Data S4: NinjaMap performance in fecal challenge experiments, related to Figures 4 and 5.

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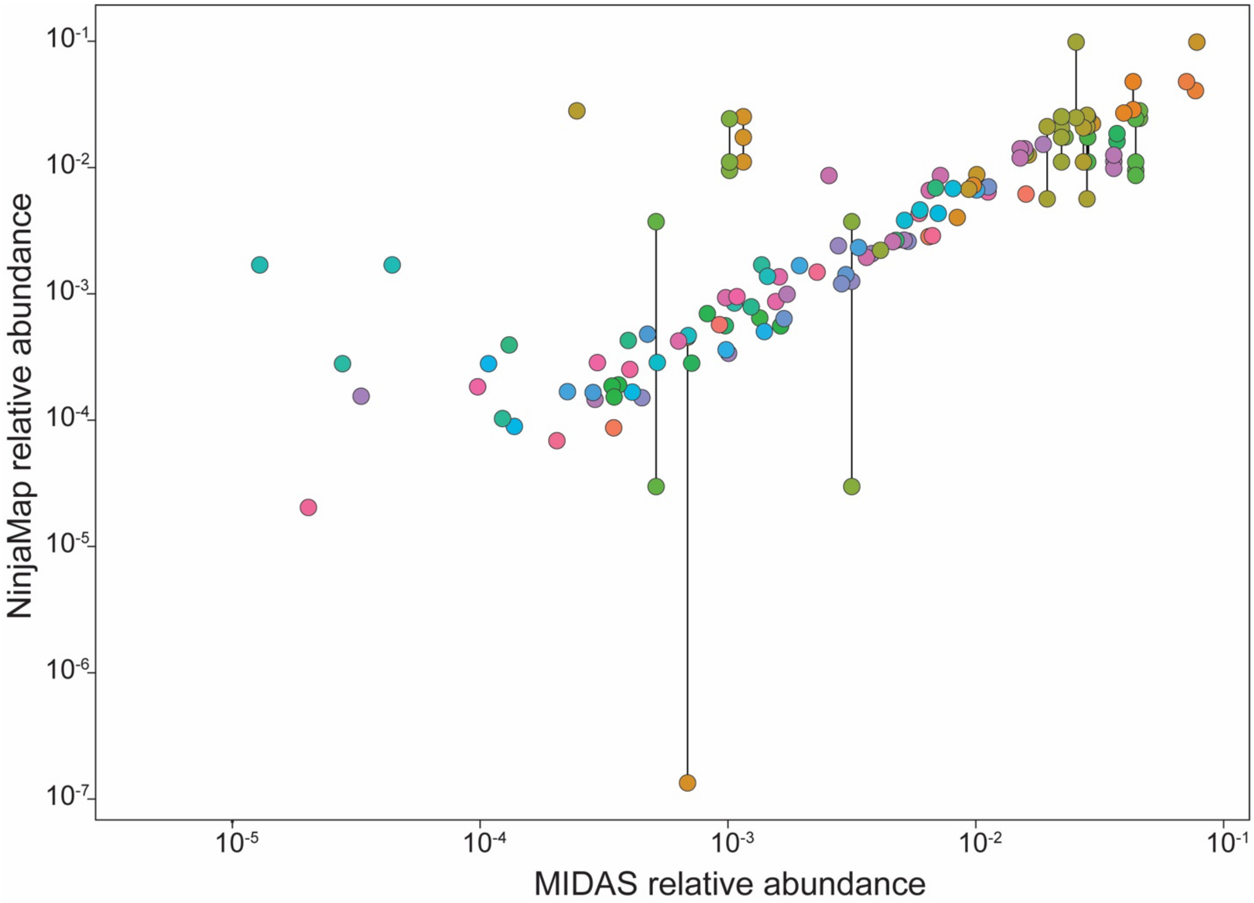
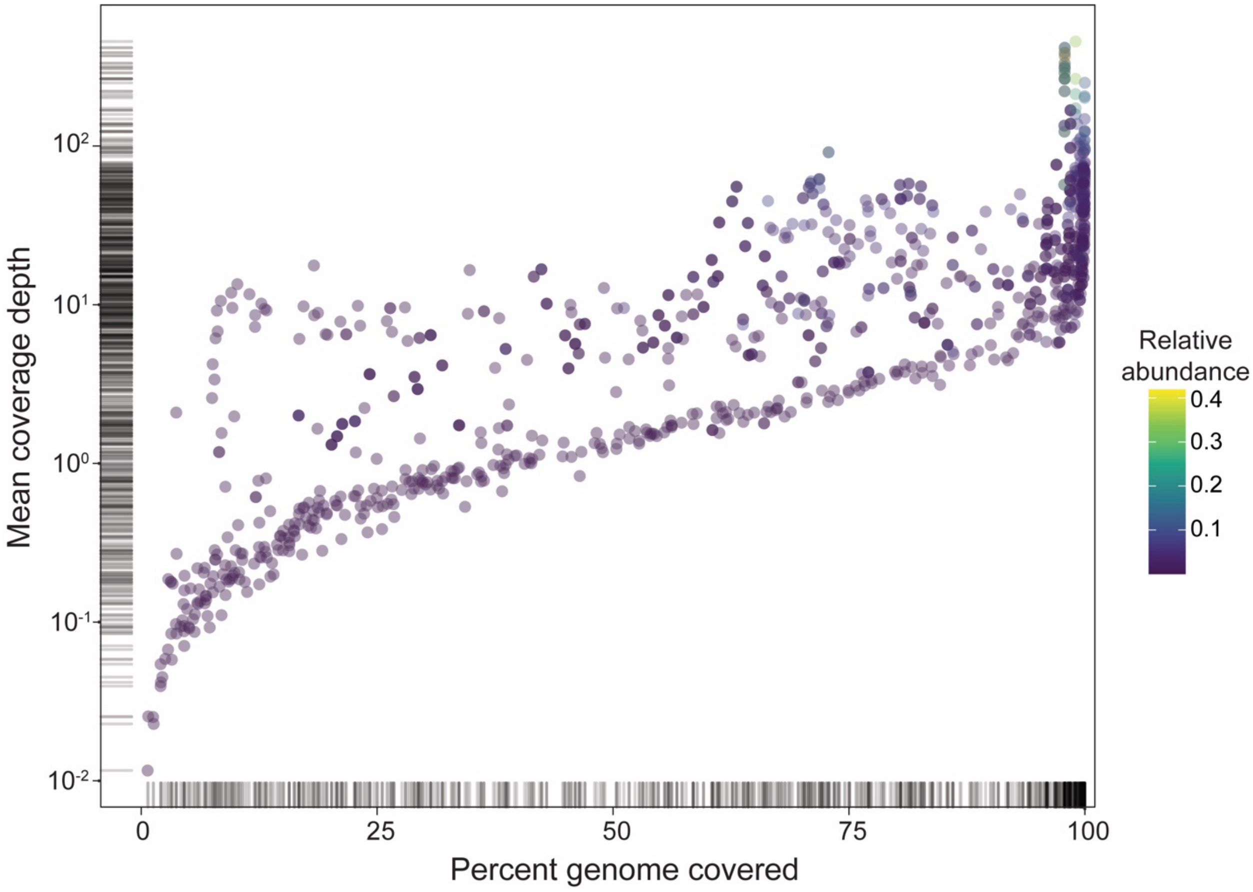
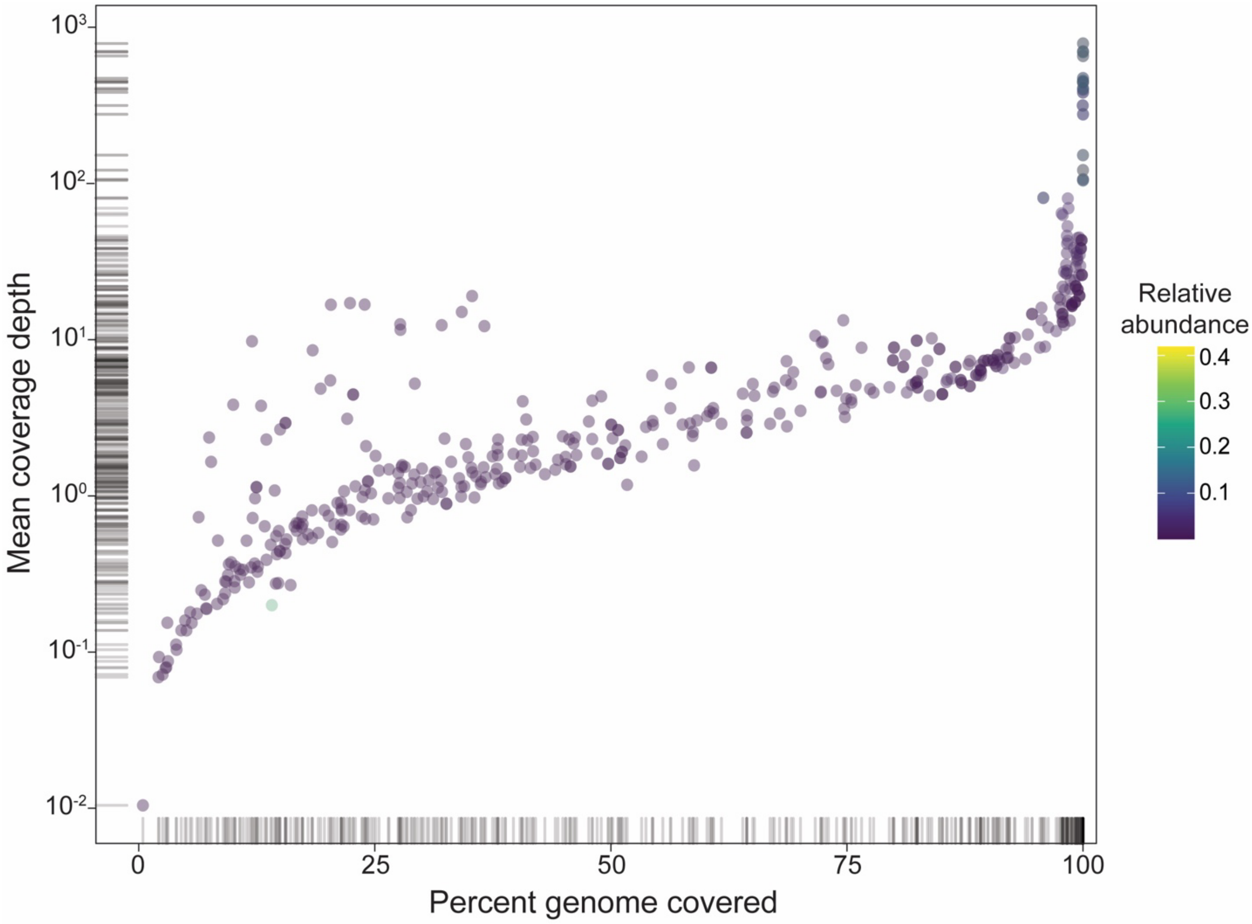


Comparison of MIDAS and NinjaMap sequencing read utilization. Mapping results are shown from the hCom2 inoculum used for the second fecal challenge experiment (**Figure 5**). Each circle represents a strain and the corresponding species bucket identified by MIDAS. Points connected by lines represent two strains that NinjaMap can distinguish but that map to the same MIDAS bin, and are therefore colored similarly. Spearman's correlation coefficient is 0.83 and the Pearson correlation coefficient is 0.717.



NinjaMap strain coverage from the first fecal challenge experiment (Figure 4). Reads from week 8 of the PBS challenge for hCom1 were aligned to the reference genomes in our database. Reads were retained only if they matched a database strain at 100% identity over 100% read length. Over 60% of strains had >95% breadth of coverage at 10x depth from perfectly matched reads.



NinjaMap strain coverage from the second fecal challenge experiment (Figure 5). Reads from week 8 of the PBS challenge for hCom2 were aligned to the reference genomes in our databases. Reads were retained only if they matched a database strain at 100% identity over 100% read length. 54% of original strains in hCom2 and 76% of the new strains in hCom2 exhibited >95% coverage of the reference genome by perfectly matched reads.