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

	Fold		
	change		
Probe ID	(log2)	AGI Code	TAIR annotation
			similar to PBS lyase HEAT-like repeat-containing protein [Arabidopsis
			thaliana] (TAIR:AT3G62530.1); similar to unnamed protein product [Vitis
		At3g62460	vinifera] (GB:CAO40196.1); contains InterPro domain Protein of unknown
251241_s_at	4.9848	At3g62530	function DUF537 (InterPro:IPR007491)
	3.1048	At1g49500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G19030.1)
	2.8498	At1g31690	copper ion binding
245757_at	2.7449	At1g35140	PHI-1PHI-1 (PHOSPHATE-INDUCED 1)
			BT2_BT2 (BTB AND TAZ DOMAIN PROTEIN 2); protein binding /
252367_at	2.5597	At3g48360	transcription factor/ transcription regulator
250228_at	2.4610	At5g13840	WD-40 repeat family protein
260283_at	2.2613	At1g80480	PTAC17PTAC17 (PLASTID TRANSCRIPTIONALLY ACTIVE17)
266142_at	2.1909	At2g39030	GCN5-related N-acetyltransferase (GNAT) family protein
			hydrophobic protein, putative / low temperature and salt responsive protein,
266566_at	1.9566	At2g24040	putative
255479_at	1.9348	At4g02380	ATLEA5_SAG21SAG21 (SENESCENCE-ASSOCIATED GENE 21)
261410_at	1.8492	At1g07610	MT1CMT1C (metallothionein 1C)
254804_at	1.8223	At4g13010	oxidoreductase, zinc-binding dehydrogenase family protein
			PETGCytochrome b6-f complex, subunit V. Disruption of homologous
	1.8147	AtCg00600	gene in Chlamydomonas results in disruption of cytochrome b6-f complex.
263046_at	1.8009	At2g05380	GRP3S_GRP3S (GLYCINE-RICH PROTEIN 3 SHORT ISOFORM)
260568_at	1.7669	At2g43570	chitinase, putative
245611_at	1.6538	At4g14390	ankyrin repeat family protein
	1.6525	At4g16710	glycosyltransferase family protein 28
248191_at	1.6353	At5g54130	calcium-binding EF hand family protein
		At3g47090	
252450_s_at		At3g47580	leucine-rich repeat transmembrane protein kinase, putative
249125_at	1.5494	At5g43450	2-oxoglutarate-dependent dioxygenase, putative
			similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42570.1);
			similar to unnamed protein product [Vitis vinifera] (GB:CAO69853.1);
266474_at	1.5398	At2g31110	contains InterPro domain Protein of unknown function DUF231, plant
247439_at	1.4982	At5g62670	AHA11AHA11 (ARABIDOPSIS H(+)-ATPASE 11); ATPase
255459_at	1.4717	At4g02890	UBQ14_UBQ14 (ubiquitin 14)
249375_at	1.4711	At5g40730	AGP24_AGP24 (ARABINOGALACTAN PROTEIN 24)
247606_at	1.4424	At5g61000	replication protein, putative
260287_at	1.4412	At1g80440	kelch repeat-containing F-box family protein
057000	4 4400	A+0 =0004.0	CYP71B23_CYP71B23 (cytochrome P450, family 71, subfamily B,
257623_at	1.4409	At3g26210	polypeptide 23); oxygen binding
259472_at	1.4295	At1g18910	protein binding / zinc ion binding
263365_at	1.4189	At2g20550	DNAJ chaperone C-terminal domain-containing protein
259800_at	1.4079	At1g72175	zinc finger (C3HC4-type RING finger) family protein
254533_at	1.3971	At4g19670	zinc finger (C3HC4-type RING finger) family protein
252437_at	1.3945	At3g47380	invertase/pectin methylesterase inhibitor family protein
000440	4 0704	At1g03140	and in the stand Day 40 for mile an action
263116_s_at		At1g54590	splicing factor Prp18 family protein
263478_at	1.3679	At2g31880	leucine-rich repeat transmembrane protein kinase, putative
050400 = 1	4 0040	A+4~20000	ATAUR1ATAUR1 (ATAURORA1); histone serine kinase(H3-S10 specific) /
253403_at	1.3612	At4g32830	kinase/ protein serine/threonine kinase

family protein
family protein
a dabudratasa family protein
e dehydratase family protein
4). h. eta. mala eta ei da e
1); beta-galactosidase
1 (TAID ATAO 70540 0)
ana] (TAIR:AT1G79510.2);
ana] (TAIR:AT1G16320.1);
ana] (TAIR:AT1G79510.1);
fera] (GB:CAO39696.1);
main containing protein 83);
DATION ()
RATION 1)
e, hydrolyzing O-glycosyl
_
rotein
ana] (TAIR:AT3G25240.1);
fera] (GB:CAO38687.1);
n function DUF506, plant
OLINE-5-CARBOXYLATE
oonsive protein-related
ana] (TAIR:AT5G52420.1);
fera] (GB:CAO49441.1)
ana] (TAIR:AT4G22310.1);
3:ABK93494.1); contains
UPF0041 (InterPro:IPR005336)
amily protein
ana] (TAIR:AT4G14450.1)
(GB:CAN76393.1)
;2 (SERINE
transferase
tein
tein carbohydrate transmembrane
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carbohydrate transmembrane

			ADR1-L2ADR1-L2 (ADR1-LIKE 2); ATP binding / nucleoside-
250829_a	1.0786	At5g04720	triphosphatase/ nucleotide binding / protein binding
247545_a		At5g61530	small G protein family protein / RhoGAP family protein
266761_a		At2g47130	short-chain dehydrogenase/reductase (SDR) family protein
255478_a		At4g02440	EID1_EID1 (EMPFINDLICHER IM DUNKELROTEN LICHT 1)
251024_a		At5g02180	amino acid transporter family protein
264121_a		At1g02280	TOC33 PPI1 TOC33 (PLASTID PROTEIN IMPORT 1)
201121_α	1	7 K 1 g 0 2 2 0 0	NTF2A_NTF2A (NUCLEAR TRANSPORT FACTOR 2A); Ran GTPase
264446_a	t 1.0578	At1g27310	binding / protein transporter
	1110010	7 K. 1 g _ 1 G 1 G	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61930.1);
			similar to unnamed protein product [Vitis vinifera] (GB:CAO17934.1);
262811_a	1.0576	At1g11700	contains InterPro domain Protein of unknown function DUF584
254818_a		At4g12470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
245264_a		At4g17245	zinc finger (C3HC4-type RING finger) family protein
255116_a		At4g08850	leucine-rich repeat family protein / protein kinase family protein
265472_a		At2g15580	zinc finger (C3HC4-type RING finger) family protein
	110110	<u> </u>	Identical to Uncharacterized protein At5g22580 [Arabidopsis Thaliana]
			(GB:Q9FK81); similar to stable protein 1-related [Arabidopsis thaliana]
			(TAIR:AT3G17210.1); similar to hypothetical protein [Vitis vinifera]
			(GB:CAN68720.1); contains InterPro domain Dimeric alpha-beta barrel
			(InterPro:IPR011008); contains InterPro domain Stress responsive alpha-
249894_a	1.0421	At5g22580	beta barrel (InterPro:IPR013097)
	111111111	119 111	UGT73B5UGT73B5 (UDP-GLUCOSYL TRANSFERASE 73B5); UDP-
265499_a	1.0226	At2g15480	glycosyltransferase/ transferase, transferring glycosyl groups
	111111111111111111111111111111111111111	<u> </u>	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13062.2);
			similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G13062.1);
			similar to unnamed protein product [Vitis vinifera] (GB:CAO41766.1);
260603_a	1.0222	At1g55960	contains InterPro domain Lipid-binding START (InterPro:IPR002913)
261366_a		At1g53100	acetylglucosaminyltransferase
_		Ť	NDHJEncodes NADH dehydrogenase subunit J. Its transcription is
245010_a	t 1.0170	AtCg00420	increased upon sulfur depletion.
259502_a		At1g15670	kelch repeat-containing F-box family protein
254286_a		At4g22950	AGL19_GL19AGL19 (AGAMOUS-LIKE 19); transcription factor
		At1g72060	
256337_a	t 1.0055	At1g72070	serine-type endopeptidase inhibitor
260875_a		At1g21410	SKP2A_SKP2A; protein binding
		Ĭ	RRS1_ATWRKY52_SLH1RRS1 (RESISTANT TO RALSTONIA
248995_a	1.0005	At5g45260	SOLANACEARUM 1)