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<b>Title</b>	Microbiota and metabolite profiling reveal specific alterations in bacterial community structure and environment in the cystic fibrosis airway during exacerbation
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**Table S2.** Sampling depth and biodiversity found by barcoded 454 sequencing of sputum samples from “stable”, “exacerbated” and “control” patient cohorts

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