

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
	A2:Vv07:850-1409:Dc07:1600-3216	A3:Vv07:539-1077:Dc01:0-747	A4:Vv07:684-1400:Dc01:3915-4301	
	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
Vv9	A1:Vv09:0-1,221:Dc02:2,556-3,042	A1:Vv09:200-1221:Dc05:1533-1993	A3:Vv08:0-1867:Dc04:2517-2877	A4:Vv08:0-1867:Dc05:0-1788
		A2:Vv09:0-1221:Dc07:2018-3216	A3:Vv08:851-1390:Dc03:2632-4040	
Vv10	A1:Vv10:0-632:Dc01:3,194-4,301	A2:Vv10:0-632:Dc08:1258-2400	A3:Vv09:0-1221:Dc05:0-684	A4:Vv09:0-1221:Dc06:1405-3449
	A1:Vv11:0-554:Dc03:2,448-2,836		A3:Vv10:0-1221:Dc02:0-1023	A4:Vv10:0-1221:Dc02:2812-3860
Vv11	A1:Vv11:0-554:Dc03:2,448-2,836	A2:Vv11:0-660:Dc08:1721-2491	A3:Vv10:0-200:Dc04:0-500	
	A1:Vv11:383-1,107:Dc04:1,747-2,440	A2:Vv11:0-660:Dc08:1721-2491		A4:Vv11:0-1000:Dc07:1132-1672
	A1:Vv12:0-967:Dc04:0-568	A2:Vv11:383-1107:Dc05:1584-2146	A3:Vv11:0-1107:Dc03:306-1714	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:Vv12:0-1481:Dc06:1175-2223	A3:Vv12:432-1481:Dc05:3449-3730	A4:Vv12:500-1481:Dc09:0-1000
	A1:Vv12:1,172-1,481:Dc02:1,713-2,200	A2:Vv12:1131-1481:Dc07:1904-2238	A3:Vv12:900-1481:Dc01:1159-1800	
Vv13	A1:Vv13:0-665:Dc03:2,914-3,344	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 A1:Vv14:0-1,729:Dc02:0-869	A2:Vv13:166-997:Dc05:2836-3193 A2:Vv13:976-1329:Dc09:100-2316 A2:Vv14:0-1500:Dc06:1788-2555 A2:Vv14:0-1729:Dc07:1878-2316 A2:Vv14:0-1062:Dc07:2316-3216	A3:Vv13:540-1329:Dc02:1380-1789 A3:Vv14:0-687:Dc01:0-1803 A3:Vv14:0-1729:258-700 A3:Vv14:750-1729:Dc03:2097-2710 A3:Vv15:0-500:Dc02:0-946 A3:Vv15:0-561:Dc02:1994-2275 A3:Vv16:0-647:Dc03:1688-2199 A3:Vv16:0-647:Dc05:1814-2400 A3:Vv17:0-1168:Dc06:1507-1891 A3:Vv17:0-1168:Dc06:3142-3449 A3:Vv18:0-415:Dc05:0-3730 A3:Vv18:953-1886:Dc05:1226-1712 A3:Vv18:415-1244:Dc05:3117-3526 A3:Vv19:0-1135:Dc05:3321-3730	A4:Vv13:976-1329:Dc06:2376-3000 A4:Vv14:479-1729:Dc04:1310-2414 A4:Vv14:667-937:Dc05:894-1431 A4:Vv14:0-1000:Dc09:0-916 A4:Vv15:0-561:Dc02:3579-3860 A4:Vv15:0-500:Dc09:0-930 A4:Vv16:0-647:DC04:1464-2312 A4:Vv17:0-292:Dc02:2531-2837 A4:Vv17:521-1168:Dc02:2122-2786 A4:Vv17:0-584:Dc03:2531-2838 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 A4:Vv19:0-1135:Dc06:869-1329 A4:Vv19:206-1135:Dc06:2453-3449
Vv14	A1:Vv14:1,042-1,729:Dc02:1,559-2,122 A1:Vv14:750-1,062:Dc02:2,531-2,889			
Vv15	A1:Vv15:0-561:Dc04:2,954-3,339	A2:Vv15:0-561:Dc07:1647-3216		
Vv16	A1:Vv16:0-647:Dc03:0-895	A2:Vv16:0-647:Dc06:0-1500		
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		
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		
Vv19	A1:Vv19:0-1,135:Dc04:283-1,233	A2:Vv19:0-1135:Dc05:0-1661		

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

Cc4	A1:Cc03:500-1632:Dc02:0-1500 A1:Cc04:0-1241:Dc02:2528-310 8 A1:Cc04:438-1727:Dc03:0-4040	A2:Cc04:0-1727:Dc07:2121-3216	A3:Cc04:486-1727:Dc04:0-3339 A3:Cc04:0-1727:Dc05:0-700	A4:Cc04:0-1727:Dc06:1298-3449
Cc5	A1:Cc05:0-1661:Dc04:0-1295	A2:Cc05:879-1295:Dc06:0-1400 A2:Cc05:0-1300:Dc06:1195-3449 A2:Cc05:1000-1661:Dc06:1700-3449 A2:Cc05:1000-1661:Dc06:0-400	A3:Cc05:0-635:Dc05:3422-3730 A3:Cc05:0-1075:Dc03:0-1438 A3:Cc05:1172-1466:Dc03:1130-1500 A3:Cc05:831-1661:Dc05:0-2000 A3:Cc06:0-281:Dc04:0-3339 A3:Cc06:0-2389:Dc04:1772-2385 A3:Cc06:0-2389:Dc04:545-1056 A3:Cc06:756-2389:Dc03:1541-2191	A4:Cc05:1466-1661:Dc03:0-1432 A4:Cc05:0-300:Dc05:811-1000 A4:Cc05:0-879:Dc05:2738-3354 A4:Cc05:879-1661:Dc05:3319-3730
Cc6	A1:Cc06:0-2389:Dc03:0-1438 A1:Cc06:0-800:Dc07:0-1026 A1:Cc06:500-2000:Dc07:0-1847	A2:Cc06:0-1536:Dc08:1672-2491 A2:Cc06:0-1073:Dc06:0-1725 A2:Cc06:1000-2389:Dc06:0-1059	A4:Cc06:0-2389:Dc03:3150-3800 A4:Cc06:0-2389:Dc05:616-2156 A4:Cc06:0-268:Dc05:2224-2806	
Cc7	A1:Cc07:0-2146:Dc03:1883-400 0 A1:Cc07:0-2146:Dc05:958-1403	A2:Cc07:1024-2176:Dc04:1193-3000 A2:Cc07:0-561:Dc06:1742-2117 A2:Cc07:439-1195:Dc06:1503-2110	A4:Cc07:0-366:Dc04:0-3339 A4:Cc07:1658-2146:Dc03:0-1154 A4:Cc07:854-2146:Dc03:1155-1746 A4:Cc07:0-2000:Dc07:1600-2804	
Cc8	A1:Cc08:0-1718:Dc01:0-1946 A1:Cc08:196-1718:Dc08:1092-2 116	A2:Cc08:0-1718:Dc01:3038-4301 A2:Cc08:1497-1718	A3:Cc08:491-1227:Dc01:2321-2901 A3:Cc08:0-1718:Dc02:0-2085	A4:Cc08:0-1718:Dc02:2664-3758
Cc9	A1:Cc09:0-1094:Dc07:513-855 A1:Cc09:0-535:Dc08:0-2491 A1:Cc09:0-1094:Dc02:2000-386 0	A2:Cc09:0-535:Dc09:0-2316 A2:Cc09:365-1094:Dc01:2357-3860	A3:Cc09:0-875:Dc01:614-2219 A3:Cc09:729-1094:Dc08:0-1638	A4:Cc09:0-802:Dc01:3516-4028 A4:Cc09:0-1094:Dc02:0-1810 A4:Cc09:500-1094:Dc06:2834-3449
Cc10	A1:Cc10:0-1653:Dc03:0-1849	A2:Cc10:0-899:Dc04:0-1295 A2:Cc10:851-1653:Dc04:1158-3339	A3:Cc10:0-267:Dc05:0-1700 A3:Cc10:0-500:Dc05:1300-2000 A3:Cc10:0-948:Dc05:2943-3730 A3:Cc10:800-1653:Dc01:0-1092 A3:Cc11:0-1000:Dc01:1604-2697 A3:Cc11:0-1753:Dc02:2050-2664	A4:Cc10:0-340:Dc06:2493-3449 A4:Cc10:0-1094:Dc06:0-1366 A4:Cc10:1021-1653:Dc01:2765-4000
Cc11	A1:Cc11:0-1753:Dc07:0-1847	A2:Cc11:0-1753:Dc09:0-2316	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.

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	In <i>D. carota</i> as to
	<i>V. vinifera</i>	<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.

Supplementary figure legends

Supplementary Figure S1. Homologous dotplot within carrot genome. The best, secondarily, and other matched homologous gene pairs were shown by red, blue, and gray dots, respectively. Mean Ks of each inferred collinear block is shown besides. The Ks values ≤ 0.65 are in red, and others in blue, often relating recent polyploidization and older polyploidization, respectively.

Supplementary Figure S2. Homologous dotplot between grape and carrot genomes. The best, secondarily, and other matched homologous gene pairs were shown by red, blue, and gray dots, respectively. Mean Ks of each inferred collinear block is shown besides. The Ks values ≤ 1.20 are in red, and others in blue, often showing orthology and outparalogy, respectively.

Supplementary Figure S3. Homologous dotplot between coffee and carrot genomes. The best, secondarily, and other matched homologous gene pairs were shown by red, blue, and gray dots, respectively. Mean Ks of each inferred collinear block is shown besides. The Ks values ≤ 1.3 are in red, and others in blue, often showing orthology and outparalogy, respectively.

Supplementary Figure S4. Examples of homologous gene dotplots between carrot and coffee. Carrot and coffee chromosome numbers were shown. Best-hit genes make red dots, secondary hits make blue dots, and the other grey.

Supplementary Figure S5. Trees with topology supporting the Dc- α and Dc- β . a-f Homoeologous groups related to the eudicot-common hexaploidy are shown with hexagons with same color, and a grape homoeolog and their corresponding carrot orthologs are shown with red rectangles and green rectangles, respectively from Dc- β .

Supplementary Figure S6. Alignment of carrot, coffee and grape genomes. The alignment was constructed by using inferred collinear genes between genomes and with the grape genome as reference. The grape chromosomes form the innermost circle, and their paralogous genes in colinearity are linked curves. A grape chromosome region has 1 and 3 orthologous regions in coffee, carrot, respectively. The homologous regions form the other circles, displayed by short

lines to show collinear genes. The short lines in grape chromosomes were coloured as to 7core-eudicot-common ancestral chromosomes inferred previously (Jaillon, et al., 2007). The short lines forming chromosomes in other genomes were coloured as to their respective source chromosomes numbers. The relating colour scheme is shown below. V: grape; C: coffee; D: carrot.

Supplementary Figure S7. Homologous dotplot between grape and lettuce

genome. The best, secondary, and other matched homologous gene pairs output by Blast were dotplotted by red, blue, and gray colors in this figure, respectively.

Supplementary Figure S8. Homologous dotplot between carrot and lettuce

genome. The best, secondary, and other matched homologous gene pairs output by Blast were dotplotted by red, blue, and gray colors in this figure, respectively.

Supplementary Figure S9. Homologous alignments and carrot subgenome gene retention along corresponding orthologous coffee chromosomes. Details in Fig. 4.

Supplementary Figure S10. Fitting a geometric distribution and gene loss rates in carrot as to the grape and coffee. a Carrot with grape as reference genome. **b** carrot with coffee as reference genome.

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