Supplemental Table 1. Differentially expressed probe sets in PBMCs of patients with FHL.

Affy. ID	***Symbol***	***Description***	***P-value[1]***	***P-value[2]***	***P-value[3]***	***Fold change 1 vs. 2***	***Fold change 1 vs. 3***	***Fold change 2 vs.3***
229444_at		Chromosome 6 open reading frame	0.230041331	0.002789511	0.020392707	0.774307309	0.378908906	0.489352097
236691_at	LOC646509	hypothetical protein LOC646509	0.942496462	0.000774242	0.00206488	1.00688562	0.698631357	0.693853744
235147_at	LOC440928	hypothetical gene supported by AK096649	0.15111957	0.004299448	0.050502918	0.659093803	0.415799309	0.630865148
236282_at		CDNA clone IMAGE:4826240	0.290353933	0.006536929	0.023805975	0.882653368	0.546740252	0.619428047
211780_x_at	DCTN1	dynactin 1 (p150, glued homolog, Drosophila)	0.014460882	0.007925613	0.156682879	0.721338258	0.598480053	0.829680177
1552393_at	ENTHD1	ENTH domain containing 1	0.113273621	0.002604583	0.027483832	0.91389876	0.739016373	0.8086414
217623_at	MYLK3,	myosin light chain kinase 3	0.137444543	0.00188591	0.002681003	0.882077668	0.719615571	0.81581883
209077_at	TXN2	thioredoxin 2	0.206524425	0.001085208	0.017978558	0.752016077	0.491861281	0.65405687
210721_s_at	PAK7	p21(CDKN1A)-activated kinase 7	0.98739611	0.000499103	0.0027308	1.000866064	0.822803871	0.822091886
220317_at	LRAT	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	0.2319042	0.004861812	0.014496534	0.932427904	0.804131796	0.862406404
205991_s_at	PRRX1	paired related homeobox 1	0.02185604	0.002111709	0.015267184	0.899927822	0.722718684	0.803085165
216443_at	LUZP2	Leucine zipper protein 2	0.359630892	0.002880742	0.013548718	0.954608131	0.815607948	0.854390321
231015_at	KLF15	Kruppel-like factor 15	0.684791023	0.002599204	0.01589571	0.980583021	0.727224103	0.741624205
1554886_a_at	MLXIP	MLX interacting protein	0.941865589	0.002778822	0.007966589	1.00545943	0.76315063	0.759006885
244130_at	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	0.227159513	0.005381187	0.021204353	0.958183647	0.844359355	0.881208271
232256_s_at	LOC401321	hypothetical LOC401321	0.80469222	0.002211828	0.009227788	0.977684399	0.481091306	0.492072193
241401_at	C4orf12	chromosome 4 open reading frame 12	0.440670239	0.007687579	0.011045439	0.969890436	0.883282407	0.910703285
1552900_a_at	MGC34034,	hypothetical protein MGC34034	0.410926211	0.000350847	0.001041785	0.969318645	0.753303937	0.777147887
244852_at	C18orf4	chromosome 18 open reading frame 4	0.071897992	0.004850086	0.029598461	0.861582465	0.733809683	0.851699881
1564785_at	LOC196913	hypothetical protein LOC196913	0.028527281	0.007273758	0.037019066	0.863985358	0.720998166	0.83450276
236173_s_at	LRIG1	Leucine-rich repeats and immunoglobulin-like domains 1	0.023468143	0.001579218	0.04860273	0.842070213	0.710018772	0.843182387
228875_at	C6orf189	chromosome 6 open reading frame 189	0.776705667	0.001400043	0.001102813	0.973559614	0.740486302	0.760596775
1561976_at	C1orf167	chromosome 1 open reading frame 167	0.0991479	0.002525658	0.012328417	0.862977705	0.718295001	0.832344795
1569937_at		CDNA clone IMAGE:4799216	0.699050625	0.003960436	0.001572685	1.025806335	0.856523857	0.834976182
243243_at	GPC3	Glypican 3	0.432362701	0.002769755	0.003782825	1.072011851	0.798580488	0.74493625
241693_at	OSBPL1A	Oxysterol binding protein-like 1A	0.94059789	0.001087377	0.003570388	0.992177599	0.706773313	0.712345566
1561229_at	LOC642376	Hypothetical protein LOC642376	0.719651148	0.000622117	0.002046376	1.015448122	0.82267585	0.810160393
204159_at	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0.004965024	0.008604145	0.084377651	0.614221938	0.381770625	0.621551596
201226_at	NDUFB8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	0.032143269	0.011254581	0.082437372	0.690932051	0.580884191	0.840725495
224947_at	RNF26	ring finger protein 26	0.014813351	0.024979848	0.20074447	0.498151776	0.402860666	0.808710689
202233_s_at	UQCRH	ubiquinol-cytochrome c reductase hinge protein	0.012189363	0.01773575	0.160691488	0.727591105	0.628471905	0.863770736
233049_x_at	STUB1	STIP1 homology and U-box containing protein 1	0.011631497	0.008012888	0.036239883	0.692432991	0.564214108	0.814828461
227625_s_at	STUB1	STIP1 homology and U-box containing protein 1	0.024070405	0.012315582	0.130639313	0.673664082	0.576624295	0.855952263
217934_x_at	STUB1	STIP1 homology and U-box containing protein 1	0.061224079	0.017458124	0.018995296	0.715686589	0.608277667	0.849921847
1566783_at	WBSCR17	Williams-Beuren syndrome chromosome region 17	0.00256191	0.01645438	0.252367124	0.850937433	0.799067491	0.939043765

202298_at	NDUFA1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	0.029111501	0.006375053	0.415216514	0.502804102	0.453452286	0.90184683
229271_x_at	COL11A1	collagen, type XI, alpha 1	0.000658241	0.037879036	0.83528716	0.781465078	0.772369834	0.988361292
207356_at	DEFB4	defensin, beta 4	0.00073384	0.030199089	0.923629694	0.77976125	0.776820345	0.996228455
219019_at	LRDD	leucine-rich repeats and death domain containing	0.032273475	0.005777222	0.528062721	0.505409606	0.449532678	0.889442293
241699_at	RY1	Putative nucleic acid binding protein RY-1	0.023510353	0.045519254	0.959572087	0.731315387	0.728433017	0.996058651
221791_s_at	CCDC72	coiled-coil domain containing 72	0.013867073	0.107948842	0.366156797	0.72094048	0.765562824	1.06189463
226791_at	KIFC2	kinesin family member C2	0.000409723	0.094904763	0.022284665	0.516297593	0.62116652	1.203117211
1555234_a_at	RHOJ	ras homolog gene family, member J	0.001079117	0.185865003	0.192673409	0.739925387	0.809815108	1.094455093
202182_at	GCN5L2	GCN5 general control of amino-acid synthesis 5-like 2 (yeast)	0.000297058	0.191857774	0.111150634	0.545275597	0.66275086	1.215441997
1563512_at	NOS1AP	Nitric oxide synthase 1 (neuronal) adaptor protein	0.000200248	0.134722526	0.002648691	0.719079479	0.819188857	1.139218795
237011_at	LOC643837,	CDNA clone IMAGE:30529307	0.007071451	0.509197661	0.007540352	0.695584628	0.97053059	1.395273199
238389_s_at		---	0.008538243	0.883038085	0.006137125	0.173594417	0.708109836	4.079104905
223496_s_at	CCDC8	coiled-coil domain containing 8	0.013664163	0.948949957	0.00973677	0.60336963	0.865276122	1.434073044
225968_at	PRICKLE2	prickle-like 2 (Drosophila)	0.001593447	0.662080758	0.025185325	0.675877675	0.851084773	1.259229006
1562822_at	NHS	Nance-Horan syndrome (congenital cataracts and dental anomalies)	0.015252299	0.481422221	0.061394237	0.708015679	0.830146585	1.172497461
241540_at		---	0.002072589	0.78294481	0.016779524	0.655576662	0.865375902	1.320022435
1569251_a_at	ZNF333	zinc finger protein 333	0.004285144	0.818599905	0.022220751	0.361329317	0.668968923	1.851410586
228207_at	SPAG6	Sperm associated antigen 6	0.002680076	0.255920645	0.125842838	0.495167293	0.618744753	1.24956709
232678_at	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9	0.015147671	0.553042659	0.009035589	0.710792288	0.967474388	1.361121109
1554931_at	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	0.006413512	0.804325277	0.011949511	0.735649439	0.946492432	1.286607972
234903_at	OR2B3	olfactory receptor, family 2, subfamily B, member 3	0.015925674	0.828303096	0.005916	0.802034113	0.960691974	1.197819343
1564075_a_at	FLJ35848	Hypothetical protein FLJ35848	0.006191702	0.217876843	0.002348481	0.7612516	1.037750538	1.363216233
236214_at	NYD-SP18	testes development-related NYD-SP18	0.006456311	0.656632834	0.009599196	0.728202846	0.917238657	1.259592245
217252_at	OSIL	oxidative stress induced like	0.008447659	0.972248511	0.0080064	0.737238585	0.933118291	1.265693778
233494_at	ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	0.005814889	0.189300363	0.032624107	0.695165875	0.842104081	1.211371432
214325_at	GP2	glycoprotein 2 (zymogen granule membrane)	0.002631467	0.216519786	0.002448775	0.632900813	0.831126037	1.313201091
240009_at	C21orf89	Chromosome 21 open reading frame 89	0.006791578	0.780975383	0.006858273	0.703915272	0.960079969	1.363914107
1559392_s_at	SYT7	synaptotagmin VII	0.015335874	0.411835882	0.000926171	0.608347832	0.993899219	1.633767996
207051_at	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	0.047220482	0.050146834	0.002147701	0.804856355	1.14037392	1.416866393
1566848_x_at		CDNA clone IMAGE:4815589	0.008091784	0.168074221	0.003397502	0.692850111	1.094166694	1.579225689
231073_at	C1orf168	chromosome 1 open reading frame 168	0.003096109	0.155508859	0.003957249	0.682335383	1.111794523	1.62939597
232638_at	COL20A1	collagen, type XX, alpha 1	0.005482253	0.104236224	0.000727909	0.74331199	1.077753366	1.449934053
211265_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)	0.022733831	0.008771585	0.000279192	0.789892068	1.197981616	1.516639634
241525_at	LOC200772	hypothetical protein LOC200772	0.023095432	0.336249612	0.006626452	0.39459836	1.009232753	2.557620245
1555843_at	HNRPM	Heterogeneous nuclear ribonucleoprotein M	0.017300481	0.738156086	0.006431701	0.412398145	0.880427953	2.13489795

211442_x_at	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	0.030259964	0.137792216	0.00295968	0.795061783	1.06223924	1.336046157
237960_at	Ccdc46	Coiled-coil domain containing 46	0.006565203	0.81941376	0.008738329	0.717178633	0.965910169	1.346819501
1561045_a_at		Homo sapiens, clone IMAGE:5548255, mRNA	0.012130656	0.848351658	0.002167605	0.708335538	0.952251917	1.344351463
210614_at	TTPA	tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with vitamin E deficiency)	0.002635466	0.343674906	0.000596598	0.682189885	1.005615885	1.47409967
239293_at	NRSN1	neurensin 1	0.052378185	0.143089841	0.002173375	0.769122976	1.056972855	1.374257288
1561037_a_at		CDNA clone IMAGE:5260914	0.009588894	0.519848105	0.007284975	0.660753503	0.996728463	1.508472463
1565777_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	0.007180608	0.336552669	0.004538528	0.298888815	1.087477626	3.638401876
1561671_at	LOC286121	hypothetical protein LOC286121	0.005242998	0.063820486	0.002631968	0.793547178	1.1127208	1.402211274
242085_at	C2orf18	Chromosome 2 open reading frame 18	0.018376901	0.089447653	0.002044351	0.820299341	1.056352275	1.287764383
238220_at	UTX	ubiquitously transcribed tetratricopeptide repeat, X chromosome	0.034040258	0.159169947	0.005949158	0.524102329	1.155474497	2.204673465
201497_x_at	MYH11	myosin, heavy polypeptide 11, smooth muscle	0.019662616	0.30804422	0.005137164	0.801551569	1.004566944	1.253277995
1558128_at	PAPOLA	Poly(A) polymerase alpha	0.023635638	0.179159701	0.002903746	0.704056453	1.054620312	1.4979201
215666_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	0.008143662	0.519651014	0.00468689	0.051829177	0.71105819	13.71926462
206746_at	BFSP1	beaded filament structural protein 1, filensin	0.005113111	0.666154737	0.00642571	0.690585089	0.942402239	1.36464319
218956_s_at	PTCD1	pentatricopeptide repeat domain 1	0.004220459	0.343516617	0.003039516	0.595735406	1.021058419	1.713946173
222117_s_at	ADCK2	aarF domain containing kinase 2	0.005482094	0.29726386	0.000769677	0.381710145	1.050060186	2.750936014
232348_at	C18orf8	Chromosome 18 open reading frame 8	0.006940941	0.237021859	0.001683575	0.52170801	1.090888133	2.090993644
242374_at	HIAT1	Hippocampus abundant transcript 1	0.135876629	0.025611009	0.001164442	0.623256706	1.589636327	2.550532247
1552315_at	GIMAP1	GTPase, IMAP family member 1	0.009630412	0.660708977	0.01894342	2.603609271	2.181207769	1.736593252
232447_at	DCAKD	Dephospho-CoA kinase domain containing	0.011235095	0.583860178	0.006360558	2.364581073	1.409919415	0.596266049
224856_at	FKBP5	FK506 binding protein 5	0.018095695	0.896331163	0.016607391	2.433388588	1.337776583	0.549758715
218692_at	FLJ20366	hypothetical protein FLJ20366	0.001944709	0.3595542	0.052105352	1.136135987	1.072372258	0.943876675
237877_at	GTPBP2	GTP binding protein 2	0.007627969	0.890309806	0.005076655	1.820182274	1.210007423	0.664772666
1554059_at	SETMAR	SET domain and mariner transposase fusion gene	0.026817434	0.927834478	0.00036231	1.179265462	1.031921643	0.875054579
207037_at	TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	0.008574983	0.234673639	0.011558871	2.48105921	1.705041912	0.687223386
236018_at	LCMT2	Leucine carboxyl methyltransferase 2	0.02114989	0.129892879	0.004103946	1.385686401	0.900562375	0.649903452
213925_at	C1orf95	Chromosome 1 open reading frame 95	0.020357894	0.064259254	0.000912331	1.145840602	0.963774909	0.841107312
229110_at	LOC100128844,	CDNA clone IMAGE:4794876	0.039828975	0.005657653	0.000631467	1.147509364	0.882418583	0.768985954
209331_s_at	MAX	MYC associated factor X	0.011436017	0.275862716	0.004195917	1.377125569	0.964346041	0.700260065
1554468_s_at	FBF1	Fas (TNFRSF6) binding factor 1	0.025150845	0.073692557	0.000924664	1.354899624	0.903094468	0.666539759
204893_s_at	ZFYVE9	zinc finger, FYVE domain containing 9	0.450971097	0.004423244	0.00534159	0.799382373	1.957013351	2.448156749
1554707_at	C9orf68	chromosome 9 open reading frame 68	0.087824722	0.007280409	0.003301936	0.906511034	1.192727047	1.315733623
1552423_at	ETV3	ets variant gene 3	0.044913011	0.008007547	0.001495638	0.581995546	2.047827498	3.51863088
207913_at	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1	0.291883776	0.001812766	0.00477919	0.944933323	1.21796319	1.288940882
227561_at	LOC651619	hypothetical protein LOC651619	0.280102988	0.008972202	0.003318287	0.925749069	1.256599594	1.357386831

203130_s_at	KIF5C	kinesin family member 5C	0.078414257	0.036923202	0.000175218	0.432674898	1.783712015	4.122522533
1557170_at	NEK8	NIMA (never in mitosis gene a)- related kinase 8	0.119397612	0.013845617	0.000257371	0.838254822	1.195279439	1.425914183
1565650_at	Arf1,	ADP-ribosylation factor 1	0.158255874	0.005330038	0.000355577	0.807242842	1.488740305	1.844228561
205836_s_at	YTHDC2	YTH domain containing 2	0.161327642	0.001793111	0.002335808	0.883007531	1.568052032	1.775808221
204094_s_at	TSC22D2	TSC22 domain family, member 2	0.382550744	0.005818723	0.01462932	1.060761132	1.418083288	1.336854496
209011_at	TRIO	triple functional domain (PTPRF interacting)	0.715884012	0.003716917	0.008369718	1.072509471	1.761218902	1.642147645
236621_at	RPS27	ribosomal protein S27 (metallopanstimulin 1)	0.401427939	0.001732732	0.013500687	1.285303062	4.105769964	3.194398336
215671_at	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	0.904220234	0.0017456	0.007223037	1.031316039	2.732987201	2.649999706
1558691_a_at	DOCK4	dedicator of cytokinesis 4	0.578998586	0.005562998	0.010843684	1.477072581	6.416805747	4.344272467
1570106_at	C1orf71	Chromosome 1 open reading frame 71	0.411597712	0.006848478	0.00367196	1.137305307	1.600100966	1.406922975
1563364_at	RFXDC2	Regulatory factor X domain containing 2	0.129081058	0.003708743	0.02249464	1.544292	3.610647743	2.338060252
209378_s_at	KIAA1128	KIAA1128	0.020502276	0.002192241	0.027478278	1.573400208	3.156574383	2.006212003
221561_at	SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	0.448772517	0.007299223	0.006712646	1.330459935	3.082488001	2.316858944
212665_at	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	0.574043604	0.002368174	0.003466833	0.887950776	1.9248289	2.167720275
1555855_at	AKR1C2	Aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2	0.938401419	0.002181243	0.000163414	1.01202727	1.562189404	1.543623824
1552931_a_at	PDE8A	phosphodiesterase 8A	0.322085775	0.001200233	0.003094381	1.159519843	2.267447997	1.955505989
241616_at	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	0.143117664	0.00519357	0.018809017	1.485714508	3.942204209	2.653406282
232574_at	XYLT1	xylosyltransferase I	0.503956909	0.00377905	0.009580863	1.061746346	1.54278746	1.453065947
241659_at	JMJD1C	Jumonji domain containing 1C	0.965724891	0.001479871	0.004794575	1.004576838	1.851317481	1.842882905
1557943_at	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	0.663532057	0.001637303	0.00290208	1.070452752	1.649779101	1.541197495
242836_at	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	0.827751906	0.00071558	0.012038399	1.102244825	5.409502673	4.907714283
244805_at		cordon-bleu homolog (mouse)	0.495029936	5.66305E-05	0.011272993	1.044859404	1.197500676	1.146087858
209978_s_at	LPA	lipoprotein, Lp(a) /// plasminogen	0.943791226	0.000422616	0.006255755	0.993859267	1.270909428	1.278761964
1552788_a_at	HELB	helicase (DNA) B	0.122361355	0.009234453	0.005268538	2.292234058	3.86641482	1.686745211
1562409_s_at		CDNA clone IMAGE:5269062	0.182580025	0.002474525	0.014347708	1.089788431	1.222522097	1.121797646
217419_x_at	AGRIN	agrin	0.409055467	0.003448221	0.001420602	1.245188478	2.117459578	1.700513308
239766_at	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	0.026590792	0.001074674	0.473002345	2.203141244	2.649098433	1.202418792
1569921_at	ADK	Adenosine kinase	0.023515103	0.001997397	0.499298166	1.520254699	1.633972867	1.07480205
217643_x_at	FLJ22795	Hypothetical protein FLJ22795	0.116806407	0.006284445	0.018015572	1.225261216	1.455247496	1.187703876
202686_s_at	AXL	AXL receptor tyrosine kinase	0.027676046	0.004537833	0.269987577	4.546163922	6.123553864	1.346971638
1562611_at	AKAP13	kinase (PRKA) anchor protein 13	0.035631552	0.00308334	0.155052971	2.463072227	4.10003525	1.66460212
210214_s_at	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	0.005972687	0.068467243	0.123888939	2.226480908	1.766742187	0.793513289
242189_at	HOMER1	Homer homolog 1 (Drosophila)	0.083063844	0.005844444	0.203990197	2.271850657	3.128670077	1.377146014
209456_s_at	FBXW11	F-box and WD-40 domain protein 11	0.048940946	0.019914544	0.3353188	1.564778756	1.716971999	1.097261828
240552_at	MTHFD1L	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	0.018243446	0.017362392	0.307182133	5.202060116	8.417214129	1.61805399
209012_at	TRIO	triple functional domain (PTPRF interacting)	0.016183031	0.006304372	0.10140656	1.564386216	1.846687555	1.180455016

222467_s_at	SAPS3	SAPS domain family, member 3	0.00187195	0.002620186	0.008784026	1.210822033	1.321564356	1.091460446
231207_at	Mrps30,	mitochondrial ribosomal protein S30	0.016982274	0.00500731	0.84838583	3.376929642	3.592726505	1.063903275
1566284_at	REV3L,	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	0.005161692	0.021140807	0.749807952	2.475338997	2.33910088	0.944961835
244567_at		Transcribed locus	0.010852954	0.007777749	0.223658584	4.305749948	5.390306619	1.251885661
204684_at	NPTX1	neuronal pentraxin I	0.00094217	0.015651274	0.561661559	2.532442962	2.899526762	1.144952445
210171_s_at	CREM	cAMP responsive element modulator	0.004652196	0.059236863	0.66416842	2.382954172	2.229091351	0.935431901
227289_at	LOC144997	hypothetical protein LOC144997	0.001752841	0.010016793	0.204900034	1.295802132	1.404433165	1.08383304
1570593_at	ATP8A1,	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	0.022205014	0.027812162	0.928343335	2.090432656	2.063268947	0.9870057
235756_at	SAMD4A	Sterile alpha motif domain containing 4A	0.002759073	0.041138901	0.449822118	2.537816528	2.279963911	0.898395879
244794_at		Transcribed locus	0.013976996	0.228196361	0.184260447	3.216756095	2.21896014	0.68981299
233377_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	0.005482514	0.150793658	0.477708781	4.724014361	3.680434304	0.779090414
227027_at	GFPT1,	glutamine-fructose-6-phosphate transaminase 1	0.010556456	0.262295027	0.118592075	2.801195159	2.062709413	0.73636762
226819_at		LSM11, U7 small nuclear RNA associated	0.026876078	0.097308588	0.315765977	3.300825053	2.760539808	0.836318122
237725_x_at	SMC5	structural maintenance of chromosomes 5	0.004487652	0.099412771	0.145944348	2.029399047	1.736219124	0.855533625
238421_at	MNAB	Membrane associated DNA binding protein	0.041848609	0.038371692	0.307030138	3.132392293	3.655081263	1.166865744
1566285_at	REV3L,	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	0.013723924	0.04626565	0.779768468	1.995894608	2.053178074	1.028700647
242059_at	ETNK1	Ethanolamine kinase 1	0.01424069	0.016905627	0.407402107	1.940661792	2.073617013	1.068510248
239596_at	SLC30A7	solute carrier family 30 (zinc transporter), member 7	0.02047263	0.081323989	0.839815888	2.33976448	2.4241411	1.036062014
231282_at	C10orf70	Chromosome 10 open reading frame 70	0.016847493	0.14161039	0.459193116	1.602141789	1.509256269	0.942024158
240490_at	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	0.003586714	0.091063148	0.380691926	1.297575176	1.239698815	0.955396525
1555405_at	UBE3C	ubiquitin protein ligase E3C	0.019907964	0.069680909	0.732049089	1.843877256	1.92837243	1.045824728
237136_at	MYO1E	Myosin IE	0.03895426	0.041856486	0.349780165	1.691237941	1.891788395	1.118582045
237218_at	RP11-82K18.3	Kynurenine aminotransferase III	0.00952218	0.077519217	0.972207677	2.83172202	2.851370611	1.006938743
240977_at	LRCH1	Leucine-rich repeats and calponin homology (CH) domain containing 1	0.002271396	0.029831154	0.811296935	2.566761819	2.636656387	1.02723064
231695_at	DIP2B	DIP2 disco-interacting protein 2 homolog B (Drosophila)	0.02621283	0.007860661	0.227286811	1.673320219	2.011867613	1.202320745
1561053_at		---	0.025903067	0.034884239	0.532049497	1.233527858	1.206757487	0.978297717

Supplemental Table 2. qRT-PCR data of patients with FHL. Validation of microarray data.

	GENE SYMBOL	CONTROL	LH1	LH1	LH1	LH2	LH2	LH2	LH3	LH3	LH3
		2^(- Avg.(Delta(Ct)	2^(- Avg.(Delta(Ct)	Fold Change	p-value	2^(- Avg.(Delta(Ct)	Fold Change	p-value	2^(- Avg.(Delta(Ct)	Fold Change	p-value
1	CDKN2C	0.001176	0.001807	1.5369	0.611834	0.000176	0.1497	0.08152	0.00013	0.1103	0.070076
2	RNF26	0.002618	0.001832	0.6998	0.396556	0.000325	0.1241	0.051762	0.000535	0.2045	0.078896
3	UQCRH	0.0965	0.109766	1.1375	0.881178	0.03224	0.3341	0.083083	0.03098	0.321	0.135701
4	LRDD	0.000181	0.00036	1.9873	0.316969	0.000255	1.4077	0.180499	0.001029	5.6798	0.016807
5	HLA-DRB4	0.003561	0.019438	5.4579	0.352544	0.024433	6.8606	0.146149	0.00216	0.6064	0.364612
6	ADCK2	0.000883	0.001425	1.6142	0.218242	0.000343	0.3885	0.083462	0.002459	2.7863	0.009224
7	C18orf8	0.003058	0.001645	0.5381	0.385879	0.00197	0.6443	0.136294	0.008897	2.9096	0.000925
8	HIAT1	0.008815	0.004953	0.5619	0.039725	0.007164	0.8127	0.885267	0.015761	1.788	0.03563
9	GIMAP1	0.001322	0.000071	0.0536	0.052552	0.002033	1.5378	0.46904	0.002815	2.13	0.120374
10	DCAKD	0.003283	0.000918	0.2795	0.101998	0.005563	1.6945	0.708894	0.005592	1.7033	0.738808
11	FKBP5	0.020428	0.002438	0.1194	0.045169	0.070073	3.4303	0.015042	0.092944	4.5499	0.009752
12	GTPBP2	0.00094	0.000384	0.4082	0.301524	0.000485	0.5158	0.272364	0.003793	4.0348	0.529303
13	FLJ20366	0.000908	0.000103	0.1134	0.050033	0.0024	2.6436	0.071886	0.001336	1.4717	0.242712
14	ETV3	0.010896	0.021456	1.9691	0.185999	0.001943	0.1783	0.063448	0.002577	0.2365	0.091723
15	KIF5C	0.000532	0.000607	1.1421	0.024687	0.000051	0.0963	0.000268	0.000264	0.4971	0.921096
16	RPS27	2.259233	1.252664	0.5545	0.519011	0.597703	0.2646	0.024225	1.276771	0.5651	0.31709
17	PDE4B	0.012076	0.017855	1.4785	0.131033	0.020761	1.7191	0.10653	0.004718	0.3907	0.087438
18	DOCK4	0.000208	0.000885	4.2526	0.000939	0.000079	0.3811	0.076677	0.000093	0.447	0.154362
19	RFX7	0.006884	0.00123	0.1786	0.029482	0.006368	0.925	0.841571	0.002971	0.4315	0.161615
20	KIAA1128	0.02864	0.020797	0.7261	0.309644	0.048111	1.6799	0.256256	0.023276	0.8127	0.987341
21	MTHFD1L	0.000439	0.002748	6.255	0.00027	0.012028	27.379	0.000005	0.007494	17.0595	0.000038
22	GAPDH	0.264102	1.134849	4.297	0.000001	0.725728	2.7479	0.000482	0.594604	2.2514	0.012192
23	B2M	1	1	1	0	1	1	0	1	1	0
24	HGDC	0.000016	0.000004	0.224	0.581275	0.000014	0.8507	0.581928	0.000016	0.9604	0.582022

	GENE SYMBOL	**CONTROL**	**LH4**	**LH4**	**LH4**	**LH6**	**LH6**	**LH6**	**LH7**	**LH7**	**LH7**
		2^(- Avg.(Delta(Ct)	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**
1	CDKN2C	0.001176	0.001909	1.6236	0.690415	0.002413	2.0527	0.104098	0.000718	0.611	0.364761
2	RNF26	0.002618	0.011951	4.5657	0.000311	0.007692	2.9383	0.027689	0.005934	2.2671	0.073996
3	UQCRH	0.0965	0.167241	1.7331	0.348502	0.226487	2.347	0.071848	0.116899	1.2114	0.934409
4	LRDD	0.000181	0.001597	8.8203	0.000089	0.000373	2.061	0.024194	0.000181	0.9983	0.59518
5	HLA-DRB4	0.003561	0.008974	2.5198	0.927332	0.002464	0.6918	0.691797	0.001375	0.386	0.223171
6	ADCK2	0.000883	0.001822	2.0646	0.049723	0.001219	1.3811	0.160901	0.000913	1.0347	0.80829
7	C18orf8	0.003058	0.007669	2.5082	0.000709	0.004172	1.3645	0.206819	0.006494	2.1238	0.012713
8	HIAT1	0.008815	0.013792	1.5646	0.215177	0.010489	1.1899	0.44013	0.017742	2.0127	0.04047
9	GIMAP1	0.001322	0.000357	0.2698	0.185329	0.00004	0.0303	0.05031	0.002113	1.5984	0.671264
10	DCAKD	0.003283	0.006896	2.1006	0.612573	0.001893	0.5767	0.382355	0.004415	1.3449	0.754051
11	FKBP5	0.020428	0.030963	1.5157	0.164629	0.001116	0.0546	0.036339	0.028756	1.4077	0.276482
12	GTPBP2	0.00094	0.002285	2.4312	0.875454	0.001032	1.0981	0.449169	0.001716	1.8256	0.848074
13	FLJ20366	0.000908	0.001818	2.0023	0.350834	0.000076	0.0838	0.05108	0.001631	1.7963	0.606003
14	ETV3	0.010896	0.003166	0.2905	0.145471	0.011801	1.083	0.844093	0.001724	0.1582	0.091264
15	KIF5C	0.000532	0.000035	0.0665	0.000722	0.003813	7.1685	0.012284	0.000047	0.0886	0.000867
16	RPS27	2.259233	0.972655	0.4305	0.09888	7.754319	3.4323	0.024861	0.747425	0.3308	0.525046
17	PDE4B	0.012076	0.052435	4.3419	0.000009	0.030029	2.4866	0.02509	0.002873	0.2379	0.335415
18	DOCK4	0.000208	0.000054	0.2578	0.067873	0.001712	8.2297	0.031144	0.00007	0.337	0.094557
19	RFX7	0.006884	0.002926	0.4251	0.133539	0.005611	0.8151	0.66295	0.000727	0.1055	0.041081
20	KIAA1128	0.02864	0.015697	0.5481	0.21847	0.039146	1.3668	0.344658	0.0066	0.2304	0.080432
21	MTHFD1L	0.000439	0.001594	3.628	0.002328	0.003325	7.5685	0.007002	0.00135	3.072	0.008397
22	GAPDH	0.264102	0.681444	2.5802	0.02654	0.60815	2.3027	0.008474	0.82932	3.1401	0.005769
23	B2M	1	1	1	0	1	1	0	1	1	0
24	HGDC	0.000016	0.000012	0.7393	0.634977	0.00003	1.8521	0.583087	0.000012	0.7565	0.634985

	GENE SYMBOL	CONTROL	LH8	LH8	LH8	LH9	LH9	LH9	LH11	LH11	LH11
		2^(- Avg.(Delta(Ct)	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**
1	CDKN2C	0.001176	0.001976	1.6808	0.289357	0.001268	1.0786	0.734114	0.003835	3.2622	0.016189
2	RNF26	0.002618	0.00883	3.3733	0.008206	0.007812	2.9845	0.019153	0.003093	1.1817	0.091146
3	UQCRH	0.0965	0.184284	1.9097	0.099609	0.093861	0.9727	0.573777	0.185995	1.9274	0.112564
4	LRDD	0.000181	0.000735	4.0582	0.018644	0.000924	5.1012	0.002771	0.000353	1.9509	0.01356
5	HLA-DRB4	0.003561	0.034674	9.736	0.040129	0.003504	0.984	0.664312	0.049836	13.9933	0.006335
6	ADCK2	0.000883	0.000477	0.5406	0.474088	0.001328	1.5044	0.193842	0.000368	0.4173	0.14142
7	C18orf8	0.003058	0.003331	1.0892	0.553152	0.006817	2.2294	0.003911	0.004225	1.3819	0.040946
8	HIAT1	0.008815	0.011125	1.2621	0.297131	0.025737	2.9197	0.00034	0.009269	1.0515	0.530452
9	GIMAP1	0.001322	0.001453	1.0994	0.817718	0.000092	0.0697	0.099026	0.000827	0.6256	0.391001
10	DCAKD	0.003283	0.002995	0.9122	0.992972	0.000683	0.2079	0.139904	0.003393	1.0335	0.815326
11	FKBP5	0.020428	0.037856	1.8532	0.045033	0.002536	0.1241	0.158783	0.089209	4.3671	0.014127
12	GTPBP2	0.00094	0.000551	0.5857	0.515585	0.000219	0.233	0.243426	0.000385	0.4094	0.31745
13	FLJ20366	0.000908	0.000661	0.7278	0.607764	0.000638	0.703	0.397078	0.000499	0.549	0.542517
14	ETV3	0.010896	0.003369	0.3092	0.138393	0.007958	0.7304	0.380826	0.007634	0.7006	0.77901
15	KIF5C	0.000532	0.000077	0.1443	0.001643	0.001764	3.3173	0.000012	0.000162	0.3043	0.823907
16	RPS27	2.259233	1.887749	0.8356	0.659571	1.761332	0.7796	0.483042	0.438303	0.194	0.046993
17	PDE4B	0.012076	0.094732	7.8444	0.000015	0.030963	2.5639	0.014002	0.016785	1.3899	0.210994
18	DOCK4	0.000208	0.000046	0.2213	0.066731	0.000182	0.8751	0.613285	0.000163	0.7832	0.775207
19	RFX7	0.006884	0.001268	0.1842	0.063657	0.000538	0.0782	0.036772	0.00128	0.1859	0.073891
20	KIAA1128	0.02864	0.007958	0.2779	0.110884	0.020146	0.7034	0.32498	0.006992	0.2441	0.101932
21	MTHFD1L	0.000439	0.001343	3.0578	0.01103	0.002079	4.7322	0.000506	0.013508	30.7497	0.000053
22	GAPDH	0.264102	0.510506	1.933	0.02001	0.403321	1.5271	0.199092	1.091768	4.1339	0.000793
23	B2M	1	1	1	0	1	1	0	1	1	0
24	HGDC	0.000016	0.000022	1.3295	0.635376	0.000012	0.7075	0.634974	0.000024	1.4414	0.635518

	GENE SYMBOL	CONTROL	LH12	LH12	LH12	LH13	LH13	LH13	LH15	LH15	LH15
		2^(- Avg.(Delta(Ct)	2^(- Avg.(Delta(Ct)	Fold Change	p-value	2^(- Avg.(Delta(Ct)	Fold Change	p-value	2^(- Avg.(Delta(Ct)	Fold Change	p-value
1	CDKN2C	0.001176	0.007289	6.201	0.002397	0.002954	2.5126	0.149588	0.003448	2.2618	0.106835
2	RNF26	0.002618	0.026142	9.9866	0.001066	0.008393	3.2061	0.010718	0.000111	0.0364	0.705512
3	UQCRH	0.0965	0.416821	4.3194	0.00349	0.193893	2.0093	0.208917	0.104145	1.7808	0.252153
4	LRDD	0.000181	0.000473	2.6132	0.051337	0.000382	2.1104	0.012395	0.0012	7.0739	0.16173
5	HLA-DRB4	0.003561	0.057016	16.0092	0.023853	0.001631	0.458	0.243113	0.005473	0.6541	0.218681
6	ADCK2	0.000883	0.00285	3.2284	0.017088	0.001052	1.1913	0.656896	0.003852	5.1159	0.001082
7	C18orf8	0.003058	0.009339	3.0543	0.000078	0.004876	1.5948	0.104858	0.002518	0.9091	0.687799
8	HIAT1	0.008815	0.038407	4.357	0.000001	0.011625	1.3187	0.035296	0.010097	1.3851	0.512229
9	GIMAP1	0.001322	0.001686	1.2753	0.817949	0.000546	0.4127	0.207384	0.000046	0.0272	0.061587
10	DCAKD	0.003283	0.013961	4.2526	0.011168	0.007239	2.2051	0.469433	0.000178	0.0363	0.068379
11	FKBP5	0.020428	0.041738	2.0432	0.152341	0.11162	5.4642	0.000027	0.001289	0.0557	0.040841
12	GTPBP2	0.00094	0.000101	0.1073	0.255229	0.000259	0.2752	0.315059	0.004613	5.1041	0.134299
13	FLJ20366	0.000908	0.000417	0.4593	0.159514	0.000191	0.2105	0.110755	0.000114	0.1124	0.05593
14	ETV3	0.010896	0.006524	0.5987	0.417609	0.004354	0.3996	0.272608	0.224793	43.2112	0.010869
15	KIF5C	0.000532	0.000149	0.2796	0.002036	0.000215	0.4043	0.019556	0.00205	4.5473	0.000072
16	RPS27	2.259233	3.5801	1.5847	0.123012	1.079228	0.4777	0.486465	0.716978	0.3675	0.09951
17	PDE4B	0.012076	0.024476	2.0267	0.063479	0.005563	0.4606	0.107699	0.153184	21.9199	0.000001
18	DOCK4	0.000208	0.0002	0.9598	0.790587	0.000117	0.5642	0.206352	0.000582	3.0543	0.000174
19	RFX7	0.006884	0.007239	1.0515	0.879411	0.002724	0.3957	0.124554	0.009981	1.4557	0.315659
20	KIAA1128	0.02864	0.024775	0.865	0.900021	0.015553	0.5431	0.238446	0.110849	3.4882	0.008097
21	MTHFD1L	0.000439	0.00349	7.9447	0.000039	0.00327	7.4427	0.000066	0.001436	3.1511	0.00386
22	GAPDH	0.264102	1.285652	4.868	0.000127	0.125	0.4733	0.69572	0.557354	2.1251	0.033944
23	B2M	1	1	1	0	1	1	0	1	1	0
24	HGDC	0.000016	0.00003	1.8585	0.582882	0.000035	2.1747	0.636127	0.000011	0.5406	0.634867

	GENE SYMBOL	**CONTROL**	**LH16**	**LH16**	**LH16**	**LH17**	**LH17**	**LH17**	**LH18**	**LH18**	**LH18**
		2^(- Avg.(Delta(Ct)	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**
1	CDKN2C	0.001176	0.018797	12.3306	0	0.004093	2.6851	0.05469	0.002563	1.6812	0.189476
2	RNF26	0.002618	0.002031	0.6666	0.100743	0.01132	3.7149	0.01267	0.011858	3.8915	0.017533
3	UQCRH	0.0965	0.038651	0.6609	0.974952	0.202361	3.4601	0.094324	0.169811	2.9036	0.253422
4	LRDD	0.000181	0.000384	2.2645	0.934406	0.000706	4.165	0.539259	0.001128	6.6522	0.069289
5	HLA-DRB4	0.003561	0.00491	0.5868	0.199954	0.014155	1.6915	0.814862	0.00736	0.8795	0.37011
6	ADCK2	0.000883	0.005226	6.9403	0.000792	0.001219	1.6189	0.08754	0.001532	2.035	0.045396
7	C18orf8	0.003058	0.005934	2.1423	0.014317	0.002791	1.0075	0.23613	0.006207	2.2405	0.008543
8	HIAT1	0.008815	0.016289	2.2346	0.009858	0.022996	3.1547	0.003122	0.016608	2.2784	0.003045
9	GIMAP1	0.001322	0.002954	1.7281	0.641109	0.000129	0.0752	0.039277	0.002766	1.6183	0.461843
10	DCAKD	0.003283	0.007581	1.5431	0.735354	0.000257	0.0523	0.045813	0.007578	1.5424	0.619768
11	FKBP5	0.020428	0.179659	7.7633	0.014441	0.001036	0.0448	0.024247	0.028008	1.2103	0.229021
12	GTPBP2	0.00094	0.001953	2.161	0.875459	0.001845	2.0408	0.110291	0.000435	0.4809	0.143959
13	FLJ20366	0.000908	0.00663	6.5281	0.000266	0.000066	0.0653	0.035069	0.000722	0.7107	0.210748
14	ETV3	0.010896	0.000676	0.13	0.139306	0.047861	9.2002	0.082222	0.000494	0.095	0.49517
15	KIF5C	0.000532	0.000586	1.2998	0.414888	0.002915	6.4643	0.07329	0.00008	0.1774	0.033732
16	RPS27	2.259233	0.907519	0.4652	0.13204	1.569168	0.8043	0.916975	0.588046	0.3014	0.069019
17	PDE4B	0.012076	0.00199	0.2847	0.160304	0.056818	8.1304	0.026481	0.00272	0.3893	0.753993
18	DOCK4	0.000208	0.000296	1.552	0.157884	0.002555	13.4078	0.000082	0.000204	1.0714	0.058327
19	RFX7	0.006884	0.008393	1.2241	0.251229	0.009958	1.4523	0.148093	0.007129	1.0398	0.449872
20	KIAA1128	0.02864	0.192109	6.0454	0.000174	0.188809	5.9415	0.036214	0.027853	0.8765	0.657418
21	MTHFD1L	0.000439	0.001522	3.3384	0.014971	0.001169	2.5654	0.015258	0.001892	4.1502	0.004692
22	GAPDH	0.264102	0.387786	1.4785	0.41088	0.05366	0.2046	0.42273	0.666187	2.54	0.004332
23	B2M	1	1	1	0	1	1	0	1	1	0
24	HGDC	0.000016	0.000024	1.156	0.635419	0.000085	4.0888	0.598718	0.000042	2.0408	0.548783

	GENE SYMBOL	**CONTROL**	**LH19**	**LH19**	**LH19**	**LH20**	**LH20**	**LH20**	**LH21**	**LH21**	**LH21**
		2^(- Avg.(Delta(Ct)	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**	**2^(- Avg.(Delta(Ct)**	**Fold Change**	**p-value**
1	CDKN2C	0.001176	0.000686	0.4498	0.355987	0.002249	1.4751	0.613127	0.001583	1.0383	0.696155
2	RNF26	0.002618	0.002249	0.738	0.650713	0.000999	0.328	0.123142	0.004007	1.3149	0.858313
3	UQCRH	0.0965	0.062789	1.0736	0.142667	0.088593	1.5148	0.258991	0.141938	2.427	0.752657
4	LRDD	0.000181	0.00012	0.7051	0.606001	0.000092	0.5406	0.388786	0.000323	1.9042	0.793416
5	HLA-DRB4	0.003561	0.043687	5.2204	0.026493	0.00174	0.2079	0.111342	0.027268	3.2584	0.397108
6	ADCK2	0.000883	0.000788	1.0461	0.868715	0.000199	0.2639	0.08338	0.001101	1.4624	0.527495
7	C18orf8	0.003058	0.008144	2.94	0.001769	0.00849	3.0649	0.0005	0.009798	3.5369	0.000012
8	HIAT1	0.008815	0.026892	3.6893	0.001366	0.027331	3.7494	0.000028	0.047257	6.483	0
9	GIMAP1	0.001322	0.000764	0.4473	0.328358	0.001646	0.9632	0.472501	0.000044	0.0259	0.061786
10	DCAKD	0.003283	0.002712	0.5519	0.233974	0.004466	0.9091	0.439337	0.000102	0.0208	0.065858
11	FKBP5	0.020428	0.014714	0.6358	0.275902	0.125579	5.4264	0.000006	0.002687	0.1161	0.051548
12	GTPBP2	0.00094	0.000399	0.4419	0.233027	0.0012	1.3272	0.398111	0.000892	0.9874	0.324726
13	FLJ20366	0.000908	0.000367	0.3618	0.117327	0.000326	0.3209	0.107521	0.000095	0.0932	0.053268
14	ETV3	0.010896	0.004721	0.9075	0.635693	0.001661	0.3194	0.190613	0.008315	1.5984	0.964702
15	KIF5C	0.000532	0.000218	0.4835	0.052185	0.000339	0.7518	0.227643	0.001387	3.0773	0.000401
16	RPS27	2.259233	1.164734	0.597	0.573194	0.420448	0.2155	0.051673	4.40762	2.2592	0.039856
17	PDE4B	0.012076	0.009552	1.3668	0.233929	0.012633	1.8077	0.524372	0.032502	4.6509	0.00053
18	DOCK4	0.000208	0.000357	1.8758	0.047223	0.000068	0.3554	0.042151	0.00284	14.9027	0
19	RFX7	0.006884	0.002737	0.3991	0.057668	0.002142	0.3124	0.02833	0.009037	1.318	0.357011
20	KIAA1128	0.02864	0.024861	0.7823	0.458399	0.008182	0.2575	0.042541	0.038562	1.2135	0.86516
21	MTHFD1L	0.000439	0.000638	1.4004	0.777727	0.00123	2.6991	0.021716	0.001704	3.7386	0.001137
22	GAPDH	0.264102	0.214641	0.8184	0.379996	0.590496	2.2514	0.020313	0.447513	1.7063	0.209719
23	B2M	1	1	1	0	1	1	0	1	1	0
24	HGDC	0.000016	0.000011	0.5443	0.6349	0.000003	0.16	0.634526	0.000006	0.2958	0.634648

	GENE SYMBOL	CONTROL	LH22	LH22	LH22	LH23	LH23	LH23	LH26	LH26	LH26
		2^(- Avg.(Delta(Ct)	2^(- Avg.(Delta(Ct)	Fold Change	p-value	2^(- Avg.(Delta(Ct)	Fold Change	p-value	2^(- Avg.(Delta(Ct)	Fold Change	p-value
1	CDKN2C	0.001176	0.01038	6.8093	0.082539	0.00235	1.5413	0.644927	0.001874	1.229	0.990752
2	RNF26	0.002618	0.024947	8.187	0.082351	0.00348	1.1421	0.852747	0.001814	0.5953	0.3333
3	UQCRH	0.0965	0.441351	7.5466	0.083411	0.109071	1.865	0.396164	0.047586	0.8137	0.073978
4	LRDD	0.000181	0.001822	10.7468	0.082811	0.000367	2.1622	0.775131	0.000436	2.5713	0.938559
5	HLA-DRB4	0.003561	0.174041	20.7974	0.082191		0.076	0.082852	0.00167	0.199	0.08439
6	ADCK2	0.000883	0.006673	8.8612	0.082364	0.000808	1.073	0.793503	0.001109	1.4726	0.63485
7	C18orf8	0.003058	0.065041	23.4796	0.082065	0.008051	2.9063	0.001297	0.005226	1.8867	0.045868
8	HIAT1	0.008815	0.195806	26.8621	0.08198	0.042101	5.7757	0.000001	0.024349	3.3404	0.00004
9	GIMAP1	0.001322	0.006754	3.9518	0.082961	0.001724	1.0087	0.638215	0.000129	0.0755	0.071155
10	DCAKD	0.003283	0.010934	2.2256	0.084378	0.001935	0.3939	0.164016	0.000279	0.0568	0.075725
11	FKBP5	0.020428	0.044041	1.9031	0.084273	0.00506	0.2186	0.071898	0.002123	0.0917	0.046188
12	GTPBP2	0.00094	0.005689	6.2948	0.083687	0.000543	0.6008	0.254129	0.000799	0.8837	0.303571
13	FLJ20366	0.000908	0.002806	2.7622	0.083681	0.000878	0.8645	0.414938	0.000059	0.0584	0.047963
14	ETV3	0.010896	0.01132	2.176	0.085987	0.020665	3.9724	0.032217	0.009596	1.8446	0.825596
15	KIF5C	0.000532	0.005931	13.1546	0.081945	0.001197	2.6543	0.000082	0.008892	19.7211	0.000028
16	RPS27	2.259233	10.39271	5.327	0.08261	2.07053	1.0613	0.997442	1.643381	0.8424	0.730797
17	PDE4B	0.012076	0.020689	2.9605	0.083829	0.01577	2.2566	0.199291	0.030678	4.3898	0.000923
18	DOCK4	0.000208	0.000436	2.2855	0.08356	0.000068	0.3546	0.043167	0.001286	6.7466	0
19	RFX7	0.006884	0.01022	1.4905	0.085064	0.002027	0.2956	0.036372	0.003844	0.5606	0.118669
20	KIAA1128	0.02864	0.105477	3.3192	0.083219	0.020054	0.6311	0.254734	0.035077	1.1038	0.780378
21	MTHFD1L	0.000439	0.012174	26.7074	0.082068	0.000888	1.9487	0.211762	0.002449	5.3734	0.000009
22	GAPDH	0.264102	0.298851	1.1394	0.534635	0.277392	1.0576	0.807601	0.224793	0.8571	0.405537
23	B2M	1	1	1	0	1	1	0	1	1	0
24	HGDC	0.000016	0.000158	7.6299	0.093221	0.000012	0.5635	0.63488	0.000016	0.7896	0.635076