

**Table S1.** List of top 10 genus that contributed to QS functional genes using PICRUSt2.

<b>Taxonomy Contributions</b>	<b>C10 (%)</b>
Pseudomonas	33.78103154
Escherichia-Shigella	5.482468212
Sphingomonas	5.031100347
Bifidobacterium	4.574227996
Bacteroides	3.759564045
Blautia	3.374250014
Catenibacterium	3.16507954
Massilia	2.928386635
o__Acidobacteriales; f__uncultured; g__uncultured	2.779765509
Enterococcus	2.510045687
	<b>C12 (%)</b>
Pseudomonas	37.68856567
Bifidobacterium	6.382978723
Sphingomonas	5.454277431
f__Comamonadaceae;NA	5.390398506
Catenibacterium	4.161957643
Massilia	4.009630976
Bacteroides	3.626357427
o__Acidobacteriales; f__uncultured; g__uncultured	2.859810329
Blautia	2.515846887
Bacillus	1.916367746
	<b>C8 (%)</b>
Pseudomonas	35.58993282
Bifidobacterium	7.342227268
Bacteroides	5.643864131
Catenibacterium	4.626738575
Sphingomonas	3.798845681
f__Comamonadaceae;NA	3.742075882
Blautia	3.694767717
Massilia	3.6900369
Polaromonas	2.838489923
Variovorax	1.717286404
	<b>BS (%)</b>
Pseudomonas	32.15302952
Bifidobacterium	8.842568617
Catenibacterium	7.651475919
Bacteroides	6.54453651
Massilia	3.845157949

Blautia	3.010098395
Variovorax	3.010098395
Bacillus	2.492232004
Sphingomonas	1.851372346
o__Acidobacteriales; f__uncultured; g__uncultured	1.728379078
	<b>W (%)</b>
Pseudomonas	29.83806618
Bifidobacterium	7.81976062
Catenibacterium	6.233278573
Bacteroides	5.862473598
Blautia	4.125792068
Massilia	3.431119456
f__Comamonadaceae;NA	2.52522882
Variovorax	2.520535086
Escherichia-Shigella	2.271767191
Sphingomonas	2.098099038