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**Mapping the Microbiota in Hidradenitis
Suppurativa**

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Dedications

I would like to dedicate this thesis to my husband Donal and to my family who have encouraged me from project conception and initiation, right up to submission. Your support is greatly appreciated.

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Declarations

This is to certify that the work I am submitting is my own and has not been submitted for another degree, either at University College Cork or elsewhere. All external references and sources are clearly acknowledged and identified within the contents. I have read and understood the regulations of University College Cork concerning plagiarism and intellectual property.

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Abstract

Hidradenitis suppurativa (HS) is a chronic inflammatory skin disease characterized by the formation of nodules, abscesses, and fistula at intertriginous sites. Pain, pruritus, malodour, and suppuration have a significant impact on quality of life for HS patients. The skin-gut axis is an area of emerging research in inflammatory skin disease and is a potential contributory factor to the pathogenesis of HS. Skin microbiome alterations in HS have become an area of expanding research with its role in the pathogenesis of HS becoming clearer. Gut microbiome alterations have been described in many inflammatory diseases including inflammatory bowel disease, rheumatoid arthritis, and cancer, but little is known about the gut microbiome in HS. Our hypothesis is that gut, as well as skin, microbiota alterations and their metabolites, may be responsible for skin inflammation in HS.

The level of pain experienced by 150 patients with HS was measured using the visual analogue scale and EQ-5D-5L questionnaires. 59 patients with HS provided faecal samples, nasal and skin swabs of affected sites for analysis. These 59 patients also provided serum samples and completed questionnaires including the Dermatology Life Quality Index (DLQI), Morisky Medication Adherence Scale, International Physical Activity Questionnaire, and Food Frequency Questionnaire. 30 healthy controls provided fecal samples and 20 healthy controls provided nasal and skin swabs. We performed bacterial 16S rRNA gene amplicon sequencing on total DNA derived from the samples. Calprotectin was determined by enzyme-linked immunoassay (CALPROLAB™ Calprotectin ELISA (HRP). Complement C5a levels were assessed using enzyme-linked immunosorbent assay (Abcam ab193695 Complement C5a Human ELISA Kit).

Pain was widely reported in 134 responders to the visual analog scale questionnaire. 82.1% reported some level of pain and 35.8% reported high levels of pain. In the EQ-5D-5L questionnaire, 81.4% of responders indicated that they felt pain or discomfort, and 31.0% expressed “severe” or “extreme” pain/discomfort. Weak correlation was seen between levels of pain and one marker of gut microbiota alpha diversity (Chao1), but this failed to be repeated for all indices of microbiota species richness. A significant impact on quality of life with a mean DLQI score of 12.15 (SD 7.67) was observed in patients with HS, which is in line with other severe dermatoses. 59% of patients reported a large or extremely large impact on their quality of life. The DLQI score did not correlate with gut microbial diversity. In this study, over 40% of patients with HS also reported some difficulty remembering to take their medications with 20% reporting that they forgot to take their medication in the previous 2 weeks. Patients with HS also reported moderate-to-high levels of physical activity; however this may be overestimated. Alterations in gut microbiota diversity did not correlate with levels of physical activity. Microbiome alpha diversity was significantly lower in the faecal, skin and nasal samples of individuals with HS which may be secondary to disease biology or related to antibiotic usage. *Ruminococcus gnavus* was more abundant in the faecal microbiome of individuals with HS, which is also reported in Crohn’s disease (CD), suggesting comorbidity due to shared gut microbiota alterations. No significant difference in faecal microbiota composition or overall habitual diet was seen in the patients with HS and diet was not associated with disease severity. Diet in HS was significantly different to controls, and similar to patients with CD. *Finegoldia magna* was over-abundant in HS skin samples relative to healthy controls. It is possible local inflammation is driven by *F. magna* through promoting the formation of neutrophil extracellular

traps (NETs). 27.1% of patients with HS had a raised faecal calprotectin level of >50mg/kg with markedly elevated levels of >150mg/kg in 8.5% suggesting occult gastrointestinal inflammation. Median complement C5a level in patients with HS was elevated at 47 ng/ml (IQR 30.55 ng/ml) which is in keeping with prior studies.

These alterations in both the gut and skin microbiome in HS warrant further exploration, and therapeutic strategies including faecal microbiota transplant or bacteriotherapy could be of benefit. Faecal calprotectin is a simple test which should be considered in patients with HS, with further investigations warranted in patients with elevated levels. C5a may provide a therapeutic target in patients with HS and serum C5a may act a biomarker of the disease.

1. Introduction

1.1 Clinical Features of Hidradenitis Suppurativa (HS)

Hidradenitis suppurativa (HS), also known as Verneuil's disease and acne inversa in the past, was first described by a French Surgeon Aristide Verneuil in 1854 in his paper 'Etudes sur les tumeurs de la peau; de quelques maladies des glandes sudoripares'(1). HS is chronic debilitating inflammatory skin disorder of mainly flexural sites bearing apocrine glands, including the axilla, inframammary and anogenital regions. Typical early lesions are solitary, painful nodules that may persist for weeks to months, with a mean duration of 7 to 15 days (2). These nodules tend to be more rounded than common boils or abscesses, with which they are commonly mistaken, and they often present with initial burning, stinging, pain and pruritus (2). These nodules can fail to rupture and resolve spontaneously, 'silent nodules', or evolve into abscesses (2). Abscesses can rupture spontaneously, or after incision, with drainage of purulent material (2). Rupture can lead to a granulomatous, foreign-body like reaction. Chronic inflammation can result in chronic sinus formation with tunnelling into neighbouring skin, resulting in chronic discharge and malodour from anaerobic colonisation (2). Ulceration and pyogenic granulomas can also occur (2). Healing with hypertrophic scarring and multiporous or uniporous 'tombstone' open pseudocomedones is characteristic (2). These pseudocomedones represent superficial microfistulae. Folliculitis, or follicular pustules, can also co-occur but is not a diagnostic feature of HS (2).

Differences in topographical distribution of lesions has been described with women reporting more lesions in the anterior part of the body (axillae, breasts and genito-femoral area) and men reporting more involvement of the back of the body, atypical sites such as the ears and chest, and the presence of pilonidal sinus (3–6). An attempt

to describe three broad phenotypic groups in HS based on sites of predilection has been published in the literature: axillary-mammary, follicular and gluteal (7). In this cross-sectional study ‘axillary-mammary’ HS presented with breast and axillary lesions and hypertrophic scars (7). ‘Follicular’ HS presented with axillary, and mammary lesions as well as lesions in the ears, chest, back or legs, follicular lesions such as pilonidal sinus and comedones, severe acne, obesity, and a family history of HS (7). ‘Follicular’ HS was described most commonly in males and current smokers, with greater disease severity (7). ‘Gluteal’ HS was characterised by gluteal involvement, papules and folliculitis, and patients had less severe disease, smoked, and had lower body mass index values (7). A study of Mediterranean patients with HS which included serum biomarker analysis identified two clusters of presentation; cluster 1 which accounted for 65% of patients were male, non-obese, had early onset disease, nodular lesions of posterior sites, a history of pilonidal sinus, high levels of IL-10, and γ -secretase mutations (8). Cluster 2 which accounted for 35% of patients were either male or female, obese, with later onset HS, more sinuses and abscesses in anterior sites rather than nodules, and higher levels of IL-27 and IL-6 (8).



Figure 1: Severe Hurley stage III hidradenitis suppurativa of the buttocks. (Taken from McCarthy S, Foley CC, Dvorakova V, Quinlan C, Murphy M, Maher M. PASH syndrome with bony destruction. *Clinical and Experimental Dermatology*. 2019 Dec;44(8):918-20.)(9)

As the diagnosis of HS is made clinically, a standard disease definition is vital to accurately determine prevalence and incidence. It is agreed that three criteria must be met for hidradenitis suppurativa to be diagnosed: 1. Typical inflammatory skin lesions as described above, 2. Occurrence in one or more sites of predilection, predominantly flexural sites, in particular the axillae and groin, and 3. Chronic or recurrent bouts of inflammation (10).

Differential diagnoses of HS include common abscesses, carbuncles and furunculosis especially in those with early lesions, infected Bartholin's gland in the genital region of women, and infected or inflamed epidermoid cysts (2). Less common differentials include lymphogranuloma venereum, scrofuloderma, actinomycosis, developmental fistulae, nodular acne and pilonidal cyst, and cutaneous Crohn's disease (2).

1.2 Clinical Course, Assessment and Severity Grading of HS

HS is a chronic skin disease. Onset is typically after puberty with symptoms tending to abate in older age groups, however, there are rare reports of prepubertal and post-menopausal onset in the literature (11–14). Complete remission after menopause is usual in females, but HS in male patients may continue to be active in old age (2,5). Pre-pubertal onset should prompt endocrinological consultation and screening tests to rule out such conditions as hyperandrogenism, hyperinsulinism and precocious puberty (14). Disease onset tends to begin earlier if there is a positive family history of HS (2).

Assessment of severity is performed by clinical assessment of lesions and disease activity, and patient reported outcome measures. Imaging and biochemistry studies are rarely required, and these are not routinely used in routine clinical practice.

No ideal assessment tool for hidradenitis suppurativa exists and attempts are ongoing to develop valid and reliable severity assessments, particularly to measure outcomes in clinical trials (15).

Hurley staging is commonly used in assessing HS severity and is composed of three stages: I - Abscess formation, single, or multiple, without sinus tracts and cicatrization, II - Recurrent abscesses with tract formation and cicatrization, single or multiple, widely separated lesions, and III – Diffuse or near-diffuse involvement or

multiple interconnected tracts and abscesses across the entire area (16). Although stage I disease is the most common, most patients presenting to dermatology have Hurley stage II and III disease (10). The disadvantage of Hurley staging is that it is a static assessment which does not reflect disease activity, and does not evaluate the severity of each affected area which may differ. Despite these limitations Hurley staging remains the most commonly used clinical assessment of HS in routine clinical practice. The Refined Hurley score divides stage I and II into A, B and C based on number of areas involved and presence or absence of sinus tracts. Hurley stage I do not have sinus tracts and IA have ≤ 2 involved areas and < 5 abscesses or nodules, IB have > 2 body areas or ≥ 5 abscesses or nodules (predominantly fixed lesions) and IC: > 2 body areas or ≥ 5 abscesses or nodules (migratory lesions). Hurley II have sinus tracts and Hurley IIA have $< 1\%$ of BSA (body surface area), without abscesses or nodules, IB have $< 1\%$ of BSA, with ≤ 2 affected body areas with abscesses or nodules and IC have $< 1\%$ of BSA, with > 2 affected body areas with abscesses or nodules. Hurley III is defined as $\geq 1\%$ of BSA of the involved body site with interconnected inflammatory sinus tracts.

The Sartorius score and modified Sartorius score are more dynamic HS scores that are based on lesion counting, however they are used mainly in the setting of clinical trials (17). Lesions including nodules, abscesses, sinus tracts and scars are counted. The longest distance between two lesions in a region is measured to determine area involved and the presence or absence of normal skin between lesions is assessed. In severe disease counting of individual lesions can be difficult as lesions merge, however it is easier in milder disease with discrete lesions. As this score is time consuming, it is rarely used in routine clinical practice.

The HS-specific physician global assessment is also used to determine HS severity, but also generally only in the setting of clinical trials. Six stages of HS are described:

1 - Clear: no inflammatory or noninflammatory nodules, 2 - Minimal: only noninflammatory nodules are present, 3 - Mild: fewer than 5 inflammatory nodules without abscesses and draining fistulas, or 1 abscess or draining fistula without additional inflammatory nodules, 4 - Moderate: fewer than 5 inflammatory nodules or 1 abscess, or draining fistula and 1 or more inflammatory nodules, or 2 to 5 abscesses or draining fistulas and less than 10 inflammatory nodules, 5- Severe: 2 to 5 abscesses or draining fistulas and 10 or more inflammatory nodules, 6 - Very severe: more than 5 abscesses or draining fistulas (18).

Newer HS scoring systems include the hidradenitis suppurativa severity index (HSSI), and the hidradenitis suppurativa clinical response (HiSCR), which have been used in clinical trials, and the international hidradenitis suppurativa severity score system (IHS 4) and the hidradenitis suppurativa area and severity index (HASI) which have recently been developed in the hope of developing a more reliable and valid assessment tool (19–22).

A summary of the HS scoring systems is outlined in Table 1.

Table 1: Summary of the common HS scoring systems used in setting of clinical practice and clinical trials

Assessment tool	Components of HS scoring system						
Hidradenitis Suppurativa Severity Index (HSSI)	Composite score range 0-19		No. of sites	Body surface area	No. of inflammatory lesions	No. of dressing changes in working hours	Pain (visual analog scale)
		Stage 0	0	0	0	0	0-1
		Stage 1	1	1	1-2	0	0-1
		Stage 2	2	2-3	2-3	1	2-4
		Stage 3	3	4-5	4-5	>1	5-7
		Stage 4	≥4	>5	>5	>1	8-10
Hurley Score	I	Single or multiple abscesses					
	II	Recurrent abscesses, sinus tract formation and scarring. Single or multiple lesions, widely separated					
	III	Diffuse involvement of entire area, multiple interconnected tracts and abscesses					
Refined Hurley Score	Absence of sinus tracts	Hurley I A: ≤2 involved areas and <5 abscesses or nodules B: >2 body areas or ≥5 abscesses or nodules – predominantly fixed lesions C: >2 body areas or ≥5 abscesses or nodules – migratory lesions					
	Presence of sinus tracts	Hurley II A: <1% of BSA, without abscesses or nodules B: <1% of BSA, with ≤2 affected body areas with abscesses or nodules C: <1% of BSA, with >2 affected body areas with abscesses or nodules					

		Hurley III: $\geq 1\%$ of BSA of the involved body site with interconnected inflammatory sinus tracts
Sartorius Score		Assessing anatomical regions involved, distance between lesions, and scoring individual lesions.
Modified Sartorius Score	Anatomic regions affected	3 points per region affected: axilla, groin, gluteal, other
	No. and type of lesions (per region)	1 point for nodule 6 points for fistula
	Longest distance between 2 lesions	1 point $< 5\text{cm}$ 3 points 5-10cm 9 points $> 10\text{cm}$
	Lesions clearly separated by normal skin	0 points if yes 9 points if no
HS-Physicians Global Assessment (HS-PGA)	Clear: 0	
	Minimal: 1	Presence of non-inflammatory nodules
	Mild: 2	< 5 inflammatory nodules or 1 abscess/fistula
	Moderate: 3	≥ 5 inflammatory nodules 1 abscess or draining fistula and ≥ 1 inflammatory nodule 2-5 abscesses or draining fistulas and < 10 inflammatory nodules

	Severe: 4	2-5 abscesses or draining fistulas and ≥ 10 inflammatory nodules
	Very severe: 5	>5 abscesses or draining fistulas
HS Clinical Response (HiSCR)		Achieving at least a 50% reduction from baseline in abscess and inflammatory nodule count with no increase in abscess/fistula counts
Hidradenitis Suppurativa Area and Severity Index (HASI)	HASI score 0-72	Modelled after the Psoriasis Activity and Severity Index (PASI) Erythema, thickness, drainage, and tenderness scored 0-3 for each body site involved, percentage body surface area (BSA) affected calculated for each body region using PASI approach (0 = none, 1 = 1–9%, 2 = 10–29%, 3 = 30–49%, 4 = 50–69%, 5 = 70–89%, 6 = 90–100%) The sum of the four clinical variable scores was multiplied by the area score of each involved region This value was then multiplied by the proportion of the BSA of that region, to give a regional HASI score Regional HASI scores were added together to give the cumulative total HASI score (range 0–72)
IHS4	Points =	(number of nodules x 1) +(number of abscesses x 2) _ (number of draining tunnels/fistulae/sinuses x 4)
	Mild	≤ 3 points
	Moderate	4-10 points
	Severe	≥ 11 points

Patient reported outcome measures can be useful in assessing disease severity in HS and its impact on quality of life. The dermatology life quality index (DLQI), EQ-5D-5L, and the Skindex-16 can be used to assess morbidity and impact on quality of life (23). Regular measurements over time are important to assess for impact of disease over time, disease activity and response to treatment. Visual analogue scales of pain and itch are also helpful in assessing patient symptoms (24).

Assessment of depression and anxiety is important in HS to ensure a holistic approach. Commonly used psychometric scales include the Beck depression inventory (BDI), patient health questionnaire-9 (PHQ9) and hospital anxiety and depression scale (HADS) (25). Furthermore, the HIDRADisk, a short visual quality of life tool has been formulated to assess burden of HS on quality of life and shows strong correlation with Skindex-16 and DLQI (26).

Imaging is not routinely used in HS; however, several studies have reported the utility of ultrasound in determining extent of disease. Similarly, MRI has also been used to delineate the extent of disease, particularly prior to extensive surgery (27). Simple clinical photography can be useful in determining response to treatment and may be an easy adjunct in most clinical settings (28).

Biochemistry studies in HS are of limited use, but raised inflammatory markers such as C-reactive protein, and a raised leucocyte count may be detected (10). Generally, biochemistry studies in HS are used to monitor systemic treatment prescribed and in the assessment of the co-morbidities that are associated with HS (10).

1.3 Epidemiology of HS

Determination of HS prevalence and incidence is challenging as it is often under-recognised and a diagnostic delay is common (29). Prevalence figures vary greatly in the literature from 0.05% to 4.1% probably due to differing data sources used, and the varying levels of HS recognition between countries (30–32). Prevalence of HS in the USA is reported at 0.1% (33). Prevalence of up to 4.1% is reported in European populations with a prevalence of 1.4% in one Irish study (32,34). Although reported US prevalence is lower than European prevalence, this is likely due to the data sources used to estimate prevalence (30). Prevalence in African Americans is three times higher than in white individuals and thus higher prevalence in Europe is unlikely due to ethnicity and genetic differences (30,33). Information on prevalence in Asian populations is lacking with one study reporting a prevalence of 0.06% in the South Korean population (35). Reports from the rest of the world include a report of prevalence of 0.67% in Australia and 0.8% in Ghana (36,37).

Incidence of HS appears to be increasing, possibly due to increasing recognition of the condition (30). Annual incidence of 11.4 in the US and 28.3 in the UK per 100,000 population is reported (38,39).

Women are more commonly affected than men (32,40). In Europe and North America, HS has a female-to-male ratio of 3:1 (13,30,33,35,38). However, interestingly, in South Korean patients the ratio is 1:1.6 presenting more commonly in males (35). In Asian populations the buttocks are most frequently affected, whereas in Europe and the US it is the groin and axillae most affected (2,35,41,42). An association with lower socioeconomic status has also been reported. This may relate to the higher prevalence of risk factors for developing HS in this group, or could be a consequence of the illness itself (50).

1.4 Histology of HS lesions

Perilesional skin demonstrates psoriasiform hyperplasia with an increased number of CD3+ T-cells and CD138+ plasma cells, dendritic cells and mast cells observed (44).

In early HS lesions, follicular occlusion with dilatation driven by endogenous and exogenous factors discussed below, is seen (45). On histology follicular hyperkeratosis is seen with plugging and dilatation of the hair follicle (44).

Occlusion of the hair follicle is also thought to lead to dysregulation of keratinocytes and the microbiome of the skin (45).

Follicular occlusion is followed by rupture of follicular contents into the dermis which triggers an immune response (45). Histologically a dense cell infiltrate is seen, consisting of monocytes, neutrophils, multinucleated giant cells, B-cells, plasma cells, T-cells and natural killer (NK) cells leading to abscess formation (45). Keratin fibres and keratinocyte debris are seen, with multinucleated giant cells often contain keratin fibres (44). CD11c+ dendritic cells are abundant, as well as CD14+ monocytes, CD68+ macrophages and FXIIIa+ dermal dendritic cells (44).

Granuloma formation has also been described (44).

Chronic lesions are characterised by expansion of the inflammatory infiltrate, with more pronounced neutrophilic inflammation (44). Chronic inflammation leads to formation of epithelialised fistula and sinus tracts, and scarring due to dysregulated matrix metalloproteinases (MMPs), tissue inhibitors of metalloproteinase (TIMPs), and increased tissue growth factor (TGF)- β 1-2-3 which causes fibrosis (45–47).

Furthermore, sinus tracts provide an ideal site for bacterial biofilm formation with subsequent maintenance of the inflammatory loop (48). Apocrinitis is not seen in all cases, confirming that apocrine involvement is a secondary phenomenon (49–53).

1.5 Aetiology of HS

Understanding the aetiology and pathogenesis of disease is of paramount importance in informing therapeutic options. Current therapies in HS are limited and treatment of severe cases can prove challenging (54). The current understanding of the aetiology and pathogenesis of HS is incomplete, with numerous hypotheses concerning the interplay of lifestyle factors, the skin microbiota, genetics, and a dysregulated immune system postulated (55).

1.5.1 Lifestyle Factors

Two widely accepted lifestyle factors which play a role in the development of HS are obesity and tobacco smoking, and higher smoking pack-year history and higher body mass index (BMI) are linked to increased disease severity (5,11,35,39,51–54). In one study assessing clinical course and prognosis in HS, it was noted non-smokers were more likely to report remission than active smokers, and similarly more non-obese patients reported remission compared to obese patients (60).

Obesity is reported in approximately 60% of patients with HS, particularly central obesity (43). An odds ratio of 3.45 (95% CI 2.20-5.38, $P < 0.001$) for HS and obesity has been reported (59). Obesity appears to predispose patients to the development of HS in a number of ways. Firstly, it enlarges the skinfolds of the body providing sites of repeated mechanical stress and friction, maceration, and anaerobic bacterial colonisation (44,45). Mechanical stress and friction are thought to contribute to the development of HS by promoting follicular occlusion and rupture in a susceptible individual (44). Mechanical stress may provoke the release of damage-associated molecules (DAMPs) and allow for entry of microbes promoting inflammation (55).

Skin-to-skin contact leads to a higher skin temperature, and humidity from sweat retention in large skin folds, with reduced oxygen availability promoting anaerobic bacterial growth and maceration (44). Obesity also creates a subclinical proinflammatory state, producing proinflammatory cytokines and dysregulated adipokines which promote the development of inflammatory disorders, including skin disease (46–50). IL-1 β and TNF- α are secreted by macrophages in visceral fat and upregulation of IL-6 and TNF- α gene expression is seen (69,70). Circulating palmitate levels are also increased in obesity and interact with toll like receptors (TLRs) to activate the innate immune system and result in inflammation (71). Furthermore, obesity increases the risk of developing metabolic syndrome and insulin-resistance, which have also been associated with HS, and contribute to the proinflammatory state (51). Weight reduction has a proven beneficial effect on morbidity and prognosis in HS and response to treatment. Obesity is associated in the literature with abnormal gut microbiota, and attempts are being made to modulate the gut microbiota for treating obesity (72).

Cigarette smoking is a common association in HS and has been attributed to the development and severity of disease (13,42,73,74). Reports of current or former cigarette smoking in HS ranges between 30% to 98% (75). A systematic review calculated an odds ratio (OR) of 4.34 (95% confidence interval (CI) 2.48-7.60, $P < 0.001$) for HS and current smoking (59). Tobacco is composed of thousands of chemicals including nicotine, and polyaromatic hydrocarbons (76). It is thought that nicotine in cigarettes may activate keratinocytes via nicotinic acetylcholine receptors and induce acanthosis, and epidermal hyperplasia (77,78). Smoking also creates an altered skin microbiome, with increased virulence of *Staphylococcus aureus* through enhanced cellular adhesion and biofilm formation (79,80). Nicotine also reduces

anti-microbial peptides, such as human-beta-defensin-2 (h β D-2) increasing susceptibility to bacteria (81,82). Smoking is proinflammatory, and has been seen to increase intracellular cAMP levels and increase IL-1 α , IL-1 β , IL-8, IL-10, IL-17 and TNF- α resulting in neutrophil chemotaxis and TH17 cell inflammatory responses (62,83,84). Altered chemotaxis of neutrophils has also been postulated in palmoplantar pustulosis to explain the predilection in smokers (85). Acquired downregulation of Notch signalling has also been reported in smokers, and this pathway plays a role in development of HS (86). Furthermore, smoking reduces blood circulation resulting in impaired wound healing from reduced tissue oxygenation, and this potentially results in poor healing of lesions in HS (87). Smoking is also associated with an altered skin and gut microbiota in the literature (88,89).

1.5.2 Hormonal Influence

HS demonstrates a female predominance, presents after puberty, and patients often report premenstrual flares when progesterone levels are high (90). Reports of improvement in HS during pregnancy or after menopause further supports the role of hormones in HS pathogenesis (90). However, one study surveying 85 women with HS reported the majority had no effect of pregnancy on their HS (72%) with 20% reporting an improvement and 8% a deterioration (60). In this study menopause was associated with an improvement in HS for the majority (48%), no difference in 38% and worsening in 15% in 61 women surveyed (60). Basal levels of major sex hormones such as oestrogen, progesterone, testosterone and dehydroepiandrosterone sulphate also do not appear to be altered compared to controls (91). However, response to anti-androgen therapy in HS has been reported (92).

1.5.3 Genetic Predisposition

A family history of HS is reported in approximately 40% of cases (93). Familial HS tends towards more severe disease and lower remission rates, implying the importance of genetic factors. Interestingly patients with no family history of HS tend to be more overweight and smoke more, suggesting different subpopulations exist in HS (7).

Early Genetic Studies

Fitzsimmons et al. provided an initial report on 3 families with 21 members affected by HS, with all three generations of one family affected (94). This report was followed by a study on HS in 23 families with 62 members affected; 3 generations affected in 5 families and 2 generations affected in 6 families (95). This prompted discussion as to whether an autosomal dominant pattern of inheritance was present in HS, despite only 34% of first-degree relatives being affected, compared to 50% in confirmed autosomal dominant conditions (95). It was postulated that incomplete penetrance or missed cases resulted in the lower familial cases (95).

Defects in Notch and γ -secretase pathways

Gao et al. assessed families exhibiting autosomal dominant inheritance of HS in a large Han Chinese family with a genome wide scan (96). Linkage to chromosome 1 was demonstrated in affected members of this family with HS (1p21.1-1q25.3) (96). This linkage was not demonstrated in a further familial HS study by Saleh Al-Ali et al. in 2010 (97).

Wang et al. first identified a mutation in the PSENEN gene in affected members of 2 families demonstrating autosomal dominant inheritance (98). This was not present in

unaffected members of the family or in a control population (98). PSENEN encodes a subunit of γ -secretase protein. In four other families, mutations in NCSTN or PSEN1 genes were seen that encode other γ -secretase subunits (98). The NCSTN gene is located at 1q22-23, which is within the region identified by the early study by Gao et al (96,98). γ -secretase is a protease that targets type-1 transmembrane proteins such as Notch, E-cadherin, or CD44 (99).

Notch signaling in particular plays a role in hair follicle development, in modulating T-cell-mediated immune responses and in suppressing Toll-like receptor-4 induced cytokine responses (98–100). Mutations in PSEN1 and PSEN2, which also encode γ -secretase subunits, have been identified in familial Alzheimer disease, with accumulation of β -amyloid peptides due to abnormal cleavage of amyloid precursor protein, a type-1 transmembrane protein (101). A link between HS and Alzheimer disease has not been found to date. In mouse models, deficiency of γ -secretase results in the development of epidermal cysts from hair follicles and an absence of sebaceous glands, mediated via the Notch signaling pathway (102). Reduced sebaceous gland number and volume are seen in HS (103). Deficiency of Nicastrin, a protein in the γ -secretase protein complex, has been shown to cause follicular and cystic hyperkeratosis (104). Further studies, however, demonstrated that γ -secretase mutations appear to represent only a minority of cases of HS, even in those with a family history (105,106). It has also been demonstrated that mutations in γ -secretase can be present in unaffected family members suggesting incomplete penetrance, and epigenetics, such as the impact of smoking, may be important in the development of HS these cases (107). Furthermore, it appears that those with γ -secretase mutations tend towards more severe disease, an atypical phenotype, and prove refractory to treatment (106).

Mutations in Proline-Serine-Threonine Phosphatase Interacting Protein 1

Proline-serine-threonine phosphatase interacting protein 1 (PSTPIP1) mutations have been identified in syndromic cases of HS. Genetics of HS with defects in inflammasome function in the setting of inflammatory syndromes will be discussed in associated conditions.

Twin studies

Twin studies give important information on the contribution of genetics and environment to the development of disease (108). One early study on the genetics of HS included a pair of female monozygotic twins who developed HS in their 20s (94). A recent Dutch study reported a prevalence of HS among twin pairs of 1.2%, with a mean age of 32.7 years (108). The calculated heritability of HS was 77% (95% CI 54-90%) suggesting a strong contribution of genetic factors in the development of HS, and was higher than in psoriasis and rheumatoid arthritis (108). Interestingly the heritability of HS was similar to Crohn's disease (108). The variance seen in this study also supports a multifactorial cause, with environmental factors contributing (108).

Other genes associated with HS

Sphingolipids are membrane lipids involved in growth regulation, cell migration, adhesion, apoptosis, senescence, and inflammatory responses in tissues (109).

Aberrant expression of the genes Ceramide synthase-2 (CerS2) and Sphingosine kinase-2 (SPHK2), involved in sphingolipid synthesis, are significantly downregulated in HS when compared with unaffected skin resulting in decreased levels of ceramide generating enzymes (110). Furthermore, galactosylceramides and

gangliosides, products of the sphingolipid pathway, are elevated in lesions of HS (110). Galactosylceramide activates natural killer cells and promotes inflammation (110).

In one study a single nucleotide polymorphism of the *IL-12Rb1* gene coding for the IL-12Rb1 receptor subunit did not genetically predispose to HS, however, this polymorphism was associated with later disease presentation in the h1 haplotype and higher risk of severe disease in the h2 haplotype, suggesting the IL-12/IL-23 pathway may be important in the pathogenesis of HS (111).

The copy number of the β -defensin gene cluster (DEFB) was found to increase risk of developing HS and determine disease phenotype in one case control study (112). HS lesions have also demonstrated higher lipocalin 2 (LCN2) mRNA expression levels compared to healthy controls and this may serve as a blood biomarker to assess activity of disease (113).

Genome Wide Association Studies

A paucity of genome wide association studies (GWAS) exists in HS. A single GWAS in HS has been undertaken in patients enrolled in two phase 3 hidradenitis suppurativa trials (PIONEER I and II) and who were responders to adalimumab (114). An intron of the BCL2 gene was discovered which reached genome-wide significance suggests that BCL2 may be repressed in HS affected tissues by adalimumab (114). A GWAS to elucidate the genetic aetiology of HS is currently being undertaken by the National Institute of Health in the United States utilising the Genetic Epidemiology Research in Adult Health and Aging (GERA) cohort and Partners Healthcare Biobank cohort and is due for completion in 2022 (115).

1.5.4 Follicular Occlusion

HS was once believed to be a disease of the apocrine gland. However, it is now known that it is primarily a disease of the hair follicle (116). The primary event in HS is follicular occlusion with infundibular hyperkeratosis of the follicle and hyperplasia of the follicular epithelium lead to collection of cellular debris, dilation of the hair follicle, rupture, an inflammatory response, abscess and sinus tract formation and scarring (117). Apocrine glands can be inflamed secondary to dermal inflammation however apocrine gland morphology, density and distribution is similar to healthy controls (117,118). A reduction in sebaceous gland volume is seen (103). Thinning of the basement membrane zone around the sebofollicular junction in HS skin has been observed and this may predispose to the rupture of follicular contents into the dermis causing inflammation (119). This is a primary phenomenon which is not caused by prior inflammation (119). Mechanical trauma, as discussed in association with obesity, contributes to follicular disruption in these weakened pilosebaceous units (119).

1.5.5 Immunopathogenesis of HS

HS was largely thought to be an infectious disease until the 1980s when early studies suggested the role of immune dysfunction, in particular the role of T-lymphocytes, in its pathogenesis (120,121). In the early 2000s, host-defence defects in HS and possible response to immunosuppression were reported in the literature (122,123). Lapins et al. noted dysfunctional neutrophils in patients with HS compared to controls (122). Links between HS and inflammatory bowel disease had been made and Martinez et al noted improvement in HS in a patient who was treated with

infliximab for Crohn's disease (123,124). Since this time it has become widely accepted that HS is an autoinflammatory disorder with alterations in the immune system (45). In the primary lesion the release of follicular contents into the dermis activates several inflammatory pathways, in particular the Th17/IL-23, NOD-like receptor protein 3 (NLRP3) and innate toll-like receptors (TLR), creating skin inflammation and an inflammatory loop (45). Resulting influx of dysregulated immune cells and the production of keratinocyte-mediated products is key to the development and maintenance of inflammation in HS (125,126).

Alterations of the innate immune system are noted in HS (127). Antimicrobial peptides (AMPs) are produced as part of the body's response to pathogens and play a role in the modulation of inflammatory responses, wound healing, and skin barrier homeostasis (128,129). Examples include the human β -defensins (h β D)1- 3, cathelicidin LL-37, ribonuclease 7, psoriasin (S100A7), calgranulin-A (S100A8), calgranulin-B (S100A9), koebnerisin (S100A15 or S100A7A), and dermcidin. The role of AMPs in HS is under investigation, with mixed results in the literature. Wolk et al. confirmed an upregulation of the AMPs h β D 2 and 3, S100A7, S100A8 and S100A9 compared to controls suggesting a role of AMPs in HS development (130). However the levels of AMPs were not as high as in psoriasis and atopic dermatitis, in particular for h β D 2 and 3 (130). Hofmann et al. noted reduced levels of h β D3 in severe HS and reduced ribonuclease 7 (131). However, a further study demonstrated elevated levels of ribonuclease 7, S100A7 and S100A8 compared to controls (132). Cathelicidin LL-37 is also elevated in HS compared to controls and correlates with the presence of inflammatory cells and cytokines (133,134). Dermcidin was downregulated in HS compared to controls in two further studies (135,136).

Lipocalin 2 (LCN2) is also increased in serum and affected skin of patients with HS as previously discussed (113).

The role of the complement cascade is another area of research in HS and recent studies have noted several complement abnormalities in HS (137). The complement system plays an important role in the innate immune system, defending against pathogens. There are three pathways in the complement cascade: the classical, lectin and alternative pathways which all converge to generate C3 convertase, which in turn generates C5 convertase, which generates C5a and C5b-9 production (137). Complement facilitates removal of pathogens through opsonization and lysis, and it also plays a role in the adaptive immune system through B and T-cell activation (137). The role of complement activation in the pathogenesis of HS is unclear and may be as a consequence of the disease (137). Elevated levels of C5a and C5b-9 are found in HS (138,139). It is thought that an altered microbiome in HS may activate C3a and C5a pathways which may result in NLRP3 inflammasome activation (nucleotide-binding oligomerization domain (NOD)-, leucine-rich repeat (LRR)-, and pyrin domain (PYD)-containing protein 3) (140). In the study by Kanni et al., which demonstrated elevated levels of C5a and C5b-9 in HS, a C5a inhibitor IFX-1 reduced TNF- α levels produced by peripheral blood mononuclear cells (PBMCs) taken from HS affected patients (138). This suggests the role of C5a in promoting cytokine production by monocytes. Furthermore, a study on IFX-1 demonstrated a significant reduction in neutrophil and serum calprotectin levels (139).

Studies determining the levels of cytokines in serum and skin, both affected and non-affected, have led to a greater understanding of HS pathogenesis. Elevated cytokines have been noted in the affected and unaffected skin, serum, and exudate of HS patients (125,126). Cytokines can contribute to follicular occlusion in the primary

lesions by contributing to hyperkeratinisation and hyperplasia of the follicular infundibulum (53). Furthermore, it is thought circulating cytokines and chemokines can prompt development of HS in distant predilection sites (45). A number of cytokines have been found to be elevated in HS.

Both IL-1 α and IL-1 β levels are elevated in HS (126,141). High IL-1 β levels result in production of neutrophil-attracting chemokines (chemokine ligand-1 (CXCL1), CXCL6 and CXCL8) and matrix metalloproteins (MMP1, MMP3, MMP10) resulting in neutrophil chemotaxis and subsequent inflammation (55). IL-

36 α , β and γ , members of the IL-1 cytokine family, are also elevated in HS, particularly in established or chronic lesions (142). IL-36 cytokines play an important role in the modulation of T-helper (Th)1 and Th17 responses (142).

Tumour necrosis factor- α (TNF- α) plays an important role in the pathogenesis of HS, as evidenced by the efficacy of TNF- α inhibitors in the disease (18,21,143,144). Elevated TNF- α has been reported in HS and correlate with severity (126,141). TNF- α recruits and activates neutrophils and lymphocytes and promotes the production of other inflammatory cytokines (145). Moran et al. observed T-cells with a Th17 skewed cytokine profile (expressing IL-17, as well as CM-CSF, IL-22, IFN- γ and TNF- α) and elevated regulatory T-cells (Treg) in lesional skin, which normalized on the introduction of a TNF- α inhibitor. This suggests that IL-17 inhibition via TNF blockade leads to clinical improvement (146). In another study Th17 inflammatory serum markers (IL-1 β , IL-6, IL-8, IL-10, IL-17A, and TNF- α), CRP and ESR were reduced significantly after 36 weeks of adalimumab, a TNF- α inhibitor (147). Mechanistic target of rapamycin complex 1 (mTORC1) pathway is upregulated in HS lesions, and this also responds to TNF- α inhibition (148).

Interferon (IFN)- γ , a cytokine predominantly secreted by natural killer (NK) cells, CD4⁺ Th1 cells, and CD8 cytotoxic cells, are also elevated in HS and appear to be a dominant response by keratinocytes in HS (149,150). IFN- γ activates macrophages and plays a synergistic role with TNF- α in mediating immune response (151).

IL-10 is highly expressed in HS lesions, both lesional and perilesional, compared to healthy control skin (126). IL-10 is an anti-inflammatory cytokine; however, it exerts a negative effect on IL-22 expression, an important stimulator of keratinocyte antimicrobial peptide (AMP) expression (152). These decreased levels of IL-22 are postulated to contribute to HS pathogenesis (152).

The IL-12/23 pathway is also thought to be important in the pathogenesis of HS. IL-23 is necessary for development of Th17 cells to produce IL-17. IL12/Th1 and IL-23/Th17 pathways are upregulated in HS (153). Clinical improvements noted by patients with HS treated with the IL-12/23 inhibitor ustekinumab further support the role of IL-12 and IL-23 in HS (154).

IL-17, mainly produced by Th17 cells and neutrophils, is significantly elevated in HS (141,155,156). IL-17 exerts a pro-inflammatory effect on the skin, promoting influx of monocytes, neutrophil, Th17 cells and myeloid cells, and feeding an inflammatory loop resulting in increased IL-17 production and further inflammatory cell infiltration (141). The role of Th17/IL-17 in HS is further supported by the fact the levels decrease after effective treatment of HS, including the use of IL-17 inhibitors (156,157).

Elevated levels of IL-36 α , β and γ is also reported in lesions of HS and is known to induce neutrophil-attracting chemokines, cytokines, and AMPs (55).

1.5.6 Role of the Microbiota in HS

The role of the skin microbiota in the development of HS is an area of expanding research. However, its role in the development of HS is controversial (158). A number of studies reported that the microbiome of HS lesional and non-lesional skin differs from healthy controls, and support its role in disease pathogenesis (159). Nevertheless, HS does not appear to be a primarily infectious disease, evidenced by the failure in most cases to develop infectious complications such as cellulitis, lymphadenopathy and systemic symptoms (160). The response to immunosuppression also suggests that the role of the microbiota is not the primary cause in HS but rather a contributing factor (161). Furthermore, it is unknown if antibiotics are effective in HS due to their anti-bacterial or anti-inflammatory properties (162). It is thought that antibiotics may attenuate the inflammatory response in HS by removing bacteria from ruptured follicles which are thought to trigger an immune response (163). Detailed discussion of the altered microbiome in HS will be provided later in this chapter.

1.5.7 Diet and HS

The gut-skin axis is an expanding area of research, and several skin conditions including HS, have gut comorbidities (164–166). An abnormal gut microbiota, or dysbiosis, has been linked to the development of skin disease (166). Diet has a significant impact on the gut microbiota composition (166,167). Study on the role of dietary factors in the development of HS is lacking (168). It has been suggested that a dairy-free diet and avoidance of high glycaemic load foods can result in improvement in HS (168,169). It is postulated that dairy products and high

glycaemic foods can act through hormonal mechanisms by triggering androgen-driven obstruction of follicles (169). Other studies suggested avoiding nightshades (Solanaceae) and foods and drinks containing brewer's yeast such as bread and beer (168). One study reported lesser severity of HS in those who follow a Mediterranean diet (170). These studies, however, provide little commentary on the effect of diet on the microbiota as a potential aetiological factor. More detailed discussion of the gut-skin axis in HS will be provided later in this chapter.

1.5.8 Drug-induced HS

HS is rarely associated with medications, however it has been reported to flare with lithium therapy and reports of 'de novo' HS with sirolimus therapy are present in the literature (2,171,172). Further reports implicated ciclosporin, vemurafenib, adalimumab, etanercept, infliximab, secukinumab, ustekinumab, tocilizumab, rituximab, and the oral contraceptive pill therapy in the development of HS, however, a systematic review found the evidence for drug-induced HS low (173,174).

1.6 HS, Associations, and Disease Complications

1.6.1 HS and Autoinflammatory Syndromes

Autoinflammatory diseases are a heterogeneous group of systemic disorders characterised by exaggerated innate immune system response with abnormal interleukin (IL)-1 signalling (175). The four recognised autoinflammatory syndromes presenting with HS as part of the spectrum of disease are PASH (Pyoderma gangrenosum, acne, and hidradenitis suppurativa), PAPASH (Pyogenic arthritis, pyoderma gangrenosum, acne, and hidradenitis suppurativa), PsAPASH (Psoriatic arthritis, pyoderma gangrenosum, acne, hidradenitis suppurativa) and PASS (Pyoderma gangrenosum, acne, and ankylosing spondylitis, with or without hidradenitis suppurativa) and have been associated with mutations related to the inflammasome, which regulates innate immunity. Diagnosis of syndromic HS is often made on clinical features, which may be atypical, severe, and resistant to treatment, and the presence of systemic inflammation. Mutations in the gene encoding PSTPIP1 (proline-serine-threonine phosphatase-interacting protein 1), which interacts with pyrin, have been found in the autosomal dominantly inherited PAPA syndrome which presents with pyogenic arthritis, acne and pyoderma gangrenosum (176). The genetic basis of PASH, and PAPASH is less understood and appears to be heterogeneous, with mutations in several genes including PSTPIP1, MEFV (Mediterranean fever), NOD (Nucleotide binding oligomerization domain containing)-2, NCSTN (Nicastrin), and NOD-like receptor protein (NLRP)-3 described (177–181). The genetic basis of PsAPASH and PASS has not been described (182–184).

An association between Familial Mediterranean Fever (FMF) and HS has been described in the literature. FMF is an autosomal recessive condition characterised by recurrent attacks of fever, peritonitis, arthritis and amyloidosis and may result in end-stage renal disease (185). The MEFV gene is mutated in FMF which encodes pyrin. Several case series report a link between FMF and HS, with an increased prevalence of 0.7% in patients with HS vs. 0.1% in controls (43–45). An association has also been seen with SAPHO syndrome (Synovitis, acne, pustulosis, hyperostosis and osteitis) (187,188). The genetics of SAPHO is still unknown, however one case report demonstrated a mutation in NCSTN in a patient with concurrent HS (189).

HS can be challenging to treat and syndromic HS, which often presents with more severe disease, can prove very resistant to standard treatment. Although standard HS treatment, such as the TNF- α inhibitors, are reported to be effective, consideration for targeting IL-1 such as Anakinra and Canakinumab should be made if patients fail first line therapies (190–192). Due to the chronicity and severity of syndromic HS, combination therapy with biologics, immunomodulating agents such as dapsone, and surgery is often required (190).

Of note, an abnormal gut microbiota has been suggested in small studies on FMF and SAPHO, with no studies exploring the microbiota in the autoinflammatory conditions in which HS forms part of the spectrum (193,194).

1.6.2 HS and Follicular Occlusion Syndrome

Follicular occlusion syndrome is an umbrella term that includes the conditions acne, HS, pilonidal sinus and dissecting cellulitis of the scalp.

A strong association is seen between HS and acne vulgaris, independent of the auto-inflammatory syndromes discussed above (38). As discussed previously, hyperkeratinisation and hyperplasia of the terminal part of the hair follicle is seen in early lesions in HS, leading to occlusion, dilatation, and rupture of the hair follicle triggering an inflammatory response (195). Similar features are seen in acne vulgaris (196). Toll-like receptor (TLR)-2 is raised in HS and acne triggering inflammation (197,198). Elevated interleukin 1 β is also seen in both conditions, driving neutrophilia and type 17 helper (Th17) T-cell response (163). Prevalence of acne vulgaris in patients with HS has been reported as 15.2% in a large cross-sectional study with a prevalence of only 2.9% in those without HS ($p < 0.001$) (199). Prevalence was greatest in females, those aged 18 to 44, non-white, obese, and in those who had polycystic ovarian syndrome (199). Acne conglobata, presenting with severe nodulocystic acne with extensive scarring, is also strongly associated with HS, with a prevalence of 4.5% (OR 5.07, 95% CI 4.69-5.49) seen in Korean patients (35,200). Acne treatments have some success in HS including the use of antibiotics and retinoids, however their efficacy is less than in acne vulgaris with mixed benefit in particular with isotretinoin (163).

An altered skin microbiome is well described in acne with an abundance of *Cutibacterium* (previously known as *Propionibacterium*) *acnes* found in the acne-prone sebum rich areas of skin (201). Other bacteria and fungi may also play a role in development of acne including *Staphylococcus epidermidis*, *Cutibacterium granulosum*, *Proteobacteria* and *Firmicutes*, and *Malassezia species* (201). The use of antibiotics in acne suppresses *C. acnes*, with an increase seen in alpha diversity or bacterial species richness, and also has an anti-inflammatory effect (201–203). An altered gut microbiome has also been described in acne, with lower gut microbiota

diversity and a higher ratio of Bacteroidetes to Firmicutes, and lower levels of beneficial bacteria *Lactobacillus* and *Bifidobacterium* (204,205). Clinical trials have demonstrated some beneficial effects of modulating the skin and gut microbiota in acne via the use of probiotics (helpful bacteria) but further study is required (201,206,207).

Pilonidal sinus (PS) is an abscess of the sacrococcygeal region which can present acutely, when inflamed and under tension, with severe pain and suppuration (208). It is more common in men, and presents usually between the ages of 25 to 30, and similar to HS rarely presents before puberty or in old age (209). Treatment in symptomatic cases is surgical, to remove the fistulating abscess, with healing by primary or secondary intention (208). PS has been associated with HS with five-fold higher odds of developing the condition in HS compared to controls (28,31,49). Similar risk factors for development are seen in both conditions including friction, increased BMI, and a positive family history (209). Anaerobic bacteria, dominate in skin samples taken from pilonidal sinus, similar to HS (211). It is thought PS may represent part of the disease spectrum in HS.

Dissecting cellulitis (DC), also known as ‘folliculitis et perifolliculitis capitis abscedens et suffoidens’, presents with perifolliculitis (inflammatory cells in skin around hair follicles), dermal abscesses, and sinus tract formation in the scalp resulting in a secondary scarring alopecia (212). An overlap of clinical features is seen with HS and the association of DC, HS, and acne conglobata is known as the follicular occlusion triad, or tetrad if pilonidal sinus is also present (212). DC presents more often in men, African-Americans and in those who are overweight or obese (212,213). Similar to HS, DC is often made worse by smoking, and hair

shaving can be a trigger (212). DC has also been associated with Crohn's disease, pyoderma gangrenosum, axial arthropathy, and SAPHO syndrome discussed previously (213–216). Again similarities between DC and HS have led some to conclude they are different localisations of the same disease (212). *Staphylococcus aureus* is the predominant bacterium found on swabs of DC, and bacterial biofilm formation, similar to the process in HS, has been described (217). Treatment of DC includes retinoids, antibiotics, steroids, and dapsone.(212). Based on its similarity to HS, biologic therapy with anti-TNF α has been trialled with reports of some success in the literature (218).

1.6.3 HS and Inflammatory Bowel Disease

Inflammatory bowel disease (IBD) is a chronic relapsing inflammatory disease of the gastrointestinal tract and includes the diagnoses of Crohn's disease (CD) and ulcerative colitis (UC). HS and inflammatory bowel disease, in particular CD, share clinical and pathogenic similarities, and an association has been proven (219,220). A prevalence of Crohn's disease of 2% in patients with HS has been reported in the USA, compared with 0.6% in controls, and a higher prevalence of 2.5% in European patients with HS (221,222). In Korean patients an association between HS and Crohn's disease was not found, but an association with UC was present (35). Meta-analysis data demonstrates a 2.12-fold increased odds for developing CD and 1.51-fold increased odds for developing UC, with one cohort demonstrating a 5.6-fold increased risk of IBD, in patients with HS (219).

Both CD and HS present with sterile abscesses, scarring, and sinus tract formation (219). Perianal HS and perianal CD are clinically similar with inflammatory fistulae

and suppuration and HS is likely to be misdiagnosed as cutaneous CD, although true cutaneous CD is very rare (220). Histology is often not helpful in distinguishing between HS and CD with granuloma formation and lymphoid follicles seen in both (220). Both HS and IBD are associated with spondyloarthropathy, smoking, and obesity, and both respond to TNF- α inhibitors (74,223–229).

HS and IBD also share genetic susceptibility with the genes *SULT1B1* and *SULT1E1* associated with both (220). HS and IBD also have an immunopathogenic link with an aberrant immune response playing a central role in both diseases.

Elevated levels of cytokines such as IL-1, IL-6, IL-17, IL-23, and TNF have been described in HS and IBD (230,231). Conventional treatment of IBD and HS includes biologic therapies, in particular TNF- α inhibitors (225,232). IBD is associated with an altered gut microbiota compared to healthy controls, known as dysbiosis, and it is thought that inflammation is as a result of abnormal immune responses in susceptible individuals to this dysbiosis (233). Although an altered skin microbiota has been described in HS compared to controls, research on the gut microbiota is lacking (227–234). The interaction between the gut and skin microbiome and the immune system, known as the gut-skin axis, is an area of emerging interest, particularly in gut pathologies that have skin co-morbidities (235). Given the role of the microbiota in driving inflammation in IBD, studies assessing the manipulation of the microbiota have also been undertaken. The use of probiotics (health-promoting gut microbiota), prebiotics (non-digestible fibres that help microbiota grow) and synbiotics (mixture of prebiotics and probiotics) in IBD have shown mixed results, with most evidence for supplementing with *Lactobacillus* and *Bifidobacterium* (236). Faecal microbiota transplantation (FMT) is the transplantation of healthy donor gut microbiota via a liquid stool suspension to the small intestine of an affected individual, with the aim

of restoring a healthy intestinal microbiota. This has proven effective in treating refractory and recurrent *Clostridium (Clostridioides) difficile* infection (237). FMT has also been used with some success in IBD (238,239). It is possible that such strategies could be effective in HS also, if an altered gut microbiome is confirmed.

1.6.4 HS, Metabolic Syndrome, and Cardiovascular Disease

HS has been associated with the metabolic syndrome. Metabolic syndrome is defined by at least three of: high serum triglycerides, low serum high density lipoprotein (HDL), hypertension, elevated fasting blood glucose, and abdominal obesity. The association between obesity and HS has been discussed above. An association between HS and hypertriglyceridaemia (OR 1.67 (95% CI 1.14-2.47)) and low HDL (OR 2.48, 95% CI 1.49-4.16) (54). An association with type 2 diabetes has also been described with an adjusted odds ratio of 1.69 (95% CI 1.50-1.91) in one review and odds ratio of 2.85 (95% CI 1.34-6.08) in another (40,46). Insulin resistance is also increased in HS, seen in 43% of patients with HS in one study (47). Hypertension has been associated with HS in case-control studies, however a significant association was not seen in the meta-analysis of these studies (OR 1.5, 95% CI 0.63-3.58) (54). Cardiovascular disease (CVD) associated mortality is significantly higher in patients with HS when compared to severe psoriasis and healthy controls with double the risk of death from CVD compared to those without HS and 1.5 times the risk compared to patients with psoriasis (48). The incidence rate ratios (95% CI) compared to healthy controls were 1.57 (1.14-2.17) for MI, 1.33 (1.01-1.76) for ischaemic stroke and 1.95 (1.42-2.67) for CV-associated death, 1.53 (1.27-1.86) for major adverse CV events (MACE) and 1.35 (1.15-1.59) for all-cause mortality (48). The incidence rate ratios (95% CI) in patients with HS were 1.00

(0.74-1.35) for MI, 0.93 (0.71-1.22) for ischemic stroke, 1.58 (1.17-2.12) for CV-associated death, 1.08 (0.90-1.29) for MACE, and 1.09 (0.94-1.28) for all-cause mortality when compared to patients with severe psoriasis (48).

The gut microbiota plays a role in the pathogenesis of the metabolic syndrome and studies have shown a transient improvement in insulin levels with faecal transplantation from lean healthy donors (245–247). Furthermore, a connection between an altered gut microbiota and atherosclerosis has been described (248,249).

1.6.5 HS and Polycystic Ovarian Syndrome

Polycystic ovarian syndrome (PCOS) is a common endocrine and metabolic disorder of women which may present with irregular menses, clinical hyperandrogenism, obesity, and polycystic ovaries (250,251). An association between PCOS and HS is recognised with anti-androgen therapy used in both conditions (250,252). A pooled OR of 2.64 (95% CI 1.69-4.11; $p < 0.00001$) of PCOS has been reported in patients with HS, however literature studying the link is lacking (252). Co-morbidities including obesity, diabetes, metabolic syndrome are seen in both conditions (252). An altered gut and vaginal microbiome has been described in PCOS, but further study is required to demonstrate on how this impacts on its pathogenesis (253,254).

1.6.6 HS and Obstructive Sleep Apnoea

HS is also associated with obstructive sleep apnoea (OSA) with a prevalence of 3.5% and an odds ratio of 1.45 compared to controls (95% CI 1.33-1.57) (255). As this association is under-recognised, screening for sleep disturbance in HS cohorts is

recommended (255). Disruption of sleep in the context of OSA has also been associated with alterations in gut microbiota (256).

1.6.7 HS and Psoriasis

An association between HS and psoriasis has been reported in the literature. A study from South Korea reported an odds ratio (OR) of 4.58 (95% CI 4.21-4.97), a study from Israel an OR of 1.8 (95% CI 1.4-2.2), and a study from Denmark an OR of 2.99 (95% CI 2.04–4.38) (35,257,258). Both HS and psoriasis share similar aggravating factors and comorbidities including smoking, obesity, cardiovascular disease, and metabolic syndrome (30,259–262). Shared inflammatory pathways including the IL-23/Th17 pathway have been implicated, and elevated levels of TNF- α are seen in both conditions (55,263). Both conditions respond to similar biological therapy, although more effectively in psoriasis (161,264). Treatment of psoriasis with biological therapy can be associated with paradoxical development of HS and vice versa (265,266). The exact pathophysiology of paradoxical eruptions is unknown, however, it is likely genetic susceptibility, and multiple immunological pathways with cytokine imbalance are involved (265). Also psoriasis and HS can co-occur in the rare autoinflammatory syndrome PsAPASH (Psoriatic arthritis, pyoderma gangrenosum, acne, hidradenitis suppurativa) (267).

The role of bacteria, in particular the role of *Streptococci* in triggering flares of psoriasis, is well recognised (268,269). An altered skin microbiome has been described in psoriasis, however, studies on the gut microbiome have yielded mixed results (270). Although alpha-diversity (a measure of species richness) was not significantly lower in psoriasis in the majority of studies, an altered microbiota or dysbiosis was seen in all studies (270).

1.6.8 HS, Alopecia Areata, and Vitiligo

An association between HS and alopecia areata (AA) has been described with an odds ratio (OR) of 1.352 (95% CI 1.235-1.481) in a population-based study from South Korea (35). In that study an association between HS and vitiligo (OR 1.233, 95% CI 1.007-1.511) was also found (35). A study from the US also confirmed a link with alopecia areata with a relative risk (RR) of 2.22 (271). The primary event in both AA and HS is hair follicle disruption, leading to subsequent inflammation (271). An altered gut microbiome was not found in one study on AA, and another described a distinct microbiome in AA compared to controls with no difference in alpha diversity (species richness) (272,273). Several cases of hair regrowth following faecal microbiota transplantation have been reported suggesting a link does exist and could provide a novel therapeutic target in AA (274,275).

1.6.9 HS and Rheumatological Disease

HS has been associated with ankylosing spondylitis, rheumatoid arthritis and psoriatic arthritis (30). An odds ratio (OR) of 1.47 for ankylosing spondylitis (95% CI 1.14-1.89), and 1.31 for rheumatoid arthritis (95% CI 1.16-1.47) has been reported in South Korean patients (35). A US study confirmed the increased link of developing ankylosing spondylitis and rheumatoid arthritis, and also confirmed a link with psoriatic arthritis (Hazard ratio 1.44, 95% CI 1.08-1.93) (276). Furthermore, an altered gut microbiome has also been reported in spondyloarthritis, rheumatoid and psoriatic arthritis (277–279).

1.6.10 HS and Pyoderma Gangrenosum

Pyoderma gangrenosum is a rare inflammatory skin condition which presents in the classical form with a painful nodule or pustule that breaks down and evolves into a painful enlarging ulcer with undermined border (280). Concomitant pyoderma gangrenosum (PG) and HS is well described in the literature and can present in the context of several autoinflammatory syndromes, as discussed above (281). HS and PG have been associated with Crohn's disease (CD) and ulcerative colitis, and both respond to treatment with TNF- α inhibitors (221,222,282–288). An odds ratio of 21.14 (95% CI 17.51-25.51) has been reported in the US of PG in patients with HS. The prevalence of PG is higher (3.68%) in those who have both HS and CD, than in those who have HS alone (0.12%), however when patients with CD are excluded the odds ratio remained high at 26.51 (95% CI 21.07-33.36) for PG in HS (289).

1.6.11 HS, Dowling-Degos disease

Dowling-Degos disease (DDD) is a rare autosomal dominant genodermatosis, characterized by reticulate pigmentation of the flexures and has been associated with HS (290). Loss of function mutations in KRT5 (keratin 5), POFUT1 (protein O-fucosyltransferase 1) and POGLUT1 (protein O-glucosyltransferase 1) have been implicated in DDD (291–293). Mutations in γ -secretase subunit encoding PSENEN have been described in DDD associated with HS, in those negative for the above mutations (294). Mutations lead to defective Notch signalling, which is important in follicular epithelial differentiation. Similar to HS, DDD has a predilection for flexural skin and also involves the hair follicle (295). The clinical presentation of DDD can also include follicular hyperkeratotic lesions, epidermoid cysts, comedo-like lesions, and pilonidal sinus (296). In patients with HS and DDD, there is often a

family history of HS, a follicular pattern and involvement of the trunk and nape of the neck (290,297).

1.6.12 HS and Down Syndrome

Down syndrome patients have been reported to have increased rates of follicular occlusion disorders (298). An association between HS and Down syndrome is well established, and is associated with earlier onset of disease (299). One meta-analysis demonstrated an odds ratio of 9.61 (95% CI 5.70-16.20) of developing HS in Down syndrome patients (299). Obesity is often associated with Down syndrome and is a risk factor for development of HS as discussed previously (40,299). However, studies have shown that Down syndrome is an risk factor for HS, independent of increased body mass index (299). Genetic factors may explain this link, with overexpression of amyloid precursor protein on chromosome 21 in Down syndrome resulting in a decline in notch signalling proposed (300). Excess amyloid precursor protein also leads to follicular plugging and keratinocyte proliferation seen in HS (301).

1.6.13 HS and Skin Cancer

A rare complication of the chronic inflammation seen in HS is the development of cutaneous squamous cell carcinoma (SCC). Higher risk of developing SCC in HS is seen in men, and in older age groups and nearly all cases of SCC in the literature involved the perianal or buttock regions (302). Patients often presented late due to difficulty distinguishing early SCC with HS lesions, and over half the cases in the literature presented with metastases (302). It is imperative that patients are

monitored for malignant transformation of chronic lesions to ensure early diagnosis and treatment.

1.6.14 HS and Lymphoedema

Lymphoedema, presenting with swelling and induration of the skin, is a recognised complication of HS which can prove difficult to treat (303). Lymphoedema most commonly complicates HS of the genital area and buttocks (303). Once lymphoedema is established, it responds poorly to HS medical management (303). Early intervention in HS should be undertaken to prevent the complication of lymphoedema, and once present early surgical intervention should be considered (303).

1.6.15 HS, Depression, and Anxiety

HS is a debilitating, painful, and chronic skin condition, and the drainage and odour from suppurating lesions can cause embarrassment and social isolation. It is therefore unsurprising that a high prevalence of depression and anxiety is seen in HS. A meta-analysis reported a prevalence of depression of 21% in HS, with an odds ratio of 1.99 (95% CI 1.63-2.43), and a prevalence of anxiety of 12% in HS, with an odds ratio of 1.97 (95% CI 1.65-2.35) (304). A higher risk of suicide was also found in the literature, with a hazard ratio for completed suicide in HS patients of 2.42 (95% CI 1.07-5.45) reported in a Danish national registry study (305).

The microbiota are a key regulator of gut-brain function, and the microbiota-gut-brain axis is an area of expanding research in determining the biological and physiological basis of psychiatric disorders (306). Gut microbiome dysbiosis has

been described in anxiety and depression, and mouse models have proven that anxiety and depressive behaviour can be transferred by faecal transplant from an affected individual (307,308). Efforts are underway to target this altered microbiota in depression and anxiety, via the use of antibiotics, faecal transplantation of a healthy microbiome, and the use of prebiotics, probiotics (or ‘psychobiotics’) and fermented foods (307).

1.6.16 HS, Body Image and Sexual Dysfunction

A further consequence of the disfigurement and painful inflammation of HS is poor body image and sexual dysfunction. Body image is significantly diminished in patients with HS compared to BMI matched controls (309). Sexual dysfunction is markedly raised in HS with a prevalence ranging between 51-62% in the literature (310). Risk factors for sexual dysfunction in HS included female sex, more severe disease activity with active lesions in the genital area, higher intensity of pain, presence of malodour, and presence of mood disorders (310).

1.7 Management of HS

Due to the phenotypic heterogeneity of HS and its multifactorial pathogenesis, it is unsurprising that HS is a complex disease which can prove challenging to manage.

1.7.1 Lifestyle measures in HS

Mild disease may respond to lifestyle modifications such as weight loss, smoking cessation, and wearing loose clothing which reduces friction (311,312).

1.7.2 Topical Therapies in HS

Treatment of HS includes the use of topical antiseptics, keratolytics or antibiotics.

Monotherapy with topical treatment is considered for mild or localised disease, however topical therapy is generally recommended as an adjunct to systemic therapy (313).

Anti-bacterial cleansers, for example those containing chlorhexidine, iodine or benzalkonium chloride, are frequently prescribed in HS to reduce the bacterial colonization in affected areas; however there are no studies of their efficacy (225,313,314). A phase II open-label study is currently evaluating topical gentian violet as an antiseptic in HS (NCT04388163) and a topical anti-biofilm surfactant wound gel is also being evaluated (NCT04648631) (315).

Topical clindamycin is recommended by the European S1 for localised Hurley stage I or mild Hurley stage II disease, twice daily for three months (311). An early study Clemmensen et al. proved that topical clindamycin reduced symptom recurrence and reduced lesion count compared to placebo (316) Topical clindamycin is well tolerated, however it increases rates of *Staphylococcus aureus* resistance (317).

Topical resorcinol (15%) is a keratolytic or exfoliant which has been proven effective in mild Hurley stage I or II disease, and also has antipruritic and antiseptic properties (318). Several small studies have demonstrated efficacy in stage I and II disease, with reduction in pain noted, and was well tolerated (318–321).

Recommended dosing is twice daily for flares, reducing to once daily for maintenance treatment (311,318).

Topical ichthammol 10% has also been trialled in HS with patients reporting some improvement (322). Topical benzoyl peroxide (5-10%) can also be used in HS, and may reduce antibiotic resistance when used in combination as seen in acne (323).

Weak evidence also exists for the use of azelaic acid and topical isotretinoin in HS (324).

A phase-II open label trial of the JAK1/2 inhibitor ruxolitinib as a topical cream (1.5%) is also currently in progress (NCT04414514)(325).

Table 2: Studies of topical therapies in HS

Study	Therapy used	Number of participants	Outcome measure	Result
Topical clindamycin				
Clemmensen et al. (1983): (316)	Topical clindamycin hydrochloride 1% in isopropanol 80%, propylene glycol 10% and water 9% versus placebo	27 participants: 13 clindamycin 14 placebo	1. Patient assessment: diary of frequency and duration of recurrences. Ranked as much improved (+2), improved (+1), unaltered (0), worse (-1), much worse (-2) 2. Lesion count	Clindamycin treatment significantly better than placebo (p <0.01)
Jemec et al. (1998): (326)	Topical clindamycin 1% twice daily versus Tetracycline 500mg twice daily	44 participants with Hurley Stage I-II disease: 22 clindamycin 22 tetracycline	1. Visual analog scale (VAS): patient global evaluation, soreness 2. Lesion count	No significant difference seen between two treatment arms
Topical Resorcinol				
Boer et al. (2009): (318)	Resorcinol 15% once daily	12 participants Hurley stage I-II	Reduction in pain by VAS over 1 year	Reduction in pain by VAS noted in all 12 participants
Pascual et al. (2017): (321)	Resorcinol 15% twice daily	32 participants Hurley stage I-II	1. Lesion size on ultrasound at day 30 2. Clinical resolution of lesions at day 30 3. Ultrasonographic (US) resolution of lesions at day 30 4. Reduction in pain by VAS at day 30	1. Reduction in lesion size (p<0.001) 2. Clinical resolution in 84.4% 3. US resolution in 65.5% 4. Reduction in mean pain score (p <0.001)

Molinelli et al. (2020): (320)	Resorcinol 15% once daily	61 participants with Hurley Stage I-II	1. HiSCR at 12 weeks 2. IHS4 at 12 weeks 3. VAS and DLQI at 12 weeks 4. Ultrasonography at baseline, 4 and 12 weeks	1. Clinical response (HiSCR) in 85.2% at 12 weeks ($p < 0.001$) 2. Reduction in IHS4 ($p < 0.05$) 3. Reduction in VAS and DLQI ($p < 0.001$) 4. Reduction in lesion numbers on ultrasound by 80.4% for nodules and 87.1% for abscesses ($p < 0.001$)
Docampo-Simón et al. (2022): (319)	Resorcinol 15% twice daily for flares, once daily maintenance	92 participants with Hurley stage I-II	Treatment Satisfaction Questionnaire for Medication (TQSM)	Mean TQSM score 317.5 out of a possible 400 with 84.4% recommending the topical treatment to others with HS
<i>Topical ichthammol</i>				
Fisher et al. (2020): (322)	Ichthammol 10% in soft yellow paraffin twice daily	20 participants	Patient reported improvement	90% reported some improvement

1.7.3 Systemic Antibiotic Therapy in HS

Systemic antibiotics are indicated in patients with mild disease which fails to respond to topical or lifestyle measures, moderate-to-severe disease, and when multiple body sites are affected (311,313,327). Monotherapy may be effective in mild-to-moderate disease, however, in more advanced disease it is used as an adjunct to other therapies. Antibiotics are thought to be effective in HS due to their anti-inflammatory properties, however antibiotics which lack an anti-inflammatory action such as ertapenem and ceftriaxone have also been shown to be effective in HS (328,329). Tetracycline antibiotics and rifampicin are the mainstay of antibiotic therapy in HS. Tetracyclines interfere with protein synthesis in bacteria at the ribosomal level (330). Inhibition of inflammation by tetracyclines is due to inhibition of mitogen-induced human lymphocytic proliferation, suppression of neutrophil migration and chemotaxis, inhibition of T-cell proliferation, inhibition of phospholipase A2, and inhibition of expression of nitric oxide synthetase (330). Rifampicin has a bacteriostatic effect via its inhibition of DNA-dependent RNA polymerase in bacteria, however its immunomodulatory effects are thought to be important in HS(331). A recent *ex vivo* culture study of rifampicin in HS noted its effect on cytokine production with decreased IL-1 β , IL-6, IL-8, IL-10 and TNF- α , and reduced expression of Toll-like receptor 2 (331).

Tetracycline antibiotics or combination therapy with rifampicin and clindamycin for a 12 week period are the usual first line choices as monotherapy for HS, or used as an adjunct in more severe disease (311). The first randomised control trial of systemic tetracyclines by Jemec et al. showed no difference between oral tetracycline 500mg twice daily and topical clindamycin twice daily (326).

Minocycline (100mg once daily) was evaluated in combination with colchicine

(0.5mg twice daily) with a significant improvement noted; however the efficacy of minocycline alone cannot be extrapolated from this (332). Doxycycline or minocycline 100mg twice daily used in a subset of patients enrolled in the PIONEER trials of adalimumab, was not linked to better outcomes (143). A small retrospective study demonstrated a marked response to doxycycline 100mg twice daily with 60% achieving HiSCR, however, numbers were small (333). A recent study by Jørgensen et al. compared oral tetracycline 500mg twice daily, doxycycline 100mg twice daily, or lymecycline therapy 300mg twice daily in HS (334). Treatment with tetracycline, doxycycline and lymecycline was effective, with a statistically significant mean improvement in Sartorius HS score (HSS), and safe in this study with greatest clinical improvement with tetracycline therapy, as measured by the HSS (334). Van Straalen et al. assessed efficacy and tolerability tetracycline, doxycycline, minocycline and lymecycline in HS and noted a significant decrease in IHS4 and 40.1% HiSCR achievement with 12 weeks treatment with a tetracycline (335). Combination therapy with clindamycin and rifampicin (300mg twice daily) has been proved to be effective in several studies, with response rates of 71% to 93% (336–340). Clindamycin is added to reduce the development of resistance to rifampicin as it is highly mutagenic; however, rifampicin significantly reduces clindamycin levels via the cytochrome p450 3A4 pathway which can explain secondary resistance (341,342). Caposiena et al. evaluated the efficacy of clindamycin alone versus combination therapy with rifampicin, and found no difference between the treatment groups, suggesting monotherapy with clindamycin as an effective alternative therapy in HS (343). In contrast, Iannone et al. noted better efficacy in patients treated with combination therapy versus clindamycin alone (344).

Join-Lambert et al. also assessed the efficacy of combination rifampicin (10mg/kg once daily), moxifloxacin (400mg once daily) and metronidazole (250 to 500mg three times daily) for 6 weeks followed by rifampicin and moxifloxacin therapy until remission to treat Hurley stage I, II, and III HS (345). Once remission was noted rifampicin and moxifloxacin was continued for a further 6-12 weeks and some were prescribed secondary prophylaxis with trimethoprim-sulfamethoxazole or doxycycline (345). Of note 50% of the participants also had induction treatment with ceftriaxone IV with oral metronidazole for 2 weeks (345). Complete remission was obtained in 57% of patients (345).

Delage et al. assessed the use of this combination therapy to treat severe Hurley stage I HS, with complete and prolonged remission noted in 75% of patients, suggesting early broad spectrum antimicrobial treatment may induce clinical remission (346). Pristinamycin was used in those who did not tolerate moxifloxacin, or had a history of tendonitis or joint pain, with no difference in outcomes (346). A retrospective study assessed efficacy of adalimumab alone versus rifampicin and clindamycin (347). Both groups achieved a significant reduction in modified Sartorius score but with a greater efficacy noted in the adalimumab group (347). A study assessing efficacy of daily ofloxacin (200-400mg) and clindamycin (600-1800mg) demonstrated similar response rates to rifampicin and clindamycin combination treatment (348).

Intravenous antibiotics have also been used in HS, such as the induction therapy with IV ceftriaxone seen in the 2011 study by Join-Lambert et al. (345). Intravenous ertapenem daily for 6 weeks was also assessed in a study by Join-Lambert et al., and was effective in 17 of 30 patients with dramatic improvement in severe cases (328). This has led to its use as a bridge to biologic or surgical treatment of severe HS.(328)

IV clindamycin for 5 days (600mg three times daily) followed by rifampicin and clindamycin combination therapy for 10 to 12 weeks, in a study by Nikolakis et al. in 2021, achieved rapid response with improved quality of life (349).

Table 3: Studies of systemic antibiotic therapy in HS

Study	Therapy used	Participants	Outcome measure used	Results
<i>Tetracycline antibiotics</i>				
Jemec et al. (1998): (326)	Topical clindamycin 1% twice daily versus Tetracycline 500mg twice daily	44 participants with Hurley Stage I-II disease: 22 clindamycin 22 tetracycline	1. Visual analog scale (VAS): patient global evaluation, soreness 2. Lesion count	No significant difference seen between two treatment arms
Armyra et al. (2017): (332)	Minocycline 100mg once daily with colchicine 500mcg twice daily	20 participants with Hurley stage I-III	1. Physician's global assessment (PGA) 2. Hurley score 3. Dermatology Life Quality Index (DLQI)	Significant improvement in 1. PGA 2. Hurley score 3. DLQI
Vural et al. (2019): (333)	Doxycycline 100mg twice daily	10 participants with Hurley stage I-III	HiSCR	60% achievement HiSCR
Jørgensen et al. (2021): (334)	Tetracycline 500mg twice daily, doxycycline 100mg twice daily, or lymecycline therapy 300mg twice daily	108 patients with Hurley stage I-III	1. Sartorius HS score (HSS) 2. DLQI 3. PGA 4. Pain numerical rating scale (NRS)	1. Mean HSS decreased by 8.13 from baseline ($p < 0.001$) 2. Mean DLQI decreased by 3 ($p < 0.001$) 3. Median PGA 'small improvement (1-29%)' 4. Mean pain NRS decreased by 1 ($p < 0.001$)

Van Straalen et al. (2021): (335)	Tetracycline 500mg twice daily, doxycycline 100mg once daily, minocycline 100mg once daily	108 participants: 42 received tetracycline, 121 received doxycycline, 17 received minocycline	1. HiSCR 2. IHS4 3. DLQI 4. Pain NRS	1. 40.1% attainment of HiSCR 2. Significant reduction in IHS4 ($P < 0.001$) 3. Significant reduction in DLQI ($p < 0.001$) 4. Significant reduction in pain ($p = 0.001$)
Caposiena et al. (2021): (350)	Group A: Lymecycline 300mg daily versus Group B: rifampicin 300mg twice daily and clindamycin 150mg four times daily for 10 weeks	52 participants with HS Group A: 26 Group B: 26	1. Sonographic score of HS 2. IHS4 3. VAS pain 4. DLQI	Significant improvement in IHS4, pain VAS and DLQI in both groups ($p < 0.001$) No significant difference in response rates in both groups ($p = 0.78$) IHS4 did not differ significantly between groups Ultrasound nodule and abscess count was lower in Group A than Group B after treatment, draining tunnel count was lower in Group B than Group A Group A had higher improvement in pain VAS ($p < 0.001$) and DLQI ($p < 0.05$)

<i>Rifampicin and Clindamycin</i>				
Mendonça et al. (2006): (337)	Rifampicin and clindamycin 300mg twice daily for 10 weeks (minocycline 100mg once daily substituted if developed diarrhoea on clindamycin)	14 participants	Retrospective review of clinical remission	10 of 14 (71%) achieved remission
Gener et al. (2009): (340)	Rifampicin 600mg daily and clindamycin 300mg twice daily for 10 weeks	70 participants with Hurley stage I-III disease	1. Sartorius score 2. Hurley stage at 10 weeks 3. Pain VAS	1. Dramatic decrease in Sartorius score ($p < 0.001$) 2. Decrease in Hurley score noted ($p=0.018$) 3. Median pain reduction from 7 to 3 ($p < 0.001$)
Van Der Zee et al. (2009): (339)	Rifampicin and clindamycin 600mg daily for 10 weeks	34 participants with Hurley stage I-III disease	1. Hurley score 2. Investigator global assessment with partial improvement: $<75\%$ clinical improvement from baseline, and total remission: $> 75\%$ improvement or total clearance	28/34 (82%) showed at least partial improvement 16/34 (47%) showed total remission
Bettoli et al. (2014): (338)	Rifampicin and clindamycin 600mg daily for 10 weeks	20 participants with Hurley stage I-III disease	1. 25% improvement in Sartorius score 2. Number of exacerbations	1. 17/20 (85%) had $>25\%$ improvement in Sartorius score ($p = 0.00098$) 2. Reduction in exacerbations ($p = 0.0091$)

Dessinioti et al. (2016): (336)	Rifampicin and clindamycin 600mg daily for 12 weeks	26 participants with Hurley stage I-III disease	Clinical response	Clinical response in 19/26 (73%) with sustained efficacy at 1 year in 7/17 (41%) and disease relapse in 10/17 (59) after a mean of 4.2 months
Ochi et al. (2018): (351)	Rifampicin and clindamycin 300mg twice daily for 10 weeks	11 participants with HS	Clinical response HS-PGA in 4 participants	63.6% reported clinical improvement 3 of 4 had improvement in HS-PGA
Caposiena et al. (2019): (343)	Group A: Clindamycin 150mg four times daily with rifampicin 300mg twice daily for 8 weeks versus Group B: Clindamycin 150mg four times daily for 8 weeks	60 participants: 30 in group A 30 in group B	Hidradenitis Suppurativa Clinical Response (HiSCR) – at least a 50% reduction from baseline in total abscess or inflammatory nodule count	17/30 (56.7%) in group A, and 19/30 (63.3%) achieved HiSCR with no significant difference between groups (p = 0.598)
Marasca et al. (2019): (347)	Adalimumab versus rifampicin and clindamycin for 10 weeks	30 participants	1. Modified Sartorius score 2. Hidradisk QOL assessment	1. Reduction in modified Sartorius score (p = 0.0052) 2. Reduction in Hidradisk (p = 0.0095)
Vural et al. (2019): (333)	Rifampicin and clindamycin 300mg twice daily for 3 months	28 participants with Hurley stage I-III disease	HiSCR	46.6% achievement HiSCR
Yao Y et al. (2021): (352)	Rifampicin and clindamycin 300mg twice daily for 6 months	54 participants with HS	1.Hidradenitis Suppurativa Score (HSS) 2.DLQI 3.VAS pain 4.HS-PGA	1. 79.6% showed improvement in HSS, with 37% achieving >50% improvement from baseline, and 13% full remission 2. Median DLQI decreased from 14.5 to 10 (p<0.0001)

				3. Median VAS decreased from 9.1 to 5.9 ($p < 0.0001$) 4. Median PGA corresponded to 'small improvement' (1-29%)
Iannone et al. (2021): (344)	Rifampicin 300mg twice daily and clindamycin 150mg four times daily for 12 weeks versus clindamycin 150mg four times daily for 12 weeks	36 participants with moderate to severe HS: 19 on clindamycin plus rifampicin, 17 on clindamycin alone	1. Modified Sartorius score 2. Acne inversa severity score (AIS) 3. DLQI	1. Greater reduction in modified Sartorius score in clindamycin plus rifampicin group ($p = 0.058$) 2. Significant reduction in AISI in clindamycin plus rifampicin group ($p = 0.034$) 3. Non-significant reduction in DLQI between groups ($p = 0.207$)
Van Straalen et al. (2021): (335)	Rifampicin and clindamycin 600mg daily for 12 weeks	103 participants with Hurley stage I-III disease	1. HiSCR 2. IHS4 3. DLQI 4. Pain NRS	1. 48.2% attainment of HiSCR 2. Significant reduction in IHS4 ($P < 0.001$) 3. Significant reduction in DLQI ($p < 0.001$) 4. Significant reduction in pain ($p = 0.001$)
Caposiena et al. (2021): (350)	Group A: Lymecycline 300mg daily versus Group B: rifampicin 300mg twice daily and clindamycin 150mg four times daily for 10 weeks	52 participants with HS Group A: 26 Group B: 26	1. Sonographic score of HS 2. IHS4 3. VAS pain 4. DLQI	Significant improvement in IHS4, pain VAS and DLQI in both groups ($p < 0.001$) No significant difference in response rates in both groups ($p = 0.78$) IHS4 did not differ significantly between groups Ultrasound nodule and abscess count was lower in Group A than Group B

				after treatment, draining tunnel count was lower in Group B than Group A Group A had higher improvement in pain VAS ($p<0.001$) and DLQI ($p<0.05$)
Bettoli et al. (2021): (353)	Rifampicin and clindamycin 300mg twice daily for 10 weeks	20 participants aged ≤ 16 years with HS	1. Sartorius Score 2. No of exacerbations during treatment compared to prior 3 months	1. Sartorius score mean reduction of 52.8% with 60% achieving $>50\%$ improvement ($p=0.001$) 2. 37.1% mean reduction in number of exacerbations ($p=0.001$)
<i>Rifampicin</i>				
Join Lambert et al. (2011): (345)	Rifampicin (10mg/kg/day), moxifloxacin (400mg daily) and metronidazole (500mg three times daily) and 50% received pre-treatment with IV ceftriaxone (1g daily) and metronidazole (500mg three times daily) for 2 weeks. Median duration was 2.4 – 12 months depending on stage.	28 participants with Hurley stage I-III disease	Remission of HS	57% achieved complete remission
Vural et al. (2019): (333)	Rifampicin, moxifloxacin and metronidazole for 3 months	2 participants with Hurley stage I disease	HiSCR	100% achievement HiSCR
Delage et al. (2020): (346)	Rifampicin (10mg/kg once daily), moxifloxacin (400mg once daily) and metronidazole (250-500mg three times daily) for 6 weeks then Rifampicin and moxifloxacin alone	28 participants with Hurley Stage 1 HS	Sartorius score	Median Sartorius score dropped from 14 to 0 ($p=6 \times 10^{-6}$) at week 12 75% reached clinical remission (Sartorius score = 0)

	for 4 weeks. (Pristinamycin 1g three times daily in those with contra-indications or intolerant of moxifloxacin)			
<i>Clindamycin</i>				
Delaunay et al. (2018): (348)	Ofloxacin (200-400mg) and clindamycin (600-1800mg daily) as per patients' weight with mean duration of treatment of 4.3 months	65 participants with Hurley stage I-III disease	Patient reported improvement	58.4% reported improvement in HS
Caposiena et al. (2019): (343)	Group A: Clindamycin 150mg four times daily with rifampicin 300mg twice daily for 8 weeks versus Group B: Clindamycin 150mg four times daily for 8 weeks	60 participants: 30 in group A 30 in group B	Hidradenitis Suppurativa Clinical Response (HiSCR) – at least a 50% reduction from baseline in total abscess or inflammatory nodule count	17/30 (56.7%) in group A, and 19/30 (63.3%) achieved HiSCR with no significant difference between groups (p = 0.598)
Rosi et al. (2019): (354)	Clindamycin 300mg twice daily for 12 weeks	31 participants	1. Sartorius score 2. HS-PGA 3. IHS4 4. VAS pain	1. Mean reduction of 15 in sartorius score (p≤0.01) 2. Mean reduction of 1 in HS-PGA (p≤0.01) 3. Mean reduction of 6 in IHS4 (p≤0.01) 4. Mean reduction of 3 in VAS pain (p≤0.01)

An et al. (2021): (355)	Clindamycin monotherapy (dose not specified) for 8 weeks	50 participants: 34 eligible for evaluation at 8 weeks	1. HiSCR - at least a 50% reduction from baseline in total abscess or inflammatory nodule count 2. HS-PGA	1. 61.76% achieved HiSCR 2. Mean HS-PGA decreased from 3.24 to 2.15 (p=0.001)

Antibiotic side-effects can be numerous and care should be taken to minimise these. Apart from specific side effects to particular antibiotics (for example photosensitivity with tetracyclines), side effects common to all antibiotics include candidiasis, and allergic reactions (329). The negative impact of antibiotic therapy on gut microbiome diversity has been established in multiple studies with repeated and prolonged courses leading to dysbiosis (356,357). Acute *Clostridioides difficile* infection can also occur with antibiotic use, and is a particular risk with clindamycin (342). *C. difficile* risk is higher in patients with inflammatory bowel disease with one study reporting a higher prevalence among patients with ulcerative colitis (3.7%) and Crohn's disease (1.1%) compared to the general population (0.5%) (358). Interestingly, this increased risk is not borne out in cases of HS treated with clindamycin. A study by Kwak et al. found no increased risk of *C. difficile* infection in patients treated with IV or oral clindamycin in HS (359). Co-prescription with rifampicin (over 75% in this study) may explain the low incidence of *C. difficile* infection, as it reduces serum clindamycin levels, and also treats the infection (341,342,359). Antibiotic resistance is also a growing concern, and prolonged use of antibiotics in HS should be discouraged. Treatment of flares with antibiotics or induction treatment with antibiotics prior to surgery or commencement of a biologic is recommended, with long-term maintenance therapy with antibiotics discouraged (329).

1.7.4 The Use of Biologic Drugs in HS

Targeted biologic therapy is now the mainstay of treatment of moderate to severe HS.

Anti-TNF- α therapy

As discussed previously TNF- α is elevated in HS. Several biologics targeting TNF- α have been trialled in HS.

Adalimumab is the first and only biologic approved (by the European Medicines Agency (EMA) and US Food and Drug Administration (FDA)) for the treatment of HS. This is based on the results of two phase III double-blind placebo-controlled trials (PIONEER I and II) (143). In these studies 633 participants with HS received either a loading subcutaneous adalimumab dose of 160mg on week 0, and 80mg on week 2 followed by 40mg weekly maintenance dose from week 4, or placebo. In PIONEER II tetracycline antibiotics were continued if required (143). The HiSCR (at least a 50% reduction from baseline in total abscess or inflammatory nodule count) was achieved in 50.6% of participants on adalimumab, versus 26.8% receiving placebo ($p < 0.001$), and Dermatology Life Quality Index (DLQI) scores also improved in the treatment arm (143). 88 participants entered the open-label extension study of adalimumab 40mg weekly with HISCAR achieved in 52.3% at week 12, 62.5% at week 36, and 52.3% at week 168 (288). Adalimumab was well tolerated in these studies. Adverse events were 4.6% or less in both PIONEER studies, with one incidence of non-melanoma skin cancer and one incidence of breast cancer, and no serious infections reported (143). Four serious infections and no adverse events of opportunistic infections excluding oral candidiasis, no active tuberculosis, lymphomas, cancers or demyelinating disorders were reported in the

open label study (288). In practice doses of 80mg weekly can be introduced in those with partial response or loss of efficacy to 40mg weekly of adalimumab (360).

Studies in Crohn's disease and ankylosing spondylitis suggest an improvement in gut microbiota composition results from adalimumab therapy (361,362).

Furthermore studies in spondyloarthritis have suggested certain microbiota patterns can predict response to TNF- α treatment (361,363). A small study assessed the gut microbiota before and after 12 weeks of adalimumab therapy in 10 patients with HS (364). It showed a shift in composition and function of the gut microbiota after adalimumab therapy, with more beneficial metabolites such as short-chain fatty acids detected (364).

Infliximab, a chimeric monoclonal antibody targeting TNF- α , was studied in a phase II randomised, placebo-controlled, double-blind study in moderate to severe HS (21). 38 patients with moderate to severe HS received 5mg/kg of infliximab on weeks 0, 2, 4, 6, 14, and 22 (21). At 8 weeks, 57% had a > 50% decrease in their HS Severity Index (HSSI) versus 5% in the placebo group ($p=0.092$), 60% had a 25-50% decrease in HSSI compared to 5.6% receiving placebo ($p<0.001$) (21). DLQI and visual analog scores of pain also improved in the treatment arm (21). Infliximab was well tolerated in the treatment group, with no serious adverse events reported (21). Higher doses of infliximab have been proposed (7.5-10mg/kg) with good control of disease (123,365).

Etanercept is a recombinant human TNF- α receptor fusion protein that binds membrane bound TNF- α receptors. No improvement was achieved in HS patients treated with etanercept in one phase II open-label, randomised controlled trial (366).

Golimumab is a fully human anti-TNF- α monoclonal antibody that binds to TNF- α . Case reports have shown some efficacy in HS (367,368).

Certolizumab Pegol, is a pegylated humanised monoclonal antigen-binding fragment of IgG which binds to TNF- α . A case series of certolizumab use in 2 patients (200mg every 2 weeks) showed no efficacy, however several case reports show improvement at higher doses (400mg every 2 weeks) (369–372). As certolizumab is pegylated it does not cross the placental barrier, therefore it has been used off-licence in pregnancy (370).

Anti-IL-1

The IL-1 pathway has been found to be hyperactive in HS, leading to skin infiltration and destruction (373). Targeting this pathway has been trialled in HS.

Anakinra is a recombinant interleukin-1 receptor antagonist, competitively inhibiting IL-1 α and IL-1 β receptor interaction. An open label study of anakinra 100mg subcutaneously for 8 weeks in patients with moderate to severe HS showed a significant mean decrease of 34.8 in their modified Sartorius score, as well as a reduction in patient and physician global assessments. Furthermore an improvement in DLQI was seen. However, rebound of HS was seen in all patients during the 8-week follow up period (374). Tzanetakou et al. reported 78% of patients treated with anakinra achieved HiSCR (at least a 50% reduction from baseline in total abscess or inflammatory nodule count) compared to 30% receiving placebo at week 12 ($p=0.04$) (192). Again, in the 12 week follow-up period control of HS was lost, with no difference in HiSCR between the groups (192). A study of long-term efficacy of anakinra followed three patients treated with anakinra for between 6 months and 7 years (375). In this study all required switching to another biologic agent due to

relapse (375). As anakinra has had mixed results in HS, and also requires daily subcutaneous injections, its use in HS is limited. However, anakinra may be an appropriate option in those with other autoinflammatory syndromes (281).

Canakinumab is a human IgG κ monoclonal antibody targeting IL-1 β with mixed evidence of efficacy in HS in the literature. Case reports have shown some efficacy in HS, however failures have also been reported (376–379).

Bermekimab (MABp1) is a recombinant human IgG1 monoclonal antibody which binds IL-1 α . In a study by Kanni et al. 60% (6/10) of patients achieved HiSCR (at least a 50% reduction from baseline in total abscess or inflammatory nodule count) after receiving bermekimab 7.5mg/kg every 2 weeks versus 10% (1/10) of those receiving placebo at 12 weeks (380). In the open label extension study 75% of those transitioned (8 patients) achieved HiSCR at week 12 (381). A further open-label phase II study of bermekimab 400mg subcutaneously weekly showed a significant reduction in lesion count and visual analog scale pain scores in patients with moderate to severe HS who were anti-TNF naïve and those who failed anti-TNF treatment (382).

A phase II trial is ongoing of lutikizumab, an anti-IL1 α/β dual variable domain immunoglobulin in HS (383). Another phase II trial is assessing MEDI8968, a fully human monoclonal antibody which binds to IL-1R1 in HS (384).

Anti-IL17

Serum IL-17 levels are elevated in patients with HS and correlate with disease severity (156). A number of biologic agents targeting IL-17 have been used to treat HS.

Secukinumab, a human monoclonal IgG1 κ antibody that binds IL-17A, has shown some efficacy in HS. A pilot trial in 9 patients with moderate to severe HS found 67% achieved HiSCR when treated with secukinumab 300mg weekly for 5 weeks then every 4 weeks for 24 weeks (385). An open label study in 20 patients with moderate to severe HS found 70% achieved HiSCR when treated with secukinumab 300mg subcutaneously weekly for 5 weeks then every 4 weeks in 9 patients, or every 2 weeks in 11 patients up to 24 weeks (386). A retrospective study of secukinumab 300mg weekly for 5 weeks then every 4 weeks up to 16 weeks in 20 patients with HS found 75% achieved HiSCR response (387). In this study, 2 of the 20 patients developed Crohn's disease after 3 and 5 months of treatment (387). HS has been associated with inflammatory bowel disease as discussed previously, and careful clinical examination to detect possible susceptibility to IBD prior to secukinumab therapy should be advised (388). It should also be avoided in those with active inflammatory bowel disease. An Italian retrospective study in 31 patients with HS treated with secukinumab 300mg weekly for 5 weeks, followed by 300mg every 4 weeks, found 41% achieved HiSCR at week 28 which was lower than previously reported (389). Several clinical trials are in progress to determine if there is a benefit to treatment with secukinumab in HS (NCT03099980, NCT04179175, NCT03713632, NCT03713619) (390).

Brodalumab is a monoclonal antibody that binds with high affinity to the IL-17RA subunit of the IL-17 receptor and blocks signalling of the pro-inflammatory cytokines IL-17A, IL-17C and IL-17F. An open label study of brodalumab 210mg subcutaneously on week 0, 1, 2, and every 2 weeks thereafter in 10 patients with moderate to severe HS found 100% achieved HiSCR at 12 weeks (391). In the maintenance period 2 patients had recurrence of drainage from their gluteal sinus tracts, and suggested higher doses for some patients with more severe disease may be required (391). Weekly brodalumab 210mg subcutaneously was then trialled in 10 patients with draining tunnels, with 100% achieving HiSCR by week 4 and sustained up to week 24 (392). Therefore weekly dosing may be indicated in those with more severe disease with tunnels and sinus tracts.

Ixekizumab is an IgG4 monoclonal antibody that binds with high affinity to IL-17A and IL-17A/F. Three case reports in the literature have suggest ixekizumab may also be effective in HS but no case series or trials have been published (393–395).

Bimekizumab is a monoclonal IgG1 antibody that inhibits ILA and IL17F. A phase II, double-blind, placebo-controlled trial was carried out, comparing bimekizumab 640mg week 0, then 320mg every 2 weeks, to placebo, and to adalimumab 160mg week 0, 80mg week 2 and then 40mg weekly from week 4 (396). 57.3% of patients receiving bimekizumab achieved HiSCR at week 12, versus 26.1% in the placebo group. 46% bimekizumab-treated patients achieved HiSCR₇₅ and 32% achieved HiSCR₉₀, 10% of placebo-treated patients achieved HiSCR₇₅ and none achieved HiSCR₉₀, and 35% of adalimumab-treated patients achieved HiSCR₇₅ and 15% achieved HiSCR₉₀ (396). Results of two phase III trials and an extension study are awaited (NCT04242446, NCT04242498, NCT04901195) (397).

CJM112 is an anti-IL17A and IL-17A/F IgG1 κ monoclonal antibody. In a phase II randomised controlled trial HS-PGA response rate was 32.3% in those treated with CJM112 300mg weekly for 5 weeks then every 2 weeks (33 patients) compared to 12.5% in those who received placebo (33 patients) at week 16 (398).

Izokibep is a potent and selective inhibitor of IL-17A that is being developed for HS and is currently in phase II trials (399). The IL17A/F nanobody sonelokimab is also being studied in HS (400).

Anti-IL12/23

Ustekinumab is a fully human IgG1 κ monoclonal antibody that binds to the shared p40 protein subunit of IL-12 and IL-23. A phase II open label study found that patients treated with ustekinumab (45mg if <100kg, 90mg if >100kg) at week 0, 4, 16, and 28 with an observation period to 40 weeks, had a marked improvement in modified Sartorius score in 35% and a moderate improvement in 47%. Furthermore 47% achieved HiSCR at week 40 (401). Several case series and case reports have reported efficacy of ustekinumab in HS (402–410). However drug survival was variable (402–410). Higher doses as used in Crohn's disease has also been trialled in HS (411–413). Romani et al evaluated an initial iv infusion of ustekinumab adjusted by weight ($\leq$ 55 kg, 260 mg; 56–85 kg, 390 mg; $\geq$ 86 kg, 520 mg) followed by a maintenance subcutaneous dose of 90mg every 8 weeks in 14 patients (413). 50% had achieved HiSCR at 16 weeks (413). A retrospective study in 6 patients with the same regimen also found 50% achieved HiSCR at week 12 (411). In another retrospective case series of 10 patients 90% achieved HiSCR with 90mg subcutaneous ustekinumab with no induction therapy (412).

Anti-IL23

Guselkumab is a recombinant human monoclonal antibody that binds to the p19 subunit of IL-23. Case reports and case series have reported efficacy with guselkumab 100mg subcutaneously at weeks 0, 4, then every 8 weeks (414–418). A retrospective study of 11 patients reported that 63.6% achieved HiSCR at week 16 ± 4 weeks, with mean drug survival of 24.54 months (419). However, one case series reported poor outcomes with a higher dosing regimen (100mg sc week 0, 4, then every 4 weeks) in 4 patients (420).

Tildrakizumab is a recombinant human monoclonal antibody to the p19 subunit of IL-23. One case series in 5 patients of Tildrakizumab 100mg week 0, 4 then 200mg every 4 weeks thereafter reported improvement in abscess and nodule count at week 8 in all patients and ongoing improvement at week 20 in 3 of the 5 patients (1 discontinued at week 8 due to pregnancy)(421)

Rizankizumab is a humanised monoclonal antibody that binds to IL-23. Clinical response has been reported in cases in the literature at a dose of 150mg on week 0, and week 4, then every 12 weeks thereafter (422–424).

Anti-IL36

IL-36 is involved in neutrophil recruitment and activation, and elevated levels of IL-36 has been found in HS lesions (425). Imsidolimab and spesolimab are monoclonal antibody that bind to IL-36 which have been developed for the treatment of pustular psoriasis (426,427). Their use in HS is being trialled currently (428,429).

Janus Kinase (JAK) inhibitors

Janus Kinase inhibitors block IL-6 signalling through the JAK-STAT pathway (430). IL-6 is known to be involved in the pathogenesis of HS (373). Tofacitinib is a JAK-1 and -3 inhibitor with reports of success in the treatment of 2 patients with HS (430). INCB054707 is a JAK1 inhibitor which was studied in 2 phase II trials in patients with moderate to severe HS (431). Ten patients received 15mg in study 1 and 9 received 30mg, 9 received 60mg, 8 received 90mg patients and 9 received placebo in study 2 (431). 70% of patients in study 1 and 81% of patients in study 2 had treatment related adverse events, with 30% in study 1 and 42% in study 2 having grade 3 adverse events (431). Of those patients eligible for evaluation, 3(43%) in study 1 and 17(65%; 30mg, 56%; 60mg, 56%;90mg, 88%) in study 2 achieved HiSCR (431). A further study evaluating efficacy and safety of INCB054707 is ongoing currently (432). Upadacitinib, a JAK1 inhibitor has been studied in HS and results are awaiting publication (433).

C5a inhibitors

IFX-1 is a monoclonal IgG4 κ antibody that selectively binds to C5a (139). A phase II study assessed efficacy of IFX-1 800mg day I, 4, 8, 15, 22, 29, 36, 43 and 50 in patients with HS (139). 12 patients were enrolled and 75% achieved positive HiSCR on day 50, and 83.3% on day 134 (139). IFX-1 was well tolerated (139). A randomised, double-blind, placebo controlled trial in 175 patients with HS, demonstrated HiSCR achievement in 40.4% receiving 400mg every 4 weeks, 51.5% receiving 800mg every 4 weeks, 38.7% receiving 800mg every 2 weeks and 35.5% receiving 1200mg every 2 weeks (434). 47.1% of those receiving placebo achieved HiSCR (434). It is thought that using HiSCR contributed to the high placebo

response rate as the data collected on draining tunnels demonstrated significant efficacy of IFX-1 compared to placebo (434,435). Avacopan is an oral C5a receptor antagonist which is also under study in HS (436).

Others

Several other treatments in HS are under study currently:

- LY3041658 is a monoclonal antibody that inhibits chemokines which bind to CXCR1 and CXCR2 which is currently in a phase II trial in HS (437).
- PF-06650833, an IL-1 receptor-associated kinase 4 (IRAK4) inhibitor (438).
- PF-06700841, a tyrosine kinase (TYK2) and JAK1 inhibitor that blocks IL-12/23 signalling (438).
- PF-06826647, a tyrosine kinase inhibitor (TYK2)(438).
- Fostamatinib, a spleen tyrosine kinase enzyme inhibitor (SYK)(439).
- KT-474, an IRAK4 inhibitor is recruiting to a phase 1 study (440).
- Iscalimab (CFZ533) is an anti-CD40 IgG1 monoclonal antibody that blocks the CD40-CD154 pathway (441).
- LYS006, a leukotriene A4 (LTA4) hydrolase inhibitor (442).
- CSL324, a recombinant anti-granulocyte colony-stimulating factor (G-CSF) receptor monoclonal antibody (443).
- RIST4721, an oral CXCR2 antagonist (444).
- BDB-001, a toll-like receptor 7 and 8 agonist (445).
- ATI-450, a small molecule inhibitor of p38a mitogen-activated protein kinase (MAPK)/MAPK-activated protein kinase 2 (MK2)(446).

1.7.4 Other Systemic Treatments

Steroid therapy

Systemic corticosteroids produce pan-cytokine inhibition and are thus effective in HS (447). However, high dose and protracted courses of oral corticosteroids are not recommended due to side effects, and due to the chronicity of HS it is not recommended to prescribe them routinely. They may however be a useful adjunct as short-term rescue therapy for flares or as a bridge to other long-term systemic therapies (313).

Intralesional steroids, however, are widely used to treat individual lesions in HS (448–452). Intralesional corticosteroids administered to inflammatory nodules can lead to rapid resolution and can be useful in treating flares (452,453). One study compared two different doses of intralesional triamcinolone, 10mg and 40mg/ml and showed no statistical difference when compared to placebo (449). Varying doses of intralesional steroid is used in the published studies, thus optimal dosing is unknown (448–454). A clinical trial is being undertaken to determine this (455).

Oral retinoid therapy

There is some evidence in the literature for the use of retinoids in HS. Acitretin at doses of 0.5-0.6mg/kg/day for 3 to 12 months have been trialled with variable outcomes in HS (456,457). Response rates are reported to be approximately 50% with high recurrence rates seen, and as such it should only be considered as a second- or third-line treatment (313,456,457). Isotretinoin may be helpful in mild disease at low doses (<1mg/kg/day) and can be considered if the patient has severe concomitant acne or as second- or third-line therapy (313,458). Alitretinoin at a dose of 10mg/kg/day has been assessed in 14 women for a period of 24 weeks in one

study with 78.5% patients having significant improvement in their modified Sartorius score (459). Alitretinoin is not available to prescribe in Ireland.

Selective PDE-4 inhibitor therapy

Apremilast is a phosphodiesterase-4 (PDE-4) inhibitor which has been studied in a placebo-controlled trial in HS (460). In this study 20 patients with moderate HS received apremilast 30mg twice daily or placebo for 16 weeks (460). HiSCR was achieved in 53.3% of those receiving apremilast and in none of those receiving placebo (460). Four of the eight responders continued apremilast in a 2 year follow-up study (2 discontinued due to pregnancy, one due to intolerable nausea, and one due to quiescence of HS)(461). Orismilast, is another PDE-4 inhibitor currently being trialled in HS (462).

Hormonal and endocrine therapies

Due to the onset of HS after puberty, presence of premenstrual flares, and the rarity of cases in postmenopausal patients hormonal therapies have been trialled in HS (463). In particular patients with polycystic ovarian syndrome (PCOS), discussed above, may benefit from hormonal therapy for their HS, although robust evidence for the use of anti-androgens does not exist in the literature due to the limited small studies (92).

Cyproterone acetate with ethinyloestradiol (50mg/50µg) versus ethinyloestradiol/norgestrel (50µg/500µg) has been evaluated in 24 patients with HS showing clinical improvement, with no difference noted between the two treatments (464).

Spironolactone (100 to 150mg daily) has also been used to some success in HS in a case series (465). A further retrospective study of spironolactone 75mg daily found that it reduced lesion count, HS-PGA score and pain (466).

Metformin 1.5g/day has also been used in HS as it has anti-androgen, and anti-inflammatory effects, and can treat concomitant PCOS and metabolic syndrome if present (467). In this retrospective study subjective clinical response was seen in 68% with 19% experiencing quiescence of disease with metformin monotherapy (467). However drug survival in this study at 12-months was 39% (467). A further study of metformin (500mg to 1500mg) in 25 patients with HS showed significant reduction in Sartorius score in 76%, as well as a significant improvement in DLQI in 64% at week 24 (468). A phase III trial is currently evaluating the efficacy of metformin and doxycycline versus doxycycline alone (469).

Finasteride, a type II 5- α reductase inhibitor has also been used with some effect in HS (470–473). Doses of between 1 and 5 mg have been trialled with success reported but relapse is common (473). A study of 7 patients who failed antibiotic therapy, treated with 5mg a day of finasteride reported improvement in 6 of 7 patients with complete healing in 3 cases (472). 2 case series report improvement in paediatric cases of HS with finasteride (470,471).

Dapsone

Dapsone has been used in HS with some success but evidence available is weak (474). A retrospective review evaluated dapsone (50-200mg/day) in 24 patients with HS with improvement noted in 38%, however none of the Hurley Stage III patients responded (475). A retrospective case series of dapsone 25-150mg/day also showed positive response in all 5 patients (476). A series of 19 patients with moderate to

severe HS taking 25-100mg/day showed clinically significant improvement in 15.8%, slight improvement in 52.6% and no improvement in 31.6% (477). A retrospective review in 25 patients receiving dapsone 50mg-200mg showed subjective clinical improvement in 64% (478). Again this study showed no improvement in Hurley Stage III disease with responders having mild to moderate HS (478). A larger case series in 56 patients with mild to moderate HS showed 62.5% of patients achieved HiSCR at 12 weeks on doses of 50-150mg/day (479). Dapsone is designated as third line treatment in mild to moderate HS (313).

Colchicine

Colchicine has been trialled in small series at a dose of 0.5mg twice daily with little effect (332). In a prospective pilot study of 8 patients with HS only 2 continued treatment at 4 months, with only 1 showing slight improvement in HS-PGA (480). When used in combination with minocycline 100mg once daily for 3 months, followed by colchicine alone for 3 months a significant improvement was noted in 20 patients (332). However, this does not support its use as monotherapy in HS (332).

Finally, a study of 44 patients who received colchicine as monotherapy, or in combination with doxycycline 100mg daily or doxycycline 40mg daily, showed significant improvement in DLQI and IHS4 scores in all groups ($p < 0.001$) (481).

Methotrexate

Methotrexate, a folate antagonist, has been shown not to be effective in HS in a single series of 3 patients treated with doses of 12.5-15mg weekly for 6-24 weeks (482). However, a review in 2020 of 15 patients suggests methotrexate may be

effective in a subset of patients with HS, in particular older patients with lower body mass index, but did not show benefit when taking concurrent biologic therapy (483). Low dose methotrexate however may be beneficial in treating anti-drug antibodies in infliximab therapy (484).

Azathioprine

Azathioprine, a disease modifying anti-rheumatic drug, is deemed to be poorly effective in treating HS (313). One series in 9 patients with HS receiving low doses of azathioprine 0.5-1mg/kg for 1-8 months showed slight improvement in 4 of the cases (485).

Ciclosporin

Ciclosporin has been reported as having poor efficacy in HS in patients receiving doses up to 5mg/kg day (486). Doses of 6mg/kg have shown some improvement in HS but relapse on discontinuing the ciclosporin and side effects make it an unpopular option in HS (487–489).

Sirolimus

Sirolimus, a mammalian target of rapamycin (mTOR) inhibitor, has been reported to be effective in one case series of 9 patients as combination rescue therapy with a TNF- α inhibitor in severe, refractory HS (490).

1.7.5 Surgery for HS

Evidence for surgical management of HS is mainly based on case series and reports. Incision and drainage is often performed to give rapid relief of acute lesions but

recurrence usually occurs (491). Deroofing is associated with less recurrence and can be performed on localised HS (492). Seton suturing of tunnels and fistulae is well tolerated and has shown some benefit for perianal disease in HS, but there is little evidence of its efficacy in the literature, in particular for axillary disease (415,493). Wide excision is recommended in those with scarring, and tunnel formation with lower recurrence rates compared to marginal excision (491). With regard to reconstruction practices, recurrence rates in one study were 22% with primary intention healing, 11% with secondary intention healing, and 2% each with flaps and grafts in a systematic review of the literature (494). Combination therapy with biologic therapy is recommended to prevent higher recurrence rates (495).

1.7.6 Laser, Light and Radiation Therapy for HS

Neodymium-doped yttrium-aluminium-garnet (Nd:YAG) laser was trialled in studies and case reports showing efficacy in HS (496). CO₂ lasers have been used in the excision of affected skin with positive outcomes (497–503). Long-pulsed alexandrite, diode lasers and intense pulsed light has been reported to be effective in causing follicular destruction and improvement in HS in case reports (504–507). Both topical and intralesional photodynamic therapy has been trialled in several series in HS with variable results (508–510). External beam radiation has shown equivocal results in the literature and thus is not recommended routinely in HS but may be an option in severe recalcitrant HS not suitable for surgery (511).

1.7.8 Wound dressings

Evidence on wound care in HS is limited. Absorptive dressings are most often used in HS but these can be costly (512). A prospective study found some benefit to using gentamicin-collagen sponges over primary closure in 124 patients, however recurrence and complication rates were similar at 3 months (513). Manuka honey with silver alginate dressings, hydrofiber, and silastic foam dressings were also found to be well tolerated by patients in 2 studies (514,515). Negative-pressure wound therapy has been used with success in surgical wounds in HS to shorten healing time and as a bridge to skin grafting or use of a dermal regeneration template (Integra®)(516–518). Several studies are in progress to determine ideal wound care in HS (519).

1.8 The Microbiome in HS

1.8.1 The Human Microbiome

The microbiome is defined as ‘the collective genetic information contained within the microbiota, including bacteria, viruses and fungi, residing in and on the human body’ (520). The microbiome and its links to health and disease is an area of rapidly expanding research. The microbiome varies from person-to-person; however, the overall functional characteristics and higher-level taxonomy is largely preserved in health (521). Factors which impact the microbiome composition include vertical mother-to-infant transmission of the microbiome (via vaginal mode of delivery at birth and breastfeeding), host genetics, ageing, diet, ethnicity, medications, and lifestyle factors such as smoking (520,521).

The gut microbiota contributes to host defence via its influence on the maturation of the immune system, however, in some susceptible groups the gut microbiota can lead to inflammation (522). Variant microbe populations in the gut have been described in many disease states including inflammatory bowel disease, colorectal cancer, Type-2 diabetes, and rheumatoid arthritis (521). However, causal relationships for many of these associations have not been proven, and the question remains whether this is ‘cause or effect?’(520). Nevertheless, describing the gut microbiome in disease states may provide therapeutic options to improve health. Examples of this includes the successful use of healthy donor faecal transplants in patients with *Clostridioides difficile* infection as a consequence of antibiotic use, to restore intestinal microbial diversity and reduce inflammation (523).

The human skin is the body's largest organ and is a physical and immunological barrier against external agents (524). Human skin is colonised by countless microorganisms, most of which are harmless or sometimes beneficial (524,525). The innate and adaptive immune systems play key roles in determining skin microbiome composition and homeostasis; however, a bidirectional relationship exists with the microbiota also informing the immune system (524,526). Studies profiling the healthy skin microbiome have been undertaken (527). The skin is colonised by a diverse microbiota, which varies greatly across and within individuals, dependent on anatomical site, and host and environmental factors such as temperature, humidity, antibiotic use, soaps, cosmetics, and UV exposure (528). Abundant microbes are found in moist skin areas, with *Staphylococcus* and *Corynebacterium* found preferentially in these areas (524). Sebaceous areas are colonised with more *Cutibacterium acnes*, and dry sites have a diverse microbial composition (524). Some skin diseases are associated with an imbalance in the skin microbiome, for example the overabundance of *C. acnes* seen in acne vulgaris, and treatment of dysbiosis can be effective in treating the disease (528).

Early studies on skin and gut microbiota in disease used culture-based methods which underestimate the total microbial diversity, as easily cultured bacteria were favoured (529). As sequencing technology has advanced, our understanding of the microbiome is greatly improved, and the complete diversity of the microbiome can be captured using sequence variation in conserved taxonomic markers to identify microbes. In our study we will focus on bacteria, and thus 16S ribosomal RNA (rRNA) gene sequencing will be used.

1.8.2 The Skin Microbiome in HS

Several attempts to profile the skin microbiome in HS has been undertaken, with more recent studies suggesting its potential role in the pathogenesis of HS (530,531). It is hypothesized that HS may be initiated by an abnormal immune response to bacteria in the skin which are released after follicular rupture, promoting inflammation via toll-like receptors, NOD-like receptors and the inflammasome (526). The majority of studies on the skin microbiome in HS utilised aerobic and anaerobic culture techniques on swab, aspirate or biopsy samples (532–545). These studies often noted a high proportion of sterile samples and *Staphylococcus aureus*, coagulase-negative *Staphylococcus*, gram-positive cocci, and Enterobacteriaceae dominated (532–545). Next generation sequencing techniques were introduced in recent years targeting pooled amplicons of 16S and 18S ribosomal RNA demonstrating a previously undiscovered microbiome alteration in the affected and non-affected skin of patients with HS compared to controls which has expanded our knowledge of the microbiota role in the pathogenesis of HS (546). *Porphyromonas*, *Prevotella*, and *Corynebacterium* were found in abundance (546). Reduced levels of *Cutibacterium acnes* was noted, as well as reduced coagulase-negative staphylococci (159,547,548). *C. acnes* is a beneficial bacterium, which helps to maintain a low skin pH (via the release of free fatty acids), and as a commensal it blocks colonisation by pathogenic *Staphylococcus aureus* and Streptococci (525). However, elevated levels of *C. acnes* appear to be pathogenic in acne vulgaris (163). Extensive bacterial biofilm formation is also seen in the chronic lesions of the disease, in particular in the sinus tracts (530).

Of note, only three of these studies on the skin microbiome in HS had matched control groups (546–548). Furthermore, only six of these studies used skin biopsies

or deep swabs during CO₂ laser ablation or deroofting procedures to describe the microbiome in HS, with superficial sampling with swabs or aspirates of lesions the most common method of sample collection (530,533,536,540,545,546,549).

Acquiring an accurate and representative sample of the microbiome of the skin is challenging and approaches adopted include swabbing, tape stripping, skin biopsies and scraping. Swabbing is the easiest and least invasive approach, however, it may not represent the microbiome of the deeper skin layers. The addition of skin scraping with swabbing increases yield and this is the approach we will adopt in this study.

Biopsies are most likely the best approach to profile the microbiome as they provide all layers of skin, however, they result in scarring and thus are generally taken during surgical treatment of HS in the literature (533,536). Tape stripping and pore stripping can be helpful in sampling the superficial and follicular microbiome. Grice et al. compared these sampling techniques and found similar microbial populations regardless of sampling method used, however Prast-Nielsen showed that biopsy specimens were superior to swabs (550,551).

Although bacteria appear to play a key role in the development of HS, HS is not a primary infectious disease, as evidenced by the low rates of cellulitis and lymph node enlargement, and the response of HS to immunosuppression (160,552). A matter for debate, however, is how antibiotic therapy works in HS, whether it is via its anti-inflammatory or anti-microbial effect.

This study of the skin microbiota in HS will add to the expanding literature in this area using next generation sequencing with a control to further elucidate the alterations seen and characterise their role in HS pathogenesis and propagating inflammation.

Alterations in the cutaneous microbiome in the studies of patients with HS are listed in Table 3.

Table 3: Skin microbiome in HS in culture and next generation sequencing studies

Methods used	Study	Samples taken	No of patients	Control group	Results
Culture studies	Highet et al. (1988):(532)	Swabs from perineum	32	No	<i>Streptococcus milleri</i> , <i>S. aureus</i> & anaerobic streptococci
	Jemec et al. (1996):(535)	Lesion aspirates from axilla, inframammary and genital area	41	No	<i>S. epidermidis</i> , <i>S. aureus</i> & anaerobes
	Brook et al. (1999):(553)	Lesion aspirates and swabs from axilla	17	No	<i>S. aureus</i> , <i>Prevotella melaninogenica</i> , <i>Peptostreptococcus</i> , <i>Streptococcus pyogenes</i>
	Lapins et al. (1999):(533)	Biopsies and swabs post CO ₂ laser ablation from axillae and perineum	25	No	<i>S. aureus</i> , <i>Prevotella</i> , <i>Peptostreptococcus</i> , <i>C. acnes</i> , <i>Lactobacillus</i> , <i>Bacteroides</i> , group c streptococci, <i>Enterobacteriaceae</i>
	Sartorius et al. (2012):(536)	Biopsies post CO ₂ laser ablation from axilla and groin	10	No	Coagulase-negative staphylococcus, anaerobes & <i>Corynebacterium</i>
	Matusiak et al. (2014): (537)	Swabs from axilla and perineum	69	No	<i>S. aureus</i> , <i>S. epidermidis</i> , <i>Proteus mirabilis</i> , & <i>Enterococcus faecalis</i>

	Katoulis et al. (2015):(540)	Lesion aspirates from axilla, breast, perianal, groin, buttocks, and scalp	22	No	<i>Staphylococcus & P. mirabilis</i>
	Hessam et al. (2016):(539)	Swabs from axilla, groin, gluteal cleft, and perineum	113	No	<i>S. aureus, P. mirabilis, E-coli, & Coagulase-negative staphylococcus</i>
	Thomas et al. (2016):(538)	Samples taken from neck, occiput, chest, face, axilla, breast, groin, perineum, gluteal cleft and perianal area, and genitals	76	No	<i>S. aureus, Prevotella, Corynebacterium, & S. epidermidis</i>
	Nikolakis et al. (2017):(544)	Swabs from axilla, breast, inguinal area, buttock and perianal area	50	No	<i>S. aureus</i> , coagulase-negative staphylococci, streptococci, Enterobacteriaceae
	Bettoli et al. (2018):(542)	Swabs from axilla, groin & perianal area	137	No	<i>S. epidermidis, S. haemolyticus, Proteus, E-coli, Streptococcus agalactiae</i>
	Jamalpour et al. (2018):(543)	Swabs from axilla, groin, scalp, neck, buttock, breast and perianal area	26	No	<i>S. aureus, E-coli & diphtheroids</i>

	Benzecry et al. (2018):(541)	Swabs from axilla, breast, groin, genitals, perineum, and buttocks	46	No	Staphylococcus, Streptococcus, Corynebacterium & Enterobacteriaceae
	Barmatz et al. (2022):(554)	Samples from genitalia, gluteal/perianal area, and axilla	97	No	Enterobacterales and coagulase-negative staphylococci higher in those prescribed antibiotics in community
Culture & Next Generation Sequencing (NGS)	Guet-Revillet et al. (2014):(545)	Swabs, aspirates, and biopsies from axilla, breast, trunk and neck, gluteal cleft, buttocks, and inguinal crease	82	No	<i>Staphylococcus lugdenesis</i> , actinomycetes, milleri group streptococci, anaerobes
Next Generation sequencing (NGS)	Ring et al. (2017):(546)	Biopsies of affected and unaffected skin groin and axilla	30	Yes – 24 controls	<u>Increased</u> <i>Corynebacterium</i> , <i>Porphyromonas</i> , & <i>Peptoniphilus</i> compared to controls <u>Decreased</u> <i>Cutibacterium acnes</i>
	Guet-Revillet et al. (2017):(549)	Swabs, aspirates and biopsies from affected areas – axilla, inguinal fold, buttocks and breast, and swabs of unaffected areas	65	No	<i>Prevotella</i> , <i>Porphyromonas</i> , anaerobes, <i>Fusobacterium</i> & <i>Parvimonas</i>
	Ring et al. (2019):(530)	Swabs of HS tunnels during derroofing of axilla and groin	32	No	<i>Prevotella</i> , <i>Porphyromonas</i> , & <i>Corynebacterium</i>

	Naik et al. (2020):(548)	Swab from axilla, gluteal cleft, and inframammary fold	12	Yes – 5 controls	<u>Increased</u> Anaerobes <u>Decreased</u> <i>C. acnes</i>
	Riverain-Gillet et al. (2020):(547)	Swabs of unaffected axilla, inguinal crease and gluteal cleft	60	Yes -17 controls	<u>Increased</u> anaerobes, <i>Prevotella</i> , <i>Actinomyces</i> , <i>Campylobacter ureolyticus</i> , & <i>Mobilinucus</i> <u>Decreased</u> <i>S. epidermidis</i> , <i>S. hominis</i> , <i>C. acnes</i> & coagulase-negative staphylococci
	Lam et al. (2021): (555)	Swabs of axilla	6	7	

1.8.3 The Gut Microbiome in HS

There are limited studies on the gut microbiome in HS (236,556). As discussed previously, HS is associated with many other disease states, including spondyloarthritis, inflammatory bowel disease (IBD), and metabolic syndrome, and an altered gut microbiome has been associated with these conditions (56,219,224,247,557–562). In Crohn's disease shifts in gut microbiota composition, in a genetically susceptible individual, are associated with a dysregulated immune system resulting in inflammation (563,564). Manipulation of the gut microbiota in IBD is a focus of current research, with the aim of reducing inflammation (240). We hypothesize that similar shifts in the gut microbiome exist in patients with HS, and could result in the immune dysregulation seen, leading to skin inflammation (564). Thus, exploration of the gut microbiome in HS is of interest, particularly as it may inform future therapies.

Three other studies on the gut microbiota composition in HS have been carried out (236,556). Eppinga et al. characterised the gut microbiome using taxon-specific quantitative polymerase chain reaction (PCR) in 17 patients with HS, 17 patients with HS and IBD, 29 patients with psoriasis, 31 patients with IBD, 13 patients with IBD and psoriasis, and 33 controls (235). In psoriasis, IBD, psoriasis and IBD, and HS and IBD groups lower abundance of the anti-inflammatory bacterium *Faecalibacterium prausnitzii* was found, with an increased relative abundance of pathogenic strains of *Escherichia coli* (556). This altered microbiome was not noted in the patients with HS alone (556). Kam et al. profiled the gut microbiome in 3 patients with HS and compared to 3 healthy controls (236). Increased levels of *Bilophila* and *Holdemanella* were found, with lower relative abundance of Firmicutes, Lachnobacterium, and Veillonella in patients with HS when compared to controls

(236). Lam et al. profiled the gut microbiome in 17 patients with HS and 20 healthy controls, and the axillary skin microbiome from 6 patients with HS and 7 healthy controls via 16S ribosomal RNA amplicon sequencing (555). No difference in bacterial richness ($p=0.483$), Shannon ($p=0.082$) and inverse Simpson ($p=0.916$) indices nor in bacterial community structure was seen (555). No differences in α - and β - diversity were found in this study.(555) *Robinsoniella* was found in the majority of HS patients (59%) and in none of the healthy controls, and could be a potential pathogen (555,565). *Sellimonas* was also more common in patients with HS than in controls and overabundance of *Sellimonas* has also been found in the gut microbiome of patients with rheumatoid arthritis and ankylosing spondylitis (555,566,567). *Christensenellaceae* was depleted in faeces of patients with HS, a phenomenon which has also been described in psoriasis (555,568). No differences were found in this study in α - and β - diversity of skin samples, however *Mesorhizobium* (a soil and environment microbe) was present in all affected skin samples (555). A recent study in 2022 has described a shift in gut microbiota composition, function, and metabolic profile after adalimumab therapy and has been discussed previously (364). Baseline gut microbial samples showed reduced alpha-diversity with a shift towards control samples after 12 weeks of adalimumab therapy with no differences noted between the two groups (364). At baseline HS patient had reduced Firmicutes and Euryarchaeota, and increased Actinobacteria and Bacteroidetes, with higher abundance of *Ruminococcus bromii* and *Coprococcus eutactus* in healthy controls (364). After Adalimumab therapy *Bifidobacterium*, *Bacteroides*, *Agathobacter*, *Prevotella_9*, *Faecalibacterium*, and *Blautia* were noted in the gut microbiota of patients with HS (364).

To date the nasal and oral microbiome have not been described in HS.

1.8.4 Peripheral Blood Bacteria in HS

A study by Ring et al. did not demonstrate a peripheral bacteraemia in 27 patients with moderate to severe HS compared to 26 healthy controls via Next Generation 16s rRNA gene Sequencing (NGS)(569).

1.9 Outline of Thesis

As discussed above, HS is a chronic, debilitating disease which can prove challenging to treat, and which has a significant impact on quality of life. In **Chapter 2** I sought to examine the limited placebo controlled trials to date in HS and the heterogeneity of outcome measures used, and to assess the placebo response rate in these trials in an attempt to determine true drug efficacy. Knowledge of placebo response will be vital in clinical trial design of microbiota based interventions in HS in future, which is of particular interest to me. In **Chapter 3** I studied pain in a cohort of patients with HS, adherence to prescribed treatment, exercise patterns, and examined the impact of HS on quality of life. I also assessed correlations between levels of pain and physical activity, and impact on quality of life with measures of gut microbiota diversity. In **Chapter 4** I described the skin microbial composition in a cohort of patients with HS compared to healthy controls, to determine if a dysbiosis or an altered skin microbiome was noted which may contribute to disease pathogenesis. In **Chapter 5** I described the gut microbial composition in a cohort of patients with HS compared to healthy controls, to determine if a dysbiosis was noted which may contribute to disease pathogenesis and may provide a therapeutic target. In **Chapter 6** I described the inflammatory markers, faecal calprotectin and serum C5a levels, in a cohort of patients with HS and correlated these to microbiota diversity. Finally in **Chapter 7** I described the diet of a cohort of patients with HS and its relationship to the gut and skin microbiome, inflammatory markers and clinical characteristics. I compared the habitual diet of those with HS to healthy controls and patients with Crohn's disease.

2. Placebo Response Rates in Hidradenitis Suppurativa

Abstract publication in the British Journal of Dermatology, 2016

A review of the placebo-controlled trials in hidradenitis suppurativa. S. McCarthy, D. Sheehan, M. Murphy, F. Shanahan (2016), Bristol Cup Posters. Br J Dermatol, 175: 25-78.

Presentation at British Association of Dermatologists Annual Meeting, 2016 and Irish Association of Dermatologists Spring Meeting, 2016

Abstract

Background

Knowledge of placebo effect is important in evaluating therapies and in planning future clinical trials. Patients with hidradenitis suppurativa (HS) experience clinical improvement without medical intervention, as in many other chronic inflammatory diseases. Due to the relapsing remitting nature of HS placebo response is likely to be high. Knowledge of placebo response will be vital in planning future microbiota based interventional trials in future.

Aim

The aim of this study was to review the literature to describe the placebo response rates in the controlled trials of hidradenitis suppurativa.

Methods

A search for placebo-controlled, randomised controlled trials (RCT) of interventions for hidradenitis suppurativa was undertaken and placebo response rates documented.

Results

The placebo rates across the studies varied greatly (range 0 to 30%). There was a significant trend for higher response rates to be associated with higher placebo rates (P-value < 0.05). Placebo rates were dependent on the scoring system used to assess severity of disease.

Conclusion

The placebo response rate in clinical trials of hidradenitis suppurativa was variable. The use of standardised validated outcome measures to assess response is essential in the future trials of hidradenitis suppurativa to compare efficacy of systemic treatments as well as placebo response.

2.1 Introduction

Knowledge of placebo response rates is important in evaluating therapies and for the design of further therapeutic trials. Studies of placebo effects in medical trials of inflammatory conditions indicate significant clinical improvement occurs in approximately 30% of patients in inactive treatment groups, and modulate active treatment outcomes (570–572). The determinants of the placebo-response are varied but include the natural history of the disease, the behaviour of clinicians, cognitive emotional biases, and the study design (570). Placebo response can be a result of the patient's expectations and beliefs about a beneficial outcome, and optimised doctor-patient relationships in the setting of a trial. Furthermore, since the natural history of chronic inflammatory diseases is characterised by recurring periods of relapse and remission, this can have a profound influence on the results of therapeutic trials. Knowledge of the impact of placebo response and its determinants can improve clinical trial design, and of particular interest to us in the design of microbiota based interventions in future. When assessed in terms of remission and response, the placebo rates for inflammatory bowel disease have been estimated at 18-19% for Crohn's disease, and 13-28% for ulcerative colitis (573,574). Similarly, mean improvements of 14-28% were reported in the placebo limbs in treatment trials for atopic dermatitis, with lower placebo response rates of ~4% in psoriasis (575,576).

Hidradenitis suppurativa is a debilitating chronic inflammatory disease characterised by recurrent abscesses in flexural sites including the axilla, groin, and inframammary area. Progress in hidradenitis suppurativa research and treatment has been limited, in part, by disease heterogeneity but also by insufficient knowledge of placebo rates and its implication on sample size and study design. Furthermore, a standardised

definition of clinical response in hidradenitis suppurativa is lacking and has resulted in significant heterogeneity between the primary and secondary outcome assessments used in HS studies (15).

Here, we review the placebo response rates in the published controlled trials in hidradenitis suppurativa.

2.2 Methods

Literature search

A search of PUBMED/MEDLINE, EMBASE, and the Cochrane Central Register of Controlled Trials (CENTRAL) was performed. Placebo-controlled, randomised controlled trials (RCT) of interventions for hidradenitis suppurativa were included. The literature search used the following combination of terms ‘hidradenitis suppurativa’, ‘acne inversa’, ‘placebo’, ‘placebo-controlled’, ‘double-blind’, ‘randomised-controlled trial’ and ‘clinical trial’.

Selection criteria

Studies were included for analysis if all the following criteria were fulfilled: 1. the study was a placebo-controlled trial, 2. all patients in the study had active disease at entry, 3. the active treatment was a systemic therapy, 4. the study reported the methodology of defining clinical response and 5. data on response or remission in patients receiving placebo was available. Ten RCT were identified (18,21,143,144,192,316,366,380,577). Eight were eligible for inclusion to the review (18,21,143,144,192,380,577). One trial was excluded because a topical therapy was used (316) and another was excluded because the placebo response was not

documented (366) and unavailable from the authors on request. We assessed the intervention response rate and the placebo-response rate in each study.

Data abstraction

Data abstraction was performed by two independent reviewers (SM and MM). Data abstracted included study design, outcome measures employed, sample size of active and placebo groups, duration of follow up and response rates.

Statistical analysis

Statistical analysis was carried out using R software (2019 r-project.org).

2.3 Results

Eight studies were included in this review (18,21,143,144,192,380,460). These studies used varying outcome measures to determine response. Characteristics of studies, outcome measures used, and placebo response rates are shown in Table 1. The components of the outcome measures used are summarised in Table 2.

Table 1: Characteristics of studies containing placebo response data

Authors	Year	Active Treatment size (N)	Placebo size (N)	Active Therapy	Follow up to placebo response	Outcome measures used and definition of response		Active Treatment Response rate	Placebo response rate	<i>p-value</i>
Grant et al.:(21)	2010	15	18	Infliximab (5mg/kg week 0,2,6)	8 weeks	1°:	50% decrease in HSSI	~27%	5.6%	0.092
						2°:	25-50% decrease in HSSI	60%	5.6%	<0.001
							Mean PGA	~1.7	~4.6	<0.001
							Mean change in DLQI	-10	~-<2	0.03
							Mean change in VAS for pain	-39.8	-0.6	<0.001
							Mean change in ESR	~ -12	~ +6.0	0.012
							Mean change in CRP	-1.0	~ + 0.4	0.062

Miller et al.:(144)	2011	15	6	Adalimumab 80mg at baseline then 40mg alternate weeks	12 weeks	1°:	Mean change in Sartorius	-11.27	+ 5.83	0.074
							Mean change in Hurley score	-0.13	0	0.4
						2°:	Mean change in % of days with lesions	-38.89	-32.14	0.4
							Mean change in VAS for pain	-13.4	+3.17	0.4
Kimball et al.:(18)	2012	103	51	Adalimumab 40mg weekly or 40mg EOW	16 weeks		Mean change in DLQI	-3.67	+1.00	0.06
						1°:	HS-PGA with at least a 2-grade improvement relative to baseline	EOW 9.6% Weekly 17.6%	3.9%	EOW 0.25 Weekly 0.025
						2°:	HS-PGA OF Clear/Minimal/Mild %	EOW 21.2% Weekly 49.0%	23.5%	0.004 (vs. weekly)
							Mean % improvement from baseline: Inflammatory nodules	EOW 30.4% ± 11.8 Weekly 43.3% ± 11.9	13.2% ± 12.9	0.089 (vs. weekly)

							Mean % improvement from baseline: Abscesses	EOW 54.3% ± 13.8 Weekly 58.2% ± 16.6	26.9% ± 14.3	0.0152 (vs. weekly)
							Mean % improvement from baseline: Draining fistulae	EOW 13.5% ± 25.3 Weekly 31.1% ± 26.3	-25.1% ± 30.4	0.166 (vs. weekly)
						Mean change from baseline ± SE	Modified Sartorius Score	EOW -32.0 ± 9.5 Weekly - 40.2 ± 9.8	17.2 ± 9.8	0.097 (vs. weekly)
							DLQI	EOW -3.2 ± 0.8 Weekly - 6.3 ± 0.9	-2.3 ± 0.9	0.001 (vs. weekly)
							TWPI	EOW -4.3 ± 3.2 Weekly - 18.4% ± 4.1		<0.001 (vs. weekly)
							PHQ-9	EOW -1.3 ± 0.8 Weekly - 3.7 ± 0.8	-0.9 ± 0.8	0.015 (vs. weekly)

Kimball et al. – 2 studies: (143)	2016	PIONEER I- 153	PIONEER I - 154	Adalimumab 160mg SC week 0, 80mg week 2, then 40mg weekly from week 4	12 weeks	1°:	Achieving positive HiSCR	41.8%	26.0%	0.003
						2°:	Total abscess and inflammatory nodule count of 0,1,2 %	28.9%	28.6%	0.96
							≥ 30% reduction and ≥1 unit reduction in skin pain	27.9%	24.8%	0.63
							Change in mean Modified Sartorius Score from baseline	-24.4	-15.7	0.12
		PIONEER II-163	PIONEER II - 163	Adalimumab 160mg SC week 0, 80mg week 2, 40mg weekly from week 4	12 weeks	1°:	Achieving positive HiSCR	58.9%	27.6%	<0.001
						2°:	Total abscess and inflammatory nodule count of 0,1,2 %	51.8%	32.2%	0.01
							≥ 30% reduction and ≥ 1 unit reduction in skin pain	45.7%	20.7%	<0.001
							Change in mean Modified Sartorius Score from baseline	-28.9	-9.5	<0.001
Tzanetakou et al.:(192)	2016	9	10	Anakinra (IL-1RA)	12 weeks	1°:	HiSCR	78%	30%	0.04
							Disease activity	67%	20%	0.04

				100mg SC daily						
							Sartorius score	~0%	~0%	
						2°:	Time to new exacerbation			0.01
Kanni et al.:(380)	2018	10	10	MABp-1 (anti- IL-1a) 7.5mg/kg IV every 14 days	12 weeks	1°:	Achieving positive HiSCR	60%	10%	0.035
						2°:	VAS for pain	70%	30%	
							Time to new exacerbation	11 weeks	7 weeks	0.159
							Decrease in at least 2 of: PGA, Disease activity, Modified Sartorius Score, VAS for pain, & DLQI)	80%	40%	0.054
							20% decrease of total lesion depth	22.2%	77.8%	0.027
Vossen et al.:(577)	2018	15	5	Apremilast PO 30mg twice daily	16 weeks	1°:	Achieving positive HiSCR	53.3%	0%	0.055
						2°:	Mean change AN count	-2.0 (-3.9 to -0.5)	2 (-0.8 to 4.8)	0.011
							Mean change DLQI	-2.3 (-5.9 to 1.3)	4.2 (-1.7 to 10.1)	0.230
							Mean change NRS for pain	-0.8 (-2.2 to 0.6)	2.2 (-0.1 to 4.5)	0.009
							Mean change NRS for itch	-1.1 (-2.5 to 0.3)	3.4 (0.1 to 4.7)	0.015

							Mean change NRS for disease burden	-1.0 (-2.3 to 0.3)	0.9 (-1.2 to 3)	0.049

AN: Abscess/Nodule; CRP: C-reactive Protein; DLQI: Dermatology Life Quality Index; EOW: every other week; ESR: Erythrocyte Sedimentation Rate; HiSCR: Hidradenitis Suppurativa Clinical Response; HSSI: Hidradenitis Suppurativa Severity Index; HS-PGA: Hidradenitis Suppurativa Physician's Global Assessment; IV: Intravenous; NRS: Numeric rating scale; PHQ-9: Patient Health Questionnaire-9; SC: Subcutaneous; TWPI: Total Work Productivity Index; VAS: Visual Analog Scale for pain

Table 2: Primary outcome measures in placebo-controlled trials in hidradenitis suppurativa

<u>Outcome measure</u>	<u>Studies</u>	<u>Assessment to determine efficacy</u>
Hidradenitis Suppurativa Severity Index (HSSI)	Grant et al.(21)	Composite score ranging from 0-19 - Assessing number of sites involved, percentage body surface involved, number of erythematous and painful lesions, number of dressing changes during working or leisure hours and pain on visual analog scale
Hurley Stage	Miller et al.(144)	Stage I = single or multiple abscesses Stage II = recurrent abscesses, sinus tract formation and scarring. Single or multiple lesions, widely separated Stage III = Diffuse involvement of entire area, multiple interconnected tracts and abscesses
Sartorius Score	Miller et al.(144)	Assessing anatomical regions involved, distance between lesions, and scoring individual lesions.
HS-Physicians Global Assessment (HS-PGA)	Kimball et al. (2012)(18)	Clear Minimal = presence of non-inflammatory nodules Mild = <5 inflammatory nodules or 1 abscess/fistula Moderate = ≥ 5 inflammatory nodules 1 abscess or draining fistula and ≥ 1 inflammatory nodule 2-5 abscesses or draining fistulas and <10 inflammatory nodules Severe = 2-5 abscesses or draining fistulas and ≥ 10 inflammatory nodules Very severe = >5 abscesses or draining fistulas
HS Clinical Response (HiSCR)	Tzanetakou et al.(192) Kimball et al. (2016)(143) Kanni et al.(380) Vossen et al.(460)	Achieving at least a 50% reduction from baseline in abscess and inflammatory nodule count with no increase in abscess/fistula counts

Outcome measures used

Five different primary outcome measures were used in the studies. The Hidradenitis Suppurativa Severity Index (HSSI)(21), and Hurley score(16,144) were used in one study each. Sartorius scoring(17,144,192) and Physician's global assessment in hidradenitis suppurativa (HS-PGA) were used in two studies each(18,21). The hidradenitis suppurativa Clinical Response score (HiSCR)(20) was the most commonly used, in the five more recent studies on hidradenitis suppurativa(143,192,380,577).

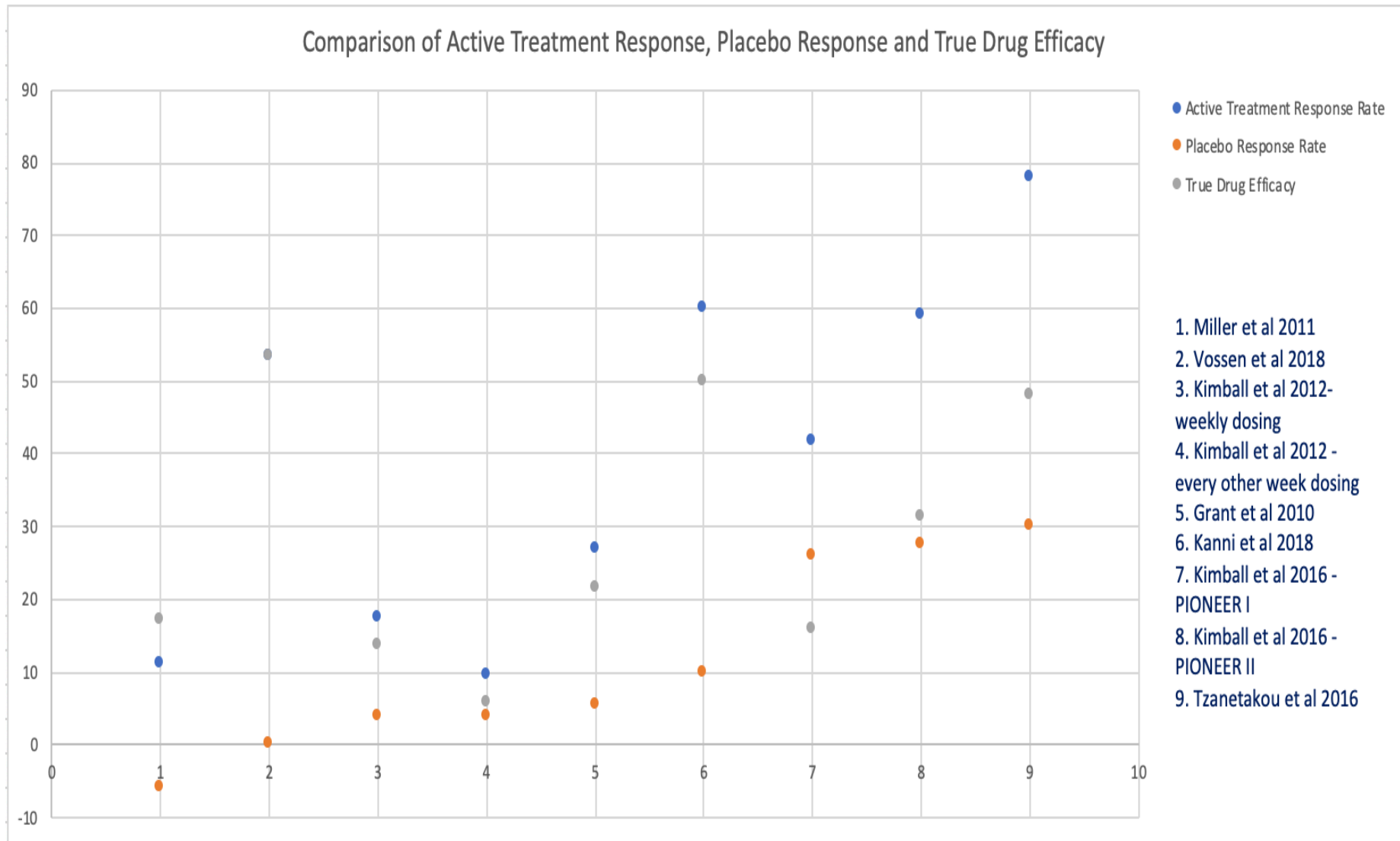
Interventions studied

Most of the interventions were biologics (6/7) with one systemic agent (1/7). Five studies compared the use of TNF-alpha inhibitors to placebo (18,21,143,144). Two agents targeted IL-1, one study comparing anakinra (anti IL-1)(192) to placebo and the other MABp1 (anti IL-1a)(380) to placebo. One study assessed response to the phosphodiesterase-4 inhibitor apremilast (577).

Placebo response rate

With significant heterogeneity among studies, the placebo rates across the studies varied from 0% to 30%. There was a significant trend for higher response rates to be associated with higher placebo rates (P-value < 0.05) when both sets of values from the Kimball et al. 2012 and the Kimball et al. 2016 studies were included (Figure 3).

Figure 3: Comparison of the active treatment response rate, placebo response rate and the true drug efficacy



The average estimate for the 5 lowest placebo response rate studies was 1.5 (+ 4.6) with an active response rate of 23.7 (+17.9). This compares to a placebo response rate of 23.4 (+9.1) with an active response rate of 59.7 (+14.8).

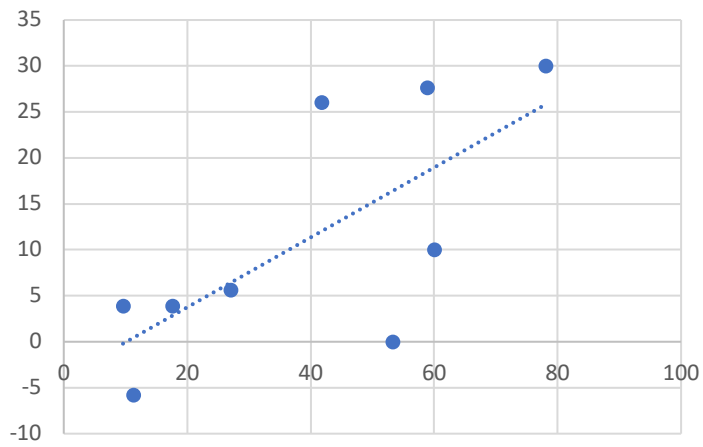
The true drug efficacy, as defined by the difference between the active and the placebo response, was calculated and investigated. There was no significant association between the placebo response rate and the true drug efficacy showing that a smaller placebo rate is not associated with a greater true drug efficacy (Figure 4b).

However, there was a strong association between a greater true drug efficacy and the active response rate ($P\text{-value} < 0.01$), showing that an increase in the active response rate was important to increase the marginal response in these studies (Figure 4c).

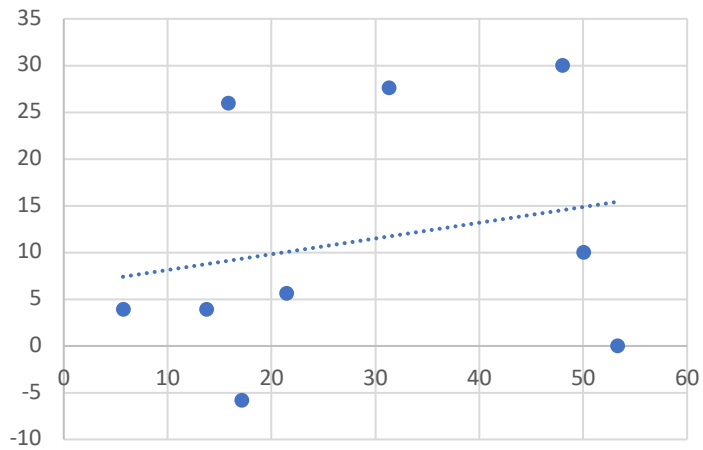
This was not statistically associated with study size, but it should be noted that the three studies with the highest true drug response rate are also three of the smaller studies.

Figure 4: (a) Association between placebo and active treatment response rate, (b) placebo response and true drug efficacy, and (c) the true drug efficacy and active drug response rate

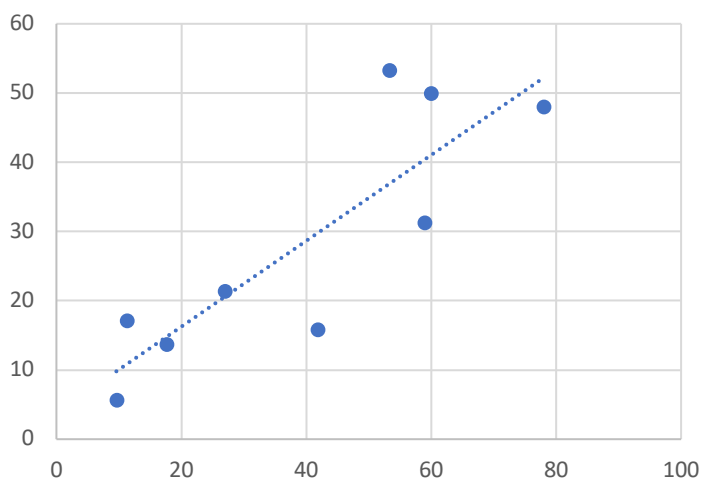
(a) Placebo / Active Response Rate



(b) Placebo / True Drug Response Rate



(c) True Drug / Active Response Rate



2.4 Discussion

Double-blind placebo-controlled randomised controlled trials are the gold standard when assessing efficacy of new therapies. The inclusion of a placebo arm is particularly important in inflammatory conditions such as hidradenitis suppurativa, which are characterised by intermittent periods of acute exacerbation alternating with remission. Knowledge of placebo response is important to inform both pharmacological and non-pharmacological treatment of disease (578). In several of these studies of HS, marked clinical improvement was noted in the placebo arm. Factors that influence the placebo response rate in inflammatory disease include the study duration, the number of study visits, disease severity at entry, and the definition of response (570,571). A longer study duration can stabilise or lower the placebo response over time. Higher disease severity at study entry can lead to a higher placebo response rate due to the natural fluctuation of the disease course. Cognitive and behavioural factors also influence the placebo response, with patient expectations of a response leading to higher placebo response rates, and clinical improvement often seen in those assessed regularly in the setting of a clinical trial. Outcome measures used to determine disease response should also be chosen carefully. Pain and depression scores used as outcome measures can be more susceptible to placebo effect than other methods, and assessment of pain, in particular, forms an integral part of evaluating disease response in HS (579). Setting the primary outcome measure to assess clinical response and the follow up period is of paramount importance in these studies. The lack of a standardised definition of clinical response in hidradenitis suppurativa has resulted in significant heterogeneity between the primary and secondary outcome assessments used (18,21,143,144,192,380,460). Rates of placebo response in the randomised

controlled trials of hidradenitis suppurativa included in this review ranged from 0 to 30% (18,21,143,144,192,380,460). There was a significant trend for higher response rates to be associated with higher placebo rates (P-value < 0.05). There was no significant association between the placebo response rate and the true drug efficacy showing that that a smaller placebo rate is not associated with a greater true drug efficacy. Variable results were also seen in reviews of placebo response in the clinical trials of ulcerative colitis (0-67%) and Crohn's disease (0-46%), as well as atopic dermatitis (14-28%)(573–575). Both active treatment, and placebo response is strongly influenced by the measure of outcomes. Heterogeneity of the outcome measures used leads to difficulty interpreting results and comparing studies. The development of the Psoriasis Area Severity Index (PASI) standardised the assessment of primary outcomes in psoriasis, with clear meta-analysis available to compare efficacy of systemic treatments as well as the placebo response (580); however, the study design and follow up period can still result in variability. There is a need for more stringent definitions of objective outcomes and follow up in the clinical trial design of future studies in hidradenitis suppurativa. Work by the HISTORIC (Hidradenitis Suppurativa cORe outcomes set International Collaboration) group of IDEOM (International Dermatology Outcome Measures group) aims to create robust objective and consistent outcome measures in HS RCTs going forward (581). These will include pain, quality of life measures, physical signs, global assessments, and progression of disease over time. Eligibility criteria for inclusion into studies is also an important factor in assessing active treatment and placebo response rates. The tendency to increase severity scores to ensure inclusion into clinical trials is well described, leading to 'eligibility creep' and resulting perceived improvement in both the active treatment and placebo arms on initial

assessment of response (582). Thus stringent application of inclusion criteria will also form an important part of study design. Knowledge of these issues in the clinical trials of HS to date, which is highlighted by the variation in placebo response, will strengthen study design in future clinical trials via the introduction of agreed standardised outcome measures, follow-up periods, and inclusion criteria. This is of particular interest to us in informing the clinical trial design of future microbiota based interventions in HS.

2.5 Limitations

Statistical pooling was limited in this review due to heterogeneity among studies and small sample sizes. Publication bias may occur such that studies showing significant response to treatment may be more likely to be published than those showing no difference.

2.6 Conclusion

In conclusion, the placebo response rate in clinical trials of hidradenitis suppurativa varied across different studies and was dependent on the method of scoring disease activity as well as the active response rate.

3. Pain, Quality of Life, Adherence to treatment, and Exercise in Hidradenitis Suppurativa

3.1 Pain and Hidradenitis Suppurativa

Data published as part of SHIP study, Journal of European Academy of Dermatology and Venereology, 2017

Delany E, Gormley G, Hughes R, **McCarthy S**, Kirthi S, Markham T, Tobin AM, Murphy M, Kirby B. A cross-sectional epidemiological study of hidradenitis suppurativa in an Irish population (SHIP). Journal of the European Academy of Dermatology and Venereology. 2018 Mar;32(3):467-73.

Presentation at European Academy of Dermatology and Venereology, September 2017 and Irish Association of Dermatologists Autumn Meeting, October 2017

Abstract

Hidradenitis suppurativa (HS) is a chronic inflammatory disease that affects apocrine-gland bearing skin and has a substantial impact on quality of life. To date, few studies have described the pain experienced by patients with HS and the management of pain associated with HS.

Patients aged ≥ 18 years with a diagnosis of HS confirmed by a consultant dermatologist were recruited. The level of pain experienced by patients was measured using the visual analogue scale (VAS; where 0=no pain and 10=worst pain possible) and EQ-5D-5L questionnaires. Additional information was collected on the use of analgesics in this population.

Pain was widely reported in 134 responders to the visual analog scale questionnaire. 110 (82.1%) reported some level of pain (score ≥ 1) and 48 (35.8%) reported a score ≥ 5 . In the EQ-5D-5L questionnaire, 118/145 (81.4%) responders indicated that they felt pain or discomfort, and 45/145 (31.0%) expressed “severe” or “extreme” pain/discomfort. The relationship between Hurley stage and EQ-5D-5L response on pain/discomfort was statistically significant ($p < 0.001$). 61/150 (40.7%) patients reported taking analgesics. A total of 99 pain medications were reported, of which 61 (61.6%) were over-the-counter medications

Many patients with HS experience considerable pain, which has a substantial impact on their quality of life. In general, patients with more severe disease reported greater pain and discomfort. It is therefore crucial that physicians and researchers be aware of the pain experienced by patients with HS, and that pain be included as a key outcome in future clinical trials.

3.1.1 Introduction

HS may lead to painful eruptions and malodorous discharge with a significant negative impact on quality of life. Few studies to date have investigated the pain experienced by patients with HS, and how this pain is managed (583). The SHIP study was a cross-sectional, epidemiological study of HS in an Irish population (34). The primary objective was to estimate the prevalence of HS at selected dermatology clinics in a hospital setting in Ireland. Secondary objectives included assessment of disease characteristics and various aspects of disease burden, including pain.

3.1.2 Methods

Data were collected from four dermatology clinics over a six-month period in 2015. A total of 15,547 patients attended these sites during the recruitment period, of whom 221 (1.4%) had a diagnosis of HS, and 150 (1.0%) formed the full analysis set (FAS). The severity of pain experienced by patients in the FAS was measured using the Visual analogue scale (VAS; where 0 = no pain and 10 = worst pain possible) and Euro Quality of Life Health Outcome Measure (EQ-5D-5L). Information was also collected on the use of analgesics in this population. Statistics were performed using Excel (version 16.65) and R (version 4.3.1).

3.1.3 Results

150 patients were recruited over a six-month period in the four centres in 2015. The average age of the patients was 37 years and the majority were female (105, 70%). The point prevalence of HS in this particular Irish population was estimated to be 1.4%. The mean Body Mass Index (BMI) was 32 (females 33, males 30). In this

population, 56% were smokers, while 22% were former smokers. The average smoking pack years was 17.0. The average alcohol consumption was 4.4 units per week (SD 6.41). Of note the majority of the patients were employed, however this population took a mean of 15.9 sick days in the preceding 12 months.

Table 1: Patient Socio-Demographics

Parameter	Mean	SD	N
Age at consent (years)	36.5	11.28	150
Female	35.3		105
Male	39.2		45
Height (cm)	167.82	10.362	150
Weight (kg)	91.18	24.536	148
BMI (kg/m²)	32.25	8.558	150
Female	33.07	9.168	105
Male	30.32	6.625	45
Gender			N (%)
Female			105 (70%)
Male			45 (30%)
Race			N (%)
White			143 (95.3%)
Black			1 (0.7%)
Asian			1 (0.7%)
Other			5 (3.5%)
Smoking and Alcohol			N (%)
Never smoked			33 (22.0%)
Smoker			84 (56.0%)
Former smoker			33 (22.0%)
Smoking pack years (for smokers and former smokers)	17	12.72	65

Alcohol consumption (units/week)	4.4	6.41	150
Work status			
Student			16 (10.7%)
Employed			76 (50.7%)
Unemployed			32 (21.3%)
Temporary Illness Disability			4 (2.7%)
Permanent Illness			10 (6.7%)
Other			12 (8.0%)
Sick Days in past 12 months	15.9	55.09	113

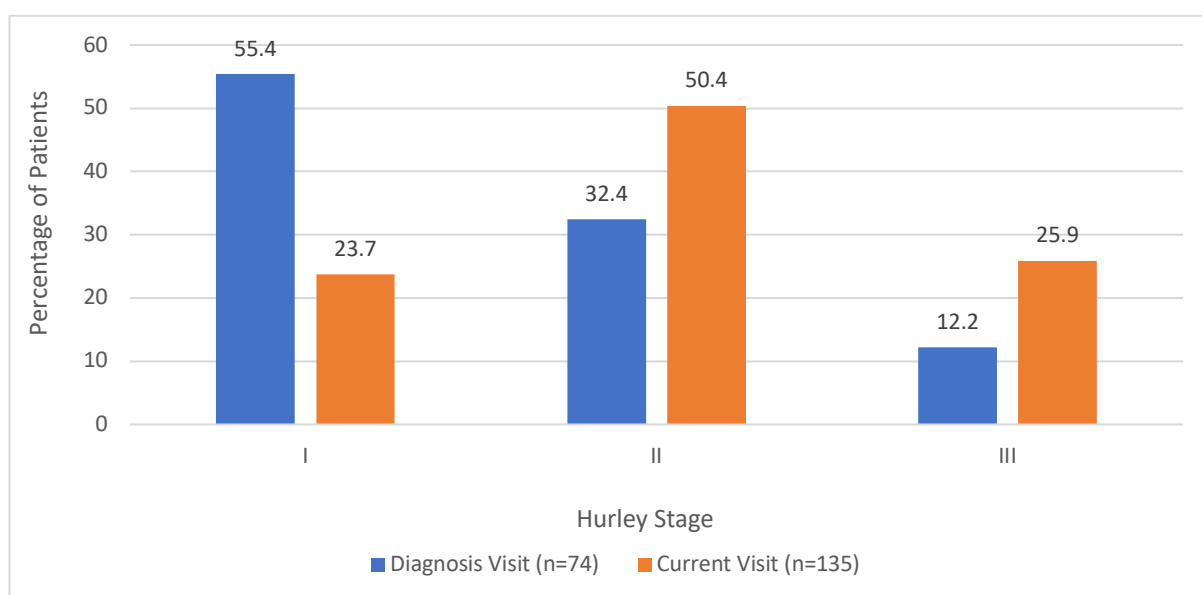
The mean age at diagnosis was 31.3 years and the mean duration of symptoms prior to diagnosis of HS was 8.49 years (SD 7.910). The average disease duration since diagnosis was 5.29 years (SD 7.246).

Table 2: Clinical profile of the study population

Parameter	Mean	SD	N	Missing
Age at time of diagnosis (years)	31.3	10.13	146	4
Female	29.6		104	1
Male	35.6		42	3
Duration of symptoms before diagnosis (years)	8.49	7.910	146	4
Female	8.67		102	3
Male	8.07		44	1
Duration of disease from diagnosis to study visit (years)	5.29	7.246	145	5
Female	5.66		103	2
Male	4.38		42	3

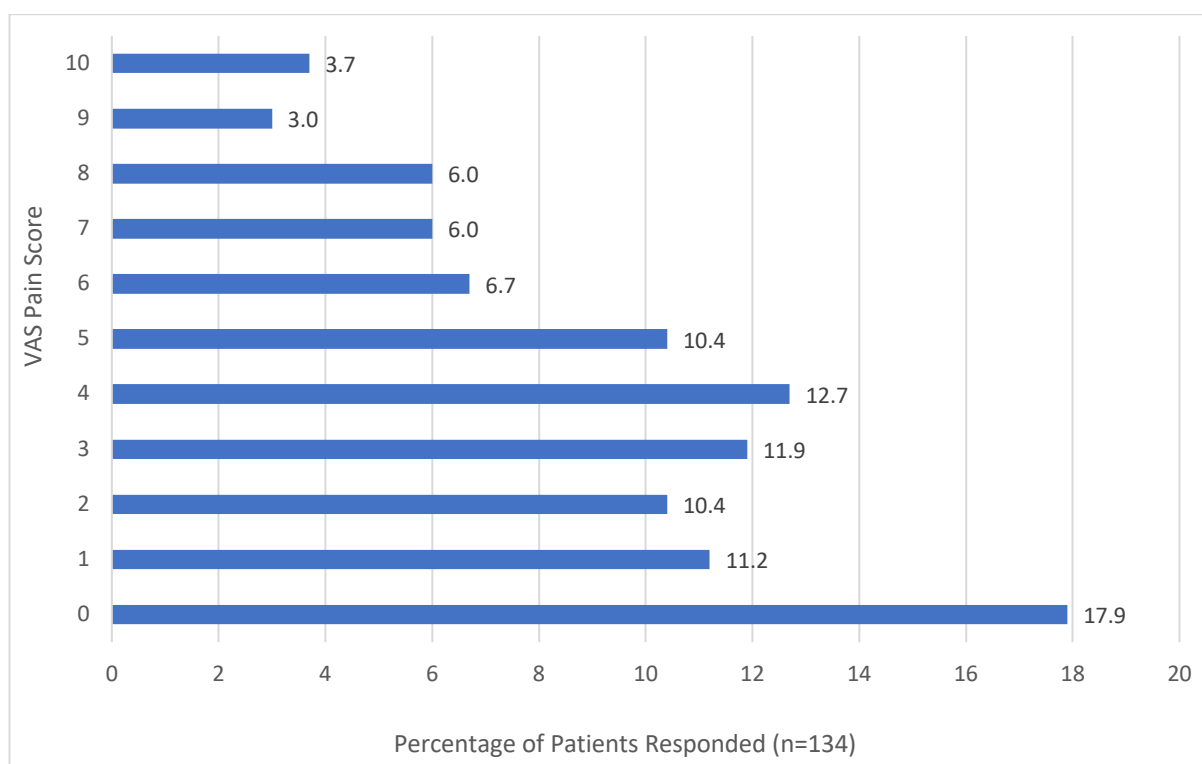
The majority of patients for whom data were available had Hurley stage I disease at the diagnosis visit (n=41; 55.4%). The majority had Hurley stage II disease at the study visit (n=68; 50.4%) (Figure 1).

Figure 1: Hurley Stage at diagnosis and at study visit



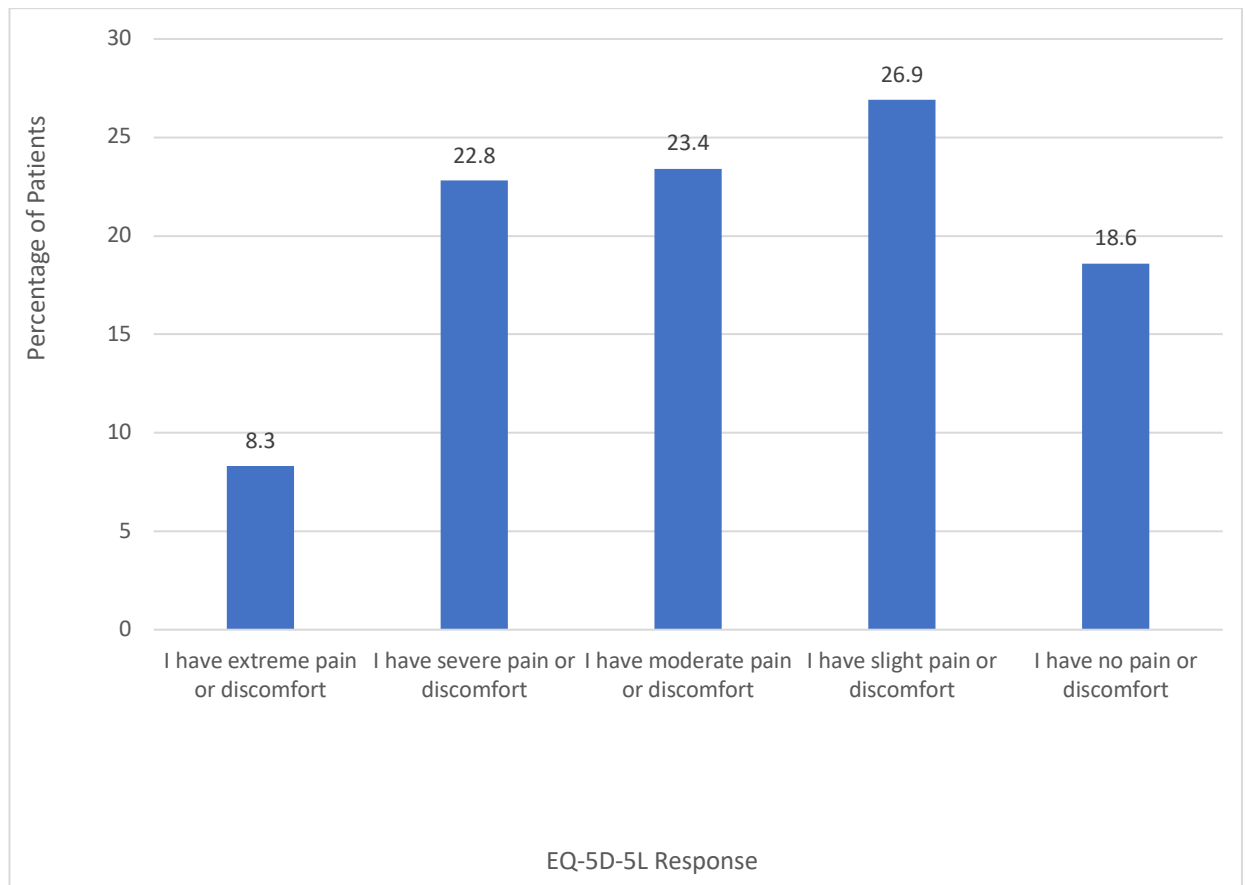
Pain was widely reported. Of 134 responders to the Visual Analog Scale, 82.1% (110) reported some degree of pain (score ≥ 1) and 35.8% (48) reported a score ≥ 5 (Figure 2).

Figure 2: Pain Intensity Scores at the Study Visit



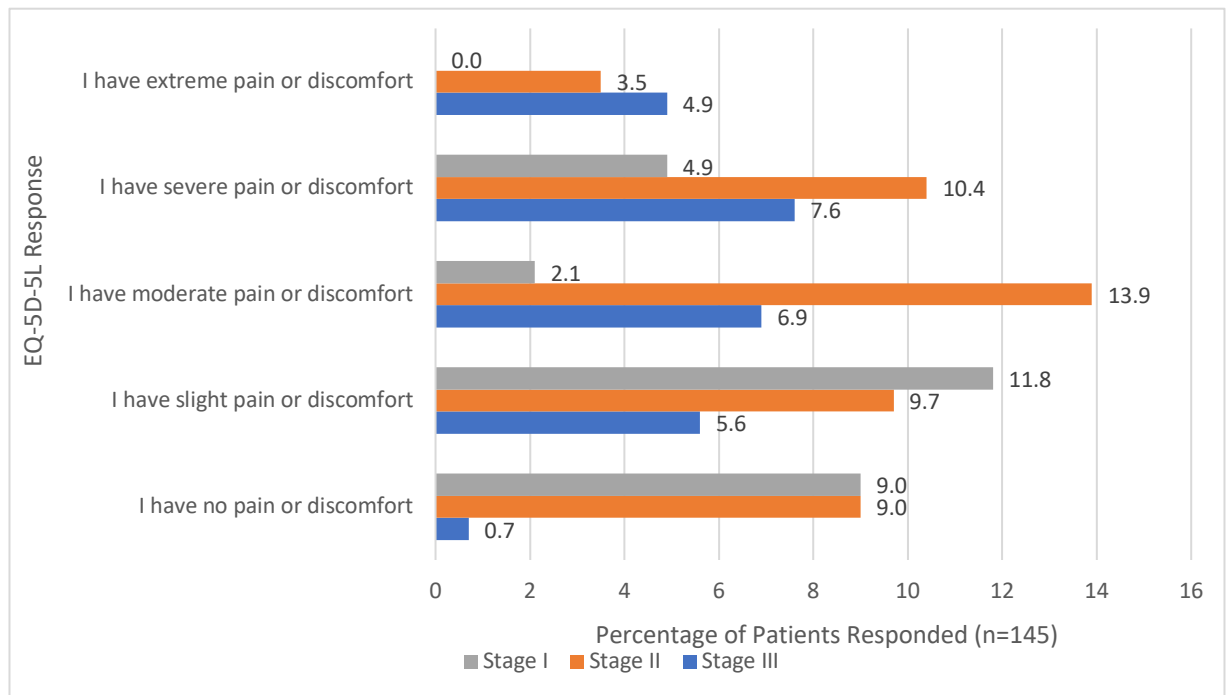
Patients also completed a Euro Quality of Life Health Outcome Measure questionnaire. The majority of patients reported pain associated with their HS, with just over 30 percent reporting severe to extreme pain (Figure 3).

Figure 3: EQ-5D-5L Responses



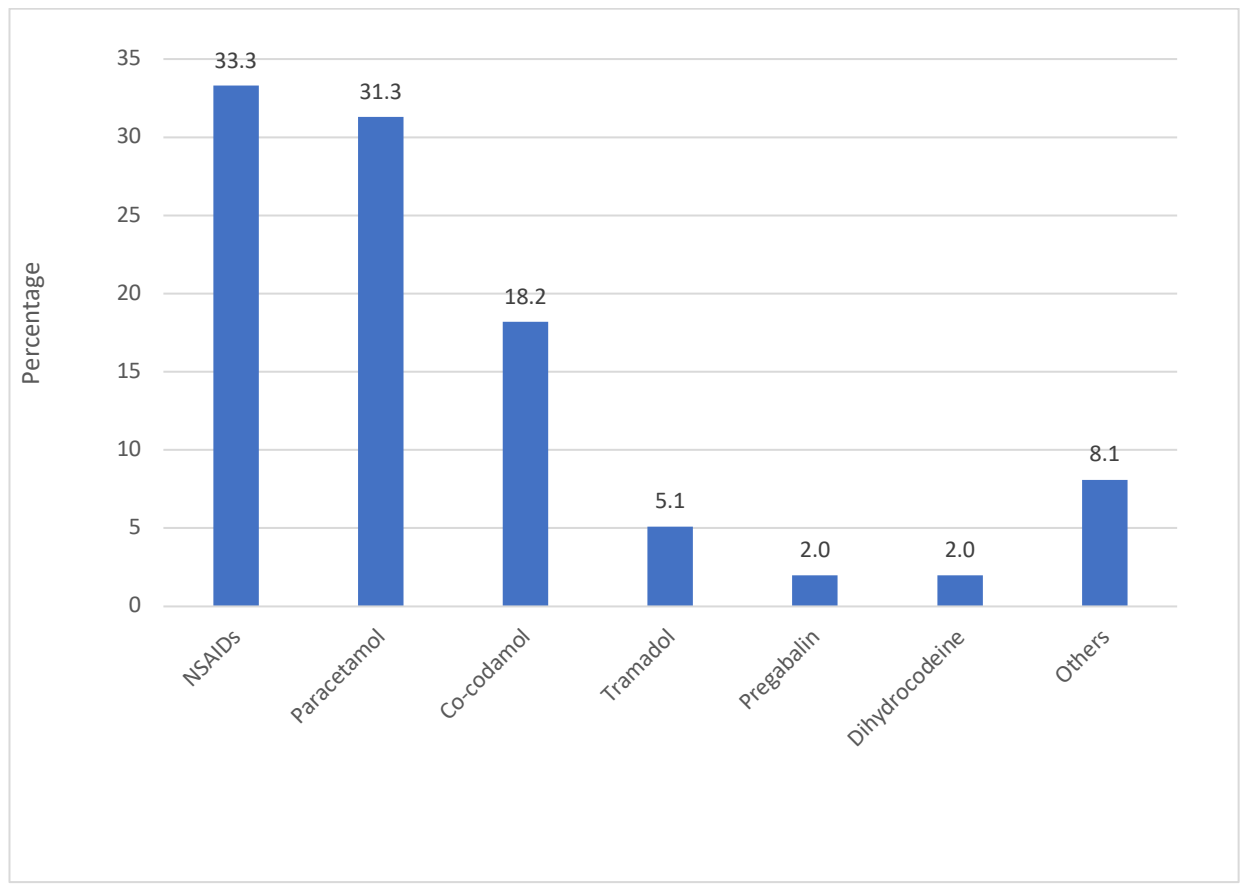
The relationship between Hurley Stage and this score was statistically significant with a p-value of <0.001 (Kruskal-Wallis). Patients who reported no pain or discomfort were predominantly Hurley stages I and II, while those reporting extreme pain or discomfort were exclusively stages II and III (Figure 4).

Figure 4: Association between Hurley stage and EQ5D-5L response



A significant proportion of patients (61/150, 40.7%) reported taking analgesics (Figure 5). A total of 99 analgesics were reported, the majority of which were over-the-counter medications accounting for 61.6% of analgesics taken. Weak negative correlation was seen between pain scores and the gut microbial diversity index chao1 ($p=0.01$), but this was not seen with other gut microbial diversity measures including Simpson and Shannon indices ($p=0.05$, $p=0.12$).

Figure 5: Reported use of analgesics in the study population



3.1.4 Discussion

Patients with HS often experience considerable pain, which has a meaningful impact on their quality of life. The characteristics of pain in HS have been described as hot, burning, pressure, stretching, cutting, sharp, taut, gnawing, throbbing, aching and splitting (584). Pain in HS correlated more highly with QoL impairment than even disease severity; however, more severe disease appears to be associated with greater pain and discomfort in the current study (24,585). The results align with a Danish study, in which patients reported a mean score of 3.9 (SD $\pm$ 3.2) on a 10-point pain VAS (586). Another Danish study reported analgesic use in 65% of the study population highlighting the burden of disease (587). Regular analgesic use

addressing pain in HS is vital in improving QoL. However, there is little evidence in the literature to guide pharmacologic analgesia in HS, and dermatologists have limited training in complex pain management resulting in patient's self-management (588). Categorizing HS pain as either acute or chronic and predominantly nociceptive versus neuropathic aids the application of pain management practices in other conditions to HS management (589). HS pain is both nociceptive, with release of signalling molecules at sites of tissue injury, and neuropathic, with somatosensory nervous system dysfunction (590,591). Addressing both nociceptive and neuropathic pain is essential in managing pain in HS, balancing optimum dosage with side effects as well as addressing acute pain with strong analgesia and approaching chronic pain with a step-wise approach. There was weak negative correlation between pain scores and some markers of gut microbial diversity, suggesting a dysbiosis or reduction in gut microbial diversity may be associated with higher pain scores. This finding however was not reproducible for all alpha diversity markers and is thus likely not significant. Recently alterations in gut microbiota and their metabolites have been found to be associated with chronic pain, however the specific characteristics of this microbiome alteration remains inconsistent across the studies (592). Nevertheless, it appears that an altered host-microbe interaction contributes to the severity and duration of chronic pain and this should be further explored (592).

3.1.5 Conclusion

Collectively, these data highlight the need for greater awareness among physicians and researchers of the pain experienced by patients with HS, and suggest that pain should be included as a key outcome in future clinical trials.

3.2 Dermatology Life Quality Index and Hidradenitis Suppurativa

Abstract

Hidradenitis suppurativa (HS) is a recurrent, debilitating skin disorder presenting with painful inflammatory lesions of the apocrine-gland bearing skin. Pain, pruritus, malodour, and suppuration have a significant impact on quality of life (QoL) for HS patients (583).

Patients aged >18 with a diagnosis of hidradenitis suppurativa made by a consultant dermatologist were recruited from 2 dermatology centres in Ireland and completed the DLQI composed of 10 questions.

59 patients completed the standardised dermatology life quality index (DLQI). Mean DLQI was 12.15 (SD 7.67) with no differences noted in relation to age or sex. Mean DLQI for patients with Hurley stage I disease was 12 (SD 7.8), Hurley stage II disease 11.75 (SD 7.26) and Hurley stage III disease 12.1 (SD 8.27). Severity of HS did not correlate with higher total DLQI score. Although there was weak negative correlation between DLQI score and the gut microbiota alpha diversity measure *chao1*, no significant correlation was seen with the Simpson and Shannon indices ($p = 0.96$, $p = 0.21$). Six had a score of 0-1 (6/59;10.2%) showing no effect on their life, seven had a score of 2-5 (7/59;11.9%) showing a small effect on their life, and eleven had a score of 6-10 (11/59;18.6%) showing a moderate effect on their life. 24 scored 11-20 (24/59;40.7%) showing a very large effect on their life and 11 scored 21-30 (11/59;18.6%) showing an extremely large effect on their life.

HS has a significant impact on quality of life with DLQI scores in line with other severe dermatoses, as seen in our study (583,593–595). Highest DLQI scores were seen in relation to embarrassment or self-consciousness relating to HS and its impact on choice of clothing, as was reported previously, likely due to associated

suppuration and malodorous discharge. A high proportion of our cohort were unemployed and reported issues related to work and social activities. A high proportion also reported relationship difficulties and sexual dysfunction related to their diagnosis.

Understanding the overall burden of disease on QoL is important in providing holistic care in HS. Optimal treatment requires a multidisciplinary approach, addressing both the physical and psychosocial impacts of the disease, with the aim of improving clinical outcomes and QoL.

3.2.1 Introduction

Hidradenitis suppurativa (HS) is a recurrent, debilitating skin disorder presenting with painful inflammatory lesions of the apocrine-gland bearing skin. Pain, pruritus, malodour, and suppuration have a significant impact on quality of life (QoL) for HS patients (583). The tool most frequently used to assess patients QoL in patients attending dermatology clinics is the Dermatology Life Quality Index (DLQI)(596). Mean DLQI scores for HS range from 8.3-12.7 which is typical for severe dermatoses (594). The aim of the questionnaire is to measure how much the skin condition has affected the patient's life over the preceding week. The questions focus on physical sensations, embarrassment, interference with activities at home, clothing selection, impact on social activities, difficulty participating in a sport, preventing work or school attendance, causing relationship problems with close friends, relatives, or a partner, sexual difficulties, and impact of treatment on life, and lifestyle (596). Response options are "very much" scoring 3, "a lot" scoring 2, "a little" scoring 1, "not at all" scoring 0 and "not relevant" (596). The minimum score is 0 and maximum score is 30. A score of 0 to 1 shows no effect at all on patient's life, 2 to 5 a small effect on patient's life, 6 to 10 a moderate effect on patient's life, 11-20 very large effect on patient's life and 21-30 an extremely large effect on patient's life (596).

3.2.2 Methods

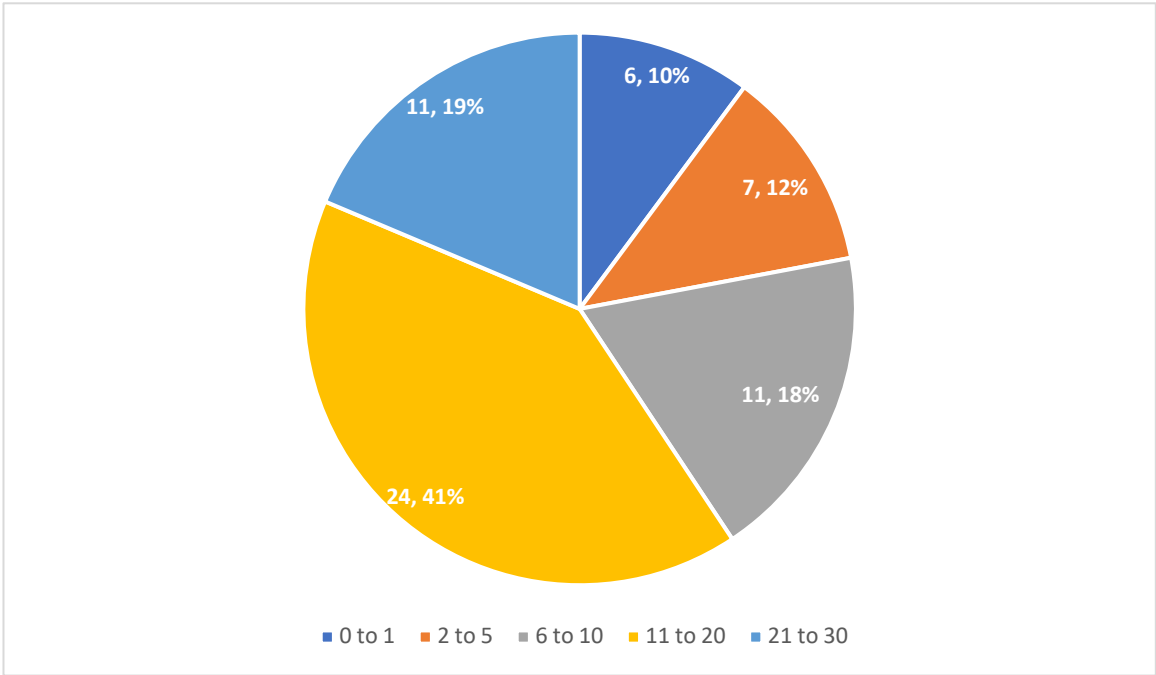
Patients with a diagnosis of hidradenitis suppurativa made by a consultant dermatologist were recruited from 2 dermatology centres in Ireland and completed the DLQI composed of 10 questions. Descriptive statistics were applied to report the questionnaire outcomes with continuous outcomes described as mean $\pm$ SD. To

calculate the differences between mean scores of two groups in normally distributed data, the independent Student's t-test was used. The Pearson correlation coefficient (r) and the Spearman correlation coefficient (r_s) were used to determine correlation. A $P < 0.05$ was considered statistically significant. Statistics were carried out using Excel (version 16.65) and R (version 4.3.1)

3.2.3 Results

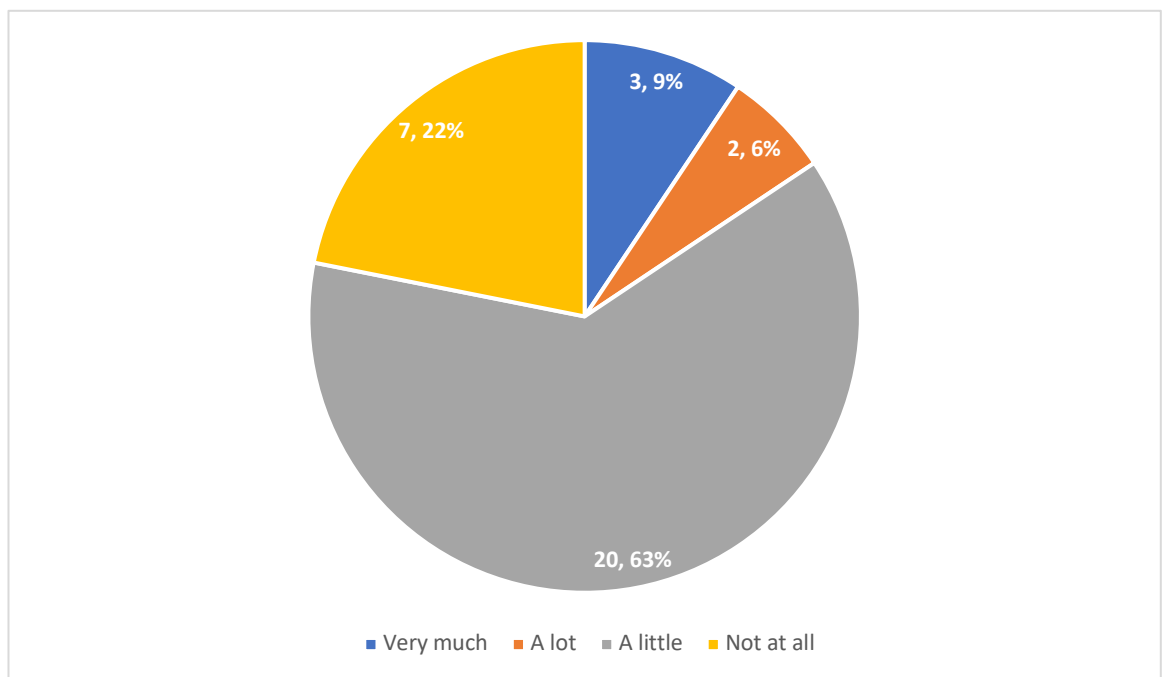
59 patients completed the standardised dermatology life quality index (DLQI). 45 were female and 14 were male. Mean age was 38.33 (SD 11.58). Mean age at diagnosis was 32.61 (SD 12.3). 17 (17/59; 29%) were Hurley stage I, 32 (32/59; 54%) were Hurley stage II, and 10 (10/59; 17%) were Hurley stage III. The majority (57/59; 97%) were white and European, and 2 were of mixed ethnic origin (2/59; 3%). 57% (34/59) were current smokers and 32% (19/59) ex-smokers for an average of 16.5 (SD 12.19) pack years. Mean BMI was 31.13 (SD 7.18). Mean DLQI was 12.15 (SD 7.67) with no differences noted in relation to age or sex. Mean DLQI for patients with Hurley stage I disease was 12 (SD 7.8), Hurley stage II disease 11.75 (SD 7.26) and Hurley stage III disease 12.1 (SD 8.27). Severity of HS did not correlate with higher total DLQI score. Six had a score of 0-1 (6/59; 10.2%) showing no effect on their life, seven had a score of 2-5 (7/59; 11.9%) showing a small effect on their life, and eleven had a score of 6-10 (11/59; 18.6%) showing a moderate effect on their life. 24 scored 11-20 (24/59; 40.7%) showing a very large effect on their life and 11 scored 21-30 (11/59; 18.6%) showing an extremely large effect on their life. (Figure 1) Although there was weak negative correlation between DLQI score and the gut microbial alpha diversity measure chao1, this was not seen for the Simpson and Shannon indices ($p=0.96$, $p=0.21$)

Figure 1: Total DLQI score



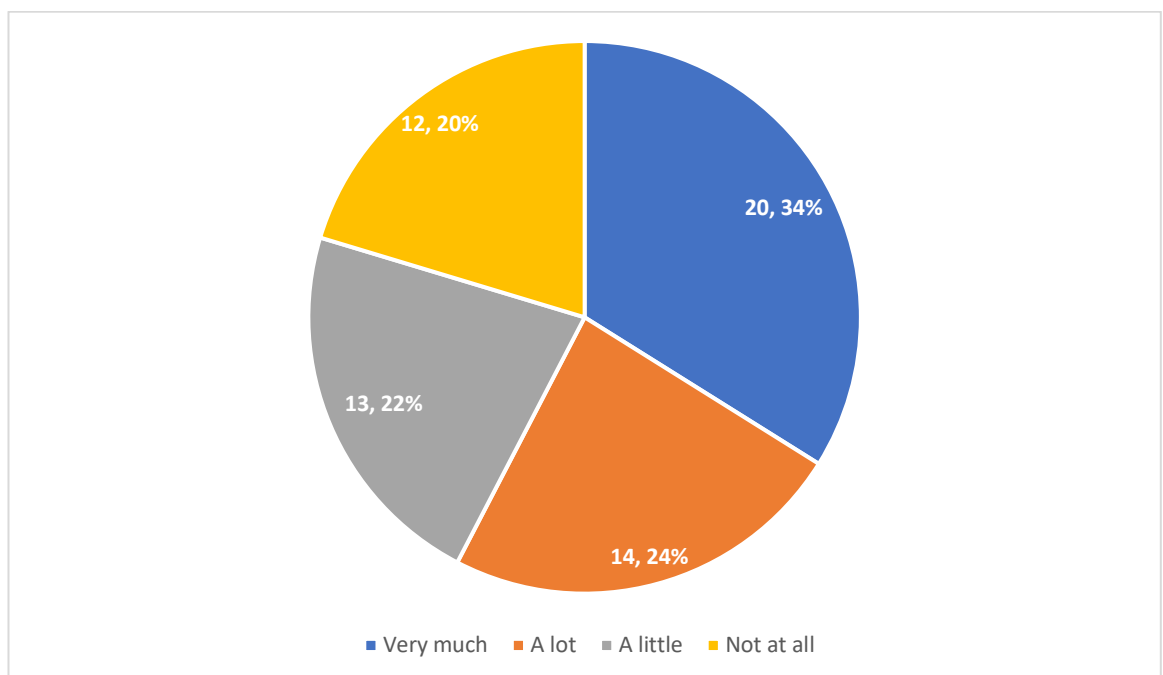
For the first question on the DLQI ‘Over the last week, how itchy, sore, painful or stinging has your skin been?’ 7 (22%) reported not at all, 20 (63%) a little, 2 (6%) a lot, and 3 (9%) very much. (Figure 2)

Figure 2: Question 1 - Over the last week, how **itchy**, **sore**, **painful** or **stinging** has your skin been?



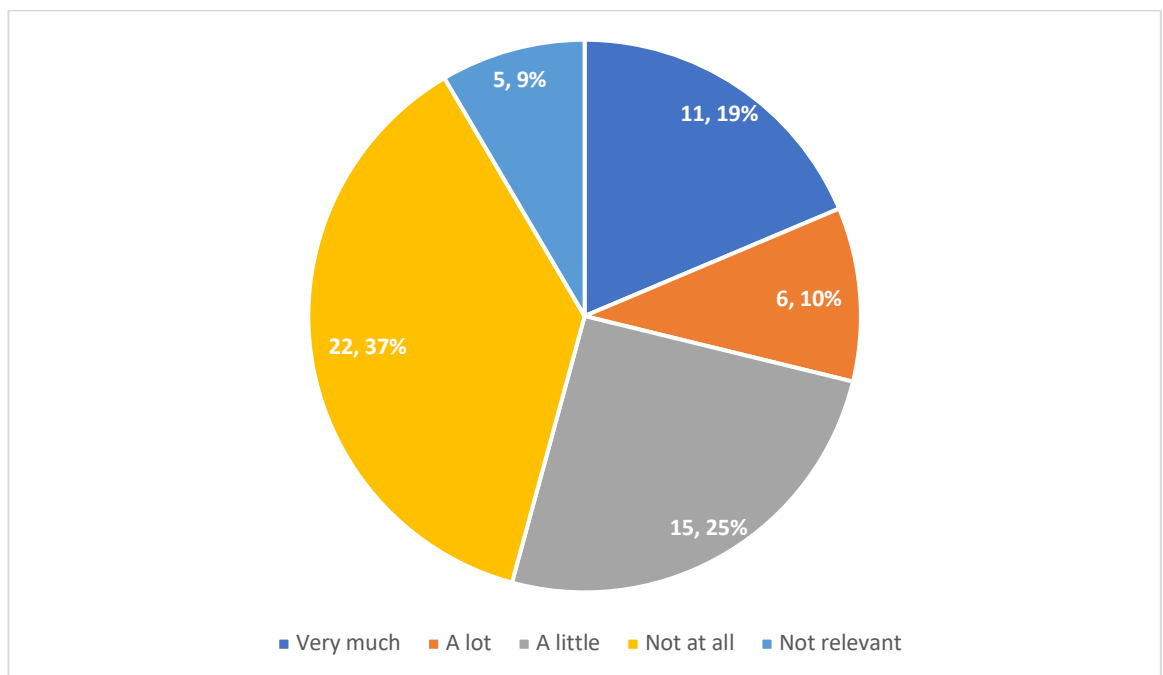
For the second question ‘Over the last week, how embarrassed or self-conscious have you been because of your skin?’ 12 (20%) reported not at all, 13 (22%) reported a little, 14 (24%) reported a lot, and 20 (34%) reported very much. (Figure 3)

Figure 3: Question 2 - Over the last week, how **embarrassed** or **self-conscious** have you been because of your skin?



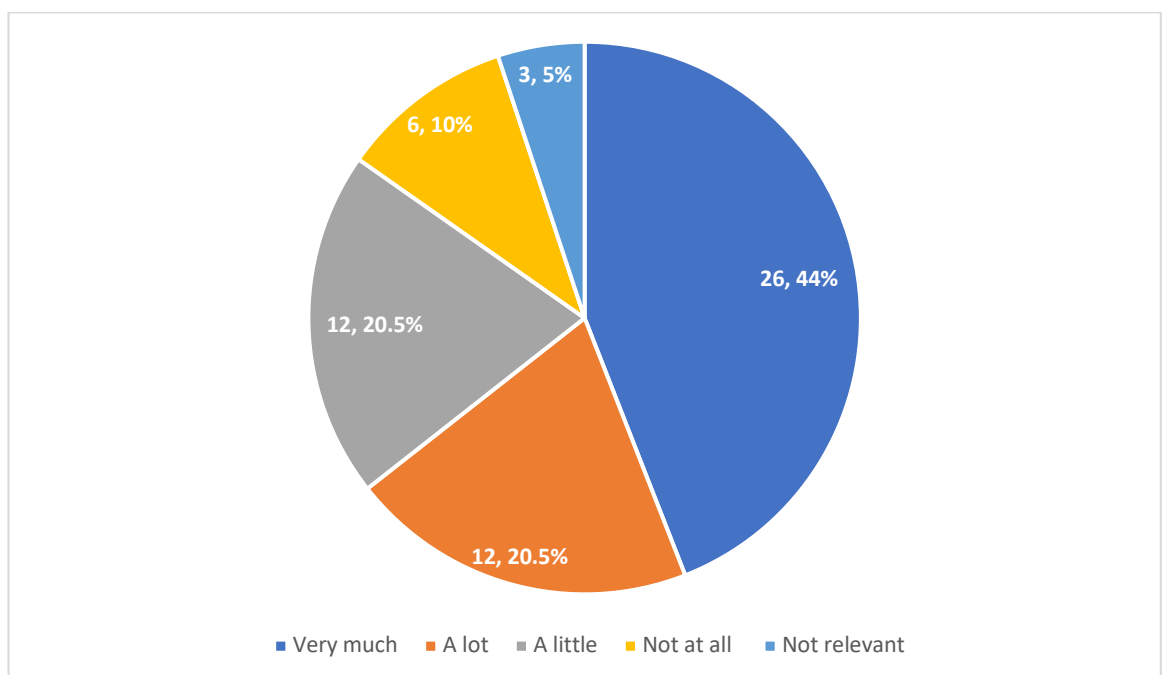
When asked ‘Over the last week, how much has your skin interfered with you going shopping or looking after your home or garden?’ 22 (37%) responded not at all, 15 (25%) a little, 6 (10%) a lot and 11 (19%) very much with 5 (9%) reporting that the question was not relevant. (Figure 4)

Figure 4: Question 3 - Over the last week, how much has your skin interfered with you going **shopping** or looking after your **home** or **garden**?



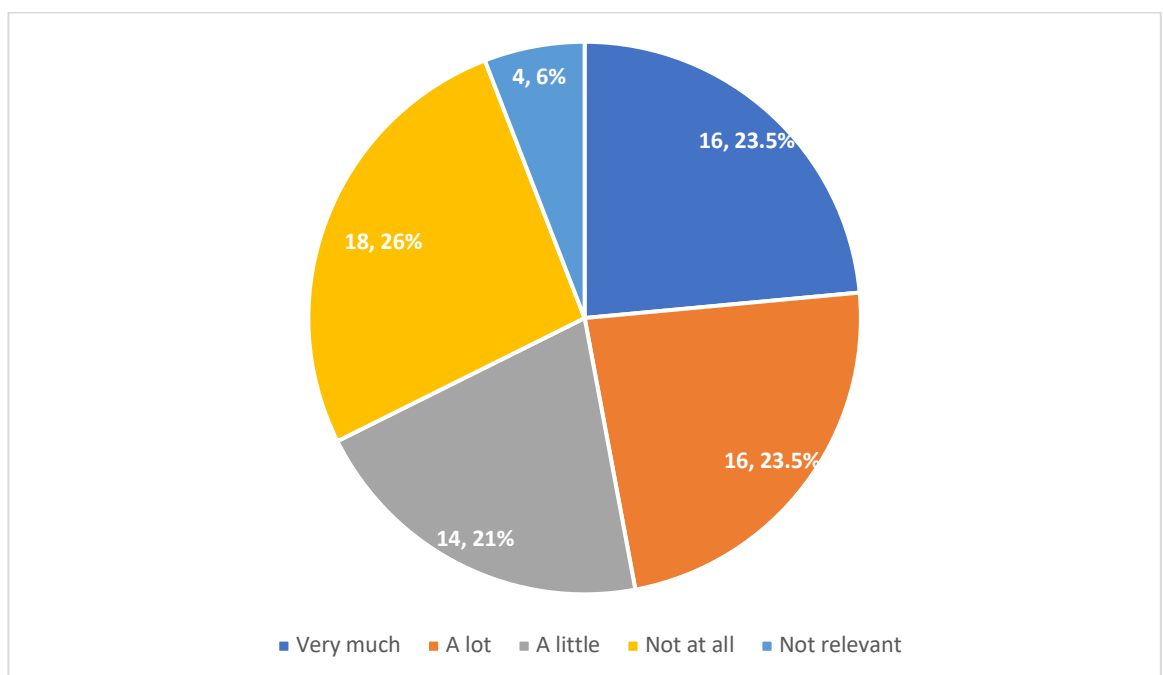
For the fourth question ‘Over the last week, how much has your skin influenced the clothes you wear?’ 6 (10%) reported not at all, 12 (20.5%) a little, 12 (20.5%) a lot, and 26 (44%) very much, with 3 (5%) reporting that the question was not relevant. (Figure 5)

Figure 5: Question 4 - Over the last week, how much has your skin influenced the clothes you wear?



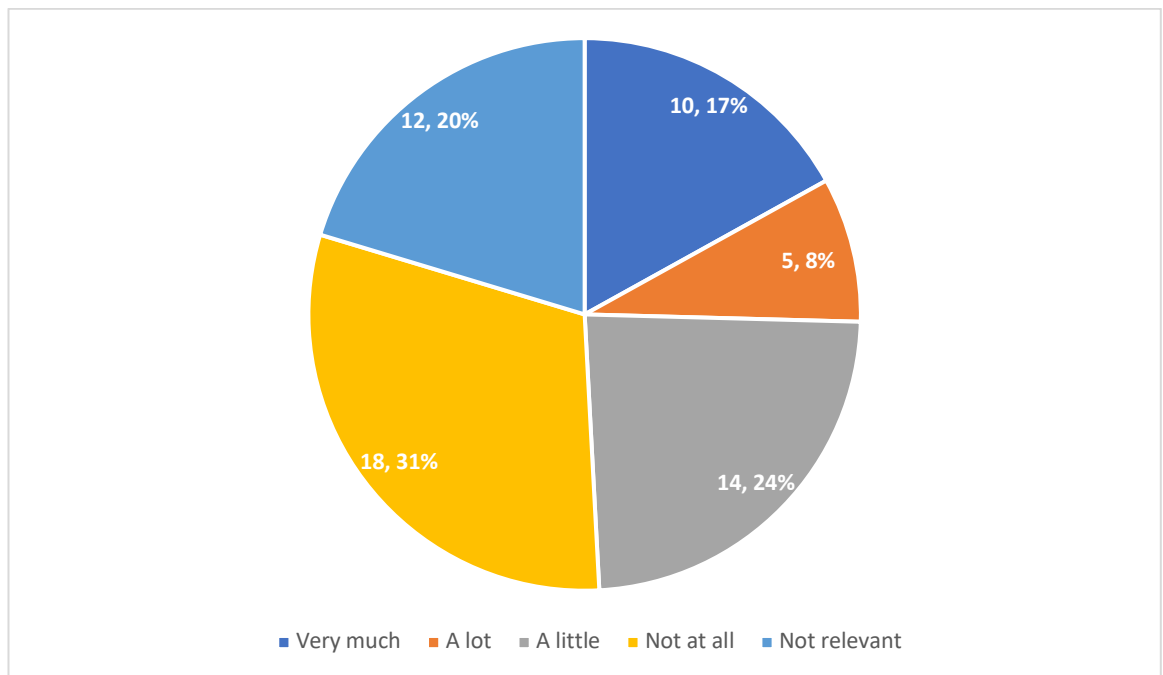
When asked ‘Over the last week, how much has your skin affected any social or leisure activities?’ 18 (26%) responded not at all, 14 (21%) a little, 16 (23.5%) a lot, and 16 (23.5%) very much, with 4 (6%) reporting that the question was not relevant. (Figure 6)

Figure 6: Question 5 - Over the last week, how much has your skin affected any social or leisure activities?



When asked ‘Over the last week, how much has your skin made it difficult for you to do any sport?’ 18 (31%) responded not at all, 14 (24%) a little, 5 (8%) a lot and 10 (17%) very much, with 12 (20%) reporting not engaging in sport. (Figure 7)

Figure 7: Question 6 - Over the last week, how much has your skin made it difficult for you to do any **sport**?



7 (12%) reported that their skin prevented them from working or studying in the previous week, with 23 (39%) not currently working or studying. (Figure 8) Of the 29 (49%) who did not report their skin preventing them from working or studying, 2 (7%) reported it was a little, and 16 (55%) a lot problematic. (Figure 9)

Figure 8: Question 7 - Over the last week, has your skin prevented you from working or studying?

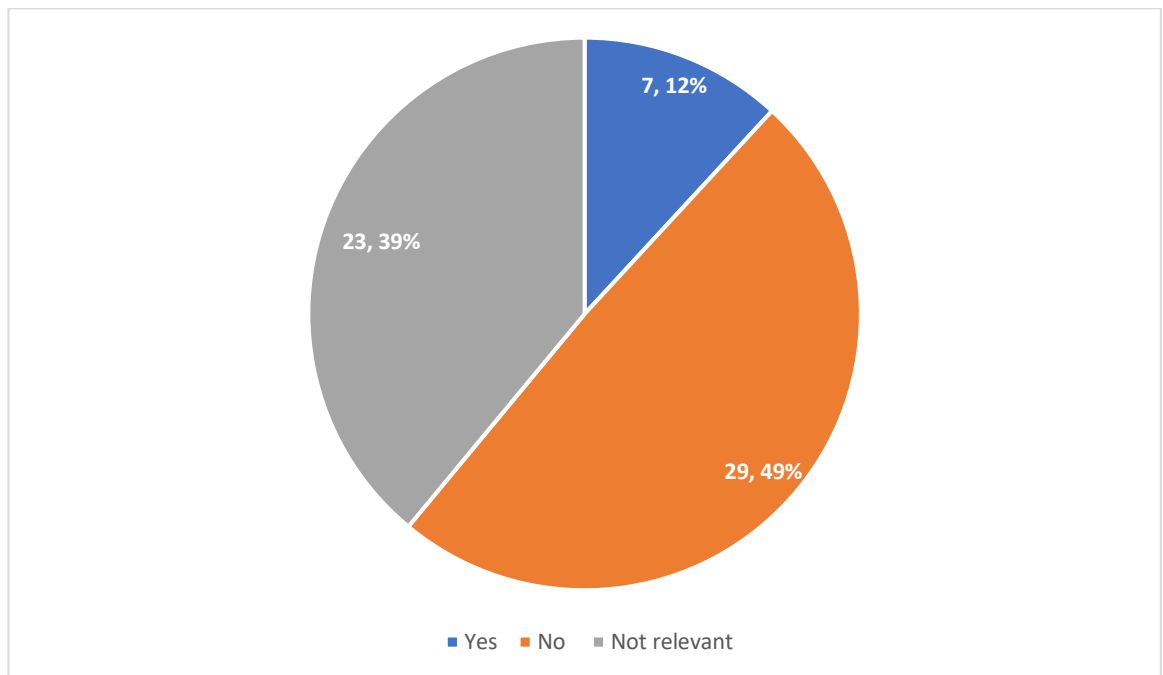
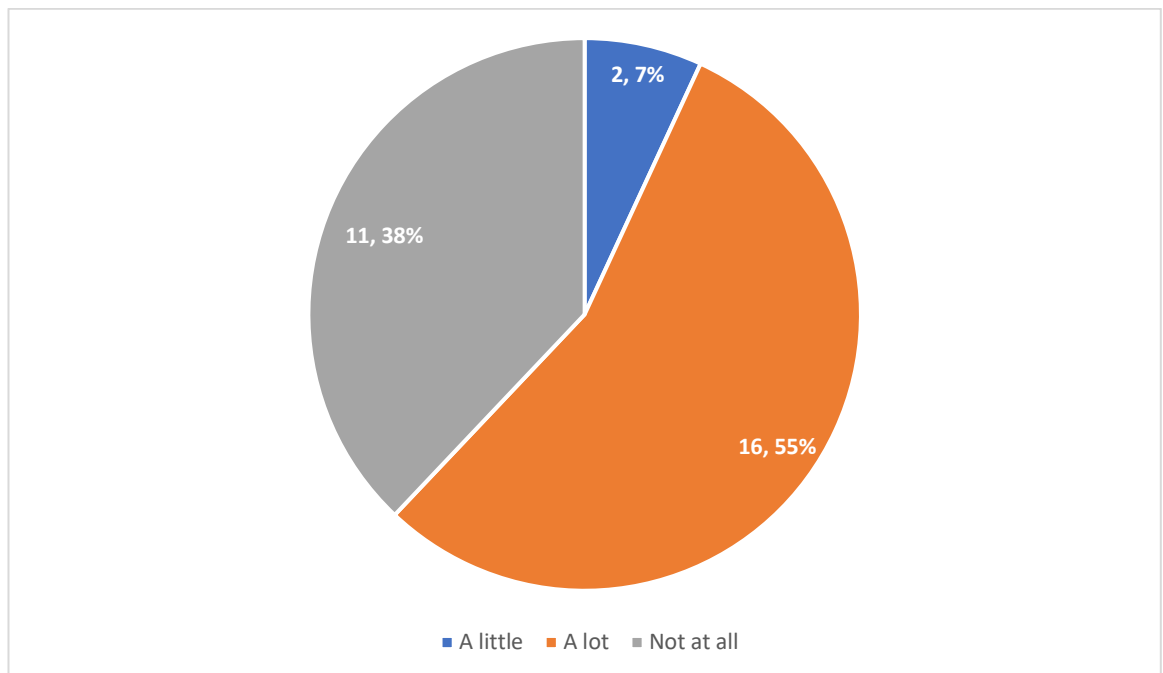
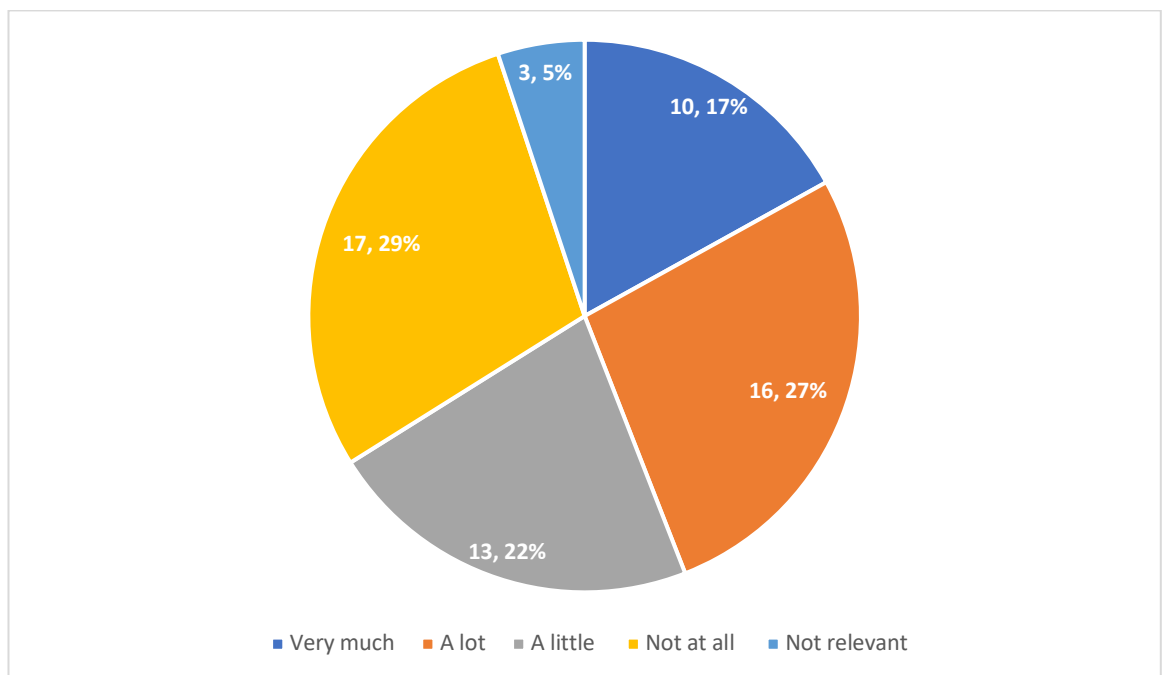


Figure 9: If "No", over the last week how much has your skin been a problem at work or studying?



When asked ‘Over the last week, how much has your skin created problems with your partner or any of your close friends or relatives?’ 17 (29%) reported not at all, 13 (22%) a little, 16 (27%) a lot, and 10 (17%) very much. 3 (5%) reported the question as irrelevant. (Figure 10)

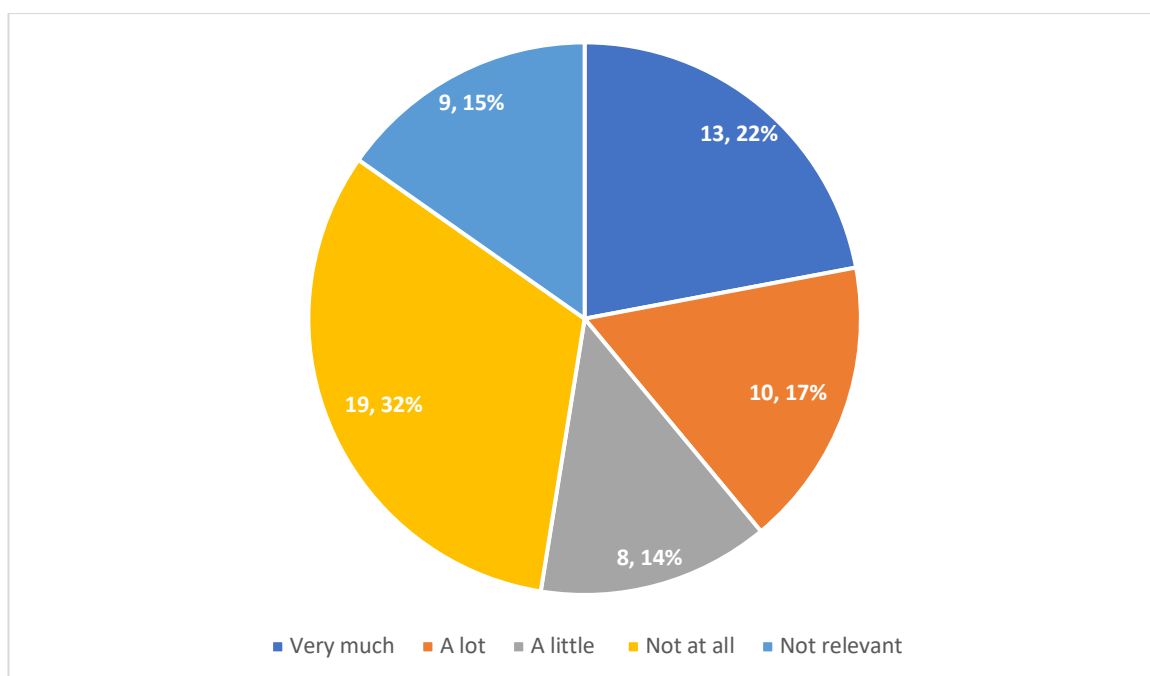
Figure 10: Question 8 - Over the last week, how much has your skin created problems with your **partner** or any of your **close friends** or **relatives**?



Of note 59% (35/59) of patients included in this study reported not being in a relationship.

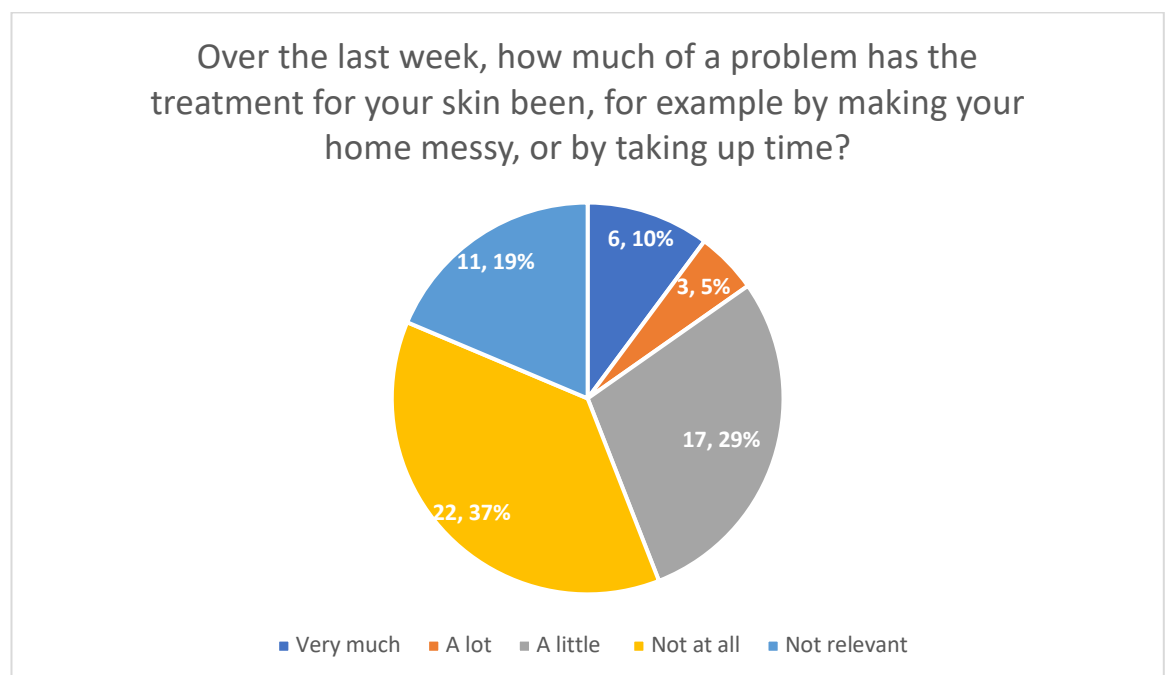
With regards how much has their skin has caused any sexual difficulties in the preceding week, 8 (14%) reported a little, 10 (17%) a lot, and 13 (22%) very much. 9 (15%) reported the question as irrelevant. (Figure 11)

Figure 11: Question 9 - Over the last week, how much has your skin caused any sexual difficulties?



17 (29%) reported that the treatment of their skin was a little bit problem, 3 (5%) a lot and 6 (10%) very much with 22 (37%) reporting no issues and 11 (19%) deeming the question irrelevant. (Figure 12)

Figure 12: Question 10 - Over the last week, how much of a problem has the **treatment** for your skin been, for example by making your home messy, or by taking up time?



3.2.4 Discussion

HS has a significant impact on quality of life with DLQI scores in line with other severe dermatoses, as seen in this study (583,593–595). However DLQI scores did not correlate with HS severity. This is contrary to prior studies which did show positive correlation of DLQI with HS severity as defined by Hurley staging (597–599). This may be due to the limitation of Hurley staging as a static measure that does not accurately account for flares of disease or subjective measures such as pain.

Gut microbial diversity also did not differ by DLQI score. Furthermore there was no correlation between DLQI score and the gut microbiota alpha diversity (a measure of species richness) metrics Shannon and Simpson indices suggesting that a severe impact on quality of life in HS does not correlate with alterations in gut microbiota. Highest DLQI scores were seen in relation to embarrassment or self-consciousness relating to HS and its impact on choice of clothing, as seen previously, likely due to associated suppuration and malodorous discharge. HS also has a significant impact on body image as previously described (600). Pain and itch once more appears to be a considerable issue in 15% of this cohort. Itch is an often underrecognized symptom which has been proven to have a significant negative impact on HS patients' psychosocial wellbeing (601).

Patients with HS also report issues in both their employment and leisure time.

Previous studies have described frequent absences in work or education resulting in reduced productivity, and sometimes leading to unemployment (595,602). This was also noted in our study with 12% reporting absences in the previous week with a further 30% reporting that HS impacted a little or a lot on their work or studies. HS is also associated with higher risk of leaving the workforce, and this is reflected in our results with 39% of our cohort unemployed (602). Activities such as shopping, housework and work in the garden was a struggle for 29% of the patients with HS in this cohort highlighting the negative impact on activities of daily life.

Impact on social life and relationships is also a considerable issue for patients with HS. Social isolation and stigmatisation are seen in patients with HS with a major impact on QoL (594,595). 44% of our cohort reported issues with relationships related to their diagnosis. In our study 59% declared not to be in a relationship currently, and this is also reflected in the literature (603). A recent study showed the

negative impact on HS patients' partners' QoL, leading to discord in their relationships and this combined with low self-esteem in HS may account for the high proportion of this cohort not in a relationship (603). Sexual health is also impaired in HS and this is reflected in the study results, with 15% not sexually active and 22% reporting a high impact with sexual difficulties (604,605). In prior studies sexual dysfunction was higher in females, which was not found in this cohort; however there was a high ratio of females to males in this study (3:1) reflecting the higher incidence of HS in women (604,605).

Psychological stress in HS may also result in making or continuing negative lifestyle choices with a large proportion of our cohort current or ex-smokers and overweight or obese. HS can also limit physical activity due to painful lesions and in our cohort a quarter of patients reported issues with engaging with sport with a further 20% reporting they did not engage in sport at all. This lack of physical activity contributes to weight gain and poor cardiovascular health. Treatment of disease can also prove a significant burden to patients. In our cohort 15% reported that treatment of their HS was bothersome. Several studies report significant personal healthcare costs with regards to HS treatment, and along with its impact on employment, could lead to considerable financial strain (594,595,603).

3.2.5 Conclusion

Understanding the overall burden of disease on QoL is important in providing holistic care in HS. Optimal treatment requires a multidisciplinary approach, addressing both the physical and psychosocial impacts of the disease, with the aim of improving clinical outcomes and QoL.

3.3 Adherence to treatment in Hidradenitis Suppurativa

Abstract

Hidradenitis is a chronic relapsing remitting inflammatory disease of the apocrine gland bearing skin presenting. Treatment of hidradenitis suppurativa can be challenging with a limited range of evidence-based therapies and no current curative treatments (54). Adherence to medication is the extent to which patients use their prescribed treatments (606). Adherence to prescribed treatment is vital to ensure therapeutic success in chronic illnesses such as hidradenitis suppurativa. Little is known about patient adherence to treatment in hidradenitis suppurativa. We sought to determine levels of adherence to prescribed medications in a cohort of patients with hidradenitis suppurativa.

Patients aged >18 with a confirmed diagnosis of hidradenitis suppurativa by a consultant dermatologist were recruited to the study in two tertiary referral centres in Ireland. Patients were invited to complete the Morisky Medication Adherence Scale, a validated scale designed to estimate the risk of medication non-adherence (607).

In this study over 40% also reported some difficulty remembering to take their medications with 20% reporting that they forgot to take their medication in the previous 2 weeks. A further 25% of this cohort cut back on or stopped medications without discussing with their doctor.

Optimising the patient-doctor relationship, simplifying the regimen and careful explanation and education may improve adherence in chronic illness, and this approach should be used in the management of HS.

3.3.1 Introduction

Hidradenitis is a chronic relapsing remitting inflammatory disease of the apocrine gland bearing skin presenting with inflammatory nodules, abscesses, often progressing to sinus tract formation and scarring. Treatment of hidradenitis suppurativa can be challenging with a limited range of evidence-based therapies and no current curative treatments (54). Adherence to medication is the extent to which patients use their prescribed treatments (606). Adherence to prescribed treatment is vital to ensure therapeutic success in chronic illnesses such as hidradenitis suppurativa. Patients can be unintentionally non-adherent due to forgetfulness or misunderstanding, some however are intentionally non-adherent due to side effects or perceived ineffectiveness of treatments (606,608). In psoriasis it is estimated that up to 40% of patients do not use their medication as prescribed and the rate of non-adherence is particularly high for topical therapy (608,609). However, little is known about patient adherence to treatment in hidradenitis suppurativa. We sought to determine levels of adherence to prescribed medications in a cohort of patients with hidradenitis suppurativa.

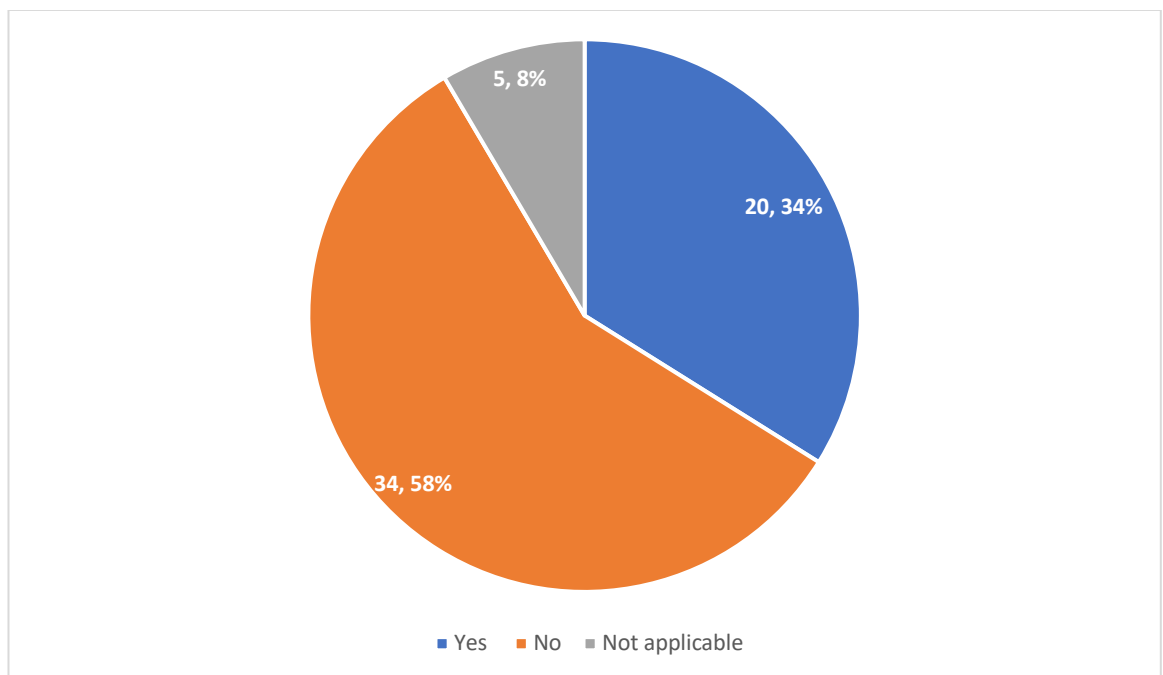
3.3.2 Methods

Patients aged >18 with a confirmed diagnosis of hidradenitis suppurativa by a consultant dermatologist were recruited to the study in two tertiary referral centres in Ireland. Patients were invited to complete the Morisky Medication Adherence Scale, a validated scale designed to estimate the risk of medication non-adherence (607). Data relating to age, sex, past medical history, and current and past medication history were collected. Statistics were performed using Excel (version 16.65).

3.3.3 Results

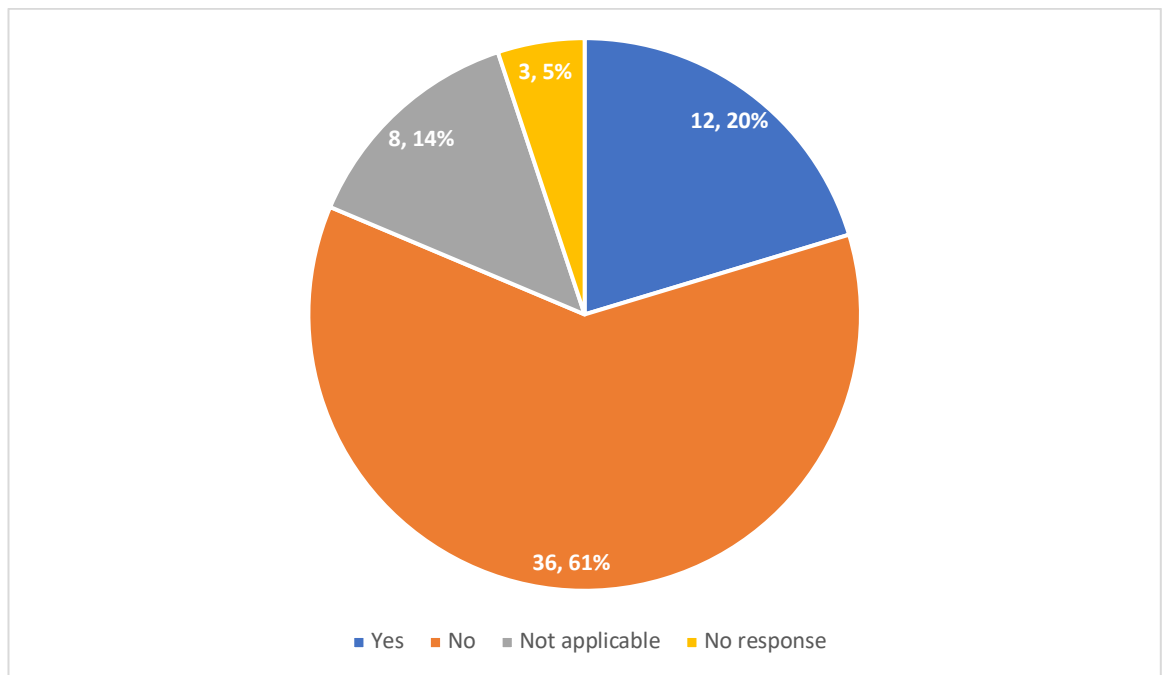
59 patients with a diagnosis of hidradenitis suppurativa completed the questionnaire, assessing adherence to all medications prescribed. Mean age was 38 (SD 12). 64.4% (38/59) were taking regular systemic medications, 2 were on topical or inhaled medications. Of the patients taking systemic medications, 10 (26%; 10/38) were prescribed subcutaneous or intravenous TNF- α inhibitors for HS and/or Crohn's disease. When asked if they sometimes forget to take their medications 33.9% (20/59) responded yes, with 57.6% (34/59) responded no. (Figure 1)

Figure 1: Do you forget to take medications sometimes?



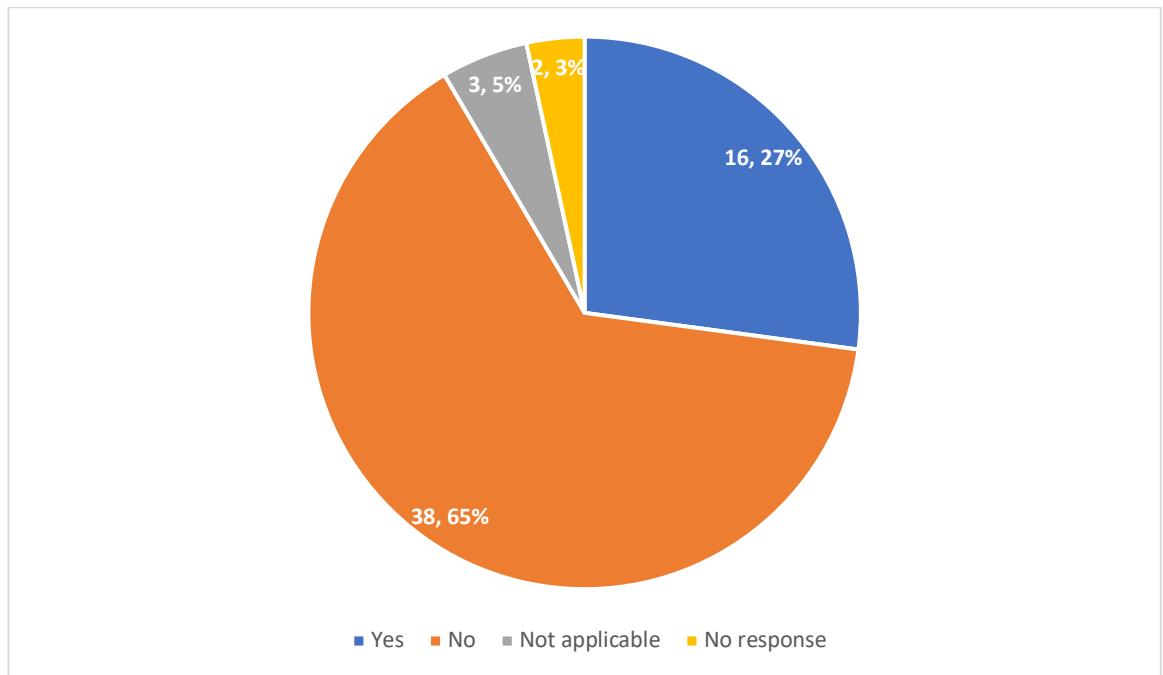
Patients were then asked if over the past two weeks were there any days when they did not take their medications. 20.3% (12/59) responded yes, and 61% (36/59) responded no. (Figure 2)

Figure 2: Thinking over the past two weeks, were there any days when you did not take your medications?



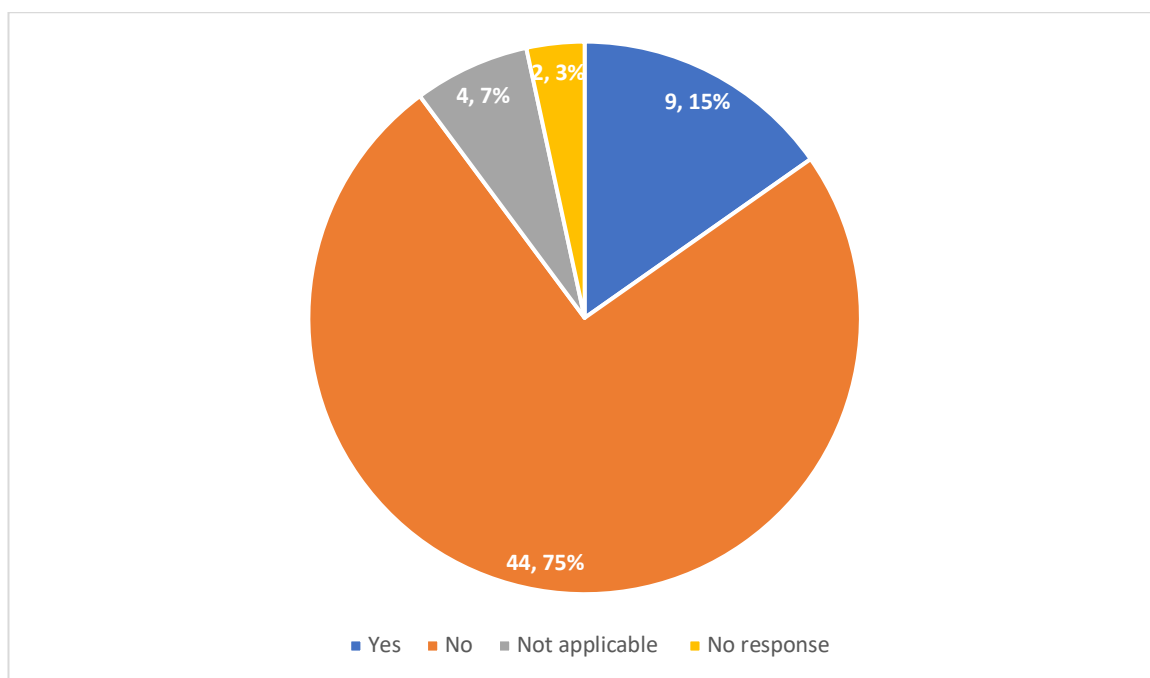
27.1% (16/59) reported cutting back or stopping medications without consulting their doctor because they felt worse when they took it. (Figure 3)

Figure 3: Have you ever cut back or stopped taking your medications without telling your doctor, because you felt worse when you took it?



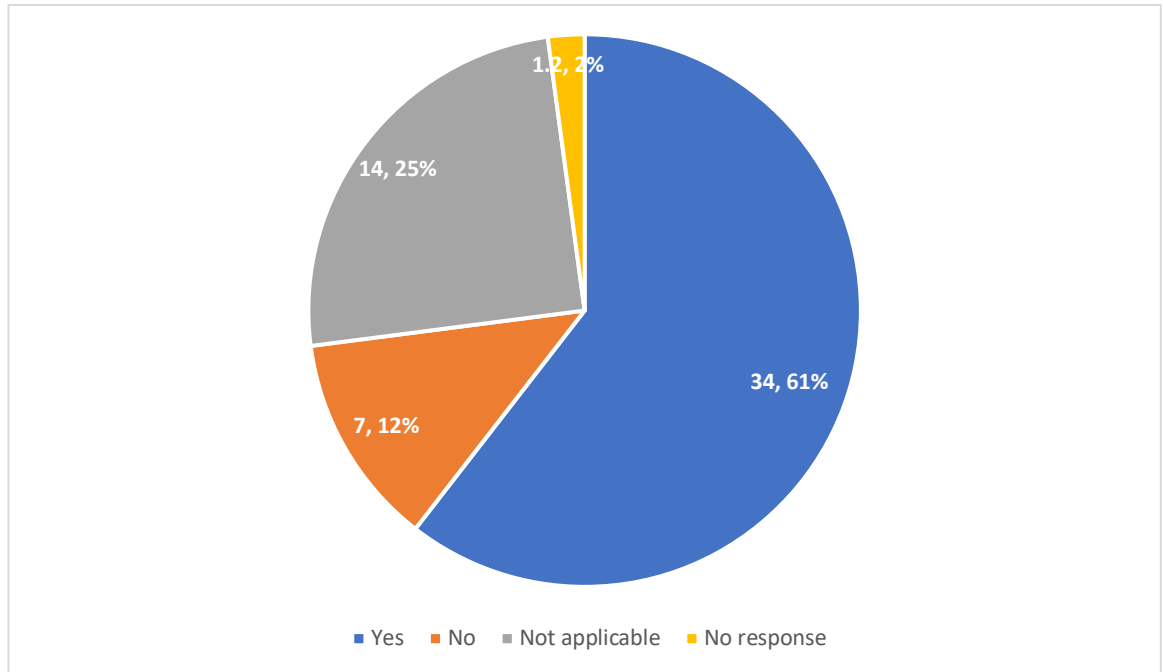
When travelling or leaving home most, 74.6% (44/59), remembered to bring their medications. (Figure 4)

Figure 4: When you travel or leave home, do you sometimes forget to bring along your medications?



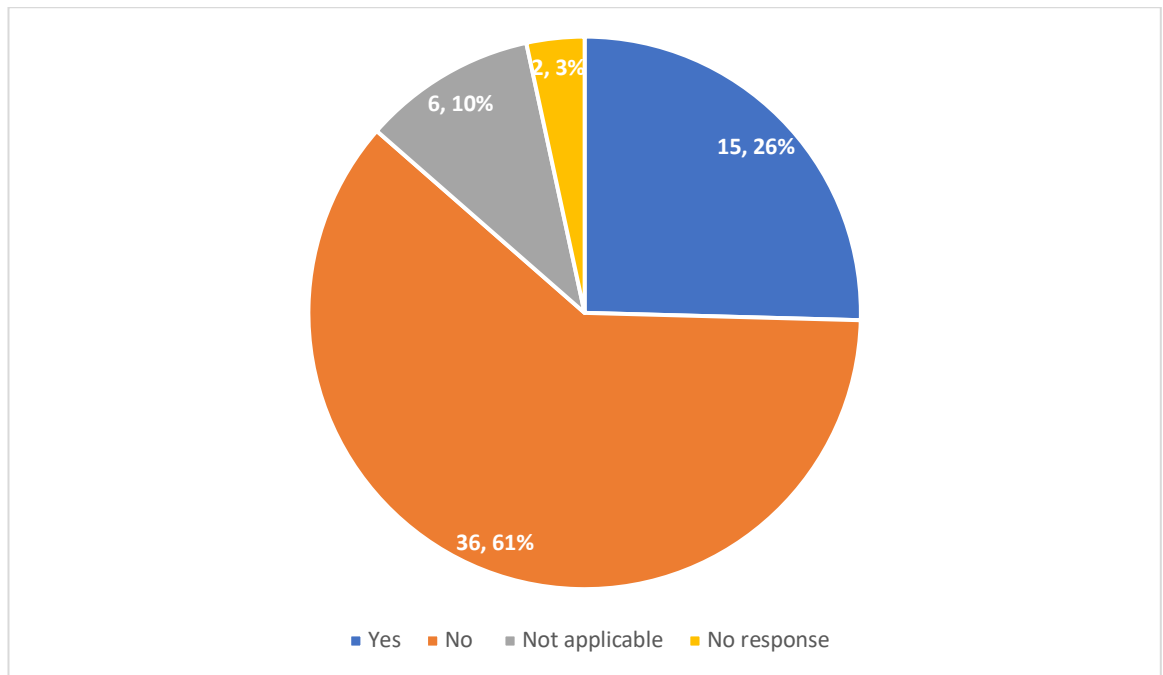
The majority reported remembering to take their medications yesterday, 57.6% (34/59). (Figure 5)

Figure 5: Did you take your medications yesterday?



25.4% (15/59) report sometimes stopping their medication when they feel like their health condition is under control. (Figure 6)

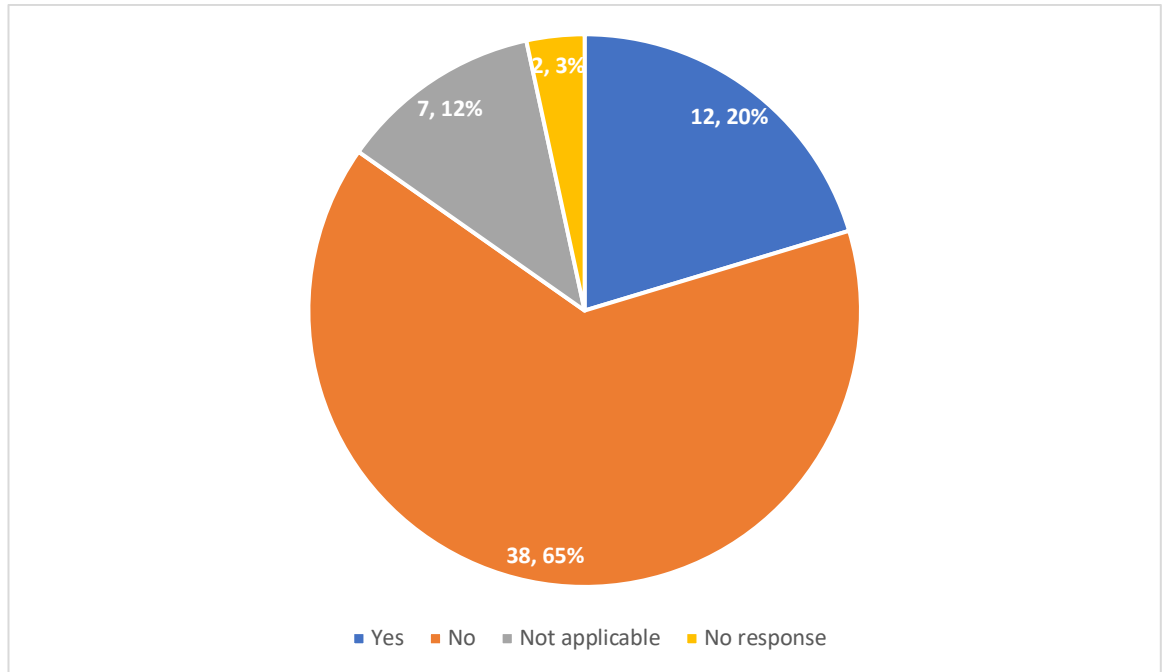
Figure 6: When you feel like your health condition is under control, do you sometimes stop taking your medications?



20% (12/59) reported feeling hassled sticking to their prescribed treatment plan.

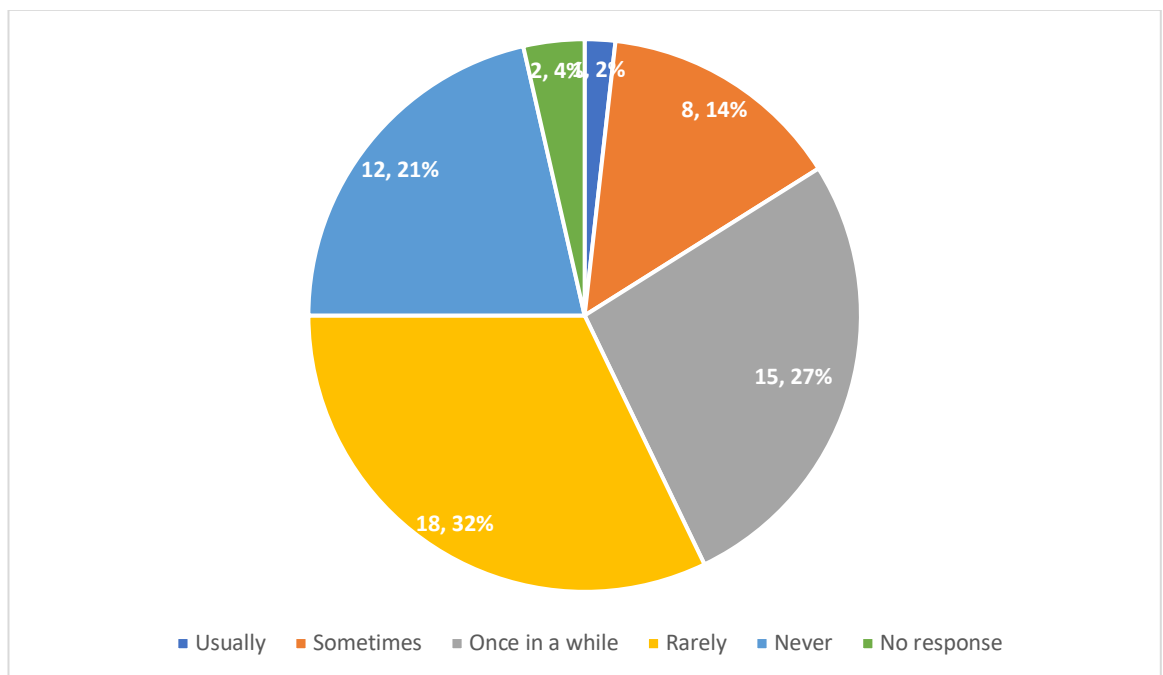
(Figure 7)

Figure 7: Do you ever feel hassled about sticking to your treatment plan?



40.7% (24/59) reported having some difficulty remembering to take their medications, while the majority, 50.8% reported this was rarely or never an issue. (Figure 8)

Figure 8: How often do you have difficulty remembering to take all your medications?



3.3.4 Discussion

In this study over 40% also reported some difficulty remembering to take their medications with 20% reporting that they forgot to take their medication in the previous 2 weeks. A further 25% of this cohort cut back on or stopped medications without discussing with their doctor. However, questionnaires measuring adherence to medications are believed to tend towards overestimating adherence which may affect our results (610). Little is published on adherence to medication in HS. One study reported low adherence to over the counter antimicrobial washes in HS (611). A tendency towards helplessness and passivity has also been described in patients

with HS which may lead to poor health maintenance, in the form of leaving appointments and non-adherence (612). It is accepted that optimising the patient-doctor relationship, simplifying the regimen and careful explanation and education may improve adherence in chronic illness, and this approach should be used in the management of HS (608). Biologic therapies are known to have high rates of adherence (613). As biologic therapy is the preferred treatment of moderate-to-severe HS which has failed standard therapy, adherence is likely to be higher in these patients.

3.3.5 Conclusion

This study suggests that non-adherence may be an issue in patients with HS, with over 40% reporting some difficulty remembering to take their medications and a quarter of patients stopping or cutting back on medications without discussing with a doctor. Further exploration is needed to determine the reasons for non-adherence in HS. Non-adherence should be explored in patients with HS, to ensure that that it is not a factor in non-response to therapies.

3.4 Physical Activity in Patients with Hidradenitis Suppurativa

Abstract

Physical activity has profound health benefits and has gained interest as an important modifiable environmental lifestyle factor in a variety of diseases, including cardiovascular disease, type II diabetes, and rheumatic disease (614–616). One study showed an inverse relationship between disease severity with intensity of physical activity in HS (170). In this study we sought to describe the physical activity of our cohort of patients with hidradenitis suppurativa.

Patients with a confirmed diagnosis of HS from two tertiary referral centres for dermatology were asked to complete the International Physical Activity Questionnaire (IPAQ) to determine their weekly physical activity scores (617). 61 patients with HS completed the questionnaire. 77% (47/61) were female and mean age was 38.33 years (SD 11.58). 18 (30%) patients had Hurley stage I disease, 33 (54%) patients had Hurley stage II disease, and 10 (16%) patients had Hurley stage III disease. 65% (40/61) reported high physical activity of >3000 MET-minutes per week. 25% (15/61) reported moderate physical activity of >600 MET-minutes per week. 10% (6/61) reported low physical activity of <600 MET-minutes per week. Median METs by Hurley score were high for Hurley stage I at 4492.5 METs per week (IQR 5722 METs), and Hurley stage II at 5964 METs per week (IQR 9375 METs), and a moderate 1917 METs per week (IQR 5040 METs) for Hurley stage III. No statistical difference was noted in physical activity scores by Hurley staging ($p=0.108$) and there was no correlation between physical activity and gut microbial diversity.

This cohort of patients with HS reported moderate to high levels of physical activity. Levels of physical activity in this study did not correlate with disease severity in

contrast to previous literature. Reporting physical activity is quite subjective relying on recall of the patient and it is therefore possible that our cohort have reported falsely elevated levels of physical activity reflecting the moderate to high levels of physical activity seen in this study.

3.4.1 Introduction

Physical activity has profound health benefits. The European guidelines for physical activity recommend a minimum of 30 minutes of daily moderate-intensity physical activity for adults including seniors (618). The World Health Organisation recommend at least 150 minutes of moderate-intensity aerobic physical activity throughout the week or to do at least 75 minutes of vigorous-intensity activity throughout the week or an equivalent of moderate- and vigorous-intensity activity and that aerobic activity should be performed in bouts of at least 10 minutes duration (619). Physical activity has gained interest as an important modifiable environmental lifestyle factor in a variety of diseases, including cardiovascular disease, type II diabetes, and rheumatic disease (614–616). Some studies have also shown that physical activity may protect against the development of cancer, neurodegenerative and inflammatory disorders, and infections (620,621). Studies evaluating the association between physical activity and development of Crohn's disease have shown mixed results, however a meta-analysis suggests that physical activity has a protective effect (622). Few studies have described the physical activity of patients with HS, nor the impact of physical activity on the development of HS. A study by Lorite-Fuentes et al. showed an inverse relationship between disease severity with

intensity of physical activity (170). In this study we sought to describe the physical activity of a cohort of patients with hidradenitis suppurativa.

3.4.2 Methods

Patients with a confirmed diagnosis of HS from two tertiary referral centres for dermatology were asked to complete the International Physical Activity Questionnaire (IPAQ) to determine their weekly physical activity scores.⁽⁶¹⁷⁾ This questionnaire comprises of five parts; (1) Job-related physical activity, (2) Transportation physical activity, (3) Housework, house maintenance, and caring for family, (4) Recreation, sport, and leisure-time physical activity, and (5) Time spent sitting over the preceding 7 days. Activities were deemed vigorous if they make a person breathe much harder than normal, and moderate if they breathe somewhat harder than normal. Physical activity (PA) was categorised into three levels; Low/Inactive, Moderate, or High. Participants were deemed to be in the moderate category if their PA level was equivalent to 'half an hour of at least moderate-intensity PA on most days'. High category included those who engage in at least one hour per day of at least moderate-intensity activity above the basal level of PA (ie those that move at least 12,500 steps per day or the equivalent in moderate or vigorous activities). PA per week was calculated by determining metabolic equivalents or METs per week per participant. A MET is the ratio of your working metabolic rate relative to your resting metabolic rate. Metabolic rate is the rate of energy expended per unit of time. One MET is defined as the energy that you expend when resting or sitting still and an activity with a value of 2 METs expends double the energy than sitting still. Standard MET values are used in the IPAQ: Walking =

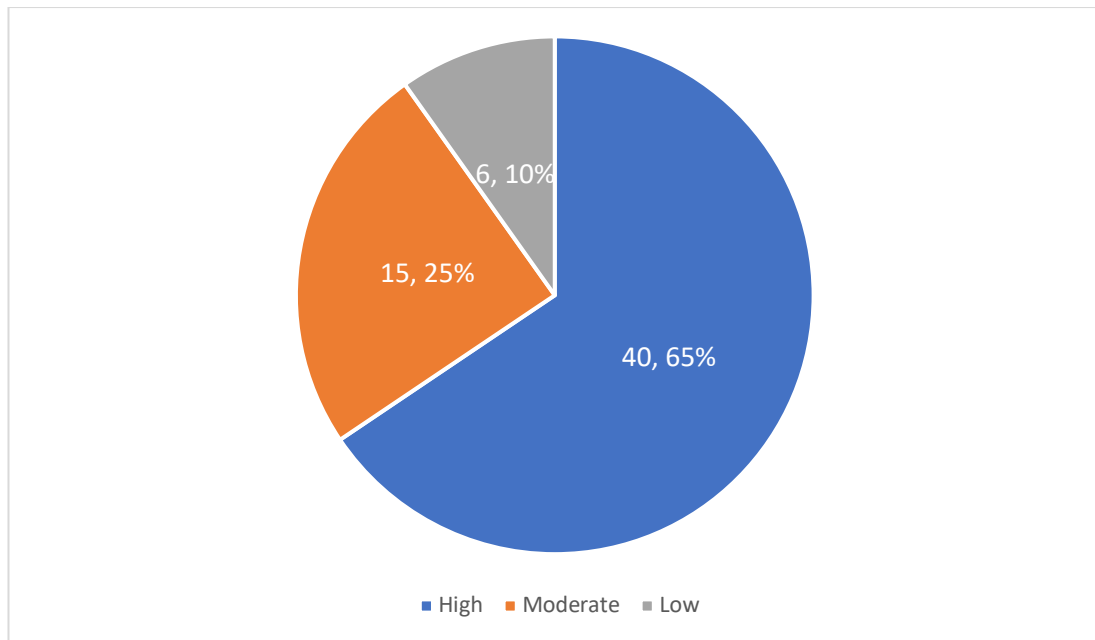
3.3 METs, Moderate PA = 4 METs and Vigorous PA = 8.0 METs. Statistics were performed using R (version 4.2.1).

3.4.3 Results

61 patients with HS completed the questionnaire. 77% (47/61) were female. Mean age was 38.33 years (SD 11.58). Mean weight was 87.7kg (SD 21.87) with a mean BMI of 31.37kg/m² (SD7.21). 18 (30%) patients had Hurley stage I disease, 33 (54%) patients had Hurley stage II disease, and 10 (16%) patients had Hurley stage III disease.

65% (40/61) reported high physical activity of >3000 MET-minutes per week. 25% (15/61) reported moderate physical activity of >600 MET-minutes per week. 10% (6/61) reported low physical activity of <600 MET-minutes per week. Median METs by Hurley score were high for Hurley stage I at 4492.5 METs per week (IQR 5722 METs), and Hurley stage II at 5964 METs per week (IQR 9375 METs), and a moderate 1917 METs per week (IQR 5040 METs) for Hurley stage III. No statistical difference was noted in physical activity scores by Hurley staging ($p=0.108$)(Kruskal-Wallis). There was no correlation seen between physical activity and the gut microbial diversity metrics chao1, Shannon and Simpson indices ($p=0.44, 0.29, 0.4$)

Figure 1: Physical activity in patients with HS



The first domain of the IPAQ was occupation related physical activity. 48% (29/61) of patients were unemployed. Of those who were employed 56% (18/32) did no vigorous work. Of those that were employed 44% (14/32) patients engaged in vigorous activity (eg heavy lifting, digging, climbing stairs) at work for an average of 9 hours a week (IQR 29 hours) and 56% (18/32) patients engaged in moderate activity (eg carrying light loads) at work for a median of 9 hours (IQR 22.9 hours) a week. 50% (16/32) walked for at least 10 minutes as part of their work for a median of 17 hours a week (IQR 33 hours).

The second domain of the IPAQ was transportation related physical activity. 89% (54/61) travelled by motor vehicle for a median of 7 hours per week (IQR 10 hours). 3% (2/61) cycled in the past 7 days for a median of 1.25 hours (IQR 0.25 hours).

67% walked from place to place for a median of 3.25 hours per week (IQR 5 hours).

The third domain of the IPAQ was household activities. 18% (11/62) reported vigorous activity in the garden or yard (eg chopping wood or digging) for a median of 4 hours per week (IQR 4.3 hours) and 43% (26/61) reported moderate activities in

the garden or yard (eg washing windows, sweeping) for a median of 4 hours a week (IQR 4 hours). 80% (49/61) engaged in moderate activity in the home (eg sweeping, scrubbing floors) for a median of 4 hours (IQR 11 hours).

The final domain of the IPAQ was leisure related physical activity. 54% (33/61) walked for leisure for a median of 3.5 hours a week (IQR 4.4 hours). 8% (5/61) engaged in vigorous exercise (eg aerobics, running, fast cycling) for a median of 3 hours per week (IQR 3 hours). 11% (7/61) engaged in moderate exercise (eg gentle cycling, swimming at regular pace) for a median of 2 hours per week (IQR 1 hour). Patients reported sitting for a median of 5 hours per day during weekdays (IQR 4 hours) and 4 hours during weekends (IQR 3 hours).

3.4.4 Discussion

Our cohort of patients with HS reported moderate to high levels of physical activity. Levels of physical activity in this study did not correlate with disease severity. In contrast to this, a previous study by Lorite-Fuentes et al. found an inverse relationship between disease severity and the intensity of activity (170). This suggests a trend towards lower disease activity in those engaging in vigorous physical activity (170). Evidence from the literature suggests that weight loss can result in resolution of HS, especially at frictional locations (623,624). Physical activity in combination with a healthy diet can result in weight loss, thus explaining the inverse relationship seen in their study (170). Furthermore, exercise has been proven to alter the gut microbiota with resulting positive health effects (625). However, in this study levels of physical activity did not correlate with gut microbial diversity.

Although using metabolic equivalent of task (MET) is the gold standard in calculating physical activity, it is prone to error as patients can overestimate physical activity leading to distortion of the results and their impact on health outcomes (626,627). Reporting physical activity is quite subjective relying on recall of the patient and it is therefore possible that this cohort have reported falsely elevated levels of physical activity reflecting the moderate-to-high levels of physical activity seen in this study.

3.4.5 Conclusion

In conclusion moderate-to-high intensity physical activity was found in our cohort of patients with HS with no correlation with disease severity. It is possible that over-estimation of physical activity may have contributed to these findings.

4. The Skin Microbiota in Hidradenitis Suppurativa

Published in Journal of Investigative Dermatology

McCarthy S, Barrett M, Kirthi S, Pellanda P, Vlckova K, Tobin AM, Murphy M, Shanahan F, O'Toole PW. Altered Skin and Gut Microbiome in Hidradenitis Suppurativa. Journal of Investigative Dermatology. 2021 Aug 6.

Presented at European Academy of Dermatology and Venereology 30th Congress, September 2021

Abstract

Hidradenitis suppurativa (HS) is a chronic inflammatory skin disease characterized by the formation of nodules, abscesses, and fistula at intertriginous sites. The skin-gut axis is an area of emerging research in inflammatory skin disease and is a potential contributory factor to the pathogenesis of HS. 59 patients with HS provided nasal and skin swabs of affected sites for analysis. 20 healthy controls provided nasal and skin swabs. We performed bacterial 16S rRNA gene amplicon sequencing on total DNA derived from the samples. Microbiome alpha diversity was significantly lower in the skin and nasal samples of individuals with HS which may be secondary to disease biology or related to antibiotic usage. *Fingoldia magna* was over-abundant in HS skin samples relative to healthy controls. It is possible local inflammation is driven by *F. magna* through promoting the formation of neutrophil extracellular traps (NET). These alterations in the skin microbiome in HS warrant further exploration, and may inform future therapeutic strategies.

4.1 Introduction

Hidradenitis suppurativa (HS) is a chronic, debilitating, follicular skin disease presenting with deep-seated, painful, inflammatory nodules of the axillary, inframammary, inguinal, and anogenital regions (628). A population prevalence of up to 4% has been reported in the literature (229,628,629). There is a female predominance, with pubertal onset (628,630,631). Smoking, obesity are associated, and a genetic predisposition has been reported (630–632). Comorbidities have been identified in patients with HS including spondyloarthropathy, metabolic syndrome and inflammatory bowel disease (IBD), particularly Crohn's disease (61,633,634). As well as significant morbidity, HS is associated with increased mortality, in particular due to cardiovascular events, with increased cancer risk also recorded (635,636). Depression, anxiety and substance misuse are also common (637,638).

The cause of HS is incompletely understood, with follicular occlusion, dysregulated inflammatory response of cytokines such as tumour necrosis factor (TNF)- α , interleukin(IL)-1 β and IL-17, and an altered microbiota are thought to play a role (141,158,630,639–642).

In this study we tested for an association between microbiota alteration in the skin and nasal mucosa, and HS. The microbiota across the various niches was compared to that of healthy controls.

4.2 Material and Methods

4.2.1 *Study Population*

Adult patients with a confirmed clinical diagnosis of hidradenitis suppurativa made by a consultant dermatologist in two tertiary referral centres in Ireland were invited to participate in the study. Ethical approval (Cork Research Ethics Committee and Tallaght University Hospital Ethics Committee), and written informed consent from patients was obtained. Exclusion criteria included topical or oral antibiotic usage in the preceding four weeks. Data including age, gender, smoking status, weight, height, body mass index, presence of co-morbidities and severity of disease (Hurley Score)(16). Healthy adult controls were recruited from the general population, and were age and gender matched.

4.2.2 *Sample collection*

In patients with HS, skin swabs (DNA-free) were taken from affected sites (axilla, inframammary, inguinal and perineal/nates) using a buffer solution with firm swabbing for 30-60 seconds. Affected sites varied by number and location in HS patients. Participants did not bathe for at least 24-48 hours prior to taking swabs and were asked to not apply anti-perspirants or emollients on the skin in that time. Skin swabs were taken from corresponding sites in controls (axilla, inframammary, inguinal and perineal/nates) using the same technique. Nasal swabs were also taken from both groups.

4.2.3 Microbial DNA extraction

Nasal and skin swabs were extracted using QIAamp UCP Pathogen Mini Kit (Qiagen, Hilden, Germany) as per manufacturer's instructions. (See Supplementary Methods Chapter)

4.2.4 Library Preparation and 16S rRNA gene sequencing

Total community DNA extracted from clinical samples underwent 16S rRNA gene PCR. The 16S rRNA gene was amplified using primers for the V3-V4 region; forward,

TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGGGNGGCWGCAG-3' and reverse, 5'-

GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTACHVGGGTATCTAATCC-3'¹⁷(643).

Microbial genomic DNA extracted from skin swab samples was amplified using MTP Taq DNA Polymerase (Merck KGaA, Darmstadt, Germany) with the PCR thermocycler protocol as follows: Initiation step of 94°C for 1 min followed by 35 cycles of 94°C for 60 s, 55 °C for 45 s, and 72 °C for 30 s, and a final extension step of 72 °C for 5 min.

A subsequent indexing PCR was carried out to add unique sample-specific DNA barcodes to the generated amplicons in accordance with the Illumina 16S Metagenomic Sequencing Protocol (Illumina, California, USA)(644). Libraries DNA concentration was quantified using a Qubit fluorimeter (Invitrogen) using the 'High Sensitivity' assay and samples were pooled at a standardised concentration (644). The pooled library was sequenced on the Illumina MiSeq platform (Illumina, California, USA) utilising 2×300 bp chemistry.

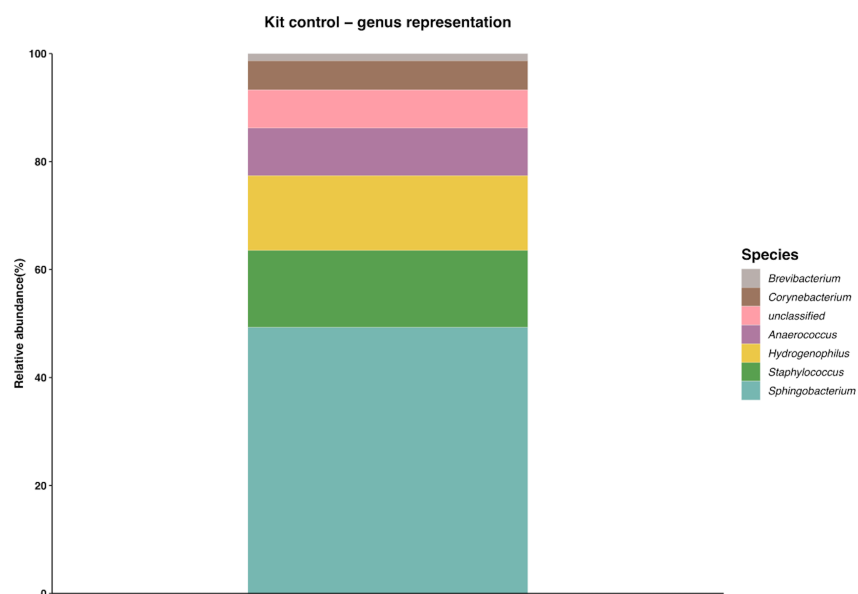
4.2.5 Bioinformatic and biostatistical analysis

The majority of the analysis was performed in R (v3.6.0). Paired reads were quality filtered, trimmed, merged and Amplicon Sequence Variants (ASV) inferred using the R package dada2 (v1.12.1)(645). Taxonomic classification was performed using the RDP Classifier within Mothur in conjugation with SPINGO, a species-level classifier (646). A confidence cut of 80% was used for taxonomic assignment. QIIME v1.9.1 and the R package vegan v2.5.6 were used to calculate β -diversity metrics (647). β -diversity was visualized via principal coordinates analysis (PCoA) plots whose coordinates were identified using with the Ape package v5.1. R-squared (R^2) and p-value were calculated using Permutational Multivariate Analysis of Variance (PERMANOVA) via the R package vegan (v2.4.2). Differential abundance analysis was carried out using DEseq2 (v1.22.2)(648). Random forest was performed in R using the package randomForest (v4.6.14). Genomic functionality was inferred using PICRUST2 with the command picrust2_pipeline.py with default (649).

4.2.6 Identification of potential microbial DNA contamination

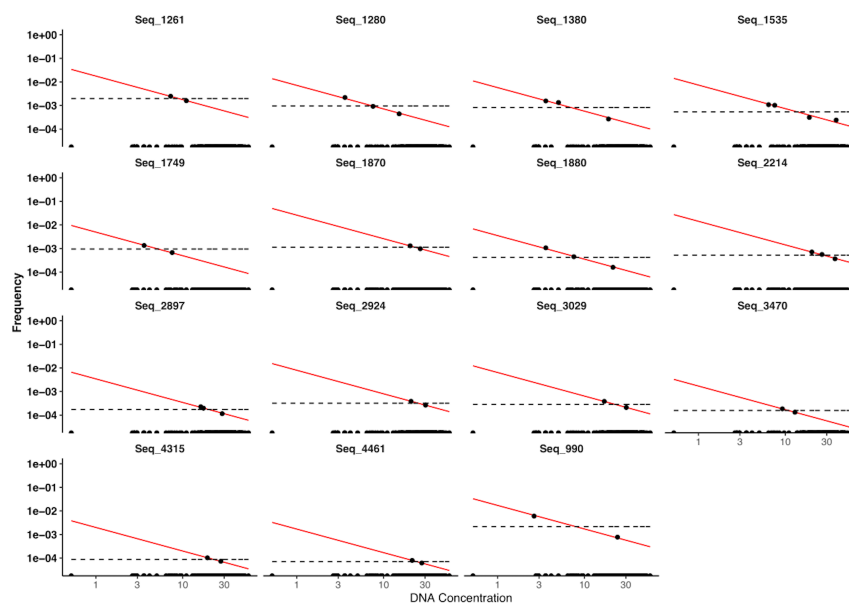
Because skin samples are considered low biomass with respect to bacterial load, we included protocols to mitigate the potential impact of contamination. Reagents used were selected based on their quality of being putatively microbial DNA free including the QIAamp Ultraclean production Pathogen Mini Kit (Qiagen, Hilden, Germany) and MTP Taq DNA Polymerase (Merck). However, these reagents can inadvertently contain contamination. Furthermore, contamination can come from a range of other sources including environmental and user-derived contamination. A negative control was run within the same sequencing batch to detect potential contamination from reagents. This negative control was dominated by taxa typical of contamination including *Sphingobacterium* and *Hydrogenophilus* (Figure 1)(650).

Figure 1: Taxonomic representation within mock extraction. Bar plots displaying the relative abundance of genera within the kit control.



Furthermore, the negative sample had atypically low DNA concentration (0.521ng/μl) relative to extracted clinical samples as measured by the qubit (Supplementary Table 1). Other non-contaminant taxa were found in the kit control but we posit that this is due to index swapping (651). We further utilized the R package decontam to detect contaminating ASVs (652). Using the ‘frequency method’ we identified 15 ASVs that reached the threshold (Supplementary Table 2). These ASVs contributed only modestly to the samples, median=0, mean=0.01881(Figure 2).

Figure 2: Decontam frequency graph. X-axis equals concentration of sample before normalisation. Y-axis equals frequency of ASV. Each dot represents a sample.



Filtering these ASVs from the ASV table had no effect on differential abundance analysis.

4.2.7 Storage of sequencing data

Datasets related to this article can be found at

<https://www.ebi.ac.uk/ena/browser/view/PRJEB43835>, hosted at European

Nucleotide Archive, accession number PRJEB43835 (653).

4.3 Results

4.3.1 Descriptive statistics of the study population

59 patients with HS were recruited providing skin swabs and nasal swabs (Table 1).

20 healthy controls provided skin and nasal swabs (Planned 3:1 ratio). Mean body mass index (BMI) in the HS group was 31.5, and 28.06 in the skin control group. Of the 59 patients with HS, 18 (30.5%) were Hurley Stage 1 (abscess formation without sinus tracts and cicatrisation), 32 (54.2%) were Hurley Stage 2 (recurrent abscesses with tract formation and scars) and 9 (15.3%) were Hurley Stage 3 (multiple interconnected tracts and abscesses throughout an entire area).

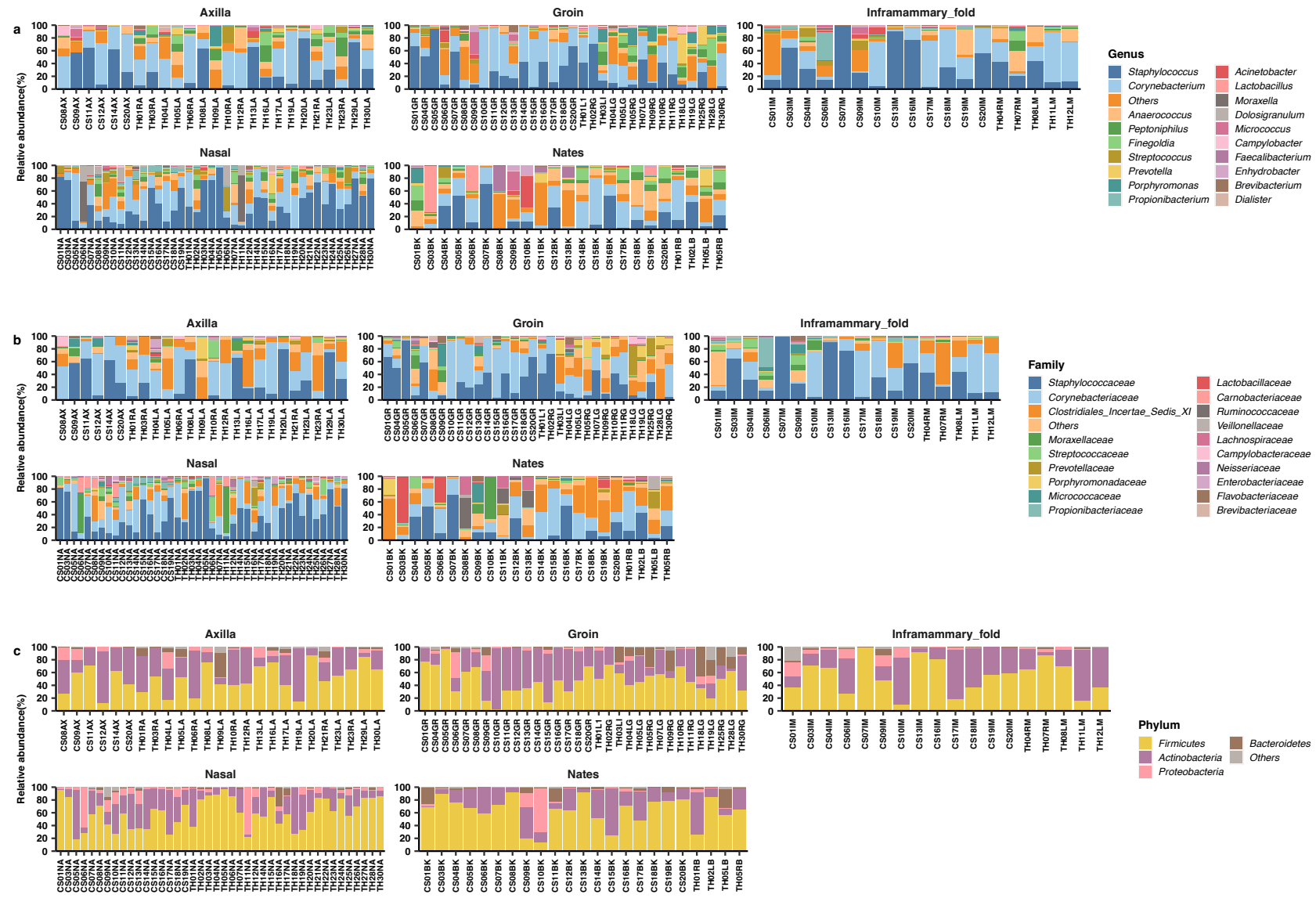
Table 1: Subject characteristics of HS subjects and healthy controls. Comparison of variables between HS cohort and healthy controls. Wilcoxon signed-rank test or χ^2 statistic was used to determine significance.

	HS	Controls	Significance
N (patients)	59	20	n/a
Gender (Female/Male)	45/14	15/5	NS
Age (mean, range)	37, 21-62	41, 24-68	NS
BMI (mean, range)	31.5, 19.6-45.0	28.06, 20.3-40	0.023
Crohn's Disease (yes/no)	4/59	0/20	NS
TNF-α inhibitor therapy	9/59	0/20	
Nasal			
N (patients)	25	17	n/a
Gender (Female/Male)	22/3	12/5	NS
Age (mean, range)	41, 24-54	36, 24-68	NS
BMI (mean, range)	33, 20.4-45.0	29	NS
Axilla			
N (patients)	19	6	n/a
Gender (Female/Male)	16/3	2/4	NS
Age (mean, range)	39, 24-54	37, 29-52	NS
BMI (mean, range)	31, 19.6-45.0	29, 22.5-39.2	NS
Groin			
N (patients)	15	17	n/a
Gender (Female/Male)	12/3	12 /5	NS
Age (mean, range)	35, 24-52	40, 24-68	NS
BMI (mean, range)	30, 20.4-44.9	29, 20.9-40.0	NS
Breast			
N (patients)	5	13	n/a
Gender (Female/Male)	5/0	13/0	NS
Age (mean, range)	39, 25-52	39, 24-54	NS
BMI (mean, range)	30.5, 19.6-38.0	28.3, 23.6-40.0	NS
Nates			
N (patients)	4	19	n/a
Gender (Female/Male)	2/2	14/5	NS
Age (mean, range)	36, 28-39	40, 24-68	NS
BMI (mean, range)	31 30.0-31.6	28, 20.9-40.0	NS

4.3.2 Ecological structure is altered in nasal and skin microbiome

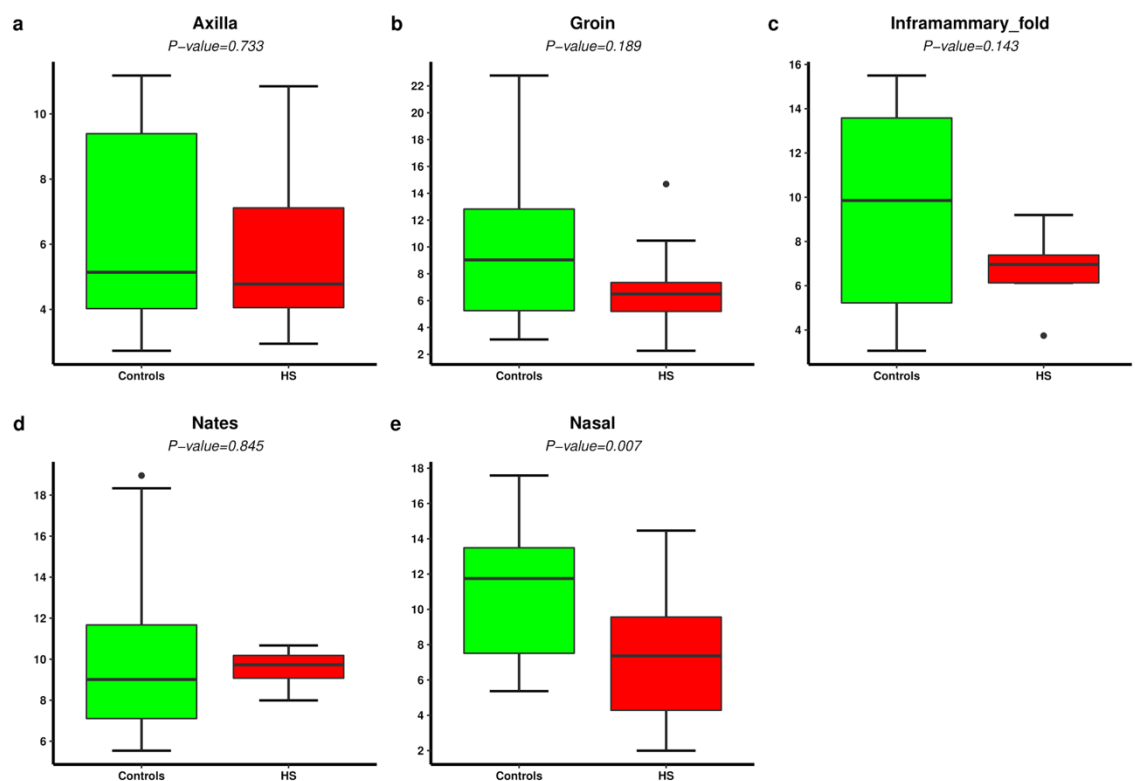
Microbial material derived from skin swabs is generally considered low biomass. In the current study, a high PCR cycle number was therefore used to maximise yield and the number of samples which produced usable amplicons. However, such a methodology is susceptible to contamination, that is, detection of microbial DNA not derived from the sample under study including reagent-derived microbial DNA. We employed a number of techniques to reduce and/or detect contaminant microbial DNA (See methods section). Although no overt level of contamination was detected, one cannot rule out all sources of contamination including environmental and user derived contamination. Skin and nasal samples with low PCR yield were excluded from the analysis resulting in differences in the final numbers of sites sampled per subject. The overall microbiome composition of nasal and skin samples studied was typical of what has been previously described, that is, mainly composed of the genera *Staphylococcus* and *Corynebacterium* (Figure 2).

Figure 2: Taxonomic representation of microbiome of nasal and skin specimens. (a) Bar plots displaying the relative abundance of genera within nasal and skin samples. Genera with a relative abundance of less than 0.5% across all samples grouped into ‘others’ with sequences not classified at the genus level. (b) Bar plots displaying the relative abundance of families within nasal and skin samples. Families with a relative abundance of less 0.5% across all samples grouped into ‘others’ with sequences not classified at the family level. (c) Bar plots displaying the relative abundance of phyla within nasal and skin samples. Families with a relative abundance of less 1% across all samples grouped into ‘others’ with sequences not classified at the phylum level.



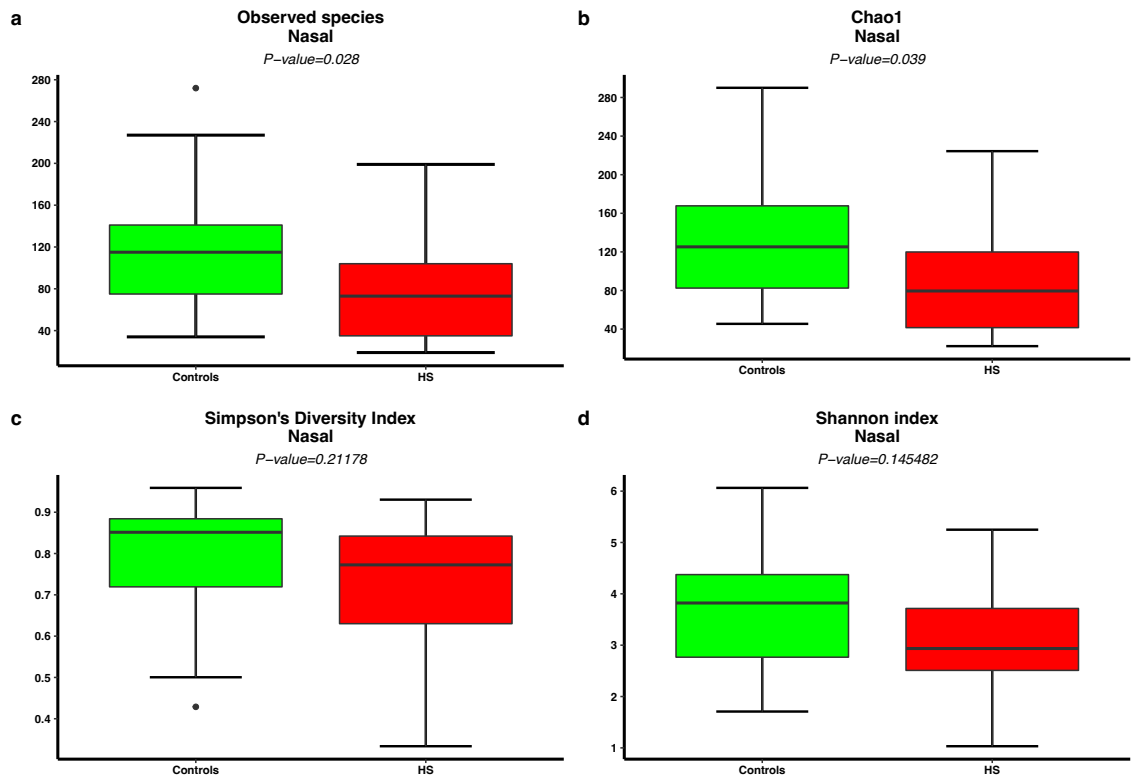
Both nasal and skins swabs showed a reduction in alpha-diversity in the HS cohort (Figure 3). However, only nasal swabs reached a statistically significant decrease.

Figure 3: Alpha-diversity comparisons across nasal and skin microbiome. Bar plots of alpha-diversity (Phylogenetic diversity) comparing healthy controls versus individuals with HS. Wilcoxon signed-rank test was used to calculate p-values.



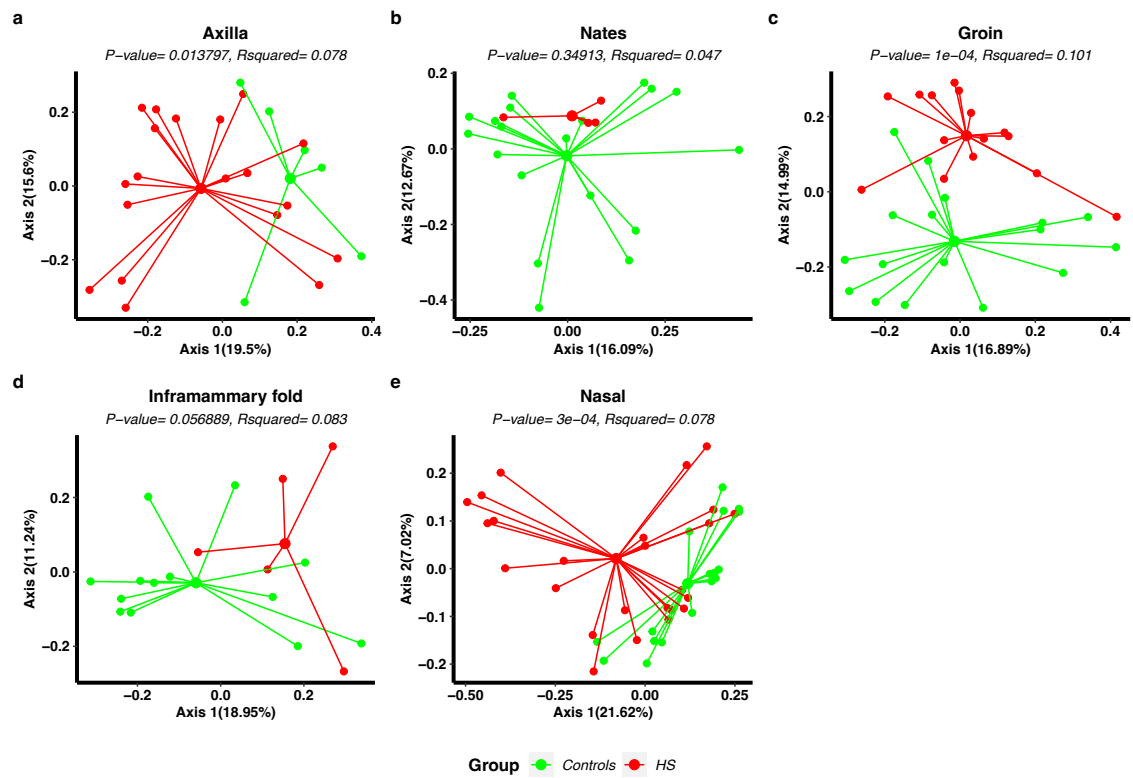
This was also true for other alpha-diversity metrics including Observed species and Chao1 but not for Simpson or Shannon indices (Figure 4).

Figure 4: Bar plots of alpha diversity metrics for nasal samples. (a) Phylogenetic diversity. (b) Chao1. (c) Simpson's Diversity Index. (d) Shannon index. Wilcoxon signed-rank test was used to calculate p-values.



The number of subjects that contributed samples to some sites was low, with a low control number, thus the statistical power was reduced and significance difficult to capture. There was a statistically significant separation in beta-diversity with respect to axilla, groin, and nasal microbiota datasets (Figure 5), showing that different microbiome communities are present at these body sites.

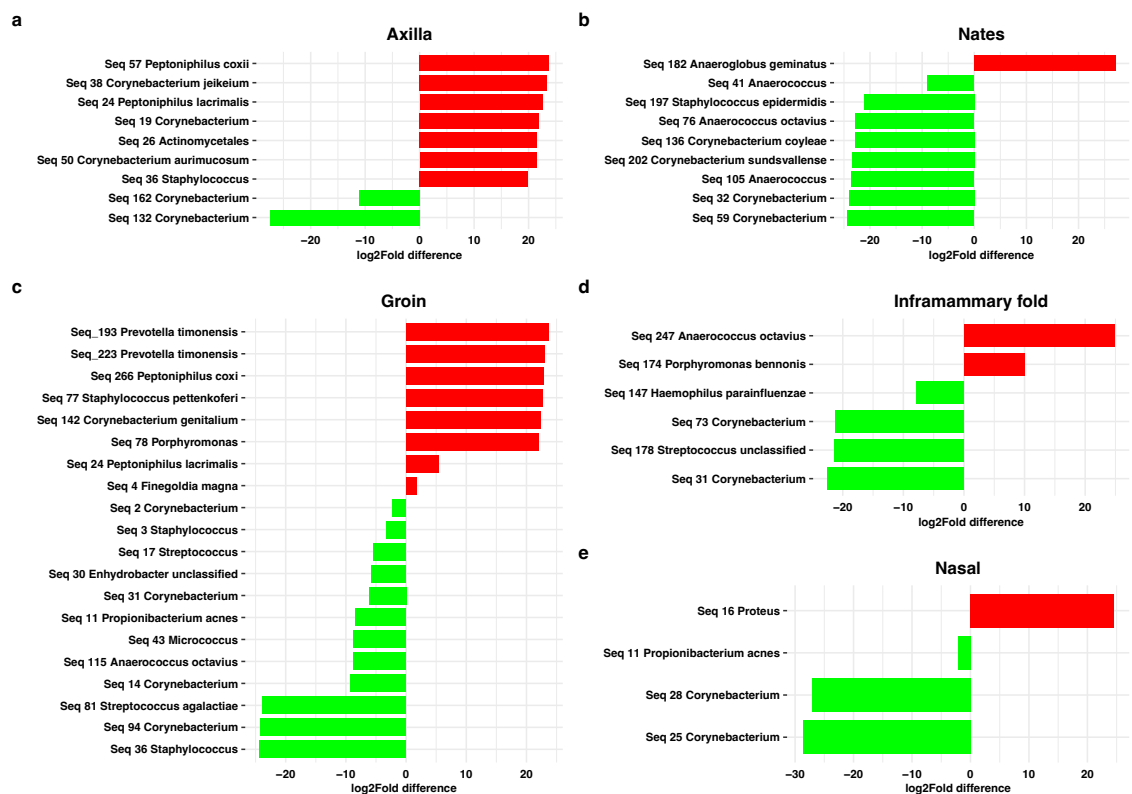
Figure 5: Beta-diversity comparisons of nasal and skin microbiome. Principal Coordinates Analysis representation of Beta diversity (Unweighted Unifrac) between individuals with HS versus healthy controls. Statistical testing was performed using Permutational Multivariate Analysis of Variance.



4.3.3 Differentially abundant ASVs and metabolic pathways in the nasal and skin microbiome of HS patients

We identified differentially abundant ASVs in the nasal microbiome and all skin sites studied (Figure 6). ASVs were collapsed to the species level and differential species abundance delineated (Figure 6).

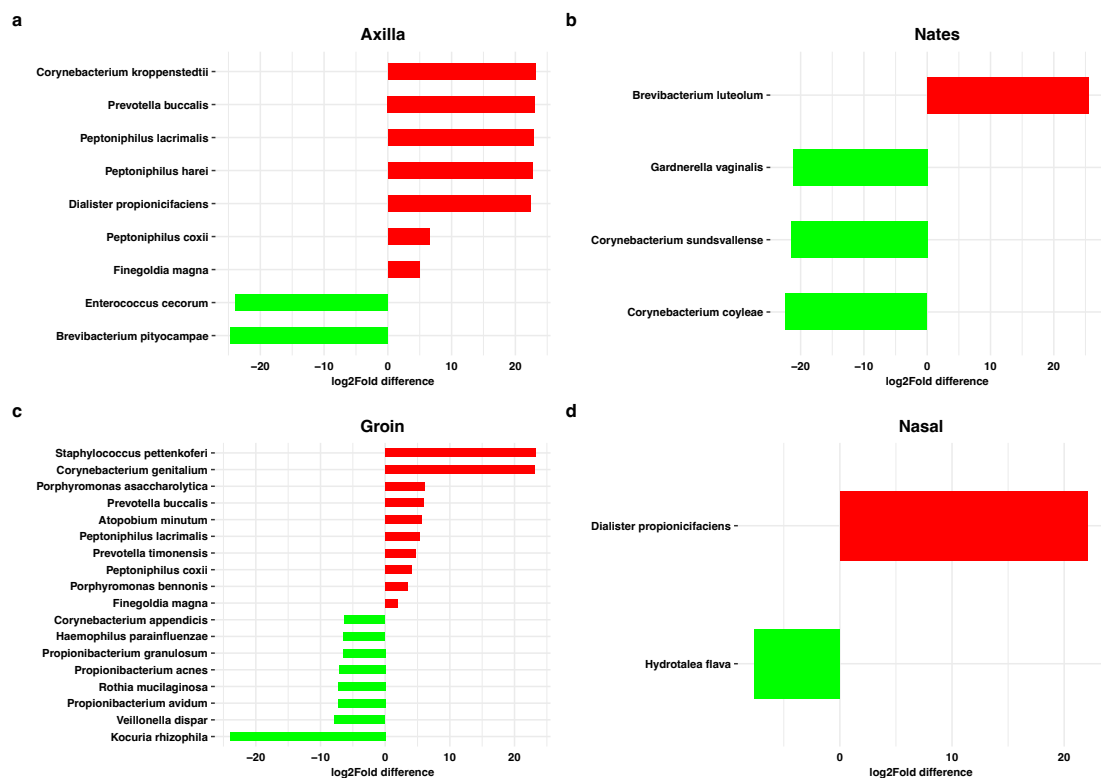
Figure 6: Bar plots of differentially abundant ASVs across nasal and skin swab samples. DESeq2 used for statistical analysis. ASVs enriched in HS samples in red. ASVs enriched in control samples in green.



An ASV, Seq 4, assigned to *Finegoldia magna* had a significantly higher abundance at the groin site in individuals with HS relative to healthy controls. Furthermore, at

the species level, *F. magna* was more abundant in HS relative to healthy controls in groin and axilla samples (Figure 7).

Figure 7: Bar plots of differentially abundant species across nasal and skin sites. DESeq2 was used to for statistical analysis. Species enriched in HS samples in red. Species enriched in control samples in green.



HS is more common in women, resulting in an expected higher ratio of female to males in this study. To correct for this confounder, we performed differential abundance analysis, integrating gender in to the DESeq model, to identify differently abundant ASVs and species (Figure 8, Figure 9).

Figure 8: Bar plots of differentially abundant ASVs across nasal and skin swab samples. DESeq2 was used for statistical analysis while controlling for gender as a confounder. ASVs enriched in HS samples in red. ASVs enriched in control samples in green.

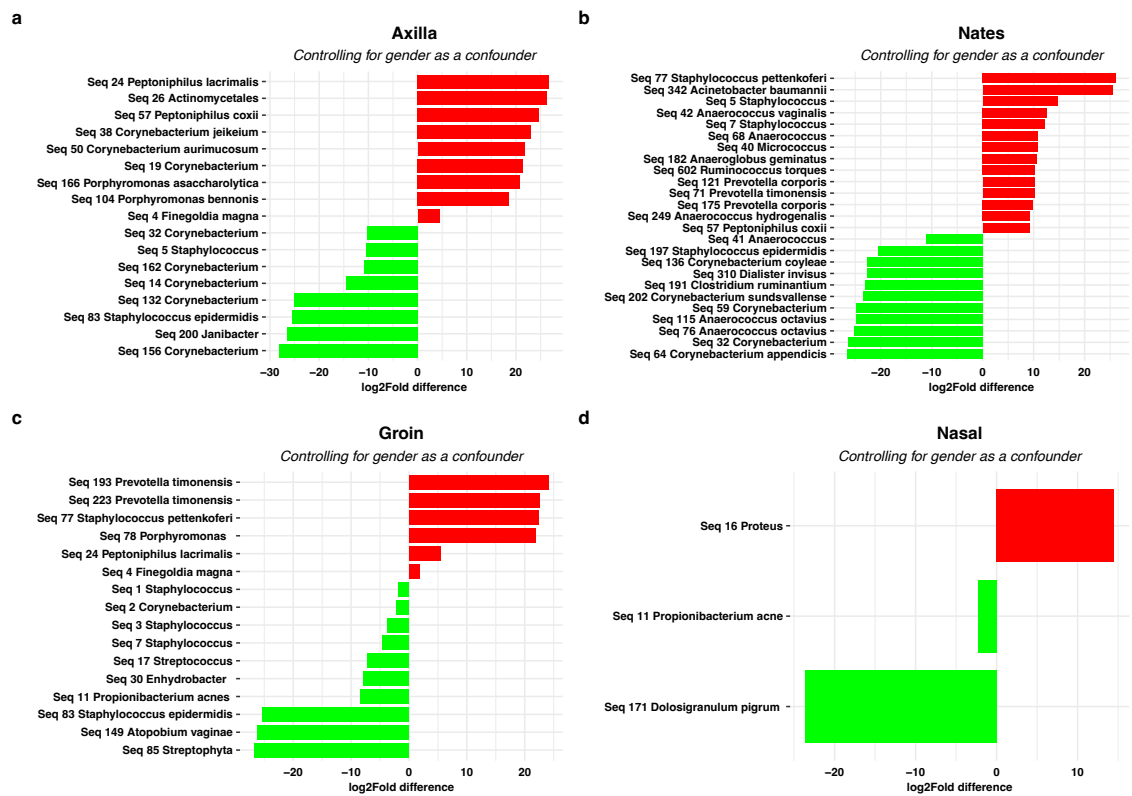
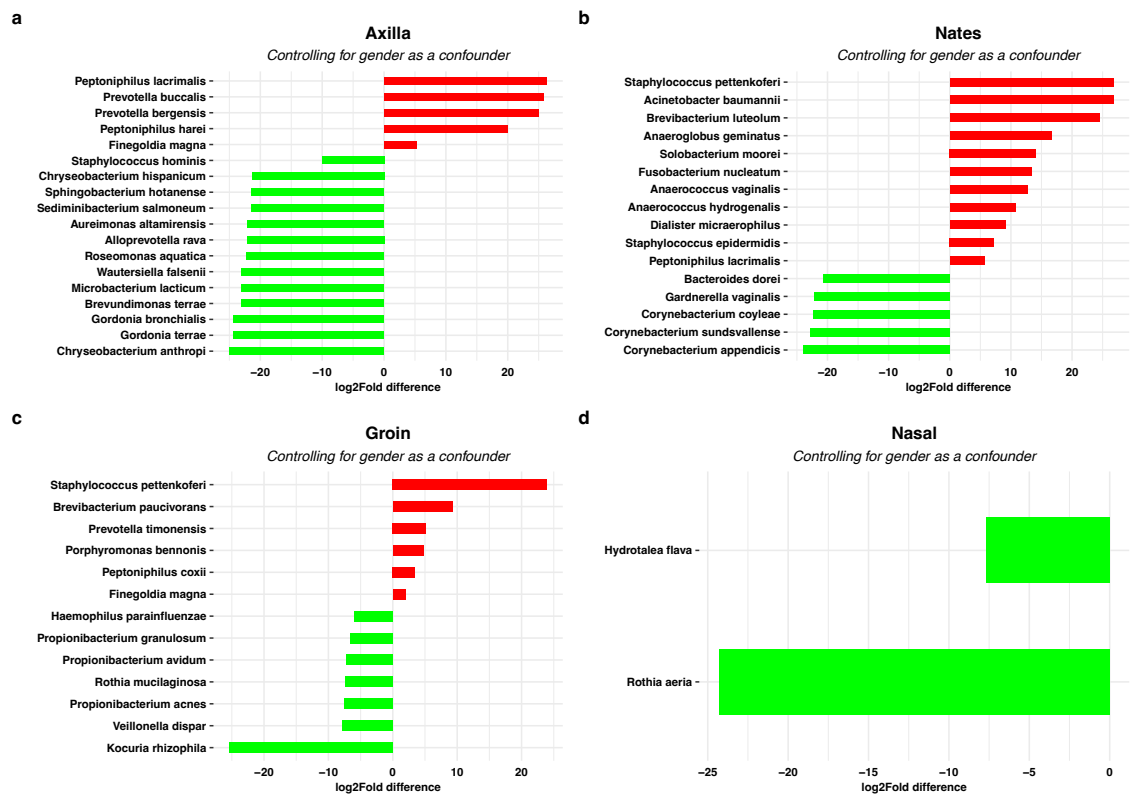


Figure 9: Bar plots of differentially abundant species across nasal and skin sites.

DESeq2 was used to for statistical analysis while controlling for gender as a confounder. Species enriched in HS samples in red. Species enriched in control samples in green.

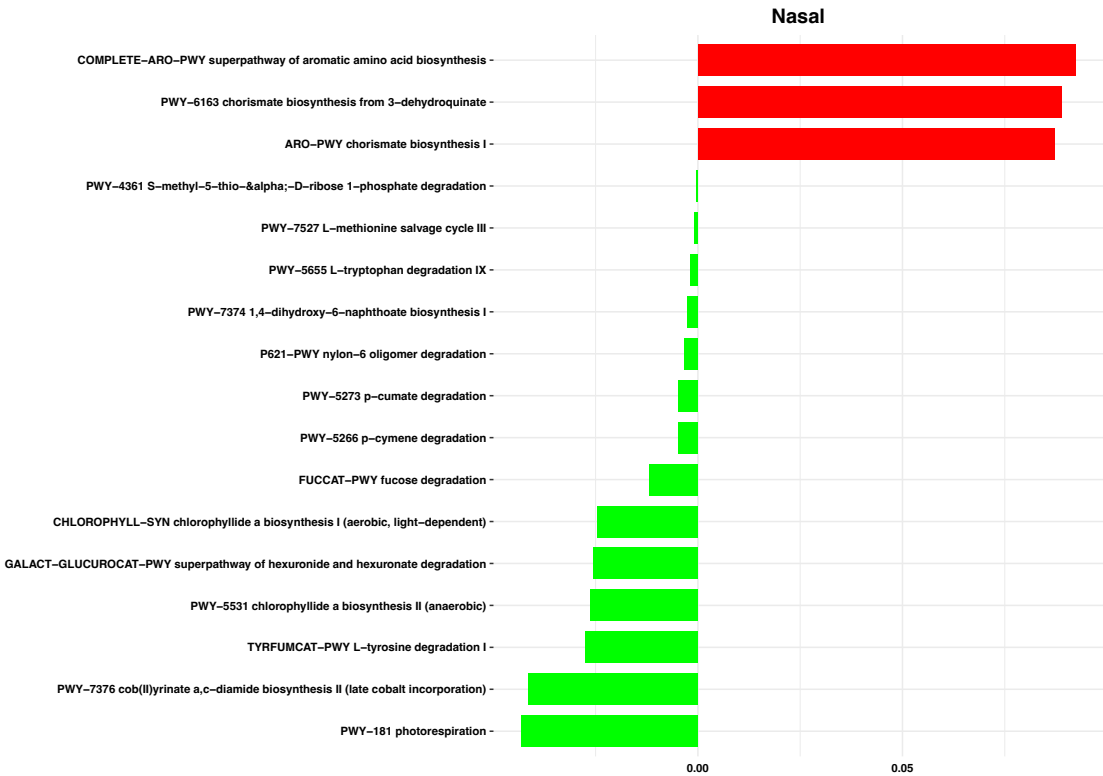


The *Finegoldia magna* assigned ASV Seq 4 was found at increased abundance in groin and axilla samples derived from individuals with HS relative to healthy controls. This was also reflected at the species level. Significantly differentially abundant pathways were found in relation to the nasal microbiome and one pathway in the groin microbiome (Figure 10).

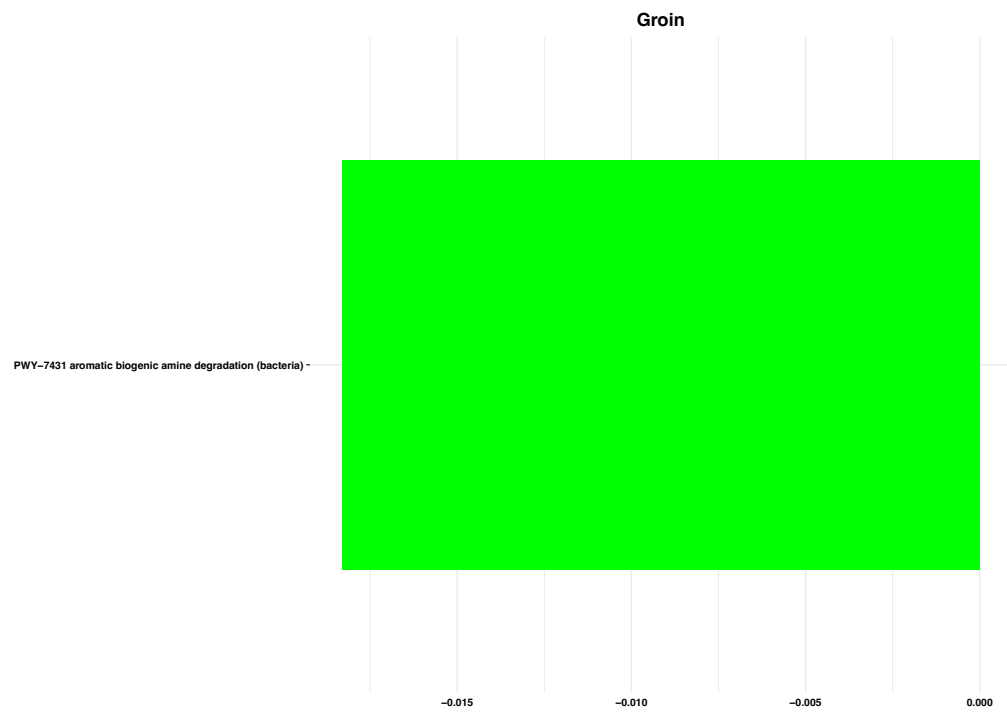
Figure 10: Differential MetaCyc pathways across skin sites. (a) Nasal. (b) Groin.

Wilcoxon signed-rank test was used to calculate p-values. MetaCyc pathways enriched in HS samples in red. MetaCyc pathways enriched in control samples in green.

(a)



(b)



4.4 Discussion

We identified a number of differences in microbiome configuration in faecal and swab samples from across a number of body sites in individuals with HS compared to healthy controls. Alpha diversity was lower in subjects with HS across most of these sites suggesting a reduction in the richness of the skin microbiota compared to controls. Decreases in alpha diversity in skin, and nasal microbiota have been reported in atopic dermatitis, with conflicting results for the gut microbiota (654–657). Alpha-diversity has been observed to be lower in skin samples from individuals with psoriasis, with even more variable results in the gut (658–660).

4.4.1 Skin Microbiome

Ring *et al* examined the difference in the skin microbiome between subjects with hidradenitis suppurativa and healthy controls using skin biopsies (159). Our analysis corroborates and extends the number of taxa found to differentially abundant. In particular there is agreement that *Peptoniphilus lacrimalis*, *Fingoldia magna*, *Peptoniphilus coxii*, *Anaerococcus murdochii*, and *Anaerococcus obesiensis* are more abundant in HS, with a higher abundance of *Cutibacterium acnes* in healthy controls (159). Colonisation and proliferation of certain strains of *C. acnes* may play a role in the pathogenesis of acne vulgaris (661,662). The depletion of *C. acnes* in individuals with HS suggests that it does not play a similar mechanistic role in HS as it does in acne. However, a decrease in *C. acnes* may alter the microbial ecological of skin and promote HS pathogenesis. Alpha diversity was reduced in nasal and groin samples. This is also found in atopic dermatitis; however, the corresponding increase in *Staphylococcus aureus* typically seen in atopic dermatitis was not detected in these patients with HS (663,664). Similarly, in psoriasis a reduction in alpha diversity is seen compared to healthy controls, featuring elevated

Streptococcus and reduction in *Propionibacterium* that was not seen in this cohort with HS (660). Higher numbers of bacteria with pathogenic capability namely *F. magna* was noted in the current study. *F. magna* has been shown to have immune modulating activities; in particular it can promote the formation of neutrophil extracellular traps (NET). These NETs feature prominently in HS lesions and their abundance is correlated with disease severity, as measured by Hurley staging (665). Thus *F. magna* may contribute to HS disease biology by stimulating NET formation. *F. magna* has also been shown to activate mast cells and basophils which in turn produce proinflammatory histamine and cytokines (666,667). In a recent study *F. magna* was demonstrated to activate proinflammatory neutrophils mediated by virulence factors protein L and FAF (*F. magna* adhesion factor)(668).

4.4.2 Potential impact

There is a lack of high-quality evidence for treatment options in HS (226,628,669). A multidisciplinary approach with a combination of medical and surgical treatment is often needed, combined with lifestyle measures: smoking cessation and weight loss (226,628,669). Antibiotics remain the initial treatment for most patients, with TNF-alpha inhibitors in those who fail to respond (226,628,669). The use of antibiotics in HS, for their anti-inflammatory rather than anti-microbial effect, may play a role in the reduction in alpha-diversity seen in this study; however, we detected no significant difference in ASVs in those who received antibiotics in the preceding year compared to those who did not. Microbiota based therapies may have potential benefits in HS, in particular targeted microbial supplementation to increase diversity and richness. The selective depletion of certain microbes such as *F. magna* and *R. gnavus*, which may play a pathogenic role, could provide therapeutic targets.

4.5 Conclusion

We have characterised the skin microbiota in patients with HS compared to healthy controls. The identification of particular taxa that may contribute to HS pathogenesis, such as *F. magna*, could inform future microbiota-based therapeutic strategies.

Supplementary Table 1: DNA concentration of samples as measured by the qubit.

Sample name	Patient	disease_state	qubit_values	skin_site	sample_type
Blank	Blank	blank	0.521	blank	blank
CS01BK	CS01	control	29.6	Buttock	swab
CS01GR	CS01	control	30.4	Groin	swab
CS01IM	CS01	control	2.63	Inframammary_fold	swab
CS01NA	CS01	control	30.7	Nasal	swab
CS03BK	CS03	control	35.1	Buttock	swab
CS03IM	CS03	control	7.25	Inframammary_fold	swab
CS03NA	CS03	control	31.7	Nasal	swab
CS04BK	CS04	control	28.6	Buttock	swab
CS04GR	CS04	control	24.9	Groin	swab
CS04IM	CS04	control	26.3	Inframammary_fold	swab
CS05BK	CS05	control	15.1	Buttock	swab
CS05GR	CS05	control	22.4	Groin	swab
CS05NA	CS05	control	8.53	Nasal	swab
CS06BK	CS06	control	28	Buttock	swab
CS06GR	CS06	control	7.55	Groin	swab
CS06IM	CS06	control	3.59	Inframammary_fold	swab
CS06NA	CS06	control	23.8	Nasal	swab
CS07BK	CS07	control	17.3	Buttock	swab
CS07GR	CS07	control	16.6	Groin	swab
CS07IM	CS07	control	16.1	Inframammary_fold	swab
CS07NA	CS07	control	40.2	Nasal	swab
CS08AX	CS08	control	18.6	Axilla	swab
CS08BK	CS08	control	25.3	Buttock	swab
CS08GR	CS08	control	24.3	Groin	swab
CS08NA	CS08	control	27.5	Nasal	swab
CS09AX	CS09	control	25.1	Axilla	swab
CS09BK	CS09	control	30.6	Buttock	swab
CS09GR	CS09	control	37.3	Groin	swab
CS09IM	CS09	control	26.4	Inframammary_fold	swab
CS09NA	CS09	control	20.2	Nasal	swab
CS10BK	CS10	control	3.55	Buttock	swab
CS10GR	CS10	control	23	Groin	swab
CS10IM	CS10	control	23.9	Inframammary_fold	swab
CS10NA	CS10	control	15.9	Nasal	swab
CS11AX	CS11	control	11	Axilla	swab
CS11BK	CS11	control	24	Buttock	swab
CS11GR	CS11	control	16.3	Groin	swab
CS11NA	CS11	control	19.6	Nasal	swab
CS12AX	CS12	control	15.9	Axilla	swab
CS12BK	CS12	control	24.5	Buttock	swab
CS12GR	CS12	control	24	Groin	swab

CS12NA	CS12	control	30.3	Nasal	swab
CS13BK	CS13	control	18.5	Buttock	swab
CS13GR	CS13	control	14.8	Groin	swab
CS13IM	CS13	control	23.8	Inframammary_fold	swab
CS13NA	CS13	control	18.9	Nasal	swab
CS14AX	CS14	control	2.98	Axilla	swab
CS14BK	CS14	control	18.2	Buttock	swab
CS14GR	CS14	control	32.7	Groin	swab
CS14NA	CS14	control	16.9	Nasal	swab
CS15BK	CS15	control	24.2	Buttock	swab
CS15GR	CS15	control	28.4	Groin	swab
CS15NA	CS15	control	19.2	Nasal	swab
CS16BK	CS16	control	5.02	Buttock	swab
CS16GR	CS16	control	13.9	Groin	swab
CS16IM	CS16	control	8.03	Inframammary_fold	swab
CS16NA	CS16	control	31.6	Nasal	swab
CS17BK	CS17	control	15.3	Buttock	swab
CS17GR	CS17	control	16.2	Groin	swab
CS17IM	CS17	control	19.2	Inframammary_fold	swab
CS17NA	CS17	control	13.6	Nasal	swab
CS18BK	CS18	control	16.2	Buttock	swab
CS18GR	CS18	control	9.69	Groin	swab
CS18IM	CS18	control	9.25	Inframammary_fold	swab
CS18NA	CS18	control	6.42	Nasal	swab
CS19BK	CS19	control	24	Buttock	swab
CS19IM	CS19	control	21.4	Inframammary_fold	swab
CS19NA	CS19	control	19.8	Nasal	swab
CS20AX	CS20	control	20.6	Axilla	swab
CS20BK	CS20	control	32	Buttock	swab
CS20GR	CS20	control	32.2	Groin	swab
CS20IM	CS20	control	27.1	Inframammary_fold	swab
TH01L1	TH01	HS	20.6	Groin	swab
TH01NA	TH01	HS	35.9	Nasal	swab
TH01RA	TH01	HS	32.5	Axilla	swab
TH01RB	TH01	HS	32.8	Buttock	swab
TH02LB	TH02	HS	20.7	Buttock	swab
TH02NA	TH02	HS	38.5	Nasal	swab
TH02RG	TH02	HS	36.2	Groin	swab
TH03LI	TH03	HS	30.7	Groin	swab
TH03NA	TH03	HS	2.76	Nasal	swab
TH03RA	TH03	HS	48	Axilla	swab
TH04LA	TH04	HS	2.95	Axilla	swab
TH04LG	TH04	HS	23.9	Groin	swab
TH04NA	TH04	HS	25.6	Nasal	swab
TH04RM	TH04	HS	20.1	Inframammary_fold	swab

TH05LA	TH05	HS	21.8	Axilla	swab
TH05LB	TH05	HS	36.5	Buttock	swab
TH05LG	TH05	HS	18.1	Groin	swab
TH05NA	TH05	HS	22.1	Nasal	swab
TH05RB	TH05	HS	29.2	Buttock	swab
TH05RG	TH05	HS	44.8	Groin	swab
TH06NA	TH06	HS	30.8	Nasal	swab
TH06RA	TH06	HS	32	Axilla	swab
TH07LG	TH07	HS	43.1	Groin	swab
TH07NA	TH07	HS	45.8	Nasal	swab
TH07RM	TH07	HS	33.5	Inframammary_fold	swab
TH08LA	TH08	HS	39.7	Axilla	swab
TH08LM	TH08	HS	44.9	Inframammary_fold	swab
TH08SP	TH08	HS	28.7	Suprapubic	swab
TH09LA	TH09	HS	31	Axilla	swab
TH09RG	TH09	HS	24.6	Groin	swab
TH10RA	TH10	HS	28	Axilla	swab
TH10RG	TH10	HS	33.7	Groin	swab
TH11LM	TH11	HS	47.8	Inframammary_fold	swab
TH11NA	TH11	HS	37.1	Nasal	swab
TH11RG	TH11	HS	18.8	Groin	swab
TH12LM	TH12	HS	33.1	Inframammary_fold	swab
TH12NA	TH12	HS	28.6	Nasal	swab
TH12RA	TH12	HS	52	Axilla	swab
TH13LA	TH13	HS	29.9	Axilla	swab
TH14NA	TH14	HS	57	Nasal	swab
TH15NA	TH15	HS	27.4	Nasal	swab
TH16LA	TH16	HS	27.9	Axilla	swab
TH16NA	TH16	HS	31.8	Nasal	swab
TH16RAB	TH16	HS	35.6	Abdomen	swab
TH17LA	TH17	HS	2.78	Axilla	swab
TH17NA	TH17	HS	44.9	Nasal	swab
TH18LG	TH18	HS	28.6	Groin	swab
TH18NA	TH18	HS	40.3	Nasal	swab
TH19LA	TH19	HS	19.7	Axilla	swab
TH19LG	TH19	HS	40.2	Groin	swab
TH19NA	TH19	HS	23.3	Nasal	swab
TH20LA	TH20	HS	37.9	Axilla	swab
TH20NA	TH20	HS	47.3	Nasal	swab
TH21NA	TH21	HS	22.9	Nasal	swab
TH21RA	TH21	HS	4.14	Axilla	swab
TH22NA	TH22	HS	32.1	Nasal	swab
TH22SP	TH22	HS	30.4	Suprapubic	swab
TH23LA	TH23	HS	38.9	Axilla	swab
TH23NA	TH23	HS	26.5	Nasal	swab

TH23RA	TH23	HS	34.7	Axilla	swab
TH24LSP	TH24	HS	27.5	Suprapubic	swab
TH24NA	TH24	HS	12.9	Nasal	swab
TH25NA	TH25	HS	31.1	Nasal	swab
TH25RG	TH25	HS	45.6	Groin	swab
TH26AB	TH26	HS	43.2	Abdomen	swab
TH26NA	TH26	HS	49.5	Nasal	swab
TH27NA	TH27	HS	31.1	Nasal	swab
TH28LG	TH28	HS	6.89	Groin	swab
TH28NA	TH28	HS	27.9	Nasal	swab
TH29LA	TH29	HS	21.3	Axilla	swab
TH29LSP	TH29	HS	40.7	Suprapubic	swab
TH30LA	TH30	HS	34.7	Axilla	swab
TH30NA	TH30	HS	34.1	Nasal	swab
TH30RG	TH30	HS	30.3	Groin	swab

Supplementary Table 2: 15 ASVs that reached the threshold using the ‘frequency method’

	Kingdom	Phylum	Class	Order	Family	Genus	Species
Seq 990	Bacteria	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Blautia	Blautia luti
Seq 1261	Bacteria	Cyanobacteria/Chloroplast	Chloroplast	Chloroplast	Streptophyta	unclassified	unclassified
Seq 1280	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Kocuria	unclassified
Seq 1380	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Sphingomonas	unclassified
Seq 1535	Bacteria	Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	Lactobacillus delbrueckii
Seq 1749	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas	Pseudomonas rhizosphaerae
Seq 1870	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Wautersiella	Wautersiella falsenii
Seq 1880	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Xanthobacter	unclassified
Seq 2214	Bacteria	Candidatus Saccharibacteria	unclassified	unclassified	unclassified	unclassified	unclassified
Seq 2897	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylobacteriaceae	Methylobacterium	Methylobacterium aquaticum
Seq 2924	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	unclassified	unclassified
Seq 3029	Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae 1	Bacillus	unclassified
Seq 3470	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	Tannerella	Tannerella forsythia
Seq 4315	Bacteria	Acidobacteria	Acidobacteria Gp4	Blastocatella	unclassified	unclassified	unclassified
Seq 4461	Bacteria	Proteobacteria	Epsilonproteobacteria	Campylobacterales	Campylobacteraceae	Campylobacter	Campylobacter ureolyticus

5. The Gut Microbiota in Hidradenitis Suppurativa

Published in Journal of Investigative Dermatology

McCarthy S, Barrett M, Kirthi S, Pellanda P, Vlckova K, Tobin AM, Murphy M, Shanahan F, O'Toole PW. Altered Skin and Gut Microbiome in Hidradenitis Suppurativa. Journal of Investigative Dermatology. 2021 Aug 6.

Presented at European Academy of Dermatology and Venereology 30th Congress, September 2021

Abstract

Hidradenitis suppurativa (HS) is a chronic inflammatory skin disease characterized by the formation of nodules, abscesses, and fistula at intertriginous sites. The skin-gut axis is an area of emerging research in inflammatory skin disease and is a potential contributory factor to the pathogenesis of HS. 59 patients with HS provided faecal samples for analysis. 30 healthy controls provided faecal samples. We performed bacterial 16S rRNA gene amplicon sequencing on total DNA derived from the samples. Microbiome alpha diversity was significantly lower in the faecal samples of individuals with HS which may be secondary to disease biology or related to antibiotic usage. *Ruminococcus gnavus* was more abundant in the faecal microbiome of individuals with HS, which is also reported in Crohn's disease (CD), suggesting comorbidity due to shared gut microbiota alterations. These alterations in gut microbiome in HS warrant further exploration, and therapeutic strategies including faecal microbiota transplant (FMT) or bacteriotherapy could be of benefit.

5.1 Introduction

Hidradenitis suppurativa (HS) is a chronic, debilitating, follicular skin disease presenting with deep-seated, painful, inflammatory nodules of the axillary, inframammary, inguinal, and anogenital regions (628). A population prevalence of up to 4% has been reported in the literature (229,628,629). There is a female predominance, with pubertal onset (628,630,631). Smoking, obesity are associated, and a genetic predisposition has been reported (630–632). Comorbidities have been identified in patients with HS including spondyloarthropathy, metabolic syndrome and inflammatory bowel disease (IBD), particularly Crohn's disease (61,633,634). As well as significant morbidity, HS is associated with increased mortality, in particular due to cardiovascular events, with increased cancer risk also recorded (635,636). Depression, anxiety and substance misuse are also common (637,638).

The cause of HS is incompletely understood, with follicular occlusion, dysregulated inflammatory response of cytokines such as tumour necrosis factor (TNF)- α , interleukin(IL)-1 β and IL-17, and an altered microbiota are thought to play a role (141,158,630,639–642).

HS and IBD share common manifestations of sterile abscesses, and sinus tract formation (670). Similar pathways are activated in Crohn's disease and HS, with elevated production of the innate immune mediators IL-1, IL-6, IL-17, IL-23 and TNF- α (671–673). Smoking and obesity are common associations, and HS and IBD respond to TNF- α inhibitor therapy (630,674–676). Research supports the role of the gut microbiota in IBD and other inflammatory conditions including rheumatoid arthritis, and psoriasis (677–683). Although the skin microbiota in HS is an area of expanding research, the gut microbiota or the 'gut-skin axis' in HS deserves greater

consideration (236,639,684). One study investigated *Faecalibacterium prausnitzii* and *Escherichia coli* levels in patients with psoriasis, concomitant psoriasis and IBD, HS, and concomitant HS and IBD (684). Increased levels of *E. coli* and decreased levels of *F. prausnitzii* was noted in patients with psoriasis. A significant difference in abundance of *E. coli* or *F. prausnitzii* was not noted in patients with HS (684). As an altered gut microbiota has been associated with various pathophysiologies involving immune dysregulation, it may play a role in the development of HS. In this study we tested for an association between microbiota alteration in faeces and HS.

5.2 Material and Methods

5.2.1 Study Population

Adult patients with a confirmed clinical diagnosis of hidradenitis suppurativa made by a consultant dermatologist in two tertiary referral centres in Ireland were invited to participate in the study. Ethical approval (Cork Research Ethics Committee and Tallaght University Hospital Ethics Committee), and written informed consent from patients was obtained. Exclusion criteria included topical or oral antibiotic usage in the preceding four weeks. Data including age, gender, smoking status, weight, height, body mass index, presence of co-morbidities and severity of disease (Hurley Score)(16) were recorded. Healthy adult controls were recruited from the general population, and were age and gender matched.

5.2.2 Sample collection

Fresh (<24 hours) faecal samples were provided by patients and controls and stored at -80°C prior to microbial DNA extraction.

5.2.3 Microbial DNA extraction

Microbial DNA was extracted from stool samples using the repeated bead beating method, with some modifications (685). (See Supplementary Methods chapter)

5.2.4 Library Preparation and 16S rRNA gene sequencing

Total community DNA extracted from clinical samples underwent 16S rRNA gene PCR. The 16S rRNA gene was amplified using primers for the V3-V4 region; forward,

TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGGGNGGCWGC

G-3' and reverse, 5'-

GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTACHVGGGTATC

TAATCC-3'¹⁷.(643)

Faecal microbial genomic DNA was amplified using Phusion High-Fidelity DNA Polymerase (Thermo Scientific, Massachusetts, USA) with the PCR thermocycler protocol as follows: Initiation step of 98 °C for 3 min followed by 25 cycles of 98 °C for 30 s, 55 °C for 60 s, and 72 °C for 20 s, and a final extension step of 72 °C for 5 min.

A subsequent indexing PCR was carried out to add unique sample-specific DNA barcodes to the generated amplicons in accordance with the Illumina 16S Metagenomic Sequencing Protocol (Illumina, California, USA)(644). Libraries DNA concentration was quantified using a Qubit fluorimeter (Invitrogen) using the 'High Sensitivity' assay and samples were pooled at a standardised concentration (644). The pooled library was sequenced on the Illumina MiSeq platform (Illumina, California, USA) utilising 2×300 bp chemistry.

5.2.5 Microbiome profiling

The microbiome composition of samples was profiled by standard 16S rRNA gene sequencing protocols as previously published by our laboratory (685). (See Supplementary Methods chapter)

5.2.6 Bioinformatic and biostatistical analysis

The majority of the analysis was performed in R (v3.6.0). Paired reads were quality filtered, trimmed, merged and Amplicon Sequence Variants (ASV) inferred using the R package dada2 (v1.12.1)(645). Taxonomic classification was performed using the RDP Classifier within Mothur in conjugation with SPINGO, a species-level classifier (646). A confidence cut of 80% was used for taxonomic assignment. QIIME v1.9.1 and the R package vegan v2.5.6 were used to calculate β -diversity metrics (647). β -diversity was visualized via principal coordinates analysis (PCoA) plots whose coordinates were identified using with the Ape package v5.1. R-squared (R^2) and p-value were calculated using Permutational Multivariate Analysis of Variance (PERMANOVA) via the R package vegan (v2.4.2). Differential abundance analysis was carried out using DEseq2 (v1.22.2)(648). Random forest was performed in R using the package randomForest (v4.6.14) Genomic functionality was inferred using PICRUST2 with the command `picrust2_pipeline.py` with default (649).

5.2.7 Storage of sequencing data

Datasets related to this article can be found at

<https://www.ebi.ac.uk/ena/browser/view/PRJEB43835>, hosted at European

Nucleotide Archive, accession number PRJEB43835 (653).

5.3 Results

5.3.1 Descriptive statistics of the study population

59 patients with HS were recruited providing faecal samples. 30 healthy controls provided faecal samples (Planned 2:1 ratio) (Table 1). Mean body mass index (BMI) in the HS group was 31.5, and 28.2 in the faecal control group. 4 (6.8%) patients in the HS group had a history of Crohn's disease. Of the 59 patients with HS, 18 (30.5%) were Hurley Stage 1 (abscess formation without sinus tracts and cicatrization), 32 (54.2%) were Hurley Stage 2 (recurrent abscesses with tract formation and scars) and 9 (15.3%) were Hurley Stage 3 (multiple interconnected tracts and abscesses throughout an entire area).

Table 1: Subject characteristics of HS subjects and healthy controls

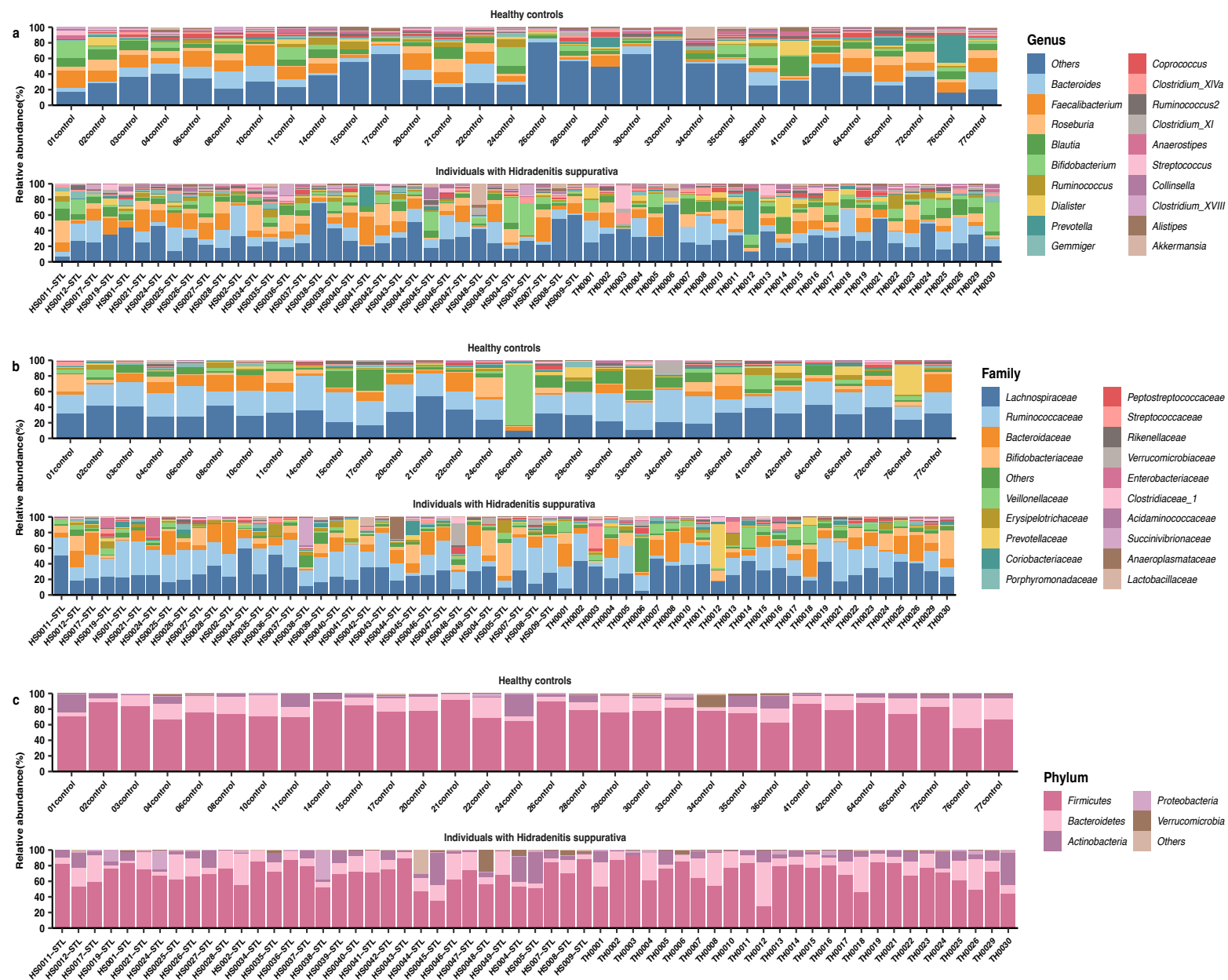
Comparison of variables between HS cohort and healthy controls. Wilcoxon signed-rank test or χ^2 statistic was used to determine significance.

	HS	Controls	Significance
N (patients)	59	30	n/a
Gender (Female/Male)	45/14	20/10	NS
Age (mean, range)	37, 21-62	38, 19-62	NS
BMI (mean, range)	31.5, 19.6-45.0	28.2, 18.7-46.3	0.023
Crohn's Disease (yes/no)	4/59	0/30	NS
TNF- α inhibitor therapy	9/59	0/30	

5.3.2 Overall structure of the faecal microbiota is altered in HS

We examined the microbiome composition of 59 and 30 faecal specimens from individuals with HS and healthy controls respectively (Figure 1).

Figure 1: Taxonomic representation of microbiome in faecal specimens. (a) Bar plots displaying the relative abundance of genera in faecal samples. Genera with a relative abundance of less than 1% across all samples were grouped into ‘others’ i.e. with sequences not classified at the genus level. (b) Bar plots displaying the relative abundance of families in faecal samples. Families with a relative abundance of less than 0.5% across all samples were grouped into ‘others’ i.e. with sequences not classified at the family level. (c) Bar plots displaying the relative abundance of phyla in faecal samples. Families with a relative abundance of less 0.5% across all samples were grouped into ‘others’ i.e. with sequences not classified at the phylum level.



Ecological metrics showed a difference between the microbiome of individuals with HS and healthy controls (Figure 2). Alpha-diversity, a marker of microbial species richness or variation within a sample, was significantly lower in individuals with HS (Figure 2a).

Figure 2: Ecological overview of faecal microbiome data. (a) Alpha-diversity.

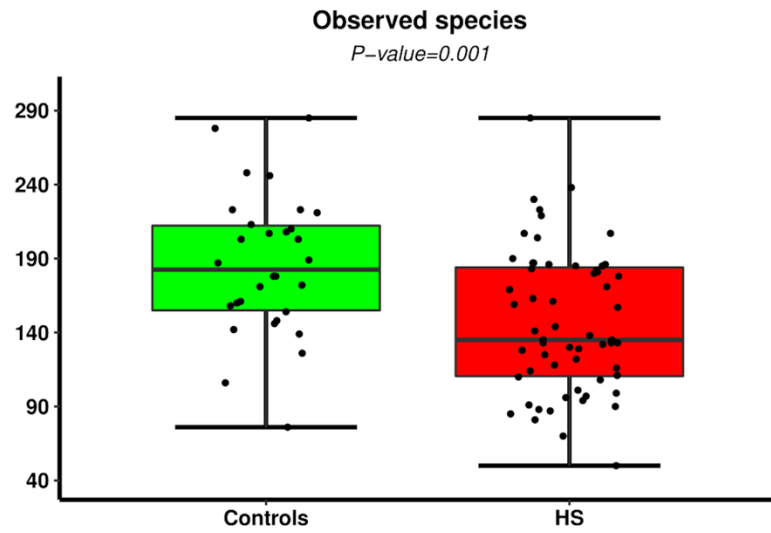
Boxplot comparing alpha diversity (observed species index) between individuals with HS versus healthy controls. Wilcoxon signed-rank test was used to calculate p-values

(b) Beta diversity. Respective distance between samples based on their microbiome composition was calculated using unweighted Unifrac. Principal Coordinates Analysis (PCoA) was performed to obtain the coordinates of the first two PCoA axes which were plotted. Statistical testing was performed using

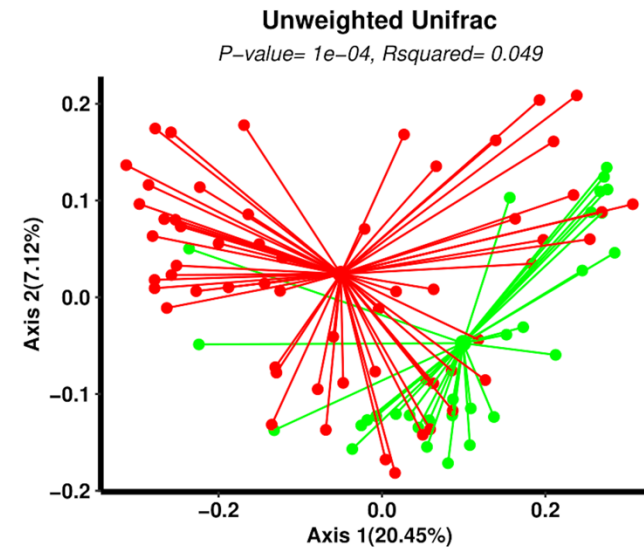
Permutational Multivariate Analysis of Variance (PERMANOVA). **(c) Hierarchical clustering.** The relatedness between samples based on their microbiome composition was calculated using Spearman's rank correlation coefficient.

Hierarchical clustering was performed using the Ward2 method and the results plotted as a dendrogram. Statistical testing was performed using Permutational Multivariate Analysis of Variance (PERMANOVA).

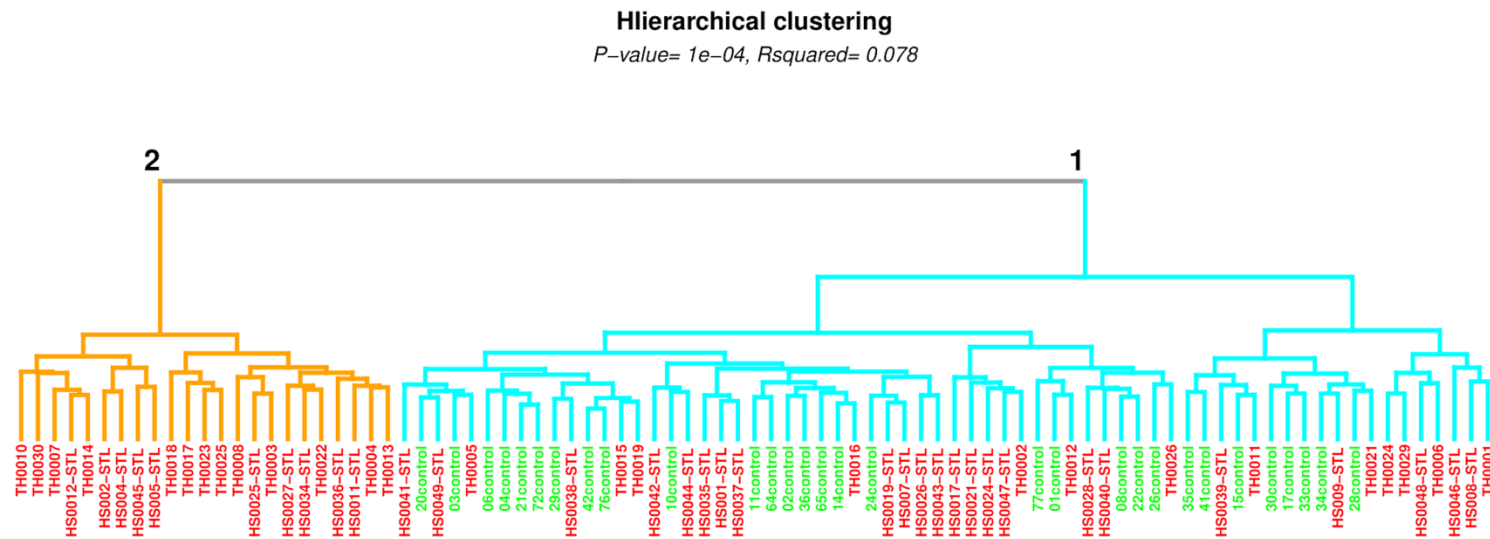
a



b

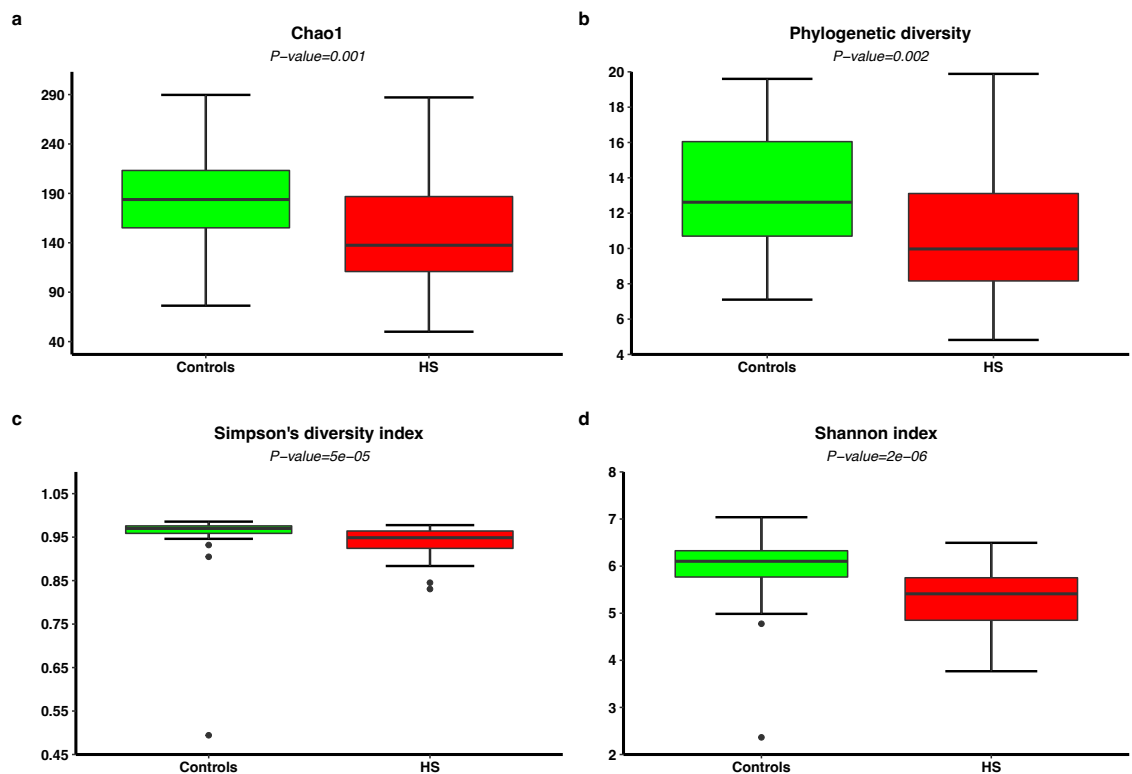


c



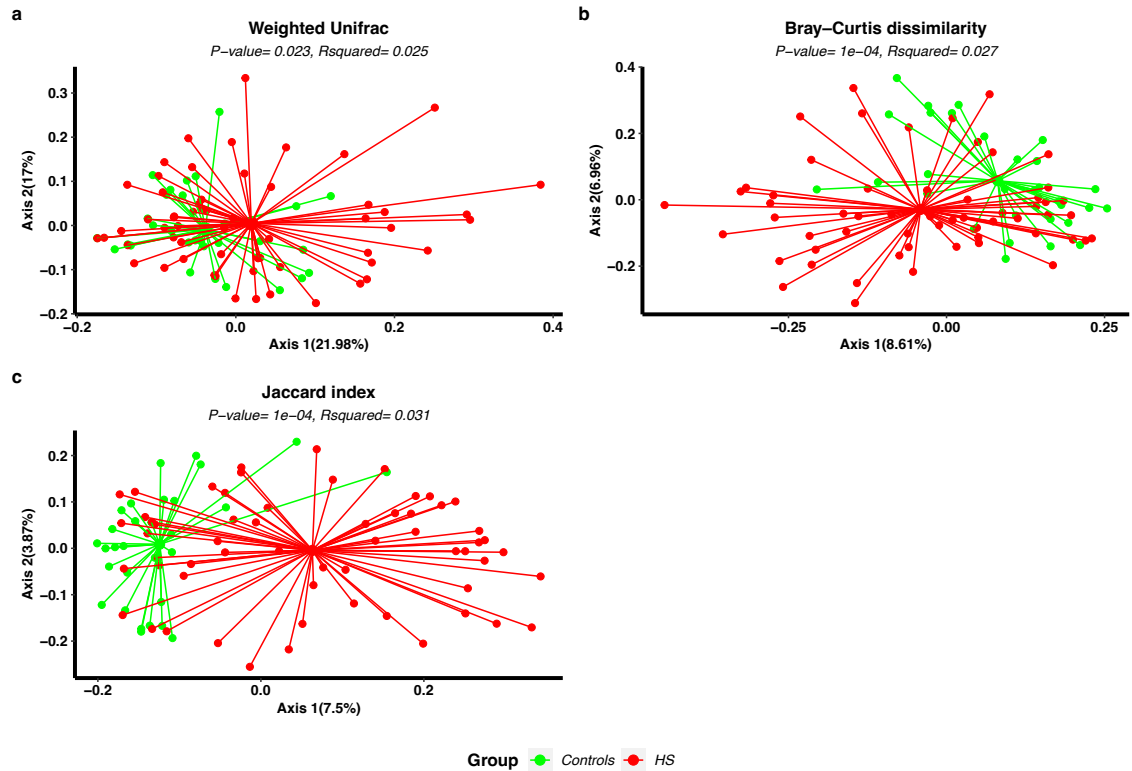
This reduction was also observed for four other metrics of alpha-diversity including Shannon and phylogenetic diversity (Figure 3).

Figure 3: Bar plots of alpha diversity metrics for faecal samples. (a) Chao1. (b) Phylogenetic diversity. (c) Simpson's Diversity Index. (d) Shannon index. Wilcoxon signed-rank test was used to calculate p-values.



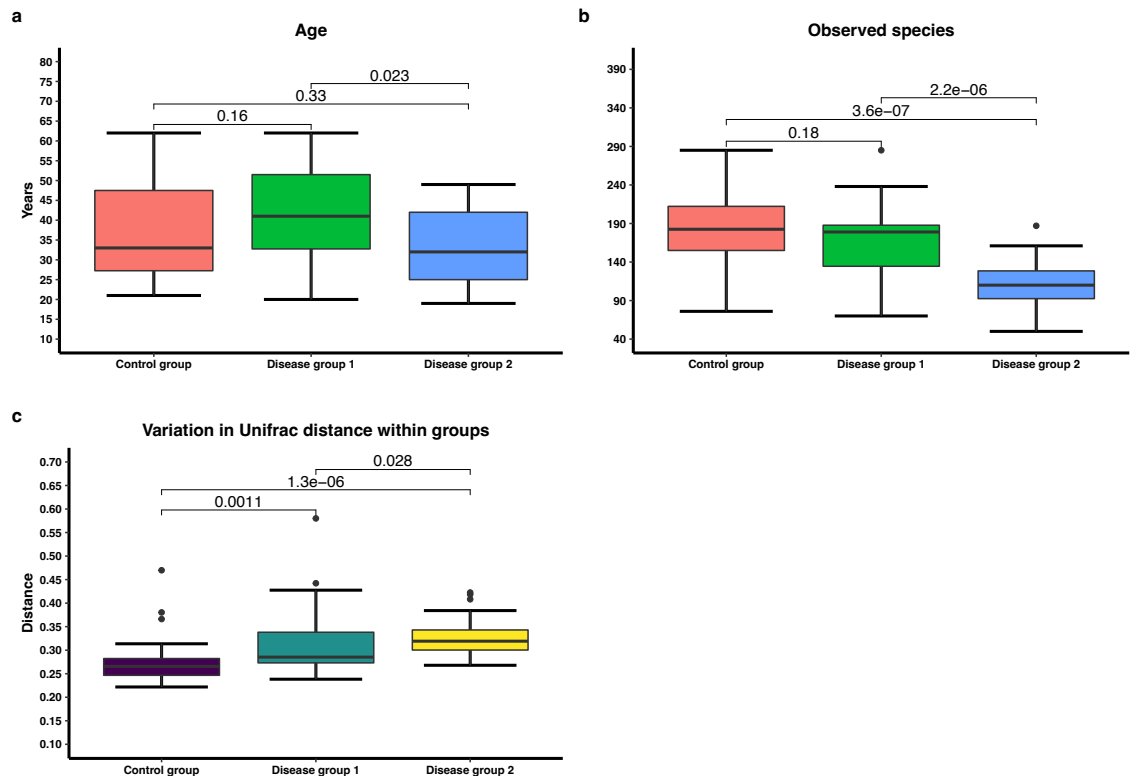
A microbiome separation in beta-diversity, (a comparison of global microbial composition in all the samples), between the HS and healthy controls was observed across all metrics tested (Figure 2b) (Figure 4), noting also less clustering within the HS samples. Hierarchical clustering replicated and reinforced this separation as seen by the presence of a cluster composed exclusively of patients with HS (Figure 4c).

Figure 4: PCoA representing Beta diversity metrics for faecal samples. (a) Weighted Unifrac. (b) Bray–Curtis Dissimilarity. (c) Jaccard index. Statistical testing was performed using Permutational Multivariate Analysis of Variance (PERMANOVA).



We further investigated this cohort by grouping the individuals informed by the hierarchical clustering that is, control group (control samples, cyan branch, branch No.1), disease group 1 (cyan branch, branch No.1) and disease group 2 (orange branch, branch No.2). We found that disease group 2 was composed of significantly younger subjects than disease group 1 but not the controls (Figure 5a). Alpha diversity was lower in disease group 2 compared to the disease group 1 and the control group (Figure 5b). There was greater within-group microbiome variation, evidenced by higher levels of Unifrac distance between samples, within disease group 2 compared to the other two groups (Figure 5c).

Figure 5: Difference in groups informed by clustering. (a) Bar plot of age differences. (b) Bar plots of observed species. (c) Differences in the Variation in Unifrac distance within groups. Wilcoxon signed-rank test was used to calculate p-values.



We found no statistical difference with respect to gender between these groups. Menopause has been previously reported to be associated with compositional changes in the microbiota.(686) Although we did not have direct information on menopausal status, we classified individuals as possibly being menopausal if over age 50 (average of menopause age in western populations being 51) and of the female sex (Table 2).(687–689)

Table 2: Menopausal status of females with HS studied

	Menopausal*	Non-menopausal*
Control group	5	25
Disease group 1	4	32
Disease group 2	0	23

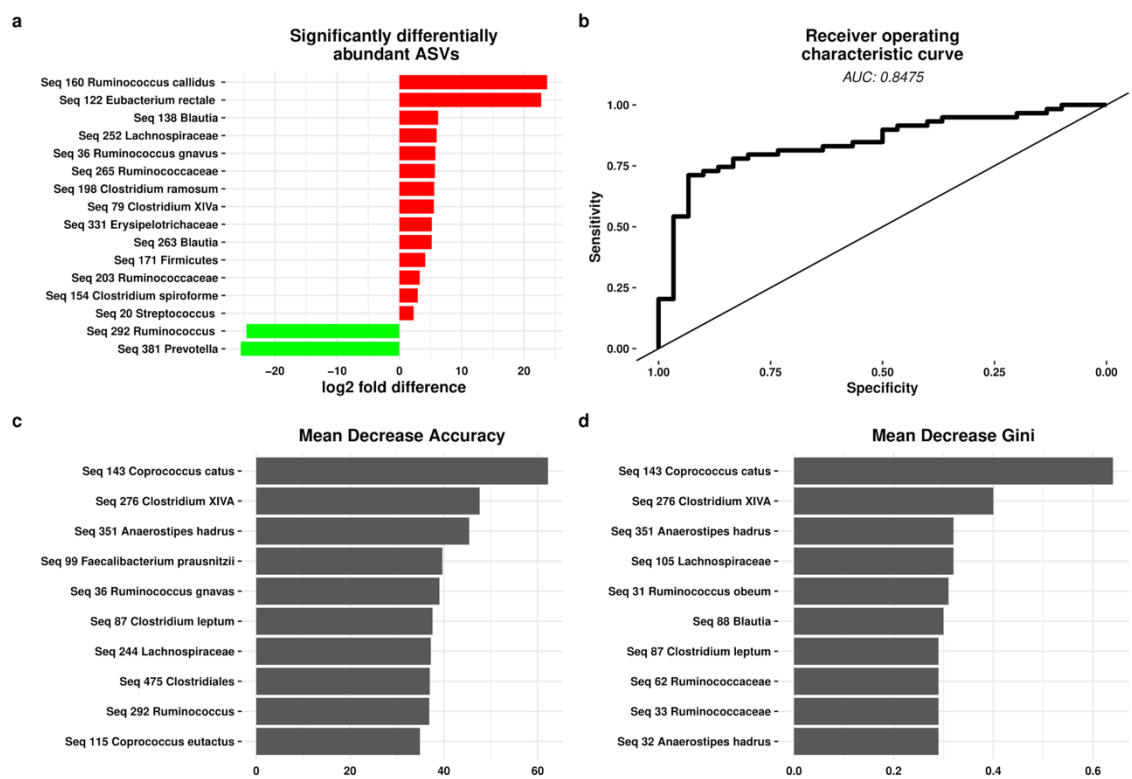
Using this as a proxy for menopausal state, we did not find a statically significant difference between the three groups (chi-squared test). Furthermore microbiome alpha diversity did not show any correlation with known Crohn's disease or calprotectin level (Pearson correlation).

5.3.3 Differentially abundant ASVs in the faecal microbiome

Microbial amplicon sequencing data can be rationalised in terms of amplicon sequence variants (ASVs) which allows the data to be resolved down to single-nucleotide difference (690). A number of ASVs were found to be differentially abundant between the faecal microbiome of patients with HS and healthy controls (Figure 6a).

Figure 6: Differentially abundant ASVs and machine learning classification. (a)

Bar plot of differential abundant ASVs expressed as log fold difference. Negative values indicate those overrepresented in controls. Positive values indicate overrepresented in individuals with HS. **(b)** Receiver operating characteristic curves (ROC). **(c,d)** Top discriminatory ASVs with regard to discriminating the HS subjects from healthy controls. **(c)** Mean Decrease Accuracy. **(d)** Mean Decrease Gini.

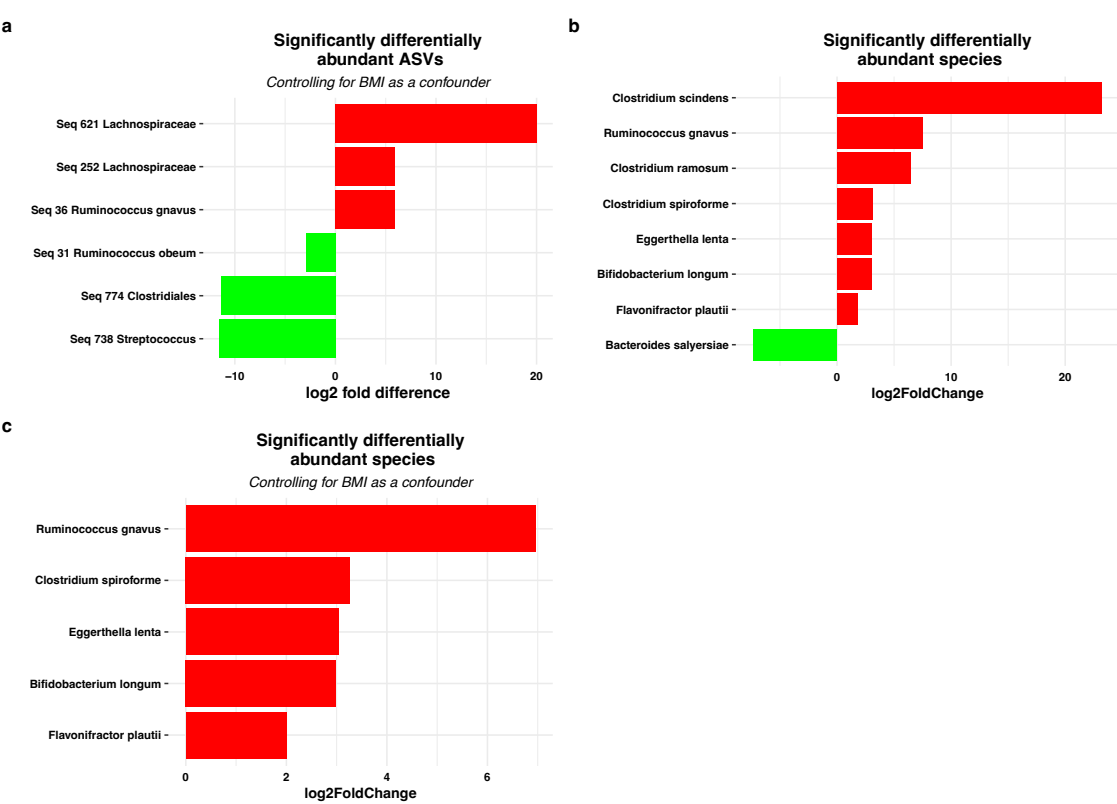


With regard to log2 fold differences, the ASVs assigned to the taxa *Ruminococcus callidus* and *Eubacterium rectale* were the most enriched in individuals with HS relative to healthy controls. However, with respect to proportional abundance, the greatest difference was detected in ASVs assigned to the taxa *Streptococcus* spp. (an

average relative abundance of 0.19% in the control cohort versus 0.95% in the HS cohort) and *Ruminococcus gnavus* (average relative abundance values of 0.01% in the control cohort versus 0.7% in the HS cohort).

As BMI was significantly different between the groups, the DESeq2 model was re-run to adjust for BMI (Figure 7). The differential over-abundance of *Ruminococcus gnavus* remained statistically significant in the HS cohort. However, an ASV assigned to *Ruminococcus obeum* was revealed to be depleted in individuals with HS. ASVs were also collapsed to the species level and differential abundance of species determined with and without BMI as a confounder (Figure 7). *R. gnavus* was retained as being significantly over-abundant in the HS cohort in both analyses.

Figure 7: Bar plots of differential abundant ASVs and species in faecal samples. (a) Significantly differentially abundant ASVs with BMI integrated into the model. (b) Significantly differentially abundant species. (c) Significantly differentially abundant species with BMI integrated into the model. DESeq2 used to for statistical analysis. ASVs/species enriched in HS samples in red. ASVs/species enriched in control samples in green.



Antibiotic usage for the previous year was recorded in the HS cohort. There were no significant ASVs that were differently abundant between those who had received antibiotic therapy in the last year and those who did not.

5.3.4 Machine learning identification of HS-related microbiota members

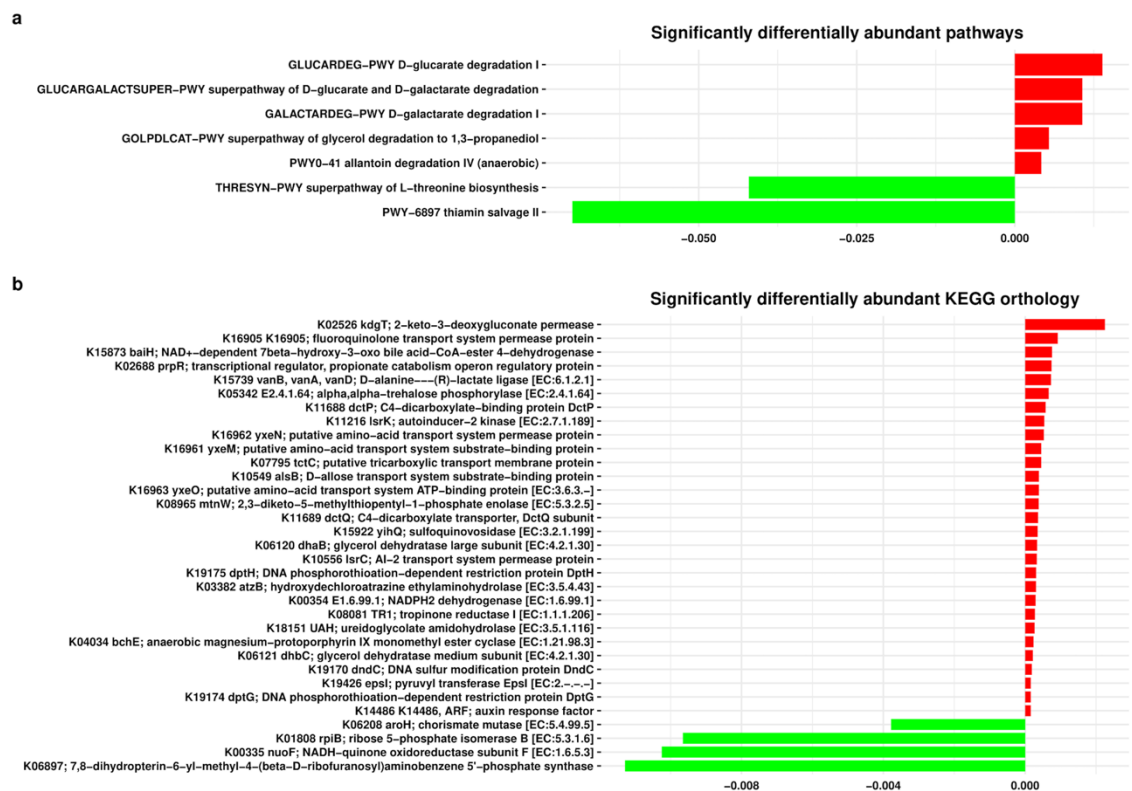
The machine learning classifier random forest (RF) was employed to test if ASVs could discriminate the HS patients from the healthy control cohort. The RF classifier performed reasonably with an area under the curve (AUC) of 0.848 (Figure 6b). A number of ASVs identified as discriminatory (i.e. as contributing to the RF model) were taxonomically assignable to butyrate-producing bacterial species including *Faecalibacterium prausnitzii*, *Coprococcus eutactus*, *Coprococcus catus* and *Anaerostipes hadrus* (Figure 6c). A number of ASVs that we had identified using the DESeq2 model as being differentially abundant were also identified including *Ruminococcus gnavus* and *Ruminococcus obeum*.

5.3.5 Changes in predicted metabolic function of the faecal microbiota

Metagenomic functionality was inferred using the algorithm PICRUSt2, which is based on the metabolic pathways of reference microbiota data to which a test-set of 16S data is compared. Several metabolic pathways were thus predicted to be differentially abundant between HS and control metagenomes (Figure 7a). Metabolic pathways for D-glucarate degradation and D-galactarate degradation, which are associated with a poor prognosis in CD, were overrepresented in individuals with HS relative to healthy controls (691).

Figure 7: Differentially abundant metabolic pathways and KEGG orthologs.

(a) Bar plot of differential abundant MetaCyc as expressed by difference in mean proportional abundance. MetaCyc pathways enriched in HS samples in red. MetaCyc pathways enriched in control samples in green. **(b)** Bar plot of differential abundant KOs as expressed by difference in mean proportional abundance. KOs enriched in HS samples in red. KOs enriched in control samples in green. Wilcoxon signed-rank test was used to calculate p-values.



5.4 Discussion

We identified a number of differences in microbiome configuration in faecal samples in individuals with HS compared to healthy controls. Alpha diversity was lower in subjects with HS suggesting a reduction in the richness of the gut microbiota compared to controls. Decreases in alpha diversity in skin, and nasal microbiota have been reported in atopic dermatitis, with conflicting results for the gut microbiota (654–657). Alpha-diversity has been observed to be lower in skin samples from individuals with psoriasis, with even more variable results in the gut (658–660).

5.4.1 Gut Microbiome in HS

Elevated levels of *Ruminococcus gnavus* and *Clostridium ramosum* were among the greatest differences in relative abundance between patients with HS and healthy control microbiomes in this study. *R. gnavus* has been consistently found to be overrepresented in subjects with Crohn's Disease and is associated with spondyloarthritis, and irritable bowel syndrome (679,692–697). *R. gnavus* is linked to development of eczema and other allergic diseases in infants, possibly due to its effect on the host immune system development (696,698). A mechanistic role of *R. gnavus* in Crohn's disease has been experimentally supported by the production of a potent proinflammatory polysaccharide which induces the production TNF- α via interacting with the toll-like receptor 4 (TLR4) of innate immune cells, such as dendritic cells (699). The production of this polysaccharide may contribute to the pathogenesis of HS. It is possible that the diseases that are comorbid with HS have a common aetiology, due, in part, to the activity of *R. gnavus*. *C. ramosum* has also been reported to be increased in Crohn's disease and obesity (680,700). In a previous

study, *R. obeum* was strongly enriched in controls relative to individuals with IBD as seen in our study (701).

We found pathways related to galactarate and glucarate degradation were more abundant in the faecal microbiome from individuals with HS. These metabolic pathways have also been implicated in Crohn's disease clinical outcome and may link to systemic inflammation. In a paired whole exome shotgun metagenomics study comparing individuals with IBD and healthy controls, immune-related gene *CABIN1* was associated with an increase of D-glucarate degradation (702). Both D-glucarate degradation and D-galactarate degradation were overrepresented in individuals with Crohn's Disease with a poor prognosis (691). Antibiotics are known to induce a host-mediated elevation in levels of galactarate and glucarate in the gut and increased expression of microbial genes responsible for galactarate and glucarate degradation may be a response to this (703). Mouse model studies demonstrated that antibiotic treatment increases galactarate and glucarate through increased expression of inducible nitric oxide synthase (iNOS)(704).

5.4.2 Potential impact

There is a lack of high-quality evidence for treatment options in HS (226,628,669). A multidisciplinary approach with a combination of medical and surgical treatment is often needed, combined with lifestyle measures; smoking cessation and weight loss (226,628,669). Antibiotics remain the initial treatment for most patients, with TNF-alpha inhibitors in those who fail to respond (226,628,669). The use of antibiotics in HS, for their anti-inflammatory rather than anti-microbial effect, may play a role in the reduction in alpha-diversity seen in this study;

however, we detected no significant difference in ASVs in those who received antibiotics in the preceding year compared to those who did not. Microbiota based therapies may have potential benefits in HS, in particular targeted microbial supplementation to increase diversity and richness. The selective depletion of certain microbes such as *R. gnavus*, which may play a pathogenic role, could provide therapeutic targets.

5.5 Conclusion

We have characterised the gut microbiota in patients with HS compared to healthy controls. We have provided evidence for a possible microbial link between IBD and HS, with *R. gnavus* abundant in both conditions. The identification of particular taxa that may contribute to HS pathogenesis, such as *R. gnavus*, could inform future microbiota-based therapeutic strategies.

6. Faecal Calprotectin and Serum C5a levels in Hidradenitis Suppurativa

6.1 Faecal Calprotectin Levels in Hidradenitis Suppurativa

Abstract

Introduction

Hidradenitis suppurativa (HS) is a chronic, painful skin disease, presenting with recurrent inflammatory nodules and abscesses in intertriginous areas, often healing with scar formation (225). HS shares common clinical manifestations, genetic susceptibility, and immunologic features with Crohn's disease (705). Faecal calprotectin is a cytosolic protein released during neutrophil activation and is a marker of gastrointestinal inflammation (706). It is a metric of disease activity, therapeutic response, and prognosis in inflammatory bowel disease (707). We sought to determine if faecal calprotectin levels were elevated in patients with HS.

Adult patients with HS were recruited and provided fresh stool samples. Calprotectin was determined by enzyme-linked immunoassay (CALPROLAB™ Calprotectin ELISA (HRP)).

Fifty-nine patients with hidradenitis suppurativa were recruited. Sixteen patients (27.1%) had a raised faecal calprotectin level of >50mg/kg. 11 (18.6%) had levels of 50mg-150mg/kg. Of these eleven patients, one had a history of Crohn's disease (9%). Five patients (8.5%) had a faecal calprotectin level of >150mg/kg. Of these five patients one had a diagnosis of Crohn's disease, on no systemic treatment.

The results show that over a quarter of patients with HS have evidence of occult gastrointestinal inflammation. Elevated faecal calprotectin levels were found in patients with HS, without concurrent Crohn's disease. Given the potential for misdiagnosis and the possibility of co-morbidity, we recommend this simple test for

all patients with HS with due consideration of further investigations in patients with an elevated faecal level of calprotectin.

6.1.1 Introduction

Hidradenitis suppurativa (HS) is a chronic, painful skin disease, presenting with recurrent inflammatory nodules and abscesses in intertriginous areas, often healing with scar formation (225). The cause of HS is unclear, with follicular occlusion, dysregulated inflammatory response of cytokines and altered microbiota thought to be contributory (705). HS shares common clinical manifestations, genetic susceptibility, and immunologic features with Crohn's disease and the two conditions are often associated (705). Due to this association, it is suggested that HS patients be screened for symptoms of IBD and symptomatic patients referred for further investigations (708). HS and Crohn's disease are also both associated with spondyloarthropathy, and common risk factors include a genetic predisposition, smoking and obesity (705). Both HS and Crohn's disease respond well to tumor necrosis factor inhibitors (705). Furthermore, an altered gut microbiome has been described in inflammatory bowel disease and in HS (709,710).

Inflammatory markers are an important adjunct in assessing disease severity and response to treatment. Calprotectin, a member of the S100 protein family, is a calcium-binding heterodimeric cytosolic protein expressed in a wide variety of cell types, including neutrophils and monocytes (711). Calprotectin has a regulatory function in inflammatory processes and elevated levels are seen in acute phase inflammatory reactions(711). Serum calprotectin has been found to be elevated in many inflammatory conditions including HS (712). Faecal calprotectin is released during neutrophil activation in the gut and is a marker of gastrointestinal

inflammation used by gastroenterologists (706). It is a metric of disease activity, therapeutic response, and prognosis in inflammatory bowel disease (707). Elevated faecal calprotectin levels have also been found in spondyloarthritis, psoriatic arthritis, and colorectal cancer (706,713,714).

Thus we sought to determine if faecal calprotectin levels were elevated in patients with HS and to compare these calprotectin levels to the altered faecal microbiome discussed in Chapter 5 (710).

6.1.2 Methods

Adult patients with a confirmed clinical diagnosis of hidradenitis suppurativa in two tertiary referral centres in Ireland were invited to participate in the study.

Demographics including age, gender, Hurley stage, body mass index (BMI), medication history, and the presence of co-morbidities were recorded. Fresh (<24 hours) stool samples were collected by the patient and were stored at -80°C prior to extraction and testing. Microbial DNA was extracted and library preparation and 16S rRNA gene sequencing was carried out (as previously discussed in Chapter 5) (710). Calprotectin was determined by an enzyme-linked immunoassay (CALPROLAB™ Calprotectin ELISA (HRP)).(See Supplementary Methods) Levels were normal if 5-50mg/kg, and elevated if >50mg/kg.(706) Results of 50-150mg/kg were deemed mildly elevated, warranting repeat testing, with levels >150mg/kg suggestive of active bowel inflammation. Statistical analysis was performed using R (v3.6.0).

6.1.3 Results

59 patients with hidradenitis suppurativa were recruited. The mean age was 38.6 years (SD 11.5); 45 were female (76.3%) and four had a history of Crohn's disease

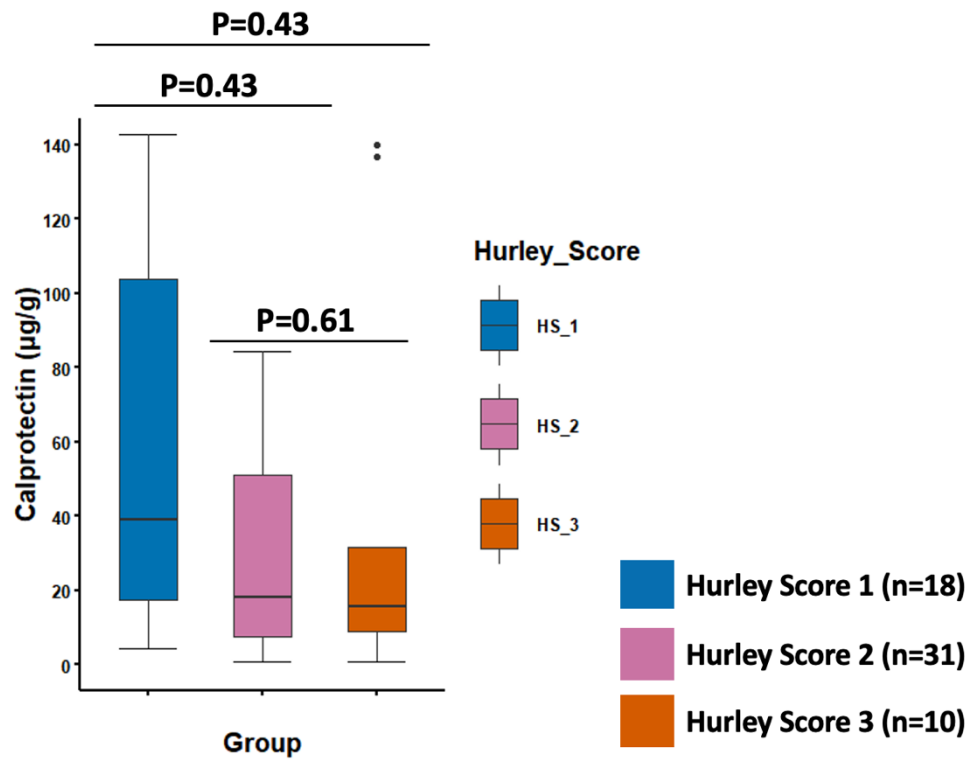
(6.8%). 18 were Hurley Stage I, 32 were Hurley Stage II, and 9 were Hurley Stage III.(Table 1).

Table 1: Patient demographics and results

All Patients	
Gender N (%)	Female 45 (76.3) Male 14 (23.7)
Mean age (SD)	38.6 years (11.5)
Mean body mass index (mg/m²) (SD)	31.9kg/m ²
Hurley Stage (N)	I 18 II 32 III 9
Positive history of Crohn's Disease N(%)	4 (6.8)
Systemic therapy:	
TNF- α N (%)	9 (15.3)
Calprotectin 50mg-150mg/kg N (%)	11 (18.6)
Calprotectin >150mg/kg N (%)	5 (8.5%)

Sixteen patients (27.1%) had a raised faecal calprotectin level of >50mg/kg. 11 (18.6%) had levels of 50mg-150mg/kg. Of these eleven patients, one had a history of Crohn's disease (9%). Five patients (8.5%) had a faecal calprotectin level of >150mg/kg. Of these five patients one had a diagnosis of Crohn's disease, on no systemic treatment. Faecal calprotectin levels did not differ by Hurley stage in those studied (p=0.43)(Figure 1).

Figure 1: Calprotectin levels as per Hurley staging



Hierarchal clustering identified two distinct microbiome groups (710)(Figure 2). No significant difference in faecal calprotectin was noted between these two groups (p=0.88)(Figure 3).

Figure 2: Two distinct faecal microbiome groups seen in patients with HS

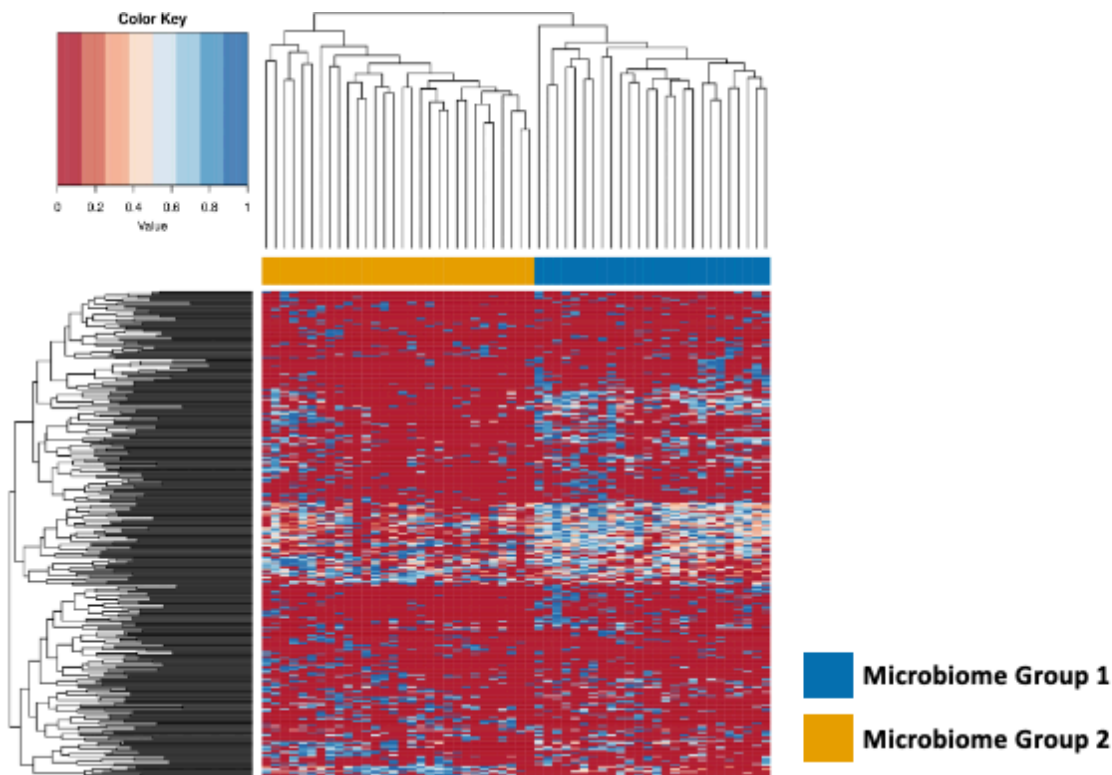
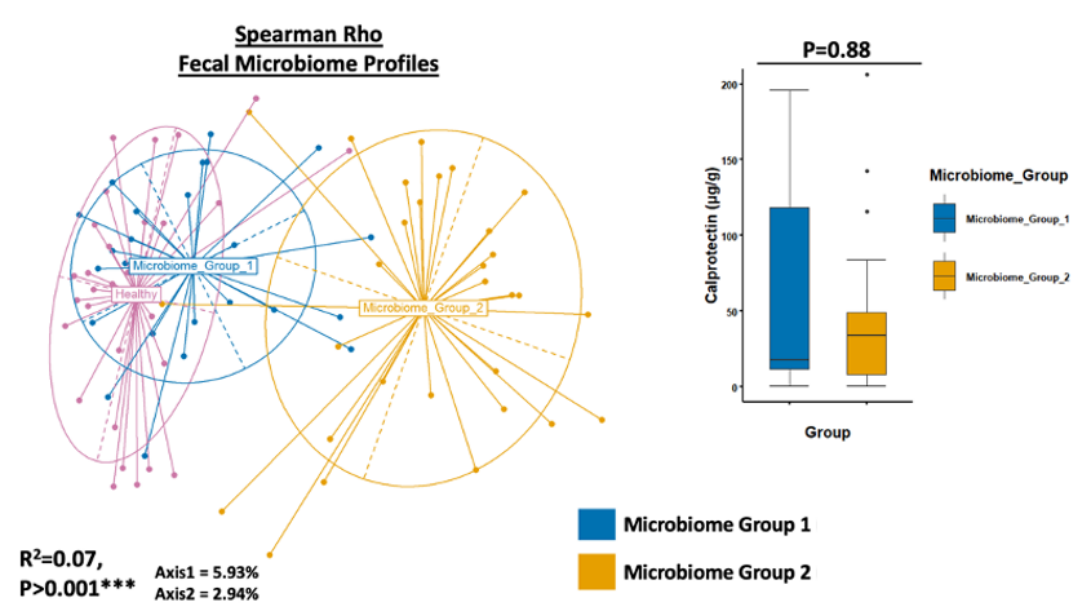


Figure 3: No significant difference in faecal calprotectin was noted between the two distinct microbiome groups noted in HS patients



Of those with no history of Crohn's disease and elevated faecal calprotectin levels, 2 (14%) were taking prophylactic aspirin, and 1 (7%) was taking a non-steroidal anti-inflammatory drugs (NSAIDs). Nine patients (15.3%) in this study were receiving treatment with a tumour necrosis factor (TNF- α) inhibitor, 2 (22%) of whom had elevated levels of calprotectin. We did not find any significant association between levels of calprotectin and TNF- α inhibitor therapy with regard to both current and previous use (Wilcoxon rank-sum test).

6.1.4 Discussion

Serum calprotectin has been used as a marker of disease activity in rheumatoid arthritis, spondyloarthritis and psoriatic arthritis, as well as sepsis and cancer and is not specific to gastrointestinal inflammation (715). Elevated serum levels of calprotectin in HS has previously been described with no correlation with Hurley disease stage, as seen in our study (712). Its use as a biomarker in HS has yet to be proven(712). Other S100 proteins, S100A4 and S100A15 have recently been found to be elevated in HS, and may play a role in HS pathogenesis by promoting inflammation and fibrosis (716).

Faecal calprotectin levels in inflammatory conditions, including HS, has become a recent area of research interest. Elevated faecal calprotectin levels have also been described in spondyloarthritis, psoriasis and psoriatic arthritis (706,714).

Interestingly in psoriatic arthritis, it appears gut inflammation perpetuates joint inflammation (714). Furthermore in spondyloarthritis, chronic gut inflammation was deemed an independent risk factor for the development of inflammatory bowel disease (717).

Faecal calprotectin levels were elevated in 16 (27.1%) of patients in this study. Of those with no history of Crohn's disease and elevated faecal calprotectin levels, 2 were taking prophylactic aspirin, which may raise calprotectin levels (718). The consistent use of non-steroidal anti-inflammatory drugs has been associated with an increase in calprotectin levels, with one patient taking an NSAIDs in this study with an elevated calprotectin level (719). Nine patients (15.3%) in this study were receiving treatment with a tumour necrosis factor (TNF- α) inhibitor, two (22%) of whom had elevated levels of calprotectin. TNF- α inhibitors are used to control inflammation in both inflammatory bowel disease and HS and thus may result in low levels of calprotectin in these patients. However, we did not find any significant association between levels of calprotectin and TNF- α inhibitor therapy with regard to both current and previous use. Studies in inflammatory bowel disease proved that a reduction in faecal calprotectin level indicated mucosal improvement in patients commenced on TNF- α inhibitor treatment (720).

Our results are consistent with other studies on faecal calprotectin levels in HS, which suggest faecal calprotectin could be used as a marker of disease activity (721,722). Faecal calprotectin does not appear to correlate with disease stage as defined by Hurley Staging, however this is a static assessment that does not evaluate disease activity (19,721). This elevated faecal calprotectin in HS suggests subclinical gut inflammation which may be related to their disease, however we cannot outrule concurrent inflammatory bowel disease, with Crohn's disease a common association (705).

Faecal calprotectin is an easy, non-invasive test which may play an role in determining risk of developing inflammatory bowel disease as suggested by a recent study on prevalence of inflammatory bowel disease in paediatric HS (723). However

the significance of subclinical gut inflammation in HS is unknown, and further study is required to determine if this inflammation is simply a marker of disease activity, if it contributes to HS flares or if it signifies a risk of developing inflammatory bowel disease in future. Furthermore, we have demonstrated an altered gut microbiota in HS (710). It is possible that this subclinical gut inflammation, as indicated by the elevated faecal calprotectin levels in this cohort, may be as a result of alterations in the gut microbiota; however, levels of calprotectin did not differ between the two distinct microbiome groups described in this study(710).

6.1.5 Conclusion

Elevated faecal calprotectin levels were found in patients with HS, without concurrent Crohn's disease. Faecal and serum calprotectin may be a marker of disease activity in HS, however its utility in assessing response to treatment is yet unknown. It is also unknown if elevated faecal calprotectin may signify a risk of developing inflammatory bowel disease in future. Given the potential for misdiagnosis and the possibility of co-morbidity, we recommend this simple test be considered in patients with HS with due consideration of further investigations in patients with an elevated faecal level of calprotectin.

6.2 Serum Complement C5a Levels in Hidradenitis Suppurativa

Abstract

The complement system plays a key role in innate immunity, enhancing the ability of antibodies and phagocytic cells to defend against pathogens. C5a is an anaphylatoxin, a product of the complement cascade, which plays a role in supporting inflammation by the recruitment of immune cells to the site of activation, and the release of granule based enzymes (724). Increased circulating levels of C5a and C5b-9 anaphylotoxins have been described in one study, with resultant high levels of TNF- α production (138). We sought to determine the serum concentration of anaphylatoxin C5a in our cohort of patients with HS.

Patients with a confirmed diagnosis of HS by a consultant dermatologist from two tertiary referral centres were invited to participate in the study. Complement C5a levels were assessed using enzyme-linked immunosorbent assay (Abcam ab193695 Complement C5a Human ELISA Kit).

54 patients with HS provided serum samples for analysis. Median complement C5a level was elevated at 47 ng/ml (IQR 30.55 ng/ml). Complement C5a levels did not correlate with disease severity as defined by Hurley staging.

The study findings are in keeping with the prior study by Kanni et al. which described levels of C5a >28 ng/ml in patients with HS, however negative correlation of C5a with HS severity was found in their study and no correlation was found by disease severity in ours (138). C5a may provide a therapeutic target in patients with HS and serum C5a may act a biomarker of the disease.

6.2.1 Introduction

Hidradenitis Suppurativa is a chronic inflammatory skin disease of primarily intertriginous sites presenting with recurrent painful nodules, abscesses and often progressing to scarring and sinus tract formation. The pathogenesis of HS is incompletely understood but genetic, endocrine, environmental, immunological and microbial factors play a role (40,725,726). The primary event is thought to be follicular hyperkeratosis and dilatation, followed by follicular rupture (725,726). This induces an exaggerated response in the innate immune system resulting in recruitment of inflammatory cells and mediators to the dermis, with resultant abscess formation and chronic inflammation (725). The complement system plays a key role in innate immunity, enhancing the ability of antibodies and phagocytic cells to defend against pathogens. C5a is an anaphylatoxin, a proinflammatory polypeptide product of the complement cascade, which plays a role in supporting inflammation by the recruitment of immune cells to the site of activation including neutrophils, eosinophils, monocytes, and T lymphocytes, the activation of phagocytic cells, and the release of granule based enzymes (724). Little research has looked at the role of the complement cascade in HS however it is thought that anaphylatoxins recruit neutrophils to the affected skin resulting in suppuration (138). Increased circulating levels of C5a and C5b-9 have been described in one study, with resultant high levels of TNF- α production (138). In this study levels of C5a exceeding 28 ng/ml were associated with a specificity of >90% with occurrence of HS (138). The addition of IFX-1, a C5a blocker, in this study led to a reduction in TNF- α suggesting a therapeutic target in HS (138). However, a further study by Prens et al. failed to show elevated serum levels of C5a in HS (727). We sought to determine the serum concentration of anaphylatoxin C5a in a cohort of patients with HS.

6.2.2 Methods

Patients with a confirmed diagnosis of HS by a consultant dermatologist from two tertiary referral centres were invited to participate in the study. Demographics including age, gender, Hurley stage, body mass index (BMI), medication history, and the presence of co-morbidities were recorded. Serum samples were obtained and stored at -80°C prior to testing. Complement C5a levels were assessed using enzyme-linked immunosorbent assay (Abcam ab193695 Complement C5a Human ELISA Kit). Statistical analysis was performed using R (version 4.1.3)

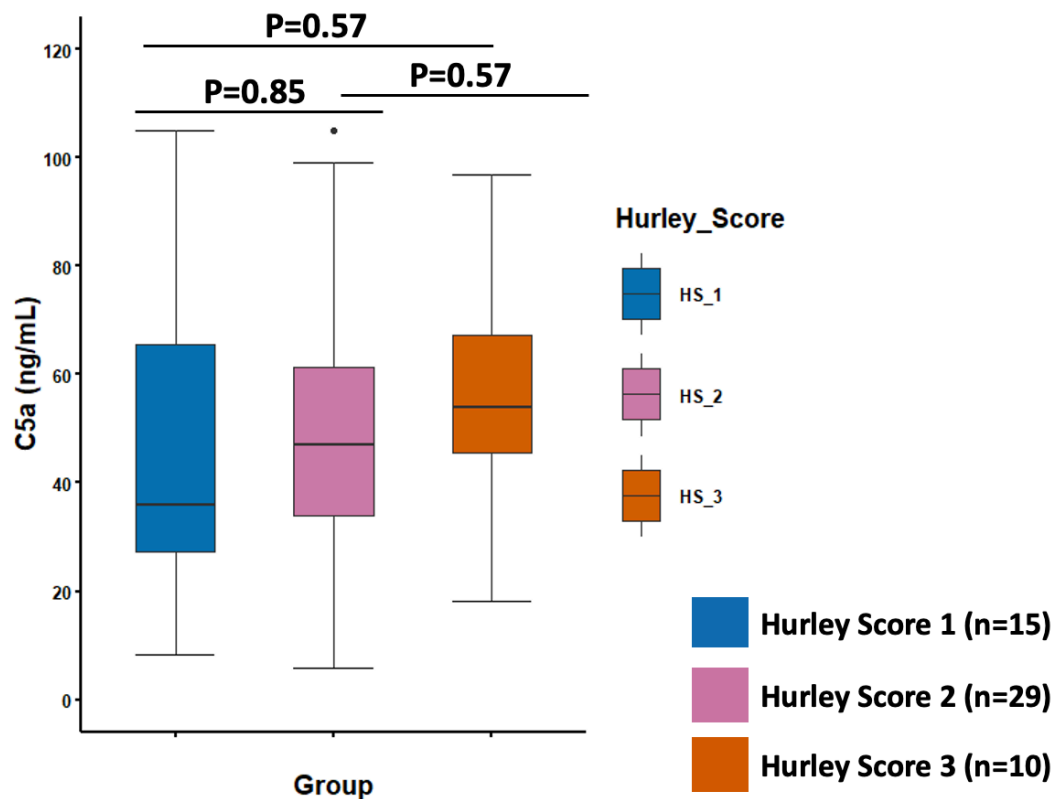
6.2.3 Results

54 patients with HS provided serum samples for analysis. Mean age was 37.1 years (SD 11.23). 43 (80%) were female and 11 (20%) were male. 15 (28%) were Hurley stage I, 29 (54%) were Hurley stage II, and 10 (18%) were Hurley stage III. 9 patients were currently prescribed adalimumab and 1 patient was prescribed infliximab, both TNF- α inhibitors, for their HS. 4 patients had inflammatory bowel disease (3 Crohn's, 1 ulcerative colitis), 4 had psoriasis, 3 had eczema, 1 had cutaneous lupus, and 1 patient had psoriatic arthritis. Median complement C5a level was 47 ng/ml (IQR 30.55 ng/ml). Complement C5a levels did not correlate with disease severity as defined by Hurley staging (Kruskal-wallis with Dunns post-hoc test)(Figure 1). Patients with Hurley stage I had a median complement C5a level of 35.8 ng/ml (IQR 38.13), Hurley stage II 47 ng/ml (IQR 27.34) and Hurley stage III 54 ng/ml (IQR 21.58).

Table 1: Patient demographics

All Patients	
Gender N (%)	Female 43 (80%) Male 11 (20%)
Mean age (SD)	37.1 years (11.23)
Mean body mass index	
Hurley Stage (N)	
I	15
II	29
III	10
History of	
Inflammatory bowel disease	4
Psoriasis	4
Eczema	3
Psoriatic arthritis	1
Cutaneous lupus	1
Systemic therapy:	
TNF- α N (%)	10 (19%)

Figure 1: The inflammatory marker C5a is not significantly different by disease severity. All p values are FDR (False discovery rate) corrected.



6.2.4 Discussion

C5a is an activation product of the complement cascade and may result in neutrophil activation and infiltration of the skin in HS lesions (138). Complement C5a levels were elevated in patients with HS in this study, however this did not correlate with disease severity. This is in keeping with the prior study by Kanni et al. which described levels of C5a >28 ng/ml in patients with HS, however they noted negative correlation of C5a with HS severity which may suggest complement activation occurs in the early stages before progression to stage II, and III (138). Our study supports further the role of systemic complement activation in HS and C5a levels may be used as a biomarker in future. The addition of IFX-1, a C5a blocker, in the study by Kanni et al. led to a reduction in TNF- α suggesting a therapeutic target in HS (138). In an open-label single-arm trial by Giamarellos-Bourboulis et al. twelve patients with HS received 800mg of IFX-1 on days 1, 4, 8, 15, 22, 29, 36, 43, and 50 and 75% achieved the primary endpoint of positive Hidradentitis Suppurativa Clinical Response score (HiSCR) on day 50, and 83.3% on day 134 (139). This further supports the role of C5a in HS and the use of C5a blockade as therapy. There is also a randomised, double-blind, placebo-controlled phase II trial ongoing targeting C5a in patients with HS, the results of which are awaited (728).

6.2.5 Conclusion

In conclusion we found elevated levels of C5a in our cohort of patients with hidradenitis suppurativa. C5a may provide a therapeutic target in patients with HS and serum C5a may act a biomarker of the disease.

7. Diet and Hidradenitis Suppurativa

Abstract

The gut-skin axis is an expanding area of research, and several skin conditions including HS, have gut comorbidities (164–166). An abnormal gut microbiota, or dysbiosis, has been linked to the development of skin disease and diet has a significant impact on the gut microbiota composition (166,167). The aim of this study was to describe the diet of a cohort of patients with HS and to determine if diet had an interaction with the gut and skin microbiome, inflammatory markers, and disease severity.

Adult patients with a confirmed clinical diagnosis of hidradenitis suppurativa made by a consultant dermatologist in two tertiary referral centres in Ireland were invited to participate in the study. Patients with HS were asked to complete a Food Frequency Questionnaire which examined their diet over the past year. Comparative analysis to 102 patients with Crohn's Disease (CD) and 95 controls was carried out. Fresh faecal samples were provided by patients and controls. Microbial DNA was extracted and library preparation and 16S rRNA gene sequencing was carried out (as previously described in Chapter 5) (710). Calprotectin was evaluated by an enzyme-linked immunosorbent assay (CALPROLAB™ Calprotectin ELISA (HRP)) and complement C5a levels were evaluated by enzyme-linked immunosorbent assay (Abcam ab193695 Complement C5a Human ELISA Kit).

No significant difference in faecal microbiota composition or overall habitual diet was seen in the patients with HS. Diet was not associated with disease severity and faecal microbiota composition did not differ by Hurley stage. Two distinct microbiome groups were noted and there was no significant difference in overall

habitual diet between the microbiome groups. Two distinct dietary groups were noted by hierarchical clustering and microbiome groups did differ by dietary group. Dietary group 1, whose members had lower calprotectin levels, had higher consumption of several dietary ingredients associated with Western diet. C5a levels were not significantly different between dietary groups. The habitual diet of patients with HS differed from healthy controls, and was similar to those with CD. In conclusion, we described the diet of a cohort of patients with HS and explored the relationships between the gut and skin microbiome, inflammatory markers, and disease severity. Modification of the gut microbiota via interventional diets may have a potential role to play in HS treatment in future.

7.1 Introduction

Hidradenitis suppurativa (HS) is a chronic inflammatory dermatosis presenting with painful nodules, abscesses, and sinus tracts in intertriginous sites. The gut-skin axis is an expanding area of research, and several skin conditions including HS, have gut comorbidities (164–166). An abnormal gut microbiota, or dysbiosis, has been linked to the development of skin disease (166). Diet has a significant impact on the gut microbiota composition (166,167). Study on the role of dietary factors in the development of HS is lacking (168). It has been suggested that a dairy-free diet and avoidance of high glycaemic load foods can result in improvement in HS (168,169). It is postulated that dairy products and high glycaemic foods can act through hormonal mechanisms by triggering androgen-driven obstruction of follicles (169). Other studies suggested avoiding nightshades (Solanaceae) and foods and drinks containing brewer's yeast such as bread and beer (168). Adherence to a Mediterranean diet in HS demonstrated lower disease activity and severity in another study (170). These studies, however, provide little information on the effect of diet on the microbiota as a potential aetiological factor. The current aim was therefore to describe the diet of a cohort of patients with HS and to determine if diet had an interaction with the gut and skin microbiome, inflammatory markers, and disease severity. We also compared the habitual diet of patients with HS, to controls and to patients with Crohn's disease (CD).

7.2 Methods

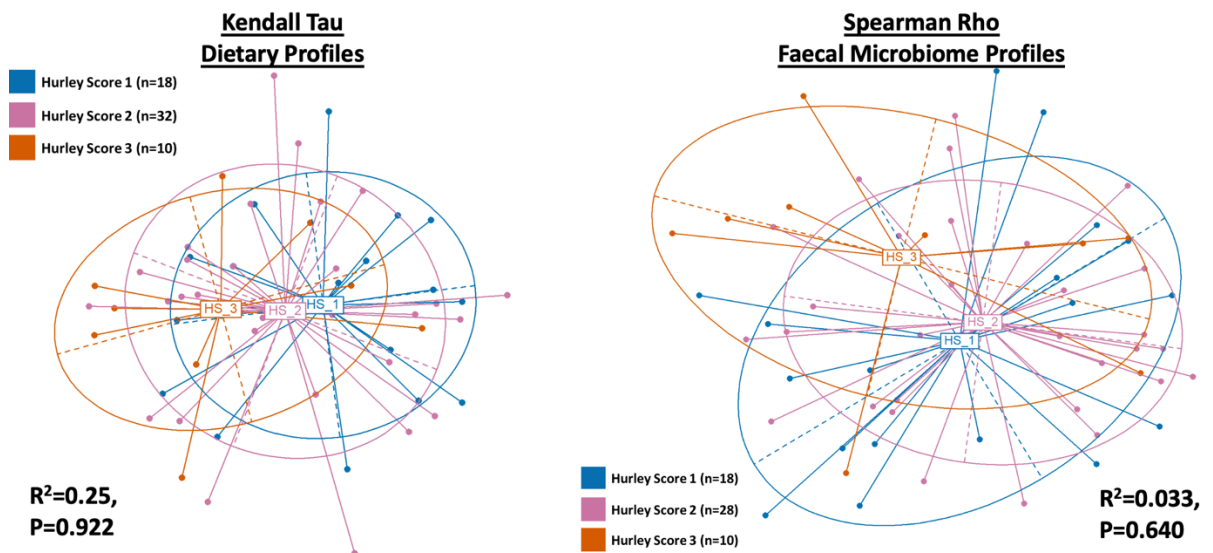
Adult patients with a confirmed clinical diagnosis of hidradenitis suppurativa made by a consultant dermatologist in two tertiary referral centres in Ireland were invited to participate in the study. Ethical approval (Cork Research Ethics Committee and

Tallaght University Hospital Ethics Committee) and written informed consent from patients was obtained. Exclusion criteria included topical or oral antibiotic usage in the preceding four weeks. Data including age, gender, smoking status, weight, height, body mass index, presence of co-morbidities and severity of disease (Hurley Score) were recorded (16). Healthy adult controls were recruited from the general population, and were age and gender matched. For comparative analysis we included data for 102 patients with Crohn's disease and 95 controls obtained from a previously published dataset (559). Patients with HS were asked to complete a Food Frequency Questionnaire which examined their diet over the past year (See Supplementary Methods). Patients were asked to estimate their average intake of specified foods, including meat, fish and poultry, bread and biscuits, cereals, potatoes, rice and pasta, dairy products, fruit, vegetables, sweets and snacks, and drinks. Intake of functional foods such as probiotics was also examined, as well as vitamin supplements, and any special diets. Fresh (<24 hours) faecal samples were provided by patients and controls and stored at -80°C prior to microbial DNA extraction. Microbial DNA was extracted and library preparation and 16S rRNA gene sequencing was carried out (as previously described in Chapter 5) (710). Calprotectin was evaluated by an enzyme-linked immunosorbent assay (CALPROLAB™ Calprotectin ELISA (HRP)) and complement C5a levels were evaluated by enzyme-linked immunosorbent assay (Abcam ab193695 Complement C5a Human ELISA Kit). (See Supplementary Methods) Statistical analysis was performed using R (version 4.2.1).

7.3 Results

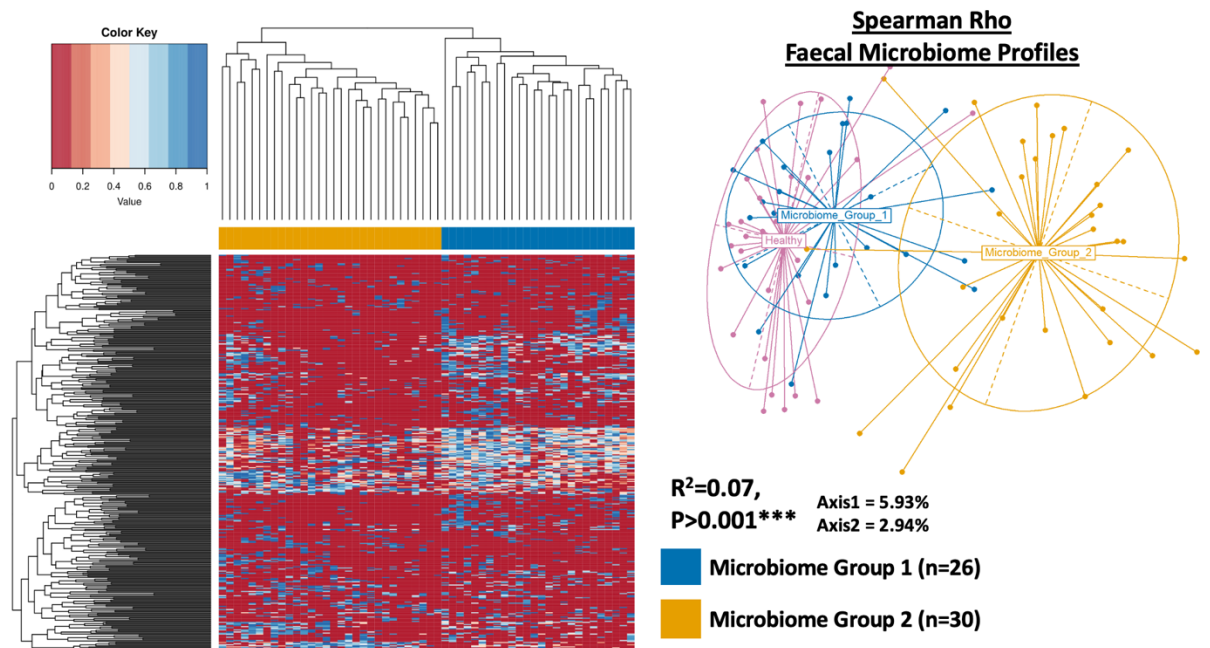
56 patients with HS and 30 healthy controls provided faecal samples for analysis and completed food frequency questionnaires. 18 had Hurley stage I disease, 28 Hurley stage II disease and 10 Hurley stage III disease. No significant difference in faecal microbiota composition or overall habitual diet was seen in the patients with HS (Figure 1). Diet was not associated with disease severity and faecal microbiota composition did not differ by Hurley stage ($p=0.640$; Figure 1).

Figure 1: Faecal microbiota composition and dietary profiles by Hurley stage



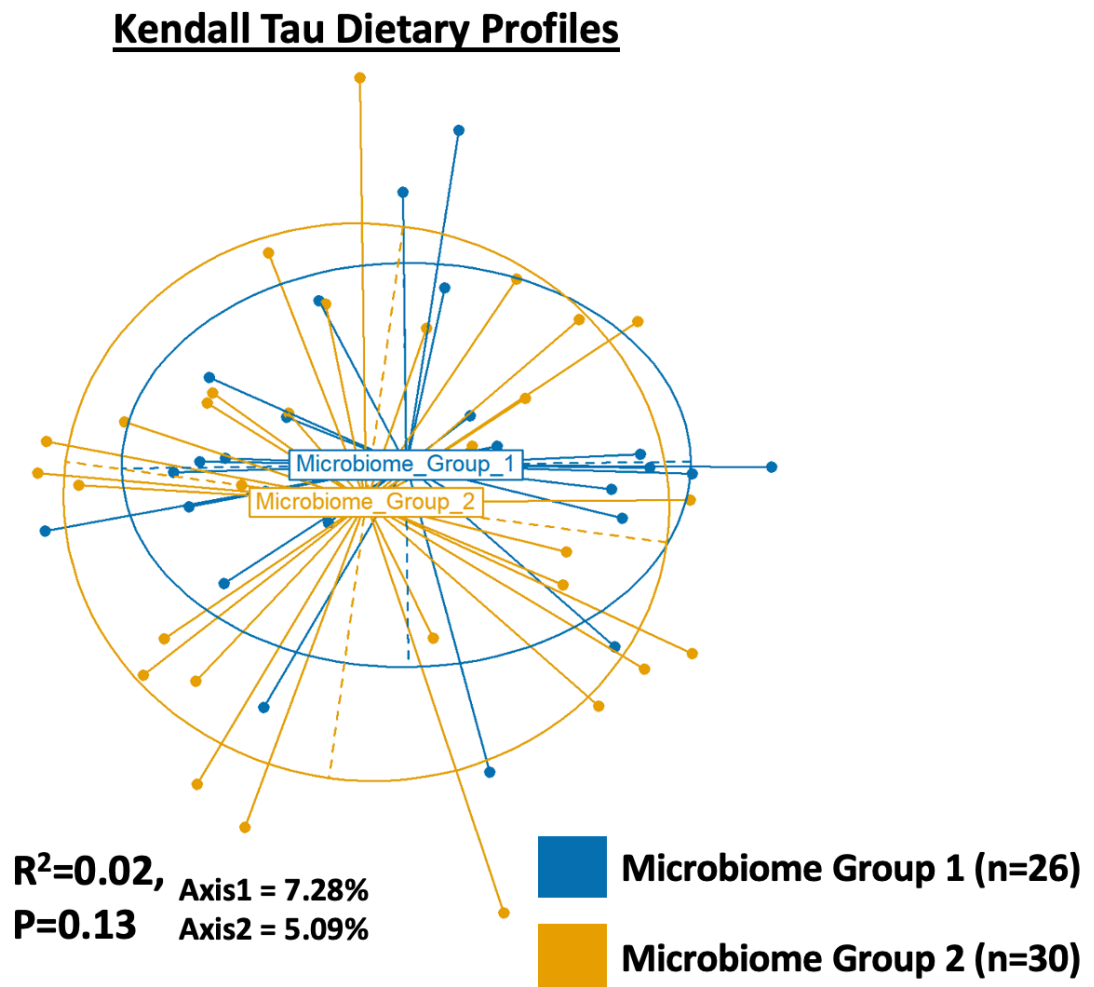
Hierarchical clustering revealed two distinct microbiome groups (as previously discussed in Chapter 5)(710)(Figure 2).

Figure 2: Hierarchical clustering of microbiome groups



Differences in individual dietary ingredients were also examined. Cohens d test was used to remove food items with small effect size and logistic regression was used to control for age, age at diagnosis, previous antibiotic use, gender, Hurley stage and body mass index (BMI). There was no significant difference in overall habitual diet between the microbiome groups ($p=0.13$)(Figure 3).

Figure 3: Dietary profiles of two distinct HS microbiome groups

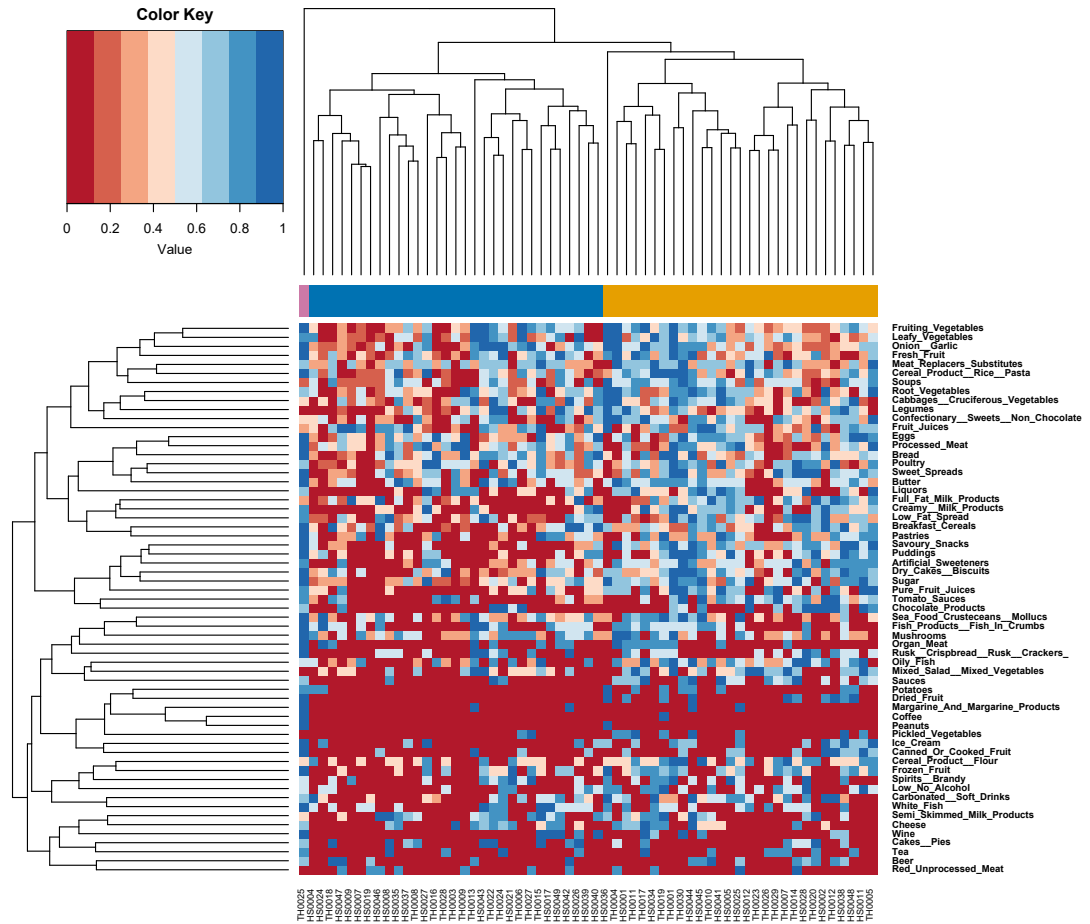


However, hierarchical clustering revealed two distinct habitual dietary patterns among HS patients with higher levels of calprotectin in dietary group 2 ($p=0.011$)(Figure 4).

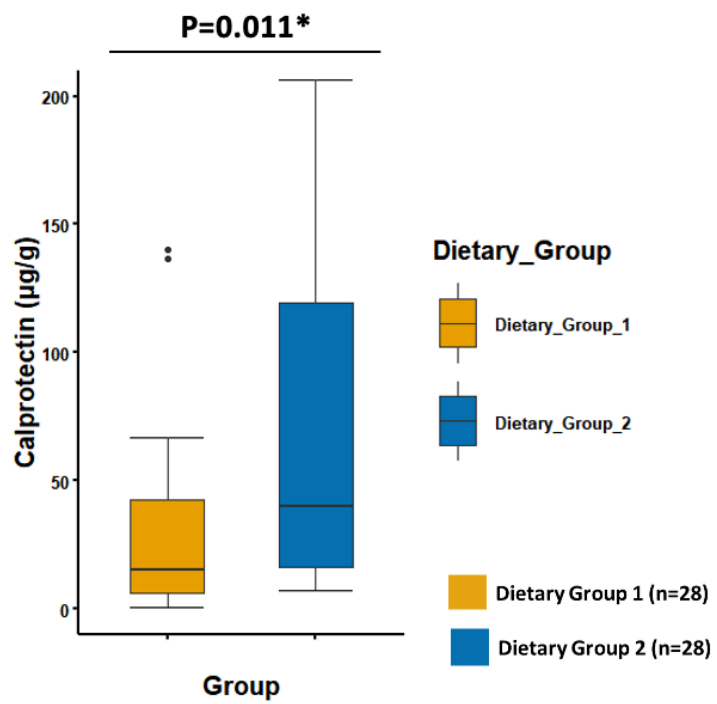
Dietary group 1, whose members had lower calprotectin levels, had higher consumption of several dietary ingredients associated with Western diet.

Figure 4: (a) Hierarchical clustering of habitual dietary patterns among HS patients, (b) with higher calprotectin levels in dietary group 2

(a)

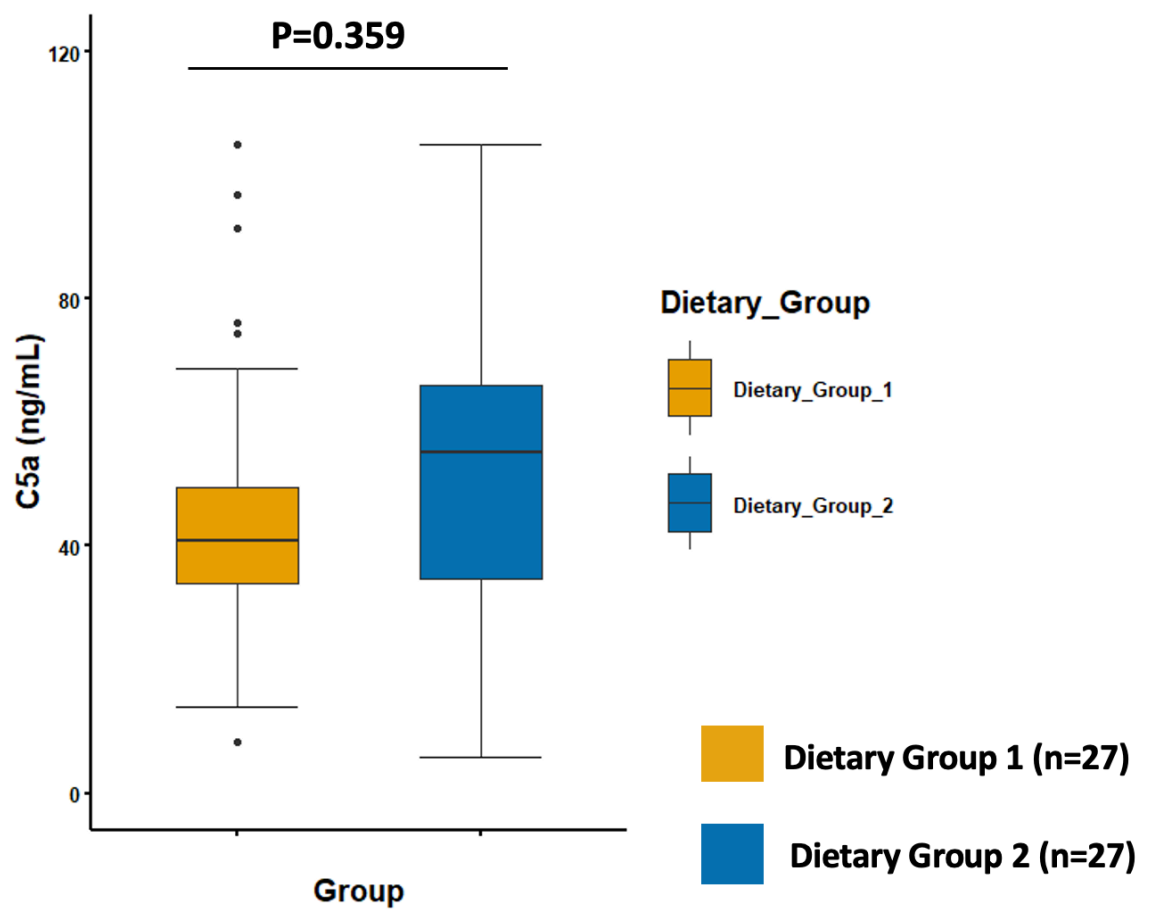


(b)



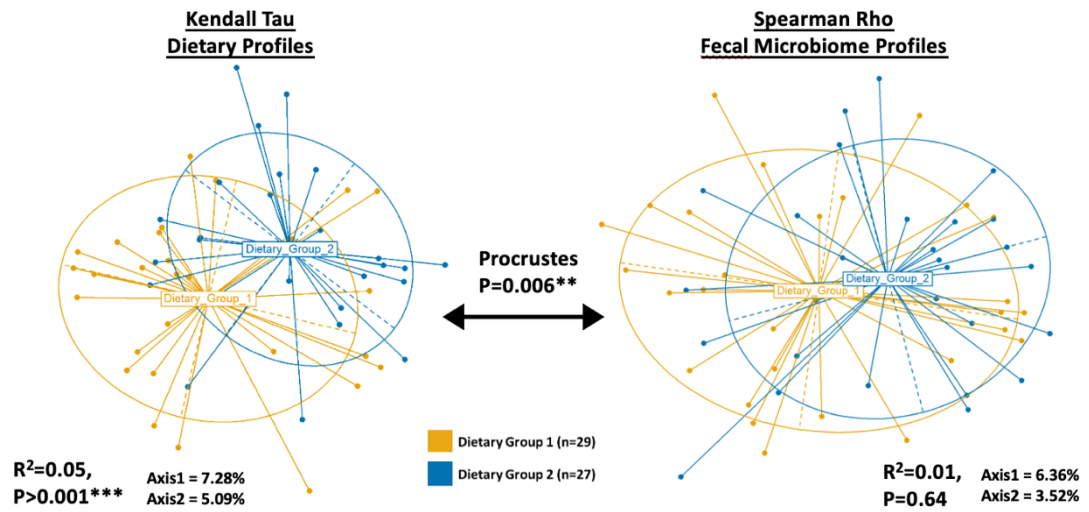
C5a levels were not significantly different between dietary groups ($p=0.359$)(Figure 5).

Figure 5: C5a levels by dietary group



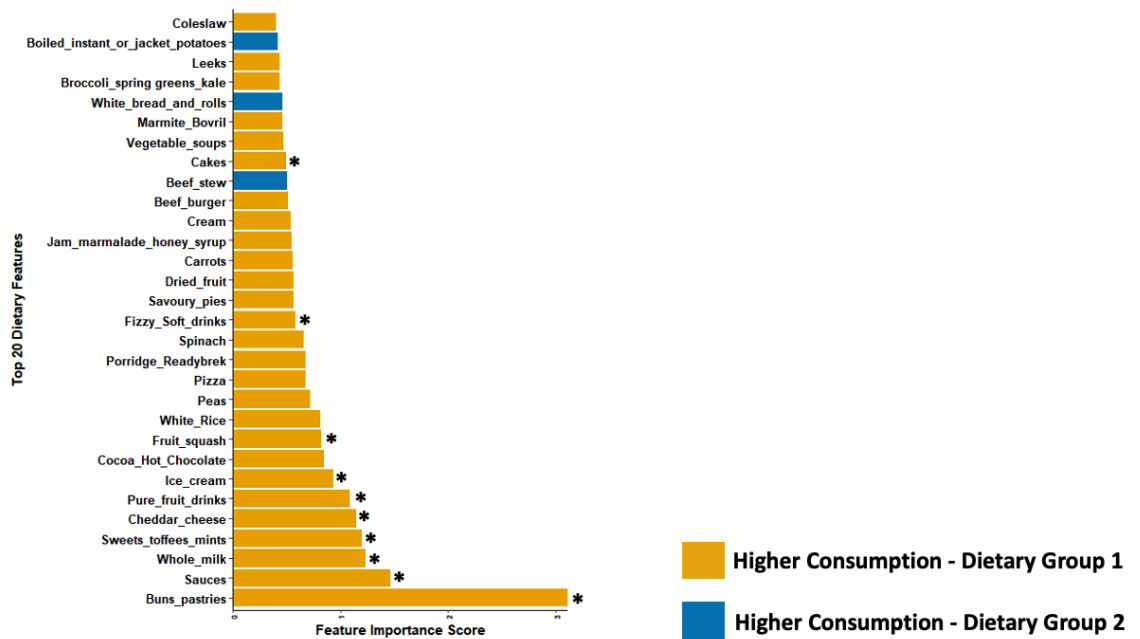
A significant association was seen between habitual diet and faecal microbiota composition (Figure 6).

Figure 6: Association between habitual diet and faecal microbiota composition



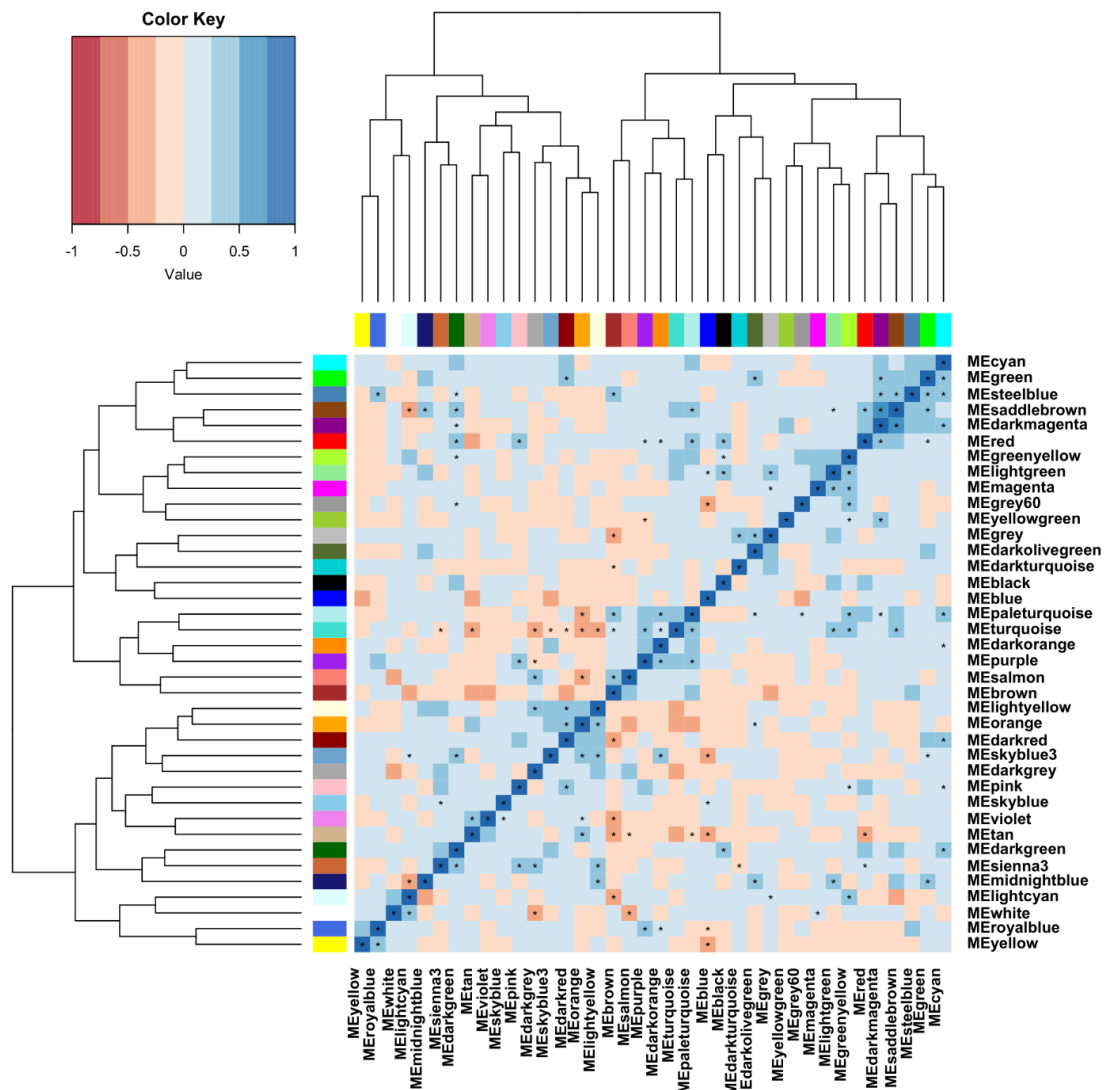
Random Forest classification was used to determine the top 30 dietary features in HS (Figure 7). Dietary group 1 had higher consumption of several dietary ingredients associated with Western diet (Cakes, buns, pastries, soft drinks, sweets, and dairy products).

Figure 7: Random Forest classification with an accuracy of 90% demonstrating top 30 dietary features (with accuracy of 90%). * denotes dietary ingredient significantly different through logistic regression



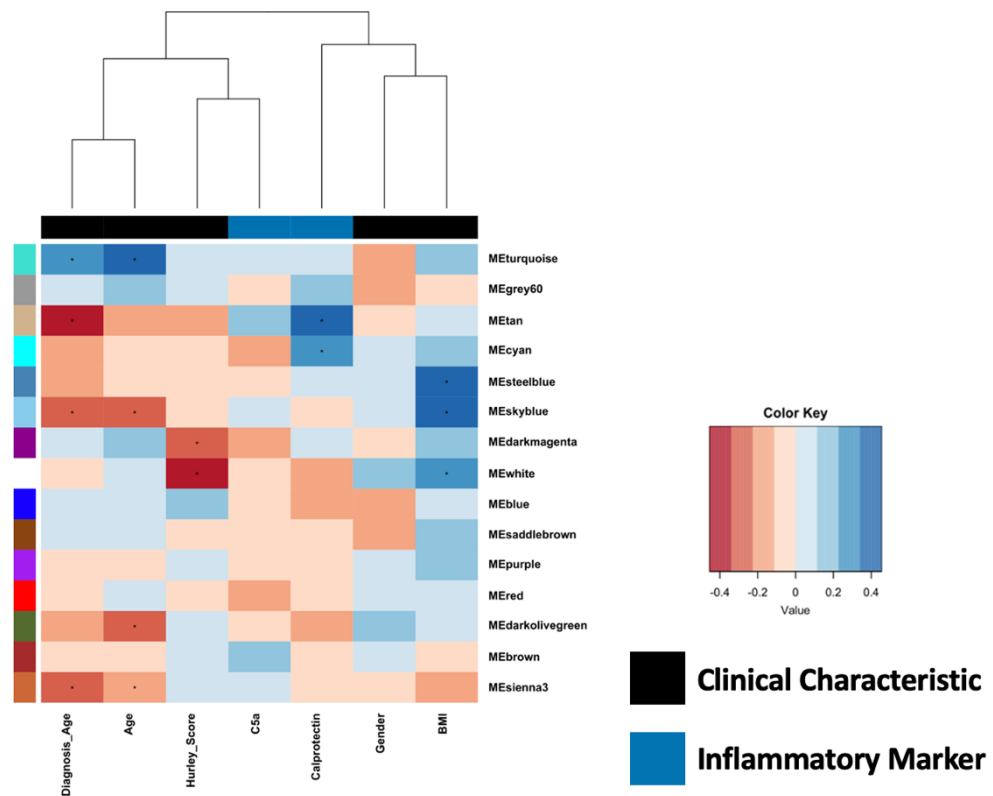
Exploration of the relationships between different gene sets (modules) via weighted gene co-expression network analysis (WGCNA) identified 38 modules of interest. WGCNA constructs co-expression networks based on correlations between the quantitative measurements of each taxon (729). Spearman correlations show associations between different modules (Figure 8). This heatmap shows correlations of the food frequency questionnaire and clinical metadata to the faecal microbiome. The modules included common gut taxa such as Lactobacilli, Ruminococcaceae, Clostridiales, and Firmicutes. The full list of module taxon content for the faecal microbiome is available in Appendix 1.

Figure 8: Spearman correlation between different modules



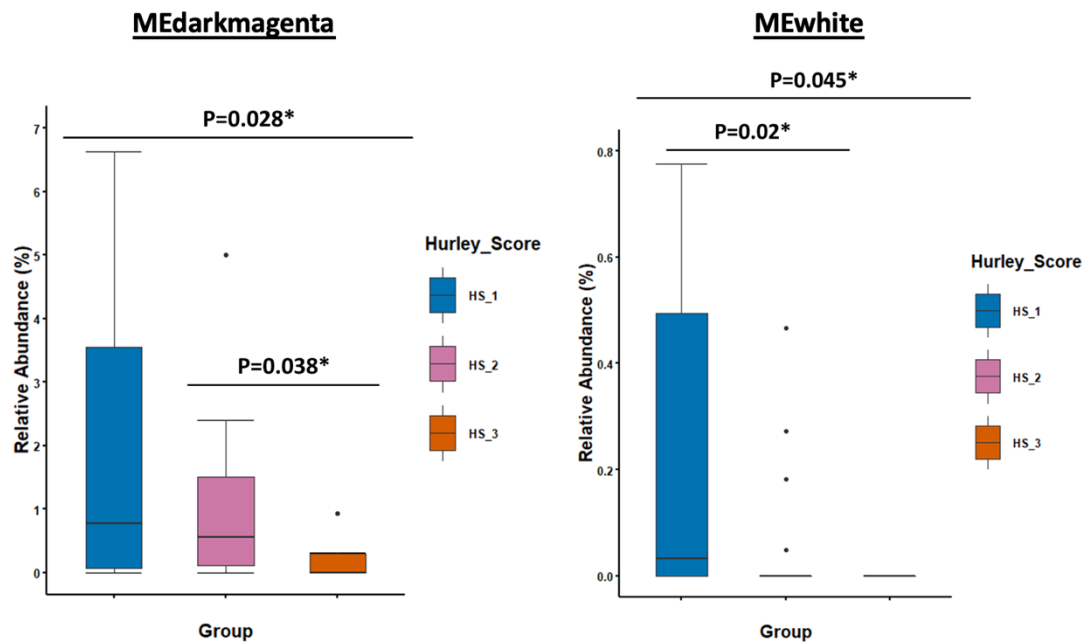
We conducted spearman correlation analysis between clinical characteristics and inflammatory markers with the top 15 most important features (WGCNA modules) in distinguishing between the HS and healthy microbiota from a random forest classifier (Figure 9).

Figure 9: Spearman correlation between modules, clinical characteristics, and inflammatory markers for faecal microbiome



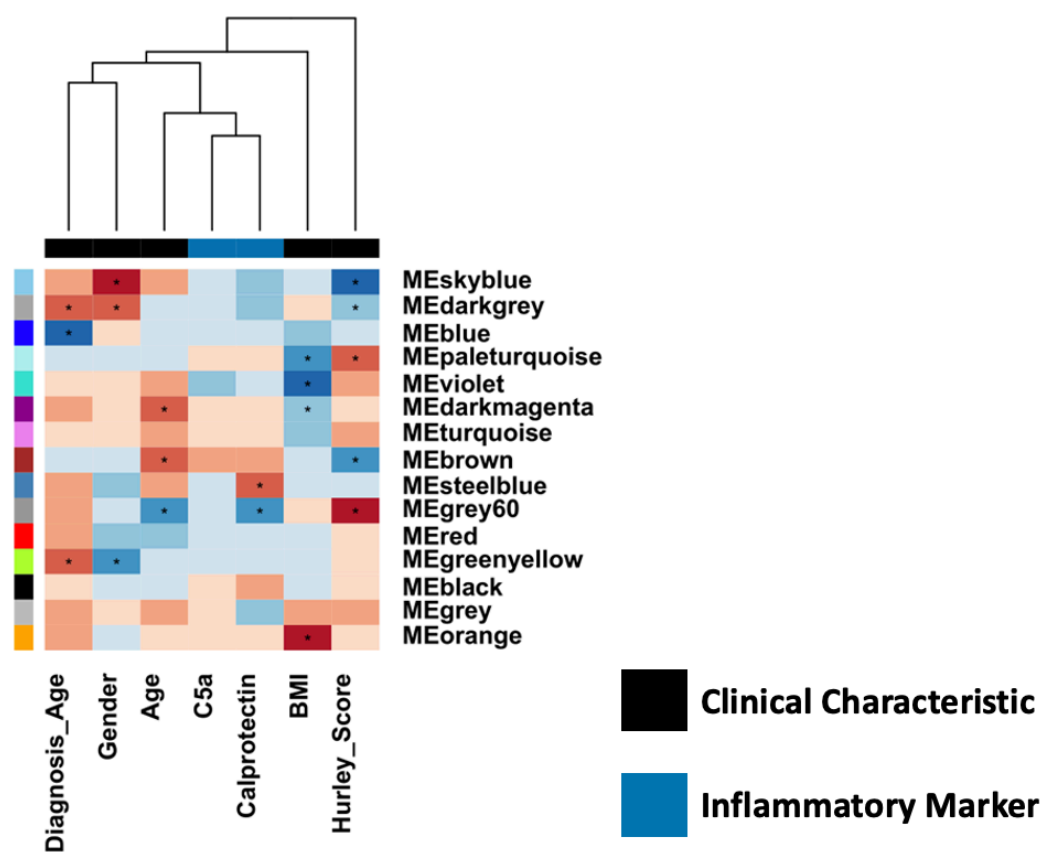
Calprotectin levels had strong positive correlation with taxa in the tan and cyan modules. The tan module included *Ruminococcus gnavus*, which was overabundant in HS as previously discussed, and the cyan module included taxa such as Ruminococcaceae, Clostridiales, and *Faecalibacterium prausnitzii*. Loss of taxa was a feature of two WGCNA modules, darkmagenta and white. Depletion of these taxa was associated with disease severity in HS (Figure 10). The darkmagenta and the white modules included Firmicutes and Lactobacilli which are beneficial bacteria.

Figure 10: Loss of taxa in two WGCNA modules (darkmagenta and white) associated with disease severity in HS patients



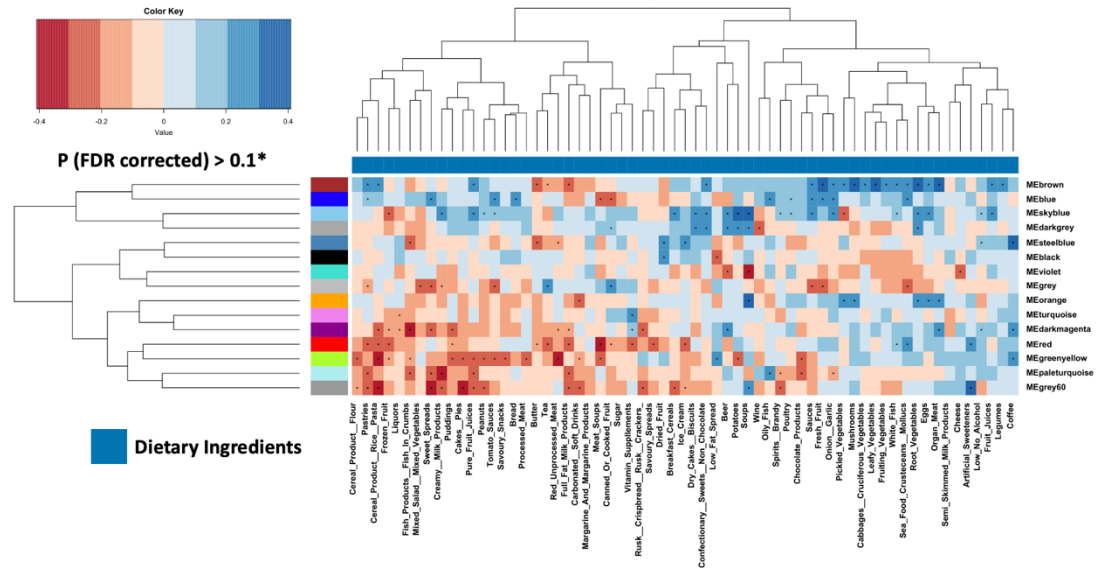
Correlation between modules and dietary ingredients for faecal microbiome was investigated using Spearman correlation analysis. (Figure 11) Positive correlation between processed carbohydrates, dairy products, and red meat were seen with several modules. These modules included the taxa Ruminococcaceae, and Clostridiales.

Figure 12: Spearman correlation between modules, clinical characteristics, and inflammatory markers for the skin microbiome



Spearman correlation was conducted between the modules and dietary ingredients for the skin microbiome showing association between processed carbohydrates, dairy products and processed meats and the taxa *Corynebacterium*, *Staphylococcus epidermidis*, Streptococci and anaerobes (Figure 13).

Figure 13: Spearman correlation between modules and dietary ingredients for skin microbiome

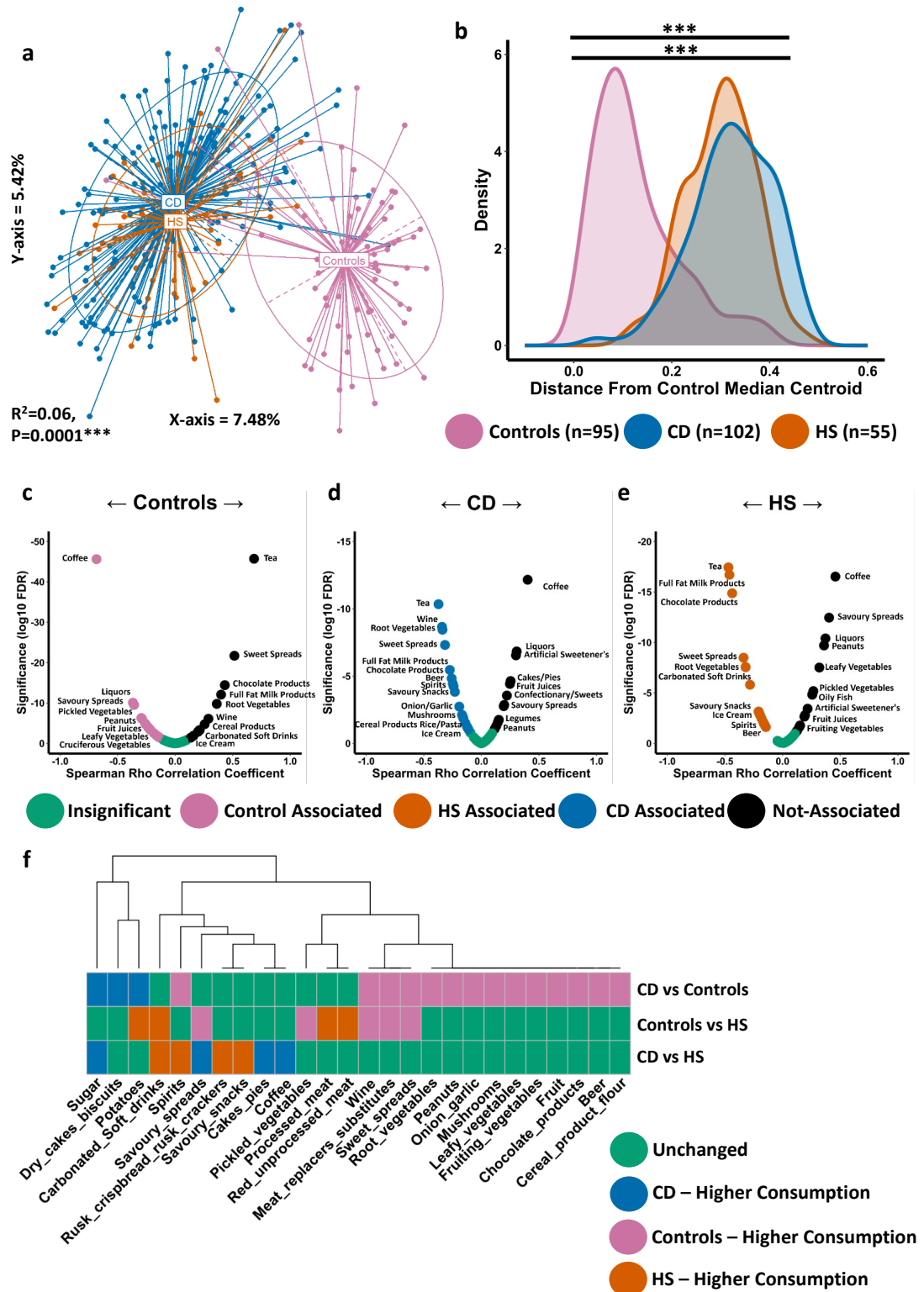


We conducted principal component analysis using the Kendall tau distance measure to investigate differences in habitual diet of patients with HS, patients with Crohn's disease (CD) and healthy controls (Figure 14a). We observed a statistically significant separation between the groups (PERMANOVA FDR-corrected $P < 0.0001$; $R^2 = 0.06$). Habitual diet in patients with HS was significantly different to controls (Figure 12a). Interestingly, the HS habitual diet was not significantly different to diet of those with CD (Figure 14a and 14b). Given the large difference in habitual diet between patients with HS and controls, we wanted to establish what specific dietary ingredients were most or least associated with the median dietary pattern of each group. We conducted Spearman correlation analysis between the consumption levels of each dietary ingredient with the distance from the median centroid of each study group respectively, as calculated from Figure 14a (Figure 14c-14e). As expected, the control group was observed to have a strong negative correlation with the distance from the

control median centroid for a number of food items considered to be health promoting and high in dietary fibre (Figure 14c). This list included a variety of vegetables (cruciferous, leafy, and pickled) as well as fish (Figure 14c). Dietary ingredients which were least associated (positive correlation) with controls using this approach included chocolate products, ice-cream and carbonated soft drinks, all of which are elements of the Western diet. Using this approach, an opposing trend was identified for CD (Figure 14d) and HS (Figure 14e). A number of food items whose consumption is typical for the Western diet were found to negatively correlate with the distance from the HS median centroid (Figure 14e), including processed meat, sugar, carbonated soft drinks, ice-cream and chocolate. Several alcoholic beverages were also found to be associated with the HS diet including beer, wine and spirits. Dietary ingredients which were least associated with the HS diet (positive correlation) included fish, a variety of vegetables (pickled, leafy and fruiting) as well as fruit (Figure 14e).

Figure 14: Habitual diet of patients with HS resembles the Western diet similar to patients with CD. (a) Principal Component Analysis (PCoA) of habitual dietary profiles (Kendall tau distance) based on daily frequency of consumption. The P Value (0.0001) obtained using a PERMONOVA shows there is statistically significant separation between the groups. The eigen values are also reported which show the variation reported in the X-axis (7.48%) and Y-axis (5.24%) of the PCoA. (b) Using the PCoA coordinates from (a) the median control centroid was calculated and the distance of all samples from those coordinates was subsequently determined and displayed here as a density plot. Density is displayed on the Y-axis while the actual reported distance from the control median centroid is displayed on the X-axis. Kruskal-Wallis with Dunn's post hoc test was used to determine significant

differences between the groups for this distance measure. The annotations used for P values are $P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***. All displayed P values are FDR corrected. (c-d) Volcano plot showing spearman correlations between the consumption of dietary ingredients and (c) the median control centroid, (d) the CD median centroid and (e) the HS median centroid. A significant negative correlation indicates that a specific dietary ingredient is associated with the median pattern of that patient group as its consumption increase the shorter the distance to the median centroid. Significant positive correlations indicate that a specific food item is not associated with the median dietary of that patient group as its consumption increases the larger the distance from the median centroid. (f) Wilcoxon test was conducted to determine what food items were differentially consumed between each pairwise comparison and shown in a colour coded heatmap. Each colour signifies whether that specific genera was unchanged (green), higher in controls (purple), higher in patients with CD (blue) or higher in patients with HS (orange).



7.4 Discussion

This study found no significant difference in faecal microbiota composition or overall habitual diet in the patients with HS. Diet was not associated with disease severity and faecal microbiota composition did not differ by Hurley stage.

Furthermore, there was no significant difference in overall habitual diet between the two distinct microbiome groups previously described. Interestingly a more western diet was associated with lower faecal calprotectin levels, the reason for which is unexplained..

Explorations of the relationships between diet, the skin and faecal microbiome, inflammatory markers, and clinical characteristics was also performed. Modules associated with the taxa Ruminococcaceae and Clostridiales positively correlated with calprotectin levels in faecal microbiome analysis. These taxa were also associated with a diet rich in processed carbohydrates, dairy products, and red meat. An abundance of *Ruminococcus gnavus* has previously been described in the faecal microbiome of patients with HS (710). Loss of beneficial taxa, including Firmicutes and Lactobacilli, in two modules correlated with disease severity in HS (730).

Regarding the skin microbiome, calprotectin levels, BMI, and Hurley staging all showed positive correlation with modules including the taxa *Corynebacterium*, *Staphylococcus epidermidis*, streptococci and anaerobes which are found to be pathogenic in HS (531). Furthermore, these skin taxa were found to correlate with a diet rich in processed carbohydrates, dairy products, and processed meat.

The dietary pattern in patients with HS resembled that of the Western diet, differed from controls, and was similar to that of Crohn's Disease. Dietary ingredients found

to positively associate with HS were high in sugar and saturated fat. In addition, food items least associated with HS included vegetables and fruit which are high in dietary fibre and health promoting. These findings highlight the need for greater nutritional support for patients with HS. Structured dietary advice and/or dietary intervention represents a promising avenue to alleviate disease burden

Diet can have a profound effect on the gut microbiome and gut microbes in turn influence the absorption, metabolism, and storage of nutrients (731). Current research shows that dietary fibres promote the growth of beneficial bacteria and suppress the growth of pathogenic species (730). The quantity and type of fat and protein also modulates both beneficial and potentially pathogenic microbes (730). Diets low in fibre and high in processed carbohydrates and fats can result in lower gut microbial diversity (731). Lower gut microbial diversity has been linked to the development of several inflammatory conditions, including inflammatory bowel disease (732–734). The response of the gut microbiota to diet may provide a valuable tool to exploit, with potential to develop interventional diets to treat diseases associated with gut dysbiosis. Such interventional diets have been trialled in inflammatory bowel disease with reported success (735). A diet rich in fibre-rich plant foods, and low in processed carbohydrates and red meat could prove to have an anti-inflammatory effect in HS, reducing disease severity and flares. Such a diet may also prevent development of HS in those who are predisposed.

7.5 Conclusion

In conclusion, we described the diet of a cohort of patients with HS and explored the relationships between the gut and skin microbiome, inflammatory markers, and

disease severity. Modification of the gut microbiota via interventional diets may have a potential role to play in HS treatment in future.

8. Conclusions and Future Perspectives

HS is a chronic, debilitating disease, the pathogenesis of which is still not completely understood. HS can prove challenging to treat as discussed in the introductory chapter, and the lack of randomised placebo-controlled trials in HS has resulted in little evidence in the literature for effective treatments for HS. Furthermore, the lack of a standardised outcome measure has made comparison of the different treatments difficult. **Chapter 2** examined the placebo-controlled trials in the literature, commenting on the placebo response rates and estimating the true drug efficacy, as well as commenting on the heterogeneity of the outcome measures used which limits a systematic approach to comparison. Knowledge of placebo response is of interest to inform design of future microbiota based intervention trials in future.

HS is a debilitating painful disorder with a significant impact on patients' quality of life. **Chapter 3** described the impact of HS on the quality of life of the cohort of patients studied here. Our findings were in keeping with the published literature, highlighting the challenges faced in patients with HS, with 59% reporting a large or extremely large effect of the disease on their life. Highest scores were recorded for levels of embarrassment and self-consciousness relating to the disease and choice of clothing. This adds to the growing literature on the impact on body image noted in patients with HS. Furthermore, a negative impact on employment and leisure time was observed, and this needs to be tackled to ensure patients can continue work and social commitments. Social isolation was also a feature of patients with HS and supports should be made available to these patients to ensure psychological stresses are addressed in addition to the physical aspects of the disease. This chapter also

studied pain in a cohort of patients with HS and emphasises the need for guidelines on the appropriate treatment of pain in HS, which is often overlooked by GPs, dermatologists and surgeons in their assessment and treatment of this cohort. Finally, some subjects reported that the treatment of their HS was bothersome. This chapter also assessed adherence to prescribed treatment in a cohort with HS. Adherence has been noted as poor in patients with HS in the literature, and this was mirrored in our results with a significant proportion reporting their difficulty remembering to take their medication and a further proportion cutting back or stopping medications without medical input. Ensuring adherence to prescribed treatment through enhanced supports tackling the perceived barriers to compliance would be of benefit in patients with HS. It is important to appreciate that non-adherence is not solely ‘the fault’ of patients but several healthcare factors including poor access and poor communication can have an impact; thus these issues should be further explored in HS. I used validated questionnaires in this study which gives important quantitative results. However, such questionnaires lack depth of information with standardised responses, and thus a mixed methods approach with more qualitative data from focus groups or interviews exploring themes surrounding pain, impact on quality of life, and adherence to prescribed treatment in HS would have added more insight into their thoughts, feelings, and experiences. I also sought to describe the physical activity undertaken by a cohort of patients with HS. In this study it appears that patients with HS had moderate to high levels of activity; however, overestimation of physical activity is a trend observed in many studies assessing exercise levels. The use of a questionnaire to assess physical activity appears to be prone to bias, and therefore the use of individual interviews to clarify responses, and objective

measurement of pedometer or smartphone-based activity would have given more robust findings.

The skin microbiome is an area of expanding research in HS, with more robust data coming to light about the bacteria found in lesions of HS, and their possible role in the pathogenesis of the disease, since the introduction of next generation sequencing in recent years. **Chapter 4** described the skin microbiome composition in a cohort of patients with HS compared to healthy controls. A dysbiosis with lower alpha diversity, a marker of species richness, and elevated levels of *Finegoldia magna* was noted in patients with HS. This is in agreement with the prior literature.

There is a paucity of data on the gut microbiome in HS in the literature to date.

Chapter 5 described the gut microbiome in a cohort of patients with HS compared to healthy controls. This is the first large study on the gut microbiome in HS showing an altered gut microbiome with low alpha diversity and an abundance of *Ruminococcus gnavus*.

As with any microbiome study, we were limited by the lack of a good definition of a 'healthy microbiome'. A strength of this study in this respect is the inclusion of a control group which was lacking in many of the prior microbiome studies in HS. Furthermore, with next generation sequencing the results can be biased due to incomplete reference databases, and varying PCR amplification frequencies used; and the clinical significance of the identified dysbiosis is unknown. Skin samples in particular prove challenging for amplicon-based sequencing as they are low biomass. The number of subjects that contributed swab samples to some sites was low, with a

low control number. Attempts to optimise sample collection were made including no cleansing of the skin for at least 24 hours before sample collection, the use of a scraping and firm swabbing method to increase yield, and the use of a buffer skin solution. Reagents and swabs were selected as reported to be DNA-free and a negative control was run within the same sequencing batch to detect contamination. A further limitation of the study is the lack of swabs from unaffected skin which has been proven to show an altered microbiome in a study by Ring et al (546). I did however attempt to sequence the microbiome of affected and unaffected skin biopsies from 9 patients. Unfortunately limited bacterial DNA concentrations were extracted, with high levels of off-target amplification of human DNA, an issue which has been encountered in other studies (736–738). This is a general feature of microbiome analysis of low biomass samples (739). Therefore, standardisation of analysis of microbial DNA in skin biopsies is required to reduce human DNA by unbiased whole genome amplification (736). From this study, it appears primer selection in sample processing and sequencing may have resulted in this contamination (737,738). Optimising DNA extraction from skin biopsies is an aim for future studies in HS and other skin conditions I plan to explore.

This research adds to the expanding knowledge of the microbiome in HS, describing an altered skin and gut microbiome. However, despite this growing knowledge of the microbiome in HS, it remains unclear whether dysbiosis is cause or effect; that is whether the skin inflammation is because of the dysbiosis or whether the dysbiosis is caused by the skin inflammation. Therefore, the true role of the gut and skin microbiome in the pathogenesis of HS needs to be further elucidated. The way forward for this should be further large cohort studies with a control group, and

standardisation of methodology to ensure the homogeneity across studies for direct comparison. Assessing the gut and skin microbiome over time in the same patients may also be of benefit, as would describing the microbiome present during flares and remissions, as well determining the role that it may play in the relapsing and remitting nature of the condition. Other areas of research, which have thus far been neglected in the literature, are the oral and genital microbiome which should be included in future microbiome studies in HS. With new technology, further research on the skin microbiome in HS, such as a prospective cohort study assessing the transient microbiota present during flares and the core microbiota present during remissions, as well as the skin microbiota present pre and post therapy, with next generation sequencing of the skin microbiome from skin swabs and biopsies of affected and unaffected areas, would add to the current knowledge. This might be challenging as the distinction between stable and transient microbiota, which may be in low abundance, can be difficult to decipher (736). Identifying these microbiota present during remissions and flares may inform future manipulation of the skin microbiota via intervention studies such as skin probiotics.

A further prospective cohort study on the gut microbiome in HS, characterising the gut microbiome during flares and remissions of the disease, and pre and post therapy would add to the growing literature and provide potential targets for HS treatment.. Other areas of further research on the gut microbiome include the impact of long-term antibiotics on the microbiome in HS. Our study evaluated patients off antibiotics for at least 4 weeks and did not note any difference between groups with no antibiotic therapy versus those who had antibiotic therapy in the preceding year. A cohort study to evaluate the gut and skin microbiome pre-antibiotic therapy for HS

and on treatment could determine the impact of the antibiotics used in HS on the gut and skin microbiome. Describing the skin and gut microbiome in HS further may also allow us to develop more targeted or narrower-spectrum antibiotics for the treatment of HS in future. This is one way to tackle the emerging issue of anti-microbial resistance, which is of concern with the current long-term use of broad-spectrum antibiotics in HS. It may also provide a way to better target the deep-seated lesions of HS which often poorly respond to antibiotic therapy due to biofilm creation, and may, too, reduce HS patients' risk of developing the antibiotic associated infection *C. difficile*.

The impact of the biologics on the skin and gut microbiome should also be further evaluated. It has been shown in studies on inflammatory bowel disease that adalimumab alters the gut microbiome towards eubiosis (740). If this is also true of anti-TNF- α therapy in HS, the implications of this are worth exploring. Studies have also described how the gut microbiome can affect patient responses to cancer immunotherapy (741). It is therefore possible that certain microbiome patterns may indicate better response to certain treatments also in HS.

High species diversity is positively correlated with resistance to pathogens in both the skin and gut microbiome. Further targeting the gut microbiome may be achieved through faecal microbiota transplantation (FMT), transferring live microorganisms from healthy donors to affected patients. FMT has proven beneficial in the management of *C. difficile*, and inflammatory bowel disease, and its use is also being explored in other areas including cancer immunotherapy (742,743). A clinical trial has also been registered assessing the safety and efficacy of FMT in patients with

chronic inflammatory diseases including several rheumatological conditions, psoriasis, and HS (FRONT) (744). Similarly in the area of treating skin disease, cutaneous microbiota transplants have been trialled in atopic dermatitis and should be explored in HS. Supplementation with pre-biotics and probiotics may also be explored via a randomised controlled trial with the aim of restoring healthy high species diversity, with possible impact on both the skin and gut microbiota. Prebiotics are non-digestible ingredients that selectively stimulate the growth of health-related bacteria such as *Bifidobacterium* and *Lactobacilli*, whereas probiotics are living microorganisms that confer a health benefit on the host. To date, no evidence exists for the benefits of prebiotics and probiotics in HS with varied results in atopic dermatitis, acne, and psoriasis (745). Restoring commensal microbial homeostasis replacing pathogenic species, using probiotic strains in HS, may be the way forward in modulating the inflammatory cascade. This is true for both the cutaneous and gut microbiomes. A randomised controlled trial assessing supplementation with beneficial bacteria such as *Ruminococcus obeum*, which was depleted in patients with HS and enriched in healthy controls, would be of interest with the aim of reducing pathogenic bacteria such as *Ruminococcus gnavus* and *Clostridium ramosum* identified in this study, increasing alpha diversity, and restoring eubiosis in the treatment group compared to controls. A randomised controlled trial of a topical probiotic in HS would also be of interest, and targets such as restoring *Propionibacterium acnes* and depleting pathogenic bacteria such as *Finegoldia magna* should be explored.

As gut microbiome research moves on to address the mechanisms influencing host health the crosstalk between the immune system, the gut, and the cutaneous

microbiome, and the role of this pathway in the development of skin disease in HS should be elucidated. A way of evaluating this may be the development of a mouse model of HS. An adequate mouse model of HS does not currently exist and development of such will be important to understand HS pathogenesis better. The first murine models focused on γ -secretase associated polymorphisms which have been described in cases of familial HS(746). Although these mouse models showed some cyst formation they failed to develop the clinical characteristics of inflammation, abscess formation, fistulation and scarring (746). Similarly NCSTN knockout mice showed inflammation of hair follicles but failed to develop abscesses. As human and murine skin differs greatly, xenograft models may be a better approach to study HS pathogenesis further and attempts are underway to complete this. The potential impact of the skin and gut microbiome on the development of HS and the utility of manipulation of the microbiome could be further elucidated via these mouse models.

Ex vivo studies of lesional human skin in HS may also give further insights into the pathogenesis of HS and response to therapy. A study by Vossen et al. of punch biopsy transwell culture demonstrated the contribution of IL-1 in driving inflammation in HS and the inhibitory effect of anti-inflammatory drugs on proinflammatory cytokines and anti-microbial peptides (AMPs)(747). Ex vivo studies are promising and optimisation of such models should be a further area of research to explore.

Calprotectin is a protein biomarker present in the serum and faeces. Gut inflammation and elevated levels may indicate undiagnosed inflammatory bowel

disease. Complement C5a is a potent anaphylatoxin which mediates inflammation and is a chemoattractant for neutrophils. **Chapter 6** described the faecal calprotectin and serum C5a levels in a cohort of patients with HS. Both calprotectin and C5a levels were raised in this study. Elevated faecal calprotectin may indicate sub-clinical inflammation of the bowel mucosa in HS and supports the close monitoring of patients in HS at risk of developing inflammatory bowel disease. Complement C5a may in future be used as a biomarker of disease activity in HS if further studies confirm such an elevation. Furthermore, clinical trials are ongoing to assess the success of targeting C5a in treating HS (728).

Diet is known to be a significant modulator of the gut microbiota (730). Diets high in fat and highly processed carbohydrates, and low in fibre content predispose to gut dysbiosis, with potential implications on health (730). **Chapter 7** described the diet of the cohort of patients with HS and its correlation with the microbial composition, clinical characteristics, serum C5a, and faecal calprotectin levels. We also compared habitual diet of those with HS to healthy controls and patients with Crohn's disease. A western diet was described in patients with HS compared to controls, and similar to those with Crohn's disease. To date little research has shown the impact of diet on development or exacerbation of HS with small sample sizes and no placebo group in the published literature. Diets high in fibre rich plant foods, and low in red meats and processed foods could reduce disease severity and flares, and enhance response to therapy in those with HS, and lower risk of HS developing in those predisposed. Dietary fibre exerts a protective effect on gut microbiota composition and is fermented to produce short chain fatty acids which exert an anti-inflammatory effect on T cells and macrophages (748,749). The next step to assess the impact of diet on

HS would be a randomised controlled trial of dietary intervention with dietary fibre to determine its effect on the altered microbiota described, comparing the gut and skin microbiota pre and post intervention, and to further explore further the role diet plays in HS.

The pathogenesis of HS is likely a result of several different factors including immune dysregulation and an altered microbiome, and so multimodal treatments are likely to be the way forward in future. I look forward to future studies exploring the microbiome further in HS. This is a young and exciting area of research with great potential, impacting on our understanding of the pathogenesis of HS, and informing the development of future treatments.

9. References

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10. Supplementary Methods and Appendices

Patient Recruitment

Inclusion Criteria

To be considered eligible for enrolment into the study, subjects must;

1. Be able to give written informed consent.
2. Be between 18 and 65 years of age.
3. Study group will compromise those with a diagnosis of hidradenitis suppurativa.
4. Control group will include healthy individuals with no chronic medical conditions.

Exclusion criteria

Subjects will be excluded from the study if they meet any of the below criteria;

1. Are less than 18 and greater than 65 years of age.
2. Have a significant acute or chronic coexisting illness (cardiovascular, gastrointestinal, immunological, metabolic or any condition which contraindicates, in the investigators judgement, entry to the study).
3. Have a condition or taking a medication that the investigator believes would interfere with the objectives of the study, pose a safety risk, or confound the interpretation of the study results.
4. Subjects may not be receiving treatment involving experimental drugs.
5. If the subject has been in a recent experimental trial, these must have been completed not less than 30 days prior to this study.

1. Pre-treatment of Microbial DNA from Nasal, and Skin Swabs

1. Equilibrate samples to room temperature (15–25°C).
2. If a precipitate has formed in Buffer ATL or Buffer APL2, dissolve by incubating at 56°C.
3. Heat a thermoshaker to 56°C.
4. Heat a water bath or heating block to 70°C.
5. Equilibrate Buffer AVE to room temperature.
6. Cut the tip off a swab and place it in a 2ml microcentrifuge tube.
7. Add 500 µl Buffer ATL.
8. Place the tube on a thermoshaker and incubate for 10 min at 56°C with continuous shaking at 600 rpm.
9. Open the 2 ml tube and carefully transfer all the liquid into a fresh 2ml tube.

2. Purification of Microbial DNA from pre-treated samples

1. Add 40 µl Proteinase K and mix the sample by vortexing for 10 s.
2. Incubate the sample at 56°C for 10 min.
3. Add 200 µl of Buffer APL2 to the sample. Close the cap and mix by pulse-vortexing for 30 s.
4. Incubate at 70°C for 10 min.
5. Briefly spin the tube to remove drops from the inside of the lid.
6. Add 300 µl ethanol to the lysate. Close the cap, and mix

thoroughly by pulse-vortexing for 15–30 s.

7. Carefully apply 600 µl of the mixture from step 6 to the QIAamp UCP Mini spin column (in a 2ml collection tube) without wetting the rim. Close the cap, and centrifuge at 6000 x g (8000 rpm) for 1 min. Place the QIAamp Mini spin column in a clean 2 ml collection tube (provided), and discard the tube containing the filtrate.
8. Repeat step 7 by applying the remaining mixture from step 6 to the QIAamp UCP Mini spin column.
9. Carefully open the QIAamp UCP Mini spin column and add 600 µl Buffer APW1 without wetting the rim. Close the cap and centrifuge at 6000 x g (8000 rpm) for 1 min. Place the QIAamp UCP Mini spin column in a clean 2 ml collection tube (not provided), and discard the collection tube containing the filtrate.
10. Carefully open the QIAamp UCP Mini spin column and add 750 µl Buffer APW2 without wetting the rim. Close the cap and centrifuge at full speed (20,000 x g; 14,000 rpm) for 3 min.
11. Place the QIAamp UCP Mini spin column in a new 2ml collection tube and discard the old collection tube with the filtrate. Centrifuge at full speed for 1 min. Place the QIAamp UCP Mini column into a new 2 ml collection tube. Open the lid and incubate the assembly at 56°C for 3 min to dry the membrane completely.

12. Place the QIAamp UCP Mini column in a clean 1.5 ml elution tube and discard the collection tube. Carefully apply 20–100 μ l of Buffer AVE to the center of the QIAamp UCP Mini membrane. Close the lid and incubate at room temperature for 1 min.

Important: Ensure that the elution buffer is equilibrated to room temperature. If elution is done in small volumes (<50 μ l) the elution buffer has to be dispensed onto the center of the membrane for complete elution of bound DNA. Elution volume is flexible and can be adapted according to the requirements of downstream applications. The recovered eluate volume will be up to 5 μ l less than the elution volume applied onto the column.

13. Centrifuge at full speed (20,000 x g; 14,000 rpm) for 1 min to elute the DNA.
14. Repeat steps 13 and 14.

1. Cell Lysis

1. Transfer 0.25g of sample into a fresh 2ml screw cap tube. Add 1ml of lysis buffer and 0.4g of sterile zirconia beads.
2. Homogenize for 60 seconds at a maximum speed on a Mini-Bead Beater.
3. Place on ice for 30-60 to allow the tube to cool. Repeat steps 2 and 3 twice more.
4. Incubate at 70°C for 15 min, with gentle shaking by hand every 5 min.
5. Centrifuge at 4°C for 5 min at full speed. Transfer the supernatant to a fresh 2ml Eppendorf tube.
6. Add 300ul of fresh lysis buffer to the lysis tube and repeat the steps 2-5, and then pool the supernatant.

2. Precipitation of nucleic acids

7. Add 347ul of 7.5M (260ul of 10M) ammonium acetate to each lysate tube, mix well and incubate on ice for 5mins.
8. Centrifuge at 4°C for 10 min at full speed.
9. Transfer the supernatant to two 1.5ml Eppendorf tubes, add one volume of isopropanol (650ul) and mix well, and incubate on ice for 30 min.
10. Centrifuge at 4°C for 15 min at full speed, remove the supernatant using aspiration(decanting), wash the nucleic acids pellet with 300ul 70% ethanol, and dry the pellet for ~30mins, or until completely dry.
11. Dissolve the nucleic acid pellet in 100ul of TE (Tris-EDTA) buffer and pool the two aliquots.

3. Removal of RNA, protein and purification

12. Add 2ul of DNase-free RNase (10mg/ml) and incubate at 37°C for 15min.
13. Add 15ul of Proteinase K and 200ul of Buffer AL (from the QIAamp DNA Stool Mini Kit), mix well, and incubate at 70°C for 10 min.
14. Add 200ul of ethanol and mix well. Transfer to a QIAamp column and centrifuge at full speed for 1 min.
15. Discard the flow through, place column in new collecting tube. Add 500ul of Buffer AW1 (Qiagen) and centrifuge for 1 min at room temperature.
16. Discard the flow through, replace the collecting tube, Add 500ul of Buffer AW2 (Qiagen) and centrifuge for 1 min at room temperature.
17. Discard the flow through and dry the column by centrifugation at room temperature for 1 min.
18. Place column in Eppendorf tube. Add 200ul of Buffer AE (Qiagen) and incubate at room temperature for 2 min.
19. Centrifuge at room temperature for 1 min to elute the DNA.
20. Discard the column and store the labelled tube at -20°C.
21. Can check quality of DNA by running on 0.8% gel.

16S Amplicon PCR - NU-AGE Standard Operating Procedure

Table 1:

Item	Supplier
NU-AGE Faecal DNA	N/A
16S Amplicon PCR Forward Primer	
16S Amplicon PCR Reverse Primer	
Nuclease-Free Water (10 x 50 ml)	Qiagen
Phusion Taq High-Fidelity Buffer (10 x 1.5 ml)	Fisher
PCR microplate Thermo-Fast 96 well natural semi-skirted Thermo Scientific ABgene	Fisher
Microtube PCR DNase and RNase free polypropylene with flat lid 0.2ml clear MBP	Fisher
Microcentrifuge tube 2 ml	Sarstedt
Microcentrifuge tube 0.5 ml	Fisher
Gilson Pipetman P1000, P200 and P20 pipettes	Fisher
Fisherbrand SureOne pipette tips 1000 µl, 200 µl, 20 µl	Fisher
Pipetting reservoir sterile polystyrene 50 ml	Fisher
PCR cap flat cap polypropylene natural cap-strip for 96-well plates	Fisher
Veriti Applied Biosystems 96-well Thermal Cycler	Fisher
Microcentrifuge	N/A
Biosafety Cabinet	N/A
Plate centrifuge	N/A

Prepare PCR Reaction:

1. Turn the safety cabinet on and place a red waste bag in the bag support.
2. Place tips, pipettes, PCR and other tubes, PCR plate, strip caps, pipetting reservoirs, tube racks, permanent markers, nuclease-free water and any other materials needed inside the cabinet and UV them for 20 min.
3. Thaw primers, 2x Phusion Taq High-Fidelity Mix and samples.
4. After thawed flick each sample to homogenise them.
5. After the 20 min, prepare the 16S Amplicon PCR Master Mix (use reaction template 16S for calculation).

Table 2: 16S Amplicon PCR Master Mix

16S Amplicon PCR Mix	Sequence (5'-3')	stock conc.	volume / well	final conc.
NU-AGE Faecal DNA		7.5 ng/ μ l	2.0 μ l	15 ng/ 30 μ l
Nuclease-Free Water		-	10.6 μ l	-
16S Amplicon PCR Forward Primer	TCGTCGGCAGCGTCAGATG TGTATAAGAGACAGCCTAC GGGNGGCWGCAG	5 μ M	1.2 μ l	0.2 μ M
16S Amplicon PCR Reverse Primer	GTCTCGTGGGCTCGGAGAT GTGTATAAGAGACAGGACT ACHVGGGTATCTAATCC	5 μ M	1.2 μ l	0.2 μ M
2x Phusion Taq High-Fidelity Mix		2x	15 μ l	1x
Total			30 μ l	

6. Distribute 28 μ l per well in all the wells of one a PCR microplate.
7. Add 2.0 μ l of each of the diluted DNA samples and 2.0 μ l of H₂O (negative control) into the corresponding well
8. Mix well by pipetting up and down.
9. Cover wells of plate with PCR cap flat strips (or adhesive film).
10. Centrifuge plate, 1000 rpm for 1 min.
11. Place plate in the preheated 96-well Thermal Cycler and run the program as below.

Table 3: 16S Amplicon PCR Cycling Conditions

Temperature	Time	Repeats	Step
98°C	30"	none	Initialisation
98°C	10"	X 25 cycles	Denaturation
55°C	15"		Annealing
72°C	20"		Extension
72°C	5'	none	Elongation

Relevant Literature:

16S Metagenomic Sequencing Library Preparation. Preparing 16S Ribosomal RNA Gene Amplicons for the Illumina MiSeq System. Part# 15044223Rev.B. Illumina.

Klindworth A, Pruesse E, Schweer T, Peplles J, Quast C, et al. (2013) Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. Nucleic Acids Res 41(1).The gene-specific sequences used in this protocol target the 16S V3 and V4 region. They are selected from the Klindworth et al. 2013. Illumina adapter overhang nucleotide sequences are added to the gene-specific sequences. The full length primer sequences, using standard IUPAC nucleotide nomenclature, to follow the protocol targeting this region are: 16S Amplicon PCR Forward Primer (S-D-Bact-0341-b-S-17) = 5' TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGGGNGGCWGA G

16S Amplicon PCR Reverse Primer (S-D-Bact-0785-a-A-21) = 5' GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTACHVGGGTATC TAATCC. The amplicon size is of 531 bp.

DERMATOLOGY LIFE QUALITY INDEX

Hospital No:

Date:

Name:

Score:

Address:

Diagnosis:

The aim of this questionnaire is to measure how much your skin problem has affected your life OVER THE LAST WEEK. Please tick ☒ one box for each question.

1.	Over the last week, how itchy, sore, painful or stinging has your skin been?	Very much ☐ A lot ☐ A little ☐ Not at all ☐
2.	Over the last week, how embarrassed or self-conscious have you been because of your skin?	Very much ☐ A lot ☐ A little ☐ Not at all ☐
3.	Over the last week, how much has your skin interfered with you going shopping or looking after your home or garden ?	Very much ☐ A lot ☐ A little ☐ Not at all ☐ Not relevant ☐
4.	Over the last week, how much has your skin influenced the clothes you wear?	Very much ☐ A lot ☐ A little ☐ Not at all ☐ Not relevant ☐
5.	Over the last week, how much has your skin affected any social or leisure activities?	Very much ☐ A lot ☐ A little ☐ Not at all ☐ Not relevant ☐
6.	Over the last week, how much has your skin made it difficult for you to do any sport ?	Very much ☐ A lot ☐ A little ☐ Not at all ☐ Not relevant ☐
7.	Over the last week, has your skin prevented you from working or studying ?	Yes ☐ No ☐ Not relevant ☐

	If "No", over the last week how much has your skin been a problem at work or studying ?	A lot	☐
		A little	☐
		Not at all	☐
8.	Over the last week, how much has your skin created problems with your partner or any of your close friends or relatives ?	Very much	☐
		A lot	☐
		A little	☐
		Not at all	☐
		Not relevant	☐
9.	Over the last week, how much has your skin caused any sexual difficulties ?	Very much	☐
		A lot	☐
		A little	☐
		Not at all	☐
		Not relevant	☐
10.	Over the last week, how much of a problem has the treatment for your skin been, for example by making your home messy, or by taking up time?	Very much	☐
		A lot	☐
		A little	☐
		Not at all	☐
		Not relevant	☐

Please check you have answered EVERY question. Thank you.

AY Finlay, GK Khan, April 1992 www.dermatology.org.uk, used with the permission of the authors.

Morisky 8 item medication adherence questionnaire

- Do you sometimes forget to take your medication?
 - Yes ☐
 - No ☐
- People sometimes miss taking their medicines for reasons other than forgetting. Thinking over the past 2 weeks, were there any days when you did not take your medicine?
 - Yes ☐
 - No ☐
- Have you ever cut back or stopped taking your medicine without telling your doctor because you felt worse when you took it?
 - Yes ☐
 - No ☐
- When you travel or leave home, do you sometimes forget to bring along your medicine?
 - Yes ☐
 - No ☐
- Did you take all your medicines yesterday?
 - Yes ☐
 - No ☐
- When you feel like your symptoms are under control, do you sometimes stop taking your medicine?
 - Yes ☐
 - No ☐
- Taking medicine every day is a real inconvenience for some people. Do you ever feel hassled about sticking to your treatment plan
 - Yes ☐
 - No ☐
- How often do you have difficulty remembering to take all your medicine?
 - Never/rarely ☐
 - Once in a while ☐
 - Sometimes ☐
 - Usually ☐
 - All of the time ☐

Score

INTERNATIONAL PHYSICAL ACTIVITY QUESTIONNAIRE (October 2002)

LONG LAST 7 DAYS SELF-ADMINISTERED FORMAT

FOR USE WITH YOUNG AND MIDDLE-AGED ADULTS (15-69 years)

The International Physical Activity Questionnaires (IPAQ) comprises a set of 4 questionnaires. Long (5 activity domains asked independently) and short (4 generic items) versions for use by either telephone or self-administered methods are available. The purpose of the questionnaires is to provide common instruments that can be used to obtain internationally comparable data on health-related physical activity.

Background on IPAQ

The development of an international measure for physical activity commenced in Geneva in 1998 and was followed by extensive reliability and validity testing undertaken across 12 countries (14 sites) during 2000. The final results suggest that these measures have acceptable measurement properties for use in many settings and in different languages, and are suitable for national population-based prevalence studies of participation in physical activity.

Using IPAQ

Use of the IPAQ instruments for monitoring and research purposes is encouraged. It is recommended that no changes be made to the order or wording of the questions as this will affect the psychometric properties of the instruments.

Translation from English and Cultural Adaptation

Translation from English is encouraged to facilitate worldwide use of IPAQ. Information on the availability of IPAQ in different languages can be obtained at www.ipaq.ki.se. If a new translation is undertaken we highly recommend using the prescribed back translation methods available on the IPAQ website. If possible please consider making your translated version of IPAQ available to others by contributing it to the IPAQ website. Further details on translation and cultural adaptation can be downloaded from the website.

Further Developments of IPAQ

International collaboration on IPAQ is on-going and an **International Physical Activity Prevalence Study** is in progress. For further information see the IPAQ website.

More Information

More detailed information on the IPAQ process and the research methods used in the development of IPAQ instruments is available at www.ipaq.ki.se and Booth, M.L. (2000). *Assessment of Physical Activity: An International Perspective*. Research Quarterly for Exercise and Sport, 71 (2): s114-20. Other scientific publications and presentations on the use of IPAQ are summarized on the website.

INTERNATIONAL PHYSICAL ACTIVITY QUESTIONNAIRE

We are interested in finding out about the kinds of physical activities that people do as part of their everyday lives. The questions will ask you about the time you spent being physically active in the **last 7 days**. Please answer each question even if you do not consider yourself to be an active person. Please think about the activities you do at work, as part of your house and yard work, to get from place to place, and in your spare time for recreation, exercise or sport.

Think about all the **vigorous** and **moderate** activities that you did in the **last 7 days**. **Vigorous** physical activities refer to activities that take hard physical effort and make you breathe much harder than normal. **Moderate** activities refer to activities that take moderate physical effort and make you breathe somewhat harder than normal.

PART 1: JOB-RELATED PHYSICAL ACTIVITY

The first section is about your work. This includes paid jobs, farming, volunteer work, course work, and any other unpaid work that you did outside your home. Do not include unpaid work you might do around your home, like housework, yard work, general maintenance, and caring for your family. These are asked in Part 3.

1. Do you currently have a job or do any unpaid work outside your home?

☐
☐

Yes

No



Skip to PART 2: TRANSPORTATION

The next questions are about all the physical activity you did in the **last 7 days** as part of your paid or unpaid work. This does not include traveling to and from work.

2. During the **last 7 days**, on how many days did you do **vigorous** physical activities like heavy lifting, digging, heavy construction, or climbing up stairs **as part of your work**? Think about only those physical activities that you did for at least 10 minutes at a time.

_____ days per week

☐

No vigorous job-related physical activity



Skip to question 4

3. How much time did you usually spend on one of those days doing **vigorous** physical activities as part of your work?

_____ hours per day

_____ minutes per day

4. Again, think about only those physical activities that you did for at least 10 minutes at a time. During the **last 7 days**, on how many days did you do **moderate** physical activities like carrying light loads **as part of your work**? Please do not include walking.

_____ days per week

☐

No moderate job-related physical activity



Skip to question 6

5. How much time did you usually spend on one of those days doing **moderate**

physical activities as part of your work?

_____ hours per day
_____ minutes per day

6. During the **last 7 days**, on how many days did you **walk** for at least 10 minutes at a time **as part of your work**? Please do not count any walking you did to travel to or from work.

_____ days per week

☐

No job-related walking



***Skip to PART 2:
TRANSPORTATION***

7. How much time did you usually spend on one of those days **walking** as part of your work?

_____ hours per day
_____ minutes per day

PART 2: TRANSPORTATION PHYSICAL ACTIVITY

These questions are about how you traveled from place to place, including to places like work, stores, movies, and so on.

8. During the **last 7 days**, on how many days did you **travel in a motor vehicle** like a train, bus, car, or tram?

_____ days per week

☐

No traveling in a motor vehicle



Skip to question 10

9. How much time did you usually spend on one of those days **traveling** in a train, bus, car, tram, or other kind of motor vehicle?

_____ hours per day
_____ minutes per day

Now think only about the **bicycling** and **walking** you might have done to travel to and from work, to do errands, or to go from place to place.

10. During the **last 7 days**, on how many days did you **bicycle** for at least 10 minutes at a time to go **from place to place**?

_____ days per week

☐

No bicycling from place to place



Skip to question 12

11. How much time did you usually spend on one of those days to **bicycle** from place to place?

_____ hours per day
_____ minutes per day

12. During the **last 7 days**, on how many days did you **walk** for at least 10 minutes at a time to go **from place to place**?

_____ days per week

☐

No walking from place to place

➔ **Skip to PART 3: HOUSEWORK**

13. How much time did you usually spend on one of those days **walking** from place to place?

_____ hours per day

_____ minutes per day

PART 3: HOUSEWORK, HOUSE MAINTENANCE, AND CARING FOR FAMILY

This section is about some of the physical activities you might have done in the **last 7 days** in and around your home, like housework, gardening, yard work, general maintenance work, and caring for your family.

14. Think about only those physical activities that you did for at least 10 minutes at a time. During the **last 7 days**, on how many days did you do **vigorous** physical activities like heavy lifting, chopping wood, shoveling snow, or digging **in the garden or yard**?

_____ days per week

☐

No vigorous activity in garden or yard

➔ **Skip to question 16**

15. How much time did you usually spend on one of those days doing **vigorous** physical activities in the garden or yard?

_____ hours per day

_____ minutes per day

16. Again, think about only those physical activities that you did for at least 10 minutes at a time. During the **last 7 days**, on how many days did you do **moderate** activities like carrying light loads, sweeping, washing windows, and raking **in the garden or yard**?

_____ days per week

☐

No moderate activity in garden or yard

➔ **Skip to question 18**

17. How much time did you usually spend on one of those days doing **moderate** physical activities in the garden or yard?

_____ hours per day

_____ minutes per day

18. Once again, think about only those physical activities that you did for at least 10 minutes at a time. During the **last 7 days**, on how many days did you do **moderate** activities like carrying light loads, washing windows, scrubbing floors and sweeping **inside your home**?

- _____ days per week
- ☐ No moderate activity inside home → **Skip to PART 4: RECREATION,**
19. How much time did you usually spend on one of those days doing **moderate** physical activities inside your home?
- _____ hours per day
_____ minutes per day

PART 4: RECREATION, SPORT, AND LEISURE-TIME PHYSICAL ACTIVITY

This section is about all the physical activities that you did in the **last 7 days** solely for recreation, sport, exercise or leisure. Please do not include any activities you have already mentioned.

20. Not counting any walking you have already mentioned, during the **last 7 days**, on how many days did you **walk** for at least 10 minutes at a time **in your leisure time**?
- _____ days per week
- ☐ No walking in leisure time → **Skip to question 22**
21. How much time did you usually spend on one of those days **walking** in your leisure time?
- _____ hours per day
_____ minutes per day
22. Think about only those physical activities that you did for at least 10 minutes at a time. During the **last 7 days**, on how many days did you do **vigorous** physical activities like aerobics, running, fast bicycling, or fast swimming **in your leisure time**?
- _____ days per week
- ☐ No vigorous activity in leisure time → **Skip to question 24**
23. How much time did you usually spend on one of those days doing **vigorous** physical activities in your leisure time?
- _____ hours per day
_____ minutes per day
24. Again, think about only those physical activities that you did for at least 10 minutes at a time. During the **last 7 days**, on how many days did you do **moderate** physical activities like bicycling at a regular pace, swimming at a regular pace, and doubles tennis **in your leisure time**?
- _____ days per week
- ☐ No moderate activity in leisure time → **Skip to PART 5: SITTING**

25. How much time did you usually spend on one of those days doing **moderate** physical activities in your leisure time?
- _____ hours per day
_____ minutes per day

PART 5: TIME SPENT SITTING

The last questions are about the time you spend sitting while at work, at home, while doing course work and during leisure time. This may include time spent sitting at a desk, visiting friends, reading or sitting or lying down to watch television. Do not include any time spent sitting in a motor vehicle that you have already told me about.

26. During the **last 7 days**, how much time did you usually spend **sitting** on a **weekday**?
- _____ hours per day
_____ minutes per day
27. During the **last 7 days**, how much time did you usually spend **sitting** on a **weekend day**?
- _____ hours per day
_____ minutes per day

This is the end of the questionnaire, thank you for participating.

1. Extraction using the weighing method (without extraction device)

1. Weigh (tare) an empty screw cap tube with an inoculation loop.
2. Take out approx. 100 mg (between 40 and 120 mg) faeces by means of the inoculation loop and place it into the screw cap tube. Avoid taking out solid, undigested material like fibres and seeds.
3. Weigh tube and loop with faeces which will give the net faeces weight.
4. Break or cut off the top half of the loop handle and leave the bottom part inside the tube.
5. Add extraction buffer to a weight: volume ratio 1:50, for instance 4.9 ml buffer to 100 mg faeces. Close the tube.
6. Mix vigorously for 30 seconds by means of a vortex mixer.
7. Continue the mixing on a shaker (at approx. 1000 rpm) for 30±5 minutes with the loop inside the tube as an agitator.
8. Allow a couple of minutes on the bench for particles to settle and pipette carefully from the top of the tube. No centrifugation is necessary, but a short centrifugation can be performed if a particle-free solution is required.
9. The extract, which represents a 1:50 dilution (weight:volume) of the stool sample, is now ready for dilution and testing.
10. For storage, transfer about 0.5 ml to a new tube. Extracts can be stored at 2 - 8°C for at least five days or frozen below -20°C for up to 2 years

2. ELISA Procedure

1. Dilute faeces extract samples 1:100 (e.g. 10 μ I sample + 990 μ I Sample Dilution Buffer) and mix well by vortexing.
2. Add 100 μ I of each standard, control and diluted sample in duplicate wells.
3. Cover the plate with a sealing foil and incubate at room temperature for 40 ± 5 min on a horizontal plate shaker (approximately 500 -700 rpm).
4. At the end of the incubation time, remove the liquid and wash the wells by adding 300 μ l Washing Solution to each well. Remove as much liquid as possible and repeat until a total of three washings have been performed. If a plate washer is used, check that all aspirating and filling probes are unblocked to ensure efficient washing of all wells. After the final wash, invert the plate and tap the well openings thoroughly on absorbent tissue to remove any remaining Washing Solution.
5. Mix the content of the Enzyme Conjugate vial gently prior to use (do not shake). Add 100 μ I of conjugate to each well, preferably using a repetitive or multichannel pipette.
6. Cover the plate with sealing foil and incubate at room temperature for 40 ± 5 min on a horizontal plate shaker.
7. Repeat the washing steps as described above, three times with 300 μ L Washing Solution per well.
8. Add 100 μ I Enzyme Substrate Solution to each well, preferably using a repetitive or multichannel pipette.
9. Incubate the plate at room temperature (without shaking) for 20 - 30

minutes, protected from light.

10. Add 100 μ L 0.2 M sulphuric acid stop solution to each well if a fixed incubation period is required.
11. Read the optical density (OD) values at 450 nm using an ELISA reader. If the plate reader has this option, shake the plate briefly (2-3 seconds) before reading.

3. Calculation of Calprotectin concentration in patient faecal samples:

1. Calculate the mean OD values of all duplicate wells (standards and samples).
2. Plot the value of each standard concentration (ng/ml) on the x axis against its mean OD value on the y-axis to obtain a standard curve. A 4-parameter curve fit function is recommended (see Figure 1 below). If a logarithmic x axis is required, a value of 0.001 ng/ml must be used for standard A (0 ng/ml).
3. Use the calibration curve to determine the Calprotectin concentration in the diluted samples (ng/ml) based on their OD values

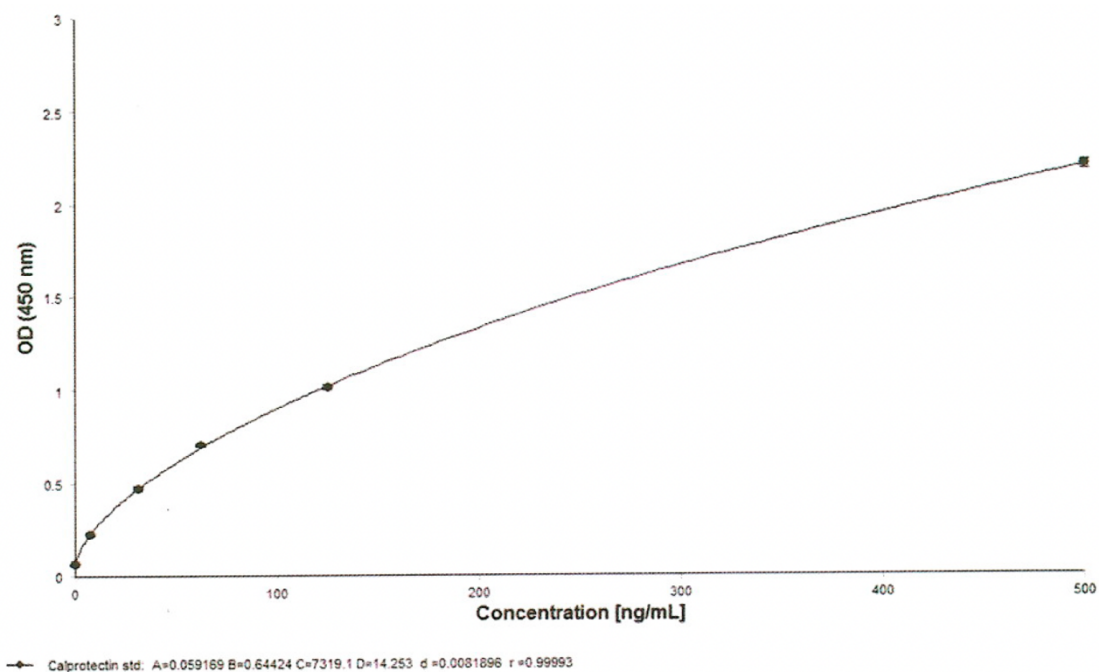


Figure 1: A representative standard curve using 4-parameter curve fit.

1. Standard Preparation

Equilibrate all reagents to room temperature (18-25°C) prior to use.

1. Briefly centrifuge the vial of Human C5a Standard and then add 400 μ L Assay Diluent A (for serum/plasma samples) or 1X Assay Diluent B (for cell culture supernatants) into the Human C5a Standard vial to prepare a 50 ng/mL Stock Standard. Mix thoroughly but gently.
2. Label tubes #1-8.
3. Prepare the 2000 pg/mL Standard #1 by adding 40 μ L Stock Standard into tube #1 along with 960 μ L Assay Diluent A or 1x Assay Diluent B. Mix thoroughly but gently.
4. Add 300 μ L Assay Diluent A or 1x Assay Diluent B into tubes 2-8.
5. Prepare Standard #2 by adding 300 μ L Standard #1 to tube #2. Mix thoroughly but gently.
6. Prepare Standard #3 by adding 300 μ L from Standard #2 to tube #3. Mix thoroughly but gently.
7. Using the table below as a guide, prepare further serial dilutions.
8. Standard #8 contains no protein and is the Blank control.

2. Sample Preparation

1. Add 100 μ L of each standard and sample into appropriate wells. Cover plate and incubate for 2.5 hours at room temperature or overnight at 4°C with gentle shaking.
2. Discard the solution and wash 4 times with 1X Wash Buffer. Wash by filling each well with 300 μ L 1X Wash Buffer using a multichannel pipette or

automatic plate washer. Complete removal of liquid at each step is essential to good performance. After the

last wash, remove any remaining Wash Buffer by aspirating or decanting.

Invert the plate and blot it by tapping gently against clean paper towels.

3. Add 100 μ L of the prepared biotinylated Human C5a Detection Antibody to each well. Incubate for 1 hour at room temperature with gentle shaking.
4. Discard the solution. Repeat the wash as in step 2.
5. Add 100 μ L of prepared 1X HRP-Streptavidin solution to each well. Incubate for 45 minutes at room temperature with gentle shaking
6. Discard the solution. Repeat the wash as in step 2.
7. Add 100 μ L of TMB One-Step Substrate Reagent to each well. Incubate for 30 minutes at room temperature in the dark with gentle shaking.
8. Add 50 μ L of Stop Solution to each well. Read at 450 nm immediately.

3. Calculations

1. Calculate the mean absorbance for each set of duplicate standards, controls and samples, and subtract the average zero standard optical density.
2. Plot the standard curve on log-log graph paper, with standard concentration on the x-axis and absorbance on the y-axis.
3. Draw the best-fit straight line through the standard points

Food Frequency Questionnaire

Name:

YOUR DIET OVER THE PAST YEAR

For each food there is an amount shown, of what we think is a “medium serving” or a common household unit such as a slice or teaspoon. Please put a tick in the box to indicate how often, **on average**, you have eaten the specified amount of each food, to the nearest whole number **during the past year**.

Please estimate your average food use as best you can. Please answer every question, do not leave ANY lines blank.

EXAMPLES:

The following are examples on how to estimate how often and how much bread and potatoes you ate over the past year. Please estimate your food intake for all foodstuffs in the same way.

Potatoes: If you ate a medium serving of potatoes 3 times per week over the past year put a tick in the box “2-4 per week”. If you think you usually ate more or less than a medium serving please try to estimate which box suits best.

	AVERAGE USE LAST YEAR								
BREAD AND SAVOURY BISCUITS (One slice or one biscuit)	Never or less than once	1-3 per month	Once a week	2-4 per week	5-6 per week	Once a day	2-3 per day	4-5 per day	6+ per day
White bread and rolls (including ciabatta and pannini bread)								✓	
	AVERAGE USE LAST YEAR								
Potatoes, Rice and Pasta (medium serving)	Never or less than once	1-3 per month	Once a week	2-4 per week	5-6 per week	Once a day	2-3 per day	4-5 per day	6+ per day

Boiled, instant or jacket potatoes				√					

For white bread a medium serving is one medium sized slice.
Therefore if you usually ate 1 medium slice 4 or 5 times per day, you should put a tick in the column headed “4-5 per day”. If you ate 2 medium slices 4 or 5 times per day, then you should put a tick in the column “6+ per day”.

Please check that you put a tick (√) on every line

	AVERAGE USE LAST YEAR								
A. MEAT, FISH AND POULTRY (Medium serving – the size of a deck of cards)	Never or less than once	1-3 per mo n th	On c e a we e k	2-4 per we e k	5-6 per we e k	On c e a day	2-3 pe r da y	4-5 pe r da y	6+ per da y
1. Beef roast									
2. Beef: steak									
3. Beef: mince									
4. Beef: stew									
5. Beef burger (1 burger)									
6. Pork: roast									
7. Pork: chops									
8. Pork: slices/escalopes									
9. Lamb: roast									
10. Lamb: chops									
11. Lamb: stew									
12. Chicken portion or other poultry e.g.									
13. Breaded chicken, chicken nuggets,									
14. Bacon									
15. Ham									
16. Corned beef, Spam, Luncheon									
17. Sausages, Frankfurters (1 sausage)									
18. Savoury pies (e.g. meat pie, pork pie, steak & kidney pie, sausage									
19. Liver, heart, kidney									
20. Liver paté									
21. Fish fried in batter, as in fish and chips									
22. Fish fried in breadcrumbs									
23. Oven baked/grilled fish (in breadcrumbs or									
24. Fish fingers/fish cakes									
25. Other white fish, fresh or frozen (e.g. cod, haddock, plaice, sole,									
26. Oily fish, fresh or canned (e.g. mackerel, kippers, tuna, salmon, sardines, herring)									
27. Shellfish (e.g. crab, prawns,									

	AVERAGE USE LAST YEAR								
B. BREAD AND SAVOURY BISCUITS (One slice or one biscuit)	Never or less than once	1-3 per mo n th	On c e a we e k	2-4 per we e k	5-6 per we e k	On c e a day	2-3 pe r da y	4-5 pe r da y	6+ per da y
1. White bread and rolls (including ciabatta and pannini)									
2. Brown bread and rolls									
3. Wholemeal bread and rolls									
4. Cream crackers, cheese biscuits									
5. Crisp bread, e.g. Ryvita									
6. Pancakes, muffins, oatcakes									

	AVERAGE USE LAST YEAR								
C. CEREALS (One medium sized bowl)	Never or less than once	1-3 per mo n th	On c e a we e k	2-4 per we e k	5-6 per we e k	On c e a day	2-3 pe r da y	4-5 pe r da y	6+ per da y
1. Porridge, Readybrek									
2. All Bran, Weetabix,									
3. Branflakes, Bran Buds									
4. Cornflakes, Rice Krispies									
5. Muesli (e.g. Country Store, Alpen, sugar									
6. Sugar Coated Cereals (e.g. Frosties, Crunchy Nut Cornflakes, Crunchy Sugar Coated Muesli)									

	AVERAGE USE LAST YEAR								
D. POTATOES, RICE AND PASTA (Medium serving – about a cupful)	Never or less than once	1-3 per month	Once a week	2-4 per week	5-6 per week	Once a day	2-3 per day	4-5 per day	6+ per day
1. Boiled, instant or jacket potatoes									
2. Mashed potatoes									
3. Chips									
4. Roast potatoes									
5. Potato Salad									
6. White Rice									
7. Brown Rice									
8. White/yellow or green pastas (e.g. spaghetti, macaroni, noodles)									
9. Wholemeal pasta									
10. Lasagne (meat based)									
11. Lasagne (vegetarian)									
12. Moussaka									
13. Pizza									
14. Macaroni Cheese									

	AVERAGE USE LAST YEAR								
E. DAIRY PRODUCTS AND FATS	Never or less than once	1-3 per mo n th	On c e a we e k	2-4 per we e k	5-6 per we e k	On c e a day	2-3 pe r da y	4-5 pe r da y	6+ per da y
1. Cream (tablespoon)									
2. Full-fat yoghurt or Greek- style Yoghurt (125g)									
3. Dairy desserts (125g carton)									
4. Cheddar cheese (medium serving)									
5. Low-fat cheddar cheese (medium									
6. Eggs as boiled, fried, scrambled, poached									
7. Quiche (medium serving)									
8. Light salad cream or light mayonnaise									
9. Salad cream, mayonnai se									
10. French dressing									
11. Other salad dressing									
12. The following on bread or vegetables									
13. Butter (teaspoon)									
14. Lite Butter e.g. Dawn Lite, Connacht Gold									
15. Sunflower margarine e.g. Flora (teaspoon)									
16. Low-fat margarine (e.g. low- low)									
17. Cholesterol Lowering Spreads e.g. Flora Pro Active, Dairy Gold Heart (teaspoon)									
18. Cream & Vegetable Oil spread e.g. Golden Pasture, Kerrymaid, Dairy Gold – teaspoon									

19. Olive oil spread e.g. Golden Olive (teaspoon)									

	AVERAGE USE LAST YEAR								
F. FRUIT (1 Fruit or medium serving)	Never or less than once	1-3 per mon th	Once a wee k	2-4 per we ek	5-6 per we ek	Once a day	2-3 per da y	4-5 per da y	6+ per da y
1. Apples									
2. Pears									
3. Oranges, satsumas, mandarins									
4. Grapefruit									
5. Bananas									
6. Grapes									
7. Melon									
8. Peaches, plums									
9. Apricots									
10. Strawberries, raspberries, kiwi fruit									
11. Tinned fruit									
12. Dried fruit e.g. raisins									
13. Frozen fruit									

	AVERAGE USE LAST YEAR								
G. VEGETABLES Fresh, frozen or tinned (Medium Serving – 2 tablespoons)	Never or less than once	1-3 per mon th	Once a wee k	2-4 per we ek	5-6 per we ek	Once a day	2-3 per da y	4-5 per da y	6+ per da y
1. Carrots									
2. Spinach									
3. Broccoli, spring greens, kale									
4. Brussel sprouts									
5. Cabbage									
6. Peas									
7. Green beans, broad beans, runner beans									
8. Courgettes									
9. Cauliflower									
10. Parsnips, turnips									
11. Leeks									
12. Onions									
13. Garlic									
14. Mushrooms									
15. Sweet peppers									
16. Beansprouts									
17. Green salad, lettuce									

18. Cucumber, celery									
19. Tomatoes									
20. Sweetcorn									
21. Beetroot									
22. Coleslaw									
23. Baked beans									
24. Dried lentils, beans, peas									Pa
25. Tofu, soya meat, TVP									

	AVERAGE USE LAST YEAR								
H. SWEETS AND SNACKS (Medium serving)	Never or less than once	1-3 per mo nt h	Onc e a we ek	2-4 per we ek	5-6 per we ek	Once a day	2-3 pe r da y	4-5 pe r da y	6+ per da y
1. Chocolate coated sweet biscuits e.g. digestive									
2. Plain sweet biscuits e.g. Marietta, digestives, rich tea (one)									
3. Cakes e.g. fruit, sponge									
4. Buns, pastries e.g. croissants,									
5. Fruit pies, tarts, crumbles									
6. Sponge puddings									
7. Milk puddings e.g. rice, custard, trifle									
8. Ice cream, choc ices, Frozen									
9. Chocolates, singles or squares									
10. Sweets, toffees, mints									
11. Sugar added to tea coffee, cereal									
12. Sugar substitute e.g. canderel added to tea coffee, cereal (teaspoon)									
13. Crisps or other packet snacks									
14. Peanuts or other nuts									

	AVERAGE USE LAST YEAR								
I. SOUPS, SAUCES AND SPREADS	Never or less than once	1-3 per month	Once a week	2-4 per week	5-6 per week	Once a day	2-3 per day	4-5 per day	6+ per day
1. Vegetable soups: homemade/fresh (1									
2. Vegetable soups: tinned/ packet (1 bowl)									
3. Meat soups: homemade/fresh (1									
4. Meat soups: tinned/ packet (1 bowl)									
5. Sauces e.g. white sauce, cheese sauce, gravy (tablespoon)									
6. Tomato based sauces e.g. pasta sauces									
7. Curry-type sauces									
8. Pickles, chutney (tablespoon)									
9. Marmite, Bovril (tablespoon)									
10. Jam, marmalade, honey, syrup (teaspoon)									
11. Peanut butter (teaspoon)									

	AVERAGE USE LAST YEAR								
J. DRINKS	Never or less than once	1-3 per month	Once a week	2-4 per week	5-6 per week	Once a day	2-3 per day	4-5 per day	6+ per day
1. Tea (cup)									
2. Coffee instant (cup)									
3. Coffee ground (cup)									
4. Coffee, decaffeinated (cup)									
5. Coffee whitener e.g. coffee-mate									
6. Cocoa, Hot Chocolate (cup)									
7. Horlicks, Ovaltine (cup)									
8. Wine (glass)									
9. Beer, Larger or Cider (half pint)									
10. Alcopops e.g. Bacardi Breezer									

11. Whole milk (cup) – cow or goat (including milk used in tea, cereal etc)									
12. Semi-skimmed milk (cup) (including milk used in tea, cereal etc)									
13. Port, Sherry, Vermouth, liqueurs									
14. Spirits e.g. Gin, Whiskey (single									
15. Low calorie or diet soft fizzy (glass)									
16. Fizzy Soft drinks e.g. Cocoa Cola									
17. Pure fruit drinks e.g. orange juice (small									
18. Fruit squash (small glass)									

	AVERAGE USE LAST YEAR								
K. Functional Foods	Never or less than once	1-3 per month	Once a week	2-4 per week	5-6 per week	Once a day	2-3 per day	4-5 per day	6+ per day
1. Probiotic drinks/yoghurt e.g. Actimel, Yakult <i>Please specify brand name:</i>									

	AVERAGE USE LAST YEAR								
K. Functional Foods	Never or less than once	1-3 per month	Once a week	2-4 per week	5-6 per week	Once a day	2-3 per day	4-5 per day	6+ per day
2. Vitamin supplements									

Please mention if you have been on any particular diets during the last 12 months, and if so, how many months/weeks ago and for how long were you on the diet:

Diet name and description	Months ago commenced diet	Months ago ceased diet (if diet ongoing say ongoing)

Appendix 1: Faecal module taxa list

Taxa	Colours
Seq 1 Eubacterium rectale	black
Seq 25 Megamonas	black
Seq 112 Veillonella ratti	black
Seq 134 Lactobacillus	black
Seq 172 Clostridiales	black
Seq 177 Ruminococcaceae	black
Seq 193 Bacteroides plebeius	black
Seq 383 Eubacterium eligens	black
Seq 501 Bacteroides xylanisolvens	black
Seq 507 Streptococcus	black
Seq 531 Eubacterium eligens	black
Seq 567 Bacteroides plebeius	black
Seq 586 Roseburia faecis	black
Seq 592 Roseburia	black
Seq 652 Haemophilus parainfluenzae	black
Seq 710 Faecalibacterium prausnitzii	black
Seq 758 Lachnospiraceae	black
Seq 789 Ruminococcus obeum	black
Seq 807 Firmicutes	black
Seq 833 Bacteroides massiliensis	black
Seq 859 Ruminococcaceae	black
Seq 896 Haemophilus	black
Seq 1029 Ruminococcus bromii	black
Seq 1032 Ruminococcus obeum	black
Seq 1054 Lachnospiraceae	black
Seq 1090 Veillonella rogosae	black
Seq 1129 Faecalibacterium prausnitzii	black
Seq 1148 Veillonella atypica	black
Seq 1155 Actinomyces odontolyticus	black
Seq 1197 Streptococcus parasanguinis	black
Seq 1203 Lachnospiraceae	black
Seq 1204 Bacteroides ovatus	black
Seq 1213 Eubacterium ruminantium	black
Seq 1237 Veillonella dispar	black
Seq 1301 Streptococcus	black
Seq 1307 Roseburia inulinivorans	black
Seq 1339 Parabacteroides merdae	black
Seq 1490 Lachnospiraceae	black
Seq 1570 Faecalibacterium prausnitzii	black
Seq 1625 Clostridium aldenense	black
Seq 1724 Eubacterium eligens	black
Seq 1730 Enterococcus	black

Seq 1763 <i>Ruminococcus albus</i>	black
Seq 1768 <i>Streptococcus</i>	black
Seq 1783 <i>Barnesiella intestinihominis</i>	black
Seq 1791 <i>Streptococcus parasanguinis</i>	black
Seq 1864 Clostridiales	black
Seq 1888 <i>Dorea</i>	black
Seq 1891 <i>Streptococcus</i>	black
Seq 1938 <i>Blautia faecis</i>	black
Seq 1940 <i>Olsenella</i>	black
Seq 1988 <i>Prevotella copri</i>	black
Seq 2016 Ruminococcaceae	black
Seq 2044 Enterobacteriaceae	black
Seq 2045 <i>Alloscardovia omnicolens</i>	black
Seq 2073 <i>Lactobacillus oris</i>	black
Seq 2090 <i>Granulicatella</i>	black
Seq 2187 <i>Collinsella aerofaciens</i>	black
Seq 2218 Ruminococcaceae	black
Seq 2321 <i>Collinsella aerofaciens</i>	black
Seq 2322 <i>Rothia mucilaginosa</i>	black
Seq 2412 <i>Allisonella histaminiformans</i>	black
Seq 2520 <i>Proteus</i>	black
Seq 2563 Streptophyta	black
Seq 2574 <i>Streptococcus</i>	black
Seq 2575 <i>Streptococcus sobrinus</i>	black
Seq 2627 <i>Lactobacillus delbrueckii</i>	black
Seq 2737 Porphyromonadaceae	black
Seq 2881 <i>Pseudoflavonifractor</i>	black
Seq 2882 <i>Atopobium parvulum</i>	black
Seq 2915 Ruminococcaceae	black
Seq 2998 Clostridiales	black
Seq 2999 <i>Gemella morbillorum</i>	black
Seq 3040 <i>Actinomyces graevenitzi</i>	black
Seq 3169 Ruminococcaceae	black
Seq 3526 Clostridiales	black
Seq 3529 Lachnospiraceae	black
Seq 3 <i>Blautia</i>	blue
Seq 32 <i>Anaerostipes hadrus</i>	blue
Seq 61 <i>Asteroleplasma anaerobium</i>	blue
Seq 63 <i>Catenibacterium mitsuokai</i>	blue
Seq 68 <i>Prevotella copri</i>	blue
Seq 81 <i>Succinivibradextrinosolvens</i>	blue
Seq 82 Clostridiales	blue
Seq 99 <i>Faecalibacterium prausnitzii</i>	blue
Seq 119 Firmicutes	blue
Seq 120 Clostridiales	blue

Seq_121	Erysipelotrichaceae	blue
Seq_129	Succinivibradextrinosolvens	blue
Seq_146	Firmicutes	blue
Seq_155	Ruminococcaceae	blue
Seq_157	Eubacterium eligens	blue
Seq_166	Ruminococcus bromii	blue
Seq_197	Paraprevotella clara	blue
Seq_205	Bacteroides massiliensis	blue
Seq_212	Ruminococcus	blue
Seq_227	Bacteroides coprocola	blue
Seq_235	Clostridium disporicum	blue
Seq_244	Lachnospiraceae	blue
Seq_255	Ruminococcaceae	blue
Seq_260	Coprococcus eutactus	blue
Seq_266	Ruminococcaceae	blue
Seq_273	Ruminococcaceae	blue
Seq_333	Lachnospiraceae	blue
Seq_337	Ruminococcaceae	blue
Seq_357	Clostridiales	blue
Seq_375	Clostridiales	blue
Seq_394	Lachnospiraceae	blue
Seq_408	Clostridium XIVa	blue
Seq_425	Bacteroides massiliensis	blue
Seq_451	Ruminococcaceae	blue
Seq_457	Lachnospiraceae	blue
Seq_505	Prevotella	blue
Seq_520	Firmicutes	blue
Seq_527	Clostridium sensu stricto	blue
Seq_545	Clostridiales	blue
Seq_553	Bacteroidetes	blue
Seq_599	Clostridium sensu stricto	blue
Seq_600	Lachnospiraceae	blue
Seq_641	Ruminococcaceae	blue
Seq_668	Phascolarctobacterium succinatutens	blue
Seq_781	Collinsella aerofaciens	blue
Seq_823	Ruminococcaceae	blue
Seq_830	Bacteroidales	blue
Seq_838	Clostridiales	blue
Seq_863	Ruminococcaceae	blue
Seq_869	Bacteroides massiliensis	blue
Seq_878	Oscillibacter	blue
Seq_932	Clostridium XIVa	blue
Seq_940	Clostridia	blue
Seq_941	Ruminococcaceae	blue
Seq_970	Bacteroidetes	blue

Seq_1015_Clostridiales	blue
Seq_1165_Prevotellaceae	blue
Seq_1193_Streptococcus	blue
Seq_1195_Mitsuokella_jalaludinii	blue
Seq_1215_Firmicutes	blue
Seq_1227_Prevotella	blue
Seq_1249_Olsenella	blue
Seq_1266_Prevotella	blue
Seq_1292_Bacteroides_eggerthii	blue
Seq_1324_Clostridiales	blue
Seq_1344_Coriobacteriaceae	blue
Seq_1345_Ruminococcaceae	blue
Seq_1356_Ruminococcaceae	blue
Seq_1366_Mogibacterium	blue
Seq_1415_Coriobacteriaceae	blue
Seq_1436_Flavonifractor_plautii	blue
Seq_1459_Bifidobacterium	blue
Seq_1477_Mitsuokella_jalaludinii	blue
Seq_1491_Bacteroidetes	blue
Seq_1515_Phascolartobacterium_succinatutens	blue
Seq_1582_Ruminococcus_callidus	blue
Seq_1617_Bacteria	blue
Seq_1626_Prevotella_copri	blue
Seq_1672_Ruminococcaceae	blue
Seq_1761_Lachnospiraceae	blue
Seq_1795_Ruminococcaceae	blue
Seq_1843_Ruminococcaceae	blue
Seq_1868_Bacteria	blue
Seq_1889_Bacteria	blue
Seq_1916_Bacteria	blue
Seq_2060_Clostridia	blue
Seq_2095_Clostridiales	blue
Seq_2126_Clostridiales	blue
Seq_2185_Ruminococcaceae	blue
Seq_2186_Ruminococcus_bromii	blue
Seq_2216_Clostridiales	blue
Seq_2268_Clostridiales	blue
Seq_2311_Bacteria	blue
Seq_2312_Clostridiales	blue
Seq_2319_Bacteroides_eggerthii	blue
Seq_2442_Butyricimonas_virosa	blue
Seq_2453_Bacteria	blue
Seq_2504_Oscillibacter	blue
Seq_2566_Bacteroides_finegoldii	blue
Seq_2692_Barnesiella_intestinihominis	blue

Seq_2693_Coriobacteriaceae	blue
Seq_2695_Firmicutes	blue
Seq_2783_Clostridiales	blue
Seq_2883_Methanosphaera_stadtmanae	blue
Seq_3001_Bacteroidetes	blue
Seq_3004_Butyricimonas	blue
Seq_3158_Bacteria	blue
Seq_3161_Coriobacteriaceae	blue
Seq_3163_Ruminococcaceae	blue
Seq_3409_Catenibacterium_mitsuokai	blue
Seq_3410_Streptophyta	blue
Seq_3414_Succinivibradextrinosolvens	blue
Seq_3417_Faecalibacterium_prausnitzii	blue
Seq_3420_Clostridiales	blue
Seq_3421_Bacteria	blue
Seq_18_Clostridium_XVIII	brown
Seq_23_Ruminococcaceae	brown
Seq_45_Alistipes_putredinis	brown
Seq_62_Ruminococcaceae	brown
Seq_90_Eubacterium_siraeum	brown
Seq_92_Prevotella_copri	brown
Seq_111_Clostridiales	brown
Seq_125_Bacteroides_caccae	brown
Seq_147_Blautia_luti	brown
Seq_156_Ruminococcaceae	brown
Seq_167_Lactobacillus_ruminis	brown
Seq_208_Bacteroides_vulgatus	brown
Seq_213_Collinsella	brown
Seq_229_Oscillibacter_valericigenes	brown
Seq_264_Clostridium_XIVb	brown
Seq_274_Bacteroides_uniformis	brown
Seq_291_Desulfovibrio_piger	brown
Seq_293_Dialister_succinatiphilus	brown
Seq_306_Ruminococcaceae	brown
Seq_310_Bacteroides	brown
Seq_332_Slackia_isoflavoniconvertens	brown
Seq_349_Clostridiales	brown
Seq_350_Gemmiger_forficilis	brown
Seq_358_Clostridiales	brown
Seq_377_Sutterella_wadsworthensis	brown
Seq_392_Ascaccharobacter	brown
Seq_435_Bacteroides_fragilis	brown
Seq_477_Bacteroidetes	brown
Seq_497_Odoribacter_splanchnicus	brown
Seq_524_Ruminococcaceae	brown

Seq 534 Clostridiales	brown
Seq 566 Ruminococcaceae	brown
Seq 606 Coriobacteriaceae	brown
Seq 620 Clostridiales	brown
Seq 625 Flavonifractor plautii	brown
Seq 716 Ruminococcaceae	brown
Seq 719 Erysipelotrichaceae	brown
Seq 728 Erysipelotrichaceae	brown
Seq 855 Ruminococcus bromii	brown
Seq 862 Lactobacillus ruminis	brown
Seq 868 Firmicutes	brown
Seq 911 Clostridium XIVb	brown
Seq 917 Clostridiales	brown
Seq 933 Clostridium XIVa	brown
Seq 987 Clostridium IV	brown
Seq 989 Clostridiales	brown
Seq 993 Lachnospiraceae	brown
Seq 1008 Parabacteroides distasonis	brown
Seq 1042 Prevotella copri	brown
Seq 1051 Enterorhabdus	brown
Seq 1077 Clostridium IV	brown
Seq 1158 Eubacterium siraeum	brown
Seq 1229 Firmicutes	brown
Seq 1244 Barnesiella intestinihominis	brown
Seq 1253 Alphaproteobacteria	brown
Seq 1283 Paraprevotella clara	brown
Seq 1294 Lachnospiraceae	brown
Seq 1323 Ruminococcaceae	brown
Seq 1355 Clostridiales	brown
Seq 1363 Prevotellaceae	brown
Seq 1434 Porphyromonadaceae	brown
Seq 1460 Clostridium leptum	brown
Seq 1487 Coriobacteriaceae	brown
Seq 1527 Lachnospiraceae	brown
Seq 1560 Bacteroides	brown
Seq 1583 Collinsella tanakaei	brown
Seq 1591 Firmicutes	brown
Seq 1638 Butyrivibrio fibrisolvens	brown
Seq 1641 Gordonibacter	brown
Seq 1682 Bacteria	brown
Seq 1713 Anaerofilum pentosovorans	brown
Seq 1738 Ruminococcaceae	brown
Seq 1780 Clostridiales	brown
Seq 1834 Sutterella stercoricanis	brown
Seq 1855 Firmicutes	brown

Seq 1862 Clostridiales	brown
Seq 1869 Firmicutes	brown
Seq 1890 Peptococcus niger	brown
Seq 2009 Clostridium leptum	brown
Seq 2014 Ruminococcaceae	brown
Seq 2035 Clostridium leptum	brown
Seq 2036 Eubacteriaceae	brown
Seq 2107 Ruminococcaceae	brown
Seq 2127 Barnesiella intestinihominis	brown
Seq 2128 Enterorhabdus	brown
Seq 2156 Howardella ureilytica	brown
Seq 2157 Clostridiales	brown
Seq 2158 Ruminococcaceae	brown
Seq 2200 Ruminococcaceae	brown
Seq 2369 Desulfovibrionales	brown
Seq 2410 Paraprevotella clara	brown
Seq 2411 Erysipelotrichaceae	brown
Seq 2457 Ruminococcaceae	brown
Seq 2505 Oscillibacter	brown
Seq 2506 Ruminococcaceae	brown
Seq 2568 Adlercreutzia equolifaciens	brown
Seq 2569 Erysipelotrichaceae	brown
Seq 2570 Parabacteroides distasonis	brown
Seq 2571 Butyricimonas virosa	brown
Seq 2625 Porphyromonadaceae	brown
Seq 2626 Clostridiales	brown
Seq 2696 Anaerotruncus colihominis	brown
Seq 2884 Ruminococcaceae	brown
Seq 2885 Coriobacteriaceae	brown
Seq 2886 Ruminococcaceae	brown
Seq 2887 Ruminococcaceae	brown
Seq 2889 Lachnospiraceae	brown
Seq 3007 Butyricimonas virosa	brown
Seq 3008 Prevotella copri	brown
Seq 3164 Clostridiales	brown
Seq 3165 Clostridium leptum	brown
Seq 3431 Clostridiales	brown
Seq 59 Bifidobacterium	cyan
Seq 97 Phascolarctobacterium faecium	cyan
Seq 102 Ruminococcus albus	cyan
Seq 116 Alistipes	cyan
Seq 176 Eubacterium desmolans	cyan
Seq 188 Bilophila wadsworthia	cyan
Seq 230 Bacteroides ovatus	cyan
Seq 303 Flavonifractor plautii	cyan

Seq 338 <i>Clostridium ruminantium</i>	cyan
Seq 511 <i>Asaccharobacter</i>	cyan
Seq 540 <i>Phascolarctobacterium faecium</i>	cyan
Seq 558 <i>Bifidobacterium longum</i>	cyan
Seq 570 <i>Lachnospiraceae</i>	cyan
Seq 610 <i>Ruminococcaceae</i>	cyan
Seq 638 <i>Lachnospiraceae</i>	cyan
Seq 678 <i>Bacteroides xylanisolvens</i>	cyan
Seq 733 <i>Coriobacteriaceae</i>	cyan
Seq 741 <i>Ruminococcus albus</i>	cyan
Seq 754 <i>Blautia</i>	cyan
Seq 812 <i>Lachnospiraceae</i>	cyan
Seq 900 <i>Firmicutes</i>	cyan
Seq 925 <i>Lachnospiraceae</i>	cyan
Seq 1036 <i>Clostridiales</i>	cyan
Seq 1192 <i>Ruminococcaceae</i>	cyan
Seq 1387 <i>Lachnospiraceae</i>	cyan
Seq 1429 <i>Lachnospiraceae</i>	cyan
Seq 1463 <i>Ruminococcaceae</i>	cyan
Seq 1553 <i>Roseburia intestinalis</i>	cyan
Seq 1595 <i>Firmicutes</i>	cyan
Seq 1636 <i>Lachnospiraceae</i>	cyan
Seq 1686 <i>Parabacteroides distasonis</i>	cyan
Seq 1732 <i>Blautia faecis</i>	cyan
Seq 1766 <i>Ruminococcus torques</i>	cyan
Seq 1767 <i>Faecalibacterium prausnitzii</i>	cyan
Seq 1782 <i>Lachnospiraceae</i>	cyan
Seq 1970 <i>Actinomyces odontolyticus</i>	cyan
Seq 2001 <i>Flavonifractor plautii</i>	cyan
Seq 2046 <i>Eubacterium tenue</i>	cyan
Seq 2076 <i>Cloacibacillus evryensis</i>	cyan
Seq 2301 <i>Parabacteroides distasonis</i>	cyan
Seq 2409 <i>Clostridiales</i>	cyan
Seq 2499 <i>Candidatus Saccharibacteria</i>	cyan
Seq 2526 <i>Clostridiales</i>	cyan
Seq 2527 <i>Clostridium XIVa</i>	cyan
Seq 2731 <i>Ruminococcaceae</i>	cyan
Seq 2733 <i>Desulfovibrionaceae</i>	cyan
Seq 2734 <i>Ruminococcaceae</i>	cyan
Seq 2735 <i>Ruminococcaceae</i>	cyan
Seq 2925 <i>Erysipelotrichaceae</i>	cyan
Seq 3046 <i>Ruminococcaceae</i>	cyan
Seq 3210 <i>Eubacteriaceae</i>	cyan
Seq 3211 <i>Clostridiales</i>	cyan
Seq 3549 <i>Clostridiales</i>	cyan

Seq 3550 Bacteria	cyan
Seq 3553 Ruminococcaceae	cyan
Seq 3554 Lachnospiraceae	cyan
Seq 10 Gemmiger formicilis	darkgreen
Seq 51 Ruminococcus bromii	darkgreen
Seq 75 Ruminococcaceae	darkgreen
Seq 101 Streptococcus	darkgreen
Seq 135 Eubacterium rectale	darkgreen
Seq 202 Porphyromonadaceae	darkgreen
Seq 353 Eubacterium rectale	darkgreen
Seq 398 Paraprevotella clara	darkgreen
Seq 454 Lachnospiraceae	darkgreen
Seq 462 Clostridium_XIVa	darkgreen
Seq 466 Bacteroides	darkgreen
Seq 585 Bacteroides ovatus	darkgreen
Seq 681 Barnesiella intestinihominis	darkgreen
Seq 712 Firmicutes	darkgreen
Seq 769 Faecalibacterium prausnitzii	darkgreen
Seq 809 Ruminococcus callidus	darkgreen
Seq 834 Adlercreutzia equolifaciens	darkgreen
Seq 949 Blautia faecis	darkgreen
Seq 1001 Bacteroidetes	darkgreen
Seq 1183 Flavonifractor plautii	darkgreen
Seq 1306 Ruminococcaceae	darkgreen
Seq 1489 Coriobacteriaceae	darkgreen
Seq 1530 Clostridium leptum	darkgreen
Seq 1616 Parabacteroides distasonis	darkgreen
Seq 1624 Bacteroidetes	darkgreen
Seq 1714 Clostridiales	darkgreen
Seq 1722 Phascolarctobacterium succinatutens	darkgreen
Seq 1803 Ruminococcus lactaris	darkgreen
Seq 1804 Bacteroidetes	darkgreen
Seq 1859 Coriobacteriaceae	darkgreen
Seq 1987 Clostridium hathewayi	darkgreen
Seq 2013 Bacteroidetes	darkgreen
Seq 2155 Eubacterium infirmum	darkgreen
Seq 2255 Barnesiella intestinihominis	darkgreen
Seq 2366 Ruminococcaceae	darkgreen
Seq 2392 Prevotella bivia	darkgreen
Seq 2690 Firmicutes	darkgreen
Seq 2691 Lachnospiraceae	darkgreen
Seq 2780 Ruminococcaceae	darkgreen
Seq 2879 Solobacterium moorei	darkgreen
Seq 2880 Prevotella corporis	darkgreen
Seq 2995 Bacteroidales	darkgreen

Seq 2996 Porphyromonas uenonis	darkgreen
Seq 2997 Prevotella buccalis	darkgreen
Seq 3404 Clostridiales	darkgreen
Seq 7 Bifidobacterium longum	darkgrey
Seq 55 Bifidobacterium bifidum	darkgrey
Seq 171 Firmicutes	darkgrey
Seq 298 Bifidobacterium breve	darkgrey
Seq 322 Veillonella parvula	darkgrey
Seq 422 Lachnospiraceae	darkgrey
Seq 496 Clostridium XVIII	darkgrey
Seq 542 Bacteria	darkgrey
Seq 577 Ruminococcaceae	darkgrey
Seq 605 Eggerthella lenta	darkgrey
Seq 621 Lachnospiraceae	darkgrey
Seq 665 Ruminococcaceae	darkgrey
Seq 715 Flavonifractor plautii	darkgrey
Seq 914 Ruminococcaceae	darkgrey
Seq 998 Blautia	darkgrey
Seq 1069 Clostridium IV	darkgrey
Seq 1100 Ruminococcaceae	darkgrey
Seq 1161 Eubacterium fissicatena	darkgrey
Seq 1303 Allisonella histaminiformans	darkgrey
Seq 1456 Escherichia/Shigella	darkgrey
Seq 1513 Ruminococcaceae	darkgrey
Seq 1518 Erysipelotrichaceae	darkgrey
Seq 1676 Clostridium ruminantium	darkgrey
Seq 1787 Ruminococcaceae	darkgrey
Seq 1871 Ruminococcaceae	darkgrey
Seq 1920 Clostridium IV	darkgrey
Seq 1962 Clostridium ruminantium	darkgrey
Seq 1986 Lactonifactor longoviformis	darkgrey
Seq 2018 Ruminococcaceae	darkgrey
Seq 2068 Allisonella histaminiformans	darkgrey
Seq 2165 Prevotella copri	darkgrey
Seq 2192 Enterococcus	darkgrey
Seq 2212 Lactobacillus vaginalis	darkgrey
Seq 2406 Butyrivibrio	darkgrey
Seq 2510 Actinomyces odontolyticus	darkgrey
Seq 2511 Prevotella bivia	darkgrey
Seq 2581 Clostridium XIVb	darkgrey
Seq 2620 Fusobacterium nucleatum	darkgrey
Seq 3023 Enterobacter	darkgrey
Seq 3024 Streptococcus agalactiae	darkgrey
Seq 3183 Atopobium minutum	darkgrey
Seq 31 Ruminococcus obeum	darkmagenta

Seq 50 Erysipelotrichaceae	darkmagenta
Seq 122 Eubacterium rectale	darkmagenta
Seq 195 Gemmiger formicilis	darkmagenta
Seq 328 Ruminococcaceae	darkmagenta
Seq 355 Alistipes finegoldii	darkmagenta
Seq 452 Parabacteroides distasonis	darkmagenta
Seq 568 Bacteroides clarus	darkmagenta
Seq 587 Dialister invisus	darkmagenta
Seq 593 Dialister invisus	darkmagenta
Seq 618 Clostridium XIVa	darkmagenta
Seq 805 Dorea longicatena	darkmagenta
Seq 861 Clostridiales	darkmagenta
Seq 880 Eubacterium rectale	darkmagenta
Seq 902 Firmicutes	darkmagenta
Seq 934 Alistipes indistinctus	darkmagenta
Seq 1058 Allisonella histaminiformans	darkmagenta
Seq 1214 Lachnospiraceae	darkmagenta
Seq 1262 Eubacterium rectale	darkmagenta
Seq 1313 Lachnospiraceae	darkmagenta
Seq 1444 Gemmiger formicilis	darkmagenta
Seq 1470 Desulfovibrilegallii	darkmagenta
Seq 1587 Lachnospiraceae	darkmagenta
Seq 1746 Bilophila wadsworthia	darkmagenta
Seq 1808 Clostridiales	darkmagenta
Seq 1965 Oscillibacter valericigenes	darkmagenta
Seq 1992 Porphyromonadaceae	darkmagenta
Seq 2064 Parabacteroides distasonis	darkmagenta
Seq 2135 Ruminococcaceae	darkmagenta
Seq 2225 Ruminococcaceae	darkmagenta
Seq 2639 Clostridium butyricum	darkmagenta
Seq 2651 Ruminococcaceae	darkmagenta
Seq 2721 Oxalobacteraceae	darkmagenta
Seq 2807 Lactobacillus	darkmagenta
Seq 2910 Bacteroidales	darkmagenta
Seq 3200 Bacteria	darkmagenta
Seq 3506 Streptophyta	darkmagenta
Seq 127 Catenibacterium mitsuokai	darkolivegreen
Seq 164 Catenibacterium mitsuokai	darkolivegreen
Seq 335 Bacteroides vulgatus	darkolivegreen
Seq 509 Bacteroides vulgatus	darkolivegreen
Seq 522 Faecalibacterium prausnitzii	darkolivegreen
Seq 543 Blautia luti	darkolivegreen
Seq 794 Coriobacteriaceae	darkolivegreen
Seq 839 Eubacterium desmolans	darkolivegreen
Seq 956 Erysipelotrichaceae	darkolivegreen

Seq_1002_Ruminococcus_bromii	darkolivegreen
Seq_1055_Phascolarctobacterium_succinatutens	darkolivegreen
Seq_1088_Roseburia_faecis	darkolivegreen
Seq_1147_Anaerostipes_hadrus	darkolivegreen
Seq_1154_Dorea	darkolivegreen
Seq_1208_Sutterella_stercoricanis	darkolivegreen
Seq_1418_Lachnospiraceae	darkolivegreen
Seq_1442_Blautia_luti	darkolivegreen
Seq_1473_Clostridium_IV	darkolivegreen
Seq_1486_Eubacterium_desmolans	darkolivegreen
Seq_1551_Eubacterium_desmolans	darkolivegreen
Seq_1631_Anaerotruncus	darkolivegreen
Seq_1635_Lachnospiraceae	darkolivegreen
Seq_1807_Slackia_piriformis	darkolivegreen
Seq_2096_Lachnospiraceae	darkolivegreen
Seq_2257_Ruminococcaceae	darkolivegreen
Seq_2288_Ruminococcaceae	darkolivegreen
Seq_2328_Erysipelotrichaceae	darkolivegreen
Seq_2372_Firmicutes	darkolivegreen
Seq_2591_Blautia	darkolivegreen
Seq_2698_Clostridiales	darkolivegreen
Seq_2699_Clostridium_leptum	darkolivegreen
Seq_2700_Clostridium_XI	darkolivegreen
Seq_2718_Enterobacteriaceae	darkolivegreen
Seq_2787_Butyricimonas_virosa	darkolivegreen
Seq_2819_Bacteroides_clarus	darkolivegreen
Seq_2909_Parasutterella_excrementihominis	darkolivegreen
Seq_3167_Clostridium_leptum	darkolivegreen
Seq_3437_Clostridiales	darkolivegreen
Seq_5_Ruminococcaceae	darkorange
Seq_206_Bacteroides_eggerthii	darkorange
Seq_219_Ruminococcaceae	darkorange
Seq_326_Faecalibacterium_prausnitzii	darkorange
Seq_363_Dorea_longicatena	darkorange
Seq_554_Ruminococcaceae	darkorange
Seq_688_Ruminococcaceae	darkorange
Seq_760_Clostridiales	darkorange
Seq_866_Clostridium_XIVa	darkorange
Seq_908_Coprococcus_eutactus	darkorange
Seq_928_Lachnospiraceae	darkorange
Seq_1065_Eubacterium	darkorange
Seq_1199_Ruminococcaceae	darkorange
Seq_1256_Eubacterium_desmolans	darkorange
Seq_1275_Lachnospiraceae	darkorange
Seq_1287_Oscillibacter_valericigenes	darkorange

Seq_1364_Clostridiales	darkorange
Seq_1457_Clostridiales	darkorange
Seq_1605_Ruminococcaceae	darkorange
Seq_1831_Flavonifractor_plautii	darkorange
Seq_2131_Parabacteroides_distasonis	darkorange
Seq_2166_Holdemania_filiformis	darkorange
Seq_2167_Lachnospiraceae	darkorange
Seq_2206_Clostridium_XIVa	darkorange
Seq_2233_Ruminococcaceae	darkorange
Seq_2259_Bacteroides_thetaiotaomicron	darkorange
Seq_2260_Pseudoflavonifractor	darkorange
Seq_2492_Firmicutes	darkorange
Seq_2512_Coprobaecillus_cateniformis	darkorange
Seq_2582_Ruminococcaceae	darkorange
Seq_2614_Ruminococcaceae	darkorange
Seq_2631_Ruminococcaceae	darkorange
Seq_2708_Prevotella_corporis	darkorange
Seq_2797_Actinomyces_turicensis	darkorange
Seq_3026_Ruminococcaceae	darkorange
Seq_3187_Bacteria	darkorange
Seq_3473_Gordonibacter_pamelaeae	darkorange
Seq_3476_Erysipelotrichaceae	darkorange
Seq_3477_Porphyromonas	darkorange
Seq_3478_Clostridiales	darkorange
Seq_89_Bacteroides_ovatus	darkred
Seq_106_Ruminococcus2	darkred
Seq_272_Ruminococcaceae	darkred
Seq_289_Ruminococcus_bromii	darkred
Seq_331_Erysipelotrichaceae	darkred
Seq_345_Blautia	darkred
Seq_365_Dialister_invisus	darkred
Seq_584_Erysipelotrichaceae	darkred
Seq_632_Flavonifractor_plautii	darkred
Seq_635_Ruminococcus	darkred
Seq_636_Bacteroides_coprophilus	darkred
Seq_742_Ruminococcus_flavefaciens	darkred
Seq_792_Lachnospiraceae	darkred
Seq_831_Blautia	darkred
Seq_915_Paraprevotella_clara	darkred
Seq_921_Bacteroides_coprophilus	darkred
Seq_938_Holdemania_filiformis	darkred
Seq_1064_Sarcina_ventriculi	darkred
Seq_1130_Lachnospiraceae	darkred
Seq_1259_Lachnospiraceae	darkred
Seq_1267_Clostridium_XIVa	darkred

Seq_1290_Ruminococcaceae	darkred
Seq_1479_Lachnospiraceae	darkred
Seq_1540_Eubacterium_desmolans	darkred
Seq_1586_Clostridium_sensu_stricto	darkred
Seq_1710_Ruminococcaceae	darkred
Seq_1897_Ruminococcus_lactaris	darkred
Seq_1922_Clostridium_XIVa	darkred
Seq_1964_Paraprevotella_clara	darkred
Seq_2019_Ruminococcaceae	darkred
Seq_2124_Erysipelotrichaceae	darkred
Seq_2151_Ruminococcaceae	darkred
Seq_2224_Ruminococcaceae	darkred
Seq_2295_Firmicutes	darkred
Seq_2373_Bacteroides	darkred
Seq_2419_Coriobacteriaceae	darkred
Seq_2449_Ruminococcaceae	darkred
Seq_2519_Erysipelotrichaceae	darkred
Seq_2592_Bacteroides	darkred
Seq_2636_Ruminococcaceae	darkred
Seq_2637_Lachnospiraceae	darkred
Seq_2638_Lachnospiraceae	darkred
Seq_2720_Paraprevotella_clara	darkred
Seq_3035_Ruminococcaceae	darkred
Seq_3504_Lachnospiraceae	darkred
Seq_3505_Clostridiales	darkred
Seq_186_Megasphaera_elsdenii	darkturquoise
Seq_220_Blautia	darkturquoise
Seq_224_Hallella	darkturquoise
Seq_389_Megasphaera_elsdenii	darkturquoise
Seq_406_Prevotella_buccae	darkturquoise
Seq_426_Prevotella_stercorea	darkturquoise
Seq_445_Megasphaera_elsdenii	darkturquoise
Seq_458_Megasphaera_elsdenii	darkturquoise
Seq_494_Megasphaera_elsdenii	darkturquoise
Seq_700_Fusobacterium	darkturquoise
Seq_722_Prevotella_buccae	darkturquoise
Seq_748_Veillonellaceae	darkturquoise
Seq_764_Prevotella_buccae	darkturquoise
Seq_796_Roseburia_faecis	darkturquoise
Seq_889_Anaeroglobus_geminatus	darkturquoise
Seq_916_Fusobacterium_nucleatum	darkturquoise
Seq_1003_Prevotella_stercorea	darkturquoise
Seq_1011_Clostridium_sensu_stricto	darkturquoise
Seq_1028_Clostridium_disporicum	darkturquoise
Seq_1252_Megasphaera_micronuciformis	darkturquoise

Seq_1288_Veillonellaceae	darkturquoise
Seq_1310_Anaeroglobus	darkturquoise
Seq_1361_Dialister	darkturquoise
Seq_1405_Veillonellaceae	darkturquoise
Seq_1417_Fusobacterium	darkturquoise
Seq_1480_Collinsella_aerofaciens	darkturquoise
Seq_1764_Campylobacter_conciscus	darkturquoise
Seq_1790_Dorea_longicatena	darkturquoise
Seq_1857_Blautia_luti	darkturquoise
Seq_1968_Pediococcus	darkturquoise
Seq_2006_Bacteria	darkturquoise
Seq_2020_Selenomonas_flueggei	darkturquoise
Seq_2072_Megasphaera_micronuciformis	darkturquoise
Seq_2137_Megasphaera_micronuciformis	darkturquoise
Seq_2160_Ruminococcaceae	darkturquoise
Seq_2188_Enterobacteriaceae	darkturquoise
Seq_2195_Coriobacteriaceae	darkturquoise
Seq_2289_Ruminococcaceae	darkturquoise
Seq_2331_Veillonellaceae	darkturquoise
Seq_2469_Campylobacter	darkturquoise
Seq_2470_Succiniclasticum_ruminis	darkturquoise
Seq_2643_Dialister_pneumosintes	darkturquoise
Seq_2722_Prevotella_stercorea	darkturquoise
Seq_3170_Ruminococcaceae	darkturquoise
Seq_16_Blautia_luti	green
Seq_142_Ruminococcus_albus	green
Seq_152_Parabacteroides_distasonis	green
Seq_153_Bacteroides_cellulosilyticus	green
Seq_242_Clostridium_leptum	green
Seq_268_Alistipes	green
Seq_301_Clostridium_scindens	green
Seq_318_Parasutterella_excrementihominis	green
Seq_324_Ruminococcaceae	green
Seq_364_Parabacteroides_distasonis	green
Seq_384_Prevotellaceae	green
Seq_419_Prevotellaceae	green
Seq_440_Ruminococcaceae	green
Seq_448_Clostridiales	green
Seq_456_Clostridium_XIVa	green
Seq_467_Eubacterium_rectale	green
Seq_472_Lachnospiraceae	green
Seq_502_Coriobacteriaceae	green
Seq_574_Ruminococcaceae	green
Seq_611_Firmicutes	green
Seq_619_Faecalibacterium_prausnitzii	green

Seq 657 Bacteroides fragilis	green
Seq 671 Oscillibacter	green
Seq 676 Blautia	green
Seq 684 Faecalibacterium prausnitzii	green
Seq 708 Alistipes indistinctus	green
Seq 744 Ruminococcaceae	green
Seq 751 Deltaproteobacteria	green
Seq 763 Prevotellaceae	green
Seq 782 Clostridium lactatifermentans	green
Seq 786 Ruminococcaceae	green
Seq 811 Ruminococcaceae	green
Seq 856 Olsenella	green
Seq 857 Ruminococcus albus	green
Seq 872 Barnesiella intestinihominis	green
Seq 887 Bacteroides vulgatus	green
Seq 955 Oscillibacter	green
Seq 957 Ruminococcaceae	green
Seq 976 Eubacterium desmolans	green
Seq 984 Lachnospiraceae	green
Seq 1021 Lachnospiraceae	green
Seq 1093 Clostridiales	green
Seq 1101 Clostridium XIVa	green
Seq 1118 Prevotella stercorea	green
Seq 1176 Anaerofustis stercorihominis	green
Seq 1184 Ruminococcaceae	green
Seq 1201 Coriobacteriaceae	green
Seq 1238 Butyrivibrio fibrisolens	green
Seq 1360 Erysipelotrichaceae	green
Seq 1416 Clostridium leptum	green
Seq 1556 Ruminococcaceae	green
Seq 1610 Ruminococcaceae	green
Seq 1611 Lachnospiraceae	green
Seq 1652 Clostridium XIVb	green
Seq 1745 Coriobacteriaceae	green
Seq 1792 Subdoligranulum variabile	green
Seq 1877 Desulfovibrionaceae	green
Seq 1923 Ruminococcus gnavus	green
Seq 1967 Eubacterium desmolans	green
Seq 1993 Porphyromonadaceae	green
Seq 2136 Ruminococcaceae	green
Seq 2266 Eubacterium	green
Seq 2327 Clostridium XIVb	green
Seq 2330 Ruminococcaceae	green
Seq 2347 Anaerotruncus colihominis	green
Seq 2375 Bilophila wadsworthia	green

Seq_2420_Clostridium_XIVa	green
Seq_2421_Deltaproteobacteria	green
Seq_2447_Ruminococcaceae	green
Seq_2587_Ruminococcaceae	green
Seq_2593_Erysipelotrichaceae	green
Seq_2640_Enterorhabdus	green
Seq_2641_Bacteria	green
Seq_2642_Anaerostipes_butyricus	green
Seq_2723_Ruminococcaceae	green
Seq_2724_Lachnospiraceae	green
Seq_2810_Clostridium_IV	green
Seq_2916_Ruminococcaceae	green
Seq_3195_Parvimonas_micra	green
Seq_3489_Bacteroides_coprocola	green
Seq_3531_Subdoligranulum	green
Seq_3533_Ruminococcaceae	green
Seq_9_Faecalibacterium_prausnitzii	greenyellow
Seq_26_Ruminococcus_bromii	greenyellow
Seq_46_Parabacteroides_merdae	greenyellow
Seq_73_Lachnospiraceae	greenyellow
Seq_151_Oscillibacter_valericigenes	greenyellow
Seq_190_Faecalibacterium_prausnitzii	greenyellow
Seq_218_Ruminococcus_bromii	greenyellow
Seq_247_Bacteroides_vulgatus	greenyellow
Seq_281_Eubacterium_rectale	greenyellow
Seq_305_Eubacterium_rectale	greenyellow
Seq_344_Lachnospiraceae	greenyellow
Seq_395_Bacteroides	greenyellow
Seq_515_Faecalibacterium_prausnitzii	greenyellow
Seq_546_Barnesiella_intestinihominis	greenyellow
Seq_603_Clostridium_XIVb	greenyellow
Seq_699_Bacteroides	greenyellow
Seq_739_Lachnospiraceae	greenyellow
Seq_755_Deltaproteobacteria	greenyellow
Seq_767_Roseburia_faecis	greenyellow
Seq_777_Lachnospiraceae	greenyellow
Seq_835_Firmicutes	greenyellow
Seq_894_Alistipes_senegalensis	greenyellow
Seq_948_Bifidobacterium_breve	greenyellow
Seq_1043_Lachnospiraceae	greenyellow
Seq_1114_Anaerostipes_hadrus	greenyellow
Seq_1120_Ruminococcus_callidus	greenyellow
Seq_1188_Ruminococcaceae	greenyellow
Seq_1218_Bifidobacterium_breve	greenyellow
Seq_1257_Lachnospiraceae	greenyellow

Seq_1278_Clostridium_leptum	greenyellow
Seq_1320_Bacteroides	greenyellow
Seq_1331_Parabacteroides_distasonis	greenyellow
Seq_1340_Lachnospiraceae	greenyellow
Seq_1367_Clostridium_leptum	greenyellow
Seq_1465_Ruminococcaceae	greenyellow
Seq_1475_Bacteroides_fragilis	greenyellow
Seq_1488_Lachnospiraceae	greenyellow
Seq_1512_Bacteroides_fragilis	greenyellow
Seq_1535_Clostridium_XIVa	greenyellow
Seq_1622_Anaerostipes_hadrus	greenyellow
Seq_1653_Parabacteroides_distasonis	greenyellow
Seq_1685_Ruminococcaceae	greenyellow
Seq_1698_Clostridium_XIVa	greenyellow
Seq_1740_Blautia_luti	greenyellow
Seq_1823_Clostridium_IV	greenyellow
Seq_1895_Ruminococcaceae	greenyellow
Seq_1912_Parabacteroides_distasonis	greenyellow
Seq_1913_Parasutterella_excrementihominis	greenyellow
Seq_1958_Bacteria	greenyellow
Seq_2034_Lachnospiraceae	greenyellow
Seq_2122_Ruminococcaceae	greenyellow
Seq_2123_Eubacterium_desmolans	greenyellow
Seq_2270_Peptococcus	greenyellow
Seq_2285_Dialister_invisus	greenyellow
Seq_2286_Megasphaera_micronuciformis	greenyellow
Seq_2324_Lachnospiraceae	greenyellow
Seq_2448_Ruminococcaceae	greenyellow
Seq_2618_Pseudoflavonifractor_capillosus	greenyellow
Seq_2683_Actinomyces	greenyellow
Seq_2796_Desulfovibrionaceae	greenyellow
Seq_2868_Ruminococcaceae	greenyellow
Seq_3021_Ruminococcaceae	greenyellow
Seq_3146_Roseburia	greenyellow
Seq_3382_Firmicutes	greenyellow
Seq_3384_Faecalibacterium_prausnitzii	greenyellow
Seq_3387_Lactococcus	greenyellow
Seq_3388_Porphyromonas_bennonis	greenyellow
Seq_3464_Bilophila_wadsworthia	greenyellow
Seq_1667_Ruminococcaceae	grey
Seq_2063_Staphylococcus	grey
Seq_29_Ruminococcus_bromii	grey60
Seq_84_Ruminococcus_albus	grey60
Seq_91_Clostridiales	grey60
Seq_130_Bacteroides_vulgatus	grey60

Seq_149_Lachnospiraceae	grey60
Seq_233_Eubacterium_ruminantium	grey60
Seq_330_Ruminococcaceae	grey60
Seq_396_Dialister_propionificiens	grey60
Seq_397_Lachnospiraceae	grey60
Seq_474_Clostridiales	grey60
Seq_493_Faecalibacterium_prausnitzii	grey60
Seq_536_Faecalibacterium_prausnitzii	grey60
Seq_591_Ruminococcaceae	grey60
Seq_604_Faecalibacterium_prausnitzii	grey60
Seq_631_Bacteroides_vulgatus	grey60
Seq_674_Bacteroides_vulgatus	grey60
Seq_687_Ruminococcus2	grey60
Seq_718_Dialister_propionificiens	grey60
Seq_759_Bacteroides	grey60
Seq_799_Gemmiger_formicilis	grey60
Seq_813_Clostridium_XIVa	grey60
Seq_864_Eubacterium_rectale	grey60
Seq_924_Clostridium_XIVa	grey60
Seq_1075_Clostridium_XVIII	grey60
Seq_1086_Roseburia	grey60
Seq_1112_Ruminococcaceae	grey60
Seq_1152_Lachnospiraceae	grey60
Seq_1286_Faecalibacterium_prausnitzii	grey60
Seq_1314_Ruminococcaceae	grey60
Seq_1414_Bacteroides	grey60
Seq_1464_Ruminococcaceae	grey60
Seq_1656_Roseburia_faecis	grey60
Seq_1683_Erysipelotrichaceae	grey60
Seq_1723_Roseburia_inulinivorans	grey60
Seq_2021_Clostridiales	grey60
Seq_2093_Ruminococcaceae	grey60
Seq_2175_Proteobacteria	grey60
Seq_2231_Streptophyta	grey60
Seq_2256_Lachnospiraceae	grey60
Seq_2318_Eubacterium_desmolans	grey60
Seq_2367_Lachnospiraceae	grey60
Seq_2368_Clostridiales	grey60
Seq_2452_Clostridium_IV	grey60
Seq_2551_Ruminococcaceae	grey60
Seq_2564_Clostridium_leptum	grey60
Seq_2565_Ruminococcaceae	grey60
Seq_2622_Ruminococcaceae	grey60
Seq_2623_Clostridiales	grey60
Seq_2707_Peptococcus_niger	grey60

Seq_3157_Pseudomonas	grey60
Seq_3184_Clostridiales	grey60
Seq_3406_Clostridiales	grey60
Seq_3468_Clostridiales	grey60
Seq_3472_Blautia_faecis	grey60
Seq_8_Dialister_invisus	lightcyan
Seq_69_Lachnospiraceae	lightcyan
Seq_77_Bacteroides_coprocola	lightcyan
Seq_158_Bacteroides_ovatus	lightcyan
Seq_180_Bacteroides_ovatus	lightcyan
Seq_386_Faecalibacterium_prausnitzii	lightcyan
Seq_441_Bacteroides_coprocola	lightcyan
Seq_455_Bacteroides	lightcyan
Seq_490_Bacteroides	lightcyan
Seq_498_Lachnospiraceae	lightcyan
Seq_537_Bacteroides	lightcyan
Seq_538_Lachnospiraceae	lightcyan
Seq_551_Oscillibacter	lightcyan
Seq_623_Ruminococcaceae	lightcyan
Seq_661_Firmicutes	lightcyan
Seq_689_Alistipes	lightcyan
Seq_720_Bacteroides_thetaiotaomicron	lightcyan
Seq_770_Clostridium_leptum	lightcyan
Seq_778_Lachnospiraceae	lightcyan
Seq_840_Bacteroides	lightcyan
Seq_1010_Parabacteroides	lightcyan
Seq_1024_Clostridium_XVIII	lightcyan
Seq_1178_Ruminococcaceae	lightcyan
Seq_1297_Porphyromonadaceae	lightcyan
Seq_1309_Bifidobacterium_dentium	lightcyan
Seq_1341_Bacteroides	lightcyan
Seq_1357_Bacteroides	lightcyan
Seq_1688_Clostridium_hathewayi	lightcyan
Seq_1707_Lachnospiraceae	lightcyan
Seq_1727_Faecalibacterium_prausnitzii	lightcyan
Seq_1728_Bacteroides	lightcyan
Seq_1825_Alistipes_shahii	lightcyan
Seq_1846_Ruminococcaceae	lightcyan
Seq_1856_Oscillospira_guilliermondii	lightcyan
Seq_1872_Bacteroides	lightcyan
Seq_1921_Lachnospiraceae	lightcyan
Seq_1944_Bacteroides	lightcyan
Seq_1990_Anaerofustis_stercorihominis	lightcyan
Seq_1991_Paraprevotella_clara	lightcyan
Seq_2098_Ruminococcaceae	lightcyan

Seq_2132_Lachnospiraceae	lightcyan
Seq_2290_Sutterella	lightcyan
Seq_2326_Clostridium_XIVa	lightcyan
Seq_2466_Parasutterella_secunda	lightcyan
Seq_2467_Firmicutes	lightcyan
Seq_2516_Alistipes_indistinctus	lightcyan
Seq_2584_Flavonifractor_plautii	lightcyan
Seq_2585_Succinatimonas_hippeii	lightcyan
Seq_2714_Clostridium_ramosum	lightcyan
Seq_2801_Ruminococcaceae	lightcyan
Seq_2802_Ruminococcaceae	lightcyan
Seq_2803_Dialister_invisus	lightcyan
Seq_3030_Bacteroides	lightcyan
Seq_3191_Oxalobacteraceae	lightcyan
Seq_21_Roseburia_faecis	lightgreen
Seq_44_Roseburia_intestinalis	lightgreen
Seq_76_Roseburia	lightgreen
Seq_209_Eubacterium_rectale	lightgreen
Seq_442_Lachnospiraceae	lightgreen
Seq_460_Bacteroides_stercoris	lightgreen
Seq_469_Erysipelotrichaceae	lightgreen
Seq_504_Eubacterium_rectale	lightgreen
Seq_564_Roseburia_intestinalis	lightgreen
Seq_656_Coriobacteriaceae	lightgreen
Seq_662_Blautia	lightgreen
Seq_683_Faecalibacterium_prausnitzii	lightgreen
Seq_693_Bacteroides_massiliensis	lightgreen
Seq_695_Roseburia_intestinalis	lightgreen
Seq_962_Lachnospiraceae	lightgreen
Seq_1037_Lactobacillus	lightgreen
Seq_1080_Streptococcus	lightgreen
Seq_1096_Lachnospiraceae	lightgreen
Seq_1260_Faecalibacterium_prausnitzii	lightgreen
Seq_1426_Bacteria	lightgreen
Seq_1427_Eggerthella_lenta	lightgreen
Seq_1476_Megasphaera	lightgreen
Seq_1499_Lachnospiraceae	lightgreen
Seq_1514_Blautia	lightgreen
Seq_1548_Faecalibacterium_prausnitzii	lightgreen
Seq_1581_Ruminococcus_torques	lightgreen
Seq_1603_Weissella	lightgreen
Seq_1604_Megasphaera	lightgreen
Seq_1623_Lactobacillus	lightgreen
Seq_1655_Clostridium_XIVa	lightgreen
Seq_1687_Clostridiales	lightgreen

Seq_1703_Lactobacillus	lightgreen
Seq_1741_Eggerthella_lenta	lightgreen
Seq_1742_Butyricimonas_virosa	lightgreen
Seq_1801_Lachnospiraceae	lightgreen
Seq_1802_Coprococcus_comes	lightgreen
Seq_1824_Clostridiales	lightgreen
Seq_1853_Dorea_formicigenerans	lightgreen
Seq_1860_Butyricimonas_virosa	lightgreen
Seq_1867_Lactobacillus	lightgreen
Seq_1960_Coprococcus_comes	lightgreen
Seq_2065_Holdemania_filiformis	lightgreen
Seq_2066_Erysipelotrichaceae	lightgreen
Seq_2094_Blautia	lightgreen
Seq_2450_Lachnospiraceae	lightgreen
Seq_2503_Lachnospiraceae	lightgreen
Seq_2872_Lachnospiraceae	lightgreen
Seq_2873_Leuconostoc	lightgreen
Seq_2874_Erysipelotrichaceae	lightgreen
Seq_2875_Odoribacter_splanchnicus	lightgreen
Seq_2878_Ruminococcaceae	lightgreen
Seq_2989_Peptostreptococcus_anaerobius	lightgreen
Seq_100_Bacteroides_thetaiotaomicron	lightyellow
Seq_108_Bacteroides_dorei	lightyellow
Seq_137_Bacteroides_fragilis	lightyellow
Seq_191_Bacteroides_ovatus	lightyellow
Seq_252_Lachnospiraceae	lightyellow
Seq_265_Ruminococcaceae	lightyellow
Seq_315_Clostridium_IV	lightyellow
Seq_412_Ruminococcaceae	lightyellow
Seq_464_Bacteria	lightyellow
Seq_548_Coprobacillus_cateniformis	lightyellow
Seq_561_Anaerostipes	lightyellow
Seq_576_Veillonellaceae	lightyellow
Seq_598_Bacteroides_ovatus	lightyellow
Seq_667_Clostridium_lactatifermentans	lightyellow
Seq_670_Anaerotruncus_colihominis	lightyellow
Seq_756_Clostridium_XIVa	lightyellow
Seq_762_Bifidobacterium_dentium	lightyellow
Seq_858_Bacteria	lightyellow
Seq_983_Ruminococcaceae	lightyellow
Seq_1004_Ruminococcaceae	lightyellow
Seq_1081_Ruminococcaceae	lightyellow
Seq_1099_Sutterella_stercoricanis	lightyellow
Seq_1139_Oscillospira_guilliermondii	lightyellow
Seq_1189_Staphylococcus	lightyellow

Seq_1226_Pseudoflavonifractor	lightyellow
Seq_1602_Clostridium_XIVa	lightyellow
Seq_1914_Lachnospiraceae	lightyellow
Seq_1915_Ruminococcaceae	lightyellow
Seq_1959_Peptococcus	lightyellow
Seq_2024_Ruminococcaceae	lightyellow
Seq_2039_Clostridium_leptum	lightyellow
Seq_2153_Ruminococcaceae	lightyellow
Seq_2154_Clostridiales	lightyellow
Seq_2184_Enterococcus	lightyellow
Seq_2254_Ruminococcaceae	lightyellow
Seq_2287_Ruminococcaceae	lightyellow
Seq_2365_Clostridiales	lightyellow
Seq_2451_Oscillibacter_valericigenes	lightyellow
Seq_2502_Eubacterium_desmolans	lightyellow
Seq_2687_Clostridium_XIVb	lightyellow
Seq_2689_Lactobacillus_fermentum	lightyellow
Seq_2779_Ruminococcaceae	lightyellow
Seq_2869_Corynebacterium	lightyellow
Seq_2876_Clostridiales	lightyellow
Seq_2877_Ruminococcaceae	lightyellow
Seq_2990_Hydrogenoanaerobacterium	lightyellow
Seq_2991_Ruminococcaceae	lightyellow
Seq_2992_Ruminococcaceae	lightyellow
Seq_2993_Acetanaerobacterium_elongatum	lightyellow
Seq_3397_Clostridium_IV	lightyellow
Seq_3401_Lachnospiraceae	lightyellow
Seq_11_Bacteroides_dorei	magenta
Seq_13_Faecalibacterium_prausnitzii	magenta
Seq_70_Bacteroides_uniformis	magenta
Seq_78_Lachnospiraceae	magenta
Seq_95_Prevotella_copri	magenta
Seq_103_Eubacterium_eligens	magenta
Seq_133_Ruminococcus_lactaris	magenta
Seq_173_Lachnospiraceae	magenta
Seq_175_Blautia_faecis	magenta
Seq_189_Parabacteroides_distasonis	magenta
Seq_210_Lachnospiraceae	magenta
Seq_232_Parasutterella_excrementihominis	magenta
Seq_240_Clostridiales	magenta
Seq_254_Firmicutes	magenta
Seq_312_Lachnospiraceae	magenta
Seq_366_Bacteroides	magenta
Seq_369_Asteroleplasma	magenta
Seq_437_Lachnospiraceae	magenta

Seq 476 Ruminococcus	magenta
Seq 518 Bacteroides intestinalis	magenta
Seq 530 Bacteria	magenta
Seq 557 Adlercreutzia equolifaciens	magenta
Seq 572 Firmicutes	magenta
Seq 589 Bilophila wadsworthia	magenta
Seq 624 Bacteria	magenta
Seq 627 Asteroleplasma	magenta
Seq 804 Lachnospiraceae	magenta
Seq 842 Ruminococcaceae	magenta
Seq 847 Lachnospiraceae	magenta
Seq 875 Clostridiales	magenta
Seq 884 Ruminococcaceae	magenta
Seq 922 Lachnospiraceae	magenta
Seq 950 Lachnospiraceae	magenta
Seq 990 Bacteria	magenta
Seq 1151 Faecalibacterium prausnitzii	magenta
Seq 1271 Ruminococcaceae	magenta
Seq 1281 Parabacteroides distasonis	magenta
Seq 1325 Faecalibacterium prausnitzii	magenta
Seq 1349 Clostridium XVIII	magenta
Seq 1370 Firmicutes	magenta
Seq 1401 Ruminococcaceae	magenta
Seq 1428 Ruminococcaceae	magenta
Seq 1440 Bacteroides vulgatus	magenta
Seq 1469 Roseburia faecis	magenta
Seq 1472 Firmicutes	magenta
Seq 1516 Parabacteroides johnsonii	magenta
Seq 1637 Lachnospiraceae	magenta
Seq 1704 Eubacterium desmolans	magenta
Seq 1725 Ruminococcaceae	magenta
Seq 1826 Butyricimonas virosa	magenta
Seq 1941 Lachnospiraceae	magenta
Seq 1961 Prevotella copri	magenta
Seq 2323 Bacteria	magenta
Seq 2370 Lachnospiraceae	magenta
Seq 2458 Lachnospiraceae	magenta
Seq 2507 Porphyromonadaceae	magenta
Seq 2508 Clostridium lactatifermentans	magenta
Seq 2703 Clostridium IV	magenta
Seq 2789 Pseudomonas	magenta
Seq 2790 Butyricimonas virosa	magenta
Seq 2791 Candidatus Saccharibacteria	magenta
Seq 2892 Bacteria	magenta
Seq 2893 Barnesiella intestinihominis	magenta

Seq_3012_Clostridiales	magenta
Seq_3013_Ruminococcaceae	magenta
Seq_3171_Ruminococcaceae	magenta
Seq_3172_Ruminococcaceae	magenta
Seq_3173_Desulfovibrionaceae	magenta
Seq_3174_Firmicutes	magenta
Seq_3444_Clostridiales	magenta
Seq_3445_Butyricimonas_virosa	magenta
Seq_3446_Clostridiales	magenta
Seq_3447_Bacteria	magenta
Seq_3450_Buttiauxella	magenta
Seq_3575_Ruminococcaceae	magenta
Seq_93_Anaerostipes_hadrus	midnightblue
Seq_194_Megasphaera	midnightblue
Seq_222_Clostridium_XIVa	midnightblue
Seq_226_Megasphaera	midnightblue
Seq_300_Bacteroidales	midnightblue
Seq_327_Dialister_invisus	midnightblue
Seq_340_Bacteroides_vulgatus	midnightblue
Seq_379_Eubacterium_rectale	midnightblue
Seq_528_Roseburia_faecis	midnightblue
Seq_535_Blautia_luti	midnightblue
Seq_547_Burkholderiales	midnightblue
Seq_639_Erysipelotrichaceae	midnightblue
Seq_643_Faecalibacterium_prausnitzii	midnightblue
Seq_822_Megasphaera	midnightblue
Seq_849_Lachnospiraceae	midnightblue
Seq_871_Erysipelotrichaceae	midnightblue
Seq_1009_Roseburia_faecis	midnightblue
Seq_1017_Ruminococcus_torques	midnightblue
Seq_1057_Coriobacteriaceae	midnightblue
Seq_1060_Lachnospiraceae	midnightblue
Seq_1107_Lachnospiraceae	midnightblue
Seq_1124_Parabacteroides_distasonis	midnightblue
Seq_1159_Parabacteroides_distasonis	midnightblue
Seq_1179_Lachnospiraceae	midnightblue
Seq_1250_Coriobacteriaceae	midnightblue
Seq_1261_Blautia	midnightblue
Seq_1302_Coprococcus_comes	midnightblue
Seq_1315_Clostridium_glycolicum	midnightblue
Seq_1520_Clostridium_bartlettii	midnightblue
Seq_1606_Clostridium_scindens	midnightblue
Seq_1607_Lachnospiraceae	midnightblue
Seq_1608_Lachnospiraceae	midnightblue
Seq_1612_Bifidobacterium_pseudolongum	midnightblue

Seq_1674_Lachnospiraceae	midnightblue
Seq_1695_Ruminococcaceae	midnightblue
Seq_1726_Blautia	midnightblue
Seq_1785_Ruminococcus_torques	midnightblue
Seq_1794_Lachnospiraceae	midnightblue
Seq_1858_Eubacterium_desmolans	midnightblue
Seq_1892_Flavonifractor_plautii	midnightblue
Seq_1893_Clostridium_XIVa	midnightblue
Seq_1949_Bacteria	midnightblue
Seq_2097_Sutterella_stercoricanis	midnightblue
Seq_2129_Lachnospiraceae	midnightblue
Seq_2161_Clostridium_XIVa	midnightblue
Seq_2162_Lachnospiraceae	midnightblue
Seq_2170_Lachnospiraceae	midnightblue
Seq_2190_Bacteroidetes	midnightblue
Seq_2196_Actinomyces	midnightblue
Seq_2413_Lachnospiraceae	midnightblue
Seq_2414_Ruminococcus2	midnightblue
Seq_2461_Clostridiales	midnightblue
Seq_2473_Bacteria	midnightblue
Seq_2814_Lachnospiraceae	midnightblue
Seq_3175_Campylobacter_troglodytis	midnightblue
Seq_3454_Oscillibacter	midnightblue
Seq_19_Bacteroides_vulgatus	orange
Seq_43_Bacteroides_vulgatus	orange
Seq_54_Bacteroides_xylanisolvens	orange
Seq_79_Clostridium_XIVa	orange
Seq_141_Ruminococcaceae	orange
Seq_170_Flavonifractor_plautii	orange
Seq_257_Bacteroides_vulgatus	orange
Seq_285_Clostridium_symbiosum	orange
Seq_359_Odoribacter_splanchnicus	orange
Seq_368_Bacteroides_vulgatus	orange
Seq_376_Bacteroides_vulgatus	orange
Seq_428_Bacteroides_vulgatus	orange
Seq_578_Ruminococcaceae	orange
Seq_790_Clostridium_IV	orange
Seq_870_Clostridium_aldenense	orange
Seq_954_Clostridium_lavalense	orange
Seq_999_Clostridium_XIVa	orange
Seq_1014_Bacteria	orange
Seq_1026_Clostridium_XIVa	orange
Seq_1035_Butyricicoccus_pullicaecorum	orange
Seq_1044_Parabacteroides_merdae	orange
Seq_1056_Alistipes	orange

Seq_1063_Clostridium_aldenense	orange
Seq_1095_Roseburia_inulinivorans	orange
Seq_1200_Clostridium_aldenense	orange
Seq_1443_Lachnospiraceae	orange
Seq_1458_Clostridium_IV	orange
Seq_1494_Clostridium_citroniae	orange
Seq_1529_Ruminococcaceae	orange
Seq_1569_Firmicutes	orange
Seq_1689_Firmicutes	orange
Seq_1947_Eggerthella_lenta	orange
Seq_2003_Lachnospiraceae	orange
Seq_2092_Clostridium_lactatifermentans	orange
Seq_2468_Subdoligranulum_variabile	orange
Seq_2635_Ruminococcaceae	orange
Seq_2719_Bifidobacterium_pseudolongum	orange
Seq_3198_Actinomycetales	orange
Seq_3199_Erysipelotrichaceae	orange
Seq_3502_Firmicutes	orange
Seq_192_Barnesiella_intestinihominis	paleturquoise
Seq_405_Firmicutes	paleturquoise
Seq_434_Phascolarctobacterium_succinatutens	paleturquoise
Seq_517_Lachnospiraceae	paleturquoise
Seq_544_Parabacteroides_distasonis	paleturquoise
Seq_666_Parabacteroides_distasonis	paleturquoise
Seq_735_Lachnospiraceae	paleturquoise
Seq_826_Ruminococcus_callidus	paleturquoise
Seq_853_Oscillibacter	paleturquoise
Seq_1034_Faecalibacterium_prausnitzii	paleturquoise
Seq_1067_Ruminococcaceae	paleturquoise
Seq_1070_Blautia	paleturquoise
Seq_1105_Ruminococcaceae	paleturquoise
Seq_1258_Faecalibacterium_prausnitzii	paleturquoise
Seq_1312_Alistipes_indistinctus	paleturquoise
Seq_1338_Phascolarctobacterium_succinatutens	paleturquoise
Seq_1413_Barnesiella_intestinihominis	paleturquoise
Seq_1462_Clostridiales	paleturquoise
Seq_1483_Clostridium_IV	paleturquoise
Seq_1600_Faecalibacterium_prausnitzii	paleturquoise
Seq_1619_Ruminococcaceae	paleturquoise
Seq_1671_Ruminococcaceae	paleturquoise
Seq_1866_Coriobacteriaceae	paleturquoise
Seq_1937_Clostridiales	paleturquoise
Seq_2144_Prevotella_buccalis	paleturquoise
Seq_2150_Ruminococcaceae	paleturquoise
Seq_2214_Bacteria	paleturquoise

Seq_2498_Clostridiales	paleturquoise
Seq_2538_Oscillibacter	paleturquoise
Seq_2561_Lachnospiraceae	paleturquoise
Seq_2562_Clostridiales	paleturquoise
Seq_2600_Anaerotruncus_colihominis	paleturquoise
Seq_2686_Porphyrromonas	paleturquoise
Seq_2778_Ruminococcaceae	paleturquoise
Seq_2870_Clostridiales	paleturquoise
Seq_2871_Ruminococcaceae	paleturquoise
Seq_3149_Clostridiales	paleturquoise
Seq_3151_Porphyrromonas_somerae	paleturquoise
Seq_22_Bacteroides_uniformis	pink
Seq_40_Bacteroides_stercoris	pink
Seq_80_Coprococcus_eutactus	pink
Seq_85_Bacteroides_stercoris	pink
Seq_96_Acidaminococcus_intestini	pink
Seq_150_Roseburia_hominis	pink
Seq_179_Bacteroides_xylanisolvens	pink
Seq_215_Bacteroides_stercoris	pink
Seq_238_Bacteroides_vulgatus	pink
Seq_279_Ruminococcus_flavefaciens	pink
Seq_284_Ruminococcaceae	pink
Seq_325_Ruminococcaceae	pink
Seq_346_Lachnospiraceae	pink
Seq_409_Firmicutes	pink
Seq_436_Faecalibacterium_prausnitzii	pink
Seq_486_Barnesiella_intestinihominis	pink
Seq_508_Parabacteroides_distasonis	pink
Seq_569_Ruminococcaceae	pink
Seq_601_Lachnospiraceae	pink
Seq_616_Bacteroidales	pink
Seq_766_Eubacterium_desmolans	pink
Seq_816_Bacteroides	pink
Seq_944_Oscillibacter_valericigenes	pink
Seq_982_Lachnospiraceae	pink
Seq_996_Parabacteroides_distasonis	pink
Seq_1006_Ruminococcaceae	pink
Seq_1019_Lachnospiraceae	pink
Seq_1047_Lachnospiraceae	pink
Seq_1102_Ruminococcaceae	pink
Seq_1125_Parasutterella_excrementihominis	pink
Seq_1174_Ruminococcaceae	pink
Seq_1198_Phascolarctobacterium_succinatutens	pink
Seq_1245_Lachnospiraceae	pink
Seq_1251_Clostridiales	pink

Seq_1285_Clostridiales	pink
Seq_1390_Clostridiales	pink
Seq_1439_Oscillibacter_valericigenes	pink
Seq_1466_Streptococcus	pink
Seq_1517_Clostridium_indolis	pink
Seq_1538_Ruminococcaceae	pink
Seq_1627_Dorea_longicatena	pink
Seq_1684_Blautia_hydrogenotrophica	pink
Seq_1705_Streptococcus	pink
Seq_1743_Ruminococcaceae	pink
Seq_1760_Clostridium_leptum	pink
Seq_1784_Parabacteroides_distasonis	pink
Seq_2040_Clostridiales	pink
Seq_2041_Ruminococcaceae	pink
Seq_2067_Gemella_sanguinis	pink
Seq_2130_Ruminococcaceae	pink
Seq_2163_Bacteria	pink
Seq_2164_Bacteria	pink
Seq_2189_Clostridium_leptum	pink
Seq_2234_Oscillibacter	pink
Seq_2416_Lactobacillus_algidus	pink
Seq_2459_Clostridium_hiranonis	pink
Seq_2460_Firmicutes	pink
Seq_2576_Clostridiales	pink
Seq_2577_Lachnospiraceae	pink
Seq_2628_Leuconostocarnosum	pink
Seq_2704_Firmicutes	pink
Seq_2792_Ruminococcaceae	pink
Seq_2793_Ruminococcaceae	pink
Seq_2794_Clostridiales	pink
Seq_2795_Oscillibacter_valericigenes	pink
Seq_2895_Abiotrophia_defectiva	pink
Seq_2896_Actinomyces_graevenitzii	pink
Seq_3014_Firmicutes	pink
Seq_3015_Eubacterium	pink
Seq_3016_Actinomyces_lingnae	pink
Seq_3017_Clostridiales	pink
Seq_3176_Clostridiales	pink
Seq_3177_Clostridiales	pink
Seq_3178_Peptococcaceae_1	pink
Seq_3456_Clostridiales	pink
Seq_3457_Bacteria	pink
Seq_27_Lachnospiraceae	purple
Seq_83_Ruminococcaceae	purple
Seq_109_Lachnospiraceae	purple

Seq 115 Coprococcus eutactus	purple
Seq 239 Eggerthella lenta	purple
Seq 317 Erysipelotrichaceae	purple
Seq 424 Bacteroides caccae	purple
Seq 430 Clostridia	purple
Seq 459 Blautia hydrogenotrophica	purple
Seq 550 Anaerostipes hadrus	purple
Seq 630 Coriobacteriaceae	purple
Seq 675 Clostridium IV	purple
Seq 677 Ruminococcaceae	purple
Seq 707 Gordonibacter pamelaee	purple
Seq 732 Ruminococcaceae	purple
Seq 771 Eubacterium desmolans	purple
Seq 852 Clostridiales	purple
Seq 860 Lachnospiraceae	purple
Seq 903 Bacteria	purple
Seq 920 Eubacterium	purple
Seq 936 Catenibacterium mitsuokai	purple
Seq 945 Erysipelotrichaceae	purple
Seq 966 Holdemania filiformis	purple
Seq 1071 Lachnospiraceae	purple
Seq 1072 Clostridium methylpentosum	purple
Seq 1153 Ruminococcaceae	purple
Seq 1164 Bacteria	purple
Seq 1171 Clostridiales	purple
Seq 1224 Turicibacter sanguinis	purple
Seq 1247 Clostridiales	purple
Seq 1263 Ruminococcaceae	purple
Seq 1276 Clostridiales	purple
Seq 1295 Ruminococcus2	purple
Seq 1351 Ruminococcus obeum	purple
Seq 1532 Firmicutes	purple
Seq 1544 Clostridiales	purple
Seq 1550 Lachnospiraceae	purple
Seq 1589 Parabacteroides distasonis	purple
Seq 1596 Clostridiales	purple
Seq 1613 Dialister invisus	purple
Seq 1620 Lachnospiraceae	purple
Seq 1647 Clostridiales	purple
Seq 1736 Clostridiales	purple
Seq 1747 Clostridiales	purple
Seq 1748 Ruminococcus bromii	purple
Seq 1762 Ruminococcaceae	purple
Seq 1769 Clostridiales	purple
Seq 1870 Ruminococcaceae	purple

Seq_1876_Ruminococcaceae	purple
Seq_1908_Clostridium_IV	purple
Seq_2043_Clostridiales	purple
Seq_2081_Firmicutes	purple
Seq_2139_Ruminococcaceae	purple
Seq_2284_Coriobacteriaceae	purple
Seq_2335_Ruminococcaceae	purple
Seq_2336_Clostridiales	purple
Seq_2337_Flavonifractor_plautii	purple
Seq_2338_Bacteria	purple
Seq_2432_Ruminococcaceae	purple
Seq_2525_Ruminococcaceae	purple
Seq_2595_Butyricimonas_virosa	purple
Seq_2646_Firmicutes	purple
Seq_2647_Lachnospiraceae	purple
Seq_2648_Lachnospiraceae	purple
Seq_2729_Ruminococcaceae	purple
Seq_2815_Clostridiales	purple
Seq_2816_Butyricimonas_virosa	purple
Seq_2921_Ruminococcaceae	purple
Seq_2922_Streptococcus	purple
Seq_2923_Butyricimonas_virosa	purple
Seq_2924_Clostridiales	purple
Seq_17_Bacteroides_vulgatus	red
Seq_35_Coproccoccus_eutactus	red
Seq_52_Clostridiales	red
Seq_57_Roseburia_inulinivorans	red
Seq_60_Faecalibacterium_prausnitzii	red
Seq_64_Dorea_formicigenerans	red
Seq_105_Lachnospiraceae	red
Seq_128_Clostridium_XIVa	red
Seq_144_Ruminococcus_torques	red
Seq_159_Bacteroides_eggerthii	red
Seq_161_Clostridium_XIVa	red
Seq_181_Clostridium_XVIII	red
Seq_184_Clostridiales	red
Seq_185_Anaerostipes_hadrus	red
Seq_187_Anaerostipes_hadrus	red
Seq_207_Bacteroides_ovatus	red
Seq_228_Clostridium_XIVb	red
Seq_276_Clostridium_XIVa	red
Seq_282_Eubacterium_desmolans	red
Seq_336_Flavonifractor_plautii	red
Seq_374_Alistipes_finegoldii	red
Seq_390_Clostridiales	red

Seq_400_Blautia	red
Seq_470_Eubacterium_siraeum	red
Seq_487_Bacteroides_finegoldii	red
Seq_521_Lachnospiraceae	red
Seq_563_Bacteroides_vulgatus	red
Seq_685_Eubacterium_desmolans	red
Seq_690_Bacteria	red
Seq_692_Bacteroides_vulgatus	red
Seq_746_Lachnospiraceae	red
Seq_779_Clostridiales	red
Seq_785_Proteobacteria	red
Seq_817_Faecalibacterium_prausnitzii	red
Seq_832_Ruminococcaceae	red
Seq_918_Lachnospiraceae	red
Seq_931_Blautia	red
Seq_937_Firmicutes	red
Seq_981_Lachnospiraceae	red
Seq_1012_Faecalibacterium_prausnitzii	red
Seq_1018_Lachnospiraceae	red
Seq_1030_Parabacteroides_distasonis	red
Seq_1073_Parabacteroides_distasonis	red
Seq_1106_Clostridium_sensu_stricto	red
Seq_1140_Bifidobacterium	red
Seq_1172_Lachnospiraceae	red
Seq_1202_Lachnospiraceae	red
Seq_1233_Lachnospiraceae	red
Seq_1268_Erysipelotrichaceae	red
Seq_1378_Clostridium_saccharogumia	red
Seq_1391_Burkholderiales	red
Seq_1446_Clostridiales	red
Seq_1471_Erysipelotrichaceae	red
Seq_1484_Streptococcus	red
Seq_1519_Lachnospiraceae	red
Seq_1549_Lachnospiraceae	red
Seq_1571_Lachnospiraceae	red
Seq_1658_Lachnospiraceae	red
Seq_1659_Ruminococcus_obeum	red
Seq_1677_Coprococcus_comes	red
Seq_1793_Coprococcus_catus	red
Seq_1820_Bacteroides_nordii	red
Seq_1832_Faecalibacterium_prausnitzii	red
Seq_1948_Ruminococcaceae	red
Seq_1969_Lachnospiraceae	red
Seq_2102_Lachnospiraceae	red
Seq_2198_Ruminococcaceae	red

Seq_2332_Clostridiales	red
Seq_2333_Collinsella_tanakaiei	red
Seq_2376_Dorea	red
Seq_2471_Collinsella	red
Seq_2522_Pediococcus	red
Seq_2523_Eubacterium_desmolans	red
Seq_2754_Clostridium_leptum	red
Seq_2811_Ruminococcaceae	red
Seq_2919_Coriobacteriaceae	red
Seq_3205_Clostridiales	red
Seq_3535_Solobacterium_moorei	red
Seq_28_Akkermansia_muciniphila	royalblue
Seq_66_Clostridium_sensu_stricto	royalblue
Seq_145_Clostridium_glycolicum	royalblue
Seq_236_Bifidobacterium_longum	royalblue
Seq_249_Firmicutes	royalblue
Seq_275_Akkermansia_muciniphila	royalblue
Seq_290_Akkermansia_muciniphila	royalblue
Seq_388_Bifidobacterium_animalis	royalblue
Seq_415_Ruminococcaceae	royalblue
Seq_495_Turicibacter_sanguinis	royalblue
Seq_532_Ruminococcaceae	royalblue
Seq_552_Ruminococcaceae	royalblue
Seq_705_Lachnospiraceae	royalblue
Seq_743_Ruminococcaceae	royalblue
Seq_791_Eubacterium_siraeum	royalblue
Seq_795_Holdemania_filiformis	royalblue
Seq_828_Clostridiales	royalblue
Seq_946_Clostridium_sensu_stricto	royalblue
Seq_1022_Lachnospiraceae	royalblue
Seq_1136_Bacteroides_fragilis	royalblue
Seq_1284_Eubacterium	royalblue
Seq_1500_Parabacteroides_johnsonii	royalblue
Seq_1539_Ruminococcaceae	royalblue
Seq_1565_Ruminococcaceae	royalblue
Seq_1628_Clostridium_baratii	royalblue
Seq_1719_Clostridiales	royalblue
Seq_1786_Alistipes_finegoldii	royalblue
Seq_1827_Clostridium_sensu_stricto	royalblue
Seq_1828_Flavonifractor_plautii	royalblue
Seq_1829_Desulfovibrio	royalblue
Seq_1894_Ruminococcaceae	royalblue
Seq_1918_Clostridium_XIVa	royalblue
Seq_1942_Ruminococcus	royalblue
Seq_1979_Ruminococcaceae	royalblue

Seq_2000_Pseudoflavonifractor	royalblue
Seq_2017_Bacteroides	royalblue
Seq_2143_Clostridiales	royalblue
Seq_2191_Bacteria	royalblue
Seq_2219_Clostridiales	royalblue
Seq_2258_Klebsiella	royalblue
Seq_2509_Butyricimonas_virosa	royalblue
Seq_2629_Clostridiales	royalblue
Seq_2630_Veillonella_dispar	royalblue
Seq_2705_Ruminococcaceae	royalblue
Seq_3019_Clostridiales	royalblue
Seq_3020_Firmicutes	royalblue
Seq_3180_Lachnospiraceae	royalblue
Seq_3459_Clostridiales	royalblue
Seq_3460_Clostridiales	royalblue
Seq_221_Erysipelotrichaceae	saddlebrown
Seq_223_Prevotella_stercorea	saddlebrown
Seq_259_Lachnospiraceae	saddlebrown
Seq_296_Parabacteroides_distasonis	saddlebrown
Seq_314_Gemmiger_formicilis	saddlebrown
Seq_367_Ruminococcus_callidus	saddlebrown
Seq_373_Lachnospiraceae	saddlebrown
Seq_481_Prevotella_copri	saddlebrown
Seq_595_Blautia	saddlebrown
Seq_680_Eubacterium_rectale	saddlebrown
Seq_697_Parasutterella_excrementihominis	saddlebrown
Seq_798_Clostridiales	saddlebrown
Seq_821_Prevotella_stercorea	saddlebrown
Seq_825_Allisonella_histaminiformans	saddlebrown
Seq_877_Prevotella	saddlebrown
Seq_939_Clostridium_XIVa	saddlebrown
Seq_947_Enterorhabdus	saddlebrown
Seq_991_Barnesiella_intestinihominis	saddlebrown
Seq_997_Phascolarctobacterium_succinatutens	saddlebrown
Seq_1038_Prevotella_stercorea	saddlebrown
Seq_1068_Blautia	saddlebrown
Seq_1166_Erysipelotrichaceae	saddlebrown
Seq_1221_Clostridiales	saddlebrown
Seq_1234_Prevotella_stercorea	saddlebrown
Seq_1272_Lachnospiraceae	saddlebrown
Seq_1369_Faecalibacterium_prausnitzii	saddlebrown
Seq_1382_Ruminococcus_callidus	saddlebrown
Seq_1657_Phascolarctobacterium_succinatutens	saddlebrown
Seq_1673_Slackia_isoflavoniconvertens	saddlebrown
Seq_1701_Clostridium_XIVb	saddlebrown

Seq 2015 Ruminococcaceae	saddlebrown
Seq 2159 Lachnospiraceae	saddlebrown
Seq 2320 Bacteroides ovatus	saddlebrown
Seq 2573 Mogibacterium	saddlebrown
Seq 2701 Sutterella wadsworthensis	saddlebrown
Seq 2788 Firmicutes	saddlebrown
Seq 2891 Bacteroides	saddlebrown
Seq 3439 Butyricimonas virosa	saddlebrown
Seq 4 Bifidobacterium	salmon
Seq 67 Bifidobacterium	salmon
Seq 86 Prevotella copri	salmon
Seq 104 Lachnospiraceae	salmon
Seq 160 Ruminococcus callidus	salmon
Seq 169 Akkermansia muciniphila	salmon
Seq 174 Prevotella copri	salmon
Seq 211 Prevotella copri	salmon
Seq 277 Bacteroides caccae	salmon
Seq 302 Bifidobacterium angulatum	salmon
Seq 323 Prevotella copri	salmon
Seq 351 Anaerostipes hadrus	salmon
Seq 429 Ruminococcaceae	salmon
Seq 471 Prevotella copri	salmon
Seq 594 Erysipelotrichaceae	salmon
Seq 596 Prevotella copri	salmon
Seq 645 Bacteroidetes	salmon
Seq 686 Lachnospiraceae	salmon
Seq 696 Eubacterium desmolans	salmon
Seq 775 Ruminococcaceae	salmon
Seq 819 Lactobacillus ruminis	salmon
Seq 906 Faecalibacterium prausnitzii	salmon
Seq 929 Sutterella wadsworthensis	salmon
Seq 986 Eubacterium desmolans	salmon
Seq 995 Lachnospiraceae	salmon
Seq 1000 Prevotella copri	salmon
Seq 1122 Barnesiella intestinihominis	salmon
Seq 1205 Phascolarctobacterium succinatutens	salmon
Seq 1319 Ruminococcaceae	salmon
Seq 1327 Phascolarctobacterium succinatutens	salmon
Seq 1328 Peptococcus niger	salmon
Seq 1358 Faecalibacterium prausnitzii	salmon
Seq 1372 Prevotella copri	salmon
Seq 1373 Prevotella copri	salmon
Seq 1374 Ruminococcaceae	salmon
Seq 1383 Prevotella copri	salmon
Seq 1404 Lachnospiraceae	salmon

Seq 1505 <i>Bacteroides fragilis</i>	salmon
Seq 1585 <i>Eubacterium desmolans</i>	salmon
Seq 1588 <i>Prevotella copri</i>	salmon
Seq 1599 Ruminococcaceae	salmon
Seq 1609 Lachnospiraceae	salmon
Seq 1630 <i>Eubacterium desmolans</i>	salmon
Seq 1709 <i>Blautia faecis</i>	salmon
Seq 1788 <i>Prevotella copri</i>	salmon
Seq 1798 <i>Prevotella copri</i>	salmon
Seq 1896 <i>Barnesiella intestinihominis</i>	salmon
Seq 1930 Coriobacteriaceae	salmon
Seq 1963 <i>Eubacterium desmolans</i>	salmon
Seq 2118 Porphyromonadaceae	salmon
Seq 2181 Lachnospiraceae	salmon
Seq 2265 Clostridiales	salmon
Seq 2329 <i>Prevotella copri</i>	salmon
Seq 2588 Clostridiales	salmon
Seq 2633 Lachnospiraceae	salmon
Seq 2634 Ruminococcaceae	salmon
Seq 2905 <i>Butyricimonas virosa</i>	salmon
Seq 2906 Coriobacteriaceae	salmon
Seq 3033 <i>Clostridium lactatifermentans</i>	salmon
Seq 3492 <i>Pseudomonas</i>	salmon
Seq 3494 <i>Sutterella stercoricanis</i>	salmon
Seq 3495 <i>Catenibacterium mitsuokai</i>	salmon
Seq 3496 <i>Bacteroides</i>	salmon
Seq 3514 Selenomonadales	salmon
Seq 47 <i>Ruminococcus torques</i>	sienna3
Seq 138 <i>Blautia</i>	sienna3
Seq 263 <i>Blautia</i>	sienna3
Seq 320 <i>Coprobacillus cateniformis</i>	sienna3
Seq 461 <i>Blautia</i>	sienna3
Seq 559 <i>Gemmiger formicilis</i>	sienna3
Seq 597 Bacteria	sienna3
Seq 608 Bacteria	sienna3
Seq 649 Lachnospiraceae	sienna3
Seq 673 Firmicutes	sienna3
Seq 713 Bacteria	sienna3
Seq 727 <i>Faecalibacterium prausnitzii</i>	sienna3
Seq 734 Firmicutes	sienna3
Seq 738 <i>Streptococcus</i>	sienna3
Seq 888 <i>Bacteroides ovatus</i>	sienna3
Seq 1109 Ruminococcaceae	sienna3
Seq 1141 <i>Eubacterium desmolans</i>	sienna3
Seq 1162 <i>Lachnospira</i>	sienna3

Seq_1173_Eubacterium_desmolans	sienna3
Seq_1209_Eubacterium_desmolans	sienna3
Seq_1220_Parasutterella_excrementihominis	sienna3
Seq_1243_Parabacteroides_distasonis	sienna3
Seq_1386_Blautia	sienna3
Seq_1430_Lachnospiraceae	sienna3
Seq_1447_Blautia	sienna3
Seq_1467_Blautia	sienna3
Seq_1511_Blautia	sienna3
Seq_1669_Blautia	sienna3
Seq_1670_Lachnospiraceae	sienna3
Seq_1851_Lachnospiraceae	sienna3
Seq_2227_Firmicutes	sienna3
Seq_2528_Eubacterium_desmolans	sienna3
Seq_2820_Eggerthella_lenta	sienna3
Seq_2982_Clostridiales	sienna3
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Seq_3358_Lachnospiraceae	sienna3
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Seq_307_Ruminococcaceae	skyblue
Seq_329_Bacteroides_ovatus	skyblue
Seq_385_Clostridiales	skyblue
Seq_402_Lachnospiraceae	skyblue
Seq_480_Alistipes_finegoldii	skyblue
Seq_499_Anaerostipes_hadrus	skyblue
Seq_519_Blautia	skyblue
Seq_523_Bacteria	skyblue
Seq_541_Bacteroides_ovatus	skyblue
Seq_653_Lactococcus	skyblue
Seq_723_Ruminococcus_albus	skyblue
Seq_772_Akkermansia_muciniphila	skyblue
Seq_810_Akkermansia_muciniphila	skyblue
Seq_971_Eubacterium_desmolans	skyblue
Seq_1160_Lachnospiraceae	skyblue
Seq_1311_Lactobacillus	skyblue
Seq_1584_Blautia	skyblue
Seq_1661_Clostridium_scindens	skyblue
Seq_1675_Bacteroides_intestinalis	skyblue
Seq_1706_Eubacterium_rectale	skyblue
Seq_1765_Lachnospiraceae	skyblue
Seq_1830_Bacteroides_intestinalis	skyblue
Seq_1873_Blautia_faecis	skyblue
Seq_1919_Anaerostipes_hadrus	skyblue
Seq_1989_Blautia_glucerasea	skyblue
Seq_2138_Lachnospiraceae	skyblue

Seq 2299 Clostridium lactatifermentans	skyblue
Seq 2300 Clostridium lavalense	skyblue
Seq 2417 Oscillibacter valericigenes	skyblue
Seq 2645 Ruminococcaceae	skyblue
Seq 2706 Gordonibacter pamelaee	skyblue
Seq 2727 Ruminococcaceae	skyblue
Seq 2897 Holdemania filiformis	skyblue
Seq 3022 Actinomycetales	skyblue
Seq 3043 Clostridiales	skyblue
Seq 3044 Staphylococcus	skyblue
Seq 3542 Ralstonia insidiosa	skyblue
Seq 3543 Alloiococcus otitis	skyblue
Seq 14 Bacteroides uniformis	skyblue3
Seq 217 Bacteroides uniformis	skyblue3
Seq 225 Lachnospiraceae	skyblue3
Seq 342 Coriobacteriaceae	skyblue3
Seq 360 Barnesiella intestinihominis	skyblue3
Seq 423 Roseburia intestinalis	skyblue3
Seq 478 Olsenella	skyblue3
Seq 565 Alistipes massiliensis	skyblue3
Seq 679 Acidaminococcaceae	skyblue3
Seq 802 Gemmiger formicilis	skyblue3
Seq 815 Roseburia intestinalis	skyblue3
Seq 892 Eubacterium rectale	skyblue3
Seq 942 Faecalibacterium prausnitzii	skyblue3
Seq 943 Lachnospiraceae	skyblue3
Seq 1558 Streptophyta	skyblue3
Seq 1885 Clostridium XIVa	skyblue3
Seq 2033 Faecalibacterium prausnitzii	skyblue3
Seq 2105 Lachnospiraceae	skyblue3
Seq 2120 Collinsella	skyblue3
Seq 2121 Acidaminococcaceae	skyblue3
Seq 2211 Butyricimonas virosa	skyblue3
Seq 2251 Erysipelotrichaceae	skyblue3
Seq 2403 Erysipelotrichaceae	skyblue3
Seq 2404 Ruminococcaceae	skyblue3
Seq 2477 Butyricimonas virosa	skyblue3
Seq 2681 Lachnospiraceae	skyblue3
Seq 2862 Ruminococcaceae	skyblue3
Seq 2863 Butyricimonas virosa	skyblue3
Seq 3359 Clostridiales	skyblue3
Seq 3571 Clostridiales	skyblue3
Seq 3572 Clostridiales	skyblue3
Seq 15 Collinsella aerofaciens	steelblue
Seq 24 Blautia faecis	steelblue

Seq_42_Ruminococcus_torques	steelblue
Seq_162_Firmicutes	steelblue
Seq_168_Lachnospiraceae	steelblue
Seq_251_Blautia_luti	steelblue
Seq_391_Dialister_succinatiphilus	steelblue
Seq_484_Coprococcus_eutactus	steelblue
Seq_612_Blautia_faecis	steelblue
Seq_626_Megasphaera	steelblue
Seq_721_Ruminococcus2	steelblue
Seq_736_Megasphaera	steelblue
Seq_803_Clostridiales	steelblue
Seq_913_Lachnospiraceae	steelblue
Seq_926_Slackia_piriformis	steelblue
Seq_988_Clostridiales	steelblue
Seq_1265_Ruminococcus_torques	steelblue
Seq_1399_Ruminococcaceae	steelblue
Seq_1468_Ruminococcaceae	steelblue
Seq_1931_Clostridiales	steelblue
Seq_1935_Clostridium_XIVb	steelblue
Seq_2171_Alistipes	steelblue
Seq_2197_Clostridiales	steelblue
Seq_2252_Actinomyces_odontolyticus	steelblue
Seq_2283_Clostridium_XIVa	steelblue
Seq_2316_Clostridiales	steelblue
Seq_2682_Ruminococcaceae	steelblue
Seq_2776_Ruminococcaceae	steelblue
Seq_2866_Clostridiales	steelblue
Seq_2983_Gordonibacter_pamelaee	steelblue
Seq_2984_Erysipelotrichaceae	steelblue
Seq_3143_Ruminococcaceae	steelblue
Seq_3369_Dialister	steelblue
Seq_3370_Haemophilus_parainfluenzae	steelblue
Seq_3372_Clostridiales	steelblue
Seq_3373_Clostridiales	steelblue
Seq_3374_Clostridiales	steelblue
Seq_3376_Lachnospiraceae	steelblue
Seq_20_Streptococcus	tan
Seq_36_Ruminococcus_gnavus	tan
Seq_37_Clostridium_bartlettii	tan
Seq_38_Escherichia/Shigella	tan
Seq_113_Veillonella_dispar	tan
Seq_114_Streptococcus	tan
Seq_118_Lachnospiraceae	tan
Seq_154_Clostridium_spiroforme	tan
Seq_163_Ruminococcus_gnavus	tan

Seq 198 <i>Clostridium ramosum</i>	tan
Seq 201 Lachnospiraceae	tan
Seq 214 Lachnospiraceae	tan
Seq 243 <i>Klebsiella</i>	tan
Seq 258 <i>Lactobacillus</i>	tan
Seq 286 <i>Escherichia/Shigella</i>	tan
Seq 308 Lachnospiraceae	tan
Seq 341 <i>Veillonella atypica</i>	tan
Seq 372 <i>Veillonella parvula</i>	tan
Seq 382 <i>Streptococcus mutans</i>	tan
Seq 393 <i>Veillonella dispar</i>	tan
Seq 401 Ruminococcaceae	tan
Seq 410 <i>Faecalibacterium prausnitzii</i>	tan
Seq 411 Lachnospiraceae	tan
Seq 446 <i>Veillonella parvula</i>	tan
Seq 447 <i>Enterococcus</i>	tan
Seq 453 Lachnospiraceae	tan
Seq 512 <i>Streptococcus</i>	tan
Seq 549 <i>Butyricicoccus pullicaecorum</i>	tan
Seq 581 <i>Butyricicoccus pullicaecorum</i>	tan
Seq 628 Ruminococcaceae	tan
Seq 648 <i>Lactobacillus</i>	tan
Seq 659 <i>Lactobacillus</i>	tan
Seq 663 <i>Erysipelotrichaceae</i>	tan
Seq 669 <i>Clostridium paraputrificum</i>	tan
Seq 701 <i>Lactobacillus</i>	tan
Seq 703 <i>Clostridium XI</i>	tan
Seq 747 <i>Veillonella</i>	tan
Seq 776 <i>Streptococcus</i>	tan
Seq 820 <i>Bifidobacterium</i>	tan
Seq 844 <i>Rothia mucilaginosa</i>	tan
Seq 893 <i>Clostridium glycolicum</i>	tan
Seq 1048 <i>Streptococcus cristatus</i>	tan
Seq 1082 <i>Clostridium bartlettii</i>	tan
Seq 1121 <i>Clostridium XI</i>	tan
Seq 1131 <i>Veillonella</i>	tan
Seq 1181 <i>Blautia</i>	tan
Seq 1191 Bifidobacteriaceae	tan
Seq 1342 <i>Streptococcus</i>	tan
Seq 1441 <i>Lactobacillus</i>	tan
Seq 1629 <i>Clostridium paraputrificum</i>	tan
Seq 1643 <i>Lactobacillus</i>	tan
Seq 1708 <i>Clostridium spiroforme</i>	tan
Seq 1886 <i>Alistipes massiliensis</i>	tan
Seq 2168 <i>Enterococcus</i>	tan

Seq 2228 Streptococcus	tan
Seq 2291 Rothia mucilaginosa	tan
Seq 2292 Fusobacterium nucleatum	tan
Seq 2400 Rothia dentocariosa	tan
Seq 2716 Haemophilus	tan
Seq 2804 Scardovia wiggsiae	tan
Seq 2805 Clostridium XIVb	tan
Seq 3032 Campylobacter gracilis	tan
Seq 3193 Megasphaera micronuciformis	tan
Seq 3194 Eikenella corrodens	tan
Seq 3579 Veillonella	tan
Seq 2 Faecalibacterium prausnitzii	turquoise
Seq 6 Faecalibacterium prausnitzii	turquoise
Seq 12 Lachnospiraceae	turquoise
Seq 33 Ruminococcaceae	turquoise
Seq 34 Dorea longicatena	turquoise
Seq 39 Ruminococcaceae	turquoise
Seq 48 Lachnospiraceae	turquoise
Seq 49 Coprococcus comes	turquoise
Seq 53 Faecalibacterium prausnitzii	turquoise
Seq 58 Prevotella copri	turquoise
Seq 71 Ruminococcaceae	turquoise
Seq 72 Faecalibacterium prausnitzii	turquoise
Seq 74 Ruminococcaceae	turquoise
Seq 87 Clostridium leptum	turquoise
Seq 88 Blautia	turquoise
Seq 107 Ruminococcaceae	turquoise
Seq 110 Bacteroides coprocola	turquoise
Seq 117 Lachnospiraceae	turquoise
Seq 124 Clostridium XIVa	turquoise
Seq 126 Catenibacterium mitsuokai	turquoise
Seq 131 Firmicutes	turquoise
Seq 136 Eubacterium desmolans	turquoise
Seq 139 Firmicutes	turquoise
Seq 140 Ruminococcaceae	turquoise
Seq 143 Coprococcus catus	turquoise
Seq 148 Prevotella copri	turquoise
Seq 165 Firmicutes	turquoise
Seq 178 Lachnospiraceae	turquoise
Seq 183 Alistipes shahii	turquoise
Seq 196 Ruminococcaceae	turquoise
Seq 199 Clostridiales	turquoise
Seq 200 Barnesiella intestinihominis	turquoise
Seq 216 Ruminococcaceae	turquoise
Seq 234 Clostridium XIVa	turquoise

Seq_237	<i>Phascolarctobacterium succinatutens</i>	turquoise
Seq_248	<i>Sutterella stercoricanis</i>	turquoise
Seq_261	<i>Flavonifractor</i>	turquoise
Seq_262	<i>Coriobacteriaceae</i>	turquoise
Seq_278	<i>Methanobrevibacter smithii</i>	turquoise
Seq_280	<i>Blautia</i>	turquoise
Seq_283	<i>Firmicutes</i>	turquoise
Seq_287	<i>Lachnospiraceae</i>	turquoise
Seq_294	<i>Clostridiales</i>	turquoise
Seq_297	<i>Ruminococcaceae</i>	turquoise
Seq_311	<i>Blautia</i>	turquoise
Seq_316	<i>Ruminococcaceae</i>	turquoise
Seq_319	<i>Clostridium_XIVa</i>	turquoise
Seq_321	<i>Ruminococcaceae</i>	turquoise
Seq_334	<i>Phascolarctobacterium succinatutens</i>	turquoise
Seq_339	<i>Bacteroides uniformis</i>	turquoise
Seq_343	<i>Ruminococcaceae</i>	turquoise
Seq_354	<i>Lachnospiraceae</i>	turquoise
Seq_370	<i>Firmicutes</i>	turquoise
Seq_378	<i>Lachnospiraceae</i>	turquoise
Seq_399	<i>Ruminococcaceae</i>	turquoise
Seq_421	<i>Ruminococcaceae</i>	turquoise
Seq_427	<i>Alistipes indistinctus</i>	turquoise
Seq_432	<i>Ruminococcaceae</i>	turquoise
Seq_433	<i>Prevotella copri</i>	turquoise
Seq_438	<i>Bacteria</i>	turquoise
Seq_439	<i>Lachnospiraceae</i>	turquoise
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Seq_449	<i>Firmicutes</i>	turquoise
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Seq_475	<i>Clostridiales</i>	turquoise
Seq_514	<i>Erysipelotrichaceae</i>	turquoise
Seq_516	<i>Ruminococcaceae</i>	turquoise
Seq_526	<i>Flavonifractor plautii</i>	turquoise
Seq_560	<i>Lachnospiraceae</i>	turquoise
Seq_573	<i>Firmicutes</i>	turquoise
Seq_582	<i>Lachnospiraceae</i>	turquoise
Seq_617	<i>Ruminococcaceae</i>	turquoise
Seq_629	<i>Sutterella stercoricanis</i>	turquoise
Seq_650	<i>Lachnospiraceae</i>	turquoise
Seq_651	<i>Ruminococcaceae</i>	turquoise
Seq_654	<i>Lachnospiraceae</i>	turquoise
Seq_658	<i>Ruminococcaceae</i>	turquoise
Seq_694	<i>Ruminococcaceae</i>	turquoise
Seq_704	<i>Lachnospiraceae</i>	turquoise

Seq_706_Bacteria	turquoise
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Seq_729_Phascolarctobacterium_succinatutens	turquoise
Seq_730_Firmicutes	turquoise
Seq_750_Bacteria	turquoise
Seq_773_Ruminococcaceae	turquoise
Seq_788_Clostridiales	turquoise
Seq_836_Clostridiales	turquoise
Seq_846_Coprococcus_catus	turquoise
Seq_851_Clostridiales	turquoise
Seq_867_Firmicutes	turquoise
Seq_874_Haemophilus	turquoise
Seq_885_Clostridiales	turquoise
Seq_890_Oscillibacter	turquoise
Seq_891_Howardella_ureilytica	turquoise
Seq_895_Bacteria	turquoise
Seq_897_Lachnospiraceae	turquoise
Seq_899_Prevotella_copri	turquoise
Seq_901_Eubacterium_xylanophilum	turquoise
Seq_905_Prevotella_copri	turquoise
Seq_963_Ruminococcaceae	turquoise
Seq_968_Ruminococcaceae	turquoise
Seq_969_Clostridiales	turquoise
Seq_975_Clostridiales	turquoise
Seq_980_Clostridium_lactatifermentans	turquoise
Seq_985_Lachnospiraceae	turquoise
Seq_992_Ruminococcaceae	turquoise
Seq_1005_Lachnospiraceae	turquoise
Seq_1013_Ruminococcaceae	turquoise
Seq_1016_Ruminococcaceae	turquoise
Seq_1061_Ruminococcaceae	turquoise
Seq_1066_Clostridiales	turquoise
Seq_1084_Oscillibacter	turquoise
Seq_1098_Dorea_longicatena	turquoise
Seq_1117_Oscillibacter	turquoise
Seq_1119_Ruminococcaceae	turquoise
Seq_1123_Ruminococcaceae	turquoise
Seq_1135_Clostridium_IV	turquoise
Seq_1145_Dorea_longicatena	turquoise
Seq_1146_Phascolarctobacterium_succinatutens	turquoise
Seq_1150_Oscillibacter	turquoise
Seq_1180_Clostridiales	turquoise
Seq_1190_Dorea_longicatena	turquoise
Seq_1219_Lachnospiraceae	turquoise
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Seq_1230_Ruminococcaceae	turquoise
Seq_1254_Lachnospiraceae	turquoise
Seq_1300_Alistipes_massiliensis	turquoise
Seq_1326_Faecalibacterium_prausnitzii	turquoise
Seq_1348_Ruminococcaceae	turquoise
Seq_1354_Clostridium_XIVa	turquoise
Seq_1371_Peptococcus_niger	turquoise
Seq_1393_Ruminococcus_callidus	turquoise
Seq_1394_Ruminococcaceae	turquoise
Seq_1425_Ruminococcaceae	turquoise
Seq_1461_Ruminococcaceae	turquoise
Seq_1524_Clostridiales	turquoise
Seq_1559_Ruminococcaceae	turquoise
Seq_1567_Actinomyces_odontolyticus	turquoise
Seq_1805_Firmicutes	turquoise
Seq_1811_Ruminococcaceae	turquoise
Seq_1813_Clostridiales	turquoise
Seq_1814_Bacteroides_xylanisolvens	turquoise
Seq_1882_Bacteria	turquoise
Seq_1932_Ruminococcaceae	turquoise
Seq_1943_Bacteria	turquoise
Seq_1997_Ruminococcaceae	turquoise
Seq_2042_Firmicutes	turquoise
Seq_2083_Clostridium_IV	turquoise
Seq_2174_Ruminococcaceae	turquoise
Seq_2220_Lachnospiraceae	turquoise
Seq_2248_Clostridiales	turquoise
Seq_2261_Puniceicoccaceae	turquoise
Seq_2273_Clostridiales	turquoise
Seq_2280_Firmicutes	turquoise
Seq_2325_Ruminococcaceae	turquoise
Seq_2418_Ruminococcaceae	turquoise
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Seq_2463_Firmicutes	turquoise
Seq_2464_Ruminococcaceae	turquoise
Seq_2488_Hydrogenoanaerobacterium_saccharovorans	turquoise
Seq_2513_Lachnospiraceae	turquoise
Seq_2514_Ruminococcaceae	turquoise
Seq_2578_Bacteroidales	turquoise
Seq_2583_Alloprevotella_rava	turquoise
Seq_2601_Clostridiales	turquoise
Seq_2632_Oscillibacter_valericigenes	turquoise
Seq_2710_Bacteroides	turquoise
Seq_2711_Ruminococcaceae	turquoise
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Seq 2799 Bacteria	turquoise
Seq 2800 Ruminococcaceae	turquoise
Seq 2900 Clostridiales	turquoise
Seq 2901 Clostridiales	turquoise
Seq 2902 Anaerotruncus colihominis	turquoise
Seq 2903 Firmicutes	turquoise
Seq 3027 Firmicutes	turquoise
Seq 3028 Anaerorhabdus furcosa	turquoise
Seq 3029 Olsenella	turquoise
Seq 3189 Syntrophomonadaceae	turquoise
Seq 3480 Deltaproteobacteria	turquoise
Seq 3481 Bacteria	turquoise
Seq 132 Streptococcus	violet
Seq 356 Klebsiella	violet
Seq 362 Catenibacterium mitsuokai	violet
Seq 483 Alistipes	violet
Seq 590 Klebsiella	violet
Seq 615 Ruminococcus bromii	violet
Seq 622 Alistipes finegoldii	violet
Seq 637 Catenibacterium mitsuokai	violet
Seq 642 Klebsiella	violet
Seq 768 Bacteroides salyersiae	violet
Seq 850 Dialister invisus	violet
Seq 1138 Lachnospiraceae	violet
Seq 1177 Blautia	violet
Seq 1186 Klebsiella	violet
Seq 1212 Faecalibacterium prausnitzii	violet
Seq 1274 Lachnospiraceae	violet
Seq 1329 Streptococcus	violet
Seq 1396 Bacteroides	violet
Seq 1445 Lachnospiraceae	violet
Seq 1509 Eubacterium desmolans	violet
Seq 1533 Alistipes shahii	violet
Seq 1666 Butyricimonas virosa	violet
Seq 2091 Clostridium XI	violet
Seq 2201 Paraprevotella clara	violet
Seq 2213 Lachnospiraceae	violet
Seq 2253 Faecalibacterium prausnitzii	violet
Seq 2297 Pyramidobacter piscolens	violet
Seq 2364 Clostridiales	violet
Seq 2560 Blautia	violet
Seq 2619 Clostridiales	violet
Seq 2777 Lachnospiraceae	violet
Seq 2911 Ruminococcaceae	violet

Seq 2986 <i>Clostridium butyricum</i>	violet
Seq 3037 <i>Parabacteroides distasonis</i>	violet
Seq 3038 Bacteria	violet
Seq 3147 <i>Rothia mucilaginosa</i>	violet
Seq 3511 Bacteroidales	violet
Seq 3580 <i>Streptococcus</i>	violet
Seq 253 <i>Bacteroides massiliensis</i>	white
Seq 267 <i>Eubacterium rectale</i>	white
Seq 271 <i>Alistipes shahii</i>	white
Seq 361 <i>Dialister invisus</i>	white
Seq 371 <i>Ruminococcus bromii</i>	white
Seq 404 <i>Bacteroides plebeius</i>	white
Seq 468 <i>Ruminococcus albus</i>	white
Seq 473 <i>Coprococcus eutactus</i>	white
Seq 503 <i>Bacteroides plebeius</i>	white
Seq 614 Ruminococcaceae	white
Seq 644 Lachnospiraceae	white
Seq 725 <i>Ruminococcus callidus</i>	white
Seq 774 Clostridiales	white
Seq 865 <i>Faecalibacterium prausnitzii</i>	white
Seq 927 <i>Blautia</i>	white
Seq 951 <i>Bacteroides stercoris</i>	white
Seq 964 <i>Faecalibacterium prausnitzii</i>	white
Seq 1206 <i>Bacteroides plebeius</i>	white
Seq 1246 <i>Clostridium disporicum</i>	white
Seq 1296 Lachnospiraceae	white
Seq 1359 <i>Clostridium ruminantium</i>	white
Seq 1375 <i>Olsenella</i>	white
Seq 1395 Coriobacteriaceae	white
Seq 1481 <i>Faecalibacterium prausnitzii</i>	white
Seq 1552 <i>Faecalibacterium prausnitzii</i>	white
Seq 1632 <i>Ruminococcus torques</i>	white
Seq 1668 Ruminococcaceae	white
Seq 1729 <i>Parasutterella excrementihominis</i>	white
Seq 1781 <i>Bacteroides plebeius</i>	white
Seq 1966 <i>Dorea longicatena</i>	white
Seq 2007 Ruminococcaceae	white
Seq 2226 Ruminococcaceae	white
Seq 2282 <i>Actinomyces odontolyticus</i>	white
Seq 2374 Ruminococcaceae	white
Seq 2809 Firmicutes	white
Seq 2912 Ruminococcaceae	white
Seq 3355 Erysipelotrichaceae	white
Seq 3516 Peptostreptococcaceae	white
Seq 3582 Erysipelotrichaceae	white

Seq_30_Clostridium_ruminantium	yellow
Seq_41_Clostridiales	yellow
Seq_56_Clostridium_disporicum	yellow
Seq_65_Ruminococcaceae	yellow
Seq_182_Clostridium_leptum	yellow
Seq_203_Ruminococcaceae	yellow
Seq_241_Turicibacter_sanguinis	yellow
Seq_245_Clostridium_leptum	yellow
Seq_250_Alistipes	yellow
Seq_348_Clostridiales	yellow
Seq_352_Barnesiella_intestinihominis	yellow
Seq_407_Clostridiales	yellow
Seq_414_Alistipes	yellow
Seq_420_Bacteroides_massiliensis	yellow
Seq_431_Bacteria	yellow
Seq_485_Akkermansia_muciniphila	yellow
Seq_489_Clostridium_hathewayi	yellow
Seq_506_Lachnospiraceae	yellow
Seq_539_Firmicutes	yellow
Seq_588_Alistipes_indistinctus	yellow
Seq_634_Clostridiales	yellow
Seq_660_Ruminococcaceae	yellow
Seq_829_Ruminococcaceae	yellow
Seq_837_Flavonifractor_plautii	yellow
Seq_873_Clostridiales	yellow
Seq_882_Firmicutes	yellow
Seq_898_Lachnospiraceae	yellow
Seq_909_Ruminococcaceae	yellow
Seq_935_Ruminococcaceae	yellow
Seq_961_Lachnospiraceae	yellow
Seq_967_Pseudoflavonifractor	yellow
Seq_1089_Clostridiales	yellow
Seq_1236_Lachnospiraceae	yellow
Seq_1280_Bacteria	yellow
Seq_1321_Clostridium_XIVa	yellow
Seq_1322_Clostridia	yellow
Seq_1385_Bacteroides_vulgatus	yellow
Seq_1400_Flavonifractor_plautii	yellow
Seq_1403_Clostridium_XI	yellow
Seq_1406_Ruminococcaceae	yellow
Seq_1408_Clostridiales	yellow
Seq_1409_Clostridia	yellow
Seq_1478_Ruminococcaceae	yellow
Seq_1493_Lachnospiraceae	yellow
Seq_1503_Clostridium_IV	yellow

Seq_1504_Clostridiales	yellow
Seq_1531_Clostridium_IV	yellow
Seq_1543_Anaerotruncus_colihominis	yellow
Seq_1644_Bacteria	yellow
Seq_1735_Alistipes_indistinctus	yellow
Seq_1744_Eubacterium_rectale	yellow
Seq_1759_Clostridiales	yellow
Seq_1779_Clostridiales	yellow
Seq_1789_Clostridiales	yellow
Seq_1806_Ruminococcaceae	yellow
Seq_1946_Erysipelotrichaceae	yellow
Seq_2037_Holdemania_filiformis	yellow
Seq_2054_Clostridiales	yellow
Seq_2070_Clostridiales	yellow
Seq_2099_Clostridium_IV	yellow
Seq_2100_Ruminococcaceae	yellow
Seq_2134_Lachnospiraceae	yellow
Seq_2169_Firmicutes	yellow
Seq_2183_Ruminococcaceae	yellow
Seq_2193_Clostridiales	yellow
Seq_2194_Bacteria	yellow
Seq_2217_Clostridiales	yellow
Seq_2223_Bacteroides_thetaiotaomicron	yellow
Seq_2263_Clostridiales	yellow
Seq_2293_Clostridiales	yellow
Seq_2294_Ruminococcaceae	yellow
Seq_2362_Clostridiales	yellow
Seq_2394_Ruminococcaceae	yellow
Seq_2415_Ruminococcaceae	yellow
Seq_2430_Ruminococcaceae	yellow
Seq_2589_Alistipes	yellow
Seq_2590_Firmicutes	yellow
Seq_2717_Anaerotruncus_colihominis	yellow
Seq_2907_Clostridiales	yellow
Seq_2908_Lachnospiraceae	yellow
Seq_3497_Bacteria	yellow
Seq_3498_Clostridiales	yellow
Seq_3499_Clostridium_IV	yellow
Seq_270_Streptococcus	yellowgreen
Seq_288_Escherichia/Shigella_coli	yellowgreen
Seq_640_Ruminococcus2	yellowgreen
Seq_714_Dorea_longicatena	yellowgreen
Seq_784_Ruminococcus_bromii	yellowgreen
Seq_793_Faecalibacterium_prausnitzii	yellowgreen
Seq_808_Faecalibacterium_prausnitzii	yellowgreen

Seq 824 <i>Blautia</i>	yellowgreen
Seq 845 <i>Clostridium</i> XIVa	yellowgreen
Seq 876 <i>Faecalibacterium prausnitzii</i>	yellowgreen
Seq 1031 <i>Faecalibacterium prausnitzii</i>	yellowgreen
Seq 1087 <i>Catenibacterium mitsuokai</i>	yellowgreen
Seq 1097 <i>Erysipelotrichaceae</i>	yellowgreen
Seq 1134 <i>Blautia luti</i>	yellowgreen
Seq 1149 <i>Rothia mucilaginosa</i>	yellowgreen
Seq 1223 <i>Anaerostipes hadrus</i>	yellowgreen
Seq 1534 <i>Faecalibacterium prausnitzii</i>	yellowgreen
Seq 1536 <i>Roseburia intestinalis</i>	yellowgreen
Seq 1566 <i>Clostridium</i> XIVa	yellowgreen
Seq 1651 <i>Blautia</i>	yellowgreen
Seq 1654 <i>Phascolarctobacterium succinatutens</i>	yellowgreen
Seq 1852 <i>Ruminococcus</i> 2	yellowgreen
Seq 1911 <i>Collinsella</i>	yellowgreen
Seq 1985 <i>Ruminococcus lactaris</i>	yellowgreen
Seq 2012 <i>Prevotella</i>	yellowgreen
Seq 2038 <i>Phascolarctobacterium succinatutens</i>	yellowgreen
Seq 2125 <i>Phascolarctobacterium succinatutens</i>	yellowgreen
Seq 2360 <i>Bacteroides caccae</i>	yellowgreen
Seq 2361 <i>Allisonella histaminiformans</i>	yellowgreen
Seq 2380 <i>Erysipelotrichaceae</i>	yellowgreen
Seq 2446 <i>Paraprevotella clara</i>	yellowgreen
Seq 2864 <i>Leuconostokimchii</i>	yellowgreen
Seq 3368 <i>Clostridiales</i>	yellowgreen
Seq 3395 <i>Roseburia</i>	yellowgreen

Appendix 2: Skin modules taxa

Taxa	Colours
Seq_2_Corynebacterium	black
Seq_454_Prevotella_timonensis	black
Seq_780_Staphylococcus_aureus	black
Seq_930_Prevotella_bivia	black
Seq_951_Corynebacterium	black
Seq_955_Staphylococcus	black
Seq_966_Anaerococcus_murdochii	black
Seq_982_Parvimonas_micra	black
Seq_997_Corynebacterium	black
Seq_1024_Corynebacterium	black
Seq_1031_Staphylococcus	black
Seq_1050_Corynebacterium_jeikeium	black
Seq_1059_Actinomycetales	black
Seq_1089_Corynebacterium	black
Seq_1092_Corynebacterium	black
Seq_1105_Corynebacterium_aurimucosum	black
Seq_1111_Corynebacterium	black
Seq_1112_Akkermansia_muciniphila	black
Seq_1140_Corynebacterium	black
Seq_1141_Corynebacterium	black
Seq_1165_Corynebacterium_aurimucosum	black
Seq_1168_Peptoniphilus_coxii	black
Seq_1172_Corynebacterium	black
Seq_1173_Actinomycetales	black
Seq_1177_Corynebacterium	black
Seq_1182_Corynebacterium	black
Seq_1207_Prevotella_bivia	black
Seq_1227_Corynebacterium	black
Seq_1234_Prevotella_denticola	black
Seq_1257_Corynebacterium	black
Seq_1272_Prevotella_timonensis	black
Seq_1286_Corynebacterium	black
Seq_1296_Brevibacterium	black
Seq_1304_Corynebacterium	black
Seq_1333_Corynebacterium_aurimucosum	black
Seq_1356_Corynebacterium_aurimucosum	black
Seq_1357_Gallicola	black
Seq_1362_Staphylococcus	black
Seq_1363_Anaerococcus_vaginalis	black
Seq_1390_Corynebacterium_aurimucosum	black
Seq_1406_Corynebacterium	black
Seq_1445_Corynebacterium	black

Seq_1471_Corynebacterium	black
Seq_1476_Prevotella_bivia	black
Seq_1516_Klebsiella	black
Seq_1517_Prevotella_bivia	black
Seq_1533_Corynebacterium_aurimucosum	black
Seq_1564_Peptoniphilus	black
Seq_1581_Corynebacterium	black
Seq_1590_Corynebacterium_jeikeium	black
Seq_1673_Corynebacteriaceae	black
Seq_1681_Corynebacterium	black
Seq_1830_Corynebacterium	black
Seq_1898_Corynebacterium	black
Seq_1965_Corynebacterium	black
Seq_2024_Corynebacterium_jeikeium	black
Seq_2258_Thermomonas_hydrothermalis	black
Seq_2272_Saccharofermentans_acetigenes	black
Seq_2362_Gluconobacter	black
Seq_2749_Prevotella_buccalis	black
Seq_8_Corynebacterium	blue
Seq_11_Propionibacterium_acnes	blue
Seq_74_Anaerococcus_octavius	blue
Seq_95_Fusobacterium_nucleatum	blue
Seq_113_Prevotella_bivia	blue
Seq_118_Streptococcus	blue
Seq_162_Corynebacterium	blue
Seq_178_Streptococcus	blue
Seq_180_Gardnerella_vaginalis	blue
Seq_282_Actinobaculum_massiliense	blue
Seq_371_Staphylococcus	blue
Seq_397_Gardnerella_vaginalis	blue
Seq_399_Enterococcus	blue
Seq_457_Paracoccus_yeei	blue
Seq_523_Ruminococcaceae	blue
Seq_684_Prevotella_melaninogenica	blue
Seq_738_Pseudoxanthomonas_spadix	blue
Seq_739_Gardnerella_vaginalis	blue
Seq_799_Corynebacterium_durum	blue
Seq_812_Staphylococcus_massiliensis	blue
Seq_839_Moryella_indoligenes	blue
Seq_946_Acinetobacter_johnsonii	blue
Seq_970_Streptophyta	blue
Seq_1022_Streptococcus_equi	blue
Seq_1082_Photobacterium	blue
Seq_1135_Alloioococcus_otitis	blue
Seq_1295_Actinomyces	blue

Seq 1376 <i>Dialister propionificiens</i>	blue
Seq 1490 <i>Howardella ureilytica</i>	blue
Seq 1521 <i>Aeromonas</i>	blue
Seq 1569 <i>Acinetobacter johnsonii</i>	blue
Seq 1660 <i>Prevotella</i>	blue
Seq 1662 <i>Sneathia</i>	blue
Seq 1748 <i>Pantoea</i>	blue
Seq 1820 <i>Pseudomonas</i>	blue
Seq 1873 <i>Pantoea calida</i>	blue
Seq 1889 <i>Acidaminococcus intestini</i>	blue
Seq 1969 <i>Acidovorax temperans</i>	blue
Seq 1995 <i>Aerococcus christensenii</i>	blue
Seq 2041 <i>Megasphaera elsdenii</i>	blue
Seq 2098 <i>Pseudomonas luteola</i>	blue
Seq 2268 <i>Corynebacterium</i>	blue
Seq 2343 <i>Campylobacter concisus</i>	blue
Seq 2350 <i>Amaricoccus</i>	blue
Seq 2414 <i>Veillonella parvula</i>	blue
Seq 2579 <i>Dermacoccus nishinomiyaensis</i>	blue
Seq 2584 <i>Solobacterium moorei</i>	blue
Seq 2619 <i>Nocardioides aquaticus</i>	blue
Seq 2721 <i>Coriobacteriaceae</i>	blue
Seq 2773 <i>Prevotella histicola</i>	blue
Seq 2795 <i>Neisseria bacilliformis</i>	blue
Seq 2810 <i>Actinomyces lingnae</i>	blue
Seq 2849 <i>Prevotella amnii</i>	blue
Seq 2966 <i>Blastocatella</i>	blue
Seq 2969 <i>Enterobacteriaceae</i>	blue
Seq 3022 <i>Prevotella</i>	blue
Seq 3155 <i>Haemophilus parainfluenzae</i>	blue
Seq 3188 <i>Streptococcus</i>	blue
Seq 3211 <i>Anaerococcus prevotii</i>	blue
Seq 3364 <i>GpI</i>	blue
Seq 3417 <i>Psychrobacter</i>	blue
Seq 3458 <i>Cyanobacteria</i>	blue
Seq 3496 <i>Brevibacterium</i>	blue
Seq 3497 <i>Psychrobacter</i>	blue
Seq 3580 <i>GpI</i>	blue
Seq 3581 <i>Zoogloea</i>	blue
Seq 3582 <i>Brevundimonas</i>	blue
Seq 3630 <i>Brachybacterium</i>	blue
Seq 3690 <i>Shinella</i>	blue
Seq 3753 <i>Neisseria</i>	blue
Seq 3781 <i>Cyanobacteria</i>	blue
Seq 3882 <i>Caulobacter</i>	blue

Seq 4041	Propionibacteriaceae	blue
Seq 4042	Rhodospirillaceae	blue
Seq 4123	Streptococcus	blue
Seq 4142	Stenotrophomonas maltophilia	blue
Seq 4206	Spirosoma	blue
Seq 4207	Proteobacteria	blue
Seq 4208	Marmoricola bigeumensis	blue
Seq 4209	Pseudomonas	blue
Seq 4342	Leptotrichia	blue
Seq 4409	Pantoea	blue
Seq 4410	Cardiobacterium hominis	blue
Seq 4411	Porphyrobacter	blue
Seq 4412	Hallella	blue
Seq 4413	Diaphorobacter	blue
Seq 4414	Rhodococcus	blue
Seq 4415	Flavobacterium	blue
Seq 4416	Prevotellaceae	blue
Seq 4640	Porphyromonas gulae	blue
Seq 4641	Selenomonas noxia	blue
Seq 4642	Enterobacteriaceae	blue
Seq 4643	Treponema amylovorum	blue
Seq 4886	Rhodocyclaceae	blue
Seq 4887	Clostridiales	blue
Seq 4888	Rhizobiales	blue
Seq 4889	Lachnospiraceae	blue
Seq 5093	Lachnospiraceae	blue
Seq 5094	Mobiluncus curtisii	blue
Seq 5215	Cyanobacteria	blue
Seq 5216	Tannerella forsythia	blue
Seq 5218	Solirubrobacter	blue
Seq 5498	Veillonella dispar	blue
Seq 5499	Jeotgalicoccus	blue
Seq 5575	Atopobium vaginae	blue
Seq 5720	Hymenobacter	blue
Seq 6198	Sphingobacteriaceae	blue
Seq 6199	Actinomycetales	blue
Seq 6201	Staphylococcus	blue
Seq 6330	Roseburia faecis	blue
Seq 6600	Sphingobacterium	blue
Seq 6601	Cyanobacteria	blue
Seq 64	Corynebacterium appendicis	brown
Seq 94	Corynebacterium	brown
Seq 102	Corynebacterium riegellii	brown
Seq 108	Faecalibacterium prausnitzii	brown
Seq 142	Corynebacterium genitalium	brown

Seq 160 <i>Faecalibacterium prausnitzii</i>	brown
Seq 170 <i>Weeksella virosa</i>	brown
Seq 184 <i>Oligella urethralis</i>	brown
Seq 201 <i>Corynebacterium sundsvallense</i>	brown
Seq 229 <i>Peptoniphilus koenoeneniae</i>	brown
Seq 311 <i>Corynebacterium tuscaniense</i>	brown
Seq 318 <i>Propionibacterium avidum</i>	brown
Seq 327 <i>Granulicatella elegans</i>	brown
Seq 330 <i>Facklamia ignava</i>	brown
Seq 409 <i>Bifidobacterium longum</i>	brown
Seq 416 <i>Abiotrophia defectiva</i>	brown
Seq 420 <i>Weeksella virosa</i>	brown
Seq 434 <i>Alishewanella</i>	brown
Seq 435 <i>Pseudomonas</i>	brown
Seq 447 <i>Weeksella virosa</i>	brown
Seq 468 <i>Staphylococcus simulans</i>	brown
Seq 472 <i>Staphylococcus simulans</i>	brown
Seq 484 <i>Clostridiales Incertae Sedis XI</i>	brown
Seq 491 <i>Staphylococcus simulans</i>	brown
Seq 539 <i>Micrococcaceae</i>	brown
Seq 667 <i>Micrococcaceae</i>	brown
Seq 668 <i>Anaerostipes hadrus</i>	brown
Seq 737 <i>Ruminococcus bromii</i>	brown
Seq 804 <i>Roseburia faecis</i>	brown
Seq 805 <i>Corynebacterium riegelii</i>	brown
Seq 825 <i>Staphylococcus simulans</i>	brown
Seq 832 <i>Corynebacterium genitalium</i>	brown
Seq 880 <i>Micrococcaceae</i>	brown
Seq 885 <i>Facklamia ignava</i>	brown
Seq 890 <i>Clostridiales</i>	brown
Seq 894 <i>Anaerostipes hadrus</i>	brown
Seq 957 <i>Anaerococcus octavius</i>	brown
Seq 993 <i>Eubacterium rectale</i>	brown
Seq 1012 <i>Roseburia faecis</i>	brown
Seq 1033 <i>Prevotellaceae</i>	brown
Seq 1039 <i>Lachnospiraceae</i>	brown
Seq 1060 <i>Staphylococcus</i>	brown
Seq 1076 <i>Succiniclasticum ruminis</i>	brown
Seq 1139 <i>Corynebacterium riegelii</i>	brown
Seq 1142 <i>Clostridiales Incertae Sedis XI</i>	brown
Seq 1329 <i>Lachnospiraceae</i>	brown
Seq 1359 <i>Porphyromonas bennonis</i>	brown
Seq 1430 <i>Megasphaera</i>	brown
Seq 1478 <i>Ruminococcaceae</i>	brown
Seq 1482 <i>Oscillibacter</i>	brown

Seq 1603	Acinetobacter	brown
Seq 1614	Clostridium XIVb	brown
Seq 1654	Gardnerella vaginalis	brown
Seq 1657	Anaerococcus	brown
Seq 1757	Ruminococcaceae	brown
Seq 1764	Ruminococcus albus	brown
Seq 1798	Ruminococcus torques	brown
Seq 1864	Parasutterella excrementihominis	brown
Seq 1980	Brevibacterium	brown
Seq 2011	Ruminococcaceae	brown
Seq 2012	Prevotella buccalis	brown
Seq 2130	Fastidiosipila sanguinis	brown
Seq 2147	Microbacteriaceae	brown
Seq 2302	Clostridium leptum	brown
Seq 2569	Bacteroides ovatus	brown
Seq 2886	Lachnospiraceae	brown
Seq 2922	Facklamia hominis	brown
Seq 3159	Actinomycetales	brown
Seq 3261	Barnesiella intestinihominis	brown
Seq 3264	Blautia glucerasea	brown
Seq 3396	Burkholderiales	brown
Seq 3427	Clostridium XIVa	brown
Seq 3669	Varibaculum cambriense	brown
Seq 3682	Streptophyta	brown
Seq 3874	Clostridium scindens	brown
Seq 3875	Bacteroides	brown
Seq 3876	Oscillibacter	brown
Seq 4006	Flavonifractor plautii	brown
Seq 4008	Nesterenkonia	brown
Seq 4009	Clostridium hathewayi	brown
Seq 4154	Blastococcus aggregatus	brown
Seq 4155	Lachnospiraceae	brown
Seq 4352	Ruminococcaceae	brown
Seq 4353	Eubacterium desmolans	brown
Seq 4564	Alistipes shahii	brown
Seq 4797	Rhodothermaceae	brown
Seq 4799	Erysipelotrichaceae	brown
Seq 5110	Eubacterium rectale	brown
Seq 5516	Ruminococcaceae	brown
Seq 5518	Prevotella buccalis	brown
Seq 5519	Bacteroidetes	brown
Seq 6232	Stenotrophomonas	brown
Seq 6233	Veillonellaceae	brown
Seq 6238	Faecalibacterium prausnitzii	brown
Seq 42	Anaerococcus vaginalis	cyan

Seq_109	<i>Prevotella buccalis</i>	cyan
Seq_111	<i>Prevotella buccalis</i>	cyan
Seq_122	<i>Neisseriaceae</i>	cyan
Seq_123	<i>Peptoniphilus coxii</i>	cyan
Seq_128	<i>Prevotella buccalis</i>	cyan
Seq_130	<i>Porphyromonadaceae</i>	cyan
Seq_199	<i>Actinobaculum schaalii</i>	cyan
Seq_213	<i>Dialister invisus</i>	cyan
Seq_222	<i>Rhodobacteraceae</i>	cyan
Seq_268	<i>Peptoniphilus coxii</i>	cyan
Seq_290	<i>Peptoniphilus coxii</i>	cyan
Seq_342	<i>Acinetobacter baumannii</i>	cyan
Seq_376	<i>Finegoldia magna</i>	cyan
Seq_388	<i>Peptoniphilus</i>	cyan
Seq_391	<i>Trueperella bernardiae</i>	cyan
Seq_417	<i>Peptoniphilus coxii</i>	cyan
Seq_542	<i>Dialister propionificiens</i>	cyan
Seq_543	<i>Streptophyta</i>	cyan
Seq_569	<i>Prevotella corporis</i>	cyan
Seq_620	<i>Olsenella</i>	cyan
Seq_699	<i>Actinomyces neuii</i>	cyan
Seq_705	<i>Actinomyces neuii</i>	cyan
Seq_743	<i>Porphyromonadaceae</i>	cyan
Seq_747	<i>Prevotella buccalis</i>	cyan
Seq_748	<i>Prevotella buccalis</i>	cyan
Seq_755	<i>Empedobacter brevis</i>	cyan
Seq_757	<i>Eremococcus coleocola</i>	cyan
Seq_769	<i>Prevotella buccalis</i>	cyan
Seq_797	<i>Anaerococcus octavius</i>	cyan
Seq_811	<i>Clostridium XVIII</i>	cyan
Seq_853	<i>Pseudomonas</i>	cyan
Seq_1606	<i>Fusobacterium nucleatum</i>	cyan
Seq_1771	<i>Peptoniphilus lacrimalis</i>	cyan
Seq_2026	<i>Sutterella wadsworthensis</i>	cyan
Seq_2230	<i>Arthrobacter</i>	cyan
Seq_2699	<i>Acetobacteraceae</i>	cyan
Seq_2706	<i>Dietzia</i>	cyan
Seq_3006	<i>Cloacibacterium normanense</i>	cyan
Seq_3281	<i>Varibaculum cambriense</i>	cyan
Seq_4192	<i>Olsenella</i>	cyan
Seq_4193	<i>Capnocytophaga gingivalis</i>	cyan
Seq_4194	<i>Murdochiella asaccharolytica</i>	cyan
Seq_4871	<i>Sunxiuqinia</i>	cyan
Seq_5197	<i>Bacteria</i>	cyan
Seq_5680	<i>Hymenobacter</i>	cyan

Seq 6539 <i>Anaerococcus vaginalis</i>	cyan
Seq 6540 <i>Anaerococcus vaginalis</i>	cyan
Seq 6546 <i>Prevotella</i>	cyan
Seq 6548 <i>Clostridiales</i>	cyan
Seq 6549 <i>Anaerococcus octavius</i>	cyan
Seq 6550 <i>Succinivibrindextrinosolvens</i>	cyan
Seq 87 <i>Porphyromonas bennonis</i>	darkgreen
Seq 328 <i>Brevundimonas</i>	darkgreen
Seq 405 <i>Corynebacterium</i>	darkgreen
Seq 451 <i>Staphylococcus</i>	darkgreen
Seq 482 <i>Porphyromonas bennonis</i>	darkgreen
Seq 493 <i>Dialister propionificiens</i>	darkgreen
Seq 844 <i>Corynebacterium imitans</i>	darkgreen
Seq 1030 <i>Faecalibacterium prausnitzii</i>	darkgreen
Seq 1047 <i>Porphyromonas bennonis</i>	darkgreen
Seq 1175 <i>Clostridium XI</i>	darkgreen
Seq 1204 <i>Streptophyta</i>	darkgreen
Seq 1223 <i>Sphingomonadaceae</i>	darkgreen
Seq 1281 <i>Porphyromonas bennonis</i>	darkgreen
Seq 1338 <i>Atopobium vaginae</i>	darkgreen
Seq 1459 <i>Bacteria</i>	darkgreen
Seq 1474 <i>Anaerococcus prevotii</i>	darkgreen
Seq 1588 <i>Actinomycetales</i>	darkgreen
Seq 1691 <i>Prevotella timonensis</i>	darkgreen
Seq 1753 <i>Clostridia</i>	darkgreen
Seq 1823 <i>Peptoniphilus coxii</i>	darkgreen
Seq 1841 <i>GpI</i>	darkgreen
Seq 1922 <i>Sphingomonas</i>	darkgreen
Seq 1962 <i>Sphingomonadaceae</i>	darkgreen
Seq 2001 <i>Corynebacterium imitans</i>	darkgreen
Seq 2037 <i>Bacillus thermoamylovorans</i>	darkgreen
Seq 2064 <i>Finegoldia magna</i>	darkgreen
Seq 2127 <i>Haemophilus</i>	darkgreen
Seq 2128 <i>Acidimicrobiales</i>	darkgreen
Seq 2219 <i>Actinomycetales</i>	darkgreen
Seq 2240 <i>Staphylococcus</i>	darkgreen
Seq 2290 <i>Bacteria</i>	darkgreen
Seq 2339 <i>Porphyromonas bennonis</i>	darkgreen
Seq 2358 <i>Bacteroides</i>	darkgreen
Seq 2624 <i>Eubacterium desmolans</i>	darkgreen
Seq 2717 <i>Rhizobium giardinii</i>	darkgreen
Seq 2816 <i>Massilia timonae</i>	darkgreen
Seq 3105 <i>Varibaculum cambriense</i>	darkgreen
Seq 3206 <i>Bacteria</i>	darkgreen
Seq 3872 <i>Moraxella</i>	darkgreen

Seq 4002 Acidobacteria Gp4	darkgreen
Seq 4559 Propionibacteriaceae	darkgreen
Seq 126 Eubacterium rectale	darkgrey
Seq 157 Anaerococcus senegalensis	darkgrey
Seq 205 Blautia	darkgrey
Seq 227 Lachnospiraceae	darkgrey
Seq 249 Anaerococcus hydrogenalis	darkgrey
Seq 299 Streptococcus	darkgrey
Seq 306 Peptoniphilus coxii	darkgrey
Seq 334 Ruminococcaceae	darkgrey
Seq 383 Peptoniphilus coxii	darkgrey
Seq 410 Porphyromonas bennonis	darkgrey
Seq 477 Brevibacterium paucivorans	darkgrey
Seq 497 Anaerococcus	darkgrey
Seq 511 Turicibacter sanguinis	darkgrey
Seq 535 Anaerococcus prevotii	darkgrey
Seq 692 Anaerococcus	darkgrey
Seq 763 Alistipes putredinis	darkgrey
Seq 1038 Lachnospiraceae	darkgrey
Seq 1065 Peptococcus niger	darkgrey
Seq 1602 Firmicutes	darkgrey
Seq 1729 Bacteroides	darkgrey
Seq 1857 Ruminococcaceae	darkgrey
Seq 2144 Blautia	darkgrey
Seq 2182 Roseburia inulinivorans	darkgrey
Seq 2838 Parabacteroides	darkgrey
Seq 2924 Erysipelotrichaceae	darkgrey
Seq 3039 Bacteroides ovatus	darkgrey
Seq 3088 Clostridium XIVa	darkgrey
Seq 3144 Lachnospiraceae	darkgrey
Seq 3157 Faecalibacterium prausnitzii	darkgrey
Seq 3207 Eggerthella lenta	darkgrey
Seq 3326 Lachnospiraceae	darkgrey
Seq 3373 Asaccharobacter	darkgrey
Seq 3472 Parasutterella excrementihominis	darkgrey
Seq 3557 Acinetobacter	darkgrey
Seq 3667 Blautia faecis	darkgrey
Seq 4497 Ruminococcaceae	darkgrey
Seq 4560 Fastidiosipila sanguinis	darkgrey
Seq 4791 Clostridiales	darkgrey
Seq 6214 Lactobacillales	darkgrey
Seq 6329 Bacteroides vulgatus	darkgrey
Seq 179 Neisseria	darkmagenta
Seq 190 Corynebacterium pseudogenitalium	darkmagenta
Seq 191 Clostridium ruminantium	darkmagenta

Seq 344 Staphylococcus auricularis	darkmagenta
Seq 387 Gallicola	darkmagenta
Seq 438 Porphyromonas uenonis	darkmagenta
Seq 440 Rothia mucilaginosa	darkmagenta
Seq 460 Anaerococcus	darkmagenta
Seq 544 Staphylococcus	darkmagenta
Seq 573 Clostridiales	darkmagenta
Seq 626 Staphylococcus	darkmagenta
Seq 772 Staphylococcus	darkmagenta
Seq 790 Finegoldia magna	darkmagenta
Seq 944 Staphylococcus	darkmagenta
Seq 1099 Streptococcus	darkmagenta
Seq 1205 Staphylococcus	darkmagenta
Seq 1511 Abiotrophia defectiva	darkmagenta
Seq 1553 Helcococcus ovis	darkmagenta
Seq 1557 Atopobium parvulum	darkmagenta
Seq 1595 Corynebacterium	darkmagenta
Seq 1669 Bacteroides vulgatus	darkmagenta
Seq 1733 Finegoldia magna	darkmagenta
Seq 1777 Staphylococcus auricularis	darkmagenta
Seq 3474 Staphylococcus	darkmagenta
Seq 3605 Gaiella occulta	darkmagenta
Seq 4010 Corynebacterium durum	darkmagenta
Seq 4565 Enterobacteriaceae	darkmagenta
Seq 4800 Prevotella disiens	darkmagenta
Seq 4801 Nocardioidea	darkmagenta
Seq 5112 Megasphaera	darkmagenta
Seq 5113 Burkholderiales	darkmagenta
Seq 5114 Sphingobium	darkmagenta
Seq 5524 Lactobacillus reuteri	darkmagenta
Seq 6245 Neisseria	darkmagenta
Seq 45 Acinetobacter	darkolivegreen
Seq 48 Peptoniphilus harei	darkolivegreen
Seq 247 Anaerococcus octavius	darkolivegreen
Seq 363 Acinetobacter ursingii	darkolivegreen
Seq 407 Rothia mucilaginosa	darkolivegreen
Seq 433 Acinetobacter	darkolivegreen
Seq 464 Staphylococcus	darkolivegreen
Seq 513 Staphylococcus	darkolivegreen
Seq 725 Pseudomonas	darkolivegreen
Seq 1034 Anaerococcus octavius	darkolivegreen
Seq 1203 Haemophilus	darkolivegreen
Seq 1302 Massilia timonae	darkolivegreen
Seq 1784 Corynebacterium	darkolivegreen
Seq 1855 Brevibacterium	darkolivegreen

Seq 1933	Porphyromonas	darkolivegreen
Seq 2049	Streptophyta	darkolivegreen
Seq 2227	Prevotella nanceiensis	darkolivegreen
Seq 2233	Truepera radiovictrix	darkolivegreen
Seq 2869	Bosea	darkolivegreen
Seq 3046	Corynebacterium	darkolivegreen
Seq 3106	Nesterenkonia lacusekhoensis	darkolivegreen
Seq 3149	Lactococcus	darkolivegreen
Seq 3162	Amaricoccus	darkolivegreen
Seq 3566	Brachybacterium	darkolivegreen
Seq 4362	Ancylobacter dichloromethanicus	darkolivegreen
Seq 4363	Corynebacterium matruchotii	darkolivegreen
Seq 4364	Aureimonas	darkolivegreen
Seq 4578	Burkholderiales	darkolivegreen
Seq 5138	Sphingobacterium	darkolivegreen
Seq 5573	Blastocatella	darkolivegreen
Seq 6311	Murdochiella asaccharolytica	darkolivegreen
Seq 6312	Spirosoma rigui	darkolivegreen
Seq 6314	Comamonadaceae	darkolivegreen
Seq 6325	Finegoldia magna	darkolivegreen
Seq 6328	Bacillariophyta	darkolivegreen
Seq 258	Corynebacterium	darkorange
Seq 266	Peptoniphilus coxii	darkorange
Seq 293	Akkermansia muciniphila	darkorange
Seq 822	Campylobacter ureolyticus	darkorange
Seq 1019	Corynebacterium	darkorange
Seq 1055	Finegoldia magna	darkorange
Seq 1113	Corynebacterium	darkorange
Seq 1116	Finegoldia magna	darkorange
Seq 1129	Corynebacterium aurimucosum	darkorange
Seq 1209	Anaerococcus	darkorange
Seq 1224	Anaerococcus murdochii	darkorange
Seq 1291	Campylobacter ureolyticus	darkorange
Seq 1299	Staphylococcus	darkorange
Seq 1305	Corynebacterium	darkorange
Seq 1306	Clostridiales Incertae Sedis XI	darkorange
Seq 1342	Corynebacterium jeikeium	darkorange
Seq 1398	Anaerococcus murdochii	darkorange
Seq 1403	Akkermansia muciniphila	darkorange
Seq 1446	Corynebacterium	darkorange
Seq 1487	Corynebacterium	darkorange
Seq 1488	Corynebacterium	darkorange
Seq 1496	Corynebacterium	darkorange
Seq 1547	Corynebacterium	darkorange
Seq 1640	Anaerococcus	darkorange

Seq 1650 Anaerococcus murdochii	darkorange
Seq 1721 Corynebacterium	darkorange
Seq 1797 Prevotella disiens	darkorange
Seq 1818 Corynebacterium	darkorange
Seq 1911 Anaerococcus	darkorange
Seq 1967 Anaerococcus murdochii	darkorange
Seq 1994 Corynebacterium jeikeium	darkorange
Seq 2025 Prevotella bivia	darkorange
Seq 2039 Prevotella disiens	darkorange
Seq 2067 Corynebacterium	darkorange
Seq 2115 Finegoldia magna	darkorange
Seq 2176 Finegoldia magna	darkorange
Seq 2575 Corynebacterium	darkorange
Seq 4402 Lachnospiraceae	darkorange
Seq 151 Anaerococcus octavius	darkred
Seq 216 Negativicoccus succinicivorans	darkred
Seq 252 Clostridium disporicum	darkred
Seq 259 Lactococcus	darkred
Seq 385 Peptoniphilus	darkred
Seq 650 Staphylococcus	darkred
Seq 689 Corynebacterium	darkred
Seq 888 Streptococcus mutans	darkred
Seq 915 Lachnospiraceae	darkred
Seq 1200 Anaerococcus octavius	darkred
Seq 1472 Alphaproteobacteria	darkred
Seq 1563 Staphylococcus	darkred
Seq 1675 Leuconostoc	darkred
Seq 1840 Eubacterium brachy	darkred
Seq 1993 Anaerococcus	darkred
Seq 2006 Staphylococcus	darkred
Seq 2143 Clostridium XIVa	darkred
Seq 2304 Cyanobacteria	darkred
Seq 2489 Lachnospiraceae	darkred
Seq 2600 Microbacteriaceae	darkred
Seq 2920 Anaerococcus vaginalis	darkred
Seq 3111 Leptotrichia shahii	darkred
Seq 3478 Atopobium rimae	darkred
Seq 3483 Corynebacterium aurimucosum	darkred
Seq 3574 Bacteroides coprocola	darkred
Seq 3770 Arthrobacter	darkred
Seq 3892 Selenomonas noxia	darkred
Seq 3893 Pseudonocardiaceae	darkred
Seq 4173 Bacteroides plebeius	darkred
Seq 4315 Blastocatella	darkred
Seq 4838 Prevotella salivae	darkred

Seq 4839 Lachnospiraceae	darkred
Seq 5163 Dorea longicatena	darkred
Seq 5165 Flavobacterium	darkred
Seq 5166 Candidatus Saccharibacteria	darkred
Seq 5167 Flavobacteriaceae	darkred
Seq 5168 Zoogloea	darkred
Seq 5628 Chryseobacterium	darkred
Seq 5629 Xanthomonadaceae	darkred
Seq 5630 Eikenella corrodens	darkred
Seq 6463 Actinobacteria	darkred
Seq 6464 Bacteroidetes	darkred
Seq 71 Prevotella timonensis	darkturquoise
Seq 131 Prevotella timonensis	darkturquoise
Seq 150 Dialister microaerophilus	darkturquoise
Seq 161 Prevotella disiens	darkturquoise
Seq 208 Staphylococcus	darkturquoise
Seq 220 Dialister propionificiens	darkturquoise
Seq 226 Peptostreptococcus anaerobius	darkturquoise
Seq 574 Roseomonas	darkturquoise
Seq 695 Leptotrichia hongkongensis	darkturquoise
Seq 911 Dialister microaerophilus	darkturquoise
Seq 1119 Dialister propionificiens	darkturquoise
Seq 1147 Pantoea	darkturquoise
Seq 1167 Capnocytophaga leadbetteri	darkturquoise
Seq 1534 Aureimonas altamirensis	darkturquoise
Seq 1634 Varibaculum cambriense	darkturquoise
Seq 1636 Prevotella buccalis	darkturquoise
Seq 1904 Leptotrichia shahii	darkturquoise
Seq 1939 Prevotella bergensis	darkturquoise
Seq 2113 Actinomyces	darkturquoise
Seq 2221 Prevotella buccalis	darkturquoise
Seq 2224 Corynebacterium	darkturquoise
Seq 2323 Rhodobacteraceae	darkturquoise
Seq 2447 Clostridium leptum	darkturquoise
Seq 2558 Anaerococcus	darkturquoise
Seq 2570 Gemella morbillorum	darkturquoise
Seq 2660 Janthinobacterium lividum	darkturquoise
Seq 2742 Varibaculum cambriense	darkturquoise
Seq 2846 Stenotrophomonas rhizophila	darkturquoise
Seq 2921 Prevotella melaninogenica	darkturquoise
Seq 3271 Rhizobium	darkturquoise
Seq 3484 Rubellimicrobium aerolatum	darkturquoise
Seq 3485 Pasteurellaceae	darkturquoise
Seq 3772 Streptococcus	darkturquoise
Seq 3930 Vibrio	darkturquoise

Seq 4681 Porphyromonas endodontalis	darkturquoise
Seq 4843 Pedobacter	darkturquoise
Seq 4844 Flavobacterium johnsoniae	darkturquoise
Seq 5169 Novosphingobium	darkturquoise
Seq 5637 Acetobacteraceae	darkturquoise
Seq 6479 Haemophilus parainfluenzae	darkturquoise
Seq 6482 Spartobacteria	darkturquoise
Seq 81 Streptococcus agalactiae	green
Seq 125 Clostridiales	green
Seq 271 Fusobacterium nucleatum	green
Seq 310 Dialister invisus	green
Seq 364 Porphyromonas bennonis	green
Seq 381 Porphyromonas uenonis	green
Seq 390 Corynebacterium	green
Seq 485 Clostridiales	green
Seq 490 Gallicola	green
Seq 512 Lactobacillus	green
Seq 575 Corynebacterium riegelii	green
Seq 631 Corynebacterium	green
Seq 736 Clostridiales	green
Seq 745 Alloprevotella tanneriae	green
Seq 774 Streptophyta	green
Seq 794 Bacteroides dorei	green
Seq 798 Eubacterium rectale	green
Seq 840 Ruminococcaceae	green
Seq 870 Parabacteroides merdae	green
Seq 891 Peptostreptococcus stomatis	green
Seq 905 Staphylococcus	green
Seq 947 Micrococcus lylae	green
Seq 978 Prevotella oris	green
Seq 1096 Atopobium rimae	green
Seq 1270 Lachnospiraceae	green
Seq 1332 Alloprevotella tanneriae	green
Seq 1353 Olsenella uli	green
Seq 1426 Corynebacterium striatum	green
Seq 1442 Prevotella oris	green
Seq 1536 Prevotella oris	green
Seq 1853 Campylobacter gracilis	green
Seq 1923 Anaerococcus obesiensis	green
Seq 1924 Staphylococcus	green
Seq 2003 Dermabacter hominis	green
Seq 2014 Anaerococcus octavius	green
Seq 2065 Veillonella	green
Seq 2108 Lachnoanaerobaculum	green
Seq 2133 Prevotella denticola	green

Seq 2242 <i>Treponema medium</i>	green
Seq 2266 <i>Eubacterium desmolans</i>	green
Seq 2285 <i>Slackia exigua</i>	green
Seq 2293 <i>Nosocomiicoccus ampullae</i>	green
Seq 2454 <i>Porphyromonas somerae</i>	green
Seq 2547 <i>Porphyromonas</i>	green
Seq 2581 <i>Peptoniphilus</i>	green
Seq 2622 <i>Selenomonas infelix</i>	green
Seq 2806 <i>Helcobacillus massiliensis</i>	green
Seq 2963 <i>Ruminococcus callidus</i>	green
Seq 3002 <i>Prevotella stercorea</i>	green
Seq 3051 <i>Selenomonas infelix</i>	green
Seq 3078 <i>Eubacterium sulci</i>	green
Seq 3898 <i>Treponema socranskii</i>	green
Seq 4034 <i>Prevotellaceae</i>	green
Seq 4180 <i>Clostridiales</i>	green
Seq 4181 <i>Facklamia</i>	green
Seq 4389 <i>Ruminococcaceae</i>	green
Seq 4455 <i>Slackia isoflavoniconvertens</i>	green
Seq 4849 <i>Clostridium glycolicum</i>	green
Seq 5176 <i>Clostridiales</i>	green
Seq 5177 <i>Hymenobacter</i>	green
Seq 5571 <i>Clostridium sensu stricto</i>	green
Seq 5648 <i>Leptotrichia</i>	green
Seq 5650 <i>Acidovorax</i>	green
Seq 5654 <i>Prevotella denticola</i>	green
Seq 6309 <i>Porphyromonas somerae</i>	green
Seq 6490 <i>Gp16</i>	green
Seq 6494 <i>Butyricimonas virosa</i>	green
Seq 40 <i>Micrococcus</i>	greenyellow
Seq 43 <i>Micrococcus</i>	greenyellow
Seq 114 <i>Corynebacterium imitans</i>	greenyellow
Seq 136 <i>Corynebacterium coyleae</i>	greenyellow
Seq 200 <i>Janibacter</i>	greenyellow
Seq 236 <i>Acinetobacter</i>	greenyellow
Seq 237 <i>Micrococcus</i>	greenyellow
Seq 331 <i>Arcanobacterium</i>	greenyellow
Seq 370 <i>Brachybacterium</i>	greenyellow
Seq 372 <i>Bacteria</i>	greenyellow
Seq 422 <i>Blautia faecis</i>	greenyellow
Seq 458 <i>Streptophyta</i>	greenyellow
Seq 549 <i>Corynebacterium</i>	greenyellow
Seq 656 <i>Acinetobacter</i>	greenyellow
Seq 746 <i>Corynebacterium</i>	greenyellow
Seq 754 <i>Aerococcaceae</i>	greenyellow

Seq_833_Pseudomonas	greenyellow
Seq_958_Diplorickettsia	greenyellow
Seq_986_Corynebacterium_imitans	greenyellow
Seq_1241_Murdochiella_asaccharolytica	greenyellow
Seq_1276_Corynebacterium	greenyellow
Seq_1367_Anaerococcus	greenyellow
Seq_1369_Acinetobacter	greenyellow
Seq_1544_Acinetobacter	greenyellow
Seq_1601_Helcococcus	greenyellow
Seq_1719_Actinomyces	greenyellow
Seq_1792_Anoxybacillus	greenyellow
Seq_1813_Acinetobacter	greenyellow
Seq_1932_Xanthobacter_autotrophicus	greenyellow
Seq_2043_Chryseobacterium	greenyellow
Seq_2418_Leuconostocarnosum	greenyellow
Seq_3067_Methylobacterium_adhaesivum	greenyellow
Seq_3115_Pseudomonas_stutzeri	greenyellow
Seq_3164_Corynebacterium	greenyellow
Seq_3407_Anaerococcus_prevotii	greenyellow
Seq_3481_Pseudomonas	greenyellow
Seq_3891_Janthinobacterium	greenyellow
Seq_4029_Sphingomonas	greenyellow
Seq_4168_Escherichia/Shigella	greenyellow
Seq_4169_Leucobacter	greenyellow
Seq_4379_Streptococcus	greenyellow
Seq_4831_Pseudomonas	greenyellow
Seq_4832_Flavobacterium_oncorhynchi	greenyellow
Seq_4833_Porphyrimonas	greenyellow
Seq_4834_Pseudomonas	greenyellow
Seq_4835_Stenotrophomonas	greenyellow
Seq_5612_Cellulomonas	greenyellow
Seq_5616_Aeromonas	greenyellow
Seq_5617_Negativicoccus_succinicivorans	greenyellow
Seq_5618_Prevotella	greenyellow
Seq_6445_Clostridiaceae_1	greenyellow
Seq_6446_Prevotella	greenyellow
Seq_6447_Ruminococcaceae	greenyellow
Seq_6448_Novispirillum_ittersonii	greenyellow
Seq_6450_Butyricimonas_virosa	greenyellow
Seq_1_Staphylococcus	grey
Seq_3_Staphylococcus	grey
Seq_4_Finegoldia_magna	grey
Seq_5_Staphylococcus	grey
Seq_6_Staphylococcus	grey
Seq_7_Staphylococcus	grey

Seq 9 Staphylococcus epidermidis	grey
Seq 10 Anaerococcus octavius	grey
Seq 12 Peptoniphilus	grey
Seq 13 Corynebacterium	grey
Seq 14 Corynebacterium	grey
Seq 15 Corynebacterium	grey
Seq 16 Proteus	grey
Seq 18 Peptoniphilus asaccharolyticus	grey
Seq 19 Corynebacterium	grey
Seq 20 Anaerococcus octavius	grey
Seq 21 Campylobacter ureolyticus	grey
Seq 22 Dolosigranulum pigrum	grey
Seq 24 Peptoniphilus lacrimalis	grey
Seq 25 Corynebacterium	grey
Seq 26 Actinomycetales	grey
Seq 27 Moraxella nonliquefaciens	grey
Seq 28 Corynebacterium	grey
Seq 31 Corynebacterium	grey
Seq 33 Staphylococcus	grey
Seq 34 Clostridiales	grey
Seq 36 Staphylococcus	grey
Seq 44 Porphyromonas bennonis	grey
Seq 47 Streptococcus	grey
Seq 49 Actinomycetales	grey
Seq 53 Proteus	grey
Seq 54 Staphylococcus hominis	grey
Seq 57 Peptoniphilus coxii	grey
Seq 59 Corynebacterium	grey
Seq 61 Anaerococcus murdochii	grey
Seq 68 Anaerococcus	grey
Seq 69 Corynebacterium	grey
Seq 72 Peptoniphilus duerdenii	grey
Seq 73 Corynebacterium	grey
Seq 80 Porphyromonas bennonis	grey
Seq 83 Staphylococcus epidermidis	grey
Seq 86 Porphyromonas bennonis	grey
Seq 96 Streptococcus	grey
Seq 101 Porphyromonas somerae	grey
Seq 107 Streptococcus sanguinis	grey
Seq 112 Corynebacterium pseudogenitalium	grey
Seq 120 Corynebacterium	grey
Seq 121 Prevotella corporis	grey
Seq 138 Anaerococcus prevotii	grey
Seq 141 Fusobacterium nucleatum	grey
Seq 152 Sneathia	grey

Seq 158 Staphylococcus epidermidis	grey
Seq 159 Staphylococcus	grey
Seq 165 Staphylococcus	grey
Seq 171 Dolosigranulum pigrum	grey
Seq 173 Fusobacterium nucleatum	grey
Seq 175 Prevotella corporis	grey
Seq 177 Dolosigranulum pigrum	grey
Seq 182 Anaeroglobus geminatus	grey
Seq 186 Anaerococcus octavius	grey
Seq 192 Dermabacter hominis	grey
Seq 193 Prevotella timonensis	grey
Seq 194 Facklamia	grey
Seq 206 Actinomyces neuii	grey
Seq 209 Corynebacterium	grey
Seq 210 Gemella haemolysans	grey
Seq 214 Peptoniphilus coxii	grey
Seq 232 Campylobacter curvus	grey
Seq 240 Prevotella denticola	grey
Seq 241 Ruminococcaceae	grey
Seq 243 Porphyromonas bennonis	grey
Seq 245 Corynebacterium	grey
Seq 254 Facklamia languida	grey
Seq 255 Corynebacterium	grey
Seq 257 Staphylococcus	grey
Seq 263 Corynebacterium	grey
Seq 270 Streptophyta	grey
Seq 272 Dolosigranulum pigrum	grey
Seq 275 Clostridiales	grey
Seq 276 Anaerococcus octavius	grey
Seq 280 Aerococcus	grey
Seq 283 Porphyromonas bennonis	grey
Seq 303 Corynebacterium kroppenstedtii	grey
Seq 309 Clostridium sensu stricto	grey
Seq 317 Staphylococcus	grey
Seq 320 Faecalibacterium prausnitzii	grey
Seq 324 Mobiluncus curtisii	grey
Seq 325 Corynebacterium	grey
Seq 340 Finegoldia magna	grey
Seq 343 Actinomyces radingae	grey
Seq 345 Porphyromonas bennonis	grey
Seq 350 Prevotella timonensis	grey
Seq 351 Corynebacterium kroppenstedtii	grey
Seq 354 Actinomycetales	grey
Seq 355 Prevotella timonensis	grey
Seq 360 Corynebacterium	grey

Seq 362	Prevotella denticola	grey
Seq 366	Clostridiales	grey
Seq 373	Prevotella buccalis	grey
Seq 377	Prevotella oris	grey
Seq 378	Prevotella bergensis	grey
Seq 380	Finegoldia magna	grey
Seq 384	Streptococcus	grey
Seq 393	Prevotella buccalis	grey
Seq 396	Chryseobacterium	grey
Seq 401	Corynebacterium	grey
Seq 402	Dolosigranulum pigrum	grey
Seq 404	Atopobium minutum	grey
Seq 411	Neisseria	grey
Seq 427	Negativicoccus succinicivorans	grey
Seq 429	Enhydrobacter	grey
Seq 431	Facklamia languida	grey
Seq 432	Enterobacteriaceae	grey
Seq 436	Porphyromonas uenonis	grey
Seq 449	Prevotella oris	grey
Seq 456	Staphylococcus	grey
Seq 467	Brochothrix thermosphacta	grey
Seq 470	Negativicoccus succinicivorans	grey
Seq 488	Finegoldia magna	grey
Seq 489	Prevotella oris	grey
Seq 494	Prevotella oris	grey
Seq 495	Haemophilus	grey
Seq 507	Corynebacterium	grey
Seq 514	Finegoldia magna	grey
Seq 515	Prevotella denticola	grey
Seq 516	Fusobacterium nucleatum	grey
Seq 521	Staphylococcus	grey
Seq 525	Staphylococcus	grey
Seq 526	Gordonia	grey
Seq 527	Coprococcus comes	grey
Seq 532	Paracoccus	grey
Seq 533	Staphylococcus	grey
Seq 536	Staphylococcus epidermidis	grey
Seq 540	Corynebacterium	grey
Seq 546	Enterobacteriaceae	grey
Seq 554	Enterobacter	grey
Seq 561	Corynebacterium mucifaciens	grey
Seq 565	Dialister propionificiens	grey
Seq 567	Corynebacterium	grey
Seq 571	Prevotella bergensis	grey
Seq 579	Enterobacteriaceae	grey

Seq 585	<i>Corynebacterium kroppenstedtii</i>	grey
Seq 589	<i>Corynebacterium kroppenstedtii</i>	grey
Seq 591	<i>Sphingomonas</i>	grey
Seq 592	<i>Finegoldia magna</i>	grey
Seq 593	<i>Lactobacillus iners</i>	grey
Seq 594	<i>Fusobacterium nucleatum</i>	grey
Seq 601	<i>Corynebacterium durum</i>	grey
Seq 607	<i>Leptotrichia</i>	grey
Seq 608	<i>Corynebacterium jeikeium</i>	grey
Seq 612	<i>Petrobacter succinatimandens</i>	grey
Seq 614	<i>Veillonella atypica</i>	grey
Seq 623	<i>Dialister pneumosintes</i>	grey
Seq 627	<i>Porphyromonas catoniae</i>	grey
Seq 628	<i>Negativicoccus succinicivorans</i>	grey
Seq 630	<i>Bifidobacterium breve</i>	grey
Seq 640	<i>Micrococcaceae</i>	grey
Seq 649	<i>Haemophilus parainfluenzae</i>	grey
Seq 652	<i>Corynebacterium</i>	grey
Seq 654	<i>Veillonella parvula</i>	grey
Seq 657	<i>Lactobacillus</i>	grey
Seq 662	<i>Xanthomonadaceae</i>	grey
Seq 666	<i>Corynebacterium</i>	grey
Seq 669	<i>Staphylococcus</i>	grey
Seq 671	<i>Staphylococcus</i>	grey
Seq 673	<i>Staphylococcus</i>	grey
Seq 674	<i>Anaerococcus octavius</i>	grey
Seq 679	<i>Fastidiosipila sanguinis</i>	grey
Seq 686	<i>Murdochella asaccharolytica</i>	grey
Seq 687	<i>Acinetobacter johnsonii</i>	grey
Seq 688	<i>Staphylococcus</i>	grey
Seq 697	<i>Parvimonas micra</i>	grey
Seq 700	<i>Porphyromonas bennonis</i>	grey
Seq 702	<i>Staphylococcus</i>	grey
Seq 710	<i>Peptoniphilus</i>	grey
Seq 711	<i>Peptoniphilus coxii</i>	grey
Seq 715	<i>Actinobacteria</i>	grey
Seq 717	<i>Bacillus thermoamylovorans</i>	grey
Seq 718	<i>Murdochella asaccharolytica</i>	grey
Seq 721	<i>Lachnospiraceae</i>	grey
Seq 729	<i>Staphylococcus</i>	grey
Seq 740	<i>Corynebacterium</i>	grey
Seq 750	<i>Staphylococcus</i>	grey
Seq 759	<i>Corynebacterium imitans</i>	grey
Seq 760	<i>Staphylococcus</i>	grey
Seq 762	<i>Hydrogenophilus</i>	grey

Seq 766 <i>Fusobacterium nucleatum</i>	grey
Seq 767 <i>Fusobacterium nucleatum</i>	grey
Seq 782 <i>Anaerococcus</i>	grey
Seq 787 <i>Porphyromonas bennonis</i>	grey
Seq 792 <i>Lactobacillus iners</i>	grey
Seq 796 <i>Tetracoccus cechii</i>	grey
Seq 813 <i>Escherichia/Shigella</i>	grey
Seq 819 <i>Acinetobacter</i>	grey
Seq 826 <i>Pseudomonas</i>	grey
Seq 828 <i>Anaerococcus prevotii</i>	grey
Seq 829 Clostridiales	grey
Seq 831 <i>Corynebacterium</i>	grey
Seq 849 <i>Actinomyces</i>	grey
Seq 854 <i>Schlegelella aquatica</i>	grey
Seq 869 <i>Anaerococcus prevotii</i>	grey
Seq 874 <i>Gallicola</i>	grey
Seq 879 <i>Varibaculum cambriense</i>	grey
Seq 883 <i>Helcococcus sueciensis</i>	grey
Seq 889 <i>Acinetobacter</i>	grey
Seq 899 <i>Neisseria elongata</i>	grey
Seq 906 <i>Haemophilus</i>	grey
Seq 917 <i>Staphylococcus</i>	grey
Seq 924 <i>Corynebacterium</i>	grey
Seq 928 <i>Actinomyces europaeus</i>	grey
Seq 929 <i>Varibaculum cambriense</i>	grey
Seq 935 Clostridiales	grey
Seq 941 <i>Actinobaculum schaalii</i>	grey
Seq 952 <i>Coprococcus catus</i>	grey
Seq 953 <i>Veillonella atypica</i>	grey
Seq 954 <i>Anaerococcus octavius</i>	grey
Seq 969 <i>Carnobacterium</i>	grey
Seq 972 Planctomycetaceae	grey
Seq 973 <i>Prevotella bergensis</i>	grey
Seq 989 <i>Corynebacterium</i>	grey
Seq 994 <i>Porphyromonas</i>	grey
Seq 996 <i>Corynebacterium</i>	grey
Seq 1002 <i>Actinomyces turicensis</i>	grey
Seq 1011 Clostridiales	grey
Seq 1013 <i>Pseudomonas</i>	grey
Seq 1015 <i>Pseudomonas</i>	grey
Seq 1023 <i>Aerococcus sanguinicola</i>	grey
Seq 1025 <i>Prevotella timonensis</i>	grey
Seq 1032 <i>Porphyromonas</i>	grey
Seq 1036 <i>Staphylococcus</i>	grey
Seq 1042 <i>Pseudomonas</i>	grey

Seq_1043	Staphylococcus	grey
Seq_1045	Staphylococcus	grey
Seq_1051	Veillonella parvula	grey
Seq_1052	Kocuria	grey
Seq_1070	Corynebacterium jeikeium	grey
Seq_1075	Pseudomonas	grey
Seq_1080	Aeromonas	grey
Seq_1083	Peptoniphilus	grey
Seq_1095	Dialister microaerophilus	grey
Seq_1101	Dermabacter hominis	grey
Seq_1107	Rhizobium	grey
Seq_1108	Proteus	grey
Seq_1109	Anaerococcus	grey
Seq_1121	Prevotella timonensis	grey
Seq_1133	Chryseobacterium	grey
Seq_1138	Corynebacterium amycolatum	grey
Seq_1143	Peptostreptococcus stomatis	grey
Seq_1159	Helcococcus	grey
Seq_1170	Fusobacterium nucleatum	grey
Seq_1179	Peptoniphilus asaccharolyticus	grey
Seq_1184	Paracoccus	grey
Seq_1190	Murdochiella asaccharolytica	grey
Seq_1197	Peptococcus niger	grey
Seq_1206	Dialister propionicifaciens	grey
Seq_1211	Enterobacter	grey
Seq_1218	Staphylococcus	grey
Seq_1219	Staphylococcus	grey
Seq_1222	Prevotella corporis	grey
Seq_1231	Negativicoccus succinicivorans	grey
Seq_1239	Methylobacterium radiotolerans	grey
Seq_1249	Staphylococcaceae	grey
Seq_1250	Deinococcus	grey
Seq_1251	Staphylococcus	grey
Seq_1260	Brevibacterium paucivorans	grey
Seq_1263	Prevotella bivia	grey
Seq_1271	Proteus mirabilis	grey
Seq_1273	Actinobaculum schaalii	grey
Seq_1278	Corynebacterium	grey
Seq_1288	Microbacteriaceae	grey
Seq_1289	Corynebacterium	grey
Seq_1301	Alishewanella jeotgali	grey
Seq_1318	Porphyromonas asaccharolytica	grey
Seq_1319	Clostridiales Incertae Sedis XI	grey
Seq_1320	Corynebacterium	grey
Seq_1322	Staphylococcus epidermidis	grey

Seq_1326	Flavobacteriaceae	grey
Seq_1330	Peptoniphilus duerdenii	grey
Seq_1334	Staphylococcus	grey
Seq_1343	Aerococcus urinae	grey
Seq_1352	Veillonella dispar	grey
Seq_1360	Anaerococcus octavius	grey
Seq_1364	Prevotella denticola	grey
Seq_1366	Streptophyta	grey
Seq_1374	Luteimonas	grey
Seq_1375	Corynebacterium	grey
Seq_1377	Moraxella	grey
Seq_1392	Peptococcus niger	grey
Seq_1393	Haemophilus parainfluenzae	grey
Seq_1420	Corynebacterium riegelii	grey
Seq_1422	Alishewanella aestuarii	grey
Seq_1428	Gemella haemolysans	grey
Seq_1429	Peptoniphilus	grey
Seq_1433	Veillonella	grey
Seq_1434	Veillonella dispar	grey
Seq_1448	Staphylococcus	grey
Seq_1463	Negativicoccus succinicivorans	grey
Seq_1466	Staphylococcus	grey
Seq_1473	Staphylococcus	grey
Seq_1485	Gp6	grey
Seq_1537	Corynebacterium	grey
Seq_1548	Clostridiales Incertae Sedis XI	grey
Seq_1566	Clostridiales	grey
Seq_1587	Facklamia ignava	grey
Seq_1612	Staphylococcus epidermidis	grey
Seq_1617	Streptococcus	grey
Seq_1629	Corynebacterium	grey
Seq_1630	Staphylococcus pettenkoferi	grey
Seq_1631	Campylobacter hominis	grey
Seq_1642	Ruminococcaceae	grey
Seq_1649	Finegoldia magna	grey
Seq_1665	Micrococcaceae	grey
Seq_1683	Aerococcus christensenii	grey
Seq_1699	Moraxella lincolnii	grey
Seq_1711	Prevotella	grey
Seq_1720	Campylobacter ureolyticus	grey
Seq_1742	Actinomyces gerencseriae	grey
Seq_1752	Prevotella buccalis	grey
Seq_1755	Prevotella bergensis	grey
Seq_1756	Corynebacterium aurimucosum	grey
Seq_1772	Negativicoccus succinicivorans	grey

Seq_1775	Streptophyta	grey
Seq_1786	Novosphingobium	grey
Seq_1787	Staphylococcus pettenkoferi	grey
Seq_1805	Moraxella	grey
Seq_1814	Prevotella oulorum	grey
Seq_1824	Acinetobacter	grey
Seq_1828	Pyramidobacter piscolens	grey
Seq_1833	Cyanobacteria	grey
Seq_1842	Prevotella bergensis	grey
Seq_1843	Corynebacterium pseudogenitalium	grey
Seq_1844	Moraxella lincolnii	grey
Seq_1850	Clostridiales	grey
Seq_1852	Schlegelella aquatica	grey
Seq_1874	Xanthomonadaceae	grey
Seq_1878	Skermanella aerolata	grey
Seq_1880	Xanthobacter	grey
Seq_1882	Clostridiales	grey
Seq_1884	Enterococcus cecorum	grey
Seq_1908	Prevotella	grey
Seq_1913	Stenotrophomonas	grey
Seq_1926	Dialister propionicifaciens	grey
Seq_1936	Finegoldia magna	grey
Seq_1957	Staphylococcus epidermidis	grey
Seq_1964	Facklamia languida	grey
Seq_1966	Staphylococcus	grey
Seq_1979	Aerococcus	grey
Seq_1981	Anaerococcus octavius	grey
Seq_1992	Hydrogenophilus	grey
Seq_1999	Flavobacteriaceae	grey
Seq_2002	Kocuria kristinae	grey
Seq_2007	Brevibacterium	grey
Seq_2018	Pseudomonas	grey
Seq_2020	Anaerococcus murdochii	grey
Seq_2023	Anoxybacillus	grey
Seq_2028	Leptotrichia buccalis	grey
Seq_2038	Veillonella parvula	grey
Seq_2042	Luteimonas	grey
Seq_2055	Corynebacterium confusum	grey
Seq_2080	Haemophilus parainfluenzae	grey
Seq_2083	Anaerococcus octavius	grey
Seq_2089	Dialister	grey
Seq_2094	Capnocytophaga gingivalis	grey
Seq_2099	Veillonella	grey
Seq_2109	Actinomyces naeslundii	grey
Seq_2120	Jeotgalicoccus	grey

Seq 2129 <i>Corynebacterium</i>	grey
Seq 2134 <i>Propionibacterium granulosum</i>	grey
Seq 2135 <i>Anaerococcus octavius</i>	grey
Seq 2142 <i>Acinetobacter johnsonii</i>	grey
Seq 2168 <i>Proteobacteria</i>	grey
Seq 2203 <i>Facklamia ignava</i>	grey
Seq 2206 <i>Clostridium sensu stricto</i>	grey
Seq 2220 <i>Clostridium disporicum</i>	grey
Seq 2241 <i>Streptococcus</i>	grey
Seq 2243 <i>Staphylococcus epidermidis</i>	grey
Seq 2244 <i>Anaerococcus octavius</i>	grey
Seq 2274 <i>Anaerococcus</i>	grey
Seq 2286 <i>Facklamia</i>	grey
Seq 2307 <i>Actinomycetales</i>	grey
Seq 2310 <i>Staphylococcus</i>	grey
Seq 2311 <i>Prevotella timonensis</i>	grey
Seq 2326 <i>Prevotella buccalis</i>	grey
Seq 2327 <i>Porphyromonadaceae</i>	grey
Seq 2333 <i>Peptococcus niger</i>	grey
Seq 2342 <i>Atopobium minutum</i>	grey
Seq 2356 <i>Pantoea agglomerans</i>	grey
Seq 2359 <i>Marmoricola</i>	grey
Seq 2365 <i>Porphyromonas uenonis</i>	grey
Seq 2393 <i>Clostridiales</i>	grey
Seq 2395 <i>Bacteria</i>	grey
Seq 2397 <i>Prevotella</i>	grey
Seq 2408 <i>Campylobacter gracilis</i>	grey
Seq 2411 <i>Anaerococcus</i>	grey
Seq 2453 <i>Staphylococcaceae</i>	grey
Seq 2455 <i>Staphylococcus lugdunensis</i>	grey
Seq 2469 <i>Facklamia languida</i>	grey
Seq 2470 <i>Porphyromonas somerae</i>	grey
Seq 2472 <i>Peptoniphilus coxii</i>	grey
Seq 2492 <i>Photobacterium phosphoreum</i>	grey
Seq 2494 <i>Corynebacterium</i>	grey
Seq 2496 <i>Kingella oralis</i>	grey
Seq 2500 <i>Streptococcus</i>	grey
Seq 2518 <i>Morganella morganii</i>	grey
Seq 2521 <i>Staphylococcus aureus</i>	grey
Seq 2534 <i>Ethanoligenens</i>	grey
Seq 2541 <i>Anaerococcus octavius</i>	grey
Seq 2566 <i>Lachnospiraceae</i>	grey
Seq 2567 <i>Facklamia languida</i>	grey
Seq 2578 <i>Staphylococcus epidermidis</i>	grey
Seq 2598 <i>Corynebacterium coyleae</i>	grey

Seq 2606 Bacteria	grey
Seq 2618 Porphyromonas asaccharolytica	grey
Seq 2625 Corynebacterium	grey
Seq 2626 Corynebacterium amycolatum	grey
Seq 2627 Acinetobacter lwoffii	grey
Seq 2630 Corynebacterium imitans	grey
Seq 2650 Facklamia languida	grey
Seq 2654 Bacteroidetes	grey
Seq 2662 Rheinheimera perlucida	grey
Seq 2684 Porphyromonas asaccharolytica	grey
Seq 2687 Facklamia languida	grey
Seq 2696 Veillonella	grey
Seq 2697 Cardiobacterium hominis	grey
Seq 2724 Nesterenkonia	grey
Seq 2729 Aeromonas	grey
Seq 2743 Aerococcus urinae	grey
Seq 2751 Ruminococcaceae	grey
Seq 2769 Streptococcus	grey
Seq 2770 Anaerococcus octavius	grey
Seq 2804 Porphyromonas	grey
Seq 2809 Streptococcus	grey
Seq 2840 Conexibacter	grey
Seq 2841 Lachnospiraceae	grey
Seq 2842 Porphyromonadaceae	grey
Seq 2843 Bacteroidales	grey
Seq 2848 Corynebacterium jeikeium	grey
Seq 2850 Mesorhizobium	grey
Seq 2877 Streptophyta	grey
Seq 2916 Prevotella intermedia	grey
Seq 2919 Aerococcus sanguinicola	grey
Seq 2940 Streptophyta	grey
Seq 2951 Peptoniphilus	grey
Seq 2952 Prevotella buccalis	grey
Seq 2998 Blautia luti	grey
Seq 3005 Peptoniphilus coxii	grey
Seq 3008 Brevundimonas	grey
Seq 3009 Pasteurellaceae	grey
Seq 3014 Capnocytophaga leadbetteri	grey
Seq 3045 Roseomonas vinacea	grey
Seq 3049 Peptoniphilus koenoenieniae	grey
Seq 3054 Clostridiales Incertae Sedis XI	grey
Seq 3055 Brachybacterium	grey
Seq 3057 Brevibacterium	grey
Seq 3108 Corynebacterium frankenforstense	grey
Seq 3112 Pseudomonas	grey

Seq 3139 Sphingomonadaceae	grey
Seq 3209 Prevotellaceae	grey
Seq 3210 Megasphaera micronuciformis	grey
Seq 3219 Prevotella timonensis	grey
Seq 3259 Oligella urethralis	grey
Seq 3268 Dermabacter hominis	grey
Seq 3329 Blautia faecis	grey
Seq 3330 Campylobacter curvus	grey
Seq 3336 Micrococcaceae	grey
Seq 3337 Anaeroglobus geminatus	grey
Seq 3340 Corynebacterium	grey
Seq 3385 Brevibacterium	grey
Seq 3393 Prevotella	grey
Seq 3395 Actinomyces	grey
Seq 3398 Actinomycetales	grey
Seq 3400 Prevotella buccalis	grey
Seq 3401 Rhizobium	grey
Seq 3408 Haemophilus parainfluenzae	grey
Seq 3416 Rothia mucilaginosa	grey
Seq 3462 Prevotella	grey
Seq 3465 Lysobacter gummosus	grey
Seq 3473 Nocardioidea	grey
Seq 3475 Actinobaculum schaalii	grey
Seq 3480 Petrobacter succinatimandens	grey
Seq 3487 Bacteroidetes	grey
Seq 3489 Anaerococcus	grey
Seq 3553 Scardovia wiggsiae	grey
Seq 3562 Prevotella bergensis	grey
Seq 3564 Ruminococcus	grey
Seq 3567 Eubacterium rectale	grey
Seq 3570 Porphyromonas benzonis	grey
Seq 3583 Rhodobacteraceae	grey
Seq 3584 Moraxellaceae	grey
Seq 3585 Prevotella oulorum	grey
Seq 3671 Helcococcus	grey
Seq 3673 Corynebacterium	grey
Seq 3675 Dialister propionificiens	grey
Seq 3759 Nocardioidea islandensis	grey
Seq 3760 Sphingomonas	grey
Seq 3777 Bacteroides uniformis	grey
Seq 3782 Peptoniphilus	grey
Seq 3783 Rhizobium giardinii	grey
Seq 3886 Corynebacterium	grey
Seq 3903 Corynebacterium doosanense	grey
Seq 3907 Aquabacterium	grey

Seq 4007 <i>Dialister propionificiens</i>	grey
Seq 4012 <i>Brevibacterium</i>	grey
Seq 4013 <i>Prevotella</i>	grey
Seq 4014 <i>Selenomonas noxia</i>	grey
Seq 4015 <i>Prevotella oris</i>	grey
Seq 4017 <i>Stenotrophomonas maltophilia</i>	grey
Seq 4022 <i>Lachnospiraceae</i>	grey
Seq 4023 <i>Ruminococcaceae</i>	grey
Seq 4024 <i>Lachnoanaerobaculum saburreum</i>	grey
Seq 4031 <i>Enhydrobacter</i>	grey
Seq 4038 <i>Actinomyces odontolyticus</i>	grey
Seq 4058 <i>Treponema amylovorum</i>	grey
Seq 4077 <i>Bacteria</i>	grey
Seq 4079 <i>Chloroplast</i>	grey
Seq 4158 <i>Murdochiella asaccharolytica</i>	grey
Seq 4159 <i>Anaerococcus vaginalis</i>	grey
Seq 4160 <i>Megasphaera elsdenii</i>	grey
Seq 4164 <i>Pantoea</i>	grey
Seq 4167 <i>Bacteria</i>	grey
Seq 4183 <i>Prevotella buccalis</i>	grey
Seq 4186 <i>Akkermansia muciniphila</i>	grey
Seq 4190 <i>Treponema lecithinolyticum</i>	grey
Seq 4201 <i>Firmicutes</i>	grey
Seq 4203 <i>Prevotella melaninogenica</i>	grey
Seq 4204 <i>Clostridiales Incertae Sedis XI</i>	grey
Seq 4205 <i>Clostridiales</i>	grey
Seq 4210 <i>Actinomycetales</i>	grey
Seq 4211 <i>Porphyromonas catoniae</i>	grey
Seq 4349 <i>Rathayibacter</i>	grey
Seq 4365 <i>Blautia</i>	grey
Seq 4373 <i>Neisseria bacilliformis</i>	grey
Seq 4376 <i>Lactobacillus</i>	grey
Seq 4384 <i>Capnocytophaga sputigena</i>	grey
Seq 4385 <i>Gemella palaticanis</i>	grey
Seq 4386 <i>Porphyromonas catoniae</i>	grey
Seq 4390 <i>Streptococcus agalactiae</i>	grey
Seq 4392 <i>Lactobacillus jensenii</i>	grey
Seq 4398 <i>Finnegoldia magna</i>	grey
Seq 4417 <i>Staphylococcus</i>	grey
Seq 4461 <i>Campylobacter ureolyticus</i>	grey
Seq 4568 <i>Mogibacterium timidum</i>	grey
Seq 4569 <i>Facklamia</i>	grey
Seq 4577 <i>Prevotella</i>	grey
Seq 4583 <i>Clostridiales</i>	grey
Seq 4587 <i>Phyllobacteriaceae</i>	grey

Seq 4588 Prevotella timonensis	grey
Seq 4599 Actinomyces odontolyticus	grey
Seq 4611 Lysobacter	grey
Seq 4613 Prevotella copri	grey
Seq 4614 Chryseobacterium	grey
Seq 4615 Cellulomonas	grey
Seq 4616 Alphaproteobacteria	grey
Seq 4623 Psychrobacter	grey
Seq 4645 Clostridiales Incertae Sedis XI	grey
Seq 4766 Mogibacterium	grey
Seq 4785 Parvimonas micra	grey
Seq 4802 Ruminococcus torques	grey
Seq 4808 Anaerococcus murdochii	grey
Seq 4809 Anaerococcus	grey
Seq 4821 Micrococcaceae	grey
Seq 4855 Rothia mucilaginosa	grey
Seq 4856 Propionibacterium acnes	grey
Seq 4857 Oligella urethralis	grey
Seq 4861 Corynebacterium	grey
Seq 4865 Rhizobiales	grey
Seq 4882 Prevotellaceae	grey
Seq 4883 Brevibacterium	grey
Seq 4884 Moryella indoligenes	grey
Seq 4885 Rhodobacteraceae	grey
Seq 4893 Firmicutes	grey
Seq 5105 Howardella ureilytica	grey
Seq 5106 Acinetobacter	grey
Seq 5107 Peptoniphilus lacrimalis	grey
Seq 5118 Bifidobacterium	grey
Seq 5119 Bacteria	grey
Seq 5120 Atopobium minutum	grey
Seq 5128 Luteibacter rhizovicius	grey
Seq 5135 Jeotgaliococcus pinnipedialis	grey
Seq 5137 Capnocytophaga ochracea	grey
Seq 5146 Selenomonas noxia	grey
Seq 5147 Porphyromonas	grey
Seq 5149 Bacteria	grey
Seq 5150 Mogibacterium	grey
Seq 5151 Ilumatobacter	grey
Seq 5162 Fusobacterium	grey
Seq 5188 Parvimonas micra	grey
Seq 5191 Bifidobacterium longum	grey
Seq 5198 Ruminococcus flavefaciens	grey
Seq 5207 Facklamia languida	grey
Seq 5209 Veillonella parvula	grey

Seq_5213	<i>Staphylococcus lugdunensis</i>	grey
Seq_5214	<i>Staphylococcus</i>	grey
Seq_5219	<i>Nocardioides</i>	grey
Seq_5221	<i>Neisseriaceae</i>	grey
Seq_5532	<i>Corynebacterium</i>	grey
Seq_5535	<i>Bacteria</i>	grey
Seq_5536	<i>Bacteria</i>	grey
Seq_5538	<i>Corynebacterium</i>	grey
Seq_5541	<i>Staphylococcus aureus</i>	grey
Seq_5542	<i>Ruminococcaceae</i>	grey
Seq_5549	<i>Bacteria</i>	grey
Seq_5550	<i>Bacteroidetes</i>	grey
Seq_5552	<i>Anaerostipes hadrus</i>	grey
Seq_5555	<i>Pseudoxanthomonas taiwanensis</i>	grey
Seq_5561	<i>Alloprevotella rava</i>	grey
Seq_5562	<i>Mycoplasma salivarium</i>	grey
Seq_5566	<i>Clostridiales</i>	grey
Seq_5567	<i>Prevotella oulorum</i>	grey
Seq_5568	<i>Clostridiales</i>	grey
Seq_5569	<i>Prevotella</i>	grey
Seq_5600	<i>Hymenobacter</i>	grey
Seq_5609	<i>Porphyromonas</i>	grey
Seq_5611	<i>Porphyromonas</i>	grey
Seq_5625	<i>Flavobacterium</i>	grey
Seq_5626	<i>Barnesiella</i>	grey
Seq_5627	<i>Porphyromonas circumdentaria</i>	grey
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Seq_5681	<i>Pseudomonas</i>	grey
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Seq_5709	<i>Ruminococcaceae</i>	grey
Seq_5711	<i>Conexibacter arvalis</i>	grey
Seq_5713	<i>Bacillus circulans</i>	grey
Seq_5715	<i>Flavobacterium noncentrifugens</i>	grey
Seq_5716	<i>Staphylococcus</i>	grey
Seq_5717	<i>Bacteria</i>	grey
Seq_5723	<i>Clostridia</i>	grey
Seq_5725	<i>Psychrobacter</i>	grey
Seq_5726	<i>Bacteria</i>	grey
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Seq_6227	<i>Ruminococcaceae</i>	grey
Seq_6228	<i>Sphingomonas</i>	grey
Seq_6259	<i>Prevotella corporis</i>	grey
Seq_6262	<i>Anaeroglobus geminatus</i>	grey

Seq 6269 Porphyromonas uenonis	grey
Seq 6273 Clostridiales	grey
Seq 6276 Firmicutes	grey
Seq 6286 Succinivibrionasolvens	grey
Seq 6288 Butyrivibrio	grey
Seq 6289 Actinomycetales	grey
Seq 6290 Murdochiella asaccharolytica	grey
Seq 6292 Actinomycetales	grey
Seq 6298 Lachnospiraceae	grey
Seq 6302 Bacteroidetes	grey
Seq 6336 Oribacterium sinus	grey
Seq 6381 Firmicutes	grey
Seq 6392 Treponema socranskii	grey
Seq 6397 Stenotrophomonas	grey
Seq 6398 Bacteria	grey
Seq 6403 Brevundimonas	grey
Seq 6404 Gammaproteobacteria	grey
Seq 6408 Ruminococcus champanellensis	grey
Seq 6437 Peptoniphilus lacrimalis	grey
Seq 6439 Porphyromonas bennonis	grey
Seq 6442 Clostridiales	grey
Seq 6462 Clostridiales	grey
Seq 6495 Bacteria	grey
Seq 6496 Bacteria	grey
Seq 6500 Prevotella copri	grey
Seq 6504 Barnesiella intestinihominis	grey
Seq 6534 Lactobacillus algidus	grey
Seq 6538 Streptophyta	grey
Seq 6541 Actinomycetales	grey
Seq 6542 Deinococcus	grey
Seq 6545 Sphingobacterium	grey
Seq 6567 Enterobacteriaceae	grey
Seq 6568 Selenomonas artemidis	grey
Seq 6572 Sutterella stercoricanis	grey
Seq 6576 Clostridium XIVa	grey
Seq 6580 Staphylococcaceae	grey
Seq 6581 Cyanobacteria	grey
Seq 6583 Clostridiales	grey
Seq 6584 Bacteria	grey
Seq 6590 Prevotella	grey
Seq 6591 Candidatus Saccharibacteria	grey
Seq 6593 Porphyromonas endodontalis	grey
Seq 6610 Clostridiales	grey
Seq 6611 Firmicutes	grey
Seq 6614 Bacteria	grey

Seq 6615 Enterobacteriaceae	grey
Seq 6618 Ilumatobacter	grey
Seq 6620 Porphyromonas	grey
Seq 6621 Firmicutes	grey
Seq 6651 Actinomycetales	grey
Seq 6670 Staphylococcus	grey
Seq 6675 Stenotrophomonas maltophilia	grey
Seq 23 Lactobacillus iners	grey60
Seq 46 Anaerococcus octavius	grey60
Seq 79 Staphylococcus	grey60
Seq 93 Pseudomonas	grey60
Seq 143 Faecalibacterium prausnitzii	grey60
Seq 149 Atopobium vaginae	grey60
Seq 155 Dermacoccus nishinomiyaensis	grey60
Seq 188 Dermacoccus	grey60
Seq 423 Corynebacterium pseudogenitalium	grey60
Seq 430 Corynebacterium pseudogenitalium	grey60
Seq 444 Dialister	grey60
Seq 459 Staphylococcus hominis	grey60
Seq 698 Staphylococcus	grey60
Seq 742 Anaerococcus	grey60
Seq 851 Pseudomonas	grey60
Seq 881 Staphylococcus	grey60
Seq 1413 Nevskia ramosa	grey60
Seq 1414 Anaerococcus prevotii	grey60
Seq 2296 Gemella asaccharolytica	grey60
Seq 2507 Bacteria	grey60
Seq 2542 Aerococcus urinae	grey60
Seq 2573 Enterobacteriaceae	grey60
Seq 2621 Veillonella montpellierensis	grey60
Seq 2628 Porphyromonas somerae	grey60
Seq 2771 Porphyromonas somerae	grey60
Seq 2896 Pseudomonas	grey60
Seq 2948 Ochrobactrum	grey60
Seq 3163 Stenotrophomonas	grey60
Seq 3212 Anaerococcus senegalensis	grey60
Seq 3213 Mycoplasma hominis	grey60
Seq 3764 Prevotella timonensis	grey60
Seq 3765 Propionimicrobium lymphophilum	grey60
Seq 3863 Clostridiales Incertae Sedis XI	grey60
Seq 4162 Neisseria	grey60
Seq 4163 Clostridiales	grey60
Seq 4366 Prevotella	grey60
Seq 4367 Lachnospiraceae	grey60
Seq 4813 Parabacteroides distasonis	grey60

Seq 4814 Enterobacteriaceae	grey60
Seq 4815 Roseomonas	grey60
Seq 5140 Bacteroides xylanisolvens	grey60
Seq 5141 Parvimonas micra	grey60
Seq 5579 Enterobacteriaceae	grey60
Seq 6340 Actinomyces odontolyticus	grey60
Seq 38 Corynebacterium jeikeium	lightcyan
Seq 50 Corynebacterium aurimucosum	lightcyan
Seq 60 Corynebacterium aurimucosum	lightcyan
Seq 135 Corynebacterium aurimucosum	lightcyan
Seq 181 Lactobacillus jensenii	lightcyan
Seq 196 Dermabacter hominis	lightcyan
Seq 359 Acinetobacter baumannii	lightcyan
Seq 408 Jonquetella anthropi	lightcyan
Seq 415 Staphylococcus	lightcyan
Seq 465 Micrococcaceae	lightcyan
Seq 503 Prevotella bivia	lightcyan
Seq 508 Corynebacterium	lightcyan
Seq 600 Micrococcaceae	lightcyan
Seq 709 Klebsiella	lightcyan
Seq 749 Coprococcus eutactus	lightcyan
Seq 753 Prevotella bergensis	lightcyan
Seq 848 Bacteroides uniformis	lightcyan
Seq 882 Enterobacteriaceae	lightcyan
Seq 931 Ruminococcaceae	lightcyan
Seq 1100 Blautia	lightcyan
Seq 1178 Klebsiella	lightcyan
Seq 1293 Micrococcaceae	lightcyan
Seq 1347 Acinetobacter	lightcyan
Seq 1437 Phascolarctobacterium faecium	lightcyan
Seq 1552 Corynebacterium	lightcyan
Seq 1562 Bacteroides coprocola	lightcyan
Seq 2345 Enterobacteriaceae	lightcyan
Seq 2357 Pseudomonas	lightcyan
Seq 2572 Paraprevotella clara	lightcyan
Seq 2686 Enterococcus	lightcyan
Seq 3103 Ruminococcaceae	lightcyan
Seq 3104 Catenibacterium mitsuokai	lightcyan
Seq 3260 Gallicola	lightcyan
Seq 3391 Ruminococcus albus	lightcyan
Seq 3471 Coriobacteriaceae	lightcyan
Seq 3666 Blautia	lightcyan
Seq 3871 Anaerococcus octavius	lightcyan
Seq 4000 Lachnospiraceae	lightcyan
Seq 4001 Sphingomonadales	lightcyan

Seq 4145 Erysipelotrichaceae	lightcyan
Seq 4343 Porphyromonadaceae	lightcyan
Seq 4344 Bifidobacterium	lightcyan
Seq 4789 Coriobacteriaceae	lightcyan
Seq 5098 Coprobacillus cateniformis	lightcyan
Seq 5099 Prevotellaceae	lightcyan
Seq 5505 Planifilum fimeticola	lightcyan
Seq 5506 Exiguobacterium	lightcyan
Seq 6209 Prevotella disiens	lightcyan
Seq 29 Moraxella	lightgreen
Seq 100 Corynebacterium appendicis	lightgreen
Seq 174 Porphyromonas bennonis	lightgreen
Seq 361 Peptoniphilus	lightgreen
Seq 367 Porphyromonas	lightgreen
Seq 382 Corynebacterium	lightgreen
Seq 398 Gallicola	lightgreen
Seq 478 Anaerococcus octavius	lightgreen
Seq 531 Anaerococcus octavius	lightgreen
Seq 562 Anaerococcus octavius	lightgreen
Seq 703 Anaerococcus octavius	lightgreen
Seq 803 Clostridiales	lightgreen
Seq 836 Anaerococcus	lightgreen
Seq 945 Corynebacterium	lightgreen
Seq 977 Anaerococcus octavius	lightgreen
Seq 1037 Anaerococcus octavius	lightgreen
Seq 1067 Peptoniphilus	lightgreen
Seq 1226 Anaerococcus octavius	lightgreen
Seq 1290 Anaerococcus octavius	lightgreen
Seq 1543 Anaerococcus octavius	lightgreen
Seq 1618 Peptoniphilus	lightgreen
Seq 1712 Clostridiales	lightgreen
Seq 1713 Anaerococcus octavius	lightgreen
Seq 1734 Clostridiales	lightgreen
Seq 1810 Corynebacterium	lightgreen
Seq 1909 Corynebacterium	lightgreen
Seq 2004 Anaerococcus octavius	lightgreen
Seq 2005 Corynebacterium	lightgreen
Seq 2013 Anaerococcus octavius	lightgreen
Seq 2257 Anaerococcus octavius	lightgreen
Seq 2382 Firmicutes	lightgreen
Seq 2428 Corynebacterium	lightgreen
Seq 2471 Anaerococcus octavius	lightgreen
Seq 2520 Anaerococcus octavius	lightgreen
Seq 2722 Clostridiales	lightgreen
Seq 2932 Ruminococcaceae	lightgreen

Seq 3000 Clostridiales	lightgreen
Seq 3215 Anaerococcus octavius	lightgreen
Seq 3335 Dialister propionificiens	lightgreen
Seq 3479 Anaerococcus octavius	lightgreen
Seq 3571 Corynebacterium riegeli	lightgreen
Seq 3890 Clostridiales	lightgreen
Seq 4026 Clostridiales Incertae Sedis XI	lightgreen
Seq 37 Corynebacterium	lightyellow
Seq 62 Staphylococcus	lightyellow
Seq 76 Anaerococcus octavius	lightyellow
Seq 91 Staphylococcus	lightyellow
Seq 119 Anaerococcus	lightyellow
Seq 139 Staphylococcus haemolyticus	lightyellow
Seq 197 Staphylococcus epidermidis	lightyellow
Seq 278 Gardnerella vaginalis	lightyellow
Seq 294 Corynebacterium	lightyellow
Seq 394 Finegoldia magna	lightyellow
Seq 455 Clostridium bartlettii	lightyellow
Seq 588 Streptococcus	lightyellow
Seq 636 Corynebacterium	lightyellow
Seq 727 Staphylococcus	lightyellow
Seq 845 Staphylococcus epidermidis	lightyellow
Seq 1086 Staphylococcus	lightyellow
Seq 1378 Staphylococcus	lightyellow
Seq 1436 Sutterella wadsworthensis	lightyellow
Seq 1452 Bifidobacterium longum	lightyellow
Seq 1594 Corynebacterium	lightyellow
Seq 1644 Ruminococcus	lightyellow
Seq 1664 Clostridiales	lightyellow
Seq 1785 Anaerococcus senegalensis	lightyellow
Seq 1989 Ruminococcus	lightyellow
Seq 2165 Amaricoccus tamworthensis	lightyellow
Seq 2433 Clostridium sensu stricto	lightyellow
Seq 2491 Porphyromonas gingivalis	lightyellow
Seq 2559 Ruminococcaceae	lightyellow
Seq 2678 Veillonellaceae	lightyellow
Seq 3486 Burkholderiales	lightyellow
Seq 3771 Bacilli	lightyellow
Seq 3773 Leptotrichia	lightyellow
Seq 3896 Rhizobium	lightyellow
Seq 4033 Actinomyces odontolyticus	lightyellow
Seq 4346 Prevotellaceae	lightyellow
Seq 4847 Capnocytophaga granulosa	lightyellow
Seq 4848 Candidatus Saccharibacteria	lightyellow
Seq 5171 Streptococcus	lightyellow

Seq 5180 <i>Gemella bergeri</i>	lightyellow
Seq 5642 <i>Eubacterium eligens</i>	lightyellow
Seq 5643 Clostridiales	lightyellow
Seq 5644 Chitinophagaceae	lightyellow
Seq 5657 <i>Corynebacterium</i>	lightyellow
Seq 84 <i>Atopobium minutum</i>	magenta
Seq 92 <i>Anaerococcus murdochii</i>	magenta
Seq 116 <i>Peptoniphilus coxii</i>	magenta
Seq 129 <i>Jonquetella anthropi</i>	magenta
Seq 133 <i>Porphyromonas</i>	magenta
Seq 134 <i>Porphyromonas</i>	magenta
Seq 146 Clostridiales Incertae Sedis XI	magenta
Seq 163 <i>Anaerococcus lactolyticus</i>	magenta
Seq 166 <i>Porphyromonas asaccharolytica</i>	magenta
Seq 286 <i>Bifidobacterium</i>	magenta
Seq 295 <i>Veillonella dispar</i>	magenta
Seq 308 <i>Corynebacterium kroppenstedtii</i>	magenta
Seq 313 Porphyromonadaceae	magenta
Seq 323 Porphyromonadaceae	magenta
Seq 333 <i>Prevotella</i>	magenta
Seq 341 <i>Prevotella</i>	magenta
Seq 474 <i>Porphyromonas bennonis</i>	magenta
Seq 505 <i>Prevotella</i>	magenta
Seq 732 <i>Prevotella</i>	magenta
Seq 843 <i>Haemophilus</i>	magenta
Seq 852 Clostridiales	magenta
Seq 892 <i>Peptoniphilus lacrimalis</i>	magenta
Seq 1003 <i>Prevotella</i>	magenta
Seq 1208 <i>Fastidiosipila sanguinis</i>	magenta
Seq 1279 <i>Prevotella</i>	magenta
Seq 1399 <i>Murdochiella</i>	magenta
Seq 1542 <i>Pyramidobacter pisciolens</i>	magenta
Seq 1568 Lachnospiraceae	magenta
Seq 1646 <i>Gemmatimonas aurantiaca</i>	magenta
Seq 1671 <i>Mogibacterium</i>	magenta
Seq 1765 <i>Porphyromonas</i>	magenta
Seq 1788 Firmicutes	magenta
Seq 2019 <i>Peptoniphilus lacrimalis</i>	magenta
Seq 2174 <i>Varibaculum cambriense</i>	magenta
Seq 2175 <i>Hymenobacter arizonensis</i>	magenta
Seq 2189 <i>Varibaculum cambriense</i>	magenta
Seq 2308 <i>Noviherbaspirillum</i>	magenta
Seq 2394 <i>Noviherbaspirillum</i>	magenta
Seq 2495 Bacteroidales	magenta
Seq 2543 <i>Gallicola barnesae</i>	magenta

Seq 2688 <i>Pyramidobacter piscolens</i>	magenta
Seq 2880 <i>Prevotella</i>	magenta
Seq 2917 <i>Porphyromonas</i>	magenta
Seq 3047 <i>Ruminococcaceae</i>	magenta
Seq 3138 <i>Lysobacter thermophilus</i>	magenta
Seq 3332 <i>Enterobacteriaceae</i>	magenta
Seq 3333 <i>Bacteria</i>	magenta
Seq 3766 <i>Veillonellaceae</i>	magenta
Seq 3883 <i>Moraxella nonliquefaciens</i>	magenta
Seq 4018 <i>Faecalibacterium prausnitzii</i>	magenta
Seq 4369 <i>Bacteroidales</i>	magenta
Seq 4579 <i>Armatimonadetes gp5</i>	magenta
Seq 4817 <i>Bacteria</i>	magenta
Seq 5142 <i>Clostridiales</i>	magenta
Seq 5584 <i>Peptoniphilus lacrimalis</i>	magenta
Seq 6350 <i>Corynebacterium imitans</i>	magenta
Seq 570 <i>Prevotella bivia</i>	midnightblue
Seq 603 <i>Corynebacterium</i>	midnightblue
Seq 622 <i>Prevotella bivia</i>	midnightblue
Seq 784 <i>Staphylococcus</i>	midnightblue
Seq 908 <i>Lachnospiraceae</i>	midnightblue
Seq 914 <i>Staphylococcus</i>	midnightblue
Seq 987 <i>Corynebacterium</i>	midnightblue
Seq 1040 <i>Corynebacterium jeikeium</i>	midnightblue
Seq 1048 <i>Staphylococcus</i>	midnightblue
Seq 1049 <i>Staphylococcus</i>	midnightblue
Seq 1054 <i>Corynebacterium</i>	midnightblue
Seq 1091 <i>Corynebacterium</i>	midnightblue
Seq 1157 <i>Peptoniphilus</i>	midnightblue
Seq 1164 <i>Clostridiales Incertae Sedis XI</i>	midnightblue
Seq 1180 <i>Finnegoldia magna</i>	midnightblue
Seq 1181 <i>Peptoniphilus harei</i>	midnightblue
Seq 1194 <i>Clostridiales Incertae Sedis XI</i>	midnightblue
Seq 1233 <i>Corynebacterium aurimucosum</i>	midnightblue
Seq 1240 <i>Corynebacterium jeikeium</i>	midnightblue
Seq 1244 <i>Corynebacterium jeikeium</i>	midnightblue
Seq 1246 <i>Anaerococcus murdochii</i>	midnightblue
Seq 1252 <i>Staphylococcus epidermidis</i>	midnightblue
Seq 1253 <i>Corynebacterium aurimucosum</i>	midnightblue
Seq 1254 <i>Bacteria</i>	midnightblue
Seq 1282 <i>Corynebacterium</i>	midnightblue
Seq 1384 <i>Corynebacterium aurimucosum</i>	midnightblue
Seq 1397 <i>Corynebacterium</i>	midnightblue
Seq 1416 <i>Corynebacterium aurimucosum</i>	midnightblue
Seq 1435 <i>Prevotella bivia</i>	midnightblue

Seq_1444	Anaerococcus_murdochii	midnightblue
Seq_1469	Corynebacterium_amycolatum	midnightblue
Seq_1470	Corynebacterium_aurimucosum	midnightblue
Seq_1475	Staphylococcus	midnightblue
Seq_1495	Actinomycetales	midnightblue
Seq_1545	Corynebacterium	midnightblue
Seq_1546	Staphylococcus	midnightblue
Seq_1573	Corynebacterium	midnightblue
Seq_1607	Corynebacterium	midnightblue
Seq_1608	Prevotella_bivia	midnightblue
Seq_1714	Corynebacterium_aurimucosum	midnightblue
Seq_1766	Corynebacterium	midnightblue
Seq_1806	Staphylococcus	midnightblue
Seq_1817	Corynebacterium_jeikeium	midnightblue
Seq_2270	Porphyromonas_uenonis	midnightblue
Seq_2292	Staphylococcus	midnightblue
Seq_2847	Murdochella_asaccharolytica	midnightblue
Seq_5175	Pseudomonadaceae	midnightblue
Seq_6489	Clostridiales	midnightblue
Seq_32	Corynebacterium	orange
Seq_67	Anaerococcus_octavius	orange
Seq_115	Anaerococcus_octavius	orange
Seq_156	Corynebacterium	orange
Seq_239	Corynebacterium	orange
Seq_277	Streptophyta	orange
Seq_300	Hydrogenophilus	orange
Seq_322	Staphylococcus	orange
Seq_661	Anaerococcus_octavius	orange
Seq_664	Anaerococcus_octavius	orange
Seq_714	Brevundimonas	orange
Seq_771	Microbacteriaceae	orange
Seq_793	Porphyromonas_uenonis	orange
Seq_1028	Candidatus_Saccharibacteria	orange
Seq_1350	Veillonella_rogosae	orange
Seq_1395	Corynebacterium	orange
Seq_1423	Intrasporangiaceae	orange
Seq_1518	Corynebacterium	orange
Seq_1710	Lactobacillus	orange
Seq_1815	Corynebacterium_urealyticum	orange
Seq_1930	Blastococcus_aggregatus	orange
Seq_2131	Rheinheimera_tangshanensis	orange
Seq_2392	Prevotella_intermedia	orange
Seq_2519	Micrococcaceae	orange
Seq_2540	Rhizobiales	orange
Seq_2596	Erwinia_rhapontici	orange

Seq 2656 <i>Corynebacterium kroppenstedtii</i>	orange
Seq 2657 <i>Paracoccus yeei</i>	orange
Seq 2719 <i>Prevotella timonensis</i>	orange
Seq 2720 <i>Streptococcus</i>	orange
Seq 2744 <i>Neisseria</i>	orange
Seq 2794 <i>Caulobacter vibrioides</i>	orange
Seq 2879 <i>Peptoniphilus coxii</i>	orange
Seq 3042 <i>Corynebacterium appendicis</i>	orange
Seq 3043 <i>Arthrobacter</i>	orange
Seq 3160 <i>Hymenobacter</i>	orange
Seq 3877 <i>Lactobacillus jensenii</i>	orange
Seq 3878 <i>Anaerococcus</i>	orange
Seq 4567 <i>Chryseobacterium</i>	orange
Seq 35 <i>Corynebacterium</i>	paleturquoise
Seq 419 <i>Rothia mucilaginosa</i>	paleturquoise
Seq 424 <i>Streptococcus</i>	paleturquoise
Seq 471 <i>Streptococcus</i>	paleturquoise
Seq 529 <i>Ruminococcus bromii</i>	paleturquoise
Seq 558 <i>Actinomyces</i>	paleturquoise
Seq 808 <i>Lactobacillus</i>	paleturquoise
Seq 821 <i>Veillonella</i>	paleturquoise
Seq 876 <i>Pantoea</i>	paleturquoise
Seq 1114 <i>Anaerococcus</i>	paleturquoise
Seq 1189 <i>Corynebacterium kroppenstedtii</i>	paleturquoise
Seq 1192 <i>Kingella oralis</i>	paleturquoise
Seq 1509 <i>Sphingomonas</i>	paleturquoise
Seq 1730 <i>Bifidobacterium longum</i>	paleturquoise
Seq 1983 <i>Haemophilus influenzae</i>	paleturquoise
Seq 2016 <i>Aggregatibacter segnis</i>	paleturquoise
Seq 2299 <i>Pseudomonas</i>	paleturquoise
Seq 2385 <i>Jeotgalicoccus huakuii</i>	paleturquoise
Seq 2386 <i>Capnocytophaga granulosa</i>	paleturquoise
Seq 2413 <i>Actinomyces odontolyticus</i>	paleturquoise
Seq 2429 <i>Enterobacteriaceae</i>	paleturquoise
Seq 2448 <i>Brachybacterium</i>	paleturquoise
Seq 2909 <i>Streptobacillus moniliformis</i>	paleturquoise
Seq 2962 <i>Selenomonas sputigena</i>	paleturquoise
Seq 3217 <i>Lachnospiraceae</i>	paleturquoise
Seq 3362 <i>Treponema medium</i>	paleturquoise
Seq 3776 <i>Prevotella pallens</i>	paleturquoise
Seq 4185 <i>Clostridiales</i>	paleturquoise
Seq 4394 <i>Prevotella veroralis</i>	paleturquoise
Seq 4395 <i>Candidatus Saccharibacteria</i>	paleturquoise
Seq 4610 <i>Saccharofermentans</i>	paleturquoise
Seq 4858 <i>Brochothrix thermosphacta</i>	paleturquoise

Seq 5185 <i>Stenotrophomonas</i>	paleturquoise
Seq 5186 <i>Helcococcus sueciensis</i>	paleturquoise
Seq 5187 <i>Murdochiella asaccharolytica</i>	paleturquoise
Seq 6510 Firmicutes	paleturquoise
Seq 6514 Gp6	paleturquoise
Seq 77 <i>Staphylococcus pettenkoferi</i>	pink
Seq 78 <i>Porphyromonas</i>	pink
Seq 228 <i>Parvimonas micra</i>	pink
Seq 230 Clostridiales	pink
Seq 274 <i>Peptoniphilus</i>	pink
Seq 329 <i>Saccharofermentans acetigenes</i>	pink
Seq 353 <i>Solobacterium moorei</i>	pink
Seq 357 <i>Mobiluncus curtisii</i>	pink
Seq 368 <i>Prevotella buccalis</i>	pink
Seq 400 <i>Porphyromonas</i>	pink
Seq 428 Clostridiales Incertae Sedis XI	pink
Seq 439 Clostridiales	pink
Seq 469 <i>Peptoniphilus coxii</i>	pink
Seq 480 <i>Prevotella</i>	pink
Seq 605 Clostridiales	pink
Seq 680 <i>Pyramidobacter piscolens</i>	pink
Seq 691 <i>Porphyromonas</i>	pink
Seq 712 <i>Fusobacterium</i>	pink
Seq 776 <i>Saccharofermentans acetigenes</i>	pink
Seq 834 <i>Porphyromonas somerae</i>	pink
Seq 1035 <i>Prevotella corporis</i>	pink
Seq 1127 <i>Prevotella corporis</i>	pink
Seq 1215 <i>Porphyromonas somerae</i>	pink
Seq 1349 <i>Treponema refringens</i>	pink
Seq 1523 <i>Corynebacterium frankenforstense</i>	pink
Seq 1647 <i>Fusobacterium nucleatum</i>	pink
Seq 1698 <i>Prevotella corporis</i>	pink
Seq 1744 <i>Prevotella</i>	pink
Seq 1829 <i>Fusobacterium nucleatum</i>	pink
Seq 1856 <i>Porphyromonas</i>	pink
Seq 1897 <i>Clostridium symbiosum</i>	pink
Seq 2149 <i>Dialister microaerophilus</i>	pink
Seq 2163 <i>Corynebacterium frankenforstense</i>	pink
Seq 2164 <i>Eggerthia catenaformis</i>	pink
Seq 2204 <i>Porphyromonas bennonis</i>	pink
Seq 2262 Clostridiales	pink
Seq 2291 <i>Anaeroglobus geminatus</i>	pink
Seq 2383 <i>Bacteroidetes</i>	pink
Seq 2427 <i>Porphyromonas bennonis</i>	pink
Seq 2844 <i>Barnesiella</i>	pink

Seq_3266_Ruminococcaceae	pink
Seq_3267_Porphyromonas_somerae	pink
Seq_3404_Bacteroidetes	pink
Seq_3767_Prevotella_buccalis	pink
Seq_3885_Saccharofermentans	pink
Seq_4021_Prevotella_buccalis	pink
Seq_4372_Lachnospiraceae	pink
Seq_5145_Prevotellaceae	pink
Seq_5592_Jonquetella_anthropi	pink
Seq_5595_Bacteroidetes	pink
Seq_6365_Bacteria	pink
Seq_6370_Prevotella	pink
Seq_6372_Bacteria	pink
Seq_6376_Saccharofermentans_acetigenes	pink
Seq_6377_Bacteroidetes	pink
Seq_6378_Prevotella_timonensis	pink
Seq_41_Anaerococcus	purple
Seq_97_Anaerococcus	purple
Seq_99_Acinetobacter_junii	purple
Seq_104_Porphyromonas_bennonis	purple
Seq_235_Anaerococcus_prevotii	purple
Seq_262_Acinetobacter_johnsonii	purple
Seq_269_Actinomyces_hominis	purple
Seq_297_Kocuria_rhizophila	purple
Seq_346_Pseudomonas	purple
Seq_448_Porphyromonas_bennonis	purple
Seq_566_Psychrobacter_sanguinis	purple
Seq_587_Acinetobacter	purple
Seq_595_Stenotrophomonas	purple
Seq_642_Paracoccus	purple
Seq_783_Staphylococcus	purple
Seq_817_Caulobacteraceae	purple
Seq_878_Anaerococcus_prevotii	purple
Seq_895_Actinomyces	purple
Seq_934_Brevibacterium	purple
Seq_959_Bacteroides_vulgatus	purple
Seq_1018_Enterobacter	purple
Seq_1216_Sphingobacterium_multivorum	purple
Seq_1386_Fusobacterium_nucleatum	purple
Seq_1465_Mycobacterium	purple
Seq_1639_Acinetobacter_calcoaceticus	purple
Seq_1851_Staphylococcus_epidermidis	purple
Seq_1877_Pseudomonas	purple
Seq_1890_Williamsia	purple
Seq_1902_Novosphingobium	purple

Seq_1952_Campylobacter_ureolyticus	purple
Seq_2231_Shewanella	purple
Seq_2372_Anaerostipes_hadrus	purple
Seq_2417_Brevundimonas	purple
Seq_2545_Rhodobacteraceae	purple
Seq_2745_Streptobacillus	purple
Seq_2747_Mycobacterium	purple
Seq_2881_Rhodobacteraceae	purple
Seq_3270_Acinetobacter	purple
Seq_3575_Aurantimonadaceae	purple
Seq_3679_Prevotella_melaninogenica	purple
Seq_3680_Enterobacteriaceae	purple
Seq_3681_Neisseriaceae	purple
Seq_3895_Conchiformibius_steedae	purple
Seq_4174_Leptotrichia	purple
Seq_4175_Enterobacteriaceae	purple
Seq_4176_Ruminococcus_bromii	purple
Seq_4387_Gardnerella_vaginalis	purple
Seq_4388_Cobetia_crustatorum	purple
Seq_4603_Pedobacter	purple
Seq_4604_Skermanella_aerolata	purple
Seq_4840_Gpl	purple
Seq_5635_Moraxellaceae	purple
Seq_6467_Cardiobacteriaceae	purple
Seq_6468_Acidobacteria_Gp4	purple
Seq_6471_Capnocytophaga	purple
Seq_51_Anaerococcus_octavius	red
Seq_58_Staphylococcus_epidermidis	red
Seq_75_Neisseriaceae	red
Seq_202_Corynebacterium_sundsvallense	red
Seq_212_Streptococcus	red
Seq_219_Moraxella	red
Seq_224_Kocuria_rhizophila	red
Seq_281_Paracoccus	red
Seq_285_Gemmiger_formicilis	red
Seq_418_Acinetobacter_johnsonii	red
Seq_452_Finegoldia_magna	red
Seq_466_Dietzia	red
Seq_509_Acinetobacter	red
Seq_518_Peptoniphilus	red
Seq_557_Veillonella	red
Seq_677_Chryseobacterium_hispanicum	red
Seq_707_Actinomyces_europaeus	red
Seq_866_Kocuria_kristinae	red
Seq_1066_Pantoea	red

Seq 1084 <i>Wautersiella falsenii</i>	red
Seq 1236 <i>Acinetobacter junii</i>	red
Seq 1269 <i>Porphyromonas catoniae</i>	red
Seq 1409 <i>Finegoldia magna</i>	red
Seq 1591 Enterobacteriaceae	red
Seq 1616 <i>Wautersiella falsenii</i>	red
Seq 1726 <i>Acinetobacter</i>	red
Seq 1807 <i>Psychrobacter</i>	red
Seq 1832 <i>Haemophilus</i>	red
Seq 1948 <i>Staphylococcus</i>	red
Seq 2053 <i>Nosocomiicoccus ampullae</i>	red
Seq 2322 <i>Rhizobium</i>	red
Seq 2341 <i>Acinetobacter</i>	red
Seq 2461 <i>Comamonas</i>	red
Seq 2761 <i>Pseudoxanthomonas</i>	red
Seq 2772 <i>Neisseria mucosa</i>	red
Seq 2815 <i>Janthinobacterium</i>	red
Seq 3004 <i>Pantoea</i>	red
Seq 3052 Enterobacteriaceae	red
Seq 3053 Enterobacteriaceae	red
Seq 3131 <i>Bosea</i>	red
Seq 3225 <i>Streptococcus sobrinus</i>	red
Seq 3491 <i>Paracoccus</i>	red
Seq 3577 <i>Neisseria flavescens</i>	red
Seq 3684 <i>Acinetobacter</i>	red
Seq 3685 <i>Brevundimonas</i>	red
Seq 4011 <i>Actinomyces odontolyticus</i>	red
Seq 4187 Enterobacteriaceae	red
Seq 4189 <i>Pseudomonas</i>	red
Seq 4400 Enterobacteriaceae	red
Seq 4401 <i>Pseudomonas</i>	red
Seq 4618 <i>Fusobacterium nucleatum</i>	red
Seq 4619 <i>Staphylococcus sciuri</i>	red
Seq 4620 <i>Flavobacterium</i>	red
Seq 5192 <i>Achromobacter</i>	red
Seq 5193 <i>Rhizobium</i>	red
Seq 5194 Gp16	red
Seq 5668 <i>Ruminococcus bromii</i>	red
Seq 5669 Betaproteobacteria	red
Seq 5671 Bacteria	red
Seq 5673 Corynebacteriaceae	red
Seq 6520 Betaproteobacteria	red
Seq 6521 Bacteria	red
Seq 6525 Bacteria	red
Seq 6530 <i>Solirubrobacter ginsenosidimutans</i>	red

Seq 6667 Firmicutes	red
Seq 6668 Pseudomonas	red
Seq 223 Prevotella timonensis	royalblue
Seq 291 Brevibacterium	royalblue
Seq 375 Corynebacterium	royalblue
Seq 462 Staphylococcus pettenkoferi	royalblue
Seq 475 Porphyromonas bennonis	royalblue
Seq 635 Dialister propionificiens	royalblue
Seq 741 Porphyromonas	royalblue
Seq 860 Anaerococcus octavius	royalblue
Seq 984 Clostridiales	royalblue
Seq 1008 Gallicola	royalblue
Seq 1064 Clostridiales	royalblue
Seq 1074 Bacteria	royalblue
Seq 1106 Coriobacteriaceae	royalblue
Seq 1126 Sutterella stercoricanis	royalblue
Seq 1150 Clostridiales	royalblue
Seq 1232 Clostridiales	royalblue
Seq 1506 Anaerococcus prevotii	royalblue
Seq 1633 Porphyromonas	royalblue
Seq 1661 Veillonellaceae	royalblue
Seq 2137 Clostridiales	royalblue
Seq 2162 Porphyromonas	royalblue
Seq 2181 Porphyromonas	royalblue
Seq 2384 Clostridiales	royalblue
Seq 2655 Actinomyces turicensis	royalblue
Seq 2685 Porphyromonas somerae	royalblue
Seq 2995 Porphyromonas	royalblue
Seq 3156 Porphyromonas	royalblue
Seq 3559 Treponema refringens	royalblue
Seq 3754 Porphyromonas	royalblue
Seq 3884 Clostridiales	royalblue
Seq 4143 Ruminococcaceae	royalblue
Seq 4144 Peptoniphilus coxii	royalblue
Seq 4370 Murdochiella asaccharolytica	royalblue
Seq 4557 Bacteria	royalblue
Seq 4580 Barnesiella intestinihominis	royalblue
Seq 4787 Firmicutes	royalblue
Seq 4818 Bacteria	royalblue
Seq 5144 Clostridiales	royalblue
Seq 6204 Bacteria	royalblue
Seq 6360 Varibaculum cambriense	royalblue
Seq 6361 Bacteria	royalblue
Seq 6364 Bacteroidetes	royalblue
Seq 39 Anaerococcus	saddlebrown

Seq 148 <i>Murdochiella asaccharolytica</i>	saddlebrown
Seq 153 <i>Anaerococcus octavius</i>	saddlebrown
Seq 248 <i>Corynebacterium pseudogenitalium</i>	saddlebrown
Seq 267 <i>Finegoldia magna</i>	saddlebrown
Seq 289 <i>Corynebacterium pseudogenitalium</i>	saddlebrown
Seq 305 <i>Anaerococcus prevotii</i>	saddlebrown
Seq 461 <i>Ruminococcus obeum</i>	saddlebrown
Seq 550 <i>Peptoniphilus coxii</i>	saddlebrown
Seq 598 <i>Gallicola</i>	saddlebrown
Seq 777 <i>Peptococcus niger</i>	saddlebrown
Seq 967 <i>Streptococcus</i>	saddlebrown
Seq 979 <i>Dialister propionificiens</i>	saddlebrown
Seq 1053 <i>Bacteroides uniformis</i>	saddlebrown
Seq 1117 <i>Lachnospiraceae</i>	saddlebrown
Seq 1373 <i>Ruminococcaceae</i>	saddlebrown
Seq 1501 <i>Ruminococcus bromii</i>	saddlebrown
Seq 1538 <i>Clostridium XIVa</i>	saddlebrown
Seq 1839 <i>Oxalobacteraceae</i>	saddlebrown
Seq 1905 <i>Ruminococcus callidus</i>	saddlebrown
Seq 1940 <i>Lachnospiraceae</i>	saddlebrown
Seq 2340 <i>Neisseria</i>	saddlebrown
Seq 2676 <i>Roseburia intestinalis</i>	saddlebrown
Seq 2831 <i>Ruminococcaceae</i>	saddlebrown
Seq 2996 <i>Ruminococcaceae</i>	saddlebrown
Seq 3208 <i>Olsenella uli</i>	saddlebrown
Seq 3262 <i>Lactobacillus</i>	saddlebrown
Seq 3312 <i>Eggerthella lenta</i>	saddlebrown
Seq 3392 <i>Lachnospiraceae</i>	saddlebrown
Seq 3560 <i>Parabacteroides</i>	saddlebrown
Seq 3561 <i>Corynebacterium</i>	saddlebrown
Seq 3757 <i>Flavobacteriaceae</i>	saddlebrown
Seq 4150 <i>Pseudomonas</i>	saddlebrown
Seq 4562 <i>Veillonella</i>	saddlebrown
Seq 4794 <i>Oscillibacter</i>	saddlebrown
Seq 5103 <i>Gp1</i>	saddlebrown
Seq 6218 <i>Treponema</i>	saddlebrown
Seq 30 <i>Enhydrobacter</i>	salmon
Seq 63 <i>Acinetobacter</i>	salmon
Seq 127 <i>Anaerococcus obesiensis</i>	salmon
Seq 145 <i>Prevotella buccalis</i>	salmon
Seq 242 <i>Chryseobacterium</i>	salmon
Seq 292 <i>Peptoniphilus lacrimalis</i>	salmon
Seq 304 <i>Acinetobacter</i>	salmon
Seq 307 <i>Jeotgalicoccus pinnipedialis</i>	salmon
Seq 338 <i>Acinetobacter parvus</i>	salmon

Seq 412 Acinetobacter	salmon
Seq 421 Acinetobacter	salmon
Seq 426 Chryseobacterium anthropi	salmon
Seq 473 Acinetobacter	salmon
Seq 499 Chryseobacterium anthropi	salmon
Seq 502 Ochrobactrum	salmon
Seq 519 Chryseobacterium	salmon
Seq 653 Chryseobacterium anthropi	salmon
Seq 676 Acinetobacter	salmon
Seq 704 Acinetobacter	salmon
Seq 706 Acinetobacter tjernbergiae	salmon
Seq 823 Acinetobacter	salmon
Seq 827 Globicatella	salmon
Seq 873 Acinetobacter	salmon
Seq 971 Acinetobacter	salmon
Seq 988 Clostridium IV	salmon
Seq 999 Bacteroides vulgatus	salmon
Seq 1027 Prevotella buccalis	salmon
Seq 1068 Microbacterium lacticum	salmon
Seq 1198 Aerococcaceae	salmon
Seq 1486 Chryseobacterium	salmon
Seq 1625 Peptoniphilus	salmon
Seq 1727 Bosea	salmon
Seq 1837 Rhodobacter	salmon
Seq 1998 Helcococcus	salmon
Seq 2319 Dialister invisus	salmon
Seq 2512 Stenotrophomonas maltophilia	salmon
Seq 2588 Brevibacterium	salmon
Seq 2599 Vogesella	salmon
Seq 2893 Bacteroides stercoris	salmon
Seq 2953 Staphylococcus simulans	salmon
Seq 3165 Burkholderia	salmon
Seq 3239 Corynebacterium	salmon
Seq 3269 Staphylococcus	salmon
Seq 3572 Massilia timonae	salmon
Seq 4030 Delftia	salmon
Seq 4171 Sphingopyxis	salmon
Seq 4383 Enterobacteriaceae	salmon
Seq 4597 Pseudomonas	salmon
Seq 4598 Xanthobacter autotrophicus	salmon
Seq 5161 Vagococcus	salmon
Seq 5621 Terrimonas	salmon
Seq 5622 Neisseria bacilliformis	salmon
Seq 6452 Porphyromonas	salmon
Seq 56 Clostridiales	skyblue

Seq 103 <i>Chryseobacterium hominis</i>	skyblue
Seq 244 Clostridiales Incertae Sedis XI	skyblue
Seq 301 <i>Brachybacterium</i>	skyblue
Seq 453 <i>Bacteroides uniformis</i>	skyblue
Seq 479 <i>Dorea longicatena</i>	skyblue
Seq 530 <i>Brevibacterium pityocampae</i>	skyblue
Seq 560 <i>Moryella indoligenes</i>	skyblue
Seq 577 <i>Saccharofermentans acetigenes</i>	skyblue
Seq 584 Clostridiales Incertae Sedis XI	skyblue
Seq 616 <i>Helcococcus</i>	skyblue
Seq 926 <i>Corynebacterium pseudogenitalium</i>	skyblue
Seq 938 <i>Staphylococcus</i>	skyblue
Seq 968 Clostridiales	skyblue
Seq 1016 <i>Porphyromonas asaccharolytica</i>	skyblue
Seq 1046 Porphyromonadaceae	skyblue
Seq 1195 <i>Finegoldia magna</i>	skyblue
Seq 1292 <i>Staphylococcus</i>	skyblue
Seq 1586 <i>Peptoniphilus</i>	skyblue
Seq 1610 <i>Corynebacterium pseudogenitalium</i>	skyblue
Seq 1611 Porphyromonadaceae	skyblue
Seq 1620 <i>Acinetobacter</i>	skyblue
Seq 1659 <i>Porphyromonas uenonis</i>	skyblue
Seq 1682 <i>Peptoniphilus</i>	skyblue
Seq 2119 <i>Slackia exigua</i>	skyblue
Seq 2177 <i>Prevotella buccalis</i>	skyblue
Seq 2187 <i>Haemophilus</i>	skyblue
Seq 2191 <i>Campylobacter ureolyticus</i>	skyblue
Seq 3492 Clostridiales	skyblue
Seq 3578 Clostridiales	skyblue
Seq 3904 <i>Moryella indoligenes</i>	skyblue
Seq 3905 <i>Aureimonas altamirensis</i>	skyblue
Seq 4626 Comamonadaceae	skyblue
Seq 4627 <i>Clostridium sensu stricto</i>	skyblue
Seq 4872 <i>Pseudomonas</i>	skyblue
Seq 4873 <i>Aeromonas</i>	skyblue
Seq 5691 Firmicutes	skyblue
Seq 6673 Prevotellaceae	skyblue
Seq 211 <i>Corynebacterium massiliense</i>	steelblue
Seq 316 <i>Corynebacterium frankenforstense</i>	steelblue
Seq 349 <i>Corynebacterium glucuronolyticum</i>	steelblue
Seq 483 <i>Corynebacterium</i>	steelblue
Seq 563 <i>Corynebacterium frankenforstense</i>	steelblue
Seq 578 <i>Fusobacterium periodonticum</i>	steelblue
Seq 648 <i>Staphylococcus</i>	steelblue
Seq 660 <i>Clostridium glycolicum</i>	steelblue

Seq_751_Peptoniphilus	steelblue
Seq_838_Porphyromonas_catoniae	steelblue
Seq_1155_Pseudomonas	steelblue
Seq_1225_Anaerococcus_vaginalis	steelblue
Seq_1238_Prevotella_salivae	steelblue
Seq_1297_Peptoniphilus	steelblue
Seq_1308_Pantoea	steelblue
Seq_1323_Streptococcus	steelblue
Seq_1361_Megasphaera_elsdenii	steelblue
Seq_1382_Gallicola	steelblue
Seq_1421_Prevotella_nanceiensis	steelblue
Seq_1567_Abiotrophia_defectiva	steelblue
Seq_1728_Actinomyces	steelblue
Seq_1938_Staphylococcus_epidermidis	steelblue
Seq_2150_Parasutterella_excrementihominis	steelblue
Seq_2155_Olsenella	steelblue
Seq_2361_Leptotrichia	steelblue
Seq_2498_Bacteroidetes	steelblue
Seq_2574_Lactobacillus	steelblue
Seq_2882_Corynebacterium	steelblue
Seq_3158_Lactobacillus	steelblue
Seq_3199_Prevotella_loescheii	steelblue
Seq_3296_Mogibacterium	steelblue
Seq_4035_Kocuria	steelblue
Seq_4608_Chryseobacterium	steelblue
Seq_4609_Piscicoccus_intestinalis	steelblue
Seq_5184_Gpl	steelblue
Seq_5658_Sphingomonas	steelblue
Seq_6508_Prevotella_melaninogenica	steelblue
Seq_82_Staphylococcus	tan
Seq_132_Corynebacterium	tan
Seq_250_Staphylococcus	tan
Seq_260_Brevibacterium_paucivorans	tan
Seq_326_Corynebacterium	tan
Seq_374_Finegoldia_magna	tan
Seq_386_Blautia_luti	tan
Seq_395_Brevibacterium_luteolum	tan
Seq_441_Corynebacterium_jeikeium	tan
Seq_496_Anaerococcus_vaginalis	tan
Seq_537_Micrococcaceae	tan
Seq_541_Staphylococcus_pettenkoferi	tan
Seq_552_Corynebacterium_jeikeium	tan
Seq_599_Prevotella_copri	tan
Seq_602_Ruminococcus_torques	tan
Seq_621_Peptococcus_niger	tan

Seq 624 Brachybacterium	tan
Seq 765 Lachnospiraceae	tan
Seq 788 Ruminococcus	tan
Seq 807 Dorea formicigenerans	tan
Seq 850 Kytococcus	tan
Seq 1088 Corynebacterium	tan
Seq 1104 Catenibacterium mitsuokai	tan
Seq 1210 Clostridiales	tan
Seq 1310 Brevibacterium luteolum	tan
Seq 1327 Bifidobacterium angulatum	tan
Seq 1351 Faecalibacterium prausnitzii	tan
Seq 1385 Clostridiales	tan
Seq 1515 Staphylococcus pettenkoferi	tan
Seq 1702 Lachnospiraceae	tan
Seq 1780 Lachnospiraceae	tan
Seq 1881 Clostridium XLVa	tan
Seq 1945 Flavonifractor	tan
Seq 2033 Bifidobacterium bifidum	tan
Seq 2148 Staphylococcus pettenkoferi	tan
Seq 2173 Prevotella copri	tan
Seq 2367 Lactobacillus ruminis	tan
Seq 2452 Staphylococcus	tan
Seq 2522 Erysipelotrichaceae	tan
Seq 2658 Prevotella copri	tan
Seq 3044 Prevotella copri	tan
Seq 3476 Ruminococcus obeum	tan
Seq 4572 Anaerostipes hadrus	tan
Seq 4573 Propionibacterium acnes	tan
Seq 4574 Erysipelotrichaceae	tan
Seq 4803 Burkholderiales	tan
Seq 4805 Barnesiella intestinihominis	tan
Seq 5547 Eubacterium desmolans	tan
Seq 5548 Candidatus Saccharibacteria	tan
Seq 6280 Bacteria	tan
Seq 6282 Lachnospiraceae	tan
Seq 6283 Roseburia	tan
Seq 6284 Acidaminococcus intestini	tan
Seq 17 Streptococcus	turquoise
Seq 70 Staphylococcus	turquoise
Seq 85 Streptophyta	turquoise
Seq 140 Micrococcaceae	turquoise
Seq 167 Rothia dentocariosa	turquoise
Seq 187 Staphylococcus	turquoise
Seq 198 Acinetobacter	turquoise
Seq 221 Staphylococcus epidermidis	turquoise

Seq 233 <i>Veillonella dispar</i>	turquoise
Seq 238 <i>Streptococcus</i>	turquoise
Seq 256 <i>Dialister</i>	turquoise
Seq 264 <i>Granulicatella</i>	turquoise
Seq 279 <i>Streptococcus</i>	turquoise
Seq 314 <i>Kocuria</i>	turquoise
Seq 319 <i>Staphylococcus</i>	turquoise
Seq 336 <i>Acinetobacter</i>	turquoise
Seq 358 <i>Rothia mucilaginosa</i>	turquoise
Seq 369 <i>Staphylococcus epidermidis</i>	turquoise
Seq 463 <i>Alloprevotella</i>	turquoise
Seq 506 <i>Fusobacterium</i>	turquoise
Seq 510 <i>Porphyromonas asaccharolytica</i>	turquoise
Seq 582 <i>Actinomyces</i>	turquoise
Seq 611 <i>Aggregatibacter</i>	turquoise
Seq 643 <i>Corynebacterium singulare</i>	turquoise
Seq 693 <i>Staphylococcus</i>	turquoise
Seq 764 <i>Veillonella</i>	turquoise
Seq 781 <i>Staphylococcus epidermidis</i>	turquoise
Seq 795 <i>Tetracoccus cechii</i>	turquoise
Seq 810 <i>Staphylococcus</i>	turquoise
Seq 835 <i>Acinetobacter</i>	turquoise
Seq 855 <i>Fusobacterium nucleatum</i>	turquoise
Seq 859 <i>Parvimonas micra</i>	turquoise
Seq 898 <i>Staphylococcus</i>	turquoise
Seq 922 <i>Rothia mucilaginosa</i>	turquoise
Seq 933 <i>Corynebacterium matruchotii</i>	turquoise
Seq 936 <i>Saccharofermentans acetigenes</i>	turquoise
Seq 983 <i>Leptotrichia buccalis</i>	turquoise
Seq 991 <i>Prevotella</i>	turquoise
Seq 995 <i>Lachnospiraceae</i>	turquoise
Seq 1021 <i>Leptotrichia</i>	turquoise
Seq 1081 <i>Actinomyces odontolyticus</i>	turquoise
Seq 1093 <i>Streptococcus</i>	turquoise
Seq 1097 <i>Ruminococcus bromii</i>	turquoise
Seq 1102 <i>Gemella</i>	turquoise
Seq 1162 <i>Gemella morbillorum</i>	turquoise
Seq 1169 <i>Leptotrichia amnionii</i>	turquoise
Seq 1187 <i>Methylobacterium</i>	turquoise
Seq 1199 <i>Pasteurellaceae</i>	turquoise
Seq 1214 <i>Enterobacteriaceae</i>	turquoise
Seq 1324 <i>Kocuria</i>	turquoise
Seq 1391 <i>Acinetobacter</i>	turquoise
Seq 1440 <i>Actinomyces georgiae</i>	turquoise
Seq 1443 <i>Leptotrichia wadei</i>	turquoise

Seq_1582_Actinomycetales	turquoise
Seq_1599_Acinetobacter_guillouiae	turquoise
Seq_1651_Sphingomonadales	turquoise
Seq_1653_Actinomycetales	turquoise
Seq_1679_Leptotrichia	turquoise
Seq_1687_Lachnoanaerobaculum	turquoise
Seq_1717_Brevibacterium	turquoise
Seq_1735_Staphylococcus_pasteuri	turquoise
Seq_1745_Corynebacterium_matruchotii	turquoise
Seq_1866_Bacteria	turquoise
Seq_1869_Selenomonas_noxia	turquoise
Seq_1891_Campylobacter	turquoise
Seq_1942_Leptotrichia	turquoise
Seq_1973_Aureimonas_jatrophae	turquoise
Seq_1977_Actinomyces	turquoise
Seq_2027_Lachnoanaerobaculum_saburreum	turquoise
Seq_2056_Rhizobium	turquoise
Seq_2075_Prevotella_melaninogenica	turquoise
Seq_2103_Acinetobacter	turquoise
Seq_2118_Leptotrichia	turquoise
Seq_2139_Serratia	turquoise
Seq_2209_Pseudomonas	turquoise
Seq_2273_Pasteurellaceae	turquoise
Seq_2282_Porphyrromonas_catoniae	turquoise
Seq_2320_Chryseobacterium	turquoise
Seq_2324_Tannerella_forsythia	turquoise
Seq_2325_Lachnospiraceae	turquoise
Seq_2376_Corynebacterium_durum	turquoise
Seq_2377_Porphyrromonas_endodontalis	turquoise
Seq_2479_Capnocytophaga_ochracea	turquoise
Seq_2501_Capnocytophaga	turquoise
Seq_2552_Leuconostoc	turquoise
Seq_2576_Fusobacterium_nucleatum	turquoise
Seq_2577_Porphyrromonas_catoniae	turquoise
Seq_2593_Pseudomonas	turquoise
Seq_2632_Fusobacterium	turquoise
Seq_2661_Haemophilus_haemolyticus	turquoise
Seq_2666_Rhodococcus	turquoise
Seq_2690_Selenomonas	turquoise
Seq_2808_Lachnospiraceae	turquoise
Seq_2883_Flavobacteriaceae	turquoise
Seq_2905_Enterobacteriaceae	turquoise
Seq_2936_Filifactor_alocis	turquoise
Seq_2955_Haemophilus	turquoise
Seq_2956_Prevotella_nigrescens	turquoise

Seq 3001 Porphyromonadaceae	turquoise
Seq 3191 Olsenella profusa	turquoise
Seq 3218 Prevotella pleuritidis	turquoise
Seq 3272 Porphyromonas bennonis	turquoise
Seq 3339 Capnocytophaga ochracea	turquoise
Seq 3413 Selenomonas sputigena	turquoise
Seq 3414 Prevotella oulorum	turquoise
Seq 3415 Prevotella saccharolytica	turquoise
Seq 3470 Tannerella forsythia	turquoise
Seq 3493 Corynebacterium imitans	turquoise
Seq 3494 Alloprevotella rava	turquoise
Seq 3495 Capnocytophaga ochracea	turquoise
Seq 3579 Prevotella maculosa	turquoise
Seq 3687 Actinomyces	turquoise
Seq 3688 Stenotrophomonas	turquoise
Seq 3696 Eubacterium saphenum	turquoise
Seq 3779 Porphyromonas catoniae	turquoise
Seq 3780 Sphingomonadaceae	turquoise
Seq 3902 Ilumatobacter fluminis	turquoise
Seq 3938 Deinococcus aerolatus	turquoise
Seq 4196 Haemophilus	turquoise
Seq 4197 Cardiobacterium valvarum	turquoise
Seq 4198 Selenomonas artemidis	turquoise
Seq 4200 Citrobacter	turquoise
Seq 4323 Bacteria	turquoise
Seq 4403 SR1	turquoise
Seq 4404 Pseudomonas	turquoise
Seq 4405 Flavobacteriaceae	turquoise
Seq 4406 Corynebacterium riegelsii	turquoise
Seq 4629 Prevotella saccharolytica	turquoise
Seq 4630 Nakamurella multipartita	turquoise
Seq 4633 Clostridiales	turquoise
Seq 4874 Treponema amylovorum	turquoise
Seq 4875 Leptotrichia	turquoise
Seq 4878 Aurantimonadaceae	turquoise
Seq 5202 Peptococcus niger	turquoise
Seq 5204 Candidatus Saccharibacteria	turquoise
Seq 5205 Treponema	turquoise
Seq 5206 Prevotella marshii	turquoise
Seq 5693 Sinobacteraceae	turquoise
Seq 5694 Veillonellaceae	turquoise
Seq 5696 Sphingobacterium	turquoise
Seq 5697 Actinobacteria	turquoise
Seq 5698 Bacteria	turquoise
Seq 5699 Bacteria	turquoise

Seq 5702 <i>Vibrio</i>	turquoise
Seq 5703 Veillonellaceae	turquoise
Seq 5705 Clostridiales	turquoise
Seq 6555 Proteobacteria	turquoise
Seq 6558 Micrococcaceae	turquoise
Seq 6564 SR1	turquoise
Seq 88 <i>Propionibacterium granulosum</i>	violet
Seq 176 <i>Propionibacterium</i>	violet
Seq 215 <i>Staphylococcus epidermidis</i>	violet
Seq 288 <i>Corynebacterium kroppenstedtii</i>	violet
Seq 302 <i>Spirosoma</i>	violet
Seq 315 <i>Staphylococcus</i>	violet
Seq 678 <i>Propionibacterium acnes</i>	violet
Seq 713 <i>Neisseria</i>	violet
Seq 733 <i>Enterococcus</i>	violet
Seq 744 <i>Wautersiella falsenii</i>	violet
Seq 961 <i>Marmoricola scoriae</i>	violet
Seq 1149 <i>Bacteroides uniformis</i>	violet
Seq 1220 <i>Sphingomonas glacialis</i>	violet
Seq 1337 <i>Turicella otitidis</i>	violet
Seq 1528 <i>Prevotella histicola</i>	violet
Seq 1556 <i>Phenylobacterium</i>	violet
Seq 1560 <i>Pseudomonas</i>	violet
Seq 1572 <i>Veillonella</i>	violet
Seq 1638 Gp4	violet
Seq 1759 <i>Pseudomonas</i>	violet
Seq 1875 Sphingomonadales	violet
Seq 1912 Actinomycetales	violet
Seq 1984 <i>Enterococcus</i>	violet
Seq 2068 <i>Candidatus Saccharibacteria</i>	violet
Seq 2085 <i>Blastocatella</i>	violet
Seq 2136 <i>Lactobacillus versmoldensis</i>	violet
Seq 2391 Comamonadaceae	violet
Seq 2398 <i>Enterococcus</i>	violet
Seq 2537 <i>Sphingomonas</i>	violet
Seq 2691 <i>Pseudomonas</i>	violet
Seq 2811 <i>Rudaeicoccus suwonensis</i>	violet
Seq 2885 Bacteria	violet
Seq 3908 <i>Sphingomonas</i>	violet
Seq 4647 Comamonadaceae	violet
Seq 5727 <i>Capnocytophaga ochracea</i>	violet
Seq 90 <i>Porphyromonas</i>	white
Seq 147 <i>Haemophilus parainfluenzae</i>	white
Seq 183 <i>Finegoldia magna</i>	white
Seq 610 <i>Haemophilus</i>	white

Seq 638 Burkholderiales	white
Seq 735 Alloprevotella rava	white
Seq 768 Alloprevotella	white
Seq 871 Rhizobium	white
Seq 896 Streptococcus sanguinis	white
Seq 1069 Alloprevotella rava	white
Seq 1264 Bacillaceae 2	white
Seq 1522 Finegoldia magna	white
Seq 1535 Lactobacillus delbrueckii	white
Seq 1667 Alloprevotella rava	white
Seq 1868 Treponema lecithinolyticum	white
Seq 1990 Actinomyces	white
Seq 2077 Leptotrichia	white
Seq 2467 Porphyromonas catoniae	white
Seq 2612 Capnocytophaga sputigena	white
Seq 2727 Pseudomonas	white
Seq 2839 Conchiformibius steedae	white
Seq 2915 Granulicatella	white
Seq 3755 Rubellimicrobium aerolatum	white
Seq 3756 Prevotella nigrescens	white
Seq 3873 Oxalobacteraceae	white
Seq 4004 Leuconostoc	white
Seq 4147 Naxibacter	white
Seq 4148 Acetobacter lovaniensis	white
Seq 4149 Intrasporangiaceae	white
Seq 4347 Armatimonadetes_gp5	white
Seq 4348 Gpl	white
Seq 4561 Candidatus Saccharibacteria	white
Seq 4792 Chlorophyta	white
Seq 4793 Rubellimicrobium	white
Seq 5102 Erwinia	white
Seq 5510 Chryseobacterium	white
Seq 5512 Clostridiales Incertae Sedis XI	white
Seq 6217 Chloroplast	white
Seq 89 Brevibacterium	yellow
Seq 137 Lactobacillus	yellow
Seq 204 Neisseria meningitidis	yellow
Seq 218 Nosocomiicoccus ampullae	yellow
Seq 225 Corynebacterium urealyticum	yellow
Seq 234 Neisseriaceae	yellow
Seq 261 Prevotella copri	yellow
Seq 298 Anaerococcus	yellow
Seq 332 Anaerococcus prevotii	yellow
Seq 335 Clostridiales Incertae Sedis XI	yellow
Seq 337 Corynebacterium urealyticum	yellow

Seq 392 <i>Collinsella aerofaciens</i>	yellow
Seq 437 <i>Corynebacterium urealyticum</i>	yellow
Seq 476 <i>Anaerococcus</i>	yellow
Seq 522 <i>Pseudomonas</i>	yellow
Seq 559 <i>Micrococcaceae</i>	yellow
Seq 580 <i>Anaerococcus</i>	yellow
Seq 632 <i>Peptoniphilus coxii</i>	yellow
Seq 644 <i>Clostridiales</i>	yellow
Seq 645 <i>Staphylococcus</i>	yellow
Seq 791 <i>Ruminococcus torques</i>	yellow
Seq 806 <i>Anaerococcus</i>	yellow
Seq 814 <i>Anaerococcus octavius</i>	yellow
Seq 903 <i>Clostridiales</i>	yellow
Seq 1077 <i>Actinomyces odontolyticus</i>	yellow
Seq 1325 <i>Carnobacteriaceae</i>	yellow
Seq 1480 <i>Pseudomonas</i>	yellow
Seq 1551 <i>Anaerococcus prevotii</i>	yellow
Seq 1626 <i>Brevundimonas</i>	yellow
Seq 1648 <i>Porphyromonas bennonis</i>	yellow
Seq 1658 <i>Streptococcus</i>	yellow
Seq 1725 <i>Staphylococcus</i>	yellow
Seq 1731 <i>Prevotella copri</i>	yellow
Seq 1816 <i>Dialister propionificaciens</i>	yellow
Seq 2054 <i>Clostridiales</i>	yellow
Seq 2138 <i>Dietzia timorensis</i>	yellow
Seq 2141 <i>Anaerococcus</i>	yellow
Seq 2375 <i>Comamonas kerstersii</i>	yellow
Seq 2412 <i>Dialister propionificaciens</i>	yellow
Seq 2549 <i>Prevotella copri</i>	yellow
Seq 2610 <i>Capnocytophaga sputigena</i>	yellow
Seq 2659 <i>Anaerococcus</i>	yellow
Seq 2667 <i>Mogibacterium</i>	yellow
Seq 2723 <i>Flavobacterium</i>	yellow
Seq 2731 <i>Negativicoccus succinicivorans</i>	yellow
Seq 2746 <i>Clostridiales</i>	yellow
Seq 2796 <i>Lachnospiraceae</i>	yellow
Seq 2845 <i>Enterobacteriaceae</i>	yellow
Seq 2999 <i>Saccharofermentans acetigenes</i>	yellow
Seq 3110 <i>Porphyromonas bennonis</i>	yellow
Seq 3214 <i>Dietzia</i>	yellow
Seq 3463 <i>Cloacibacterium normanense</i>	yellow
Seq 3676 <i>Micrococcaceae</i>	yellow
Seq 3704 <i>Micrococcaceae</i>	yellow
Seq 3768 <i>Actinomycetales</i>	yellow
Seq 3889 <i>Corynebacterium</i>	yellow

Seq 4378	Massilia	yellow
Seq 4589	Peptococcus niger	yellow
Seq 4590	Actinomycetales	yellow
Seq 4593	Veillonella	yellow
Seq 4594	Eubacterium desmolans	yellow
Seq 4795	Bacteroidetes	yellow
Seq 4822	Sphingobacterium faecium	yellow
Seq 4824	Prevotella bergensis	yellow
Seq 4825	Chryseobacterium	yellow
Seq 4827	Megasphaera elsdenii	yellow
Seq 4829	Selenomonas artemidis	yellow
Seq 4830	Bacteroidetes	yellow
Seq 5069	Clostridiales Incertae Sedis XI	yellow
Seq 5104	Facklamia	yellow
Seq 5152	Prevotella nanceiensis	yellow
Seq 5153	Atopostipes suicloacalis	yellow
Seq 5154	Prostheco bacter	yellow
Seq 5155	Stenotrophomonas maltophilia	yellow
Seq 5603	Prevotella buccalis	yellow
Seq 5604	Bacteria	yellow
Seq 5605	Sphingomonadaceae	yellow
Seq 5606	Moheibacter	yellow
Seq 5607	Moraxella	yellow
Seq 6221	Staphylococcus	yellow
Seq 6222	Ruminococcus champanellensis	yellow
Seq 6410	Peptostreptococcus anaerobius	yellow
Seq 6417	Burkholderiales	yellow
Seq 6418	Porphyromonas	yellow
Seq 6432	Bacteria	yellow