

Table S7. A list of sample identifiers and geographic locations for the coastal Douglas-fir trees comprising the diversity panel that was used to discover single nucleotide polymorphisms (SNPs) within 121 candidate genes putatively associated with cold-hardiness phenotypes. A maximum of 24 samples were used for each gene (cf. Materials and Methods). These represent a subset of the samples analyzed by Krutovsky and Neale (22). NF = National Forest.

Population	Population id	Sample ID	Latitude (°N)	Longitude (°W)
Coastal Douglas-fir				
Cascade	22	22-1	47.3302	-121.4303
		22-2	47.3500	-121.4550
		22-3	47.3302	-121.4303
		22-4	47.1225	-121.5616
		22-5	47.1225	-121.5616
Vail	24	24-1	46.4310	-122.5357
		24-2	46.5020	-122.0951
		24-3	46.4310	-122.5357
		24-4	46.5009	-122.4310
Twin Harbors	26	26-1	46.1453	-122.4837
		26-2	46.0925	-122.3437
		26-3	46.1453	-122.4842
		26-4	46.1453	-122.4842
Longview	28	28-1	46.5605	-123.2259
		28-2	47.0306	-123.2000
		28-3	46.5555	-123.2235
		28-4	46.3913	-123.1630
Springfield	30	30-1	44.2721	-122.2705
		30-2	44.0555	-122.3722
		30-3	44.0555	-122.3722
		30-4	44.2721	-122.2721
Coos Bay	32	32-1	43.2151	-124.0418
		32-2	43.2151	-124.0418
		32-3	43.2415	-124.0010
		32-4	43.2405	-123.5951
Bigcone Douglas-fir				
Angeles NF	na	06019	na	na

Table S8. Annotation for the 121 candidate genes resequenced for coastal Douglas-fir. Annotations were based on tBLASTx analysis using the non-redundant nucleotide (nr/nt) collection available from GenBank. All analyses were conducted using the Douglas-fir EST or EST contig from which resequencing primers were designed as the query sequence. Hits against organisms without fully sequenced genomes were verified for similar gene functionality against the *Arabidopsis thaliana* and *Oryza sativa* genomes whenever possible. Douglas-fir candidate genes with similar gene products were designated as separate members of a gene family when nucleotide sequence similarity for overlapping EST or EST contigs was < 90%.

Locus	Organism	tBLASTx	Accession	Gene Product
CD028057.1	<i>Oryza sativa</i>	7.00E-76	NM_001050147	calcium-dependent protein kinase
CN634517.1	<i>Pseudotsuga menziesii</i>	2.00E-65	Z49764	luminal binding protein
CN634677.1	<i>Arabidopsis thaliana</i>	4.00E-50	NM_111157	LRR receptor-like protein kinase
CN635137.1	<i>Picea mariana</i>	1.00E-57	AF051202	aquaporin
CN635490.1	<i>Arabidopsis thaliana</i>	3.00E-13	NM_111463	rare cold inducible protein
CN635596.1	<i>Arabidopsis thaliana</i>	3.00E-42	NM_125822	phosphate-responsive protein
CN635661.1 ^a	<i>Arabidopsis thaliana</i>	na	NM_117347	auxilin-related protein
CN635674.1	<i>Arabidopsis thaliana</i>	4.00E-47	NM_121534	pentatricopeptide (PPR) containing protein
CN635691.1	<i>Picea abies</i>	5.00E-112	AF328842	homeodomain protein (HB2)
CN636014.1	<i>Arabidopsis thaliana</i>	2.00E-112	NM_112093	heat shock protein 70 kDa
CN636043.1	<i>Pseudotsuga menziesii</i>	1.00E-95	U41902	cysteine protease pseudotzain
CN636093.1	<i>Cryptomeria japonica</i>	2.00E-19	AB211741	calmodulin
CN636149.1	<i>Pinus taeda</i>	6.00E-30	Z37992	cinnamyl alcohol dehydrogenase
CN636303.1	<i>Pinus radiata</i>	2.00E-91	EU301694	actin depolymerizing factor
CN636471.1	<i>Pinus pinaster</i>	8.00E-100	AY321089	phenylalanine ammonia-lyase
CN636492.1	<i>Oryza sativa</i>	2.00E-55	NM_001050492	phosphoethanolamine methyltransferase
CN636784.1	<i>Pinus contorta</i>	1.00E-127	AF187821	S-adenosylmethionine synthetase
CN636795.1	<i>Arabidopsis thaliana</i>	1.00E-59	NM_101028	xyloglucan:xyloglucosyl transferase
CN636901.1	<i>Oryza sativa</i>	8.00E-27	NM_001065251	alanine aminotransferase
CN636999.1 ^a	<i>Arabidopsis thaliana</i>	na	NM_103822	BURP domain-containing protein
CN637166.1	<i>Arabidopsis thaliana</i>	2.00E-26	NM_100889	phloem protein
CN637226.1	<i>Arabidopsis thaliana</i>	7.00E-75	NM_100698	prephenate dehydratase family protein
CN637244.1	<i>Zea mays</i>	1.00E-28	NM_001112543	cysteine protease inhibitor
CN637306.1	<i>Picea glauca</i>	3.00E-61	EF601068	MYB-like transcription factor
CN637339.1	<i>Arabidopsis thaliana</i>	3.00E-45	NM_129573	unknown hypothetical protein
CN637910.1	<i>Arabidopsis thaliana</i>	3.00E-38	NM_101012	ABC family protein
CN637944.1	<i>Arabidopsis thaliana</i>	2.00E-32	NM_129387	bet v I domain containing protein
CN638015.1	<i>Picea sitchensis</i>	6.00E-15	EF084692	unknown hypothetical protein
CN638070.1	<i>Arabidopsis thaliana</i>	2.00E-24	NM_119071	acid phosphatase class B family protein
CN638367.1	<i>Oryza sativa</i>	1.00E-90	NM_001051693	ATP-dependent RNA helicase-like protein
CN638381.1	<i>Oryza sativa</i>	3.00E-117	NM_001069063	iron-inhibited ABC transporter
CN638489.1	<i>Oryza sativa</i>	2.00E-114	AF247164	alpha-expansin

CN638545.1	<i>Pinus taeda</i>	7.00E-90	AF096998	trans-cinnamate 4-hydroxylase
CN638556.1	<i>Arabidopsis thaliana</i>	1.00E-25	NM_120637	transcription regulation protein
CN638735.1	<i>Pinus taeda</i>	1.00E-123	DQ641986	cellulose synthase-like A1
CN639074.1	<i>Pinus contorta</i>	1.00E-34	U38186	S-adenosylmethionine synthetase
CN639087.1	<i>Arabidopsis thaliana</i>	7.00E-68	NM_124213	LRR receptor-like protein kinase
CN639130.1	<i>Arabidopsis thaliana</i>	4.00E-55	NM_118561	chloroplast heat shock protein 70 kDa
CN639236.1	<i>Oryza sativa</i>	3.00E-96	NM_001050445	guanine nucleotide-binding beta subunit protein
CN639311.1	<i>Oryza sativa</i>	2.00E-66	AB111916	replication protein
CN639346.1	<i>Pinus radiata</i>	5.00E-32	U90346	MADS-box transcription factor
CN639480.1	<i>Arabidopsis thaliana</i>	9.00E-41	NM_100032	2-hydroxyacid dehydrongenase
CN640037.1	<i>Pinus tabuliformis</i>	9.00E-79	DQ062681	tau class glutathione S-transferase
CN640110.1	<i>Arabidopsis thaliana</i>	4.00E-66	NM_110969	galacturonosyltransferase
CN640155.1	<i>Oryza sativa</i>	6.00E-38	NM_001068919	bicoid-interacting 3 domain containing protein
CN640247.1	<i>Picea mariana</i>	6.00E-87	AF227627	chalcone synthase
CN640289.1	<i>Oryza sativa</i>	9.00E-50	NM_001074378	serine hydroxymethyltransferase
CN640361.1	<i>Arabidopsis thaliana</i>	9.00E-92	NM_100263	zinc-finger (C2H2 type) family protein
CN640419.1	<i>Glycine max</i>	3.00E-96	AB210900	heat shock protein 70 kDa
CN640485.1	<i>Oryza sativa</i>	1.00E-69	NM_001070907	HNH endonuclease domain containing protein
CN640493.1	<i>Arabidopsis thaliana</i>	1.00E-39	NM_180904	nuclear transport factor
CN640521.1	<i>Arabidopsis thaliana</i>	6.00E-40	NM_179270	DNA-binding bromodomain-containing protein
CN640670.1	<i>Oryza sativa</i>	6.00E-55	NM_001062995	GH3 auxin-responsive promotor family protein
CN640738.1	<i>Ginkgo biloba</i>	1.00E-27	AY750963	anthocyanidin reductase
CN641116.1	<i>Oryza sativa</i>	3.00E-59	NM_001065234	carboxy-terminal kinesin
CN641171.1	<i>Arabidopsis thaliana</i>	4.00E-34	NM_106730	cinnamoyl CoA reductase
CN641226.1	<i>Glycine max</i>	1.00E-31	AB092811	LRR receptor-like protein kinase
ES418315.1	<i>Pinus pinaster</i>	3.00E-47	AJ309081	flavenoid 3-hydroxylase
ES418915.1	<i>Pinus radiata</i>	4.00E-24	AY262820	cellulose synthase-like protein
ES419198.1	<i>Pinus taeda</i>	7.00E-52	AY670436	LIM domain protein
ES419223.1 ^a	<i>Arabidopsis thaliana</i>	na	NM_125984	phytosulfokine precursor
ES419242.1	<i>Oryza sativa</i>	1.00E-10	NM_001060766	response regulator protein
ES419657.1	<i>Arabidopsis thaliana</i>	1.00E-48	NM_114249	calmodulin
ES420171.1	<i>Arabidopsis thaliana</i>	1.00E-62	NM_114943	cold regulated plasma membrane protein
ES420250.1	<i>Picea abies</i>	6.00E-24	EF522166	dehydrin-like protein
ES420603.1	<i>Picea abies</i>	7.00E-21	EF522171	dehydrin-like protein
ES420757.1	<i>Arabidopsis thaliana</i>	6.00E-22	NM_123503	unknown hypothetical protein
ES420771.1	<i>Arabidopsis thaliana</i>	1.00E-30	NM_111461	anaphase promoting complex/cyclosome protein
ES420862.1	<i>Picea glauca</i>	3.00E-56	L42465	late embryo abundance (LEA) protein
ES421219.1	<i>Oryza sativa</i>	1.00E-46	NM_001065800	UDP-glucosyltransferase family protein
ES421311.1	<i>Picea sitchensis</i>	1.00E-52	EF084165	unknown hypothetical protein
ES421603.1	<i>Arabidopsis thaliana</i>	7.00E-64	NM_124985	heat shock protein 90 kDa

ES421877.1	<i>Arabidopsis thaliana</i>	4.00E-56	NM_128767	ccr4-NOT transcription complex protein
ES422367.1	<i>Pinus radiata</i>	2.00E-21	EU394120	ferritin
ES424016.1	<i>Glycine max</i>	6.00E-35	AF243377	glutathione S-transferase
ES428620.1	<i>Picea glauca</i>	3.00E-60	AF121198	14-3-3 protein
Pm_CL135Contig1	<i>Arabidopsis thaliana</i>	2.00E-152	NM_114400	cysteine proteinase
Pm_CL1400Contig1	<i>Oryza sativa</i>	2.00E-32	NM_001060573	alpha-L-arabinofuranosidase/beta-D-xylosidase
Pm_CL150Contig1	<i>Arabidopsis thaliana</i>	9.00E-24	NM_202741	phloem protein
Pm_CL1692Contig1	<i>Oryza sativa</i>	5.00E-23	NM_001064601	zinc-finger containing protein
Pm_CL1811Contig1	<i>Arabidopsis arenosa</i>	7.00E-74	AY333120	Swi2/Snf2-related chromatin remodeling ATPase
Pm_CL1814Contig1	<i>Arabidopsis thaliana</i>	2.00E-51	NM_124040	tetraspanin
Pm_CL1868Contig1	<i>Arabidopsis thaliana</i>	1.00E-61	NM_128676	actin depolymerizing factor
Pm_CL1982Contig1	<i>Oryza sativa</i>	8.00E-94	NM_001057633	peptide transporter
Pm_CL1994Contig1	<i>Picea abies</i>	5.00E-154	AJ868575	caffeate O-methyltransferase
Pm_CL1997Contig1	<i>Pinus taeda</i>	6.00E-50	EF619967	sucrose synthase
Pm_CL1Contig2	<i>Picea glauca</i>	2.00E-89	AF109917	glycine-rich RNA-binding protein
Pm_CL2089Contig1	<i>Arabidopsis thaliana</i>	4.00E-52	NM_119920	putative formide amidohydrolase
Pm_CL2133Contig1	<i>Arabidopsis thaliana</i>	6.00E-41	NM_179926	mitochondrial transcription termination factor
Pm_CL214Contig1	<i>Zea mays</i>	1.00E-62	NM_001111956	beta-tubulin
Pm_CL2282Contig1	<i>Arabidopsis thaliana</i>	5.00E-22	NM_114895	unknown hypothetical protein
Pm_CL234Contig1	<i>Arabidopsis thaliana</i>	8.00E-110	NM_104107	Rab GTPase
Pm_CL618Contig1	<i>Arabidopsis thaliana</i>	3.00E-66	NM_120688	tropinone reductase
Pm_CL61Contig1	<i>Picea abies</i>	3.00E-106	AJ271126	cyclosporin A-binding protein
Pm_CL73Contig1	<i>Arabidopsis thaliana</i>	5.00E-94	NM_124900	glycosyl hydrolase family protein
Pm_CL783Contig1	<i>Arabidopsis thaliana</i>	7.00E-34	NM_129353	SOUL heme-binding family protein
Pm_CL795Contig1	<i>Arabidopsis thaliana</i>	2.00E-47	NM_202438	WD-40 repeat family protein
Pm_CL855Contig1	<i>Vitis vinifera</i>	2.00E-85	DQ786632	flavonoid 3-hydroxylase
Pm_CL908Contig1	<i>Arabidopsis thaliana</i>	1.00E-32	NM_121323	GRAM-containing/ABA-responsive protein
Pm_CL919Contig1	<i>Arabidopsis thaliana</i>	1.00E-44	NM_106112	HVA22-like protein
Pm_CL922Contig1	<i>Arabidopsis thaliana</i>	5.00E-49	NM_001035987	thaumatin-like protein
Pm_CL939Contig1	<i>Arabidopsis thaliana</i>	1.00E-85	AY045869	aluminum-induced protein
Pm_CL969Contig1	<i>Oryza sativa</i>	6.00E-57	NM_001055522	cell division cycle protein
Pm_CL988Contig1	<i>Arabidopsis thaliana</i>	5.00E-14	NM_101026	thioredoxin-like protein
sM13Df243	<i>Pinus taeda</i>	5.00E-14	AY648093	arabinogalactan 4
sSPcDFD005F06506	<i>Arabidopsis thaliana</i>	3.00E-27	NM_115415	regulator of chromosome condensation protein
sSPcDFD015C12212	<i>Arabidopsis thaliana</i>	4.00E-49	NM_112443	phospholipase D
sSPcDFD024D11311	<i>Arabidopsis thaliana</i>	8.00E-53	NM_102304	polcalcin
sSPcDFD040B03103	<i>Pinus radiata</i>	4.00E-34	U42400	MADS-box transcription factor
sSPcDFE002A03003	<i>Picea glauca</i>	1.00E-33	L42466	ACC oxidase
sSPcDFE025C06206	<i>Oryza sativa</i>	9.00E-48	NM_001059265	purple acid phosphatase
sSPcDFE028B10110	<i>Arabidopsis thaliana</i>	6.00E-28	NM_117813	beta-amylase

sSPcDFE038D06306	<i>Arabidopsis thaliana</i>	8.00E-32	NM_130225	calcium binding protein with EF-hand motif
sSPcDFE044F10510	<i>Arabidopsis thaliana</i>	4.00E-35	NM_127816	mitochondrial substrate carrier family protein
sSPcDFE049B06106	<i>Arabidopsis thaliana</i>	2.00E-23	NM_130234	auxin-responsive family protein
sSPcDFE049E11411	<i>Arabidopsis thaliana</i>	3.00E-42	NM_202131	pentatricopeptide (PPR) containing protein
sSPcDFF014F08508	<i>Oryza sativa</i>	3.00E-34	NM_001056474	hypothetical water stress induced protein
sSPcDFF015H05705	<i>Oryza sativa</i>	1.00E-34	NM_001055452	cytochrome P450 family protein
sSPcDFF044H10710	<i>Arabidopsis thaliana</i>	6.00E-31	NM_125091	auxin:hydrogen symporter/transporter
U22458.1	<i>Populus tremula</i>	3.00E-159	AM_072292	phytochrome B
Z49715.1 ^a	<i>Arabidopsis thaliana</i>	na	NM_104147	late embryogenesis abundant (LEA) protein

^aThese candidate genes had an extreme expression differences in Douglas-fir cold-hardiness EST libraries and were chosen based on this and results from blastp searches.

Table S9. A list of primers by locus for all 121 candidate genes resequenced within the diversity panel of coastal Douglas-fir. Genomic DNA was amplified in 384-well format PCR setup. Each PCR reaction contained 10 ng Dna, 1x HotStart buffer (Qiagen), 0.8 mM dNTPs, 1 mM MgCl₂, 0.2 U HotStart polymerase (Qiagen) and 0.2 uM forward and reverse primers in 10 ul reactions. PCR cycling parameters were: one cycle of 95°C for 15 min, 35 cycles of 95°C for 20 s, 55-60°C for 30 s and 72°C for 1 min, followed by one cycle of 72°C for 3 min. The resultant PCR products were purified using the AMPure[®] solid phase reversible immobilization chemistry (Agencourt Bioscience, Boston, MA) followed by bidirectional dideoxy sequencing with universal M13 primers and the Big-Dye v. 3.1 chemistry (Applied Biosystems, Foster City, CA). Sequencing was carried out via capillary electrophoresis using ABI Prism 3730XL DNA analyzers. AT = annealing temperature.

Locus	Forward primer (5'-3')	Reverse primer (5'-3')	AT (°C)	Primer sets
CD028057.1	AACGTCTTACGGCTGCTGAG	GGCTTGACCAATACCACAGAA	57	1
CN634517.1	AATCAGGAGTGCCAAGACCG GGACAAGCACCAGAGCACGA	GCCTCTCTTTGATTTTATTCTCCA CGAGGGAAGTCCAAATCTGAAGTA	55 55	2
CN634677.1	AACACGCTCTCGTATTGCC	GCTTTTCCAGTCAGAATC	60	1
CN635137.1	CAAGGGAATGAACTGAAGTTGGTG	CAAATGGCTCCCAAACACTGA	55	1
CN635490.1	TCAACACATACCCATAGTCGCAC	GGTTGGGTGTGTGTAATATGTC	55	1
CN635596.1	GTTTTTTTCAGGGCGACGG	AGTAAAAGGATTTGTAAACAGCCACCAG	60	1
CN635661.1	AAGAAGGGCAGAAAGAGCAGCAC	TGCTCTCTCTGCCCGTTCCCTTG	55	1
CN635674.1	CTTCATAGGCGTTTTGTC	GCTTCAGGTTTTACTGG	60	1
CN635691.1	GAGAAAATTCGCCTTCAG	CATCGTCATCAATGTTACC	60	1
CN636014.1	TTGTCTCTTGGATTGGAAGTGC TGAAGGTGAAAGAGCAAGGA	TTCATCCTCAGCGTTGTATTTCTCT ACCAGAAGCTCCACCAAAG	55 55	2
CN636043.1	TATGACTTTGGGGTACTGCTATG	ATTGACGAGAACACTGAGGGGAA	55	1
CN636093.1	GAGCCAGCACAGCGAAACAT	ACTATGATGTGGAAAGCAAAC	55	1
CN636149.1	TCCAAACAACCTTCTCGCAGTATT	ACGACGTAACATTCAAGGTAGCA	55	1
CN636303.1	CCCCATCCAAAAGTTAAT	CAAACCTTATGGCGACTTCAC	55	1
CN636471.1	GCGTGGTCTCTCAGGTGGC	CCTTTCCGATGTATTCACCCG	55	1
CN636492.1	GGAGAAGGATTTGTCAGTACGGGA	CTCAAATTCAACAGCACATCGTC	55	1
CN636784.1	GGTTGAGACCAGATGGGAAA TCCCTGAGGTGCTGTTCTCT	TTTCCTTGTCTGGGATCCTG AGGGCTCTGCTGTTCAATGT	55 55	2
CN636795.1	ACAGATTCGGGTGGTTCAGCAT	ACGAAGATACAAATGGAGCAGC	55	1
CN636901.1	CCTGGTTCAGGATTCGGTCAA	GCGTGTGTTTATGATTTTATGATGTG	55	1
CN636999.1	AGGATTTGCTTTCCTGAGAGA	CATTCACCTCCCTTGCCA	55	1
CN637166.1	CCAGAAGATGAAGAATCC	TGAAGCCCTGTAAGAACTCC	60	1
CN637226.1	AATCGGGTCATTAGCC	CGTTGTTACAGTCGTC	60	1
CN637244.1	AAATGCCGACGAGATGCTGC	GCCGCATACAGCTTGTTTTTA	55	1
CN637306.1	CTAAACAATGGGAAGGG	ATCTCGTTGTCCGTTT	60	1
CN637339.1	AGGATGGAGATGGCAAC	CTGAACTGAAGACGAG	60	1
CN637910.1	GCACCGTCACATAAATTTTC	TTCATCAAGTCGCAGCC	60	1
CN637944.1	ATGTCTGGTCCGTGTTG	TCCCATCTTTCTCCTC	60	1

CN638015.1	TCCAATCTACTCAAGGCGTCCA	CAGTCTTAGCAGCGAAATAACAACA	55	1
CN638070.1	GTTTCTCTTGTTCCCTCCTC	GCATCATATACTTCTTCACATAGCC	60	1
CN638367.1	CTTCCTGAGCAAACCCTGAGC	GCATAAAGTGTGCGGAAGGAAAGGAT	55	1
CN638381.1	TTGAGGAAAACCAGATGAAGCAGT	CTGCTACCAAAGTCAAACATAATCAATACA	57	1
CN638489.1	ACCAATTTCTGCCCTCC	GATAAAGTCTGCCCAACC	60	1
CN638545.1	TTCCGCTCCTCGTTCCTCACAT	GCAAACTACTGACAGCAAAAACAA	55	1
CN638556.1	ATGGGGTGAGCGTTATCTGG	CAACTCTCAGTCATATCAGG	60	1
CN638735.1	CCTTTTACTGTGTTGTGATTCC	GAAGAAGAGATAGACACC	60	1
CN639074.1	AGTGCCCGAACCTCTGTCTGT	AAGCCATTACATCCAAAGCGT	57	1
CN639087.1	AGACAGAAAAGCAGTTCAAG	ATAACCCAAGTCACCAAATCACC	60	1
CN639130.1	CTCATTGAGAGATGCAAAG	GGATTCACAGTAACATTTGG	60	1
CN639236.1	TTCTCCATTGATAACCGCCAG	ATAGTAACTCCGTCTTTGCCGCCGT	55	1
CN639311.1	CTATGGCATCTGTTGG	GCTGAAGGATTTGCTC	60	1
CN639346.1	CAACTGAGCAACTCCGACTGATT	CCACTTCGGCATCGCAGAGC	55	1
CN639480.1	ATCATTGCGATGAGGG	GGGTTTCTTCATCATAACAG	60	1
CN640037.1	CTGCTGCAATCAAACC	TCAACCAACCAATCCC	60	1
CN640110.1	ATTGTCTCACTCTGCGG	CGAATTTCAATATGCGTCTC	60	1
CN640155.1	GAAGATAAGGGCAGAG	CGAATCAACCATTTCATCAC	60	1
CN640247.1	TATTTACGCTTTCTCCCGAT	AATTCTTCCCGACAGCGACG	55	1
CN640289.1	AGCCGATTTTGAGAAGATTGGAGAG	TATGCTATTCTATGGTCACTTATCGG	55	1
CN640361.1	AATCCAATGTTACTTCTGCTGCTTC	ATCTCCTTGCTAGTCCGCTGTCTC	60	1
CN640419.1	TGGAGAAGGTGGAGAAGAAA	TTCCAGTGCCATTGTCCTCT	55	1
CN640485.1	CACATTTATCCCCTCTC	TTGGCAATTCTCAACTGTAGTC	60	1
CN640493.1	ATGTTCTCCACCAGTCTCCCCAAATG	GGTTGTAAGAATCCTGAGAGTCCA	55	1
CN640521.1	AGCGGATGTCAGATTG	GGGTAGACTTTGTAGG	60	1
CN640670.1	ATATTGGGAATTGGTACGG	TTCTGGTGAGGATGTGG	60	1
CN640738.1	ACATCCAGGTTGCCATTGCG	CGCAGAAGGCCGCTACATTT	55	1
CN641116.1	TTCTCGCACCTTTTCCC	GCCATAATGACATCCCC	60	1
CN641171.1	AACTCAGGTATATGTGGATGTAAGGG	CCGAGGAACAGTGGAGAGAG	55	1
CN641226.1	GTGAGATCACCAATATTCAG	CTCCAAACATTGAAGGAATC	60	1
ES418315.1	GCAGCGGTGGTGAAAGAGACT	CAGATGGGAAGGAAGACGAGCA	55	1
ES418915.1	AGCCATTGCCTACTATTCTGTG	CTTCTTGCATCCATATTCTCCCTG	55	1
ES419198.1	TGGTGTGTCATCAGTCCCTCA	GTCATACACAAGCCATAGCGATTAC	55	1
ES419223.1	CCCAAGTTCAAGTTTATTTTCATCATC	AAATGAAGGATACAAACAACTGCTC	55	1
ES419242.1	ATTGCATGCCCAGGAACTACAG	AGTCTTCGGCTCCTTCATCTAAA	57	1
ES419657.1	AAGCATTCCGGGTTTTTCGAC	TATCACCCAGGACATTCAAAAAGTTAT	55	1
ES420171.1	CAAGAGCACATCCGACGCAA	ATTCCTCGGTCCATCCTTCTCT	55	1
ES420250.1	GTGGTGTGAGGTGGAAGGACAGT	CATCAAAGAGAAAATACAGTCGGC	55	1
ES420603.1	GAAGGAAGAAGAGGAAGGCCGAGA	TCCGACGCATCTTACACATTATTA	55	1
ES420757.1	CCAATGCGGCGTGTGTTTCAGTA	TTTTACAAGTTCAGCAAGACCACA	55	1

ES420771.1	CATTGGTATGGGGTGCCTGTA	TTCCAAGCAATGGCTGTTTAC	55	1
ES420862.1	AAAGACAGAGGTGAAAGAGATTGC	AACATCTCAAAGTATTCATCATCTCAA	55	1
ES421219.1	GGCGTTGGGAGAGGATTTTTTC	AATCTTCTCTTCTAATGCCACCA	55	1
ES421311.1	ATCCTTAGTCCGACATTTTGCTGCT	AAGGCACTACACAATACAAACGACAC	55	1
ES421603.1	CGACCTCCTCCATCTTGCTG	CGACCGTGTGTGGATTCTC	55	2
	TCAAGCAAGAAGACAATGGAATAAAT	GTCCACATAAATCCAAAATAAAACAGT	57	
ES421877.1	ATTCCATCGAGTTGCTACGCCAG	CCAACATAATAGGTCTCCATCAACG	55	1
ES422367.1	GACAATGCTGAGAAGGGCGA	ATACAAATCGCGGCTACCAAAT	55	1
ES424016.1	TGTCAACCAGCGGGGATACTCA	TCTTTTGTTCGTCACCTCCC	55	1
ES428620.1	ATAGACTCCACCAATCCGCT	TTGAATTCGCCAGATAGAGC	55	1
Pm_CL135Contig1	CTCACTAACACCATAACC	GAGCATTTAACAACTTTGGG	60	1
Pm_CL1400Contig1	TGCGTCACTCTAATGCC	ATCTGTCAAAGTAGAGAACACC	60	1
Pm_CL150Contig1	CACTCTTTCTTTTCAAGTTAC	CAAATCCTTCATTGTCTCCTTC	60	1
Pm_CL1692Contig1	CTTCAGGGTTAAAGAATGG	TGCGGAGAAGATGATG	60	1
Pm_CL1811Contig1	GTTTGTGCGCATTGATGG	TGGAGCAACGCAAGTAG	60	1
Pm_CL1814Contig1	TAATGCCTCAGCCATCC	GCAGTAAGCAACAGTATTACAG	60	1
Pm_CL1868Contig1	GTCTCCTGACAAATCC	GTAGACCGTAGAATCC	60	1
Pm_CL1982Contig1	CTGAAAAAGTCGGAATTTGG	GCTAATAACATCAAATGCGG	60	1
Pm_CL1994Contig1	TGTGGGTGGAGATATG	CCAAGTGAATATGGAATGAAG	60	2
	GAGATACAACAGTATTTTCAACAGGGG	AAGTGTCATGCAATAATTATCACCCC	60	
Pm_CL1997Contig1	GATTAATGACGCTGTCTG	CCCCTCCATACAAAATAC	60	1
Pm_CL1Contig2	CTGGTTCTCTTTGGTTC	TGCCATTCATTGCGTC	60	1
Pm_CL2089Contig1	GTTGTGAAAGACTTCCC	CACCCCCACTAAAATC	60	1
Pm_CL2133Contig1	GCCAACACTCTATTTTTTGC	CTCAACATCGTTTTCAACC	60	1
Pm_CL214Contig1	CCAACAATGTGAAATCCAG	GCCTACGAAACAACAAGAAATG	60	1
Pm_CL2282Contig1	AAATCCTGCCCTTGTC	AAATCTCTTCTCCTCC	60	1
Pm_CL234Contig1	GAAGTGAAGTGAAGATAG	ACATTCATGTCCTCCTTAGCTG	60	1
Pm_CL618Contig1	CAGCTTATCATCTGTCTC	TTGTCACTTGCCCACTC	60	1
Pm_CL61Contig1	AACCTGCTGAAAACCC	TCTTCGGTCAAGTCGTC	60	1
Pm_CL73Contig1	GATTGCCAGCAGATTCAACC	AATAAGTAAGAATGATACAGCCAGCCC	60	1
Pm_CL783Contig1	AAAGCTCTCCAGAGTCCCAACC	GTCGAAAAGAAAACCCATATTCCCC	60	1
Pm_CL795Contig1	GGACATTCATACACGG	TAGACTTTGGGATGTTAGG	60	1
Pm_CL855Contig1	ACATTCCCAAGAACGCC	CACTTCAAATGTCTGCC	60	1
Pm_CL908Contig1	CAAACCTCTGGACAACAC	CGGAACTCTGTATATCTC	60	1
Pm_CL919Contig1	ATCAACAGTGGCTGAC	CAGTATATGATCCAAATGGG	60	1
Pm_CL922Contig1	CAACTACATTTTTCGTCGG	GGATGGCTACAATCTTC	60	1
Pm_CL939Contig1	CAGACCAGAGGAAAAC	GGAAGTGGAGTCATAAG	60	1
Pm_CL969Contig1	GGAGGATGATACTGAAG	CAGATTTCCATAGCATAGAC	60	1
Pm_CL988Contig1	TTATCAGGCTTCGGCTTCGG	TCTGAAGGTGGACTCTGAC	60	1
sM13Df243	AGTCCGTAAACGGGCTTTCT	CGTGAAACCGAGGAAGTAG	55	1

sSPcDFD005F06506	GAAGGTACAGTATAGGAATG	AAGTCTTTTGCTGGGG	60	1
sSPcDFD015C12212	CTCTAAAGACTTCTCTCTG	TTACCTGCCACCCATTC	60	1
sSPcDFD024D11311	CATCAATCTACAGTCCTCC	TCGAATCAAATCGAATCCAGCC	60	1
sSPcDFD040B03103	GCGGGAGAAAAATTAAGG	GGAGAAGGAAAGAATGG	60	1
sSPcDFE002A03003	CATTAACCCAACAAACCAC	TCATACAGATGGAGGAG	60	1
sSPcDFE025C06206	CAACTCCAATGTGCTTC	CCAATACAAGTGGCTTC	60	1
sSPcDFE028B10110	GAGATTTGAGATGTGTTGAG	CTGCTTTGAGATGAAGG	60	1
sSPcDFE038D06306	TTACAGTTGGTTAGGGTTTC	AATTGGGGTTTTCAATCAAGGCTTC	60	1
sSPcDFE044F10510	GTCCTTGAAAACCTTCC	CATGATCGTTGACAGCC	60	1
sSPcDFE049B06106	CAACCATAACAGCAACAC	GCCACGATTTTCACAAG	60	1
sSPcDFE049E11411	CAACACCTGCAAAACTC	GGCATCTATGTACTGGTTAATC	60	1
sSPcDFF014F08508	TGACGTGAAGGAACTG	CTGAGAATGTGGATTTGG	60	1
sSPcDFF015H05705	CAGCAGCATTAAAGATGG	GGATGGAGAGTGTTTTGG	60	1
sSPcDFF044H10710	CTGTGTTTTAGGTCTCTC	TCGCAATGGCTGTTAG	60	1
U22458.1	CAATTTTGGTCCACTCCAAG	AATCCCAAAAACCTTGCATCA	57	1
Z49715.1	AGGCAACTGAAACGACCAAGG	TAAAACCAGCCAAGCCAAACAA	57	2
	CGACGATGAAGAGGAGGGAG	TAATCAAACCACACAACACGCAC	57	

Table S10. Data summary and annotation information for 121 candidate genes. SD = standard deviation, UTR = untranslated region.

Locus	Length ^a (bp)	Missing ^b (bp)	<i>n</i>	SDR ^c	BDR ^d	Frame ^e	5' UTR ^f	Exon ^f	Intron ^f	3' UTR ^f
CD028057.1	686	0	20	0	20	3		1-38, 177-292, 370-537, 668-686	39-176, 293-369, 538-667	
CN634517.1	777	2	23	0/0	23/23	1	1-71, 191-686	72-190		687-777
CN634677.1	288	0	23	3	20	3	1-288			
CN635137.1	738	3	21	0	21	2	1-231	232-738		
CN635490.1	448	27	23	1	22	1	1-99, 222-311	100-221		312-448
CN635596.1	311	0	23	7	16	2	1-212			213-311
CN635661.1	254	12	20	0	20	3	1-166			167-254
CN635674.1	163	0	19	9	10	2	1-163			
CN635691.1	635	16	23	0	23	2	1-56, 181-355, 510-635	57-180, 356-509		
CN636014.1	675	0	24	0/0	24/24	2	1-675			
CN636043.1	1176	32	22	0	22	2	1-83, 959-1033	84-958		1034-1176
CN636093.1	353	0	22	0	22	2	1-80			81-353
CN636149.1	341	0	18	0	18	1	1-89, 187-341	90-186		
CN636303.1	650	0	23	0	23	1	1-104, 239-389	105-238		390-650
CN636471.1	433	1	23	0	23	2	1-433			
CN636492.1	406	0	24	0	24	3	1-29, 207-406	30-206		
CN636784.1	803	0	24	0/0	24/24	3	1-803			
CN636795.1	676	14	23	0	23	1	200-396, 520-676	1-199, 397-519		
CN636901.1	569	0	23	0	23	1	1-14, 143-269	15-142		270-569
CN636999.1	357	0	23	0	23	2	1-53, 164-357	54-163		
CN637166.1	366	48	16	0	16	3	1-366			
CN637226.1	188	23	20	0	20	3	1-188			
CN637244.1	366	2	22	0	22	3	1-169, 263-366	170-262		
CN637306.1	670	5	23	1	22	2	1-90, 196-325, 627-670	91-195, 326-626		
CN637339.1	533	0	22	0	22	1	1-32, 109-280, 377-533	33-108, 281-376		
CN637910.1	303	0	23	0	23	1	1-303			
CN637944.1	237	0	20	5	15	2	1-237			
CN638015.1	395	2	21	0	21	2	1-139, 229-268	140-228		269-395
CN638070.1	185	0	12	0	12	3	1-185			
CN638367.1	889	4	23	0	23	2	1-101, 483-575, 696-781, 864-889	102-482, 576-695, 782-863		

CN638381.1	959	0	16	0	16	3		1-853		854-959
CN638489.1	456	30	15	3	12	3		1-147, 253-456	148-252	
CN638545.1	512	0	23	0	23	2		1-386		387-512
CN638556.1	380	0	23	0	23	3		1-380		
CN638735.1	596	0	23	0	23	2		1-79, 251-442, 589-596	80-250, 443-588	
CN639074.1	547	0	24	0	24	3		1-238		239-547
CN639087.1	370	0	23	3	20	1		1-370		
CN639130.1	117	0	21	0	21	3		1-117		
CN639236.1	308	0	20	0	20	2		1-308		
CN639311.1	812	22	22	0	22	3		1-43, 144-304	44-143, 305-812	
CN639346.1	189	2	17	2	15	1	1-57	58-189		
CN639480.1	422	0	23	0	23	3		1-422		
CN640037.1	458	0	22	0	22	2		1-188, 300-458	189-299	
CN640110.1	364	0	23	0	23	2		1-364		
CN640155.1	318	36	17	1	16	3		1-318		
CN640247.1 ^g	754	1	24	0	24	2		1-602 (605)		603 (606)-754 209-228
CN640289.1	228	0	23	0	23	3		1-208		
CN640361.1	757	7	22	6	16	1		1-82, 687-757	83-686	
CN640419.1	618	1	22	0	22	2		1-15, 114-268, 358-440, 548-618	16-113, 269-357, 441-547	
CN640485.1	528	2	23	0	23	1	1-72	73-298, 502-528	299-501	
CN640493.1	247	0	16	0	16	3		1-94, 215-247	95-214	
CN640521.1	418	0	23	0	23	1		1-418		
CN640670.1	197	0	23	1	22	2		1-197		
CN640738.1	542	0	21	0	21	2		1-88, 199-340	89-198	341-542
CN641116.1	739	40	23	0	23	1		1-77, 322-403, 525-629, 735-739	78-321, 404-524, 630-734	
CN641171.1	470	0	22	0	22	2		1-157, 244-445	158-243	446-470
CN641226.1	375	0	23	0	23	2		1-375		
ES418315.1	426	1	22	0	22	1		1-426		
ES418915.1	401	0	23	0	23	3		1-100		101-401
ES419198.1	368	1	23	0	23	1		1-147		148-368
ES419223.1	445	5	22	0	22	3		1-34, 134-292	35-133	293-445
ES419242.1	831	0	16	0	16	1		1-11, 529-727	12-528	728-831
ES419657.1	377	0	23	0	23	3		1-178		179-377
ES420171.1	235	0	23	0	23	1		1-90		91-235
ES420250.1	884	13	23	0	23	1	1-124	125-241, 368-655	242-367	656-884
ES420603.1	425	0	23	0	23	3		1-295		296-425

ES420757.1	648	0	19	0	19	2		1-23, 174-329, 474-648	24-173, 330-473	
ES420771.1	292	0	20	0	20	3		1-127		128-292
ES420862.1	679	49	23	0	23	3		1-10, 143-583	11-142	584-679
ES421219.1	499	0	22	0	22	2		1-494		495-499
ES421311.1	729	0	21	0	21	1		1-113, 397-532	114-396	533-729
ES421603.1	528	0	23	0	23	1		1-411		412-528
ES421877.1	550	0	19	0	19	2		1-488		489-550
ES422367.1	1038	24	16	0	16	2		273-334, 453-518, 625-688, 850-929	1-272, 335-452, 519-624, 689-849	930-1038
ES424016.1	397	0	21	0	21	1		1-345		346-397
ES428620.1	686	0	17	0	17	1		206-322, 433-492	1-205, 323-432	493-686
Pm_CL135Contig1	769	1	8	6	2	1		1-132, 256-387, 761-769	133-255, 388-760	
Pm_CL1400Contig1	378	1	23	2	21	3		1-325		326-378
Pm_CL150Contig1	356	40	16	0	16	2		1-356		
Pm_CL1692Contig1	358	4	22	1	21	1	1-16	17-358		
Pm_CL1811Contig1	672	32	16	0	16	1		204-323, 527-625	1-203, 324-526, 626-672	
Pm_CL1814Contig1	368	0	23	0	23	1		1-368		
Pm_CL1868Contig1	398	1	21	0	21	3		1-151		152-398
Pm_CL1982Contig1	271	0	23	0	23	1		1-271		
Pm_CL1994Contig1	831	0	23	0/0	23/23	2		1-210, 299-363, 484-783	211-298, 364-483	784-831
Pm_CL1997Contig1	711	12	21	0	21	2		227-339, 462-581	1-226, 340-461	582-711
Pm_CL1Contig2	631	19	16	0	16	1	1-103	104-217, 532-631	218-531	
Pm_CL2089Contig1	400	0	23	0	23	1	1-123, 222-234	235-400	124-221	
Pm_CL2133Contig1	334	0	23	1	22	3		1-334		
Pm_CL214Contig1	360	0	22	9	13	3		1-259		260-360
Pm_CL2282Contig1	351	3	23	0	23	1		1-351		
Pm_CL234Contig1	753	5	18	0	18	1		74-223, 334-414, 733-753	1-73, 224-333, 415-732	
Pm_CL618Contig1	348	44	23	3	20	2		1-126, 297-348	127-296	
Pm_CL61Contig1	392	28	21	1	20	2		1-116		117-392
Pm_CL73Contig1	462	31	23	0	23	1		1-151, 265-299	152-264	300-462
Pm_CL783Contig1	406	0	22	2	20	2		1-380		381-406
Pm_CL795Contig1	417	7	23	0	23	3		1-316		317-417
Pm_CL855Contig1	394	0	23	0	23	3		1-358		359-394
Pm_CL908Contig1	501	5	18	0	18	2		1-101, 204-449	102-203	450-501

Pm_CL919Contig1	738	10	22	1	21	2	1-13, 110-344, 693-738	14-109, 345-692	
Pm_CL922Contig1	433	0	22	1	21	3	1-349		350-433
Pm_CL939Contig1	437	0	21	0	21	2	1-133, 218-437	134-217	
Pm_CL969Contig1	404	0	23	1	22	3	1-247		248-404
Pm_CL988Contig1	555	8	23	0	23	1	1-45, 241-555	46-240	
sM13Df243	286	0	19	0	19	1	1-231		232-286
sSPcDFD005F06506	507	56	21	0	21	2	1-35, 161-280	36-160	281-507
sSPcDFD015C12212	152	0	23	10	13	3	1-28		29-152
sSPcDFD024D11311	388	16	23	1	22	1	1-388		
sSPcDFD040B03103	378	0	22	0	22	3	1-210		211-378
sSPcDFE002A03003	501	0	12	1	11	2	1-140, 223-465	141-222	466-501
sSPcDFE025C06206	456	9	13	3	10	2	1-197, 410-456	198-409	
sSPcDFE028B10110	431	0	22	0	22	2	1-407		408-431
sSPcDFE038D06306	386	44	23	0	23	1	1-38	39-386	
sSPcDFE044F10510	353	33	23	0	23	1	1-353		
sSPcDFE049B06106	358	3	21	0	21	2	1-293		294-358
sSPcDFE049E11411	407	0	20	0	20	3	1-325		326-407
sSPcDFF014F08508	499	0	13	0	13	2	1-53, 168-404	54-167	405-499
sSPcDFF015H05705	286	0	23	11	12	3	1-271		272-286
sSPcDFF044H10710	674	0	16	0	16	3	1-61, 260-336, 425-491	62-259, 337-424, 512-588	492-511, 589-674
U22458.1	706	0	23	0	23	3	1-706		
Z49715.1	984	91	20	0/0	20/20	2	1-5, 410-697, 821-934	6-409, 698-820	935-984
Total	59173	928	----						
Average (± 1 SD)	489	8	21						
	(± 204)	(± 15)	(± 3)						

^aThe length in base pairs of the aligned data.

^bThe number of aligned positions where at least one sample has missing data or an insertion-deletion (indel) event.

^cSDR = single direction read. The number of samples with single, either forward or reverse, reads. Loci with two primer sets give results for each set separated by a slash.

^dBDR = bidirectional reads. The number of samples with both forward and reverse reads. Loci with two primer sets give results for each set separated by a slash.

^eFrame is given as the codon position of the first base in the alignment or the first base within the coding region.

^fRanges are given as positions in the alignment with the numbering starting at 1.

^gThis locus had a point mutation in some samples that extended the coding region for an extra amino acid. Values for this haplotype are given in parentheses.