

**Legends for Supplementary Online Materials.**

**Figure S1. SB203580 and Bay 11-7082 inhibit of p38<sup>mapk</sup> and NF- $\kappa$ B in lung fibroblastic cells.** (A) The p38<sup>mapk</sup> inhibitor SB203580 (20  $\mu$ M) blocks both basal, and TNF- $\alpha$  (10 ng/ml) and IFN- $\gamma$  (50 U/ml) induced phosphorylation of HSP27, a downstream target of p38<sup>mapk</sup>, in the human MRC-5 lung fibroblastic cells. Equal loading of protein was verified by blotting for  $\beta$ -actin. The upper panel is a representative blot from one of three independent experiments, while the lower panel shows the mean $\pm$ SEM for all three experiments. (B) The NF- $\kappa$ B inhibitor Bay 11-7082 (3  $\mu$ M) blocks TNF- $\alpha$  and IFN- $\gamma$  induced degradation of I $\kappa$ B- $\alpha$  in the MRC-5 fibroblasts. Equality in protein loading is illustrated by the  $\beta$ -actin blot. The upper panel is a representative blot from one of three independent experiments, while the lower panel displays the mean  $\pm$ SEM for all three experiments. The untreated, without vehicle, control is labeled Utr.

**Table S1.** Transcripts differentially expressed in fibroblast cell lines treated with TNF- $\alpha$  (10 ng/ml) and IFN- $\gamma$  (50 U/ml) for 36 hr. These 603 transcripts meet the statistical criteria for differential expression (unpaired t-test, FDR<0.05). The fold ratio (stimulated/unstimulated) for each fibroblast cell line is given along with the associated p-value for the group.



Probeset ID	Symbol	Fold Ratio (Stim/Con)			p-value	Gene Title
		FS087	MRC5	N78		
203915_at	CXCL9	5360.6	5251.0	5104.1	4.49E-09	chemokine (C-X-C motif) ligand 9
210029_at	IDO1	4745.4	4316.5	4080.0	1.21E-08	indoleamine 2,3-dioxygenase 1
205890_s_at	GABBR1 /// UBD	4318.1	3644.9	4808.9	4.58E-08	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D
211122_s_at	CXCL11	2409.2	2738.5	2224.0	1.42E-07	chemokine (C-X-C motif) ligand 11
1405_i_at	CCL5	2010.2	2818.3	2381.2	1.69E-07	chemokine (C-C motif) ligand 5
228501_at	GALNTL2	0.034	0.030	0.032	2.53E-07	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase
1555759_a_at	CCL5	4927.9	3794.2	5586.6	4.73E-07	chemokine (C-C motif) ligand 5
238581_at	GBP5	280.1	283.0	245.0	7.01E-07	guanylate binding protein 5
239206_at	CR1L	11.7	14.3	12.4	1.11E-06	complement component (3b/4b) receptor 1-like
239205_s_at	CR1 /// CR1L	31.5	27.9	34.6	1.20E-06	complement component (3b/4b) receptor 1 (Knops blood group) /// complement compo
230178_s_at	---	0.201	0.199	0.216	1.74E-06	---
33304_at	ISG20	808.6	823.8	884.5	1.90E-06	interferon stimulated exonuclease gene 20kDa
242625_at	RSAD2	894.2	589.6	1355.3	2.87E-06	radical S-adenosyl methionine domain containing 2
226609_at	DCBLD1	3.8	4.6	4.2	3.06E-06	discoidin, CUB and LCCL domain containing 1
217933_s_at	LAP3	14.6	14.5	16.9	3.29E-06	leucine aminopeptidase 3
224597_at	---	0.421	0.423	0.414	3.38E-06	---
213797_at	RSAD2	1298.2	552.6	1167.5	3.57E-06	radical S-adenosyl methionine domain containing 2
225162_at	SH3D19	0.082	0.100	0.107	3.76E-06	SH3 domain containing 19
215485_s_at	ICAM1	197.4	238.3	119.2	3.91E-06	intercellular adhesion molecule 1
204655_at	CCL5	3474.2	1772.9	3855.3	4.35E-06	chemokine (C-C motif) ligand 5
238455_at	---	0.127	0.109	0.145	4.75E-06	---
210163_at	CXCL11	1358.7	2347.8	1134.0	4.91E-06	chemokine (C-X-C motif) ligand 11
207181_s_at	CASP7	4.2	4.0	4.5	5.04E-06	caspase 7, apoptosis-related cysteine peptidase
222868_s_at	IL18BP	317.2	320.3	356.3	5.24E-06	interleukin 18 binding protein
202902_s_at	CTSS	459.6	664.0	815.1	5.44E-06	cathepsin S
219684_at	RTP4	138.1	126.7	174.3	5.46E-06	receptor (chemosensory) transporter protein 4
204698_at	ISG20	1046.9	1060.1	1436.9	5.53E-06	interferon stimulated exonuclease gene 20kDa
201980_s_at	RSU1	2.7	2.8	2.9	5.62E-06	Ras suppressor protein 1
220358_at	BATF3	81.8	124.9	88.6	6.13E-06	basic leucine zipper transcription factor, ATF-like 3
225483_at	VPS26B	0.336	0.302	0.334	6.27E-06	vacuolar protein sorting 26 homolog B (S. pombe)
210190_at	STX11	7.5	7.1	6.0	6.38E-06	syntaxin 11
230966_at	IL411	74.3	92.4	122.0	6.61E-06	interleukin 4 induced 1

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		FS087	MRC5	N78		
202901_x_at	CTSS	110.7	135.2	83.8	6.74E-06	cathepsin S
224225_s_at	ETV7	61.3	36.0	58.7	6.96E-06	ets variant 7
209545_s_at	RIPK2	18.3	20.1	22.0	7.54E-06	receptor-interacting serine-threonine kinase 2
232617_at	CTSS	294.9	254.3	433.5	7.65E-06	cathepsin S
204224_s_at	GCH1	603.1	831.5	520.0	8.24E-06	GTP cyclohydrolase 1
239582_at	PML	15.0	13.6	20.1	8.49E-06	promyelocytic leukemia
219357_at	GTPBP1	6.0	7.0	7.5	8.50E-06	GTP binding protein 1
200878_at	EPAS1	0.177	0.137	0.148	8.53E-06	endothelial PAS domain protein 1
1555515_a_at	C1orf2	5.0	6.4	5.7	8.55E-06	chromosome 1 open reading frame 2
212933_x_at	RPL13	0.605	0.629	0.592	9.00E-06	ribosomal protein L13
205660_at	OASL	403.5	255.8	602.7	9.75E-06	2'-5'-oligoadenylate synthetase-like
204748_at	PTGS2	30.2	23.7	27.7	1.06E-05	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxyge
224626_at	SLC35A4	2.2	2.2	2.4	1.10E-05	solute carrier family 35, member A4
222905_s_at	TMEM143	0.540	0.509	0.525	1.13E-05	transmembrane protein 143
1569030_s_at	NUB1	5.0	6.5	6.5	1.15E-05	negative regulator of ubiquitin-like proteins 1
209544_at	RIPK2	13.2	14.0	13.7	1.16E-05	receptor-interacting serine-threonine kinase 2
212818_s_at	ASB1	0.150	0.172	0.124	1.20E-05	ankyrin repeat and SOCS box-containing 1
202590_s_at	PDK2	0.204	0.265	0.232	1.22E-05	pyruvate dehydrogenase kinase, isozyme 2
227677_at	JAK3	27.5	20.1	35.9	1.25E-05	Janus kinase 3 (a protein tyrosine kinase, leukocyte)
235574_at	GBP4	179.5	294.6	135.0	1.37E-05	guanylate binding protein 4
204211_x_at	EIF2AK2	3.2	2.7	2.9	1.51E-05	eukaryotic translation initiation factor 2-alpha kinase 2
219716_at	APOL6	19.7	12.4	13.4	1.58E-05	apolipoprotein L, 6
209761_s_at	SP110	7.2	9.5	10.1	1.58E-05	SP110 nuclear body protein
204683_at	ICAM2	13.1	14.1	10.2	1.62E-05	intercellular adhesion molecule 2
217739_s_at	NAMPT	7.4	7.8	10.5	1.65E-05	nicotinamide phosphoribosyltransferase
212217_at	PREPL	0.244	0.258	0.277	1.68E-05	prolyl endopeptidase-like
219950_s_at	TIAM2	1.0	1.0	1.0	1.69E-05	T-cell lymphoma invasion and metastasis 2
200905_x_at	HLA-E	6.3	6.4	5.7	1.71E-05	major histocompatibility complex, class I, E
216841_s_at	SOD2	29.0	25.8	36.1	1.72E-05	superoxide dismutase 2, mitochondrial
223776_x_at	TINF2	5.3	4.4	5.2	1.77E-05	TERF1 (TRF1)-interacting nuclear factor 2
228690_s_at	NDUFA11	0.500	0.550	0.541	1.84E-05	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa
215223_s_at	SOD2	79.1	57.5	88.5	1.96E-05	superoxide dismutase 2, mitochondrial
228439_at	BATF2	194.5	144.1	157.7	1.99E-05	basic leucine zipper transcription factor, ATF-like 2
1559530_at	---	4.5	5.1	4.4	2.02E-05	---
212505_s_at	KIAA0892	1.9	1.9	2.1	2.07E-05	KIAA0892
212733_at	KIAA0226	4.6	5.2	6.5	2.07E-05	KIAA0226
58916_at	KCTD14	129.2	81.0	87.3	2.09E-05	potassium channel tetramerisation domain containing 14
205599_at	TRAF1	209.8	85.6	126.8	2.09E-05	TNF receptor-associated factor 1

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		FS087	MRC5	N78		
202644_s_at	TNFAIP3	135.5	286.1	146.6	2.16E-05	tumor necrosis factor, alpha-induced protein 3
201891_s_at	B2M	1.6	1.6	1.5	2.16E-05	beta-2-microglobulin
243176_at	---	0.360	0.318	0.388	2.16E-05	---
AFFX-HUMISGF	STAT1	3.5	3.4	3.8	2.21E-05	signal transducer and activator of transcription 1, 91kDa
224738_x_at	RPL7L1	0.487	0.524	0.484	2.23E-05	ribosomal protein L7-like 1
38241_at	BTN3A3	10.3	7.4	9.4	2.28E-05	butyrophilin, subfamily 3, member A3
226865_at	---	0.074	0.098	0.068	2.34E-05	---
219202_at	RHBDF2	26.3	31.9	22.2	2.39E-05	rhomoid 5 homolog 2 (Drosophila)
201649_at	UBE2L6	5.7	6.3	7.1	2.41E-05	ubiquitin-conjugating enzyme E2L 6
238025_at	MLKL	30.4	21.5	31.1	2.41E-05	mixed lineage kinase domain-like
208771_s_at	LTA4H	0.311	0.318	0.337	2.44E-05	leukotriene A4 hydrolase
219590_x_at	DPH5	0.457	0.419	0.442	2.50E-05	DPH5 homolog (S. cerevisiae)
229625_at	GBP5	483.2	667.5	250.3	2.55E-05	guanylate binding protein 5
224452_s_at	MGC12966	0.602	0.620	0.561	2.66E-05	hypothetical protein LOC84792
211588_s_at	LOC652346 /// PML	14.0	9.5	11.2	2.67E-05	similar to promyelocytic leukemia protein isoform 1 /// promyelocytic leukemia
213413_at	STON1	0.048	0.032	0.037	2.67E-05	stonin 1
202643_s_at	TNFAIP3	336.5	615.2	249.8	2.73E-05	tumor necrosis factor, alpha-induced protein 3
229699_at	LOC100129 550	0.148	0.126	0.114	2.74E-05	Hypothetical protein LOC100129550 (LOC100129550), mRNA
208848_at	ADH5	0.373	0.436	0.380	2.78E-05	alcohol dehydrogenase 5 (class III), chi polypeptide
212017_at	FAM168B	0.174	0.141	0.142	2.81E-05	family with sequence similarity 168, member B
218776_s_at	TMEM62	10.4	15.1	17.9	2.92E-05	transmembrane protein 62
203828_s_at	IL32	523.8	965.5	1231.9	2.92E-05	interleukin 32
227918_s_at	ZYG11B	0.420	0.390	0.442	3.05E-05	zyg-11 homolog B (C. elegans)
204858_s_at	TYMP	86.5	47.1	73.8	3.09E-05	thymidine phosphorylase
210797_s_at	OASL	363.0	158.6	420.4	3.09E-05	2'-5'-oligoadenylate synthetase-like
219424_at	EBI3	58.7	109.6	115.4	3.17E-05	Epstein-Barr virus induced 3
202741_at	PRKACB	0.257	0.254	0.260	3.20E-05	protein kinase, cAMP-dependent, catalytic, beta
226757_at	IFIT2	49.1	59.7	111.4	3.29E-05	interferon-induced protein with tetratricopeptide repeats 2
223085_at	RNF19A	2.2	1.9	2.3	3.35E-05	ring finger protein 19A
32069_at	N4BP1	4.9	4.8	5.0	3.37E-05	NEDD4 binding protein 1
233540_s_at	CDK5RAP2	0.274	0.342	0.272	3.42E-05	CDK5 regulatory subunit associated protein 2
240214_at	---	0.505	0.530	0.501	3.43E-05	---
206553_at	OAS2	23.0	43.2	30.3	3.46E-05	2'-5'-oligoadenylate synthetase 2, 69/71kDa
225906_at	---	0.059	0.080	0.092	3.53E-05	---
217982_s_at	MORF4L1	0.770	0.768	0.802	3.58E-05	mortality factor 4 like 1
214459_x_at	HLA-C	3.1	3.0	3.6	3.62E-05	major histocompatibility complex, class I, C

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		FS087	MRC5	N78		
1553293_at	MRGPRX3	368.4	152.8	317.1	3.63E-05	MAS-related GPR, member X3
238226_at	FAM70B	2.4	2.0	2.2	3.91E-05	family with sequence similarity 70, member B
202727_s_at	IFNGR1	1.9	1.9	2.2	3.93E-05	interferon gamma receptor 1
226233_at	B3GALNT2	0.330	0.265	0.338	4.00E-05	beta-1,3-N-acetylgalactosaminyltransferase 2
219181_at	LIPG	13.1	13.8	20.6	4.09E-05	lipase, endothelial
208812_x_at	HLA-C	3.0	2.6	2.7	4.23E-05	major histocompatibility complex, class I, C
203927_at	NFKBIE	26.4	28.4	40.3	4.24E-05	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, ep
225338_at	ZYG11B	0.282	0.325	0.366	4.26E-05	zyg-11 homolog B (C. elegans)
235964_x_at	---	12.9	15.0	15.7	4.44E-05	---
217986_s_at	BAZ1A	5.8	6.2	7.2	4.51E-05	bromodomain adjacent to zinc finger domain, 1A
201339_s_at	SCP2	0.456	0.426	0.386	4.53E-05	sterol carrier protein 2
204785_x_at	IFNAR2	4.3	3.8	5.2	4.60E-05	interferon (alpha, beta and omega) receptor 2
213620_s_at	ICAM2	40.1	24.2	52.7	4.61E-05	intercellular adhesion molecule 2
1553118_at	THEM4	0.394	0.373	0.430	4.62E-05	thioesterase superfamily member 4
202687_s_at	TNFSF10	436.7	546.5	1171.7	4.64E-05	tumor necrosis factor (ligand) superfamily, member 10
208745_at	ATP5L	0.495	0.428	0.487	4.66E-05	ATP synthase, H+ transporting, mitochondrial FO complex, subunit G
220751_s_at	C5orf4	0.065	0.097	0.085	4.70E-05	chromosome 5 open reading frame 4
204533_at	CXCL10	4062.9	1500.4	5830.3	4.70E-05	chemokine (C-X-C motif) ligand 10
214329_x_at	TNFSF10	294.0	190.9	376.2	4.73E-05	tumor necrosis factor (ligand) superfamily, member 10
205552_s_at	OAS1	327.7	271.0	728.0	5.11E-05	2',5'-oligoadenylate synthetase 1, 40/46kDa
212605_s_at	---	0.259	0.205	0.173	5.12E-05	---
201857_at	ZFR	0.669	0.711	0.717	5.17E-05	zinc finger RNA binding protein
217738_at	NAMPT	8.1	7.7	12.7	5.24E-05	nicotinamide phosphoribosyltransferase
226833_at	CYB5D1	0.327	0.388	0.378	5.26E-05	cytochrome b5 domain containing 1
202136_at	ZMYND11	0.427	0.378	0.329	5.30E-05	zinc finger, MYND domain containing 11
229174_at	C3orf38	5.1	5.4	5.9	5.39E-05	chromosome 3 open reading frame 38
240013_at	---	7.8	7.3	11.1	5.41E-05	---
212741_at	MAOA	0.047	0.058	0.059	5.50E-05	monoamine oxidase A
238007_at	ZNF271	0.451	0.394	0.386	5.51E-05	zinc finger protein 271
203607_at	INPP5F	0.446	0.423	0.514	5.54E-05	inositol polyphosphate-5-phosphatase F
208073_x_at	TTC3	0.126	0.129	0.118	5.55E-05	tetratricopeptide repeat domain 3
202108_at	PEPD	0.598	0.621	0.659	5.58E-05	peptidase D
200817_x_at	RPS10	0.573	0.612	0.571	5.64E-05	ribosomal protein S10
204019_s_at	SH3YL1	0.173	0.188	0.212	5.70E-05	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)
209619_at	CD74	740.5	242.9	1351.8	5.76E-05	CD74 molecule, major histocompatibility complex, class II invariant chain
214440_at	NAT1	2.5	2.2	2.6	5.78E-05	N-acetyltransferase 1 (arylamine N-acetyltransferase)

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		FS087	MRC5	N78		
213138_at	ARID5A	6.9	6.3	9.2	5.98E-05	AT rich interactive domain 5A (MRF1-like)
225729_at	C6orf89	0.283	0.335	0.345	6.05E-05	chromosome 6 open reading frame 89
229653_at	VPS53	0.326	0.330	0.309	6.07E-05	vacuolar protein sorting 53 homolog (S. cerevisiae)
204389_at	MAOA	0.129	0.100	0.160	6.18E-05	monoamine oxidase A
204187_at	GMPR	23.4	23.4	40.8	6.27E-05	guanosine monophosphate reductase
202688_at	TNFSF10	1057.9	1084.1	1012.8	6.27E-05	tumor necrosis factor (ligand) superfamily, member 10
207375_s_at	IL15RA	55.7	39.5	94.2	6.28E-05	interleukin 15 receptor, alpha
224763_at	RPL37	0.189	0.199	0.216	6.57E-05	Ribosomal protein L37, mRNA (cDNA clone IMAGE:6671394)
225216_at	CXorf39	0.411	0.436	0.357	6.61E-05	CDNA: FLJ21191 fis, clone COL00104
235505_s_at	---	0.139	0.185	0.172	6.68E-05	---
222582_at	PRKAG2	0.357	0.330	0.357	6.73E-05	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
208012_x_at	SP110	7.9	8.9	12.4	6.83E-05	SP110 nuclear body protein
219634_at	CHST11	4.0	4.9	5.6	6.84E-05	carbohydrate (chondroitin 4) sulfotransferase 11
204249_s_at	LMO2	26.9	51.9	32.9	6.94E-05	LIM domain only 2 (rhombotin-like 1)
225123_at	---	0.075	0.046	0.087	7.19E-05	---
235529_x_at	---	15.4	14.2	15.9	7.20E-05	---
202307_s_at	TAP1	25.7	29.8	42.4	7.20E-05	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
232666_at	OAS3	18.6	35.7	18.8	7.23E-05	2'-5'-oligoadenylate synthetase 3, 100kDa
203652_at	MAP3K11	1.6	1.8	1.6	7.33E-05	mitogen-activated protein kinase kinase kinase 11
210538_s_at	BIRC3	133.0	134.4	127.3	7.56E-05	baculoviral IAP repeat-containing 3
229553_at	PGM2L1	0.427	0.421	0.408	7.57E-05	phosphoglucomutase 2-like 1
226551_at	RIPK1	2.9	3.9	3.5	7.58E-05	receptor (TNFRSF)-interacting serine-threonine kinase 1
219809_at	WDR55	2.5	2.4	2.3	7.62E-05	WD repeat domain 55
201076_at	NHP2L1	0.563	0.611	0.575	7.66E-05	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)
201814_at	TBC1D5	0.483	0.433	0.464	7.68E-05	TBC1 domain family, member 5
225414_at	RNF149	3.3	3.9	4.4	7.72E-05	ring finger protein 149
225944_at	NLN	0.328	0.383	0.418	7.80E-05	neurolysin (metallopeptidase M3 family)
224809_x_at	TINF2	5.7	4.2	5.4	7.87E-05	TERF1 (TRF1)-interacting nuclear factor 2
235170_at	ZNF92	2.1	1.8	1.8	7.94E-05	zinc finger protein 92
239246_at	FARP1	0.179	0.225	0.205	7.98E-05	CDEP
213932_x_at	HLA-A	2.3	2.6	2.4	8.13E-05	major histocompatibility complex, class I, A
238029_s_at	SLC16A14	0.071	0.046	0.085	8.31E-05	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)
209762_x_at	SP110	7.8	9.9	12.4	8.48E-05	SP110 nuclear body protein
225625_at	ALKBH2	0.450	0.496	0.434	8.53E-05	alkB, alkylation repair homolog 2 (E. coli)
223192_at	SLC25A28	7.8	10.7	13.9	8.66E-05	solute carrier family 25, member 28
213716_s_at	SECTM1	34.8	36.2	97.0	8.91E-05	secreted and transmembrane 1
1552323_s_at	FAM122C	12.4	17.3	11.3	8.98E-05	family with sequence similarity 122C

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222572_at	PPM2C	2.2	2.3	2.1	9.35E-05	protein phosphatase 2C, magnesium-dependent, catalytic subunit
217780_at	C19orf56	0.668	0.678	0.739	9.41E-05	chromosome 19 open reading frame 56
226474_at	NLR5	17.3	21.7	18.8	9.46E-05	NLR family, CARD domain containing 5
204999_s_at	ATF5	8.4	10.7	11.7	9.54E-05	activating transcription factor 5
211678_s_at	RNF114	4.2	5.0	5.7	9.63E-05	ring finger protein 114
211528_x_at	HLA-G	4.2	3.7	4.5	9.63E-05	major histocompatibility complex, class I, G
220744_s_at	IFT122	0.424	0.496	0.494	9.73E-05	intraflagellar transport 122 homolog (Chlamydomonas)
225228_at	TMEM77	0.710	0.713	0.772	9.83E-05	transmembrane protein 77
228797_at	---	0.245	0.181	0.245	9.84E-05	---
231779_at	IRAK2	21.9	23.0	15.7	9.92E-05	interleukin-1 receptor-associated kinase 2
231137_at	---	0.390	0.461	0.450	9.99E-05	---
226883_at	---	0.358	0.338	0.282	9.99E-05	---
217947_at	CMTM6	0.728	0.667	0.709	1.00E-04	CKLF-like MARVEL transmembrane domain containing 6
205606_at	LRP6	0.225	0.228	0.186	0.0001	low density lipoprotein receptor-related protein 6
235175_at	GBP4	208.8	96.3	246.9	0.0001	guanylate binding protein 4
216526_x_at	HLA-C	2.5	2.4	3.0	0.0001	major histocompatibility complex, class I, C
210785_s_at	C1orf38	29.4	30.5	42.2	0.0001	chromosome 1 open reading frame 38
203137_at	WTAP	5.2	4.2	6.5	0.0001	Wilms tumor 1 associated protein
201422_at	IFI30	67.0	159.6	295.9	0.00011	interferon, gamma-inducible protein 30
201962_s_at	RNF41	0.279	0.256	0.190	0.00011	ring finger protein 41
204821_at	BTN3A3	8.8	7.2	9.7	0.00011	butyrophilin, subfamily 3, member A3
203449_s_at	TERF1	0.597	0.627	0.658	0.00011	telomeric repeat binding factor (NIMA-interacting) 1
205236_x_at	SOD3	12.3	6.5	10.6	0.00011	superoxide dismutase 3, extracellular
217752_s_at	CNDP2	4.7	4.1	5.0	0.00011	CNDP dipeptidase 2 (metallopeptidase M20 family)
209124_at	MYD88	6.7	4.7	6.8	0.00011	myeloid differentiation primary response gene (88)
219863_at	HERC5	61.1	72.1	142.3	0.00011	hect domain and RLD 5
201317_s_at	PSMA2	2.5	3.2	2.7	0.00011	proteasome (prosome, macropain) subunit, alpha type, 2
209815_at	PTCH1	0.158	0.085	0.090	0.00011	patched homolog 1 (Drosophila)
219283_at	C1GALT1C1	6.5	4.9	6.5	0.00011	C1GALT1-specific chaperone 1
212993_at	NACC2	0.411	0.381	0.317	0.00011	NACC family member 2, BEN and BTB (POZ) domain containing
232021_at	GLT8D3	0.451	0.486	0.425	0.00011	glycosyltransferase 8 domain containing 3
243141_at	SGMS2	0.160	0.106	0.126	0.00011	sphingomyelin synthase 2
203550_s_at	C1orf2	3.8	4.3	5.7	0.00011	chromosome 1 open reading frame 2
204439_at	IFI44L	230.8	115.7	690.6	0.00012	interferon-induced protein 44-like
226395_at	HOO3	0.272	0.230	0.270	0.00012	hook homolog 3 (Drosophila)
211529_x_at	HLA-G	4.0	5.3	4.8	0.00012	major histocompatibility complex, class I, G



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		FS087	MRC5	N78		
206272_at	RAB4A /// SPHAR	0.171	0.227	0.267	0.00012	RAB4A, member RAS oncogene family /// S-phase response (cyclin-related)
200887_s_at	STAT1	2.9	2.5	3.2	0.00012	signal transducer and activator of transcription 1, 91kDa
220975_s_at	C1QTNF1	16.0	15.0	21.2	0.00012	C1q and tumor necrosis factor related protein 1
206065_s_at	DPYS	1.6	1.4	1.4	0.00012	dihydropyrimidinase
217502_at	IFIT2	210.8	129.3	249.9	0.00012	interferon-induced protein with tetratricopeptide repeats 2
219540_at	ZNF267	10.8	9.2	14.7	0.00012	zinc finger protein 267
201064_s_at	PABPC4	0.183	0.198	0.168	0.00012	poly(A) binding protein, cytoplasmic 4 (inducible form)
203241_at	UVRAG	3.8	3.7	4.7	0.00012	UV radiation resistance associated gene
225199_at	---	0.225	0.222	0.286	0.00012	---
212163_at	KIDINS220	0.431	0.482	0.452	0.00012	kinase D-interacting substrate, 220kDa
200813_s_at	PAFAH1B1	0.537	0.507	0.557	0.00012	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit 45kDa
219691_at	SAMD9	7.2	14.1	13.3	0.00012	sterile alpha motif domain containing 9
226502_at	ELMOD2	0.369	0.309	0.287	0.00013	ELMO/CED-12 domain containing 2
225468_at	PATL1	2.5	3.4	3.2	0.00013	protein associated with topoisomerase II homolog 1 (yeast)
238417_at	PGM2L1	0.532	0.535	0.612	0.00013	phosphoglucomutase 2-like 1
210119_at	KCNJ15	19.1	23.5	38.1	0.00013	potassium inwardly-rectifying channel, subfamily J, member 15
204804_at	TRIM21	7.2	6.1	9.0	0.00013	tripartite motif-containing 21
219545_at	KCTD14	83.3	81.2	68.0	0.00013	potassium channel tetramerisation domain containing 14
221827_at	RBCK1	3.3	2.8	3.3	0.00013	RanBP-type and C3HC4-type zinc finger containing 1
221731_x_at	VCAN	0.155	0.119	0.102	0.00013	versican
226157_at	TFDP2	0.106	0.132	0.103	0.00013	CDNA clone IMAGE:4817695
219210_s_at	RAB8B	4.8	5.4	4.7	0.00013	RAB8B, member RAS oncogene family
228495_at	CCDC75	0.160	0.192	0.163	0.00013	coiled-coil domain containing 75
204806_x_at	HLA-F	7.4	7.1	10.7	0.00013	major histocompatibility complex, class I, F
222864_s_at	ZNF219	1.0	1.0	1.0	0.00013	zinc finger protein 219
227026_at	MPHOSPH 8	0.526	0.494	0.567	0.00014	M-phase phosphoprotein 8
226175_at	TTC9C	3.6	3.1	3.7	0.00014	tetratricopeptide repeat domain 9C
205486_at	TESK2	6.0	6.0	7.7	0.00014	testis-specific kinase 2
216862_s_at	LOC100133 946 /// MTCP1	0.232	0.333	0.266	0.00014	similar to mature T-cell proliferations 1 /// mature T-cell proliferation 1
222288_at	---	0.049	0.026	0.026	0.00014	---
218611_at	IER5	1.8	1.7	1.8	0.00014	immediate early response 5

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		FS087	MRC5	N78		
217436_x_at	HLA-A, A29, B, G, H, J	6.0	8.1	9.1	0.00015	major histocompatibility complex, class I, A /// major histocompatibility comple
36129_at	SGSM2	0.432	0.498	0.506	0.00015	small G protein signaling modulator 2
226207_at	RILPL1	2.7	2.5	3.6	0.00015	Rab interacting lysosomal protein-like 1
204620_s_at	VCAN	0.136	0.144	0.138	0.00015	versican
205546_s_at	TYK2	2.0	1.9	2.3	0.00015	tyrosine kinase 2
235229_at	---	904.9	328.5	1470.6	0.00015	---
229673_at	---	0.343	0.294	0.295	0.00015	---
223834_at	CD274	100.1	46.6	59.1	0.00015	CD274 molecule
201429_s_at	RPL37A	0.740	0.750	0.794	0.00015	ribosomal protein L37a
224643_at	PRRC1	0.441	0.420	0.420	0.00015	proline-rich coiled-coil 1
221477_s_at	SOD2	15.0	19.8	32.6	0.00016	superoxide dismutase 2, mitochondrial
1555736_a_at	AGTRAP	3.0	3.8	3.1	0.00016	angiotensin II receptor-associated protein
1554997_a_at	PTGS2	20.0	20.0	11.0	0.00016	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxyge
209770_at	BTN3A1	6.7	7.3	8.1	0.00016	butyrophilin, subfamily 3, member A1
229351_at	---	0.654	0.686	0.613	0.00016	---
200012_x_at	LOC653737	0.449	0.460	0.421	0.00016	hypothetical LOC653737 /// ribosomal protein L21-like /// ribosomal protein L21
55692_at	ELMO2	5.0	5.5	7.7	0.00017	engulfment and cell motility 2
204084_s_at	CLN5	2.3	2.3	2.8	0.00017	ceroid-lipofuscinosis, neuronal 5
204303_s_at	KIAA0427	0.246	0.168	0.228	0.00017	KIAA0427
208617_s_at	PTP4A2	0.509	0.436	0.450	0.00017	protein tyrosine phosphatase type IVA, member 2
211506_s_at	IL8	539.6	2763.7	689.5	0.00017	interleukin 8
210563_x_at	CFLAR	7.8	9.4	10.4	0.00017	CASP8 and FADD-like apoptosis regulator
240054_at	---	12.3	10.5	6.6	0.00017	---
208392_x_at	SP110	13.7	11.0	25.1	0.00017	SP110 nuclear body protein
225376_at	C20orf11	0.451	0.402	0.519	0.00017	chromosome 20 open reading frame 11
226656_at	CRTAP	0.363	0.274	0.253	0.00017	cartilage associated protein
212432_at	GRPEL1	1.5	1.6	1.8	0.00017	GrpE-like 1, mitochondrial (E. coli)
202859_x_at	IL8	145.7	777.2	333.8	0.00017	interleukin 8
219013_at	GALNT11	0.189	0.241	0.239	0.00017	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase
233090_at	---	0.474	0.422	0.488	0.00018	---
204098_at	RBMX2	0.668	0.620	0.688	0.00018	RNA binding motif protein, X-linked 2
222916_s_at	HDLBP	0.187	0.208	0.130	0.00018	high density lipoprotein binding protein
238531_x_at	---	111.1	61.2	238.3	0.00018	---
1559433_at	LOC149773	5.1	8.2	7.0	0.00018	CDNA FLJ33293 fis, clone BNGH42000675
226009_at	RP11-529I10.4	0.277	0.394	0.349	0.00018	deleted in a mouse model of primary ciliary dyskinesia
225973_at	TAP2	14.4	12.8	20.9	0.00018	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)

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		FS087	MRC5	N78		
203552_at	MAP4K5	0.438	0.408	0.351	0.00019	mitogen-activated protein kinase kinase kinase kinase 5
204828_at	RAD9A	5.8	9.0	7.7	0.00019	RAD9 homolog A (S. pombe)
1556629_a_at	SNAP25	0.389	0.409	0.420	0.00019	HUMSNAP25B(F)
218817_at	SPCS3	2.2	1.9	2.2	0.00019	signal peptidase complex subunit 3 homolog (S. cerevisiae)
204972_at	OAS2	394.1	133.0	498.5	0.00019	2'-5'-oligoadenylate synthetase 2, 69/71kDa
219364_at	DHX58	26.9	33.0	24.6	0.00019	DEXH (Asp-Glu-X-His) box polypeptide 58
205692_s_at	CD38	149.2	401.4	677.2	0.00019	CD38 molecule
202126_at	PRPF4B	1.5	1.3	1.5	0.00019	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
221253_s_at	TXNDC5	0.549	0.460	0.478	0.00019	thioredoxin domain containing 5
208453_s_at	XPNPEP1	2.6	3.3	3.1	0.00019	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble
206633_at	CHRNA1	30.4	31.7	86.3	0.0002	cholinergic receptor, nicotinic, alpha 1 (muscle)
203236_s_at	LGALS9	45.7	109.9	144.8	0.0002	lectin, galactoside-binding, soluble, 9
207630_s_at	CREM	6.0	4.8	4.9	0.0002	cAMP responsive element modulator
204070_at	RARRES3	47.3	42.7	30.0	0.0002	retinoic acid receptor responder (tazarotene induced) 3
219092_s_at	IPPK	2.1	2.0	1.9	0.0002	inositol 1,3,4,5,6-pentakisphosphate 2-kinase
225424_at	GPAM	0.146	0.183	0.147	0.0002	glycerol-3-phosphate acyltransferase, mitochondrial
215342_s_at	RABGAP1L	2.3	2.6	3.1	0.0002	RAB GTPase activating protein 1-like
226756_at	---	4.1	5.0	4.7	0.0002	---
217922_at	---	0.088	0.131	0.161	0.00021	---
214791_at	SP140L	2.5	3.4	2.7	0.00021	SP140 nuclear body protein-like
220091_at	SLC2A6	29.7	16.9	42.7	0.00021	solute carrier family 2 (facilitated glucose transporter), member 6
204470_at	CXCL1	42.9	124.8	94.7	0.00021	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
201115_at	POLD2	0.476	0.363	0.430	0.00021	polymerase (DNA directed), delta 2, regulatory subunit 50kDa
235157_at	---	16.9	23.3	28.6	0.00021	---
235046_at	---	0.186	0.246	0.311	0.00021	---
226603_at	SAMD9L	5.5	10.0	12.2	0.00021	sterile alpha motif domain containing 9-like
231175_at	BEND6	0.291	0.268	0.292	0.00021	BEN domain containing 6
227125_at	---	20.0	15.7	21.1	0.00021	---
204769_s_at	TAP2	19.4	15.9	14.8	0.00021	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)
231296_at	---	0.407	0.372	0.338	0.00021	---
200704_at	LITAF	2.3	2.7	3.0	0.00022	lipopolysaccharide-induced TNF factor
220052_s_at	TINF2	4.8	3.8	5.1	0.00022	TERF1 (TRF1)-interacting nuclear factor 2

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		FS087	MRC5	N78		
224645_at	EIF4EBP2	0.221	0.200	0.282	0.00022	eukaryotic translation initiation factor 4E binding protein 2
239218_at	PDE1C	0.070	0.078	0.069	0.00022	phosphodiesterase 1C, calmodulin-dependent 70kDa
209203_s_at	BICD2	0.449	0.453	0.473	0.00022	bicaudal D homolog 2 (Drosophila)
205875_s_at	ATRIP /// TREX1	12.8	25.9	39.0	0.00022	ATR interacting protein /// three prime repair exonuclease 1
219209_at	IFIH1	125.4	49.1	132.5	0.00022	interferon induced with helicase C domain 1
202588_at	AK1	0.466	0.371	0.399	0.00022	adenylate kinase 1
225302_at	TXNDC10	0.297	0.367	0.312	0.00022	thioredoxin domain containing 10
227270_at	LOC285550	0.258	0.299	0.361	0.00022	hypothetical protein LOC285550
218793_s_at	SCML1	2.5	3.5	3.0	0.00023	sex comb on midleg-like 1 (Drosophila)
225279_s_at	C3orf17	0.514	0.572	0.579	0.00023	chromosome 3 open reading frame 17
222394_at	PDCD6IP	0.223	0.276	0.355	0.00023	programmed cell death 6 interacting protein
209239_at	NFKB1	4.2	5.7	3.8	0.00023	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
1570253_a_at	RHEBL1	8.3	13.2	7.3	0.00023	Ras homolog enriched in brain like 1
225012_at	HDLBP	0.273	0.190	0.267	0.00023	high density lipoprotein binding protein
37549_g_at	BBS9	0.517	0.387	0.424	0.00023	Bardet-Biedl syndrome 9
231769_at	FBXO6	19.0	15.7	28.1	0.00023	F-box protein 6
221798_x_at	---	0.763	0.785	0.711	0.00023	---
204747_at	IFIT3	56.0	28.1	133.8	0.00023	interferon-induced protein with tetratricopeptide repeats 3
223454_at	CXCL16	18.2	33.0	44.7	0.00023	chemokine (C-X-C motif) ligand 16
212206_s_at	H2AFV	0.111	0.090	0.105	0.00024	H2A histone family, member V
209774_x_at	CXCL2	53.7	51.2	19.3	0.00024	chemokine (C-X-C motif) ligand 2
204494_s_at	C15orf39	1.7	1.8	1.6	0.00024	chromosome 15 open reading frame 39
201287_s_at	SDC1	0.280	0.163	0.160	0.00024	syndecan 1
212734_x_at	RPL13	0.560	0.664	0.561	0.00024	ribosomal protein L13
213151_s_at	7-Sep	0.624	0.532	0.543	0.00024	septin 7
200668_s_at	UBE2D3	1.5	1.5	1.4	0.00024	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)
224619_at	CASC4	0.540	0.617	0.576	0.00025	cancer susceptibility candidate 4
212830_at	MEGF9	0.107	0.061	0.071	0.00025	multiple EGF-like-domains 9
221476_s_at	RPL15	0.331	0.313	0.349	0.00025	ribosomal protein L15
202251_at	PRPF3	3.8	3.7	4.1	0.00025	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)
226047_at	MRVI1	0.019	0.058	0.021	0.00025	murine retrovirus integration site 1 homolog
209630_s_at	FBXW2	0.298	0.222	0.329	0.00025	F-box and WD repeat domain containing 2
200717_x_at	RPL7	0.470	0.543	0.402	0.00025	ribosomal protein L7
207616_s_at	TANK	2.2	3.1	2.9	0.00025	TRAF family member-associated NFKB activator
211799_x_at	HLA-C	5.3	5.4	5.7	0.00025	major histocompatibility complex, class I, C

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		FS087	MRC5	N78		
222870_s_at	B3GNT2	5.7	4.1	8.1	0.00025	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
205299_s_at	BTN2A2	4.5	4.8	6.1	0.00025	butyrophilin, subfamily 2, member A2
230214_at	MRVI1	0.038	0.065	0.026	0.00025	murine retrovirus integration site 1 homolog
212657_s_at	IL1RN	32.6	18.3	45.4	0.00026	interleukin 1 receptor antagonist
224784_at	MLLT6	4.0	5.4	5.6	0.00026	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran
235513_at	---	0.231	0.343	0.252	0.00026	---
227069_at	---	0.180	0.239	0.174	0.00026	---
225929_s_at	RNF213	14.0	12.6	14.1	0.00026	ring finger protein 213
221528_s_at	ELMO2	4.9	6.1	9.4	0.00026	engulfment and cell motility 2
222997_s_at	MRPS21	0.666	0.754	0.698	0.00026	mitochondrial ribosomal protein S21
227085_at	H2AFV	0.410	0.282	0.275	0.00026	H2A histone family, member V
225849_s_at	SFT2D1	1.5	1.7	1.7	0.00026	SFT2 domain containing 1
201783_s_at	RELA	4.7	4.2	7.8	0.00026	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
203283_s_at	HS2ST1	0.418	0.480	0.433	0.00027	heparan sulfate 2-O-sulfotransferase 1
217781_s_at	ZFP106	0.204	0.270	0.216	0.00027	zinc finger protein 106 homolog (mouse)
243271_at	---	14.7	27.6	26.7	0.00027	---
226648_at	HIF1AN	0.262	0.268	0.347	0.00027	hypoxia inducible factor 1, alpha subunit inhibitor
217336_at	Various'	0.484	0.505	0.601	0.00027	hypothetical LOC376693 /// similar to ribosomal protein S10 /// similar to hCG20
210443_x_at	OGFR	3.4	3.9	5.5	0.00027	opioid growth factor receptor
201273_s_at	hCG_1781062 /// SRP9	0.657	0.684	0.712	0.00027	hCG1781062 /// signal recognition particle 9kDa
226501_at	XPNPEP3	0.285	0.332	0.233	0.00027	X-prolyl aminopeptidase (aminopeptidase P) 3, putative
228347_at	SIX1	4.3	4.2	4.0	0.00028	SIX homeobox 1
201502_s_at	NFKBIA	19.7	11.2	35.9	0.00028	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, al
227221_at	---	0.268	0.250	0.335	0.00028	---
208860_s_at	ATRX	0.273	0.293	0.200	0.00028	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevi
241347_at	KIAA1618	11.2	12.2	6.7	0.00028	KIAA1618
216231_s_at	B2M	1.5	1.8	1.7	0.00028	beta-2-microglobulin
205500_at	C5	0.533	0.591	0.525	0.00028	complement component 5
226333_at	IL6R	0.173	0.167	0.098	0.00028	interleukin 6 receptor
211542_x_at	RPS10	0.594	0.630	0.586	0.00029	ribosomal protein S10
225923_at	---	0.121	0.184	0.152	0.00029	---
226516_at	C19orf28	3.2	3.0	3.1	0.00029	chromosome 19 open reading frame 28
226805_at	---	0.099	0.083	0.082	0.00029	---
204072_s_at	FRY	0.026	0.045	0.024	0.00029	furry homolog (Drosophila)

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		FS087	MRC5	N78		
212736_at	C16orf45	0.205	0.290	0.184	0.00029	chromosome 16 open reading frame 45
210645_s_at	TTC3	0.093	0.164	0.101	0.00029	tetratricopeptide repeat domain 3
218213_s_at	C11orf10	0.547	0.630	0.589	0.0003	chromosome 11 open reading frame 10
224702_at	TMEM167 A	0.552	0.429	0.434	0.0003	transmembrane protein 167A
211256_x_at	BTN2A1	4.8	4.2	6.5	0.0003	butyrophilin, subfamily 2, member A1
221726_at	RPL22	0.246	0.231	0.151	0.0003	ribosomal protein L22
226117_at	TIFA	13.6	13.7	12.8	0.0003	TRAF-interacting protein with forkhead-associated domain
215313_x_at	HLA-A	2.4	2.4	3.1	0.0003	major histocompatibility complex, class I, A
209417_s_at	IFI35	84.4	32.3	44.6	0.0003	interferon-induced protein 35
223220_s_at	PARP9	15.8	7.2	18.4	0.0003	poly (ADP-ribose) polymerase family, member 9
205945_at	IL6R	0.100	0.108	0.046	0.0003	interleukin 6 receptor
228505_s_at	TMEM170 A	4.7	5.7	3.7	0.0003	transmembrane protein 170A
219774_at	CCDC93	2.6	2.7	3.2	0.00031	coiled-coil domain containing 93
206469_x_at	AKR7A3	0.455	0.451	0.522	0.00031	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)
225617_at	ODF2	0.479	0.373	0.432	0.00031	outer dense fiber of sperm tails 2
217751_at	GSTK1	4.4	4.0	5.6	0.00031	glutathione S-transferase kappa 1
200790_at	ODC1	0.389	0.359	0.287	0.00031	ornithine decarboxylase 1
202906_s_at	NBN	4.0	5.5	5.9	0.00031	nibrin
225147_at	CYTH3	0.306	0.380	0.457	0.00031	cytohesin 3
208661_s_at	TTC3	0.096	0.153	0.121	0.00032	tetratricopeptide repeat domain 3
221953_s_at	LOC729580	0.359	0.282	0.333	0.00032	PREDICTED: Homo sapiens hypothetical LOC729580 (LOC729580), mRNA
223598_at	RAD23B	0.287	0.397	0.352	0.00032	RAD23 homolog B ( <i>S. cerevisiae</i> )
209636_at	NFKB2	14.1	18.7	15.5	0.00032	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
203299_s_at	AP1S2	0.586	0.572	0.478	0.00032	adaptor-related protein complex 1, sigma 2 subunit
201335_s_at	ARHGEF12	0.291	0.278	0.251	0.00032	Rho guanine nucleotide exchange factor (GEF) 12
226771_at	ATP8B2	0.521	0.449	0.383	0.00032	ATPase, class I, type 8B, member 2
233880_at	RNF213	16.9	14.6	13.9	0.00033	ring finger protein 213
219104_at	RNF141	0.128	0.234	0.161	0.00033	ring finger protein 141
219563_at	C14orf139	0.176	0.252	0.210	0.00033	chromosome 14 open reading frame 139
222455_s_at	PARVA	0.663	0.567	0.588	0.00033	parvin, alpha
224769_at	---	0.733	0.627	0.634	0.00033	---
219593_at	SLC15A3	34.9	22.0	67.5	0.00033	solute carrier family 15, member 3
227531_at	---	0.350	0.446	0.289	0.00033	---
225931_s_at	RNF213	14.0	16.0	14.5	0.00033	ring finger protein 213
207571_x_at	C1orf38	25.1	21.0	36.8	0.00033	chromosome 1 open reading frame 38
1553982_a_at	RAB7B	0.286	0.287	0.322	0.00033	RAB7B, member RAS oncogene family
226512_at	ZMYM2	0.401	0.462	0.516	0.00034	zinc finger, MYM-type 2

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		FS087	MRC5	N78		
208619_at	DDB1	0.400	0.514	0.431	0.00034	damage-specific DNA binding protein 1, 127kDa
212042_x_at	RPL7	0.469	0.493	0.410	0.00034	ribosomal protein L7
211373_s_at	PSEN2	3.8	5.7	4.6	0.00034	presenilin 2 (Alzheimer disease 4)
200867_at	RNF114	4.4	6.6	7.4	0.00034	ring finger protein 114
221740_x_at	LRRC37A2	0.226	0.265	0.183	0.00034	CDNA FLJ34414 fis, clone HEART2003168, highly similar to Homo sapiens c114 SLIT-
215719_x_at	FAS	4.0	6.1	8.1	0.00034	Fas (TNF receptor superfamily, member 6)
217456_x_at	HLA-E	4.7	3.9	2.8	0.00034	major histocompatibility complex, class I, E
218130_at	C17orf62	3.0	2.7	4.3	0.00034	chromosome 17 open reading frame 62
215602_at	FGD2	1.0	1.0	1.0	0.00034	FYVE, RhoGEF and PH domain containing 2
202209_at	LSM3	0.605	0.506	0.544	0.00034	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)
233310_at	---	3.8	5.7	5.2	0.00034	---
234987_at	---	18.6	18.1	14.6	0.00034	---
201665_x_at	RPS17	0.513	0.457	0.482	0.00035	ribosomal protein S17
202381_at	ADAM9	0.717	0.781	0.746	0.00035	ADAM metallopeptidase domain 9 (meltrin gamma)
223983_s_at	C19orf12	2.4	2.7	3.1	0.00035	chromosome 19 open reading frame 12
214318_s_at	FRY	0.269	0.157	0.200	0.00035	furry homolog (Drosophila)
241991_at	---	3.4	4.3	5.3	0.00035	---
1558102_at	---	0.314	0.312	0.245	0.00035	---
209878_s_at	RELA	6.7	5.5	10.6	0.00035	v-rel reticuloendotheliosis viral oncogene homolog A (avian)
225415_at	DTX3L	6.8	4.9	9.4	0.00035	deltex 3-like (Drosophila)
204413_at	TRAF2	3.1	4.0	2.8	0.00035	TNF receptor-associated factor 2
218943_s_at	DDX58	50.4	35.4	118.8	0.00035	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
221011_s_at	LBH	0.152	0.092	0.100	0.00035	limb bud and heart development homolog (mouse)
221680_s_at	ETV7	16.3	13.1	20.7	0.00035	ets variant 7
212613_at	BTN3A2	6.8	5.9	6.9	0.00035	butyrophilin, subfamily 3, member A2
202942_at	ETFB	0.239	0.256	0.289	0.00036	electron-transfer-flavoprotein, beta polypeptide
220960_x_at	RPL22	0.538	0.624	0.488	0.00036	ribosomal protein L22
222592_s_at	ACSL5	15.1	32.2	28.4	0.00036	acyl-CoA synthetase long-chain family member 5
226116_at	---	0.255	0.270	0.206	0.00037	---
218613_at	PSD3	0.069	0.062	0.132	0.00037	pleckstrin and Sec7 domain containing 3
206574_s_at	LOC100131062 /// PTP4A3	0.979	0.978	0.984	0.00037	similar to protein tyrosine phosphatase type IVA, member 3 /// protein tyrosine
210681_s_at	USP15	3.3	5.9	4.4	0.00037	ubiquitin specific peptidase 15
202531_at	IRF1	21.4	16.5	43.7	0.00037	interferon regulatory factor 1
218962_s_at	TMEM168	0.362	0.387	0.406	0.00037	transmembrane protein 168
204440_at	CD83	111.6	54.9	61.1	0.00037	CD83 molecule
204017_at	KDEL3	0.410	0.279	0.290	0.00037	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3

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		FS087	MRC5	N78		
221875_x_at	HLA-F	7.7	5.2	11.5	0.00037	major histocompatibility complex, class I, F
203968_s_at	CDC6	0.332	0.195	0.286	0.00037	cell division cycle 6 homolog ( <i>S. cerevisiae</i> )
225636_at	STAT2	3.0	2.9	4.6	0.00038	signal transducer and activator of transcription 2, 113kDa
209451_at	TANK	2.1	2.8	2.9	0.00038	TRAF family member-associated NFKB activator
221492_s_at	ATG3	1.7	2.1	1.8	0.00038	ATG3 autophagy related 3 homolog ( <i>S. cerevisiae</i> )
209817_at	PPP3CB	0.351	0.412	0.304	0.00038	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform
203340_s_at	SLC25A12	5.7	5.7	6.5	0.00038	solute carrier family 25 (mitochondrial carrier, Aralar), member 12
1570261_at	---	17.5	46.2	41.1	0.00038	---
210514_x_at	HLA-G	4.2	3.7	4.9	0.00038	major histocompatibility complex, class I, G
227009_at	---	0.248	0.166	0.245	0.00038	---
218810_at	ZC3H12A	10.7	18.6	19.5	0.00038	zinc finger CCCH-type containing 12A
211012_s_at	LOC161527 /// PML	9.2	16.8	15.6	0.00038	hypothetical protein LOC161527 /// promyelocytic leukemia
223106_at	TMEM14C	0.696	0.727	0.695	0.00039	transmembrane protein 14C
216252_x_at	FAS	4.0	6.6	8.6	0.00039	Fas (TNF receptor superfamily, member 6)
204994_at	MX2	246.3	59.5	369.6	0.00039	myxovirus (influenza virus) resistance 2 (mouse)
235459_at	---	0.225	0.194	0.155	0.00039	---
34689_at	ATRIP /// TREX1	9.1	15.1	30.9	0.00039	ATR interacting protein /// three prime repair exonuclease 1
201413_at	HSD17B4	0.359	0.378	0.315	0.00039	hydroxysteroid (17-beta) dehydrogenase 4
213474_at	KCTD7	0.281	0.329	0.193	0.00039	potassium channel tetramerisation domain containing 7
238629_x_at	---	99.2	40.5	152.8	0.00039	---
235116_at	TRAF1	29.2	12.5	18.8	0.0004	TNF receptor-associated factor 1
226401_at	PARP10	3.5	6.9	6.0	0.0004	poly (ADP-ribose) polymerase family, member 10
219582_at	OGFRL1	2.6	3.1	3.8	0.0004	opioid growth factor receptor-like 1
238725_at	IRF1	27.0	24.8	82.4	0.0004	interferon regulatory factor 1
239461_at	GALNTL2	0.117	0.203	0.129	0.0004	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase
240469_at	---	1.0	1.0	1.0	0.0004	---
219100_at	OBFC1	0.404	0.411	0.509	0.0004	oligonucleotide/oligosaccharide-binding fold containing 1
202869_at	OAS1	327.5	186.8	1317.6	0.00041	2',5'-oligoadenylate synthetase 1, 40/46kDa
236018_at	---	0.685	0.642	0.692	0.00041	---
204521_at	C12orf24	0.185	0.182	0.196	0.00041	chromosome 12 open reading frame 24
202637_s_at	ICAM1	996.8	275.5	159.5	0.00041	intercellular adhesion molecule 1
1553976_a_at	RP11- 529I10.4	0.275	0.323	0.428	0.00041	deleted in a mouse model of primary ciliary dyskinesia



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		FS087	MRC5	N78		
223551_at	PKIB	4.1	7.7	4.9	0.00042	protein kinase (cAMP-dependent, catalytic) inhibitor beta
210312_s_at	IFT20	0.472	0.535	0.449	0.00042	intraflagellar transport 20 homolog (Chlamydomonas)
205476_at	CCL20	515.5	169.7	1087.6	0.00042	chemokine (C-C motif) ligand 20
204388_s_at	MAOA	0.062	0.133	0.090	0.00042	monoamine oxidase A
201517_at	NCBP2	0.547	0.494	0.534	0.00042	nuclear cap binding protein subunit 2, 20kDa
202313_at	PPP2R2A	2.1	2.5	2.9	0.00042	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform
201350_at	FLOT2	1.7	1.5	1.9	0.00042	flotillin 2
227319_at	---	0.211	0.223	0.256	0.00042	---
226795_at	---	3.1	2.9	4.5	0.00042	---
235279_at	---	0.135	0.142	0.078	0.00043	---
221485_at	B4GALT5	4.4	3.5	4.5	0.00043	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5
225633_at	DPY19L3	0.142	0.148	0.112	0.00043	dpy-19-like 3 (C. elegans)
230098_at	PHF20L1	0.282	0.392	0.390	0.00043	PHD finger protein 20-like 1
212288_at	FNBP1	0.353	0.304	0.207	0.00043	formin binding protein 1
217719_at	EIF3L	0.348	0.341	0.253	0.00043	eukaryotic translation initiation factor 3, subunit L
200006_at	PARK7	0.592	0.708	0.592	0.00043	Parkinson disease (autosomal recessive, early onset) 7
202509_s_at	TNFAIP2	6.2	5.4	8.9	0.00044	tumor necrosis factor, alpha-induced protein 2
235742_at	RHOC	7.2	6.0	12.5	0.00044	Full length insert cDNA clone YP95A10
212037_at	PNN	0.467	0.378	0.411	0.00044	pinin, desmosome associated protein
218633_x_at	ABHD10	0.267	0.318	0.270	0.00044	abhydrolase domain containing 10
214042_s_at	RPL22	0.309	0.392	0.238	0.00044	ribosomal protein L22
207850_at	CXCL3	21.3	55.3	20.6	0.00044	chemokine (C-X-C motif) ligand 3
1553959_a_at	B3GALT6	2.5	2.0	2.4	0.00044	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6
243222_at	---	4.2	5.1	5.4	0.00044	---
201743_at	CD14	11.8	30.7	19.5	0.00044	CD14 molecule
202734_at	TRIP10	2.1	1.8	1.9	0.00044	thyroid hormone receptor interactor 10
200814_at	PSME1	3.7	3.7	5.4	0.00044	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
207196_s_at	TNIP1	8.1	15.9	16.7	0.00044	TNFAIP3 interacting protein 1
1552378_s_at	RDH10	0.083	0.103	0.037	0.00044	retinol dehydrogenase 10 (all-trans)
214838_at	SFT2D2	12.0	7.8	11.4	0.00045	SFT2 domain containing 2
226711_at	FOXN2	2.1	3.0	2.7	0.00045	forkhead box N2
222068_s_at	LRR50	28.2	15.9	23.8	0.00045	leucine rich repeat containing 50
209694_at	PTS	0.324	0.354	0.360	0.00045	6-pyruvoyltetrahydropterin synthase
224606_at	KLF6	3.5	2.8	4.1	0.00045	DNA-binding protein CPBP (CPBP)
218124_at	RETSAT	0.663	0.680	0.579	0.00046	retinol saturase (all-trans-retinol 13,14-reductase)
204924_at	TLR2	46.6	17.2	79.8	0.00046	toll-like receptor 2

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		FS087	MRC5	N78		
235812_at	TMEM188	1.7	1.8	1.5	0.00046	transmembrane protein 188
234523_at	---	1.0	1.0	1.0	0.00046	---
225394_s_at	ZCRB1	0.614	0.539	0.604	0.00046	zinc finger CCHC-type and RNA binding motif 1
223502_s_at	TNFSF13B	243.5	582.7	187.6	0.00046	tumor necrosis factor (ligand) superfamily, member 13b
225850_at	SFT2D1	1.6	1.6	1.6	0.00046	SFT2 domain containing 1
219685_at	TMEM35	0.051	0.037	0.059	0.00046	transmembrane protein 35
224973_at	FAM46A	4.0	4.7	7.3	0.00046	family with sequence similarity 46, member A
208973_at	ERI3	0.475	0.573	0.493	0.00046	exoribonuclease 3
207388_s_at	PTGES	20.0	25.8	56.4	0.00046	prostaglandin E synthase
240088_at	PDE5A	0.179	0.177	0.186	0.00046	phosphodiesterase 5A, cGMP-specific
202510_s_at	TNFAIP2	41.1	31.5	149.4	0.00047	tumor necrosis factor, alpha-induced protein 2
1553286_at	ZNF555	0.406	0.379	0.532	0.00047	zinc finger protein 555
823_at	CX3CL1	65.5	24.5	111.6	0.00047	chemokine (C-X3-C motif) ligand 1
233632_s_at	XRN1	2.2	3.2	3.2	0.00047	5'-3' exoribonuclease 1
229958_at	CLN8	0.093	0.189	0.175	0.00047	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)
208768_x_at	RPL22	0.465	0.546	0.388	0.00047	ribosomal protein L22
201227_s_at	NDUFB8	0.489	0.445	0.530	0.00047	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
1562966_at	KIAA1217	8.9	7.0	6.2	0.00047	KIAA1217
201641_at	BST2	276.1	314.8	1074.3	0.00047	bone marrow stromal cell antigen 2
1558250_s_at	---	0.162	0.212	0.313	0.00047	---
1553713_a_at	RHEBL1	9.3	5.4	6.7	0.00047	Ras homolog enriched in brain like 1
200904_at	HLA-E	5.3	5.5	8.5	0.00047	major histocompatibility complex, class I, E
205240_at	GPSM2	0.461	0.425	0.326	0.00047	G-protein signaling modulator 2 (AGS3-like, C. elegans)
220363_s_at	ELMO2	3.8	5.6	6.9	0.00048	engulfment and cell motility 2
217771_at	GOLM1	13.6	12.9	20.7	0.00048	golgi membrane protein 1
202432_at	PPP3CB	0.400	0.356	0.523	0.00048	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform
235042_at	XIRP1	84.9	25.0	75.6	0.00048	xin actin-binding repeat containing 1
203803_at	PCYOX1	0.199	0.260	0.203	0.00048	prenylcysteine oxidase 1
205205_at	RELB	25.9	20.4	23.0	0.00049	v-rel reticuloendotheliosis viral oncogene homolog B
218421_at	CERK	0.112	0.132	0.249	0.00049	ceramide kinase
225076_s_at	ZNFX1	5.1	8.3	9.1	0.00049	zinc finger, NFX1-type containing 1
202961_s_at	ATP5J2	0.731	0.804	0.742	0.00049	ATP synthase, H <sup>+</sup> transporting, mitochondrial FO complex, subunit F2
231959_at	LIN52	4.3	6.0	9.4	0.00049	lin-52 homolog (C. elegans)
204589_at	NUAK1	0.115	0.115	0.115	0.00049	NUAK family, SNF1-like kinase, 1
209390_at	TSC1	0.431	0.382	0.470	0.00049	tuberous sclerosis 1
215646_s_at	VCAN	0.114	0.105	0.092	0.0005	versican
202863_at	SP100	3.1	4.1	5.2	0.0005	SP100 nuclear antigen

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		FS087	MRC5	N78		
220731_s_at	NECAP2	2.3	2.4	2.3	0.0005	NECAP endocytosis associated 2
223268_at	C11orf54	0.459	0.398	0.482	0.0005	chromosome 11 open reading frame 54
1558115_at	RECK	0.687	0.607	0.656	0.0005	reversion-inducing-cysteine-rich protein with kazal motifs
224232_s_at	PRELID1	2.1	2.4	2.0	0.0005	PRELI domain containing 1
215078_at	SOD2	6.6	17.3	10.6	0.0005	superoxide dismutase 2, mitochondrial
221021_s_at	CTNBL1	5.8	4.8	10.1	0.0005	catenin, beta like 1
226336_at	PPIA	0.297	0.236	0.336	0.0005	peptidylprolyl isomerase A (cyclophilin A)
207740_s_at	NUP62	4.1	6.4	3.6	0.00051	nucleoporin 62kDa
207761_s_at	METTL7A	0.139	0.109	0.187	0.00051	methyltransferase like 7A
230893_at	DNAJC21	0.155	0.272	0.206	0.00051	DnaJ (Hsp40) homolog, subfamily C, member 21
227092_at	---	0.196	0.320	0.329	0.00051	---
230499_at	---	12.0	18.7	36.1	0.00051	---
214508_x_at	CREM	9.3	5.1	8.5	0.00051	cAMP responsive element modulator
213191_at	TICAM1	4.1	3.7	3.3	0.00051	toll-like receptor adaptor molecule 1
238601_at	PHKB	0.216	0.238	0.176	0.00051	phosphorylase kinase, beta
230266_at	RAB7B	0.088	0.157	0.080	0.00051	RAB7B, member RAS oncogene family
216466_at	NAV3	4.7	3.2	3.8	0.00051	neuron navigator 3
224994_at	CAMK2D	2.0	2.0	2.1	0.00052	calcium/calmodulin-dependent protein kinase II delta
203045_at	NINJ1	18.9	12.4	41.2	0.00052	ninjurin 1
223443_s_at	FLJ32065	0.220	0.342	0.353	0.00052	hypothetical protein FLJ32065
229441_at	PRSS23	0.065	0.163	0.061	0.00052	CDNA PSEC0048 fis, clone NT2RP2000028, highly similar to Serine protease 23 prec
204088_at	P2RX4	3.8	3.1	2.5	0.00053	purinergic receptor P2X, ligand-gated ion channel, 4
201486_at	RCN2	0.412	0.421	0.422	0.00053	reticulocalbin 2, EF-hand calcium binding domain
226748_at	LYSMD2	2.7	4.4	3.7	0.00053	LysM, putative peptidoglycan-binding, domain containing 2
221766_s_at	FAM46A	5.0	4.7	8.2	0.00053	family with sequence similarity 46, member A
206790_s_at	NDUFB1	0.692	0.743	0.733	0.00053	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa
237287_at	WDR34	0.904	0.878	0.858	0.00053	CDNA FLJ57659 complete cds, highly similar to WD repeat protein 34
202365_at	UNC119B	0.185	0.124	0.154	0.00054	unc-119 homolog B (C. elegans)
228955_at	---	0.173	0.188	0.196	0.00054	---
226793_at	LOC283267	0.470	0.430	0.460	0.00054	hypothetical LOC283267
226282_at	---	0.171	0.099	0.120	0.00054	---
233748_x_at	PRKAG2	0.412	0.349	0.485	0.00054	protein kinase, AMP-activated, gamma 2 non-catalytic subunit
236253_at	---	1.0	1.0	1.0	0.00054	---
201540_at	FHL1	0.114	0.170	0.085	0.00054	four and a half LIM domains 1
209476_at	TXNDC1	3.9	4.7	4.5	0.00054	thioredoxin domain containing 1

Probeset ID	Symbol	Fold Ratio (Stim/Con)			p-value	Gene Title
		FS087	MRC5	N78		
224116_at	---	1.0	1.0	1.1	0.00054	---
239050_s_at	---	0.349	0.312	0.452	0.00054	---
204958_at	PLK3	2.4	3.5	2.6	0.00055	polo-like kinase 3 (Drosophila)
222064_s_at	AARSD1	0.466	0.455	0.511	0.00055	alanyl-tRNA synthetase domain containing 1
213038_at	RNF19B	10.8	28.7	16.1	0.00055	ring finger protein 19B
212498_at	---	0.358	0.352	0.470	0.00055	---
226161_at	SLC30A6	0.601	0.710	0.610	0.00055	solute carrier family 30 (zinc transporter), member 6