

Table S1. The number of the 16S rRNA gene sequences obtained from the non-secretor samples, the secretor samples and the samples with different FUT2 genotypes by pyrosequencing.

	Non-secretor (AA)	Secretor (AG/GG)	Secretor, AG	Secretor, GG	Total
Samples	12	12	7	5	24
total # of Reads	118 507	127 299	72 843	54 456	245 806
# of reads passing QC	60 184	67 168	38 532	28 636	127 352
Average # (range) of reads per sample	5 015 (2529 - 7276)	5 597 (3509 - 7257)	5505 (3509-7257)	5727 (5187-6137)	5306 (2529-7276)
Good's coverage	0.796	0.787	0.733	0.794	0.792