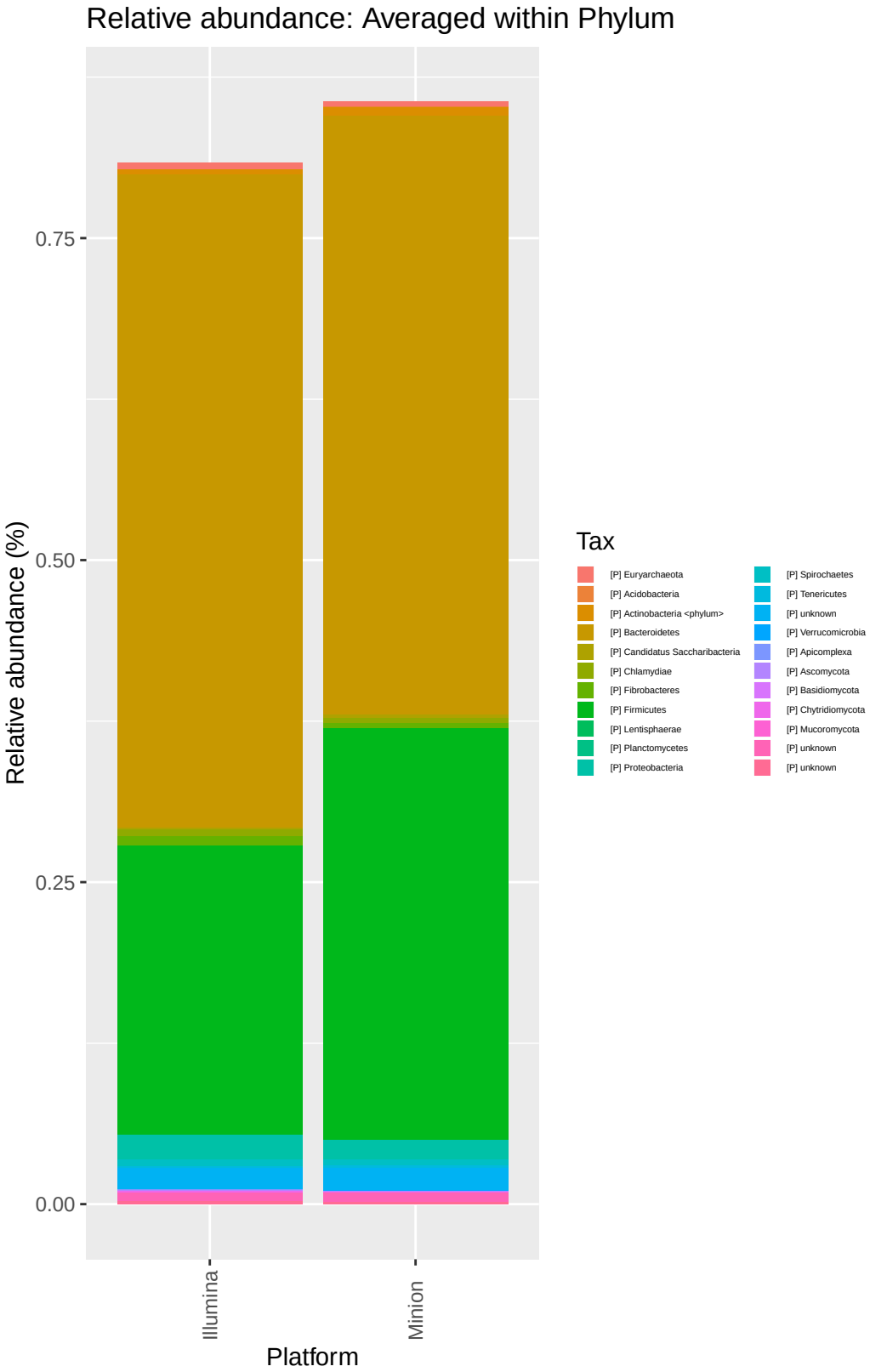
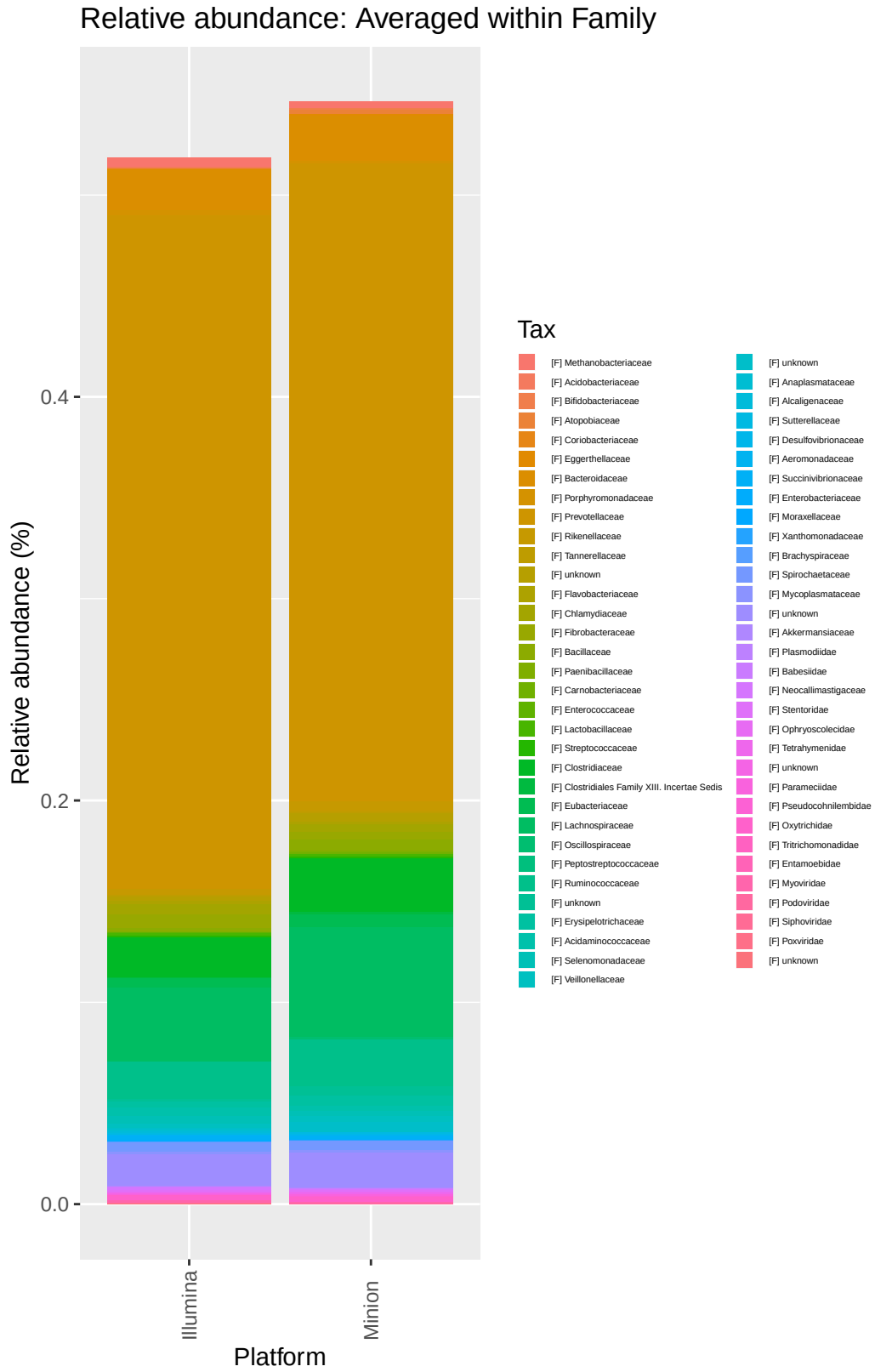
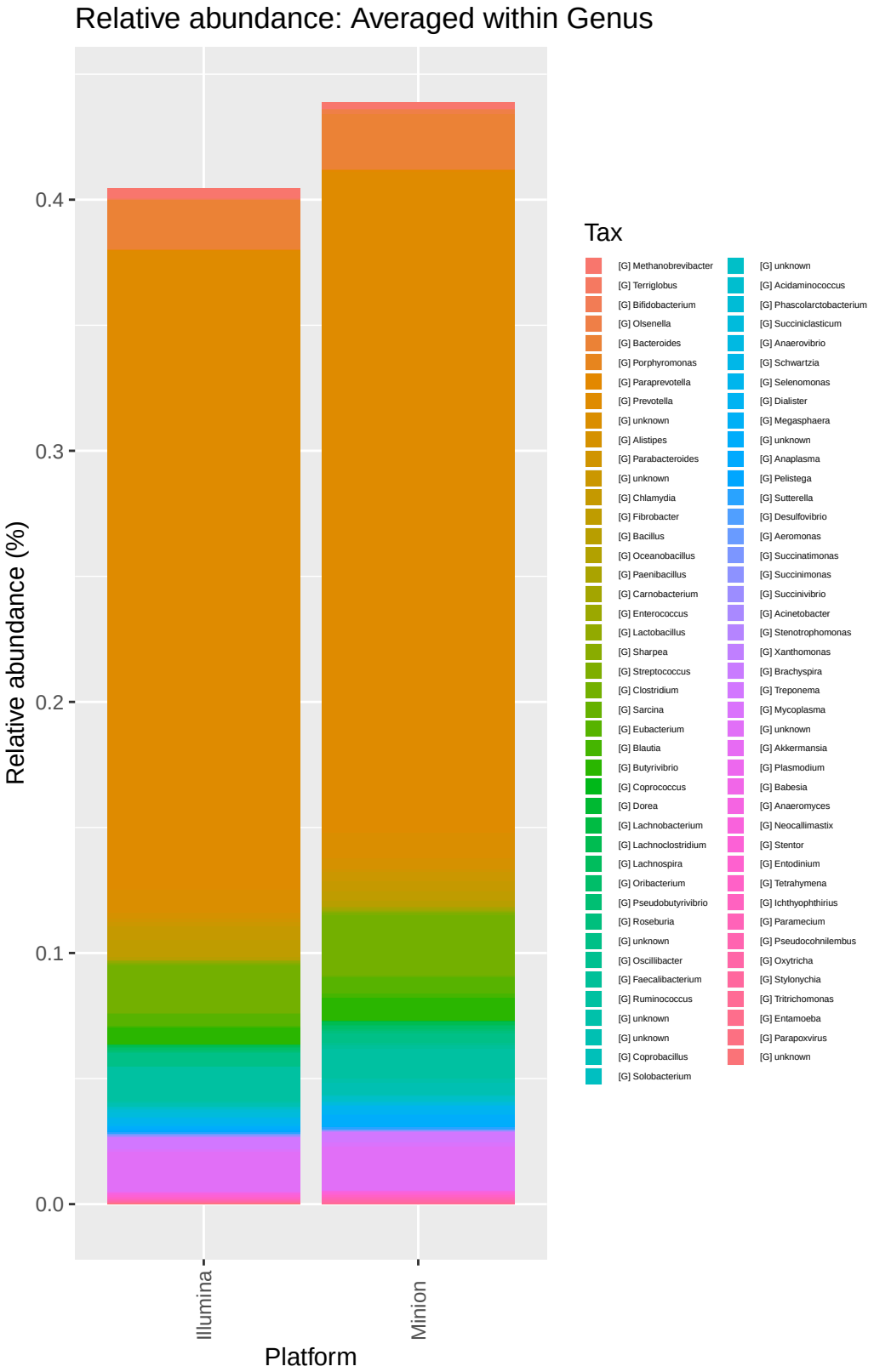
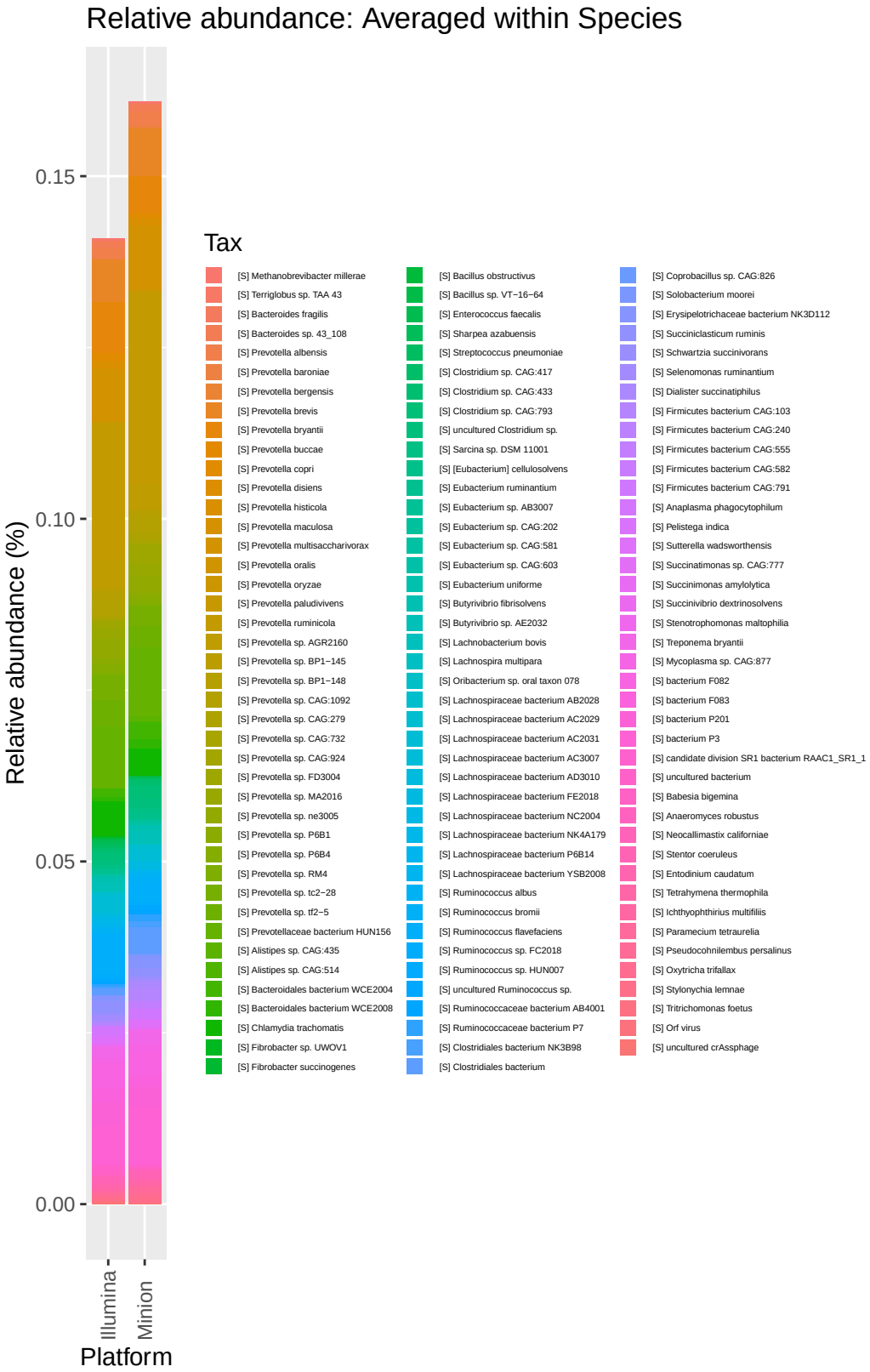

Relative abundance: Averaged within Phylum
Relative abundance (%)
0.75
0.50
0.25
0.00
Illumina
Minion
Platform
Tax
[P] Euryarchaeota
[P] Acidobacteria
[P] Actinobacteria <phylum>
[P] Bacteroidetes
[P] Candidatus Saccharibacteria
[P] Chlamydiae
[P] Fibrobacteres
[P] Firmicutes
[P] Lentisphaerae
[P] Planctomycetes
[P] Proteobacteria
[P] Spirochaetes
[P] Tenericutes
[P] unknown
[P] Verrucomicrobia
[P] Apicomplexa
[P] Ascomycota
[P] Basidiomycota
[P] Chytridiomycota
[P] Mucoromycota
[P] unknown
[P] unknown


Relative abundance: Averaged within Family
Relative abundance (%)
0.4
0.2
0.0
Illumina
Minion
Platform
Tax
[F] Methanobacteriaceae
[F] Acidobacteriaceae
[F] Bifidobacteriaceae
[F] Atopobiaceae
[F] Coriobacteriaceae
[F] Eggerthellaceae
[F] Bacteroidaceae
[F] Porphyromonadaceae
[F] Prevotellaceae
[F] Rikenellaceae
[F] Tannerellaceae
[F] unknown
[F] Flavobacteriaceae
[F] Chlamydiaceae
[F] Fibrobacteraceae
[F] Bacillaceae
[F] Paenibacillaceae
[F] Carnobacteriaceae
[F] Enterococcaceae
[F] Lactobacillaceae
[F] Streptococcaceae
[F] Clostridiaceae
[F] Clostridiales Family XIII. Incertae Sedis
[F] Eubacteriaceae
[F] Lachnospiraceae
[F] Oscillospiraceae
[F] Peptostreptococcaceae
[F] Ruminococcaceae
[F] unknown
[F] Erysipelotrichaceae
[F] Acidaminococcaceae
[F] Selenomonadaceae
[F] Veillonellaceae
[F] unknown
[F] Anaplasmataceae
[F] Alcaligenaceae
[F] Sutterellaceae
[F] Desulfovibrionaceae
[F] Aeromonadaceae
[F] Succinivibrionaceae
[F] Enterobacteriaceae
[F] Moraxellaceae
[F] Xanthomonadaceae
[F] Brachyspiraceae
[F] Spirochaetaceae
[F] Mycoplasmataceae
[F] unknown
[F] Akkermansiaceae
[F] Plasmodiidae
[F] Babesiidae
[F] Neocallimastigaceae
[F] Stentoridae
[F] Ophryoscolecidae
[F] Tetrahymenidae
[F] unknown
[F] Parameciidae
[F] Pseudocohnilembidae
[F] Oxytrichidae
[F] Tritrichomonadidae
[F] Entamoebidae
[F] Myoviridae
[F] Podoviridae
[F] Siphoviridae
[F] Poxviridae
[F] unknown


Relative abundance: Averaged within Genus
Relative abundance (%)
0.0
0.1
0.2
0.3
0.4
Illumina
Minion
Platform
Tax
[G] Methanobrevibacter
[G] Terriglobus
[G] Bifidobacterium
[G] Olsenella
[G] Bacteroides
[G] Porphyromonas
[G] Paraprevotella
[G] Prevotella
[G] unknown
[G] Alistipes
[G] Parabacteroides
[G] unknown
[G] Chlamydia
[G] Fibrobacter
[G] Bacillus
[G] Oceanobacillus
[G] Paenibacillus
[G] Carnobacterium
[G] Enterococcus
[G] Lactobacillus
[G] Sharpea
[G] Streptococcus
[G] Clostridium
[G] Sarcina
[G] Eubacterium
[G] Blautia
[G] Butyrivibrio
[G] Coprococcus
[G] Dorea
[G] Lachnobacterium
[G] Lachnoclostridium
[G] Lachnospira
[G] Oribacterium
[G] Pseudobutyrivibrio
[G] Roseburia
[G] unknown
[G] Oscillibacter
[G] Faecalibacterium
[G] Ruminococcus
[G] unknown
[G] unknown
[G] Coprobacillus
[G] Solobacterium
[G] unknown
[G] Acidaminococcus
[G] Phascolarctobacterium
[G] Succiniclasticum
[G] Anaerovibrio
[G] Schwartzia
[G] Selenomonas
[G] Dialister
[G] Megasphaera
[G] unknown
[G] Anaplasma
[G] Pelistega
[G] Sutterella
[G] Desulfovibrio
[G] Aeromonas
[G] Succinatimonas
[G] Succinimonas
[G] Succinivibrio
[G] Acinetobacter
[G] Stenotrophomonas
[G] Xanthomonas
[G] Brachyspira
[G] Treponema
[G] Mycoplasma
[G] unknown
[G] Akkermansia
[G] Plasmodium
[G] Babesia
[G] Anaeromyces
[G] Neocallimastix
[G] Stentor
[G] Entodinium
[G] Tetrahymena
[G] Ichthyophthirius
[G] Paramecium
[G] Pseudocohnilembus
[G] Oxytricha
[G] Stylonychia
[G] Tritrichomonas
[G] Entamoeba
[G] Parapoxvirus
[G] unknown


Relative abundance: Averaged within Species
Relative abundance (%)
0.00
0.05
0.10
0.15
Illumina
Minion
Platform
Tax
[S] Methanobrevibacter millerae
[S] Terriglobus sp. TAA 43
[S] Bacteroides fragilis
[S] Bacteroides sp. 43_108
[S] Prevotella albensis
[S] Prevotella baroniae
[S] Prevotella bergensis
[S] Prevotella brevis
[S] Prevotella bryantii
[S] Prevotella buccae
[S] Prevotella copri
[S] Prevotella disiens
[S] Prevotella histicola
[S] Prevotella maculosa
[S] Prevotella multisaccharivorax
[S] Prevotella oralis
[S] Prevotella oryzae
[S] Prevotella paludivivens
[S] Prevotella ruminicola
[S] Prevotella sp. AGR2160
[S] Prevotella sp. BP1−145
[S] Prevotella sp. BP1−148
[S] Prevotella sp. CAG:1092
[S] Prevotella sp. CAG:279
[S] Prevotella sp. CAG:732
[S] Prevotella sp. CAG:924
[S] Prevotella sp. FD3004
[S] Prevotella sp. MA2016
[S] Prevotella sp. ne3005
[S] Prevotella sp. P6B1
[S] Prevotella sp. P6B4
[S] Prevotella sp. RM4
[S] Prevotella sp. tc2−28
[S] Prevotella sp. tf2−5
[S] Prevotellaceae bacterium HUN156
[S] Alistipes sp. CAG:435
[S] Alistipes sp. CAG:514
[S] Bacteroidales bacterium WCE2004
[S] Bacteroidales bacterium WCE2008
[S] Chlamydia trachomatis
[S] Fibrobacter sp. UWOV1
[S] Fibrobacter succinogenes
[S] Bacillus obstructivus
[S] Bacillus sp. VT−16−64
[S] Enterococcus faecalis
[S] Sharpea azabuensis
[S] Streptococcus pneumoniae
[S] Clostridium sp. CAG:417
[S] Clostridium sp. CAG:433
[S] Clostridium sp. CAG:793
[S] uncultured Clostridium sp.
[S] Sarcina sp. DSM 11001
[S] [Eubacterium] cellulosolvens
[S] Eubacterium ruminantium
[S] Eubacterium sp. AB3007
[S] Eubacterium sp. CAG:202
[S] Eubacterium sp. CAG:581
[S] Eubacterium sp. CAG:603
[S] Eubacterium uniforme
[S] Butyrivibrio fibrisolvens
[S] Butyrivibrio sp. AE2032
[S] Lachnobacterium bovis
[S] Lachnospira multipara
[S] Oribacterium sp. oral taxon 078
[S] Lachnospiraceae bacterium AB2028
[S] Lachnospiraceae bacterium AC2029
[S] Lachnospiraceae bacterium AC2031
[S] Lachnospiraceae bacterium AC3007
[S] Lachnospiraceae bacterium AD3010
[S] Lachnospiraceae bacterium FE2018
[S] Lachnospiraceae bacterium NC2004
[S] Lachnospiraceae bacterium NK4A179
[S] Lachnospiraceae bacterium P6B14
[S] Lachnospiraceae bacterium YSB2008
[S] Ruminococcus albus
[S] Ruminococcus bromii
[S] Ruminococcus flavefaciens
[S] Ruminococcus sp. FC2018
[S] Ruminococcus sp. HUN007
[S] uncultured Ruminococcus sp.
[S] Ruminococcaceae bacterium AB4001
[S] Ruminococcaceae bacterium P7
[S] Clostridiales bacterium NK3B98
[S] Clostridiales bacterium
[S] Coprobacillus sp. CAG:826
[S] Solobacterium moorei
[S] Erysipelotrichaceae bacterium NK3D112
[S] Succiniclasticum ruminis
[S] Schwartzia succinivorans
[S] Selenomonas ruminantium
[S] Dialister succinatiphilus
[S] Firmicutes bacterium CAG:103
[S] Firmicutes bacterium CAG:240
[S] Firmicutes bacterium CAG:555
[S] Firmicutes bacterium CAG:582
[S] Firmicutes bacterium CAG:791
[S] Anaplasma phagocytophilum
[S] Pelistega indica
[S] Sutterella wadsworthensis
[S] Succinatimonas sp. CAG:777
[S] Succinimonas amylolytica
[S] Succinivibrio dextrinosolvens
[S] Stenotrophomonas maltophilia
[S] Treponema bryantii
[S] Mycoplasma sp. CAG:877
[S] bacterium F082
[S] bacterium F083
[S] bacterium P201
[S] bacterium P3
[S] candidate division SR1 bacterium RAAC1_SR1_1
[S] uncultured bacterium
[S] Babesia bigemina
[S] Anaeromyces robustus
[S] Neocallimastix californiae
[S] Stentor coeruleus
[S] Entodinium caudatum
[S] Tetrahymena thermophila
[S] Ichthyophthirius multifiliis
[S] Paramecium tetraurelia
[S] Pseudocohnilembus persalinus
[S] Oxytricha trifallax
[S] Stylonychia lemnae
[S] Tritrichomonas foetus
[S] Orf virus
[S] uncultured crAssphage