Supplementary table 10: Interaction of OTUs with Helicobacter pylori

OTU code	Status of interaction	OTU_Taxonomy greengenes database	OTU representative sequence	q value
Otu000023	Co-exluding in IM	k__Bacteria;p__Firmicutes;c__Bacilli;o__Lactobacillales;f__Lactobacillaceae;g__Lactobacillus;	TACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGAAGAATAAGTCTGATGTGAAAGCCCTCGGCTTAA	0.016
Otu000029	Co-occuring in IM	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Prevotellaceae;g__Prevotella;s__melaninogenica;	TACGGAAGGTCCAGGCGTTATCCGGATTTATTGGGTTTAAAGGGAGCGTAGGCTGGAGATTAAGTGTGTTGTGAAATGTAGACGCTCAA	0.029
Otu000039	Co-exluding in IM	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae;g__SMB53;	TACGTAGGGGGCTAGCGTTATCCGGAATTACTGGGCGTAAAGGGTGCGTAGGTGGTTTCTTAAGTCAGAGGTGAAAGGCTACGGCTCAA	0.038
Otu000044	Co-excluding in SG and IM	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Methylophilales;f__Methylophilaceae;g__Methylobacillus;	TACGTAGGGTGCGAGCGTTAATCGGAATTACTGGGCGTAAAGCGAGCGCAGGCGGTTCTGCAAGTCAGATGTGAAATCCCCGGGCTCAA	0.027
Otu000080	Co-exluding in IM	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;o__Bacillales_unclassified;o__Bacillales_unclassified;	TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGCAGGTGGTTTCTTAAGTCTGATGTGAAAGCCCACGGCTCAA	0.0093
Otu000087	Co-occuring in IM	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Helicobacteraceae;g__Helicobacter;s__ganmani;	TACGGAGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAAGAGCGCGTAGGCGGGATAGCAAGTCAGATGTGAAATCCTATGGCTTAA	0.0047
Otu000108	Co-occuring in SG and IM	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Micrococcaceae;g__Arthrobacter;s__psychrolactophilus;	TACGTAGGGCGCAAGCGTTATCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGTTTGTCGCGTCTGCCGTGAAAGTCCGGGGCTCAA	0.023
Otu000142	Co-exluding in IM	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__Ruminococcus;	TACGTAGGGAGTAAGCGTTATCCGGAATTACTGGGTGTAAAGGGAGTGTAGGCGGGACTTTAAGTCAGATGTGAAAATTATGGGCTCAA	0.016
Otu000294	Co-occuring in IM	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;f__Ruminococcaceae;g__Moryella	TACGTAGGTTGCAAGCGTTGTCCGGATTTACTGGGTGTAAAGGGCGTGTAGGCGGAGCTGCAAGTCAGATGTGAAATCCCGGGGCTCAA	0.038

OTU: Operational taxonomic unit
SG: Superficial gastritis
IM: Intestinal metaplasia