

## Supplementary Tables

**Table S1. Summary statistics of Illumina re-sequencing data per sample**

<b>SampleID</b>	<b>Location</b>	<b>Latitude</b>	<b>Longitude</b>	<b>Mapping rate (%)</b>	<b>Mean Coverage</b>
<i>P. tremula</i>					
SwAsp001	Simlang	56.6925	13.2147	91.34%	20.50
SwAsp009	Simlang	56.7336	13.2517	90.52%	23.70
SwAsp011	Ronneby	56.3478	15.025	90.06%	48.58
SwAsp014	Ronneby	56.3081	15.1269	88.78%	24.53
SwAsp021	Vargarda	57.9917	12.9119	89.54%	18.50
SwAsp025	Vargarda	57.9869	12.9358	88.62%	17.25
SwAsp032	Ydre	57.8492	15.3217	88.56%	20.32
SwAsp033	Ydre	57.8281	15.3103	90.27%	20.11
SwAsp045	Brunsborg	59.6425	12.9408	88.90%	20.25
SwAsp047	Brunsborg	59.6308	12.9608	89.72%	19.46
SwAsp055	Uppsala	59.8131	17.9817	88.66%	22.25
SwAsp057	Uppsala	59.7761	17.9889	88.43%	23.88
SwAsp067	Alvdalen	61.1978	13.8092	88.56%	22.25
SwAsp068	Alvdalen	61.3017	13.7222	88.78%	22.27
SwAsp076	Delsbo	61.7106	16.7311	90.34%	36.74
SwAsp078	Delsbo	61.6925	16.67	88.88%	21.01
SwAsp087	Dorotea	64.3406	16.3992	90.00%	24.44
SwAsp088	Dorotea	64.3358	16.3736	89.94%	23.22
SwAsp096	Umea	63.9781	20.7056	90.48%	23.43
SwAsp098	Umea	63.8656	20.4986	90.27%	24.60
SwAsp103	Arjeplog	66.0247	18.5742	91.27%	22.23
SwAsp110	Arjeplog	66.2592	18	90.62%	36.83
SwAsp111	Lulea	65.6703	21.8986	90.68%	31.39
SwAsp114	Lulea	65.5544	22.3939	91.25%	34.62
Mean				89.77%	25.10
<i>P. tremuloides</i>					
Alb10-3	Alberta	51.0718	-115.0044	90.47%	21.08
Alb13-1	Alberta	51.0479	-115.0232	91.66%	23.22
Alb16-1	Alberta	51.0838	-115.3892	90.75%	19.63
Alb17-4	Alberta	51.0809	-115.3946	90.82%	18.13
Alb18-3	Alberta	51.0686	-115.3516	91.20%	21.49
Alb25-4	Alberta	51.0524	-114.9131	90.32%	18.29
Alb27-1	Alberta	51.0405	-114.8939	91.50%	29.02
Alb31-1	Alberta	51.0435	-114.8352	91.09%	23.06
Alb33-2	Alberta	51.0431	-114.7568	90.91%	27.76
Alb35-2	Alberta	51.0234	-115.0640	90.58%	17.87
Alb6-3	Alberta	51.1324	-115.0664	91.92%	28.77

Albb15-3	Alberta	51.0811	-115.3767	91.79%	22.14
Dan1-1C13	UW Arboreturn	43.0520	-89.4242	91.08%	24.12
Dan2-1B7	UW Arboreturn	43.0526	-89.4253	90.95%	30.61
PG1-1B4	Parfrey's Glenn	43.4249	-89.6445	91.59%	18.66
PG2-1B9	Parfrey's Glenn	43.4184	-89.6417	91.65%	24.14
PG3-1B6	Parfrey's Glenn	43.4198	-89.6532	91.27%	21.74
PI3-1B3	Pine Island area	43.5402	-89.5666	90.99%	23.13
Sau1-1B10	Boxter's Hollow	43.4036	-89.8176	90.05%	17.99
Sau2-1B2	Boxter's Hollow	43.4048	-89.8243	90.79%	11.79
Sau3-1B13	Boxter's Hollow	43.4053	-89.8141	91.25%	16.49
Wau1-1B5	Waushara country	44.1314	-89.2082	91.01%	36.65
Mean				91.07%	22.53

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**Table S2.** Tracy-Widom statistics for the first three eigenvalues in PCA analysis

<b>Eigenvalues</b>	<b>Eigenvalues</b>	<b>Twstat</b>	<b>P-value</b>
1	21.40	15.374	2.506e-19
2	2.09	3.290	9.651e-4
3	1.98	-3.62	0.980302

**Table S3.** Mean ( $\pm$ standard deviation) values of population genomic statistics ( $\Theta_\pi$ , Tajima's D, Fay&Wu's H,  $F_{ST}$  and  $d_{xy}$ ) comparisons between Alberta and Wisconsin population of *P. tremuloides* per chromosome.

	$\Theta_\pi$		Tajima's D		Fay & Wu's H		$F_{ST}$	$d_{xy}$
	Alberta	Wisconsin	Alberta	Wisconsin	Alberta	Wisconsin		
<b>Chr01</b>	0.0168 ( $\pm 0.0080$ )	0.0165 ( $\pm 0.0080$ )	-0.9086 ( $\pm 0.4671$ )	-0.7125 ( $\pm 0.4732$ )	-0.3064 ( $\pm 0.2545$ )	-0.3003 ( $\pm 0.2752$ )	0.0425 ( $\pm 0.0236$ )	0.0172 ( $\pm 0.0082$ )
<b>Chr02</b>	0.0149 ( $\pm 0.0068$ )	0.0143 ( $\pm 0.0068$ )	-1.0459 ( $\pm 0.4326$ )	-0.8487 ( $\pm 0.4353$ )	-0.2822 ( $\pm 0.2282$ )	-0.2898 ( $\pm 0.2649$ )	0.0643 ( $\pm 0.0767$ )	0.0155 ( $\pm 0.0074$ )
<b>Chr03</b>	0.0163 ( $\pm 0.0084$ )	0.0158 ( $\pm 0.0083$ )	-0.9533 ( $\pm 0.4599$ )	-0.7716 ( $\pm 0.4457$ )	-0.2575 ( $\pm 0.2463$ )	-0.2539 ( $\pm 0.2696$ )	0.0403 ( $\pm 0.0216$ )	0.0165 ( $\pm 0.0085$ )
<b>Chr04</b>	0.0166 ( $\pm 0.0083$ )	0.0161 ( $\pm 0.0083$ )	-0.9466 ( $\pm 0.4725$ )	-0.7604 ( $\pm 0.4599$ )	-0.2817 ( $\pm 0.2458$ )	-0.2703 ( $\pm 0.2495$ )	0.0416 ( $\pm 0.0268$ )	0.0169 ( $\pm 0.0084$ )
<b>Chr05</b>	0.0152 ( $\pm 0.0072$ )	0.0148 ( $\pm 0.0072$ )	-0.9376 ( $\pm 0.4464$ )	-0.7292 ( $\pm 0.4617$ )	-0.2880 ( $\pm 0.2405$ )	-0.2831 ( $\pm 0.2607$ )	0.0442 ( $\pm 0.0268$ )	0.0155 ( $\pm 0.0074$ )
<b>Chr06</b>	0.0155 ( $\pm 0.0075$ )	0.0150 ( $\pm 0.0074$ )	-0.9574 ( $\pm 0.4387$ )	-0.7354 ( $\pm 0.4552$ )	-0.2948 ( $\pm 0.2460$ )	-0.2913 ( $\pm 0.2574$ )	0.0453 ( $\pm 0.0286$ )	0.0158 ( $\pm 0.0077$ )
<b>Chr07</b>	0.0153 ( $\pm 0.0076$ )	0.0150 ( $\pm 0.0077$ )	-0.9841 ( $\pm 0.4379$ )	-0.7912 ( $\pm 0.4535$ )	-0.3132 ( $\pm 0.2700$ )	-0.3042 ( $\pm 0.2686$ )	0.0425 ( $\pm 0.0225$ )	0.0156 ( $\pm 0.0078$ )
<b>Chr08</b>	0.0141 ( $\pm 0.0066$ )	0.0136 ( $\pm 0.0066$ )	-1.0507 ( $\pm 0.4213$ )	-0.8231 ( $\pm 0.4283$ )	-0.2421 ( $\pm 0.2127$ )	-0.2099 ( $\pm 0.2241$ )	0.0496 ( $\pm 0.0321$ )	0.0144 ( $\pm 0.0068$ )
<b>Chr09</b>	0.0142 ( $\pm 0.0059$ )	0.0138 ( $\pm 0.0057$ )	-1.0441 ( $\pm 0.3974$ )	-0.8018 ( $\pm 0.4133$ )	-0.2202 ( $\pm 0.1959$ )	-0.2144 ( $\pm 0.2224$ )	0.0419 ( $\pm 0.0221$ )	0.0144 ( $\pm 0.0060$ )
<b>Chr10</b>	0.0141 ( $\pm 0.0069$ )	0.0136 ( $\pm 0.0069$ )	-1.0274 ( $\pm 0.4114$ )	-0.8046 ( $\pm 0.4256$ )	-0.2473 ( $\pm 0.2174$ )	-0.2411 ( $\pm 0.2419$ )	0.0415 ( $\pm 0.0230$ )	0.0143 ( $\pm 0.0070$ )
<b>Chr11</b>	0.0179 ( $\pm 0.0081$ )	0.0175 ( $\pm 0.0081$ )	-0.9106 ( $\pm 0.4568$ )	-0.7215 ( $\pm 0.4747$ )	-0.2784 ( $\pm 0.2335$ )	-0.2732 ( $\pm 0.2496$ )	0.0400 ( $\pm 0.0207$ )	0.0182 ( $\pm 0.0083$ )
<b>Chr12</b>	0.0173 ( $\pm 0.0085$ )	0.0170 ( $\pm 0.0085$ )	-0.9653 ( $\pm 0.4471$ )	-0.7729 ( $\pm 0.4571$ )	-0.2653 ( $\pm 0.2351$ )	-0.2463 ( $\pm 0.2462$ )	0.0396 ( $\pm 0.0205$ )	0.0177 ( $\pm 0.0088$ )
<b>Chr13</b>	0.0157 ( $\pm 0.0082$ )	0.0153 ( $\pm 0.0082$ )	-0.9588 ( $\pm 0.4870$ )	-0.7818 ( $\pm 0.4885$ )	-0.2729 ( $\pm 0.2554$ )	-0.2646 ( $\pm 0.2665$ )	0.0410 ( $\pm 0.0231$ )	0.0160 ( $\pm 0.0084$ )
<b>Chr14</b>	0.0161 ( $\pm 0.0096$ )	0.0158 ( $\pm 0.0095$ )	-0.9975 ( $\pm 0.4573$ )	-0.8029 ( $\pm 0.4545$ )	-0.2678 ( $\pm 0.2527$ )	-0.2534 ( $\pm 0.2648$ )	0.0402 ( $\pm 0.0236$ )	0.0164 ( $\pm 0.0097$ )
<b>Chr15</b>	0.0169 ( $\pm 0.0083$ )	0.0165 ( $\pm 0.0083$ )	-0.9280 ( $\pm 0.4514$ )	-0.7261 ( $\pm 0.4385$ )	-0.2580 ( $\pm 0.2459$ )	-0.2523 ( $\pm 0.2525$ )	0.0440 ( $\pm 0.0274$ )	0.0173 ( $\pm 0.0086$ )
<b>Chr16</b>	0.0176 ( $\pm 0.0086$ )	0.0169 ( $\pm 0.0083$ )	-0.8526 ( $\pm 0.4589$ )	-0.6576 ( $\pm 0.4619$ )	-0.2846 ( $\pm 0.2403$ )	-0.2826 ( $\pm 0.2719$ )	0.0444 ( $\pm 0.0314$ )	0.0179 ( $\pm 0.0088$ )
<b>Chr17</b>	0.0181 ( $\pm 0.0094$ )	0.0181 ( $\pm 0.0095$ )	-0.7841 ( $\pm 0.5009$ )	-0.6659 ( $\pm 0.5073$ )	-0.2760 ( $\pm 0.2742$ )	-0.2673 ( $\pm 0.2921$ )	0.0398 ( $\pm 0.0226$ )	0.0186 ( $\pm 0.0097$ )
<b>Chr18</b>	0.0167 ( $\pm 0.0081$ )	0.0162 ( $\pm 0.0079$ )	-0.9224 ( $\pm 0.4688$ )	-0.6992 ( $\pm 0.4718$ )	-0.2829 ( $\pm 0.2499$ )	-0.2809 ( $\pm 0.2669$ )	0.0427 ( $\pm 0.0230$ )	0.0170 ( $\pm 0.0083$ )
<b>Chr19</b>	0.0207 ( $\pm 0.0104$ )	0.0202 ( $\pm 0.0107$ )	-0.6935 ( $\pm 0.5026$ )	-0.5612 ( $\pm 0.4814$ )	-0.2739 ( $\pm 0.2598$ )	-0.2813 ( $\pm 0.2695$ )	0.0451 ( $\pm 0.0356$ )	0.0212 ( $\pm 0.0111$ )
<b>Total</b>	0.0161 ( $\pm 0.0081$ )	0.0157 ( $\pm 0.0080$ )	-0.9494 ( $\pm 0.4584$ )	-0.7512 ( $\pm 0.4604$ )	-0.2768 ( $\pm 0.2436$ )	-0.2699 ( $\pm 0.2610$ )	0.0443 ( $\pm 0.0325$ )	0.0165 ( $\pm 0.0083$ )

**Table S4.** Relative likelihood of the different models shown in Figure S2.

<b>Model</b>	<b>Max(log<sub>10</sub>(Lhood<sub>i</sub>)<sup>a</sup></b>	<b>No. Of parameters(d)</b>	<b>AIC<sub>i</sub><sup>b</sup></b>	<b>Δ<sub>i</sub><sup>b</sup></b>	<b>Model normalized relative likelihood (w<sub>i</sub>)<sup>b</sup></b>
model1	-101984901	4	469657833.5	4348409.527	~0
model2	-101543009	6	467622849.6	2313425.664	~0
model3	-101904750	4	469288724.5	3979300.532	~0
model4	-101040655	6	465309424.0	0	1
model5	-101921512	4	469365916.4	4056492.395	~0
model6	-101088118	6	465527999.2	218575.193	~0
model7	-101579670	9	467791685.8	2482261.808	~0
model8	-101522598	9	467528859.5	2219435.535	~0
model9	-101984994	7	469658267.8	4348843.808	~0
model10	-101601501	9	467892221.3	2582797.278	~0
model11	-101523956	9	467535113.3	2225689.356	~0
model12	-101990034	7	469681477.8	4372053.866	~0
model13	-101606614	9	467915767.5	2606343.513	~0
model14	-101607050	9	467917775.3	2608351.367	~0
model15	-101982056	11	469644745.8	4335321.818	~0
model16	-101685141	13	468277405.7	2967981.712	~0
model17	-101617365	13	467965285.7	2655861.698	~0
model18	-101686006	13	468281389.2	2971965.185	~0

<sup>a</sup>Based on the best likelihood among the 50 independent runs for each model (Figure S2).

<sup>b</sup>The calculation of AIC<sub>i</sub>, Δ<sub>i</sub> and w<sub>i</sub> are according to the methods shown in Excoffier *et al.* (2013).

**Table S5.** Demographic parameters used in *msms* simulations, with parameters corresponding to the models shown in Figure S5.

Model	N0	N1	N2	N3	T1	T2	m12	m21	m23	m32
Model1 <sup>a</sup>	56235	102814	309500	-	0.51	-	0.1	0.4	-	-
Model2 <sup>b</sup>	56235	102814	309500	309500	0.51	0.03	0.1	0.4	0	0
Model3 <sup>b</sup>	56235	102814	309500	309500	0.51	0.11	0.1	0.4	10	10

<sup>a</sup> All values in model 1 are based on the best-fitting model predicted by *fastsimcoal2*. Divergence times (T) are represented in units of 4N1 generations and gene flow are represented as 4Nm where N is the effective population size of the source (donor) species/populations and m is the per generation migration rate.

<sup>b</sup> N2, N3, T2, m23, m32 in model 2 and 3 correspond to the effective population sizes, divergence time and gene flow between subpopulation of Alberta and Wisconsin in *P. tremuloides*, respectively. All other parameters are the same as in model 1.

**Table S6.** Summary statistics comparing regions displaying extreme genetic differentiation with the rest of the genomic regions in both *P. tremula* and *P. tremuloides* (the mean±standard deviation values are shown).

Parameters	Species	Regions displaying high differentiation	Regions displaying low differentiation	Background
$\theta_s$	<i>P. tremula</i>	0.0076(±0.0048) <sup>***</sup>	0.0356(±0.0166) <sup>***</sup>	0.0147(±0.0077)
	<i>P. tremuloides</i>	0.0094(±0.0054) <sup>***</sup>	0.0358(±0.0161) <sup>***</sup>	0.0160(±0.0078)
Tajima's D	<i>P. tremula</i>	-0.9285(±0.5202) <sup>***</sup>	-0.0660(±0.5327) <sup>***</sup>	-0.2994(±0.5083)
	<i>P. tremuloides</i>	-1.6589(±0.4177) <sup>***</sup>	-0.6047(±0.5534) <sup>***</sup>	-1.1554(±0.4561)
Fay&Wu's H	<i>P. tremula</i>	-0.6800(±0.3886) <sup>***</sup>	-0.1171(±0.2598) <sup>***</sup>	-0.3984(±0.2793)
	<i>P. tremuloides</i>	-0.5154(±0.3024) <sup>***</sup>	-0.1144(±0.2451) <sup>***</sup>	-0.3222(±0.2196)
$r^2$	<i>P. tremula</i>	0.2886(±0.1406) <sup>***</sup>	0.1985(±0.0964)	0.2114(±0.1206)
	<i>P. tremuloides</i>	0.2481(±0.1372) <sup>***</sup>	0.1662(±0.0957) <sup>*</sup>	0.1577(±0.1110)
$\rho/\theta_s$	<i>P. tremula</i>	0.1627(±0.2634) <sup>***</sup>	0.1139(±0.1291) <sup>**</sup>	0.2395(±0.3533)
	<i>P. tremuloides</i>	0.2595(±0.3535) <sup>***</sup>	0.2087(±0.2388) <sup>**</sup>	0.5384(±0.5222)
Fixed (%)	<i>P. tremula</i>	0.0568(±0.0327) <sup>***</sup>	~0(±0.0000) <sup>***</sup>	0.0055(±0.0098)
	<i>P. tremuloides</i>	0.0431(±0.0290) <sup>***</sup>	~0(±0.0000) <sup>***</sup>	0.0035(±0.0073)
Shared (%)		0.0788(±0.0338) <sup>***</sup>	0.3468(±0.0937) <sup>***</sup>	0.1678(±0.0629)
$F_{ST}$		0.7402(±0.0438) <sup>***</sup>	0.1121(±0.0180) <sup>***</sup>	0.3804(±0.1216)
$d_{xy}$		0.0323(±0.0181) <sup>***</sup>	0.0401(±0.0180) <sup>***</sup>	0.0249(±0.0110)
RND		0.7313(±0.2013) <sup>***</sup>	0.6887(±0.1970) <sup>***</sup>	0.5516(±0.1431)

Asterisks designate significant differences between the regions displaying exceptionally genetic differentiation and the rest of genomic regions by Mann-Whitney U test (\*  $P$ -value < 0.05; \*\*  $P$ -value < 1e-4; \*\*\* $P$ -value <2.2e-16).

**Table S7.** List of the genes located in regions displaying significantly high genetic differentiation between *P. tremula* and *P. tremuloides*.

<b>Poplar gene</b>	<b>Best Arabidopsis hit</b>	<b>Synonyms</b>	<b>Annotated description</b>
Potri.001G003900 Potri.001G004000	AT1G55350	ATDEK1,DEK1,EMB1275,EMB80	calpain-type cysteine protease family
Potri.001G015400 Potri.001G025100	AT3G45140	ATLOX2,LOX2	lipoxygenase 2
Potri.001G030700 Potri.001G030800	AT1G29940	NRPA2	nuclear RNA polymerase A2
Potri.001G030900 Potri.001G031000	AT1G29940	NRPA2	nuclear RNA polymerase A2
Potri.001G046500 Potri.001G049400	AT2G32700	LUH	LEUNIG_homolog
Potri.001G050100 Potri.001G062900	AT2G02230	AtPP2-B1,PP2-B1	phloem protein 2-B1
Potri.001G078500  Potri.001G078600	AT1G33410	ATNUP160,NUP160,SAR1	SUPPRESSOR OF AUXIN RESISTANCE1
Potri.001G080900 Potri.001G083700	AT2G43000	anac042,NAC042	NAC domain containing protein 42
Potri.001G083800  Potri.001G083900	AT2G46680	ATHB-7,ATHB7,HB-7	homeobox 7
Potri.001G083900 Potri.001G098600	AT2G46660	CYP78A6	cytochrome P450, family 78, subfamily A, polypeptide 6
Potri.001G098700  Potri.001G102700	AT4G11240	TOPP7	Calcineurin-like metallo-phosphoesterase superfamily protein
Potri.001G102800 Potri.001G102900	AT1G12780	ATUGE1,UGE1	UDP-D-glucose/UDP-D-galactose 4-epimerase 1
Potri.001G108200 Potri.001G108300	AT1G63700	EMB71,MAPKKK4,YDA	Protein kinase superfamily protein
Potri.001G124000 Potri.001G128200	AT2G45760	BAL,BAP2	BON association protein 2
Potri.001G155900 Potri.001G156000	AT4G25230	RIN2	RPM1 interacting protein 2
Potri.001G156100 Potri.001G161600	AT1G53730	SRF6	STRUBBELIG-receptor family 6
Potri.001G161700 Potri.001G165800	AT1G53750	RPT1A	regulatory particle triple-A 1A
Potri.001G171000	AT5G13640	ATPDAT,PDAT,PDAT1	phospholipid:diacylglycerol



Potri.001G171100	AT1G54170	CID3	acyltransferase
Potri.001G171200			CTC-interacting domain 3
Potri.001G181100			
Potri.001G181600	AT4G12560	CPR30	F-box and associated interaction domains-containing protein
Potri.001G182200			
Potri.001G186000	AT1G79810	ATPEX2,PEX2,TED3	Pex2/Pex12 N-terminal domain-containing protein / zinc finger (C3HC4-type RING finger) family protein
Potri.001G189700	AT1G79750	ATNADP-ME4,NADP-ME4	NADP-malic enzyme 4
Potri.001G189800			
Potri.001G191000			
Potri.001G191100			
Potri.001G191400			
Potri.001G191500	AT3G16380	PAB6	poly(A) binding protein 6
Potri.001G191600			
Potri.001G194000			
Potri.001G194100			
Potri.001G194400	AT1G17730	CHMP1B,VPS46.1	vacuolar protein sorting 46.1
Potri.001G195300			
Potri.001G195900			
Potri.001G196000	AT1G51760	IAR3,JR3	peptidase M20/M25/M40 family protein
Potri.001G196100			
Potri.001G196500			
Potri.001G196600			
Potri.001G196700			
Potri.001G197000	AT3G13890	ATMYB26,MS35,MYB26	myb domain protein 26
Potri.001G205700			
Potri.001G205800			
Potri.001G206600			
Potri.001G206700	AT4G33430	ATBAK1,ATSERK3,BAK1,ELG,RKS10,SERK3	BRI1-associated receptor kinase
Potri.001G206800	AT5G64570	ATBXL4,XYL4	beta-D-xylosidase 4
Potri.001G229900			
Potri.001G230000	AT2G31960	ATGSL03,ATGSL3,GSL03	glucan synthase-like 3
Potri.001G239600			
Potri.001G244300			
Potri.001G244400			
Potri.001G260500	AT5G13800	CRN1,PPH	pheophytinase
Potri.001G260600			
Potri.001G260700	AT3G51970	ASAT1,ATASAT1,ATSAT1	acyl-CoA sterol acyl transferase 1
Potri.001G276900			
Potri.001G285800			
Potri.001G290500			
Potri.001G290600	AT5G14930	SAG101	senescence-associated gene 101

Potri.001G307700			
Potri.001G318800			
Potri.001G318900			
Potri.001G319000			
Potri.001G328400	AT2G22540	AGL22,SVP	K-box region and MADS-box transcription factor family protein
Potri.001G331900			
Potri.001G332000			
Potri.001G332100	AT5G40870	ATUK/UPRT1,UK/UPRT1,UKL1	uridine kinase/uracil phosphoribosyltransferase 1
Potri.001G347000	AT5G15380	DRM1	domains rearranged methylase 1
Potri.001G347100			
Potri.001G347200	AT3G27785	ATMYB118,MYB118,PGA37	myb domain protein 118
Potri.001G351400	AT3G01480	ATCYP38,CYP38	cyclophilin 38
Potri.001G351700			
Potri.001G351800	AT4G18240	ATSS4,SS4,SSIV	starch synthase 4
Potri.001G358400	AT2G34640	HMR,PTAC12	plastid transcriptionally active 12
Potri.001G359100	AT3G20440	BE1,EMB2729	Alpha amylase family protein
Potri.001G359300			
Potri.001G359700	AT5G55310	TOP1,TOP1BETA	DNA topoisomerase 1 beta
Potri.001G359800			
Potri.001G359900	AT5G55390	EDM2	ENHANCED DOWNY MILDEW 2
Potri.001G360100	AT4G26700	ATFIM1,FIM1	fimbrin 1
Potri.001G368000	AT4G25434	ATNUDT10,NUDT10	nudix hydrolase homolog 10
Potri.001G368100	AT5G55760	SRT1	sirtuin 1
Potri.001G378400	AT1G78440	ATGA2OX1,GA2OX1	Arabidopsis thaliana gibberellin 2-oxidase 1
Potri.001G379800	AT1G53590	NTMC2T6.1,NTMC2TYPE6.1	Calcium-dependent lipid-binding (CaLB domain) family protein
Potri.001G396000			
Potri.001G402500			
Potri.001G402600			
Potri.001G406200			
Potri.001G415900			
Potri.001G416000			
Potri.001G416100	AT5G54650	ATFH5,Fh5	formin homology5
Potri.001G449000	AT4G10570	UBP9	ubiquitin-specific protease 9
Potri.001G449100			
Potri.001G457800			
Potri.001G466800			
Potri.002G000200			
Potri.002G013100	AT1G62830	ATLSD1,ATSWP1,LDL1,LSD1,SWP1	LSD1-like 1
Potri.002G013200	AT1G20450	ERD10,LTI29,LTI45	Dehydrin family protein
Potri.002G024100	AT1G75660	AtXRN3,XRN3	5'-3' exoribonuclease 3
Potri.002G027200	AT1G19910	ATVHA-C2,AVA-2PE,AVA-P2	ATPase, F0/V0 complex, subunit C protein
Potri.002G027300			
Potri.002G033100			

Potri.002G035900	AT1G03950	VPS2.3	vacuolar protein sorting-associated protein 2.3
Potri.002G036000	AT4G28540	CKL6,PAPK1	casein kinase I-like 6
Potri.002G045900	AT3G54610	BGT,GCN5,HAC3,HAG01,HAG1,HAT1	histone acetyltransferase of the GNAT family 1
Potri.002G046000			
Potri.002G053900	AT2G31530	EMB2289,SCY2	SecY protein transport family protein
Potri.002G054000	AT1G03190	ATXPD,UVH6	RAD3-like DNA-binding helicase protein
Potri.002G074400	AT1G43890	ATRAB-C1,ATRAB18,ATRABC1,RAB18,RAB18-1,RABC1	RAB GTPASE HOMOLOG B18
Potri.002G074500			
Potri.002G076800	AT5G54160	ATOMT1,OMT1	O-methyltransferase 1
Potri.002G076900			
Potri.002G079100	AT1G77300	ASHH2,CCR1,EFS,SDG8	histone methyltransferases(H3-K4 specific);histone methyltransferases(H3-K36 specific)
Potri.002G088700			
Potri.002G088800			
Potri.002G088900	AT4G08500	ARAKIN,ATMEKK1,MAPKKK8,MEK K1	MAPK/ERK kinase kinase 1
Potri.002G104100			
Potri.002G105100			
Potri.002G107400			
Potri.002G110700	AT1G58250	SAB	Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain
Potri.002G111000			
Potri.002G124100	AT1G46480	WOX4	WUSCHEL related homeobox 4
Potri.002G124200	AT2G23350	PAB4,PABP4	poly(A) binding protein 4
Potri.002G124500			
Potri.002G124600			
Potri.002G124700	AT1G45976	SBP1	S-ribonuclease binding protein 1
Potri.002G126700			
Potri.002G126800			
Potri.002G126900			
Potri.002G129200	AT1G47720	OSB1	Primosome PriB/single-strand DNA-binding
Potri.002G129300	AT4G33300	ADR1-L1	ADR1-like 1
Potri.002G143000			
Potri.002G143200			
Potri.002G150000			
Potri.002G151400	AT3G61130	GAUT1,LGT1	galacturonosyltransferase 1
Potri.002G151500	AT2G45640	ATSAP18,SAP18	SIN3 associated polypeptide P18
Potri.002G151600			
Potri.002G152100	AT2G42010	PLDBETA,PLDBETA1	phospholipase D beta 1
Potri.002G160500	AT1G01650	ATSPPL4,SPPL4	SIGNAL PEPTIDE PEPTIDASE-LIKE 4
Potri.002G160600	AT3G61415	ASK21,SK21	SKP1-like 21
Potri.002G164000			

Potri.002G164100	AT5G12370	SEC10	exocyst complex component sec10
Potri.002G175600			
Potri.002G176700	AT2G46700	ATCRK3,CRK3	CDPK-related kinase 3
Potri.002G204200			
Potri.002G207200	AT2G47940	DEGP2	DEGP protease 2
Potri.002G208700			
Potri.002G217000			
Potri.002G230000	AT1G05200	ATGLR3.4,GLR3.4,GLUR3	glutamate receptor 3.4
Potri.002G230100			
Potri.002G235700			
Potri.002G237700			
Potri.002G237800			
Potri.002G245400	AT3G25070	RIN4	RPM1 interacting protein 4
Potri.002G245500			
Potri.002G246800			
Potri.002G246900			
Potri.002G257700			
Potri.002G257800	AT4G28610	AtPHR1,PHR1	phosphate starvation response 1
Potri.002G260100			
Potri.002G260200			
Potri.003G005700	AT1G33980	ATUPF3,UPF3	Smg-4/UPF3 family protein
Potri.003G005800			
Potri.003G009900	AT4G25880	APUM6,PUM6	pumilio 6
Potri.003G015400	AT1G60940	SNRK2-10,SNRK2.10,SRK2B	SNF1-related protein kinase 2.10
Potri.003G045700	AT4G19210	ATRLI2,RLI2	RNAse I inhibitor protein 2
Potri.003G046800	AT1G31770	ABCG14	ATP-binding cassette 14
Potri.003G047600			
Potri.003G047700	AT5G56600	PFN3,PRF3	profilin 3
Potri.003G077500			
Potri.003G086400	AT5G47010	ATUPF1,LBA1,UPF1	RNA helicase, putative
Potri.003G100000	AT4G19020	CMT2	chromomethylase 2
Potri.003G101000			
Potri.003G101100			
Potri.003G117500			
Potri.003G117600			
Potri.003G117700	AT1G62960	ACS10	ACC synthase 10
Potri.003G117800			
Potri.003G123300			
Potri.003G123400			
Potri.003G132900			
Potri.003G134500	AT4G24220	AWI31,VEP1	NAD(P)-binding Rossmann-fold superfamily protein
Potri.003G134600			
Potri.003G140500			
Potri.003G140600			
Potri.003G140700			
Potri.003G147700			

Potri.003G147800			
Potri.003G147900	AT1G64690	BLT	branchless trichome K-box region and MADS-box transcription factor family protein
Potri.003G169800	AT5G10140	AGL25,FLC,FLF	
Potri.003G169900	AT5G60910	AGL8,FUL	AGAMOUS-like 8
Potri.003G170200	AT5G60910	AGL8,FUL	AGAMOUS-like 8
Potri.003G189500			
Potri.003G214200	AT5G13000	ATGSL12,gs112	glucan synthase-like 12
Potri.003G215600			
Potri.004G037900	AT1G61120	GES,TPS04,TPS4	terpene synthase 04
Potri.004G040900			
Potri.004G047700	AT1G28380	NSL1	MAC/Perforin domain-containing protein
Potri.004G051600	AT2G33880	HB-3,STIP,WOX9	homeobox-3
Potri.004G085400	AT5G37600	ATGLN1;1,ATGSR1,GLN1;1,GSR 1	glutamine synthase clone R1
Potri.004G092400			
Potri.004G101200	AT1G67140	SWEETIE	HEAT repeat-containing protein
Potri.004G101300	AT1G67140	SWEETIE	HEAT repeat-containing protein
Potri.004G103900	AT3G21630	CERK1,LYSM RLK1	chitin elicitor receptor kinase 1
Potri.004G104000	AT1G26110	DCP5	decapping 5
Potri.004G104100			
Potri.004G106600	AT3G25180	CYP82G1	cytochrome P450, family 82, subfamily G, polypeptide 1
Potri.004G106700	AT5G15930	PAM1	plant adhesion molecule 1
Potri.004G121800	AT5G39660	CDF2	cycling DOF factor 2 Domain of unknown function (DUF298)
Potri.004G122100	AT3G28970	AAR3	
Potri.004G124800	AT5G15450	APG6,CLPB-P,CLPB3	casein lytic proteinase B3
Potri.004G127400			
Potri.004G129900			
Potri.004G131400			
Potri.004G133700			
Potri.004G133800			
Potri.004G143200			
Potri.004G147800	AT1G50030	TOR	target of rapamycin Phosphatidylinositol 3- and 4-kinase family protein
Potri.004G152400	AT1G49340	ATPI4K ALPHA	
Potri.004G155600	AT1G19440	KCS4	3-ketoacyl-CoA synthase 4
Potri.004G178000			
Potri.004G178100			
Potri.004G178200			
Potri.004G185700	AT1G08260	ABO4,EMB142,EMB2284,EMB529,ES D7,POL2A,TIL1	DNA polymerase epsilon catalytic subunit C2H2 zinc-finger protein SERRATE (SE)
Potri.004G196400	AT2G27100	SE	
Potri.004G235200			
Potri.004G235300	AT4G19350	EMB3006	embryo defective 3006
Potri.005G001200			
Potri.005G001300	AT3G62020	GLP10	germin-like protein 10

Potri.005G001700			
Potri.005G001800	AT1G09530	PAP3,PIF3,POC1	phytochrome interacting factor 3
Potri.005G005900	AT1G09420	G6PD4	glucose-6-phosphate dehydrogenase 4
Potri.005G006000			
Potri.005G006100	AT1G09420	G6PD4	glucose-6-phosphate dehydrogenase 4
Potri.005G007000			
Potri.005G049100			
Potri.005G049200			
Potri.005G059000	AT5G64070	PI-4KBETA1,PI4KBETA1	phosphatidylinositol 4-OH kinase beta1
Potri.005G062700	AT4G16990	RLM3	disease resistance protein (TIR-NBS class), putative
Potri.005G065500			
Potri.005G067500			
Potri.005G067600			
Potri.005G067700	AT5G09260	VPS20.2	vacuolar protein sorting-associated protein 20.2
Potri.005G067800			
Potri.005G082400	AT4G39620	ATPPR5,EMB2453	Tetratricopeptide repeat (TPR)-like superfamily protein
Potri.005G082500			
Potri.005G082600			
Potri.005G096400			
Potri.005G100700			
Potri.005G100800			
Potri.005G108800			
Potri.005G114700	AT2G17950	PGA6,WUS,WUS1	Homeodomain-like superfamily protein
Potri.005G128900	AT4G36860	DAR1	LIM domain-containing protein
Potri.005G142700	AT4G37270	ATHMA1,HMA1	heavy metal atpase 1
Potri.005G142800	AT4G37270	ATHMA1,HMA1	heavy metal atpase 1
Potri.005G143000			
Potri.005G143100			
Potri.005G148000	AT1G43130	LCV2	like COV 2
Potri.005G152100			
Potri.005G152200			
Potri.005G152300	AT5G49680	KIP	Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain
Potri.005G152400	AT1G58250	SAB	
Potri.005G152500			
Potri.005G153100			
Potri.005G157400	AT4G24580	REN1	Rho GTPase activation protein (RhoGAP) with PH domain
Potri.005G157500			
Potri.005G172100			
Potri.005G172200	AT4G08500	ARAKIN,ATMEKK1,MAPKKK8,MEK K1	MAPK/ERK kinase kinase 1
Potri.005G182100	AT1G77300	ASHH2,CCR1,EFS,SDG8	histone methyltransferases(H3-K4

Potri.005G193100	AT1G43620	TT15,UGT80B1	specific);histone methyltransferases(H3-K36 specific) UDP-Glycosyltransferase superfamily protein
Potri.005G203400	AT1G16120	WAKL1	wall associated kinase-like 1
Potri.005G207700	AT5G37020	ARF8,ATARF8	auxin response factor 8 jasmonic acid carboxyl methyltransferase
Potri.005G230100	AT1G19640	JMT	LSD1-like 3
Potri.005G235400	AT4G16310	LDL3	basic pentacysteine 6
Potri.005G235900	AT5G42520	ATBPC6,BBR/BPC6,BPC6	
Potri.005G236000			
Potri.005G237100			
Potri.005G242700			
Potri.005G242800			
Potri.005G259100			
Potri.006G002600	AT5G14420	RGLG2	RING domain ligase2
Potri.006G002700			
Potri.006G002800	AT5G56000	AtHsp90.4,Hsp81.4	HEAT SHOCK PROTEIN 81.4 UDP-Glycosyltransferase superfamily protein
Potri.006G023100	AT1G22400	ATUGT85A1,UGT85A1	UDP-glucosyl transferase 85A4
Potri.006G023200	AT1G78270	AtUGT85A4,UGT85A4	jasmonate-zim-domain protein 8
Potri.006G023300	AT1G30135	JAZ8,TIFY5A	Telomerase activating protein Est1
Potri.006G038500	AT5G19400	SMG7	
Potri.006G038600			
Potri.006G055300	AT3G57660	NRPA1	nuclear RNA polymerase A1
Potri.006G070500	AT3G10700	GalAK	galacturonic acid kinase
Potri.006G079800			
Potri.006G079900	AT5G58190	ECT10	evolutionarily conserved C-terminal region 10
Potri.006G080000			
Potri.006G097900	AT4G00430	PIP1;4,PIP1E,TMP-C	plasma membrane intrinsic protein 1;4
Potri.006G105800	AT2G38440	ATSCAR2,DIS3,ITB1,SCAR2,WAVE4	SCAR homolog 2
Potri.006G108200	AT3G08760	ATSIK	Protein kinase superfamily protein
Potri.006G109200	AT5G04930	ALA1	aminophospholipid ATPase 1 Malectin/receptor-like protein kinase family protein
Potri.006G110000	AT3G51550	FER	heat shock transcription factor A3
Potri.006G115700	AT5G03720	AT-HSFA3,HSFA3	Protein kinase superfamily protein
Potri.006G115800	AT5G03730	AtCTR1,CTR1,SIS1	
Potri.006G120200			
Potri.006G120300			
Potri.006G120400			
Potri.006G120500			
Potri.006G120600	AT3G53150	UGT73D1	UDP-glucosyl transferase 73D1
Potri.006G120700	AT2G26830	emb1187	Protein kinase superfamily protein
Potri.006G130400			
Potri.006G130500			
Potri.006G135600	AT5G58010	LRL3	LJRHL1-like 3
Potri.006G135700			

Potri.006G137900			
Potri.006G141300	AT5G20570	ATRBX1,HRT1,RBX1,ROC1	RING-box 1
Potri.006G145100	AT1G72830	ATHAP2C,HAP2C,NF-YA3	nuclear factor Y, subunit A3
Potri.006G163400			
Potri.006G163500			
Potri.006G163600	AT5G19690	STT3A	staurosporin and temperature sensitive 3-like A
Potri.006G163700	AT1G77180	SKIP	chromatin protein family Galactose oxidase/kelch repeat superfamily protein
Potri.006G166300	AT5G57360	ADO1,FKL2,LKP1,ZTL	
Potri.006G167000	AT4G30220	RUXF	small nuclear ribonucleoprotein F
Potri.006G170700			
Potri.006G174700	AT4G30340	ATDGK7,DGK7	diacylglycerol kinase 7
Potri.006G175500	AT2G18700	ATTPS11,ATTPSB,TPS11	trehalose phosphatase/synthase 11
Potri.006G197000	AT1G55310	ATSCL33,SCL33,SR33	SC35-like splicing factor 33
Potri.006G197100			
Potri.006G197200			
Potri.006G197300			
Potri.006G197400			
Potri.006G197500			
Potri.006G201100	AT5G22030	UBP8	ubiquitin-specific protease 8
Potri.006G204600			
Potri.006G208900	AT3G11540	SPY	Tetratricopeptide repeat (TPR)-like superfamily protein exocyst subunit exo70 family protein H4
Potri.006G214300	AT3G09520	ATEXO70H4,EXO70H4	
Potri.006G216900	AT3G43300	ATMIN7,BEN1	HOPM interactor 7
Potri.006G222100			
Potri.006G265100			
Potri.006G275900	AT1G22640	ATMYB3,MYB3	myb domain protein 3
Potri.006G276000			
Potri.006G276100			
Potri.006G279900			
Potri.006G280000			
Potri.007G000200	AT3G20000	TOM40	translocase of the outer mitochondrial membrane 40
Potri.007G000300	AT3G20020	ATPRMT6,PRMT6	protein arginine methyltransferase 6
Potri.007G000700			
Potri.007G001200			
Potri.007G001300			
Potri.007G002200	AT2G07050	CAS1	cycloartenol synthase 1
Potri.007G002300			
Potri.007G009600	AT4G18240	ATSS4,SS4,SSIV	starch synthase 4
Potri.007G009700			
Potri.007G036800	AT3G50440	ATMES10,MES10	methyl esterase 10
Potri.007G045800	AT2G23380	CLF,ICU1,SDG1,SET1	SET domain-containing protein
Potri.007G056200	AT4G38630	ATMCB1,MBP1,MCB1,RPN10	regulatory particle non-ATPase 10
Potri.007G059100	AT2G17510	EMB2763	ribonuclease II family protein



Potri.007G059200			
Potri.007G059900			
Potri.007G060000			
Potri.007G060100			
Potri.007G060300	AT4G35790	ATPLDDELTA,PLDDELTA	phospholipase D delta
Potri.007G060400	AT5G66055	AKRP,EMB16,EMB2036	ankyrin repeat protein
Potri.007G060800			
Potri.007G060900	AT4G35830	ACO1	aconitase 1
Potri.007G061400			
Potri.007G061500	AT2G17800	ARAC1,ATGP2,ATRAC1,ATROP3,RO P3	Arabidopsis RAC-like 1
Potri.007G061600	AT2G17790	VPS35A,ZIP3	VPS35 homolog A
Potri.007G061700			
Potri.007G062700			
Potri.007G063200			
Potri.007G063800			
Potri.007G063900	AT2G26000	BRIZ2	zinc finger (C3HC4-type RING finger) family protein
Potri.007G064000	AT4G35260	IDH-I,IDH1	isocitrate dehydrogenase 1
Potri.007G066800	AT3G12890	ASML2	activator of spomin::LUC2
Potri.007G082700			
Potri.007G086800			
Potri.007G086900			
Potri.007G107800			
Potri.007G113300	AT1G32750	GTD1,HAC13,HAF01,HAF1,TAF1	HAC13 protein (HAC13)
Potri.007G115400			
Potri.007G147000			
Potri.007G147100			
Potri.007G147200	AT2G44150	ASHH3,SDG7	histone-lysine N-methyltransferase ASHH3
Potri.008G002100	AT5G23450	ATLCBK1,LCBK1	long-chain base (LCB) kinase 1
Potri.008G008200	AT3G21180	ACA9,ATACA9	autoinhibited Ca(2+)-ATPase 9
Potri.008G008300			
Potri.008G032800	AT5G04290	KTF1,SPT5L	kow domain-containing transcription factor 1
Potri.008G035600	AT3G54860	ATVPS33,VPS33	Sec1/munc18-like (SM) proteins superfamily
Potri.008G035700	AT3G54850	ATPUB14,PUB14	plant U-box 14
Potri.008G045400			
Potri.008G070300	AT5G05560	EMB2771	E3 ubiquitin ligase, putative
Potri.008G078600			
Potri.008G078700			
Potri.008G101200	AT5G49930	emb1441	zinc knuckle (CCHC-type) family protein
Potri.008G101300	AT3G17205	UPL6	ubiquitin protein ligase 6
Potri.008G107700			
Potri.008G107800	AT4G02080	ASAR1,ATSAR2,ATSARA1C,SAR2	secretion-associated RAS super family 2
Potri.008G107900			

Potri.008G109300			
Potri.008G117000			
Potri.008G133300			
Potri.008G133400	AT3G17860	JAI3,JAZ3,TIFY6B	jasmonate-zim-domain protein 3
Potri.008G133600			
Potri.008G133700	AT2G01650	PUX2	plant UBX domain-containing protein 2
Potri.008G148000	AT2G02800	APK2B	protein kinase 2B
Potri.008G148100	AT2G02860	ATSUC3,ATSUT2,SUC3,SUT2	sucrose transporter 2
Potri.008G151900			
Potri.008G158800	AT5G43810	AGO10,PNH,ZLL	Stabilizer of iron transporter SufD / Polynucleotidyl transferase
Potri.008G163400			
Potri.008G163500			
Potri.008G163600			
Potri.008G177100			
Potri.008G202000	AT3G63088	DVL14,RTFL14	ROTUNDIFOLIA like 14
Potri.008G202100			
Potri.008G203300	AT3G06100	NIP7;1,NLM6,NLM8	NOD26-like intrinsic protein 7;1
Potri.008G205600	AT3G06400	CHR11	chromatin-remodeling protein 11
Potri.008G205900			
Potri.008G206000	AT1G48270	GCR1	G-protein-coupled receptor 1
Potri.008G206100			
Potri.008G206200			
Potri.008G217300	AT4G02570	ATCUL1,AXR6,CUL1	cullin 1
Potri.008G217400			
Potri.008G219100			
Potri.009G007700			
Potri.009G007800	AT5G60790	ATGCN1,GCN1	ABC transporter family protein
Potri.009G011000			
Potri.009G015000	AT5G60410	ATSIZ1,SIZ1	DNA-binding protein with MIZ/SP-RING zinc finger, PHD-finger and SAP domain
Potri.009G047700	AT2G13360	AGT,AGT1,SGAT	alanine:glyoxylate aminotransferase
Potri.009G047800	AT2G13370	CHR5	chromatin remodeling 5
Potri.009G054600	AT4G34890	ATXDH1,XDH1	xanthine dehydrogenase 1
Potri.009G056900			
Potri.009G057000			
Potri.009G057100			
Potri.009G078000	AT5G37060	ATCHX24,CHX24	cation/H <sup>+</sup> exchanger 24
Potri.009G078600	AT2G14170	ALDH6B2	aldehyde dehydrogenase 6B2
Potri.009G078700	AT2G14170	ALDH6B2	aldehyde dehydrogenase 6B2
Potri.009G078800			
Potri.009G078900			
Potri.009G094800	AT1G49820	ATMTK,MTK	S-methyl-5-thioribose kinase
Potri.009G094900	AT2G15230	ATLIP1,LIP1	lipase 1
Potri.009G095000			
Potri.009G095100	AT4G15480	UGT84A1	UDP-Glycosyltransferase superfamily

Potri.009G098300	AT2G15480	UGT73B5	protein UDP-glucosyl transferase 73B5
Potri.009G098400	AT2G15480	UGT73B5	UDP-glucosyl transferase 73B5
Potri.009G098500			
Potri.009G108200	AT2G15890	MEE14	maternal effect embryo arrest 14
Potri.009G108300			
Potri.009G108400			
Potri.009G109400	AT2G23460	ATXLG1,XLG1	extra-large G-protein 1
Potri.009G134200	AT2G20990	ATSYTA,NTMC2T1.1,NTMC2TYPE1.1,SYT1,SYTA	synaptotagmin A
Potri.009G165600	AT4G38360	LAZ1	Protein of unknown function (DUF300)
Potri.009G165700	AT3G50360	ATCEN2,CEN1,CEN2	centrin2
Potri.009G166900			
Potri.009G167000			
Potri.010G028200			
Potri.010G028300			
Potri.010G028400			
Potri.010G044100	AT1G10760	GWD,GWD1,SEX1,SOP,SOP1	Pyruvate phosphate dikinase, PEP/pyruvate binding domain
Potri.010G078600			
Potri.010G079300	AT2G26640	KCS11	3-ketoacyl-CoA synthase 11
Potri.010G081400			
Potri.010G092900	AT1G69830	AMY3,ATAMY3	alpha-amylase-like 3
Potri.010G104600			
Potri.010G109700			
Potri.010G109800			
Potri.010G114000	AT4G38620	ATMYB4,MYB4	myb domain protein 4
Potri.010G115400			
Potri.010G115500			
Potri.010G115700	AT2G01270	AtQSOX2,QSOX2	quiescin-sulfhydryl oxidase 2
Potri.010G122200	AT3G18290	BTS,EMB2454	zinc finger protein-related
Potri.010G133000			
Potri.010G146800			
Potri.010G152000			
Potri.010G152100			
Potri.010G152200			
Potri.010G198300			
Potri.010G198400	AT3G55610	P5CS2	delta 1-pyrroline-5-carboxylate synthase 2
Potri.010G198500			
Potri.010G207100			
Potri.010G207200	AT2G28760	UXS6	UDP-XYL synthase 6
Potri.010G210100	AT3G55320	PGP20	P-glycoprotein 20
Potri.010G210200	AT3G55330	PPL1	PsbP-like protein 1
Potri.010G211100	AT3G07100	ERMO2,SEC24A	Sec23/Sec24 protein transport family protein
Potri.010G211200			

Potri.010G211300	AT2G39450	ATMTP11,MTP11	Cation efflux family protein exocyst subunit exo70 family protein H2
Potri.010G212400	AT2G39380	ATEXO70H2,EXO70H2	
Potri.010G215300	AT2G37250	ADK,ATPADK1	adenosine kinase
Potri.010G215400			
Potri.010G215500	AT3G55005	TON1B	tonneau 1b (TON1b) DNA-binding protein with MIZ/SP- RING zinc finger, PHD-finger and SAP domain
Potri.010G219600	AT5G60410	ATSIZ1,SIZ1	
Potri.010G219700			
Potri.010G219800			
Potri.010G220000			
Potri.010G228500			
Potri.010G230400			
Potri.010G230500	AT5G04430	BTR1,BTR1L,BTR1S	binding to TOMV RNA 1L (long form)
Potri.010G234300			
Potri.010G238400			
Potri.010G238500			
Potri.010G246400			
Potri.010G246500			
Potri.010G246600	AT3G07040	RPM1,RPS3	NB-ARC domain-containing disease resistance protein
Potri.010G246700			
Potri.010G246800	AT5G17770	ATCBR,CBR,CBR1	NADH:cytochrome B5 reductase 1 ferredoxin/thioredoxin reductase subunit A (variable subunit) 2
Potri.010G255500	AT5G08410	FTRA2	long-chain base (LCB) kinase 1
Potri.010G255600	AT5G23450	ATLCBK1,LCBK1	calcium-dependent protein kinase 21
Potri.011G003400	AT4G04720	CPK21	PCF11P-similar protein 4
Potri.011G024800	AT4G04885	PCFS4	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related
Potri.011G046400	AT1G61140	EDA16	
Potri.011G046500			
Potri.011G068900			
Potri.011G069000			
Potri.011G069100			
Potri.011G077200	AT4G18040	AT.EIF4E1,CUM1,EIF4E,eIF4E1	eukaryotic translation initiation factor 4E
Potri.011G090900	AT1G30450	ATCCC1,CCC1,HAP5	cation-chloride co-transporter 1 multidrug resistance-associated protein 1
Potri.011G091200	AT1G30400	ATABCC1,ATMRP1,EST1,MRP1	calcineurin B-like 3
Potri.011G094900	AT4G26570	ATCBL3,CBL3	MAP kinase 19
Potri.011G102500	AT3G14720	ATMPK19,MPK19	
Potri.011G102600			
Potri.011G123800			
Potri.011G123900	AT5G54440	AfTRS130,CLUB	CLUB
Potri.011G144500			
Potri.011G144700			
Potri.011G158000			

Potri.011G167700	AT3G13330	PA200	proteasome activating protein 200
Potri.012G048400			
Potri.012G059000			
Potri.012G060100			
Potri.012G060700			
Potri.012G061000	AT3G18480	AtCASP,CASP	CCAAT-displacement protein alternatively spliced product
Potri.012G061100			
Potri.012G061900			
Potri.012G065600	AT5G61150	VIP4	leo1-like family protein
Potri.012G076800			
Potri.012G077900	AT5G40200	DegP9	DegP protease 9
Potri.013G001100			
Potri.013G001200			
Potri.013G001300	AT1G09530	PAP3,PIF3,POC1	phytochrome interacting factor 3
Potri.013G035100			
Potri.013G035200	AT3G04940	ATCYSD1,CYSD1	cysteine synthase D1
Potri.013G039500			
Potri.013G039600	AT5G49570	AtPNG1,PNG1	peptide-N-glycanase 1
Potri.013G053500	AT5G18280	APY2,ATAPY2	apyrase 2
Potri.013G053600			
Potri.013G068100			
Potri.013G076800			
Potri.013G076900			
Potri.013G078200			
Potri.013G081300	AT1G15750	TPL,WSIP1	Transducin family protein / WD-40 repeat family protein
Potri.013G081400			
Potri.013G081600			
Potri.013G081700			
Potri.013G083500			
Potri.013G083800			
Potri.013G084700			
Potri.013G084800	AT3G03340	UNE6	LUC7 related protein
Potri.013G086700			
Potri.013G087300			
Potri.013G087400			
Potri.013G087900			
Potri.013G088000			
Potri.013G088100	AT1G31800	CYP97A3,LUT5	cytochrome P450, family 97, subfamily A, polypeptide 3
Potri.013G088200	AT1G31800	CYP97A3,LUT5	cytochrome P450, family 97, subfamily A, polypeptide 3
Potri.013G089000	AT3G14050	AT-RSH2,ATRSH2,RSH2	RELA/SPOT homolog 2
Potri.013G099500	AT4G19710	AK-HSDH,AK-HSDH II	aspartate kinase-homoserine dehydrogenase ii
Potri.013G108300	AT4G23710	VAG2,VATG2,VHA-G2	vacuolar ATP synthase subunit G2
Potri.013G108400			

Potri.013G108500	AT2G16920	PFU2,UBC23	ubiquitin-conjugating enzyme 23
Potri.013G108600	AT1G72050	TFIIIA	transcription factor IIIA
Potri.013G108700			
Potri.013G108800			
Potri.013G114100			
Potri.013G115700			
Potri.013G127000			
Potri.013G129400			
Potri.013G129500			
Potri.013G159500			
Potri.013G159600	AT1G26910	RPL10B	Ribosomal protein L16p/L10e family protein
Potri.013G161100	AT5G58240	FHIT	FRAGILE HISTIDINE TRIAD
Potri.013G161200			
Potri.014G014700	AT1G10130	ATECA3,ECA3	endoplasmic reticulum-type calcium-transporting ATPase 3
Potri.014G014800			
Potri.014G025300	AT1G46480	WOX4	WUSCHEL related homeobox 4
Potri.014G025400	AT1G49760	PAB8,PABP8	poly(A) binding protein 8
Potri.014G025500			
Potri.014G028500	AT5G11210	ATGLR2.5,GLR2.5	glutamate receptor 2.5
Potri.014G028600			
Potri.014G028700			
Potri.014G028800	AT2G29120	ATGLR2.7,GLR2.7	glutamate receptor 2.7
Potri.014G028900			
Potri.014G029000	AT5G42900	COR27	cold regulated gene 27
Potri.014G109900			
Potri.014G117800	AT2G47230	ATDUF6,DUF6	DOMAIN OF UNKNOWN FUNCTION 724 6
Potri.014G128200	AT4G02390	APP,ATPARP1,PARP1,PP	poly(ADP-ribose) polymerase
Potri.014G136000			
Potri.014G141800	AT2G42810	PAPP5,PP5,PP5.2	protein phosphatase 5.2
Potri.014G167800	AT4G14540	NF-YB3	nuclear factor Y, subunit B3
Potri.014G171800	AT5G48300	ADG1,APS1	ADP glucose pyrophosphorylase 1
Potri.014G185300			
Potri.014G189500			
Potri.014G189900			
Potri.014G194300	AT2G20300	ALE2	Protein kinase superfamily protein
Potri.014G195100			
Potri.014G195200			
Potri.014G195300			
Potri.014G195700			
Potri.014G195800	AT5G44070	ARA8,ATPCS1,CAD1,PCS1	phytochelatin synthase 1 (PCS1)
Potri.014G196700			
Potri.014G196800			
Potri.015G032300			
Potri.015G032400			

Potri.015G032500			
Potri.015G035600			
Potri.015G048700	AT2G03800	GEK1	D-aminoacyl-tRNA deacylases
Potri.015G049700			
Potri.015G049800			
Potri.015G050800	AT1G73960	TAF2	TBP-associated factor 2
Potri.015G051000			
Potri.015G051200			
Potri.015G051800			
Potri.015G051900			
Potri.015G052100			
Potri.015G052200	AT5G23060	CaS	calcium sensing receptor
Potri.015G052400			
Potri.015G052500			
Potri.015G052600			
Potri.015G053300			
Potri.015G055400			
Potri.015G062100	AT5G61410	EMB2728,RPE	D-ribulose-5-phosphate-3-epimerase light-harvesting chlorophyll-protein complex I subunit A4
Potri.015G062200	AT3G47470	CAB4,LHCA4	
Potri.015G075800	AT5G14750	ATMYB66,MYB66,WER,WER1	myb domain protein 66
Potri.015G079800	AT4G24680	MOS1	modifier of snc1
Potri.015G104500	AT3G05020	ACP,ACP1	acyl carrier protein 1
Potri.015G104600			
Potri.015G106400			
Potri.016G029200	AT1G65440	GTB1	global transcription factor group B1
Potri.016G069100	AT3G05680	EMB2016	embryo defective 2016
Potri.016G079200			
Potri.016G094300	AT1G07570	APK1,APK1A	Protein kinase superfamily protein
Potri.016G094700			
Potri.016G094800	AT3G47620	AtTCP14,TCP14	TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14
Potri.016G095400			
Potri.016G095500			
Potri.016G095700	AT5G03730	AtCTR1,CTR1,SIS1	Protein kinase superfamily protein
Potri.016G095800	AT5G03730	AtCTR1,CTR1,SIS1	Protein kinase superfamily protein
Potri.016G095900	AT5G03770	KDTA	KDO transferase A
Potri.016G096300			
Potri.016G096700			
Potri.016G096800			
Potri.016G096900			
Potri.016G097000			
Potri.016G097300			
Potri.016G097800	AT5G03530	ATRAB,ATRAB ALPHA,ATRAB18B,ATRABC2A,RAB C2A	RAB GTPase homolog C2A
Potri.016G097900			
Potri.016G098000			

Potri.016G098100			
Potri.016G101400	AT2G37740	ATZFP10,ZFP10	zinc-finger protein 10
Potri.016G103300			
Potri.016G132000	AT3G08850	ATRAPTOR1B,RAPTOR1,RAPTOR1B	HEAT repeat ;WD domain, G-beta repeat protein protein
Potri.016G141500			
Potri.016G141600			
Potri.016G141700			
Potri.016G142400	AT2G48110	MED33B,REF4	reduced epidermal fluorescence 4
Potri.016G142500	AT3G23590	MED33A,RFR1	REF4-related 1
Potri.017G039100			
Potri.017G041300			
Potri.017G041700			
Potri.017G042100			
Potri.017G044100			
Potri.017G044200	AT2G22540	AGL22,SVP	K-box region and MADS-box transcription factor family protein
Potri.017G044600			
Potri.017G051300	AT1G17840	ABCG11,ATWBC11,COF1,DSO,WBC11	white-brown complex homolog protein 11
Potri.017G073100	AT3G02020	AK3	aspartate kinase 3
Potri.017G073200	AT5G40280	ATFTB,ERA1,WIG	Prenyltransferase family protein
Potri.017G087900	AT3G01090	AKIN10,KIN10,SNRK1.1	SNF1 kinase homolog 10
Potri.017G092600	AT5G15540	ATSCC2,EMB2773,SCC2	PHD finger family protein
Potri.017G101100	AT3G02260	ASA1,BIG,CRM1,DOC1,LPR1,TIR3,UMB1	auxin transport protein (BIG)
Potri.017G112200			
Potri.017G128300	AT3G03380	DegP7	DegP protease 7
Potri.017G141000	AT5G37020	ARF8,ATARF8	auxin response factor 8
Potri.017G141100	AT1G17880	ATBTF3,BTF3	basic transcription factor 3
Potri.017G141200			
Potri.017G142000			
Potri.017G142100			
Potri.017G142200			
Potri.018G019100	AT3G23780	DMS2,DRD2,NRPD2,NRPD2A,NRPE2	nuclear RNA polymerase D2A
Potri.018G047700	AT2G26280	CID7	CTC-interacting domain 7
Potri.018G047800	AT5G21930	ATHMA8,HMA8,PAA2	P-type ATPase of Arabidopsis 2
Potri.018G047900	AT2G26330	ER,QRP1	Leucine-rich receptor-like protein kinase family protein
Potri.018G059400	AT4G32940	GAMMA-VPE,GAMMAVPE	gamma vacuolar processing enzyme
Potri.018G060000			
Potri.018G061800			
Potri.018G066000			
Potri.018G066100	AT2G19450	ABX45,AS11,ATDGAT,DGAT1,RDS1, TAG1	membrane bound O-acyl transferase (MBOAT) family protein
Potri.018G072600	AT2G26890	GRV2,KAM2	DNAJ heat shock N-terminal domain-containing protein
Potri.018G089700	AT4G30160	ATVLN4,VLN4	villin 4
Potri.018G139900	AT5G57110	ACA8,AT-ACA8	autoinhibited Ca <sup>2+</sup> -ATPase, isoform 8



Potri.018G140200			
Potri.018G140300			
Potri.018G141100	AT1G51590	MANIB,MNS1	alpha-mannosidase 1
Potri.018G141200			
Potri.018G142300			
Potri.018G142400	AT4G29940	PRHA	pathogenesis related homeodomain protein A
Potri.019G047300	AT5G16750	TOZ	Transducin family protein / WD-40 repeat family protein
Potri.019G078300	AT5G47850	CCR4	CRINKLY4 related 4
Potri.019G080300	AT1G22620	ATSAC1	Phosphoinositide phosphatase family protein
Potri.019G129700			
Potri.019G129800			
Potri.019G129900	AT5G66750	ATDDM1,CHA1,CHR01,CHR1,DDM1, SOM1,SOM4	chromatin remodeling 1

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**Table S8.** List of the genes located in regions displaying significantly low genetic differentiation between *P. tremula* and *P. tremuloides*.

<b>Poplar gene</b>	<b>Best Arabidopsis hit</b>	<b>Synonyms</b>	<b>Annotated description</b>
Potri.001G017800			
Potri.001G017900			
Potri.001G043500			
Potri.001G043600	AT5G15350	AtENODL17,ENODL17	early nodulin-like protein 17
Potri.001G043700			
Potri.001G061400	AT5G50850	MAB1	Transketolase family protein
Potri.001G064800	AT1G74170	AtRLP13,RLP13	receptor like protein 13
Potri.001G064900	AT1G74190	AtRLP15,RLP15	receptor like protein 15
Potri.001G159200			
Potri.001G212000	AT1G22020	SHM6	serine hydroxymethyltransferase 6
Potri.001G276800			
Potri.001G293600			
Potri.001G394000			
Potri.001G394100			
Potri.001G398900	AT5G53860	emb2737,EMB64	embryo defective 2737
Potri.001G399000			
Potri.001G424600	AT4G27040	VPS22	EAP30/Vps36 family protein
Potri.001G424700	AT4G27030	FAD4,FADA	fatty acid desaturase A
Potri.001G424800			
Potri.001G432100			
Potri.001G432200			
Potri.001G432300			
Potri.001G440800			
Potri.001G440900			
Potri.001G441000			
Potri.001G441100			
Potri.001G445600			
Potri.001G445900			
Potri.002G116500			
Potri.002G116600			
Potri.002G116700			
Potri.002G116800	AT1G02000	GAE2	UDP-D-glucuronate 4-epimerase 2
Potri.002G117000	AT2G45330	emb1067	RNA 2'-phosphotransferase, Tpt1 / KptA family
Potri.002G119800			
Potri.002G119900	AT5G43130	TAF4,TAF4B	TBP-associated factor 4

Potri.002G146600			
Potri.002G146700			
Potri.002G215100	AT2G30950	FTSH2,VAR2	FtsH extracellular protease family
Potri.003G000200			
Potri.003G000300			
Potri.003G027300			
Potri.003G061200			
Potri.003G181600			
Potri.003G181700			
Potri.003G198700			
Potri.003G198800			
Potri.003G199100			
Potri.003G199600			
Potri.003G199700			
Potri.003G200100			
Potri.003G200200			
Potri.003G200400	AT3G54480	SKIP5,SKP5	SKP1/ASK-interacting protein 5
Potri.003G200500			
Potri.003G201700	AT1G29050	TBL38	TRICHOME BIREFRINGENCE-LIKE 38
Potri.003G201800			
Potri.003G201900			
Potri.003G202000			
Potri.003G202100	AT1G50420	SCL-3,SCL3	scarecrow-like 3
Potri.003G207600			
Potri.003G207700			
Potri.003G207800			
Potri.003G209700			
Potri.003G209800			
Potri.003G209900			
Potri.003G210000			
Potri.003G210100			
Potri.003G210200			
Potri.004G000100			
Potri.004G011300			
Potri.004G011400			
Potri.004G025300			
Potri.004G025600	AT4G05200	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25
Potri.004G025700	AT4G23180	CRK10,RLK4	cysteine-rich RLK (RECEPTOR-like protein kinase) 10
Potri.004G095000			
Potri.004G096700			
Potri.004G096800			
Potri.004G117300			

Potri.004G117400			
Potri.004G169400			
Potri.004G169500			
Potri.004G186300			
Potri.004G194200	AT3G03740	ATBPM4,BPM4	BTB-POZ and MATH domain 4
Potri.004G194300			
Potri.004G194400	AT5G17770	ATCBR,CBR,CBR1	NADH:cytochrome B5 reductase 1
Potri.004G194500			
Potri.004G194600	AT3G62020	GLP10	germin-like protein 10
Potri.004G194700			
Potri.004G194800			
Potri.004G195200			
Potri.004G195300			
Potri.005G003900			
Potri.005G004000			
Potri.005G004100			
Potri.005G004200			
Potri.005G004300	AT1G02500	AtSAM1,MAT1,SAM-1,SAM1	S-adenosylmethionine synthetase 1
Potri.005G004400			
Potri.005G004500			
Potri.005G004600			
Potri.005G011800			
Potri.005G011900			
Potri.005G012000			
Potri.005G012200	AT5G37640	UBQ9	ubiquitin 9
Potri.005G012300			
Potri.005G014700	AT4G21390	B120	S-locus lectin protein kinase family protein
Potri.005G014800	AT4G21390	B120	S-locus lectin protein kinase family protein
Potri.005G041300	AT4G26090	RPS2	NB-ARC domain-containing disease resistance protein
Potri.005G042900			
Potri.005G043000			
Potri.005G043100			
Potri.005G125200	AT2G18500	ATOFP7,OFP7	ovate family protein 7
Potri.005G241600			
Potri.006G013500			
Potri.006G060900			
Potri.006G082400			
Potri.006G082500	AT3G53620	AtPPa4,PPa4	pyrophosphorylase 4
Potri.006G117800	AT3G53030	SRPK4	ser/arg-rich protein kinase 4
Potri.006G189400			
Potri.006G189500			
Potri.006G194700	AT5G06650	GIS2	C2H2 and C2HC zinc fingers superfamily protein
Potri.006G271500	AT2G24610	ATCNGC14,CNGC14	cyclic nucleotide-gated channel

Potri.006G271600			
Potri.006G271700			
Potri.006G271800			
Potri.006G273300			
Potri.006G273400			
Potri.006G273500			
Potri.006G273600			
Potri.006G273700			
Potri.006G273800			
Potri.006G273900			
Potri.006G274000			
Potri.006G274100	AT2G24490	ATRPA2,ATRPA32A,ROR1,RPA2,RPA32A	replicon protein A2
Potri.006G274200			
Potri.006G274300			
Potri.007G087200	AT2G22125	CSII	binding
Potri.007G116900	AT1G77120	ADH,ADH1,ATADH,ATADH1	alcohol dehydrogenase 1
Potri.007G117000	AT5G38280	PR5K	PR5-like receptor kinase
Potri.007G117100			
Potri.007G117200	AT2G43840	UGT74F1	UDP-glycosyltransferase 74 F1
Potri.007G132100			
Potri.007G132200			
Potri.007G132300			
Potri.007G132900			
Potri.007G133000	AT2G01570	RGA,RGA1	GRAS family transcription factor family protein
Potri.007G133100			
Potri.007G133200			
Potri.007G133300			
Potri.007G141000	AT5G38280	PR5K	PR5-like receptor kinase
Potri.007G141100			
Potri.007G141200			
Potri.007G141600			
Potri.007G142500			
Potri.007G143100			
Potri.007G143200			
Potri.008G022800			
Potri.008G022900			
Potri.008G023000			
Potri.008G023500			
Potri.008G024800			
Potri.008G024900			
Potri.008G025000			
Potri.008G174500	AT5G43900	ATMYA2,MYA2,XI-2,XI-6	myosin 2
Potri.008G190200			
Potri.009G055500			
Potri.009G055600			

Potri.009G139500			
Potri.009G139600	AT4G38460	GGR	geranylgeranyl reductase
Potri.010G007000			
Potri.010G007100			
Potri.010G044400			
Potri.010G044500	AT1G70560	SAV3,TAA1,WEI8	tryptophan aminotransferase of Arabidopsis 1
Potri.010G044600			
Potri.010G044700	AT1G60780	HAP13	Clathrin adaptor complexes medium subunit family protein
Potri.011G016100			
Potri.011G016200			
Potri.011G018000			
Potri.011G018100			
Potri.011G019500			
Potri.011G019600			
Potri.011G019700			
Potri.011G068600	AT4G18710	ATSK21,BIN2,DWF12,SK21,UCU1	Protein kinase superfamily protein
Potri.011G117400			
Potri.012G007700			
Potri.012G011800			
Potri.012G012000			
Potri.012G012100			
Potri.012G012200			
Potri.012G012500			
Potri.012G012600			
Potri.012G029600			
Potri.012G029700			
Potri.012G029800			
Potri.012G029900			
Potri.012G030600			
Potri.012G030700			
Potri.012G030800			
Potri.012G046200	AT1G74000	SS3	strictosidine synthase 3
Potri.012G046300			
Potri.012G051300			
Potri.012G051400	AT1G08510	FATB	fatty acyl-ACP thioesterases B
Potri.012G070600			
Potri.012G095800	AT5G63420	emb2746	RNA-metabolising metallo-beta-lactamase family protein
Potri.012G122800			
Potri.013G037700	AT3G04870	PDE181,SPC1,ZDS	zeta-carotene desaturase
Potri.013G037800			
Potri.013G089400			
Potri.013G101800			
Potri.013G104400	AT1G58350	ZW18	Putative serine esterase family protein

Potri.013G104500	AT1G33980	ATUPF3,UPF3	Smg-4/UPF3 family protein
Potri.013G104600			
Potri.013G104700	AT4G09900	ATMES12,MES12	methyl esterase 12
Potri.013G105400			
Potri.013G105500			
Potri.013G105600			
Potri.013G105700			
Potri.013G105800			
Potri.013G133800			
Potri.013G133900			
Potri.013G146200	AT2G20810	GAUT10,LGT4	galacturonosyltransferase 10
Potri.013G146300			
Potri.013G146400			
Potri.013G146500			
Potri.014G002800			
Potri.014G003000			
Potri.014G003100			
Potri.014G004100	AT3G20000	TOM40	translocase of the outer mitochondrial membrane 40
Potri.014G004200			
Potri.014G004500			
Potri.014G004600			
Potri.014G005400			
Potri.014G010100			
Potri.014G010200	AT3G20000	TOM40	translocase of the outer mitochondrial membrane 40
Potri.014G010300	AT3G20020	ATPRMT6,PRMT6	protein arginine methyltransferase 6
Potri.014G033900	AT2G26560	PLA IIA,PLA2A,PLP2	phospholipase A 2A
Potri.014G054200			
Potri.014G054300			
Potri.014G054400			
Potri.014G054500	AT4G39120	HISN7,IMPL2	myo-inositol monophosphatase like 2
Potri.014G128300			
Potri.014G128400	AT3G53760	ATGCP4,GCP4	GAMMA-TUBULIN COMPLEX PROTEIN 4
Potri.015G019000			
Potri.015G019100	AT5G53130	ATCNGC1,CNGC1	cyclic nucleotide gated channel 1
Potri.015G021700			
Potri.015G024400			
Potri.015G024500			
Potri.015G024900			
Potri.015G025000			
Potri.015G025100			
Potri.015G026200			
Potri.015G026300			
Potri.015G041000	AT1G18100	E12A11,MFT	PEBP

Potri.015G041300	AT3G18080	BGLU44	(phosphatidylethanolamine-binding protein) family protein
Potri.015G041400			B-S glucosidase 44
Potri.015G059200			
Potri.015G059300			
Potri.015G094200			
Potri.015G111900	AT2G35160	SGD9,SUVH5	SU(VAR)3-9 homolog 5
Potri.015G112000			
Potri.015G112300	AT4G25130	PMSR4	peptide met sulfoxide reductase 4
Potri.015G112400			
Potri.015G112500			
Potri.015G112600			
Potri.015G112700			
Potri.015G113000	AT5G45130	ATRAB-F2A,ATRAB5A,ATRABF2A,RAB-F2A,RAB5A,RABF2A,RHA1	RAB homolog 1
Potri.015G113100			
Potri.015G113200			
Potri.015G113300	AT5G14345	AtENODL21,ENODL21	early nodulin-like protein 21
Potri.015G113400			
Potri.015G113800			
Potri.015G113900			
Potri.015G115400	AT5G45110	ATNPR3,NPR3	NPR1-like protein 3
Potri.015G115500			
Potri.015G115600	AT5G14345	AtENODL21,ENODL21	early nodulin-like protein 21
Potri.015G118600			
Potri.015G118700			
Potri.015G118800	AT1G31200	ATPP2-A9,PP2-A9	phloem protein 2-A9
Potri.015G118900	AT1G10155	ATPP2-A10,PP2-A10	phloem protein 2-A10
Potri.015G119400			
Potri.015G119500			
Potri.015G119600			
Potri.015G119700			
Potri.015G119800			
Potri.015G119900			
Potri.015G120000	AT1G31200	ATPP2-A9,PP2-A9	phloem protein 2-A9
Potri.015G120300	AT5G24560	AtPP2-B12,PP2-B12	phloem protein 2-B12
Potri.015G120400	AT1G31190	IMPL1	myo-inositol monophosphatase like 1
Potri.015G120500			
Potri.015G120600			
Potri.015G120700			
Potri.015G121900			
Potri.015G122000	AT5G38280	PR5K	PR5-like receptor kinase
Potri.015G122100	AT2G35150	EXL1	EXORDIUM like 1
Potri.015G122200			
Potri.015G122300			



Potri.015G123700			
Potri.015G123800			
Potri.015G123900	AT2G35110	GRL,NAP1,NAPP	transcription activators
Potri.016G011500			
Potri.016G012200			
Potri.016G027500			
Potri.016G027600	AT3G56910	PSRP5	plastid-specific 50S ribosomal protein 5
Potri.016G027700			
Potri.016G038900	AT3G57090	BIGYIN,FIS1A	Tetratricopeptide repeat (TPR)-like superfamily protein
Potri.016G039000	AT1G16390	3-Oct,ATOCT3	organic cation/carnitine transporter 3
Potri.016G039100			
Potri.016G039200			
Potri.016G039500			
Potri.016G039600			
Potri.016G039700			
Potri.016G039800			
Potri.016G039900			
Potri.016G040000			
Potri.016G092700			
Potri.016G092800			
Potri.017G015100			
Potri.017G015200			
Potri.017G015500			
Potri.017G015600			
Potri.017G024200			
Potri.017G024900			
Potri.017G025000			
Potri.017G027900	AT3G13710	PRA1.F4	prenylated RAB acceptor 1.F4
Potri.017G081200			
Potri.017G092200			
Potri.017G095600	AT3G51550	FER	Malectin/receptor-like protein kinase family protein
Potri.017G095700	AT3G29780	RALFL27	ralf-like 27
Potri.017G095800			
Potri.017G095900	AT3G51550	FER	Malectin/receptor-like protein kinase family protein
Potri.017G104300			
Potri.017G108200			
Potri.017G108300			
Potri.017G108400			
Potri.017G117200			
Potri.017G117300			
Potri.017G117400			
Potri.017G123500			
Potri.017G123600			

Potri.017G123700	AT3G45980	H2B,HTB9	Histone superfamily protein
Potri.017G123800			
Potri.017G137000	AT5G40990	GLIP1	GDSL lipase 1
Potri.017G152200			
Potri.017G152300			
Potri.017G152500			
Potri.017G152600			
Potri.017G152700			
Potri.018G004500			
Potri.018G004600			
Potri.018G004800	AT4G16130	ARA1,ATISA1,ISA1	arabinose kinase
Potri.018G004900			
Potri.018G005000			
Potri.018G008300			
Potri.018G008400	AT4G31540	ATEXO70G1,EXO70G1	exocyst subunit exo70 family protein G1
Potri.018G108000			
Potri.018G108100			
Potri.018G145500	AT5G35330	ATMBD2,MBD02,MBD2	methyl-CPG-binding domain protein 02
Potri.018G145600			
Potri.018G145700	AT4G16130	ARA1,ATISA1,ISA1	arabinose kinase
Potri.018G148300	AT1G16120	WAKL1	wall associated kinase-like 1
Potri.018G148400			
Potri.019G005900			
Potri.019G006000			
Potri.019G014900	AT2G26560	PLA IIA,PLA2A,PLP2	phospholipase A 2A
Potri.019G015000	AT2G14050	MCM9	minichromosome maintenance 9
Potri.019G015700			
Potri.019G019700			
Potri.019G020000	AT3G04460	APM4,ATPEX12,PEX12	peroxin-12
Potri.019G020100			
Potri.019G020200			
Potri.019G020300			
Potri.019G041400			
Potri.019G069400			
Potri.019G069500			
Potri.019G094700			
Potri.019G094800			
Potri.019G096500			
Potri.019G096600			
Potri.019G096700			
Potri.019G096800			
Potri.019G096900			
Potri.019G097000			
Potri.019G105200	AT4G03320	tic20-IV	translocon at the inner envelope membrane of chloroplasts 20-IV

Potri.019G105300

Potri.019G106200

Potri.019G106800

Potri.019G106900

Potri.019G108300

Potri.019G108400

Potri.019G108700

Potri.019G108800 AT4G03320 tic20-IV

Potri.019G110800

Potri.019G110900

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translocon at the inner envelope  
membrane of chloroplasts 20-IV

**Table S9.** Functional gene categories enriched for genes located within regions displaying significantly low genetic differentiation between *P. tremula* and *P. tremuloides*.

GO term	Ontology	Description	P-value	FDR
GO:0012501	P	programmed cell death	4.1e-17	2.7e-15
GO:0006915	P	apoptosis	4.1e-17	2.7e-15
GO:0016265	P	death	1.5e-16	4.8e-15
GO:0008219	P	cell death	1.5e-16	4.8e-15
GO:0002376	P	immune system process	1.8e-07	3.4e-06
GO:0006955	P	immune response	1.8e-07	3.4e-06
GO:0045087	P	innate immune response	1.8e-07	3.4e-06
GO:0006952	P	defense response	2.3e-06	3.8e-05
GO:0009987	P	cellular process	7.2e-06	0.00011
GO:0007165	P	signal transduction	0.00014	0.0019
GO:0006796	P	phosphate metabolic process	0.00036	0.004
GO:0006793	P	phosphorus metabolic process	0.00036	0.004
GO:0023046	P	signaling process	0.00046	0.0043
GO:0023060	P	signal transmission	0.00046	0.0043
GO:0016310	P	phosphorylation	0.00051	0.0045
GO:0023052	P	signaling	0.00077	0.0064
GO:0043687	P	post-translational protein modification	0.0013	0.01
GO:0006468	P	protein amino acid phosphorylation	0.0014	0.01
GO:0006950	P	response to stress	0.0015	0.011
GO:0006464	P	protein modification process	0.0035	0.023
GO:0065004	P	protein-DNA complex assembly	0.0047	0.024
GO:0050896	P	response to stimulus	0.0048	0.024
GO:0043412	P	macromolecule modification	0.0051	0.024
GO:0034728	P	nucleosome organization	0.0047	0.024
GO:0031497	P	chromatin assembly	0.0047	0.024
GO:0006334	P	nucleosome assembly	0.0047	0.024
GO:0006333	P	chromatin assembly or disassembly	0.0052	0.024
GO:0006323	P	DNA packaging	0.0047	0.024
GO:0071103	P	DNA conformation change	0.0074	0.034
GO:0006996	P	organelle organization	0.0093	0.041
GO:0051049	P	regulation of transport	0.012	0.047
GO:0032879	P	regulation of localization	0.012	0.047
GO:0044070	P	regulation of anion transport	0.012	0.047
GO:0043269	P	regulation of ion transport	0.012	0.047
GO:0043531	F	ADP binding	2.4e-17	2.1e-15
GO:0005524	F	ATP binding	7,00E-12	2.1e-10
GO:0032559	F	adenyl ribonucleotide binding	7,00E-12	2.1e-10
GO:0032555	F	purine ribonucleotide binding	1.4e-11	2.4e-10
GO:0032553	F	ribonucleotide binding	1.4e-11	2.4e-10
GO:0030554	F	adenyl nucleotide binding	9.9e-11	1.2e-09

GO:0001882	F	nucleoside binding	1.1e-10	1.2e-09
GO:0001883	F	purine nucleoside binding	9.9e-11	1.2e-09
GO:0017076	F	purine nucleotide binding	1.8e-10	1.8e-09
GO:0000166	F	nucleotide binding	1.5e-09	1.3e-08
GO:0005515	F	protein binding	3.8e-06	2.6e-05
GO:0004888	F	transmembrane receptor activity	3.6e-06	2.6e-05
GO:0004872	F	receptor activity	3.9e-06	2.6e-05
GO:0060089	F	molecular transducer activity	0.00039	0.0023
GO:0004871	F	signal transducer activity	0.00039	0.0023
GO:0005488	F	binding	0.0019	0.0098
GO:0004672	F	protein kinase activity	0.0018	0.0098
GO:0016301	F	kinase activity	0.004	0.02
GO:0016772	F	transferase activity, transferring phosphorus-containing groups	0.0055	0.024
GO:0016773	F	phosphotransferase activity, alcohol group as acceptor	0.0056	0.024
GO:0004437	F	inositol or phosphatidylinositol phosphatase activity	0.0097	0.041
GO:0044422	C	organelle part	0.0024	0.025
GO:0000785	C	chromatin	0.0027	0.025
GO:0000786	C	nucleosome	0.0027	0.025
GO:0044446	C	intracellular organelle part	0.0024	0.025
GO:0032993	C	protein-DNA complex	0.0027	0.025

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