**S1 Table.** Microbiome association with disease severity. Multiple genera associated with disease severity by Lund-Makay CT score were identified. Correlated genera were different between disease subtypes (CRSwNP or CRSsNP) and tissue types (nasal polyp or uncinate tissue).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Disease subtype** | **Tissue type** | **Genus** | **Linear regression** | **Correlation coefficient** | **Spearman's rho** | **P-value** |
| CRSwNP | Nasal polyp | *Prevotella* | -2732.02\*RA+18.87 | 0.7119 | -0.771 | 0.025 |
| *Finegoldia* | 6484.72\*RA + 8.64 | 0.6641 | 0.718 | 0.045 |
| CRSwNP | Uncinate tissue | *Lachnospira* | 2398.59\*RA + 8.21 | 0.7366 | 0.745 | 0.034 |
| *Bacteroides* | -298.69\*RA + 14.97 | 0.6972 | -0.807 | 0.015 |
| *Paraburkholderia* | 2780.38\*RA + 8.61 | 0.6944 | 0.718 | 0.045 |
| *Agathobacter* | 3121.39\*RA + 7.96 | 0.6653 | 0.745 | 0.034 |
| CRSsNP | Uncinate tissue | *Roseburia* | -1548.44\*RA + 14.94 | 0.9142 | -0.971 | 0.001 |
| *Lachnoanaerobaculum* | -2944.35\*RA + 11.8 | 0.8859 | -0.823 | 0.044 |
| AB185816 | -1177.74\*RA + 11.8 | 0.8859 | -0.823 | 0.044 |
| *Rothia* | -2349.65\*RA + 18.21 | 0.8817 | -0.928 | 0.008 |
| *Streptococcus* | -234.27\*RA + 14.59 | 0.8713 | -0.899 | 0.015 |

Abbreviations: CRSwNP, chronic rhinosinusitis with nasal polyp; CRSsNP, chronic rhinosinusitis without nasal polyp; RA, relative abundance.