Appendix 2e Genes differentially regulated between *A. l. petraea* populations. This table contains the full set of genes that were expressed more highly in Helin than Leitrim (P <0.05, log2 fold change >-1).

Probe ID	Fold change (log2)	AGI Code	TAIR annotation
248197_at	-3.9290	At5g54190	PORA__PORA (Protochlorophyllide reductase A); oxidoreductase/ protochlorophyllide reductase
265111_at	-3.1763	At1g62510	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
259799_at	-2.8856	At1g72290	trypsin and protease inhibitor family protein / Kunitz family protein
250558_at	-2.6549	At5g07990	TT7_CYP75B1_D501__TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding
259431_at	-2.6379	At1g01620	PIP1;3_PIP1C_PIP1;3_TMP-B__PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3)
258224_at	-2.3351	At3g15670	late embryogenesis abundant protein, putative / LEA protein, putative
255080_at	-2.2984	At4g09030	AGP10__AGP10 (Arabinogalactan protein 10)
253879_s_at	-2.2570	At4g27560 At4g27570	glycosyltransferase family protein
245307_at	-2.2390	At4g16770	oxidoreductase, 2OG-Fe(II) oxygenase family protein
264672_at	-2.0912	At1g09750	chloroplast nucleoid DNA-binding protein-related
246038_s_at	-2.0523	At5g19460 At5g19470	ATNUDT20__ATNUDT20 (Arabidopsis thaliana Nudix hydrolase homolog 20); hydrolase
249761_at	-2.0443	At5g23970	transferase family protein
255786_at	-2.0441	At1g19670	ATCLH1_ATHCOR1_CORI1__ATCLH1 (CORONATINE-INDUCED PROTEIN 1)
254915_s_at	-2.0028	At4g11310 At4g11320	RD21__cysteine proteinase, putative
260309_at	-2.0025	At1g70580	AOAT2_GGT2__AOAT2 (GLUTAMATE:GLYOXYLATE AMINOTRANSFERASE 2); alanine transaminase
249690_at	-1.9402	At5g36210	serine-type peptidase
255619_s_at	-1.9080	At4g01350 At5g59920	DC1 domain-containing protein
245465_at	-1.7552	At4g16590	ATCSLA01_ATCSLA1_CSLA01__ATCSLA01 (Cellulose synthase-like A1); glucosyltransferase/ transferase, transferring glycosyl groups
264160_at	-1.7465	At1g65450	transferase family protein
264741_at	-1.7263	At1g62290	aspartyl protease family protein
254098_at	-1.6985	At4g25100	FSD1__FSD1 (FE SUPEROXIDE DISMUTASE 1); iron superoxide dismutase
265722_at	-1.6875	At2g40100	LHCB4.3__LHCB4.3 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding
250083_at	-1.6363	At5g17220	ATGSTF12_GST26_TT19__ATGSTF12 (GLUTATHIONE S-TRANSFERASE 26); glutathione transferase
259941_s_at	-1.6332	At1g71280 At1g71370	DEAD/DEAH box helicase, putative
267349_at	-1.5785	At2g40008 At2g40010	
247944_at	-1.5437	At5g57100	transporter-related
248647_at	-1.4909	At5g49190	SUS2_SSA__SUS2 (SUCROSE SYNTHASE 2); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups
247450_at	-1.4831	At5g62350	invertase/pectin methylesterase inhibitor family protein / DC 1.2 homolog (FL5-2I22)
251262_at	-1.4547	At3g62080	SNF7 family protein
246550_at	-1.4404	At5g14920	gibberellin-regulated family protein
252973_s_at	-1.4298	At4g38740	ROC1__ROC1 (rotamase CyP 1); peptidyl-prolyl cis-trans isomerase
260227_at	-1.4292	At1g74450	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G18740.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43630.1); contains InterPro domain Protein of unknown function DUF793 (InterPro:IPR008511)

254492_at	-1.4148	At4g20260	DREPP plasma membrane polypeptide family protein
262128_at	-1.4078	At1g52690	late embryogenesis abundant protein, putative / LEA protein, putative
248967_at	-1.4035	At5g45350	proline-rich family protein
245736_at	-1.3874	At1g73330	ATDR4__ATDR4 (Arabidopsis thaliana drought-repressed 4)
266358_at	-1.3814	At2g32280	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G21310.1); similar to unknown [Populus trichocarpa] (GB:ABK92874.1); contains InterPro domain Protein of unknown function DUF1218 (InterPro:IPR009606)
263549_at	-1.3808	At2g21650	MEE3__MEE3 (maternal effect embryo arrest 3); DNA binding / transcription factor
266813_at	-1.3689	At2g44920	thylakoid lumenal 15 kDa protein, chloroplast
256780_at	-1.3650	At3g13640	ATRLI1__ATRLI1 (Arabidopsis thaliana RNase L inhibitor protein 1)
262751_at	-1.3551	At1g16310	cation efflux family protein
259609_at	-1.3521	At1g52410	TSA1__TSA1 (TSK-ASSOCIATING PROTEIN 1)
258158_at	-1.3498	At3g17790	ATPAP17_PAP17_ATACP5__ATACP5 (acid phosphatase 5); acid phosphatase/ protein serine/threonine phosphatase
247925_at	-1.3391	At5g57560	TCH4_XTH22__TCH4 (TOUCH 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase
261534_at	-1.3297	At1g01820	PEX11C__PEX11C
257641_s_at	-1.3224	At3g25760 At3g25770	AOC1_ERD12__AOC1 (ALLENE OXIDE CYCLASE 1)
254759_at	-1.3052	At4g13180	short-chain dehydrogenase/reductase (SDR) family protein
253643_at	-1.3006	At4g29780	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G12010.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43835.1); contains domain PTHR22930 (PTHR22930)
248964_at	-1.2935	At5g45340	CYP707A3__CYP707A3 (cytochrome P450, family 707, subfamily A, polypeptide 3); oxygen binding
254120_at	-1.2881	At4g24570	mitochondrial substrate carrier family protein
245275_at	-1.2838	At4g15210	BMY1_ATBETA-AMY_AT-BETA-AMY_RAM1__ATBETA-AMY (BETA-AMYLASE); beta-amylase
263333_at	-1.2823	At2g03890	phosphatidylinositol 3- and 4-kinase family protein
266989_at	-1.2772	At2g39330	jacalin lectin family protein
256577_at	-1.2732	At3g28220	meprin and TRAF homology domain-containing protein / MATH domain-containing protein
264657_at	-1.2533	At1g09100	RPT5B__RPT5B (26S PROTEASOME AAA-ATPASE SUBUNIT RPT5B); ATPase/ calmodulin binding
264240_at	-1.2517	At1g54820	protein kinase family protein
249264_s_at	-1.2502	At5g41740 At5g41750	disease resistance protein (TIR-NBS-LRR class), putative
252389_at	-1.2497	At3g47833	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G62575.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64387.1)
267095_at	-1.2486	At2g38280	FAC1_ATAMPD__FAC1 (EMBRYONIC FACTOR1); AMP deaminase
254304_at	-1.2470	At4g22270	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G03820.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23242.1)
252181_at	-1.2309	At3g50685	similar to unnamed protein product [Vitis vinifera] (GB:CAO22868.1)
257666_at	-1.1815	At3g20270	lipid-binding serum glycoprotein family protein
258641_at	-1.1781	At3g08030	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G41800.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40802.1); contains InterPro domain Protein of unknown function DUF642 (InterPro:IPR006946)
252633_x_at	-1.1688	At3g44490 At3g44660	HDA17__HDA17 (histone deacetylase 17); histone deacetylase
258239_at	-1.1669	At3g27690	LHCB2:4_LHCB2__LHCB2:4 (Photosystem II light harvesting complex gene 2.3); chlorophyll binding
251340_at	-1.1624	At3g60830	ATARP7_ARP7__ATARP7 (ACTIN-RELATED PROTEIN 7); structural constituent of cytoskeleton
245323_at	-1.1528	At4g16500	cysteine protease inhibitor family protein / cystatin family protein
261642_at	-1.1504	At1g27680	APL2__APL2 (large subunit of AGP 2)

245088_at	-1.1217	At2g39850	subtilase
250102_at	-1.1204	At5g16590	leucine-rich repeat transmembrane protein kinase, putative
256983_at	-1.1198	At3g13470	chaperonin, putative
251899_at	-1.1170	At3g54400	aspartyl protease family protein
248007_at	-1.1115	At5g56260	dimethylmenaquinone methyltransferase family protein
256578_at	-1.1068	At3g28200	peroxidase, putative
255604_at	-1.1043	At4g01080	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G01430.1); similar to unknown protein Cr17 [Brassica napus] (GB:AAX51387.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253)
254283_s_at	-1.0983	At4g22870 At4g22880	leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative
261586_at	-1.0937	At1g01640	speckle-type POZ protein-related
267090_at	-1.0818	At2g38270	CXIP2__CXIP2 (CAX-INTERACTING PROTEIN 2); electron carrier/ protein disulfide oxidoreductase
253344_at	-1.0807	At4g33550	similar to protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] (TAIR:AT4G30880.1); similar to unknown [Setaria italica] (GB:AAP93138.1); contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140)
259532_at	-1.0795	At1g12470	Pep3/Vps18/deep orange family protein
247288_at	-1.0789	At5g64330	NPH3_JK218_RPT3__NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3)
258750_at	-1.0783	At3g05910	pectinacetylesterase, putative
248793_at	-1.0764	At5g47240	ATNUDT8__ATNUDT8 (Arabidopsis thaliana Nudix hydrolase homolog 8);
254926_at	-1.0736	At4g11280	ACS6__ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6)
251151_at	-1.0729	At3g63170	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26310.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22529.1); contains InterPro domain Chalcone isomerase-like (InterPro:IPR016087)
262086_at	-1.0705	At1g56050	GTP-binding protein-related
260877_at	-1.0702	At1g21500	similar to hypothetical protein OsI_030994 [Oryza sativa (indica cultivar-group)] (GB:EAZ09762.1); similar to Os09g0517000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063677.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD33829.1)
248719_at	-1.0586	At5g47910	RBOHD__RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)
265680_at	-1.0584	At2g32150	haloacid dehalogenase-like hydrolase family protein
267645_at	-1.0519	At2g32860	glycosyl hydrolase family 1 protein
249208_at	-1.0430	At5g42650	AOS_CYP74A__AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ oxygen binding
265057_at	-1.0350	At1g52140	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G16330.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64915.1)
245688_at	-1.0264	At1g28290	AGP31__AGP31 (ARABINOGALACTAN-PROTEIN 31)
246880_s_at	-1.0239	At5g25980 At5g26000	TGG2__TGG2 (GLUCOSIDE GLUCOHYDROLASE 2); hydrolase, hydrolyzing O-glycosyl compounds
267256_s_at	-1.0237	At2g23000 At2g23010	SCPL10__SCPL10 (serine carboxypeptidase-like 10); serine carboxypeptidase
250207_at	-1.0189	At5g13930	CHS_TT4__ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase
253300_at	-1.0185	At4g33580	carbonic anhydrase family protein / carbonate dehydratase family protein
253975_at	-1.0174	At4g26600	nucleolar protein, putative
258321_at	-1.0168	At3g22840	ELIP1_ELIP__ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN); chlorophyll binding
258373_at	-1.0159	At3g14290	PAE2__PAE2 (20S proteasome alpha subunit E2); peptidase
263421_at	-1.0147	At2g17230	phosphate-responsive 1 family protein
261788_at	-1.0137	At1g15980	similar to unnamed protein product [Vitis vinifera] (GB:CAO49411.1); contains domain G3DSA:3.40.50.2000 (G3DSA:3.40.50.2000); contains domain SSF53756 (SSF53756)

264342_at	-1.0128	At1g12080	contains domain PTHR22683 (PTHR22683)
263161_at	-1.0068	At1g54020	myrosinase-associated protein, putative
257835_at	-1.0056	At3g25180	CYP82G1__CYP82G1 (cytochrome P450, family 82, subfamily G, polypeptide 1); oxygen binding
250072_at	-1.0049	At5g17210	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61065.1); similar to Os06g0114700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001056606.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62222.1); contains InterPro domain Protein of unknown function DUF1218 (InterPro:IPR009606)
262098_at	-1.0034	At1g56170	HAP5B__HAP5B (Heme activator protein (yeast) homolog 5B)
266588_at	-1.0030	At2g14890	AGP9__AGP9 (ARABINOGALACTAN PROTEIN 9)
261059_at	-1.0029	At1g01250	AP2 domain-containing transcription factor, putative
252996_s_at	-1.0021	At4g38460	GGR__GGR (GERANYLGERANYL REDUCTASE); farnesyltranstransferase
263715_at	-1.0006	At2g20570	GPRI1_GLK1__GPRI1 (GOLDEN2-LIKE 1); transcription factor