

1 **Supplementary Table 5. Simulation of 16S rDNA amplicon sequences from NCBI 16S rRNA RefSeq database**

16S region	Forward (5'→3')	Reverse (5'→3')	Amplicon size of <i>E. coli</i> 16S template	Size selection of amplicons		Count of sequences (strains) of NCBI 16S rRNA RefSeq	
				min.	max.	Input before simulation	After simulation
V1-V3	AGAGTTTGATCATGGCTCAG	CCAGCAGCCGCGGTAAT	490	420	510	20,160	90% input
V3-V5	CCTACGGGAGGCAGCAG	ACTCAAATGAATTGACGG	551	525	561	20,160	90% input
V4	CCAGCAGCCGCGGTAA	ATTAGATACCCTGGTAGTCC	253	248	258	20,160	99% input
V6V9	AACGCGAAGAACCTTAC	AAGTCGTAACAAGGTAACCGTA	507	477	527	20,160	75% input

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