Nucleotide substitution variant count distributions (input samples) input2 input1 input3 0.4 0.2 0.0 10.0 7.5 5.0 2.5 0.0 9 -Hamming_distance 6 -Density 15 10 5 15 10 5 10 5 -1e+05 1e+01 1e+03 1e+05 1e+01 1e+03 1e+01 1e+03 1e+05 variant count + 1 (log scale)