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Supplemental information

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Running Title: CitCYP97B hydroxylates β -cryptoxanthin

Supplemental Figures

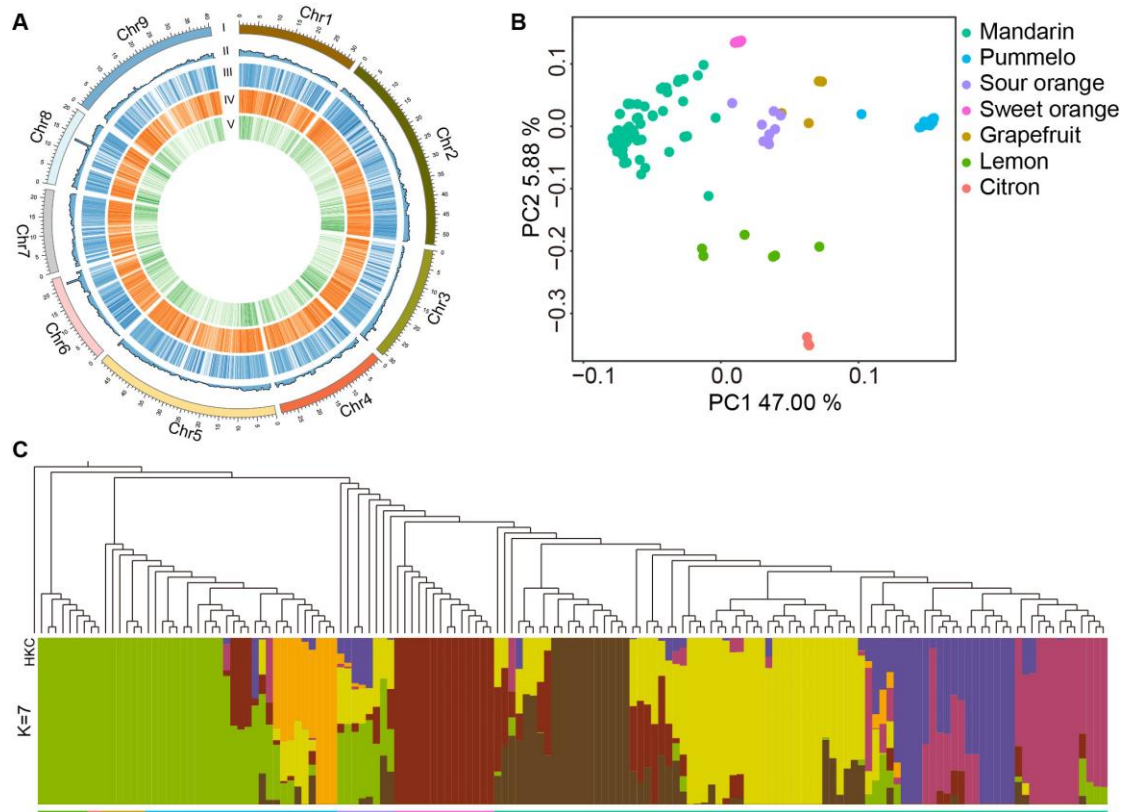


Figure S1. Phylogenetic analysis of the 150 citrus accessions.

Overview of the variance map (A) and population admixture analysis (B, C) of 150 citrus accessions based on the SNP dataset. (I) Chromosomes; (II) Gene density; (III) SNP density; (IV) InDel density; (V) SV density. The colored dots and lines indicate different citrus groups in the principal component analysis (B) and population admixture (C).

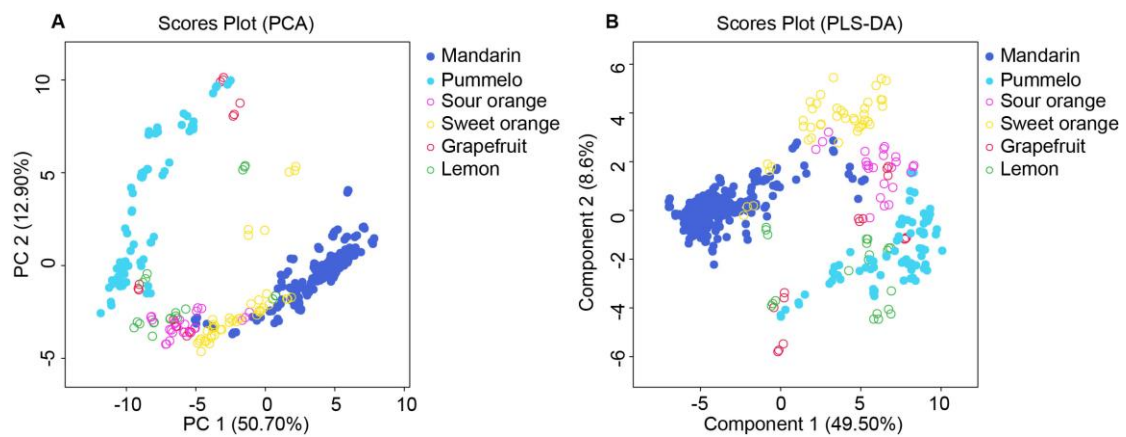


Figure S2. Multivariate analysis of carotenoids and carotenoid derivatives.

Principal component analysis (A) and partial least squares discriminant analysis (B) of carotenoids and carotenoid derivatives that accumulate in 148 citrus accessions.

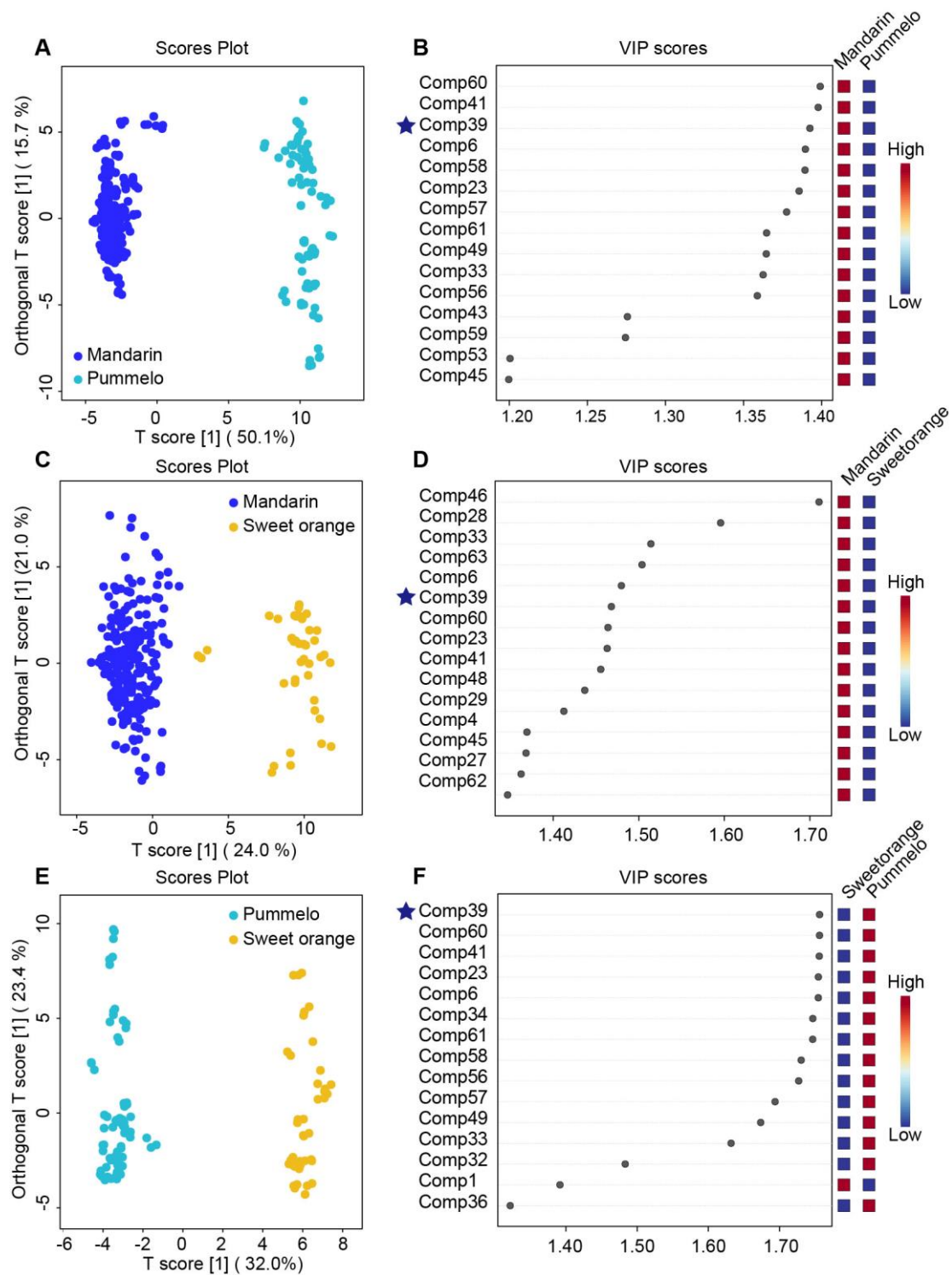


Figure S3. Orthogonal PLS-DA of carotenoids and carotenoid derivatives among mandarin, pummelo, and sweet orange.

Score plots (A, C, E) based on Orthogonal PLS-DA and top 15 variables (B, D, F) based on Component 1 (T score). The star indicates β -cryptoxanthin.

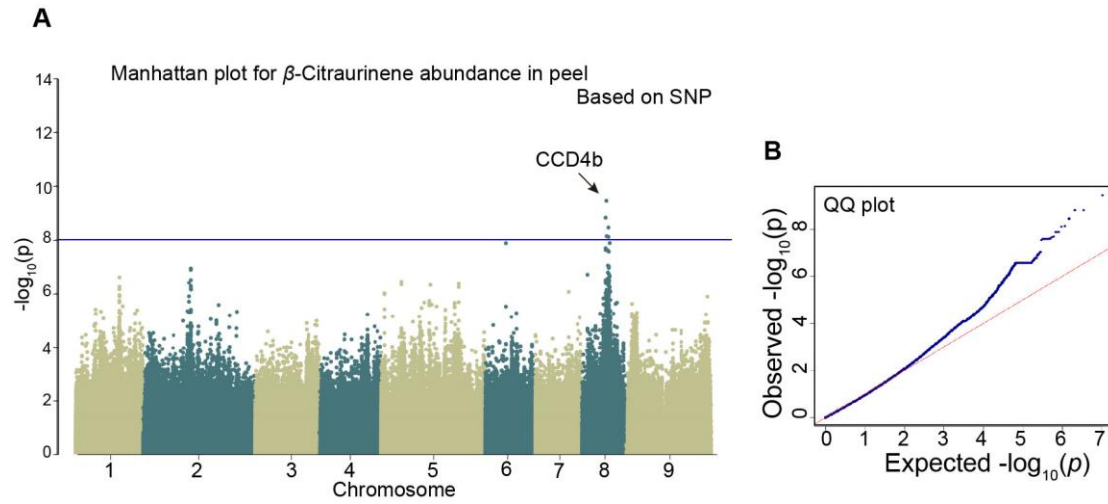


Figure S4. Genome-wide association study for β -citraurine.

Manhattan plot (A) and QQ plot (B) of β -citraurine abundance based on a SNP-GWAS for citrus peel.

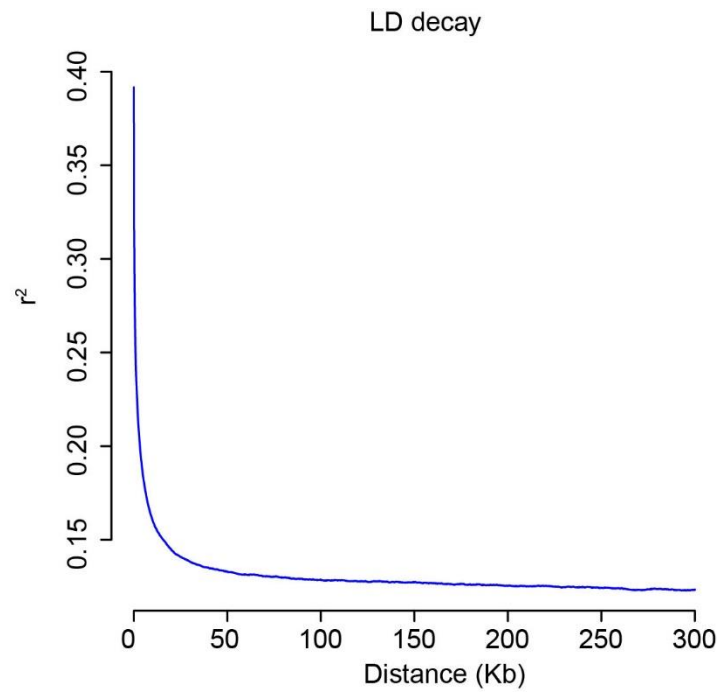


Figure S5. Linkage disequilibrium (LD) decay in the studied population.

LD level represented by r^2 with physical distance in the whole population.

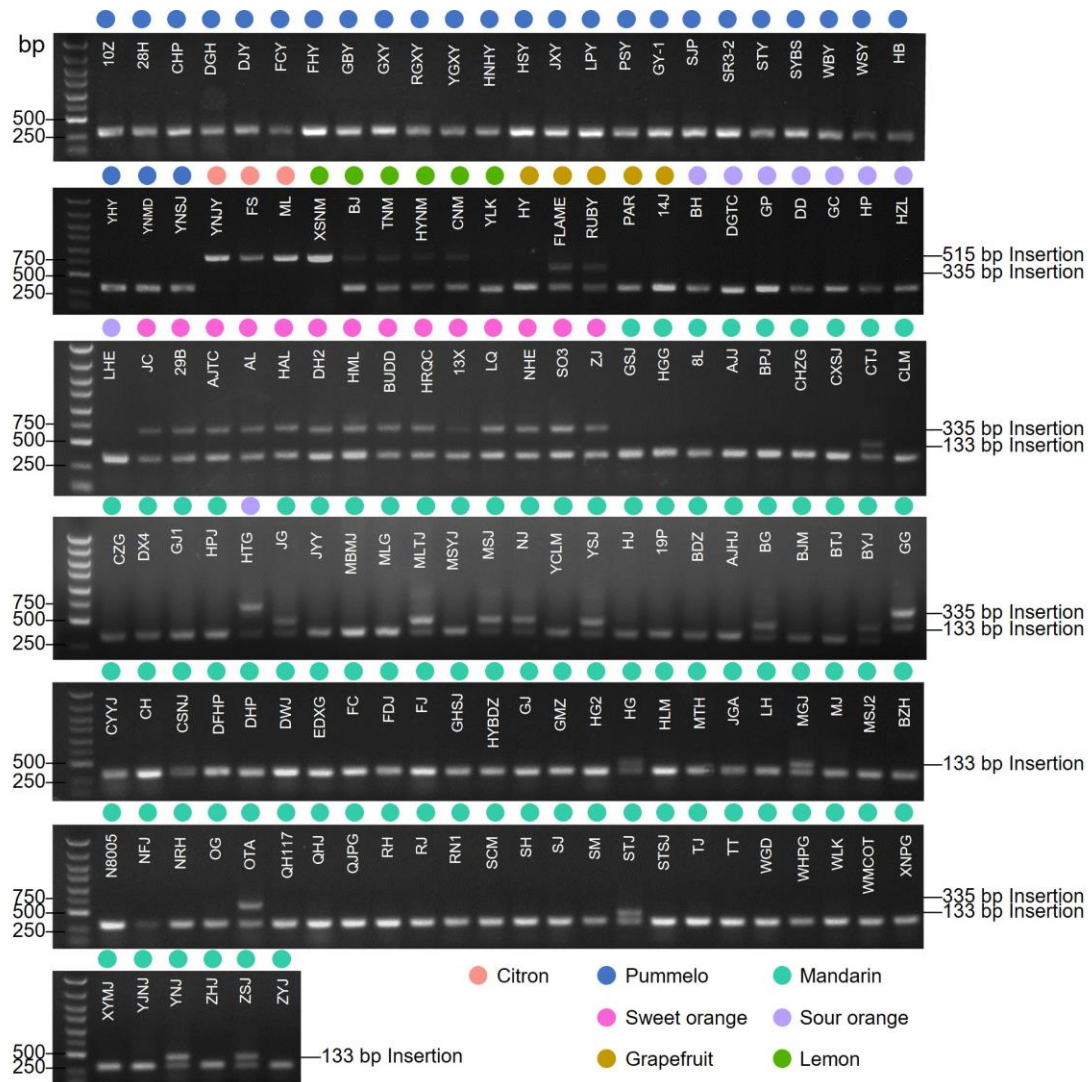


Figure S6. Validation of structural variation using PCR-based markers.

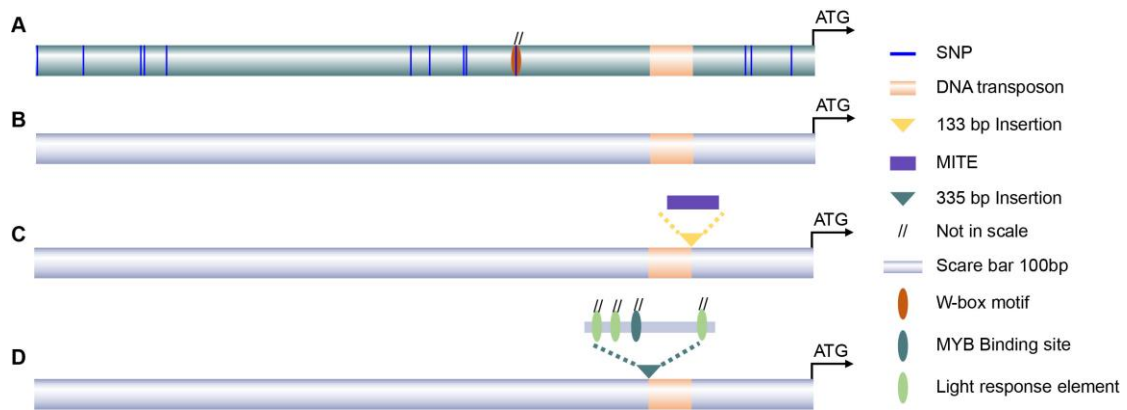


Figure S7. Schematic of *CitCYP97B* promoter sequence variation.

Schematic of *CitCYP97B* promoter sequence variation in Haplotype 1 (A), Haplotype 3 (B), Haplotype 4 (C), Haplotype 5 (D). The hooked arrow indicates the start site of transcription.

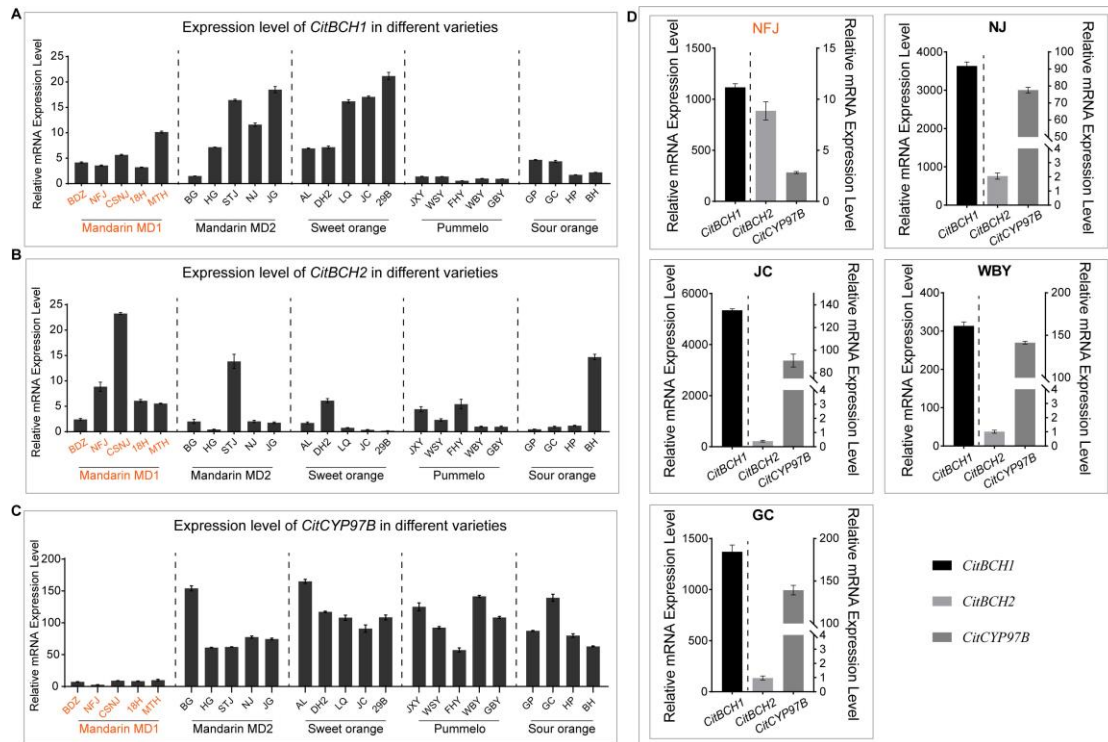


Figure S8. The expression level of carotene hydroxylase genes in different citrus varieties. (A) The expression levels of *CitBCH1* in the pulp of mature citrus varieties. (B) The expression levels of *CitBCH2* in the pulp of mature citrus varieties. (C) The expression levels of *CitCYP97B* in the pulp of mature citrus varieties. (D) Comparison of the expression levels of carotene hydroxylase genes in different citrus varieties. The expression level of *CitBCH1* corresponds to the left Y-axis, and both the expression levels of *CitBCH2* and *CitCYP97B* correspond to the right Y-axis. Data are presented as mean values \pm standard error in triplicate. Orange font indicates the varieties that accumulate a high proportion of β -cryptoxanthin.

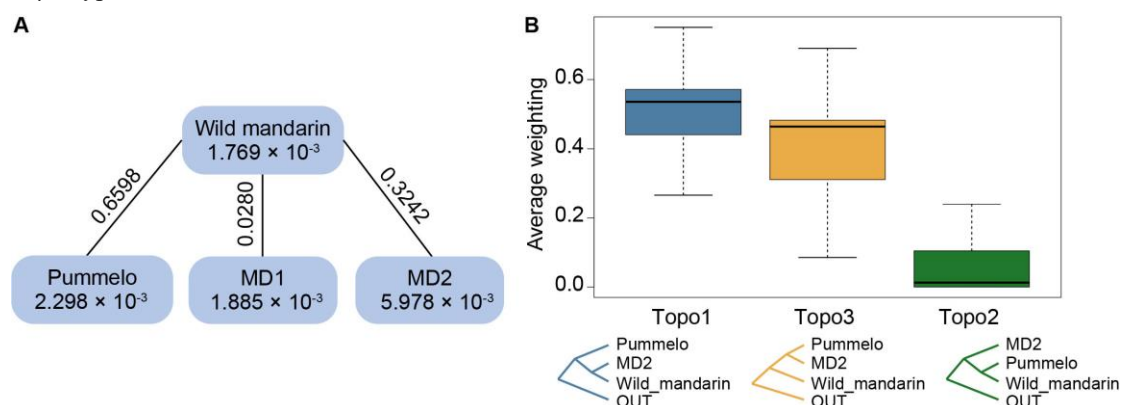


Figure S9. Genetic diversity and introgression analysis of wild mandarin, cultivated mandarin MD2, and pummelo. Genetic diversity and population differentiation in the window containing *CitCYP97B* (A) and topology weighting of the 1-Mb region around *CitCYP97B* in wild mandarin, cultivated mandarin MD2, and pummelo (B). Rectangles represent the genetic diversity (π) of citrus groups. Lines represent F_{ST} values between citrus groups.

Supplemental Tables

Table S1. Information and statistics for genome sequence data of *Citrus* accessions used in this study.

Accession	Common name	Scientific name	Category	Reads Length	Mean Coverage	GC percentage	Mean Mapping Quality	SRR id on NCBI	Source	Collection Source
18H	Red Tangerine	<i>Citrus reticulata</i>	Cultivated mandarin MD1	125	33.07	38.96	38.92	SRR3749605	Wang et al, 2017	Hubei Province, China
19P	Ponkan	<i>C. reticulata</i>	Cultivated mandarin MD1	90	35.57	37.44	38.34	SRR3747617	Wang et al, 2017	Hubei Province, China
20H	Bendizao	<i>C. reticulata</i>	Cultivated mandarin MD1	90	35.50	37.37	38.64	SRR3747635	Wang et al, 2018	Hubei Province, China
AJHJ	Anjianghongju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	31.78	37.93	40.65	SRR25409391	sequenced in this study	Hunan Province, China
BJM	Baiju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	36.01	37.90	40.41	SRR25409390	sequenced in this study	Chongqing, China
CH	Chihong	<i>C. reticulata</i>	Cultivated mandarin MD1	150	33.73	37.33	40.98	SRR25409379	sequenced in this study	Hunan Province, China
CSNJ	Changshananju	<i>C. reticulata</i>	Cultivated mandarin MD1	125	28.05	38.07	39.45	SRR3747609	Wang et al, 2018	Chongqing, China
DFHP	Dafeng Huangpiju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	33.37	37.18	40.67	SRR25409368	sequenced in this study	Chongqing, China
DHP	Dahongpao	<i>C. reticulata</i>	Cultivated mandarin MD1	150	41.68	37.60	40.21	SRR25409357	sequenced in this study	Chongqing, China
DWJ	Diwangju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	34.81	37.69	40.57	SRR25409346	sequenced in this study	Chongqing, China
EDXG	Edangxianggan	<i>C. reticulata</i>	Cultivated mandarin MD1	150	39.69	37.79	40.78	SRR25409336	sequenced in this study	Chongqing, China
FDJ	Fengdongju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	34.18	37.73	40.66	SRR25409335	sequenced in this study	Chongqing, China
FJ	Fuju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	35.84	37.74	40.49	SRR25409334	sequenced in this study	Zhejiang Province, China

GJ	Guangju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	36.16	37.81	42.67	SRR25409333	sequenced in this study	Chongqing, China
GJ1	Guiju-1	<i>C. reticulata</i>	Cultivated mandarin MD1	150	40.73	37.47	40.48	SRR25409389	sequenced in this study	Guangxi Province, China
HG2	Huagan-2	<i>C. reticulata</i>	Cultivated mandarin MD1	150	42.52	38.63	40.22	SRR25409388	sequenced in this study	Hubei Province, China
HLM	Huanglinmiao	<i>C. reticulata</i>	Cultivated mandarin MD1	150	36.93	36.99	40.43	SRR25409387	sequenced in this study	Hubei Province, China
HYBDZ	Huangyan Bendizao	<i>C. reticulata</i>	Cultivated mandarin MD1	150	31.70	37.28	40.99	SRR25409386	sequenced in this study	Hubei Province, China
JGA	Jiangan	<i>C. reticulata</i>	Cultivated mandarin MD1	125	32.02	40.65	39.34	SRR5796822	Wang et al, 2018	Chongqing, China
LH	Liaohong	<i>C. reticulata</i>	Cultivated mandarin MD1	150	31.41	36.77	40.66	SRR25409385	sequenced in this study	Zhejiang Province, China
MJ	Manju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	32.43	37.18	40.75	SRR25409384	sequenced in this study	Zhejiang Province, China
MTH	Mantouhong	<i>C. reticulata</i>	Cultivated mandarin MD1	150	40.52	38.41	40.13	SRR25409383	sequenced in this study	Chongqing, China
N8005	Tiqie mandarin	<i>C. reticulata</i>	Cultivated mandarin MD1	150	35.46	37.70	40.48	SRR25409382	sequenced in this study	Chongqing, China
NFJ	Nanfengmiju	<i>C. reticulata</i>	Cultivated mandarin MD1	100	33.71	42.20	38.84	SRR5796630	Wang et al, 2017	Hubei Province, China
NRH	Niurouhong	<i>C. reticulata</i>	Cultivated mandarin MD1	150	40.07	38.31	40.27	SRR25409381	sequenced in this study	Guizhou Province, China
OG	Ougan	<i>C. reticulata</i>	Cultivated mandarin MD1	150	42.02	38.38	41.13	SRR25409380	sequenced in this study	Chongqing, China
QHJ	Qinghongju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	35.91	37.71	40.51	SRR25409378	sequenced in this study	Zhejiang Province, China
QJPG	Qingjiang Ponkan	<i>C. reticulata</i>	Cultivated mandarin MD1	150	34.65	37.51	40.61	SRR25409377	sequenced in this study	Hubei Province, China

RH	Sunki	<i>C. reticulata</i>	Cultivated mandarin MD1	150	39.53	37.76	41.21	SRR25409376	sequenced in this study	Hubei Province, China
RJ	Ruju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	40.99	37.21	40.32	SRR25409375	sequenced in this study	Chongqing, China
SH	Suhong	<i>C. reticulata</i>	Cultivated mandarin MD1	150	33.17	37.39	42.19	SRR25409374	sequenced in this study	Chongqing, China
TJ	Tu mandarin	<i>C. reticulata</i>	Cultivated mandarin MD1	150	34.76	37.32	41.08	SRR25409373	sequenced in this study	Chongqing, China
TT	Taitian Ponkan	<i>C. reticulata</i>	Cultivated mandarin MD1	150	32.60	37.71	40.53	SRR25409372	sequenced in this study	Hubei Province, China
WGD	Wuganda mandairn	<i>C. reticulata</i>	Cultivated mandarin MD1	150	33.65	38.14	40.26	SRR25409371	sequenced in this study	Chongqing, China
WHPG	Seedless Ponkan	<i>C. reticulata</i>	Cultivated mandarin MD1	125	26.05	38.34	39.25	SRR5796644	Wang et al, 2018	Chongqing, China
XNPG	Xinnv Ponkan	<i>C. reticulata</i>	Cultivated mandarin MD1	150	35.08	37.53	40.62	SRR25409370	sequenced in this study	Hubei Province, China
XYMJ	Xinyumiju	<i>C. reticulata</i>	Cultivated mandarin MD1	150	33.63	36.97	40.89	SRR25409369	sequenced in this study	Jiangxi Province, China
YJNJ	Yuanjiangnanju	<i>C. reticulata</i>	Cultivated mandarin MD1	125	30.64	36.69	39.76	SRR5796865	Wang et al, 2018	Hunan Province, China
ZHJ	Zhuhongju	<i>C. reticulata</i>	Cultivated mandarin MD1	125	27.61	40.60	38.88	SRR5796927	Wang et al, 2018	Chongqing, China
BG	Biangan	<i>C. reticulata</i>	Cultivated mandarin MD2	150	33.87	37.74	40.91	SRR25409367	sequenced in this study	Chongqing, China
BTJ	Bingtangju	<i>C. reticulata</i>	Cultivated mandarin MD2	125	30.36	37.90	39.68	SRR3756893	Wang et al, 2017	Hubei Province, China
BYJ	Bayueju	<i>C. reticulata</i>	Cultivated mandarin MD2	150	38.95	38.65	40.19	SRR25409366	sequenced in this study	Guangdong Province, China
CTJ	Chutianju	<i>C. reticulata</i>	Cultivated mandarin MD2	150	34.15	37.10	40.55	SRR25409365	sequenced in this study	Guangdong Province, China

CZG	Chachigan	<i>C. reticulata</i>	Cultivated mandarin MD2	125	28.83	38.03	39.22	SRR3747583	Wang et al, 2018	Chongqing, China
HG	Hanggan	<i>C. reticulata</i>	Cultivated mandarin MD2	150	41.51	38.56	40.56	SRR25409364	sequenced in this study	Guangdong Province, China
MGJ	Manguju	<i>C. reticulata</i>	Cultivated mandarin MD2	150	35.31	38.36	40.65	SRR25409363	sequenced in this study	Chongqing, China
MLTJ	Mingliutianju	<i>C. reticulata</i>	Cultivated mandarin MD2	125	24.97	38.69	39.24	SRR3750679	Wang et al, 2018	Guangdong Province, China
MSJ	Mashuiju	<i>C. reticulata</i>	Cultivated mandarin MD2	125	26.37	38.89	39.20	SRR3751832	Wang et al, 2017	Hubei Province, China
NJ	Nianju	<i>C. reticulata</i>	Cultivated mandarin MD2	125	30.77	38.06	39.04	SRR3750668	Wang et al, 2018	Chongqing, China
STJ	Shatangju	<i>C. reticulata</i>	Cultivated mandarin MD2	125	30.33	39.51	38.73	SRR3756933	Wang et al, 2018	Chongqing, China
YNJ	Vietnamju	<i>C. reticulata</i>	Cultivated mandarin MD2	150	36.52	37.75	40.90	SRR25409362	sequenced in this study	Chongqing, China
YSJ	Yangshan mandarin	<i>C. reticulata</i>	Cultivated mandarin MD2	125	32.29	37.81	39.55	SRR3750648	Wang et al, 2018	Guangdong Province, China
ZSJ	Zhushaju	<i>C. reticulata</i>	Cultivated mandarin MD2	150	39.68	37.61	40.27	SRR25409361	sequenced in this study	Chongqing, China
AJJ	Aijiju	<i>C. reticulata</i>	Mandarin hybrid	150	36.50	37.43	40.61	SRR25409360	sequenced in this study	Chongqing, China
BZH	Buzhihuo	<i>C. reticulata</i>	Mandarin hybrid	150	18.67	36.83	41.81	SRR25409359	sequenced in this study	Hubei Province, China
CLM	Clementin	<i>C. reticulata</i>	Mandarin hybrid	100	117.39	35.05	40.52	SRR5807898	Wu et al, 2018	Hubei Province, China
FC	Fairchild	<i>C. reticulata</i>	Mandarin hybrid	150	36.80	37.42	41.14	SRR25409358	sequenced in this study	Chongqing, China
GG	Gonggan	<i>C. reticulata</i>	Mandarin hybrid	150	35.27	37.91	41.68	SRR25409356	sequenced in this study	Guangxi Province, China

JG	Jiaogan	<i>C. reticulata</i>	Mandarin hybrid	150	42.49	38.04	41.50	SRR25409355	sequenced in this study	Chongqing, China
MLG	Moluogesianju	<i>C. reticulata</i>	Mandarin hybrid	150	33.22	37.81	41.09	SRR25409354	sequenced in this study	Chongqing, China
Ota	Ortanique tangor	<i>C. reticulata</i>	Mandarin hybrid	150	37.19	37.51	41.79	SRR25409353	sequenced in this study	Hubei Province, China
QH117	Qihui	<i>C. reticulata</i>	Mandarin hybrid	150	39.48	37.62	40.12	SRR3822244	Wang et al, 2017	Hubei Province, China
SM	Satsuma Mandarin	<i>C. unshiu</i>	Mandarin hybrid	90	38.77	36.97	39.99	SRR5807909	Wang et al, 2018	Hubei Province, China
GMZ	Guangmingzao	<i>C. unshiu</i>	Mandarin hybrid	150	34.05	37.22	41.98	SRR25409352	sequenced in this study	Hubei Province, China
RN1	Rinan-1 Satsuma	<i>C. unshiu</i>	Mandarin hybrid	150	38.81	36.95	42.05	SRR25409351	sequenced in this study	Hubei Province, China
WLK	Wilking	<i>C. reticulata</i>	Mandarin hybrid	100	26.47	38.69	38.97	SRR3820551	Wang et al, 2017	Hubei Province, China
WMCot	W-Mcot	<i>C. reticulata</i>	Mandarin hybrid	150	38.52	38.20	41.07	SRR25409350	sequenced in this study	Hubei Province, China
YCLM	MA-10	<i>C. reticulata</i>	Mandarin hybrid	150	42.23	37.85	40.34	SRR25409349	sequenced in this study	Hubei Province, China
ZYJ	Zhuanyouju	<i>C. reticulata</i>	Mandarin hybrid	150	31.41	38.39	41.04	SRR25409348	sequenced in this study	Chongqing, China
HGG	Huangguogan	<i>C. reticulata</i>	Mandarin hybrid	150	44.47	38.06	42.89	SRR25409347	sequenced in this study	Chongqing, China
HPJ	Daoxian huapi	<i>C. reticulata</i>	domesticated mandarin	100	21.76	38.22	38.19	SRR3750611	Wang et al, 2017	Hubei Province, China
8L	Tachibana Mandarin	<i>C. reticulata</i>	Wild mandarin	90	35.86	39.30	38.18	SRR3747335	Wang et al, 2017	Chongqing, China
CYY	Chongyi wild mandarin	<i>C. reticulata</i>	Wild mandarin	100	22.72	36.87	38.67	SRR3747399	Wang et al, 2017	Jiangxi Province, China

DX4	Daoxian wild mandarin	<i>C. reticulata</i>	Wild mandarin	90	35.50	37.57	38.47	SRR5796645	Wang et al, 2018	Hubei Province, China
JYY	Jiangyong wild mandarin	<i>C. reticulata</i>	Wild mandarin	150	44.88	37.07	40.63	SRR5796862	Wang et al, 2018	Hubei Province, China
MS1	Mangshan wild mandarin	<i>C. reticulata</i>	Wild mandarin	90	35.21	37.72	38.41	SRR5796818	Wang et al, 2018	Hubei Province, China
BPJ	Bianpingju	<i>C. reticulata</i>	Mandarin unclassified	150	41.65	37.73	40.25	SRR25409345	sequenced in this study	Chongqing, China
CX SJ	Cengxisuanju	<i>C. reticulata</i>	Mandarin unclassified	150	36.91	37.37	40.56	SRR25409344	sequenced in this study	Guangxi Province, China
GHSJ	Guihusuanju	<i>C. reticulata</i>	Mandarin unclassified	150	41.08	38.47	40.05	SRR25409343	sequenced in this study	Guangdong Province, China
MBMJ	Mabimiju	<i>C. reticulata</i>	Mandarin unclassified	150	35.20	37.63	40.34	SRR25409342	sequenced in this study	Chongqing, China
MSJ2	Mashiju	<i>C. reticulata</i>	Mandarin unclassified	150	31.33	37.57	40.43	SRR25409341	sequenced in this study	Chongqing, China
SCM	Sun Chu Sha Kat	<i>C. reticulata</i>	Mandarin unclassified	100	39.43	35.38	39.39	SRR6188448	Wu et al, 2018	Chongqing, China
SJ	Suanju	<i>C. reticulata</i>	Mandarin unclassified	150	35.36	37.44	40.36	SRR25409340	sequenced in this study	Chongqing, China
STSJ	Shantousuanju	<i>C. reticulata</i>	Mandarin unclassified	150	36.10	37.65	40.44	SRR25409339	sequenced in this study	Chongqing, China
CHZG	Chaozhougan	<i>C. reticulata</i>	Mandarin unclassified	150	30.94	37.65	40.58	SRR25409338	sequenced in this study	Chongqing, China
GSJ	Gongsunju	<i>C. reticulata</i>	Mandarin unclassified	150	31.81	37.64	40.93	SRR25409337	sequenced in this study	Hunan Province, China
10Z	Zipi Pummelo	<i>C. maxima</i>	Pummelo	90	32.18	37.34	43.75	SRR3823645	Wang et al, 2017	Hubei Province, China
28H	Huazhoujuhong	<i>C. maxima</i>	Pummelo	90	37.74	37.53	43.52	SRR3823225	Wang et al, 2017	Guangxi Province, China

CHP	Chandler	<i>C. maxima</i>	Pummelo	100	26.11	36.30	44.64	SRR1023627	Wu et al, 2014	Hubei Province, China
DGH	Daguohong Pummelo	<i>C. maxima</i>	Pummelo	150	34.38	37.77	45.99	SRR25409048	sequenced in this study	Hunan Province, China
DJY	Dianjiang red Pummelo	<i>C. maxima</i>	Pummelo	150	42.12	38.91	45.77	SRR25409047	sequenced in this study	Chongqing, China
FCY	Feicui Pummelo	<i>C. maxima</i>	Pummelo	150	43.54	39.06	45.91	SRR25409044	sequenced in this study	Zhejiang Province, China
FHY	Fenghuang Pummelo	<i>C. maxima</i>	Pummelo	150	33.78	37.20	48.28	SRR25409043	sequenced in this study	Hubei Province, China
GBY	Kaopan Pummelo	<i>C. maxima</i>	Pummelo	125	29.04	37.66	45.72	SRR3823447	Wang et al, 2017	Chongqing, China
GXY	Guanximi Pummelo	<i>C. maxima</i>	Pummelo	90	37.74	37.52	43.84	SRR5802549	Wang et al, 2018	Chongqing, China
GY-1	Gui-1 Pummelo	<i>C. maxima</i>	Pummelo	150	40.03	37.32	46.32		Liang et al, 2020	Guangxi Province, China
HB	HB Pummelo	<i>C. maxima</i>	Pummelo	150	41.83	37.34	46.03	SRR9127779	Liang et al, 2020	Hubei Province, China
HNHY	Huanonghong Pummelo	<i>C. maxima</i>	Pummelo	125	30.31	37.62	45.13	SRR3823230	Wang et al, 2017	Hubei Province, China
HSY	Suan hongrou Pummelo	<i>C. maxima</i>	Pummelo	150	34.84	37.85	46.09	SRR25409042	sequenced in this study	Guangxi Province, China
JXY	Jinxiang Pummelo	<i>C. maxima</i>	Pummelo	150	45.74	38.51	44.46	SRR25409041	sequenced in this study	Chongqing, China
LPY	Liangping Pummelo	<i>C. maxima</i>	Pummelo	150	33.24	37.35	48.23	SRR25409040	sequenced in this study	Chongqing, China
PSY	Pingshan Pummelo	<i>C. maxima</i>	Pummelo	150	38.80	37.36	46.14	SRR25409039	sequenced in this study	Chongqing, China
RGXY	Red Guanxi Pummelo	<i>C. maxima</i>	Pummelo	150	44.77	38.42	45.75	SRR25409038	sequenced in this study	Chongqing, China
SJP	Sijipao Pummelo	<i>C. maxima</i>	Pummelo	150	36.63	37.54	45.97	SRR25409037	sequenced in this study	Chongqing, China

SR3-2	Majia Pummelo	<i>C. maxima</i>	Pummelo	125	28.15	37.94	44.88	SRR3822290	Wang et al, 2017	Jiangxi Province, China
STY	Shatian Pummelo	<i>C. maxima</i>	Pummelo	100	35.06	44.43	42.86	SRR5796631	Wang et al, 2017	Chongqing, China
SYBS	Suanyou In Baishazhen	<i>C. maxima</i>	Pummelo	125	30.24	38.27	45.04	SRR3844987	Wang et al, 2017	Guangxi Province, China
WBY	Wanbai Pummelo	<i>C. maxima</i>	Pummelo	125	34.11	38.06	45.01	SRR3823251	Wang et al, 2017	Chongqing, China
WSY	Acidless Pummelo	<i>C. maxima</i>	Pummelo	100	32.37	42.26	43.53	SRR5796633	Wang et al, 2017	Hubei Province, China
YGXY	Yellow Guanxi Pummelo	<i>C. maxima</i>	Pummelo	150	43.82	38.16	45.88	SRR25409046	sequenced in this study	Chongqing, China
YHY	Yuhuan Pummelo	<i>C. maxima</i>	Pummelo	150	38.72	37.55	46.41	SRR25409045	sequenced in this study	Chongqing, China
YNMD	Yunnanmiandian	<i>C. maxima</i>	Pummelo	150	28.86	36.65	46.16		Liang et al, 2020	Yunnan Province, China
YNSJ	Yunnanshuijing Pummelo	<i>C. maxima</i>	Pummelo	150	47.39	38.02	47.31	SRR9127776	Liang et al, 2020	Yunnan Province, China
HP	Huangpi Sour orange	<i>C. aurantium</i>	Sour orange	150	21.38	39.32	40.29	SRR25394378	sequenced in this study	Chongqing, China
BH	Bianhong lemon	<i>C. aurantium</i>	Sour orange	150	27.30	37.67	43.09	SRR9127844	Liang et al, 2020	Chongqing, China
DD	Daidai	<i>C. aurantium</i>	Sour orange	90	36.77	37.64	40.89	SRR3885049	Wang et al, 2017	Hubei Province, China
DGTC	Dagoutoucheng	<i>C. aurantium</i>	Sour orange	150	18.59	36.83	43.05	SRR9127839	Liang et al, 2020	Chongqing, China
GC	Gaocheng	<i>C. aurantium</i>	Sour orange	150	20.87	36.37	43.33	SRR25394377	sequenced in this study	Chongqing, China
GP	Guangpi Sour orange	<i>C. aurantium</i>	Sour orange	150	28.54	38.06	42.67	SRR9127856	Liang et al, 2020	Chongqing, China
HTG	Hutougan	<i>C. aurantium</i>	Sour orange	150	48.37	37.56	42.22	SRR25394376	sequenced in this study	Hubei Province, China
HZL	Zhuluanhongguo	<i>C. aurantium</i>	Sour orange	150	28.00	37.87	42.45	SRR9127851	Liang et al, 2020	Chongqing, China
LHE	Lianhe Sour orange	<i>C. aurantium</i>	Sour orange	150	32.60	37.56	43.20	SRR25394375	sequenced in this study	Chongqing, China

13X	Blood Orange	<i>C. sinensis</i>	Sweet orange	90	29.85	37.06	40.35	SRR3884813	Wang et al, 2017	Chongqing, China
29B	Bingtangcheng	<i>C. sinensis</i>	Sweet orange	90	36.34	39.77	39.84	SRR3926732	Wang et al, 2017	Chongqing, China
AJTC	Succari	<i>C. sinensis</i>	Sweet orange	150	44.09	37.34	42.49	SRR10321654	Wang et al, 2021	Chongqing, China
AL	Anliu Sweet orange	<i>C. sinensis</i>	Sweet orange	125	30.69	38.44	41.14	SRR3883626	Wang et al, 2017	Hubei Province, China
BuDD	BuDD blood orange	<i>C. sinensis</i>	Sweet orange	150	43.50	38.22	42.32	SRR25408882	sequenced in this study	Hubei Province, China
DH2	Dahongtiancheng	<i>C. sinensis</i>	Sweet orange	125	35.70	39.33	41.07	SRR5801193	Wang et al, 2021	Chongqing, China
HAL	Honganliu	<i>C. sinensis</i>	Sweet orange	150	46.99	41.09	41.91	SRR5801703	Wang et al, 2021	Hubei Province, China
HML	Hamlin Sweet orange	<i>C. sinensis</i>	Sweet orange	125	26.22	40.72	40.49	SRR3883647	Wang et al, 2017	Chongqing, China
HRQC	Caracara	<i>C. sinensis</i>	Sweet orange	150	53.48	41.49	41.91	SRR5801917	Wang et al, 2021	Hubei Province, China
JC	Jincheng	<i>C. sinensis</i>	Sweet orange	125	29.53	37.57	41.55	SRR3884491	Wang et al, 2017	Hubei Province, China
LQ	Robertson navel orange	<i>C. sinensis</i>	Sweet orange	90	35.76	36.88	40.43	SRR3884773	Wang et al, 2017	Chongqing, China
NHE	Newhall navel orange	<i>C. sinensis</i>	Sweet orange	150	38.29	37.10	41.94	SRR3927459	Wang et al, 2017	Hubei Province, China
SO3	Valencia Orange	<i>C. sinensis</i>	Sweet orange	90	55.46	37.34	40.37	SRR5799051	Wang et al, 2017	Hubei Province, China
ZJ	Zaojin Sweet orange	<i>C. sinensis</i>	Sweet orange	150	50.38	38.70	42.15	SRR25408881	sequenced in this study	Hubei Province, China
FS	Buddha'S Hand	<i>C. medica</i>	Citron	100	29.03	37.65	35.81	SRR3948163	Wang et al, 2017	Hubei Province, China
JY	Citron	<i>C. medica</i>	Citron	90	35.90	37.21	35.83	SRR3938734	Wang et al, 2017	Yunnan Province, China
14J	Coctail Grapefruit	<i>C. maxima</i>	Grapefruit	90	36.39	36.91	41.30	SRR3926757	Wang et al, 2017	Hubei Province, China

Flame	Flame grapefruit	<i>C. maxima</i>	Grapefruit	100	28.82	41.40	41.37	SRR3927405	Wang et al, 2017	Hubei Province, China
HY	Huyou	<i>C. maxima</i>	Grapefruit	150	28.55	38.77	42.03	SRR25609456	Data waiting for release	Chongqing, China
PAR	Marsh grapefruit	<i>C. maxima</i>	Grapefruit	100	107.26	32.25	43.40	SRR6188447	Wu et al, 2018	Hubei Province, China
Ruby	Star Ruby grapefruit	<i>C. maxima</i>	Grapefruit	100	30.81	39.49	41.94	SRR3927447	Wang et al, 2017	Hubei Province, China
BJ	Beijing lemon	<i>C. limon</i>	Lemon	150	37.01	37.65	39.60		Liang et al, 2020	Yunnan Province, China
CNM	Rough lemon	<i>C. limon</i>	Lemon	150	46.47	38.13	38.68	SRR25409056	sequenced in this study	Hubei Province, China
HYNM	Huaye lemon	<i>C. limon</i>	Lemon	150	50.45	38.55	39.92	SRR25409055	sequenced in this study	Hubei Province, China
ML	Muli	<i>C. limon</i>	Lemon	90	35.82	37.04	38.63		Liang et al, 2020	Chongqing, China
TNM	Tu lemon	<i>C. limon</i>	Lemon	150	35.61	36.85	39.00	SRR25409054	sequenced in this study	Guangdong Province, China
XSNM	Xiangshui lemon	<i>C. limon</i>	Lemon	150	33.16	37.33	38.22	SRR25409053	sequenced in this study	Yunnan Province, China
YLK	Eureka Lemon	<i>C. limon</i>	Lemon	125	34.63	40.58	38.45	SRR3952134	Wang et al, 2017	Hubei Province, China

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5. Liang, M. et al. (2020). Evolution of self-compatibility by a mutant Sm-RNase in citrus. *Nature Plants* 6:131–142.
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Table S2. Information on carotenoids and carotenoid derivatives.

No.	Putative component name	Level ^a
Comp1	(11cis,13cis,13'cis)-1,2,7,7',8,8',11',12'-Octahydro-1,2-epoxy-psi,psi-carotene	B
Comp2	1,2,7,7',8,8',11',12'-Octahydro-psi,psi-caroten-1-ol-isomer	B
Comp3	10'-Apo- β -carotene-isomer2	B
Comp4	1-Methoxy-1,2,7',8',11',12'-hexahydro-psi,psi-carotene	B
Comp5	3'-Hydroxyechinenone/3'-OH-Echinenone	B
Comp6	3'-Hydroxyechinenone/3'-OH-Echinenone-isomer	B
Comp7	4,4'-Diapolycopene	B
Comp8	4_4'-diapophytoene	B
Comp9	4_4'-Diapophytoene-isomer2	B
Comp10	4_4'-Diapophytoene-isomer3	B
Comp11	Phytofluene	A
Comp12	Phytofluene-isomer	B
Comp13	Phytoene	A
Comp14	Phytoene-isomer	B
Comp15	Phytoene-isomer2	B
Comp16	Phytoene-isomer3	B
Comp17	Phytoene-isomer4	B
Comp18	α -Carotene	A
Comp19	All-trans axerophthene-isomer1	B
Comp20	All-trans axerophthene-isomer2	B
Comp21	All-Trans-3,4-Didehydrolycopene	B
Comp22	All-Trans-3,4-Didehydrolycopene-isomer	B
Comp23	All-Trans-3,5-Didehydrolycopene-isomer2	B
Comp24	All-Trans-3,6-Didehydrolycopene-isomer3	B
Comp25	All-Trans-3,7-Didehydrolycopene-isomer4	B
Comp26	All-Trans-3,8-Didehydrolycopene-isomer5	B
Comp27	Alpha-Zeacarotene	B
Comp28	Alpha-Zeacarotene-isomer	B
Comp29	Alpha-Zeacarotene-isomer2	B
Comp30	Alpha-Zeacarotene-isomer3	B
Comp31	Alpha-Zeacarotene-isomer4	B
Comp32	Antheraxanthin	A
Comp33	Antheraxanthin-isomer3	B
Comp34	Apo-10'-zeaxanthin	B
Comp35	APO-11-zeaxanthin	B
Comp36	APO-12'-capsorubin-isomer	B
Comp37	APO-9-zeaxanthinone-isomer	B
Comp38	β -Carotene	A
Comp39	β -Cryptoxanthin	A
Comp40	β -Ionene	B
Comp41	Bisdehydrolycopene/ Tetradehydrolycopene	B
Comp42	Bisdehydrolycopene/ Tetradehydrolycopene-isomer	B
Comp43	Citranaxanthin-isomer	B
Comp44	δ -Carotene	A

Comp45	Dihydrospheroidene/Methoxyneurosporene	B
Comp46	Dihydrospheroidene/Methoxyneurosporene-isomer	B
Comp47	Dihydrospheroidene/Methoxyneurosporene-isomer2	B
Comp48	Echinenone/(Myxoxanthin)-isomer1	B
Comp49	Echinenone/(Myxoxanthin)-isomer2	B
Comp50	γ -Carotene	A
Comp51	Ionene-isomer	B
Comp52	Lactucaxanthin-isomer1	B
Comp53	Lactucaxanthin-isomer2	B
Comp54	Lutein-H2O	A
Comp55	Lycopene	A
Comp56	Neoxanthin-isomer	B
Comp57	Violaxanthin	A
Comp58	Violaxanthin-isomer	B
Comp59	Zeaxanthin	A
Comp60	Zeaxanthin-isomer	B
Comp61	Zeinoxanthin	A
Comp62	ζ -Carotene	B
Comp63	ζ -Carotene-isomer	B
Comp64	ζ -Carotene-isomer2	B
Comp65	ζ -Carotene-isomer3	B

^a: Level of identification. (A) standard; (B) Public databases and MS/MS.

Table S3. The proportion level of β -cryptoxanthin in citrus accessions.

Accession	Common name	Category	Proportion Level of β -Cryptoxanthin	Ratio of β -Cryptoxanthin to Violaxanthin
FS	Buddha'S Hand	Citron	Low	0.00
JY	Citron	Citron	Low	0.00
14J	Coctail Grapefruit	Grapefruit	Low	0.05
Flame	Flame grapefruit	Grapefruit	Low	0.00
HY	Huyou	Grapefruit	Low	0.08
PAR	Marsh grapefruit	Grapefruit	Low	0.00
Ruby	Star Ruby grapefruit	Grapefruit	Low	0.00
BJ	Beijing lemon	Lemon	Low	0.00
CNM	Rough lemmon	Lemon	Low	0.00
HYNM	Huaye lemon	Lemon	Low	0.00
ML	Muli	Lemon	Low	0.00
TNM	Tu lemmon	Lemon	High	14.01
XSNM	Xiangshui lemmon	Lemon	Low	0.00
YLK	Eureka Lemon	Lemon	Low	0.00
18H	Red Tangerine	Cultivated mandarin MD1	High	1.73
19P	Ponkan	Cultivated mandarin MD1	High	3.39
20H	Bendizao	Cultivated mandarin MD1	High	2.24
AJHJ	Anjianghongju	Cultivated mandarin MD1	High	1.33
BJM	Baiju	Cultivated mandarin MD1	High	3.49
CH	Chihong	Cultivated mandarin MD1	High	1.41
CSNJ	Changshananju	Cultivated mandarin MD1	High	1.60
DFHP	Dafeng Huangpiju	Cultivated mandarin MD1	High	3.30
DHP	Dahongpao	Cultivated mandarin MD1	High	2.13
DWJ	Diwangju	Cultivated mandarin MD1	High	2.84
EDXG	Edangxianggan	Cultivated mandarin MD1	High	4.07
FDJ	Fengdongju	Cultivated mandarin MD1	High	4.51
FJ	Fuju	Cultivated mandarin MD1	High	1.72
GJ	Guangju	Cultivated mandarin MD1	High	8.81
GJ1	Guiju-1	Cultivated mandarin MD1	High	1.43

GMZ	Guangmingzao	Cultivated mandarin MD1	High	9.65
HG2	Huagan-2	Cultivated mandarin MD1	High	2.37
HLM	Huanglinmiao	Cultivated mandarin MD1	High	2.71
HYBDZ	Huangyan Bendizao	Cultivated mandarin MD1	High	1.78
JGA	Jiangan	Cultivated mandarin MD1	High	1.38
LH	Liaohong	Cultivated mandarin MD1	High	1.24
MJ	Manju	Cultivated mandarin MD1	High	3.21
MTH	Mantouhong	Cultivated mandarin MD1	High	1.87
N8005	Tiqie mandarin	Cultivated mandarin MD1	High	4.76
NFJ	Nanfengmiju	Cultivated mandarin MD1	High	3.00
NRH	Niurouhong	Cultivated mandarin MD1	High	1.42
OG	Ougan	Cultivated mandarin MD1	Low	0.56
QHJ	Qinghongju	Cultivated mandarin MD1	High	1.46
QJPG	Qingjiang Ponkan	Cultivated mandarin MD1	High	3.87
RH	Sunki	Cultivated mandarin MD1	High	1.72
RJ	Ruju	Cultivated mandarin MD1	High	2.39
RN1	Rinan-1 Satsuma	Cultivated mandarin MD1	High	7.11
SH	Suhong	Cultivated mandarin MD1	High	1.08
TJ	Tu mandarin	Cultivated mandarin MD1	High	4.85
TT	Taitian Ponkan	Cultivated mandarin MD1	High	2.08
WGD	Wuganda mandairn	Cultivated mandarin MD1	High	3.50
WHPG	Seedless Ponkan	Cultivated mandarin MD1	High	2.59
XNPG	Xinnv Ponkan	Cultivated mandarin MD1	High	5.88
XYMJ	Xinyumiju	Cultivated mandarin MD1	High	3.64
YJNJ	Yuanjiangnanju	Cultivated mandarin MD1	High	1.38
ZHJ	Zhuhongju	Cultivated mandarin MD1	High	1.78
BG	Biangan	Cultivated mandarin MD2	Low	0.73
BTJ	Bingtangju	Cultivated mandarin MD2	High	1.61
BYJ	Bayueju	Cultivated mandarin MD2	Low	0.32
CTJ	Chutianju	Cultivated mandarin MD2	Low	0.21
CZG	Chachigan	Cultivated mandarin MD2	High	6.42

HG	Hanggan	Cultivated mandarin MD2	Low	0.36
MGJ	Manguju	Cultivated mandarin MD2	Low	0.48
MLTJ	Mingliutianju	Cultivated mandarin MD2	Low	0.24
MSJ	Mashuiju	Cultivated mandarin MD2	Low	0.27
NJ	Nianju	Cultivated mandarin MD2	Low	0.28
STJ	Shatangju	Cultivated mandarin MD2	Low	0.29
YNJ	Vietnamju	Cultivated mandarin MD2	Low	0.50
YSJ	Yangshan mandarin	Cultivated mandarin MD2	Low	0.19
ZSJ	Zhushaju	Cultivated mandarin MD2	High	2.10
AJJ	Aijiju	Mandarin hybrid	High	5.34
BZH	Buzhihuo	Mandarin hybrid	High	1.91
CLM	Clementin	Mandarin hybrid	High	2.40
FC	Fairchild	Mandarin hybrid	High	3.01
GG	Gonggan	Mandarin hybrid	Low	0.06
JG	Jiaogan	Mandarin hybrid	Low	0.43
MLG	Moluogesuanju	Mandarin hybrid	High	2.65
Ota	Ortanique tangor	Mandarin hybrid	Low	0.27
QH117	Qihui	Mandarin hybrid	High	2.11
SM	Satsuma Mandarin	Mandarin hybrid	High	6.88
WLK	Wilking	Mandarin hybrid	Low	0.24
WMCot	W-Mcot	Mandarin hybrid	High	2.75
YCLM	MA-10	Mandarin hybrid	High	4.51
ZYJ	Zhuanyouju	Mandarin hybrid	High	1.41
BPJ	Bianpingju	Mandarin unclassified	High	5.57
CXSJ	Cengxisuanju	Mandarin unclassified	High	2.94
GHSJ	Guihusuanju	Mandarin unclassified	High	1.82
MBMJ	Mabimiju	Mandarin unclassified	High	6.23
MSJ2	Mashiju	Mandarin unclassified	High	2.03
SCM	Sun Chu Sha Kat	Mandarin unclassified	High	1.18
SJ	Suanju	Mandarin unclassified	High	3.93
STSJ	Shantousuanju	Mandarin unclassified	High	2.29

HPJ	Daoxian huapi	Semi domesticated mandarin	High	4.20
8L	Tachibana Mandarin	Wild mandarin	Low	0.03
CYY	Chongyi wild mandarin	Wild mandarin	High	4.47
DX4	Daoxian wild mandarin	Wild mandarin	High	3.62
JYY	Jiangyong wild mandarin	Wild mandarin	High	8.45
MS1	Mangshan wild mandarin	Wild mandarin	High	4.32
CHZG	Chaozhogan	Mandarin unclassified	High	0.84
G SJ	Gongsunju	Mandarin unclassified	Low	0.65
10Z	Zipi Pummelo	Pummelo	Low	0.00
28H	Huazhoujuhong	Pummelo	Low	0.00
CHP	Chandler	Pummelo	Low	0.00
DGH	Daguohong Pummelo	Pummelo	Low	0.00
DJY	Dianjiang red Pummelo	Pummelo	Low	0.00
FCY	Feicui Pummelo	Pummelo	Low	0.00
FHY	Fenghuang Pummelo	Pummelo	Low	0.00
GBY	Kaopan Pummelo	Pummelo	Low	0.00
GXY	Guanximi Pummelo	Pummelo	Low	0.00
GY-1	Gui-1 Pummelo	Pummelo	Low	0.00
HB	HB Pummelo	Pummelo	Low	0.00
HNHY	Huanonghong Pummelo	Pummelo	Low	0.00
HSY	Suan hongrou Pummelo	Pummelo	Low	0.00
JXY	Jinxiang Pummelo	Pummelo	Low	0.00
LPY	Liangping Pummelo	Pummelo	Low	0.00
PSY	Pingshan Pummelo	Pummelo	Low	0.00
RGXY	Red Guanxi Pummelo	Pummelo	Low	0.00
SJP	Sijipao Pummelo	Pummelo	Low	0.00
SR3-2	Majia Pummelo	Pummelo	Low	0.00
STY	Shatian Pummelo	Pummelo	Low	0.00
SYBS	Suanyou In Baishazhen	Pummelo	Low	0.00
WBY	Wanbai Pummelo	Pummelo	Low	0.00
WSY	Acidless Pummelo	Pummelo	Low	0.00

YGXY	Yellow Guanxi Pummelo	Pummelo	Low	0.00
YHY	Yuhuan Pummelo	Pummelo	Low	0.00
YNMD	Yunnanmiandian	Pummelo	Low	0.00
YNSJ	Yunnanshuijing Pummelo	Pummelo	Low	0.00
HP	Huangpi Sour orange	Unclassified	Low	0.11
HGG	Huangguogan	Mandarin hybrid	Low	0.42
BH	Bianhong lemon	Sour orange	Low	0.10
DD	Daidai	Sour orange	High	3.60
DGTC	Dagoutoucheng	Sour orange	Low	0.74
GC	Gaocheng	Sour orange	Low	0.10
GP	Guangpi Sour orange	Sour orange	Low	0.19
HTG	Hutougan	Sour orange	Low	0.37
HZL	Zhuluanhongguo	Sour orange	Low	0.22
LHE	lianhe Sour orange	Sour orange	Low	0.76
13X	Blood Orange	Sweet orange	Low	0.38
29B	Bingtangcheng	Sweet orange	Low	0.09
AJTC	Aijitangcheng	Sweet orange	Low	0.05
AL	Anliu Sweet orange	Sweet orange	Low	0.09
BuDD	BuDD blood orange	Sweet orange	Low	0.17
DH2	Dahongtiancheng	Sweet orange	Low	0.09
HAL	Honganliu	Sweet orange	Low	0.17
HML	Hamlin Sweet orange	Sweet orange	Low	0.09
HRQC	Caracara	Sweet orange	Low	0.16
JC	Jincheng	Sweet orange	Low	0.09
LQ	Robertson navel orange	Sweet orange	Low	0.17
NHE	Newhall navel orange	Sweet orange	Low	0.17
SO3	Valencia Orange	Sweet orange	Low	0.52
ZJ	Zaojin Sweet orange	Sweet orange	Low	0.07

Table S4. Annotation of proteins encoded by candidate genes.

ID	Annotation
Cg6g012040	Pfam: FAR1 DNA-binding domain; PANTHER: Protein FAR1-related sequence 10-related
Cg6g012050	Pfam: FAR1 DNA-binding domain; PANTHER: Protein FAR1-related sequence 10-related
Cg6g012060	Pfam: Cytochrome P450; PANTHER: Cytochrome P450 97B3
Cg6g012070	Pfam: VQ motif; PANTHER: VQ motif-containing protein 2
Cg6g012080	Pfam: Pectinesterase 1; PANTHER: Pectinesterase 8-related 1

Table S5. CYP97 family homologs from other plants.

Name	Accession ID in NCBI
At-CYP97A3	AAL08302
Dc-CYP97A3	JQ655297
Os-CYP97A4	EEC74248.1
Mt-CYP97A10	ABD28565.1
Sl-CYP97A29	ACJ25969
Rc-CYP97A	XP_002512609.1
OS-CYP97A4	AK068163
Ps-CYP97B1	CAA89260
Gm-CYP97B2	AAB94586
At-CYP97B3	CAB10290
OS-CYP97B4	AK100596
At-CYP97C1	AAM13903
Dc-CYP97C1	ABB52076
Os-CYP97C2	AAK20054
Mt-CYP97C10	ABC59096
Sl-CYP97C11	ACJ25968
Rc-CYP97C	XP_002519427.1

Table S6. Haplotypes and SV types of the *CitCYP97B* promoter in *Citrus* accessions used in this study.

Accession	Genotypes	Haplotypes	SV type of alleles		SNP16	SNP15	SNP14	SNP10	SNP9	SNP8	SNP7	SNP6	SNP5	SNP4	SNP3	SNP2	SNP1
18H	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
19P	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
20H	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
BJM	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
BZH	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
CHZG	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
CSNJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
CXSJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
DFHP	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
DHP	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
DWJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
EDXG	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
FC	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
FDJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
FJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
GHSJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
GJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
GJ1	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
GMZ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
HG2	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
HLM	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
HPJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
HYBDZ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
JGA	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
MBMJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
MJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
MLG	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
MS1	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
MSJ2	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T

MTH	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
N8005	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
NFJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
QH117	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
QHJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
QJPG	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
RH	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
RJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
RN1	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
SCM	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
SH	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
SJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
SM	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
STSJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
TJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
TT	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
WGD	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
WHPG	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
WMCot	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
XNPG	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
XYMJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
YJNJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
ZYJ	Geno.1	Hap.1/Hap.1	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
10Z	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
28H	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
CHP	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
DGH	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
DJY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
FCY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
FHY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
GBY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C

GXY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
GY-1	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
HB	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
HNHY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
HSY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
HY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
JXY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
LPY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
PSY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
RGXY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
SJP	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
SR3-2	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
STY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
SYBS	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
WBY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
WSY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
YGXY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
YHY	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
YNMD	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
YNSJ	Geno.2	Hap.3/Hap.3	/	/	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
FS	Geno.3	Hap.6/Hap.6	515 bp Insertion	515 bp Insertion	A/A	T/T	C/C	T/T	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
JY	Geno.3	Hap.6/Hap.6	515 bp Insertion	515 bp Insertion	A/A	T/T	C/C	T/T	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
XSNM	Geno.3	Hap.6/Hap.6	515 bp Insertion	515 bp Insertion	A/A	T/T	C/C	T/T	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
BG	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
BYJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
CTJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HG	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
JG	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
MGJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
MLTJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
MSJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C

NJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
STJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
YNJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
YSJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
ZSJ	Geno.4	Hap.1/Hap.4	/	133 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
13X	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
29B	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
AJTC	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
AL	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
BuDD	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
DH2	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
Flame	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HAL	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HML	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HRQC	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
JC	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
LQ	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
NHE	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HTG	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
Ota	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
Ruby	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
SO3	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
ZJ	Geno.5	Hap.1/Hap.5	/	335 bp Insertion	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
14J	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
BH	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
BTJ	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
DD	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
DGTC	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
GC	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HGG	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HZL	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C

LHE	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
OG	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
PAR	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
WLK	Geno.6	Hap.1/Hap.3	/	/	G/A	C/T	C/T	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
CNM	Geno.7	Hap.1/Hap.6	/	515 bp Insertion	G/A	C/T	C/C	T/T	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HYNM	Geno.7	Hap.1/Hap.6	/	515 bp Insertion	G/A	C/T	C/C	T/T	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
TNM	Geno.7	Hap.1/Hap.6	/	515 bp Insertion	G/A	C/T	C/C	T/T	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
AJHJ	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
CH	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
CYY	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
DX4	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
JYY	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
LH	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
NRH	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
ZHJ	Geno.8	Hap.1/Hap.2	/	/	G/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
AJJ	Geno.9	Hap.1/Hap.7	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/A	G/A	A/G	A/G	T/C
CLM	Geno.9	Hap.1/Hap.7	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/A	G/A	A/G	A/G	T/C
CZG	Geno.9	Hap.1/Hap.7	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/A	G/A	A/G	A/G	T/C
YCLM	Geno.9	Hap.1/Hap.7	/	/	G/G	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/A	G/A	A/G	A/G	T/C
GG	Geno.10	Hap.4/Hap.5	133 bp Insertion	335 bp Insertion	A/A	T/T	T/T	G/G	G/G	A/A	C/C	A/A	A/A	A/A	G/G	G/G	C/C
BPJ	Geno.11	Hap.2/Hap.2	/	/	A/A	C/C	C/C	T/T	C/C	G/G	T/T	G/G	G/G	G/G	A/A	A/A	T/T
8L	Geno.12	Hap.2/Hap.8	/	/	A/A	C/T	C/C	T/T	C/C	G/A	T/T	G/G	G/A	G/A	A/G	A/A	T/T
BJ	Geno.13	Hap.2/Hap.6	/	515 bp Insertion	A/A	C/T	C/C	T/T	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
ML	Geno.14	Hap.6/Hap.9	515 bp Insertion	515 bp Insertion	G/A	C/T	C/C	T/T	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
YLK	Geno.15	Hap.1/Hap.10	/	/	G/A	C/T	C/C	T/T	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
GP	Geno.16	Hap.1/Hap.11	/	/	G/A	C/C	C/C	T/G	C/G	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
GSJ	Geno.17	Hap.1/Hap.12	/	/	G/A	C/T	C/T	T/T	C/C	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C
HP	Geno.17	Hap.1/Hap.12	/	/	G/A	C/T	C/T	T/T	C/C	G/A	T/C	G/A	G/A	G/A	A/G	A/G	T/C

Table S7. Primers used in this study.

Notes	Name	Primer sequences (5'-3')
Gene cloning	CitCYP97B-F	GTGGCTCGCTGGCCTTATT
	CitCYP97B-R	TACAGTCAGTGGACAGCCGA
	CitCYP97B-pro-F	AGTCATCATTATGGCGATGGGGTAAC
	CitCYP97B-pro-R	TGCAAGCCAAAATGCAATAAGGCC
	CitBCH1-F	TGTGGTCTGCGTCCATTTAA
	CitBCH1-R	TTTACGCTCACGCCATTA
	CitBCH2-F	ATGGCAAGTGGAATGTCATC
	CitBCH2-R	CAGTTGAGCCTTAATTTAGC
Marker for SV validation	CitCYP97B-pro-insert-F	CCCGGTGCTGTTGATTTTATACA
	CitCYP97B-pro-insert-R	CACTTCCATGTTCTGTATTTTGA
LUC vector construction	pGreen0800-CitCYP97B-pro-F	GGTCGACGGTATCGATAAGCTTAGTCATCATTATGGCGAT
	pGreen0800-CitCYP97B-pro-R	TTTATGTTTTTGGCGTCTTCCATGGTGCAAGCCAAAATGCAATAAGGCC
Subcellular localization vector construction	pRI121-CitCYP97B-F	TGTTGATACATATGCCCGTCGACATGGCTACTACAACAACCTGTATCTTTCATCA
	pRI121-CitCYP97B-R	TGCTCACCATGAATTCGGATCCGTGGACAGCCGATCTCTCCC
Prokaryotic expression vector construction	pRSFDuet-CitBCH1-F	CGGCGCGCCTGCAGGTCGACATGGCGGTCGGACTA
	pRSFDuet-CitBCH1-R	CATTATGCGGCCGCAAGCTTTTTTGGAAACCCTGTTGTATGATTTG
	pRSFDuet-CitBCH2-F	CGGCGCGCCTGCAGGTCGACATGGCAAGTGGAATGTCATCAGC
	pRSFDuet-CitBCH2-R	GCGGCCGCAAGCTTGTCGACCGTTTCTTTATCTAATCCTTCCGTGCCT
	pRSFDuet-CitCYP97B-F	GCGATCGCTGACGTCGGTACCATGTCTCCGTCTGTCAGA
	pRSFDuet-CitCYP97B-R	GCGGTTTCTTTACCAGACTCGAGGTGGACAGCCGATCTCTCCC
RNA interference and overexpression vector construction	Adapter-attB1-F	GGGGACAAGTTTGTACAAAAAAGCAGGCT
	Adapter-attB2-R	GGGGACCACTTTGTACAAGAAAGCTGGGT
	attB1-pHellgate8-CitCYP97B-F	AAAAAGCAGGCTTATCTCTTCAGCAGTTGGTTATGGC
	attB2-pHellgate8-CitCYP97B-R	AGAAAGCTGGGTTTGAACCAAGACTTCCGCCAC

Primers used for qRT-PCR

MTGB-CitCYP97B-F	AGTCCGGAGCTAGCTCTAGAATGGCTACTACAACAAC
MTGB-CitCYP97B-R	CCCTTGCTCACCATGGATCCGTGGACAGCCGATCTCTCCC
Actin-qPCR-F	CCAAGCAGCATGAAGATCAA
Actin-qPCR-R	ATCTGCTGGAAGGTGCTGAG
CitCYP97B-qPCR-F	ACCATACTTCTGGGACCGGC
CitCYP97B-qPCR-R	TGTTGCTCCAGTAACAAGTTCCAC
CrtB-qPCR-F	TGGATTCCCAGTGAAGAAGGTC
CrtB-qPCR-R	CATAATCTGCGCCATCATCAAG
GGPPS-qPCR-F	TAGAGTTCCTCAGTTACGCACAG
GGPPS-qPCR-R	GCCAGTTCTCTGTCTTTTGTATCC
PSY1-qPCR-F	CCCGGACTGCTGTGTTTAAT
PSY1-qPCR-R	GAGCAAGGATGCCTCAAATC
CRTISO-qPCR-F	TTCTTTCCATTACATGGGTGTT
CRTISO-qPCR-R	TCATCCTCAAGCACAAAATGGT
PDS-qPCR-F	ATAATTGGCGGACAGGCATA
PDS-qPCR-R	CCTCTGTGCTCACTCGATCA
ZDS-qPCR-F	ATCAGTGCTCGTTGTATGCTTACTATATT
ZDS-qPCR-R	CCCTTGAGCATCCGCAAT
LCYE-qPCR-F	CAACTGGATATTGAGGGCATCA
LCYE-qPCR-R	CAAGGAAACCGTGCCACATC
LCYB1-qPCR-F	GGCTATATGGTGGCAAGGACTT
LCYB1-qPCR-R	CAGAATTGAGGCTTCGAACGA
LCYB2-qPCR-F	CCCTATTTCCATTAGGCCGC
LCYB2-qPCR-R	CACGTCATATCGAATACGATC
BCH1-qPCR-F	TTTGGGATGGCCTACATGTTC
BCH1-qPCR-R	GGCACGTCGGCAATGG

BCH2-qPCR-F	TTTGGGCAAGGTGGGCTCATAG
BCH2-qPCR-R	GAGTCCTGGAACGATGCCTTTG
CYP97C1-qPCR-F	TCTATGTTAGTTGCGGGCCA
CYP97C1-qPCR-R	GGAGGATGTGGGTAGAGACG
CYP97A3-qPCR-F	AGAGGCGAAAGGGACAATCA
CYP97A3-qPCR-R	ACGCCATATCTCCCCATCTG
CCD4B-qPCR-F	CAGCAAGAAATTTGGAGTTG
CCD4B-qPCR-R	CGTAAAATCTTCTTGAGAC
ZEP-qPCR-F	GAAGCAATTCTTCGACGTGACA
ZEP-qPCR-R	ACCGAGTCCCCAAGCAAAGT
VDE-qPCR-F	GTACTGGCTTGCATGTTTTTGGTC
VDE-qPCR-R	GCCGATTGTTGCAGGTTTGA
