Supporting Information Table S1. Summary of all loci typed in lodgepole (Lp), and jack pine (Jp), including diversity measures (observed heterozygosity (Ho), expected heterozygosity (UHe)), their estimated linkage group, the data subset they were included in ('Data'), the frequency they were detected as an outlier for each subset of data, the direction of selection, and their putative annotation.

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Jackc1080p157	368	0.003	0.003	-0.001	100	0.270	0.263	-0.031		species/Jp				0.53		RPM1-interacting protein 4 (RIN4) family protein
Jackc1237p470	368	0.082	0.083	0.020	100	0.560	0.495	-0.136		all		1		0.046	Negative	OT U-like cysteine protease
Jackc1315p459	368	0.000	0.000		100	0.370	0.339	-0.096		species/Jp				0.523		bZIP transcription factor/ABA-responsive element binding protein
Jackc1384p110					100	0.430	0.426	-0.014		Jp						transcribed locus
Jackc1410p116	364	0.052	0.051	-0.027	100	0.500	0.495	-0.015		all		1		0.927		postsynaptic protein-related/microtubule-associated protein CRIPT
Jackc1450p228	367	0.008	0.008	-0.004	100	0.500	0.422	-0.190		species/Jp				0.08		transcribed locus
Jackc1483p368	345	0.006	0.006	-0.003	100	0.410	0.426	0.033		species/Jp				0.044		ubiquitin-specific protease 3
Jackc149p234	368	0.003	0.003	-0.001	100	0.270	0.249	-0.089		species/Jp				0.973		4-hydroxy-3-methylbut-2-enyl diphosphate reductase
Jackc1504p209	368	0.003	0.003	-0.001	100	0.300	0.309	0.025		species/Jp			2	0.002	Positive	transcribed locus
Jackc152p517	368	0.160	0.170	0.056	100	0.390	0.392	-0.001		all				0.788		L-asparaginase/ amidohydrolase
Jackc1570p273	367	0.000	0.000		99	0.505	0.496	-0.023		species/Jp				0.325		protein tyrosine kinase superfamily
Jackc1579p429					100	0.300	0.322	0.062		Jp						Pleckstrin homology (PH) domain superfamily protein
Jackc1735p209	364	0.003	0.003	-0.001	100	0.460	0.444	-0.040		species/Jp				LL+LJ-JJ-		mRNA splicing factor/thioredoxin-like/Dim1 family
Jackc1859p368	364	0.088	0.084	-0.046	100	0.480	0.457	-0.055		all				0.788		
Jackc2307p219					98	0.224	0.200	-0.126		Jp						DnaJ/Hsp40 cystein-rich domain superfamily protein
Jackc2433p173	368	0.003	0.003	-0.001	100	0.480	0.478	-0.009		species/Jp				LL+LJ-; LL-		pentatricopeptide repeat (PPR)/tetratricopeptide repeat (TPR)-like
Jackc2551p179					93	0.495	0.493	-0.009	JP01	Jp						WD-40 repeat family protein/beige/BEACH domain-related
Jackc2623p916	368	0.008	0.008	-0.004	100	0.560	0.482	-0.167		species/Jp				0.034		transcribed locus
Jackc2888p563	368	0.090	0.091	0.010	99	0.374	0.374	-0.003		all				0.604		cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis
Jackc291p82					98	0.602	0.487	-0.241		Jp						Heavy metal transport/detoxification superfamily protein
Jackc3017p105	368	0.011	0.011	-0.005	100	0.450	0.502	0.100	JP01	species/Jp				0.077		
Jackc3080p108	368	0.003	0.003	-0.001	100	0.340	0.309	-0.105		species/Jp			1	0.125	Negative	myb domain protein 3r-4
Jackc3589p359					92	0.522	0.488	-0.076		Jp						cytochrome C1 family
Jackc3789p280	364	0.003	0.003	-0.001	100	0.240	0.227	-0.061		species/Jp				0.142		transcribed locus
Jackc391p162					100	0.290	0.290	-0.004		Jp						photosystem I, PsaA/PsaB protein
Jackc4003p197					99	0.414	0.364	-0.144	JP02	Jp						O-acetyltransferase protein/Cas1p-like protein
Jackc402p99	368	0.000	0.000		100	0.420	0.457	0.077		species/Jp	1			0	Positive	NADH-ubiquinone oxidoreductase related
Jackc406p342	368	0.030	0.035	0.139	100	0.560	0.502	-0.122	JP07	all		1		0.876		heat shock cognate protein 70-1
Jackc408p413	365	0.005	0.005	-0.003	100	0.580	0.486	-0.199		species/Jp				0.045		protein of unknown function (DUF3411)
Jackc452p299	366	0.003	0.003	-0.001	97	0.361	0.369	0.017		species/Jp				0.531		BEL1-like homeodomain/DNA binding transcription factor
Jackc473p320					99	0.485	0.459	-0.061	JP03	Jp						Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
Jackc480p274	367	0.289	0.274	-0.056	100	0.270	0.263	-0.031		all	1			0.025	Negative	Heavy metal transport/detoxification superfamily protein
Jackc616p315					100	0.460	0.457	-0.011	JP04	Jp						septin
Jackc722p712	355	0.521	0.494	-0.056	99	0.465	0.491	0.049	LP01/JP05	all				0.037		cinnamoyl-CoA reductase/NAD dependent epimerase/dehydratase
Jackc816p105	367	0.011	0.011	-0.005	100	0.330	0.290	-0.143		species/Jp				0.087		
Jackc833p224	352	0.548	0.501	-0.097					LP02	Lp						CCCH-type zinc finer family protein
Jackc915p369	368	0.329	0.360	0.086	100	0.540	0.490	-0.108	LP03/JP06	all				0.187		ribosomal protein L2 family
Jackc924p449					97	0.309	0.317	0.018		Jp						response regulator
Jackc961p604	368	0.003	0.003	-0.001	100	0.360	0.414	0.126	JP01	species/Jp				N; LL-,LJ+		protochlorophyllide oxidoreductase A/short chain dehydrogenase
Jp_c00039p703	368	0.011	0.011	-0.005	100	0.390	0.382	-0.026	JP02	species/Jp				0.337		adenosine kinase
Jp_c00242p897					97	0.629	0.502	-0.260	JP07	Jp						ribosomal protein S5 family protein

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Jp_c00433p427	368	0.024	0.024	-0.012	100	0.360	0.422	0.143		all				0.544		GDSL-link lipase/acylhydrolase
Jp_c00542p351	368	0.049	0.048	-0.025	100	0.450	0.466	0.029		all				0.172		transcribed locus
Jp_c00704p802	367	0.313	0.307	-0.021	100	0.280	0.284	0.008		all				0.004		peroxidase 2
Jp_c01249p362	349	0.610	0.425	-0.439	93	0.516	0.466	-0.113	JP03	all	2			0	Negative	short-chain dehydrogenase-reductase B/KR domain
Jp_c01798p762					95	0.337	0.309	-0.097		Jp						coatomer gamma subunit putative
Jp_c01946p291					100	0.470	0.454	-0.040	JP04	Jp						xyloglucan endo-transflycosylase
Jp_c01993p623	364	0.223	0.219	-0.017	99	0.192	0.206	0.065	JPLP01	all				0.628		protein kinase superfamily
Jp_c01993p67	367	0.218	0.224	0.024	91	0.099	0.133	0.254	JPLP01	all				0.386		protein kinase superfamily
Jp_c02124p853	335	0.069	0.066	-0.036	99	0.202	0.229	0.114		all	1			0.748	Negative	NUP50/nucleoporin
Jp_c02580p908	368	0.011	0.011	-0.005	100	0.490	0.496	0.008		species/Jp				0.002		ubiquitin-conjugating enzyme
Jp_c03167p296	368	0.024	0.024	-0.012	100	0.290	0.263	-0.107	LP11/JP08	all				0.841		auxin response factor 1/B3 DNA binding domain
Jp_c03167p428					99	0.222	0.214	-0.043		Jp						auxin response factor 1/B3 DNA binding domain
Jp_c03968p478	368	0.424	0.370	-0.147	100	0.360	0.333	-0.085	LPL1	all				0.044		plasma membrane intrinsic protein 2;8/aquaporin PIP2
Jp_c03968p72	368	0.620	0.496	-0.250	100	0.110	0.104	-0.058	LPL1	all				0.02		plasma membrane intrinsic protein 2;8/aquaporin PIP2
Jp_c04973p670	343	0.510	0.493	-0.036	100	0.470	0.491	0.038	LP01/JP05	all				0.042		alcohol dehydrogenase/zinc-binding dehydrogenase
Jp_c05130p655	368	0.011	0.011	-0.005	100	0.400	0.478	0.159		species/Jp				0.223		voltage dependent anion channel
Jp_c05171p407	367	0.104	0.103	-0.005	98	0.643	0.484	-0.336		all				0.063		translocase of outer membrane 22-V
Jp_c06398p643	368	0.543	0.501	-0.087	100	0.380	0.367	-0.042	LP02	all				0.003		thylakoid rhondanese-like
Jp_c06551p422	368	0.095	0.100	0.052	100	0.540	0.495	-0.096		all				0.92		photosynthetic electron transfer C
Jp_c07427p1497	368	0.003	0.003	-0.001	100	0.180	0.197	0.081		species/Jp				0.972		tranlocon outer complex protein/DUF3406
Jp_c09653p489	367	0.324	0.358	0.093	100	0.540	0.490	-0.108	LP03/JP06	all				0.071		photosystem II reaction center PSB29 protein/thylakoid formation protein
Jp_c12031p335	367	0.387	0.423	0.083	93	0.624	0.454	-0.382		all	1			0	Negative	protein of unknown function (DUF538)
Jp_c12214p1395	368	0.071	0.073	0.035	100	0.460	0.482	0.042		all				LL-; LJ-,JJ+		homeobox domain
Jp_c12920p1329	366	0.025	0.024	-0.012	100	0.280	0.270	-0.042		all				0.302		inner membrane family protein
Jp_c13093p749	364	0.025	0.024	-0.013	100	0.550	0.496	-0.113	LP04/JP11	all		2		0.001	Positive	HSP20-like chaperones superfamily protein
Jp_c13875p1478	367	0.071	0.068	-0.037					LP05	Lp		2				pectin methylesterase
Jp_c15855p785	368	0.185	0.202	0.086	100	0.310	0.290	-0.074		all	1			0	Negative	A20/AN1-like zinc finger family protein
Jp_c15992p560	368	0.014	0.014	-0.007	96	0.219	0.313	0.297		species/Jp				0.061		transducin/WD-40 repeat-like superfamily/homologue of yeast autophagy
Jp_c17571p991	368	0.003	0.003	-0.001	100	0.500	0.474	-0.061		species/Jp				0.413		high cyclic electron flow 1/fructose 1-6-bisphosphatase
Jp_c18278p614					95	0.368	0.446	0.169		Jp						thioredoxin superfamily protein
Jp_c18600p510	353	0.003	0.003	-0.001	99	0.293	0.279	-0.055		species/Jp				0.009		ribosomal protein L32
Jp_c19293p339					99	0.404	0.500	0.188		Jp						glutathione s-transerfase/translation elongation factor
Jp_c20036p1123	367	0.079	0.076	-0.041	100	0.390	0.361	-0.085		all				0.345		S-formylglutathione hydrolase/esterase
Jp_c20182p499	367	0.079	0.076	-0.041	100	0.230	0.263	0.122		all				0.054		transcribed locus
Jp_c20432p742	368	0.005	0.005	-0.003	100	0.230	0.235	0.015		species/Jp	1			0.073	Positive	phytoene desaturation 1/4-hydroxyphenylpyruvate/Glyoxalase/Bleomycin
Jp_c20538p910	344	0.523	0.481	-0.089	99	0.505	0.502	-0.010		all	1			0	Negative	transcribed locus/glycine rich protein
Jp_c20590p588	354	0.045	0.044	-0.023	100	0.480	0.486	0.008		all		1		0.136		RNA -binding protein/RNA recognition motif
Jp_c20770p419	368	0.008	0.008	-0.004	100	0.590	0.426	-0.392		species/Jp				0.017		eukaryotic translation initiation factor 2 beta subunit
Jp_c20964p544	368	0.076	0.073	-0.040	100	0.350	0.351	-0.004		all				0.793		NAD(P)-binding Rossmann-fold superfamily protein/short chain dehydrogenase
Jp_c21015p448	368	0.168	0.154	-0.092	100	0.420	0.414	-0.020		all				0.861		P-loop containing nucleoside triphosphate hydrolase/SRP54-type, GTPase domain
Jp_c21018p454	365	0.003	0.003	-0.001	100	0.560	0.502	-0.122		species/Jp				0.201		erythronate-4 phosphate dehydrogenase family protein
Jp_c21171p1069	353	0.445	0.485	0.082	99	0.323	0.324	-0.003		all				0.114		S-adenosyl-L-homocysteine hydrolase/NAD binding domain
Jp_c21224p439	368	0.402	0.381	-0.057	100	0.350	0.351	-0.004		all	2			0.547	Negative	transketolase/dehydrogenase-5-phosphate synthase

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Jp_c21306p1347	367	0.000	0.000		92	0.511	0.459	-0.118		species/Jp				0.816		glyceraldehyde 3-phosphate dehydrogenase of plastid 1
Jp_c21401p474	367	0.177	0.171	-0.040	100	0.510	0.494	-0.038		all				0.303		pyridine nucleotide-disulphide oxidoreductase/monodehydroascorbate reductase 1
Jp_c21871p717	352	0.020	0.020	-0.010	99	0.414	0.473	0.120		all				0.618		methionine sulfoxide reductase B 2
Jp_c21979p359					100	0.320	0.284	-0.134		Jp						ribosomal protein S26e
Jp_c22176p294	352	0.006	0.006	-0.003	100	0.510	0.466	-0.100		species/Jp				0.348		Protein of unknown function (DUF1230)
Jp_c22804p650					98	0.429	0.427	-0.009		Jp						aldose 1-epimerase/galactose mutartotase-like superfamily protein
Jp_c23049p629	367	0.379	0.393	0.036	100	0.290	0.351	0.168		all				0.183		papain family cysteine protease/cathepsin propeptide inhibitor domain
Jp_c23259p1067	368	0.016	0.016	-0.008	100	0.400	0.396	-0.015		species/Jp				0.05		SIT4 phosphatase-associated family protein
Jp_c23409p668	368	0.024	0.024	-0.012	100	0.560	0.499	-0.127		all		2		0.205	Positive	glyoxalase/bleomycin resistance protein/dioxygenase superfamily
Jp_c23680p1524	368	0.014	0.019	0.279	100	0.390	0.484	0.191		all		1		0.115		copper amine oxidase family protein
Jp_c23867p705	367	0.003	0.003	-0.001	100	0.400	0.387	-0.040		species/Jp				0.374		peroxin 11D
Jp_c23884p704	368	0.011	0.011	-0.005	100	0.540	0.503	-0.080		species/Jp				0.572		signal peptide peptidase like-2
Jp_c24821p611	368	0.027	0.027	-0.014	100	0.320	0.284	-0.134		all	1	2		0.494	Positive	nodulin MtN3 family protein
Jp_c25025p252	339	0.024	0.035	0.321	100	0.470	0.496	0.048		all				0.341		ubiquitin-like superfamily/UBL5
Jp_c25075p377	368	0.416	0.419	0.005	100	0.560	0.451	-0.248		all	2			0	Negative	phenylcoumaran benzylic ether reductase/NmrA-like negative transcriptional regulator
Jp_c25220p628	368	0.033	0.032	-0.017	100	0.470	0.480	0.017		all				0.168		ribosomal protein L19e
Jp_c25513p539	359	0.435	0.456	0.046	100	0.450	0.476	0.050	LP06	all			1	0.033	Negative	ribosomal protein L6
Jp_c26007p766	368	0.003	0.003	-0.001	100	0.280	0.242	-0.163		species/Jp				0.102		glycine cleavage T-protein/aminomethyltransferase folate binding domain
Jp_c26456p564	368	0.171	0.170	-0.007						Lp						40S ribosomal protein S4; Provisional
Jp_c26537p1091	368	0.068	0.076	0.103	100	0.320	0.322	0.000		all		1		0.133		homeobox domain/Homeobox-leucine zipper protein family
Jp_c26967p1321	368	0.008	0.008	-0.004	100	0.530	0.500	-0.065		species/Jp			1	0.06	Negative	S-adenosylmethionine-dependent methyltransferase superfamily protein
Jp_c27011p1002	368	0.005	0.005	-0.003	100	0.530	0.494	-0.078		species/Jp				0.865		targeting protein for Xklp2 (TPX2)
Jp_c27188p1706	368	0.003	0.003	-0.001	99	0.505	0.475	-0.068		species/Jp				0.32		suppressor of abi3-5
Jp_c27585p643	367	0.409	0.455	0.100	100	0.460	0.502	0.080		all	1			0	Negative	alpha-L-arabinofuranosidase/kelch motif
Jp_c27768p690	368	0.285	0.271	-0.053	100	0.460	0.501	0.077		all				0.079		papain family cysteine protease/cathepsin propeptide inhibitor domain
Jp_c27995p367	363	0.008	0.014	0.396	100	0.540	0.499	-0.087		species/Jp				0.05		transcribed locus/BES1-interacting Myc-like protein 2
Jp_c28163p1406	368	0.022	0.027	0.189	100	0.160	0.148	-0.087		all		1		0.019		CCT motif family protein
Jp_c28414p495	303	0.251	0.398	0.369	97	0.423	0.489	0.131		all				0		cytochrome c oxidase;electron carriers
Jp_c28904p670	368	0.011	0.011	-0.005	100	0.350	0.488	0.279		species/Jp			2	0	Positive	ubiquitin-conjugating enzyme 28//E3 interaction residues
Jp_c28943p445	362	0.011	0.011	-0.006	100	0.380	0.387	0.012		species/Jp				0.543		ubiquitin-conjugating enzyme/ IQ-domain 26
Jp_c28993p1003	368	0.459	0.475	0.032	100	0.440	0.405	-0.091	JPL1	all				0.452		GRAS family transcription factor
Jp_c28993p897	367	0.019	0.019	-0.010	100	0.440	0.414	-0.068	JPL1	all	1	1		0.224	Positive	GRAS family transcription factor
Jp_c29875p506	368	0.003	0.003	-0.001	100	0.420	0.437	0.035		species/Jp				0.992		transcribed locus
Jp_c30646p698	363	0.003	0.003	-0.001	100	0.300	0.284	-0.063		species/Jp				0.135		mitochondrial carrier family protein (isoform 1)
Jp_c31376p1552	368	0.043	0.043	-0.022	100	0.560	0.497	-0.131		all				0.445		ATP binding;ATP-dependent helicases;DNA helicases
Jp_c31636p544	367	0.281	0.287	0.019	100	0.420	0.405	-0.042		all				0.477		methylenetetrahydrofolate reductase
Jp_c32144p353					99	0.535	0.489	-0.099		Jp						Protein kinase superfamily protein
Jp_c32861p648					95	0.326	0.414	0.207		Jp						ubiquitin-related modifier
Jp_c33062p504	362	0.008	0.008	-0.004	100	0.400	0.451	0.109		species/Jp				0.963		cytochrome c oxidase related
Jp_c33476p566	368	0.087	0.088	0.013	99	0.485	0.470	-0.036		all				0.897		CLP protease regulatory subunit
Jp_c34152p781	347	0.127	0.124	-0.024	99	0.515	0.502	-0.031		all			2	0.018	Positive	ribosomal protein L27
Jp_c34224p545	368	0.011	0.011	-0.005	100	0.450	0.418	-0.082		species/Jp				0.434		transcribed locus
Jp_c34823p887					95	0.516	0.495	-0.048		Jp						ribosomal S3A

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Jp_c34902p455	365	0.005	0.005	-0.003	100	0.490	0.488	-0.009		species/Jp	1			0.768	Positive	copper/zinc superoxide dismutase
Jp_c38919p628	362	0.304	0.288	-0.057						Lp						caleosin-related family protein/responsive to dessication 20
Jp_c40483p485	368	0.005	0.005	-0.003	100	0.430	0.410	-0.055	JPL3	species/Jp	1			0.57	Positive	pyridine nucleotide-disulphide oxidoreductase
Jp_c40483p739	368	0.008	0.008	-0.004	100	0.430	0.410	-0.055	JPL3	species/Jp	1			0.624	Positive	pyridine nucleotide-disulphide oxidoreductase
Jp_c40635p369	368	0.000	0.000		100	0.510	0.480	-0.067		species/Jp				0.931		photosystem II subunit Q-2/Oxygen evolving enhancer protein 3
Jp_c43016p279	352	0.014	0.014	-0.007	100	0.340	0.309	-0.105		species/Jp				0.02		transcribed locus
Jp_c43058p705	366	0.011	0.011	-0.005	100	0.380	0.405	0.058		species/Jp	1			0.001	Positive	HSP20-like chaperones superfamily protein
Jp_c43213p458	368	0.019	0.019	-0.010	100	0.900	0.499	-0.812	LP07	all		2		0	Positive	lipid transfer protein/seed storage 25 albumin superfamily protein
Jp_c43596p385	367	0.005	0.005	-0.003	100	0.510	0.471	-0.088	JP13	species/Jp				0.106		peptide transporter
Jp_c43942p268	367	0.213	0.232	0.081	100	0.330	0.410	0.190		all				0.837		alpha/beta hydrolases superfamily/dienelactone hydrolase family
Jp_c43969p509	366	0.123	0.116	-0.066	99	0.525	0.501	-0.053		all				0.883		ribosomal protein L13e/breat basic conserved 1
Jp_c44066p1378	368	0.019	0.019	-0.010	100	0.410	0.401	-0.028		all				0.7		little nuclei like
Jp_c44467p708	368	0.005	0.005	-0.003	100	0.380	0.414	0.077		species/Jp				0.207		ubiquitin-conjugating enzyme
Jp_c44595p1466	363	0.146	0.181	0.193	100	0.460	0.414	-0.117		all				0.079		alpha-galactosidase 2/glycosyl hydrolase family 31
Jp_c44637p536	368	0.022	0.022	-0.011	100	0.470	0.502	0.059	LP07	all		2		0.579	Positive	coatomer alpha subunit/glycine-rich protein
Jp_c44933p494	368	0.024	0.024	-0.012	100	0.390	0.410	0.043		all	1	2		0.139	Positive	photosystem II reaction center protein
Jp_c45253p360					99	0.354	0.364	0.024		Jp						ribosomal L22e protein family
Jp_c45986p341	360	0.008	0.008	-0.004	100	0.450	0.496	0.089		species/Jp				0.089		ribosomal protein S14p/S29e family protein
Jp_c46035p392					100	0.390	0.410	0.043		Jp						ribosomal protein S13/S18 family
Jp_c46992p573	367	0.016	0.016	-0.008	100	0.370	0.372	0.000		species/Jp				0.21		zinc finer (C2H2 type) family protein
JpLpc00337p904	367	0.311	0.302	-0.029	100	0.040	0.039	-0.020	LP08	all			1	0.207		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
JpLpc00745p1003	368	0.457	0.473	0.034	100	0.030	0.030	-0.015	LP09	all	removed			0.326		protein kinases/ubiquitin-protein ligase
JpLpc00988p408	368	0.011	0.011	-0.005	100	0.460	0.463	0.002		species/Jp				0.252		WRKY DNA binding domain
JpLpc01929p219	368	0.495	0.501	0.011	100	0.210	0.205	-0.032	JP09	all				0.001		CHASE domain containing histidine kinase protein
JpLpc02715p437	367	0.112	0.110	-0.013	99	0.515	0.495	-0.046		all				0		transcribed locus
JpLpc02733p310	368	0.011	0.011	-0.005	100	0.270	0.339	0.200		species/Jp	1			0.998	Positive	transcribed locus
JpLpc03397p578	359	0.206	0.203	-0.019	100	0.030	0.030	-0.015		all				0.33		SNARE associated golgi protein
JpLpc03587p814	367	0.395	0.375	-0.056	100	0.010	0.010	-0.005		species/Lp				0.615		protein kinase/casein kinase 1
JpLpc04112p1237	365	0.008	0.014	0.396	100	0.490	0.494	0.003	JP01	species/Jp				0.01		SSXT family protein
JpLpc04112p131	368	0.046	0.045	-0.024	100	0.010	0.010	-0.005		species/Lp	1			0.123	Positive	SSXT family protein
JpLpc04689p1306	325	0.403	0.405	0.004					LPL2	Lp						similar to Arabisopsis thaliana At1g70160/
JpLpc04689p1619	364	0.448	0.438	-0.024	100	0.000	0.000		LPL2	species/Lp				0.105		similar to Arabisopsis thaliana At1g70160/
JpLpc05265p1240	368	0.024	0.029	0.169	100	0.000	0.000			species/Lp				0.073		transcribed locus
JpLpc06142p940	368	0.497	0.488	-0.021	100	0.450	0.476	0.050		all	1			0.782	Negative	transcribed locus
JpLpc07372p371	368	0.484	0.497	0.025	100	0.040	0.039	-0.020		all				0.726		stabilizer of ion transporter SufD/polynucelotidyl transferase
JpLpc07589p2036	367	0.278	0.306	0.090	100	0.280	0.284	0.008		all	1			0.283	Negative	NADH-ubiquinone dehydrogenase/molybdopterin oxidoreductase
JpLpc08428p772	368	0.011	0.011	-0.005	100	0.530	0.448	-0.190		species/Jp				0.012		alpha and gamma adaptin binding protein
JpLpc09880p1739	362	0.086	0.082	-0.045	99	0.172	0.206	0.164		all				0		methyltransferase domain/tellurite resistance protein
JpLpc10450p806	368	0.440	0.434	-0.015	100	0.050	0.049	-0.026		all				0.166		myb-like DNA-binding domain
JpLpc11477p234	368	0.098	0.093	-0.051	99	0.000	0.000			species/Lp				0.075		Tetratricopeptide repeat (TRP)/FKBP-type peptidyl-prolyl cis-trans isomerase
JpLpc15608p1838	337	0.151	0.140	-0.082						Lp		3			Positive	Transducin family protein / WD-40 repeat family protein
JpLpc16915p385	368	0.111	0.105	-0.059	99	0.182	0.166	-0.100		all				0.056		transcribed locus
JpLpc18130p528	368	0.171	0.175	0.018	99	0.152	0.158	0.035		all				0.26		similar to Arabisopsis thaliana thaliana At5g13030

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
JpLpc21364p981	368	0.052	0.056	0.069	100	0.140	0.131	-0.075		all	1	3		0	Positive	myb-like DNA binding domain
JpLpc21779p551	368	0.079	0.076	-0.041	100	0.040	0.039	-0.020		all	1			0.377	Positive	Rab5-interacting family protein
JpLpc23919p3213	367	0.384	0.424	0.092	100	0.030	0.030	-0.015		all				0.811		response regulator 2
JpLpc24416p627	368	0.008	0.008	-0.004	100	0.460	0.474	0.024		species/Jp				0		HOPW1-1 interacting 1/aminotransferase class III
JpLpc24944p305	368	0.008	0.008	-0.004	99	0.535	0.473	-0.138		species/Jp				0.011		transcribed locus
JpLpc26435p293	368	0.484	0.501	0.032	100	0.060	0.058	-0.031		all				0.26		TATA-binding protein/cullin-associated and neddylation dissociated/HEAT repeats
JpLpc30315p463	367	0.305	0.299	-0.022	100	0.000	0.000			species/Lp				0.137		basic pentacysteine 6/GAGA binding protein-like family
JpLpc30743p1175	368	0.168	0.163	-0.032	100	0.370	0.382	0.026		all				0.563		thylakoid lumenal P17.1 protein
JpLpc30808p665	368	0.011	0.011	-0.005	97	0.371	0.341	-0.094		species/Jp	1			0.44	Positive	BTB/POZ domain and MATH domain 2
JpLpc31632p126	363	0.325	0.347	0.062	100	0.320	0.284	-0.134		all				0.31		cystatin domain
JpLpc31862p774	367	0.278	0.285	0.023	100	0.010	0.010	-0.005		species/Lp				0.432		chalcone-flavanone isomerase
JpLpc31990p707	368	0.019	0.019	-0.010	99	0.343	0.416	0.171	JPL2	all		1		0.024		homeobox 1
JpLpc31990p90	368	0.027	0.027	-0.014	100	0.460	0.495	0.067	JPL2	all		1		0.021		homeobox 1
JpLpc32323p740	367	0.022	0.027	0.189	100	0.240	0.227	-0.061		all	1		1	0.032	Positive	Aluminum induced protein with YGL and LRDR motifs
JpLpc32835p1047	368	0.457	0.475	0.037	100	0.060	0.058	-0.031		all				0.337		transcribed locus
JpLpc33893p239	368	0.016	0.016	-0.008	100	0.070	0.104	0.327		species/Jp	3			0.585	Positive	auxin-F-box protein 5
JpLpc34244p1745	365	0.890	0.495	-0.800	98	0.459	0.431	-0.071		all	1			0	Negative	Basic-leucine zipper transcription factor family protein
JpLpc34265p968	364	0.327	0.306	-0.070	100	0.110	0.104	-0.058		all				0		F-box like family protein
JpLpc34784p179	367	0.044	0.043	-0.022	99	0.455	0.456	-0.001		all				0.995		calreticulin family
JpLpc35530p946	358	0.310	0.313	0.009	99	0.182	0.183	-0.001		all				0.082		ethelene response factor
JpLpc36107p918	366	0.268	0.267	-0.004	100	0.180	0.165	-0.099		all				0.292		transcribed locus
JpLpc36252p1327	368	0.082	0.078	-0.042	100	0.020	0.020	-0.010		all	1			0.002	Positive	histone chaperone/global transription factor C
JpLpc36728p680	366	0.115	0.108	-0.061	100	0.560	0.490	-0.149		all				0		anitcondon-binding domain/RNA-processing
JpLpc37132p434	336	0.467	0.464	-0.008	100	0.000	0.000			species/Lp				0		
JpLpc37447p1264	368	0.011	0.011	-0.005	100	0.530	0.484	-0.100		species/Jp				0.082		Fcf2 pre-rRNA processing protein
JpLpc38316p430	305	0.148	0.142	-0.037						Lp						sucrose-6F-phosphate synthase
JpLpc38375p1504	367	0.439	0.471	0.066	100	0.100	0.095	-0.053	LP10/JP10	all				0.04		homeodomain-like superfamily
JpLpc39429p214	368	0.163	0.177	0.076	99	0.071	0.069	-0.037		all				0.23		SIN3-like 4
JpLpc39841p549	367	0.401	0.366	-0.094	99	0.374	0.384	0.023		all				0.034		similar to Arabisopsis thaliana At4g09830
JpLpc39929p732	368	0.087	0.083	-0.045	100	0.490	0.448	-0.100		all				0.109		SSXT family protein/translation elongation factor EF1A
JpLpc39993p867	368	0.033	0.037	0.126	100	0.210	0.189	-0.117		all		1		0.062		uncharacterized conserved protein (DUF2358)/SnoaL-like domain
JpLpc39995p1987	368	0.030	0.029	-0.015	100	0.520	0.486	-0.075	LP04/JP11	all				0		Telomerase activating protein Est1
JpLpc40356p1400	367	0.302	0.287	-0.057	97	0.031	0.031	-0.016		all	1			0	Negative	inorganic H+ pyrophosphatase
JpLpc40793p1901	368	0.014	0.014	-0.007	100	0.310	0.303	-0.028		species/Jp	1			0.062	Positive	Rtr1/RPAP2 family
JpLpc41024p554	368	0.071	0.068	-0.037						Lp						F-box family
JpLpc41037p1156	368	0.378	0.374	-0.011	100	0.010	0.010	-0.005		species/Lp				0.577		TMPIT-like protein
JpLpc41319p340	368	0.027	0.032	0.153	100	0.030	0.049	0.385		all	2	1		0.992	Positive	uncharacterized BCR, YbaB family COG0718
JpLpc42885p286	368	0.563	0.498	-0.130	100	0.300	0.356	0.153		all				0.158		DDRGK domain
JpLpc44209p446	368	0.073	0.071	-0.038	100	0.290	0.263	-0.107	LP11/JP08	all	removed			0.22		auxin response factor 1
JpLpc44494p452	366	0.019	0.019	-0.010	100	0.560	0.502	-0.122		all		1		0.053		transcribed locus
JpLpc44713p1218					98	0.531	0.442	-0.206		Jp			1		Negative	SEUSS-like 2
JpLpc44713p1452	368	0.410	0.429	0.043	100	0.120	0.131	0.078	LP07	all				0.016		SEUSS-like 2
JpLpc44782p470	368	0.022	0.022	-0.011	100	0.320	0.297	-0.084		all	1	2		0.335	Positive	KNOX1/2 domain/KNOTTED-like

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
JpLpc44961p330	368	0.429	0.426	-0.009	99	0.525	0.494	-0.069		all				0.735		transcribed locus
JpLpc45225p571	368	0.043	0.043	-0.022	99	0.202	0.183	-0.112	LP07	all	1	3		0.002	Positive	B-cell receptor-associated protein 31-like
JpLpc45900p1071	368	0.476	0.473	-0.007	95	0.032	0.031	-0.016		all				0.527		AP2 domain/integrase-type DNA-binding/eukaryotic translation initiation factor
JpLpc47089p1628	368	0.486	0.445	-0.095	100	0.050	0.049	-0.026		all				0.422		Dof-type zinc finger DNA-binding family protein
JpLpc47089p1831	366	0.016	0.016	-0.008	100	0.190	0.173	-0.105		species/Jp	2		1	0.249	Positive	Dof-type zinc finger DNA-binding family protein
JpLpc47519p1846	367	0.008	0.008	-0.004	100	0.200	0.212	0.053		species/Jp				0.259		ankyrin repeat family protein with DHHC zinc finger domain
JpLpc47519p2237	365	0.474	0.462	-0.028	99	0.131	0.123	-0.070		all				0.022		ankyrin repeat family protein with DHHC zinc finger domain
JpLpc47778p1036					100	0.030	0.030	-0.015		Jp						chlorophyll A-B binding family protein
JpLpc48195p543	366	0.505	0.501	-0.011	100	0.060	0.058	-0.031		all				0.342		NAD(P)-binding Rossmann-fold superfamily protein/short chain dehydrogenase
JpLpc48449p524					100	0.280	0.270	-0.042		Jp						transcribed locus
JpLpc49274p383	367	0.267	0.259	-0.033	100	0.000	0.000			species/Lp				0.015		double-stranded DNA binding
JpLpc49873p886	368	0.003	0.003	-0.001	100	0.480	0.499	0.034	JP11	species/Jp				0.234		protein of unknown function (DUF1118)
JpLpc50195p453	291	0.113	0.119	0.048						Lp						complex I subunit
JpLpc50715p1991	368	0.033	0.032	-0.017	100	0.470	0.494	0.044		all				0.012		ubiquitin-like superfamily
JpLpc50903p425	368	0.005	0.005	-0.003	100	0.390	0.434	0.096		species/Jp				0.917		transcribed locus
JpLpc54166p882	368	0.304	0.315	0.033	100	0.020	0.020	-0.010		all				0.123		
JpLpc54814p220	368	0.247	0.268	0.075	100	0.020	0.020	-0.010	LPL3	all				0		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
JpLpc54814p513	367	0.300	0.316	0.050	100	0.050	0.049	-0.026	LPL3	all			1	0.114		basic helix-loop-helix (bHLH) DNA-binding superfamily protein
JpLpc56344p652	368	0.451	0.444	-0.018	100	0.150	0.139	-0.081		all				0.026		cell elongation protein/DWARF 1/calmodulin binding
JpLpc57540p66	366	0.508	0.439	-0.158	100	0.240	0.297	0.187		all				0		RNA binding motif/dicer-like 1
JpLpc60957p494	368	0.470	0.473	0.004	100	0.110	0.104	-0.058		all				0		cysteine proteinases superfamily protein
JpLpc61376p1097	368	0.386	0.408	0.054	100	0.010	0.010	-0.005		species/Lp				0.259		protein kinase/mitogen-activated protein kinase
JpLpc63491p915	368	0.019	0.019	-0.010	100	0.240	0.256	0.059		all	2	1		0.002	Positive	cytokinin response factor/AP2 domain
JpLpc65526p1833	368	0.473	0.490	0.034	100	0.040	0.039	-0.020		all				0.108		AP2 domain/integrase-type DNA-binding superfamily
JpLpc66545p1207	368	0.019	0.019	-0.010	99	0.081	0.078	-0.042		all	2		1	0.02	Positive	transcribed locus
JpLpc66974p221	365	0.438	0.453	0.030	100	0.550	0.448	-0.234		all	1			0.048	Negative	enhanced downy mildew 2 (EDM2)
JpLpc68435p382	367	0.510	0.494	-0.033	100	0.050	0.049	-0.026		all				0.661		Acyl-CoA N-acyltransferases superfamily protein
JpLpc71773p809	365	0.471	0.500	0.057	99	0.465	0.440	-0.062		all				0.166		ribosomal protein L18ae family
JpLpc72416p369	364	0.349	0.377	0.073	100	0.020	0.020	-0.010		all				0.037		ARF-GAP domain 8/putative GTPase activating protein for Arf
JpLpc72792p1173	367	0.033	0.048	0.317					LP12	Lp		1				polyketide cyclase/dehydrase and lipid transport superfamily/START_STARD2_7 like
JpLpc73084p710					100	0.360	0.345	-0.049		Jp						phytochrome-associated protein phosphatase type 2C
JpLpc74417p752	367	0.534	0.497	-0.077						Lp						Protein of unknown function (DUF2488)
JpLpc74576p546	368	0.003	0.003	-0.001	100	0.220	0.227	0.027		species/Jp				0.309		transcribed locus
JpLpc75275p653	368	0.098	0.113	0.130	100	0.530	0.401	-0.329		all				0		transcribed locus
JpLpc75741p1236	368	0.489	0.486	-0.009	100	0.100	0.095	-0.053		all				0.229		kinase related protein of unknown functin
JpLpc79147p1879	368	0.063	0.061	-0.032	100	0.090	0.104	0.134		all	1	1		0.45	Positive	transcribed locus
JpLpc79197p531	368	0.497	0.493	-0.011	100	0.070	0.068	-0.036	LP10/JP1	all			1	0.286		homolog of anti-oxidant 1/heavy-metal associated domain/copper chaperone
JpLpc79522p772					83	0.434	0.414	-0.055		Jp						transcribed locus
JpLpc79566p1158	368	0.514	0.500	-0.029	100	0.200	0.181	-0.111		all				0.164		transcribed locus
JpLpc80697p862	368	0.465	0.501	0.070	100	0.400	0.345	-0.166		all				0.002		AWPM-19 family (membrane)/ peptidoglycan-binding LysM domain-containing
JpLpc82733p437	365	0.496	0.499	0.004	100	0.020	0.020	-0.010		all				0.031		basic transcription factor 3/NAC domain
JpLpc82733p81	366	0.005	0.005	-0.003	100	0.550	0.502	-0.101		species/Jp				0.015		basic transcription factor 3/NAC domain
JpLpc85542p1333					94	0.468	0.458	-0.027		Jp						geranylgeranyl pyrophosphate synthase 1

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
JpLpc86157p398	367	0.161	0.166	0.031	100	0.090	0.086	-0.047	JPLP2	all	1		1	0.169	Positive	RNA recognition motif/SC35-like splicing factor 28
JpLpc86157p76	340	0.179	0.178	-0.010	99	0.091	0.087	-0.048	JPLP2	all	1		1	0.289	Positive	RNA recognition motif/SC35-like splicing factor 28
Lodgc103p389	368	0.467	0.426	-0.098	100	0.210	0.220	0.040		all				0.039		4-hydroxy-3-methylbut-2-enyl diphosphate reductase
Lodgc1040p150	368	0.117	0.129	0.094	100	0.010	0.010	-0.005		species/Lp				0.221		ADR1-like/leucine rich repeat/NB-ARC domain
Lodgc1065p551	368	0.052	0.050	-0.026						Lp						ubiquitin-specific protease 13
Lodgc1073p453	367	0.360	0.371	0.028	100	0.010	0.010	-0.005		species/Lp				0.402		glutamyl-tRNA reductase family protein
Lodgc1087p211	368	0.239	0.270	0.112	100	0.000	0.000		LP13	species/Lp	1	3		0.005	Positive	proteasome alpha type 7
Lodgc1092p492	363	0.267	0.267	-0.002	100	0.010	0.010	-0.005		species/Lp				0.068		zinc-binding dehydrogenase/oxidoreductase
Lodgc1110p421	368	0.408	0.426	0.042	100	0.050	0.049	-0.026		all				0.002		NAC domain containing protein 71
Lodgc1141p278	363	0.215	0.254	0.152	100	0.000	0.000			species/Lp				0.042		DnaJ homolog 3
Lodgc118p350	365	0.427	0.467	0.083	100	0.010	0.010	-0.005	LP13	species/Lp	2	3		0	Positive	sedoheptulose-bisphosphate/fructose-1-6-bisphosphate - chloroplast like
Lodgc1193p223	365	0.323	0.304	-0.066	100	0.010	0.010	-0.005		species/Lp				0.069		transcribed locus
Lodgc1214p281	366	0.363	0.337	-0.078	100	0.000	0.000			species/Lp				0.239		delta subunit of Mt ATP synthase
Lodgc123p319	368	0.337	0.331	-0.018	100	0.010	0.010	-0.005		species/Lp				0.983		LSD1 like zinc finger
Lodgc1249p448	302	0.487	0.412	-0.183						Lp						pyruvate phosphate dikinase/pyruvate binding domain
Lodgc1316p295	362	0.276	0.291	0.051						Lp						adolase superfamily protein/fructose-bisphosphate adolase class I
Lodgc1407p248	324	0.043	0.111	0.609	100	0.000	0.000			species/Lp				0		stress-inducible protein, putative/sialyltransferase family protein
Lodgc1490p507	368	0.057	0.056	-0.029						Lp						ubiquinal cytochrome reductase transmembrane region/iron-sulfur subunit
Lodgc1496p263	368	0.144	0.148	0.023	100	0.000	0.000			species/Lp				0.369		beta-ketoacyl reductase/KR domain/short chain dehydrogenase
Lodgc1562p404	368	0.486	0.493	0.011	100	0.030	0.030	-0.015		all				0.63		fibrillin family protein/Plastid-lipid associated protein PAP
Lodgc157p477	352	0.134	0.154	0.131	100	0.020	0.020	-0.010		all				0.01		adenosylmethionine decarboxylase
Lodgc15p411	366	0.369	0.370	0.002	100	0.260	0.270	0.033		all				0.009		YGGT family protein
Lodgc1623p352	365	0.299	0.302	0.009						Lp						B-box type zinc finger protein with CCT domain
Lodgc1794p389	360	0.422	0.431	0.020	100	0.450	0.392	-0.155		all				0.177		4-coumarate-CoA ligase enzyme (PT4CL1)
Lodgc1891p418	368	0.283	0.284	0.004	100	0.580	0.482	-0.208		all				0.04		transcribed locus
Lodgc189p276	367	0.267	0.244	-0.098	100	0.010	0.010	-0.005		species/Lp				0.083		ATP-citrate synthase
Lodgc1909p373	365	0.255	0.277	0.079	100	0.110	0.104	-0.058		all				0.519		beta-ketoacyl synthase, N-terminal domain/fatty acid biosynthesis 1
Lodgc1931p524	368	0.277	0.277	-0.002	100	0.020	0.020	-0.010		all				0.021		transcribed locus
Lodgc2047p463	368	0.546	0.494	-0.108	100	0.380	0.333	-0.145		all				0.058		helix-loop-helix DNA binding domain
Lodgc2049p390	368	0.215	0.221	0.028	100	0.010	0.010	-0.005		species/Lp				0.634		RING/U-box superfamily protein
Lodgc218p506	367	0.112	0.115	0.029	100	0.000	0.000			species/Lp		1		0.126	Negative	transcribed locus
Lodgc2226p408	366	0.372	0.354	-0.051	100	0.330	0.328	-0.012		all				0.334		IQ calmodulin-binding motif
Lodgc2304p514	367	0.240	0.274	0.123	100	0.010	0.010	-0.005	LP14	species/Lp	1	3		0.24	Positive	triosephosphate isomerase
Lodgc2347p440	358	0.263	0.233	-0.131	98	0.429	0.492	0.125	JP12	all				0.497		serine-rich protein-related
Lodgc2413p445	368	0.111	0.120	0.068	99	0.000	0.000			species/Lp		1		0.02		histone deacetylase
Lodgc2449p408	366	0.189	0.197	0.042	100	0.110	0.104	-0.058		all				0.118		membrane-associated mannitol-induced
Lodgc2458p469					100	0.280	0.270	-0.042		Jp						CLP protease
Lodgc2485p527	367	0.428	0.465	0.079	100	0.440	0.469	0.056		all				0.705		transcribed locus
Lodgc2532p1120	368	0.492	0.489	-0.006	100	0.050	0.049	-0.026		all				0.081		Ras family/miro-like protein/signal recognition particle receptor beta subunit
Lodgc2606p320	367	0.180	0.182	0.008	100	0.190	0.173	-0.105	JP13	all				0.003		ADP-ribosylation factor family/G protein alpha subunit
Lodgc2627p673	367	0.471	0.497	0.050	100	0.080	0.077	-0.042		all				0.357		2-oxoglutarate (2OG) and Fe(II) dependent oxygenase superfamily protein
Lodgc2649p345	368	0.117	0.120	0.023	100	0.010	0.010	-0.005		species/Lp				0.388		thioredoxin
Lodgc2743p497	359	0.223	0.244	0.086	100	0.030	0.030	-0.015		all				0.007		eIF4-gamma/ARM repeat superfamily protein

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Lodgc2792p662	366	0.448	0.496	0.095	98	0.235	0.253	0.069		all				0.184		
Lodgc2798p514	368	0.486	0.467	-0.042	100	0.010	0.010	-0.005		species/Lp				0.193		rhamnose biosynthesis 1/polysaccharide biosynthesis/NAD dependent epimerase
Lodgc2800p195	367	0.158	0.146	-0.086	100	0.000	0.000			species/Lp				0.67		myb-like DNA-binding domain
Lodgc2828p334	367	0.365	0.353	-0.034	100	0.010	0.010	-0.005		species/Lp				0.177		polysaccharide biosynthesis/NAD dependent epimerase/dyhydroflavonol 4-reductase
Lodgc3011p422	314	0.643	0.499	-0.291						Lp						elongation factor
Lodgc3248p281					85	0.024	0.023	-0.012		Jp						protein kinase/tyrosine superfamily protein
Lodgc3290p342	356	0.292	0.292	-0.003	100	0.000	0.000			species/Lp				0.032		photosystem II reaction center PSB28 protein
Lodgc3293p323	364	0.503	0.481	-0.048	100	0.020	0.020	-0.010		all				0.654		Tetratricopeptide repeat (TRP) superfamily protein
Lodgc3482p180	366	0.527	0.485	-0.089	100	0.000	0.000			species/Lp				0.59		RAN GTPase 3/RNA helicase/miro-like protein/Ras family
Lodgc348p360	368	0.516	0.482	-0.074	99	0.040	0.040	-0.021		all				0.187		glutamate:glyoxylate aminotransferase
Lodgc389p393	367	0.319	0.337	0.052	99	0.030	0.030	-0.015		all				0.002		dehydrin
Lodgc408p638	367	0.267	0.251	-0.064	100	0.030	0.030	-0.015		all				0.006		IQ calmodulin-binding motif
Lodgc4104p268	358	0.849	0.501	-0.699	100	0.200	0.197	-0.021		all				0		purine biosynthesis 4
Lodgc415p436	367	0.256	0.278	0.076	100	0.000	0.000			species/Lp				0.072		ribosomal protein 1/L3
Lodgc4293p449	368	0.141	0.131	-0.076	100	0.000	0.000			species/Lp				0.341		trypsin family protein
Lodgc4306p424	366	0.467	0.475	0.015	100	0.280	0.309	0.090		all				0.012		nucleotide-diphospho-sugar transferases superfamily
Lodgc4405p428	368	0.212	0.219	0.031	100	0.010	0.010	-0.005		species/Lp				0.014		peroxin 14/peroxisomal membrane anchor protein
Lodgc4407p669	368	0.266	0.277	0.037	100	0.060	0.058	-0.031		all			1	0.042		PGRS-like
Lodgc4455p208	367	0.436	0.414	-0.055	99	0.455	0.501	0.088		all	1			0.318	Negative	Plant protein of unknown function (DUF868)
Lodgc447p278	367	0.447	0.356	-0.255					LP12	Lp						actin depolymerizing factor/tropomyosin-type actin-binding protein
Lodgc4517p609	334	0.368	0.369	0.002						Lp						protein tyrosine phosphatase
Lodgc469p206	357	0.353	0.372	0.050	99	0.000	0.000			species/Lp				0.002		cysteine proteinases/cathepsin propeptide inhibitor domain/papain cysteine protease
Lodgc478p476	367	0.153	0.164	0.068	100	0.320	0.333	0.036		all	1			0.012	Negative	alpha/beta hydrolase family
Lodgc4922p383	368	0.505	0.499	-0.014	100	0.090	0.104	0.134		all				0.588		2-oxoglutarate (2OG) and Fe(II) dependent oxygenase superfamily protein
Lodgc5121p406	367	0.376	0.402	0.063	100	0.020	0.020	-0.010		all				0.19		Protein of unknown function (DUF1218)
Lodgc5297p86	367	0.150	0.143	-0.046	100	0.330	0.466	0.288	JP12	all				0.649		RING 1A
Lodgc5447p89	368	0.288	0.288	-0.002	100	0.020	0.020	-0.010		all				0.983		Alba DNA/RNA binding protein
Lodgc5453p480	368	0.239	0.235	-0.018	100	0.270	0.290	0.065		all	2			0.118	Negative	nodulin-like/major facilitator superfamily protein
Lodgc5567p169	368	0.188	0.175	-0.076	100	0.000	0.000			species/Lp				0.085		photosystem I reaction centre (PSAN or PSI-N)
Lodgc5620p213	363	0.171	0.201	0.148						Lp						dormancy-auxin associated protein/heat shock protein
Lodgc5646p131	360	0.136	0.127	-0.073	91	0.066	0.085	0.216		all				0		ARM repeat superfamily protein
Lodgc570p462	368	0.101	0.105	0.044	100	0.000	0.000			species/Lp				0.765		similar to ewsr1b
Lodgc576p498	367	0.324	0.327	0.008	100	0.070	0.068	-0.036		all				0.329		cysteine-rich receptor like protein kinase/similar to copia protein (gag-int-pol protein)
Lodgc6047p607	366	0.139	0.135	-0.037	100	0.120	0.113	-0.064	LP06	all	1			0.672	Negative	ACD1-like
Lodgc623p588	368	0.266	0.315	0.154	100	0.010	0.010	-0.005		species/Lp				0.649		lactate/malate dehydrogenase, NAD binding domain
Lodgc6246p531	368	0.291	0.293	0.006	100	0.020	0.020	-0.010		all				0.671		peroxin 22
Lodgc624p1141	368	0.410	0.398	-0.033	100	0.020	0.020	-0.010		all				0.974		chloroplast sulphur E/Fe-S metabolism associated domain
Lodgc642p886	366	0.503	0.459	-0.098	100	0.010	0.010	-0.005		species/Lp				0.087		GATA type zinc finger transcription factor family protein
Lodgc6501p370	352	0.608	0.494	-0.232						Lp						Annexin
Lodgc6505p421	368	0.261	0.247	-0.058	100	0.430	0.401	-0.078		all				0.911		RING/U-box superfamily protein
Lodgc654p579	365	0.312	0.320	0.024	100	0.020	0.020	-0.010		all				0.66		cupin domain/1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase
Lodgc6568p554	368	0.329	0.366	0.100	100	0.100	0.131	0.232	JP09	all			2	0.01		flavanone 3-hydroxylase
Lodgc6868p131	368	0.367	0.354	-0.037	100	0.080	0.095	0.158		all				0.046		Drought-responsive family protein

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Lodgc7085p286	366	0.385	0.378	-0.020	100	0.040	0.039	-0.020		all				0.15		Peptidase M76 family/Ku70-binding protein
Lodgc7446p377	365	0.523	0.491	-0.068	100	0.010	0.010	-0.005		species/Lp				0.674		flavin-binding monooxygenase family protein
Lodgc758p388	368	0.226	0.241	0.063	100	0.000	0.000			species/Lp				0.367		2-phosphoglycolate pohsphatase 1
Lodgc7681p243	361	0.363	0.489	0.256						Lp						cytochrome B5 isoform B
Lodgc792p190	368	0.207	0.215	0.038	100	0.020	0.020	-0.010		all				0.043		4-aminobutyrate transaminase/pyridoxal phosphate dependent transferases
Lodgc889p498	368	0.465	0.489	0.049	100	0.030	0.030	-0.015		all				0.001		UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain
Lodgc910p162	336	0.420	0.380	-0.106	91	0.011	0.011	-0.006		species/Lp				0.191		glutamate decarboxylase/pyridoxal-dependent
Lodgc914p496	368	0.139	0.134	-0.037	100	0.000	0.000			species/Lp				0.862		tetraspanin family
Lodgc978p318	367	0.436	0.423	-0.033	100	0.550	0.491	-0.125	JP05	all				0.002		phosphoglycerate kinase
Lp_c00150p459	367	0.014	0.014	-0.007	100	0.130	0.173	0.244		species/Jp	2			0.353	Positive	circadian clock associated 1
Lp_c00150p61	368	0.351	0.345	-0.017	100	0.020	0.020	-0.010		all				0.011		circadian clock associated 1
Lp_c00228p801	362	0.533	0.495	-0.079	100	0.460	0.501	0.077		all				0.577		ribosomal protein L19 family
Lp_c00318p734	368	0.342	0.364	0.059	100	0.110	0.122	0.095		all				0.262		phosphofruktokinase family protein
Lp_c00579p455	362	0.434	0.473	0.082	100	0.030	0.030	-0.015		all				0.002		AUX/IAA family
Lp_c00925p827	367	0.253	0.238	-0.068	100	0.010	0.010	-0.005		species/Lp				0.546		calcineurin-like metallo-phosphoesterase superfamily protein
Lp_c00983p1180	367	0.354	0.376	0.057	100	0.520	0.499	-0.047		all	1			0.271	Negative	tetratricopeptide repeat like/basic-leucine zipper transcription factor
Lp_c01140p845	366	0.262	0.244	-0.076	100	0.000	0.000			species/Lp				0.133		tetratricopeptide repeat
Lp_c01467p496	368	0.147	0.150	0.020	100	0.120	0.113	-0.064		all	1			0	Negative	protein of unknown function (DUF538)
Lp_c01502p915	354	0.506	0.495	-0.022	94	0.340	0.360	0.051		all				0.003		calcineurin-like metallo-phosphoesterase superfamily protein
Lp_c01813p1225	367	0.240	0.228	-0.055	100	0.020	0.020	-0.010		all			1	0.299		biotin/lipoyl attachment domain-containing protein
Lp_c02035p862	368	0.416	0.425	0.021	100	0.050	0.049	-0.026		all				0.341		protein containing PDZ domain, K-box domain, and TPR region
Lp_c02191p296	368	0.492	0.498	0.012	100	0.030	0.030	-0.015	LPL4	all				0.917		transketolase
Lp_c02191p997	368	0.277	0.277	-0.002	100	0.010	0.010	-0.005	LPL4	species/Lp				0.71		transketolase
Lp_c02598p1040	316	0.481	0.464	-0.039						Lp						similar to Arabisopsis thaliana At1g62780
Lp_c02648p549	314	0.484	0.492	0.014						Lp						GHMP kinase family protein
Lp_c02821p599					98	0.459	0.459	-0.007		Jp						protein kinase superfamily protein
Lp_c03449p321	368	0.427	0.492	0.131	100	0.010	0.010	-0.005		species/Lp				0.214		B-Box type zinc-finger like protein
Lp_c04005p661	363	0.854	0.491	-0.742	99	0.010	0.010	-0.005		species/Lp				0		xyloglucan endo-transflycosylase
Lp_c04005p977	364	0.473	0.485	0.025	100	0.010	0.010	-0.005		species/Lp				0.005		xyloglucan endo-transflycosylase
Lp_c04157p375	368	0.239	0.227	-0.054	100	0.000	0.000			species/Lp				0.1		endoplasmic reticulum vesicle transporter
Lp_c04318p2154	368	0.207	0.215	0.038	100	0.000	0.000		LP14	species/Lp		3		0.267	Positive	carbohydrate binding molecule/starch branching enzyme 2.2
Lp_c04466p3014	346	0.486	0.459	-0.060						Lp						transducin/WD-40 repeat-like superfamily
Lp_c04493p319	366	0.462	0.494	0.064	100	0.040	0.058	0.313		all				0.087		magnesium transporter
Lp_c05328p985	368	0.375	0.381	0.014	100	0.190	0.189	-0.011		all				0.679		phosphogluconate dehydrogenase/glyoxylate reductase 1
Lp_c07286p308	367	0.433	0.406	-0.070	100	0.280	0.242	-0.163		all				0.115		chloroplast stem-loop binding protein/NAD dependent epimerase/dehydratase family
Lp_c07630p326	368	0.519	0.493	-0.054	100	0.330	0.316	-0.051		all				0.503		pectin lyase-like superfamily protein/glycosyl hydrolases family 28
Lp_c07997p838	365	0.515	0.484	-0.066	100	0.050	0.049	-0.026		all				0.27		cobalamin synthesis/plastid transcriptionaly active 17
Lp_c08410p197	367	0.455	0.466	0.023	100	0.040	0.039	-0.020		all			1	0.115		proteasome beta subunit
Lp_c09201p186	366	0.396	0.394	-0.007	99	0.020	0.020	-0.010	LPL5	all				0.988		ATP synthase delta-subunit
Lp_c09201p641	367	0.417	0.383	-0.090	100	0.030	0.030	-0.015	LPL5	all				0.346		ATP synthase delta-subunit
Lp_c10619p774	368	0.413	0.424	0.025	100	0.500	0.490	-0.026		all			1	0.043	Negative	dehydration responsive/ S-adenosyl-L-methionine-dependent methyltransferase
Lp_c10940p79	366	0.456	0.481	0.050	100	0.020	0.020	-0.010		all				0.372		Glycosyl transferase family 90
Lp_c11275p339	368	0.508	0.482	-0.056	100	0.020	0.020	-0.010		all				0.886		thioredoxin superfamily protein

Locus	Lodgepole pine				Jack pine				Linkage group	Data	Outlier Detection			Introgress	Direction	Annotation
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Lp_c12025p1415	368	0.231	0.229	-0.009	100	0.030	0.030	-0.015		all				0.738		core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
Lp_c13667p869	368	0.166	0.157	-0.059	100	0.010	0.010	-0.005		species/Lp				0.39		proteasome beta subunit/N-terminal nucleophile aminohydrolasses superfamily protein
Lp_c13778p292	347	0.369	0.480	0.230	100	0.470	0.488	0.032	JPLP3	all	1		1	0.001	Negative	purple acid phosphatase 18
Lp_c13778p747	367	0.411	0.442	0.067	100	0.300	0.396	0.239	JPLP3	all	1		1	0.145	Negative	purple acid phosphatase 18
Lp_c14079p1373	363	0.551	0.488	-0.130	99	0.455	0.394	-0.159		all	1			0.186	Negative	enolase
Lp_c14699p1329	368	0.046	0.045	-0.024						Lp						haloacid dehalogenase-like hydrolase superfamily protein
Lp_c14699p706	368	0.500	0.500	-0.001	100	0.130	0.122	-0.070		all			1	0.04		haloacid dehalogenase-like hydrolase superfamily protein
Lp_c14947p720	368	0.429	0.488	0.119	100	0.060	0.058	-0.031		all				0.019		ribosomal protein L1p/L10e family
Lp_c15030p593	304	0.368	0.379	0.026						Lp						senescence associated family protein
Lp_c16370p922	367	0.308	0.311	0.008	100	0.040	0.039	-0.020		all				0.989		MAP kinase kinase 6/protein tyrosine kinase
Lp_c16943p1584	368	0.109	0.108	-0.010	100	0.030	0.030	-0.015		all				0.005		3-ketoacyl-CoA synthase/chalcone and stilbene synthases/FAE1-Type III polyketide synthase
Lp_c17356p659	356	0.480	0.476	-0.010	97	0.258	0.270	0.040		all				0.001		myb-domain protein/DNA-binding
Lp_c18494p368	368	0.478	0.476	-0.006	100	0.050	0.049	-0.026		all				0.603		glucose-6-phosphate dehydrogenase 6
Lp_c18615p1158	366	0.194	0.193	-0.007	100	0.040	0.039	-0.020		all				0.749		ATP citrate lyase/succinyl-CoA sythetase beta-chain
Lp_c19125p748	352	0.040	0.039	-0.020	98	0.000	0.000			species/Lp				0		pyruvate kinase family protein
Lp_c19571p508	368	0.293	0.277	-0.061	100	0.010	0.010	-0.005		species/Lp				0.013		RNA 3'-terminal phosphate cyclase/enolpyruvate transferase, alpha/beta
Lp_c19870p302	368	0.486	0.498	0.022	100	0.080	0.077	-0.042		all				0.005		protease inhibitor/seed storage/LTP family
Lp_c20503p566	368	0.299	0.302	0.008	100	0.000	0.000		LP08	species/Lp				0.195		RAN binding domain protein
Lp_c20831p1035	356	0.140	0.145	0.031	99	0.020	0.020	-0.010		all				0		NIN like protein 7/PB1 domain
Lp_c21093p679	368	0.514	0.489	-0.051	100	0.010	0.010	-0.005		species/Lp				0.008		proteasome subunit alpha type 1
Lp_c21261p452	368	0.451	0.469	0.038						Lp						RNA-binding KH domain-containing protein
Lp_c21366p1031	363	0.375	0.425	0.118	100	0.010	0.010	-0.005		species/Lp				0.01		GDSL-like lipase acylhydrolase superfamily protein
Lp_c21536p992	367	0.226	0.230	0.014	100	0.440	0.437	-0.011		all				0		glycosyl hydrolase superfamily protein/endoxyloglucan transferase A3
Lp_c21696p443	368	0.440	0.404	-0.092	100	0.000	0.000			species/Lp				0.194		fatty acid hydroxylase superfamily
Lp_c21731p403	368	0.500	0.479	-0.045	100	0.080	0.077	-0.042		all				0.546		haloacid dehalogenase-like hydrolase superfamily protein
Lp_c21879p397	368	0.209	0.200	-0.046	100	0.090	0.086	-0.047		all				0.338		Acyl CoA binding protein
Lp_c22300p474	366	0.030	0.035	0.139						Lp						serine carbosypeptidase like
Lp_c22393p548	368	0.427	0.423	-0.010	100	0.010	0.010	-0.005	LP09	species/Lp				0.599		protein kinases/ubiquitin-protein ligase
Lp_c22542p803	368	0.429	0.430	0.001	100	0.410	0.410	-0.006		all				0.777		glutamate synthase (ferrodoxin)/NADH-dependent
Lp_c22767p940	360	0.197	0.196	-0.009	99	0.242	0.214	-0.138		all				0.133		arabinogalactan protein 2
Lp_c23304p610	368	0.421	0.439	0.040	99	0.455	0.443	-0.031		all				0		chaperonin-60 alpha/TCP-1
Lp_c23425p1676	311	0.354	0.342	-0.035						Lp						BEL1-like homeodomain/DNA binding transcription factor
Lp_c23768p576	368	0.473	0.492	0.038	100	0.430	0.494	0.125		all				0.001		casein kinase/protein tyrosine kinase
Lp_c23779p298	365	0.153	0.156	0.013						Lp						zinc-binding alcohol dehydrogenase, NAD binding/cinnamyl alcohol dehydrogenase 5
Lp_c23779p894	363	0.201	0.224	0.100						Lp						zinc-binding alcohol dehydrogenase, NAD binding/cinnamyl alcohol dehydrogenase 5
Lp_c24197p836	368	0.435	0.428	-0.017	100	0.030	0.030	-0.015		all				0.462		RED-like protein
Lp_c24207p657					95	0.063	0.100	0.367		Jp						chalcone-flavanone isomerase
Lp_c24391p1138	368	0.473	0.501	0.054	100	0.050	0.049	-0.026	JPLP4	all				0.305		ARF-GAP domain 6/putative GTPase activating protein for Arf
Lp_c24391p444	367	0.482	0.501	0.035	100	0.050	0.049	-0.026	JPLP4	all				0.464		ARF-GAP domain 6/putative GTPase activating protein for Arf
Lp_c24502p363	367	0.460	0.486	0.052	99	0.020	0.020	-0.010		all				0.001		modified of rudimentary protein (Mod (r))
Lp_c24551p196	367	0.057	0.056	-0.029						Lp						glycosyl hydrolase superfamily protein
Lp_c24551p2210	368	0.332	0.335	0.008	100	0.000	0.000			species/Lp				0.949		glycosyl hydrolase superfamily protein
Lp_c24582p834	368	0.448	0.463	0.030	100	0.000	0.000			species/Lp				0.059		ATPase family associated (AAA)/trisphosphate hydrolases superfamily

Locus	Lodgepole pine				Jack pine				Linkage group	**Data**	Outlier Detection			**Introgress**	**Direction**	**Annotation**
	N	Ho	UHe	F	N	Ho	UHe	F			Species	Lodge	Jack			
Lp_c24702p966	363	0.471	0.482	0.021	100	0.030	0.030	-0.015		all		1		0.452	Positive	FAR-17a/AIG1-like protein
Lp_c24728p554	368	0.429	0.498	0.137	100	0.030	0.049	0.385		all				0.002		ribosomal protein S4 (RPS4A)
Lp_c25137p1866	368	0.514	0.499	-0.031	100	0.030	0.030	-0.015		all				0.933		COBRA-like extracellular glycosyl-phosphatidyl inositol-anchored protein family
Lp_c25194p1160	341	0.422	0.496	0.147	100	0.070	0.068	-0.036		all				0.274		Aluminum induced protein with YGL and LRDR motifs
Lp_c25309p582	368	0.424	0.432	0.018	100	0.030	0.030	-0.015		all				0.008		chaperone protein dnaJ-related
Lp_c25811p401	367	0.436	0.439	0.005	100	0.040	0.039	-0.020		all				0.023		alto/keto reductase family/NAD(P)-linked oxidoreductase superfamily
Lp_c26195p495	367	0.093	0.108	0.141	100	0.010	0.010	-0.005		species/Lp				0.964		iron binding zinc finger CDGSH type/similar to kinesin like protein
Lp_c26630p901	356	0.404	0.412	0.016						Lp						peptidase c65 otubain/ubiquitin thioesterase otubain
Lp_c26844p544	365	0.334	0.304	-0.102	100	0.000	0.000			species/Lp				0.243		ornithine-delta-aminotransferase/aminotransferase class III
Lp_c26937p895	330	0.342	0.369	0.072						Lp						pollen Ole e 1 allergen and extensin family protein
Lp_c27142p1396	363	0.416	0.355	-0.174						Lp						ATPase/hydrogen-exporting ATPase/phosphenolpyruvate carboxylase
Lp_c27765p734	361	0.524	0.501	-0.047	99	0.515	0.492	-0.051		all				0.731		late embryogenesis abundant protein (LEA) family protein
Lp_c28145p330	367	0.319	0.340	0.061	100	0.320	0.297	-0.084	LPL6	all			1	0.022	Positive	NifU-like protein 2
Lp_c28145p756	368	0.245	0.258	0.052	100	0.010	0.010	-0.005	LPL6	species/Lp				0.445		NifU-like protein 2
Lp_c28426p547	368	0.188	0.175	-0.076	100	0.000	0.000			species/Lp				0.879		ribosomal protein L16p/L10e family
Lp_c28483p683	352	0.497	0.479	-0.039						Lp						Protein of unknown function (DUF760)
Lp_c29024p781	361	0.504	0.498	-0.013	100	0.300	0.297	-0.016		all				0.65		GDP-mannose 3,5-epimerase/NAD
Lp_c30198p360	368	0.380	0.422	0.097	100	0.010	0.010	-0.005		species/Lp				0.324		prohibitin
Lp_c30954p847	367	0.433	0.408	-0.064	100	0.000	0.000			species/Lp				0.12		BSD domain-containing protein
Lp_c31191p1428	366	0.331	0.359	0.077	100	0.010	0.010	-0.005		species/Lp				0.081		Duplicated homeodomain-like superfamily protein
Lp_c31206p1180	368	0.397	0.406	0.022	100	0.110	0.104	-0.058		all				0.002		Protein of unknown function (DUF1423)/potyviral VPg interacting protein 1
Lp_c31229p1539	368	0.473	0.461	-0.028	100	0.130	0.122	-0.070		all			1	0.08		galactose oxidase/kelch repeat
Lp_c31410p562	360	0.472	0.484	0.023	100	0.010	0.010	-0.005		species/Lp				0.066		aldehyde dehydrogenase family
Lp_c31430p340	367	0.417	0.456	0.084	100	0.450	0.494	0.085		all	1			0.313	Negative	coatomer beta subunit
Lp_c31693p433	368	0.063	0.061	-0.032	100	0.230	0.220	-0.051		all				0.683		fatty acid desaturase 2 (FAD2)
Lp_c32359p509	368	0.519	0.501	-0.038	100	0.020	0.020	-0.010		all				0.707		ribosomal L28 family
Lp_c32518p1291	368	0.478	0.495	0.033	100	0.040	0.039	-0.020		all				0.32		glycosyl transferase family 8/plant glycogenin-like starch initiation protein
Lp_c32989p661	368	0.342	0.350	0.020	100	0.040	0.039	-0.020		all				0.564		NAD(P)-binding Rossmann-fold/3-beta hydroxysteroid dehydrogenase/isomerase
Lp_c33326p690	367	0.409	0.402	-0.018	100	0.370	0.316	-0.179		all	1			0.13	Negative	heavy metal transport/myb-like HTH transcriptional regulator family protein
Lp_c33380p839	368	0.481	0.498	0.034	100	0.070	0.086	0.186		all				0.593		Aluminum induced protein with YGL and LRDR motifs
Lp_c33543p797	367	0.455	0.495	0.080	100	0.040	0.039	-0.020		all				0.986		similar to Arabisopsis thaliana At1g68490
Lp_c33997p220	368	0.280	0.268	-0.047	100	0.500	0.463	-0.085		all				0.353		ATP synthase alpha/beta family
Lp_c34571p636	366	0.197	0.191	-0.033	100	0.080	0.077	-0.042		all	1			0.353	Negative	cytochrome B5 isoform B
Lp_c34658p813	356	0.503	0.483	-0.043	100	0.010	0.010	-0.005		species/Lp				0.28		triosephosphate isomerase
Lp_c35003p642	366	0.350	0.336	-0.043	100	0.000	0.000			species/Lp				0.295		Oxygen evolving enhancer protein 3
Lp_c35144p736	352	0.466	0.484	0.036	99	0.374	0.443	0.153		all				0.013		S1/P1 nuclease/endonuclease 4
Lp_c38820p1995	353	0.544	0.496	-0.099	99	0.051	0.049	-0.026	LP03	all				0.525		SGNH hydrolase-type esterase superfamily protein
Lp_c38837p2392	367	0.259	0.272	0.047	100	0.040	0.039	-0.020		all				0.385		TUDOR-SN protein 1/Staphylococcal nuclease homologue
Lp_c41343p893	367	0.504	0.501	-0.008	100	0.290	0.290	-0.004		all				0.048		LUC7 N_terminus domain-containing protein
Lp_c42715p803	368	0.043	0.043	-0.022						Lp						importin alpha isoform/armadillo/beta-catenin-like repreat
Lp_c44052p679	367	0.515	0.472	-0.093	100	0.050	0.049	-0.026	LP05	all				0.123		UDP-glucuronate decarboxylase/dehydrogenase-isomerase family
Lp_c46762p868	365	0.348	0.302	-0.154						Lp						nucleic-acid binding domain OB-fold-like protein
Lp_c47525p1103	368	0.443	0.387	-0.145	98	0.000	0.000			species/Lp				0.088		Protein of unknown function (DUF1218)
Lp_c49110p1018	366	0.404	0.333	-0.217	99	0.202	0.199	-0.023		all				0.011		ATP synthase/gamma subunit/Cellulose synthase family protein