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

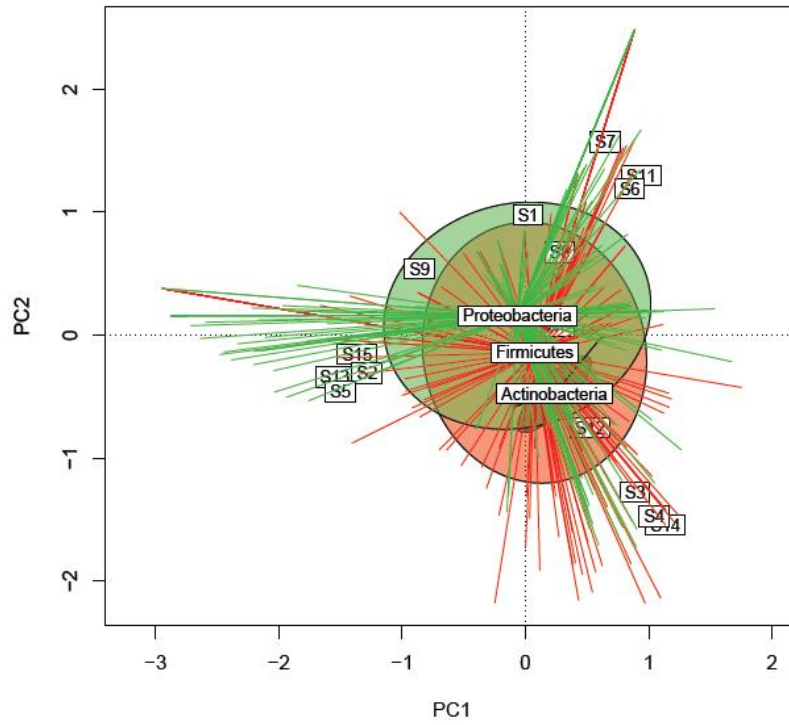


FIG S1. Principal component analysis results at the genus/species composition among samples from the human gut microbiota of athletes

Figure S2

LRH -----MTASPWDLRKVLDELKQDPQQYHETDVQVDPDAELAGVYRYIGAGGTV
LPL -----MAEQPWLRRVLDEIKDDPKNYHETDVEVDPNAELSGVYRYIGAGGTV
PET -----MAKKDVYDLRKVLDELKKEPGQYHETNVEVDPDAELSGVYRYIGAGGTV
ERA -----MSTPYDLRKVLAELEQEMPGEYHETNVEVDPHAELSGVYRYIGAGGTV
SGA -----MSEQPYDLRKVLEELKEIPGQYHETDVEIDPNAEISGVYRYIGAGGTV
ECL -----MQNPINDLRSALALLQRHPGHYIETDHPVDPNAELAGVYRHIGAGGTV
ACH MEQP---FPAFIDFPPINDLRSALARLQQVPGQLLHTDHPVDPHGELAGVYKRVGAGGTV
KIN ----MNRTDHTANSPVIDLRSALARLEQSPDELISTDHEIDPRSELAGVYKRVGAGGTV
ATR MEDNVMDRTDHAANSPIVLDLRSALARLEAFPGELISTDQEVDPSELAGVYKRVGAGGTV
AGL -----MNDTIHDLRSALDYLRDMPGQLLETDTDEVDCDAEVSQVYRHHVAGGTV
ERY -----MKEPYDLRSALQQLEAEEGQLLITDKLTNTDDELAGVYRYIGGGGTL
COP -----MSKKKVRDLRSALALLQSIDGQLVETDVEVDPPLGELSGVYRHHVAGGTV
BLA -----MAEKVRDLRSALALLQMPDQLIETEVEVDPMAELAGVYRHHVAGGTV
FIR -----MADKVRDLRSALERLKTMEGQYIETDVEVDPMAELAGVYRYVAGGTV
AHA -----MQDKVRDLRSALKRKLQMEGQYIETDVEVDPMAELAGVYRYVAGGTV
LAC -----MQDKVRDLRSALKRKLQMEGQYIETDVEVDPMAELAGVYRYVAGGTV
DLO -----MAAKVTDLRSALKMLEDMPGQLIETDVEVEPMAELSGVYRHHVAGGTV
IBA -----MNKVRDLRSALALLNMPGQLIETDVEVDPMAELSGVYRHHVAGGTV
CBU -----MSNKVYDLRSALALLKTLPGQLIETDVEVDPMAELAGVYRYVAGGTV
HHA -----MVEDLRSAVEELKQYENQIACDTEVDSYAEVAGIYRYVAGGTV
TSA ---MKIKERVNKMANQIHDLSAIEFLKQHENQIVYTNSEVDCEAEISGIYRYVAGGTV
PAG -----MSGKESKVNDLRSALALLSQYDNELIYTDPEVDPVAELSGVYRYVAGGTV
HAL ----MANNADNKIKNP IHDLSALEFLKNQPGELVSTNVEVDPCAELSGVYRYVAGGTV
SBL -----MKNKDKIPVHDLRSALALLKTLPGEYVETDTEVDPHAELSGVYRYVAGGTV
KRA ----MSNSENKNTSGVTDLRSALALLKTLPGEYVETDTEVDPHAELSGVYRYVAGGTV
KMI ----MANSNDKTPSSVHDLRSALALLKTLPGEYVETDTEVDPHAELSGVYRYVAGGTV

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LRH ERPTQ-EGPAMMFNNVVGFPTRVLIIGLMSRKRKRVGKMFHQDYHTLGRFLNKAVLNPIQP
LPL QRPTQ-EGPAMMFNNVKGFPDTRVLTGLMASRRRVGKMFHHDYQTLGQYLNEAVSNPVAP
PET QRPTQ-EGPAMMFNNVKGFPDTRVLMGLMASRKRKRVGKMFHHDYHTLGQFLNDSVENPVDP
ERA KRPTK-EGPAMMFNCVKGFPDTRVLIGI IASRDRVGKILHHDPKHLGRLLKDSVQNPVKP
SGA ERPTQ-EGPAMTFNNIKGFPNVRVNI GTMASRKRVGHI LHHDYKDLGHLNKAVERNPKP
ECL KRPTR-TGPAMMFNSVKGYPGSRILVGMHASRERAALLGCVPSKLAQHVQAVKNPVAP
ACH KRPTR-LGPAMMFNHKIGYPDSRVLVGMASRERVALLLDTPDRLAERMGEAIEKAIDP
KIN MRPTR-TGPAMMFENVKGYPGARVLVGLMAKRERVALLLDSRPEELGRRMGEAVLNGIAP
ATR MRPTR-TGPAMMFENVKGYPGARVLVGLMAKRERVALLLDSRPEELGRRMGEAVLNGIAP
AGL ARPTK-EGPAMVFNNVKGFPDARVAIGLLSSRKRVAALLGMDEQYLGQLIGQKLAETIPP
ERY QRPTQ-LGPAMLFTNIQNHGSRVLI GLLGDRQRCASLLNTTSEQLPFLMNKAYSKRLLDP
COP MRPTQ-EGPAMIFNHVKGHPGARVAIGLLASRRRVGYLLDCEPQKLGFLKDSVNNPIKP
BLA KRPTK-EGPAMIFNRKIGHPDARVAIGLLASRKRVAALLDTPENLGMMLCKSVENPIPP
FIR KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKRVAALLDCKPEELGKKLYHSVDNPIPP
AHA KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKHVAALLDCKPEELGKKLYHSVDNPIAP
LAC KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKRVAALLDCKPEELGKKLYHSVDNPIAP
DLO MRPTK-EGPAMIFNNVKGHPGARVAIGVLASRTRVGALLECDPKDLGKKLYHSVDNPIPP
IBA QRPTK-EGPAMIFNNVKGHKDARVLI GLLASRKRVAALLGTEPEDLGKLLYHSVDNPIPP
CBU QRPTK-EGPAMIFNNIKGHKDARVLI GLLASRRRVAALLDCEPENLGMMLCKSVENPIPP
HHA KRPTK-EGPALLFRNIKGFDPKQVLI GLLASRKRVGYYLLDCPPDKLGFLKDAANPVMP
TSA MRPTK-IGPAMLFNHVKDYEHKSVLIGL FASRERVGLMLGCEPDRLGFLNLDALNHPVDP
PAG KRPTR-VGPAMVFNKIKGFNDMRVLI GLLSSRQRVARLFGTSPENLAFMLKDSVKNPIPP
HAL QRPTRKNGPAMVFNKIKGFDDISVTI GLNGSRKRKRVGHFLNCAPELGHLLKDSVKNAIQP
SBL QRPTRKNGPAMVFHNKIGFRNTNVAI GLNGSRKRKRVGHFLNCAPEKLGFLKDSVKHAIAP
KRA QRPTRKNGPVMVFNKIKGFQDISVAI GLNGSRKRKRVSHFLNCAPEKLGFLKDSVQNPPIPP
KMI QRPTRKNGPVMVFNKIKGFKDISVAI GLNGSRQRVSHFLQCEPAKLGHLKDSVENAIAP

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LRH VTVE-ESAAPAHEVVAKASDPDFDIRKLVAAPTNTPQDAGPYITCGVVLGSNMAK-TMTD
LPL ETVA-EADAPAHDVVYKATDEGFDIRKLVAAPTNTPQDAGPYITVGVVFGSSMDK-SKSD
PET VMVD-EADAPTHEVVHKSTDAADFDIRKLVAAPTNTPRDAGPYITVGVVYGSNPK-TMSD
ERA VKVA-KTDAPAQEVVHLATDEGFDIRKILAAPTNTEYDAGPYITMGVVFVGSNDPK-TMSD
SGA VKVS-KDQAPAQEVVHLATDDDFDIRKILAAPTNTEYDAGPYITGLVYGSTPDK-SMSD
ECL VVVP-ASQAPCQEQVFYADDPDFDLRKLPAPTNTPIDAGPFFCLGLVLASDPEDTSLTD
ACH VVVP-REQAPCQEQIVHRAEDPGFDLRLLPAPTNTEEDAGPFFCLGLVLASDPEDTSLTD
KIN VVLK-GQSAPCQEQIFRADDPHFDLRNLLPAPTNTEEDAGPYFCLGLLLGSDDPN-GHTD
ATR VVFK-EGSAPCQEQVFRADDPNFDLRHLLPAPTNTEEDAGPYFCLGLLLGSDDPN-GHTD
AGL APIAEGKHIDCQEVVHLATDPDFDLRLLPAPTNTPEDAGPYVTMGLIAGHSPFN-SDTD
ERY VVVA---KGICQEQIVHREDEGFDIRRLLPAIKATKEDAGPYITMGLCYASEPET-KESD
COP VVIP-HEQAKCQEVKYFADDPDFDIRKLVPAPTNTEEDAGPYITLMGMCYASSPET-GESD
BLA VDLE-G-DAPCQQVHKAADPDFDLYKLVPAPTNTPDDAGPYITLMGMCYATHPDT-GVHD
FIR VEYQ-G-APPCQQVHKAEDPDFNLYDLVPAPTNTPDDAGPYITLMGMCYATHPDT-GVHD
AHA VEYQ-G-DAPCQQVHKAEDPDFNLYDLVPAPTNTPDDAGPYITLMGMCYATHPDT-GVHD
LAC VEYQ-G-DAPCQQVHKAEDPDFNLYDLVPAPTNTPDDAGPYITLMGMCYATHPDT-GVHD
DLO VLTE-EA-APCQEVVHKATDPDFDLYKLVPAPTNTPVDAGPYITLMGMCYASHPDT-GVSD
IBA VLTD--KTPLCQEVVHRATDEDFDLYKLVPAPTNTPDDAGPYITLMGMCYASHPDT-GCSD
CBU VLTD-AKLPLCQQVHKAADPDFDLNKLVPAPTNTPDDAGPYITLMGMCYASHPDT-KFSD
HHA EFTE-SGDVPCQEEIHYASDEGFDIRKILPAPQNTTEEDAGPYITMGMCYASDPVT-GDGD
TSA IEIP-QAKAKCQEVVHLSTDEGFDIRKILPAPKNTLEEDAGPYITMGLCYASDPDT-KAGD
PAG IVIP-REHAVCQEVVHLATDPDFDILKILPTPTNTEEDAGPYITLMGMCYAADPET-GEHD
HAL VTVS-ADKAVCQQVTHFAEDADFDLRKLLPAPTNTEEDAGPYITMGLCYASDPDT-HESD
SBL VDVS-TGNAVCQEVVHLATDPDFDLRKLPAPTNTEEDAGPYITMGLCYASDPDT-HESD
KRA IL-T-KDNAVCQQVHLASDTNFDLRKLLPAPTNTEEDAGPYITMGLCYASDPET-HESD
KMI VM-A-QGAAVCQQVHLASADAFDLRKLPAPTNTEEDAGPYITMGLCYASDPET-HESD
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LRH VTIHRMVLEDKDTLGIYIMPGGRHIGHFAEEYEKANKPMPVTINIGLDPAITIGATFEPP
LPL VTIHRMVLEDKDKLGIYIMPGGRHIGHFAEEYEKANKPMPITINIGLDPAITIGATFEPP
PET VTIHRMVLEDKDKLGIYIMPGGRHIGHKFAEEYEKMNKMPITINIGLDPAITIGATFEPP
ERA VTIHRMVLEDEDTIGMYIMPGGRHIGHFQKQYEALNKMPITINIGLDPAISIGTTFEPP
SGA VTIHRMVLEDKDTIGIYIMPGGRHIGHAFLESEYQKLNKMPITINIGLDPAILIGATFEPP
ECL VTIHRLCVQERDELSMFLAAG-RHIEVFRKKAEEAAGKPLPVTINMGLDPAIYIGACFEAP
ACH VTIHRLCVQGRDRLSIFFAPD-RHIDKFRQKAEAAAGKPLPVTINMGLDPAILIGSCFEAP
KIN VTIHRLCVQGRDELSVFFAPG-RHIDAFRAKAEERGEALPITINMGLDPAIPIGACFEAP
ATR VTIHRLCVQGRDELSVFFAPG-RHIDAFRAKAEERGEALPITINMGLDPAIPIGACFEAP
AGL VTIHRLCIESKDTMGMWITPGSRHLGAFFEQWKEKGEDMPVTVSIGLDPAVYMCAGFEAP
ERY VTIHRLCLQSKDEMTMFFTPGIRHLDVFRKKAEEAKNKALPISISIGVDPALIEIACFEPP
COP VTIHRMCFQSKDEISIFLQPGARHIGYFRELAEAKGEALPISISIGVDPALIEIACFEAP
BLA VTIHRLCIQKDELSIFFTPGARHIGAMAERAEELGQRLPISISIGVDPALIEIACFEPP
FIR VTIHRLCIQKDELSIFFTPGARHIGAMAERAEELGQKLPISISIGVDPALIEIACFEAP
AHA VTIHRLCIQKDELSIFFTPGARHIGAMAERAEELGQKLPISISIGVDPALIEIACFEAP
LAC VTIHRLCIQKDELSIFFTPGARHIGAMAERAEELGQKLPISISIGVDPALIEIACFEAP
DLO VTIHRLCIQKDELSIFFTPGARHIGAMAERAEELGQRLPISISIGVDPALIEIACFEPP
IBA VTIHRLCIQKDELSIFFTPGARHIGAMAERAEELGQKLPISISIGVDPALIEIACFEPP
CBU VTIHRLCIQKDELSIFFTPGARHIGAMAERAEELGQNLPLISISIGVDPALIEIACFEPP
HHA VTIHRLCLQSADEMTMFFTPGVRHLDAFREKAEREGVNLPLISISIGVDPALIEIACFEPP
TSA ITIHRMCLQSKDELTMFFTPGVRHLDAFREKAEREGVNLPLISISIGVDPALIEIACFEPP
PAG VTIHRLCVQSKDEISMYFVPG-RHLDTFRQKAEAAAGKPLPITISIGVDPALIEIACFEPP
HAL ITIHRMCLQSKDELTMWLTTPG-RHIDAFRMAKAEAAAGKPLPISISIGVDPALIEIACFEPP
SBL ITIHRMCLQSKDELTMWLTTPG-RHIDAFRIKAEAAAGKALPISISIGVDPALIEIACFEPP
KRA ITIHRMCLQSKDELTMWLTTPG-RHIDAFRMAKAEAAAGKPLPISISIGVDPALIEIACFEPP
KMI ITIHRMCLQSKDELTMWLTTPG-RHIDAFRMAKAEAAAGQPLPISISIGVDPALIEIACFEPP
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LRH TTPLGYDELGVAGAIRQEPVQLVQAVTVDEKAIARSEFTLEGYIMPNTRIQEDINTHTGK
LPL TTPFGYNELGVAGAIRNQAVQLVDGVTVDEKAIARSEYTLEGYIMPNERIQEDINTHTGK
PET TTPLGYNELGVAGAIRQEPVQLVKGLTVDEKAIARSEYTLEGYIMPNERIQEDINTHTGK
ERA TTPLGYNELWVAGALRQEPVQLVDGVAVDEVGIARSEFIEAEILPHETIQEDINTNTGK
SGA TTPLGYNELWVAGALRNEPVQLVDSIAVDEVGIARSEFIEGEILPNETIQEDINTHTGH
ECL TTPFGYNELGVAGALRQQPVQLVQGVAVKEKAIARAEIIIEGELLPGVRVREDQHTNTGH
ACH TTPLGYDELKVIAGGLRGRPVLEVAVSIGQKAIARAEVIEGEILPHERLREDINTDSGR
KIN TTPLGFDELTVAGGLRGRAVELVDAVTVKERSIARAEIVIEGEILPGRRIREDVNTNTGH
ATR TTPLGFDELTVAGGLRGRAVELVDAVTVKERSIARAEIVIEGEILPGRRIQEDVNTNTGH
AGL TTPLGYNELQIAGGIRGRAVELAPALTVPETCIAHAAYVIEGYLSITDVTREDVNTNTGK
ERY TTPLGFNELSIAGGIRNKPVLEKCKVSDIEYAIHSEYVIEGELLPGKRMREDQHTGLGK
COP TTPLGYDELQVAGAIRNEPVLEVECLTINERAIANAAYVIEGEILPGKRIREDIHSNTGK
BLA TTPLGYDELSVAGALRKEPVLEKCKLTVNERAIANAAYVIEGEVILNVRVQEDQNSNTGY
FIR TTPLGYDELAVAGALRNEPVLEKCKLTVNEMAIANAAYVIEGEVILNVRVQEDQNSHTGY
AHA TTPLGYDELSVAGALRNEPVLEKCKLTVNEMAIANAAYVIEGEVILNVRVQEDQNSHTGY
LAC TTPLGYDELSVAGALRNEPVLEKCKLTVNEMAIANAAYVIEGEVILNVRVQEDQNSHTGY
DLO TTPMGYDELAVAGALRGEVRLCKLTVNERAIANAAYVIEGEVVPNVRVQEDQNSHTGY
IBA TTPMGYDELAVAGALRGEAVELCNCLTVNEKAIANAAYVIEGEVILNVRVQEDQNSHTGY
CBU TTPLGYDELSVAGALRGPVLEKCKITVNERAIANAAYVIEGEVILNVRVQEDKNSNTGY
HHA TTPMGFNELSIAGALRKKPVRMAKCRITIDEYAIANAAYVIEGELVAGKRMREDINTNTGK
TSA ATPLGFNELSIAGGLRGPVLETKCLTIDEMAIANAAYVIEGELVFGQRMREDINTNTGK
PAG TTPLGFDELAVAGALRNEPVLEKCKLTVNARGIANAEIVIEGELVFNVRVREDQNTNTGK
HAL TTPLGFDELAVAGALRNEPVLEKCKLTVNARGIANAEIVIEGELVFNVRVREDQNTNTGK
SBL TTPLGFNELSIAGALRGRAVEMVQCKTINEKAIHAEIVIEGELVFNVRVREDQNTNTGK
KRA TTPLGFDELAVAGALRNEPVLEKCKLTVNARGIANAEIVIEGELVFNVRVREDQNTNTGK
KMI TTPLGFNELSIAGALRGAVEMVQCKTINEKAIHAEIVIEGELVFNVRVREDQNTHTGR
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LRH AMPEFFPGYDGDANPALQVIKVTAVTHRDRHPIMQSVIGPSEEHVSMAGIPTEASILQLVD
LPL AMPEFFPGYDGDANPALQVIKVTAVTHRKN-NAIMQSVIGPSEEHVSMAGIPTEASILQLVN
PET AMPEFFPGYDGDANPALQVIKVTAVTHRKN-DPIMQSVIGPSEEHVSMAGIPTEASILSLTN
ERA AMPEFFPGYDGDANPAVNQVVKVKAITHRKDRPIMQTTIGPSEEHVSMAGIPTEASILDLDVD
SGA AMPEFFPGYDGDANPALNVIKVAVTHRKNPIMQTTIGPSEEHVSMAGIPTEASILNLVD
ECL AMPEFFPGYDGDANPNSLPVIKVAVTMRN-HAILQTLVGPGEHHTLAGLIPTEASIRNAVE
ACH AMPEFFPGYDGDANPNSLPVIRVAVTMRN-QAILQTLVGPGEHHTLAGIPTEASIRNAVE
KIN AMPEFFPGYDGDANPALPVIKVAVTMRN-NAILQTLVGPGEHHTLAGIPTEASIFNACD
ATR AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASIFNACD
AGL AMPEFFPGYDGDANPNSLPVIRVAVTMRN-HPIMQSVIGPSEEHVSMAGIPTEASILQKME
ERY AMPEFFPGYDGDANPNSLPVIRVKAITHRK-NPIMRVCLGPGEEHVNLAGIPTEASILSLCE
COP AMPEFFPGYDGDANPELPIIKVAVTTRK-NPIMQTCIGPSEEHVSMAGIPTEASILTMVD
BLA AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
FIR AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
AHA AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
LAC AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
DLO AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
IBA AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
CBU AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
HHA AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
TSA AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
PAG AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
HAL AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
SBL AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
KRA AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
KMI AMPEFFPGYDGDANPNSLPVIKVTAVTMRN-NAILQTLVGPGEHHTLAGIPTEASILQKME
***** * .. ::::*.** * : : :**.**.**.**:***:*****

LRH RAI PGKVKNVYNPPAGGGKLMTIMQIHKDNPADEGIQRQAALLAFSAFKEKLTVWL VDDD
LPL RAI PGKVTNVYNPPAGGGKLMTIMQIHKDNEADEGIQRQAALLAFSAFKEKLTVIL VDED
PET RAI PGKVLNVYNPPAGGGKLMTIMQIHKDNEADEGIQRQAALLAFSSFKELKTVFL VDED
ERA KAI PGKVTNVYNPPAGGGKLMSTILQIHKESEADEGIQRQAAILLALSAFKEKLTVIL VDDD
SGA KAI PGKVLNVYNPPAGGGKLMTIMQIRKENPADEGIQRQAALLAFSSFKELKTVIL VDED
ECL EAI PGFQLQNVYAHTAGGGKFLGILQVKKRQPSDEGRQQAALIALATYSELKNIIL VDED
ACH RAMPGLLNVAHTAGGGKLLAVLQVAKRRPGDEGRQRQAALIALAVYRELKNVIL VDED
KIN KALPGFVKNVYAHSAAGGGKLLAILQVCQRSAGDVGKARQAALIALAVYRELKNIIVDDD
ATR KALPGFVKNVYAHSAAGGGKLLAILQVCQRSAGDAGKARQAALIALAVYRELKNIIVDDD
AGL TAI PGRLNVAHAAPCGGGKFVAVLQFKKSSINDEGRQRNAAMLAFSAFSELKHFVFL VDED
ERY KAMPGNVRNVHCASSGGGKYIAVLQFVKRMESDEGRQRQAALLAFSAFSELKHFVFL VDED
COP KAMPGLQNVYCSSAGGGKYIAVMQFKKSVPSDEGRQRQAALLAFSAFAELKHFVFL VDED
BLA KAMPGLQNVYCSSAGGGKYMAVLQFKKLSQSDEGRQRQAALLAFSAFSELKNVFL VDED
FIR KAMPGLQNVYCSSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHFVFL VDED
AHA KAMPGLQNVYCSSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHFVFL VDED
LAC KAMPGLQNVYCSSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHFVFL VDED
DLO KAMPGLQNVYCSSAGGGKYMAVLQFKKLTASDEGRQRQAALLAFSAFSELKHFVFL VDED
IBA KAMPGLQNVYCSSAGGGKYMAVLQFKKSVASDEGRQRQAALLAFSAFSELKNIFIVDED
CBU KAMPGLQNVYCSSAGGGKFMAVLQFKKTVASDEGRQRQAALLAFSAFSELKNIFL VDED
HHA KALAGRVKNVYAHSSGGGKYMAVIQFAKQVPSDEGRQRQAALIALTAFPELKHVIV VDED
TSA RAMPGRVLNVYAHSSGGGKYLAAILQFKKSI PSDEGRQRQAALVAFSAFPELKHVIL VDED
PAG RALPGFVQNVHCPSPGTGKYLAVLQVKKRFVAVDEGRQRQAALLAFSAFSELKHFVFL VDED
HAL RAMPGLLNVAFAHSAGGGKLLAVMQFKKSAVDEGRQRQAALLAFSAFSELKHFVIL VDED
SBL RAMPGLLNVAFAHSAGGGKLLAVMQFKKSSVNDEGRQRQAALLAFSAFPELKHVIL VDED
KRA RAMPGLLNVAFAHSAGGGKLLAVMQFKKSSPADEGRQRQAALLAFSAFPELKHVIL VDED
KMI RAMPGLLNVAFAHSAGGGKLLAVLQFKKSSPADEGRQRQAALLAFSAFPELKHVIL VDED
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LRH VDI FDMNDVWWTMNTREFQGDQDIMVLPGMRNHPLDP SERPQYDPKSI RVRGMSSKTVIDG
LPL VDI FDMNDVIWWTMNTREFQADQDIMVLSGMRNHPLDP SERPQYDPKSI RFRGMSSKLVIDG
PET VDI FDMNDVWWTINTREFQADQDIMVLPGMRNHPLDP SERPEYDPKSI RTRGMSSKLVIDG
ERA VDI FDMNDVMWTLNTRFQGDQDILVLPGMRNHPLDP SERPEYDPKSI RFRGMSSKTI LDG
SGA VDI FDMNDVMWTINTREFQAHKDIMSLGMRNHPLDP SERPEYSPEHIRVRGMSSKLVLDG
ECL VDI FDSDDILWAMTTRMQGDVSTITTLPGIRGHQLDPSQSPDYST-SIRNGISCKTIFDC
ACH VDPFDSDDVLWAMQTRYQGDVDTIFVPGVPGHVLDPSQVPEYSP-SIAARGLTCKTIFDC
KIN VDLFDSNDVLWAMQTRYQGNVDTMFLPGVTGHVLDPSQVPEYDP-SIPAKGVSCKTIFDC
ATR VDLFDSNDVLWAMQTRYQGNVDTMFLPGVTGHVLDPSQVPDYDP-SIPAKGVSCKTIFDC
AGL VDI FDMSDVMWAMTTRFQADTGLITIPGAHCHVLDPSNDPAFAP-SIRVHGIACKAIFDC
ERY VDI FDMKDVLWAMTTRFQSDIDCISIPGVRCHPLDPSNDTTYDP-SIRDARGIACKTIFDC
COP VDPFDMKDVMWAMTTRFQADLDLITIPGVQCHPLDPSNQPEYSA-HIRARGIACKAIFDC
BLA VDCE DMNDVLWAMNTRFQGDVDVITIPGVRCHPLDPSNDPAFSP-SIRDHGIACKTIFDC
FIR VDCE DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSP-SIRDHGIACKTIFDC
AHA VDCE DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSS-SIRDHGIACKTIFDC
LAC VDCE DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSS-SIRDHGIACKTIFDC
DLO VDCE DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPSCSG-SIRDHGIACKTIFDC
IBA VDCE DMNDVLWAMNTRFQGDVDVITIPGVRCHPLDPSNDPSFSP-SIRDHGIACKTIFDC
CBU VDCE DMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPDYSP-SIKNHGIACKTIFDC
HHA VDI FDSDDVLWALNTRYQGDVDTITIPGVRCHPLDPTEGPEYNP-MLKDRGISCKTIFDC
TSA VDI FDSNDVLWALTTRYQGDLDTVFIPGVRCHPLDPSNLYHP-SILSTGIACKTIYDC
PAG VDVE DLSVDMWAMTTRYQGDVSTVFIPGVRCHPLDPSNDPAFSP-SVRDHGITCKTIFDC
HAL VDI FDSDDVMWAMQTRYQGDVDTVFIPGVRCHPLDPSQMPDYSP-SILOEGMSCKTIFDC
SBL VDI FTDDVLWAMQTRYQGDIDTITIPGVRCHPLDPSQVPEYSP-FITQQGMTCKTIFDC
KRA VDI FDSDDVLWAMQTRYQGDVDTVTIPGVRCHPLDPSQIPAYSP-SILOQGMCKTLFDC
KMI VDI FDSDDVLWAMQTRYQGDVDTIVIPGVRCHPLDPSQVPEYSP-SILOQGMCKTIFDC
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LRH      TVPFDMRDQFKRAAFKKVS--DWQKYLK-----
LPL      TVPFDMKDQFERAQFMKVA--DWEKYLK-----
PET      TVPFDMKDQFERAQFKEVK--DWEKYLK-----
ERA      TVPFDLKDDFIRAEFKEVP--DWEKYLK-----
SGA      TVPFDMKDQFERAKFKEVP--DWKKYLD-----
ECL      TVPWALKARFERAPFMEVDPTWAPPELFSDDK-
ACH      TAPWHLRERFERAKFRDVPDHPFAPPELFPQARS
KIN      TYPWKLKEHFVRAQFRDVPDHPFAPSIFPKAGM
ATR      TYPWKLKEHFVRAQFREVDHPFAPSIFPKAGM
AGL      TYPYDLKDEFQRCRFLDIDQDKWAAELAH----
ERY      TVPFSQKERFQRAAFQVEEASQWLK-----
COP      TVPFDQKARFERAKFMDVDPKCWLPDMLK----
BLA      TVPYDLKEDFHRARFMELDPEKWLKK-----
FIR      TVPYDQKERFKRARFMEVDPEHWL-----
AHA      TVPYDQKERFKRARFMEVDPEHWLS-----
LAC      TVPYDQKERFKRARFMEVDPEHWLS-----
DLO      TVPYDQKDRFKRAQFMDVDPEHWVK-----
IBA      TVPFEQKERFKRARFMDVDPEHWLKDIDK-----
CBU      TVPFHMKERFKRAKFMVDPEHWL-----
HHA      TVPYGLKDRFQRSKFKEVNMEDEIRPLV----
TSA      TVPFIQKERFKRSSFKEVNLSYDIKPLK----
PAG      TVPYNLKANFHRSEFLEVDVNRFI PGFNQK---
HAL      TVPFHLKAHFERSRFKEADVVKRFLPDFE-----
SBL      TVPFHLKTHFERSTFKEVDVKRFLPDFE-----
KRA      TVPFHLKSHFERSKFKEVDVKRFLPDFE-----
KMI      TVPFHLKHTFQRSRFKEVDVKRFLPDFE-----
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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.