

Supplementary Table 1. Differential abundance of genera between cases and controls.
P-values were computed with Metastats [1]

| Genus | <i>p</i> value (Metastats) | Case | | Control | |
|----------------|-------------------------------|-------|------|---------|------|
| | | Mean | SEM | Mean | SEM |
| Selenomonas | <0.01 | 3.54 | 0.47 | 0.61 | 0.21 |
| Prevotella | <0.01 | 24.84 | 4.33 | 2.95 | 1.95 |
| Tannerella | <0.01 | 0.89 | 0.26 | 0.02 | 0.01 |
| Granulicatella | 0.01 | 0.04 | 0.01 | 0.61 | 0.21 |
| Actinomyces | 0.01 | 1.70 | 0.23 | 19.06 | 6.55 |
| Streptococcus | 0.02 | 1.15 | 0.26 | 20.31 | 7.54 |
| Catonella | 0.02 | 0.72 | 0.28 | 0.04 | 0.02 |
| Treponema | 0.03 | 3.66 | 1.17 | 0.71 | 0.49 |
| Haemophilus | 0.04 | 0.05 | 0.02 | 1.90 | 0.83 |
| Gemella | 0.07 | 0.40 | 0.23 | 1.15 | 0.31 |
| Fusobacterium | 0.08 | 13.30 | 3.04 | 5.78 | 2.51 |
| Filifactor | 0.10 | 0.82 | 0.42 | 0.07 | 0.07 |