

Statistics of apple genome assemblies

	Gala	<i>M. sieversii</i>	<i>M. sylvestris</i>
Estimated heterozygosity rate	0.01282	0.0085	0.01053
Haploid consensus size (Mb)	652.4	667.7	661.1
Contig (#)	7,560	6,703	5,144
Contig N50 (bp)	2,317,231	3,483,045	18,878,997
Max contig length (bp)	29,855,514	14,355,387	49,357,370
Scaffold (#)	877	506	3,100
Scaffold N50 (bp)	23,924,958	16,839,475	35,683,067
Max scaffold length	38,215,415	34,030,144	55,646,331
Gaps (#)	6,682	6,193	2,043
Scaffolds anchored (%)	96.7	97.8	96.7
BUSCO completeness (%)	97.9	97.9	97.9
Repeat content (%)	58.72	59.36	59.31
Protein coding genes (#)	45,352	45,210	45,199
Diploid genome size (bp)	1,311,623,508	1,323,434,086	1,309,264,564
Contig (#)	118,849	50,832	53,436
Contig N50 (bp)	144,199	1,233,539	1,942,904
Max contig length	6,630,327	6,619,014	18,807,287
Scaffolds (#)	94,713	44,462	46,260
Scaffold N50 (bp)	3,307,266	3,833,162	4,295,302
Max scaffold length	20,876,489	16,940,064	31,614,455
Gaps (#)	24,151	6,367	7,251
Haplome A size (bp)	657,696,253	661,956,187	627,665,831
Haplome B size (bp)	577,209,808	608,988,016	601,478,285
BUSCO completeness (%)	97.7	97.7	97.7
Protein coding genes (#)	90,507	90,147	90,193