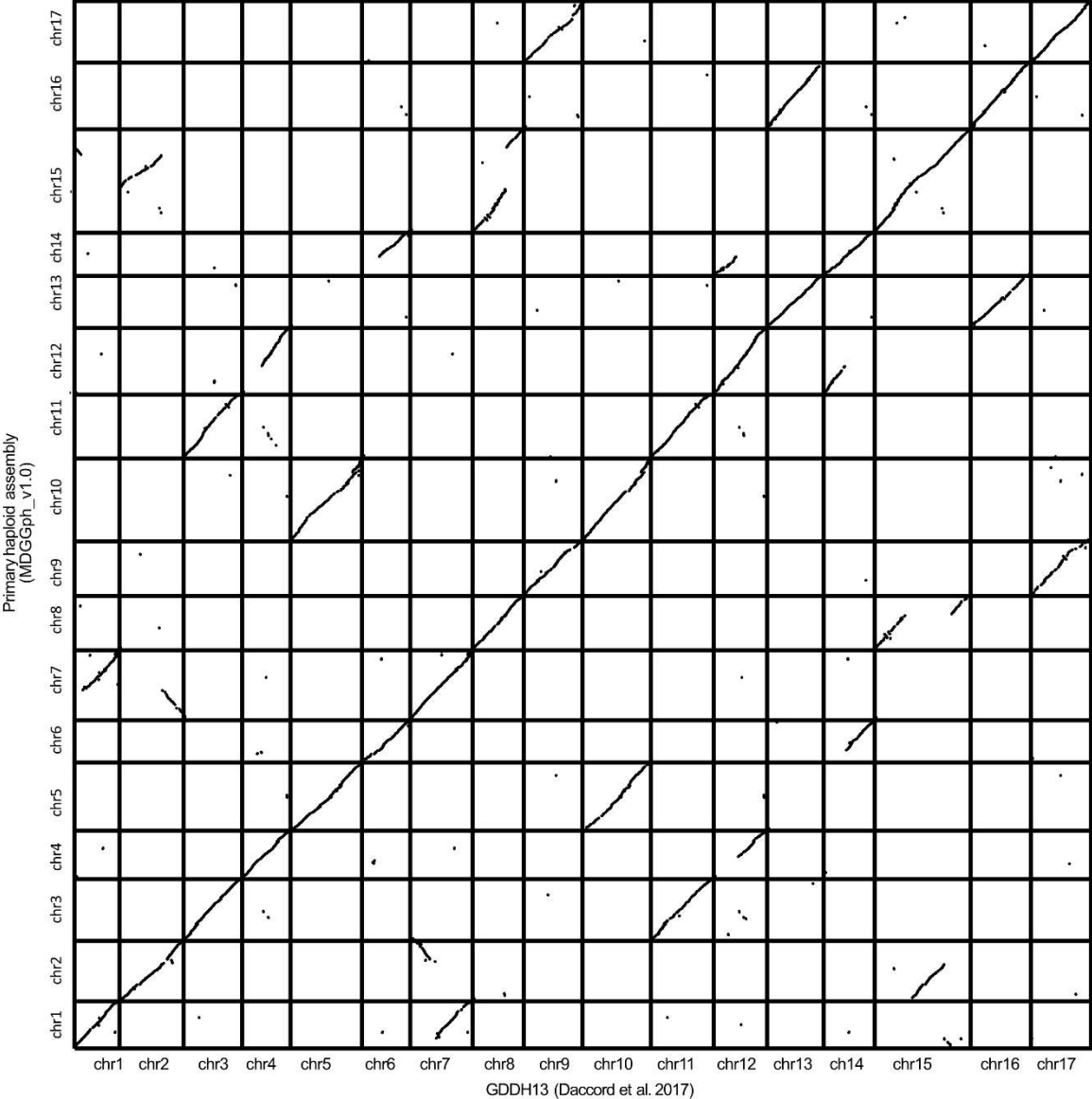


Supplementary figure 1: Syntenic dotplot generated comparing the 17 apple chromosomes (chr1-chr17) of the GDDH13 assembly (x-axis, Daccord et al 2017) versus the primary haploid assembly MDGGph\_v1.0 (y-axis). Each dot indicates a syntenic gene pair between the two assemblies.



Supplementary table 1: Chromosome lengths of the haploid assemblies MDGGph\_v1.0 and MDGGsh\_v1.0 compared to HFTH1 (Zhang et al. 2019) and GDDH13 (Daccord et al 2017).

MDGGph_v1.0 (primary haploid assembly)			MDGGsh_v1.0 (secondary haploid assembly)			HFTH1 (Zhang et al. 2019)			GDDH13 (Daccord et al 2017)		
	Length (bp)	Scaffolds		Length (bp)	Scaffolds		Length (bp)	Scaffolds		Length (bp)	Scaffolds
chr1	34,957,745	2	chr_s1	20,900,120	189	chr1	32,944,118	13	chr1	32,625,452	86
chr2	43,219,086	2	chr_s2	42,574,754	180	chr2	38,449,405	9	chr2	37,577,729	88
chr3	41,865,124	2	chr_s3	35,827,395	240	chr3	37,138,690	5	chr3	37,524,076	81
chr4	36,846,674	2	chr_s4	26,433,372	183	chr4	31,012,745	8	chr4	32,301,874	65
chr5	46,262,512	3	chr_s5	58,045,489	239	chr5	47,891,858	14	chr5	47,952,461	108
chr6	37,227,775	3	chr_s6	46,706,699	155	chr6	35,567,198	6	chr6	37,137,259	89
chr7	42,138,739	3	chr_s7	23,675,059	246	chr7	35,934,761	6	chr7	36,691,129	76
chr8	37,261,338	1	chr_s8	25,480,337	200	chr8	31,511,015	8	chr8	31,609,270	67
chr9	42,757,514	1	chr_s9	30,211,764	217	chr9	34,800,404	10	chr9	37,604,908	80
chr10	49,447,705	2	chr_s10	46,315,672	241	chr10	43,815,736	14	chr10	41,762,413	83
chr11	46,034,967	3	chr_s11	48,391,545	218	chr11	42,456,296	15	chr11	43,059,885	91
chr12	37,592,879	1	chr_s12	19,120,998	191	chr12	32,285,079	9	chr12	33,050,054	75
chr13	40,714,413	1	chr_s13	37,617,649	237	chr13	44,866,511	13	chr13	44,339,518	119
chr14	36,122,606	1	chr_s14	39,177,835	148	chr14	31,515,206	6	chr14	32,513,452	62
chr15	60,319,455	2	chr_s15	48,141,362	339	chr15	56,644,392	16	chr15	54,945,402	129
chr16	47,681,219	1	chr_s16	28,833,803	228	chr16	41,670,059	15	chr16	41,389,449	93
chr17	39,000,747	1	chr_s17	23,971,657	211	chr17	33,998,825	8	chr17	34,748,701	76
			Unanchored	80,621,795	2583	Unanchored	7,992,922		Unanchored	52,728,359	

Supplementary table 2: Results of the Benchmarking Universal Single-Copy Orthologs (BUSCO) analysis on the assemblies MDGGph\_v1.0, MDGGdi\_v1.0 and on GDDH13 (Daccord *et al.* 2017).

	<b>MDGGph_v1.0</b>		<b>MDGGdi_v1.0</b>		<b>GDDH13</b>	
	<b>(primary haploid assembly)</b>		<b>(diploid assembly)</b>		<b>(Daccord et al. 2017)</b>	
<b>Complete BUSCOs (C)</b>	1,347	93.5%	1,387	96.3%	1,383	96.0%
<b>Complete and single-copy BUSCOs (S)</b>	943	65.5%	467	32.4%	894	62.1%
<b>Complete and duplicated BUSCOs (D)</b>	404	28.1%	920	63.9%	489	34.0%
<b>Fragmented BUSCOs (F)</b>	20	1.4%	11	0.8%	13	0.9%
<b>Missing BUSCOs (M)</b>	73	5.1%	42	2.9%	44	3.1%
<b>Total BUSCO groups searched</b>	1,440		1,440		1,440	