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Supplementary Information for

The genome of *Crucihimalaya himalaica*, a close relative of *Arabidopsis*, shows ecological adaptation to high altitude

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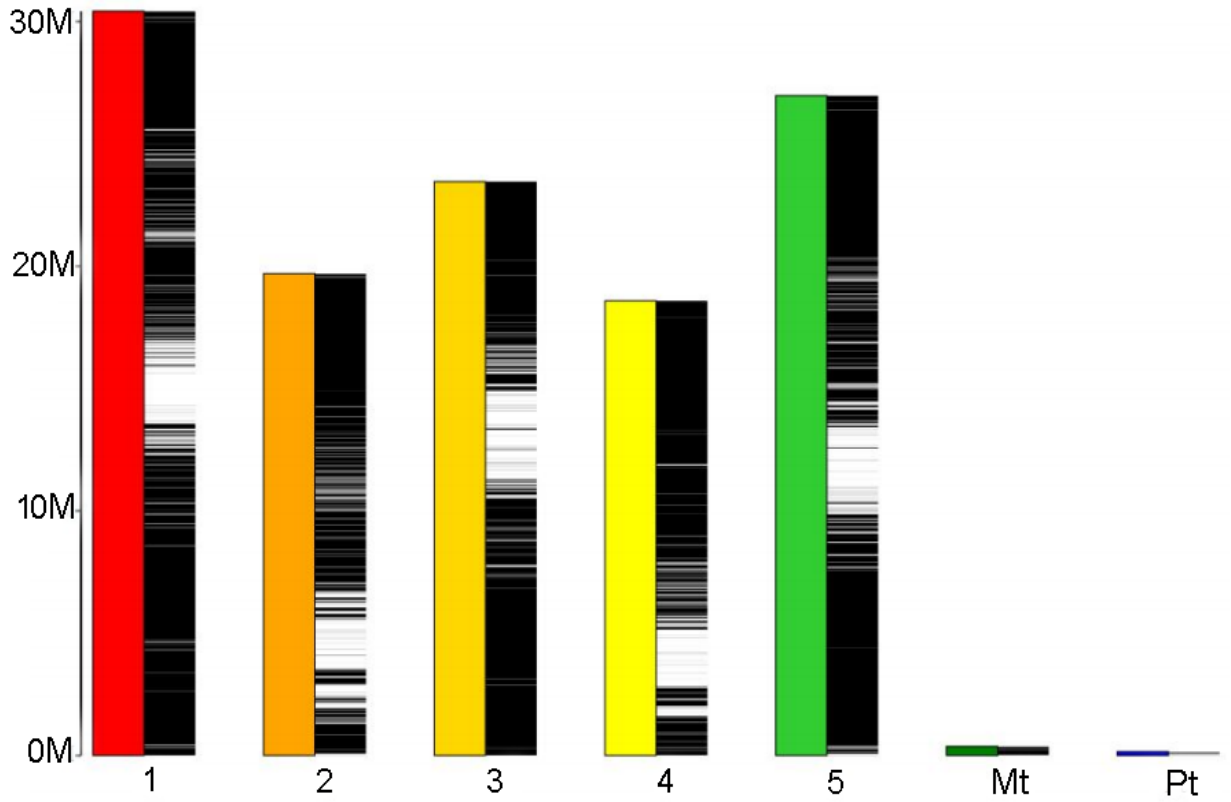

Figure S1. The coverage diagram using raw reads mapped to the chromosomes of *Arabidopsis thaliana* by Lastz software.

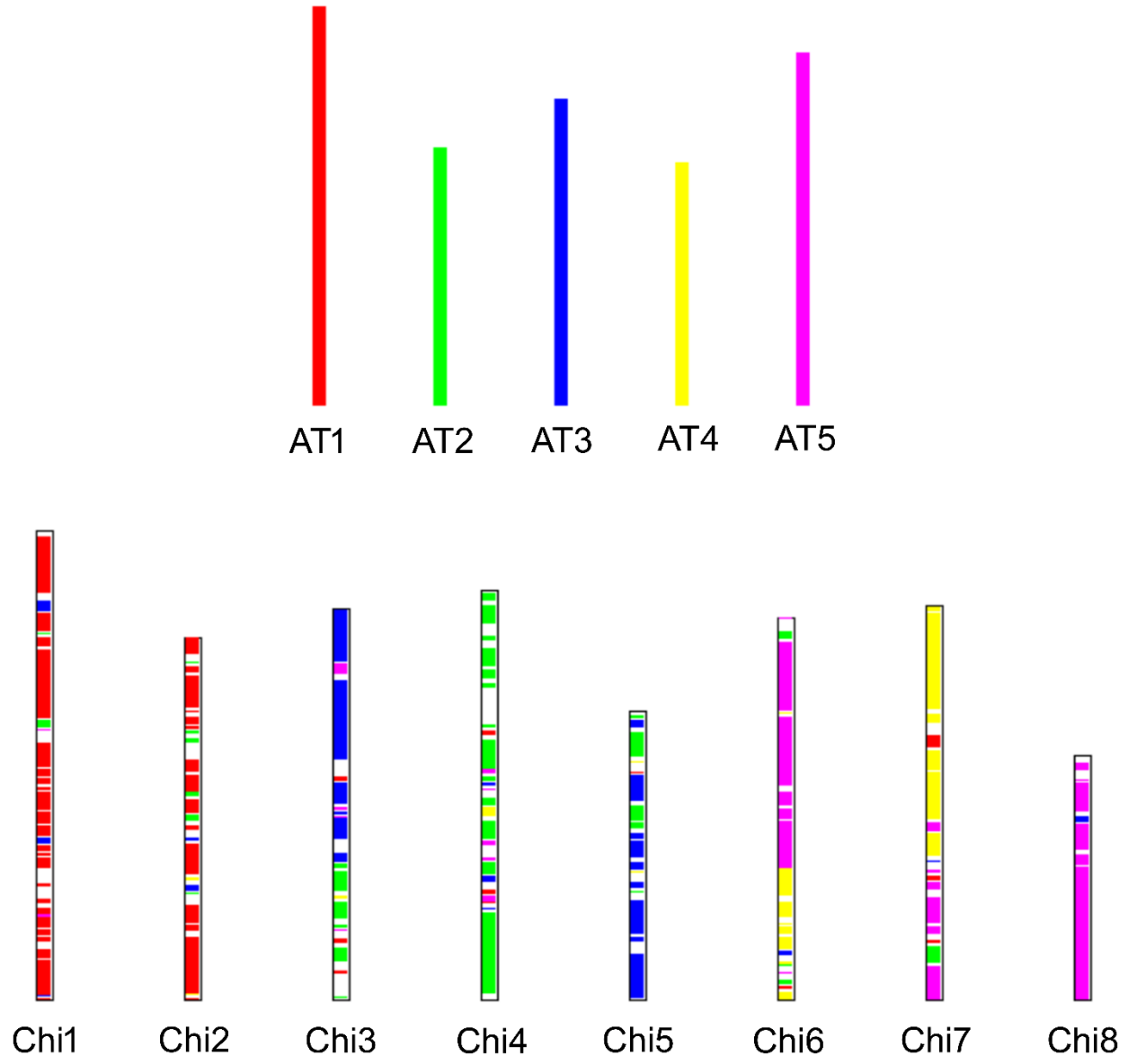

Figure S2. The genomic collinearity analysis between chromosomes of *A. thaliana* (AT) and pseudo-chromosomes of *Crucihimalaya himalaica* (Chi) using MCscanX software. We first identified the orthologs between *C. himalaica* and *A. thaliana*. Then we locate the scaffolds of *C. himalaica* to the ancestral Brassicaceae karyotype chromosomes (1) by corresponding genome blocks which include the same orthologs of *A. thaliana*. We have not used the pseudo-chromosomes of *C. himalaica* for further analyses because there are many genome gaps.

1. Cheng S, et al. (2013) The *Tarenaya hassleriana* genome provides insight into reproductive trait and genome evolution of crucifers. *Plant Cell* 25(8):2813-2830.

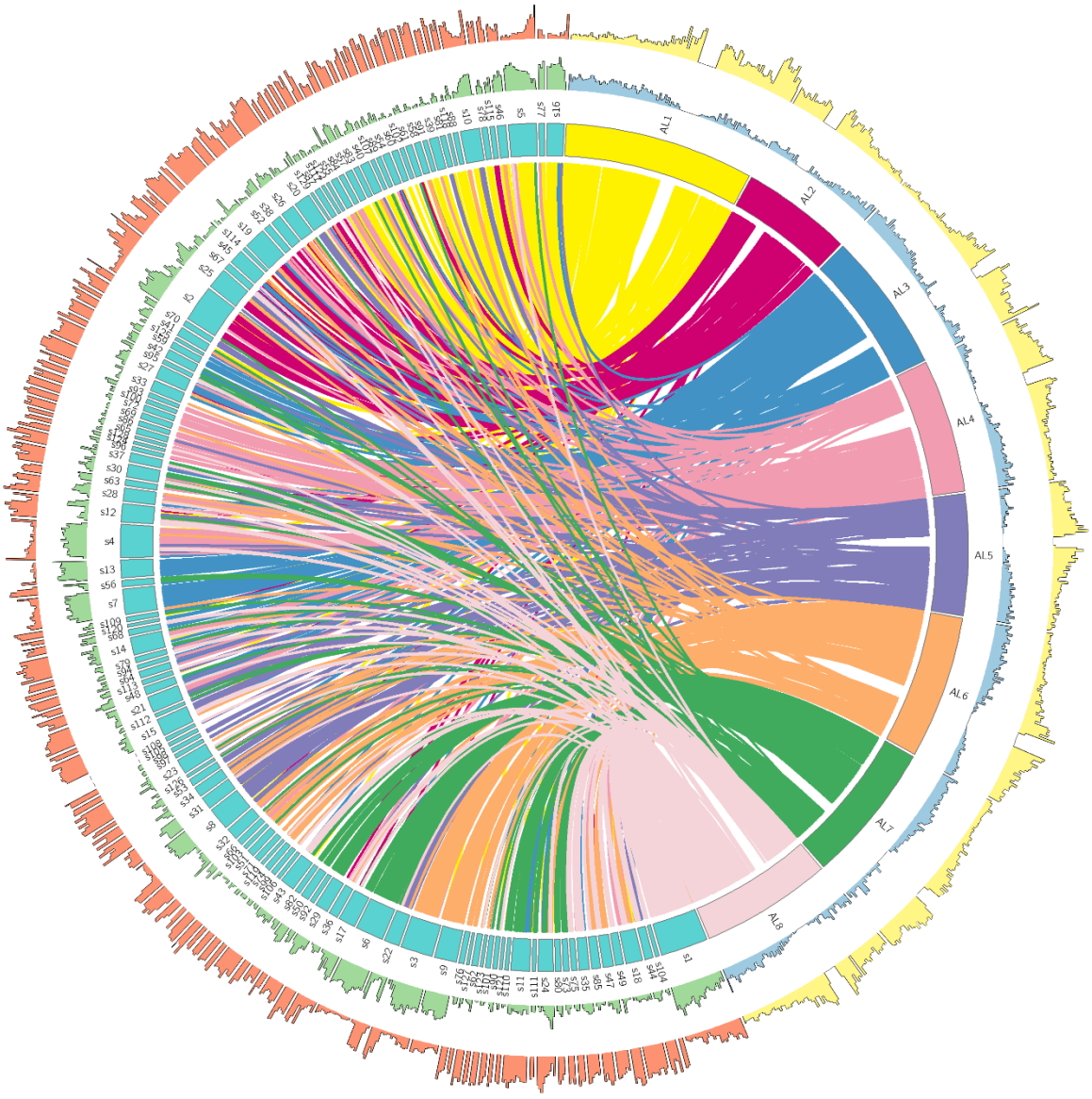

Figure S3. Comparative genomic analyses and Circos plot of *C. himalaica* vs. *A. lyrata* genomic features. Tracks from inside to outside are: collinearity blocks between both genomes, number of chromosomes/scaffolds, gene density, and transposable element density.

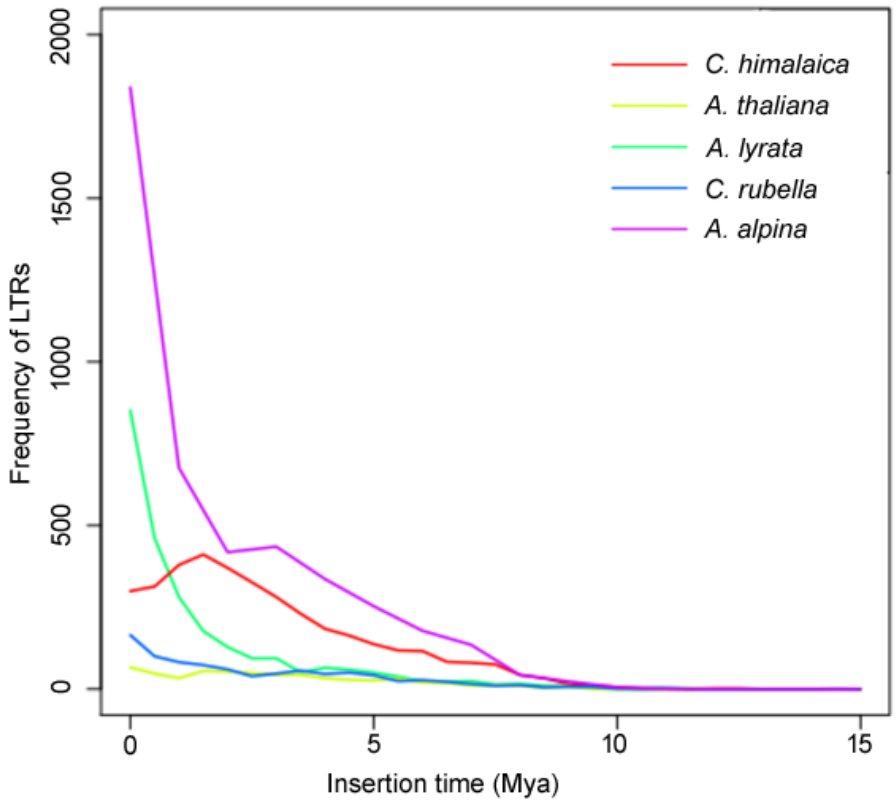

Figure S4. Insertion time distribution of long terminal repeat retrotransposons in five relatives. There is comparably dramatic proliferation of LTR retrotransposons in *A. alpina*. The different pattern of proliferation of LTR retrotransposons between *A. alpina* and *C. himalaica* might reflect different processes of genome adaptive evolution and geological history.

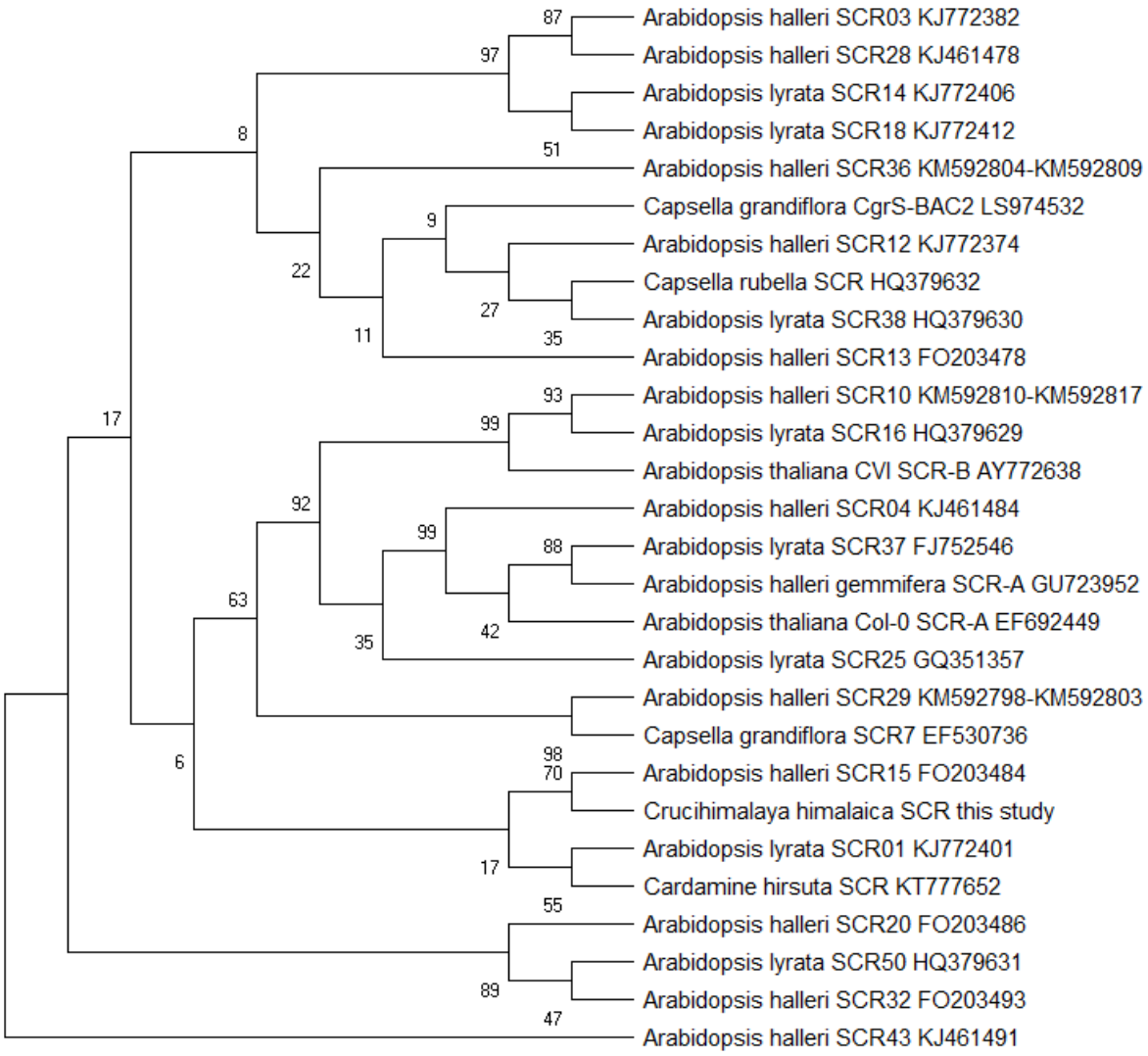

Figure S5. Molecular phylogeny of the SCR sequences from *A. lyrata*, *A. halleri*, *A. thaliana*, *C. hirsuta*, *C. grandiflora*, *C. rubella* and *C. himalaica*. Names of the SCR sequences are followed by the accession numbers. The phylogeny was generated using maximum likelihood algorithm with 500 bootstrap replicates.

Table S1. Statistics of characteristics of *C. himalaica* genome (*K*-mer=17)

Characteristics	
K-mer	17
Depth	66
N *K*-mer	18,107,540,600
Genome size	274.36 Mb
Revised Genome size	265.23 Mb
Heterozygous rate	0.70%
Repeat rate	49.82%

Table S2. Sequencing and quality filtering statistics.

Pair-end libraries	Insert size	Total data(G)	Sequence coverage (X)
Illumina reads	250 bp	15.22	67.45
	450 bp	8.16	36.16
	2 Kbp	5.95	26.37
	5 Kbp	5.52	24.46
	10 Kbp	4.71	20.87
	15 Kbp	4.93	21.85
Pacbio reads	/	6.19	27.43
Total	/	50.68	224.59

Table S3. Assessment of genome assembly quality by PE reads.

	Type	Percentage
Reads	Mapping rate (%)	96.69%
	Average sequencing depth	79.46%
	Coverage (%)	96.43%
Genome	Coverage (%)	95.82%
	Coverage at least 10X (%)	95.23%
	Coverage at least 20X (%)	94.05%

Table S4. Statistics of predicted protein-coding genes in *C. himalaica* and relatives

Species	Number	Average gene length (bp)	Average CDS length (bp)	Average exons per gene	Average exon length (bp)	Average intron length (bp)
C. himalaica	27,019	1,969.20	1,145.15	4.98	229.78	206.86
A. thaliana	27,173	1,879.97	1,218.93	5.16	236.26	158.93
A. lyrata	32,036	1,878.02	1,089.46	4.89	222.60	202.49
Capsella rubella	26,634	1,941.40	1,238.98	5.16	240.23	168.96

Table S5. Information of function annotation in *C. himalaica* genes.

#Database		Annotated Number	Annotated Percent (%)
NR		26,795	99.2
Swiss-Prot		21,163	78.3
KEGG		19,450	72
	All	22,639	83.8
InterPro	Pfam	21,008	77.8
	GO	15,078	55.8
Annotated		26,806	99.2
Total		27,019	-

Table S6. Statistics of noncoding RNA in *C. himalaica* genome.

Type		Copy	Average length (bp)	Total length (bp)	Percent of genome (%)
miRNA		448	118.647321	53,154	0.022645
tRNA		577	74.8544194	43,191	0.018401
rRNA	rRNA	153	126.052288	19,286	0.008217
	18S	9	350.666667	3,156	0.001345
	28S	12	133.166667	1,598	0.000681
	5.8S	1	167	167	0.000071
	5S	131	109.656489	14,365	0.00612
snRNA	snRNA	974	109.306982	106,465	0.045358
	CD-box	824	104.850728	86,397	0.036808
	HACA-box	51	127.960784	6,526	0.00278
	splicing	99	136.787879	13,542	0.005769

Table S7. Assessment of the *C. himalaica* genome assembly using transcriptome sequences from reads of different tissues assembled by trinity software.

Data	Number	Total length (bp)	Sequences covered by assembly (%)	With >90% sequence in one scaffold	Number Percent (%)	With >50% sequence in one scaffold	Number Percent (%)
>0bp	29,420	27,458,144	99.74	27,174	92.37	29,102	98.92
>200bp	29,420	27,458,144	99.74	27,174	92.37	29,102	98.92
>500bp	15,754	23,039,370	99.87	14,804	93.97	15,629	99.21
>1k	9,156	18,350,856	99.92	8,679	94.79	9,096	99.35
>2k	3,354	9,994,990	99.94	3,166	94.4	3,331	99.31

Table S8. Scaffolds from the *C. himalaica* assembly were aligned to conserved genes using BUSCO method.

Species	Genome Size	BUSCO annotation assessment results
C. himalaica	234.72 Mbp	C:96% [D:16%], F:1.4%, M:2.1%, n:956

C: Complete Single-Copy BUSCOs

D: Complete Duplicated BUSCOs

F: Fragmented BUSCOs

M: Missing BUSCOs

n: Total BUSCO groups searched

Table S9. Statistics of transcription factors (TFs) and transcription regulators (TRs) in *C. himalaica* genome.

TFs	***C. himalaica***	***C. rubella***	***A. thaliana***	***A. lyrata***
Alfin-like	7	7	7	7
AP2/ERF-AP2	12	14	14	13
AP2/ERF-ERF	112	129	128	128
AP2/ERF-RAV	4	3	4	5
B3	62	67	66	80
B3-ARF	15	19	22	20
BBR-BPC	7	6	7	8
BES1	9	9	8	9
bHLH	137	131	137	139
BSD	2	1	2	1
bZIP	68	69	72	78
C2C2-CO-like	15	16	16	17
C2C2-Dof	34	35	36	34
C2C2-GATA	33	30	30	28
C2C2-LSD	3	3	3	3
C2C2-YABBY	7	6	6	6
C2H2	114	105	105	116
C3H	54	53	57	60
CAMTA	6	6	6	6
CPP	8	8	8	7
CSD	4	2	4	17
DBB	4	3	6	4
DBP	2	2	2	2
DDT	5	6	5	5
E2F-DP	8	8	8	7
EIL	7	6	6	6
FAR1	13	20	17	5
GARP-ARR-B	8	10	10	10
GARP-G2-like	47	44	41	46
GeBP	15	17	20	21
GRAS	39	35	34	37
GRF	9	8	9	9
HB-BELL	12	13	13	13
HB-HD-ZIP	43	45	42	29
HB-KNOX	7	7	8	8
HB-other	12	11	11	12

HB-PHD	2	2	2	2
HB-WOX	16	15	16	16
HRT	2	2	2	2
HSF	27	30	24	38
LFY	1	46	43	47
LIM	6	1	1	1
LOB	44	6	6	6
MADS-MIKC	30	35	39	34
MADS-M-type	51	90	69	47
MYB	136	151	142	148
MYB-related	75	58	63	61
NAC	94	110	112	119
NF-X1	2	2	2	3
NF-YA	9	9	10	12
NF-YB	14	12	13	16
NF-YC	14	12	14	15
NOZZLE	1	1	1	1
OFP	19	18	17	22
PLATZ	11	12	12	13
RWP-RK	16	15	14	16
S1Fa-like	2	3	3	3
SAP	1	1	1	1
SBP	16	15	17	15
SRS	11	10	10	10
STAT	2	2	2	3
TCP	24	25	24	25
Tify	13	14	16	16
Trihelix	26	26	26	27
TUB	10	11	11	11
ULT	2	2	2	2
VOZ	2	2	2	3
Whirly	3	3	3	4
WRKY	68	74	73	80
zf-HD	17	17	17	17
Total	1711	1786	1779	1832
TRs	*C. himalaica*	*C. rubella*	*A. thaliana*	*A. lyrata*
ARID	12	15	10	8
AUX/IAA	30	29	29	35
Coactivator p15	2	3	3	3
GNAT	32	35	33	36

HMG	9	10	11	12
IWS1	11	8	9	9
Jumonji	18	19	16	19
LUG	2	2	2	2
MBF1	3	3	3	3
MED6	1	1	1	1
MED7	2	2	2	3
mTERF	33	36	35	46
Others	77	76	89	86
PHD	34	32	34	39
Pseudo ARR-B	4	5	5	5
RB	1	1	1	1
Rcd1-like	4	5	4	4
SET	40	41	43	42
SNF2	37	38	39	39
SOH1	1	1	1	1
SWI/SNF-BAF60b	19	16	18	19
SWI/SNF-SWI3	4	4	4	4
TAZ	10	10	10	10
TRAF	27	26	26	29
Total	413	418	428	456

TableS10. Statistics of repeat sequences (above) and transposable elements (TEs, below) in *C. himalaica* genome.

Type	Repeat size	Percent of genome (%)
Trf	7,839,117	3.339737
Repeatmasker	98,349,552	41.900333
Proteinmask	49,048,563	20.896395
Total	110,107,416	46.909592

	Repeatmasker (repbase+*de novo*)		Repeatmasker (*de novo* only)		Combined TEs (without Trf)	
Type	Length (bp)	Percent of genome (%)	Length (bp)	Percent of genome (%)	Length (bp)	Percent of genome (%)
DNA	21,439,954	9.134167	10,403,085	4.432076	25,451,841	10.84337
LINE	3,019,542	1.28643	6,676,747	2.844527	7,645,679	3.257325
SINE	107,893	0.045966	0	0	107,893	0.045966
LTR	68,720,558	29.27735	32,053,891	13.656073	71,284,904	30.369851
Simple repeat	427,789	0.182253	0	0	427,789	0.182253
Unknown	6,294,682	2.681754	0	0	6,294,682	2.681754
Total	98,349,552	41.900333	49,048,563	20.896395	107,449,857	45.77738

Table S11. De novo identification of LTR retrotransposons in multiple species

Species	*A. lyrata*	*A. thaliana*	*C. himalaica*	*C. rubella*
Family Number	696	258	1,038	390
LTR Number	2,523	593	3,752	922
Average LTR Number	3.625	2.298	3.615	2.364
Max Family	143	31	190	98
Min Family	1	1	1	1
Top10	687	188	739	281
Top20	969	253	1,023	360
Top30	1,143	293	1,228	415
Top40	1,250	323	1,389	457
Top50	1,332	346	1,516	490
Top100	1,594	435	1,962	603

Table S12. Summary of gene ortholog analysis conducted on nine sequenced genomes.

Species	Name	Gene
A. thaliana	*Arabidopsis thaliana*	26,867
A. lyrata	*Arabidopsis lyrata*	31,988
C. rubella	*Capsella rubella*	26,521
E. salsugineum	*Eutrema salsugineum*	26,351
B. rapa	*Brassica rapa*	41,173
C. hirsuta	*Cardamine hirsuta*	29,453
S. parvula	*Schrenkiella parvula*	26,706
A. arabicum	*Aethionema arabicum*	23,167
C. himalaya	*Crucihimalaya himalaya*	27,019

Table S13. Summary of significantly expanded and contracted orthogroups in five closely related species.

Expansive 150 orthogroups	*A. thaliana*	*A. lyrata*	*Capsella rubella*	*C. himalaica*	*Cardamine hirsuta*	*P* value
my_prefix71	1	0	0	48	0	1.76E-54
my_prefix128	1	0	0	35	0	6.76E-41
my_prefix165	0	0	0	31	0	6.14E-36
my_prefix177	0	0	0	30	0	1.06E-34
my_prefix179	0	0	0	30	0	1.06E-34
my_prefix178	1	1	0	27	1	5.47E-31
my_prefix215	0	0	0	27	0	5.47E-31
my_prefix233	1	0	0	25	0	1.62E-28
my_prefix263	0	0	0	25	0	1.62E-28
my_prefix492	1	0	0	16	1	7.98E-20
my_prefix602	0	0	0	16	0	7.98E-20
my_prefix603	1	0	0	15	0	1.43E-18
my_prefix782	1	0	0	14	0	2.56E-17
my_prefix201	1	3	4	20	0	2.02E-16
my_prefix942	0	0	0	13	0	4.58E-16
my_prefix943	1	0	0	12	0	8.20E-15
my_prefix1033	0	0	0	12	0	8.20E-15
my_prefix1039	0	0	0	12	0	8.20E-15
my_prefix553	0	3	0	13	0	8.86E-14
my_prefix1035	0	1	0	11	0	1.47E-13
my_prefix1233	0	0	0	11	0	1.47E-13
my_prefix1036	1	0	1	10	0	2.63E-12
my_prefix1018	2	0	0	10	0	2.63E-12
my_prefix2055	0	0	0	10	0	2.63E-12
my_prefix2060	0	0	0	10	0	2.63E-12
my_prefix867	3	0	0	11	0	2.37E-11
my_prefix2059	0	1	0	9	0	4.71E-11
my_prefix2070	1	0	0	9	0	4.71E-11
my_prefix2401	0	0	0	9	0	4.71E-11
my_prefix2412	0	0	0	9	0	4.71E-11
my_prefix2416	0	0	0	9	0	4.71E-11
my_prefix2705	0	0	0	8	0	8.44E-10
my_prefix2709	0	0	0	8	0	8.44E-10
my_prefix2711	0	0	0	8	0	8.44E-10
my_prefix412	2	0	1	12	5	5.74E-09
my_prefix2407	0	1	0	7	1	1.51E-08

my_prefix2718	1	0	0	7	0	1.51E-08
my_prefix3021	0	0	0	7	0	1.51E-08
my_prefix3032	0	0	0	7	0	1.51E-08
my_prefix3061	0	0	0	7	0	1.51E-08
my_prefix142	1	9	6	15	3	7.94E-08
my_prefix2409	1	1	1	6	0	2.71E-07
my_prefix2410	1	0	1	6	1	2.71E-07
my_prefix2411	1	1	1	6	0	2.71E-07
my_prefix2704	1	1	0	6	0	2.71E-07
my_prefix3723	0	0	0	6	0	2.71E-07
my_prefix941	2	1	2	7	1	1.48E-06
my_prefix571	0	2	2	8	4	4.70E-06
my_prefix2408	1	1	1	5	1	4.85E-06
my_prefix2860	0	2	0	5	0	4.85E-06
my_prefix3770	1	0	0	5	0	4.85E-06
my_prefix3802	1	0	0	5	0	4.85E-06
my_prefix4315	0	0	0	5	0	4.85E-06
my_prefix4321	0	0	0	5	0	4.85E-06
my_prefix4326	0	0	0	5	0	4.85E-06
my_prefix4340	0	0	0	5	0	4.85E-06
my_prefix4341	0	0	0	5	0	4.85E-06
my_prefix4422	0	0	0	5	0	4.85E-06
my_prefix4423	0	0	0	5	0	4.85E-06
my_prefix1232	1	2	2	6	0	2.21E-05
my_prefix1993	2	0	0	6	2	2.21E-05
my_prefix2677	0	0	0	6	2	2.21E-05
my_prefix2697	1	1	1	4	1	8.68E-05
my_prefix2701	1	1	1	4	1	8.68E-05
my_prefix2707	1	1	1	4	1	8.68E-05
my_prefix2710	1	1	1	4	1	8.68E-05
my_prefix2716	1	1	1	4	1	8.68E-05
my_prefix3020	1	1	1	4	0	8.68E-05
my_prefix2604	0	4	0	4	0	8.68E-05
my_prefix3416	2	0	0	4	0	8.68E-05
my_prefix3750	0	2	0	4	0	8.68E-05
my_prefix4327	1	0	0	4	0	8.68E-05
my_prefix15758	0	0	0	4	0	8.68E-05
my_prefix15759	0	0	0	4	0	8.68E-05
my_prefix15763	0	0	0	4	0	8.68E-05
my_prefix15771	0	0	0	4	0	8.68E-05

my_prefix15776	0	0	0	4	0	8.68E-05
my_prefix15777	0	0	0	4	0	8.68E-05
my_prefix15784	0	0	0	4	0	8.68E-05
my_prefix15843	0	0	0	4	0	8.68E-05
my_prefix15844	0	0	0	4	0	8.68E-05
my_prefix877	2	2	1	5	3	0.000318672
my_prefix888	3	2	2	5	1	0.000318672
my_prefix1084	1	2	2	5	1	0.000318672
my_prefix2690	0	1	0	5	2	0.000318672
my_prefix1034	1	1	3	6	1	0.000906578
my_prefix2784	1	2	1	3	0	0.00155421
my_prefix2869	1	2	1	3	0	0.00155421
my_prefix2935	1	1	0	3	2	0.00155421
my_prefix2996	1	2	0	3	1	0.00155421
my_prefix3615	1	1	1	3	0	0.00155421
my_prefix3678	1	1	0	3	1	0.00155421
my_prefix3730	1	0	1	3	1	0.00155421
my_prefix3749	1	0	1	3	1	0.00155421
my_prefix3786	1	1	1	3	0	0.00155421
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my_prefix4346	0	1	1	3	0	0.00155421
my_prefix4362	1	1	0	3	0	0.00155421
my_prefix4424	1	0	1	3	0	0.00155421
my_prefix4276	0	0	0	3	2	0.00155421
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my_prefix17882	0	0	0	3	0	0.00155421
my_prefix17884	0	0	0	3	0	0.00155421
my_prefix17885	0	0	0	3	0	0.00155421
my_prefix17886	0	0	0	3	0	0.00155421
my_prefix17887	0	0	0	3	0	0.00155421
my_prefix17888	0	0	0	3	0	0.00155421
my_prefix17889	0	0	0	3	0	0.00155421
my_prefix17895	0	0	0	3	0	0.00155421
my_prefix17903	0	0	0	3	0	0.00155421
my_prefix17905	0	0	0	3	0	0.00155421
my_prefix17989	0	0	0	3	0	0.00155421
my_prefix17990	0	0	0	3	0	0.00155421
my_prefix17991	0	0	0	3	0	0.00155421
my_prefix17992	0	0	0	3	0	0.00155421
my_prefix17993	0	0	0	3	0	0.00155421
my_prefix17994	0	0	0	3	0	0.00155421
my_prefix17995	0	0	0	3	0	0.00155421
my_prefix17996	0	0	0	3	0	0.00155421
my_prefix17997	0	0	0	3	0	0.00155421
my_prefix17998	0	0	0	3	0	0.00155421
my_prefix17999	0	0	0	3	0	0.00155421
my_prefix18000	0	0	0	3	0	0.00155421
my_prefix79	8	9	8	13	8	0.00194091
my_prefix947	1	4	2	4	1	0.00743951
my_prefix1931	1	2	2	4	1	0.00743951
my_prefix2414	1	1	2	4	1	0.00743951
my_prefix2061	2	2	2	4	0	0.00743951
my_prefix2703	1	1	2	4	0	0.00743951
my_prefix535	0	12	0	4	0	0.00743951

Contract 89 orthogroups	*A. thaliana*	*A. lyrata*	*Capsella rubella*	*C. himalaica*	*Cardamine hirsuta*	*P* value
my_prefix7	34	15	47	15	37	5.03E-11
my_prefix14	16	16	29	6	25	1.26E-10
my_prefix126	16	3	11	0	6	2.02E-09

my_prefix42	25	7	14	4	15	4.64E-08
my_prefix2	32	28	52	26	54	1.75E-07
my_prefix9	27	25	23	12	32	4.02E-07
my_prefix78	13	6	14	3	10	1.45E-06
my_prefix57	15	10	17	4	8	3.02E-06
my_prefix56	12	12	15	5	11	5.73E-06
my_prefix407	3	4	4	0	9	6.62E-06
my_prefix410	10	1	4	0	5	6.62E-06
my_prefix572	4	4	4	0	4	6.62E-06
my_prefix80	21	2	13	3	7	3.55E-05
my_prefix92	11	13	12	3	3	3.55E-05
my_prefix35	19	12	17	7	15	3.72E-05
my_prefix187	11	2	12	1	3	6.51E-05
my_prefix203	7	5	5	1	9	6.51E-05
my_prefix163	7	12	8	2	2	0.000138711
my_prefix213	7	4	7	2	7	0.000138711
my_prefix231	6	6	10	2	2	0.000138711
my_prefix355	1	1	16	0	3	0.000199561
my_prefix522	2	7	5	0	3	0.000199561
my_prefix778	8	1	4	0	2	0.000199561
my_prefix909	4	4	3	0	2	0.000199561
my_prefix950	1	4	4	0	3	0.000199561
my_prefix166	0	0	29	0	2	0.000199561
my_prefix6	30	42	27	19	35	0.000202751
my_prefix107	10	10	8	3	8	0.000259537
my_prefix11	25	9	24	14	28	0.000324624
my_prefix41	12	17	17	8	12	0.000329454
my_prefix23	18	17	16	9	17	0.000454826
my_prefix28	16	15	15	9	18	0.000454826
my_prefix269	6	4	5	1	8	0.000557948
my_prefix352	9	2	5	1	4	0.000557948
my_prefix425	5	7	5	1	1	0.000557948
my_prefix483	3	4	4	1	6	0.000557948
my_prefix528	4	2	5	1	5	0.000557948
my_prefix262	7	0	13	1	4	0.000557948
my_prefix13	21	20	17	11	23	0.000799865
my_prefix58	11	12	11	6	13	0.00102558
my_prefix267	4	6	8	2	4	0.00116835
my_prefix33	13	25	12	7	14	0.00144968
my_prefix132	7	8	7	3	10	0.0020644

my_prefix135	5	6	8	3	13	0.0020644
my_prefix180	8	6	7	3	5	0.0020644
my_prefix1016	3	2	5	0	2	0.00215496
my_prefix1205	2	2	6	0	1	0.00215496
my_prefix1213	2	3	2	0	4	0.00215496
my_prefix2100	1	2	4	0	2	0.00215496
my_prefix2142	1	3	4	0	1	0.00215496
my_prefix2267	3	2	2	0	2	0.00215496
my_prefix2279	1	3	2	0	3	0.00215496
my_prefix2284	3	3	2	0	1	0.00215496
my_prefix2466	1	2	4	0	1	0.00215496
my_prefix2517	3	2	2	0	1	0.00215496
my_prefix2622	3	2	2	0	1	0.00215496
my_prefix2937	1	2	2	0	2	0.00215496
my_prefix873	2	1	11	0	0	0.00215496
my_prefix874	1	2	11	0	0	0.00215496
my_prefix1030	1	0	8	0	3	0.00215496
my_prefix2278	2	3	4	0	0	0.00215496
my_prefix2314	0	3	3	0	3	0.00215496
my_prefix2343	3	1	5	0	0	0.00215496
my_prefix2587	1	4	3	0	0	0.00215496
my_prefix2591	3	3	2	0	0	0.00215496
my_prefix2852	2	3	2	0	0	0.00215496
my_prefix2947	2	0	2	0	3	0.00215496
my_prefix3100	2	2	2	0	0	0.00215496
my_prefix3438	2	0	2	0	2	0.00215496
my_prefix3466	2	0	2	0	2	0.00215496
my_prefix1038	0	0	10	0	2	0.00215496
my_prefix2723	0	0	6	0	2	0.00215496
my_prefix98	9	11	7	4	10	0.00326544
my_prefix113	14	4	13	4	4	0.00326544
my_prefix146	12	2	8	4	8	0.00326544
my_prefix34	13	13	20	10	15	0.00333104
my_prefix77	6	17	12	5	6	0.0047797
my_prefix97	12	10	9	5	5	0.0047797
my_prefix275	2	15	4	1	2	0.00569599
my_prefix393	6	6	3	1	4	0.00569599
my_prefix476	6	5	3	1	3	0.00569599
my_prefix570	3	4	5	1	3	0.00569599
my_prefix607	4	4	5	1	1	0.00569599

my_prefix864	2	3	4	1	4	0.00569599
my_prefix939	3	1	3	1	5	0.00569599
my_prefix965	3	4	3	1	1	0.00569599
my_prefix938	1	0	6	1	5	0.00569599
my_prefix1	61	64	37	35	95	0.00647362
my_prefix8	21	16	20	15	47	0.00868273

Table S14. List of 610 positively selected genes in *C. himalaica* (Chi) genome.

orthogroups	Ks/Ks value	χ^2 square test	*C. himalaica*	Orthologs in *A. thaliana*
my_prefix8199	999	7.04606E-58	Chi|21.54	AT2G22530
my_prefix8675	999	9.43586E-48	Chi|4.600	AT2G41080
my_prefix4981	999	1.85719E-43	Chi|8.748.1	AT3G63400
my_prefix5832	999	6.51373E-43	Chi|16.499	AT1G03160
my_prefix8730	998.9946	2.82378E-40	Chi|4.819	AT2G43370
my_prefix11989	999	4.98088E-38	Chi|24.37.1	AT5G66850
my_prefix11800	999	4.70655E-36	Chi|1.1026	AT5G60450
my_prefix11581	999	4.44968E-32	Chi|1.287	AT5G52790
my_prefix14718	999	2.9231E-31	Chi|9.720	AT5G20680
my_prefix8289	999	7.36471E-31	Chi|5.987	AT2G26930
my_prefix12977	999	1.80631E-30	Chi|10.285	AT1G10660
my_prefix10457	256.6443	8.72039E-27	Chi|22.314	AT4G38380
my_prefix10487	999	1.33888E-26	Chi|22.405	AT4G39410
my_prefix5603	999	2.98105E-26	Chi|24.16	AT5G01930
my_prefix6789	999	3.46548E-26	Chi|63.63	AT1G64600
my_prefix7671	106.5766	4.04042E-26	Chi|7.654	AT3G13490
my_prefix4851	999	4.92021E-26	Chi|4.365	AT2G38780
my_prefix13985	179.9911	1.11134E-25	Chi|28.145	AT2G32900
my_prefix11037	998.9987	2.60525E-25	Chi|17.377	AT4G19140
my_prefix9496	999	3.71289E-25	Chi|8.711.1	AT3G61860
my_prefix11158	127.9338	4.98163E-25	Chi|42.24	AT4G14850
my_prefix13443	150.8536	2.91815E-24	Chi|4.583	AT2G40890
my_prefix5669	999	3.22797E-24	Chi|22.311	AT4G38360
my_prefix8086	86.29101	4.30376E-24	Chi|144.2.1	AT2G16900
my_prefix4322	357.5595	1.67526E-23	Chi|189.11	AT4G04320
my_prefix15094	127.1085	3.57445E-23	Chi|17.167.1	AT4G24240
my_prefix10586	999	1.18597E-22	Chi|6.325	AT4G35180
my_prefix8871	703.7999	1.61277E-22	Chi|22.7	AT2G48120
my_prefix13638	998.9999	1.79443E-22	Chi|7.831	AT3G11620
my_prefix6710	999	2.343E-22	Chi|57.150.2	AT1G53560
my_prefix13675	96.90223	3.45717E-22	Chi|7.567	AT3G14220
my_prefix4629	73.63647	4.30094E-22	Chi|115.17	AT1G67790
my_prefix13436	999	7.75494E-22	Chi|2.720	AT1G73805
my_prefix4760	320.2743	1.03196E-21	Chi|48.55.1	AT3G20070
my_prefix14276	170.1041	2.26116E-21	Chi|172.18	AT3G47440
my_prefix12245	187.0145	6.33277E-21	Chi|76.20	AT5G25340
my_prefix9643	97.29217	2.07716E-20	Chi|3.784.1	AT5G04740
my_prefix9461	119.7033	3.7351E-20	Chi|8.606	AT3G60690

my_prefix6996	999	6.78406E-20	Chi|2.968.1	AT1G69230
my_prefix8895	999	7.27061E-20	Chi|70.108	AT2G01690
my_prefix4547	719.0144	1.00175E-19	Chi|178.1	AT1G32770
my_prefix14847	877.9543	1.12898E-19	Chi|189.3	AT4G04470
my_prefix8642	999	2.13951E-19	Chi|4.499.1	AT2G40095
my_prefix13962	886.5911	2.20275E-19	Chi|37.57.2	AT2G30695
my_prefix9931	395.5537	2.48824E-19	Chi|9.202.1	AT5G15170
my_prefix13530	999	2.6299E-19	Chi|13.708	AT3G02420
my_prefix7884	999	5.00915E-19	Chi|109.7	AT3G21215
my_prefix10911	138.6568	1.33254E-18	Chi|17.175	AT4G24175
my_prefix6394	999	1.56212E-18	Chi|46.214	AT1G27520
my_prefix12113	999	1.75498E-18	Chi|92.62	AT4G18070
my_prefix12585	107.32	2.07263E-18	Chi|2.928	AT1G69540
my_prefix11706	771.2728	2.79514E-18	Chi|1.734.1	AT5G57300
my_prefix11914	999	8.34407E-18	Chi|1.1392	AT5G64200
my_prefix12827	999	8.50341E-18	Chi|1.822	AT5G58200
my_prefix9056	700.0196	8.99269E-18	Chi|44.96	AT3G43540
my_prefix5602	999	1.24535E-17	Chi|8.759	AT3G63500
my_prefix14175	999	1.69481E-17	Chi|84.28.1	AT2G47710
my_prefix5751	998.9999	2.47198E-17	Chi|1.1094	AT5G61150
my_prefix13226	49.25852	2.68864E-17	Chi|107.13	AT1G49130
my_prefix5854	999	2.71126E-17	Chi|16.413	AT1G04130
my_prefix10652	722.2215	3.01312E-17	Chi|6.570	AT4G32720
my_prefix6491	658.4021	3.44181E-17	Chi|88.15	AT1G32190
my_prefix11886	999	3.71599E-17	Chi|1.1295.1	AT5G63220
my_prefix7163	595.9938	7.34238E-17	Chi|2.551	AT1G75490
my_prefix6194	999	2.21762E-16	Chi|5.324	AT1G17210
my_prefix10793	999	3.89519E-16	Chi|6.1041	AT4G28025
my_prefix8783	724.7912	5.81904E-16	Chi|4.975	AT2G45010
my_prefix5893	66.7493	5.99786E-16	Chi|16.261	AT1G05577
my_prefix12161	999	1.15496E-15	Chi|200.20	AT5G01660
my_prefix4995	140.2265	1.17415E-15	Chi|3.738.1	AT5G05240
my_prefix9440	975.4896	1.53327E-15	Chi|8.532	AT3G59960
my_prefix12694	552.8538	1.72451E-15	Chi|5.662	AT1G20890
my_prefix13913	97.66143	1.82282E-15	Chi|181.2	AT2G25420
my_prefix5054	999	2.17702E-15	Chi|28.4	AT4G06676
my_prefix4484	999	2.30707E-15	Chi|5.46	AT1G14310
my_prefix6372	214.486	2.4317E-15	Chi|46.93	AT1G25540
my_prefix10923	934.3238	2.61372E-15	Chi|17.209	AT4G23860
my_prefix13340	991.5837	3.11178E-15	Chi|130.9.1	AT1G65030

my_prefix10194	999	5.18199E-15	Chi|47.106.1	AT5G25150
my_prefix12577	985.6077	7.00357E-15	Chi|29.10	AT1G67570
my_prefix5579	998.9995	7.06497E-15	Chi|31.255	AT3G51360
my_prefix15301	755.8708	9.08976E-15	Chi|44.80	AT5G43300
my_prefix10158	999	1.17004E-14	Chi|26.51	AT5G23570
my_prefix6786	101.4926	1.18473E-14	Chi|63.74.1	AT1G64680
my_prefix9500	739.8918	1.40557E-14	Chi|8.724	AT3G61970
my_prefix14172	763.652	1.72226E-14	Chi|84.17	AT2G47600
my_prefix9715	56.06483	1.9564E-14	Chi|3.572	AT5G06980
my_prefix12087	999	2.31175E-14	Chi|6.976	AT4G28670
my_prefix13888	999	2.31962E-14	Chi|40.110.2	AT2G21385
my_prefix14795	999	2.52392E-14	Chi|14.133.1	AT5G27390
my_prefix9542	998.9987	3.28023E-14	Chi|200.13	AT5G01730
my_prefix13579	999	5.97944E-14	Chi|13.197	AT3G07170
my_prefix8666	999	6.34838E-14	Chi|4.579	AT2G40840
my_prefix9707	187.645	7.83516E-14	Chi|3.592	AT5G06780
my_prefix6778	882.3825	1.59535E-13	Chi|84.61	AT1G56460
my_prefix10030	747.5815	1.95667E-13	Chi|9.514	AT5G18540
my_prefix7672	728.484	2.20672E-13	Chi|7.649.1	AT3G13550
my_prefix14138	632.4499	2.30873E-13	Chi|4.993	AT2G45210
my_prefix8380	325.9039	2.51287E-13	Chi|37.58	AT2G30700
my_prefix5749	178.3868	2.79878E-13	Chi|1.1089	AT5G61100
my_prefix4883	702.1731	3.01066E-13	Chi|4.1181	AT2G47115
my_prefix9844	409.3438	4.36218E-13	Chi|3.108	AT5G12300
my_prefix9483	101.5436	4.52335E-13	Chi|8.663	AT3G61410
my_prefix11908	77.5604	4.71293E-13	Chi|1.1379	AT5G64050
my_prefix6254	100.0227	5.79349E-13	Chi|5.573.1	AT1G19860
my_prefix6882	999	6.49342E-13	Chi|175.5	AT1G58170
my_prefix5515	376.9078	9.58236E-13	Chi|19.163	AT2G24700
my_prefix7319	306.2678	9.90446E-13	Chi|13.793	AT3G01470
my_prefix12650	412.9086	1.07076E-12	Chi|16.75	AT1G07540
my_prefix8607	147.7658	1.244E-12	Chi|4.387	AT2G39000
my_prefix7099	976.1028	1.65257E-12	Chi|2.775	AT1G73210
my_prefix9648	999	1.80341E-12	Chi|3.770	AT5G04890
my_prefix15005	999	2.20548E-12	Chi|6.614	AT4G32320
my_prefix11811	335.8491	2.27457E-12	Chi|1.1068	AT5G60870
my_prefix6901	179.4789	4.9062E-12	Chi|87.53	AT1G65410
my_prefix5552	999	5.1661E-12	Chi|70.126	AT2G01510
my_prefix9959	186.3312	6.03195E-12	Chi|9.283	AT5G16020
my_prefix8037	107.1065	6.59379E-12	Chi|103.7.1	AT2G14910

my_prefix12186	999	1.08739E-11	Chi|3.394	AT5G09250
my_prefix8865	84.0506	1.11034E-11	Chi|22.30.1	AT2G47890
my_prefix12380	99.33731	1.15419E-11	Chi|65.17	AT2G27500
my_prefix12304	793.8369	1.15697E-11	Chi|97.8.1	AT3G29760
my_prefix13008	999	1.15983E-11	Chi|5.71	AT1G14520
my_prefix5693	624.0751	1.52386E-11	Chi|173.42	AT4G25990
my_prefix9012	64.9394	1.56628E-11	Chi|15.49	AT3G27860
my_prefix5790	295.1486	2.81085E-11	Chi|84.41	AT1G01770
my_prefix12230	649.6275	3.08892E-11	Chi|9.632	AT5G19710
my_prefix10529	998.9986	4.41373E-11	Chi|6.164	AT4G37050
my_prefix13532	998.9966	4.92364E-11	Chi|13.705	AT3G02450
my_prefix5506	999	5.46118E-11	Chi|42.158	AT2G18800
my_prefix4823	998.9985	6.04882E-11	Chi|30.83	AT2G31530
my_prefix12325	223.9698	6.87259E-11	Chi|31.163	AT3G50360
my_prefix15407	998.9997	6.89227E-11	Chi|1.541	AT5G55130
my_prefix10358	799.2069	8.44083E-11	Chi|15.214.1	AT4G05060
my_prefix7215	69.727	1.0853E-10	Chi|2.340	AT1G77765
my_prefix4662	998.9992	1.12863E-10	Chi|2.649	AT1G74490
my_prefix6339	71.32238	1.22505E-10	Chi|5.947	AT1G23890
my_prefix5788	120.946	1.24497E-10	Chi|84.48.2	AT1G01860
my_prefix6988	63.09138	1.52059E-10	Chi|2.989	AT1G69020
my_prefix13515	998.9992	1.53828E-10	Chi|194.8	AT1G80030
my_prefix10425	999	1.93707E-10	Chi|185.27	AT4G01250
my_prefix12148	396.8602	2.11099E-10	Chi|80.76	AT5G40645
my_prefix6452	772.0402	2.26649E-10	Chi|78.84	AT1G30090
my_prefix9021	999	2.44695E-10	Chi|47.1	AT3G28370
my_prefix10756	62.98033	2.63864E-10	Chi|6.938	AT4G29070
my_prefix12232	638.0679	3.67181E-10	Chi|9.750	AT5G21040
my_prefix13148	514.2844	3.85848E-10	Chi|115.66	AT1G29195
my_prefix7601	79.70386	3.99273E-10	Chi|7.868	AT3G11220
my_prefix13441	998.9979	4.41331E-10	Chi|2.668	AT1G74320
my_prefix7382	169.5409	5.80496E-10	Chi|13.581	AT3G03550
my_prefix13945	767.0305	7.23013E-10	Chi|18.20	AT2G28050
my_prefix12312	108.9272	7.31872E-10	Chi|98.38	AT3G45280
my_prefix8479	999	8.41748E-10	Chi|12.204	AT2G34925
my_prefix12384	229.5282	8.87643E-10	Chi|38.11	AT2G27760
my_prefix10212	133.4873	9.20985E-10	Chi|7.991	AT5G26040
my_prefix13539	562.1473	1.06895E-09	Chi|13.621.1	AT3G03180
my_prefix6162	998.9999	1.14718E-09	Chi|5.184	AT1G15740
my_prefix8477	629.5224	1.70803E-09	Chi|12.211	AT2G34860

my_prefix13193	999	1.88176E-09	Chi|80.92.2	AT1G35160
my_prefix5033	999	1.90561E-09	Chi|9.472	AT5G18100
my_prefix14634	806.2232	2.18465E-09	Chi|9.187	AT5G15010
my_prefix4787	786.5175	2.27078E-09	Chi|95.33	AT2G19385
my_prefix9480	59.59266	2.3016E-09	Chi|3G61230	AT3G61230
my_prefix13124	182.1656	2.39037E-09	Chi|46.177	AT1G24350
my_prefix6522	999	2.66356E-09	Chi|54.14	AT1G33980
my_prefix6785	54.70671	3.0099E-09	Chi|63.76	AT1G64700
my_prefix11726	200.5147	3.33732E-09	Chi|1.785.1	AT5G57860
my_prefix11911	114.011	3.42685E-09	Chi|1.1385.1	AT5G64130
my_prefix15278	85.58334	3.63287E-09	Chi|36.48	AT5G45980
my_prefix11121	999	3.67804E-09	Chi|50.133	AT4G16460
my_prefix6913	154.8865	3.79916E-09	Chi|19.93	AT1G66260
my_prefix12635	126.7407	4.55782E-09	Chi|16.456	AT1G03687
my_prefix7085	999	4.56086E-09	Chi|2.828.2	AT1G72740
my_prefix11567	88.24252	5.48167E-09	Chi|1.253	AT5G52270
my_prefix13411	998.9978	6.19353E-09	Chi|25.260	AT1G71420
my_prefix11809	999	8.27915E-09	Chi|1.1057	AT5G60750
my_prefix7328	999	8.39985E-09	Chi|13.755	AT3G01140
my_prefix6223	97.76815	8.53215E-09	Chi|5.466	AT1G18700
my_prefix7293	998.9998	8.63522E-09	Chi|194.21	AT1G79890
my_prefix10085	206.2081	9.38394E-09	Chi|9.681	AT5G20240
my_prefix10472	173.6853	9.88852E-09	Chi|22.354	AT4G38940
my_prefix8683	999	1.11035E-08	Chi|4.634.1	AT2G41420
my_prefix10538	998.9989	1.33197E-08	Chi|6.141	AT4G36850
my_prefix15544	722.0865	1.35611E-08	Chi|1.1516.1	AT5G65480
my_prefix14158	59.3121	1.36217E-08	Chi|4.1145	AT2G46770
my_prefix5248	999	1.364E-08	Chi|1.582	AT5G55570
my_prefix8603	38.00033	1.61544E-08	Chi|4.370	AT2G38823
my_prefix8713	999	1.74316E-08	Chi|4.758	AT2G42760
my_prefix14474	64.01463	1.77511E-08	Chi|24.18	AT5G01910
my_prefix7185	82.26793	1.83174E-08	Chi|2.464	AT1G76450
my_prefix6199	999	1.87514E-08	Chi|5.335	AT1G17330
my_prefix15157	67.94037	1.87651E-08	Chi|50.55	AT4G17220
my_prefix14900	998.9973	1.98143E-08	Chi|22.306	AT4G38260
my_prefix15175	999	2.26927E-08	Chi|50.191	AT4G16008
my_prefix4691	999	2.28045E-08	Chi|194.34	AT1G79780
my_prefix12475	347.8758	2.37399E-08	Chi|13.119	AT3G07970
my_prefix10674	53.70784	2.41162E-08	Chi|6.645	AT4G31990
my_prefix5942	80.93217	2.61655E-08	Chi|16.45.1	AT1G07890

my_prefix12848	124.0201	2.74442E-08	Chi|24.38	AT5G66840
my_prefix6000	105.5329	3.84312E-08	Chi|77.61	AT1G09760
my_prefix4888	129.6384	3.89638E-08	Chi|22.17	AT2G48030
my_prefix7299	670.6131	3.90176E-08	Chi|22.224	AT1G79730
my_prefix6706	94.94362	3.99135E-08	Chi|57.176	AT1G53250
my_prefix13555	172.9931	4.42089E-08	Chi|13.488	AT3G04560
my_prefix9469	346.2925	4.62596E-08	Chi|8.625	AT3G60870
my_prefix6711	999	5.45047E-08	Chi|57.149	AT1G53570
my_prefix4443	58.70073	5.67982E-08	Chi|16.621	AT1G01290
my_prefix11091	913.101	5.84376E-08	Chi|50.32	AT4G17440
my_prefix10452	531.8559	5.96713E-08	Chi|2.38	AT1G05940
my_prefix11669	999	7.05262E-08	Chi|1.607	AT5G55850
my_prefix12620	94.19065	7.42946E-08	Chi|2.81	AT1G80320
my_prefix8150	545.1781	7.65778E-08	Chi|27.161	AT2G20515
my_prefix9028	25.78219	7.73134E-08	Chi|66.72	AT3G28840
my_prefix6197	212.3401	8.0522E-08	Chi|5.332	AT1G17285
my_prefix10229	999	8.78224E-08	Chi|127.41	AT5G26960
my_prefix14301	999	1.0515E-07	Chi|31.83.2	AT3G49430
my_prefix13635	999	1.07731E-07	Chi|7.847	AT3G11460
my_prefix11765	998.9999	1.27714E-07	Chi|1.908	AT5G59020
my_prefix6517	999	1.28129E-07	Chi|81.55	AT1G33470
my_prefix12357	89.85695	1.37504E-07	Chi|40.107.1	AT2G21370
my_prefix9160	999	1.65953E-07	Chi|31.122	AT3G49840
my_prefix8594	150.1622	1.66342E-07	Chi|4.351	AT2G38660
my_prefix14817	998.9995	1.6699E-07	Chi|74.52.1	AT4G09140
my_prefix7743	999	1.91575E-07	Chi|7.402	AT3G15770
my_prefix9065	48.38557	1.97799E-07	Chi|191.5	AT3G44460
my_prefix14077	64.84437	2.17797E-07	Chi|4.538	AT2G40430
my_prefix5654	32.11977	2.44527E-07	Chi|62.21	AT5G28000
my_prefix8010	66.76146	2.51503E-07	Chi|58.36	AT2G06530
my_prefix11900	79.4558	2.61379E-07	Chi|1.1358.1	AT5G63880
my_prefix6142	112.4607	2.62897E-07	Chi|5.115	AT1G14990
my_prefix14644	998.9991	2.72627E-07	Chi|9.246.1	AT5G15640
my_prefix7437	346.3074	2.72742E-07	Chi|13.412	AT3G05210
my_prefix10621	168.3125	2.86257E-07	Chi|6.465	AT4G33760
my_prefix9450	94.41276	3.42648E-07	Chi|8.571	AT3G60370
my_prefix14874	576.026	3.86439E-07	Chi|32.30	AT4G02405
my_prefix10564	179.7999	3.93384E-07	Chi|6.253	AT4G35880
my_prefix14554	81.0842	4.19292E-07	Chi|3.468	AT5G08130
my_prefix11263	851.5797	4.2483E-07	Chi|24.272	AT5G40450

my_prefix12193	84.36774	4.25203E-07	Chi|3.237	AT5G10890
my_prefix11976	938.1487	4.41909E-07	Chi|1.1590	AT5G67370
my_prefix8459	998.9995	4.56839E-07	Chi|12.273	AT2G34310
my_prefix8798	561.7236	5.17291E-07	Chi|4.1031	AT2G45650
my_prefix8859	998.9967	5.55542E-07	Chi|84.16	AT2G47590
my_prefix10400	999	5.82002E-07	Chi|3.7	AT4G02075
my_prefix10447	44.44427	6.29216E-07	Chi|2.53	AT4G00120
my_prefix13623	239.493	6.51485E-07	Chi|7.954	AT3G10380
my_prefix6024	107.7665	6.73931E-07	Chi|10.286.1	AT1G10657
my_prefix6911	31.4903	6.83238E-07	Chi|2.1072	AT1G66235
my_prefix8761	169.7608	6.87761E-07	Chi|4.918.2	AT2G44440
my_prefix15432	999	6.99338E-07	Chi|1.696	AT5G56970
my_prefix11310	95.21405	7.05162E-07	Chi|49.42.1	AT5G47570
my_prefix10767	998.9982	7.09482E-07	Chi|6.978	AT4G28640
my_prefix11818	999	7.24278E-07	Chi|1.1088	AT5G61090
my_prefix6106	76.63039	7.70816E-07	Chi|24.150	AT1G13620
my_prefix12698	789.1717	8.01765E-07	Chi|5.826	AT1G22130
my_prefix15462	998.9999	9.64434E-07	Chi|1.926	AT5G59070
my_prefix5523	91.03238	9.98975E-07	Chi|2G31430	AT2G31430
my_prefix8421	212.7964	1.17994E-06	Chi|2.891	AT2G32640
my_prefix11826	300.2767	1.21795E-06	Chi|1.1113	AT5G61380
my_prefix6209	113.3037	1.33797E-06	Chi|5.369	AT1G17680
my_prefix4966	25.43761	1.3645E-06	Chi|8.408	AT3G58290
my_prefix8958	999	1.51105E-06	Chi|113.69	AT3G26050
my_prefix14646	177.5176	1.57745E-06	Chi|9.254	AT5G15730
my_prefix13755	999	1.65054E-06	Chi|48.125	AT3G20740
my_prefix6399	999	1.74486E-06	Chi|46.232	AT1G27700
my_prefix12465	305.1899	1.8164E-06	Chi|13.387	AT3G05450
my_prefix6467	998.9993	1.98181E-06	Chi|78.11	AT1G30755
my_prefix11719	998.9995	2.02169E-06	Chi|1.768	AT5G57670
my_prefix12936	998.9997	2.12648E-06	Chi|16.138	AT1G06900
my_prefix10856	999	2.13271E-06	Chi|17.24	AT4G25600
my_prefix11769	214.5701	2.3558E-06	Chi|1.927	AT5G59050
my_prefix9186	999	2.4318E-06	Chi|31.211	AT3G50920
my_prefix9044	998.9821	2.45983E-06	Chi|3G29385	AT3G29385
my_prefix12305	83.3862	2.45991E-06	Chi|97.20	AT3G43850
my_prefix6454	125.3496	2.53228E-06	Chi|78.79	AT1G30130
my_prefix4842	60.36018	2.69795E-06	Chi|4.127	AT2G36570
my_prefix14221	50.48689	2.80045E-06	Chi|113.65	AT3G26010
my_prefix9418	833.6189	2.81427E-06	Chi|8.447	AT3G58780

my_prefix12392	999	2.84777E-06	Chi|66.13	AT2G30933
my_prefix12879	33.63933	2.93959E-06	Chi|16.500	AT1G03150
my_prefix6005	998.9996	3.17543E-06	Chi|77.47	AT1G09830
my_prefix12134	998.8046	3.27229E-06	Chi|43.51	AT4G14120
my_prefix14585	24.74489	3.34273E-06	Chi|3.231	AT5G10950
my_prefix13431	90.24286	3.36027E-06	Chi|2.765	AT1G73340
my_prefix15327	866.3165	3.60245E-06	Chi|45.21	AT5G47840
my_prefix4317	58.5822	3.66812E-06	Chi|13.802	AT3G01550
my_prefix10619	466.3052	3.80896E-06	Chi|6.462	AT4G33800
my_prefix13136	999	3.83881E-06	Chi|55.29	AT1G28200
my_prefix7735	999	3.89863E-06	Chi|7.417	AT3G15630
my_prefix9837	998.9972	4.27528E-06	Chi|3.133	AT5G12040
my_prefix7766	999	4.62026E-06	Chi|7.314	AT3G16690
my_prefix12919	204.0776	5.0445E-06	Chi|16.206	AT1G06070
my_prefix5617	110.2945	5.06764E-06	Chi|3.537	AT5G07360
my_prefix11780	388.3799	5.76479E-06	Chi|1.957	AT5G59570
my_prefix8379	456.5172	5.76738E-06	Chi|37.49	AT2G30620
my_prefix12112	999	5.78371E-06	Chi|92.69	AT4G18150
my_prefix4681	58.90847	5.86907E-06	Chi|2.213	AT1G79070
my_prefix7823	999	7.33914E-06	Chi|7.130	AT3G18610
my_prefix11523	749.3293	7.52827E-06	Chi|1.97	AT5G50830
my_prefix4755	75.28426	8.00582E-06	Chi|7.50.1	AT3G19260
my_prefix4540	71.5994	8.8318E-06	Chi|159.43	AT1G29860
my_prefix11269	80.17857	8.97409E-06	Chi|111.1	AT5G40020
my_prefix13238	998.9999	1.0349E-05	Chi|139.23	AT1G50730
my_prefix14074	69.91767	1.05017E-05	Chi|4.516	AT2G40240
my_prefix8279	681.7103	1.10619E-05	Chi|84.77	AT2G26580
my_prefix4543	998.9967	1.2069E-05	Chi|78.20	AT1G30670
my_prefix12142	220.0772	1.20733E-05	Chi|187.10	AT5G37730
my_prefix12267	571.6226	1.29335E-05	Chi|99.13	AT4G11340
my_prefix14192	999	1.29725E-05	Chi|70.52	AT2G02140
my_prefix10533	999	1.3028E-05	Chi|6.153	AT4G37170
my_prefix12277	90.30626	1.32466E-05	Chi|66.33	AT4G03140
my_prefix6652	998.9925	1.36709E-05	Chi|139.48.2	AT1G50440
my_prefix11499	558.1408	1.41651E-05	Chi|12.49	AT5G49970
my_prefix5364	82.30505	1.4281E-05	Chi|5.916	AT1G23420
my_prefix14155	999	1.44135E-05	Chi|4.1135	AT2G46640
my_prefix14050	998.9993	1.57884E-05	Chi|4.281	AT2G37960
my_prefix8091	114.0414	1.60978E-05	Chi|144.27	AT2G17033
my_prefix7181	999	1.63446E-05	Chi|2.474	AT1G76360

my_prefix10631	100.7907	1.77397E-05	Chi|6.500	AT4G33467
my_prefix4976	67.37005	1.85065E-05	Chi|22.104	AT3G62990
my_prefix10643	998.9658	1.99319E-05	Chi|6.551	AT4G32915
my_prefix5094	998.9982	2.21043E-05	Chi|6.117	AT4G36600
my_prefix12197	999	2.26094E-05	Chi|3.147	AT5G11870
my_prefix15515	138.7241	2.27839E-05	Chi|1.1305	AT5G63380
my_prefix12295	999	2.29165E-05	Chi|41.94	AT2G04025
my_prefix7114	998.9998	2.31219E-05	Chi|2.716	AT1G73840
my_prefix5127	70.52328	2.48663E-05	Chi|4G28395D2	AT4G28395
my_prefix14857	290.1295	2.6163E-05	Chi|15.154	AT4G03510
my_prefix9474	24.30771	2.85757E-05	Chi|8.633	AT3G61080
my_prefix5862	63.81644	3.01568E-05	Chi|16.375	AT1G04530
my_prefix15370	998.9996	3.0301E-05	Chi|1.257	AT5G52310
my_prefix8406	999	3.03052E-05	Chi|30.66	AT2G31730
my_prefix8234	432.7004	3.124E-05	Chi|32.133	AT2G24395
my_prefix11934	998.9996	3.36234E-05	Chi|1.1442	AT5G64690
my_prefix7440	29.20617	3.37238E-05	Chi|13.407	AT3G05260
my_prefix5957	998.9998	3.38015E-05	Chi|77.184	AT1G08540
my_prefix8685	82.27136	3.9024E-05	Chi|4.646	AT2G41550
my_prefix14174	330.0121	3.97972E-05	Chi|84.23	AT2G47670
my_prefix11416	999	4.30618E-05	Chi|44.81	AT5G43310
my_prefix8269	140.7871	4.45762E-05	Chi|17.420	AT2G26240
my_prefix5580	999	4.48958E-05	Chi|31.272	AT3G51540
my_prefix12069	97.59169	4.5271E-05	Chi|6.251	AT4G35900
my_prefix4795	73.05752	4.53729E-05	Chi|13.5	AT2G19010
my_prefix8155	998.9992	4.58446E-05	Chi|33.60	AT2G20710
my_prefix7900	394.0559	4.74141E-05	Chi|68.119	AT3G22200
my_prefix7386	999	4.9516E-05	Chi|13.575	AT3G03610
my_prefix11868	188.5749	4.95726E-05	Chi|1.1249	AT5G62720
my_prefix13665	641.3279	5.04711E-05	Chi|7.650	AT3G13540
my_prefix6266	313.4884	5.13568E-05	Chi|5.623	AT1G20450
my_prefix15004	858.9091	5.1365E-05	Chi|6.611	AT4G32342
my_prefix8447	999	5.19629E-05	Chi|28.76	AT2G33690
my_prefix14219	129.7074	5.20547E-05	Chi|113.58	AT3G25950
my_prefix4616	998.9999	5.2361E-05	Chi|61.34.1	AT1G61100
my_prefix7079	998.9995	5.3198E-05	Chi|2.852	AT1G72490
my_prefix6004	998.9983	5.39211E-05	Chi|77.49	AT1G09820
my_prefix13394	998.9663	5.53719E-05	Chi|25.137	AT1G70210
my_prefix5150	47.03799	5.60768E-05	Chi|29.109	AT4G22140
my_prefix8633	288.7016	5.87355E-05	Chi|4.478	AT2G39910

my_prefix13427	47.62543	6.37285E-05	Chi|1G72690	AT1G72690
my_prefix6188	998.9992	6.37517E-05	Chi|5.293	AT1G16900
my_prefix8045	699.4892	6.4524E-05	Chi|45.60	AT2G15580
my_prefix8574	60.15156	7.12858E-05	Chi|4.289.1	AT2G38025
my_prefix12838	522.5459	7.45252E-05	Chi|1.1297	AT5G63270
my_prefix5449	94.86623	7.84468E-05	Chi|190.28	AT1G80240
my_prefix14103	156.0301	7.88499E-05	Chi|4.707	AT2G42200
my_prefix11387	45.66227	8.1502E-05	Chi|35.75	AT5G44450
my_prefix15339	18.89066	8.20307E-05	Chi|104.19	AT5G49150
my_prefix5571	998.9998	8.34866E-05	Chi|172.5	AT3G47590
my_prefix5412	67.65267	8.91951E-05	Chi|29.54	AT1G67260
my_prefix5711	999	9.4112E-05	Chi|50.216	AT4G15810
my_prefix11458	576.9053	9.54214E-05	Chi|79.3	AT5G48220
my_prefix12754	58.6141	9.70648E-05	Chi|1G53930	AT1G53930
my_prefix4889	998.9999	9.82714E-05	Chi|22.11	AT2G48080
my_prefix10376	97.65838	0.000101008	Chi|32.85	AT4G02880
my_prefix5842	95.60409	0.000101793	Chi|16.449.1	AT1G03780
my_prefix5761	201.161	0.000109162	Chi|1.1502	AT5G65320
my_prefix10415	24.62808	0.000117436	Chi|24.195	AT4G01650
my_prefix7837	67.96291	0.000128695	Chi|7.55	AT3G19210
my_prefix6251	998.9999	0.000129468	Chi|5.567	AT1G19790
my_prefix9057	102.9464	0.000133245	Chi|97.19	AT3G43860
my_prefix4701	999	0.000138591	Chi|13.554	AT3G03800
my_prefix7097	122.0106	0.00014202	Chi|2.778	AT1G73180
my_prefix14233	999	0.000150502	Chi|112.46	AT3G27410
my_prefix15115	33.25592	0.000150723	Chi|29.138	AT4G21902
my_prefix5815	998.9983	0.000155878	Chi|16.555	AT5G61710
my_prefix5610	999	0.000156348	Chi|3.994.1	AT5G02520
my_prefix7020	91.34044	0.000156928	Chi|25.123	AT1G70100
my_prefix14237	11.01764	0.000161727	Chi|15.59.1	AT3G27730
my_prefix5566	999	0.000164508	Chi|215.4	AT3G28960
my_prefix5592	268.126	0.000165452	Chi|8.236	AT3G56550
my_prefix4853	998.9997	0.000166806	Chi|4.394	AT2G39060
my_prefix6225	26.0238	0.000176003	Chi|5.473	AT1G18750
my_prefix5545	21.06962	0.000184822	Chi|4.854	AT2G43745
my_prefix11634	89.558	0.000189743	Chi|1.493	AT5G54730
my_prefix10905	25.80087	0.000193811	Chi|17.161	AT4G24270
my_prefix9860	70.09114	0.000210389	Chi|3.63	AT5G13090
my_prefix5745	80.6629	0.000245542	Chi|1.847	AT5G58450
my_prefix7147	270.1612	0.000268083	Chi|2.614.1	AT1G74880

my_prefix10170	999	0.000269904	Chi|26.108.1	AT5G24165
my_prefix7327	675.6113	0.000276479	Chi|13.759	AT3G01175
my_prefix4690	999	0.000279929	Chi|190.39	AT1G80140
my_prefix10163	52.65273	0.000294459	Chi|26.78	AT5G23910
my_prefix10429	40.63975	0.000304304	Chi|9.22	AT4G01023
my_prefix7242	368.5846	0.000306004	Chi|2.243	AT1G78810
my_prefix9173	41.15435	0.000306887	Chi|31.175	AT3G50520
my_prefix7605	998.9993	0.000311204	Chi|7.853	AT3G11405
my_prefix8757	137.7538	0.000315949	Chi|4.908	AT2G44330
my_prefix8073	998.9988	0.000318819	Chi|27.59	AT2G19450
my_prefix11625	999	0.000331699	Chi|1.465	AT5G54470
my_prefix12816	39.46566	0.000335766	Chi|1.407	AT5G53870
my_prefix12738	42.60003	0.000341223	Chi|13.23	AT1G48170
my_prefix12543	998.996	0.000362031	Chi|11.231	AT2G16440
my_prefix10883	30.24497	0.000368029	Chi|17.108	AT4G24880
my_prefix4539	998.9917	0.000386962	Chi|1G29041	AT1G29041
my_prefix10657	999	0.000388253	Chi|6.587	AT4G32551
my_prefix7032	18.00434	0.000394656	Chi|25.192	AT1G70650
my_prefix6111	53.80938	0.000421027	Chi|24.134	AT1G13790
my_prefix14394	999	0.000427826	Chi|8.182	AT3G55970
my_prefix15086	999	0.000435044	Chi|17.100	AT4G24960
my_prefix12151	425.0267	0.000446726	Chi|111.40	AT5G39820
my_prefix10558	998.9997	0.000447124	Chi|6.236	AT4G36050
my_prefix14392	35.91415	0.000447837	Chi|8.180	AT3G55950
my_prefix12517	50.12879	0.000451414	Chi|48.126	AT3G20750
my_prefix5999	998.9981	0.000456977	Chi|77.62	AT1G09750
my_prefix10454	998.9998	0.000467784	Chi|22.294.1	AT4G38160
my_prefix12238	87.1775	0.000471788	Chi|9.839	AT5G22650
my_prefix11540	49.29172	0.000473387	Chi|1.158	AT5G51330
my_prefix7351	688.443	0.000478814	Chi|13.673	AT3G02710
my_prefix5320	19.78179	0.000490638	Chi|16.195	AT1G06170
my_prefix5202	999	0.000507886	Chi|49.30	AT5G47680
my_prefix7850	117.5766	0.000537943	Chi|48.32.1	AT3G19860
my_prefix7038	123.2116	0.000600607	Chi|25.214	AT1G70900
my_prefix8700	259.5516	0.000601344	Chi|4.699	AT2G42120
my_prefix7659	999	0.000622657	Chi|7.685	AT3G13190
my_prefix12508	999	0.000651103	Chi|7.236	AT3G17600
my_prefix6820	726.8614	0.000664953	Chi|38.103	AT1G63460
my_prefix4785	18.42758	0.000673904	Chi|27.125	AT2G20180
my_prefix11145	999	0.000693317	Chi|82.70	AT4G15620

my_prefix6967	190.0007	0.000716591	Chi|2.1069	AT1G68460
my_prefix10348	325.0909	0.00071964	Chi|103.60	AT4G04920
my_prefix8244	998.9955	0.000763319	Chi|19.172	AT2G24800
my_prefix13805	817.7722	0.000783809	Chi|21.22	AT2G04620
my_prefix8860	271.0489	0.000801068	Chi|84.27	AT2G47700
my_prefix10408	60.77211	0.000805857	Chi|24.176	AT4G01870
my_prefix14101	560.2535	0.000807102	Chi|4.701	AT2G42140
my_prefix8233	58.48555	0.000835184	Chi|32.127	AT2G24350
my_prefix13523	999	0.000860611	Chi|13.766	AT3G01230
my_prefix4694	157.5723	0.000865465	Chi|13.825	AT3G01800
my_prefix14492	75.81865	0.000893644	Chi|3.1004	AT5G02420
my_prefix13386	999	0.000909935	Chi|2.960	AT1G69295
my_prefix12355	46.33486	0.000927081	Chi|40.92	AT2G21195
my_prefix9578	999	0.000931639	Chi|3.992	AT5G02540
my_prefix5750	76.56984	0.000962124	Chi|1.1090	AT5G61110
my_prefix5919	21.04126	0.000977835	Chi|16.152	AT1G06720
my_prefix14431	53.99517	0.001003108	Chi|8.545	AT3G60110
my_prefix4536	134.2839	0.00101137	Chi|46.262	AT1G28040
my_prefix15382	999	0.00101637	Chi|1.355	AT5G53330
my_prefix4527	73.89131	0.001049089	Chi|46.16	AT1G26790
my_prefix9614	27.4188	0.001061558	Chi|3.870	AT5G03800
my_prefix7939	108.6514	0.001069424	Chi|156.11	AT3G23740
my_prefix9930	58.12079	0.001076022	Chi|9.199	AT5G15140
my_prefix9748	118.5274	0.001077132	Chi|3.446	AT5G08340
my_prefix12806	999	0.001081884	Chi|1.200	AT5G51790
my_prefix7556	738.762	0.001158421	Chi|56.128	AT3G09580
my_prefix5689	106.7894	0.00116163	Chi|6.958	AT4G28840
my_prefix13509	998.9992	0.001201096	Chi|2.80	AT1G80310
my_prefix5244	525.838	0.001204755	Chi|1.441	AT5G54225
my_prefix12228	999	0.001224601	Chi|9.560	AT5G19030
my_prefix4799	665.8389	0.001240523	Chi|40.113	AT2G21400
my_prefix8343	999	0.0012413	Chi|128.21	AT2G28880
my_prefix7002	32.18497	0.001241321	Chi|2.949	AT1G69400
my_prefix7325	998.9963	0.001279753	Chi|13.763	AT3G01200
my_prefix5766	278.61	0.001321624	Chi|1.1593	AT5G67340
my_prefix5740	13.07457	0.001361824	Chi|1.594	AT5G55690
my_prefix4706	998.9998	0.001411028	Chi|13.382	AT3G05510
my_prefix8369	998.9981	0.001461484	Chi|96.60	AT2G30340
my_prefix11639	999	0.001468021	Chi|1.519	AT5G54920
my_prefix7716	998.9993	0.001468572	Chi|7.468	AT3G15260

my_prefix11569	998.9989	0.001499717	Chi|1.261	AT5G52380
my_prefix11262	36.64303	0.00155663	Chi|24.275	AT5G40470
my_prefix10869	998.9942	0.001628513	Chi|17.75	AT4G25190
my_prefix8991	23.73896	0.001675189	Chi|21.157	AT3G26940
my_prefix12118	306.739	0.001689673	Chi|50.102	AT4G16695
my_prefix10916	157.8309	0.001690943	Chi|17.198	AT4G23940
my_prefix4537	999	0.001711346	Chi|46.266	AT1G28080
my_prefix9615	615.5523	0.001759102	Chi|3.867	AT5G03840
my_prefix8742	83.71412	0.001764001	Chi|4.848	AT2G43670
my_prefix6994	999	0.001765875	Chi|2.974	AT1G69180
my_prefix9827	999	0.001850534	Chi|3.153	AT5G11810
my_prefix12248	107.7819	0.001929865	Chi|145.11	AT5G25890
my_prefix12655	185.2164	0.001932687	Chi|77.92	AT1G09460
my_prefix4804	999	0.001935422	Chi|85.48	AT2G23530
my_prefix10853	998.9992	0.001947324	Chi|17.21	AT4G25630
my_prefix4673	998.9965	0.002036681	Chi|2.416	AT1G76952
my_prefix8638	999	0.002347761	Chi|4.485	AT2G39970
my_prefix13457	998.9996	0.002354483	Chi|2.559.2	AT1G75400
my_prefix10044	32.60263	0.002386377	Chi|9.567	AT5G19100
my_prefix7050	998.9992	0.002422551	Chi|25.238	AT1G71160
my_prefix12821	90.34266	0.002469867	Chi|1.652	AT5G56369
my_prefix11892	475.6043	0.002494046	Chi|1.1303	AT5G63350
my_prefix5829	998.9999	0.002625594	Chi|16.510	AT1G03055
my_prefix6363	999	0.002678054	Chi|46.40	AT1G26580
my_prefix12742	57.34158	0.002695838	Chi|67.103	AT1G49420
my_prefix12390	998.9999	0.00279398	Chi|18.114	AT2G30280
my_prefix6674	17.17488	0.002822458	Chi|83.74	AT1G52050
my_prefix6374	56.78627	0.002824791	Chi|46.105	AT1G25440
my_prefix12293	12.03367	0.002878434	Chi|41.14	AT2G03060
my_prefix5774	81.21372	0.002922637	Chi|140.14	AT4G12840
my_prefix11853	48.47368	0.00292934	Chi|1.1200	AT5G62240
my_prefix11929	245.9141	0.003033758	Chi|1.1434	AT5G64630
my_prefix11051	999	0.003048039	Chi|92.1	AT4G18600
my_prefix11664	999	0.00308861	Chi|1.593	AT5G55670
my_prefix6606	17.3855	0.003123516	Chi|89.6	AT1G48330
my_prefix5717	21.99707	0.003172492	Chi|30.19	AT4G13630
my_prefix13950	37.31183	0.003212734	Chi|22.250	AT2G28600
my_prefix9182	908.4888	0.003330223	Chi|31.204	AT3G50850
my_prefix14267	291.6385	0.003334939	Chi|98.36	AT3G45275
my_prefix9899	999	0.003430347	Chi|9.103	AT5G14070

my_prefix11806	999	0.003442343	Chi|1.1046	AT5G60650
my_prefix13009	202.1174	0.003541797	Chi|5.73	AT1G14540
my_prefix12444	15.14492	0.003562966	Chi|4.1019	AT2G45500
my_prefix10444	748.0653	0.003694153	Chi|2.60	AT4G00200
my_prefix6320	66.93992	0.00370801	Chi|5.876	AT1G23050
my_prefix11023	998.9996	0.003744628	Chi|17.412	AT4G19590
my_prefix15372	998.9997	0.003795121	Chi|1.267	AT5G52440
my_prefix12034	20.21999	0.003870251	Chi|142.17	AT4G12970
my_prefix11321	27.9224	0.003877623	Chi|15.107	AT5G47220
my_prefix4997	998.9897	0.003922273	Chi|5G05365	AT5G05365
my_prefix14500	998.9999	0.004008745	Chi|3.905	AT5G03510
my_prefix14612	58.40446	0.004042662	Chi|3.73	AT5G12980
my_prefix14961	9.78871	0.004057262	Chi|6.329	AT4G35130
my_prefix11173	998.9999	0.004119395	Chi|43.88	AT4G14330
my_prefix8178	334.257	0.0041604	Chi|93.46	AT2G21690
my_prefix12454	749.6593	0.004178934	Chi|13.723	AT3G02260
my_prefix8532	12.19401	0.004199138	Chi|4.133	AT2G36640
my_prefix11750	998.9998	0.004356053	Chi|1.854	AT5G58530
my_prefix5593	9.18249	0.004410907	Chi|8.314	AT3G57240
my_prefix9080	25.92553	0.004475049	Chi|53.57	AT3G45830
my_prefix9688	998.9997	0.004527465	Chi|3.644	AT5G06250
my_prefix5310	239.0403	0.004528009	Chi|8.778	AT1G02040
my_prefix13943	998.9999	0.004602903	Chi|18.50	AT2G28190
my_prefix6049	999	0.004638993	Chi|10.178	AT1G11710
my_prefix13013	48.52214	0.004666663	Chi|5.85	AT1G14680
my_prefix12653	921.7209	0.004674729	Chi|77.210	AT1G08310
my_prefix14134	40.35453	0.00472843	Chi|4.978	AT2G45050
my_prefix13000	30.24992	0.00474554	Chi|24.135	AT1G13770
my_prefix8341	246.8276	0.005160195	Chi|128.12	AT2G28810
my_prefix7109	218.8859	0.005175041	Chi|1G73640	AT1G73640
my_prefix5530	188.5859	0.005312021	Chi|4.28	AT2G35640
my_prefix13978	999	0.005317319	Chi|63.111	AT2G32020
my_prefix6405	998.9983	0.00534541	Chi|46.254	AT1G27960
my_prefix6213	66.26749	0.005405377	Chi|5.422	AT1G18265
my_prefix7350	93.90512	0.005628248	Chi|13.674	AT3G02700
my_prefix14120	32.72467	0.005676639	Chi|4.846	AT2G43650
my_prefix12708	15.25104	0.005714091	Chi|46.58	AT1G26330
my_prefix5924	998.9969	0.005746145	Chi|16.132	AT1G06930
my_prefix14197	87.80688	0.00574945	Chi|70.14	AT2G02750
my_prefix11427	6.94369	0.005784427	Chi|75.60	AT5G42810

my_prefix13420	998.9999	0.005808203	Chi|25.335	AT1G72220
my_prefix9665	124.733	0.005874343	Chi|3.716	AT5G05500
my_prefix9514	27.09612	0.005965836	Chi|22.73	AT3G62670
my_prefix12190	999	0.005974583	Chi|3.336	AT5G09850
my_prefix13470	998.9963	0.006005702	Chi|2.435	AT1G76740
my_prefix8848	145.5055	0.006083866	Chi|4.1200	AT2G47310
my_prefix14057	13.28329	0.006114031	Chi|4.332	AT2G38440
my_prefix11670	9.22851	0.006177529	Chi|1.608	AT5G55860
my_prefix6090	14.31292	0.006194014	Chi|195.32	AT1G13030
my_prefix10458	171.6672	0.006218553	Chi|22.317	AT4G38410
my_prefix14164	998.9996	0.006243921	Chi|4.1166	AT2G46970
my_prefix10079	38.3723	0.006324211	Chi|9.668	AT5G20110
my_prefix5650	37.22081	0.006348835	Chi|34.35	AT5G26690
my_prefix8827	20.75572	0.006409	Chi|4.1104	AT2G46360
my_prefix8345	22.69874	0.006417434	Chi|128.24	AT2G28910
my_prefix7419	502.0434	0.006482623	Chi|13.473	AT3G04700
my_prefix12254	998.9979	0.006568196	Chi|18.141	AT5G27220
my_prefix15499	999	0.006907614	Chi|1.1188	AT5G62130
my_prefix4870	27.84611	0.006992284	Chi|4.766	AT2G42830
my_prefix8697	999	0.007089553	Chi|4.695	AT2G42070
my_prefix8898	178.4879	0.007326026	Chi|70.99	AT2G01770
my_prefix13727	31.19663	0.007380647	Chi|7.154	AT3G18370
my_prefix7705	998.9995	0.007459208	Chi|7.494	AT3G15000
my_prefix7687	998.9998	0.007464917	Chi|7.575	AT3G14170
my_prefix13257	12.68886	0.007482742	Chi|83.39	AT1G52380
my_prefix10726	275.883	0.007552905	Chi|6.847	AT4G29930
my_prefix14996	94.58159	0.007854513	Chi|6.561	AT4G32820
my_prefix7316	51.24457	0.008002566	Chi|13.799	AT3G01516
my_prefix15392	88.89382	0.008014491	Chi|1.466	AT5G54480
my_prefix12130	33.34813	0.0080221	Chi|42.29	AT4G14815
my_prefix8940	999	0.00811397	Chi|41.84	AT2G03830
my_prefix13893	999	0.008157594	Chi|21.99	AT2G22260
my_prefix6556	15.21695	0.008159022	Chi|39.57	AT1G36390
my_prefix5770	998.9993	0.008207524	Chi|152.4	AT4G13440
my_prefix12404	883.8172	0.008333765	Chi|12.301	AT2G33880
my_prefix12623	137.8095	0.008344539	Chi|84.40.3	AT1G01760
my_prefix8812	20.72617	0.008478964	Chi|4.1073	AT2G46020
my_prefix10045	23.33591	0.008485478	Chi|9.570	AT5G19120
my_prefix8021	73.65928	0.008529343	Chi|75.71	AT2G13350
my_prefix9401	12.73507	0.008635437	Chi|8.395	AT3G58130

my_prefix15514	38.77324	0.008648097	Chi|1.1288	AT5G63140
my_prefix14224	20.94047	0.008649515	Chi|21.215	AT3G26390
my_prefix10708	766.2287	0.008683115	Chi|117.36	AT4G30820
my_prefix5640	998.9999	0.008690481	Chi|9.789	AT5G22090
my_prefix10460	998.9999	0.00914436	Chi|22.325	AT4G38500
my_prefix15533	999	0.009150489	Chi|1.1474	AT5G64970
my_prefix8136	365.7003	0.00941695	Chi|42.143	AT2G18650
my_prefix8558	256.3622	0.009417393	Chi|4.201	AT2G37270
my_prefix5337	999	0.009440767	Chi|10.158	AT1G11905
my_prefix4457	62.29567	0.009724965	Chi|16.192	AT1G06210
my_prefix13356	999	0.009860859	Chi|45.128	AT1G66670
my_prefix10705	49.20184	0.009930246	Chi|6.746	AT4G30880

Table S15. KEGG functional categories of PSGs in *C. himalaica*.

KEGG terms	Input number	*P* value
Zeatin biosynthesis	3	0.01831
Sulfur relay system (Ubiquitin related)	2	0.04626
Peroxisome	5	0.05029
Folate biosynthesis	2	0.09506
Alanine, aspartate and glutamate metabolism	3	0.09905
Riboflavin metabolism	1	0.19725
Nucleotide excision repair	3	0.2061
Mismatch repair	2	0.22368
Base excision repair	2	0.25595
Aminoacyl-tRNA biosynthesis	4	0.25968
Spliceosome	6	0.26199
Plant hormone signal transduction	8	0.26251
Vitamin B6 metabolism	1	0.28079
DNA replication	2	0.31244
Arachidonic acid metabolism	1	0.32669
Arginine and proline metabolism	2	0.33641
Glutathione metabolism	3	0.34684
Basal transcription factors	2	0.35226
Homologous recombination	2	0.36013
Phenylalanine, tyrosine and tryptophan biosynthesis	2	0.36797
Flavonoid biosynthesis	1	0.38336
Lysine degradation	1	0.44756
Inositol phosphate metabolism	2	0.45128
mRNA surveillance pathway	3	0.46876
Purine metabolism	4	0.46921
Carotenoid biosynthesis	1	0.48283
Propanoate metabolism	1	0.52638
Ubiquinone biosynthesis	1	0.54676
Fatty acid elongation	1	0.54676
Circadian rhythm - plant	1	0.55662
Glycerophospholipid metabolism	2	0.57291
beta-Alanine metabolism	1	0.59397
Phenylalanine metabolism	1	0.61145
N-Glycan biosynthesis	1	0.62818
Stilbenoid, diarylheptanoid and gingerol biosynthesis	1	0.64418
protein ubiquitination	10	0.65115
Porphyrin and chlorophyll metabolism	1	0.65951
Phenylpropanoid biosynthesis	3	0.6786
Glycerolipid metabolism	1	0.69499
Galactose metabolism	1	0.70812
RNA transport	3	0.72487
Terpenoid backbone biosynthesis	1	0.72677
Glycolysis / Gluconeogenesis	2	0.73387

Fructose and mannose metabolism	1	0.76059
Phosphatidylinositol signaling system	1	0.78077
Glycine, serine and threonine metabolism	1	0.79926
Endocytosis	2	0.82322
Protein processing in endoplasmic reticulum	3	0.84884
Phagosome	1	0.85254
Plant-pathogen interaction	2	0.88468
RNA degradation	1	0.91687
Biosynthesis of amino acids	3	0.92117
Pyrimidine metabolism	1	0.92389
Starch and sucrose metabolism	2	0.93805
Ubiquitin mediated proteolysis	1	0.95712
Biosynthesis of secondary metabolites	15	0.98026
Ribosome	1	0.99968

Table S16. GO categories of PSGs in *C. himalaica*.

GO terms	Function	# input list	# in background	*P* value	FDR
GO:0048608	Reproductive structure development	79	1722	4.50E-10	2.00E-06
GO:0022414	Reproductive process	91	2224	4.60E-09	5.10E-06
GO:0003006	Reproductive developmental process	86	2050	4.40E-09	5.10E-06
GO:0009791	Post-embryonic development	90	2188	4.50E-09	5.10E-06
GO:0000003	Reproduction	92	2272	6.10E-09	5.40E-06
GO:0007275	Multicellular organismal development	135	3864	9.50E-09	6.90E-06
GO:0032501	Multicellular organismal process	136	4020	5.50E-08	3.50E-05
GO:0016070	RNA metabolic process	128	3734	7.50E-08	4.10E-05
GO:0009908	Flower development	48	948	1.00E-07	4.90E-05
GO:0032502	Developmental process	136	4094	1.60E-07	6.90E-05
GO:0048437	Floral organ development	34	605	8.80E-07	0.00035
GO:0048569	Post-embryonic organ development	34	608	9.80E-07	0.00036
GO:0048438	Floral whorl development	30	510	1.60E-06	0.00055
GO:0048856	Anatomical structure development	113	3396	2.20E-06	0.00064
GO:0048646	Anatomical structure formation involved in morphogenesis	23	331	2.10E-06	0.00064
GO:0010468	Regulation of gene expression	94	2695	2.90E-06	0.00081
GO:0019219	Regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	88	2496	4.30E-06	0.00095
GO:0006139	Nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	147	4798	4.30E-06	0.00095
GO:0010556	Regulation of macromolecule biosynthetic process	88	2491	3.90E-06	0.00095
GO:0060255	Regulation of macromolecule metabolic process	97	2829	4.00E-06	0.00095
GO:0009889	Regulation of biosynthetic process	91	2634	6.30E-06	0.0011
GO:0006355	Regulation of transcription, DNA-dependent	84	2372	6.20E-06	0.0011
GO:0051171	Regulation of nitrogen compound metabolic process	88	2517	5.80E-06	0.0011
GO:0031326	Regulation of cellular biosynthetic process	91	2631	6.00E-06	0.0011
GO:0045449	Regulation of transcription	84	2376	6.60E-06	0.0012
GO:0051252	Regulation of RNA metabolic process	84	2388	7.90E-06	0.0013
GO:0048645	Organ formation	16	192	9.30E-06	0.0015
GO:0048449	Floral organ formation	15	174	1.20E-05	0.0019
GO:0080090	Regulation of primary metabolic process	93	2761	1.30E-05	0.002
GO:0006350	Transcription	89	2620	1.50E-05	0.0021
GO:0006351	Transcription, DNA-dependent	89	2618	1.50E-05	0.0021
GO:0032774	RNA biosynthetic process	89	2621	1.50E-05	0.0021
GO:0019222	Regulation of metabolic process	103	3186	2.20E-05	0.0029
GO:0048563	Post-embryonic organ morphogenesis	17	233	2.50E-05	0.0031
GO:0048444	Floral organ morphogenesis	17	233	2.50E-05	0.0031
GO:0031323	Regulation of cellular metabolic process	96	2928	2.60E-05	0.0032
GO:0006807	Nitrogen compound metabolic process	164	5675	2.70E-05	0.0032
GO:0048481	Ovule development	13	159	7.50E-05	0.0087
GO:0048465	Corolla development	11	117	8.50E-05	0.0091
GO:0048440	Carpel development	17	258	8.10E-05	0.0091

GO:0048441	Petal development	11	117	8.50E-05	0.0091
GO:0000398	Nuclear mRNA splicing, via spliceosome	11	120	0.0001	0.011
GO:0048467	Gynoecium development	17	268	0.00012	0.013
GO:0048518	Positive regulation of biological process	37	896	0.00019	0.019
GO:0006396	RNA processing	39	967	0.0002	0.02
GO:0000375	RNA splicing, via transesterification reactions	11	131	0.00021	0.02
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	11	131	0.00021	0.02
GO:0006397	mRNA processing	13	179	0.00023	0.021
GO:0048580	Regulation of post-embryonic development	23	459	0.00026	0.023
GO:0008284	Positive regulation of cell proliferation	8	72	0.00028	0.024
GO:0048731	System development	69	2083	0.0003	0.026
GO:0048513	Organ development	69	2083	0.0003	0.026
GO:0016071	mRNA metabolic process	20	381	0.00036	0.03
GO:0048522	Positive regulation of cellular process	33	793	0.00036	0.03
GO:0009886	Post-embryonic morphogenesis	24	503	0.00037	0.03
GO:0042440	Pigment metabolic process	19	361	0.00049	0.038
GO:0007131	Reciprocal meiotic recombination	11	145	0.00048	0.038