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Title	Functional environmental screening of a metagenomic library identifies stlA; a unique salt tolerance locus from the human gut microbiome
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Figure S4. Comparisons of gene arrangement on SMG 25 fosmid insert and scaffolds with *stlA* homologues from Human Microbiome Project.

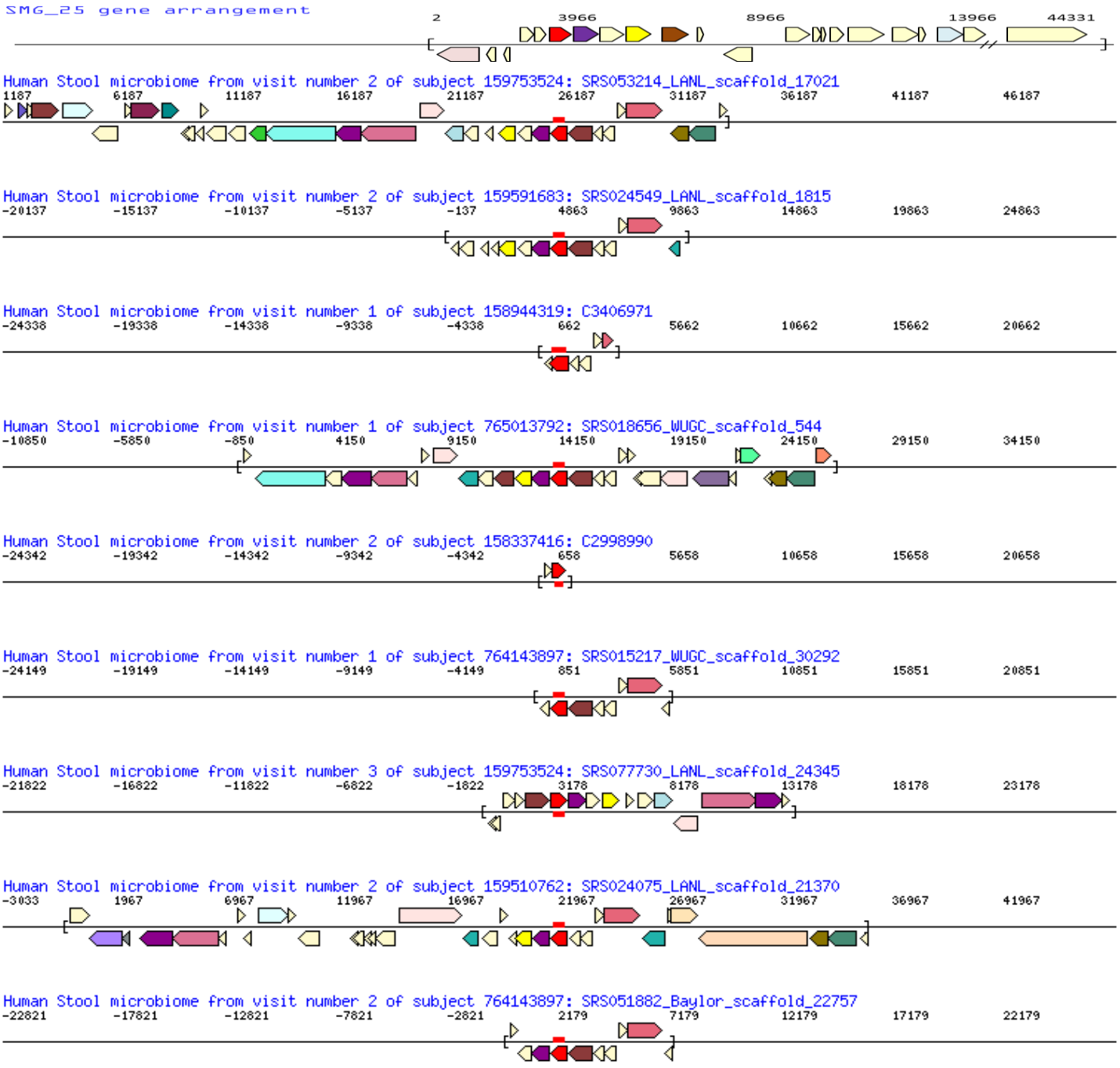


Figure S4. The gene neighbourhood region of the *stlA* gene from SMG 25 is compared with gene neighbourhoods from scaffolds with an *stlA* homologue. Homologues of *stlA* were identified through similarity searches (BLASTP; 1e-^{50} cut-off) to the Human Microbiome Project (HMP) datasets. Ten *stlA* homologues were identified and only from the stool microbiome. A legend describing putative

gene functions is presented below datasets. Ten *stlA* homologues were identified and only from the stool microbiome. A legend describing putative gene functions is presented below.

Legend: Red = Hypothetical/membrane protein (*stlA* and homologues); Cream = Hypothetical protein; Dark purple = NADH:ubiquinone oxidoreductase (COG0838); Medium brown = Fucose permease (COG0838); Light blue = Site-specific recombinase, XerD (COG4974); Dark brown = Uncharacterized protein related to capsule biosynthesis enzymes (COG3550); Dark blue/grey = Predicted restriction endonuclease (COG3183); Green = Predicted metal-dependent hydrolase (COG1451); Light-medium blue = Type I site-specific restriction-modification system (COG0610); Light purple = Restriction endonuclease (COG0732); Light maroon = Type I restriction-modification system methyltransferase subunit (COG0286); Light pink = Restriction endonuclease (COG1715); Medium blue = ATP-dependent nuclease (COG3857); Yellow = Predicted membrane protein (TM2 domain) (COG2314); Purple = DnaJ-class molecular chaperone with C-terminal Zn finger domain (COG0484); Brown = Ankyrin repeat protein (COG0666); Dark pink = Serine/threonine protein kinase (COG0515); Olive = Uncharacterized protein with von Willebrand factor (vWF) domain (COG4245); Dark blue = Uncharacterized protein with protein kinase and helix-hairpin-helix DNA-binding domains (COG4248); Light mint green = Virulence protein (COG3943); Mint green = RecB family exonuclease (COG2887); Pink = Predicted oxidoreductase (COG0667); Purple/grey = Hydrolases of the alpha/beta superfamily (COG1073); Light green = Transcriptional regulator, AraC-type DNA-binding domain-containing proteins (COG2207); Orange = Predicted ATPase (AAA+ superfamily) (COG1373); Light grey = Site-specific recombinase, DNA invertase Pin homologs (COG1961); Dark cream = Filamentation induced by cAMP protein (COG3177); Light orange = Predicted helicase (COG4889).