Nucleotide substitution variant count distributions (input samples) input2 input1 input3 0.4 0.2 0.0 7.5 5.0 2.5 0.0 12 9 . Hamming_distance 6 3 -Density 25 20 15 10 5 -20 15 10 5. 15 10 5 1e+01 1e+01 1e+03 1e+05 1e+01 1e+03 1e+03 1e+05 1e+05 variant count + 1 (log scale)