

The explanations for all the columns in the output of the differential analysis in Table S1 and Table S2 is as follows from the DESeq2 manual. The columns include:
baseMean = the average of the normalized counts taken over all samples; **log2FoldChange** = log2 fold change between the groups. E.g. value 2 means that the expression has increased 4-fold; **lfcSE** = standard error of the log2FoldChange estimate; **stat** = Wald statistic; **pvalue** = Wald test p-value; **padj** = Benjamini-Hochberg adjusted p-value

Table S1 Genes for which the levels of expression were significantly higher in the 67°N population as compared to the 56°N population in response to SHADE in Norway spruce

Gene_ID	TAIR	Primary Gene Symbol	Gene Model Description	Expression	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
MA_93016g0010	AT1G01490		Heavy metal transport/detoxification superfamily protein	shade67>shade56	171.99156	19.31080551	3.3123768	5.8298938	5.55E-09	4.05E-06
MA_10436915g0010	AT1G01630		Sec14p-like phosphatidylinositol transfer family protein	shade67>shade56	181.74323	0.890249942	0.2256632	3.9450378	7.98E-05	0.00785557
MA_9801637g0010	AT1G02080		transcription regulator;(source:Araport11)	shade67>shade56	213.33803	24.54497744	4.3990602	5.5795957	2.41E-08	1.52E-05
MA_11144g0010	AT1G02205	ECERIFERUM 1 (CER1)	Expression of the CER1 gene associated with plant cuticle development	shade67>shade56	108.46666	2.068137632	0.5135865	4.0268533	5.65E-05	0.00616581
MA_10107572g0010	AT1G02800	CELLULOSE 2 (CEL2)	Encodes a protein with similarity to endo-1,4-beta-D-glucanase	shade67>shade56	139.88385	8.882139059	1.4882152	5.9683163	2.40E-09	1.91E-06
MA_4984597g0010	AT1G03230		Eukaryotic aspartyl protease family protein;(source:Araport11)	shade67>shade56	411.38787	21.9613859	4.8673892	4.5119436	6.42E-06	0.00109619
MA_388691g0010	AT1G03600	(PSB27)	PSB27 is a chloroplast lumen localized protein	shade67>shade56	742.76598	0.648168009	0.1545924	4.192755	2.76E-05	0.00353428
MA_45121g0010	AT1G05670		Pentatricopeptide repeat (PPR-like) superfamily protein	shade67>shade56	184.58984	23.3255113	4.6756254	4.9887468	6.08E-07	0.00015401
MA_5724086g0010	AT1G10170	NF-X-LIKE 1 (NXFL1)	Encodes ATNXFL1, a homologue of the putative NF-X-Like 1	shade67>shade56	39.044387	21.84528163	5.5538392	3.9332777	7.81E-05	0.00803983
MA_12361g0010	AT1G10390	DRACULA2 (DRA2)	DRA2 is a homolog of mammalian nucleoporin	shade67>shade56	95.148831	2.635868046	0.5869981	4.4904199	7.11E-06	0.00116898
MA_640601g0010	AT1G10640		Pectin lyase-like superfamily protein;(source:Araport11)	shade67>shade56	120.66502	1.686576144	0.3424242	4.9253994	8.42E-07	0.00020244
MA_10430253g0010	AT1G10740		alpha/beta-Hydrolases superfamily protein;(source:Araport11)	shade67>shade56	43.387063	19.20864968	4.2782117	4.4898782	7.13E-06	0.00116898
MA_10432704g0020	AT1G11290	CHLORORESPIRATORY REDUCTASE	Pentatricopeptide Repeat Protein containing two pentatricopeptide repeats	shade67>shade56	388.93827	2.036870563	0.4773711	4.2668492	1.98E-05	0.00270169
MA_500971g0010	AT1G12050	FUMARYLACETOACETATE HYDROLASE	Encodes a fumarylacetoacetase that converts fumarylacetoacetate to fumarate	shade67>shade56	137.11908	30	6.0065614	4.9945381	5.90E-07	0.00015401
MA_10435025g0010	AT1G13520		hypothetical protein (DUF1262);(source:Araport11)	shade67>shade56	139.92554	2.605127449	0.6168562	4.223233	2.41E-05	0.00318496
MA_15382g0010	AT1G13570		F-box/RNI-like superfamily protein;(source:Araport11)	shade67>shade56	63.129848	19.75701806	4.5405589	4.3512304	1.35E-05	0.00200323
MA_179350g0020	AT1G23740	ALKENAL/ONE OXIDOREDUCTASE	AOR is an alkenal/one oxidoreductase that acts on alkenals	shade67>shade56	467.58936	25.98001962	4.9570437	5.2410309	1.60E-07	7.51E-05
MA_470965g0010	AT1G25440	B-BOX DOMAIN PROTEIN 15 (BBP15)	B-box type zinc finger protein with CCT domain	shade67>shade56	455.31386	1.121153225	0.2626287	4.2689661	1.96E-05	0.00268966
MA_89572g0010	AT1G26760	SET DOMAIN PROTEIN 35 (SDG35)	SET domain protein 35;(source:Araport11)	shade67>shade56	42.735581	20.65022444	4.404534	4.6504765	3.31E-06	0.00060152
MA_129800g0010	AT1G27170		transmembrane receptors / ATP binding protein	shade67>shade56	61.243749	23.9648196	5.8925165	4.0669613	4.76E-05	0.00538973
MA_190687g0010	AT1G28750		SGNH hydrolase-type esterase superfamily protein	shade67>shade56	221.37196	19.19121621	4.3179928	4.4444762	8.81E-06	0.00140178
MA_10265740g0010	AT1G34300		lectin protein kinase family protein;(source:Araport11)	shade67>shade56	13.049835	6.827765434	1.6550327	4.1254566	3.70E-05	0.00443591
MA_9827161g0010	AT1G50510		indigoidine synthase A family protein;(source:Araport11)	shade67>shade56	350.65976	24.79895514	5.8990002	4.2104203	2.55E-05	0.00332946
MA_2734g0010	AT1G55790		ferredoxin-fold anticodon-binding domain protein	shade67>shade56	35.061281	22.4663389	5.5747433	4.0302022	5.58E-05	0.00613067
MA_119176g0010	AT1G56145		Leucine-rich repeat transmembrane protein kinase	shade67>shade56	212.29721	11.61665618	2.5818513	4.4993514	6.82E-06	0.00114018
MA_242575g0010	AT1G56720		Protein kinase superfamily protein;(source:Araport11)	shade67>shade56	144.14445	23.65612586	5.7870066	4.0878	4.35E-05	0.00502182
MA_650284g0010	AT1G59740	NRT1/ PTR FAMILY 4.3 (NPF4.3)	Major facilitator superfamily protein;(source:Araport11)	shade67>shade56	117.29519	24.4485448	4.7248031	5.1745109	2.29E-07	0.00010074
MA_1734g0010	AT1G65450	GLAUCE (GLC)	Contains dual transcription units and alternative splicing	shade67>shade56	67.713142	2.31918862	0.5679646	4.0831891	4.44E-05	0.00509479
MA_52897g0010	AT1G66920		Protein kinase superfamily protein;(source:Araport11)	shade67>shade56	214.04324	22.16541059	4.3848556	5.1132985	3.17E-07	0.00012624
MA_9239567g0010	AT1G69930	GLUTATHIONE S-TRANSFERASE	Encodes glutathione transferase belonging to theta class	shade67>shade56	48.887639	6.951129764	1.4925065	4.6573532	3.20E-06	0.00058802
MA_129851g0010	AT1G72470	EXOCYST SUBUNIT EXO70 FAMILY	A member of EXO70 gene family, putative exocyst subunit	shade67>shade56	68.886724	23.1219094	5.8916095	3.9245489	8.69E-05	0.00824038
MA_553396g0010	AT1G74310	HEAT SHOCK PROTEIN 101 (HSP101)	Encodes ClpB1, which belongs to the Casein lytic protease family	shade67>shade56	229.3189	24.41459867	4.582808	5.3274321	9.96E-08	5.34E-05
MA_88684g0010	AT1G74460		GDSL-motif esterase/acyltransferase/lipase. Encodes a	shade67>shade56	198.59424	0.780591597	0.1767749	4.4157374	1.01E-05	0.00158375
MA_180495g0010	AT1G78060		Glycosyl hydrolase family protein;(source:Araport11)	shade67>shade56	104.55114	1.492501596	0.3435133	3.4484148	1.39E-05	0.00205549
MA_108157g0010	AT1G78800		UDP-Glycosyltransferase superfamily protein;(source:Araport11)	shade67>shade56	288.92213	24.91890254	5.4512999	5.4864128	4.10E-08	2.44E-05
MA_10348903g0010	AT1G78895		Reticulon family protein;(source:Araport11)	shade67>shade56	95.841286	17.97643928	3.2894734	5.464838	4.63E-08	2.72E-05
MA_10429874g0010	AT1G80160	GLYOXYLASE I 7 (GLYI7)	Vincinal oxygen chelate (VOC) superfamily member	shade67>shade56	161.27715	23.12495978	5.8609333	3.9456105	7.96E-05	0.00785557
MA_395055g0010	AT1G80820	CINNAMOYL COA REDUCTASE (CCR)	Encodes a cinnamoyl CoA reductase isoform	shade67>shade56	40.899254	30	6.0094577	4.992131	5.97E-07	0.00015401
MA_19208g0010	AT2G01850	ENDOXYGLOGUCAN TRANSFERASE	EXGT-A3 has homology to xyloglucan endotransferase	shade67>shade56	124.3984	22.68203697	4.60999	4.9201922	8.65E-07	0.00020673
MA_16619g0010	AT2G02450	LONG VEGETATIVE PHASE 1 (LOV1)	NAC domain containing protein 35;(source:Araport11)	shade67>shade56	76.088784	22.14299267	4.3836582	5.0512589	4.39E-07	0.00015401
MA_78676g0020	AT2G13600	SLOW GROWTH 2 (SLO2)	Encodes a pentatricopeptide repeat protein	shade67>shade56	196.9592	21.58842311	4.6065824	4.6864294	2.78E-06	0.0005233
MA_101849g0010	AT2G17040	NAC DOMAIN CONTAINING PROTEIN 35 (NAC35)	Member of the NAC transcription factor family	shade67>shade56	461.71542	26.84616555	5.2685729	5.0955289	3.48E-07	0.00013233
MA_7493784g0010	AT2G17130	CINNAMYL ALCOHOL DEHYDROGENASE	cinnamyl alcohol dehydrogenase homolog 2;(source:Araport11)	shade67>shade56	143.36126	22.94004279	4.4972198	5.1009388	3.38E-07	0.00013122
MA_455g0010	AT2G22250	ASPARTATE AMINOTRANSFERASE	Encodes a prokaryotic-type plastidic aspartate aminotransferase	shade67>shade56	154.31616	21.73531843	4.5262512	4.8020575	1.57E-06	0.00033066
MA_7330598g0010	AT2G22590		UDP-Glycosyltransferase superfamily protein;(source:Araport11)	shade67>shade56	341.19687	20.19612958	4.4945833	4.4934376	7.01E-06	0.00116312
MA_177197g0020	AT2G24130		Leucine-rich receptor-like protein kinase family protein	shade67>shade56	107.67222	26.02330665	5.9568443	4.4139586	1.01E-05	0.00158504
MA_10427649g0020	AT2G26700	PINOID2 (PID2)	Member of AGC VIIa Kinase gene family. Encodes a	shade67>shade56	145.97226	3.016886255	0.6021253	5.0103961	5.43E-07	0.00015401
MA_20782g0010	AT2G27610		Tetratricopeptide repeat (TPR)-like superfamily protein	shade67>shade56	185.7094	1.647532558	0.361988	4.5513464	5.33E-06	0.00093994
MA_906876g0010	AT2G29380	HIGHLY ABA-INDUCED PP2C GENE	highly ABA-induced PP2C protein 3;(source:Araport11)	shade67>shade56	101.08365	2.557108004	0.6497897	3.9352856	8.31E-05	0.0080187
MA_116552g0010	AT2G32010	CVP2 LIKE 1 (CVL1)	Encodes an inositol polyphosphate 57-phosphatase	shade67>shade56	203.68622	1.477916508	0.3769251	3.9209823	8.82E-05	0.00831233
MA_161036g0010	AT2G33150	PEROXISOMAL 3-KETOACYL-COA	Encodes an organellar (peroxisome, glyoxysome) 3-ketoacyl-CoA	shade67>shade56	62.413835	22.23258589	5.6952758	3.9036891	4.97E-05	0.008787
MA_10432854g0010	AT2G34930		disease resistance family protein / LRR family protein	shade67>shade56	246.28107	19.21591367	4.4020052	4.3652638	1.27E-05	0.00191227
MA_10434829g0020	AT2G35730		Heavy metal transport/detoxification superfamily protein	shade67>shade56	257.51116	1.652742878	0.419015	3.9443524	8.00E-05	0.00785557
MA_26811g0010	AT2G36750	UDP-GLUCOSYL TRANSFERASE 7	UDP-glucosyl transferase 73C1;(source:Araport11)	shade67>shade56	642.45689	20.92464441	3.062855	3.831745	8.39E-12	2.09E-08
MA_8644998g0010	AT2G36830	GAMMA TONOPLAST INTRINSIC	Encodes a tonoplast intrinsic protein, which functions in	shade67>shade56	57.502335	22.85053915	5.8929248	3.8776228	0.00010548	0.00957963
MA_159120g0010	AT2G38300		myb-like HTH transcriptional regulator family protein	shade67>shade56	61.559852	20.2489734	3.19972	6.3333346	2.40E-10	2.99E-07
MA_41286g0020	AT2G39210		Major facilitator superfamily protein;(source:Araport11)	shade67>shade56	265.38725	9.774556004	2.4734683	3.9517612	7.76E-05	0.00778006
MA_10429137g0020	AT2G44460	BETA GLUCOSIDASE 28 (BGLU28)	beta glucosidase 28;(source:Araport11)	shade67>shade56	610.9023	11.28373972	2.8598257	3.945604	7.96E-05	0.00785557
MA_9544285g0010	AT2G45660	AGAMOUS-LIKE 20 (AGL20)	Controls flowering and is required for CO to promote flowering	shade67>shade56	59.14217	24.48104131	5.4303222	4.5082115	6.54E-06	0.00110231
MA_9957507g0010	AT2G45670	LYSOPHOSPHATIDYLETHANOLAM	Encodes an acyl-CoA: lysophosphatidylethanolamine	shade67>shade56	77.389898	1.950904293	0.3984553	4.8961686	9.77E-07	0.000226
MA_10431662g0010	AT3G01160		pre-rRNA-processing ESF1-like protein;(source:Araport11)	shade67>shade56	39.915146	21.71071847	5.5445025	3.9157199	9.01E-05	0.00843675
MA_187159g0010	AT3G01190		Peroxidase superfamily protein;(source:Araport11)	shade67>shade56	72.076916	23.3149957	5.5560126	4.196354	2.71E-05	0.00349982
MA_9076332g0010	AT3G04140		Ankyrin repeat family protein;(source:Araport11)	shade67>shade56	16.847116	3.1738832	0.8031452	3.9518174	7.76E-05	0.0078006
MA_8035959g0010	AT3G04720		Encodes a protein similar to the antifungal chitinase	shade67>shade56	137.62157	25.66154289	5.4483365	4.7099776	2.48E-06	0.00048095
MA_101858g0010	AT3G11980	MALE STERILITY 2 (MS2)	Similar to fatty acid reductases.	shade67>shade56	21.755398	30	6.0094222	4.9921605	5.97E-07	0.00015401
MA_9825276g0010	AT3G12390		Nascent polypeptide-associated complex (NAC)	shade67>shade56	64.092653	25.42688374	5.896436	4.3122462	1.62E-05	0.00230278
MA_85286g0010	AT3G13080		encodes an ATP-dependent MRP-like ABC transporter	shade67>shade56	68.252939	25.17279858	5.8945496	4.2705211	1.95E-05	0.00267964
MA_10432070g0010	AT3G17611	RHOMBOID-LIKE PROTEIN 14 (RHOM14)	RHOMBOID-like protein 14;(source:Araport11)	shade67>shade56	308.39347	9.53088024	1.4137652	6.7571957	1.41E-11	3.31E-08
MA_10208460g0010	AT3G18090	NUCLEAR RNA POLYMERASE D2	Encodes a subunit of RNA polymerase IV (aka RNA polymerase D2)	shade67>shade56	358.56828	25.8970636	5.8899104	4.3968519	1.10E-05	0.00170264
MA_9208522g0010	AT3G19640	MAGNESIUM TRANSPORTER 4 (MGT4)	Transmembrane magnesium transporter. One of two isoforms	shade67>shade56	73.279952	30	5.5599977	5.3956857	6.83E-08	3.85E-05
MA_10342550g0010	AT3G21000		Gag-Pol-related retrotransposon family protein	shade67>shade56	43.666787	30	6.0073801	4.9938575	5.92E-07	0.00015401
MA_226036g0010	AT3G27970		Exonuclease family protein;(source:Araport11)	shade67>shade56	173.81697	10.14610409	1.5841105	6.4049221	1.50E-10	2.20E-07
MA_9736190g0010	AT3G43660		The gene encodes a putative nodulin-like21 protein	shade67>shade56	72.609617	7.897492333	1.4711915	5.3654377	8.08E-08	4.50E-05
MA_218285g0010	AT3G44050		P-loop containing nucleoside triphosphate hydrolase	shade67>shade56	82.801515	23.49644132	5.6822669	4.1347303	3.55E-05	0.004297

MA_4231108g0010	AT4G16970	Protein kinase superfamily protein;(source:Arabidopsis thaliana)	shade67>shade56	132.69181	23.24712591	5.8316618	3.9863638	6.71E-05	0.00702839	
MA_10426824g0010	AT4G17785	MYB DOMAIN PROTEIN 39 (MYB39)	Encodes a putative transcription factor (MYB39)	shade67>shade56	74.263519	2.386550787	0.5503552	4.3363827	1.45E-05	0.0021182
MA_10433704g0010	AT4G18550	DAD1-LIKE SEEDING ESTABLISHMENT	DSEL is cytosolic acylhydrolase that shows preference for DAD1	shade67>shade56	190.61376	2.085062526	0.3396734	6.1384327	8.33E-10	8.82E-07
MA_10428179g0010	AT4G19450	Major facilitator superfamily protein;(source:Arabidopsis thaliana)	shade67>shade56	415.5138	2.267466224	0.5375758	4.2179469	2.47E-05	0.00323386	
MA_12346g0010	AT4G23290	CYSTEINE-RICH RLK (RECEPTOR-LIKE KINASE)	Encodes a cysteine-rich receptor-like protein kinase	shade67>shade56	22.587358	21.92887916	3.1855846	6.883785	5.83E-12	1.64E-08
MA_178762g0010	AT4G23440	Disease resistance protein (TIR-NBS class);(source:Arabidopsis thaliana)	shade67>shade56	94.75764	30	5.8085164	5.16483	2.41E-07	0.000105	
MA_498754g0010	AT4G24130	DUF538 family protein (Protein of unknown function)	shade67>shade56	45.012723	2.359532685	0.5523136	4.2720886	1.94E-05	0.00266954	
MA_475302g0010	AT4G26090	RESISTANT TO P. SYRINGAE 2 (RPS2)	Encodes a plasma membrane protein with leucine-rich repeats	shade67>shade56	69.501895	18.84260247	3.8365974	4.9112795	9.05E-07	0.00021201
MA_5382714g0010	AT4G26330	UNFERTILIZED EMBRYO SAC 17 (UNF17)	Subtilisin-like serine endopeptidase family protein	shade67>shade56	217.52282	22.4460546	3.6951903	6.0743975	1.24E-09	1.20E-06
MA_9399920g0010	AT4G26740	SEED GENE 1 (ATS1)	Encodes caleosin, a 27-kDa protein found with caleosin	shade67>shade56	122.09961	9.820074023	2.017926	4.8664193	1.14E-06	0.00025446
MA_551848g0020	AT4G26970	ACONITASE 2 (ACO2)	Encodes an aconitase that can catalyze the conversion of aconitate to isocitrate	shade67>shade56	60.353095	24.89660816	5.8941381	4.2239608	2.40E-05	0.00318463
MA_7354451g0010	AT4G28250	EXPANSIN B3 (EXPB3)	putative beta-expansin/allergen protein. Nomenclature	shade67>shade56	143.08438	1.612388608	0.3690315	4.3692442	1.25E-05	0.00188536
MA_9930140g0010	AT4G30170	Peroxidase family protein;(source:Arabidopsis thaliana)	shade67>shade56	62.037677	21.58697676	4.2647119	5.0617667	4.15E-07	0.00015287	
MA_36985g0020	AT4G33300	ADR1-LIKE 1 (ADR1-L1)	Encodes a member of the ADR1 family nucleotide-binding domain	shade67>shade56	45.027778	8.91149957	2.2191578	4.0157124	5.93E-05	0.00639851
MA_501572g0010	AT4G33720	(ATCAPE3)	CAP (Cysteine-rich secretory proteins, Antigen processing)	shade67>shade56	178.30396	19.21367128	4.4740714	4.294449	1.75E-05	0.00244747
MA_15237g0010	AT4G34100	ECERIFERUM 9 (CER9)	Encodes a protein involved in cuticular wax biosynthesis	shade67>shade56	34.446299	20.08009195	4.3147584	4.6538161	3.26E-06	0.0005944
MA_10427611g0010	AT4G38190	CELLULOSE SYNTHASE LIKE D4 (CLSD4)	encodes a gene similar to cellulose synthase	shade67>shade56	70.581856	9.382576657	1.4742493	6.3643081	1.96E-10	2.62E-07
MA_27312g0010	AT5G02900	CYTOCHROME P450, FAMILY 96C	member of CYP96A	shade67>shade56	41.060459	24.59198292	5.1543598	4.7711033	1.83E-06	0.00037641
MA_10425930g0010	AT5G04895	ABA OVERLY SENSITIVE 6 (ABOG6)	DEA(D/H)-box RNA helicase family protein;(source:Arabidopsis thaliana)	shade67>shade56	167.21642	30	6.0068133	4.9943287	5.90E-07	0.00015401
MA_10238446g0010	AT5G05170	CONSTITUTIVE EXPRESSION OF	Encodes a cellulose synthase isomer. CESA3	shade67>shade56	166.18441	24.65722666	5.8904557	4.1859625	2.84E-05	0.00363066
MA_9328561g0010	AT5G05850	PLANT INTRACELLULAR RAS GTPase	Encodes PIRL1, a member of the Plant intracellular Ras GTPase	shade67>shade56	56.744221	30	6.0076142	4.9936629	5.92E-07	0.00015401
MA_422924g0010	AT5G06360	Ribosomal protein S8e family protein;(source:Arabidopsis thaliana)	shade67>shade56	99.352722	19.00542484	4.5153843	4.2090382	2.56E-05	0.00333958	
MA_9786598g0010	AT5G07580	(ERF106)	encodes a member of the ERF (ethylene response factor) family	shade67>shade56	57.692637	21.18347183	4.4742683	4.7345109	2.20E-06	0.00043835
MA_6332848g0010	AT5G08570	Pyruvate kinase family protein;(source:Arabidopsis thaliana)	shade67>shade56	61.577376	7.314099244	1.5687699	4.6623147	3.13E-06	0.00057784	
MA_10432569g0010	AT5G09970	CYTOCHROME P450, FAMILY 78C	member of CYP78A	shade67>shade56	399.65958	10.03243663	1.4394621	6.9695734	3.18E-12	9.61E-09
MA_8066361g0010	AT5G17540	HXXXD-type acyl-transferase family protein;(source:Arabidopsis thaliana)	shade67>shade56	70.935852	23.08690862	5.8129366	3.971643	7.14E-05	0.00729666	
MA_10192245g0010	AT5G17920	METHIONINE SYNTHESIS 1 (ATM1)	Encodes a cytosolic cobalamin-independent methionine synthase	shade67>shade56	120.13048	23.46768982	5.8905826	3.9839336	6.78E-05	0.00708316
MA_10428851g0010	AT5G18980	ARM repeat superfamily protein;(source:Arabidopsis thaliana)	shade67>shade56	300.34056	19.39280001	3.3221509	5.8374231	5.30E-09	3.94E-06	
MA_960556g0010	AT5G19930	PLASMA MEMBRANE GLUCOSE-RESPONSE	PGR is putative plasma membrane glucose-respon	shade67>shade56	111.16564	24.59536423	4.3200391	5.6933199	1.25E-08	8.24E-06
MA_121630g0010	AT5G20480	EF-TU RECEPTOR (EFR)	Encodes a predicted leucine-rich repeat receptor	shade67>shade56	26.649066	22.00904044	5.479014	4.016971	5.90E-05	0.00638073
MA_41345g0010	AT5G20950	(BGLC1)	Encodes a beta-glucosidase involved in xyloglucan	shade67>shade56	64.774986	9.855500114	1.8217342	5.409955	6.30E-08	3.61E-05
MA_10437273g0010	AT5G24080	Protein kinase superfamily protein;(source:Arabidopsis thaliana)	shade67>shade56	128.58433	25.06420688	5.8916771	4.2541718	2.10E-05	0.00281904	
MA_132981g0010	AT5G24760	GroES-like zinc-binding dehydrogenase family	shade67>shade56	11339.414	1.617442195	0.4114815	3.9307775	8.47E-05	0.00810721	
MA_10434521g0010	AT5G27100	GLUTAMATE RECEPTOR 2.1 (GLR2.1)	member of Putative ligand-gated ion channel	shade67>shade56	195.80201	27.11057913	5.3083363	5.1071706	3.27E-07	0.00012934
MA_510832g0010	AT5G33406	hAT dimerization domain-containing protein /	shade67>shade56	79.296602	3.724433237	0.8859067	4.2040921	2.62E-05	0.00340297	
MA_8760260g0010	AT5G36930	Disease resistance protein (TIR-NBS-LRR class)	shade67>shade56	35.361848	23.57751423	5.8966228	3.9984776	6.38E-05	0.00672822	
MA_494813g0010	AT5G39320	UDP-GLUCOSE DEHYDROGENASE	UDP-glucose 6-dehydrogenase family protein;(source:Arabidopsis thaliana)	shade67>shade56	118.97449	21.89497984	4.3769355	5.0023537	5.66E-07	0.00015401
MA_183130g0020	AT5G44030	CELLULOSE SYNTHASE A4 (CESA4)	Encodes a cellulose synthase involved in secondary cell wall	shade67>shade56	130.7649	18.39774898	4.2813283	4.2972058	1.73E-05	0.00244001
MA_10428737g0010	AT5G44380	(ATBBE28)	FAD-binding Berberine family protein;(source:Arabidopsis thaliana)	shade67>shade56	93.64181	23.02795435	4.4935545	5.1246635	2.98E-07	0.00012247
MA_986218g0010	AT5G44700	GASSHO 2 (GSO2)	Encodes GASSHO2 (GSO2), a putative leucine-rich repeat	shade67>shade56	165.23896	21.02946968	4.4369235	4.7396512	2.14E-06	0.0004294
MA_10319538g0010	AT5G45370	USUALLY MULTIPLE ACIDS MOVING	nodulin MtN21-like transporter family protein	shade67>shade56	17.447841	14.92039355	3.6351066	4.1045272	4.05E-05	0.00477606
MA_90634g0010	AT5G46610	aluminum activated malate transporter family	shade67>shade56	64.971654	7.108339214	1.802015	3.9446614	7.99E-05	0.00785557	
MA_83446g0020	AT5G50400	PURPLE ACID PHOSPHATASE 27	purple acid phosphatase 27;(source:Arabidopsis thaliana)	shade67>shade56	317.71611	21.33455177	3.4619624	6.1625602	7.16E-10	7.77E-07
MA_321195g0010	AT5G51780	basic helix-loop-helix (bHLH) DNA-binding superfamily	shade67>shade56	168.47283	12.79658274	2.427048	5.2724885	1.35E-07	6.64E-05	
MA_39500g0010	AT5G53470	ACYL-COA BINDING PROTEIN 1 (ACBP1)	Encodes an acyl-CoA binding protein that is located in the	shade67>shade56	109.56587	1.789931901	0.3968894	4.509901	6.49E-06	0.00109794
MA_766568g0010	AT5G54930	METABOLIC NETWORK MODULATOR	AT hook motif-containing protein;(source:Arabidopsis thaliana)	shade67>shade56	81.183942	10.29709703	2.5140508	4.0958189	4.21E-05	0.00493173
MA_10426326g0020	AT5G55090	MITOGEN-ACTIVATED PROTEIN	member of MEKK subfamily	shade67>shade56	233.8183	9.34552367	1.3981422	6.6842442	2.32E-11	4.82E-08
MA_10428846g0020	AT5G55250	IAA CARBOXYLMETHYLTRANSFERASE	Encodes an enzyme which specifically converts IAA-Me to IAA	shade67>shade56	48.710255	17.97497551	3.8356595	4.6862803	2.78E-06	0.0005233
MA_10426320g0010	AT5G56960	basic helix-loop-helix (bHLH) DNA-binding family	shade67>shade56	94.262969	23.53511908	5.4073855	4.3524027	1.35E-05	0.00199954	
MA_10434319g0010	AT5G58360	OVATE FAMILY PROTEIN 3 (OPF3)	ovate family protein 3;(source:Arabidopsis thaliana)	shade67>shade56	177.21754	1.223426997	0.2913975	4.1984811	2.69E-05	0.00347772
MA_5587g0010	AT5G60700	glycosyltransferase family protein 2;(source:Arabidopsis thaliana)	shade67>shade56	186.46586	1.205843312	0.3092628	3.8990898	9.66E-05	0.00892206	
MA_92381g0010	AT5G64140	RIBOSOMAL PROTEIN S28 (RPS28)	Encodes a putative ribosomal protein S28.	shade67>shade56	121.24359	23.74769686	5.7573079	4.1247919	3.71E-05	0.00443618
MA_261256g0010	AT5G64570	BETA-D-XYLOSIDASE 4 (XYL4)	Encodes a beta-d-xylosidase that belongs to family 4	shade67>shade56	41.297439	22.53010886	5.4595113	4.1267629	3.68E-05	0.00442333

Table S2 Genes for which the levels of expression were significantly higher in the 56°N population as compared to the 67°N population in response to SHADE in Norway spruce

Gene_ID	TAIR	Primary Gene Symbol	Gene Model Description	Expression	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
MA_10325260g0010	AT1G04580	ALDEHYDE OXIDASE 4 (AO4)	Encodes aldehyde oxidase AA04 preferentially	shade67<shade56	81.315393	-22.88013074	5.8918542	-3.88335	0.00010303	0.00941731
MA_35645g0010	AT1G05200	GLUTAMATE RECEPTOR 3.4 (GLR3.4)	Encodes a putative glutamate receptor GLR3 w	shade67<shade56	272.51679	-25.55209379	4.2803869	-5.969576	2.38E-09	1.91E-06
MA_355745g0010	AT1G05270		TraB family protein;(source:Araport11)	shade67<shade56	214.99011	-12.54145848	2.4921623	-5.03236	4.84E-07	0.00015401
MA_213682g0010	AT1G06640		encodes a protein whose sequence is similar to	shade67<shade56	210.29368	-23.77830423	5.8901633	-4.036952	5.42E-05	0.00599576
MA_10427341g0010	AT1G07650		Leucine-rich repeat transmembrane protein kin	shade67<shade56	2798.077	-3.098507079	0.7826282	-3.959105	7.52E-05	0.00761091
MA_496233g0010	AT1G1180	SECRETORY CARRIER MEMBRAN	Secretory carrier membrane protein (SCAMP) f	shade67<shade56	464.85582	-4.803988131	0.7783166	-6.17228	6.73E-10	7.50E-07
MA_10435231g0010	AT1G12860	SCREAM 2 (SCRM2)	Encodes ICE2 (Inducer of CBF Expression 2), a t	shade67<shade56	1036.0692	-2.995103713	0.7645977	-3.917321	8.95E-05	0.00840214
MA_447489g0010	AT1G15100	RING-H2 FINGER A2A (RHA2A)	Encodes a putative RING-H2 finger protein RHA	shade67<shade56	2475.4907	-2.089481029	0.5191656	-4.024691	5.71E-05	0.00619083
MA_1026335g0020	AT1G15780	NON-RECOGNITION-OF-BTH 4 (N	mediator of RNA polymerase II transcription su	shade67<shade56	34.011685	-23.05216854	5.5165931	-4.178697	2.93E-05	0.00369282
MA_10431686g0010	AT1G18090		5-3 exonuclease family protein;(source:Arapor	shade67<shade56	133.77856	-1.707936457	0.3775515	-4.523718	6.08E-06	0.00104411
MA_3340g0010	AT1G20510	OPC-8:0 COA LIGASE1 (OPCL1)	OPC-8:0 CoA ligase1;(source:Araport11)	shade67<shade56	73.538753	-30	6.0072541	-4.993962	5.92E-07	0.00015401
MA_7115g0010	AT1G22640	MYB DOMAIN PROTEIN 3 (MYB3)	MYB-type transcription factor (MYB3) that rep	shade67<shade56	172.44193	-23.14887515	5.8902415	-3.930038	8.49E-05	0.00811381
MA_939384g0010	AT1G26500		Pentatricopeptide repeat (PPR) superfamily pr	shade67<shade56	76.036931	-23.46362023	5.8912287	-3.982806	6.81E-05	0.00709934
MA_15946g0010	AT1G30220	INOSITOL TRANSPORTER 2 (INT2)	Inositol transporter presenting conserved extra	shade67<shade56	338.30772	-19.37093044	4.3878454	-4.414679	1.01E-05	0.00158504
MA_10433153g0020	AT1G30290		unknown protein	shade67<shade56	262.51475	-27.08410624	4.3695575	-6.198364	5.71E-10	6.71E-07
MA_9974774g0010	AT1G32300	L -GULONOL-1,4-LACTONE (L -GU	D-arabinono-1,4-lactone oxidase family protei	shade67<shade56	59.887848	-20.72426353	4.3067491	-4.812043	1.49E-06	0.00031613
MA_10432360g0020	AT1G37130	NITRATE REDUCTASE 2 (NIA2)	Identified as a mutant resistant to chlorate. En	shade67<shade56	1268.3351	-1.297015908	0.25408	-5.104754	3.31E-07	0.00012979
MA_19887g0010	AT1G48500	JASMONATE-ZIM-DOMAIN PRO	jasmonate-zim-domain protein 4;(source:Arap	shade67<shade56	22.796923	-30	6.0105393	-4.991233	6.00E-07	0.00015401
MA_86183g0010	AT1G54200	BIG GRAIN 3 (BG3)	DNA mismatch repair Msh6-like protein;(sourc	shade67<shade56	296.12841	-3.275875616	0.7906427	-4.143307	3.42E-05	0.00416318
MA_564894g0010	AT1G55910	ZINC TRANSPORTER 11 PRECUR	member of Putative zinc transporter ZIP2 - like	shade67<shade56	182.443	-8.543741989	1.4440798	-5.916392	3.29E-09	2.58E-06
MA_464469g0010	AT1G56120		Leucine-rich repeat transmembrane protein kin	shade67<shade56	43.755794	-21.51556729	4.4004257	-4.889429	1.01E-06	0.00023135
MA_401306g0010	AT1G61065		1,3-beta-glucan synthase component (DUF121	shade67<shade56	232.08101	-24.50516034	5.8901333	-4.160375	3.18E-05	0.00389277
MA_16626g0010	AT1G61250	SECRETORY CARRIER 3 (SC3)	Encodes a putative secretory carrier membran	shade67<shade56	444.83114	-2.131529526	0.5017083	-4.248544	2.15E-05	0.00288164
MA_167711g0010	AT1G64680		beta-carotene isomerase D27;(source:Araport2	shade67<shade56	3312.6325	-1.089032164	0.2432001	-4.477872	7.54E-06	0.00122246
MA_38922g0010	AT1G71050	HEAVY METAL ASSOCIATED ISO	Heavy metal transport/detoxification superfam	shade67<shade56	323.46382	-9.342012204	2.2831081	-4.091796	4.28E-05	0.00497479
MA_10180304g0010	AT1G72840		Disease resistance protein (TIR-NBS-LRR class)	shade67<shade56	165.28471	-24.62843545	5.6158972	-4.385499	1.16E-05	0.00178087
MA_10370672g0010	AT1G77460	CELLULOSE SYNTHASE INTERAC	Encodes a plasma membrane, microtubule ass	shade67<shade56	31.994045	-4.57047869	1.000288	-4.529582	5.91E-06	0.00101675
MA_441084g0010	AT1G77840		Translation initiation factor IF2/IF5;(source:Ara	shade67<shade56	367.29826	-24.06317044	5.8899652	-4.085452	4.40E-05	0.00509509
MA_14341g0010	AT1G78020	FCS LIKE ZINC FINGER 6 (FLZ6)	FCS like zinc finger 6 is induced during energ	shade67<shade56	412.05258	-11.32909104	1.5438017	-7.338437	2.16E-13	1.83E-09
MA_587505g0010	AT1G79620	VASCULAR-RELATED RLK 1 (VRL	VRK1 is a LRR kinase involved in switching bet	shade67<shade56	16.397498	-8.007723581	1.7295361	-6.429984	3.66E-06	0.00065858
MA_8433628g0010	AT2G01610		Plant invertase/pectin methyltransferase inhibi	shade67<shade56	47.351166	-22.33584837	5.3966668	-4.138823	3.49E-05	0.00423322
MA_8300751g0010	AT2G04570		GDSL-motif esterase/acyltransferase/lipase. Er	shade67<shade56	61.237582	-18.88374371	3.705427	-5.09624	3.46E-07	0.00013233
MA_10429950g0020	AT2G13540	ABA HYPERSENSITIVE 1 (ABH1)	Encodes a nuclear cap-binding protein that for	shade67<shade56	357.93022	-3.055303903	0.7643503	-3.997256	6.41E-05	0.0067462
MA_349646g0010	AT2G14080		Disease resistance protein (TIR-NBS-LRR class)	shade67<shade56	101.04164	-11.15758155	1.5849578	-7.039671	1.93E-12	6.54E-09
MA_17793g0010	AT2G16850	PLASMA MEMBRANE INTRINSIC	plasma membrane intrinsic protein 2;(source:A	shade67<shade56	62.714376	-24.34183127	5.9383296	-4.130053	3.63E-05	0.00437292
MA_8866128g0010	AT2G17570	CIS-PRENYLTRANSFERASE 1 (CP	Undecaprenyl pyrophosphate synthetase famil	shade67<shade56	486.50293	-3.685883792	0.8846408	-4.166531	3.09E-05	0.00383343
MA_5951905g0010	AT2G18050	HISTONE H1-3 (H1S1-3)	encodes a structurally divergent linker histone	shade67<shade56	236.99984	-26.56529095	5.8901749	-4.510102	6.48E-06	0.00109794
MA_346860g0010	AT2G19130		S-locus lectin protein kinase family protein;(so	shade67<shade56	207.98178	-2.253851841	0.3374051	-6.679957	2.39E-11	4.82E-08
MA_63882g0010	AT2G19790	ADAPTOR PROTEIN COMPLEX 4	Encodes a component of the AP4 complex and	shade67<shade56	224.03066	-21.39560558	4.2691118	-5.011723	5.39E-07	0.00015401
MA_266310g0010	AT2G23910		NAD(P)-binding Rossmann-fold superfamily pr	shade67<shade56	449.84823	-2.093146683	0.484531	-5.072523	2.54E-06	0.00048775
MA_10431396g0010	AT2G26490	JINGUBANG (JGB)	JGB contains seven WD40 repeats and is highl	shade67<shade56	17.775076	-24.01944223	5.9027062	-4.069225	4.72E-05	0.00535193
MA_780853g0010	AT2G28160	FER-LIKE IRON DEFICIENCY INDU	Encodes a putative transcription factor that reg	shade67<shade56	68.760449	-24.30070684	5.5800542	-4.354923	1.33E-05	0.00198363
MA_9765350g0010	AT2G28800	ALBINO 3 (ALB3)	member of Chloroplast membrane protein ALB	shade67<shade56	180.19431	-26.40437984	5.8904643	-4.482563	7.38E-06	0.00120048
MA_206815g0010	AT2G29690	ANTHRANILATE SYNTHASE 2 (AS	Encode a functional anthranilate synthase prot	shade67<shade56	140.64084	-1.878720942	0.4452341	-4.219625	2.45E-05	0.00322627
MA_279076g0010	AT2G30933		Carbohydrate-binding X8 domain superfamily	shade67<shade56	57.035001	-19.49922833	4.3004765	-4.534202	5.78E-06	0.00100058
MA_10436215g0020	AT2G31750	UDP-GLUCOSYL TRANSFERASE 7	Encodes an auxin glycosyltransferase that is lik	shade67<shade56	305.02062	-12.53572629	2.8605809	-4.382231	1.17E-05	0.00180033
MA_564534g0010	AT2G31900	MYOSIN-LIKE PROTEIN XI(F) (XIF	Encodes an novel myosin isoform.	shade67<shade56	76.765086	-10.83403494	2.767198	-3.915262	9.03E-05	0.00843675
MA_1160818g0020	AT2G32850		Protein kinase superfamily protein;(source:Ara	shade67<shade56	88.015676	-21.26675086	4.2646005	-4.98681	6.14E-07	0.00015463
MA_960018g0020	AT2G34050		ATP synthase F1 complex assembly factor;(sou	shade67<shade56	371.48094	-13.99385857	2.3307011	-6.004141	1.92E-09	1.66E-06
MA_834070g0010	AT2G35340		Zinc finger C-x8-C-x5-C-x3-H-type family protei	shade67<shade56	89.347434	-21.25102673	4.3980546	-4.831915	1.35E-06	0.00028904
MA_10351640g0010	AT2G35800	S-ADENOSYL METHIONINE TRAN	Encodes a predicted calcium-dependent S-ade	shade67<shade56	41.524372	-23.62600107	4.2967167	-5.498617	3.83E-08	2.31E-05
MA_122962g0010	AT2G38120	AUXIN RESISTANT 1 (AUX1)	Encodes an auxin influx transporter. AUX1 res	shade67<shade56	592.19336	-1.797521412	0.3642197	-4.935267	8.00E-07	0.00019484
MA_95687g0010	AT2G38940	PHOSPHATE TRANSPORTER 1;4	Encodes Pht1;4, a member of the Pht1 family c	shade67<shade56	134.32187	-25.46575205	5.793003	-4.321354	1.55E-05	0.00223228
MA_1042839480	AT2G39480	ATP-BINDING CASSETTE B6 (ABC	P-glycoprotein 6;(source:Araport11)	shade67<shade56	46.515492	-9.455428442	1.7703551	-5.340979	2.94E-08	5.08E-05
MA_4183720g0010	AT2G40610	EXPANSIN A8 (EXPA8)	member of Alpha-Expansin Gene Family. Nami	shade67<shade56	61.370234	-23.02511844	5.8923518	-3.907628	9.32E-05	0.00866945
MA_634100g0010	AT2G42360		RING/U-box superfamily protein;(source:Arapo	shade67<shade56	174.80972	-23.15469167	5.7896012	-3.999359	6.35E-05	0.00672822
MA_3206652g0010	AT2G42850	CYTOCHROME P450, FAMILY 71	cytochrome P450, family 718;(source:Araport1	shade67<shade56	42.720765	-30	5.3576359	-5.599485	2.15E-08	1.38E-05
MA_253584g0010	AT2G45550	CYTOCHROME P450, FAMILY 76	member of CYP76C	shade67<shade56	156.33341	-3.129882756	0.7288422	-4.294321	1.75E-05	0.00244747
MA_10427075g0010	AT2G45560	CYTOCHROME P450, FAMILY 76	cytochrome P450 monooxygenase	shade67<shade56	59.97644	-2.642012325	0.4197184	-6.294726	3.08E-10	3.72E-07
MA_1925g0010	AT2G48130	(LTPG15)	Encodes a plasma membrane-localized glycos	shade67<shade56	196.7309	-1.606474795	0.3603114	-4.458573	8.25E-06	0.00132264
MA_7555671g0010	AT3G02470	S-ADENOSYLMETHIONINE DECA	Encodes a S-adenosylmethionine decarboxylas	shade67<shade56	91.999685	-22.6108394	5.6409809	-4.008317	6.12E-05	0.00652739
MA_80461g0010	AT3G04220		Disease resistance protein (TIR-NBS-LRR class)	shade67<shade56	39.54445	-30	6.0078069	-4.993503	5.93E-07	0.00015401
MA_909045g0010	AT3G07880	SUPERCENTIPEDE1 (SCN1)	RhoGTPase GDP dissociation inhibitor (RhoGDI	shade67<shade56	96.913487	-21.61953728	4.3552138	-4.964059	6.90E-07	0.00016986
MA_10429484g0010	AT3G14075		Mono-/di-acylglycerol lipase, N-terminal;(sour	shade67<shade56	60.455908	-23.47161132	5.8943013	-3.982085	6.83E-05	0.00710304
MA_5681263g0010	AT3G14360	OIL BODY LIPASE 1 (ATOBL1)	alpha/beta-Hydrolases superfamily protein;(so	shade67<shade56	146.95975	-21.7894401	3.6013222	-6.0504	1.44E-09	1.32E-06
MA_403867g0010	AT3G14820		GDSL-motif esterase/acyltransferase/lipase. Er	shade67<shade56	239.45738	-26.41920125	5.893083	-4.483087	7.36E-06	0.00120048
MA_16493g0010	AT3G16520	UDP-GLUCOSYL TRANSFERASE 8	UDP-glucosyl transferase 88A1;(source:Arapor	shade67<shade56	195.61151	-27.88664738	5.8930942	-4.732089	2.22E-06	0.00044153
MA_9959752g0010	AT3G20630	UBIQUITIN-SPECIFIC PROTEASE	Encodes a ubiquitin-specific protease. Identica	shade67<shade56	65.003028	-30	6.0070734	-4.994112	5.91E-07	0.00015401
MA_10428105g0010	AT3G22060		contains Pfam profile: PF01657 Domain of unk	shade67<shade56	46.626838	-18.84022474	3.4184677	-5.511307	3.56E-08	2.18E-05
MA_10367103g0010	AT3G22220		hAT transposon superfamily;(source:Araport11	shade67<shade56	206.49539	-23.52400821	3.6648839	-6.418759	1.37E-10	2.15E-07
MA_51552g0010	AT3G24503	ALDEHYDE DEHYDROGENASE 20	Arabidopsis thaliana aldehyde dehydrogenase	shade67<shade56	45.01806	-22.24427383	4.4359404	-5.014557	5.32E-07	0.00015401
MA_12314g0010	AT3G28917	MINI ZINC FINGER 2 (MIF2)	mini zinc finger 2;(source:Araport11)	shade67<shade56	123.11633	-13.05871064	3.2825001	-3.978282	6.94E-05	0.0071539
MA_10426995g0010	AT3G33550		GDSL-motif esterase/acyltransferase/lipase. Er	shade67<shade56	139.89151	-23.49012238	5.4596462	-4.302499	1.69E-05	0.00239039
MA_10428913g0020	AT3G44630		Disease resistance protein (TIR-NBS-LRR class)	shade67<shade56	41.32858	-3.62680913	0.895874	-4.048347	5.16E-05	0.00577497
MA_9820002g0010	AT3G45970	EXPANSIN-LIKE A1 (EXLA1)	member of EXPANSIN-LIKE. Naming convention	shade67<shade56	135.18542	-23.59508938	5.8868045	-4.008132	6.12E-05	0.00652739
MA_4364416g0010	AT3G4652									

MA_111976g0010	AT4G04970	GLUCAN SYNTHASE-LIKE 1 (GSL1)	encodes a gene similar to callose synthase The	shade67<shade56	111.36636	-4.093241089	0.7300074	-5.607123	2.06E-08	1.34E-05
MA_169781g0010	AT4G09340		SPLA/Ryanodine receptor (SPRY) domain-conta	shade67<shade56	55.161341	-19.17770461	4.0645158	-4.718325	2.38E-06	0.00046377
MA_10435813g0010	AT4G10310	HIGH-AFFINITY K+ TRANSPORTER	encodes a sodium transporter (HKT1) expresse	shade67<shade56	325.95917	-22.18232556	3.1536734	-7.033806	2.01E-12	6.54E-09
MA_179643g0010	AT4G10500	DMR6-LIKE OXYGENASE 1 (DLO1)	2-oxoglutarate (2OG) and Fe(II)-dependent oxy	shade67<shade56	377.3487	-12.92130221	2.8225575	-4.57787	4.70E-06	0.00083178
MA_58710g0010	AT4G10550		Subtilase family protein;(source:Araport11)	shade67<shade56	284.90435	-1.187277451	0.3004241	-3.952005	7.75E-05	0.00778006
MA_423032g0010	AT4G10780		LRR and NB-ARC domains-containing disease re	shade67<shade56	327.37919	-15.04072897	3.6782994	-4.089044	4.33E-05	0.00500861
MA_92659g0010	AT4G18390	TEOSINTE BRANCHED 1, CYCLOPEPTIDE	TEOSINTE BRANCHED 1, cycloidea and PCF tran	shade67<shade56	81.598303	-22.31837131	4.4340774	-5.033374	4.82E-07	0.00015401
MA_456473g0010	AT4G23140	CYSTEINE-RICH RLK (RECEPTOR-LIKE KINASE)	Arabidopsis thaliana receptor-like protein kin	shade67<shade56	98.792615	-19.52952353	4.4650202	-4.373894	1.22E-05	0.00185801
MA_945672g0010	AT4G23340		2-oxoglutarate (2OG) and Fe(II)-dependent oxy	shade67<shade56	172.16112	-24.69937417	5.8902701	-4.19325	2.75E-05	0.00353428
MA_128616g0010	AT4G26050	PLANT INTRACELLULAR RAS GTPase	Encodes PIRL8, a member of the Plant Intracell	shade67<shade56	96.865151	-25.06625578	5.8910747	-4.254955	2.09E-05	0.00281814
MA_17530g0010	AT4G26890	MITOGEN-ACTIVATED PROTEIN KINASE	member of MEKK subfamily	shade67<shade56	338.17932	-24.49086995	5.8898861	-4.158123	3.21E-05	0.00391345
MA_31254g0010	AT4G28200		U3 small nucleolar RNA-associated-like protein	shade67<shade56	114.00041	-20.96888821	4.4917221	-4.668341	3.04E-06	0.0005661
MA_5708g0010	AT4G32300	S-DOMAIN-2 5 (SD2-5)	S-domain-2 5;(source:Araport11)	shade67<shade56	205.36017	-12.85435167	2.6516443	-4.847691	1.25E-06	0.0002739
MA_96242g0010	AT4G34160	CYCLIN D3;1 (CYCD3;1)	encodes a cyclin D-type protein involved in the	shade67<shade56	28.327684	-30	6.0098127	-4.991836	5.98E-07	0.00015401
MA_13722g0010	AT4G37520	TRANSPARENT TESTA 7 (TT7)	Peroxidase superfamily protein;(source:Arapor	shade67<shade56	129.64975	-21.47274279	4.4832093	-4.789592	1.67E-06	0.00034841
MA_10357974g0010	AT4G38070		transcription factor bHLH131-like protein;(sour	shade67<shade56	147.69388	-2.410789851	6.0004615	-0.014895	5.95E-05	0.00640439
MA_351763g0010	AT5G02230		Haloacid dehalogenase-like hydrolase (HAD) su	shade67<shade56	75.443171	-18.97876163	3.3107345	-5.732943	9.90E-09	6.76E-06
MA_19871g0020	AT5G02960		Ribosomal protein S12/S23 family protein;(sou	shade67<shade56	188.10599	-25.08343565	5.8905345	-4.258261	2.06E-05	0.00278748
MA_96757g0010	AT5G05340	PEROXIDASE 52 (PRX52)	Encodes a protein with sequence similarity to p	shade67<shade56	157.26187	-1.263494658	0.3037252	-4.159993	3.18E-05	0.00389277
MA_10280064g0010	AT5G07990	TRANSPARENT TESTA 7 (TT7)	Required for flavonoid 3' hydroxylase activity.	shade67<shade56	591.00163	-2.52383258	0.6503736	-3.880589	0.0001042	0.0094839
MA_10308567g0040	AT5G08020	RPA70-KDA SUBUNIT B (RPA70B)	Encodes a homolog of Replication Protein A. rp	shade67<shade56	235.74736	-1.878923288	0.3928419	-4.782899	1.73E-06	0.0003567
MA_93721g0020	AT5G09810	ACTIN 7 (ACT7)	Member of Actin gene family.Mutants are defe	shade67<shade56	86.773394	-30	5.4063976	-5.548981	2.87E-08	1.79E-05
MA_9106g0010	AT5G13700	POLYAMINE OXIDASE 1 (PAO1)	Encodes a protein with polyamine oxidase acti	shade67<shade56	133.92391	-24.89671027	5.8905269	-4.226568	2.37E-05	0.00315788
MA_73048g0010	AT5G15780		Pollen Ole e 1 allergen and extensin family prot	shade67<shade56	3059.7929	-2.976854627	0.682619	-4.360931	1.30E-05	0.00193675
MA_7491716g0010	AT5G17680		disease resistance protein (TIR-NBS-LRR class);	shade67<shade56	155.4035	-21.7115806	5.5174828	-3.935052	8.32E-05	0.0080187
MA_8256257g0010	AT5G20680	TRICHOME BIREFRINGENCE-LIKE 1 (TBL1)	Encodes a member of the TBL (TRICHOME BIRE	shade67<shade56	223.31806	-22.76446823	4.6127576	-4.93511	8.01E-07	0.00019484
MA_95738g0010	AT5G20700		senescence-associated family protein, putative	shade67<shade56	104.26097	-4.201242853	0.89282	-4.705588	2.53E-06	0.00048775
MA_19854g0020	AT5G21960		encodes a member of the DREB subfamily A-5	shade67<shade56	36.547943	-21.52738551	5.5151606	-3.903311	9.49E-05	0.008787
MA_10434800g0010	AT5G23230	NICOTINAMIDASE 2 (NIC2)	nicotinamidase 2;(source:Araport11)	shade67<shade56	23.253605	-16.06965962	3.6305816	-4.426194	9.59E-06	0.00152023
MA_59443g0010	AT5G26220	GAMMA-GLUTAMYL CYCLOTRANSFERASE 16 (WRKY16)	ChC-like family protein;(source:Araport11)	shade67<shade56	522.51603	-6.937424699	0.9367568	-7.40579	1.30E-13	1.83E-09
MA_7706481g0010	AT5G45050		Encodes a member of the WRKY Transcription	shade67<shade56	78.771933	-11.19808893	2.3505736	-4.763981	1.90E-06	0.0003862
MA_10434773g0030	AT5G47500	PECTIN METHYLESTERASE 5 (PM5)	predicted to encode a pectin methylesterase	shade67<shade56	31.715567	-18.86120083	3.5596116	-5.298668	1.17E-07	5.95E-05
MA_9957075g0010	AT5G48930	HYDROXYCINNAMOYL-COA SHIKIMATE 3-HYDROXYLASE	At5g48930 has been shown to encode for the	shade67<shade56	22.009697	-30	6.0103004	-4.991431	5.99E-07	0.00015401
MA_29890g0010	AT5G49890	CHLORIDE CHANNEL C (CLC-C)	member of Anion channel protein family	shade67<shade56	191.2228	-22.09201482	3.634185	-6.078946	1.21E-09	1.19E-06
MA_838949g0010	AT5G53350	CLP PROTEASE REGULATORY SUBUNIT 1 (CLPR1)	CLP protease regulatory subunit CLPX mRNA, n	shade67<shade56	206.92373	-10.40859199	2.6518131	-3.925085	8.67E-05	0.00824038
MA_652482g0010	AT5G55490	GAMETE EXPRESSED PROTEIN 1 (GEP1)	Encodes a transmembrane domain containing	shade67<shade56	61.204977	-24.14644217	5.8929358	-4.097523	4.18E-05	0.00409917
MA_10153873g0010	AT5G56150	UBIQUITIN-CONJUGATING ENZYME 30 (UBC30)	ubiquitin-conjugating enzyme 30;(source:Arap	shade67<shade56	135.84427	-20.51991807	4.4386793	-4.622978	3.78E-06	0.00067834
MA_23239g0010	AT5G58490		NAD(P)-binding Rossmann-fold superfamily pro	shade67<shade56	492.44562	-1.143730454	0.2256147	-5.069397	3.99E-07	0.00014815
MA_83574g0010	AT5G59970		Histone superfamily protein;(source:Araport11)	shade67<shade56	223.28613	-25.64928987	3.5723895	-7.179869	6.98E-13	3.03E-09
MA_3003293g0010	AT5G60390	(EF1ALPHA)	GTP binding Elongation factor Tu family protei	shade67<shade56	52.962014	-22.97246948	5.8933811	-3.898012	9.70E-05	0.00894233
MA_183219g0010	AT5G63960	GIGANTEA SUPPRESSOR5 (GIS5)	Encodes the catalytic subunits of DNA polymer	shade67<shade56	72.570338	-23.25206085	5.7098909	-4.072243	4.66E-05	0.00529725
MA_10437110g0010	AT5G64790		O-Glycosyl hydrolases family 17 protein;(sourc	shade67<shade56	11.086688	-30	6.0115883	-4.990362	6.03E-07	0.00015401
MA_205355g0010	AT5G64950	MITOCHONDRIAL TRANSCRIPTOMER 1 (MTM1)	mTERF family protein which functions in the re	shade67<shade56	69.227533	-24.0330073	5.8934183	-4.07794	4.54E-05	0.00519707
MA_10238024g0010	AT5G66580		hypothetical protein;(source:Araport11)	shade67<shade56	13.514632	-30	6.0106723	-4.991122	6.00E-07	0.00015401
MA_904305g0010	AT4G02750		Tetratricopeptide repeat (TPR)-like superfamily	shade67<shade56	99.713923	-1.960704561	0.4126041	-4.752024	2.01E-06	0.00040586

Table S3 Allele and genotype frequencies of missense mutations in the nine candidate DEGs in response to SHADE in Norway spruce that show cline

Gene name	SNP	Gene_ID	Reference allele frequency p-value	Alternate allele frequency p-value	Genotype frequency p-value
MYB3	T132R	MA_7115g0010	C: 2.98E-40	G: 1.64E-06	4.77E-52
LOV1	R156K	MA_16619g0010	G: 0.424181	A: 0.139508	8.94E-07
LOV1	D190N	MA_16619g0010	G: 0.036124	A: 0.016444	8.78E-11
SCRM2	T208M	MA_10435231g0010	C: 7.00E-11	T: 0.017001	3.59E-29
SCRM2	S238N	MA_10435231g0010	G: 2.38E-20	A: 0.014526	2.64E-39
TCP2	F4S	MA_92659g0010	T: 0.000215	C: 4.47E-27	9.13E-38
TCP2	V25A	MA_92659g0010	T: 6.18E-07	C: 7.93E-11	1.87E-12
TCP2	E32G	MA_92659g0010	A: 5.11E-07	G: 5.81E-11	1.31E-12
TCP2	E51K	MA_92659g0010	G: 3.03E-23	A: 0.001302	6.37E-36
TCP2	I53F	MA_92659g0010	A: 0.001336	T: 1.93E-22	5.44E-34
NAC036	D206E	MA_101849g0010	T: 8.36E-05	A: 3.48E-09	1.13E-09
NAC036	T237M	MA_101849g0010	C: 0.758596	T: 0.090354	0.008645
EXPB3	K3R	MA_7354451g0010	A: 1.14E-06	G: 0.358795	4.10E-09
EXPB3	R6S	MA_7354451g0010	G: 4.67E-11	T: 0.317117	4.71E-16
EXPB3	C32R	MA_7354451g0010	T: 3.02E-09	C: 3.02E-09	3.02E-09
FLZ6	L88V	MA_14341g0010	C: 7.35E-06	G: 0.434854	8.07E-10
VRLK1	A265V	MA_587505g0010	C: 0.160674	T: 0.005841	0.001393
VRLK1	V283L	MA_587505g0010	G: 1.85E-07	C: 0.020671	4.64E-08
RPS2	S123N	MA_475302g0010	G: 1.24E-27	A: 0.35738	1.36E-37
RPS2	E166A	MA_475302g0010	A: 1.43E-22	C: 0.590028	2.69E-29

Significant p-values (p-value<0.05) are in bold

Table S4 Tukey's post-hoc test for genotype frequencies of missense mutations in the nine candidate DEGs in response to SHADE in Norway spruce that show cline

Gene name	SNP	Gene_ID	Tukey's p-value S1 vs S2	Bonferroni p-value S1 vs S2	Tukey's p-value S1 vs S3	Bonferroni p-value S1 vs S3	Tukey's p-value S1 vs S4	Bonferroni p-value S1 vs S4	Tukey's p-value S1 vs S5	Bonferroni p-value S1 vs S5	Tukey's p-value S1 vs S6	Bonferroni p-value S1 vs S6	Tukey's p-value S2 vs S3	Bonferroni p-value S2 vs S3	Tukey's p-value S2 vs S4	Bonferroni p-value S2 vs S4	Tukey's p-value S2 vs S5	Bonferroni p-value S2 vs S5	Tukey's p-value S2 vs S6	Bonferroni p-value S2 vs S6	Tukey's p-value S3 vs S4	Bonferroni p-value S3 vs S4	Tukey's p-value S3 vs S5	Bonferroni p-value S3 vs S5	Tukey's p-value S3 vs S6	Bonferroni p-value S3 vs S6	Tukey's p-value S4 vs S5	Bonferroni p-value S4 vs S5	Tukey's p-value S4 vs S6	Bonferroni p-value S4 vs S6	Tukey's p-value S5 vs S6	Bonferroni p-value S5 vs S6
MYB3_1132R	T132R	MA_7115g0010	0.9	4.438543	0.3809	0.7933012	0.00101	8.41E-07	0.00101	0.00E+00	0.00101	0.00E+00	0.89999	5.5308979	0.00101	0.0002866	0.00101	0.00E+00	0.00101	0.00E+00	0.01416	0.0167036	0.00101	9.99E-15	0.00101	0.00E+00	0.00101	0.0001467	0.001	1.44E-08	0.03717	0.047318
LOV1_R156K	R156K	MA_16619g0010	0.7743	3.0534676	0.89999	9.9629893	0.89999	8.96E+00	0.53796	1.39E+00	0.00101	1.58E-06	0.89999	6.6357244	0.89999	7.0910793	0.89999	1.37E+01	0.00137	1.46E-03	0.89999	14.124039	0.89999	4.60E+00	0.00101	8.42E-05	0.89999	4.9076422	0.001	5.80E-05	0.00101	5.79E-05
LOV1_D190N	D190N	MA_16619g0010	0.6904	2.3489015	0.89999	10.477417	0.21985	3.78E-01	0.00101	4.49E-04	0.00101	1.92E-09	0.89999	5.1359826	0.89999	6.2452656	0.18041	2.95E-01	0.00101	1.80E-05	0.51207	1.2670546	0.01062	1.23E-02	0.00101	2.59E-07	0.74445	2.7870975	0.001	9.97E-04	0.00371	0.0064232
SCRM2_T208M	T208M	MA_10435231g0010	0.9	6.6801453	0.0351	0.0444439	0.00101	6.92E-05	0.00101	0.00E+00	0.00101	0.00E+00	0.25272	0.4531943	0.00288	0.0031488	0.00101	2.97E-12	0.00101	6.66E-15	0.67395	2.2262969	0.00101	1.06E-04	0.00101	1.12E-07	0.0466	0.0607834	0.001	1.33E-04	0.12701	0.1927665
SCRM2_S238N	S238N	MA_10435231g0010	0.9	6.9390908	0.05953	0.0798303	0.00101	2.51E-05	0.00101	0.00E+00	0.00101	0.00E+00	0.00911	0.0104674	0.00101	1.41E-06	0.00101	0.00E+00	0.00101	0.00E+00	0.45082	1.0189796	0.00101	3.44E-07	0.00101	1.45E-08	0.00534	0.0059807	0.001	1.74E-04	0.51272	1.2701007
TCP2_F4S	F4S	MA_92659g0010	0.2461	0.4377259	0.00321	0.00353	0.00101	1.20E-10	0.00101	0.00E+00	0.00101	0.00E+00	0.63803	1.9760238	0.00101	9.49E-05	0.00101	5.59E-08	0.00101	0.00E+00	0.0431	0.0557163	0.00139	1.50E-03	0.00101	1.03E-13	0.89999	9.9550509	0.001	7.58E-06	0.00101	1.87E-07
TCP2_V25A	V25A	MA_92659g0010	0.1101	0.1619267	0.00829	0.0094848	0.00101	2.74E-06	0.00101	2.18E-10	0.00101	8.44E-10	0.89999	5.3953807	0.10321	0.150322	0.00763	8.69E-03	0.00174	1.88E-03	0.59302	1.693677	0.23279	4.07E-01	0.05774	7.72E-02	0.89999	11.063088	0.7961	3.26E+00	0.83888	3.693338
TCP2_E32G	E32G	MA_92659g0010	0.0808	0.1127966	0.0067	0.0075799	0.00101	1.99E-06	0.00101	1.32E-10	0.00101	5.73E-10	0.89999	5.7752225	0.11513	0.1705974	0.00884	1.02E-02	0.00205	2.22E-03	0.59257	1.691056	0.22973	4.00E-01	0.05752	7.68E-02	0.89999	10.999381	0.7957	3.26E+00	0.84157	3.7218412
TCP2_E51K	E51K	MA_92659g0010	0.9	8.2469537	0.00101	0.0001536	0.00101	3.33E-13	0.00101	0.00E+00	0.00101	4.33E-14	0.00264	0.002883	0.00101	1.17E-10	0.00101	0.00E+00	0.00101	2.27E-11	0.03883	0.0496521	0.00101	5.35E-05	0.02435	2.99E-02	0.82337	3.5318492	0.9	1.37E+01	0.87929	4.1384781
TCP2_I53F	I53F	MA_92659g0010	0.7579	2.9050206	0.00101	0.0002009	0.00101	2.23E-13	0.00101	0.00E+00	0.00101	2.33E-14	0.03086	0.0386213	0.00101	7.27E-09	0.00101	0.00E+00	0.00101	1.49E-09	0.02786	0.0345557	0.00101	2.71E-05	0.01593	1.89E-02	0.81671	3.4639986	0.9	1.35E+01	0.88391	4.1916593
NAC036_D206E	D206E	MA_101849g0010	0.9	7.1059258	0.56717	1.5466731	0.02361	2.89E-02	0.00101	6.94E-07	0.00101	4.23E-06	0.89999	5.4945844	0.19113	0.3168462	0.00101	2.10E-04	0.00101	3.24E-04	0.73195	2.680765	0.02404	2.95E-02	0.01654	1.97E-02	0.62414	1.8852176	0.4121	8.89E-01	0.89999	6.9681642
NAC036_T237M	T237M	MA_101849g0010	0.9	5.9875681	0.89999	5.2107547	0.79673	3.27E+00	0.09522	1.37E-01	0.00663	7.51E-03	0.89999	13.521499	0.89999	10.60103	0.64544	2.03E+00	0.11318	1.67E-01	0.89999	12.162953	0.77311	3.04E+00	0.18419	3.03E-01	0.89999	4.4701953	0.2571	4.63E-01	0.60649	1.7746104
EXPB3_K3R	K3R	MA_7354451g0010	0.9	12.011758	0.89999	4.9009516	0.00942	1.08E-02	0.00101	2.56E-05	0.00101	1.63E-05	0.89999	7.1191219	0.03005	0.0375134	0.00101	3.17E-04	0.00101	1.23E-04	0.2375	0.417652	0.01826	2.19E-02	0.0048	5.36E-03	0.89999	8.2555587	0.7049	2.46E+00	0.88391	4.1915974
EXPB3_R6S	R6S	MA_7354451g0010	0.8347	3.6497194	0.48448	1.1474042	0.00101	1.97E-04	0.00101	9.30E-11	0.00101	4.42E-10	0.89999	7.9913453	0.02596	0.0308244	0.00101	3.37E-06	0.00101	1.90E-06	0.17021	0.2737278	0.00101	3.89E-04	0.00101	1.09E-04	0.6542	2.0857852	0.2455	4.36E-01	0.85008	3.813265
EXPB3_C32R	C32R	MA_7354451g0010	0.9	4.6678307	0.00522	0.0058414	0.00359	3.97E-03	1.01E-03	3.56E-08	0.00101	1.07E-04	0.12507	0.1892671	0.10978	0.1614217	0.00101	9.58E-05	0.01019	1.18E-02	0.89999	14.621978	0.73263	2.69E+00	0.89999	6.94E+00	0.66994	2.1971697	0.9	6.41E+00	0.89999	9.1855594
FLZ6_L88V	L88V	MA_14341g0010	0.9	11.374357	0.01786	0.0214026	0.01842	2.21E-02	0.00101	5.09E-07	0.00101	7.60E-06	0.06004	0.0806038	0.06363	0.0860072	0.00101	1.82E-05	0.00101	9.26E-05	0.89999	14.028657	0.71543	2.54E+00	0.60262	1.75E+00	0.63245	1.9391767	0.5326	1.37E+00	0.89999	9.3941199
VRUK1_A265V	A265V	MA_587505g0010	0.9	11.032665	0.89999	5.6330672	0.88508	4.2049855	0.04405	0.0570795	0.31754	0.6161669	0.83226	3.6237187	0.89999	7.1254889	0.175	0.2836421	0.56364	1.5273451	0.42623	0.9351913	0.00381	0.0042099	0.06251	0.0843104	0.64787	2.0422428	0.9	5.4142459	0.89999	10.204831
VRUK1_V283L	V283L	MA_587505g0010	0.9	13.13935	0.89999	10.859847	0.0046	5.12E-03	0.00101	8.20E-05	0.00267	2.91E-03	0.89999	12.620119	0.01182	0.0137868	0.00101	5.13E-04	0.00743	8.45E-03	0.03127	0.03918	0.00274	3.00E-03	0.02127	2.58E-02	0.89999	13.291233	0.9	1.39E+01	0.89999	14.528704
RPS2_S123N	S123N	MA_475302g0010	0.9	6.875651	0.00974	0.0112368	0.00101	1.61E-11	0.00101	0.00E+00	0.00101	0.00E+00	0.00119	0.0012757	0.00101	7.76E-13	0.00101	0.00E+00	0.00101	0.00E+00	0.00772	0.0088055	0.00101	1.25E-05	0.00101	2.90E-05	0.89999	5.6641515	0.7174	2.56E+00	0.89999	6.5902257
RPS2_E166A	E166A	MA_475302g0010	0.9	11.677818	0.00448	0.0049875	0.00101	6.33E-13	0.00101	3.33E-15	0.00101	3.06E-13	0.00233	0.0025296	0.00101	3.73E-13	0.00101	3.33E-15	0.00101	1.87E-13	0.00376	0.0041582	0.01089	1.26E-02	0.0032	3.51E-03	0.89999	4.3988266	0.9	1.49E+01	0.88747	4.2329841

Significant p-values (p-value<0.05) are highlighted

Table S5 Hardy Weinberg Equilibrium(HWE) for genotype frequencies of missense mutations in the nine candidate DEGs in response to SHADE in Norway spruce that show cline

Gene name	SNP	Gene_Id	S1 (lat 55-57) HWE p-value	S2 (lat 58) HWE p-value	S3 (lat 59-60) HWE p-value	S4 (lat 61-62) HWE p-value	S5 (lat 63-64) HWE p-value	S6 (lat 65-67) HWE p-value
MYB3_T132R	T132R	MA_7115g0010	0.6305073	0.7079489	0.09879334	0.8456276	0.5690967	0.2102694
LOV1_R156K	R156K	MA_16619g0010	0.5444456	0.7613816	0.7349385	0.8755682	0.3548293	0.418793
LOV1_D190N	D190N	MA_16619g0010	0.5665429	0.00543298	0.420296	0.01394043	0.001147745	0.02871752
SCRM2_T208M	T208M	MA_10435231g0010	0.5657677	0.85023	0.05895691	0.05068066	0.4412498	0.2792934
SCRM2_S238N	S238N	MA_10435231g0010	0.08930325	0.2158439	0.01860447	0.1180562	0.4398115	0.1794888
TCP2_F4S	F4S	MA_92659g0010	0.001170066	0.0171661	0.003380215	0.4064667	0.01912685	0.000335543
TCP2_V25A	V25A	MA_92659g0010	0.7798684	0.6814202	0.2724744	1	0.6166626	0.1421518
TCP2_E32G	E32G	MA_92659g0010	0.7805884	0.6788518	0.2724744	1	0.6166373	0.1421518
TCP2_E51K	E51K	MA_92659g0010	0.3382155	0.00067806	0.1981032	1	0.7584974	0.1178837
TCP2_I53F	I53F	MA_92659g0010	0.3402181	0.00071409	0.1205355	1	0.758248	0.1163396
NAC036_D206E	D206E	MA_101849g0010	0.07351378	1	0.3554533	0.08390553	0.05158337	0.03029547
NAC036_T237M	T237M	MA_101849g0010	0.3934845	0.4284897	0.5779759	0.3071086	0.6738657	0.8415818
EXPB3_K3R	K3R	MA_7354451g0010	0.07548853	0.2311453	0.1825768	1	0.000137283	0.01557581
EXPB3_R6S	R6S	MA_7354451g0010	0.1956392	0.4769058	0.0299857	0.8717671	4.78E-06	0.01553658
EXPB3_C32R	C32R	MA_7354451g0010	1	1	1	1	1	1
FLZ6_L88V	L88V	MA_14341g0010	7.04E-08	0.00107311	0.05147672	0.02159798	1.80E-05	0.002130486
VRK1_A265V	A265V	MA_587505g0010	0.1128199	0.2850072	0.338132	1	0.1760774	0.3675938
VRK1_V283L	V283L	MA_587505g0010	0.0179411	0.4710266	0.001521785	0.01064617	2.25E-06	0.03230442
RPS2_S123N	S123N	MA_475302g0010	3.62E-09	0.00015184	0.000284223	2.97E-09	7.97E-18	3.74E-08
RPS2_E166A	E166A	MA_475302g0010	2.82E-10	0.00047369	0.000236755	6.31E-06	5.82E-11	5.95E-06

Significant p-values (p-value<0.05) are highlighted

Table S6 Allele frequencies of missense mutations in the nine candidate DEGs in response to SHADE in Norway spruce that do not show cline

Population-wise allele frequency										
ContigID:SnpPosition	Gene_ID	Gene name	Amino acid change	Allele	S1	S2	S3	S4	S5	S6
MA_7115:46740	MA_7115g0010	MYB3	Arg162Gln	Reference (G)	0.995851	0.992788	0.989247	0.990148	0.99195	0.99095
				Alternate (A)	0.00414938	0.00721154	0.0107527	0.00985222	0.00805009	0.00904977
MA_7115:46905	MA_7115g0010	MYB3	Pro107Leu	Reference (C)	0.985356	0.992857	0.989247	0.987923	0.992958	0.988636
				Alternate (T)	0.0146444	0.00714286	0.0107527	0.0120773	0.00704225	0.0113636
MA_7115:46944	MA_7115g0010	MYB3	His94Leu	Reference (A)	0.642857	0.617925	0.6	0.611111	0.653641	0.702703
				Alternate (T)	0.357143	0.382075	0.4	0.388889	0.346359	0.297297
MA_7115:46972	MA_7115g0010	MYB3	Pro85Thr	Reference (C)	0.82582	0.82783	0.818182	0.85782	0.879159	0.847534
				Alternate (A)	0.17418	0.17217	0.181818	0.14218	0.120841	0.152466
MA_7115:47037	MA_7115g0010	MYB3	His63Arg	Reference (A)	0.806122	0.775943	0.794118	0.754717	0.769702	0.860987
				Alternate (G)	0.193878	0.224057	0.205882	0.245283	0.230298	0.139013
MA_7115:47067	MA_7115g0010	MYB3	Pro53Arg	Reference (C)	0.975309	0.96934	0.975806	0.99763	0.999123	0.997738
				Alternate (G)	0.0246914	0.0306604	0.0241935	0.00236967	0.000877193	0.00226244
MA_16619:4719	MA_16619g0010	LOV1	Glu41Lys	Reference (G)	0.940816	0.924528	0.927807	0.898058	0.914613	0.842342
				Alternate (A)	0.0591837	0.0754717	0.0721925	0.101942	0.0853873	0.157658
MA_16619:4858	MA_16619g0010	LOV1	Asp87Val	Reference (A)	0.984375	0.992308	0.983051	0.992063	0.98	0.983333
				Alternate (T)	0.015625	0.00769231	0.0169492	0.00793651	0.02	0.0166667
MA_10435231:4572	MA_10435231g0010	SCRM2	Thr26Ala	Reference (A)	0.962963	0.950472	0.981183	0.992788	0.996466	0.993243
				Alternate (G)	0.037037	0.0495283	0.0188172	0.00721154	0.00353357	0.00675676
MA_10435231:4578	MA_10435231g0010	SCRM2	Leu28Val	Reference (C)	0.95082	0.931604	0.882353	0.879808	0.838028	0.80543
				Alternate (G)	0.0491803	0.0683962	0.117647	0.120192	0.161972	0.19457
MA_92659:15358	MA_92659g0010	TCP2	Gly364Val	Reference (G)	0.955752	0.97	0.945355	0.968599	0.936364	0.956019
				Alternate (T)	0.0442478	0.03	0.0546448	0.031401	0.0636364	0.0439815
MA_101849:25488	MA_101849g0010	NAC036	Ser56Leu	Reference (C)	0.835417	0.832524	0.808743	0.84	0.795495	0.819635
				Alternate (T)	0.164583	0.167476	0.191257	0.16	0.204505	0.180365
MA_101849:25632	MA_101849g0010	NAC036	Thr104Ile	Reference (C)	0.668724	0.670616	0.693548	0.71875	0.737676	0.702703
				Alternate (T)	0.331276	0.329384	0.306452	0.28125	0.262324	0.297297
MA_101849:25646	MA_101849g0010	NAC036	Ser109Pro	Reference (T)	0.199588	0.130332	0.172043	0.18599	0.149558	0.144796
				Alternate (C)	0.800412	0.869668	0.827957	0.81401	0.850442	0.855204
MA_101849:25689	MA_101849g0010	NAC036	Lys123Arg	Reference (A)	0.971193	0.966667	0.97043	0.983333	0.977837	0.988636
				Alternate (G)	0.0288066	0.0333333	0.0295699	0.0166667	0.0221631	0.0113636
MA_14341:1048	MA_14341g0010	FLZ6	Val14Ile	Reference (G)	0.781633	0.739437	0.666667	0.71934	0.757867	0.578829
				Alternate (A)	0.218367	0.260563	0.333333	0.28066	0.242133	0.421171
MA_14341:1231	MA_14341g0010	FLZ6	Ser75Pro	Reference (T)	0.161088	0.135468	0.181564	0.232673	0.272556	0.172018
				Alternate (C)	0.838912	0.864532	0.818436	0.767327	0.727444	0.827982
MA_14341:1244	MA_14341g0010	FLZ6	Gly79Val	Reference (G)	0.975104	0.985714	0.983696	0.995215	0.987365	0.99095
				Alternate (T)	0.0248963	0.0142857	0.0163043	0.00478469	0.0126354	0.00904977
MA_14341:1265	MA_14341g0010	FLZ6	Ala86Val	Reference (C)	0.981481	0.975962	0.964088	0.907317	0.871087	0.945701
				Alternate (T)	0.0185185	0.0240385	0.0359116	0.0926829	0.128913	0.0542986
MA_587505:1178	MA_587505g0010	VRLK1	Thr271Pro	Reference (A)	0.959016	0.959716	0.948925	0.956522	0.953488	0.948198
				Alternate (C)	0.0409836	0.0402844	0.0510753	0.0434783	0.0465116	0.0518018
MA_587505:1244	MA_587505g0010	VRLK1	Pro249Ala	Reference (C)	0.97479	0.956311	0.945355	0.974874	0.973535	0.953917
				Alternate (G)	0.0252101	0.0436893	0.0546448	0.0251256	0.026465	0.0460829
MA_475302:3505	MA_475302g0010	RPS2	Glu150Asp	Reference (G)	0.932773	0.936893	0.909341	0.8225	0.76588	0.873832
				Alternate (T)	0.0672269	0.0631068	0.0906593	0.1775	0.23412	0.126168
MA_475302:3524	MA_475302g0010	RPS2	Gly144Asp	Reference (G)	0.981172	0.985366	0.958791	0.938424	0.950271	0.943662
				Alternate (A)	0.0188285	0.0146341	0.0412088	0.0615764	0.0497288	0.056338
MA_475302:3557	MA_475302g0010	RPS2	Val133Ala	Reference (T)	0.42766	0.376238	0.544199	0.733831	0.758272	0.68599
				Alternate (C)	0.57234	0.623762	0.455801	0.266169	0.241728	0.31401

Table S7 Allele frequencies of synonymous mutations in the nine candidate DEGs in response to SHADE in Norway spruce that show mild cline

				Population-wise allele frequency						
ContigID:SnpPosition	Gene_ID	Gene name	Amino acid change	Allele	S1	S2	S3	S4	S5	S6
MA_92659:14474	MA_92659g0010	TCP2	Tyr69Tyr	Reference (T)	T:0.964912	T:0.958115	T:0.985955	T:0.992537	T:0.992767	T:0.992991
				Alternate (C)	C:0.0350877	C:0.0418848	C:0.0140449	C:0.00746269	C:0.00723327	C:0.00700935
MA_92659:15344	MA_92659g0010	TCP2	Arg359Arg	Reference (C)	C:0.948661	C:0.8925	C:0.826705	C:0.728856	C:0.70941	C:0.564286
				Alternate (A)	A:0.0513393	A:0.1075	A:0.173295	A:0.271144	A:0.29059	A:0.435714
MA_16619:4700	MA_16619g0010	LOV1	Ala34Ala	Reference (G)	G:0.979508	G:0.992925	G:0.967914	G:0.954327	G:0.939367	G:0.91704
				Alternate (A)	A:0.0204918	A:0.00707547	A:0.0320856	A:0.0456731	A:0.0606327	A:0.0829596
MA_14341:1032	MA_14341g0010	FLZ6	Phe8Phe	Reference (T)	T:0.963265	T:0.959906	T:0.938172	T:0.915094	T:0.925569	T:0.849099
				Alternate (C)	C:0.0367347	C:0.0400943	C:0.061828	C:0.0849057	C:0.0744308	C:0.150901
MA_101849:25612	MA_101849g0010	NAC036	Phe97Phe	Reference (T)	T:0.884774	T:0.850711	T:0.859459	T:0.86019	T:0.847711	T:0.808559
				Alternate (C)	C:0.115226	C:0.149289	C:0.140541	C:0.13981	C:0.152289	C:0.191441
MA_101849:25633	MA_101849g0010	NAC036	Thr104Thr	Reference (T)	T:0.584362	T:0.535545	T:0.58871	T:0.581731	T:0.545936	T:0.513514
				Alternate (G)	G:0.415638	G:0.464455	G:0.41129	G:0.418269	G:0.454064	G:0.486486
MA_101849:25735	MA_101849g0010	NAC036	Tyr138Tyr	Reference (T)	T:0.965021	T:0.944175	T:0.951613	T:0.953431	T:0.928187	T:0.884091
				Alternate (C)	C:0.0349794	C:0.0558252	C:0.0483871	C:0.0465686	C:0.0718133	C:0.115909
MA_101849:25762	MA_101849g0010	NAC036	Phe147Phe	Reference (C)	C:0.944215	C:0.93	C:0.942935	C:0.936893	C:0.927549	C:0.974654
				Alternate (T)	T:0.0557851	T:0.07	T:0.0570652	T:0.0631068	T:0.0724508	T:0.0253456

Table S8 Allele frequencies of synonymous mutations in the nine candidate DEGs in response to SHADE in Norway spruce that do not show cline

Population-wise allele frequency										
ContigID:Snpposition	Gene_ID	Gene name	Amino acid change	Allele	S1	S2	S3	S4	S5	S6
MA_7115:46700	MA_7115g0010	MYB3	Leu175Leu	Reference (A)	0.914583	0.87799	0.863388	0.856061	0.85118	0.920814
				Alternate (G)	0.0854167	0.12201	0.136612	0.143939	0.14882	0.0791855
MA_16619:4622	MA_16619g0010	LOV1	Arg8Arg	Reference (G)	0.983607	0.988152	0.962366	0.963768	0.983186	0.986547
				Alternate (A)	0.0163934	0.0118483	0.0376344	0.0362319	0.0168142	0.0134529
MA_16619:4679	MA_16619g0010	LOV1	His27His	Reference (C)	0.979508	0.985782	0.983957	0.976077	0.972711	0.975336
				Alternate (T)	0.0204918	0.014218	0.0160428	0.0239234	0.0272887	0.0246637
MA_10435231:4637	MA_10435231g0010	SCRM2	Cys47Cys	Reference (C)	0.967347	0.978673	0.967914	0.96875	0.976232	0.975113
				Alternate (T)	0.0326531	0.021327	0.0320856	0.03125	0.0237676	0.0248869
MA_10435231:4643	MA_10435231g0010	SCRM2	Leu49Leu	Reference (G)	1	0.990521	0.989305	0.973558	0.970018	0.9819
				Alternate (T)	0	0.00947867	0.0106952	0.0264423	0.0299824	0.0180995
MA_92659:14336	MA_92659g0010	TCP2	Asn23Asn	Reference (T)	0.933884	0.914286	0.918919	0.910628	0.917845	0.909502
				Alternate (C)	0.0661157	0.0857143	0.0810811	0.089372	0.0821555	0.0904977
MA_101849:25543	MA_101849g0010	NAC036	Gly74Gly	Reference (T)	0.197531	0.135071	0.183784	0.193627	0.150995	0.145455
				Alternate (C)	0.802469	0.864929	0.816216	0.806373	0.849005	0.854545
MA_101849:25549	MA_101849g0010	NAC036	Cys76Cys	Reference (T)	0.981557	0.978774	0.964865	0.978365	0.992895	0.995495
				Alternate (C)	0.0184426	0.0212264	0.0351351	0.0216346	0.0071048	0.0045045
MA_7354451:133	MA_7354451g0010	EXPB3	Leu28Leu	Reference (T)	0.973361	0.966981	0.978495	0.938679	0.93838	0.929545
				Alternate (C)	0.0266393	0.0330189	0.0215054	0.0613208	0.0616197	0.0704545
MA_14341:1083	MA_14341g0010	FLZ6	Pro25Pro	Reference (C)	0.826531	0.800469	0.763441	0.816038	0.847636	0.754505
				Alternate (T)	0.173469	0.199531	0.236559	0.183962	0.152364	0.245495

Table S9 Allele frequencies of missense mutations in the DEGs other than nine candidate genes in response to SHADE in Norway spruce

				Population-wise allele frequency						
ContigID:Snpposition	Gene_ID	Gene name	Amino acid change	Allele	S1	S2	S3	S4	S5	S6
MA_86183:6248	MA_86183g0010	BIG GRAIN 3 (BG3)	Ala30Val	Reference (C) Alternate (T)	C:0.952869 T:0.0471311	C:0.95283 T:0.0471698	C:0.935135 T:0.0648649	C:0.884058 T:0.115942	C:0.864675 T:0.135325	C:0.819005 T:0.180995
MA_10351640:1873	MA_10351640g0010	S-ADENOSYL METHIONINE TRANSPORTER-LIKE (SAMTL)	Gln119Lys	Reference (C) Alternate (A)	C:0.972803 A:0.0271967	C:0.971154 A:0.0288462	C:0.964865 A:0.0351351	C:0.927184 A:0.0728155	C:0.921147 A:0.078853	C:0.925676 A:0.0743243
MA_15920:34530	MA_15920g0010	MYB-like HTH transcriptional regulator family protein	Val9Met	Reference (G) Alternate (A)	G:0.959916 A:0.0400844	G:0.954545 A:0.0454545	G:0.949153 A:0.0508475	G:0.914216 A:0.085784	G:0.869091 A:0.130909	G:0.815421 A:0.184579
MA_20782:9490	MA_20782g0010	Tetratricopeptide repeat (TPR)-like superfamily protein	Ala180Val	Reference (C) Alternate (T)	C:0.212185 T:0.787815	C:0.220588 T:0.779412	C:0.287634 T:0.712366	C:0.355392 T:0.644608	C:0.366667 T:0.633333	C:0.372146 T:0.627854
MA_80461:1299	MA_80461g0010	Disease resistance protein	Asp154Ala	Reference (A) Alternate (C)	A:0.991416 C:0.00858369	A:0.995074 C:0.00492611	A:0.991279 C:0.00872093	A:0.992105 C:0.00789474	A:0.985102 C:0.0148976	A:0.987805 C:0.0121951
MA_227006:3453	MA_227006g0010	Diphthamide synthesis DPH2 family protein	Arg21Trp	Reference (C) Alternate (T)	C:0.946721 T:0.0532787	C:0.933962 T:0.0660377	C:0.884409 T:0.115591	C:0.866995 T:0.133005	C:0.859929 T:0.140071	C:0.777027 T:0.222973
MA_423032:1006	MA_423032g0010	Disease resistance protein	Ala51Ser	Reference (G) Alternate (T)	G:0.981405 T:0.018595	G:0.981221 T:0.0187793	G:0.986559 T:0.0134409	G:0.973171 T:0.0268293	G:0.968582 T:0.0314183	G:0.965438 T:0.0345622
MA_447489:1980	MA_447489g0010	RING-H2 FINGER A2A (RHA2A)	Ser92Thr	Reference (T) Alternate (A)	T:0.995885 A:0.00411523	T:0.995283 A:0.00471698	T:0.986559 A:0.0134409	T:0.983412 A:0.0165877	T:0.956714 A:0.0432862	T:0.945946 A:0.0540541
MA_904305:7873	MA_904305g0010	Tetratricopeptide repeat (TPR)-like superfamily protein	Arg55Ser	Reference (G) Alternate (C)	G:0.973333 C:0.0266667	G:0.976923 C:0.0230769	G:0.956395 C:0.0436047	G:0.937173 C:0.0628272	G:0.913424 C:0.0865759	G:0.917073 C:0.0829268
MA_904305:8387	MA_904305g0010	Tetratricopeptide repeat (TPR)-like superfamily protein	Ala227Thr	Reference (G) Alternate (A)	G:0.971311 A:0.0286885	G:0.973934 A:0.0260664	G:0.957219 A:0.0427807	G:0.949761 A:0.0502392	G:0.938163 A:0.0618375	G:0.938914 A:0.061086
MA_918643:2547	MA_918643g0010	Protein kinase superfamily protein	Try87His	Reference (T) Alternate (C)	T:0.653061 C:0.346939	T:0.601415 C:0.398585	T:0.521505 C:0.478495	T:0.464789 C:0.535211	T:0.367544 C:0.632456	T:0.335586 C:0.664414
MA_945672:6851	MA_945672g0010	Oxygenase superfamily protein	Asp71Val	Reference (A) Alternate (T)	A:0.900826 T:0.0991736	A:0.887019 T:0.112981	A:0.852151 T:0.147849	A:0.816425 T:0.183575	A:0.833037 T:0.166963	A:0.718182 T:0.281818
MA_945672:7014	MA_945672g0010	Oxygenase superfamily protein	Ser17Gly	Reference (A) Alternate (G)	A:0.904564 G:0.0954357	A:0.889952 G:0.110048	A:0.860215 G:0.139785	A:0.822967 G:0.177033	A:0.831541 G:0.168459	A:0.726852 G:0.273148
MA_945672:7341	MA_945672g0010	Oxygenase superfamily protein	Arg115Ser	Reference (C) Alternate (A)	C:0.971074 A:0.0289256	C:0.978469 A:0.0215311	C:0.959677 A:0.0403226	C:0.934466 A:0.065534	C:0.935599 A:0.0644007	C:0.936364 A:0.0636364
MA_10430253:15461	MA_10430253g0010	Alpha/beta-Hydrolases superfamily protein	Phe61Tyr	Reference (T) Alternate (A)	T:0.168103 A:0.831897	T:0.207729 A:0.792271	T:0.265537 A:0.734463	T:0.308081 A:0.691919	T:0.313528 A:0.686472	T:0.375 A:0.625
MA_10432704:73817	MA_10432704g0020	CHLORORESPIRATORY REDUCTION22 (CRR22)	Ala219Val	Reference (C) Alternate (T)	C:0.997908 T:0.00209205	C:0.992857 T:0.00714286	C:0.991848 T:0.00815217	C:0.9875 T:0.0125	C:0.979204 T:0.0207957	C:0.96789 T:0.0321101
MA_96757:12081	MA_96757g0010	PEROXIDASE 52 (PRX52)	Ala55Thr	Reference (G) Alternate (A)	G:0.993878 A:0.00612245	G:0.992891 A:0.007109	G:0.997312 A:0.00268817	G:0.978673 A:0.021327	G:0.975177 A:0.0248227	G:0.975225 A:0.0247748
MA_90634:8021	MA_90634g0010	Aluminum activated malate transporter family protein	Pro43Ser	Reference (C) Alternate (T)	C:0.997925 T:0.00207469	C:0.987923 T:0.0120773	C:0.986486 T:0.0135135	C:0.981043 T:0.0189573	C:0.97331 T:0.0266904	C:0.958904 T:0.0410959
MA_89572:19598	MA_89572g0010	SET DOMAIN PROTEIN 35 (SDG35)	Leu35Ser	Reference (A) Alternate (G)	A:0.738589 G:0.261411	A:0.722222 G:0.277778	A:0.765027 G:0.234973	A:0.77451 G:0.22549	A:0.852415 G:0.147585	A:0.844037 G:0.155963
MA_8433628:1321	MA_8433628g0010	Plant invertase/pectin methylesterase inhibitor superfamily protein	Met85Leu	Reference (T) Alternate (A)	T:0.970464 A:0.0295359	T:0.953202 A:0.046798	T:0.980447 A:0.0195531	T:0.987113 A:0.0128866	T:0.996176 A:0.00382409	T:0.995327 A:0.0046729
MA_83446:30566	MA_83446g0020	purple acid phosphatase 27;(source:Araport11)	Trp38Ser	Reference (G) Alternate (C)	G:0.868313 C:0.131687	G:0.848341 C:0.151659	G:0.892473 C:0.107527	G:0.929612 C:0.0703883	G:0.974245 C:0.0257549	G:0.979638 C:0.020362
MA_8344:30649	MA_83446g0020	purple acid phosphatase 27;(source:Araport11)	Glu66Lys	Reference (G) Alternate (A)	G:0.865702 A:0.134298	G:0.841346 A:0.158654	G:0.895161 A:0.104839	G:0.919903 A:0.0800971	G:0.975979 A:0.0240214	G:0.972727 A:0.0272727
MA_8344:30651	MA_83446g0020	purple acid phosphatase 27;(source:Araport11)	Glu66Asp	Reference (G) Alternate (T)	G:0.865702 T:0.134298	G:0.841346 T:0.158654	G:0.895161 T:0.104839	G:0.92029 T:0.0797101	G:0.975133 T:0.0248668	G:0.972851 T:0.0271493
MA_8344:30830	MA_83446g0020	purple acid phosphatase 27;(source:Araport11)	Leu126His	Reference (T) Alternate (A)	T:0.880753 A:0.119247	T:0.885167 A:0.114833	T:0.905405 A:0.0945946	T:0.871287 A:0.128713	T:0.857923 A:0.142077	T:0.818605 A:0.181395
MA_58710:10558	MA_58710g0010	Subtilase family protein	Cys24Tyr	Reference (G) Alternate (A)	G:0.761224 A:0.238776	G:0.755924 A:0.244076	G:0.737838 A:0.262162	G:0.71327 A:0.28673	G:0.738011 A:0.261989	G:0.717489 A:0.282511
MA_5587:58879	MA_5587g0010	glycosyltransferase family protein 2	Cys294Ser	Reference (A) Alternate (T)	A:0.932735 T:0.0672646	A:0.957286 T:0.0427136	A:0.921512 T:0.0784884	A:0.959459 T:0.0405405	A:0.954373 T:0.0456274	A:0.987923 T:0.0120773
MA_5587:58921	MA_5587g0010	glycosyltransferase family protein 2	Llu280Lys	Reference (C) Alternate (T)	C:0.886076 T:0.113924	C:0.90625 T:0.09375	C:0.879121 T:0.120879	C:0.935 T:0.065	C:0.933028 T:0.0669725	C:0.962441 T:0.0375587

MA_5587:58936	MA_5587g0010	glycosyltransferase family protein 2	Gln275Lys	Reference (G) Alternate (T)	G:0.866109 T:0.133891	G:0.900474 T:0.0995261	G:0.863388 T:0.136612	G:0.921182 T:0.0788177	G:0.925551 T:0.0744485	G:0.949074 T:0.0509259
MA_5587:58946	MA_5587g0010	glycosyltransferase family protein 2	Gln271His	Reference (C) Alternate (A)	C:0.983402 A:0.0165975	C:0.973934 A:0.0260664	C:0.978261 A:0.0217391	C:0.987745 A:0.0122549	C:0.99543 A:0.00457038	C:0.997706 A:0.00229358
MA_5587:58965	MA_5587g0010	glycosyltransferase family protein 2	Ala265Val	Reference (G) Alternate (A)	G:0.968487 A:0.0315126	MG:0.966667 A:0.0333333	G:0.983784 A:0.0162162	G:0.97 A:0.03	G:0.979204 A:0.0207957	G:0.990868 A:0.00913242
MA_5587:59010	MA_5587g0010	glycosyltransferase family protein 2	Ile250Thr	Reference (A) Alternate (G)	A:0.968619 G:0.0313808	A:0.968447 G:0.0315534	A:0.989011 G:0.010989	A:0.9675 G:0.0325	A:0.974074 G:0.0259259	A:0.979167 G:0.0208333
MA_5587:59031	MA_5587g0010	glycosyltransferase family protein 2	Pro243Leu	Reference (G) Alternate (A)	G:0.968354 A:0.0316456	G:0.968293 A:0.0317073	G:0.986111 A:0.0138889	G:0.972081 A:0.0279188	G:0.975791 A:0.0242086	G:0.981132 A:0.0188679
MA_52897:17848	MA_52897g0010	Protein kinase superfamily protein	Gly194Arg	Reference (C) Alternate (T)	C:0.57377 T:0.42623	C:0.561905 T:0.438095	C:0.601093 T:0.398907	C:0.629268 T:0.370732	C:0.590909 T:0.409091	C:0.625 T:0.375
MA_52897:18331	MA_52897g0010	Protein kinase superfamily protein	Val33Ile	Reference (C) Alternate (T)	C:0.89959 T:0.10041	C:0.899522 T:0.100478	C:0.948925 T:0.0510753	C:0.939904 T:0.0600962	C:0.949558 T:0.0504425	C:0.958904 T:0.0410959
MA_510832:1492	MA_510832g0010	hAT dimerization domain-containing protein / transposase-like protein	Ala52Thr	Reference (C) Alternate (T)	C:0.985656 T:0.0143443	C:0.971564 T:0.028436	C:0.973118 T:0.0268817	C:0.898551 T:0.101449	C:0.919183 T:0.0808171	C:0.910314 T:0.0896861
MA_4984597:670	MA_4984597g0010	Eukaryotic aspartyl protease family protein	Val224Met	Reference (G) Alternate (A)	G:0.983673 A:0.0163265	G:0.971698 A:0.0283019	G:0.97027 A:0.0297297	G:0.952381 A:0.047619	G:0.944938 A:0.0550622	G:0.950673 A:0.0493274
MA_38922:6655	MA_38922g0010	HEAVY METAL ASSOCIATED ISOPRENYLATED PLANT PROTEIN 20 (HIP20)	Phe2Cys	Reference (T) Alternate (G)	T:0.946721 G:0.0532787	T:0.940758 G:0.0592417	T:0.943243 G:0.0567568	T:0.969484 G:0.0305164	T:0.97242 G:0.0275801	T:0.974886 G:0.0251142
MA_31254:22109	MA_31254g0010	U3 small nucleolar RNA-associated-like protein	Glu30Asp	Reference (T) Alternate (G)	T:0.724066 G:0.275934	T:0.758294 G:0.241706	T:0.76087 G:0.23913	T:0.806763 G:0.193237	T:0.814286 G:0.185714	T:0.809417 G:0.190583
MA_1925:30754	MA_1925g0010	LTPG15	Pro6Leu	Reference (G) Alternate (A)	G:0.836735 A:0.163265	G:0.866197 A:0.133803	G:0.897849 A:0.102151	G:0.930622 A:0.069378	G:0.941441 A:0.0585586	G:0.928241 A:0.0717593
MA_17793:51035	MA_17793g0010	PLASMA MEMBRANE INTRINSIC PROTEIN 2;8 (PIP2;8)	Gly37Glu	Reference (G) Alternate (A)	G:0.958678 A:0.0413223	G:0.913043 A:0.0869565	G:0.932432 A:0.0675676	G:0.874408 A:0.125592	G:0.855098 A:0.144902	G:0.772936 A:0.227064
MA_17793:51051	MA_17793g0010	PLASMA MEMBRANE INTRINSIC PROTEIN 2;8 (PIP2;8)	Lys42Asn	Reference (G) Alternate (T)	G:0.966805 T:0.033195	G:0.978049 T:0.0219512	G:0.991892 T:0.00810811	G:0.990431 T:0.00956938	G:0.985714 T:0.0142857	G:0.990826 T:0.00917431
MA_169781:13449	MA_169781g0010	SPla/Ryanodine receptor (SPRY) domain-containing protein	Arg46Ile	Reference (C) Alternate (A)	C:0.997826 A:0.00217391	C:0.976923 A:0.0230769	C:0.988827 A:0.0111732	C:0.974619 A:0.0253807	C:0.943916 A:0.0560837	C:0.947005 A:0.0529954
MA_15382:33084	MA_15382g0010	F-box/RNI-like superfamily protein	Leu249Gln	Reference (T) Alternate (A)	T:0.991632 A:0.0083682	T:0.990476 A:0.00952381	T:0.98913 A:0.0108696	T:0.956731 A:0.0432692	T:0.925267 A:0.0747331	T:0.958716 A:0.0412844
MA_15382:33180	MA_15382g0010	F-box/RNI-like superfamily protein	Leu281Pro	Reference (T) Alternate (C)	T:0.958678 C:0.0413223	T:0.976303 C:0.0236967	T:0.9 C:0.1	T:0.865385 C:0.134615	T:0.840708 C:0.159292	T:0.763636 C:0.236364
MA_15382:33267	MA_15382g0010	F-box/RNI-like superfamily protein	Gly310Glu	Reference (G) Alternate (A)	G:0.689956 A:0.310044	G:0.711905 A:0.288095	G:0.585165 A:0.414835	G:0.556931 A:0.443069	G:0.567935 A:0.432065	G:0.461187 A:0.538813
MA_14234:43020	MA_14234g0010	Adenine nucleotide alpha hydrolases-like superfamily protein	Arg25Gly	Reference (C) Alternate (G)	C:0.985417 G:0.0145833	C:0.995098 G:0.00490196	C:0.975543 G:0.0244565	C:0.977273 G:0.0227273	C:0.962523 G:0.0374771	C:0.956019 G:0.0439815
MA_129478:6147	MA_129478g0010	BRASSINOSTEROID-RESPONSIVE RING-H2 (BRH1)	Ile64Val	Reference (A) Alternate (G)	A:0.103306 G:0.896694	A:0.11165 G:0.88835	A:0.145946 G:0.854054	A:0.141791 G:0.858209	A:0.138989 G:0.861011	A:0.334101 G:0.665899
MA_116552:11911	MA_116552g0010	CVP2 LIKE 1 (CVL1)	Arg141Thr	Reference (G) Alternate (C)	G:0.993534 C:0.00646552	G:0.978155 C:0.0218447	G:0.988827 C:0.0111732	G:0.967822 C:0.0321782	G:0.969203 C:0.0307971	G:0.969626 C:0.0303738
MA_10265740:3728	MA_10265740g0010	lectin protein kinase family protein	Phe60Ser	Reference (T) Alternate (C)	T:0.975207 C:0.0247934	T:0.983254 C:0.0167464	T:0.931319 C:0.0686813	T:0.930952 C:0.0690476	T:0.901596 C:0.0984043	T:0.905405 C:0.0945946
MA_10265740:5430	MA_10265740g0010	lectin protein kinase family protein	Asn627Lys	Reference (C) Alternate (G)	C:1 G:0	C:0.992424 G:0.00757576	C:0.980114 G:0.0198864	C:0.976562 G:0.0234375	C:0.958333 G:0.0416667	C:0.960094 G:0.0399061
MA_10265740:5624	MA_10265740g0010	lectin protein kinase family protein	Arg692His	Reference (G) Alternate (A)	G:0.959184 A:0.0408163	G:0.966981 A:0.0330189	G:0.882353 A:0.117647	G:0.866029 A:0.133971	G:0.826585 A:0.173415	G:0.830317 A:0.169683
MA_10265740:5737	MA_10265740g0010	lectin protein kinase family protein	Val730Leu	Reference (G) Alternate (T)	G:0.971074 T:0.0289256	G:0.966667 T:0.0333333	G:0.895161 T:0.104839	G:0.877404 T:0.122596	G:0.83659 T:0.16341	G:0.844595 T:0.155405
MA_10265740:5784	MA_10265740g0010	lectin protein kinase family protein	Gln745His	Reference (A) Alternate (C)	A:0.946502 C:0.0534979	A:0.96875 C:0.03125	A:0.893443 C:0.106557	A:0.855392 C:0.144608	A:0.832423 C:0.167577	A:0.845622 C:0.154378
MA_10238024:5310	MA_10238024g0010	hypothetical protein	Glu147Lys	Reference (G) Alternate (A)	G:0.960905 A:0.0390947	G:0.95 A:0.05	G:0.932796 A:0.0672043	G:0.908213 A:0.0917874	G:0.922662 A:0.0773381	G:0.864679 A:0.135321

MA_10208460:670	MA_10208460g0010	NUCLEAR RNA POLYMERASE D2B (NRPD2B)	Val31Leu	Reference (G) Alternate (C)	G:0.954918 C:0.045082	G:0.943128 C:0.056872	G:0.975806 C:0.0241935	G:0.971292 C:0.0287081	G:0.97043 C:0.0295699	G:0.984018 C:0.0159817
MA_388691:5378	MA_388691g0010	Photosystem II lipoprotein (PSB27)	Cys52Tyr	Reference (G) Alternate (A)	G:0.246835 A:0.753165	G:0.256098 A:0.743902	G:0.23743 A:0.76257	G:0.275862 A:0.724138	G:0.27808 A:0.72192	G:0.3 A:0.7

Table S10 Gene expression of non-DEGs (controls) in response to SHADE in Norway spruce

Gene_ID	TAIR	Primary Gene Symbol	Gene Model Description	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj
MA_10021g0010	AT5G07040	RING/U-box superfamily prot	RING/U-box superfamily protein	14.570416	1.938381436	0.7522544	2.5767632	0.00997303	0.27745053
MA_10061g0010	AT2G43120	PIRIN2, PRN2	Encodes a member of the function	177.11837	-0.177315276	0.2075426	-0.854356	0.39290785	0.99992075
MA_100380g0010	AT1G24330	ARM repeat superfamily prot	ARM repeat superfamily protein	226.52852	0.361978156	0.2558102	1.4150264	0.15706076	0.94760895
MA_100868g0010	AT2G40610	ATEXP8	member of Alpha-Expansin Gene	17.060885	1.611278446	0.7906084	2.0380233	0.0415476	0.61826162
MA_101097g0010	AT3G11750	FOLB1	Encodes an enzyme that can act a	127.67383	0.103704993	0.29544	0.3510188	0.72557425	0.99992075
MA_10048552g0010	AT1G17650	ATGLYR2	Glyoxylate reductase located in ch	410.32766	-0.29535518	0.3698652	-0.798548	0.42455241	0.99992075
MA_10055565g0010	AT2G41475	ATS3A	Embryo-specific protein 3, (ATS3)	47.664244	0.006263711	0.3115459	0.0201053	0.98395941	0.99992075
MA_10085364g0010	AT3G48730	GSAM	glutamate-1-semialdehyde 2,1-an	309.56684	0.163151046	0.1892884	0.8619177	0.38873283	0.99992075
MA_10111432g0010	AT4G34050	CCOAOMT1	Methyltransferase in the lignin bi	54.675449	0.564759944	1.1107334	0.5084568	0.61113304	0.99992075
MA_10086651g0010	AT5G59250	HP59, PLASTIDIC SUGAR TRAN	Encodes a chloroplast localized H-	146.98322	0.077330586	0.348358	0.221986	0.8243248	0.99992075

Table S11 Allele frequencies of the non-DEGs (controls) in response to SHADE in Norway spruce

				Population-wise allele frequency						
ContigID:Snpposition	Gene_ID	Gene name	Amino acid change	Allele	S1	S2	S3	S4	S5	S6
MA_10021:11111	MA_10021g0010	RING/U-box supe	Gln116Glu	Reference (C)	0.987552	0.968293	0.991892	0.972772	0.975655	0.984018
				Reference (G)	0.0124481	0.0317073	0.00810811	0.0272277	0.0243446	0.0159817
MA_10021:11118	MA_10021g0010	RING/U-box supe	Ser113Ser	Reference (C)	0.927083	0.939614	0.959239	0.970732	0.955473	0.942922
				Reference (A)	0.0729167	0.0603865	0.0407609	0.0292683	0.0445269	0.0570776
MA_10021:11258	MA_10021g0010	RING/U-box supe	Thr67Ala	Reference (A)	0.983673	0.957346	0.991935	0.97381	0.972855	0.982063
				Reference (G)	0.0163265	0.042654	0.00806452	0.0261905	0.0271454	0.0179372
MA_10021:11300	MA_10021g0010	RING/U-box supe	Gly53Ser	Reference (G)	0.863265	0.876777	0.787634	0.644231	0.6	0.671946
				Reference (A)	0.136735	0.123223	0.212366	0.355769	0.4	0.328054
MA_10021:11309	MA_10021g0010	RING/U-box supe	His50Tyr	Reference (C)	0.944898	0.947867	0.924731	0.890476	0.923759	0.905405
				Reference (T)	0.055102	0.0521327	0.0752688	0.109524	0.0762411	0.0945946
MA_10061:6620	MA_10061g0010	PIRIN2, PRN2	Val34Ala	Reference (T)	0.343621	0.345972	0.409836	0.368421	0.283036	0.266204
				Reference (C)	0.656379	0.654028	0.590164	0.631579	0.716964	0.733796
MA_10061:6652	MA_10061g0010	PIRIN2, PRN2	Pro23Pro	Reference (C)	0.936475	0.933649	0.921622	0.911905	0.884071	0.927928
				Reference (G)	0.0635246	0.0663507	0.0783784	0.0880952	0.115929	0.0720721
MA_10061:6670	MA_10061g0010	PIRIN2, PRN2	Leu17Leu	Reference (T)	0.887295	0.889151	0.856757	0.868421	0.867908	0.855204
				Reference (A)	0.112705	0.110849	0.143243	0.131579	0.132092	0.144796
MA_100380:7172	MA_100380g0010	ARM repeat supe	Val159Ile	Reference (G)	0.989451	0.980392	0.97541	1	0.999094	1
				Reference (A)	0.0105485	0.0196078	0.0245902	0	0.0009058	0
MA_100380:7185	MA_100380g0010	ARM repeat supe	Thr154Thr	Reference (T)	0.925847	0.948529	0.925824	0.878788	0.894737	0.857143
				Reference (G)	0.0741525	0.0514706	0.0741758	0.121212	0.105263	0.142857
MA_100380:7212	MA_100380g0010	ARM repeat supe	His145Gln	Reference (T)	0.783843	0.7725	0.798343	0.870558	0.864545	0.892523
				Reference (G)	0.216157	0.2275	0.201657	0.129442	0.135455	0.107477
MA_100868:5630	MA_100868g0010	ATEXP8	Glu104Lys	Reference (G)	0.910042	0.903382	0.895161	0.888614	0.933996	0.917431
				Reference (A)	0.0899582	0.0966184	0.104839	0.111386	0.0660036	0.0825688
MA_100868:5663	MA_100868g0010	ATEXP8	Ser93Cys	Reference (A)	0.954936	0.956311	0.940217	0.972772	0.971296	0.955399
				Reference (T)	0.0450644	0.0436893	0.0597826	0.0272277	0.0287037	0.0446009
MA_101097:19803	MA_101097g0010	FOLB1	Ser17Asn	Reference (G)	0.944215	0.971564	0.954054	0.978261	0.983186	0.984091
				Reference (A)	0.0557851	0.028436	0.0459459	0.0217391	0.0168142	0.0159091
MA_101097:19843	MA_101097g0010	FOLB1	Gly4Arg	Reference (G)	0.921488	0.954762	0.967391	0.97619	0.969697	0.961538
				Reference (A)	0.0785124	0.0452381	0.0326087	0.0238095	0.030303	0.0384615
MA_10048552:1277	MA_10048552g0010	ATGLYR2	Gly6Val	Reference (G)	0.975309	0.992925	0.986559	0.988038	0.975439	0.986486
				Reference (T)	0.0246914	0.00707547	0.0134409	0.0119617	0.0245614	0.0135135
MA_10048552:1293	MA_10048552g0010	ATGLYR2	Gly11Gly	Reference (C)	0.362705	0.375	0.400538	0.419431	0.490317	0.412162
				Reference (A)	0.637295	0.625	0.599462	0.580569	0.509683	0.587838
MA_10055565:3050	MA_10055565g0010	ATS3A	Asp21Asp	Reference (C)	0.969828	0.965517	0.983425	0.971939	0.982143	0.961905
				Reference (T)	0.0301724	0.0344828	0.0165746	0.0280612	0.0178571	0.0380952
MA_10055565:3055	MA_10055565g0010	ATS3A	Ala20Thr	Reference (G)	0.980851	0.985222	0.97486	0.94359	0.954545	0.943128
				Reference (A)	0.0191489	0.0147783	0.0251397	0.0564103	0.0454545	0.056872
MA_10085364:3481	MA_10085364g0010	GSAM	Glu211Glu	Reference (A)	0.863043	0.893564	0.840782	0.914508	0.925414	0.908451
				Reference (G)	0.136957	0.106436	0.159218	0.0854922	0.0745856	0.0915493
MA_10085364:3493	MA_10085364g0010	GSAM	Gly207Gly	Reference (A)	0.978992	0.985646	0.983607	0.972222	0.979167	0.972222
				Reference (T)	0.0210084	0.0143541	0.0163934	0.0277778	0.0208333	0.0277778
MA_10085364:3886	MA_10085364g0010	GSAM	Ala76Ala	Reference (A)	0.973361	0.980952	0.981183	0.962085	0.976357	0.961712
				Reference (T)	0.0266393	0.0190476	0.0188172	0.0379147	0.0236427	0.0382883
MA_10085364:3907	MA_10085364g0010	GSAM	Asp69Glu	Reference (T)	0.985656	0.995238	0.983871	0.988152	0.987741	0.997758
				Reference (A)	0.0143443	0.0047619	0.016129	0.0118483	0.0122592	0.00224215
MA_10085364:3926	MA_10085364g0010	GSAM	Glu63Gly	Reference (A)	0.985714	0.995238	0.983871	0.988152	0.988616	0.997748
				Reference (G)	0.0142857	0.0047619	0.016129	0.0118483	0.0113835	0.00225225
MA_10111432:302	MA_10111432g0010	CCOAOMT1	Val53Asp	Reference (T)	0.983607	0.969194	0.978495	0.938095	0.920635	0.959459
				Reference (A)	0.0163934	0.0308057	0.0215054	0.0619048	0.0793651	0.0405405
MA_10111432:322	MA_10111432g0010	CCOAOMT1	Arg60Arg	Reference (A)	0.967078	0.936019	0.886486	0.858173	0.794484	0.790541
				Reference (C)	0.0329218	0.063981	0.113514	0.141827	0.205516	0.209459
MA_10111432:336	MA_10111432g0010	CCOAOMT1	Glu64Asp	Reference (G)	0.843621	0.851415	0.857527	0.787081	0.740675	0.791855
				Reference (T)	0.156379	0.148585	0.142473	0.212919	0.259325	0.208145
MA_10111432:340	MA_10111432g0010	CCOAOMT1	Ala66Thr	Reference (G)	0.738683	0.787736	0.798387	0.695238	0.633628	0.710407
				Reference (A)	0.261317	0.212264	0.201613	0.304762	0.366372	0.289593
MA_10086651:5150	MA_10086651g0010	HP59, PLASTIDIC	Pro41Pro	Reference (A)	0.945607	0.939904	0.928962	0.908213	0.956912	0.961009
				Reference (G)	0.0543933	0.0600962	0.0710383	0.0917874	0.043088	0.0389908
MA_10086651:5166	MA_10086651g0010	HP59, PLASTIDIC	Trp36Ser	Reference (G)	0.943983	0.940476	0.92973	0.903846	0.952509	0.961187
				Reference (C)	0.0560166	0.0595238	0.0702703	0.0961538	0.047491	0.0388128

Fig.S1 Developmental stage of the Norway spruce seedlings with fully developed hypocotyls when the seedlings were harvested for all the experiments included in the study.

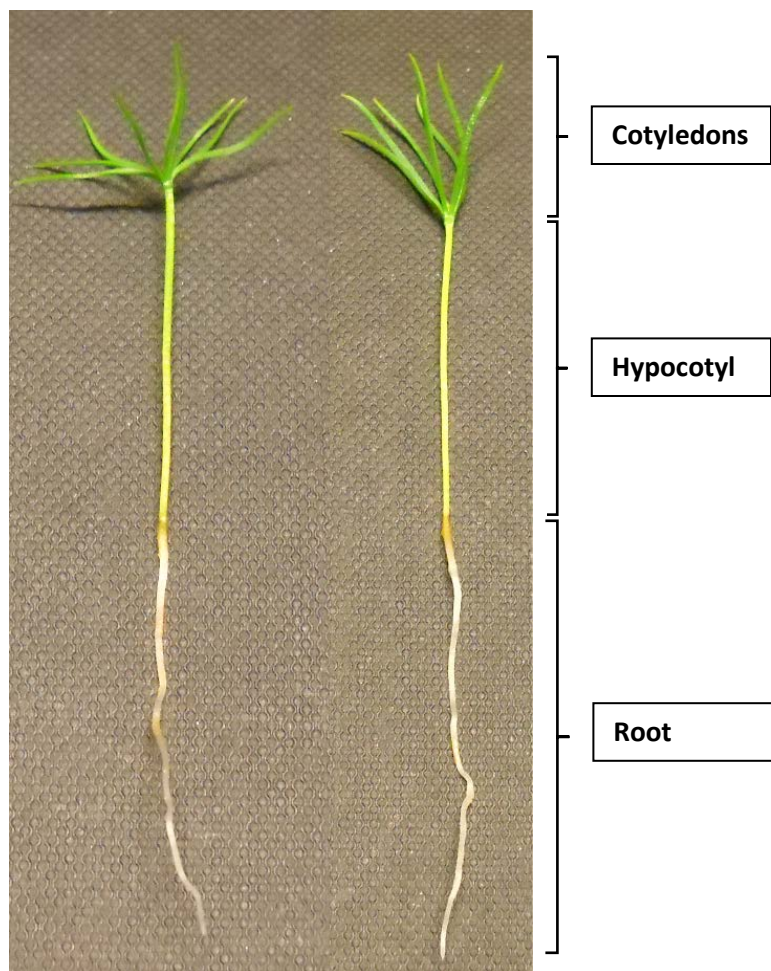


Fig.S2 Metabolism overview with the DEGs in response to shade in the northern and southern populations of Norway spruce. The network map represents the gene regulation in the northern population as compared to the southern one

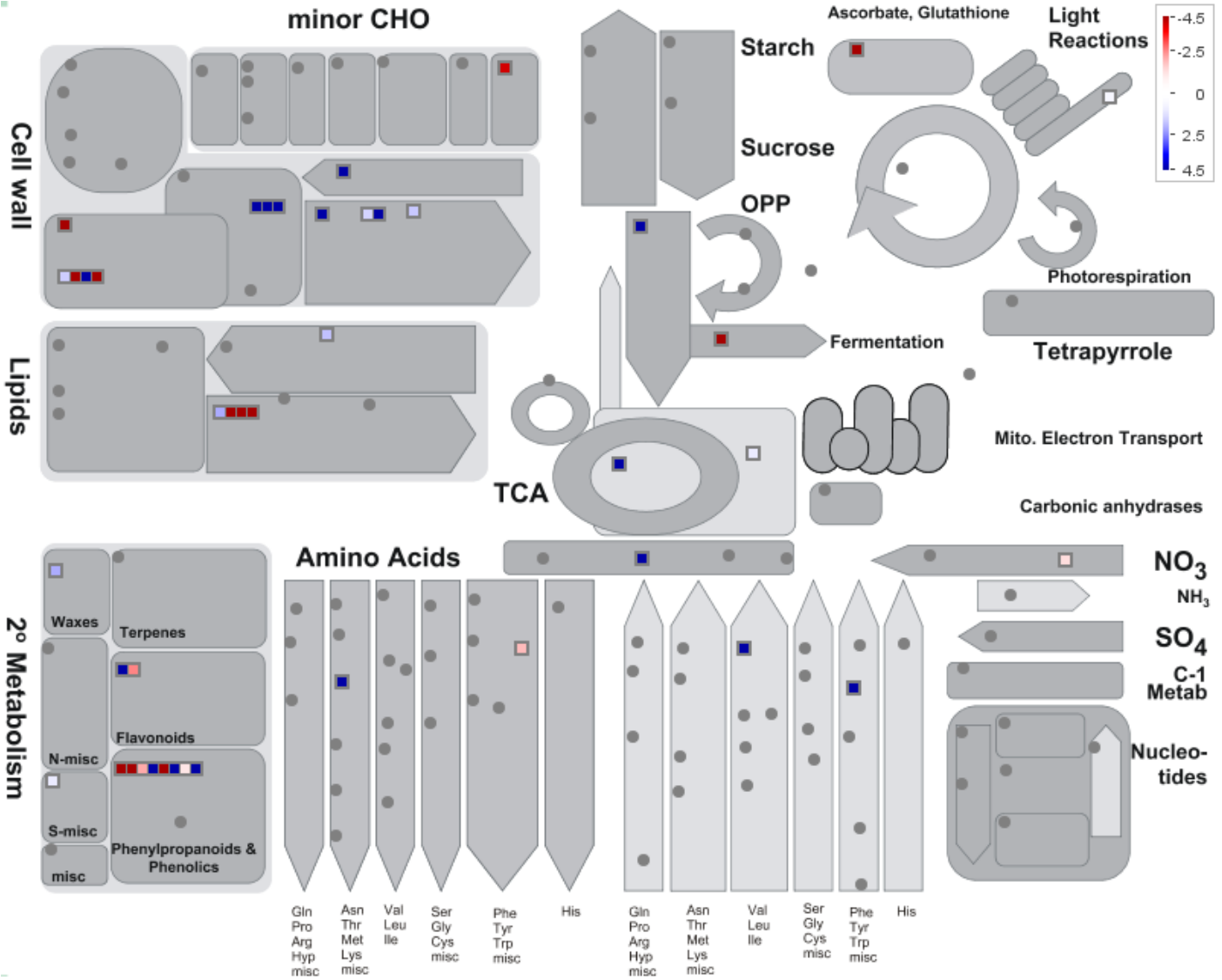


Fig.S3 Secondary metabolism with the DEGs in response to shade in the northern and southern populations of Norway spruce. The network map represents the gene regulation in the northern population as compared to the southern one

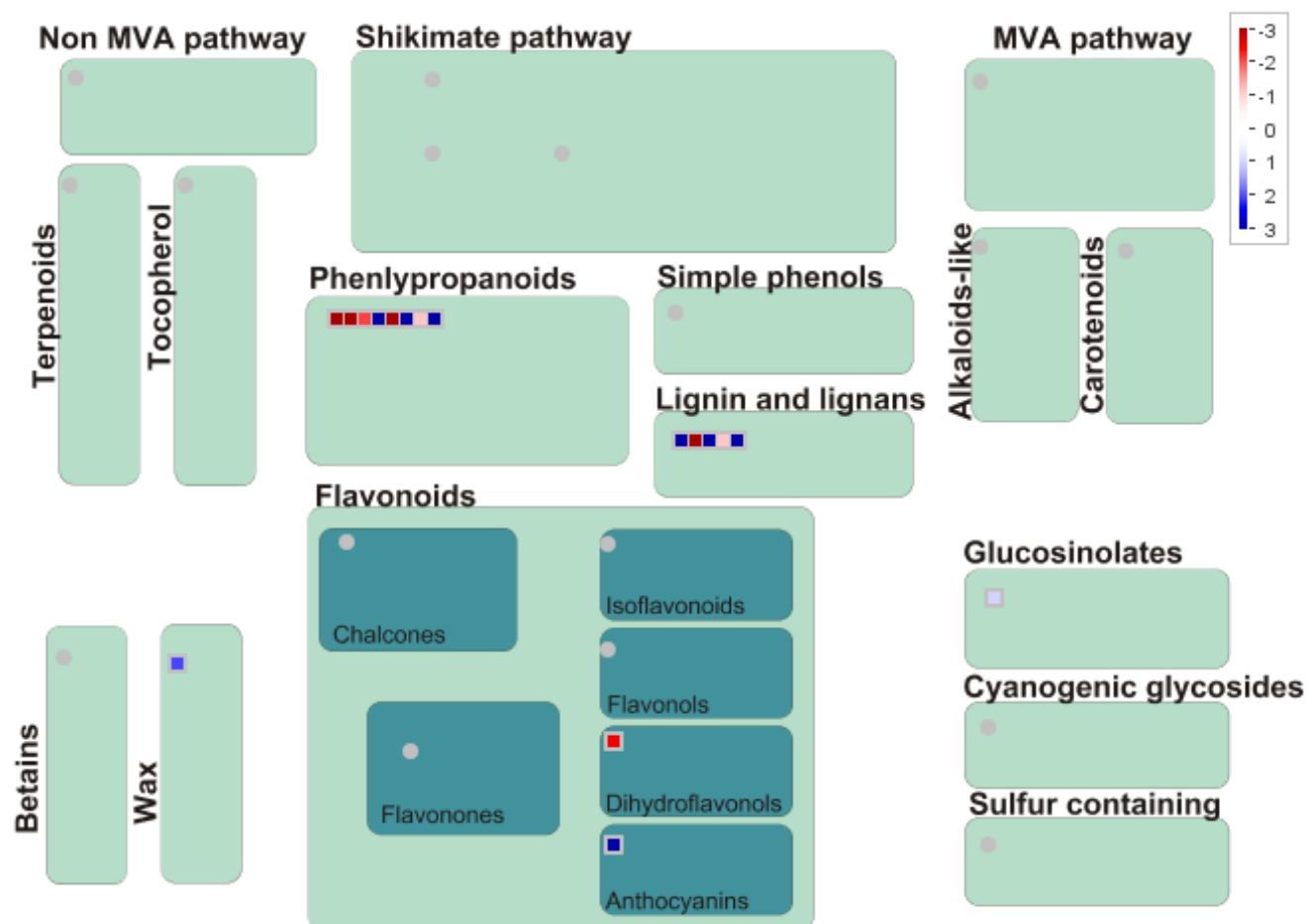


Fig.S4 Phenylpropanoid pathway with the DEGs in response to shade in the northern and southern populations of Norway spruce. The network map represents the gene regulation in the northern population as compared to the southern one

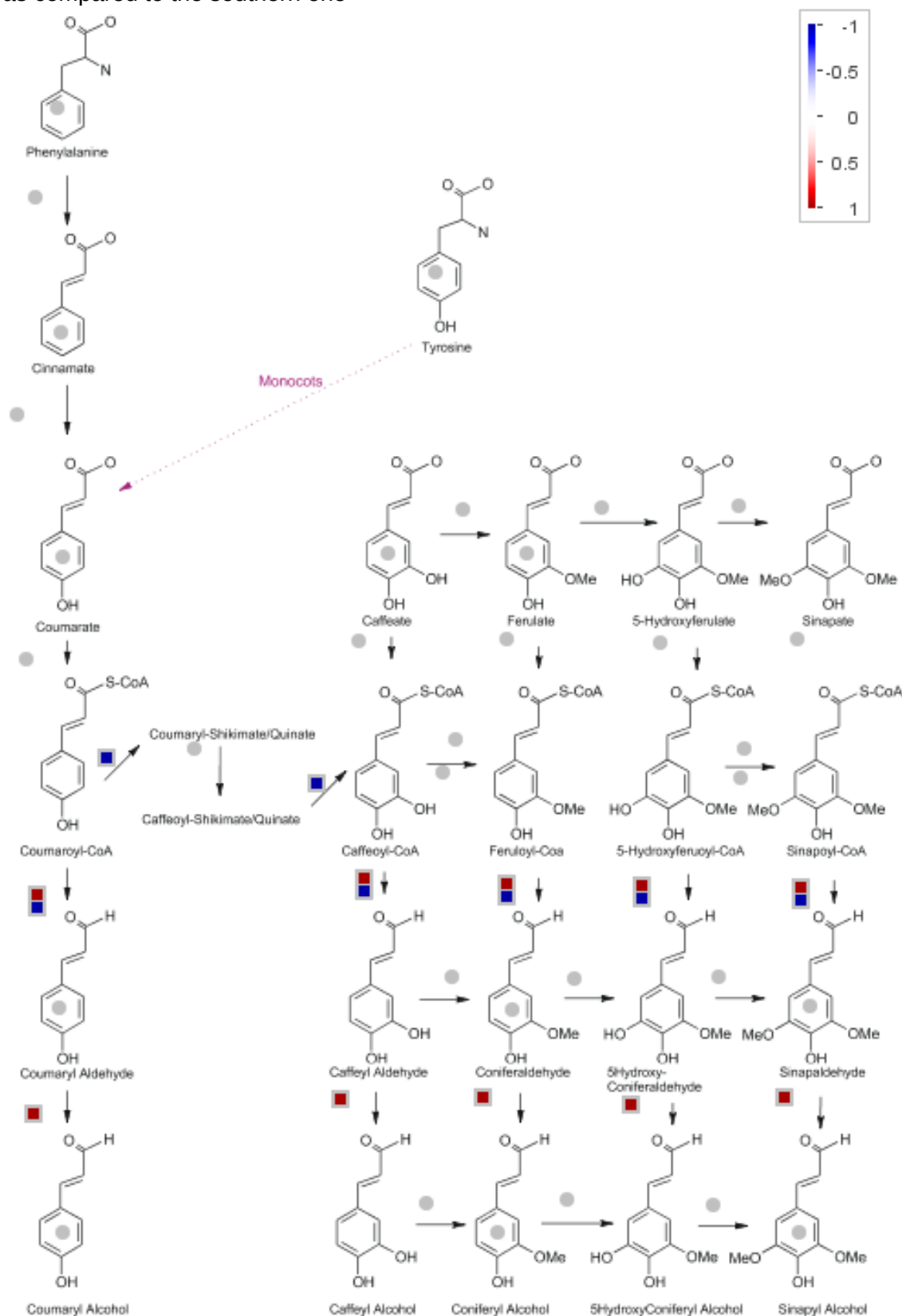


Fig.S5 Regulation overview with the DEGs in response to shade in the northern and southern populations of Norway spruce. The network map represents the gene regulation in the northern population as compared to the southern one

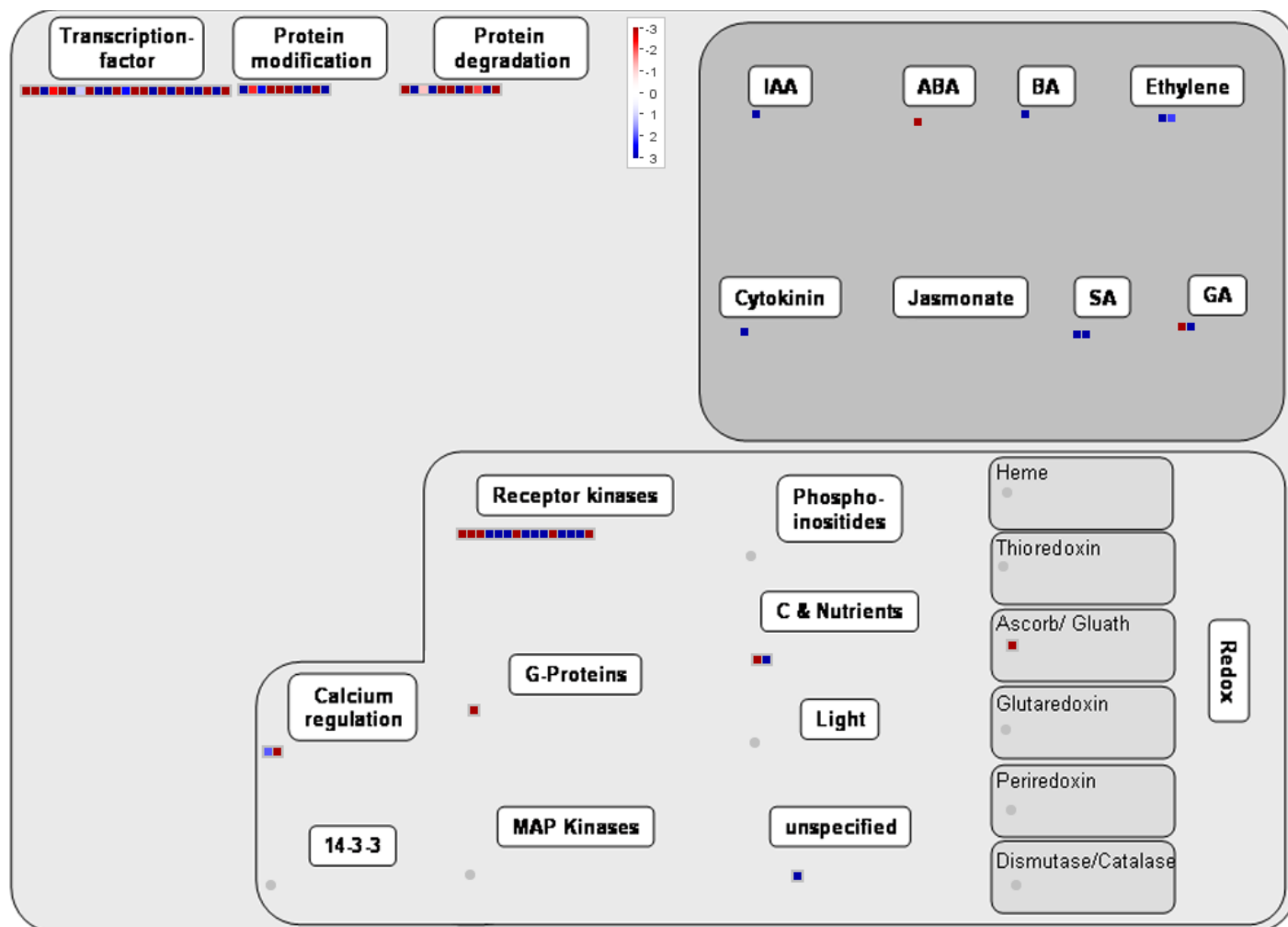


Fig.S6 Cellular response overview with the DEGs in response to shade in the northern and southern populations of Norway spruce. The network map represents the gene regulation in the northern population as compared to the southern one

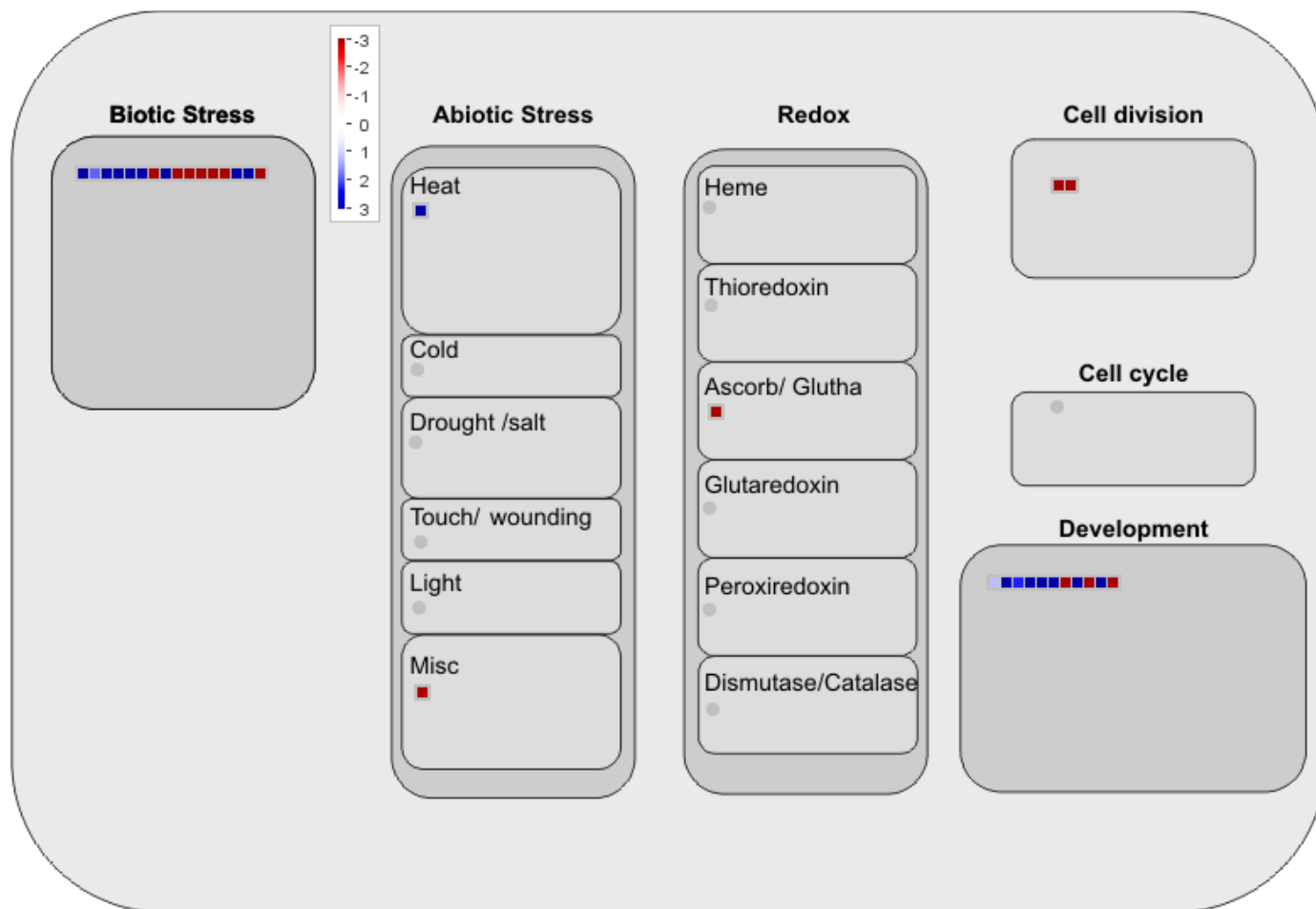
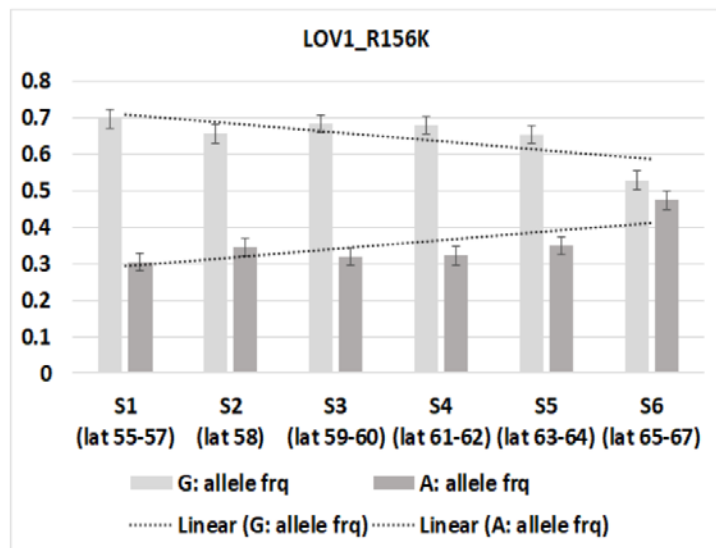


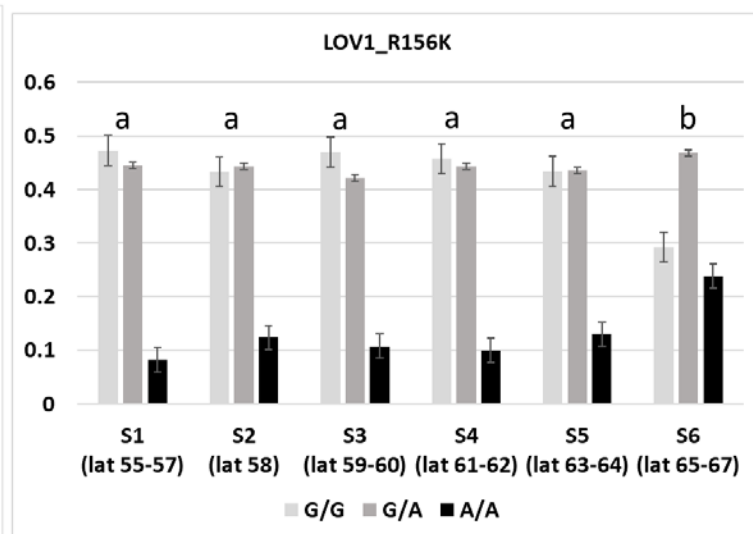
Fig.S7 Cline with reference to variation in allele and genotype frequencies of SNPs in the *LOV1* gene in Norway spruce populations across Sweden

a and c: allele frequencies of R156K and D190N respectively

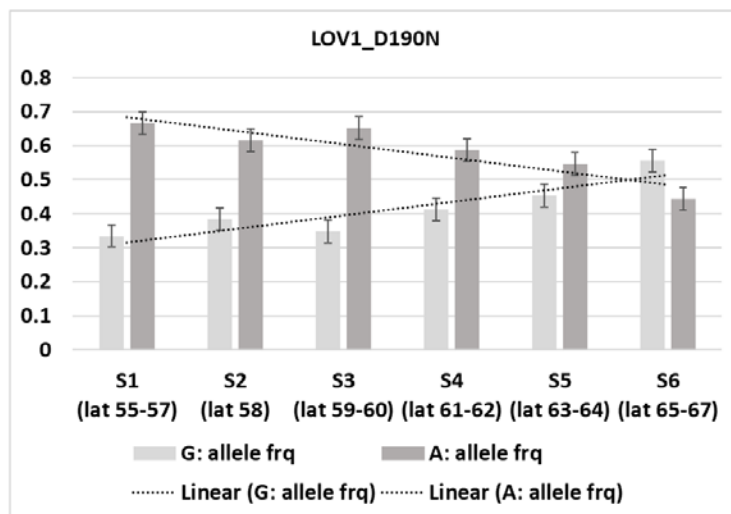
b and d: genotype frequencies of R156K and D190N respectively, Tukey's *post-hoc* categorization is indicated above the bars



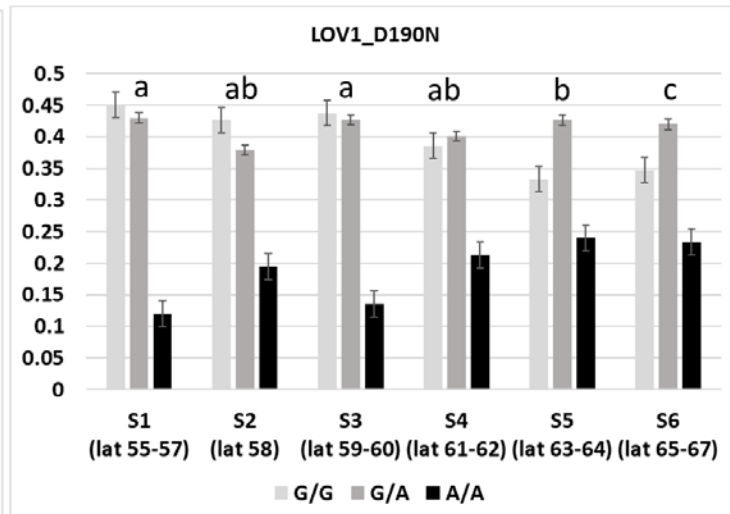
a



b



c



d

Fig.S8 Cline with reference to variation in allele and genotype frequencies of SNPs in the *SCRM2* gene in Norway spruce populations across Sweden

a and c: allele frequencies of T208M and S238N respectively
b and d: genotype frequencies of T208M and S238N respectively, Tukey's *post-hoc* categorization is indicated above the bars

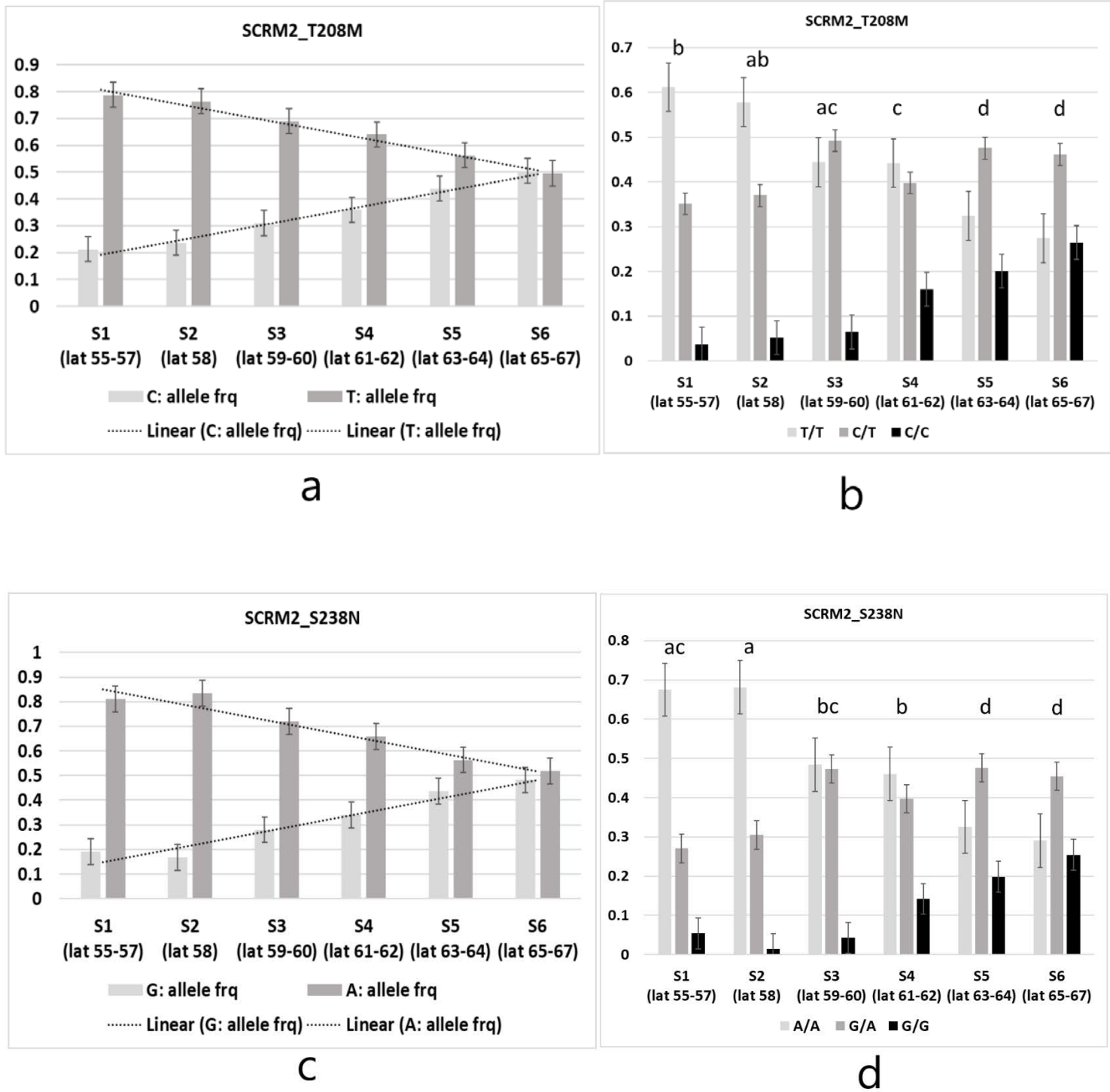
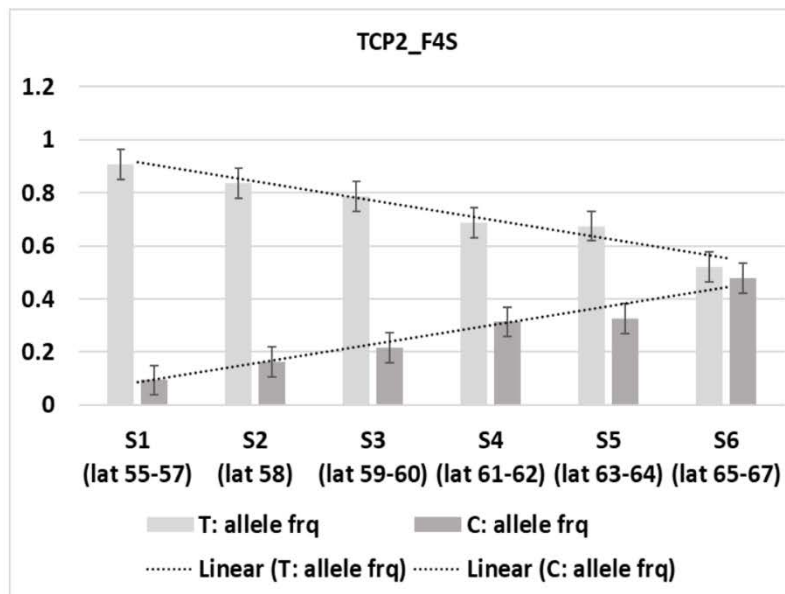


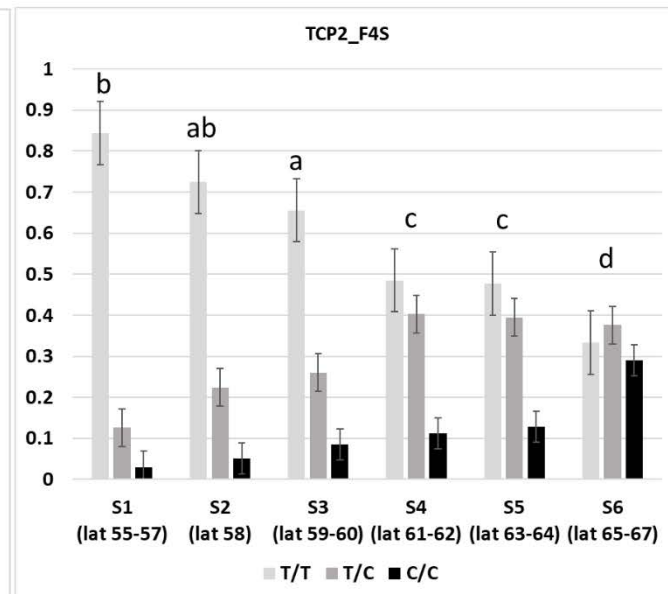
Fig.S9 Cline with reference to variation in allele and genotype frequencies of SNPs in the *TCP2* gene in Norway spruce populations across Sweden

a c e g and i: allele frequencies of F4S, V25A, E32G, E51K and I53F respectively

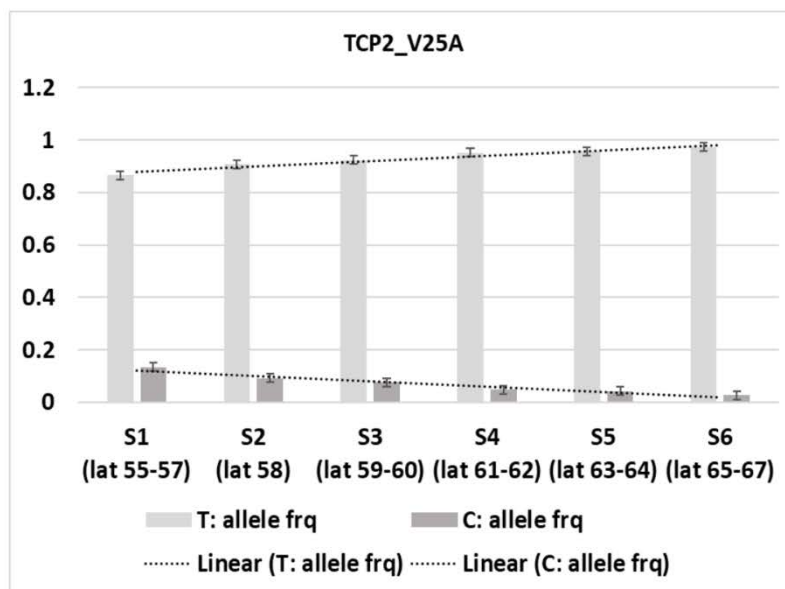
b d f h and j: genotype frequencies of F4S, V25A, E32G, E51K and I53F respectively, Tukey's *post-hoc* categorization is indicated above the bars



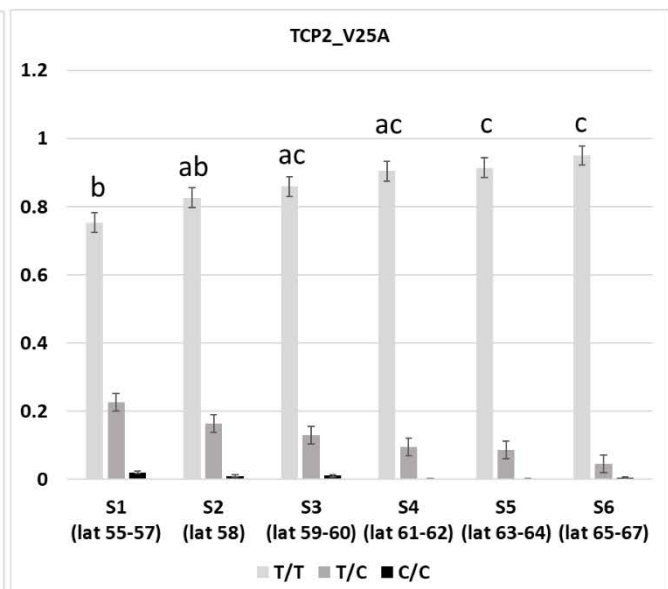
a



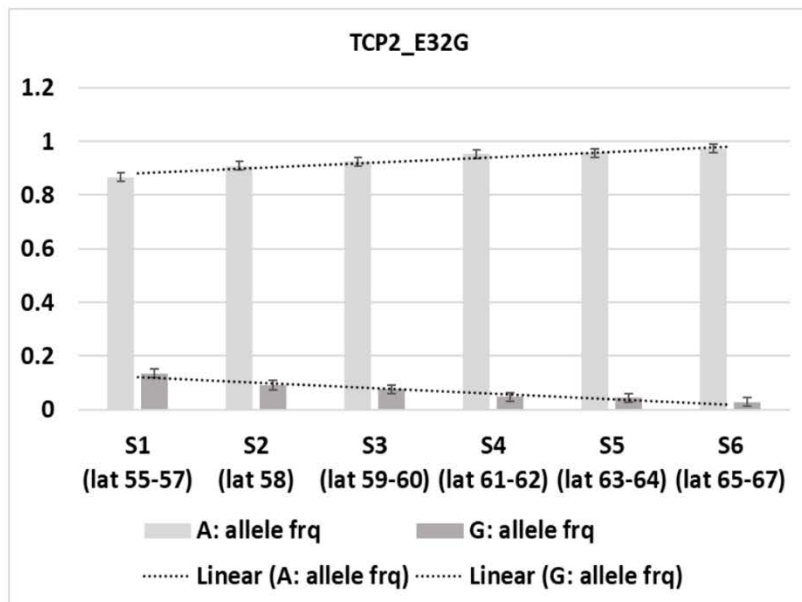
b



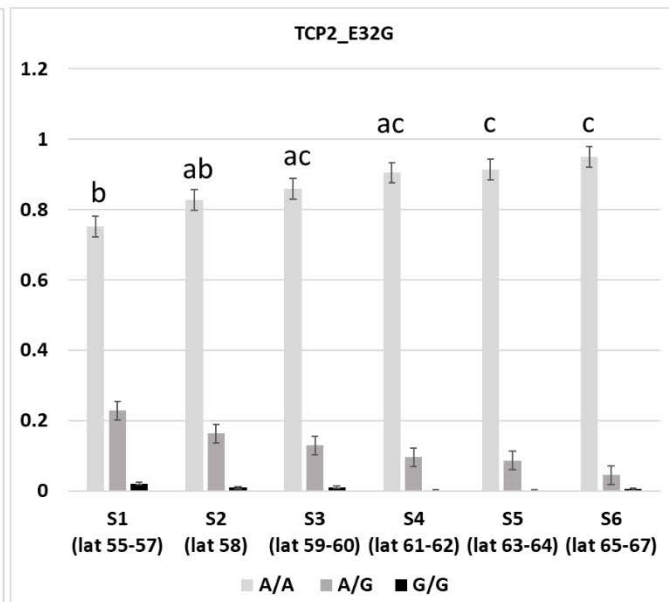
c



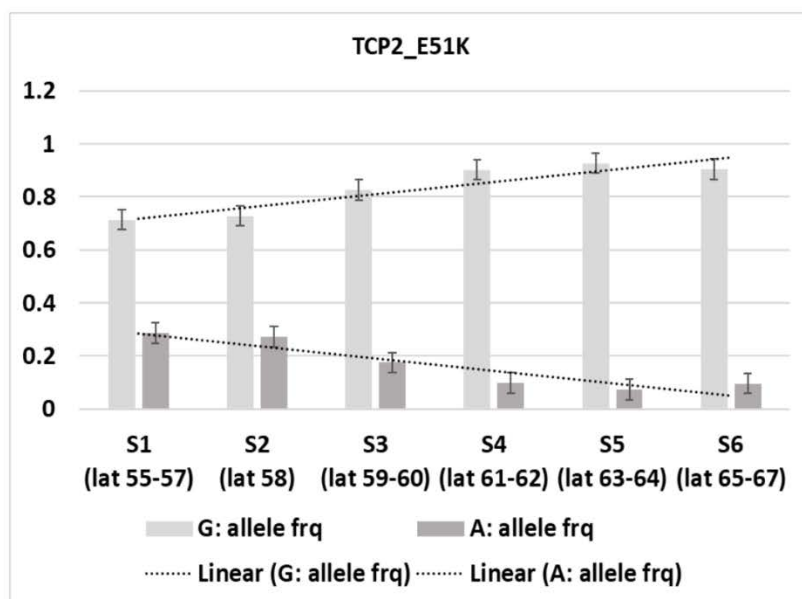
d



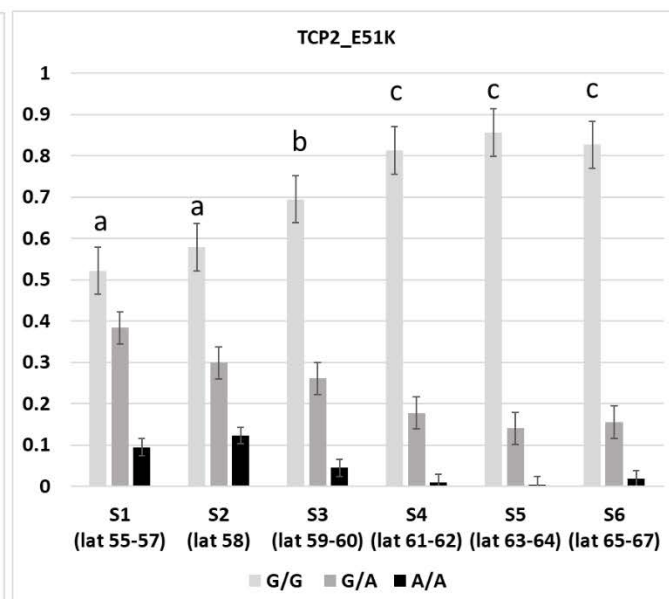
e



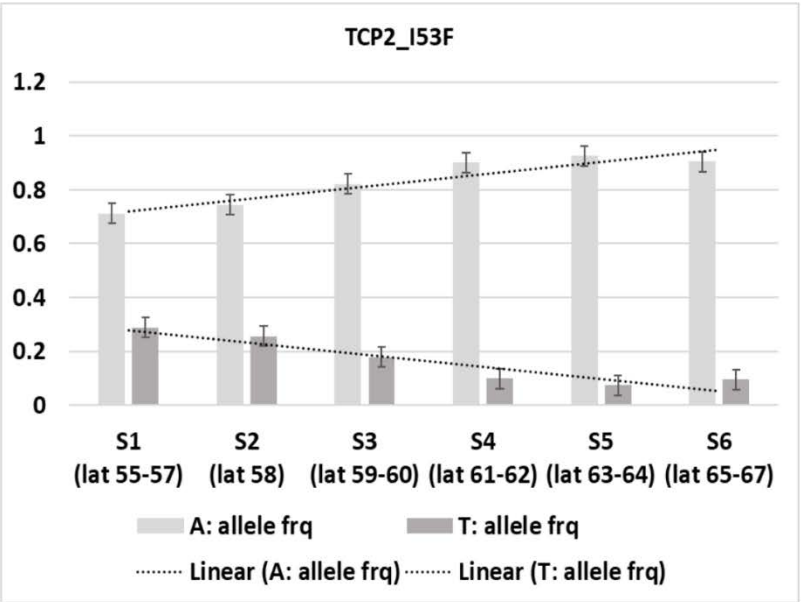
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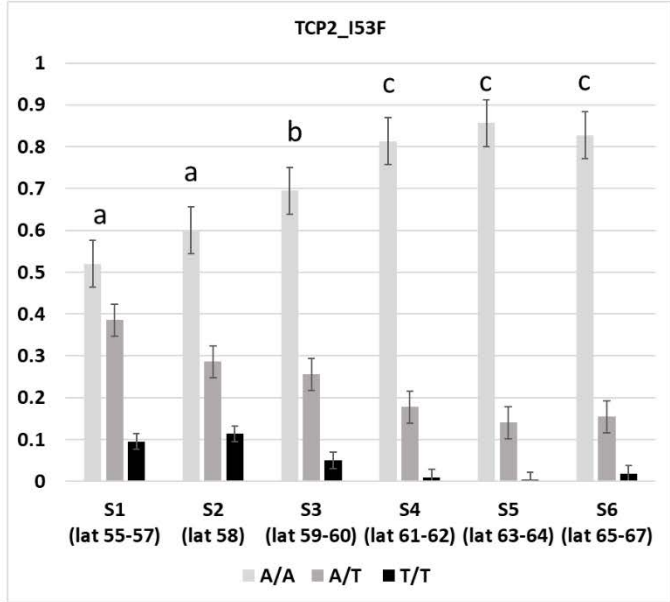
g



h



i

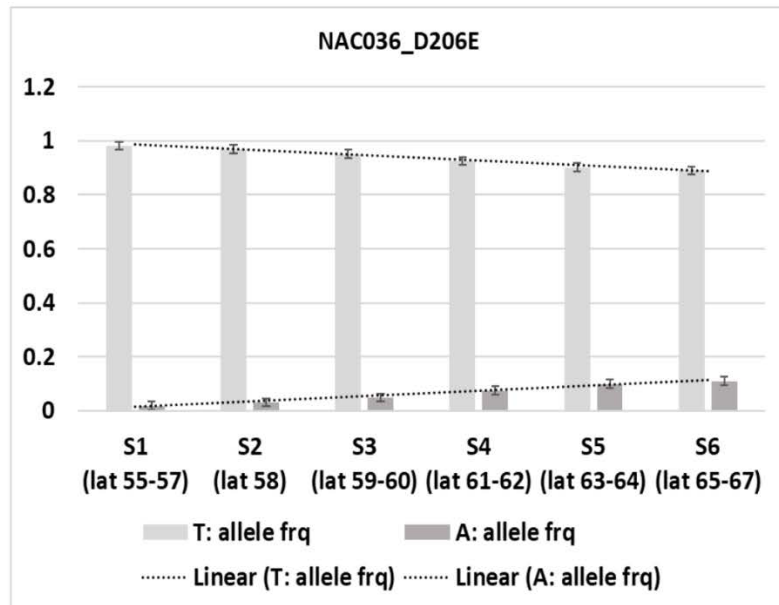


j

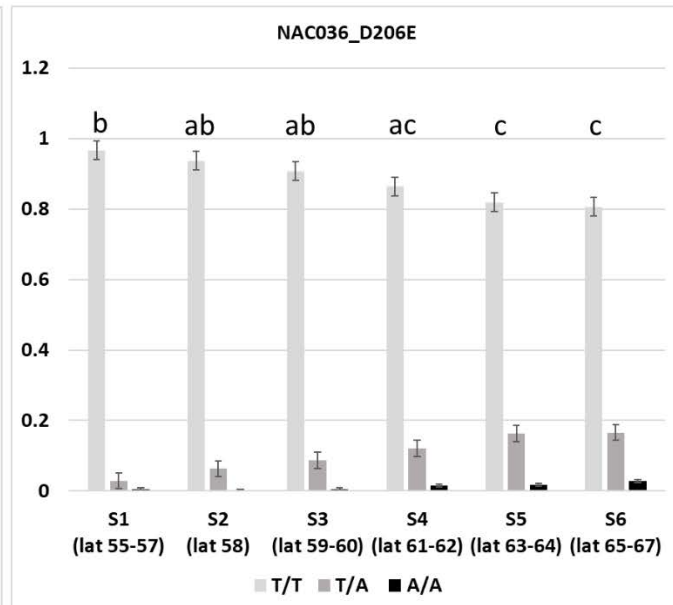
Fig.S10 Cline with reference to variation in allele and genotype frequencies of SNPs in the *NAC036* gene in Norway spruce populations across Sweden

a and c: allele frequencies of D206E and T237M respectively

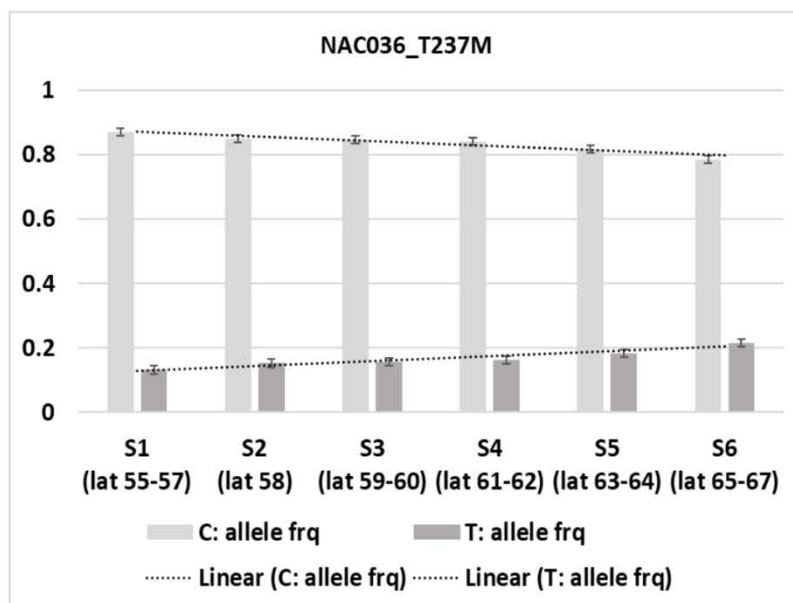
b and d: genotype frequencies of D206E and T237M respectively, Tukey's *post-hoc* categorization is indicated above the bars



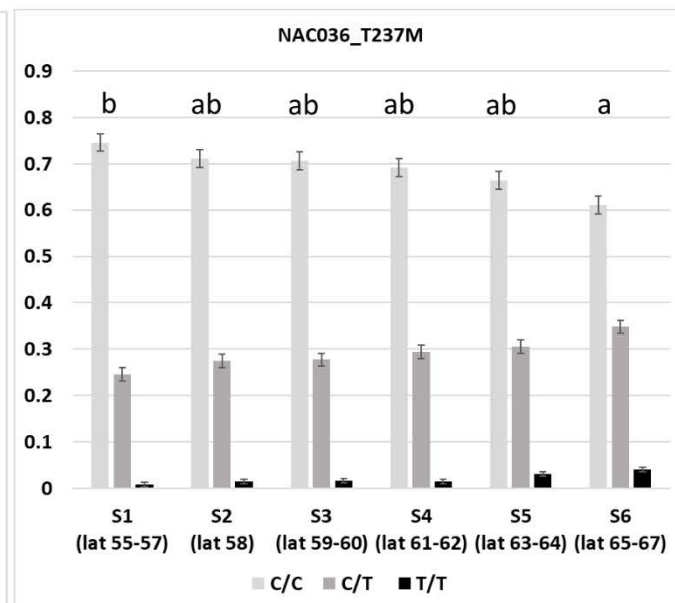
a



b



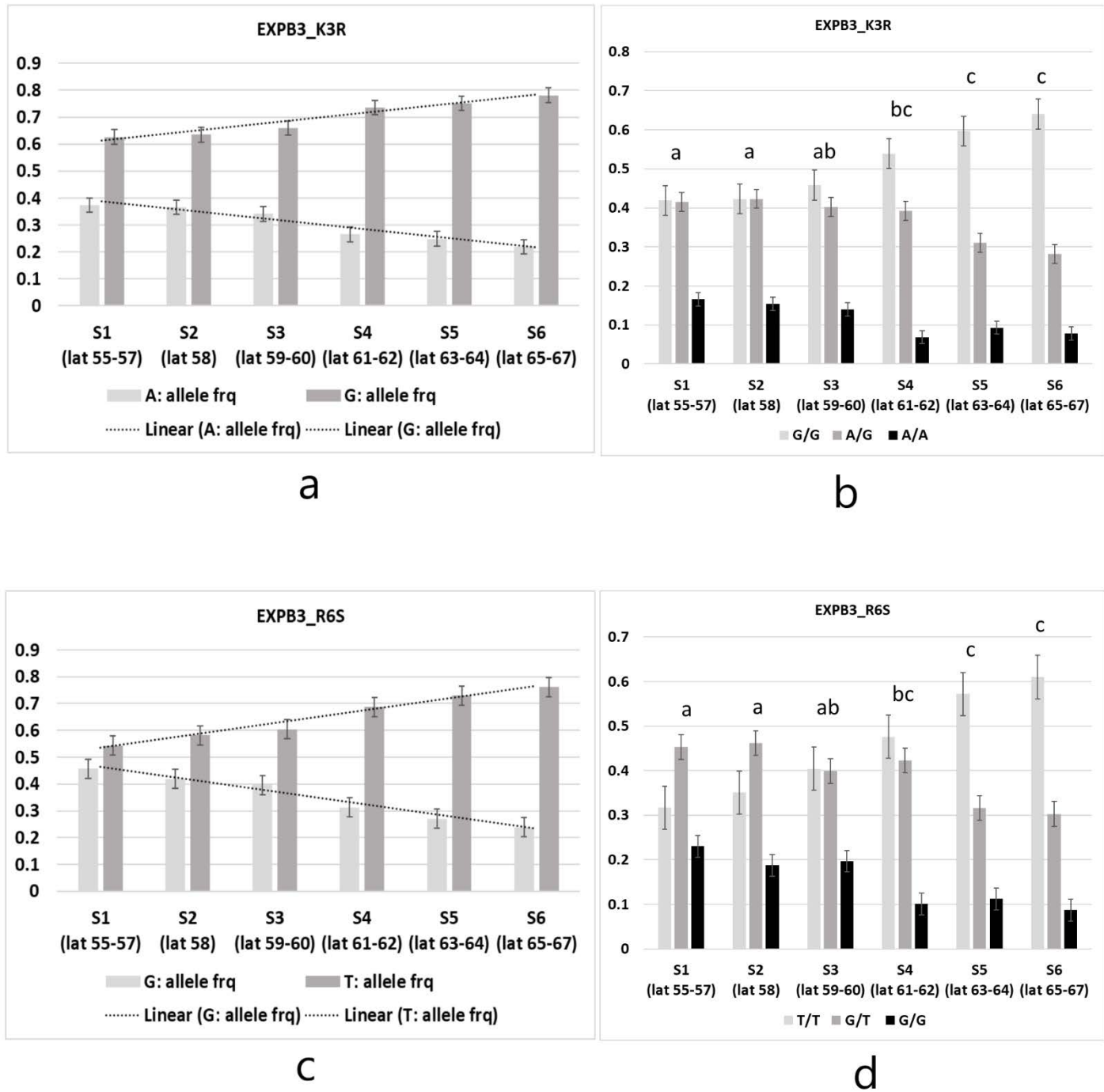
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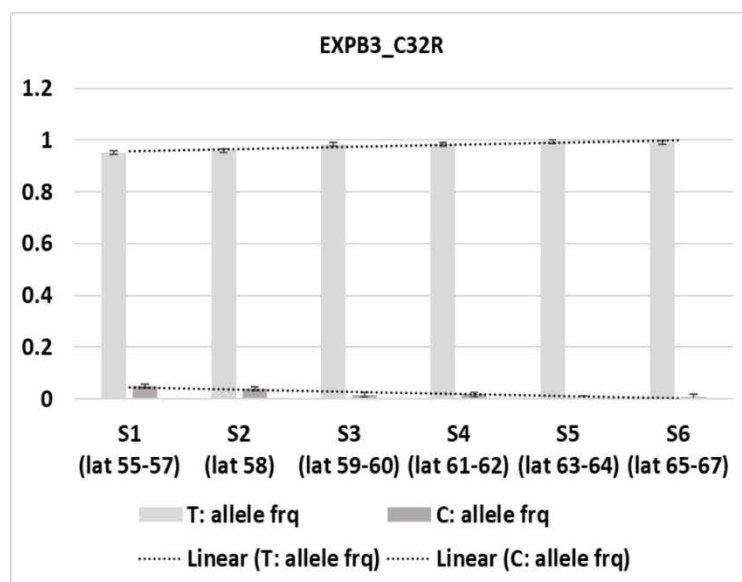


d

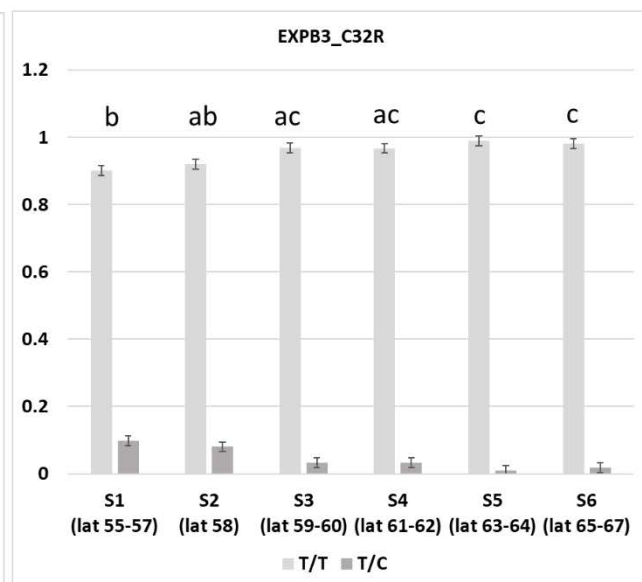
Fig.S11 Cline with reference to variation in allele and genotype frequencies of SNPs in the *EXPB3* gene in Norway spruce populations across Sweden

a c and e: allele frequencies of K3R, R6S and C32R respectively
b d and f: genotype frequencies of K3R, R6S and C32R respectively, Tukey's *post-hoc* categorization is indicated above the bars





e



f

Fig.S12 Cline with reference to variation in allele and genotype frequencies of SNP in the *FLZ6* gene in Norway spruce populations across Sweden

a allele frequencies of L88V

b genotype frequencies of L88V, Tukey's *post-hoc* categorization is indicated above the bars

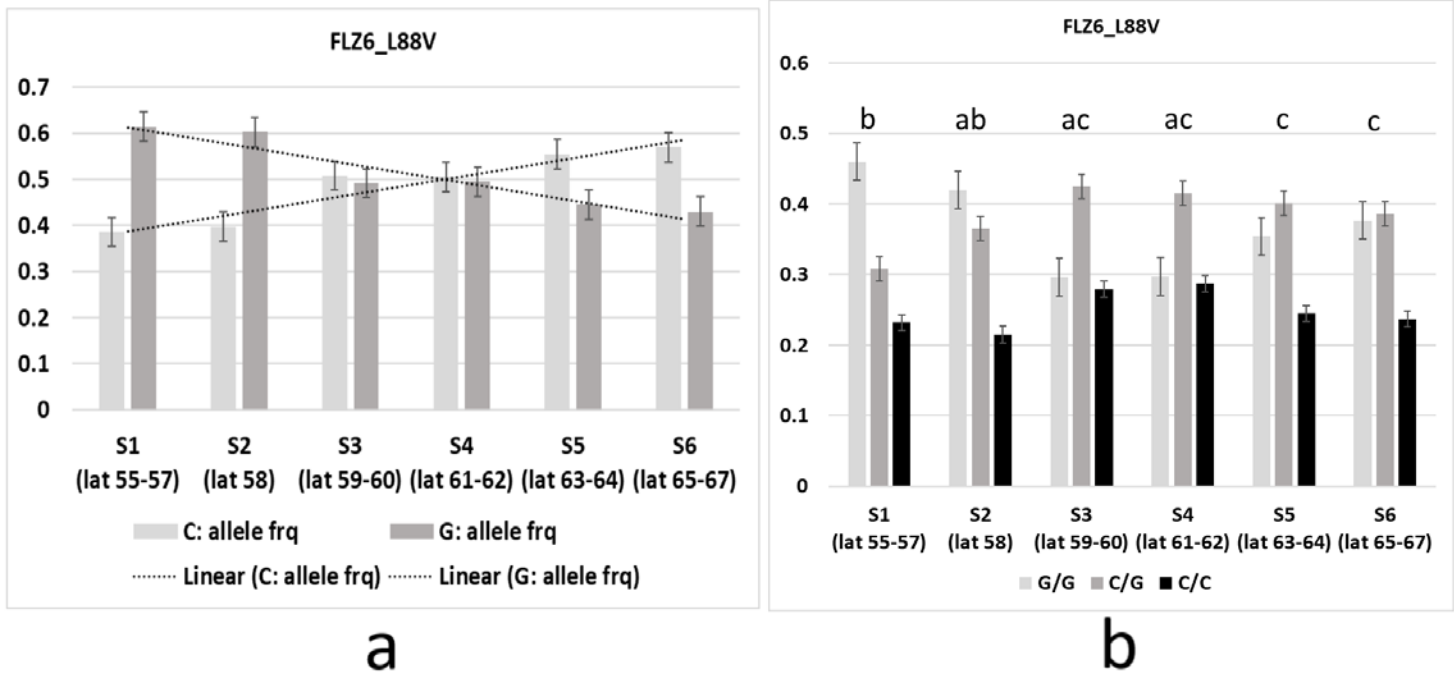
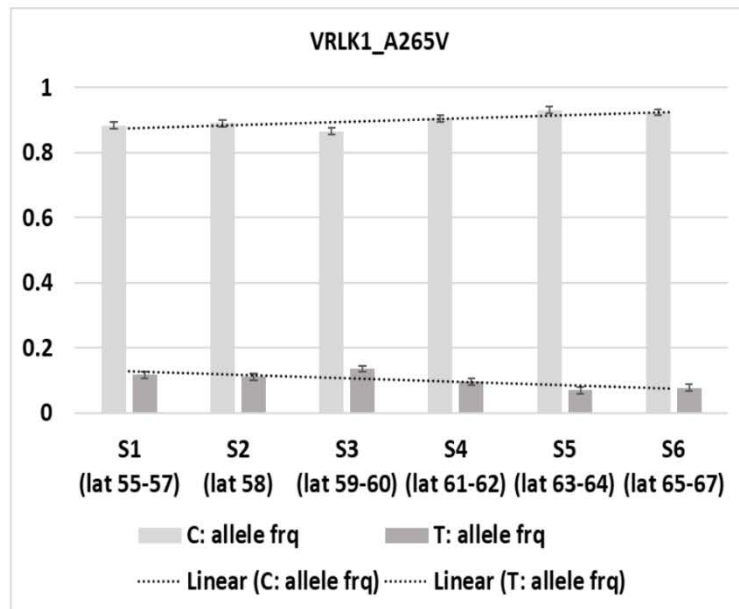


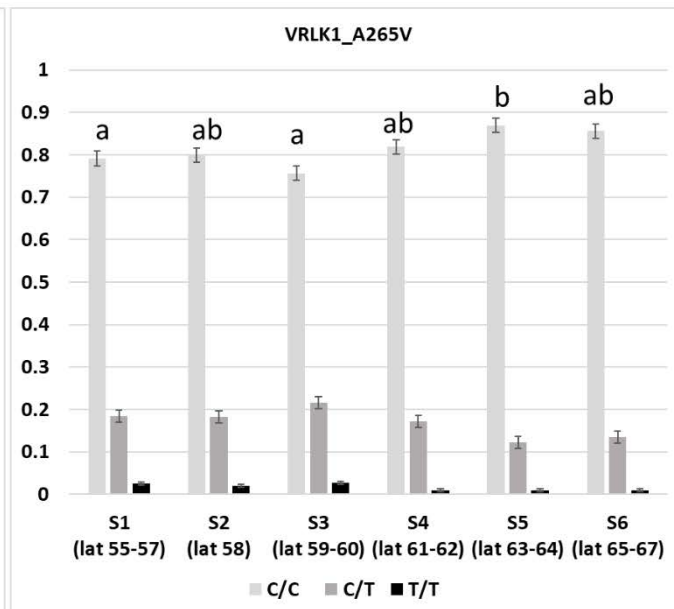
Fig.S13 Cline with reference to variation in allele and genotype frequencies of SNPs in the *VRLK1* gene in Norway spruce populations across Sweden

a and c: allele frequencies of A265V and V283L respectively

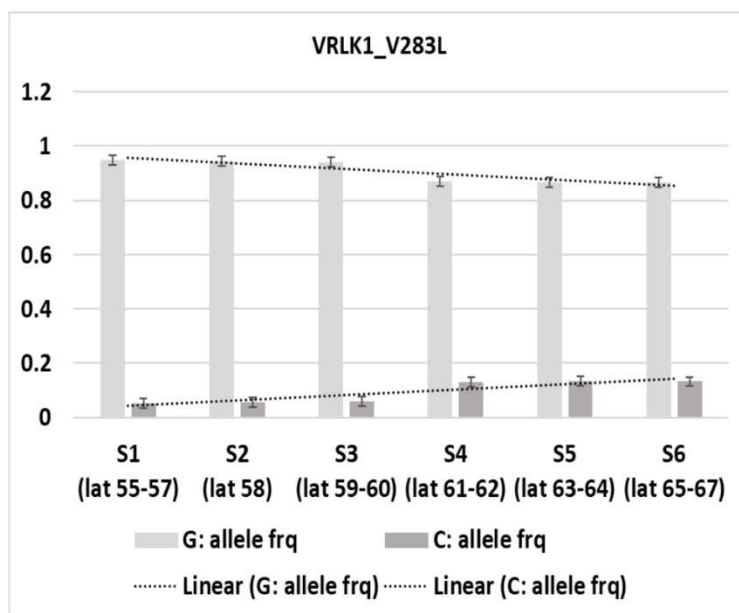
b and d: genotype frequencies of A265V and V283L respectively, Tukey's *post-hoc* categorization is indicated above the bars



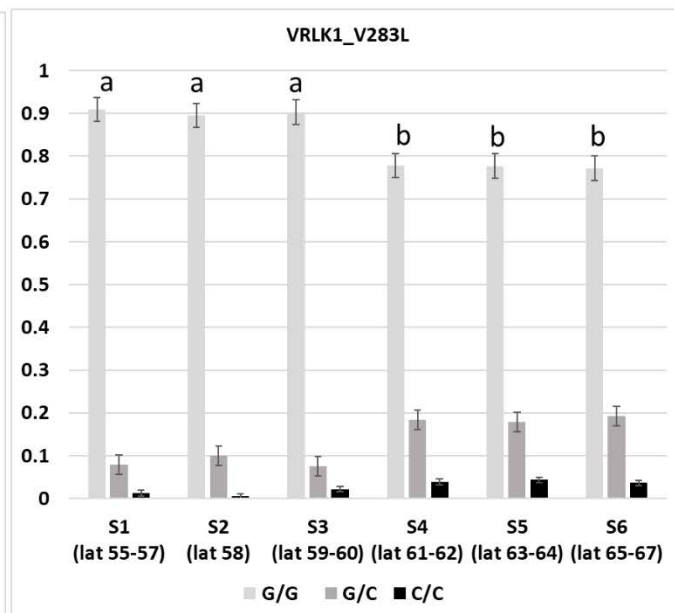
a



b



c

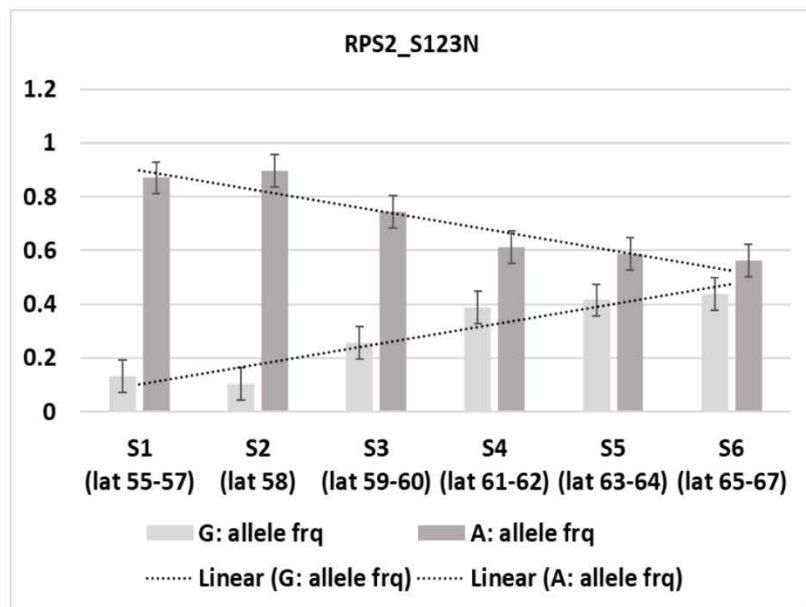


d

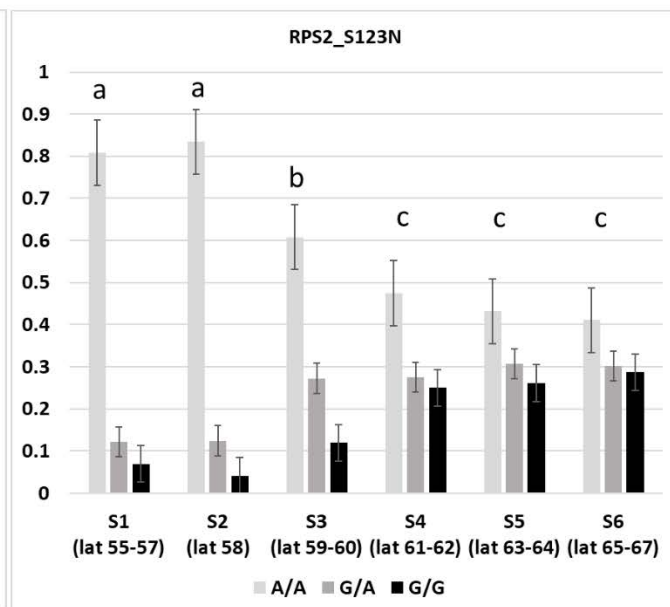
Fig.S14 Cline with reference to variation in allele and genotype frequencies of SNPs in the *RPS2* gene in Norway spruce populations across Sweden

a and c: allele frequencies of S123N and E166A respectively

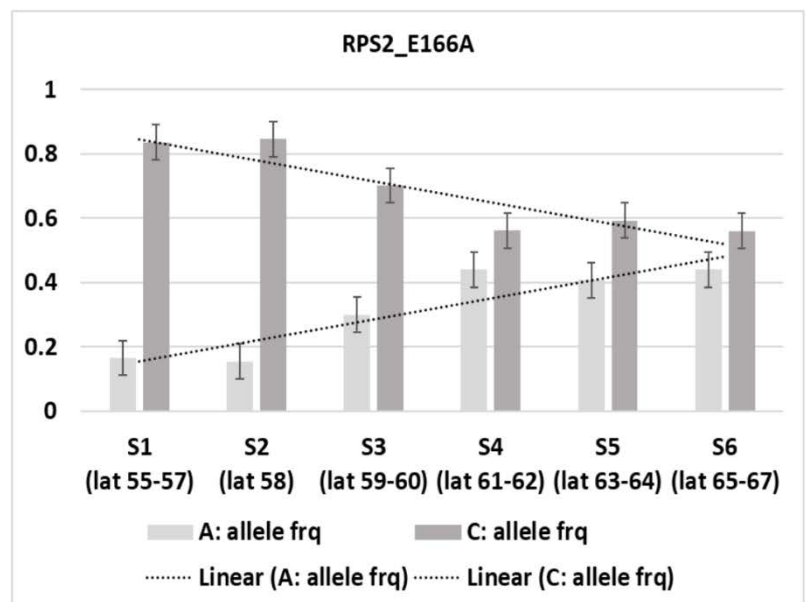
b and d: genotype frequencies of S123N and E166A respectively, Tukey's *post-hoc* categorization is indicated above the bars



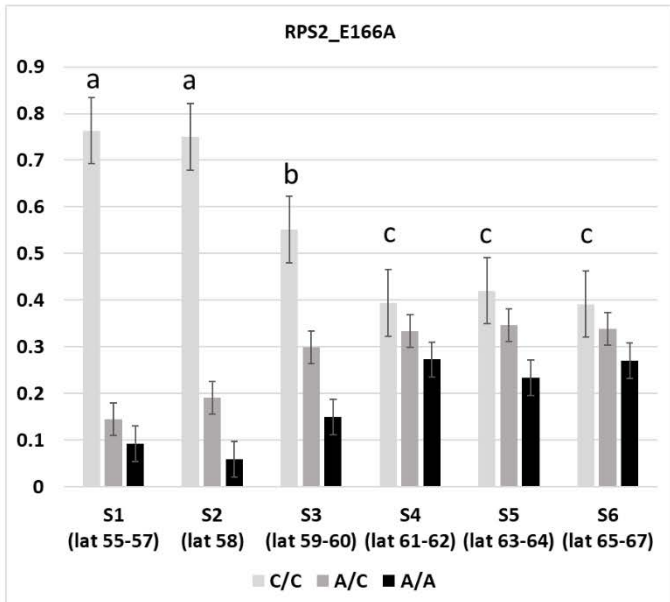
a



b



c



d

AT4G18390 [365 residues] *Arabidopsis thaliana* (<https://www.arabidopsis.org>)

MA_92659p0010	--	551
AT4G18390	KN	365

MA_16619p0010	-----MDLPGRFYPT	11
AT2G02450	MAIVSSTTSIIPMSNQVNNNEKGIEDNDHRGGQESHVQNEDEADDHDHDMVMPGFRFHPT	60
	* : * * * * * : *	
MA_16619p0010	EEELVG FYLKKRIQGSHPMNFDIVIPTLDL YRYDPCELP SLAHDVEERQWFFFVPRDHKN	71
AT2G02450	EEELIEFYLRKKEGKRFN - - VELITFLDL YRYDPWELPAMAA - IGEKEWYFYVPRDRKY	117
	*** : * * * : : * : : * * * * * * * * : * : * : * : * * * : *	
MA_16619p0010	SS-GRPNRLTKSGYWKATGSDRAIRNELLQCIGLKKILVFYK GKAPY GQKTDWIMNEYRL	130
AT2G02450	RNGDRPNRVTTSGYWKATGADRMIRSETSRPIGLKKT LVEYSGKAPKGTRTSWIMNEYRL	177
	. * * * * : * * * * * * * * * * * * * * : * * * * * * * * * * * * *	
	51-198: NAC domain: DNA-binding and dimerization domain	
	R or K	
MA_16619p0010	PDLRSSSVKVRDIVLCRIYRKAASQSMELQAKPD - -HVVKEE - - - -TAVSGDEYEDTS	183
AT2G02450	PHHETEKYQKAEISLCRVYKRPGVEDHPSVPRSLSTRHHNHSSTSSRLALRQQQHSSS	237
	* : * * * * : : . : . . * : : * : : : * *	
	D or N	
MA_16619p0010	---YSTTLNDGGQLSNPMTEIEVSSLYYQKRERVCS-S-----DQSKTNNGDSLYECL--	232
AT2G02450	SNHSDNNLNNNN---NINNLEKLSTEYSGDGSTTTTTTNSDVTIALANQNIYRPMY	293
	. . . * * . : : * * * . . : : * : : . : * . :	
MA_16619p0010	---E-PIMLSEETRVLKNPKACKTALLELPNMSL-----N	263
AT2G02450	DTSNNTLIVSTRNHQDDDETAIVDDLQRLVNYQISDGGNINHQYFQIAQQFHHTQQQAN	353
	: : : * . . : . : * * * * . :	
MA_16619p0010	CPLSQPIATPPALLSTPPPFQPSL---I-----	288
AT2G02450	ANALQLVAAATTATLMPQTQAALAMNMIPAGTIPNNALWDMWNP IVPDGNRDHYTNIPF	413
	. * : * : : * * : *	
MA_16619p0010	- 288	
AT2G02450	K 414	

Accession	Protein Name	Length
MA_10435231p0010	MNSDGVWLDGSGESPEVNNGEASWVRNPDEDWFNNPPPPQHTNQNDRFRNGGFPLNPSE	60
MA_10435231p0010	NLLLLLQSIDSSSSSSPLLHPFTLDAASQQQQQQQQQQEQSFLATKACIVSLLNVPTIN	120
MA_10435231p0010	LRAMLDDGGGEDGFYATMDANGWTLLEALLGSSLSPPGGSVLSNVGGSI ---NA--SHHLS	171
MA_10435231p0010	NNTFDDFGFDSGFLGQQ-----FHGN-HQSPNSMNFTGLNHSVPDFLPAPENSSGS	170
MA_10435231p0010	CSMSTS-----VHTLEGGPGSDQLGLLHRRDVIESGIHKNGGNQKPNG---GVG	117
MA_10435231p0010	CGLSPLFSNRAKVLKPLQVMAS- GS-QPTLFQKRAAMRQSSSKCMNSESSSEMRKSSY	228
MA_10435231p0010	ERGA---DSVVAV-DSNNNKYVNAANAGRGGKNGPLPAKNLMAERRRRKKLNDRLMLRS	172
MA_10435231p0010	EREIDDTSTGIIDISGLNYESDDHNTNNNGKGGKKGMPAKNLMAERRRRKKLNDRLYMLRS	288
MA_10435231p0010	VVPKVSMDRSSILGDAAEYLQELLQRIGDLHTELISGSCNSK---PLADTLADFPCRLN	229
MA_10435231p0010	VVPKISKMDRASILGDAIDYKELLQRINDLHTELESTPPSSSLHPLTPTPQTLSYRVK	348
MA_10435231p0010	GELQASF--SIVTEPAKVEVRSREGKSLHINMFCSEKPGLLLSTIRALDELGLDVKQAV	286
MA_10435231p0010	EELCPSSSLSPKGGQPRVEVRLREGKAVNIHMFCCRPPGLLLSTMRALDNLGLDVQQAV	408
MA_10435231p0010	ISCLNGFALDVLQEKQSM-GGDVTAEEIKTLLLHTAGYQAGL	327
MA_10435231p0010	ISCFNGFALDVFRAEQCEDHDVLPEQIKAVLLDTAGYAGLV	450

Fig.S18 Domains of NAC DOMAIN CONTAINING PROTEIN 36 (NAC036)Missense polymorphism sites are highlighted in **green** in the Norway spruce gene sequences

Reference and alternative amino acids are displayed in dotted box

Well characterized domains of the genes are highlighted in other colors in the *Arabidopsis thaliana* gene sequences**MA_101849g0010** [306 residues] Norway spruce (<http://congenie.org/>)**AT2G17040** [276 residues] *Arabidopsis thaliana* (<https://www.arabidopsis.org>)

CLUSTAL O(1.2.4) multiple sequence alignment

MA_101849p0010	-----MAMPDKICN-----DGVVQGEMLDLPGRFYPT	29
AT2G17040	MNSDG VWLDGSGESPEVNNGEAASWVRNPDEDWFNNPPPPQHTNQNDFRENGGFLLNPSE	60
	: **:	
MA_101849p0010	EELLSFYMKKKIQAGHS-----LN-----F-----DKIIPT	55
AT2G17040	NLLLLL--QQSIDSSSSSPLLHPFTLDAASQQQQQQQQEQSFLATKACIVSLLNVPT	118
	: ** : : : * : : : : *	
	6-152: NAC domain: DNA-binding and dimerization domain	
MA_101849p0010	MDLYQYDPWELPGFAHDAGEQQWFFVPRYHNKRARNRLAVSGYWKATGSDRAVRNELL	115
AT2G17040	INNNTFDD-----FGFDSG-----FLGQQFHGNHQSPNSMNFTGLNHSVPDFLPAPENSS	168
	: : * : * : * : * : : * : : * : : : : : : :	
MA_101849p0010	QCIGLKILV-----FYKGKSPYGQKTDWIMNEYRMPEFSSSAPKKKMDMVLCCRIYRK	168
AT2G17040	GSCGLSPLFSNRAKVLKPLQVMASGSGSPTLFQKRAAMRQ-----SSSSKMCNSES	220
	. ** . : : : : * : : : : * : : : : * . . : *	
MA_101849p0010	TATRKSLQRAKTNGVDKEEPVSSDVYEDKSHSLT-----V	205
AT2G17040	SEMRKSSYEREIDDT-STGIIDISGLNYESDDHNTNNNGKGGKMPAKNLMAERRRRKKL	279
	: *** : * : . : * . * * :	
	D or E	
MA_101849p0010	D VRCLSN---PM-----IEAK	218
AT2G17040	NDRLYMLRSVVPKISKMDRASILGDAIDYKELLQRINDLHTELESTPPSSSSSLHPLTPT	339
	: * : *	
	T or M	
MA_101849p0010	VSSVQYLDDEGVCSSRSK T KDESS-----LFDCLPIMFCEDEETTTLKTSK----	265
AT2G17040	PQTLSYRVKEELCPSSSLPSPKGQQPRVEVRLREGKAVNIHMFGRRLGLLLSTMRALDN	399
	. : : * . * : * * * . : : . : : * * . : * * :	
MA_101849p0010	-----PKACKPPQLELPKLPMDFLFGQKITTPYALLATPSPFQ	303
AT2G17040	LGLDVQQAIVISCFNGFALDVFAEQCQEDHDVLPEQIKAVLLD---TAGYAGLV-----	450
	: * : : * * : * . : * * * .	
MA_101849p0010	IPL 306	
AT2G17040	--- 450	

	K or R	R or S	C or R	
MA_7354451p0010 AT4G28250	MRKTVRLQWPLVPNFCLDVTAFCFVLLLLFS	KEPALGLEHTELNRRDDLEWRPATATWYG	60	
	-----MQLFPVMLATLCIVLQLLIGSS----	ALATTNRHVSNSHWLPAVATWYG	45	
	: * : ::::*:** *:... . *	* : : . : * ** ,*****		
MA_7354451p0010 AT4G28250	SPDGDGSDGIL-----	SPNGDGSDGGACGYGTLDVKPLHARVGAVNPILFKNGEGCGACYKVRCLDKSICSRRAV	71 105	
	** ,*****			
MA_7354451p0010 AT4G28250	-----	TVIITDECPGCSKTSTHFDLSGAVFGRLAIAGESGPLRNRGLIPVIYRRTACKYRGKNIA	71 165	
		54-162: Domain: Expansin-like EG45		
MA_7354451p0010 AT4G28250	-----	FHVNEGSTDFWLSLLVEFEDGEIGDSMHIRQAGAREWLEMKHVWGAWNCIIGGPLKGPF	71 225	
		175-256: Domain: Expansin-like CBD		
MA_7354451p0010 AT4G28250	-----	SIKLTTLSAGKTLSATDVVPRNWAPKATYSSLNLFSPVL	71 264	

MA_14341p0010 KMKE-SSAPANNRQSSSTNQSVRAGTVAAA- 180
AT1G78020 AKEPAVTAPARAKPG-----KGRAAAAV 162

: *** : * ***

AT1G79620 [971 residues] *Arabidopsis thaliana* (<https://www.arabidopsis.org>)

CLUSTAL 0(1.2.4) multiple sequence alignment

Accession	Protein Name	Length
MA_587505p0010	MVGSNTVTATSRLLLLICFAYSFTVFSMISSVTDPRDAAALRSLMDQWDNTPPSWGGSDDP	60
MA_587505p0010	CGTPWEGVSCNNSRITALGLSTMGLKGRLSGDIGELAE LRSLDLSFNRLTGSLTSRLGD	120
MA_587505p0010	LQKLNILILAGCGFTGTIPNELGYLKDLSFLALNSNFTGKIPASLGNLTKVYWLADN	180
MA_587505p0010	QLTGPIPISSGSSPGLDLLKAKHFHFNKNQLSGTIPPKLFSSEMILIHVLF DGNRFTGS	240
MA_587505p0010	LILPIAVIITIAG--VMATGMKGKDESKCPYDLTVASRMIP-----IPSTLGLIQTLEVLRLDRNTLTG---KVPENLSNLTNIIELNLAHNKLVGSLPDLSDMK	296
MA_587505p0010	SSCYANNTDQTIE-KNTCCWS-VFASYVFSISLYANRTGTVLLDANGS-----RHCTN-SMNYVDLSNNSFDPSESPLWFSTLP SLTTLVMEYGS LQGPLPNKLF GFPQLQQVRLKKNA	356
MA_587505p0010	FNGTLSLGD TVGPELQLVDLQDNDISSVTLSSGYTNTLILEGNPVCTTA-----LSNT	409
MA_587505p0010	RYATLGDISNVIDVGNASIACDGPSLN-----ESKACERC--QEK-VISKALELLNLTNSNYCQIQQQQVKRIYSTSLANCGGKSCPLDQKVSPQSC ECAYPYEGTLYFRGPMFRDLSNV	469
MA_587505p0010	KEFVPCGMAITMGIWGRDP---SEE-----RFGGYVGCVLQVLGNIG-----NTY---HSLEMSLWVKLGLTPGSVSLQNPFFNDDYLQIQ LALFPPMGKYFN RTEVQRI	525
MA_587505p0010	GLGTSSLIPSPPPP--PLPAS---HEPSGGNKK-GRGRVRIAVAGIAATS VLLVFAAGFDLSNQYKPPPLFGPYFYFIASPYTFPADGNHGSLSSRMVTG IITGCSALVLCLVALGI	585
MA_587505p0010	LI LKSKKTNGPSEESTASSSLQVLTRSLMGIDKRTETVAREPLPTEGLYLFTKRELQRAYAMWQKRRAEQA-----IGLSRPFVSWASSGKDS-GGAPQLKGARWFSYEELKKI	634
MA_587505p0010	TEDFSEARVLGTGGSGKVYLGLKLP SGKQVAIKRIVQKRK--VDEFYKEVELLSRLRHPNL TNNFSVSSELGYGGYGKVYKGLMQDGHMVAIKRAQQGSTQGGLFEKTEIELLSRVVHKNL	694
638-912: Domain: Protein kinase		
MA_587505p0010	ASLLGYCQHRREHILVY EYMPGGDLGCLLFRREDPVL PDRRLRIALDCAEGLAHLHLFPVGLVGFCFEQGEQILVY EYMSNGSLKDSL TGRSGITLDWKRRRLRVALG SARGLAYLHELA	754

MA_587505p0010	EGAIVHRDIKPTKLSDFGISKLIAPDISHASTEIKGTTGFLDPEYFFVGKLNILLNESGQ	518
AT1G79620	DPPIIHRDVKST-----NILLDENLT	775
	: *:*:*:* * * *:*:*:	
MA_587505p0010	AKLSDFGVSKLIAP-DFSHASTEIKGTTGYVDPEYFTVGRLTDASDVYSFGVVLLQLISG	577
AT1G79620	AKVADFGLSKLVSDCTKGHVSTQVKGT LGYLDPEYYTTQKLTEKSDVYSFGVMMELITA	835
	*:	
MA_587505p0010	QKAVISTPSGGADSVVYMAHVFMSGEDPDVRNLVDPRIADAMDARDLGSIK--MVL DIA	634
AT1G79620	KQPIEG-----KYIVREIKLVMNKSDDDFYGLRDKMDR--SLRDVGTLPELGRYMELA	887
	::: . .:*:::*. * * . * * . *:*:*::: :::*	
MA_587505p0010	Y-----	635
AT1G79620	LKCVDETADERPTMSEVKEIEIIIQNSGASSSSSASASSSATDFGEKLLYGGTLKKKEA	947
MA_587505p0010	-----	635
AT1G79620	RDGDGGGAFDYSGGYSVPTKIEPK	971

AT1G22640 [257 residues] *Arabidopsis thaliana* (<https://www.arabidopsis.org>)

CLUSTAL 0(1.2.4) multiple sequence alignment

MA_7115p0010	MG-RSCSSKEGLNRGSAWSRKEDMILSEYIRIHGDGGWTNLPQAGLKRCKGKSCRLRWNTY	59
AT1G22640	MGRSPCC ^E KAHMNKGAWTKEEDQLLV^DYIRKHGEGCW^RSLPRAAGLQRCGKSCRLRW^MNY	60
	** * * : : * * * : : * * : * * * * * : * * : * * : * * * * * * * * *	
	9-61: Myb-type1 HTH DNA-binding domain	
MA_7115p0010	LRPDIKLGNI ^S PD ^E DELII ^R MRHLLGN ^R WSLIAGRLPGRTDNEIKNYWNTRL ^S SKLL ^S ID	119
AT1G22640	L^RPD^LKRG^NFT^EEE^DELII^KLH^SLLGN^KWSLIAGRLPGRTDNEIKNYWN^THI^KR^LLSRG	120
	**** * * : : * * * : : * * : * * : * * * * * * * * * * * : : * * *	
	62-116: Myb-type2 HTH DNA-binding domain	
MA_7115p0010	DSQSKSTARNLE ^T SSKSPPPPPNHVFKTTPIKIT ^T AVKFSETVGP ^K KRCNG-YG-RSNCSS	177
AT1G22640	IDPNS--HRLINESV ^S PS ^S LQNDV ^V ETIHL-----DFSGPVKPEPVREEIGMVN ^N NCES	172
	. . . * : : * * * * . * : * : . ** * * : . * . * * *	
MA_7115p0010	AEA ^I KLCNI ^K ENTNSIPHDDSEHIV ^F DMT-----DVN ^L LLETEAGNCTSAI ^W SL ^E E	227
AT1G22640	SGT-----TSEKDYGN ^E EDW ^L NLELSVG ^S PSYRYESTR ^K VS ^V DSAESTRRW ^G SE-	222
	: : * . . : . . * . * : : : : * . *	
MA_7115p0010	ERSPHSY ^F FAVD ^T ATL ^D ESLSELN ^V LSSPDCN ^L LYSASGSST ^D FELEEFY ^R EAT ^L AT ^G I	287
AT1G22640	-----LFGA ^H ESDA ^V CLC ^R IGLFR ^N ESC ^R NC-----RVSD ^V RT ^H -----	257
	* . . . : . . : : . *	
MA_7115p0010	NDSVFT 293	
AT1G22640	----- 257	

Fig.S23 Domains of RESISTANT TO P. SYRINGAE 2 (RPS2)

Missense polymorphism sites are highlighted in green in the Norway spruce gene sequences

Reference and alternative amino acids are displayed in dotted box

Well characterized domains of the genes are highlighted in other colors in the *Arabidopsis thaliana* gene sequences

MA_475302g0010 [303 residues] Norway spruce (<http://congenie.org/>)

AT4G26090 [910 residues] *Arabidopsis thaliana* (<https://www.arabidopsis.org>)

CLUSTAL O(1.2.4) multiple sequence alignment

MA_475302p0010	-----	0
AT4G26090	MDFISSLIVGCAQVLCESMNAERRGHKTDLRQAITDLETAIGDLKAIRDLLTRIQQDG	60
29-58: Coiled coil domain - essential for the resistance to AvrRpt2		
MA_475302p0010	-----	0
AT4G26090	LEGRSCSNRAREWLSAVQVTETKTALLVRFRRREQRTRMRRRYLSCFGCADIYKLCCKVS	120
MA_475302p0010	-----	0
AT4G26090	AILKSIGELRERSEAIKTDGGSIQVTCREIPIKSVVGNTTMMEQVLEFLSEEEERGIIGV	180
135-440: NB-ARC domain - nucleotide-binding domain		
MA_475302p0010	-----	0
AT4G26090	YGPGGVGKTTLMQSINNELITKGHQYDVLIWVQMSREFGECTIQQAVGARLGLSWDEKET	240
MA_475302p0010	-----	0
AT4G26090	GENRALKIYRALRQKRFLLLDDVWEEIDLEKTGVPRPDRENCKVMFTTRSIACNNMG	300
MA_475302p0010	-----	0
AT4G26090	AEYKLRVEFLEKKHAWELFCSKVWRKDLLLESSSIRRLAEIIVSKCGGLPLALITLGGAMA	360
MA_475302p0010	-----	0
AT4G26090	HRETEEEWIHASEVLTRFPAEMKGMNYVFALLKFSYDNLESDLLRSCFLYCALFPEEHSI	420
MA_475302p0010	-----	0
AT4G26090	EIEQLVEYVWVGEGFLTSSHGVNTIYKGYFLIGDLKAACLETGDEKTQVKMHNVVRSFAL	480
MA_475302p0010	-----	0
AT4G26090	WMASEQGTYKELILVEPSMGHTEAPKAENWRQALVISLLDNRIQTLPEKLICPKLTTLML	540
512-533: Leucine-rich repeat 1 (LRR) - probably act as specificity determinant of pathogen recognition		
MA_475302p0010	---MKLKEIP-----ALDIGNQAAHGGFPMSNAKTMQLQILKIQGCRVLKTR	46
AT4G26090	QQNSSLKKIPTGFFMHPVLRVLDLSFTS-ITEIPLSI-KYLVELYHLSMSGTKIS--VL	596
534-556: LRR 2 559-580: LRR 3		
MA_475302p0010	VEELPNLRKLG---ISHCAELKELSMES-----GG	73
AT4G26090	POELGNLRKLKHLDLQRTQFLQTIPRDAICWLSKLEVLNLYSYAGWELQSFGEDEAEEL	656
582-604: LRR 4 605-627: LRR 5		
MA_475302p0010	GLLRRLERL-----DLWSLQRLESIVWNAKTMQLQIFFGISNCHVLKTFGVEELP---	122
AT4G26090	GFADLEYLENLTTLGITVLSLETCLKTLFEFGALHKHIQHLHVEECNELLYFNLPSTLNHG	716
MA_475302p0010	-SLKEINISNCVELKESFM---ESGGSLPMLIEILEYSLEIRSIVWNEKTM----LQLQS	174
AT4G26090	RNLRRLSIKSCHDLEYLVTADFENDWLPSEVLTLHSLHNLTRVWGNVSVDCLRNIRC	776
MA_475302p0010	FYISYCRVLKTF-RVEELPNLKEIEIKQCPQLVQIGS-----VPMLKKLTLEG	222

AT4G26090	INISHCNKLKNVSWVQKLPKLEVIELFDCREIEELISEHESPSVEDPTLFPSLKTLRTRD	836
	: **:*. **.. *:***: **: ;* *: :* **	
MA_475302p0010	LKSESIARASSVWNKETMPKLEYINITGCPLLRRLPMEMDK-LPNLKKIVGEVGWWEIGI	281
AT4G26090	LPELNSI-----LPSRFSFQKVETLVITNCPRVKKLPFQERRTQMNLPVYCEEKWWKAL	891
	* : :** : .: :: *: * : **, ** :*:*: : : ** .: * **::	
MA_475302p0010	NWEIDNVKIKLSELFREDEDED 303	
AT4G26090	EKDQPNEELCYLPRFVPN---- 909	
	: : * :: * :	