

Supplemental Table 1: The genes correlated with the sensitivity of a panel of 28 cell lines to IGF1R inhibitor BMS-536924 as identified by Affymetrix gene array. The genes were selected by two statistic analyses: two sample t-test to compare gene expression of 16 sensitive cell lines to that of 12 resistant cell lines ($p < 0.001$ and 2 fold); and the Pearson correlations between the $\log_2(\text{IC}_{50})$ data and the expression level of each gene in the 28 cell lines ($p < 0.001$). The genes overlapped from the two analyses are listed here with p values and fold change between the sensitive and resistant cell line groups indicated. The genes are rank ordered by the fold changes. The positive fold changes indicate the genes having higher expression level in the sensitive cell lines and the negative fold changes indicate the genes having higher expression level in the resistant cell lines.

Probe ID	Accession #	Gene Title	Gene Symbol	p-value in t-test	Fold (S/R) ¹	p-value (correlation) ²
Genes higher expressed in the group of sensitive cell lines						
214451_at	NM_003221	transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	TFAP2B	1.3E-05	56.6	4.3E-04
212713_at	R72286	microfibrillar-associated protein 4	MFAP4	1.7E-06	14.5	9.9E-05
204915_s_at	AB028641	SRY (sex determining region Y)-box 11	SOX11	1.7E-07	13.4	4.3E-05
216623_x_at	AK025084	trinucleotide repeat containing 9	TNRC9	3.2E-04	13.2	5.5E-04
221011_s_at	NM_030915	limb bud and heart development homolog (mouse) /// limb bud and heart development homolog (mouse)	LBH	7.1E-05	12.2	4.7E-04
202517_at	NM_001313	collapsin response mediator protein 1	CRMP1	3.0E-06	11.3	4.1E-04
205888_s_at	A1962693	janus kinase and microtubule interacting protein 2 /// myelin transcription factor 1-like	JAKMIP2 /// MYT1L	3.1E-08	9.3	1.1E-05
207781_s_at	NM_021998	zinc finger protein 711	ZNF711	9.2E-12	8.1	3.6E-07
221748_s_at	AL046979	tensin 1 /// tensin 1	TNS1	5.4E-05	7.8	4.3E-04
213170_at	AA406605	glutathione peroxidase 7	GPX7	2.0E-05	7.4	1.6E-04
205123_s_at	NM_003692	transmembrane protein with EGF-like and two follistatin-like domains 1	TMEFF1	1.2E-05	6.9	1.0E-04
203999_at	AV731490	---	---	1.6E-06	6.7	9.2E-04

218445_at	NM_018649	H2A histone family, member Y2	H2AFY2	1.2E-07	6.3	9.7E-05
215043_s_at	X83301	SMA3 /// SMA5	SMA3 /// SMA5	4.0E-07	6.2	1.5E-05
209598_at	AB020690	paraneoplastic antigen MA2	PNMA2	2.5E-05	6.1	1.4E-04
212382_at	BF433429	Transcription factor 4	TCF4	1.3E-06	5.8	1.0E-04
212386_at	BF592782	CDNA FLJ11918 fis, clone HEMBB1000272	---	1.6E-06	5.7	6.0E-06
205889_s_at	NM_014790	janus kinase and microtubule interacting protein 2	JAKMIP2	9.6E-08	5.5	4.5E-06
205830_at	NM_004362	calmegin	CLGN	5.6E-08	5.4	4.4E-07
211071_s_at	BC006471	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11 /// myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	MLLT11	1.9E-05	5.3	5.7E-04
212599_at	AK025298	autism susceptibility candidate 2	AUTS2	2.1E-05	5.3	1.8E-05
206440_at	NM_004664	lin-7 homolog A (C. elegans)	LIN7A	9.1E-04	4.8	3.2E-04
206565_x_at	NM_006780	SMA3	SMA3	9.0E-07	4.7	4.6E-06
219855_at	NM_018159	nudix (nucleoside diphosphate linked moiety X)-type motif 11	NUDT11	3.8E-04	4.7	8.1E-04
213131_at	R38389	olfactomedin 1	OLFM1	1.6E-04	4.7	6.0E-04
200884_at	NM_001823	creatine kinase, brain	CKB	2.8E-07	4.6	9.8E-07
206655_s_at	NM_000407	glycoprotein Ib (platelet), beta polypeptide /// septin 5	GP1BB /// SEPT5	1.2E-05	4.5	9.1E-04
214023_x_at	AL533838	tubulin, beta 2B	TUBB2B	5.4E-04	4.5	1.5E-04
204860_s_at	A1817801	NLR family, apoptosis inhibitory protein /// similar to Baculoviral IAP repeat-containing protein 1 (Neuronal apoptosis inhibitory protein)	NAIP /// LOC728519	3.0E-05	4.2	1.1E-04
208998_at	U94592	uncoupling protein 2 (mitochondrial, proton carrier)	UCP2	2.6E-06	4.2	6.1E-06
204165_at	NM_003931	WAS protein family, member 1	WASF1	2.7E-07	4.1	1.1E-05

212847_at	AL036840	Far upstream element (FUSE) binding protein 1	FUBP1	1.0E-07	4.1	1.2E-04
213216_at	AL537463	OTU domain containing 3	OTUD3	9.8E-06	3.9	1.9E-05
213547_at	AB014567	cullin-associated and neddylation-dissociated 2 (putative)	CAND2	3.3E-05	3.7	2.1E-05
204742_s_at	NM_015032	androgen-induced proliferation inhibitor	APRIN	8.9E-06	3.5	1.5E-05
213605_s_at	AL049987	Similar to Beta-glucuronidase precursor	LOC728411	1.6E-05	3.5	3.5E-05
204457_s_at	NM_002048	growth arrest-specific 1	GAS1	1.4E-04	3.4	1.1E-04
214102_at	AK023737	centaurin, delta 1	CENTD1	1.9E-06	3.4	5.6E-06
201449_at	AL567227	TIA1 cytotoxic granule-associated RNA binding protein	TIA1	1.3E-08	3.4	2.4E-05
205347_s_at	NM_021992	thymosin-like 8	TMSL8	7.6E-05	3.3	1.2E-04
212816_s_at	BE613178	cystathionine-beta-synthase	CBS	5.8E-05	3.2	5.6E-04
214850_at	X75940	glucuronidase, beta pseudogene 1	GUSBP1	4.9E-06	3.2	1.4E-04
212731_at	U79297	ankyrin repeat domain 46	ANKRD46	1.8E-07	3.2	2.2E-06
221965_at	AI990326	M-phase phosphoprotein 9	MPHOSPH9	1.6E-07	3.1	8.2E-06
213283_s_at	BG285616	sal-like 2 (Drosophila)	SALL2	2.7E-06	3.1	2.4E-05
200644_at	NM_023009	MARCKS-like 1	MARCKSL1	2.8E-05	3.1	1.8E-05
210882_s_at	U04811	trophinin	TRO	2.2E-05	3.0	4.4E-05
204040_at	NM_014746	ring finger protein 144	RNF144	1.8E-04	3.0	1.9E-04
203069_at	NM_014849	synaptic vesicle glycoprotein 2A	SV2A	3.1E-04	3.0	8.0E-04
215146_s_at	AB028966	tetratricopeptide repeat domain 28	TTC28	7.9E-07	3.0	1.4E-08
213610_s_at	BE326381	kelch-like 23 (Drosophila)	KLHL23	7.0E-06	2.9	5.1E-05
202967_at	NM_001512	glutathione S-transferase A4	GSTA4	1.2E-04	2.9	3.1E-04
218223_s_at	NM_016274	pleckstrin homology domain containing, family O member 1	PLEKHO1	5.9E-07	2.9	1.2E-07
221261_x_at	NM_030801	melanoma antigen family D, 4 /// melanoma antigen family D, 4	MAGED4	1.9E-05	2.9	9.3E-06
212624_s_at	BF339445	chimerin (chimaerin) 1	CHN1	9.7E-05	2.9	1.5E-04
215599_at	X83300	SMA4 /// similar to SMA4	SMA4 /// LOC730390	9.8E-06	2.8	1.3E-04
212126_at	BG391282	CDNA clone IMAGE:4842353	---	1.4E-07	2.8	7.4E-05

209153_s at	M31523	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	TCF3	1.4E-06	2.8	9.7E-05
214724_at	AF070621	DIX domain containing 1	DIXDC1	1.8E-05	2.7	2.8E-04
208986_at	AL559478	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	TCF12	2.3E-06	2.7	2.7E-07
213626_at	AL049442	carbonyl reductase 4	CBR4	9.6E-06	2.7	3.3E-04
218868_at	NM_020445	ARP3 actin-related protein 3 homolog B (yeast)	ACTR3B	6.8E-06	2.6	6.9E-04
203298_s at	NM_004973	jumonji, AT rich interactive domain 2	JARID2	1.3E-07	2.6	1.6E-04
37577_at	U79256	Rho GTPase activating protein 19	ARHGAP19	4.1E-05	2.6	1.1E-04
212482_at	BF671894	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	RMND5A	1.8E-06	2.5	1.9E-04
204173_at	NM_002475	myosin, light chain 6B, alkali, smooth muscle and non-muscle	MYL6B	9.9E-04	2.5	7.4E-04
203151_at	AW296788	microtubule-associated protein 1A	MAP1A	2.3E-04	2.5	7.7E-04
212919_at	AV715578	DCP2 decapping enzyme homolog (S. cerevisiae)	DCP2	1.1E-06	2.5	3.3E-05
213694_at	AW027347	round spermatid basic protein 1	RSBN1	9.2E-07	2.5	2.8E-04
203625_x at	BG105365	melanoma cell adhesion molecule	MCAM	1.8E-04	2.5	1.4E-04
204795_at	NM_025263	proline rich 3	PRR3	1.0E-05	2.5	2.0E-04
212670_at	AA479278	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)	ELN	2.0E-05	2.5	1.4E-04
212547_at	N34842	FLJ35348	FLJ35348	9.4E-07	2.5	7.2E-05
210567_s at	BC001441	S-phase kinase-associated protein 2 (p45)	SKP2	6.7E-04	2.4	4.1E-04
209748_at	AB029006	spastin	SPAST	4.0E-07	2.4	3.8E-04
215128_at	AV704232	CDNA FLJ11682 fis, clone HEMBA1004880	---	4.7E-05	2.4	4.5E-04
203825_at	NM_007371	bromodomain containing 3	BRD3	1.2E-06	2.4	4.5E-05
214220_s at	AW003635	Alstrom syndrome 1	ALMS1	1.4E-06	2.4	1.6E-05
210045_at	AU151428	isocitrate dehydrogenase 2 (NADP+), mitochondrial	IDH2	6.1E-06	2.4	5.7E-04

218683_at	NM_021190	polypyrimidine tract binding protein 2	PTBP2	1.5E-06	2.4	5.8E-04
218457_s_at	NM_022552	DNA (cytosine-5-)-methyltransferase 3 alpha	DNMT3A	2.2E-06	2.4	7.2E-05
204061_at	NM_005044	protein kinase, X-linked	PRKX	6.2E-06	2.4	2.3E-05
210649_s_at	AF231056	AT rich interactive domain 1A (SWI-like)	ARID1A	7.1E-07	2.4	7.2E-08
212153_at	AB007930	pogo transposable element with ZNF domain	POGZ	8.7E-08	2.4	6.1E-05
218265_at	NM_024077	SECIS binding protein 2	SECISBP2	1.1E-06	2.4	2.2E-05
210543_s_at	U34994	protein kinase, DNA-activated, catalytic polypeptide	PRKDC	5.0E-04	2.3	1.3E-04
220443_s_at	NM_012476	ventral anterior homeobox 2	VAX2	2.0E-04	2.3	5.1E-04
202561_at	AF070613	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	TNKS	1.4E-04	2.3	4.6E-04
203795_s_at	NM_020993	B-cell CLL/lymphoma 7A	BCL7A	3.1E-06	2.3	3.3E-04
213387_at	AB033066	ATPase family, AAA domain containing 2B	ATAD2B	2.5E-06	2.3	1.0E-04
203046_s_at	NM_003920	timeless homolog (Drosophila)	TIMELESS	6.7E-07	2.3	7.1E-06
211929_at	AA527502	heterogeneous nuclear ribonucleoprotein A3	HNRPA3	1.8E-05	2.3	1.8E-04
222101_s_at	BF222893	dachsous 1 (Drosophila)	DCHS1	5.2E-04	2.3	2.3E-04
203940_s_at	NM_014909	vasohibin 1	VASH1	6.0E-04	2.3	1.8E-04
203026_at	NM_014872	zinc finger and BTB domain containing 5	ZBTB5	3.7E-08	2.3	5.5E-05
212164_at	AL522296	transmembrane protein 183A	TMEM183A	1.1E-06	2.2	1.7E-04
207705_s_at	NM_025176	KIAA0980 protein	RP4-691N24.1	1.4E-04	2.2	9.6E-05
210962_s_at	AB019691	A kinase (PRKA) anchor protein (yotiao) 9	AKAP9	5.2E-08	2.2	2.0E-05
210555_s_at	U85430	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NFATC3	5.4E-07	2.2	5.1E-05
220040_x_at	NM_018684	KIAA1166	KIAA1166	1.8E-05	2.2	8.6E-04
220735_s_at	NM_020654	SUMO1/sentrin specific peptidase 7	SEN7	1.0E-04	2.2	2.3E-04
220143_x_at	NM_018032	LUC7-like (S. cerevisiae)	LUC7L	3.0E-06	2.2	2.0E-04
221203_s_at	NM_018023	YEATS domain containing 2	YEATS2	6.8E-08	2.2	1.1E-08

212710_at	AL043774	calmodulin regulated spectrin-associated protein 1	CAMSAP1	2.0E-05	2.2	8.7E-04
208838_at	AB020636	---	---	1.4E-04	2.2	5.7E-06
218724_s_at	NM_021809	TGFB-induced factor 2 (TALE family homeobox)	TGIF2	3.2E-04	2.2	7.7E-05
206554_x_at	NM_006515	SET domain and mariner transposase fusion gene	SETMAR	6.6E-04	2.2	1.7E-04
202540_s_at	NM_000859	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	HMGCR	4.0E-05	2.2	4.6E-05
204060_s_at	NM_005044	protein kinase, X-linked /// protein kinase, Y-linked	PRKX /// PRKY	6.8E-05	2.2	4.9E-05
203859_s_at	NM_002579	paralemmin	PALM	2.4E-05	2.1	7.1E-04
209431_s_at	AF254083	POZ (BTB) and AT hook containing zinc finger 1	PATZ1	5.4E-06	2.1	4.5E-04
212704_at	AI049962	zinc finger, CCHC domain containing 11	ZCCHC11	5.6E-06	2.1	5.2E-05
207401_at	NM_002763	prospero-related homeobox 1	PROX1	3.7E-04	2.1	5.1E-04
204557_s_at	NM_014934	DAZ interacting protein 1	DZIP1	6.7E-04	2.1	6.8E-06
212753_at	AI692203	polycomb group ring finger 3	PCGF3	8.9E-08	2.1	1.9E-04
201051_at	BE560202	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	ANP32A	5.9E-05	2.1	5.0E-04
212693_at	BE670928	MDN1, midasin homolog (yeast)	MDN1	2.3E-04	2.1	9.3E-04
201741_x_at	M69040	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	SFRS1	2.4E-07	2.1	7.8E-05
208644_at	M32721	poly (ADP-ribose) polymerase family, member 1	PARP1	2.0E-05	2.0	1.3E-04
218306_s_at	NM_003922	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	HERC1	1.2E-05	2.0	1.0E-04
213743_at	BE674119	cyclin T2	CCNT2	8.7E-07	2.0	4.2E-04
208073_x_at	NM_003316	tetratricopeptide repeat domain 3	TTC3	1.6E-06	2.0	9.5E-04
209043_at	AF033026	3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1	6.6E-06	2.0	3.4E-05

209715_at	L07515	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	CBX5	9.9E-05	2.0	3.1E-05
Genes higher expressed in the group of resistant cell lines						
209016_s_at	BC002700	keratin 7	KRT7	8.9E-05	-81.0	3.5E-06
222108_at	AC004010	adhesion molecule with Ig-like domain 2	AMIGO2	1.0E-06	-46.4	1.6E-05
209008_x_at	U76549	keratin 8 /// keratin 8	KRT8	1.1E-05	-45.6	2.5E-04
202858_at	NM_006758	U2 small nuclear RNA auxiliary factor 1	U2AF1	1.3E-08	-42.3	4.4E-06
204070_at	NM_004585	retinoic acid receptor responder (tazarotene induced) 3	RARRES3	4.1E-04	-40.9	3.0E-05
201324_at	NM_001423	epithelial membrane protein 1	EMP1	6.9E-12	-40.0	3.4E-06
211506_s_at	AF043337	interleukin 8	IL8	1.7E-06	-39.6	3.5E-05
209835_x_at	BC004372	CD44 molecule (Indian blood group)	CD44	2.5E-11	-38.7	3.3E-06
201858_s_at	J03223	proteoglycan 1, secretory granule	PRG1	7.6E-07	-37.9	1.5E-04
202638_s_at	NM_000201	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	ICAM1	1.8E-04	-34.2	2.6E-04
201596_x_at	NM_000224	keratin 18	KRT18	2.3E-07	-33.3	2.0E-05
204855_at	NM_002639	serpin peptidase inhibitor, clade B (ovalbumin), member 5	SERPINB5	9.3E-04	-30.4	5.9E-05
217901_at	BF031829	Desmoglein 2	DSG2	8.6E-05	-30.2	7.5E-04
205083_at	NM_001159	aldehyde oxidase 1	AOX1	7.5E-07	-28.3	3.1E-05
202855_s_at	AL513917	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	SLC16A3	6.4E-08	-25.5	3.1E-06
215034_s_at	A1189753	transmembrane 4 L six family member 1	TM4SF1	2.5E-06	-25.1	1.1E-04
221530_s_at	BE857425	basic helix-loop-helix domain containing, class B, 3	BHLHB3	1.1E-06	-24.5	3.6E-07
202854_at	NM_000194	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	HPRT1	2.6E-08	-24.1	3.5E-06
201798_s_at	NM_013451	fer-1-like 3, myoferlin (C. elegans)	FER1L3	2.4E-10	-23.5	2.5E-06
209803_s_at	AF001294	pleckstrin homology-like domain, family A, member 2	PHLDA2	2.2E-11	-23.2	3.3E-06
210916_s_at	AF098641	CD44 molecule (Indian blood group) /// mitogen-activated protein kinase 10	CD44 /// MAPK10	5.1E-11	-21.7	1.1E-05

203108_at	NM_003979	G protein-coupled receptor, family C, group 5, member A	GPRC5A	5.8E-09	-20.7	1.3E-05
204420_at	BG251266	FOS-like antigen 1	FOSL1	6.7E-09	-20.5	4.7E-05
206632_s_at	NM_004900	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	APOBEC3B	3.2E-09	-20.3	1.5E-05
212444_at	AA156240	CDNA clone IMAGE:6025865	---	1.2E-07	-18.4	1.0E-04
204470_at	NM_001511	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	CXCL1	1.1E-04	-17.7	2.8E-05
201109_s_at	AV726673	thrombospondin 1	THBS1	4.0E-04	-17.5	9.9E-04
205627_at	NM_001785	cytidine deaminase	CDA	5.9E-05	-17.5	5.4E-05
209278_s_at	L27624	tissue factor pathway inhibitor 2	TFPI2	3.3E-04	-15.7	4.7E-04
208747_s_at	M18767	complement component 1, s subcomponent	C1S	1.5E-04	-15.3	8.1E-04
201842_s_at	A1826799	EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	8.3E-04	-14.0	8.7E-04
210592_s_at	M55580	spermidine/spermine N1-acetyltransferase 1	SAT1	1.2E-08	-13.9	6.3E-06
204222_s_at	NM_006851	GLI pathogenesis-related 1 (glioma)	GLIPR1	2.6E-05	-13.8	5.6E-04
202627_s_at	AL574210	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	SERPINE1	1.6E-04	-13.2	6.7E-04
203851_at	NM_002178	insulin-like growth factor binding protein 6	IGFBP6	1.8E-06	-13.2	3.0E-04
208949_s_at	BC001120	lectin, galactoside-binding, soluble, 3 (galectin 3)	LGALS3	2.3E-04	-13.1	6.4E-04
210042_s_at	AF073890	cathepsin Z	CTSZ	3.0E-07	-12.9	2.1E-05
206513_at	NM_004833	absent in melanoma 2	AIM2	1.1E-04	-12.6	1.9E-04
202202_s_at	NM_002290	laminin, alpha 4	LAMA4	2.5E-05	-12.2	8.0E-04
204363_at	NM_001993	coagulation factor III (thromboplastin, tissue factor)	F3	3.0E-04	-11.9	5.4E-04
202832_at	NM_014635	GRIP and coiled-coil domain containing 2	GCC2	6.1E-04	-11.9	5.5E-05

202267_at	NM_005562	laminin, gamma 2	LAMC2	3.7E-04	-11.7	1.6E-04
219759_at	NM_022350	leukocyte-derived arginine aminopeptidase	LRAP	1.2E-06	-11.6	1.5E-05
217744_s_at	NM_022121	PERP, TP53 apoptosis effector	PERP	1.0E-06	-11.4	4.0E-05
204279_at	NM_002800	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	PSMB9	1.3E-05	-11.2	8.0E-06
201474_s_at	NM_002204	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	ITGA3	2.2E-08	-11.1	3.3E-07
201468_s_at	NM_000903	NAD(P)H dehydrogenase, quinone 1	NQO1	3.8E-05	-10.8	2.4E-05
205798_at	NM_002185	interleukin 7 receptor /// interleukin 7 receptor	IL7R	3.2E-07	-10.7	7.5E-04
221059_s_at	NM_021615	coactosin-like 1 (Dictyostelium)	COTL1	3.8E-09	-10.5	2.5E-06
218211_s_at	NM_024101	melanophilin	MLPH	6.2E-06	-10.4	6.7E-05
201042_at	AL031651	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	TGM2	1.4E-04	-10.1	6.7E-04
212473_s_at	BE965029	microtubule associated monooxygenase, calponin and LIM domain containing 2	MICAL2	1.8E-05	-10.1	9.7E-04
201631_s_at	NM_003897	immediate early response 3	IER3	1.9E-06	-9.3	4.3E-05
210896_s_at	AF306765	aspartate beta-hydroxylase	ASPH	9.8E-08	-9.2	1.4E-04
208581_x_at	NM_005952	metallothionein 1X	MT1X	3.8E-06	-8.9	1.9E-04
214446_at	NM_012081	elongation factor, RNA polymerase II, 2	ELL2	4.9E-10	-8.7	3.2E-05
201170_s_at	NM_003670	basic helix-loop-helix domain containing, class B, 2	BHLHB2	2.5E-07	-8.5	3.5E-06
202862_at	NM_000137	fumarylacetoacetate hydrolase (fumarylacetoacetase)	FAH	4.0E-07	-8.5	1.6E-05
203234_at	NM_003364	uridine phosphorylase 1	UPP1	1.7E-06	-8.5	2.2E-05
218322_s_at	NM_016234	acyl-CoA synthetase long-chain family member 5	ACSL5	9.4E-05	-8.3	1.9E-06
206461_x_at	NM_005951	metallothionein 1H	MT1H	1.1E-06	-8.2	8.6E-05
212185_x_at	NM_005953	metallothionein 2A	MT2A	1.4E-06	-8.1	1.9E-04

208790_s_at	AF312393	polymerase I and transcript release factor	PTRF	3.4E-05	-7.8	8.7E-04
36711_at	AL021977	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	MAFF	7.4E-09	-7.7	9.7E-07
218084_x_at	NM_014164	FXYD domain containing ion transport regulator 5	FXYD5	5.2E-06	-7.6	5.1E-06
217996_at	AA576961	pleckstrin homology-like domain, family A, member 1	PHLDA1	3.8E-07	-7.5	2.5E-04
211456_x_at	AF333388	metallothionein 1H-like protein	LOC645745	1.3E-06	-7.4	1.1E-04
213865_at	AI378788	discoidin, CUB and LCCL domain containing 2	DCBLD2	2.3E-07	-7.4	5.7E-04
209514_s_at	BE502030	RAB27A, member RAS oncogene family	RAB27A	2.3E-05	-7.3	3.2E-04
209310_s_at	U25804	caspase 4, apoptosis-related cysteine peptidase	CASP4	1.4E-05	-7.1	1.3E-04
209040_s_at	U17496	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	PSMB8	1.8E-05	-7.1	6.9E-06
205100_at	NM_005110	glutamine-fructose-6-phosphate transaminase 2	GFPT2	3.3E-06	-7.1	2.1E-04
213572_s_at	AI554300	serpin peptidase inhibitor, clade B (ovalbumin), member 1	SERPINB1	1.4E-07	-7.0	1.4E-07
209679_s_at	BC003379	small trans-membrane and glycosylated protein	LOC57228	2.4E-06	-7.0	1.1E-04
203821_at	NM_001945	heparin-binding EGF-like growth factor	HBEGF	3.8E-05	-6.9	9.8E-05
220016_at	NM_024060	AHNAK nucleoprotein (desmoyokin)	AHNAK	5.1E-05	-6.9	2.4E-05
212070_at	AL554008	G protein-coupled receptor 56	GPR56	6.1E-05	-6.8	1.6E-07
211429_s_at	AF119873	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	SERPINA1	5.0E-04	-6.8	5.1E-05
202863_at	NM_003113	SP100 nuclear antigen	SP100	1.7E-07	-6.7	1.4E-05
216336_x_at	AL031602	metallothionein 1M	MT1M	5.3E-06	-6.6	1.3E-05
217165_x_at	M10943	metallothionein 1F (functional)	MT1F	5.6E-06	-6.6	1.9E-04

201983_s at	AW157070	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	EGFR	1.6E-06	-6.5	2.8E-04
210538_s at	U37546	baculoviral IAP repeat-containing 3	BIRC3	1.6E-04	-6.5	5.4E-05
201926_s at	BC001288	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	CD55	3.6E-06	-6.5	3.4E-04
208944_at	D50683	transforming growth factor, beta receptor II (70/80kDa)	TGFB2	1.2E-06	-6.5	9.7E-04
208690_s at	BC000915	PDZ and LIM domain 1 (elfin)	PDLIM1	1.6E-04	-6.4	5.6E-05
210117_at	AF311312	sperm associated antigen 1	SPAG1	3.6E-05	-6.4	4.2E-04
210138_at	AF074979	regulator of G-protein signalling 20	RGS20	5.9E-06	-6.3	1.4E-05
217478_s at	X76775	major histocompatibility complex, class II, DM alpha	HLA-DMA	2.9E-04	-6.2	1.3E-04
202499_s at	NM_006931	solute carrier family 2 (facilitated glucose transporter), member 3	SLC2A3	1.1E-06	-6.2	2.0E-04
214791_at	AK023116	hypothetical protein BC004921	LOC93349	1.1E-06	-6.1	2.6E-06
209457_at	U16996	dual specificity phosphatase 5	DUSP5	1.5E-05	-6.1	1.7E-04
207574_s at	NM_015675	growth arrest and DNA-damage-inducible, beta	GADD45B	1.2E-06	-6.0	1.6E-04
214866_at	X74039	plasminogen activator, urokinase receptor	PLAUR	8.1E-07	-5.8	3.8E-04
211612_s at	U62858	interleukin 13 receptor, alpha 1 /// interleukin 13 receptor, alpha 1	IL13RA1	1.5E-07	-5.7	1.1E-05
207265_s at	NM_016657	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	KDELR3	1.4E-07	-5.6	5.0E-04
213274_s at	AA020826	cathepsin B	CTSB	6.6E-05	-5.6	2.2E-04
200632_s at	NM_006096	N-myc downstream regulated gene 1	NDRG1	5.2E-05	-5.5	2.1E-04
222150_s at	AK026747	hypothetical protein LOC54103	LOC54103	8.8E-07	-5.5	1.1E-06
210136_at	AW070431	myelin basic protein	MBP	1.8E-06	-5.4	5.9E-04
216985_s at	AJ002077	syntaxin 3	STX3	1.7E-06	-5.4	3.5E-06
201412_at	NM_014045	low density lipoprotein receptor-related protein 10	LRP10	3.9E-06	-5.3	1.2E-04

205579_at	NM_000861	histamine receptor H1	HRH1	1.0E-06	-5.3	9.3E-06
202733_at	NM_004199	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II	P4HA2	5.2E-04	-5.3	3.8E-04
210987_x_at	M19267	tropomyosin 1 (alpha)	TPM1	1.7E-04	-5.2	3.2E-04
204032_at	NM_003567	breast cancer anti-estrogen resistance 3	BCAR3	2.8E-06	-5.1	7.4E-04
209706_at	AF247704	NK3 transcription factor related, locus 1 (Drosophila)	NKX3-1	2.0E-05	-5.1	2.3E-05
205499_at	NM_014467	sushi-repeat-containing protein, X-linked 2	SRPX2	6.7E-06	-5.0	1.2E-05
202085_at	NM_004817	tight junction protein 2 (zona occludens 2)	TJP2	9.4E-04	-4.9	5.0E-04
219620_x_at	NM_017723	hypothetical protein FLJ20245	FLJ20245	7.0E-07	-4.9	2.3E-04
212923_s_at	AK024828	chromosome 6 open reading frame 145	C6orf145	2.4E-08	-4.9	6.1E-05
212463_at	BE379006	CD59 molecule, complement regulatory protein	CD59	1.8E-07	-4.8	2.4E-04
201506_at	NM_000358	transforming growth factor, beta-induced, 68kDa	TGFBI	1.9E-04	-4.8	6.6E-04
202180_s_at	NM_017458	major vault protein	MVP	6.1E-05	-4.7	9.6E-05
203726_s_at	NM_000227	laminin, alpha 3	LAMA3	9.8E-04	-4.6	6.6E-04
212543_at	U83115	absent in melanoma 1	AIM1	4.0E-04	-4.6	1.4E-04
205266_at	NM_002309	leukemia inhibitory factor (cholinergic differentiation factor)	LIF	2.5E-07	-4.6	3.7E-06
203939_at	NM_002526	5'-nucleotidase, ecto (CD73)	NT5E	8.0E-04	-4.6	6.7E-04
222294_s_at	AW971415	CDNA clone IMAGE:5745639	---	4.1E-05	-4.6	1.2E-04
206034_at	NM_002640	serpin peptidase inhibitor, clade B (ovalbumin), member 8	SERPINB8	5.9E-06	-4.6	5.9E-04
214459_x_at	M12679	major histocompatibility complex, class I, C	HLA-C	9.7E-04	-4.6	1.3E-04
202990_at	NM_002863	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	PYGL	1.5E-05	-4.6	8.0E-04

205896_at	NM_003059	solute carrier family 22 (organic cation transporter), member 4	SLC22A4	2.3E-05	-4.5	1.8E-04
203041_s_at	J04183	lysosomal-associated membrane protein 2	LAMP2	1.2E-04	-4.5	2.7E-05
201471_s_at	NM_003900	sequestosome 1	SQSTM1	3.9E-06	-4.5	2.0E-04
218631_at	NM_021732	arginine vasopressin-induced 1	AVPI1	2.9E-05	-4.5	3.1E-05
204981_at	NM_002555	solute carrier family 22 (organic cation transporter), member 18	SLC22A18	6.9E-06	-4.5	1.1E-04
203005_at	NM_002342	lymphotoxin beta receptor (TNFR superfamily, member 3)	LTBR	2.5E-07	-4.5	2.8E-07
200766_at	NM_001909	cathepsin D	CTSD	3.4E-05	-4.4	9.5E-06
204745_x_at	NM_005950	metallothionein 1G	MT1G	4.0E-06	-4.4	2.8E-04
219165_at	NM_021630	PDZ and LIM domain 2 (mystique)	PDLIM2	9.2E-06	-4.3	9.7E-04
201482_at	NM_002826	quiescin Q6	QSCN6	1.7E-05	-4.3	6.1E-05
218368_s_at	NM_016639	tumor necrosis factor receptor superfamily, member 12A	TNFRSF12A	7.6E-07	-4.2	6.7E-05
209873_s_at	AF053719	plakophilin 3	PKP3	3.2E-04	-4.2	7.3E-05
204254_s_at	NM_000376	vitamin D (1,25-dihydroxyvitamin D3) receptor	VDR	3.1E-05	-4.2	5.6E-06
203430_at	NM_014320	heme binding protein 2	HEBP2	4.5E-05	-4.2	9.1E-05
202531_at	NM_002198	interferon regulatory factor 1	IRF1	4.4E-05	-4.1	3.0E-05
205398_s_at	NM_005902	SMAD family member 3	SMAD3	4.4E-06	-4.1	7.5E-04
203518_at	NM_000081	lysosomal trafficking regulator	LYST	5.2E-04	-4.1	2.4E-04
218273_s_at	NM_018444	protein phosphatase 2C, magnesium-dependent, catalytic subunit	PPM2C	8.3E-08	-4.0	2.1E-04
202087_s_at	NM_001912	cathepsin L	CTSL	9.0E-05	-4.0	1.6E-04
218764_at	NM_024064	protein kinase C, eta	PRKCH	7.8E-05	-3.9	1.2E-05
201422_at	NM_006332	interferon, gamma-inducible protein 30	IFI30	7.7E-04	-3.9	2.7E-04
212196_at	AW242916	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	IL6ST	4.5E-05	-3.9	8.0E-04
202201_at	NM_000713	biliverdin reductase B (flavin reductase (NADPH))	BLVRB	3.3E-05	-3.8	4.3E-06

209417_s_at	BC001356	interferon-induced protein 35	IFI35	6.6E-05	-3.8	2.9E-04
203329_at	NM_002845	protein tyrosine phosphatase, receptor type, M	PTPRM	3.9E-06	-3.8	5.8E-05
200701_at	NM_006432	Niemann-Pick disease, type C2	NPC2	1.2E-04	-3.7	8.2E-04
219622_at	NM_017817	RAB20, member RAS oncogene family	RAB20	8.5E-04	-3.7	8.7E-04
207467_x_at	NM_001750	calpastatin	CAST	6.6E-06	-3.6	4.1E-04
205640_at	NM_000694	aldehyde dehydrogenase 3 family, member B1	ALDH3B1	7.4E-07	-3.6	1.5E-07
203215_s_at	AA877789	myosin VI	MYO6	9.1E-04	-3.5	4.0E-05
217998_at	NM_007350	pleckstrin homology-like domain, family A, member 1 /// hypothetical LOC652993	PHLDA1 /// LOC652993	4.5E-07	-3.4	2.1E-04
204158_s_at	NM_006019	T-cell, immune regulator 1, ATPase, H ⁺ transporting, lysosomal V0 subunit A3	TCIRG1	5.4E-05	-3.4	7.5E-04
208637_x_at	BC003576	actinin, alpha 1	ACTN1	1.2E-07	-3.4	4.4E-05
218844_at	NM_025149	hypothetical protein FLJ20920	FLJ20920	1.5E-04	-3.4	8.3E-05
219716_at	NM_030641	apolipoprotein L, 6	APOL6	1.4E-05	-3.4	2.2E-08
204747_at	NM_001549	interferon-induced protein with tetratricopeptide repeats 3	IFIT3	1.7E-06	-3.4	4.2E-04
202693_s_at	AW194730	serine/threonine kinase 17a (apoptosis-inducing)	STK17A	1.6E-04	-3.3	6.4E-04
210276_s_at	AF281030	TRIO and F-actin binding protein	TRIOBP	2.5E-04	-3.3	3.4E-04
205730_s_at	NM_014945	actin binding LIM protein family, member 3	ABLIM3	3.2E-05	-3.3	1.2E-04
202861_at	NM_002616	period homolog 1 (Drosophila)	PER1	4.8E-05	-3.3	5.6E-05
217739_s_at	NM_005746	pre-B-cell colony enhancing factor 1	PBEF1	7.8E-06	-3.3	1.4E-04
221044_s_at	NM_021616	tripartite motif-containing 34 /// tripartite motif-containing 6 and tripartite motif-containing 34	TRIM34 /// TRIM6-TRIM34	4.7E-06	-3.3	3.1E-04
207375_s_at	NM_002189	interleukin 15 receptor, alpha	IL15RA	1.1E-05	-3.3	1.3E-04
213816_s_at	AA005141	met proto-oncogene (hepatocyte growth factor receptor)	MET	1.8E-06	-3.2	9.9E-04
221843_s_at	AA195017	KIAA1609	KIAA1609	4.6E-05	-3.2	3.4E-05

218983_at	NM_016546	complement component 1, r subcomponent-like	C1RL	3.6E-04	-3.2	3.1E-04
207357_s_at	NM_017540	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	GALNT10	3.9E-06	-3.2	7.3E-05
218292_s_at	NM_016203	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	PRKAG2	1.2E-06	-3.2	1.4E-04
207643_s_at	NM_001065	tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A	1.5E-05	-3.2	2.6E-04
204629_at	NM_013327	parvin, beta	PARVB	1.1E-04	-3.1	7.5E-04
212552_at	BE617588	hippocalcin-like 1	HPCAL1	1.5E-04	-3.1	3.1E-04
204682_at	NM_000428	latent transforming growth factor beta binding protein 2	LTBP2	1.1E-05	-3.1	4.0E-06
219691_at	NM_017654	sterile alpha motif domain containing 9	SAMD9	6.1E-05	-3.1	3.5E-05
200885_at	NM_005167	ras homolog gene family, member C	RHOC	1.6E-06	-3.1	2.0E-04
212737_at	AL513583	GM2 ganglioside activator	GM2A	1.7E-05	-3.0	7.2E-06
210514_x_at	AF226990	HLA-G histocompatibility antigen, class I, G	HLA-G	7.8E-04	-3.0	7.4E-04
201944_at	NM_000521	hexosaminidase B (beta polypeptide)	HEXB	9.4E-07	-2.9	4.2E-04
218849_s_at	NM_006663	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	PPP1R13L	4.5E-05	-2.9	2.4E-04
204693_at	NM_007061	CDC42 effector protein (Rho GTPase binding) 1	CDC42EP1	5.0E-05	-2.9	2.8E-04
209546_s_at	AF323540	apolipoprotein L, 1	APOL1	3.7E-06	-2.9	1.2E-05
204034_at	NM_014297	ethylmalonic encephalopathy 1	ETHE1	3.8E-06	-2.9	4.2E-05
202307_s_at	NM_000593	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	TAP1	3.3E-04	-2.9	2.4E-04
210978_s_at	BC002616	transgelin 2	TAGLN2	2.5E-04	-2.9	8.6E-05
202275_at	NM_000402	glucose-6-phosphate dehydrogenase	G6PD	3.7E-04	-2.9	3.0E-04
217150_s_at	S73854	neurofibromin 2 (bilateral acoustic neuroma)	NF2	3.3E-05	-2.9	1.2E-04
202545_at	NM_006254	protein kinase C, delta	PRKCD	1.5E-05	-2.9	7.9E-04

214783_s_at	BG177920	annexin A11	ANXA11	7.0E-07	-2.8	6.2E-05
214077_x_at	H15129	Meis1 homolog 3 (mouse) pseudogene 1	MEIS3P1	7.1E-04	-2.8	9.5E-04
213083_at	AJ005866	solute carrier family 35, member D2	SLC35D2	4.3E-04	-2.8	4.9E-04
220049_s_at	NM_025239	programmed cell death 1 ligand 2	PDCD1LG2	2.7E-04	-2.8	3.1E-05
211926_s_at	AI827941	myosin, heavy chain 9, non-muscle	MYH9	1.6E-05	-2.8	6.2E-04
221291_at	NM_025217	UL16 binding protein 2	ULBP2	1.6E-04	-2.8	2.4E-04
208613_s_at	AV712733	filamin B, beta (actin binding protein 278)	FLNB	5.2E-04	-2.7	6.0E-04
218747_s_at	NM_018009	TAP binding protein-like	TAPBPL	3.6E-04	-2.7	7.4E-05
219684_at	NM_022147	receptor (chemosensory) transporter protein 4	RTP4	1.4E-04	-2.7	8.0E-04
206284_x_at	NM_001834	clathrin, light chain (Lcb)	CLTB	2.0E-04	-2.6	1.5E-06
201847_at	NM_000235	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	LIPA	3.7E-05	-2.6	9.1E-04
205192_at	NM_003954	mitogen-activated protein kinase kinase kinase 14	MAP3K14	3.4E-05	-2.6	2.4E-04
221473_x_at	U49188	serine incorporator 3	SERINC3	1.5E-07	-2.6	6.7E-05
218194_at	NM_015523	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	REXO2	8.9E-06	-2.6	6.6E-04
205084_at	NM_018844	B-cell receptor-associated protein 29	BCAP29	2.8E-06	-2.6	4.9E-04
202996_at	NM_021173	polymerase (DNA-directed), delta 4	POLD4	6.3E-05	-2.6	5.3E-04
208872_s_at	AA814140	receptor accessory protein 5	REEP5	4.6E-05	-2.6	2.8E-04
60471_at	AA625133	Ras and Rab interactor 3	RIN3	1.5E-05	-2.6	6.8E-05
203925_at	NM_002061	glutamate-cysteine ligase, modifier subunit	GCLM	6.8E-05	-2.5	5.9E-06
201587_s_at	NM_001569	interleukin-1 receptor-associated kinase 1	IRAK1	1.1E-05	-2.5	8.4E-05
204769_s_at	M74447	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	TAP2	9.5E-06	-2.5	9.6E-06
201953_at	NM_006384	calcium and integrin binding 1 (calmyrin)	CIB1	2.1E-06	-2.5	5.0E-04

215723_s_at	AJ276230	phospholipase D1, phosphatidylcholine-specific	PLD1	8.6E-06	-2.5	4.7E-05
205032_at	NM_002203	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	ITGA2	6.5E-04	-2.5	7.1E-04
203045_at	NM_004148	ninjurin 1	NINJ1	2.9E-05	-2.5	4.0E-04
221641_s_at	AF241787	acyl-CoA thioesterase 9	ACOT9	8.9E-05	-2.5	5.5E-04
209039_x_at	AF001434	EH-domain containing 1	EHD1	5.2E-05	-2.5	8.8E-04
209179_s_at	BC003164	leukocyte receptor cluster (LRC) member 4	LENG4	3.1E-06	-2.4	1.5E-04
206670_s_at	NM_013445	glutamate decarboxylase 1 (brain, 67kDa) /// LAG1 homolog, ceramide synthase 6 (S. cerevisiae)	GAD1 /// LASS6	2.9E-04	-2.4	8.0E-04
201360_at	NM_000099	cystatin C (amyloid angiopathy and cerebral hemorrhage)	CST3	5.6E-05	-2.4	7.7E-04
53720_at	AI862559	hypothetical protein FLJ11286	FLJ11286	3.2E-04	-2.4	4.4E-04
201975_at	NM_002956	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	RSN	1.4E-04	-2.4	3.7E-04
200618_at	NM_006148	LIM and SH3 protein 1	LASP1	3.8E-05	-2.4	8.0E-04
209575_at	BC001903	interleukin 10 receptor, beta	IL10RB	4.2E-04	-2.3	9.6E-06
220761_s_at	NM_016281	TAO kinase 3	TAOK3	3.7E-04	-2.3	5.2E-06
208659_at	AF034607	chloride intracellular channel 1	CLIC1	1.9E-08	-2.3	4.1E-05
213272_s_at	AF070596	transmembrane protein 159	TMEM159	2.0E-05	-2.3	1.1E-04
219710_at	NM_024577	SH3 domain and tetratricopeptide repeats 2	SH3TC2	3.3E-04	-2.3	5.1E-05
203258_at	NM_006442	DR1-associated protein 1 (negative cofactor 2 alpha)	DRAP1	1.9E-05	-2.3	5.7E-04
221534_at	AF073483	chromosome 11 open reading frame 68	C11orf68	2.1E-04	-2.3	1.5E-04
202122_s_at	NM_005817	mannose-6-phosphate receptor binding protein 1	M6PRBP1	6.5E-07	-2.3	4.4E-04
202205_at	NM_003370	vasodilator-stimulated phosphoprotein	VASP	7.5E-06	-2.2	1.6E-05
203920_at	NM_005693	nuclear receptor subfamily 1, group H, member 3	NR1H3	3.6E-04	-2.2	5.5E-04

207196_s at	NM_006058	TNFAIP3 interacting protein 1	TNIP1	1.1E-05	-2.2	4.1E-04
218881_s at	NM_024530	FOS-like antigen 2	FOSL2	1.1E-07	-2.2	1.8E-06
204398_s at	NM_012155	echinoderm microtubule associated protein like 2	EML2	4.9E-05	-2.2	2.5E-06
202378_s at	NM_017526	leptin receptor overlapping transcript	LEPROT	3.7E-04	-2.2	1.3E-04
219332_at	NM_024723	MICAL-like 2	MICALL2	4.4E-05	-2.2	6.4E-04
203454_s at	NM_004045	ATX1 antioxidant protein 1 homolog (yeast)	ATOX1	5.9E-06	-2.2	3.0E-04
208757_at	BC001123	transmembrane emp24 protein transport domain containing 9	TMED9	7.9E-07	-2.2	8.7E-05
209584_x at	AF165520	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	APOBEC3C	4.1E-05	-2.2	2.0E-04
220174_at	NM_025061	leucine rich repeat containing 8 family, member E	LRRC8E	9.7E-05	-2.2	6.2E-04
200709_at	NM_000801	FK506 binding protein 1A, 12kDa	FKBP1A	2.7E-06	-2.2	5.8E-05
215037_s at	U72398	BCL2-like 1	BCL2L1	5.9E-04	-2.2	4.3E-04
221926_s at	BF196320	interleukin 17 receptor C	IL17RC	2.2E-06	-2.2	5.7E-06
203279_at	NM_014674	ER degradation enhancer, mannosidase alpha-like 1	EDEM1	8.4E-06	-2.2	5.7E-04
218109_s at	NM_022736	major facilitator superfamily domain containing 1	MFSD1	1.7E-04	-2.2	1.5E-04
221561_at	L21934	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	SOAT1	5.8E-05	-2.2	8.8E-04
214703_s at	AW954107	mannosidase, alpha, class 2B, member 2	MAN2B2	2.4E-04	-2.1	9.9E-04
202377_at	AW026535	---	---	1.5E-04	-2.1	7.5E-05
202908_at	NM_006005	Wolfram syndrome 1 (wolframin)	WFS1	7.7E-05	-2.1	5.1E-04
40420_at	AB015718	serine/threonine kinase 10	STK10	1.6E-07	-2.1	1.1E-04
209940_at	AF083068	poly (ADP-ribose) polymerase family, member 3	PARP3	7.4E-06	-2.1	1.7E-04
208701_at	BC000373	Amyloid beta (A4) precursor-like protein 2	APLP2	1.2E-04	-2.1	8.5E-05

218065_s_at	NM_020644	TMEM9 domain family, member B	TMEM9B	6.5E-06	-2.1	1.3E-04
204458_at	AL110209	lysophospholipase 3 (lysosomal phospholipase A2)	LYPLA3	8.0E-05	-2.1	5.9E-04
218749_s_at	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	SLC24A6	2.0E-07	-2.1	2.1E-05
220189_s_at	NM_014275	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	MGAT4B	7.0E-05	-2.1	1.4E-04
218498_s_at	NM_014584	ERO1-like (<i>S. cerevisiae</i>)	ERO1L	1.5E-06	-2.1	8.2E-05
201022_s_at	NM_006870	destrin (actin depolymerizing factor)	DSTN	5.2E-06	-2.1	3.3E-06
208407_s_at	NM_001331	catenin (cadherin-associated protein), delta 1	CTNND1	4.0E-04	-2.1	7.8E-04
336_at	D38081	thromboxane A2 receptor	TBXA2R	4.7E-04	-2.0	8.4E-05
221087_s_at	NM_014349	apolipoprotein L, 3	APOL3	1.5E-04	-2.0	2.1E-05
218154_at	NM_024736	gasdermin domain containing 1	GSDMDC1	9.5E-06	-2.0	1.3E-04

1. Fold difference in gene expression level at baseline between the 16 sensitive cell lines and the 12 resistant cell lines as determined by IC₅₀ with the cut off 0.3 μM. The cell lines with IC₅₀ below 0.3 μM are defined as sensitive whereas the cell lines with IC₅₀ above 0.3 μM are defined as resistant to the IGF-1R inhibitor BMS-536924.
2. Pearson correlations between the expression level of each gene and the log₂(IC₅₀) data in the 28 cell lines

Supplemental Table 2: The proteins correlated with the sensitivity of 26 sarcoma cell lines to IGF1R inhibitor BMS-536924 as identified by LC/MS based “label free” protein profiling. The peptide ions were selected by the overlaps between the two statistic analyses: t-test ($p < 0.001$ between 14 sensitive cell lines and 12 resistant cell lines) and the Pearson correlations between the log₂ (IC₅₀) data and the expression level of each peptide ion in the 26 cell lines ($p < 0.001$). The peptide ions generated from statistical analyses were sequenced by tandem mass spectrometry to get the identification of the proteins which are listed in this Table. The name of protein and gene, the sequence of each peptide ion associated with identified protein, the p values and fold change between the sensitive and resistant cell line groups for each peptide ion are listed. The positive fold changes indicate the peptide ions having higher expression level in the sensitive cell lines and the negative fold changes indicate the peptide ions having higher expression level in the resistant cell lines. The overlap with Affymetrix gene expression results (Supplemental Table 1) is also indicated.

Protein name	Swiss-protein ID	Gene name	Identified by microarray ¹	Peptide sequence	p-value in t-test	Fold change (S/R) ²	p-value (correlation) ³
Creatine Kinase, brain		CKB	Yes	FCTGLTQIETLFK	5.36E-11	12.6	2.62E-06
				KENPLQFKFR	3.92E-05	12.0	2.84E-04
thymoprotein		TMPO		YGVNPGPIVGTTR	1.22E-04	4.0	9.62E-07
Stathmin	P16949	STMN1	Yes	DLSLEEIQK	4.40E-08	3.9	2.13E-09
heterogeneous nuclear ribonucleoprotein A1	P09651	HNRPA1	Yes	NQGGYGGSSSSSSYGSGR	8.49E-07	3.7	1.97E-09
				YQLLQLVEPFGVISNHLILNK	3.17E-05	3.7	2.95E-07
high mobility protein 2	P26583	HMGB2	Yes	LGEMWSEQSAK	2.83E-04	3.5	9.73E-05
Radixin	P35241	RDX		KALELDQER	4.10E-05	3.4	2.25E-05
high mobility protein 1		HMGB1		KHPDASVNFSEFSK	2.48E-04	3.4	5.48E-06
				DLSAAGIGLLAAATQSLSPASLGR	6.06E-05	3.2	7.10E-06
matrin 3		MATR3	Yes	MKSQAFIEMETR	6.29E-05	3.1	1.56E-07
				MSSYAFFVQTCR	2.38E-04	3.0	7.44E-04
				EDSQRPGAHLTVK	4.38E-04	2.9	3.83E-06
				HVNPVQALSEFK	5.47E-05	2.8	6.60E-06
				AAMRETWLSNQQR	7.89E-04	2.8	1.09E-05

spectrin, beta		SPTBN2		ALAVEGK	1.70E-04	2.7	7.41E-04
				YANVIAYDHSR	2.12E-05	2.7	4.50E-07
lactate dehydrogenase		LDHB		IVVVTAGVR	3.87E-04	2.7	9.45E-05
				ESYSVYVYK	7.20E-07	2.7	2.18E-04
				TSPVEGLSGNPADLEK	7.54E-04	2.6	4.78E-07
Plasma membrane calcium-transporting ATPase 4	P23634	ATP2B4		SMSTVIRNPNGGFR	2.00E-04	2.6	9.64E-06
catenin		CTNNA1	Yes	TLAVER	1.10E-04	2.3	8.49E-04
poly rC binding protein		PCBP2	Yes	IITLTGPTNAIFK	5.71E-05	2.2	5.00E-07
				DAVYTEHAK	3.31E-04	2.2	3.69E-04
				PADGILIQNDLK	2.45E-04	2.2	9.34E-04
histone 3		H3F3B	Yes	EIAQDFK	5.14E-05	2.2	4.54E-04
protein tyrosine phosphatase, receptor type, F		PTPRF		TFALHK	9.87E-04	2.1	5.40E-04
KH domain containing, RNA binding, signal transduction associated 1	Q07666	KHDRBS1	Yes	DSLDPSTHAMQLLTAEIEK	8.62E-04	2.1	2.35E-04
heterogeneous nuclear ribonucleoprotein M		HRNPM	Yes	AFITNIPFDVK	6.65E-04	2.1	4.00E-05
histone 3		HIST3H3	Yes	YRPGTVALR	6.96E-05	2.0	2.70E-04
heterogeneous nuclear ribonucleoprotein D	Q14103	HNRPD	Yes	IFVGGLSPDTPEEK	6.39E-06	1.9	5.09E-05
				MFIGGLSWDTTK	1.25E-04	1.9	5.40E-04
tublin, alpha		NP_006073		FDLMYAK	1.37E-04	1.9	1.58E-04
heterogeneous nuclear ribonucleoprotein A2		HNRPA2	Yes	IDTIEIITDR	4.59E-04	1.9	2.33E-04
histone 2		H2AFY2	Yes	EIQTAVR	3.44E-05	1.9	8.41E-04
heterogeneous nuclear ribonucleoprotein	P22626	HNRPA2	Yes	GFGFVTFDDHDPVVK	8.04E-05	1.9	6.93E-05
splicing factor proline/glutamine rich		SFPQ		LFVGNLPADITEDEFKR	8.88E-04	1.9	2.85E-05
histone H2B		NP_00351	Yes	AMGIMNSFVNDIFER	1.49E-04	1.9	1.30E-04
heterogeneous nuclear ribonucleoprotein		HNRPA3	Yes	LTDCVVMR	1.98E-04	1.8	1.69E-04
				GFGFVLFK	5.18E-05	1.8	1.95E-04
histone 1		HIST1H4I		TLYGFGG	3.54E-04	1.8	2.90E-04
heat shock protein 60		CPN60		VGEVIVTK	1.41E-04	1.8	2.12E-04
cleavage and polyadenylation specific factor 1	Q10570	CPSF1	Yes	MYAVYK	1.98E-04	1.7	8.49E-04
ATP synthase, H ⁺ transporting, mitochondrial F1 complex	Q9Y653	ATP5G	Yes	TIAMDGTEGLVR	9.36E-04	1.6	1.40E-04
heterogeneous nuclear ribonucleoprotein K		HRNPK	Yes	IILDISESPIK	7.40E-04	1.6	3.85E-05
peroxiredoxin		PRDX6	Yes	LPPFIIDDR	1.72E-04	1.5	1.41E-05

				LQQELDDLLVLDLHQQR	5.51E-04	-2.3	8.39E-04
myosin light chain 6	O00159	MYL6	Yes	HVLVTLGEEK	1.47E-04	-2.3	3.82E-04
				VLDFEHFLPMLQTVAK	8.48E-07	-2.7	9.65E-04
destrin	P60981	DSTN	Yes	YALYDASFETK	5.35E-07	-2.7	2.64E-05
				IGFSGPKLEGGEVDLKGPK	5.74E-05	-2.7	1.21E-06
myosin heavy chain 9		MYH9	Yes	VVFQEFR	2.27E-04	-3.0	3.26E-04
actinin, alpha	O43707	ACTN4	Yes	DYETATLSDIK	3.05E-06	-3.0	6.40E-05
calpain		CAPN2		SMVAVMDSDTTGK	1.00E-05	-3.1	5.44E-05
				ELLTTMGDR	2.54E-04	-3.3	8.89E-04
				SNTENLSQHFR	9.37E-08	-3.6	2.76E-08
				DGFIDKEDLHDMLASLGK	5.20E-07	-3.6	1.74E-05
				EAFQLFDR	3.53E-07	-3.7	5.83E-06
				FAIQDISVEETSAAK	6.22E-05	-3.7	8.97E-08
				ISMFDIDLNLK	1.33E-06	-3.9	1.99E-04
AHNAK nucleoprotein	Q09666	AHNAK	Yes	VPGIDATTK	4.66E-06	-4.0	7.91E-04
LIM domain and actin binding	Q9UHB6	LIMA1		YPHIKDGEDLK	1.92E-05	-4.0	5.51E-05
chloride intracellular protein 1	O00299	CLIC1	Yes	GVTFNVTVDTK	1.38E-08	-4.0	4.77E-06
				GEGPEVDVNLPK	1.90E-05	-4.3	2.23E-04
filamin B		FLNB	Yes	GDYVLAVK	2.41E-06	-4.5	4.80E-06
				ISMPDFDLHLK	3.28E-05	-4.7	3.22E-04
				TINEVENQILTR	3.51E-08	-4.7	3.53E-07
actinin, alpha	P12814	ACTN1	Yes	VGWEQLLTTIAR	8.55E-10	-4.8	1.09E-06
				IAEFTTNLTETEEK	1.89E-06	-5.0	1.86E-05
				FSMPGFK	6.72E-06	-5.2	1.71E-04
myoferlin	Q9NZM1	FER1L3	Yes	VGETIIDLENR	4.52E-05	-5.3	7.00E-04
				VISGVLQLGNIVFK	3.87E-05	-5.5	3.72E-05
				LDPHLVLDQLR	5.41E-06	-5.5	1.68E-04
Syntaxin	O15400	STX7	Yes	TLNQLGTPQDSPELR	7.85E-07	-5.6	5.27E-04

1. Also identified by gene expression profiling as listed in Supplemental Table 1.
2. Fold difference in gene expression level at baseline between the 14 sensitive cell lines and the 12 resistant cell lines as determined by IC₅₀ with the cut off is 0.3 μ M. The cell lines with IC₅₀ below 0.3 μ M are defined as sensitive whereas the cell lines with IC₅₀ above 0.3 μ M are defined as resistant to the IGF-1R inhibitor BMS-536924.
3. Pearson correlations between the expression level of each gene and the log₂(IC₅₀) data in the 26 cell lines.

Supplemental Table 3: Common genes correlated with both the primary resistance and the acquired resistance to IGF-1R inhibitor BMS-536924.

Gene	Gene Symbol	Fold in primary resistant vs. sensitive ¹	Fold in acquired resistant vs. sensitive ²
calpastatin	CAST	3.6	2.5
CD44 molecule (Indian blood group)	CD44	38.7	2
CD55 molecule, decay accelerating factor for complement (Cromer blood group)	CD55	6.5	6.1
cystatin C (amyloid angiopathy and cerebral hemorrhage)	CST3	2.4	3
discoidin, CUB and LCCL domain containing 2	DCBLD2	7.4	11.3
Desmoglein 2	DSG2	30.2	13.9
ethylmalonic encephalopathy 1	ETHE1	2.9	2
FOS-like antigen 2	FOSL2	2.2	2.1
FXFD domain containing ion transport regulator 5	FXFD5	7.6	2
glutamate decarboxylase 1 (brain, 67kDa)/ LAG1 homolog, ceramide synthase 6 (S. cerevisiae)	GAD1/ LASS6	2.4	6.5
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	GALNT10	3.2	2.5
glutamine-fructose-6-phosphate transaminase 2	GFPT2	7.1	4.6
G protein-coupled receptor, family C, group 5, member A	GPRC5A	20.7	3
hippocalcin-like 1	HPCAL1	3.1	2.8
immediate early response 3	IER3	9.3	3.2
interleukin 13 receptor, alpha 1	IL13RA1	5.7	2.1
keratin 18	KRT18	33.3	2.1
lysosomal-associated membrane protein 2	LAMP2	4.5	2.3
lectin, galactoside-binding, soluble, 3 (galectin 3)	LGALS3	13.1	2.3
latent transforming growth factor beta binding protein 2	LTBP2	3.1	2.5
major vault protein	MVP	4.7	2
Niemann-Pick disease, type C2	NPC2	3.7	2

5'-nucleotidase, ecto (CD73)	NT5E	4.6	3.2
pleckstrin homology-like domain, family A, member 2	PHLDA2	23.2	2
plasminogen activator, urokinase receptor	PLAUR	5.8	2.3
regulator of G-protein signalling 20	RGS20	6.3	2
Ras and Rab interactor 3	RIN3	2.6	2.6
solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	SLC16A3	25.5	2.1
solute carrier family 22 (organic cation transporter), member 18	SLC22A18	4.5	2.8
solute carrier family 2 (facilitated glucose transporter), member 3	SLC2A3	6.2	2
SP100 nuclear antigen	SP100	6.7	2
TAO kinase 3	TAOK3	2.3	2
tissue factor pathway inhibitor 2	TFPI2	15.7	194
thrombospondin 1	THBS1	17.5	6.1
transmembrane 4 L six family member 1	TM4SF1	25.1	6.1
vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR	4.2	2.6

¹. Fold difference in gene expression level at baseline between the 12 resistant cell lines and 16 sensitive cell lines as determined by IC₅₀ with the cut off 0.35 µM.

². Fold difference in gene expression level between acquired resistant RD-1^R cells (IC₅₀=2.0µM) and the sensitive parental RD-1^S (IC₅₀=0.238µM) cells

Supplemental Table 4: Global pathway analyses. RMA normalized baseline gene expression data from 28 cell lines were first filtered (Max>5 and CV>3%) down to 17276 probe sets. The global pathway analysis was performed on the filtered data using Bioconductor's *globaltest* package (Geoman J, Oosting J. Testing association of a pathway with a clinical variable. Version 4.4.0.) against a collection of 182 KEGG pathways to compare sensitive and resistant cell lines groups and identify pathways that were different between two groups and may contribute to the sensitivity of cells to BMS-536924. For Rh41 drug treatment studies, expression datasets were first filtered to remove probe sets with Max<5, which resulted in 9269 probe sets. The *Globaltest* was also performed on expression data for the BMS-536924 treated Rh41 cells compared to that for the untreated control cells to identify pathways that were modulated by BMS-536924 treatment. The p-value, indicating the association between expression values and resistant/sensitive classifications, as well as its multiplicity-adjusted version, FWER (Holm's method), were reported for each pathway.

Pathway	Basal expression (sensitive vs. resistant)							Modulated by drug treatment (drug treated vs control)					
	# of Genes ¹	# of Genes Tested ²	Statistic Q	Expected Q	sd of Q	p-value	FWER adjusted p-value ³	Tested ²	Statistic Q	Expected Q	sd of Q	p-value	FWER adjusted p-value ³
Circadian rhythm	36	32	100.23	9.13	6.79	3.7E-06	0.0007	17	33.03	10.81	8.57	0.0271	1.0000
Epithelial cell signaling in Helicobacter pylori infection	128	113	103.05	11.87	7.23	3.9E-06	0.0007	64	38.84	10.79	7.33	0.0077	0.8214
Atrazine degradation	10	8	268.20	19.62	18.76	4.7E-06	0.0009	2	5.80	3.90	4.16	0.2210	1.0000
ECM-receptor interaction	191	146	209.61	26.49	15.82	4.9E-06	0.0009	66	50.34	15.42	10.80	0.0129	1.0000
Cysteine metabolism	28	23	70.91	8.33	5.23	5.7E-06	0.0010	11	35.04	8.27	6.12	0.0039	0.5373
Hematopoietic cell lineage	176	108	237.83	25.20	17.91	6.3E-06	0.0011	29	35.88	12.70	9.27	0.0284	1.0000
Adherens junction	190	150	81.13	11.75	6.33	6.9E-06	0.0012	99	69.89	13.20	9.99	0.0018	0.3078
Cytokine-cytokine receptor interaction	386	252	100.83	14.61	7.52	8.6E-06	0.0015	63	54.63	11.41	7.96	0.0021	0.3418
Valine, leucine and isoleucine degradation	91	81	77.65	11.00	6.30	1.1E-05	0.0019	60	41.43	9.10	6.13	0.0020	0.3297
Keratan sulfate biosynthesis	22	20	73.74	7.57	5.61	1.3E-05	0.0023	9	40.67	8.58	6.81	0.0037	0.5116
Neurodegenerative Disorders	74	60	130.45	18.64	10.93	1.4E-05	0.0024	37	39.06	11.32	8.34	0.0138	1.0000
Aminosugars metabolism	39	34	45.05	7.25	3.82	1.7E-05	0.0030	21	20.49	9.21	6.12	0.0553	1.0000
Complement and coagulation cascades	102	66	201.63	24.78	15.98	1.8E-05	0.0031	18	53.72	13.72	10.02	0.0061	0.7042

Toll-like receptor signaling pathway	147	115	66.20	10.26	5.60	1.9E-05	0.0032	46	60.69	11.87	9.54	0.0033	0.4772
Huntington's disease	69	52	115.29	13.77	9.41	2.0E-05	0.0034	37	46.56	9.50	7.09	0.0023	0.3694
MAPK signaling pathway	518	437	60.21	11.26	5.36	2.2E-05	0.0037	190	54.71	11.76	8.47	0.0028	0.4270
Arginine and proline metabolism	75	62	122.94	21.14	11.15	2.3E-05	0.0038	35	48.21	11.56	8.17	0.0039	0.5390
Leukocyte transendothelial migration	217	159	87.38	16.54	8.21	2.4E-05	0.0040	83	39.16	9.69	6.49	0.0038	0.5258
Basal transcription factors	48	43	19.31	3.54	1.73	2.6E-05	0.0042	27	25.58	7.12	4.87	0.0077	0.8214
Colorectal cancer	146	131	87.28	14.96	8.09	2.6E-05	0.0043	68	78.27	15.73	11.64	0.0020	0.3297
Cell Communication	200	138	148.96	26.53	14.05	2.8E-05	0.0045	69	37.62	10.59	7.32	0.0078	0.8214
Nicotinate and nicotinamide metabolism	50	43	178.71	22.29	15.37	3.4E-05	0.0055	17	33.37	12.81	9.43	0.0397	1.0000
Pyrimidine metabolism	110	100	45.16	7.07	3.89	3.4E-05	0.0055	71	51.52	10.43	7.68	0.0020	0.3297
Regulation of actin cytoskeleton	376	306	55.40	11.50	5.37	3.5E-05	0.0056	160	50.86	10.55	7.63	0.0023	0.3631
Biosynthesis of steroids	33	32	123.05	11.59	10.25	3.7E-05	0.0059	23	180.94	23.37	23.27	0.0010	0.1805
Glutathione metabolism	47	43	99.79	15.45	8.91	3.8E-05	0.0060	28	38.61	9.08	6.45	0.0045	0.5905
Ubiquitin mediated proteolysis	83	71	31.66	5.56	2.90	3.9E-05	0.0061	54	25.48	8.40	5.64	0.0168	1.0000
Vitamin B6 metabolism	14	13	177.14	14.99	14.74	3.9E-05	0.0061	7	57.41	13.80	11.17	0.0076	0.8214
Butanoate metabolism	67	59	65.53	11.17	6.25	4.3E-05	0.0066	44	30.97	8.84	5.68	0.0060	0.7004
Dorso-ventral axis formation	49	43	57.93	8.56	5.56	4.6E-05	0.0071	19	20.69	7.53	5.47	0.0317	1.0000
RNA polymerase	30	27	20.95	3.76	2.04	4.6E-05	0.0071	24	51.66	9.37	7.50	0.0019	0.3201
Focal adhesion	413	329	90.03	18.90	9.16	4.9E-05	0.0074	175	60.45	13.20	9.50	0.0027	0.4130
Methionine metabolism	22	20	48.85	6.28	4.37	5.5E-05	0.0083	13	94.02	16.38	15.58	0.0040	0.5438
TGF-beta signaling pathway	144	121	94.72	14.97	8.55	5.5E-05	0.0083	48	50.26	11.80	8.12	0.0032	0.4666
Propanoate metabolism	61	55	70.03	12.46	6.98	5.6E-05	0.0084	36	91.01	14.28	12.37	0.0014	0.2444
Axon guidance	225	183	56.69	11.59	5.49	6.0E-05	0.0089	100	34.25	10.39	6.79	0.0102	0.9094
Reductive carboxylate cycle (CO2 fixation)	16	15	50.54	6.69	4.86	7.2E-05	0.0106	14	100.13	13.69	13.07	0.0010	0.1867
ATP synthesis	60	44	27.79	4.21	2.54	7.4E-05	0.0108	43	27.03	7.17	5.46	0.0106	0.9094
beta-Alanine metabolism	43	35	93.68	14.82	9.51	7.7E-05	0.0112	19	38.99	8.30	5.88	0.0022	0.3572
Glutamate metabolism	52	48	73.12	10.67	6.98	8.7E-05	0.0125	30	30.05	10.54	6.81	0.0182	1.0000
Glycan structures - biosynthesis 1	129	115	45.14	9.39	4.57	8.8E-05	0.0126	64	31.48	8.93	6.14	0.0089	0.8789
Prion disease	20	15	76.27	9.52	7.48	9.0E-05	0.0127	10	32.79	8.99	7.19	0.0136	1.0000
Taurine and hypotaurine metabolism	16	13	42.07	4.84	4.01	9.2E-05	0.0130	4	6.78	4.95	4.72	0.2379	1.0000
Tryptophan metabolism	129	108	72.49	13.66	7.56	9.3E-05	0.0130	58	64.19	10.93	8.77	0.0015	0.2559
Jak-STAT signaling pathway	246	170	58.41	11.75	6.01	9.6E-05	0.0133	52	36.39	11.59	7.65	0.0128	1.0000
Tyrosine metabolism	93	64	87.56	15.78	9.51	0.0001	0.0154	35	23.63	7.55	4.79	0.0104	0.9094
Lysine degradation	69	63	53.50	9.83	5.50	0.0001	0.0155	42	39.49	10.64	8.03	0.0111	0.9294
Terpenoid biosynthesis	12	12	72.25	7.05	6.89	0.0001	0.0157	8	308.49	30.60	37.64	0.0007	0.1291
GnRH signaling pathway	209	169	46.08	9.08	4.81	0.0001	0.0174	81	44.05	10.10	7.08	0.0033	0.4772

Dentatorubropallidolusian atrophy (DRPLA)	44	32	106.23	12.11	10.20	0.0001	0.0175	16	13.63	6.83	5.12	0.0955	1.0000
Fatty acid elongation in mitochondria	17	17	18.47	3.14	1.95	0.0002	0.0201	16	14.40	5.70	3.75	0.0333	1.0000
Sphingolipid metabolism	57	49	57.93	11.78	6.31	0.0002	0.0205	24	23.09	9.11	6.10	0.0346	1.0000
Insulin signaling pathway	245	205	24.32	6.52	2.78	0.0002	0.0251	104	44.97	10.80	7.86	0.0052	0.6653
Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	37	32	20.60	4.31	2.36	0.0002	0.0251	14	47.73	12.21	9.44	0.0087	0.8747
Selenoamino acid metabolism	53	48	47.63	6.83	4.80	0.0002	0.0251	29	54.82	10.97	8.43	0.0027	0.4094
Citrate cycle (TCA cycle)	42	39	38.08	6.03	3.91	0.0002	0.0262	33	58.13	11.10	8.85	0.0023	0.3677
Apoptosis	162	141	44.52	9.59	4.81	0.0002	0.0285	55	35.81	9.77	6.35	0.0057	0.6958
Cell adhesion molecules (CAMs)	251	183	94.01	20.89	10.55	0.0002	0.0297	68	37.04	11.59	7.29	0.0095	0.8805
Oxidative phosphorylation	157	120	14.45	3.62	1.62	0.0002	0.0301	128	25.31	6.64	4.57	0.0058	0.6958
VEGF signaling pathway	136	115	48.21	10.28	5.49	0.0003	0.0324	58	25.63	9.22	6.05	0.0221	1.0000
Glycerolipid metabolism	78	59	55.93	12.25	6.37	0.0003	0.0334	28	31.31	9.64	6.87	0.0154	1.0000
Natural killer cell mediated cytotoxicity	227	168	64.33	11.69	7.00	0.0003	0.0334	75	21.93	8.52	4.99	0.0215	1.0000
Glycosaminoglycan degradation	33	23	42.89	7.00	4.92	0.0003	0.0345	13	17.59	9.66	7.59	0.1298	1.0000
Fatty acid metabolism	83	63	40.55	8.84	4.58	0.0003	0.0351	44	25.72	8.17	5.00	0.0089	0.8789
Adipocytokine signaling pathway	125	101	32.68	7.96	3.88	0.0003	0.0375	42	31.46	9.29	6.14	0.0094	0.8805
Hedgehog signaling pathway	75	57	64.22	10.43	7.11	0.0003	0.0375	31	30.03	11.71	8.51	0.0409	1.0000
Tight junction	217	171	56.28	13.29	6.70	0.0003	0.0377	99	34.88	9.77	6.58	0.0071	0.7968
Styrene degradation	7	2	116.58	11.96	13.24	0.0004	0.0409	1	1.06	4.41	6.23	0.6232	1.0000
Fc epsilon RI signaling pathway	136	111	47.07	10.39	5.65	0.0004	0.0459	39	29.69	8.25	5.53	0.0071	0.7968
Taste transduction	54	39	34.05	5.95	3.92	0.0004	0.0461	18	27.41	7.14	5.11	0.0072	0.7969
Alanine and aspartate metabolism	42	36	76.85	11.98	8.88	0.0004	0.0484	27	35.08	8.19	5.89	0.0040	0.5438
Purine metabolism	219	179	30.10	8.26	3.68	0.0004	0.0484	106	45.39	9.62	6.80	0.0021	0.3438
Pathogenic Escherichia coli infection - EHEC	109	70	79.15	16.00	9.26	0.0004	0.0490	72	51.54	10.37	7.70	0.0020	0.3297
Pathogenic Escherichia coli infection - EPEC	109	70	79.15	16.00	9.26	0.0004	0.0490	72	51.54	10.37	7.70	0.0020	0.3297
Glycerophospholipid metabolism	111	91	27.87	7.09	3.44	0.0005	0.0497	50	33.33	10.61	7.86	0.0209	1.0000
Cell cycle	206	182	47.25	11.25	5.80	0.0005	0.0510	123	41.25	12.56	8.53	0.0112	0.9294
mTOR signaling pathway	91	76	31.91	8.09	4.02	0.0005	0.0559	41	35.80	9.59	6.82	0.0075	0.8214
ABC transporters - General	63	42	48.76	11.45	6.25	0.0005	0.0580	10	15.58	9.84	7.55	0.1681	1.0000
Benzoate degradation via CoA ligation	49	41	47.74	9.58	5.87	0.0006	0.0595	28	40.22	10.38	7.20	0.0055	0.6894
O-Glycan biosynthesis	23	20	83.53	16.15	10.74	0.0007	0.0686	7	27.29	9.14	8.74	0.0458	1.0000
Galactose metabolism	38	33	30.35	7.83	4.05	0.0007	0.0718	20	36.77	10.09	7.38	0.0101	0.9094
Parkinson's disease	29	21	96.76	18.74	12.94	0.0007	0.0721	18	20.06	7.42	4.62	0.0201	1.0000
Olfactory transduction	61	49	21.05	5.50	2.75	0.0007	0.0721	21	57.87	10.90	9.00	0.0026	0.4060

Cholera - Infection	82	65	21.19	5.54	2.79	0.0008	0.0764	57	39.40	8.55	6.21	0.0031	0.4590
Wnt signaling pathway	261	219	53.40	12.43	6.73	0.0008	0.0764	121	43.13	11.20	7.55	0.0049	0.6382
Gap junction	206	160	49.96	12.13	6.50	0.0008	0.0771	93	61.41	11.06	8.46	0.0013	0.2365
Cyanoamino acid metabolism	14	11	18.42	3.53	2.53	0.0008	0.0775	8	25.30	7.48	6.41	0.0233	1.0000
SNARE interactions in vesicular transport	64	64	35.79	7.77	4.50	0.0008	0.0775	32	35.50	9.09	6.37	0.0060	0.6990
Nitrogen metabolism	39	31	42.00	10.13	5.60	0.0008	0.0784	10	60.02	16.60	15.23	0.0224	1.0000
Antigen processing and presentation	164	111	80.04	11.95	9.80	0.0008	0.0786	68	29.28	9.96	6.00	0.0115	0.9450
Glycine, serine and threonine metabolism	56	42	54.90	13.02	7.44	0.0008	0.0786	24	45.97	11.71	7.74	0.0036	0.5115
Glycan structures - degradation	51	38	34.08	7.57	4.64	0.0009	0.0825	19	20.62	9.29	7.16	0.0746	1.0000
Phosphatidylinositol signaling system	136	113	44.86	10.79	5.86	0.0009	0.0828	51	37.85	10.09	6.95	0.0067	0.7546
Starch and sucrose metabolism	90	70	48.01	11.86	6.58	0.0010	0.0874	41	27.35	8.19	5.87	0.0146	1.0000
One carbon pool by folate	28	24	23.60	4.63	3.06	0.0010	0.0886	14	31.66	7.48	5.61	0.0046	0.6026
gamma-Hexachlorocyclohexane degradation	39	23	71.24	14.34	9.56	0.0010	0.0899	13	35.32	11.83	8.14	0.0183	1.0000
Limonene and pinene degradation	58	43	59.25	12.56	7.92	0.0010	0.0899	29	35.26	8.57	5.76	0.0035	0.4937
Type I diabetes mellitus	98	68	116.46	20.54	15.05	0.0010	0.0899	21	24.88	9.22	5.53	0.0179	1.0000
Bile acid biosynthesis	50	35	50.46	10.82	6.70	0.0011	0.0927	22	18.01	9.22	6.34	0.0880	1.0000
DNA polymerase	31	28	24.26	4.76	3.09	0.0011	0.0927	21	28.17	9.65	7.74	0.0332	1.0000
Pentose phosphate pathway	42	31	25.75	6.72	3.53	0.0011	0.0927	22	44.82	10.05	8.76	0.0083	0.8481
Benzoate degradation via hydroxylation	8	6	30.40	5.07	4.23	0.0012	0.0965	6	2.00	4.79	4.13	0.7195	1.0000
Bisphenol A degradation	18	14	112.46	22.37	15.85	0.0013	0.1015	9	37.73	15.04	11.03	0.0444	1.0000
Urea cycle and metabolism of amino groups	30	26	89.59	20.21	12.54	0.0013	0.1067	14	93.30	15.66	13.34	0.0017	0.2945
1- and 2-Methylnaphthalene degradation	38	25	60.83	11.49	8.30	0.0014	0.1072	18	35.22	9.99	7.10	0.0096	0.8805
Heparan sulfate biosynthesis	26	23	36.36	7.88	5.14	0.0014	0.1072	13	29.25	9.93	8.15	0.0340	1.0000
PPAR signaling pathway	118	88	47.26	13.95	6.75	0.0014	0.1072	34	66.64	11.44	8.81	0.0012	0.2179
Glycan structures - biosynthesis 2	99	84	24.19	7.19	3.49	0.0014	0.1082	28	18.41	8.33	5.31	0.0525	1.0000
Nucleotide sugars metabolism	17	16	42.92	8.30	5.83	0.0014	0.1082	11	24.77	11.05	7.95	0.0629	1.0000
Glycolysis / Gluconeogenesis	102	64	35.59	9.36	4.96	0.0015	0.1088	50	41.35	8.93	6.73	0.0032	0.4666
Neuroactive ligand-receptor interaction	418	237	43.06	11.50	5.81	0.0015	0.1131	41	36.52	8.90	6.40	0.0057	0.6958
Calcium signaling pathway	332	246	40.88	10.62	5.59	0.0016	0.1144	90	52.62	10.83	7.55	0.0017	0.2945
Ubiquinone biosynthesis	8	8	14.21	3.04	2.13	0.0017	0.1188	6	21.89	4.40	3.56	0.0031	0.4650
Sulfur metabolism	19	16	90.30	14.98	12.72	0.0017	0.1207	8	12.37	7.63	7.92	0.1777	1.0000
Type II diabetes mellitus	78	50	30.01	8.14	4.49	0.0018	0.1215	11	33.62	9.80	6.82	0.0092	0.8805
B cell receptor signaling pathway	114	97	47.48	11.90	6.88	0.0018	0.1246	40	42.57	11.38	8.30	0.0091	0.8803
Arachidonic acid metabolism	86	52	40.67	10.74	6.00	0.0019	0.1254	18	48.84	10.09	8.03	0.0035	0.4937

Ethylbenzene degradation	28	23	63.04	12.72	9.12	0.0019	0.1259	15	39.35	9.40	6.82	0.0045	0.5911
Phenylalanine metabolism	49	33	73.44	14.55	10.92	0.0020	0.1277	19	30.39	7.52	5.42	0.0057	0.6958
Inositol phosphate metabolism	81	68	35.03	9.60	5.15	0.0020	0.1293	32	24.00	8.85	6.18	0.0302	1.0000
Linoleic acid metabolism	61	32	29.78	7.81	4.67	0.0020	0.1293	14	56.66	11.09	8.69	0.0025	0.3883
Folate biosynthesis	56	50	25.34	6.80	3.90	0.0026	0.1604	35	15.93	6.58	4.11	0.0345	1.0000
Long-term potentiation	142	110	40.53	9.65	6.05	0.0028	0.1698	51	44.43	10.06	7.44	0.0040	0.5438
Pyruvate metabolism	63	52	37.54	10.91	5.87	0.0028	0.1698	37	33.82	8.51	6.14	0.0057	0.6958
Synthesis and degradation of ketone bodies	11	10	35.55	8.19	5.72	0.0029	0.1698	9	83.47	16.00	13.28	0.0024	0.3762
Glyoxylate and dicarboxylate metabolism	15	12	21.46	4.54	3.39	0.0032	0.1834	12	15.09	5.09	3.84	0.0258	1.0000
Fructose and mannose metabolism	63	50	21.96	7.10	3.53	0.0033	0.1909	31	33.90	8.61	5.79	0.0044	0.5877
Nitrobenzene degradation	20	14	8.73	2.75	1.47	0.0039	0.2169	9	21.31	6.08	4.30	0.0092	0.8805
T cell receptor signaling pathway	168	128	20.54	7.06	3.27	0.0039	0.2169	56	36.77	10.89	8.00	0.0148	1.0000
Metabolism of xenobiotics by cytochrome P450	95	52	79.49	20.21	13.25	0.0042	0.2268	21	21.54	8.29	5.12	0.0239	1.0000
Histidine metabolism	59	47	52.36	13.77	8.80	0.0046	0.2412	22	26.85	7.18	4.76	0.0052	0.6619
Peptidoglycan biosynthesis	4	4	104.97	13.04	18.21	0.0046	0.2412	3	49.73	20.08	22.35	0.0905	1.0000
Ascorbate and aldarate metabolism	19	17	69.33	16.28	12.07	0.0048	0.2439	12	27.49	10.08	7.18	0.0299	1.0000
Glycosphingolipid biosynthesis - ganglioseries	21	17	23.65	7.20	4.15	0.0049	0.2439	6	16.66	9.34	8.39	0.1420	1.0000
Alzheimer's disease	45	37	62.12	17.34	10.93	0.0054	0.2634	26	18.81	12.23	7.86	0.1657	1.0000
Protein export	15	13	9.11	2.70	1.66	0.0054	0.2634	13	39.28	9.47	7.48	0.0079	0.8259
Fatty acid biosynthesis	11	9	43.40	7.82	7.78	0.0057	0.2664	4	216.63	26.13	30.54	0.0016	0.2833
Aminophosphonate metabolism	26	21	8.08	3.06	1.44	0.0066	0.3058	12	19.02	6.43	4.00	0.0126	1.0000
Biotin metabolism	13	12	10.81	3.12	2.02	0.0068	0.3058	5	54.40	14.23	16.64	0.0352	1.0000
N-Glycan biosynthesis	58	50	18.82	6.01	3.37	0.0068	0.3058	36	32.52	8.84	6.44	0.0092	0.8805
Long-term depression	148	111	34.04	10.55	6.06	0.0071	0.3072	48	37.93	9.53	6.70	0.0054	0.6843
Notch signaling pathway	79	69	23.19	7.75	4.26	0.0075	0.3146	50	20.43	8.34	5.96	0.0459	1.0000
Porphyrin and chlorophyll metabolism	43	34	51.69	12.23	9.63	0.0077	0.3146	19	20.94	7.32	5.24	0.0261	1.0000
Valine, leucine and isoleucine biosynthesis	16	15	37.05	7.62	7.26	0.0089	0.3544	10	10.45	6.24	5.01	0.1496	1.0000
Diterpenoid biosynthesis	3	3	53.19	10.79	11.21	0.0106	0.4135	1	3.93	7.04	9.96	0.4553	1.0000
Aminoacyl-tRNA biosynthesis	40	38	10.84	4.18	2.08	0.0111	0.4220	33	64.61	11.35	9.44	0.0020	0.3297
Chondroitin sulfate biosynthesis	21	20	32.66	10.43	6.64	0.0117	0.4332	12	32.07	8.81	7.86	0.0210	1.0000
Proteasome	48	29	6.22	2.53	1.24	0.0142	0.5115	45	32.19	7.40	5.86	0.0056	0.6916
Retinol metabolism	5	5	100.63	21.53	23.67	0.0157	0.5487	1	4.32	7.61	10.76	0.4512	1.0000
Caprolactam degradation	26	25	12.75	4.93	2.71	0.0171	0.5765	14	12.40	6.18	4.20	0.0809	1.0000

N-Glycan degradation	20	17	29.27	8.57	6.65	0.0170	0.5765	8	12.89	8.67	7.18	0.1956	1.0000
Novobiocin biosynthesis	4	2	16.22	3.91	3.98	0.0171	0.5765	2	54.00	10.25	13.06	0.0164	1.0000
Phenylalanine, tyrosine and tryptophan biosynthesis	18	13	35.87	9.78	8.31	0.0175	0.5765	10	63.66	12.59	9.97	0.0024	0.3701
Amyotrophic lateral sclerosis (ALS)	34	28	73.95	24.39	18.89	0.0266	0.7980	16	39.63	10.47	7.73	0.0082	0.8419
Androgen and estrogen metabolism	62	42	30.43	10.89	7.52	0.0280	0.8129	11	19.95	5.96	3.98	0.0087	0.8747
Pentose and glucuronate interconversions	21	15	67.73	18.38	18.63	0.0284	0.8129	7	22.83	6.22	5.20	0.0149	1.0000
Streptomycin biosynthesis	12	11	33.09	12.55	8.44	0.0301	0.8129	6	44.94	9.23	8.10	0.0058	0.6958
Alkaloid biosynthesis I	7	5	164.60	40.45	48.96	0.0318	0.8199	2	54.00	10.25	13.06	0.0164	1.0000
Alkaloid biosynthesis II	33	26	28.46	10.32	7.53	0.0329	0.8199	17	25.28	6.61	4.64	0.0062	0.7122
Tetrachloroethene degradation	7	6	37.77	10.27	10.88	0.0315	0.8199	4	13.78	13.88	11.37	0.3867	1.0000
Glycosphingolipid biosynthesis - globoseries	21	15	24.27	9.26	7.12	0.0430	0.9261	7	17.15	8.07	6.55	0.0879	1.0000
Regulation of autophagy	40	24	15.18	5.99	4.29	0.0415	0.9261	12	40.34	11.30	9.77	0.0201	1.0000
Ribosome	201	48	22.00	8.01	6.34	0.0403	0.9261	163	39.46	8.01	8.07	0.0103	0.9094
1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation	3	1	27.59	16.44	23.25	0.1951	1	1	1441.12	128.38	181.56	0.0008	0.1468
2,4-Dichlorobenzoate degradation	7	5	1.76	5.11	4.33	0.7870	1	4	17.03	2.66	2.72	0.0028	0.4156
C21-Steroid hormone metabolism	12	6	28.63	13.76	10.95	0.0954	1	0	NA	NA	NA	NA	NA
C5-Branched dibasic acid metabolism	3	3	0.38	2.70	2.74	0.8668	1	3	17.40	13.25	14.91	0.2507	1.0000
Carbon fixation	42	24	18.55	8.80	6.32	0.0732	1	19	48.39	10.23	10.02	0.0109	0.9268
D-Glutamine and D-glutamate metabolism	9	9	6.85	3.92	3.47	0.1446	1	3	14.09	5.65	5.34	0.0702	1.0000
Fluorene degradation	3	1	11.09	5.96	8.43	0.1725	1	1	0.26	0.96	1.35	0.5995	1.0000
Glycosphingolipid biosynthesis - lactoseries	14	9	15.35	7.08	6.71	0.1020	1	3	6.99	6.54	6.91	0.3173	1.0000
Glycosphingolipid biosynthesis - neolactoseries	39	30	15.64	6.49	4.97	0.0556	1	11	10.39	6.38	4.11	0.1435	1.0000
Inositol metabolism	7	5	2.17	9.34	12.32	0.6841	1	5	174.46	20.25	24.31	0.0015	0.2711
Lysine biosynthesis	6	5	15.25	6.48	6.94	0.0951	1	4	14.06	10.04	10.97	0.2285	1.0000
Maturity onset diabetes of the young	38	19	42.63	16.52	13.90	0.0539	1	4	5.22	7.18	7.73	0.4537	1.0000
Methane metabolism	18	11	9.49	4.26	3.08	0.0641	1	8	13.88	7.58	6.90	0.1349	1.0000
Pantothenate and CoA biosynthesis	31	27	30.34	14.07	9.64	0.0646	1	12	9.40	7.83	6.11	0.2848	1.0000
Riboflavin metabolism	25	22	20.64	13.72	10.88	0.1777	1	14	20.57	9.60	6.00	0.0561	1.0000
Stilbene, coumarine and lignin biosynthesis	12	7	13.58	6.20	5.73	0.0953	1	4	33.20	8.01	8.57	0.0219	1.0000
Thiamine metabolism	10	9	11.30	5.14	3.65	0.0660	1	5	6.84	6.66	6.14	0.3449	1.0000
Carbazole degradation	2	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
D-Arginine and D-ornithine metabolism	1	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA

Monoterpenoid biosynthesis	8	0	NA	NA	NA	NA	NA	0	NA	NA	NA	NA	NA
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1. Number of genes associated with the specified pathway.
2. Number of genes tested by this dataset that are associated with the specified pathway
3. FWER: Multiplicity-adjusted p value by Holm's method