# Constructed from biom file	Bastu	
#OTU ID	PUR200801	
k Bacteria;p Actinobacteria;c Actinobacteria;o Bifidobacteriales;f Bifidobacteriaceae;g Bifidobacterium	0.94%	
k Bacteria;p Actinobacteria;c Coriobacteriia;o Coriobacteriales;f Coriobacteriaceae;g Adlercreutzia-Asaccharobacter	0.16%	
k Bacteria;p Actinobacteria;c Coriobacteriia;o Coriobacteriales;f Coriobacteriaceae;g Collinsella	10.12%	
k Bacteria;p Actinobacteria;c Coriobacteriia;o Coriobacteriales;f Coriobacteriaceae;g Denitrobacterium	0.02%	
k Bacteria;p Actinobacteria;c Coriobacteriia;o Coriobacteriales;f Coriobacteriaceae;g NA	0.21%	
k Bacteria;p Actinobacteria;c Coriobacteriia;o Coriobacteriales;f Coriobacteriaceae;g Slackia	0.17%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Bacteroidaceae;g Bacteroides	6.66%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Porphyromonadaceae;g Barnesiella	0.08%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Porphyromonadaceae;g Odoribacter	0.22%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Porphyromonadaceae;g Parabacteroides	1.14%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Prevotellaceae;g Alloprevotella	5.62%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Prevotellaceae;g NA	4.55%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Prevotellaceae;g Prevotella	16.02%	
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Rikenellaceae;g Alistipes	0.02%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Christensenellaceae;g NA	0.03%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Clostridiaceae;g Clostridium	1.68%	
k Bacteria:p Firmicutes;c Clostridia:o Clostridiales:f Eubacteriaceae;g Eubacterium	0.04%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Family XIII;g Eubacterium	0.02%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Family XIII;g NA	0.16%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia	4.05%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Lachnoclostridium	8.19%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Lactonifactor	1.37%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g NA	4.17%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Roseburia	0.47%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Tyzzerella	0.15%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f NA;g NA	1.58%	
k Bacteria:p Firmicutes;c Clostridia:o Clostridiales:f Peptococcaceae;g Peptococcus	0.81%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Peptostreptococcaceae;g Peptoclostridium	0.05%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g *Soleaferrea	0.02%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcacea;g Anaerotruncus	0.88%	
k Bacteria:p Firmicutes;c Clostridia:o Clostridiales:f Ruminococcaceae:g Butyricicoccus	0.09%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Eubacterium	0.09%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Faecalibacterium	0.31%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Flavonifractor	0.27%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g NA	2.22%	
k Bacteria:p Firmicutes;c Clostridia:o Clostridiales:f Ruminococcaceae;g Ruminiclostridium	3.87%	
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Subdoligranulum	6.75%	
k Bacteria;p Firmicutes;c Erysipelotrichia;o Erysipelotrichales;f Erysipelotrichaceae;g Catenibacterium	1.19%	
k Bacteria;p Firmicutes;c Erysipelotrichia;o Erysipelotrichales;f Erysipelotrichaceae;g Holdemanella	2.67%	
k Bacteria;p Firmicutes;c Negativicutes;o Selenomonadales;f Acidaminococcaceae;g Megamonas	8.99%	
k Bacteria;p Firmicutes;c Negativicutes;o Selenomonadales;f Veillonellaceae;g Allisonella	0.11%	
k Bacteria;p Fusobacteria;c Fusobacteriia;o Fusobacteriales;f Fusobacteriaceae;g Fusobacterium	0.62%	
k Bacteria;p Proteobacteria;c Betaproteobacteria;o Burkholderiales;f Alcaligenaceae;g Sutterella	2.94%	
k Bacteria;p Proteobacteria;c Gammaproteobacteria;o Enterobacteriales;f Enterobacteriaceae;g Escherichia-Shigella	0.22%	
None;Other;Other;Other;Other	0.08%	
Tonic, outer, outer, outer, outer	0.0070	

# Constructed from biom file	Bastu
#OTU ID	PUR200801
kBacteria;pActinobacteria;cActinobacteria;oBifidobacteriales;fBifidobacteriaceae;gBifidobacterium;ssaeculare	0.94%
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia-Asaccharobacter;s_celatus-equolifaciens	0.16%
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_aerofaciens	3.72%
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_intestinalis-stercoris	1.47%
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_sp10410	0.07%
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_tanakaei	4.86%
kBacteria;pActinobacteria;cCoriobacteriia;oCoriobacteriales;fCoriobacteriaceae;gDenitrobacterium;sdetoxificans	0.02%
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_NA;s_sp10524	0.21%
k_Bacteria;p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Slackia;s_piriformis	0.17%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_coprocola	0.89%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Bacteroidaceae;g Bacteroides;s finegoldii	0.03%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Bacteroidaceae;g Bacteroides;s plebeius	4.35%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Bacteroidaceae;g Bacteroides;s sp12254	0.50%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Bacteroidaceae;g Bacteroides;s sp12324	0.27%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Bacteroidaceae;g Bacteroides;s stercoris	0.18%
Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Bacteroidaceae;g Bacteroides;s uniformis	0.04%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidale;f Bacteroidaceae;g Bacteroides;s vulgatus	0.38%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_xylanisolvens	0.02%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Porphyromonadaceae;g Barnesiella;s intestinihominis	0.08%
k Bacteria;p Bacteroidetes;c Bacteroidia;o Bacteroidales;f Porphyromonadaceae;g Odoribacter;s sp13171	0.08%
	0.15%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Odoribacter;s_sp13171-sp13184	
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Parabacteroides;s_distasonis	0.59%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Parabacteroides;s_merdae	0.55%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Alloprevotella;s_sp13496-sp13497	5.62%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_NA;s_sp13942	4.55%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella;s_copri	9.44%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella;s_copri-sp13942	6.58%
k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes;s_sp14354	0.02%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae;g_NA;s_sp30180	0.03%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium;s_perfringens	1.68%
kBacteria;pFirmicutes;cClostridia;oClostridiales;fEubacteriaceae;gEubacterium;scallanderi-limosum	0.04%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Family XIII;g_Eubacterium;s_sp31674	0.02%
kBacteria;pFirmicutes;cClostridia;oClostridiales;fFamily XIII;gNA;ssp31533-sp31552	0.04%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Family XIII;g_NA;s_sp31561	0.03%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Family XIII;g_NA;s_sp31623-sp31633-sp31678	0.08%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s hansenii-producta	1.15%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s hydrogenotrophica	0.04%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s NA	0.04%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s sp31973	0.06%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s sp31989	0.86%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s sp32027	0.04%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s sp32032	0.69%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s sp32042	0.88%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Blautia;s sp32046	0.27%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Lachnoclostridium;s sp32341-sp32430	0.10%
	6.16%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32350	0.04%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32350-sp32432-sp33707	0.05%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32362	0.06%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32364	0.99%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32371-sp32374	0.09%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32374	0.07%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32386	0.09%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32424	0.13%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lachnoclostridium;s_sp32445	0.41%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Lactonifactor;s_longoviformis	1.37%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp32166	0.02%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp32167	0.10%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp32615-sp32802	0.49%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp33387	0.85%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp33479	0.14%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp33635	0.13%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp33656	0.46%
kBacteria;pFirmicutes;cClostridia;oClostridiales;fLachnospiraceae;gNA;ssp33707	0.07%
kBacteria;pFirmicutes;cClostridia;oClostridiales;fLachnospiraceae;gNA;ssp33728-sp33748	1.76%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp33756	0.07%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_NA;s_sp33769	0.08%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Roseburia;s_sp33161-sp33189	0.35%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Lachnospiraceae;g Roseburia;s sp33185	0.11%
ik Bacteria,p Firmicutes,c Ciostriuia,o Ciostriuiaies,i Lacrinospiraceae,g Roseburia,s Spootoo	
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Tyzzerella;s_sp33302	0.15%

k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Peptococcaceae;g Peptococcus;s sp34119	0.81%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Peptostreptococcaceae;g Peptoclostridium;s sp34340	0.05%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_**Soleaferrea;s_sp34492	0.03%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Anaerotruncus;s colihominis	0.02%
	0.86%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Anaerotruncus;s_sp34474	
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Butyricicoccus;s_pullicaecorum	0.09%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Eubacterium;s_sp35686	0.09%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Faecalibacterium;s_prausnitzii	0.31%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Flavonifractor;s_plautii	0.27%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp34734	0.11%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp34743	0.02%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp34794	0.08%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp34815	0.25%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp34850	0.06%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp35059	0.17%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp35099	0.04%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp35327	0.29%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp35413	0.02%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp35436	0.04%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp35662	0.05%
k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_NA;s_sp35690	0.38%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g NA;s sp35707	0.30%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g NA;s sp35736	0.16%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g NA;s sp35758	0.04%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g NA;s sp35805	0.02%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g NA;s sp35829	0.12%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g NA;s sp35834	0.07%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Ruminiclostridium;s sp34905-sp34937	0.06%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Ruminiclostridium;s sp34921	0.02%
k Bacteria;p Firmicutes;c Clostridiale; Clostridiales;f Ruminococcaceae;g Ruminiclostridium;s sp34921-sp34937	0.03%
k Bacteria;p Firmicutes;c Clostridiales;f Ruminococcaceae;g Ruminiclostridium;s sp34949	3.39%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Ruminiclostridium;s sp34950	0.38%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Subdoligranulum;s sp35580-sp35585-variabile	0.17%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Subdoligranulum;s sp35590	0.07%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Subdoligranulum;s sp35591	4.17%
k Bacteria;p Firmicutes;c Clostridia;o Clostridiales;f Ruminococcaceae;g Subdoligranulum;s variabile	2.34%
k_Bacteria;p_Firmicutes;c_Erysipelotrichia;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Catenibacterium;s_mitsuokai	1.19%
k_Bacteria;p_Firmicutes;c_Erysipelotrichia;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Holdemanella;s_sp36738	2.67%
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Selenomonadales;f_Acidaminococcaceae;g_Megamonas;s_funiformis	8.99%
k_Bacteria;p_Firmicutes;c_Negativicutes;o_Selenomonadales;f_Veillonellaceae;g_Allisonella;s_histaminiformans	0.11%
k_Bacteria;p_Fusobacteria;c_Fusobacteria;o_Fusobacteriales;f_Fusobacteriaceae;g_Fusobacterium;s_sp37458	0.62%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Sutterella;s_sp48275	0.09%
k_Bacteria;p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Sutterella;s_wadsworthensis	2.84%
k_Bacteria;p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_Escherichia-Shigella;s_coli	0.22%
None;Other;Other;Other;Other	0.08%