

Species

SP10 <i>Bacteroides intestinalis</i>	SP8 <i>Romboutsia ilealis</i>	SPN423 <i>Pseudoflavonifractor phocaeensis</i> _nov_94.191%
SP107 <i>Bacteroides thetaiotaomicron</i>	SP80 <i>Parabacteroides goldsteinii</i>	SPN43 <i>Pseudoflavonifractor phocaeensis</i> _nov_92.340%
SP109 <i>Atopostipes</i> sp._MOT–200	SP83 <i>Staphylococcus haemolyticus</i>	SPN434 <i>Oscillospiraceae</i> _ [G–4] bacterium_MOT–151_nov_92.116%
SP111 <i>Haemophilus parainfluenzae</i>	SP87 <i>Akkermansia muciniphila</i>	SPN447 <i>Lachnospiraceae</i> _ [G–3] bacterium_MOT–168_nov_94.154%
SP115 <i>Kosakonia sacchari</i>	SP91 <i>Adlercreutzia equolifaciens</i>	SPN456 <i>Oscillospiraceae</i> _ [G–3] bacterium_MOT–150_nov_90.702%
SP119 <i>Corynebacterium marinum</i>	SP93 <i>Monoglobus pectinilyticus</i>	SPN467 <i>Oscillibacter valericigenes</i> _nov_94.595%
SP12 <i>Clostridium disporicum</i>	SP99 <i>Bacteroides uniformis</i>	SPN47 <i>Coprococcus eutactus</i> _nov_95.085%
SP126 <i>Microbacterium hydrocarbonoxydans</i>	SPN1 <i>Lachnospiraceae</i> _ [G–3] bacterium_MOT–168_nov_94.154%	SPN478 <i>Lachnospiraceae</i> _ [G–4] bacterium_MOT–169_nov_97.065%
SP129 <i>Corynebacterium amycolatum</i>	SPN107 <i>Niveispirillum fermenti</i> _nov_85.242%	SPN479 <i>Lachnospiraceae</i> _ [G–6] bacterium_MOT–171_nov_94.340%
SP13 <i>Enterococcus avium</i>	SPN110 <i>Rothia nasimurium</i> _nov_97.228%	SPN489 <i>Mediterraneibacter</i> [Ruminococcus] gnnavus_nov_94.990%
SP138 <i>Odoribacter laneus</i>	SPN12 <i>Streptococcus</i> sp._MOT–045_nov_97.764%	SPN498 <i>Lachnospiraceae</i> _ [G–8] bacterium_MOT–173_nov_89.189%
SP14 <i>Collinsella aerofaciens</i>	SPN120 <i>Anaerotrignum aminivorans</i> _nov_92.812%	SPN509 <i>Oscillospiraceae</i> _ [G–3] bacterium_MOT–150_nov_91.304%
SP147 <i>Erysipelatoclostridium</i> [Clostridium] <i>saccharogumia</i>	SPN13 <i>Kiloniella majae</i> _nov_85.144%	SPN519 <i>Caproiciproducens galactitolivorans</i> _nov_91.083%
SP15 <i>Phocaeicola vulgatus</i>	SPN132 <i>Blautia luti</i> _nov_96.008%	SPN523 <i>Arthrospira platensis</i> _nov_90.531%
SP17 <i>Enterobacter cancerogenus</i>	SPN133 <i>Frisingiococcus caecimuris</i> _nov_96.451%	SPN531 <i>Lachnospira multipara</i> _nov_84.298%
SP18 <i>Shigella sonnei</i>	SPN144 <i>Blautia glucerasea</i> _nov_97.899%	SPN541 <i>Lacrimispora xylanolytica</i> _nov_96.436%
SP19 <i>Shigella flexneri</i>	SPN156 <i>Eubacterium xylanophilum</i> _nov_91.313%	SPN551 <i>Propioniferax innocua</i> _nov_95.207%
SP22 <i>Escherichia coli</i>	SPN164 <i>Turicibacter sanguinis</i> _nov_96.137%	SPN562 <i>Blautia hydrogenotrophica</i> _nov_93.582%
SP23 <i>Ligilactobacillus murinus</i>	SPN168 <i>Lachnospiraceae</i> _ [G–6] bacterium_MOT–171_nov_94.130%	SPN572 <i>Oscillospiraceae</i> _ [G–7] bacterium_MOT–154_nov_94.612%
SP25 <i>Blautia glucerasea</i>	SPN180 <i>Eubacterium coprostanoligenes</i> _nov_91.379%	SPN580 <i>Muribaculaceae</i> _ [G–2] bacterium_MOT–104_nov_86.228%
SP27 <i>Cutibacterium acnes</i>	SPN202 <i>Coprococcus eutactus</i> _nov_92.704%	SPN581 <i>Faecalicatena fissicatena</i> _nov_96.042%
SP31 <i>Granulicatella adiacens</i>	SPN213 <i>Agathobaculum desmolans</i> _nov_86.345%	SPN582 <i>Eubacterium coprostanoligenes</i> _nov_91.845%
SP36 <i>Bacteroides xylanisolvens</i>	SPN218 <i>Butyricicoccus pullicaecorum</i> _nov_87.216%	SPN583 <i>Lachnospiraceae</i> _ [G–1] bacterium_MOT–166_nov_93.983%
SP37 <i>Bifidobacterium pseudolongum</i>	SPN226 <i>Oscillospiraceae</i> _ [G–6] bacterium_MOT–153_nov_97.831%	SPN584 <i>Lacrimispora saccharolytica</i> _nov_90.625%
SP39 <i>Rothia kristinae</i>	SPN238 <i>Longibaculum muris</i> _nov_92.754%	SPN585 <i>Lachnospiraceae</i> _ [G–2] bacterium_MOT–167_nov_96.646%
SP4 <i>Longicatena caecimuris</i>	SPN25 <i>Glucerbacter canis</i> _nov_95.388%	SPN586 <i>Glucerbacter canis</i> _nov_93.946%
SP40 <i>Geobacillus stearothermophilus</i>	SPN250 <i>Blautia faecicola</i> _nov_93.111%	SPN588 <i>Eisenbergiella massiliensis</i> _nov_86.486%
SP41 <i>Lactobacillus intestinalis</i>	SPN252 <i>Oscillospiraceae</i> _ [G–4] bacterium_MOT–151_nov_90.496%	SPN589 <i>Oscillospiraceae</i> _ [G–2] bacterium_MOT–149_nov_88.017%
SP42 <i>Shigella dysenteriae</i>	SPN264 <i>Lachnoclostridium</i> [Clostridium] <i>herbivorans</i> _nov_92.723%	SPN59 <i>Blautia schinkii</i> _nov_94.340%
SP44 <i>Rothia aerolata</i>	SPN275 <i>Lachnospiraceae</i> _ [G–3] bacterium_MOT–168_nov_93.750%	SPN590 <i>Oscillospiraceae</i> _ [G–4] bacterium_MOT–151_nov_93.347%
SP45 <i>Eisenbergiella massiliensis</i>	SPN284 <i>Ruminococcus albus</i> _nov_91.045%	SPN591 <i>Lachnospiraceae</i> _ [G–3] bacterium_MOT–168_nov_92.500%
SP46 <i>Triticum aestivum</i>	SPN286 <i>Lawsonibacter asaccharolyticus</i> _nov_90.909%	SPN592 <i>Duncaniella freteri</i> _nov_89.024%
SP5 <i>Staphylococcus urelyticus</i>	SPN298 <i>Acutalibacter muris</i> _nov_95.661%	SPN593 <i>Lachnospiraceae</i> _ [G–6] bacterium_MOT–171_nov_96.226%
SP51 <i>Actinidia eriantha</i>	SPN309 <i>Barnesiella viscericola</i> _nov_90.447%	SPN603 <i>Alistipes finegoldii</i> _nov_94.835%
SP53 <i>Fusicatenibacter saccharivorans</i>	SPN321 <i>Fusicatenibacter saccharivorans</i> _nov_89.474%	SPN616 <i>Blautia producta</i> _nov_96.017%
SP54 <i>Parasutterella excrementihominis</i>	SPN334 <i>Oscillospiraceae</i> _ [G–1] bacterium_MOT–147_nov_95.218%	SPN627 <i>Ruminococcus albus</i> _nov_92.225%
SP55 <i>Ruthenibacterium lactatiformans</i>	SPN343 <i>Lachnospiraceae</i> _ [G–9] bacterium_MOT–174_nov_96.855%	SPN639 <i>Chryseobacterium culicis</i> _nov_97.280%
SP57 <i>Stenotrophomonas pavanii</i>	SPN355 <i>Erysipelatoclostridium</i> [Clostridium] <i>saccharogumia</i> _nov_96.042%	SPN71 <i>Oscillospiraceae</i> _ [G–2] bacterium_MOT–149_nov_96.473%
SP58 <i>Streptococcus agalactiae</i>	SPN36 <i>Anaerostipes hadrus</i> _nov_92.754%	SPN83 <i>Blautia producta</i> _nov_95.178%
SP61 <i>Veillonella parvula</i>	SPN364 <i>Fusicatenibacter saccharivorans</i> _nov_97.479%	SPN95 <i>Spongiibacter marinus</i> _nov_80.142%
SP64 <i>Enterococcus faecalis</i>	SPN365 <i>Faecalimonas umblicata</i> _nov_96.033%	SPP4 <i>Staphylococcus argenteus_aureus_roterodami</i>
SP66 <i>Bilophila wadsworthia</i>	SPN377 <i>Lachnospiraceae</i> _ [G–11] bacterium_MOT–178_nov_94.929%	SPP5 <i>Streptococcus parasanguinis_parasanguinis_clade_721</i>
SP69 <i>Streptococcus</i> sp._HMT_064	SPN388 <i>Oscillospiraceae</i> _ [G–4] bacterium_MOT–151_nov_92.946%	SPP7 <i>Veillonella dispar_parvula</i>
SP7 <i>Streptococcus mutans</i>	SPN400 <i>Anaerotruncus rubifantisi</i> _nov_88.820%	SPP8 <i>Staphylococcus saprophyticus_xylosus</i>
SP75 <i>Mammalicoccus sciuri</i>	SPN405 <i>Oscillospiraceae</i> _ [G–3] bacterium_MOT–150_nov_91.097%	SPPN3 <i>Kordiimonas multispecies_sppn3_2_nov_79.121%</i>
SP79 <i>Alistipes finegoldii</i>	SPN411 <i>Zhongshania marina</i> _nov_79.765%	