Simulated ZIKV mix (20 000x, 3 strains)

	# contigs $\geq$ 500bp	largest contig	N50	MAC length (%)	target genomes (%)	N-rate (%)	mismatches (%)	indels (%)
MLEHaplo	-	-	-	-	-	-	-	-
PredictHaplo-h-ref	3	10258	10258	0	100.0	0.029	0	0.042
PredictHaplo-b-ref	3	10270	10270	0	100.0	0	0	0.003
ShoRAH-h-ref	-	-	-	-	-	-	-	-
ShoRAH-b-ref	156	10251	10251	0	99.8	0.039	2.938	0.003
SAVAGE-de-novo	6	10257	10203	0	99.9	0.006	0	0
SAVAGE-h-ref	6	10264	10231	0	99.9	0.006	0	0
SAVAGE-b-ref	4	10267	10263	0	99.9	0.003	0	0
SGA	19	1437	631	0	29.0	0	1.377	0
SOAPdenovo2	38	651	513	0	39.5	0	0.616	0
SPAdes	11	10269	3261	0	99.6	0	0	0
metaSPAdes	12	8620	4969	0	33.4	0	0.691	0

Supplemental Table S2: Assembly results per method for the 20.000x simulated 3-ZIKV-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 $\geq$ 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.