	Simulated mix 600x		*Simulated mix 20 000x*		*Lab mix 20 000x*	
	CPU time (minutes)	Peak memory usage (GB)	CPU time (minutes)	Peak memory usage (GB)	CPU time (minutes)	Peak memory usage (GB)
MLEHaplo	54	2.2	-	-	-	-
SAVAGE-denovo	19	0.6	5296	0.9	7495	1.1
SAVAGE-ref-bg	6.4	1.3	449	1.7	850	3.0
ShoRAH	12	1.2	32375	10	22256	12
PredictHaplo	7	0.04	223	1.1	158	0.9
SGA	24	0.09	164	0.5	300	0.7
SOAPdenovo2	0.15	0.7	5	9.5	6	8.3
SPAdes	2.0	8.4	46	8.7	166	8.8
metaSPAdes	1.3	8.4	37	8.6	130	8.7

Supplemental Table S4: Runtime and memory usage comparison for specialized viral quasispecies tools MLEHaplo, SAVAGE-denovo, SAVAGE-ref-bg, ShoRAH, and PredictHaplo, and for generic assemblers SGA, SOAPdenovo2, SPAdes, and metaSPAdes. The first four columns show results on simulated HIV data (*simulated mix*, 600x and 20 000x respectively), while the last two columns show results on real HIV data (*lab mix*). SAVAGE-denovo uses more CPU time than SAVAGE-ref-bg, because it has to find all approximate suffix-prefix overlaps without using a reference genome.