

Sequential paleotetraploidization shaped carrot genome

Additional tables

Table S1. Number of homologous blocks and gene pairs within a genome or between genomes.

Homologous Blocks within and among genome	BL ^a > 4	BL > 10	BL > 20	BL > 50	ACGP ^b	LDB ^c	LDB on chromosomes
<i>Vitis vinifera</i>	1,831/169	1,230/55	783/24	111/2	10.83, 22.36, 32.63, 55.50	61	VV05-VV07
<i>Coffea canephora</i>	2,436/270	1,301/45	1,048/26	408/6	9.02, 28.91, 40.31, 68.00	95	CC01-CC06
<i>Daucus carota</i>	7,142/745	3,913/166	2,545/62	1,192/15	9.59, 23.57, 41.05, 79.47	122	DC01-DC02
<i>V. vinifera</i> vs <i>C. canephora</i>	15,712/1,283	10,288/232	9,108/145	6,325/56	12.25, 44.34, 62.81, 112.95	326	VV05-CC03
<i>V. vinifera</i> vs <i>D. carota</i>	17,427/1,684	10,503/442	7,032/181	2,548/34	10.35, 23.76, 38.85, 74.94	142	VV05-DC08
<i>C. canephora</i> vs <i>D. carota</i>	20,939/2,001	12,346/423	9,378/200	5,352/64	10.46, 29.19, 46.89, 83.63	194	CC03-DC08

^aBL: block_length; ^bACGP: average colinear gene pairs respectively per block; ^cLDB: number of colinear gene pairs reside in longest duplicated block

Table S2. Number of homologous genes within a genome or between genomes.

Homologous Blocks within and among genome	BL ^a > 4	BL> 10	BL> 20	BL> 50	LDB ^b	LDB on chromosomes
<i>Vitis vinifera</i>	3,049	2,184	1,469	222	61	VV05-VV07
<i>Coffea canephora</i>	3,701	2231	1812	800	95	CC01-CC06
<i>Daucus carota</i>	8904	5957	4232	1967	122	DC02-DC02
<i>V. vinifera</i> vs <i>C. canephora</i>	9887 vs 9994	8364 vs 8309	7634 vs 7632	5836 vs 5814	326	VV05-CC03
<i>V. vinifera</i> vs <i>D. carota</i>	9270 vs 12133	7048 vs 9031	5294 vs 6681	2120 vs 2548	142	VV05- DC08
<i>C. canephora</i> vs <i>D. carota</i>	10551 vs 13819	7998 vs 10622	6645 vs 8675	4359 vs 5345	194	CC03-DC08

^aBL: block_length; ^bLDB: number of colinear gene pairs reside in longest duplicated block

Table S3. Orthologous genomic regions between grape and carrot.

Grape chromosomes	Corresponding orthologous regions between grape and carrot			
Vv1	A1:Vv01:0-1,327:Dc01:1,726-2,3			A4:Vv01:0-211:Dc01:3257-4301
	18	A2:Vv01:0-1327:Dc01:3091-3528	A3:Vv01:0-1327:Dc07:0-1466	A4:Vv01:0-400:Dc09:993-1323
	A1:Vv01:0-1,327:Dc02:2,122-2,7	A2:Vv01:0-1327:Dc08:0-1207	A3:Vv01:0-211:Dc01:644-979	A4:Vv01:380-1327:Dc09:993-1552
	61			A4:Vv01:674-1327:Dc09:1934-2316
Vv2	A1:Vv02:0-741:Dc02:1,432-2,09			
	6	A2:Vv02:0-1237:Dc02:3272-3758	A3:Vv02:0-244:Dc07:1801-2161	A4:Vv02:0-1237:Dc01:3657-4301
	A1:Vv02:0-443:Dc02:1,994-2,20	A2:Vv02:0-433:Dc02:3630-3860	A3:Vv02:247-1237:Dc01:0-567	A4:Vv02:0-1000:Dc02:0-409
	0			A4:Vv02:392-887:Dc02:716-971
Vv3	A1:Vv02:0-1,237:Dc08:1,207-2,1			
	57			
	A1:Vv03:371-1,000:Dc01:901-1,			
	442	A2:Vv03:0-1000:Dc01:2601-3168	A3:Vv03:0-1000:Dc09:0-1000	A4:Vv03:0-542:Dc06:3015-3270
Vv4	A1:Vv01:0-438:Dc06:2,810-3,06			A4:Vv03:417-1000:Dc06:1865-2402
	6			
	A1:Vv04:0-995:Dc01:0-1,159			
	A1:Vv04:1,348-1638:Dc01:0-1,1	A2:Vv04:0-954:Dc01:3760-4198	A3:Vv04:0-871:Dc01:2292-2730	A4:Vv04:0-1600:Dc02:2812-3579
Vv5	59	A2:Vv04:394-995:Dc02:562-1559	A3:Vv04:0-500:Dc01:3065-3322	A4:Vv04:800-1683:Dc06:1431-1967
	A1:Vv04:518-1,140:Dc07:0-900	A2:Vv04:829-1638:Dc05:0-1405	A3:Vv04:800-1638:Dc03:0-256	A4:Vv04:1000-1683:Dc04:1438-1824
	A1:Vv04:1,016-1,638:Dc07:2,26		A3:Vv04:601-1638:Dc03:2148-3119	
	4-3216			
Vv6	A1:Vv05:0-1,131:Dc01:1,623-2,1			
	38	A2:Vv05:0-1748:Dc07:0-1544	A3:Vv05:0-1748:Dc08:0-1335	A4:Vv05:0-1700:Dc09:1349-2316
	A1:Vv05:1,131-1,748:Dc02:0-92			A4:Vv05:800-1748:Dc09:0-1171
	0			A4:Vv05:900-1748:Dc08:1644-2491
Vv6	A1:Vv06:0-1,779:Dc01:1,288-1,7	A2:Vv06:0-290:Dc07:0-1600	A3:Vv06:0-1779:Dc04:2671-3110	A4:Vv06:0-848:Dc05:2631-2964
	51	A2:Vv06:0-1000:Dc02:0-818		A4:Vv06:786-1779:Dc05:1942-3730

Vv7	A1:Vv06:265-1,779:Dc02:997-1,406	A2:Vv06:0-1779:Dc02:2428-2761		
	A1:Vv06:1,262-1,799:Dc09:0-1,800	A2:Vv06:786-1779:Dc03:3426-4040		
	A1:Vv07:0-1,309:Dc03:3,529-4,040	A2:Vv06:800-1779:Dc07:1600		
	A1:Vv07:1,140-1,409:Dc03:0-2,000	A2:Vv07:0-1409:Dc05:2044-2606	A3:Vv07:0-1036:Dc01:2060-2575	A4:Vv07:0-912:Dc02:741-1329
	A1:Vv07:700-1,409:Dc03:1,943-2,327	A2:Vv07:850-1409:Dc07:1600-3216	A3:Vv07:539-1077:Dc01:0-747	A4:Vv07:684-1400:Dc01:3915-4301
	A1:Vv07:1,181-1,409:Dc03:2,608-3,068	A2:Vv07:1098-1409:Dc01:489-1004	A3:Vv07:974-1409:Dc06:0-1865	A4:Vv07:808-1409:Dc04:0-800
				A4:Vv07:800-1409:Dc04:1233-2000
Vv8	A1:Vv08:0-1,867:Dc03:143-918	A2:Vv08:0-1867:Dc06:0-1780	A3:Vv08:0-1867:Dc04:488-1053	A4:Vv08:0-643:Dc05:2325-2759
	A1:Vv08:0-1,867:Dc07:0-952	A2:Vv08:0-1867:Dc08:2209-2491	A3:Vv08:0-1867:Dc04:2055-2414	A4:Vv08:975-1245:Dc05:2453-2785
			A3:Vv08:0-1867:Dc04:2517-2877	A4:Vv08:0-1867:Dc05:0-1788
			A3:Vv08:851-1390:Dc03:2632-4040	
Vv9	A1:Vv09:0-1,221:Dc02:2,556-3,042	A1:Vv09:200-1221:Dc05:1533-1993	A3:Vv09:0-1221:Dc05:0-684	A4:Vv09:0-1221:Dc06:1405-3449
		A2:Vv09:0-1221:Dc07:2018-3216		
Vv10	A1:Vv10:0-632:Dc01:3,194-4,301	A2:Vv10:0-632:Dc08:1258-2400	A3:Vv10:0-1221:Dc02:0-1023	A4:Vv10:0-1221:Dc02:2812-3860
	A1:Vv11:0-554:Dc03:2,448-2,836		A3:Vv10:0-200:Dc04:0-500	
Vv11	A1:Vv11:383-1,107:Dc04:1,747-2,440	A2:Vv11:0-660:Dc08:1721-2491	A3:Vv11:0-1107:Dc03:306-1714	A4:Vv11:0-1000:Dc07:1132-1672
	A1:Vv12:0-967:Dc04:0-568	A2:Vv11:383-1107:Dc05:1584-2146		A4:Vv11:490-1107:Dc06:0-1686
Vv12	A1:Vv12:658-1,481:Dc04:568-1,721	A2:Vv12:0-1481:Dc06:1175-2223	A3:Vv12:0-638:Dc03:300-1278	A4:Vv12:0-987:Dc05:485-3347
	A1:Vv12:1,172-1,481:Dc02:1,713-2,200	A2:Vv12:1131-1481:Dc07:1904-2238	A3:Vv12:432-1481:Dc05:3449-3730	A4:Vv12:500-1481:Dc09:0-1000
			A3:Vv12:900-1481:Dc01:1159-1800	
Vv13	A1:Vv13:0-665:Dc03:2,914-3,34	A2:Vv13:0-644:Dc07:1389-1724	A3:Vv13:0-636:Dc03:1602-1977	A4:Vv13:0-727:Dc08:1002-2311

	1 A1:Vv13:166-768:Dc04:2,337-2,671 A1:Vv13:810-1,329:Dc01:2,498-2,962 A1:Vv14:0-1,729:Dc01:2,395-3,000	A2:Vv13:166-997:Dc05:2836-3193 A2:Vv13:976-1329:Dc09:100-2316	A3:Vv13:540-1329:Dc02:1380-1789	A4:Vv13:976-1329:Dc06:2376-3000
Vv14	A1:Vv14:0-1,729:Dc02:0-869 A1:Vv14:1,042-1,729:Dc02:1,559-2,122 A1:Vv14:750-1,062:Dc02:2,531-2,889	A2:Vv14:0-1500:Dc06:1788-2555 A2:Vv14:0-1729:Dc07:1878-2316 A2:Vv14:0-1062:Dc07:2316-3216	A3:Vv14:0-687:Dc01:0-1803 A3:Vv14:0-1729:258-700 A3:Vv14:750-1729:Dc03:2097-2710	A4:Vv14:479-1729:Dc04:1310-2414 A4:Vv14:667-937:Dc05:894-1431 A4:Vv14:0-1000:Dc09:0-916
Vv15	A1:Vv15:0-561:Dc04:2,954-3,339	A2:Vv15:0-561:Dc07:1647-3216	A3:Vv15:0-500:Dc02:0-946 A3:Vv15:0-561:Dc02:1994-2275	A4:Vv15:0-561:Dc02:3579-3860 A4:Vv15:0-500:Dc09:0-930
Vv16	A1:Vv16:0-647:Dc03:0-895	A2:Vv16:0-647:Dc06:0-1500	A3:Vv16:0-647:Dc03:1688-2199 A3:Vv16:0-647:Dc05:1814-2400	A4:Vv16:0-647:DC04:1464-2312
Vv17	A1:Vv17:0-542:Dc04:1,824-3,339 A1:Vv17:0-1,168:Dc05:0-792 A1:Vv18:352-1,161:Dc03:0-256 A1:Vv18:0-725:Dc03:716-1,304	A2:Vv17:0-1168:Dc07:2521-3216	A3:Vv17:0-1168:Dc06:1507-1891 A3:Vv17:0-1168:Dc06:3142-3449	A4:Vv17:0-292:Dc02:2531-2837 A4:Vv17:521-1168:Dc02:2122-2786 A4:Vv17:0-584:Dc03:2531-2838
Vv18	A1:Vv18:1,036-1,886:Dc03:665-1,764 A1:Vv18:20-725:Dc01:2,859-3,271 A1:Vv19:248-1,135:Dc03:1,202-1,534	A2:Vv18:0-435:Dc04:1053-1824 A2:Vv18:100-1886:Dc04:0-514 A2:Vv18:953-1886:Dc04:0-1515	A3:Vv18:0-415:Dc05:0-3730 A3:Vv18:953-1886:Dc05:1226-1712 A3:Vv18:415-1244:Dc05:3117-3526	A4:Vv18:0-622:Dc06:3015-3449 A4:Vv18:0-2000:Dc06:0-434 A4:Vv18:0-1886:Dc06:996-1303 A4:Vv18:100-1886:Dc06:2376-2759 A4:Vv18:1205-1886:Dc06:2970-3449
Vv19	A1:Vv19:0-1,135:Dc04:283-1,233	A2:Vv19:0-1135:Dc05:0-1661	A3:Vv19:0-1135:Dc05:3321-3730	A4:Vv19:0-1135:Dc06:869-1329 A4:Vv19:206-1135:Dc06:2453-3449

Each grape genomic region corresponds to four or fewer independent carrot regions, denoted from A1-A4. The chromosome identification

numbers and ranges (measured in genes) that contain orthologous genes from both species have been shown.

Table S4. Orthologous genomic regions between coffee and carrot.

Coffee chromosomes		Corresponding orthologous regions between coffee and carrot		
Cc1	A1:Cc01:0-1100:Dc01:0-2150	A2:Cc01:0-1000:Dc09:886-2316 A2:Cc01:855-2198:Dc05:2019-3303	A3:Cc01:1000-2200:Dc01:0-542 A3:Cc01:1661-2198:Dc01:2032-2574 A3:Cc01:0-1470:Dc02:0-655 A3:Cc01:800-2000:Dc02:1900-3860 A3:Cc01:0-2198:Dc03:1000-3000 A3:Cc01:800-2000:Dc06:1700-3449 A3:Cc01:0-1100:Dc07:0-821	A4:Cc01:0-1100:Dc07:822-1700 A4:Cc01:0-1472:Dc02:650-1482 A4:Cc01:1500-2198:Dc02:620-1482 A4:Cc01:1100-2198:Dc01:3960-4301
	A1:Cc01:0-1100:Dc03:2150-4301			
	A1:Cc01:1514-2198:Dc03:3457-4040			
	A1:Cc01:500-2198:Dc04:2657-339			
	A1:Cc02:0-878:Dc03:1335-3355			
	A1:Cc02:0-634:Dc05:1848-2327			
	A1:Cc02:805-1220:Dc05:2738-730			
	A1:Cc02:1098-1659:Dc02:2972-3518			
	A1:Cc02:1660-2439:Dc01:785-673			
	A1:Cc02:2268-3049:Dc04:2828-3339			
Cc2	A1:Cc02:2634-3610:Dc01:2594-4000	A2:Cc02:0-561:Dc06:0-1500 A2:Cc02:561-1683:Dc08:0-2116 A2:Cc02:854-1224:Dc02:0-1879 A2:Cc02:1512-4000:Dc06:1878-3449 A2:Cc02:2098-4000:Dc07:1608-2326	A3:Cc02:0-310:Dc03:0-993 A3:Cc02:2941-4000:Dc01:1000-1820 A3:Cc02:0-2000:Dc07:0-992 A3:Cc02:400-2585:Dc01:2970-4301 A3:Cc02:2000-4000:Dc09:2009-2316 A3:Cc02:2902-4000:Dc02:0-1127 A3:Cc02:3390-4000:Dc04:2800-3339	A4:Cc02:1235-1600:Dc02:0-500 A4:Cc02:0-610:Dc04:0-2249 A4:Cc02:0-1573:Dc07:1266-1779 A4:Cc02:200-4000:Dc09:0-1090 A4:Cc02:3585-4000:Dc02:3655-3860
	A1:Cc02:2610-4000:Dc02:1298-3000			
	A1:Cc03:0-1632:Dc01:1000-2185			
Cc3		A2:Cc03:0-1632:Dc07:0-2000	A3:Cc03:0-1632:Dc08:0-2000	A4:Cc03:0-1632:Dc09:732-2316

Cc4	A1:Cc03:500-1632:Dc02:0-1500			
	A1:Cc04:0-1241:Dc02:2528-310			
	8	A2:Cc04:0-1727:Dc07:2121-3216	A3:Cc04:486-1727:Dc04:0-3339	A4:Cc04:0-1727:Dc06:1298-3449
Cc5	A1:Cc04:438-1727:Dc03:0-4040		A3:Cc04:0-1727:Dc05:0-700	
		A2:Cc05:879-1295:Dc06:0-1400	A3:Cc05:0-635:Dc05:3422-3730	A4:Cc05:1466-1661:Dc03:0-1432
	A1:Cc05:0-1661:Dc04:0-1295	A2:Cc05:0-1300:Dc06:1195-3449	A3:Cc05:0-1075:Dc03:0-1438	A4:Cc05:0-300:Dc05:811-1000
Cc6		A2:Cc05:1000-1661:Dc06:1700-3449	A3:Cc05:1172-1466:Dc03:1130-1500	A4:Cc05:0-879:Dc05:2738-3354
		A2:Cc05:1000-1661:Dc06:0-400	A3:Cc05:831-1661:Dc05:0-2000	A4:Cc05:879-1661:Dc05:3319-3730
	A1:Cc06:0-2389:Dc03:0-1438	A2:Cc06:0-1536:Dc08:1672-2491	A3:Cc06:0-281:Dc04:0-3339	A4:Cc06:0-2389:Dc03:3150-3800
Cc7	A1:Cc06:0-800:Dc07:0-1026	A2:Cc06:0-1073:Dc06:0-1725	A3:Cc06:0-2389:Dc04:1772-2385	A4:Cc06:0-2389:Dc05:616-2156
	A1:Cc06:500-2000:Dc07:0-1847	A2:Cc06:1000-2389:Dc06:0-1059	A3:Cc06:0-2389:Dc04:545-1056	A4:Cc06:0-268:Dc05:2224-2806
			A3:Cc06:756-2389:Dc03:1541-2191	
Cc8	A1:Cc07:0-2146:Dc03:1883-400	A2:Cc07:1024-2176:Dc04:1193-3000		A4:Cc07:0-366:Dc04:0-3339
	0	A2:Cc07:0-561:Dc06:1742-2117	A3:Cc07:0-2146:Dc01:0-3140	A4:Cc07:1658-2146:Dc03:0-1154
	A1:Cc07:0-2146:Dc05:958-1403	A2:Cc07:439-1195:Dc06:1503-2110	A3:Cc07:1700-2146:Dc06:0-300	A4:Cc07:854-2146:Dc03:1155-1746
Cc9				A4:Cc07:0-2000:Dc07:1600-2804
	A1:Cc08:0-1718:Dc01:0-1946	A2:Cc08:0-1718:Dc01:3038-4301	A3:Cc08:491-1227:Dc01:2321-2901	
	A1:Cc08:196-1718:Dc08:1092-2116	A2:Cc08:1497-1718	A3:Cc08:0-1718:Dc02:0-2085	A4:Cc08:0-1718:Dc02:2664-3758
Cc10	A1:Cc09:0-1094:Dc07:513-855			A4:Cc09:0-802:Dc01:3516-4028
	A1:Cc09:0-535:Dc08:0-2491	A2:Cc09:0-535:Dc09:0-2316	A3:Cc09:0-875:Dc01:614-2219	A4:Cc09:0-1094:Dc02:0-1810
	A1:Cc09:0-1094:Dc02:2000-3860	A2:Cc09:365-1094:Dc01:2357-3860	A3:Cc09:729-1094:Dc08:0-1638	A4:Cc09:500-1094:Dc06:2834-3449
Cc11			A3:Cc10:0-267:Dc05:0-1700	
	A1:Cc10:0-1653:Dc03:0-1849	A2:Cc10:0-899:Dc04:0-1295	A3:Cc10:0-500:Dc05:1300-2000	A4:Cc10:0-340:Dc06:2493-3449
		A2:Cc10:851-1653:Dc04:1158-3339	A3:Cc10:0-948:Dc05:2943-3730	A4:Cc10:0-1094:Dc06:0-1366
Cc12			A3:Cc10:800-1653:Dc01:0-1092	A4:Cc10:1021-1653:Dc01:2765-4000
	A1:Cc11:0-1753:Dc07:0-1847	A2:Cc11:0-1753:Dc09:0-2316	A3:Cc11:0-1000:Dc01:1604-2697	
			A3:Cc11:0-1753:Dc02:2050-2664	A4:Cc11:0-1753:Dc08:0-1491

Each coffee genomic region corresponds to four or fewer independent carrot regions, denoted from A1-A4. The chromosome identification

numbers and ranges (measured in genes) that contain orthologous genes from both species have been shown.

Table S5. Paralogous, orthologous and out-paralogous gene pairs within a genome or between genomes.

Genomes	Grape	Coffee	Carrot
Grape	2424	7471	9639
Coffee	3759	1640	11256
Carrot	5713	7850	5511

Numbers on the main diagonal denote paralogous gene pairs within a genome, numbers above the diagonal denote orthologous gene pairs between two genomes, and numbers below the diagonal denote out-paralogous gene pairs between two genomes.

Table S6. Paralogous, orthologous and out-paralogous genes within a genome or between genomes.

Genomes	Grape	Coffee	Carrot
Grape	3853	7355/7387	7013/9096
Coffee	3023/3199	2768	8152/10907
Carrot	4324/3544	5480/4724	6777

See the legends of Supplementary Table S5. In non-diagonal cells, gene numbers in two corresponding species were shown, from vertical and horizontal lists respectively.

Table S7. Paralogous, orthologous and out-paralogous blocks within a genome or between genomes.

Genomes	Grape	Coffee	Carrot
Grape	86	152	537
Coffee	154	92	488
Carrot	396	467	224

See the legends of Supplementary Table S5. In non-diagonal cells, gene numbers in two corresponding species were shown, from vertical and horizontal lists respectively.

Table S10. Kernel function analysis of Ks distribution related to duplication events within each genome and between genomes (before

evolutionary rate correction).

Intragenomic/Intergenomic colinear gene pairs	Weight coefficient related to duplication event or speciation	Peak of Ks distribution (μ)	Deviation (σ)	Correction coefficient (λ)
Grape ECH-related	0.569	1.053	0.120	1
Coffee ECH-related	0.137	1.400	0.070	0.752
Carrot ECH-related	0.116	1.390	0.099	0.758
Carrot Dc- β -related	0.498	0.944	0.176	0.758
Carrot Dc- α -related	0.171	0.551	0.060	0.758
Lettuce- ECH-related	0.298	1.486	0.060	0.732
Lettuce- sWGT-related	0.322	0.872	0.131	0.732
Grape-Coffee	0.264	1.085	0.094	0.858
Coffee-Carrot (Split)	0.202	1.195	0.116	0.755
Coffee-Carrot (ECH)	0.139	1.496	0.129	0.755
Lettuce-Carrot	0.716	1.175	0.256	0.758

Table S11. Kernel function analysis of Ks distribution related to duplication events within each genome and between genomes (after evolutionary rate correction).

Intragenomic/Intergenomic colinear gene pairs	Weight coefficient related to duplication event or speciation	Peak of Ks distribution (μ)	Deviation (σ)	Correction coefficient (λ)
Grape ECH-related	0.569	1.053	0.120	1
Coffee ECH-related	0.224	1.053	0.070	0.752
Carrot ECH-related	0.058	1.053	0.049	0.758
Carrot Dc- β -related	0.631	0.703	0.148	0.758
Carrot Dc- α -related	0.139	0.421	0.049	0.758
Lettuce- ECH-related	0.331	1.053	1.131	0.732
Lettuce- sWGT-related	0.405	0.619	0.072	0.732
Grape-Coffee	0.331	0.935	0.094	0.858
Coffee-Carrot (Split)	0.666	0.901	0.180	0.755
Coffee-Carrot (ECH)	0.430	1.053	0.189	0.755

Supplementary Table S12. Homologous depth within carrot, coffee and grape genome.

Genome	<i>V. vinifera</i>	<i>C. canephora</i>	<i>D. carota</i>
Intergenomic homologous depth level			
0	9728/0(0.411)	10064/0(0.458)	6047/0(0.197)
1	6280/1118(0.266)	5797/993(0.264)	7628/1900(0.248)
2	7310/2912(0.309)	5940/2166(0.270)	7708/3449(0.251)
3	322/180(0.014)	170/87(0.008)	6480/4081(0.211)
4	7/8(0.000)		2101/1619(0.068)
5			548/534(0.018)
6			205/249(0.007)
7			25/28(0.001)

In each cell, we show the genes number in the reference genome and the corresponding homologous regions piled up to certain depth in the compared plant genome, and the percentage of genes covered in the compared genome.

Supplementary Table S13. Intergenomic homologous depth of carrot genome with grape or coffee as reference.

Intragenomic homologous depth level	In <i>D. carota</i> as to <i>V. vinifera</i>	In <i>D. carota</i> as to <i>C. canephora</i>
0	3392/0(0.143)	3578/0(0.163)
1	2398/481(0.101)	2044/365(0.093)
2	3013/1169(0.127)	2270/991(0.103)
3	3614/2197(0.153)	2979/1835(0.136)
4	3727/3030(0.158)	3474/3082(0.158)
5	2812/2702(0.119)	2769/2955(0.126)
6	2338/2502(0.099)	2286/2805(0.104)
7	1502/2027(0.064)	1463/2012(0.067)
8	682/1016(0.029)	736/1134(0.034)
9	154/242(0.007)	297/556(0.014)
10	15/30(0.001)	63/127(0.003)
11		3/7(0.000)
12		9/24(0.000)

In each cell, we show the genes number in the reference genome and the corresponding homologous regions piled up to certain depth in the compared plant genome, and the percentage of genes covered in the compared genome.

Table S14. Carrot gene loss rates and gene translocation with grape as reference genome.

Grape		Carrot homoelogenous subgenomes					
Chr #	Gene #	AAT- 1	AAT-2	AAT 1-2 difference	ART-1	ART-2	ART 1-2 difference
1	1327	0.79	0.82	0.03	0.8	0.86	0.06
2	1237	0.71	0.79	0.08	0.86	0.82	0.04
3	1000	0.9	0.86	0.04	0.91	0.84	0.07
4	1638	0.84	0.83	0.01	0.84	0.9	0.06
5	1748	0.87	0.85	0.02	0.86	0.88	0.02
6	1779	0.85	0.86	0.01	0.9	0.8	0.1
7	1409	0.83	0.81	0.02	0.82	0.87	0.05
8	1867	0.86	0.81	0.05	0.78	0.85	0.07
9	1221	0.86	0.88	0.02	0.9	0.9	0
10	632	0.85	0.83	0.02	0.83	0.86	0.03
11	1107	0.88	0.82	0.06	0.9	0.88	0.02
12	1481	0.84	0.85	0.01	0.87	0.88	0.01
13	1329	0.81	0.86	0.05	0.87	0.88	0.01
14	1729	0.88	0.83	0.05	0.86	0.85	0.01
15	561	0.92	0.88	0.04	0.91	0.86	0.05
16	647	0.86	0.89	0.03	0.89	0.92	0.03
17	1168	0.83	0.84	0.01	0.86	0.89	0.03
18	1886	0.84	0.84	0	0.79	0.86	0.07
19	1135	0.81	0.82	0.01	0.88	0.84	0.04
Total/Aver.	24901	0.84	0.84	0.03	0.86	0.87	0.04

Table S15. Carrot gene loss rates and gene translocation with coffee as reference genome.

Coffee		Carrot homoeologous subgenomes					
Chr #	Gene #	T1- A	T1-B	T1 A-B difference	T2-A	T2-B	T2 A-B difference
1	2198	0.85	0.74	0.11	0.86	0.64	0.22
2	4000	0.80	0.80	0	0.89	0.60	0.29
3	1632	0.85	0.81	0.04	0.85	0.64	0.21
4	1727	0.78	0.83	0.05	0.84	0.62	0.22
5	1661	0.82	0.84	0.02	0.87	0.62	0.25
6	2389	0.85	0.80	0.05	0.81	0.54	0.27
7	2146	0.80	0.85	0.05	0.77	0.54	0.23
8	1718	0.78	0.86	0.08	0.83	0.61	0.22
9	1094	0.86	0.85	0.01	0.85	0.72	0.13
10	1653	0.80	0.82	0.02	0.84	0.67	0.17
11	1753	0.87	0.81	0.06	0.87	0.64	0.23
Total/Aver.	21971	0.82	0.82	0.04	0.84	0.62	0.22

Table S16. The observed distribution of gene loss and translocation numbers fitted by using different density curves of geometry distribution.

Reference genome	Genomes	Parameter of geometry distribution	Fitness (R-square)	P-value (F-test)
<i>Vitis Vinifera</i>	<i>Daucus Carota</i>	0.2205	0.9797	0.9306
<i>Coffea canephora</i>	<i>Daucus Carota</i>	0.2489	0.9941	0.9259

Table S19. Carotenoid accumulation gene family.

Name	original number	Carrot				Grape		Coffee	
		Homologous (evaluation≤1e-10, Score ≥150)	related to γ-duplication	related to Dc-β duplication	related to Dc-α duplication	Homologous (evaluation≤1e-10, Score ≥150)	related to γ-duplication	Homologous (evaluation≤1e-10, Score ≥150)	related to γ-duplication
DXS	4	4	2(50.00%)	4(100.00%)	3(75.00%)	9	2(22.22%)	4	3(75.00%)
DXR	1	1	0(-)	1(100.00%)	1(100.00%)	1	1(100.00%)	2	2(100.00%)
MCT	2	2	0(-)	1(50.00%)	0(-)	1	0(-)	1	0(-)
CMK	1	1	0(-)	0(-)	0(-)	1	0(-)	1	0(-)
MTS	1	1	0(-)	1(100.00%)	1(100.00%)	1	1(100.00%)	1	1(100.00%)
HDS	2	2	1(50.00%)	2(100.00%)	1(50.00%)	1	1(100.00%)	1	1(100.00%)
HDR	3	3	0(-)	3(100.00%)	3(100.00%)	1	1(100.00%)	1	1(100.00%)
IPPI	2	2	0(-)	1(50.00%)	1(50.00%)	1	0(-)	1	1(100.00%)
GPPS	1	4	0(-)	3(75.00%)	3(75.00%)	2	0(-)	2	1(50.00%)
GGPS	6	7	2(28.57%)	6(85.71%)	5(71.43%)	5	4(80.00%)	3	3(100.00%)
PSY	3	3	1(33.33%)	2(66.67%)	1(33.33%)	3	1(33.33%)	2	1(50.00%)
CCD	6	17	0(-)	15(88.24%)	14(82.35%)	14	6(42.86%)	9	9(100.00%)
PDS	1	1	0(-)	1(100.00%)	1(100.00%)	1	1(100.00%)	1	1(100.00%)
ZISO	1	1	0(-)	1(100.00%)	1(100.00%)	1	0(-)	1	0(-)
CRTISO	2	2	0(-)	2(100.00%)	1(50.00%)	2	0(-)	2	2(100.00%)
ZDS	2	2	0(-)	1(50.00%)	1(50.00%)	2	2(100.00%)	2	1(50.00%)
LCYE	1	3	0(-)	3(100.00%)	2(66.67%)	3	1(33.33%)	3	3(100.00%)
LCYB	1	3	0(-)	3(100.00%)	2(66.67%)	3	1(33.33%)	3	3(100.00%)
CYP97B3	1	4	1(25.00%)	4(100.00%)	4(100.00%)	6	2(33.33%)	6	4(66.67%)
BCH1/C	1	3	0(-)	3(100.00%)	2(66.67%)	2	1(50.00%)	1	1(100.00%)

HXB									
BCH2	1	3	0(-)	3(100.00%)	2(66.67%)	2	1(50.00%)	1	1(100.00%)
CHXE	1	5	1(20.00%)	5(100.00%)	5(100.00%)	8	3(37.50%)	6	4(66.67%)
VDE	1	1	0(-)	1(100.00%)	1(100.00%)	1	0(-)	1	0(-)
ZEP	1	2	1(50.00%)	2(100.00%)	1(50.00%)	2	1(50.00%)	1	1(100.00%)
NCED	9	15	0(-)	14(93.33%)	13(86.67%)	11	4(36.36%)	6	6(100.00%)

Table S20. Information of genomic data.

Order	Species name	Common name	Version	Data source	Genes	Anchored Genes ^a	Reference
1	<i>Vitis vinifera L.</i>	Grape	Genoscope.12X	JGI (https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Vvinifera)	37,829	24,901	(Jaillon <i>et al.</i> , 2007)
2	<i>Coffea canephora</i>	Coffee	v1.0	(http://coffee-genome.org/)	25574	21,971	(Denoeud <i>et al.</i> , 2014)
3	<i>Daucus carota L.</i>	Carrot	v2.0	JGI (https://phytozome.jgi.doe.gov/pz/portal.html#!info?alias=Org_Dcarota)	32,113	30,742	(Iorizzo <i>et al.</i> , 2016)

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