	L = 10 K			L = 100 K			L = 1 M		
p =	0.001	0.1	0.2	0.001	0.1	0.2	0.001	0.1	0.2
k = 21	95.4	95.3	94.7	95.0	95.2	95.06	95.0	95.0	94.6
k = 51	95.4	94.8	N/A	94.8	94.6	N/A	94.9	95.1	94.4
k = 100	94.7	N/A	N/A	94.6	N/A	N/A	95.4	93.7	N/A

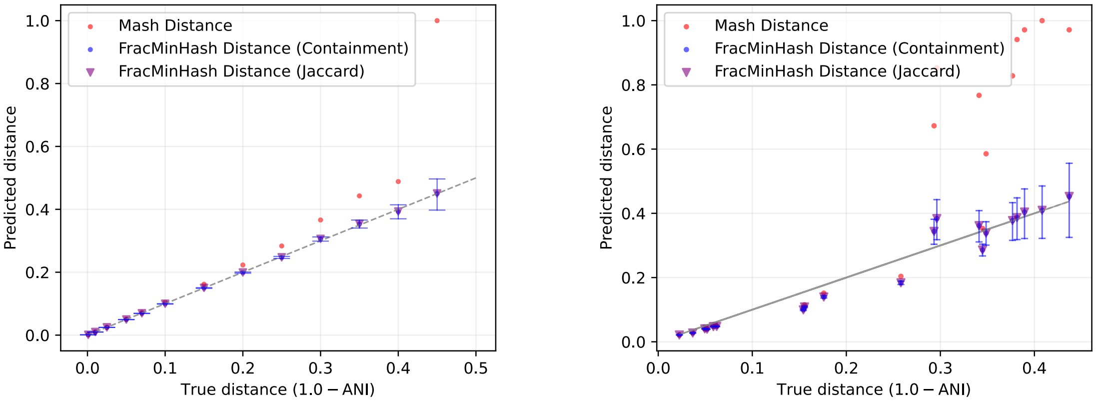
Table S1: The percentage of experiments that resulted in the true mutation rate falling within the 95% confidence interval given in Theorem 8 when using various mutation rates across multiple k-mer sizes and L values. A scale factor of 0.2 was used. The results show an average over 10,000 simulations for each setting. N/A entries indicate that the parameters are not particularly meaningful and will not produce interpretable results, either because $E[N_{\text{mut}}] \approx L$ in these cases (almost all k-mers are mutated), or because the scale factor is too small to differentiate between the two FracMinHash sketches.

	L = 10 K			L = 100 K			L = 1 M		
p =	0.001	0.1	0.2	0.001	0.1	0.2	0.001	0.1	0.2
k = 21	96.3	95.0	96.0	95.1	95.0	95.3	95.0	95.2	94.9
k = 51	94.9	94.5	N/A	94.7	95.3	N/A	94.7	95.0	N/A
k = 100	95.2	N/A	N/A	95.2	N/A	N/A	94.5	N/A	N/A

Table S2: The percentage of experiments that resulted in the true mutation rate falling within the 95% confidence interval given in Theorem 8 when using various mutation rates across multiple k-mer sizes and L values. A scale factor of 0.05 was used. The results show an average over 10,000 simulations for each setting. N/A entries indicate that the parameters are not particularly meaningful and will not produce interpretable results, either because $E[N_{\text{mut}}] \approx L$ in these cases (almost all k-mers are mutated), or because the scale factor is too small to differentiate between the two FracMinHash sketches.

	$L = 10$ K			$L = 100$ K			$L = 1$ M		
$p =$	0.001	0.1	0.2	0.001	0.1	0.2	0.001	0.1	0.2
$k = 21$	9792.1	1094.2	92.2	97920.9	10941.9	922.3	979208.7	109419.0	9223.3
$k = 51$	9502.5	46.4	0.11	95025.4	463.8	1.1	950254.4	4638.4	11.4
$k = 100$	9047.9	0.26	2.04E-6	90479.2	2.7	2.04E-5	904792.1	26.6	2.04E-4

Table S3: The expected number of non-mutated k-mers after undergoing the simple mutation process, shown across multiple k-mer sizes, L values, and mutation rates.



(a) Estimates of evolutionary distances between original and mutated *Staphylococcus* genome

(b) Estimates of evolutionary distances between pairs of real bacterial genomes

Fig. S1: Mash distances and FracMinHash estimates of evolutionary distance (given in terms of one minus the average nucleotide identity: ANI) when (a) introducing point mutations to a *Staphylococcus* genome at a known rate, and (b) between pairs of real bacterial genomes.