

Figure S1: K-mer (K=17) analysis of the two genomes. The X-axis is depth; the y-axis represents the frequency. The left peak is the heterozygous peak and the right peak was the homozygous peak. A: *A. altilis*, B: *A. heterophyllus*.

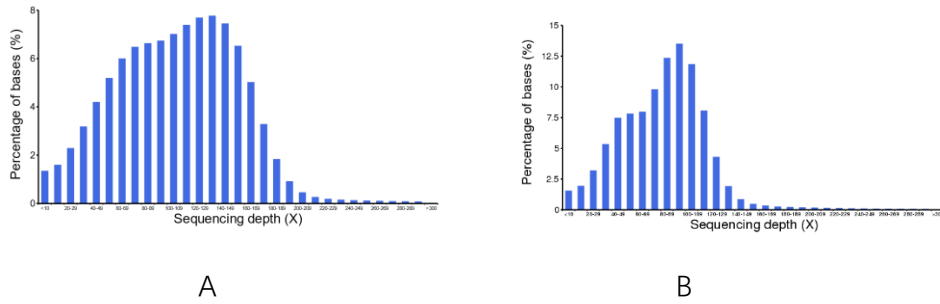


Figure S2: Distribution of sequencing depth of the assembly data. The X-axis is the depth and the y-axis show the percentage of bases at each depth. The results show that <1% of bases have a sequencing depth less than 10. A: *A. altilis*, B: *A. heterophyllus*.

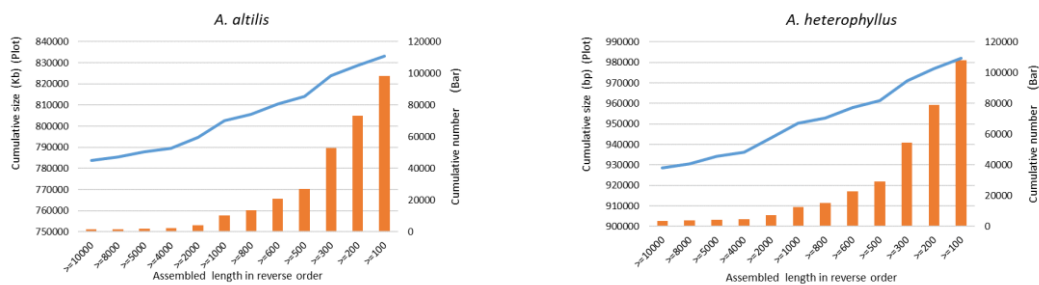


Figure S3: Distribution of the length and number of the scaffold in two species. The blue lines show the size, and the orange bars show the number.

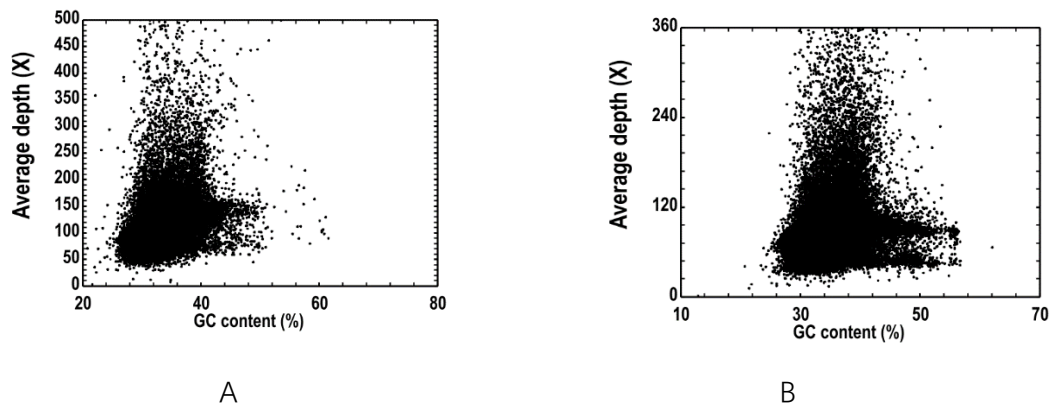


Figure S4: The distribution of GC content. The GC content and the average depth were calculated from 10 kb non-overlapping sliding windows. The distribution pattern of GC content indicates a relatively pure single genomic sample without contamination and no GC bias. A: *A. altilis*, B: *A. heterophyllum*.

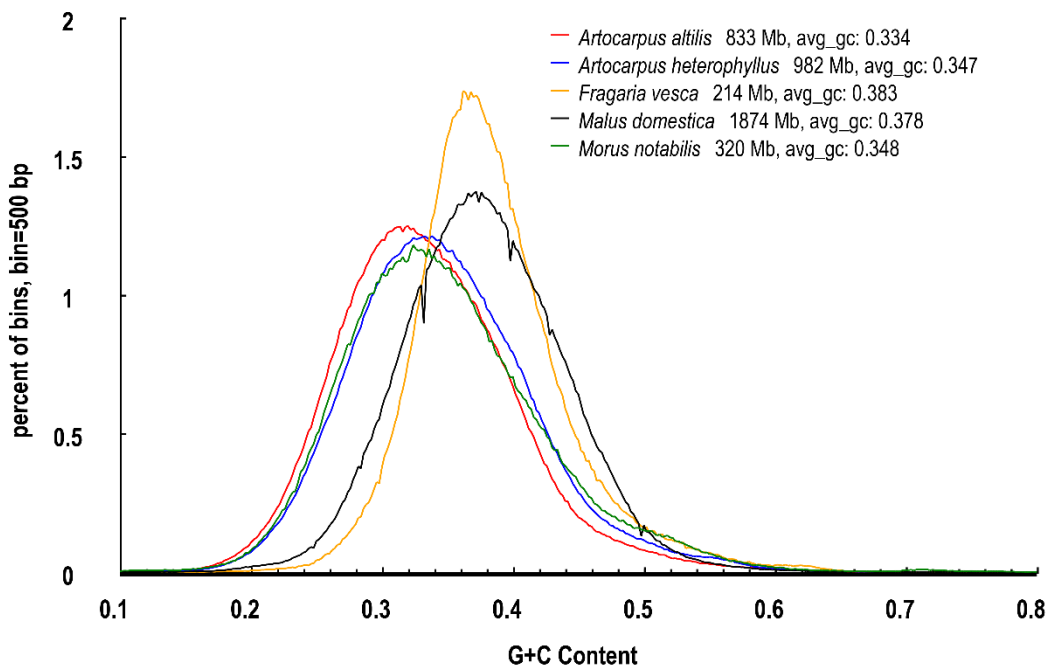


Figure S5: Comparison of GC content across closely related species. The *A. altilis*, *A. heterophyllum* and *M. notabilis* belong to the same family, and they show the same peaks of GC content.

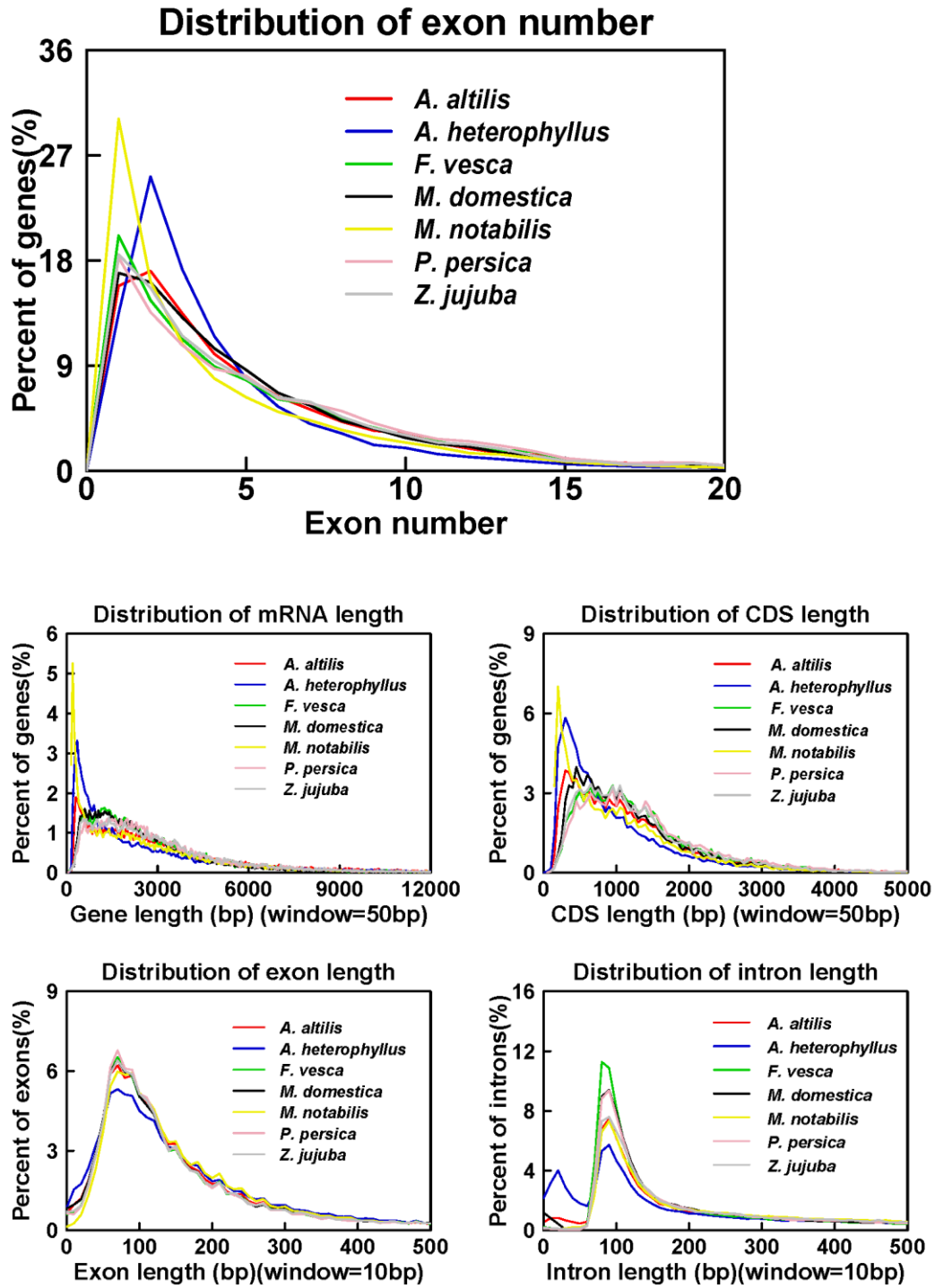


Figure S6: Statistics of gene models in *A. altilis*, *A. heterophyllus*, *F. vesca*, *M. domestica*, *M. notabilis*, *Prunus persica* and *Ziziphus jujuba*.

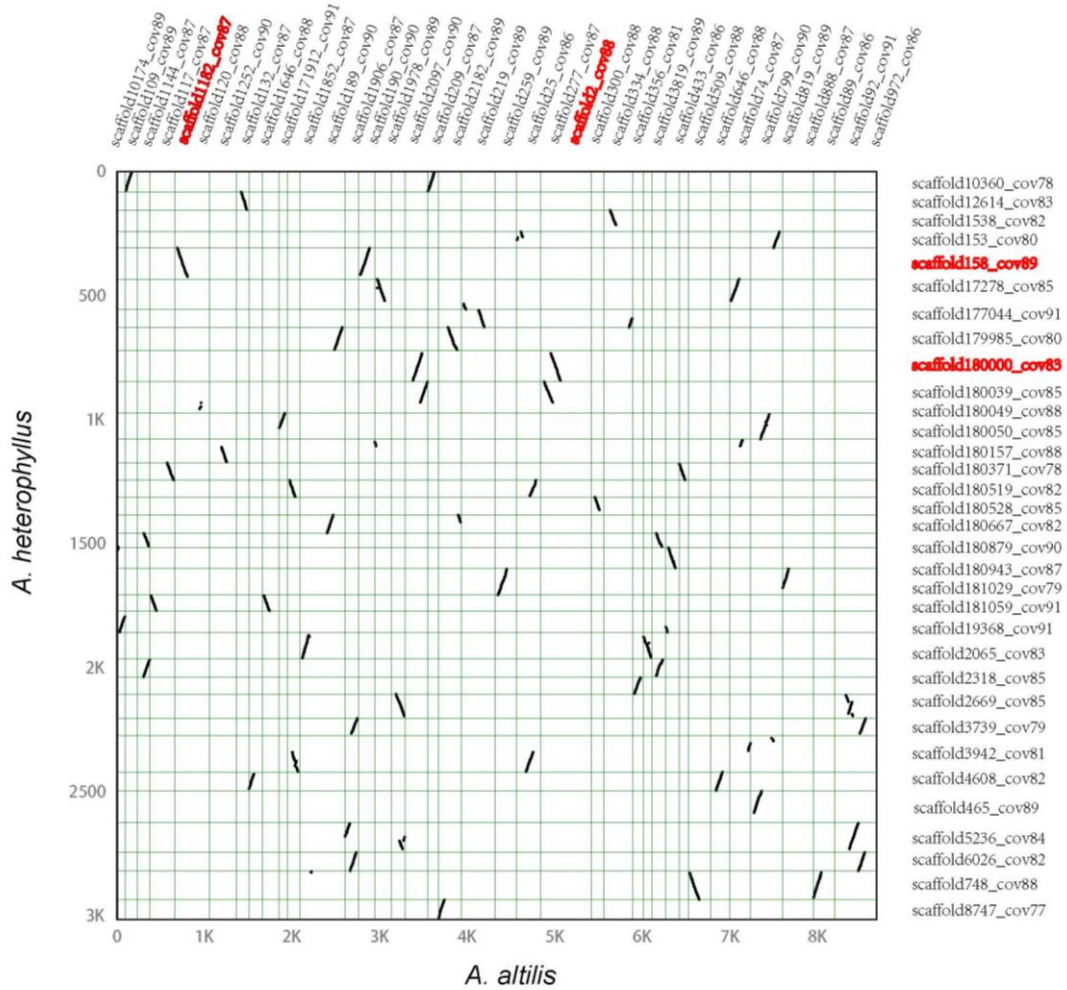
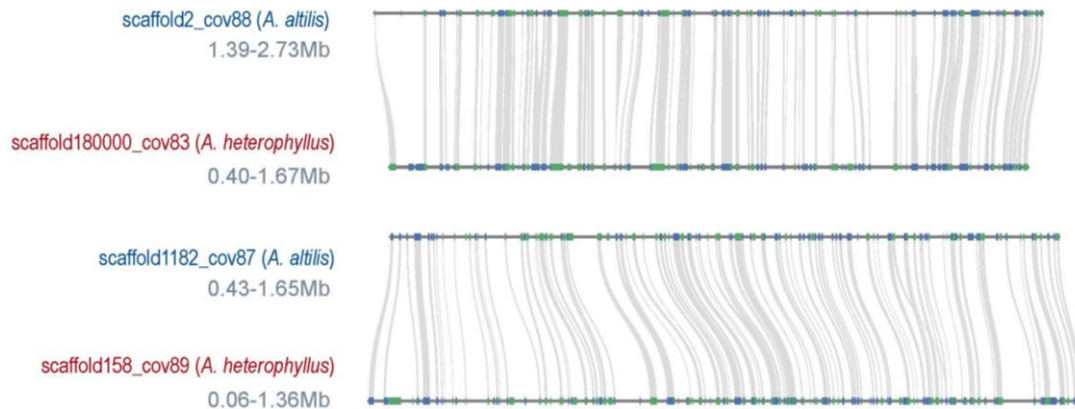
AInter-genomic comparison: *A. altilis* vs *A. heterophyllus* (3,132 gene pairs)**B**

Figure S7: (A) The collinearity between two species. The X-axis is the *A. heterophyllus*; Y-axis is the *A. altilis*. (B) Preservation of co-localized genes on the two largest overlapping orthologous scaffolds of *A. altilis* and *A. heterophyllus*.

Table S1. Statistics of the raw and clean data of DNA sequencing. Clean data were obtained by filtering raw data as described in the article. The sequencing depth calculated based on a genome size of 811, 1005 Mb of *A. attilis* and *A. heterophyllus*, respectively.

Species	Library	Read insert length (bp)	Raw data			Clean data		
			base number (bp)	Reads number (bp)	Depth (X)	base number (bp)	Reads number (bp)	Depth (X)
<i>A. attilis</i>	170	PE100	27,997,546,200	279,975,462	34.51	24,457,319,840	257,445,472	30.15
	350	PE100	37,756,156,600	377,561,566	46.54	32,314,250,380	323,142,504	39.83
	500	PE100	17,016,336,900	170,163,369	20.98	14,394,991,000	143,949,910	17.74
	800	PE100	27,820,793,600	278,207,936	34.29	23,427,277,780	234,272,778	28.88
	2000	PE100	29,259,701,000	292,597,010	36.07	11,676,799,030	116,767,990	14.39
	6000	PE100	26,886,185,600	268,861,856	33.14	10,018,166,480	100,181,665	12.35
	10000	PE100	34,525,749,400	345,257,494	42.56	10,295,921,210	102,959,212	12.69
	20000	PE100	25,992,313,200	259,923,132	32.04	3,530,699,890	35,306,999	4.35
	Total		227,254,782,500	2,272,547,825	280.13	130,115,425,610	1,314,026,530	160.39
<i>A. heterophyllus</i>	170	PE100	38,595,699,600	385,956,996	38.38	33,017,200,030	330,172,000	32.83
	350	PE100	32,428,208,400	324,282,084	32.25	27,992,453,380	279,924,534	27.84
	500	PE100	14,831,029,800	148,310,298	14.75	12,425,626,520	124,256,265	12.36
	800	PE100	22,618,262,000	226,182,620	22.49	19,410,382,710	194,103,827	19.30
	2000	PE100	76,821,363,600	768,213,636	76.39	36,971,268,180	369,712,682	36.77
	6000	PE100	32,718,039,600	327,180,396	32.54	14,483,081,550	144,830,816	14.40
	10000	PE100	22,875,623,600	228,756,236	22.75	4,204,951,180	42,049,512	4.18
	20000	PE100	32,777,398,400	327,773,984	32.59	4,311,498,050	43,114,981	4.29
	Total		273,665,625,000	2,736,656,250	272.14	152,816,461,600	1,528,164,616	151.96

Table S2. Summary statistics of the transcriptome data.

Species	Abbreviation	Raw data		Clean data		Sample
		Base number (bp)	Reads number (bp)	Base number (bp)	Reads number (bp)	
<i>A. altilis</i>	AALBd	4,629,731,282	19,131,121	611,897,508	2,886,309	Leaf bud
	AAYL	11,655,613,464	48,163,692	1,117,701,948	5,272,179	Young leaf
	AASL	10,178,838,956	42,061,318	1,024,350,292	4,831,841	Semi mature leaf
	AAML	19,051,406,682	78,724,821	2,635,339,776	12,430,848	Mature leaf
	AAST	8,529,531,032	35,245,996	916,693,088	4,324,024	stem
	Total	54,045,121,416	223,326,948	6,305,982,612	29,745,201	
<i>A. heterophyllus</i>	AHLB	1,174,736,970	9,708,570	20,728,520	180,248	Leaf bud
	AHYL	11,510,346,914	95,126,834	194,000,860	1,686,964	Young leaf
	AHML	928,769,616	7,675,782	66,734,270	580,298	Mature leaf
	AHSL	13,289,054,416	109,826,896	200,927,310	1,747,194	Semi mature leaf
	AHRT	2,612,876,178	21,594,018	232,498,720	2,021,728	Roots
	AHSDL	12,200,805,826	100,833,106	1,097,277,560	9,541,544	Seedling
	AHS	6,078,062,078	50,231,918	1,001,884,60	871,204	Stem
	Total	47,794,651,998	394,997,124	1,812,167,240	16,629,180	

Table S3. Estimation of the genome size based on K-mer statistics.

Species	Kmer value	Kmer number	Peak depth(X)	Genome size (Mb)	Used bases (Gb)	Used reads (Mb)	Depth (X)
<i>A. altilis</i>	17	59,221,955,980	73	811.26	70.08	678.89	44.96
<i>A. heterophyllus</i>	17	39,218,751,230	39	1,005.61	46.29	442.23	46.03

Table S4. BUSCO evaluation of the annotated protein-coding genes in *A. altilis* and *A. heterophyllus*.

BUSCOs	<i>A. altilis</i>		<i>A. heterophyllus</i>	
	N	P (%)	N	P (%)
Complete BUSCOs	1,319	91.6	1,288	89.5
Complete single-copy	977	67.8	885	61.5
Complete duplicated	342	23.8	403	28.0
Fragmented	32	2.2	30	2.1
Missing	89	6.2	122	8.4

Table S5. Analysis of gene families of different species.

Species	Genes number	Genes in families	Unclustered genes	Family number	Unique families	Average genes per family
<i>A. thaliana</i>	26,637	23,011	3,626	12,620	769	1.8
<i>A. altilis</i>	33,986	27,354	6,632	15,614	136	1.8
<i>A. heterophyllus</i>	35,845	28,969	6,876	15,768	242	1.8
<i>F. vesca</i>	34,301	26,703	7,598	15,188	1,427	1.8
<i>M. domestica</i>	61,721	45,647	16,074	17,385	3,352	2.6
<i>M. notabilis</i>	27,085	20,805	6,280	14,955	567	1.4
<i>P. mume</i>	31,128	25,702	5,426	16,060	566	1.6
<i>P. persica</i>	28,701	25,385	3,316	15,654	231	1.6
<i>Z. jujuba</i>	36,942	34,050	2,892	14,170	755	2.4

Table S6. Enriched GO terms (level 3) of genes in families with expansion.

Species	GO ID	GO Term	Type	P-value	Number of genes
<i>A. altilis</i>	GO:0036094	small molecule binding	Molecular Function	5.74E-27	862
	GO:0043167	ion binding	Molecular Function	4.10E-22	1,239

	GO:0016740	transferase activity	Molecular Function	1.43E-11	763
	GO:0097159	organic cyclic compound binding	Molecular Function	2.28E-07	1,274
	GO:1901363	heterocyclic compound binding	Molecular Function	2.28E-07	1,274
	GO:0001871	pattern binding	Molecular Function	0.000227	13
	GO:0005515	protein binding	Molecular Function	0.003724	630
	GO:0016049	cell growth	Biological Process	1.21E-06	12
	GO:0044700	single organism signaling	Biological Process	0.000533	72
	GO:0022857	transmembrane transporter activity	Molecular Function	1.45E-17	332
	GO:0022892	substrate-specific transporter activity	Molecular Function	1.53E-09	151
	GO:0016491	oxidoreductase activity	Molecular Function	8.81E-07	547
	GO:0036094	small molecule binding	Molecular Function	2.11E-06	983
	GO:0038023	signaling receptor activity	Molecular Function	1.00E-05	27
	GO:0048037	cofactor binding	Molecular Function	0.000102	164
	GO:0019208	phosphatase regulator activity	Molecular Function	0.000673	15
	GO:0016829	lyase activity	Molecular Function	0.002478	86
	GO:0030246	carbohydrate binding	Molecular Function	0.006209	63
	GO:0005515	protein binding	Molecular Function	0.008019	892
A. <i>heterophyllus</i>	GO:0003682	chromatin binding	Molecular Function	0.014389	17
	GO:0044703	multi-organism reproductive process	Biological Process	1.28E-38	96
	GO:0044706	multi-multicellular organism process	Biological Process	1.28E-38	96
	GO:0048610	cellular process involved in reproduction	Molecular Function	2.68E-37	97
	GO:0022414	reproductive process	Biological Process	3.57E-36	96
	GO:0044707	single-multicellular organism process	Biological Process	2.67E-27	100
	GO:0044700	single organism signaling	Biological Process	2.31E-14	149
	GO:0044763	single-organism cellular process	Biological Process	3.69E-11	831
	GO:0051716	cellular response to stimulus	Biological Process	1.07E-08	180
	GO:0044765	single-organism transport	Biological Process	5.90E-06	438

GO:0044710	single-organism metabolic process	Biological Process	2.90E-05	739
GO:0051234	establishment of localization	Biological Process	0.000225	493
GO:0009605	response to external stimulus	Biological Process	0.002533	7
GO:0051606	detection of stimulus	Biological Process	0.007408	5
GO:0031224	intrinsic to membrane	Cellular Component	4.87E-06	326
GO:0008287	protein serine/threonine phosphatase complex	Cellular Component	0.001066	13
GO:0044425	membrane part	Cellular Component	0.003813	362
GO:0044421	extracellular region part	Cellular Component	0.007408	5

Table S7. Enriched pathways of genes in families with expansion.

Species	Pathway ID	KEGG description	Number of genes	P-value (<=0.05)
<i>A. attilis</i>	ko04626	Plant-pathogen interaction	265	1.33679E-15
	ko04144	Endocytosis	127	1.55321E-11
	ko04146	Peroxisome	79	7.69212E-10
	ko04141	Protein processing in endoplasmic reticulum	179	1.75141E-06
	ko03040	Spliceosome	150	9.27025E-06
	ko00300	Lysine biosynthesis	16	6.66998E-05
	ko00450	Selenocompound metabolism	22	0.000214547
	ko00072	Synthesis and degradation of ketone bodies	8	0.000814513
	ko00190	Oxidative phosphorylation	74	0.002151087
	ko00195	Photosynthesis	34	0.006288728
	ko00260	Glycine, serine and threonine metabolism	44	0.00738846
	ko00564	Glycerophospholipid metabolism	50	0.007535005
	ko03060	Protein export	28	0.007913934
	ko03050	Proteasome	30	0.008523159
	ko03430	Mismatch repair	88	1.09E-14

A.	ko04626	Plant-pathogen interaction	339	1.9E-13
<i>heterophyllus</i>	ko03030	DNA replication	98	6E-13
	ko03440	Homologous recombination	84	1.28E-12
	ko00380	Tryptophan metabolism	40	3.05E-08
	ko01110	Biosynthesis of secondary metabolites	811	1.21E-07
	ko03420	Nucleotide excision repair	92	1.64E-07
	ko00908	Zeatin biosynthesis	59	2.94E-06
	ko00941	Flavonoid biosynthesis	90	7.46E-06
	ko00052	Galactose metabolism	80	2.83E-05
	ko04712	Circadian rhythm - plant	78	4.5E-05
	ko03040	Spliceosome	185	5.32E-05
	ko00940	Phenylpropanoid biosynthesis	189	5.41E-05
	ko00903	Limonene and pinene degradation	36	6.01E-05
	ko00620	Pyruvate metabolism	85	7.13E-05
	ko00130	Ubiquinone and other terpenoid-quinone biosynthesis	53	0.000353
	ko04144	Endocytosis	136	0.00072
	ko00604	Glycosphingolipid biosynthesis - ganglio series	31	0.000844
	ko02010	ABC transporters	74	0.000855

Table S8. The gene list of starch biosynthesis in *Glycine max.*

Category	ID in <i>Glycine max</i>
AGPL	Glyma.04G011900
AGPL	Glyma.04G030300
AGPL	Glyma.06G011700
AGPL	Glyma.06G030400
AGPL	Glyma.11G116600
AGPL	Glyma.12G042400
AGPL	Glyma.17G252500
AGPL	Glyma.19G223100
AGPS	Glyma.02G304500
AGPS	Glyma.14G009300

BE	Glyma.03G192300
BE	Glyma.04G017700
BE	Glyma.06G018000
BE	Glyma.19G192800
DPE	Glyma.03G121100
DPE	Glyma.04G219500
DPE	Glyma.06G146400
DPE	Glyma.19G125800
GBSS	Glyma.07G049900
GBSS	Glyma.20G218100
ISA	Glyma.03G151200
ISA	Glyma.06G100600
ISA	Glyma.08G028400
ISA	Glyma.19G153700
PHOH	Glyma.08G334000
PHOH	Glyma.13G057800
PHOH	Glyma.13G235600
PHOH	Glyma.18G067200
PHOH	Glyma.19G028400
PHOH	Glyma.20G026700
PUL	Glyma.10G197000
SS	Glyma.04G235200
SS	Glyma.05G127800
SS	Glyma.06G129400
SS	Glyma.07G260500
SS	Glyma.08G082600
SS	Glyma.13G062700
SS	Glyma.13G204700
SS	Glyma.15G108000
SS	Glyma.19G022900
