

Title	A diverse range of human gut bacteria have the potential to metabolize the dietary component gallic acid
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Figure S1

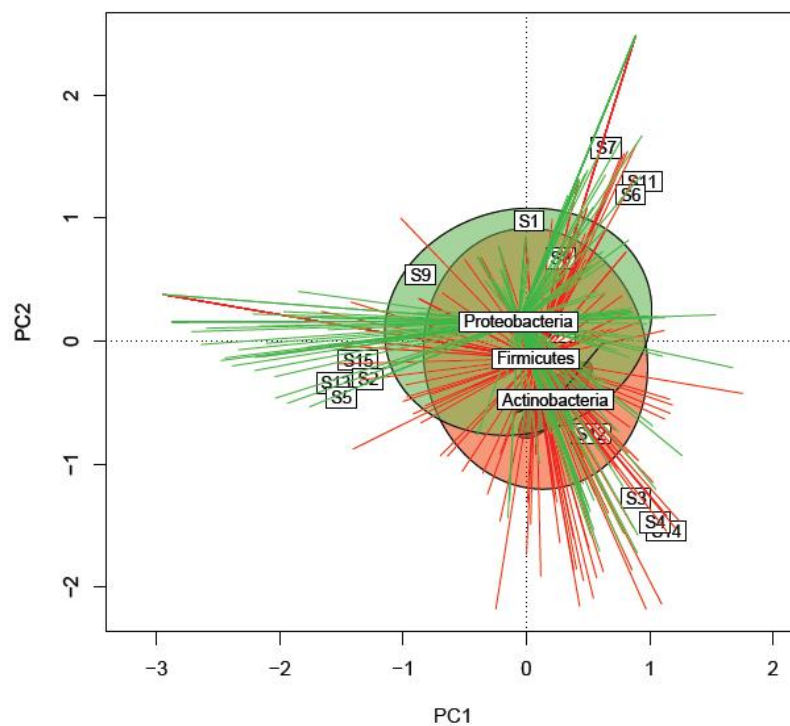


FIG S1. Principal component analysis results at the genus/species composition among samples from the human gut microbiota of athletes

Figure S2

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LRH      -----MTASPWDLRKVLDELKQDPQQYHETDVQVDPDAELAGVYRYIGAGGTV
LPL      -----MAEQPWDLRRVLDEIKDDPKNYHETDVEVDPNAELSGVYRYIGAGGTV
PET      -----MAKKDVYDLRKVLDELKKEPGQYHETNVEVDPDAELSGVYRYIGAGGTV
ERA      -----MSTPYDLRKVLAELQEMPGEYHETNVEVDPHAELSGVYRYIGAGGTV
SGA      -----MSEQPYDLRKVLEELKEIPGQYHETDVEIDPNAEISGVYRYIGAGGTV
ECL      -----MQNPINDLRSAILLQRHPGHYIETDHPVDPNAELAGVYRHIGAGGTV
ACH      MEQP---FPAFIDFPPINDLRSALARLQQVPGQLLHTDHPVDPHGELAGVYKRVGAGGTV
KIN      ----MNRTDHTANSPVIDLRSALARLEQSPDELISTDHEIDPRSELAGVYKRVGAGGTV
ATR      MEDNVMDRTDHAANSFVIDLRSALARLEAFPGELISTDQEVDPSELAGVYKRVGAGGTV
AGL      -----MNDTIHDLRSALDYLRDMPGQLLETDTDEVDCDAEVSGVYRHVGAGGTV
ERY      -----MKEPYDLRSALQQLEAEEGQLLITDKLTNTDGELAGVYRYIGGGGTL
COP      -----MSKKKVRDLRSALELLQSIDGQLVETDVEVDPLGELSGVYRHVGAGGTV
BLA      -----MAEKVRDLRSALALLEQMPDQLIETEVEVDPMaelAGVYRYVGAGGTV
FIR      -----MADKVRDLRSALERLKTMEGQYIETDVEVDPMaelAGVYRYVGAGGTV
AHA      -----MQDKVRDLRSALKRKLQMEGQYIETDVEVDPMaelAGVYRYVGAGGTV
LAC      -----MQDKVRDLRSALKRKLQMEGQYIETDVEVDPMaelAGVYRYVGAGGTV
DLO      -----MAAKVTDLRSALKMLEDMPGQLIETDVEVEPMaelSGVYRHVGAGGTV
IBA      -----MNKVRDLRSALELLENMPGQLIETDVEVDPMaelSGVYRHVGAGGTV
CBU      -----MSNKVYDLRSALELLKTLPGQLIETDVEVDPMaelAGVYRYVGAGGTV
HHA      -----MVEDLRSAVEELKKYENQIACDTDEVDSYAEVAGIYRYVGAGGTV
TSA      ---MKIKERVNKMANKIHDLSAIEFLKQHENQIVYTNSEVDCEAEISGIYRYVGAGGTV
PAG      -----MSGKESKVNDLRSALALLSQYDNELIYTDEPVDPAELSGVYRYVGAHGTV
HAL      ----MANNADNKIKNPIHDLRSALEFLKNQPGELVSTNVEVDPCAELSGVYRYVGAGGTC
SBL      -----MKNKDKIPVHDLRSALELLKTLPGEYVETFTTEVDPHAELSGVYRYVGAGGTC
KRA      ----MSNSENKNTSGVTDLRSALIELLKTLPGEYVETDTEVDPHAELSGVYRYVGAGGTC
KMI      ----MANSDNKTPSSVHDLRSALELLKTLPGEYVETDTEVDPHAELSGVYRYVGAGGTC
          ***  .:  :      .      *      :      .*:*:*:*: :*. **

LRH      ERPTQ-EGPAMMFNNVVGFPDTRVLIGLMSARKRVGKMFHQDYHTLGRFLNKAVLNPIQP
LPL      QRPTQ-EGPAMMFNNVKGFPDTRVLITGLMASRRRVGKMFHHDYQTLGQYLNEAVSNPVAP
PET      QRPTQ-EGPAMMFNNVKGFPDTRVLMGLMASARKRVGKMFHHDYHTLGQFLNDSVENPVDP
ERA      KRPTK-EGPAMMFNCVKGFPDTRVLIGI IASRDRVGKILHHDPKHLGRLLKDSVQNPVKP
SGA      ERPTQ-EGPAMTFNNIKGFPNVRVNIGTMASARKRVGHILHHDYKDLGHLLNKAVENPVKP
ECL      KRPTR-TGPAMMFNSVKGYPGSRILVGMHASRERAALLLGCVP SKLAQHVGQAVKNPVAP
ACH      KRPTR-LGPAMMFNHIKGYPDSRVLVGMASRERVALLLDTTPDRLAERMGEAIEKAIDP
KIN      MRPTR-TGPAMMFENVKGYPGARVLVGLMAKRERVALLLDSRPEELGRRMGEAVLNGIAP
ATR      MRPTR-TGPAMMFENVKGYPGARVLVGLMAKRERVALLLDSKPEELGQRMGEAVLNGIAP
AGL      ARPTK-EGPAMVFNNVKGFPDPAKVAIGLLSSRKRVAALLGMDEQYLGQLIGQKLAETIPP
ERY      QRPTQ-LGPAMLFTNIQNHGPSRVLIGLLGDRQRCASLLNTTSEQLPFLMNKAYSKRLDP
COP      MRPTQ-EGPAMIFNHVKGHPGARVAIGLLASRRRVGYLLDCEPQKLGFLLKDSVNNPIKP
BLA      KRPTK-EGPAMIFNRIKGHPDARVAIGLLASRKRVAALLDTPENLGKMLCKSVENPIPP
FIR      KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKRVAALLDCKPEELGKKLYYSVDNPIPP
AHA      KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKHVAALLDCKPEELGKKLYHSVDNPIAP
LAC      KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKRVAALLDCKPEELGKKLYHSVDNPIAP
DLO      MRPTK-EGPAMIFNNVKGHPGARVAIGVLASRTRVGALLECDPKDLGKKLYHSVDNPIPP
IBA      QRPTK-EGPAMIFNNVKGHKDARVLIGLLASRKRVAALLGTEPEDLGKKLYRSVDNPIPP
CBU      QRPTK-EGPAMIFNNIKGHK DARVLIGLLASRRRVVAALLDCEPENLGKKLYRSVDNPIAP
HHA      KRPTK-EGPALLFRNIKGFPDQVLIIGLLASRKRVG YLLDCCPDKLGFLLLKDAAANPVMP
TSA      MRPTK-IGPAMLFNHVKDYEHSKVLIGLFASRERVGLMLGCEPDRLGFLLLNDALNHPVDP
PAG      KRPTR-VGPAMVFNKIKGFNDMRVLIGLLSSRQRVARLFGTSPENLAFMLKDSVLNPIPP
HAL      QRPTRKNGPAMVFNKIKGFDDISVTIGLNGSRKRVG HFLNCAPERLGHLLKDSVKNAIQP
SBL      QRPTRKNGPAMVFNKIKGFRNTNVAIGLNGSRKRVG HFLNCAPEKLGHLLKDSVKHAIAP
KRA      QRPTRKNGPVMVFNKIKGFKDISVAIGLNGSRKRVS HFLNCAPEKLGHLLKDSVQNPPIPP
KMI      QRPTRKNGPVMVFNKIKGFKDISVAIGLNGSRQRVSHFLQCEPAKLGHLLKDSVENAIAP
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LRH	VTVE-ESAAPAHEVVAKASDPDFDIRKLVAAPTNTPQDAGPYITCGVVLGSNMAK-TMTD
LPL	ETVA-EADAPAHDVVYKATDEGFDIRKLVAAPTNTPQDAGPYITVGVVFGSSMDK-SKSD
PET	VMVD-EADAPTHEVVHKSTDAADFDIRKLVAAPTNTPRDAGPYITVGVVYGSNPDK-TMSD
ERA	VKVA-KTDAPAQEVVHLATDEGFDIRKILAAPTNTEYDAGPYITMGVVFGSDPEK-TMSD
SGA	VKVS-KDQAPAQEVVHLATDDDFDIRKILAAPTNTEYDAGPYITTLGVYGSTPDK-SMSD
ECL	VVVP-ASQAPCQEQVFYADDPDFDLRKLLPAPTNTPIDAGPFFCLGLVLASDPEDTSLTD
ACH	VVVP-REQAPCQEQIVHRAEDPGFDLRTLLPAPTNTDEDAGPFFCLGLVLGSDPEE-GHAD
KIN	VVLK-GQSAPCQEQIFRADDPHFDLRNLLPAPTNTTEEDAGPYFCLGLLLGSDDPN-GHTD
ATR	VVFK-EGSAPCQEQVFRADDPNFDLRHLLPAPTNTTEEDAGPYFCLGLLLGSDDPN-GHTD
AGL	APIAEGKHIDCQEVVHLATDPDFDLRRLVPAPTNTPEDAGPYVTMGLIAGHSPFN-SDTD
ERY	VVVA---KGICQEQIVHHREDEGFDIRLLPAIKATKEDAGPYITMGLCYASEPET-KESD
COP	VVIP-HEQAKCQEVKYFADDPDFDIRKLVPAPTNTLEDAGPYITLGMCYASSPET-GESD
BLA	VDLE-G-DAPCQQVVHKAADPDFDLYKLVPAPTNTPDAGPYITLGMCYATHPDT-GVHD
FIR	VEYQ-G-APPCQQVVHKAEDPDFNLYDLVPAPTNTPDAGPYITLGMCYATHPDT-GVHD
AHA	VEYQ-G-DAPCQQVVHKVEDPDFNLYDLVPAPTNTPDAGPYITLGMCYATHPDT-GVHD
LAC	VEYQ-G-DAPCQQVVHKVEDPDFNLYDLVPAPTNTPDAGPYITLGMCYATHPDT-GVHD
DLO	VLTE-EA-APCQEVVHKATDPDFDLYKLVPAPTNTPDAGPYITLGMCYASHPDT-GVSD
IBA	VLTD--KTPLCQEVVHRATDEDFDLYKLVPAPTNTPDAGPYITLGMCYASHPDT-GCSD
CBU	VLTD-AKLPLCQQVVHKATDPDFDLNKLVPAPTNTPDAGPYITLGMCYASHPDT-KFSD
HHH	EFTE-SGDVPCQEEIHYASDEGFDIRKILPAPQNTTEEDAGPYITMGMCYASDPVT-GDGD
TSA	IEIP-QAKAKCQEVVHLSTDEGFDIRKILPAPKNTLEDAGPYITMGLCYASDPDT-KAGD
PAG	IVIP-REHAVCQEVVHLATDPDFDILKILPTPTNTPEDAGPYITLGMCYAADPET-GEHD
HAL	VTVS-ADKAVCQQVTHFAEDADDFDLRKLLPAPTNTTEEDAGPYITMGLCYASDPDT-HESD
SBL	VDVS-TGNAVCCQEVVHLATDPDFDLRKLLPAPTNTTEEDAGPYITMGLCYASDPQT-HESD
KRA	IL-T-KDNAVCQQVVHLASDTNFDLRKLLPAPTNTTEEDAGPYITMGLCYASDPET-HESD
KMI	VM-A-QGAAVCQQVVHLASDADFDRKLLPAPTNTTEEDAGPYITMGLCYASDPET-HESD
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LRH	VTIHRMVLEDKDTLGIYIMPGGRHIGHFAEEYEKANKKMPVTINIGLDPAITIGATFEPP
LPL	VTIHRMVLEDKDKLGIYIMPGGRHIGAFAEYEKANKKMPITINIGLDPAITIGATFEPP
PET	VTIHRMVLEDKDKLGIYIMPGGRHIGKFAEEYEKMNKMPITINIGLDPAITIGATFEPP
ERA	VTIHRMVLEDEDTIGMYIMPGGRHIGHFQKQYEALNKMPITINIGLDPAISIGTTFEPP
SGA	VTIHRMVLEDKDTIGIYIMPGGRHIGAFLESEYQKLNKMPITINIGLDPAILIGATFEPP
ECL	VTIHRLCVQERDELSMFLAAG-RHIEVFRKKAEAAAGKPLPVTINMGLDPAIYIGACFEAP
ACH	VTIHRLCVQGRDRLSIFFAPD-RHIDKFRQKAEAAAGKPLPVTINMGLDPAIIGSCFEAP
KIN	VTIHRLCVQGRDELSVFFAPG-RHIDAFRAKAEERGEALPITINMGLDPAIPIGACFEAP
ATR	VTIHRLCVQGRDELSVFFAPG-RHIDAFRAKAEERGEALPITINMGLDPAIPIGACFEAP
AGL	VTIHRLCIESKDTMGMWITPGSRHLGAFFEQWKEKGEDMPVTVSIGLDPAVYMCAGFEAP
ERY	VTIHRCLCQSKDEMTMFFTPGIRHLDVFRKKAEAKNKALPISISIGVDPALIEIAACFEPP
COP	VTIHRMCFQSKDEISIFLQPGARHIGYFRELAEAKGEALPISISIGVDPALIEIASCFEAP
BLA	VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEEELGQRLPISISIGVDPALIEIGSCFEPP
FIR	VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEEELGQKLPIISISIGVDPALIEIGSCFEAP
AHA	VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEEELGQKLPIISISIGVDPALIEIGSCFEAP
LAC	VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEEELGQKLPIISISIGVDPALIEIGSCFEAP
DLO	VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEEELGQRLPISISIGVDPALIEIGSCFEPP
IBA	VTIHRLCIQSKDELSIFFTPGARHIGAMAERAEEELGQKLPIISISIGVDPALIEIGSCFEPP
CBU	VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEEELGQNLPIISISIGVDPALIEIGSCFEPP
HHH	VTIHRCLCQSADEMTMFFTPGVRHLDAFREKAEREQVNLPIISISIGVDPALIEIASCFEPP
TSA	ITIHRCLCQSKDELTMFFTPGVRHIDAFRKKAEAGQNNLPISISIGVDPALIEIYVTSFEPP
PAG	VTIHRLCVQSKDEISMYFVPG-RHLDTFRQKAEAAAGKPLPITISIGVDPALIEIGACFEPP
HAL	ITIHRLCVQSRDELSMWLTPG-RHIDAFRMKAEAAQKPLPIISISIGVDPALIEIAACFEPP
SBL	ITIHRLCVQSKDELTMWLTPG-RHIDAFRIKAEAAAGKALPIISISIGVDPALIEVAACFEPP
KRA	ITIHRLCVQSRDELSMWLTPG-RHIDAFRMKAEAAAGKPLPIISISIGVDPALIEIAACFEPP
KMI	ITIHRLCVQSRDELSMWLTPG-RHIDAFRMKAEAAAGQPLPIISISIGVDPALIEIAACFEPP
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LRH	TTPLGYDELGVAGAIRQEPVQLVQAVTVDEKAIARSEFTLEGYIMPNTRIQEDINTHTGK
LPL	TTPFGYNELGVAGAIRNQAVQLVDGVTVDKAIARSEYTLLEGYIMPNERIQEDINTHTGK
PET	TTPLGYNELGVAGAIRQEPVQLVKGLTVDEKAIARSEYTLLEGYIMPNERIQEDINTHTGK
ERA	TTPLGYNELWVAGALRQEPVQLVDGVAVDEVGIARSEFIIIEAEILPHETIQEDINTNTGK
SGA	TTPLGYNELWVAGALRNEPVQLVDSIAVDEVGIARSEFIIIEGEILPNETIQEDINTHTGH
ECL	TTPFGYNELGVAGALRQQPVVELVQGVAVKEKAIARAEIIIEGELLPGVRVREDQHTNTGH
ACH	TTPLGYDELKIIAGGLRGRPVELVEAVSIGQKAIARAEVVIIEGEILPHERLREDINTDSGR
KIN	TTPLGFDELTVAGGLRGRAVELVDVAVTVKERSIARAEIVIEGEILPGRRIREDVNTNTGH
ATR	TTPLGFDELTVAGGLRGRAVELVDVAVTVKERSIARAEIVIEGEILPGRRIQEDVNTNTGH
AGL	TTPLGYNELQIAGGIRGRAVELAPALTVPETCIAHAEYVIEGYLSITDTVREDVNTNTGK
ERY	TTPLGFNELSIIAGGIRNKPVELCKCVSIIIDEYAIHASEYVIEGELLPGKRMREDQHTGLGK
COP	TTPLGYDELQVAGAIRNEPVELVECLTINERAIANAAYVIEGEILPGKRIREDIHSNTGK
BLA	TTPLGYDELSVAGALRKEPVELCKCLTVNRAIANAEYVIEGEVILPGVRKREDQNSNTGY
FIR	TTPLGYDELAVAGALRNEPVELCKCLTVNEMAIAANAAYVIEGEVILNVRVQEDQNSHTGY
AHA	TTPLGYDELSVAGALRNEPVELCKCLTVNEMAIAANAAYVIEGEVILPNVRVQEDQNSHTGY
LAC	TTPLGYDELSVAGALRNEPVELCKCLTVNEMAIAANAAYVIEGEVILPNVRVQEDQNSHTGY
DLO	TTPMGYDELAVAGALRGEPVRLCKCLTVNRAIANAEYVIEGEVVPNVRVQEDQNSHTGY
IBA	TTPMGYDELAVAGALRGEAVELCNCLTVNEKAIANAAYVIEGEVILPNVRVQEDQNSNTGY
CBU	TTPLGYDELSVAGALRGKPVLECKCITVNERAIANAAYVIEGEVILPNLRVQEDKNSNTGY
HHA	TTPLGFNELSIIAGALRKKPVMAKCRITIDEYAIANAFAVIEGELVAGKRMREDINTNTGK
TSA	ATPLGFNELSIIAGGLRGKPVLETKCLTIDEMAIAANAAYVIEGELVFGQRMREDINTNTGK
PAG	TTPLGFDELSVAGSLRNQAVELVDCLTVNARGIANAEIVIEGELVPNYRVREDQNTNTGK
HAL	TTPLGFDELSIIAGALRGHAVEMVQCKTINEKAIHAEIVIEGELLPNLRVREDQNTNTGK
SBL	TTPLGFNELSIIAGALRGRAVEMVQCKTINEKAIHAEIVIEGELLPDVRMQEDINTHTGR
KRA	TTPLGYDELSVAGALRGKAVEMVQCKTINERAIHAEIVIEGELLPNVRLREDQNTNTGK
KMI	TTPLGFNELSIIAGALRGKAVEMTQCKTINEKAIHAEIVIEGELRPNARVREDQNTHTGR
	***:** ** * * * * * * * * * *

[illegible]

LRH	RAIPGKVKNVYNPPAGGGKLMTIMQIHKDNPADEGIQRQAALLAFSAFKEKLTWVL	VDDD
LPL	RAIPGKVTNVYNPPAGGGKLMTIMQIHKDNEADEGIQRQAALLAFSAFKEKLTVIL	VDED
PET	RAIPGKVLNVYNPPAGGGKLMTIMQIHKDNAADEGIQRQAALLAFSSFKELKTVFL	VDED
ERA	KAIPGKVTNVYNPPAGGGKLMSTILQIHKESEADEGIQRQAAILALSFAFKEKLTVIL	VDDD
SGA	KAIPGKVLNVYNPPAGGGKLMTIMQIRKENPADEGIQRQAALLAFSSFKELKTVIL	VDED
ECL	EAIPGFLQNVYAHTAGGGKFLGILQVKKRQPSDEGRQQAALIALATYSELKNIIIL	VDED
ACH	RAMPGLLKNVYAHTAGGGKLLAVLQVAKRRPGDEGRQRQAALIALAVYRELKNVIL	VDED
KIN	KALPGFVKNVYAHSAGGGKLLAILQVCQRSAGDVGKARQAALIALAVYRELKNVII	VDDD
ATR	KALPGFVKNVYAHSAGGGKLLAILQVCQRSAGDAGKARQAALIALAVYRELKNII	VDDD
AGL	TAIPGRLNVHAAPCGGGKFVAVLQFKKSSINDEGRQRNAAMLAFSAFSELKHVFL	VDED
ERY	KAMPGNVRNVHCASSGGGKYIAVLQFVKRMESDEGRQRQAALLAFSAFSELKHVFL	VDED
COP	KAMPGKLQNVYCASSGGGKYIAVMQFKKSVPSDEGRQRQAALLAFSAFAELKHVFL	VDED
BLA	KAMPGRLQNVYCASSAGGGKYMAVLQFKKLSQSDEGRQRQAALLAFSAFSELKNVFL	VDED
FIR	KAMPGRLQNVYCGSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHVFL	VDED
AHA	KAMPGRLQNVYCGSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHVFL	VDED
LAC	KAMPGRLQNVYCGSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHVFL	VDED
DLO	KAMPGRLQNVYCASPGGGKYMAVLQFKKLTASDEGRQRQAALLAFSAFSELKHVFL	VDED
IBA	KAMPGRLQNVYCASSAGGGKYMAVLQFKKSVASDEGRQRQAALLAFSAFSELKNIFI	VDED
CBU	KAMPGRLQNVYCCSSGGGKFMAVLQFKKTVASDEGRQRQAALLAFSAFSELKNIFL	VDED
HHH	KALAGRVKNVYAHRSGGGKYMAVIQFAQVPSDEGRQRQAALIALTAFPELKHVIV	VDED
TSA	RAMPGRVLNVYAHSSGGGKYLAAILQFKKSI PSDEGRQRQAALVAFSAFPELKHVIL	VDED
PAG	RALPGFVQNVHCPSPGTGKYLAVLQVKKRFVDEGRQRQAALLAFSAFSELKHVML	VDED
HAL	RAMPGKLLNVFAHSAGGGKLLAVMQFKKSAPVDEGRQRQAALLAFSAFSELKHVIL	VDED
SBL	RAMPGKLLNVFAHSAGGGKLLAVMQFKKSSVNDEGRQRQAALLAFSAFPELKHVIL	VDED
KRA	RAMPGKLLNVFAHSAGGGKLLAVMQFKKFS PADEGRQRQAALLAFSAFPELKHVIL	VDED
KMI	RAMPGKLLNVFAHSAGGGKLLAVLQFKKSSPADEGRQRQAALLAFSAFPELKHVIL	VDED

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LRH	VDIE	DMNDVVWMTMNTRFQGDQDIMVLPGMRNHPLDPSERPQYDPKSI RVRGMSSKTVIDG
LPL	VDIE	DMNDVIWMTMNTRFQADQDLMVLSGMRNHPLDPSERPQYDPKSI RFRGMSSKLVIDG
PET	VDIE	DMNDVVWMTINTRFQADQDIMVLPGMRNHPLDPSERPQYDPKSI RTRGMSSKLVIDG
ERA	VDIE	DMNDVMWMTLNTRFQGDQDILVLPGMRNHPLDPSERPQYDPKSI RFRGMSSKTIIDG
SGA	VDIE	DMNDVMWMTINTRFQAHKDIMSLEGMRNHPLDPSERPQYDPKSI RVRGMSSKLVLIDG
ECL	VDIE	DSDDILWAMTTRMQGDVSIITLPGIRGHQLDPSQSPDYST-SIRNGNISCKTIFDC
ACH	VDIE	DSDDVLWAMQTRYQGDVDTIFVPGVPGHVLDPQVPEYSP-SIAARGLTCKTIFDC
KIN	VDIE	DSNDVLWAMQTRYQGNVDTMFLPGVTGHVLDPQVPEYDP-SIPAKGVSKTIFDC
ATR	VDIE	DSNDVLWAMQTRYQGNVDTMFLPGVTGHVLDPQVPEYDP-SIPAKGVSKTIFDC
AGL	VDIE	DMSDVMWAMTTRFQADTGLITIPGAHCHVLDPNDPAFAP-SIRVHGIACKAIFDC
ERY	VDIE	DMKDVLWAMTTRFQSDIDCISIPGVRCHPLDPSNDTTYDP-SIRDRGIACKAIFDC
COP	VDIE	DMKDVMWAMTTRFQADLDLITIPGVQCHPLDPSNQPEYSA-HIRARGVACKAIFDC
BLA	VDIE	DMNDVLWAMNTRFQGDVDVITIPGVRCHPLDPSNDPAFSP-SIRDHGIACKTIFDC
FIR	VDIE	DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSP-SIRDHGIACKTIFDC
AHA	VDIE	DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSS-SIRDHGIACKTIFDC
LAC	VDIE	DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSS-SIRDHGIACKTIFDC
DLO	VDIE	DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPSCSG-SIRDHGIACKTIFDC
IBA	VDIE	DMNDVLWAMNTRFQGDVDVITIPGVRCHPLDPSNDPSFSP-SIRDHGIACKTIFDC
CBU	VDIE	DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPDYSP-SIKNHGIACKTIFDC
HHH	VDIE	DSDDVLWALNTRYQGDVDTITIPGVRCHPLDPTEGPEYNP-MLKDRGISCKTIFDC
TSA	VDIE	DSNDVLWALTTRYQGDLDTVFIPGVRCHPLDPSSSNLYHP-SILSTGIACKTIYDC
PAG	VDIE	DLSDVMWAMTTRYQGDVSTVFIPGVRCHPLDPSSDPAFSP-SVRDHGITCKTIFDC
HAL	VDIE	DSDDVMWAMQTRYQGDVDTVFIPGVRCHPLDPSQMPDYSP-SILQEGMSCKTIFDC
SBL	VDIE	DTDDVLWAMQTRYQGDIDTITIPGVRCHPLDPSQVPEYSP-FITQQGMTCKTIFDC
KRA	VDIE	DSDDVLWAMQTRYQGDVDTVTIPGVRCHPLDPSQIPAYSP-SILQQGMSCKTLFDC
KMI	VDIE	DSDDVLWAMQTRYQGDVDTIVIPGVRCHPLDPSQVPEYSP-SILQQGMSCKTIFDC

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LRH	TVPFDMRDQFKRAAFKKVS--DWQKYLK-----
LPL	TVPFDMKDQFERAQFMKVA--DWEKYLK-----
PET	TVPFDMKDQFERAQFKEVK--DWEKYLK-----
ERA	TVPFDLKDDFIRAEFKEVP--DWEKYLK-----
SGA	TVPFDMKDQFERAKFKEVP--DWKKYLD-----
ECL	TVPWALKARFERAPFMEVDPTWAPELFSDKK-
ACH	TAPWHLRERFERAKFRDVPHPFAPELFPQARS
KIN	TYPWKLKEHFVRAQFRDVPHPFAPSIFPKAGM
ATR	TYPWKLKEHFVRAQFREVDHPHPFAPSIFPKAGM
AGL	TVPYDLKDEFQRCRFLDIDQDKWAAELAH----
ERY	TVPFSQKERFQRAAFQEVEASQWLK-----
COP	TVPFDQKARFERAKFMDVDPKCWLPLDMLK----
BLA	TVPYDLKEDFHRARFMELDPEKWLKK-----
FIR	TVPYDQKERFKRARFMEVDPEHWL-----
AHA	TVPYDQKERFKRARFMEVDPEHWLS-----
LAC	TVPYDQKERFKRARFMEVDPEHWLS-----
DLO	TVPYDQKDRFKRAQFMDVDPEHWVK-----
IBA	TVPFEQKERFKRARFMDVDPEHWLKDIDK-----
CBU	TVPFHMKERFKRAKFMEVDPEHWL-----
HHA	TVPYGLKDRFQRSKFKEVNMEDEIRPLV----
TSA	TVPFIQKERFKRSSFKEVNLSYDIKPLK----
PAG	TVPYNLKANFHRSEFLEVDVNRFI PGFNQK---
HAL	TVPFHLKAHFERSRFKEADV KRFLPDFE-----
SBL	TVPFHLKTHFERSTFKEVDV KRFLPDFE-----
KRA	TVPFHLKSHFERSKFKEVDV KRFLPDFE-----
KMI	TVPFHLKHTFQRSRFKEVDV KRFLPDFE-----
	* *: : * *. * . :

FIG S2. Comparison of amino acid sequences of subunit C of putative gallate decarboxylase proteins from bacteria identified by HTS from athlete faecal microbiota. Multiple alignments were done using the programs ClustalOmega after retrieval of sequences from BLAST homology searches. The C subunits are from *Acetobacter tropicalis* (ATR) (WP_006559787.1), *Actinomyces glycerinitolerans* (AGL) (WP_073329259.1), *Anaerostipes hadrus* (AHA) (WP_009204323.1), *Azotobacter chroococcum* (ACH) (WP_052264016.1), *Blautia* sp. KLE 1732 (BLA) (WP_021650680.1), *Clostridium butyricum* (CBU) (WP_058371993.1), *Coprobacillus* (COP) (WP_008787659.1), *Dorea longicatena* CAG:42 (DLO) (CDE20644.1), *Enterobacter cloacae* subsp. *cloacae* ATCC 13047 (ECL) (YP_003612445.1), *Enterococcus* (ERA) (WP_010743655.1), *Erysipelotrichaceae* bacterium 3_1_53 (ERY) (EFP59895.1), Firmicutes bacterium CAG:270 (FIR) (CDD72954), *Hafnia*

alvei ATCC 51873 (HAL) (WP_004092226.1), *Hungatella hathewayi* (HHA) (WP_006771947.1), *Intestinibacter bartlettii* (IBA) (WP_007285641.1), *Klebsiella michiganensis* KCTC 1686 (KMI) (AEX02211.1), *Komagataeibacter intermedius* (KIN) (WP_039733191.1), *Kosakonia* (KRA) (WP_071921386.1), *Lachnospiraceae* bacterium 5_163FAA (LAC) (EFV16561), *Lactobacillus rhamnosus* (LRH) (WP_005712295.1), *Lactobacillus plantarum* ATCC 14917T (LPL) (D7VDD5), *Pantoea agglomerans* strain FDAARGOS_160 (PAG) (AMG60167.1), *Pediococcus ethanolidurans* (PET) (WP_057806460.1), *Shimwellia blattae* (SBL) (WP_002441866.1), *Streptococcus* (SGA) (WP_003065832.1), and *Turicibacter sanguinis* (TSA) (WP_040763984.1). Residues that are identical (*), conserved (:) or semiconserved (.) in all sequences are indicated. Dashes indicated gaps introduced to maximize similarities. Degenerate primers were designed on the conserved domains highlighted.