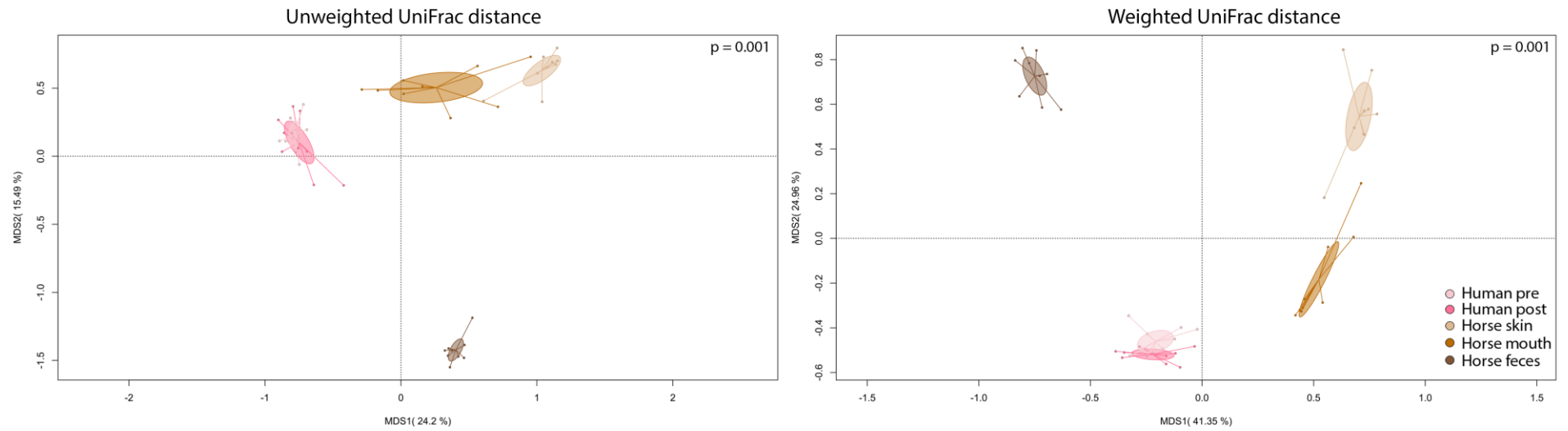
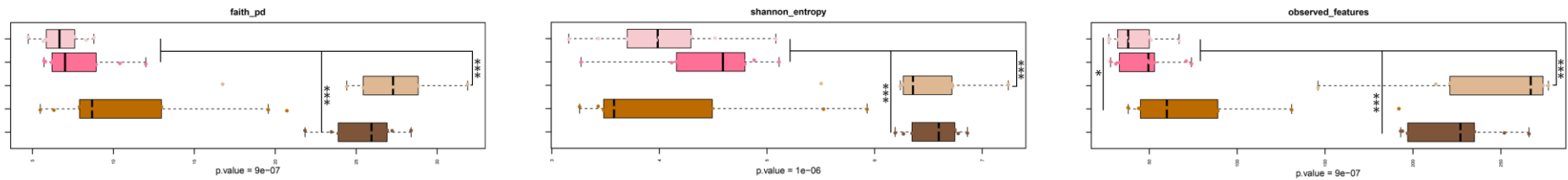
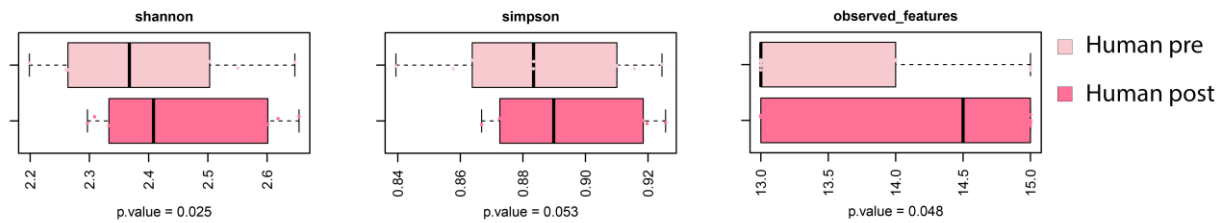


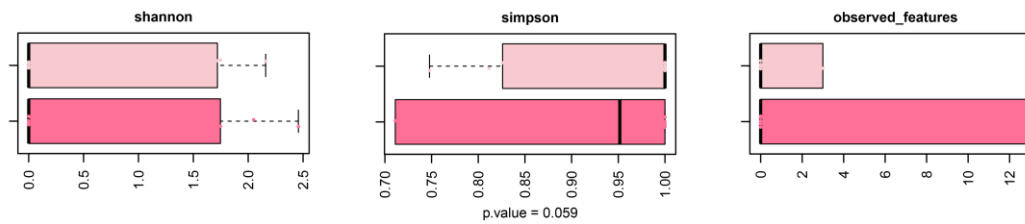
A**B**

Supplementary Figure 1.

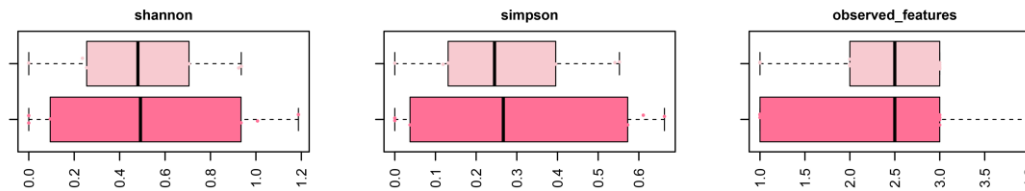
Faecalibacterium species



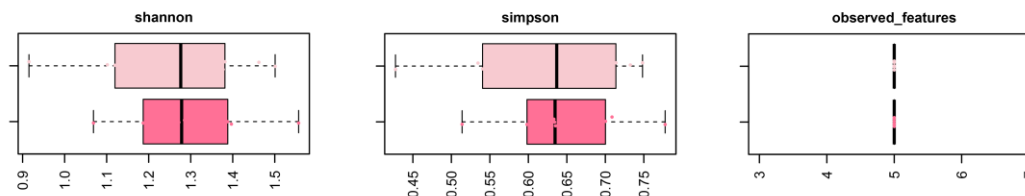
Prevotella species



Phascolarctobacterium species



Blautia species



Supplementary Figure 2.

Supplementary Table 1. Dietary habits of enrolled subjects, kept constant during the 15-days biodiversity intervention

[illegible]

Supplementary Table 2. Log2FC variation of CAZymes families compared to the children gut microbiome before the biodiversity intervention

Gene	log_FC	diffexpressed	CAZymes Family
GH108	-2.301	DOWN	Glycoside Hydrolases
GH97	-1.756	DOWN	Glycoside Hydrolases
GH44	-1.604	DOWN	Glycoside Hydrolases
GT19	-1.920	DOWN	GlycosylTransferases
GT87	-2.586	DOWN	GlycosylTransferases
GH98	-1.898	DOWN	Glycoside Hydrolases
GH48	-2.929	DOWN	Glycoside Hydrolases
GH57	-1.952	DOWN	Glycoside Hydrolases
CE11	-1.974	DOWN	Carbohydrate Esterases
GT31	-2.684	DOWN	GlycosylTransferases
GT13	-1.977	DOWN	GlycosylTransferases
GT25	-2.221	DOWN	GlycosylTransferases
GH55	-2.392	DOWN	Glycoside Hydrolases
GT89	-4.322	DOWN	GlycosylTransferases
AA5	-4.322	DOWN	Auxiliary Activities
GH67	-4.322	DOWN	Glycoside Hydrolases
GH54	-4.322	DOWN	Glycoside Hydrolases
AA9	-4.322	DOWN	Auxiliary Activities
GT53	-4.322	DOWN	GlycosylTransferases
PL15	-4.322	DOWN	Polysaccharide Lyases
CE13	-4.322	DOWN	Carbohydrate Esterases
PL21	-4.322	DOWN	Polysaccharide Lyases
GH124	-3.597	DOWN	Glycoside Hydrolases
GT66	2.102	UP	GlycosylTransferases
CE5	2.524	UP	Carbohydrate Esterases
PL10	1.667	UP	Polysaccharide Lyases
GT7	2.524	UP	GlycosylTransferases

Supplementary Table 3. Log2FC variation of SCFAs-related KO genes abundance compared to the children gut microbiome before the biodiversity intervention.

Gene	log_FC	diffexpressed	Interested Pathway	KEGG Orthology name
K00158	-1.546134643	DOWN	Pyruvate metabolism	pyruvate oxidase [EC:1.2.3.3]
K00174	-3.321928095	DOWN	Glycolysis / Gluconeogenesis	2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase subunit alpha [EC:1.2.7.3 1.2.7.11]
K00208	-3.321928095	DOWN	Fatty acid biosynthesis	enoyl-[acyl-carrier protein] reductase I [EC:1.3.1.9 1.3.1.10]
K00246	-3.321928095	DOWN	Citrate cycle (TCA cycle)	succinate dehydrogenase subunit C
K00247	-3.321928095	DOWN	Citrate cycle (TCA cycle)	succinate dehydrogenase subunit D
K00627	-2.454217273	DOWN	Glycolysis / Gluconeogenesis	pyruvate dehydrogenase E2 component (dihydrolipoyllysine-residue acetyltransferase) [EC:2.3.1.12]
K01060	-3.321928095	DOWN	Penicillin and cephalosporin biosynthesis	cephalosporin-C deacetylase [EC:3.1.1.41]
K01644	-1.501444498	DOWN	Two-component system	citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.34]
K01646	-1.94963261	DOWN	Two-component system	citrate lyase subunit gamma (acyl carrier protein)
K01760	-2.164628423	DOWN	Cysteine and methionine metabolism	cysteine-S-conjugate beta-lyase [EC:4.4.1.13]
K01903	-1.693800836	DOWN	Citrate cycle (TCA cycle)	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
K03342	-3.321928095	DOWN	Folate biosynthesis	para-aminobenzoate synthetase / 4-amino-4-deoxychorismate lyase [EC:2.6.1.85 4.1.3.38]
K09011	-3.321928095	DOWN	Valine, leucine and isoleucine biosynthesis	(R)-citramalate synthase [EC:2.3.3.21]
K11258	-1.910419635	DOWN	Valine, leucine and isoleucine biosynthesis	acetolactate synthase II small subunit [EC:2.2.1.6]
K14682	-3.321928095	DOWN	Arginine biosynthesis	amino-acid N-acetyltransferase [EC:2.3.1.1]
K00135	3.256352548	UP	Alanine, aspartate and glutamate metabolism	succinate-semialdehyde dehydrogenase / glutarate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.79 1.2.1.20]
K00156	3.256352548	UP	Pyruvate metabolism	pyruvate dehydrogenase (quinone) [EC:1.2.5.1]
K00161	3.256352548	UP	Glycolysis / Gluconeogenesis	pyruvate dehydrogenase E1 component subunit alpha [EC:1.2.4.1]
K00240	2.393078354	UP	Citrate cycle (TCA cycle)	succinate dehydrogenase iron-sulfur subunit [EC:1.3.5.1]
K00241	1.581705105	UP	Citrate cycle (TCA cycle)	succinate dehydrogenase cytochrome b subunit
K01039	3.256352548	UP	Styrene degradation	glutaconate CoA-transferase, subunit A [EC:2.8.3.12]
K01631	3.256352548	UP	Galactose metabolism	2-dehydro-3-deoxyphosphogalactonate aldolase [EC:4.1.2.21]
K01639	3.256352548	UP	Amino sugar and nucleotide sugar metabolism	N-acetylneuraminate lyase [EC:4.1.3.3]
K01640	3.256352548	UP	Valine, leucine and isoleucine degradation	hydroxymethylglutaryl-CoA lyase [EC:4.1.3.4]
K01667	1.939682764	UP	Tryptophan metabolism	tryptophanase [EC:4.1.99.1]
K01902	3.256352548	UP	Citrate cycle (TCA cycle)	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
K01958	3.256352548	UP	Citrate cycle (TCA cycle)	pyruvate carboxylase [EC:6.4.1.1]
K02535	3.256352548	UP	Lipopolysaccharide biosynthesis	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [EC:3.5.1.108]
K03119	3.256352548	UP	Taurine and hypotaurine metabolism	taurine dioxygenase [EC:1.14.11.17]
K03416	3.256352548	UP	Propanoate metabolism	methylmalonyl-CoA carboxyltransferase 5S subunit [EC:2.1.3.1]
K03777	3.256352548	UP	Pyruvate metabolism	D-lactate dehydrogenase (quinone) [EC:1.1.5.12]
K04020	3.256352548	UP	Pyruvate metabolism	phosphotransacetylase
K07248	3.256352548	UP	Pyruvate metabolism	lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase [EC:1.2.1.22 1.2.1.21]
K08324	3.256352548	UP	Alanine, aspartate and glutamate metabolism	succinate-semialdehyde dehydrogenase [EC:1.2.1.16 1.2.1.24]
K11533	3.256352544	UP	Fatty acid biosynthesis	fatty acid synthase, bacteria type [EC:2.3.1.-]
K12339	3.256352548	UP	Cysteine and methionine metabolism	S-sulfo-L-cysteine synthase (O-acetyl-L-serine-dependent) [EC:2.5.1.144]
K16363	2.139417173	UP	Fatty acid biosynthesis	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase / 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:3.5.1.108 4.2.1.59]
K16704	3.256352548	UP	O-Antigen nucleotide sugar biosynthesis	dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase [EC:2.3.1.210]

Supplementary Table 4. KEGG Orthology pathways assigned to bacterial Infectious disease identified within our dataset. Abundance is expressed as Copies per Milion reads within each children gut microbiome sample.

	Infectious disease: bacterial		
sample_ID	ko05100 (CoPM)	ko05120 (CoPM)	ko05150 (CoPM)
A03T0	0	0.0027	0.0001
A05T0	0	0.0018	0.0000
A09T0	0	0.0015	0.0005
M02T0	0	0.0019	0.0001
M08T0	0	0.0026	0.0000
PT01T0	0	0.0012	0.0001
PT03T0	0	0.0002	0.0002
PT04T0	0	0.0011	0.0000
PT05T0	0	0.0006	0.0003
PT07T0	0	0.0015	0.0001
A03T1	0	0.0025	0.0002
A05T1	0	0.0012	0.0000
A09T1	1.21E-05	0.0028	0.0002
M02T1	0	0.0018	0.0003
M08T1	2.53E-06	0.0027	0.0000
PT01T1	0	0.0017	0.0002
PT03T1	0	0.0004	0.0003
PT04T1	0	0.0019	0.0001
PT05T1	0	0.0008	0.0005
PT07T1	0	0.0015	0.0002

Supplementary Table 5. Genome Taxonomy Database (GTB) assigned to each SGB within our dataset.

SGBs_ID	GTDB taxonomy
A03T0_bin.14	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus_A;s_Coprococcus_A catus_A
A03T0_bin.19	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Slackia_A;s_Slackia_A isoflavoniconvertens
A03T0_bin.5	d_Bacteria;p_Bacillota_A;c_Clostridia;o_TANB77;f_CAG-508;g_CAG-269;s_CAG-269 sp000431335
A03T0_bin.6	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Actinomycetaceae;g_Pauljensenia;s_Pauljensenia bouchesdurhonensis
A03T0_bin.7	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Gordonibacter;s_Gordonibacter pamelaee
A03T1_bin.10	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter;s_Agathobacter rectalis
A03T1_bin.11	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A;s_Blautia_A massiliensis
A03T1_bin.12	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Eubacterium_R;s_Eubacterium_R sp000436835
A03T1_bin.13	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_D;s_Ruminococcus_D bicirculans
A03T1_bin.15	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Acetatifactor;s_Acetatifactor intestinalis
A03T1_bin.16	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Vescimonas;s_Vescimonas sp900548615
A03T1_bin.18	d_Bacteria;p_Bacillota_C;c_Negativicutes;o_Veillonellales;f_Dialisteraceae;g_Dialister;s_Dialister invisus
A03T1_bin.19	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Christensenellales;f_CAG-138;g_SFEL01;s_SFEL01 sp004557245
A03T1_bin.21	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Fimenecus;s_Fimenecus sp000432435
A03T1_bin.22	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Dorea_A;s_Dorea_A longicatena
A03T1_bin.25	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Evtepia;s_Evtepia sp004556345
A03T1_bin.26	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_RUG115;s_RUG115 sp900066395
A03T1_bin.5	d_Bacteria;p_Bacillota_A;c_Clostridia;o_TANB77;f_CAG-508;g_CAG-452;s_CAG-452 sp000434035
A03T1_bin.6	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Angelakisella;s_Angelakisella sp900547385
A03T1_bin.7	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Christensenellales;f_CAG-138;g_RUG472;s_RUG472 sp900545265
A03T1_bin.8	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_Faecalibacterium prausnitzii_A
A05T0_bin.10	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Ruminococcus_E;s_Ruminococcus_E sp003526955
A05T0_bin.11	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Adlercreutzia;s_Adlercreutzia hattorii
A05T0_bin.12	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiales;f_Akkermansiaceae;g_Akkermansia;s_Akkermansia muciniphila
A05T0_bin.13	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Vescimonas;s_Vescimonas sp000435555
A05T0_bin.14	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Evtepia;s_Evtepia gabavorous
A05T0_bin.21	d_Bacteria;p_Bacillota;c_Bacilli;o_RF39;f_UBA660;g_Aphodocola;s_Aphodocola sp000434835
A05T0_bin.23	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Mediterraneibacter;s_Mediterraneibacter lactaris
A05T0_bin.3	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1417;s_UBA1417 sp003531055
A05T0_bin.4	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_Faecalibacterium prausnitzii_D
A05T0_bin.5	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_Bifidobacterium adolescentis
A05T0_bin.6	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coprococcus;s_Coprococcus eutactus
A05T1_bin.12	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Scatavimonas;s_Scatavimonas sp900540275
A05T1_bin.15	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_Faecalibacterium duncaniae
A05T1_bin.16	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_Faecalibacterium longum
A05T1_bin.19	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Hominisplanchenecus;s_Hominisplanchenecus faecis
A05T1_bin.2	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger formicilis
A05T1_bin.24	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Fusicatenibacter;s_Fusicatenibacter saccharivorans
A05T1_bin.25	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Oliverpabstia;s_Oliverpabstia intestinalis
A05T1_bin.27	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_Ruminococcus_C sp000437175
A05T1_bin.4	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Agathobacter;s_Agathobacter faecis
A05T1_bin.9	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_Bifidobacterium animalis
A09T0_bin.1	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Lactococcus;s_Lactococcus cremoris

A09T0_bin.12	d_Bacteria;p_Bacillota_A;c_Clostridia;o_UBA1381;f_UBA1381;g_CAG-41;s_CAG-41 sp900066215
A09T0_bin.16	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactiplantibacillus;s_Lactiplantibacillus plantarum
A09T0_bin.17	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_Ruminococcus_C sp900545285
A09T0_bin.18	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger sp900539695
A09T0_bin.4	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella;s_Prevotella copri_A
A09T0_bin.6	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Wujia;s_Wujia chipingensis
A09T0_bin.7	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Christensenellales;f_CAG-74;g_UBA11524;s_UBA11524 sp000437595
A09T1_bin.1	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A;s_Blautia_A faecis
A09T1_bin.10	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_Ruminococcus_E;s_Ruminococcus_E bromii_B
A09T1_bin.13	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus salivarius
A09T1_bin.14	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Butyricocccaceae;g_Agathobaculum;s_Agathobaculum butyriciproducens
A09T1_bin.15	d_Bacteria;p_Actinomyetota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_Collinsella sp900547345
A09T1_bin.5	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Coproccoccus;s_Coproccoccus eutactus_A
A09T1_bin.6	d_Bacteria;p_Actinomyetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Anaerotardibacter;s_Anaerotardibacter sp900540345
Horse_bin.1	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_WCHB1-69;g_RUG11690;s_RUG11690 sp024400715
Horse_bin.10	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_UBA1179;s_
Horse_bin.11	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Actinomycetales;f_Brevibacteriaceae;g_Brevibacterium;s_Brevibacterium yomogidense_A
Horse_bin.12	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Mycobacteriales;f_Mycobacteriaceae;g_Dietzia;s_
Horse_bin.13	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_UBA1189;s_
Horse_bin.14	d_Bacteria;p_Bacillota_A;c_Clostridia;o_UBA1381;f_UBA1381;g_UBA1738;s_
Horse_bin.15	d_Bacteria;p_Chloroflexota;c_Chloroflexia;o_Thermomicrobiales;f_UBA6265;g_UBA6265;s_
Horse_bin.16	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Actinomycetales;f_Micrococcaceae;g_Citricoccus;s_
Horse_bin.17	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella;s_
Horse_bin.18	d_Bacteria;p_Chloroflexota;c_Chloroflexia;o_Thermomicrobiales;f_UBA6265;g_UBA6265;s_
Horse_bin.19	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_
Horse_bin.2	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_CAG-177;s_
Horse_bin.20	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Actinomycetales;f_Dermatophilaceae;g_Ornithinococcus;s_
Horse_bin.21	d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Neisseriaceae;g_Neisseria;s_
Horse_bin.22	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Carnobacteriaceae;g_Marinilactibacillus;s_
Horse_bin.23	d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_;
Horse_bin.24	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaceae;g_Akkermansia;s_
Horse_bin.25	d_Bacteria;p_Gemmatimonadota;c_Gemmatimonadetes;o_Longimicrobiales;f_Longimicrobiaceae;g_Longimicrobium;s_
Horse_bin.26	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG099;s_RUG099 sp024403055
Horse_bin.27	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Mycobacteriales;f_Mycobacteriaceae;g_Rhodococcus;s_Rhodococcus sp012844225
Horse_bin.28	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_UBA1189;s_
Horse_bin.29	d_Bacteria;p_Fibrobacterota;c_Fibrobacteria;o_Fibrobacteriales;f_Fibrobacteraceae;g_Fibrobacter;s_Fibrobacter sp900142465
Horse_bin.3	d_Bacteria;p_Synergistota;c_Synergistia;o_Synergistales;f_Synergistaceae;g_E4-60;s_E4-60 sp018065065
Horse_bin.30	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Mycobacteriales;f_Mycobacteriaceae;g_Corynebacterium;s_Corynebacterium casei
Horse_bin.31	d_Bacteria;p_Pseudomonadota;c_Alphaproteobacteria;o_Rhodobacterales;f_Rhodobacteriaceae;g_Paracoccus;s_Paracoccus sp021491915
Horse_bin.32	d_Bacteria;p_Chloroflexota;c_Chloroflexia;o_Thermomicrobiales;f_UBA6265;g_UBA6265;s_
Horse_bin.33	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_UBA1786;s_
Horse_bin.34	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Actinomycetales;f_Micrococcaceae;g_Glutamicibacter;s_Glutamicibacter arilaitensis
Horse_bin.35	d_Bacteria;p_Actinomyetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Phoenicibacter;s_
Horse_bin.36	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Actinomycetales;f_Actinomycetaceae;g_Pauljensenia;s_
Horse_bin.37	d_Bacteria;p_Actinomyetota;c_Actinomycetia;o_Mycobacteriales;f_Mycobacteriaceae;g_Corynebacterium;s_Corynebacterium glutamicum
Horse_bin.38	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_

Horse_bin.39	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_WM01;s_
Horse_bin.4	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Propionibacteriales;f_Propionibacteriaceae;g_Brevilactibacter;s_
Horse_bin.40	d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Acinetobacter;s_Acinetobacter pecorum
Horse_bin.41	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Vescimonas;s_
Horse_bin.42	d_Bacteria;p_Verrucomicrobiota;c_Kiritimatiellia;o_LD1-PB3_B;f_Lenti-01;g_RGIG3636;s_
Horse_bin.43	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Microbacteriaceae;g_Pseudoclavibacter;s_
Horse_bin.44	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Microbacteriaceae;g_Agrococcus;s_Agrococcus casei
Horse_bin.45	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_UBA932;g_Cryptobacteroides;s_
Horse_bin.46	d_Bacteria;p_Verrucomicrobiota;c_Verrucomicrobiae;o_Verrucomicrobiales;f_Akkermansiaceae;g_Akkermansia;s_
Horse_bin.48	d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Staphylococcaceae;g_Staphylococcus;s_Staphylococcus xylosus
Horse_bin.49	d_Bacteria;p_Spirochaetota;c_Spirochaetia;o_Treponematales;f_Treponemataceae;g_UBA1240;s_UBA1240 sp024402495
Horse_bin.5	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_UBA738;s_UBA738 sp018065965
Horse_bin.50	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_RUG708;s_
Horse_bin.51	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_UBA932;g_Cryptobacteroides;s_Cryptobacteroides sp900771005
Horse_bin.52	d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Salinicoccaceae;g_Jeotgalicoccus;s_Jeotgalicoccus sp003513765
Horse_bin.53	d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Psychrobacter;s_Psychrobacter alimentarius_A
Horse_bin.54	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Aerococcus;s_Aerococcus urinaeequi
Horse_bin.55	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Brevibacteriaceae;g_Brevibacterium;s_Brevibacterium aurantiacum
Horse_bin.56	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Propionibacteriales;f_Propionibacteriaceae;g_Arachnia;s_
Horse_bin.57	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Limivacinus;s_
Horse_bin.58	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Micrococcaceae;g_Kocuria;s_
Horse_bin.59	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_UBA932;g_Cryptobacteroides;s_
Horse_bin.6	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Saccharofermentanales;f_Saccharofermentanaceae;g_Saccharofermentans;s_Saccharofermentans sp024403855
Horse_bin.60	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Dermatophilaceae;g_Ornithinimicrobium;s_
Horse_bin.61	d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Salinicoccaceae;g_Aliicoccus;s_
Horse_bin.62	d_Bacteria;p_Bacillota;c_Bacilli;o_Bacillales;f_Planococcaceae;g_Planococcus;s_Planococcus sp021513255
Horse_bin.63	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Limivacinus;s_
Horse_bin.64	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Limivacinus;s_
Horse_bin.65	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Propionibacteriales;f_Propionibacteriaceae;g_Brevilactibacter;s_
Horse_bin.66	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Acutalibacteraceae;g_UBA1227;s_
Horse_bin.67	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_F23-B02;s_
Horse_bin.68	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Avilachnospira;s_Avilachnospira sp024405155
Horse_bin.7	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_WM01;s_
Horse_bin.70	d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Staphylococcaceae;g_Staphylococcus;s_Staphylococcus equorum
Horse_bin.71	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Ligilactobacillus;s_Ligilactobacillus equi
Horse_bin.72	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_RGIG3159;s_
Horse_bin.73	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus equinus
Horse_bin.74	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Micrococcaceae;g_Rothia;s_
Horse_bin.77	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Micrococcaceae;g_Kocuria;s_Kocuria rosea
Horse_bin.78	d_Bacteria;p_Pseudomonadota;c_Gammaproteobacteria;o_Burkholderiales;f_Neisseriaceae;g_Neisseria;s_
Horse_bin.79	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_UBA1179;s_UBA1179 sp024398695
Horse_bin.8	d_Bacteria;p_Bacillota;c_Bacilli;o_Staphylococcales;f_Staphylococcaceae;g_Macrococcus;s_Macrococcus caroulesicus
Horse_bin.80	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Christensenellales;f_CAG-74;g_ZC3RG03;s_
Horse_bin.9	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_UBA932;g_Cryptobacteroides;s_Cryptobacteroides sp024401795
M02T0_bin.11	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes;s_Anaerostipes hadrus_A
M02T0_bin.16	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_CAG-103;s_CAG-103 sp900543625

M02T1_bin.1	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Senegalimassilia;s_Senegalimassilia anaerobia
M02T1_bin.8	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Oliverpabstia;s_Oliverpabstia faecicola
M08T0_bin.14	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_Collinsella tanakaei
M08T0_bin.15	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Atopobiaceae;g_Thermophilibacter;s_Thermophilibacter provencensis
M08T0_bin.18	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Atopobiaceae;g_Coprovincinus;s_Coprovincinus sp900551595
M08T0_bin.2	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Ellagibacter;s_Ellagibacter isourolithinifaciens
M08T0_bin.20	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Zhenpiania;s_Zhenpiania hominis
M08T0_bin.5	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_Bifidobacterium bifidum
M08T0_bin.6	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_Collinsella sp900541055
M08T0_bin.8	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Atopobiaceae;g_Tractidigestivibacter;s_Tractidigestivibacter sp000752675
M08T0_bin.9	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger qucibialis
M08T1_bin.1	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Anaerotardibacter;s_Anaerotardibacter sp000436075
M08T1_bin.11	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_Bifidobacterium catenulatum
M08T1_bin.12	d_Bacteria;p_Bacteroidota;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Prevotella;s_Prevotella rara
M08T1_bin.16	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Faecalibacterium;s_Faecalibacterium hattorii
M08T1_bin.2	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Christensenellales;f_CAG-74;g_Ventricola;s_Ventricola sp900542395
M08T1_bin.7	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_CAG-103;s_CAG-103 sp000432375
PT01T0_bin.10	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_Collinsella sp900541855
PT01T0_bin.12	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Mediterraneibacter;s_Mediterraneibacter faecis
PT01T0_bin.4	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A;s_Blautia_A wexlerae
PT01T0_bin.9	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A;s_Blautia_A sp900066335
PT01T1_bin.5	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Latilactobacillus;s_Latilactobacillus sakei
PT01T1_bin.6	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Anaerotardibacter;s_Anaerotardibacter sp000435675
PT03T0_bin.10	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruthenibacterium;s_Ruthenibacterium merdipullorum
PT03T0_bin.14	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Actinomycetaceae;g_Pauljensenia;s_Pauljensenia sp018375675
PT03T0_bin.15	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Ruminococcus_C;s_Ruminococcus_C sp000980705
PT03T0_bin.5	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A;s_Blautia_A obeum
PT03T0_bin.7	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Clostridium_AP;s_Clostridium_AP scindens
PT03T0_bin.9	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus_B;s_Enterococcus_B lactis
PT03T1_bin.2	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerobutyricum;s_Anaerobutyricum hallii
PT03T1_bin.8	d_Bacteria;p_Bacillota;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus;s_Streptococcus thermophilus
PT04T0_bin.1	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_Collinsella sp003487125
PT05T0_bin.10	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia;s_Blautia sp001304935
PT05T0_bin.11	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_Collinsella intestinalis
PT05T0_bin.15	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Rubneribacter;s_Rubneribacter badeniensis
PT05T0_bin.17	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Anaerostipes;s_Anaerostipes hadrus
PT05T0_bin.2	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_Bifidobacterium pullorum_B
PT05T0_bin.3	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger avicola
PT05T0_bin.5	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_Lentihominibacter excrementipullorum
PT05T0_bin.7	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A;s_Blautia_A hydrogenotrophica
PT05T0_bin.8	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Eggerthella;s_Eggerthella lenta
PT05T0_bin.9	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Vescimonas;s_Vescimonas sp001916855
PT05T1_bin.3	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Lachnoclostridium_B;s_Lachnoclostridium_B sp900066555
PT05T1_bin.5	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Actinomycetaceae;g_Pauljensenia;s_Pauljensenia sp000466265
PT05T1_bin.8	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Gordonibacter;s_Gordonibacter urolithinifaciens
PT07T0_bin.12	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_

PT07T0_bin.3	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Lachnospirales;f_Lachnospiraceae;g_Blautia_A;s_Blautia_A sp000436615
PT07T0_bin.6	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Oscillospiraceae;g_Evtepia;s_Evtepia excrementipullorum
PT07T0_bin.8	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_Bifidobacterium pseudocatenulatum
PT07T0_bin.9	d_Bacteria;p_Actinomycetota;c_Actinomycetia;o_Actinomycetales;f_Bifidobacteriaceae;g_Bifidobacterium;s_Bifidobacterium longum
PT07T1_bin.18	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_Eggerthellaceae;g_Anaerotardibacter;s_Anaerotardibacter sp000435475
PT07T1_bin.2	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Oscillospirales;f_Ruminococcaceae;g_Gemmiger;s_Gemmiger sp900540775
PT07T1_bin.4	d_Bacteria;p_Actinomycetota;c_Coriobacteriia;o_Coriobacteriales;f_QAMH01;g_QAMH01;s_QAMH01 sp900544245
PT07T1_bin.9	d_Bacteria;p_Bacillota_A;c_Clostridia;o_Peptostreptococcales;f_Anaerovoracaceae;g_Lentihominibacter;s_Lentihominibacter faecis
Horse_bin.76	d_Archaea;p_Halobacteriota;c_Methanomicrobia;o_Methanomicrobiales;f_Methanocorpusculaceae;g_Methanocorpusculum;s__

Supplementary Table 6. Log2FC variation of SGBs abundance, in terms of Genome copies per milion reads, compared to the children gut microbiome before the biodiversity intervention.

SGBs_ID	log_FC	diffexpressed	GTDB taxonomy
Horse_bin.64	6.803	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Limivacinus;s__
Horse_bin.27	6.803	UP	d__Bacteria;p__Actinomycetota;c__Actinomycetia;o__Mycobacteriales;f__Mycobacteriaceae;g__Rhodococcus;s__Rhodococcus sp012844225
Horse_bin.5	6.803	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__UBA738;s__UBA738 sp018065965
A03T1_bin.7	6.803	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Christensenellales;f__CAG-138;g__RUG472;s__RUG472 sp900545265
A03T1_bin.6	6.057	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Angelakisella;s__Angelakisella sp900547385
A03T1_bin.5	5.396	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__TANB77;f__CAG-508;g__CAG-452;s__CAG-452 sp000434035
A05T1_bin.12	4.973	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Acutalibacteraceae;g__Scatavimonas;s__Scatavimonas sp900540275
A03T1_bin.19	3.909	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Christensenellales;f__CAG-138;g__SFEL01;s__SFEL01 sp004557245
A03T1_bin.16	3.589	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Vescimonas;s__Vescimonas sp900548615
M08T1_bin.16	3.445	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium;s__Faecalibacterium hattorii
M08T1_bin.12	3.331	UP	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Prevotella;s__Prevotella rara
PT01T1_bin.5	2.789	UP	d__Bacteria;p__Bacillota;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Latilactobacillus;s__Latilactobacillus sakei
PT05T0_bin.2	2.763	UP	d__Bacteria;p__Actinomycetota;c__Actinomycetia;o__Actinomycetales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium pullorum_B
A03T1_bin.15	2.702	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Acetatifactor;s__Acetatifactor intestinalis
A05T1_bin.9	2.472	UP	d__Bacteria;p__Actinomycetota;c__Actinomycetia;o__Actinomycetales;f__Bifidobacteriaceae;g__Bifidobacterium;s__Bifidobacterium animalis
A03T1_bin.8	2.367	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium;s__Faecalibacterium prausnitzii_A
A03T1_bin.13	2.287	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus_D;s__Ruminococcus_D bicirculans
A05T1_bin.19	2.235	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Hominisplanchenecus;s__Hominisplanchenecus faecis
M08T1_bin.7	2.149	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__CAG-103;s__CAG-103 sp000432375
M02T1_bin.8	2.023	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Oliverpabstia;s__Oliverpabstia faecicola
A05T1_bin.15	1.930	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Faecalibacterium;s__Faecalibacterium duncaniae
Horse_bin.41	1.899	UP	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Vescimonas;s__
A03T1_bin.18	1.569	UP	d__Bacteria;p__Bacillota_C;c__Negativicutes;o__Veillonellales;f__Dialisteraceae;g__Dialister;s__Dialister invisus
A09T0_bin.17	-1.577	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus_C;s__Ruminococcus_C sp900545285
A05T0_bin.21	-1.698	DOWN	d__Bacteria;p__Bacillota;c__Bacilli;o__RF39;f__UBA660;g__Aphodocola;s__Aphodocola sp000434835
PT05T0_bin.10	-1.734	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Blautia;s__Blautia sp001304935
PT05T0_bin.5	-1.750	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Peptostreptococcales;f__Anaerovoracaceae;g__Lentihominibacter;s__Lentihominibacter excrementipullorum
PT05T0_bin.11	-1.858	DOWN	d__Bacteria;p__Actinomycetota;c__Coriobacteriia;o__Coriobacteriales;f__Coriobacteriaceae;g__Collinsella;s__Collinsella intestinalis
A05T0_bin.10	-1.880	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Acutalibacteraceae;g__Ruminococcus_E;s__Ruminococcus_E sp003526955
A05T0_bin.3	-2.207	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Acutalibacteraceae;g__UBA1417;s__UBA1417 sp003531055
PT03T0_bin.15	-2.224	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Ruminococcus_C;s__Ruminococcus_C sp000980705
A09T0_bin.6	-2.277	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Wujia;s__Wujia chipingensis
A05T0_bin.12	-2.405	DOWN	d__Bacteria;p__Verrucomicrobiota;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Akkermansiaceae;g__Akkermansia;s__Akkermansia muciniphila
PT05T0_bin.3	-2.528	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Ruminococcaceae;g__Gemmiger;s__Gemmiger avicola
A09T0_bin.4	-2.623	DOWN	d__Bacteria;p__Bacteroidota;c__Bacteroidia;o__Bacteroidales;f__Bacteroidaceae;g__Prevotella;s__Prevotella copri_A
A05T0_bin.13	-2.838	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Vescimonas;s__Vescimonas sp000435555
PT05T0_bin.9	-3.114	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Oscillospirales;f__Oscillospiraceae;g__Vescimonas;s__Vescimonas sp001916855
A05T0_bin.6	-3.119	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__Lachnospirales;f__Lachnospiraceae;g__Coprococcus;s__Coprococcus eutactus
A09T0_bin.1	-4.887	DOWN	d__Bacteria;p__Bacillota;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Lactococcus;s__Lactococcus cremoris
A09T0_bin.16	-5.529	DOWN	d__Bacteria;p__Bacillota;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactiplantibacillus;s__Lactiplantibacillus plantarum
A03T0_bin.5	-5.645	DOWN	d__Bacteria;p__Bacillota_A;c__Clostridia;o__TANB77;f__CAG-508;g__CAG-269;s__CAG-269 sp000431335
PT03T0_bin.9	-5.831	DOWN	d__Bacteria;p__Bacillota;c__Bacilli;o__Lactobacillales;f__Enterococcaceae;g__Enterococcus_B;s__Enterococcus_B lactis
Horse_bin.19	-9.966	DOWN	d__Bacteria;p__Bacillota;c__Bacilli;o__Lactobacillales;f__Streptococcaceae;g__Streptococcus;s__