

Supplemental Table 3. Mammary tumor transcripts differentially regulated by virulent surface metastasis ($Q < 0.05$, $n = 66$ microarrays). The gene expression data from individual mammary tumor samples were ordered such that 25% (33 samples) of the total samples came from mice with no surface- or section- metastatic lesions and the longest tumor onset. Gene expression data from these 33 samples served as the reference group when paired with the gene expression data of 33 mammary tumor samples from mice that had the most surface metastatic lesions detected (MET66). Annotation was performed with Ingenuity Pathway Analysis Knowledge Base.

*Positive fold change is significant fold change increase in gene expression from mammary tumors with virulent surface metastasis relative to mammary tumors with no metastasis. Negative fold change is significant fold change increase in gene expression from mammary tumors with no metastasis relative to mammary tumors with virulent surface metastasis.

†Identification of transcript by RefSeq or Illumina probe ID where RefSeq was not available.

‡Highlights significant transcripts that appear in duplicate due to the redundancy of transcript representation on Illumina Bead Chips.

§Official symbolic name of transcript

||Official descriptive name of transcript

	A	B	C	D	E	F
1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
2	1.427	4.108	NM_029639.1		1600029D21RIK	RIKEN cDNA 1600029D21 gene
3	1.128	3.214	XM_001472446.1		2010315B03RIK	RIKEN cDNA 2010315B03 gene
4	1.139	2.38	NM_028314.1		2700097O09RIK	RIKEN cDNA 2700097O09 gene
5	-0.895	3.214	NM_029849.1		4632433K11RIK	RIKEN cDNA 4632433K11 gene
6	-0.832	2.708	NM_144829.1		AARSD1	alanyl-tRNA synthetase domain containing 1
7	-0.867	4.108	NM_145140		ABCC10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10
8	1.694	0	NM_203502		ABPB	androgen binding protein beta
9	-0.82	2.38	NM_177470.2		ACAA2	acetyl-Coenzyme A acyltransferase 2
10	-0.776	0	NM_007382		ACADM	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain
11	1.149	2.708	NM_133225.1		ACBD3	acyl-Coenzyme A binding domain containing 3
12	1.351	4.108	NM_207625.1		ACSL4	acyl-CoA synthetase long-chain family member 4
13	-0.796	0.797	NM_007393.1		ACTB	actin, beta
14	1.127	2.127	NM_019785.1		ACTR10	actin-related protein 10 homolog (<i>S. cerevisiae</i>)
15	-0.768	0	NM_175643.1	D	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2
16	-0.83	2.708	NM_175643.1	D	ADAMTS2	ADAM metallopeptidase with thrombospondin type 1 motif, 2
17	-0.884	4.108	NM_025748.2		ADAT2	adenosine deaminase, tRNA-specific 2, TAD2 homolog (<i>S. cerevisiae</i>)
18	1.31	2.127	NM_013758.2		ADD3	adducin 3 (gamma)
19	-0.831	2.38	NM_009636.1		AEBP1	AE binding protein 1
20	1.168	0.633	NM_026375.1		AHCTF1	AT hook containing transcription factor 1
21	1.233	2.127	NM_145542		AHCYL1	S-adenosylhomocysteine hydrolase-like 1
22	-0.812	1.138	NM_025337.2		AKR7A2	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
23	-0.859	4.108	NM_020332.2		ANKH	ankylosis, progressive homolog (mouse)
24	1.272	0	NM_024204		ANKRD22	ankyrin repeat domain 22
25	1.139	3.214	NM_133872.1		AOF2	amine oxidase (flavin containing) domain 2
26	-0.883	2.38	NM_194341.1		AP1GBP1	AP1 gamma subunit binding protein 1
27	1.187	2.708	NM_007460.1		AP3D1	adaptor-related protein complex 3, delta 1 subunit
28	1.235	1.345	NM_009681.2		AP3S1	adaptor-related protein complex 3, sigma 1 subunit
29	-0.801	0	NM_007470.1		APOD	apolipoprotein D
30	1.262	0.633	NM_173743.2		APOL9B	apolipoprotein L 9b
31	1.207	1.01	NM_009705.1		ARG2	arginase, type II
32	-0.888	2.38	NM_008488.1		ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1
33	1.224	2.38	NM_025859.1		ARL1	ADP-ribosylation factor-like 1
34	1.21	4.108	NM_178050.2		ARL6IP2	ADP-ribosylation factor-like 6 interacting protein 2
35	-0.821	1.401	NM_026369.1		ARPC5	actin related protein 2/3 complex, subunit 5, 16kDa
36	1.47	0	NM_012055.1		ASNS	asparagine synthetase
37	-0.829	2.127	NM_007494.2		ASS1	argininosuccinate synthetase 1
38	-0.851	1.138	NM_016755.2		ATP5J	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6
39	1.234	4.108	NP_536848.1		ATP6	ATP synthase 6; ATPase subunit 6
40	1.141	2.38	NM_023721.1		ATP6V1D	ATPase, H ⁺ transporting, lysosomal 34kDa, V1 subunit D
41	1.157	4.108	NM_178640		B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
42	-0.888	4.108	NM_019517.2		BACE2	beta-site APP-cleaving enzyme 2
43	-0.823	4.108	XM_148990.3		BAT2D1	BAT2 domain containing 1
44	-0.857	2.127	NM_175002.1		BC025076	cDNA sequence BC025076
45	-0.877	2.127	NM_175044.1		BCOR	BCL6 co-repressor
46	-0.804	0	NM_007542.3		BGN	biglycan
47	1.31	0	NM_010800.2	D	BHLHB8	basic helix-loop-helix domain containing, class B, 8
48	1.264	0	NM_010800.2	D	BHLHB8	basic helix-loop-helix domain containing, class B, 8
49	-0.805	0	NM_031397.1		BICC1	bicaudal C homolog 1 (Drosophila)
50	1.182	2.38	NM_008528.3		BLNK	B-cell linker
51	-0.884	4.108	NM_009755.2		BMP1	bone morphogenetic protein 1
52	1.239	0	NM_009761.2		BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like
53	-0.858	3.214	NM_175277.2		BOLA3	bolA homolog 3 (E. coli)
54	-0.845	1.401	NM_023336.2		BRD3	bromodomain containing 3
55	-0.732	2.127	NM_007569.1		BTG1	B-cell translocation gene 1, anti-proliferative
56	-0.764	3.214	NM_013483.1		BTN1A1	butyrophilin, subfamily 1, member A1
57	-0.865	1.401	NM_172280.2		C11ORF30	chromosome 11 open reading frame 30
58	-0.898	4.108	NM_138757.1		C12ORF11	chromosome 12 open reading frame 11
59	1.168	0.633	AK049325	D	C12ORF30	chromosome 12 open reading frame 30
60	1.09	2.708	NM_172722	D	C12ORF30	chromosome 12 open reading frame 30
61	1.129	4.108	NM_025427.1		C13ORF15	chromosome 13 open reading frame 15
62	-0.85	4.108	NM_021446		C14ORF1	chromosome 14 open reading frame 1
63	-0.854	2.38	NM_198609		C15ORF15	chromosome 15 open reading frame 15
64	-0.878	2.708	NM_178901.2		C16ORF54	chromosome 16 open reading frame 54
65	1.118	2.127	NM_175287.2		C1ORF174	chromosome 1 open reading frame 174
66	-0.768	0	NM_198860.1		C22ORF36	chromosome 22 open reading frame 36
67	1.22	2.127	NM_029554.2		C4ORF19	chromosome 4 open reading frame 19
68	1.208	0	NM_133697.1		C4ORF34	chromosome 4 open reading frame 34
69	1.158	3.214	AK050607		C5ORF28	chromosome 5 open reading frame 28
70	1.115	3.214	NM_025879.1		C5ORF44	chromosome 5 open reading frame 44
71	-0.802	2.38	NM_027457.2		C6ORF35	chromosome 6 open reading frame 35
72	1.584	1.345	NM_026336.1		C6ORF58	chromosome 6 open reading frame 58
73	1.16	3.214	NM_177682.3		C7ORF28A	chromosome 7 open reading frame 28A
74	-0.857	3.214	NM_178116.2		CAMTA2	calmodulin binding transcription activator 2
75	-0.868	4.108	AK017510		CBX6	chromobox homolog 6
76	-0.849	4.108	NM_177045.2		CC2D1B	coiled-coil and C2 domain containing 1B
77	-0.792	0.797	NM_026439.1		CCDC80	coiled-coil domain containing 80
78	-0.851	2.127	BC001984		CCNDBP1	cyclin D-type binding-protein 1
79	1.207	3.214	NM_023243.2		CCNH	cyclin H
80	-0.824	3.214	NM_009836.1		CCT3	chaperonin containing TCP1, subunit 3 (gamma)
81	-0.882	3.214	NM_023223.1		CDC20	cell division cycle 20 homolog (S. cerevisiae)
82	-0.876	2.708	NM_194444.1		CDK10	cyclin-dependent kinase 10

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83	-0.843	3.214	NM_026373.1		CDK2AP2	CDK2-associated protein 2
84	1.185	4.108	NM_007669.2		CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
85	-0.82	1.138	NM_009876.2		CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
86	1.138	1.01	NM_173370.3		CDS1	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1
87	-0.759	1.138	NM_009885.1		CEL	carboxyl ester lipase (bile salt-stimulated lipase)
88	-0.686	3.214	NM_017392		CELSR2	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)
89	1.389	2.708	NM_008198.1		CFB	complement factor B
90	1.412	0	NM_026929.2		CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)
91	1.232	0	NM_023543.1		CHN2	chimerin (chimaerin) 2
92	-0.843	3.214	NM_023850.1		CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
93	-0.888	0	NM_029738.1		CLUAP1	clusterin associated protein 1
94	-0.725	2.38	NM_007742.2		COL1A1	collagen, type I, alpha 1
95	1.199	3.214	NM_007736		COL4A5	collagen, type IV, alpha 5 (Alport syndrome)
96	-0.839	3.214	NM_015734.1		COL5A1	collagen, type V, alpha 1
97	-0.78	0	NM_009933.1	D	COL6A1	collagen, type VI, alpha 1
98	-0.794	3.214	NM_009933.1	D	COL6A1	collagen, type VI, alpha 1
99	1.144	3.214	NM_173185		CSNK1G1	casein kinase 1, gamma 1
100	-0.839	3.214	NM_134002.1		CSNK1G2	casein kinase 1, gamma 2
101	-0.885	4.108	NM_013884.2		CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)
102	1.274	4.108	NM_033616.2		CSPRS	component of Sp100-rs
103	-0.862	3.214	NM_018761.2		CTNNA1	catenin (cadherin-associated protein), alpha-like 1
104	-0.828	1.138	NM_007802.2		CTSK	cathepsin K
105	1.239	0	NM_022325.3		CTSZ	cathepsin Z
106	-0.878	2.38	NM_009987.2		CX3CR1	chemokine (C-X3-C motif) receptor 1
107	-0.863	2.38	NM_028868.1		CXXC1	CXXC finger 1 (PHD domain)
108	-0.896	2.38	XM_109819		CYB5D2	cytochrome b5 domain containing 2
109	1.23	3.214	NM_010022		DBT	dihydrolipoamide branched chain transacylase E2
110	1.163	3.214	NM_033623.1		DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)
111	1.312	0.633	NM_029083.1		DDIT4	DNA-damage-inducible transcript 4
112	1.294	0.633	XM_131083.2		DENND2D	DENN/MADD domain containing 2D
113	1.116	1.345	NM_021428.3		DEXI	dexamethasone-induced transcript
114	-0.732	2.38	NM_138306.1		DGKZ	diacylglycerol kinase, zeta 104kDa
115	-0.871	3.214	NM_013764.1		DGUOK	deoxyguanosine kinase
116	1.264	1.01	NM_007839.1		DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15
117	1.129	3.214	NM_148948.2		DICER1	dicer 1, ribonuclease type III
118	-0.871	3.214	NM_015814.2		DKK3	dickkopf homolog 3 (Xenopus laevis)
119	1.351	3.214	NM_172899.1		DMKN	dermokine
120	-0.843	2.38	NM_010068.1		DNMT3B	DNA (cytosine-5-)-methyltransferase 3 beta
121	-0.863	2.38	NM_007879.1		DRG1	developmentally regulated GTP binding protein 1

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
122	1.156	3.214	NM_007904.2		EDNRB	endothelin receptor type B
123	-0.842	4.108	NM_023240.1		EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
124	-0.807	4.108	NM_026007		EEF1G	eukaryotic translation elongation factor 1 gamma
125	-0.823	0.797	NM_028889.1		EFHD1	EF-hand domain family, member D1
126	1.121	3.214	NM_010107.2		EFNA1	ephrin-A1
127	1.599	0	NM_028133.1		EGLN3	egl nine homolog 3 (C. elegans)
128	-0.86	2.127	NM_146200		EIF3C	eukaryotic translation initiation factor 3, subunit C
129	-0.847	2.127	NM_025344		EIF3F	eukaryotic translation initiation factor 3, subunit F
130	1.18	2.38	NM_080635.1		EIF3H	eukaryotic translation initiation factor 3, subunit H
131	-0.712	0	NM_007925.2		ELN	elastin (supravalvular aortic stenosis, Williams-Beuren syndrome)
132	-0.779	0	NM_080595.1		EMID1	EMI domain containing 1
133	-0.869	1.401	NM_010129.1		EMP3	epithelial membrane protein 3
134	1.146	3.214	NM_028013.1		ENDOD1	endonuclease domain containing 1
135	-0.834	3.214	NM_013813.1		EPB41L3	erythrocyte membrane protein band 4.1-like 3
136	1.16	2.127	NM_010144.2		EPHB4	EPH receptor B4
137	-0.881	3.214	NM_007949.2		ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D)
138	-0.859	3.214	NM_007953.1		ESRRA	estrogen-related receptor alpha
139	1.175	4.108	AK049827		ETNK1	ethanolamine kinase 1
140	1.165	2.708	NM_027148.2		EXOSC8	exosome component 8
141	-0.828	0.797	NM_010169.2		F2R	coagulation factor II (thrombin) receptor
142	1.13	3.214	NM_007974		F2RL1	coagulation factor II (thrombin) receptor-like 1
143	-0.821	4.108	NM_138587.3		FAM3C	family with sequence similarity 3, member C
144	-0.856	3.214	NM_010180		FBLN1	fibulin 1
145	1.186	4.108	NM_015822.1		FBXL3	F-box and leucine-rich repeat protein 3
146	-0.874	3.214	NM_023605.1		FBXO9	F-box protein 9
147	-0.897	3.214	NM_013907.1		FBXW4	F-box and WD repeat domain containing 4
148	-0.815	2.38	NM_010189		FCGRT	Fc fragment of IgG, receptor, transporter, alpha
149	1.135	3.214	NM_172591.2		FCHO2	FCH domain only 2
150	1.196	0	NM_146054.1		FERMT2	fermitin family homolog 2 (Drosophila)
151	-0.853	1.401	NM_054071.1		FGFRL1	fibroblast growth factor receptor-like 1
152	-0.857	1.401	NM_153573.1		FKBP14	FK506 binding protein 14, 22 kDa
153	1.188	0	NM_010220.2		FKBP5	FK506 binding protein 5
154	-0.825	2.127	NM_177394.2		FLJ35220	hypothetical protein FLJ35220
155	-0.818	2.127	NM_008028.1		FLOT2	flotillin 2
156	-0.854	2.127	XM_129845.3		FN1	fibronectin 1
157	-0.855	3.214	NM_021899.2		FOXJ2	forkhead box J2
158	-0.814	2.708	NM_008047.2		FSTL1	follistatin-like 1
159	-0.721	1.138	NM_010239.1		FTH1	ferritin, heavy polypeptide 1
160	-0.869	2.708	NM_011936.1		FTO	fat mass and obesity associated

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
161	1.188	4.108	NM_008056		FZD6	frizzled homolog 6 (Drosophila)
162	-0.871	2.38	NM_021356.2		GAB1	GRB2-associated binding protein 1
163	-0.871	3.214	NM_183358.2		GADD45GIP1	growth arrest and DNA-damage-inducible, gamma interacting protein 1
164	-0.89	4.108	NM_144908.1		GALNT11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11 (GalNAc-T11)
165	1.273	0	NM_008084.1	D	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
166	1.167	2.38	NM_008084.2	D	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
167	1.151	3.214	NM_020619.2		GCS1	glucosidase I
168	-0.885	1.138	NM_010279.2		GFRA1	GDNF family receptor alpha 1
169	-0.82	2.708	NM_008116		GGT1	gamma-glutamyltransferase 1
170	1.186	4.108	NM_078478.1		GHITM	growth hormone inducible transmembrane protein
171	1.3	2.127	NM_010288.2		GJA1	gap junction protein, alpha 1, 43kDa
172	1.2	0	NM_015828		GNE	glucosamine (UDP-N-acetyl)-2-epimerase/N-acetylmannosamine kinase
173	-0.849	1.401	NM_175193.2		GOLIM4	golgi integral membrane protein 4
174	1.122	4.108	NM_146133.2		GOLPH3L	golgi phosphoprotein 3-like
175	-0.801	0.797	NM_016696.1		GPC1	glypican 1
176	1.159	0.633	NM_173866.1		GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2
177	1.098	4.108	NM_172768.1		GRAMD1B	GRAM domain containing 1B
178	-0.846	3.214	NM_013541		GSTP1	glutathione S-transferase pi 1
179	-0.8	4.108	XM_126043.3		H2AFV	H2A histone family, member V
180	1.233	4.108	NM_008211.2		H3F3B	H3 histone, family 3B (H3.3B)
181	-0.796	0	NM_145558		HADHB	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
182	-0.844	4.108	NM_025641.2		HCG_25371	hCG25371
183	-0.861	4.108	NM_008233.1		HDGF2	hepatoma-derived growth factor-related protein 2
184	1.326	2.127	NM_178206		HIST1H3B	histone cluster 1, H3b
185	1.186	0	NM_178192.1		HIST1H4F	histone cluster 1, H4f
186	1.2	2.127	NM_175655.1		HIST1H4I	histone cluster 1, H4i
187	1.307	3.214	NM_178215		HIST2H3B	histone cluster 2, H3b
188	1.181	0	NM_178211.1	D	HIST4H4	histone cluster 4, H4
189	1.168	1.345	NM_178210.1	D	HIST4H4	histone cluster 4, H4
190	1.27	0	NM_013820.1		HK2	hexokinase 2
191	-0.76	2.127	NM_207105.1	D	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2
192	-0.797	4.108	NM_010379.2	D	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2
193	-0.689	0	NM_182650.2		HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1
194	1.188	0	NM_152134.1	D	HOMER1	homer homolog 1 (Drosophila)
195	1.177	0	NM_152134.1	D	HOMER1	homer homolog 1 (Drosophila)
196	-0.849	3.214	XM_133550.4		HOMER2	homer homolog 2 (Drosophila)

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197	1.208	1.345	NM_133255		HOOK2	hook homolog 2 (Drosophila)
198	-0.779	0	NM_017370.1		HPR	haptoglobin-related protein
199	-0.802	0.797	NM_008288		HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1
200	1.227	0.633	NM_019657.2		HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12
201	-0.721	0.797	NM_008302.2	D	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
202	-0.81	1.138	NM_008302.2	D	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1
203	1.189	1.01	NM_173752.1		HSPC159	galectin-related protein
204	-0.838	3.214	NM_008305.2		HSPG2	heparan sulfate proteoglycan 2
205	1.189	0	NM_008307.1		HTF9C	Hpall tiny fragments locus 9C
206	1.116	3.214	NM_019752.2		HTRA2	HtrA serine peptidase 2
207	1.323	0	NM_026790.1		IFI27	interferon, alpha-inducible protein 27
208	1.234	3.214	NM_008332.2		IFIT2	interferon-induced protein with tetratricopeptide repeats 2
209	1.359	2.38	NM_026820		IFITM1	interferon induced transmembrane protein 1 (9-27)
210	1.577	0	NM_025378.1	D	IFITM3	interferon induced transmembrane protein 3 (1-8U)
211	1.467	0	NM_025378.1	D	IFITM3	interferon induced transmembrane protein 3 (1-8U)
212	-0.835	1.138	XM_194109.2		IGSF3	immunoglobulin superfamily, member 3
213	-0.755	2.127	NM_010549.1		IL11RA	interleukin 11 receptor, alpha
214	-0.835	3.214	NM_008361		IL1B	interleukin 1, beta
215	-0.886	3.214	AK020663		IL6R	interleukin 6 receptor
216	-0.879	2.127	NM_011919.3		ING1	inhibitor of growth family, member 1
217	1.207	0.633	NM_029665.2		IPO11	importin 11
218	-0.866	3.214	NM_025526.1		ISCU	iron-sulfur cluster scaffold homolog (E. coli)
219	-0.889	4.108	NM_012043.2		ISLR	immunoglobulin superfamily containing leucine-rich repeat
220	1.246	0	XM_194279		JMJD1A	jumonji domain containing 1A
221	-0.817	1.138	NM_008416.1		JUNB	jun B proto-oncogene
222	-0.829	0	NM_172872.2		KANK4	KN motif and ankyrin repeat domains 4
223	-0.874	2.127	NM_145958.1		KBTBD2	kelch repeat and BTB (POZ) domain containing 2
224	-0.812	1.138	XM_133614.4		KCTD14	potassium channel tetramerisation domain containing 14
225	-0.886	3.214	NM_011317.2		KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1
226	1.15	1.345	NM_028791.3		KIAA0082	KIAA0082
227	-0.76	3.214	NM_020568.1		KIAA1881	KIAA1881
228	-0.852	0	XM_358544.1		KIF1A	kinesin family member 1A
229	-0.617	4.108	NM_008443.2		KIF3A	kinesin family member 3A
230	1.116	4.108	NM_010629.1		KIFAP3	kinesin-associated protein 3
231	1.124	4.108	NM_010685.2		LAMP2	lysosomal-associated membrane protein 2
232	-0.802	3.214	NM_010688.2		LASP1	LIM and SH3 protein 1
233	-0.864	1.401	NM_008879.2		LCP1	lymphocyte cytosolic protein 1 (L-plastin)
234	1.218	2.127	NM_010708.1		LOC284194	galectin-9 like
235	-0.871	1.401	NM_007905.1		LOC653441	similar to polyhomeotic 1-like
236	1.111	3.214	NM_028894.1		LONRF3	LON peptidase N-terminal domain and ring finger 3
237	-0.816	1.138	NM_010729.2		LOXL1	lysyl oxidase-like 1

	A	B	C	D	E	F
1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
238	-0.727	2.127	NM_029796.2		LRG1	leucine-rich alpha-2-glycoprotein 1
239	-0.857	0	NM_177152.4		LRIG3	leucine-rich repeats and immunoglobulin-like domains 3
240	-0.748	0	XM_358823.1		LRRC15	leucine rich repeat containing 15
241	1.202	0	NM_025948.1		LSM14A	LSM14A, SCD6 homolog A (<i>S. cerevisiae</i>)
242	-0.872	2.38	NM_030597.2		LSM2	LSM2 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)
243	-0.801	3.214	NM_010741		LY6C1	lymphocyte antigen 6 complex, locus C1
244	-0.863	3.214	NM_172778.1		MAOB	monoamine oxidase B
245	-0.889	4.108	NM_009006		MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2
246	1.181	4.108	NM_027314.2		MARCH5	membrane-associated ring finger (C3HC4) 5
247	-0.855	2.708	AK031598.1		MASP1	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)
248	-0.834	0.797	NM_008567.1		MCM6	minichromosome maintenance complex component 6
249	1.412	4.108	AK042346		MED23	mediator complex subunit 23
250	-0.882	2.708	NM_145426.1		MFAP3	microfibrillar-associated protein 3
251	-0.855	2.127	NM_015776		MFAP5	microfibrillar associated protein 5
252	-0.682	2.127	NM_008594		MFGE8	milk fat globule-EGF factor 8 protein
253	1.123	3.214	AK007898		MFSD11	major facilitator superfamily domain containing 11
254	1.134	3.214	NM_026050.1		MGC12966	hypothetical protein LOC84792
255	-0.767	0.797	NM_012022.1		MGI:1349458	per-pentamer repeat gene
256	1.472	0	NM_010806.1	D	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to, 4
257	1.119	4.108	NM_010806.1	D	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to, 4
258	-0.776	2.38	NM_026178.2		MMD	monocyte to macrophage differentiation-associated
259	-0.741	0	NM_008610.1		MMP2	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)
260	-0.876	4.108	NM_010809.1		MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatinase)
261	-0.862	0.797	XM_357108.1		MRPL44	mitochondrial ribosomal protein L44
262	-0.826	2.127	NM_028722.1		MSL-1	male-specific lethal-1 homolog
263	-0.812	0	NM_010833.1		MSN	moesin
264	-0.849	3.214	NM_054082.1		MTA3	metastasis associated 1 family, member 3
265	-0.859	3.214	NM_019880.2	D	MTCH1	mitochondrial carrier homolog 1 (<i>C. elegans</i>)
266	-0.864	2.127	NM_019880.2	D	MTCH1	mitochondrial carrier homolog 1 (<i>C. elegans</i>)
267	1.138	4.108	NM_026002.3		MTDH	metadherin
268	-0.869	4.108	NM_178051.3		MTERFD2	MTERF domain containing 2
269	-0.821	2.127	NM_013827.1		MTF2	metal response element binding transcription factor 2
270	1.137	1.345	NM_172308.2		MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
271	1.304	0	NM_008638		MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase
272	-0.865	2.708	AK010766		MTIF2	mitochondrial translational initiation factor 2
273	-0.844	2.127	NM_013604.1		MTX1	metaxin 1

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
274	1.279	0.633	NM_013606		MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
275	-0.854	1.138	NM_139300	D	MYLK	myosin light chain kinase
276	-0.859	2.708	NM_139300	D	MYLK	myosin light chain kinase
277	1.135	4.108	NM_010863.1		MYO1B	myosin IB
278	1.207	0	NM_021524.1		NAMPT	nicotinamide phosphoribosyltransferase
279	-0.812	1.138	NM_173437.1		NAV1	neuron navigator 1
280	1.258	3.214	NM_025987.1		NDUFA6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa
281	-0.831	2.127	NM_026703.1		NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
282	1.347	2.38	NM_023172.2		NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
283	-0.921	3.214	NM_010890.2		NEDD4	neural precursor cell expressed, developmentally down-regulated 4
284	-0.774	0.797	NM_010906.1	D	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)
285	-0.861	3.214	S81451	D	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)
286	-0.861	2.708	NM_010917.1		NID1	nidogen 1
287	1.217	0.633	NM_008695.1		NID2	nidogen 2 (osteonidogen)
288	1.182	2.127	NM_021303.1		NOC2L	nucleolar complex associated 2 homolog (S. cerevisiae)
289	-0.869	3.214	NM_133800.2		NOL12	nucleolar protein 12
290	-0.885	2.708	NM_025533.1		NOSIP	nitric oxide synthase interacting protein
291	1.131	2.708	NM_145469.1		NPAL2	NIPA-like domain containing 2
292	-0.903	3.214	NM_010151.1		NR2F1	nuclear receptor subfamily 2, group F, member 1
293	-0.871	4.108	NM_008737.1		NRP1	neuropilin 1
294	-0.851	0.797	NM_008740.2		NSF	N-ethylmaleimide-sensitive factor
295	-0.898	3.214	NM_010947.2		NTN2L	netrin 2-like (chicken)
296	1.197	2.38	NM_139144.2		OGT	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)
297	-0.911	4.108	NM_146332.1		OLFR135	olfactory receptor 135
298	1.197	3.214	NM_130885.1		OXR1	oxidation resistance 1
299	1.461	0	NM_008774.2		PABPC1	poly(A) binding protein, cytoplasmic 1
300	-0.854	3.214	NM_011960.1		PARG	poly (ADP-ribose) glycohydrolase
301	1.212	0.633	NM_030253.1		PARP9	poly (ADP-ribose) polymerase family, member 9
302	-0.833	0.797	NM_008788.1		PCOLCE	procollagen C-endopeptidase enhancer
303	1.139	2.708	XM_133378.3		PDCD2L	programmed cell death 2-like
304	-0.882	4.108	AK011999		PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)
305	1.16	3.214	NM_008808		PDGFA	platelet-derived growth factor alpha polypeptide
306	-0.849	2.38	NM_011058.1		PDGFRA	platelet-derived growth factor receptor, alpha polypeptide
307	-0.857	3.214	NM_016861.1		PDLIM1	PDZ and LIM domain 1 (elfin)
308	-0.865	3.214	NM_026441.2		PEF1	penta-EF-hand domain containing 1
309	1.146	2.38	NM_008827.2		PGF	placental growth factor
310	1.413	0	NM_008828		PGK1	phosphoglycerate kinase 1
311	1.299	3.214	NM_016783.2		PGRMC1	progesterone receptor membrane component 1

	A	B	C	D	E	F
1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
312	1.159	2.38	NM_007531.1		PHB2	prohibitin 2
313	-0.884	3.214	NM_146135.1		PIAS3	protein inhibitor of activated STAT, 3
314	1.415	2.127	NM_133779.1		PIGT	phosphatidylinositol glycan anchor biosynthesis, class T
315	1.953	0.633	NM_008843.1		PIP	prolactin-induced protein
316	-0.868	3.214	NM_008850.1		PITPNA	phosphatidylinositol transfer protein, alpha
317	-0.874	4.108	NM_008873.2		PLAU	plasminogen activator, urokinase
318	-0.838	2.38	NM_011962.2		PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
319	-0.808	3.214	NM_025802.1		PNPLA2	patatin-like phospholipase domain containing 2
320	-0.827	1.401	XM_282920.1		POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa
321	1.301	3.214	NM_023127		POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
322	-0.882	4.108	NM_008854		PRKACA	protein kinase, cAMP-dependent, catalytic, alpha
323	-0.817	3.214	NM_011100.3		PRKACB	protein kinase, cAMP-dependent, catalytic, beta
324	-0.786	0	NM_011101.3		PRKCA	protein kinase C, alpha
325	-0.865	0	XM_131444.4		PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)
326	1.134	4.108	NM_133701.1		PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)
327	-0.805	1.401	NM_028195		PSCD4	pleckstrin homology, Sec7 and coiled-coil domains 4
328	-0.882	2.38	NM_133948.2		PSIP1	PC4 and SFRS1 interacting protein 1
329	1.215	4.108	NM_011191.1		PSME2B-PS	protease (prosome, macropain) 28 subunit beta B, pseudogene
330	-0.872	3.214	XM_127497.2		PTCD2	pentatricopeptide repeat domain 2
331	-0.916	4.108	NM_008984		PTPRM	protein tyrosine phosphatase, receptor type, M
332	-0.878	4.108	AK032604		PTPRS	protein tyrosine phosphatase, receptor type, S
333	1.161	2.127	NM_021888.1		QTRT1	queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase)
334	-0.797	0	NM_008997.1		RAB11B	RAB11B, member RAS oncogene family
335	-0.861	4.108	NM_009000.2		RAB24	RAB24, member RAS oncogene family
336	-0.896	2.708	NM_009005.1		RAB7A	RAB7A, member RAS oncogene family
337	-0.854	3.214	NM_009015.2		RAD54L	RAD54-like (S. cerevisiae)
338	-0.876	2.38	NM_009058.1		RALGDS	ral guanine nucleotide dissociation stimulator
339	-0.84	1.401	NM_178045.3	D	RASSF4	Ras association (RalGDS/AF-6) domain family member 4
340	-0.843	2.127	NM_178045.3	D	RASSF4	Ras association (RalGDS/AF-6) domain family member 4
341	-0.777	0	NM_009031.2		RBBP7	retinoblastoma binding protein 7
342	1.217	2.127	XM_131139.4		RBM15	RNA binding motif protein 15
343	1.164	0	NM_178608.2		REEP1	receptor accessory protein 1
344	-0.816	0	NM_007874.2		REEP5	receptor accessory protein 5
345	1.15	4.108	NM_139292.1		REEP6	receptor accessory protein 6
346	1.515	2.127	NR_003278.1		RN18S	18S RNA
347	-0.862	2.708	NM_013876.2		RNF11	ring finger protein 11
348	1.098	4.108	NM_153503.1		RNF113A1	ring finger protein 113A1
349	-0.884	2.708	NM_028019.1		RNF135	ring finger protein 135
350	-0.846	3.214	NM_207204.1		RP4-691N24.1	ninein-like
351	1.23	2.127	NM_009076		RPL12	ribosomal protein L12
352	-0.846	0.797	NM_022891.1		RPL23	ribosomal protein L23

	A	B	C	D	E	F
1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
353	1.244	4.108	NM_026055.1		RPL39	ribosomal protein L39
354	1.143	3.214	NM_011297.2		RPS24	ribosomal protein S24
355	1.433	0.633	NM_021384.2		RSAD2	radical S-adenosyl methionine domain containing 2
356	-0.89	2.708	NM_019685.1		RUVBL1	RuvB-like 1 (E. coli)
357	1.369	1.01	NM_009112.1		S100A10	S100 calcium binding protein A10
358	-0.865	4.108	NM_016926.1		SART3	squamous cell carcinoma antigen recognized by T cells 3
359	-0.846	2.127	NM_153790.1		SCARF2	scavenger receptor class F, member 2
360	-0.731	0	NM_011325.1		SCNN1B	sodium channel, nonvoltage-gated 1, beta (Liddle syndrome)
361	-0.881	3.214	NM_011327.1		SCP2	sterol carrier protein 2
362	1.306	3.214	NM_025468.1		SEC11C	SEC11 homolog C (S. cerevisiae)
363	1.164	1.01	NM_153055.2		SEC63	SEC63 homolog (S. cerevisiae)
364	-0.888	2.127	XM_127336.2		SECISBP2	SECIS binding protein 2
365	-0.698	0	NM_011340.2		SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
366	-0.834	1.401	NM_030261		SESN3	sestrin 3
367	-0.783	0.797	NM_009186		SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)
368	-0.794	0.797	NM_172755.2		SFRS14	splicing factor, arginine/serine-rich 14
369	-0.875	2.127	NM_024480.2		SH3BP5L	SH3-binding domain protein 5-like
370	1.186	4.108	NM_009194.1		SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
371	1.283	0	NM_018861.2		SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4
372	-0.802	0.797	NM_153150.1		SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
373	1.385	0	NM_011400.1		SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1
374	-0.9	2.38	NM_021435.1		SLC35B4	solute carrier family 35, member B4
375	1.161	2.127	NM_032008.2		SLMAP	sarcolemma associated protein
376	-0.886	3.214	NM_020618.3		SMARCE1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
377	-0.823	1.401	NM_022315.1		SMOC2	SPARC related modular calcium binding 2
378	1.158	2.38	NM_029701.1		SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)
379	1.263	0	NM_011451.1		SPHK1	sphingosine kinase 1
380	-0.849	4.108	NM_025287.1		SPOP	speckle-type POZ protein
381	-0.879	2.127	NM_029035.2		SPSB1	splA/ryanodine receptor domain and SOCS box containing 1
382	-0.805	0.797	NM_175836.1		SPTBN1	spectrin, beta, non-erythrocytic 1
383	1.213	2.38	NM_026130.1		SRPR	signal recognition particle receptor ('docking protein')
384	1.258	3.214	NM_026155.1		SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)
385	1.178	0	NM_153091.2		ST7L	suppression of tumorigenicity 7 like
386	1.234	3.214	BC057690.1		STAT1	signal transducer and activator of transcription 1, 91kDa

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
387	-0.812	4.108	NM_028800		STK40	serine/threonine kinase 40
388	-0.862	3.214	NM_175162.2		STOX2	storkhead box 2
389	-0.834	4.108	NM_009304.1		SYNGR2	synaptogyrin 2
390	1.398	0.633	NM_020047.2		TACSTD2	tumor-associated calcium signal transducer 2
391	1.204	3.214	NM_001081499.2		TBC1D8B	TBC1 domain family, member 8B (with GRAM domain)
392	-0.788	1.401	NM_009368.1		TGFB3	transforming growth factor, beta 3
393	-0.885	3.214	XM_129857.4		TGFBRAP1	transforming growth factor, beta receptor associated protein 1
394	-0.799	1.138	NM_009382.2		THY1	Thy-1 cell surface antigen
395	-0.78	0	NM_011593		TIMP1	TIMP metalloproteinase inhibitor 1
396	-0.721	0	NM_009388.2		TKT	transketolase (Wernicke-Korsakoff syndrome)
397	1.194	3.214	NM_134020.1		TMED4	transmembrane emp24 protein transport domain containing 4
398	1.129	4.108	NM_201359.1		TMEM106C	transmembrane protein 106C
399	-0.866	1.401	NM_133804.1		TMEM132A	transmembrane protein 132A
400	1.131	2.38	NM_028264.2		TMEM55A	transmembrane protein 55A
401	1.149	2.127	NM_024246.3		TMEM79	transmembrane protein 79
402	1.138	3.214	NM_152800.1		TOR2A	torsin family 2, member A
403	1.185	2.38	NM_009413.1		TPD52L1	tumor protein D52-like 1
404	-0.635	2.38	NM_022314		TPM3	tropomyosin 3
405	1.191	4.108	NM_009418.1		TPP2	tripeptidyl peptidase II
406	-0.86	1.401	NM_176842.2		TPRKB	TP53RK binding protein
407	1.243	1.01	NM_028173.1		TRAM1	translocation associated membrane protein 1
408	1.291	0	NM_144554.1		TRIB3	tribbles homolog 3 (Drosophila)
409	1.194	0.633	XM_126545.2		TRIM25	tripartite motif-containing 25
410	1.269	2.38	NM_026473.2		TUBB6	tubulin, beta 6
411	-0.828	3.214	NM_026872.1		UBAP2	ubiquitin associated protein 2
412	-0.879	3.214	NM_009458.3		UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)
413	1.198	4.108	NM_019586		UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)
414	-0.776	3.214	NM_080562.2		UBOX5	U-box domain containing 5
415	-0.862	4.108	NM_138668.1		UFSP2	UFM1-specific peptidase 2
416	1.127	4.108	XM_620754.3		ULK3	unc-51-like kinase 3 (C. elegans)
417	-0.814	2.708	NM_029012.1		UNQ1887	signal peptide peptidase 3
418	1.207	3.214	NM_021522.2		USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)
419	1.289	1.01	NM_011909.1		USP18	ubiquitin specific peptidase 18
420	1.137	1.345	NM_144937.2		USP3	ubiquitin specific peptidase 3
421	1.188	4.108	AK082943		USP33	ubiquitin specific peptidase 33
422	-0.818	0	NM_144826.2		UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)
423	1.181	3.214	NM_009502		VCL	vinculin
424	1.541	0	NM_009505.2		VEGFA	vascular endothelial growth factor A
425	1.26	0	NM_013703.1	D	VLDLR	very low density lipoprotein receptor
426	1.213	0	NM_013703	D	VLDLR	very low density lipoprotein receptor
427	1.173	2.38	NM_022997		VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)

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1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
428	-0.573	4.108	NM_011709.2		WAP	whey acidic protein
429	1.153	0.633	NM_027057		WDFY1	WD repeat and FYVE domain containing 1
430	-0.865	4.108	NM_177267.3		WDR22	WD repeat domain 22
431	-0.789	0	NM_009525.2		WNT5B	wingless-type MMTV integration site family, member 5B
432	1.174	3.214	NM_019653.2		WSB1	WD repeat and SOCS box-containing 1
433	-0.835	3.214	NM_133791.3		WWC2	WW and C2 domain containing 2
434	1.131	2.127	NM_028198		XPO5	exportin 5
435	-0.875	4.108	NM_009534.1		YAP1	Yes-associated protein 1, 65kDa
436	-0.848	2.38	NM_011732.1		YBX1	Y box binding protein 1
437	-0.804	4.108	NM_138303.1		YIPF2	Yip1 domain family, member 2
438	-0.891	2.38	XM_358776.1		ZDHH8	zinc finger, DHHC-type containing 8
439	-0.824	2.127	NM_007496.1		ZFH3	zinc finger homeobox 3
440	1.191	2.708	NM_013844.1		ZFP68	zinc finger protein 68
441	-0.863	3.214	NM_146175.2		ZNF282	zinc finger protein 282
442	-0.907	4.108	NM_173769.2		ZNF641	zinc finger protein 641
443	1.715	0.633	XM_359007.1			This ID not mapped to the IPAKB
444	1.432	0.633	XM_148611.1			This ID not mapped to the IPAKB
445	1.426	2.708	XM_356892.1			This ID not mapped to the IPAKB
446	1.337	1.01	XM_485210			This ID not mapped to the IPAKB
447	1.328	0	XM_147335.2			This ID not mapped to the IPAKB
448	1.287	0	NM_010156.2			This ID not mapped to the IPAKB
449	1.252	0	XM_355081.1			This ID not mapped to the IPAKB
450	1.242	3.214	XM_139474.1			This ID not mapped to the IPAKB
451	1.235	0	XM_124389.1			This ID not mapped to the IPAKB
452	1.234	4.108	XM_356224.1			This ID not mapped to the IPAKB
453	1.209	2.127	NM_020573.1			This ID not mapped to the IPAKB
454	1.2	2.38	XM_489186			This ID not mapped to the IPAKB
455	1.182	2.38	XM_356873.1			This ID not mapped to the IPAKB
456	1.156	2.127	XM_132529.2			This ID not mapped to the IPAKB
457	1.141	3.214	XM_283274.2			This ID not mapped to the IPAKB
458	1.134	4.108	C330006P03Rik			This ID not mapped to the IPAKB
459	1.126	3.214	9830115L13Rik			This ID not mapped to the IPAKB
460	1.115	2.127	XM_130797.3			This ID not mapped to the IPAKB
461	1.114	1.345	XM_284356.2			This ID not mapped to the IPAKB
462	-0.662	0.797	XM_354700			This ID not mapped to the IPAKB
463	-0.718	3.214	XM_145698.4			This ID not mapped to the IPAKB
464	-0.79	1.401	NM_012059.2			This ID not mapped to the IPAKB
465	-0.82	2.127	XM_484355			This ID not mapped to the IPAKB
466	-0.824	2.38	1110003O08Rik			This ID not mapped to the IPAKB
467	-0.834	2.127	XM_148568.1			This ID not mapped to the IPAKB
468	-0.834	2.127	XM_358661.1			This ID not mapped to the IPAKB

	A	B	C	D	E	F
1	Fold Change*	False Discovery Rate (q-value)	ID†	Notes‡	Molecules§	Description
469	-0.838	3.214	NM_177062.2			This ID not mapped to the IPAKB
470	-0.845	2.38	XM_109767.2			This ID not mapped to the IPAKB
471	-0.859	2.38	9530083O12Rik			This ID not mapped to the IPAKB
472	-0.862	2.38	XM_195728.3			This ID not mapped to the IPAKB
473	-0.863	3.214	NG_005838.1			This ID not mapped to the IPAKB
474	-0.864	3.214	XM_150337.1			This ID not mapped to the IPAKB
475	-0.867	1.401	XM_134183.4			This ID not mapped to the IPAKB
476	-0.874	2.708	XM_489155			This ID not mapped to the IPAKB
477	-0.874	2.127	XM_127605.4			This ID not mapped to the IPAKB
478	-0.908	3.214	NG_005612.1			This ID not mapped to the IPAKB
479	-0.924	4.108	XM_143254.3			This ID not mapped to the IPAKB