

Genomic convergence underlying high-altitude adaptation in alpine plants

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SUPPORTING INFORMATION

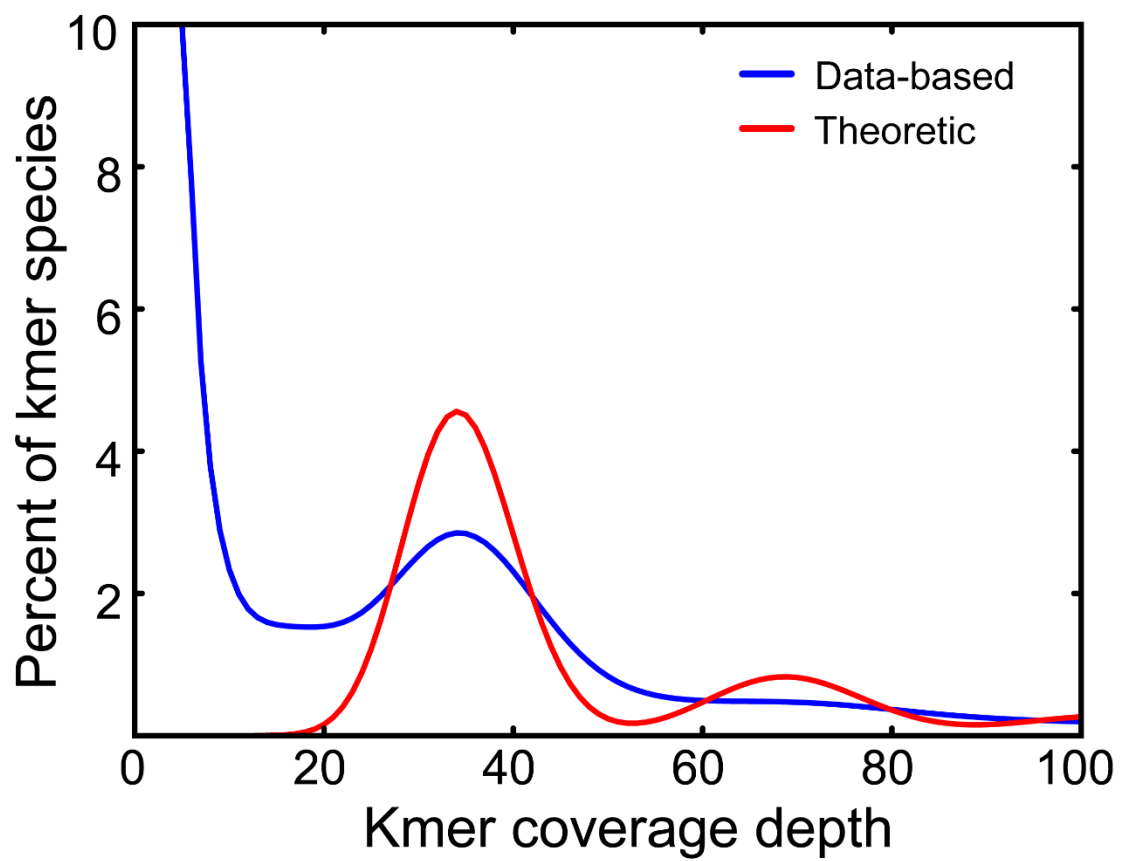


Figure S1. K-mer based analysis to estimate the genome size of *S. obvallata*

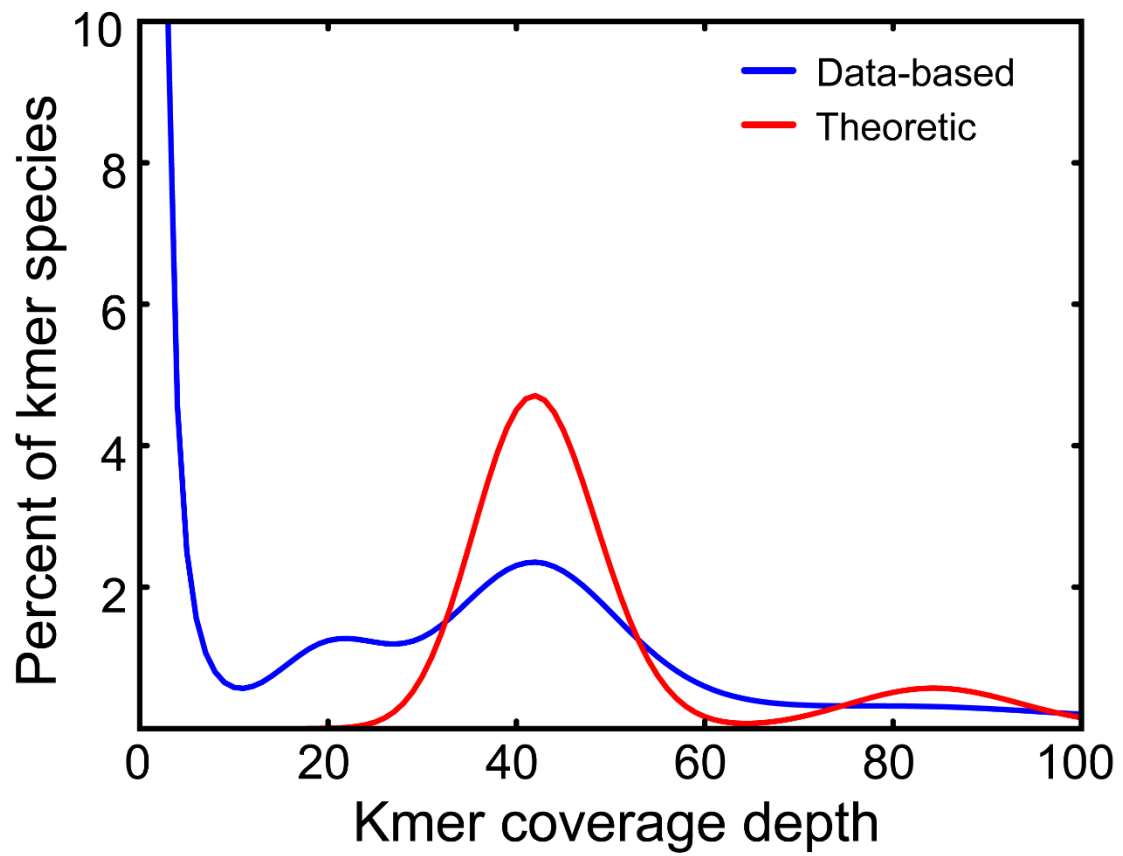


Figure S2. K-mer based analysis to estimate the genome size of *R. alexandrae*

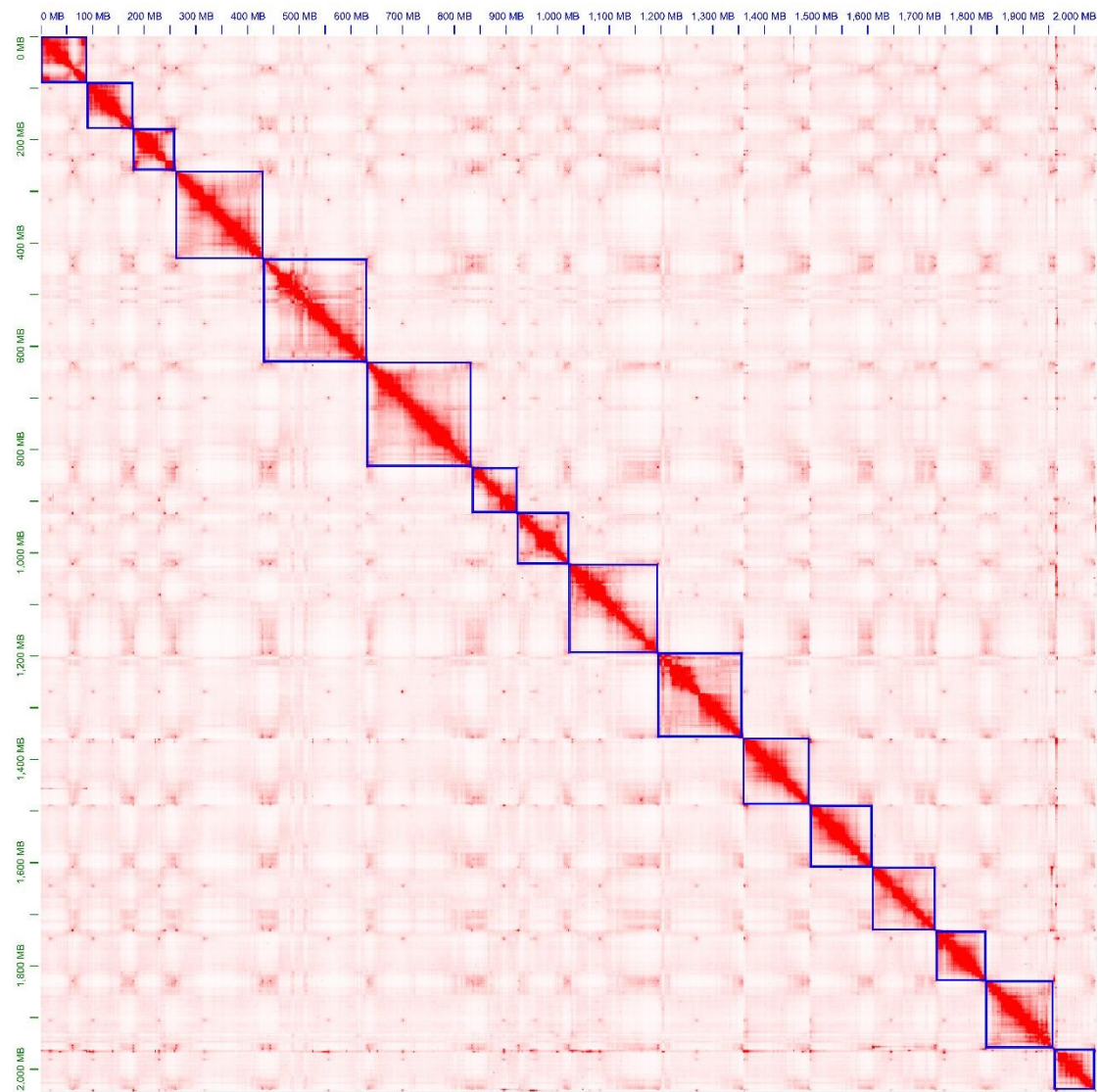


Figure S3. The Hi-C assisted assembly of *S. obvallata* pseudomolecules
Heatmap showing Hi-C interactions with darker red color indicating a higher contact probability.

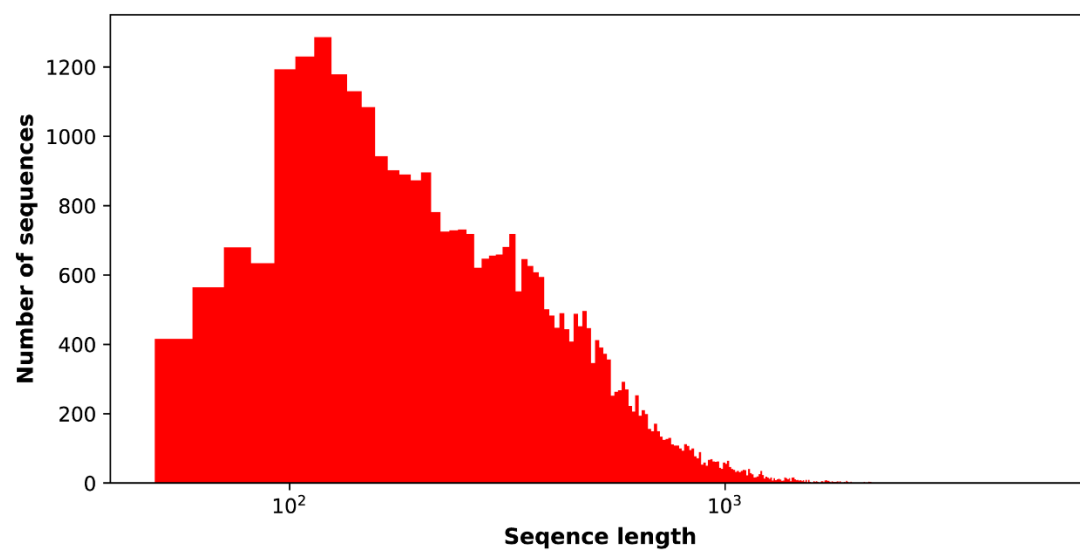


Figure S4. The distribution of sequence length of predicted protein-coding genes in *S. obvallata* genome

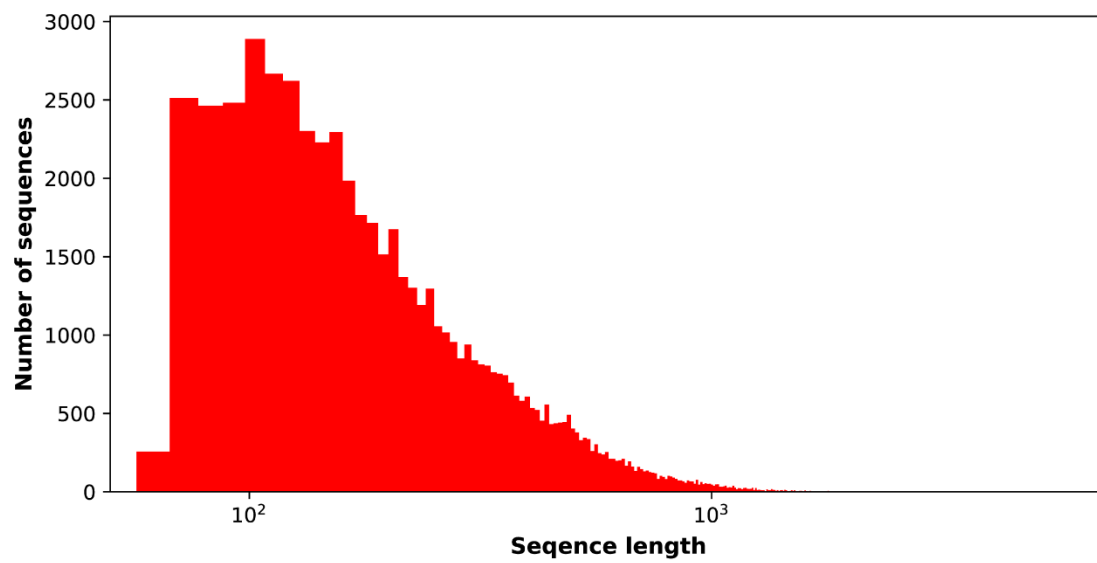


Figure S5. The distribution of sequence length of predicted protein-coding genes in *R. alexandrae* genome

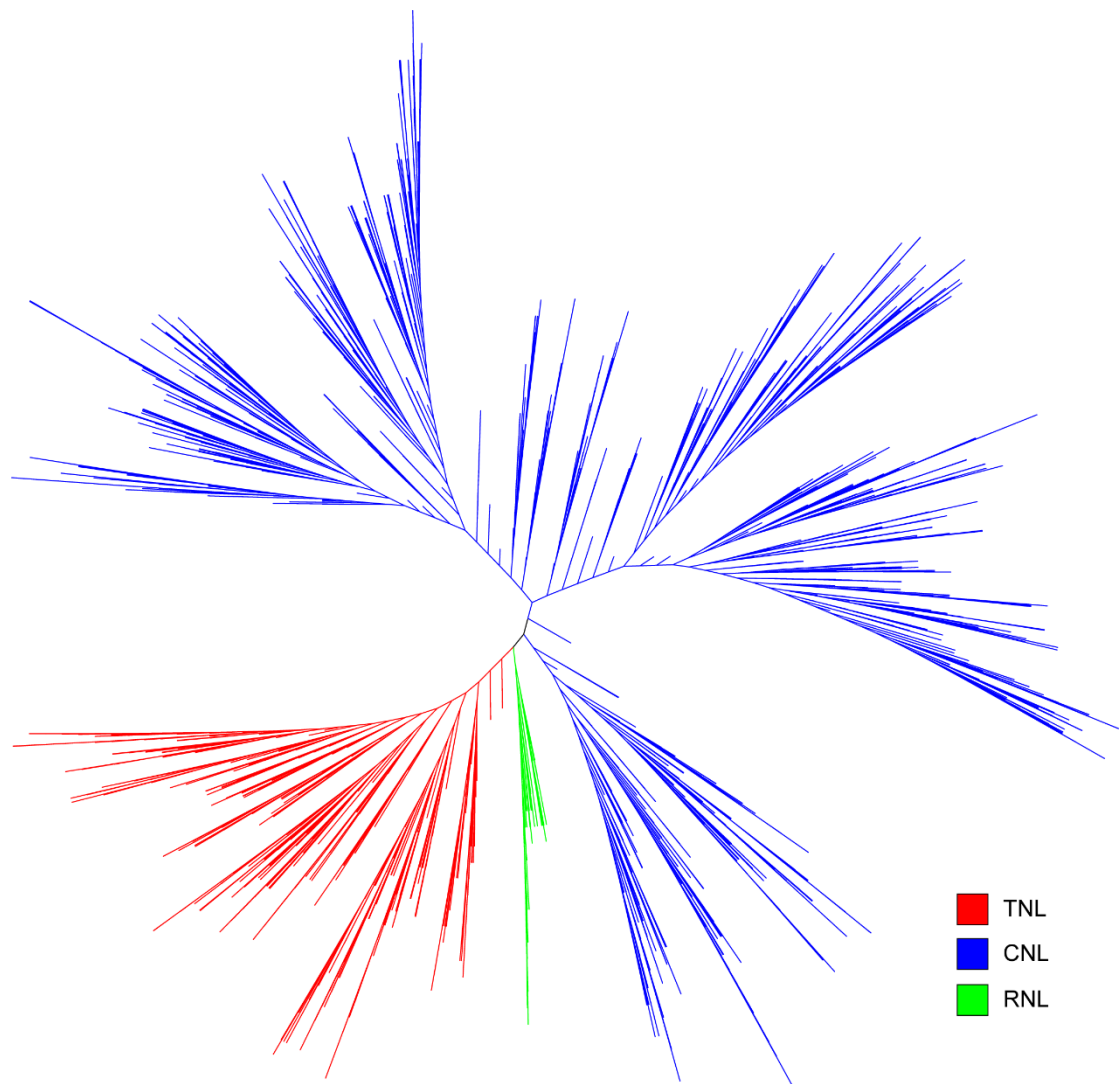


Figure S6. Gene tree of the nucleotide-binding site and leucine-rich-repeat domain receptor (NBS-LRR) genes
Three subclasses, TIR-NBS-LRR (TNL), CC-NBS-LRR (CNL) and RPW8-NBS-LRR (RNL) with 1,024, 4,058, and 173 genes are included.

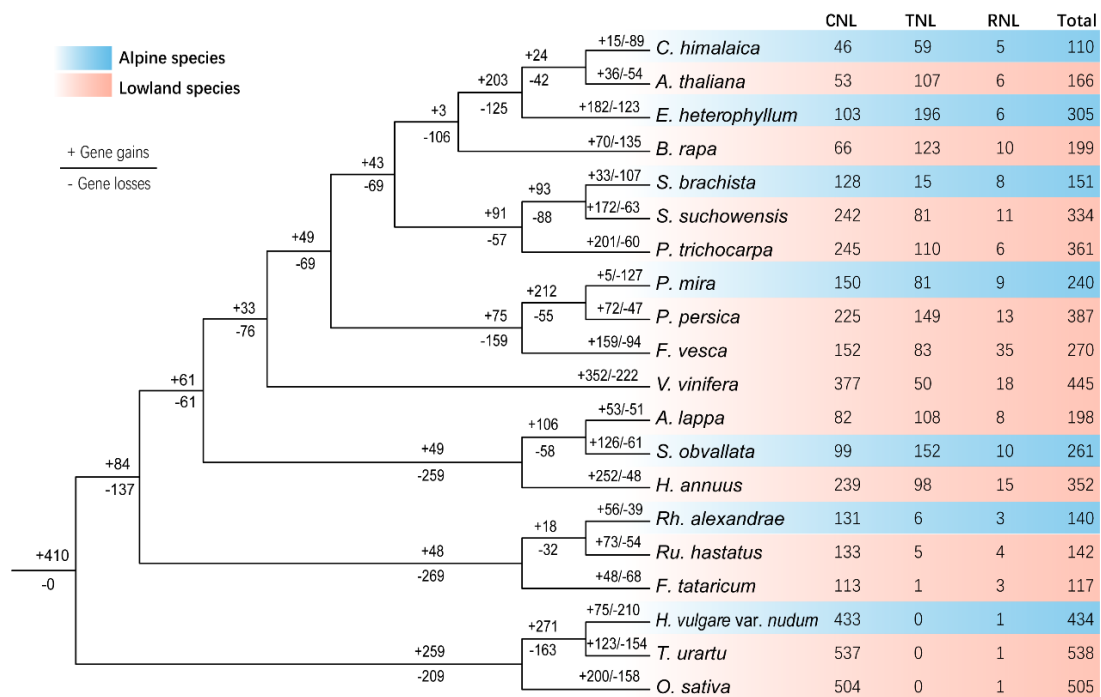


Figure S7. Loss and gain events of NBS-LRR genes in sampled species
Three NBS-LRR gene subclasses, CC-NBS-LRR (CNL), TIR-NBS-LRR (TNL), and RPW8-NBS-LRR (RNL), are included. ‘-’ or ‘+’ indicates the number of gene losses and gains on each branch.

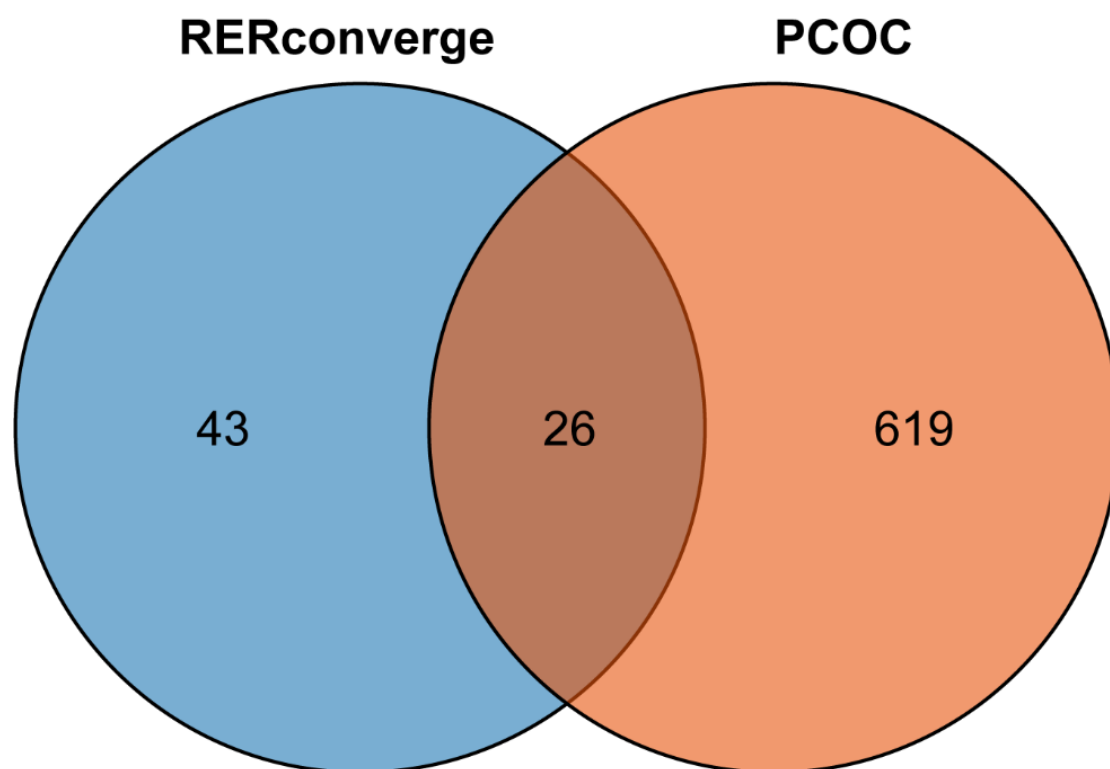


Figure S8. Venn plot showing the number of genes undergoing molecular convergence detected by RERconverge and PCOC analysis

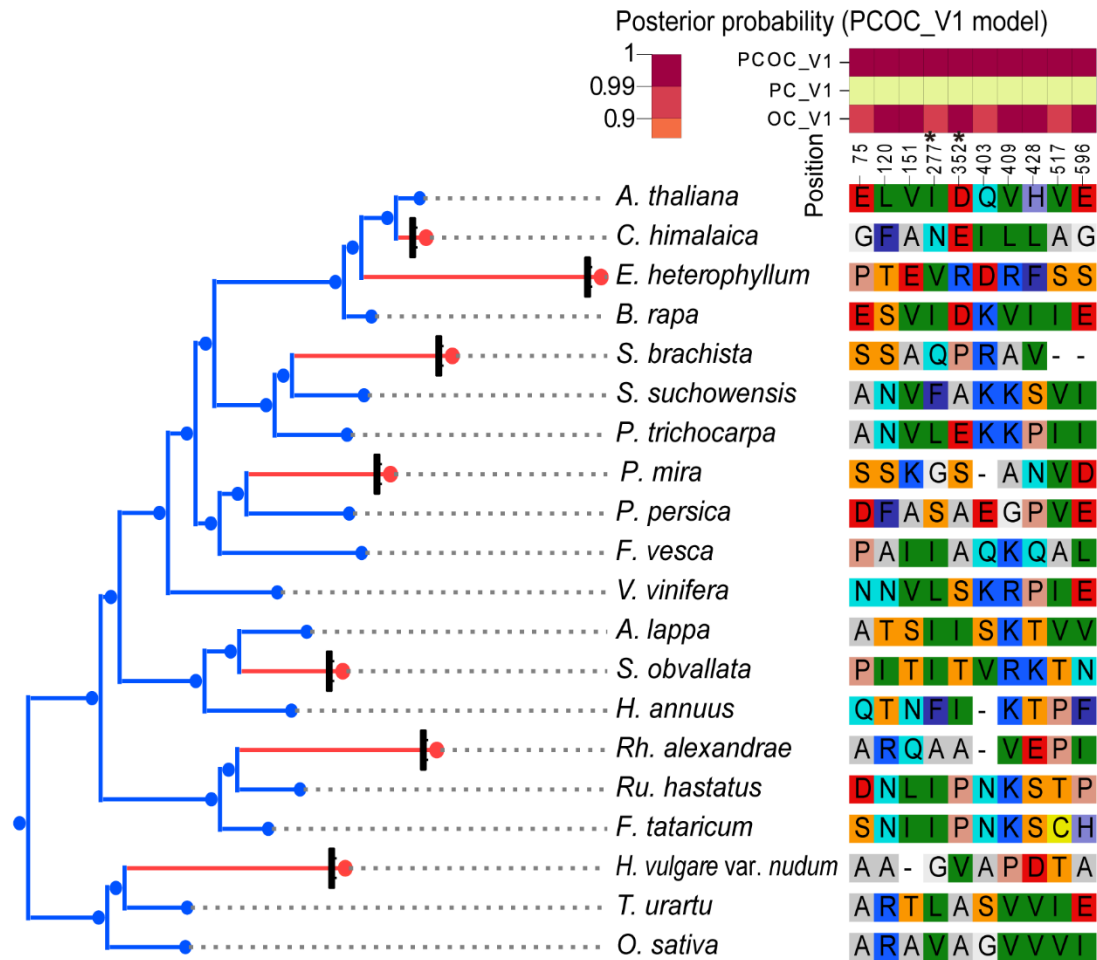


Figure S9. Site-based estimation of convergent amino acid evolution on S-locus genes using PCOC method

Only sites with a posterior probability above 0.9 according to the PCOC model are represented. Alpine species are in red, and their low-land sisters are in blue. Two sites located on the S-locus glycoprotein domain are labeled with stars.

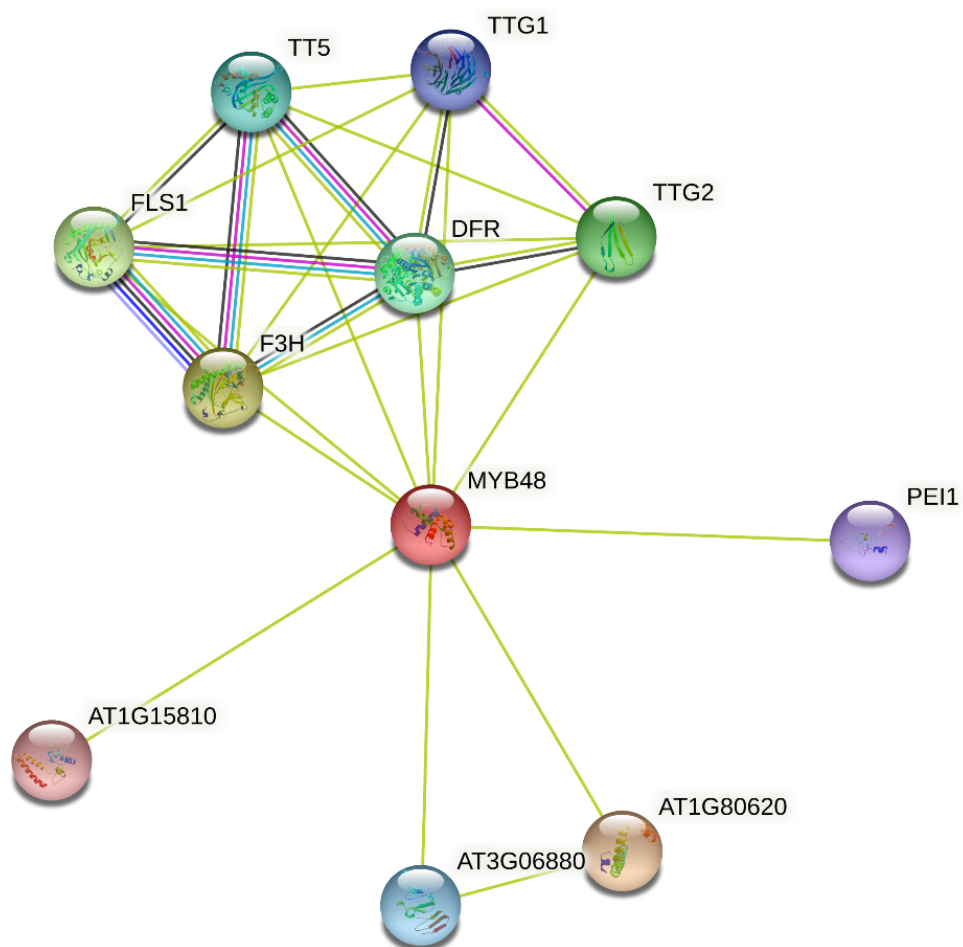


Figure S10. The predicted STRING network of Arabidopsis MYB48
Network nodes represent proteins and edges represent protein-protein interactions.

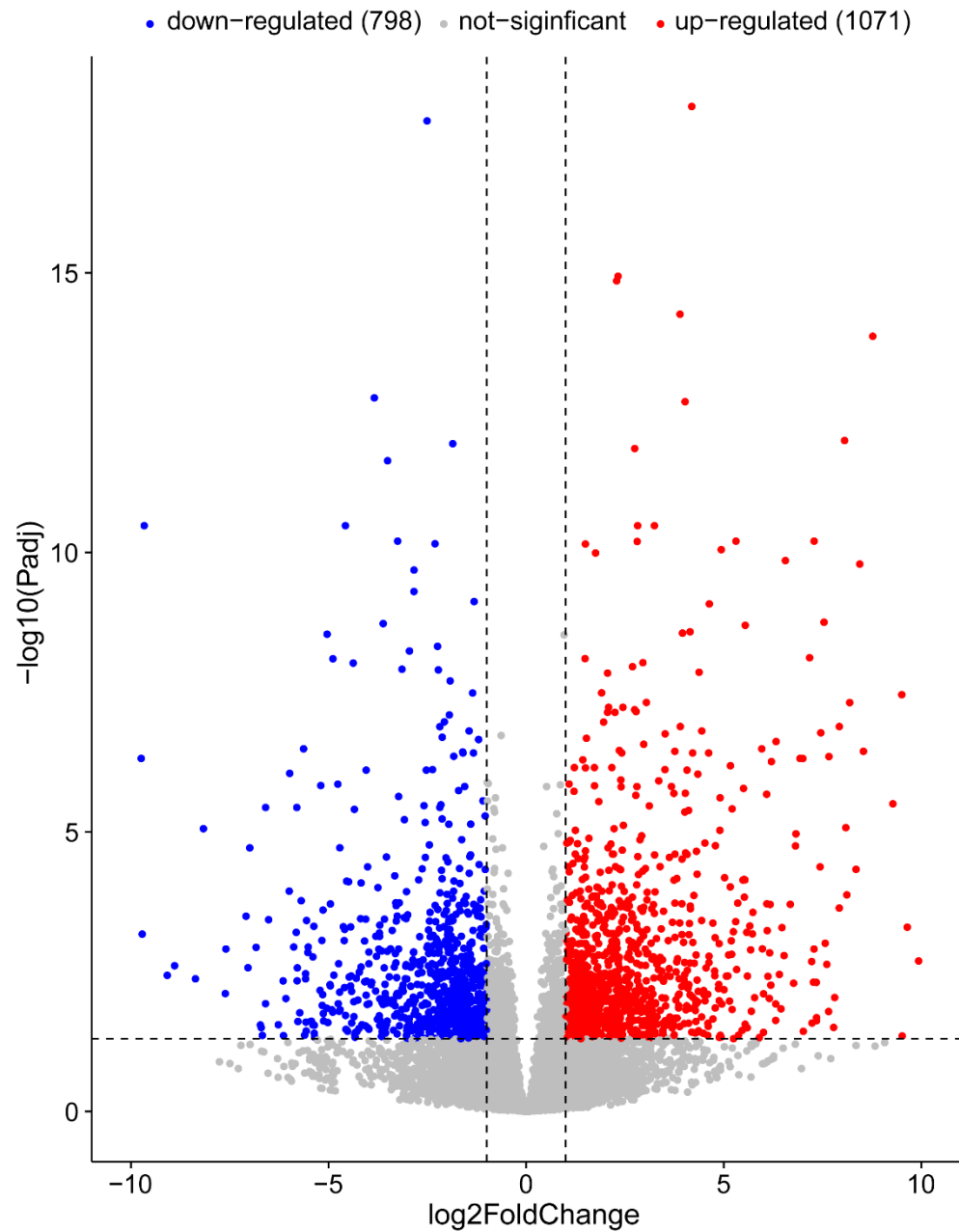


Figure S11. Volcano plot of differentially expressed genes between bract leaves and normal leaves

Significantly up-regulated genes are represented as red dots and significant down-regulated genes are represented as blue dots in volcano plot. “Padj” refers to the adjusted p -value using the Benjamini–Hochberg method.

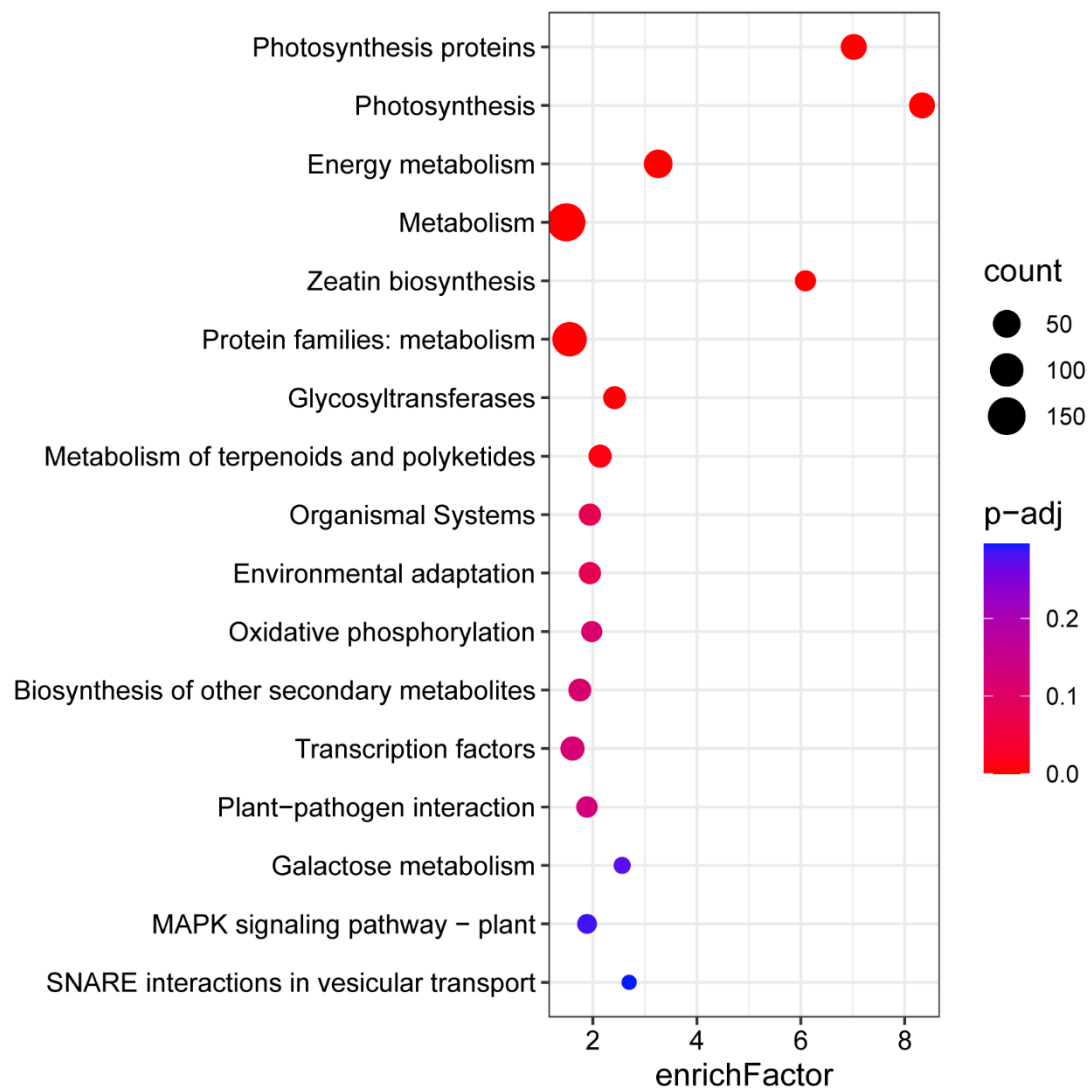


Figure S12. KEGG pathways of significantly down-regulated genes in bract leaves

“p-adj” refers to the adjusted *p*-value using the Benjamini–Hochberg method.

Table S1. Genome sequences of 20 species used for comparative analysis, including seven alpine plants (bold) and 13 representative lowland sisters. NCBI: the National Center for Biotechnology Information. TAIR: The Arabidopsis Information Resource.

Family	Species	Database	Reference
Brassicaceae	<i>A. thaliana</i>	TAIR	(Lamesch et al., 2012)
	<i>B. rapa</i>	Ensembl Plants	(Wang et al., 2011)
	<i>C. himalaica</i>	NCBI	(Zhang et al., 2019)
	<i>E. heterophyllum</i>	NCBI	(Guo et al., 2018)
Polygonaceae	<i>F. tataricum</i>	Tartary Buckwheat Genome Project	(Zhang et al., 2017)
	<i>Rh. alexandrae</i>	Newly generated	This study
	<i>Ru. hastatus</i>	NCBI	(Rifkin et al., 2021)
Rosaceae	<i>F. vesca</i>	Ensembl Plants	(Shulaev et al., 2011)
	<i>P. mira</i>	Genome Database for Rosaceae	(Wang et al., 2021)
	<i>P. persica</i>	Ensembl Plants	(Verde et al., 2013)
Asteraceae	<i>A. lappa</i>	NCBI	(Yang et al., 2022)
	<i>H. annuus</i>	Ensembl Plants	(Badouin et al., 2017)
	<i>S. obvallata</i>	Newly generated	This study
Poaceae	<i>H. vulgare</i> var. <i>nudum</i>	Ensembl Plants	(Zeng et al., 2015)
	<i>O. sativa</i>	Ensembl Plants	(Yu et al., 2002)
	<i>T. urartu</i>	Ensembl Plants	(Ling et al., 2018)
Salicaceae	<i>P. trichocarpa</i>	Ensembl Plants	(Tuskan et al., 2006)
	<i>S. brachista</i>	NCBI	(Chen et al., 2019)
	<i>S. suchowensis</i>	NCBI	(Dai et al., 2014)
Vitaceae	<i>V. vinifera</i>	Ensembl Plants	(Jaillon et al., 2007)

Table S2. Estimation of genome sizes for *S. obvallata* and *R. alexandrae* based on *K*-mer statistics

Species	<i>K</i> -mer	<i>K</i> -mer count	Peak depth	Genome size (bp)
<i>S. obvallata</i>	17	78,809,693,159	34	2,250,587,609
<i>R. alexandrae</i>	17	92,775,947,880	42	2,084,855,059

Table S3. The total sequencing data for genome assembly

Species	Library	Total Base (bp)	Total Reads	Average Length (bp)	N50 (bp)	Q20 (%)
<i>S. obvallata</i>	ONT	143,303,536,196	11,784,529	22,917	60,615	-
	Illumina	95,142,395,400	634,282,636	150	150	96.11
	Hi-C	205,914,823,800	1,372,765,492	150	150	97.87
<i>R. alexandrae</i>	ONT	144,007,146,545	8,605,927	16,733	34,697	-
	Illumina	103,853,673,000	692,357,820	150,	150	97.05

Table S4. The information of transcriptomic data of *S. obvallata* used in the study

Tissue	Name	Total Base (bp)	Total Reads	Q20 (%)
Base leaf	JL-1	11,004,025,506	73,608,710	98.10
	JL-2	10,494,272,308	70,156,674	98.26
	JL-3	10,227,039,340	68,431,730	98.39
Middle leaf	ML-1	10,422,933,558	69,743,294	98.38
	ML-2	10,385,815,346	69,485,058	98.28
	ML-3	10,277,264,344	68,692,336	98.28
Bract leaf	BL-1	9,590,764,446	64,087,306	98.34
	BL-2	10,989,175,450	73,458,712	98.30
	BL-3	10,969,678,684	73,321,792	98.31
Flower	F-1	11,435,046,272	76,473,416	98.27
	F-2	10,349,894,180	69,276,056	98.19
	F-3	10,134,792,130	67,828,610	98.24
Stem	S-1	10,888,411,306	72,793,584	98.16
	S-2	10,378,851,842	69,437,830	98.33
	S-3	9,931,403,162	66,407,362	98.40
Total	-	157,479,367,874	1,053,202,470	98.28

Table S5. Statistics of initial genome assembly of *S. obvallata* and *R. alexandrae*

Statistic	<i>S. obvallata</i>	<i>R. alexandrae</i>
Total length (bp)	2,044,030,733	2,039,881,226
Number of contigs	145	129
Largest contig (bp)	126,457,859	160,815,976
GC (%)	37.94	41.41
Contig N50 (bp)	36,958,263	36,323,674
Contig N75 (bp)	18,497,281	18,056,298

Table S6. Summary of the chromosome lengths of *S. obvallata* genome

Chromosome	Length (bp)
chr1	91,194,000
chr2	90,574,642
chr3	82,964,075
chr4	108,979,119
chr5	201,268,011
chr6	202,229,626
chr7	87,271,487
chr8	94,844,151
chr9	173,197,562
chr10	165,923,688
chr11	125,735,984
chr12	121,890,839
chr13	120,237,955
chr14	98,231,984
chr15	107,747,241
chr16	79,213,330
Total	1,951,503,694

Table S7. Genome completeness measured by Benchmarking Universal Single-Copy Orthologs (BUSCO) of *S. obvallata* genome

Type	Number	Percent (%)
Complete BUSCOs (C)	1526	94.6
Complete and single-copy BUSCOs (S)	1420	88.0
Complete and duplicated BUSCOs (D)	106	6.6
Fragmented BUSCOs (F)	12	0.7
Missing BUSCOs (M)	76	4.7
Total BUSCO groups searched	1614	100

Table S8. Genome completeness measured by Benchmarking Universal Single-Copy Orthologs (BUSCO) of *R. alexandrae* genome

Type	Number	Percent (%)
Complete BUSCOs (C)	2190	94.1
Complete and single-copy BUSCOs (S)	2017	86.7
Complete and duplicated BUSCOs (D)	173	7.4
Fragmented BUSCOs (F)	35	1.5
Missing BUSCOs (M)	101	4.4
Total BUSCO groups searched	2326	100

Table S9. Prediction of repetitive elements in the assembled *S. obvallata* genome

TE type	Length (bp)	Percentage of sequence
TE total	1,597,806,979	81.88%
LINEs	18,132,623	0.93%
LTR/Copia	502,728,577	25.76%
LTR/Gypsy	355,031,153	18.19%
DNA transposons	39,617,754	2.03%
Unclassified	657,623,138	33.70%

Table S10. Prediction of repetitive elements in the assembled *R. alexandrae* genome

TE type	Length (bp)	Percentage of sequence
TE total	1,665,563,021	81.65%
LINEs	55,688,757	2.73%
LTR/Copia	129,074,158	6.33%
LTR/Gypsy	774,739,843	37.98%
DNA transposons	832,271,540	4.08%
Unclassified	592,993,472	29.07%

Table S11. Functional annotation of predicted genes of *S. obvallata* and *R. alexandrae* genomes

Database	<i>S. obvallata</i>		<i>R. alexandrae</i>	
	Annotated proteins	Percent (%)	Annotated proteins	Percent (%)
InterPro	28,261	74.49	32,170	80.56
NR	36,433	96.03	47,268	76.90
Swiss-Prot	28,641	75.49	32,861	53.46
eggNOG	34,347	90.53	40,806	66.39
Total annotated	36,542	96.32	47,535	77.34
Total genes	37,938	100	61,463	100

Table S12. Summary of gene family clustering among the 20 species used

Species	Total Genes	Genes in families	Unassigned genes	Gene families	Unique families	Gene per family
<i>A. thaliana</i>	48,455	46,894	1,561	15,545	571	3.7
<i>A. lappa</i>	32,771	30,564	2,207	14,663	402	4.5
<i>B. rapa</i>	41,025	38,865	2,160	14,968	558	5.4
<i>C. himalaica</i>	27,019	26,346	673	14,893	113	1.1
<i>E. heterophyllum</i>	42,586	40,279	2,307	15,341	646	5.6
<i>F. tataricum</i>	34,544	30,574	3,970	14,247	572	4.7
<i>F. vesca</i>	64,597	61,202	3,395	16,117	1,735	13.3
<i>H. annuus</i>	70,864	59,704	11,160	18,537	2,856	22.9
<i>H. vulgare</i> var. <i>nudum</i>	37,961	36,678	1,283	15,470	449	11.6
<i>O. sativa</i>	42,246	35,414	6,832	17,121	1,483	9.9
<i>P. trichocarpa</i>	73,012	68,079	4,933	16,535	930	4.0
<i>P. mira</i>	28,519	27,686	833	15,080	144	5.6
<i>P. persica</i>	47,089	45,081	2,008	15,438	363	2.6
<i>R. alexandrae</i>	61,463	57,793	3,670	17,798	2,670	27.2
<i>R. hastatus</i>	38,271	34,959	3,312	15,034	1,016	11.0
<i>S. brachista</i>	30,209	28,899	1,310	14,091	196	2.1
<i>S. suchowensis</i>	36,449	33,543	2,906	14,770	216	1.8
<i>S. obvallata</i>	37,938	36,338	1,600	15,095	503	4.6
<i>T. urartu</i>	41,449	34,952	6,497	16,308	1,335	9.4
<i>V. vinifera</i>	41,097	37,297	3,800	15,630	1,174	12.3

Table S13. Significantly enriched GO terms of convergently expanded gene families in alpine plant genomes based on the hypergeometric test

ID	Description	Gene Ratio	Background Ratio	p-adjust value
GO:0042542	response to hydrogen peroxide	10/156	76/26032	1.21E-08
GO:0051259	protein complex oligomerization	9/156	56/26032	1.21E-08
GO:0010817	regulation of hormone levels	13/156	303/26032	6.74E-06
GO:0000302	response to reactive oxygen species	10/156	166/26032	8.60E-06
GO:0010345	suberin biosynthetic process	5/156	22/26032	1.72E-05
GO:0071456	cellular response to hypoxia	11/156	242/26032	1.72E-05
GO:0036294	cellular response to decreased oxygen levels	11/156	244/26032	1.72E-05
GO:0071453	cellular response to oxygen levels	11/156	244/26032	1.72E-05
GO:0009150	purine ribonucleotide metabolic process	10/156	195/26032	1.72E-05
GO:0006163	purine nucleotide metabolic process	10/156	203/26032	2.24E-05
GO:0009117	nucleotide metabolic process	11/156	272/26032	3.05E-05
GO:0006074	(1->3)-beta-D-glucan metabolic process	4/156	13/26032	3.05E-05
GO:0006075	(1->3)-beta-D-glucan biosynthetic process	4/156	13/26032	3.05E-05
GO:0036293	response to decreased oxygen levels	12/156	335/26032	3.05E-05
GO:0070482	response to oxygen levels	12/156	336/26032	3.05E-05
GO:0009259	ribonucleotide metabolic process	10/156	221/26032	3.05E-05
GO:0006753	nucleoside phosphate metabolic process	11/156	282/26032	3.40E-05
GO:0001709	cell fate determination	4/156	14/26032	3.40E-05
GO:0072521	purine-containing compound metabolic process	10/156	228/26032	3.40E-05
GO:0019693	ribose phosphate metabolic process	10/156	230/26032	3.50E-05
GO:0009926	auxin polar transport	7/156	100/26032	5.98E-05
GO:0006457	protein folding	9/156	200/26032	8.23E-05
GO:0001666	response to hypoxia	11/156	327/26032	0.000108
GO:0009851	auxin biosynthetic process	5/156	44/26032	0.00014
GO:0006637	acyl-CoA metabolic process	5/156	49/26032	0.000208
GO:0035383	thioester metabolic process	5/156	49/26032	0.000208
GO:1901568	fatty acid derivative metabolic process	5/156	49/26032	0.000208
GO:0060918	auxin transport	7/156	126/26032	0.000208
GO:0009914	hormone transport	7/156	129/26032	0.000234
GO:0009408	response to heat	10/156	299/26032	0.000237
GO:0055086	nucleobase-containing small molecule metabolic process	11/156	380/26032	0.000325
GO:0042446	hormone biosynthetic process	6/156	105/26032	0.000669
GO:0033865	nucleoside bisphosphate metabolic process	5/156	66/26032	0.000711
GO:0033875	ribonucleoside bisphosphate metabolic process	5/156	66/26032	0.000711
GO:0034032	purine nucleoside bisphosphate metabolic process	5/156	66/26032	0.000711
GO:0009850	auxin metabolic process	5/156	75/26032	0.00127
GO:0010540	basipetal auxin transport	3/156	15/26032	0.00127
GO:0045165	cell fate commitment	5/156	100/26032	0.004686

GO:0042445	hormone metabolic process	6/156	160/26032	0.005523
GO:0009142	nucleoside triphosphate biosynthetic process	4/156	60/26032	0.006013
GO:0010150	leaf senescence	7/156	230/26032	0.00617
GO:0009699	phenylpropanoid biosynthetic process	5/156	111/26032	0.006847
GO:0009638	phototropism	3/156	28/26032	0.007415
GO:0009141	nucleoside triphosphate metabolic process	4/156	65/26032	0.007415
GO:0090693	plant organ senescence	7/156	248/26032	0.008773
GO:0016998	cell wall macromolecule catabolic process	3/156	33/26032	0.01131
GO:0009723	response to ethylene	7/156	261/26032	0.01131
GO:0006754	ATP biosynthetic process	3/156	34/26032	0.011607
GO:0015986	proton motive force-driven ATP synthesis	3/156	34/26032	0.011607
GO:0044264	cellular polysaccharide metabolic process	8/156	353/26032	0.013909
GO:0051274	beta-glucan biosynthetic process	4/156	82/26032	0.015277
GO:0009698	phenylpropanoid metabolic process	5/156	145/26032	0.018099
GO:0006545	glycine biosynthetic process	2/156	11/26032	0.018099
GO:0080086	stamen filament development	2/156	11/26032	0.018099
GO:0051273	beta-glucan metabolic process	4/156	89/26032	0.018483
GO:0009205	purine ribonucleoside triphosphate metabolic process	3/156	42/26032	0.018483
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	3/156	42/26032	0.018483
GO:0046034	ATP metabolic process	5/156	150/26032	0.018998
GO:0009145	purine nucleoside triphosphate biosynthetic process	3/156	43/26032	0.019112
GO:0044036	cell wall macromolecule metabolic process	6/156	228/26032	0.022181
GO:0009144	purine nucleoside triphosphate metabolic process	3/156	46/26032	0.022181
GO:0006566	threonine metabolic process	2/156	13/26032	0.022181
GO:0009637	response to blue light	5/156	163/26032	0.025047
GO:0009733	response to auxin	8/156	414/26032	0.029032
GO:0009199	ribonucleoside triphosphate metabolic process	3/156	54/26032	0.032729
GO:0009201	ribonucleoside triphosphate biosynthetic process	3/156	54/26032	0.032729
GO:0006544	glycine metabolic process	2/156	18/26032	0.039478
GO:0006119	oxidative phosphorylation	3/156	63/26032	0.048904

“*p*-adjust value” refers to the adjusted *p*-value of the Benjamini–Hochberg false discovery rate (FDR), and the same below.

Table S14. Significantly enriched KEGG pathways of convergently expanded gene families in alpine plant genomes based on the hypergeometric test

ID	Description	Gene Ratio	Background Ratio	p-adjust value
ath00073	Cutin, suberine and wax biosynthesis	5/53	37/5098	0.000883
ath00190	Oxidative phosphorylation	8/53	163/5098	0.002715
ath04141	Protein processing in endoplasmic reticulum	9/53	215/5098	0.002715
ath00380	Tryptophan metabolism	5/53	64/5098	0.003121
ath04146	Peroxisome	5/53	87/5098	0.010104
ath00260	Glycine, serine and threonine metabolism	4/53	70/5098	0.02493

Table S15. Significantly enriched GO terms of convergently contracted gene families in alpine plant genomes based on the hypergeometric test

ID	Description	Gene Ratio	Background Ratio	p-adjust value
GO:0051923	sulfation	17/3445	17/26032	2.28E-12
GO:0007010	cytoskeleton organization	94/3445	325/26032	6.17E-11
GO:0030029	actin filament-based process	49/3445	128/26032	6.52E-10
GO:0002229	defense response to oomycetes	39/3445	91/26032	1.14E-09
GO:0030036	actin cytoskeleton organization	46/3445	119/26032	1.14E-09
GO:0000209	protein polyubiquitination	44/3445	111/26032	1.14E-09
GO:0007015	actin filament organization	43/3445	109/26032	2.08E-09
GO:0097435	supramolecular fiber organization	57/3445	177/26032	1.26E-08
GO:0046618	xenobiotic export	26/3445	50/26032	1.26E-08
GO:1990961	xenobiotic detoxification by transmembrane export across the plasma membrane	26/3445	50/26032	1.26E-08
GO:0042908	xenobiotic transport	28/3445	57/26032	1.26E-08
GO:0002239	response to oomycetes	43/3445	116/26032	1.34E-08
GO:0051640	organelle localization	54/3445	165/26032	1.34E-08
GO:0030048	actin filament-based movement	16/3445	22/26032	3.89E-08
GO:0099515	actin filament-based transport	16/3445	22/26032	3.89E-08
GO:0030050	vesicle transport along actin filament	14/3445	18/26032	1.13E-07
GO:0006928	movement of cell or subcellular component	34/3445	87/26032	1.75E-07
GO:0098754	detoxification	49/3445	155/26032	2.64E-07
GO:0043173	nucleotide salvage	14/3445	19/26032	3.00E-07
GO:0099518	vesicle cytoskeletal trafficking	14/3445	19/26032	3.00E-07
GO:0051648	vesicle localization	21/3445	40/26032	3.22E-07
GO:0051650	establishment of vesicle localization	21/3445	40/26032	3.22E-07
GO:0140115	export across plasma membrane	34/3445	91/26032	5.09E-07
GO:0043547	positive regulation of GTPase activity	20/3445	40/26032	2.07E-06
GO:0009896	positive regulation of catabolic process	43/3445	138/26032	2.84E-06
GO:0015914	phospholipid transport	13/3445	19/26032	3.60E-06
GO:0009636	response to toxic substance	51/3445	180/26032	4.74E-06
GO:0140352	export from cell	50/3445	175/26032	4.74E-06
GO:0043087	regulation of GTPase activity	20/3445	43/26032	8.02E-06
GO:0022406	membrane docking	22/3445	51/26032	9.34E-06
GO:0140056	organelle localization by membrane tethering	22/3445	51/26032	9.34E-06
GO:0031331	positive regulation of cellular catabolic process	40/3445	130/26032	9.58E-06
GO:0030705	cytoskeleton-dependent intracellular transport	17/3445	33/26032	9.69E-06
GO:0043094	cellular metabolic compound salvage	29/3445	81/26032	1.30E-05
GO:0006325	chromatin organization	66/3445	268/26032	1.79E-05
GO:0051345	positive regulation of hydrolase activity	20/3445	46/26032	2.53E-05
GO:0031497	chromatin assembly	35/3445	112/26032	3.21E-05
GO:0009845	seed germination	49/3445	184/26032	4.78E-05

GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	21/3445	53/26032	7.72E-05
GO:0009123	nucleoside monophosphate metabolic process	20/3445	49/26032	7.72E-05
GO:0051656	establishment of organelle localization	32/3445	103/26032	9.98E-05
GO:0006334	nucleosome assembly	18/3445	42/26032	0.000105
GO:0045732	positive regulation of protein catabolic process	24/3445	67/26032	0.00011
GO:0030243	cellulose metabolic process	26/3445	76/26032	0.000113
GO:0051247	positive regulation of protein metabolic process	41/3445	149/26032	0.000122
GO:0006108	malate metabolic process	11/3445	18/26032	0.000122
GO:0032434	regulation of proteasomal ubiquitin-dependent protein catabolic process	21/3445	55/26032	0.000126
GO:1901800	positive regulation of proteasomal protein catabolic process	21/3445	55/26032	0.000126
GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	21/3445	55/26032	0.000126
GO:0065004	protein-DNA complex assembly	28/3445	86/26032	0.000126
GO:0009124	nucleoside monophosphate biosynthetic process	19/3445	47/26032	0.000131
GO:0071215	cellular response to abscisic acid stimulus	75/3445	338/26032	0.000143
GO:0097306	cellular response to alcohol	75/3445	338/26032	0.000143
GO:0046777	protein autophosphorylation	46/3445	177/26032	0.000147
GO:0046112	nucleobase biosynthetic process	13/3445	25/26032	0.000149
GO:0009966	regulation of signal transduction	89/3445	421/26032	0.000149
GO:0018958	phenol-containing compound metabolic process	24/3445	69/26032	0.000151
GO:0034728	nucleosome organization	20/3445	52/26032	0.000159
GO:1901605	alpha-amino acid metabolic process	81/3445	375/26032	0.000161
GO:0006869	lipid transport	38/3445	137/26032	0.000173
GO:0045332	phospholipid translocation	9/3445	13/26032	0.000176
GO:0032270	positive regulation of cellular protein metabolic process	38/3445	138/26032	0.000197
GO:0006220	pyrimidine nucleotide metabolic process	15/3445	33/26032	0.000197
GO:0006221	pyrimidine nucleotide biosynthetic process	15/3445	33/26032	0.000197
GO:0006305	DNA alkylation	20/3445	53/26032	0.000197
GO:0006306	DNA methylation	20/3445	53/26032	0.000197
GO:0043648	dicarboxylic acid metabolic process	28/3445	89/26032	0.000199
GO:0006338	chromatin remodeling	30/3445	99/26032	0.000214
GO:0071824	protein-DNA complex subunit organization	30/3445	99/26032	0.000214
GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	21/3445	58/26032	0.000232
GO:2000058	regulation of ubiquitin-dependent protein catabolic process	21/3445	58/26032	0.000232
GO:0009132	nucleoside diphosphate metabolic process	25/3445	76/26032	0.000233
GO:0042537	benzene-containing compound metabolic process	25/3445	76/26032	0.000233
GO:0008154	actin polymerization or depolymerization	18/3445	46/26032	0.000278
GO:0000281	mitotic cytokinesis	17/3445	42/26032	0.000278

GO:0006538	glutamate catabolic process	8/3445	11/26032	0.000278
GO:0006904	vesicle docking involved in exocytosis	8/3445	11/26032	0.000278
GO:0023051	regulation of signaling	89/3445	431/26032	0.000279
GO:0045862	positive regulation of proteolysis	21/3445	59/26032	0.000279
GO:1903364	positive regulation of cellular protein catabolic process	21/3445	59/26032	0.000279
GO:0009894	regulation of catabolic process	49/3445	200/26032	0.000282
GO:0006536	glutamate metabolic process	13/3445	27/26032	0.000299
GO:0009738	abscisic acid-activated signaling pathway	61/3445	268/26032	0.00031
GO:0034204	lipid translocation	9/3445	14/26032	0.000312
GO:0090158	endoplasmic reticulum membrane organization	9/3445	14/26032	0.000312
GO:0030244	cellulose biosynthetic process	23/3445	69/26032	0.000351
GO:0072528	pyrimidine-containing compound biosynthetic process	17/3445	43/26032	0.000356
GO:0032268	regulation of cellular protein metabolic process	82/3445	393/26032	0.000367
GO:0010646	regulation of cell communication	90/3445	442/26032	0.000389
GO:0061640	cytoskeleton-dependent cytokinesis	22/3445	65/26032	0.000389
GO:0048584	positive regulation of response to stimulus	58/3445	254/26032	0.000411
GO:0009696	salicylic acid metabolic process	19/3445	52/26032	0.000411
GO:0051246	regulation of protein metabolic process	86/3445	419/26032	0.000418
GO:0009833	plant-type primary cell wall biogenesis	13/3445	28/26032	0.000422
GO:0009185	ribonucleoside diphosphate metabolic process	21/3445	61/26032	0.000422
GO:0051273	beta-glucan metabolic process	27/3445	89/26032	0.000422
GO:0009161	ribonucleoside monophosphate metabolic process	17/3445	44/26032	0.000457
GO:0045893	positive regulation of transcription, DNA-templated	99/3445	500/26032	0.00046
GO:0042026	protein refolding	15/3445	36/26032	0.00047
GO:0090351	seedling development	50/3445	211/26032	0.000489
GO:0009789	positive regulation of abscisic acid-activated signaling pathway	19/3445	53/26032	0.000494
GO:0006241	CTP biosynthetic process	10/3445	18/26032	0.000494
GO:0009208	pyrimidine ribonucleoside triphosphate metabolic process	10/3445	18/26032	0.000494
GO:0009209	pyrimidine ribonucleoside triphosphate biosynthetic process	10/3445	18/26032	0.000494
GO:0046036	CTP metabolic process	10/3445	18/26032	0.000494
GO:0061136	regulation of proteasomal protein catabolic process	21/3445	62/26032	0.000503
GO:0030388	fructose 1,6-bisphosphate metabolic process	8/3445	12/26032	0.000524
GO:0046033	AMP metabolic process	8/3445	12/26032	0.000524
GO:0009299	mRNA transcription	9/3445	15/26032	0.000536
GO:0009593	detection of chemical stimulus	13/3445	29/26032	0.000583
GO:0000097	sulfur amino acid biosynthetic process	16/3445	41/26032	0.000599
GO:0006096	glycolytic process	19/3445	54/26032	0.000609
GO:0006757	ATP generation from ADP	19/3445	54/26032	0.000609
GO:0008643	carbohydrate transport	21/3445	63/26032	0.000609

GO:0051606	detection of stimulus	21/3445	63/26032	0.000609
GO:0071496	cellular response to external stimulus	56/3445	249/26032	0.000698
GO:0031329	regulation of cellular catabolic process	43/3445	176/26032	0.000698
GO:0030042	actin filament depolymerization	12/3445	26/26032	0.000768
GO:0050801	ion homeostasis	79/3445	386/26032	0.000772
GO:0009156	ribonucleoside monophosphate biosynthetic process	16/3445	42/26032	0.000786
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	10/3445	19/26032	0.000795
GO:2000026	regulation of multicellular organismal development	97/3445	497/26032	0.000795
GO:0048278	vesicle docking	15/3445	38/26032	0.000811
GO:0006167	AMP biosynthetic process	7/3445	10/26032	0.000925
GO:0008655	pyrimidine-containing compound salvage	7/3445	10/26032	0.000925
GO:0043102	amino acid salvage	7/3445	10/26032	0.000925
GO:0045596	negative regulation of cell differentiation	7/3445	10/26032	0.000925
GO:0071267	L-methionine salvage	7/3445	10/26032	0.000925
GO:0009135	purine nucleoside diphosphate metabolic process	19/3445	56/26032	0.000947
GO:0009179	purine ribonucleoside diphosphate metabolic process	19/3445	56/26032	0.000947
GO:0046031	ADP metabolic process	19/3445	56/26032	0.000947
GO:0030001	metal ion transport	51/3445	224/26032	0.000952
GO:0030837	negative regulation of actin filament polymerization	8/3445	13/26032	0.000971
GO:0140029	exocytic process	8/3445	13/26032	0.000971
GO:0044728	DNA methylation or demethylation	23/3445	75/26032	0.000998
GO:0016311	dephosphorylation	50/3445	219/26032	0.001005
GO:0048580	regulation of post-embryonic development	84/3445	421/26032	0.001005
GO:0048467	gynoecium development	28/3445	100/26032	0.001038
GO:0034220	ion transmembrane transport	67/3445	319/26032	0.001073
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	21/3445	66/26032	0.001086
GO:0009147	pyrimidine nucleoside triphosphate metabolic process	10/3445	20/26032	0.001207
GO:0009826	unidimensional cell growth	85/3445	431/26032	0.00134
GO:0002221	pattern recognition receptor signaling pathway	11/3445	24/26032	0.001431
GO:0051274	beta-glucan biosynthetic process	24/3445	82/26032	0.001493
GO:0010629	negative regulation of gene expression	87/3445	445/26032	0.001493
GO:0009129	pyrimidine nucleoside monophosphate metabolic process	9/3445	17/26032	0.001493
GO:0009218	pyrimidine ribonucleotide metabolic process	12/3445	28/26032	0.001493
GO:0009220	pyrimidine ribonucleotide biosynthetic process	12/3445	28/26032	0.001493
GO:0051094	positive regulation of developmental process	35/3445	140/26032	0.001679
GO:0048582	positive regulation of post-embryonic development	25/3445	88/26032	0.001765
GO:0019856	pyrimidine nucleobase biosynthetic process	8/3445	14/26032	0.001765
GO:0043649	dicarboxylic acid catabolic process	8/3445	14/26032	0.001765

GO:0070262	peptidyl-serine dephosphorylation	7/3445	11/26032	0.001872
GO:0071265	L-methionine biosynthetic process	7/3445	11/26032	0.001872
GO:0006470	protein dephosphorylation	35/3445	141/26032	0.001877
GO:0031668	cellular response to extracellular stimulus	53/3445	243/26032	0.001912
GO:1903362	regulation of cellular protein catabolic process	21/3445	69/26032	0.001975
GO:0006098	pentose-phosphate shunt	13/3445	33/26032	0.002035
GO:0009991	response to extracellular stimulus	64/3445	309/26032	0.002035
GO:0006090	pyruvate metabolic process	24/3445	84/26032	0.002035
GO:0015748	organophosphate ester transport	16/3445	46/26032	0.002071
GO:0007018	microtubule-based movement	20/3445	65/26032	0.002295
GO:0009064	glutamine family amino acid metabolic process	20/3445	65/26032	0.002295
GO:0097035	regulation of membrane lipid distribution	9/3445	18/26032	0.002377
GO:0005984	disaccharide metabolic process	22/3445	75/26032	0.00239
GO:0042176	regulation of protein catabolic process	24/3445	85/26032	0.00239
GO:0006304	DNA modification	23/3445	80/26032	0.00239
GO:0002764	immune response-regulating signaling pathway	14/3445	38/26032	0.002515
GO:0005992	trehalose biosynthetic process	10/3445	22/26032	0.002722
GO:0009395	phospholipid catabolic process	10/3445	22/26032	0.002722
GO:0016052	carbohydrate catabolic process	50/3445	230/26032	0.002839
GO:0032507	maintenance of protein location in cell	11/3445	26/26032	0.002839
GO:0045185	maintenance of protein location	11/3445	26/26032	0.002839
GO:0006535	cysteine biosynthetic process from serine	8/3445	15/26032	0.00287
GO:0031333	negative regulation of protein-containing complex assembly	8/3445	15/26032	0.00287
GO:0032272	negative regulation of protein polymerization	8/3445	15/26032	0.00287
GO:0032776	DNA methylation on cytosine	8/3445	15/26032	0.00287
GO:0098660	inorganic ion transmembrane transport	51/3445	237/26032	0.003112
GO:0006165	nucleoside diphosphate phosphorylation	19/3445	62/26032	0.00318
GO:0009311	oligosaccharide metabolic process	24/3445	87/26032	0.003245
GO:0009733	response to auxin	80/3445	414/26032	0.003251
GO:0006607	NLS-bearing protein import into nucleus	7/3445	12/26032	0.003329
GO:0051643	endoplasmic reticulum localization	7/3445	12/26032	0.003329
GO:0061817	endoplasmic reticulum-plasma membrane tethering	7/3445	12/26032	0.003329
GO:0007017	microtubule-based process	52/3445	244/26032	0.003361
GO:0048468	cell development	88/3445	465/26032	0.003361
GO:0010214	seed coat development	17/3445	53/26032	0.003429
GO:0006740	NADPH regeneration	13/3445	35/26032	0.003429
GO:0055075	potassium ion homeostasis	9/3445	19/26032	0.003442
GO:1905428	regulation of plant organ formation	9/3445	19/26032	0.003442
GO:0048437	floral organ development	58/3445	281/26032	0.003665
GO:0031408	oxylipin biosynthetic process	10/3445	23/26032	0.003741
GO:0046470	phosphatidylcholine metabolic process	10/3445	23/26032	0.003741
GO:0044087	regulation of cellular component biogenesis	36/3445	153/26032	0.00375
GO:0000904	cell morphogenesis involved in differentiation	63/3445	313/26032	0.004193

GO:0050776	regulation of immune response	28/3445	110/26032	0.004229
GO:0048481	plant ovule development	18/3445	59/26032	0.004399
GO:0009130	pyrimidine nucleoside monophosphate biosynthetic process	8/3445	16/26032	0.004515
GO:0030162	regulation of proteolysis	21/3445	74/26032	0.004515
GO:0000911	cytokinesis by cell plate formation	20/3445	69/26032	0.004515
GO:0035556	intracellular signal transduction	90/3445	484/26032	0.004874
GO:0045944	positive regulation of transcription by RNA polymerase II	41/3445	184/26032	0.004951
GO:0048440	carpel development	23/3445	85/26032	0.005121
GO:0070588	calcium ion transmembrane transport	14/3445	41/26032	0.005121
GO:0019344	cysteine biosynthetic process	9/3445	20/26032	0.005121
GO:0005991	trehalose metabolic process	10/3445	24/26032	0.005274
GO:0006094	gluconeogenesis	10/3445	24/26032	0.005274
GO:0006816	calcium ion transport	20/3445	70/26032	0.005331
GO:0010876	lipid localization	38/3445	168/26032	0.005553
GO:0006739	NADP metabolic process	15/3445	46/26032	0.005571
GO:0048199	vesicle targeting, to, from or within Golgi	7/3445	13/26032	0.005571
GO:0009112	nucleobase metabolic process	13/3445	37/26032	0.00568
GO:0009787	regulation of abscisic acid-activated signaling pathway	31/3445	129/26032	0.005726
GO:1901419	regulation of response to alcohol	31/3445	129/26032	0.005726
GO:1905957	regulation of cellular response to alcohol	31/3445	129/26032	0.005726
GO:0009639	response to red or far red light	77/3445	405/26032	0.005755
GO:1901657	glycosyl compound metabolic process	60/3445	300/26032	0.006025
GO:0000096	sulfur amino acid metabolic process	18/3445	61/26032	0.006179
GO:0035670	plant-type ovary development	18/3445	61/26032	0.006179
GO:0046939	nucleotide phosphorylation	19/3445	66/26032	0.006195
GO:0009832	plant-type cell wall biogenesis	63/3445	319/26032	0.00621
GO:0051261	protein depolymerization	14/3445	42/26032	0.006216
GO:0010029	regulation of seed germination	24/3445	92/26032	0.006382
GO:0051494	negative regulation of cytoskeleton organization	8/3445	17/26032	0.006667
GO:1902904	negative regulation of supramolecular fiber organization	8/3445	17/26032	0.006667
GO:0006073	cellular glucan metabolic process	48/3445	229/26032	0.006705
GO:0044042	glucan metabolic process	49/3445	235/26032	0.006705
GO:0000910	cytokinesis	40/3445	182/26032	0.006788
GO:0009959	negative gravitropism	10/3445	25/26032	0.006898
GO:0031407	oxylipin metabolic process	10/3445	25/26032	0.006898
GO:0048768	root hair cell tip growth	10/3445	25/26032	0.006898
GO:0090630	activation of GTPase activity	10/3445	25/26032	0.006898
GO:0032259	methylation	57/3445	284/26032	0.006898
GO:0051017	actin filament bundle assembly	9/3445	21/26032	0.006903
GO:0061572	actin filament bundle organization	9/3445	21/26032	0.006903

GO:0045089	positive regulation of innate immune response	14/3445	43/26032	0.007625
GO:0071483	cellular response to blue light	12/3445	34/26032	0.007823
GO:0009267	cellular response to starvation	39/3445	178/26032	0.007988
GO:0040029	regulation of gene expression, epigenetic	32/3445	138/26032	0.008152
GO:0010608	post-transcriptional regulation of gene expression	54/3445	268/26032	0.008228
GO:0018105	peptidyl-serine phosphorylation	26/3445	105/26032	0.008461
GO:0009066	aspartate family amino acid metabolic process	18/3445	63/26032	0.008502
GO:0042126	nitrate metabolic process	7/3445	14/26032	0.008535
GO:0042128	nitrate assimilation	7/3445	14/26032	0.008535
GO:0006995	cellular response to nitrogen starvation	13/3445	39/26032	0.008678
GO:0042546	cell wall biogenesis	90/3445	496/26032	0.008832
GO:1900140	regulation of seedling development	24/3445	95/26032	0.009395
GO:0009741	response to brassinosteroid	28/3445	117/26032	0.009477
GO:0018209	peptidyl-serine modification	26/3445	106/26032	0.009477
GO:0002682	regulation of immune system process	39/3445	180/26032	0.009477
GO:0006206	pyrimidine nucleobase metabolic process	8/3445	18/26032	0.009477
GO:0009065	glutamine family amino acid catabolic process	8/3445	18/26032	0.009477
GO:0006812	cation transport	67/3445	351/26032	0.009565
GO:0048588	developmental cell growth	58/3445	295/26032	0.009593
GO:0032535	regulation of cellular component size	19/3445	69/26032	0.00961
GO:0090066	regulation of anatomical structure size	19/3445	69/26032	0.00961
GO:0043414	macromolecule methylation	47/3445	228/26032	0.00961
GO:0048438	floral whorl development	46/3445	222/26032	0.00961
GO:0009809	lignin biosynthetic process	17/3445	59/26032	0.009782

Only p-adjust value < 0.01 are provided.

Table S16. Significantly enriched KEGG pathways of convergently contracted gene families in alpine plant genomes based on the hypergeometric test

ID	Description	Gene Ratio	Background Ratio	p-adjust value
ath00620	Pyruvate metabolism	39/869	97/5098	4.73E-06
ath00710	Carbon fixation in photosynthetic organisms	30/869	69/5098	1.15E-05
ath01200	Carbon metabolism	78/869	272/5098	2.41E-05
ath00960	Tropane, piperidine and pyridine alkaloid biosynthesis	19/869	36/5098	2.73E-05
ath01232	Nucleotide metabolism	31/869	84/5098	0.000197
ath01230	Biosynthesis of amino acids	67/869	244/5098	0.000381
ath00250	Alanine, aspartate and glutamate metabolism	21/869	51/5098	0.00053
ath04075	Plant hormone signal transduction	76/869	291/5098	0.00053
ath03015	mRNA surveillance pathway	38/869	119/5098	0.00053
ath00270	Cysteine and methionine metabolism	39/869	124/5098	0.000556
ath00430	Taurine and hypotaurine metabolism	8/869	11/5098	0.000716
ath00630	Glyoxylate and dicarboxylate metabolism	27/869	78/5098	0.001077
ath00590	Arachidonic acid metabolism	11/869	20/5098	0.001077
ath04145	Phagosome	28/869	83/5098	0.001207
ath00240	Pyrimidine metabolism	23/869	64/5098	0.001502
ath04144	Endocytosis	44/869	158/5098	0.002732
ath00010	Glycolysis / Gluconeogenesis	34/869	119/5098	0.007067
ath00350	Tyrosine metabolism	15/869	41/5098	0.012192
ath04136	Autophagy - other	15/869	41/5098	0.012192
ath04120	Ubiquitin mediated proteolysis	40/869	155/5098	0.017982
ath00564	Glycerophospholipid metabolism	28/869	99/5098	0.017982
ath00220	Arginine biosynthesis	13/869	36/5098	0.023298
ath03040	Spliceosome	47/869	192/5098	0.023298
ath04626	Plant-pathogen interaction	49/869	204/5098	0.027774
ath04016	MAPK signaling pathway - plant	35/869	139/5098	0.039598
ath00910	Nitrogen metabolism	14/869	43/5098	0.040714
ath00909	Sesquiterpenoid and triterpenoid biosynthesis	9/869	23/5098	0.040714

Table S17. Annotation information of 36 convergent selected genes

Orthologs	Species	Genes	Annotations
OG0004760	<i>C. himalaica</i> , <i>E. heterophyllum</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>R. alexandrae</i>	<i>AT5G13310</i> , <i>AT5G13970</i>	Fruit development, heterocycle catabolic process
OG0000832	<i>C. himalaica</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>R. alexandrae</i> , <i>S. obvallata</i>	<i>MYB48</i> , <i>MYB27</i> , <i>MYB59</i>	Regulation of flavonol biosynthesis, regulation of cell cycle progression and root elongation
OG0012010	<i>E. heterophyllum</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>R. alexandrae</i> , <i>S. brachista</i>	<i>AT5G52220</i>	Mitotic sister chromatid cohesion
OG0000329	<i>C. himalaica</i> , <i>E. heterophyllum</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>R. alexandrae</i>	<i>SEP1</i> , <i>SEP2</i> , <i>SEP3</i> , <i>SEP4</i>	Development of sepals, petals, stamens and carpels, determination of flower meristem and organ identity
OG0005233	<i>C. himalaica</i> , <i>E. heterophyllum</i> , <i>R. alexandrae</i> , <i>S. brachista</i>	<i>BBX11</i>	Circadian rhythm, response to blue light, response to light stimulus, response to red light
OG0000556	<i>C. himalaica</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>S. brachista</i>	<i>AT5G21090</i> , <i>AT3G43740</i>	Signal transduction
OG0001948	<i>C. himalaica</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>R. alexandrae</i> , <i>S. brachista</i>	<i>AT5P1</i> , <i>AT1G71710</i>	Phosphatidylinositol dephosphorylation, seed germination, seedling development
OG0001928	<i>C. himalaica</i> , <i>P. mira</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>PMDH1</i> , <i>PMDH2</i>	Regulation of fatty acid beta-oxidation, regulation of photorespiration
OG0009364	<i>E. heterophyllum</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>R. alexandrae</i>	<i>OHP2</i>	Photosystem II assembly, response to light intensity
OG0009704	<i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>R. alexandrae</i> , <i>S. obvallata</i>	<i>HSA32</i> , <i>AT4G21323</i>	Heat acclimation, response to heat
OG0007885	<i>C. himalaica</i> , <i>E. heterophyllum</i> , <i>H. vulgare</i> var. <i>nudum</i>	<i>SVL4</i> , <i>SVL5</i>	Pollen tube growth, lipid metabolic process
OG0005129	<i>C. himalaica</i> , <i>E. heterophyllum</i> , <i>H. vulgare</i> var. <i>nudum</i>	<i>AT3G55470</i>	Regulation of defense response, response to water deprivation, shoot system development
OG0004460	<i>C. himalaica</i> , <i>E. heterophyllum</i> , <i>P. mira</i>	<i>LIN37A</i> , <i>LIN37B</i>	Cellular component biogenesis, organelle organization
OG0004639	<i>C. himalaica</i> , <i>E. heterophyllum</i> , <i>S. brachista</i>	<i>EMB2777</i> , <i>AT3G28230</i>	Maturation of SSU-rna from tricistronic rna transcript (SSU-rna, 5.8S rna, LSU-rna)
OG0001094	<i>C. himalaica</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>S. brachista</i>	<i>NUC-L1</i> , <i>NUC-L2</i>	Rna processing, leaf development, root development, shoot system development
OG0006408	<i>C. himalaica</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>S. brachista</i>	<i>AT1G12730</i> , <i>AT1G63110</i>	Response to temperature stimulus, protein localization to cell surface

OG0001067	<i>C. himalaica</i> , <i>H. vulgare</i> var. <i>nudum</i> , <i>S. brachista</i>	<i>CAT1</i> , <i>CAT2</i> , <i>CAT3</i>	Response to cold, response to light stimulus, response to hydrogen peroxide, response to oxidative stress
OG0007544	<i>C. himalaica</i> , <i>P. mira</i> , <i>S. brachista</i>	<i>LSP1</i>	Response to virus, translational initiation
OG0006996	<i>C. himalaica</i> , <i>P. mira</i> , <i>S. brachista</i>	<i>HPR</i>	Photorespiration, cellular response to light stimulus
OG0000803	<i>C. himalaica</i> , <i>P. mira</i> , <i>S. obvallata</i>	<i>AEP1</i> , <i>AEP2</i> , <i>AEP3</i>	Leaf senescence, protein catabolic process, response to ethylene
OG0001859	<i>C. himalaica</i> , <i>R. alexandrae</i> , <i>S. obvallata</i>	<i>AT1G32610</i> , <i>VQ9</i> , <i>IKU1</i> , <i>AT5G46780</i>	Endosperm development, regulation of seed growth
OG0001302	<i>C. himalaica</i> , <i>R. alexandrae</i> , <i>S. obvallata</i>	<i>KPNB1</i> , <i>AT3G08947</i> , <i>AT3G08943</i>	Protein import into nucleus, drought stress
OG0003962	<i>E. heterophyllum</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>DUF726</i> , <i>AT4G36210</i>	Response to lipid, shoot system development, signal transduction
OG0002378	<i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>S. brachista</i>	<i>SLP3</i> , <i>AT4G30020</i>	Cell differentiation, cell division, proteolysis, tissue development
OG0007327	<i>H. vulgare</i> var. <i>nudum</i> , <i>P. mira</i> , <i>S. brachista</i>	<i>TPC1</i>	Calcium ion transport, regulation of stomatal movement, seed germination
OG0000811	<i>H. vulgare</i> var. <i>nudum</i> , <i>R. alexandrae</i> , <i>S. brachista</i>	<i>NOT4A</i> , <i>NOT4B</i> , <i>NOT4C</i>	Protein ubiquitination, regulation of chloroplast protein synthesis
OG0001877	<i>H. vulgare</i> var. <i>nudum</i> , <i>R. alexandrae</i> , <i>S. brachista</i>	<i>PRP4KA</i> , <i>PRP4KB</i> , <i>AT3G53640</i>	Mrna cis splicing, via spliceosome, protein phosphorylation
OG0012347	<i>H. vulgare</i> var. <i>nudum</i> , <i>R. alexandrae</i> , <i>S. brachista</i>	<i>AT5G64730</i>	Regulation of developmental process, mrna splicing, via spliceosome
OG0001378	<i>H. vulgare</i> var. <i>nudum</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>AT1G49750</i> , <i>AT3G19320</i> , <i>AT4G06744</i>	Response to jasmonic acid, response to wounding, secondary metabolic process
OG0003532	<i>H. vulgare</i> var. <i>nudum</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>MMD1</i> , <i>AT2G01810</i> , <i>AT2G07714</i> , <i>ATMG00550</i>	Meiotic cell cycle, male meiosis chromosome segregation, pollen sperm cell differentiation
OG0005907	<i>H. vulgare</i> var. <i>nudum</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>AT3G06868</i> , <i>AT5G49100</i>	Cell wall biogenesis, plant-type cell wall organization or biogenesis
OG0001368	<i>P. mira</i> , <i>R. alexandrae</i> , <i>S. brachista</i>	<i>AT1G14670</i> , <i>AT2G01970</i> , <i>AT5G37310</i>	Protein localization to membrane
OG0004363	<i>P. mira</i> , <i>R. alexandrae</i> , <i>S. obvallata</i>	<i>PEPKR2</i>	Intracellular signal transduction, peptidyl-serine phosphorylation, protein autophosphorylation
OG0001613	<i>P. mira</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>PME21</i> , <i>PMEI-PME28</i> , <i>PME58</i> , <i>AT3G06830</i>	Cell wall modification, pectin catabolic process, seed coat development
OG0006829	<i>P. mira</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>AT5G14580</i>	RNA catabolic process, mitochondrial RNA processing

OG0004220	<i>R. alexandrae</i> , <i>S. brachista</i> , <i>S. obvallata</i>	<i>NBS1</i>	DNA repair, cellular response to DNA damage stimulus, double-strand break repair via homologous recombination, mitotic recombination
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Gene functions are adopted from The Arabidopsis Information Resource (TAIR) database.

Table S18. Significantly enriched GO terms of genes undergoing convergent positive selection in alpine plant genomes

ID	Description	Gene Ratio	Background Ratio	p-adjust value
GO:0009970	cellular response to sulfate starvation	3/75	14/26032	0.003228
GO:0019217	regulation of fatty acid metabolic process	3/75	28/26032	0.007984
GO:0045292	mRNA cis splicing, via spliceosome	3/75	31/26032	0.007984
GO:0042744	hydrogen peroxide catabolic process	3/75	32/26032	0.007984
GO:0048440	carpel development	4/75	85/26032	0.007984
GO:0046488	phosphatidylinositol metabolic process	4/75	91/26032	0.007984
GO:0030258	lipid modification	4/75	95/26032	0.007984
GO:0045490	pectin catabolic process	4/75	98/26032	0.007984
GO:0006995	cellular response to nitrogen starvation	3/75	39/26032	0.007984
GO:0048467	gynoecium development	4/75	100/26032	0.007984
GO:0009853	photorespiration	3/75	46/26032	0.011032
GO:0043562	cellular response to nitrogen levels	3/75	48/26032	0.011032
GO:0050994	regulation of lipid catabolic process	2/75	10/26032	0.011032
GO:0006606	protein import into nucleus	3/75	55/26032	0.014248
GO:0042743	hydrogen peroxide metabolic process	3/75	55/26032	0.014248
GO:0051170	import into nucleus	3/75	58/26032	0.015241
GO:0048481	plant ovule development	3/75	59/26032	0.015241
GO:0016485	protein processing	3/75	60/26032	0.015241
GO:0035670	plant-type ovary development	3/75	61/26032	0.015241
GO:0000272	polysaccharide catabolic process	4/75	143/26032	0.015489
GO:0080113	regulation of seed growth	2/75	15/26032	0.015787
GO:0034504	protein localization to nucleus	3/75	68/26032	0.018067
GO:0006650	glycerophospholipid metabolic process	4/75	159/26032	0.019216
GO:0006108	malate metabolic process	2/75	18/26032	0.019216
GO:0080112	seed growth	2/75	18/26032	0.019216
GO:0042542	response to hydrogen peroxide	3/75	76/26032	0.021093

GO:0045488	pectin metabolic process	4/75	171/26032	0.021603
GO:0010393	galacturonan metabolic process	4/75	172/26032	0.021603
GO:0042545	cell wall modification	4/75	173/26032	0.021603
GO:0043094	cellular metabolic compound salvage	3/75	81/26032	0.021959
GO:0016036	cellular response to phosphate starvation	3/75	82/26032	0.022013
GO:0045944	positive regulation of transcription by RNA polymerase II	4/75	184/26032	0.023147
GO:0046855	inositol phosphate dephosphorylation	2/75	23/26032	0.023147
GO:0071545	inositol phosphate catabolic process	2/75	23/26032	0.023147
GO:0071555	cell wall organization	5/75	313/26032	0.023848
GO:0019216	regulation of lipid metabolic process	3/75	90/26032	0.024735
GO:0046486	glycerolipid metabolic process	4/75	197/26032	0.026456
GO:0046838	phosphorylated carbohydrate dephosphorylation	2/75	26/26032	0.026456
GO:0051604	protein maturation	3/75	96/26032	0.027094
GO:0046856	phosphatidylinositol dephosphorylation	2/75	27/26032	0.027094
GO:0006506	GPI anchor biosynthetic process	2/75	30/26032	0.031801
GO:0046839	phospholipid dephosphorylation	2/75	30/26032	0.031801
GO:0006505	GPI anchor metabolic process	2/75	31/26032	0.033142
GO:0048438	floral whorl development	4/75	222/26032	0.035007
GO:0046174	polyol catabolic process	2/75	33/26032	0.035826
GO:0006644	phospholipid metabolic process	4/75	228/26032	0.036311
GO:0045229	external encapsulating structure organization	5/75	370/26032	0.036311
GO:0016052	carbohydrate catabolic process	4/75	230/26032	0.036374
GO:0010565	regulation of cellular ketone metabolic process	3/75	117/26032	0.038068
GO:0006913	nucleocytoplasmic transport	3/75	121/26032	0.040125
GO:0051169	nuclear transport	3/75	121/26032	0.040125
GO:0031668	cellular response to extracellular stimulus	4/75	243/26032	0.040125
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2/75	38/26032	0.040125
GO:0000398	mRNA splicing, via spliceosome	4/75	246/26032	0.040754
GO:0098813	nuclear chromosome segregation	3/75	125/26032	0.040754
GO:0071496	cellular response to external stimulus	4/75	249/26032	0.041196
GO:0043647	inositol phosphate metabolic process	2/75	40/26032	0.041243
GO:0044282	small molecule catabolic process	4/75	253/26032	0.041699
GO:0046164	alcohol catabolic process	2/75	41/26032	0.041699
GO:0072593	reactive oxygen species metabolic process	3/75	131/26032	0.041699
GO:0006635	fatty acid beta-oxidation	2/75	42/26032	0.041699

GO:0009960	endosperm development	2/75	42/26032	0.041699
GO:0007059	chromosome segregation	3/75	137/26032	0.045802
GO:0000375	RNA splicing, via transesterification reactions	4/75	272/26032	0.048201
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	4/75	272/26032	0.048201

Table S19. Significantly enriched KEGG pathways of genes undergoing convergent positive selection in alpine plant genomes

ID	Description	Gene Ratio	Backgroun d Ratio	p-adjust value
ath00630	Glyoxylate and dicarboxylate metabolism	6/21	78/5105	7.58E-06
ath01200	Carbon metabolism	6/21	272/5105	0.004073
ath00040	Pentose and glucuronate interconversions	4/21	108/5105	0.004073
ath03018	RNA degradation	4/21	113/5105	0.004073
ath00380	Tryptophan metabolism	3/21	64/5105	0.006808
ath00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	2/21	26/5105	0.011642
ath04146	Peroxisome	3/21	87/5105	0.011642
ath03013	Nucleocytoplasmic transport	3/21	103/5105	0.016293
ath04016	MAPK signaling pathway - plant	3/21	139/5105	0.032616
ath00020	Citrate cycle (TCA cycle)	2/21	64/5105	0.044605
ath00710	Carbon fixation in photosynthetic organisms	2/21	69/5105	0.046611

Table S20. Significantly enriched GO terms of gene families undergoing convergently accelerated evolutionary rate in alpine plant genomes

ID	Description	Gene Ratio	Background Ratio	p-adjust value
GO:0048544	recognition of pollen	27/255	50/26032	6.72E-39
GO:0008037	cell recognition	27/255	52/26032	1.46E-38
GO:0009875	pollen-pistil interaction	27/255	72/26032	8.09E-34
GO:0009856	pollination	35/255	374/26032	5.89E-22
GO:0044706	multi-multicellular organism process	35/255	374/26032	5.89E-22
GO:0009696	salicylic acid metabolic process	11/255	52/26032	2.46E-10
GO:0006955	immune response	20/255	283/26032	5.40E-10
GO:0009694	jasmonic acid metabolic process	11/255	57/26032	5.40E-10
GO:0045087	innate immune response	18/255	237/26032	1.52E-09
GO:0018958	phenol-containing compound metabolic process	11/255	69/26032	3.85E-09
GO:0042537	benzene-containing compound metabolic process	11/255	76/26032	1.04E-08
GO:0009736	cytokinin-activated signaling pathway	10/255	80/26032	2.78E-07
GO:0071368	cellular response to cytokinin stimulus	10/255	86/26032	5.25E-07
GO:0009735	response to cytokinin	10/255	133/26032	3.11E-05
GO:0032270	positive regulation of cellular protein metabolic process	10/255	138/26032	4.07E-05
GO:0051247	positive regulation of protein metabolic process	10/255	149/26032	7.67E-05
GO:0031408	oxylipin biosynthetic process	5/255	23/26032	8.07E-05
GO:0031407	oxylipin metabolic process	5/255	25/26032	0.000118
GO:0032268	regulation of cellular protein metabolic process	15/255	393/26032	0.00025
GO:0070534	protein K63-linked ubiquitination	4/255	15/26032	0.000306
GO:0051246	regulation of protein metabolic process	15/255	419/26032	0.000457
GO:0031398	positive regulation of protein ubiquitination	4/255	17/26032	0.000457
GO:1903322	positive regulation of protein modification by small protein conjugation or removal	4/255	17/26032	0.000457
GO:0006301	postreplication repair	4/255	18/26032	0.000559
GO:0044772	mitotic cell cycle phase transition	7/255	89/26032	0.000602
GO:1901615	organic hydroxy compound metabolic process	15/255	440/26032	0.000681
GO:0072350	tricarboxylic acid metabolic process	4/255	21/26032	0.000949
GO:0003008	system process	4/255	22/26032	0.000971
GO:0003013	circulatory system process	4/255	22/26032	0.000971
GO:0003018	vascular process in circulatory system	4/255	22/26032	0.000971
GO:0010232	vascular transport	4/255	22/26032	0.000971
GO:0010233	phloem transport	4/255	22/26032	0.000971
GO:0031396	regulation of protein ubiquitination	4/255	23/26032	0.001132
GO:1903320	regulation of protein modification by small protein conjugation or removal	4/255	24/26032	0.001308
GO:0035556	intracellular signal transduction	15/255	484/26032	0.001459
GO:0090630	activation of GTPase activity	4/255	25/26032	0.001459
GO:0000209	protein polyubiquitination	7/255	111/26032	0.001671

GO:0044770	cell cycle phase transition	7/255	112/26032	0.001721
GO:0031399	regulation of protein modification process	9/255	197/26032	0.002006
GO:0007623	circadian rhythm	8/255	155/26032	0.002006
GO:0048511	rhythmic process	8/255	155/26032	0.002006
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	5/255	54/26032	0.002341
GO:1904029	regulation of cyclin-dependent protein kinase activity	5/255	54/26032	0.002341
GO:0071900	regulation of protein serine/threonine kinase activity	5/255	59/26032	0.00348
GO:0000160	phosphorelay signal transduction system	7/255	130/26032	0.003653
GO:0006448	regulation of translational elongation	3/255	14/26032	0.003685
GO:0010114	response to red light	6/255	101/26032	0.00561
GO:0043547	positive regulation of GTPase activity	4/255	40/26032	0.007046
GO:0009309	amine biosynthetic process	4/255	42/26032	0.008159
GO:0042401	cellular biogenic amine biosynthetic process	4/255	42/26032	0.008159
GO:0045859	regulation of protein kinase activity	5/255	74/26032	0.008578
GO:0043087	regulation of GTPase activity	4/255	43/26032	0.008584
GO:0043549	regulation of kinase activity	5/255	76/26032	0.009317
GO:0051345	positive regulation of hydrolase activity	4/255	46/26032	0.010682
GO:0006415	translational termination	3/255	21/26032	0.010704
GO:0043244	regulation of protein-containing complex disassembly	3/255	24/26032	0.015656
GO:0045727	positive regulation of translation	3/255	25/26032	0.017353
GO:0001932	regulation of protein phosphorylation	5/255	90/26032	0.018133
GO:0034250	positive regulation of cellular amide metabolic process	3/255	27/26032	0.021016
GO:0042325	regulation of phosphorylation	5/255	97/26032	0.024323
GO:0042752	regulation of circadian rhythm	4/255	61/26032	0.026852
GO:0050790	regulation of catalytic activity	9/255	302/26032	0.026852
GO:0051726	regulation of cell cycle	8/255	247/26032	0.026852
GO:0051338	regulation of transferase activity	5/255	101/26032	0.026852
GO:0031401	positive regulation of protein modification process	4/255	62/26032	0.026852
GO:0016126	sterol biosynthetic process	3/255	33/26032	0.033097
GO:1990573	potassium ion import across plasma membrane	2/255	10/26032	0.033097
GO:0006545	glycine biosynthetic process	2/255	11/26032	0.03366
GO:0007094	mitotic spindle assembly checkpoint signaling	2/255	11/26032	0.03366
GO:0031577	spindle checkpoint signaling	2/255	11/26032	0.03366
GO:0033046	negative regulation of sister chromatid segregation	2/255	11/26032	0.03366
GO:0033047	regulation of mitotic sister chromatid segregation	2/255	11/26032	0.03366
GO:0033048	negative regulation of mitotic sister chromatid segregation	2/255	11/26032	0.03366
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	2/255	11/26032	0.03366
GO:0051985	negative regulation of chromosome segregation	2/255	11/26032	0.03366
GO:0071173	spindle assembly checkpoint signaling	2/255	11/26032	0.03366
GO:0071174	mitotic spindle checkpoint signaling	2/255	11/26032	0.03366
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	2/255	11/26032	0.03366

GO:1905819	negative regulation of chromosome separation	2/255	11/26032	0.03366
GO:2000816	negative regulation of mitotic sister chromatid separation	2/255	11/26032	0.03366
GO:0012501	programmed cell death	6/255	161/26032	0.034837
GO:0019430	removal of superoxide radicals	2/255	12/26032	0.037772
GO:0071450	cellular response to oxygen radical	2/255	12/26032	0.037772
GO:0071451	cellular response to superoxide	2/255	12/26032	0.037772
GO:0071484	cellular response to light intensity	2/255	12/26032	0.037772
GO:0048278	vesicle docking	3/255	38/26032	0.038421
GO:0065009	regulation of molecular function	9/255	338/26032	0.039785
GO:0008219	cell death	7/255	231/26032	0.048022
GO:0000303	response to superoxide	2/255	14/26032	0.048022
GO:0000305	response to oxygen radical	2/255	14/26032	0.048022
GO:2001251	negative regulation of chromosome organization	2/255	14/26032	0.048022
GO:0046777	protein autophosphorylation	6/255	177/26032	0.048048
GO:0071478	cellular response to radiation	6/255	178/26032	0.048798

Table S21. Significantly enriched KEGG pathways of gene families undergoing convergently accelerated evolutionary rate in alpine plant genomes

ID	Description	Gene Ratio	Background Ratio	p-adjust value
ath00040	Pentose and glucuronate interconversions	12/57	107/5095	3.05E-08
ath03430	Mismatch repair	5/57	37/5095	0.000584
ath03030	DNA replication	5/57	48/5095	0.001392
ath04075	Plant hormone signal transduction	11/57	289/5095	0.001717
ath03440	Homologous recombination	5/57	64/5095	0.003245
ath03420	Nucleotide excision repair	5/57	67/5095	0.003339
ath04144	Endocytosis	7/57	158/5095	0.005942
ath00999	Biosynthesis of various plant secondary metabolites	4/57	64/5095	0.016304
ath00073	Cutin, suberine and wax biosynthesis	3/57	37/5095	0.021013
ath00940	Phenylpropanoid biosynthesis	5/57	128/5095	0.032743
ath04130	SNARE interactions in vesicular transport	3/57	47/5095	0.033166
ath00670	One carbon pool by folate	2/57	21/5095	0.045072

Table S22. Tests for relaxed selection on S-locus genes of alpine plants using RELAX model

Species	<i>k</i>	<i>p</i> -value
<i>C. himalaica</i>	0.78	0.025
<i>E. heterophyllum</i>	0.43	0.042
<i>H. vulgare</i> var. <i>nudum</i>	0.15	0.002
<i>P. mira</i>	1.54	0.078
<i>R. alexandrae</i>	0.80	0.201
<i>S. brachista</i>	0.60	0.001
<i>S. obvallata</i>	0.72	0.007

k: estimated selection intensity. *p*-values are calculated by likelihood ratio test and significant results ($p < 0.05$) are in bold.

Table S23. Functional annotation of genes predicted to interact with *MYB48*

Gene	Identifier	Annotations
<i>DFR</i>	AT5G42800.1	Bifunctional dihydroflavonol 4-reductase/flavanone 4-reductase; Dihydroflavonol reductase. Catalyzes the conversion of dihydroquercetin to leucocyanidin in the biosynthesis of anthocyanins
<i>F3H</i>	AT3G51240.1	Naringenin,2-oxoglutarate 3-dioxygenase; Catalyzes the 3-beta-hydroxylation of 2S-flavanones to 2R,3R-dihydroflavonols which are intermediates in the biosynthesis of flavonols, anthocyanidins, catechins and proanthocyanidins in plants
<i>FLS1</i>	AT5G08640.1	Flavonol synthase/flavanone 3-hydroxylase; Catalyzes the formation of flavonols from dihydroflavonols. It can act on dihydrokaempferol to produce kaempferol, on dihydroquercetin to produce quercetin and on dihydromyricetin to produce myricetin.
<i>PEI1</i>	AT5G07500.1	Zinc finger C-x8-C-x5-C-x3-H type family protein; Embryo-specific transcription factor required at the globular to heart stage transition in embryo development
<i>TT5</i>	AT3G55120.1	Chalcone-flavanone isomerase family protein; Catalyzes the intramolecular cyclization of bicyclic chalcones into tricyclic (S)-flavanones. Responsible for the isomerization of 4,2',4',6'-tetrahydrochalcone (also termed chalcone) into naringenin
<i>TTG1</i>	AT5G24520.1	Transducin/WD40 repeat-like superfamily protein; Required for the accumulation of purple anthocyanins in leaves and stems. Involved in trichome and root hair development. Controls epidermal cell fate specification. Affects dihydroflavonol 4-reductase gene expression.
<i>TTG2</i>	AT2G37260.1	Wrky family transcription factor family protein; Encodes a protein similar to WRKY transcription factors that is expressed in the seed integument and endosperm. Mutants are defective in proanthocyanidin synthesis and seed mucilate deposition. Seeds are yellow colored
<i>AT1G15810</i>	AT1G15810.1	S15/NS1, RNA-binding protein; Its function is described as structural constituent of ribosome; Involved in translation
<i>AT1G80620</i>	AT1G80620.1	Uncharacterized protein T21F11.5; S15/NS1, RNA-binding protein; Its function is described as structural constituent of ribosome; Involved in translation
<i>AT3G06880</i>	AT3G06880.2	Transducin/WD40 repeat-like superfamily protein; Its function is described as binding, nucleotide binding; Located in cellular

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