

Species (sequence length in MB)	Large STR (cutoff >=350nt)			Medium STR (150nt<=cutoff<350nt)			Short STR (12nt<=cutoff<150nt)			Memory requirement	
	No. of STR	Avg. STR length(nt)	CPU time (sec)	No. of STR	Avg. STR length(nt)	CPU time (sec)	No. of STR	Avg. STR length(nt)	CPU time (sec)	Total memory required in MB	Processing memory in MB
Reference genomes											
C elegans (100.27 MB)	2	496	5	33	187	5	94697	12	5	104.256	3.986
Drosophila (137.05 MB)	12	619	8	26	240	8	223123	13	8	140.675	3.625
Canis familiaris (2317.59 MB)	2	418	158	55	196	158	3877732	15	157	2321.486	3.896
Bos taurus (2640.16 MB)	2	411	179	14	197	180	2850953	13	178	2644.146	3.986
Mus musculus (2647.52 MB)	57	592	178	1058	186	177	4062928	17	178	2651.416	3.896
Macaca mulata (2763.46 MB)	2	545	187	29	205	187	3267234	14	187	2767.322	3.862
Pan troglodytes (2803.62 MB)	1	443	180	33	205	179	3190500	14	181	2807.587	3.967
Homo sapiens (2937.63 MB)	8	558	196	41	206	199	3211310	14	196	2941.564	3.934
Assembled human genomes											
NA12878 (2798.04 MB)	2	368	191	39	195	190	3213613	14	193	2801.974	3.934
HG00514 (2805.67 MB)	8	489	187	75	210	190	3192268	14	195	2809.615	3.945
NA19240 (2815.57 MB)	6	578	188	47	201	191	3221358	14	195	2819.238	3.668
CHM1.1 (2827.65 MB)	1	465	188	30	197	191	3191074	14	196	2831.584	3.934
HG00733 (2864.15 MB)	1	552	192	72	221	190	3240565	14	191	2868.117	3.967

Supplementary Table 7: Performance evaluation on whole genome sequences