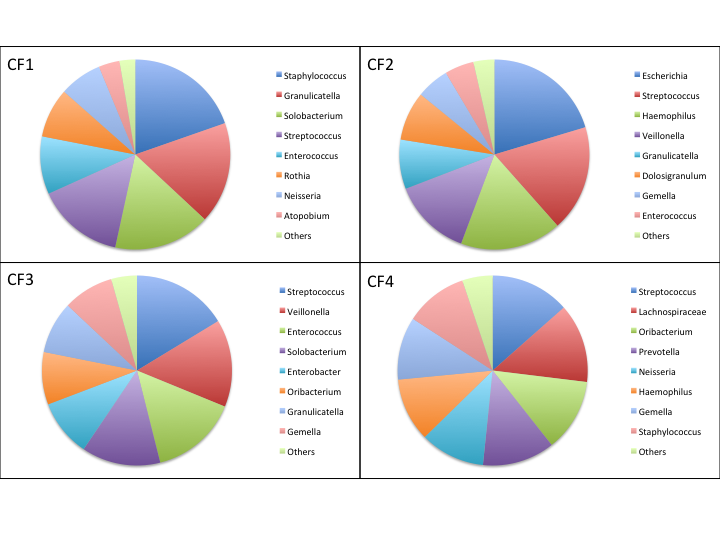
**MetaGeniE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing**

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**Figure S4.** Distribution of microbial community across the four cystic fibrosis samples (Top Hit per Genus is represented; Minimum genome coverage percent >10%, Genome Size >100,000; Scaffolds do not represent whole genomes and might be overrepresented).