Simulated HIV mix (600x)

	# contigs ≥ 500bp	largest contig	N50	MAC length (%)	target genomes (%)	N-rate (%)	mismatches (%)	indels (%)
MLEHaplo	17	1673	1288	0	10.7	0	2.09	0.116
PredictHaplo-h-ref	4	9710	9710	0	79.5	0.659	1.374	0.091
PredictHaplo-b-ref	3	9800	9800	100	59.1	0.289	1.628	0.175
ShoRAH-h-ref	39	9526	9526	0	98.0	0.318	0.394	0.087
ShoRAH-b-ref	63	9657	9657	1.6	97.2	0.307	1.356	0.151
SAVAGE-de-novo	26	7667	3381	0	97.9	0	0.004	0
SAVAGE-h-ref	34	8261	2628	0	96.6	0	0.028	0.002
SAVAGE-b-ref	33	6308	2400	0	98.4	0	0	0
SGA	3	583	520	0	3.3	0	0	0
SOAPdenovo2	31	4813	1639	0	78.9	0	0.005	0.003
SPAdes	15	9455	5476	0	87.8	0	0.047	0.005
metaSPAdes	3	4706	4706	0	18.8	0	1.321	0.022

Supplemental Table S1: Assembly results per method for the 600x simulated 5-strain HIV mix. For reference guided methods we present results using an established, high quality reference genome (h-ref) as well as an ad-hoc, bootstrap reference genome (b-ref). All assemblies were evaluated on the following criteria: number of contigs ≥ 500 bp, length of the largest contig, N50 statistic, MissAssembled Contigs (MAC) length relative to total contig length, percentage of the target genomes recovered, percentage of undetermined bases (N), and percentage of mismatches and indels compared to the ground truth.