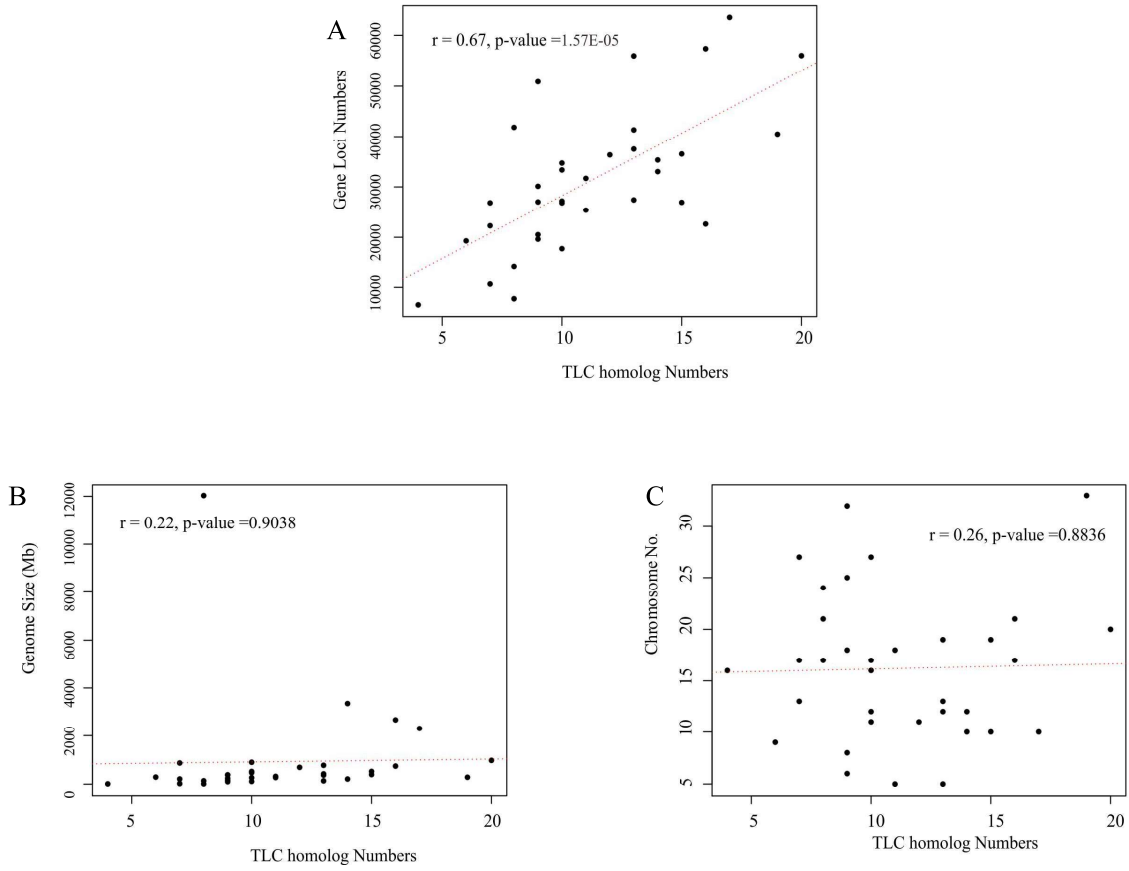
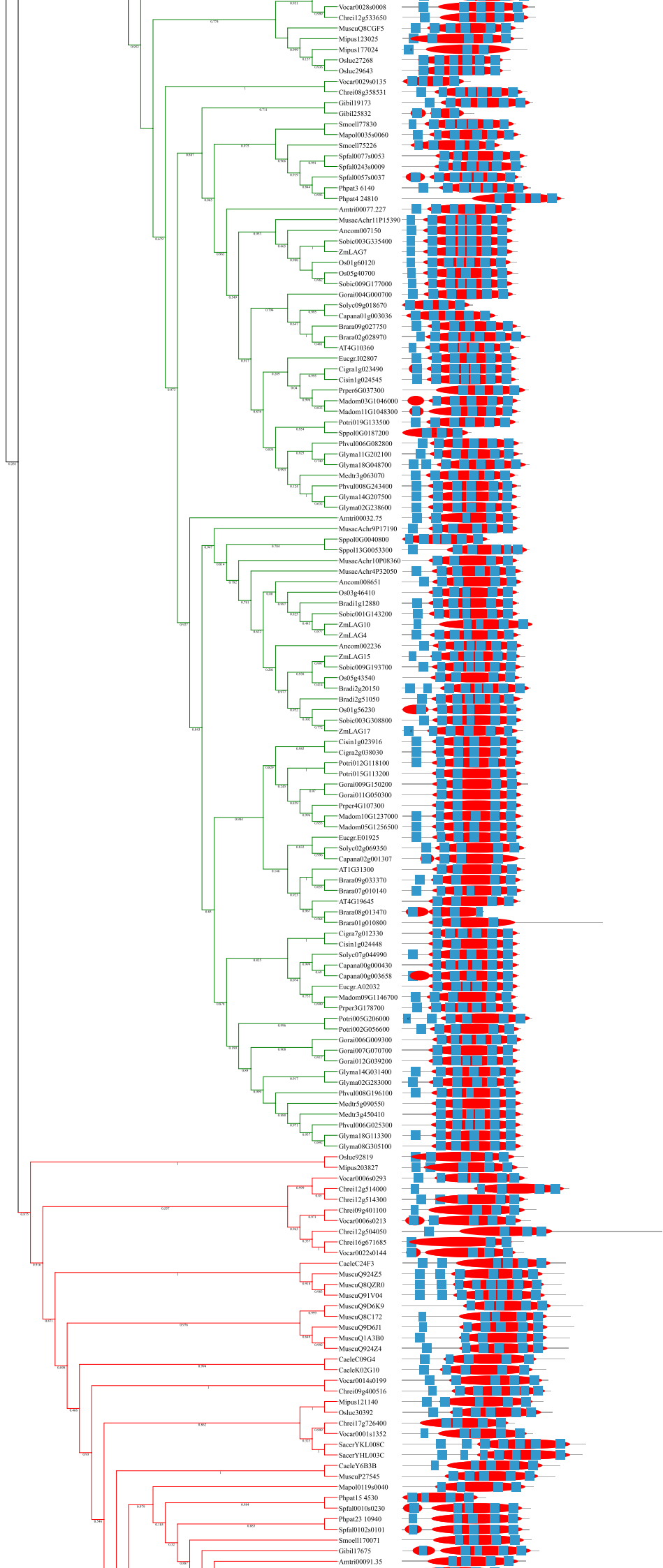


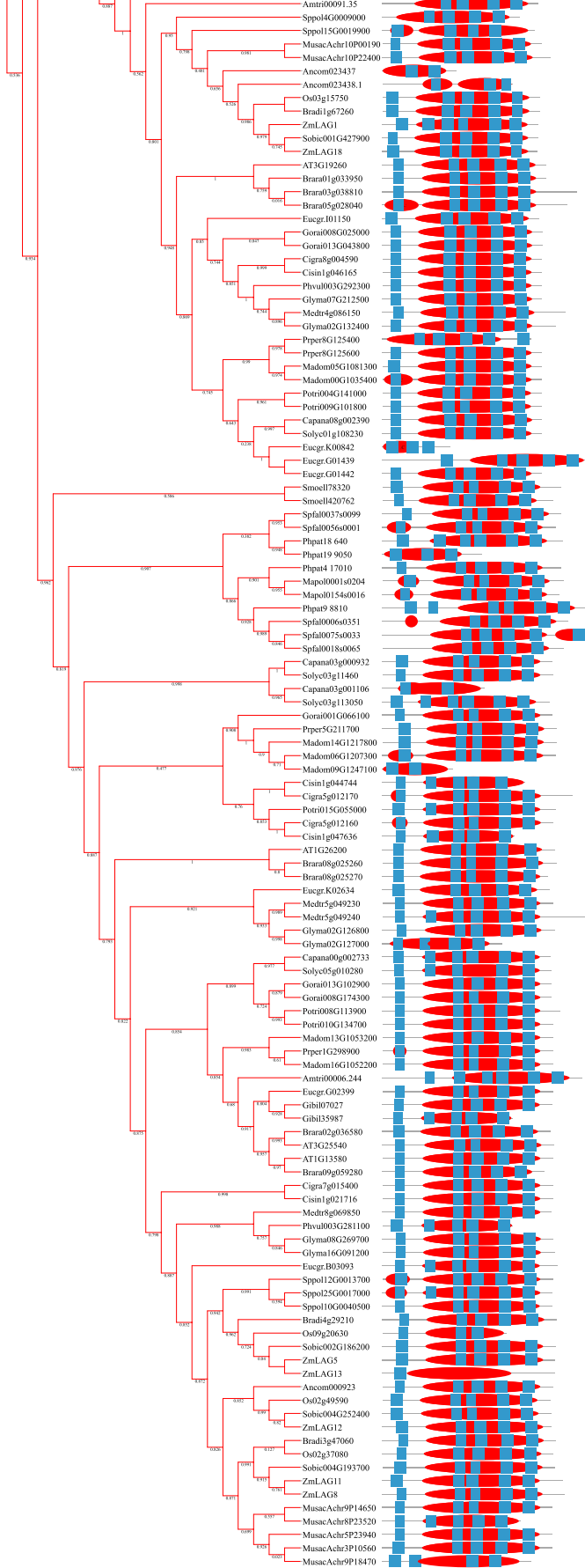
FigureS1 Correlation analysis between TLC numbers with genome-wide protein-encoding gene numbers (A), genome size (B) and chromosome number (C), respectively.



FigureS2 The ML Phylogenetic tree built by TLC proteins from 31 plant species and three out-group species.







TableS1 Genome information of 31 plant species and three outgroup species.

Taxonomy	Species name	Abrr.	Genome Size(Mb)	Gene Loci number	Chromosome number	TLC number
Bathycoccaceae	<i>Ostreococcus lucimarinus</i>	Osluc	13.2	7796	21	8
Mamiellophyceae	<i>Micromonas pusilla</i>	Mipus	22	10660	17	7
Chlamydomonadaceae	<i>Chlamydomonas reinhardtii</i>	Chrei	111.1	17741	17	10
Chlorophyceae	<i>Volvox carteri</i>	Vocar	138	14247	17	8
Bryophyta	<i>Physcomitrella patens</i>	Phpat	473	33362	27	10
<i>Sphagnaceae</i>	<i>Sphagnum fallax</i>	Spfal	395	26939	19	15
<i>Marchantiaceae</i>	<i>Marchantia polymorpha</i>	Mapol	290	19287	9	6
Selaginellaceae	<i>Selaginella moellendorffii</i>	Smoell	212.5	22273	27	7
Ginkgoaceae	<i>Ginkgo biloba</i>	Gibil	12032	41840	24	8
Amborellaceae	<i>Amborella trichopoda</i>	Amtri	870	26846	13	7
Musaceae	<i>Musa acuminata</i>	Musac	523	36528	10	15
Bromeliaceae	<i>Ananas comosus</i>	Ancom	382	27024	25	9
Araceae	<i>Spirodela polyrhiza</i>	Sppol	158.00	19623	32	9
Poaceae	<i>Zea mays</i>	Zm	2300	63480	10	18
Poaceae	<i>Sorghum Bicolor</i>	Sobic	211	33032	10	14
Poaceae	<i>Brachypodium distachyon</i>	Bradi	272	31694	5	11
Poaceae	<i>Oryza sativa</i>	Os	372	55986	12	13
Solanaceae	<i>Capsicum annuum</i>	Capana	3349	35336	12	14
Solanaceae	<i>Solanum lycopersicum</i>	Solyc	900	34727	12	10
Salicaceae	<i>Populus trichocarpa</i>	Potri	422.9	41335	19	13
Rosaceae	<i>Prunus persica</i>	Prper	265	26837	16	10
Rosaceae	<i>Malus domestica</i>	Madom	742.3	57386	17	16
Fabaceae	<i>Medicago truncatula</i>	Medtr	241	50894	8	9
Fabaceae	<i>Phaseolus vulgaris</i>	Phvul	521.1	27197	11	10
Fabaceae	<i>Glycine max</i>	Glyma	978	56044	20	20
Myrtaceae	<i>Eucalyptus grandis</i>	Eucgr	691	36349	11	12
Malvaceae	<i>Gossypium raimondii</i>	Gorai	775	37505	13	13
Rutaceae	<i>Citrus grandis</i>	Cigra	380	30120	18	9
Rutaceae	<i>Citrus sinensis</i>	Cisin	319	25376	18	11
Brassicaceae	<i>Brassica rapa</i>	Brara	283.8	40492	33	19
<i>Brassicaceae</i>	<i>Arabidopsis thaliana</i>	AT	135	27416	5	13
nematode	<i>Caenorhabditis elegans</i>	Caele	100	20512	6	9
Ascomycota	<i>Saccharomyces cerevisiae</i>	Sacer	12	6604	16	4
mammalia	<i>Mus musculus</i>	Muscu	2662.4	22619	21	16

TableS2 Inbred and wild maize used in the present study.

Accession number	Name	Type
1	B73_SRR1575495	Inbred
2	CH10_SRR1575496	Inbred
3	D06_SRR1575497	Inbred
4	D09_SRR1575498	Inbred
5	D152_SRR1575499	Inbred
6	DK105_SRR1575500	Inbred
7	EC169_SRR1575501	Inbred
8	EC49A_SRR1575502	Inbred
9	EP1_SRR1575503	Inbred
10	EP44_SRR1575504	Inbred
11	EZ5_SRR1575505	Inbred
12	F03802_SRR1575506	Inbred
13	F252_SRR1575508	Inbred
14	F283_SRR1575509	Inbred
15	F2_SRR1575507	Inbred
16	F353_SRR1575510	Inbred
17	F618_SRR1575511	Inbred
18	F64_SRR1575512	Inbred
19	F7_SRR1575513	Inbred
20	F98902_SRR1575514	Inbred
21	FF0721H-7_SRR1575515	Inbred
22	Lo11_SRR1575516	Inbred
23	Mo17_SRR1575517	Inbred
24	PH207_SRR1575518	Inbred
25	UH006_SRR1575520	Inbred
26	UH007_SRR1575521	Inbred
27	UH009_SRR1575522	Inbred
28	UH250_SRR1575523	Inbred
29	UH304_SRR1575524	Inbred
30	W117_SRR1575525	Inbred
31	TIL01	Wild
32	TIL02	Wild
33	TIL03	Wild
34	TIL04-TIP285	Wild
35	TIL04-TIP454	Wild
36	TIL05	Wild
37	TIL06-TIP260	Wild
38	TIL06-TIP496	Wild
39	TIL07	Wild
40	TIL08	Wild
41	TIL09	Wild

42	TIL10	Wild
43	TIL11	Wild
44	TIL12	Wild
45	TIL14-TIP498	Wild
46	TIL15	Wild
47	TIL16	Wild
48	TIL17	Wild
49	TIL25-TIP489	Wild
50	TIP489.2	Wild
51	TIP498.2	Wild
52	Teosinte	Wild

TableS3 Primer sequences used for RT-qPCR analysis.

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>ZmTLC1</i>	CTTCTGTTCAAGCATGGGTCCTCA	TTTCCCAAGCAACAAGAGCACC
<i>ZmTLC2</i>	CTTCGGTGTCTCCACCACAATC	CAGCAGGTCAGGAAGACGAAGA
<i>ZmTLC3</i>	GGTGGCTGTTCCCGTTGTTC	GATCAGGCAGCTGGCGC
<i>ZmTLC4</i>	AGATGGCGACGATGACTGC	AGCACAGAGGTGTACGGAACGA
<i>ZmTLC5</i>	TCCTAGAGATTGGGAAGATGGC	GGAACATAACGAGCCGAAGAAGTA
<i>ZmTLC6</i>	CGCCGTATCGCTTCTCCAC	ACTGCCACCAAATAGTTCTTCATG
<i>ZmTLC7</i>	TCTTCACCGAAATCACGACTCC	ATTATCCGAGCAATCAGCCATC
<i>ZmTLC8</i>	TGCTACTGTCGTCCTGATTGTT	CGGAGAAGAACCCATGAAATAAC
<i>ZmTLC9</i>	CGTCATTCCGTGGTGGGTG	CTTCTTTGACTTGGGAGGGG
<i>ZmTLC10</i>	GCCTTGATGAGGGACTATCTGCT	CAATATTGAGTGAAATCGTAAGCC
<i>ZmTLC11</i>	GGTGGGTTTTAATATATCGGATGC	TGAATCTCGTGAGGAACAATGC
<i>ZmTLC12</i>	GGTTCAGTTGTCCTTGCCATTCAT	GCTCGTGCTCCAGAGAATCCAG
<i>ZmTLC13</i>	CGTGGCATCGTGGATACTTCTC	TTTCTCCTTGTCAGGGTCAGC
<i>ZmTLC14</i>	GCGTGCTGCCACCTCAAC	CTTGAGCATCTCCCGCAGGT
<i>ZmTLC15</i>	CAATGTTTGTTACTTGGCTGATGG	TAGTGAACAGTATGGTGGGGGC
<i>ZmTLC16</i>	CTCGTCGCTGATGCTCACAAAT	CAATCCTGATGGCTCTGCTGGT
<i>ZmTLC17</i>	GTCCTTCACCATATGCTGTCGC	ATCGGAGGTTGATTCCAGGTGT
<i>ZmTLC18</i>	CGCCTCGTCTACAAGCCATTA	CTTGACAATCTTTGCTTGCCTG
<i>ZmGADPH</i>	CTTCGGCATTGTTGAGGGTTTG	TCCTTGGCTGAGGGTCCGTC
<i>ZmActin1</i>	GGGATTGCCGATCGTATGAG	GAGCCACCGATCCAGACACT

TableS4 Ka, Ks and Ka/Ks ratio of WGD/SD and LD duplicated gene pairs in surveyed angiosperms.

Gene1	Gene2	Ks	Ka	Ka/Ks	Duplication pairs
Aco023437	Aco023438	9.1895	1.5284	0.1663	Aco_LD1
Aco002236	Aco008651	0.922	0.1188	0.1288	Aco_WGD1
AT1G35170.1	AT1G35180.1	0.0572	0.0292	0.5112	AT_LD1
AT1G31300.1	AT4G19645.1	3.4969	0.1849	0.0529	AT_WGD1
Bradi2g09580	Bradi2g09607	0.8721	0.135	0.1548	Bd_LD1
Bradi2g20150	Bradi2g51050	0.8881	0.1725	0.1943	Bd_WGD1
BraA08g025260.3C	BraA08g025270.3C	0.1145	0.0737	0.6431	Brapa_LD1
BraA01g010800.3C	BraA08g013470.3C	0.2289	0.0884	0.3864	Brapa_WGD1
BraA01g010800.3C	BraA09g033370.3C	2.8028	0.2725	0.0972	Brapa_WGD2
BraA01g033950.3C	BraA03g038810.3C	54.0486	1.3985	0.0259	Brapa_WGD3
BraA01g033950.3C	BraA05g028040.3C	0.3769	0.1013	0.2687	Brapa_WGD4
BraA02g028970.3C	BraA09g027750.3C	0.2529	0.0647	0.256	Brapa_WGD5
BraA03g038810.3C	BraA05g028040.3C	51.9784	1.1822	0.0227	Brapa_WGD6
BraA07g010140.3C	BraA09g033370.3C	0.3335	0.0165	0.0495	Brapa_WGD7
BraA08g025260.3C	BraA09g059280.3C	3.5269	0.3445	0.0977	Brapa_WGD8
Cg5g012160.1	Cg5g012170.1	0.5174	0.1647	0.3183	Cgrandis_LD1
Cg5g012160.1	Cg7g015400.1	2.8258	0.2427	0.0859	Cgrandis_WGD1
Eucgr.G01439	Eucgr.G01442	0.0201	0.0205	1.019	Eu_LD1
Eucgr.B03093	Eucgr.G02399	0.9497	0.1327	0.1397	Eu_WGD1
Eucgr.G01439	Eucgr.I01150	1.5345	0.1925	0.1254	Eu_WGD2
Glyma.02G126800	Glyma.02G127000	0.0464	0.0135	0.2901	Gmax_LD1
Glyma.02G132400	Glyma.07G212500	0.0927	0.0285	0.307	Gmax_WGD1
Glyma.02G238600	Glyma.11G202100	0.4503	0.1471	0.3267	Gmax_WGD2
Glyma.02G238600	Glyma.14G207500	0.1312	0.0322	0.2451	Gmax_WGD3
Glyma.02G238600	Glyma.18G048700	0.451	0.1396	0.3096	Gmax_WGD4
Glyma.02G283000	Glyma.08G305100	0.3628	0.1078	0.2971	Gmax_WGD5
Glyma.02G283000	Glyma.14G031400	0.0894	0.0178	0.1985	Gmax_WGD6
Glyma.02G283000	Glyma.18G113300	0.3653	0.1088	0.298	Gmax_WGD7
Glyma.04G249500	Glyma.06G113400	0.1661	0.0461	0.2774	Gmax_WGD8
Glyma.08G305100	Glyma.14G031400	0.3776	0.0949	0.2513	Gmax_WGD9
Glyma.08G305100	Glyma.18G113300	0.0686	0.0251	0.3656	Gmax_WGD10
Glyma.11G202100	Glyma.14G207500	0.5063	0.1704	0.3366	Gmax_WGD11
Glyma.11G202100	Glyma.18G048700	0.0483	0.0276	0.572	Gmax_WGD12
Glyma.14G031400	Glyma.18G113300	0.3567	0.0922	0.2585	Gmax_WGD13
Glyma.14G071100	Glyma.17G253500	0.2205	0.056	0.2541	Gmax_WGD14
Glyma.14G207500	Glyma.18G048700	0.4909	0.1627	0.3315	Gmax_WGD15

Glyma.16G062400	Glyma.19G076700	2.0046	0.3119	0.1556	Gmax_WGD16
Gorai.008G025000.1	Gorai.013G043800.1	0.3998	0.1041	0.2603	Graim_WGD1
Gorai.008G174300.1	Gorai.013G102900.1	0.3881	0.0934	0.2406	Graim_WGD2
Gorai.009G150200.1	Gorai.011G050300.1	0.3756	0.1029	0.2738	Graim_WGD3
GSMUA_Achr3G10560_001	GSMUA_Achr5G23940_001	0.355	0.059	0.1661	Mac_WGD1
GSMUA_Achr3G10560_001	GSMUA_Achr9G18470_001	0.7028	0.3837	0.546	Mac_WGD2
GSMUA_Achr8G23520_001	GSMUA_Achr9G14650_001	0.3336	0.1335	0.4003	Mac_WGD3
Medtr5g049230.1	Medtr5g049240.1	0.3525	0.0948	0.2689	Mt_LD1
Medtr3g450410.1	Medtr5g090550.1	0.6917	0.0919	0.1329	Mt_WGD1
Os01g56230	Os05g43540	0.6953	0.1588	0.2284	Os_WGD1
Os01g60120	Os05g40700	0.8186	0.1601	0.1956	Os_WGD2
Potri.002G056600.1	Potri.005G206000.1	0.1912	0.0634	0.3316	Potri_WGD1
Potri.002G083300.1	Potri.005G178200.1	0.2665	0.0668	0.2507	Potri_WGD2
Potri.004G141000.1	Potri.009G101800.1	0.169	0.0689	0.408	Potri_WGD3
Potri.008G113900.1	Potri.010G134700.1	0.1884	0.0584	0.31	Potri_WGD4
Potri.012G118100.1	Potri.015G113200.1	0.1395	0.0379	0.2719	Potri_WGD5
Pp3c18_640	Pp3c19_9050	1.6134	0.3856	0.239	Ppaten_WGD1
Prupe.1G298900.1	Prupe.5G211700.1	1.1559	0.2387	0.2065	Ppersica_WGD1
Prupe.1G233600.1	Prupe.3G301200.1	4.4423	0.2962	0.0667	Ppersica_WGD2
Prupe.8G125400.1	Prupe.8G125600.1	0.1591	0.0994	0.6246	Ppersics_LD1
Sobic.003G120500	Sobic.003G120600	0.2886	0.0385	0.1335	Sbi_LD1
Sobic.003G308800	Sobic.009G193700	0.8609	0.1675	0.1945	Sbi_WGD1
Sobic.003G335400	Sobic.009G177000	1.1523	0.178	0.1545	Sbi_WGD2
Solyc04g080750.2.1	Solyc12g089230.1.1	0.863	0.1539	0.1783	Sly_WGD1
Spipo10G0040500	Spipo12G0013700	0.83	0.156	0.188	Spipo_WGD1
Spipo10G0040500	Spipo25G0017000	1.1894	0.184	0.1547	Spipo_WGD2
Spipo12G0013700	Spipo25G0017000	1.3714	0.1681	0.1225	Spipo_WGD3
Spipo15G0019900	Spipo4G0009000	1.3817	0.3589	0.2598	Spipo_WGD4
Zm00001d005671	Zm00001d020296	0.0886	0.0259	0.2922	Zm_WGD1
Zm00001d034572	Zm00001d013028	0.3092	0.0106	0.0343	Zm_WGD2
Zm00001d042699	Zm00001d012265	0.1321	0.0192	0.1456	Zm_WGD3
Zm00001d050910	Zm00001d016993	0.1617	0.0676	0.4179	Zm_WGD4
Zm00001d013028	Zm00001d030772	0.6296	0.1617	0.2569	Zm_TD1
Zm00001d005671	Zm00001d028534	3.072	0.5971	0.1944	Zm_TD2