NEW INSIGHTS INTO THE PHYLOGENY AND SPECIATION OF KUMQUAT (*FORTUNELLA* SPP.) BASED ON CHLOROPLAST SNP, NUCLEAR SSR AND WHOLE-GENOME SEQUENCING

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SUPPLEMENTARY MATERIALS (Fig. S1–S5; Tables S1–S11)

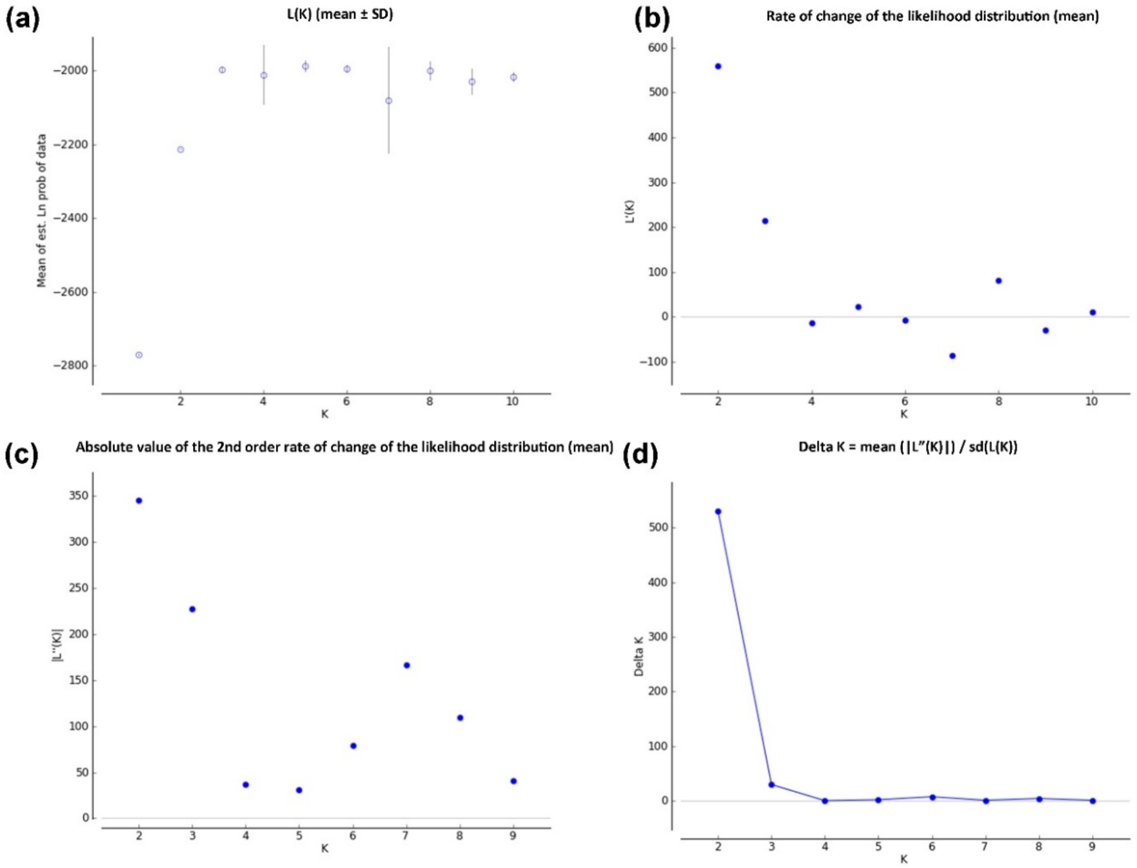

Fig. S1 Estimation of K value among the 34 *Fortunella* accessions using *Structure Harvester* based on nSSR data. Note: four *Fortunella* hybrids were excluded here. (a) The L(K) (mean likelihoods per K value), including standard deviation bars to display likelihood variance. (b) Rate of change of the likelihood distribution (mean) calculated as $L'(K) = L(K) - L(K-1)$. (c) Absolute values of the second order rate of change of the likelihood distribution (mean) calculated according to the formula: $|L''(K)| = |L'(K+1) - L'(K)|$. (d) Delta K ($\Delta K$) calculated as $\Delta K = m|L''(K)|/s[L(K)]$. The modal value of this distribution is the true K(*) or the uppermost level of structure.

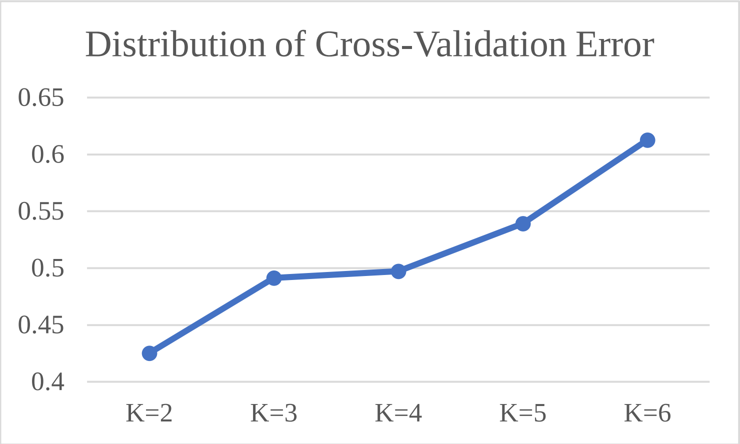

Fig. S2 Cross-validation error distribution of *K* = 2 to *K* = 6 among cultivated *Fortunella* (CUL) and Hongkong kumquat (HK) populations using *ADMIXTURE* based on SNP data.

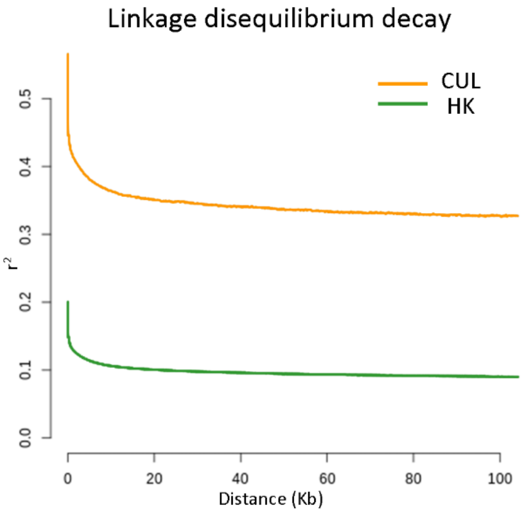

Fig. S3 Linkage disequilibrium decay analysis of cultivated *Fortunella* (CUL, orange curve) and wild Hongkong kumquat (HK, green curve) populations.

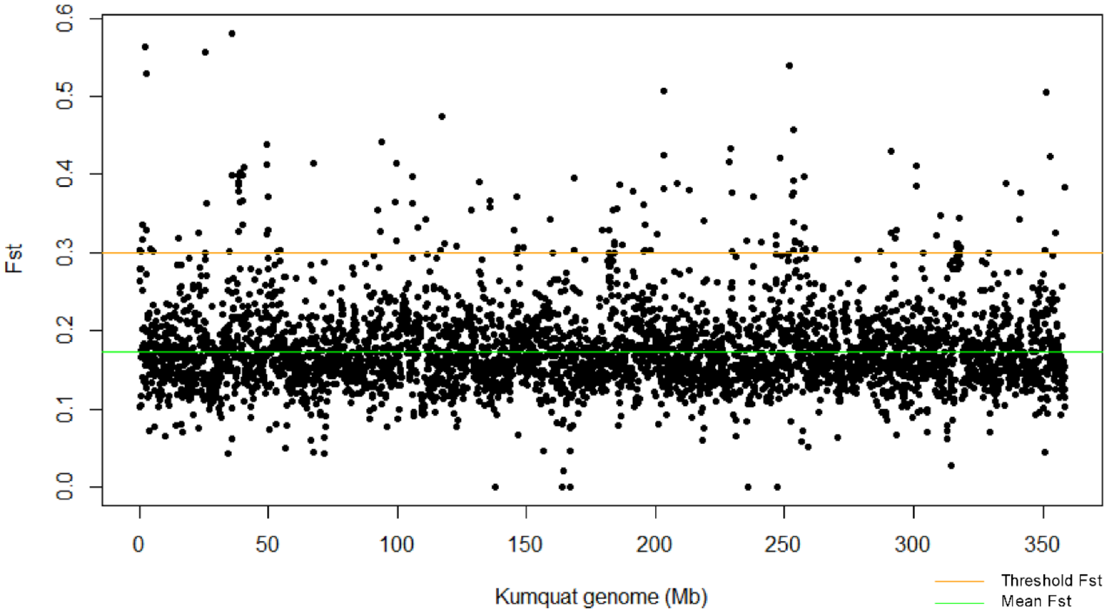

Fig. S4 Screening of the highly divergent genomic regions between cultivated *Fortunella* (CUL) and wild Hongkong kumquat (HK). The orange line indicates the screening threshold, *Fst* = 0.3; the green line indicates the mean *Fst* value, 0.17.

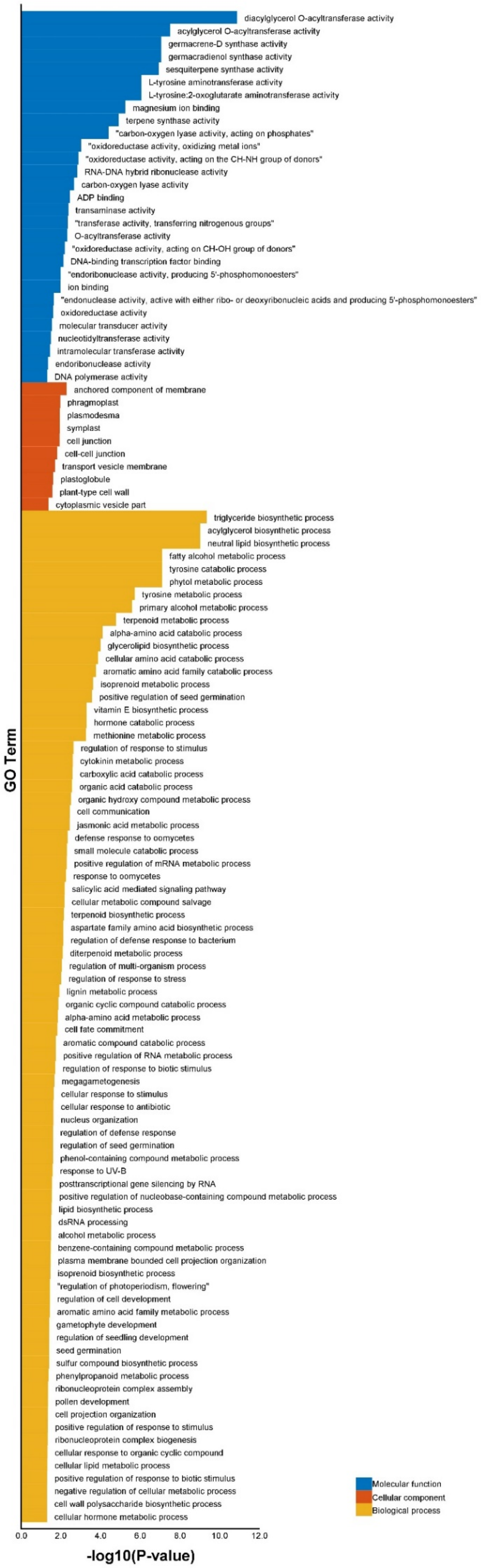

Fig. S5 GO enrichment analysis of the 747 genes in the highly divergent genomic regions between cultivated *Fortunella* (CUL) and wild Hongkong kumquat (HK) populations.

Table S1 Chloroplast loci and primers information

Locus	Type	Primers	Temperature (℃)	Location
*trn*K-*mat*K	Spacer	GGACGGATTTGGTATTTGGA	53	1878–2151
		ACTCTACCGTTGAGTTAGCAA	53	1766–2154
*trn*Q-*psb*K	Spacer	AAACCCGTTGCCTTACCACTT	55	7544–7897
		AAAGCGTAGGCCTCGGGTAAT	57	7519–7976
*rpl*16	Intron	TCCCTTTCATTCTTCCTC	50	85664–86698
		GAGAAATTCCGCAATTCTAT	49	85688–86730
*rps*16	Intron	ACCCACTTTCCGAAGATC	52	5234–6120
		AGAAAGCAACGTGCGACT	52	5184–6100
*mat*K	Gene	ACCGTATCGCACTATGTATC	53	2151–3680
		GAACTAGTCGGATGGAGTAG	55	1915–3709

Table S2 Summary of nSSR primers

ID	Front-primer	Reverse-primer
A03	CGAGAGGAATCATGGGATCT	TGTGTTCAGTGTGGAGTTGC
A05	AACAGTGTAGCATCGCACTTTCAC	GATACAAGGGACTTGCCCATCTC
A13	CCTCAGCTCTAGCAAAAGCACATT	AGAGGCTATAGATCGTGGATGCAG
A14	CCAGAGCAAAACATAGAAAGAGCG	ACTCTAGCTCTGCTCCCTTCATCA
A17	GAAAGACCAAGCGAGTGAGC	TGAAACCTGGCGGTAACTCT
A18	CAAAGGTGGGACAGCAAGTT	ACCCTCTACAGGCCATCCTT
A21	AGAGTCTCGGTGAAGCAAGC	TAGCGGTAAACAAGGGATGG
A23	CCGAACCAAACCAGTGACTT	TTTGCTTTCGAGACCAGACC
A24	GCAGCAACAACAACCACATC	CCCTTTCCCTCTGATGATGA
A28	AACCAAGTCACCTCACAGCC	TCGGACCATACTTCCTCCAC
A31	CCCTTACCCATTTTTCCCTC	TACGGGCATCAATAGCCTTC
B04	GATCCAGCAAAACCCTTTCA	AGCGATGAAGAAGCAGAAGC
B18	CTTACAACACAACTGCTGCAAAGC	TTATAAGTGGGGCCCATCAAAACT
B26	GCTTTCGATCCCTCCACATA	GATCCCTACAATCCTTGGTCC
B28	GACACTTTGGTGGAAATGGG	TTCTGTTGCTGGTTTTGGCT
B30	ATCCTCATTTGTTTTCCCCC	GTTGGCTTGTGATCGGAGTT
B31	TCTAACCCAAAAATCTGCCG	AGGGGCTTAGAGAACGTGGT
B33	TTTCTTCGTCAACCCCAAAG	TAGAAGAAGGACCCCGAACC
B36	AACAATCGGCAACTCCAATC	AGCCATTGAAGGAATGATCC
B37	CAATCACAGGAGCGACTTCA	CTCAATTCAGCAAACCGACA
B39	AATCAAAACCACCCAGCAAC	GGAAATCCGCTGCATAAAGA
B40	ACAGTGTGTCCGCATGAAAA	ATTTCCTTCACAACCGTGCT
B6	GGGTTTGCATGGCATAATTC	GTCGTCAGCGATTCCAATTT
B9	GCAGATTTGGCAGATTGAGA	CATACACCCCATTCAACAGC
C02	AAAGACCCTTGGGACTGCTT	TGAAAGTGACATATCAAGCCCA
C03	CTTAATGTCGGGAAGGCTGA	CGAAGAAATTGCAGAAGAGAGA
C04	GTTTTCTTTTGCCGGGTGTA	AAAATCCAACATGGTTGACACA
C10	GCACCTTTTATACCTGACTCGG	TTCAGCATTTGAGTTGGTTACG
C11	TTTTTCTTTCCCCCTCATCA	ATAACTCCCCGACTGCCTCT
C13	GTAGCCATCTCAGCCACCAT	TTTGTTCCATCAGCATCCAA
D03	TTCATTTGGAACAAAACCCAATTC	GCTGCTAATCACAGCATCAAGAGA
D04	GTTTTCTTTTGCCGGGTGTA	AAAATCCAACATGGTTGACACA
D17	CGCCAAGCTTACCACTCACTAC	GCCACGATTTGTAGGGGATAG
D18	GAAAGGGTTACTTGACCAGGC	CTTCCCAGCTGCACAAGC
D6	TCCAATCCCATTGTTTGTGTT	TTAACTGGGGTGGTGGTGAT
D8	CACGCGTCCGTCACTTTATT	GCAAATGTTGGCTAGAAATGG
E1	CCTTAAGAGGCTTTGCTGGA	CCAAACCCCAGATAATCAACA
E12	CCGTTGCGGTCTACCATTAT	CCAGCCACAGAGTTTTCACA
E27	GGACTTGTCGCAAAACCATT	CTCCTGCATTATTGGTCGGT
E28	TTGTTCAAGTAAGGAAGAAACTCG	CACGCAAAGCAATGCTAAAG
E29	GTCTGGGTCAGTGTGGGAGT	CGAAAAAGACAGCCAAATCC
E3	GTGACATACGCACACACACG	TGTGGTGATTGACAAGTTTTTG
E30	GTTTTCTTTTGCCGGGTGTA	AAAATCCAACATGGTTGACACA
E5	TTTCTTCGTCAACCCCAAAG	TAGAAGAAGGACCCCGAACC
E6	AACAATCGGCAACTCCAATC	AGCCATTGAAGGAATGATCC
E7	ATCATTTCAACAAGGGACGG	TCGCCAATCAAACAACAAAA

Table S3 Chloroplast genetic diversity of 38 *Fortuenlla* accessions

Statistics	*trn*K-*mat*K	*trn*Q-*psb*K	*rpl16*	*rps16*	*mat*K	Overall
Type	spacer	spacer	intron	intron	gene	
Length (bp)	285	435	1070	859	1764	4413
Polymorphic sites (Np)	12	1	2	5	5	25
Haplotype number (Nh)	5	2	3	4	4	11
Haplotype diversity (Hd)	0.45	0.15	0.44	0.25	0.15	0.69
Nucleotide diversity (Pi, 10-4)	63.9	3.5	4.7	5.9	1.5	7.3
Average number of nucleotide differences (Nk)	1.75	0.15	0.48	0.50	0.26	3.14

Table S4 Summary of diagnostic SNPs

No.	Sequence	Locus	Diagnosis
1	TTGGA**G(C)**TGGAA	*trnQ-psbK* spacer	*Fortunella*/*Citrus*
2	TCCAA**A(T)**AAAAT	*rpl16* intron	*Fortunella*/*Citrus*
3	ATTTT**A(C)**TTTCA	*rpl16* intron	*Fortunella*/*Citrus*
4	TTGAC**C(T)**GGTTC	*rpl16* intron	*Fortunella*/*Citrus*
5	AATTT**T(G)**AGTAT	*matK* cds	*Fortunella*/*Citrus*
6	ATTCT**G(A)**TGAAG	*matK* cds	*Fortunella*/*Citrus*
7	TTCTC**G(T)**GATTC	*matK* cds	*Fortunella*/*Citrus*
8	ATCTG**T(G)**TTAAT	*matK* cds	*Fortunella*/*Citrus*

Table S5 Summary of chloroplast haplotypes

Haplotype code	Sample number	Sample code
Hap_1	21	[F._margarita_(LF) F._margarita_(DGLF) F._margarita_(JZLF) F._margarita_(WZLF) F._margarita_(LFHY) F._japonica_(LW) F._japonica_(GXCP) F._crassifolia_(LCHP) F._crassifolia_(HPJG) F._crassifolia_(LSHY) F._crassifolia_(JX4) F._crassifolia_(WZJD) F._crassifolia_(LSJG) F._crassifolia_(NBJD) F._crassifolia_(HCYJG) F._crassifolia_(YSJG) F._crassifolia_(G1) F._crassifolia_(G2) C._madurensis_(SJJ) F._japonica_(RAJG) F._margarita_(XLF)]
Hap_2	1	[F._margarita_(QZLF)]
Hap_3	2	[F._crassifolia_(YXBZQ) F._crassifolia_(YXJG)]
Hap_4	2	[F._crassifolia_(LYJD) F._crassifolia_(YCJD)]
Hap_5	1	[F._crassifolia_(LYJG)]
Hap_6	3	[F._hindsii_(DJD) F._hindsii_(XJD) F._hindsii_(CZ)]
Hap_7	4	[F._hindsii_(WTD) Hybird_(WGJ) Hybird_(JGZ) F._obovata_(CS)]
Hap_8	1	[F._hindsii_(JD)]
Hap_9	1	[F._hindsii_(DR01)]
Hap_10	1	[F._hindsii_(DB02)]
Hap_11	1	[F._hindsii_(MJS)]
Hap_12	1	[C._aurantifolia_(Lime)]
Hap_13	1	[C._sinensis_(Sweet_orange)]
Hap_14	1	[Poncirus_trifoliata]
Hap_15	1	[C._medica_(Citron)]
Hap_16	1	[C._ichangensis_(Papeda)]
Hap_17	1	[C._maxima_(Pummelo)]
Hap_18	1	[C._reticulata_(Mandarin)]
Hap_19	1	[Severinia_buxifolia]
Hap_20	1	[C._limon_(Lemon)]
Hap_21	1	[C._aurantium_(Sour_orange)]

Note: The bold code indicates the haplotypes specific to *Fotunella*.

Table S6 Genetic diversity of 38 kumquat accessions based on the 47 nSSR loci

Locus	No. different alleles (Na)	Effective No. alleles (Ne)	Shannon’s information index (I)	Observed heterozygosity (Ho)	Expected heterozygosity (He)	Unbiased expected heterozygosity (uHe)
A05	7	2.14	1.14	0.50	0.53	0.54
A13	3	1.62	0.69	0.47	0.38	0.39
A14	5	1.87	0.89	0.58	0.47	0.47
B06	3	2.01	0.74	0.71	0.50	0.51
B09	4	1.21	0.41	0.08	0.17	0.18
B18	5	2.64	1.15	0.76	0.62	0.63
B26	6	2.87	1.34	0.37	0.65	0.66
B28	6	2.90	1.26	0.71	0.65	0.66
B30	7	4.16	1.57	0.76	0.76	0.77
B31	3	1.95	0.73	0.18	0.49	0.49
B33	5	1.39	0.63	0.16	0.28	0.29
B39	5	2.68	1.17	0.82	0.63	0.64
B40	5	3.27	1.34	0.76	0.69	0.70
E1	7	3.98	1.58	0.79	0.75	0.76
E3	3	2.89	1.08	0.00	0.65	0.66
E5	3	2.09	0.83	0.82	0.52	0.53
E6	8	3.79	1.58	0.21	0.74	0.75
E7	6	3.41	1.45	0.71	0.71	0.72
E12	7	3.33	1.40	0.79	0.70	0.71
C02	6	2.53	1.13	0.61	0.60	0.61
C03	4	2.29	1.01	0.76	0.56	0.57
C11	3	1.34	0.50	0.24	0.26	0.26
C13	2	1.23	0.34	0.11	0.19	0.19
D6	4	2.13	0.95	0.16	0.53	0.54
D17	5	3.19	1.29	0.89	0.69	0.70
C10	4	2.56	1.06	0.87	0.61	0.62
D08	4	2.64	1.07	0.79	0.62	0.63
C04	6	2.56	1.29	0.50	0.61	0.62
D18	4	1.39	0.61	0.24	0.28	0.29
D03	5	1.82	0.81	0.29	0.45	0.46
D04A	6	1.88	0.98	0.13	0.47	0.47
D04B	2	1.05	0.12	0.05	0.05	0.05
A03	2	1.87	0.66	0.68	0.47	0.47
A17	4	1.21	0.38	0.16	0.17	0.17
A21	2	1.50	0.51	0.37	0.33	0.34
A24	2	1.05	0.12	0.05	0.05	0.05
A28	4	2.32	0.98	0.92	0.57	0.58
A31	4	3.12	1.25	0.68	0.68	0.69
A18	2	1.11	0.21	0.11	0.10	0.10
A23	4	2.81	1.15	0.84	0.64	0.65
B04	3	2.92	1.09	0.68	0.66	0.67
B36	5	1.73	0.91	0.24	0.42	0.43
B37	7	3.70	1.53	0.92	0.73	0.74
E27	2	1.11	0.21	0.11	0.10	0.10
E28	2	1.99	0.69	0.95	0.50	0.51
E29	6	2.56	1.29	0.55	0.61	0.62
E30	2	1.05	0.12	0.05	0.05	0.05
Mean	4.34	2.27	0.92	0.49	0.49	0.49
SE	0.25	0.13	0.06	0.05	0.03	0.03

Note: Na, number of alleles; Ne, effective of number alleles; I, Shannon’s informative index; Ho, observed heterozygosity; He, expected heterozygosity; uHe, unbiased expected heterozygosity.

Table S7 Genetic diversity of 38 kumquat accessions and 10 citrus accessions based on the 47 nSSR loci

Locus	No. different alleles (Na)	Effective No. alleles (Ne)	Shannon's information index (I)	Observed heterozygosity (Ho)	Expected heterozygosity (He)	Unbiased expected heterozygosity (uHe)
A05	10	3.10	1.55	0.46	0.68	0.68
A13	6	2.18	1.10	0.48	0.54	0.55
A14	10	2.34	1.30	0.54	0.57	0.58
B06	4	2.10	0.83	0.66	0.52	0.53
B09	4	1.51	0.66	0.17	0.34	0.34
B18	7	3.12	1.40	0.69	0.68	0.69
B26	15	4.43	1.99	0.48	0.77	0.78
B28	10	4.07	1.67	0.63	0.75	0.76
B30	10	5.51	1.95	0.69	0.82	0.83
B31	9	2.82	1.33	0.29	0.65	0.65
B33	10	2.11	1.28	0.25	0.53	0.53
B39	9	3.18	1.50	0.71	0.69	0.69
B40	8	4.18	1.66	0.69	0.76	0.77
E1	9	5.19	1.84	0.65	0.81	0.82
E3	5	3.91	1.44	0.04	0.74	0.75
E5	5	2.97	1.24	0.65	0.66	0.67
E6	11	4.19	1.76	0.25	0.76	0.77
E7	8	4.67	1.79	0.62	0.79	0.79
E12	11	4.74	1.81	0.71	0.79	0.80
C02	9	3.20	1.47	0.65	0.69	0.69
C03	9	3.08	1.49	0.73	0.68	0.68
C11	4	1.60	0.70	0.25	0.37	0.38
C13	4	1.59	0.74	0.15	0.37	0.37
D6	4	2.30	0.98	0.19	0.57	0.57
D17	7	3.45	1.47	0.83	0.71	0.72
C10	6	3.19	1.37	0.81	0.69	0.69
D08	8	3.56	1.52	0.81	0.72	0.73
C04	8	3.57	1.61	0.46	0.72	0.73
D18	9	2.14	1.22	0.29	0.53	0.54
D03	6	2.52	1.18	0.38	0.60	0.61
D04A	6	2.36	1.17	0.17	0.58	0.58
D04B	4	1.55	0.72	0.15	0.36	0.36
A03	5	2.11	0.87	0.60	0.53	0.53
A17	7	1.73	0.96	0.27	0.42	0.43
A21	3	1.59	0.66	0.33	0.37	0.38
A24	4	1.27	0.47	0.13	0.21	0.21
A28	6	3.07	1.34	0.83	0.67	0.68
A31	6	4.20	1.56	0.56	0.76	0.77
A18	4	1.42	0.63	0.17	0.30	0.30
A23	6	3.32	1.40	0.77	0.70	0.71
B04	7	3.39	1.38	0.63	0.71	0.71
B36	7	2.20	1.22	0.29	0.55	0.55
B37	7	4.81	1.74	0.79	0.79	0.80
E27	2	1.16	0.26	0.15	0.14	0.14
E28	3	2.25	0.88	0.88	0.56	0.56
E29	8	3.73	1.66	0.58	0.73	0.74

E30	5	1.55	0.75	0.17	0.36	0.36
Mean	6.91	2.94	1.27	0.48	0.60	0.61
SE	2.64	1.14	0.42	0.25	0.17	0.17

Note: Na, number of alleles; Ne, effective of number alleles; I, Shannon's informative index; Ho, observed heterozygosity; He, expected heterozygosity; uHe, unbiased expected heterozygosity.

Table S8 Annotation of the SNPs used in population-genomic analysis

Type	Count	Percent
SNP number	5104141	
HIGH	9456	0.0006
LOW	365396	0.0248
MODERATE	324508	0.0221
MODIFIER	14010870	0.9525
MISSENSE	326075	0.5453
NONSENSE	4917	0.0082
SILENT	266941	0.4464
3_prime_UTR_variant	589154	0.0399
5_prime_UTR_premature_start_codon_gain_variant	51407	0.0035
5_prime_UTR_variant	326599	0.0221
downstream_gene_variant	3811756	0.2581
initiator_codon_variant	128	0
intergenic_region	3514535	0.238
intragenic_variant	986	0.0001
intron_variant	1849688	0.1253
missense_variant	324508	0.022
non_coding_transcript_variant	957	0.0001
splice_acceptor_variant	1503	0.0001
splice_donor_variant	1597	0.0001
splice_region_variant	58055	0.0039
start_lost	631	0
stop_gained	4917	0.0003
stop_lost	808	0.0001
stop_retained_variant	431	0
synonymous_variant	266510	0.0181
upstream_gene_variant	3963362	0.2684
DOWNSTREAM	3811756	0.2591
EXON	592827	0.0403
INTERGENIC	3514535	0.2389
INTRON	1803521	0.1226
SPLICE_SITE_ACCEPTOR	1503	0.0001
SPLICE_SITE_DONOR	1597	0.0001
SPLICE_SITE_REGION	52026	0.0035
TRANSCRIPT	1943	0.0001
UPSTREAM	3963362	0.2694
UTR_3_PRIME	589154	0.0401
UTR_5_PRIME	378006	0.0257
Transitions	31901014	
Transversions	18456414	
Ts/Tv ratio	1.73	
A to C	230600	
A to G	645282	
A to T	276365	
T to A	277202	
T to C	643941	
T to G	231225	
C to A	276983	
C to G	172746	
C to T	949604	
G to A	951356	
G to C	172752	
G to T	276085	

Table S9 Archiving information of 30 sequencing data

Data code	Accession code	Species
A01	DGLF	*F. margarita*
A02	LF	*F. margarita*
A03	G2	*F. crassifolia*
A04	LYJG	*F. crassifolia*
A05	HPJG	*F. crassifolia*
A06	YXBZQ	*F. crassifolia*
A07	LW	*F. japonica*
A09	RAJD	*F. japonica*
A10	LSJG	*F. crassifolia*
A11	XLF	*F. margarita*
A12	WZJD	*F. crassifolia*
A13	YSJG	*F. crassifolia*
A14	GXCP	*F. japonica*
A17	JX4	*F. crassifolia*
A18	HCYJG	*F. crassifolia*
B1	MJS	*F. hindsii*
D2	LY43	*F. hindsii*
F2	ZX9	*F. hindsii*
G1	CZ	*F. hindsii*
I1	HC27	*F. hindsii*
J1	XMS	*F. hindsii*
K1	JIEX	*F. hindsii*
L3	DB02	*F. hindsii*
N1	CFX	*F. hindsii*
O1	JLS	*F. hindsii*
P3	LH08	*F. hindsii*
Q1	DYT01	*F. hindsii*
S3	DYS02	*F. hindsii*
Y6	DR01	*F. hindsii*
Z3	WTD	*F. hindsii*

Table S10 Highly divergent genomic regions between cultivated *Fortunella* (CUL) and wild Hongkong kumquat (HK) populations

Location Contig ID	Start Position	End Position
tig00011921_arrow_pilon	200001	600000
tig00010673_arrow_pilon	200001	400000
tig00040360_arrow_pilon	1	100000
tig00005381_arrow_pilon	1	100000
tig00013765_arrow_pilon	1	100000
tig00001836_arrow_pilon	1	100000
tig00001315_arrow_pilon	1	100000
tig00040109_arrow_pilon	1	100000
tig00004152_arrow_pilon	1	100000
tig00010229_arrow_pilon	100001	500000
tig00000584_arrow_pilon	600001	700000
tig00012142_arrow_pilon	1	400000
tig00040184_arrow_pilon	1	700000
tig00002340_arrow_pilon	1200001	1600000
tig00005724_arrow_pilon	1	100000
tig00001777_arrow_pilon	1	700000
tig00003129_arrow_pilon	2700001	2800000
tig00040198_arrow_pilon	300001	400000
tig00040277_arrow_pilon	700001	800000
tig00040100_arrow_pilon	9200001	11300000
tig00040133_arrow_pilon	1400001	1500000
tig00007591_arrow_pilon	600001	700000
tig00015758_arrow_pilon	1	100000
tig00015401_arrow_pilon	1	100000
tig00006955_arrow_pilon	1	100000
tig00003671_arrow_pilon	1	100000
tig00040120_arrow_pilon	3600001	3700000
tig00001541_arrow_pilon	1900001	2100000
tig00040136_arrow_pilon	800001	900000
tig00013772_arrow_pilon	1	100000
tig00002619_arrow_pilon	5000001	5100000
tig00007311_arrow_pilon	400001	500000
tig00040137_arrow_pilon	1	100000
tig00040266_arrow_pilon	200001	300000
tig00000053_arrow_pilon	1	4800000
tig00001399_arrow_pilon	100001	200000
tig00000014_arrow_pilon	100001	200000
tig00040288_arrow_pilon	1	100000
tig00001140_arrow_pilon	100001	200000
tig00040088_arrow_pilon	400001	500000
tig00008693_arrow_pilon	500001	900000
tig00000734_arrow_pilon	1	100000
tig00040155_arrow_pilon	900001	2000000
tig00004748_arrow_pilon	600001	700000
tig00040092_arrow_pilon	500001	3700000
tig00040083_arrow_pilon	1	100000
tig00001293_arrow_pilon	1	200000

tig00007648_arrow_pilon	1	100000
tig00010755_arrow_pilon	200001	300000
tig00000852_arrow_pilon	2800001	2900000
tig00040123_arrow_pilon	300001	400000
tig00000268_arrow_pilon	1	100000
tig00003120_arrow_pilon	100001	700000
tig00000197_arrow_pilon	1	100000
tig00007327_arrow_pilon	300001	400000
tig00001762_arrow_pilon	1700001	1800000
tig00040089_arrow_pilon	500001	700000
tig00002643_arrow_pilon	1	100000
tig00005284_arrow_pilon	1	100000
tig00040186_arrow_pilon	1	1000000
tig00003837_arrow_pilon	800001	900000
tig00040079_arrow_pilon	200001	1300000
tig00040317_arrow_pilon	600001	700000
tig00002834_arrow_pilon	1	100000
tig00040194_arrow_pilon	1	200000
tig00005260_arrow_pilon	100001	200000
tig00013237_arrow_pilon	1	100000
tig00001692_arrow_pilon	1900001	2100000
tig00006415_arrow_pilon	1	100000
tig00040201_arrow_pilon	1000001	1100000
tig00040081_arrow_pilon	600001	2500000
tig00008366_arrow_pilon	1	100000
tig00001669_arrow_pilon	100001	200000
tig00040265_arrow_pilon	800001	1400000
tig00040154_arrow_pilon	1	100000
tig00003840_arrow_pilon	1	100000
tig00000397_arrow_pilon	1	100000
tig00040253_arrow_pilon	900001	1000000
tig00002844_arrow_pilon	1	100000

Table S11 Functional annotation of the 36 genes involved in tricarboxylic acid cycle identified in highly divergent genomic regions between cultivated *Fortunella* (CUL) and wild Hong Kong kumquat (HK) populations

Gene ID	Annotation database (Swiss-Prot; TrEMBL; BlastProDom; Coil; FPrintScan; Gene3D; HAMAP; HMMPIR; HMMPanther; HMMPfam; HMMSmart; HMMTigr; PatternScan; ProfileScan; Seg; superfamily; IPR; GO)
sjg003210	Ribulose bisphosphate carboxylase large chain (Fragment) no description; RIBOSOMAL PROTEIN S15, BACTERIAL AND ORGANELLAR; OS12G0207600 PROTEIN; seg; RuBisCo, C-terminal domain; RuBisCO, large subunit, small (N-terminal) domain; Ribulose bisphosphate carboxylase, large subunit, C-terminal; NULL; Ribulose bisphosphate carboxylase, large subunit, ferrodoxin-like N-terminal; Molecular Function: magnesium ion binding (GO:0000287); Biological Process: carbon fixation (GO:0015977), Molecular Function: ribulose-bisphosphate carboxylase activity (GO:0016984)
sjg003350	Ribulose bisphosphate carboxylase large chain (Fragment) no description; RIBOSOMAL PROTEIN S15, BACTERIAL AND ORGANELLAR; OS12G0207600 PROTEIN; RuBisCO_large; RuBisCo, C-terminal domain; NULL; Ribulose bisphosphate carboxylase, large subunit, C-terminal; Molecular Function: magnesium ion binding (GO:0000287)
sjg304970	Probable polygalacturonase no description; FAMILY NOT NAMED; Glyco_hydro_28; Parallel beta-helix repeats; seg; Pectin lyase-like; Pectin lyase fold/virulence factor; Parallel beta-helix repeat; Glycoside hydrolase, family 28; NULL; Pectin lyase fold; Molecular Function: polygalacturonase activity (GO:0004650), Biological Process: carbohydrate metabolic process (GO:0005975)
sjg305080	Probable polygalacturonase no description; FAMILY NOT NAMED; NULL; Pectin lyase fold
sjg305110	Probable polygalacturonase Uncharacterized protein no description; SUBFAMILY NOT NAMED; FAMILY NOT NAMED; Pectin lyase-like; Pectin lyase fold/virulence factor; NULL; Pectin lyase fold
sjg018240	60S ribosomal protein L14-2 coiled-coil; no description; 60S RIBOSOMAL PROTEIN L14; Ribosomal_L14e; seg; Ribosomal protein L2 domain 2; NULL; Ribosomal protein L14; Molecular Function: structural constituent of ribosome (GO:0003735), Cellular Component: intracellular (GO:0005622), Cellular Component: ribosome (GO:0005840), Biological Process: translation (GO:0006412)
sjg254330	Probable indole-3-acetic acid-amido synthetase GH3.5 FAMILY NOT NAMED; GH3; seg; GH3 auxin-responsive promoter; NULL
sjg149060	Sugar transport protein 1 SUGRTRNSPORT; no description; SUBFAMILY NOT NAMED; FAMILY NOT NAMED; Sugar_tr; SP: MFS transporter, sugar porter (SP) family; SUGAR_TRANSPORT_1; SUGAR_TRANSPORT_2; MFS; seg; MFS general substrate transporter; General substrate transporter;Sugar transporter, conserved site; NULL; Major facilitator superfamily domain, general substrate transporter; Sugar/inositol transporter; Major facilitator superfamily domain; Molecular Function: transporter activity (GO:0005215), Biological Process: transport (GO:0006810), Cellular Component: membrane (GO:0016020), Biological Process: transmembrane transport (GO:0055085); Cellular Component: integral to membrane (GO:0016021), Molecular Function: transmembrane transporter activity (GO:0022857), Biological Process: transmembrane transport (GO:0055085); Cellular Component: membrane (GO:0016020), Molecular Function: substrate-specific transmembrane transporter activity (GO:0022891), Biological Process: transmembrane transport (GO:0055085)
sjg292700	Protein TIC 20-IV, chloroplastic seg; NULL
sjg067480	Galacturonosyltransferase 8 no description; SUBFAMILY NOT NAMED; FAMILY NOT NAMED; Glyco_transf_8; Nucleotide-diphospho-sugar transferases; NULL; Glycosyl transferase, family 8; Molecular Function: transferase activity, transferring glycosyl groups (GO:0016757)
sjg067610	Flavonoid 3',5'-hydroxylase no description; Cytochrome P450; Molecular Function: iron ion binding (GO:0005506), Molecular Function: electron carrier activity (GO:0009055), Molecular Function: oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen (GO:0016705), Molecular Function: heme binding (GO:0020037), Biological Process: oxidation-reduction process (GO:0055114)
sjg263150	Endoglucanase 9 no description; ENDO-1,4-BETA-GLUCANASE; Glyco_hydro_9 GLYCOSYL_HYDROL_F9_1; GLYCOSYL_HYDROL_F9_2; seg; Six-hairpin glycosidases; Six-hairpin glycosidase;Glycoside hydrolase, family 9;Glycoside hydrolase, family 9, active site; NULL; Six-hairpin glycosidase-like; Molecular Function: catalytic activity (GO:0003824); Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Biological Process: carbohydrate metabolic process (GO:0005975)
sjg264280	Mannan endo-1,4-beta-mannosidase 5 no description; FAMILY NOT NAMED; Cellulase; (Trans)glycosidases; NULL; Glycoside hydrolase, superfamily; Glycoside hydrolase, catalytic domain; Glycoside hydrolase, family 5; Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Biological Process: carbohydrate metabolic process (GO:0005975); Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975)
sjg267420	O-acyltransferase WSD1 coiled-coil; SUBFAMILY NOT NAMED; FAMILY NOT NAMED DUF1298; WES_acyltransf; seg; NULL; O-acyltransferase, WSD1, C-terminal; O-acyltransferase, WSD1, N-terminal; Molecular Function: diacylglycerol O-acyltransferase activity (GO:0004144); Molecular Function: diacylglycerol O-acyltransferase activity (GO:0004144), Biological Process: glycerolipid biosynthetic process (GO:0045017)
sjg097660	Probable inactive shikimate kinase like 1, chloroplastic SHIKIMTKNASE; no description; SHIKIMATE KINASE; SKI; P-loop containing nucleoside triphosphate hydrolases; NULL; Shikimate kinase/Threonine synthase-like 1; P-loop containing nucleoside triphosphate hydrolase
sjg097970	Glucuronoxylan 4-O-methyltransferase 1 Uncharacterized protein FAMILY NOT NAMED; Polysacc_synt_4; A_thal_3515: uncharacterized plant-specific domain; seg; Xylan biosynthesis protein IRX15/IRX15L; Putative polysaccharide biosynthesis protein; NULL
sjg098170	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (Fragment) no description; GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE; Gp_dh_C; seg; Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain; Glyceraldehyde/Erythrose phosphate dehydrogenase family; NULL; Glyceraldehyde 3-phosphate dehydrogenase, catalytic domain; Molecular Function: oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor (GO:0016620), Biological Process: oxidation-reduction process (GO:0055114)

sjg098860	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial no description; SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN; Fer2_3;Fer4_17; dhsB: succinate dehydrogenase and fumarate reducta; 2FE2S_FER_1; 4FE4S_FER_1; 4FE4S_FER_2; 2FE2S_FER_2; seg; 2Fe-2S ferredoxin-like;alpha-helical ferredoxin; 4Fe-4S ferredoxin, iron-sulphur binding, conserved site; Succinate dehydogenase/fumarate reductase N-terminal; NULL; Beta-grasp domain; 4Fe-4S ferredoxin-type, iron-sulpur binding domain; 2Fe-2S ferredoxin-type domain; Alpha-helical ferredoxin; 2Fe-2S ferredoxin, iron-sulphur binding site; Succinate dehydrogenase/fumarate reductase iron-sulphur protein; Biological Process: tricarboxylic acid cycle (GO:0006099), Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: electron carrier activity (GO:0009055), Molecular Function: iron-sulfur cluster binding (GO:0051536); Molecular Function: 2 iron, 2 sulfur cluster binding (GO:0051537); Molecular Function: iron-sulfur cluster binding (GO:0051536)
sjg100150	Callose synthase 12 Uncharacterized protein FAMILY NOT NAMED; Glucan_synthase; FKS1_dom1; seg; NULL; 1,3-beta-glucan synthase subunit FKS1-like, domain-1; Glycosyl transferase, family 48; Cellular Component: 1,3-beta-D-glucan synthase complex (GO:0000148), Molecular Function: 1,3-beta-D-glucan synthase activity (GO:0003843), Biological Process: (1->3)-beta-D-glucan biosynthetic process (GO:0006075), Cellular Component: membrane (GO:0016020)
sjg100460	Mannan endo-1,4-beta-mannosidase 2 no description; FAMILY NOT NAMED; Cellulase; seg; (Trans)glycosidases; NULL; Glycoside hydrolase, superfamily; Glycoside hydrolase, catalytic domain; Glycoside hydrolase, family 5; Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Biological Process: carbohydrate metabolic process (GO:0005975);Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975)
sjg102290	Ribulose-phosphate 3-epimerase, cytoplasmic isoform Uncharacterized protein no description; RIBULOSE-5-PHOSPHATE-3-EPIMERASE; SUBFAMILY NOT NAMED; Ribul_P_3_epim; RIBUL_P_3_EPIMER_2; Ribulose-phoshate binding barrel; NULL; Aldolase-type TIM barrel; Ribulose-phosphate 3-epimerase-like;Ribulose-phosphate binding barrel; Molecular Function: catalytic activity (GO:0003824);Biological Process: carbohydrate metabolic process (GO:0005975), Molecular Function: racemase and epimerase activity, acting on carbohydrates and derivatives (GO:0016857); Molecular Function: catalytic activity (GO:0003824), Biological Process: metabolic process (GO:0008152)
sjg299220	Glucan endo-1,3-beta-glucosidase 1 PRICHEXTENSN; no description; SUBFAMILY NOT NAMED; FAMILY NOT NAMED; X8; Possibly involved in carbohydrate binding; seg; NULL; Glycoside hydrolase, catalytic domain; X8; Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975)
sjg139810	Glycerol-3-phosphate dehydrogenase SDP6, mitochondrial Glycerol-3-phosphate dehydrogenase FADG3PDH; no description; SUBFAMILY NOT NAMED;GLYCEROL-3-PHOSPHATE DEHYDROGENASE; DAO; FAD_G3PDH_2; FAD_G3PDH_1; seg; FAD-linked reductases, C-terminal domain; FAD/NAD(P)-binding domain; FAD-dependent glycerol-3-phosphate dehydrogenase; NULL; FAD dependent oxidoreductase; Molecular Function: glycerol-3-phosphate dehydrogenase activity (GO:0004368), Biological Process: glycerol-3-phosphate metabolic process (GO:0006072), Cellular Component: glycerol-3-phosphate dehydrogenase complex (GO:0009331), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114)
sjg139870	Malate dehydrogenase [NADP], chloroplastic no description; MALATE DEHYDROGENASE; Ldh_1_N; Ldh_1_C; MalateDH-SF1: malate dehydrogenase; MDH; seg; NAD(P)-binding Rossmann-fold domains; LDH C-terminal domain-like; NULL; Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal; NAD(P)-binding domain; Malate dehydrogenase, active site; Lactate/malate dehydrogenase, N-terminal; Malate dehydrogenase, type 2; Lactate/malate dehydrogenase, C-terminal; Biological Process: malate metabolic process (GO:0006108), Molecular Function: malate dehydrogenase activity (GO:0016615), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975), Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Biological Process: oxidation-reduction process (GO:0055114)
sjg140840	Pullulanase 1, chloroplastic no description; ALPHA-AMYLASE;PULLULANASE; DUF3372;CBM_48; Alpha-amylase; pullul_strch: alpha-1,6-glucosidases, pullulanase-; seg; E set domains; (Trans)glycosidases; Glycoside hydrolase, family 13, N-terminal; NULL; Immunoglobulin-like fold; Alpha-1,6-glucosidases, pullulanase-type; Glycoside hydrolase, family 13; Immunoglobulin E-set; Glycoside hydrolase, catalytic domain; Glycoside hydrolase, superfamily; Alpha-1,6-glucosidases, pullulanase-type, C-terminal; Glycosyl hydrolase, family 13, catalytic domain; Molecular Function: catalytic activity (GO:0003824); Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975), Molecular Function: cation binding (GO:0043169); Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Biological Process: carbohydrate metabolic process (GO:0005975); Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975); Biological Process: carbohydrate metabolic process (GO:0005975), Molecular Function: pullulanase activity (GO:0051060)
sjg000200	Beta-glucosidase 18 GLHYDRLASE1; no description; GLYCOSYL HYDROLASE; Glyco_hydro_1; GLYCOSYL_HYDROL_F1_2; seg; (Trans)glycosidases; Glycoside hydrolase, family 1, active site; NULL; Glycoside hydrolase, superfamily; Glycoside hydrolase, catalytic domain; Glycoside hydrolase, family 1; Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Biological Process: carbohydrate metabolic process (GO:0005975);Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975)

sjg000430	Malate dehydrogenase, mitochondrial no description; L-lactate/malate dehydrogenase; MALATE AND LACTATE DEHYDROGENASE;MALATE DEHYDROGENASE; Ldh_1_N;Ldh_1_C; MDH_euk_gproteo: malate dehydrogenase, NAD-depende; MDH; seg; NAD(P)-binding Rossmann-fold domains; LDH C-terminal domain-like; L-lactate/malate dehydrogenase; Malate dehydrogenase, type 1; NULL; Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal; NAD(P)-binding domain; Lactate/malate dehydrogenase, N-terminal; Malate dehydrogenase, active site; Lactate/malate dehydrogenase, C-terminal; Biological Process: malate metabolic process (GO:0006108), Molecular Function: malate dehydrogenase activity (GO:0016615), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Biological Process: cellular carbohydrate metabolic process (GO:0044262), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975), Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Biological Process: oxidation-reduction process (GO:0055114); Biological Process: malate metabolic process (GO:0006108), Molecular Function: L-malate dehydrogenase activity (GO:0030060), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Biological Process: oxidation-reduction process (GO:0055114)
sjg000970	Xylosyltransferase 2 GLYCOSYLTRANSFERASE 14 FAMILY MEMBER; GLYCOSYLATION ENZYME-LIKE PROTEIN; Branch; Glycosyl transferase, family 14; NULL; Molecular Function: acetylglucosaminyltransferase activity (GO:0008375), Cellular Component: membrane (GO:0016020)
sjg147470	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase no description; UDPGT; UDPGT; seg; UDP-glucuronosyl/UDP-glucosyltransferase; NULL; Biological Process: metabolic process (GO:0008152), Molecular Function: transferase activity, transferring hexosyl groups (GO:0016758)
sjg104210	Alpha-galactosidase Alpha-galactosidase GLHYDRLASE27; no description; SUBFAMILY NOT NAMED; ALPHA-GALACTOSIDASE/ALPHA-N-ACETYLGALACTOSAMINIDASE; seg; Glycosyl hydrolase domain;(Trans)glycosidases; NULL; Glycoside hydrolase, superfamily; Glycosyl hydrolase, family 13, all-beta; Aldolase-type TIM barrel; Glycoside hydrolase, family 27; Molecular Function: catalytic activity (GO:0003824);Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Biological Process: carbohydrate metabolic process (GO:0005975)
sjg241520	ATP-dependent 6-phosphofructokinase 2 PHFRCTKINASE; no description; ATP-dependent phosphofructokinase, TP0108 type; PHOSPHOFRUCTOKINASE; PFK; Phosphofructokinase; Phosphofructokinase domain; NULL; Phosphofructokinase; Pyrophosphate-dependent phosphofructokinase TP0108; Molecular Function: 6-phosphofructokinase activity (GO:0003872), Molecular Function: ATP binding (GO:0005524), Biological Process: glycolysis (GO:0006096); Molecular Function: 6-phosphofructokinase activity (GO:0003872), Biological Process: fructose 6-phosphate metabolic process (GO:0006002), Biological Process: glycolysis (GO:0006096); Molecular Function: 6-phosphofructokinase activity (GO:0003872), Cellular Component: 6-phosphofructokinase complex (GO:0005945), Biological Process: glycolysis (GO:0006096)
sjg241550	Glucan endo-1,3-beta-glucosidase 5 no description; SUBFAMILY NOT NAMED; FAMILY NOT NAMED; Glyco_hydro_17;X8; Possibly involved in carbohydrate binding; GLYCOSYL_HYDROL_F17; seg; (Trans)glycosidases; Glycoside hydrolase, family 17; NULL; Glycoside hydrolase, superfamily; Glycoside hydrolase, catalytic domain; X8; Molecular Function: hydrolase activity, hydrolyzing O-glycosyl compounds (GO:0004553), Biological Process: carbohydrate metabolic process (GO:0005975); Molecular Function: catalytic activity (GO:0003824), Biological Process: carbohydrate metabolic process (GO:0005975)
sjg104140	Probable 3-hydroxyisobutyrate dehydrogenase-like 3, mitochondrial no description; SUBFAMILY NOT NAMED; 3-HYDROXYISOBUTYRATE DEHYDROGENASE-RELATED; NAD_binding_11;NAD_binding_2; seg; 6-phosphogluconate dehydrogenase C-terminal domain-like; NAD(P)-binding Rossmann-fold domains; 6-phosphogluconate dehydrogenase, NADP-binding; NULL; Dehydrogenase, multihelical; NAD(P)-binding domain; Hydroxy monocarboxylic acid anion dehydrogenase, HIBADH-type;6-phosphogluconate dehydrogenase, C-terminal-like; Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity (GO:0016491), Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Molecular Function: coenzyme binding (GO:0050662), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: phosphogluconate dehydrogenase (decarboxylating) activity (GO:0004616), Biological Process: pentose-phosphate shunt (GO:0006098), Biological Process: oxidation-reduction process (GO:0055114); Biological Process: oxidation-reduction process (GO:0055114)
sjg104360	Probable 3-hydroxyisobutyrate dehydrogenase-like 3, mitochondrial no description; SUBFAMILY NOT NAMED; 3-HYDROXYISOBUTYRATE DEHYDROGENASE-RELATED; NAD_binding_11;NAD_binding_2; 6-phosphogluconate dehydrogenase C-terminal domain-like; NAD(P)-binding Rossmann-fold domains; 6-phosphogluconate dehydrogenase, NADP-binding; NULL; Dehydrogenase, multihelical; NAD(P)-binding domain;6-phosphogluconate dehydrogenase, C-terminal-like; Hydroxy monocarboxylic acid anion dehydrogenase, HIBADH-type; Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114);Molecular Function: phosphogluconate dehydrogenase (decarboxylating) activity (GO:0004616), Biological Process: pentose-phosphate shunt (GO:0006098), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity (GO:0016491), Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Molecular Function: coenzyme binding (GO:0050662), Biological Process: oxidation-reduction process (GO:0055114); Biological Process: oxidation-reduction process (GO:0055114)

sjg104370	Probable 3-hydroxyisobutyrate dehydrogenase-like 3, mitochondrial no description; SUBFAMILY NOT NAMED; 3-HYDROXYISOBUTYRATE DEHYDROGENASE-RELATED; NAD_binding_11; NAD_binding_2; seg; 6-phosphogluconate dehydrogenase C-terminal domain-like; NAD(P)-binding Rossmann-fold domains; 6-phosphogluconate dehydrogenase, NADP-binding; NULL; Dehydrogenase, multihelical; NAD(P)-binding domain; 6-phosphogluconate dehydrogenase, C-terminal-like; Hydroxy monocarboxylic acid anion dehydrogenase, HIBADH-type; Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity (GO:0016491), Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Molecular Function: coenzyme binding (GO:0050662), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: phosphogluconate dehydrogenase (decarboxylating) activity (GO:0004616), Biological Process: pentose-phosphate shunt (GO:0006098), Biological Process: oxidation-reduction process (GO:0055114); Biological Process: oxidation-reduction process (GO:0055114)
sjg104390	Probable 3-hydroxyisobutyrate dehydrogenase-like 3, mitochondrial Uncharacterized protein no description; SUBFAMILY NOT NAMED;3-HYDROXYISOBUTYRATE DEHYDROGENASE-RELATED; NAD_binding_11;NAD_binding_2; seg; 6-phosphogluconate dehydrogenase C-terminal domain-like; NAD(P)-binding Rossmann-fold domains; 6-phosphogluconate dehydrogenase, NADP-binding; NULL; Dehydrogenase, multihelical; NAD(P)-binding domain;6-phosphogluconate dehydrogenase, C-terminal-like; Hydroxy monocarboxylic acid anion dehydrogenase, HIBADH-type; Molecular Function: oxidoreductase activity (GO:0016491), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: oxidoreductase activity (GO:0016491), Molecular Function: oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616), Molecular Function: coenzyme binding (GO:0050662), Biological Process: oxidation-reduction process (GO:0055114); Molecular Function: phosphogluconate dehydrogenase (decarboxylating) activity (GO:0004616), Biological Process: pentose-phosphate shunt (GO:0006098), Biological Process: oxidation-reduction process (GO:0055114); Biological Process: oxidation-reduction process (GO:0055114)