**Supporting information**

Table S1. Bacterial taxa with adjusted P-values obtained from SILVA. P-values are adjusted for multiple testing
correction in order to reduce false positive results

|  |  |  |
| --- | --- | --- |
| **Operational Taxonomic Unit** | **Stat** | **Padjusted** |
| *Synergistaceae* unclassified | -7.3808154872676 | 1.66762284764966\*10-11 |
| *Atopobium* spp. | 6.44115283003831 | 6.28417833059817\*10-9 |
| Human oral bacteria BD1-5 | -5.97344706711132 | 8.20765704263695\*10-8 |
| *Lactobacillus* spp. | 5.79192208476946 | 1.84401376196454\*10-7 |
| *Butyrivibrio* spp. | 4.49192635861786 | 0.00010744826924249 |
| *Peptostreptococcaceae* Unclassified | -4.4141529062156 | 0.000134363306731825 |
| *Solobacterium* spp. | 4.37725914643883 | 0.000141546570828339 |
| *Megasphaera* spp. | 3.82639216611577 | 0.00125306525070144 |
| *Capnocytophaga* spp. | -3.71622930326129 | 0.00178625965271426 |
| *Slackia* spp. | 3.68935550987769 | 0.00183317110352649 |
| *Bifidobacterium* spp. | 3.60381542833573 | 0.00207746602402593 |
| *Prevotella* spp. | 3.62774342664091 | 0.00207746602402593 |
| *Moryella* spp. | 3.61479440791409 | 0.00207746602402593 |
| *Clostridiales* uncultured family  | -3.47069906446576 | 0.00318961870678213 |
| *Eikenella* spp.  | -3.44468553682608 | 0.00318961870678213 |
| *Treponema* spp. | -3.45549391277486 | 0.00318961870678213 |
| *Actinomyces* spp. | 3.40579549660307 | 0.00349649354877567 |
| Candidate division SR1  | -3.15114617344019 | 0.00820899720377545 |
| *Peptococcus* spp.  | -2.95271153098626 | 0.0151770882544323 |
| *Anaeroglobus* spp. | -2.9085185050637 | 0.0167362793442853 |
| *Dialister* spp.  | 2.85002300816242 | 0.0185356122414987 |
| *Pasteurellaceae* unclassified | -2.85262356650637 | 0.0185356122414987 |
| *Fusobacterium* spp.  | -2.76470473390749 | 0.0223677043943404 |
| *Actinobacillus* spp. | 2.57588363170221 | 0.037851195377557 |
| *Mogibacterium* spp.  | 2.54009698023371 | 0.0405072547191099 |
| *Cryptobacterium* spp.  | 2.52546116174981 | 0.0408264485245026 |
| *Clostridiales* Family XIII unclassified  | -2.50630790703424 | 0.0417158992705353 |
| *Lachnospiraceae* unclassified  | -2.47339682099731 | 0.0443329908323991 |
| *Staphylococcus* spp.  | 2.45949550217167 | 0.0446910265024849 |
| *Mycoplasma* spp.  | -2.32425433737055 | 0.0609102245083872 |
| *Bifidobacteriaceae* unclassified  | 2.27507122456351 | 0.0656101540044277 |
| *Neisseria* spp.  | -2.15476249447586 | 0.0847467949973194 |
| *Streptococcus* spp.  | 2.08339956023919 | 0.0986192685632586 |
| *Tannerella* spp.  | -1.9615996339307 | 0.128774784951411 |
| *Actinobaculum* spp.  | 1.94095374693255 | 0.131744664494361 |
| *Veillonella* spp.  | 1.9313192009483 | 0.131744664494361 |
| *Porphyromonas spp.*  | -1.89714731105984 | 0.139265928252837 |
| Candidate division TM7  | 1.88168191558443 | 0.141048821322945 |
| *Clostridiales* Family\_XIII unclassified  | 1.864544117002 | 0.143434895958703 |
| *Corynebacterium* spp.  | -1.80705250546809 | 0.159573060732671 |
| *Prevotellaceae* unclassified  | -1.77289174739652 | 0.168378010836963 |
| *Scardovia* spp.  | 1.66123492145293 | 0.204932502011363 |
| *Bulleidia* spp.  | 1.53089915624901 | 0.256426878609273 |
| *Aestuariimicrobium* spp. | 1.39437716944387 | 0.320362894383997 |
| *Rothia* spp.  | -1.35187799888229 | 0.32806878526881 |
| *Lachnospiraceae* unclassified  | -1.36132819450511 | 0.32806878526881 |
| *Haemophilus* spp.  | -1.35390259424212 | 0.32806878526881 |
| *Oribacterium* spp.  | 1.31508293429885 | 0.342701473962645 |
| *Cardiobacterium* spp.  | -1.30836678277671 | 0.342701473962645 |
| *Neisseriaceae* unclassified  | 1.17534636604343 | 0.410076680620721 |
| *Kingella* spp.  | -1.07336775221857 | 0.476337327294068 |
| Unassigned bacteria | 0.949694322694806 | 0.566880704788816 |
| *Gemella* spp.  | 0.910467780594551 | 0.585308526389668 |
| *Veillonellaceae* unclassified  | 0.90694216067989 | 0.585308526389668 |
| *Clostridiales* unclassified family  | -0.780380999486458 | 0.625675090149152 |
| *Parvimonas* spp.  | 0.757755721252263 | 0.625675090149152 |
| *Catonella* spp.  | -0.779836525422117 | 0.625675090149152 |
| *Leptotrichia* spp.  | -0.777968461102738 | 0.625675090149152 |
| *Neisseriaceae* unclassified  | -0.771147774659251 | 0.625675090149152 |
| *Peptostreptococcaceae* unclassified  | 0.723772485540723 | 0.645919154884058 |
| *Filifactor* spp.  | -0.673465518484677 | 0.67175980909181 |
| *Abiotrophia* spp.  | -0.518220350498138 | 0.781174158371704 |
| *Anaerococcus* spp.  | 0.492817294386512 | 0.785083560778642 |
| *Streptococcaceae* unclassified  | 0.477938965895177 | 0.789006194443737 |
| *Aggregatibacter* spp.  | -0.437353148945581 | 0.806398357894685 |
| *Granulicatella* spp.  | -0.37081639665193 | 0.856159937732391 |
| Unassigned bacteria | -0.247627507194918 | 0.90711487588156 |
| Unassigned bacilli | 0.276687284735486 | 0.90711487588156 |
| *Peptostreptococcaceae* unclassified  | -0.288446460828179 | 0.90711487588156 |
| *Alysiella* spp.  | 0.247916136351445 | 0.90711487588156 |
| *Firmicutes* Unclassified | -0.201049173084341 | 0.918867342398189 |
| *Mitsuokella* spp.  | 0.152842191111398 | 0.940640493335124 |
| *Shuttleworthia* spp.  | 0.0894581802750933 | 0.969073097952939 |
| *Johnsonella* spp. | -0.027354889049866 | 0.987332121183642 |
| *Flavobacteriaceae* unclassified  | 0.215353503817065 | NA |
| *Erysipelotrichaceae* unclassified  | -0.14722439979293 | NA |
| *Moraxella* spp.  | 0.0668955580300727 | NA |

Table S2. Bacterial taxa with adjusted P-values obtained from Human Oral Microbiome Database (HOMD). P-values are adjusted for multiple testing correction in order to reduce false positive results

|  |  |  |
| --- | --- | --- |
| **OTU** | **Stat** | **Padjusted** |
| *Lactobacillus* spp. | -6.45409479474323 | 1.00158240008095\*10-8 |
| *Fretibacterium* spp. | 6.34234307252394 | 1.04096470860236\*10-8 |
| *Atopobium* spp. | -6.13208265092909 | 2.65990457824073\*10-8 |
| GN02 [G-2] | 5.82008532257433 | 1.35280467284957\*10-7 |
| *Solobacterium* spp. | -4.88862369655286 | 1.86839829221903\*10-5 |
| *Butyrivibrio* spp. | -4.84319234933199 | 1.95913217979891\*10-5 |
| *Lachnospiraceae* [G-3] | 4.5371194342896 | 7.49508403213552\*10-5 |
| Stomatobaculum spp. | -4.33679526344865 | 0.000166261450318532 |
| *Peptostreptococcaceae* [XI][G-7] | 4.19637141529889 | 0.000277252560309419 |
| *Peptostreptococcaceae* [XI][G-5] | 4.14105930587059 | 0.000318049109768394 |
| *Bifidobacterium* spp. | -3.85307502705096 | 0.000975564899313541 |
| *Megasphaera* spp. | -3.79912648977577 | 0.00111325345556533 |
| *Capnocytophaga* spp. | 3.73275557978932 | 0.00134034347744363 |
| *Bacteroidetes* [G-5]  | 3.6243361119194 | 0.00184041245953167 |
| *Bacteroidales* [G-2]  | 3.59848871852137 | 0.00184041245953167 |
| TM7 [F-1] Unclassified | -3.60108780487205 | 0.00184041245953167 |
| *Dialister* spp. | -3.54469236163852 | 0.00212721084096414 |
| *Eikenella* spp. | 3.49462849983156 | 0.00242635702207807 |
| Ruminococcaceae [G-2] | -3.27584159317344 | 0.00510104316088404 |
| *Bacteroidetes* [G-3] | 3.21313404741977 | 0.00601220150989153 |
| *Peptostreptococcaceae* [XI][G-4] | 3.20040409084809 | 0.00601220150989153 |
| *Prevotella* spp. | -3.17401139386961 | 0.0062872711652855 |
| GN02 [G-1] | 3.14548739349753 | 0.00663241363058447 |
| *Cryptobacterium* spp. | -3.10479004889174 | 0.0072992083770579 |
| *Treponema* spp. | 3.02821798378423 | 0.00905282091527167 |
| SR1 [G-1]  | 2.97871560919919 | 0.0102424059954776 |
| *Actinomyces* spp. | -2.91716823985772 | 0.0116059705730353 |
| *Alloprevotella* spp. | -2.92482437708152 | 0.0116059705730353 |
| *Clostridiales* [F-1][G-1] | 2.82073852171429 | 0.0152000621001537 |
| *Alloscardovia* spp. | -2.80686618773451 | 0.0152336506136489 |
| *Fusobacterium* spp. | 2.79856158850104 | 0.0152336506136489 |
| *Bulleidia* spp. | -2.64303320256354 | 0.0236230060000929 |
| *Ruminococcaceae* [G-1] | -2.62732411651554 | 0.0239922949032303 |
| *Slackia* spp. | -2.59446988299858 | 0.0256346941567233 |
| *Lachnospiraceae* [G-2] | -2.49811070989331 | 0.0328196051814825 |
| *Mogibacterium* spp. | -2.41574111523442 | 0.0401304557074349 |
| *Staphylococcus* spp. | -2.38418820617003 | 0.0414407847808214 |
| *Peptococcus* spp. | 2.39299118611006 | 0.0414407847808214 |
| *Peptostreptococcaceae* [XI][G-2] | -2.34369763989509 | 0.0450414145300286 |
| *Streptococcus* spp. | -2.28830932984125 | 0.0508748812162072 |
| *Lachnospiraceae* [G-8] | 2.27788129109764 | 0.0510120954772045 |
| *Streptococcaceae* Unclassified | -2.20793794143074 | 0.0596874084560669 |
| *Bergeyella* spp. | 2.09296387089537 | 0.0777771847710425 |
| *Actinobaculum* spp. | -2.08248285459677 | 0.0779875372247281 |
| *Veillonella* spp. | -2.02263820812174 | 0.088136944358989 |
| *Peptostreptococcaceae* [XI][G-1] | -1.96586295913614 | 0.0986288855804254 |
| *Scardovia* spp. | -1.85351350821255 | 0.12490231588979 |
| *Porphyromonas* spp. | 1.81290675163069 | 0.133871892393926 |
| *Stenotrophomonas* spp. | -1.76410047668451 | 0.145096489789445 |
| TM7 [G-6] | -1.75735811457737 | 0.145096489789445 |
| *Neisseria* spp. | 1.69341416736933 | 0.163032406381274 |
| *Selenomonas* spp. | -1.63912847084439 | 0.179022281156862 |
| *Corynebacterium* spp. | 1.62267807008069 | 0.181670910158161 |
| *Mitsuokella* spp. | -1.57600337565595 | 0.195968561557164 |
| TM7 [G-5] | 1.55948304918045 | 0.198857319998214 |
| *Propionibacterium* spp. | -1.52013502705406 | 0.209299818081401 |
| *Tannerella* spp. | 1.51538518378556 | 0.209299818081401 |
| *Oribacterium* spp. | -1.40606026531796 | 0.253327123548147 |
| *Mycoplasma* spp. | 1.3571676687232 | 0.270369862914956 |
| *Veillonellaceae* [G-1] | 1.35214738465248 | 0.270369862914956 |
| *Rothia* spp. | 1.29260609869692 | 0.295828758838883 |
| *Gemella* spp. | -1.14958991035011 | 0.371431920172595 |
| *Campylobacter* spp. | -1.09521053422064 | 0.399286442454863 |
| *Cardiobacterium* spp. | 1.05179741312851 | 0.421032977609626 |
| *Lautropia* spp. | -1.03309598970945 | 0.426821940776593 |
| *Pseudomonas* spp. | -0.955302493025047 | 0.473137526312782 |
| *Olsenella* spp. | -0.932631152786705 | 0.481984488788975 |
| *Parvimonas* spp. | -0.920687501524083 | 0.48328899282398 |
| *Peptostreptococcus* spp. | -0.797906460225923 | 0.566566365568136 |
| *Shuttleworthia* spp. | -0.71741769712723 | 0.621810129840504 |
| *Mobiluncus* spp. | -0.636544812741282 | 0.637362792923263 |
| *Bacteroides* spp. | -0.674503535068853 | 0.637362792923263 |
| *Abiotrophia* spp. | -0.622755893966515 | 0.637362792923263 |
| *Catonella* spp. | 0.682927255705345 | 0.637362792923263 |
| *Johnsonella* spp. | 0.649680787555039 | 0.637362792923263 |
| *Lachnospiraceae* [G-7] | -0.63897851562877 | 0.637362792923263 |
| *Haemophilus* spp. | 0.631908936486933 | 0.637362792923263 |
| TM7 [G-3] | -0.549758914282798 | 0.687033285753241 |
| *Lachnospiraceae* [XIV] Unclassified | -0.504781439100348 | 0.714702994183027 |
| Unassigned Other  | 0.429635408659645 | 0.754192337880151 |
| *Enterococcus* spp. | 0.423110132730617 | 0.754192337880151 |
| *Filifactor* spp. | 0.425683799778011 | 0.754192337880151 |
| *Kingella* spp. | 0.386162884757101 | 0.7752119956042 |
| *Peptostreptococcaceae* [XI][G-9] | 0.339503149211114 | 0.794696784803174 |
| *Moraxella* spp. | -0.34208891440522 | 0.794696784803174 |
| *Ottowia* spp. | 0.272130020737771 | 0.835290169380453 |
| *Aggregatibacter* spp. | -0.26644830861666 | 0.835290169380453 |
| *Lachnoanaerobaculum* spp. | -0.244262125116703 | 0.843710897418313 |
| *Peptostreptococcaceae* [XI][G-6] | 0.20189743513477 | 0.868311409745663 |
| *Granulicatella* spp. | 0.107298439102738 | 0.930594099230161 |
| *Leptotrichia* spp. | 0.0998304338996341 | 0.930594099230161 |
| TM7 [G-1] | -0.043120118205251 | 0.965605782204658 |

Figure S3-S5. Venn diagrams showing OTU overlaps between family members