

Table S2. Sampling depth and biodiversity found by barcoded 454 sequencing of sputum samples from “stable”, “exacerbated” and “control” patient cohorts

Sampling depth	Average from stable CF samples	Average from exacerbated CF samples	Average from non-CF samples
Total sequences	60,500	65,000	71,000
High quality pyrosequences	49,000	50,000	51,000
Unique sequences (100% ID)	1,600	1,550	1,700
OTU (98% ID)	400	450	450
Genera	25-35	15-20	20-28