
Relative abundance of Genus (%)
Age
0
5
10
15
20
25
[Anaerorhabdus] furcosa group
r = 0.36 , P = 0.00018
[Eubacterium] coprostanoligenes group
r = 0.62 , P = 1.4E−12
[Eubacterium] ventriosum group
r =− 0.53 , P = 7.7E−09
[Eubacterium] xylanophilum group
r = 0.22 , P = 0.025
[Ruminococcus] gauvreauii group
r =− 0.16 , P = 0.11
[Ruminococcus] torques group
r =− 0.54 , P = 4.3E−09
Actinobacillus
r =− 0.62 , P = 1.7E−12
Agathobacter
r =− 0.36 , P = 0.00018
Alloprevotella
r =− 0.61 , P = 7.7E−12
Anaerobiospirillum
r =− 0.3 , P = 0.0018
Anaerococcus
r = 0.27 , P = 0.0053
Anaerofustis
r = 0.3 , P = 0.002
Anaeroplasma
r =− 0.4 , P = 2.5E−05
Anaerostipes
r =− 0.34 , P = 0.00039
Anaerovibrio
r =− 0.28 , P = 0.0036
Azoarcus
r = 0.41 , P = 1.4E−05
Bifidobacterium
r = 0.34 , P = 0.00042
Blautia
r =− 0.33 , P = 0.00057
Brachyspira
r =− 0.54 , P = 4.4E−09
Butyricicoccus
r =− 0.34 , P = 0.00048
Butyrivibrio
r =− 0.33 , P = 0.00056
CAG−352
r = 0.46 , P = 8E−07
CAG−873
r = 0.44 , P = 3E−06
Campylobacter
r =− 0.6 , P = 2.5E−11
Candidatus Methanogranum
r =− 0.23 , P = 0.021
Candidatus Saccharimonas
r =− 0.42 , P = 1.1E−05
Candidatus Soleaferrea
r = 0.62 , P = 2.4E−12
Caproiciproducens
r = 0.3 , P = 0.0016
Catenibacterium
r =− 0.3 , P = 0.0017
Cetobacterium
r =− 0.52 , P = 1.9E−08
Christensenellaceae R−7 group
r = 0.59 , P = 6E−11
Clostridium sensu stricto 6
r = 0.33 , P = 0.00064
Collinsella
r = 0.33 , P = 0.00057
Coprococcus 1
r =− 0.47 , P = 5.9E−07
Coprococcus 2
r =− 0.43 , P = 5.5E−06
Coriobacteriaceae UCG−003
r = 0.24 , P = 0.013
Corynebacterium 1
r = 0.35 , P = 0.00029
Desulfovibrio
r = 0.33 , P = 0.00071
Dorea
r = -0.35 , P = 0.00022
Enterorhabdus
r = 0.3 , P = 0.0022
Erysipelotrichaceae UCG−003
r =− 0.21 , P = 0.037
Erysipelotrichaceae UCG−004
r = 0.082 , P = 0.41
Faecalibacterium
r = -0.55 , P = 1.1E−09
Family XIII AD3011 group
r = 0.33 , P = 0.00058
Flavonifractor
r = 0.29 , P = 0.0025
Fournierella
r =− 0.45 , P = 1.7E−06
Fusicatenibacter
r =− 0.56 , P = 5.8E−10
Fusobacterium
r =− 0.36 , P = 0.00016
GCA−900066225
r = 0.33 , P = 0.00064
GCA−900066575
r =− 0.68 , P = 1.5E−15
Gemella
r =− 0.48 , P = 3.4E−07
Haemophilus
r =− 0.31 , P = 0.0012
Helicobacter
r =− 0.44 , P = 2.6E−06
Holdemanella
r =− 0.24 , P = 0.014
Howardella
r =− 0.23 , P = 0.019
Intestinimonas
r =− 0.39 , P = 3.7E−05
Lachnoclostridium
r =− 0.41 , P = 1.6E−05
Lachnospira
r =− 0.4 , P = 2.5E−05
Lachnospiraceae FCS020 group
r = 0.24 , P = 0.013
Lachnospiraceae NC2004 group
r =− 0.25 , P = 0.0094
Lachnospiraceae ND3007 group
r =− 0.42 , P = 9.3E−06
Lachnospiraceae NK3A20 group
r = 0.32 , P = 0.00078
Lachnospiraceae UCG−001
r =− 0.63 , P = 1.1E−12
Lachnospiraceae UCG−003
r =− 0.6 , P = 2.1E−11
Lachnospiraceae UCG−004
r =− 0.65 , P = 1.3E−13
Lachnospiraceae UCG−007
r = 0.54 , P = 2.3E−09
Lachnospiraceae UCG−008
r =− 0.52 , P = 1.1E−08
Lachnospiraceae UCG−010
r =− 0.42 , P = 1.1E−05
Lachnospiraceae XPB1014 group
r =− 0.41 , P = 1.5E−05
Lactobacillus
r = 0.29 , P = 0.0025
Libanicoccus
r = 0.54 , P = 3.1E−09
Marvinbryantia
r =− 0.3 , P = 0.0022
Megasphaera
r = 0.24 , P = 0.015
Methanobrevibacter
r = 0.48 , P = 3.2E−07
Mitsuokella
r =− 0.37 , P = 9.3E−05
Mogibacterium
r = 0.46 , P = 1.2E−06
Mucispirillum
r =− 0.46 , P = 1.1E−06
Negativibacillus
r = 0.29 , P = 0.0033
Neisseria
r =− 0.32 , P = 0.001
Olsenella
r = 0.33 , P = 0.00057
Oscillibacter
r = 0.49 , P = 1.8E−07
p−1088−a5 gut group
r = 0.31 , P = 0.0012
Parabacteroides
r = 0.051 , P = 0.61
Phascolarctobacterium
r =− 0.36 , P = 0.00019
Phoenicibacter
r = 0.26 , P = 0.0073
Prevotella 2
r =− 0.54 , P = 2.3E−09
Prevotella 9
r =− 0.4 , P = 3.1E−05
Prevotellaceae UCG−001
r =− 0.33 , P = 0.00076
Prevotellaceae UCG−003
r = 0.34 , P = 0.00046
Prevotellaceae UCG−004
r = 0.23 , P = 0.017
Rikenellaceae RC9 gut group
r = 0.6 , P = 1.1E−11
Roseburia
r =− 0.61 , P = 5.7E−12
Ruminobacter
r =− 0.34 , P = 0.00038
Ruminococcaceae NK4A214 group
r = 0.54 , P = 2.3E−09
Ruminococcaceae UCG−002
r = 0.57 , P = 2.8E−10
Ruminococcaceae UCG−008
r =− 0.35 , P = 0.00033
Ruminococcaceae UCG−010
r = 0.5 , P = 7.6E−08
Ruminococcaceae UCG−013
r = 0.55 , P = 1.1E−09
Sarcina
r =− 0.3 , P = 0.0023
Senegalimassilia
r = 0.32 , P = 0.001
Slackia
r = 0.35 , P = 0.00028
Sphaerochaeta
r = 0.28 , P = 0.0044
Stenotrophomonas
r = 0.45 , P = 1.6E−06
Subdoligranulum
r =− 0.38 , P = 6.9E−05
Succinivibrio
r = 0.34 , P = 0.00043
Sutterella
r =− 0.4 , P = 2.2E−05
Treponema 2
r = 0.53 , P = 9E−09
Tyzzerella 3
r =− 0.23 , P = 0.017
U29−B03
r = 0.33 , P = 0.00064
uncultured alpha proteobacterium
r =− 0.3 , P = 0.0023
uncultured Erysipelotrichaceae bacterium
r = 0.24 , P = 0.013
uncultured Lachnospiraceae bacterium
r =− 0.43 , P = 5.9E−06
Veillonella
r =− 0.47 , P = 3.5E−07
Weissella
r = 0.35 , P = 3E−04
Z20
r = 0.39 , P = 4.5E−05