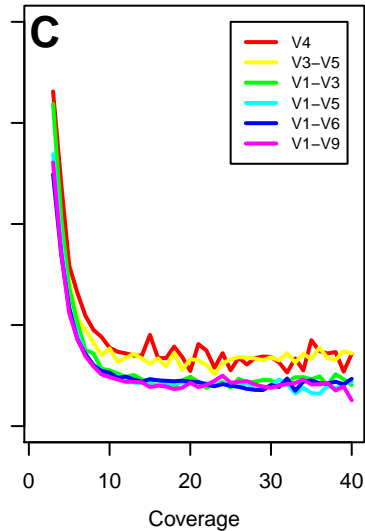
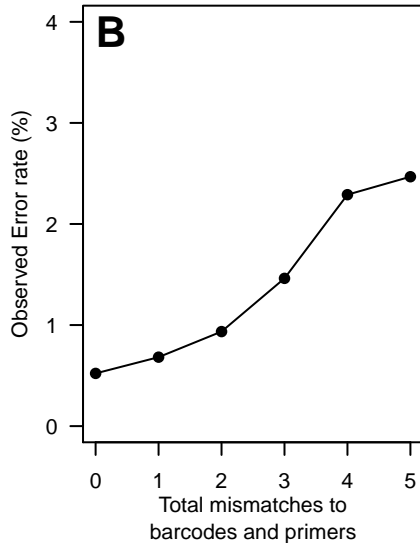
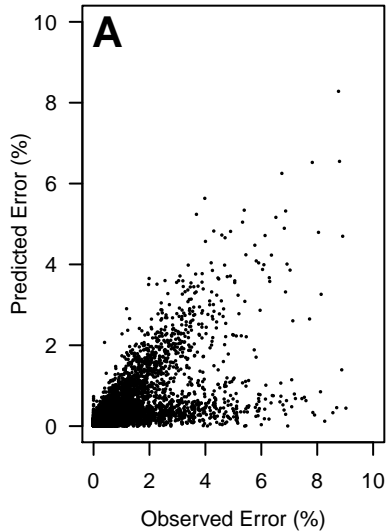


Table 1. Summary of the primer pairs used to generate the 16S rRNA gene fragment fragments and the characteristics of each region.

Region	Forward	Reverse	<i>E. coli</i> Coordinates	Amplicon Length	Sequences (N)
V4	GTGCCAGCMGCCGCGGTAA	GGACTACHVGGGTWTCTAAT	515-806	253	21,934
V1-V3	AGRGTTTGATYMTGGCTCAG	ATTACCGCGGCTGCTGG	8-534	490	36,545
V3-V5	CCTACGGGAGGCAGCAG	CCCGTCAATTCMTTTRAGT	341-927	551	16,694
V1-V5	AGRGTTTGATYMTGGCTCAG	CCCGTCAATTCMTTTRAGT	8-927	881	51,759
V1-V6	AGRGTTTGATYMTGGCTCAG	ACRACACGAGCTGACGAC	8-1078	1033	64,599
V1-V9	AGRGTTTGATYMTGGCTCAG	GGYTACCTTGTTACGACTT	8-1510	1464	61,721



Mock

V1-V9
V1-V6
V1-V5
V1-V3
V3-V5
V4

Human

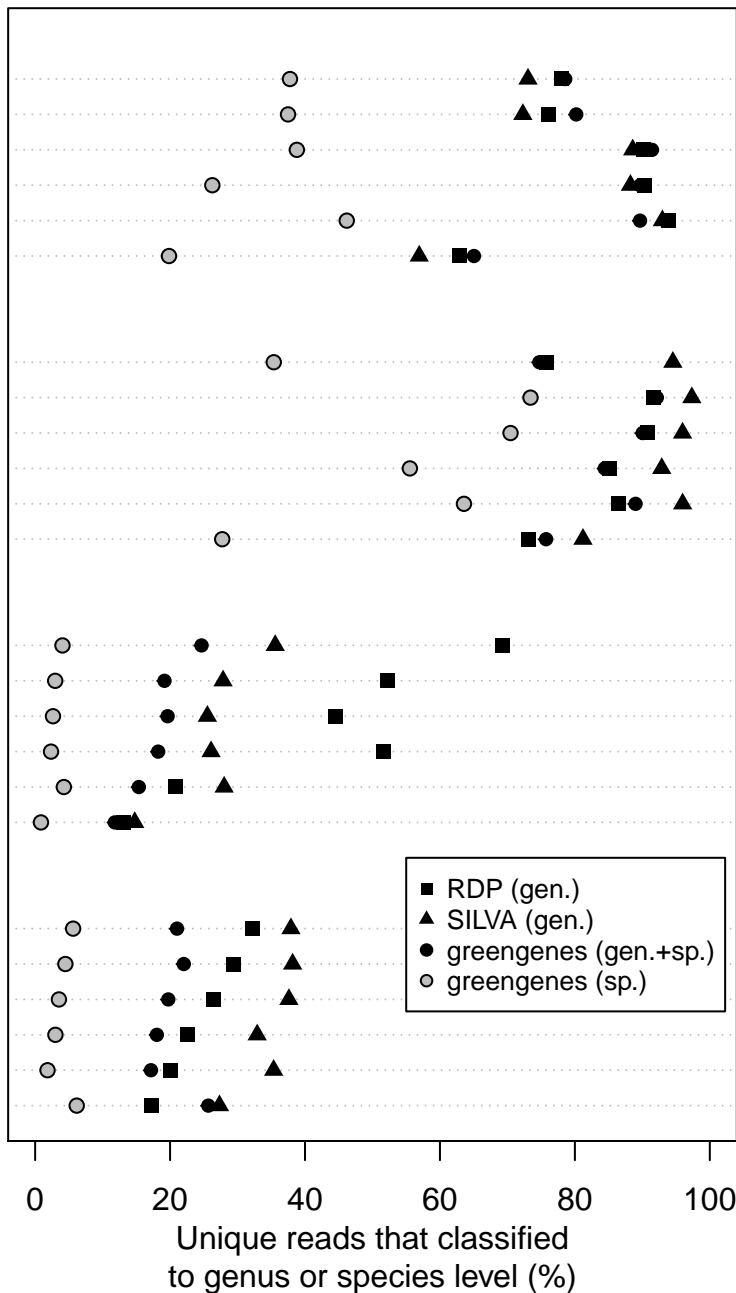
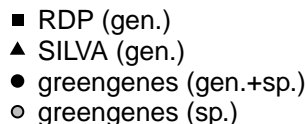
V1-V9
V1-V6
V1-V5
V1-V3
V3-V5
V4

Mouse

V1-V9
V1-V6
V1-V5
V1-V3
V3-V5
V4

Soil

V1-V9
V1-V6
V1-V5
V1-V3
V3-V5
V4



Percentage of 1-nt variants

