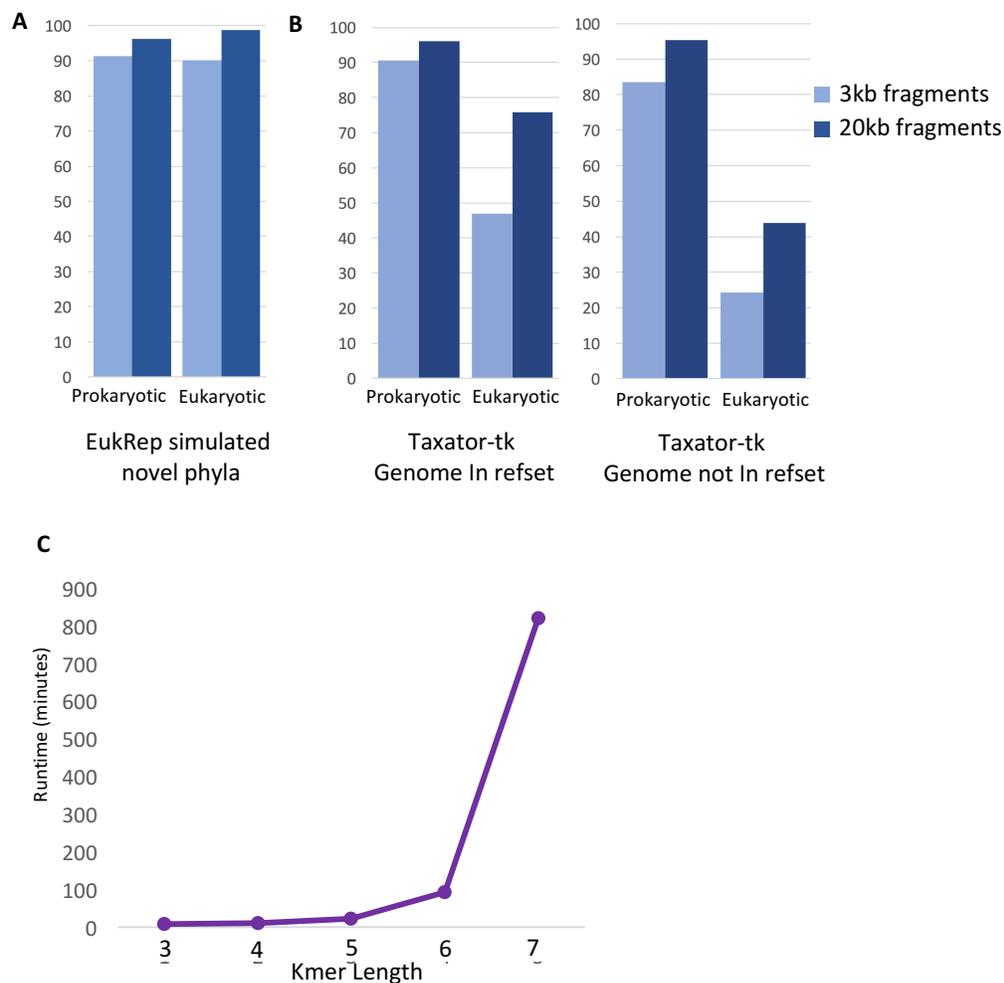Supplemental Figure S3 Effect of *k*-mer length and sequence length on prediction accuracy. (A) Proportion of total sequence tested accurately recovered as either prokaryotic or eukaryotic for both eukaryotes (n=18) and prokaryotes (n=46) from phyla not represented in EukRep's training set. (B) Proportion of total sequence tested accurately recovered as either prokaryotic or eukaryotic for both eukaryotes (n=18) and prokaryotes (n=46) with taxator-tk both with the genomes present in its reference set used for mapping or with the genomes removed from its reference set. (C) EukRep runtime on the CG_WC metagenome (874 Mbp in assembled length) on a single core utilizing *k*-mer lengths of 3-7bp.