List of selected genes on scatter plot: HT-X; HT-MT-Y; HT-siRNA-Z

TargetID	Signal_	Signal_	Signal_	Symbol	Accession	Synonyms	GO	GO	GO
GI_10047089-S	89.9	103.5	87.3	SMPX	NM_014332.1		DNA	nucleus	striated
GI_10047091-S	517.6	748.7	756	NP25	NM_013259.1	NP22			central
GI_10047093-S	659.1	725.4	696.9	HSP70-4	NM_016299.1		ATP		proteolysis
GI_10047099-S	283.9	274.7	242.8	LOC51186	NM_016303.1		DNA	nucleus	regulation
GI_10047103-S	2088.6	2034.1	1908.2	SS18L2	NM_016305.1	KIAA-iso			
GI_10047105-S	611.3	2625.4	2103.2	CPA4	NM_016352.1	CPA3	carboxype	cellular_co	histogene
GI_10047121-S	89.9	88	93.2	MCFP	NM_018843.1		binding	mitochond	transport
GI_10047123-S	875.5	825.4	702.1	LOC55974	NM_018845.1	SCP			
GI_10047133-A	146.8	158.5	147.4	EB-1	NM_020140.1	AIDA;MGC26087			
GI_10047133-I	116.4	141.6	112.7	EB-1	NM_020140.1	AIDA;MGC26087			
GI_10092578-S	126.3	140.7	133.1	ITIH3	NM_002217.1	H3P	endopepti		
GI_10092585-S	166.9	186.8	150.3	ZNF236	NM_007345.1	ZNF236A;ZNF236B	transcripti	nucleus	regulation
GI_10092596-S	350	410.9	509	MCOLN1	NM_020533.1	ML4;MLIV			
GI_10092600-S	1119.6	1175.8	1083.2	EIF4G3	NM_003760.2	eIF4GII	mRNA	eukaryotic	regulation
GI_10092602-S	155.5	183.9	160	PRG3	NM_006093.2	MBPH	sugar		immune
GI_10092603-S	146	183.7	184.4	C10orf1	NM_020527.1	HUG1	transcripti	nucleus	transcripti
GI_10092611-A	798.4	752.1	875.1	CKLF	NM_016326.2	C32;CKLF1;CKLF2;CKLF3;CKLF4;UCK-	cytokine	integral to	chemotaxi
GI_10092616-S	135.9	157.5	140.1	PCBP3	NM_020528.1	ALPHA-CP3	nucleic	nucleus	mRNA
GI_10092618-S	911.6	668.6	511.1	NFKBIA	NM_020529.1	IKBA;MAD-3;NFKBI	transcripti	cytoplasm	response
GI_10092638-S	482.7	659	460.4	CRIM1	NM_016441.1		insulin-like	extracellul	neurogene
GI_10092658-S	162.9	149.1	141.4	FLJ12886	NM_019108.1	F17127_1;DKFZp564H1322			
GI_10092668-S	176.1	192.3	186.7	OR2S2	NM_019897.1	OST715	olfactory	integral to	olfaction
GI_10092672-S	949	878.3	802.8	LOC57019	NM_020313.1				
GI_10092690-S	122.6	120.1	108.2	TJP3	NM_014428.1	ZO-3	protein	tight	intracellula
GI_10190657-S	107.2	116.3	110.7	HSA404617	NM_018722.1	KCNQ1DN	molecular	cellular_co	biological_
GI_10190665-I	155.8	163.8	141.6	ATP6V0A4	NM_020632.1	a4;Stv1;VPP2;Vph1;RTA1C;RTADR;ATP6N2			
GI_10190669-S	108.6	102.7	107.8	GDF3	NM_020634.1		cytokine	extracellul	cell growth
GI_10190671-S	108.4	111	102.3	FGF22	NM_020637.1				
GI_10190679-S	417	505.5	444.2	ASCL3	NM_020646.1		DNA	nucleus	regulation
GI_10190681-S	135.8	129.6	142	CBX8	NM_020649.1	PC3;RC1;HPC3	chromatin	chromatin	chromatin
GI_10190685-S	253.8	299.2	254.9	ZNF286	NM_020652.1	KIAA1874	DNA	nucleus	regulation
GI_10190687-S	94.8	88.7	91.8	ZNF287	NM_020653.1		transcripti	nucleus	regulation
GI_10190695-S	158.9	150.4	163.6	ZNF304	NM_020657.1		DNA	nucleus	regulation
GI_10190697-S	128.6	162.7	149.1	CX36	NM_020660.1	GJA9	connexon	connexon	cell
GI_10190699-S	130.6	139.7	139.1	AICDA	NM_020661.1	AID;ARP2;CDA2;HIGM2	cytidine	cellular_co	mRNA
GI_10190701-S	170.2	184.8	194.6	MRS2L	NM_020662.1	HPT;MRS2			
GI_10190705-S	248.9	320.9	289	CLK4	NM_020666.1		ATP	nucleus	protein
GI_10190709-S	95.7	100.9	108.6	LOC57399	NM_020669.1				
GI_10190711-S	314.4	415.4	378.4	S100A14	NM_020672.1	BCMP84;S100A15	calcium		
GI_10190741-S	91.6	103.2	104.6	USP29	NM_020903.1		cysteine-	cellular_co	ubiquitin-
GI_10190743-S	147.9	192.7	121.2	PLEKHA4	NM_020904.1	PEPP1	DNA	nucleus	regulation

GI_10190745-S	600.1	644.9	567.2	RDH14	NM_020905.1	PAN2	oxidoredu		metabolis
GI_10190747-S	134.1	153	150.8	SCUBE2	NM_020974.1	CEGP1	calcium		
GI_10198655-S	94.9	97.7	90.5	AMHR2	NM_020547.1	AMHR	protein	integral to	signal
GI_10257436-S	332.6	402.6	378	TTYH1	NM_020659.1		iron ion	integral to	iron ion
GI_10280617-S	229.9	296.2	277.8	ATP12A	NM_001676.2	ATP1AL1	hydrogen/	hydrogen/	proton
GI_10280625-S	193.3	235.7	230.8	APS	NM_020979.1		JAK	cytoplasm	signal
GI_10337584-S	110.3	135.6	124.1	DEFA5	NM_021010.1	DEF5;HD-5	antimicrob	extracellul	antimicrob
GI_10337586-S	94.6	87.6	85.2	FGF6	NM_020996.1	HST2;HBGF-6	growth	extracellul	oncogene
GI_10337596-S	212.4	274.3	200.9	SCN2A2	NM_021007.1	HBSCII	voltage-	voltage-	sodium
GI_10337606-S	324.6	393.9	465.3	PTTG3	NM_021000.1				
GI_10337608-S	479.1	515.5	557.9	CTAG2	NM_020994.1	ESO2;CAMEL;LAGE1;LAGE-1;LAGE-			
GI_10337610-S	371.4	459.6	393.9	NEUROG3	NM_020999.1	ngn3;Atoh5;Math4B	transcripti	nucleus	peripheral
GI_10346128-S	103.4	259.8	110.7	DDX43	NM_018665.1	HAGE;DKFZp434H2114	ATP		
GI_10346134-S	232.7	445.4	333	MAPRE2	NM_014268.1	EB1;EB2;RP1	microtubul		cellular
GI_10440557-S	110.1	140.7	131.2	RFPL1	NM_021026.1	RNF78			
GI_10440561-S	146.2	181.4	155.3	FHR-3	NM_021023.1	FHR3;HLF4;DOWN16		extracellul	
GI_10440563-S	116.5	122.6	115	TLX3	NM_021025.1	RNX;HOX11L2	transcripti	nucleus	regulation
GI_10440565-S	141.1	187.4	138.7	LZTS1	NM_021020.1	F37;FEZ1	transcripti		
GI_10442821-S	578.6	612.4	598.7	BIRC6	NM_016252.1	KIAA1289	cysteine	intracellula	ubiquitin
GI_10518496-S	159.6	156.3	146.2	DLL1	NM_005618.2	DELTA1	structural	extracellul	cell
GI_10518498-S	1051.6	1169.5	690.2	RNF24	NM_007219.2	G1L			
GI_10518499-S	199.7	339.4	176.9	F3	NM_001993.2	TF;TFA;CD142	blood	integral to	blood
GI_10518500-S	165.3	192.4	162.2	F5	NM_000130.2	FVL;PCCF	blood		blood
GI_10518501-I	91.5	107.5	97.4	F7	NM_000131.2		serine-	extracellul	blood
GI_10518502-A	172.6	205.3	180.5	F7	NM_019616.1		serine-	extracellul	blood
GI_10518504-I	100.3	88.6	92.9	F8	NM_000132.2	AHF;F8B;F8C;HEMA;FVIII;DXS1253E	blood		blood
GI_10518505-A	433.3	538	520.1	F8	NM_019863.1	AHF;F8B;F8C;HEMA;FVIII;DXS1253E	blood		blood
GI_10518505-I	169.3	187.1	183.3	F8	NM_019863.1	AHF;F8B;F8C;HEMA;FVIII;DXS1253E	blood		blood
GI_10518507-S	94.9	99.5	102.7	F9	NM_000133.2	FIX;PTC;HEMB	blood	extracellul	blood
GI_10567815-I	171.3	208.8	193.5	GNAO1	NM_020988.1	GNAO;G-ALPHA-o	heterotrim	peripheral	axon
GI_10567821-S	98.4	101.9	91.1	ZNF253	NM_021047.1	BMZF1;BMZF-1;FLJ90391	zinc ion	nucleus	regulation
GI_10567823-S	151.1	184.9	167.5	LOC57830	NM_021046.1		structural	intermedia	biological_
GI_10645198-S	96.6	99.7	97.1	ADAMTS7	NM_014272.1	ADAM-TS7;DKFZp434H204	metallope	extracellul	proteolysis
GI_10800141-S	146.2	169.7	150.2	IFNA7	NM_021057.1	IFNA-J	interferon-	extracellul	response
GI_10800147-S	238.9	263.9	230.9	KIAA0186	NM_021067.1				
GI_10800407-S	112.1	112.2	103	CGA	NM_000735.2	HCG;LHA;FSHA;GPHa;TSHA;GPHA1;CG-	hormone	soluble	signal
GI_10800411-S	325.1	496.1	514.7	MAPRE3	NM_012326.2	EB3;RP3;EBF3	microtubul		microtubul
GI_10800413-S	485.8	573.6	523.9	SC5DL	NM_006918.2	ERG3;SC5D	C-5 sterol	endoplas	lipid
GI_10800414-S	172.3	255.5	747.8	NDN	NM_002487.2	HsT16328	DNA	nucleus	negative
GI_10800415-S	1091.6	1250.8	807.7	SCG2	NM_003469.2	CHGC;SgII	calcium	secretory	protein
GI_10800416-S	425.3	561	483.6	BRAP	NM_006768.2	IMP;BRAP2;RNF52	nuclear	soluble	nucleocyto
GI_10800418-S	228.3	282.1	248.3	CHGA	NM_001275.2	CGA	calcium	synaptic	regulation
GI_10801344-S	8363.6	8084.4	6790.3	eIF3k	NM_013234.1	M9;ARG134;PTD001;HSPC029;PLAC-			
GI_10834965-S	2262.2	2409	2245.1	GLB1	NM_000404.1		beta-	lysosome	

GI_10834967-S	280.9	320.5	316.7	MAN2B1	NM_000528.1	MANB;LAMAN	alpha-	lysosome	protein
GI_10834979-S	106.7	117.5	93.8	IL9	NM_000590.1	P40;HP40;IL-9	interleukin-	extracellul	positive
GI_10834981-S	94.1	105	99.9	IGFBP5	NM_000599.1	IBP5	insulin-like	extracellul	signal
GI_10834983-S	230.4	326.5	172.6	IL6	NM_000600.1	HGF;HSF;BSF2;IL-6;IFNB2	interleukin-	extracellul	negative
GI_10834989-A	165.9	217.9	125.5	NCAM1	NM_000615.1	CD56;NCAM;MSK39	cell	integral to	synaptic
GI_10834999-S	124.4	139.3	128.6	PNLIP	NM_000936.1		triacylglyc		triacylglyc
GI_10835001-S	2819.9	1383	270.4	ARHGDIB	NM_001175.1	D4;GDIA2;GDID4;LYGDI;RAP1GN1	Rho GDP-	cytoplasmi	negative
GI_10835009-S	694.4	870.5	585.5	CTNND1	NM_001331.1	CAS;CTNND;P120CAS;P120CTN;KIAA0384	structural	kinesin	cell
GI_10835012-S	111.1	126.2	118.1	ESR2	NM_001437.1	Erb;ESRB;NR3A2;ER-BETA;ESR-BETA	steroid	nucleus	signal
GI_10835020-S	294.3	361.9	304.1	IGFBP4	NM_001552.1	IBP4	insulin-like	extracellul	skeletal
GI_10835022-S	1733.8	1146.9	1101.4	ITPR1	NM_002222.1	IP3R;IP3R1;Insp3r1	inositol-	endoplas	small
GI_10835024-S	5232.7	7320.5	6048.4	NDUFV2	NM_021074.1		iron-sulfur	NADH	mitochond
GI_10835040-S	237.9	288.9	256	ZNF202	NM_003455.1		specific	nucleus	lipid
GI_10835046-S	1711.7	1868.1	1400.2	SGCE	NM_003919.1	ESG;DYT11		sarcoglyca	muscle
GI_10835048-S	8196	9678.8	7287.9	ARHA	NM_001664.1	RHOA;ARH12;RHO12;RHOH12	Rho small	cytoskelet	Rho
GI_10835070-S	174.7	933.7	232.6	CD74	NM_004355.1	DHLAG;HLADG;Ia-GAMMA	class II	integral to	immune
GI_10835082-S	139	162.6	148	RS1	NM_000330.1	RS;XLRS1	cell	extracellul	vision
GI_10835084-S	1084.6	894.1	1459.1	MT1H	NM_005951.1	MT1	heavy		
GI_10835092-S	1451.6	1707.6	1685.4	PTTG2	NM_006607.1				
GI_10835094-S	562.6	531	490.2	SAA4	NM_006512.1	CSAA	amyloid	extracellul	acute-
GI_10835100-S	457.2	549.6	628.5	GCN5L2	NM_021078.1	GCN5	transcripti	nucleoso	protein
GI_10835102-S	87.8	87.9	90	IFNA4	NM_021068.1	INFA4	interferon-	extracellul	response
GI_10835118-S	611.3	647	631.7	MYO5A	NM_000259.1	GS1;MYO5;MYH12;MYOXIN	myosin	kinesin	nonselecti
GI_10835134-S	103.6	129.6	119.2	CRP	NM_000567.1	PTX1	binding	extracellul	inflammat
GI_10835138-S	117	121.7	122.4	FCGR3B	NM_000570.1	CD16;FCG3;FCGR3	receptor		immune
GI_10835156-S	107.1	261.8	103.3	IGFBP2	NM_000597.1	IBP2			
GI_10835158-S	2265.2	3582.8	3677	SERPINE1	NM_000602.1	PAI;PAI1;PAI-1;PLANH1	endopepti		blood
GI_10835168-S	673.5	670.1	984.9	SLC11A2	NM_000617.1	DCT1;DMT1;NRAMP2	iron ion	integral to	iron ion
GI_10835170-S	131.7	164.4	129.1	IFNG	NM_000619.1	IFG;IFI	interferon-	extracellul	cell
GI_10835172-S	120.4	150.4	124.3	NOS1	NM_000620.1	NOS	nitric-	membran	synaptic
GI_10835174-S	199.8	216.5	195.9	HTR2A	NM_000621.1	HTR2	serotonin	integral to	serotonin
GI_10835182-S	149.8	166.6	173.2	IFNAR1	NM_000629.1	AVP;IFRC;IFNAR;IFNBR	interferon-	integral to	JAK-STAT
GI_10835186-S	475.2	653.3	628.5	SOD2	NM_000636.1	IPO-B;MNSOD	manganes	mitochond	response
GI_10835188-S	665.1	737.9	740.3	GSR	NM_000637.1		glutathion	mitochond	response
GI_10835196-S	114	114	102.1	HTR1F	NM_000866.1	MR77;HTR1EL	serotonin	integral to	G-protein
GI_10835229-S	330.1	410	366.4	MT1G	NM_005950.1	MT1;MGC12386	heavy		
GI_10835235-S	227.3	289.1	257.3	SPRR1A	NM_005987.1	SPRK	structural		epidermal
GI_10835237-S	742.5	838.6	397	IFITM2	NM_006435.1	1-8D		integral to	immune
GI_10835241-S	105.1	109.6	102.2	PRKG1	NM_006258.1	PGK;CGKI;PRKG1B;PRKGR1B;cGKI-			actin
GI_10835249-S	119.6	132.2	113.4	REGL	NM_006508.1	RS			cell
GI_10835253-S	120.4	150.3	141.5	SPRR2C	NM_006518.1				
GI_10862687-S	122.9	134.4	123.6	LATS1	NM_004690.2	wts;WARTS	protein		regulation
GI_10862688-S	143.4	108	97	ZFPM2	NM_012082.2	FOG2;hFOG-2	transcripti		regulation
GI_10862689-S	180.8	235.2	167	LMAN1	NM_005570.2	MR60;gp58;F5F8D;FMFD1;MCFD1;ERGIC5	mannose	Golgi	ER to

GI_10862690-S	2190.4	2176.7	1119.5	ACVR1	NM_001105.2	ALK2;SKR1;ACTRI;ACVRLK2	transmem	integral to	transmem
GI_10862696-S	360.8	374.1	338.5	ACVR2	NM_001616.2	ACTRII	transmem	integral to	transmem
GI_10862697-S	265.2	245.3	264.4	ACVR2B	NM_001106.2	ACTR-IIB	transmem	integral to	transmem
GI_10863870-S	305.9	385.7	325.9	RYR1	NM_000540.1	CCO;MHS;RYR;MHS1;RYDR	calcium-	smooth	calcium
GI_10863872-S	124.7	126.7	114.1	TGFB1	NM_000660.1	CED;DPD1;TGFB	transformi		anti-
GI_10863874-S	65577.5	64467	60037	RPL41	NM_021104.1		structural	cytosolic	protein
GI_10863876-S	630	411.7	392.1	PLSCR1	NM_021105.1	MMTRA1B	calcium	integral to	phospholi
GI_10863878-S	724.7	658.9	794.9	SLC5A6	NM_021095.1	SMVT	sodium	membran	small
GI_10863884-S	108.2	125.6	125.8	RUNX2	NM_004348.1	CCD;AML3;CCD1;OSF2;CBFA1;PEBP2A1;P	RNA	nucleus	ossificatio
GI_10863902-S	1554.6	1992.9	1252.3	TRIP12	NM_004238.1				
GI_10863904-S	364.1	484	344.9	TRIP11	NM_004239.1	CEV14;TRIP230;GMAP-210	protein		transcripti
GI_10863908-S	104.6	119.4	96.7	SPINT2	NM_021102.1	Kop;HAI2;HAI-2	serine	soluble	cell
GI_10863910-S	85.6	105.2	95.8	SPINK2	NM_021114.1	HUSI-II	endopepti		
GI_10863912-S	199.5	252.1	232.4	SLC8A1	NM_021097.1	NCX1	sodium	integral to	sodium
GI_10863920-S	98	96.4	96.7	DLG3	NM_021120.1	NEDLG;SAP102;KIAA1232	guanylate	cellular_co	negative
GI_10863922-S	1636.3	1385.6	701.9	PMAIP1	NM_021127.1	APR;NOXA			oncogene
GI_10863934-S	530.8	338	705.8	RTN1	NM_021136.1	NSP	molecular	endoplas	signal
GI_10863940-S	93.4	99.5	98.1	UGT2B4	NM_021139.1	UGT2B11	glucurono	microsom	xenobiotic
GI_10863942-S	226.5	224.1	208.4	UTX	NM_021140.1			nucleus	
GI_10863946-S	733.9	722.8	628.5	DMTF1	NM_021145.1	DMP1;DMTF;hDMP1	transcripti	nucleus	regulation
GI_10863950-S	300.1	283.2	364.4	UNG2	NM_021147.1		uracil DNA	nucleus	base-
GI_10863968-S	149.8	154	145.9	POLD4	NM_021173.1	p12;POLDS	delta DNA	nucleus	DNA
GI_10863972-S	139.5	132.4	126.3	HAMP	NM_021175.1	HEPC;HFE2B;LEAP1;LEAP-1	antifungal	extracellul	xenobiotic
GI_10863974-S	137.4	177.7	157.6	IGRP	NM_021176.1				
GI_10863982-S	82.9	87.3	94.9	HB-1	NM_021182.1				
GI_10863984-S	732.5	836.1	806.7	C6orf47	NM_021184.1	G4;NG34;D6S53E	molecular	cellular_co	biological_
GI_10863992-S	102.7	123.5	108.5	CYP4F11	NM_021187.1		cytochrom	membran	electron
GI_10863994-S	797.1	778.1	757.3	ZNF410	NM_021188.1	APA1;APA-1	DNA	nucleus	regulation
GI_10863996-S	255.8	393.5	292.6	PTBP2	NM_021190.1	PTB;MIBP;nPTB;PTBLP;brPTB	nucleic		
GI_10863998-S	126.8	138.4	122.6	NEUROD4	NM_021191.1	ATH-3;Atoh3;MATH-3	DNA	nucleus	regulation
GI_10864008-I	1736.4	1619	1927.4	CTDSP1	NM_021198.1	SCP1;NLIIF			
GI_10864010-S	1373.1	2143.3	2349.2	SQRDL	NM_021199.1	CGI-44	disulfide	mitochond	electron
GI_10864012-S	174.4	292.9	218.5	PLEKHB1	NM_021200.1	KPL1;PHR1;PHRET1	signal	membran	phototrans
GI_10864016-S	1844.9	1501.4	1267.4	MASA	NM_021204.1	FLJ12594;DKFZp586M0524	hydrolase		metabolis
GI_10864018-S	107.7	94.4	96.9	C9orf27	NM_021208.1	EST-YD1	molecular	cellular_co	biological_
GI_10864022-S	991.3	1215.6	1022.3	LOC58486	NM_021211.1		DNA		
GI_10864024-S	415.5	745.9	581.4	ZF	NM_021212.1		antiviral	nucleus	transcripti
GI_10864026-S	275.9	334.3	364.8	PCTP	NM_021213.1	STARD2			
GI_10864030-S	1263.3	1738.3	1501.4	ZNF339	NM_021220.1	OVOL2;EUROIMAGE566589	DNA	nucleus	regulation
GI_10864032-S	137.9	163.1	137.6	LY6G5B	NM_021221.1	G5b;C6orf19			
GI_10864034-S	172.1	198.3	173	PROL1	NM_021225.1	BPLP;PRL1	molecular	cellular_co	biological_
GI_10864036-S	109.7	123.1	111.2	MYL7	NM_021223.1	MYL2A;MYLC2A	myosin	myosin	smooth
GI_10864040-A	128.6	147.5	130.8	MLL3	NM_021230.1	HALR;FLJ12625;KIAA1506	methyltran	nucleus	regulation
GI_10864040-I	122.1	145.3	144.5	MLL3	NM_021230.1	HALR;FLJ12625;KIAA1506	methyltran	nucleus	regulation

GI_10864042-S	98.5	109.5	90.6	PRODH2	NM_021232.1	HSPOX1			
GI_10864046-S	414.3	536.7	442.9	EPS15L1	NM_021235.1	EPS15R	calcium		
GI_10864048-S	4919.7	4205.7	3458.5	C12orf14	NM_021238.1	TERA			
GI_10864054-S	117	138.3	109.7	LY6G6D	NM_021246.1	G6D;NG25;LY6-D;MEGT1;C6orf23			
GI_10864056-S	108.5	111.4	98.8	PRM3	NM_021247.1		molecular	cellular_co	biological_
GI_10864062-S	319.5	466.3	443.6	PELI2	NM_021255.1				
GI_10864068-S	419.3	481	478.5	TMEM8	NM_021259.1	M83	molecular	integral to	biological_
GI_10864076-S	338.4	395.1	359.4	CACNA1H	NM_021098.1	CACNA1HB	low	voltage-	myoblast
GI_10864080-S	100	124.5	108	PLXNB3	NM_005393.1	PLEXR;PLXN6;PLEXB3	receptor	membran	developm
GI_10864649-S	113.2	141	125.6	PRKCZ	NM_002744.2	PKC2	atypical	cytoplasm	anti-
GI_10880123-A	332	474.6	476	PSCD2	NM_004228.3	ARNO;CTS18.1;Sec7p-L	ARF	kinesin	actin
GI_10880124-S	86.1	77.5	78.3	SAG	NM_000541.2	ARRESTIN	protein	soluble	rhodopsin
GI_10880125-S	104.4	104.8	109.9	XPNPEP2	NM_003399.3		aminopept	membran	proteolysis
GI_10880133-A	174	172.5	155	ARRB1	NM_020251.1	ARB1;ARR1	enzyme	heterotrim	signal
GI_10880974-S	108.9	108.2	102.1	LOC57821	NM_021179.1				
GI_10880978-S	149.7	182.9	157.7	LSP1	NM_002339.1	WP34;pp52	actin	actin	cellular
GI_10880984-S	86.2	79.9	86.4	IFNA17	NM_021268.1		interferon-	extracellul	response
GI_10938004-S	93.8	113.9	109	CDKL2	NM_003948.2	P56;KKIAMRE	protein		sex
GI_10938005-S	405.3	395.1	426.2	SLC10A3	NM_019848.2	P3;DXS253E	bile	integral to	organic
GI_10938006-I	91.7	100.3	93.8	TSC2	NM_000548.2	LAM;TUBERIN	Rab	cytosol	pathogene
GI_10938009-A	736.4	750.8	640.6	TSC2	NM_021056.1	LAM;TUBERIN	Rab	cytosol	pathogene
GI_10938011-S	107	124	113.7	ACTC	NM_005159.2		structural	actin	regulation
GI_10938012-S	234.9	264.1	239.9	E4F1	NM_004424.2	E4F	transcripti		cell
GI_10938013-S	3917.3	7535	8219.3	JUND	NM_005354.2		RNA	chromatin	regulation
GI_10938017-S	1443.4	1694.8	1722.3	CCNB2	NM_004701.2	HsT17299	cyclin-	nucleus	cytokinesi
GI_10938018-S	122.4	128.8	117.2	DSPG3	NM_004950.2	SLRR3B	glycosami	extracellul	pregnancy
GI_10938019-S	92.7	115.4	96.2	FABP2	NM_000134.2	FABPI	lipid		fatty acid
GI_10938020-S	155.6	176.8	152.1	FABP3	NM_004102.2	MDGI;FABP11;O-FABP	lipid	soluble	negative
GI_10938021-S	9396.9	10820	10098	CAP1	NM_006367.2	CAP;CAP1-PEN		membran	establish
GI_10938022-S	82	90.3	84.2	PAMCI	NM_005447.2	P-CIP1		endosome	nonselecti
GI_10947028-S	179.9	205.8	198.1	SCGB1D2	NM_006551.2	LIPB;LPHB		extracellul	
GI_10947029-S	95.2	81.2	84.9	SERPINI2	NM_006217.2	MEPI;PI14;PANCPIN;TSA2004;SERPIN12	serpin		cell
GI_10947030-S	5595	6750.3	6151.7	PM5	NM_014287.2		molecular	cellular_co	biological_
GI_10947032-S	3705.4	3846.8	4277.9	M6PR	NM_002355.2	SMPR;MPR46;CD-MPR	transmem	lysosome	endosome
GI_10947033-S	1398.6	2162.3	3237.5	MXD4	NM_006454.2	MAD4	transcripti		negative
GI_10947034-S	306.5	305.1	287.8	EIF4ENIF1	NM_019843.2	4E-T;Clast4;FLJ21601	protein	cytoplasm	nucleocyto
GI_10947049-A	91.1	80.4	90.6	ANK1	NM_020481.1	ANK;SPH1;SPH2	structural	actin	
GI_10947051-I	102.3	109.3	105.4	ANK2	NM_001148.2	LQT4	structural	membran	signal
GI_10947053-A	142.4	149.4	134.6	ANK2	NM_020977.1	LQT4	structural	membran	signal
GI_10947058-S	2532.7	1787.4	2020.4	ADCY3	NM_004036.2	AC3;KIAA0511	adenylate	integral to	signal
GI_10947059-I	142.7	186.7	152.2	ADCY6	NM_015270.2	KIAA0422	calcium/ca	integral to	cAMP
GI_10947062-S	113.4	129.9	105.3	ADCYAP1	NM_001117.2	PACAP	neuropepti	soluble	adenylate
GI_10947110-S	217.1	167	117.2	ARG2	NM_001172.2		arginase	mitochond	nitric oxide
GI_10947121-I	94.5	92.4	80.3	ABCC9	NM_020297.1	SUR2;ABC37	sulfonylur	integral to	potassium

GI_10947123-A	115.3	103.4	104.2	ABCC9	NM_020298.1	SUR2;ABC37	sulfonylur	integral to	potassium
GI_10947125-S	293	437.7	399.3	ABCD3	NM_002858.2	ABC43;PMP70;PXMP1	ATP-	integral to	peroxisom
GI_10947128-A	165.8	208.5	183.9	ABCD4	NM_020324.1	P70R;P79R;ABC41;PMP69;PXMP1L;EST352	ATP	peroxisom	small
GI_10947130-I	110.8	126.6	113.8	ABCD4	NM_020325.1	P70R;P79R;ABC41;PMP69;PXMP1L;EST352	ATP	peroxisom	small
GI_10947134-S	3244.6	3000.7	2931.3	ABCF1	NM_001090.1	ABC27;ABC50;EST123147	translation		protein
GI_10947138-S	121.2	122.8	133	ARG1	NM_000045.2		arginase	cytoplasm	urea cycle
GI_11024640-S	521.6	391.6	395.4	GAGE7	NM_021123.1	GAGE-7			
GI_11024646-S	90.4	93	89.6	ADH6	NM_000672.2	ADH-5	alcohol		ethanol
GI_11024685-S	662.9	701.4	538.8	FLJ10637	NM_018164.1	FLJ10630			
GI_11024693-S	322.2	302	229.5	DDX26	NM_012141.1	HDB;DBI-1;DICE1;Notchl2;DKFZP434B105	tumor		cell growth
GI_11024697-S	3150.1	2588.8	2236.9	MGEA5	NM_012215.1	MEA5;KIAA0679;O-GLCNACASE	hyalurono		glycoprote
GI_11024703-S	597.4	465.9	454.7	FLJ10287	NM_019083.1	FLJ11219			
GI_11024711-S	106.4	103.2	90.8	MYH4	NM_017533.1	MYH2B;MyHC-2B;MyHC-IIb	muscle	muscle	striated
GI_11034818-S	236.7	204.6	359.2	NRIP3	NM_020645.1	C11orf14	sugar		
GI_11034834-I	192.4	247.2	196.1	ZNF302	NM_018675.1	ZNF327;ZNF135L;ZNF140L	DNA	nucleus	regulation
GI_11034854-S	1533.1	1757.9	1804.8	C11orf15	NM_020644.1			integral to	
GI_11036631-S	121	123.8	125	DSPP	NM_014208.1	DPP;DSP;DGI1;DTDP2;DFNA39	collagen	extracellul	ossificatio
GI_11036639-S	1293.7	1435.6	791.5	PPP3CB	NM_021132.1	CALNB;CALNA2	calmoduli	calcineurin	transcripti
GI_11036645-S	971.2	1479.2	1401.2	H2BFS	NM_017445.1				
GI_11036647-S	111.5	106	107.7	PPY2	NM_021092.1				
GI_11036649-S	148.8	199.1	163.4	PYY2	NM_021093.1				
GI_11036657-S	90.2	84.8	70.1	DAZ3	NM_020364.1	pDP1679	nucleic		
GI_11036659-S	86.1	91.6	81.6	DAZ2	NM_020363.1	pDP1678	nucleic		
GI_11037054-S	171.3	162.7	166.8	SPAG4	NM_003116.1		structural	kinesin	spermatog
GI_11037056-S	1941.5	2119.1	1258.5	MYO10	NM_012334.1	KIAA0799	actin	cytoskelet	neuropepti
GI_11037060-A	1067.7	1107.7	1021.6	C21orf59	NM_021254.1	C21orf48;FLJ20467			
GI_11037060-I	132.3	141.7	123.6	C21orf59	NM_021254.1	C21orf48;FLJ20467			
GI_11037062-S	251.2	283.3	177.2	PELI1	NM_020651.2				
GI_11037064-S	473.6	406.3	277	DISC1	NM_018662.1	KIAA0457	protein	kinesin	biological_
GI_11038618-S	17086.3	19495	15662	ACTG1	NM_001614.2	ACTG;DFNA20;DFNA26	structural	actin	
GI_11038619-A	155.3	181.7	159	CHAT	NM_020986.1	FIMG2	acyltransf	cytoplasm	synaptic
GI_11038623-S	1119.1	961.8	834.8	PHC1	NM_004426.1	EDR1;HPH1;RAE28	protein	nucleus	developm
GI_11038625-S	120.7	125.6	108	ACTG2	NM_001615.2	ACTE;ACTA3;ACTSG	structural	actin	muscle
GI_11038626-I	249.9	296	256.5	CHAT	NM_020549.2	FIMG2	acyltransf	cytoplasm	synaptic
GI_11038629-I	155.5	187.3	176.8	CHAT	NM_020984.1	FIMG2	acyltransf	cytoplasm	synaptic
GI_11038636-I	137.8	152.7	142.7	GRIN1	NM_007327.1	NR1;NMDA1;NMDAR1	N-methyl-	integral to	small
GI_11038638-I	111.4	124.1	128.8	BCR	NM_004327.2	ALL;CML;PHL;BCR1;D22S11;D22S662	protein		protein
GI_11038640-A	146	180.6	167.9	BCR	NM_021574.1	ALL;CML;PHL;BCR1;D22S11;D22S662	protein		protein
GI_11038640-I	566.1	649.5	636.3	BCR	NM_021574.1	ALL;CML;PHL;BCR1;D22S11;D22S662	protein		protein
GI_11038642-A	14961.4	18266	15834	AP2S1	NM_021575.1	AP17;CLAPS2;AP17-DELTA	vesicle	coated	
GI_11038644-I	7800.3	9636.4	8130.8	AP2S1	NM_004069.2	AP17;CLAPS2;AP17-DELTA	vesicle	coated	
GI_11038645-S	1295.1	1527.5	1280.5	BANF1	NM_003860.2	BAF;BCRP1;D14S1460	DNA	nucleus	response
GI_11038647-S	284.8	244.4	269.2	CDC7	NM_003503.2	Hsk1;CDC7L1;HsCDC7;huCDC7	protein	cytoplasm	G1/S
GI_11038650-S	1066.5	1178.6	1104.2	IK	NM_006083.2	RED;CSA2	cytokine	soluble	immune

GI_11038651-S	1292.5	1444.3	1461.5	PTTG1	NM_004219.2	EAP1;PTTG;HPTTG;TUTR1;SECURIN	transcripti	cytoplasm	spermatog
GI_11038652-S	139.2	185.5	159.2	AQP9	NM_020980.2	SSC1;HsT17287	water	integral to	water
GI_11038653-S	89.9	98.5	81	ADAMTS1	NM_006988.2	C3-C5;METH1;KIAA1346	integrin	extracellul	integrin-
GI_11038658-A	114.9	160.2	411	ADAMTS2	NM_021599.1	NPI;PCINP;PCPNI;hPCPNI;ADAM-	collagenas	extracellul	collagen
GI_11038661-S	119.4	132.1	120.7	C1QB	NM_000491.2		compleme	compleme	compleme
GI_11038670-S	9906.4	9079	8421.4	PTTG1IP	NM_004339.2	PBF;C21ORF1;C21ORF3	molecular	integral to	protein-
GI_11038671-A	250.9	317.4	298.8	CD79A	NM_021601.1	IGA;MB-1	transmem	integral to	defense
GI_11038673-I	174.9	225.3	171.4	CD79B	NM_000626.1	B29;IGB	transmem	integral to	signal
GI_11038675-A	142.6	169.5	140.4	CD79B	NM_021602.1	B29;IGB	transmem	integral to	signal
GI_11055991-S	621.9	880.4	717.4	RISC	NM_021626.1	HSCP1	serine		proteolysis
GI_11055993-S	342.6	376.4	455.9	SENP2	NM_021627.1	AXAM2;SMT3IP2;KIAA1331	cysteine-	nuclear	regulation
GI_11055995-S	101.1	113.5	112.9	ALOXE3	NM_021628.1		lipoxygena		electron
GI_11056001-S	98.3	101.9	88.1	FKSG2	NM_021631.1		molecular	cytoplasm	apoptosis
GI_11056007-S	100.9	104.2	106.2	LGR7	NM_021634.1		rhodopsin-	integral to	G-protein
GI_11056009-S	284.9	356.2	284.4	PBOV1	NM_021635.1	UC28;UROC28;dJ171N11.2			
GI_11056011-S	128.7	130.1	130.5	FLJ14084	NM_021637.1				
GI_11056017-S	911.2	817.4	773.5	C12orf10	NM_021640.1	MYG;MYG1			
GI_11056035-S	1227.1	1282.2	1161.8	KIAA0153	NM_015140.1		tubulin-		protein
GI_11056051-S	285.9	339.5	292.4	FCGR2A	NM_021642.1	CD32;FCG2;FcGR;CDw32;FCGR2;IGFR2;F	receptor	integral to	immune
GI_11056053-S	491.9	1392.8	726.3	TRB2	NM_021643.1	TRIB2;GS3955	protein		protein
GI_11056055-I	217.1	245.6	232.6	MRPS12	NM_021107.1	RPS12;RPMS12;RPSM12;MPR-S12;MT-	structural	mitochond	protein
GI_11063982-S	637.9	705.4	638.5	KIAA0266	NM_021645.1				
GI_11067750-S	105.9	123.6	110.5	IFNA2	NM_000605.2	INFA2	interferon-	extracellul	induction
GI_11068002-S	166.7	234.4	276.4	IGF1R	NM_000875.2	JTK13	insulin-like	integral to	insulin
GI_11068140-S	186	228.5	221.2	C11orf16	NM_020643.1				
GI_11072092-I	2664.1	2412.6	2625.8	WDR6	NM_018031.2	FLJ10218	molecular	cellular_co	biological_
GI_11072100-S	230.4	245.3	219.4	C22orf3	NM_012265.1	HS984G1A			
GI_11079227-S	1991.5	2258.9	2208.4	NSF	NM_006178.1	SKD2	ATP-	Golgi	proteolysis
GI_11079650-S	148.9	173.1	157.1	PNOC	NM_006228.2	PPNOC	neuropepti	extracellul	sensory
GI_11095446-S	91.7	103.8	101.6	HLA-DQA2	NM_020056.1	HLA-DXA			
GI_11096339-S	2108.5	3151.7	3824.1	C3orf4	NM_019895.1	HSPC174;GENX-3745;DKFZP564P0462		integral to	
GI_11119413-S	1569.7	1233.1	1243.9	TACC2	NM_006997.1	AZU-1		kinesin	oncogene
GI_11119427-S	3966.3	3024.8	3698.1	VIP32	NM_021732.1	VIT32;PP5395			
GI_11119429-S	112.1	112.6	98.8	TSKS	NM_021733.1	TSKS1	kinase		
GI_11120735-S	131.9	151.2	158.2	DUX1	NM_012146.1		transcripti	nucleus	transcripti
GI_11120737-S	185.4	228.3	192.2	DUX5	NM_012149.1		transcripti	nucleus	regulation
GI_11125767-S	950.5	1041.4	949	HRI	NM_014413.2		ATP		protein
GI_11125769-S	2374.3	2665.3	2223.1	JTV1	NM_006303.2	P38;PRO0992	DNA		protein
GI_11125771-S	103.1	104.8	93.6	MARCKS	NM_002356.4	MACS;80K-L;PKCSL;MRACKS;PRKCSL	calmoduli	actin	cell
GI_11125773-S	266.7	248.9	263	PMS2	NM_000535.2	PMSL2;HNPCC4;PMS2CL	DNA	nucleus	mismatch
GI_11125774-S	90.8	98.4	94	REN	NM_000537.2		renin		regulation
GI_11128014-S	91.3	101.9	81.9	IFNA6	NM_021002.1		hematopoi	extracellul	response
GI_11128020-S	107.4	87.6	104.8	DKFZP434AC	NM_018991.1				
GI_11136625-S	106.4	125	107.3	NOX3	NM_015718.1	GP91-3	oxidoredu	membran	electron

GI_11138122-S	114.4	131.7	125.8	CHRNA10	NM_020402.2		extracellul	integral to	synaptic
GI_11140810-S	2235.2	1813	1581.3	CUL4A	NM_003589.1		tumor		induction
GI_11140814-S	310.9	376.9	335	FTCD	NM_006657.1		folic acid	cytoplasm	folic acid
GI_11141874-S	119.6	128.4	125.5	IL21	NM_021803.1				
GI_11141876-S	204.1	200.4	417.5	SIGIRR	NM_021805.1		interleukin-	membran	
GI_11141882-S	259.4	307.3	273.2	BPESC1	NM_021812.1		molecular	cellular_co	biological_
GI_11141886-S	137.9	125.3	109.3	HAPLN2	NM_021817.1	BRAL1	hyaluronic	extracellul	cell
GI_11141890-S	113.9	116.7	112.6	LMAN1L	NM_021819.1	ERGL;CPXIII;FLJ13993;ERGIC-53L			
GI_11141892-S	402.8	452.6	381.5	C6orf75	NM_021820.1	MDS024;dJ187J11.2			
GI_11141898-S	2361.9	2041.9	2350.3	NIF3L1	NM_021824.1	CALS-7;MDS015;ALS2CR1			
GI_11141904-S	102.4	115.4	95.9	FLJ23514	NM_021827.1				
GI_11181769-I	102.2	110.5	106.9	XT3	NM_020208.1		transporte	plasma	small
GI_11184225-S	996	808.5	438.8	RGS10	NM_002925.2		signal		signal
GI_11184232-S	157.2	166.1	145.6	HAO1	NM_017545.2	GOX;GOX1;HAOX1	(S)-2-	peroxisom	electron
GI_11184237-S	72.2	79.7	76.4	LBX1	NM_006562.3	LBX1H	transcripti	nucleus	embryoge
GI_11225606-S	128.8	138.7	123.6	IL1RAPL2	NM_017416.1	IL1R9;IL-1R9;TIGIRR-1;IL1RAPL-2	interleukin-	membran	central
GI_11225608-S	148.1	164	130.3	ACE2	NM_021804.1	ACEH;DKFZP434A014	zinc ion	membran	proteolysis
GI_11231178-A	445.7	541.9	490.1	LAIR1	NM_021708.1	LAIR-1	transmem	integral to	immune
GI_11231178-I	127.3	159.4	145.6	LAIR1	NM_021708.1	LAIR-1	transmem	integral to	immune
GI_11276084-S	100.2	98.8	102.4	UGT1A9	NM_021027.1	HLUGP4	UDP-	microsom	metabolis
GI_11277467-I	1023.2	829.1	945.7	SIVA	NM_006427.2	CD27BP	receptor		induction
GI_11277469-A	2206.4	1843.4	2187	SIVA	NM_021709.1	CD27BP	receptor		induction
GI_11321560-S	237.7	271.9	240.6	HPX	NM_000613.1		heme	extracellul	heme
GI_11321570-S	91.8	102.3	81.5	SLIT3	NM_003062.1	MEGF5;SLIL2;SLIT1;Slit-3	protein	extracellul	developm
GI_11321574-S	130.2	153.9	129.9	LY6D	NM_003695.1	E48	cell	peripheral	cell
GI_11321578-S	236.6	259.6	262	MYH13	NM_003802.1	MyHC-eo	muscle	striated	striated
GI_11321580-S	1404.4	1596.1	1363.9	SUCLG1	NM_003849.1	SUCLA1	GTP	mitochond	glycolysis
GI_11321582-S	525.3	687	681.4	SUCLA2	NM_003850.1	A-BETA	succinate-	mitochond	succinyl-
GI_11321586-S	237.1	262.1	241.1	HFL1	NM_002113.1	CFHL;FHR1;H36-1	plasma	extracellul	compleme
GI_11321592-S	684.3	1249.2	1411.2	IGFBP6	NM_002178.1				
GI_11321594-S	158	187.9	183.4	ITGA9	NM_002207.1	RLC;ITGA4L;ALPHA-RLC	cell	integrin	cell
GI_11321596-S	448.5	539.2	469.4	KDR	NM_002253.1	FLK1;VEGFR;VEGFR2	vascular	integral to	transmem
GI_11321604-S	661.6	773.4	902	JARID1C	NM_004187.1	SMCX;XE169;DXS1272E	DNA	nucleus	regulation
GI_11321616-S	130.1	151	124.2	DPYSL4	NM_006426.1	CRMP3;DRP-4;ULIP4	hydrolase		neurogene
GI_11321627-S	157.5	192.1	158.5	CTRC	NM_007272.1	CLCR	peptidase		proteolysis
GI_11321629-S	1020.6	1324.8	1522.7	NR1H2	NM_007121.1	NER;UNR;LXR-b;NER-I;RIP15	ligand-	nucleus	regulation
GI_11321633-S	63.3	67	67.5	CD2AP	NM_012120.1	CMS;DKFZP586H0519	structural	actin	substrate-
GI_11321635-S	104.5	111.8	109.6	TPSD1	NM_012217.1		serine-		proteolysis
GI_11321641-S	228.2	193.4	198.4	BRD1	NM_014577.1	BRL;BRPF1;BRPF2;DKFZP434B094			
GI_11342663-S	125.5	271.1	153.4	MX2	NM_002463.1	MXB	GTPase	cytoplasm	defense
GI_11342665-S	2210.6	4563.3	2621.8	MMP2	NM_004530.1	CLG4;CLG4A;TBE-1	gelatinase	extracellul	proteolysis
GI_11342671-S	209.7	235.7	207.7	MYH3	NM_002470.1	MYHSE1;MYHC-EMB	myosin	striated	muscle
GI_11345453-S	545.7	364.9	422.5	FANCE	NM_021922.1	FAE;FACE	molecular	nucleus	
GI_11345457-S	297.9	347.9	272.7	FLJ21820	NM_021925.1		catalytic		lipid

GI_11345459-S	325.5	391.2	321	FLJ13220	NM_021927.1		small		small
GI_11345461-S	425.7	731.3	594.9	FLJ22649	NM_021928.1		peptidase	microsom	
GI_11345471-S	499	269.3	318.1	FLJ12438	NM_021933.1	IIP45			
GI_11345479-S	3775.4	3216.3	3390.6	C21orf97	NM_021941.1	FLJ21324			
GI_11345483-S	704.1	584.5	505.2	TEX27	NM_021943.1	FLJ13222	molecular		
GI_11345485-S	574.2	384.8	337	C14orf93	NM_021944.1	FLJ12154			
GI_11345491-S	209	262.3	233	SRR	NM_021947.1		lyase		L-serine
GI_11386138-S	142.4	141.6	151.8	PLCB3	NM_000932.1		phospholi	membran	intracellula
GI_11386142-S	222.5	283	221.1	SERPINF2	NM_000934.1	AAP;API;PLI;A2AP;ALPHA-2-PI	serpin	Golgi	acute-
GI_11386146-S	7984.3	6679.3	7930.5	PSAP	NM_002778.1	GLBA;SAP1	lipid	lysosome	glycosphin
GI_11386152-S	348.6	486.5	420.8	OR1E2	NM_003554.1	OR1E4;OR17-93;OR17-135	receptor	integral to	chemosen
GI_11386154-S	147.8	170.1	152.9	ATP2B3	NM_021949.1	PMCA3	adenosine	integral to	small
GI_11386156-S	941.5	3018.6	2361.6	CDA	NM_001785.1	CDD	cytidine		nucleobas
GI_11386170-S	105.8	105.9	117.9	CEACAM5	NM_004363.1	CEA;CD66e	tumor	membran	
GI_11386172-S	90.8	96.5	89.5	DMRT1	NM_021951.1	DMT1	transcripti	nucleus	male
GI_11386174-A	2597.7	2571.9	2687.5	PPP1R11	NM_021959.1	HCGV;HCG-V;TCTE5;TCTEX5	protein	soluble	
GI_11386184-S	2434.6	2653.8	2103.6	CBARA1	NM_006077.1	CALC;DKFZp564C246	calcium	intracellula	defense
GI_11386190-S	2935.5	2149.4	2225.7	LGTN	NM_006893.1		receptor	cytoplasm	intracellula
GI_11386194-S	328.8	428.4	349.2	FOXB1	NM_012182.1	FKH5;HFKH-5	transcripti	nucleus	regulation
GI_11386196-S	196.1	252.9	228	FOXE3	NM_012186.1	ASMD;FKHL12;FREAC8	transcripti	nucleus	regulation
GI_11386198-S	737.4	612.1	691.3	PVRL3	NM_015480.1	PPR3;PRR3;PVRR3;nectin-			
GI_11386200-S	607.5	686	656.4	UGCGL2	NM_020121.2	HUGT2;FLJ10873;FLJ11485	transferas	endoplas	carbohydr
GI_11415027-S	121.6	151.6	142.4	TCL1A	NM_021966.1	TCL1		microsom	developm
GI_11415031-S	133.6	149.3	123	OR1D4	NM_003552.1	OR17-30;OLFR17-30	G-protein	integral to	sensory
GI_11415033-S	164.5	191.8	165.3	OR1G1	NM_003555.1	OR1G2;OR17-130;OR17-209	olfactory	integral to	G-protein
GI_11415035-S	541.1	549.9	607.9	ZNF148	NM_021964.1	BERF-1;BFCOL1;ZBP-89;ZFP148;pHZ-	specific	DNA-	cellular
GI_11415045-S	195.4	247.2	237.3	SERF1A	NM_021967.1	4F5;H4F5;FAM2A;SERF1;SMAM1	molecular	cellular_co	neurogene
GI_11496238-S	1556.7	1686.6	1811.8	RELA	NM_021975.1	NFKB3	protein	transcripti	toxin
GI_11496266-S	118.1	118	129.2	ALX4	NM_021926.1	FPP;PFM;PFM1;PFM2;KIAA1788	transcripti	nucleus	regulation
GI_11496268-S	1365.3	1591	1180.9	ZNF277	NM_021994.1	NRIF4			
GI_11496272-S	172.9	231.9	153.3	TMSNB	NM_021992.1		actin	cytoskelet	biological_
GI_11496274-S	113.2	96.5	104.2	OR1E1	NM_003553.1	HGM071;OR17-2;OR1E9P;OR17-32	olfactory	integral to	perception
GI_11496280-S	104.2	116.2	109.5	KLK13	NM_015596.1	KLKL4;KLK-L4;DKFZP586J1923	trypsin	extracellul	proteolysis
GI_11496282-S	215.7	203	152	PLAC1	NM_021796.1		molecular	cellular_co	biological_
GI_11496880-S	1170.8	1380.9	1586.7	ELK1	NM_005229.2		transcripti	nucleus	oncogene
GI_11496883-S	98.4	85.6	90.3	CLPS	NM_001832.2		enzyme	soluble	lipid
GI_11496886-S	190.7	241.5	225.6	ADH1A	NM_000667.2	ADH1	alcohol	cytoplasm	ethanol
GI_11496888-S	101.2	112.3	106.3	ADH1C	NM_000669.2	ADH3	alcohol	cytoplasm	ethanol
GI_11496889-S	92.5	100.6	97.1	ADH4	NM_000670.2	ADH-2	electron-		aldehyde
GI_11496890-S	2068.8	1911.6	1760.2	ADH5	NM_000671.2	FDH;ADHX;ADH-3	formaldeh		ethanol
GI_11496969-S	83.2	94.8	84.3	ADH7	NM_000673.2	ADH-4	alcohol		regulation
GI_11496970-A	208	250.8	224	GRIN1	NM_000832.4	NR1;NMDA1;NMDAR1	N-methyl-	integral to	small
GI_11496977-S	1458.4	1320	1527.4	NFYC	NM_014223.2	HSM;CBFC;HAP5;CBF-C;NF-YC;H1TF2A	RNA		protein
GI_11496979-S	517.9	411.4	365.2	PMS1	NM_000534.2	PMSL1;hPMS1;HNPCC3	DNA	nucleus	mismatch

GI_11496980-A	257.7	439.6	357.6	SVIL	NM_003174.2		membran	actin	cytoskelet
GI_11496980-I	101.4	134.7	132.7	SVIL	NM_003174.2		membran	actin	cytoskelet
GI_11496981-I	104.5	107	97.1	SVIL	NM_021738.1		membran	actin	cytoskelet
GI_11496985-S	114.3	98.7	108.4	C1QR1	NM_012072.2	CD93;C1qRP;C1qR(P);dJ737E23.1	receptor	integral to	antimicrob
GI_11496986-S	127.4	142.7	135.4	PART1	NM_016590.2	DKFZP586D0823			
GI_11496987-S	120.8	144.8	138.1	RENBP	NM_002910.4	RBP;RNBP	endopepti		regulation
GI_11496988-S	405.2	588.1	426.4	GAA	NM_000152.2	LYAG	alpha-	lysosome	glycogen
GI_11496989-S	3291.9	2850.7	2977.4	ADPRT	NM_001618.2	PARP;PPOL;ADPRT1;PARP-1;pADPRT-1	NAD ADP-	nucleus	protein
GI_11496990-S	121.9	122.9	127	ADPRTL1	NM_006437.2	PH5P;p193;PARPL;VPARP;VAULT3;KIAA01	NAD ADP-	nucleus	DNA
GI_11496991-S	575.2	464.1	531	ADPRTL2	NM_005484.2	PARP2;ADPRT2;PARP-	catalytic	nucleus	protein
GI_11496992-S	728.1	707.3	726.7	ADPRTL3	NM_005485.2	PARP3;ADPRT3;PARP-	NAD ADP-	nucleus	protein
GI_11496993-A	114.8	112.8	98.2	ADAM28	NM_021777.1	MDCL;ADAM23;MDC-Lm;MDC-Ls;eMDCII	metallope	integral to	spermatog
GI_11496993-I	98.4	94	94	ADAM28	NM_021777.1	MDCL;ADAM23;MDC-Lm;MDC-Ls;eMDCII	metallope	integral to	spermatog
GI_11496997-A	199.2	253.6	243.7	ADAM11	NM_021612.1	MDC	integrin	integral to	integrin-
GI_11496999-A	157.1	180.8	163	ADAM12	NM_021641.1	MCMP;MLTN;MLTNA;MCMPMltna	metallope	integral to	myoblast
GI_11496999-I	96.4	95.2	88.4	ADAM12	NM_021641.1	MCMP;MLTN;MLTNA;MCMPMltna	metallope	integral to	myoblast
GI_11497001-S	913.2	745.6	463.8	ADAM15	NM_003815.2	MDC15	metallope	peripheral	cell-matrix
GI_11497005-A	1065	1130.6	853	ADAM17	NM_021832.1	TACE;cSVP;CD156b	metallope	peripheral	cell-cell
GI_11497600-I	172.7	213.2	208.6	ADAM29	NM_014269.2	svph1	metallope	integral to	spermatog
GI_11497602-A	106.4	122.5	119.9	ADAM29	NM_021779.1	svph1	metallope	integral to	spermatog
GI_11497606-S	90.1	89	83.4	ADAM2	NM_001464.2	FTNB;PH30;PH-30b	integrin	integral to	fusion of
GI_11497611-A	571	665	478.6	GABBR1	NM_021903.1	GPRC3A;GABABR1	GABA-B	kinesin	negative
GI_11497611-I	242.8	310.1	276	GABBR1	NM_021903.1	GPRC3A;GABABR1	GABA-B	kinesin	negative
GI_11545742-S	754.4	1418.1	1813.7	SDF2L1	NM_022044.1			membran	
GI_11545750-S	107.1	122.9	108.4	CSNK1G1	NM_022048.1		ATP		protein
GI_11545752-S	99.6	113.5	110.9	GPR88	NM_022049.1	STRG	receptor	integral to	G-protein
GI_11545756-S	123.3	121.1	124.6	NXF3	NM_022052.1		protein	nucleus	protein-
GI_11545760-S	164.9	139.6	107.2	KCNK12	NM_022055.1	THIK2;THIK-2	voltage-	integral to	potassium
GI_11545764-S	417.2	462.6	349.3	CXCL16	NM_022059.1	SRPSOX;CXCLG16;SR-PSOX	cytokine	integral to	chemotaxi
GI_11545766-S	1311.9	927.3	683.5	ABHD4	NM_022060.1	FLJ12816	hydrolase		aromatic
GI_11545768-S	98.3	123.1	102.8	PKNOX2	NM_022062.1	PREP2;FLJ13074	transcripti	nucleus	regulation
GI_11545770-S	183.9	192.9	173.9	C10orf84	NM_022063.1	FLJ13188;bA319I23.1			
GI_11545792-S	888.5	827.1	911.8	FLJ12455	NM_022078.1		nucleic	intracellula	
GI_11545796-A	290.4	275.4	276.3	C1orf24	NM_022083.1	NIBAN	molecular	cellular_co	biological_
GI_11545800-S	920.7	839.1	1248.7	GALNT11	NM_022087.1	FLJ21634			
GI_11545810-S	118.6	137.2	139.6	LOC63928	NM_022097.1		calcium		
GI_11545816-S	631.8	638.2	376.4	GPSM3	NM_022107.1	G18;NG1;G18.2;C6orf9;G18.1a;G18.1b			
GI_11545826-S	225.1	252.2	241.3	P53AIP1	NM_022112.1		molecular	mitochond	apoptosis
GI_11545834-S	341.4	401.5	381.7	SE20-4	NM_022117.1	CDA1;CTCL;DENTT;HRIHFB2216	DNA	nucleus	nucleoso
GI_11545840-S	110.8	135.2	117.8	OXCT2	NM_022120.1	FKSG25;SCOT-T;FLJ00030	CoA-		metabolis
GI_11545844-S	102.8	94.6	92.3	MMP27	NM_022122.1	MMP-27	zinc ion	extracellul	proteolysis
GI_11545846-I	130.6	123.7	125.5	NPAS3	NM_022123.1	MOP6			
GI_11545852-S	125.8	113.3	118.7	SLC28A3	NM_022127.1	CNT3	nucleoside	membran	transport
GI_11545854-S	260.4	299.2	279.3	RBKS	NM_022128.1	RBSK	ribokinase		D-ribose

GI_11545856-S	126.3	151.9	164.2	MAWBP	NM_022129.1		molecular	cellular_co	biological_
GI_11545860-S	135.7	177.8	141.8	CLSTN2	NM_022131.1	CS2;CSTN2	calcium	integral to	homophili
GI_11545866-S	134.1	139	124	GP3ST	NM_022134.1	GAL3ST2	sulfotransf	membran	biological_
GI_11545882-S	118	135.3	115	TNMD	NM_022144.1	TEM;CHM1L;BRICD4;CHM1-LIKE		integral to	
GI_11545886-S	124.8	140	127.1	OT7T022	NM_022146.1	NPFF1	neuropepti	integral to	G-protein
GI_11545889-S	141.8	168	160.3	IFRG28	NM_022147.1			integral to	
GI_11545911-S	101.9	161.1	103.3	CARD15	NM_022162.1	CD;ACUG;BLAU;IBD1;NOD2;PSORAS1	ATP	intracellula	apoptosis
GI_11545913-S	361.7	514.9	548.2	XYLT2	NM_022167.1	XT2;XT-II;xylT-II	acetylgluc	membran	glycosami
GI_11545917-S	122.7	288.4	168	LCN7	NM_022164.1	ARG1;LIECG3	extracellul	extracellul	transport
GI_11545919-S	153.6	133	178.7	LIN7B	NM_022165.1	VELI2;LIN-7B;MALS-2	protein		intracellula
GI_11545925-S	113.2	116.5	103.6	DAMS	NM_022001.1				
GI_11559922-I	202.8	253.7	235	WBSCR1	NM_022170.1	EIF4H;WSCR1;KIAA0038	translation	eukaryotic	regulation
GI_11559926-S	736	880.5	810.6	MRPS14	NM_022100.1	MRP-S14;HSMRPS14;DJ262D12.2	structural	mitochond	protein
GI_11560140-S	505.5	702.7	753.3	TCTA	NM_022171.1		tumor		
GI_11612654-S	185.2	207.9	163	FXYD6	NM_022003.1		ion	integral to	ion
GI_11612658-S	491.2	647.9	555.8	FXYD7	NM_022006.1		ion	integral to	ion
GI_11612673-I	126.9	135.8	135.4	FXYD3	NM_021910.1	MAT8;PLML;MAT-8	chloride	integral to	chloride
GI_11612675-A	218.5	263.8	237.8	FXYD3	NM_005971.2	MAT8;PLML;MAT-8	chloride	integral to	chloride
GI_11641230-S	261.8	318.1	283.4	EDAR	NM_022336.1	DL;ED3;ED5;ED1R;EDA3;EDA-A1R	transmem	integral to	apoptosis
GI_11641236-S	109.5	116.2	107.9	RAB38	NM_022337.1	NY-MEL-1	GTP	cellular_co	small
GI_11641238-S	427.5	651.9	509.4	C11orf24	NM_022338.1	DM4E3			
GI_11641240-S	108.5	112.3	119.6	ZFYVE20	NM_022340.1	Rabenosyn-5	zinc ion	endosome	endosome
GI_11641242-S	176.4	213.2	180.4	PDF	NM_022341.1		molecular	mitochond	protein
GI_11641254-S	171.6	192.4	165.8	IFRG15	NM_022347.1				
GI_11641260-S	1112.1	1400.5	1333.4	LRAP	NM_022350.1	L-RAP			
GI_11641264-S	445.8	388.8	336.6	OSGEPL1	NM_022353.1				
GI_11641266-S	108.8	105.1	96.2	SPATA1	NM_022354.1	SP-2;SPAP1			
GI_11641268-S	168.4	232.9	196.2	DPEP2	NM_022355.1				
GI_11641272-S	171.4	201.1	175.2	DPEP3	NM_022357.1		membran		proteolysis
GI_11641288-S	1871.9	1568.5	1471.9	TFB2M	NM_022366.1	Hkp1;FLJ22661;FLJ23182	rRNA		rRNA
GI_11641302-S	104.7	104.1	100.7	ARL6IP2	NM_022374.1	FLJ23293			
GI_11641403-S	221.5	287.6	266	CKMT1	NM_020990.2	CKMT;UMTCK	creatine	mitochond	
GI_11641404-S	147.5	165.5	144.1	CLCN4	NM_001830.2	CLC4;ClC-4	voltage-	membran	small
GI_11641410-A	712	857	553.3	CDC25B	NM_021872.1		protein		positive
GI_11641414-I	123.4	140.4	130.3	CDC25B	NM_021874.1		protein		positive
GI_11641417-S	111.9	117.3	100	GDF10	NM_004962.2	BMP3B;BMP-3b	growth	nucleus	TGFbeta
GI_11641418-S	110.5	124.9	129.8	GDF11	NM_005811.2	BMP11;BMP-11	cytokine	cellular_co	mesoderm
GI_11641419-S	91	89.7	86.2	GDF1	NM_001492.3		cytokine	extracellul	cell growth
GI_11641422-A	1076.5	1308.7	1049.2	USP9X	NM_021906.1	DFFRX	cysteine-		deubiquiti
GI_11641426-S	246.3	263.4	243.7	USP9Y	NM_004654.2	DFFRY	ubiquitin-		deubiquiti
GI_11761614-A	266.8	451.9	538.1	PC	NM_022172.1	PCB	pyruvate	mitochond	biotin
GI_11761614-I	102.6	108.3	115.4	PC	NM_022172.1	PCB	pyruvate	mitochond	biotin
GI_11761618-I	215.5	248.1	250	GMPPB	NM_013334.2	KIAA1851			
GI_11761620-A	182.2	278.4	271.4	GMPPB	NM_021971.1	KIAA1851			

GI_11761622-I	182.7	206.2	188.6	PC	NM_000920.2	PCB	pyruvate	mitochond	biotin
GI_11761623-A	458	421.7	570.7	ST7	NM_018412.2	HELG;RAY1;SEN4;TSG7;ETS7q;FAM4A1;S			
GI_11761623-I	612.3	497.8	728	ST7	NM_018412.2	HELG;RAY1;SEN4;TSG7;ETS7q;FAM4A1;S			
GI_11761625-I	427.1	355.4	383.7	ST7	NM_021908.1	HELG;RAY1;SEN4;TSG7;ETS7q;FAM4A1;S			
GI_11761627-I	100.7	89.6	85.6	FGA	NM_000508.2		fibrinogen	soluble	positive
GI_11761628-A	101.3	108.7	102.1	FGA	NM_021871.1		fibrinogen	soluble	positive
GI_11761628-I	121.4	114.6	97.1	FGA	NM_021871.1		fibrinogen	soluble	positive
GI_11761630-S	107.6	93.2	95	FGB	NM_005141.1		fibrinogen	fibrinogen	positive
GI_11761632-I	107.8	129.1	108.2	FGG	NM_021870.1		fibrinogen	fibrinogen	positive
GI_11761634-A	107.2	117.4	92	FGG	NM_000509.3		fibrinogen	fibrinogen	positive
GI_11761634-I	90.5	98.6	91.7	FGG	NM_000509.3		fibrinogen	fibrinogen	positive
GI_11761636-S	104.6	104.9	97.5	ACTL7A	NM_006687.2		structural	cytoskelet	
GI_11761637-S	108.7	96.2	107.2	ACTL7B	NM_006686.2		structural	actin	
GI_11863127-A	468	422.4	558.2	PIGA	NM_020473.1	GPI3;PIG-A	catalytic	endoplas	biosynthes
GI_11863129-I	132.9	152.5	153.9	PIGA	NM_002641.1	GPI3;PIG-A	catalytic	endoplas	biosynthes
GI_11863131-A	138.1	150.7	143	NR1I2	NM_022002.1	BXR;PAR;PRR;PXR;SAR;SXR;ONR1;PAR1;	ligand-		steroid
GI_11863131-I	101.9	112.6	99.1	NR1I2	NM_022002.1	BXR;PAR;PRR;PXR;SAR;SXR;ONR1;PAR1;	ligand-		steroid
GI_11863151-S	801.2	1058.5	1127.2	JARID2	NM_004973.2	JMJ	DNA	nucleus	central
GI_11863155-S	145.8	172.6	114.8	RECK	NM_021111.1	ST15;hRECK	metalloen	membran	cell growth
GI_11863157-S	2952.1	3062	3203.1	RING1	NM_002931.2	RNF1	zinc ion	nucleus	regulation
GI_11863158-S	4976.8	5662.3	3539.8	RYK	NM_002958.1	RYK1;D3S3195	transmem	integral to	signal
GI_11863160-A	490.2	931.3	602.3	TIA1	NM_022037.1		poly(A)	secretory	induction
GI_11863164-S	340.1	337.2	281	TPRT	NM_014317.2	TPT	transferas		isoprenoid
GI_11967980-S	106.1	127.8	99.9	RAB17	NM_022449.1	FLJ12538	GTP		small
GI_11967986-S	457.9	534.1	511.7	FBS1	NM_022452.1	FBS;FLJ11618			
GI_11968022-S	579.5	536	540.1	ZFP106	NM_022473.1	ZNF474			
GI_11968026-S	1077.8	947.8	692.6	FTS	NM_022476.1	FT1;FLJ13258	ubiquitin		ubiquitin
GI_11968040-S	471.4	432.8	467.2	DCLRE1C	NM_022487.1	SCIDA;SNM1C;ARTEMIS;RS-			
GI_11968044-S	6394.6	4257.7	4295.6	FLJ22056	NM_022489.1				
GI_11968046-S	2092.5	1479.2	1279.7	PAF53	NM_022490.1	FLJ13390;FLJ13970			
GI_11968048-S	769.9	814.6	846.1	FLJ12788	NM_022492.1				
GI_11968050-S	187.3	215.7	215.8	NARFL	NM_022493.1	PRN;HPRN;FLJ21988			
GI_11968052-S	1864.6	1353.5	1293.8	ZDHHC6	NM_022494.1	ZNF376;FLJ21952	zinc ion	integral to	regulation
GI_11968151-S	122.1	137	123.4	SHANK1	NM_016148.1	SSTRIP;SPANK-1;synamon	protein	nucleus	intracellula
GI_11968153-S	187	200.8	214.3	KIR2DL5	NM_020535.1	CD158F	receptor		
GI_11991659-S	110.8	113.3	106.2	SEMA6A	NM_020796.1	VIA;SEMA;HT018;SEMAQ;SEMA6A1;KIAA1			
GI_11993934-S	328.6	535.9	416.8	CHI3L2	NM_004000.1	YKL39;YKL-39	hydrolase	extracellul	metabolis
GI_11993942-S	3431.7	4733.4	5508.4	TIP-1	NM_014604.1		protein	cytoplasm	intracellula
GI_11995467-S	15807.6	19271	10971	IFITM3	NM_021034.1	1-8U		integral to	immune
GI_11995473-S	146.9	173.4	144.8	GSK3A	NM_019884.1		cAMP-		protein
GI_12007645-S	131.4	130.9	122.2	NYX	NM_022567.1	CLRP;CSNB1;CSNB4	molecular	extracellul	vision
GI_12007649-S	104.4	100	100.9	NDST4	NM_022569.1		sulfotransf		
GI_12025664-S	1482.4	1813.8	1457.9	UBE2V2	NM_003350.2	MMS2;UEV2;EDPF1;UEV-2;DDVIT1;EDAF-	ubiquitin		protein
GI_12025666-S	115	141.8	137.7	CLCA4	NM_012128.2	CaCC;CaCC2	chloride	integral to	small

GI_12025669-S	4690.3	5387.8	5017.5	ACTN1	NM_001102.2		structural	actin	
GI_12025672-A	501.4	502.9	418.7	CLCN6	NM_021737.1	CLC-6;KIAA0046	chloride	membran	small
GI_12056462-S	163	1704.6	3584.6	F8A	NM_012151.2	HAP40;DXS522E	molecular	cellular_co	biological_
GI_12056464-S	3112.8	2064.4	1821.1	FBL	NM_001436.2	FIB;FLRN;RNU3IP1	RNA	small	rRNA
GI_12056466-S	188.5	204.1	186.4	CRYBB3	NM_004076.3	CRYB3	structural		vision
GI_12056467-A	317.2	1957.4	1489.5	JUP	NM_021991.1	DP3;PDGB;PKGB;DPIII	cytoskelet	soluble	cell
GI_12056469-S	213.6	269.9	233	RAI2	NM_021785.2		molecular	cellular_co	embryonic
GI_12056470-S	610.9	2181.8	1670.3	RAI3	NM_003979.2	RAIG1;GPRC5A	G-protein	membran	signal
GI_12056472-S	1151.3	1053.2	1032.7	NANS	NM_018946.2	SAS			
GI_12056477-S	890.6	667	426.6	UCN	NM_003353.2	UI;UROC	neuropepti	extracellul	G-protein
GI_12056478-I	104.2	107.3	117.3	UTS2	NM_021995.1	UII;U-II;UCN2	G-protein	extracellul	pan-neural
GI_12056480-A	162.3	212.1	201.2	UTS2	NM_006786.2	UII;U-II;UCN2	G-protein	extracellul	pan-neural
GI_12056480-I	133	146.5	122.3	UTS2	NM_006786.2	UII;U-II;UCN2	G-protein	extracellul	pan-neural
GI_12056481-S	208.8	227.8	204.1	ZNF235	NM_004234.3	HZF6;ZFP93;ANF270;ZNF270	DNA	nucleus	regulation
GI_12056483-S	228.8	170.9	159.1	ZNF197	NM_006991.2	P18;VHLaK;ZNF20;ZNF166;D3S1363E	transcripti		
GI_12056970-S	1913.4	1459.5	1390.7	ANAPC1	NM_022662.1	APC1;MCPR;TSG24			
GI_12056972-S	136.7	136.1	125.2	EBF2	NM_022659.1	COE2;FLJ11500	DNA	nucleus	regulation
GI_12056974-S	81.8	92.7	80.7	CTAGE-1	NM_022663.1				
GI_12225239-S	101	118.1	102.2	STAB1	NM_015136.1	FEEL-1;FELE-1;STAB-1;KIAA0246	hyaluronic		electron
GI_12232372-S	1519.6	1581	1575.5	RABGAP1	NM_012197.2	GAPCENA;TBC1D11	tubulin	centrosom	cell cycle
GI_12232384-S	1112.3	1227	1338.3	COPS7B	NM_022730.1	FLJ12612			
GI_12232386-S	2985.4	3701.1	2833.9	NUCKS	NM_022731.1	JC7;FLJ21480	DNA	nucleus	regulation
GI_12232388-S	1123.4	1188.8	1050	FLJ20859	NM_022734.1				
GI_12232392-S	1740.8	2495.2	2673.7	FLJ14153	NM_022736.1				
GI_12232394-S	481.9	681.1	638.8	LPPR2	NM_022737.1	FLJ13055			
GI_12232400-S	1068.8	1159	909.6	SMYD3	NM_022743.1	ZMYND1;ZNFN3A1;FLJ21080			
GI_12232402-S	3437.3	3362.6	3102.1	FLJ13868	NM_022744.1				
GI_12232406-S	116.6	118.3	102	C14orf136	NM_022747.1	FLJ22558			
GI_12232412-S	275.6	326.6	281.4	ZC3HDC1	NM_022750.1	FLJ22693	nucleic		
GI_12232414-S	114.7	133.9	170	C18orf11	NM_022751.1	FLJ21610			
GI_12232418-S	713.7	601.9	590.6	FLJ12903	NM_022753.1				
GI_12232428-S	452.2	412.3	345	FLJ21865	NM_022759.1	DKFZp434P174			
GI_12232430-S	168.6	192.9	162.3	C11orf1	NM_022761.1	FLJ23499			
GI_12232436-S	382.2	406.2	295.8	FLJ12998	NM_022764.1	FLJ13893	nucleic		metabolis
GI_12232446-S	1291.2	907.5	805.2	TORC3	NM_022769.1	FLJ21868			
GI_12232454-S	275	359.7	287.5	FLJ12681	NM_022773.1	FLJ22302			
GI_12232456-S	230.2	294.6	250.8	FLJ21144	NM_022774.1	FLJ11445;FLJ13183			
GI_12232462-S	122	132.5	140.4	RABL5	NM_022777.1	FLJ13225;FLJ14117;DKFZp761N0823			
GI_12232472-S	137.7	316.8	154.9	DEPDC6	NM_022783.1	DEP.6;FLJ12428;FLJ13854;DKFZp564B1778	protein		intracellula
GI_12232474-S	102.2	96.1	96.2	FLJ12476	NM_022784.1	DKFZp434F2114			
GI_12232478-S	1486.7	1402.3	1399.7	ARV1	NM_022786.1				
GI_12383050-S	93.4	103.1	101.8	TMEFF2	NM_016192.2	TR;HPP1;TENB2	serine		
GI_12383052-S	742	739.4	499.8	TULP4	NM_020245.2	TUSP;KIAA1397	transcripti	cellular_co	response
GI_12383057-S	148.6	169	153.4	PLA2G2F	NM_022819.1		calcium-	cellular_co	biological_

GI_12383061-S	1640.6	1722.4	2591.1	KLC2	NM_022822.1	FLJ12387	microtubul	kinesin	microtubul
GI_12383063-S	123.7	149.2	123.7	FNDC4	NM_022823.1	FRCP1;FLJ22362			
GI_12383065-S	639.5	728.9	657.3	AXOT	NM_022826.1	AXO;DKFZP586F1122			
GI_12383073-S	2060.4	1748.5	1602.9	FLJ22347	NM_022830.1	FLJ21850;FLJ22267	nucleic		
GI_12383075-S	604.5	669.2	507.7	FLJ12806	NM_022831.1				
GI_12383083-S	93.7	110.8	103.9	FLJ22833	NM_022837.1	FLJ13624			
GI_12383091-S	182.9	192.1	161	FLJ12994	NM_022841.1	FLJ21104			
GI_12408637-A	97.8	101.7	102.1	XT3	NM_022405.1		transporte	plasma	small
GI_12408641-S	1025.7	954.1	930.8	BRD2	NM_005104.2	NAT;RNF3;FSRG1;RING3;D6S113E;KIAA90	protein	nucleus	spermatog
GI_12408642-S	485.1	594.9	638.5	BRD3	NM_007371.2	ORFX;RING3L;KIAA0043	molecular	nucleus	biological_
GI_12408643-A	265.6	447.9	360	XRCC4	NM_003401.2				double-
GI_12408644-S	171.5	149.7	159.1	XRCC3	NM_005432.2		DNA	nucleus	response
GI_12408645-S	16603.5	13853	12662	CAPN2	NM_001748.3	mCANP;CANPL2;CANPml	cysteine-	intracellula	proteolysis
GI_12408650-S	7748.5	7672.4	7408.3	XRCC5	NM_021141.2	KU80;Ku86;NFIV;KARP1;KARP-1	double-	nucleus	double-
GI_12408653-S	554	866.7	1004.6	B3GAT3	NM_012200.2	GLCATI;GlcAT-I	galactosyl	Golgi	glycosami
GI_12408655-S	3493.4	3796.1	4232.1	CAPN1	NM_005186.2	CANP;muCL;CANPL1;muCANP	calpain	intracellula	positive
GI_12408657-A	126.3	121.3	129.3	CDC25C	NM_022809.1	CDC25	prenylated	nucleus	regulation
GI_12408659-I	128.9	136.2	148.7	CDC25C	NM_001790.2	CDC25	prenylated	nucleus	regulation
GI_12408664-A	140.5	149.4	150.2	MAL	NM_022440.1		channel/p	insoluble	hemocyte
GI_12408674-S	6227.5	4699.4	4314	PFDN2	NM_012394.2	PFD2	chaperone	prefoldin	protein
GI_12408676-S	156	149.2	160.2	PFDN4	NM_002623.2	C1;C-1;PFD4	co-	cytosol	protein
GI_12545377-A	115.1	116.1	118.3	CSHL1	NM_022580.1	CSL;CS-5;CSHP1;hCS-L	hormone	extracellul	biological_
GI_12545379-S	101.4	109	95.6	SCT	NM_021920.2		hormone	extracellul	pancreatic
GI_12545383-S	93.3	105.6	91.3	HAND2	NM_021973.1	Hed;dHand;DHAND2;Thing2	transcripti	nucleus	heart
GI_12545386-S	144.5	179.9	165.6	CPNE6	NM_006032.2	N-COPINE	transporte		vesicle-
GI_12545388-S	1223.2	1126.1	1072	HS2ST1	NM_012262.2	KIAA0448	transferas		
GI_12545394-I	96.2	115.1	119.2	ICA1	NM_022307.1	ICA69;ICAp69		cytoplasm	
GI_12545396-I	267.4	277.1	237.9	ICA1	NM_022308.1	ICA69;ICAp69		cytoplasm	
GI_12545398-S	441.4	539.2	109	ICAM2	NM_000873.2	CD102	integrin	integral to	cell-cell
GI_12545399-S	325.1	322	308.9	ICAM3	NM_002162.2	CD50;CDW50;ICAM-R	integrin	proteoglyc	cell-cell
GI_12545400-A	124	137.2	123.7	ICAM4	NM_001544.2	LW	integrin	integral to	
GI_12545401-I	125.9	106.6	119.7	ICAM4	NM_022377.1	LW	integrin	integral to	
GI_12545403-S	199.3	513.9	452.6	ICAM5	NM_003259.2	TLN;TLCN	cell	integral to	cell-cell
GI_12545405-A	4380.5	2888.2	2542.2	RASA1	NM_022650.1	GAP;PKWS;RASA;CMAVM;RASGAP;p120G	Ras		cell growth
GI_12545405-I	115.5	119.8	93.7	RASA1	NM_022650.1	GAP;PKWS;RASA;CMAVM;RASGAP;p120G	Ras		cell growth
GI_12545407-S	131.6	120.1	124.5	RASA2	NM_006506.2	GAP1M	Ras		signal
GI_12548775-S	205.6	239.1	208.9	GABRB1	NM_000812.2		GABA-A	integral to	small
GI_12548784-I	154.4	160.6	142.3	GABRB2	NM_021911.1		GABA-A	integral to	gamma-
GI_12597621-S	556.4	573.7	515	CLPX	NM_006660.3		chaperoni	mitochond	protein
GI_12597624-S	1023.3	696.5	986.7	ATF5	NM_012068.2	ATFX	transcripti	nucleus	regulation
GI_12597630-S	261.4	284.8	303.9	FLJ12448	NM_022895.1				
GI_12597640-S	87.7	88.7	78.9	LRRC19	NM_022901.1	FLJ21302			
GI_12597648-S	266.6	292.4	287.1	FLJ13195	NM_022906.1		electron		electron
GI_12597650-S	101.5	101	100	FLJ23053	NM_022907.1				

GI_12597652-S	612.7	991.2	799.8	FLJ12442	NM_022908.1				
GI_12597656-S	138.4	155.4	137.6	FLJ13110	NM_022912.1				
GI_12597658-S	3390.5	2608	2620.8	24432	NM_022914.1				
GI_12621915-S	90.7	96	95.9	DEFA1	NM_004084.2	MRS;DEF1;HP-1;HNP-1	antimicrob	extracellul	chemotaxi
GI_12621916-S	121.9	121.5	121.2	DEFA3	NM_005217.2	DEF3;HNP3;HP-3;HNP-3	antimicrob	extracellul	chemotaxi
GI_12621917-S	87.4	99.1	91.9	DEFA6	NM_001926.2	DEF6;HD-6	antimicrob	extracellul	antimicrob
GI_12621918-S	127.4	407.8	131.1	TAGLN	NM_003186.2	SM22;SMCC;WS3-10	actin		muscle
GI_12669906-S	680.3	408.3	669.4	FACL2	NM_021122.2				
GI_12669908-I	107.6	109.9	112.7	ACSL4	NM_022977.1	ACS4;FACL4;LACS4;MRX63	long-chain-		learning
GI_12669910-S	184.9	212.4	228.3	E2F1	NM_005225.1	RBP3;E2F-1;RBBP3	transcripti	transcripti	G1 phase
GI_12669913-S	1384	1269.6	666.6	E2F3	NM_001949.2	E2F-3;KIAA0075	protein	transcripti	transcripti
GI_12669916-S	1190.5	590.1	480.2	E2F5	NM_001951.2	E2F-5	protein	transcripti	regulation
GI_12707557-I	107.5	112.7	103.4	GABRE	NM_021990.1		GABA-A	integral to	gamma-
GI_12707559-A	348.4	462.3	403.2	GABRE	NM_004961.2		GABA-A	integral to	gamma-
GI_12707560-A	203.9	231.8	206.2	PER2	NM_003894.3	FASPS;KIAA0347			circadian
GI_12707561-I	494.2	380.5	175.7	PER2	NM_022817.1	FASPS;KIAA0347			circadian
GI_12707563-S	116.1	102.3	117.9	DUSP2	NM_004418.2	PAC1;PAC-1	protein	nucleus	inactivatio
GI_12707564-I	234.2	307.8	258.9	ECM1	NM_004425.2			extracellul	
GI_12707565-S	5398	2426.6	1880.9	DUSP5	NM_004419.2	HVH3	protein	nucleus	heat
GI_12707569-S	7229.4	7064.3	7372.7	ECHS1	NM_004092.2	SCEH	enoyl-CoA	mitochond	fatty acid
GI_12707571-A	706.5	766.1	684.2	ECM1	NM_022664.1			extracellul	
GI_12707573-S	104.7	91.2	85.3	OCM	NM_006188.2	OM;ONCM	calcium	cellular_co	biological_
GI_12707574-S	107.4	111.6	107.8	OXT	NM_000915.2	OT;OT-NPI	hormone	extracellul	parturition
GI_12707576-A	113.2	127.6	125.5	PRRX1	NM_022716.1	PMX1;PRX1;PHOX1	transcripti	nucleus	regulation
GI_12707578-I	161.3	186.5	157.4	PRRX1	NM_006902.2	PMX1;PRX1;PHOX1	transcripti	nucleus	regulation
GI_12707579-S	97.7	121.2	123.9	PHOX2B	NM_003924.2	PMX2B;NBPHOX	transcripti	nucleus	neurogene
GI_12711659-S	142.6	153.8	163.6	PRKWNK1	NM_018979.1	KDP;WNK1;PHA2C;KIAA0344			
GI_12711661-S	187.1	204.6	194.8	DO	NM_021071.1	ART4;DOK1	NAD(P)-	membran	protein
GI_12711669-S	152.5	165.4	161.2	FLJ12517	NM_023007.1				
GI_12711681-S	258.5	265.8	290.4	FLJ21870	NM_023016.1				
GI_12718865-S	235.9	309.2	257.6	DNAI2	NM_023036.1		motor	dynein	microtubul
GI_12719454-A	142.8	153.8	137.4	FOLR1	NM_016731.2	FBP;FOLR;MOv18;FR-alpha	folic acid	peripheral	receptor
GI_12738830-S	108.8	113.2	106.4	LOC65121	NM_023013.1				
GI_12738833-S	108.9	123.3	113.8	LOC65122	NM_023014.1				
GI_12746589-I	100.3	114.9	107.9	CTBP2	NM_022802.1		tumor		viral
GI_12751474-S	521.9	880.9	710.3	SLC39A6	NM_012319.2	LIV-1	heavy	membran	heavy
GI_12751478-S	119.2	126.7	106	LOC65243	NM_023070.1		nucleic	membran	proteolysis
GI_12751480-S	409	429.4	320.8	SPATS2	NM_023071.1	SCR59;SPATA10;FLJ13117			
GI_12751490-S	510.7	419.9	456.1	FLJ12439	NM_023077.1				
GI_12751492-S	749.9	674.9	882.6	FLJ13852	NM_023078.1		pyrroline-5-		proline
GI_12751496-S	609.8	482.3	519.1	FLJ20989	NM_023080.1				
GI_12957487-S	131.9	144	150.8	13CDNA73	NM_023037.1	CG003			
GI_12963480-S	832	799.2	1028	MGC5560	NM_019054.1				
GI_12965168-S	139.2	160.1	154.7	ATP1B4	NM_012069.2		monovale	integral to	small

GI_12965169-S	299.8	371	362.5	SPEC1	NM_020239.2	SCIP1	GTPase	plasma	regulation
GI_12965171-S	128	141.5	128.6	TAS2R9	NM_023917.1	T2R9;TRB6	taste	integral to	G-protein
GI_12965173-S	106.6	105.3	107.4	TAS2R8	NM_023918.1	T2R8;TRB5	taste	integral to	G-protein
GI_12965175-S	144.7	160.6	142.6	TAS2R7	NM_023919.1	T2R7;TRB4	taste	integral to	G-protein
GI_12965177-S	93.6	81.5	86.2	TAS2R13	NM_023920.1	TRB3;T2R13	taste	integral to	biological_
GI_12965179-S	89.1	92.5	96.2	TAS2R10	NM_023921.1	TRB2;T2R10	taste	integral to	biological_
GI_12965181-S	200.3	216.4	202.5	TAS2R14	NM_023922.1	TRB1;T2R14	taste	integral to	biological_
GI_12965190-S	929	1029.2	879	BRD9	NM_023924.1	FLJ13441			
GI_12965196-S	305	201.6	186	NS3TP2	NM_023927.1	FLJ21313			
GI_13027379-S	337.4	407.1	537.8	ALS2CR3	NM_015049.1	GRIF1;OIP98;CALS-C;GRIF-1;KIAA0549	intracellula	cytoplasm	neurotran
GI_13027599-S	958.5	944.5	1049.4	MGC2494	NM_023933.1				
GI_13027601-S	342.2	347.3	225.5	C20orf116	NM_023935.1	MGC2592;dJ1187M17.3	DNA	nucleus	regulation
GI_13027603-S	1208	1299.7	1360.3	MRPS34	NM_023936.1	MGC2616;MRP-S12;MRP-S34	structural	mitochond	
GI_13027615-S	113.1	117.4	108.8	MGC3036	NM_023942.1	FLJ22216			
GI_13027629-S	201.3	235.4	236.8	DGCR14	NM_022719.1	ES2;DGSI;DGS-I;Ese2el	molecular	nucleus	neurogene
GI_13027631-S	207.4	258.4	224	SERF1B	NM_022978.1	FAM2B;H4F5C			
GI_13027633-S	187.5	252.7	176.9	MDFI	NM_005586.2	I-MF	transcripti	cytoplasm	embryoge
GI_13027635-S	609.4	396.3	228.5	EDG1	NM_001400.2	ECGF1;CHEDG1;D1S3362	G-protein	integral to	G-protein
GI_13027637-S	2643.2	2828.8	2484.5	UGP2	NM_006759.2	UDPG;UGPP2;UDPGP2;pHC379	UTP-		UDP-
GI_13027639-S	131.5	156.3	133.9	AASS	NM_005763.2	LKRSDH;LORSDH;LKR/SDH	peroxidas		electron
GI_13027654-A	1439.8	1616	1276.6	SNURF	NM_022804.1		molecular	nucleus	biological_
GI_13027789-I	106.7	91.7	94.4	MMP19	NM_022790.1	MMP18;RASI-1			
GI_13027793-A	148.8	214.2	164.9	MMP19	NM_022792.1	MMP18;RASI-1			
GI_13027795-S	169.5	201.3	214.1	MMP11	NM_005940.2	ST3;SL-3;STMY3	stromelysi	extracellul	proteolysis
GI_13027796-S	106	110.8	91.8	MMP13	NM_002427.2	CLG3	collagenas	extracellul	proteolysis
GI_13027797-S	8521	7070.6	191.1	MMP14	NM_004995.2	MMP-X1;MTMMP1;MT1-MMP	zinc ion	extracellul	proteolysis
GI_13027798-S	200.8	303.4	186.4	MMP1	NM_002421.2	CLG;CLGN	collagenas	extracellul	proteolysis
GI_13027799-A	175.4	197	180.5	MMP16	NM_022564.1	MMP-X2;MT-MMP2;MT-MMP3;MT3-MMP	enzyme	extracellul	proteolysis
GI_13027799-I	121.2	125.9	128.5	MMP16	NM_022564.1	MMP-X2;MT-MMP2;MT-MMP3;MT3-MMP	enzyme	extracellul	proteolysis
GI_13027801-I	122.6	155.6	153.4	MMP16	NM_005941.2	MMP-X2;MT-MMP2;MT-MMP3;MT3-MMP	enzyme	extracellul	proteolysis
GI_13027803-S	401.1	155.9	128.3	MMP3	NM_002422.2	SL-1;STMY;STR1;STMY1;TRANSIN	stromelysi	extracellul	proteolysis
GI_13027804-S	115.8	127.3	103.4	MMP7	NM_002423.2	MMP-7;MPSL1;PUMP-1	metalloen	extracellul	proteolysis
GI_13027806-S	170.2	174.4	191.2	MMP24	NM_006690.2	MMP25;MT5-MMP	enzyme	extracellul	proteolysis
GI_13027808-A	178.9	158.3	129	MMP25	NM_022718.1	MMP20;MT6-MMP;LEUKOLYSIN	zinc ion	membran	proteolysis
GI_13027810-S	113.1	130.4	128.7	MMP26	NM_021801.2		zinc ion	extracellul	collagen
GI_13112046-I	117.8	134.7	115.6	FGFR3	NM_000142.2	ACH;CEK2;JTK4;HSFGFR3EX	fibroblast	integral to	JAK-STAT
GI_13112047-A	145.1	216.5	170.1	FGFR3	NM_022965.1	ACH;CEK2;JTK4;HSFGFR3EX	fibroblast	integral to	JAK-STAT
GI_13112049-A	178.2	161.5	93.5	FGFR4	NM_022963.1	TKF;JTK2	fibroblast	integral to	FGF
GI_13112049-I	96.8	103.9	91.8	FGFR4	NM_022963.1	TKF;JTK2	fibroblast	integral to	FGF
GI_13112051-I	143.7	149	138.8	FGFR4	NM_002011.2	TKF;JTK2	fibroblast	integral to	FGF
GI_13112053-S	892.4	1118.4	1296.7	FGFRL1	NM_021923.2	FGFR5			
GI_13112055-S	182	208	201.9	AVPR1B	NM_000707.2	AVPR3	vasopress	endosome	cytosolic
GI_13123771-S	1717	1772.9	1658.2	CNOT10	NM_015442.1	FLJ12890;FLJ13165;DKFZP434K115			
GI_13123773-S	350.2	299.9	306.4	POT1	NM_015450.1	DKFZP586D211			

GI_13123777-S	133.2	169.3	161	BRUNOL4	NM_020180.1	CELF4;BRUNOL-4	nucleic		
GI_13124755-S	118	123.2	106.7	KIAA0582	NM_015147.1				
GI_13124760-I	88.3	90.1	84.7	HOM-TES-10	NM_015438.1	FLJ20703;DKFZP586I2223			
GI_13124762-S	96.2	88.7	87.5	DKFZP566F0	NM_015653.1				
GI_13124772-S	751.6	590.6	698.5	LOC51236	NM_016458.2				
GI_13124878-A	526.9	668.4	639.5	MYH11	NM_002474.1	SMHC;SMMHC	actin	muscle	striated
GI_13124880-A	3679.5	3265.7	4013.5	CBFB	NM_022845.1	PEBP2B	RNA		oncogene
GI_13124884-S	100.2	112.2	114.8	DEFB1	NM_005218.2	BD1;HBD1;HBD-1;DEFB-1;DEFB101	antimicrob	extracellul	chemotaxi
GI_13124885-S	96.6	105.4	98.9	DEFB4	NM_004942.2	SAP1;DEFB2;HBD-2;DEFB-2;DEFB102	antimicrob	extracellul	response
GI_13124886-S	128.5	118.9	120.7	DEFB103	NM_018661.2	HBD3;HBP3;DEFB3;HBD-3;HBP-3;DEFB-3	antimicrob	extracellul	xenobiotic
GI_13124887-S	103	96.7	98.6	EGFL6	NM_015507.2	W80;MAEG;DKFZP564P2063	integrin	extracellul	cell cycle
GI_13124889-S	3284.5	2465.9	2516.7	C12orf8	NM_006817.2	ERP28;ERP29;ERp31;PDI-DB	protein	endoplas	intracellula
GI_13124890-S	395.7	657.5	458.1	GALNT1	NM_020474.2	GALNAC-T1	polypeptid	Golgi	O-linked
GI_13124893-S	723.4	839.4	627.2	GALNT6	NM_007210.2	GalNAcT6;GALNAC-T6	polypeptid		O-linked
GI_13128859-S	3713.2	4997.2	5188.9	HDAC1	NM_004964.2	HD1;RPD3;RPD3L1	histone	nucleus	regulation
GI_13128861-S	1131.2	1137.9	1114.8	HDAC3	NM_003883.2	HD3;RPD3;RPD3-2	histone	nucleus	regulation
GI_13128863-S	178.3	213.4	234.3	HDAC6	NM_006044.2	HD6;JM21;KIAA0901	zinc ion	cytoplasm	histone
GI_13128865-S	127.3	133.6	149.3	HEXA	NM_000520.2	TSD	beta-N-	lysosome	glycosphin
GI_13128866-S	10220.4	8189.5	6226.8	HEXB	NM_000521.2		beta-N-	lysosome	glycosphin
GI_13128949-S	89.8	101.1	100.1	IFNA1	NM_024013.1	IFL;IFN;IFNA@;IFN-ALPHA			
GI_13128959-S	105.2	119.9	108.2	GJB3	NM_024009.1	CX31;DFNA2	connexon	connexon	hearing
GI_13128965-S	102.2	124.2	116.1	IFNA13	NM_006900.2		interferon-	extracellul	defense
GI_13128967-S	151	163.1	147.9	MGC1136	NM_024025.1	MGC2627	protein	nucleus	protein
GI_13128985-S	108.4	118.7	114.1	MGC3113	NM_024035.1	FLJ22850			
GI_13128989-S	232.5	217.3	241.9	MGC2603	NM_024037.1	FLJ14264			
GI_13128993-S	1075.6	1008.1	837.3	MIS12	NM_024039.1	hMis12;MGC2488			
GI_13128995-S	1856	1902.1	1626.2	CUEDC2	NM_024040.1	MGC2491;C10orf66;bA18I14.5			
GI_13128997-S	511.1	440.7	455.6	SCNM1	NM_024041.1	MGC3180			
GI_13129005-S	2956.2	2400.9	1603.9	DDX50	NM_024045.1	GU2;GUB;MGC3199;RH-II/GuB			
GI_13129013-S	109.8	150.4	137.2	MGC5566	NM_024049.1				
GI_13129023-S	554.6	589.8	670.4	C7orf25	NM_024054.1	MGC2821;FLJ21167			
GI_13129029-S	92.1	96.8	91.9	MGC5590	NM_024058.1				
GI_13129033-S	216.4	213.9	167.8	MGC5395	NM_024060.1		protein		intracellula
GI_13129039-S	589.6	546.4	531.8	SPATA5L1	NM_024063.1	MGC5347;FLJ12286	nucleotide		
GI_13129059-S	104.7	95.6	96.7	MGC3169	NM_024074.1				
GI_13129061-S	834.3	885	1033.8	LENG5	NM_024075.1				
GI_13129063-S	304.8	264.8	223.5	KCTD15	NM_024076.1	MGC2628;MGC25497	voltage-	membran	potassium
GI_13129067-S	387.6	321.9	391.1	MGC3162	NM_024078.1				
GI_13129085-S	239.1	325.6	316	KDELC1	NM_024089.1	EP58;KDEL1;MGC5302			
GI_13129087-S	519.8	757.6	531.5	ELOVL6	NM_024090.1	FAE;LCE;MGC5487;FLJ23378		integral to	
GI_13129091-S	1799.5	1880.9	2494.1	MGC5508	NM_024092.1				
GI_13129093-S	664.8	680.2	536.7	MGC5509	NM_024093.1				
GI_13129095-S	441.9	382.7	476.7	MGC5528	NM_024094.1	DCC1			
GI_13129099-S	1089.2	970.6	1023.3	XTP3TPA	NM_024096.1	CDA03;RS21C6;MGC5627			

GI_13129101-S	620.7	733.8	614.6	MGC955	NM_024097.1				
GI_13129103-S	396.7	403.3	325.8	MGC2574	NM_024098.1	FLJ22321	DNA	nucleus	regulation
GI_13129105-S	1175.3	1390.6	1239.8	MGC2477	NM_024099.1				
GI_13129115-S	256.2	282.3	250.3	ZNF426	NM_024106.1	MGC2663	nucleic	intracellula	regulation
GI_13129117-A	1923.9	2017.4	2045.7	MGC3123	NM_024107.1				
GI_13129119-S	486.2	657.4	429.6	MGC2650	NM_024108.1				
GI_13129121-S	742.3	955.3	558.4	MGC2654	NM_024109.1	FLJ12433			
GI_13129133-S	91.5	113.1	91.5	MGC4309	NM_024115.1				
GI_13129135-S	475.7	507.3	670.4	MGC5306	NM_024116.1				
GI_13129141-S	282.3	407.4	337.3	LGP2	NM_024119.1	FLJ11354	nucleic		
GI_13129143-S	291.6	367.3	314	C20orf7	NM_024120.1	FLJ22324;dJ842G6.1			
GI_13162281-S	268.2	235.2	312.1	STS	NM_000351.2	ES;ASC;ARSC;SSDD;ARSC1	steryl-	endosome	steroid
GI_13162284-S	478.7	528	592.8	MGC5242	NM_024033.1	FLJ22450			
GI_13184045-S	166.9	196.2	161.7	CYP4F12	NM_023944.1	F22329_1	monooxyg	membran	electron
GI_13184051-S	101.7	107	103.3	BTN2A3	NM_024018.1				
GI_13186246-A	121.6	163.7	120.9	FGFR1	NM_023110.1	H2;H3;H4;H5;CEK;FLG;FLT2;KAL2;BFGFR;	fibroblast	integral to	fibroblast
GI_13186246-I	161.5	186.9	163.4	FGFR1	NM_023110.1	H2;H3;H4;H5;CEK;FLG;FLT2;KAL2;BFGFR;	fibroblast	integral to	fibroblast
GI_13186256-I	111.7	97	89	FGFR2	NM_022971.1	BEK;JWS;CEK3;CFD1;ECT1;KGFR;TK14;TK			
GI_13186266-A	114.2	98.6	92.4	FGFR2	NM_022976.1	BEK;JWS;CEK3;CFD1;ECT1;KGFR;TK14;TK			
GI_13186299-S	121.6	111.3	116.6	U2AF1L1	NM_005083.2	U2AF1P;U2AFBPL;U2AF1RS1;U2AF1-RS1	RNA	nucleus	biological_
GI_13186300-A	119.8	123.9	120.2	CAPN10	NM_021251.2		calpain	cytoplasm	proteolysis
GI_13186309-I	214.4	269.4	256.6	CAPN10	NM_023087.1		calpain	cytoplasm	proteolysis
GI_13186313-I	102.6	100.8	82.6	CAPN10	NM_023089.1		calpain	cytoplasm	proteolysis
GI_13186315-S	177.4	188	162.6	CAPN6	NM_014289.2	CANPX;CAPNX;CalpM;DJ914P14.1	calpain	intracellula	proteolysis
GI_13186317-I	99.5	107.1	99.4	METTL1	NM_023032.1	C12orf1;YDL201w	methyltran	membran	transport
GI_13186319-A	965.7	862.6	1002.8	METTL1	NM_023033.1	C12orf1;YDL201w	methyltran	membran	transport
GI_13194196-S	720.5	796.5	784.1	KIF13B	NM_015254.1	GAKIN;KIAA0639	ATP	kinesin	microtubul
GI_13194198-S	106.1	116.5	94.3	TM6SF1	NM_023003.1		molecular	integral to	biological_
GI_13236491-S	150.6	180.3	176.3	LY6G6E	NM_024123.1	G6e;C6orf22			
GI_13236496-S	84.4	82.8	82.1	HTR5A	NM_024012.1		serotonin	integral to	G-protein
GI_13236498-S	83.7	89.2	82	LOC55871	NM_018491.2				
GI_13236513-S	174.2	198.8	172.9	MGC4614	NM_024294.1				
GI_13236519-S	3850.6	4116	4159.8	MGC2941	NM_024297.1	FLJ22884	DNA		regulation
GI_13236531-S	142.4	173.3	132.7	ZNF495	NM_024303.1	MGC4161	transcripti	nucleus	regulation
GI_13236539-S	175.1	153.5	140.3	MGC4171	NM_024307.1	FLJ22603	glyceroph		glycerol
GI_13236552-S	390.3	329.4	402.1	MGC3731	NM_024313.1				
GI_13236564-S	132.1	150.3	149.8	MGC11266	NM_024322.1				
GI_13236574-S	413	532.6	491.1	ZNF576	NM_024327.1	MGC2508;FLJ22700			
GI_13236578-S	316.2	250.1	172.4	SLC27A3	NM_024330.1	FATP3;MGC4365			
GI_13236584-S	875.6	875.9	859	FSD1	NM_024333.1	MIR1;MGC3213		intracellula	
GI_13236586-S	2380.6	2662	2100.8	MGC3222	NM_024334.1	DKFZp586G1919			
GI_13236592-S	154.2	168.3	154.5	ZNF557	NM_024341.1	MGC4054	nucleic	nucleus	regulation
GI_13236596-S	813.9	752.4	533.3	MGC10765	NM_024345.1	FLJ23201			
GI_13249345-S	86.8	91.9	88.3	NPPC	NM_024409.1	CNP	hormone	extracellul	regulation

GI_13259496-I	105.2	122.3	112.2	ARID4A	NM_002892.2	RBP1;RBBP1;RBP-1	protein	chromatin	transcripti
GI_13259500-A	182.3	194.4	206.9	ARID4A	NM_023001.1	RBP1;RBBP1;RBP-1	protein	chromatin	transcripti
GI_13259502-S	123	148.6	138.1	NR0B2	NM_021969.1	SHP;SHP1	transcripti	nucleus	cholestero
GI_13259504-S	1939.2	1599.8	2022.3	RBBP7	NM_002893.2	RbAp46		nucleus	developm
GI_13259505-S	225.6	137.6	357	ESM1	NM_007036.2		insulin-like	extracellul	biological_
GI_13259507-A	488.4	547.2	597.2	DCTN1	NM_023019.1	P135;DP-150;DAP-150	motor	kinesin	mitosis
GI_13259509-I	111.9	114.2	110.3	DCTN1	NM_004082.2	P135;DP-150;DAP-150	motor	kinesin	mitosis
GI_13259511-A	829.4	681.4	633.9	SMN1	NM_022874.1	SMN;SMA1;SMA2;SMA3;SMA4;SMNT;BCD5			
GI_13259517-I	103.8	104.3	94.7	ADAM12	NM_003474.2	MCMP;MLTN;MLTNA;MCMPMltna	metallope	integral to	myoblast
GI_13259519-S	608.5	593.5	554	HDAC4	NM_006037.2	HD4;HDACA;HA6116;HDAC-A;KIAA0288	transcripti	histone	neurogene
GI_13259521-I	107.6	118.5	121.8	HDAC7A	NM_015401.1	HDAC7;DKFZP586J0917			
GI_13259523-A	109.4	115.4	108.9	HDAC7A	NM_016596.2	HDAC7;DKFZP586J0917			
GI_13259530-A	126.6	121.1	110.9	SMN2	NM_022877.1	SMNC;BCD541;C-BCD541			
GI_13259532-S	133.9	147.3	130.5	AVP	NM_000490.2	VP;ADH;ARVP;AVRP;AVP-NPII	neuropepti	soluble	water
GI_13259536-S	90.3	92.7	101.4	IBSP	NM_004967.2	BSP;BNSP;SP-II;BSP-II	cell	extracellul	ossificatio
GI_13259537-S	491.9	466.7	367.3	KAI1	NM_002231.2	R2;4F9;C33;IA4;ST6;CD82;GR15;SAR2	tumor	integral to	
GI_13259538-S	582.3	392.1	370.7	MSRA	NM_012331.2		protein-		methionin
GI_13259540-S	90	100.6	90.8	UCP2	NM_003355.2	UCPH;SLC25A8	uncouplin	mitochond	proton
GI_13259542-A	1006.9	1145.3	1145.6	SLC25A14	NM_022810.1	UCP5;BMCP1	carrier	mitochond	aerobic
GI_13259544-I	97.6	99.7	99.6	UCP3	NM_003356.2	SLC25A9	uncouplin	mitochond	proton
GI_13259545-A	100.9	102.7	110.6	UCP3	NM_022803.1	SLC25A9	uncouplin	mitochond	proton
GI_13259545-I	106.1	86.7	88.9	UCP3	NM_022803.1	SLC25A9	uncouplin	mitochond	proton
GI_13259551-A	637.3	1599.5	956.5	G1P3	NM_002038.2	6-16;IFI616		integral to	immune
GI_13324673-S	102.8	116.1	84	TSPY	NM_003308.2	DYS14;pJA923			sex
GI_13324676-S	490.7	1225.7	550	ENPP1	NM_006208.1	M6S1;NPP1;NPPS;PC-1;PCA1;PDNP1	nucleotide	membran	response
GI_13324681-S	371.3	421.1	420.6	FAM3A	NM_021806.1	2-19;2.19;XAP-7;DXS560S			
GI_13324689-S	115.5	142.2	118	ILT8	NM_024318.1	LILRB6			
GI_13325053-S	199.6	297.8	300.3	CYP1A1	NM_000499.2	AHH;AHRR;CP11;CYP1;P1-450;P450-	cytochrom	membran	oncogene
GI_13325054-S	81.9	92.6	73.8	SLC27A6	NM_014031.1	FATP6;VLCS-H1	long-chain-		very-long-
GI_13325056-S	377.8	282.8	320.6	SLC27A5	NM_012254.1	FATP5;FACVL3;VLACSR;VLCSH2;VLCS-	long-chain-	endoplas	very-long-
GI_13325058-S	3535.7	3912.2	4537.6	ACTR1A	NM_005736.2	ARP1	motor	microtubul	vesicle-
GI_13325059-S	100.4	99.3	93.8	CYP1B1	NM_000104.2	CP1B;GLC3A	cytochrom	membran	eye
GI_13325060-S	835.6	984	983.8	ACTR1B	NM_005735.2	ARP1B;CTRN2	motor	microtubul	
GI_13325061-S	674.3	830.1	695	CYP1A2	NM_000761.2	CP12;P3-450;P450(PA)	cytochrom	microsom	electron
GI_13325062-S	163.1	236.7	156.6	JAK2	NM_004972.2		protein-	cytoskelet	JAK-STAT
GI_13325063-S	307.7	405.6	429.2	CELSR2	NM_001408.1	EGFL2;MEGF3;CDHF10;KIAA0279;Flamingo	G-protein	integral to	neuropepti
GI_13325065-S	1086.5	732.3	938.9	CELSR3	NM_001407.1	FMI1;EGFL1;HFMI1;MEGF2;CDHF11	G-protein	integral to	neuropepti
GI_13325067-I	88.4	96.2	87.2	MTRR	NM_024010.1	MSR	electron	mitochond	amino
GI_13325073-S	131.8	152.4	135.7	MYBPC3	NM_000256.2	FHC;CMH4;MYBP-C	structural	striated	regulation
GI_13325074-S	5529.5	6292.2	5717.6	QSCN6	NM_002826.2	Q6			negative
GI_13346499-S	259.4	224	260.4	BITE	NM_024491.1				
GI_13346505-S	90.7	106.1	97	SFTPA2	NM_006926.1	SP-A2;SPAII;COLEC5	lectin [goid	extracellul	respiratory
GI_13374556-S	137.2	132.3	136.6	ZNF117	NM_024498.1	HPF9	zinc ion	nucleus	regulation
GI_13375617-S	883	1395.6	1030.7	DHCR24	NM_014762.1	KIAA0018;SELADIN1	oxidoredu	Golgi	electron

GI_13375631-S	77.3	80.5	80.2	HOXD1	NM_024501.1	HOX4;HOX4G	transcripti	nucleus	regulation
GI_13375633-S	179.7	216.2	196.4	HIVEP3	NM_024503.1	KRC;KBP1;KIAA1555	transcripti	nucleus	regulation
GI_13375635-S	99.4	79.8	89.1	PRDM14	NM_024504.1	PFM11;MGC59730	DNA	nucleus	regulation
GI_13375643-S	88.9	99.2	79.1	ZBED2	NM_024508.1	MGC10796	transporte	membran	transport
GI_13375645-S	673.6	687.1	792.6	LRFN3	NM_024509.1	MGC2656	DNA	nucleus	regulation
GI_13375655-S	84	98.1	98.5	ULBP3	NM_024518.1	RAET1N	MHC	membran	immune
GI_13375659-S	1222.3	1191	1239.8	FLJ22555	NM_024520.1				
GI_13375663-S	131	134.9	125	FLJ12650	NM_024522.1				
GI_13375675-S	605.3	559.5	528.3	NKAP	NM_024528.1	FLJ22626	DNA	nucleus	regulation
GI_13375679-S	425.8	526.3	468.4	FLJ23306	NM_024530.1				
GI_13375689-S	382.6	452.3	397.1	FLJ22021	NM_024535.1		serine-		proteolysis
GI_13375694-S	2466.5	1685.2	2592.3	FLJ12118	NM_024537.1		ATP		cysteinyl-
GI_13375700-S	310.9	300.7	391.5	C10orf76	NM_024541.1	FLJ13114			
GI_13375704-S	389.2	485.3	430.1	FLJ12875	NM_024544.1				
GI_13375716-S	94.8	101	88.2	LASS4	NM_024552.1	Trh1;FLJ12089	transcripti	nucleus	regulation
GI_13375720-S	229.2	247.5	235.2	FLJ21103	NM_024556.1				
GI_13375724-S	132.7	147.2	155.7	C14orf138	NM_024558.1	FLJ13920			
GI_13375737-S	382.8	383.6	400.1	FLJ21616	NM_024567.1				
GI_13375741-S	633.7	629	448	FLJ11712	NM_024570.1				
GI_13375743-S	342	356	279.5	GALNT14	NM_024572.1	FLJ12691;GalNac-T10;GalNac-T14			
GI_13375745-S	322.6	371.2	322.2	C6orf211	NM_024573.1	FLJ12910			
GI_13375749-S	168	198.2	188.4	FLJ23467	NM_024575.1				
GI_13375755-S	1385	1290.1	1643.1	FLJ22709	NM_024578.1		DNA	nucleus	regulation
GI_13375757-S	299.9	537	329.7	FLJ23221	NM_024579.1				
GI_13375763-S	168.5	244.6	169.9	FLJ23056	NM_024582.1				
GI_13375778-S	229.8	243.4	248.6	FLJ22386	NM_024589.1				
GI_13375784-S	111	128.5	119.2	FLJ13352	NM_024592.1		copper,	integral to	superoxid
GI_13375790-S	391.8	439	444.8	FLJ12666	NM_024595.1				
GI_13375792-S	163.8	173.5	152.4	FLJ12847	NM_024596.1	MCPH1		intracellula	
GI_13375800-S	375.7	365.3	209	FLJ20898	NM_024600.1				
GI_13375806-S	191.9	220.1	160	FLJ11588	NM_024603.1				
GI_13375808-S	610.1	643.4	590.6	FLJ21908	NM_024604.1				
GI_13375814-S	151.9	163.4	150.5	PPP1R3B	NM_024607.1	GL;PPP1R4;FLJ14005			
GI_13375816-S	125.4	130.2	130.4	NEIL1	NM_024608.1	NEI1;hFPG1;FLJ22402			DNA
GI_13375829-S	100.7	103.2	88.2	FLJ13197	NM_024614.1				
GI_13375833-S	339.3	312.7	421.9	FLJ23186	NM_024616.1				
GI_13375845-S	459.2	425	483.1	FLJ13491	NM_024623.1		procollage	endoplas	protein
GI_13375849-S	174.4	222.3	173.8	B7-H4	NM_024626.1	B7X;B7S1;FLJ22418			
GI_13375859-S	370.9	452.3	405	FLJ23342	NM_024631.1				
GI_13375867-S	106.6	122.1	115.1	FLJ23153	NM_024636.1	TIARP			
GI_13375882-S	112.2	134.9	115.2	C14orf140	NM_024643.1	FLJ23093			
GI_13375884-S	125.5	141.9	127.5	C14orf169	NM_024644.1	FLJ21802			
GI_13375886-S	120.2	126.9	108	FLJ13842	NM_024645.1		RNA	nucleus	
GI_13375890-A	941.7	1052.1	1048.3	FLJ22222	NM_024648.1				

GI_13375900-S	567.8	637.6	490.3	PRKRIP1	NM_024653.1	C114;FLJ13902			
GI_13375912-S	176.3	166.5	319.1	FLJ22573	NM_024660.1				
GI_13375918-S	146.9	177.4	166.5	FLJ11838	NM_024664.1				
GI_13375925-S	6930.6	5807.7	6156.3	FLJ12750	NM_024667.1				
GI_13375927-S	78.4	93.1	78.5	FLJ11795	NM_024669.1				
GI_13375951-S	202.8	193.8	251.6	TBC1D17	NM_024682.1	FLJ12168			
GI_13375953-S	555	643.5	626.6	FLJ22729	NM_024683.1				
GI_13375959-S	130.6	113.8	103.4	FLJ23049	NM_024687.1				
GI_13375961-S	90.2	106.6	91.1	C10orf68	NM_024688.1	FLJ13031			
GI_13375963-S	127.8	125.6	134.1	FLJ14103	NM_024689.1				
GI_13375978-S	252.5	263.5	215.3	FLJ23058	NM_024696.1				
GI_13375980-S	189.1	205.8	206.6	FLJ22419	NM_024697.1		RNA	nucleus	
GI_13375984-S	1024.5	703.9	556.9	FLJ14007	NM_024699.1		molecular		
GI_13375990-S	120.8	113.6	108.6	FLJ13841	NM_024702.1				
GI_13375996-S	229.8	260	236.4	FLJ13639	NM_024705.1				
GI_13376000-S	190.5	226.8	214.7	GEMIN7	NM_024707.1	FLJ13956	pre-mRNA	spliceoso	nuclear
GI_13376006-S	534	530	363	FLJ23469	NM_024710.1		catalytic		metabolis
GI_13376012-S	204.3	203.9	196.6	FLJ22557	NM_024713.1				
GI_13376022-S	108.9	121.2	104.7	GRTP1	NM_024719.1	TBC1D6;FLJ22474	hormone	extracellul	
GI_13376024-S	119.8	135.8	136.9	FLJ23510	NM_024720.1				
GI_13376028-S	294.8	340.4	312.2	ACBD4	NM_024722.1	FLJ13322	acyl-CoA		
GI_13376030-A	254.6	300.9	265.9	FLJ23471	NM_024723.1				
GI_13376039-S	142.2	168.2	166.9	FLJ23259	NM_024727.1				
GI_13376041-S	1276.9	1374.5	1100.9	C7orf10	NM_024728.1	ORF19;DERP13;FLJ11808			metabolis
GI_13376049-S	150	166.7	152	FLJ14351	NM_024732.1				
GI_13376059-S	209.3	236.5	263.1	FLJ21415	NM_024738.1				
GI_13376061-S	856.5	744.3	834.9	DIBD1	NM_024740.1	FLJ21845;DKFZp586M2420			
GI_13376063-S	292.8	271.4	249	ZNF408	NM_024741.1	FLJ12827	DNA	nucleus	regulation
GI_13376075-S	180.3	190.3	177	FLJ11539	NM_024748.1				
GI_13376079-S	169.7	201.5	177.9	FLJ13273	NM_024751.1				
GI_13376087-S	791.3	674.7	516.7	FLJ13213	NM_024755.1	FLJ10005			
GI_13376090-S	397.1	548.3	436.9	MMRN2	NM_024756.1	FLJ13465;ENDOGLYX1;EndoGlyx-1		extracellul	
GI_13376096-S	133.1	148.9	147.5	FLJ13955	NM_024759.1				
GI_13376098-S	114.1	154.4	103.9	FLJ14009	NM_024760.1				
GI_13376104-S	106.5	128.5	108.7	C14orf161	NM_024764.1	FLJ14298			
GI_13376108-S	394.2	520.6	438.4	FLJ23451	NM_024766.1				
GI_13376112-S	96.3	99.7	90.4	FLJ12057	NM_024768.1				
GI_13376118-S	137.2	155.7	172	FLJ13848	NM_024771.1		N-		
GI_13376122-S	136.8	130.2	129	FLJ13798	NM_024773.1				
GI_13376139-S	92.1	96.1	83.1	FLJ23594	NM_024781.1				
GI_13376141-S	267.8	311.9	289.1	FLJ12610	NM_024782.1				
GI_13376149-S	104	99.4	102.4	ZDHHC11	NM_024786.1	ZNF399;FLJ13153			
GI_13376161-S	1764.6	1500.7	1250.6	CT120	NM_024792.1	FLJ22282	structural	ribosome	protein
GI_13376163-S	305.1	400.1	349.9	ABHD9	NM_024794.1	FLJ22408	epoxide		response

GI_13376165-S	90.3	86.3	99	FLJ22800	NM_024795.1			integral to	
GI_13376167-S	99.6	107.1	95.4	FLJ22639	NM_024796.1				
GI_13376169-S	97.9	104.6	104.3	SNX22	NM_024798.1	FLJ13952	protein		intracellula
GI_13376172-S	106.7	109.1	97.8	FLJ13224	NM_024799.1				
GI_13376180-S	93.2	114.3	106.1	FLJ21665	NM_024803.1		GTP	microtubul	microtubul
GI_13376182-S	184	295.5	231.1	FLJ12606	NM_024804.1		nucleic	intracellula	regulation
GI_13376184-S	427.5	351.4	401.4	FLJ21172	NM_024805.1				rRNA
GI_13376186-I	117.3	147.9	101.3	FLJ23554	NM_024806.1				
GI_13376188-S	114.5	129.4	108.2	C6orf76	NM_024807.1	TLT2;FLJ13693			
GI_13376194-S	380.1	476.6	417.1	FLJ23018	NM_024810.1				
GI_13376199-S	337.2	363.7	323.4	BAALC	NM_024812.1	FLJ12015			
GI_13376201-S	369.2	257.7	204.8	FLJ13150	NM_024813.1				
GI_13376203-S	381.6	447.1	374.6	CBLL1	NM_024814.1	HAKAI;FLJ23109			
GI_13376207-S	782.4	1031.7	1403.2	FRA	NM_024816.1	FLJ23282	catalytic		
GI_13376209-S	342.5	357.3	412.7	FLJ13710	NM_024817.1				
GI_13376215-S	101.8	124.3	109.3	FLJ22349	NM_024821.1				
GI_13376219-S	129	146	131.9	FLJ21596	NM_024823.1				
GI_13376225-S	97.8	98.8	101.8	FLJ21159	NM_024826.1				
GI_13376227-S	193.6	219.7	201.8	HDAC11	NM_024827.1	FLJ22237	hydrolase	nucleus	regulation
GI_13376229-S	930.5	961.2	910.9	C9orf82	NM_024828.1	FLJ13657			
GI_13376239-S	281	260.1	491.1	FLJ23506	NM_024833.1		nucleic	intracellula	regulation
GI_13376242-S	237.1	254.2	260.6	FLJ13081	NM_024834.1				
GI_13376244-S	1519.4	1462.1	1295.6	ZNF403	NM_024835.1	DIF3;LZK1;DIF-			
GI_13376246-S	286.6	361.6	353.7	FLJ22301	NM_024836.1				
GI_13376252-S	3973	3047.9	3535.3	RPP21	NM_024839.1	FLJ22638			
GI_13376260-S	225.2	271	247.7	FLJ14154	NM_024845.1		N-		
GI_13376262-S	132.4	153.3	141.3	FLJ11710	NM_024846.1				
GI_13376266-S	133.5	125.5	114.7	FLJ13941	NM_024848.1		DNA	nucleus	regulation
GI_13376268-S	177.6	215.1	207.6	FLJ14126	NM_024849.1				
GI_13376270-S	161.8	184.2	179.7	FLJ21458	NM_024850.1				
GI_13376276-S	118.8	118.6	108.5	FLJ13385	NM_024853.1				
GI_13376278-S	387.7	342.5	532.8	FLJ22028	NM_024854.1		disulfide		electron
GI_13376285-S	97.1	110.2	109.1	FLJ21687	NM_024859.1	JM10	protein	nucleus	intracellula
GI_13376287-S	426.2	427	446.4	FLJ21148	NM_024860.1				
GI_13376289-S	167.9	196.5	166.3	FLJ22671	NM_024861.1				
GI_13376291-S	185.7	196.3	178.4	FLJ13962	NM_024862.1				
GI_13376297-S	121	127.5	121	NANOG	NM_024865.1	FLJ12581;FLJ40451			
GI_13376301-S	149	163.5	152.9	FLJ14124	NM_024868.1				
GI_13376303-S	141	175.8	149.4	FLJ14050	NM_024869.1		DNA	nucleus	regulation
GI_13376305-S	223	201.5	198.3	FLJ12748	NM_024871.1				
GI_13376307-S	112.1	119	121	FLJ22570	NM_024872.1				
GI_13376313-S	90.8	91.5	71.2	SYNPO2L	NM_024875.1	FLJ12921			
GI_13376317-S	161.3	211.2	181.7	FLJ13265	NM_024877.1		cyclin-		cytokinesi
GI_13376321-S	220.7	250.4	250.5	FLJ23556	NM_024880.1				

GI_13376326-S	99.5	92.9	103.9	C6orf155	NM_024882.1	FLJ13189;dJ288M22.3	DNA	nucleus	regulation
GI_13376328-S	138.8	102.1	140.8	FLJ22202	NM_024883.1				
GI_13376330-S	263.4	280.3	294.7	C14orf160	NM_024884.1	FLJ12618			
GI_13376332-S	94	102.8	85.4	TAF7L	NM_024885.1	TAF2Q;FLJ23157;dJ738A13.1			
GI_13376334-S	86.2	75.9	81.2	FLJ14280	NM_024886.1				
GI_13376338-S	99.8	151.8	121.6	FLJ11535	NM_024888.1				
GI_13376342-S	114.8	117.1	109.2	FLJ11783	NM_024891.1				
GI_13376346-S	158.2	271.7	178.5	C20orf39	NM_024893.1	FLJ14220			
GI_13376352-S	128.3	146.7	116.7	FAM31C	NM_024898.1	FLJ22757			
GI_13376362-S	102.5	97.6	82.3	SCD4	NM_024906.1	ACOD4;FLJ21032			
GI_13376366-S	207.7	199.3	183.3	FLJ12973	NM_024908.1				
GI_13376368-S	235.9	339.6	307.8	C6orf134	NM_024909.1	FLJ13158			
GI_13376370-S	116.7	122.2	104.6	FLJ12700	NM_024910.1				
GI_13376375-S	286.1	365	330.8	FLJ14327	NM_024912.1				
GI_13376379-S	194.6	206.6	194.7	FLJ13262	NM_024914.1				
GI_13376381-S	109.3	126.2	117.3	TFCP2L3	NM_024915.1	DFNA28;FLJ13782			
GI_13376383-S	111.3	106.5	94.6	FLJ22814	NM_024916.1				
GI_13376399-S	181.5	241.5	173.7	FLJ12571	NM_024926.1				
GI_13376403-S	96.2	112	111	C6orf59	NM_024929.1	FLJ23112			
GI_13376405-S	145.3	171	164.3	FLJ22659	NM_024934.1				
GI_13376418-S	201.1	260.9	264.3	FLJ13611	NM_024941.1				
GI_13376420-S	390.1	320.3	306.7	C10orf88	NM_024942.1	FLJ13490	ATP	membran	transport
GI_13376422-S	397.1	529.4	292.8	FLJ23235	NM_024943.1				
GI_13376426-S	359.4	310.4	308.2	C9orf76	NM_024945.1	FLJ12888			
GI_13376428-S	334.7	430.3	371.2	NIP30	NM_024946.1	CDA10;CDA018;FLJ21799		nucleus	
GI_13376430-S	695.4	700.8	553.7	FLJ13397	NM_024948.1	CARP	calcium		
GI_13376434-S	294.9	331.6	296.7	FLJ12891	NM_024950.1				
GI_13376446-S	770.5	822.4	809.5	C20orf98	NM_024958.1	FLJ23329;dJ1103G7.6		integral to	
GI_13376452-S	101.5	112.2	98.7	FLJ11370	NM_024961.1				
GI_13376459-S	102.2	108.5	95.4	ZNF556	NM_024967.1	FLJ11637	nucleic	nucleus	regulation
GI_13376465-S	225.5	268.9	224.2	FLJ11722	NM_024970.1				
GI_13376473-S	115.4	126	110.3	FLJ11800	NM_024974.1				
GI_13376475-S	171.1	239.8	191.9	FLJ11996	NM_024976.1				
GI_13376477-S	183.4	206.3	186.5	FLJ12078	NM_024977.1				
GI_13376479-S	103.1	113.6	100	FLJ12121	NM_024978.1				
GI_13376487-S	96	96.9	93.3	FLJ12331	NM_024986.1		structural	ribosome	protein
GI_13376491-S	126.9	136.1	134.7	FLJ12355	NM_024988.1		DNA	nucleus	regulation
GI_13376493-S	91.1	99.2	92.4	PGAP1	NM_024989.1	FLJ12377	catalytic		lipid
GI_13376495-S	178.3	205.2	161	FLJ12547	NM_024992.1				
GI_13376499-S	321.4	414.9	348.3	FLJ12595	NM_024994.1				
GI_13376510-S	227.7	251.4	249.7	FLJ13096	NM_025000.1				
GI_13376514-S	81.7	89.9	79.2	C6orf208	NM_025002.1	FLJ13162;dJ182D15.1			
GI_13376518-S	150.2	169.7	148.2	FLJ13215	NM_025004.1				
GI_13376520-S	80.9	90.5	92.7	FLJ13315	NM_025005.1				

GI_13376526-S	125.4	121.3	107.4	FLJ13544	NM_025008.1				
GI_13376528-S	6035.5	8181.9	6357.5	FLJ13621	NM_025009.1				
GI_13376530-S	98.7	116.3	103.7	FLJ13744	NM_025011.1				
GI_13376532-S	122.3	127.8	120.9	FLJ13769	NM_025012.1				
GI_13376538-S	113.6	102.4	103.7	TUBA4	NM_025019.1	FLJ13940	GTP	microtubul	microtubul
GI_13376540-S	126.9	145.8	125.4	FLJ14069	NM_025023.1				
GI_13376542-S	112.2	142.5	111.7	FLJ14082	NM_025024.1				
GI_13376545-S	150	174.3	165.2	FLJ14100	NM_025025.1				
GI_13376547-S	252.2	277.4	258.2	FLJ14107	NM_025026.1				
GI_13376551-S	198.8	211.2	187.5	FLJ14346	NM_025029.1				
GI_13376553-S	516.6	625.4	550.3	FLJ20972	NM_025030.1				
GI_13376555-S	98.3	96.8	89.6	FLJ21075	NM_025031.1				
GI_13376557-S	174.2	172.9	154.7	FLJ21272	NM_025032.1				
GI_13376561-S	129.6	151.1	126.5	FLJ21290	NM_025034.1				
GI_13376565-S	180.6	230.5	201.7	FLJ22173	NM_025041.1				
GI_13376573-S	126.7	141.3	140.2	FLJ22595	NM_025047.1		GTP		protein
GI_13376575-S	94.4	111.7	103.4	FLJ22684	NM_025048.1				
GI_13376577-S	117.1	144.4	146.3	C15orf20	NM_025049.1	FLJ22692			
GI_13376579-S	120.6	136.9	125.2	FLJ23022	NM_025051.1				
GI_13376581-S	181.2	221.5	211.9	FLJ23074	NM_025052.1		protein-		protein
GI_13376588-S	133.1	110.2	119.2	FLJ23185	NM_025056.1				
GI_13376590-S	124.4	196.1	153.7	C14orf45	NM_025057.1	FLJ23189			
GI_13376600-S	99	118	96.5	FLJ23550	NM_025063.1				
GI_13376602-S	95.8	97.5	91	FLJ23604	NM_025064.1				
GI_13376606-S	125.1	130.9	121.7	FLJ14106	NM_025067.1				
GI_13376610-S	397.4	418.5	335.6	FLJ14299	NM_025069.1				
GI_13376614-S	90.3	92.8	90.4	FLJ12190	NM_025071.1				
GI_13376618-S	116.6	138.3	133.5	FLJ21168	NM_025073.1				
GI_13376622-S	3889.9	3930.5	3655.1	NIF3L1BP1	NM_025075.1	FLJ23445			
GI_13376631-S	289.6	332.5	284.1	FLJ23231	NM_025079.1				
GI_13376635-S	535.4	576.8	566.5	FLJ13111	NM_025082.1				
GI_13376641-S	127.4	134.4	111.5	FLJ22596	NM_025086.1				
GI_13376643-S	105.6	121.7	93.7	FLJ21511	NM_025087.1				
GI_13376645-S	137.5	156.9	157.7	FLJ13241	NM_025088.1				
GI_13376651-S	193.4	254.1	175.2	FLJ22635	NM_025092.1				
GI_13376653-S	79.4	76.2	73.2	FLJ11827	NM_025093.1				
GI_13376657-S	87.5	107.9	85.3	FLJ23558	NM_025095.1				
GI_13376659-S	3246.1	4051.7	3606.6	FLJ21106	NM_025097.1				
GI_13376664-S	639.1	517.2	382.4	FLJ22170	NM_025099.1				
GI_13376666-S	102.2	104.2	101.5	C14orf157	NM_025100.1				
GI_13376668-S	356	386.7	411.8	CCDC2	NM_025103.1	CMG1;CMG-1;FLJ22621			
GI_13376672-S	124.9	126.9	129	FLJ12409	NM_025105.1				
GI_13376676-S	218.4	257.2	207.9	MYCT1	NM_025107.1	MTLC;FLJ21269			
GI_13376678-S	659	458.3	667.4	FLJ13909	NM_025108.1				

GI_13376686-S	134	165.3	143.8	C13orf18	NM_025113.1	FLJ21562			
GI_13376688-S	84	90.8	79.4	FLJ13615	NM_025114.1				
GI_13376690-S	663.4	741.1	698.9	FLJ23263	NM_025115.1				
GI_13376694-S	101.1	161.1	280.1	FLJ11871	NM_025117.1				
GI_13376696-S	259.6	315.1	285.5	FLJ13310	NM_025118.1				
GI_13376700-S	388	441.3	424.7	FLJ21749	NM_025124.1				
GI_13376716-S	379.6	407.4	389.6	OPA3	NM_025136.1	MGA3;FLJ22187		kinesin	vision
GI_13376724-S	302.1	289	209.1	FLJ22471	NM_025140.1				
GI_13376728-S	165.4	183.6	158	C21orf96	NM_025143.1				
GI_13376734-S	712.1	753.1	613.1	MAK3P	NM_025146.1	FLJ13194	N-		
GI_13376746-S	630.2	701.6	609	C14orf127	NM_025152.1	FLJ12660	ATP		
GI_13376748-S	130.2	163.6	151.5	FLJ21477	NM_025153.1		ATP	membran	cation
GI_13376750-S	1248	1448	1134.3	FLJ11848	NM_025155.1				
GI_13376758-S	104.7	96.8	109.4	FLJ11577	NM_025159.1		oxidoredu		metabolis
GI_13376767-S	172.7	142.2	157.5	ELL3	NM_025165.1	FLJ22637			
GI_13376779-S	174.5	148.8	150.8	TRIM45	NM_025188.1	RNF99;FLJ13181	zinc ion	intracellula	
GI_13376797-S	150.7	152.4	146	FLJ21945	NM_025203.1	PP384			
GI_13376801-S	513.7	588.1	490.8	EG1	NM_025205.1	DKFZP434N185			
GI_13376811-S	96.3	115.7	101.2	I-4	NM_025210.1		protein	cellular_co	protein
GI_13376815-S	320.6	337.3	318.2	CXXC4	NM_025212.1	IDAX	zinc ion	cellular_co	negative
GI_13376817-S	260.3	325	275.8	SE57-1	NM_025214.1				
GI_13376825-S	202.6	244.7	217.4	ULBP1	NM_025218.1	RAET1I	MHC	membran	immune
GI_13376833-S	222.7	219.6	205.5	ZNF435	NM_025231.1	FLJ22191	transcripti	nucleus	regulation
GI_13376839-S	1863.8	2352.3	2410.2	REC14	NM_025234.1				
GI_13376845-S	157.3	191.1	174.1	SOST	NM_025237.1		molecular	cellular_co	negative
GI_13376847-S	1502.6	1800.4	1468.1	BTBD1	NM_025238.1	FLJ20724	protein	cellular_co	biological_
GI_13376851-S	253.3	330.3	324.7	B7H3	NM_025240.1		molecular	cellular_co	immune
GI_13376853-S	1334.8	1287.5	1284.6	UBXD1	NM_025241.1	UBXDC2			
GI_13376857-A	138.7	156.8	139.3	TSGA10	NM_025244.1		porin	mitochond	
GI_13376859-S	1096.3	1056.1	1095.4	TMEM22	NM_025246.1	MGC3295;DKFZp564K2464		membran	
GI_13376861-S	107.9	105.2	90.2	C6orf27	NM_025258.1	G7c;NG37			
GI_13376867-A	159.2	195.8	170.4	C6orf29	NM_025257.1	CTL4;NG22;FLJ14491			
GI_13376873-S	91	96	107.4	LY6G6C	NM_025261.1	G6c;NG24;C6orf24			
GI_13376875-S	220.3	302	235.3	LY6G5C	NM_025262.1	G5c;NG33;C6orf20;LY6G5CA;LY6G5CB			
GI_13376877-S	1737.1	1339	1046.3	PRR3	NM_025263.1	CAT56	nucleic	nucleus	regulation
GI_13376994-S	756	911.7	698.3	ME2	NM_002396.2		malate	mitochond	pyruvate
GI_13376995-S	231.1	326.3	288.4	WFS1	NM_006005.2	WFS;WFRS;DFNA6;DFNA14;DFNA38;DIDM		integral to	vision
GI_13376997-S	161.5	182	164.9	FES	NM_002005.2	FPS	protein-		protein
GI_13376998-S	129.5	137.9	136.6	CRYGA	NM_014617.2	CRYG1;CRYG5;CRY-g-A	structural		vision
GI_13376999-S	111.1	109.9	108	CRYGB	NM_005210.2	CRYG2	structural	cellular_co	biological_
GI_13377000-S	119.6	136	131.4	CRYGC	NM_020989.2	CCL;CRYG3	structural	cellular_co	biological_
GI_13377001-S	93.1	94.7	99.4	CRYGD	NM_006891.2	CACA;CRYG4;cry-g-D	structural		vision
GI_13377003-S	114.5	124.3	110.8	CRYGS	NM_017541.2	CRYG8	structural		cell shape
GI_13378148-A	115.6	115.4	112.7	LRRC1	NM_025168.1	LANO;FLJ10775;FLJ11834;dJ523E19.1			

GI_13378148-I	110.5	112.6	106.7	LRRC1	NM_025168.1	LANO;FLJ10775;FLJ11834;dJ523E19.1			
GI_13384595-S	1408.5	1041.8	727.6	ZNF330	NM_014487.2	NOA36;HSA6591	electron	centromer	mitosis
GI_13384599-S	700.8	641.9	491	SPATA7	NM_018418.1	HSD3;HSD-3.1			
GI_13384601-S	102.8	193.3	112	FLJ23403	NM_022068.1	FLJ23144			
GI_13385593-S	2874.2	3030.1	3027.8	CYB5-M	NM_030579.1			mitochond	electron
GI_13386461-A	391.9	431.1	460.1	MASK	NM_024668.1	FLJ10042;FLJ11979;FLJ14127;FLJ20288;KI			
GI_13386461-I	534.2	435.1	547	MASK	NM_024668.1	FLJ10042;FLJ11979;FLJ14127;FLJ20288;KI			
GI_13386481-S	107.2	109.2	94.7	MGC10946	NM_030572.1				
GI_13386483-S	386.4	421.9	385.8	THAP7	NM_030573.1	MGC10963	DNA		
GI_13386487-S	3611.2	2432.7	2469.9	MGC10334	NM_030575.1		DNA	nucleus	regulation
GI_13386491-S	291.1	263.5	241.4	MGC10993	NM_030577.1				
GI_13386499-A	96	92.9	80.6	CACNA1A	NM_000068.2	EA2;FHM;MHP;APCA;HPCA;MHP1;SCA6;C	voltage-	voltage-	small
GI_13386501-S	133.6	138.2	127.8	BARX1	NM_021570.2		transcripti	nuclear	transcripti
GI_13386504-S	92.2	101.1	95.5	CYP3A7	NM_000765.2	CP37;P450-HFLA	cytochrom	membran	electron
GI_13386511-A	208.6	244.1	206.8	WT1	NM_000378.2	GUD;WAGR;WT33;WIT-2	transcripti	nucleus	regulation
GI_13399295-S	120.4	147.6	132.8	MAZ	NM_002383.1	PUR1;ZF87;SAF-1;SAF-2	RNA		transcripti
GI_13399303-S	184.8	401.1	321	APOBEC3G	NM_021822.1	ARP9;CEM15;MDS019;FLJ12740;bK150C2.7	zinc ion		
GI_13399321-S	1918.8	1859.7	1426.6	FLJ10774	NM_024662.1	ALP;FLJ12179;KIAA1709;DKFZp434C116	N-	nucleus	biological_
GI_13430847-S	261.7	325.8	307.3	NR1D1	NM_021724.1	EAR1;hRev;THRA1;THRAL;ear-1	transcripti	nucleus	regulation
GI_13430851-S	153.9	197.9	172.9	DKFZp434L0	NM_017558.1	FLJ12871			
GI_13430853-A	173.3	96.7	75.7	NXF2	NM_022053.1	TAPL-2;FLJ20416	protein	nucleus	protein-
GI_13430853-I	136.1	142.7	125.2	NXF2	NM_022053.1	TAPL-2;FLJ20416	protein	nucleus	protein-
GI_13430855-S	543	459.1	625.8	C6orf79	NM_022102.1	FLJ20958			
GI_13430859-S	313.9	394.2	355.9	HIPK2	NM_022740.1	PRO0593	transcripti	nucleus	
GI_13430863-A	185.9	461.9	213	NDRG4	NM_022910.1	SMAP-8;KIAA1180;MGC19632		cytoplasm	response
GI_13430867-S	170.4	187	156.9	MGC2615	NM_024103.1				
GI_13430871-S	97.2	107	109.7	FLJ14075	NM_024894.1	FLJ13938			
GI_13430873-S	112.9	114.4	116.2	FLJ12985	NM_024924.1				
GI_13430877-S	127.8	152	141	KIAA0795	NM_025010.1	FLJ13703	protein		
GI_13430881-A	287.5	292.2	291.7	MECT1	NM_025021.1	TORC1;WAMTP1;FLJ14027;KIAA0616			
GI_13435126-S	113.1	140.4	103.7	T3JAM	NM_025228.1	DJ434O14.3			
GI_13435128-S	327	518.7	341.8	HSA9947	NM_022089.1		ATP	integral to	cation
GI_13435134-S	85	103.4	85.2	TSPYQ1	NM_022573.1		DNA	nucleus	nucleoso
GI_13435144-S	248	264.4	230.1	KIAA0643	NM_024793.1	FLJ13297			
GI_13435146-S	155	159.6	165.5	FLJ14297	NM_024903.1				
GI_13435148-S	131.9	135.9	132.1	FLJ21918	NM_024939.1	FLJ22248	nucleic		
GI_13435160-A	153	156.2	145.8	SPTBN4	NM_025213.1	QV;SPTBN3;KIAA1642			
GI_13435349-A	2259.4	2621.4	2197	FDXR	NM_024417.1	ADXR	ferredoxin-	mitochond	electron
GI_13435352-A	140.7	200	159.8	L1CAM	NM_024003.1	S10;HSAS;MASA;MIC5;SPG1;CAML1;CD17	cell	integral to	cell
GI_13435355-S	4371.1	3933.9	3526.9	HAX1	NM_006118.2		DNA	nuclear	regulation
GI_13435358-S	1434.9	2010	1751.8	DDB1	NM_001923.2	DDBA;XAP1;XPCE;XPE-BF;UV-DDB1	damaged	nucleus	pyrimidine-
GI_13435360-A	212.6	247	228.3	DSC1	NM_024421.1	CDHF1;DG2/DG3	cell	gap	cell shape
GI_13435367-A	156.5	184	155.6	DSC3	NM_001941.2	DSC;DSC1;DSC2;DSC4;CDHF3;HT-CP	cell	cytoskelet	cell
GI_13435374-A	154.4	170.7	184.3	GMEB1	NM_024482.1	PIF96;P96PIF	transcripti	kinesin	

GI_13435378-S	713.6	670.3	857.7	GMEB2	NM_012384.2	PIF79;P79PIF;KIAA1269	RNA	kinesin	invasive
GI_13435379-S	167.2	172.5	154.4	RETN	NM_020415.2	ADSF;RSTN;FIZZ3;RETN1	hormone	extracellul	biological_
GI_13435380-S	5204.3	5536.4	4669.4	GPS1	NM_004127.3	COPS1	GTPase		JNK
GI_13435382-S	252.8	229.9	226.3	FLJ20628	NM_017910.2	DKFZp564I2178	S-		
GI_13435384-S	634.2	829.2	754.4	GTF2B	NM_001514.2	TF2B;TFIIB	general	transcripti	transcripti
GI_13435387-S	501.5	583.9	586.1	CYP4A11	NM_000778.2	CP4Y;CYP4A2;CYP4AII	fatty acid	microsom	fatty acid
GI_13435388-S	104.5	93.3	91.7	CYP4B1	NM_000779.2	P-450HP	cytochrom	membran	electron
GI_13435389-S	119.4	130.8	120.4	CYP4F8	NM_007253.2	CPF8;CYPIVF8	fatty acid	membran	prostaglan
GI_13435390-S	109.4	119	91.8	CYP4F2	NM_001082.3	CPF2	monooxyg	membran	leukotrien
GI_13435392-A	891.7	878.6	758.3	TIAL1	NM_003252.2	TCBP;TIAR	antimicrob	lysosome	induction
GI_13435392-I	188.2	207	185.2	TIAL1	NM_003252.2	TCBP;TIAR	antimicrob	lysosome	induction
GI_13435393-I	119	136.2	107	TIAL1	NM_022333.1	TCBP;TIAR	antimicrob	lysosome	induction
GI_13435396-I	181.6	168.2	186.4	PHF1	NM_024165.1	PHF2	transcripti	nucleus	regulation
GI_13435400-S	416	656.8	487.9	ME1	NM_002395.2	MES;HUMNDME	malate	cytosol	tricarboxyli
GI_13435401-S	250.9	314	277.6	CCL7	NM_006273.2	FIC;MARC;MCP3;NC28;MCP-3;SCYA7	chemokin	extracellul	chemotaxi
GI_13435403-S	341.1	370.3	242.2	HRH1	NM_000861.2	H1-R;hisH1	histamine	integral to	G-protein
GI_13435404-S	118.5	116.8	101	HRH2	NM_022304.1	H2R	histamine	integral to	G-protein
GI_13442997-S	136.2	155.6	129.4	DPF3	NM_012074.1	CERD4;cer-d4;FLJ14079	zinc ion	nucleus	regulation
GI_13443001-S	418.6	350.2	275.9	FLJ22795	NM_025084.1				
GI_13443013-S	385.9	378.1	253.7	ASB9	NM_024087.1	MGC4954;FLJ20636;DKFZP564L0862			intracellula
GI_13443017-S	638.1	711.9	957.4	C16orf33	NM_024571.1	FLJ22940			
GI_13443019-S	120.6	135.4	140.8	ZNF552	NM_024762.1	FLJ21603			
GI_13443025-S	262.1	311.6	223.7	FLJ10178	NM_018015.2	FLJ14191			
GI_13443032-A	1256.8	1285.7	1553.4	FLJ20297	NM_017951.1	FLJ20756			
GI_13443032-I	230.9	293.2	238.2	FLJ20297	NM_017951.1	FLJ20756			
GI_13446228-S	331.3	401.1	374.9	MESDC1	NM_022566.1				
GI_13449264-S	901.2	1024.5	888.1	KIAA1608	NM_024820.1	FAM31A;FLJ21129			
GI_13449266-S	121.1	134.4	116.8	FLJ21628	NM_030613.1			nucleus	
GI_13449278-S	109.6	116.7	116.4	SLC25A21	NM_030631.1	ODC;ODC1	binding	mitochond	transport
GI_13449286-S	106.8	116	102	EGFL8	NM_030652.1	NG3;C6orf8	calcium		
GI_13470085-S	4521.9	4107.4	3897.7	RAI14	NM_015577.1	RAI13;NORPEG;KIAA1334;DKFZp564G013			
GI_13470087-S	139	146.2	179.5	GPR107	NM_020960.1	LUSTR1;FLJ20998;FLJ22591;KIAA1624;MG			
GI_13470091-S	1019.4	864.8	499.2	FYCO1	NM_024513.1	RUFY3;ZFYVE7;FLJ13335	zinc ion		
GI_13470093-S	272.4	338.2	294.5	APOL5	NM_030642.1	APOL-V	high-	cellular_co	lipid
GI_13487903-S	103.4	123.2	121.2	DKFZp434M	NM_017600.1				
GI_13489072-S	196.1	232.8	163.6	EGLN1	NM_022051.1	PHD2;SM-20;HIFPH2;ZMYND6;C1orf12	oxidoredu	cytosol	protein
GI_13489082-S	935.4	926.2	854.6	C11orf23	NM_018312.2	SAPL;SAPLa;FLJ11058			
GI_13489098-S	119.9	144.1	133.1	FLJ12242	NM_024681.1		voltage-	membran	potassium
GI_13489104-S	384.4	460.7	419.3	DEPDC2	NM_025170.2	DEP.2;FLJ12987;FLJ14017	protein		intracellula
GI_13491165-S	1638.7	1911.8	1617.7	PUM1	NM_014676.1	PUMH;PUMH1;PUML1;KIAA0099	RNA		
GI_13491167-S	1210.6	1101.7	990.9	PUM2	NM_015317.1	PUMH2;PUML2;KIAA0235			
GI_13491171-I	162.6	164.3	167.4	PRX	NM_020956.1	CMT4F;KIAA1620	molecular	membran	nerve
GI_13514808-S	87.9	94	95.8	DDX3Y	NM_004660.2	DBY	ATP		
GI_13514812-I	1598.6	1844	1265.2	DDX3X	NM_001356.2	DBX;DDX3;HLP2;DDX14	ATP		

GI_13514816-A	204.4	272.4	251.9	DDX3X	NM_024005.1	DBX;DDX3;HLP2;DDX14	ATP		
GI_13514816-I	114.3	146.7	151	DDX3X	NM_024005.1	DBX;DDX3;HLP2;DDX14	ATP		
GI_13514819-I	123.9	126.4	125.7	DHX9	NM_001357.2	LKP;RHA;DDX9;NDHII;NDH II	ATP	cytoplasm	
GI_13514821-A	657.9	802.9	765.4	DHX9	NM_030588.1	LKP;RHA;DDX9;NDHII;NDH II	ATP	cytoplasm	
GI_13514826-S	3991.3	4877	4553.9	DDX5	NM_004396.2	P68;HLR1;G17P1;HUMP68	ATP	nucleus	cell growth
GI_13514830-S	1050.5	982.5	904.3	DDX10	NM_004398.2	HRH-J8	RNA		
GI_13518012-A	260.4	326.3	171.1	MJD	NM_030660.1	ATX3;MJD1;SCA3		nucleoplas	nucleotide-
GI_13518014-I	84.7	82.8	78.5	DDX4	NM_024415.1	VASA	nucleic		developm
GI_13518016-I	93.9	88.6	88.4	WNT2B	NM_004185.2	WNT13;XWNT2	signal	extracellul	embryoge
GI_13518018-I	98.4	100.2	85.3	MJD	NM_004993.2	ATX3;MJD1;SCA3		nucleoplas	nucleotide-
GI_13518020-A	108.5	121.6	106.3	WNT2B	NM_024494.1	WNT13;XWNT2	signal	extracellul	embryoge
GI_13518020-I	163.8	213.5	186.2	WNT2B	NM_024494.1	WNT13;XWNT2	signal	extracellul	embryoge
GI_13518022-S	92.2	96.2	87.3	OPCML	NM_002545.2	OPCM;OBCAM	opioid	integral to	neuronal
GI_13518024-S	150.6	172.8	149.8	HRG	NM_000412.2	HPRG;HRGP	plasma	extracellul	
GI_13518025-S	617.2	762.3	570.1	LIMS1	NM_004987.2	PINCH;PINCH1			cell aging
GI_13518027-S	235.3	205.9	138.4	BFSP1	NM_001195.2	CP94;CP115;LIFL-H;FILENSIN	structural	intermedia	RNA
GI_13518031-S	723.1	742.9	615.4	GLI3	NM_000168.2	PHS;GCPS;PAPA;PAPB;PAP-	transcripti	cytoplasm	protein-
GI_13518035-S	83.2	98.2	97.2	MATN1	NM_002379.2	CMP;CRTM	extracellul	extracellul	cartilage
GI_13518036-I	95.4	124.7	90.4	MATN2	NM_002380.2				
GI_13518038-A	246.9	588.9	258.7	MATN2	NM_030583.1				
GI_13518040-S	153.1	188.2	171.8	MATN3	NM_002381.2	HOA;EDM5	extracellul	extracellul	skeletal
GI_13518226-A	137.2	169.2	132.7	GLI2	NM_005270.2	THP2	transcripti	nucleus	histogene
GI_13518227-S	811.1	866.1	843.9	MCCC1	NM_020166.2	MCCA;MCC-B	biotin	mitochond	biotin
GI_13540470-S	184.3	189.4	162.5	TCF7L2	NM_030756.1	TCF4;TCF-4	RNA	nucleus	oncogene
GI_13540472-S	3101	3834.1	3197.4	TCP1	NM_030752.1	CCT1;Ccta;D6S230E	chaperone	cytosol	protein
GI_13540481-S	98.6	116.1	112.9	C14orf102	NM_017970.1	FLJ10008;FLJ14051			
GI_13540489-S	122.4	133.7	133.1	BACH2	NM_021813.1		protein	nucleus	regulation
GI_13540500-S	110.8	105.7	111.2	ZNF442	NM_030824.1	FLJ14356	nucleic	intracellula	regulation
GI_13540508-S	117.2	139.5	120.6	MKRN4	NM_030757.1	RNF64;ZNF-Xp;ZNF127L1	nucleic		
GI_13540512-S	153.4	165.7	123.3	OSBP2	NM_030758.1	ORP4;ORP-4;OSBPL1;KIAA1664		membran	lipid
GI_13540514-S	984.6	925.2	875.5	NRBF2	NM_030759.1	COPR1;COPR2;NRBF-2;FLJ30395			
GI_13540520-S	144.3	174.4	227.7	BHLHB3	NM_030762.1	DEC2;SHARP1;SHARP-1	transcripti	nucleus	regulation
GI_13540522-S	187.5	223.2	186.8	NSBP1	NM_030763.1		chromatin	chromatin	regulation
GI_13540528-I	128.1	139.8	121.7	BCL2L14	NM_030766.1	BCLG			
GI_13540532-S	131.6	155.4	128.8	NPL	NM_030769.1	NPL1;c112;C1orf13			
GI_13540534-S	162.2	204.6	181.1	TMPRSS5	NM_030770.1	SPINESIN	trypsin	integral to	proteolysis
GI_13540544-S	157.1	163.2	143	ZBP1	NM_030776.1	DLM1;DLM-1;C20ORF183;dJ718J7.3	DNA	cellular_co	biological_
GI_13540554-S	698.6	548.2	596.9	PTDSS2	NM_030783.1	PSS2			phosphati
GI_13540556-S	164.1	146.4	129.9	GPR63	NM_030784.1	PSP24B;PSP24(beta)	molecular	integral to	G-protein
GI_13540558-S	176.6	215.7	201.3	RSHL1	NM_030785.1	RSP4;RSP6	ferric iron	extracellul	iron ion
GI_13540560-S	170.5	419.5	445.6	SYNCOILIN	NM_030786.1	SYNC			
GI_13540562-S	89.2	92.7	84.4	FHR5	NM_030787.1	FHR-5	compleme	extracellul	compleme
GI_13540575-S	487.7	392.8	399.5	TDRD3	NM_030794.1	FLJ21007	nucleic	nucleus	regulation
GI_13540579-S	305.8	443	417.3	DKFZP566A1	NM_030797.1	FLJ11080			

GI_13540585-S	586.4	577	526.2	DKFZP564O1	NM_030800.1				
GI_13540593-S	470.5	526.2	446.4	LMAN2L	NM_030805.1	VIPL;MGC11139;DKFZp564L2423	sugar	endoplas	protein
GI_13540601-S	302.9	309.1	265.1	C12orf22	NM_030809.1	C12ORF2;TAIP-12			
GI_13540609-S	216.2	263.5	285.4	DKFZP566D1	NM_030816.1	dJ677H15.3			
GI_13540611-S	114.4	206.4	107.1	DKFZP434F0	NM_030817.1				
GI_13562087-S	106.9	113.7	109.5	LRRC3	NM_030891.1	C21orf102			
GI_13562103-S	106.2	109	99.8	OR3A3	NM_012373.1	OR3A6;OR3A7;OR17-16;OR17-137;OR17-	receptor	integral to	signal
GI_13569839-S	273	216.7	153.2	LRP16	NM_014067.2				
GI_13569844-S	1070.2	860.8	840.4	MYNN	NM_018657.2	SBBIZ1	zinc ion		transcripti
GI_13569847-I	164.4	184.7	160.5	TBRG4	NM_030900.1	CPR2;KIAA0948			cell cycle
GI_13569857-S	863.8	656.7	600.1	FLJ14129	NM_030895.1		DNA	nucleus	regulation
GI_13569859-S	168.5	187.6	173.1	CD1E	NM_030893.1	HSCDIEL	defense/i	integral to	immune
GI_13569863-S	101.8	88.4	87	CDADC1	NM_030911.1	NYD-SP15			
GI_13569865-S	3045.8	2244.1	1946.8	TRIM8	NM_030912.1	GERP;RNF27	zinc ion	kinesin	biological_
GI_13569869-S	1936.7	1837	2183.3	C9orf74	NM_030914.1	MGC2668			
GI_13569871-S	239	667.9	502.2	LBH	NM_030915.1	DKFZP566J091			
GI_13569886-S	104.5	117.4	95.4	FLJ12577	NM_030925.1				
GI_13569888-S	372.6	502	527.9	DC-TM4F2	NM_030927.1	MGC11352			
GI_13569896-S	135.7	156.2	136.7	C1orf14	NM_030933.1	GE36			
GI_13569912-S	197.4	211.2	227.1	LOC81691	NM_030941.1	DKFZp434J0315			
GI_13569914-S	117.9	111.3	110.1	AMN	NM_030943.1			integral to	developm
GI_13569916-S	85.8	82.3	79.3	C15orf5	NM_030944.1				
GI_13569918-A	93.3	102.3	99.7	C1QTNF3	NM_030945.1	CTRP3;CORS26;FLJ37576		microfibril	
GI_13569918-I	198.2	232.8	217.7	C1QTNF3	NM_030945.1	CTRP3;CORS26;FLJ37576		microfibril	
GI_13569921-S	141.8	131.7	108.5	SNARK	NM_030952.1	DKFZP434J037	protein-		protein
GI_13569927-S	108.8	123.5	105.3	ADAMTS12	NM_030955.1		zinc ion	extracellul	proteolysis
GI_13569929-S	93.6	100.6	98.2	TLR10	NM_030956.1		interleukin-	integral to	immune
GI_13569931-S	124.1	142.1	116.2	SLCO5A1	NM_030958.1	OATP-J;OATP5A1;OATPRP4;SLC21A15	transporte	integral to	transport
GI_13569937-S	81.1	89.9	95.7	SIAT7E	NM_030965.1	MGC3184;ST6GalNAcV	sialyltransf	Golgi	protein
GI_13569939-S	113.7	112.8	95.6	KRTAP1-3	NM_030966.1	KAP1.2;KAP1.3;KAP1.9;KAP1.8A;KAP1.8B;K			
GI_13569947-S	984.7	1050.4	1288.7	TCBAP0758	NM_030973.1	P78;DKFZp434K0512			
GI_13569955-S	2599.1	2427.9	2074.1	ARPC5L	NM_030978.1	ARC16-2;MGC3038			
GI_13569959-S	334.7	350.7	376.7	FLJ12671	NM_030980.1		exonuclea	intracellula	
GI_13569961-S	274.2	328.8	339.6	RAB1B	NM_030981.1				
GI_13591857-S	826.7	900.6	722.4	PADI1	NM_013358.1	PDI;PDI1;HPAD10	protein-		protein
GI_13624324-S	135.9	152.5	134.1	OR7C2	NM_012377.1	OR7C3;OR19-18;CIT-HSP-87M17	olfactory	integral to	chemosen
GI_13624328-S	101.4	128.5	110.8	OR2W1	NM_030903.1	hs6M1-15	olfactory	integral to	olfaction
GI_13624330-S	97.8	121.2	103.6	OR2J2	NM_030905.1	OR6-8;hs6M1-6;dJ80I19.4	olfactory	integral to	olfaction
GI_13654234-A	378.9	545	700.5	RGS20	NM_003702.2	RGSZ1;ZGAP1	protein	peripheral	regulation
GI_13654273-S	866.7	819.2	1027.2	DKFZP566J2	NM_031208.1				
GI_13654275-S	342.3	288.5	302.2	QTRT1	NM_031209.1	TGT	queuine	ribosome	tRNA
GI_13654285-S	164.1	190.9	178.9	AF311304	NM_031214.1				
GI_13654291-S	102	112.4	99.8	ZNF505	NM_031218.1	FLJ12488	metallope	nucleus	proteolysis
GI_13654295-S	115.5	115.3	115.7	PITPNM3	NM_031220.1	NIR1;RDGBA3	phosphati	integral to	transmem

GI_13676856-S	123.4	161.2	132.9	HSPA2	NM_021979.2		chaperone		male
GI_13677215-A	139	143.5	141.6	PTPRO	NM_030668.1	PTPU2;GLEPP1;PTP-U2	transmem	integral to	protein
GI_13699810-I	102.9	115.3	99.4	WHSC1L1	NM_023034.1	NSD3;FLJ20353			
GI_13699812-A	112.5	100.9	107.4	WHSC1L1	NM_017778.2	NSD3;FLJ20353			
GI_13699812-I	782.4	847.6	637.1	WHSC1L1	NM_017778.2	NSD3;FLJ20353			
GI_13699815-S	118.9	128.6	119.9	CYP2C18	NM_000772.1	CPCI;CYP2C;CYP2C17;P450IIC17;P450-	monooxyg	membran	electron
GI_13699817-S	242.1	280	238.2	CYP2C9	NM_000771.2	CPC9;CYP2C10;P450IIC9;P450 MP-4;P450			
GI_13699820-S	3826.2	4902.5	4157.7	NDUFA1	NM_004541.2	MWFE;CI-MWFE	NADH	NADH	energy
GI_13699821-S	118.8	157.1	146	NDUFA5	NM_005000.2	B13;NUFM;UQOR13;FLJ12147;CI-13KD-B	NADH	NADH	
GI_13699823-S	279.5	297.3	360.6	KIF11	NM_004523.2	EG5;HKSP;KNSL1;TRIP5	microtubul	kinesin	mitotic
GI_13699825-I	115.8	130.4	110	KIF25	NM_030615.1	KNSL3	microtubul	kinesin	organelle
GI_13699827-A	78.8	86.1	92	KIF25	NM_005355.2	KNSL3	microtubul	kinesin	organelle
GI_13699829-I	87.8	76.4	98	MATN4	NM_003833.2	HE6WCR54		extracellul	
GI_13699832-S	1345	892.5	1066.9	KIF2C	NM_006845.2	MCAK;KNSL6	microtubul	kinesin	centromer
GI_13699835-A	173.7	159.9	107.2	MATN4	NM_030592.1	HE6WCR54		extracellul	
GI_13699837-S	184.8	222.8	176.4	CYP2E1	NM_000773.2	CPE1;CYP2E;P450-J;P450C2E	monooxyg	membran	electron
GI_13699838-I	101.3	91.2	90.8	TBXAS1	NM_001061.2	TS;TXS;CYP5;THAS;TXAS;CYP5A1			blood
GI_13699839-A	91.5	95.9	99.2	TBXAS1	NM_030984.1	TS;TXS;CYP5;THAS;TXAS;CYP5A1			blood
GI_13699841-S	110.1	105.8	111.4	TPS1	NM_003293.2	TPS2;alpha II	serine-		defense
GI_13699860-S	194.2	216.2	187.1	SLC22A14	NM_004803.2	OCTL2;OCTL4;ORCTL4	organic	membran	small
GI_13699861-S	262.5	382.7	370.8	HYOU1	NM_006389.2	ORP150	ATP	endoplas	response
GI_13699866-S	2677.3	1975.2	1990.6	MAP1LC3B	NM_022818.2	MAP1A/1BLC3			microtubul
GI_13699867-S	447.1	461.9	440.9	MTHFD1	NM_005956.2	MTHFC;MTHFD	methylene	mitochond	amino
GI_13699869-S	4119.2	2487.9	1164.1	MTHFD2	NM_006636.2	NMDMC	methylene	mitochond	one-
GI_13702710-S	96.3	98.3	101.8	PSG2	NM_031246.1	PSBG2;PSGGB	molecular	cellular_co	pregnancy
GI_13775161-S	131.6	133	132.7	OR7A17	NM_030901.1	HTPCRX19	olfactory	integral to	olfaction
GI_13775163-S	186.6	218.4	213.8	MGC3771	NM_030970.1	MGC1912			
GI_13775165-S	117.7	153.4	175	MGC5384	NM_030972.1				
GI_13775177-S	102.2	107	119.4	TEX13B	NM_031273.1				
GI_13775183-S	107.1	102	94.5	TEX11	NM_031276.1				
GI_13775185-I	97.5	100.4	113.2	RNF17	NM_031277.1	Mmip-2			
GI_13775195-S	5556.3	6148	3690.7	PP1057	NM_031285.1				
GI_13775201-S	348.9	382	336	HMGA1L4	NM_031288.1	PAPA-1;HMGIYL4			
GI_13775203-A	101.5	109.8	98.3	GSG1	NM_031289.1	MGC3146			
GI_13775203-I	147	179.5	164.1	GSG1	NM_031289.1	MGC3146			
GI_13775205-S	95	101	99.5	DKFZP434K1	NM_031290.1				
GI_13775207-S	138.7	159.7	146.6	DKFZP434N1	NM_031291.1		binding	integral to	transport
GI_13775209-S	168.9	152.7	131	DKFZP434G1	NM_031292.1		molecular		
GI_13775211-S	99.6	94.2	88.4	PMFBP1	NM_031293.1	DKFZP434G131			
GI_13775219-S	718.6	638.9	803.4	MGC2963	NM_031298.1				
GI_13775223-S	394	647	535	PSFL	NM_031301.1	APH1B;APH-1B;DKFZp564D0372		integral to	
GI_13775229-S	116.5	124.3	105.7	DKFZP564B1	NM_031305.1				
GI_13775231-S	88.2	98.1	84	DKFZP564B1	NM_031306.1		nucleic		
GI_13775237-S	236	282.3	235.8	PLVAP	NM_031310.1	PV1;FELS;PV-1;gp68			

GI_13775594-S	137.5	124.9	130.5	TPSB1	NM_003294.2	TPS1;TPS2;beta I;tryptase-II	serine-		proteolysis
GI_13775596-S	458.7	552.6	493.3	TPSB2	NM_024164.2	beta II			
GI_13775598-S	395.5	390.1	402.6	SIRT1	NM_012238.3	SIR2L1	NAD ADP-	chromatin	chromatin
GI_13775601-A	201.4	216.5	203.4	SIRT2	NM_030593.1	SIR2L;SIR2L2	NAD ADP-	cytoplasm	protein
GI_13775603-S	454.3	489.6	477.2	SIRT3	NM_012239.3	SIR2L3	NAD ADP-	chromatin	protein
GI_13786122-S	272.4	209.6	176.9	TCF7L1	NM_031283.1	TCF3;TCF-3	transcripti	nucleus	establish
GI_13786128-S	109	122.7	107.6	RAB33B	NM_031296.1	DKFZP434G099	GTP	Golgi	small
GI_13787185-S	81.1	83.3	88.3	CYP7A1	NM_000780.2	CP7A;CYP7	monooxyg	microsom	bile acid
GI_13787188-A	211.1	267.3	229.5	CYP2C8	NM_000770.2	CPC8;P450 MP-12/MP-20	monooxyg	membran	electron
GI_13787190-S	79.1	92.4	87	CYP7B1	NM_004820.2	CP7B	oxysterol	microsom	bile acid
GI_13787191-S	510.9	616.5	566.6	ALPI	NM_001631.2	IAP			
GI_13787192-S	178	218.5	188.4	ALPL	NM_000478.2	HOPS;TNAP;TNSALP;AP-TNAP	magnesiu	integral to	skeletal
GI_13787194-S	167.1	202.4	139.7	ALPP	NM_001632.2	ALP;PLAP		peripheral	
GI_13787208-S	4460	4122.2	3349.3	DDX21	NM_004728.1	GUA;GURDB;RH-II/GU;RH-II/GuA	ATP	nucleolus	
GI_13787213-A	196.7	170.2	158.4	SIRT5	NM_012241.2	SIR2L5	NAD ADP-		chromatin
GI_13787213-I	589.7	439.1	443	SIRT5	NM_012241.2	SIR2L5	NAD ADP-		chromatin
GI_13787214-I	720.1	590.6	524.3	SIRT5	NM_031244.1	SIR2L5	NAD ADP-		chromatin
GI_13787216-S	111.3	110.5	112.4	FAT2	NM_001447.1	CDHF8;HFAT2;MEGF1	calcium	integral to	homophili
GI_13899218-S	533.3	614.5	491.2	GABARAPL1	NM_031412.1	GEC1	receptor		
GI_13899220-S	92.7	113.7	108.6	MLZE	NM_031415.1				
GI_13899222-S	209.2	263.2	248.5	C18orf2	NM_031416.1		molecular	cellular_co	biological_
GI_13899226-S	89.3	94.1	95.8	TMEM16C	NM_031418.1	C11orf25;GENX-3947			
GI_13899228-S	314.5	251.3	192.3	MAIL	NM_031419.1	IKBZ;INAP			
GI_13899232-S	105.7	126.7	103.3	DKFZP434H0	NM_031421.1				
GI_13899234-S	113.9	128.7	112.8	CHST9	NM_031422.1	GALNAC4ST-2	N-	cellular_co	glycosami
GI_13899238-S	830.2	1054.4	1142.4	MGC10812	NM_031425.1				
GI_13899240-S	245.8	265	170.8	C9orf58	NM_031426.1	IBA2;FLJ12783	calcium		
GI_13899242-S	120.9	137.2	113.5	C14orf168	NM_031427.1	MGC12435			
GI_13899246-S	326.3	430.5	382.8	RTBDN	NM_031429.1				
GI_13899248-S	193.6	193.7	202.6	RILP	NM_031430.1		transporte	membran	transport
GI_13899252-S	718.9	929	862.3	UCK1	NM_031432.1				
GI_13899254-S	231.5	268.6	259.1	MFRP	NM_031433.1	FLJ30570	transmem	membran	developm
GI_13899258-S	140.1	162.4	108.4	DKFZP564I04	NM_031435.1		DNA		
GI_13899262-S	308	370.1	297	TMEM7	NM_031440.1	LTM1		integral to	
GI_13899280-S	1157	800.2	758	MGC13033	NM_031447.1				
GI_13899294-S	117.2	143.7	130.1	MS4A8B	NM_031457.1	MS4A4;4SPAN4	transporte	integral to	transport
GI_13899296-S	331.4	484.5	330.6	BAL	NM_031458.1			nucleus	
GI_13899304-S	1700.2	3848.5	2377	CD99L2	NM_031462.1	MIC2L1;DKFZp761H2024			
GI_13899310-S	177.7	182.6	161.3	MGC13204	NM_031465.1				
GI_13899314-S	145.2	166.1	134	CALN1	NM_031468.1		calcium		
GI_13899316-S	589	386.6	387.6	SH3BGRL2	NM_031469.1			nucleus	
GI_13899326-S	231.7	261.2	248.7	NRIP2	NM_031474.1	DKFZP761G1913	aspartic-	nucleus	proteolysis
GI_13899328-S	124.8	156.5	135.2	ESPN	NM_031475.1	DKFZP434A196			
GI_13899331-S	234.6	331.9	645.2	DKFZP434B0	NM_031476.1			extracellu	

GI_13899341-S	271.9	327.5	297	SLC25A18	NM_031481.1	GC2	binding	mitochond	transport
GI_13899343-S	1356.6	1761.2	2165.5	MRVLDC1	NM_031484.1	GB14;MARVD1;MGC4415;FLJ22343;FLJ234	transporte	membran	transport
GI_13899351-S	148.6	189.1	161.5	RBP5	NM_031491.1	CRBP3;CRBPIII;CRBP-III	intracellula	cytoplasm	transport
GI_13904851-S	147.2	200.6	175.2	CYP3A4	NM_017460.3	HLP;CP33;CP34;CYP3A;NF-	monooxyg	microsom	lipid
GI_13904852-S	346.2	431.6	369.6	CYP11B1	NM_000497.2	FHI;CPN1;CYP11B;P450C11	steroid 11-	mitochond	steroid
GI_13904854-S	298.3	342.9	285	CYP17A1	NM_000102.2	CPT7;CYP17;S17AH;P450C17	steroid 17-	microsom	sex
GI_13904855-S	100.5	93.6	104.6	CYP11B2	NM_000498.2	CPN2;ALDOS;CYP11B;CYP11BL;P-	steroid 11-	membran	glucocorti
GI_13904857-A	113.7	135	127.1	CYP19A1	NM_000103.2	ARO;ARO1;CPV1;CYAR;CYP19;P-	aromatase	microsom	steroid
GI_13904859-I	81.8	90.5	90.8	CYP19A1	NM_031226.1	ARO;ARO1;CPV1;CYAR;CYP19;P-	aromatase	microsom	steroid
GI_13904862-S	80.1	76.7	88.4	CYP24A1	NM_000782.2	CP24;CYP24;P450-CC24	monooxyg	mitochond	electron
GI_13904863-S	103.1	129	101	CYP27A1	NM_000784.2	CTX;CP27;CYP27	steroid	membran	electron
GI_13904864-S	257.4	310.4	295.4	CYP27B1	NM_000785.2	VDR;CP2B;CYP1;PDDR;VDD1;VDDR;VDDR	cytochrom	membran	vitamin
GI_13904867-S	28687	25804	20903	RPS10	NM_001014.2		structural	cytosolic	protein
GI_13904868-S	23007.7	20324	15684	RPS29	NM_001032.2		structural	cytosolic	regulation
GI_13904869-S	45065.7	46449	39609	RPS5	NM_001009.2		structural	cytosolic	protein
GI_13929211-S	108.9	120.2	114.2	OR2A4	NM_030908.1	OR2A10	olfactory	integral to	olfaction
GI_13929427-S	2326.2	1981	1495.9	CYP51A1	NM_000786.2	LDM;CP51;CYP51;CYPL1;P450L1;P450-	sterol 14-	integral to	electron
GI_13929428-S	194.6	227.8	204.7	CYP8B1	NM_004391.1	CP8B;CYP12	sterol 12-	microsom	electron
GI_13929430-S	96.4	97.8	92.4	CCR8	NM_005201.2	CY6;TER1;CKRL1;CKR-	chemokin	integral to	cytosolic
GI_13929435-A	571.4	683.7	606	CABP2	NM_031204.1		calcium		signal
GI_13929441-A	66	77.1	70.8	MUCDHL	NM_017717.3	MU-PCDH;FLJ20219			
GI_13929441-I	112.5	134.6	121.4	MUCDHL	NM_017717.3	MU-PCDH;FLJ20219			
GI_13929444-I	158.7	169.2	155.2	MUCDHL	NM_031265.1	MU-PCDH;FLJ20219			
GI_13929461-S	545.6	907.6	623.8	B4GALT1	NM_001497.2	GT1;GTB;GGTB2;B4GAL-T1;beta4Gal-T1	N-	Golgi	lactose
GI_13929463-A	571.9	515.9	500.5	B4GALT2	NM_003780.2	B4Gal-T2;B4Gal-T3;beta4Gal-T2	galactosylt		
GI_13929464-I	136.5	144.6	142	B4GALT2	NM_030587.1	B4Gal-T2;B4Gal-T3;beta4Gal-T2	galactosylt		
GI_13929468-S	759.4	818.1	971.9	B4GALT3	NM_003779.2	beta4Gal-T3	galactosylt		
GI_13929469-S	637.2	734.5	659.8	B4GALT4	NM_003778.2	B4Gal-T4;beta4Gal-T4	galactosylt	Golgi	membran
GI_13929470-S	940.3	2145.3	1179.2	B4GALT5	NM_004776.2	B4Gal-T5;beta4Gal-T5;beta4GalT-V;BETA4-	galactosylt	Golgi	carbohydr
GI_13929471-S	219.5	162.4	211.1	B4GALT6	NM_004775.2	B4Gal-T6;beta4Gal-T6	galactosylt	Golgi	
GI_13929472-S	145.2	175.1	153.7	CDC10	NM_001788.2	7-Sep	GTP	kinesin	cytokinesi
GI_13929473-S	85.3	83.5	91.1	NAT8	NM_003960.2	GLA;CML1;TSC501;TSC510	N-		drug
GI_13937360-S	193.6	196.4	197.9	TRF4-2	NM_022447.1		nucleic		
GI_13994189-S	826	798.2	996.3	FZD8	NM_031866.1	FZ-8;hFZ8	frizzled	integral to	frizzled
GI_13994233-S	99.7	105.9	100.9	ENAM	NM_031889.1		structural	extracellul	bone
GI_13994235-S	203.5	243.3	209.5	CECR6	NM_031890.1				
GI_13994241-S	5427.2	5473.4	6045.2	SH3KBP1	NM_031892.1	CIN85		kinesin	
GI_13994243-S	178.4	173.4	143.1	FTHL17	NM_031894.1		binding		iron ion
GI_13994249-S	243.6	305.7	279.3	TEKT3	NM_031898.1		structural	kinesin	microtubul
GI_13994254-S	98.9	119.3	102.7	AGXT2	NM_031900.1	AGT2	alanine-	mitochond	amino
GI_13994260-S	284.4	330	259.4	MRPL32	NM_031903.1	L32mt;HSPC283;MRP-L32;bMRP-59b	structural	mitochond	protein
GI_13994267-S	199.8	203.4	135.1	USP26	NM_031907.1		cysteine-	signal	ubiquitin-
GI_13994272-S	97.2	106.5	86.7	C1QTNF4	NM_031909.1	CTRP4;ZACRP4			
GI_13994281-S	507.1	359.4	341.5	SETDB2	NM_031915.1	CLLD8;CLLL8;C13orf4	DNA	nucleus	chromatin

GI_13994286-S	426	404.1	435.4	KLF16	NM_031918.1	DRRF;BTEB4;NSLP2	DNA	nucleus	regulation
GI_13994288-S	102.4	106.4	124.6	CSDUFD1	NM_031919.1		molecular	cellular_co	biological_
GI_13994299-S	505.9	352.7	579.1	TMPIT	NM_031925.1				
GI_13994301-S	144.6	188.2	183.6	TTY7	NM_031926.1				
GI_13994315-A	97.1	95.1	104.8	WNT8A	NM_031933.1	WNT8D	signal	extracellul	developm
GI_13994321-S	156	258.3	215.3	TBC1D10	NM_031937.1	EPI64	PDZ-	microvillus	biological_
GI_13994332-S	444.3	442.2	391.3	IFP38	NM_031943.1		translation		translation
GI_13994334-S	112.6	111.1	103.6	MIXL1	NM_031944.1	MIXL;MILD1	transcripti	nucleus	regulation
GI_13994340-S	137.6	151.7	150.3	SLC25A2	NM_031947.1	ORNT2	L-ornithine	mitochond	mitochond
GI_13994348-S	125.6	127	130.6	SPATA9	NM_031952.1	FLJ35906;NYD-SP16			
GI_13994357-S	115.1	146.7	141.1	NYD-SP14	NM_031956.1				
GI_13994359-S	112.5	172.8	114.9	KRTAP1-5	NM_031957.1	KAP1.5;KRTAP1.5	receptor		
GI_13994361-S	142.8	183.3	161.9	KRTAP3-1	NM_031958.1	KAP3.1;KRTAP3.1		intermedia	
GI_13994371-S	145.9	172.8	160.8	KRTAP17-1	NM_031964.1	KAP17.1;KRTAP16.1;KRTAP17.1			
GI_13994373-S	179.6	194.6	198	GSG2	NM_031965.1		ATP		protein
GI_14028874-S	146.1	148.3	165.8	SLC35D1	NM_015139.1	UGTREL7;KIAA0260	sugar	endoplas	transport
GI_14042922-S	1124.8	905.8	1104.4	C9orf5	NM_032012.1	CG2;CG-2	molecular	integral to	biological_
GI_14042940-S	5886.3	6020.1	4370.1	eIF2A	NM_032025.1	CDA02			
GI_14042942-S	656.7	610.1	499.3	CDA11	NM_032026.1				
GI_14042948-S	156.2	156.3	155.6	FKSG87	NM_032029.1				
GI_14042950-S	75.5	82.7	83.9	FKSG83	NM_032030.1	6p22.2-p21.31	pheromon	integral to	G-protein
GI_14042952-S	110.9	119.3	113.9	FKSG17	NM_032031.1				
GI_14042954-S	101.8	116.3	111.5	FKSG42	NM_032032.1				
GI_14042956-S	116.8	124	112.7	FKSG43	NM_032033.1			cytoskelet	
GI_14042959-S	247.7	276.4	262	SLC4A11	NM_032034.1	BTR1;dJ794I6.2	inorganic	membran	anion
GI_14042961-S	1055.9	602.7	533.8	C14orf141	NM_032035.1	MSTP031			
GI_14042963-S	457	646.8	598.1	FAM14A	NM_032036.1	TLH29		integral to	
GI_14042965-S	284.2	228	240.3	SSTK	NM_032037.1		ATP		protein
GI_14042967-S	2034.5	2449.5	2322.4	SPINL	NM_032038.1				
GI_14042969-S	1033.7	1653.8	1714.2	DKFZP761D0	NM_032039.1		cell	integrin	cell-matrix
GI_14042971-S	137.4	144.6	132.6	CCDC8	NM_032040.1	DKFZP564K0322			
GI_14042973-S	303.3	265.6	279.4	NCALD	NM_032041.1		tubulin	cytosol	vesicle-
GI_14042977-S	182.7	197.3	188.2	BRIP1	NM_032043.1	OF;BACH1	ATP	nucleus	nucleotide-
GI_14042983-S	109.9	111.9	103	MSP	NM_032046.1				
GI_14042987-S	294.6	483.4	142.6	EMILIN2	NM_032048.1	FOAP-10;EMILIN-2;FLJ33200	protein	extracellul	biological_
GI_14043021-S	8016	7037.8	6688.8	MARS	NM_004990.2	METRS;MTRNS	methionin	soluble	protein
GI_14043023-S	2567.8	3695.9	2931	BAG3	NM_004281.2	BIS;BAG-3;CAIR-1;DKFZp434E0610	apoptosis	cellular_co	protein
GI_14043025-S	237.2	353.1	186.5	VAMP8	NM_003761.2	EDB		synaptic	nonselecti
GI_14043031-A	1624.4	1949.1	871.5	C20orf18	NM_031227.1	XAP4;RNF54;UBCE7IP3		kinesin	
GI_14043043-A	124.7	119	106.8	CCR9	NM_006641.2	GPR-9-6	chemokin	integral to	cytosolic
GI_14043059-S	110.5	103.3	101.6	CRYAA	NM_000394.2	CRYA1	chaperone		vision
GI_14043065-A	136.2	143.3	139.5	AGTR1	NM_032049.1	AT1;AG2S;AT1B;AT2R1;HAT1R;AGTR1A;A	angiotensi	integral to	cytosolic
GI_14043065-I	352.7	423.1	371.6	AGTR1	NM_032049.1	AT1;AG2S;AT1B;AT2R1;HAT1R;AGTR1A;A	angiotensi	integral to	cytosolic
GI_14043068-S	160.9	191.2	165.6	HBA2	NM_000517.3			hemoglobi	

GI_14043069-I	413.7	389.6	209.4	HNRPA1	NM_031157.1	HNRNPA1	heterogen	nucleoplas	RNA-
GI_14043073-A	2206.9	2769	2742.8	HNRPA2B1	NM_002137.2	RNPA2;HNRPA2;HNRPB1;SNRPB1;HNRNP	heterogen	nucleus	RNA
GI_14110370-S	2726.6	2203.1	2089.7	CDC16	NM_003903.2	APC6		centrosom	regulation
GI_14110374-A	2827.1	2681.3	2447.1	M17S2	NM_005899.2	NBR1;CA125;KIAA0049	tumor		
GI_14110374-I	117.5	122.3	104.7	M17S2	NM_005899.2	NBR1;CA125;KIAA0049	tumor		
GI_14110377-I	135.5	148.9	137.6	M17S2	NM_031858.1	NBR1;CA125;KIAA0049	tumor		
GI_14110380-I	1443.4	1517.7	1389.5	M17S2	NM_031862.1	NBR1;CA125;KIAA0049	tumor		
GI_14110386-I	119.5	127.4	112.8	CDC2L5	NM_003718.2	CHED;CDC2L;KIAA1791	protein		regulation
GI_14110389-A	315.5	328.7	307	CDC2L5	NM_031267.1	CHED;CDC2L;KIAA1791	protein		regulation
GI_14110394-S	3604.9	1978.2	1477.7	XBP1	NM_005080.2	XBP2;TREB5	DNA	nucleus	immune
GI_14110398-S	150.9	172.6	139.9	ALPPL2	NM_031313.1	ALPG;GCAP;ALPPL	magnesiu	integral to	metabolis
GI_14110401-A	2526	2883.9	2721.5	HNRPAB	NM_004499.2	ABBP1	mRNA	ribonucleo	mRNA
GI_14110403-I	549.2	593.4	585.9	HNRPAB	NM_031266.1	ABBP1	mRNA	ribonucleo	mRNA
GI_14110406-A	911.5	962.5	912.3	HNRPDL	NM_031372.1	HNRNP;JKTBP;JKTBP2;laAUF1	double-	nucleus	RNA
GI_14110410-I	1960.6	1325.2	870.9	HNRPDL	NM_005463.2	HNRNP;JKTBP;JKTBP2;laAUF1	double-	nucleus	RNA
GI_14110413-A	7876.1	7511.2	6375.9	HNRPD	NM_002138.2	P37;AUF1;AUF1A;hnRNPD0	RNA	nucleus	RNA
GI_14110425-S	1023.3	1090.3	798	HNRPA0	NM_006805.2	hnRNPA0	heterogen	ribonucleo	mRNA
GI_14110430-A	4606.7	5450.1	3805.9	HNRPC	NM_004500.2	C1;C2;HNRNP;SNRPC;hnRNPC	heterogen	ribonucleo	mRNA
GI_14140235-S	109.6	107	91.8	SLC5A4	NM_014227.1	SAAT1;SGLT3;DJ90G24.4	transporte	integral to	sodium
GI_14141149-S	776	724.6	539.2	MTA1	NM_004689.2		transcripti	nucleus	signal
GI_14141150-S	271.2	282.1	225.2	HNRPF	NM_004966.2	HNRNPF;mcs94-1	heterogen	ribonucleo	RNA
GI_14141151-I	148.4	143.8	155.5	HNRPM	NM_005968.2	HTGR1;NAGR1;HNRNPM;HNRPM4;HNRNP	transmem	membran	
GI_14141153-A	6503.2	6918.4	6035.2	HNRPM	NM_031203.1	HTGR1;NAGR1;HNRNPM;HNRPM4;HNRNP	transmem	membran	
GI_14141155-S	704.8	928.1	922.9	HNRPH2	NM_019597.2	FTP3;HNRPH';hnRNPH'	heterogen	ribonucleo	
GI_14141158-A	925	858.8	827.6	HNRPH3	NM_021644.2	2H9;DKFZP586F0222	heterogen	ribonucleo	RNA
GI_14141160-A	5468.4	5940.1	4693.3	HNRPU	NM_004501.2	SAF-A;U21.1;HNRNPU	heterogen	nucleoplas	RNA
GI_14141162-I	126.4	134.4	108.1	HNRPU	NM_031844.1	SAF-A;U21.1;HNRNPU	heterogen	nucleoplas	RNA
GI_14141164-S	6587.1	7605.8	8233.1	PCBP1	NM_006196.2	HNRPX;HNRPE1;hnRNP-X;hnRNP-E1	single-	cytoplasm	mRNA
GI_14141165-A	4347.2	4917.5	5427.4	PCBP2	NM_031989.1	HNRPE2;hnRNP-E2	RNA	cytoplasm	mRNA
GI_14141169-S	651.7	809.3	816.6	MTA2	NM_004739.2	PID;MTA1L1;MTA1-L1	transcripti	histone	chromatin
GI_14141171-S	87	84.2	86.9	MTNR1A	NM_005958.2	MEL-1A-R	melatonin	integral to	mating
GI_14141172-S	100.1	106	109.7	MTNR1B	NM_005959.2	MEL-1B-R	melatonin	integral to	G-protein
GI_14141173-S	3159.6	2361.5	1993.4	HMGB2	NM_002129.2	HMG2	DNA	nuclear	chromoso
GI_14141174-S	106.4	105.5	90.1	ABCG5	NM_022436.2		nucleotide	integral to	transport
GI_14141179-S	1139.1	1025.7	881	FADS1	NM_013402.3	D5D;TU12;FADSD5;LLCDL1	C-5 sterol	integral to	fatty acid
GI_14141180-S	653.2	495.2	132.6	FADS2	NM_004265.2	D6D;DES6;TU13;FADSD6;LLCDL2;SLL0262		membran	fatty acid
GI_14141182-S	4120.5	1607.5	1400.6	HMGA2	NM_003483.3	BABL;LIPO;HMGIC	AT DNA	chromatin	establish
GI_14141183-S	137.7	135.7	138.1	NBR2	NM_005821.2				
GI_14141188-S	2059.1	2584.8	2440.2	HNRPR	NM_005826.2	HNRNPR;hnRNP-R	heterogen	ribonucleo	mRNA
GI_14141189-S	28828.3	27769	20714	RPL27A	NM_000990.2		structural	cytosolic	protein
GI_14141190-S	135.9	143.4	124	HOXB13	NM_006361.2		transcripti	nucleus	epidermal
GI_14141191-S	41768.5	40136	34120	RPS14	NM_005617.2	EMTB	structural	cytosolic	protein
GI_14141192-S	16654.1	13615	11172	RPS9	NM_001013.2		structural	cytosolic	protein
GI_14141194-S	1042.7	1401.5	1342.8	SDF2	NM_006923.2		dolichyl-	membran	protein

GI_14141725-S	295.2	343	358.1	SLC30A1	NM_021194.1	ZNT1	cation	integral to	zinc ion
GI_14149608-S	661.3	941.8	618	EXTL2	NM_001439.1	EXTR2	tumor	endoplas	
GI_14149614-S	2197.5	2555.3	1978.2	MGC4189	NM_032308.1				
GI_14149616-S	5114.2	5206.5	4386.1	NCOA4	NM_005437.1	RFG;ELE1;PTC3;ARA70;DKFZp762E1112	transcripti	nucleus	male
GI_14149626-S	324.7	298.5	284.8	USP15	NM_006313.1	UNPH4;KIAA0529	ubiquitin-		deubiquiti
GI_14149628-S	1377	1529.8	1503.8	XAB1	NM_007266.1	MBDIN;NTPBP	nucleotide		small
GI_14149650-S	104.1	99.3	98.1	NSG-X	NM_014411.1				
GI_14149652-S	513.2	585.2	539.9	TOR1B	NM_014506.1	DQ1;MGC4386	adenosine		
GI_14149656-S	3581	4129.3	3952.6	KIAA1049	NM_014972.1				
GI_14149666-S	170.9	311.3	270	SARM1	NM_015077.1	SARM;SAMD2;KIAA0524	transmem	membran	
GI_14149670-S	582.3	488.3	466.1	MAST2	NM_015112.1	MTSSK;MAST205;KIAA0807			
GI_14149674-S	440.7	389.5	300.9	CSTF2T	NM_015235.1	CstF-64T;KIAA0689;DKFZp434C1013	nucleic		
GI_14149676-S	187.7	166.5	162.7	LPHN3	NM_015236.1	LEC3;KIAA0768			
GI_14149679-S	2713.9	2901.1	2707.4	MBC2	NM_015292.1	KIAA0747	rhodopsin-	integral to	G-protein
GI_14149687-S	5086.4	4973.4	4731.3	NICE-3	NM_015449.1	HSPC012;DKFZp586G1722			
GI_14149689-S	264.2	272.5	263.8	DKFZP434F0	NM_015453.1		molecular		
GI_14149693-S	100.8	104.6	107.4	LRRC21	NM_015613.1	PAL;DKFZP434K091	transmem	integral to	photorece
GI_14149701-S	541.5	561.5	604.5	DKFZP566H	NM_015528.1				
GI_14149707-S	189.5	200.9	173.5	DKFZP434C1	NM_015621.1				
GI_14149711-S	135.6	158.5	129.8	C1QTNF5	NM_015645.1	CTRP5;DKFZp586B0621		microfibril	
GI_14149715-S	168.7	174.3	162.8	PPP1R12C	NM_017607.1	p84;DKFZp434D0412			
GI_14149719-S	727.3	769.6	735.7	FLJ11301	NM_018385.1		DNA	nucleus	regulation
GI_14149723-S	157.7	159.5	153.4	MESP1	NM_018670.1	IR1899308			
GI_14149729-S	501.8	507.4	479.2	SMARCAD1	NM_020159.1	ETL1;KIAA1122;DKFZp762K2015	ATP	nucleus	regulation
GI_14149733-S	478	543.5	530.5	CORO1B	NM_020441.1	CORONIN-2;DKFZP762I166	actin	kinesin	
GI_14149737-S	409.1	387.2	260.2	NLN	NM_020726.1	KIAA1226			
GI_14149741-S	416.7	556.9	502.6	KIAA1536	NM_020898.1				
GI_14149772-S	224.2	270.7	234.2	DKFZP564O	NM_032120.1				
GI_14149778-S	372.1	438.3	428.8	DKFZP564D	NM_032125.1		electron		electron
GI_14149780-S	221.6	274	267	DKFZP564J0	NM_032126.1				
GI_14149782-S	571.8	576.2	468.5	DKFZP566M	NM_032127.1	FLJ22665;KIAA1759			
GI_14149784-S	85.6	85.4	89.7	DKFZP566M	NM_032128.1				
GI_14149786-S	97.5	100.1	98.4	DKFZP434H	NM_032129.1				
GI_14149788-S	115.2	117.2	121.3	DKFZP434J0	NM_032130.1				
GI_14149792-S	116.9	128.8	118.4	DKFZP434P	NM_032134.1				
GI_14149798-S	283.1	314.4	309.8	RAB6C	NM_032144.1	WTH3	GTP	intracellula	protein
GI_14149802-S	1338.1	1002.2	864.5	ANKRD27	NM_032139.1	FLJ00040;DKFZP434L0718			
GI_14149804-S	1223.1	1165.5	1261	DKFZP434A1	NM_032140.1				
GI_14149806-S	557.1	429.5	374.8	DKFZP434K1	NM_032141.1				
GI_14149810-S	109.5	118.8	119.9	DKFZP434B1	NM_032143.1		nucleic		electron
GI_14149816-S	92.3	90.7	96.3	USP44	NM_032147.1	FLJ14528;DKFZP434D0127	cysteine-		ubiquitin-
GI_14149820-S	114.9	131.7	127.6	DKFZP434G	NM_032149.1				
GI_14149832-S	124.8	138.4	131.1	DKFZp547I0	NM_032155.1				
GI_14149848-S	86.4	83.9	83	FLJ12363	NM_032167.1				

GI_14149856-S	84	96.8	89.3	FLJ12787	NM_032175.1				
GI_14149858-S	216.2	231.1	172.6	PHAX	NM_032177.1	FLJ13193			
GI_14149860-S	168.7	151.1	125.1	FLJ13291	NM_032178.1				
GI_14149862-A	844	945.2	723.8	FLJ20542	NM_032179.1	FLJ13294			
GI_14149864-S	1429.2	1695	1133.8	FLJ13391	NM_032181.1				
GI_14149874-S	1120	1050.5	714.2	MYST1	NM_032188.1	MOF;hMOF;FLJ14040			
GI_14149901-S	242.8	232.4	211	FLJ21742	NM_032207.1				
GI_14149903-I	3507.3	4039.1	2832.2	ANTXR1	NM_032208.1	ATR;TEM8;FLJ10601;FLJ21776	receptor	integral to	
GI_14149905-S	103.7	91.7	82.7	FLJ21777	NM_032209.1				
GI_14149929-S	1185.1	1534.4	1339.1	FLJ22679	NM_032227.1	FLJ20173			
GI_14149947-S	223.4	280.2	253.5	FLJ23416	NM_032238.1				
GI_14149955-S	1639.8	1766.2	2028.4	DKFZp564A1	NM_032242.1				
GI_14149959-S	297.9	263.8	321.9	DKFZp434I1	NM_032245.1				
GI_14149963-S	150.4	167.1	157.4	DKFZp434E0	NM_032247.1				
GI_14149965-S	132.6	150.2	131.1	DKFZp434F1	NM_032248.1				
GI_14149967-S	121.4	119	121.5	DKFZp434F1	NM_032249.1				
GI_14149970-S	91.7	103.3	88.5	DKFZp434A1	NM_032250.1				
GI_14149976-S	233.8	288.7	281.6	DKFZp434F1	NM_032254.1				
GI_14149978-S	208.7	227.2	208.1	ZNF541	NM_032255.1	DKFZp434I1930			
GI_14149980-S	304.7	345.8	468.3	DKFZp434K2	NM_032256.1				
GI_14149984-S	175.2	210.7	186.7	TBC1D3	NM_032258.1	PRC17;DKFZp434P2235	GTPase		cell growth
GI_14149986-S	141.2	133.3	192.4	DKFZp434F0	NM_032259.1		electron		electron
GI_14149994-S	162.8	194.1	279.3	DKFZp434N0	NM_032262.1	DKFZp434G1017			
GI_14149996-S	255.6	245.1	231.6	AE2	NM_032264.1	DKFZp434D177			
GI_14149998-S	169.4	186.6	180.9	ZMYND15	NM_032265.1	DKFZp434N127			
GI_14150000-S	212.8	240.9	220.7	C2orf16	NM_032266.1	DKFZp434G118			
GI_14150002-S	91.9	117.5	100.8	RGSL2	NM_032267.1	DKFZp434E169	signal		
GI_14150018-S	98.9	97	91.4	DKFZp547F0	NM_032274.1				
GI_14150026-S	1171.2	787.9	803.3	ZCCHC9	NM_032280.1	DKFZp761J139	nucleic		
GI_14150028-S	223.1	235.7	228.9	DKFZp547J0	NM_032281.1				
GI_14150030-S	1307.5	1598.1	1866.3	DKFZp761O1	NM_032287.1				
GI_14150034-S	169.3	198.7	186.4	DKFZp761B0	NM_032289.1				
GI_14150036-S	224.6	206.2	213	DKFZp761C1	NM_032290.1				
GI_14150038-S	185	209.7	204	DKFZp761D2	NM_032291.1				
GI_14150040-S	1648.7	1345.8	1519.9	HAGHL	NM_032304.1	MGC2605			
GI_14150046-S	610.1	824.6	615.1	SLC37A3	NM_032295.1	DKFZp761N0624			
GI_14150048-S	530.7	583.3	392.6	DKFZp761A1	NM_032296.1	KIAA1552			
GI_14150051-S	172.5	224.2	229.3	DKFZp761D1	NM_032297.1				
GI_14150053-S	232	289.9	264.3	SYT3	NM_032298.1	SytIII;DKFZp761O132	transporte	synaptic	transport
GI_14150057-S	514.7	731.6	633.2	MGC10870	NM_032301.1				
GI_14150059-S	796.7	732.9	684.4	MGC10911	NM_032302.1				
GI_14150063-S	546.2	616.4	576	MGC3200	NM_032305.1				
GI_14150079-S	1100.7	1274.9	1141.3	MGC4767	NM_032314.1				
GI_14150081-S	921	823.7	576.4	MGC4399	NM_032315.1		binding	mitochond	transport

GI_14150087-S	263.1	358.4	503	HIATL2	NM_032318.1	MGC12945	transporte	membran	transport
GI_14150089-S	227.2	220.5	235.7	C2orf7	NM_032319.1	MGC13004	peptidase		proteolysis
GI_14150093-S	110	111	106.6	MGC13057	NM_032321.1				
GI_14150097-S	425.7	366.1	331	MGC13102	NM_032323.1				
GI_14150099-S	1436.1	1512	1497	MGC13186	NM_032324.1		ATP-		proteolysis
GI_14150107-S	122.8	126.6	124.2	MGC12458	NM_032328.1		calcium		
GI_14150117-S	238.4	231.9	210.5	MGC14595	NM_032334.1				
GI_14150119-A	137.6	151.9	144.6	PHF6	NM_032335.1	BFLS;KIAA1823;MGC14797	electron		electron
GI_14150119-I	79.2	82.9	82.8	PHF6	NM_032335.1	BFLS;KIAA1823;MGC14797	electron		electron
GI_14150121-S	101.2	109.4	110.2	MGC14799	NM_032336.1				
GI_14150127-S	1086	1105.4	1015.8	C6orf125	NM_032340.1	MGC14833;bA6B20.2			
GI_14150131-S	91.9	490.7	160.7	MGC12992	NM_032342.1				
GI_14150133-S	539.3	524.7	559.3	CHCHD6	NM_032343.1	MGC13016			
GI_14150136-S	953.2	991	1012.1	MGC13045	NM_032344.1				
GI_14150138-S	249	355.7	319.7	PYM	NM_032345.1	MGC13064			
GI_14150140-S	858.4	742.8	611.8	MGC13096	NM_032346.1		apoptosis	cytoplasm	apoptosis
GI_14150142-S	124.9	144.3	144.2	ZNF397	NM_032347.1	ZNF47;MGC13250			
GI_14150170-S	2483.2	2695.4	2704.6	THOC3	NM_032361.1	TEX1;MGC5469	RNA	nucleus	transport
GI_14150172-S	210.9	254.2	220	HEIL1	NM_032362.1				
GI_14150184-S	229.6	177.5	157.6	ZBED3	NM_032367.1	MGC15435	DNA		
GI_14150188-S	177.8	231.8	192.3	MGC15619	NM_032369.1		cation	membran	cation
GI_14150190-S	263	344.7	307	MGC15716	NM_032370.1				
GI_14150216-I	108.7	135	125.9	C5orf4	NM_032385.1	FLJ13758			
GI_14150228-S	84.3	88	93.4	RAP140	NM_015224.1	se89-1;KIAA1105			
GI_14161691-S	113	120.7	94.2	CAPNS2	NM_032330.1	MGC12536;MGC14804	calcium		
GI_14165257-S	123.3	141.5	141.1	CYLD	NM_015247.1	EAC;CDMT;CYLD1;HSPC057;KIAA0849			
GI_14165263-I	235.1	263.2	251.2	NDRG4	NM_020465.1	SMAP-8;KIAA1180		cytoplasm	response
GI_14165271-S	1350.8	1882.1	1920.8	PINK1	NM_032409.1	BRPK	protein-		protein
GI_14165275-S	98.6	89	94.3	ECRG4	NM_032411.1				
GI_14165281-S	99.4	108.2	99	PROK1	NM_032414.1	PK1;PRK1;EGVEGF	growth		cell
GI_14165285-S	207.9	188.3	181.5	RHOBTB2	NM_015178.1	DBC2;KIAA0717	RAS small		protein
GI_14165380-A	129.3	142.3	123.2	PCDHA10	NM_031859.1	CNR8;CNRN8;CNRS8;CRNR8;PCDH-	cell	integral to	cell
GI_14165380-I	84.7	79.6	74.3	PCDHA10	NM_031859.1	CNR8;CNRN8;CNRS8;CRNR8;PCDH-	cell	integral to	cell
GI_14165386-A	112.9	122.5	112.3	PCDHA11	NM_031861.1	CNR7;CNRN7;CNRS7;CRNR7;PCDH-	cell	integral to	cell
GI_14165389-A	101	108	87.2	PCDHA6	NM_031848.1	CNR2;CNRN2;CNRS2;CRNR2;PCDH-	cell	integral to	cell
GI_14165391-A	104.5	101.5	101.9	PCDHA12	NM_031864.1	PCDH-ALPHA12	calcium	integral to	homophili
GI_14165396-A	88	92	91.9	PCDHA13	NM_031865.1	CNR5;CNRN5;CNRS5;CRNR5;PCDH-	calcium	integral to	homophili
GI_14165399-A	77.2	89.1	75	PCDHA1	NM_031410.1	PCDH-ALPHA1	cell	integral to	cell
GI_14165399-I	85.8	100.2	102.5	PCDHA1	NM_031410.1	PCDH-ALPHA1	cell	integral to	cell
GI_14165404-A	87.6	102	93.6	PCDHA2	NM_031495.1	PCDH-ALPHA2	cell	integral to	cell
GI_14165404-I	76.7	77.7	83.8	PCDHA2	NM_031495.1	PCDH-ALPHA2	cell	integral to	cell
GI_14165406-I	126.2	128.3	122	PCDHA2	NM_031496.1	PCDH-ALPHA2	cell	integral to	cell
GI_14165409-A	104.8	103.6	98.3	PCDHA3	NM_031497.1	PCDH-ALPHA3	cell	integral to	cell
GI_14165409-I	119.9	123.9	112.9	PCDHA3	NM_031497.1	PCDH-ALPHA3	cell	integral to	cell

GI_14165412-A	132.4	140.7	126.4	PCDHA4	NM_031500.1	CNR1;CNRN1;CRNR1;PCDH-ALPHA4	cell	integral to	cell
GI_14165415-A	89.5	82.1	84.1	PCDHA5	NM_031501.1	CNR6;CNRN6;CNRS6;CRNR6;PCDH-	cell	integral to	cell
GI_14165415-I	169	192.1	179.2	PCDHA5	NM_031501.1	CNR6;CNRN6;CNRS6;CRNR6;PCDH-	cell	integral to	cell
GI_14165418-A	119.5	108.6	113.5	PCDHA7	NM_031852.1	CNR4;CNRN4;CNRS4;CRNR4;PCDH-	cell	integral to	cell
GI_14165421-A	306	386.7	362.8	PCDHA8	NM_031856.1	PCDH-ALPHA8	cell	integral to	cell
GI_14165421-I	87.3	90	84.7	PCDHA8	NM_031856.1	PCDH-ALPHA8	cell	integral to	cell
GI_14165424-A	171.7	215.4	185.7	PCDHA9	NM_031857.1	KIAA0345;PCDH-ALPHA9	calcium	integral to	homophili
GI_14165436-A	293.7	382	315.6	HNRPK	NM_031263.1	CSBP;TUNP;HNRNPK	heterogen	nucleoplas	RNA
GI_14165449-A	337.1	385.2	357.8	COL4A3	NM_031366.1	TUMSTATIN	collagen	collagen	negative
GI_14165451-A	346	346.1	376.3	COL4A3BP	NM_031361.1	GPBP;CERTL;STARD11	protein	kinesin	protein
GI_14165455-A	300.8	381.6	350.3	MAP1B	NM_032010.1	MAP5;FUTSCH	structural	microtubul	cell shape
GI_14165455-I	103.9	119.3	101.5	MAP1B	NM_032010.1	MAP5;FUTSCH	structural	microtubul	cell shape
GI_14165457-I	98	106	113.3	MAP1B	NM_005909.2	MAP5;FUTSCH	structural	microtubul	cell shape
GI_14165459-A	699.8	862.9	816.8	NARF	NM_012336.2	FLJ10067;DKFZp434G0420	lamin	nuclear	
GI_14165460-I	199	228.1	210.9	NARF	NM_031968.1	FLJ10067;DKFZp434G0420	lamin	nuclear	
GI_14165467-S	21816	19998	17633	RPS18	NM_022551.2	KE3;HKE3;KE-3	structural	small	protein
GI_14165470-S	1136.9	1238.7	1251.6	CDC42EP4	NM_012121.3	CEP4;BORG4;KAIA1777			
GI_14165471-S	1301.7	1382	1251.9	SUGT1	NM_006704.2	SGT1		kinetochor	centromer
GI_14192940-S	95.7	108.6	90.5	MEGF11	NM_032445.1	KIAA1781	ubiquinol-	membran	electron
GI_14192942-S	135.8	265.9	101	MEGF10	NM_032446.1	KIAA1780	structural		
GI_14195591-S	89.2	103.3	90.1	PCDHB10	NM_018930.2	PCHB10;PCDH-BETA10	cell	integral to	cell
GI_14195592-S	147	178.1	156.4	PCDHB11	NM_018931.2	ME2;PCDH-BETA11	cell	integral to	cell
GI_14195593-S	134.1	151.6	146	PCDHB12	NM_018932.2	PCDH-BETA12	cell	integral to	cell
GI_14195594-S	122.2	111.8	127.2	PCDHB13	NM_018933.2	PCDH-BETA13	calcium-	integral to	synaptoge
GI_14195596-A	154.4	155	142.9	PPP1R12B	NM_032103.1	MYPT2	enzyme		regulation
GI_14195602-S	132.7	128.7	133.4	PCDHB14	NM_018934.2	PCDH-BETA14	cell	integral to	cell
GI_14195603-S	194.4	170.8	224	PCDHB15	NM_018935.2	PCDH-BETA15	cell	integral to	cell
GI_14195604-S	104.5	111.8	99.2	PCDHB16	NM_020957.1	ME1;PCDH3X;PCDHB8a;KIAA1621;PCDH-	calcium-	integral to	synaptoge
GI_14195606-S	80.9	83.2	84.6	PCDHB1	NM_013340.2	PCDH-BETA1	calcium	integral to	homophili
GI_14195608-S	129	120.9	117.6	PCDHB2	NM_018936.2	PCDH-BETA2	cell	integral to	cell
GI_14195609-S	114	130.3	115.8	PCDHB3	NM_018937.2	PCDH-BETA3	cell	integral to	cell
GI_14195610-S	175.1	210.5	164.8	PCDHB4	NM_018938.2	PCDH-BETA4	cell	integral to	cell
GI_14195611-S	188	336.6	179.7	PCDHB5	NM_015669.2	PCDH-BETA5;DKFZP586B0217	calcium-	integral to	synaptoge
GI_14195612-S	105.2	135.3	106.4	PCDHB6	NM_018939.2	PCDH-BETA6	cell	integral to	cell
GI_14195613-S	113.8	170.5	119.4	PCDHB7	NM_018940.2	PCDH-BETA7	calcium	integral to	homophili
GI_14195614-S	110.8	128.5	101	PCDHB8	NM_019120.2	PCDH3I;PCDH-BETA8	calcium	integral to	homophili
GI_14195617-A	110.6	125.5	122.4	MAP2	NM_031845.1	MAP2A;MAP2B;MAP2C	structural	microtubul	microtubul
GI_14195629-A	125.1	134.3	121.9	MAP4	NM_030983.1		structural	microtubul	
GI_14195631-I	146.9	148.7	150.8	MAP4	NM_002375.2		structural	microtubul	
GI_14195632-S	121.9	142	117.7	MAGEC1	NM_005462.2	CT7;MAGE-C1	tumor		
GI_14195633-S	1910.6	3334.1	2257.6	MAGED1	NM_006986.2	NRAGE;DLXIN-1	tumor		
GI_14196447-A	119.2	116.1	109.2	PCDHGA10	NM_032090.1	PCDH-GAMMA-A10	calcium	integral to	homophili
GI_14196447-I	93.6	90.8	81	PCDHGA10	NM_032090.1	PCDH-GAMMA-A10	calcium	integral to	homophili
GI_14196450-A	120.8	152.3	123.1	PCDHGA11	NM_032091.1	PCDH-GAMMA-A11	calcium	integral to	homophili

GI_14196450-I	142.4	148.9	144.7	PCDHGA11	NM_032091.1	PCDH-GAMMA-A11	calcium	integral to	homophili
GI_14196456-A	109.8	118.1	121.2	PCDHGA12	NM_032094.1	FIB3;CDH21;KIAA0588;PCDH-GAMMA-A12	calcium	integral to	homophili
GI_14196458-A	88.6	97.6	91.7	PCDHGA1	NM_031993.1	PCDH-GAMMA-A1	calcium	integral to	homophili
GI_14196458-I	99.2	97.6	86.6	PCDHGA1	NM_031993.1	PCDH-GAMMA-A1	calcium	integral to	homophili
GI_14196461-A	107.7	103	110	PCDHGA2	NM_032009.1	PCDH-GAMMA-A2	calcium	integral to	homophili
GI_14196464-A	84.1	85.6	78	PCDHGA3	NM_032011.1	PCDH-GAMMA-A3	calcium	integral to	homophili
GI_14196464-I	95.8	93	88.1	PCDHGA3	NM_032011.1	PCDH-GAMMA-A3	calcium	integral to	homophili
GI_14196467-A	120.9	151.5	134.6	PCDHGA4	NM_032053.1	PCDH-GAMMA-A4	calcium	integral to	homophili
GI_14196467-I	103.4	122.7	108.9	PCDHGA4	NM_032053.1	PCDH-GAMMA-A4	calcium	integral to	homophili
GI_14196470-A	106.9	122.3	112	PCDHGA5	NM_032054.1	ME3;CDH-GAMMA-A5;PCDH-GAMMA-A5	calcium	integral to	homophili
GI_14196473-A	94.6	106.6	105.9	PCDHGA6	NM_032086.1	PCDH-GAMMA-A6	calcium	integral to	homophili
GI_14196476-A	92.7	80.1	94.6	PCDHGA7	NM_032087.1	PCDH-GAMMA-A7	calcium	integral to	homophili
GI_14196476-I	88.3	92.1	77.8	PCDHGA7	NM_032087.1	PCDH-GAMMA-A7	calcium	integral to	homophili
GI_14210483-S	102.8	126.4	124.2	GPR145	NM_032503.1	SLT;MCH2;MCH2R;MCHR2	receptor	integral to	G-protein
GI_14210505-S	764.2	485.1	362.3	LOC84524	NM_032494.1		nucleic	nucleus	regulation
GI_14210509-S	418.7	241.9	144.7	ARHGAP9	NM_032496.1	10C;RGL1;MGC1295			
GI_14210533-S	110.5	126.4	107.4	KRTAP4-4	NM_032524.1	KAP4.4;KRTAP4.4	receptor	intermedia	
GI_14210535-S	2300	2005.3	1273.7	MGC4083	NM_032525.1	TUBB-5	GTP	microtubul	microtubul
GI_14210537-S	99.4	107.6	91.7	NT5C1A	NM_032526.1	CN-I;CN1A;CN-IA	5'-	cytosol	nucleoside
GI_14211539-S	460.4	523.7	407.1	MOV10	NM_020963.1	KIAA1631			
GI_14211842-S	1112.7	1215.3	1107.2	SCOC	NM_032547.1	SCOCO;HRIHFB2072			
GI_14211844-S	418.5	514.6	461.6	IMMP2L	NM_032549.1	IMP2		mitochond	
GI_14211848-S	142.4	111	104.4	FKSG79	NM_032553.1		rhodopsin-	integral to	G-protein
GI_14211858-S	928.2	947.4	1181.9	FLJ14753	NM_032558.1				
GI_14211866-S	97.3	112.5	104.7	PLA2G12B	NM_032562.1	FKSG71;GXIIIsPLA2	calcium-		lipid
GI_14211868-S	125.1	139.3	138.4	SPRL6A	NM_032563.1	LEP16			
GI_14211872-S	1871.4	1736.8	1207.2	EBRP	NM_032565.1		isomerase	endoplas	
GI_14211880-S	138.8	125.1	136.9	NAG73	NM_032570.1				
GI_14211888-S	1594.4	1578.9	1671.9	LOC84661	NM_032574.1			nucleus	
GI_14211890-S	155.9	171	153.4	GLIS2	NM_032575.1				
GI_14211892-S	245.9	292.1	212.1	CYorf15B	NM_032576.1				
GI_14211894-S	124.1	141.3	125.3	FLJ14437	NM_032578.1				
GI_14211896-S	192.4	227.9	197.9	RETNLB	NM_032579.1	FIZZ1;FIZZ2;HXCP2;RELMb;RELMbeta	hormone	cellular_co	cell
GI_14211898-S	112.1	107.6	107.1	HES7	NM_032580.1		DNA	nucleus	mesoderm
GI_14211906-S	103.7	123.8	114	ZNF347	NM_032584.1	ZNF1111	DNA	nucleus	regulation
GI_14211918-S	176.8	205	189.3	SLC9A7	NM_032591.1	NHE7	ion	integral to	sodium
GI_14211920-S	237.3	288	241.4	PHACS	NM_032592.1	ACS	transamin		biosynthes
GI_14211922-S	1049.8	1055.7	1287.7	HINT2	NM_032593.1	HIT-17			
GI_14211926-S	89.6	86.5	88	PPP1R9B	NM_032595.1	SPINO;PPP1R9	transporte	membran	transport
GI_14211934-S	175.3	193.1	180.8	NYD-SP18	NM_032599.1				
GI_14211940-S	102.9	99.3	93.3	CX62	NM_032602.1		connexon	connexon	cell
GI_14211948-S	291.4	369.2	357.3	CREB3L3	NM_032607.1	CREB-H			
GI_14249118-S	219	258.6	221.7	PEPP-2	NM_032498.1		transcripti	nucleus	regulation
GI_14249125-S	935.4	672.1	735.9	GTPBP3	NM_032620.1	MSS1;MTGP1;THDF1;GTPBG3;FLJ14700	GTPase		tRNA

GI_14249127-S	102.9	111.8	106.1	LNX	NM_032622.1	MPDZ	protein		intracellula
GI_14249145-S	132.5	123.8	124.7	C7orf13	NM_032625.1	MY040			
GI_14249149-S	1483.1	2434.9	1866.5	SSBP4	NM_032627.1	MGC3181			
GI_14249161-S	105.8	112.8	105.2	MGC5457	NM_032633.1				
GI_14249177-S	663.1	696.2	840.9	GRCC9	NM_032641.1	SSB2;SSB-2;MGC2519	molecular	cellular_co	intracellula
GI_14249183-S	280.3	303.1	289.8	MGC2452	NM_032644.1				
GI_14249191-S	123.7	157.3	126.1	MGC10820	NM_032648.1			kinesin	
GI_14249201-S	212.9	239.3	219.7	C21orf122	NM_032653.1				
GI_14249203-S	99.8	121.3	108.9	MGC10981	NM_032654.1				
GI_14249217-S	300.3	338.3	362	MGC5139	NM_032661.1				
GI_14249219-S	218.7	323.1	219.2	MGC10600	NM_032662.1				
GI_14249231-S	115.6	122.7	115.2	MGC4771	NM_032668.1				
GI_14249237-S	234	222.6	256	MGC10814	NM_032671.1				
GI_14249239-S	545.1	524.3	518.8	NSPC1	NM_032673.1	MGC10882			
GI_14249251-S	132.8	138.8	130.9	ZNF577	NM_032679.1	MGC4400	nucleic	nucleus	regulation
GI_14249255-S	103.5	103.1	106.2	TRIM51	NM_032681.1	MGC10977			
GI_14249259-S	314.5	373.5	373.1	MGC12972	NM_032683.1				
GI_14249265-S	238.4	264.5	234.9	MGC13008	NM_032686.1				
GI_14249273-S	653	708.6	670.9	MGC13198	NM_032690.1				
GI_14249275-S	319.7	369.1	326.7	MGC11082	NM_032691.1				
GI_14249281-S	127.3	124.8	124.8	MGC12935	NM_032694.1				
GI_14249285-S	105.6	114.8	99.5	MGC12262	NM_032696.1				
GI_14249303-S	1107.8	801.2	716.9	MGC12966	NM_032706.1				
GI_14249307-S	350.7	507.8	190	C10orf33	NM_032709.1	FLJ23849;MGC13047	oxidoredu		electron
GI_14249309-S	925.4	1095.5	899.7	MGC13053	NM_032710.1				
GI_14249311-S	143.4	155.2	200.6	MGC13090	NM_032711.1				
GI_14249315-S	223.8	231.6	348.2	MGC13251	NM_032714.1				
GI_14249355-S	89.8	103.4	94.5	MGC13168	NM_032735.1		molecular		
GI_14249363-S	273.6	410.3	368.4	MGC5370	NM_032739.1				
GI_14249371-S	103.2	104.9	109.1	C6orf105	NM_032744.1	MGC12335;dJ413H6.1			
GI_14249373-S	102.8	96.4	86	MGC12538	NM_032746.1				
GI_14249375-S	197.3	195.6	100	USMG5	NM_032747.1	MGC14697;bA792D24.4			
GI_14249381-S	3636.1	3172.1	3471.4	MGC15429	NM_032750.1		catalytic	nucleus	
GI_14249383-S	242.7	370.6	459.3	C14orf128	NM_032751.1				
GI_14249385-S	227.4	263.6	210.3	ZNF496	NM_032752.1	MGC15548			
GI_14249391-S	162.9	182.9	198.2	MGC15634	NM_032755.1				
GI_14249393-S	118.3	129.1	118	MGC15668	NM_032756.1				
GI_14249395-S	90.6	93.5	93.9	MGC15705	NM_032757.1				
GI_14249407-S	99.5	101.5	86.9	MGC16142	NM_032763.1				
GI_14249413-S	159.2	152.6	145.3	MGC16179	NM_032766.1				
GI_14249445-S	198.4	256.3	207.5	FLJ14431	NM_032783.1		oxidoredu		metabolis
GI_14249449-S	101.1	111.1	102.5	FLJ14442	NM_032785.1		carboxype		proteolysis
GI_14249451-S	292.4	244.8	215.7	FLJ14451	NM_032786.1		nucleic		
GI_14249453-S	75.1	74.8	69.5	GPR128	NM_032787.1	FLJ14454	G-protein	membran	neuropepti

GI_14249455-S	91.3	110.5	84.3	ZNF514	NM_032788.1	FLJ14457	nucleic	nucleus	regulation
GI_14249457-S	730.9	820.4	670.5	FLJ14464	NM_032789.1				
GI_14249467-I	1788.4	2103.4	1800.6	C6orf29	NM_032794.1	CTL4;NG22;FLJ14491			
GI_14249469-S	631	636.7	583.8	FLJ14494	NM_032795.1		pseudouri		
GI_14249477-S	440.7	473.9	605.4	FLJ14525	NM_032800.1	MGC10710			
GI_14249487-S	163.3	217.1	201.9	ZNF206	NM_032805.1	FLJ14549	transcripti	nucleus	regulation
GI_14249499-S	111.8	110.8	114.5	TBRG1	NM_032811.1	TB-5;FLJ14621	DNA	nucleus	
GI_14249503-S	241.1	215.5	158	FLJ14624	NM_032813.1				
GI_14249505-S	98.5	98.7	92.8	FLJ14627	NM_032814.1				
GI_14249511-S	96.5	82.8	75.7	FLJ14641	NM_032817.1				
GI_14249513-S	126.1	154	163.6	C9orf100	NM_032818.1	FLJ14642;MGC44886			
GI_14249519-S	1216.7	938.1	974.3	FLJ14668	NM_032822.1		odorant		transport
GI_14249523-S	129.5	152.9	135.3	FLJ14681	NM_032824.1		phospholi		lipid
GI_14249531-S	157.6	153.4	134.6	ZNF587	NM_032828.1	ZF6;UBF-fl;FLJ14710;FLJ20813			
GI_14249533-S	189.4	236.8	215	FLJ14721	NM_032829.1				
GI_14249535-S	5331	3997.8	3480.2	CIRH1A	NM_032830.1	NAIC;CIRHIN;TEX292;FLJ14728;KIAA1988			
GI_14249537-S	416.9	563.6	582.3	C7orf19	NM_032831.1	CBCIP2;FLJ12474;FLJ14733			
GI_14249549-S	1166.9	1359.9	962.2	FLJ14775	NM_032837.1		DNA	nucleus	regulation
GI_14249551-S	1031.4	1057.1	1150.3	DIRC2	NM_032839.1	RCC4;FLJ14784			
GI_14249553-S	659.7	606.5	981.9	FLJ14800	NM_032840.1		hormone	extracellul	developm
GI_14249557-S	1510.5	1109.7	958.3	FLJ14803	NM_032842.1				
GI_14249561-S	349.6	377.1	405	MASTL	NM_032844.1	THC2;FLJ14813	ATP		protein
GI_14249563-S	99.7	104.6	102.5	FLJ14816	NM_032845.1		DNA	nucleus	regulation
GI_14249567-S	1636.1	1747.5	1445.5	FLJ14825	NM_032847.1				
GI_14249569-S	2840.3	2584.5	2381	FLJ14827	NM_032848.1				
GI_14249581-S	111.6	156.2	86.4	FLJ14871	NM_032854.1				
GI_14249585-S	315.8	330	287.3	FLJ14888	NM_032856.1				
GI_14249589-S	103.9	97.4	96.6	FLJ14904	NM_032858.1				
GI_14249591-S	90.4	81.9	83.6	FLJ14906	NM_032859.1		catalytic		
GI_14249607-S	136	118.5	143.1	FLJ14966	NM_032867.1				
GI_14249613-S	251.2	194.1	127.9	JFC1	NM_032872.1	FLJ14996			
GI_14249619-S	544.3	659.8	605.9	MGC15482	NM_032875.1		electron		electron
GI_14249631-S	579	632.8	596.3	LSM10	NM_032881.1	MGC15749	pre-mRNA	small	mRNA
GI_14249635-S	9711.1	6405.1	9361.9	C20orf100	NM_032883.1	MGC15880;dJ495O3.1;dJ1108D11.2	DNA	nucleus	regulation
GI_14249641-S	124.9	119.9	121.6	MGC15912	NM_032886.1				
GI_14249643-S	165.1	178.2	155.3	MGC16037	NM_032887.1				
GI_14249653-S	420	349.3	245.4	MGC14161	NM_032892.1		translation	cytoskelet	translation
GI_14249657-S	959.4	782.4	459.6	MGC14376	NM_032895.1				
GI_14249661-S	89.6	96	97.9	MGC14436	NM_032897.1				
GI_14249683-S	108.9	111.5	98	MGC14407	NM_032908.1				
GI_14249687-S	421	567.6	519.8	C21orf119	NM_032910.1				
GI_14249699-S	304.9	263	259.4	MGC16279	NM_032916.1				
GI_14249701-S	117.9	124.2	111.6	MGC2848	NM_032917.1				
GI_14249703-S	201.1	198.6	175	RERG	NM_032918.1	MGC15754	RAS small		small

GI_14249705-S	324.8	358.6	327.3	C21orf124	NM_032920.1	PRED79;FLJ31940;MGC15873			
GI_14249707-A	380	470	369.7	MGC15875	NM_032921.1	MGC45484			
GI_14249725-S	89	213.6	150.4	MGC13040	NM_032930.1				
GI_14249741-S	96.7	92.4	100.3	LOC84664	NM_032577.1				
GI_14251204-S	88	106.7	97.3	HRH4	NM_021624.2	H4;H4R;BG26;HH4R;AXOR35;GPRv53;GPC	histamine	integral to	G-protein
GI_14251206-S	170	202.4	181.3	MOV10L1	NM_018995.1	DJ402G11.8;DKFZp434B0717	ATP	intracellula	developm
GI_14251208-S	7059.3	7848.3	7807.2	CLIC1	NM_001288.3	G6;NCC27	chloride	nuclear	small
GI_14251210-S	447.8	764	665.2	MCCC2	NM_022132.3	MCCB	biotin	mitochond	leucine
GI_14251211-S	307.8	302.8	243	DDX20	NM_007204.3	DP103;GEMIN3;DKFZP434H052	ATP	cytoskelet	assembly
GI_14251213-S	1094.4	1658.3	1504.5	DDX24	NM_020414.3				
GI_14251214-S	308.3	186.4	183.5	KLF5	NM_001730.2	CKLF;IKLF;BTEB2	RNA	nucleus	transcripti
GI_14251216-S	617	717	584.2	CRYZ	NM_001889.2		alcohol		vision
GI_14251217-S	114.7	125.3	111.5	CRYBA1	NM_005208.3	CRYB1	structural		vision
GI_14269577-S	218	280.9	274.7	MT4	NM_032935.1	MTIV	copper ion	cytoplasm	biological_
GI_14270477-I	126.9	141.3	160.7	GPS2	NM_032442.1	AMF-1;KIAA1787	GTPase		JNK
GI_14270480-A	108.6	128.6	112.5	GPS2	NM_032938.1	AMF-1;KIAA1787	GTPase		JNK
GI_14270482-A	124.7	129.8	124.8	PCDHGA8	NM_014004.2	KIAA0327;PCDH-GAMMA-A8	calcium	integral to	homophili
GI_14270482-I	76.8	88.2	82.8	PCDHGA8	NM_014004.2	KIAA0327;PCDH-GAMMA-A8	calcium	integral to	homophili
GI_14270486-A	264.1	346.8	299.6	PCDHGA9	NM_032089.1	PCDH-GAMMA-A9	calcium	integral to	homophili
GI_14270489-A	200.2	242.4	210.8	PCDHGB1	NM_032095.1	PCDH-GAMMA-B1	calcium	integral to	homophili
GI_14270492-A	103.4	114.8	123.3	PCDHGB2	NM_032096.1	PCDH-GAMMA-B2	calcium	integral to	homophili
GI_14270495-A	105.2	111.9	108.1	PCDHGB3	NM_032097.1	PCDH-GAMMA-B3	calcium	integral to	homophili
GI_14270498-A	297.7	317.5	287.5	PCDHGB4	NM_032098.1	FIB2;CDH20;PCDH-GAMMA-B4	calcium-	membran	cell
GI_14270501-A	96.1	103.8	95.9	PCDHGB6	NM_032100.1	PCDH-GAMMA-B6	calcium	integral to	homophili
GI_14270504-A	114.1	125.6	118.6	PCDHGB5	NM_032099.1	PCDH-GAMMA-B5	calcium	integral to	homophili
GI_14270504-I	91.4	93	81.4	PCDHGB5	NM_032099.1	PCDH-GAMMA-B5	calcium	integral to	homophili
GI_14270507-A	110.1	123.9	106.3	PCDHGB7	NM_032101.1	ME6;PCDH-GAMMA-B7	calcium	integral to	homophili
GI_14270507-I	82.6	84.6	81.7	PCDHGB7	NM_032101.1	ME6;PCDH-GAMMA-B7	calcium	integral to	homophili
GI_14277673-S	228.6	341.3	198.8	LMCD1	NM_014583.2		molecular	cellular_co	biological_
GI_14277676-I	178.3	193.4	194	PCDHGC3	NM_032402.1	PC43;PCDH2;PCDH-GAMMA-C3			
GI_14277678-A	120.8	127.4	107.4	PCDHGC3	NM_032403.1	PC43;PCDH2;PCDH-GAMMA-C3			
GI_14277681-A	166.2	191	184.4	PCDHGC4	NM_032406.1	PCDH-GAMMA-C4	calcium	integral to	homophili
GI_14277681-I	104.2	109.7	105	PCDHGC4	NM_032406.1	PCDH-GAMMA-C4	calcium	integral to	homophili
GI_14277684-A	95.5	88.8	93.5	PCDHGC5	NM_032407.1	PCDH-GAMMA-C5	calcium	integral to	homophili
GI_14277684-I	98.1	108.8	97.6	PCDHGC5	NM_032407.1	PCDH-GAMMA-C5	calcium	integral to	homophili
GI_14277687-S	141.5	162.9	123.3	TEX13A	NM_031274.2				
GI_14277688-S	96.7	95.1	108.8	TEX15	NM_031271.2	DKFZP434M2415			
GI_14277689-S	173.5	262.9	185.8	C6orf32	NM_015864.2	PL48;DIFF40;DIFF48;KIAA0386			
GI_14277693-I	103	102.5	94.9	NXF2	NM_017809.2	TAPL-2;FLJ20416	protein	nucleus	protein-
GI_14277695-A	108.2	96.2	100.4	RNF17	NM_031994.1	Mmip-2			
GI_14277695-I	103.2	113.9	103.1	RNF17	NM_031994.1	Mmip-2			
GI_14277699-S	31646.9	33058	23463	RPS12	NM_001016.2		structural	cytosolic	protein
GI_14277701-A	161.7	172	187.2	APBA2BP	NM_031231.1	NIP1;XB51;EFCBP3;NECAB3;SYTIP2;dJ63M			
GI_14456711-S	106.5	120.7	114	HBA1	NM_000558.3		protein	hemoglobi	oxygen

GI_14456712-S	115.3	169.2	144.4	HBQ1	NM_005331.3		globin	hemoglobi	oxygen
GI_14550404-S	375.2	477.1	416.1	RAD18	NM_020165.2	RNF73	damaged	nucleus	response
GI_14550413-S	120	128	123.7	IRTA2	NM_031281.1	BXMAS1	receptor		
GI_14550415-S	150	181.1	168	IRTA1	NM_031282.1				
GI_14574565-A	128.7	136	117.4	AIF1	NM_032955.1	IBA1;AIF-1;IRT-1		nucleus	cell cycle
GI_14574565-I	217.7	249.6	230	AIF1	NM_032955.1	IBA1;AIF-1;IRT-1		nucleus	cell cycle
GI_14574567-I	203.2	234.1	211.4	AIF1	NM_001623.3	IBA1;AIF-1;IRT-1		nucleus	cell cycle
GI_14574569-S	150.8	175.3	142.5	BAG4	NM_004874.2	SODD;BAG-4	apoptosis		anti-
GI_14574570-S	189.9	124.2	153.4	BCL2A1	NM_004049.2	GRS;BFL1;HBPA1;BCL2L5	apoptosis		anti-
GI_14574571-S	303	284.3	298.6	BCL2L2	NM_004050.2	BCLW;BCL-W;KIAA0271	apoptosis		anti-
GI_14577915-S	99.9	111	120.9	EBI2	NM_004951.2		G-protein	integral to	virulence
GI_14577916-S	181.7	202.8	147.3	EBI3	NM_005755.2		receptor	membran	humoral
GI_14577918-S	99.2	121.6	94.3	C4A	NM_007293.1	C4S;CO4	compleme	extracellul	compleme
GI_14577920-S	87.1	97.6	88.1	C4B	NM_000592.3	C4F;CO4	compleme	extracellul	compleme
GI_14577927-S	3746.7	4378.8	2399.1	TRIM16	NM_006470.2	EBBP	transcripti	cytoplasm	
GI_14577931-I	94.8	117.7	102.1	DNAH9	NM_001372.2	DYH9;HL20;DNAL1;DNEL1;HL-	adenosine	cytoskelet	spermatog
GI_14589846-S	129.2	163	151.2	SEC61A2	NM_018144.2	FLJ10578	protein	integral to	protein
GI_14589848-S	129.4	199	143	GNGT2	NM_031498.1	GNG8;GNG9;GNGT8;G-GAMMA-8;G-	signal	heterotrim	phototrans
GI_14589850-S	479.9	633	528.4	KCNK2	NM_014217.1	TREK;TPKC1;TREK-1	outward	voltage-	potassium
GI_14589853-A	418.9	454.4	319.8	PTP4A3	NM_007079.2	PRL3;PRL-3;PRL-R	prenylated		
GI_14589855-I	99.3	113.4	90.5	PTP4A3	NM_032611.1	PRL3;PRL-3;PRL-R	prenylated		
GI_14589858-A	178.3	193.2	145.5	ASPH	NM_020164.2	BAH;HAAH;JCTN;CASQ2BP1	peptide-	endoplas	muscle
GI_14589859-I	3916.6	3794.5	2952.4	ASPH	NM_032466.1	BAH;HAAH;JCTN;CASQ2BP1	peptide-	endoplas	muscle
GI_14589865-I	181.5	198.6	168.6	ASPH	NM_004318.2	BAH;HAAH;JCTN;CASQ2BP1	peptide-	endoplas	muscle
GI_14589867-A	91.1	96.5	81.2	BLR1	NM_001716.2	CXCR5;MDR15	G-protein	integral to	G-protein
GI_14589867-I	135	152.6	131.1	BLR1	NM_001716.2	CXCR5;MDR15	G-protein	integral to	G-protein
GI_14589868-I	101.7	107.6	96.1	BLR1	NM_032966.1	CXCR5;MDR15	G-protein	integral to	G-protein
GI_14589873-A	492.3	499.5	506.1	DOM3Z	NM_032419.1	NG6;DOM3L			
GI_14589875-A	288.7	344.6	333.3	EFS	NM_032459.1	SIN;EFS1;EFS2;HEFS	cell	cytoplasm	intracellula
GI_14589877-I	196.7	225.7	201.6	EFS	NM_005864.2	SIN;EFS1;EFS2;HEFS	cell	cytoplasm	intracellula
GI_14589887-S	106.4	125.1	106.6	CDH1	NM_004360.2	UVO;CDHE;ECAD;LCAM	calcium-		
GI_14589888-S	2844.1	3461.9	3592.9	CDH2	NM_001792.2	CDHN;NCAD	cell	integral to	cell
GI_14589892-S	188.9	194.3	208.4	CDH4	NM_001794.2	CAD4;RCAD	calcium-	plasma	cell
GI_14589894-S	113.2	130.5	112.9	CDH5	NM_001795.2	7B4	calcium-	integral to	homophili
GI_14589898-S	2008	2115	2105.4	MAP2K1	NM_002755.2	MEK1;MKK1;MAPKK1;PRKMK1	MAP		chemotaxi
GI_14589899-I	93.6	119.2	132.2	MAP2K6	NM_002758.2	MEK6;MKK6;MAPKK6;PRKMK6;SAPKK3	MAP		DNA
GI_14589901-A	96.9	107.9	100.9	MAP2K6	NM_031988.1	MEK6;MKK6;MAPKK6;PRKMK6;SAPKK3	MAP		DNA
GI_14589901-I	109.2	124.2	113	MAP2K6	NM_031988.1	MEK6;MKK6;MAPKK6;PRKMK6;SAPKK3	MAP		DNA
GI_14589910-A	131	112.7	122.7	MMP28	NM_024302.2	MM28;MMP25			
GI_14589913-A	128	117.6	115.1	PCDH10	NM_020815.1	PCDH19;OL-			
GI_14589913-I	89.4	93.2	84.4	PCDH10	NM_020815.1	PCDH19;OL-			
GI_14589915-I	93.2	93.1	93.1	PCDH10	NM_032961.1	PCDH19;OL-			
GI_14589925-S	112.7	116.9	112.4	PCDH12	NM_016580.2	VECAD2;VE-cadherin-2	cell	cytoskelet	neuronal
GI_14589926-S	99.4	102.2	104.5	PCDH17	NM_014459.2	PCH68;PCDH68	calcium	membran	homophili

GI_14589930-A	200.6	258.9	226.3	PCDH7	NM_002589.2	BHPCDH;BH-Pcdh	calcium	integral to	homophili
GI_14589930-I	129.4	176.3	172.4	PCDH7	NM_002589.2	BHPCDH;BH-Pcdh	calcium	integral to	homophili
GI_14589932-I	78.5	80	73.2	PCDH7	NM_032456.1	BHPCDH;BH-Pcdh	calcium	integral to	homophili
GI_14589934-I	176.2	208.1	194.3	PCDH7	NM_032457.1	BHPCDH;BH-Pcdh	calcium	integral to	homophili
GI_14589936-A	146	186	150.5	PCDH8	NM_032949.1	PAPC;ARCADLIN	calcium-	integral to	cell-cell
GI_14589941-A	89.8	95.8	84.2	PCDH11Y	NM_032971.1	PCDHY;PCDH22			
GI_14589941-I	93.9	98.4	94.2	PCDH11Y	NM_032971.1	PCDHY;PCDH22			
GI_14589945-I	90.4	118	93.3	PCDH11Y	NM_032973.1	PCDHY;PCDH22			
GI_14589948-S	1649.8	1819.8	1601.1	POLR2A	NM_000937.2	RPB1;RPO2;POLR2;POLRA;RPBh1;RPOL2;	DNA-	DNA-	transcripti
GI_14589949-S	574.6	511.8	504.9	POLR2D	NM_004805.2	RBP4;HSRBP4;HSRPB4	DNA-	DNA-	transcripti
GI_14589950-S	2074.1	2169.6	2236.2	POLR2E	NM_002695.2	RPB5;XAP4;RPABC1;hRPB25;hsRPB5	DNA-	DNA-	transcripti
GI_14589952-S	6926	6743.4	5153.8	POLR2H	NM_006232.2	RPB8;RPB17;RPABC3;hsRPB8	DNA-	DNA-	transcripti
GI_14589954-S	1900.4	1541.6	1634.4	POLR2I	NM_006233.3	RPB9;hsRPB9;hRPB14.5	DNA-	DNA-	transcripti
GI_14589955-S	2293.2	2756.8	2592.8	POLR2K	NM_005034.2	RPB12;RPABC4;RPB7.0;hRPB7.0;hsRPB10	zinc ion	DNA-	regulation
GI_14589957-S	499.1	444.5	609.3	POLR3K	NM_016310.2	C11;RPC10;RPC11;hRPC11	DNA-	DNA-	transcripti
GI_14591901-A	462.5	550.9	438.5	RECQL	NM_032941.1	RecQ1;RECQL1	DNA	nucleus	DNA
GI_14591903-I	269.5	375.6	251.4	RECQL	NM_002907.2	RecQ1;RECQL1	DNA	nucleus	DNA
GI_14591905-S	27596	25323	22605	RPL13A	NM_012423.2		structural	large	protein
GI_14591906-S	4921.4	4166.9	2291.9	RPL17	NM_000985.2	rpL23	structural	ribosome	
GI_14591907-S	25257.9	23409	17461	RPL23	NM_000978.2	rpL17	structural	ribosome	protein
GI_14591908-S	18153.7	15942	12511	RPL5	NM_000969.2	MSTP030	structural	cytosolic	protein
GI_14591910-S	11588.8	11010	8741.8	RPS13	NM_001017.2		structural	cytosolic	protein
GI_14591911-S	4086.4	3650.3	3033.9	RPS15	NM_001018.2	RIG	structural	cytosolic	protein
GI_14591913-S	16250.4	14912	10724	RPS17	NM_001021.2	RPS17L1;RPS17L2	structural	cytosolic	protein
GI_14591914-S	23532.8	21220	17363	RPS19	NM_001022.2	DBA	structural	cytosolic	hemocyte
GI_14591915-S	24286.3	22844	18407	RPS20	NM_001023.2		structural	cytosolic	protein
GI_14591916-S	22173.9	21345	17584	RPS25	NM_001028.2		structural	cytosolic	protein
GI_14591917-S	862.6	816.3	829.9	SEC13L	NM_031216.2	Seh1;SEH1A;SEH1B	porin	mitochond	intracellula
GI_14591918-S	648.3	643	597.4	SEC22L2	NM_012430.2	SEC22A	vesicle	endoplas	ER to
GI_14591930-S	558.5	662.8	514	COG3	NM_031431.2	SEC34			
GI_14591931-S	1291.2	1819.1	1391.4	SEC61A1	NM_013336.2	HSEC61			
GI_14591932-S	868.6	1366.4	1200.2	SEC61B	NM_006808.2		protein	integral to	nonselecti
GI_14591933-S	3920.3	6027.6	3952	SEC61G	NM_014302.2	SSS1	protein	endoplas	protein
GI_14591934-S	644.9	853.7	517.3	SEC63	NM_007214.2	SEC63L;PRO2507	endoplas	endoplas	protein-
GI_14600335-S	146.5	151	141.7	PCDHB9	NM_019119.3	PCDH3H;PCDH-BETA9	calcium-	integral to	synaptoge
GI_14602425-S	1779	1694	1733.8	TLOC1	NM_003262.2	HTP1;Dtrp1;SEC62	endoplas	integral to	cotranslati
GI_14602426-I	175.7	204	186.3	ZWINT	NM_032997.1	HZwint-1		kinesin	
GI_14602428-A	294.4	276.2	390.1	ZWINT	NM_007057.2	HZwint-1		kinesin	
GI_14602440-A	99.3	104.8	106.1	WBSCR14	NM_032994.1	MIO;CHREBP;MONDOB;WS-bHLH	DNA	transcripti	embryoge
GI_14602442-A	96.7	112.4	89.4	STK31	NM_031414.2		cAMP-		protein
GI_14602442-I	100.5	120.1	117.1	STK31	NM_031414.2		cAMP-		protein
GI_14602444-I	241.9	290.3	278.7	STK31	NM_032944.1		cAMP-		protein
GI_14602451-S	4071.5	4143.1	3981.9	POLR2F	NM_021974.2	RPB6;RPABC2;hsRPB6;HRBP14.4;hRPB14.	DNA-	DNA-	transcripti
GI_14602452-I	96.3	93.9	90	TMPRSS3	NM_032401.1	DFNB8;DFNB10;ECHOS1;TADG12	trypsin	integral to	proteolysis

GI_14602454-I	216.6	287.4	260.6	TMPRSS3	NM_032404.1	DFNB8;DFNB10;ECHOS1;TADG12	trypsin	integral to	proteolysis
GI_14602456-A	127.4	161.1	124.9	TMPRSS3	NM_032405.1	DFNB8;DFNB10;ECHOS1;TADG12	trypsin	integral to	proteolysis
GI_14602456-I	167.3	208	169.4	TMPRSS3	NM_032405.1	DFNB8;DFNB10;ECHOS1;TADG12	trypsin	integral to	proteolysis
GI_14602458-S	95.9	99.9	90.4	TMPRSS2	NM_005656.2	PRSS10	serine-	integral to	proteolysis
GI_14670357-A	234.7	281.7	236.1	GTF2I	NM_033003.1	DIWS;SPIN;IB291;BAP135;BTKAP1;TFII-	protein	nucleus	transcripti
GI_14670359-I	184.7	216.6	195.1	ZNF278	NM_014323.2	ZSG;MAZR;PATZ;RIAZ;dJ400N23	protein	membran	transport
GI_14670363-A	143.5	151.5	132.5	ZNF278	NM_032051.1	ZSG;MAZR;PATZ;RIAZ;dJ400N23	protein	membran	transport
GI_14670363-I	317	281.9	266.5	ZNF278	NM_032051.1	ZSG;MAZR;PATZ;RIAZ;dJ400N23	protein	membran	transport
GI_14670367-I	105.1	95.9	98.2	PCBP4	NM_020418.2	LIP4;MCG10	nucleic	nucleus	DNA
GI_14670368-I	162.3	194.5	163.9	PCBP4	NM_033008.1	LIP4;MCG10	nucleic	nucleus	DNA
GI_14670372-A	753.1	915.6	871.9	PCBP4	NM_033010.1	LIP4;MCG10	nucleic	nucleus	DNA
GI_14670374-S	2476	2329.4	3669.4	STMN3	NM_015894.2	SCLIP		kinesin	neurogene
GI_14670378-I	250.1	313	259.3	TBL2	NM_032988.1	WBSCR13;WS-betaTRP;DKFZP43N024	molecular	cellular_co	biological_
GI_14670380-S	804.7	786.2	823.1	CENPF	NM_016343.2	CENF;PRO1779		kinetochor	regulation
GI_14670382-S	134.1	149	152.5	DAPK2	NM_014326.2	DRP-1	calmoduli	cytoplasm	induction
GI_14670384-S	1604.9	1373.2	1462.9	AATF	NM_012138.2	DED;CHE1;CHE-1	apoptosis	nucleus	anti-
GI_14670385-S	32456.2	28199	29647	RPS21	NM_001024.2		structural	cytosolic	protein
GI_14670386-I	250	320.9	283.3	BAD	NM_004322.2	BBC2;BCL2L8	protein	mitochond	apoptotic
GI_14670387-A	647.6	711.8	825.9	BAD	NM_032989.1	BBC2;BCL2L8	protein	mitochond	apoptotic
GI_14670387-I	171.7	181	176.4	BAD	NM_032989.1	BBC2;BCL2L8	protein	mitochond	apoptotic
GI_14670389-I	94.8	126.9	107.1	BAZ1B	NM_023005.2	WSTF;WBSCR9;WBSCR10	zinc ion	kinesin	transcripti
GI_14670391-A	693.7	690.3	668	BAZ1B	NM_032408.1	WSTF;WBSCR9;WBSCR10	zinc ion	kinesin	transcripti
GI_14670393-I	736.7	789.9	735.7	DEDD	NM_032998.1	DEFT;KE05;DEDD1;FLDED1;CASP8IP1	DNA	nucleolus	induction
GI_14670395-A	1113.5	1120.7	1146	DEDD	NM_004216.2	DEFT;KE05;DEDD1;FLDED1;CASP8IP1	DNA	nucleolus	induction
GI_14702160-I	107.5	111.5	106.9	CYLN2	NM_003388.3	CLIP;CLIP2;WSCR4;WBSCR4;CLIP-		microtubul	
GI_14702161-A	6204	4437	3667.1	CYLN2	NM_032421.1	CLIP;CLIP2;WSCR4;WBSCR4;CLIP-		microtubul	
GI_14702166-A	975.4	4101.7	8796.4	PLAT	NM_000931.2	TPA;T-PA	t-		proteolysis
GI_14702170-I	1583.5	1642.4	1216.9	POLR2C	NM_032940.1	RPB3;RPB31;hRPB33;hsRPB3	DNA-	DNA-	transcripti
GI_14702172-A	3398.1	3366.7	2473.1	POLR2C	NM_002694.2	RPB3;RPB31;hRPB33;hsRPB3	DNA-	DNA-	transcripti
GI_14702179-A	1487	1695.6	1455.1	WBSCR1	NM_031992.1	EIF4H;WSCR1;KIAA0038	translation	eukaryotic	regulation
GI_14702185-A	293.1	282.9	276.8	WBSCR5	NM_032464.1	LAB;NTAL;WSCR5;HSPC046;WBSCR15	DNA	nucleus	regulation
GI_14702187-I	108	116.6	105.7	WBSCR5	NM_022040.2	LAB;NTAL;WSCR5;HSPC046;WBSCR15	DNA	nucleus	regulation
GI_14717399-A	129.6	135.1	145.1	PCDHAC2	NM_031883.2	PCDH-ALPHA-C2	cell	integral to	cell
GI_14717399-I	126.3	156.4	128.9	PCDHAC2	NM_031883.2	PCDH-ALPHA-C2	cell	integral to	cell
GI_14717402-A	101	105.6	97.1	PCDHAC1	NM_031882.2	PCDH-ALPHA-C1	cell	integral to	cell
GI_14717402-I	89.9	107.4	104.2	PCDHAC1	NM_031882.2	PCDH-ALPHA-C1	cell	integral to	cell
GI_14717405-I	105.2	107.2	99.5	PCDHA9	NM_014005.3	KIAA0345;PCDH-ALPHA9	calcium	integral to	homophili
GI_14717406-S	359.4	337.1	401.2	TAF7	NM_005642.2	TAF2F;TAFII55	protein	transcripti	regulation
GI_14719417-I	266.2	308.5	261.1	TRIM5	NM_033034.1	RNF88	zinc ion	intracellula	
GI_14719419-I	97.4	101.9	92.4	CCNB3	NM_033031.1				
GI_14719421-S	205.1	255.4	233.4	LMLN	NM_033029.1	Msp;Gp63			
GI_14719425-S	226.3	275.8	259.4	GAL3ST2	NM_033036.1	GAL3ST3	transferas		
GI_14719429-S	3070.5	3035.8	3312.8	PNMA1	NM_006029.3	MA1	tumor	nucleolus	central
GI_14719432-I	100.8	86.2	84.6	LRRC2	NM_024512.2				

GI_14719826-S	104.8	126	101	COL1A1	NM_000088.2	OI4	structural	collagen	epidermal
GI_14734386-S	738.1	887.3	820	LOC90024	XM_028217.1				
GI_14758391-S	692.2	617.7	896.7	FLJ12221	XM_031342.1				
GI_14769619-S	122.7	126.9	110.2	KIAA1701	XM_042087.1				
GI_14780893-S	83.6	90.6	74.6	GPR91	NM_033050.1				
GI_14780899-S	150.7	171.5	162.1	OR2B2	NM_033057.1	OR2B9;OR6-1;hs6M1-10;dJ193B12.4	olfactory	integral to	olfaction
GI_14780901-S	479.8	381	286.1	MPP4	NM_033066.1	DLG6	protein		intracellula
GI_14780903-S	89.2	94.5	90	KLHL1	NM_020866.1	KIAA1490			
GI_14790114-A	994.7	780.9	290.5	CASP3	NM_032991.1	CPP32;SCA-1;CPP32B;APOPAIN	caspase-3		induction
GI_14790118-I	123.6	118	123.8	CASP3	NM_004346.2	CPP32;SCA-1;CPP32B;APOPAIN	caspase-3		induction
GI_14790123-I	147.4	145.4	154.7	CASP9	NM_001229.2	MCH6;APAF3;APAF-3;ICE-LAP6	caspase-9	intracellula	caspase
GI_14790127-A	471.2	527.2	767.4	CASP9	NM_032996.1	MCH6;APAF3;APAF-3;ICE-LAP6	caspase-9	intracellula	caspase
GI_14790134-S	335.5	392.7	386.2	MTERF	NM_006980.2		transcripti	mitochond	RNA
GI_14790137-S	559.9	550.6	541.5	POLRMT	NM_005035.2	APOLMT;MTRPOL	DNA-	mitochond	DNA
GI_14790142-S	31986.4	31938	24986	RPS23	NM_001025.2		structural	cytosolic	protein
GI_14790145-S	135.1	144.2	121.8	CXCL11	NM_005409.3	IP9;H174;IP-9;b-R1;I-TAC;SCYB11;SCYB9B	chemokin	extracellul	response
GI_14790148-I	115.5	141.2	119.8	TNFSF11	NM_003701.2	ODF;OPGL;sOdf;RANKL;TRANCE;hRANKL2	cytokine	extracellul	positive
GI_14790166-A	310	400	414.6	TNFRSF6B	NM_003823.2	M68;TR6;DCR3;DJ583P15.1.1	apoptosis	soluble	anti-
GI_14790166-I	129.9	126.3	103.6	TNFRSF6B	NM_003823.2	M68;TR6;DCR3;DJ583P15.1.1	apoptosis	soluble	anti-
GI_14790189-S	1087.1	907.1	854.8	SHARP	NM_015001.2	MINT;KIAA0929	nucleic	nucleus	regulation
GI_14861835-A	1416.8	1479.8	1114	ALG2	NM_033087.1	CDGIi;hALPG2;FLJ14511			
GI_14861857-S	136.2	136.1	127.2	C6orf114	NM_033069.1	ADG-90			
GI_14916436-S	260.1	275.9	221.6	Prostein	NM_033102.1	PRST			
GI_14916444-S	90.2	95.6	81.3	GALP	NM_033106.1		neuropepti	cellular_co	neuropepti
GI_14916454-S	84	96.4	82.9	PSKH2	NM_033126.1		ATP		protein
GI_14916472-S	1995.9	2445.2	2035.3	SCIN	NM_033128.1	KIAA1905			
GI_14916476-S	143.8	134.1	131.1	RGPR	NM_033127.1	KIAA1928			
GI_14916482-I	168.3	209.2	212.2	CASP6	NM_001226.2	MCH2	cysteine-		induction
GI_14916484-A	154.3	175.3	179.2	CASP6	NM_032992.1	MCH2	cysteine-		induction
GI_14916487-A	137.1	148	130.7	CASP10	NM_032974.1	MCH4;ALPS2;FLICE2	caspase-		induction
GI_14916487-I	1327.2	1455.2	1409.7	CASP10	NM_032974.1	MCH4;ALPS2;FLICE2	caspase-		induction
GI_14916493-I	80.3	88.3	85.6	RARB	NM_000965.2	HAP;RRB2;NR1B2	retinoic	nucleus	oncogene
GI_14916495-A	130.3	187.8	202.2	RARB	NM_016152.2	HAP;RRB2;NR1B2	retinoic	nucleus	oncogene
GI_14916496-A	104.6	128.6	101.2	OGN	NM_014057.2	OIF;SLRR3A;DKFZP586P2421	growth	cellular_co	biological_
GI_14916497-I	89.9	87	84.9	OGN	NM_033014.1	OIF;SLRR3A;DKFZP586P2421	growth	cellular_co	biological_
GI_14916502-A	19370.8	19972	15449	RPS24	NM_001026.2		structural	cytosolic	protein
GI_14916516-S	188.6	199.6	133.9	AP1M2	NM_005498.3	MU1B;MU-1B;HSMU1B	protein	coated pit	nonselecti
GI_14916517-S	1624	1214.1	1272.9	AP3M1	NM_012095.2		protein	lysosome	protein-
GI_14916518-S	786.5	625.9	458.5	AP3M2	NM_006803.2	P47B;AP47B;CLA20	protein	clathrin	intracellula
GI_14917108-S	2695.8	3753.1	3130.1	AP2M1	NM_004068.2	AP50;CLAPM1	vesicle	coated	nonselecti
GI_14917110-S	424.8	507.5	376.3	AP4M1	NM_004722.2	MU-4;MU-ARP2	vesicle	clathrin	vesicle-
GI_14917112-S	2134.7	2426.5	2239	SRPRB	NM_021203.2	APMCF1	GTP	signal	
GI_14917114-S	266.1	333.8	294.7	KRTHA1	NM_002277.2	HA1;hHa1	structural	intermedia	epidermal
GI_14917116-S	125.3	136.6	133	KRTHA3A	NM_004138.2	HA3I;Krt1-3;hHa3-I		kinesin	cell shape

GI_14917118-S	124.8	127.9	138.4	KRTHA4	NM_021013.3	HA4;hHa4	structural	intermedia	epidermal
GI_14917120-S	111.1	110.7	117.5	KRTHA7	NM_003770.3	HA7;hHa7	structural	cytoskelet	
GI_14971410-A	1587.5	1455	1501.1	TRIM33	NM_033020.1	PTC7;RFG7;TF1G;TIF1G;FLJ11429;KIAA11	transcripti	kinesin	regulation
GI_14971412-I	95.3	85.2	74.8	TRIM33	NM_015906.2	PTC7;RFG7;TF1G;TIF1G;FLJ11429;KIAA11	transcripti	kinesin	regulation
GI_14971414-S	380.7	617.6	708.1	TIF1	NM_003852.2	PTC6;TF1A;RNF82;TIF1A;hTIF1;TRIM24;TIF	specific	kinesin	transcripti
GI_14971416-S	1100.1	1148.3	1250	TRIM28	NM_005762.2	KAP1;TF1B;RNF96;TIF1B	transcripti	nucleus	regulation
GI_15011879-S	635	676.5	562.3	MST4	NM_016542.2	MASK			
GI_15011885-S	198.6	209.7	192.7	MGC5356	NM_024059.2				
GI_15011886-S	537	818.3	670.3	MGC5338	NM_024062.2				
GI_15011899-A	623.3	541.7	453.7	SYTL2	NM_032379.2	SLP2;CHR11SYT;FLJ20163;FLJ21219			
GI_15011899-I	98.8	93	101.1	SYTL2	NM_032379.2	SLP2;CHR11SYT;FLJ20163;FLJ21219			
GI_15011901-I	117.4	115.8	110.3	SYTL2	NM_032943.1	SLP2;CHR11SYT;FLJ20163;FLJ21219			
GI_15011911-S	125.9	140.9	122.5	CDH6	NM_004932.2	KCAD	calcium-	integral to	cell
GI_15011912-S	917.9	2155.1	1078.9	COL6A1	NM_001848.1	OPLL	collagen	microfibril	histogene
GI_15011914-I	282.2	265.4	232.2	NOLA1	NM_018983.2	GAR1	cation	membran	
GI_15011915-A	1203.7	932.7	788.1	NOLA1	NM_032993.1	GAR1	cation	membran	
GI_15011917-S	4570	5805.8	5648.7	ATP6AP2	NM_005765.2	M8-9;ATP6IP2;APT6M8-9;ATP6M8-9	hydrogen	integral to	proton
GI_15011919-S	6788.7	6549.4	7465	NOLA2	NM_017838.2	NHP2;NHP2P;FLJ20479			
GI_15011920-S	5043.6	4936.1	5404.2	NOLA3	NM_018648.2	NOP10;NOP10P	molecular	small	pseudouri
GI_15011921-S	2074.3	1706	1537	DKC1	NM_001363.2	DKC;NAP57;NOLA4;XAP101;dyskerin	RNA	nucleoplas	rRNA
GI_15011922-S	113	110	101.1	FGF19	NM_005117.2		growth		neurogene
GI_15011923-A	577.1	488.1	515.2	GTF2IRD1	NM_005685.2	GTF3;RBAP2;CREAM1;MUSTRD1;WBSCR1	transcripti	nucleus	regulation
GI_15011925-I	200	206.9	214.5	PCTK1	NM_033018.1	PCTAIRE1;PCTGAIRE	protein		protein
GI_15011927-A	847.3	1103	966.8	PCTK1	NM_033019.1	PCTAIRE1;PCTGAIRE	protein		protein
GI_15011935-S	7448.4	7417.4	6122.8	RPS26	NM_001029.2		structural	cytosolic	protein
GI_15011937-S	31234.6	26094	23936	RPS27	NM_001030.2	MPS1;MPS-1	structural	ribosome	protein
GI_15011938-S	11484.8	9659.1	7964.5	RPS28	NM_001031.2		structural	cytosolic	protein
GI_15011940-A	1959	1651.7	1253.7	TRIM4	NM_033091.1	RNF87			
GI_15011942-S	465.5	383.9	380.3	TRIM2	NM_015271.2	RNF86;KIAA0517	zinc ion	cytoplasm	biological_
GI_15011943-A	130.7	161.5	143.7	TRIM5	NM_033092.1	RNF88	zinc ion	intracellula	
GI_15011943-I	155.8	172	171.1	TRIM5	NM_033092.1	RNF88	zinc ion	intracellula	
GI_15011973-S	2729.9	1671.5	1518.5	ARHGEF2	NM_004723.2	GEF;P40;GEFH1;LFP40;GEF-	guanyl-	microtubul	cell
GI_15011975-S	176.2	212.5	127.8	ARHGEF5	NM_005435.2	P60;TIM;GEF5;TIM1	GTP		oncogene
GI_15011976-S	98.6	113.3	104.5	ARHGEF16	NM_014448.2	NBR;GEF16			
GI_15011978-A	127.3	578.2	1142.5	ARHGEF4	NM_015320.2	ASEF;GEF4;STM6;KIAA1112;DKFZp434G20			
GI_15011980-I	120.1	134	116.5	ARHGEF4	NM_032995.1	ASEF;GEF4;STM6;KIAA1112;DKFZp434G20			
GI_15022798-S	371.9	361.5	337.3	STARD10	NM_006645.1	PCTP2;CGI-52;NY-CO-28;SDCCAG28	tumor		
GI_15022800-A	563.9	797.4	977.6	HYAL2	NM_003773.2	LUCA2;LuCa-2	hyalurono	lysosome	glycosami
GI_15022800-I	94.7	92.6	72.4	HYAL2	NM_003773.2	LUCA2;LuCa-2	hyalurono	lysosome	glycosami
GI_15022816-S	99.3	106.9	109.3	KRTHA3B	NM_002279.3	HA3II;KRTHA3A;hHa3-II		kinesin	cell shape
GI_15029523-S	127.7	149.2	133	DKFZP434F1	NM_015643.1				
GI_15029525-S	200.7	227.9	233.8	DNAH8	NM_001371.1	hdhc9	axonemal	axonemal	cell
GI_15042936-S	214.4	275.6	251.3	PADI2	NM_007365.1	PDI2;KIAA0994	protein-		protein
GI_15042948-S	169.6	163.4	180	PRDM12	NM_021619.2	PFM9	DNA	nucleus	regulation

GI_15042952-S	108.6	114.7	107.7	MUC13	NM_033049.1	DRCC1;FLJ20063			
GI_15042958-A	224.7	282.5	263	SLC4A5	NM_021196.2	NBC4			
GI_15042962-S	203.8	219.7	209	DUX4	NM_033178.1		transcripti	nucleus	regulation
GI_15042964-S	314.1	407.2	298.7	OR51B4	NM_033179.1	HOR5'Beta1	olfactory	integral to	olfaction
GI_15042966-S	112.3	121.3	101.1	OR51B2	NM_033180.1	OR51B1P;HOR5'Beta3	olfactory	integral to	G-protein
GI_15055534-S	100.6	107.9	103.7	BPIL1	NM_025227.1	RYSR;LPLUNC2;dJ726C3.2	lipid		
GI_15055536-S	156.1	186.9	155.4	SCGN	NM_006998.2	SEGN;SECRET;DJ501N12.8	calcium	cytoplasm	biological_
GI_15055538-S	59473.8	55188	39023	RPS2	NM_002952.2	LLREP3	structural	cytosolic	protein
GI_15055542-S	807.4	844.9	827.4	SRP46	NM_032102.1		nucleic	nucleus	regulation
GI_15055544-A	221.7	228.3	198.3	FGF1	NM_033137.1	AFGF;ECGF;FGFA;ECGFA;ECGFB;HBGF1;	fibroblast	extracellul	embryoge
GI_15055546-I	120.2	117.5	110.6	FGF1	NM_000800.2	AFGF;ECGF;FGFA;ECGFA;ECGFB;HBGF1;	fibroblast	extracellul	embryoge
GI_15055547-S	135.8	161	151.5	FGF23	NM_020638.2	ADHR;HYPF;HPDR2	growth	extracellul	cell
GI_15055548-A	179.7	186.3	176.6	FGF5	NM_033143.1	FGF5S	fibroblast	extracellul	FGF
GI_15055550-I	98.1	130.3	110.6	FGF5	NM_004464.2	FGF5S	fibroblast	extracellul	FGF
GI_15082233-S	113.9	116.5	112.8	LDHL	NM_033195.1		L-lactate		glycolysis
GI_15082237-S	214.7	262.5	247.2	HspB9	NM_033194.1		heat		
GI_15082251-S	118.7	113.6	94.1	MGC12466	NM_033213.1		nucleic	nucleus	regulation
GI_15082255-I	123.5	140.1	137.2	LCMT1	NM_016015.2	LCMT;CGI-68	S-		protein
GI_15082260-S	113.7	111.5	88.3	WNT9A	NM_003395.1	WNT14	extracellul	extracellul	signal
GI_15100150-S	383.9	482.3	386.3	BAT5	NM_021160.1	NG26;D6S82E	catalytic	integral to	
GI_15100157-S	119.4	105.4	110.9	NYD-SP12	NM_031955.2				
GI_15100159-S	101.9	87.9	95.1	LOC84643	NM_032559.2		ATP	kinesin	microtubul
GI_15100161-S	101.2	118.8	112.9	NYD-SP21	NM_032597.2	DKFZp434H092			
GI_15100169-I	118.5	125.4	122.2	TRIM15	NM_033229.1	RNF93;ZNFB7	zinc ion	kinesin	
GI_15147227-S	1728.5	3033	5486.9	BEX1	NM_018476.2	HBEX2;HGR74-h	signal	nucleus	regulation
GI_15147233-S	124.8	141.5	127.6	CAM-KIIN	NM_033259.1				
GI_15147245-S	79.6	87.7	94.9	GNG8	NM_033258.1		signal	heterotrim	G-protein
GI_15147247-S	135.7	114.4	107	EPSTI1	NM_033255.1	BRESI1			
GI_15147249-S	444.2	384.5	420.8	PPP1R14A	NM_033256.1	CPI-17;PPP1INL			
GI_15147251-S	2005	2180.3	1342.5	SH3BP1	NM_018957.2	dJ37E16;FLJ21318			
GI_15147327-A	104	122.7	102.4	CYP2A7	NM_030589.2	CPA7;CPAD;CYPIIA7;P450-IIA4	cytochrom	membran	electron
GI_15147331-S	104.3	106.1	106.5	CYP3A5	NM_000777.2	CP35;PCN3;P450PCN3	monooxyg	microsom	steroid
GI_15147332-S	936.1	868.5	877.5	TRIM37	NM_015294.1	MUL;TEF3;KIAA0898	zinc ion	intracellula	
GI_15147334-S	257.3	247.3	248.8	NCOA5	NM_020967.1	CIA;KIAA1637;bA465L10.6		nucleus	regulation
GI_15147344-S	81.1	81.6	74.1	FGF7	NM_002009.2	KGF;HBGF-7	growth	extracellul	epidermal
GI_15147349-A	104.1	109.9	92.7	FGF8	NM_033165.1	AIGF;HBGF-8	fibroblast	cellular_co	gastrulatio
GI_15149469-S	1336.9	1216.7	1218.2	JJAZ1	NM_015355.1	CHET9;SUZ12;KIAA0160		nucleus	cell growth
GI_15149471-S	94.3	86.9	89.3	PBX4	NM_025245.1		transcripti	nucleus	regulation
GI_15149473-I	113.7	109	121.4	ABCC11	NM_033151.2	MRP8			
GI_15149477-I	144.2	145.8	129.3	COL2A1	NM_001844.3	SEDC;COL11A3	collagen	collagen	skeletal
GI_15149478-A	137.6	164	143.3	COL2A1	NM_033150.1	SEDC;COL11A3	collagen	collagen	skeletal
GI_15149480-S	101.1	110.8	95.6	COL3A1	NM_000090.2		collagen	collagen	circulation
GI_15150800-S	123.5	123.3	121.8	LOC91120	NM_033196.1				
GI_15150802-S	148.4	184.7	162.1	OPN4	NM_033282.1	MOP	G-protein	integral to	phototrans

GI_15150808-S	432.9	450.1	674.5	LOC90701	NM_033280.1		peptidase	microsom	proteolysis
GI_15187163-S	83.6	87.1	90.1	LACRT	NM_033277.1				
GI_15193291-A	172.3	207.5	208.3	NALP12	NM_033297.1	RNO2;PYPAF7			
GI_15193291-I	87.4	109	97.5	NALP12	NM_033297.1	RNO2;PYPAF7			
GI_15193293-S	4835.1	6287.7	5593.1	PGR1	NM_033296.1				
GI_15193297-S	104.5	102.3	103.7	GABRG3	NM_033223.1		extracellul	integral to	chloride
GI_15208630-S	183.3	454.7	481.4	MGC4655	NM_033309.1		galactosylt	membran	protein
GI_15208644-S	437.2	467.2	415.6	BYSL	NM_004053.2	BYSTIN	cell	cytoplasm	pregnancy
GI_15208647-A	140	135.2	144.6	CNR1	NM_033181.1	CB1;CNR;CB-R;CB1A;CANN6;CB1K5	cannabino	integral to	G-protein
GI_15208649-S	496.3	573.9	590.1	TRIM32	NM_012210.2	HT2A;TATIP;LGMD2H	transcripti	nucleus	virulence
GI_15208650-S	212.2	248.7	237.2	HYAL3	NM_003549.2	LUCA3;LUCA-3;LUCA14;Minna14	hyalurono		carbohydr
GI_15208652-S	292.2	323.3	295.7	ZNF147	NM_005082.2	EFP;Z147;RNF147;TRIM25	transcripti	kinesin	
GI_15208653-S	207.1	250.3	218	DGCR6	NM_005675.2		cell	extracellul	histogene
GI_15208655-A	761.2	811.5	898	PDGFA	NM_033023.1	PDGF1	platelet-	extracellul	cell
GI_15208659-S	331.5	365.9	395.5	SSA1	NM_003141.2	SSA;RO52;RNF81;TRIM21	ribonucleo	ribonucleo	pathogene
GI_15208661-S	870.1	1218.5	725.2	TRIM22	NM_006074.2	RNF94;STAF50;GPSTAF50	transcripti	nucleus	regulation
GI_15208662-I	129.4	156	143.5	TRIM14	NM_014788.2	KIAA0129	protein	cytoplasm	cell growth
GI_15208664-A	119.2	130.4	119.1	TRIM14	NM_033219.1	KIAA0129	protein	cytoplasm	cell growth
GI_15208666-I	115.8	123.8	125.1	TRIM14	NM_033220.1	KIAA0129	protein	cytoplasm	cell growth
GI_15277412-S	146.5	150.8	140.6	SOX6	NM_033326.1	HSSOX6	transcripti	kinesin	establish
GI_15277420-A	1151.7	988.5	903.8	UBE2J1	NM_016336.2	Ubc6p;CGI-	ubiquitin		ubiquitin
GI_15281149-S	113.3	111.5	111.7	UNKL	NM_024023.1				
GI_15426251-S	347.6	451.3	421.5	CGB8	NM_033183.1				
GI_15431284-S	137.7	131.3	111.2	ZBTB10	NM_023929.2	RINZF;FLJ12752	protein		
GI_15431286-S	344.9	447.2	421.7	LHB	NM_000894.2	CGB4;LSH-B	receptor	soluble	male
GI_15431287-S	26992.1	25290	20105	RPL10A	NM_007104.3	NEDD6;Csa-19	structural	cytosolic	embryoge
GI_15431289-S	31924.7	30887	22175	RPL11	NM_000975.2		structural	cytosolic	protein
GI_15431291-S	39601.4	32762	23163	RPL12	NM_000976.2		structural	cytosolic	protein
GI_15431292-S	15017.9	14831	11868	RPL15	NM_002948.2	EC45;RPL10;RPLY10;RPYL10	structural	ribosome	protein
GI_15431294-I	599	753.2	796.3	RPL13	NM_033251.1	BBC1;D16S444E	structural	cytosolic	protein
GI_15431296-A	10564	9637.9	7638.8	RPL13	NM_000977.2	BBC1;D16S444E	structural	cytosolic	protein
GI_15431298-S	23117.4	19597	17895	RPL18	NM_000979.2		structural	cytosolic	protein
GI_15431299-S	38947.5	33738	29026	RPL18A	NM_000980.2		structural	cytosolic	protein
GI_15431300-S	4169.3	3914.6	3209.3	RPL7	NM_000971.2		structural	cytosolic	protein
GI_15431302-S	1716	1518.8	1156.2	RPL9	NM_000661.2		structural	ribosome	protein
GI_15431304-A	7096.4	6153.5	6420.8	RPL8	NM_000973.2		structural	cytosolic	protein
GI_15431305-I	367	461.5	455.8	RPL8	NM_033301.1		structural	cytosolic	protein
GI_15431308-S	32831.3	26563	25327	RPS7	NM_001011.2		structural	cytosolic	protein
GI_15431309-S	409.2	517	431.4	KRT14	NM_000526.3	K14;CK14;EBS3;EBS4	structural	intermedia	epidermal
GI_15431311-S	87.2	92.7	94.9	KRTHA2	NM_002278.2	HA2;hHa2		kinesin	epidermal
GI_15431313-S	134.5	151.5	145.7	KRTHA5	NM_002280.3	HA5;hHa5		kinesin	embryoge
GI_15431315-S	332.3	346.3	297.1	KRTHB4	NM_033045.2	HB4;Hb-4;hHb4	structural	kinesin	biological_
GI_15431317-S	478.9	562.5	497.8	KRTHA8	NM_006771.3	HA8;hHa8	structural	intermedia	
GI_15431319-S	13786.1	11039	17263	KRTHB1	NM_002281.2	HB1;Hb-1;MLN137;ghHkb1;hHAKB2-1		kinesin	cell shape

GI_15431322-S	276.3	351.8	297.5	KRTHB3	NM_002282.2	HB3;Hb-3	serine	kinesin	epidermal
GI_15431324-S	129.6	154.7	148.8	KRTHB5	NM_002283.2	HB5;Hb-5;hHb5	structural	intermedia	epidermal
GI_15431325-S	546.9	1110.1	359.9	KRTHB6	NM_002284.2	HB6;MNX;hHb6		kinesin	
GI_15431327-I	105.4	117.5	112.1	CASP1	NM_033292.1	ICE;P45;IL1BC	thiol	intracellula	pathogene
GI_15431333-A	86.1	85.6	79.1	CASP1	NM_033295.1	ICE;P45;IL1BC	thiol	intracellula	pathogene
GI_15451747-S	113.1	129.8	106	CGB5	NM_033043.1	HCG			
GI_15451749-S	108	109.2	112	CGB7	NM_033142.1	CG-beta-a	hormone	soluble	female
GI_15451751-S	156.7	192	181.6	CGB	NM_000737.2	CGB3	hormone	soluble	female
GI_15451756-I	130.9	155.7	131	ADRA1A	NM_033302.1	ADRA1C;ADRA1L1	alpha1-	integral to	protein
GI_15451758-I	143	182	155	ADRA1A	NM_033303.1	ADRA1C;ADRA1L1	alpha1-	integral to	protein
GI_15451760-A	96.6	102	100.6	ADRA1A	NM_033304.1	ADRA1C;ADRA1L1	alpha1-	integral to	protein
GI_15451760-I	83.8	83.9	86.4	ADRA1A	NM_033304.1	ADRA1C;ADRA1L1	alpha1-	integral to	protein
GI_15451762-I	154.5	142.5	103.8	PML	NM_033238.1	MYL;RNF71;TRIM19	transcripti	nucleus	oncogene
GI_15451776-A	156.3	152.8	140.7	PML	NM_033247.1	MYL;RNF71;TRIM19	transcripti	nucleus	oncogene
GI_15451783-S	129.8	150	131.8	ADRA1B	NM_000679.2	ADRA1	alpha1-	integral to	protein
GI_15451784-S	329.1	410	345.2	ADRA1D	NM_000678.2	ADRA1;ADRA1A;ADRA1R	alpha1-	integral to	cell growth
GI_15451785-A	409.5	466.8	418.8	PDGFB	NM_033016.1	SIS;SSV;PDGF2;c-sis	platelet-	membran	response
GI_15451787-S	88.7	87.2	79.6	PDGFRA	NM_006206.2	CD140A;PDGFR2	platelet-	integral to	cell
GI_15451788-S	331.3	778.9	430.6	PDGFRB	NM_002609.2	JTK12;PDGFR;CD140B;PDGFR1;PDGF-R-	platelet-	integral to	signal
GI_15451836-I	103.3	114.5	116.2	ABCA7	NM_019112.2	ABCX;ABCA-SSN	ATP	integral to	
GI_15451837-A	108.5	133.7	133.4	ABCA7	NM_033308.1	ABCX;ABCA-SSN	ATP	integral to	
GI_15451837-I	121.2	125.8	118.3	ABCA7	NM_033308.1	ABCX;ABCA-SSN	ATP	integral to	
GI_15451841-A	122.6	127.9	128.3	ADAM19	NM_023038.2	MLTNB;FKSG34;MADDAM	zinc ion	integral to	proteolysis
GI_15451841-I	122.3	106.8	108.6	ADAM19	NM_023038.2	MLTNB;FKSG34;MADDAM	zinc ion	integral to	proteolysis
GI_15451843-I	4283.1	6794.4	5584	ADAM19	NM_033274.1	MLTNB;FKSG34;MADDAM	zinc ion	integral to	proteolysis
GI_15451847-I	127.3	148.8	128.6	NR6A1	NM_033334.1	RTR;GCNF;NR61;GCNF1	ligand-	nucleus	spermatog
GI_15451849-A	82	99.2	83.9	NR6A1	NM_033335.1	RTR;GCNF;NR61;GCNF1	ligand-	nucleus	spermatog
GI_15451851-A	491.8	702.4	581.9	MID1	NM_033290.1	OS;FXY;OSX;OGS1;XPRF;BBBG1;GBBB1;R	protein	microtubul	pattern
GI_15451851-I	100.4	104.6	120.5	MID1	NM_033290.1	OS;FXY;OSX;OGS1;XPRF;BBBG1;GBBB1;R	protein	microtubul	pattern
GI_15451855-S	1474.9	1303.1	868.3	CAV1	NM_001753.3	CAV;VIP21	structural	caveola	
GI_15451858-A	92.8	91.1	87.9	CAV3	NM_001234.3	VIP21;LGMD1C;VIP-21		caveola	muscle
GI_15451859-I	104.2	129.9	110.1	CAV3	NM_033337.1	VIP21;LGMD1C;VIP-21		caveola	muscle
GI_15451863-A	151.1	191.5	181	B3GNT1	NM_033252.1	B3GNT;B3GN-T1;B3GN-T2;B3GNT-	N-	Golgi	protein
GI_15451865-A	190.3	274	313	LRP8	NM_017522.2	APOER2;HSZ75190	LDL	plasma	lipid
GI_15451869-I	117.5	104.4	105.8	LRP8	NM_004631.2	APOER2;HSZ75190	LDL	plasma	lipid
GI_15451870-S	159.5	191.4	185	B3GALT1	NM_020981.2	beta3Gal-T1	UDP-	Golgi	protein
GI_15451871-S	99.9	90.5	86.2	B3GALT2	NM_003783.2	GLCT2;BETA3GALT2;beta3Gal-T2	UDP-	Golgi	protein
GI_15451872-S	111.6	120.6	153.8	B3GALT4	NM_003782.2	GalT4;Gal-	UDP-	Golgi	protein
GI_15451873-I	90.1	299.5	95.1	B3GALT3	NM_003781.2	P;P1;GLCT3;galT3;beta3Gal-T3	UDP-	Golgi	protein
GI_15451876-I	75.1	73.8	73.2	B3GALT3	NM_033168.1	P;P1;GLCT3;galT3;beta3Gal-T3	UDP-	Golgi	protein
GI_15451878-A	108.4	184.9	111.5	B3GALT3	NM_033169.1	P;P1;GLCT3;galT3;beta3Gal-T3	UDP-	Golgi	protein
GI_15451878-I	127.4	134.3	113	B3GALT3	NM_033169.1	P;P1;GLCT3;galT3;beta3Gal-T3	UDP-	Golgi	protein
GI_15451880-A	165.2	191.7	164.1	B3GALT5	NM_033170.1	B3T5;GLCT5;B3GalTx;B3GalT-V;beta3Gal-	UDP-	Golgi	protein
GI_15451886-I	98.2	102.8	94.7	B3GALT5	NM_033173.1	B3T5;GLCT5;B3GalTx;B3GalT-V;beta3Gal-	UDP-	Golgi	protein

GI_15451888-A	148.2	103	211.1	GAD1	NM_013445.2	GAD;GAD25;GAD67			glutamate
GI_15451888-I	331.4	274	487.8	GAD1	NM_013445.2	GAD;GAD25;GAD67			glutamate
GI_15451891-S	1647.6	2053.2	1646.9	EIF5B	NM_015904.2	IF2;FLJ10524;KIAA0741;DKFZp434I036	translation	nucleus	translation
GI_15451894-S	100.5	110.4	105.8	B3GNT3	NM_014256.2	TMEM3;B3GN-T3;B3GNT-	galactosylt	Golgi	protein
GI_15451896-I	88.1	101	87.7	CCR2	NM_000647.3	CKR2;CCR2A;CCR2B;CKR2A;CKR2B;CMKB	chemokin	soluble	negative
GI_15451899-S	186.9	238.2	217.2	FGF3	NM_005247.2	INT2;HBGF-3	growth	extracellul	embryoge
GI_15451900-S	267.5	263.5	172.9	KCNK1	NM_002245.2	DPK;HOHO;TWIK1;TWIK-1	inward	voltage-	potassium
GI_15451901-S	284.4	270.2	255.9	MAP4K3	NM_003618.2	GLK;MAPKKKK3;RAB8IPL1	protein		JNK
GI_15451903-S	127.6	164.1	143.8	MOX2	NM_005944.3	MRC;MOX1;OX-2;CD200		integral to	
GI_15451905-S	117.4	137.6	133.8	NAALAD2	NM_005467.2	NAADALASE2;NAALADASE2	dipeptidyl-	integral to	proteolysis
GI_15451906-S	835	1108.6	866.8	NPEPPS	NM_006310.2	PSA;MP100	aminopept	cytosol	proteolysis
GI_15451908-A	2362.1	1304.1	837.8	CASP4	NM_001225.2	TX;ICH-2;Mih1/TX;ICEREL-II;ICE(rel)II	thiol	cytoplasm	induction
GI_15451909-I	116.6	103.2	98.9	CASP4	NM_033306.1	TX;ICH-2;Mih1/TX;ICEREL-II;ICE(rel)II	thiol	cytoplasm	induction
GI_15451911-I	94.6	96.1	92.3	CASP4	NM_033307.1	TX;ICH-2;Mih1/TX;ICEREL-II;ICE(rel)II	thiol	cytoplasm	induction
GI_15451913-S	126.9	114.3	118.7	BAIAP3	NM_003933.3	BAP3;KIAA0734	protein C-		neurotran
GI_15451920-A	113.9	125.4	126.2	PDGFD	NM_033135.1	IEGF;MSTP036;SCDGF-B			
GI_15451924-S	5230.5	6126.4	8306.9	SPOCK	NM_004598.2	TIC1;SPOCK1;TESTICAN	proteoglyc	extracellul	cell
GI_15451925-S	151.3	181.3	165.3	PIK3C2B	NM_002646.2	C2-PI3K	phosphati	microsom	intracellula
GI_15451927-S	132.7	156.2	129.7	PIK3C2G	NM_004570.2	PI3K-C2GAMMA	1-	membran	intracellula
GI_15451928-I	139.9	125.5	123.8	CDC14A	NM_003672.2	cdc14;hCDC14;Cdc14A1;Cdc14A2	protein	nucleus	regulation
GI_15451930-I	103.4	104.5	97.5	CDC14A	NM_033312.1	cdc14;hCDC14;Cdc14A1;Cdc14A2	protein	nucleus	regulation
GI_15451932-A	107.8	112.4	100.6	CDC14A	NM_033313.1	cdc14;hCDC14;Cdc14A1;Cdc14A2	protein	nucleus	regulation
GI_15451932-I	99.3	85.3	81.7	CDC14A	NM_033313.1	cdc14;hCDC14;Cdc14A1;Cdc14A2	protein	nucleus	regulation
GI_15451934-A	120.7	133.5	123.5	CDC14B	NM_003671.2	CDC14B3;Cdc14B1;Cdc14B2;hCDC14B			
GI_15451934-I	1763.6	2355.6	1900.1	CDC14B	NM_003671.2	CDC14B3;Cdc14B1;Cdc14B2;hCDC14B			
GI_15451935-I	194.3	167.8	187.7	CDC14B	NM_033331.1	CDC14B3;Cdc14B1;Cdc14B2;hCDC14B			
GI_15451937-I	113.1	107.1	115.8	CDC14B	NM_033332.1	CDC14B3;Cdc14B1;Cdc14B2;hCDC14B			
GI_15451941-S	7415.8	7135.2	6042.7	UBA52	NM_003333.2	CEP52;RPL40;HUBCEP52	ubiquitin	cytoplasm	protein
GI_15451942-S	84.4	92.7	83.7	ZNF6	NM_021998.2	ZNF4;ZNF5;CMPX1	transcripti	nucleus	regulation
GI_15487665-A	98.6	112.7	104	NXF5	NM_033154.1		RNA	nucleus	transport
GI_15487667-I	89.1	95	99.4	NXF5	NM_033155.1		RNA	nucleus	transport
GI_15529971-S	205.9	257.1	226.5	MCART1	NM_033412.1	CG7943;MGC14836	binding	mitochond	transport
GI_15529981-S	2127.6	1989.1	2021.4	IMP4	NM_033416.1	MGC19606			
GI_15529995-S	237.1	260.4	250.7	SOS1	NM_005633.2	GF1;HGF;GGF1;GINGF	Rho		RAS
GI_15553096-S	646.8	569.3	505.5	MGC9084	NM_033418.1				
GI_15559204-S	344.9	319.2	180.7	SLAMF9	NM_033438.1	SF2001;CD2F-10;CD84-H1			
GI_15559206-S	131	131.7	112.6	ELA2A	NM_033440.1		pancreatic		proteolysis
GI_15559208-S	109	129.9	126.6	C9orf26	NM_033439.1	DVS27;NF-HEV;DKFZp586H0523			
GI_15618994-S	103.4	118	108.6	KRT6IRS	NM_033448.1	K6IRS1;KRT6IRS1		kinesin	
GI_15619000-S	436.2	522.9	514.8	CGB1	NM_033377.1				
GI_15619002-S	101.8	92.9	102.5	CGB2	NM_033378.1				
GI_15619004-S	90.4	91	102.7	KRTAP1-1	NM_030967.2	HB2A;KAP1.1;KAP1.6;KAP1.7;KAP1.1A;KAP	structural	intermedia	biological_
GI_15619005-S	215.7	243	224	VIPR1	NM_004624.2	II;HVR1;RCD1;RDC1;VIPR;VIRG;VPAC1;PA	vasoactive	integral to	positive
GI_15619007-A	137.6	131.5	125.7	VPS13A	NM_015186.1	CHAC;KIAA0986	intracellula	intracellula	protein

GI_15619007-I	85.5	104.7	86.9	VPS13A	NM_015186.1	CHAC;KIAA0986	intracellula	intracellula	protein
GI_15619009-I	287.9	363.9	302	VPS13A	NM_033305.1	CHAC;KIAA0986	intracellula	intracellula	protein
GI_15619014-S	112.1	119.1	103.7	PRKACG	NM_002732.2	KAPG	cAMP-		male
GI_15619016-I	282.7	241.5	219.7	PTPN22	NM_015967.2	LYP;Lyp1;Lyp2	protein		signal
GI_15619017-A	274.7	287.6	239.6	PTPN22	NM_012411.2	LYP;Lyp1;Lyp2	protein		signal
GI_15619017-I	91.7	91.5	86.2	PTPN22	NM_012411.2	LYP;Lyp1;Lyp2	protein		signal
GI_15627000-S	89.9	105.1	92.5	ZNF257	NM_033468.1	BMZF4;BMZF-4	zinc ion	nucleus	regulation
GI_15718669-S	93.5	90	92.5	ADRA2A	NM_000681.2	ADRA2;ADRAR;ZNF32;ADRA2R	alpha2-	integral to	activation
GI_15718672-S	150.1	151.5	149.9	ADRA2C	NM_000683.2	ADRA2L2;ADRARL2;ADRA2RL2	alpha2-	endosome	activation
GI_15718673-S	454.9	551.7	445.3	ADRB2	NM_000024.3	BAR;B2AR;ADRBR;ADRB2R	beta2-	endosome	transmem
GI_15718674-S	358.2	531.1	491.2	ALOX5AP	NM_001629.2	FLAP	enzyme	integral to	leukotrien
GI_15718677-S	2158.1	2028.7	1984.7	DGCR6L	NM_033257.2	FLJ10666	transcripti	kinesin	regulation
GI_15718678-S	249.7	303.4	266.9	INHBC	NM_005538.2	IHBC	transformi	extracellul	cell growth
GI_15718681-S	167.2	227.3	204.5	LAG3	NM_002286.4	CD223	antigen	integral to	
GI_15718683-S	439.7	562.3	673.7	SERTAD3	NM_013368.2	RBT1			
GI_15718685-S	95	101.2	114.3	RPL10	NM_006013.2	QM;NOV;DXS648;DXS648E;FLJ23544	tumor	cytosolic	
GI_15718686-S	20285.9	16704	13764	RPS3	NM_001005.2		structural	cytosolic	protein
GI_15718688-A	27936.5	24981	21840	RPS3A	NM_001006.2	FTE1	structural	cytosolic	protein
GI_15718701-A	206.1	221.9	213.8	CASP7	NM_033340.1	MCH3;CMH-1;ICE-LAP3	cysteine-	cytoplasm	apoptotic
GI_15718701-I	81	80.1	78.9	CASP7	NM_033340.1	MCH3;CMH-1;ICE-LAP3	cysteine-	cytoplasm	apoptotic
GI_15718703-I	90.7	97.4	89.5	CASP8	NM_001228.2	MACH;MCH5;FLICE	caspase-8	cytoskelet	apoptotic
GI_15718707-I	90.1	106.8	85.9	CASP8	NM_033356.1	MACH;MCH5;FLICE	caspase-8	cytoskelet	apoptotic
GI_15718709-I	86.1	92.8	97	CASP8	NM_033357.1	MACH;MCH5;FLICE	caspase-8	cytoskelet	apoptotic
GI_15718711-A	153.7	158.2	144.4	CASP8	NM_033358.1	MACH;MCH5;FLICE	caspase-8	cytoskelet	apoptotic
GI_15718713-S	103.2	105.9	91.3	HIST1H2AI	NM_003509.2	H2A/c;H2AFC			
GI_15718714-S	105	112.6	114.4	HIST1H2AK	NM_003510.2	H2A/d;H2AFD;HIST1H2AI	DNA	chromoso	nucleoso
GI_15718715-S	68.4	63.3	70.4	HIST1H2AJ	NM_021066.2	H2A/E;H2AFE;HIST1H2AK;dJ160A22.4	DNA	chromoso	nucleoso
GI_15718716-S	127	140.4	130.2	HIST1H1B	NM_005322.2	H1;H1.5;H1F5	DNA	chromoso	nucleoso
GI_15718717-S	101.6	118.6	107.4	HIST1H2AL	NM_003511.2	H2A.i;H2A/i;H2AFI;dJ193B12.9	DNA	chromoso	nucleoso
GI_15718718-S	102.8	128.3	110.6	HIST1H2AM	NM_003514.2	H2A.1;H2A/n;H2AFN;dJ193B12.1			
GI_15718719-S	140.5	168.6	157.9	HIST1H2BL	NM_003519.3	H2B/c;H2BFC;dJ97D16.4	DNA	chromoso	nucleoso
GI_15718720-S	113.4	100	109.7	HIST1H2BN	NM_003520.3	H2B/d;H2BFD;MGC9388	DNA	chromoso	nucleoso
GI_15718721-S	285.1	357.2	322.4	HIST1H2BM	NM_003521.2	H2B/e;H2BFE;dJ160A22.3	DNA	chromoso	nucleoso
GI_15718723-S	113.4	130.5	118.1	HIST1H3I	NM_003533.2	H3.f;H3/f;H3FF			
GI_15718724-S	273.2	320.7	303.2	HIST1H3J	NM_003535.2	H3/j;H3FJ			
GI_15718725-S	136.4	219.2	170.1	HIST1H3H	NM_003536.2	H3/k;H3FK;H3F1K	DNA	chromoso	nucleoso
GI_15718726-S	110.4	109.8	98	HIST1H4K	NM_003541.2	H4/D;H4FD;dJ160A22.1			
GI_15718728-S	88.7	95.4	94.9	HIST1H4L	NM_003546.2	H4.k;H4/k;H4FK			
GI_15718764-I	190.4	234.6	226	KCNK4	NM_016611.2	TRAAK;DKFZP566E164	potassium		potassium
GI_15718766-A	122.3	123.6	111.5	KCNK4	NM_033310.1	TRAAK;DKFZP566E164	potassium		potassium
GI_15718766-I	154.2	175	162.7	KCNK4	NM_033310.1	TRAAK;DKFZP566E164	potassium		potassium
GI_15718768-I	124.7	122.2	109.3	KCNK4	NM_033311.1	TRAAK;DKFZP566E164	potassium		potassium
GI_15718770-S	114.8	123.8	117.4	KCNK5	NM_003740.2	TASK2;TASK-2;FLJ11035	potassium	membran	potassium
GI_15718773-S	414.5	545.6	564.1	SPA17	NM_017425.2	SP17;SP17-1	cAMP-	membran	fertilization

GI_15721936-S	2505.6	2752.1	2572.5	MRPS24	NM_032014.1	HSPC335;MRP-S24			
GI_15723369-S	125.3	135	120.2	SLC38A5	NM_033518.1	SN2;JM24			
GI_15723373-S	98.7	109.6	88	sdolf	NM_033519.1		olfactory	integral to	olfaction
GI_15743546-S	937	792.6	668.9	NOL7	NM_016167.3	RARG-1;dJ223E5.2			
GI_15743547-S	96.2	110.2	92.7	LIMS3	NM_033514.1				
GI_15743557-S	147.7	184.9	158.9	KRTAP2-4	NM_033184.2	KAP2.4;KRTAP2.4			
GI_15812177-S	251.4	219.1	209.5	ZFP36L2	NM_006887.3	BRF2;ERF2;ERF-2;TIS11D	transcripti	nucleus	oncogene
GI_15812179-S	22079.1	15543	8170.6	ZFP36L1	NM_004926.2	BRF1;ERF1;cMG1;ERF-1;Berg36;TIS11B	transcripti	nucleus	
GI_15812181-S	124.6	138.7	129.7	ADAM20	NM_003814.3		metallope	integral to	fertilization
GI_15812182-S	117	113.9	95.7	ADAM21	NM_003813.2	ADAM31	metallope	integral to	fertilization
GI_15812185-I	218.2	283.3	308.9	FBXO3	NM_012175.2	FBA;FBX3;DKFZp564B092	ubiquitin		proteolysis
GI_15812187-A	295.3	404.3	434.4	FBXO3	NM_033406.1	FBA;FBX3;DKFZp564B092	ubiquitin		proteolysis
GI_15812187-I	109.7	119	98.5	FBXO3	NM_033406.1	FBA;FBX3;DKFZp564B092	ubiquitin		proteolysis
GI_15812190-S	1080.2	674.3	692	FBXO5	NM_012177.2	EMI1;FBX5	ubiquitin		proteolysis
GI_15812191-S	222.2	202	232.8	FBXO6	NM_018438.2	FBG2;FBX6	ubiquitin		proteolysis
GI_15812192-S	1407.5	1749.1	1767	FBXO7	NM_012179.2	FBX;FBX7;FBX07	ubiquitin-	ubiquitin	ubiquitin-
GI_15812194-A	121.8	106.1	108.1	FBXO24	NM_012172.2	FBX24;DKFZp434I1122	ubiquitin-	ubiquitin	protein
GI_15812195-I	123.1	143	138.5	FBXO24	NM_033506.1	FBX24;DKFZp434I1122	ubiquitin-	ubiquitin	protein
GI_15812197-S	353.8	479.3	412.7	FBXO2	NM_012168.2	FBG1;FBX2;NFB42	ubiquitin		proteolysis
GI_15812199-A	1301.2	1369.6	1383.8	FBXO9	NM_012347.2	FBX9;NY-REN-57;DKFZp434C0118			
GI_15812199-I	74.2	70.6	63.9	FBXO9	NM_012347.2	FBX9;NY-REN-57;DKFZp434C0118			
GI_15812200-I	94.7	102.6	90.9	FBXO9	NM_033480.1	FBX9;NY-REN-57;DKFZp434C0118			
GI_15812202-I	131.5	127.8	126.4	FBXO9	NM_033481.1	FBX9;NY-REN-57;DKFZp434C0118			
GI_15812204-S	91.7	94.1	100	KRTAP3-2	NM_031959.2	KAP3.2;KRTAP3.2		intermedia	
GI_15812205-S	89.2	80.6	88	KRTAP3-3	NM_033185.2	KAP3.3;KRTAP3.3		intermedia	
GI_15812207-S	1093.9	1038	1282.3	FBXO8	NM_012180.1	FBS;DC10;FBX8	ubiquitin	ubiquitin	proteolysis
GI_15812211-A	112.3	126.6	123	PDE5A	NM_033430.1	CN5A;PDE5;PDE5A1;CGB-PDE	3',5'-cyclic-	cellular_co	cyclic
GI_15812215-I	113.3	112.4	94.4	PDE5A	NM_033437.1	CN5A;PDE5;PDE5A1;CGB-PDE	3',5'-cyclic-	cellular_co	cyclic
GI_15812217-S	173.2	204.5	185.1	RBM8A	NM_005105.2	Y14;RBM8;ZNRP;RBM8B;ZRNP1;BOV-	mRNA	cytoplasm	RNA
GI_15812218-S	13746.4	12051	9780.2	RPL30	NM_000989.2		structural	cytosolic	protein
GI_15812219-S	29261.4	26115	20609	RPL31	NM_000993.2		structural	cytosolic	protein
GI_15812220-S	23694.3	23802	18069	RPL32	NM_000994.2		structural	cytosolic	protein
GI_15812223-A	419.8	516.1	387.7	TRERF1	NM_033501.1	RAPA;TReP-132;HSA277276;dJ139D8.5			
GI_15812225-I	170	197.7	168.3	TRERF1	NM_033502.1	RAPA;TReP-132;HSA277276;dJ139D8.5			
GI_15834618-A	134.2	155.3	127.6	FBXO4	NM_012176.1	FBX4;FLJ10141;DKFZp547N213			
GI_15834618-I	493.8	461.2	396.8	FBXO4	NM_012176.1	FBX4;FLJ10141;DKFZp547N213			
GI_15834620-I	105.3	100.8	98.3	FBXO4	NM_033484.1	FBX4;FLJ10141;DKFZp547N213			
GI_15834622-S	171.8	219.8	175.2	SLPI	NM_003064.2	ALP;ALK1;BLPI;HUSI;WAP4;WFDC4;HUSI-I	endopepti		
GI_15834623-S	1802.1	1446.1	1360	SRPK1	NM_003137.2	SFRSK1	cell cycle	nucleus	RNA
GI_15887357-S	95.5	101	89	GUCA1B	NM_002098.2	GCAP2;GUCA2	calcium		receptor
GI_15890082-S	141.4	155.9	148.1	REST	NM_005612.3	XBR;NRSF			
GI_15890083-S	98.7	96.1	76	COL4A4	NM_000092.2	CA44	collagen	collagen	regulation
GI_15890084-A	691.9	1606.6	1386.1	COL4A5	NM_000495.3	ATS;ASLN;CA54	collagen	collagen	
GI_15967154-I	215	328	435	SCAND1	NM_016558.2	RAZ1;SDP1	transcripti	nucleus	regulation

GI_15967155-A	1045.9	1713.1	2110.2	SCAND1	NM_033630.1	RAZ1;SDP1	transcripti	nucleus	regulation
GI_15967157-I	87.1	90.4	78.1	GCK	NM_000162.2	GK;GLK;HK4;HKIV;HXKP;MODY2;NIDDM	glucokinas		glycolysis
GI_15967158-A	152.5	160.6	149	GCK	NM_033507.1	GK;GLK;HK4;HKIV;HXKP;MODY2;NIDDM	glucokinas		glycolysis
GI_15967160-I	121	135.4	122.4	GCK	NM_033508.1	GK;GLK;HK4;HKIV;HXKP;MODY2;NIDDM	glucokinas		glycolysis
GI_15991812-S	97.9	114.1	100	MMEL2	NM_033467.1	NL2	metallope	membran	proteolysis
GI_15991814-I	92.3	93	87.8	SCAND2	NM_022050.2		molecular	nucleus	regulation
GI_15991816-I	93.8	96.8	92.1	SCAND2	NM_033633.1		molecular	nucleus	regulation
GI_15991818-I	103.3	102	100.8	SCAND2	NM_033634.1		molecular	nucleus	regulation
GI_15991820-A	118.8	128.9	118.6	SCAND2	NM_033635.1		molecular	nucleus	regulation
GI_15991824-I	114.7	135	119.5	SCAND2	NM_033640.1		molecular	nucleus	regulation
GI_15991826-I	118.7	120.3	113.5	HK1	NM_033496.1	HKI;HXK1	hexokinas	membran	glycolysis
GI_15991832-I	84.8	92	89.4	HK1	NM_033500.1	HKI;HXK1	hexokinas	membran	glycolysis
GI_16117774-S	161.3	192.5	174	R29124_1	NM_033543.1	FLJ13540			
GI_16117776-S	87.4	100.6	82.6	RGS8	NM_033345.1		signal		signal
GI_16117778-A	461.7	468.6	433.9	FBXW7	NM_018315.2	AGO;CDC4;FBW7;FBX30;FBXW6;SEL10;SE			
GI_16117778-I	124.6	125.1	117.8	FBXW7	NM_018315.2	AGO;CDC4;FBW7;FBX30;FBXW6;SEL10;SE			
GI_16117780-I	272.8	299.8	274.5	FBXW7	NM_033632.1	AGO;CDC4;FBW7;FBX30;FBXW6;SEL10;SE			
GI_16117786-A	632.9	889.9	654.3	RPL34	NM_000995.2		structural	cytosolic	protein
GI_16117788-I	1137.9	1570.6	1209.4	RPL34	NM_033625.1		structural	cytosolic	protein
GI_16117790-S	31893.6	30889	23885	RPL35A	NM_000996.2		structural	cytosolic	protein
GI_16117792-S	41467.1	36165	28536	RPL35	NM_007209.2		structural	cytosolic	protein
GI_16117793-I	266.9	314.8	337.3	RPL36	NM_015414.2	DKFZP566B023	structural	cytosolic	protein
GI_16117795-A	27158.5	22326	20164	RPL36	NM_033643.1	DKFZP566B023	structural	cytosolic	protein
GI_16118221-S	142	157.9	155	KRTAP4-10	NM_033060.2	KAP4.10;KRTAP4.10		intermedia	
GI_16118222-S	96.2	116	103	KRTAP4-14	NM_033059.2	KAP4.14;KRTAP4.14	receptor	intermedia	
GI_16118223-S	159.9	174.1	148.3	KRTAP4-2	NM_033062.2	KAP4.2;KRTAP4.2	receptor	intermedia	
GI_16118224-S	154.7	185.7	163.1	KRTAP4-5	NM_033188.2	KAP4.5;KRTAP4.5	sugar	intermedia	
GI_16118226-S	103.7	111.2	111.8	KRTAP4-7	NM_033061.2	KAP4.7;KRTAP4.7		intermedia	
GI_16118228-S	163.9	194.2	169.3	KRTAP9-4	NM_033191.2	KAP9.4;KRTAP9.4		intermedia	
GI_16118230-A	137.8	142.3	117.2	KCNK7	NM_033347.1	TWIK3	potassium	membran	potassium
GI_16118236-S	79.1	105	86.8	KRTAP4-12	NM_031854.2	KAP4.12;KRTAP4.12		intermedia	
GI_16118239-S	105.8	108.5	97.8	KRTAP9-2	NM_031961.2	KAP9.2;KRTAP9.2			
GI_16118241-S	105.8	118.9	107.5	KRTAP9-3	NM_031962.2	KAP9.3;KRTAP9.3	receptor	intermedia	
GI_16157523-S	128.1	132.2	120.6	DKFZp762K2	XM_048721.2				
GI_16159362-S	919	222.4	275.3	NEDL2	XM_038999.2				
GI_16262451-S	149.9	173.6	130.4	CGN	NM_020770.1	KIAA1319	actin	kinesin	biological_
GI_16306478-S	485.4	572.6	735.5	TSGA14	NM_018718.1	DKFZp762H1311			
GI_16306484-S	96.5	106.6	91.8	PALMD	NM_017734.2	PALML;C1orf11;FLJ20271			
GI_16306485-S	157.8	175.7	152.5	RBAK	NM_021163.2		nucleic	nucleus	regulation
GI_16306486-A	99.5	99.5	100.2	CDH7	NM_033646.1	CDH7L1	calcium	integral to	homophili
GI_16306486-I	136.9	150.2	132.7	CDH7	NM_033646.1	CDH7L1	calcium	integral to	homophili
GI_16306488-I	108.2	106.6	97.2	CDH7	NM_004361.2	CDH7L1	calcium	integral to	homophili
GI_16306490-I	261.3	303.6	355.9	CDC2	NM_001786.2	CDK1	cyclin-	nucleus	start
GI_16306493-I	102.8	104.6	89.4	FBXW1B	NM_012300.1	BTRC2;FBW1B;BTRCP2;KIAA0696	ubiquitin-	ubiquitin	protein

GI_16306495-I	95.7	96.5	93.2	FBXW1B	NM_033644.1	BTRC2;FBW1B;BTRCP2;KIAA0696	ubiquitin-	ubiquitin	protein
GI_16306497-A	2349.4	2680.5	2177.5	FBXW1B	NM_033645.1	BTRC2;FBW1B;BTRCP2;KIAA0696	ubiquitin-	ubiquitin	protein
GI_16306499-A	1213.7	1508.7	1389.6	FBXO21	NM_015002.1	FBX21;KIAA0875;DKFZp434G058			
GI_16306505-S	304.2	317.4	336.9	CASP8AP2	NM_012115.2	CED-4;FLASH;RIP25;FLJ11208;KIAA1315	death		induction
GI_16306508-S	145.9	505.8	444.7	CASPR3	NM_033655.1	FLJ14195;KIAA1714			
GI_16306524-A	113.7	109.3	106.7	CCNB3	NM_033670.1				
GI_16306528-S	108.6	137.9	161.4	CCNA1	NM_003914.2		cyclin-	cytosol	male
GI_16306529-S	114	151.9	137.5	CDH10	NM_006727.2		calcium-	integral to	homophili
GI_16306531-A	137.4	1389.9	488.6	CDH11	NM_001797.2	OB;CAD11;CDHOB;OSF-4	calcium-	integral to	skeletal
GI_16306533-I	134	172.8	146.2	CDH11	NM_033664.1	OB;CAD11;CDHOB;OSF-4	calcium-	integral to	skeletal
GI_16306535-S	131.8	132.6	124.3	CDH19	NM_021153.2	CDH7;CDH7L2	calcium	integral to	homophili
GI_16306536-S	105.1	121.8	108.3	CDH20	NM_031891.2	Cdh7;CDH7L3	calcium	integral to	homophili
GI_16306538-S	95.6	88.7	103.4	CDH8	NM_001796.2		calcium-	integral to	cell
GI_16306540-S	124.5	143.5	128.1	CDH9	NM_016279.2		calcium	integral to	homophili
GI_16306542-A	123.4	99.9	147.1	FGF13	NM_033642.1	FGF2;FHF2	growth	extracellul	signal
GI_16306542-I	93.6	104	103.1	FGF13	NM_033642.1	FGF2;FHF2	growth	extracellul	signal
GI_16306544-I	111.3	114.6	104.9	FGF13	NM_004114.2	FGF2;FHF2	growth	extracellul	signal
GI_16306545-A	138.3	170.2	142.3	FGF18	NM_033649.1	ZFGF5;FGF-18	growth	extracellul	positive
GI_16306547-S	8080.9	7618.1	5880.3	SARS	NM_006513.2	SERS;SERRS	serine-	soluble	tRNA
GI_16306549-S	108.4	110.8	106.9	SELENBP1	NM_003944.2	LPSB;SP56;hSBP;hSP56;FLJ13813	selenium		
GI_16306551-S	257.5	308.5	281.9	SEMA6C	NM_030913.2	SEMAY;KIAA1869;m-Sema Y;m-Sema-Y		integral to	neurogene
GI_16306554-S	111.4	162.9	125.6	KCNK13	NM_022054.2	THIK1;THIK-1	voltage-	integral to	potassium
GI_16306560-S	13304.5	11597	9166.5	RPL37	NM_000997.2		structural	cytosolic	protein
GI_16306561-S	29378.1	25668	20501	RPL37A	NM_000998.2		structural	cytosolic	protein
GI_16306562-S	26851.6	23718	20132	RPL38	NM_000999.2		structural	cytosolic	protein
GI_16306563-S	20860.9	19259	16315	RPL39	NM_001000.2		structural	cytosolic	protein
GI_16306565-S	161.2	198.2	161.6	HIST1H2BO	NM_003527.4	H2B.2;H2B/n;H2BFN;dJ193B12.2	DNA	chromoso	nucleoso
GI_16306567-S	86.1	97.9	102	PAPOLG	NM_022894.2	FLJ11805;FLJ12972;FLJ13482;FLJ14187	RNA	nucleus	transcripti
GI_16306569-S	1096.6	1071.5	1068	MAPK6	NM_002748.2	ERK3;PRKM6;p97MAPK;HsT17250	protein		protein
GI_16306577-A	245.5	348.6	288.8	FBXL6	NM_024555.2	FBL6;FLJ22888	ubiquitin		proteolysis
GI_16306579-S	322.3	409	336.9	FBXL11	NM_012308.1	FBL7;CXXC8;FBL11;LILINA;FLJ00115;KIAA	zinc ion		electron
GI_16306581-S	264.3	307.7	293.6	FBXL2	NM_012157.2	FBL2;FBL3;DKFZP564P0622	protein	cytoplasm	proteolysis
GI_16306583-S	336.7	344.6	291	FBXL3A	NM_012158.1	FBL3;FBL3A	ubiquitin	ubiquitin	ubiquitin-
GI_16306585-S	125	116	116.6	FBXL3B	NM_012159.1	FBL3B	ubiquitin	ubiquitin	ubiquitin-
GI_16306590-S	148.8	200	182.2	FBXL9	NM_012163.1	FBL9	ubiquitin		proteolysis
GI_16306592-S	149.3	213.9	163.7	HIST1H4J	NM_021968.3	H4/E;H4FE;dJ160A22.2			
GI_16306593-A	128.2	190.4	185.4	SKP2	NM_032637.2	FBL1;FLB1;FBXL1;MGC1366			G1/S
GI_16306593-I	487.2	781.4	791.9	SKP2	NM_032637.2	FBL1;FLB1;FBXL1;MGC1366			G1/S
GI_16306594-I	114.7	130.3	115.9	SKP2	NM_005983.2	FBL1;FLB1;FBXL1;MGC1366			G1/S
GI_16332359-A	408.4	482	486	CDC2L1	NM_033487.1	p58;PK58;CLK-1;p58CLK-1;p58CDC2L1	tumor	cytoplasm	protein
GI_16357469-S	145.4	154.9	154.8	CDC6	NM_001254.2	CDC18L;HsCDC6;HsCDC18	nucleotide	cytoplasm	negative
GI_16357470-I	884.7	887.3	573.4	CDC42	NM_001791.2	G25K;CDC42Hs	Rho small	filopodium	actin
GI_16357471-A	1006.1	1365.3	697.6	CDC42	NM_044472.1	G25K;CDC42Hs	Rho small	filopodium	actin
GI_16357471-I	90.6	109.6	127.6	CDC42	NM_044472.1	G25K;CDC42Hs	Rho small	filopodium	actin

GI_16357473-S	408.7	487.4	408.3	CDC42BPB	NM_006035.2	MRCKB;KIAA1124	protein	cytoskelet	regulation
GI_16357476-S	638.4	598.2	675.6	CDC34	NM_004359.1	UBE2R1;E2-CDC34	ubiquitin	nucleus	DNA
GI_16357489-A	86.3	94.6	88.9	CDC2L2	NM_033534.1	CDC2L3;p58GTA;PITSLRE	protein-	nucleus	mitosis
GI_16357499-S	1000.4	1020.7	1109.5	CDC5L	NM_001253.2	hCDC5;PCDC5RP;KIAA0432	DNA	nucleus	cytokinesi
GI_16357500-A	88.8	88.6	91	COL4A6	NM_001847.1		collagen	collagen	oncogene
GI_16357500-I	261.5	303.4	274.6	COL4A6	NM_001847.1		collagen	collagen	oncogene
GI_16357502-I	97.5	121.3	92.5	COL4A6	NM_033641.1		collagen	collagen	oncogene
GI_16418033-S	130.7	185.6	90.1	CG018	NM_052818.1				
GI_16418350-S	540.1	586.8	582.8	MGC20255	NM_052848.1		DNA	nucleus	regulation
GI_16418354-S	213.4	316.2	239.6	CREB3L1	NM_052854.1	OASIS	transcripti	nucleus	regulation
GI_16418362-S	198.6	204.4	217.2	MGC21675	NM_052861.1				
GI_16418366-S	110.1	113	97.2	SCGB3A1	NM_052863.1	HIN1;HIN-1;LU105;UGRP2;PnSP-2	cytokine	extracellul	negative
GI_16418370-S	79.9	92.6	78.8	SNAG1	NM_052870.1	SNX18	protein	Golgi	intracellula
GI_16418372-S	96	116.3	94.8	MGC4677	NM_052871.1				
GI_16418376-S	596.5	779	667.2	MGC16028	NM_052873.1				
GI_16418378-S	106.6	112.2	109.6	STX1B2	NM_052874.1				
GI_16418390-S	100.3	87.3	89.7	ZIM3	NM_052882.1		DNA	nucleus	regulation
GI_16418392-S	109.9	108.2	118.2	SIGLEC11	NM_052884.1		lectin [goid	integral to	cell
GI_16418394-S	153.8	175	151.2	SLC2A13	NM_052885.1	HMIT	transporte	integral to	carbohydr
GI_16418396-S	106.8	105.9	101	MAL2	NM_052886.1		transporte	synaptic	transport
GI_16418400-S	224.6	238	203.8	LOC114659	NM_052888.1				
GI_16418404-S	116.9	116.5	109.3	PGLYRP3	NM_052891.1	PGRPIA	protein	membran	peptidogly
GI_16418408-S	3232.8	4238.4	2902.7	PORIMIN	NM_052932.1	KCT3			
GI_16418432-S	424.9	887.9	164.4	HAK	NM_052947.1		protein		protein
GI_16418442-S	137.6	164.1	159.7	DIRC1	NM_052952.1				
GI_16418446-S	88	96.5	94.4	CYYR1	NM_052954.1	C21orf95	molecular	integral to	biological_
GI_16418448-S	108.9	111.1	112.9	BUCS1	NM_052956.1	MACS1			
GI_16418450-S	97.6	108.1	91.4	VEST1	NM_052958.1				
GI_16418454-S	107.1	91.4	106.6	RBP7	NM_052960.1	CRBP4;CRBPIV	lipid		transport
GI_16418460-S	396.7	280.7	259.8	TOP1MT	NM_052963.1		DNA	mitochond	DNA
GI_16418462-S	98	96.6	102.8	MAS1L	NM_052967.1	MRG;MAS-L;dJ994E9.2	rhodopsin-	integral to	G-protein
GI_16418464-S	111.3	98.7	100.9	LEAP-2	NM_052971.1				xenobiotic
GI_16418466-S	229.5	253.2	165.9	LRG1	NM_052972.1	LRG	molecular	membran	biological_
GI_16445028-S	321.7	423.4	416	IGSF8	NM_052868.1	EWI2;PGRL;CD81P3			
GI_16445034-S	103	112	103.7	TGM7	NM_052955.1	TGMZ	acyltransf		peptide
GI_16445349-A	88.1	89.8	80.5	TRIM15	NM_052812.1	RNF93;ZNFB7	zinc ion	kinesin	
GI_16445351-I	104.6	100.7	86.4	TRIM31	NM_007028.2	RNF;HCG1;HCGI;C6orf13			
GI_16445353-A	244.3	284.7	232.9	TRIM31	NM_052816.1	RNF;HCG1;HCGI;C6orf13			
GI_16445355-S	1315.3	1194.6	1222.7	MGC19595	NM_033415.2	R30923_1			
GI_16445392-S	101.8	103.6	103.5	CDH12	NM_004061.2	CDHB	calcium	integral to	homophili
GI_16445394-S	91.4	88.7	88.2	CDH18	NM_004934.2	CDH14;CDH24;CDH14L;EY-CADHERIN	calcium-	integral to	homophili
GI_16445399-A	226.3	264.1	242.8	DRD3	NM_033660.1	D3DR	dopamine	integral to	dopamine
GI_16445404-S	106.5	107.6	100.2	DRD1	NM_000794.2	DADR;DRD1A	dopamine	cell [goid	dopamine
GI_16445406-S	110.4	118	100.8	KCNK9	NM_016601.2	KT3.2;TASK3;TASK-3	voltage-	integral to	potassium

GI_16445407-I	83.1	101.5	91.4	MID2	NM_012216.2	FXY2;RNF60;TRIM1		microtubul	embryoge
GI_16445408-A	157.2	166.8	168.1	MID2	NM_052817.1	FXY2;RNF60;TRIM1		microtubul	embryoge
GI_16445410-A	1262.8	1206.7	1143.9	RFP2	NM_005798.2	CAR;LEU5;RNF77;TRIM13	tumor	kinesin	embryoge
GI_16445411-I	222.5	279.4	269	RFP2	NM_052811.1	CAR;LEU5;RNF77;TRIM13	tumor	kinesin	embryoge
GI_16445417-S	454.4	486.8	512.7	SCAMP2	NM_005697.3		protein	integral to	post-Golgi
GI_16445418-I	612.9	798.8	897.3	SCAMP3	NM_005698.2	C1ORF3;PROPIN1;Propin 1	protein	integral to	post-Golgi
GI_16445420-A	6006.6	6820.7	7793.8	SCAMP3	NM_052837.1	C1ORF3;PROPIN1;Propin 1	protein	integral to	post-Golgi
GI_16445423-S	1667.2	1363.3	1268.8	WDR12	NM_018256.2	YTM1;FLJ10881;FLJ12719;FLJ12720			
GI_16445433-S	850.7	774	668.9	WDR8	NM_017818.2	FLJ20430			
GI_16445440-S	278.5	309	317.1	TRIM26	NM_003449.2	AFP;RNF95;ZNF173	protein	kinesin	
GI_16506284-S	111.8	95.7	101.7	NY-BR-1	NM_052997.1		aspartic-	nucleus	proteolysis
GI_16506290-S	156.8	174.1	157.1	OSR2	NM_053001.1		electron		electron
GI_16506300-S	4379.9	2583.7	1501.3	TIGA1	NM_053000.1				
GI_16506819-S	1161.8	479.5	314.7	C1orf17	NM_015101.1	KIAA0584			lipopolysa
GI_16506825-A	91.6	91.8	87.1	SIGLECL1	NM_033329.1	S2V;SLG;FLJ38600	lectin [goid	integral to	cell
GI_16506825-I	197.1	212.1	180.6	SIGLECL1	NM_033329.1	S2V;SLG;FLJ38600	lectin [goid	integral to	cell
GI_16507197-S	199.2	168.2	167.5	ZNF291	NM_020843.1	MSTP063;KIAA1454			
GI_16507203-S	549.4	652.6	835	UHRF1	NM_013282.2	Np95;ICBP90;RNF106;FLJ21925	RNA		regulation
GI_16507207-S	277	311.2	311.1	CIC	NM_015125.2	KIAA0306	transporte		transport
GI_16507234-S	101.6	109.4	100.1	DNAH11	NM_003777.1	DNHBL;DPL11;DNAHBL;DNAHC11	axonemal	axonemal	cell
GI_16507949-S	119.8	120.1	101.9	TEKT2	NM_014466.2	h-tektin-t	structural	kinesin	microtubul
GI_16507951-S	109.8	159	124.8	CARD11	NM_032415.2	BIMP3;CARMA1	apoptosis	intracellula	intracellula
GI_16507953-I	115.2	146.9	135.2	CARD14	NM_024110.2	BIMP2;CARMA2	protein	kinesin	intracellula
GI_16507954-A	96.5	113.5	92.4	CARD14	NM_052819.1	BIMP2;CARMA2	protein	kinesin	intracellula
GI_16507954-I	227.1	290.7	245.9	CARD14	NM_052819.1	BIMP2;CARMA2	protein	kinesin	intracellula
GI_16507956-S	615.5	626.9	645.8	CDH13	NM_001257.2	CDHH	tumor	membran	cell
GI_16507957-S	287.7	458	320.5	CDH15	NM_004933.2	CDH3;CDHM;MCAD;CDH14	cell	integral to	cell
GI_16507958-S	112.1	116.8	113.7	CDH16	NM_004062.2		calcium-	integral to	cell
GI_16507959-S	118.1	125.4	111.1	CDH17	NM_004063.2	HPT1;CDH16;HPT-1	calcium-	membran	small
GI_16507961-I	254	326.9	275.9	CDH23	NM_022124.2	USH1D;DFNB12;KIAA1774;KIAA1812;DKFZ			
GI_16507963-A	101.4	118.4	106.5	CDH23	NM_052836.1	USH1D;DFNB12;KIAA1774;KIAA1812;DKFZ			
GI_16507963-I	106.1	113.8	114.1	CDH23	NM_052836.1	USH1D;DFNB12;KIAA1774;KIAA1812;DKFZ			
GI_16507965-S	37301.6	36592	32032	ENO1	NM_001428.2	NNE;PPH;MPB1;MBP-1;ENO1L1	phosphop		negative
GI_16507966-S	959.6	1085	544.1	ENO2	NM_001975.2	NSE	phosphop	phosphop	glycolysis
GI_16507967-S	88.9	104	103.2	KCNK15	NM_022358.2	KT3.3;TASK5;KCNK11;KCNK14;TASK-	voltage-	integral to	potassium
GI_16507968-S	22378.6	20595	15951	RPL3	NM_000967.2	TARBP-B	structural	cytosolic	protein
GI_16519560-I	102	100.9	107.9	TRIM10	NM_052828.1	RNF9;HERF1;RFB30	transcripti	kinesin	mesoderm
GI_16519562-A	183.8	218.4	188.8	TRIM10	NM_006778.2	RNF9;HERF1;RFB30	transcripti	kinesin	mesoderm
GI_16519562-I	103.3	110	105.3	TRIM10	NM_006778.2	RNF9;HERF1;RFB30	transcripti	kinesin	mesoderm
GI_16519563-A	108.6	105.7	106.6	EEF1B2	NM_021121.2	EF1B;EEF1B;EEF1B1	translation	eukaryotic	translation
GI_16519563-I	1141.1	1653.6	1286.2	EEF1B2	NM_021121.2	EF1B;EEF1B;EEF1B1	translation	eukaryotic	translation
GI_16519564-I	4033.9	4010	2827.5	EEF1B2	NM_001959.2	EF1B;EEF1B;EEF1B1	translation	eukaryotic	translation
GI_16554557-I	81.8	88.8	85.6	CARD9	NM_022352.2		apoptosis	kinesin	apoptosis
GI_16554563-S	156.3	181.9	173.7	CARD6	NM_032587.2	CINCIN1	apoptosis	intracellula	apoptosis

GI_16554565-I	170.8	202.6	204.4	CCNDBP1	NM_012142.2	DIP1;GCIP			
GI_16554567-A	836.9	940.5	1267.4	CCNDBP1	NM_037370.1	DIP1;GCIP			
GI_16554567-I	246.3	323.5	274.4	CCNDBP1	NM_037370.1	DIP1;GCIP			
GI_16554575-S	1617	1439.2	1621.1	CDC23	NM_004661.2	APC8		anaphase-	mitotic
GI_16554576-S	678.3	960.6	833.5	CDC27	NM_001256.2	APC3;HNUC;D0S1430E;D17S978E		centrosom	mitotic
GI_16554578-S	1239.6	3212.5	814.4	COL5A1	NM_000093.2		collagen	collagen	cell
GI_16554580-S	126.8	162.8	143.5	COL5A2	NM_000393.2		extracellul	collagen	cell growth
GI_16554581-S	314.4	556.7	344.3	COL5A3	NM_015719.2		collagen	collagen	muscle
GI_16554582-I	261.7	302.9	278.4	CORO2A	NM_003389.2	IR10;WDR2;CLIPINB	protein	kinesin	intracellula
GI_16554586-I	182.2	214.4	216.6	CTDP1	NM_004715.2	FCP1	DNA-		transcripti
GI_16554588-A	826.3	1028.8	1200.2	CTDP1	NM_048368.1	FCP1	DNA-		transcripti
GI_16554591-A	266.4	339.4	366.5	ENO3	NM_053013.1	MSE	phosphop	phosphop	glycolysis
GI_16554595-A	7315.9	12699	7627.7	IER3	NM_003897.2	DIF2;IEX1;PRG1;DIF-2;GLY96;IEX-1;IEX-1L	apoptosis		anti-
GI_16554596-I	115.6	170.3	121.6	IER3	NM_052815.1	DIF2;IEX1;PRG1;DIF-2;GLY96;IEX-1;IEX-1L	apoptosis		anti-
GI_16554600-S	585.5	675.9	585.6	MRPS18A	NM_018135.2	S18bmt;FLJ10548;MRPS18-	structural	ribosome	protein
GI_16554601-S	6196	4356.4	4205.7	MRPS18B	NM_014046.2	PTD017;S18amt;C6orf14;HSPC183;MRPS18-	structural	ribosome	protein
GI_16554602-S	3105.1	3235.8	2904.8	MRPS22	NM_020191.2	GIBT;GK002;C3orf5;RPMS22;MRP-S22	structural	mitochond	biological_
GI_16554603-S	4014	4261.5	3841	MRPS23	NM_016070.2	CGI-138;HSPC329;MRP-S23	structural	mitochond	
GI_16554605-S	2011.8	2337.9	1586.6	MRPS2	NM_016034.2	CGI-91;MRP-S2	structural	small	protein
GI_16554606-S	313.3	293.9	307.4	MRPS10	NM_018141.2	MRP-S10;FLJ10567;PNAS-122	structural	mitochond	protein
GI_16554608-I	438.6	553.8	534.5	MRPS11	NM_022839.2	HCC-2;FLJ22512;FLJ23406	structural	ribosome	protein
GI_16554610-S	3472.3	3305.8	3287.3	MRPS15	NM_031280.2	DC37;RPMS15;MPR-S15;FLJ11564	structural	ribosome	protein
GI_16554612-S	1758.1	1767.2	1528.5	MRPS16	NM_016065.2	RPMS16;CGI-132;MRP-S16;FLJ22062	structural	ribosome	protein
GI_16554613-S	1328.4	1393	1429.7	MRPS17	NM_015969.2	RPMS17;HSPC011;MRP-S17	structural	ribosome	protein
GI_16554617-S	1220.5	1406.1	1523.1	MRPS7	NM_015971.2	MRP-S;RP-S7;RPMS7;MRP-S7	structural	ribosome	protein
GI_16554620-I	233.4	264.3	241.8	WDR10	NM_052985.1	SPG;WDR10p;WDR140;FLJ00025;FLJ10897			
GI_16554624-A	286.5	346.4	315.5	WDR10	NM_052990.1	SPG;WDR10p;WDR140;FLJ00025;FLJ10897			
GI_16554626-I	654.4	632.6	672.5	WDR5	NM_017588.1	BIG-3	signal	heterotrim	G-protein
GI_16579829-S	102	99.4	94.1	RPL39L	NM_052969.1	RPL39L1	structural	ribosome	protein
GI_16579882-S	774.4	766.4	786.4	MRPS28	NM_014018.2	MRPS35;HSPC007;MRP-S28;MRP-	structural	mitochond	biological_
GI_16579883-S	81.3	82.7	75.1	RPL3L	NM_005061.2		structural	ribosome	protein
GI_16579884-S	38186.1	34317	28489	RPL4	NM_000968.2	HRPL4	structural	cytosolic	protein
GI_16579887-S	144.3	148.2	130.3	FBP1	NM_000507.2	FBP	fructose-		fructose
GI_16579889-I	144.2	146.3	132.2	WDR7	NM_015285.1	TRAG;KIAA0541			
GI_16579891-A	306.6	344	369.8	WDR7	NM_052834.1	TRAG;KIAA0541			
GI_16596679-S	110.9	118.6	107.1	UGT2B28	NM_053039.1		glucurono	microsom	xenobiotic
GI_16596683-S	92.3	99.2	97.3	MGC20460	NM_053043.1				
GI_16596685-S	1664.7	1799.9	1769.9	MGC14327	NM_053045.1	MGC15961			
GI_16596687-S	307.1	385.3	436.7	MGC16063	NM_053047.1				
GI_16604251-S	680.1	712.8	558.3	ZNF300	NM_052860.1		DNA	nucleus	regulation
GI_16604255-S	101.2	95.7	106.3	PALM2	NM_053016.1				
GI_16604257-A	775.7	614.8	583	GPR74	NM_053036.1	NPFF2;NPGPR	G-protein	integral to	perception
GI_16716338-S	152	169.7	152.2	PVRL4	NM_030916.1	LNIR;PRR4;nectin-4			
GI_16751832-S	198.9	114.7	336.7	COP	NM_052889.1		apoptosis	intracellula	apoptosis

GI_16751916-S	77.4	91.9	89.4	GPR102	NM_053278.1	TA5;TAR5;TRAR5	receptor	integral to	G-protein
GI_16751920-S	106	109.2	92	DCD	NM_053283.1	AIDD	antifungal	extracellul	cell growth
GI_16751922-S	103.6	95.2	95	WFIKKN	NM_053284.1	RJD2			
GI_16753201-S	96.2	112.4	101	KCNK16	NM_032115.2	TALK1;TALK-1	voltage-	integral to	potassium
GI_16753204-A	330	497.2	392.9	UBQLN1	NM_053067.1	DA41;DSK2;XDRP1;PLIC-1			
GI_16753206-S	991.8	1081.6	1097.7	UBQLN2	NM_013444.2	Dsk2;CHAP1;LIC-2;N4BP4;PLIC2;PLIC-			
GI_16753208-S	212.9	300.4	325.7	UBQLN3	NM_017481.2				ubiquitin
GI_16753209-S	131.9	96.4	88.9	SCAP1	NM_003726.2	SKAP55	protein-		signal
GI_16753213-S	24212.6	28701	26105	PFN1	NM_005022.2		actin	actin	cytoskelet
GI_16753214-I	120.8	162.8	162.7	PFN2	NM_053024.1	PFL;D3S1319E	actin	actin	regulation
GI_16753216-A	4900.3	5450.8	4222.5	PFN2	NM_002628.2	PFL;D3S1319E	actin	actin	regulation
GI_16753217-S	156.9	168.8	176.4	PURA	NM_005859.2	PUR1;PURALPHA;PUR-ALPHA	single-	nucleus	DNA
GI_16753219-S	130.1	135.3	129.5	ADAMDEC1	NM_014479.2	M12.219	integrin	integral to	negative
GI_16753220-S	107.3	104.5	96.7	CDH22	NM_021248.1	C20orf25;dJ998H6.1	calcium	integral to	homophili
GI_16753224-S	12653.6	12107	9663	RPL14	NM_003973.2	L14;RL14;hRL14;CTG-B33;CAG-ISL-7	structural	cytosolic	protein
GI_16753226-S	17520.3	16433	12412	RPL6	NM_000970.2	TAXREB107	structural	cytosolic	regulation
GI_16753228-S	481.2	392.5	556.4	PAG	NM_018440.2		transmem	integral to	signal
GI_16753230-S	121.1	131.5	118.6	TEKT1	NM_053285.1		structural	kinesin	microtubul
GI_16753232-S	425.3	566.5	489.7	TLN1	NM_006289.2	TLN;KIAA1027			
GI_16757969-I	2345.4	796.2	1008.1	C1orf24	NM_052966.1	NIBAN	molecular	cellular_co	biological_
GI_16876434-S	124.7	122.8	119.5	GPR101	NM_054021.1	GPCR6	receptor	integral to	G-protein
GI_16876446-S	106.7	109.9	104.8	AMAC	NM_054028.1			membran	
GI_16876448-S	112	113.7	99.7	C8orf14	NM_054029.1	VIR35			
GI_16876452-S	110	111.5	104.4	MRGX3	NM_054031.1		receptor	integral to	G-protein
GI_16876454-S	132.5	151.9	136.5	MRGX4	NM_054032.1		receptor	integral to	G-protein
GI_16904380-S	842.7	880.8	746.7	LRBA	NM_006726.1	BGL;LBA;CDC4L;LAB300	molecular	cellular_co	biological_
GI_16904382-S	95	102.4	93.8	KIAA1365	NM_020794.1				
GI_16904386-S	177.8	318.2	115.6	PCOLCE2	NM_013363.2	PCPE2	ATP	membran	transport
GI_16905072-S	484.4	373.8	450.1	FKSG14	NM_022145.2	P33;Solt;AF5alpha			
GI_16905366-S	86.4	96.4	86	HRLP5	NM_054108.1				
GI_16905370-S	83.9	99.6	90.4	IHPK3	NM_054111.1	IP6K3;INSP6K3	inositol-		
GI_16905372-S	242.2	287	271.3	DEFB118	NM_054112.1	ESC42;DEFB-18;C20orf63;dJ1018D12.3	antibacteri	perinuclea	xenobiotic
GI_16905502-A	1140.5	1626.6	1016.1	SEC23B	NM_032985.2		protein	membran	vesicle-
GI_16905503-I	117	116.5	108.7	SEC23B	NM_032986.2		protein	membran	vesicle-
GI_16905508-A	150.1	109.3	108.4	B3GAT1	NM_018644.2	HNK-1;GLCATP;GlcAT-P	glucurono	integral to	protein
GI_16905509-I	922.2	1006.6	854.1	B3GAT1	NM_054025.1	HNK-1;GLCATP;GlcAT-P	glucurono	integral to	protein
GI_16905511-S	34088.1	30799	25677	RPLP1	NM_001003.2	P1;RPP1	structural	cytosolic	protein
GI_16905512-S	14576.7	12460	10690	RPLP2	NM_001004.2	P2;RPP2	structural	cytosolic	protein
GI_16905513-S	709.9	778.6	603.3	RDX	NM_002906.2		actin	actin	cytoskelet
GI_16905514-S	1041.8	1268.1	1148.5	RFX5	NM_000449.2		DNA	nucleus	transcripti
GI_16905515-A	800.4	957.8	838.6	FUSIP1	NM_006625.3	NSSR;TASR;SRp38;TASR1;TASR2;FUSIP2;	pre-mRNA	nucleus	mRNA
GI_16905515-I	974.7	1107.7	1015	FUSIP1	NM_006625.3	NSSR;TASR;SRp38;TASR1;TASR2;FUSIP2;	pre-mRNA	nucleus	mRNA
GI_16905516-I	390.5	496.1	422.6	FUSIP1	NM_054016.1	NSSR;TASR;SRp38;TASR1;TASR2;FUSIP2;	pre-mRNA	nucleus	mRNA
GI_16905519-I	376.8	455.7	397.1	GOSR2	NM_054022.1	GS27;MEMBRIN	v-SNARE	ER-Golgi	membran

GI_16905521-A	318.9	380.2	311.9	GOSR2	NM_004287.2	GS27;MEMBRIN	v-SNARE	ER-Golgi	membran
GI_16905521-I	380.2	509.2	430.1	GOSR2	NM_004287.2	GS27;MEMBRIN	v-SNARE	ER-Golgi	membran
GI_16905523-S	132.6	143.2	126.2	CES1	NM_001266.3	CEH;CES2;HMSE;SES1;HMSE1	serine	endoplas	response
GI_16905527-A	3777.5	3654.8	2895.3	DAP3	NM_004632.2	DAP-3;MRPS29;MRP-S29;bMRP-10	structural	mitochond	induction
GI_16915927-A	144.6	123.5	140.5	CPB2	NM_016413.2	CPU;PCPB;TAFI	lysine	extracellul	proteolysis
GI_16915931-I	86.3	85.5	95.2	CPB2	NM_001872.2	CPU;PCPB;TAFI	lysine	extracellul	proteolysis
GI_16915933-A	10176.1	7362.7	9512.5	MGAT4B	NM_014275.2	GNT-IV;GnT-Ivb	alpha-1,3-		N-glycan
GI_16915933-I	573.7	730.9	690.7	MGAT4B	NM_014275.2	GNT-IV;GnT-Ivb	alpha-1,3-		N-glycan
GI_16915935-I	122.4	127.1	120.7	MGAT4B	NM_054013.1	GNT-IV;GnT-Ivb	alpha-1,3-		N-glycan
GI_16933524-S	114.5	116.5	111.3	UNC5C	NM_003728.2	UNC5H3	netrin		brain
GI_16933527-I	93.2	103.8	89.5	CYP26A1	NM_057157.1	CP26;CYP26;P450RAI;P450RAI1	retinoic	membran	metabolis
GI_16933529-A	144.2	158.4	160.6	CYP26A1	NM_000783.2	CP26;CYP26;P450RAI;P450RAI1	retinoic	membran	metabolis
GI_16933529-I	195.3	229.4	224.6	CYP26A1	NM_000783.2	CP26;CYP26;P450RAI;P450RAI1	retinoic	membran	metabolis
GI_16933536-I	112.9	124	114.1	GLMN	NM_053274.1	GVM;GLML;FAB68;FAP48;FKBPAP;VMGLO	receptor		protein
GI_16933538-A	546.8	576.8	592.7	GLMN	NM_007070.2	GVM;GLML;FAB68;FAP48;FKBPAP;VMGLO	receptor		protein
GI_16933539-S	226.5	284.8	256.6	FAP	NM_004460.2	FAPA;DPPIV;SEPRASE	dipeptidyl-	integral to	cell-cell
GI_16933541-I	18812.7	32210	11550	FN1	NM_002026.1	FN;CIG;FINC;LETS	cell	extracellul	cell
GI_16933543-A	412.8	830.1	315.2	FN1	NM_054034.1	FN;CIG;FINC;LETS	cell	extracellul	cell
GI_16933543-I	289.8	583.7	192.4	FN1	NM_054034.1	FN;CIG;FINC;LETS	cell	extracellul	cell
GI_16933547-A	25026.1	22062	18943	RPLP0	NM_001002.2	P0;L10E;RPP0;PRLP0	structural	cytosolic	protein
GI_16933548-A	142.6	179.8	190.2	MFI2	NM_033316.2	MTF1;MAP97;MGC4856	iron ion	extracellul	iron ion
GI_16933548-I	425.8	825.4	1012.3	MFI2	NM_033316.2	MTF1;MAP97;MGC4856	iron ion	extracellul	iron ion
GI_16933549-I	119.4	129.8	115.6	MFI2	NM_005929.3	MTF1;MAP97;MGC4856	iron ion	extracellul	iron ion
GI_16933550-A	524.3	913.5	575.5	ANTXR1	NM_053034.1	ATR;TEM8;FLJ10601;FLJ21776	receptor	integral to	
GI_16933550-I	91.7	103	87.7	ANTXR1	NM_053034.1	ATR;TEM8;FLJ10601;FLJ21776	receptor	integral to	
GI_16933552-I	1312.7	2253.1	1254.6	ANTXR1	NM_018153.2	ATR;TEM8;FLJ10601;FLJ21776	receptor	integral to	
GI_16933554-S	96.4	103	99.1	PCDH15	NM_033056.2	USH1F	calcium	integral to	hearing
GI_16933556-S	127.6	113.3	108.6	PCDH16	NM_003737.1	FIB1;CDH25;FLJ11790;KIAA1773	calcium-	integral to	cell
GI_16933558-S	149.8	157.9	145.2	PC-LKC	NM_017675.2	FLJ20124;FLJ20383	calcium	membran	homophili
GI_16933560-S	79.6	99.9	89	SSPN	NM_005086.3	KRAG;SPN1;SPN2	DNA	dystrophin-	muscle
GI_16933562-S	4881.1	5270	4660.9	TCEB1	NM_005648.2	SIII	protein	nucleus	regulation
GI_16933563-I	273.7	350.5	387.4	DNM1L	NM_012062.2	DLP1;DRP1;DVLP;VPS1;DYMPLE;HDYNIV	GTPase	Golgi cis-	mitochond
GI_16933564-S	113.8	120.6	124.6	PCDH21	NM_033100.1	KIAA1775;DKFZp434A132	calcium	membran	homophili
GI_16936519-S	142.8	202.6	179.3	WNT10A	NM_025216.2	FLJ14301	signal	extracellul	developm
GI_16936521-S	186.1	196.9	170.6	WNT10B	NM_003394.2	WNT-12	signal	extracellul	oncogene
GI_16936523-S	191.5	220	189.8	WNT1	NM_005430.2	INT1	signal	soluble	central
GI_16936525-S	94.7	118.5	103.5	WNT6	NM_006522.2		extracellul	extracellul	developm
GI_16936527-I	225.6	260.8	201.3	CDK2	NM_001798.2	p33(CDK2)	cyclin-	cytoplasm	regulation
GI_16936529-A	785.9	1105.9	866.8	CDK2	NM_052827.1	p33(CDK2)	cyclin-	cytoplasm	regulation
GI_16936531-I	3559.9	3195.6	3176.5	CDK4	NM_000075.2	CMM3;PSK-J3;MGC14458	cyclin-		G1/S
GI_16936532-A	6282.1	5421.8	5388	CDK4	NM_052984.1	CMM3;PSK-J3;MGC14458	cyclin-		G1/S
GI_16936534-I	177.9	190	186.2	UNC119	NM_054035.1	HRG4		cytosol	phototrans
GI_16936537-A	680.4	717.4	617.7	UNC119	NM_005148.2	HRG4		cytosol	phototrans
GI_16936539-I	130.2	132.1	108.9	CRYBA2	NM_057093.1		structural	cellular_co	biological_

GI_16945965-S	127.3	132.8	146.3	CENTB5	NM_030649.1	KIAA1716			
GI_16945967-S	131.8	157.5	151.2	TMEM10	NM_033207.2	TMP10;HTMP10		integral to	
GI_16945968-S	153.4	112	98.1	LRP15	NM_052953.2				
GI_16945969-A	96.1	105.5	97.5	PSIP1	NM_021144.2	p52;p75;PAIP;DFS70;LEDGF;PSIP2	DNA	nucleus	regulation
GI_16945969-I	1159.5	1106	1159.3	PSIP1	NM_021144.2	p52;p75;PAIP;DFS70;LEDGF;PSIP2	DNA	nucleus	regulation
GI_16950590-A	2472.1	2590.7	2736.3	MRPS12	NM_033363.1	RPS12;RPMS12;RPSM12;MPR-S12;MT-	structural	mitochond	protein
GI_16950592-I	1015	1183.8	904.3	MRPS21	NM_018997.1	MDS016;RPMS21;MRP-S21			
GI_16950596-A	1859.6	2237.1	1808.2	MRPS33	NM_053035.1	PTD003;CGI-139;MRP-S33;FLJ21123	structural	mitochond	protein
GI_16950598-S	1739.2	1738.8	1673.6	MRPS30	NM_016640.2	PAP;PDCD9;MRP-S30;DKFZp566B2024			apoptosis
GI_16950599-S	1468.8	1164.5	1280.8	MRPS31	NM_005830.2	IMOGN38;MRP-S31	structural	mitochond	regulation
GI_16950602-S	1607.6	1357.7	1442.2	MRPS35	NM_021821.2	MDS023;MRPS28;MRP-			
GI_16950606-S	2836.4	3816.6	3271.6	MRPL51	NM_016497.2	CDA09;MRP64;bMRP64;HSPC241	structural	mitochond	
GI_16950608-S	2004.2	2359.3	2037.8	MRPS27	NM_015084.1	MRP-S27;FLJ21764;FLJ23348;KIAA0264	structural	mitochond	
GI_16950622-A	450.4	422.9	212.4	MYLK	NM_053031.1	KRP;MLCK;MLCK108;MLCK210;FLJ12216	myosin-		protein
GI_16950626-A	755.2	695.8	852.5	AP1S1	NM_001283.2	AP19;CLAPS1;SIGMA1A	vesicle	coated	nonselecti
GI_16950626-I	834.8	718.8	916.1	AP1S1	NM_001283.2	AP19;CLAPS1;SIGMA1A	vesicle	coated	nonselecti
GI_16950627-I	2064.5	1857	2320.8	AP1S1	NM_057089.1	AP19;CLAPS1;SIGMA1A	vesicle	coated	nonselecti
GI_16950629-A	94.5	94.9	92.2	AQP6	NM_001652.2	AQP2L	water	integral to	small
GI_16950630-I	103.1	112.4	98.5	AQP6	NM_053286.1	AQP2L	water	integral to	small
GI_16950632-I	131.8	152.5	123.6	ASS	NM_054012.1	ASS1;CTLN1	ligase	cytoplasm	urea cycle
GI_16950634-A	368.7	557.3	357.1	ASS	NM_000050.2	ASS1;CTLN1	ligase	cytoplasm	urea cycle
GI_16950639-I	154.9	160.9	157.6	ARTN	NM_003976.2	EVN;NBN	receptor		neuroblast
GI_16950642-I	117	122.4	111.7	ARTN	NM_057091.1	EVN;NBN	receptor		neuroblast
GI_16950644-A	123.7	122.7	104.2	ARTN	NM_057160.1	EVN;NBN	receptor		neuroblast
GI_16950644-I	150.1	188.1	163.8	ARTN	NM_057160.1	EVN;NBN	receptor		neuroblast
GI_16950653-S	451.6	518.7	582.4	CCNA2	NM_001237.2	CCN1;CCNA	cyclin-	nucleus	mitotic G2
GI_16950654-S	5100.4	3382.9	4106	CCND1	NM_053056.1	BCL1;PRAD1;U21B31;D11S287E	cyclin-	nucleus	G1/S
GI_16950656-S	168	390.4	125.8	CCND2	NM_001759.2	KIAK0002	cyclin-	nucleus	regulation
GI_16950657-S	418.8	791.5	856.7	CCND3	NM_001760.2		cyclin-	nucleus	regulation
GI_16950659-S	2312.3	2293.3	2204.3	CDK7	NM_001799.2	CAK1;STK1;CDKN7;p39MO15	cyclin-	nucleus	transcripti
GI_16975495-S	130.5	150.8	139.2	CORTBP2	NM_033427.1	Orf4;C7orf8;KIAA1758			
GI_17017962-A	134.8	149	133.5	FOXP2	NM_014491.1	SPCH1;CAGH44;TNRC10	transcripti		neurogene
GI_17017969-S	28477.9	27546	22845	RPL24	NM_000986.2		structural	cytosolic	protein
GI_17017970-S	19230.9	17915	13855	RPL26	NM_000987.2		structural	cytosolic	protein
GI_17017971-S	2931.3	3720.6	3261.7	RPL26L1	NM_016093.2	RPL26P1	structural	large	protein
GI_17017972-S	25182	23581	19157	RPL27	NM_000988.2		structural	ribosome	protein
GI_17017973-S	136.2	139.8	130.7	WNT11	NM_004626.2	HWNT11			embryoge
GI_17017975-S	112.6	113	111.6	WNT9B	NM_003396.1	WNT15;WNT14B	extracellul	extracellul	signal
GI_17017978-S	176.8	230.2	171.3	WNT3A	NM_033131.2		extracellul	extracellul	morphoge
GI_17017979-A	320.9	441	339.8	KLHL4	NM_057162.1	KHL4;DKELCHL;KIAA1687	actin	cytoskelet	actin
GI_17017983-S	1200.3	1293.2	1373.7	CDK9	NM_001261.2	TAK;C-2k;CDC2L4;PITALRE	cyclin-	transcripti	RNA
GI_17017984-S	237.6	304	220.6	CDKL3	NM_016508.2	NKIAMRE	protein		protein
GI_17017985-S	10164.2	9689.7	8065	COX4I1	NM_001861.2	COX4;COXIV	cytochrom	mitochond	energy
GI_17017986-S	6735.9	5503.4	5324.2	COX5A	NM_004255.2	VA;COX;COX-VA	cytochrom	inner	electron

GI_17017987-S	5236.1	5941.1	5517.9	COX5B	NM_001862.2	COXVB	cytochrom	mitochond	respiratory
GI_17017990-S	991.8	1087.5	976.3	FTSJ3	NM_017647.2	EPCS3;FLJ20062			
GI_17017992-S	174.3	170	152.8	STK22C	NM_052841.2	TSSK3;SPOGA3;STK22D	ATP		protein
GI_17025229-S	104.7	117.7	100.3	KCNK17	NM_031460.2	TALK2;TASK4;TALK-2;TASK-4	voltage-	integral to	potassium
GI_17025233-S	150.5	185.8	160.2	KEL	NM_000420.2		endopepti	cytoskelet	N-linked
GI_17105380-S	119.7	108.7	95.5	CLIC2	NM_001289.3	XAP121	chloride	membran	small
GI_17105393-S	32163.9	32673	28057	RPL23A	NM_000984.2	MDA20	structural	cytosolic	protein
GI_17105395-S	14680.7	13233	11218	RPL29	NM_000992.2	HIP;HUMRPL29	heparin	cytosolic	embryo
GI_17105396-I	422.4	410.1	388.9	RFP	NM_006510.3	RNF76;TRIM27	nucleic	membran	spermatog
GI_17105397-I	1119.9	1286.7	859.5	WDR1	NM_017491.2	NORI-1	protein	cytoskelet	hearing
GI_17105398-A	5886.1	5796.6	4414.1	WDR1	NM_005112.3	NORI-1	protein	cytoskelet	hearing
GI_17105399-I	113.9	148.1	131.8	PIK4CA	NM_058004.1	pi4K230;PI4K-ALPHA	1-	Golgi	phosphati
GI_17105401-I	104.3	152.7	91	FEZ1	NM_022549.2			kinesin	axon
GI_17105402-A	133.1	229.2	134.3	FEZ1	NM_005103.3			kinesin	axon
GI_17105402-I	115.7	714.8	97.4	FEZ1	NM_005103.3			kinesin	axon
GI_17136074-S	921.2	804.4	836	AXUD1	NM_033027.2	URAX1;TAIP-3;DKFZp566F164		nucleus	apoptosis
GI_17136075-I	225.4	264	220	KLHL4	NM_019117.3	KHL4;DKELCHL;KIAA1687	actin	cytoskelet	actin
GI_17136076-S	181.3	262.6	123.4	MYLK2	NM_033118.2	KMLC;MLCK;skMLCK	myosin-		protein
GI_17136077-S	120.9	94.9	116.5	VGF	NM_003378.2		growth	cellular_co	biological_
GI_17136079-I	235.6	290.9	303.2	PEX16	NM_057174.1			integral to	peroxisom
GI_17136146-S	162.8	198	100.4	ADORA2A	NM_000675.3	RDC8;hA2aR;ADORA2	adenosine	membran	phagocyto
GI_17136150-S	863.6	943.4	935.9	ZW10	NM_004724.2	HZW10	centromeri	kinetochor	centromer
GI_17149810-A	9705.6	12136	6524	COL6A3	NM_057167.1		collagen	microfibril	muscle
GI_17149812-S	3362.8	4226.9	3525.7	KLHDC3	NM_057161.2	PEAS;HPEAS;dJ20C7.3			
GI_17149826-A	535.2	456	409.6	TBDN100	NM_025085.2	Ga19;NATH;FLJ13340			
GI_17149833-S	149.5	151.6	132.2	SORT1	NM_002959.3	NT3;Gp95	transmem	Golgi	nonselecti
GI_17149835-A	2422.9	2755.6	993.5	FKBP1A	NM_054014.1	FKBP1;PKC12;PKCI2;FKBP12;PPIASE;FKB	receptor	nucleus	protein
GI_17149835-I	849.7	1026.4	379.1	FKBP1A	NM_054014.1	FKBP1;PKC12;PKCI2;FKBP12;PPIASE;FKB	receptor	nucleus	protein
GI_17149837-I	5859.2	7257.2	3037	FKBP1A	NM_000801.2	FKBP1;PKC12;PKCI2;FKBP12;PPIASE;FKB	receptor	nucleus	protein
GI_17149840-A	158	187.7	167.2	FKBP1B	NM_004116.2	OTK4;FKBP9;FKBP1L;PKBP1L;PPIase;FKB	cyclophilin	cytoplasm	muscle
GI_17149841-I	102.3	110.9	114.4	FKBP2	NM_004470.2	PPIase;FKBP-13	FK506	endoplas	protein
GI_17149843-A	195.7	250.9	213.1	FKBP2	NM_057092.1	PPIase;FKBP-13	FK506	endoplas	protein
GI_17149843-I	341.5	438.1	357.2	FKBP2	NM_057092.1	PPIase;FKBP-13	FK506	endoplas	protein
GI_17149845-S	1536.4	1662	2003.1	FKBP3	NM_002013.2	PPIase;FKBP-25	receptor	nucleus	protein
GI_17149846-S	1295	1328.4	1415.5	FKBP4	NM_002014.2	HBI;p52;Hsp56;FKBP52;FKBP59;PPIase	Hsp70/Hs	nucleus	protein
GI_17149847-S	409.1	409.7	256.3	FKBP5	NM_004117.2	P54;FKBP51;FKBP54;PPIase;Ptg-10	peptidyl-	nucleus	protein
GI_17149848-S	112.1	114.4	105.5	FKBP6	NM_003602.2	FKBP36;PPIase	peptidyl-		protein
GI_17149850-S	222	242.7	253.8	FKBP8	NM_012181.2	FKBP38;FKBPr38			intracellula
GI_17157994-S	104.3	102.2	92.7	DGAT2L1	NM_058165.1	MGAT1;DGAT2L	acyltransf		
GI_17158002-S	1701.6	1689.8	1536.8	ANTXR2	NM_058172.1	ISH;JHF;CMG2;CMG-2;FLJ31074			
GI_17158004-S	171.2	197.4	180.5	LOC118430	NM_058173.1				
GI_17158012-S	171.8	180.9	166.7	C21orf42	NM_058184.1				
GI_17158018-S	200.8	254.5	242.2	C21orf67	NM_058188.1	PRED54			
GI_17158020-A	157.8	172.2	154.6	C21orf69	NM_058189.1	PRED54			

GI_17158020-I	604.4	716.4	633.3	C21orf69	NM_058189.1	PRED54			
GI_17158022-S	192.6	177	136.1	C21orf70	NM_058190.1	PRED56			
GI_17158034-S	98.5	118.4	106.3	TECTB	NM_058222.1				
GI_17158040-A	112.6	103.4	88.8	HDAC9	NM_058177.1	HD7;HDAC;HDRP;MITR;HDAC7;HDAC7B;H	histone	nucleus	regulation
GI_17158040-I	99.2	105.3	109.5	HDAC9	NM_058177.1	HD7;HDAC;HDRP;MITR;HDAC7;HDAC7B;H	histone	nucleus	regulation
GI_17158042-S	21737.3	21394	17970	RPL19	NM_000981.2		structural	cytosolic	protein
GI_17158043-S	33004.2	29048	24081	RPS6	NM_001010.2		structural	cytosolic	protein
GI_17196625-S	132.5	160.7	158.6	C22orf20	NM_025225.2	FLJ22012;dJ796I17.1	catalytic	integral to	
GI_17318558-I	132.9	137.3	123.4	CCNE1	NM_001238.1	CCNE	cyclin-	nucleus	G1/S
GI_17318560-A	129.5	161.3	152.3	CCNE1	NM_057182.1	CCNE	cyclin-	nucleus	G1/S
GI_17318566-A	229.8	331.1	353.4	CCNE2	NM_004702.2	CYCE2	cyclin-	nucleus	cell cycle
GI_17318568-S	202.6	219.4	207.8	KRT1	NM_006121.2	K1;CK1;KRT1A	structural	intermedia	epidermal
GI_17318571-S	89.4	97.4	89.9	KRT3	NM_057088.1	K3;CK3	structural	kinesin	cytoskelet
GI_17318573-S	100	117.4	108.7	KRT4	NM_002272.1	K4;CK4;CYK4;FLJ31692	structural	intermedia	epidermal
GI_17318577-S	342.9	375.1	339.1	KRT5	NM_000424.2	K5;CK5;EBS2;KRT5A	structural	intermedia	epidermal
GI_17352499-S	181.9	309.9	384.9	BDKRB2	NM_000623.2	B2R;BK2;BK-2;BKR2;BRB2	bradykinin	integral to	phosphati
GI_17388802-S	3381.6	2880.1	2085.4	PAICS	NM_006452.2	AIRC;PAIS;ADE2H1	phosphori	phosphori	purine
GI_17402869-I	354.4	323.5	248.4	BCCIP	NM_016567.2	TOK-1		nucleus	regulation
GI_17402870-A	824.4	783.3	629.2	BCCIP	NM_078468.1	TOK-1		nucleus	regulation
GI_17402870-I	1934	1888	1566.1	BCCIP	NM_078468.1	TOK-1		nucleus	regulation
GI_17402872-I	165.2	157.2	157.2	BCCIP	NM_078469.1	TOK-1		nucleus	regulation
GI_17402874-I	7894	12384	5740.5	COL6A2	NM_001849.2	PP3610;DKFZp586E1322	collagen	collagen	muscle
GI_17402876-A	480.5	850.4	461.8	COL6A2	NM_058174.1	PP3610;DKFZp586E1322	collagen	collagen	muscle
GI_17402878-I	250.3	296.5	284.9	COL6A2	NM_058175.1	PP3610;DKFZp586E1322	collagen	collagen	muscle
GI_17402880-I	87.8	78	77.7	DLAD	NM_021233.2		deoxyribo		DNA
GI_17402881-A	97.8	94.1	85.1	DLAD	NM_058248.1		deoxyribo		DNA
GI_17402881-I	112.6	116.7	114.1	DLAD	NM_058248.1		deoxyribo		DNA
GI_17402883-A	98.3	109	106.6	KIAA1622	NM_020958.2				
GI_17402883-I	116.5	117.8	111.8	KIAA1622	NM_020958.2				
GI_17402885-I	160.6	196.5	226.1	KIAA1622	NM_058237.1				
GI_17402889-A	523.5	614.1	597.1	NPTXR	NM_058178.1	NPR	receptor	integral to	
GI_17402894-A	855	767.3	764.3	RAD51C	NM_002876.2	RAD51L2	adenosine	nucleus	DNA
GI_17402894-I	74.6	78.5	78.8	RAD51C	NM_002876.2	RAD51L2	adenosine	nucleus	DNA
GI_17402895-I	401	456.5	417.7	RAD51C	NM_058216.1	RAD51L2	adenosine	nucleus	DNA
GI_17402899-S	570.6	642.1	523.5	FUBP1	NM_003902.2	FBP;FUBP	single-	nucleus	transcripti
GI_17402901-S	520.2	693.1	580.7	GNB1L	NM_053004.1	GY2;FKSG1;WDR14;WDVCF;DGCRK3;KIAA	molecular	internal	G-protein
GI_17402905-S	3794.5	3536.4	2636.6	RPL22	NM_000983.2	EAP;HBP15;HBP15/L22	structural	cytosolic	protein
GI_17402906-A	114.3	102.1	106.6	TRIM29	NM_058193.1	ATDC	transcripti		transcripti
GI_17402906-I	76.3	92.4	72.9	TRIM29	NM_058193.1	ATDC	transcripti		transcripti
GI_17402908-I	346.7	418.5	330.6	TRIM29	NM_012101.2	ATDC	transcripti		transcripti
GI_17402910-A	1648.8	1856.5	1870.7	VPS29	NM_016226.2	DC7;DC15;PEP11;FLJ20492;DKFZp564F022	protein		intracellula
GI_17402913-A	98.1	125.2	112.7	WNT16	NM_016087.2		extracellul	extracellul	developm
GI_17402913-I	133.9	131.3	126.9	WNT16	NM_016087.2		extracellul	extracellul	developm
GI_17402915-I	109	116.9	105.6	WNT16	NM_057168.1		extracellul	extracellul	developm

GI_17402917-S	508.6	1713.6	1456.4	WNT5A	NM_003392.2	hWNT5A	receptor	soluble	embryoge
GI_17402918-A	199.7	379.6	292.1	WNT5B	NM_030775.2	MGC2648	signal	extracellul	developm
GI_17402918-I	114.7	130.4	119.7	WNT5B	NM_030775.2	MGC2648	signal	extracellul	developm
GI_17402920-I	143	162.4	144.7	WNT5B	NM_032642.2	MGC2648	signal	extracellul	developm
GI_17402930-I	101.3	122.3	118	SPAG11	NM_058203.1	EP2;HE2;EP2C;EP2D		extracellul	spermatog
GI_17402934-A	91	89.9	87.6	SPAG11	NM_058207.1	EP2;HE2;EP2C;EP2D		extracellul	spermatog
GI_17435003-S	82.4	97.3	84.2	LOC129614	XM_065316.1				
GI_17436546-S	298	368.1	340.9	LOC132706	XM_067994.1				
GI_17436980-S	101.2	82.9	84.5	LOC127059	XM_060301.1				
GI_17437014-S	113.8	134.2	118.1	LOC127066	XM_060307.1				
GI_17437031-S	172.8	211.4	187.9	LOC127069	XM_060310.1				
GI_17437058-S	91.9	82.8	88.5	LOC127074	XM_060315.1				
GI_17437334-S	12086.6	10948	8552.2	LOC127099	XM_060328.1				
GI_17437350-S	164.9	149.5	150.1	LOC130063	XM_059396.1				
GI_17437660-S	77.8	113.8	91	LOC130402	XM_065715.1				
GI_17438568-S	107.6	109.8	107.7	LOC131086	XM_067193.1				
GI_17443792-S	81.7	88.9	84.3	LOC127482	XM_060509.1				
GI_17444700-S	1621.7	1488.4	1267.5	LOC127545	XM_060535.1				
GI_17445393-S	235.9	310.5	296.8	LOC127617	XM_060572.1				
GI_17446452-S	101.5	104.2	99	LOC133185	XM_068229.1				
GI_17446851-S	1063.1	1249.9	967.5	LOC130678	XM_065828.1				
GI_17448143-S	110.6	105.8	107.8	C9orf11	XM_035953.2				
GI_17449884-S	200.3	229.1	224.1	LOC134505	XM_068889.1				
GI_17451521-S	103.7	109.4	107.9	LOC128371	XM_060956.1				
GI_17454506-S	7979.7	7461.4	6673.7	LOC122585	XM_063202.1				
GI_17456752-S	103.7	104.9	92.4	LOC119682	XM_061614.1				
GI_17456788-S	192.5	203.5	201.7	LOC119692	XM_061624.1				
GI_17459234-S	127.4	148.3	130.1	LOC139061	XM_066452.1				
GI_17459487-S	101.5	115.8	109.9	LOC139116	XM_066484.1				
GI_17460102-S	103.5	114.3	109.6	LOC120586	XM_062162.1				
GI_17461456-S	351	434	394.9	LOC120775	XM_062285.1				
GI_17461543-S	87.6	92.8	91.3	LOC120787	XM_062263.1				
GI_17462608-S	98.5	103.5	100	LOC132870	XM_059608.1				
GI_17466805-S	212.3	250.1	229.2	LOC137485	XM_059909.1				
GI_17470104-S	312.7	378.3	356.8	LOC138881	XM_071150.1				
GI_17470112-S	307.4	396.3	364.1	LOC138883	XM_071152.1				
GI_17474308-S	94.2	100.8	90.4	LOC121129	XM_062467.1				
GI_17474608-S	184.9	192.8	206.1	LOC121275	XM_062553.1				
GI_17475183-S	116.8	133.5	115.6	LOC121792	XM_062788.1				
GI_17475713-S	113.6	119.8	132.9	LOC122038	XM_062912.1				
GI_17476687-S	125.8	131.4	112.9	LOC122742	XM_063310.1				
GI_17476953-S	122.5	131.2	121.6	LOC122867	XM_063336.1				
GI_17480196-S	89.5	101.6	88	LOC124871	XM_058857.1				
GI_17482322-S	10465.7	10901	8368.1	LOC125910	XM_064859.1				

GI_17482451-S	242.8	307.9	250.7	LOC125963	XM_064884.1				
GI_17482470-S	171.9	182.3	217.9	MGC20533	XM_050564.2				
GI_17484248-S	191.2	211.4	207.8	RPS4L	XM_066040.1	dJ843L14.2			
GI_17484446-S	148.4	194.2	167.3	RPL7AL2	XM_066102.1	dJ189G13.1			
GI_17484710-S	113.7	122.7	105.5	SLC25A5L	XM_066162.1	dJ1065O2.2			
GI_17484771-S	85.1	90.2	83.8	LOC128820	XM_066176.1				
GI_17484775-S	114.9	118.8	109.2	LOC128822	XM_066177.1				
GI_17484794-S	100.1	120.5	103.7	GGTLA3	XM_066189.1	dJ831C21.1			
GI_17486064-S	74	71.2	81	LOC139542	XM_066752.1				
GI_17488773-S	90.9	111	107.9	LOC127665	XM_060597.1				
GI_17505186-S	195.1	219	187.1	KRT6A	NM_005554.2	K6A;CK6A	structural	intermedia	ectoderm
GI_17505187-S	153.9	180	161.6	KRT6B	NM_005555.2	K6B;PC2;CK6B	structural	intermedia	ectoderm
GI_17505188-S	205.2	231.6	209.5	KRT6C	NM_058242.1	K6C;CK6C	structural	kinesin	cytoskelet
GI_17505192-S	115.2	151.2	169.5	WNT7B	NM_058238.1		extracellul	extracellul	developm
GI_17505194-I	170.7	179.1	172.4	WNT8A	NM_058244.1	WNT8D	signal	extracellul	developm
GI_17505196-S	124.1	126	120.3	WNT8B	NM_003393.2		signal	extracellul	embryoge
GI_17505197-S	83.2	93.7	95.3	ACSL6	NM_015256.1	ACS2;FACL6;LACS2;LACS5;KIAA0837	long-chain-	mitochond	acyl-CoA
GI_17505233-A	250.5	271.5	297.8	NUSAP1	NM_018454.4	LNP;ANKT;SAPL;BM037;Q0310;FLJ13421;P			
GI_17511204-S	346.9	408.3	276.1	GPR124	NM_032777.6	TEM5;FLJ14390;KIAA1531;DKFZp434C211;			
GI_17511208-S	2713	2547.2	2170.5	TENS1	NM_022748.6	TEM6;FLJ13732;H_NH049I23.2	protein-		intracellula
GI_17511260-S	180.7	209.2	174.5	PPP1R14D	NM_017726.6	FLJ20251;CPI17-like			
GI_17511434-S	599.9	630.6	521.7	ROBO4	NM_019055.4	FLJ20798			
GI_17530790-S	148.9	143.8	121.9	ZNF354B	NM_058230.1	KID2;FLJ25008	nucleic	intracellula	regulation
GI_17572803-S	450.5	529.7	502.9	ASPSCR1	NM_024083.2	TUG;ASPL;ASPS;RCC17;ASPCR1			
GI_17572806-S	210.6	287.9	259.6	ASP	NM_031916.2		cAMP-		signal
GI_17572809-S	951.2	1184.2	1245.7	THOC4	NM_005782.1	ALY;BEF	transcripti	nucleus	protein
GI_17572813-S	121.9	126.3	113.9	ABT1	NM_013375.2	hABT1	general	nucleus	transcripti
GI_17572819-S	95.5	103.9	107.2	ARS	NM_020427.2	MDM;ANUP;SLURP1	cytokine	extracellul	biological_
GI_17572823-S	99.7	101.4	89.9	AVIL	NM_006576.2	p92;DOC6;ADVIL;FLJ12386	actin	actin	neurogene
GI_17738286-S	2549.8	2867.5	3151	SCAMP4	NM_079834.1	SCAMP-4			
GI_17738293-I	97.5	116.6	94.7	CDKN2A	NM_058195.1	ARF;MLM;P16;p14;p19;CMM2;INK4;MTS1;T	cyclin-	nucleus	cell cycle
GI_17738295-A	275.6	329.4	309.6	CDKN2A	NM_058196.1	ARF;MLM;P16;p14;p19;CMM2;INK4;MTS1;T	cyclin-	nucleus	cell cycle
GI_17738297-I	92.3	91.4	100.7	CDKN2A	NM_058197.1	ARF;MLM;P16;p14;p19;CMM2;INK4;MTS1;T	cyclin-	nucleus	cell cycle
GI_17738300-S	405.3	560	435.2	COL7A1	NM_000094.2	EBD1;EBR1;EBDCT	collagen	basement	epidermal
GI_17738304-S	120.9	129.7	139.2	ARHD	NM_014578.2	Rho;RHOM;RhoD;RHOHP1	Rho small		Rho
GI_17738306-S	101.2	99.3	102	CPLX2	NM_006650.2	CPX2;921-L	vesicle		nonselecti
GI_17738307-S	1211.7	1156.4	1361.7	FREQ	NM_014286.2	FLUP;NCS1;NCS-1;DKFZp761L1223	calcium-	cellular_co	cell
GI_17738309-S	1411.3	1738.8	1721.2	BBP	NM_032027.2				
GI_17738311-S	201.3	250.4	245.6	CCIN	NM_005893.1		structural	cytoskelet	spermatog
GI_17738313-S	577.2	575.3	538.2	CCNH	NM_001239.2	CAK;p34;p37	cyclin-	nucleus	regulation
GI_17738314-S	7603.6	7488.6	4586.1	CCNI	NM_006835.2	CYI;CYC1	cyclin-		spermatog
GI_17738315-A	112.8	150.6	115.6	CYP3A43	NM_057096.2				
GI_17864089-S	361.1	324	359.5	AUTS2	NM_015570.1	KIAA0442	molecular	cellular_co	biological_
GI_17864091-S	221.7	261.6	237	DNAH7	NM_018897.1	KIAA0944	nucleotide	dynein	microtubul

GI_17865794-I	180.2	203.9	205.8	BLP1	NM_031940.2				
GI_17865796-A	993.8	1218	941.1	BLP1	NM_078473.1				
GI_17865798-A	2594.1	2961.8	2375.8	BLP2	NM_025141.2	FLJ22604			
GI_17865799-I	262.2	321.3	280.8	BLP2	NM_078474.1	FLJ22604			
GI_17865801-S	1480.1	1526.1	1402.7	VPS4B	NM_004869.2	SKD1;VPS4-2	peroxisom		membran
GI_17865806-S	659	666.6	732.6	VPS4A	NM_013245.2	SKD1;SKD2;VPS4;VPS4-1;FLJ22197	ATP	cytosol	nonselecti
GI_17865813-I	137.6	151.1	127.2	VNN2	NM_004665.2	FOAP-4;GPI-80	hydrolase		cell
GI_17865815-A	290.7	321	314	VNN2	NM_078488.1	FOAP-4;GPI-80	hydrolase		cell
GI_17865815-I	126.3	151.8	135.4	VNN2	NM_078488.1	FOAP-4;GPI-80	hydrolase		cell
GI_17865817-I	107	114.7	95.6	VNN3	NM_018399.2	HSA238982			
GI_17865818-A	99.5	96.4	97.1	VNN3	NM_078625.1	HSA238982			
GI_17865818-I	91.5	81.2	83.6	VNN3	NM_078625.1	HSA238982			
GI_17921981-S	529.5	491.7	421	COX10	NM_001303.2		farnesyltra	mitochond	heme
GI_17921983-S	252.2	240.9	215.1	COX11	NM_004375.2	COX11P	cytochrom	integral to	cytochrom
GI_17921988-S	2854.5	2616.8	1924	TUBA1	NM_006000.1	FLJ30169;H2-ALPHA	structural	microtubul	
GI_17921990-A	1104.5	952.7	1036.1	TUBA2	NM_079836.1	bA408E5.3	structural	microtubul	microtubul
GI_17921992-I	1158.2	926.9	837.5	TUBA2	NM_006001.1	bA408E5.3	structural	microtubul	microtubul
GI_17921994-S	136.2	128.1	130	COL9A3	NM_001853.2	IDD;MED;EDM3;DJ885L7.4.1	collagen	collagen	
GI_17921996-S	104.4	114.8	106.8	MYL4	NM_002476.2	GT1;ALC1;AMLC;PRO1957	structural	muscle	
GI_17933755-S	103.2	100.7	105.8	GBA3	NM_020973.2	GLUC;CBGL1	hydrolase		carbohydr
GI_17933771-S	4954.4	4442	5619.4	S100A16	NM_080388.1	S100F;DT1P1A7;MGC17528	calcium		
GI_17939343-S	127.2	211.6	107.1	TTYH2	NM_032646.4	MGC4837			
GI_17939347-S	131.8	148.7	136.3	DEFB104	NM_080389.1	DEFB4;DEFB-4			xenobiotic
GI_17941284-S	104.4	100.1	100.8	KST1	NM_052944.2	RKST1;SMIT2	transporte	membran	transport
GI_17975596-S	790.6	1208.5	1099.6	SELM	NM_080430.1		selenium		
GI_17975754-I	328.7	420.8	451	MSL3L1	NM_078628.1	DKFZP586J1822	transcripti	nucleus	transcripti
GI_17975758-A	340.8	412.6	373.4	MSL3L1	NM_078630.1	DKFZP586J1822	transcripti	nucleus	transcripti
GI_17975760-I	103.9	134.5	103.4	MSL3L1	NM_006800.2	DKFZP586J1822	transcripti	nucleus	transcripti
GI_17975764-A	3118.5	2388.6	2653.5	EPHB2	NM_017449.1	DRT;ERK;Hek5;EPHT3;Tyro5	transmem	integral to	oncogene
GI_17975771-I	105.1	110.8	110	BTN2A1	NM_078476.1	BTF1;BT2.1		integral to	lipid
GI_17975773-A	330.9	384.2	349.4	BTN2A1	NM_007049.2	BTF1;BT2.1		integral to	lipid
GI_17978302-S	109.2	111.3	101.4	SERPINB11	NM_080475.1	EPIPIN	serpin		
GI_17978464-S	387	473.7	495.4	TWIST1	NM_000474.2	SCS;ACS3;BPES2;BPES3;TWIST	enzyme	nucleus	chromoso
GI_17978465-S	278.6	320.2	283.9	CCNT1	NM_001240.2	CCNT;CYCT1	cyclin-	kinesin	regulation
GI_17978467-A	317.5	433.9	444.8	CCNT2	NM_001241.2		cyclin-	kinesin	regulation
GI_17978468-I	560.7	705.6	595.8	CCNT2	NM_058241.1		cyclin-	kinesin	regulation
GI_17978470-S	77.3	98.2	89.5	ATP8A1	NM_006095.1	ATPIA;ATPP2;ATPASEII	ATP	integral to	aminopho
GI_17978473-S	131.7	128.2	122.9	HHEX	NM_002729.2	HEX;PRH;HMPH;PRHX;HOX11L-PEN	DNA	nucleus	developm
GI_17978474-S	181.6	190.6	175.3	OLIG2	NM_005806.1	BHLHB1;RACK17;PRKCBP2	DNA	nucleus	cell growth
GI_17978476-S	243.4	302.4	316.1	VPS11	NM_021729.3	END1;PEP5;RNF108;hVPS11	ATP	kinesin	intracellula
GI_17978478-I	173.9	184	156.4	VPS16	NM_022575.2	hVPS16	protein	membran	intracellula
GI_17978482-A	1876.2	1960.6	1151.6	VPS16	NM_080414.1	hVPS16	protein	membran	intracellula
GI_17978482-I	347.8	396.2	371	VPS16	NM_080414.1	hVPS16	protein	membran	intracellula
GI_17978486-S	1963.8	2740.6	2621.2	VPS18	NM_080432.1	KIAA1475	protein	membran	intracellula

GI_17978488-A	1505.1	2130.1	2128	CD97	NM_001784.2	TM7LN1	G-protein	integral to	G-protein
GI_17978490-I	131.9	143.5	126	CD97	NM_078481.1	TM7LN1	G-protein	integral to	G-protein
GI_17978492-S	3795.4	4438.3	4835.6	CDK2AP1	NM_004642.2	DOC1;ST19;DORC1;doc-1;p12DOC-1	tumor	cytoplasm	S phase
GI_17978494-I	110.6	107.7	107.1	CDKN1A	NM_078467.1	P21;CIP1;SDI1;WAF1;CAP20;CDKN1;MDA-6	cyclin-	nucleus	induction
GI_17978496-A	9008.7	12007	9372.8	CDKN1A	NM_000389.2	P21;CIP1;SDI1;WAF1;CAP20;CDKN1;MDA-6	cyclin-	nucleus	induction
GI_17978497-S	622.4	1020.5	998.7	CDKN1B	NM_004064.2	KIP1;CDKN4;P27KIP1	cyclin-	nucleus	cell cycle
GI_17978499-A	585.1	623.9	619	CNOT7	NM_054026.1	CAF1;hCAF-1	signal	nucleus	carbohydr
GI_17978499-I	177.7	194.7	199.4	CNOT7	NM_054026.1	CAF1;hCAF-1	signal	nucleus	carbohydr
GI_17978501-A	98.3	105.5	84	COL9A1	NM_001851.2	MED;DJ149L1.1.2	collagen	microfibril	histogene
GI_17978501-I	113.3	150.8	114	COL9A1	NM_001851.2	MED;DJ149L1.1.2	collagen	microfibril	histogene
GI_17978503-A	176.2	194.1	179.8	COL9A1	NM_078485.1	MED;DJ149L1.1.2	collagen	microfibril	histogene
GI_17978503-I	94.6	87.4	87.1	COL9A1	NM_078485.1	MED;DJ149L1.1.2	collagen	microfibril	histogene
GI_17978510-A	4985.2	5496.3	5641.2	SIAHBP1	NM_014281.3	FIR;PUF60;RoBPI			
GI_17978513-S	184.4	208.7	186.8	TNS	NM_022648.2	TNS1;PRO0929;FLJ10923;DKFZP434G162			
GI_17978517-S	86.2	106.8	98	TNFRSF13C	NM_052945.2	BAFFR	receptor	integral to	immune
GI_17978518-S	4008	3147.9	3539.3	VPS26	NM_004896.2	HB58;Hbeta58;FLJ12930	protein	cytosol	intracellula
GI_17981693-A	79.3	82.8	79	CDKN2B	NM_004936.2	P15;MTS2;TP15;INK4B	cyclin-		cell cycle
GI_17981695-I	96.6	81.3	97.7	CDKN2B	NM_078487.1	P15;MTS2;TP15;INK4B	cyclin-		cell cycle
GI_17981697-I	210.6	279.3	325.8	CDKN2C	NM_001262.2	p18;INK4C;p18-INK4C	cyclin-	cytoplasm	cell cycle
GI_17981698-A	245.9	454	584.8	CDKN2C	NM_078626.1	p18;INK4C;p18-INK4C	cyclin-	cytoplasm	cell cycle
GI_17981698-I	219.7	326.9	302.7	CDKN2C	NM_078626.1	p18;INK4C;p18-INK4C	cyclin-	cytoplasm	cell cycle
GI_17981701-I	96.7	92.4	97.5	CDKN2D	NM_079421.1	p19;INK4D;p19-INK4D			
GI_17981703-S	1054.1	1234.9	866.4	CDKN3	NM_005192.2	KAP;CDI1;CIP2;KAP1	protein		G1/S
GI_17981706-S	8344.7	7126	5798.7	RPS4Y	NM_001008.2	RPS4Y1	structural	ribosome	protein
GI_17981707-S	2193.7	1685.3	1781.9	TWIST2	NM_057179.1	DERMO1	DNA	cytoplasm	cell
GI_17981709-S	13529.3	11953	10737	FAU	NM_001997.2	FAU1;RPS30	ubiquitin	ribosome	protein
GI_17986244-I	131.5	131.7	121.8	PNUTL2	NM_080415.1	H5;ARTS;CE5B3;SEPT4;hucep-7;hCDCREL-	GTPase		cytokinesi
GI_17986246-A	116.4	157.2	114.3	PNUTL2	NM_080416.1	H5;ARTS;CE5B3;SEPT4;hucep-7;hCDCREL-	GTPase		cytokinesi
GI_17986248-I	117.4	135.1	126	PNUTL2	NM_080417.1	H5;ARTS;CE5B3;SEPT4;hucep-7;hCDCREL-	GTPase		cytokinesi
GI_17986251-A	462.1	466.2	485	SP110	NM_004510.2	IFI41;IFI75;FLJ22835	hematopoi	nucleus	regulation
GI_17986251-I	570	564.9	728.6	SP110	NM_004510.2	IFI41;IFI75;FLJ22835	hematopoi	nucleus	regulation
GI_17986253-I	129.6	130.5	104	SP110	NM_080424.1	IFI41;IFI75;FLJ22835	hematopoi	nucleus	regulation
GI_17986259-A	5735	9838.3	7924.7	MYL6	NM_079423.1	ESMLC;LC17A;LC17B;MLC1SM;MLC3NM;M	structural	non-	
GI_17986267-A	236.4	229.9	236.2	BANP	NM_079837.1	SMAR1;FLJ10177;FLJ20538;DKFZp761H17			
GI_17986269-A	107.1	202.4	415.1	DRD2	NM_016574.2	D2R;D2DR	dopamine	intermedia	dopamine
GI_17986271-I	104.4	118	148.6	DRD2	NM_000795.2	D2R;D2DR	dopamine	intermedia	dopamine
GI_17986272-I	102.6	98	90.9	MYL1	NM_079420.1	MLC1F;MLC3F	structural	muscle	
GI_17986274-I	130.8	158.8	142.7	MYL1	NM_079422.1	MLC1F;MLC3F	structural	muscle	
GI_17986276-S	4423.1	6193.5	3140.3	COL4A2	NM_001846.1	FLJ22259	collagen	collagen	extracellul
GI_17986278-S	282.4	301.5	277.7	MC3R	NM_019888.2	MC3	melanocor	integral to	G-protein
GI_17986280-S	8248.5	8671.2	6182.6	MLC1SA	NM_002475.2		structural	muscle	muscle
GI_17986281-S	1172	1831.4	1543.2	PTP4A1	NM_003463.2	HH72;PRL1;PRL-1;PTPCAAX1;PTP(CAAX1)	protein	nucleus	oncogene
GI_17986282-S	6130.9	11727	7288.7	TUBA3	NM_006009.2	FLJ25113;B-ALPHA-1	structural	microtubul	glia cell
GI_17998550-S	97.5	107.6	92.5	SERPINB12	NM_080474.1	YUKOPIN	serpin	cytoplasm	negative

GI_17999523-S	110.6	108.5	90.2	ACRBP	NM_032489.2	SP32;OY-TES-1			
GI_17999525-S	92.9	108.8	105.2	COX4I2	NM_032609.2	COX4;COX4B;COX4-2;COXIV-	aa3-type	mitochond	electron
GI_17999527-S	6376.4	8124.2	6693.8	COX6A1	NM_004373.2	COX6A;COX6AL			energy
GI_17999529-S	196.1	224.5	212.9	COX6A2	NM_005205.2	COX6AH;COXVIAH	aa3-type	mitochond	energy
GI_17999530-S	3799.6	4669.5	4001.9	COX6B	NM_001863.3	COXG	aa3-type	mitochond	electron
GI_17999531-S	4344.5	5385.7	4694	COX6C	NM_004374.2		aa3-type	mitochond	energy
GI_17999532-S	615.9	543.7	780.5	PHYH	NM_006214.2	PAHX	catalytic	peroxisom	lipid
GI_17999533-S	408	478.6	419.9	PRPF18	NM_003675.2	PRP18;hPrp18	pre-mRNA	spliceoso	mRNA
GI_17999536-S	2085.9	2643.5	2583.8	PRPF8	NM_006445.2	PRP8;RP13;HPRP8;PRPC8	pre-mRNA	snRNP U5	mRNA
GI_18034689-S	857.7	1147.8	1469.9	C20orf4	NM_015511.2	CGI-23;bA234K24.2;DKFZp564N1363			
GI_18034691-I	4176.3	4351.2	4316.4	CDW92	NM_080546.2	CTL1;CHTL1			
GI_18079215-S	92	82.9	87.8	CASKIN1	NM_020764.1	KIAA1306			
GI_18079315-S	1649.9	1242.9	1285.9	TJP4	NM_080604.1	PILT			
GI_18079320-S	152.9	164.5	142.3	C20orf102	NM_080607.1	dJ1118M15.2			
GI_18079322-S	158.7	141.5	150	GAB3	NM_080612.1				
GI_18079324-S	297.5	266.8	338.4	C20orf112	NM_080616.1	dJ1184F4.2			
GI_18087810-S	940	654.8	678.3	THRAP6	NM_080651.1	TRAP25;MGC9890	transcripti	nucleus	transcripti
GI_18087816-S	96.9	104.7	102.5	NY-REN-41	NM_080654.1				
GI_18087818-S	1693.9	2060.5	2166.2	MGC17337	NM_080655.1				
GI_18087820-S	154.7	177.6	167.8	MGC13017	NM_080656.1				
GI_18087824-S	205.3	265.5	210.8	ACY-3	NM_080658.1	HCBP1;MGC9740			
GI_18087826-S	86.6	93.7	89.7	MGC14839	NM_080659.1	FLJ25219			
GI_18087834-S	111.4	127.6	114.7	MGC16943	NM_080663.1	KIAA1504	exonuclea	intracellula	
GI_18087836-S	191.3	176.5	174.7	C14orf126	NM_080664.1	MGC9912	hydrolase	cytoplasm	D-amino
GI_18087840-S	104.8	115.5	111.1	LOC112840	NM_080666.1	MGC9907		extrachro	
GI_18087850-S	94.6	103	103.6	KCNE4	NM_080671.1	MIRP3;MGC20353	voltage-	integral to	potassium
GI_18087854-S	508.3	581.4	619.9	Dlc2	NM_080677.1	MGC17810	microtubul	microtubul	microtubul
GI_18087856-S	927.5	1070.3	1063.5	NCE2	NM_080678.1	MGC18120	ubiquitin		ubiquitin
GI_18104939-S	119.4	127.7	122.4	CST9L	NM_080610.1	bA218C14.1	cysteine		
GI_18104947-S	5949.4	5746.4	4396.7	RPL21	NM_000982.2	L21	structural	cytosolic	protein
GI_18104949-A	102.1	115.9	96.9	TBX1	NM_080646.1	DGS;TGA;CAFS;CTHM;DGCR;DORV;VCFS;	RNA	nucleus	heart
GI_18104949-I	101.5	89.8	92.3	TBX1	NM_080646.1	DGS;TGA;CAFS;CTHM;DGCR;DORV;VCFS;	RNA	nucleus	heart
GI_18104951-I	125.3	153.7	143.2	TBX1	NM_080647.1	DGS;TGA;CAFS;CTHM;DGCR;DORV;VCFS;	RNA	nucleus	heart
GI_18104955-A	547.7	664.7	612.7	MAG	NM_002361.2	GMA;S-MAG;SIGLEC-4A	sugar	membran	cell
GI_18104958-S	105.5	125.3	100.8	APACD	NM_005783.2		electron		electron
GI_18104960-S	2515.9	2188.2	2231.6	APPBP1	NM_003905.2	A-116A10.1;DKFZP434P241	catalytic	cytoplasm	signal
GI_18104961-S	271.4	279.6	235.2	APPBP2	NM_006380.2	PAT1;HS.84084;KIAA0228	microtubul	microtubul	intracellula
GI_18104963-A	255.4	326.2	332.3	CAPS	NM_080590.1	CAPS1	calcium		intracellula
GI_18104965-I	125.5	162	142.9	CAPS	NM_004058.2	CAPS1	calcium		intracellula
GI_18104966-I	107.6	123.2	107.7	PTGS1	NM_000962.2	COX1;COX3;PHS1;PCOX1;PGHS1;PTGHS;	prostaglan	membran	physiologi
GI_18104968-A	202	418.3	161.5	PTGS1	NM_080591.1	COX1;COX3;PHS1;PCOX1;PGHS1;PTGHS;	prostaglan	membran	physiologi
GI_18104972-A	837.8	916.5	725	PTP4A2	NM_080392.1	HH13;OV-1;PRL2;HH7-2;PRL-2;PTP4A;HU-	protein		
GI_18104974-I	2145.4	1902	1741.3	PTP4A2	NM_003479.2	HH13;OV-1;PRL2;HH7-2;PRL-2;PTP4A;HU-	protein		
GI_18104975-S	636.9	477.1	348.6	PTPLA	NM_014241.2		protein		signal

GI_18104977-S	1547.4	2294.3	1783.5	PTPN1	NM_002827.2	PTP1B	protein	soluble	signal
GI_18104978-I	398.2	541.2	427	PTPN2	NM_002828.2	PTPT;TCPTP;TC-PTP;TCELLPTP	protein		protein
GI_18104981-A	383.5	339.2	256	PTPN2	NM_080423.1	PTPT;TCPTP;TC-PTP;TCELLPTP	protein		protein
GI_18104985-S	192.5	232.3	183.9	PTPN3	NM_002829.2	PTPH1	structural	cytoskelet	protein
GI_18104987-S	215.7	266.1	255.7	PTPN4	NM_002830.2	PTPMEG;PTPMEG1	non-	cytoskelet	protein
GI_18104994-A	488.9	869.8	791.2	AP1G2	NM_003917.2	G2AD	protein	Golgi	nonselecti
GI_18104995-I	160.5	178.3	161.9	AP1G2	NM_080545.1	G2AD	protein	Golgi	nonselecti
GI_18105001-A	128.4	133.8	119.6	AP1GBP1	NM_080551.1	SYNG		secretory	intracellula
GI_18105001-I	125.3	145.9	132	AP1GBP1	NM_080551.1	SYNG		secretory	intracellula
GI_18105005-S	465	510.6	622	AP1M1	NM_032493.2	AP47;CLTNM;MU-1A;CLAPM2	protein	coated pit	endocytosi
GI_18105006-S	259.8	221	217.7	CAD	NM_004341.2		carbamoyl-	cytoplasm	'de novo'
GI_18105008-S	3166.1	2770.9	2357.9	CAMLG	NM_001745.2	CAML		integral to	defense
GI_18105009-S	166.5	184.6	165	2-Apr	NM_014318.2				apoptosis
GI_18105011-I	393.6	417.6	438.8	3-Apr	NM_016085.2	p18;HSPC013			
GI_18105013-A	5174.2	4952.1	5072.1	3-Apr	NM_080592.1	p18;HSPC013			
GI_18105017-I	112.5	115.5	116.5	COLQ	NM_080538.1	EAD	DNA	basal	acetylcholi
GI_18105025-I	139.8	150.6	147.3	COLQ	NM_080542.1	EAD	DNA	basal	acetylcholi
GI_18105029-A	125.4	177.3	127.6	COLQ	NM_080544.1	EAD	DNA	basal	acetylcholi
GI_18105031-S	141.6	149.6	136.8	COL10A1	NM_000493.2		collagen	collagen	skeletal
GI_18105033-S	95.4	122.9	108.7	COLEC10	NM_006438.2	CLL1	lectin [goid	cytoplasm	
GI_18105034-S	93.2	96	100.4	COX7A1	NM_001864.2	COX7A;COX7AH;COX7AM	cytochrom	inner	energy
GI_18105035-S	3839.5	5180.1	4292.7	COX7A2	NM_001865.2	COX7AL;COX7AL1;COXVIIa-L	aa3-type	inner	electron
GI_18105036-S	3135.4	3053	2624.9	COX7A2L	NM_004718.2	EB1;SIG81;COX7AR;COX7RP	cytochrom	mitochond	electron
GI_18105038-S	4706.1	7407.6	5482.4	COX7B	NM_001866.2		cytochrom	mitochond	
GI_18105039-S	11696.8	12412	10785	COX7C	NM_001867.2		aa3-type	mitochond	energy
GI_18105040-I	102.1	106.4	96.9	GAB2	NM_012296.2	KIAA0571			
GI_18105041-A	781.3	514.7	437.2	GAB2	NM_080491.1	KIAA0571			
GI_18105041-I	112.1	113.1	101.8	GAB2	NM_080491.1	KIAA0571			
GI_18105044-S	459.9	677.5	775	HIST1H2AH	NM_080596.1	H2A/S;H2AFALii;dJ86C11.1	DNA	nucleus	nucleoso
GI_18105047-S	5106.9	7187.7	6409.6	HIST1H2BK	NM_080593.1	H2B/S;H2BFT;H2BFAiii	DNA	chromoso	nucleoso
GI_18105049-S	100.7	108.6	104.4	DES	NM_001927.2	CSM1;CSM2;CMD1I;FLJ12025	structural	intermedia	regulation
GI_18105051-S	140.5	170.2	153.2	MAGEH1	NM_014061.3	1-Apr			apoptosis
GI_18105052-S	2065.3	1791.3	1565.8	RAE1	NM_003610.2	MRNP41;Mnrp41;FLJ30608;dJ481F12.3;dJ8	RNA	nuclear	mRNA-
GI_18105053-S	445.4	480.7	492.3	KIFAP3	NM_014970.2	KAP3;SMAP;Smg GDS;Smg-	molecular	endoplas	signal
GI_18105057-S	440.5	497.2	567.3	VPS33B	NM_018668.2	FLJ14848	protein	membran	protein
GI_18105059-I	227.1	261.6	243.8	VPS41	NM_014396.2	HVSP41			
GI_18105060-A	751.2	777.6	714.3	VPS41	NM_080631.1	HVSP41			
GI_18105062-S	661.3	808.1	695.4	VPS45A	NM_007259.2	H1;VPS45;VSP45;VPS45B;VSP45A;H1VPS4	protein	Golgi	intracellula
GI_18105064-S	194.5	214.7	196.5	VN1R1	NM_020633.2	V1RL1;ZVNH1;ZVNR1;VNR19I1			
GI_18105065-S	97.6	111.1	109	HIST1H4I	NM_003495.2	H4M;H4/m;H4FM			
GI_18129625-S	95.8	101.5	92.9	MGC4473	NM_080719.1				
GI_18129633-S	193.9	229.3	223.1	C20orf86	NM_080674.1	bA196N14.3			
GI_18129689-S	115	113.1	106.7	TBX4	NM_018488.2		transcripti	nucleus	regulation
GI_18139548-S	170.3	181.1	169.3	SET7	NM_030648.1	SET9;FLJ21193;KIAA1717	methyltran	nucleus	chromatin

GI_18141296-I	82.4	87.5	90	SCRIB	NM_015356.1	CRIB1;SCRB1;SCRIB1;Vartul;KIAA0147	protein		intracellula
GI_18141306-S	4742.5	4962.6	4144.3	SLC7A11	NM_014331.2	xCT;CCBR1	cystine:glu	integral to	protein
GI_18141314-S	112.6	110	111.9	EDG8	NM_030760.2	S1P5;Edg-8;SPPR-1;SPPR-2			
GI_18141315-S	314.1	335.5	329.6	SSB1	NM_025106.2	FLJ22393			intracellula
GI_18141577-A	481.5	551.7	515.4	EGLN2	NM_080732.1	EIT6;PHD1;HIFPH1;DKFZp434E026			
GI_18152766-S	230.6	236.9	253	SYTL4	NM_080737.1		transporte	membran	transport
GI_18152772-S	121.3	128.3	123.8	NEU4	NM_080741.1	MGC18222	exo-alpha-		carbohydr
GI_18152774-S	92.3	91.2	113.7	B3GAT2	NM_080742.1	GLCATS;GlcAT-S;KIAA1963;bA156I14.1	galactosyl	Golgi	carbohydr
GI_18152778-S	450.4	1202.3	218.4	SRCRB4D	NM_080744.1	S4D-SRCRB;SRCRB-S4D			
GI_18152784-S	4503.1	6034.9	6996.2	C20orf52	NM_080748.1	bA353C18.2		integral to	
GI_18152788-S	215.4	265.5	260.2	ZSWIM3	NM_080752.1	FLJ32079;C20orf164;dJ337O18.7			
GI_18201869-S	93.3	92.7	86.1	GPR82	NM_080817.1		rhodopsin-	integral to	G-protein
GI_18201877-S	396.9	473.5	640.1	C20orf108	NM_080821.1	5A3;dJ1167H4.1;DKFZP434A1114		integral to	
GI_18201879-S	240.5	320.6	310.4	OVCA2	NM_080822.1				
GI_18201883-S	100.6	97.4	87.6	C20orf173	NM_080828.1	FLJ25360;dJ477O4.4			
GI_18201885-S	132.9	139.9	143.8	C20orf175	NM_080829.1	FLJ32230;dJ530I15.2	chemokin	extracellul	immune
GI_18201887-S	92.1	79.2	80.6	PABPC5	NM_080832.1	PABP5	RNA		
GI_18201889-S	134.9	131.8	128	C20orf152	NM_080834.1	dJ954P9.1			
GI_18201895-A	111.9	128.2	114.8	TBX5	NM_080718.1	HOS	RNA		heart
GI_18201897-A	153.6	146.7	157.6	TBX6	NM_080758.1		DNA		mesoderm
GI_18201897-I	343.9	406	382	TBX6	NM_080758.1		DNA		mesoderm
GI_18201899-I	276.6	362.1	319.6	TBX6	NM_004608.2		DNA		mesoderm
GI_18201901-S	1794.4	1629.8	1272.3	HARSL	NM_012208.2	HO3;HARSR	ATP	cytoplasm	histidyl-
GI_18201902-S	3449.8	4514.1	3997.1	HARS	NM_002109.3	HRS;FLJ20491	ATP	cytoplasm	histidyl-
GI_18201903-S	183.8	193.8	182.6	EPHA8	NM_020526.2	EEK;HEK3;KIAA1459	signal	integral to	protein
GI_18201904-S	4176.7	4539.8	3851.8	GPI	NM_000175.2	AMF;NLK;PGI;PHI;GNPI;SA-36	cytokine		hemostasi
GI_18201906-S	1196	1755.5	1241.3	PRAME	NM_006115.2	MAPE;OIP4	tumor		
GI_18201907-I	223.5	235.6	199.4	VCAM1	NM_001078.2	INCAM-100	cell	integral to	cell-cell
GI_18201908-A	93.1	96.7	108.6	VCAM1	NM_080682.1	INCAM-100	cell	integral to	cell-cell
GI_18201910-S	93.5	103.5	96.3	VTN	NM_000638.2	V75;VNT	cell	extracellul	cell
GI_18201912-S	148.2	198.1	175.8	FOXN1	NM_003593.2	WHN;FKHL20	specific	nucleus	epidermal
GI_18201914-A	128.3	155.9	132.3	COL11A2	NM_080679.1	HKE5;PARP;STL3;DFNA13	collagen	collagen	skeletal
GI_18201916-I	141.7	168	154.2	COL11A2	NM_080680.1	HKE5;PARP;STL3;DFNA13	collagen	collagen	skeletal
GI_18201920-A	147.8	317.7	332.3	COL12A1	NM_080645.1	COL12A1L;BA209D8.1;DJ234P15.1	collagen	collagen	skeletal
GI_18201922-I	103.9	104.4	97.4	COL12A1	NM_004370.4	COL12A1L;BA209D8.1;DJ234P15.1	collagen	collagen	skeletal
GI_18254455-S	125.7	142.7	131	TSGA2	NM_080860.1	FLJ32753			meiosis
GI_18254459-S	98.4	114.8	96.4	SSB4	NM_080862.1	SSB-4			intracellula
GI_18254463-S	109.8	102.4	102.7	RLN3	NM_080864.1	H3;RXN3;ZINS4;insl7	hormone	extracellul	physiologi
GI_18254471-S	160.3	176.6	172.4	UNC5D	NM_080872.1	Unc5h4;KIAA1777	serpin		signal
GI_18254473-S	101.5	104.8	95.7	ASB11	NM_080873.1				intracellula
GI_18266677-S	85.6	82.3	83.6	LOC129026	NM_080842.1				
GI_18373304-S	205.4	206.7	213	ARRDC2	NM_015683.1	PP2703;CLONE24945			sensory
GI_18373307-S	2087.9	1937.8	2290.7	RAB40C	NM_021168.1	RARL;RASL8C	GTP		protein
GI_18373330-S	110.2	122.9	100.4	RAB40A	NM_080879.1	RAR2A;Rar-2;FLJ32297	GTP		protein

GI_18373333-S	924.9	981.7	964.3	TMEM14B	NM_030969.2	MGC1223	molecular	integral to	
GI_18375500-I	721.9	826.8	703.6	APEX1	NM_001641.2	APE;APX;APE1;APEN;APEX;HAP1;REF1;R	DNA-	obsolete	base-
GI_18375502-A	4563.4	5167.2	4510.7	APEX1	NM_080648.1	APE;APX;APE1;APEN;APEX;HAP1;REF1;R	DNA-	obsolete	base-
GI_18375506-S	825.7	822.5	975.8	APEX2	NM_014481.2	APE2;XTH2;APEXL2	endonucle		DNA
GI_18375508-S	405	524.7	210.6	APXL	NM_001649.2	HSAPXL	amiloride-		intracellula
GI_18375514-S	174.5	206.9	166.7	APCS	NM_001639.2	SAP;PTX2	amyloid	extracellul	protein
GI_18375515-A	316	367.7	339.7	ACPT	NM_080791.1				
GI_18375517-I	109.7	112.3	107.4	COL11A1	NM_001854.2	STL2;COLL6	collagen	collagen	cartilage
GI_18375519-I	97.9	97.4	82.2	COL11A1	NM_080629.1	STL2;COLL6	collagen	collagen	cartilage
GI_18375521-A	106.9	118	116.6	COL11A1	NM_080630.1	STL2;COLL6	collagen	collagen	cartilage
GI_18375523-I	194.9	151.4	187.3	UPF3A	NM_023011.2	UPF3;HUPF3A;RENT3A	nucleocyto	cytoplasm	mRNA
GI_18375524-A	749.9	604.3	626.5	UPF3A	NM_080687.1	UPF3;HUPF3A;RENT3A	nucleocyto	cytoplasm	mRNA
GI_18375526-A	384.6	313.9	259.4	UPF3B	NM_023010.2	UPF3X;HUPF3B;RENT3B			
GI_18375529-I	197.6	253.7	218	TREX1	NM_016381.2	DRN3;ATRIP;FLJ12343;DKFZp434J0310	3'-5'		DNA
GI_18375534-A	365.4	330.8	381.1	TREX1	NM_033629.1	DRN3;ATRIP;FLJ12343;DKFZp434J0310	3'-5'		DNA
GI_18375536-I	191.3	211.1	217.8	TREX2	NM_007205.2	UIP1;XQ28ORF	3'-5'		DNA
GI_18375537-A	946.4	777	747.6	TREX2	NM_017518.3	UIP1;XQ28ORF	3'-5'		DNA
GI_18375537-I	597.4	484.9	460.3	TREX2	NM_017518.3	UIP1;XQ28ORF	3'-5'		DNA
GI_18375604-I	649.9	838.5	1005.8	TBX3	NM_016569.2	UMS;XHL;TBX3-ISO	RNA	nucleus	skeletal
GI_18375606-A	132.8	153.5	169.1	TBX3	NM_005996.2	UMS;XHL;TBX3-ISO	RNA	nucleus	skeletal
GI_18375606-I	238.1	275.9	239.7	TBX3	NM_005996.2	UMS;XHL;TBX3-ISO	RNA	nucleus	skeletal
GI_18375608-A	124	115.4	103.3	DACH	NM_004392.2	DACH1;FLJ10138		nucleus	eye
GI_18375610-I	336.6	413.2	373.9	DACH	NM_080759.1	DACH1;FLJ10138		nucleus	eye
GI_18375616-I	105	101.8	105.6	DATF1	NM_022105.2	DIO1;FLJ11265;KIAA0333	DNA	nucleus	transcripti
GI_18375618-I	91.9	117.8	103.7	DATF1	NM_080796.1	DIO1;FLJ11265;KIAA0333	DNA	nucleus	transcripti
GI_18375620-A	273.5	501	893.9	DATF1	NM_080797.1	DIO1;FLJ11265;KIAA0333	DNA	nucleus	transcripti
GI_18375627-A	798.8	779.4	695.2	BAT2	NM_004638.2	G2;D6S51;D6S51E	MHC-		
GI_18375629-A	1088.1	1381.3	1204.4	BAT3	NM_080702.1	G3;D6S52E	MHC-		
GI_18375635-S	274.2	309.6	291.5	BAT4	NM_033177.2	G5;D6S54E	nucleic	intracellula	
GI_18375636-I	135.1	152.5	133.7	BAT8	NM_006709.2	G9A;NG36;NG36/G9a	methyltran	nucleus	chromatin
GI_18375640-S	108.1	113.7	108	BATF	NM_006399.2	B-ATF;SFA-2	RNA	nucleus	antimicrob
GI_18375647-A	386.1	450	336.5	PTPN13	NM_080684.1	PNP1;FAP-1;PTP1E;PTPL1;PTPLE;PTP-	non-	kinesin	protein
GI_18375651-S	1207.5	878.7	1029.5	PTPN12	NM_002835.2	PTPG1;PTP-PEST	tumor	soluble	protein
GI_18375654-S	174.2	200.4	191.3	PTPN18	NM_014369.2	BDP1	non-		protein
GI_18375656-S	163.3	177.6	152.1	PTPN21	NM_007039.2	PTPD1;PTPRL10	protein	peripheral	protein
GI_18375659-I	115.2	134.7	116.7	PTPN7	NM_080588.1	LPTP;HEPTP;PTPNI;BPTP-4;LC-PTP	protein	cytoplasm	protein
GI_18375661-A	269.8	332.3	291.1	PTPN7	NM_080589.1	LPTP;HEPTP;PTPNI;BPTP-4;LC-PTP	protein	cytoplasm	protein
GI_18375663-S	434.2	544.6	449.9	PTPN9	NM_002833.2	MEG2	non-	intracellula	protein
GI_18375664-A	188.5	219.7	213	TRPV1	NM_018727.3	VR1;DKFZp434K0220	calcium	integral to	chemosen
GI_18375664-I	132.6	144.1	126.2	TRPV1	NM_018727.3	VR1;DKFZp434K0220	calcium	integral to	chemosen
GI_18375666-I	88.1	94.9	99.3	TRPV1	NM_080704.1	VR1;DKFZp434K0220	calcium	integral to	chemosen
GI_18375668-I	82	90.6	82.9	TRPV1	NM_080705.1	VR1;DKFZp434K0220	calcium	integral to	chemosen
GI_18375670-I	98.3	108	90.5	TRPV1	NM_080706.1	VR1;DKFZp434K0220	calcium	integral to	chemosen
GI_18375672-S	482.2	540	447.5	RENT1	NM_002911.2	UPF1;HUPF1;NORF1;pNORF1;KIAA0221	helicase	cytoplasm	mRNA

GI_18375674-A	1681.9	1300.4	1203.7	UPF2	NM_015542.2	HUPF2;RENT2;KIAA1408;DKFZP434D222	RNA		protein
GI_18375674-I	158.8	163.6	168	UPF2	NM_015542.2	HUPF2;RENT2;KIAA1408;DKFZP434D222	RNA		protein
GI_18375675-I	100.7	104.4	96.4	UPF2	NM_080599.1	HUPF2;RENT2;KIAA1408;DKFZP434D222	RNA		protein
GI_18375679-S	3089.3	3333.1	3281.3	WBP11	NM_016312.2	NPWBP	single-	nucleus	regulation
GI_18375680-S	104.5	97.9	92.4	WBSCR23	NM_025042.2	FLJ22367			
GI_18378730-S	855.2	995.5	1036.3	BBX	NM_020235.2	MDS001			
GI_18378734-S	238.8	232.4	182	CAP350	NM_014810.2	KIAA0480			
GI_18379326-S	1026	1039.4	868.7	RNUT1	NM_005701.2	KPNBL	snRNA	nuclear	nucleocyto
GI_18379329-I	99.6	112.5	106.5	WAC	NM_100264.1	Wwp4;BM-			
GI_18379331-A	2487	2032.8	1665.9	WAC	NM_100486.1	Wwp4;BM-			
GI_18379333-A	1961.1	1820.1	1831.5	RNPS1	NM_080594.1	E5.1	RNA	nucleus	RNA
GI_18379335-I	126.5	142	126.2	RNPS1	NM_006711.2	E5.1	RNA	nucleus	RNA
GI_18379336-I	264.6	326.5	273.1	VPS52	NM_080564.1	ARE1;SAC2;ARE-1;SACM2L;RP5-	vesicle		nonselecti
GI_18379338-S	167.5	207.8	202.2	IL27RA	NM_004843.2	CRL1;TCCR;WSX1;IL27R;zcytor1	transmem	integral to	cell
GI_18379339-A	855	893.8	834.5	VPS52	NM_022553.3	ARE1;SAC2;ARE-1;SACM2L;RP5-	vesicle		nonselecti
GI_18379341-S	208	136.3	139.9	SORCS1	NM_052918.2	BA446H13.1		integral to	
GI_18379343-S	111.3	101.9	105.3	SORCS2	NM_020777.1	KIAA1329	protein	integral to	intracellula
GI_18379345-S	138.2	156.9	137.3	SORCS3	NM_014978.1	SORCS;KIAA1059	protein	integral to	intracellula
GI_18379347-S	144.7	134.4	127.9	SORL1	NM_003105.3	LR11;LRP9;SORLA;gp250;SorLA-1	internaliza	integral to	receptor
GI_18379348-S	282.8	318.8	340.3	VAT1	NM_006373.2	VATI;FLJ20230		synaptic	
GI_18379350-S	110.1	117.6	104.4	VPREB1	NM_007128.2	IGI;IGVPB;VPREB	antigen	extracellul	immune
GI_18379351-S	329.8	356.1	327.5	WDFY2	NM_052950.2	WDF2;ZFYVE22	zinc ion		electron
GI_18379352-S	180.6	205.2	185.4	WFDC1	NM_021197.2	PS20	molecular	extracellul	negative
GI_18379354-S	93.4	104	85.8	WIF1	NM_007191.2	WIF-1	protein-		signal
GI_18379355-I	113.9	107.4	108.8	WFDC2	NM_080733.1	HE4;WAP5;dJ461P17.6	endopepti	extracellul	proteolysis
GI_18379359-I	223.6	280.9	250.2	WFDC2	NM_080735.1	HE4;WAP5;dJ461P17.6	endopepti	extracellul	proteolysis
GI_18379361-A	162.6	184.2	162.4	WFDC2	NM_080736.1	HE4;WAP5;dJ461P17.6	endopepti	extracellul	proteolysis
GI_18379361-I	102.6	119.7	97.3	WFDC2	NM_080736.1	HE4;WAP5;dJ461P17.6	endopepti	extracellul	proteolysis
GI_18379365-S	2035.9	2420.2	2901.3	ZMPSTE24	NM_005857.2	STE24;FACE-1;Ste24p;FLJ14968	metalloex	Golgi	proteolysis
GI_18390318-S	160.2	179.5	172.6	DKFZp564I19	NM_015419.1		vascular		protein
GI_18390348-S	23194.2	22454	18813	RPL7A	NM_000972.2	TRUP;SURF3	structural	cytosolic	protein
GI_18426870-S	400.3	235.7	126.6	ASGR1	NM_001671.2	ASGPR;Hs.12056	asialoglyc	integral to	receptor
GI_18426872-I	143.3	165	154	ASGR2	NM_080912.1	L-H2;ASGP-R;Hs.1259	asialoglyc	integral to	cell
GI_18426876-A	93.8	106.8	93.8	ASGR2	NM_080914.1	L-H2;ASGP-R;Hs.1259	asialoglyc	integral to	cell
GI_18426878-A	478.1	558.9	545.4	BAT8	NM_025256.4	G9A;NG36;NG36/G9a	methyltran	nucleus	chromatin
GI_18426887-S	212.7	271.5	209.8	LOC91219	NM_080924.1				
GI_18426889-S	641.1	632.5	587.8	LOC96610	NM_080926.1				
GI_18426895-S	971.7	1388.7	1315.9	DCTN6	NM_006571.2	WS-3	cell	dynactin	mitochond
GI_18426897-I	103.4	90.6	93.3	GNAS	NM_080425.1	AHO;GSA;GSP;POH;GPSA;NESP;GNAS1;P	heterotrim	peripheral	Golgi to
GI_18426899-A	8285.8	9799.6	9910.3	GNAS	NM_080426.1	AHO;GSA;GSP;POH;GPSA;NESP;GNAS1;P	heterotrim	peripheral	Golgi to
GI_18426901-I	288.5	334.8	255.9	WRNIP1	NM_020135.2	WHIP;FLJ22526;bA420G6.2			
GI_18426903-A	1829.9	1978.2	1398.6	WRNIP1	NM_130395.1	WHIP;FLJ22526;bA420G6.2			
GI_18426905-S	89.8	114.9	90.8	DBH	NM_000787.2		catalytic	soluble	synaptic
GI_18426907-I	98	114.9	100.8	SIRPB2	NM_018556.2	SIRP-B2;bA77C3.1		integral to	negative

GI_18426908-A	184.5	253.2	191.9	SIRPB2	NM_080816.1	SIRP-B2;bA77C3.1		integral to	negative
GI_18426910-S	1144.5	1317.4	321.2	PTPNS1	NM_080792.1	BIT;MFR;P84;SIRP;MYD-1;SHPS1;SHPS-	receptor	plasma	cell
GI_18426912-I	460.3	569.4	483.5	DBN1	NM_080881.1	D0S117E;DKFZp434D064	actin	actin	
GI_18426914-A	2454.4	2785.4	1798.4	DBN1	NM_004395.2	D0S117E;DKFZp434D064	actin	actin	
GI_18426914-I	98.2	116.1	99.2	DBN1	NM_004395.2	D0S117E;DKFZp434D064	actin	actin	
GI_18426962-A	4391.1	4363.3	3856.8	DGUOK	NM_001929.2	DGK	deoxygua	mitochond	guanosine
GI_18426964-I	160.6	169.7	152.2	DGUOK	NM_080915.1	DGK	deoxygua	mitochond	guanosine
GI_18426972-S	1659.4	1805.8	1450.5	DRAP1	NM_006442.2	NC2-alpha	transcripti		negative
GI_18426974-S	187.8	225.4	202.9	HLA-DQA1	NM_002122.2	DQA1;HLA-DQ;CELIAC1;HLA-DQA	class II	integral to	pathogene
GI_18450368-I	90.2	91.1	84	PTPRA	NM_080840.1	LRP;HLPR;PTPA;HEPTP;HPTPA;RPTPA;PT	transmem	integral to	protein
GI_18450370-A	1003.9	898.8	546.7	PTPRA	NM_080841.1	LRP;HLPR;PTPA;HEPTP;HPTPA;RPTPA;PT	transmem	integral to	protein
GI_18450370-I	313.9	394	338.1	PTPRA	NM_080841.1	LRP;HLPR;PTPA;HEPTP;HPTPA;RPTPA;PT	transmem	integral to	protein
GI_18482382-S	98.6	121.8	127	KLHL6	NM_130446.1	FLJ00029	protein		
GI_18482384-S	81.8	95.2	72.1	SLC38A4	NM_018018.2	ATA3;NAT3;PAAT;FLJ10191			
GI_18490979-A	1057.2	761.7	609.6	HOM-TES-10	NM_080731.1	FLJ20703;DKFZP586I2223			
GI_18490979-I	227.9	281.6	220.7	HOM-TES-10	NM_080731.1	FLJ20703;DKFZP586I2223			
GI_18490981-S	187.9	131.5	149.6	THSD2	NM_032784.2	PWTSR;FLJ14440	electron		electron
GI_18490985-S	95.5	106.5	96.1	RPL10L	NM_080746.2		structural	ribosome	protein
GI_18490986-S	873.9	1023.4	937.6	C1orf33	NM_016183.2	dJ657E11.4	structural	ribosome	protein
GI_18490988-S	12703.9	14602	11067	RPS27L	NM_015920.2		zinc ion	ribosome	protein
GI_18490989-S	349	829.8	298.8	MX1	NM_002462.2	MX;MxA;IFI78;IFI-78K	GTPase	cytoplasm	induction
GI_18490990-S	1006.7	1362.2	1501.9	TOPK	NM_018492.2	SPK;Nori-3;FLJ14385	ATP		protein
GI_18490992-I	116.4	108.5	109.8	MRVI1	NM_130385.1	IRAG	tumor	endoplas	oncogene
GI_18490994-A	96.1	107.4	109.4	MRVI1	NM_006069.2	IRAG	tumor	endoplas	oncogene
GI_18490994-I	221.9	309.3	259.9	MRVI1	NM_006069.2	IRAG	tumor	endoplas	oncogene
GI_18490996-A	102.3	94.8	97.3	CR1	NM_000573.2	C3BR;CD35	compleme	integral to	compleme
GI_18490998-I	106.2	102.8	101.8	WISP1	NM_003882.2	CCN4	insulin-like	soluble	oncogene
GI_18490999-A	110.4	120.5	104.7	WISP1	NM_080838.1	CCN4	insulin-like	soluble	oncogene
GI_18491001-S	246.6	288.1	267.2	WISP2	NM_003881.2	CCN5;CT58;CTGF-L	insulin-like	soluble	oncogene
GI_18491002-I	93	89.9	99.1	WISP3	NM_003880.2	PPD;CCN6;LIBC;PPAC		soluble	oncogene
GI_18491003-A	146.8	160.8	136.5	WISP3	NM_130396.1	PPD;CCN6;LIBC;PPAC		soluble	oncogene
GI_18491003-I	98	118.4	106.1	WISP3	NM_130396.1	PPD;CCN6;LIBC;PPAC		soluble	oncogene
GI_18491007-S	201.5	189.6	113.9	CYP2J2	NM_000775.2	CPJ2	arachidoni	membran	regulation
GI_18491009-S	195.7	136	109.3	PTPRB	NM_002837.2	PTPB;HPTPB;HPTP-BETA;R-PTP-BETA	transmem	membran	phosphate
GI_18491011-I	148	143.7	153.9	FLJ14249	NM_022460.2				intracellula
GI_18491013-A	2462.8	1808.5	2135.2	FLJ14249	NM_106552.1				intracellula
GI_18491021-S	223.7	227.4	176.2	C20orf12	NM_018152.2	C20orf84;FLJ10600;FLJ30892;dJ568F9.2;bA			
GI_18491023-I	184.8	251.4	304.4	DPP3	NM_005700.2	FLJ11387;FLJ22331	dipeptidyl-	cytoplasm	proteolysis
GI_18491025-A	1747.5	2703.3	3281	DPP3	NM_130443.1	FLJ11387;FLJ22331	dipeptidyl-	cytoplasm	proteolysis
GI_18491027-S	10983.1	10205	8100.9	C15orf15	NM_016304.2	L30;RLP24;RPL24;RPL24L;HRP-L30-iso	structural	ribosome	protein
GI_18496982-S	277.2	508.4	264.4	CLIPR-59	NM_015526.1	CLIPR59;DKFZp586N1922			
GI_18497285-S	1440.2	1289	1012.3	DHX36	NM_020865.1	DDX36;MLEL1;KIAA1488	nucleic		
GI_18497287-S	585.1	1564.1	2195.9	LTBP3	NM_021070.2	LTBP2;DKFZP586M2123			
GI_18497297-S	237.5	277	296.3	TOR2A	NM_130459.1	TORP1;FLJ14771			

GI_18543372-S	884.9	1006.6	748.4	MMP17	NM_016155.2	MT4-MMP	enzyme	extracellul	proteolysis
GI_18543374-S	96	100.4	105.3	PURG	NM_013357.2	PURG-A;PURG-B			
GI_18546481-S	135.1	157.7	161.5	LOC148713	XM_086287.1				
GI_18548545-S	200.8	226.1	202.8	KIAA1337	XM_052561.5				
GI_18549712-S	311	377	353	LOC128372	XM_060957.2				
GI_18549722-S	113.8	127.4	116	LOC128368	XM_060953.2				
GI_18549724-S	156.5	198.8	154.9	LOC128367	XM_060952.2				
GI_18550284-S	110	121.7	101.2	KIAA1912	XM_055636.2				
GI_18552042-S	163.6	173.6	155.4	LOC151154	XM_098008.1				
GI_18552201-S	120.5	145.3	145.5	LOC151200	XM_098022.1				
GI_18553076-S	110.5	112.7	100.1	LOC151443	XM_087200.1				
GI_18553091-S	105.3	110	89.6	LOC130839	XM_059473.2				
GI_18553104-S	285.3	326.6	304.9	LOC151451	XM_087208.1				
GI_18555356-S	162	170	164.4	LOC152118	XM_098163.1				
GI_18555449-S	120.6	127.2	121.6	LOC152138	XM_093644.1				
GI_18555804-S	211.6	230.5	212.5	LOC131920	XM_059548.2				
GI_18560129-S	118.1	132	119.7	LOC153297	XM_098350.1				
GI_18562551-S	96.5	95	87.6	LOC153959	XM_098450.1				
GI_18562991-S	244.9	307.7	270.2	PLEKHG1	XM_027307.2				
GI_18563960-S	101.7	111.5	96.4	LOC154323	XM_098512.1				
GI_18564472-S	279.7	365.7	305.9	LOC154449	XM_087928.1				
GI_18566487-S	81.3	90.3	81.9	LOC154907	XM_088072.1				
GI_18570944-S	90.8	87.9	81.9	C8orf7	XM_088376.1				
GI_18572392-S	82.9	86	84.3	LOC158131	XM_088491.1				
GI_18572749-S	133.2	145.4	134.3	LOC158226	XM_088516.1				
GI_18573403-S	99.7	102	92.3	C9orf4	XM_088565.1				
GI_18575382-S	94.5	98.2	78.1	LOC143034	XM_096376.1				
GI_18577864-S	98.4	101.6	88.2	LOC143678	XM_096472.1				
GI_18580213-S	115.5	176.1	141	KIAA0984	XM_037557.2				
GI_18580675-S	151	172	158.9	LOC144631	XM_096642.1				
GI_18582778-S	95.8	91.9	105.7	LOC145197	XM_096734.1				
GI_18584496-S	164.7	168.7	161.7	LOC145846	XM_096883.1				
GI_18589705-S	121	137	122.8	LOC147649	XM_085830.1				
GI_18590346-S	120.7	143	126.2	LOC147941	XM_097347.1				
GI_18590348-S	115.1	128.5	103.9	LOC147942	XM_085967.1				
GI_18591447-S	78.3	108.6	96.4	LOC126520	XM_059051.2				
GI_18591841-S	177.1	188.2	162.9	LOC149709	XM_086637.1				
GI_18591846-S	112.1	110.3	126.9	LOC149710	XM_086659.1				
GI_18592730-S	467.3	366.2	319	LOC149934	XM_086725.1				
GI_18592785-S	156.1	169.5	176	LOC149950	XM_086732.1				
GI_18594428-S	450.4	474.6	368.1	KIAA0767	XM_027105.3				
GI_18594499-S	158.5	196.2	180.4	FLJ13330	NM_025091.2				
GI_18595513-S	126.9	98.7	91.5	LOC158724	XM_098981.1	MGC27003			
GI_18595832-S	106.5	98.7	100.7	LOC158813	XM_088680.1				

GI_18598508-S	495.1	413.3	374.9	CDR2	XM_071866.2				
GI_18599649-S	107.3	111.1	113.5	LOC152920	XM_087561.1				
GI_18599776-S	899.5	810.4	812.1	FLJ13456	XM_038291.5				
GI_18602338-S	106.9	113.2	102.5	LOC145760	XM_085225.1				
GI_18605326-S	180.6	192.3	183.8	LOC120776	XM_062286.2				
GI_18605333-S	187.9	234.8	213.5	LOC144125	XM_090203.1				
GI_18640735-S	252.1	331.6	269.2	CACH-1	NM_130767.1		serine		fatty acid
GI_18640737-S	108.7	119.9	110	GASZ	NM_130768.1		signal	cytoplasm	germ-cell
GI_18640739-S	195.7	205.6	189.5	HTR3C	NM_130770.1		extracellul	integral to	ion
GI_18640743-S	101.8	118.7	99.7	S100Z	NM_130772.1		calcium		
GI_18640747-S	1910.6	1617.4	1179.9	RAB24	NM_130781.1				
GI_18640749-S	100.7	134.5	104.2	RGS18	NM_130782.1	RGS13	signal		signal
GI_18640753-S	347.4	398.2	313.1	C10orf94	NM_130784.1	bA108K14.6			
GI_18641280-A	2508.1	2157.2	1558	RFP	NM_030950.2	RNF76;TRIM27	nucleic	membran	spermatog
GI_18641344-A	117.5	128.6	120.5	TRIM34	NM_130390.1	IFP1;RNF21			
GI_18641344-I	84.2	78.7	77.6	TRIM34	NM_130390.1	IFP1;RNF21			
GI_18641346-I	214.2	216.9	216.6	PTPRC	NM_002838.2	LCA;LY5;B220;CD45;T200;GP180	transmem	integral to	cell
GI_18641348-S	168.5	266.7	231.2	TRIM6	NM_058166.2	RNF89	zinc ion	kinesin	
GI_18641349-S	118.2	870.4	176.5	COL15A1	NM_001855.2		collagen	collagen	cell
GI_18641351-S	218.6	416.4	355	COL16A1	NM_001856.2	447AA	collagen	collagen	pregnancy
GI_18641353-I	122	151.8	118.1	COL17A1	NM_000494.2	BP180;BPAG2;LAD-1;BA16H23.2		intercellula	epidermal
GI_18641355-A	243.7	193.4	162.7	COL17A1	NM_130778.1	BP180;BPAG2;LAD-1;BA16H23.2		intercellula	epidermal
GI_18641357-I	103.2	107.8	114.9	COLEC12	NM_030781.2	CLP1;SRCL;SCARA4	sugar	nucleus	regulation
GI_18641359-A	97.3	177	87.3	COLEC12	NM_130386.1	CLP1;SRCL;SCARA4	sugar	nucleus	regulation
GI_18641365-A	90.2	84.8	83.3	PTPRC	NM_080923.1	LCA;LY5;B220;CD45;T200;GP180	transmem	integral to	cell
GI_18641365-I	122.7	122.2	132.1	PTPRC	NM_080923.1	LCA;LY5;B220;CD45;T200;GP180	transmem	integral to	cell
GI_18641367-A	681.7	748.1	668.5	MXI1	NM_130439.1	MAD2;MXD2	transcripti	nucleus	negative
GI_18641367-I	154.2	155.7	164.5	MXI1	NM_130439.1	MAD2;MXD2	transcripti	nucleus	negative
GI_18641369-I	126.9	126.8	106.8	MXI1	NM_005962.2	MAD2;MXD2	transcripti	nucleus	negative
GI_18641371-S	239.7	334.8	273.9	HLA-DRB3	NM_022555.3	HLA-DR3B	class II	integral to	signal
GI_18641372-S	139.2	672.4	283.6	HLA-DRB4	NM_021983.3	HLA-DR4B	class II	integral to	signal
GI_18641376-S	146.6	410.9	172.4	HLA-DMB	NM_002118.3	RING7;D6S221E	MHC-	integral to	perception
GI_18641377-S	182.2	234	206.2	HLA-DOB	NM_002120.2		class II	integral to	immune
GI_18641378-S	134.3	456.8	222.5	HLA-DRA	NM_019111.2	HLA-DRA1	MHC	integral to	immune
GI_18644731-A	110.5	115.2	112.8	CST11	NM_080830.2	SC13;dJ322G13.6			
GI_18644735-I	103.5	88	100.5	RGS3	NM_130795.1	C2PA;RGP3;FLJ20370;PDZ-RGS3	GTPase	cytosol	regulation
GI_18644884-S	592.2	615.9	718.2	PDXK	NM_003681.2	PKH;PNK	pyridoxal		
GI_18677727-S	224.2	256	244	RAB3D	NM_004283.2	GOV;D2-2;RAB16;RAD3D	RAB small		hemocyte
GI_18677732-S	101.9	117.6	104.7	CPNE4	NM_130808.1	CPN4;COPN4;MGC15604			
GI_18677736-S	91.5	96	100.1	DYX1C1	NM_130810.1	EKN1;FLJ37882			
GI_18677769-S	157.4	160.6	141.2	DCNP1	NM_130848.1				
GI_18699719-S	531	466.4	358.2	PPP1R13B	NM_015316.1	p85;ASPP1;KIAA0771;p53BP2-like	defense/i	nucleus	apoptosis
GI_18699721-S	651.4	733.3	417.8	ShrmL	NM_020859.1	Shroom;KIAA1481	protein		
GI_18699723-S	708.3	773.8	513.8	C6orf111	NM_032870.1	FLJ14752;FLJ14992;bA98I9.2;DKFZp564B07			

GI_18699731-A	1986.8	2637.2	2712.3	Cab45	NM_016176.2				
GI_18702322-S	94.6	127.9	101.6	DNCL2B	NM_130897.1	DNLC2B	microtubul	cytoplasmi	microtubul
GI_18702326-S	100.3	105.7	111.9	MGC26988	NM_130899.1				
GI_18702328-S	93.5	92.2	82.9	RAET1L	NM_130900.1			membran	immune
GI_18702330-S	109.6	112.4	107.6	C15orf16	NM_130901.1	CEZANNE2			
GI_18702332-S	138.7	166.8	154.6	COX7B2	NM_130902.1				
GI_18765691-S	207	228.4	195.4	LAMC3	NM_006059.2	DKFZp434E202	structural	membran	cell shape
GI_18765693-S	128.3	150.7	134.1	DPP4	NM_001935.2	CD26;ADABP;ADCP2;DPPIV;TP103	dipeptidyl-	peripheral	immune
GI_18765695-A	207.8	228.2	200	DPP6	NM_001936.2	DPPX	dipeptidyl-	integral to	proteolysis
GI_18765695-I	108.8	131.2	106.2	DPP6	NM_001936.2	DPPX	dipeptidyl-	integral to	proteolysis
GI_18765697-I	112.2	107.7	99.7	DPP6	NM_130797.1	DPPX	dipeptidyl-	integral to	proteolysis
GI_18765699-I	96.7	118.9	113.8	ELMO1	NM_014800.8	CED12;KIAA0281	SH3-	cytoskelet	phagocyto
GI_18765701-A	176.3	350.1	433	ELMO1	NM_130442.1	CED12;KIAA0281	SH3-	cytoskelet	phagocyto
GI_18765701-I	101.4	115	118.3	ELMO1	NM_130442.1	CED12;KIAA0281	SH3-	cytoskelet	phagocyto
GI_18765703-A	341	405	356.8	PLUNC	NM_016583.2	LUNX;NASG;SPURT;SPLUNC1;bA49G10.5	defense/i	extracellul	response
GI_18765704-I	300.5	365.9	327.2	PLUNC	NM_130852.1	LUNX;NASG;SPURT;SPLUNC1;bA49G10.5	defense/i	extracellul	response
GI_18765706-I	166.5	208.6	187.4	SKIP	NM_130766.1		inositol-	cytoplasm	actin
GI_18765710-S	891.6	535.6	541.9	FJX1	NM_014344.2	FLJ22416		extracellul	
GI_18765712-S	3900.9	3873.8	3768	TSG101	NM_006292.2	TSG10	transcripti	kinesin	ubiquitin
GI_18765714-S	784.7	1382.8	577.8	HLA-DMA	NM_006120.2	HLADM;RING6;D6S222E	MHC-	integral to	perception
GI_18765719-S	95.4	114.8	113.6	MAB21L1	NM_005584.2	CAGR1			embryoge
GI_18765720-S	100.3	101	105.7	MAB21L2	NM_006439.3	FLJ31103		nucleus	neurogene
GI_18765721-S	294.2	318.1	299.3	MAGEL2	NM_019066.2	nM15;NDNL1	molecular	cellular_co	biological_
GI_18765724-S	179.3	194.5	166.9	MPP2	NM_005374.2	DLG2;DKFZp761D0712	guanylate	membran	signal
GI_18765726-S	105.9	102.7	111.2	MYOG	NM_002479.2	MYF4;MYOGENIN	transcripti	nucleus	myogenes
GI_18765728-I	282.9	289.3	259.2	SNAP23	NM_003825.2	SNAP23A;SNAP23B;HsT17016	t-SNARE	secretory	nonselecti
GI_18765730-A	355.2	313.8	264.3	SNAP23	NM_130798.1	SNAP23A;SNAP23B;HsT17016	t-SNARE	secretory	nonselecti
GI_18765734-A	637.2	1314.8	538.4	SNAP25	NM_130811.1	SNAP;SNAP-	molecular	cellular_co	regulation
GI_18765736-S	315.4	379.5	358.9	SNAP29	NM_004782.2	SNAP-29;FLJ21051	SNAP	kinesin	nonselecti
GI_18765737-A	1161	1605.5	1373.6	SMG1	NM_014006.2	ATX;LIP;KIAA0421	inositol/ph		
GI_18765738-I	159.8	152.8	130.5	SMG1	NM_015092.2	ATX;LIP;KIAA0421	inositol/ph		
GI_18765740-S	159.5	192.4	162.2	SNAI1	NM_005985.2	SNA;SNAH;SLUGH2;dJ710H13.1	DNA	nucleus	cartilage
GI_18765742-S	949.1	696.8	1099.9	SNTA1	NM_003098.2	SNT1;TACIP1;dJ1187J4.5	protein	membran	muscle
GI_18765743-S	182.4	232.5	211.9	SN	NM_023068.2	CD169;FLJ00051;FLJ00055;FLJ00073;FLJ32	lectin [goid	integral to	cell-matrix
GI_18765747-A	122.9	382.5	124.4	COL18A1	NM_130445.1	KNO	tumor	collagen	negative
GI_18765747-I	259.7	318.9	263.7	COL18A1	NM_130445.1	KNO	tumor	collagen	negative
GI_18765749-I	109.6	126.7	123.5	DYRK1A	NM_101395.1	MNB;DYRK;HP86;MNBH;DYRK1	protein	nucleus	neurogene
GI_18765751-I	122.1	125.1	112.3	DYRK1A	NM_130436.1	MNB;DYRK;HP86;MNBH;DYRK1	protein	nucleus	neurogene
GI_18765755-A	780.6	927	860.4	DYRK1A	NM_130438.1	MNB;DYRK;HP86;MNBH;DYRK1	protein	nucleus	neurogene
GI_18780268-S	93	101.1	88.3	COL19A1	NM_001858.2	COL9A1L;D6S228E	collagen	collagen	skeletal
GI_18780272-S	77.7	80.8	95.8	COL21A1	NM_030820.2	COLA1L;dJ708F5.1;dJ682J15.1;DKFZp564B	structural	microfibril	cell
GI_18780284-A	209.6	258.3	219.1	MADCAM1	NM_130762.1	MACAM1	cell	integral to	cell
GI_18860830-A	885.6	957.5	887	OPA1	NM_130831.1	NPG;NTG;largeG;FLJ12460;KIAA0567	GTP	mitochond	vision
GI_18860850-A	421.2	504.9	457.8	MEN1	NM_130801.1	MEAI;SCG2	protein	nucleus	regulation

GI_18860852-I	126.9	153.2	134.5	MEN1	NM_130802.1	MEAI;SCG2	protein	nucleus	regulation
GI_18860854-I	95	88.9	88.3	MEN1	NM_130803.1	MEAI;SCG2	protein	nucleus	regulation
GI_18860861-I	100.2	98.3	103	MADD	NM_130470.1	DENN;IG20;KIAA0358	death	cytoplasm	cell
GI_18860869-A	304.8	332.6	279.1	MADD	NM_130474.1	DENN;IG20;KIAA0358	death	cytoplasm	cell
GI_18860883-I	131.1	154.6	138.2	WWOX	NM_130791.1	FOR;FRA16D;HHCMA56;PRO0128;D16S43	catalytic		steroid
GI_18860887-A	138.7	148.2	143.3	WWOX	NM_130844.1	FOR;FRA16D;HHCMA56;PRO0128;D16S43	catalytic		steroid
GI_18860887-I	109.1	111.2	108.1	WWOX	NM_130844.1	FOR;FRA16D;HHCMA56;PRO0128;D16S43	catalytic		steroid
GI_18860893-A	128.4	131.9	121.3	PTPRD	NM_130393.1	HPTP;PTPD;HPTPD;HPTP-DELTA;R-PTP-	transmem	integral to	transmem
GI_18860895-A	1808.6	1358	1682.6	PTPRF	NM_130440.1	LAR	transmem	integral to	transmem
GI_18860897-S	435.1	536.6	363.6	PTPRG	NM_002841.2	PTPG;HPTPG;RPTPG;R-PTP-GAMMA	transmem	integral to	transmem
GI_18860899-S	109.9	129	107.2	PTPRJ	NM_002843.2	DEP1;SCC1;CD148;HPTPeta;R-PTP-ETA	transmem	integral to	transmem
GI_18860901-S	1245.7	1858	1119.8	PTPRK	NM_002844.2	R-PTP-kappa	transmem	integral to	protein
GI_18860903-S	695.6	1134.1	1136.5	PTPRM	NM_002845.2	RPTPM;RPTPU;PTPRL1;hR-PTPu;R-PTP-	transmem	integral to	protein
GI_18860905-S	509.1	360.5	2663.4	PTPRN	NM_002846.2	IA2;IA-2;ICA512;R-PTP-N;IA-2/PTP	transmem	integral to	protein
GI_18860906-S	298.1	353.3	301.6	USP31	NM_032236.3	USP48;FLJ11328;FLJ20103;FLJ23054;FLJ2	peptidase		ubiquitin-
GI_18860908-S	419	405.8	874.8	SNTB1	NM_021021.2	A1B;SNT2;BSYN2;DAPA1B;SNT2B1;TIP-	actin	peripheral	muscle
GI_18860909-A	1193.5	958.1	1223.9	SNTB2	NM_130845.1	SNT3;SNTL;SNT2B2;EST25263;D16S2531E	protein	dystrophin-	intracellula
GI_18860911-I	298.2	278.9	318.7	SNTB2	NM_006750.2	SNT3;SNTL;SNT2B2;EST25263;D16S2531E	protein	dystrophin-	intracellula
GI_18860912-S	870.6	853.7	791.5	SNW1	NM_012245.2	SKIP;NCOA-62	transcripti	nucleus	oncogene
GI_18860913-S	396.9	387.2	355.3	SAV1	NM_021818.2	SAV;WW45;WWP4;salvador		kinesin	
GI_18860914-S	113.4	114.9	98.9	XK	NM_021083.2	KX	transporte	integral to	small
GI_18860915-S	2556.7	3335.5	1701.2	XRN2	NM_012255.2	FLJ10711;FLJ20077;dJ198K11.2;DKFZp434	nuclease	nucleus	recombina
GI_18860917-S	207	153.4	160.1	XYLB	NM_005108.2	FLJ10343;FLJ12539;FLJ22075	xylulokina		energy
GI_18860919-S	234.7	236.6	179.4	ESRRA	NM_004451.3	ERR1;ERRa;ESRL1;NR3B1;ERRalpha	ligand-	nucleus	regulation
GI_18874095-S	459.8	347.4	456.1	PI4K2B	NM_018323.2	PI4KIIB;FLJ11105	inositol/ph		
GI_18874098-S	689.6	827.5	698.5	IPO4	NM_024658.2	Imp4;FLJ23338	phospholi	nuclear	protein-
GI_18921092-S	89.5	102	97.4	TRPM6	NM_017662.3	HSH;HMGX;HOMG;CHAK2;FLJ20087;FLJ22			
GI_18959199-S	157.9	166.6	166.1	LATS2	NM_014572.1		tumor	nucleus	protein
GI_18959203-S	146.1	173.4	160.3	GIPC3	NM_133261.1		protein		intracellula
GI_18959211-S	118.7	126.9	113.2	GSH-2	NM_133267.1		transcripti	nucleus	regulation
GI_19071572-S	95.9	85.8	88	C20orf51	NM_022099.2	bA305P22.4			
GI_19111149-S	389.6	441.1	476.2	AMOT	NM_133265.1	FLJ14282;KIAA1071			
GI_19115953-S	139	136.2	132.8	DNAH5	NM_001369.1	HL1;PCD;CILD3;Dnahc5;KIAA1603	axonemal	axonemal	cell
GI_19115957-A	634.1	588.8	651.7	SLC39A4	NM_130849.1	AEZ;ZIP4;FLJ20327	metal ion	membran	metal ion
GI_19115957-I	96.7	119.2	110	SLC39A4	NM_130849.1	AEZ;ZIP4;FLJ20327	metal ion	membran	metal ion
GI_19115959-S	382.1	264.3	206	C6orf33	NM_133367.1	MPRB;LMPB1;FLJ32521		integral to	
GI_19115963-S	145.2	175.6	174.9	PLCD3	NM_133373.1		calcium		lipid
GI_19224662-S	85.7	94.1	75.7	my048	NM_080390.2	MY0876G05	DNA	nucleus	regulation
GI_19263339-S	2870.2	1745.4	1444	GPT2	NM_133443.1	ALT2	transamin		biosynthes
GI_19263342-S	217.6	264.4	247.9	MRIP2	NM_133446.1		DNA	nucleus	
GI_19263344-S	101.5	123.6	100.4	EMID1	NM_133455.1	EMI5;EMU1;hEmu1	DNA	extracellul	regulation
GI_19263346-S	108.7	100.6	102.4	EMID2	NM_133457.1	EMI6;EMU2;hEmu2;COL26A1	DNA	extracellul	regulation
GI_19311005-S	128.7	269.9	278.9	PPP1R14C	NM_030949.1	KEPI;NY-BR-81;CPI17-like			
GI_19311007-A	202.8	280.5	216.1	GEFT	NM_133483.1				

GI_19311007-I	113	107.1	101.8	GEFT	NM_133483.1				
GI_19311011-S	3021.7	2336.6	2247.3	BRIX	NM_018321.2	FLJ11100	molecular	nucleolus	ribosomal
GI_19387843-I	105.8	102.3	104.8	MBNL3	NM_018388.2	CHCR;MBLX;MBXL;MBLX39;FLJ11316	nucleic	nucleus	developm
GI_19387853-S	308.1	375.9	271.2	NTNG2	NM_032536.1	Lmnt2;NTNG1;KIAA1857;MGC21884	structural	extracellul	axonogen
GI_19424121-S	214.9	255.4	238.3	SLC26A10	NM_133489.1		transcripti	intracellula	regulation
GI_19424127-S	93.1	98.4	94.6	ASAH3	NM_133492.1	ACER1			
GI_19424129-S	661.3	470.9	343.6	CD109	NM_133493.1	FLJ38569;DKFZp762L1111	endopepti		
GI_19424131-S	99.6	115.2	92.1	NEK7	NM_133494.1		protein-		protein
GI_19482155-A	347.1	381	343.8	LOC56965	NM_020214.1				
GI_19482155-I	177.3	168.2	165.2	LOC56965	NM_020214.1				
GI_19482173-S	1421.8	1440.6	1622	CUL2	NM_003591.2		tumor		induction
GI_19525732-S	450.9	461.8	450.8	HEL308	NM_133636.1	MGC20604	nucleic		
GI_19525734-S	121.8	124.7	125.7	DQX1	NM_133637.1	FLJ23757	ATP		
GI_19525736-S	115.9	136.7	111.2	ADAMTS19	NM_133638.1		zinc ion	extracellul	proteolysis
GI_19526470-S	1152.5	1376.6	1101.4	RTKN	NM_033046.1	B5			
GI_19526752-I	69.4	83.2	71	SYNE1	NM_015293.1	8B;CPG2;MYNE1;MYNE-1;SYNE-1;SYNE-	lamin	nuclear	Golgi
GI_19526766-I	1868.6	1845.7	1792.6	ZAK	NM_133646.1	MLTK;mlklak			
GI_19528648-I	98.8	113.2	98.6	BMP4	NM_001202.2	ZYME;BMP2B;BMP2B1	signal		mesoderm
GI_19528651-A	473.5	348.8	156.4	BMP4	NM_130851.1	ZYME;BMP2B;BMP2B1	signal		mesoderm
GI_19528651-I	91	103.1	92.5	BMP4	NM_130851.1	ZYME;BMP2B;BMP2B1	signal		mesoderm
GI_19528653-I	616.6	500.4	513.1	FAF1	NM_007051.2	hFAF1;CGI-03;HFAF1s	protein	nucleus	apoptosis
GI_19528654-A	1308.7	904.8	1053.9	FAF1	NM_131917.1	hFAF1;CGI-03;HFAF1s	protein	nucleus	apoptosis
GI_19528662-A	731.2	915.1	845	APBB3	NM_133174.1	FE65L2	protein	cytoplasm	
GI_19549324-S	87.1	88	83.5	ARPM1	NM_032487.2	MGC15664	structural	actin	
GI_19549332-S	407.5	340.6	257.7	LOC51619	NM_015983.2		ubiquitin		ubiquitin
GI_19557632-I	238.2	287.9	275.6	PPIL3	NM_032472.3				
GI_19557635-A	2983.4	2780.8	2262.6	PPIL3	NM_130906.1				
GI_19557639-I	112.9	118	110.2	PPIL3	NM_131916.1				
GI_19557644-S	172.5	212.7	191.8	SCG3	NM_013243.2	SGIII	transmem	membran	protein
GI_19557649-S	153.7	195.9	139.5	HIST1H2AE	NM_021052.2	H2A.1;H2A.2;H2A/a;H2AFA	DNA	chromoso	nucleoso
GI_19557652-S	89.9	85.2	94.8	HIST1H2AD	NM_021065.2	H2A.3;H2A/g;H2AFG	DNA	chromoso	nucleoso
GI_19557655-S	142.7	153.6	133.6	HIST1H2AB	NM_003513.2	H2A/m;H2AFM	DNA	chromoso	nucleoso
GI_19557676-S	4753.7	5391.2	3444.1	HLA-C	NM_002117.3	D6S204;HLA-JY3	class I	integral to	immune
GI_19557683-S	1591.5	1527.4	1511	SURF1	NM_003172.2		cytochrom	mitochond	cytochrom
GI_19557686-S	610	466.2	423.2	SURF2	NM_017503.2	SURF-2	molecular	cellular_co	biological_
GI_19593984-S	3629.6	4825.6	4219.5	SURF4	NM_033161.2	ERV29;FLJ22993	molecular	endoplas	biological_
GI_19705425-S	2027.3	2004.6	2386	MANBAL	NM_022077.2	dJ1141E15.2		integral to	
GI_19718730-I	386.9	441	377.3	BRD4	NM_058243.1	CAP;MCAP;HUNKI			
GI_19718733-S	95.3	237.2	90.6	TLR2	NM_003264.2	TIL4	antibacteri	integral to	induction
GI_19718735-S	123.9	131.4	94.1	TLR3	NM_003265.2		antibacteri	integral to	signal
GI_19718736-S	94.4	87.8	103.3	TLR5	NM_003268.3	TIL3	antibacteri	integral to	signal
GI_19718744-I	135.3	149	134.2	UNG	NM_003362.2	DGU;UDG;UNG1;HIGM4;UNG15	uracil DNA	mitochond	base-
GI_19718745-A	996.5	622.5	1043.1	OSBPL1A	NM_018030.3	ORP1;OSBPL1B;FLJ10217	phospholi	intracellula	lipid
GI_19718745-I	100.6	105.1	99	OSBPL1A	NM_018030.3	ORP1;OSBPL1B;FLJ10217	phospholi	intracellula	lipid

GI_19718747-A	212.1	242.4	182.9	IDN3	NM_015384.2	IDN3-			
GI_19718747-I	87.1	89.9	87.3	IDN3	NM_015384.2	IDN3-			
GI_19718748-I	234.6	225.6	198.3	IDN3	NM_133433.1	IDN3-			
GI_19718750-A	352.2	357.1	407.2	UNG	NM_080911.1	DGU;UDG;UNG1;HIGM4;UNG15	uracil DNA	mitochond	base-
GI_19718750-I	179.1	192.1	160.4	UNG	NM_080911.1	DGU;UDG;UNG1;HIGM4;UNG15	uracil DNA	mitochond	base-
GI_19718752-S	403.5	426.8	485.9	BAP1	NM_004656.2	hucep-6;HUCEP-13;KIAA0272	ubiquitinyl	nucleus	negative
GI_19718753-A	100.5	113.2	96.1	RANBP2L1	NM_032260.2	BS-	RAN		
GI_19718753-I	91.5	101.6	81.1	RANBP2L1	NM_032260.2	BS-	RAN		
GI_19718756-S	600.1	517.4	557.6	RANBP2	NM_006267.3	NUP358	RAN	nuclear	protein-
GI_19718758-A	4613.2	3541.8	2344.6	FER1L3	NM_133337.1	MYOF;KIAA1207		nuclear	circulation
GI_19718761-A	2913.5	1980.8	1650.5	UBE3A	NM_130838.1	AS;ANCR;E6-AP;EPVE6AP	ubiquitin		brain
GI_19718763-I	205.7	259.9	236.3	UBE3A	NM_130839.1	AS;ANCR;E6-AP;EPVE6AP	ubiquitin		brain
GI_19718770-S	195.3	221.4	197.6	ELMO3	NM_024712.2	CED12;FLJ13824		membran	phagocyto
GI_19718771-A	7498.1	4470	3265.2	ASNS	NM_001673.2	TS11	asparagin	soluble	metabolis
GI_19718773-I	167.9	229.4	182	ASNS	NM_133436.1	TS11	asparagin	soluble	metabolis
GI_19718775-S	609	762.2	850.7	WEE1	NM_003390.2	WEE1hu	protein-	nucleus	regulation
GI_19718776-S	1099.4	1430.6	1979.9	FEN1	NM_004111.4	MF1;RAD2;FEN-1	double-	nucleus	UV
GI_19718777-A	284.3	311.2	314.5	SEMA6B	NM_020241.2	SEMAN;semaZ;SEMA-VIB;Sema VIb;SEM-			
GI_19718779-I	306.6	381.5	354.7	SEMA6B	NM_032108.2	SEMAN;semaZ;SEMA-VIB;Sema VIb;SEM-			
GI_19718789-A	425	473.9	485.7	RAD17	NM_133341.1	R24L;Rad24;HRAD17;RAD17Sp		nucleus	DNA
GI_19718793-I	131.7	141.3	129.9	RAD17	NM_133343.1	R24L;Rad24;HRAD17;RAD17Sp		nucleus	DNA
GI_19718798-A	288.1	258.4	274	RAD1	NM_133282.1	HRAD1	3'-5'	nucleus	DNA
GI_19718800-I	125.3	133.8	124.2	RAD1	NM_133377.1	HRAD1	3'-5'	nucleus	DNA
GI_19743563-S	160.1	197.5	186.8	CYP2A13	NM_000766.3	CPAD	monooxyg	membran	electron
GI_19743564-S	185.2	207.2	170.7	CYP2F1	NM_000774.3	C2F1;CYP2F	monooxyg	membran	electron
GI_19743568-I	989.7	1251.9	1005.4	TANK	NM_004180.2	I-TRAF	protein		signal
GI_19743570-A	268.2	286.7	242.1	TANK	NM_133484.1	I-TRAF	protein		signal
GI_19743570-I	120.4	132.9	123.1	TANK	NM_133484.1	I-TRAF	protein		signal
GI_19743572-S	118.4	115.3	105.2	WIT-1	NM_015855.2	dJ74J1.1	molecular	cellular_co	cell
GI_19743791-S	311	255.5	190	BNC	NM_001717.2	BNC1;HsT19447	transcripti	nucleus	epidermal
GI_19743793-I	81	80.7	80	SHANK2	NM_012309.1	SHANK;CORTBP1;ProSAP1;SPANK-	protein	kinesin	intracellula
GI_19743795-A	90.1	88.4	81.2	SHANK2	NM_133266.1	SHANK;CORTBP1;ProSAP1;SPANK-	protein	kinesin	intracellula
GI_19743795-I	109.4	111.2	105.4	SHANK2	NM_133266.1	SHANK;CORTBP1;ProSAP1;SPANK-	protein	kinesin	intracellula
GI_19743797-A	832.2	668.2	707.1	ZNF274	NM_016324.2	ZF2;HFB101	transcripti	nucleolus	regulation
GI_19743800-I	116.4	113.6	107.9	ZNF274	NM_133502.1	ZF2;HFB101	transcripti	nucleolus	regulation
GI_19743802-S	105.4	111.5	119.4	FBLN5	NM_006329.2	EVEC;UP50;DANCE	integrin	extracellul	cell-matrix
GI_19743804-A	120.5	128.8	129.3	ROBO1	NM_002941.2	SAX3;DUTT1;FLJ21882	axon	integral to	cell
GI_19743804-I	146.1	162.5	156.2	ROBO1	NM_002941.2	SAX3;DUTT1;FLJ21882	axon	integral to	cell
GI_19743805-I	132.7	181.8	142.6	ROBO1	NM_133631.1	SAX3;DUTT1;FLJ21882	axon	integral to	cell
GI_19743807-S	208.9	311.1	116.9	RODH	NM_003725.2	HSE	catalytic		androgen
GI_19743809-S	203.6	227.7	223.3	ROM1	NM_000327.2	ROSP1	G-protein	integral to	vision
GI_19743810-S	1380.3	1569.1	1671.9	TBK1	NM_013254.2	NAK;T2K;FLJ11330	protein		NIK-I-
GI_19743811-S	133.6	150.8	140.6	T	NM_003181.2	TFT	transcripti	nucleus	determinat
GI_19743812-I	15358.3	15810	14217	ITGB1	NM_002211.2	CD29;FNRB;MDF2;VLAB;GPIIA;MSK12	cell		homophili

GI_19743814-I	103.5	111.6	102.8	ITGB1	NM_033666.1	CD29;FNRB;MDF2;VLAB;GPIIA;MSK12	cell		homophili
GI_19743818-A	5760.9	6968	6249.3	ITGB1	NM_033668.1	CD29;FNRB;MDF2;VLAB;GPIIA;MSK12	cell		homophili
GI_19743818-I	97.6	93.9	88	ITGB1	NM_033668.1	CD29;FNRB;MDF2;VLAB;GPIIA;MSK12	cell		homophili
GI_19743822-I	122.6	139.6	126.8	ITGB1	NM_133376.1	CD29;FNRB;MDF2;VLAB;GPIIA;MSK12	cell		homophili
GI_19743828-S	102.4	104.3	104.8	HIST1H3A	NM_003529.2	H3/A;H3FA			
GI_19743834-S	95.8	109.4	95.9	HIST3H3	NM_003493.2	H3T;H3/g;H3FT	DNA	chromoso	nucleoso
GI_19743835-S	415.5	444.4	532.8	TARBP1	NM_005646.2	TRP185;TRP-185;FLJ30482	RNA	nucleus	pathogene
GI_19743837-A	1737.9	1882.6	2456.8	TARBP2	NM_004178.3		RNA	nucleus	pathogene
GI_19743844-I	116.3	120.9	117.9	DCN	NM_001920.2	PG40;PGII;PGS2;DSPG2;SLRR1B	chondroiti	extracellul	histogene
GI_19743853-A	95.7	107.7	99.4	DCN	NM_133507.1	PG40;PGII;PGS2;DSPG2;SLRR1B	chondroiti	extracellul	histogene
GI_19743870-I	349.9	376.4	313.2	FCAR	NM_133279.1	CD89	receptor	integral to	immune
GI_19743872-A	152.2	148.8	136.9	FCAR	NM_133280.1	CD89	receptor	integral to	immune
GI_19743874-S	897.3	836.7	762.2	FH	NM_000143.2	MCL;LRCC;HLRCC;MCUL1;FUMARASE	fumarate	TCA cycle	fumarate
GI_19743876-S	469.7	438.2	437.2	RFX1	NM_002918.2	EF-C	RNA	nucleus	immune
GI_19743878-A	128.8	149.4	124.6	RFX2	NM_134433.1	FLJ14226	RNA	nucleus	regulation
GI_19743882-I	175.3	194.3	189.1	RFX3	NM_002919.2	bA32F11.1	transcripti	nucleus	regulation
GI_19743883-A	172.6	221.7	198.7	RFX3	NM_134428.1	bA32F11.1	transcripti	nucleus	regulation
GI_19743883-I	115.3	119.5	104.1	RFX3	NM_134428.1	bA32F11.1	transcripti	nucleus	regulation
GI_19743885-I	99.7	110.4	114.7	RFX4	NM_032491.2	NYD-SP10	DNA	nucleus	
GI_19743887-A	92.5	93.4	77.3	RFX4	NM_002920.3	NYD-SP10	DNA	nucleus	
GI_19743887-I	118.9	124.5	123	RFX4	NM_002920.3	NYD-SP10	DNA	nucleus	
GI_19743888-I	241.6	232.1	272.3	TADA2L	NM_001488.2	ADA2;KL04P;hADA2;FLJ12705	transcripti	nucleus	regulation
GI_19743890-A	209	184.9	218	TADA2L	NM_133439.1	ADA2;KL04P;hADA2;FLJ12705	transcripti	nucleus	regulation
GI_19743890-I	96.4	112.6	95.4	TADA2L	NM_133439.1	ADA2;KL04P;hADA2;FLJ12705	transcripti	nucleus	regulation
GI_19743892-I	1629.2	2489.8	2649.7	TADA3L	NM_006354.2	ADA3;hADA3;FLJ20221;FLJ21329	transcripti	nucleus	regulation
GI_19743893-I	256.5	275.6	266.7	TADA3L	NM_133480.1	ADA3;hADA3;FLJ20221;FLJ21329	transcripti	nucleus	regulation
GI_19743895-A	605.5	978.9	968.9	TADA3L	NM_133481.1	ADA3;hADA3;FLJ20221;FLJ21329	transcripti	nucleus	regulation
GI_19743897-S	111.3	210.6	111.1	ROR2	NM_004560.2	BDB;BDB1;NTRKR2	transmem	integral to	signal
GI_19743899-I	109.2	119.5	114.9	RORA	NM_002943.2	ROR1;ROR2;ROR3;RZRA;NR1F1	ligand-	nucleus	signal
GI_19743900-I	111.1	104	95.8	RORA	NM_134260.1	ROR1;ROR2;ROR3;RZRA;NR1F1	ligand-	nucleus	signal
GI_19743902-I	157.9	176.7	170.3	RORA	NM_134261.1	ROR1;ROR2;ROR3;RZRA;NR1F1	ligand-	nucleus	signal
GI_19743904-A	169.4	254.9	163.4	RORA	NM_134262.1	ROR1;ROR2;ROR3;RZRA;NR1F1	ligand-	nucleus	signal
GI_19743904-I	231.4	286.3	251.2	RORA	NM_134262.1	ROR1;ROR2;ROR3;RZRA;NR1F1	ligand-	nucleus	signal
GI_19743906-S	109	100.9	106.8	RORB	NM_006914.2	RZRB;NR1F2;ROR-BETA;bA133M9.1	protein	nucleus	regulation
GI_19743908-S	101.9	107.2	111.1	RORC	NM_005060.2	TOR;RORG;RZRG;NR1F3	ligand-	nucleus	regulation
GI_19743913-A	119.3	148	120.4	PTPRN2	NM_130843.1	IAR;ICAAR;PTPRP;PHOGRIN;IA-	transmem	integral to	protein
GI_19743915-I	99.5	103.9	81	PTPRR	NM_002849.2	EC-PTP;PCPTP1;PTP-SL;PTPBR7	transmem	integral to	protein
GI_19743916-A	1078.5	408.9	597.4	PTPRR	NM_130846.1	EC-PTP;PCPTP1;PTP-SL;PTPBR7	transmem	integral to	protein
GI_19743916-I	122.5	140.3	131.4	PTPRR	NM_130846.1	EC-PTP;PCPTP1;PTP-SL;PTPBR7	transmem	integral to	protein
GI_19743920-A	139.3	184.3	163.4	PTPRS	NM_130853.1	PTPSIGMA	transmem	integral to	
GI_19743926-I	90.6	95.8	93.4	PTPRT	NM_133170.1	RPTPrho;KIAA0283	transmem	integral to	transmem
GI_19743928-A	234.4	285.4	260.2	PTPRT	NM_007050.3	RPTPrho;KIAA0283	transmem	integral to	transmem
GI_19743932-A	225.7	289.1	420.7	PTPRU	NM_133178.1	FMI;PTP;PCP-2;PTP-	transmem	integral to	transmem
GI_19743936-S	1255.8	1210	1284.7	DDX27	NM_017895.6	RHLP;Rrp3p;PP3241;HSPC259;MGC1018;F	nucleic	nucleus	

GI_19743938-S	413.3	650.3	391.9	DYSF	NM_003494.2	FER1L1;LGMD2B;FLJ00175		integral to	muscle
GI_19743939-S	192.9	245.3	195.8	PAGE-5	NM_130467.2				
GI_19745147-S	148	143.2	129.3	RC3	NM_015263.1	KIAA0856			
GI_19745161-S	96.9	126.5	102	NALP4	NM_134444.1	PAN2;RNH2;PYPAF4;FLJ32126			
GI_19745179-S	2032.9	3209.2	3394.6	MO25	NM_016289.2	CGI-66			
GI_19747266-I	374.2	460.6	401.8	TTN	NM_133378.1	TMD;CMD1G;CMPD4;FLJ32040	structural	cytoskelet	regulation
GI_19747268-A	122.9	134.4	128.7	PLAC6	NM_130776.1	XAGE-3;pp9012			
GI_19747268-I	112.9	125.7	130.5	PLAC6	NM_130776.1	XAGE-3;pp9012			
GI_19747270-I	116.7	144.1	127	PLAC6	NM_133179.1	XAGE-3;pp9012			
GI_19747272-S	147.9	199.2	168.4	XAGE-5	NM_130775.1				
GI_19747274-A	2651.9	2059.4	1474.6	PHF10	NM_018288.2	XAP135;FLJ10975			
GI_19747277-S	189.7	198.3	164.7	ARHU	NM_021205.3	WRCH1;hG28K;WRCH-	Rho small		small
GI_19747278-A	110.8	113.5	115.1	GAGED2	NM_133430.1	XAGE1;XAGE-1			
GI_19747280-I	96.3	102.4	102.6	GAGED2	NM_133431.1	XAGE1;XAGE-1			
GI_19747282-S	109.5	127.6	109.2	GAGED3	NM_130777.1	XAGE2;XAGE-2			
GI_19747284-S	88.3	97.1	87.5	GAGEC1	NM_007003.2	JM27;PAGE4;GAGE-9;PAGE-1;PAGE-4	molecular	cellular_co	biological_
GI_19882212-S	157.3	175.7	166.3	MASS1	NM_032119.1	FEB4;GPR98;USH2C;VLGR1;KIAA0686;DKF	G-protein	membran	neuropepti
GI_19882216-I	95	92.5	84	MTO1	NM_133645.1	CGI-02	molecular		electron
GI_19882236-S	111.5	112.7	105.7	RHPN1	NM_052924.1	ODF5;RHPN;KIAA1929			
GI_19882238-S	121.5	131.4	123.5	GNRHR2	NM_057163.1		rhodopsin-	integral to	G-protein
GI_19882240-S	184.8	123	117.3	NOPE	NM_020962.1	DDM36;KIAA1628			
GI_19882248-I	101.3	109.5	109.7	CST11	NM_130794.1	SC13;dJ322G13.6			
GI_19882250-S	90.5	97.9	95.1	CST1	NM_001898.2		cysteine		
GI_19882252-S	233.5	268.4	237.5	CST2	NM_001322.2		cysteine		
GI_19882253-S	4344.9	4342.7	2747.7	CST3	NM_000099.2	AD8	cysteine		
GI_19882254-S	165.5	184.2	161.5	CST4	NM_001899.2		cysteine		
GI_19882255-S	96.6	118.3	106.6	CST5	NM_001900.2		cysteine		
GI_19882257-S	94.3	108.4	88.5	CST8	NM_005492.2	CRES	cysteine		
GI_19882258-S	106.6	113.4	103.6	CSTL1	NM_138283.1	dJ322G13.4	cysteine		
GI_19913344-S	1494.7	1522.5	1570.8	SLBP	NM_006527.2	HBP	ribonucleo	nucleus	histone
GI_19913345-I	96.5	92.4	98.1	WHSC1	NM_014919.1	NSD2;TRX5;MMSET;REIIBP;KIAA1090			embryoge
GI_19913355-I	146.1	168.8	137.7	WHSC1	NM_133334.1	NSD2;TRX5;MMSET;REIIBP;KIAA1090			embryoge
GI_19913359-S	1768.7	1476	1927.6	TBL1X	NM_005647.2	EBI;TBL1	heterotrim	peripheral	hearing
GI_19913360-A	271.8	245.6	211.9	WHSC1	NM_133336.1	NSD2;TRX5;MMSET;REIIBP;KIAA1090			embryoge
GI_19913360-I	108.4	116.9	108.4	WHSC1	NM_133336.1	NSD2;TRX5;MMSET;REIIBP;KIAA1090			embryoge
GI_19913362-S	328.9	330	300.9	WHSC2	NM_005663.2	NELFA;FLJ10442;FLJ25112;P/OKcl.15			developm
GI_19913366-A	100.8	103	98.3	TBL1Y	NM_134259.1	TBL1			
GI_19913368-S	493.1	615.2	497.5	TBL3	NM_006453.2	SAZD	receptor		G-protein
GI_19913370-S	1104.7	1132.7	988.4	IRA1	NM_024665.2	C21;DC42;TBLR1;FLJ12894			
GI_19913380-A	98.5	101.6	100.9	C6orf25	NM_138275.1	G6b;NG31			
GI_19913382-I	311.2	350.2	310.1	C6orf25	NM_138276.1	G6b;NG31			
GI_19913384-I	92.4	94.9	96.5	C6orf25	NM_138277.1	G6b;NG31			
GI_19913386-S	119.5	135.6	116.3	GRAP2	NM_004810.2	P38;GADS;GRID;GRPL;GrbX;Mona;GRB2L;	SH3/SH2	cytoplasm	RAS
GI_19913387-S	106.1	136.3	111.5	GRAP	NM_006613.2		SH3/SH2	cytoplasm	RAS

GI_19913388-I	115.2	138	129.7	RGS3	NM_021106.2	C2PA;RGP3;FLJ20370;PDZ-RGS3	GTPase	cytosol	regulation
GI_19913391-A	3222.4	3486.7	1850.9	RGS3	NM_134427.1	C2PA;RGP3;FLJ20370;PDZ-RGS3	GTPase	cytosol	regulation
GI_19913391-I	164.4	179.2	165.1	RGS3	NM_134427.1	C2PA;RGP3;FLJ20370;PDZ-RGS3	GTPase	cytosol	regulation
GI_19913393-A	273.7	326.1	382.6	SMTN	NM_006932.3		structural	cytoskelet	muscle
GI_19913395-I	355.4	438.8	512.8	SMTN	NM_134269.1		structural	cytoskelet	muscle
GI_19913399-I	81.5	79.4	79.6	SLCO1A2	NM_021094.2	OATP;OATP-A;OATP1A2;SLC21A3	organic	integral to	organic
GI_19913400-A	114.7	141.6	122.8	SLCO1A2	NM_005075.2	OATP;OATP-A;OATP1A2;SLC21A3	organic	integral to	organic
GI_19913400-I	578.2	722.9	644.2	SLCO1A2	NM_005075.2	OATP;OATP-A;OATP1A2;SLC21A3	organic	integral to	organic
GI_19913402-I	81.9	90.5	79	SLCO1A2	NM_134431.1	OATP;OATP-A;OATP1A2;SLC21A3	organic	integral to	organic
GI_19913404-S	2529.8	1607.7	2029.2	TOP1	NM_003286.2	TOPI	DNA		DNA
GI_19913405-S	1628.9	1717.6	1644.6	TOP2A	NM_001067.2	TOP2;TP2A	DNA	nucleus	DNA
GI_19913407-S	1825.1	1966.5	1585.9	TOP2B	NM_001068.2	TOPIIB	DNA	nucleus	DNA
GI_19913411-A	858.1	1314	1372.3	MVP	NM_005115.3	LRP;VAULT1		ribonucleo	drug
GI_19913413-I	152.4	167.7	149	AP2A1	NM_014203.2	ADTAA;CLAPA1;AP2-ALPHA	protein	coated pit	nonselecti
GI_19913415-A	284.1	342.1	314.8	AP2A1	NM_130787.2	ADTAA;CLAPA1;AP2-ALPHA	protein	coated pit	nonselecti
GI_19913417-S	1234	1584.5	2026.3	ATP6V0A1	NM_005177.2	a1;Stv1;VPP1;Vph1;ATP6N1;ATP6N1A	hydrogen	coated	proton
GI_19913419-A	106.7	122.6	128.4	ATP6V0A4	NM_130840.1	a4;Stv1;VPP2;Vph1;RTA1C;RTADR;ATP6N2			
GI_19913421-I	153.3	190.3	159.2	ATP6V0A4	NM_130841.1	a4;Stv1;VPP2;Vph1;RTA1C;RTADR;ATP6N2			
GI_19913423-S	3531.1	3895.9	3507.9	ATP6V1A	NM_001690.2	HO68;VA68;VPP2;Vma1;ATP6A1;ATP6V1A1	ATP-	vacuolar	small
GI_19913425-S	125.4	134.6	146.8	ATP6V1B1	NM_001692.2	VATB;VPP3;Vma2;RTA1B;ATP6B1	ATP-	vacuolar	proton
GI_19913427-S	4816.2	4018.3	4870.3	ATP6V1B2	NM_001693.2	HO57;VATB;VPP3;Vma2;ATP6B2;ATP6B1B	hydrogen	vacuolar	proton
GI_19913429-S	4498.2	5103.8	4235.5	ATP5J	NM_001685.3	ATP5;ATPM;ATP5A	adenosine	mitochond	energy
GI_19913430-S	585.7	727.2	770.5	ATP6V1C1	NM_001695.2	VATC;Vma5;ATP6C;ATP6D;FLJ20057	hydrogen-	vacuolar	proton
GI_19913433-S	3472	4734.1	5585.5	ATP6V1E1	NM_001696.2	P31;Vma4;ATP6E;ATP6E2;ATP6V1E	hydrogen-	vacuolar	proton
GI_19913434-S	3207.6	3992.8	4096.8	ATP6V0B	NM_004047.2	ATP6F;HATPL;VMA16	adenosine	vacuolar	proton
GI_19913435-S	3842.8	5325.2	5498.3	ATP6V0E	NM_003945.2	M9.2;ATP6H;Vma21;Vma21p	adenosine	vacuolar	proton
GI_19913436-S	7883.2	9954.8	10477	ATP6V0C	NM_001694.2	ATPL;VATL;Vma3;ATP6C;ATP6L	hydrogen	vacuolar	proton
GI_19913437-S	3006.3	3968.3	4423.9	ATP6V1D	NM_015994.2	VATD;VMA8;ATP6M			
GI_19913440-A	7239.7	15979	24778	HPCAL1	NM_002149.2	BDR1;HLP2;VILIP-3	calcium	cytosol	vesicle-
GI_19913440-I	229	408.8	581.4	HPCAL1	NM_002149.2	BDR1;HLP2;VILIP-3	calcium	cytosol	vesicle-
GI_19913442-I	135.1	140.5	152.5	HPCAL1	NM_134421.1	BDR1;HLP2;VILIP-3	calcium	cytosol	vesicle-
GI_19913444-S	107.5	113.7	109.5	HPCAL4	NM_016257.2	HLP4;DKFZp761G122	calcium		central
GI_19913445-S	117.2	123.6	123.2	HPCA	NM_002143.2	BDR2	binding	cytosol	vesicle-
GI_19920316-S	3191.7	3502.5	2666.5	CKAP4	NM_006825.2	P63;CLIMP-63		integral to	nonselecti
GI_19920322-A	652.9	657.2	634.4	CDW92	NM_022109.2	CTL1;CHTL1			
GI_19923075-S	290.4	314.9	301.4	ACTRT1	NM_138289.1	ARP-T1;MGC26590	structural	actin	
GI_19923077-S	110.1	119.5	103.8	LOC148213	NM_138286.1	FLJ31526		nucleus	
GI_19923079-I	202.6	250.3	198.7	BNIPL	NM_138278.1	PP753;BNIP-S;BNIPL1;BNIPL2;BNIPL-			
GI_19923081-S	295.9	388.8	311.8	PATE	NM_138294.1		phospholi		electron
GI_19923085-S	322.6	389.4	371.1	NS3BP	NM_138291.1				
GI_19923089-S	102.6	99.1	101.6	RPIB9	NM_138290.1	RPIP9;FLJ30671;MGC26655			
GI_19923095-S	157.4	190.4	170.3	CRLF2	NM_022148.2	CRL2;TSLPR;CRLF2Y	receptor	integral to	
GI_19923101-S	271.3	323.8	291.1	HLCS	NM_000411.3	HCS	biotin-		protein
GI_19923110-S	104	108.5	162.1	IGFBP3	NM_000598.2				

GI_19923111-S	109.9	107.8	100.5	IGF1	NM_000618.2				
GI_19923121-S	125.4	141.1	120.4	CHRNA3	NM_000743.2		nicotinic	nicotinic	small
GI_19923125-S	253.6	295	254.3	GNRH1	NM_000825.2	GRH;GNRH;LHRH;LNRH	luteinizing	soluble	negative
GI_19923128-S	100	130.6	92.2	IFNAR2	NM_000874.2	IFNABR	interferon-	extracellul	JAK-STAT
GI_19923130-S	596.2	624.5	476.6	PPP3CA	NM_000944.2	CALN;CCN1;CNA1;CALNA;PPP2B;CALNA1	protein	calcineurin	protein
GI_19923133-S	467.7	526	544.5	CHUK	NM_001278.2	IKK1;IKKA;IKBKA;TCF16;NFKBIKA;IKK-	IkappaB	cytoplasm	I-kappaB
GI_19923135-S	89.2	94.7	98.9	CX3CR1	NM_001337.2	V28;CCRL1;GPR13;CMKDR1;GPRV28;CMK	chemokin	integral to	virulence
GI_19923138-S	107.6	124.4	95.9	ID4	NM_001546.2		transcripti	nucleus	regulation
GI_19923143-S	142.3	184.6	173	MYD88	NM_002468.2		death		cell
GI_19923154-S	273.3	308.9	282.4	SH3BP2	NM_003023.2	CRBM;CRPM;RES4-23	SH3/SH2		signal
GI_19923156-S	161.3	197.2	167.2	SLC6A12	NM_003044.2	BGT1;BGT-1	betaine/G	integral to	small
GI_19923159-S	395.1	325.8	232.5	SNAPC1	NM_003082.2	SNAP43;PTFgamma			transcripti
GI_19923163-S	422.7	390.2	361.1	TMEM1	NM_003274.2	EHOC1;GT334;EHOC-1	sodium	Golgi	sodium
GI_19923175-S	1361.3	1178.7	1128.3	SLC4A7	NM_003615.2	NBC2;NBC3;SBC2;SLC4A6			
GI_19923177-S	165.8	213.6	202.1	C22orf19	NM_003678.2	Fmip;PK1.3	tumor		
GI_19923180-S	123.5	137	128.7	PDLIM4	NM_003687.2	RIL	tumor	nucleus	intracellula
GI_19923194-S	126.5	155.9	110	CEACAM1	NM_001712.2	BGP;BGP1;BGPI;CD66;CD66A	tumor	membran	immune
GI_19923197-S	1091.8	728.3	768.8	RUNX1	NM_001754.2	AML1;CBFA2;AMLCR1;PEBP2A2;PEBP2aB	transcripti	nucleus	oncogene
GI_19923201-S	225.6	205	214.8	EZH1	NM_001991.2	KIAA0388	chromatin	nucleus	embryoge
GI_19923203-S	98.3	94.2	98.3	GLP1R	NM_002062.2		transmem	integral to	adenylate
GI_19923214-S	272	225.9	206.7	MEF2C	NM_002397.2		RNA	nucleus	muscle
GI_19923216-S	230.9	283.8	315.7	MKI67	NM_002417.2	KIA	ATP	nucleolus	regulation
GI_19923222-S	240.5	198.2	210.7	NFKB2	NM_002502.2	LYT10;LYT-10	transcripti	nucleus	oncogene
GI_19923224-S	85.8	104	99.3	OMG	NM_002544.2	OMGP	cell	membran	cell
GI_19923232-S	1320.4	2075.3	1926	SCP2	NM_002979.2	SCPX	sterol	peroxisom	steroid
GI_19923235-S	5451.2	6062	6574.4	SP100	NM_003113.2		DNA	kinesin	regulation
GI_19923241-S	352.6	392	387	ZFP161	NM_003409.2	ZF5;ZNF478	protein	nucleus	negative
GI_19923243-S	4298.5	4410.4	4593.1	ARHGAP1	NM_004308.2	RHOGAP;RHOGAP1;CDC42GAP	SH3/SH2		Rho
GI_19923244-S	137.5	155.8	133.5	CRHR1	NM_004382.2	CRF1;CRHR;CRF-R;CRFR1	corticotrop	integral to	adenylate
GI_19923246-S	463.3	387.9	294.8	CRY1	NM_004075.2	PHLL1	G-protein	mitochond	circadian
GI_19923256-S	100.4	92.5	91.7	TRPC6	NM_004621.3	TRP6	nonselecti	integral to	cation
GI_19923257-S	1625.5	2284.1	2426.7	PFKFB4	NM_004567.2		fructose-	cellular_co	fructose
GI_19923259-S	206.5	403.4	270.4	RAB4A	NM_004578.2	RAB4	RAB small		nonselecti
GI_19923267-S	2600.9	2267.4	2130.4	PRKRIR	NM_004705.2	DAP4;P52rIPK	protein		negative
GI_19923271-S	390.8	466.7	447.3	XPR1	NM_004736.2	X3;SYG1	G-protein	integral to	pathogene
GI_19923273-S	343.6	429.5	405.5	DLGAP1	NM_004746.2	GKAP;DAP-1;SAPAP1;DAP-1-BETA;DAP-1-	protein	membran	synaptic
GI_19923275-S	182.1	205.5	182.2	CD163	NM_004244.2	M130;MM130	scavenger	membran	antimicrob
GI_19923278-S	735.1	1031.4	1031.7	SEMA4F	NM_004263.2	SEMAM;SEMAW;M-SEMA;PRO2353;m-		membran	axon
GI_19923280-S	510.4	495.7	636.4	CHST3	NM_004273.2	C6ST;C6ST1	sulfotransf	Golgi	
GI_19923286-S	658.5	632.8	661.9	ATBF1	NM_006885.2		RNA	nucleus	transcripti
GI_19923288-S	1980.3	2863.5	1266.3	PIK3CD	NM_005026.2	p110D	phosphati	phosphoin	protein
GI_19923304-S	814.8	662.8	517.8	GTF2H1	NM_005316.2	BTF2;TFIIH			
GI_19923305-S	107.3	136.7	103.2	INMT	NM_006774.3		methyltran		
GI_19923309-S	118.4	136.3	134.5	MCF2	NM_005369.2	DBL	guanyl-	cytosol	oncogene

GI_19923318-S	81.4	73.4	73	TLX1	NM_005521.2	TCL3;HOX11	transcripti	nucleus	oncogene
GI_19923320-S	4493	3068.2	3935	KIFC3	NM_005550.2		microtubul	kinesin	vision
GI_19923322-S	291.8	402.6	467	MADH6	NM_005585.2	MADH7;SMAD6;HsT17432	inhibitory	intracellula	regulation
GI_19923324-S	201.1	210	224.1	EVI5	NM_005665.2	NB4S	protein	membran	developm
GI_19923326-S	1329	1479.6	1910.8	NET1	NM_005863.2	NET1A;ARHGEF8	guanyl-		signal
GI_19923328-S	438.2	544.9	462.9	NHLH1	NM_005598.2	HEN1;NSCL;NSCL1	DNA		central
GI_19923329-S	5049.5	4422.8	4302.4	CTDSP2	NM_005730.2	OS4;SCP2		soluble	oncogene
GI_19923332-S	99.7	99.3	103.6	FARSLB	NM_005687.2	FRSB;PheHB	phenylala	soluble	phenylala
GI_19923334-S	390.7	336.4	326.2	SCAM-1	NM_005775.2		structural	focal	cell
GI_19923342-S	967.3	1216.6	1153.2	CITED2	NM_006079.2	MRG1;P35SRJ	transcripti	nucleus	regulation
GI_19923347-S	1077.8	912.1	764	NAB1	NM_005966.2		transcripti	nucleus	regulation
GI_19923351-S	226.3	235.5	296.2	NKX3-1	NM_006167.2	NKX3A;NKX3.1	transcripti	nucleus	oncogene
GI_19923360-S	140.7	158.2	149	RPP30	NM_006413.2	TSG15	ribonuclea	nucleolar	tRNA
GI_19923361-S	92.5	94.6	90.8	THY1	NM_006288.2	CD90		integral to	
GI_19923363-S	647.8	798.4	753.9	ARPP-19	NM_006628.2	ARPP16;ARPP19;ARPP-16	potassium	cytoplasm	glucose
GI_19923364-I	101.6	116.6	108.7	DMRT2	NM_006557.3		transcripti	nucleus	male
GI_19923365-S	281.8	358.3	201.6	HPSE	NM_006665.2	HPA;HPR1;HSE1;HPSE1	beta-		proteoglyc
GI_19923366-S	2342.6	3105.2	3107.9	MSF	NM_006640.2	MSF1;SEPT9;SINT1;PNUTL4;AF17q25;KIAA	GTPase	cytoplasm	
GI_19923369-S	895.2	1783	1233.5	JARID1B	NM_006618.2	PUT1;PLU-1;RBBP2H1A	transcripti	nucleus	oncogene
GI_19923371-S	860.9	719.7	689.1	PVR	NM_006505.2	PVS;HVED;CD155;TAGE4	receptor	integral to	invasive
GI_19923373-S	124.4	142.3	128.2	HIVEP2	NM_006734.2	MBP-2;HIV-EP2	DNA	nucleus	regulation
GI_19923380-S	96.8	97.4	92.3	SCN3A	NM_006922.2	NAC3	voltage-	membran	sodium
GI_19923386-S	5198.6	5166.2	4263.2	NCBP2	NM_007362.2	NIP1;CBP20	RNA cap	nucleus	snRNA-
GI_19923388-S	138.6	243.8	178.9	PLA2R1	NM_007366.2	PLA2R;PLA2-R;PLA2IR;PLA2G1R	receptor	integral to	polysacch
GI_19923392-S	2161.6	2204.3	1659.6	RERE	NM_012102.2	ARG;ARP;DNB1;ATN1L;KIAA0458	poly-	nucleus	NLS-
GI_19923396-S	130.7	1231.9	447.4	ITGA11	NM_012211.2	HsT18964	collagen	integrin	muscle
GI_19923400-S	94.5	90.9	89.9	SERPINB13	NM_012397.2	HUR7;PI13;headpin	serpin	cellular_co	response
GI_19923401-S	3828.7	2989.6	2530.9	PITPNB	NM_012399.2	VIB1B	phosphati	intracellula	lipid
GI_19923408-S	1859.3	2285.5	1605.8	SERP1	NM_014445.2	RAMP4		ribosome	plasma
GI_19923412-S	165.1	158.8	148	USP25	NM_013396.2	USP21	ubiquitin-		deubiquiti
GI_19923414-S	201.5	252	229.4	HEYL	NM_014571.2		DNA	nucleus	embryoge
GI_19923415-S	264.3	305.1	260.4	DIS3	NM_014953.2	KIAA1008	exonuclea	nucleus	rRNA
GI_19923419-S	101.3	108.8	85.6	KIAA0998	NM_015072.2				
GI_19923429-S	134	125.8	120.5	COMMD5	NM_014066.2	HCARG;HT002			
GI_19923431-S	238.5	278.4	216.7	HSPC065	NM_014157.2	FLJ23555;DKFZP434N1418			
GI_19923436-S	1732.4	2163.6	1896.9	AK3L1	NM_016282.2	AK3;AKL3L;AKL3L1	adenylate	mitochond	
GI_19923439-S	89.9	85.3	86.7	PDE11A	NM_016953.2	PDE11A1	3',5'-cyclic-		signal
GI_19923441-S	1920	2326.3	2306.9	CGI-100	NM_016040.2		protein	endoplas	intracellula
GI_19923443-S	635.6	678.9	798.9	CGI-141	NM_016072.2			integral to	vesicle-
GI_19923444-A	145.5	130.5	125.4	SPG3A	NM_015915.2	FSP1;GBP3;SPG3;AD-FSP	GTPase	nucleus	immune
GI_19923448-S	601.2	373.1	330.5	DREV1	NM_016025.2	DREV			
GI_19923450-S	432.2	339.2	422.7	DCTN4	NM_016221.2			centrosom	
GI_19923451-S	531.2	507.7	335.2	LEF1	NM_016269.2	TCF1ALPHA	DNA	nucleus	regulation
GI_19923454-S	182.2	150.4	146.7	PLCE1	NM_016341.2	PLCE;KIAA1516			

GI_19923458-S	1729.4	1822.1	1630.2	PAIP2	NM_016480.2				
GI_19923461-S	931.5	975.8	539.2	BHC80	NM_016621.2	BM-006;KIAA1696			
GI_19923463-S	110.8	90.2	90.3	JIK	NM_016281.2	DPK	protein		JNK
GI_19923465-S	1223.7	1373.2	1002.5	SRRM2	NM_016333.2	300-KD;SRL300;SRM300;KIAA0324			
GI_19923467-S	1103	1153.8	952.6	PRKD2	NM_016457.2	PKD2;HSPC187;DKFZp586E0820	ATP	intracellula	protein
GI_19923478-S	290.1	326.8	247.5	SUFU	NM_016169.2	SUFUH;SUFUXL	transcripti	cytoplasm	nucleocyto
GI_19923482-S	144.6	152.4	149.6	RAB14	NM_016322.2	DKFZp762K0911	GTP	cellular_co	small
GI_19923484-S	204.8	213.9	184.6	LUC7A	NM_016424.2	CROP		nucleus	RNA
GI_19923486-S	86.7	75.3	82.6	MYOZ2	NM_016599.2	CS-1;C4orf5			
GI_19923492-S	465.9	387.1	427.1	PEPP2	NM_019012.2	FLJ10667;KIAA1686			
GI_19923494-S	901	1122.6	913.6	MTRF1L	NM_019041.2		translation		translation
GI_19923496-S	1029.7	1116.9	896.1	EML4	NM_019063.2	C2orf2;ELP120;ROPP120;FLJ10942			
GI_19923500-S	250.4	273.4	191.7	FLJ20445	NM_017824.2				
GI_19923501-S	2700.2	2474.2	2491	p66alpha	NM_017660.2	FLJ20085			
GI_19923511-S	91.2	109.1	89.7	C14orf119	NM_017924.2	FLJ20671			
GI_19923513-S	461.9	512.7	546.2	ESRRBL1	NM_018010.2	HIPPI;MHS4R2;FLJ10147			
GI_19923516-S	239.4	193.7	233.8	FLJ10520	NM_018124.2				
GI_19923518-S	159.9	194.2	199	RCBTB1	NM_018191.2	CLLD7;CLLL7;FLJ10716	protein		
GI_19923520-S	422.1	451.2	448	CKAP2	NM_018204.2	LB1;TMAP;se20-10;FLJ10749			
GI_19923522-S	133.4	127.6	113.3	QRSL1	NM_018292.2	GatA;FLJ10989;FLJ12189;FLJ13447;DKFZP			
GI_19923528-S	373.1	391.8	341.4	WDR33	NM_018383.2	WDC146;FLJ11294			
GI_19923532-S	280.7	251.7	306.8	PI4KII	NM_018425.2	DKFZP761G1923	inositol/ph		
GI_19923535-S	383.6	400.1	322.5	ERMAP	NM_018538.2	PRO2801			
GI_19923537-S	769.3	893.7	748.1	VEZATIN	NM_017599.2	DKFZp761C241		kinesin	
GI_19923539-S	247.3	386.6	289	UPLC1	NM_017707.2	FLJ20199	binding	nucleus	transport
GI_19923541-S	515.7	516.6	497.8	URG4	NM_017920.2	FLJ20654;KIAA1507			
GI_19923547-S	295.2	252.8	276.7	CENPJ	NM_018451.2	LAP;CPAP;LIP1;BM032			
GI_19923550-S	516.7	480.9	444.6	LANCL2	NM_018697.2	TASP;GPR69B	translation	eukaryotic	translation
GI_19923554-S	766.4	745.6	609.3	LOC56270	NM_019613.2				
GI_19923555-S	881.1	658.9	636.3	AD-020	NM_020141.2				
GI_19923558-S	209.4	262.9	258	C11orf30	NM_020193.2	EMSY;GL002			
GI_19923563-S	111.7	119.8	124.5	SENP7	NM_020654.2	KIAA1707	cysteine-	nucleus	protein
GI_19923565-S	926.9	921.8	886	SCYL1	NM_020680.2	GKLP;NKTL;NTKL;P105;TAPK;TRAP;HT019			
GI_19923567-S	769.6	802	738.9	ZNF317	NM_020933.2	KIAA1588	DNA	nucleus	regulation
GI_19923571-S	451.9	475.7	143.3	SLAMF7	NM_021181.3	19A;CS1;CRACC			
GI_19923579-S	91.1	93	89.4	FLJ11785	NM_021930.2	RINT1;RINT-1			
GI_19923589-S	877.4	925.9	842.4	FLJ21657	NM_022483.2				
GI_19923594-S	227.7	272	212.4	DDX54	NM_024072.2	DP97;APR-5;MGC2835			
GI_19923596-S	1152.4	1133.3	1270.7	SAP130	NM_024545.2	FLJ12761			
GI_19923598-S	961.1	956	1114.8	CLMN	NM_024734.2	calmin;FLJ12383;KIAA1188	actin	integral to	
GI_19923602-S	822.8	732	611	CYBRD1	NM_024843.2	DCYTB;FLJ23462		integral to	electron
GI_19923608-S	502.6	437.3	495.7	JADE1	NM_024900.2	FLJ22479;KIAA1807	DNA		regulation
GI_19923612-S	2512.8	2288.2	2062.7	FLJ21128	NM_025083.2		molecular		
GI_19923616-S	1821.6	1727.9	1454	FLJ22175	NM_025161.2				

GI_19923618-S	418.5	588.9	600.3	C1orf22	NM_025191.2				
GI_19923620-S	544.3	370.8	683.3	HSD3B7	NM_025193.2	PFIC4			
GI_19923628-I	140.3	148.8	132.9	SPAP1	NM_030764.2	FCRH2;IFGP4;IRTA4;SPAP1A;SPAP1B;SPA			
GI_19923630-S	101.3	98.3	85.6	OR51E2	NM_030774.2	PSGR	olfactory	integral to	olfaction
GI_19923633-S	961.5	1010.8	1043.1	SLC25A28	NM_031212.2	MRS3/4;NPD016	binding	mitochond	transport
GI_19923635-S	112.6	113.8	112.2	PMCHL1	NM_031887.2				
GI_19923637-S	99.9	116.1	111.6	GPR61	NM_031936.2	BALGR;GPCR3	G-protein	integral to	G-protein
GI_19923645-S	148.8	154	132.7	DRCTNNB1A	NM_032581.2				
GI_19923649-S	260.5	306.6	286.6	ZNF607	NM_032689.2	FLJ14802;MGC13071		nucleus	
GI_19923651-S	264.1	331.2	353.9	C9orf54	NM_032809.2	FLJ00199;FLJ14596			
GI_19923652-I	2027.3	1348.2	1359.1	PSIP1	NM_033222.2	p52;p75;PAIP;DFS70;LEDGF;PSIP2	DNA	nucleus	regulation
GI_19923654-S	1709.9	3056.8	2988.4	DPYSL2	NM_001386.3	DRP2;CRMP2;DRP-2;DHPRP2	dihydropyr		nucleobas
GI_19923657-S	1501	1241.7	755.1	C20orf72	NM_052865.2	FLJ14597;bA504H3.4			
GI_19923658-S	212.1	245.6	218.4	LOXL4	NM_032211.5	LOXC;FLJ21889	protein-	membran	
GI_19923660-S	228.2	227.6	200.5	NCOA6IP	NM_024831.5	PIMT;PIPMT;FLJ22995	S-		
GI_19923668-S	190.3	217.1	223	SEL1L	NM_005065.3	IBD2;SEL1-LIKE			
GI_19923670-S	2803.3	2533.6	2123.4	FOXP1	NM_032682.3	QRF1;MGC12942			
GI_19923712-A	138.4	140.2	131.8	BNIPL	NM_138279.1	PP753;BNIP-S;BNIPL1;BNIPL2;BNIPL-			
GI_19923712-I	105.6	101.6	100.7	BNIPL	NM_138279.1	PP753;BNIP-S;BNIPL1;BNIPL2;BNIPL-			
GI_19923714-S	407	191.8	136.5	IL17D	NM_138284.1	IL27;IL-22;IL-27;IL-17D			
GI_19923718-S	389.3	596.1	519.4	C14orf147	NM_138288.1	MGC24447			
GI_19923720-S	107.1	133.7	92.6	PTCRA	NM_138296.1	PTA;PT-ALPHA			
GI_19923722-S	1765.8	2114.2	1626.1	RPS6KC1	NM_012424.2	RPK118;humS6PKh1	protein		signal
GI_19923724-S	4569.2	4839.5	4164.2	ANAPC11	NM_016476.9	APC11;Apc11p;HSPC214		nucleus	cell cycle
GI_19923725-S	291.4	324.2	928.6	NOV	NM_002514.2	CCN3;NOVH;IGFBP9	insulin-like	extracellul	regulation
GI_19923728-S	332.4	320.6	267.1	AD158	NM_032270.2	DKFZp586J1119			
GI_19923737-S	684	735.1	756.1	PRPS1	NM_002764.2	PRSI;PRS I	ribose-		purine
GI_19923741-S	762.8	1041.7	1062.8	BECN1	NM_003766.2			kinesin	anti-
GI_19923742-S	5470.7	2945.3	4450	SQSTM1	NM_003900.2	p60;p62;PDB3;ZIP3	molecular	cytosol	transmem
GI_19923749-S	201.6	195.8	199.9	RAB3B	NM_002867.2		RAB small		nonselecti
GI_19923751-S	568.7	689.4	761.9	RPA3	NM_002947.2	REPA3	single-	DNA	DNA
GI_19923752-S	133.2	160.2	130.3	SLC16A1	NM_003051.2	MCT;MCT1	mevalonat	integral to	mevalonat
GI_19923760-S	333.5	489.6	465.5	MINPP1	NM_004897.2	MIPP;HIPER1;MINPP2;DKFZP564L2016	phosphohi	endoplas	polyphosp
GI_19923769-S	625.6	449.5	371.4	HLX1	NM_021958.2	HB24	DNA	nucleus	transcripti
GI_19923778-S	749.1	554.5	837.7	PIR51	NM_006479.2		double-	nucleus	recombina
GI_19923779-S	144.3	170.4	140.8	SLCO1B1	NM_006446.2	LST-1;OATP2;OATP-C;OATP1B1;SLC21A6	sodium-	membran	organic
GI_19923781-S	168.1	180	161.5	LILRB1	NM_006669.2	CD85;ILT2;LIR1;MIR7;CD85J;LIR-1;MIR-7	protein	integral to	response
GI_19923783-S	1258.7	1640.3	1392.2	PC4	NM_006713.2	P15	single-	transcripti	regulation
GI_19923785-S	385.6	343.9	436.5	UQCR	NM_006830.2		electron	ubiquinol-	energy
GI_19923786-S	4056.5	4648.3	4141.9	RER1	NM_007033.2		molecular	Golgi	retrograde
GI_19923789-S	2341	1890.5	1690.7	RAB3-GAP15	NM_012414.2	KIAA0839;DKFZP434D245	enzyme	soluble	intracellula
GI_19923793-S	819.5	833	1087.6	CARD10	NM_014550.2	BIMP1;CARMA3	protein	kinesin	apoptosis
GI_19923795-S	601.2	773.3	543.3	CGI-07	NM_015938.2	NMD3	electron		electron
GI_19923799-S	554.9	478.9	330.2	MGC:13379	NM_016499.2				

GI_19923809-S	428.3	568.1	495.4	FLJ20254	NM_017727.2		calcium	extracellul	
GI_19923815-S	643.2	874.3	625.6	PARVA	NM_018222.2	FLJ10793;FLJ12254	actin	cytoskelet	cell
GI_19923816-S	582.6	780.6	721.2	PECR	NM_018441.2	TERP;HSA250303	apoptosis	peroxisom	fatty acid
GI_19923820-S	628.4	806.5	696.3	DPYSL5	NM_020134.2	CRAM;CRMP5;Ulip6;CRMP-5	hydrolase		axon
GI_19923825-S	1786	1534.7	1267.5	LOC57149	NM_020424.2				
GI_19923826-S	2228	2686.6	2813.4	KIAA1191	NM_020444.2	FLJ21022			
GI_19923828-S	887.7	660.8	705.3	LOC57228	NM_020467.2				
GI_19923829-S	351.9	757.7	678.1	PBXIP1	NM_020524.2	HPIP			
GI_19923835-S	134.6	143.9	135.4	CPEB1	NM_030594.2	CPEB;FLJ13203	nucleic		
GI_19923839-S	127.4	152.7	152.3	FLJ13910	NM_022780.2	FLJ12753;FLJ21795			
GI_19923843-S	88.4	97.6	100.3	FLJ23518	NM_024725.2				
GI_19923847-S	1567.1	861.8	989.6	CDT1	NM_030928.2	DUP	DNA	nucleus	regulation
GI_19923852-S	176.2	211.5	222.2	DKFZP547N	NM_032018.2	dJ876B10.3			
GI_19923854-S	877.7	1137.4	970.4	SYAP1	NM_032796.2	PRO3113;FLJ14495			
GI_19923874-S	122.7	118.9	115.4	C21orf41	NM_138332.1				
GI_19923878-S	926.4	984.8	1133.7	SBBI54	NM_138334.1			integral to	
GI_19923880-S	804.2	868.8	661.3	GNPDA2	NM_138335.1	SB52	glucosami		N-
GI_19923882-S	104.6	105.7	103.2	LOC150678	NM_138336.1				
GI_19923886-S	138.1	138.1	129.2	DKFZp761H2	NM_138339.1				
GI_19923898-S	998.2	889.5	729.6	LOC90799	NM_138363.1				
GI_19923900-S	519.9	511.7	451.3	MGC16044	NM_138371.1				
GI_19923904-S	164.1	200.4	185.4	LOC91937	NM_138379.1				
GI_19923906-S	266.3	253.2	239	MGC15763	NM_138381.1		oxidoredu		electron
GI_19923908-S	743.6	713.5	672.1	LOC92305	NM_138385.1				
GI_19923910-S	181.4	175.2	173.1	LOC92345	NM_138386.1				
GI_19923916-S	515.2	518.1	635.6	LOC92799	NM_138392.1		voltage-	membran	potassium
GI_19923918-S	339.2	247.8	269.5	DP1L1	NM_138393.1				
GI_19923924-S	302.2	377.8	349.9	LOC93082	NM_138397.1		DNA	nucleus	regulation
GI_19923926-S	993.3	1197.5	1198	C6orf51	NM_138408.1	bA397G5.3			
GI_19923934-S	393.1	355.9	369.9	LOC112869	NM_138414.1				
GI_19923936-S	161.2	110.1	91.5	LOC112885	NM_138415.1		DNA	nucleus	regulation
GI_19923938-S	608.4	712	692.9	LOC112970	NM_138417.1				
GI_19923942-S	2011.7	2048	1976.7	LOC113174	NM_138421.1				
GI_19923944-S	348.3	310.8	366	LOC113179	NM_138422.1		zinc ion		
GI_19923948-S	90.1	106.4	101.1	KIF12	NM_138424.1		ATP	kinesin	microtubul
GI_19923956-S	2247.9	2653.6	2937.5	LOC113655	NM_138431.1				
GI_19923960-S	225.1	278.5	247.9	C7orf29	NM_138434.1				
GI_19923962-S	121.8	142.5	121.1	LOC113828	NM_138435.1				
GI_19923976-S	3083.2	3147.1	2889.6	C7orf30	NM_138446.1		molecular		
GI_19923980-S	114.6	149.7	115.9	LOC115811	NM_138451.1		DNA	nucleus	regulation
GI_19923982-S	876.1	870.9	1188.5	DHRS1	NM_138452.1	FLJ25430;MGC20204	oxidoredu		metabolis
GI_19923986-S	97.6	93.4	101.7	LOC115861	NM_138454.1		electron		electron
GI_19923994-S	416.7	341.1	321.4	LOC116211	NM_138461.1			integral to	
GI_19924006-S	133.7	144.1	148.8	LOC144845	NM_138474.1				

GI_19924014-S	148.4	154.8	139.7	LOC151534	NM_138482.1				
GI_19924022-S	131.6	163.4	138.9	LOC158435	NM_138497.1		receptor		
GI_19924096-A	114.3	134	115.4	SYN1	NM_133499.1	SYNI;SYN1a;SYN1b	actin	secretory	nonselecti
GI_19924098-I	171.5	192.9	183.3	SYN1	NM_006950.2	SYNI;SYN1a;SYN1b	actin	secretory	nonselecti
GI_19924100-I	231.8	277.8	245.1	SYN2	NM_003178.2	SYNII;SYNIIa;SYNIIb		peripheral	synaptic
GI_19924102-A	211.9	235.1	213.2	SYN2	NM_133625.1	SYNII;SYNIIa;SYNIIb		peripheral	synaptic
GI_19924102-I	115.1	113.6	111.3	SYN2	NM_133625.1	SYNII;SYNIIa;SYNIIb		peripheral	synaptic
GI_19924108-A	138	184.1	160.7	SYN3	NM_133633.1		ATP	synaptic	neurotran
GI_19924110-S	154.2	212.9	183.2	PRODH	NM_016335.2	PIG6;HSPOX2;PRODH1;PRODH2;TP53I6	proline		proline
GI_19924112-S	158.9	183.3	164	RAD9A	NM_004584.2	RAD9		nucleus	DNA
GI_19924114-I	4197.4	5312.2	4411.9	RAD51L1	NM_133509.1	REC2;R51H2;hREC2;RAD51B	adenosine	nucleus	meiotic
GI_19924116-A	443.8	543	490.8	RAD51L1	NM_133510.1	REC2;R51H2;hREC2;RAD51B	adenosine	nucleus	meiotic
GI_19924116-I	110.1	96.6	106.5	RAD51L1	NM_133510.1	REC2;R51H2;hREC2;RAD51B	adenosine	nucleus	meiotic
GI_19924124-A	390.1	419.4	464.8	RAD51L3	NM_133629.1	Trad;R51H3;HsTRAD;RAD51D	DNA	nucleus	meiotic
GI_19924128-I	86.3	91.8	81.8	RAD50	NM_005732.2	hRad50;RAD50-2	single-	nucleus	regulation
GI_19924130-A	153.7	126.9	87.7	RAD50	NM_133482.1	hRad50;RAD50-2	single-	nucleus	regulation
GI_19924132-I	120.5	142.7	153.4	RAD51	NM_002875.2	RECA;HRAD51;RAD51A;HsRad51;HsT1693	adenosine	nucleus	mitotic
GI_19924134-A	101.3	104.9	99.6	RAD51	NM_133487.1	RECA;HRAD51;RAD51A;HsRad51;HsT1693	adenosine	nucleus	mitotic
GI_19924136-S	328	304.9	336.4	RAD54L	NM_003579.2	HR54;hHR54;HRAD54;RAD54A	adenosine	nucleus	meiosis
GI_19924137-S	2941.3	2327.7	2144.3	RAD23A	NM_005053.2	HHR23A	single-	nucleus	nucleotide-
GI_19924138-S	1630.1	1800.1	1472.7	RAD23B	NM_002874.2	P58;HR23B;HHR23B	single-	nucleus	nucleotide-
GI_19924139-I	92.8	97.5	89.2	LARGE	NM_004737.2	KIAA0609	acetylgluc	kinesin	N-
GI_19924140-A	321.5	197.2	381.1	LARGE	NM_133642.1	KIAA0609	acetylgluc	kinesin	N-
GI_19924142-S	95.7	101.6	105.1	LUZP1	NM_033631.1	LUZP;FLJ00226	binding	mitochond	transport
GI_19924144-I	127.7	134.4	126.6	TCIRG1	NM_006019.2	a3;Stv1;Vph1;Atp6i;OC116;OPTB1;TIRC7;AT	transporte	integral to	proton
GI_19924146-A	1606.9	1489.1	1091.9	TCIRG1	NM_006053.2	a3;Stv1;Vph1;Atp6i;OC116;OPTB1;TIRC7;AT	transporte	integral to	proton
GI_19924146-I	306.2	388.9	368.1	TCIRG1	NM_006053.2	a3;Stv1;Vph1;Atp6i;OC116;OPTB1;TIRC7;AT	transporte	integral to	proton
GI_19924152-A	163.4	182.5	179.9	TLR4	NM_138557.1	TOLL;hToll	antibacteri	lipopolysa	signal
GI_19924154-I	301.8	337.4	317.2	RFXANK	NM_003721.2	BLS;RFX-B;ANKRA1;F14150_1	transcripti	nucleus	humoral
GI_19924155-A	502.3	530.3	571.6	RFXANK	NM_134440.1	BLS;RFX-B;ANKRA1;F14150_1	transcripti	nucleus	humoral
GI_19924157-S	91.7	98.7	82.7	RFXAP	NM_000538.2		DNA	nucleus	transcripti
GI_19924160-A	4957	4178	3995.1	C19orf2	NM_134447.1	RMP;URI;NNX3;FLJ10575	transcripti	DNA-	pathogene
GI_19924162-S	94.1	90.6	94.9	RNF28	NM_032588.2	IRF;SMRZ;MURF1;MURF2;FLJ32380	zinc ion	kinesin	signal
GI_19924164-S	113.6	116.6	100.7	ROS1	NM_002944.2	ROS;MCF3	protein-	sodium/po	oncogene
GI_19924171-S	501.8	366.7	409.9	WRN	NM_000553.2	RECQ3;RECQL2;RECQL3	helicase	nucleus	aging
GI_19924176-S	2494.4	2630	2241.4	SUPT16H	NM_007192.2	FACT;CDC68;FACTP140;FLJ10857;FLJ1401	positive		nucleoso
GI_19924297-S	95.6	98.3	102.1	FIGF	NM_004469.2	VEGFD;VEGF-D	platelet-	membran	positive
GI_19924298-S	414.6	454.4	580.7	FRAP1	NM_004958.2	FRAP;MTOR;FRAP2;RAFT1;RAPT1	inositol/ph	phosphoin	DNA
GI_19924299-S	137.2	117.2	110.9	TCAP	NM_003673.2	TELE;CMD1N;T-cap;LGMD2G;telethonin	structural	cytoplasm	sarcomere
GI_19924300-S	1210.6	788.8	1053.5	VEGFC	NM_005429.2	VRP;Flt4-L	growth	membran	lymph
GI_19924303-S	83	104.3	104.8	HIST1H2BB	NM_021062.2	H2B.1;H2B/f;H2BFF	DNA	chromoso	nucleoso
GI_20069857-S	281.1	352.5	283.8	WFDC12	NM_080869.1	WAP2;C20orf122;dJ211D12.4	serine	extracellul	biological_
GI_20070102-S	611.3	2069.9	825.1	TEAD2	NM_003598.1	ETF;TEF4;TEF-4	transcripti	nucleus	regulation
GI_20070108-I	350.9	428.1	336.5	DAB2IP	NM_032552.1	AF9Q34;DIP1/2;KIAA1743			

GI_20070124-S	7736.4	12294	9632	P4HB	NM_000918.2	DSI;GIT;PDI;PO4DB;PO4HB;PROHB;ERBA2	protein	endoplas	electron
GI_20070126-S	70	100.9	86.7	PDE3A	NM_000921.2	CGI-PDE	cGMP-	membran	lipid
GI_20070128-S	151.3	157.6	157	PTAFR	NM_000952.2		platelet	integral to	pathogene
GI_20070134-S	8469.6	8663.9	7984.7	G22P1	NM_001469.2	ML8;KU70;TLAA;D22S671;D22S731	double-	membran	DNA
GI_20070136-S	599.6	511.6	548.8	NDUFA6	NM_002490.2	B14	NADH	NADH	
GI_20070140-S	464.2	575.8	502.3	PLD2	NM_002663.2		phospholi	plasma	small
GI_20070145-S	186.4	238.4	136.9	SH3GL3	NM_003027.2	CNSA3;EEN-B2;SH3D2C;SH3P13;HsT19371		kinesin	central
GI_20070149-S	455.6	446.3	430.7	SPR	NM_003124.2		sepiapteri		tetrahydro
GI_20070157-S	7565.6	7998.8	8078.2	STK24	NM_003576.2	MST3;STK3;MST-3;MST3B	protein		signal
GI_20070169-S	150.9	169.9	149.1	PLGL	NM_002665.2		plasmin		
GI_20070171-S	1951.3	1880.9	1801.2	RPA1	NM_002945.2	HSSB;RF-A;RP-A;REPA1;RPA70	single-	DNA	DNA
GI_20070179-S	5986.1	4934.1	4133.4	EIF4EBP1	NM_004095.2	4EBP1;PHAS-I	translation		regulation
GI_20070184-S	379.6	411.9	406.2	USP14	NM_005151.2	TGT	ubiquitin-		deubiquiti
GI_20070185-S	286.4	299.4	234.8	PTER	NM_030664.2	RPR-1	zinc ion		catabolis
GI_20070198-S	1549.9	1463	1462.3	NR2F6	NM_005234.2				
GI_20070207-S	4644.3	4719.7	3978	RHEB	NM_005614.2	RHEB2	GTPase	membran	signal
GI_20070210-S	14780.4	11291	8415.8	SUI1	NM_005801.2	A121;ISO1	translation	cytoplasm	cell growth
GI_20070219-S	1637.2	1429.2	1098.1	SKB1	NM_006109.2	JBP1;IBP72;PRMT5;SKB1Hs			regulation
GI_20070223-S	872.4	728.3	734.1	ZNF297	NM_005453.3	BING1	DNA	nucleus	regulation
GI_20070225-S	91	103.4	91.1	AGR2	NM_006408.2	AG2;GOB-4;HAG-2;XAG-2			oncogene
GI_20070229-S	104.9	176	127.6	ENPP2	NM_006209.2	ATX;PDNP2;LysoPLD;PD-IALPHA	phosphodi	integral to	phosphate
GI_20070231-S	277	307.9	284	UQCRB	NM_006294.2	QPC;QP-C;UQBC;UQBP;UQPC	ubiquinol-	mitochond	oxidative
GI_20070233-S	549.1	692.1	598.7	TXNL4	NM_006701.2	DIM1;HsT161;U5-15kD			
GI_20070234-S	380.5	344.8	415	EVI2B	NM_006495.2	EVDB;D17S376		integral to	oncogene
GI_20070240-S	4835.5	4905.1	4237.6	D1S155E	NM_007158.2	UNR	RNA		male
GI_20070258-S	166.5	275.6	211.3	FEM1B	NM_015322.2	FIAA;KIAA0396	death	cellular_co	induction
GI_20070259-S	1075.3	1050	1101.4	COBRA1	NM_015456.2	NELFB;NELF-B;DKFZP586B0519		nucleus	regulation
GI_20070261-S	153.3	171.1	163.2	TRAF3IP1	NM_015650.2	MIPT3;MIP-T3;DKFZp434F124	receptor		
GI_20070263-S	1514.2	2323.2	2332.4	XTP3TPB	NM_015701.2	CL24936;CL25084			
GI_20070268-S	122.5	128.2	102.4	PDCD1LG1	NM_014143.2	B7-H;B7H1;PDL1;PD-L1;PDCD1L1			cell
GI_20070269-S	94.2	114.4	89	G0S2	NM_015714.2		molecular	cellular_co	cell growth
GI_20070270-I	88.5	109.2	103.4	TRNT1	NM_016000.2	CCA1;MtCCA;CGI-47	nucleotide	mitochond	tRNA
GI_20070271-S	3563.2	3619.4	3505.2	RDH11	NM_016026.2	MDT1;PSDR1;RALR1;SCALD;ARSDR1;CGI-	oxidoredu	endoplas	metabolis
GI_20070274-S	229.4	247.7	226	KLF3	NM_016531.2	BKLF	transcripti	nucleus	developm
GI_20070275-S	1830.4	1658.7	1636.4	GMPR2	NM_016576.2		GMP		nucleotide
GI_20070278-S	757.3	1026.4	990.4	COMMD10	NM_016144.2	PTD002;FLJ11285			
GI_20070283-S	87	92.5	92	EMCN	NM_016242.2	EMCN2			
GI_20070287-S	616.8	605.5	553.5	FLJ10458	NM_018096.2	Nle	signal	heterotrim	G-protein
GI_20070288-S	626.6	731.4	739.1	PLEKHA3	NM_019091.2	FAPP1;FLJ20067	phospholi	cellular_co	biological_
GI_20070290-S	299.5	307.4	293.1	FLJ20013	NM_017621.2				
GI_20070291-S	248.9	349	409.1	CHST12	NM_018641.2	C4S-2;C4ST2;C4ST-2	transferas		
GI_20070295-S	1068.1	917.8	1043.5	RNPEPL1	NM_018226.2	FLJ10806	aminopept		proteolysis
GI_20070301-S	151.2	231.5	136.8	DOK4	NM_018110.2	FLJ10488	insulin		
GI_20070304-S	730.5	621.7	756.2	MDS031	NM_018466.2				

GI_20070311-S	122.3	117.4	104	AMY2B	NM_020978.2	AMY2	alpha-		carbohydr
GI_20070320-S	236.1	272.5	224.4	NMNAT1	NM_022787.2	NMNAT;PNAT1;PNAT-1	protein	nucleus	NADH
GI_20070322-I	578.7	850.3	787.4	SLC30A5	NM_022902.2	ZNT5;ZTL1;ZNTL1;ZnT-			
GI_20070325-S	1583.5	1616.4	1596	FLJ13052	NM_023018.2	dJ283E3.1			
GI_20070327-I	91.6	93.4	92.7	MS4A4A	NM_024021.2	MS4A4;MS4A7;4SPAN1;CD20L1;CD20-			
GI_20070329-S	496.9	493.3	301.6	ZFYVE21	NM_024071.2	MGC2550			
GI_20070332-S	181.5	199.5	179.6	NPEPL1	NM_024663.2	FLJ11583;bA261P9.2	aminopept	intracellula	proteolysis
GI_20070334-S	200.1	200.4	209.6	FLJ11506	NM_024666.2				
GI_20070338-A	177.7	359.5	220.6	ZNF323	NM_030899.2	FLJ23407	transcripti	nucleus	regulation
GI_20070341-S	367.2	368.1	399.7	FLJ23375	NM_024956.2				
GI_20070345-S	204.5	333.1	367.6	ULBP2	NM_025217.2	RAET1H	MHC	membran	immune
GI_20070346-S	89.9	105.7	86.8	SLC2A11	NM_030807.2	GLUT10;GLUT11	glucose	integral to	carbohydr
GI_20070348-S	358	350.6	246.3	VMP1	NM_030938.2	DKFZP566I133			
GI_20070355-S	2382.3	2336.4	2409.8	NUMB	NM_003744.3	S171		integral to	
GI_20070357-S	114.4	110.3	108.4	LGR8	NM_130806.2	GREAT;GPR106	rhodopsin-	integral to	G-protein
GI_20070359-S	133	207.4	127.3	ARHV	NM_133639.2	Chp;WRCH2	Rho small		small
GI_20070361-S	86.6	82.6	83.1	SDPR	NM_004657.3	SDR;PS-p68	phospholi	caveola	
GI_20070373-S	112.4	127.2	113.9	C6orf142	NM_138569.1	MGC18257			
GI_20070375-S	191.5	207.7	182.3	MGC15523	NM_138570.1				
GI_20070377-S	151.6	164.4	151.6	TBN	NM_138572.1	TAF8;FLJ32821			
GI_20070379-S	92.8	102.4	87.3	LOC145957	NM_138573.1		growth	integral to	
GI_20070381-S	206.5	242.4	205.2	PWWP1	NM_138574.1	dJ309H15.1	DNA	nucleus	regulation
GI_20070383-S	142.5	169.7	165	MGC5352	NM_138575.1		catalytic		metabolis
GI_20127147-S	451.4	632.9	554.7	ZNF451	NM_015555.1	COASTER;KIAA0576;dJ417I1.1	DNA	nucleus	regulation
GI_20127403-S	150.8	171.6	144	RCP	NM_025151.2	FLJ22524;FLJ22622;rab11-FIP1			
GI_20127419-S	449.9	404.2	382.8	CHEK1	NM_001274.2	CHK1	tumor	nucleus	gametoge
GI_20127421-S	161.7	176.1	167.2	DSCAM	NM_001389.2	CHD2-42;CHD2-52	cell	membran	cell
GI_20127429-S	3076.1	3375.8	3080.3	PPP6C	NM_002721.3		protein		G1/S
GI_20127439-S	5850.4	6325.4	5398.3	TETRAN	NM_001120.2	TETTRAN	tetracyclin	integral to	small
GI_20127447-S	850.4	818.9	1011.6	POLA2	NM_002689.2		molecular	nucleus	DNA
GI_20127455-S	1253.5	2674.4	3055.3	GNG11	NM_004126.2		heterotrim	peripheral	signal
GI_20127456-S	3829.2	3588.2	3637.8	GYG	NM_004130.2		glycogenin		glycogen
GI_20127458-S	135	142.5	163.3	CITED1	NM_004143.2	MSG1	transcripti	nucleus	regulation
GI_20127459-S	1486.1	1244.5	1115.2	XPC	NM_004628.2	XP3;XPCC	damaged	nucleus	nucleotide-
GI_20127461-S	87.5	105.3	91	SLC16A5	NM_004695.2	MCT5	monocarb	membran	monocarb
GI_20127465-S	225	243.4	248.6	HOMER1	NM_004272.2	SYN47;Ves-1;HOMER-1B	protein	proteoglyc	metabotro
GI_20127466-S	286.9	307.5	372.5	CHST10	NM_004854.2	HNK1ST;HNK-1ST	sulfotransf	Golgi	cell
GI_20127469-S	1603	1322.3	1306.6	EEF1E1	NM_004280.2	P18			protein
GI_20127471-S	173.3	163.5	105.5	ETS2	NM_005239.2		DNA	nucleus	skeletal
GI_20127480-S	238.2	251.7	267.2	EPM2A	NM_005670.2	LD;LDE;EPM2;MELF;LAFORIN	protein	polysome	glycogen
GI_20127481-S	243.8	278.5	261.2	NKG7	NM_005601.2	GIG1		integral to	
GI_20127485-S	2644.5	2979.9	3785.3	M6PRBP1	NM_005817.2	PP17;TIP47		endosome	vesicle-
GI_20127489-S	688.5	577.3	489.9	MADH2	NM_005901.2	JV18;MADR2;SMAD2;JV18-1	protein	nucleus	signal
GI_20127493-S	372.6	478.6	439.5	ANP32A	NM_006305.2	LANP;MAPM;PP32;PHAP1;PHAPI;I1PP2A	MHC-	nucleus	intracellula

GI_20127494-S	83	85.1	77.3	POU4F1	NM_006237.2	BRN3A;RDC-1	transcripti	nucleus	synaptoge
GI_20127496-S	381.3	449.2	408.2	PPP5C	NM_006247.2	PP5;PPP5	protein	nucleus	transcripti
GI_20127497-S	1759.6	1654	1893.8	RRAS	NM_006270.2		RAS small		RAS
GI_20127505-S	378.1	378.6	409.4	PMVK	NM_006556.2	PMK;PMKA;PMKASE;HUMPMKI	phosphom	peroxisom	protein
GI_20127508-S	758	699.9	858.1	RAB32	NM_006834.2		GTP	mitochond	protein
GI_20127520-S	435.2	534.7	518.3	C22orf5	NM_012264.2	HS5O6A;DKFZP586A1024		integral to	
GI_20127526-S	920.4	664.1	323.7	NXT1	NM_013248.2	P15;MTR2	protein	nuclear	nucleocyto
GI_20127527-S	583.9	644.2	542.4	PARVB	NM_013327.2	CGI-56;BK414D7.C22.1.MRNA			
GI_20127535-S	383.6	762.1	416.2	RGL1	NM_015149.2	RGL;KIAA0959	Ral guanyl	cellular_co	small
GI_20127543-S	1213	1355.4	1017.1	CGI-27	NM_015955.2				
GI_20127554-S	3790.2	3613.9	2652.6	HSPC111	NM_016391.2	HSPC185		nucleus	
GI_20127557-S	4906.9	5308.1	4504.3	C9orf83	NM_016410.2	CGI-34;HSPC177	molecular		
GI_20127565-S	744.7	652.2	593	FLJ20457	NM_017832.2				
GI_20127566-S	143	135.6	121	C1orf27	NM_017847.2	FLJ20505			
GI_20127571-S	161.9	139.9	170.9	ZNF331	NM_018555.3	RITA;ZNF361;ZNF463	nucleic	nucleus	regulation
GI_20127573-S	863.5	694.4	317.1	C14orf116	NM_018589.2	PRO1635			
GI_20127576-S	1838.5	1884.5	2031.4	PNRC2	NM_017761.2	FLJ20312	receptor		
GI_20127579-S	7933.2	6092.2	5341.9	BTBD2	NM_017797.2	FLJ20386	protein		
GI_20127585-S	706.5	570.8	525.6	TDP1	NM_018319.2	SCAN1;FLJ11090	hydrolase	nucleus	DNA
GI_20127593-S	143.3	165.4	157.3	C12orf6	NM_020367.2	HIN1L			
GI_20127594-S	1266.2	2199.2	926.3	PDLIM1	NM_020992.2	CLIM1;CLP36;ELFIN;CLP-36;hCLIM1	protein	cytoskelet	response
GI_20127595-S	89	96.3	87.6	CDT6	NM_021146.2	dJ647M16.1		soluble	killer
GI_20127596-S	1643.6	3107.5	2361.8	Hes4	NM_021170.2		DNA	nucleus	regulation
GI_20127599-S	305.1	170.5	162.9	RRAGD	NM_021244.2	RAGD;bA11D8.2.1;DKFZP761H171	small	cytoplasm	cell growth
GI_20127606-S	926.9	1211.9	1021.3	C14orf133	NM_022067.2	FLJ12707			
GI_20127610-S	584.8	643	777.3	FLJ22405	NM_022485.2	FLJ90311	protein		protein
GI_20127615-S	1618.6	1957.2	1410.3	NICAL	NM_022765.2	MICAL;MICAL-			
GI_20127622-S	946	1108.7	799.9	MEP50	NM_024102.2	MGC2722			
GI_20127623-S	100.2	117.2	106.8	NOX5	NM_024505.2	NOX5A;NOX5B	binding	membran	transport
GI_20127625-S	74.5	120.1	103.3	C14orf139	NM_024633.2	FLJ21276			
GI_20127628-S	1432.6	1029.4	993.3	FLJ23436	NM_024671.2		DNA-	DNA-	transcripti
GI_20127633-S	196.2	188.5	160.1	FLJ12598	NM_024754.2				
GI_20127635-S	101.2	133	103	CHODL	NM_024944.2	MT75;PRED12;C21orf68;FLJ12627	lectin [goid	integral to	heterophili
GI_20127637-S	95.4	124.8	106.5	GPR157	NM_024980.2	FLJ12132	G-protein	membran	
GI_20127641-S	188	144	195	GKAP42	NM_025211.2	FKSG21			
GI_20127646-S	84.9	91	78.3	ITIH5	NM_030569.2	MGC10848			
GI_20127649-S	951.2	883.4	729.5	KIAA0157	NM_032182.2				
GI_20127651-S	3521.3	3252.3	2694.7	PSARL	NM_018622.3	PARL;PSARL1;PRO2207;PSENIP2			
GI_20127653-S	97.6	106.7	105.2	MGC15631	NM_032753.2		transcripti	nucleus	regulation
GI_20127658-S	1128.5	1189.1	1049.9	LGALS12	NM_033101.2	GRIP1;GALECTIN-12			
GI_20127661-S	614	1228.4	1437.4	TP53INP1	NM_033285.2	SIP;Teap;FLJ22139;P53DINP1;TP53DINP1;			
GI_20127665-S	105.2	122.4	109	MGC4766	NM_031451.3	NYD-SP8			
GI_20143481-S	128.9	135	138.2	KIAA1587	NM_020932.1	HCA1;DAMAGE			
GI_20143483-S	89.2	108.5	94.1	OSAP	NM_032623.2				

GI_20143909-I	138.7	203.8	144.9	WSB1	NM_134264.1	SWIP1;WSB-1	molecular	cellular_co	intracellula
GI_20143911-A	395.5	473.2	340.3	WSB1	NM_134265.1	SWIP1;WSB-1	molecular	cellular_co	intracellula
GI_20143915-A	87.8	91.2	82.6	TTN	NM_133379.1	TMD;CMD1G;CMPD4;FLJ32040	structural	cytoskelet	regulation
GI_20143915-I	96.4	92.2	89	TTN	NM_133379.1	TMD;CMD1G;CMPD4;FLJ32040	structural	cytoskelet	regulation
GI_20143917-I	117.8	106.3	105.6	TTN	NM_133432.1	TMD;CMD1G;CMPD4;FLJ32040	structural	cytoskelet	regulation
GI_20143921-I	145.1	169.2	150.2	TTN	NM_133437.1	TMD;CMD1G;CMPD4;FLJ32040	structural	cytoskelet	regulation
GI_20143928-I	89.2	84.9	88.1	RAD54B	NM_012415.2		DNA		mitotic
GI_20143929-A	175.5	185.3	203.5	RAD54B	NM_134434.1		DNA		mitotic
GI_20143931-S	90.3	108.6	104	RLN1	NM_006911.2	RLXH1;bA12D24.3.1;bA12D24.3.2	peptide	extracellul	pregnancy
GI_20143932-A	95.5	108.5	90.5	RLN2	NM_134441.1	RLXH2;bA12D24.1.1;bA12D24.1.2	hormone	extracellul	pregnancy
GI_20143934-I	94.3	92.8	85.3	RLN2	NM_005059.2	RLXH2;bA12D24.1.1;bA12D24.1.2	hormone	extracellul	pregnancy
GI_20143940-A	143.8	198.5	144.6	MUC4	NM_138297.1	HSA276359	Neu/ErbB-	integral to	
GI_20143942-I	135.9	132.6	121.1	KCNK10	NM_021161.3	TREK2;TREK-2	potassium	membran	small
GI_20143943-I	126.5	133.5	118.9	KCNK10	NM_138317.1	TREK2;TREK-2	potassium	membran	small
GI_20143945-A	108.7	118.9	107.9	KCNK10	NM_138318.1	TREK2;TREK-2	potassium	membran	small
GI_20143945-I	99.5	119	100	KCNK10	NM_138318.1	TREK2;TREK-2	potassium	membran	small
GI_20143947-S	276.9	283.4	273.9	TOP3A	NM_004618.2	TOP3	DNA	nucleus	meiosis
GI_20143948-S	679.2	583.7	594.7	TOPBP1	NM_007027.2	KIAA0259	protein C-	nucleus	DNA
GI_20143949-A	430.6	523.1	496.8	ITGB1BP1	NM_022334.2	ICAP1;ICAP1A;ICAP1B;ICAP-1A;ICAP-1B	protein C-	peripheral	protein
GI_20143950-I	1791	1497.6	1261	ITGB1BP1	NM_004763.2	ICAP1;ICAP1A;ICAP1B;ICAP-1A;ICAP-1B	protein C-	peripheral	protein
GI_20143951-A	159.2	193.4	143.1	RAD52	NM_002879.2		DNA	nucleus	mitotic
GI_20143953-I	154.4	169	163	RAD52	NM_134422.1		DNA	nucleus	mitotic
GI_20143955-I	95.4	111.6	101.9	RAD52	NM_134423.1		DNA	nucleus	mitotic
GI_20143959-A	160.4	179.8	153.3	DLX4	NM_001934.2	BP1;DLX7;DLX8;DLX9	transcripti		
GI_20143961-I	259	324	297.1	DLX4	NM_138281.1	BP1;DLX7;DLX8;DLX9	transcripti		
GI_20143963-S	95.6	88.7	86.3	GRIN3A	NM_133445.1	NR3A;NMDAR-L			
GI_20143965-A	628	658.6	873.3	KIF23	NM_004856.4	CHO1;KNSL5;MKLP1;MKLP-1	microtubul	kinesin	mitotic
GI_20143966-I	177.9	175.1	179.8	KIF23	NM_138555.1	CHO1;KNSL5;MKLP1;MKLP-1	microtubul	kinesin	mitotic
GI_20143970-S	110.8	124.7	125.5	TLR6	NM_006068.2		defense/i	phagocytic	signal
GI_20143972-S	1002.6	2069.2	279.2	HHIP	NM_022475.1	HIP;FLJ20992			
GI_20143974-S	333.3	416.9	373	ABCG4	NM_022169.2	WHITE2	nucleotide	integral to	transport
GI_20143978-S	188.8	223.2	236.7	ATR	NM_001184.2	FRP1;SCKL;SCKL1	protein		recombina
GI_20143980-S	387.5	399.6	460.8	HSD17B8	NM_014234.3	KE6;FABG;HKE6;FABGL;RING2;H2-	alcohol	cellular_co	lipid
GI_20149303-S	938.7	1190.9	1089.9	KIAA1160	NM_020701.1				
GI_20149305-S	19074.2	22059	20448	UBC	NM_021009.1				
GI_20149319-A	130.2	133	140.3	CLDN15	NM_138429.1	MGC19536			
GI_20149319-I	302.4	357	326	CLDN15	NM_138429.1	MGC19536			
GI_20149497-S	18198.9	18416	14709	FTL	NM_000146.2	PRO2760	iron ion	ferritin	iron ion
GI_20149499-S	473.3	501	597.4	HMBS	NM_000190.2	AIP;UPS;PBGD	hydroxym		heme
GI_20149501-S	146.9	171.9	135.5	PLA2G2A	NM_000300.2	MOM1;PLA2B;PLA2L;PLA2S;PLAS1	calcium-	membran	oncogene
GI_20149508-S	433.5	499.4	602.9	BUB1B	NM_001211.3	BUBR1;Bub1A;MAD3L	protein	kinetochor	mitotic
GI_20149512-S	1006.6	970.7	369.3	CHC1	NM_001269.2	RCC1	Ran	nucleus	chromoso
GI_20149514-S	664.3	905.9	1629.2	CXADR	NM_001338.2	CAR;HCAR	receptor	integral to	
GI_20149519-S	2678.3	2139.4	1967.5	PAFAH1B3	NM_002573.2		1-alkyl-2-	soluble	lipid

GI_20149523-S	1186.7	1168	1193	SUPT5H	NM_003169.2	SPT5;SPT5H	transcripti	nucleus	chromatin
GI_20149527-S	132.7	161.7	119.8	PSTPIP1	NM_003978.2	H-		peripheral	response
GI_20149546-S	154.7	171.4	146.7	RPS6KA1	NM_002953.2	RSK;HU-1;RSK1;MAPKAPK1A	protein		signal
GI_20149548-S	2069.8	2802.1	2650.6	SRP54	NM_003136.2		RNA	signal	protein
GI_20149554-S	158.6	886.3	878	SERPINB1	NM_030666.2	EI;LEI;PI2;MNEI;M/NEI;ELANH2	serpin	cytoplasm	
GI_20149561-S	1431.9	1119.9	1244.3	TRIP13	NM_004237.2	16E1BP	transcripti	nucleus	transcripti
GI_20149567-S	6539.7	6121	5162.9	NDUFV1	NM_007103.2	UQOR1	NADH	mitochond	energy
GI_20149569-I	115.5	129.3	116.1	RASGRP2	NM_005825.2	CDC25L;CALDAG-GEFI	lipid		signal
GI_20149573-S	189.4	232.8	199.5	KLK2	NM_005551.2		tissue		proteolysis
GI_20149575-S	2099.4	2577.4	1959.7	NFE2L2	NM_006164.2	NRF2	transcripti	nucleus	transcripti
GI_20149579-S	1036.2	962.6	855	SLC35A1	NM_006416.2	CST;hCST;CMPST	CMP-sialic	Golgi	CMP-sialic
GI_20149581-S	102.7	102.3	106.5	MARCO	NM_006770.2	SCARA2	macropha	integral to	response
GI_20149585-S	130.5	149.9	128.6	SAA2	NM_030754.2		acute-	extracellul	acute-
GI_20149591-S	4903.2	5315.6	4380.2	UNRIP	NM_007178.2	MAWD;PT-WD			invasive
GI_20149593-S	5352	7533.7	5790.4	HSPCB	NM_007355.2	HSPC2;D6S182;HSP90B;HSP90-BETA	ATP	cytoplasm	protein
GI_20149595-S	97.7	99	91.4	CBLC	NM_012116.2	CBL-3;RNF57;CBL-SL	protein	nucleus	negative
GI_20149599-S	1692.2	2215.2	2319	MSRB	NM_012228.2	CBS1;PILB;CBS-1;CGI-131	transcripti		
GI_20149601-S	2512	2588	2288.5	NT5C2	NM_012229.2	GMP;NT5B;PNT5;cN-II	5'-	cytosol	
GI_20149602-S	855.3	451.2	497.6	HEY1	NM_012258.2	CHF2;CHF-2;HERP2;HESR1;HRT-1;HESR-1	DNA	nucleus	histogene
GI_20149604-S	246	393.5	230.7	TTLL1	NM_012263.2	C22ORF7;KIAA0173;HS323M22B	molecular	cellular_co	protein
GI_20149611-S	94.6	97.8	99.5	ERVWE1	NM_014590.2	HERVW;HERV-W;HERV-W-ENV	structural	viral	syncytium
GI_20149616-S	600.9	321.1	387.4	NPDC1	NM_015392.2	CAB;CAB-;CAB1;CAB-1;DKFZP586J0523		integral to	
GI_20149620-S	263.3	304.6	303.5	DKFZP586B1	NM_015533.2		glycerone		glycerol
GI_20149630-S	105.5	116	111.5	DUSP13	NM_016364.2	BEDP;TMDP;FLJ32450	protein		meiosis
GI_20149632-S	589.6	543	466.3	SITPEC	NM_016581.2				
GI_20149636-S	199.9	223.8	196	ARTS-1	NM_016442.2	ALAP;A-	aminopept		proteolysis
GI_20149638-S	235.1	131.3	119.7	NOX4	NM_016931.2	KOX;KOX-1;RENOX	nucleotide	membran	energy
GI_20149642-S	1970.4	1530.5	981	FLJ20729	NM_017953.2	FLJ20760			
GI_20149644-S	2411.1	2236.8	2514.8	SARS2	NM_017827.2	SYS;SARS;SERS;SARSM;SerRSmt;mtSerR	serine-	mitochond	seryl-
GI_20149649-S	378.5	594.7	572.4	CHST11	NM_018413.2	C4ST;C4ST1;C4ST-1;HSA269537	transferas		
GI_20149650-S	1047.9	887	828.8	FLJ10233	NM_018034.2				
GI_20149671-S	3664.2	3620.8	3306.3	FLJ13855	NM_023079.2	HOYS7	ubiquitin		ubiquitin
GI_20149672-A	1844.7	1321.3	1376.6	SLC30A5	NM_024055.2	ZNT5;ZTL1;ZNTL1;ZnT-			
GI_20149672-I	182.5	180.9	159.4	SLC30A5	NM_024055.2	ZNT5;ZTL1;ZNTL1;ZnT-			
GI_20149678-S	311.5	381.6	363.5	FLJ22160	NM_024585.2				
GI_20149679-S	667.2	619.4	764.2	FN3KRP	NM_024619.2	FLJ12171	kinase		
GI_20149694-S	769.5	572.7	611.8	FLJ22246	NM_025232.2	PP432;FLJ22277			
GI_20149699-S	168.6	180.8	174.7	MYCBPAP	NM_032133.2	AMAP-1;DKFZp434N1415			
GI_20149708-S	194.1	282	241.6	LOC92906	NM_138394.2				
GI_20149710-S	1708.9	1372.5	1018.2	LOC93349	NM_138402.2				
GI_20149715-S	100	104.3	101.6	KIAA0626	NM_021647.3				
GI_20162553-S	120.3	130	137.4	KLF14	NM_138693.1	BTEB5	DNA	nucleus	regulation
GI_20162565-S	2418.6	2233.2	1319.4	C7orf11	NM_138701.1	ORF20	DNA	nucleus	regulation
GI_20162567-I	84.7	95.4	93.2	MAGEC3	NM_138702.1	HCA2;MAGE-C3			

GI_20162573-S	113.2	101.9	91.6	LOC163688	NM_138705.1		calcium		
GI_20162575-S	197.3	247.4	217.1	IMAGE:4907	NM_138706.1	B3Gn-T6	galactosylt	membran	protein
GI_20270187-S	172.4	232.1	197.3	ETV3	NM_005240.1	PE1;METS;PE-1;bA110J1.4	DNA	nucleus	regulation
GI_20270211-S	915	1130.3	954.1	TNKS1BP1	NM_033396.1	TAB182;KIAA1741	enzyme	chromoso	telomeras
GI_20270264-A	103	95.5	100.2	SPAP1	NM_138739.1	FCRH2;IFGP4;IRTA4;SPAP1A;SPAP1B;SPA			
GI_20270264-I	125.8	135.2	103.6	SPAP1	NM_138739.1	FCRH2;IFGP4;IRTA4;SPAP1A;SPAP1B;SPA			
GI_20270302-S	5785.7	6154.9	5675.4	ARHT2	NM_138769.1	MIRO-2;C16orf39			
GI_20270304-S	161.5	191.3	163.4	SYTL5	NM_138780.1	slp5	electron		electron
GI_20270306-S	125.8	148.1	157.9	LOC90557	NM_138770.1				
GI_20270310-S	1048.7	1159.7	1289.5	LOC91137	NM_138773.1		binding	mitochond	transport
GI_20270314-S	112.2	113	98.9	LOC91801	NM_138775.1		structural	ribosome	protein
GI_20270320-S	682.4	571.6	471.4	LOC113386	NM_138781.1				
GI_20270322-S	512.1	571.8	549.3	LOC115950	NM_138783.1		DNA	nucleus	regulation
GI_20270324-S	114.8	121.2	107	LOC116123	NM_138784.1		monooxyg		electron
GI_20270326-S	187.8	212.3	192.9	LOC116441	NM_138786.1			integral to	
GI_20270334-S	140.9	169	140.9	LOC122618	NM_138790.1		catalytic		metabolis
GI_20270340-S	2107.1	1787.1	1480.4	LYPLAL1	NM_138794.1	Q96AV0	catalytic		
GI_20270346-S	360.3	445.3	530.1	LOC129138	NM_138797.1				
GI_20270348-S	655.2	551.6	513.2	LOC129531	NM_138798.1				
GI_20270352-S	129.4	156.8	126.9	TRIM43	NM_138800.1		zinc ion	intracellula	
GI_20270354-S	120.8	133	123.7	GALM	NM_138801.1				
GI_20270356-S	430.5	382.9	423.7	LOC130617	NM_138802.1		molecular		
GI_20270368-S	249.6	297.9	260	LOC132200	NM_138808.1				
GI_20270376-S	85.1	80.8	80	LOC143241	NM_138812.1				
GI_20270382-S	130.9	156.1	145.9	SLC7A13	NM_138817.1	AGT1;XAT2;AGT-1	amino	membran	amino
GI_20270386-S	101	116.3	109.3	LOC159091	NM_138819.1				
GI_20270388-S	1516.6	1536.5	1626.4	MGC2198	NM_138820.1				
GI_20302037-S	970	1103.3	991.5	C6orf72	NM_138785.1	dJ12G14.2			
GI_20302039-S	153.2	163	140.2	LOC122945	NM_138791.1		pyrroline-5		proline
GI_20302136-S	86.2	112.8	93.6	KIAA0125	NM_014792.2				
GI_20302137-S	148.3	184.3	176.5	CST6	NM_001323.2		cysteine		embryoge
GI_20302138-S	419.9	553.3	269	CST7	NM_003650.2	CMAP	cysteine		immune
GI_20302146-A	192.3	242.1	204.9	KLK15	NM_138564.1	ACO;HSRNASPH	serine-	extracellul	proteolysis
GI_20302148-S	693.9	914.4	781	LYPLA1	NM_006330.2	LPL1;APT-1;LYSOPLA	lysophosp	membran	
GI_20302149-S	1368.1	1525.7	1809.3	LYPLA2	NM_007260.2	APT-2;DJ886K2.4	catalytic		
GI_20302150-S	529.4	559.6	646	LYPLA3	NM_012320.2	ACS;LLPL;DKFZp564A0122	lysophosp		fatty acid
GI_20302151-S	112.1	116.4	110.2	HABP2	NM_004132.2	FSAP;HABP;PHBP;HGFAL	glycosami	extracellul	cell
GI_20302152-I	153.7	178.5	182.8	HAS3	NM_005329.2			integral to	carbohydr
GI_20302154-A	103.2	93.4	86.6	HAS3	NM_138612.1			integral to	carbohydr
GI_20302154-I	150.1	161.2	152.3	HAS3	NM_138612.1			integral to	carbohydr
GI_20302156-I	103.2	112.9	90.8	MSMB	NM_002443.2	MSP;PSP;IGBF;MSPB;PN44;PRPS;PSP57;P	molecular	extracellul	biological_
GI_20302157-A	99.8	122.9	111.2	MSMB	NM_138634.1	MSP;PSP;IGBF;MSPB;PN44;PRPS;PSP57;P	molecular	extracellul	biological_
GI_20302159-S	731.6	888.6	814.2	TSNAX	NM_005999.2	TRAX	protein	nucleus	
GI_20302160-S	90.3	102.8	96.3	TSN	NM_004622.2	TRSLN;BCLF-1;REHF-1	DNA	nucleus	DNA

GI_20302161-S	118.5	120.1	111.1	GCG	NM_002054.2	GLP1;GLP2;GRPP	receptor	soluble	G-protein
GI_20302162-S	297	424	323.9	PIP5K2A	NM_005028.3	PIPK;PIP5KII-alpha	1-		glyceroph
GI_20302163-S	94.2	91	81.8	LGALS13	NM_013268.2	PP13;PLAC8	lysophosp		phospholi
GI_20302164-S	142.3	173.8	137.8	TLR7	NM_016562.2		transmem	integral to	immune
GI_20302165-I	97.2	108.8	98.1	TLR8	NM_016610.2		transmem	integral to	NIK-I-
GI_20302167-A	202.3	223.6	207.8	TLR8	NM_138636.1		transmem	integral to	NIK-I-
GI_20302169-I	180.7	204.9	200.7	TLR9	NM_017442.2		antibacteri	extracellul	response
GI_20302170-A	113.7	110.6	122.6	TLR9	NM_138688.1		antibacteri	extracellul	response
GI_20304090-S	145	139.3	133.8	ZNF2	NM_021088.1	A1-5			
GI_20304092-S	159.2	196.4	187.1	TMC2	NM_080751.1	C20orf145;dJ686C3.3	DNA	integral to	regulation
GI_20304126-S	177.9	185.5	188.5	LOC150379	NM_138814.1	dJ388M5.4	catalytic		
GI_20336185-A	243.8	161.5	139.7	PACE4	NM_138322.1	SPC4;PCSK6	subtilase		proteolysis
GI_20336185-I	120.2	127.8	114.6	PACE4	NM_138322.1	SPC4;PCSK6	subtilase		proteolysis
GI_20336193-S	633.5	895.7	752.2	FURIN	NM_002569.2	FUR;PACE;SPC1;PCSK3	furin	Golgi	proteolysis
GI_20336194-I	105.5	109.7	84	AKAP7	NM_016377.2	AKAP18	protein	plasma	ion
GI_20336195-I	132.3	143.7	135.1	AKAP7	NM_138633.1	AKAP18	protein	plasma	ion
GI_20336197-A	512.3	390.2	310.9	AKAP7	NM_004842.2	AKAP18	protein	plasma	ion
GI_20336200-A	117.7	123.2	119.4	ATM	NM_138293.1	AT1;ATA;ATC;ATD;ATE;ATDC	protein	nucleus	DNA
GI_20336200-I	102.6	110.4	103.9	ATM	NM_138293.1	AT1;ATA;ATC;ATD;ATE;ATDC	protein	nucleus	DNA
GI_20336202-I	154.7	178.4	157.3	ATM	NM_000051.2	AT1;ATA;ATC;ATD;ATE;ATDC	protein	nucleus	DNA
GI_20336204-A	822.6	849.5	801.9	ATRX	NM_138270.1	SHS;XH2;XNP;ATR2;MRXS3;RAD54;RAD54	helicase	nuclear	DNA
GI_20336206-I	90.2	91.4	83.6	ATRX	NM_138271.1	SHS;XH2;XNP;ATR2;MRXS3;RAD54;RAD54	helicase	nuclear	DNA
GI_20336210-I	906.1	1324.1	1135.5	GAMT	NM_000156.4	PIG2;TP53I2	methyltran		creatine
GI_20336211-A	326.1	452.4	408.2	GAMT	NM_138924.1	PIG2;TP53I2	methyltran		creatine
GI_20336211-I	114.3	129.2	117.9	GAMT	NM_138924.1	PIG2;TP53I2	methyltran		creatine
GI_20336213-I	79.7	80.8	77.8	GLS2	NM_013267.2	GA;GLS;LGA;hLGA	glutamina	mitochond	amino
GI_20336215-A	212.9	246.9	215.4	GLS2	NM_138566.1	GA;GLS;LGA;hLGA	glutamina	mitochond	amino
GI_20336218-A	132.2	135.6	137.3	RHCE	NM_138616.1	RHC;RHE;Rh4;RHPI;RhVI;RH30A;RHIXB;Rh	blood	integral to	transport
GI_20336224-I	101.8	127.3	98.1	RHD	NM_016124.2	RH;Rh4;RH30;RhII;RhPI;DIIIc;RHCED;RHPII	blood	integral to	transport
GI_20336226-A	123	128.8	120	RHD	NM_016225.2	RH;Rh4;RH30;RhII;RhPI;DIIIc;RHCED;RHPII	blood	integral to	transport
GI_20336228-I	89	97.5	90	PPARG	NM_015869.2	NR1C3;PPARG1;PPARG2;HUMPPARG	ligand-	nucleus	response
GI_20336230-A	146.1	344.2	153.8	PPARG	NM_005037.3	NR1C3;PPARG1;PPARG2;HUMPPARG	ligand-	nucleus	response
GI_20336236-I	289.3	351.7	341.5	PPP1R8	NM_002713.2	ARD1;NIPP1;NIPP-1;PRO2047	ribonuclea	nucleus	RNA
GI_20336237-A	181.4	180.3	160.8	PPP1R8	NM_014110.3	ARD1;NIPP1;NIPP-1;PRO2047	ribonuclea	nucleus	RNA
GI_20336240-S	242.8	296.3	267	PCSK1N	NM_013271.2	SAAS;PROSAAS	endopepti	soluble	
GI_20336241-S	130.5	182.3	152.7	PCSK1	NM_000439.3	PC1;PC3;NEC1;SPC3	subtilase		proteolysis
GI_20336243-S	85.2	89.7	80.7	PCSK2	NM_002594.2	PC2;NEC2;SPC2	subtilase	Golgi	proteolysis
GI_20336245-S	425.7	215	359.3	PCSK5	NM_006200.2	PC5;PC6;PC6A;SPC6	serine-	extracellul	proteolysis
GI_20336247-S	360.6	475.9	420.3	PCSK7	NM_004716.2	LPC;PC7;PC8;SPC7	subtilase	integral to	proteolysis
GI_20336250-A	176.5	177.1	277.6	PPT2	NM_138717.1	G14;DKFZp564P1516	palmitoyl-	lysosome	protein
GI_20336250-I	141.5	165.4	155.2	PPT2	NM_138717.1	G14;DKFZp564P1516	palmitoyl-	lysosome	protein
GI_20336252-I	164.6	158.1	141.8	PPT2	NM_138934.1	G14;DKFZp564P1516	palmitoyl-	lysosome	protein
GI_20336255-A	264.9	270.6	356.6	PIP5K2B	NM_138687.1	Pip4k2B;PIP5KIIB	1-	cytoplasm	cell
GI_20336255-I	2960.3	3495.4	3123.2	PIP5K2B	NM_138687.1	Pip4k2B;PIP5KIIB	1-	cytoplasm	cell

GI_20336257-I	144.7	163.1	138.2	PRDM2	NM_012231.2	RIZ;RIZ1;RIZ2;MTB-ZF;HUMHOXY1	zinc ion	nucleus	regulation
GI_20336259-A	93.6	104.1	91.8	PRDM2	NM_015866.2	RIZ;RIZ1;RIZ2;MTB-ZF;HUMHOXY1	zinc ion	nucleus	regulation
GI_20336259-I	321.9	375.6	381.2	PRDM2	NM_015866.2	RIZ;RIZ1;RIZ2;MTB-ZF;HUMHOXY1	zinc ion	nucleus	regulation
GI_20336261-S	604.2	834.2	748.6	GGA1	NM_013365.2		protein	kinesin	intra-Golgi
GI_20336262-I	336.7	435.1	376.6	GGA2	NM_015044.2	VEAR;FLJ20966;KIAA1080	protein	Golgi	intra-Golgi
GI_20336263-A	474.2	575.3	587.5	GGA2	NM_138640.1	VEAR;FLJ20966;KIAA1080	protein	Golgi	intra-Golgi
GI_20336263-I	147.8	157.4	150.2	GGA2	NM_138640.1	VEAR;FLJ20966;KIAA1080	protein	Golgi	intra-Golgi
GI_20336265-A	348.9	390.5	374.5	GGA3	NM_014001.2	KIAA0154	protein	Golgi	intra-Golgi
GI_20336266-I	108.2	101.9	99.2	GGA3	NM_138619.1	KIAA0154	protein	Golgi	intra-Golgi
GI_20336268-A	519.5	518.8	530.3	GNB5	NM_006578.2	GB5;DKFZP586O1922			
GI_20336268-I	383.8	477.2	435.6	GNB5	NM_006578.2	GB5;DKFZP586O1922			
GI_20336269-I	194.3	203.3	193.5	GNB5	NM_016194.2	GB5;DKFZP586O1922			
GI_20336271-I	123.1	122.4	110.4	SLC26A1	NM_022042.2	EDM4;SAT1;SAT-1			
GI_20336273-A	173.1	195.9	164.9	SLC26A1	NM_134425.1	EDM4;SAT1;SAT-1			
GI_20336273-I	132.4	105	120	SLC26A1	NM_134425.1	EDM4;SAT1;SAT-1			
GI_20336278-A	269.8	401.9	421.9	SLC26A6	NM_134426.1	DKFZp586E1422			
GI_20336280-I	97.2	103.7	87.2	SLC26A7	NM_052832.2	SUT2	sulfate	membran	sulfate
GI_20336281-A	89.6	106.6	99.7	SLC26A7	NM_134266.1	SUT2	sulfate	membran	sulfate
GI_20336281-I	140.6	170.6	159.4	SLC26A7	NM_134266.1	SUT2	sulfate	membran	sulfate
GI_20336283-I	115	113	92.9	SLC26A8	NM_052961.2	TAT1	sulfate	membran	sulfate
GI_20336284-A	232.2	304.2	263.6	SLC26A8	NM_138718.1	TAT1	sulfate	membran	sulfate
GI_20336284-I	111.7	106.4	97.4	SLC26A8	NM_138718.1	TAT1	sulfate	membran	sulfate
GI_20336286-I	105.1	114.1	116.4	SLC26A9	NM_052934.2		sulfate	membran	sulfate
GI_20336287-A	101.2	113.6	114.3	SLC26A9	NM_134325.1		sulfate	membran	sulfate
GI_20336291-A	699.8	931.2	918.1	DHX30	NM_138614.1	DDX30;FLJ11214;KIAA0890			
GI_20336291-I	153.2	165.7	159	DHX30	NM_138614.1	DDX30;FLJ11214;KIAA0890			
GI_20336295-S	341.4	319.2	346.8	DDX28	NM_018380.2	MDDX28;FLJ11282	nucleic		
GI_20336296-I	269.2	271.8	244.2	DDX31	NM_022779.7	FLJ13633;FLJ14578;FLJ23349	nucleic		
GI_20336297-A	186.6	194	175.5	DDX31	NM_138620.1	FLJ13633;FLJ14578;FLJ23349	nucleic		
GI_20336297-I	89.1	85.1	89.8	DDX31	NM_138620.1	FLJ13633;FLJ14578;FLJ23349	nucleic		
GI_20336299-S	1332	1520	1449.2	DHX32	NM_018180.2	DDX32;DHLP1;FLJ10694;FLJ10889			
GI_20336301-S	749.5	838	667.3	DHX33	NM_020162.2	DDX33;FLJ21972;DKFZp762F2011	nucleic		
GI_20336304-I	422.2	624.1	399.7	BCL11A	NM_022893.2	EVI9;CTIP1;BCL11A-L;BCL11A-			
GI_20336312-A	107.4	118.2	103.9	BCL11A	NM_138559.1	EVI9;CTIP1;BCL11A-L;BCL11A-			
GI_20336322-I	117.1	142.6	139.5	BCL2L11	NM_138625.1	BAM;BIM;BOD;BimL;BimEL		membran	induction
GI_20336326-A	127	115.2	123.9	BCL2L11	NM_138627.1	BAM;BIM;BOD;BimL;BimEL		membran	induction
GI_20336328-S	161.7	200.5	179.7	BCL2L10	NM_020396.2	Boo;Diva;BCL-B	apoptosis	mitochond	caspase
GI_20336329-I	726.1	893	808.8	BCL2L12	NM_138639.1				apoptosis
GI_20336331-A	835.9	748	830.3	BCL2L12	NM_052842.2				apoptosis
GI_20336333-A	2689.4	2078.1	3184.5	BCL2L1	NM_001191.2	BCLX;BCL2L;Bcl-X;bcl-xL;bcl-xS;BCL-XL/S	apoptosis	integral to	apoptotic
GI_20336334-I	270.7	252	365.8	BCL2L1	NM_138578.1	BCLX;BCL2L;Bcl-X;bcl-xL;bcl-xS;BCL-XL/S	apoptosis	integral to	apoptotic
GI_20336470-S	238.8	281.1	265.9	BCL10	NM_003921.2	CLAP;mE10;CIPER;c-E10;CARMEN	tumor	intracellula	induction
GI_20336471-S	455.9	584.6	522.4	BCL3	NM_005178.2	BCL4	translation	nucleus	cytoplasmi
GI_20336472-I	267.7	284.1	275.3	BCL7B	NM_001707.2				

GI_20336474-A	1286	1123.7	1200.2	BCL7B	NM_138707.1				
GI_20336476-S	403	411.4	415.6	BCL7C	NM_004765.2				
GI_20336723-S	246.4	271.3	231.1	ZNF333	NM_032433.1	KIAA1806	DNA	nucleus	regulation
GI_20336744-I	100.9	90.9	88	H2AFY	NM_004893.2	H2A.y;H2A/y;H2AFJ;mH2A1;H2AF12M;MAC	DNA	chromoso	nucleoso
GI_20336745-A	5909.2	6673.7	7131.5	H2AFY	NM_138609.1	H2A.y;H2A/y;H2AFJ;mH2A1;H2AF12M;MAC	DNA	chromoso	nucleoso
GI_20336745-I	542.8	634.1	187.2	H2AFY	NM_138609.1	H2A.y;H2A/y;H2AFJ;mH2A1;H2AF12M;MAC	DNA	chromoso	nucleoso
GI_20336749-S	7269.9	8410.4	8880.2	H2AFZ	NM_002106.2	H2AZ	DNA	chromoso	nucleoso
GI_20336750-A	414.3	751.1	351.6	HIST1H2BD	NM_021063.2	H2B/b;H2BFB;H2B.1B;HIRIP2;dJ221C16.6	DNA	chromoso	nucleoso
GI_20336750-I	89.6	104.2	93.6	HIST1H2BD	NM_021063.2	H2B/b;H2BFB;H2B.1B;HIRIP2;dJ221C16.6	DNA	chromoso	nucleoso
GI_20336751-I	604.3	1199.1	411.9	HIST1H2BD	NM_138720.1	H2B/b;H2BFB;H2B.1B;HIRIP2;dJ221C16.6	DNA	chromoso	nucleoso
GI_20336753-S	122	141.5	145.3	HIST1H2BJ	NM_021058.3	H2B/r;H2BFR	DNA	chromoso	nucleoso
GI_20336758-S	3480.9	2078.3	2756.6	H1F0	NM_005318.2	H10;H1FV;MGC5241	DNA	chromoso	nucleoso
GI_20336759-S	8763	6387.8	6464.3	H1FX	NM_006026.2	H1X;MGC8350;MGC15959	DNA	chromoso	nucleoso
GI_20336760-S	1627.5	1293.7	1374.2	HEBP1	NM_015987.2	HBP;HEBP	binding		circadian
GI_20336762-A	138.3	167.8	252.2	HRIHFB2122	NM_138632.1	KIAA1662;dJ37E16.4	F-actin	kinesin	actin
GI_20336762-I	223.6	279.4	814.6	HRIHFB2122	NM_138632.1	KIAA1662;dJ37E16.4	F-actin	kinesin	actin
GI_20336764-S	121.3	135.8	113.6	ACYP2	NM_138448.2	ACYM;ACYP	acylphosp		phosphate
GI_20357503-I	104.6	105.6	89.4	BPAG1	NM_020388.2	BPA;BP240;CATX-		basement	cytoskelet
GI_20357509-A	141.2	163.9	147.8	MSR1	NM_002445.2	SR-A;phSR1;phSR2;SCARA1	scavenger	integral to	receptor
GI_20357509-I	112.2	111.3	96	MSR1	NM_002445.2	SR-A;phSR1;phSR2;SCARA1	scavenger	integral to	receptor
GI_20357511-I	80.1	93.5	83.7	MSR1	NM_138715.1	SR-A;phSR1;phSR2;SCARA1	scavenger	integral to	receptor
GI_20357519-S	833.5	1023.6	914.6	UMPK	NM_012474.3	UK;UMK;UCK2;TSA903	uridine		carbohydr
GI_20357521-S	1598.9	1918.9	1992.3	JMJD1	NM_018433.2	TSGA;KIAA0742			
GI_20357526-S	5452.1	5327.1	5477.1	GNB1	NM_002074.2		heterotrim	peripheral	acetyl
GI_20357528-S	3039.1	3083.8	3184.6	GNB2	NM_005273.2		heterotrim	peripheral	G-protein
GI_20357531-S	135.3	128.7	125.8	GNB4	NM_021629.2		signal	heterotrim	G-protein
GI_20357534-S	2931.1	2881.4	3021.6	ATP6V1G1	NM_004888.2	ATP6J;Vma10;ATP6G1;ATP6GL	hydrogen		proton
GI_20357536-I	158.3	206.5	219.1	ATP6V1G2	NM_130463.2	NG38;ATP6G;Vma10;ATP6G2	hydrogen		proton
GI_20357538-A	248.1	435.4	520.2	ATP6V1G2	NM_138282.1	NG38;ATP6G;Vma10;ATP6G2	hydrogen		proton
GI_20357541-A	120.9	134.1	113.9	ATP6V1G3	NM_133262.2	Vma10;ATP6G3	hydrogen		proton
GI_20357546-S	3238.2	3071.9	4303.3	ATP6V1F	NM_004231.2	VATF;Vma7;ATP6S14	hydrogen	coated	proton
GI_20357549-S	909	1139.9	1247.9	SMP1	NM_014313.2			integral to	
GI_20357551-I	157.4	186.9	159.3	EMS1	NM_005231.2	Cttn		soluble	
GI_20357555-A	3037.3	2833.1	3728.3	EMS1	NM_138565.1	Cttn		soluble	
GI_20357561-S	149.8	136.7	108.3	CSTA	NM_005213.2	STF1;STFA	cysteine		
GI_20357564-S	2696.8	2529.6	2388.6	CSTB	NM_000100.2	PME;CST6;STFB	endopepti	nucleus	
GI_20357567-S	570.8	578.1	670.1	AASDHPPT	NM_015423.2	LYS2;LYS5;CGI-80;AASD-			
GI_20357571-A	111.8	118	110.5	ACF	NM_014576.2	ASP;ACF64;ACF65	RNA		mRNA
GI_20357577-I	80.5	88.3	75.7	ACF	NM_138933.1	ASP;ACF64;ACF65	RNA		mRNA
GI_20357584-I	157.6	208.2	184.2	TAF1	NM_004606.2	OF;BA2R;CCG1;CCGS;P250;NSCL2;TAF2A;	general	transcripti	G1-
GI_20357587-A	162.7	169.9	162	TAF1	NM_138923.1	OF;BA2R;CCG1;CCGS;P250;NSCL2;TAF2A;	general	transcripti	G1-
GI_20357590-S	627.8	697.3	620.2	TAF2	NM_003184.2	TAF2B;CIF150;TAFII150	RNA	transcripti	transcripti
GI_20357592-S	90.2	97.7	87.3	BSND	NM_057176.2	BART			
GI_20357594-S	278.8	308.1	335.3	GLTP	NM_016433.2				lipid

GI_20357598-I	602.8	690.4	898.5	H2AV	NM_138635.1	MGC1947;MGC10170;MGC10831			
GI_20373152-S	521.2	955.3	307.1	MYO18B	NM_032608.4	BK125H2.1	ATP	myosin	
GI_20373170-S	187.9	238	224.8	VANGL1	NM_138959.1	LPP2;STB2;MGC5338		integral to	
GI_20373176-S	10344.2	8888.1	6565.8	RPS4Y2	NM_138963.1		structural	ribosome	protein
GI_20428651-S	169.2	252.9	184.1	LCK	NM_005356.2		protein-	membran	RAS
GI_20428653-S	13813.5	13745	12100	CALM2	NM_001743.3	PHKD;CAMII;PHKD2	calcium	cytoplasm	G-protein
GI_20428778-S	93.9	110.5	98.9	MYO3B	NM_138995.1		ATP	myosin	protein
GI_20452463-S	207	177.9	111.2	ESAM	NM_138961.1	W117m			
GI_20452469-A	149.9	183.9	164	NETO1	NM_138999.1	BCTL1;BTCL1			
GI_20452469-I	98.6	102.2	110.4	NETO1	NM_138999.1	BCTL1;BTCL1			
GI_20468179-S	142.6	177	156.9	LOC196752	XM_113596.1				
GI_20471320-S	167.8	201	171.2	LOC199897	XM_117152.1				
GI_20472483-S	117.6	109.1	100.3	LOC220973	XM_166707.1				
GI_20476634-S	112.7	104.8	86	DKFZp667E0	XM_117353.1				
GI_20477602-S	74.9	69.9	69.7	LOC201651	XM_114355.1				
GI_20478094-S	129.4	143.8	131.1	LOC203235	XM_117514.1				
GI_20479073-S	212.7	187.9	246.1	LOC200205	XM_114152.1				
GI_20481373-S	109.3	130.3	102.1	LOC219797	XM_166747.1				
GI_20481991-S	129.8	134.8	116	LOC219437	XM_166878.1				
GI_20481995-S	123.2	139.7	130.6	LOC219438	XM_166879.1				
GI_20482069-S	102.2	125.1	97.9	LOC219473	XM_166825.1				
GI_20482090-S	201.1	267.7	235.4	LOC219479	XM_166831.1				
GI_20482131-S	304.4	373.3	347.2	LOC219493	XM_166845.1				
GI_20482337-S	88	90.1	97.5	LOC219954	XM_166912.1				
GI_20482350-S	114.7	127.1	112.9	LOC219959	XM_166917.1				
GI_20482352-S	100.8	102.2	96.6	LOC219960	XM_166918.1				
GI_20482378-S	162.2	189	165.2	LOC219968	XM_166926.1				
GI_20482422-S	100.3	105.3	98.6	LOC219981	XM_166898.1				
GI_20485835-S	502.8	615	567.8	LOC199680	XM_117112.1				
GI_20502985-S	380	415.2	416.2	ERK8	NM_139021.1		MAP		protein
GI_20514779-A	135.3	147.5	126.9	SPPL2B	NM_020172.1	IMP4;PSL1;KIAA1532	peptidase	integral to	proteolysis
GI_20522237-S	210.2	249.4	206.3	CYP21A2	NM_000500.4	CAH1;CPS1;CA21H;CYP21;CYP21B;P450c2	steroid		
GI_20522238-S	254.5	344.7	253.9	CYP2S1	NM_030622.5		monooxyg		electron
GI_20522239-S	182.1	204.9	207.8	CYP2A6	NM_000762.4	CPA6;CYP2A;CYP2A3;P450PB;P450C2A	coumarin	microsom	electron
GI_20522261-S	146.7	158.4	129.8	CYP2B6	NM_000767.4	CPB6;IIB1;P450;CYP2B;CYPIIB6	monooxyg	membran	electron
GI_20531764-S	246.8	211	202.5	C13orf1	NM_020456.1	CLLD6			
GI_20532905-S	117.6	126.6	130.8	LOC152122	XM_098164.4				
GI_20533843-S	79.8	89.7	80.3	MYT1L	XM_039762.4				
GI_20534043-S	103.5	111.4	112.4	LOC200475	XM_117236.1				
GI_20534796-S	224.1	275.4	249.9	LOC90342	XM_031009.5				
GI_20534826-S	275.3	312.4	283.3	LOC127623	XM_060580.4				
GI_20535783-S	99.2	93	93.4	LOC200624	XM_117257.1				
GI_20537324-S	145.5	165.4	180.2	LOC200731	XM_117268.1				
GI_20537349-S	123.4	129.2	112	CIP98	XM_027012.2				

GI_20537481-S	79.8	83.5	78.4	LOC157943	XM_098847.4				
GI_20540354-S	101.4	113.7	104.7	LOC153134	XM_098317.2				
GI_20543127-S	91.7	107.9	91.4	LOC202201	XM_116384.1				
GI_20543268-S	280	354.3	317	LOC196913	XM_113776.1				
GI_20544128-S	316	260.2	412.2	DHX35	NM_021931.2	DDX35;C20orf15;FLJ22759;KAIA0875	nucleic		
GI_20544135-I	96.9	96.7	98.7	CASPR4	NM_033401.2	KIAA1763			
GI_20544136-A	103	90.5	86.7	CASPR4	NM_138994.1	KIAA1763			
GI_20544136-I	80.6	84.6	77	CASPR4	NM_138994.1	KIAA1763			
GI_20544138-I	163.9	184	154	caspr5	NM_130773.2	FLJ31966			
GI_20544140-S	377.5	366.6	492	TAF4	NM_003185.2	TAF2C;TAF4A;TAF2C1;TAFII130;TAFII135	protein	transcripti	regulation
GI_20544141-A	110.3	119.7	121.5	caspr5	NM_138996.1	FLJ31966			
GI_20544143-A	4636.9	4226.7	5542.2	CSNK1D	NM_001893.3	HCKID	casein		protein
GI_20544144-I	952.9	1112.6	1103.3	CSNK1D	NM_139062.1	HCKID	casein		protein
GI_20544150-I	991.9	1239.7	767.4	CBX3	NM_016587.2	HECH;GAMMA;HP1-GAMMA;HP1Hs-gamma	chromatin	chromatin	chromatin
GI_20544152-A	3440.2	3270.3	2410.2	CBX3	NM_007276.3	HECH;GAMMA;HP1-GAMMA;HP1Hs-gamma	chromatin	chromatin	chromatin
GI_20544152-I	484.3	608.7	522.8	CBX3	NM_007276.3	HECH;GAMMA;HP1-GAMMA;HP1Hs-gamma	chromatin	chromatin	chromatin
GI_20544161-S	97.1	107.1	95.7	HIST1H1D	NM_005320.2	H1.3;H1F3	DNA	chromoso	nucleoso
GI_20544164-S	107.3	120.1	114.5	HIST1H1E	NM_005321.2	H1.4;H1F4;dJ221C16.5	DNA	chromoso	nucleoso
GI_20544167-S	81.6	94.5	80.7	HIST1H1T	NM_005323.3	H1t;H1FT;dJ221C16.2	DNA	chromoso	spermatog
GI_20544171-S	114.4	157.3	211.1	BDKRB1	NM_000710.2	B1R;BKR1;B1BKR;BRADYB1	bradykinin	endoplas	cytosolic
GI_20544175-S	104	93.9	101.8	BHMT2	NM_017614.3	FLJ20001	homocyst		
GI_20544178-S	571.5	569.5	502.7	TBP	NM_003194.2	GTF2D;SCA17;TFIID;GTF2D1	RNA	transcripti	transcripti
GI_20544181-S	1182.8	1139.3	1260.3	WDR13	NM_017883.3	FLJ20563		nucleus	
GI_20544184-S	260.1	278.7	260.2	YAF2	NM_005748.2		transcripti	nucleus	negative
GI_20544188-I	111.4	118.9	107.8	TNXB	NM_019105.4	XB;TNX;XBS;HXBL;TENX;TNXB1;TNXB2;T			
GI_20545519-S	93.9	128.7	84.8	LOC202324	XM_117385.1				
GI_20546300-S	110.2	120.6	107.7	LOC153770	XM_087761.2				
GI_20546504-S	288.4	321.5	314.1	KIAA1957	XM_065166.2				
GI_20547346-S	132.8	146.6	132.4	LOC203413	XM_117548.1				
GI_20547782-S	118.8	122.4	99.9	LOC134701	XM_059730.2				
GI_20550092-S	261.7	324.2	343.6	LOC145788	XM_085236.4				
GI_20552934-S	117.9	108.3	109.9	LOC202546	XM_117408.1				
GI_20553753-S	199.6	177.6	183.2	KIAA1971	XM_058720.5				
GI_20554311-S	119.7	123.2	127.5	LOC158830	XM_088684.2				
GI_20554837-S	131.4	129.7	114.3	HMGCLL1	XM_166383.1				
GI_20554839-S	323.3	409	365.5	LOC221344	XM_168073.1				
GI_20555412-S	910.5	817.8	975.7	BRPF3	XM_166450.1				
GI_20555643-S	1349.6	1203.5	1009.6	KIAA1949	XM_166376.1				
GI_20557667-S	118.5	102.7	106.5	LOC201109	XM_117044.1				
GI_20558728-S	257.6	312.4	278.3	LOC219858	XM_166757.1				
GI_20558763-S	201.3	229	226.8	LOC219870	XM_166777.1				
GI_20558775-S	130.8	101.8	123.4	LOC219874	XM_166781.1				
GI_20559322-S	108.4	120.4	117.6	LOC201201	XM_117056.1				
GI_20559681-S	87.4	90.4	93.1	LOC220061	XM_169227.1				

GI_20561649-S	451.6	429.1	442.1	ZNF319	XM_168030.1				
GI_20562142-S	819.6	793.9	551.4	KIAA1977	XM_058800.3	FLJ32345;FLJ32767			
GI_20562449-S	99.1	105.6	117.5	LOC197387	XM_117030.1				
GI_20589957-S	300.8	358.4	274.6	TPCN2	NM_139075.1	TPC2	cation	integral to	cation
GI_20589960-S	670.6	476.6	351.4	FLJ13614	NM_139076.1	FLJ11520;FLJ12642			
GI_20631970-S	344.3	408.5	344.7	C2	NM_000063.3	CO2	trypsin	compleme	compleme
GI_20631976-S	692.4	876.8	1161	CREBL1	NM_004381.3	G13;CREB-RP	transcripti	endoplas	transcripti
GI_20631979-I	394.3	443.3	423.9	DOM3Z	NM_005510.2	NG6;DOM3L			
GI_20631983-S	3815.1	3214.5	2785.2	RDBP	NM_002904.4	RD;RDP;D6S45;NELF-E	RNA	nucleus	biological_
GI_20631986-S	3106.8	4062.7	3433.7	SKIV2L	NM_006929.3	HLP;SKI2;DDX13;SKI2W;SKIV2	ATP		regulation
GI_20665033-A	233.9	243.9	264.4	TNXB	NM_032470.2	XB;TNX;XBS;HXBL;TENX;TNXB1;TNXB2;T			
GI_20665033-I	128.5	141	135.5	TNXB	NM_032470.2	XB;TNX;XBS;HXBL;TENX;TNXB1;TNXB2;T			
GI_20806090-S	224.9	258.3	227.1	STAB2	NM_017564.8	FELL;FEX2;HARE;FEEL-2;FELL-2;STAB-	hyaluronic		cell
GI_20806094-S	91	97.5	90.7	ALS2CR8	NM_024744.1;	CARF;FLJ21579;NYD-SP24			
GI_20809252-A	98.2	113.9	107.5	GH1	NM_022562.2	GH;GHN;GH-N	peptide		signal
GI_20809253-A	99.1	99	87.5	GH2	NM_022556.2	GHL;GHV;GH-V	peptide		
GI_20809254-I	126.7	144.3	123.6	GH2	NM_022557.2	GHL;GHV;GH-V	peptide		
GI_20819960-I	142.7	155.6	149.1	CSH1	NM_022640.2	PL;CSA;CSMT	growth	extracellul	pregnancy
GI_20819972-A	95.8	92.3	103.1	CSH1	NM_022642.2	PL;CSA;CSMT	growth	extracellul	pregnancy
GI_20819984-I	141.9	151.6	135.4	CSH2	NM_022644.2	CSB	growth	extracellul	pregnancy
GI_20819996-A	97.2	102.2	97.6	CSH2	NM_022646.2	CSB	growth	extracellul	pregnancy
GI_20911032-S	141.8	144.9	137	LOC90346	NM_138351.2				
GI_20977540-S	186.9	190.2	179.1	ARHGAP21	NM_020824.1	ARHGAP10;KIAA1424	protein		intracellula
GI_20986484-S	1811.7	1757.2	1889	YAP1	NM_006106.2	YAP;YAP2;YAP65	protein		
GI_20986485-I	96.4	103.1	93.8	YAP	NM_018253.2	HCCA2;FLJ10875;FLJ13914			
GI_20986494-I	118.6	120.8	111	YAP	NM_139121.1	HCCA2;FLJ10875;FLJ13914			
GI_20986496-I	85.4	97.4	87.2	MAPK7	NM_002749.2	BMK1;ERK4;ERK5;PRKM7	MAP		signal
GI_20986498-A	599.9	778.5	836.6	MAPK7	NM_139032.1	BMK1;ERK4;ERK5;PRKM7	MAP		signal
GI_20986504-I	158.3	176.1	160.6	MAPK10	NM_002753.2	JNK3;JNK3A;PRKM10;p493F12;FLJ12099;p	JUN	nucleus	signal
GI_20986505-I	107	108.9	103.2	MAPK10	NM_138980.1	JNK3;JNK3A;PRKM10;p493F12;FLJ12099;p	JUN	nucleus	signal
GI_20986507-A	143.2	188.6	146.4	MAPK10	NM_138981.1	JNK3;JNK3A;PRKM10;p493F12;FLJ12099;p	JUN	nucleus	signal
GI_20986507-I	106.4	106.2	99.6	MAPK10	NM_138981.1	JNK3;JNK3A;PRKM10;p493F12;FLJ12099;p	JUN	nucleus	signal
GI_20986513-A	153.6	143.8	138.9	MAPK14	NM_139013.1	RK;p38;EXIP;Mxi2;CSBP1;CSBP2;CSPB1;P	MAP	cytoplasm	chemotaxi
GI_20986513-I	98.4	111.4	104.4	MAPK14	NM_139013.1	RK;p38;EXIP;Mxi2;CSBP1;CSBP2;CSPB1;P	MAP	cytoplasm	chemotaxi
GI_20986517-S	266.6	276.1	329.2	MAPK8IP1	NM_005456.2	IB1;JIP-1;PRKM8IP	protein	cytoplasm	vesicle-
GI_20986522-A	121	127.8	112.4	MAPK8	NM_139049.1	JNK;JNK1;PRKM8;SAPK1;JNK1A2;JNK21B1	JUN	nucleus	response
GI_20986524-I	458	537.8	468.1	MAPK11	NM_002751.4	P38B;SAPK2;p38-	MAP	cellular_co	response
GI_20986525-A	197.9	176.3	166.1	MAPK11	NM_138993.1	P38B;SAPK2;p38-	MAP	cellular_co	response
GI_20986527-S	136.3	305.9	385.1	MAPK13	NM_002754.3	SAPK4;PRKM13;p38delta	MAP		response
GI_20986528-I	1601.4	2035.1	1666.6	MAPK1	NM_002745.2	ERK;p38;p40;p41;ERK2;ERT1;MAPK2;PRK	protein		induction
GI_20986530-A	318.1	347.7	326	MAPK1	NM_138957.1	ERK;p38;p40;p41;ERK2;ERT1;MAPK2;PRK	protein		induction
GI_20986530-I	321.2	295.3	292.8	MAPK1	NM_138957.1	ERK;p38;p40;p41;ERK2;ERT1;MAPK2;PRK	protein		induction
GI_21040234-S	110.1	124.2	113.6	ALS2CR7	NM_139158.1		ATP		protein
GI_21040238-S	94.3	102.1	100.1	LOC91614	NM_139160.1	dJ85M6.4			intracellula

GI_21040244-S	103	105.7	114.7	ALS2CR12	NM_139163.1			kinesin	
GI_21040246-S	93.5	108.4	98.7	STARD4	NM_139164.1		cholestero		lipid
GI_21040248-S	133.5	162.4	139.4	RAET1E	NM_139165.1	LETAL;ULBP4;bA350J20.7			
GI_21040252-S	115.2	104.3	101.3	SGCZ	NM_139167.1	ZSG1			
GI_21040254-S	184.4	197.9	204.4	SFRS12	NM_139168.1	SRrp86;SRrp508;DKFZp564B176	nucleic	spliceoso	nuclear
GI_21040258-S	95.6	97.4	90.5	LOC146562	NM_139170.1				
GI_21040260-S	120.5	136.2	130.9	STARD6	NM_139171.1		lipid		lipid
GI_21040262-S	136.4	147.6	130.4	MDAC1	NM_139172.1				
GI_21040264-S	147.3	148.4	132.9	LOC150159	NM_139173.1				
GI_21040268-S	120.1	142.1	125	RNF133	NM_139175.1	MGC27072	peptidase		proteolysis
GI_21040270-S	102	101.7	98.9	NALP7	NM_139176.1	NOD12;PYPAF3	ATP		
GI_21040274-S	1891	1411.9	1473.5	DEPC-1	NM_139178.1				
GI_21040276-S	529	545.3	510.5	LOC221955	NM_139179.1		triacylglyc		lipid
GI_21040313-I	181.5	201	198.9	SON	NM_032195.1	SON3;BASS1;DBP-	DNA	nucleus	anti-
GI_21040317-I	233.2	220.1	226	SON	NM_058183.2	SON3;BASS1;DBP-	DNA	nucleus	anti-
GI_21040319-A	244.5	313.3	279.8	SON	NM_138925.1	SON3;BASS1;DBP-	DNA	nucleus	anti-
GI_21040321-I	220.7	282.9	221.9	SON	NM_138926.1	SON3;BASS1;DBP-	DNA	nucleus	anti-
GI_21040323-A	1822.4	1479.6	1284.8	BCL6	NM_001706.2	BCL5;LAZ3;ZNF51	transcripti	nucleus	positive
GI_21040323-I	163.3	196.8	174.1	BCL6	NM_001706.2	BCL5;LAZ3;ZNF51	transcripti	nucleus	positive
GI_21040329-I	116.2	119.7	124.8	BCL2L14	NM_138723.1	BCLG			
GI_21040331-A	108.3	108.2	89.3	BCL2L14	NM_138724.1	BCLG			
GI_21040331-I	136	159.3	147.9	BCL2L14	NM_138724.1	BCLG			
GI_21040333-A	142.2	158.9	145.4	BCL11B	NM_138576.1	RIT1;CTIP2;CTIP-2			
GI_21040333-I	144.1	145.3	140.3	BCL11B	NM_138576.1	RIT1;CTIP2;CTIP-2			
GI_21040335-I	92.6	88.1	102.2	BCL6	NM_138931.1	BCL5;LAZ3;ZNF51	transcripti	nucleus	positive
GI_21040337-I	110.7	119.9	123.7	HFE	NM_000410.2	HH;HFE1;HLA-H		cytoplasm	iron ion
GI_21040356-A	168.8	179.7	171.7	HFE	NM_139011.1	HH;HFE1;HLA-H		cytoplasm	iron ion
GI_21040361-A	2466.7	2417.6	2711.3	BACE2	NM_138992.1	ASP1;BAE2;DRAP;AEPLC;ALP56;ASP21;CD	aspartic-	membran	protein
GI_21040367-A	705.6	1109.2	489.9	BACE	NM_138973.1	ASP2;BACE1;HSPC104;KIAA1149	beta-	membran	pathogene
GI_21040370-A	3260.7	3000.9	3968	DDX39	NM_005804.2	BAT1;DDXL;MGC8417;MGC18203		nucleus	
GI_21040372-I	144.2	159.8	148.6	DDX39	NM_138998.1	BAT1;DDXL;MGC8417;MGC18203		nucleus	
GI_21070955-A	1514.8	1845.7	1504.8	COG4	NM_015386.1	COD1;DKFZp586E1519			
GI_21070965-I	105.4	111.2	100.1	NRXN1	NM_004801.2	Hs.22998;KIAA0578	receptor	integral to	axon
GI_21070966-A	98.4	98	94	NRXN1	NM_138735.1	Hs.22998;KIAA0578	receptor	integral to	axon
GI_21070966-I	117.1	133.3	115.7	NRXN1	NM_138735.1	Hs.22998;KIAA0578	receptor	integral to	axon
GI_21070970-I	175.6	203.6	178	NRXN3	NM_138970.1	KIAA0743			
GI_21070979-A	7317.6	7094.5	6660.3	PAM	NM_138821.1	PAL;PHM	peptidylgly	soluble	protein
GI_21070992-A	201.3	243.7	220.9	PAP	NM_138937.1	HIP;PAP1;INGAP;PAP-H;REG-III	lectin [goid	soluble	cell
GI_21070994-I	105.2	109.4	101	PAP	NM_138938.1	HIP;PAP1;INGAP;PAP-H;REG-III	lectin [goid	soluble	cell
GI_21070996-S	323.3	309.4	310.1	STIM1	NM_003156.2	GOK;D11S4896E	protein	kinesin	positive
GI_21070998-S	141.2	153.2	147.9	STIM2	NM_020860.1	KIAA1482	protein	kinesin	cell-cell
GI_21071000-I	228.8	251.7	256.1	AMFR	NM_001144.3	GP78;RNF45	receptor	membran	cell
GI_21071002-A	1585	1779.2	1759.3	AMFR	NM_138958.1	GP78;RNF45	receptor	membran	cell
GI_21071004-S	4624.9	3087.4	4111.4	PHLDA2	NM_003311.2	IPL;BRW1C;BWR1C;HLDA2;TSSC3	DNA	nucleus	imprinting

GI_21071005-S	1970.2	1740.4	1780.3	TSSC4	NM_005706.2		tumor		
GI_21071007-S	245	198.5	167.2	TCN1	NM_001062.2	TC1;TCI	binding		vitamin
GI_21071009-S	361.8	537	546.8	TCN2	NM_000355.2	TC2;D22S676;D22S750	vitamin	extracellul	vitamin
GI_21071011-S	101.4	127.2	101.8	PRSS1	NM_002769.2	TRP1;TRY1;TRY4;TRYP1	trypsin	extracellul	proteolysis
GI_21071012-S	168.9	630.1	161.7	PRSS2	NM_002770.2	TRY2;TRY8;TRYP2	trypsin		proteolysis
GI_21071013-A	136.2	133.9	123.7	EPS8L3	NM_024526.2	EPS8R3;FLJ21522;MGC16817			
GI_21071019-A	534.3	638.2	665.3	ADCY6	NM_020983.2	KIAA0422	calcium/ca	integral to	cAMP
GI_21071022-S	113.7	126	123.5	HIST1H3C	NM_003531.2	H3.1;H3/c;H3FC			
GI_21071023-S	150	141.2	127.8	HIST1H4D	NM_003539.3	H4/b;H4FB;dJ221C16.9			
GI_21071024-S	16329	13285	11326	HIST1H4C	NM_003542.3	H4/g;H4FG;dJ221C16.1			
GI_21071025-S	888.8	2253.3	1492.2	HIST1H1C	NM_005319.3	H1.2;H1F2;MGC:3992	DNA	chromoso	nucleoso
GI_21071027-S	96.3	84.3	83.2	ANP32D	NM_012404.2	PP32R2			oncogene
GI_21071029-S	160.8	197.9	179	A1BG	NM_130786.2	A1B;ABG;GAB	molecular	extracellul	biological_
GI_21071031-S	870.4	928.3	819.6	DDX41	NM_016222.2	ABS;MGC8828	ATP	nucleus	regulation
GI_21071033-S	108.3	129.9	107.9	AHRR	NM_020731.2	AHH;AHHR;KIAA1234	signal		signal
GI_21071035-A	95.8	91.2	95.9	BCOR	NM_020926.2	FLJ20285;KIAA1575			
GI_21071035-I	95.9	96.7	102	BCOR	NM_020926.2	FLJ20285;KIAA1575			
GI_21071036-I	516	500.3	616.5	BCOR	NM_017745.4	FLJ20285;KIAA1575			
GI_21071038-S	160.9	192.3	161.1	CN1	NM_032649.4	CPGL2;MGC10825	carboxype		proteolysis
GI_21071040-S	83.6	87.8	87.6	CNTNAP2	NM_014141.3	NRXN4;CASPR2;KIAA0868	cell	integral to	neuronal
GI_21071041-S	683.4	992.2	715.1	YES1	NM_005433.2	Yes;C-YES;HsT441;P61-YES	protein-		protein
GI_21071042-S	123.2	128.5	123.7	SHH	NM_000193.2	HHG1;HLP3;HPE3;SMMCI	peptidase		ventral
GI_21071045-A	2340.6	2583.8	693.3	SMARCA1	NM_139035.1	SWI2;SNF2L;SNF2L1;SNF2LB	helicase	nucleus	chromatin
GI_21071047-I	94.2	112.8	107.1	SMARCA2	NM_003070.2	hBRM;Sth1p;BAF190;SNF2L2;SNF2LA;hSNF	helicase	nucleoplas	regulation
GI_21071049-A	1004.6	981.5	1155.9	SMARCA2	NM_139045.1	hBRM;Sth1p;BAF190;SNF2L2;SNF2LA;hSNF	helicase	nucleoplas	regulation
GI_21071051-I	657.4	551.6	599.8	SMARCA3	NM_003071.2	HLTF;ZBU1;HLTF1;RNF80;HIP116;SNF2L3;	adenosine	nucleus	regulation
GI_21071053-A	2423.1	1843.7	1914.4	SMARCA3	NM_139048.1	HLTF;ZBU1;HLTF1;RNF80;HIP116;SNF2L3;	adenosine	nucleus	regulation
GI_21071055-S	1454	1675.5	1611.8	SMARCA4	NM_003072.2	BRG1;BAF190;SNF2L4;SNF2LB;hSNF2B;SN	helicase	nucleoplas	regulation
GI_21071057-S	597.8	613.2	577.1	SMARCA5	NM_003601.2	SNF2H;hSNF2H;WCRF135	helicase	nucleoplas	chromatin
GI_21071059-S	759.4	652.5	642.3	SMARCAL1	NM_014140.2	HARP;HHARP	DNA	nucleus	DNA
GI_21071064-A	343.7	315.9	352.5	TAF5	NM_139052.1	TAF2D;TAFII100	transcripti	transcripti	regulation
GI_21071066-I	175.9	185.9	183.2	TAF5	NM_006951.2	TAF2D;TAFII100	transcripti	transcripti	regulation
GI_21071068-S	1653.1	1865.2	1569	TBPL1	NM_004865.2	TLF;TLP;STUD;TRF2;MGC:8389;MGC:9620	molecular	transcripti	transcripti
GI_21071069-S	101.8	90.4	95.7	TMC1	NM_138691.2	DFNB7;DFNA36;DFNB11		integral to	hearing
GI_21071072-A	152.8	178.2	155.1	KLF12	NM_016285.2	AP2REP;AP-2rep;HSPC122	transcripti	nucleus	regulation
GI_21071072-I	255.7	315.7	283	KLF12	NM_016285.2	AP2REP;AP-2rep;HSPC122	transcripti	nucleus	regulation
GI_21071073-I	303.2	336.2	329.2	KLF12	NM_007249.3	AP2REP;AP-2rep;HSPC122	transcripti	nucleus	regulation
GI_21071075-S	104.1	105.4	110.5	BMF	NM_033503.2				
GI_21071076-S	598.1	766.2	682.6	DAAM1	NM_014992.1	KIAA0666	actin	kinesin	cytokinesi
GI_21071078-S	161.8	199.1	201.9	EKI1	NM_018638.3	EKI	ethanolam	cytoplasm	phosphati
GI_21071079-S	375.5	426.2	403.1	FBXL7	NM_012304.3	FBL6;FBL7;FLJ11609;KIAA0840			
GI_21071080-S	350.2	430.7	379.2	GNB3	NM_002075.2		heterotrim	peripheral	regulation
GI_21071083-S	2614.7	2046.8	2225.3	RRM1	NM_001033.2	R1;RR1;RIR1	ribonucleo	ribonucleo	DNA
GI_21166354-S	2741.6	2159.5	1741	YT521	NM_133370.1	KIAA1966	DNA	nucleus	mRNA

GI_21166356-S	2658.4	1900.7	1424	HCCR1	NM_015416.2	HCCR-2;DKFZp586A011			
GI_21166358-S	105.4	100.2	104.3	GRK7	NM_139209.1	GPRK7	ATP		vision
GI_21166360-S	364.6	396.1	369	COG8	NM_032382.2	DOR1;FLJ22315	protein	membran	intracellula
GI_21166374-S	2266	2608.6	2589.9	TAF10	NM_006284.2	TAF2A;TAF2H;TAFII30	RNA	transcripti	transcripti
GI_21166377-S	485.5	613.1	715	TAF9L	NM_015975.3	DN7;DN-7;TAFII31L;TFIID-31	DNA	transcripti	transcripti
GI_21166381-I	268.2	330.1	304	NRXN2	NM_138734.1	KIAA0921	cell	integral to	cell
GI_21166383-A	152.6	102	84.4	HEPH	NM_014799.2	KIAA0698	copper ion		
GI_21166383-I	96.6	92.6	90.4	HEPH	NM_014799.2	KIAA0698	copper ion		
GI_21166384-I	192.4	231.1	194.8	HEPH	NM_138737.1	KIAA0698	copper ion		
GI_21166386-S	950.8	1526.6	1410	HIST1H2BH	NM_003524.2	H2B/j;H2BFJ	DNA	chromoso	nucleoso
GI_21166387-S	89.7	101.4	100	HIST1H2BI	NM_003525.2	H2B/k;H2BFK			
GI_21166388-S	124	148.5	130.9	HIST1H2BC	NM_003526.2	H2B.1;H2B/l;H2BFL;dJ221C16.3	DNA	chromoso	nucleoso
GI_21166390-S	92.8	97.4	96.9	HIST1H4A	NM_003538.3	H4/a;H4FA	DNA	chromoso	nucleoso
GI_21166391-S	102.7	116.4	104.2	HIST1H4F	NM_003540.3	H4;H4/c;H4FC			
GI_21166392-S	109	109.4	111.9	HIST1H4B	NM_003544.2	H4/I;H4FI			
GI_21166393-S	93.3	123.3	106.6	HIST1H4G	NM_003547.2	H4/l;H4FL	DNA	nucleus	nucleoso
GI_21218437-S	228.7	281.7	305.5	P66beta	NM_020699.1	KIAA1150	transcripti	nucleus	regulation
GI_21237722-S	936.1	1028.7	798.7	ST13	NM_003932.3	HIP;HOP;P48;SNC6;HSPABP;FAM10A1;HS	Hsp70/Hs	cytoplasm	protein
GI_21237724-S	126.2	123.4	114.7	PIK3CG	NM_002649.2	PI3K;PIK3;PI3CG;PI3Kgamma	1-	phosphoin	G-protein
GI_21237727-S	1166.8	1284.1	1232.2	DHX16	NM_003587.3	DBP2;PRP8;DDX16	RNA	nucleus	RNA
GI_21237729-A	90.9	95.1	100.6	MLC1	NM_015166.2	VL;LVM;MLC;KIAA0027	ion	integral to	transport
GI_21237729-I	125	139.9	127.7	MLC1	NM_015166.2	VL;LVM;MLC;KIAA0027	ion	integral to	transport
GI_21237731-I	144.2	152.2	137	MLC1	NM_139202.1	VL;LVM;MLC;KIAA0027	ion	integral to	transport
GI_21237744-A	628.6	546.4	599.9	MAPK9	NM_139070.1	JNK2;JNK2A;JNK2B;PRKM9;JNK-	JUN		response
GI_21237756-S	110.3	124.9	106.9	CD53	NM_000560.2	MOX44		integral to	signal
GI_21237760-S	15315.6	17028	15643	CD81	NM_004356.2	S5.7;TAPA1		integral to	defense
GI_21237762-S	190.5	253.1	111.6	CD9	NM_001769.2	BA2;P24;MIC3;MRP-1;DRAP-27		integral to	
GI_21237764-A	610.7	494.5	522.8	MAPKAPK5	NM_003668.2	PRAK	MAP		response
GI_21237772-I	286	332.6	297.6	MAPK8IP2	NM_016431.2	IB2;JIP2;PRKM8IPL	structural	cytoplasm	JNK
GI_21237774-A	97.8	103.7	99.2	MAPK8IP2	NM_139124.1	IB2;JIP2;PRKM8IPL	structural	cytoplasm	JNK
GI_21237780-S	1241.2	1346.4	1366.9	WASF3	NM_006646.3	SCAR3;WAVE3;KIAA0900	actin	kinesin	protein
GI_21237782-S	748.4	867.9	765.5	COG1	NM_018714.1	LDLB;KIAA1381;DKFZP762L1710	protein	membran	Golgi
GI_21237793-A	120.1	161.3	161.1	GIT2	NM_139201.1	CAT-2;KIAA0148	ARF	nucleus	regulation
GI_21237793-I	248.7	299	330.4	GIT2	NM_139201.1	CAT-2;KIAA0148	ARF	nucleus	regulation
GI_21237796-A	615.6	582.3	581	HDAC5	NM_005474.3	HD5;NY-CO-9;KIAA0600	histone	cytoplasm	chromatin
GI_21237796-I	136.6	138.3	143.9	HDAC5	NM_005474.3	HD5;NY-CO-9;KIAA0600	histone	cytoplasm	chromatin
GI_21237798-I	123.1	125.9	109.2	HDAC5	NM_139205.1	HD5;NY-CO-9;KIAA0600	histone	cytoplasm	chromatin
GI_21237801-S	2037.6	2083	2255.8	SMARCC1	NM_003074.2	Rsc8;SRG3;SWI3;BAF155;CRACC1	transcripti	nucleoplas	chromatin
GI_21237804-I	156.8	156.1	201.6	SMARCC2	NM_003075.2	Rsc8;BAF170;CRACC2	transcripti	nucleoplas	chromatin
GI_21237807-A	877.5	1029.7	943.6	SMARCC2	NM_139067.1	Rsc8;BAF170;CRACC2	transcripti	nucleoplas	chromatin
GI_21237807-I	93.6	104	109.2	SMARCC2	NM_139067.1	Rsc8;BAF170;CRACC2	transcripti	nucleoplas	chromatin
GI_21245099-A	199.3	255.5	229.2	TA-NFKBH	NM_032721.2	MGC11314			
GI_21245105-S	116	116.6	117.8	LIPH	NM_139248.1	PLA1B;mPA-PLA1	catalytic		lipid
GI_21245119-S	162.6	209.2	181.9	PPM1L	NM_139245.1	PP2CE;PP2C-epsilon	catalytic		

GI_21245123-S	96.5	100.1	104.3	Tenr	NM_139243.1	FLJ32741	adenosine	intracellula	RNA
GI_21245127-S	90.9	92.4	92.8	FGD4	NM_139241.1	FRABP;FRABIN;ZFYVE6	zinc ion		
GI_21245131-S	123.7	131.3	126.9	TA-KRP	NM_032505.1	KIAA1842	protein		
GI_21245133-S	83.2	92.7	89.1	TA-LRRP	NM_015350.1	KIAA0231			
GI_21264319-S	115.3	105.1	111.2	NALP6	NM_138329.1	PYPAF5	defense/i		defense
GI_21264321-S	100.6	107.6	99.4	TIZ	NM_138330.1	TBZF	nucleic	intracellula	regulation
GI_21264323-S	91.4	105	97.8	TAR1	NM_138327.1	TA1	receptor	integral to	G-protein
GI_21264325-S	112.6	121.8	113.4	RHBDL4	NM_138328.1	VRHO	serine-	integral to	
GI_21264327-S	116.9	136.7	127.5	ACMSD	NM_138326.1		lyase		
GI_21264329-S	458.5	458.6	426.5	LOC142678	NM_080875.1				
GI_21264335-S	136.9	164.1	147	RDS	NM_000322.2	RP7;AVMD;PRPH;AOFMD;PRPH2	G-protein	integral to	vision
GI_21264336-S	813.2	1175.5	730.1	ARAP3	NM_022481.4	FLJ21065	DNA	nucleus	neuropepti
GI_21264338-S	145.5	139.2	131.1	SOX12	NM_006943.2	SOX22	molecular	nucleus	regulation
GI_21264340-S	3589.9	3365	3706.4	SMS	NM_004595.2	SpS;SPMSY	spermidin		methionin
GI_21264342-S	141.5	140.7	147.1	SAFB	NM_002967.2	HAP;HET;SAFB1	double-	nucleus	establish
GI_21264344-S	224.8	270.3	214.3	PRPH	NM_006262.2	NEF4	structural	intermedia	
GI_21264347-A	3085.4	2562.8	2829.5	SMARCD1	NM_139071.1	BAF60A;CRACD1	transcripti	nucleoplas	chromatin
GI_21264349-I	115.3	122.8	108.1	SMARCD1	NM_003076.3	BAF60A;CRACD1	transcripti	nucleoplas	chromatin
GI_21264350-S	1370.5	1414	1557.3	SMARCD2	NM_003077.2	BAF60B;CRACD2;PRO2451	transcripti	nucleoplas	chromatin
GI_21264352-S	457.9	704.4	378	SMARCD3	NM_003078.2	BAF60C;CRACD3	transcripti	nucleoplas	chromatin
GI_21264354-S	1520.9	1821	1761.7	SMARCE1	NM_003079.3	BAF57	chromatin	nuclear	nucleoso
GI_21264356-I	188	212	185.4	MASP1	NM_001879.3	MASP;RaRF;CRARF;PRSS5;CRARF1	serine-		compleme
GI_21264358-A	103.6	104.6	90.4	MASP1	NM_139125.1	MASP;RaRF;CRARF;PRSS5;CRARF1	serine-		compleme
GI_21264358-I	143.8	144.4	129.3	MASP1	NM_139125.1	MASP;RaRF;CRARF;PRSS5;CRARF1	serine-		compleme
GI_21264360-A	80.1	87	71.7	MASP2	NM_139208.1	sMAP;MAP19	serine-		compleme
GI_21264360-I	187.8	253.3	193.5	MASP2	NM_139208.1	sMAP;MAP19	serine-		compleme
GI_21264362-I	111.9	119.1	110.9	MASP2	NM_006610.2	sMAP;MAP19	serine-		compleme
GI_21264368-A	318.2	341.1	340.6	NUP98	NM_139131.1	ADIR2;NUP196	transporte	nuclear	protein-
GI_21264368-I	536.3	533	513.4	NUP98	NM_139131.1	ADIR2;NUP196	transporte	nuclear	protein-
GI_21264372-S	142.3	195	144.6	UPK1A	NM_007000.2	UPIA;UPKA;MGC14388			
GI_21264373-S	102.7	97.8	96.6	UPK1B	NM_006952.2	UPIB;UPK1	structural	integral to	physiologi
GI_21264557-S	1146.1	1096.8	661.8	SMAP1	NM_021940.2	SMAP-1;FLJ13159			
GI_21264564-I	151.7	167.1	153	ARID1A	NM_006015.3	B120;P270;BM029;BAF250;C1orf4;SMARCF			
GI_21264566-S	88	108.1	94	HIST1H3E	NM_003532.2	H3.1;H3/d;H3FD			
GI_21264567-S	173.3	194.3	182.2	TM4SF12	NM_012338.2	NET-2		integral to	
GI_21264568-A	878	712.7	702.3	ARID1A	NM_018450.4	B120;P270;BM029;BAF250;C1orf4;SMARCF			
GI_21264570-S	104.7	107.2	102.6	HIST1H3G	NM_003534.2	H3/h;H3FH			
GI_21264571-S	90.5	95.5	92.2	HIST1H1A	NM_005325.2	H1.1;H1F1;HIST1	DNA	chromoso	spermatog
GI_21264572-S	285.5	349	306.7	NET-5	NM_006675.2			membran	
GI_21264573-S	122.2	139.8	132.2	TM4SF13	NM_014399.2	NET-6;FLJ22934		membran	
GI_21264576-S	91.3	105.5	108.2	NET-7	NM_012339.2			membran	
GI_21264577-S	186.4	365.3	378.8	TSPAN-1	NM_005727.2	NET-1		integral to	mystery
GI_21264579-S	83.5	99.4	101.7	TSPAN-2	NM_005725.2	FLJ12082		integral to	mystery
GI_21264582-S	445.7	418.1	290	TM4SF9	NM_005723.2	NET-4;TSPAN-5		integral to	mystery

GI_21264584-I	108.3	94.8	91.6	HOP	NM_032495.3	OB1;LAGY;Toto;Cameo;NECC1;SMAP31			
GI_21264586-A	91.7	89	77.3	HOP	NM_139211.1	OB1;LAGY;Toto;Cameo;NECC1;SMAP31			
GI_21264590-S	232.8	168.6	188.4	CENPH	NM_022909.3		molecular	kinetochor	centromer
GI_21264591-I	95.8	114.6	103.9	CENTD1	NM_015230.2	ARAP2;FLJ13675;KIAA0580			
GI_21264593-A	114.1	112.3	116.6	CENTD1	NM_139182.1	ARAP2;FLJ13675;KIAA0580			
GI_21264593-I	85.1	88.9	81.2	CENTD1	NM_139182.1	ARAP2;FLJ13675;KIAA0580			
GI_21264595-A	326	315.8	313.4	CENTD2	NM_015242.2	ARAP1;KIAA0782	DNA	nucleus	neuropepti
GI_21264595-I	106.8	118.7	106.1	CENTD2	NM_015242.2	ARAP1;KIAA0782	DNA	nucleus	neuropepti
GI_21264596-I	106.3	112.1	105.6	CENTD2	NM_139181.1	ARAP1;KIAA0782	DNA	nucleus	neuropepti
GI_21264599-S	140.1	205.4	134.9	HIST1H4H	NM_003543.3	H4/h;H4FH			
GI_21264600-S	81.5	106.1	80.6	HIST1H4E	NM_003545.3	H4/j;H4FJ			
GI_21264601-S	5743.5	826	555.5	LAMA5	NM_005560.3	KIAA1907	structural	basal	
GI_21264603-S	1326.5	649	277.4	LOX	NM_002317.3		protein-	extracellul	protein
GI_21264605-I	98.8	133.4	108.6	EPS8L1	NM_017729.2	DRC3;EPS8R1;MGC4642;FLJ20258;MGC23			
GI_21264607-I	112	110.3	104	EPS8L1	NM_133180.1	DRC3;EPS8R1;MGC4642;FLJ20258;MGC23			
GI_21264609-A	258.2	320.1	318.7	EPS8L1	NM_139204.1	DRC3;EPS8R1;MGC4642;FLJ20258;MGC23			
GI_21264609-I	112.5	105.5	100.7	EPS8L1	NM_139204.1	DRC3;EPS8R1;MGC4642;FLJ20258;MGC23			
GI_21264611-I	143.3	155.6	151.8	ST5	NM_005418.2	P70;P82;HTS1;P126	tumor		
GI_21264613-A	439.3	750.2	412.3	ST5	NM_139157.1	P70;P82;HTS1;P126	tumor		
GI_21264615-S	700.9	750.8	532.3	EPS8L2	NM_022772.2	EPS8R2;MGC3088;FLJ21935;FLJ22171			
GI_21264629-S	104	121.7	114.7	ST14	NM_021978.2	HAI;MTSP1;SNC19;MT-SP1;MTSP-	serine-	integral to	proteolysis
GI_21265024-S	107.1	123.4	104.9	ADAMTS10	NM_030957.1	ADAM-TS10	zinc ion	extracellul	proteolysis
GI_21265027-S	434.5	583.5	759.5	STAM	NM_003473.2	STAM1	SH3/SH2		signal
GI_21265030-S	109	102.4	100.5	STAM2	NM_005843.3	Hbp;STAM2A;STAM2B;DKFZP564C047			intracellula
GI_21265033-I	241.5	243.3	237.5	ADAMTS13	NM_139025.1	TTP;VWFCP;C9orf8;vWF-			
GI_21265036-S	101.6	127.4	105.7	ADAMTS3	NM_014243.1	ADAMTS-4;KIAA0366	heparin	extracellul	collagen
GI_21265039-S	2254.7	1996.6	1981.8	MRPL22	NM_014180.2	RPML25;HSPC158;MRP-L25			
GI_21265048-A	126.5	151.3	128.5	ADAMTS13	NM_139028.1	TTP;VWFCP;C9orf8;vWF-			
GI_21265048-I	158.8	195.8	178.9	ADAMTS13	NM_139028.1	TTP;VWFCP;C9orf8;vWF-			
GI_21265051-A	106.9	106.5	101	ADAMTS14	NM_080722.2		metalloen	extracellul	collagen
GI_21265057-S	87.1	97.3	80.1	ADAMTS15	NM_139055.1		zinc ion	extracellul	integrin-
GI_21265060-S	102.2	120.2	104.2	ADAMTS16	NM_139056.1		peptidase	extracellul	integrin-
GI_21265063-S	149	147.7	148.1	ADAMTS17	NM_139057.1	FLJ32769	zinc ion	extracellul	integrin-
GI_21265074-S	842.8	902.3	800.8	MRPL14	NM_032111.1	RMPL32;RPML32;MRP-L32	structural	ribosome	protein
GI_21265077-S	3747.5	3399.6	4217.5	MRPL15	NM_014175.2	RPML7;MRP-L7;HSPC145	structural	large	protein
GI_21265079-S	1134	1236.2	763.1	MRPL18	NM_014161.2	HSPC071;MRP-L18	structural	mitochond	
GI_21265083-S	1232.7	1201.9	1105.5	MRPL1	NM_020236.2	L1mt;BM022			
GI_21265087-S	1130.3	1417.4	1396.5	MRPL36	NM_032479.2	RPMJ;BRIP1;L36mt;PRPL36	structural	ribosome	protein
GI_21265090-S	5721.4	5303.2	4240.2	MRPL3	NM_007208.2	MRL3;RPML3	structural	cytosolic	protein
GI_21265092-S	899.1	1106.2	1309.6	MRPL41	NM_032477.1	RPML27;MRP-L27	structural		
GI_21265095-S	951	1119.3	1124.4	MRPL50	NM_019051.1	MRP-L50;FLJ20493	structural	mitochond	
GI_21265098-S	119.5	117.6	107.8	TM4-B	NM_012466.2			integral to	
GI_21265100-S	122.5	161.5	121.4	TM4SF1	NM_014220.1	L6;H-L6;M3S1;TAAL6	molecular	integral to	N-linked
GI_21265103-S	127.4	138.2	121.6	TM4SF2	NM_004615.2	A15;MXS1;CD231;CCG-B7;TALLA-		integral to	N-linked

GI_21265107-S	113	107.4	91.9	TM4SF3	NM_004616.2	CO-029	signal	membran	pathogene
GI_21265109-S	148.8	148.5	137	TM4SF4	NM_004617.2	ILTMP;il-TMP;FLJ31015		membran	negative
GI_21265112-S	107.6	100	106.9	TM4SF5	NM_003963.2		tumor	integral to	N-linked
GI_21265115-S	545	605.2	454.4	TM4SF6	NM_003270.2	T245;TSPAN-6	cell	integral to	cell
GI_21265128-A	332.9	348.1	376.6	USP21	NM_016572.2	USP16;USP23;MGC3394	cysteine-	cellular_co	ubiquitin-
GI_21269863-S	613.3	899.2	811.1	TAF11	NM_005643.2	TAF2I;PRO2134;TAFII28;MGC:15243	protein	transcripti	
GI_21269865-S	346.3	323.7	270.2	TAF5L	NM_014409.2	PAF65B	transcripti		transcripti
GI_21269867-S	626.7	776.8	873.1	TAF6L	NM_006473.2	PAF65A;MGC4288;FLJ11136	DNA	histone	chromatin
GI_21269869-I	176.6	171.3	212.9	ACAS2	NM_018677.2	ACS;ACSA;AceCS;dJ1161H23.1	acetate-	cytoplasm	metabolis
GI_21269871-A	2273	1482.1	2767.2	ACAS2	NM_139274.1	ACS;ACSA;AceCS;dJ1161H23.1	acetate-	cytoplasm	metabolis
GI_21269871-I	119.8	120.8	117.5	ACAS2	NM_139274.1	ACS;ACSA;AceCS;dJ1161H23.1	acetate-	cytoplasm	metabolis
GI_21269874-A	7248.1	5890.9	4893.7	CARS	NM_001751.3	CYSRS;MGC:11246	tRNA	soluble	protein
GI_21281666-S	760.8	566.5	455.4	C7orf36	NM_020192.1	GK003			
GI_21281668-S	138.2	153.3	152.8	BDP1	NM_018429.1	TFC5;TFNR;TAF3B1;KIAA1241;KIAA1689;T			
GI_21281672-S	89.5	82.4	86.9	LGI4	NM_139284.1	LGIL3			
GI_21281674-S	108.3	130.5	107.5	GAR17	NM_139285.1				
GI_21281676-S	229.7	248.9	228.2	WDR36	NM_139281.1	TA-WDRP	catalytic		metabolis
GI_21281678-S	209.5	190.1	178.7	TA-PP2C	NM_139283.1		catalytic		
GI_21281684-S	1653.1	1346.5	1282.7	LAGE2A	NM_139250.1				
GI_21281688-S	90.3	108.8	88.8	FLJ12056	NM_024933.1				
GI_21284382-I	229.5	251.6	229.6	ABLIM1	NM_002313.4	abLIM;LIMAB1;LIMATIN;KIAA0059	actin	actin	vision
GI_21284386-A	113.4	117.7	121.2	ABLIM1	NM_006720.2	abLIM;LIMAB1;LIMATIN;KIAA0059	actin	actin	vision
GI_21284386-I	98	115	100.7	ABLIM1	NM_006720.2	abLIM;LIMAB1;LIMATIN;KIAA0059	actin	actin	vision
GI_21312133-S	430.7	559.4	490.4	PCQAP	NM_015889.2	TIG1;CAG7A;TIG-	transcripti		neurogene
GI_21312135-S	107.5	121.4	114.8	CHST6	NM_021615.2	MCDC1	transferas	Golgi	proteoglyc
GI_21313637-S	170.9	170.1	155.9	LGI2	NM_018176.2	LGIL2;FLJ10675;KIAA1916			
GI_21314599-S	261.2	315.7	254.3	CEACAM8	NM_001816.2	CD67;CGM6;CD66b;NCA-95	tumor	extracellul	immune
GI_21314612-S	5405.7	4809.2	3600.1	EIF2S3	NM_001415.2	EIF2;EIF2G;EIF2gamma	GTPase	cytosolic	translation
GI_21314613-S	168.3	210	186.8	CD4	NM_000616.2		internaliza	integral to	enzyme
GI_21314616-S	206.1	363.5	205.5	PECAM1	NM_000442.2	CD31	cell	proteoglyc	cell
GI_21314620-S	263.6	311.9	243.6	RNASE6	NM_005615.2	RNS6;RNASEK6;RNase k6	ribonuclea	secretory	RNA
GI_21314621-S	110.2	100.9	99.2	GPR34	NM_005300.2	GPCR	G-protein	integral to	G-protein
GI_21314623-S	766.6	848.2	831.9	PGS1	NM_024419.2	DKFZP762M186			
GI_21314628-S	108.5	109.5	101.7	RAB27B	NM_004163.3		RAB small		protein
GI_21314629-S	246.3	302.5	224.6	C3AR1	NM_004054.2	AZ3B;C3AR;HNFAG09	compleme	integral to	phosphati
GI_21314630-S	94.2	192.5	99.3	GNG4	NM_004485.2		heterotrim	peripheral	regulation
GI_21314631-S	503	362.8	225.5	SLC1A4	NM_003038.2	SATT;ASCT1	neutral	membran	neutral
GI_21314634-S	156.1	154.4	153.5	PSG9	NM_002784.2	PSG11	plasma	extracellul	pregnancy
GI_21314637-S	229.1	273.5	237.8	NEUROD2	NM_006160.2	NDRF	transcripti	nucleus	regulation
GI_21314639-S	5126.8	4668.7	3340.2	SRPX	NM_006307.2	ETX1	cell	membran	cell
GI_21314640-S	313.5	406.4	362	LILRB4	NM_006847.2	HM18;ILT3;LIR5;CD85K;LIR-5	antigen	plasma	defense
GI_21314642-S	397.8	597.3	472.6	MFAP3	NM_005927.3		extracellul	extracellul	
GI_21314643-S	218.3	242.1	206.7	FRS2	NM_006654.2	SNT;SNT1;FRS2A;SNT-1;FRS2alpha	insulin	peripheral	FGF
GI_21314646-S	1631.4	2447.5	2078	RNP24	NM_006815.2	P24A	protein	microsom	intracellula

GI_21314647-S	133.1	166.3	142.2	CMRF35	NM_006678.2	LIR;CMRF35A;CMRF-35A;CMRF35A1	lymphocyt	integral to	cellular
GI_21314649-S	93.9	98.6	104.3	PPP1R1A	NM_006741.2		type 1		glycogen
GI_21314652-S	100	112	101.7	PLA2G2D	NM_012400.2	SPLASH;sPLA2S	secreted	extracellul	phospholi
GI_21314657-S	699.3	674.5	594.6	PGCP	NM_016134.2		metallocar	extracellul	peptide
GI_21314659-S	560.9	542.4	557.6	NCB5OR	NM_016230.2	b5+b5R;dJ676J13.1	cytochrom	cytoplasm	chemosen
GI_21314660-S	130.1	146.5	131.8	RND1	NM_014470.2	ARHS;RHO6	Rho small	cytoskelet	negative
GI_21314665-S	322.5	302.2	279.6	LSM8	NM_016200.2	YJR022W	pre-mRNA	small	mRNA
GI_21314666-S	2868.9	2581.4	2745.2	CPSF3	NM_016207.2	CPSF;CPSF73	RNA	nucleoplas	mRNA
GI_21314667-S	113.2	103.2	96.8	APLN	NM_017413.2		receptor		lactation
GI_21314670-S	446.9	410.9	367.3	TRPM4	NM_017636.2	TRPM4B;FLJ20041	cation	integral to	cation
GI_21314672-S	121.8	122.5	116.6	CLST11240	NM_016438.2	CLST11240-15			
GI_21314673-S	10296.1	10625	4677.3	MIG-6	NM_018948.2	MIG6;RALT;GENE-33	Rho	cytoplasm	response
GI_21314674-S	312.3	317.6	432.8	DKFZp434G0	NM_017566.2				
GI_21314678-S	118.1	114.7	104.2	SHC3	NM_016848.2	NSHC;SHCC;N-Shc	signal	nucleus	transmem
GI_21314680-S	499.3	325.4	911.4	KIAA1598	NM_018330.2	FLJ11122			
GI_21314681-S	150.8	161.8	152.7	TRPV6	NM_018646.2	CAT1;CATL;ZFAB;ECAC2;ABP/ZF;HSA2779			
GI_21314683-A	235.9	272.9	229.6	SSBP3	NM_018070.2	SSDP;SSDP1;SSDP3;FLJ10355	single-	nucleus	regulation
GI_21314683-I	108.7	121	105.2	SSBP3	NM_018070.2	SSDP;SSDP1;SSDP3;FLJ10355	single-	nucleus	regulation
GI_21314689-S	1550.7	1259.5	1020.8	NGLY1	NM_018297.2	PNG1;FLJ11005			
GI_21314691-S	117	122.3	107.6	HRMT1L3	NM_019854.2				
GI_21314694-S	802.3	798.4	823.9	KIAA1449	NM_020839.2	P80			
GI_21314699-S	177.3	627.7	341.5	FLJ12541	NM_022369.2	Stra6			
GI_21314703-S	90.5	80	77.8	GMCL	NM_022471.2	GCL	protein		
GI_21314708-S	99.3	87.2	74.2	ZNFN1A5	NM_022466.2	PEGASUS;FLJ22973			
GI_21314710-S	235.2	273.8	245.2	MGC3020	NM_024048.2				
GI_21314717-S	286	320.7	333.9	ZBTB3	NM_024784.2	FLJ23392	protein	nucleus	regulation
GI_21314718-S	95.3	103.5	107.3	FLJ11767	NM_024593.2		calcium		
GI_21314719-S	478.8	563	562.4	SNIP1	NM_024700.2	FLJ12553	DNA	nucleus	regulation
GI_21314723-S	714.7	582.7	556.3	FLJ22490	NM_024790.2				
GI_21314727-S	307.3	325.7	305.3	C18orf9	NM_024899.2	HsT1705;FLJ12542			
GI_21314730-S	248.8	244.6	211	MGC2776	NM_025265.2	MGC4440	tRNA-	tRNA-	tRNA
GI_21314735-S	99.1	113.6	101.9	LOC80298	NM_025198.2	FLJ14062			
GI_21314737-S	127	181.5	140.8	LOC83468	NM_031302.2		transferas		carbohydr
GI_21314738-S	176.7	166.6	157.5	MFTC	NM_030780.2		folate	mitochond	folate
GI_21314740-S	98.9	93.7	96.3	LOC83690	NM_031461.2			extracellul	
GI_21314741-S	350.5	283.4	311.3	DKFZP434G2	NM_031217.2		ATP	kinesin	microtubul
GI_21314743-S	97.7	97.9	100.5	STK22D	NM_032028.2	TSSK1;FKSG81;SPOGA4	protein-		protein
GI_21314751-S	173.9	202.7	180.8	GPR81	NM_032554.2	FKSG80	receptor	integral to	G-protein
GI_21314754-S	564	929.6	911.8	SPPL2A	NM_032802.2	IMP3;PSL2;FLJ14540	peptidase	integral to	proteolysis
GI_21314756-S	1042.7	1005.4	944.8	C14orf142	NM_032490.2	PNAS-127			
GI_21314757-S	166.6	290	177.9	HAVCR2	NM_032782.2	TIM3;KIM-3;TIMD3;Tim-3;FLJ14428			
GI_21314759-S	698.8	757	777.4	ZNF499	NM_032792.2	FLJ14486	protein		
GI_21314760-S	493.4	557.1	649.6	SLC35B4	NM_032826.2	YEA;YEA4;FLJ14697	nucleotide-	integral to	nucleotide-
GI_21314761-S	311.2	366.7	260.8	MCEE	NM_032601.2				

GI_21314763-S	252.8	314.7	254.8	FCRH3	NM_052939.2	SPAP2			
GI_21314766-S	356.2	365.8	332.9	MADP-1	NM_033114.2		nucleic		
GI_21314771-S	8019.6	8954.3	7215.9	ESDN	NM_080927.2	CLCP1			
GI_21314777-S	448.5	586.3	508.5	CSNK1G2	NM_001319.5	CK1g2	casein		protein
GI_21314780-S	130.8	152.1	136	NEURL	NM_004210.3	RNF67;h-neu	tumor		neurogene
GI_21314782-S	127.7	125.8	127	LOC130951	NM_138804.2				
GI_21314788-S	443.7	635	464.7	TWSG1	NM_020648.3	TSG	protein		embryonic
GI_21322233-S	98.8	85	86	SLC17A8	NM_139319.1	VGLUT3	transporte	membran	transport
GI_21322251-S	217.3	279.5	240.8	AR	NM_000044.2	KD;AIS;TFM;DHTR;SBMA;NR3C4;SMAX1;H	androgen	nucleus	sex
GI_21327676-S	1283.4	1754.2	556.5	HLA-B	NM_005514.4		MHC	integral to	immune
GI_21327678-S	10114.2	11568	12861	ATP5E	NM_006886.2	ATPE	hydrogen	proton-	proton
GI_21327679-S	122.7	163.1	131.5	ASIP	NM_001672.2	ASP;AGSW;AGTI;AGTIL	receptor	extracellul	energy
GI_21327681-S	2090.7	1922.1	2166.1	ACADM	NM_000016.2	MCAD;ACAD1;MCADH	acyl-CoA	mitochond	fatty acid
GI_21327682-S	2160	2283.5	1967.9	CINP	NM_032630.2	MGC849	kinase		
GI_21327686-A	944.1	1173	829.8	YME1L1	NM_139313.1	FTSH;MEG4;PAMP;YME1L			
GI_21327689-S	1611.4	1669.7	1617.3	SART3	NM_014706.2	TIP110;KIAA0156;p110(nrb);RP11-13G14	nucleic	intracellula	RNA
GI_21327690-A	115.9	124	126.4	ADAMTSL1	NM_052866.2	ADAMTSR1;MGC40193		extracellul	
GI_21327690-I	98.4	105.6	89.2	ADAMTSL1	NM_052866.2	ADAMTSR1;MGC40193		extracellul	
GI_21327692-I	192.5	206.1	197.4	ADAMTSL1	NM_139238.1	ADAMTSR1;MGC40193		extracellul	
GI_21327694-I	119.9	134.7	122.6	ADAMTSL1	NM_139264.1	ADAMTSR1;MGC40193		extracellul	
GI_21327696-S	115.6	132.6	121.2	DDX25	NM_013264.2	GRTH	translation	cytoplasm	regulation
GI_21327698-S	96.7	106.7	98.9	TAF13	NM_005645.2	TAF2K;TAFII18;MGC22425	protein	transcripti	transcripti
GI_21327700-A	1274.6	1507.4	1189.2	TAF15	NM_139215.1	RBP56;TAF2N;TAFII68;hTAFII68	single-	transcripti	cell growth
GI_21327702-S	160.2	236	170.4	KLK6	NM_002774.2	Bssp;Klk7;SP59;PRSS9;PRSS18;MGC9355;	serine-	extracellul	pathogene
GI_21327704-A	102.6	117.7	113.8	KLK7	NM_139277.1	SCCE;PRSS6	serine-		epidermal
GI_21327706-A	4227.3	3626.5	3092.6	NAP1L1	NM_004537.3	NRP;NAP1;NAP1L;MGC8688;MGC23410		chromatin	nucleoso
GI_21327707-I	4034.4	3935.9	3346.7	NAP1L1	NM_139207.1	NRP;NAP1;NAP1L;MGC8688;MGC23410		chromatin	nucleoso
GI_21327711-S	2372.9	2564.1	2284.1	NAP1L4	NM_005969.2	NAP2;NAP2L;hNAP2;MGC4565	chaperone	chromatin	nucleoso
GI_21327712-S	2464.6	7971.9	7095.8	PRSS11	NM_002775.2	L56;HtrA;HTRA1;ORF480	serine-	extracellul	cell growth
GI_21327713-S	100.9	114	102.4	PRSS12	NM_003619.2	BSSP3;BSSP-3;MGC12722;MOTOPSIN	serine-	membran	proteolysis
GI_21327714-S	492.4	487.3	411.7	TCERG1	NM_006706.2	CA150;TAF2S	RNA	nucleus	transcripti
GI_21328445-S	109.3	131.9	112	LIPE	NM_005357.2	HSL;LHS	hydrolase		fatty acid
GI_21328450-A	98.3	102.7	98.9	ANGPT1	NM_139290.1	AGP1;AGPT;ANG1;KIAA0003	receptor	kinesin	signal
GI_21328450-I	97.7	100.3	101.7	ANGPT1	NM_139290.1	AGP1;AGPT;ANG1;KIAA0003	receptor	kinesin	signal
GI_21328452-I	123.4	171.1	146.3	ANGPT1	NM_001146.3	AGP1;AGPT;ANG1;KIAA0003	receptor	kinesin	signal
GI_21328453-S	100.8	106.1	97.6	ANGPT4	NM_015985.2	AGP4;ANG4;ANG-3	molecular	kinesin	biological_
GI_21328454-S	741.9	1421	1012.4	HIST2H2AA	NM_003516.2	H2A;H2A.2;H2A/O;H2AFO;H2a-615	DNA	chromoso	nucleoso
GI_21359817-S	156.3	157.4	135.9	SLAC2-B	NM_015065.1	KIAA0624			
GI_21359821-S	1346.2	1286.2	1165.4	RNASE3L	NM_013235.2	RN3;DROSHA;HSA242976	double-	nucleus	ribosome
GI_21359830-S	124.3	108.6	108.3	AMY2A	NM_000699.2	AMY2	alpha-	extracellul	carbohydr
GI_21359835-S	8130.2	6517.2	5648.3	PEA15	NM_003768.2	PED;MAT1;HMAT1;MAT1H;PEA-			small
GI_21359839-S	1432.5	1761.6	1516.9	SNRPG	NM_003096.2	SMG	small	spliceoso	mRNA
GI_21359840-S	2625.8	2851.4	2409.6	TTC3	NM_003316.2	TPRD;DCRR1;TPRDI;RNF105;TPRDII;TPRD			pathogene
GI_21359847-S	245.3	285.1	257.4	HCN2	NM_001194.2	BCNG2;HAC-1;BCNG-2	cation	voltage-	cation

GI_21359849-S	158.3	175.3	170.5	CRMP1	NM_001313.2	DRP1;DRP-1;DPYSL1	dihydropyr		nucleobas
GI_21359850-S	103	113.3	113.1	C4BPA	NM_000715.2	C4BP		extracellul	compleme
GI_21359853-S	890.3	806.6	580.4	RABGGTB	NM_004582.2	GGTB	prenyltran		vision
GI_21359858-S	102.7	105.6	101.4	LUM	NM_002345.2	LDC;SLRR2D	proteoglyc	extracellul	cartilage
GI_21359859-S	6321.8	6818.9	5184.8	PTMA	NM_002823.2	TMSA		nucleus	transcripti
GI_21359861-S	124.9	130.7	106.6	EDN1	NM_001955.2	ET1	peptide	soluble	positive
GI_21359863-S	131.2	122.5	108.4	HTN1	NM_002159.2	HIS1	antifungal	extracellul	ossificatio
GI_21359866-S	5901	6026.1	5934.7	CYC1	NM_001916.2		cytochrom	mitochond	electron
GI_21359870-S	104.4	94.9	96.5	SPARCL1	NM_004684.2	SC1;HEVIN;MAST9	calcium	extracellul	
GI_21359876-S	971.6	870	699.2	GGPS1	NM_004837.2	GGPPS;GGPPS1	geranyltra		lipid
GI_21359880-S	399.3	504.8	421.8	ZNF193	NM_006299.2	PRD51	protein	nucleus	regulation
GI_21359891-S	3537	4207.5	3745.4	MKRN1	NM_013446.2	RNF61	nucleic	cellular_co	biological_
GI_21359892-S	1735.4	1031.6	867.7	TIMM9	NM_012460.2	TIM9;TIM9A	zinc ion	mitochond	mitochond
GI_21359895-S	628.4	695.2	567.8	KLHL2	NM_007246.2	MAYVEN;ABP-KELCH			
GI_21359898-S	709.9	761.8	577.2	C22orf2	NM_015373.2	CBY;arb1;HS508I15A			
GI_21359899-S	85.9	86.5	79.5	C20orf28	NM_015417.2	DKFZP434I114			
GI_21359901-S	3943.2	4208.3	2989.8	TINP1	NM_014886.2	YR-29;HCL-G1	structural	ribosome	protein
GI_21359902-S	1262.1	1511.6	906	HDGFRP3	NM_016073.2	HDGF2;CGI-142		nucleus	cell
GI_21359903-S	304.4	365.5	333.5	TFE3	NM_006521.3	RCCP2	tumor	nucleus	oncogene
GI_21359904-S	471	549.2	446.2	SH3GLB1	NM_016009.2	Bif-1;CGI-61;KIAA0491			
GI_21359905-S	17070.5	12312	11320	GLTSCR2	NM_015710.2		tumor		
GI_21359908-S	456.9	340.4	363.5	ZNF593	NM_015871.2	ZT86	transcripti	nucleus	negative
GI_21359910-S	601.3	522.2	454.9	ACP6	NM_016361.2	LPAP;ACPL1;PACPL1	acid	mitochond	lipid
GI_21359917-S	995.7	964.3	950.7	AWP1	NM_019006.2				
GI_21359919-S	125.5	148.5	135.7	ROPN1	NM_017578.2	ODF6;RHPNAP1;ropporin;DKFZp434B1222			
GI_21359921-S	1033.9	906.8	1072.3	FLJ10581	NM_018146.2	HC90	RNA		RNA
GI_21359925-S	647.2	752.2	534.8	HMG20A	NM_018200.2	FLJ10739	transcripti	nucleus	establish
GI_21359926-S	724	674.7	743.9	FLJ10842	NM_018238.2		diacylglyc		protein
GI_21359927-S	114.4	133.8	110	SIAT7A	NM_018414.2	HSY11339;ST6GalNAcI			
GI_21359928-S	3238.6	4715.5	3078.2	XPNPEP1	NM_020383.2	SAMP;XPNPEP;XPNPEPL	aminopept		
GI_21359931-S	92.6	109.4	105.1	C8orf4	NM_020130.2	TC1;TC-1;hTC-1			
GI_21359932-S	108.9	110.3	90	LXN	NM_020169.2				
GI_21359934-S	406.6	506.8	462.6	DSCAML1	NM_020693.2	KIAA1132	carboxype		proteolysis
GI_21359936-S	198.2	218.5	196.2	KIAA1173	NM_020707.2	C3orf3	molecular	cytoplasm	biological_
GI_21359942-S	3577	3001	3083.8	RHBDF1	NM_022450.2	Dist1;C16orf8;EGFR-RS;FLJ2235;FLJ22357			
GI_21359944-S	681.7	634	839.1	HCAP-G	NM_022346.2	CAPG;CHCG;CAP-G;NY-MEL-3		nucleus	mitotic
GI_21359948-S	253.8	320.8	278.2	MYOZ1	NM_021245.2	CS-2;FATZ;MYOZ			
GI_21359954-S	942.6	799.9	861.6	SBP2	NM_024077.2	MGC3156;DKFZp434B216	structural	ribosome	protein
GI_21359956-S	662.9	811.9	889	FLJ21047	NM_024569.2				
GI_21359958-S	493.1	560.6	489.5	FLJ23584	NM_024588.2				
GI_21359959-S	126.7	130.9	122.9	BGR	NM_030924.2	PRTD-NY3;DKFZp434K1635	catalytic		metabolis
GI_21359961-S	2226.9	2746.7	2650	C6orf62	NM_030939.2	FLJ12619;dJ30M3.2;DKFZP564G182			
GI_21359962-S	1009	1092.9	1094.6	COP1	NM_022457.4	FLJ10416			
GI_21359964-S	3846.4	4466.6	4059	CRR9	NM_030782.2	DKFZP761M2324			

GI_21359970-S	1177.2	1048.1	1521	ALS2CR2	NM_018571.4	PAPK;ILPIP;ILPIPA;CALS-21;PRO1038	ATP	cellular_co	protein
GI_21359973-S	130.8	148.5	145.1	VIT	NM_053276.2				
GI_21359975-S	135.8	144.9	133	SCGB3A2	NM_054023.2	LU103;PNSP1;UGRP1			
GI_21359977-S	237.5	298.9	260.6	PHC3	NM_024947.2	EDR3;HPH3;FLJ12729;FLJ12967			
GI_21359981-S	184.2	170.8	181.4	HINT3	NM_138571.3	HINT4;FLJ33126;MGC:22976			
GI_21359983-S	7243.9	7080.4	4642	CSDA	NM_003651.3	DBPA;ZONAB	double-	perinuclea	response
GI_21361069-S	5639.5	5233	6463.3	PFKL	NM_002626.2		magnesiu	6-	fructose
GI_21361071-S	1009.9	947.8	829	RAB2L	NM_004761.2	RGL2;KE1.5;HKE1.5	Ras	cellular_co	neuropepti
GI_21361076-S	96	105.2	102.4	CACNA1I	NM_021096.2		voltage-	voltage-	small
GI_21361081-S	429.8	257.6	114.7	CRLF1	NM_004750.2	NR6;CISS;CLF-1	receptor	extracellul	antimicrob
GI_21361085-S	100.2	100.6	100.1	TNFRSF10A	NM_003844.2	DR4;APO2;MGC9365;TRAILR1;TRAILR-1	death	integral to	induction
GI_21361087-A	865.3	626.8	1140.7	SPHK1	NM_021972.2	SPHK	diacylglyc	cytosol	sphingosin
GI_21361089-S	123.8	133	121.6	SCN2B	NM_004588.2		voltage-	integral to	sodium
GI_21361092-S	1792	1691.8	1252.1	TPST1	NM_003596.2		protein-	Golgi	peptidyl-
GI_21361093-S	1225.1	1639.1	2034.3	IKBKG	NM_003639.2	IP2;FIP3;NEMO;FIP-3;Fip3p;IKK-gamma	signal	kinesin	NIK-I-
GI_21361096-S	1325.6	1463.8	1210.4	GNG10	NM_004125.2		heterotrim	peripheral	signal
GI_21361098-S	757.5	888.3	864.5	CGGBP1	NM_003663.2	CGGBP;p20-CGGBP	double-	nucleus	
GI_21361102-S	213	198.6	205.7	SLC25A12	NM_003705.2	ARALAR;ARALAR1	solute:cati	mitochond	small
GI_21361104-S	203.4	250.5	208.4	RODH-4	NM_003708.2		retinol	microsom	lipid
GI_21361107-S	79.3	85	81.8	ELF3	NM_004433.2	ERT;ESX;EPR-1;ESE-1	transcripti		embryoge
GI_21361108-S	130.3	157.2	130.2	NR2E1	NM_003269.2	TLL;TLX;XTLL	steroid	nucleus	neurogene
GI_21361115-S	420.7	3414.6	1342.5	CSPG2	NM_004385.2	VERSICAN	glycosami	extracellul	cell
GI_21361125-S	710.7	695	706.2	SLC37A4	NM_001467.2	G6PT1;GSD1b;PRO0685;MGC15729	transporte	microsom	glycogen
GI_21361134-S	361.4	289.8	352.7	NFKBIB	NM_002503.2	IKBB;TRIP9	transcripti		transcripti
GI_21361147-S	106.1	111.4	106.7	CHRNA6	NM_004198.2	CHNRA6	nicotinic	nicotinic	small
GI_21361148-S	279.8	318.6	290.3	RGS7	NM_002924.2		signal	heterotrim	regulation
GI_21361154-S	143.9	181.1	176.1	EIF2AK3	NM_004836.2	PEK;WRS;PERK	protein	endoplas	translation
GI_21361156-S	552.2	437.4	545.8	HOMER3	NM_004838.2	HOMER-3			metabotro
GI_21361160-S	119.8	103.4	103.8	SURB7	NM_004264.2	SRB7	DNA-	DNA-	regulation
GI_21361162-S	343	266.3	159.7	GGCX	NM_000821.2	VKCFD1	gamma-	integral to	blood
GI_21361164-I	76.3	89.6	81.8	HTR4	NM_000870.2		serotonin	integral to	G-protein
GI_21361166-S	179.3	219	182.4	ART3	NM_001179.2		NAD ADP-	integral to	protein
GI_21361190-S	96.3	112.3	104.8	FCGR2B	NM_004001.2	CD32;FCG2;FCGR2;IGFR2	internaliza	integral to	signal
GI_21361192-S	5318.5	5252.6	5837.7	CD44	NM_000610.2	IN;INLU;MC56;MDU2;MDU3;MIC4;Pgp1;CD4	collagen	integral to	cell-matrix
GI_21361197-S	117.1	198.6	150.3	SERPINA1	NM_000295.2	PI;A1A;AAT;PI1;A1AT;alpha-1-antitrypsin	endopepti		acute-
GI_21361201-S	123.8	154.9	133.6	PCYT1B	NM_004845.2	CTB;CCT-beta	choline-	endoplas	phosphati
GI_21361206-S	157.7	295.6	184.7	ITGB4	NM_000213.2		cell	integrin	cell
GI_21361211-S	116.8	122.7	114.7	CTLA4	NM_005214.2	CD152		integral to	immune
GI_21361242-S	2200.3	3369.7	1850.2	HSPA5	NM_005347.2	BIP;MIF2;GRP78	chaperone	endoplas	response
GI_21361243-S	531.9	475.5	430.8	PEX6	NM_000287.2	PAF2;PAF-2;PXAAA1	peroxisom	cytoplasm	protein-
GI_21361251-S	1854.4	1695.6	1717.8	SMC4L1	NM_005496.2	CAPC;CAP-C;hCAP-C	DNA	cytoplasm	mitotic
GI_21361253-S	107.2	116.4	98.7	DNASE1	NM_005223.2	DNL1	endonucle	extracellul	apoptosis
GI_21361257-S	3207	1381.8	1920.9	ARHE	NM_005168.2	RHOE;RND3	Rho small	peripheral	actin
GI_21361259-S	351.6	437.2	356.1	APLP1	NM_005166.2	APLP	amyloid	basement	histogene

GI_21361261-S	109.8	114.4	113.1	PDE1A	NM_005019.2	HCAM1;HSPDE1A	calmoduli		signal
GI_21361267-S	1409.5	1776.7	1086.2	TNIP1	NM_006058.2	VAN;NAF1;ABIN-1;KIAA0113	protein	kinesin	pathogene
GI_21361270-S	149.6	161.9	136.8	MADH9	NM_005905.2	MADH6;SMAD9;SMAD8A;SMAD8B		intracellula	regulation
GI_21361271-S	8132.6	7900.6	6643.3	MLLT1	NM_005934.2	ENL;LTG19	RNA	nucleus	oncogene
GI_21361279-S	1638.8	1651.2	1747.3	TSFM	NM_005726.2	EF-TS;EF-Tsmt	transcripti	mitochond	translation
GI_21361283-S	677.9	747.5	628.9	SMNDC1	NM_005871.2	SMNR;SPF30	pre-mRNA	spliceoso	induction
GI_21361284-S	739.6	811.1	520.4	RCL1	NM_005772.2	RNAC;RPCL1	RNA-3'-	nucleolus	biological_
GI_21361288-S	68	69	65.2	PLAA	NM_004253.2	PLAP;PLA2P	phospholi		phospholi
GI_21361291-S	741.5	803.7	771.1	RBL2	NM_005611.2	Rb2;P130	protein	nucleus	oncogene
GI_21361293-S	132.6	166.1	158.9	KLRG1	NM_005810.2	2F1;MAFA;MAFAL;MAFA-L;MAFA-2F1	lectin [goid	integral to	cell
GI_21361295-S	134.5	161.6	147.2	PSG5	NM_002781.2	FL-NCA-3	plasma	extracellul	pregnancy
GI_21361297-S	99.8	99.7	88.1	ELA3A	NM_005747.2	ELA3	pancreatic		cholestero
GI_21361299-S	231.4	254.4	220.1	LIM2	NM_030657.2	MP19	structural	integral to	intercellula
GI_21361301-S	105.2	118.8	101.9	SERPINA4	NM_006215.2	KAL;KST;PI4;KLST;kallistatin	protein		
GI_21361305-S	171.5	211.4	192.1	NTRK2	NM_006180.2	TRKB	neurotrop	integral to	transmem
GI_21361307-S	101.8	102.4	90.3	PDE6C	NM_006204.2	PDEA2	cGMP-	membran	vision
GI_21361309-S	187.6	157.3	124.7	IFI44	NM_006417.2	p44;MTAP44	antiviral	cytoplasm	response
GI_21361321-S	200.1	221.4	204.5	TUBB5	NM_006087.2		structural	cytoskelet	
GI_21361323-S	1387.6	1620.7	1129	NDUFV3	NM_021075.2		NADH	NADH	mitochond
GI_21361328-S	98.2	97.4	106.1	RGR	NM_002921.2		G-protein	integral to	vision
GI_21361330-S	478.2	611.4	508	CPS1	NM_001875.2		carbamoyl-	mitochond	urea cycle
GI_21361335-S	863.2	976.6	990.9	DUT	NM_001948.2	dUTPase	dUTP	mitochond	nucleobas
GI_21361338-S	121.9	127.1	134.8	ELAVL4	NM_021952.2	HUD;PNEM	mRNA 3'		RNA
GI_21361339-S	794.5	667.1	832.6	GSK3B	NM_002093.2		glycogen		glycogen
GI_21361347-S	1901.2	1593.7	1357.8	SDCCAG16	NM_006649.2	NY-CO-16	tumor		
GI_21361349-S	3410	2221.1	2105.8	SDCCAG3	NM_006643.2	NY-CO-3	tumor		
GI_21361351-S	153.8	165.9	163.8	IMP-1	NM_006546.2	IMP1;CRDBP;CRD-BP;VICKZ1	RNA	cytoplasm	translation
GI_21361362-S	511.9	386.4	320.4	RALBP1	NM_006788.2	RIP;RIP1;RLIP76	GTPase	membran	chemotaxi
GI_21361365-S	1220	1109.3	1278.5	IFRD2	NM_006764.2	SM15;IFNRP;SKMc15	molecular	cellular_co	cell
GI_21361367-S	1482.3	1728.9	875.3	PYCS	NM_002860.2	GSAS;P5CS	N-acetyl-	mitochond	proline
GI_21361371-S	142.2	170.8	156.2	SLC14A2	NM_007163.2	UT2;UTR;HUT2	urea	integral to	urea
GI_21361373-S	519.8	540.5	449.1	SP140	NM_007237.2	LYSP100-A;LYSP100-B	transcripti	nuclear	defense
GI_21361377-S	329.1	368.7	250.1	SARDH	NM_007101.2	SAR;SDH;SARD;DMGDHL1	sarcosine	mitochond	
GI_21361379-S	1380.6	1976.8	1659.6	EAP30	NM_007241.2		RNA		regulation
GI_21361381-S	1179	1081.9	1037.9	POMT1	NM_007171.2	RT	mannosylt	integral to	O-linked
GI_21361386-S	119.5	135.7	131	RXRG	NM_006917.2	RXRC;NR2B3	retinoid-X	nucleus	regulation
GI_21361387-S	172.2	195.8	155.5	SMT3H2	NM_006937.2	HSMT3;SMT3B;SUMO-2			small
GI_21361391-S	81.9	89.1	99.3	PSG1	NM_006905.2	SP1;B1G1;PBG1;CD66f;PSBG1;PSGGA	plasma	extracellul	pregnancy
GI_21361393-S	112.6	116.3	120.7	AP4S1	NM_007077.2	AP47B;CLA20;CLAPS4	vesicle	coated	nonselecti
GI_21361396-S	784	776.6	966.3	RACGAP1	NM_013277.2	ID-GAP;MgcRacGAP			intracellula
GI_21361404-S	644.4	366	824.5	RGS17	NM_012419.3	RGSZ2;RGS-17	signal	membran	signal
GI_21361406-S	1874.5	2111.7	2287.8	HSPBP1	NM_012267.2		enzyme		protein
GI_21361410-S	364.3	564	619.7	HBP1	NM_012257.2		DNA		regulation
GI_21361412-S	142.5	173.2	150.5	DNAJB5	NM_012266.2	Hsc40	heat		response

GI_21361426-S	108.9	110.8	100.3	E2IG5	NM_014367.2				
GI_21361430-S	965.4	898.6	940.9	RCD-8	NM_014329.2	Ge-1	molecular	nucleus	biological_
GI_21361432-S	376.6	322.5	372.3	PLK4	NM_014264.2	SAK;STK18	protein		protein
GI_21361439-S	1138.3	417.8	333.7	RAB3IL1	NM_013401.2				
GI_21361441-S	829.8	1065.6	1058.3	C18orf8	NM_013326.2	MIC1;HsT2591			
GI_21361446-S	89.5	100.8	82.2	RGS1	NM_002922.2	1R20;BL34;IER1;IR20	GTPase	plasma	G-protein
GI_21361448-S	484.6	461.4	459.7	SLC2A8	NM_014580.2	GLUT8;GLUTX1	glucose	integral to	glucose
GI_21361451-S	383.1	533.9	395.7	GLS	NM_014905.2	GLS1;KIAA0838	glutamina	mitochond	glutamine
GI_21361453-S	1468	1119.3	1088.7	PYCR2	NM_013328.2	P5CR2	pyrroline-5-		proline
GI_21361457-S	502.1	563.1	396.1	ARHGEF17	NM_014786.2	TEM4;KIAA0337;P164RHOGEF;p164-			
GI_21361461-S	826.3	1288.5	1654.9	EHD2	NM_014601.2		nucleic	nucleus	
GI_21361467-S	1461.7	1385.9	1328.6	DKFZP586L0	NM_015462.2				
GI_21361469-S	741.3	742	756.7	DC8	NM_015471.2	DKFZP566O1646			
GI_21361471-S	2344.8	1344.2	1102.1	NEDD4L	NM_015277.2	RSP5;KIAA0439;hNedd4-2			
GI_21361481-S	284.5	278	248.4	RWDD3	NM_015485.2	DKFZP566K023			
GI_21361484-S	437.8	541.9	510.1	DKFZP434P1	NM_015527.2		catalytic		metabolis
GI_21361486-S	173	164.6	155.7	DKFZP434D1	NM_015595.2	SGEF;CSGEF			
GI_21361488-S	330.5	342.8	310.4	DKFZP566F2	NM_015630.2				
GI_21361494-S	287.2	261.9	240	PTD012	NM_014039.2				
GI_21361498-S	642.9	758.3	686.3	SENP3	NM_015670.2	SSP3;SMT3IP1;DKFZP586K0919	cysteine-	nucleus	proteolysis
GI_21361500-S	175.1	204.1	186.1	LR8	NM_014020.2				histogene
GI_21361502-S	537	658.1	416.8	SLC35B3	NM_015948.2	CGI-19;C6orf196;dJ453H5.1			
GI_21361508-S	442.8	662	764.7	RAB4B	NM_016154.2		GTP	cellular_co	small
GI_21361510-S	222.2	273.9	257.9	LOC51061	NM_015914.2		electron		electron
GI_21361512-S	283.6	287.7	379.3	CGI-14	NM_015944.2				
GI_21361518-S	3297.5	4349.3	5343.8	ADIPOR1	NM_015999.2	CGI-45	receptor	integral to	fatty acid
GI_21361522-S	612.2	551.2	599.2	MGC14560	NM_016301.2	MGC32810	ATP		
GI_21361524-S	565.3	592	584.6	CGI-41	NM_015997.2				
GI_21361528-S	193.7	207.5	209.5	LOC51136	NM_016125.2				
GI_21361533-S	6629.1	7612.8	6776.6	C13orf12	NM_015932.2	HSPC014			
GI_21361534-S	3176.3	3395.8	3030.5	HSPC138	NM_016401.2	HSPC179			
GI_21361536-S	875.4	1203.2	1165.2	C14orf100	NM_016475.2	HSPC213			
GI_21361540-S	118.4	114.6	109.8	HYPK	NM_016400.2	HSPC136	protein		
GI_21361544-S	1976.6	1928.2	1877.6	NIPA	NM_016478.2	HSPC216			
GI_21361550-S	495.1	562.4	725	SLC4A2	NM_003040.2	AE2;HKB3;BND3L;NBND3;EPB3L1	anion	membran	anion
GI_21361554-S	101.5	108.2	94.5	TNNI1	NM_003281.2		tropomyos	troponin	regulation
GI_21361560-S	496.8	664.6	684.9	ZNF35	NM_003420.2	HF10;HF.10	transcripti	nucleus	regulation
GI_21361562-S	135.3	198.6	111.1	SLC7A7	NM_003982.2	LPI;LAT3;Y+LAT1;y+LAT-1	basic	integral to	small
GI_21361564-S	8842.4	10272	8628	ATP5F1	NM_001688.2		hydrogen-	mitochond	proton
GI_21361570-S	157.7	192.3	154.1	CD48	NM_001778.2	BCM1;BLAST;hCD48;mCD48;BLAST1;SLAM	lymphocyt	integral to	defense
GI_21361572-S	605.6	874.7	487	CHN1	NM_001822.2	CHN;ARHGAP2;RHOGAP2	SH3/SH2		intracellula
GI_21361575-S	451.2	449.3	429.5	PS1D	NM_016505.2	pNO40;HSPC251			
GI_21361580-S	142.7	164	168.7	SLC6A13	NM_016615.2	GAT2;GAT-2			
GI_21361584-S	2093.3	2391.8	1390.2	KIAA0992	NM_016081.2	SIH002;CGI-151			amino

GI_21361594-S	112.1	102.8	87.8	SLCO1C1	NM_017435.2	OATP1;OATP-F;OATP1C1;SLC21A14	transporte	integral to	ion
GI_21361595-S	3757.8	3381.1	3107.4	FLJ21174	NM_024863.3				
GI_21361597-S	467.4	374.6	354.7	MPP6	NM_016447.2	VAM1;p55T;PALS2;VAM-1	protein	membran	intracellula
GI_21361599-S	155.8	132	108.1	SLC37A1	NM_018964.2	G3PP	sugar	integral to	transport
GI_21361603-S	144.4	158.2	119.9	SH3TC1	NM_018986.2	FLJ20356			
GI_21361605-S	3867	3576.8	2379.4	MDS025	NM_021825.3	MDS011			
GI_21361610-S	999.9	1297.9	968.7	CKIP-1	NM_016274.3				
GI_21361611-A	256	283.1	267.1	HTF9C	NM_022727.3	D22S1733E	S-		
GI_21361611-I	225.7	273.2	227.2	HTF9C	NM_022727.3	D22S1733E	S-		
GI_21361613-S	398	478	367	STK11	NM_000455.3	PJS;LKB1	protein		protein
GI_21361614-S	632.7	778.7	647.7	SARA1	NM_020150.3	SAR1;Sara;SAR1A;masra2	GTP	Golgi	small
GI_21361615-S	72.2	90	84.2	CHST8	NM_022467.3		transferas		
GI_21361616-S	141.6	137.3	132.3	FLJ20152	NM_019000.2				
GI_21361618-S	395.3	431.6	497.2	TOLLIP	NM_019009.2	IL-1RAcPIP			signal
GI_21361620-S	1677.7	2863.6	2513.4	PGM1	NM_002633.2		magnesiu	cytoplasm	glucose
GI_21361622-S	137.1	138.6	119.4	FLJ10996	NM_019044.2	MGC13033			
GI_21361628-S	534.8	480.3	384.6	ELP4	NM_019040.2	PAXNEB;PAX6NEB;C11orf19;FLJ20498			
GI_21361630-S	1058.8	959	727.2	RRN3	NM_018427.2	DKFZp566E104	RNA		transcripti
GI_21361632-S	118.3	132.7	120	FLJ20331	NM_017768.3		acid		
GI_21361636-S	404.1	494	684.3	TBC1D13	NM_018201.2	FLJ10743			
GI_21361644-S	377.6	582.8	627.9	DLG7	NM_014750.3	DLG1;HURP;KIAA0008	molecular	cellular_co	biological_
GI_21361646-S	2771	4340.1	2793.4	AHCYL1	NM_006621.3	DCAL;IRBIT;XPVKONA	adenosylh		one-
GI_21361648-S	277.7	324	306.1	OBDPF	NM_017711.2	GDE3;FLJ20207			
GI_21361652-S	584.4	530	559	FLJ20364	NM_017785.2				
GI_21361654-S	107.2	117.4	109.9	APIN	NM_017855.2	FLJ20513			
GI_21361656-S	5251.6	8007.2	6069.1	GRP58	NM_005313.3	P58;ERp57;ERp60;ERp61;GRP57;PI-	phospholi	endoplas	protein-
GI_21361658-S	250.7	303.6	313.3	IPO9	NM_018085.3	Imp9;FLJ10402			
GI_21361660-S	141.1	163.4	146.5	COMMD4	NM_017828.2	FLJ20452			
GI_21361662-S	199.8	195.3	189.3	FLJ20546	NM_017872.2		signal	heterotrim	G-protein
GI_21361667-S	460.8	474.8	482.5	VCY2IP1	NM_018174.3	C19ORF5;FLJ10669;VCY2IP-1			
GI_21361673-S	220.4	293.7	262.8	ZCWPW1	NM_017984.2	FLJ10057			
GI_21361675-S	173.5	209.9	178.4	FEZL	NM_018008.2	TOF;FKSG36;FLJ10142			
GI_21361681-S	2552.4	2789.3	2414	TAX1BP1	NM_006024.4	T6BP;TXBP151	apoptosis		anti-
GI_21361683-S	252.3	209.7	243.8	ECGP	NM_018025.2	FLJ10206;FLJ38686	nucleic	intracellula	
GI_21361685-S	134.6	126.8	131.7	FLJ10292	NM_018048.2			nucleus	sex
GI_21361686-S	262.8	336.7	278.9	FLJ10300	NM_018051.2				
GI_21361690-S	135.6	126.8	86.1	TRPM8	NM_024080.3	TRPP8;LTRPC6;MGC2849			
GI_21361692-I	773	628.4	717.9	SLC6A15	NM_018057.2	V7-3;NTT73;hv7-3;FLJ10316			
GI_21361696-I	699.4	764.6	929.5	C14orf130	NM_018108.2	MGC9518;FLJ10483	ubiquitin-		ubiquitin
GI_21361698-S	2408.6	1853.5	1964.7	SPHK2	NM_020126.3		diacylglyc	cytosol	anti-
GI_21361700-S	99.9	99.9	84.4	ZDHHC4	NM_018106.2	ZNF374;FLJ10479		integral to	
GI_21361703-S	374.8	349.7	341	FLJ10486	NM_018109.2		nucleic		
GI_21361708-S	2633.9	2416.2	1802.9	P15RS	NM_018170.2	FLJ10656	kinase		
GI_21361710-S	261.7	279.3	255.2	HCNGP	NM_013260.3				

GI_21361711-I	141.9	162.5	150.1	USP2	NM_004205.3	USP9;UBP41	cysteine-		deubiquiti
GI_21361719-S	313.3	454.5	406.2	TMEM19	NM_018279.2	FLJ10936			
GI_21361721-S	169.1	204.9	192.1	KIF13A	NM_022113.3	bA500C11.2			
GI_21361723-S	1171.5	1159.5	927.5	NXT2	NM_018698.3	P15-2	protein	nucleus	protein-
GI_21361727-S	164	200.2	181.7	FLJ10979	NM_018289.2				
GI_21361729-S	508.3	670.5	587.9	FLJ10986	NM_018291.2				carbohydr
GI_21361733-S	1839.9	1489.7	1593.9	FLJ10081	NM_017991.3	KIAA1310			
GI_21361735-S	1140.7	1117.1	1008.1	RICH1	NM_018054.3	NADRIN;FLJ10308;FLJ13219			
GI_21361737-S	149	138.2	146.7	ARHT1	NM_018307.2	MIRO-1;FLJ11040			
GI_21361740-S	1952.8	1857.5	1903.5	C6orf55	NM_016485.3	My012;HSPC228			
GI_21361742-S	86.5	90.6	80.2	NIPSNAP3B	NM_018376.2	FLJ11275			
GI_21361744-S	586.7	673.8	571.9	STRBP	NM_018387.2	SPNR;MGC3405;FLJ11307;FLJ14223;FLJ14			
GI_21361746-S	543.1	605	657.3	DKFZp762E1	NM_018410.2				
GI_21361756-S	364.8	325.2	321.4	PRO0971	NM_018569.2				
GI_21361758-S	148	187.6	168.1	MTMR8	NM_017677.2	FLJ20126			
GI_21361764-S	848	822.3	912.1	H17	NM_017547.2		oxidoredu		electron
GI_21361765-S	584.8	541.4	366.5	FLJ20531	NM_017865.2				
GI_21361767-S	144.9	1093.3	319.4	GLUL	NM_002065.3	GLNS	glutamate-		glutamine
GI_21361768-S	264.8	310.1	275.7	CFLAR	NM_003879.3	CASH;FLIP;MRIT;CLARP;FLAME;Casper;FL	apoptosis		induction
GI_21361770-S	777.3	617.3	645.9	FLJ20477	NM_017837.2				
GI_21361775-S	363.7	467.6	467.6	C14orf108	NM_018229.2	FLJ10813			
GI_21361780-S	1781.8	1941.8	1935.8	FLJ10350	NM_018067.2				
GI_21361782-S	94.3	90.7	89.8	SRrp35	NM_080743.2		nucleic	nucleus	regulation
GI_21361788-S	239.3	204.9	257	ZNF83	NM_018300.2	HPF1;FLJ11015			
GI_21361790-S	2116.8	1718.5	1968.7	FLJ20257	NM_019606.3		methyltran		
GI_21361793-S	748.7	852.6	830.3	TIP120A	NM_018448.2	CAND1;TIP120;KIAA0829			
GI_21361797-S	108.3	112.1	111.5	FAM3B	NM_058186.2	2-21;ORF9;PRED44;C21orf11;C21orf76	cytokine	extracellul	insulin
GI_21361804-S	224.4	249.7	360.2	MDS028	NM_018463.2				
GI_21361808-S	162.9	168.6	168.3	LOC56267	NM_019610.2		nucleic		
GI_21361810-S	177.9	214.2	143.2	C21orf51	NM_058182.2		molecular	cellular_co	biological_
GI_21361811-I	234.4	295.8	256.1	EPB41L4B	NM_019114.2	CG1;EHM2;DKFZp761N1814	structural	cytoskelet	cell shape
GI_21361813-S	451.8	557.2	461.8	RP4-622L5	NM_019118.2	dJ622L5.7			
GI_21361815-S	83.2	96.1	95.8	CNGB3	NM_019098.2	ACHM3	intracellula	integral to	vision
GI_21361817-S	368.3	390.5	339.5	SBBI26	NM_018846.2				
GI_21361819-S	328.7	382.3	388.7	FLJ21827	NM_020153.2				
GI_21361821-S	5426.4	6533.8	5911.9	GRIM19	NM_015965.3		NADH	mitochond	apoptosis
GI_21361824-S	121.5	134.3	147.5	C11ORF4	NM_020155.2				
GI_21361826-S	1035.3	899.9	962	METTL3	NM_019852.2	M6A;Spo8	methyltran	nucleus	RNA
GI_21361830-S	104.7	100.6	101.4	PARD3	NM_019619.2	ASIP;PAR3;SE2-5T2;SE2-5L16;SE2-		tight	asymmetri
GI_21361832-S	128.2	143.6	148	TRPV5	NM_019841.3	CAT2;ECAC1	calcium	integral to	cation
GI_21361833-I	84.7	91.8	94.5	SLC22A17	NM_020372.2	BOCT;BOIT;hBOIT	transporte	integral to	transport
GI_21361836-S	1217.1	1183.4	999.6	HT014	NM_020362.2				
GI_21361838-S	100.3	92.1	93.4	RPGRIP1	NM_020366.2	LCA6;RGI1;CORD9;RGRIP			
GI_21361844-S	289.7	338.9	297.9	PGLYRP2	NM_052890.2	tagL;PGRPL;PGRP-L;PGLYRPL;TAGL-	peptidogly	membran	detection

GI_21361846-S	241.8	270.8	230.6	CA10	NM_020178.2	CARPX;CA-RPX;HUCEP-15	carbonate	cellular_co	brain
GI_21361850-S	1242	1132	1008.2	LOC57117	NM_020395.2		electron		electron
GI_21361852-S	95	93.1	93.9	PLXDC1	NM_020405.3	TEM3;TEM7	receptor	membran	developm
GI_21361855-S	193.1	193.2	178.9	IDI2	NM_033261.2	IPPI2	isopenten	peroxisom	isoprenoid
GI_21361860-S	117.3	115.4	126.7	FANCD2	NM_033084.2	FA4;FAD;FACD;FAD2;FA-D2;FANCD			
GI_21361862-S	91	92.6	89.5	STN2	NM_033104.2	STNB		membran	endocytosi
GI_21361864-S	136.7	170.5	160.9	NX17	NM_020665.2	NX-17			
GI_21361865-I	499.6	738	569.7	ZNF3	NM_032924.2	A8-			
GI_21361869-A	555.1	584.6	529.5	C11orf17	NM_020642.2	BCA3			
GI_21361869-I	1187.8	1147.7	1101.7	C11orf17	NM_020642.2	BCA3			
GI_21361878-S	110.8	124.5	114.7	NGB	NM_021257.2		globin	hemoglobi	oxygen
GI_21361882-S	130.5	162.9	132.7	IGSF4B	NM_021189.2	BIgR;NECL1;TSLL1;FLJ10698	receptor		
GI_21361883-S	1148.8	1164.7	1139.1	RAB2B	NM_032846.2	FLJ14824			
GI_21361885-S	73.6	90.6	83.3	FLJ14834	NM_032849.2				
GI_21361889-S	1480.5	1001.3	1003.8	KLHL12	NM_021633.2	C3IP1	protein		
GI_21361890-S	119.1	169.9	206.6	FLJ20967	NM_022071.2	SH2A			intracellula
GI_21361894-S	808.5	1046.4	796.5	FKBP10	NM_021939.2	FKBP65;hFKBP65;FLJ22041			
GI_21361898-S	121.4	113.2	110.9	SLC5A7	NM_021815.2	CHT;CHT1;hCHT	transporte	membran	transport
GI_21361899-S	308.1	424.9	365.4	MDS018	NM_021823.2				
GI_21361903-S	2263.1	2086.7	1816.1	ELOVL5	NM_021814.2	HELO1;DJ483K16.1		integral to	
GI_21361906-S	147.8	102.3	108.4	ATP10A	NM_024490.2	ATPVA;ATPVC;ATP10C;KIAA0566	ATP	integral to	cation
GI_21361907-S	323.9	320.1	285.1	GBL	NM_022372.2				
GI_21361911-S	663.9	1083.4	673.2	DNAJC1	NM_022365.2	HTJ1;DNAJL1	chaperone	microsom	negative
GI_21361913-S	151.7	157.3	139.4	FLJ12287	NM_022367.2		receptor	integral to	developm
GI_21361917-S	698.5	1724.8	737.1	LEPRE1	NM_022356.2	GROS1			
GI_21361921-S	80.3	86.9	83.6	SAMSN1	NM_022136.2	HACS1			
GI_21361926-S	247.7	295.4	252.4	C6orf31	NM_030651.2	NG5		integral to	
GI_21361928-S	1405.4	1359.5	1104.5	SLC38A1	NM_030674.2	ATA1;NAT2;SAT1;SNAT1	amino	membran	amino
GI_21361930-S	108.5	132.6	110.2	C6orf148	NM_030568.2	MGC10818;bA257K9.4			
GI_21361932-S	94	101.5	93.2	CDA08	NM_030790.2	TIP			
GI_21361936-S	1787.9	1775.1	1646.9	MGC10772	NM_030567.2				
GI_21361938-S	315.4	404.3	337.9	SLC19A3	NM_025243.2		folic acid	integral to	transport
GI_21361941-S	694.9	764.7	533.6	MGC11335	NM_030819.2		oxidoredu		electron
GI_21361945-S	128.9	143.7	137.4	TNKS2	NM_025235.2	TNKL;TANK2	NAD ADP-	telomere	telomeras
GI_21361946-S	112.7	125.9	111.7	STMN4	NM_030795.2	RB3		kinesin	intracellula
GI_21361948-S	226.5	281	251.9	C19orf27	NM_031213.2	MGC5244	catalytic	membran	transport
GI_21361950-S	275.4	343.3	291.9	PRO2730	NM_025222.2				
GI_21361953-S	222.9	206.4	171.7	DKFZP564A	NM_030954.2				
GI_21361958-S	338.3	407.3	347.7	SLC35F5	NM_025181.2	FLJ22004			
GI_21361962-S	532.6	470.7	382.6	PNAS-131	NM_031446.2	PNAS-124			
GI_21361964-S	228.4	266.4	236.1	FLJ22944	NM_025145.2	FLJ36006			
GI_21361968-S	297.2	184.9	214.6	LAK	NM_025144.2	FLJ22670;KIAA1527			
GI_21361976-A	109.8	119.5	114.2	TRPM3	NM_024971.2	MLSN2;LTRPC3;FLJ11726;KIAA1616			
GI_21361976-I	91.7	113.9	100.1	TRPM3	NM_024971.2	MLSN2;LTRPC3;FLJ11726;KIAA1616			

GI_21361978-S	580.2	595.9	333.3	BOMB	NM_024949.2	FLJ22029			
GI_21361980-S	98.6	112.6	116.2	FLJ11467	NM_024963.2				
GI_21361986-A	118.4	139.3	134.6	ARG99	NM_031920.2				
GI_21361986-I	116.3	130.1	108.8	ARG99	NM_031920.2				
GI_21361994-S	386.1	485.1	482	ADCK4	NM_024876.2	FLJ12229			
GI_21361999-S	184.5	228	186	TNIP3	NM_024873.2	LIND;FLJ21162			
GI_21362001-S	145.7	185.3	145.5	FLJ13840	NM_024746.2				
GI_21362002-S	369.5	397.4	374.2	FLJ13590	NM_024840.2				
GI_21362004-S	397.9	367.5	291.9	MGC15419	NM_024735.2	MGC9527;FLJ22477;DKFZP434B027			
GI_21362006-S	131.2	135	124.5	B29	NM_031939.2				
GI_21362011-S	467.2	458.7	407.5	FLJ22625	NM_024715.2		electron		electron
GI_21362013-S	143.5	127.7	127.8	FLJ22344	NM_024717.2				
GI_21362021-S	791.1	710.5	508.4	FLJ23233	NM_024691.2				
GI_21362023-S	596.2	654.7	610.7	FLJ12436	NM_024661.2				
GI_21362025-S	104.6	99.9	107.1	FLJ22938	NM_024676.2				
GI_21362027-S	955.3	1131.9	631	ZCWCC2	NM_024657.2	FLJ11565			
GI_21362039-S	96.6	97.4	96.2	RIC3	NM_024557.2	FLJ11608			
GI_21362043-S	2865.8	3228.1	3994.8	C9orf89	NM_032310.2	MGC11115;bA370F5.1			
GI_21362045-S	847.9	625.1	679.7	C13orf7	NM_024546.2	FLJ13449			
GI_21362049-S	482.2	496.8	582.7	MGC12981	NM_032357.2				
GI_21362051-I	94.5	107.6	91.5	CHST5	NM_024533.2	FLJ22167	sulfotransf	integral to	protein
GI_21362053-S	415.1	563.8	570.4	MGC4368	NM_024510.2				
GI_21362055-S	101.4	114.6	124	AFURS1	NM_024524.2		magnesiu	integral to	cation
GI_21362059-S	607.7	544.1	453.4	MGC13114	NM_032366.2		DNA	nucleus	regulation
GI_21362065-S	132	143.4	147.7	MGC3329	NM_024086.2				
GI_21362069-S	1026.5	1104.8	1053.9	C7orf26	NM_024067.2	MGC2718			
GI_21362071-S	148.7	179.4	164	C22orf23	NM_032561.2	EVG1;FLJ32787	molecular	cellular_co	biological_
GI_21362077-S	116	115.9	133.1	FLJ12644	NM_023074.2		nucleic	intracellula	regulation
GI_21362081-S	106.5	113	105.3	NYD-SP20	NM_032598.2				
GI_21362082-S	373.7	368.7	314.5	ANKRA2	NM_023039.2	ANKRA	low-	membran	biological_
GI_21362085-S	235.4	227.4	211.3	FLJ12572	NM_022905.2	FLJ12939			
GI_21362087-S	561.2	523.7	604.4	FLJ13912	NM_022770.2				
GI_21362093-S	464	453.1	534.3	FLJ12484	NM_022767.2	FLJ12562			
GI_21362095-S	4703.7	3955.4	2300.8	C20orf81	NM_022760.3	FLJ22376;bA12M19.1;DKFZp547L054			
GI_21362099-S	182.9	279.8	234.2	ELOVL4	NM_022726.2	ADMD;STGD2;STGD3	G-protein	endoplas	vision
GI_21362100-S	373.1	284.5	251.4	SMURF2	NM_022739.2		ubiquitin-	nucleus	ubiquitin
GI_21362101-S	311.6	389.9	346.7	FLJ13576	NM_022484.2				
GI_21362103-S	3504.4	5262.8	4036.8	TXNL5	NM_032731.2	TRP14;MGC14353	electron		electron
GI_21362104-S	177.8	210.9	197.6	FLJ12587	NM_022480.2		protein		
GI_21362109-S	280.5	308.2	274.5	TPK1	NM_022445.2	HTPK1	thiamin		thiamin
GI_21362111-S	1194	1149.5	739.7	C7orf2	NM_022458.2	ACHP;LMBR1;FLJ11665			
GI_21389306-S	124.5	143.4	122.8	FLJ32312	NM_144709.1				
GI_21389314-S	896.1	976.2	842.8	SLC25A1	NM_005984.1	CTP;SLC20A3	sodium:di	mitochond	mitochond
GI_21389332-S	223.7	246	218.4	FLJ32334	NM_144565.1				

GI_21389334-S	1696.2	1393.8	2270.4	C14orf9	NM_144568.1	MGC26684;DKFZp434M0519		integral to	
GI_21389336-S	969.4	660	711.8	RPIA	NM_144563.1	RPI	ribose-5-	intracellula	pentose-
GI_21389338-S	212.9	221.5	211.3	NEXN	NM_144573.1	NELIN;nexilin			
GI_21389342-S	108.1	111.1	89.1	CAPN13	NM_144575.1		calpain	intracellula	proteolysis
GI_21389346-S	282.5	349.9	298	FLJ32926	NM_144577.1				
GI_21389350-S	139.2	174.5	222.5	SFXN5	NM_144579.1	BBG-TCC	cation	membran	cation
GI_21389358-S	94.4	93.9	88.5	FLJ30525	NM_144584.1				
GI_21389360-S	774.8	647.6	404.9	FLJ25436	NM_144581.1				
GI_21389364-S	112.4	128.5	118.7	ATP6V1C2	NM_144583.1	VMA5;ATP6C2	hydrogen-		proton
GI_21389370-S	331.8	322.8	342.3	MGC22805	NM_144590.1				
GI_21389372-S	137.2	152.1	117.9	C10orf87	NM_144587.1	FLJ25359			
GI_21389374-A	107.5	107.9	117.2	C10orf6	NM_144592.1	FLJ10512;FLJ25012			
GI_21389374-I	160.7	187.1	167	C10orf6	NM_144592.1	FLJ10512;FLJ25012			
GI_21389378-S	99.5	95.6	101.9	FLJ32942	NM_144594.1				
GI_21389380-S	550.7	514.6	466.9	C10orf32	NM_144591.1	FLJ40752;MGC27171			
GI_21389382-I	86.1	88	81.1	TTC8	NM_144596.1	BBS8			
GI_21389384-S	247.7	238.4	212.2	RHEBL1	NM_144593.1	FLJ25797;MGC34869	small		small
GI_21389390-S	1462.8	1165.3	1061.9	FLJ31153	NM_144600.1				
GI_21389392-S	427.4	385.3	389.8	MGC29937	NM_144597.1				
GI_21389406-S	462.3	536.2	513.8	FLJ32384	NM_144608.1				
GI_21389408-S	145.6	168	153.8	FLJ25410	NM_144605.1		GTP		cell cycle
GI_21389410-S	105.9	114.7	104.3	FLJ25006	NM_144610.1		copper ion		electron
GI_21389416-S	734.3	917.9	528	FLJ31795	NM_144609.1				
GI_21389426-S	1273.1	1524	1363.2	MGC29891	NM_144618.1				
GI_21389428-S	145.2	159.3	153.5	MGC23244	NM_144615.1		DNA	nucleus	regulation
GI_21389430-S	96.4	129.8	112.7	MGC14816	NM_144620.1				
GI_21389432-S	213.6	255.8	209.1	FLJ32389	NM_144617.1		heat		
GI_21389434-S	177.9	200.2	162.5	FLJ32934	NM_144622.1				
GI_21389438-A	167.8	198.1	193.4	KIS	NM_144624.1		cAMP-	cytoplasm	peptidyl-
GI_21389442-S	94	110.2	107.3	MGC17299	NM_144626.1				
GI_21389444-S	101.7	108	93.9	FLJ32784	NM_144623.1				
GI_21389446-S	657.4	531.3	279.8	C20orf140	NM_144628.1	dJ852M4.2		integral to	
GI_21389448-S	102.4	94.3	87.6	FLJ32978	NM_144625.1				
GI_21389452-S	181.7	208.6	210.4	SSTK-IP	NM_144627.1	MGC26877			
GI_21389456-S	259.4	332.8	277.9	C2orf11	NM_144629.1	FLJ30574			
GI_21389466-S	152.6	174.9	156.5	FLJ31300	NM_144639.1		lyase		histidine
GI_21389468-S	2111.1	1702	1672	CHCHD4	NM_144636.1	FLJ31709			
GI_21389470-S	729.7	755.2	556.9	FLJ32332	NM_144641.1	PP2C{eta}			
GI_21389472-S	252.9	526.1	454.7	MGC29956	NM_144638.1				
GI_21389474-S	154.9	141.3	145.6	FLJ30655	NM_144643.1				
GI_21389478-S	98.4	100.7	100.7	MGC26744	NM_144645.1				
GI_21389482-S	112.6	122.9	119.6	FLJ32786	NM_144648.1				
GI_21389490-S	102.2	91	87.5	FLJ32954	NM_144713.1				
GI_21389492-S	112.2	118	104.2	FLJ25449	NM_144714.1		catalytic		

GI_21389496-S	867.9	854.7	887.8	MGC23918	NM_144716.1				
GI_21389502-S	143.8	158.1	157.1	FLJ25467	NM_144719.1				
GI_21389504-S	86	84.1	74.9	MARLIN1	NM_144720.1	FLJ31564			
GI_21389510-S	871.8	864.7	978.3	FLJ31121	NM_144723.1		RNA	nucleus	
GI_21389514-S	972.1	1497.9	1027.7	FLJ31951	NM_144726.1				
GI_21389516-S	104.2	108.8	93.6	CRYGN	NM_144727.1				
GI_21389518-S	183	189.9	161.7	ADHFE1	NM_144650.1	ADH8;FLJ32430	iron ion		metabolis
GI_21389522-S	592.9	377	268.7	FLJ25409	NM_144652.1				
GI_21389524-S	716.9	398.3	452.9	FLJ33069	NM_144649.1				
GI_21389526-S	616.7	857.3	788.1	MGC29761	NM_144654.1				
GI_21389528-S	164.9	132.9	158.7	FLJ25471	NM_144651.1		peroxidas	nucleus	peroxidas
GI_21389534-S	275.3	290.8	235.2	TCP10L	NM_144659.1	PRED77		kinesin	
GI_21389542-S	406.3	425.5	363.3	1-Nov	NM_144663.1				
GI_21389544-S	100.9	95.7	94	SAMD8	NM_144660.1	FLJ25082			
GI_21389548-S	92.4	97.3	93.1	MGC26605	NM_144662.1		peptidase	cytosol	ubiquitin-
GI_21389550-S	135	159.2	133.5	FLJ32894	NM_144667.1				
GI_21389554-S	353.7	420.1	261.3	FLJ32752	NM_144666.1				
GI_21389558-S	207.5	277.6	235.9	FLJ31978	NM_144669.1				biosynthes
GI_21389560-S	114.1	119.6	112.6	FLJ25179	NM_144670.1		endopepti		
GI_21389568-S	129.4	154.6	116.1	FLJ32871	NM_144674.1			microtubul	microtubul
GI_21389570-S	98.4	113.6	105.9	MGC18079	NM_144675.1				
GI_21389572-S	93.8	99.4	85	MGC23911	NM_144676.1		protein	membran	intracellula
GI_21389576-S	968.1	894.8	1072.3	FLJ31528	NM_144679.1				
GI_21389578-S	91.4	94.5	89	FLJ32734	NM_144681.1				
GI_21389584-S	311.1	318.5	287.7	MGC32104	NM_144684.1		nucleic	nucleus	regulation
GI_21389588-S	475.9	476	410	TMC4	NM_144686.1	MGC39329			
GI_21389592-S	99.7	108.7	99.1	ZNF582	NM_144690.1	FLJ30927	nucleic	nucleus	regulation
GI_21389596-S	276.2	342.8	337.5	LOC148137	NM_144692.1				
GI_21389598-S	107.9	112.6	137	ZNF570	NM_144694.1	FLJ30791	nucleic	nucleus	regulation
GI_21389600-S	143.4	148.2	142.3	FLJ32421	NM_144695.1				
GI_21389608-S	115.1	119.6	131	C20orf40	NM_144703.1	FT005;FLJ25473;bA11M20.3			
GI_21389614-S	113.1	116.1	106.2	FLJ32884	NM_144702.1				
GI_21389616-S	101.8	121.6	98.7	FLJ30473	NM_144704.1		disulfide		electron
GI_21389622-S	118.1	155.3	133	PROM2	NM_144707.1	PROM-2			
GI_21396476-A	94.8	99.2	86.2	MEOX1	NM_013999.2	MOX1			developm
GI_21396477-I	123.1	107.9	104	MEOX1	NM_004527.2	MOX1			developm
GI_21396478-S	131.3	155.5	145.5	MEOX2	NM_005924.2	GAX;MOX2	transcripti	nucleus	circulation
GI_21396479-A	1392	1501	1762.2	RALY	NM_007367.2	P542	heterogen	ribonucleo	
GI_21396481-S	375.2	606.7	389	HIST1H2AC	NM_003512.3	H2A/l;H2AFL;dJ221C16.4	DNA	chromoso	nucleoso
GI_21396482-S	158.7	192.3	172.7	HIST1H2BF	NM_003522.3	H2B/g;H2BFG			
GI_21396483-S	544.9	792.2	601.1	HIST1H2BE	NM_003523.2	H2B.h;H2B/h;H2BFH;dJ221C16.8	DNA	chromoso	nucleoso
GI_21396485-I	5287.5	6005.5	5399.3	PRO1853	NM_018607.4				
GI_21396488-S	1195.5	882.4	881	PRSS15	NM_004793.2	LON;LONP;hLON;LonHS;MGC1498	ATP-	mitochond	proteolysis
GI_21396490-S	112.6	109.6	106.2	PRSS16	NM_005865.2	TSSP	serine-	cellular_co	protein

GI_21396492-A	849.6	837.3	943.2	OCRL	NM_001587.3	LOCR;OCRL1;INPP5F	phosphoin	Golgi	lipid
GI_21396495-I	282.6	349.3	324.1	OGG1	NM_016819.2	HMMH;MUTM;OGH1;HOGG1	purine-	nucleoplas	base-
GI_21396497-S	90.8	94.4	78.7	HIST1H3F	NM_021018.2	H3/i;H3FI			
GI_21396498-S	105.4	101.3	104.2	HIST1H3B	NM_003537.3	H3/l;H3FL			
GI_21396499-S	341.9	284.5	294	HIRIP3	NM_003609.2			nucleus	chromatin
GI_21396501-S	102.5	81	85.9	ELSPBP1	NM_022142.3	E12;HE12			
GI_21396502-S	90.1	93.9	127.2	EPHB1	NM_004441.2	ELK;NET;Hek6;EPHT2	transmem	integral to	signal
GI_21426826-S	695.1	800.3	802.4	APOA1BP	NM_144772.1	AIBP	molecular		
GI_21426832-S	113.3	110.3	96.9	RBM11	NM_144770.1				
GI_21426842-S	114.7	124.1	113.4	SMCR5	NM_144774.1				
GI_21426844-S	143.8	154.7	145.9	SMCR8	NM_144775.1				
GI_21450642-S	256.4	342.3	291.8	FLJ23790	NM_144963.1		globin		oxygen
GI_21450644-S	97.9	107.2	110.5	TTC16	NM_144965.1	FLJ32780			
GI_21450646-S	144.9	168.2	148.6	MGC22776	NM_144962.1				
GI_21450650-S	188.2	176.2	172.4	RG9MTD3	NM_144964.1	FLJ31455;bA3J10.9	calcium		
GI_21450652-S	79.6	88.9	83.6	ZDHHC15	NM_144969.1	FLJ31812	zinc ion	integral to	regulation
GI_21450654-S	115.8	110.3	95.5	FLJ25461	NM_144966.1		peptidase	membran	proteolysis
GI_21450656-S	85.8	87.5	82.8	MGC23940	NM_144972.1		L-lactate		glycolysis
GI_21450658-S	155.7	167.1	174.1	FLJ32783	NM_144968.1				
GI_21450662-S	224.3	302.8	310.9	MGC39350	NM_144970.1				
GI_21450664-S	449.8	384.6	427.1	FLJ32745	NM_144978.1				
GI_21450668-S	93	93	80.7	C6orf118	NM_144980.1	MGC23884;bA85G2.1			
GI_21450670-S	117.4	117.5	118.1	FAM31B	NM_144977.1	MGC27044			
GI_21450676-S	134	144.8	124.8	C10orf72	NM_144984.1	FLJ31737			
GI_21450678-S	255.2	266.6	228.3	FLJ25059	NM_144981.1		serine-	membran	proteolysis
GI_21450688-S	99.7	108.9	95.7	FLJ23878	NM_144990.1				
GI_21450690-S	843.9	936.1	842	U2AF1L3	NM_144987.1	MGC33901;U2AF1RS3;U2AF1-RS3	nucleic	nucleus	
GI_21450708-S	119.6	114.7	119.4	MGC22688	NM_145001.1		ATP		protein
GI_21450710-S	1516.1	1359.4	1417.3	STRA13	NM_144998.1	MGC14480			
GI_21450718-S	145	156.3	174.8	FLJ31164	NM_145003.1				
GI_21450724-S	112.3	104.8	95.2	NALP11	NM_145007.1	NOD17;PYPAF6	ATP		
GI_21450726-S	125.8	141.7	151	FLJ30213	NM_145008.1				
GI_21450728-S	98.1	85	86	MGC35558	NM_145013.1				
GI_21450730-S	310.2	228.8	276.2	FLJ32915	NM_145014.1				
GI_21450742-S	168.4	188.8	167.4	FLJ32771	NM_145017.1				
GI_21450744-S	166.4	169.4	158.8	C10orf25	NM_145022.1	FLJ30567			
GI_21450748-S	206.9	243.1	213.4	FLJ31547	NM_145024.1		hydrolase		
GI_21450760-S	2019.3	1530.9	1422.2	MGC22793	NM_145030.1				
GI_21450764-S	97.5	101.2	102.2	C21orf100	NM_145033.1				
GI_21450766-S	662.2	652.1	795.4	C6orf136	NM_145029.1	MGC15854			
GI_21450774-S	294.6	412.7	336.4	LOC163590	NM_145034.1				
GI_21450776-S	98.6	118.1	88.1	MGC16372	NM_145038.1	FLJ32660			
GI_21450778-S	111.5	106.7	110.6	MGC33887	NM_145036.1				
GI_21450780-S	168.3	230.7	184.2	MGC15606	NM_145037.1	FLJ30102			

GI_21450786-S	237.3	249	236.8	PRKCDBP	NM_145040.1	SRBC;HSRBC			
GI_21450791-S	262.9	301.6	294.8	MGC16385	NM_145039.1	FLJ23771;FLJ31569			
GI_21450795-S	175.7	194.1	165.8	MGC20235	NM_145041.1				
GI_21450799-S	416.6	356.6	376.9	NEIL2	NM_145043.1	NEH2;MGC2832;MGC4505;FLJ31644	DNA	nucleus	DNA
GI_21450801-S	1775.3	1764.6	1204.6	MGC10067	NM_145049.1	FLJ25267	peptidase		
GI_21450811-S	166.6	193.2	187.7	MGC27434	NM_145050.1				
GI_21450813-S	135.7	182.7	156.6	MGC12909	NM_145055.1				
GI_21450815-S	403.4	495.3	410.2	MGC23937	NM_145052.1				
GI_21450821-S	189.3	220.6	238.8	FUK	NM_145059.1		ATP	cytoplasm	metabolis
GI_21450823-S	296.1	361	295.4	MGC15476	NM_145056.1				
GI_21450827-S	542.7	621.3	503.2	MGC7036	NM_145058.1	FLJ30380;FLJ32372			
GI_21450831-S	903.2	574.9	801.9	MGC10200	NM_145060.1				
GI_21450833-S	140.3	139.7	126.9	MGC35521	NM_145065.1				
GI_21450835-S	370	367.4	346.1	C6orf113	NM_145062.1	dJ412I7.3			
GI_21450837-S	117.6	117.8	118	MGC2793	NM_145064.1				intracellula
GI_21450841-I	97.8	85.6	86.9	MATK	NM_002378.2	CHK;CTK;HYL;Lsk;HYLTK;HHYLTK;MGC17	protein-	soluble	mesoderm
GI_21450843-A	122.9	124.3	117.7	MATK	NM_139354.1	CHK;CTK;HYL;Lsk;HYLTK;HHYLTK;MGC17	protein-	soluble	mesoderm
GI_21450845-I	170.4	203.4	178.4	MATK	NM_139355.1	CHK;CTK;HYL;Lsk;HYLTK;HHYLTK;MGC17	protein-	soluble	mesoderm
GI_21450847-A	288.1	282.8	230.9	ATRN	NM_012070.2	MGCA;DPPT-L;KIAA0548	receptor	extracellul	developm
GI_21450849-S	103.4	96	94.2	OR12D2	NM_013936.2	hs6M1-20;dJ994E9.8	olfactory	integral to	olfaction
GI_21450851-A	645.5	790.2	913.4	OSBPL2	NM_014835.2	ORP2;ORP-			lipid
GI_21450854-I	145.5	166.2	143.4	STARD7	NM_020151.2	GTT1			
GI_21450855-A	4194.6	3974.4	4677.8	STARD7	NM_139267.1	GTT1			
GI_21450857-S	149.5	152.3	142.6	TRIM36	NM_018700.2	RNF98;RBCC728	zinc ion	intracellula	
GI_21450858-S	103.8	106.7	93.4	TRPM1	NM_002420.3	MLSN1;LTRPC1	calcium	membran	cell growth
GI_21450860-I	374.7	505.6	316.7	ATRN	NM_139321.1	MGCA;DPPT-L;KIAA0548	receptor	extracellul	developm
GI_21464100-S	712.8	998.7	943.6	YWHAG	NM_012479.2	14-3-3GAMMA	protein		signal
GI_21464102-S	4446.7	3641.7	3374.4	YWHAH	NM_003405.2	YWHA1	protein		protein
GI_21464103-S	7168.2	7273.9	6972.7	YWHAQ	NM_006826.2	1C5;HS1	protein		exocytosis
GI_21464104-S	1571.5	1629.1	1746.8	YY1	NM_003403.3	DELTA;NF-E1;UCRBP;YIN-YANG-1	transcripti	nucleus	regulation
GI_21464106-A	265.8	362.7	270.5	F11R	NM_144501.1	JAM;KAT;JAM1;JCAM;JAM-1;PAM-1	cell	intercellula	cell
GI_21464110-I	105.6	91.5	93.9	F11R	NM_144503.1	JAM;KAT;JAM1;JCAM;JAM-1;PAM-1	cell	intercellula	cell
GI_21464114-A	245.7	247.3	218.7	MBD1	NM_015845.2	PCM1;CXXC3	transcripti		transcripti
GI_21464120-I	279.5	355	311.1	MBD2	NM_015832.2	DMTase;NY-CO-41	satellite	nucleus	
GI_21464121-A	100.8	101.8	100.8	MBD2	NM_003927.3	DMTase;NY-CO-41	satellite	nucleus	
GI_21464122-S	2389.7	2617.7	2770.1	MBD3	NM_003926.5		DNA		
GI_21464123-A	132.5	157.2	124.4	MBNL2	NM_005757.3	MBLL;MBLL39;PRO2032			
GI_21464123-I	85.8	88.2	81.4	MBNL2	NM_005757.3	MBLL;MBLL39;PRO2032			
GI_21464124-I	681.5	929.7	703.1	MBNL2	NM_144778.1	MBLL;MBLL39;PRO2032			
GI_21464126-I	111.6	133.9	122.4	KLK8	NM_144505.1	NP;HNP;NRPN;PRSS19;TADG14	serine-		neurogene
GI_21464130-A	103	126.5	127.6	KLK8	NM_144507.1	NP;HNP;NRPN;PRSS19;TADG14	serine-		neurogene
GI_21464133-I	128.1	135.8	129.5	RGS3	NM_144488.1	C2PA;RGP3;FLJ20370;PDZ-RGS3	GTPase	cytosol	regulation
GI_21464138-A	151.1	160.8	137.3	RGS13	NM_144766.1	MGC17173	signal		signal
GI_21464140-I	1128.8	1383.2	1167.4	AKAP11	NM_016248.2	PRKA11;AKAP220;FLJ11304;KIAA0629	protein		protein

GI_21464141-A	109.2	123.9	122	AKAP11	NM_144490.1	PRKA11;AKAP220;FLJ11304;KIAA0629	protein		protein
GI_21464141-I	121.8	135.7	135.6	AKAP11	NM_144490.1	PRKA11;AKAP220;FLJ11304;KIAA0629	protein		protein
GI_21483180-I	222.5	248.7	230.4	ZFP95	NM_014569.2	KIAA1015;MGC33710	zinc ion	nucleus	regulation
GI_21483181-A	277.6	306.9	274.3	ZFP95	NM_145102.1	KIAA1015;MGC33710	zinc ion	nucleus	regulation
GI_21483181-I	91.4	95.5	98.3	ZFP95	NM_145102.1	KIAA1015;MGC33710	zinc ion	nucleus	regulation
GI_21493021-I	151.1	174.8	154.8	AKAP12	NM_005100.2	AKAP250	protein	cytoplasm	G-protein
GI_21493023-A	511.1	595.8	694.3	AKAP12	NM_144497.1	AKAP250	protein	cytoplasm	G-protein
GI_21493023-I	102.2	115.1	106.1	AKAP12	NM_144497.1	AKAP250	protein	cytoplasm	G-protein
GI_21493027-A	239.3	305.4	254.5	AKAP1	NM_003488.2	AKAP;PRKA1;AKAP84;AKAP121;AKAP149;	protein	mitochond	
GI_21493032-S	307.5	317	284.2	AKAP10	NM_007202.2	PRKA10;D-AKAP2;MGC9414	protein	mitochond	protein
GI_21493034-I	121.1	137.1	134.6	AKAP1	NM_139275.1	AKAP;PRKA1;AKAP84;AKAP121;AKAP149;	protein	mitochond	
GI_21493036-I	106.8	97.2	108.2	AKAP4	NM_003886.2	HI;p82;FSC1;AKAP82;hAKAP82	protein	cytoskelet	fertilization
GI_21493038-A	176.9	193.7	183.2	AKAP4	NM_139289.1	HI;p82;FSC1;AKAP82;hAKAP82	protein	cytoskelet	fertilization
GI_21493038-I	119	156.9	140.4	AKAP4	NM_139289.1	HI;p82;FSC1;AKAP82;hAKAP82	protein	cytoskelet	fertilization
GI_21493040-S	107.1	112.5	113.8	AKAP3	NM_006422.2	SOB1;FSP95;PRKA3;AKAP110	protein		acrosome
GI_21493042-S	85.3	103	88.9	AKAP5	NM_004857.2	H21;AKAP75;AKAP79	protein	plasma	synaptic
GI_21493044-S	167.5	187.2	165.1	AKAP6	NM_004274.3	ADAP6;PRKA6;mAKAP;ADAP100;AKAP100;	protein	nuclear	protein
GI_21493046-S	1146.8	1230.6	1121	AKAP8	NM_005858.2	AKAP95;DKFZp586B1222	protein	nucleus	mitosis
GI_21495177-S	391.1	426	391.4	DKFZp727G1	NM_145111.1				
GI_21536251-S	232.1	266.7	220.1	NBEA	NM_015678.2	BCL8B;FLJ10197;KIAA1544	protein	Golgi	post-Golgi
GI_21536270-I	360.9	290.1	120.8	EVA1	NM_005797.2	EVA;MPZL2	cell	cytoskelet	homophili
GI_21536273-S	100.1	122.1	97.2	CASQ1	NM_001231.2	CASQ;CALMITINE	calcium	smooth	
GI_21536277-S	240.5	259.2	253.4	CREBL2	NM_001310.2		transcripti	nucleus	transcripti
GI_21536278-S	895.4	833.4	838	CRTAP	NM_006371.2	CASP		extracellul	
GI_21536279-S	94.4	100.8	90.3	CRYBB1	NM_001887.3		structural		vision
GI_21536280-S	99.8	99.1	109.2	CABP5	NM_019855.3		calcium	cellular_co	signal
GI_21536281-S	90.3	255.7	281.2	CAMK1	NM_003656.3	CAMKI	calcium/ca		protein
GI_21536283-S	301.7	367.4	318.4	CHRNA7	NM_000746.2	NACHRA7	nicotinic	nicotinic	activation
GI_21536287-S	164.7	185.5	174	CKM	NM_001824.2	CKMM;M-CK	creatine		
GI_21536289-S	96	93.3	86.9	COL1A2	NM_000089.2	OI4	structural	collagen	skeletal
GI_21536290-S	329.1	366.7	128.1	CSPG4	NM_001897.2	NG2;MCSP;MCSPG;MSK16;MEL-CSPG	chondroiti	proteoglyc	oncogene
GI_21536291-S	181.8	208.3	170.6	CUBN	NM_001081.2	IFCR;MGA1;gp280	vesicle	membran	vitamin
GI_21536292-S	125.2	156.2	189.5	CLCA2	NM_006536.3	CaCC	chloride	integral to	small
GI_21536293-I	111.9	120.3	121.6	CLDN14	NM_144492.1	DFNB29	structural	tight	protein
GI_21536295-A	89.6	96.3	94.3	CLDN14	NM_012130.2	DFNB29	structural	tight	protein
GI_21536295-I	891.3	1046.8	796.4	CLDN14	NM_012130.2	DFNB29	structural	tight	protein
GI_21536296-S	114.3	140.6	134.6	CLDN16	NM_006580.2	PCLN1	magnesiu	tight	metal ion
GI_21536297-S	81.8	89	86.7	CLDN1	NM_021101.3	CLD1;SEMP1	structural	tight	cell
GI_21536298-S	116.2	130.2	124.5	CLDN3	NM_001306.2	RVP1;HRVP1;CPE-R2;CPETR2	transmem	tight	
GI_21536299-I	1057.8	1666.7	1241.3	STAT1	NM_007315.2	ISGF-3;STAT91	hematopoi	cytoplasm	tyrosine
GI_21536300-A	350.6	798	473.5	STAT1	NM_139266.1	ISGF-3;STAT91	hematopoi	cytoplasm	tyrosine
GI_21536300-I	690.7	1461.6	1096.5	STAT1	NM_139266.1	ISGF-3;STAT91	hematopoi	cytoplasm	tyrosine
GI_21536304-S	844.4	610.5	399.4	SOCS2	NM_003877.3	CIS2;SSI2;Cish2;SSI-2;SOCS-2;STATI2	JAK		JAK-STAT
GI_21536305-A	89.4	84.5	94.9	SCEL	NM_003843.2	FLJ21667;MGC22531		cytoplasm	epidermal

GI_21536309-A	557.3	647.9	657.5	SEC22L3	NM_032970.2	SEC22C;MGC5373;MGC13261	vesicle	integral to	nonselecti
GI_21536309-I	171.8	217.2	263.9	SEC22L3	NM_032970.2	SEC22C;MGC5373;MGC13261	vesicle	integral to	nonselecti
GI_21536310-I	847.8	801.5	1001.7	SEC22L3	NM_004206.2	SEC22C;MGC5373;MGC13261	vesicle	integral to	nonselecti
GI_21536313-A	78.7	92.3	87.4	RET	NM_020629.2	PTC;MTC1;HSCR1;MEN2A;MEN2B;RET51;	protein-		posterior
GI_21536314-I	155.5	168.4	152	RET	NM_020630.2	PTC;MTC1;HSCR1;MEN2A;MEN2B;RET51;	protein-		posterior
GI_21536317-S	2079.1	1576.6	1571.9	DPF2	NM_006268.3	REQ;UBID4;MGC10180	DNA	nucleus	induction
GI_21536318-S	1017.9	1009.3	978.3	RXRA	NM_002957.3	NR2B1	retinoid-X	nucleus	vitamin
GI_21536323-A	2313.9	2878.6	2998.2	HNRPUL1	NM_144734.1	E1BAP5;E1B-AP5;FLJ12944	heterogen	nucleus	response
GI_21536328-I	326.2	378.6	362.6	DDX11	NM_030655.2	CHL1;KRG2;CHLR1;MGC9335	helicase	nucleolus	mitotic
GI_21536329-S	106.8	106.3	108.4	DDX6	NM_004397.3	P54;RCK;HLR2	helicase	nucleus	oncogene
GI_21536330-I	103.1	129.4	108.8	DUSP10	NM_144728.1	MKP5;MKP-5	protein	cytoplasm	JNK
GI_21536332-A	758.3	727	697	DUSP10	NM_144729.1	MKP5;MKP-5	protein	cytoplasm	JNK
GI_21536334-I	295.7	295.1	270.5	DUSP10	NM_007207.3	MKP5;MKP-5	protein	cytoplasm	JNK
GI_21536335-I	138.7	159.9	139.8	DUSP4	NM_057158.2	TYP;HVH2;MKP2;MKP-2	protein	nucleus	MAPKKK
GI_21536336-A	157.5	169.3	127	EVA1	NM_144765.1	EVA;MPZL2	cell	cytoskelet	homophili
GI_21536336-I	143.7	132.3	104.5	EVA1	NM_144765.1	EVA;MPZL2	cell	cytoskelet	homophili
GI_21536343-I	152	186.8	160.4	TCL6	NM_020553.2	TNG1;TNG2;TCL6e1			
GI_21536345-A	89.3	91.5	83.4	TCL6	NM_020554.2	TNG1;TNG2;TCL6e1			
GI_21536348-A	1896.1	2557.9	1325.2	ACCN2	NM_001095.2	ASIC;BNaC2;ASIC1A	amiloride-	integral to	response
GI_21536350-I	155	170.9	167.5	ACCN2	NM_020039.2	ASIC;BNaC2;ASIC1A	amiloride-	integral to	response
GI_21536352-S	808.8	853.7	709.2	ACTL6	NM_016188.3	BAF53B	structural	actin	establish
GI_21536354-A	272.5	295.5	336.1	TAF6	NM_139122.1	TAF2E;TAFII70;TAFII80;TAFII85;MGC:8964	protein	transcripti	transcripti
GI_21536361-A	323	198.9	173.1	TAF1A	NM_139352.1	SL1;RAFI48;TAFI48;MGC:17061	RNA		transcripti
GI_21536363-I	138.8	121.7	102.9	TAF1A	NM_005681.2	SL1;RAFI48;TAFI48;MGC:17061	RNA		transcripti
GI_21536364-S	519.5	364.7	363.9	TAF1B	NM_005680.1	SL1;RAF1B;RAFI63;TAFI63;MGC:9349	RNA		transcripti
GI_21536366-A	887.9	998.4	715.4	TAF1C	NM_139353.1	SL1;TAFI95;TAFI110;MGC:39976	RNA		transcripti
GI_21536368-I	294.4	359.7	328.8	TAF1C	NM_005679.2	SL1;TAFI95;TAFI110;MGC:39976	RNA		transcripti
GI_21536370-S	325.8	372.4	339.1	TEP1	NM_007110.3	TP1;TLP1;p240;VAULT2	protein	nucleus	DNA
GI_21536372-S	2761.5	2402.3	1865.6	TERF2	NM_005652.2	TRF2;TRBF2	DNA	telomere	telomere
GI_21536373-S	494	554.8	503.1	ZNF498	NM_145115.1	FLJ32468			
GI_21536375-S	2175.7	4340.3	6331.2	ABCA1	NM_005502.2	TGD;ABC1;CERP;HDLDT1	anion	membran	phagocyto
GI_21536377-S	113.3	103.9	110.7	ABCB11	NM_003742.2	BSEP;PGY4;SPGP;ABC16;PFIC2;PFIC-2	bile acid	membran	small
GI_21536379-S	84.7	89.9	91.2	ABCD2	NM_005164.2	ALDR;ABC39;ALDL1;ALDRP	ATP	peroxisom	fatty acid
GI_21536380-I	109.9	107.6	114.6	ABCD4	NM_020326.2	P70R;P79R;ABC41;PMP69;PXMP1L;EST352	ATP	peroxisom	small
GI_21536384-A	168.8	180.8	171.2	ADAM22	NM_021721.2	MDC2	integrin	integral to	central
GI_21536385-I	79.2	85	84.7	ADAM22	NM_021722.2	MDC2	integrin	integral to	central
GI_21536389-S	107.2	119.9	99.6	ADAMTS6	NM_014273.2	ADAM-TS6	metallope	extracellul	proteolysis
GI_21536391-S	176.6	179.3	181.4	ADAMTS8	NM_007037.2	METH2;ADAM-TS8	integrin	extracellul	negative
GI_21536395-A	103.8	105.3	94.2	ANGPTL4	NM_016109.2	ARP4;FIAF;PGAR;HFARP;PPARG;pp1158;A		kinesin	
GI_21536397-I	108.3	105.6	105.5	ANGPTL4	NM_139314.1	ARP4;FIAF;PGAR;HFARP;PPARG;pp1158;A		kinesin	
GI_21536405-I	83.5	95.1	90.9	AMPH	NM_001635.2	AMPH1		synaptic	endocytosi
GI_21536416-A	1294.7	1244.4	1193.1	BIN1	NM_139351.1	AMPH2;AMPHL;SH3P9;MGC10367;DKFZp5	tumor	actin	nonselecti
GI_21536418-S	161.7	133.2	142.6	BIK	NM_001197.3	BP4;NBK;BBC1;BIP1	apoptosis	integral to	apoptotic
GI_21536419-A	152.3	168.7	148.3	BIRC7	NM_022161.2	KIAP;LIVIN;MLIAP;RNF50;ML-IAP	apoptosis	intracellula	activation

GI_21536422-A	94.9	85.3	125.6	AMPH	NM_139316.1	AMPH1		synaptic	endocytosi
GI_21536424-S	542.2	508.7	508.7	WBP4	NM_007187.3	FBP21	RNA	nucleus	
GI_21536425-A	536	598.4	582.1	WDR5	NM_052821.2	BIG-3	signal	heterotrim	G-protein
GI_21536426-S	132.3	168.1	182.3	WNT3	NM_030753.3	INT4	extracellul	extracellul	morphoge
GI_21536427-S	573.4	749.2	733.9	WRB	NM_004627.2	CHD5		nucleus	
GI_21536429-I	89.8	94.6	95.2	WWOX	NM_018560.4	FOR;FRA16D;HHCMA56;PRO0128;D16S43	catalytic		steroid
GI_21536430-S	78.8	106.9	94.7	TF	NM_001063.2	PRO1557;PRO2086	iron ion	extracellul	iron ion
GI_21536431-S	1454.8	7022	1085.1	TIMP3	NM_000362.3	SFD;K222TA2;HSMRK222	metalloen		proteolysis
GI_21536432-A	136.8	149.2	135.4	TNFSF11	NM_033012.2	ODF;OPGL;sOdf;RANKL;TRANCE;hRANKL2	cytokine	extracellul	positive
GI_21536432-I	119.8	138.5	118.4	TNFSF11	NM_033012.2	ODF;OPGL;sOdf;RANKL;TRANCE;hRANKL2	cytokine	extracellul	positive
GI_21536433-S	231.1	236.7	214.8	TRIAD3	NM_019011.3	ZIN;U7I1;UBCE7IP1		kinesin	apoptosis
GI_21536437-S	329.8	333.9	348.6	FBXL4	NM_012160.3	FBL4;FBL5		ubiquitin	ubiquitin-
GI_21536438-A	1505.4	2187.4	1277.5	FBXL5	NM_012161.2	FBL4;FBL5;FLR1	ubiquitin		proteolysis
GI_21536439-I	71.5	79.1	68.2	FBXL5	NM_033535.2	FBL4;FBL5;FLR1	ubiquitin		proteolysis
GI_21536440-S	180.9	190.4	168.6	BARX2	NM_003658.3		RNA	nucleus	transcripti
GI_21536441-S	182.3	285.1	229.7	BCL7A	NM_020993.2	BCL7	actin		oncogene
GI_21536442-S	209.8	253.5	244.3	BFSP2	NM_003571.2	CP47;CP49;LIFL-L;PHAKININ	structural	intermedia	vision
GI_21536443-A	12458.1	10935	7267.6	BZRP	NM_007311.2	MBR;PBR	benzodiaz	mitochond	mitochond
GI_21536444-I	1454.6	1189.6	776	BZRP	NM_000714.3	MBR;PBR	benzodiaz	mitochond	mitochond
GI_21536446-S	140.2	157.2	131.2	PAK6	NM_020168.3	PAK5	protein-		protein
GI_21536448-S	1191.6	1275.8	1278.2	PFDN1	NM_002622.3	PDF;PFD1	transcripti		cell cycle
GI_21536450-A	556.2	556.6	581	PHF1	NM_002636.3	PHF2	transcripti	nucleus	regulation
GI_21536451-S	148.5	392.4	155.8	PRSS3	NM_002771.2	MTG;TRY3;TRY4;PRSS4	trypsin	extracellul	proteolysis
GI_21536453-S	106.3	115.1	100.6	PRSS8	NM_002773.2	PROSTASIN	serine-	integral to	proteolysis
GI_21536454-I	145.3	166.5	138.6	PSEN1	NM_000021.2	AD3;FAD;PS1;S182		integral to	chromoso
GI_21536455-S	122.5	150.9	136.2	PTGIS	NM_000961.2	CYP8;PGIS;PTGI;CYP8A1	prostaglan	endoplas	prostaglan
GI_21536456-S	910.5	823.5	760.6	MOAP1	NM_022151.3	MAP-1;PNMA4			apoptosis
GI_21536459-S	239	198.8	230.2	MAP3K5	NM_005923.3	ASK1;MEKK5;MAPKKK5	MAP		activation
GI_21536460-S	158	204.7	188.1	MFNG	NM_002405.2		transferas	Golgi	pattern
GI_21536462-I	269	147	114.7	MMP25	NM_022468.3	MMP20;MT6-MMP;LEUKOLYSIN	zinc ion	membran	proteolysis
GI_21536463-S	138.1	145.6	131.8	MPP3	NM_001932.2	DLG3	guanylate	integral to	oncogene
GI_21536467-A	10759.3	6615.1	5777.7	AXL	NM_001699.3	UFO	transmem	integral to	signal
GI_21536469-S	106.2	113.4	117	DAO	NM_001917.3	DAAO;OXDA;DAMOX;MGC35381	D-amino-	peroxisom	electron
GI_21536471-S	86.8	86.2	78.9	DAZ	NM_004081.3	DAZ1;SPGY	RNA		fertilization
GI_21536472-I	106.1	107.5	107.6	DLEC1	NM_007338.2	F56;DLC1	tumor		negative
GI_21536473-S	96.5	102.9	93.2	DMXL1	NM_005509.3		protein		proteolysis
GI_21536478-I	94.7	97.1	90.8	L3MBTL	NM_015478.4	L3MBTL1;KIAA0681;H-	transcripti	nucleus	regulation
GI_21536480-A	114.5	113.5	101.9	L3MBTL	NM_032107.2	L3MBTL1;KIAA0681;H-	transcripti	nucleus	regulation
GI_21536480-I	187.1	221.5	188.8	L3MBTL	NM_032107.2	L3MBTL1;KIAA0681;H-	transcripti	nucleus	regulation
GI_21536482-S	159.2	189.9	166.3	HIST1H2BG	NM_003518.3	H2B/a;H2BFA;H2B.1A	DNA	chromoso	nucleoso
GI_21536483-S	770.9	903.5	674.7	HIP2	NM_005339.3	LIG;HYPG	ubiquitin		small
GI_21536484-S	231.4	205.4	198	HIRA	NM_003325.3	TUP1;DGCR1;TUPLE1	transcripti	nucleus	embryoge
GI_21539662-A	326.2	336.8	327.3	PJA1	NM_022368.2	RNF70;FLJ11830	ligase		
GI_21553310-S	183	208.3	181.8	HSPC105	NM_145168.1		3-beta-		steroid

GI_21553312-S	298.9	347.3	355	C14orf52	NM_145165.1	My015;FLJ33064			developm
GI_21553314-S	619.6	825.4	922.2	PIGM	NM_145167.1	MGC29896	transferas		
GI_21553316-S	2804.1	2967.5	3334.7	C6orf83	NM_145169.1	pRGR1;MGC19825			
GI_21553320-S	95.3	106.4	97.8	NYD-SP29	NM_145172.1	FLJ30067			
GI_21553322-S	91.5	117.6	105.3	DIRAS1	NM_145173.1	RIG;GBTS1;Di-Ras1	small		small
GI_21553324-S	194.8	220.7	223.3	DHRSX	NM_145177.1	DHRS5X;DHRSXY;CXorf11	oxidoredu		metabolis
GI_21553330-S	214.2	367.8	301.3	SLC2A12	NM_145176.1	GLUT8;GLUT12	transporte	integral to	carbohydr
GI_21553334-S	98.3	101	101	DNAJB7	NM_145174.1	HSC3			
GI_21553338-S	156.4	173.9	168.2	C21orf93	NM_145179.1				
GI_21614495-S	261	176	159.9	VAV3	NM_006113.3		SH3/SH2		small
GI_21614497-S	1474.7	1660.6	1549.6	VBP1	NM_003372.3	PFD3;PFDN3;VBP-1	protein	prefoldin	protein
GI_21614498-S	3936.7	3945	4198.8	VIL2	NM_003379.3	CVL;CVIL;MGC1584;DKFZp762H157		microvillus	cytoskelet
GI_21614500-A	3751.6	3894.8	4227.5	DEGS	NM_144780.1	MLD;DES1;Des-1;MGC5079	electron	membran	fatty acid
GI_21614503-I	1064.3	1339.8	1517.8	DEGS	NM_003676.2	MLD;DES1;Des-1;MGC5079	electron	membran	fatty acid
GI_21614504-I	113.1	132.5	123.6	CISH	NM_013324.4	CIS;G18;SOCS;CIS-1	molecular	cellular_co	intracellula
GI_21614506-A	859.8	958.3	870.6	CISH	NM_145071.1	CIS;G18;SOCS;CIS-1	molecular	cellular_co	intracellula
GI_21614508-I	782.8	545.3	561	DIAPH2	NM_006729.2	DIA;POF;DIA2;POF2	receptor	kinesin	cytokinesi
GI_21614509-A	191.8	190.7	178.7	FGF12	NM_021032.2	FHF1;FGF12B	growth	extracellul	heart
GI_21614509-I	122.4	121.5	115.6	FGF12	NM_021032.2	FHF1;FGF12B	growth	extracellul	heart
GI_21614510-I	132.4	152.3	125.1	FGF12	NM_004113.3	FHF1;FGF12B	growth	extracellul	heart
GI_21614512-I	453	704.8	398	FTHFD	NM_012190.2		catalytic		10-
GI_21614514-A	460.8	684.6	287.1	FTHFD	NM_144776.1		catalytic		10-
GI_21614516-A	109.3	104.5	101.6	GYPC	NM_016815.2	GE;GPC	blood	integral to	N-linked
GI_21614517-S	265.2	311.7	281	GABRR1	NM_002042.2		GABA-A	integral to	gamma-
GI_21614518-S	100.5	95	86.9	GAN	NM_022041.2	GAN1	protein	neurofilam	biological_
GI_21614519-S	408.9	719.5	667.7	G6PD	NM_000402.2	G6PD1	glucose-6-	cellular_co	glucose 6-
GI_21614521-S	290.4	207.1	155.1	GCA	NM_012198.2	GCL	calcium	cytoplasm	membran
GI_21614524-S	139.6	154	122.4	GPC4	NM_001448.2		glypican	proteoglyc	embryoge
GI_21614526-S	1397	1638.9	1119.1	MAP2K1IP1	NM_021970.2	MP1	enzyme		activation
GI_21614527-S	11048.2	10348	9491.4	MAP2K2	NM_030662.2	MEK2;MKK2;MAPKK2;PRKMK2	protein-	extracellul	protein
GI_21614528-S	133.6	142.1	124.2	NAP1L2	NM_021963.2	BPX;MGC26243	DNA	chromatin	nucleoso
GI_21614529-I	311.8	396.5	338.1	NOX1	NM_007052.3	MOX1;NOH1;NOH-1;GP91-2	superoxid	integral to	proton
GI_21614532-A	417.4	523.9	468.8	PRSS21	NM_144957.1	ESP-1;TEST1	serine-	cytoplasm	proteolysis
GI_21614535-S	116.2	126.1	110.7	PRSS22	NM_022119.2	BSSP-4;MGC9599;SP001LA;hBSSP-4	trypsin		proteolysis
GI_21614536-I	602	610.1	530.8	PRSS25	NM_013247.3	OMI;HtrA2	serine-	endoplas	response
GI_21614537-A	611.9	671.2	599.4	PRSS25	NM_145074.1	OMI;HtrA2	serine-	endoplas	response
GI_21614540-S	155.1	176.3	167.1	SAC	NM_018417.2	HCA2	adenylate	soluble	intracellula
GI_21614541-S	145.6	152.8	132.9	SIM1	NM_005068.2		DNA	nucleus	embryoge
GI_21614543-S	87.6	98.7	81.3	S100A8	NM_002964.3	P8;MIF;NIF;CAGA;CFAG;CGLA;L1Ag;MRP8;	calcium	extracellul	inflammat
GI_21614545-S	462.7	388.7	279.7	PSPH	NM_004577.2	PSP	phosphos		L-serine
GI_21614546-S	150.9	172.8	153.1	PSPN	NM_004158.2	PSP	receptor		central
GI_21614547-S	180.8	193.4	191.2	IRAK2	NM_001570.2	IRAK-2	NF-		NIK-I-
GI_21614549-S	172.9	192.7	187.6	ITK	NM_005546.3	EMT;LYK;PSCTK2	non-		cellular
GI_21614550-S	152.7	171.4	152.9	UCP1	NM_021833.3	UCP;SLC25A7	uncouplin	mitochond	proton

GI_21614551-S	127.8	144.8	133.3	SPRL1B	NM_014357.2	XP5;LEP10	molecular	cellular_co	epidermal
GI_21618324-S	428.7	537.8	485.5	FOXE1	NM_004473.3	TTF2;TITF2;TTF-2;FKHL15	RNA	nucleus	ectoderm
GI_21618326-I	130.1	159.2	136.3	FOXI1	NM_012188.3	HFH3;FKHL10;FREAC6	DNA	nucleus	regulation
GI_21618328-A	98.7	108.8	92.7	FOXI1	NM_144769.1	HFH3;FKHL10;FREAC6	DNA	nucleus	regulation
GI_21618332-S	238.5	242.5	222.2	STAT4	NM_003151.2		transcripti	nucleus	JAK-STAT
GI_21618333-I	351.7	400.3	361.2	CRAT	NM_004003.2	CAT1		peroxisom	energy
GI_21618335-A	727.7	884.8	899.3	CRAT	NM_144782.1	CAT1		peroxisom	energy
GI_21618337-A	528.5	893.4	938.8	STAT3	NM_003150.2	APRF	hematopoi	cytoplasm	JAK-STAT
GI_21618341-S	146.9	129.4	109.7	STAT5A	NM_003152.2	MGF;STAT5	transcripti	nucleus	JAK-STAT
GI_21618345-S	113.1	119.3	108.7	OTOR	NM_020157.2	FDP;MIAL			hearing
GI_21618346-I	99.8	109.3	97.1	MAP2K3	NM_002756.2	MEK3;MKK3;MAPKK3;PRKMK3	MAP		signal
GI_21618348-A	178.7	163.5	157.4	MAP2K3	NM_145109.1	MEK3;MKK3;MAPKK3;PRKMK3	MAP		signal
GI_21618348-I	161.2	163.7	158.8	MAP2K3	NM_145109.1	MEK3;MKK3;MAPKK3;PRKMK3	MAP		signal
GI_21618350-I	109.6	125.9	98	MAP2K3	NM_145110.1	MEK3;MKK3;MAPKK3;PRKMK3	MAP		signal
GI_21618355-A	253.2	287.7	268.6	KLK11	NM_006853.2	TLSP;PRSS20;MGC33060	serine-		proteolysis
GI_21618355-I	166.5	183.7	175.3	KLK11	NM_006853.2	TLSP;PRSS20;MGC33060	serine-		proteolysis
GI_21618356-I	81.9	80.4	92.7	KLK11	NM_144947.1	TLSP;PRSS20;MGC33060	serine-		proteolysis
GI_21618360-S	4210.3	2581	3071.1	FXYD5	NM_014164.3	RIC;IWU1;KCT1;IWU-1;dysad;HSPC113	ion	integral to	ion
GI_21624640-S	349.5	427.4	372.5	CABP4	NM_145200.1		calcium	cellular_co	signal
GI_21624647-S	142.7	149.9	147.5	VTI1A	NM_145206.1	MVti1;Vti1-rp2	protein	kinesin	intracellula
GI_21624653-S	99	112.4	101.3	SPATA5	NM_145207.1	SPAF	nucleotide		
GI_21624655-S	107.7	124.5	110.6	MBD3L1	NM_145208.1	MBD3L			
GI_21626459-S	656.4	3594.5	1626.3	AF1Q	NM_006818.2		molecular	cellular_co	cell growth
GI_21626460-S	188.4	227.4	191.8	AIPL1	NM_014336.2	LCA4;AIPL2	chaperone	nucleus	vision
GI_21626462-S	129	134.9	119.3	APC	NM_000038.2	GS;DP2;DP3;FAP;FPC;DP2.5	beta-	kinesin	cell
GI_21626463-S	2217.2	3409.8	2904.3	ARCN1	NM_001655.3	COPD	protein	membran	intracellula
GI_21626467-S	936.3	898.4	750.4	NP220	NM_014497.2	MGC26130	double-	nucleoplas	mRNA
GI_21630256-S	135.4	121.4	122.9	MTBP	NM_022045.2	MDM2BP			
GI_21630284-S	130.8	164.5	142.7	PDZK2	NM_024791.2	IKEPP;PDZD3;FLJ22756			
GI_21686972-S	97.6	98.2	94.7	LOC196549	NM_145293.1				
GI_21686976-S	129	153	129.8	IGSF4C	NM_145296.1	TSLL2			
GI_21686978-S	128.7	132.2	162.4	LOC200383	NM_145299.1		nucleotide		
GI_21686980-S	107	105.9	108.7	LOC200420	NM_145300.1				
GI_21686994-S	128.4	148.1	139.7	STOML3	NM_145286.1	SRO;Epb7.2l		membran	
GI_21686996-S	169.8	180.4	148.7	ZNF519	NM_145287.1	HsT2362	nucleic	intracellula	regulation
GI_21687002-S	106.4	104.2	103.5	DUX2	NM_012147.2		transcripti	nucleus	regulation
GI_21687023-S	113.7	125.9	118.6	NPCR	NM_145318.1				
GI_21687040-S	112.8	93.6	115.2	C14orf6	NM_145250.1		pancreatic		
GI_21687046-S	106.7	115.6	108.9	X102	NM_030879.2				
GI_21687047-S	123	135.6	129.6	WDR31	NM_145241.1		transporte	membran	transport
GI_21687049-S	96.5	95.2	84.9	LOC115131	NM_145242.1		olfactory	integral to	G-protein
GI_21687059-S	302.6	611.6	238.4	LOC124220	NM_145252.1				
GI_21687061-S	224.4	265	227.7	LOC124402	NM_145253.1				
GI_21687067-S	115.2	122.8	91.8	LOC202459	NM_145303.1				

GI_21687071-S	109.3	94.6	101.1	LOC124491	NM_145254.1				
GI_21687081-S	105.2	110.3	119	LOC126731	NM_145257.1				
GI_21687083-S	97.9	91	86.9	MGC22773	NM_145258.1				
GI_21687097-S	99.6	110	104.9	ACVR1C	NM_145259.1	ALK7;ACVRLK7	protein-	membran	protein
GI_21687111-S	274.6	287	264.5	LOC112476	NM_145239.1				
GI_21687118-S	111.1	328.9	135.3	LOC132671	NM_145263.1				
GI_21687122-S	220.9	267	240.4	LOC221044	NM_145314.1				
GI_21687134-S	134.2	148.7	137.7	C6orf57	NM_145267.1				
GI_21687138-S	112.3	94.5	102.8	B3GNT7	NM_145236.1		galactosylt	membran	protein
GI_21687142-S	113.6	122.4	102.8	RNASE8	NM_138331.1		pancreatic		
GI_21687148-S	130.5	122.2	132.6	LOC148823	NM_145278.1				
GI_21687150-S	1120	854.7	770	LOC203427	NM_145305.1		structural	ribosome	transport
GI_21687152-S	627.9	364.5	284.7	C10orf35	NM_145306.1				
GI_21687174-S	181.9	199.3	233.9	LOC220074	NM_145309.1				
GI_21687176-S	172.8	205.3	186.2	RASGEF1A	NM_145313.1	CG4853	guanyl-		small
GI_21687187-S	160	194.5	160.4	LOC146325	NM_145270.1				
GI_21687211-S	341.7	337.9	307.3	UVRAG	NM_003369.2			kinesin	DNA
GI_21687219-S	1577.5	1228	808.1	MGC21518	NM_145274.1				
GI_21687223-S	140.2	132.6	136.7	SLC30A6	NM_017964.2	ZNT6;FLJ31101;MGC45055			
GI_21687227-S	245	262	267.4	C14orf143	NM_145231.1		calcium		
GI_21687234-A	108.3	107.4	116.5	KLC2L	NM_145275.1	KLC2;KLCt;KNS2B			
GI_21687234-I	164.8	174.8	160	KLC2L	NM_145275.1	KLC2;KLCt;KNS2B			
GI_21687236-S	110.2	109.7	109.6	ZNF563	NM_145276.1		nucleic	intracellula	regulation
GI_21687251-S	202.4	231.1	208.7	ZNF342	NM_145288.1		DNA	nucleus	regulation
GI_21687261-S	86.3	102.9	96.6	LOC91661	NM_138372.1		nucleic	intracellula	regulation
GI_21687263-S	147.5	343.2	522.3	ZNF558	NM_144693.1	FLJ30932	nucleic	nucleus	regulation
GI_21687265-S	133.8	166.2	136.3	LOC115648	NM_145326.1		nucleic	intracellula	regulation
GI_21687267-S	91.9	86.5	83	CNOT6L	NM_144571.1	FLJ23561;FLJ25459;DKFZp434K098			
GI_21687269-S	100.8	114.8	111.4	MRVLDC2	NM_144724.1	MARVD2;FLJ30532	transporte	synaptic	transport
GI_21699053-S	93.1	95.8	92	FLJ31846	NM_144974.1				
GI_21699059-S	86.2	89.1	104.2	ZNF564	NM_144976.1	MGC26914	nucleic	intracellula	regulation
GI_21699063-S	127	115.3	116.6	ZNF501	NM_145044.1	MGC21738		nucleus	
GI_21699069-S	964.4	1052.9	1353.1	FAM14B	NM_145249.1			integral to	
GI_21699077-S	135.1	147.5	129.1	NKX2-3	NM_145285.1	NKX2C;NKX2.3	transcripti	nucleus	regulation
GI_21699081-S	157.6	107.7	180.6	LOC199777	NM_145297.1		DNA	intracellula	regulation
GI_21699083-S	87	72.6	68.3	LOC158046	NM_145283.1				
GI_21700762-S	1335.9	1847.5	2119.7	C16orf34	NM_144570.1	HN1L;FLJ13092			
GI_21702732-A	166.5	181.8	163.3	TNRC6	NM_020847.1	CAGH26;KIAA1460			
GI_21702732-I	134.1	144.7	131.6	TNRC6	NM_020847.1	CAGH26;KIAA1460			
GI_21702741-I	858.6	887.2	678	TNRC6	NM_014494.1	CAGH26;KIAA1460			
GI_21703361-A	200.1	271	243.7	SOC	NM_145345.1				
GI_21703366-S	289.6	395.1	364.3	DIRAS2	NM_017594.2	Di-Ras2;DKFZp761C07121			
GI_21703709-S	2533.6	2785.5	3080.4	SCOTIN	NM_016479.3				
GI_21704266-I	233.8	259.5	246	MAX	NM_145114.1	MGC10775;MGC11225;MGC18164;MGC346	transcripti		oncogene

GI_21704268-I	104.1	115.5	101.7	MAX	NM_145116.1	MGC10775;MGC11225;MGC18164;MGC346	transcripti		oncogene
GI_21704270-A	2107.4	2390.6	2102.6	POLR2J2	NM_032958.2	HRPB11B	DNA-		transcripti
GI_21704273-I	104.3	120	104.1	POLR2J2	NM_145325.1	HRPB11B	DNA-		transcripti
GI_21704275-S	2614.8	2729.2	2503.1	POLR2J	NM_006234.3	RPB11;RPB11A;RPB11m;hRPB14;POLR2J1	DNA-	DNA-	transcripti
GI_21704276-I	114.3	102.4	98.6	JAG2	NM_002226.3	HJ2	Notch	integral to	mystery
GI_21704278-A	234.6	226.1	155.9	JAG2	NM_145159.1	HJ2	Notch	integral to	mystery
GI_21704282-S	195.8	226.2	206.3	JPH3	NM_020655.2	JP3;HDL2;JP-3;TNRC22;CAGL237			
GI_21704284-S	115.2	121.9	97.9	JAM2	NM_021219.2	VEJAM;VE-JAM;C21orf43		integral to	cell-cell
GI_21704285-S	2075.6	1897.4	1063.7	JAM3	NM_032801.3	FLJ14529			
GI_21704286-S	143	150.1	129.5	NEU3	NM_006656.4	SIAL3	catalytic	membran	gangliosid
GI_21717802-S	1444.9	1348	1529.9	WBSCR20B	NM_145645.1				
GI_21717806-S	446.9	396.7	415.2	MGC21654	NM_145647.1				
GI_21717813-S	102.9	117.1	109.6	RYD5	NM_145651.1				
GI_21717815-S	1250.2	2096.9	1160	SLC15A4	NM_145648.1	PHT1;PTR4	copper ion	membran	oligopepti
GI_21717823-S	121.5	109.4	103	TCEB3C	NM_145653.1	HsT829;TCEB3L2	translation	nucleus	transcripti
GI_21717829-S	107.9	122.7	115	C8orf6	NM_145656.1				
GI_21717831-S	93	97.9	88.7	SPESP1	NM_145658.1	MGC24663			
GI_21729875-A	99.7	119.4	98.5	ABCC11	NM_145186.1	MRP8			
GI_21729877-I	140.3	129.4	125.3	LIPT1	NM_145196.1	MGC12290;MGC13378	ligase	mitochond	lipid
GI_21729879-I	107.8	87.9	94	LIPT1	NM_145197.1	MGC12290;MGC13378	ligase	mitochond	lipid
GI_21729881-I	140.7	176.4	138.4	LIPT1	NM_145198.1	MGC12290;MGC13378	ligase	mitochond	lipid
GI_21729883-A	391.7	259.6	242.7	LIPT1	NM_145199.1	MGC12290;MGC13378	ligase	mitochond	lipid
GI_21729887-A	128.5	137.2	122.3	ABCC12	NM_145188.1	MRP9			
GI_21729898-A	724.5	612.9	512.8	MAP2K5	NM_145162.1	MEK5;MAPKK5;PRKMK5;HsT17454	protein		signal
GI_21729898-I	89.8	92.7	82.2	MAP2K5	NM_145162.1	MEK5;MAPKK5;PRKMK5;HsT17454	protein		signal
GI_21735416-S	98.6	118	101.4	BICD2	NM_015250.1	KIAA0699			
GI_21735418-S	986.5	790.6	942.3	BDG29	NM_015144.1	BDG-29;MGC14139			
GI_21735486-S	145.3	183	154.3	ACBD5	NM_145698.1	KIAA1996;DKFZp434A2417	acyl-CoA		
GI_21735491-I	146.3	172.7	154.6	PPP1R1B	NM_032192.2	DARPP32;DARPP-32;FLJ20940	protein	cytoplasm	signal
GI_21735547-S	215.5	248.7	327.7	CEP2	NM_007186.2	C-NAP1;CEP250	DNA	cytoskelet	DNA
GI_21735549-S	119.1	133	110.1	MAP3K10	NM_002446.2	MST;MLK2	protein		JNK
GI_21735551-S	215.2	279.2	285.6	MAP3K12	NM_006301.2	DLK;MUK;ZPK	protein	cytoplasm	JNK
GI_21735553-S	287.4	342.1	323.9	MAP3K11	NM_002419.2	MLK3;PTK1;SPRK;MLK-3;MGC17114	protein		JNK
GI_21735555-S	190.1	198.7	177.7	MAP3K2	NM_006609.2	MEKK2;MEKK2B	protein		activation
GI_21735557-A	210.6	211.6	185.3	MAP3K7IP2	NM_015093.2	TAB2;FLJ21885;KIAA0733			
GI_21735558-I	93.6	95.1	94	MAP3K7IP2	NM_145342.1	TAB2;FLJ21885;KIAA0733			
GI_21735565-A	1311.8	1490.9	1227.8	MAP3K7	NM_145333.1	TAK1;TGF1a	MAP		TGFbeta
GI_21735567-S	1255.5	1154.7	1079.4	CEPT1	NM_006090.2	MGC45223	ethanolam	integral to	lipid
GI_21735568-S	119.4	116	114	CLSPN	NM_022111.2	CLASPIN	protein	cellular_co	biological_
GI_21735570-S	227.4	268.8	256.8	CMA1	NM_001836.2	CYH;MCT1	serine-		proteolysis
GI_21735571-S	1323.8	1006.1	1260.2	ECT2	NM_018098.4	FLJ10461	guanyl-	intracellula	cell growth
GI_21735574-S	176	198.9	189	JPH1	NM_020647.1	JP1;JP-1	molecular	integral to	biological_
GI_21735576-S	135.3	165.9	123.4	SDK2	NM_019064.2	FLJ10832;KIAA1514			
GI_21735583-A	882.2	720.8	672.2	OSBPL3	NM_145322.1	ORP3;ORP-3;OSBP3;KIAA0704;MGC21526			lipid

GI_21735591-A	728.2	664.7	678.8	PDCD2	NM_002598.2	RP8;ZMYND7;MGC12347	DNA	cytoplasm	apoptosis
GI_21735591-I	1700.8	1428.4	975.3	PDCD2	NM_002598.2	RP8;ZMYND7;MGC12347	DNA	cytoplasm	apoptosis
GI_21735593-I	1510.3	1408.5	1868	PDCD2	NM_144781.1	RP8;ZMYND7;MGC12347	DNA	cytoplasm	apoptosis
GI_21735599-S	1215.8	947.9	1033.8	PDCD5	NM_004708.2	TFAR19;MGC9294			induction
GI_21735600-S	1059.7	1178.7	1049	MRPL19	NM_014763.2	RLX1;RPML15;MRP-	structural	cytosolic	protein
GI_21735601-A	782.9	771.7	671.9	MRPL30	NM_016503.2	RPML28;MGC3314;MRP-L28;MGC24095			
GI_21735601-I	99.7	114.9	107	MRPL30	NM_016503.2	RPML28;MGC3314;MRP-L28;MGC24095			
GI_21735603-I	338.4	311.9	278.1	MRPL30	NM_145212.1	RPML28;MGC3314;MRP-L28;MGC24095			
GI_21735607-I	2763.4	3133.3	2289.7	MRPL33	NM_004891.2	C2orf1;RPL33L;MGC13694;MGC23922	structural	ribosome	protein
GI_21735608-A	3938.8	5140	4269.6	MRPL33	NM_145330.1	C2orf1;RPL33L;MGC13694;MGC23922	structural	ribosome	protein
GI_21735610-S	568.4	714.2	666.1	MRPL44	NM_022915.2	FLJ12701;FLJ13990	double-	intracellula	RNA
GI_21735615-I	107.4	102.5	99.1	APOL1	NM_145343.1	APOL;APO-L;APOL-I	high-	extracellul	lipid
GI_21735617-A	316.7	461.1	347.1	APOL1	NM_145344.1	APOL;APO-L;APOL-I	high-	extracellul	lipid
GI_21735619-S	4923.9	5702.9	5188.3	MDH1	NM_005917.2	MDHA;MOR2;MDH-s;MGC:1375	malic	cytosol	tricarboxyli
GI_21735620-S	10245.3	11966	9955.2	MDH2	NM_005918.2	MDH;MOR1;M-MDH;MGC:3559	oxidoredu	mitochond	tricarboxyli
GI_21735622-S	139	148.8	135.2	NTSR2	NM_012344.2	NTR2	G-protein	integral to	sensory
GI_21735623-A	5543.3	7042.8	6212.9	YWHAZ	NM_003406.2	KCIP-1	protein		
GI_21735623-I	165.5	163.9	149.3	YWHAZ	NM_003406.2	KCIP-1	protein		
GI_21902518-S	1015.8	1160.9	1060.9	PCNX	NM_014982.1	KIAA0805;KIAA0995		integral to	
GI_21902536-S	221.8	208.4	183.4	ISYNA1	NM_016368.3				
GI_21914861-A	2100	2236.3	1961.1	CECR5	NM_017829.4	FLJ20454			
GI_21914880-S	728.4	1232.8	380.1	LGMN	NM_005606.3	LGMN1;PRSC1	legumain	lysosome	proteolysis
GI_21914924-S	103.5	97.1	86.5	PDZK7	NM_024895.3	FLJ23209;bA108L7.8			
GI_21918830-S	1711.5	1967	971.7	NFE2L3	NM_004289.4	NRF3	transcripti	nucleus	transcripti
GI_21918871-S	237.4	254.2	241.4	LACE1	NM_145315.2	LACE-1			
GI_21945057-S	272.4	333.9	311.7	LOC201158	NM_145301.1		DNA	nucleus	regulation
GI_21945060-A	167.7	203.7	169.7	ZNF258	NM_145310.1	MYM;ZNF198L4	DNA		developm
GI_21945060-I	175.7	182.5	165	ZNF258	NM_145310.1	MYM;ZNF198L4	DNA		developm
GI_21955121-S	182.2	233.5	194.9	LOC94431	NM_145237.1				
GI_21955153-I	141.9	150.4	155	NALP12	NM_144687.1	RNO2;PYPAF7			
GI_21955169-I	588.6	717.8	572.4	SSBP3	NM_145716.1	SSDP;SSDP1;SSDP3;FLJ10355	single-	nucleus	regulation
GI_21955171-S	877.5	905.6	685.6	PHLDB2	NM_145753.1	LL5b;LL5beta;FLJ21791			
GI_21955236-S	111.5	103.5	98.3	STI2	NM_145755.1				
GI_21955238-S	94.5	92.3	102	ZNF396	NM_145756.1	FLJ31213	transcripti	nucleus	regulation
GI_21956638-S	390.1	456	707.5	ABTB2	NM_145804.1	DKFZP586C1619	protein		
GI_21956640-S	157.9	152.7	154	ISL2	NM_145805.1	FLJ10160	transcripti	nucleus	regulation
GI_21956644-S	883.8	1122.1	933.8	MTPN	NM_145808.1	V-1;GCDP	protein	cellular_co	regulation
GI_21956646-S	108.7	120.3	99.9	LOC220594	NM_145809.1		cysteine-		ubiquitin-
GI_22001414-S	27119.1	17692	22377	RIS1	NM_015444.1	p40BBP;DKFZp586E1621			
GI_22001416-S	175.7	202	172.4	GEMIN5	NM_015465.1	DKFZP586M1824	pre-mRNA	spliceoso	nuclear
GI_22001419-S	271.8	318.4	276	C21orf29	NM_144991.2	TSPEAR;MGC11251	structural		cell
GI_22003857-S	329.5	215.1	150.5	FLJ12604	NM_024621.1	KIAA1692			
GI_22004646-S	96.3	91.8	96	FLJ38819	NM_145865.1				
GI_22024384-S	3296	3771.1	2672.6	FPGS	NM_004957.2		tetrahydrof	cytosol	nucleobas

GI_22027467-S	235	288.4	271.2	TRPV3	NM_145068.2	VRL3			
GI_22027468-I	516.9	529	481.4	POGZ	NM_015100.1	KIAA0461;Nbla00003			
GI_22027470-S	136.9	107	125.5	NPAS2	NM_002518.2	MOP4;FLJ23138	transcripti		central
GI_22027474-I	140.7	159.7	138.9	CDIPT	NM_145752.1	PIS;PIS1;MGC1328	phosphati	integral to	phospholi
GI_22027476-A	448.9	503.4	600.6	CDIPT	NM_006319.2	PIS;PIS1;MGC1328	phosphati	integral to	phospholi
GI_22027477-A	1154.6	1005.8	970.1	POGZ	NM_145796.1	KIAA0461;Nbla00003			
GI_22027479-S	1540.1	1150.8	1103.8	POGK	NM_017542.3	BASS2;LST003;KIAA1513;KIAA15131			
GI_22027481-S	250.9	255.7	229.6	NPAS1	NM_002517.2	MOP5	transcripti	nucleus	central
GI_22027483-S	1116	1477.7	1488.9	CMAS	NM_018686.3				
GI_22027484-S	104.9	170.8	110.1	RASD1	NM_016084.3	AGS1;DEXRAS1;MGC:26290	GTPase		cell growth
GI_22027485-S	430.3	580.9	493.3	RASD2	NM_014310.3	Rhes;TEM2;MGC:4834	RAS small	cellular_co	small
GI_22027487-S	171.6	140.1	157.8	STEAP	NM_012449.2	PRSS24;STEAP1;MGC19484	transporte	intercellula	
GI_22027491-S	141.6	142.1	130.9	SPANXB2	NM_145664.1	SPANX;SPANXB			
GI_22027493-S	133.4	158	133.6	SPANXC	NM_022661.2	CTP11	molecular	nucleus	biological_
GI_22027494-S	101.2	131	122.6	SPANXD	NM_032417.2	dJ171K16.1			
GI_22027495-S	120.6	196.8	140.2	SPANXE	NM_145665.1				
GI_22027497-S	389.3	359.8	329.1	CABIN1	NM_012295.2	CAIN;KIAA0330			
GI_22027498-S	143.7	166.5	164.3	CACNG7	NM_031896.3		voltage-	voltage-	ion
GI_22027499-S	97.8	100.7	80.4	CA8	NM_004056.3	CALS;CARP;CA-VIII	carbonate		one-
GI_22027504-S	716.1	640.1	869.2	CDC91L1	NM_080476.3	PIGU;MGC40420;bA346K17.2		integral to	
GI_22027505-A	201.7	206.3	203.6	CDCA1	NM_031423.2	NUF2R			
GI_22027506-I	158.9	167.5	155.5	CDCA1	NM_145697.1	NUF2R			
GI_22027508-I	937.7	825.5	787.5	CDCA4	NM_017955.2	HEPP;FLJ20764;MGC:19517			
GI_22027510-A	1076.9	1072.8	1317.3	CDCA4	NM_145701.1	HEPP;FLJ20764;MGC:19517			
GI_22027512-I	89.4	105.7	103.7	CDCA7	NM_031942.3	JPO1;FLJ14722;FLJ14736;MGC34109			
GI_22027513-A	580.4	550.4	278	CDCA7	NM_145810.1	JPO1;FLJ14722;FLJ14736;MGC34109			
GI_22027517-A	115.9	100.8	96	CPVL	NM_031311.2	HVLP;MGC10029	serine		proteolysis
GI_22027519-A	154.4	173.6	160.3	GNAT1	NM_000172.2	GBT1;GNATR	heterotrim	peripheral	vision
GI_22027521-I	87.2	88.2	98.8	GNAT1	NM_144499.1	GBT1;GNATR	heterotrim	peripheral	vision
GI_22027523-S	246.2	275.1	267.4	GNAT2	NM_005272.2	ACHM4;GNATC	heterotrim	peripheral	G-protein
GI_22027524-S	1034.1	774.3	660.7	ARHGEF6	NM_004840.1	PIXA;COOL2;MRX46;Cool-	Rho	intracellula	JNK
GI_22027526-A	130.6	140.8	119.3	ARHGEF7	NM_003899.2	P50;P85;PAK3;PIXB;COOL1;P50BP;P85SPR	guanyl-		signal
GI_22027526-I	1030.7	1091.5	936.9	ARHGEF7	NM_003899.2	P50;P85;PAK3;PIXB;COOL1;P50BP;P85SPR	guanyl-		signal
GI_22027527-I	94.6	91.5	89.3	ARHGEF7	NM_145735.1	P50;P85;PAK3;PIXB;COOL1;P50BP;P85SPR	guanyl-		signal
GI_22027529-S	321.2	396.1	403.9	ARH	NM_015627.1	ARH2;FHCB1;FHCB2;MGC34705;DKFZp586			
GI_22027531-A	270.7	265.4	267.7	MOCS1	NM_138928.1	MOCOD;MOCS1A;MOCS1B	catalytic		Mo-
GI_22027537-S	567.6	729.1	670.6	PDCD6IP	NM_013374.2	AIP1;Alix;HP95;KIAA1375;MGC17003	signal	cytosol	signal
GI_22027539-S	6170.5	7013.5	6347.3	PDCD6	NM_013232.2	ALG-2;MGC9123	calcium		induction
GI_22027540-S	712.6	629	601.7	PDCD7	NM_005707.1	ES18;HES18;MGC22015	DNA	nucleus	regulation
GI_22027542-S	195.4	246.7	209	CACNG1	NM_000727.2	CACNLG	dihydropyr	voltage-	small
GI_22027543-S	215.6	280.5	245.9	CACNG2	NM_006078.2		voltage-	voltage-	small
GI_22027545-S	93.3	102.6	89.9	CACNG3	NM_006539.2		voltage-	voltage-	ion
GI_22027547-S	93.9	111.6	88.1	CACNG4	NM_014405.2	MGC11138;MGC24983	voltage-	integral to	small
GI_22027550-A	205	243.4	209.2	CACNG5	NM_145811.1		ion	membran	small

GI_22027550-I	158.4	177.7	153.3	CACNG5	NM_145811.1		ion	membran	small
GI_22027553-I	99.8	116.1	97	CACNG6	NM_145814.1		voltage-	voltage-	ion
GI_22027559-A	96.8	237.2	103.8	CACNG6	NM_031897.2		voltage-	voltage-	ion
GI_22027608-A	2359.9	2133.5	2481.1	COL13A1	NM_080815.2		collagen	collagen	
GI_22027610-S	278.2	302.5	225.4	TRAF1	NM_005658.2	EBI6;MGC:10353		cytoplasm	protein
GI_22027613-A	950.8	756.1	791.4	TRAF2	NM_145718.1	TRAP;TRAP3;MGC:45012			
GI_22027615-A	186.7	175	159.3	TRAF3	NM_003300.2	LAP1;CAP-1;CRAF1;CD40bp	signal	kinesin	induction
GI_22027621-I	128.6	140.8	165.8	TRAF4	NM_004295.2	CART1;MLN62;RNF83	DNA	nucleus	signal
GI_22027623-A	304	437.7	390.7	TRAF4	NM_145751.1	CART1;MLN62;RNF83	DNA	nucleus	signal
GI_22027625-I	319	408.4	372.3	TRAF5	NM_004619.2	RNF84;MGC:39780	zinc ion	kinesin	signal
GI_22027626-A	500.8	455.1	240.4	TRAF5	NM_145759.1	RNF84;MGC:39780	zinc ion	kinesin	signal
GI_22027626-I	126.6	148.3	152.9	TRAF5	NM_145759.1	RNF84;MGC:39780	zinc ion	kinesin	signal
GI_22027628-A	205.1	233.7	264.5	TRAF6	NM_004620.2	RNF85;MGC:3310	nucleic		signal
GI_22027629-I	98.4	119	114.1	TRAF6	NM_145803.1	RNF85;MGC:3310	nucleic		signal
GI_22027631-I	87.9	100	89.1	DGKB	NM_004080.1	DGK;DAGK2;DGK-BETA;KIAA0718	ATP	plasma	protein
GI_22027633-A	122.1	109.9	119.9	DGKB	NM_145695.1	DGK;DAGK2;DGK-BETA;KIAA0718	ATP	plasma	protein
GI_22027633-I	85.4	93.1	98.4	DGKB	NM_145695.1	DGK;DAGK2;DGK-BETA;KIAA0718	ATP	plasma	protein
GI_22027637-I	136.5	165.6	155.5	DMN	NM_145728.1	SYN;KIAA0353	structural	intermedia	
GI_22027639-S	641.5	1427.2	1267.9	HIST2H2BE	NM_003528.2	H2B;GL105;H2B.1;H2B/q;H2BFQ	DNA	chromoso	nucleoso
GI_22027640-S	1513	2502.3	2405.1	H3F3A	NM_002107.2	H3F3;H3.3A			
GI_22027643-S	191	171.8	126.2	KLK1	NM_002257.2	KLKR;Klk6	tissue	cellular_co	proteolysis
GI_22027645-S	197.1	245.5	224	AMOTL1	NM_130847.1	JEAP			
GI_22027647-S	1377.9	1277.1	1381.5	LPIN1	NM_145693.1	KIAA0188	molecular	nucleus	adipocyte
GI_22027649-S	318.6	209.6	310.8	LPIN2	NM_014646.2	KIAA0249		nucleus	
GI_22027652-A	720.2	902.1	533.6	AP1B1	NM_145730.1	ADTB1;BAM22;AP105A;CLAPB2	vesicle	coated pit	nonselecti
GI_22027654-S	2758.5	1919.5	798.1	AP1S2	NM_003916.3	DC22;SIGMA1B;MGC:1902	protein	clathrin	endocytosi
GI_22035547-S	476	556.6	531.3	APBA1	NM_001163.2	X11;X11A;MINT1;D9S411E;X11ALPHA	vesicle	synaptic	axon
GI_22035549-S	251.8	264.2	199.3	APBA2	NM_005503.2	X11L;MINT2;LIN-	amyloid		pathogene
GI_22035551-S	970.2	962.6	906.4	APBA3	NM_004886.2	X11L2;mint3;MGC:15815	protein	membran	intracellula
GI_22035552-I	117	125.5	100.2	APBB1	NM_001164.2	RIR;FE65;MGC:9072	protein C-		signal
GI_22035553-A	198.2	253.2	242.9	APBB1	NM_145689.1	RIR;FE65;MGC:9072	protein C-		signal
GI_22035553-I	124.8	138.3	140.9	APBB1	NM_145689.1	RIR;FE65;MGC:9072	protein C-		signal
GI_22035555-I	116.2	114.9	120.2	BRF1	NM_001519.2	BRF;hBRF;GTF3B;TAF3C;TAF3B2;TF3B90;	RNA	transcripti	tRNA
GI_22035559-A	861.8	725.7	765.3	BRF1	NM_145696.1	BRF;hBRF;GTF3B;TAF3C;TAF3B2;TF3B90;	RNA	transcripti	tRNA
GI_22035559-I	116.9	131.4	111.1	BRF1	NM_145696.1	BRF;hBRF;GTF3B;TAF3C;TAF3B2;TF3B90;	RNA	transcripti	tRNA
GI_22035561-S	573.8	510.9	385	BRF2	NM_018310.2	BRFU;FLJ11052;TFIIIB50			
GI_22035563-A	119.2	116.2	106.4	C21orf66	NM_058191.2	GCFC;BM-020			
GI_22035568-I	214.3	235	203.9	C21orf66	NM_013329.2	GCFC;BM-020			
GI_22035573-A	151.8	164.1	154.3	3-Sep	NM_145734.1	SEP3;bK250D10.3			
GI_22035582-I	146.3	144	169.2	DONSON	NM_017613.2	B17;C21ORF60;DKFZP434M035	molecular	cellular_co	biological_
GI_22035585-A	370.9	405.2	534.3	DONSON	NM_145795.1	B17;C21ORF60;DKFZP434M035	molecular	cellular_co	biological_
GI_22035587-A	3344.2	3514.8	3508.8	MRPL24	NM_024540.2	MGC9831;MRP-L18;FLJ20917;MGC22737	structural	ribosome	protein
GI_22035591-I	245.1	321.8	239.7	MRPL35	NM_016622.2				
GI_22035593-A	637.2	652	491.4	MRPL35	NM_145644.1				

GI_22035595-S	2703.3	2802.7	2434.7	MRPL53	NM_053050.2	MGC20402			
GI_22035596-S	541.9	583.4	563.4	MRPL9	NM_031420.2	L9mt	structural	ribosome	protein
GI_22035597-S	93.9	103	91.1	MAP3K8	NM_005204.2	COT;EST;ESTF;TPL2;Tpl-2;c-COT	protein	cytosol	protein
GI_22035599-S	1288.7	1208.7	1673.4	MAP4K2	NM_004579.2	GCK;BL44;RAB8IP	protein	Golgi	hemocyte
GI_22035601-A	6801.8	6528.5	3415.8	MAP4K4	NM_004834.2	HGK;NIK;FLH21957;KIAA0687	protein	cellular_co	signal
GI_22035603-I	207.2	260.1	210.6	MAP4K4	NM_145686.1	HGK;NIK;FLH21957;KIAA0687	protein	cellular_co	signal
GI_22035607-I	153	182.1	146.4	OSBPL5	NM_020896.2	ORP5;OBPH1;FLJ31948;KIAA1534;DKFZp5			
GI_22035608-A	369	321.2	277.7	OSBPL5	NM_145638.1	ORP5;OBPH1;FLJ31948;KIAA1534;DKFZp5			
GI_22035610-I	217.8	271.1	240.4	OSBPL6	NM_032523.2	ORP6;FLJ36583			
GI_22035611-A	601	374	414.9	OSBPL6	NM_145739.1	ORP6;FLJ36583			
GI_22035611-I	92.9	104.4	98.8	OSBPL6	NM_145739.1	ORP6;FLJ36583			
GI_22035613-I	493.8	518	423.4	OSBPL7	NM_017731.3	ORP7;FLJ20260			lipid
GI_22035615-A	121.7	131.4	123.2	OSBPL7	NM_145798.1	ORP7;FLJ20260			lipid
GI_22035617-S	746.8	691	453	OSBPL8	NM_020841.3	ORP8;KIAA1451			
GI_22035621-A	299.8	725.2	338.4	ASC	NM_145183.1	TMS1;CARD5;PYCARD;MGC10332	apoptosis	intracellula	induction
GI_22035623-S	334.1	465.8	525.5	CDS1	NM_001263.2	CDS	diacylglyc	endoplas	vision
GI_22035625-S	403.1	416.4	337.9	CDS2	NM_003818.2		phosphati	integral to	phospholi
GI_22035626-S	138.8	139.4	135	CSL4	NM_016046.2	p13;SKI4	exonuclea	nuclear	mRNA
GI_22035627-S	1718.8	1457.8	1884.7	LDOC1	NM_012317.2	BCUR1		nucleus	negative
GI_22035628-A	122.2	135.2	125.3	LTC4S	NM_145867.1	MGC33147	leukotrien	microsom	glutathion
GI_22035630-I	131.8	124.7	114.9	LTC4S	NM_000897.2	MGC33147	leukotrien	microsom	glutathion
GI_22035632-I	232.2	321.1	281.7	MGST1	NM_020300.3	MGST;GST12;MGST-I;MGC14525	glutathion	microsom	
GI_22035633-I	86.7	93.5	81.9	MGST1	NM_145764.1	MGST;GST12;MGST-I;MGC14525	glutathion	microsom	
GI_22035635-I	107.7	130.3	103.5	MGST1	NM_145791.1	MGST;GST12;MGST-I;MGC14525	glutathion	microsom	
GI_22035637-A	1116.7	1622.1	1251.2	MGST1	NM_145792.1	MGST;GST12;MGST-I;MGC14525	glutathion	microsom	
GI_22035639-S	141.5	140.4	124.2	MGST2	NM_002413.3	GST2;MGST-II;MGC14097	glutathion	microsom	leukotrien
GI_22035640-S	4412.8	3461.2	4415	MGST3	NM_004528.2	GST-III	peroxidas	microsom	lipid
GI_22035645-A	174.4	310.1	139.6	APOL3	NM_145640.1	CG12-1;APOLIII	apolipopro		inflammat
GI_22035647-I	122.8	148.2	117.8	APOL3	NM_145641.1	CG12-1;APOLIII	apolipopro		inflammat
GI_22035651-I	273.9	362.8	313.3	APOL3	NM_014349.2	CG12-1;APOLIII	apolipopro		inflammat
GI_22035652-I	118.1	137.1	123.4	APOL2	NM_145637.1	APOL-II	high-	intracellula	lipid
GI_22035654-A	146.3	187.5	172.9	APOL2	NM_030882.2	APOL-II	high-	intracellula	lipid
GI_22035654-I	107.7	98.2	102.6	APOL2	NM_030882.2	APOL-II	high-	intracellula	lipid
GI_22035658-A	116	109.9	105.6	APOL4	NM_145661.1	APOLIV;APOL-IV			
GI_22035658-I	162.5	203.1	176.5	APOL4	NM_145661.1	APOLIV;APOL-IV			
GI_22035660-S	140.4	144.5	146.3	APOL6	NM_030641.2	APOL-VI	lipid	cytoplasm	lipid
GI_22035661-I	102.6	107.3	98	LPAL2	NM_024492.2	APOARGC	molecular	cellular_co	biological_
GI_22035662-A	98.9	113.9	108.6	LPAL2	NM_145727.1	APOARGC	molecular	cellular_co	biological_
GI_22035662-I	129.4	119.8	113.3	LPAL2	NM_145727.1	APOARGC	molecular	cellular_co	biological_
GI_22035664-S	1046.2	469.9	389.2	TLN2	NM_015059.1	KIAA0320	actin	cytoskelet	cell
GI_22035666-S	310.2	450.8	482.6	TOB1	NM_005749.2	TOB;TROB;APRO6;TROB1;MGC34446	SH3/SH2		negative
GI_22035667-I	134.4	149.3	130.5	TXNRD2	NM_145747.1	TR;TR3;SELZ;TRXR2;TR-BETA	thioredoxi	mitochond	electron
GI_22035669-A	398.4	249	211.3	TXNRD2	NM_145748.1	TR;TR3;SELZ;TRXR2;TR-BETA	thioredoxi	mitochond	electron
GI_22035669-I	342.5	412.4	369.9	TXNRD2	NM_145748.1	TR;TR3;SELZ;TRXR2;TR-BETA	thioredoxi	mitochond	electron

GI_22035671-I	173.1	201.9	180.6	TXNRD2	NM_006440.2	TR;TR3;SELZ;TRXR2;TR-BETA	thioredoxi	mitochond	electron
GI_22035675-S	737.2	672.3	664.8	PPIL1	NM_016059.3	CYPL1;hCyPX;MGC678;PPIase;CGI-124	cyclophilin		protein
GI_22035676-I	133.9	148.5	134.7	ARID4B	NM_016374.4	BCAA;BRCAA1;RBP1L1;SAP180;RBBP1L1			
GI_22035678-A	643.7	881.6	687.1	ARID4B	NM_031371.2	BCAA;BRCAA1;RBP1L1;SAP180;RBBP1L1			
GI_22035680-A	142.2	154.7	155.5	DRF1	NM_025104.2	ASKL1;FLJ13087;MGC15009			
GI_22035680-I	93.1	91	83	DRF1	NM_025104.2	ASKL1;FLJ13087;MGC15009			
GI_22035681-I	223.6	224.6	226.5	DRF1	NM_145663.1	ASKL1;FLJ13087;MGC15009			
GI_22035683-S	166.1	207.2	207.8	AREG	NM_001657.2	AR;SDGF;CRDGF;MGC13647	growth	integral to	cell
GI_22035684-S	108	108.1	114.5	FZD10	NM_007197.2	FzE7;FZ-10;hFz10	frizzled	integral to	frizzled
GI_22035685-S	180.8	100.3	108.8	FZD3	NM_017412.2	Fz-3;hFz3	frizzled	integral to	frizzled
GI_22035686-S	108.6	124.8	113.2	ESRRB	NM_004452.2	ERR2;ERRb;ESRL2;NR3B2;ERRbeta;ERRbe	ligand-	nucleus	regulation
GI_22035688-S	157.1	159.6	143.5	GCAT	NM_014291.2	KBL;MGC23053	acyltransf	mitochond	amino
GI_22035689-S	254	282.2	275.3	SCRT1	NM_031309.2	SCRT	transcripti	nucleus	regulation
GI_22035691-A	136.2	156	139.8	GFRA1	NM_145793.1	GDNFR;RET1L;RETL1;TRNR1;GDNFRA;M	glial cell	peripheral	cell
GI_22035699-A	269.4	320.3	194	SYNGR1	NM_145738.1	MGC:1939	transporte	synaptic	transport
GI_22035699-I	82.3	104.1	100	SYNGR1	NM_145738.1	MGC:1939	transporte	synaptic	transport
GI_22035701-S	155.1	181.1	176.9	SYNGR4	NM_012451.2		transporte	synaptic	transport
GI_22040879-S	109.8	122.6	108.3	LOC257039	XM_172230.1				
GI_22041538-S	96	82.2	89.1	LOC200842	XM_115974.2				
GI_22041854-S	170.9	195.6	178.3	CAMTA1	XM_042323.8				
GI_22042061-S	79.3	101.1	86.2	LOC254938	XM_173120.1				
GI_22042087-S	24406	19420	17068	LOC150978	XM_087062.2				
GI_22042250-S	118.8	107.7	94.9	LOC256085	XM_172389.1				
GI_22042868-S	117.4	143.9	134.3	LOC253584	XM_173068.1				
GI_22042949-S	325.9	317.2	279.7	KIAA1530	XM_042661.5				
GI_22043462-S	92.8	100.2	95.2	LOC256483	XM_173015.1				
GI_22044796-S	130	139.5	137.1	LOC256880	XM_173135.1				
GI_22045019-S	112.7	109.3	116.5	LOC169831	XM_095964.5				
GI_22046514-S	100.7	117.4	102.6	LOC253883	XM_171154.1				
GI_22047129-S	195.1	704.9	669.8	IRX1	XM_098320.3				
GI_22047411-S	124.2	135.1	122.5	LOC253314	XM_171094.1				
GI_22047801-S	104	111.3	102.4	LOC253254	XM_173140.1				
GI_22049288-S	125.6	126.2	118.7	LOC202378	XM_114475.2				
GI_22049345-S	97.2	100.8	97.1	KIAA1061	XM_048786.5				
GI_22049497-S	188.9	235.4	217.2	LOC137797	XM_070613.2				
GI_22049632-S	126.6	156.6	141.6	LOC256453	XM_172917.1				
GI_22050438-S	282.3	372.5	416	LOC116412	XM_058097.2				
GI_22050996-S	151.4	178.1	106.7	KIAA1274	XM_166125.2				
GI_22051590-S	101.8	110.8	106	LOC255809	XM_172995.1				
GI_22053417-S	149.9	172.2	160	KIAA1623	XM_050644.2				
GI_22053572-S	537.7	681	638.2	KIAA0841	XM_049237.5				
GI_22053647-S	128.9	141.9	129.8	LOC221140	XM_167908.2				
GI_22054253-S	114.9	114	112.3	LOC256096	XM_173164.1				
GI_22054273-S	95	86.3	80.3	LOC253582	XM_173166.1				

GI_22054302-S	182.8	212.1	202.6	LOC145660	XM_085200.2				
GI_22054399-S	122.4	132.5	127.9	LOC145741	XM_096852.2				
GI_22055338-S	287.8	364.4	277.1	KIAA1465	XM_027396.5				
GI_22055650-S	988.1	1213	976.5	KIAA1600	XM_049351.3				
GI_22055838-S	173.5	146.5	117.1	KIAA1024	XM_044580.5				
GI_22056189-S	99.8	100.3	110.8	KIAA1233	XM_032181.3				
GI_22056336-S	140.4	155	143.6	LOC253724	XM_172874.1				
GI_22058592-S	221.4	267.5	325	KIAA0701	XM_045423.3				
GI_22059218-S	83.2	85.8	101.2	KIAA1384	XM_035405.6				
GI_22060272-S	288.9	421.9	546	LOC221424	XM_168060.2				
GI_22060692-S	138.3	190.8	179.1	LOC201484	XM_117100.2				
GI_22061507-S	110.2	120.8	106.3	LOC143970	XM_096516.2				
GI_22061830-S	147	212.8	159.7	LOC256892	XM_171424.1				
GI_22061836-S	256.4	314	292.3	LOC119695	XM_061627.2				
GI_22062022-S	1609.7	1329.3	1065.8	KIAA0033	XM_084530.5				
GI_22062495-S	5084	5681.4	5477.2	DKFZp762C1	XM_170658.1				
GI_22062556-S	157.1	179.5	167.5	LOC254439	XM_170659.1				
GI_22062795-S	77	83.9	82.2	LOC254750	XM_171156.1				
GI_22062991-S	136.9	143.6	126.8	LOC255849	XM_172855.1				
GI_22063015-S	149.3	160.2	132.8	LOC219873	XM_166780.2				
GI_22063727-S	125.7	118.7	111.3	LOC219482	XM_166834.2				
GI_22064848-S	223.1	245	244.3	LOC255244	XM_171495.1				
GI_22066239-S	133.6	118	120.1	LOC253013	XM_171892.1				
GI_22066626-S	96	99.4	85.1	LOC255725	XM_171528.1				
GI_22067432-S	128.4	134.8	148.5	KIAA1348	XM_043826.5				
GI_22068066-S	145	172.3	146.6	LOC197317	XM_117014.2				
GI_22068828-S	150.1	214.6	151.6	LOC150371	XM_086879.2				
GI_22070290-S	130.1	145.8	134.2	LOC146599	XM_085517.3				
GI_22091444-S	148.9	178.5	169.2	GFRA2	NM_001495.3	NTNRA;RETL2;TRNR2;GDNFRB;NRTNR-	glial cell	peripheral	transmem
GI_22091446-A	83.9	99	88.5	GFRA4	NM_022139.2		receptor	membran	
GI_22091447-I	219.9	229.9	212.9	GFRA4	NM_145762.1		receptor	membran	
GI_22091451-S	108	118.4	123	APOM	NM_019101.2	G3a;NG20;HSPC336;MGC:22400	apolipopro	integral to	membran
GI_22091453-S	87.9	99.1	97.3	GSTA1	NM_145740.1	GST2;GTH1;GSTA1-1	glutathion	cytoplasm	glutathion
GI_22091455-S	255.1	253	258.4	SYNGR2	NM_004710.2		transporte	synaptic	transport
GI_22091456-S	210.5	285.5	290.2	SYNGR3	NM_004209.4	MGC:20003		integral to	
GI_22091457-S	132.8	162.4	126.4	APOA5	NM_052968.2	RAP3;APOAV;APOA-V	lipid		lipid
GI_22091458-S	1605.6	1687.6	1599	PES1	NM_014303.2	PES		kinesin	embryoge
GI_22091459-S	2681.4	4146.6	3821.7	RBX1	NM_014248.2	ROC1;RNF75;MGC1481;MGC13357;BA554	eukaryotic	ubiquitin	ubiquitin-
GI_22094078-S	2550	2609.7	2414.7	TRIP3	NM_004773.1	ZNHIT3	transcripti		transcripti
GI_22094120-S	500.5	461.8	364.6	KIAA0648	NM_015200.1	SCC-112			
GI_22094124-S	101.5	103.6	99.6	ZFP28	NM_020828.1	KIAA1431			
GI_22094134-S	131.9	111.5	133.5	DOT1L	NM_032482.1	DOT1;KIAA1814	histone-	nucleus	regulation
GI_22094142-I	287.7	194	147.1	NEK11	NM_024800.2	FLJ23495	protein-		protein
GI_22094986-S	331.8	411.3	572.6	raptor	NM_020761.1	KIAA1303			

GI_22095330-S	1051.4	1719.2	1376.3	KIAA0090	NM_015047.1				
GI_22095338-S	1336	2174.5	1700.1	PGK1	NM_000291.2	PGKA	phosphogl		glycolysis
GI_22095339-S	480	1024.7	733.6	KCNJ2	NM_000891.2	IRK1;LQT7;HHIRK1;KIR2.1;HHBIRK1	inward	membran	potassium
GI_22095341-S	1674.1	1480.5	1407.2	CCT6A	NM_001762.2	CCT6;Cctz;HTR3;TCPZ;TCP20;TTCP20	chaperone	cytoplasm	protein
GI_22095346-S	439.2	2100.7	5024.7	IGSF4	NM_014333.2	BL2;ST17;NECL2;TSLC1;SYNCAM			
GI_22095348-S	344.1	393.3	404.5	WDTC1	NM_015023.2	KIAA1037			
GI_22095350-S	449.8	452.4	418.1	XPO7	NM_015024.2	RANBP16;KIAA0745	protein	nuclear	protein-
GI_22095352-S	149.5	151.7	157.1	BCAS3	NM_017679.2	MAAB;GAOB1;MGC4973;FLJ20128		nucleus	cell growth
GI_22095354-S	460.3	352.3	329.8	BIVM	NM_017693.2				
GI_22095357-S	301.8	309.1	254.2	C12orf4	NM_020374.2				
GI_22095359-S	128.4	135.1	124.4	CD209	NM_021155.2	CDSIGN;DC-SIGN;DC-SIGN1			
GI_22095361-S	428.4	463.5	381.1	C9orf19	NM_022343.2	GAPR-1;GLIPR2			
GI_22095362-S	2178.7	1542.1	1047.4	C14orf135	NM_022495.2	FLJ12799			
GI_22095364-S	273.8	328.7	287.3	RANBP17	NM_022897.2		GTP	nuclear	protein-
GI_22095366-S	169.3	210.3	173.6	FLJ13386	NM_025180.2				
GI_22095370-S	790.2	917	704.6	RUFY1	NM_025158.2	ZFYVE12;FLJ22251	zinc ion		electron
GI_22095372-S	123.5	129.3	133.5	MGC10986	NM_030576.2		electron		electron
GI_22095373-S	1985.8	4601.1	1404.4	LOXL3	NM_032603.2		protein-	membran	biological_
GI_22095374-S	105.3	111.3	107	PTPN5	NM_032781.2	STEP;PTPSTEP;FLJ14427	prenylated	integral to	protein
GI_22095383-S	550.5	556.3	456.3	RBM15	NM_022768.3	OTT;SPEN;FLJ12479;FLJ21943	RNA		cell growth
GI_22095387-S	149.1	181.5	161.4	ALS2CR15	NM_138468.3	DKFZp434E1919			
GI_22095394-S	3127.9	3366.5	2911.9	DPCK	NM_025233.3	NBP;PPAT;UKR1;CoASY;pOV-2	nucleotide	cellular_co	biological_
GI_22095396-S	163.9	165.9	137.9	CRELD1	NM_015513.2	AVSD2;CIRRIN;DKFZP566D213			
GI_22129771-S	97.6	131.4	70.4	PF20	NM_024532.2	WDR29;FLJ22724;DKFZp666P1710			
GI_22129777-S	3250.9	2733.7	1429.9	C20orf139	NM_080725.1	dJ850E9.2	DNA	extrachro	
GI_22165415-A	249.6	276.3	240.5	GALT	NM_000155.2		UTP-		galactose
GI_22165415-I	730.3	720.5	613.3	GALT	NM_000155.2		UTP-		galactose
GI_22165417-I	123.1	136.6	143.3	GALT	NM_147131.1		UTP-		galactose
GI_22165421-S	101	81.9	82.2	AQP3	NM_004925.3		transporte	membran	small
GI_22165422-I	107.7	111	104.4	DCTN3	NM_024348.2	DCTN22;DCTN-22	structural	dynactin	cytokinesi
GI_22165423-A	1443.2	1846.6	2115.6	DCTN3	NM_007234.3	DCTN22;DCTN-22	structural	dynactin	cytokinesi
GI_22165424-S	111.2	115.4	105.1	CCL19	NM_006274.2	ELC;CKb11;MIP3B;MIP-	chemokin	extracellul	chemotaxi
GI_22165425-S	259.3	293.7	289.2	CCL21	NM_002989.2	SLC;CKb9;TCA4;SCYA21;MGC34555	chemokin	extracellul	chemotaxi
GI_22165426-S	94.7	107.1	113.7	CCL24	NM_002991.2	Ckb-6;MPIF2;MPIF-2;SCYA24	chemokin	extracellul	chemotaxi
GI_22165428-S	136.1	153.9	140.6	CCL27	NM_006664.2	ALP;ILC;CTAK;CTACK;PESKY;ESKINE;SCY	chemokin	extracellul	chemotaxi
GI_22165429-A	6568.5	6162.1	5865.8	ANXA11	NM_001157.2	ANX11;CAP50	phospholi	cytoplasm	immune
GI_22165432-I	98.9	99.4	93.4	ANXA11	NM_145869.1	ANX11;CAP50	phospholi	cytoplasm	immune
GI_22202605-A	154.4	179.4	164.8	BVES	NM_147147.1	POP1;HBVES;POPDC1;MGC42413		integral to	muscle
GI_22202605-I	100.9	120.9	101.4	BVES	NM_147147.1	POP1;HBVES;POPDC1;MGC42413		integral to	muscle
GI_22202607-I	112.3	119.3	107.4	BVES	NM_007073.2	POP1;HBVES;POPDC1;MGC42413		integral to	muscle
GI_22202610-S	1424.9	1817.8	1617.7	CPD	NM_001304.3		carboxype	integral to	proteolysis
GI_22202613-I	258	232.4	243.9	CRYZL1	NM_145311.1	4P11;QOH-1	NADPH:q		
GI_22202615-I	138.2	139.7	139.4	CRYZL1	NM_145858.1	4P11;QOH-1	NADPH:q		
GI_22202617-I	159.9	176.2	181.9	CTSL	NM_001912.2	MEP;CATL	cathepsin	lysosome	proteolysis

GI_22202618-A	3640.7	3166.6	5188.1	CTSL	NM_145918.1	MEP;CATL	cathepsin	lysosome	proteolysis
GI_22202620-S	100.3	92.7	85	GSTA2	NM_000846.3	GST2;GTA2;GTH2;GSTA2-2;MGC10525	glutathion		glutathion
GI_22202621-I	140.4	125.3	129.4	GSTZ1	NM_001513.2	MAI;MAAI;GSTZ1-1;MGC2029	maleylacet	cytoplasm	phenylala
GI_22202625-A	330.2	387.9	385.7	GSTZ1	NM_145871.1	MAI;MAAI;GSTZ1-1;MGC2029	maleylacet	cytoplasm	phenylala
GI_22202627-I	176.8	216.8	224.4	PDCD8	NM_004208.2	AIF	electron	mitochond	DNA
GI_22202628-I	114.2	106.6	101.5	PDCD8	NM_145812.1	AIF	electron	mitochond	DNA
GI_22202630-A	277.7	370.3	405.4	PDCD8	NM_145813.1	AIF	electron	mitochond	DNA
GI_22202636-A	8718.7	8984.2	7766.5	PFDN5	NM_145897.1	MM1;MM-1;PFD5;MGC5329	transcripti	nucleus	regulation
GI_22203764-S	164.3	401.4	452.2	GALNT12	NM_024642.2	FLJ21212	transferas		
GI_22208950-A	851.4	1026.4	873.4	ASB3	NM_145863.1	ASB-			intracellula
GI_22208952-I	251.4	283.8	218.1	ASB3	NM_016115.3	ASB-			intracellula
GI_22208953-S	130.1	136	139.4	ASB10	NM_080871.2				intracellula
GI_22208954-S	94.8	103.4	100.6	ASB12	NM_130388.2	FLJ39577			
GI_22208956-S	239.1	233.5	227.2	ASB13	NM_024701.2	FLJ13134;MGC19879			intracellula
GI_22208961-S	761.7	744.1	823.3	ASB1	NM_016114.3	ASB-1;KIAA1146;MGC11165	molecular	intracellula	intracellula
GI_22208962-S	405	627.5	479.5	ASB2	NM_016150.3	ASB-2;MGC40044			signal
GI_22208963-I	86.6	96.5	88.1	ASB4	NM_145872.1	ASB-4			
GI_22208965-S	92.4	90	84.8	ASB5	NM_080874.2				intracellula
GI_22208974-A	2605.5	1624.6	2925.4	HMGA1	NM_145903.1	HMG-	AT DNA		regulation
GI_22208976-I	103.7	101.1	97.2	HMGA1	NM_145904.1	HMG-	AT DNA		regulation
GI_22208978-I	122.3	120.5	114.6	HMGA1	NM_145905.1	HMG-	AT DNA		regulation
GI_22208981-I	95.6	112.1	102.4	KLK10	NM_002776.3	NES1;PRSSL1	serine-	extracellul	cell growth
GI_22208983-A	91.6	88.2	89.6	KLK10	NM_145888.1	NES1;PRSSL1	serine-	extracellul	cell growth
GI_22208988-A	154.7	170.1	149.1	KLK12	NM_145895.1	KLK-L5			
GI_22208990-I	110.6	122.6	109.9	KLK3	NM_001648.2	APS;PSA	serine-		
GI_22208991-A	253.4	293.3	254.2	KLK3	NM_145864.1	APS;PSA	serine-		
GI_22208991-I	474.6	525.6	446.6	KLK3	NM_145864.1	APS;PSA	serine-		
GI_22208993-S	200.4	217.5	195.9	KLK5	NM_012427.3	SCTE;KLKL2;KLK-L2	serine-	extracellul	epidermal
GI_22208996-S	953.3	741	678.6	BBS2	NM_031885.2	BBS;MGC20703	cell	integrin	cell-matrix
GI_22208998-S	99.4	110.9	111.5	JRK	NM_003724.1	JH8			
GI_22209000-S	292.3	286	259.2	TIGD1	NM_145702.1	EEYORE			
GI_22209002-S	200.2	249.6	219.9	P11	NM_006025.2	PP11;PRSS26-PENDING	serine-	extracellul	proteolysis
GI_22209003-S	111.7	118.2	112	POPDC2	NM_022135.2	POP2	molecular	integral to	biological_
GI_22209005-S	127.5	145.4	132.7	RTDR1	NM_014433.2	MGC16968	peroxidas	cellular_co	biological_
GI_22209006-S	702.5	636	847.2	1-Sep	NM_052838.2	LARP;SEP1;DIFF6;PNUTL3;MGC20394	GTP		cytokinesi
GI_22209007-S	1727.7	2335	2669	SPRY2	NM_005842.2	hSPRY2;MGC23039		membran	histogene
GI_22209008-A	382.5	311.5	265.1	CHEK2	NM_145862.1	CDS1;CHK2;RAD53;HuCds1;PP1425;bA444			
GI_22209010-I	83.5	94.7	79.6	CHEK2	NM_007194.2	CDS1;CHK2;RAD53;HuCds1;PP1425;bA444			
GI_22212916-A	368.1	485.8	404.6	CNTFR	NM_001842.3	MGC1774	ciliary	membran	signal
GI_22212917-I	267	346.7	300.6	CNTFR	NM_147164.1	MGC1774	ciliary	membran	signal
GI_22212919-S	115.8	114.3	122.1	DNAI1	NM_012144.2	ICS;PCD;CILD1;MGC26204	motor	cilium	microtubul
GI_22212920-I	212.9	293	198.4	IL11RA	NM_004512.3	MGC2146	transmem	membran	
GI_22212921-A	233.1	270.2	210.9	IL11RA	NM_147162.1	MGC2146	transmem	membran	
GI_22212921-I	239.8	280.8	248	IL11RA	NM_147162.1	MGC2146	transmem	membran	

GI_22212923-I	302.3	431.4	449.7	NFX1	NM_002504.3	NFX2;MGC20369	transcripti	nucleus	transcripti
GI_22212924-A	354.5	343.9	331.1	NFX1	NM_147133.1	NFX2;MGC20369	transcripti	nucleus	transcripti
GI_22212924-I	84.6	111.3	95.2	NFX1	NM_147133.1	NFX2;MGC20369	transcripti	nucleus	transcripti
GI_22212926-I	470.5	453.2	415.5	NFX1	NM_147134.1	NFX2;MGC20369	transcripti	nucleus	transcripti
GI_22212935-A	3651	3136.4	3213.4	OPRS1	NM_147158.1	SR-BP1;MGC3851;SIGMAR1;FLJ25585	drug	integral to	
GI_22212941-S	631.6	740	436.3	UBAP1	NM_016525.3	UAP;UBAP;NAG20;MGC8710			
GI_22212942-S	4313.3	3737.9	3506.7	UBE2R2	NM_017811.2	UBC3B;CDC34B;FLJ20419;MGC10481	ubiquitin		ubiquitin
GI_22218338-S	197.3	249.6	283.9	MGC39325	NM_147189.1				
GI_22218340-S	164.5	176.6	167.6	MMP21	NM_147191.1		zinc ion	extracellul	proteolysis
GI_22218342-S	203.9	238.9	207.9	FLJ36155	NM_147193.1	GLIS1			
GI_22218344-S	903.7	834.9	655.7	LASS5	NM_147190.1	Trh4;FLJ25304;MGC45411	transcripti	nucleus	regulation
GI_22218346-S	117.3	117.9	119.2	TMIE	NM_147196.1	DFNB6			
GI_22218352-S	268	361.1	316.1	MGC35361	NM_147194.1				
GI_22218356-S	110.9	102.2	103.4	MRGX1	NM_147199.1		receptor	integral to	G-protein
GI_22218618-S	1012.1	1130.1	1060.4	KIAA1892	NM_015397.1	MGC1058;DKFZP434O125			
GI_22218620-S	522	668.8	639	C9orf25	NM_147202.1	FLJ39031;bA573M23.5			
GI_22219459-A	460.9	539.2	495.4	CREB1	NM_004379.2	CREB;MGC9284	transcripti	nucleus	transcripti
GI_22219466-A	531.5	545.4	536.2	NUDT2	NM_147173.1	APAH1;MGC10404	bis(5'-		nucleobas
GI_22219470-A	192.4	251.1	227.3	C9orf24	NM_147169.1	MGC32921;MGC33614;NYD-			
GI_22219472-I	155	194.7	154.9	C9orf24	NM_032596.3	MGC32921;MGC33614;NYD-			
GI_22219473-S	349.4	384.9	402.2	FADD	NM_003824.2	MORT1;MGC8528	death	cytoplasm	induction
GI_22219475-S	156.4	196.3	185.3	KLK14	NM_022046.3	KLK-L6	trypsin	extracellul	proteolysis
GI_22265328-S	483.4	775	659.3	CRADD	NM_003805.2	RAIDD;MGC9163	death	intracellula	induction
GI_22265329-I	212.7	149.5	144.4	NUDT2	NM_001161.3	APAH1;MGC10404	bis(5'-		nucleobas
GI_22267435-S	98.2	104.5	88.4	NIPSNAP3A	NM_015469.1	HSPC299;FLJ13953;MGC14553;DKFZp564			
GI_22296883-S	849	818.7	787.7	FAM11A	NM_032508.1	CXorf13			
GI_22325354-I	2211	1794.7	759.6	AKAP2	NM_007203.3	PRKA2;AKAPKL;KIAA0920;DKFZp564L0716		kinesin	
GI_22325355-A	472	379.4	285.1	AKAP2	NM_147150.1	PRKA2;AKAPKL;KIAA0920;DKFZp564L0716		kinesin	
GI_22325357-I	214.2	265.2	247.3	LRDD	NM_018494.2	PIDD;MGC16925	death		signal
GI_22325359-I	92.1	108.3	89.7	LRDD	NM_145886.1	PIDD;MGC16925	death		signal
GI_22325361-A	1210.3	1135.4	1004.1	LRDD	NM_145887.1	PIDD;MGC16925	death		signal
GI_22325365-A	1225	1210	1279.6	UBAP2	NM_020867.1	FLJ22435;KIAA1491;bA176F3.5			
GI_22325369-A	658.9	756.8	736.6	C9orf23	NM_148178.1	MGC29635;bA296L22.5			
GI_22325371-I	226.2	254.9	249.7	C9orf23	NM_148179.1	MGC29635;bA296L22.5			
GI_22325373-I	96.7	104.5	107.3	EDARADD	NM_080738.2		death	cytoplasm	NIK-I-
GI_22325374-A	172.3	245.2	162.6	EDARADD	NM_145861.1		death	cytoplasm	NIK-I-
GI_22325374-I	103.1	112.2	110.2	EDARADD	NM_145861.1		death	cytoplasm	NIK-I-
GI_22325376-A	2026.4	2349.2	2013.1	RIOK3	NM_003831.2	SUDD	molecular		chromoso
GI_22325378-I	71.4	83.8	81.7	RIOK3	NM_145906.1	SUDD	molecular		chromoso
GI_22325382-A	108.7	113.4	109.7	ITSN2	NM_147152.1	SWA;SWAP;SH3D1B;SH3P18;KIAA1256	SH3/SH2	kinesin	endocytosi
GI_22325382-I	97.2	96	96.6	ITSN2	NM_147152.1	SWA;SWAP;SH3D1B;SH3P18;KIAA1256	SH3/SH2	kinesin	endocytosi
GI_22325386-I	239.4	243.8	268.3	FBXO26	NM_024907.5	FBG4;MGC9379;FLJ11798;FLJ25205			
GI_22325387-A	765.8	407.1	473.2	FBXO26	NM_148169.1	FBG4;MGC9379;FLJ11798;FLJ25205			
GI_22325387-I	106.5	96.5	93.9	FBXO26	NM_148169.1	FBG4;MGC9379;FLJ11798;FLJ25205			

GI_22325389-I	102.5	113.5	119	OPRS1	NM_147160.2	SR-BP1;MGC3851;SIGMAR1;FLJ25585	drug	integral to	
GI_22325390-S	168.2	197.2	172.3	TIGD6	NM_030953.2	DKFZP761E2110	DNA	nucleus	
GI_22325391-S	228.4	210.2	238.9	TIGD7	NM_033208.2	Sancho	DNA	nucleus	
GI_22380642-S	299.1	351.2	303.4	DSCR10	NM_148676.1		molecular	cellular_co	biological_
GI_22507315-S	245.3	316.6	242.5	SPTB	NM_000347.3		actin	spectrin	cell shape
GI_22507370-I	122.8	112.1	101.1	AMPD2	NM_004037.5		AMP	cellular_co	purine
GI_22507371-S	107.9	98.7	89.7	CLDN19	NM_148960.1		structural	tight	
GI_22507379-S	95.5	89.7	96.7	GPRC6A	NM_148963.1	bA86F4.3	metabotro	membran	
GI_22507381-S	520.2	436.9	267.1	C20orf6	NM_016649.3	FLJ20368;HDCMC28P;bA526K24.1			
GI_22507386-S	98.9	104.8	104.1	ELA1	NM_001971.3		pancreatic		proteolysis
GI_22507387-S	175.6	222.7	215.9	ALG12	NM_024105.2	ECM39;MGC3136			
GI_22507392-S	158.3	186.4	143.7	PERQ1	NM_022574.2	GIGYF1;AF053356-CDS2			
GI_22507393-S	89.3	82.2	85.3	C20orf77	NM_021215.2	dJ1057B20.2;DKFZp434P0735			
GI_22507395-S	102.2	95.1	98.1	GJA8	NM_005267.2	CAE;CAE1;CX50;CZP1;MP70	channel/p	connexon	vision
GI_22507396-S	5766.1	15463	10398	MYH9	NM_002473.2	MHA;FTNS;DFNA17;NMMHCA	adenosine	non-	hearing
GI_22507398-S	121.6	119.1	105.6	FLJ33215	NM_148894.1				
GI_22507400-S	109.9	106.4	101	MDS2	NM_148895.1				
GI_22507402-S	112.6	114.4	110.3	NPB	NM_148896.1	PPL7;PPNPB			neuropepti
GI_22507404-S	92.2	103.7	95.5	SDR-O	NM_148897.1	RDHS	oxidoredu		metabolis
GI_22507406-S	89.6	96.4	97.8	FLJ35740	NM_147195.1	FLJ40632			
GI_22507408-S	1228.5	1111.1	1184.6	C22orf4	NM_014346.1	HSC79E021	DNA	nucleus	regulation
GI_22507412-S	142.6	154.4	139.7	C20orf144	NM_080825.2	dJ63M2.6			
GI_22507413-S	125	139.9	126.6	SRMS	NM_080823.2	SRM;C20orf148;dJ697K14.1	protein-		protein
GI_22507414-S	178.1	218	185	C20orf136	NM_080621.2	dJ591C20.7			
GI_22507416-S	92.2	94.1	86.6	PRY	NM_004676.2	PTPN13LY			
GI_22535295-S	87	97.7	95.8	SMC1L2	NM_148674.1	bK268H5;SMC1BETA;bK268H5.5	ATP	membran	chromoso
GI_22538388-A	101.1	101.3	96.1	AKAP9	NM_147166.1	PRKA9;CG-	N-methyl-	centrosom	small
GI_22538388-I	99.7	103.3	103.6	AKAP9	NM_147166.1	PRKA9;CG-	N-methyl-	centrosom	small
GI_22538399-S	141.8	145	143.1	CCL11	NM_002986.2	SCYA11;MGC22554	chemokin	extracellul	response
GI_22538400-S	104.2	110.6	96.2	OAZ	NM_015069.1	KIAA0760			
GI_22538402-A	236.5	277.8	250.2	A2BP1	NM_018723.2	FOX1;HRNBP1	RNA	Golgi	
GI_22538402-I	136.1	165	126.4	A2BP1	NM_018723.2	FOX1;HRNBP1	RNA	Golgi	
GI_22538416-I	199.2	186.9	166.2	OAZIN	NM_015878.3	OAZI;MGC691;MGC3832	enzyme		polyamine
GI_22538417-A	905	814.8	724	OAZIN	NM_148174.1	OAZI;MGC691;MGC3832	enzyme		polyamine
GI_22538419-S	111.5	105.7	109	AQP10	NM_080429.2	AQPA_HUMAN	transporte	integral to	transport
GI_22538421-S	253.6	310.1	255.1	ATF2	NM_001880.2	HB16;TREB7;CRE-BP1	RNA		
GI_22538424-S	311.7	370.7	391.4	ATPAF2	NM_145691.2	ATP12;ATP12p;MGC29736			
GI_22538425-A	464.4	604.5	511.1	C6orf4	NM_147200.1	ACT1;CIKS;C6orf5;C6orf6;MGC3581;DKFZP	molecular	cellular_co	intracellula
GI_22538425-I	100.3	108.8	111.5	C6orf4	NM_147200.1	ACT1;CIKS;C6orf5;C6orf6;MGC3581;DKFZP	molecular	cellular_co	intracellula
GI_22538427-I	118.9	137.4	119.2	C6orf4	NM_147686.1	ACT1;CIKS;C6orf5;C6orf6;MGC3581;DKFZP	molecular	cellular_co	intracellula
GI_22538429-A	9739.1	8272.7	6743.6	CTSB	NM_001908.2	APPS;CPSB	cathepsin	lysosome	proteolysis
GI_22538438-I	105.8	116.3	101.2	CTSC	NM_001814.2	HMS;PLS;CPPI;DPP1;DPPI;PALS	cysteine-	lysosome	proteolysis
GI_22538439-A	104	100.8	96.5	CTSC	NM_148170.1	HMS;PLS;CPPI;DPP1;DPPI;PALS	cysteine-	lysosome	proteolysis
GI_22538439-I	107.9	110.2	101.9	CTSC	NM_148170.1	HMS;PLS;CPPI;DPP1;DPPI;PALS	cysteine-	lysosome	proteolysis

GI_22538441-S	3609	4781.1	4903	CTSZ	NM_001336.2	CTSX	cysteine-	lysosome	proteolysis
GI_22538443-I	156.6	194	179.4	TP53I3	NM_004881.2	PIG3			
GI_22538445-A	511.3	833.6	864.7	TP53I3	NM_147184.1	PIG3			
GI_22538447-S	822.8	964.2	904.2	PIGB	NM_004855.3	MGC21236	catalytic	endoplas	GPI
GI_22538449-I	108.2	126.9	108.9	PIGQ	NM_004204.2	GPI1;hGPI1;MGC12693	transferas	integral to	carbohydr
GI_22538452-A	207.5	269.5	213.5	PIGQ	NM_148920.1	GPI1;hGPI1;MGC12693	transferas	integral to	carbohydr
GI_22538456-I	122.4	159.1	137.7	NCOA1	NM_147223.1	SRC1;NCoA-1;F-SRC-1	transcripti	nucleus	transcripti
GI_22538458-A	338.8	403.8	372.4	NCOA1	NM_147233.1	SRC1;NCoA-1;F-SRC-1	transcripti	nucleus	transcripti
GI_22538460-S	379.6	372.9	378	NCOR1	NM_006311.2	N-CoR;TRAC1;hN-	transcripti		transcripti
GI_22538462-S	10421.9	12505	11049	PSMB1	NM_002793.2	HC5;PSC5;PMSB1;FLJ25321	peptidase	26S	ubiquitin-
GI_22538463-S	2001.6	2561.9	2087.2	PSMB2	NM_002794.3	HC7-I	peptidase	26S	ubiquitin-
GI_22538464-S	3576.1	5008.2	4939.1	PSMB3	NM_002795.2	HC10-II;MGC4147	peptidase	26S	ubiquitin-
GI_22538466-S	5231.7	6055.1	5066.7	PSMB4	NM_002796.2	HN3;HsN3;PROS26	peptidase	26S	ubiquitin-
GI_22538468-S	3335.9	4477.6	4363.7	PSMB5	NM_002797.2	X;MB1;LMPX	peptidase	26S	ubiquitin-
GI_22538469-S	128.2	126.3	143.5	EOMES	NM_005442.2	TBR2	DNA	nucleus	embryoge
GI_22538474-S	27856.2	31852	28930	UBB	NM_018955.2	MGC8385	ubiquitin		protein
GI_22538475-S	508.3	633.2	585.4	UREB1	NM_031407.2				
GI_22538477-I	275.9	271.1	234.1	PEMT	NM_148172.1	PNMT;PEAMT;PEMPT;PEMT2;MGC2483	phosphati		phosphati
GI_22538479-A	1267.4	962.8	897.4	PEMT	NM_148173.1	PNMT;PEAMT;PEMPT;PEMT2;MGC2483	phosphati		phosphati
GI_22538481-I	93	89	78.5	PEMT	NM_007169.2	PNMT;PEAMT;PEMPT;PEMT2;MGC2483	phosphati		phosphati
GI_22538483-S	1739.6	1303	1181.5	PPIL4	NM_139126.2	HDCME13P	cyclophilin		protein
GI_22538484-S	604.9	649.8	603.2	PRPSAP2	NM_002767.2	PAP41	enzyme		nucleobas
GI_22538485-S	122.2	122.5	121.4	PTCH2	NM_003738.2		tumor	integral to	epidermal
GI_22538487-I	147.6	183.7	183.8	SMCR7	NM_139162.2	MGC23130			
GI_22538489-A	186.4	222.1	258.2	SMCR7	NM_148886.1	MGC23130			
GI_22538491-A	279.6	312.1	349.4	WBSCR16	NM_030798.2	MGC44931;DKFZp434D0421			
GI_22538491-I	345.7	369.9	362.1	WBSCR16	NM_030798.2	MGC44931;DKFZp434D0421			
GI_22538492-I	193	230.2	213.9	WBSCR16	NM_148842.1	MGC44931;DKFZp434D0421			
GI_22538494-S	259.8	313.6	284	WBSCR17	NM_022479.1	DKFZp761D2324	transferas		
GI_22538496-S	127.8	141.1	150.3	WBSCR18	NM_032317.2	MGC12943	chaperone		protein
GI_22538790-I	101.9	103.5	103	PDCD10	NM_007217.3	TFAR15;MGC1212;MGC24477			
GI_22538791-I	309.5	373.5	362.1	PDCD10	NM_145859.1	TFAR15;MGC1212;MGC24477			
GI_22538793-A	984	1395.4	1148.6	PDCD10	NM_145860.1	TFAR15;MGC1212;MGC24477			
GI_22538795-I	82.3	92.7	88.9	CCL25	NM_005624.2	TECK;Ckb15;SCYA25	chemokin	soluble	chemotaxi
GI_22538797-A	232.4	317.3	273.3	CCL25	NM_148888.1	TECK;Ckb15;SCYA25	chemokin	soluble	chemotaxi
GI_22538799-S	90.2	93	91.4	CCL13	NM_005408.2	NCC1;CKb10;MCP-4;NCC-	chemokin	membran	chemotaxi
GI_22538800-S	133.3	163.1	146.6	CCL16	NM_004590.2	LEC;LMC;NCC4;CKb12;HCC-4;LCC-1;Mtn-	chemokin	extracellul	chemotaxi
GI_22538801-S	117	117	108	CCL17	NM_002987.2	TARC;ABCD-2;SCYA17;A-152E5.3	chemokin	extracellul	chemotaxi
GI_22538803-S	120.2	117.4	123	CCL22	NM_002990.3	MDC;ABCD-1;SCYA22;STCP-1;DC/B-	chemokin	extracellul	chemotaxi
GI_22538805-I	86.3	90.5	94.2	CCL23	NM_005064.3	CKb8;MIP3;Ckb-8;MIP-3;MPIF-	chemokin	extracellul	negative
GI_22538807-A	106.5	116	108.2	CCL23	NM_145898.1	CKb8;MIP3;Ckb-8;MIP-3;MPIF-	chemokin	extracellul	negative
GI_22538809-I	180.7	222.7	194.5	CCL28	NM_019846.3	MEC;CCK1;SCYA28	chemokin	extracellul	chemotaxi
GI_22538810-A	114.8	112.7	99.8	CCL28	NM_148672.1	MEC;CCK1;SCYA28	chemokin	extracellul	chemotaxi
GI_22538812-S	136.1	1460.1	234.3	CCL2	NM_002982.2	HC11;MCAF;MCP1;MCP-1;SCYA2;GDCF-	chemokin	membran	response

GI_22538813-S	138.5	306.5	159.1	CCL5	NM_002985.2	SISd;SCYA5;RANTES;TCP228;D17S136E;M	chemokin	extracellul	response
GI_22538815-S	165.2	189.8	168.6	CCL8	NM_005623.2	HC14;MCP2;MCP-2;SCYA8;SCYA10	chemokin	extracellul	response
GI_22547111-S	119.4	112.9	98.8	TNFRSF11A	NM_003839.2	EOF;FEO;OFE;ODFR;PDB2;RANK;TRANCE	receptor	integral to	positive
GI_22547113-A	3971.4	3616.6	3707.3	MRPL10	NM_145255.2	RPML8;MRP-L8;MGC17973			
GI_22547115-I	115.2	126.9	131.2	TNFRSF10B	NM_003842.3	DR5;KILLER;TRICK2;TRICKB;ZTNFR9;TRAI	death	integral to	induction
GI_22547118-A	9087.7	10572	10228	TNFRSF10B	NM_147187.1	DR5;KILLER;TRICK2;TRICKB;ZTNFR9;TRAI	death	integral to	induction
GI_22547120-S	311.6	399.8	331.9	TNFRSF10C	NM_003841.2	LIT;DCR1;TRID;TRAILR3	transmem	integral to	signal
GI_22547122-S	374.8	409	182.9	TNFRSF11B	NM_002546.2	OPG;TR1;OCIF;MGC29565	cytokine	extracellul	skeletal
GI_22547127-A	1549.1	1690.5	1657.3	MRPL27	NM_016504.2	L27mt;MGC23716	structural	ribosome	protein
GI_22547128-I	146.5	148.6	155.9	MRPL27	NM_148570.1	L27mt;MGC23716	structural	ribosome	protein
GI_22547130-I	99.7	110	101.8	MRPL27	NM_148571.1	L27mt;MGC23716	structural	ribosome	protein
GI_22547132-S	1177.3	1311.9	1233.1	MRPL34	NM_023937.2	L34mt;MGC2633;MGC24974	structural	ribosome	protein
GI_22547133-S	5368.3	5065.5	5096.8	MRPL37	NM_016491.2	MRPL2;RPML2;MGC878;MRP-L2			
GI_22547137-A	322.1	359.6	337.9	MRPL4	NM_146387.1	L4mt;CGI-28;MGC2681;MGC16367			
GI_22547139-I	98.2	105.3	104.7	MRPL4	NM_146388.1	L4mt;CGI-28;MGC2681;MGC16367			
GI_22547142-I	439	1034.8	1220.4	FBXO32	NM_058229.2	MAFbx;ATROGIN1;FLJ32424;MGC33610	odorant		transport
GI_22547143-A	2189	4072.6	3660.8	FBXO32	NM_148177.1	MAFbx;ATROGIN1;FLJ32424;MGC33610	odorant		transport
GI_22547143-I	100.3	104.4	92.3	FBXO32	NM_148177.1	MAFbx;ATROGIN1;FLJ32424;MGC33610	odorant		transport
GI_22547145-S	165.9	199.8	205.5	FBXL8	NM_018378.2	FLJ11278;MGC19959			
GI_22547147-A	975.9	958	906.9	FBXO22	NM_012170.2	FBX22;FLJ13986	ubiquitin		ubiquitin-
GI_22547147-I	126	151.7	125.3	FBXO22	NM_012170.2	FBX22;FLJ13986	ubiquitin		ubiquitin-
GI_22547148-I	276.7	327.1	321.7	FBXO22	NM_147188.1	FBX22;FLJ13986	ubiquitin		ubiquitin-
GI_22547150-S	208.4	252.3	224.8	CCL18	NM_002988.2	CKb7;PARC;AMAC1;DCCK1;MIP-4;AMAC-	chemokin	extracellul	response
GI_22547151-S	274.8	342.5	310.3	CCL26	NM_006072.3	IMAC;TSC-1;MIP-4a;SCYA26;eotaxin-3;MIP-	chemokin	extracellul	chemotaxi
GI_22547155-S	1835.9	1411.9	1671.1	FLII	NM_002018.2	FLI;FLIL;Fli1;MGC39265	actin		muscle
GI_22547156-S	149.6	163.4	146.9	ABHD8	NM_024527.2	MGC2512;FLJ11743;MGC14280	epoxide		response
GI_22547158-S	2945.7	8028.6	6420.9	FLJ20343	NM_017775.2	MGC19520			
GI_22547160-S	195.7	284.1	305.6	FZD4	NM_012193.2	EVR1;Fz-4;FzE4;GPCR;FZD4S;MGC34390	frizzled	integral to	frizzled
GI_22547170-A	110	113	106.1	OSBPL9	NM_148907.1	ORP9;FLJ12492;FLJ14629;FLJ14801;FLJ32			
GI_22547175-I	145.2	151.9	146.7	OSBPL9	NM_148909.1	ORP9;FLJ12492;FLJ14629;FLJ14801;FLJ32			
GI_22547178-S	1081	991	1252.2	TRPV2	NM_016113.3	VRL;VRL1;VRL-1;MGC12549	ion	integral to	sensory
GI_22547179-A	810.6	1329.4	522.1	TRPV4	NM_147204.1	VRL2;TRP12;VRL-2;VROAC;OTRPC4			
GI_22547181-S	98.1	95.7	95.9	ZIC1	NM_003412.2	ZIC;ZNF201	DNA	nucleus	brain
GI_22547183-I	102.6	132.2	113	TRPV4	NM_021625.3	VRL2;TRP12;VRL-2;VROAC;OTRPC4			
GI_22547185-I	200.1	224.5	248.7	SHMT1	NM_004169.3	CSHMT;MGC15229;MGC24556	glycine	cytosol	L-serine
GI_22547188-A	690.9	690.8	795.9	SHMT1	NM_148918.1	CSHMT;MGC15229;MGC24556	glycine	cytosol	L-serine
GI_22547190-I	116.5	119	119.2	SNX15	NM_013306.2	HSAF001435	protein	membran	intracellula
GI_22547192-A	873.4	565.1	991	SNX15	NM_147777.1	HSAF001435	protein	membran	intracellula
GI_22547194-S	680.8	823.1	949.4	SREBF1	NM_004176.2	SREBP1	RNA	nuclear	lipid
GI_22547196-S	576.1	470.5	553.5	ZIC2	NM_007129.2	HPE5	DNA	nucleus	brain
GI_22547199-S	96.7	100.9	94.7	ZIC3	NM_003413.2	HTX;HTX1;ZNF203	DNA	nucleus	determinat
GI_22547200-S	111.4	108.9	91.7	ZIC4	NM_032153.2		DNA	nucleus	
GI_22547202-S	339.4	405.5	354.8	ZIC5	NM_033132.2		DNA	nucleus	
GI_22547203-I	117	146.4	126.9	HR	NM_005144.2	AU;ALUNC;HSA277165	transcripti	nucleus	epidermal

GI_22547206-A	120.7	141.9	114.4	HR	NM_018411.2	AU;ALUNC;HSA277165	transcripti	nucleus	epidermal
GI_22547209-A	126.8	128.4	114.1	PPIL2	NM_014337.2	CYC4;CYP60;MGC787;hCyP-60;MGC33174	cyclophilin	kinesin	protein
GI_22547209-I	413.5	477.6	442.4	PPIL2	NM_014337.2	CYC4;CYP60;MGC787;hCyP-60;MGC33174	cyclophilin	kinesin	protein
GI_22547211-I	193.5	214.9	215.6	PPIL2	NM_148175.1	CYC4;CYP60;MGC787;hCyP-60;MGC33174	cyclophilin	kinesin	protein
GI_22547217-I	204.1	230.5	226.3	TIRAP	NM_052887.2	Mal;wyatt			
GI_22547218-A	137.5	149.9	151.3	TIRAP	NM_148910.1	Mal;wyatt			
GI_22547218-I	117.3	139.1	139.8	TIRAP	NM_148910.1	Mal;wyatt			
GI_22547220-S	98.6	90.5	82.9	TLL1	NM_012464.3	TLL	metallope		skeletal
GI_22547222-S	111.9	110.5	101.9	TLL2	NM_012465.2	KIAA0932	metallope		proteolysis
GI_22547223-S	160.7	161.9	134.2	JRKL	NM_003772.2	HHMJG	DNA	nucleus	central
GI_22547226-S	136.4	140.8	123.9	LLGL1	NM_004140.2	DLG4;LLGL;HUGL1	structural	cytoskelet	
GI_22547228-S	87.5	91.6	80.1	MYO15A	NM_016239.2	DFNB3;MYO15	structural	actin	hearing
GI_22547230-S	397.3	395.1	224.6	NT5M	NM_020201.2	mdN;DNT2;dNT-2	nucleotida	mitochond	pyrimidine
GI_22547231-S	110.3	118	114.7	TBR1	NM_006593.2	TES-56	transcripti	nucleus	brain
GI_22547233-S	476.8	467.6	455.7	WDR11	NM_018117.1	DR11;WDR15;FLJ10506;KIAA1351		integral to	cell growth
GI_22726178-S	9952.1	9991.9	8237.7	LDHB	NM_002300.3		L-lactate		glycolysis
GI_22726202-S	322	387.4	345.1	TAS1R2	NM_152232.1	TR2;T1R2;GPR71	metabotro	membran	
GI_22748614-S	1383.6	1969.1	1527.4	MGC17943	NM_152261.1				
GI_22748616-S	106	114.2	96.5	DEFB105	NM_152250.1	BD-5;DEFB-5			xenobiotic
GI_22748618-A	586.3	769.7	336.6	TPM3	NM_152263.1	TRK;NEM1			
GI_22748618-I	234.7	291.7	255.7	TPM3	NM_152263.1	TRK;NEM1			
GI_22748622-S	722.1	741.1	670.7	MGC32020	NM_152266.1				
GI_22748624-S	94.8	100.1	92.7	ZNF439	NM_152262.1	DKFZp571K0837	nucleic	nucleus	regulation
GI_22748626-S	198.5	175.1	146.1	FLJ38663	NM_152269.1		translation		translation
GI_22748634-S	290.4	333.1	239	DC-UbP	NM_152277.1	MGC30022			
GI_22748638-S	169	166	166.9	FLJ11752	NM_152281.1	NTKLBP1			
GI_22748640-S	1253.1	1211.1	1258.1	MGC29816	NM_152272.1		molecular		
GI_22748650-S	1571.2	1880.2	2040.1	MGC13024	NM_152288.1				
GI_22748652-S	245.2	293.4	278.5	ARRDC1	NM_152285.1	MGC40555			sensory
GI_22748654-S	108.3	90.9	105.9	MGC35194	NM_152290.1				
GI_22748660-S	152	184.3	159	ZNF561	NM_152289.1	MGC45408		nucleus	
GI_22748664-S	103.3	100.6	104	MUC7	NM_152291.1	MGC34772			
GI_22748674-S	101.2	106.3	95.6	MGC45806	NM_152304.1		GTP		protein
GI_22748678-S	362.8	241.2	251.9	FLJ40452	NM_152307.1				
GI_22748680-S	209.5	267.7	215.5	ZNF554	NM_152303.1	FLJ34817	nucleic	nucleus	regulation
GI_22748684-S	132.5	170.6	144.6	MGC32871	NM_152311.1				
GI_22748688-S	975.7	1058.1	797.3	MGC34830	NM_152314.1				
GI_22748690-S	98.4	118.6	106.7	MGC34290	NM_152315.1				
GI_22748692-S	736.6	764.2	526	FLJ38968	NM_152316.1				
GI_22748694-S	82.9	88.1	80.7	DEPDC4	NM_152317.1	DEP.4;FLJ33505			intracellula
GI_22748696-S	465.3	399.5	337.2	MGC40397	NM_152318.1				
GI_22748700-S	497.7	567	476.9	FLJ31295	NM_152320.1		nucleic	intracellula	regulation
GI_22748702-S	121.4	127.1	118.5	FLJ32115	NM_152321.1		oxidoredu	microfibril	
GI_22748704-S	2612.9	1793.2	1873.3	BTBD11	NM_152322.1	FLJ33957	protein		

GI_22748706-S	98.3	107	101.9	SPIC	NM_152323.1	SPI-C;MGC40611	transcripti	nucleus	regulation
GI_22748708-S	111.8	123	105.6	MGC35169	NM_152324.1				
GI_22748710-S	136.7	164.7	151.5	MGC40178	NM_152325.1				
GI_22748712-S	718.3	683	866.9	ANKRD9	NM_152326.1	MGC21990		extrachro	
GI_22748714-S	119.2	107	110.2	AK7	NM_152327.1	FLJ32864	ATP		
GI_22748722-S	81.9	75	76.4	PTE2B	NM_152331.1	PTE1B;PTE-Ib;FLJ31235			
GI_22748726-S	692.4	696.6	584.1	SLC25A29	NM_152333.1	C14orf69;FLJ38975	binding	mitochond	transport
GI_22748730-S	313.7	385.1	329.3	FLJ38190	NM_152335.1				
GI_22748732-S	100.8	113.7	97.9	FLJ32310	NM_152336.1		carboxype		proteolysis
GI_22748734-S	127.9	132	135.3	FLJ32702	NM_152337.1				
GI_22748736-S	132.5	148.9	137.9	ZG16	NM_152338.1	MGC34820			
GI_22748742-S	122.1	155.8	138.5	CDYL2	NM_152342.1	FLJ38866	chromatin	chromatin	chromatin
GI_22748744-S	112.3	130.6	125	FLJ25414	NM_152343.1				
GI_22748746-S	1817.4	1903.1	1596.7	FLJ30656	NM_152344.1				
GI_22748750-S	169.8	277.9	462.2	MGC34680	NM_152346.1				
GI_22748754-S	209.5	332.5	289.3	FLJ33817	NM_152348.1				
GI_22748756-S	148.7	178.8	141.5	MGC45562	NM_152349.1			intermedia	
GI_22748758-S	14059.8	11682	9910.7	MGC40157	NM_152350.1				
GI_22748762-S	869.6	770.5	644.8	MGC24180	NM_152352.1				
GI_22748764-S	129.5	151.3	177.1	MGC33839	NM_152353.1			membran	
GI_22748768-S	105.1	111.7	105.8	ZNF441	NM_152355.1	FLJ38637	DNA	nucleus	regulation
GI_22748772-S	202.3	232.3	206.6	ZNF440	NM_152357.1	FLJ37933	nucleic	nucleus	regulation
GI_22748774-S	95.2	98.5	91	MGC33947	NM_152358.1				
GI_22748776-S	118.6	148.5	110.1	CPT1C	NM_152359.1	CPTIC;FLJ23809	acyltransf		
GI_22748780-S	159.7	179.3	171.7	MGC17791	NM_152362.1				
GI_22748786-S	152.8	157.4	166.5	FLJ34633	NM_152365.1		DNA	nucleus	regulation
GI_22748790-S	117.1	110.4	95.8	FLJ38716	NM_152367.1				
GI_22748798-S	428.7	405.4	485.8	MGC26818	NM_152371.1				
GI_22748804-S	659.9	730.4	749.8	FLJ38984	NM_152374.1				
GI_22748806-S	230.2	282.4	243.6	FLJ38753	NM_152375.1				
GI_22748810-S	119.5	133.7	124.5	MGC34837	NM_152377.1		sugar		phosphoe
GI_22748812-S	680.6	852.7	1058.1	FLJ31052	NM_152378.1				
GI_22748814-S	654	685.4	589.4	DKFZp547B1	NM_152379.1				
GI_22748818-S	91	88	81.8	FLJ37953	NM_152382.1				
GI_22748822-S	154	252.4	278.5	DKFZp762I1	NM_152384.1				
GI_22748824-S	219.7	223.7	213.3	FLJ31438	NM_152385.1				
GI_22748828-S	178.5	222.8	214.3	FLJ31322	NM_152387.1	FLJ37818	voltage-	membran	potassium
GI_22748830-S	500.5	492.5	540.5	ALS2CR4	NM_152388.1	FLJ33282			
GI_22748832-S	114.1	125.1	119.3	MGC35338	NM_152389.1				
GI_22748834-S	124.5	146.6	112.5	MGC33926	NM_152390.1		structural	tight	
GI_22748838-S	501.6	528.8	456.1	AHSA2	NM_152392.1	Hch1;DKFZp564C236	transporte	membran	transport
GI_22748844-S	421	399.7	403.8	MGC24132	NM_152396.1		S-		
GI_22748846-S	102	96	96.3	MGC39725	NM_152397.1				
GI_22748848-S	186.3	711.5	667.2	MGC45416	NM_152398.1				

GI_22748850-S	142.7	148.4	152.9	FLJ30834	NM_152399.1				
GI_22748852-S	523.4	375.8	339.1	FLJ39370	NM_152400.1				
GI_22748854-S	94	82.7	95.8	PDCL2	NM_152401.1	GCPHLP			phototrans
GI_22748860-S	216.5	211.9	209.2	JMY	NM_152405.1	FLJ37870	tubulin-		chaperoni
GI_22748864-S	666.8	449.9	517	FLJ35779	NM_152408.1				
GI_22748868-S	212.1	252.2	213.9	PACRG	NM_152410.1	FLJ32724;PARK2CRG			
GI_22748870-S	276	316.1	281.5	DKFZp762I13	NM_152411.1		nucleic	intracellula	regulation
GI_22748872-S	118.9	135.7	115	ZNF572	NM_152412.1	FLJ38002		nucleus	
GI_22748874-S	126.2	132.6	118	MGC33309	NM_152413.1		transamin		amino
GI_22748878-S	81.6	84.7	88.6	FLJ32642	NM_152415.1	HCRP1			
GI_22748880-S	320.5	308.8	333.9	MGC40214	NM_152416.1				
GI_22748882-S	579.4	520.3	479.8	FLJ32370	NM_152417.1				
GI_22748888-S	111.4	130	127.9	C9orf41	NM_152420.1	FLJ25795			
GI_22748896-S	187.9	337.7	336.9	FLJ39827	NM_152424.1				
GI_22748898-S	144.5	138.9	120.5	FLJ40249	NM_152425.1				
GI_22748900-S	111.5	114.2	124	MGC35136	NM_152427.1		actin	intracellula	
GI_22748904-S	94.2	114.1	89.6	HIWI2	NM_152431.1	FLJ36156			
GI_22748910-S	91.4	76.8	92.3	MGC24137	NM_152430.1		olfactory	integral to	G-protein
GI_22748912-S	101.4	136.9	142.2	MGC35366	NM_152435.1		hydrolase	cytoplasm	histidine
GI_22748916-S	1060.2	1201.7	1124.5	DKFZp761B1	NM_152437.1			nucleus	
GI_22748918-S	702.5	624.4	599.2	CWF19L2	NM_152434.1	FLJ32343			
GI_22748920-S	213.3	216.3	215	FLJ32549	NM_152440.1				
GI_22748922-S	159.7	177	159.6	MGC39497	NM_152436.1			extracellul	
GI_22748926-S	134.5	138	139.5	VMD2L3	NM_152439.1	MGC40411			
GI_22748928-S	100.8	103.6	96	ZADH1	NM_152444.1	FLJ39091	alcohol		
GI_22748930-S	242.8	249	191	FBXL14	NM_152441.1	MGC40195			
GI_22748932-S	167.5	121	123.3	C14orf145	NM_152446.1				
GI_22748934-S	114.1	129.6	105	RDH12	NM_152443.1	FLJ30273	oxidoredu		metabolis
GI_22748936-S	1218.8	1007.9	1061.2	XPO5	NM_020750.1	KIAA1291			
GI_22748940-S	93.2	88.7	88.7	MGC33951	NM_152448.1				
GI_22748942-S	121.1	143.4	123.6	C14orf44	NM_152445.1	FLJ31697;c14_5547		kinesin	
GI_22748944-S	170.6	175.2	165	MGC26690	NM_152450.1				
GI_22748948-S	732	974.5	1246.5	MGC18216	NM_152452.1				
GI_22748952-S	194.9	224.6	226.7	FLJ31461	NM_152454.1				
GI_22748954-S	109.8	139.9	140.9	FLJ30973	NM_152451.1				
GI_22748956-S	104.3	113.6	107.7	MGC34647	NM_152456.1				
GI_22748964-S	247.6	340.5	425.8	FLJ30999	NM_152461.1				
GI_22748966-S	134.7	131.4	130.4	ZNF597	NM_152457.1	FLJ33071	nucleic	intracellula	regulation
GI_22748968-S	170.2	178.3	164.4	EME1	NM_152463.1	MMS4L;FLJ31364	ATP		hydrogen
GI_22748970-S	240.1	259.7	234.1	FLJ31882	NM_152460.1				
GI_22748972-S	109.4	115.2	117.6	MGC39650	NM_152465.1		phospholi		lipid
GI_22748974-S	104.2	114.4	99.3	TMEM21A	NM_152462.1	AMAC1;FLJ40154		membran	
GI_22748976-S	125.3	118.9	122.3	KLHL10	NM_152467.1	FLJ32662	protein	nucleus	
GI_22748978-S	448.9	506.1	533.6	MGC45714	NM_152464.1				

GI_22748980-S	116.6	111.7	98.1	FLJ31338	NM_152469.1				
GI_22748982-S	239.8	236.1	203.9	FLJ25168	NM_152466.1				
GI_22748984-S	309.8	310.9	334	MGC17515	NM_152471.1				
GI_22748988-S	143.2	158.6	139.3	FLJ32214	NM_152473.1		structural	viral	
GI_22748990-S	316.7	360.8	354.1	FLJ34218	NM_152470.1				
GI_22748992-S	1263.2	1512.9	1246.4	MGC34079	NM_152475.1		nucleic	intracellula	regulation
GI_22748994-S	186.1	215.6	176	ZNF578	NM_152472.1	FLJ31384	electron	nucleus	electron
GI_22748996-S	145.2	163.6	164.2	ZNF565	NM_152477.1	FLJ36991	nucleic	nucleus	regulation
GI_22749000-S	111.6	100.1	111.5	FLJ30373	NM_152479.1				
GI_22749002-S	101.9	101.7	114.8	ZNF560	NM_152476.1	FLJ31986	nucleic	intracellula	regulation
GI_22749004-S	110.4	104	100.9	FLJ25660	NM_152481.1				
GI_22749006-S	184.2	226.7	201	ZNF583	NM_152478.1	FLJ31030	nucleic	intracellula	regulation
GI_22749008-S	109.4	116.8	105.4	FLJ25328	NM_152483.1				
GI_22749010-S	445.6	521.7	502.3	C19orf23	NM_152480.1	MGC39338			
GI_22749012-S	233.8	260	217.2	MGC45873	NM_152486.1				
GI_22749014-S	170.6	192.2	199.3	C19orf25	NM_152482.1	FLJ36666			
GI_22749016-S	129.6	133.5	122	FLJ32833	NM_152488.1				
GI_22749020-S	141.2	147.5	124.6	MGC39558	NM_152490.1		galactosylt	membran	protein
GI_22749022-S	117.8	129.6	135.3	FLJ31842	NM_152487.1				
GI_22749024-S	80	78.5	66.4	FLJ32825	NM_152492.1				
GI_22749026-S	126.6	131	126.2	MGC35130	NM_152489.1		ubiquitin		ubiquitin
GI_22749028-S	178.6	220.1	200.9	FLJ32785	NM_152494.1				
GI_22749032-S	595.8	329.8	715.5	FLJ31434	NM_152496.1				
GI_22749036-S	100.4	116.4	104.1	FLJ32000	NM_152498.1				
GI_22749038-S	5799.3	3915.2	3453.8	FLJ38993	NM_152495.1			integral to	intracellula
GI_22749040-S	218.5	264.9	236.8	FLJ33084	NM_152500.1				
GI_22749042-S	114.9	112.3	119.2	FLJ32206	NM_152497.1				
GI_22749044-S	78.7	78.6	74.5	FLJ32154	NM_152502.1				
GI_22749046-S	297.8	394.5	393.5	MGC45441	NM_152499.1				
GI_22749050-S	146.6	167.1	162.2	IFIX	NM_152501.1	MGC23885			
GI_22749052-S	117.9	133.3	119.6	C21orf128	NM_152507.1	FLJ33471			
GI_22749056-S	135.7	147.3	146.2	FLJ31568	NM_152509.1				
GI_22749058-S	101.4	103	96.3	C21orf129	NM_152506.1	PRED76;FLJ32835			
GI_22749062-S	89.9	99.4	89.9	FLJ32575	NM_152508.1				
GI_22749066-S	104	91.9	98.2	MGC26710	NM_152510.1				
GI_22749072-S	94.7	119.5	132.1	FLJ30990	NM_152517.1				
GI_22749078-S	572.7	701.9	716.6	COMMD1	NM_152516.1	MURR1;C2orf5;MGC27155			
GI_22749082-S	92.5	100.4	90	FLJ38359	NM_152518.1				
GI_22749084-S	189.5	224.8	275.9	FLJ40432	NM_152523.1		cyclin-		cytokinesi
GI_22749094-S	92.6	86.6	90.4	TRIPIN	NM_152524.1	FLJ25211			
GI_22749102-S	557.7	413.1	430	FLJ36175	NM_152528.1				
GI_22749104-S	125.5	135.1	137.5	MGC34728	NM_152533.1				
GI_22749110-S	148.7	132.1	123.1	FLJ31715	NM_152532.1				
GI_22749114-S	105.5	119.5	95.2	FLJ32685	NM_152534.1		ATP		protein

GI_22749116-S	132.2	149.7	128.9	FLJ32859	NM_152539.1				
GI_22749120-S	103.6	123.1	115	FLJ30194	NM_152541.1				
GI_22749122-S	122.9	136.6	133.3	IGSF11	NM_152538.1	Igsf13;BT-IgSF;MGC35227			
GI_22749124-S	79.4	101.7	80.2	FLJ25371	NM_152543.1				
GI_22749128-S	95.2	98	99.4	RASGEF1B	NM_152545.1	GPIG4;FLJ31695	guanyl-		small
GI_22749132-S	93.5	82.2	86.9	FLJ32535	NM_152547.1				
GI_22749134-S	174.5	196	148	FLJ35725	NM_152544.1				
GI_22749136-S	137.2	122.9	128	MGC39633	NM_152549.1				
GI_22749138-S	345.1	345.9	329.5	FLJ25286	NM_152546.1				
GI_22749142-S	124.3	129.6	117	FLJ25333	NM_152548.1				
GI_22749146-S	434.1	335.9	427.5	SH3RF2	NM_152550.1	RNF158;FLJ23654			
GI_22749150-S	88.5	105.3	85.5	SAMD3	NM_152552.1	FLJ34032;MGC35163;bA73O6.2			
GI_22749154-S	98.3	100	92.9	C6orf195	NM_152554.1	FLJ31934;bA145H9.2			
GI_22749158-S	193.4	273.6	262.1	FLJ31818	NM_152556.1				
GI_22749164-S	230.6	285.4	279.8	ATP6V0D2	NM_152565.1	VMA6;ATP6D2;FLJ38708	hydrogen-		hydrogen
GI_22749166-S	731.5	952.8	1554.8	FLJ32205	NM_152561.1				
GI_22749168-S	166.4	226.9	197.9	FLJ25402	NM_152567.1				
GI_22749172-S	120.1	119.9	110.7	C9orf66	NM_152569.1	FLJ31158	DNA	nucleus	regulation
GI_22749176-S	306.1	385.4	352.6	FLJ36779	NM_152571.1				
GI_22749178-S	104.3	108.9	100.4	FLJ25169	NM_152568.1		transcripti	nucleus	regulation
GI_22749180-S	139	159.3	135.3	FLJ31614	NM_152573.1		calcium		
GI_22749182-S	122.1	122.1	112.8	FLJ31810	NM_152570.1				
GI_22749184-S	91.9	111.6	100.2	FLJ31713	NM_152575.1				
GI_22749188-S	109.2	118.2	102.2	FLJ25735	NM_152577.1				
GI_22749190-S	197.8	198.7	178.2	C9orf52	NM_152574.1	FLJ33868	peptidase	membran	proteolysis
GI_22749192-S	720.4	747.7	450.8	FLJ38564	NM_152579.1				
GI_22749194-S	133.8	160.3	131.8	MGC24103	NM_152576.1				
GI_22749196-S	267.9	291.7	265.1	MOSPD2	NM_152581.1	MGC26706	structural		cell
GI_22749198-S	100.7	105.6	98.3	FMR1NB	NM_152578.1	FLJ25736;NY-SAR-35			
GI_22749200-S	94.6	113	102.2	FLJ32742	NM_152580.1				
GI_22749204-S	100.8	105.8	107.2	MGC40053	NM_152583.1				
GI_22749206-S	844.8	749.8	632.7	USP54	NM_152586.1	C10orf29;FLJ37318			
GI_22749210-S	123.4	124.1	137	DKFZp762A2	NM_152588.1				
GI_22749212-S	95.9	101.7	105.4	FLJ35821	NM_152589.1				
GI_22749214-S	232.8	305.1	284.4	FLJ36004	NM_152590.1				
GI_22749216-S	102.4	131.5	99.5	FLJ35843	NM_152591.1				
GI_22749220-S	2132.4	2168.2	1982.7	SPRED1	NM_152594.1	FLJ33903			
GI_22749228-S	115.9	134.4	112.4	FLJ35757	NM_152598.1				
GI_22749230-S	114.4	112.6	104.4	FLJ35773	NM_152599.1				
GI_22749232-S	1965	1891.4	1472.9	ZNF579	NM_152600.1	FLJ35453	DNA	nucleus	regulation
GI_22749234-S	110.1	122.8	112.3	FLJ38281	NM_152601.1		nucleic	intracellula	regulation
GI_22749236-S	99.5	100.1	75.5	ZNF433	NM_152602.1	FLJ40981	nucleic	nucleus	regulation
GI_22749242-S	111	116.5	128.6	FLJ40201	NM_152607.1				
GI_22749246-S	672.4	583.1	491.1	FLJ32001	NM_152609.1				

GI_22749248-S	320.7	382.2	353.2	FLJ35728	NM_152610.1				
GI_22749254-S	116.2	129	105.7	MGC26816	NM_152613.1				
GI_22749258-S	82.3	92.2	81.8	FLJ40597	NM_152615.1				
GI_22749266-S	314.4	237.9	217.6	MGC45428	NM_152619.1				
GI_22749274-S	151.1	176.5	161.3	FLJ37927	NM_152623.1	G6VTS76519			
GI_22749278-S	116.6	113.2	119.1	ZNF366	NM_152625.1	FLJ39796	DNA	nucleus	regulation
GI_22749288-S	84.3	84.7	87.9	FLJ35782	NM_152631.1				
GI_22749290-S	115.6	104.1	118	MGC34831	NM_152632.1				
GI_22749292-S	112.7	103.4	114.6	FLJ34064	NM_152633.1				
GI_22749296-S	138.8	153.4	143.1	FLJ39116	NM_152635.1	LZP	calcium		
GI_22749298-S	360.2	333.6	252.3	FLJ33979	NM_152636.1		methyltran		
GI_22749300-S	109.2	122.3	110.7	MGC17301	NM_152637.1		S-		
GI_22749304-S	183.1	199.9	195.4	MGC30156	NM_152639.1				
GI_22749312-S	369.9	306.8	215.6	MGC45962	NM_152644.1				
GI_22749318-S	150.3	178.5	151.9	FLJ32800	NM_152647.1				
GI_22749324-S	119.6	113	109.6	ZNF553	NM_152652.1	FLJ31751	DNA	nucleus	regulation
GI_22749326-S	1958	1413.8	1235.5	UBE2E2	NM_152653.1	UBCH8;FLJ25157	ubiquitin		ubiquitin
GI_22749328-S	222.9	278.6	226.3	FLJ38607	NM_152654.1				
GI_22749336-S	236.7	320.3	364.1	THAP8	NM_152658.1	FLJ32891	DNA		
GI_22749340-S	431.5	494.3	490.7	MGC34648	NM_152660.1				
GI_22749342-S	533.7	693.3	630.5	DKFZp761G	NM_152661.1				
GI_22749344-S	115	111.4	109.5	FLJ23867	NM_152662.1				
GI_22749348-S	88.3	97.6	102.8	FLJ31401	NM_152664.1				
GI_22749350-S	87.4	104.1	86.2	FLJ40873	NM_152665.1				
GI_22749352-S	100.6	90.4	90	FLJ40773	NM_152666.1		catalytic		metabolis
GI_22749356-S	159.2	187.7	172.4	FLJ25369	NM_152670.1		electron		electron
GI_22749358-S	238.3	294.5	267.9	MGC40423	NM_152671.1				
GI_22749362-S	109.4	142.5	114.4	FBXO15	NM_152676.1	FBX15;MGC39671			
GI_22749364-S	139.2	149.5	123	ZNF494	NM_152677.1	FLJ35105	transcripti	nucleus	regulation
GI_22749366-S	692.6	542.9	609.9	FLJ32028	NM_152680.1				
GI_22749370-S	1130.1	1130.4	786.7	MGC10198	NM_152682.1				
GI_22749372-S	285.5	241.2	233.7	FLJ33167	NM_152683.1				
GI_22749374-S	180.3	237	184	FLJ39653	NM_152684.1				
GI_22749376-S	216.3	211	198.9	MGC29463	NM_152686.1		N-		DNA
GI_22749378-S	112.3	116.2	99	FLJ33641	NM_152687.1				
GI_22749380-S	99.5	88.6	83.1	KHDRBS2	NM_152688.1	SLM1;MGC26664	nucleic	nucleus	regulation
GI_22749386-S	260.4	246.8	129.6	ZCCHC5	NM_152694.1	FLJ38865	nucleic		
GI_22749392-S	98.9	118.2	97	FLJ38377	NM_152698.1				
GI_22749400-S	119.2	115.7	119.3	C9orf94	NM_152702.1	FLJ35283			
GI_22749406-S	676.6	1035.7	825.8	MGC9850	NM_152705.1		DNA	nucleus	regulation
GI_22749412-S	195.6	242.2	222.7	C10orf27	NM_152710.1	FLJ32820			
GI_22749416-S	287.2	344.4	295.7	MGC10233	NM_152715.1				
GI_22749418-S	165.9	179.7	174.9	MGC43033	NM_152711.1				
GI_22749420-S	103.8	104.8	105.4	MGC35295	NM_152717.1				

GI_22749422-S	103	109.3	92.6	FLJ30719	NM_152714.1				
GI_22749424-S	177.7	222	207.9	NURIT	NM_152719.1	FLJ35810			
GI_22749426-S	2234.7	1921.1	1745.8	FLJ36874	NM_152716.1				
GI_22749428-S	124.2	168.7	129.7	FLJ38159	NM_152723.1				
GI_22749430-S	262	316.7	244.1	FLJ32009	NM_152718.1	URG11	sugar		
GI_22749432-S	147.2	184.6	158.6	SLC39A12	NM_152725.1	FLJ30499	heavy	membran	heavy
GI_22749442-S	234.8	305	297	FLJ34588	NM_152726.1		calcium		
GI_22749444-S	100.7	99.4	107.7	MGC39571	NM_152728.1				
GI_22749448-S	161.7	159.1	122.4	C6orf65	NM_152731.1	FLJ30162;bA203B9.1			
GI_22749452-S	397.5	479	437.9	C6orf89	NM_152734.1	FLJ25357			
GI_22749454-S	854.5	558.8	625.7	MGC33993	NM_152737.1				
GI_22749456-S	198.6	241.1	232.2	MGC40222	NM_152738.1				
GI_22749458-S	153.4	185.4	140.5	GPC2	NM_152742.1	DKFZp547M109		extracellul	
GI_22749462-S	116	126.7	131.1	DKFZp434L1	NM_152746.1				
GI_22749464-S	131	130.5	133.2	DKFZp586I14	NM_152747.1				
GI_22749470-S	95.2	92.9	90	C10orf30	NM_152751.1	FLJ40283			
GI_22749478-S	186.5	247	244.7	MGC40499	NM_152755.1				
GI_22749480-S	128	135.2	134.1	MGC39830	NM_152756.1				
GI_22749482-S	137.8	132.9	124.9	FLJ30313	NM_152757.1				
GI_22749488-S	159.7	184.2	170.9	FLJ30934	NM_152760.1				intracellula
GI_22749492-S	99	115.4	103	FLJ32880	NM_152762.1				
GI_22749494-S	132.7	153	132.9	MGC35212	NM_152764.1				
GI_22749496-S	109.4	103.9	99.5	FLJ25444	NM_152761.1				
GI_22749502-S	100.2	130.7	121.4	C19orf26	NM_152769.1	MGC40084			
GI_22749506-S	84.7	81.9	73.5	FLJ25378	NM_152768.1				
GI_22749508-S	80.5	91.4	102	MGC35043	NM_152770.1				
GI_22749510-S	310.1	371.8	331	MGC39696	NM_152771.1				
GI_22749514-S	167.4	119.2	98.6	MGC33607	NM_152775.1				
GI_22749516-S	143.1	127.2	140	MGC40368	NM_152772.1				
GI_22749518-S	315.1	316.9	269.6	MGC42090	NM_152774.1				
GI_22749520-S	124.1	143.5	114.4	MGC40579	NM_152776.1				carbohydr
GI_22749524-S	161.3	168.9	158	MGC33302	NM_152778.1		transporte	integral to	transport
GI_22749526-S	106.7	112.3	109.9	MGC26856	NM_152779.1		rhodopsin-	extracellul	G-protein
GI_22749528-S	131.6	150.9	149.6	FLJ32830	NM_152781.1				
GI_22749538-S	111.7	130.3	115.2	C9orf43	NM_152786.1	MGC17358	subtilase		proteolysis
GI_22749542-S	625.6	532.8	494.7	MGC40405	NM_152789.1				
GI_22758131-S	109.3	118.6	117.4	FLJ12616	NM_152642.1				
GI_22758145-S	130.2	117.5	110.8	FLJ25084	NM_152792.1		aspartic-		proteolysis
GI_22779859-S	122.2	142.7	134.1	FOXL1	NM_005250.1	FKH6;FKHL11;FREAC7	DNA	nucleus	regulation
GI_22779869-S	210.4	208.5	268.1	LOC149420	NM_152835.1		protein-		protein
GI_22779872-S	691	1078.3	1239.7	MTVR1	NM_152832.1		receptor		
GI_22779876-S	116.5	122.1	97.6	GJA3	NM_021954.2	CAE2;CAE3;CX46;CZP2;CZP3	connexon	connexon	visual
GI_22779931-A	738.7	411.9	391	SYNE1	NM_133650.1	8B;CPG2;MYNE1;MYNE-1;SYNE-1;SYNE-	lamin	nuclear	Golgi
GI_22779931-I	90.4	86.1	84	SYNE1	NM_133650.1	8B;CPG2;MYNE1;MYNE-1;SYNE-1;SYNE-	lamin	nuclear	Golgi

GI_22779933-S	577.9	541.6	601	PWDMP	NM_025132.2	FLJ23127;KIAA1638			
GI_22779935-S	96.2	94.9	85.8	WFDC6	NM_080827.1	WAP6;C20orf171;dJ461P17.11	serine		
GI_22902135-S	167	194.3	180.7	SP7	NM_152860.1	OSX;osterix	DNA	nucleus	regulation
GI_22907022-S	285.5	464.8	512.8	EPPB9	NM_015681.2	B9			
GI_22907024-S	271.1	294.1	334.8	APOBEC3B	NM_004900.3	ARP4;ARCD3;PHRBNL;APOBEC1L;FLJ2120	hydrolase		
GI_22907027-S	115.2	122.1	106.5	FBP2	NM_003837.2		fructose-		fructose
GI_22907036-S	3554.2	4523.6	3553.8	APOBEC3A	NM_145699.2	ARP3;PHRBN;phorbolin I	zinc ion	cellular_co	mRNA
GI_22907038-S	389.3	480.8	461.6	APOBEC3C	NM_014508.2	PBI;ARP5;ARDC2;ARDC4;APOBEC1L;MGC	zinc ion	cellular_co	biological_
GI_22907040-S	131.9	159.2	143.2	APOBEC3D	NM_152426.1	ARP6;MGC8979	zinc ion		
GI_22907046-S	379	1019.1	635.5	ADORA2B	NM_000676.2	ADORA2	adenosine	integral to	activation
GI_22907048-S	246.8	302.3	256.4	ALDH3A1	NM_000691.3	ALDH3;ALDHIII;MGC10406	aldehyde	cytosol	aldehyde
GI_22907051-S	5284.4	5607	5612.6	ARPC1A	NM_006409.2	SOP2L;SOP2Hs	actin	actin	actin
GI_22907055-S	3806.4	3373.6	4846.6	ARPC1B	NM_005720.2	ARC41;p40-ARC;p41-ARC	structural	Arp2/3	cell
GI_22907057-S	434.1	563.5	436.4	MED25	NM_018019.2	FLJ10193			
GI_22907059-S	145.7	157.5	150.8	FLJ10847	NM_018242.2		drug	membran	multidrug
GI_23065521-S	386.6	433.3	362.6	DKFZp566O	NM_015510.3	CGI-93;MGC8916			
GI_23065525-A	1116	1477.6	1027.1	GAS2L1	NM_152236.1	GAR22;MGC17243			cell growth
GI_23065528-I	327	389.8	343.6	GAS2L1	NM_152237.1	GAR22;MGC17243			cell growth
GI_23065531-I	253.4	325.1	272.8	HIF3A	NM_022462.2	IPAS;HIF-3A			
GI_23065534-I	169.1	197	167.5	HIF3A	NM_152794.1	IPAS;HIF-3A			
GI_23065537-I	110.4	110.1	96.7	HIF3A	NM_152795.1	IPAS;HIF-3A			
GI_23065540-A	102.8	99.7	101.4	HIF3A	NM_152796.1	IPAS;HIF-3A			
GI_23065540-I	114.1	123.4	108.7	HIF3A	NM_152796.1	IPAS;HIF-3A			
GI_23065543-I	455.5	467.1	423.9	GSTM1	NM_000561.2	MU;H-B;GST1;GTH4;GTM1;MU-1;GSTM1-	glutathion	cytoplasm	
GI_23065546-A	475.2	508.8	397.6	GSTM1	NM_146421.1	MU;H-B;GST1;GTH4;GTM1;MU-1;GSTM1-	glutathion	cytoplasm	
GI_23065549-S	240.5	374.6	242.2	GSTM2	NM_000848.2	GST4;GSTM;GTHMUS;GSTM2-2	glutathion		glutathion
GI_23065556-I	267.9	316.2	299.2	GSTM4	NM_147148.1	GTM4;GSTM4-4;MGC9247	glutathion		
GI_23065559-A	108.3	116.5	104.7	GSTM4	NM_147149.1	GTM4;GSTM4-4;MGC9247	glutathion		
GI_23065562-S	100.8	102.1	111.6	GSTM5	NM_000851.2	GTM5;GSTM5-5	glutathion		glutathion
GI_23065565-S	108.6	110.5	108.7	GPR24	NM_005297.2	SLC1;MCHR1;MGC32129	neuropepti	integral to	cytosolic
GI_23065568-S	103.8	109	91	GSTA4	NM_001512.2	GTA4;GSTA4-4	glutathion		response
GI_23065570-S	123	145.7	132.1	GTPBP1	NM_004286.3	GP1;GP-1;HSPC018;MGC20069	GTP		signal
GI_23097237-S	136.2	142.6	133.8	CHST13	NM_152889.1	C4ST3	transferas		
GI_23097239-S	1271.5	1419.2	1330.5	DKFZp434K1	NM_152892.1				
GI_23097243-S	102.2	91.5	98	EOS	NM_152891.1		trypsin		proteolysis
GI_23097245-S	114.8	128.3	118.1	PYC1	NM_152901.1	POP1			
GI_23097259-S	136.3	129.2	155.8	HCMOGT-1	NM_152904.1				
GI_23097269-S	625.8	733.3	653.5	MGC33894	NM_152914.1				
GI_23097271-S	124.5	127.7	120.8	PAOX	NM_152911.1	PAO;DKFZp434J245			electron
GI_23097273-S	187.1	224	195.3	DKFZp761L1	NM_152913.1				
GI_23097278-S	694.9	561.9	532.6	C20orf158	NM_152302.1	MGC16140;dJ885L7.8;DKFZp434P1115	DNA	nucleus	regulation
GI_23097280-S	148.5	153.2	153.1	KIAA1023	NM_152558.1				
GI_23097284-I	281.1	244.2	258.8	384D8-2	NM_152299.1	384D8_6;MGC2455;MGC4133;MGC5305;M			
GI_23097291-S	247.2	292.7	224.4	POP1	NM_015029.1	KIAA0061;MGC17365	ribonuclea	nucleolus	rRNA

GI_23097298-I	453	516.1	474.4 PLAC3	NM_020318.1	PAPPE;PAPP-A2			
GI_23097300-A	147.1	177.9	175.3 PLAC3	NM_021936.1	PAPPE;PAPP-A2			
GI_23097300-I	103.3	96.8	111.8 PLAC3	NM_021936.1	PAPPE;PAPP-A2			
GI_23097307-I	155.9	180.1	152.7 SYNE1	NM_033071.1	8B;CPG2;MYNE1;MYNE-1;SYNE-1;SYNE-	lamin	nuclear	Golgi
GI_23097309-S	153.7	192.8	156.2 ELOVL3	NM_152310.1	CIG30;CIG-30;MGC21435		endoplas	fatty acid
GI_23097312-S	133.6	133	127.4 FLJ39075	NM_152340.1		DNA	nucleus	regulation
GI_23097314-S	1380.9	972.8	773.3 ZFP62	NM_152283.1	ZET;FLJ34231		nucleus	
GI_23097320-S	152.2	159.7	123.8 FLJ35863	NM_152604.1		nucleic	nucleus	regulation
GI_23097324-S	101.9	92.9	102.5 FLJ23754	NM_152675.1				
GI_23097326-S	101.6	101	93.9 FLJ37549	NM_152605.1				
GI_23097330-S	135.4	141.5	132.8 MUC20	NM_152673.1	FLJ14408;KIAA1359			
GI_23097337-S	109	124.1	172 NXPH1	NM_152745.1	NPH1			
GI_23097339-A	185.7	202.5	181.4 MAGI-3	NM_152900.1		kinase		intracellula
GI_23110923-S	2710.7	2723.9	2135.3 PSMB10	NM_002801.2	LMP10;MECL1;MGC1665	peptidase	26S	humoral
GI_23110924-S	5287	6359.2	6303.5 PSMB6	NM_002798.1	Y;LMPY;DELTA;MGC5169	peptidase	cytosol	ubiquitin-
GI_23110926-S	11588.8	11582	11663 PSMB7	NM_002799.2	Z	peptidase	26S	ubiquitin-
GI_23110931-A	1027	1478.2	793.1 PSMB9	NM_148954.1	LMP2;RING12	peptidase	26S	proteolysis
GI_23110933-A	5225.1	6177.1	5654.3 PSMA1	NM_002786.2	NU;HC2;PROS30;MGC1667;MGC14542;MG	RNA	polysome	ubiquitin-
GI_23110933-I	1016.8	1348.9	1039.6 PSMA1	NM_002786.2	NU;HC2;PROS30;MGC1667;MGC14542;MG	RNA	polysome	ubiquitin-
GI_23110934-I	88.4	89	86.2 PSMA1	NM_148976.1	NU;HC2;PROS30;MGC1667;MGC14542;MG	RNA	polysome	ubiquitin-
GI_23110938-A	1829.2	2503.5	2117.3 PSMA3	NM_152132.1	HC8;PSC3;MGC12306;MGC32631	peptidase	26S	ubiquitin-
GI_23110940-S	1949.5	2404.9	2067.9 PSMA4	NM_002789.3	HC9;HsT17706;MGC12467;MGC24813	peptidase	26S	ubiquitin-
GI_23110941-S	2843.2	3842.2	3445.7 PSMA5	NM_002790.2	PSC5;ZETA	peptidase	26S	ubiquitin-
GI_23110943-S	2563.1	2823.7	2224.6 PSMA6	NM_002791.1	IOTA;p27K;PROS27;MGC2333;MGC22756;	peptidase	cytosol	ubiquitin-
GI_23110945-A	10751.2	14224	15602 PSMA7	NM_002792.2	C6;HSPC;RC6-1;XAPC7;MGC3755	transcripti	26S	ubiquitin-
GI_23110947-I	89.8	103.2	105.2 PSMA7	NM_152255.1	C6;HSPC;RC6-1;XAPC7;MGC3755	transcripti	26S	ubiquitin-
GI_23110949-S	1205.7	1104.7	1368.4 CTSD	NM_001909.3	CPSD;MGC2311	cathepsin	lysosome	proteolysis
GI_23110950-I	123.8	128.6	114.7 CTSE	NM_001910.2				proteolysis
GI_23110951-A	401.5	466.6	429.9 CTSE	NM_148964.1				proteolysis
GI_23110953-S	120.5	116	123.7 CTSG	NM_001911.2	CG;MGC23078	cathepsin	insoluble	proteolysis
GI_23110956-A	1208.8	867.6	726.1 CTSH	NM_148979.1	CPSB;MGC1519	cathepsin	lysosome	proteolysis
GI_23110958-S	152.4	159.4	150.3 CTSK	NM_000396.2	PKND;CTS02;CTSO1;CTSO2;MGC23107	cathepsin	lysosome	proteolysis
GI_23110959-S	219.1	283.9	371.7 CTSL2	NM_001333.2	CTSU;CTSV;CATL2	cathepsin	lysosome	proteolysis
GI_23110961-S	162.5	175.1	138 CTSS	NM_004079.3	MGC3886	cathepsin	lysosome	proteolysis
GI_23110963-S	306.5	352.5	326 CTSW	NM_001335.2	LYPN	cysteine-		immune
GI_23110965-I	103.6	117.3	107.1 HPS4	NM_022081.4	LE;KIAA1667	protein	lysosome	lysosome
GI_23110967-I	218.3	238	203.7 HPS4	NM_152840.1	LE;KIAA1667	protein	lysosome	lysosome
GI_23110971-I	174.4	197.2	188.7 HPS4	NM_152842.1	LE;KIAA1667	protein	lysosome	lysosome
GI_23110973-A	214.7	252.1	223.6 HPS4	NM_152843.1	LE;KIAA1667	protein	lysosome	lysosome
GI_23110975-S	174.1	214.3	218.3 IFNK	NM_020124.1		hematopoi	extracellul	defense
GI_23110977-I	127.8	156.8	133.1 IGLL1	NM_020070.2	IGO;14.1;IGL1;IGL5;IGLL;IGVPB;CD179b;VP	defense/i	membran	immune
GI_23110979-A	113.2	112.1	99.4 IGLL1	NM_152855.1	IGO;14.1;IGL1;IGL5;IGLL;IGVPB;CD179b;VP	defense/i	membran	immune
GI_23110983-I	103	115.8	106.2 KCNJ4	NM_152868.1	HIR;HRK1;HIRK2;Kir2.3	inward	voltage-	potassium
GI_23110985-S	863.6	841.6	809.1 PHF16	NM_014735.2	JADE3;KIAA0215	DNA		regulation

GI_23110986-A	96.9	106.1	100.4	MS4A1	NM_021950.2	B1;S7;Bp35;CD20;MS4A2;LEU-16;MGC3969	calcium	integral to	humoral
GI_23110988-I	108.5	113.1	97.4	MS4A1	NM_152866.1	B1;S7;Bp35;CD20;MS4A2;LEU-16;MGC3969	calcium	integral to	humoral
GI_23110992-S	104.1	92.3	97.9	MS4A3	NM_006138.3	HTM4;CD20L	receptor	membran	cell
GI_23110994-A	98.9	96.1	94.1	MS4A4A	NM_148975.1	MS4A4;MS4A7;4SPAN1;CD20L1;CD20-			
GI_23110996-S	149.5	174.5	162.6	MS4A5	NM_023945.2	TETM4;CD20L2;CD20-L2;MGC34184	receptor	integral to	
GI_23110998-S	114.3	134.7	117.9	MS4A6E	NM_139249.2		receptor	integral to	
GI_23110999-S	105.2	108.6	89	MS4A7	NM_021201.3	CFFM4;MS4A8;CD20L4	receptor	integral to	
GI_23111001-I	101.5	101.3	97.5	MAFF	NM_012323.2	U-MAF	transcripti	nucleus	parturition
GI_23111002-A	170.9	148.5	121.9	MAFF	NM_152878.1	U-MAF	transcripti	nucleus	parturition
GI_23111002-I	105.7	97.4	85.9	MAFF	NM_152878.1	U-MAF	transcripti	nucleus	parturition
GI_23111004-S	696.6	834.6	739.8	MFAP4	NM_002404.1		extracellul	extracellul	embryoge
GI_23111006-S	138.4	164.9	144.6	MGC3048	NM_024052.3				
GI_23111008-S	65.7	77.9	76.9	MYOD1	NM_002478.3	PUM;MYF3;MYOD	RNA	nucleus	myogenes
GI_23111010-I	791.3	764.4	776.8	RAI1	NM_017574.1	SMS;SMCR;KIAA1820;MGC12824;DKFZP43			
GI_23111012-A	77.9	88	81.9	RAI1	NM_152256.1	SMS;SMCR;KIAA1820;MGC12824;DKFZP43			
GI_23111016-I	119.1	113.5	115.5	RBM10	NM_005676.3	MGC997;MGC1132;DXS8237E;KIAA0122			
GI_23111017-A	541.1	562.1	494.6	RBM10	NM_152856.1	MGC997;MGC1132;DXS8237E;KIAA0122			
GI_23111019-I	137.3	138.3	144.2	RGN	NM_004683.3	RC;SMP30	calcium		
GI_23111020-A	128.2	142.4	129.9	RGN	NM_152869.1	RC;SMP30	calcium		
GI_23111022-S	665.5	691.7	147.6	SNX10	NM_013322.2	MGC33054			
GI_23111025-A	501.4	588.5	633.6	SNX11	NM_013323.2		protein		intracellula
GI_23111027-I	97.5	99.5	100	SNX11	NM_152244.1		protein		intracellula
GI_23111029-S	166.4	178.1	187.9	SNX12	NM_013346.2		protein		intracellula
GI_23111031-A	417.7	591.6	567.6	SNX1	NM_148955.1	SNX1A;MGC8664;HsT17379	protein	peripheral	endocytosi
GI_23111037-S	2334	1617.7	1224.8	SNX2	NM_003100.2	MGC5204	protein	peripheral	endocytosi
GI_23111040-A	6359.2	6992.2	6046.2	SNX3	NM_152827.1	SDP3;SNX3A;MGC17570		peripheral	endocytosi
GI_23111044-S	718.3	886	943.3	SNX4	NM_003794.2		protein	peripheral	endocytosi
GI_23111045-A	559.3	506.8	271.5	SNX5	NM_014426.2	FLJ10931			nonselecti
GI_23111046-I	589.7	708.6	347	SNX5	NM_152227.1	FLJ10931			nonselecti
GI_23111048-I	315.3	339.2	318.4	SNX6	NM_021249.2	TFAF2;MGC3157			
GI_23111050-A	1879.9	1475.9	1039.3	SNX6	NM_152233.1	TFAF2;MGC3157			
GI_23111053-I	107	130.3	109	SNX7	NM_015976.2	MGC8717;DKFZP564F052	protein		intracellula
GI_23111054-A	635.5	834.1	656.8	SNX7	NM_152238.1	MGC8717;DKFZP564F052	protein		intracellula
GI_23111054-I	134.7	140.7	141.5	SNX7	NM_152238.1	MGC8717;DKFZP564F052	protein		intracellula
GI_23111056-S	98.8	116.1	86.5	SNX9	NM_016224.3	SDP1;WISP;SH3PX1	SH3/SH2		protein
GI_23111057-S	598.3	400.8	353.5	OSBPL10	NM_017784.3	ORP10;OSBP9;FLJ20363			lipid
GI_23111058-S	212.6	254.1	255.4	OSBPL11	NM_022776.3	ORP11;ORP-			lipid
GI_23111059-S	537.1	554.2	592.4	SF3B4	NM_005850.3	SAP49;SF3B49;MGC10828	pre-mRNA	spliceoso	mRNA
GI_23111060-S	557.7	584.7	521.4	SFRS11	NM_004768.2	p54;dJ677H15.2	pre-mRNA	nucleus	mRNA
GI_23111063-A	607.1	646.6	477.8	SFRS8	NM_152235.1	SWAP	pre-mRNA	nucleus	mRNA
GI_23111065-S	111.9	102.3	104.7	SLC27A2	NM_003645.2	VLCS;FATP2;VLACS;FACVL1;hFACVL1;HsT	long-chain-	peroxisom	very-long-
GI_23111066-S	112.7	130.1	120.2	SPACA1	NM_030960.2	SAMP32;MGC32952			
GI_23199968-A	125.2	135.9	126.6	TAGAP	NM_138810.2	FKSG15;FLJ32631;FLJ39771;MGC27381			
GI_23199968-I	80.3	84.1	96.4	TAGAP	NM_138810.2	FKSG15;FLJ32631;FLJ39771;MGC27381			

GI_23199972-I	521.9	510.7	518.4	WTAP	NM_004906.3	MGC3925;KIAA0105			
GI_23199973-A	705.7	671.8	547.4	WTAP	NM_152857.1	MGC3925;KIAA0105			
GI_23199973-I	103.8	109.8	102.9	WTAP	NM_152857.1	MGC3925;KIAA0105			
GI_23199977-A	1505.3	1861.2	1573.6	WIG1	NM_152240.1	WIG-1;PAG608;FLJ12296;MGC10613			
GI_23199980-S	524.8	582.9	573.4	WIRE	NM_133264.2	FLJ23260;FLJ30495;DKFZp547N082			
GI_23199981-S	221.3	274.9	231.5	ZNF179	NM_007148.2	BFP;RNF112	zinc ion	cellular_co	biological_
GI_23199982-S	951.8	1133	847.8	PIGK	NM_005482.1	GPI8;MGC22559	GPI-		GPI
GI_23199984-S	102.4	97	92.8	ULK2	NM_014683.2	KIAA0623	protein-		protein
GI_23199988-S	347.2	425.5	385.2	CXCL14	NM_004887.3	KS1;Kec;BMAC;BRAK;NJAC;MIP-	chemokin	extracellul	chemotaxi
GI_23199992-S	281.6	337.5	279.7	LIG4	NM_002312.2		DNA	nucleus	single
GI_23199994-S	1686.6	1484.3	1351	WBSCR22	NM_017528.2	WBMT;PP3381;HUSSY-	S-	nucleus	biological_
GI_23199996-I	138.3	127.5	120.7	WBSCR20A	NM_018044.2	NOL1R;MGC986;WBSCR20;FLJ10267;p120			
GI_23199997-A	597.7	583.5	691.7	WBSCR20A	NM_148956.1	NOL1R;MGC986;WBSCR20;FLJ10267;p120			
GI_23200001-A	329.2	392.6	442.1	WBSCR20C	NM_148936.1	NOL1R2;FLJ11626;MGC15057;WBSCR20B;			
GI_23200003-I	113.1	113.3	107.5	WBSCR20C	NM_148980.1	NOL1R2;FLJ11626;MGC15057;WBSCR20B;			
GI_23200005-I	212.9	276.9	209.9	WBSCR20C	NM_149379.1	NOL1R2;FLJ11626;MGC15057;WBSCR20B;			
GI_23200009-I	119.1	135.8	133.5	WBSCR21	NM_031295.2	PP1226			
GI_23200013-A	138.4	168.3	161.5	WBSCR21	NM_148914.1	PP1226			
GI_23200017-I	155.9	179.2	155.9	WBSCR21	NM_148916.1	PP1226			
GI_23200030-A	714.9	691.6	556.6	TNFRSF25	NM_148970.1	DR3;TR3;DDR3;LARD;APO-3;TRAMP;WSL-	NGF/TNF	cytosol	induction
GI_23200040-S	756.7	678.2	816.4	TNFRSF14	NM_003820.2	TR2;ATAR;HVEA;HVEM;LIGHTR	NGF/TNF	integral to	cell
GI_23238186-I	235.2	307.5	259.6	TES	NM_015641.2	TESS;TESS-			
GI_23238187-A	271.8	485.1	413.7	TES	NM_152829.1	TESS;TESS-			
GI_23238189-S	129.6	147.8	146	WFDC9	NM_147198.2	WAP9;dJ688G8.2			
GI_23238191-S	100.5	118.5	109	TNFRSF17	NM_001192.2	BCM;BCMA	receptor	integral to	signal
GI_23238193-A	111.4	122.4	113.7	TNFRSF18	NM_148901.1	AITR;GITR;GITR-D	NGF/TNF	integral to	anti-
GI_23238195-S	144.9	469.5	108.7	IL2RB	NM_000878.2	P70-75	interleukin-	integral to	signal
GI_23238198-I	109.5	103.6	117.9	TNFRSF19L	NM_032871.3	RELT;FLJ14993	receptor	integral to	
GI_23238199-A	126.6	129.7	131.3	TNFRSF19L	NM_152222.1	RELT;FLJ14993	receptor	integral to	
GI_23238199-I	113.9	128.7	127.3	TNFRSF19L	NM_152222.1	RELT;FLJ14993	receptor	integral to	
GI_23238201-A	113.8	157.3	142.6	TNFRSF19	NM_018647.2	TAJ;TROY;TRADE;TAJ-alpha	tumor	integral to	JNK
GI_23238201-I	108.1	124.9	122.9	TNFRSF19	NM_018647.2	TAJ;TROY;TRADE;TAJ-alpha	tumor	integral to	JNK
GI_23238205-S	201.7	249.3	232.4	TNFRSF13B	NM_012452.2	TACI	receptor	integral to	cell
GI_23238206-S	3372.7	4361.9	2470.8	TNFRSF21	NM_014452.3	DR6;BM-018			
GI_23238207-S	163.7	186.1	177.7	IL17R	NM_014339.3	IL17RA;IL-17RA;hIL-17R;MGC10262	receptor	integral to	cell
GI_23238209-A	9364.7	9592.2	9861.4	ARPC2	NM_005731.2	ARC34;PRO2446;p34-Arc;PNAS-139	structural	Arp2/3	cell
GI_23238209-I	711.1	939	838.5	ARPC2	NM_005731.2	ARC34;PRO2446;p34-Arc;PNAS-139	structural	Arp2/3	cell
GI_23238210-I	167	197.3	168.2	ARPC2	NM_152862.1	ARC34;PRO2446;p34-Arc;PNAS-139	structural	Arp2/3	cell
GI_23238212-S	3265.8	3854.1	3287	ARPC5	NM_005717.2	ARC16;p16-ARC;dJ127C7.3	structural	Arp2/3	actin
GI_23238213-A	126.6	133.9	123.1	ACE	NM_152830.1	DCP;ACE1;DCP1;CD143;MGC26566	peptidyl-	soluble	regulation
GI_23238215-A	86.5	94.1	86.7	ACE	NM_152831.1	DCP;ACE1;DCP1;CD143;MGC26566	peptidyl-	soluble	regulation
GI_23238215-I	117.9	103.9	106.3	ACE	NM_152831.1	DCP;ACE1;DCP1;CD143;MGC26566	peptidyl-	soluble	regulation
GI_23238217-I	119.8	122.6	112.5	ACE	NM_000789.2	DCP;ACE1;DCP1;CD143;MGC26566	peptidyl-	soluble	regulation
GI_23238218-S	305	394.8	373.9	DMC1	NM_007068.2	DMC1H;LIM15;HsLim15;dJ199H16.1	ATP	meiotic	meiosis

GI_23238220-S	7295.9	5620.3	4498.1	EIF3S7	NM_003753.2	MGC17258;eIF3-p66;eIF3-zeta	translation	eukaryotic	regulation
GI_23238221-S	957.4	974.3	972.6	COPS3	NM_003653.2	SGN3		cytoplasm	response
GI_23238227-S	242.4	295.4	231.2	CHST7	NM_019886.2	C6ST-2	sulfotransf		
GI_23238230-A	639.7	763.6	1047.1	HMGN3	NM_138730.1	TRIP7;PNAS-24	transcripti		transcripti
GI_23238232-S	2557.9	2358.4	1800.3	HMGN4	NM_006353.2	NHC;HMG17L3;MGC5145	DNA	chromatin	regulation
GI_23238233-A	112	126.6	111.7	MS4A6A	NM_022349.2	CDA01;MS4A6;4SPAN3;CD20L3;4SPAN3.2;	receptor	integral to	
GI_23238233-I	122.5	131.1	130.8	MS4A6A	NM_022349.2	CDA01;MS4A6;4SPAN3;CD20L3;4SPAN3.2;	receptor	integral to	
GI_23238239-S	104.5	106.6	116.8	AGTR2	NM_000686.3	AT2	angiotensi	integral to	regulation
GI_23238241-S	180.2	199.3	184.6	WFDC5	NM_145652.2	PRG5;WAP1;dJ211D12.5	serine		
GI_23238242-S	312.8	429.2	424.1	SNX13	NM_015132.2	RGS-PX1;KIAA0713			
GI_23238243-I	85.4	96.2	86.8	SNX16	NM_022133.2	DKFZp666H147	protein	kinesin	intracellula
GI_23238247-A	501.5	461.5	361.3	SNX16	NM_152837.1	DKFZp666H147	protein	kinesin	intracellula
GI_23238249-S	1427.9	2066.8	2254	SNX17	NM_014748.2	KIAA0064	protein C-	early	neuropepti
GI_23238250-S	574.9	397.6	496.3	TIGD5	NM_032862.2	FLJ14926;MGC44883	DNA	nucleus	
GI_23238255-A	158.9	188	168.9	CPT1B	NM_152246.1	CPT1-M;M-CPT1;KIAA1670	carnitine	mitochond	fatty acid
GI_23238259-A	202.1	218.3	190.2	CHKL	NM_005198.3	CHETK	choline		
GI_23238259-I	446.7	501.8	390.8	CHKL	NM_005198.3	CHETK	choline		
GI_23270402-A	603.4	755.2	693.2	CRYZL1	NM_005111.5	4P11;QOH-1	NADPH:q		
GI_23308500-S	190.8	223.1	214.9	FLJ31606	NM_153025.1				
GI_23308504-S	302.1	342.7	316.1	FLJ32112	NM_153035.1				transcripti
GI_23308506-S	170.3	207.1	203.1	FLJ31166	NM_153022.1				
GI_23308508-S	100.9	101.2	98.6	FLJ31958	NM_153030.1				
GI_23308510-S	122.2	117.8	115.3	FLJ30726	NM_153018.1			nucleus	
GI_23308512-S	111.3	123.1	112.4	FLJ32831	NM_153040.1				
GI_23308516-S	279.9	271.4	256	ZNF75A	NM_153028.1	FLJ31529	nucleic	nucleus	regulation
GI_23308518-S	415.2	595.9	378.5	PRICKLE1	NM_153026.1	RILP;FLJ31627;FLJ31937			
GI_23308520-S	383.9	445.6	484.3	FLJ30634	NM_153014.1				
GI_23308524-S	234.6	268.9	278.8	FLJ35801	NM_153044.1				
GI_23308526-S	119.8	119.4	121.1	FLJ30679	NM_153017.1				
GI_23308528-S	167.5	206.8	180.5	FLJ32063	NM_153031.1				
GI_23308530-S	182.1	191.4	179.9	FLJ30430	NM_153009.1				
GI_23308532-S	85	91.2	78.8	FLJ30594	NM_153011.1		nucleic		
GI_23308536-S	97.4	105.6	95.2	FLJ32447	NM_153038.1				
GI_23308538-S	319	399.4	364.3	FLJ32955	NM_153041.1				
GI_23308540-S	217	196.7	214.4	FLJ31659	NM_153027.1				
GI_23308544-S	95	90.7	89.7	FLJ30668	NM_153015.1				
GI_23308546-S	521.1	442.8	409.7	FLJ32803	NM_153039.1				
GI_23308548-S	107.3	108.3	106.7	FLJ32065	NM_153032.1				
GI_23308550-S	104.4	111.7	109.9	KCTD7	NM_153033.1	FLJ32069	voltage-	membran	potassium
GI_23308552-S	265.2	327.4	289.9	SPATA13	NM_153023.1	FLJ31208	DNA	nucleus	chromoso
GI_23308556-S	116.9	110	98.7	FLJ32293	NM_153037.1				
GI_23308558-S	149.8	143.5	121.9	FLJ31393	NM_153024.1		olfactory	integral to	G-protein
GI_23308560-S	103.5	100.7	102.9	RNPC6	NM_153020.1	FLJ30829;dJ259A10.1			
GI_23308562-S	181.4	210.5	200.6	C6orf78	NM_153036.1	FLJ32239			

GI_23308566-S	95.1	118	103.5	ASRGL1	NM_025080.2	ALP;ALP1;FLJ22316	asparagin		glycoprote
GI_23308570-S	106.8	108.3	104.3	SLC3A1	NM_000341.2	D2H;ATR1;NBAT;RBAT;CSNU1	amino	membran	basic
GI_23308571-S	722.3	1169.9	1159.2	LENG4	NM_024298.2	BB1			
GI_23308573-S	493.1	403.8	371.4	SPRY4	NM_030964.2				
GI_23308576-S	13505.5	7954.4	3274.3	PHGDH	NM_006623.2	PDG;PGD;PGAD;PGDH;SERA;3PGDH;MGC	phosphogl		brain
GI_23308578-S	5143.7	5909.7	5372.5	TEBP	NM_006601.4	P23	protein		signal
GI_23308584-S	128.4	142.8	135.4	GPR156	NM_153002.1	PGR28;GABABL	GABA-B	membran	peroxidas
GI_23308586-S	141.8	142.3	142	NAGS	NM_153006.1	NAT7;FLJ23827	acyltransf		amino
GI_23308590-S	143	158	153.8	C4orf7	NM_152997.1	FDC-SP			
GI_23308598-S	96.6	91.6	88.5	OFCC1	NM_153003.1	MRDS1			
GI_23308602-S	111.5	110.3	99.2	MYRIP	NM_015460.1	SLAC2C;SLAC2-C;DKFZp586F1018	actin		
GI_23308686-A	110.2	139.9	122.8	KIAA0889	NM_152257.1	dJ469A13.6.1			
GI_23308686-I	89.9	105.4	91.5	KIAA0889	NM_152257.1	dJ469A13.6.1			
GI_23308688-S	1083.9	1037.5	1160	C18B11	NM_152260.1				
GI_23308690-S	105.9	97.3	96.8	BTBD9	NM_152733.1	KIAA1880;dJ322I12.1	protein		
GI_23308696-S	1326.3	1953.4	1837.6	SRPR	NM_003139.2	DP;MGC3650;MGC9571;Sralpha;MGC17355	signal	signal	cotranslati
GI_23308700-S	451.7	508.4	425.3	DRB1	NM_152945.1		nucleic		
GI_23308723-S	116.3	119.4	115.1	SIAT7C	NM_152996.1	ST6GALNACIII	sialyltransf	membran	protein
GI_23308726-S	178.1	224.2	186.4	TGFBR2	NM_003242.3	HNPCC6	type II	integral to	TGFbeta
GI_23308728-A	107.6	106.4	97.1	ZNF268	NM_003415.1	HZF3	transcripti	nucleus	developm
GI_23308730-S	2936.4	3071	2841.5	TRIP6	NM_003302.1	OIP1;ZRP-	protein	cellular_co	biological_
GI_23308736-S	308.1	313.9	237.3	ZNF23	NM_145911.1	KOX16;ZNF359	DNA	nucleus	developm
GI_23308744-S	106.2	106.8	96.9	C20orf132	NM_152503.1	FLJ36113;dJ621N11.4;DKFZp434N0426			
GI_23308748-S	219.6	252.8	229.9	C20orf147	NM_152667.1	MGC26833;dJ694B14.3	hydrolase		metabolis
GI_23312361-I	110.8	122.9	104.1	UHRF2	NM_152306.2	NIRF;URF2;RNF107;MGC33463	DNA		regulation
GI_23312363-A	642.6	464.2	317.8	UHRF2	NM_152896.1	NIRF;URF2;RNF107;MGC33463	DNA		regulation
GI_23312365-S	134.9	136.2	131.1	TNFRSF1B	NM_001066.2	p75;TBPII;TNFBR;TNFR2;CD120b;TNFR80;	tumor	integral to	apoptosis
GI_23312366-S	206	275.1	194.4	TNFRSF4	NM_003327.2	OX40;ACT35;CD134;TXGP1L	NGF/TNF	integral to	immune
GI_23312370-A	106.5	121.3	84.7	TNFRSF5	NM_152854.1	p50;Bp50;CD40;CDW40;MGC9013	receptor	proteoglyc	developm
GI_23312372-S	3327.4	3455.7	2796.4	TNFRSF1A	NM_001065.2	FPF;p55;p60;TBP1;TNF-	tumor	extracellul	signal
GI_23312375-A	128.9	157	119.9	PPEF1	NM_152225.1	PP7;PPEF;PPP7C	protein		protein
GI_23312381-I	95.8	98.7	90.5	PPEF2	NM_152933.1		protein		protein
GI_23312385-A	144.6	158.2	148.3	PPEF2	NM_006239.2		protein		protein
GI_23312387-I	84.7	89.3	87.5	CHRFAM7A	NM_139320.1	D-10;CHRNA7-DR1			
GI_23312389-A	107.3	100.9	113.2	CHRFAM7A	NM_148911.1	D-10;CHRNA7-DR1			
GI_23312391-S	341.9	316.2	311.9	TIGD2	NM_145715.1				
GI_23312393-S	90.6	75.9	88.4	TIGD3	NM_145719.1				
GI_23346408-S	1998.4	1915.7	2297.2	C20orf111	NM_016470.6	HSPC207;dJ1183I21.1			
GI_23346411-S	217	230.7	236.1	TAIP-2	NM_024969.2	FLJ11703		nucleus	apoptosis
GI_23346413-S	1673.2	1418.4	1074.2	MARK3	NM_002376.3	KP78;CTAK1;PAR1A	protein-		protein
GI_23346417-S	715.5	571.2	513.6	MINA	NM_032778.3	MDIG;MINA53;FLJ14393			
GI_23346419-S	265.1	299	255.7	NFRKB	NM_006165.2		specific	nucleus	transcripti
GI_23346423-S	84.2	89.6	97.1	IGSF4D	NM_153184.1	NECL3			
GI_23346425-S	10222.7	10289	8785.4	ATP5A1	NM_004046.3	OMR;ORM;ATPM;ATP5A;hATP1;ATP5AL2	transporte	proton-	ATP

GI_23346426-S	1824.3	1680.4	1921.2	C21orf56	NM_032261.3	DKFZp434N0650			
GI_23346635-S	121.5	117.9	108.5	DHH	NM_021044.2	HHG-3;MGC35145	peptidase		developm
GI_23346636-S	297.7	231.2	188.2	PRO1580	NM_018502.2				
GI_23346638-S	1806.5	1590.1	1644.4	TUSC4	NM_006545.3	NPR2L;NPRL2			
GI_23397408-S	115.7	137.3	123.6	MGC23947	NM_152278.1	MPMGp800C04260Q003			
GI_23397426-S	1455.4	2588.3	2518.9	SYNCRIP	NM_006372.3	pp68;NSAP1;GRY-RBP;dJ3J17.2	ribonucleo	nucleus	RNA
GI_23397428-S	8627.2	8519.3	7030.1	GA17	NM_006360.2				
GI_23397430-S	113.9	132.5	132.7	C21orf74	NM_153203.1	PRED16			
GI_23397448-S	112.3	116.7	118.9	C21orf90	NM_153204.1				
GI_23397450-S	133.9	137.3	126.5	AMICA	NM_153206.1	JAML;FLJ37080			
GI_23397455-S	468.3	496.1	242.4	MGC35048	NM_153208.1				
GI_23397457-S	135.5	149.6	125.5	FLJ37300	NM_153209.1				
GI_23397461-S	485.2	583.3	561.1	FLJ33761	NM_153211.1				
GI_23397463-S	113	113.9	111	GJB4	NM_153212.1	CX30.3;MGC21116	connexon	integral to	perception
GI_23397470-S	108.5	126	108.7	FLJ37440	NM_153214.1		calcium		
GI_23397472-S	99.9	98.9	96.6	FLJ38608	NM_153215.1				
GI_23397474-S	103.1	121.3	110.8	MGC13034	NM_153217.1				
GI_23397476-S	105	125.3	110.8	FLJ38725	NM_153218.1		electron		electron
GI_23397482-S	215	229	199.6	FLJ36090	NM_153223.1				
GI_23397486-S	111.5	137.8	126.4	RPESP	NM_153225.1	FLJ40021			
GI_23397491-S	264.6	252.1	296.1	TMEM20	NM_153226.1	C10orf60;FLJ33990		membran	
GI_23397493-S	101.7	115.5	111.3	MGC34800	NM_153227.1				
GI_23397495-S	102.6	116.4	98.4	FLJ38335	NM_153228.1				
GI_23397497-S	105	126.5	100	FLJ33318	NM_153229.1				
GI_23397499-S	96.8	105.3	86.3	MGC35179	NM_153230.1				
GI_23397509-S	183.6	220.3	202.2	FLJ36445	NM_153233.1				
GI_23397517-S	70.3	88	85.9	MGC34760	NM_153237.1				
GI_23397519-S	96.3	112	97.3	MGC22001	NM_153238.1				
GI_23397529-S	85.4	103.2	91.9	MGC42157	NM_153241.1				
GI_23397531-S	120.4	133.7	121.5	MGC35468	NM_153244.1				
GI_23397533-S	116.6	134.3	111.8	MGC45491	NM_153246.1				
GI_23397535-S	506.3	703.8	424.7	SLC29A4	NM_153247.1	ENT4;FLJ34923	nucleoside	membran	transport
GI_23397543-S	126.3	146.7	141	FLJ36119	NM_153254.1		tubulin-		protein
GI_23397553-S	162.2	160	181.8	FLJ36812	NM_153260.1				
GI_23397557-S	140.9	162.4	139.2	SYT14	NM_153262.1	sytXIV;FLJ34198	transporte	membran	transport
GI_23397559-S	613.9	723.6	611.5	ZNF549	NM_153263.1	FLJ34917	nucleic	intracellula	regulation
GI_23397563-S	2014.7	1770.5	1561.8	FLJ35827	NM_153265.1				
GI_23397569-S	110.2	106.7	85.3	FLJ31579	NM_153268.1		phospholi		intracellula
GI_23397571-S	88.5	100.1	97.3	FLJ34960	NM_153270.1		protein		
GI_23397573-S	438.3	466.2	448.5	MGC32065	NM_153271.1				
GI_23397575-S	111.6	104.7	109.9	VMD2L2	NM_153274.1		molecular	integral to	biological_
GI_23397638-A	157.8	177.2	166.9	EMR3	NM_152939.1		G-protein	membran	neuropepti
GI_23397640-S	107.6	119.8	102	MS4A2	NM_000139.2	FCERI;MS4A1;FCER1B	receptor	integral to	immune
GI_23397641-I	228.2	243.9	180.9	GREB1	NM_014668.2	KIAA0575			

GI_23397643-I	101	112.8	91.7	GREB1	NM_033090.1	KIAA0575			
GI_23397645-A	90.5	101.9	88.7	GREB1	NM_148903.1	KIAA0575			
GI_23397645-I	92.3	84	91.5	GREB1	NM_148903.1	KIAA0575			
GI_23397647-I	288.9	354.3	330.6	PIGO	NM_032634.2	MGC3079;FLJ00135;MGC20536;DKFZp434	molecular	endoplas	GPI
GI_23397651-S	649.1	1085.2	1079.9	PIGS	NM_033198.2				
GI_23397652-S	4868.4	4687.9	6973.3	PIGT	NM_015937.2	CGI-06;MGC8909			
GI_23397656-A	98.9	113.9	105.9	ABHD1	NM_152870.1	LABH1;FLJ36128	molecular		
GI_23397665-S	1045	1110.5	992.1	SIN3A	NM_015477.1	KIAA0700;DKFZP434K2235	transcripti	nucleus	regulation
GI_23397667-S	5365	7258.3	6720	ARPC3	NM_005719.2	ARC21;p21-Arc	structural	Arp2/3	cell
GI_23397668-S	1239.8	1732.5	2088.4	ARPC4	NM_005718.2	ARC20;p20-ARC;MGC13544	structural	Arp2/3	cell
GI_23397671-S	102.7	116.7	111.5	HOXD4	NM_014621.2	HOX4;HOX4B;HHO.C13;HOX-5.1;Hox-4.2	transcripti	nucleus	regulation
GI_23397673-S	242.9	284.4	254.6	HOXD9	NM_014213.2	HOX4;HOX4C;Hox-4.3;Hox-5.2	RNA	nucleus	transcripti
GI_23397677-S	856.6	867.8	871.7	STAT6	NM_003153.3	STAT6B;STAT6C;D12S1644;IL-4-STAT	transcripti	nucleus	signal
GI_23397679-S	104.5	126.4	106.1	ZP4	NM_021186.2	ZBP;ZP1;ZPB	molecular	cellular_co	biological_
GI_23397686-A	104.2	183	200.6	EMR2	NM_152918.1				
GI_23397697-A	1733.4	2656	3904.9	CPNE1	NM_152926.1	CPN1;COPN1;MGC1142	transporte		vesicle-
GI_23463288-S	491.8	557	464.3	FAM10A5	NM_153291.1				
GI_23463298-S	553.3	576	489.6	FAM10A4	NM_153290.1				
GI_23463320-S	89.7	103.6	96	ANP32E	NM_030920.2	LANPL;LANP-L;MGC5350	phosphata	cytoplasmi	
GI_23463325-S	107.6	118.6	105.9	FLJ25680	NM_153216.1		transcripti	nucleus	regulation
GI_23503232-I	358.7	418.8	378.9	C1QDC1	NM_032156.1	EEG1;EEG-1;FLJ11391;FLJ22569			
GI_23503234-A	477.7	579.1	498.5	C1QDC1	NM_023925.2	EEG1;EEG-1;FLJ11391;FLJ22569			
GI_23503234-I	90.5	94.5	88.3	C1QDC1	NM_023925.2	EEG1;EEG-1;FLJ11391;FLJ22569			
GI_23503240-S	84.3	94.4	80.9	DNAJB8	NM_153330.1	MGC33884	chaperone		
GI_23503242-S	114.6	118.6	98.3	C12orf2	NM_007211.2	HoJ-1			neuropepti
GI_23503246-S	2574.6	2511.3	1934.5	MGC45400	NM_153333.1		DNA	nucleus	regulation
GI_23503254-I	102.5	103.6	90	SLIC1	NM_153337.1	MGC35578			
GI_23503258-S	371.7	304.2	264	FLJ90811	NM_153339.1		pseudouri		tRNA
GI_23503260-S	274.4	225.6	245.3	C10orf89	NM_153336.1	MGC35392			
GI_23503262-S	289.7	345.7	265.2	IBRDC3	NM_153341.1	FLJ90005			
GI_23503264-S	128.6	136.9	140.7	FLJ90165	NM_153338.1		gamma-		
GI_23503270-S	233.7	297.1	250.5	FLJ90586	NM_153345.1				
GI_23503272-S	491.7	407.6	457.4	FLJ90024	NM_153342.1				
GI_23503274-S	179.5	230.1	129	FLJ90119	NM_153347.1				
GI_23503276-S	189.6	224.9	244.2	C6orf141	NM_153344.1	MGC46457	DNA	nucleus	regulation
GI_23503282-S	143.4	131.9	125.5	MGC34741	NM_153356.1				
GI_23503286-S	335.9	369.1	375	FLJ90396	NM_153358.1		nucleic	nucleus	regulation
GI_23503290-S	368.2	798	952.8	FLJ90166	NM_153360.1				
GI_23503292-S	325.9	402.5	353.9	SLC16A11	NM_153357.1	FLJ90193	copper,		superoxid
GI_23503296-S	126.1	151.5	157.6	C6orf158	NM_153362.1	MGC46520;dJ223E3.1	trypsin		proteolysis
GI_23503298-S	427.1	441	342.1	MGC24975	NM_153359.1				
GI_23503300-S	98.3	93.8	84.9	MGC39520	NM_153364.1				
GI_23503306-S	91.6	102	86.6	MGC42415	NM_153363.1		nucleic	intracellula	regulation
GI_23503310-S	148.1	148.6	114.3	FLJ90013	NM_153365.1				

GI_23503312-S	1084.9	733.6	362.2	MGC35274	NM_153374.1				cell wall
GI_23503314-S	1103.5	1312.9	986.4	FLJ90798	NM_153367.1		nucleic	nucleus	electron
GI_23503316-S	114.4	136.9	154.8	FLJ90575	NM_153376.1		DNA	nucleus	regulation
GI_23503318-S	426.2	568.4	498.9	PI16	NM_153370.1	MGC45378;dJ90K10.5	peroxidas	extracellul	response
GI_23503320-S	289.3	367.8	318.4	PLAC2	NM_153375.1	FLJ90734			
GI_23503326-A	209.2	254.3	189.5	MLL5	NM_018682.2	FLJ10078;FLJ14026;HDCMC04P			
GI_23503334-S	501.5	666.6	640.6	FLJ25952	NM_153251.1				
GI_23510242-S	821.8	651.6	579	KIAA1797	NM_017794.2	FLJ20375			
GI_23510282-S	1462.7	1341.8	1157.6	ELP3	NM_018091.3	FLJ10422			
GI_23510284-S	102.9	105.9	101.3	CILP2	NM_153221.1	CLIP-2;MGC45771			
GI_23510288-S	123.6	132.1	124.8	SGPP2	NM_152386.2	SPP2;FLJ39004	hydrolase	integral to	
GI_23510318-S	103	114.4	101.6	NPPA	NM_006172.1	ANF;ANP;PND;CDD-ANF	hormone	extracellul	regulation
GI_23510324-I	101.2	84.9	85.4	PMCHL2	NM_031888.1		molecular	cellular_co	synaptic
GI_23510330-S	149.1	176.9	181.7	XTP1	NM_018369.1	FLJ11252			intracellula
GI_23510334-S	272.7	270.7	284.2	IHPK1	NM_153273.1	IP6K1;MGC9925;KIAA0263	inositol-		
GI_23510339-A	1194.7	2084	2003.2	UBE1	NM_153280.1	A1S9;A1ST;GXP1;A1S9T;UBE1X;MGC4781	ubiquitin		DNA
GI_23510339-I	157.7	166.2	151.5	UBE1	NM_153280.1	A1S9;A1ST;GXP1;A1S9T;UBE1X;MGC4781	ubiquitin		DNA
GI_23510343-I	112.7	126.3	117.8	C20orf161	NM_033421.2	SNX-	protein		intracellula
GI_23510344-I	380.3	446.2	281.9	FYN	NM_002037.3	SLK;SYN;MGC45350	protein-		learning
GI_23510345-I	182	203.8	186.6	AD-017	NM_152932.1	FLJ14611			
GI_23510347-S	111.1	112.2	113.5	TTRAP	NM_016614.2	EAP2;AD022;MGC9099;dJ30M3.3	transcripti		cell
GI_23510349-A	181.2	186.7	197.5	C20orf161	NM_152897.1	SNX-	protein		intracellula
GI_23510351-S	1115.8	874.9	1482.7	AD023	NM_020679.2	MGC45027			
GI_23510353-S	281.1	346.1	334.7	Spc25	NM_020675.3	AD024;MGC22228			
GI_23510354-S	314.1	407.4	301.3	AD031	NM_032021.2				
GI_23510355-I	209.7	184	171.1	RIOK1	NM_031480.2	AD034;FLJ30006;MGC12903;bA288G3.1	protein-		protein
GI_23510357-A	1769.8	1217.8	963.2	RIOK1	NM_153005.1	AD034;FLJ30006;MGC12903;bA288G3.1	protein-		protein
GI_23510357-I	102.2	107.1	105.8	RIOK1	NM_153005.1	AD034;FLJ30006;MGC12903;bA288G3.1	protein-		protein
GI_23510361-I	164.2	147.3	196	FYN	NM_153047.1	SLK;SYN;MGC45350	protein-		learning
GI_23510363-A	3356.2	3116.9	2008.3	FYN	NM_153048.1	SLK;SYN;MGC45350	protein-		learning
GI_23510365-S	133.8	138.7	114	HOXD10	NM_002148.2	HOX4;HOX4D;HOX4E	RNA	nucleus	regulation
GI_23510367-S	271.6	276.3	200.5	HOXD11	NM_021192.2	HOX4;HOX4F	transcripti	nucleus	regulation
GI_23510369-S	103.8	94.4	91.3	HOXD12	NM_021193.2	HOX4H	transcripti	nuclear	regulation
GI_23510371-S	93	91.4	88.7	HOXD13	NM_000523.2	SPD;HOX4I	DNA	nucleus	regulation
GI_23510372-S	211.6	250.5	215.4	HOXD3	NM_006898.4	HOX4;HOX4A;Hox-4.1;MGC10470	transcripti	nucleus	embryoge
GI_23510373-S	504.3	420.1	356.2	HOXD8	NM_019558.2	HOX4;HOX4E;HOX5.4	transcripti	nucleus	determinat
GI_23510374-A	262.6	397.1	255	ANKRD15	NM_015158.1	KANK;KIAA0172	GTPase		immune
GI_23510374-I	97.7	98.3	86.5	ANKRD15	NM_015158.1	KANK;KIAA0172	GTPase		immune
GI_23510376-I	97.4	104.8	104.3	ANKRD15	NM_153186.1	KANK;KIAA0172	GTPase		immune
GI_23510378-I	136.6	151.6	130.5	TNPO1	NM_002270.2	MIP;TRN;IPO2;MIP1;KPNB2	nuclear	nuclear	protein-
GI_23510380-A	438.2	368	409.2	TNPO1	NM_153188.1	MIP;TRN;IPO2;MIP1;KPNB2	nuclear	nuclear	protein-
GI_23510380-I	117	127.8	126.3	TNPO1	NM_153188.1	MIP;TRN;IPO2;MIP1;KPNB2	nuclear	nuclear	protein-
GI_23510382-I	181.4	209.9	175.6	EZH2	NM_004456.3	EZH1;ENX-1;MGC9169	DNA	nucleus	establish
GI_23510383-A	364.3	311.9	279.6	EZH2	NM_152998.1	EZH1;ENX-1;MGC9169	DNA	nucleus	establish

GI_23510385-I	110.5	126.6	123.4	MTMR3	NM_021090.2	ZFYVE10;KIAA0371;FYVE-DSP1	protein	membran	protein
GI_23510388-A	579.9	540.3	590.7	MTMR3	NM_153051.1	ZFYVE10;KIAA0371;FYVE-DSP1	protein	membran	protein
GI_23510390-I	127.1	136.6	128.9	NEK3	NM_002498.1	HSPK36;MGC29949	cAMP-	nucleus	cell cycle
GI_23510392-A	142	150.4	137.5	NEK3	NM_152720.1	HSPK36;MGC29949	cAMP-	nucleus	cell cycle
GI_23510392-I	91	96.5	97.1	NEK3	NM_152720.1	HSPK36;MGC29949	cAMP-	nucleus	cell cycle
GI_23510394-I	97.1	108.4	99.6	NETO1	NM_138966.2	BCTL1;BTCL1			
GI_23510397-A	588.7	633.1	665.2	PANK1	NM_138316.2	PANK;PANK1a;PANK1b;MGC24596	ATP		coenzyme
GI_23510399-I	166.1	170.7	172.6	PANK1	NM_148977.1	PANK;PANK1a;PANK1b;MGC24596	ATP		coenzyme
GI_23510405-A	202	241.6	258.1	POMZP3	NM_152992.1	POM121;MGC8359;POM-ZP3			
GI_23510407-S	381.1	376.9	319.4	SAP18	NM_005870.3	SAP18p;2HOR0202;MGC27131	transcripti	histone	regulation
GI_23510408-I	185.1	221.2	232.1	SLC22A1	NM_003057.2	OCT1;HOCT1	organic	membran	organic
GI_23510409-A	130.7	111.7	113.3	SLC22A1	NM_153187.1	OCT1;HOCT1	organic	membran	organic
GI_23510411-A	621.5	648.3	538.8	SLC22A2	NM_003058.2	2-Oct	organic	membran	organic
GI_23510412-S	165.5	179.3	178.3	SNX26	NM_052948.2	TCGAP;FLJ39019			
GI_23510414-I	117.3	129.1	110.3	SLC22A2	NM_153191.1	2-Oct	organic	membran	organic
GI_23510416-I	230.4	277.4	257.6	SPAM1	NM_003117.3	HYA1;PH20;HYAL1;HYAL3;PH-		plasma	binding of
GI_23510417-A	130.9	120.1	119.7	SPAM1	NM_153189.1	HYA1;PH20;HYAL1;HYAL3;PH-		plasma	binding of
GI_23510417-I	80.2	81	80.2	SPAM1	NM_153189.1	HYA1;PH20;HYAL1;HYAL3;PH-		plasma	binding of
GI_23510430-A	250.8	294.2	277.3	TNFRSF6	NM_152876.1	FAS;APT1;CD95;APO-1;FASTM	transmem	proteoglyc	anti-
GI_23510432-I	113.7	130.1	109.2	TNFRSF8	NM_001243.2	CD30;KI-1;D1S166E	transmem	integral to	negative
GI_23510435-S	101.7	110	108.7	TNFRSF7	NM_001242.3	T14;CD27;S152;Tp55;MGC20393	transmem	integral to	apoptosis
GI_23510436-A	125.2	133.2	136.3	TNFRSF8	NM_152942.1	CD30;KI-1;D1S166E	transmem	integral to	negative
GI_23510438-S	413.8	523.2	473.5	TNFRSF9	NM_001561.4	ILA;4-1BB;CD137;CDw137;MGC2172	receptor	integral to	negative
GI_23510439-S	105	159.8	115.8	TNFSF10	NM_003810.2	TL2;APO2L;TRAIL;Apo-2L	receptor	soluble	induction
GI_23510440-I	113.4	117.6	112.3	TNFSF12	NM_153012.1	APO3L;DR3LG;TWEAK;MGC20669	receptor	integral to	induction
GI_23510442-A	265.7	294.3	169.7	TNFSF12	NM_003809.2	APO3L;DR3LG;TWEAK;MGC20669	receptor	integral to	induction
GI_23510443-S	121.9	172.1	147	TNFSF13B	NM_006573.3	BAFF;BLYS;TALL1;THANK;ZTNF4;TALL-	receptor	soluble	positive
GI_23510444-S	128.6	145.6	127.7	TNFSF15	NM_005118.2	TL1;TL1A;VEGI	receptor	soluble	signal
GI_23510446-S	185.8	206.9	140.8	TNFSF4	NM_003326.2	GP34;OX4OL;TXGP1;CD134L;OX-40L	receptor	integral to	positive
GI_23510447-S	858.1	735.8	1135.3	MCM5	NM_006739.2	CDC46;MGC5315;P1-CDC46	cell cycle	nucleus	DNA
GI_23510449-S	735.2	624	591.4	MPST	NM_021126.3	MST;TST2;MGC24539	thiosulfate	mitochond	cyanate
GI_23510450-S	2264.9	2695.9	2841.6	APEH	NM_001640.3	APH;OPH;ACPH;D3S48E;MGC2178	acylamino		proteolysis
GI_23510452-S	5732.8	6439.4	6431	COTL1	NM_021149.2	CLP;MGC19733	protein	cytoskelet	leukotrien
GI_23510453-S	126.8	130.2	108	ZNF157	NM_003446.2	HZF22	transcripti	nucleus	negative
GI_23510454-I	123.7	133.8	119.3	ZNF41	NM_153380.1	MGC8941	transcripti	nucleus	regulation
GI_23510456-A	111	138.9	123.1	ZNF41	NM_007130.1	MGC8941	transcripti	nucleus	regulation
GI_23510456-I	78.4	93.6	82.4	ZNF41	NM_007130.1	MGC8941	transcripti	nucleus	regulation
GI_23592219-S	108.1	116.6	125.2	GPR26	NM_153442.1		receptor	integral to	G-protein
GI_23592221-S	118.8	137.4	125.5	JCG3	NM_153444.1		olfactory	integral to	olfaction
GI_23592223-S	155.7	173.8	163.9	GALGT2	NM_153446.1	Cad;Sda;B4GALT	transferas		
GI_23592225-S	117.5	140.3	133.3	KIR3DL3	NM_153443.1	KIR44;KIRC1;KIR3DL7	receptor		
GI_23592229-S	206	237.9	229	JCG1	NM_153445.1		olfactory	integral to	olfaction
GI_23592231-S	840.9	826.7	740.3	LCMR1	NM_153450.1				
GI_23592235-S	171.7	194.4	172.9	C21orf86	NM_153454.1				

GI_23592241-A	140.3	150.1	155	VGLL2	NM_153453.1	VGL2;VITO1			
GI_23592243-S	109.1	117.8	127.7	C21orf87	NM_153455.1				
GI_23618862-S	391.5	378.4	339.6	Ells1	NM_152793.1	FLJ25903			
GI_23618866-S	1110.8	1069.3	1284.5	SFXN1	NM_022754.3	FLJ12876	cation	mitochond	cation
GI_23618915-A	175.5	213.9	177.5	CSE-C	NM_018978.1				
GI_23618915-I	119.7	135.8	124.5	CSE-C	NM_018978.1				
GI_23618925-S	319.9	175	216.4	ZNF559	NM_032497.1	MGC13105	nucleic	nucleus	regulation
GI_23680884-S	760.9	878.2	1103.3	FLJ20522	NM_017861.1				
GI_23821012-S	771.2	650.6	621.4	KIAA1285	NM_015694.1				
GI_23821014-S	174.6	171.5	163.6	RBJ	NM_016544.1		small		small
GI_23821022-A	430.2	676.7	217.9	IL4I1	NM_152899.1	FIG1	amine		electron
GI_23821022-I	127.3	146.1	112.6	IL4I1	NM_152899.1	FIG1	amine		electron
GI_23943784-S	205.9	260.8	234	SOSTDC1	NM_015464.1	USAG1;ECTODIN;DKFZp564D206			
GI_23943786-S	131.1	154.2	136	NCAG1	NM_032160.1	FLJ11477	sulfotransf		
GI_23943808-S	2857.1	2654.7	3164.6	TLP19	NM_015913.2	ERP18;ERP19	electron	endoplas	electron
GI_23943811-S	487.6	581.2	537.2	CTEN	NM_032865.3	FLJ14950			intracellula
GI_23943813-S	234.4	223	221.5	UEV3	NM_018314.2	ATTP;FLJ11068			
GI_23943849-I	277.8	634.3	730.3	CAMK1D	NM_153498.1	CKLiK	ATP		protein
GI_23943853-S	125.6	137.1	129.2	PGA5	NM_014224.1		pepsin A		vacuolar
GI_23943855-S	112.8	114	107.9	SIGLEC9	NM_014441.1	OBBP-LIKE	serine-	integral to	cell
GI_23943857-S	447.7	476.4	532.1	SNX8	NM_013321.1		protein		intracellula
GI_23943859-S	109.7	107	115	PTDSR	NM_015167.1	PSR;PTDSR1;KIAA0585			
GI_23943865-S	100.4	95.3	103	LOC57795	NM_021165.1	KIAA1747			protein
GI_23943871-S	793.5	991.8	923.6	LOC64744	NM_022733.1		DNA	nucleus	
GI_23943877-S	116.1	135.3	124.4	DKFZp434D1	NM_032253.1				
GI_23943879-S	204.5	256.7	229.7	MGC3207	NM_032285.1		translation	eukaryotic	translation
GI_23943883-S	2554.5	1758.2	1502.5	MGC5309	NM_032286.1				
GI_23943885-S	141.5	173.3	143.7	OTEX	NM_139282.1	PEPP1;PEPP2	transcripti	nucleus	regulation
GI_23943891-S	181.8	200.3	174.2	ORAOV1	NM_153451.1	TAOS1			
GI_23943903-S	129.6	136.2	132.7	CIDE-3	NM_022094.2	FLJ20871	apoptosis	intracellula	apoptosis
GI_23943905-S	111.8	118	115	THH	NM_007113.1	THL	calcium	intermedia	cytoskelet
GI_23943911-S	422.9	548.5	488.3	PIK3R4	NM_014602.1	P150;VPS15	enzyme	cellular_co	nonselecti
GI_23943913-S	395.3	458.3	352.3	ZRANB1	NM_017580.1	TRABID			
GI_23943919-S	113	259.6	527.6	PLA2G4A	NM_024420.1	PLA2G4;cPLA2-alpha	calcium-	cytoplasmi	icosanoid
GI_23943927-S	89.3	94.9	91.5	C20orf96	NM_153269.1	FLJ40075;dJ1103G7.2		kinesin	
GI_23957679-S	84.9	81.9	82.1	Rgr	NM_153615.1		guanyl-		intracellula
GI_23957681-S	108.7	112.4	105.4	HS3ST5	NM_153612.1	3-OST-5;HS3OST5	sulfotransf	integral to	heparan
GI_23957689-S	162.3	166.7	174.4	COG7	NM_153603.1		protein	membran	intracellula
GI_23957691-S	187	194.8	184.9	MYOCD	NM_153604.1	MYCD	DNA	nucleus	regulation
GI_23957695-S	104.1	109.6	109.9	FLJ32796	NM_153606.1				
GI_23957697-S	272.6	253.8	346	LOC153222	NM_153607.1		DNA	nucleus	regulation
GI_23957699-S	97.8	103.1	95.2	MGC17986	NM_153608.1		nucleic	intracellula	regulation
GI_23957701-I	91.3	106.7	104.9	TMPRSS6	NM_153609.1	FLJ30744	trypsin	integral to	proteolysis
GI_23957707-S	1370.8	987.1	900.2	LOC254531	NM_153613.1	FLJ10257			

GI_24041011-I	125.6	135.8	125.7	KREMEN1	NM_032045.3	KRM1;KREMEN;FLJ31863	molecular	integral to	cell
GI_24041013-A	113.8	118.9	105.9	KREMEN1	NM_153379.1	KRM1;KREMEN;FLJ31863	molecular	integral to	cell
GI_24041013-I	104	128.3	105.3	KREMEN1	NM_153379.1	KRM1;KREMEN;FLJ31863	molecular	integral to	cell
GI_24041015-A	3570.5	3276.4	3365.7	UXT	NM_004182.2	ART-27			
GI_24041017-I	124.3	152.1	150.5	UXT	NM_153477.1	ART-27			
GI_24041019-A	998.5	894.2	774.9	EED	NM_003797.2	HEED;WAIT1	transcripti	nucleus	negative
GI_24041022-I	106.3	130.7	104.4	EED	NM_152991.1	HEED;WAIT1	transcripti	nucleus	negative
GI_24041025-S	1123.7	1448.3	1927.9	NETO2	NM_018092.3	NEOT2;FLJ10430;FLJ14724;FLJ90456			
GI_24041028-I	236.5	284.2	252.6	NOS2A	NM_000625.3	NOS;INOS;NOS2;HEP-NOS	nitric-	cytoplasm	nitric oxide
GI_24041031-A	85	85.4	86.5	NOS2A	NM_153292.1	NOS;INOS;NOS2;HEP-NOS	nitric-	cytoplasm	nitric oxide
GI_24041034-S	368.5	421.4	437	NOTCH2	NM_024408.2	hN2			
GI_24041037-I	135.2	134.8	142.3	ADAM33	NM_025220.2	FLJ35308;FLJ36751;DJ964F7.1;DKFZp434K			
GI_24041039-A	320.6	369.8	354.3	ADAM33	NM_153202.1	FLJ35308;FLJ36751;DJ964F7.1;DKFZp434K			
GI_24111254-S	102.8	119.2	94.9	CPA6	NM_020361.2	CPAH			
GI_24119161-S	327.3	345.5	198.8	TNFSF7	NM_001252.2	CD70;CD27L;CD27LG	receptor	integral to	signal
GI_24119162-S	111.8	120.5	116.3	TNFSF8	NM_001244.2	CD153;CD30L;CD30LG	receptor	integral to	induction
GI_24119163-S	458.6	512.3	398.3	TNFSF9	NM_003811.2	4-1BB-L	receptor	integral to	signal
GI_24119165-I	114.8	120	92.8	RBBP9	NM_006606.2	BOG;RBBP10;MGC9236		nucleus	oncogene
GI_24119167-A	498.2	579.1	407.8	RBBP9	NM_153328.1	BOG;RBBP10;MGC9236		nucleus	oncogene
GI_24119273-S	106.8	118.2	126.2	VGCNL1	NM_052867.1	bA430M15.1			
GI_24119276-I	99.9	100.8	86.4	MGC15875	NM_153373.1	MGC45484			
GI_24119284-S	97.9	90.3	95.9	MGC34007	NM_153205.1				
GI_24158475-S	118.3	121.5	108.2	KIAA1919	NM_153369.1	NaGLT1;MGC33953			
GI_24158495-S	155	115.7	121.4	GIOT-1	NM_153257.1	MGC33911	DNA	nucleus	regulation
GI_24211014-A	221.2	253.6	251.6	FLJ10661	NM_152563.1	MGC45068			
GI_24211016-A	79.6	84.1	80.4	HSFY	NM_152584.1	HSF2L	transcripti	nucleus	regulation
GI_24211016-I	79.2	89	83.4	HSFY	NM_152584.1	HSF2L	transcripti	nucleus	regulation
GI_24211028-S	674.8	689.8	781.5	ASPM	NM_018136.2	MCPH5;FLJ10517;FLJ10549			
GI_24233516-S	377.4	481.3	427.2	FLJ31051	NM_153687.1				
GI_24233529-S	896.7	1111.4	930	LOC91526	NM_153697.1				
GI_24233531-S	142	149.7	146	ZFP1	NM_153688.1	ZNF475;FLJ34243		nucleus	
GI_24233571-S	114.4	142	115.1	ZNF367	NM_153695.1	FLJ33970			
GI_24233573-S	123.7	145.8	139.8	DEFB125	NM_153325.1	DEFB-25			xenobiotic
GI_24234682-S	496.7	510.1	518	USP11	NM_004651.2	UHX1	ubiquitin-	nucleus	deubiquiti
GI_24234684-I	6078.4	8810.2	10602	HSPA8	NM_006597.3	LAP1;HSC54;HSC70;HSC71;HSP71;HSP73;	ATP	intracellula	protein
GI_24234685-A	5744.1	9691.8	12131	HSPA8	NM_153201.1	LAP1;HSC54;HSC70;HSC71;HSP71;HSP73;	ATP	intracellula	protein
GI_24234689-A	98.9	90.2	96.3	MRE11A	NM_005590.2	ATLD;HNGS1;MRE11;MRE11B	single-	nucleoplas	regulation
GI_24234689-I	108.1	105.5	113.4	MRE11A	NM_005590.2	ATLD;HNGS1;MRE11;MRE11B	single-	nucleoplas	regulation
GI_24234691-I	376.8	377.6	422	MRE11A	NM_005591.2	ATLD;HNGS1;MRE11;MRE11B	single-	nucleoplas	regulation
GI_24234693-A	174.6	214.7	191	KRT13	NM_002274.2	K13;CK13;MGC3781	structural	intermedia	epidermal
GI_24234701-S	170.8	174.5	170.8	PITX1	NM_002653.3	BFT;POTX;PTX1	transcripti	nucleus	skeletal
GI_24234707-I	84.8	96.4	81.3	PITX2	NM_153426.1	RS;RGS;ARP1;Brx1;IDG2;IGDS;IHG2;PTX2;	transcripti	nucleus	determinat
GI_24234710-A	170.9	181.1	178.9	PITX2	NM_153427.1	RS;RGS;ARP1;Brx1;IDG2;IGDS;IHG2;PTX2;	transcripti	nucleus	determinat
GI_24234713-S	161	177.4	168.5	PITX3	NM_005029.3	PTX3;MGC12766	transcripti	nucleus	histogene

GI_24234714-S	202.1	229.1	206.6	KLK4	NM_004917.2	ARM1;EMSP;PSTS;EMSP1;KLK-L1;PRSS17	serine-	extracellul	
GI_24234719-A	2471	2967.1	2676.9	DNAJB6	NM_005494.2	MRJ;HHDJ1;HSJ-2;MSJ-	heat	cellular_co	biological_
GI_24234719-I	5683.1	5823.1	6297.6	DNAJB6	NM_005494.2	MRJ;HHDJ1;HSJ-2;MSJ-	heat	cellular_co	biological_
GI_24234721-S	127.9	146.4	138.5	DNAJC3	NM_006260.2	P58;HP58;PRKRI;P58IPK;P58IPK HP58	protein	cytoplasm	regulation
GI_24234723-A	679.6	717.6	1213.4	TRADD	NM_003789.2	Hs.89862;MGC11078			induction
GI_24234723-I	124.2	172.3	173.4	TRADD	NM_003789.2	Hs.89862;MGC11078			induction
GI_24234725-I	94	102.4	81.9	TRADD	NM_153425.1	Hs.89862;MGC11078			induction
GI_24234731-A	106.2	108	102.4	SEMA6D	NM_024966.2	FLJ11598;KIAA1479			
GI_24234731-I	94.1	93.5	97.5	SEMA6D	NM_024966.2	FLJ11598;KIAA1479			
GI_24234740-I	86.9	90.2	76.3	SEMA6D	NM_153618.1	FLJ11598;KIAA1479			
GI_24234746-S	3342.2	4116	3858.2	ILF2	NM_004515.2	NF45;MGC8391	RNA	nucleus	immune
GI_24234749-I	904.7	966.3	836.2	ILF3	NM_012218.2	MMP4;MPP4;NF90;NFAR;TCP80;DRBP76;N	RNA	nucleus	
GI_24234752-I	534	656.4	668.7	ILF3	NM_004516.2	MMP4;MPP4;NF90;NFAR;TCP80;DRBP76;N	RNA	nucleus	
GI_24234755-A	603.3	720.9	669.5	ILF3	NM_153464.1	MMP4;MPP4;NF90;NFAR;TCP80;DRBP76;N	RNA	nucleus	
GI_24234758-S	122.9	125.6	121.6	CFC1	NM_032545.2	HTX2;CRYPTIC	molecular	cellular_co	determinat
GI_24234759-I	289.3	266.6	214.4	CSAGE	NM_153478.1	CSAG1			
GI_24234762-A	2620.3	2751.3	2293.4	CSAGE	NM_153479.1	CSAG1			
GI_24307870-S	2238	2165	3071.4	MGC31963	NM_144580.1				
GI_24307874-S	252.8	317.1	285.9	ZNF11B	NM_006955.1	KOX2			
GI_24307876-S	205.7	225.8	261.6	POR	NM_000941.1	CYPOR	NADPH-	membran	electron
GI_24307878-S	1290.2	1412.1	1260.7	DNCI2	NM_001378.1	IC2	microtubul	cytoplasm	microtubul
GI_24307882-S	587.5	491.7	393.6	ETV4	NM_001986.1	E1A-F;PEAS3	RNA	nucleus	viral
GI_24307886-S	102.7	109.7	120.9	ONECUT1	NM_004498.1	HNF6;HNF-6;HNF6A	transcripti	nucleus	regulation
GI_24307888-S	1104.2	1241.6	1017.5	USP10	NM_005153.1	UBPO;KIAA0190	peptidase		deubiquiti
GI_24307898-S	376.6	411.3	403.6	ERAL1	NM_005702.1	ERA;ERAL1A;HERA-A;HERA-B			
GI_24307902-S	135.5	144.8	219.5	CORO2B	NM_006091.1	CLIPINC;KIAA0925	membran	kinesin	actin
GI_24307904-S	88.4	139.2	137.5	SPON1	NM_006108.1	KIAA0762;MGC10724;f-spondin		extracellul	
GI_24307908-S	184.8	216.8	225.3	RALGDS	NM_006266.1	RGF;RalGEF	Ral guanyl-		RAS
GI_24307912-S	215.2	247	214.6	ZNF234	NM_006630.1	HZF4;ZNF269	DNA	nucleus	developm
GI_24307916-S	1056.2	1240.6	1221.7	HELIC1	NM_006828.1	RNAH;ASC1p200;dJ121G13.4	nucleic	nucleus	
GI_24307918-S	1091.4	1047	1162.1	RY1	NM_006857.1		DNA	cellular_co	biological_
GI_24307920-S	144.2	155.1	182.8	ATE1	NM_007041.1		acyltransf	cytoplasm	protein
GI_24307922-S	546.5	638.9	449.7	RPE	NM_006916.1	MGC2636	ribulose-		carbohydr
GI_24307924-S	292	380	322.1	ZNF32	NM_006973.1	KOX30			
GI_24307928-S	372.7	320.8	377.6	OIP5	NM_007280.1		protein	cellular_co	cell
GI_24307932-S	181.1	238.9	217.6	TFEB	NM_007162.1	TCFEB	transcripti	transcripti	humoral
GI_24307934-S	252.6	303.9	248.2	ZNF184	NM_007149.1		zinc ion	nucleus	regulation
GI_24307936-S	381.7	354.3	311.8	ZNF79	NM_007135.1	pT7	DNA	nucleus	regulation
GI_24307942-S	3684.5	3928.6	3765.3	SCAP	NM_012235.1	KIAA0199	chaperone	Golgi	cholestero
GI_24307946-S	345.3	284.8	338.2	HABP4	NM_014282.1	IHABP4;Ki-1/57	DNA	nucleus	regulation
GI_24307948-S	331.9	380.2	385.4	NCDN	NM_014284.1	KIAA0607			
GI_24307950-S	430.2	438.7	420.1	PCTAIRE2BF	NM_014290.1		nucleic		
GI_24307952-S	3096.4	2863.3	2730.5	NIFU	NM_014301.1				
GI_24307954-S	511.6	487.8	384.2	CYFIP2	NM_014376.1	PIR121;PRO1331			

GI_24307956-S	292.1	358.7	325.3	PIB5PA	NM_014422.1	PIPP;INPP5	inositol/ph		
GI_24307958-S	118.5	123.5	129.2	PIPPIN	NM_014460.1	dJ347H13.2			
GI_24307960-S	1590.5	1412.5	1763.6	KIAA0406	NM_014657.1				
GI_24307962-S	249.6	305.8	192.6	ZDHHC1	NM_013304.1	ZNF377;C16orf1;HSU90653	DNA	integral to	regulation
GI_24307966-S	168.9	294.8	202.4	SRGAP2	NM_014850.1	WRP;MEGAP;SRGAP3;ARHGAP14;KIAA04			
GI_24307968-S	2542.6	2728.8	1820.6	CYFIP1	NM_014608.1	SHYC;KIAA0068;P140SRA-1			
GI_24307970-S	254.6	293.1	211.9	STK38L	NM_015000.1	KIAA0965	protein-		protein
GI_24307972-S	1643.2	1590.2	1606.9	ch-TOG	NM_014756.1	KIAA0097	molecular	cellular_co	biological_
GI_24307976-S	103.2	105.2	92.4	RIMS1	NM_014989.1	RIM;RIM1;RAB3IP2;KIAA0340	protein		vision
GI_24307982-S	786.7	781.2	828.3	KIAA0082	NM_015050.1		nucleic	intracellula	
GI_24307986-S	158.2	174.5	167.8	JMJD2C	NM_015061.1	GASC1;KIAA0780			
GI_24307990-S	347.7	358.2	277.5	PARC	NM_015089.1	H7AP1;KIAA0708	ligase		electron
GI_24307992-S	99.8	89.8	86.9	NEDL1	NM_015052.1	KIAA0322	ubiquitin-	intracellula	protein
GI_24307994-S	195	221.3	203.2	SRISNF2L	NM_015106.1	KIAA0809	ATP		
GI_24308002-S	101.6	106.6	86.4	C21orf106	NM_015151.1	DIP2;KIAA0184			
GI_24308006-S	2161.2	2385.6	2658	ARL6IP	NM_015161.1	AIP1;ARMER;ARL6IP1;KIAA0069		integral to	
GI_24308008-S	1311.1	1164.5	939.8	METAP1	NM_015143.1	KIAA0094	methionyl		proteolysis
GI_24308012-S	1262.3	1413.1	1227.4	PMPCA	NM_015160.1	KIAA0123;Alpha-MPP	protein	mitochond	proteolysis
GI_24308016-S	898	942.1	868	TBC1D1	NM_015173.1	TBC;TBC1;KIAA1108			
GI_24308026-S	120.7	128.4	115.4	KIAA1043	NM_015281.1				
GI_24308028-S	867	550.8	415.7	DOCK9	NM_015296.1	ZIZ1;KIAA1058;zizimin1	guanyl-	kinesin	biological_
GI_24308032-S	1120.1	1189.1	1167.7	FNBP4	NM_015308.1	FBP30;KIAA1014			
GI_24308034-S	1691.7	1712.9	1765.9	EXOC7	NM_015219.1	EXO70;Exo70p;YJL085W;KIAA1067			
GI_24308040-S	408.3	310.4	369.1	EST1B	NM_015327.1	SMG-5;KIAA1089			
GI_24308042-S	195.8	217.3	192.1	KIAA0828	NM_015328.1		adenosylh		one-
GI_24308048-S	466.8	391.8	377.3	KIAA0073	NM_015342.1		cyclophilin		protein
GI_24308052-S	1030.5	1091.2	951.6	SUMF2	NM_015411.1	DKFZp66I1024	molecular	endoplas	
GI_24308054-S	1262.9	1304.4	1114.8	DKFZP434F2	NM_015412.1				
GI_24308056-S	117	134.5	133.4	DKFZP586H2	NM_015430.1		trypsin		proteolysis
GI_24308058-S	1412.5	988.1	776.3	DKFZP586D0	NM_015433.1				
GI_24308060-S	288.1	240.1	193.8	ZNF363	NM_015436.1	ARNIP;CHIMP;PIRH2;hARNIP;PRO1996;DK			
GI_24308064-S	177.7	205.1	184.6	LOC126147	NM_145807.1		structural		
GI_24308068-S	801.7	685.9	967.1	EHZF	NM_015461.1	DKFZp564D0764	electron		electron
GI_24308070-S	375.1	275.9	179.7	DKFZP566K1	NM_015463.1				
GI_24308072-S	2245.9	1771.1	1864.1	PTPN23	NM_015466.1	HDPTP;HD-PTP;KIAA1471;DKFZP564F0923	protein		signal
GI_24308074-S	474	474.4	469.4	GAF1	NM_015470.1	pp75;RIP11;KIAA0857;DKFZP434H018			
GI_24308076-S	664.9	1028.7	874.1	C18orf10	NM_015476.1	HsT3006;DKFZP586M1523			
GI_24308078-S	422.3	513.9	477	ZNF385	NM_015481.1	HZF;ZFP385;DKFZP586G1122			
GI_24308080-S	352.2	428.4	331.1	SH2B	NM_015503.1	SH2-B;DKFZP547G1110	JAK		
GI_24308084-S	125.5	345.4	326	MOXD1	NM_015529.1	MOX;dJ248E1.1;DKFZP564G202	copper ion		catechola
GI_24308086-S	797.2	953.3	199	LRIG1	NM_015541.1	LIG1;LIG-1;DKFZP586O1624			
GI_24308088-S	128	121.2	114.5	CHD5	NM_015557.1	KIAA0444;DKFZp434N231			
GI_24308092-S	2184	1929.3	1654.9	C19orf13	NM_015578.1	DKFZP434D1335	DNA	nucleus	regulation
GI_24308106-S	1091.3	1146.2	848.3	DKFZp566C0	NM_015609.1				

GI_24308108-S	400.8	465.8	387.4	DKFZP564D1	NM_015631.1				
GI_24308110-S	203.5	202.3	188.2	DKFZp564O1	NM_015633.1	HSPC123-like			
GI_24308112-S	549.6	649.4	751	KIAA1279	NM_015634.1	DKFZP586B0923			
GI_24308114-S	139.1	168.8	163.6	IRF2BP1	NM_015649.1	DKFZP434M154			
GI_24308118-S	110.2	120.9	89.2	DKFZP434I0	NM_015668.1				
GI_24308126-S	1926.4	2166.7	1980.1	ERdj5	NM_018981.1	JPDI;DKFZp434J1813			
GI_24308130-S	627.1	755.1	523.1	KIAA1128	NM_018999.1		exo-alpha-	membran	carbohydr
GI_24308132-S	3002.6	3767.7	3233	LOC54499	NM_019026.1				
GI_24308140-S	114.2	128.9	111.3	SGTB	NM_019072.1	SGT2			
GI_24308146-S	228.5	165.9	117.1	IL17RD	NM_017563.1	SEF;IL-			
GI_24308152-S	160.5	159	146.6	FLJ20400	NM_017804.1				
GI_24308154-S	1474.3	1607.1	775.7	UACA	NM_018003.1	FLJ10128;KIAA1561	molecular	extracellul	biological_
GI_24308156-S	268.9	393.5	193.5	GBP3	NM_018284.1	FLJ10961			
GI_24308160-S	261.8	210.8	234.1	SLC22A15	NM_018420.1	FLIPT1;DKFZp761G0313	transporte	integral to	transport
GI_24308162-S	1029.5	1098.6	1230.9	FEM1A	NM_018708.1	DKFZp762M136			
GI_24308164-S	535	433.1	495.8	DKFZp762O	NM_018710.1				
GI_24308166-S	105	115.7	89.6	DKFZp761H0	NM_018711.1		ion	integral to	ion
GI_24308168-S	108.9	114.7	101.7	DNAH3	NM_017539.1	DLP3;DNAHC3B;Hsadhc3;DKFZp434N074	nucleotide	dynein	microtubul
GI_24308174-S	2052.4	1745	1737.8	FLJ20719	NM_017940.1	KIAA1693			
GI_24308176-S	635.4	722.1	650.2	FLJ10006	NM_017969.1				
GI_24308178-S	350.2	472.2	341.6	DKFZp547A0	NM_018704.1				
GI_24308180-S	1333.4	1438.9	1540.9	KIAA1354	NM_018847.1	FLJ13568	protein		
GI_24308184-S	846.6	925.3	906.2	LOC56926	NM_020170.1		peptidase		proteolysis
GI_24308186-S	434.6	323.9	360.2	LOC56931	NM_020175.1				
GI_24308188-S	92.2	100.1	89.1	RGMA	NM_020211.1	RGM			
GI_24308194-S	950.9	1122.6	1153.9	VARS2L	NM_020442.1				
GI_24308198-S	117.8	111.4	116.8	KIAA1181	NM_020462.1				
GI_24308206-S	5199	5173.5	4827.3	KIAA1185	NM_020710.1				
GI_24308210-S	147.9	157.3	162	KIAA1287	NM_020748.1				
GI_24308214-S	255.3	288.8	260.7	KIAA1318	NM_020769.1				
GI_24308216-S	362.4	406.4	368	MIDORI	NM_020778.1	KIAA1330	ATP		protein
GI_24308222-S	174.8	187.6	189.5	KIAA1407	NM_020817.1				
GI_24308226-S	216.1	237.9	247.4	KIAA1441	NM_020832.1				
GI_24308228-S	121.7	124.6	119.3	PACSIN1	NM_020804.1	KIAA1379	protein	kinesin	endocytosi
GI_24308230-S	502.5	534.8	637.8	ZNF537	NM_020856.1	KIAA1474	transcripti	nucleus	regulation
GI_24308232-S	110	151.9	115.4	SYT13	NM_020826.1	KIAA1427	transporte	membran	transport
GI_24308234-S	112.5	121.5	109.3	DPP10	NM_020868.1	DPRP3;KIAA1492	dipeptidyl-	membran	proteolysis
GI_24308236-S	310.3	385.3	346.7	PITPNM2	NM_020845.1	NIR3;RDGB2;RDGBA2;KIAA1457			
GI_24308238-S	347.3	337	359.1	KIAA1524	NM_020890.1				
GI_24308240-S	180.4	146.4	147.4	ZBTB2	NM_020861.1	ZNF437;KIAA1483;bA351K16.2	protein	nucleus	regulation
GI_24308244-S	1053.9	549	829.4	MGC24665	NM_152308.1				
GI_24308252-S	1861.7	1215.9	1071	DTX2	NM_020892.1	RNF58;KIAA1528	sugar	nucleus	
GI_24308254-S	555.9	427.3	353.9	ZNF529	NM_020951.1	KIAA1615		nucleus	
GI_24308256-S	568.4	499.3	383.3	KIAA1576	NM_020927.1		alcohol		

GI_24308260-S	683.9	621.6	505.8	MI-ER1	NM_020948.1	ER1;KIAA1610			
GI_24308262-S	343	439.4	310.2	HTCD37	NM_021222.1				
GI_24308268-S	2987.9	3549	3042	C9orf80	NM_021218.1	HSPC043			
GI_24308276-S	101.4	114.8	111.2	SMOC2	NM_022138.1	SMAP2	calcium	extracellul	
GI_24308286-S	8154.1	6139.9	8117.7	C9orf88	NM_022833.1	FLJ13518;FLJ22151;FLJ22298;bA356B19.6;			
GI_24308288-S	257.4	280.5	273.8	LENG1	NM_024316.1		DNA	nucleus	regulation
GI_24308296-S	165.8	180.6	182.6	ZNF306	NM_024493.1	ZF47;Zfp47	transcripti	nucleus	regulation
GI_24308298-S	145.5	213.8	193.5	ZNF436	NM_030634.1	KIAA1710	DNA	nucleus	regulation
GI_24308300-S	149.5	190.6	152	KIAA1706	NM_030636.1		DNA	intracellula	
GI_24308302-S	488.2	737.3	706.5	KIAA1720	NM_030645.1				
GI_24308304-S	278.6	309.1	479.2	C20orf129	NM_030919.1	dJ616B8.3			
GI_24308313-S	94.4	105	103	SLC4A9	NM_031467.1	AE4	inorganic	membran	anion
GI_24308321-S	1628.2	1282.8	1131.2	ZCCHC7	NM_032226.1	FLJ22611	nucleic		
GI_24308325-S	141.3	160.6	129.2	KIAA1811	NM_032430.1		cAMP-		protein
GI_24308329-S	126.7	127.2	119	KIAA1804	NM_032435.1	MLK4	protein-		protein
GI_24308331-S	391	348.5	350.8	BTBD12	NM_032444.1	KIAA1784	protein		
GI_24308333-S	1227	1838.6	1482.3	KIAA1838	NM_032448.1				carbohydr
GI_24308335-S	303.8	318.8	319.3	C6orf168	NM_032511.1	MGC2817;dJ273F20			
GI_24308337-S	183.8	402	202.4	KIAA1914	NM_032550.1	FLJ14564			
GI_24308341-S	123.7	139.2	122.3	DMRTC2	NM_033052.1		transcripti	nucleus	sex
GI_24308345-S	139.8	136.4	146	LOC85865	NM_033107.1				
GI_24308349-S	2263.1	2771.9	2860	C6orf153	NM_033112.1	dJ20C7.4			
GI_24308351-S	236.2	271.8	262.5	DMRTB1	NM_033067.1		transcripti	nucleus	sex
GI_24308353-S	328.5	382.9	364.4	BC008967	NM_033201.1				
GI_24308355-S	3373.6	3145.2	3330.9	BC002942	NM_033200.1				
GI_24308357-S	96.4	102.6	101.4	NT5C1B	NM_033253.1	AIRP;CN-IB			
GI_24308361-S	126.1	137	133.2	MGC12518	NM_033548.1		nucleic	intracellula	regulation
GI_24308363-S	969.5	1117.8	1559.8	LOC90522	NM_033557.1				
GI_24308367-S	221	198.5	234.3	FLJ38944	NM_152361.1				
GI_24308369-S	266.8	292.9	293.9	FLJ31265	NM_152395.1				
GI_24308371-S	427.2	459.2	440	MGC20398	NM_052857.1				
GI_24308375-S	768.3	665.1	833.5	STK11IP	NM_052902.1	LIP1;LKB1IP;KIAA1898;STK11IP1			
GI_24308377-S	139.8	162.3	185.8	TUBGCP5	NM_052903.1	GCP5;KIAA1899	microtubul	gamma-	microtubul
GI_24308379-S	92.1	84.7	85.8	KIAA1900	NM_052904.1		protein		
GI_24308381-S	750.8	957.9	843	LENG8	NM_052925.1	pp13842;KIAA1932;MGC40108			
GI_24308383-S	92.9	92	85.5	PNMA5	NM_052926.1	KIAA1934			
GI_24308385-S	279.3	319.6	317	LOC115294	NM_052937.1				
GI_24308387-S	818.1	757.9	982.5	DT1P1A10	NM_058163.1	MGC20451			
GI_24308389-S	2972.6	1897.3	1603.7	C1orf19	NM_052965.1				
GI_24308393-S	191	230.6	202.8	C20orf151	NM_080833.1	dJ908M14.3	DNA	nucleus	regulation
GI_24308395-S	171.9	163.9	206.7	LOC90379	NM_138353.1				
GI_24308397-S	350.7	320.6	346.8	LOC89894	NM_138341.1				
GI_24308399-S	434	479.2	403.7	C10orf42	NM_138357.1	FLJ46135			
GI_24308405-S	2638.9	3426.3	2965.2	Ses2	NM_138355.1				

GI_24308407-S	361.8	399.1	226.2	CABLES1	NM_138375.1	HsT2563			cell cycle
GI_24308411-S	174.6	293.1	140	EAT2	NM_053282.1		molecular	cellular_co	biological_
GI_24308417-S	128.7	135	118.9	MGC20785	NM_152721.1		insulin		
GI_24308421-S	177.6	222	201.6	MGC35450	NM_153708.1			integral to	
GI_24308423-S	123.7	147.7	143.1	MGC40168	NM_153709.1				
GI_24308425-S	102.6	120.1	108.3	Sprn	NM_138384.1				
GI_24308431-S	664.1	785.4	790.3	TTC5	NM_138376.1				
GI_24308433-S	3179.8	3886	3934.5	G6PC3	NM_138387.1	UGRP			
GI_24308439-S	7739.4	7558.2	5922	LOC93343	NM_138401.1				
GI_24308441-S	135.3	208.5	238	C6orf117	NM_138409.1				
GI_24308443-S	316.7	320.6	286.5	LOC116143	NM_138458.1				
GI_24308447-S	188.8	168.7	192.2	LOC151648	NM_138484.1				
GI_24308449-S	1366.7	1589.8	1628.6	LOC152217	NM_138487.1				
GI_24308451-S	2752.3	2340.2	2000.6	LOC92715	NM_138778.1				
GI_24308453-S	110.9	184.4	162.7	C6orf188	NM_153711.1	MGC45451;dJ493F7.3			
GI_24308455-S	301.7	429	335.3	MGC10084	NM_153702.1				
GI_24308457-S	433	448	418.5	MGC46719	NM_153713.1				
GI_24308459-S	127.1	124.7	121.6	C10orf67	NM_153714.1	MGC46732			
GI_24308463-S	104	124.2	102.8	MGC35182	NM_153707.1				
GI_24308513-S	118.6	128.3	101.9	GSTA5	NM_153699.1				
GI_24308523-S	4496.9	4721.5	5207.6	TMEM9	NM_016456.2		molecular	lysosome	transport
GI_24371247-S	633.1	826.1	741.9	HCBP6	NM_023934.2	DC44;MGC2495			
GI_24371249-S	203.7	230.1	205.2	C21orf81	NM_153750.1				
GI_24371253-S	92.9	106.4	121.3	C21orf84	NM_153752.1				
GI_24371255-S	90.2	101.5	87.8	C21orf88	NM_153754.1				
GI_24371257-S	103.9	113	109	C21orf82	NM_153751.1				
GI_24371259-S	108.7	119.7	107.4	FNDC5	NM_153756.1	FRCP2			
GI_24371261-S	173.1	204.9	181.3	MCM3APAS	NM_153753.1	C21orf85;FLJ10508		integral to	
GI_24371263-S	93.5	93.8	84.2	C21orf89	NM_153755.1				
GI_24371267-S	215.7	487.7	495.2	NAP1L5	NM_153757.1	DRLM	DNA	nucleus	nucleoso
GI_24371271-A	619.7	261.8	518.5	ZDHHC14	NM_153746.1	NEW1CP;FLJ20984	zinc ion	integral to	regulation
GI_24415382-S	784.4	475.5	529.7	PELP1	NM_014389.1	MNAR;P160			
GI_24415399-S	134	147.7	137.4	MYO1C	NM_033375.1	myr2;MYO1E	myosin	unconvent	perception
GI_24415403-S	172.7	190.1	177	MDN1	NM_014611.1	KIAA0301	nucleotide	nucleus	protein
GI_24415991-S	110.3	109	97.4	C21orf99	NM_153773.1				
GI_24415993-S	1194.9	993.9	866.3	SFRS7	NM_006276.3	9G8;HSSG1	pre-mRNA	nucleus	mRNA
GI_24416001-S	1710.8	1596.7	1475	RBAF600	NM_020765.1	KIAA0462;KIAA1307			
GI_24429563-I	97.6	118.6	88.8	PDE7A	NM_002604.1	HCP1	cAMP-		
GI_24429565-A	92.6	106.1	97.9	PDE7A	NM_002603.1	HCP1	cAMP-		
GI_24429565-I	109.2	121.5	102.7	PDE7A	NM_002603.1	HCP1	cAMP-		
GI_24429571-S	218.1	234	206.7	TAF1L	NM_153809.1	TAF2A2			
GI_24429573-S	913.8	749.3	563.5	SLC38A6	NM_153811.1	NAT-1	transcripti	membran	regulation
GI_24429581-S	580.3	490.1	548.1	ZFPM1	NM_153813.1	FOG;FOG1;ZNF408			
GI_24429585-S	108.1	101.3	102.6	FCGR3A	NM_000569.4	CD16;FCG3;FCGR3;IGFR3	receptor	integral to	immune

GI_24429591-S	397.6	584.9	639.1	GALNACT-2	NM_018590.3	PRO0082;MGC40204;CSGalNAcT-2	transferas		
GI_24430130-S	3310	4899	4466.7	WBP1	NM_012477.2	WBP-1;MGC15305	receptor		
GI_24430131-S	360.8	468.8	658.9	WBP2	NM_012478.2	WBP-2;MGC18269	protein		signal
GI_24430133-I	99.4	103.8	101.9	DPM3	NM_018973.3	MGC34275		endoplas	carbohydr
GI_24430136-S	1847.8	1828.5	1896.6	DXS9879E	NM_006014.2	CVG5;ESO3;ITBA2;DXS9951E	molecular	cellular_co	biological_
GI_24430138-S	355.3	418.3	410	RPAP1	NM_015540.2	MGC858;FLJ12732;KIAA1403;DKFZP727M1			
GI_24430140-S	910.8	1545.1	1284.6	FBN1	NM_000138.2	FBN;SGS;MASS;MFS1;OCTD	extracellul	extracellul	vision
GI_24430142-S	98.7	95.1	91.5	GFAP	NM_002055.2		structural	intermedia	
GI_24430143-S	165.4	182.2	164.6	GSTA3	NM_000847.3	GTA3;GSTA3-3;MGC22232	glutathion		response
GI_24430145-S	701.5	606.1	504.1	NUP153	NM_005124.2	N153;HNUP153	transporte	nuclear	nucleocyto
GI_24430147-A	985.6	852.6	788.9	NUP155	NM_004298.2	N155;KIAA0791	transporte	nuclear	nucleocyto
GI_24430147-I	113	141.2	124.2	NUP155	NM_004298.2	N155;KIAA0791	transporte	nuclear	nucleocyto
GI_24430148-I	99.1	112.8	92	NUP155	NM_153485.1	N155;KIAA0791	transporte	nuclear	nucleocyto
GI_24430150-S	10021.5	10593	9480.9	PSMC1	NM_002802.2	S4;p56;P26S4;MGC8541;MGC24583	proteasom	26S	protein
GI_24430152-S	2581.9	3002.2	2549.4	PSMC2	NM_002803.2	S7;MSS1;MGC3004	adenosine	26S	virulence
GI_24430153-S	2762.1	2907.3	3062.2	PSMC3	NM_002804.3	TBP1;MGC8487	transcripti	26S	protein
GI_24430154-A	5057.3	5717.2	5256.6	PSMC4	NM_153001.1	S6;TBP7;MIP224;MGC8570;MGC13687;MG	proteasom	26S	proteolysis
GI_24430156-I	1228.9	1330.8	1313.2	PSMC4	NM_006503.2	S6;TBP7;MIP224;MGC8570;MGC13687;MG	proteasom	26S	proteolysis
GI_24430159-S	2338	2693.9	2376.9	PSMC6	NM_002806.2	P42;P44;SUG2;CADP44;MGC12520	proteasom	26S	protein
GI_24430161-I	108.1	132.1	99.3	PMP22	NM_000304.2	DSS;HNPP;CMT1A;CMT1E;GAS-		membran	negative
GI_24430162-I	127.1	162.8	209.6	PMP22	NM_153321.1	DSS;HNPP;CMT1A;CMT1E;GAS-		membran	negative
GI_24430164-A	627.1	1347.9	1851.1	PMP22	NM_153322.1	DSS;HNPP;CMT1A;CMT1E;GAS-		membran	negative
GI_24430166-I	88.6	93.5	89.4	PANK2	NM_024960.3	HSS;HARP;PKAN;NBIA1;C20orf48;FLJ11729			
GI_24430168-A	913.6	794.6	467.4	PANK2	NM_153637.1	HSS;HARP;PKAN;NBIA1;C20orf48;FLJ11729			
GI_24430178-S	181.1	240.3	208.7	PANK3	NM_024594.2	FLJ12899;MGC16863	ATP		coenzyme
GI_24430179-S	104.9	120.3	113.4	ODF1	NM_024410.2	ODF;RT7;ODF2;ODFP;SODF;ODF27;ODFP	structural	outer	spermatog
GI_24430180-I	554.5	756.4	693.6	ODF2	NM_002540.3	ODF84;ODF2/1;ODF2/2;MGC9034	structural		cell shape
GI_24430182-A	636.7	645.2	605.3	ODF2	NM_153437.1	ODF84;ODF2/1;ODF2/2;MGC9034	structural		cell shape
GI_24430182-I	174.1	178.9	190.5	ODF2	NM_153437.1	ODF84;ODF2/1;ODF2/2;MGC9034	structural		cell shape
GI_24430185-S	1874.6	1645.8	1999.9	PIGC	NM_153747.1	GPI2;MGC2049	catalytic	endoplas	GPI
GI_24430187-S	727.7	632.9	584.2	PIGH	NM_004569.2	GPI-H	catalytic	endoplas	GPI
GI_24430188-S	148.1	150.5	128.7	PIGL	NM_004278.2		hydrolase	endoplas	GPI
GI_24430189-S	1013	979.9	1204.7	KRT15	NM_002275.2	K15;CK15;K1CO	structural	intermedia	epidermal
GI_24430191-S	125.2	112.6	122.5	KRT16	NM_005557.2	K16;CK16;K1CP;NEPPK;KRT16A	structural	intermedia	epidermal
GI_24430193-I	110.7	121.1	108.8	IL17RC	NM_032732.2	IL17-RL;MGC10763			
GI_24430196-I	134.2	158.5	132	IL17RC	NM_153461.1	IL17-RL;MGC10763			
GI_24430200-A	331.8	346.9	270.4	IL17RC	NM_153463.1	IL17-RL;MGC10763			
GI_24430200-I	205.4	241.3	204.1	IL17RC	NM_153463.1	IL17-RL;MGC10763			
GI_24430205-A	123	115	110.8	IL17RE	NM_153481.1	FLJ23658			
GI_24430207-I	110.2	112.3	103.6	IL17RE	NM_153482.1	FLJ23658			
GI_24430209-I	212.4	241.5	223.8	IL17RE	NM_153483.1	FLJ23658			
GI_24430211-S	107.3	134.7	110.2	IL23R	NM_144701.2		receptor		
GI_24430213-S	275.9	317.6	279.3	IL10RA	NM_001558.2	IL10R;CDW210A;HIL-10R;IL-10R1	interleukin-	integral to	
GI_24430214-S	1378.8	1627.8	1592.3	IL10RB	NM_000628.3	CRFB4;CRF2-4;CDW210B;IL-10R2	interleukin-	integral to	signal

GI_24430216-S	221.7	264.1	236.9	IL10	NM_000572.2	CSIF;TGIF;IL-10;IL10A	cytokine	soluble	positive
GI_24430217-S	2057.9	3444.7	3585.4	IL11	NM_000641.2	AGIF;IL-11	cytokine	extracellul	positive
GI_24430218-S	283.4	270.4	165.2	IL12A	NM_000882.2	CLMF;NFSK;NKSF1;IL-12A	interleukin-	extracellul	immune
GI_24430220-I	734.7	676	914.1	IL1RAP	NM_002182.2	IL1R3;IL-1RACP	signal	integral to	immune
GI_24430221-A	185.2	216.5	248.6	IL1RAP	NM_134470.2	IL1R3;IL-1RACP	signal	integral to	immune
GI_24430221-I	112.8	111.8	105.4	IL1RAP	NM_134470.2	IL1R3;IL-1RACP	signal	integral to	immune
GI_24431938-S	316.7	570.8	181.5	FLJ13236	NM_024902.2				
GI_24431940-S	84.6	110.2	76.6	FCGR1A	NM_000566.2	CD64;FCRI;IGFR1	receptor	integral to	phagocyto
GI_24431942-S	147.2	188.1	170.9	PDE1B	NM_000924.2	PDE1B1;PDES1B	calmoduli		apoptosis
GI_24431943-S	416.6	393.9	499.7	GLRB	NM_000824.2		glycine-	integral to	small
GI_24431944-S	125	139.1	124.1	SOAT1	NM_003101.2	ACAT;SOAT;STAT;ACACT;ACAT1	acyltransf	membran	cholestero
GI_24431948-S	87.1	90	104	CDX2	NM_001265.2	CDX3;CDX-3	transcripti	nucleus	histogene
GI_24431954-S	469.4	379.7	418.7	ZNF267	NM_003414.3	HZF2	DNA	nucleus	developm
GI_24431956-S	1072.8	965.6	904.4	C10orf69	NM_006459.2	KE04;KEO4			
GI_24431959-S	263.6	388.6	292.1	DNAJB4	NM_007034.3	HLJ1;DNAJW	chaperone		response
GI_24431962-S	132.6	151.6	138.2	CD5	NM_014207.2	T1;LEU1	scavenger	integral to	cell
GI_24431963-S	117.5	132.7	103.7	HBS1L	NM_006620.2	ERFS;HBS1;EF-	GTP		protein
GI_24431967-S	287.5	357.2	308.8	ARC	NM_015193.2	KIAA0278			
GI_24431968-S	215.8	237.1	238.7	PTD004	NM_013341.2		GTP		
GI_24431972-S	2529.1	2224.8	2359.8	FLJ20241	NM_017721.2				
GI_24431974-S	155.6	167.9	144.2	C10orf12	NM_015652.2	FLJ13022;DKFZP564P1916			
GI_24431976-S	2015.6	1732.3	2508.3	FLJ10307	NM_018053.2				
GI_24431981-S	792.7	653.3	581.2	USP47	NM_017944.2	FLJ20727			
GI_24431984-S	105	134.8	111.9	PIWIL2	NM_018068.2	HILI;mili;PIWIL1L;FLJ10351			
GI_24431986-S	136	142.3	118.6	C6orf35	NM_018452.2	BM033			
GI_24431990-S	248.7	424.4	680.7	C6orf85	NM_021945.2	FLJ22174			
GI_24431993-S	625.3	803.7	919.1	MGC3234	NM_023947.2				
GI_24431995-S	297	324.1	321.1	SH3GLB2	NM_020145.2	KIAA1848			
GI_24431998-S	292.9	254.9	285	DCLRE1B	NM_022836.2	SNM1B;FLJ12810;FLJ13998			
GI_24432005-S	884.9	700.7	679.2	FLJ22341	NM_024599.2				
GI_24432008-S	490.6	459	278.2	FLJ21308	NM_024615.2				
GI_24432010-S	246.4	286.1	130.7	PAQR6	NM_024897.2	FLJ22672			
GI_24432015-S	582.7	742.3	637.8	FLJ12529	NM_024811.2	MGC9315;FLJ39024	nucleic		
GI_24432019-S	254.9	275.1	268	FRMD1	NM_024919.2	FLJ00181;FLJ22615;FLJ40260;bA164L23.1;			
GI_24432021-S	83	100.2	100.8	NYD-TSP1	NM_032567.2				
GI_24432025-S	614.5	597.1	432.8	FLJ14360	NM_032775.2		protein		
GI_24432029-S	118.5	118.2	87	BRUNOL6	NM_052840.2		nucleic		
GI_24432033-S	147	157.6	155	NR5A1	NM_004959.3	ELP;SF1;FTZ1;SF-1;AD4BP;FTZF1	ligand-	nucleus	primary
GI_24432034-S	106.4	118.7	110.1	NYD-SP25	NM_033516.2				
GI_24432036-S	265.4	260.7	265.2	LOC83693	NM_031463.3		cysteine-		proteolysis
GI_24432038-S	895.9	656.2	667.6	ODAG	NM_021167.2	FLJ22489;RG083M05.2			
GI_24432041-S	1798.8	1280	1391	CHRAC1	NM_017444.3	YCL1;CHARC1;CHARC15;CHRAC15	epsilon	kinesin	chromatin
GI_24432048-S	99.8	108.9	95	HCA3	NM_138703.2				
GI_24432049-S	366.4	443.9	380.3	RYBP	NM_012234.3	YEAF1	transcripti	nucleus	developm

GI_24432051-S	2144.7	1290.4	821.6	FLJ25348	NM_144569.2				
GI_24432055-S	284.6	329.6	308.3	FLJ32356	NM_144671.2				
GI_24432057-S	165.2	421.3	196.9	C9orf3	NM_032823.3	C90RF3;FLJ14675			
GI_24432059-S	112.6	98.6	101.5	MGC26733	NM_144992.2				
GI_24432063-S	354.6	399.9	381.9	C10orf63	NM_145010.2	MGC26778			
GI_24432064-S	140.9	153.7	134.7	FLJ25124	NM_144698.2				
GI_24432066-S	124	114	93.8	C10orf4	NM_145246.2	FRA10AC1;F26C11.1-like			
GI_24432071-S	100.5	93.7	87.8	FBXL13	NM_145032.2	MGC21636			
GI_24432073-S	700.1	774.6	764.8	MGC33338	NM_152366.2				
GI_24432075-S	102	103.5	100.7	LOC136263	NM_145268.2				
GI_24432076-S	433.9	325.8	324.9	FLJ33516	NM_152423.2				
GI_24432082-S	109.1	109.5	109.5	FLJ34658	NM_152404.2		transferas		metabolis
GI_24432084-S	132.6	142.2	141.8	MGC39715	NM_152628.2				intracellula
GI_24432088-S	111.6	113.6	108.8	GPR66	NM_006056.2	GPC-R;NMU1R;(FM-3)	neuropepti	integral to	G-protein
GI_24432092-S	676.4	759.1	893.2	PHF13	NM_153812.1	MGC43399	DNA		regulation
GI_24432094-S	209.3	198.4	202.9	FLJ23614	NM_152695.2				
GI_24432099-I	142.3	161.1	132.9	GSG1	NM_153823.1	MGC3146			
GI_24432101-I	127.1	119.6	86.1	HS6ST2	NM_147175.2				
GI_24432103-I	139.5	142.3	117.5	SLA/LP	NM_153825.1		tRNA		
GI_24462252-S	503	607.3	457.1	ZNF25	NM_145011.2	KOX19;FLJ31890	DNA	nucleus	regulation
GI_24469782-S	1377.7	1406.1	2436	AGTRAP	NM_020350.3	ATRAP			
GI_24475585-S	1336	2446.8	2340.5	UCC1	NM_017549.1	MERP1	calcium	extracellul	cell-matrix
GI_24475588-S	317.3	244.2	225.3	BBC3	NM_014417.2	JFY1;PUMA;PUMA/JFY1			
GI_24475617-S	233.3	255.6	221.9	NUMBL	NM_004756.2	NBL;CAG3A;CTG3a;NUMBR;NUMB-			neurogene
GI_24475618-S	372.1	351.4	171.2	CD83	NM_004233.2	BL11;HB15	lymphocyt	integral to	humoral
GI_24475622-S	404.2	1273.8	374.5	MDK	NM_002391.2	NEGF2	heparin	extracellul	signal
GI_24475623-S	93.2	100.5	85.1	TYR	NM_000372.2	OCA1A;OCAIA	monophen	Golgi	eye
GI_24475624-S	3913.4	4918.7	5094.8	DBI	NM_020548.2	ACBP;ACBD1	diazepam-		transport
GI_24475625-S	140.9	146.3	112.5	SERPINA7	NM_000354.2	TBG	protein	soluble	
GI_24475626-S	262.2	297.9	271.2	TSC1	NM_000368.2	LAM;TSC;HAMARTIN;KIAA0243	tumor	kinesin	Rho
GI_24475627-S	108.1	99.5	107	TRPM5	NM_014555.2	MTR1;LTRPC5	ion	integral to	oncogene
GI_24475633-S	241.2	282.9	251.5	EP400	NM_015409.2	P400;CAGH32;TNRC12;KIAA1498;KIAA1818			
GI_24475636-S	124.4	121.1	129.4	GNMT	NM_018960.2		N-		protein
GI_24475638-S	224.2	241.4	151	KIAA1295	NM_017963.2	FLJ20831			
GI_24475639-S	2065.2	1851.9	1990.1	HSA272196	NM_018405.2		molecular	cellular_co	biological_
GI_24475643-S	985.6	1169.7	935.1	RARSL	NM_020320.2	PRO1992;MGC14993;MGC23778;dJ382I10.	ATP		arginyl-
GI_24475645-S	224.8	245.2	221	TUBGCP6	NM_020461.2	GCP6;KIAA1669;DJ402G11.6	microtubul	gamma-	microtubul
GI_24475647-S	282.5	333.8	284.8	KIAA1468	NM_020854.2	HsT885			
GI_24475651-S	94.9	86.3	102.4	NTN4	NM_021229.2	PRO3091	structural	extracellul	
GI_24475652-S	300.1	306.8	285.8	ZNF143	NM_003442.3	SBF;STAF;pHZ-1	RNA	nucleus	regulation
GI_24475653-S	98	89.9	94.4	PROK2	NM_021935.2	BV8;PK2;MIT1	molecular	cellular_co	neuropepti
GI_24475655-S	270.2	287.4	347.5	SHFM3	NM_022039.2	DAC;SHSF3;dactylin	molecular	ubiquitin	ubiquitin-
GI_24475656-S	248.7	422.7	267.5	SMOC1	NM_022137.2		calcium	basement	
GI_24475660-S	120.3	136.9	113.4	DIO3OS	NM_022345.2	C14orf134			

GI_24475700-S	1000.6	1158	1011.5	FLJ21673	NM_030898.2				
GI_24475703-S	153.3	186.2	162.3	EPC1	NM_025209.2		transcripti	nucleus	transcripti
GI_24475708-S	3306.8	4172.7	2573.6	CCNL2	NM_030937.2	PCEE;SB138;HLA-ISO;ania-6b;HCLA-ISO			
GI_24475709-S	1315.1	1555.8	1700.9	HBLD2	NM_030940.2	MGC4276	molecular		
GI_24475711-S	1121.5	694.9	980.3	HT036	NM_031207.2				
GI_24475719-S	98.1	97.6	84.6	C10orf11	NM_032024.2	CDA017			
GI_24475722-S	374	358.8	387.9	C6orf200	NM_032519.2				
GI_24475723-S	85.5	88.5	83.5	CAPS2	NM_032606.2		calcium		
GI_24475724-S	110.6	95.7	87.2	ZNF566	NM_032838.2	FLJ14779;MGC12515	nucleic	nucleus	regulation
GI_24475725-S	1509.7	1479.5	1531.5	C7orf35	NM_032936.2	DC32			
GI_24475727-S	398.3	450	444.7	C9orf37	NM_032937.2				
GI_24475729-S	92.7	89.1	78.7	NYD-SP28	NM_033124.2				
GI_24475732-S	123.9	123.8	124.7	LOC94105	NM_033209.2		molecular	cellular_co	biological_
GI_24475733-S	609.2	570.5	623.4	CASC3	NM_007359.3	BTZ;MLN51	molecular	cellular_co	biological_
GI_24475740-S	475.2	525.8	242.4	HTRA3	NM_053044.2		insulin-like	extracellul	proteolysis
GI_24475742-S	196.9	222.6	203.3	C8orf12	NM_054017.2				
GI_24475750-S	83.4	87	91.5	GDEP	NM_058168.2				
GI_24475778-S	355.5	459.4	406	GPHA2	NM_130769.2	GPA2;ZSIG51	hormone	extracellul	
GI_24475808-S	124.6	148	153.8	BRI3BP	NM_080626.4	KG19			
GI_24475811-S	837.6	1028.5	837.1	LOC56181	NM_019557.3				
GI_24475812-S	833.7	945.2	778.3	MKL1	NM_020831.2	MAL;AMKL;BSAC;KIAA1438	DNA	nucleus	cell growth
GI_24475813-S	194.1	237	249.2	RPC8	NM_138338.1	KIAA1665;MGC29654	protein	DNA-	transcripti
GI_24475827-S	112.7	125.4	125.6	C21orf94	NM_145180.2				
GI_24475831-S	113.8	132.5	117.9	NCR3	NM_147130.1	1C7;LY117;NKp30			
GI_24475836-S	154.9	155.2	160.6	ZBTB9	NM_152735.2	MGC23166	protein		
GI_24475838-S	145.3	158.3	148.5	STEPP	NM_152990.2				
GI_24475840-S	113.8	94.6	94	DEFB123	NM_153324.2	DEFB-23			xenobiotic
GI_24475843-S	152	176.1	186.5	SLC2A14	NM_153449.2	GLUT14	glucose	integral to	carbohydr
GI_24475844-S	645.1	805.4	906.6	MDGA1	NM_153487.2	GPIM	nitrogenas	membran	nitrogen
GI_24475845-S	311.8	388	226	ZNF532	NM_018181.3	FLJ10697			
GI_24475846-S	422.3	514	340.3	IVNS1ABP	NM_006469.2	ND1;NS-1;NS1-BP;HSPC068;KIAA0850	protein	transcripti	response
GI_24475850-S	165.1	133.5	127.4	POF1B	NM_024921.2	FLJ22792			
GI_24475852-A	84.1	97	88.9	AF15Q14	NM_020380.2				
GI_24475858-S	207.8	238.7	222.9	ZNF101	NM_033204.2	HZF12;DKFZp570I0164	metallope	intracellula	proteolysis
GI_24475860-S	2520.7	3299	3449.7	PHP14	NM_014172.2	CGI-202;HSPC141;DKFZp564M173	phosphohi	cytosol	dephosph
GI_24475862-S	133.9	167	147.3	H1FOO	NM_153833.1	osH1	DNA	nucleus	nucleoso
GI_24475864-S	114.7	139.5	122.7	GPR112	NM_153834.1	PGR17;RP1-299I16	G-protein	membran	neuropepti
GI_24475866-S	122.9	149.6	131.4	GPR113	NM_153835.1	PGR23;hGPCR37	G-protein	membran	neuropepti
GI_24475868-S	270.6	317.4	280.3	CREG2	NM_153836.1				
GI_24475870-S	115.9	139.5	127.9	GPR114	NM_153837.1	PGR27			
GI_24475872-S	122.6	197.4	239.9	GPR115	NM_153838.1	PGR18;FLJ38076	G-protein	membran	neuropepti
GI_24475874-S	174.7	206.6	183	GPR111	NM_153839.1	PGR20;hGPCR35	G-protein	integral to	neuropepti
GI_24475876-S	208	216.9	213.6	GPR110	NM_153840.1	PGR19;hGPCR36	G-protein	membran	neuropepti
GI_24475878-S	641.2	1631.6	787.7	FUCA1	NM_000147.2		alpha-L-	lysosome	carbohydr

GI_24475879-S	2181.7	2287	2192.9	PCCB	NM_000532.2		propionyl-	mitochond	fatty acid
GI_24475884-S	780.3	877.2	1177	C11orf13	NM_003475.2	HRC1;HRAS1	DNA	kinesin	neuropepti
GI_24475885-S	155.8	173.1	141.3	SOAT2	NM_003578.2	ACAT2;ARGP2;ACACT2	acyltransf	endoplas	cholestero
GI_24475886-S	241.6	297.9	251.9	GPR49	NM_003667.2	FEX;HG38;LGR5;GPR67;GRP49	G-protein	integral to	G-protein
GI_24475887-S	149.7	163.9	159.3	RIPK1	NM_003804.2	RIP	protein		apoptosis
GI_24475891-S	919.1	757.7	780.7	CSPG6	NM_005445.2	BAM;HCAP;SMC3;SMC3L1	chondroiti	nuclear	DNA
GI_24475893-S	40862.4	33459	32258	GNB2L1	NM_006098.2	H12.3;RACK1;Gnb2-rs1	protein	peripheral	protein
GI_24475894-S	325.3	235.8	340.1	PBX3	NM_006195.2		DNA		anterior
GI_24475897-S	320.1	475.3	457	USF1	NM_007122.2	UEF;MLTF;FCHL1;MLTFI;HYPLIP1	specific	nucleus	transcripti
GI_24475949-S	1912.4	1829.7	1863.8	LAT	NM_014387.2		SH3/SH2	integral to	immune
GI_24475953-S	121.1	131.1	128	TNPO2	NM_013433.2	IPO3;TRN2;KPNB2B;FLJ12155	nuclear	cytoplasm	nucleocyto
GI_24475957-S	96	96.2	81.4	PRO0297	NM_014081.2				
GI_24475961-S	301.8	301.7	277.5	LOC51058	NM_015911.2				
GI_24475963-S	2578.6	2904.1	2599.3	LOC51234	NM_016454.2				
GI_24475964-S	100.9	95.7	89.7	LOC51057	NM_015910.2				
GI_24475966-S	117.8	152.3	131.6	LOC51059	NM_015912.2				
GI_24475968-S	186	217.9	191.8	PACAP	NM_016459.2	FLJ32987			
GI_24475971-S	2362.3	2124.7	1925.4	LOC51249	NM_016486.2				
GI_24475975-S	1258	1555.8	2174.6	TBC1D7	NM_016495.2	dJ257A7.3			
GI_24475976-S	470.1	491	397.5	C6orf203	NM_016487.2	PRED31;HSPC230			
GI_24475978-S	3592.1	3731.9	3331.5	LOC51255	NM_016494.2				
GI_24475981-S	1128.4	1168.6	1168.5	HSPC196	NM_016464.2				
GI_24475982-A	1585.8	1013.9	1099.1	FLJ10597	NM_016501.2				
GI_24475984-S	4600	4471.4	4222.9	C6orf53	NM_016462.2	HSPC194;bA421M1.6	molecular	integral to	
GI_24475985-S	840.6	805.2	865.7	HSPC242	NM_016498.2				
GI_24475986-S	247.3	318.7	310.1	C14orf129	NM_016472.2	HSPC210			
GI_24475987-S	1436.2	919.9	782.8	ZNF581	NM_016535.2	HSPC189	DNA	nucleus	regulation
GI_24475997-S	4674.3	3564.9	3070.1	H41	NM_017548.2		molecular	cellular_co	cell
GI_24476001-S	895.9	659	1752.9	HSCARG	NM_020677.2				
GI_24476003-S	107.2	109.9	104.3	CYT19	NM_020682.2		S-		
GI_24476006-S	84	92	92	HT017	NM_020678.2				
GI_24476008-S	697.2	924.7	973.5	NPD007	NM_020684.2				
GI_24476015-I	152	161.8	130.8	GPR161	NM_153832.1	RE2			
GI_24496766-S	5797.4	6086	7776.8	HGS	NM_004712.3	HRS;ZFYVE8		endosome	negative
GI_24496784-I	137.8	158.6	139.5	AF15Q14	NM_170589.1				
GI_24496788-S	1502.1	1199.2	989.9	LARS	NM_020117.8	LEUS;LARS1;RNTLS;HSPC192;FLJ10595;F			
GI_24497434-S	6716.2	7409.6	6380.4	PSMC5	NM_002805.4	S8;P45;SUG1;TBP10;TRIP1;p45/SUG	proteasom	26S	transcripti
GI_24497436-I	89.1	82.6	83.4	SIGLECL1	NM_053003.2	S2V;SLG;FLJ38600	lectin [goid	integral to	cell
GI_24497437-S	208.3	236.2	202.7	IL12B	NM_002187.2	CLMF;NKSF;CLMF2;NKSF2;IL-12B	interleukin-	membran	JAK-STAT
GI_24497439-A	111.5	121.9	98.6	IL12RB1	NM_153701.1	IL12RB;MGC34454;IL-12R-BETA1	interleukin	integral to	positive
GI_24497439-I	193.9	222.4	184.4	IL12RB1	NM_153701.1	IL12RB;MGC34454;IL-12R-BETA1	interleukin	integral to	positive
GI_24497441-S	96.7	91.9	95.9	IL12RB2	NM_001559.2		interleukin	integral to	positive
GI_24497442-S	603.7	553.9	549.2	NUP214	NM_005085.2	CAN;CAIN;N214;D9S46E	transporte	nuclear	nucleocyto
GI_24497446-A	221.6	293.6	202.5	NUP50	NM_153645.1	NPAP60;NPAP60L;MGC39961;DKFZP564A0		nuclear	

GI_24497446-I	103.7	99.5	90.4	NUP50	NM_153645.1	NPAP60;NPAP60L;MGC39961;DKFZP564A0		nuclear	
GI_24497452-S	2258.4	2128	2048.8	NUP88	NM_002532.3	MGC8530	transporte	nuclear	nucleocyto
GI_24497454-S	116.3	126.7	105	KCNC1	NM_004976.2	KV4;NGK2;KV3.1	voltage-	voltage-	potassium
GI_24497455-A	97.2	85.8	90.2	KCNC2	NM_139137.2	KV3.2			
GI_24497455-I	107.8	135.6	129.5	KCNC2	NM_139137.2	KV3.2			
GI_24497459-S	117.7	114.8	108	KCNC3	NM_004977.2	KV3.3;KSHIIID	voltage-	voltage-	potassium
GI_24497461-I	218.8	262.1	237.9	KCNC4	NM_004978.2	KV3.4;KSHIIIC;HKSHIIIC	potassium	voltage-	potassium
GI_24497463-A	93	94.2	104.9	KCNC4	NM_153763.1	KV3.4;KSHIIIC;HKSHIIIC	potassium	voltage-	potassium
GI_24497463-I	140.4	132.6	130.7	KCNC4	NM_153763.1	KV3.4;KSHIIIC;HKSHIIIC	potassium	voltage-	potassium
GI_24497465-A	104.9	116.1	98.1	KCNJ1	NM_000220.2	ROMK;ROMK1;KIR1.1	inward	voltage-	potassium
GI_24497465-I	126.8	146.8	138.7	KCNJ1	NM_000220.2	ROMK;ROMK1;KIR1.1	inward	voltage-	potassium
GI_24497477-A	103.2	94.7	104	SLC22A6	NM_153277.1	OAT1;PAHT;HOAT1;ROAT1;MGC45260	organic	membran	alpha-
GI_24497483-S	135.4	140.9	136.8	SLC22A11	NM_018484.2	OAT4;hOAT4;MGC34282	sodium-	integral to	small
GI_24497484-I	367.6	475.7	418.3	SLC22A12	NM_144585.2	RST;OAT4L;URAT1	transporte	integral to	transport
GI_24497486-A	575.3	726.7	704.8	SLC22A12	NM_153378.1	RST;OAT4L;URAT1	transporte	integral to	transport
GI_24497488-S	103.9	122.8	98.4	SLC22A3	NM_021977.2	EMT;EMTH;OCT3	organic	membran	organic
GI_24497489-S	186.1	216.6	407.5	SLC22A4	NM_003059.2	OCTN1;MGC34546	organic	integral to	organic
GI_24497491-S	166	176.2	175.4	SLC22A5	NM_003060.2	OCTN2	carnitine	integral to	carnitine
GI_24497492-S	317.4	325	346	HOXA4	NM_002141.2	HOX1D	transcripti	nucleus	embryoge
GI_24497494-I	153	156.5	145.6	SLC22A7	NM_153320.1	NLT;OAT2;MGC24091;MGC45202	sodium-	membran	organic
GI_24497496-A	384.2	454	393.6	SLC22A7	NM_006672.2	NLT;OAT2;MGC24091;MGC45202	sodium-	membran	organic
GI_24497498-S	339.5	449.8	384.8	SLC22A8	NM_004254.2	OAT3;MGC24086	organic	membran	organic
GI_24497500-S	164	133.8	187.5	FOXA1	NM_004496.2	HNF3A;TCF3A;MGC33105	transcripti	nucleus	regulation
GI_24497502-I	113.6	107.6	105.7	FOXA2	NM_021784.3	HNF3B;TCF3B;MGC19807	transcripti	nucleus	regulation
GI_24497503-A	155.1	154	123.2	FOXA2	NM_153675.1	HNF3B;TCF3B;MGC19807	transcripti	nucleus	regulation
GI_24497503-I	81	93.3	95.1	FOXA2	NM_153675.1	HNF3B;TCF3B;MGC19807	transcripti	nucleus	regulation
GI_24497505-S	168.1	193.7	131.3	FOXA3	NM_004497.2	FKHH3;HNF3G;TCF3G;MGC10179	specific	nucleus	regulation
GI_24497507-I	111.9	119.3	119.3	HOXA1	NM_005522.3	HOX1F;MGC45232	RNA	nucleus	developm
GI_24497508-A	100.8	113.7	109.7	HOXA1	NM_153620.1	HOX1F;MGC45232	RNA	nucleus	developm
GI_24497511-I	99.5	111.9	98.5	HOXA3	NM_030661.3	HOX1E;MGC10155	transcripti	nucleus	regulation
GI_24497512-I	103.6	105.6	96.5	HOXA3	NM_153631.1	HOX1E;MGC10155	transcripti	nucleus	regulation
GI_24497514-A	101	109	98.3	HOXA3	NM_153632.1	HOX1E;MGC10155	transcripti	nucleus	regulation
GI_24497514-I	97.9	101.7	98	HOXA3	NM_153632.1	HOX1E;MGC10155	transcripti	nucleus	regulation
GI_24497516-S	593.6	794.5	697.3	HOXA5	NM_019102.2	HOX1C;HOX1.3;MGC9376	transcripti	nucleus	regulation
GI_24497518-S	251.3	228.8	200.8	MAN1A1	NM_005907.2	MAN9;HUMM3;HUMM9	mannosid	Golgi	protein
GI_24497520-S	584	629.2	646.5	MAP2K4	NM_003010.2	JNKK;MEK4;MKK4;SEK1;JNKK1;SERK1;MA	protein		JNK
GI_24497521-I	219.9	245.1	302.2	MAP3K6	NM_004672.2	MAPKKK6;MGC20114	MAP		activation
GI_24497523-A	340.8	295.6	414.1	MAP3K6	NM_145319.1	MAPKKK6;MGC20114	MAP		activation
GI_24497525-S	269.9	313.2	282.4	HOXB1	NM_002144.2	HOX2;HOX2I;Hox-2.9	transcripti	nucleus	regulation
GI_24497527-S	1134	957.4	786.3	HOXB2	NM_002145.2	K8;HOX2;HOX2H;Hox-2.8	transcripti		circulation
GI_24497529-I	863.6	1183.9	1243.8	EVC	NM_014556.2	DWF-1		integral to	muscle
GI_24497530-A	145.1	162.8	152.9	EVC	NM_153717.1	DWF-1		integral to	muscle
GI_24497530-I	119.3	111.3	121.6	EVC	NM_153717.1	DWF-1		integral to	muscle
GI_24497532-S	371	480.4	437	HOXC10	NM_017409.2	HOX3I;MGC5259	RNA	nucleus	positive

GI_24497534-S	102.2	122.2	105.4	HOXC11	NM_014212.2	HOX3H;MGC4906	RNA	nucleus	endoderm
GI_24497535-S	314	436.4	454	HOXC13	NM_017410.2	HOX3;HOX3G	RNA	nucleus	embryoge
GI_24497537-I	171.6	193.8	167.4	HOXC4	NM_014620.2	HOX3;cp19;HOX3E	transcripti	nucleus	regulation
GI_24497539-A	114.4	119.5	110.4	HOXC4	NM_153633.1	HOX3;cp19;HOX3E	transcripti	nucleus	regulation
GI_24497541-S	290.9	331	416.6	HOXC5	NM_018953.2	CP11;HOX3;HOX3D	transcripti	nucleus	regulation
GI_24497542-A	872.1	868.2	1028.7	HOXC6	NM_004503.2	CP25;HOX3;HOX3C;HHO.C8	transcripti	nucleus	oncogene
GI_24497542-I	216.7	265.2	250.1	HOXC6	NM_004503.2	CP25;HOX3;HOX3C;HHO.C8	transcripti	nucleus	oncogene
GI_24497546-S	169.5	205.4	205.2	HOXC9	NM_006897.1	HOX3;HOX3B	transcripti	nucleus	transcripti
GI_24497548-I	338.8	430.8	416.2	HOXA10	NM_018951.2	PL;HOX1H;HOX1.8;MGC12859	transcripti	nucleus	spermatog
GI_24497550-A	615.8	708.8	891.5	HOXA10	NM_153715.1	PL;HOX1H;HOX1.8;MGC12859	transcripti	nucleus	spermatog
GI_24497550-I	116.1	142.7	134.3	HOXA10	NM_153715.1	PL;HOX1H;HOX1.8;MGC12859	transcripti	nucleus	spermatog
GI_24497552-S	187.1	222.8	179.5	HOXA11	NM_005523.4	HOX1I	transcripti	nucleus	embryoge
GI_24497553-S	118.4	140.4	120.9	HOXA13	NM_000522.2	HOX1J	DNA	nucleus	skeletal
GI_24497555-S	123.9	143.1	126.2	HOXA7	NM_006896.2	ANTP;HOX1A;HOX1.1	transcripti	nucleus	regulation
GI_24497557-I	131.2	176.6	172.2	HOXA9	NM_152739.2	ABD-B;HOX1G;HOX1.7;MGC1934			oncogene
GI_24497558-A	860.4	1360.9	1748.5	HOXA9	NM_002142.3	ABD-B;HOX1G;HOX1.7;MGC1934			oncogene
GI_24497560-I	104.2	122.3	112.4	HYAL1	NM_007312.3	NAT6;LUCA1;HYAL-1;MGC45987	hyalurono	lysosome	
GI_24497563-I	97.7	96.1	93.4	HYAL1	NM_153281.1	NAT6;LUCA1;HYAL-1;MGC45987	hyalurono	lysosome	
GI_24497573-A	174.6	218.8	183	HYAL1	NM_153286.1	NAT6;LUCA1;HYAL-1;MGC45987	hyalurono	lysosome	
GI_24497575-I	143.8	133.3	124.8	AKR1A1	NM_006066.2	ALR;ALDR1;MGC1380;MGC12529	aldehyde		aldehyde
GI_24497576-A	4323.2	3687.3	2620.7	AKR1A1	NM_153326.1	ALR;ALDR1;MGC1380;MGC12529	aldehyde		aldehyde
GI_24497578-S	105.7	379.1	182.2	AKR1B10	NM_020299.3	HIS;HSI;ARL1;ARL-	aldehyde	cellular_co	aldehyde
GI_24497579-S	3069.1	4654.1	4711	AKR1B1	NM_001628.2	AR;ADR;ALDR1;MGC1804	aldehyde	extracellul	carbohydr
GI_24497580-S	154.2	299.1	491.2	AKR1C1	NM_001353.4	C9;DD1;DDH;DDH1;H-	aldo-keto	cytoplasm	xenobiotic
GI_24497582-S	345.4	872.3	1214.3	AKR1C3	NM_003739.4	DD3;HAKRB;HAKRe;HA1753;HSD17B5;hluP	aldo-keto		prostaglan
GI_24497584-S	110.9	162.9	160.6	AKR1C4	NM_001818.2	C11;CDR;DD4;CHDR;HAKRA;MGC22581;3-	aldo-keto	cytoplasm	androgen
GI_24497586-S	96.9	102	105.8	ADCY4	NM_139247.2		calcium/ca	integral to	intracellula
GI_24497588-S	103.7	99.5	121.3	ARX	NM_139058.1	ISSX;PRTS;MRX36;MRXS1	transcripti	nucleus	regulation
GI_24497590-I	165.3	154.5	167.9	DPM2	NM_152690.1	MGC21559		endoplas	protein
GI_24497592-I	1942.8	2222.9	2276.5	EDF1	NM_003792.2	MBF1;EDF-1;MGC9058	DNA	intracellula	cell growth
GI_24497593-A	2684.4	2536.6	2783.8	DPM2	NM_003863.2	MGC21559		endoplas	protein
GI_24497594-I	274.6	300.8	287.2	DSCR5	NM_016430.2	DCRC;DSRC;PIGP;DCRC-S	molecular	integral to	biological_
GI_24497596-I	117.5	119	114.4	DSCR5	NM_153681.1	DCRC;DSRC;PIGP;DCRC-S	molecular	integral to	biological_
GI_24497598-A	1061	1233.6	1156.6	DSCR5	NM_153682.1	DCRC;DSRC;PIGP;DCRC-S	molecular	integral to	biological_
GI_24497600-A	2998.9	3238.6	3322.5	EDF1	NM_153200.1	MBF1;EDF-1;MGC9058	DNA	intracellula	cell growth
GI_24497600-I	95	107.6	97.3	EDF1	NM_153200.1	MBF1;EDF-1;MGC9058	DNA	intracellula	cell growth
GI_24497610-S	571.3	711.5	639	EVX1	NM_001989.2		transcripti	nucleus	regulation
GI_24497611-S	118.2	174	131.8	KIAA1959	NM_032873.2	MGC15437	catalytic		metabolis
GI_24497613-A	91.1	94.5	108.8	KL	NM_004795.2		beta-	soluble	
GI_24497617-S	335.1	331.4	455	PRO2000	NM_014109.2	MGC5254;MGC29843;DKFZp667N1320	nucleotide		
GI_24497619-S	1594.4	1785.9	1523.1	SRP68	NM_014230.2		RNA	signal	
GI_24497621-S	674.1	548.7	565.7	TRIM11	NM_145214.2	BIA1;RNF92			
GI_24497622-S	399.9	392	364.6	TRIM38	NM_006355.2	RNF15;RORET;MGC8946	zinc ion	intracellula	biological_
GI_24497623-S	96.5	109.3	83.8	IRF6	NM_006147.2	LPS;PIT;PPS;VWS	transcripti	nucleus	regulation

GI_24497624-S	103.1	117.1	118.2	OTP	NM_032109.2	MGC3161			
GI_24497625-S	670.7	698.6	513.7	SNAI2	NM_003068.3	SLUG;SLUGH1;MGC10182	transcripti	nucleus	ectoderm/
GI_24497626-A	253.1	252.9	308.4	SIPA1	NM_006747.2	SPA1;MGC17037	GTPase	peripheral	signal
GI_24497628-I	106.7	122.9	92.8	SIPA1	NM_153253.2	SPA1;MGC17037	GTPase	peripheral	signal
GI_24497630-S	160.8	210.2	135.9	RHBDL2	NM_017821.2	RRP2;FLJ20435;MGC16997	serine-	integral to	
GI_24586652-I	119.3	138.5	118.9	MLL3	NM_170606.1	HALR;FLJ12625;KIAA1506	methyltran	nucleus	regulation
GI_24586660-S	330	279.9	286	ZNF271	NM_006629.3	HZF7;ZNFEB	zinc ion		
GI_24586662-S	471.5	509.8	406.5	DIP13B	NM_018171.2	FLJ10659			
GI_24586664-S	575.1	535.9	434.6	SLC39A8	NM_022154.4	BIGM103	heavy	membran	heavy
GI_24586672-A	481.4	602	600.3	SSH-3	NM_018276.2	SSH3;FLJ10928;FLJ20515			
GI_24586674-I	159.9	181.6	171.2	SSH-3	NM_017857.2	SSH3;FLJ10928;FLJ20515			
GI_24586683-A	186.9	252.4	371.1	DMN	NM_015286.4	SYN;KIAA0353	structural	intermedia	
GI_24586685-S	92.6	103.6	101.3	CACNG8	NM_031895.4		voltage-	voltage-	calcium
GI_24586687-S	364.6	443	400.4	ASB16	NM_080863.4	FLJ30165			
GI_24638432-S	6668.6	7845.2	6981.5	NCSTN	NM_015331.1	APH2;KIAA0253	molecular	integral to	proteolysis
GI_24638434-I	80.6	84.4	81.2	OTOA	NM_144672.2	DFNB22;FLJ32773			
GI_24638451-A	343.4	367	342.7	OTOA	NM_170664.1	DFNB22;FLJ32773			
GI_24638451-I	262.6	158.4	164.3	OTOA	NM_170664.1	DFNB22;FLJ32773			
GI_24762231-S	110.1	100.4	101.8	BRUNOL5	NM_021938.2	CELF5;BRUNOL-5	nucleic		
GI_24762235-I	407.8	462.6	430.4	FLJ14936	NM_032864.2	MGC3320			
GI_24762238-I	139.3	160.1	159.6	RASGRP3	NM_170672.1	GRP3;KIAA0846	guanyl-		small
GI_24762247-I	277.6	318.7	293	ITGB1BP3	NM_170678.1	MIBP	protein	peripheral	myoblast
GI_24797064-S	397.4	482.2	446.6	ZNF212	NM_012256.2	MGC9707;ZNFC150;C2H2-150			
GI_24797066-S	117.7	141.8	127.5	HLA-A	NM_002116.4				
GI_24797068-S	138.4	152.6	129.9	HLA-DQB1	NM_002123.2	IDDM1;CELIAC1;HLA-DQB			
GI_24797070-S	759.5	670.7	517.1	HLA-E	NM_005516.3	HLA-6.2	class I	integral to	immune
GI_24797072-S	360.6	475.6	408.7	HLA-G	NM_002127.3	TCA;HLA60;HLA-6.0	class I	integral to	perception
GI_24797073-S	263	2740.5	504.6	HLA-DPA1	NM_033554.2	HLADP;HLASB;HLA-DP1A	MHC	integral to	immune
GI_24797075-S	758.9	1773.5	319.6	HLA-DPB1	NM_002121.4	HLA-DP1B	class II		perception
GI_24797083-S	2280.5	2875.6	2710.8	KPNA6	NM_012316.3	IPOA7;KPNA7;FLJ11249;MGC17918	protein	importin,	NLS-
GI_24797084-S	5554.1	4735.2	4615.2	KPNB1	NM_002265.4	IMB1;IPOB;Impnb;NTF97;MGC2155;MGC21	nuclear	importin,	NLS-
GI_24797085-S	510.5	689.5	540.3	KPNB3	NM_002271.3	IMB3;IPO5;RANBP5;MGC2068	GTPase	importin,	NLS-
GI_24797087-A	351.9	369.9	376.1	PEX10	NM_002617.3	NALD;RNF69;MGC1998	zinc ion	peroxisom	peroxisom
GI_24797088-I	116.1	128.7	126.4	PEX10	NM_153818.1	NALD;RNF69;MGC1998	zinc ion	peroxisom	peroxisom
GI_24797090-A	376.5	371.6	457.3	PHF2	NM_024517.1	GRC5;KIAA0662	transcripti	nucleus	regulation
GI_24797092-I	124.1	110.2	109	PHF2	NM_005392.2	GRC5;KIAA0662	transcripti	nucleus	regulation
GI_24797094-A	2353.5	1362.1	1034.3	PYCR1	NM_153824.1	P5C;P5CR;PYCR;PP222	pyrroline-5-		proline
GI_24797096-I	441.1	366	243.9	PYCR1	NM_006907.2	P5C;P5CR;PYCR;PP222	pyrroline-5-		proline
GI_24797098-I	124.2	114.8	114.6	RASGRF1	NM_002891.3	GNRP;GRF1;CDC25;GRF55;CDC25L;H-	Ras		signal
GI_24797100-A	123.6	146.5	122.4	RASGRF1	NM_153815.1	GNRP;GRF1;CDC25;GRF55;CDC25L;H-	Ras		signal
GI_24797100-I	113.1	110.3	106.3	RASGRF1	NM_153815.1	GNRP;GRF1;CDC25;GRF55;CDC25L;H-	Ras		signal
GI_24797102-A	215.1	268.8	251.1	RASGRP2	NM_153819.1	CDC25L;CALDAG-GEFI	lipid		signal
GI_24797104-I	2079	1486.6	1882.6	EPHB2	NM_004442.4	DRT;ERK;Hek5;EPHT3;Tyro5	transmem	integral to	oncogene
GI_24797105-S	3963.4	3840.4	2820.2	ETEA	NM_014613.1	KIAA0887			

GI_24797117-A	113.7	114.3	110.1	CABYR	NM_153770.1	CBP86;FSP-2;MGC9117			
GI_24797131-S	1218.9	1380.6	1192.4	HOXA6	NM_024014.2	HOX1B;HOX1.2	transcripti	nucleus	regulation
GI_24797132-S	276.2	285.6	206.8	HOXB5	NM_002147.2	HOX2;HU-1;HOX2A;Hox2.1;HHO.C10	transcripti	nucleus	embryoge
GI_24797133-I	130.2	125.3	118.1	HOXB6	NM_018952.3	HOX2;HU-2;HOX2B;Hox-2.2	transcripti	nucleus	determinat
GI_24797134-I	141.5	143.1	139.5	HOXB6	NM_156036.1	HOX2;HU-2;HOX2B;Hox-2.2	transcripti	nucleus	determinat
GI_24797136-A	363	393.7	306.1	HOXB6	NM_156037.1	HOX2;HU-2;HOX2B;Hox-2.2	transcripti	nucleus	determinat
GI_24797138-S	2295.1	1638.5	1119.1	HOXB9	NM_024017.3	HOX2;HOX2E;HOX-2.5	transcripti	nucleus	transcripti
GI_24797139-S	106.5	114.8	111.4	KCNJ3	NM_002239.2	GIRK1;KIR3.1	G-protein	voltage-	potassium
GI_24797140-S	101.4	111.5	103.2	KCNJ5	NM_000890.3	CIR;GIRK4;KATP1;KIR3.4	G-protein	voltage-	potassium
GI_24797146-S	1105.7	749.5	702.4	SEPHS2	NM_012248.2	SPS2	ATP	cellular_co	selenocyst
GI_24797149-S	176.3	205.7	193.3	BMP5	NM_021073.2	MGC34244	cytokine	cellular_co	skeletal
GI_24797150-S	126	129.6	133.3	DMGDH	NM_013391.2	DMGDHD;ME2GLYDH	electron	mitochond	electron
GI_24797152-S	431.4	377.2	401.6	FGD1	NM_004463.2	AAS;FGDY;ZFYVE3	guanyl-		histogene
GI_24797154-A	739.5	905.7	835.3	ICMT	NM_012405.2	PCMT;PPMT;PCCMT;HSTE14;MST098;MST	C-terminal	membran	C-terminal
GI_24797155-I	117.7	142.3	136.8	ICMT	NM_170705.1	PCMT;PPMT;PCCMT;HSTE14;MST098;MST	C-terminal	membran	C-terminal
GI_24797157-S	851.3	822.1	668.5	MANBA	NM_005908.2	MANB1	beta-	lysosome	protein
GI_24797159-S	954.6	1421.4	1267.2	TAP1	NM_000593.4	APT1;PSF1;ABC17;ABCB2;RING4;D6S114E	peptide	membran	peptide
GI_24850106-S	135.1	142.5	126.3	RUFY2	NM_017987.2	RABIP4R;ZFYVE13;FLJ10063;KIAA1537			
GI_24850108-S	131.3	129.2	132.5	GPBAR1	NM_170699.1	BG37;GPCR;TGR5;GPR131	receptor	integral to	G-protein
GI_24850110-S	159.4	334.7	198.4	PSTPIP2	NM_024430.2	MAYP;MGC34175		kinesin	
GI_24850112-S	4444.3	5313.4	4825.1	SHCBP1	NM_024745.2	FLJ22009;MGC26900			
GI_24850114-I	444.9	584.9	545.7	CSE-C	NM_170601.1				
GI_24850132-S	1071	1098.9	1284.1	PIASY	NM_015897.2	MGC35296	zinc ion	nucleus	regulation
GI_24850455-S	121.6	123.8	111.1	SMC5L1	NM_015110.1	SMC5;KIAA0594	ATP	nucleus	chromoso
GI_24942125-S	6535.5	5421.2	4147.3	SHMT2	NM_005412.3	GLYA;SHMT		mitochond	
GI_25006531-S	298.2	302.1	254.3	SERHL	NM_170694.1	HS126B42;BK126B4.1;BK126B4.2			
GI_25014087-S	119.4	130.9	137.5	SLC34A3	NM_080877.1	NPTIIc;FLJ38680	sodium-	membran	phosphate
GI_25014092-S	248.3	251.6	203	ZNF585B	NM_152279.2	SZFP41;FLJ14928	nucleic	nucleus	regulation
GI_25014098-S	957.1	1130.4	955	SELK	NM_021237.2	HSPC030			
GI_25014108-S	5402.5	4606.2	3666.1	SELH	NM_170746.1		DNA	nucleus	regulation
GI_25014110-S	1367.3	2594.5	2206	DNAJB11	NM_016306.3	EDJ;HEDJ;ABBP2;ABBP-2	chaperone	endoplas	protein
GI_25072198-S	627.7	487	514.9	FLJ25416	NM_145018.2	FLJ13936			
GI_25092600-S	356.2	282.8	358.4	STEAP2	NM_152999.2	STMP;IPCA1;IPCA-1;STAMP1;PCANAP1		integral to	electron
GI_25092657-S	2527.9	1767.5	2396.8	C7orf27	NM_152743.1	MGC22916			
GI_25092724-S	345.1	372.9	314.2	CGI-96	NM_015703.2	BK126B4.3	nucleic		
GI_25121934-A	176.9	210.8	175.8	RASAL2	NM_004841.2	nGAP	Ras		signal
GI_25121935-A	222.4	278.3	226	RASAL2	NM_170692.1	nGAP	Ras		signal
GI_25121935-I	179.6	213.6	164.9	RASAL2	NM_170692.1	nGAP	Ras		signal
GI_25121937-I	125.8	137.6	109.5	GRLF1	NM_024342.1	GRF-1;P190A;P190-	transcripti	nucleus	transcripti
GI_25121939-A	1093.1	1232.1	1089.6	GRLF1	NM_004491.2	GRF-1;P190A;P190-	transcripti	nucleus	transcripti
GI_25121957-I	146	149.8	135	PSMD4	NM_153822.1	AF;ASF;S5A;AF-1;MCB1;Rpn10;pUB-R5		26S	
GI_25121959-S	150.2	163.1	156.3	PTCH	NM_000264.2	PTC;BCNS;HPE7;PTC1;NBCCS	tumor	integral to	embryoge
GI_25121960-S	126.8	148.3	120.9	HOXB3	NM_002146.3	HOX2;HOX2G;Hox-2.7	transcripti	nucleus	regulation
GI_25121962-S	855.8	723.3	867.8	HOXB7	NM_004502.2	HOX2;HOX2C;HHO.C1;Hox-2.3	transcripti	nucleus	regulation

GI_25121964-S	782.5	753.5	497.6	HOXB8	NM_024016.2	HOX2;HOX2D;Hox-2.4	transcripti	nucleus	regulation
GI_25121965-S	212	242.1	225	KCNJ10	NM_002241.2	KIR1.2;KIR4.1;BIRK-10;KCNJ13-PEN	ATP-	integral to	potassium
GI_25121967-S	115	193.3	120.1	KCNJ6	NM_002240.2	BIR1;GIRK2;KATP2;KCNJ7;KIR3.2;hiGIRK2	G-protein	voltage-	potassium
GI_25121968-S	119.4	135.2	127.5	KCNJ8	NM_004982.2	KIR6.1;uKATP-1	inward	voltage-	potassium
GI_25121969-S	105.8	113.3	109.6	KCNJ9	NM_004983.2	GIRK3;KIR3.3	inward	integral to	potassium
GI_25121973-S	260.8	290.3	267.6	LOC151835	NM_153635.1				
GI_25121977-S	122.6	114.5	125.2	DAZL	NM_001351.2	DAZH;DAZL1;DAZLA;SPGYLA;MGC26406	RNA	cytoplasm	germ-cell
GI_25121979-S	683.2	890.2	721.4	DISP2	NM_033510.1	DISPB;HsT16908;KIAA1742			
GI_25121981-I	118.6	115.9	119.7	CRISP1	NM_001131.2	ARP;AEGL1;HUMARP;CRISP-		extracellul	fusion of
GI_25121983-A	114.8	89	102.3	CRISP1	NM_170609.1	ARP;AEGL1;HUMARP;CRISP-		extracellul	fusion of
GI_25121985-S	250.4	290.4	216.5	BAPX1	NM_001189.2	NKX3B;NKX3-2;NKX3.2	RNA	nucleus	skeletal
GI_25121986-S	213.4	247.4	298.4	BRRN1	NM_015341.2	HCAP-H;MGC4616		nucleus	mitotic
GI_25121988-S	216.7	210.1	205	MCSP	NM_030663.2	MCS;SMCP;MGC26305;MGC26519;HSMCS	molecular	mitochond	fertilization
GI_25121990-S	113.8	105.8	101.2	MSI1	NM_002442.2		RNA		neurogene
GI_25121991-A	124.6	140	154.6	MSI2	NM_138962.2	MSI2H;MGC3245;FLJ36569			
GI_25121991-I	266.5	313.5	279.4	MSI2	NM_138962.2	MSI2H;MGC3245;FLJ36569			
GI_25121992-I	124.5	142.7	219.2	MSI2	NM_170721.1	MSI2H;MGC3245;FLJ36569			
GI_25141321-I	124.9	116.8	111	NMNAT2	NM_015039.2	PNAT2;PNAT-			
GI_25141322-S	151.5	173.5	151.8	CPNE5	NM_020939.1	CPN5;COPN5;KIAA1599			
GI_25141326-I	116.3	124.4	101.8	CPNE7	NM_014427.3	MGC34192	transporte		lipid
GI_25141327-A	157.6	195.9	227.6	CPNE7	NM_153636.1	MGC34192	transporte		lipid
GI_25168259-I	144.1	166.9	154.2	SGK2	NM_016276.3	H-SGK2;dJ138B7.2	protein	cellular_co	protein
GI_25168260-A	96.9	102.6	91.8	SGK2	NM_170693.1	H-SGK2;dJ138B7.2	protein	cellular_co	protein
GI_25168260-I	106.6	106.3	109.9	SGK2	NM_170693.1	H-SGK2;dJ138B7.2	protein	cellular_co	protein
GI_25168262-S	2183.2	3332.6	1757.9	SGK	NM_005627.2	SGK1	protein	nucleus	sodium
GI_25168264-I	175.5	196.7	185.9	SGKL	NM_013257.3	CISK;SGK2;SGK3	protein		protein
GI_25168266-A	257.5	268.9	278.5	SGKL	NM_170709.1	CISK;SGK2;SGK3	protein		protein
GI_25188178-S	4082.4	3839.7	3828.8	VDAC3	NM_005662.3	HD-VDAC3	voltage-	mitochond	adenine
GI_25188180-S	87.3	91.7	87.1	WFDC13	NM_172005.1	WAP13;C20orf138;dJ601O1.3			
GI_25188188-S	165.7	191.2	180.1	HE9	NM_172000.1				
GI_25188192-S	105.3	142.4	132.1	RAB39B	NM_171998.1		small		small
GI_25188194-S	90.2	114.3	92.2	SALL3	NM_171999.1		DNA	nucleus	developm
GI_25188200-S	91	85.2	81.6	PLCZ1	NM_033123.2	NYD-SP27			
GI_25282390-S	1732.5	1381.1	1794.2	NRM	NM_007243.1	NRM29	molecular	nuclear	biological_
GI_25282406-S	831.8	1066.2	1090.9	ISGF3G	NM_006084.3	p48;IRF9;IRF-9;ISGF3	transcripti	cytoplasm	cell
GI_25282468-S	370.9	450.9	466.3	RDH10	NM_172037.1		oxidoredu		metabolis
GI_25286702-S	1140.4	1289.8	1438.2	MGC33867	NM_138346.1	KIAA2013			
GI_25306271-A	954.6	966.2	934.6	MRPL11	NM_170738.1	L11mt;CGI-113	structural	ribosome	protein
GI_25306274-I	202.3	191.8	179.9	MRPL11	NM_170739.1	L11mt;CGI-113	structural	ribosome	protein
GI_25306276-S	1990	2441.6	2482.2	EFG1	NM_024996.5	EFG;GFM;hEFG1;FLJ12662;FLJ13632;FLJ2			
GI_25306282-A	192.9	213.6	191.7	EFG2	NM_170681.1	hEFG2;MST027;FLJ21661			
GI_25306282-I	123.4	144.6	132	EFG2	NM_170681.1	hEFG2;MST027;FLJ21661			
GI_25453469-S	48899.2	49381	39689	EEF1A1	NM_001402.4	EF1A;PTI1;EEF-1;EEF1A;EF-Tu;PTI-	GTP	eukaryotic	translation
GI_25453470-S	2655.9	2067.4	3098.3	EEF1A2	NM_001958.2	HS1;STN;EF1A;EEF1AL;EF-1-alpha-2	translation	cytoplasm	translation

GI_25453471-A	27441.2	26581	24405	EEF1D	NM_001960.2	EF-1D;FLJ20897	translation	eukaryotic	
GI_25453473-I	142.2	150.3	143.1	EEF1D	NM_032378.2	EF-1D;FLJ20897	translation	eukaryotic	
GI_25453475-S	48869.8	40245	34548	EEF1G	NM_001404.3	EF1G			
GI_25453476-S	22534.5	22381	19145	EEF2	NM_001961.2	EF2;EEF-2	translation		translation
GI_25453477-S	966.9	714.8	807.9	EEF2K	NM_013302.2	EEF-2K;HSU93850;MGC45041	translation	cytoplasm	translation
GI_25453478-S	124.1	134.3	137	ENPP3	NM_005021.2	B10;NPP3;PDNP3;CD203c;PD-IBETA	phosphodi	integral to	phosphate
GI_25453479-I	271.2	338.8	311.5	CDY1	NM_004680.2	CDY	chromatin	chromatin	spermatog
GI_25453480-A	107.8	90.8	83	CDY1	NM_170723.1	CDY	chromatin	chromatin	spermatog
GI_25453480-I	133	151.6	137.6	CDY1	NM_170723.1	CDY	chromatin	chromatin	spermatog
GI_25453482-S	96.2	103.3	110.7	CDY2	NM_004825.2	CDY	chromatin	chromatin	spermatog
GI_25453483-S	223.5	204	203.1	COQ7	NM_016138.3	CAT5;CLK-1		mitochond	ubiquinon
GI_25470885-A	828.7	883.5	727.5	DAZAP1	NM_018959.2	MGC19907	RNA		spermatog
GI_25470889-I	110.3	115.2	104.4	DAZAP1	NM_170711.1	MGC19907	RNA		spermatog
GI_25777594-S	217.4	251.7	261	CLOCK	NM_004898.2	KIAA0334	transcripti	nucleus	response
GI_25777595-A	491.1	545.6	460.2	DGKD	NM_003648.2	dgkd-2;DGKdelta;KIAA0145	diacylglyc		signal
GI_25777595-I	93.1	94.4	83.9	DGKD	NM_003648.2	dgkd-2;DGKdelta;KIAA0145	diacylglyc		signal
GI_25777597-I	198.4	207.4	177	DGKD	NM_152879.2	dgkd-2;DGKdelta;KIAA0145	diacylglyc		signal
GI_25777599-S	1160	1939	1859.6	PSMD1	NM_002807.2	S1;P112		proteasom	
GI_25777601-S	1992.5	2433.2	2853.5	PSMD2	NM_002808.3	S2;P97;TRAP2;MGC14274		proteasom	
GI_25777603-I	93.6	88.7	75.1	FLJ12661	NM_025138.2	FLJ23780	oxidoredu		metabolis
GI_25777605-A	764.1	661	370.3	FLJ12661	NM_170719.1	FLJ23780	oxidoredu		metabolis
GI_25777607-I	537.8	677.2	623.3	NOD9	NM_024618.2	FLJ21478;MGC21025			
GI_25777609-A	1176.8	1494.6	1669.5	NOD9	NM_170722.1	FLJ21478;MGC21025			
GI_25777611-S	402	511.5	482.7	PSMD3	NM_002809.2	S3;P58;RPN3		26S	
GI_25777613-S	303	317.4	255.7	PSMD5	NM_005047.2	S5B;KIAA0072;MGC23145		26S	
GI_25777616-I	128.6	147.4	130.5	CDYL	NM_004824.2	CDYL1;DKFZP586C1622	chromatin	nucleus	spermatog
GI_25777620-A	1163.7	993.2	1103.7	CDYL	NM_170752.1	CDYL1;DKFZP586C1622	chromatin	nucleus	spermatog
GI_25777625-A	904	836.6	1206.3	ABTB1	NM_172028.1	BPOZ;EF1ABP;MGC20585			
GI_25777627-A	104.5	108.6	99.1	KCNJ16	NM_170741.1	KIR5.1;MGC33717	voltage-	integral to	potassium
GI_25777629-I	92.9	113.3	109.4	KCNJ16	NM_170742.1	KIR5.1;MGC33717	voltage-	integral to	potassium
GI_25777631-S	83.4	84.6	78.5	KCNJ11	NM_000525.2	BIR;PHHI;IKATP;KIR6.2	inward	membran	potassium
GI_25777633-A	119.2	113.1	113.2	KCNJ14	NM_013348.2	IRK4;KIR2.4;MGC46111	inward	voltage-	potassium
GI_25777633-I	158	169.4	129.6	KCNJ14	NM_013348.2	IRK4;KIR2.4;MGC46111	inward	voltage-	potassium
GI_25777634-I	241.6	247.4	243.5	KCNJ14	NM_170720.1	IRK4;KIR2.4;MGC46111	inward	voltage-	potassium
GI_25777637-I	181.4	242.2	211.6	KCNJ15	NM_170736.1	KIR1.3;KIR4.2;MGC13584	inward	membran	potassium
GI_25777639-A	235.5	410.9	311	KCNJ15	NM_170737.1	KIR1.3;KIR4.2;MGC13584	inward	membran	potassium
GI_25777641-S	307.8	379.3	318.1	KCNMB1	NM_004137.2	SLO-BETA;hslo-beta;K(VCA)beta	potassium		potassium
GI_25777642-S	116.9	135.4	126.2	KCNN1	NM_002248.3	SK1;hSK1;SKCA1;KCa2.1	calcium-	voltage-	potassium
GI_25777644-I	233.3	266.1	240.9	KCNN2	NM_021614.2	SK2;hSK2;SKCA2;KCa2.2	ion	integral to	potassium
GI_25777646-A	96.9	95.1	95.9	KCNN2	NM_170775.1	SK2;hSK2;SKCA2;KCa2.2	ion	integral to	potassium
GI_25777646-I	489.5	524.5	596.5	KCNN2	NM_170775.1	SK2;hSK2;SKCA2;KCa2.2	ion	integral to	potassium
GI_25777648-I	275.9	344.3	299.6	KCNN3	NM_002249.3	SK3;hSK3;SKCA3;KCa2.3	calcium-	voltage-	potassium
GI_25777649-A	112	113.5	102	KCNN3	NM_170782.1	SK3;hSK3;SKCA3;KCa2.3	calcium-	voltage-	potassium
GI_25777649-I	89.7	92.7	87.5	KCNN3	NM_170782.1	SK3;hSK3;SKCA3;KCa2.3	calcium-	voltage-	potassium

GI_25777651-S	1401.2	980.1	966.4	KCNN4	NM_002250.2	IK1;SK4;KCA4;hSK4;IKCA1;hKCa4;KCa3.1;h	calcium-	voltage-	potassium
GI_25777652-S	178.9	195	188.1	KCNS1	NM_002251.3	KV9.1	potassium	voltage-	potassium
GI_25777656-A	166.6	196.9	169.1	CD200R	NM_138940.1	OX2R;MOX2R;HCRTR2	receptor	integral to	
GI_25777664-I	102.9	109.9	104.9	PKHD1	NM_138694.2	FCYT;ARPKD;TIGM1	receptor	integral to	
GI_25777666-A	103.7	105.5	97.1	PKHD1	NM_170724.1	FCYT;ARPKD;TIGM1	receptor	integral to	
GI_25777666-I	111.9	127.9	105.7	PKHD1	NM_170724.1	FCYT;ARPKD;TIGM1	receptor	integral to	
GI_25777668-S	159.1	199.8	175.6	FAM12A	NM_006683.3	EP3A;HE3A;HE3ALPHA;HE3-ALPHA	pancreatic	extracellul	sperm
GI_25777669-S	320.8	383.4	326.8	FAM12B	NM_022360.2	EP3B;HE3B;HE3BETA;HE3-BETA	molecular	extracellul	spermatid
GI_25777670-S	354.8	371.7	354.6	PPP1R10	NM_002714.2	FB19;CAT53;PNUTS	nucleic	nucleus	protein-
GI_25777672-I	118.8	115.2	115.7	PPP1R11	NM_170781.1	HCGV;HCG-V;TCTE5;TCTEX5	protein	soluble	
GI_25777674-A	103.1	117.6	85.2	RASSF2	NM_170773.1	KIAA0168			neuropepti
GI_25777674-I	177.3	214.7	204.5	RASSF2	NM_170773.1	KIAA0168			neuropepti
GI_25777679-A	249.2	257.5	228.5	RASSF1	NM_170712.1	123F2;RDA32;NORE2A;RASSF1A;REH3P21			
GI_25777679-I	97	108.7	97.9	RASSF1	NM_170712.1	123F2;RDA32;NORE2A;RASSF1A;REH3P21			
GI_25777681-I	103.1	111	101	RASSF1	NM_170713.1	123F2;RDA32;NORE2A;RASSF1A;REH3P21			
GI_25777691-A	167.5	132.8	152	TRIM35	NM_015066.1	HLS5;MAIR;KIAA1098;MGC17233			
GI_25777693-I	90	96.8	98	TRIM35	NM_171982.1	HLS5;MAIR;KIAA1098;MGC17233			
GI_25777695-I	103.9	112.6	104.1	TRIM39	NM_021253.2	TFP;RNF23;MGC32984	zinc ion	kinesin	biological_
GI_25777697-A	868.6	662.4	640.5	TRIM39	NM_172016.1	TFP;RNF23;MGC32984	zinc ion	kinesin	biological_
GI_25777699-I	2368.6	2656.9	2834.3	ZFP91	NM_053023.2	PZF;FKSG11			
GI_25777700-A	216.2	286.2	275.6	ZFP91	NM_170768.1	PZF;FKSG11			
GI_25777702-I	101.4	98.5	103.6	ZNF398	NM_020781.2	P51;P71;ZER6;KIAA1339	DNA	nucleus	regulation
GI_25777703-A	397.1	407.1	376.2	ZNF398	NM_170686.1	P51;P71;ZER6;KIAA1339	DNA	nucleus	regulation
GI_25777705-A	760.3	611	476.2	ZNRD1	NM_014596.4	Rpa12;hZR14;HTEX-6;tctex-6;MGC13376	DNA-	nucleus	nucleobas
GI_25777706-I	755.7	550.7	469.7	ZNRD1	NM_170783.1	Rpa12;hZR14;HTEX-6;tctex-6;MGC13376	DNA-	nucleus	nucleobas
GI_25777708-A	143.6	163.2	133.5	THEA	NM_015547.2	BFIT;BFIT1;BFIT2;THEM1;STARD14;KIAA07	serine	cytoplasm	response
GI_25777708-I	126.7	146.3	129.3	THEA	NM_015547.2	BFIT;BFIT1;BFIT2;THEM1;STARD14;KIAA07	serine	cytoplasm	response
GI_25777709-I	167.1	211	135.4	THEA	NM_147161.2	BFIT;BFIT1;BFIT2;THEM1;STARD14;KIAA07	serine	cytoplasm	response
GI_25777710-I	97.5	92.8	80.9	SKP1A	NM_006930.2	OCP2;SKP1;EMC19;OCP-			
GI_25777712-A	7216	8891.5	6864.9	SKP1A	NM_170679.1	OCP2;SKP1;EMC19;OCP-			
GI_25777714-I	119.7	137.9	109.4	RNF39	NM_025236.2	HZF;HZFW;LIRF;HZFW1			
GI_25777717-A	124.4	122.8	124.9	RNF39	NM_170770.1	HZF;HZFW;LIRF;HZFW1			
GI_25777719-A	212.5	135.2	113.7	ALDH5A1	NM_001080.3	SSDH;SSADH	succinate-	mitochond	aminobuty
GI_25777722-S	101.8	96.7	79	ALDH1A1	NM_000689.3	ALDC;ALDH1;PUMB1;ALDH11;RALDH1;ALD	aldehyde	cytosol	aldehyde
GI_25777727-A	120.4	118.2	109.9	ALDH1A2	NM_170697.1	RALDH2;MGC26444;RALDH2-T;RALDH(II)	aldehyde		vitamin A
GI_25777729-S	380.8	424.8	249.8	ALDH1B1	NM_000692.3	ALDH5;ALDHX;MGC2230	aldehyde	mitochond	carbohydr
GI_25777731-S	376.9	536.5	283	ALDH2	NM_000690.2	ALDM;ALDHI;ALDH-E2;MGC1806	aldehyde	mitochond	alcohol
GI_25777733-I	209.5	262.8	273.1	ALDH4A1	NM_003748.2	P5CD;ALDH4;P5CDH;P5CDhL;P5CDhS	1-pyrroline-	mitochond	proline
GI_25777735-A	150.5	253.4	292.6	ALDH4A1	NM_170726.1	P5CD;ALDH4;P5CDH;P5CDhL;P5CDhS	1-pyrroline-	mitochond	proline
GI_25777737-S	353.8	416.6	379.9	ALDH6A1	NM_005589.2	MMSDH;MMSADHA;MGC40271	methylmal	mitochond	pyrimidine
GI_25777738-S	3885.3	3845.2	4456.6	ALDH9A1	NM_000696.2	E3;ALDH4;ALDH7;ALDH9;TMABADH	aldehyde		aldehyde
GI_25777740-S	217.9	228.7	227.4	PGBD1	NM_032507.2	HUCEP-4;dJ874C20.4	scavenger	membran	regulation
GI_25777741-S	171.1	200.8	167.1	PGBD2	NM_170725.1				
GI_25777743-S	152.7	180.6	171.3	PGBD3	NM_170753.1	FLJ90201	electron		electron

GI_25777745-S	166.6	182.6	168.3	PGBD4	NM_152595.2	FLJ32638;FLJ37497			
GI_25777747-S	121.2	135.7	138.7	PGBD5	NM_024554.2	FLJ11413;DKFZp761A0620			
GI_25914748-S	581.4	711.4	923.5	ABCC10	NM_033450.2	MRP7;SIMRP7;EST182763	nucleotide	membran	transport
GI_25914751-I	81.6	76.8	90.8	MKKS	NM_018848.2	KMS;MKS;BBS6;HMCS	chaperone		gonad
GI_25914753-A	1384.7	1628.2	667.6	MKKS	NM_170784.1	KMS;MKS;BBS6;HMCS	chaperone		gonad
GI_25914753-I	321.8	336.9	232.8	MKKS	NM_170784.1	KMS;MKS;BBS6;HMCS	chaperone		gonad
GI_25952067-I	104.2	113.9	109.5	ABCC13	NM_138726.2	PRED6;C21orf73			
GI_25952070-I	330.6	383.7	344.4	ABCC13	NM_172024.1	PRED6;C21orf73			
GI_25952073-A	109.3	117.4	114.9	ABCC13	NM_172025.1	PRED6;C21orf73			
GI_25952079-S	227.2	301.7	276.5	KCNA2	NM_004974.2	HK4;MK2;HBK5;NGK1;RBK2;HUKIV;KV1.2	potassium	voltage-	potassium
GI_25952081-S	113.5	134.7	126.1	KCNA3	NM_002232.2	MK3;HGK5;HLK3;PCN3;HPCN3;KV1.3;HUKII	voltage-	voltage-	potassium
GI_25952084-S	122.3	121.5	112	KCNA4	NM_002233.2	HK1;HBK4;PCN2;HPCN2;HUKII;KCNA8;KV1	potassium	voltage-	potassium
GI_25952086-S	151.4	197.9	185.5	KCNA5	NM_002234.2	HK2;HCK1;PCN1;HPCN1;KV1.5	delayed	voltage-	potassium
GI_25952089-S	108.8	132.7	118.8	KCNA6	NM_002235.2	HBK2;KV1.6	voltage-	voltage-	potassium
GI_25952091-S	103.3	93.9	108.1	KCNA7	NM_031886.2	HAK6;KV1.7	voltage-	voltage-	cation
GI_25952098-A	149.8	174.8	167.7	KCNMB3	NM_171828.1		potassium		
GI_25952098-I	150.9	165.8	153.8	KCNMB3	NM_171828.1		potassium		
GI_25952101-I	114.5	149.9	116.8	KCNMB3	NM_171829.1		potassium		
GI_25952104-I	153	193.5	170.4	KCNMB3	NM_171830.1		potassium		
GI_25952107-S	429.1	425.4	530.9	KCNS3	NM_002252.3	KV9.3;MGC9481	potassium	voltage-	potassium
GI_25952110-S	108.1	113.3	117.8	TNF	NM_000594.2	DIF;TNFA;TNFSF2;CACHECTIN	tumor	soluble	response
GI_25952117-A	93.7	116	106.5	CAMK2A	NM_171825.1	CAMKA;KIAA0968	calmoduli		protein
GI_25952121-S	424.2	421.6	330.9	BBS4	NM_033028.2				vision
GI_25952130-S	141.3	156.6	146.6	ADCY2	NM_020546.1	HBAC2;KIAA1060	adenylate	integral to	signal
GI_25952133-S	136.6	161.1	131.3	DISP1	NM_032890.2	DISPA;MGC13130;MGC16796;DKFZP434I04			
GI_25952136-S	137.8	135.5	114.4	CNTF	NM_000614.2	HCNTF	ciliary	extracellul	synaptic
GI_25952143-I	144.6	166.9	160.9	TNFSF14	NM_003807.2	LTg;TR2;HVEML;LIGHT	receptor	integral to	induction
GI_25952146-A	112.5	104.6	110.2	TNFSF14	NM_172014.1	LTg;TR2;HVEML;LIGHT	receptor	integral to	induction
GI_25952149-I	97	99.7	99	ALDH8A1	NM_022568.2	ALDH12;DJ352A20.2	oxidoredu		metabolis
GI_25952151-A	125.9	146.3	103.5	ALDH8A1	NM_170771.1	ALDH12;DJ352A20.2	oxidoredu		metabolis
GI_26006460-S	539.4	714	627.1	KIRREL3	NM_032531.1	KIRRE;NEPH2;KIAA1867			
GI_26006850-S	107.3	114.8	87.6	PDE8B	NM_003719.1		signal	cellular_co	cyclic
GI_26006854-S	212.1	250.3	221.1	FLJ30317	NM_172136.1				
GI_26024192-S	1380.1	1214.2	992.5	IMAGE34514	NM_053052.2				
GI_26024194-S	270.9	327.4	290.9	LOC84518	NM_032488.2				
GI_26024196-S	210	169.8	149.6	DGAT2	NM_032564.2				
GI_26024208-S	97.8	106.9	94.2	LOC51270	NM_016521.2		transcripti	transcripti	regulation
GI_26024216-A	211.6	252.1	226	NRAP	NM_006175.2		structural	actin	actin
GI_26024320-S	84.5	90.1	91.4	IL28A	NM_172138.1	IFNL2;IL-28A			
GI_26024324-S	196	221.7	211.6	IL29	NM_172140.1	IFNL1;IL-29			
GI_26024330-S	4906.9	7796.6	7287.7	TPI1	NM_000365.3	TPI	triose-		pentose-
GI_26024341-S	83.9	94.4	93.6	FLJ23356	NM_032237.2		ATP		protein
GI_26051203-I	86.5	96.8	79.9	CAMK2B	NM_001220.3	CAM2;CAMK2;CAMKB;MGC29528	calcium/ca		protein
GI_26051217-A	550.4	661.1	581.2	CAMK2B	NM_172084.1	CAM2;CAMK2;CAMKB;MGC29528	calcium/ca		protein

GI_26051219-S	667.1	594.9	476.4	CATSPER1	NM_053054.2	CATSPER;MGC33335;MGC33368	cation	integral to	cation
GI_26051226-A	138.2	137.1	128.8	CATSPER2	NM_172097.1	MGC33346			
GI_26051226-I	759.7	817.2	796.9	CATSPER2	NM_172097.1	MGC33346			
GI_26051230-I	2799.8	2474.9	1548.4	LACTB	NM_032857.2	G24;MRPL56;FLJ14902	structural	mitochond	
GI_26051232-A	855.4	883.5	531.3	LACTB	NM_171846.1	G24;MRPL56;FLJ14902	structural	mitochond	
GI_26051232-I	347.1	535	339.7	LACTB	NM_171846.1	G24;MRPL56;FLJ14902	structural	mitochond	
GI_26051234-S	862.8	881.2	765.9	NUP133	NM_018230.2	hNUP133;FLJ10814;MGC21133	nucleocyto	nucleus	transport
GI_26051236-S	402.2	374.9	343.9	NUP54	NM_017426.2	MGC13407		nuclear	nucleocyto
GI_26051238-S	956.1	1360.5	1129.5	TNFAIP1	NM_021137.3	B12;B61;EDP1;MGC2317	voltage-	membran	potassium
GI_26051239-S	442.4	684.1	520.2	TNFAIP2	NM_006291.2	B94		extracellul	angiogene
GI_26051241-S	191.5	241.8	193.8	TNFAIP3	NM_006290.2	A20;TNFA1P2	apoptosis	nucleus	apoptosis
GI_26051242-S	134.3	131.2	131.5	TNFAIP6	NM_007115.2	TSG6	hyaluronic	extracellul	signal
GI_26051249-A	473.6	579.7	515.8	TNFSF13	NM_172089.1	APRIL;TALL2;TWE-PRIL	receptor	membran	positive
GI_26051251-I	291	361.3	320.5	RASGRP4	NM_052949.2				
GI_26051257-A	109.8	125.3	116.4	RASGRP4	NM_170604.1				
GI_26051257-I	139.5	181.6	156.3	RASGRP4	NM_170604.1				
GI_26051259-I	89.4	83.9	93	KCNQ2	NM_004518.2	BFNC;EBN1;ENB1;HNSPC;KV7.2;KVEBN1	potassium	voltage-	potassium
GI_26051263-I	102	112.3	109.8	KCNQ2	NM_172107.1	BFNC;EBN1;ENB1;HNSPC;KV7.2;KVEBN1	potassium	voltage-	potassium
GI_26051267-A	96.7	94.9	86.1	KCNQ2	NM_172109.1	BFNC;EBN1;ENB1;HNSPC;KV7.2;KVEBN1	potassium	voltage-	potassium
GI_26051267-I	142.9	150.3	135.2	KCNQ2	NM_172109.1	BFNC;EBN1;ENB1;HNSPC;KV7.2;KVEBN1	potassium	voltage-	potassium
GI_26051270-A	116.7	126.7	122.3	KCNH2	NM_172056.1	ERG1;HERG;LQT2;HERG1;Kv11.1	potassium	voltage-	potassium
GI_26051270-I	112.1	122	110.3	KCNH2	NM_172056.1	ERG1;HERG;LQT2;HERG1;Kv11.1	potassium	voltage-	potassium
GI_26051272-I	120.3	122.2	118.8	KCNH2	NM_172057.1	ERG1;HERG;LQT2;HERG1;Kv11.1	potassium	voltage-	potassium
GI_26051274-S	277.6	244.2	203.7	KCNMB4	NM_014505.4		potassium	membran	potassium
GI_26051277-S	4111.4	3496.4	3521	POM121	NM_172020.1	MGC3792;KIAA0618;DKFZP586G1822;DKF			
GI_26080430-S	115.2	105.8	91.3	FLJ12735	NM_024857.3		nucleotide		
GI_26080432-S	476.8	488.3	701.2	DPP9	NM_139159.2	DPRP2	dipeptidyl-	membran	proteolysis
GI_26105977-S	625.1	801.5	610	CENPB	NM_001810.4		satellite	centromer	chromoso
GI_26190607-S	210.3	309.1	256.6	SYNJ2	NM_003898.1	INPP5H	inositol-	insoluble	signal
GI_26190609-S	105.2	98.7	106.1	ST6GalII	NM_032528.1	KIAA1877			
GI_26190613-S	109.8	134.7	135.8	PLEKHK1	NM_145307.2	RTKN2		intracellula	signal
GI_26190615-S	247.5	252.9	246.6	KLHDC1	NM_172193.1	MST025;c14_5298			
GI_26449156-S	99.7	94.2	91.2	TAC4	NM_170685.1	HK-1;Pptc;PPT-C			tachykinin
GI_26553431-S	394.2	420.6	455.4	DHX29	NM_019030.1	DDX29	nucleic		
GI_26638649-S	6042	4731.6	3400.9	KCNMA1	NM_002247.2	SLO;BKTM;MaxiK;SAKCA;KCa1.1;SLO-	calcium-	voltage-	potassium
GI_26638651-S	119.1	113.8	107.8	KCNQ3	NM_004519.2	EBN2;BFNC2;KV7.3	potassium	voltage-	potassium
GI_26638652-I	121.9	127.4	127.6	KCNQ4	NM_004700.2	DFNA2;KV7.4	potassium	voltage-	potassium
GI_26638654-A	112.5	109.1	95.2	KCNQ4	NM_172163.1	DFNA2;KV7.4	potassium	voltage-	potassium
GI_26638656-S	6641.5	7272.2	6526.3	MRPL20	NM_017971.2	L20mt;MGC4779;FLJ10024			
GI_26638658-S	754.5	894	769.8	MRPL40	NM_003776.2	URIM;NLVCF;MGC9400;MRP-L22	structural	nucleus	embryoge
GI_26638660-I	130.9	121.4	109.2	MSH5	NM_002441.2	NG23;MutSH5;C6orf26;MGC2939			meiotic
GI_26638661-I	227.8	260.3	232.5	MSH5	NM_025259.3	NG23;MutSH5;C6orf26;MGC2939			meiotic
GI_26638665-A	282.2	320.1	284	MSH5	NM_172166.1	NG23;MutSH5;C6orf26;MGC2939			meiotic
GI_26665868-S	298.2	376.5	229.6	TUWD12	NM_172240.1				

GI_26665874-S	82.9	93.7	84.3	GOR	NM_172239.1		exonuclea	intracellula	
GI_26665876-S	93.2	108.2	101.5	APBB1IP	NM_019043.2	RIAM;INAG1			neuropepti
GI_26665878-S	101.4	108.8	107.9	CTAGE-2	NM_172241.1				
GI_26665888-I	544.6	660.8	535.2	AK2	NM_013411.2	ADK2	adenylate	mitochond	
GI_26665889-I	2097.3	2892.9	2354.9	AK2	NM_001625.2	ADK2	adenylate	mitochond	
GI_26665890-A	1175.6	1547.3	1288.7	AK2	NM_172199.1	ADK2	adenylate	mitochond	
GI_26665892-S	290.8	500.9	362	HLA-DRB5	NM_002125.3		class II	integral to	perception
GI_26667164-S	636.5	658.8	793.3	MRPL38	NM_032478.2	RPML3;MRP-L3;HSPC262;MGC4810			
GI_26667166-A	987	1110.9	489.7	MRPL42	NM_014050.2	MRPS32;PTD007;RPML31;HSPC204;MRP-	structural	mitochond	protein
GI_26667176-S	1392.5	1296.7	1221.4	MRPL46	NM_022163.2	LIECG2;P2ECSL;C15orf4;MGC22762			
GI_26667179-A	295.3	200.3	151.8	CAMK2D	NM_001221.2	CAMKD;MGC44911			
GI_26667179-I	109.3	123.5	120.3	CAMK2D	NM_001221.2	CAMKD;MGC44911			
GI_26667182-I	89	83.5	90.5	CAMK2D	NM_172115.1	CAMKD;MGC44911			
GI_26667190-A	607.8	610.4	528.6	CAMK2G	NM_001222.2	CAMK;CAMKG;CAMK-II;MGC26678	calcium/ca		protein
GI_26667213-I	111.2	108.6	102.9	EYA1	NM_000503.3	BOP;BOR			hearing
GI_26667218-A	126.5	196.8	206.7	EYA1	NM_172059.1	BOP;BOR			hearing
GI_26667229-A	112.1	148	115.5	EYA2	NM_172110.1	EAB1;MGC10614			mesoderm
GI_26667231-I	144.4	176.1	150.5	EYA2	NM_172111.1	EAB1;MGC10614			mesoderm
GI_26667234-I	97.2	106.8	91.6	EYA2	NM_172112.1	EAB1;MGC10614			mesoderm
GI_26667239-I	91.4	90.4	89.2	EYA2	NM_172113.1	EAB1;MGC10614			mesoderm
GI_26667242-I	129.9	140.5	135.9	EYA3	NM_001990.2	DKFZp686C132	hydrolase		vision
GI_26667245-A	189.3	227.5	302.8	EYA3	NM_172098.1	DKFZp686C132	hydrolase		vision
GI_26667245-I	134.5	138.2	138.7	EYA3	NM_172098.1	DKFZp686C132	hydrolase		vision
GI_26667254-A	258.9	189.8	198.4	EYA4	NM_172104.1	DFNA10	hydrolase		vision
GI_26667256-I	119.1	111.5	117.3	EYA4	NM_172105.1	DFNA10	hydrolase		vision
GI_26787960-I	113	119.7	108.9	AGER	NM_001136.3	RAGE;MGC22357	transmem	integral to	response
GI_26787961-A	134.8	141.8	143.7	AGER	NM_172197.1	RAGE;MGC22357	transmem	integral to	response
GI_26787963-A	1133.1	1655.6	1159.2	AGPAT1	NM_032741.3	G15;LPAATA;MGC4007;MGC5423;1-	lysophosp	endoplas	phosphati
GI_26787963-I	98.4	91.8	89.8	AGPAT1	NM_032741.3	G15;LPAATA;MGC4007;MGC5423;1-	lysophosp	endoplas	phosphati
GI_26787964-I	198.3	236	211.4	AGPAT1	NM_006411.2	G15;LPAATA;MGC4007;MGC5423;1-	lysophosp	endoplas	phosphati
GI_26787965-A	106.3	103.8	86.2	ALF	NM_172196.1	MGC26254	RNA	nucleus	transcripti
GI_26787965-I	130.9	153.9	128.7	ALF	NM_172196.1	MGC26254	RNA	nucleus	transcripti
GI_26787969-S	210.5	250.4	233.7	CDSN	NM_001264.2	HTSS;D6S586E	cell	intercellula	epidermal
GI_26787971-S	5173.7	5582.4	4977.1	CSNK2B	NM_001320.5	G5A;CK2B;CK2N;CSK2B	protein	protein	signal
GI_26787973-S	275	375.8	572.2	HSPA1A	NM_005345.4	HSP72;HSPA1;HSP70-1	heat	cytoplasm	mRNA
GI_26787974-S	566.6	906.2	1264.3	HSPA1B	NM_005346.3	HSP70-2	heat	cytoplasm	heat
GI_26787975-S	1505.7	2162.6	2230.2	IL13RA1	NM_001560.2	NR4;IL-13RA	receptor	interleukin-	cell
GI_26787976-S	106.8	111.1	218.3	IL13RA2	NM_000640.2	IL-13R;IL13BP	interleukin	soluble	
GI_26787977-S	94.7	91.2	90.9	IL13	NM_002188.2	ALRH;P600;IL-13	cytokine	soluble	pathogene
GI_26787979-A	244.6	229.6	268.7	IL15	NM_000585.2	IL-15;MGC9721	cytokine	endosome	positive
GI_26787980-A	227.7	225.2	176.8	IL15RA	NM_002189.2		interleukin		signal
GI_26787980-I	124.3	121.8	111.1	IL15RA	NM_002189.2		interleukin		signal
GI_26787981-I	129.6	143.4	135.1	IL15RA	NM_172200.1		interleukin		signal
GI_26787983-I	182.3	197.4	185.5	IL15	NM_172174.1	IL-15;MGC9721	cytokine	endosome	positive

GI_26787985-I	148.4	139.5	127.3	IL15	NM_172175.1	IL-15;MGC9721	cytokine	endosome	positive
GI_26787987-S	190.9	240.7	219.1	MICB	NM_005931.2	PERB11.2	protein	integral to	cell
GI_26787990-S	321.8	273.3	222.8	NFKBIL1	NM_005007.2	IKBL;NFKBIL	transcripti		
GI_26787992-S	232.1	294.9	255.3	SBLF	NM_006873.2	STNB1	transcripti	clathrin	intracellula
GI_26892294-S	142.9	155.1	140.3	MMAA	NM_172250.1		ATP	mitochond	
GI_26986531-A	2155.8	2065.5	2213.1	EIF2B4	NM_015636.2	EIF2B;EIF-2B;EIF2Bdelta;DKFZP586J0119	translation	eukaryotic	translation
GI_26986533-S	1102.4	826.8	889.6	ARHGAP12	NM_018287.4	FLJ10971;FLJ20737;FLJ21785			
GI_27262621-S	1883.1	2799.9	2098.9	NAV1	NM_020443.2	POMFIL3;FLJ12560;FLJ14203;KIAA1151;M	nucleotide	membran	metabolis
GI_27262623-I	117.6	121.4	107.5	ABCA5	NM_018672.2	ABC13;EST90625	nucleotide	membran	transport
GI_27262625-A	145	138.7	139.9	ABCA5	NM_172232.1	ABC13;EST90625	nucleotide	membran	transport
GI_27262625-I	101.3	98.5	83.2	ABCA5	NM_172232.1	ABC13;EST90625	nucleotide	membran	transport
GI_27262629-A	431.5	633	686.8	NASP	NM_152298.2	FLB7527;MGC2297;PRO1999;FLJ31599;FLJ		nucleus	DNA
GI_27262631-S	679.5	480.4	458.4	C11orf11	NM_006133.1	NSDDR;KIAA0659	triacylglyc		lipid
GI_27262633-I	83.8	84.7	91.7	NASP	NM_172164.1	FLB7527;MGC2297;PRO1999;FLJ31599;FLJ		nucleus	DNA
GI_27262635-I	111	106.4	104.5	SPAG1	NM_003114.3	SP75;TPIS;HSD-3.8;FLJ32920	DNA	nucleus	fertilization
GI_27262637-A	111.4	120.9	101	SPAG1	NM_172218.1	SP75;TPIS;HSD-3.8;FLJ32920	DNA	nucleus	fertilization
GI_27262637-I	93.2	96.5	87.2	SPAG1	NM_172218.1	SP75;TPIS;HSD-3.8;FLJ32920	DNA	nucleus	fertilization
GI_27262639-I	91.7	105.4	102.2	SPAG6	NM_012443.2	pf16;MGC26276;Repro-SA-1;DKFZp434I153		axoneme	spermatid
GI_27262640-A	172	185.8	181.8	SPAG6	NM_172242.1	pf16;MGC26276;Repro-SA-1;DKFZp434I153		axoneme	spermatid
GI_27262642-A	850.4	1011.8	942.6	A2LP	NM_017492.2	A2D;A2LG;A2RP			
GI_27262646-I	128	131.4	120.6	A2LP	NM_007245.2	A2D;A2LG;A2RP			
GI_27262654-A	147.5	170.5	152	IL16	NM_004513.3	LCF;IL-16;prIL-16;HsT19289	cytokine	extracellul	chemotaxi
GI_27262656-I	145.3	176	157.8	IL16	NM_172217.1	LCF;IL-16;prIL-16;HsT19289	cytokine	extracellul	chemotaxi
GI_27262658-S	715.9	893.3	536.8	CSF1R	NM_005211.2	FMS;CSFR;FIM2;C-FMS;CD115	macropha	integral to	signal
GI_27262662-A	119.1	140.4	125.4	CSF1	NM_172210.1	MCSF;MGC31930	macropha	cellular_co	positive
GI_27262666-I	188.9	223	200.5	CSF1	NM_172212.1	MCSF;MGC31930	macropha	cellular_co	positive
GI_27312028-S	115.3	118.1	105	C14orf50	NM_172365.1				
GI_27312030-S	115.4	128.1	114.7	LOST1	NM_172367.1		DNA	nucleus	regulation
GI_27363459-S	122.6	122.9	117.4	C20orf143	NM_080750.2				
GI_27363460-S	1067.7	926.5	876.5	Magmas	NM_016069.8	CGI-136	molecular	mitochond	
GI_27363462-S	145.6	141.6	139.7	C20orf133	NM_080676.2	dJ631M13.5			
GI_27363466-A	170.2	159.6	175.2	PACE-1	NM_020423.4	PACE1	ATP		protein
GI_27363469-S	80	95.7	97	DAOA	NM_172370.1	G72			
GI_27363481-S	102.1	115.1	100.6	G30	NM_172368.1				
GI_27363485-S	108.6	115.8	111.8	TFAP2BL1	NM_172238.1		transcripti	nucleus	regulation
GI_27363487-S	157.4	173.2	161.3	C1QG	NM_172369.1	C1QC	defense/i	extracellul	compleme
GI_27369496-S	141.5	160.3	149.6	CHST2	NM_004267.2	C6ST	sulfotransf		developm
GI_27370564-S	131.6	116.3	196.1	AQP11	NM_173039.1		cysteine-	mitochond	transport
GI_27374999-S	2697.1	3172.8	3110.2	GABARAPL2	NM_007285.6	GEF2;GEF-2	actin	cytoskelet	intracellula
GI_27413157-S	103	115.3	103.5	SCUBE1	NM_173050.1		calcium	membran	blood
GI_27413907-S	342.1	431.3	401	GBA2	NM_020944.2	AD035;KIAA1605;MGC16895;DKFZp762K05			
GI_27414254-S	295.4	293.8	251.8	HSC20	NM_172002.2	HSCB;JAC1	co-		
GI_27414494-S	132.5	141.7	123.4	MT1B	NM_005947.1	MT1;MTP	heavy	cytoplasm	biological_
GI_27414496-S	1099.8	858.4	628.1	HSPC055	NM_014153.2	FLJ20318	nucleic		

GI_27436868-S	266.1	345.4	297.8	SPRR4	NM_173080.1				
GI_27436872-S	305.1	328.4	303.4	SHPRH	NM_173082.1	FLJ90837;KIAA2023	ATP	nucleus	nucleoso
GI_27436874-S	484	583.9	530.7	RUNDC1	NM_173079.1	DKFZp761H0421			
GI_27436876-S	105.3	109.3	96.3	TSBF1	NM_173084.1	MRF1	zinc ion	intracellula	
GI_27436878-S	99.8	82.7	92.9	ARMC3	NM_173081.1	FLJ25845;FLJ32827			
GI_27436880-S	369.2	468	383.1	EBAF	NM_003240.2	LEFTA;TGFB4;LEFTY2;LEFTYA;MGC46222	transformi		oocyte
GI_27436882-I	116.3	131.1	125.5	EHF	NM_012153.2	ESE3;ESEJ	tumor	nucleus	developm
GI_27436884-A	113.5	120.7	119.7	EHF	NM_172233.1	ESE3;ESEJ	tumor	nucleus	developm
GI_27436886-S	726.9	663.6	705.5	PBX2	NM_002586.3	G17;HOX12;PBX2MHC	DNA	nucleus	anterior
GI_27436888-I	418.7	445.7	669.6	POFUT1	NM_015352.1	FUT12;O-FUT;MGC2482;O-Fuc-	fucosyltra	integral to	fucose
GI_27436890-A	125.1	146.5	147.8	POFUT1	NM_172236.1	FUT12;O-FUT;MGC2482;O-Fuc-	fucosyltra	integral to	fucose
GI_27436890-I	114.4	123.9	136.2	POFUT1	NM_172236.1	FUT12;O-FUT;MGC2482;O-Fuc-	fucosyltra	integral to	fucose
GI_27436892-I	8300.4	7952.3	7620.4	TAPBP	NM_003190.3	TPN;TAPA;TPSN;NGS17	peptide	endoplas	immune
GI_27436894-I	134.6	136.8	126.6	TAPBP	NM_172208.1	TPN;TAPA;TPSN;NGS17	peptide	endoplas	immune
GI_27436896-A	234.3	266.9	237.1	TAPBP	NM_172209.1	TPN;TAPA;TPSN;NGS17	peptide	endoplas	immune
GI_27436898-S	113.3	116.6	123.2	TIMM13	NM_012458.2	ppv1;TIM13;TIM13B;TIMM13A;TIMM13B	zinc ion	mitochond	mitochond
GI_27436899-S	3268.9	2967.3	3083	TXN2	NM_012473.3	TRX2;MT-TRX	thioredoxi	mitochond	electron
GI_27436900-S	7067.3	7602	6461.1	MRPL12	NM_002949.2	5c5-	structural	mitochond	protein
GI_27436902-S	1269.7	1361.7	1290.5	MRPL16	NM_017840.2	L16mt;FLJ20484;PNAS-111			
GI_27436903-S	2111.9	2406.8	2490.7	MRPL23	NM_021134.2	RPL23;L23MRP;RPL23L	structural	mitochond	protein
GI_27436906-S	1229	1225.8	1284.8	MRPL49	NM_004927.2	NOF;NOF1;L49mt;MGC10656	structural	mitochond	cell growth
GI_27436907-S	910.3	947.8	1091.1	MRPL54	NM_172251.1				
GI_27436909-S	500.8	530.8	525.2	FLJ21816	NM_024675.2	DKFZp667I166			
GI_27436915-A	101.5	104.5	104	MINK	NM_015716.2	MGC21111	protein		JNK
GI_27436916-I	104.7	119	104.8	MINK	NM_153827.2	MGC21111	protein		JNK
GI_27436919-I	480.2	507	430.6	SPAG9	NM_003971.3	HSS;JLP;PHET;FLJ13450;FLJ14006;FLJ346		integral to	spermatog
GI_27436921-A	209.8	199.6	180.8	SPAG9	NM_172345.1	HSS;JLP;PHET;FLJ13450;FLJ14006;FLJ346		integral to	spermatog
GI_27436921-I	190.7	189.8	189.2	SPAG9	NM_172345.1	HSS;JLP;PHET;FLJ13450;FLJ14006;FLJ346		integral to	spermatog
GI_27436923-S	600.5	1188.5	869.5	HIST2H2AC	NM_003517.2	H2A/q;H2AFQ;H2A-GL101	DNA	chromoso	nucleoso
GI_27436924-A	1485.3	1756.8	1955.4	HRD1	NM_032431.1	KIAA1810;MGC40372			
GI_27436928-S	169.9	201.6	247.5	HSPA1L	NM_005527.2	hum70t;HSP70-HOM	heat		
GI_27436930-S	110.1	100.1	108.2	OTX1	NM_014562.2	FLJ38361;MGC15736	DNA	nucleus	brain
GI_27436931-I	129	148.1	137.7	OTX2	NM_021728.2	MGC45000	transcripti	nucleus	regulation
GI_27436932-A	86.3	89.1	89	OTX2	NM_172337.1	MGC45000	transcripti	nucleus	regulation
GI_27436935-A	184.4	226.7	207.4	OTX3	NM_172225.1	MBX;PAXB			
GI_27436939-A	115.6	108.8	102.2	RELN	NM_173054.1	RL	serine-	extracellul	cell
GI_27436941-S	20534.9	19335	14114	RPS27A	NM_002954.3	CEP80;UBA80;UBCEP1;HUBCEP80	structural	ribosome	protein
GI_27436942-S	783.6	697.5	727.5	RXRB	NM_021976.3	NR2B2;DAUDI6;RCoR-1;MGC1831;H-	retinoid-X	nucleus	regulation
GI_27436943-S	114.6	121.7	110.2	LEFTB	NM_020997.2	LEFTY1;LEFTYB	transformi		TGFbeta
GI_27436944-A	1849.4	3164.4	3486.5	LMNA	NM_005572.2	FPL;LFP;EMD2;FPLD;HGPS;LDP1;LMN1;LM	structural	nuclear	muscle
GI_27436944-I	2303	3221.4	4137.6	LMNA	NM_005572.2	FPL;LFP;EMD2;FPLD;HGPS;LDP1;LMN1;LM	structural	nuclear	muscle
GI_27436949-S	210.3	309	256.6	LMNB1	NM_005573.2	LMN;LMN2;LMNB	structural	nuclear	
GI_27436950-S	1869.9	2047	2266.7	LMNB2	NM_032737.2	LMN2;LAMB2;MGC2721		lamin	S-specific
GI_27436952-I	113.4	128.5	113.8	ABCA6	NM_080284.2	EST155051	nucleotide	membran	transport

GI_27436954-A	110.5	110.3	104.6	ABCA6	NM_172346.1	EST155051	nucleotide	membran	transport
GI_27436956-S	279.6	311.4	312.9	AIP1	NM_012301.2	ARIP1;MAGI-2;ACVRIP1;KIAA0705	protein		intracellula
GI_27436958-S	220.7	232.1	225	ALMS1	NM_015120.2	ALSS;KIAA0328			
GI_27436961-I	93.3	107.5	95.7	KCNAB1	NM_003471.2	hKvb3;AKR6A3;KCNA1B;Kvb1.3;hKvBeta3;K	potassium	integral to	potassium
GI_27436963-I	111	133.1	116.2	KCNAB1	NM_172159.1	hKvb3;AKR6A3;KCNA1B;Kvb1.3;hKvBeta3;K	potassium	integral to	potassium
GI_27436965-A	149.3	158.3	159.2	KCNAB1	NM_172160.1	hKvb3;AKR6A3;KCNA1B;Kvb1.3;hKvBeta3;K	potassium	integral to	potassium
GI_27436965-I	75.8	86.6	82.6	KCNAB1	NM_172160.1	hKvb3;AKR6A3;KCNA1B;Kvb1.3;hKvBeta3;K	potassium	integral to	potassium
GI_27436968-A	240.3	275.8	253	KCNAB2	NM_172130.1	AKR6A5;KCNA2B;HKvbeta2;KV-BETA-	potassium	integral to	potassium
GI_27436970-S	158.2	175.9	170.3	KCNAB3	NM_004732.2	AKR6A9;KCNA3B;KCNA3.1B;KV-BETA-3	potassium	integral to	potassium
GI_27436972-S	99.3	95.2	95.3	KCNB1	NM_004975.2	DRK1;KV2.1;h-DRK1	delayed	voltage-	cation
GI_27436973-S	95.4	94.5	88.9	KCNB2	NM_004770.2	KV2.2	delayed	voltage-	potassium
GI_27436975-S	124.1	125.6	117	KCNE1L	NM_012282.2	KCNE5		voltage-	regulation
GI_27436977-S	102.9	104.3	99.8	KCNE2	NM_172201.1	LQT5;LQT6;MIRP1	voltage-	voltage-	potassium
GI_27436979-S	109.9	140.2	116.7	KCNE3	NM_005472.2	HOKPP;MiRP2	voltage-	voltage-	potassium
GI_27436980-S	347.3	480.6	280.3	KCND1	NM_004979.3	KV4.1	protein	voltage-	cation
GI_27436982-S	103.2	129.1	105.9	KCND2	NM_012281.2	RK5;KV4.2;KIAA1044	voltage-	voltage-	cation
GI_27436983-I	116.7	140.6	135.4	KCND3	NM_004980.3	KV4.3;KCND3L;KCND3S;KSHIVB	A-type	voltage-	potassium
GI_27436985-A	441.3	529.4	492	KCND3	NM_172198.1	KV4.3;KCND3L;KCND3S;KSHIVB	A-type	voltage-	potassium
GI_27436987-A	154.3	125.9	98.9	KCNG1	NM_002237.2	K13;KH2;KCNG;KV6.1;MGC12878	potassium	voltage-	potassium
GI_27436987-I	428.9	316.5	245.5	KCNG1	NM_002237.2	K13;KH2;KCNG;KV6.1;MGC12878	potassium	voltage-	potassium
GI_27436989-I	107.4	119	109.4	KCNG1	NM_172318.1	K13;KH2;KCNG;KV6.1;MGC12878	potassium	voltage-	potassium
GI_27436992-A	97.5	96.9	97.4	KCNG3	NM_172344.1	KV6.3;KV10.1	voltage-	voltage-	cation
GI_27436994-I	129.7	155.3	130.1	KCNG4	NM_133490.2	KV6.3;KV6.4;MGC4558	voltage-	voltage-	cation
GI_27436995-A	178.1	214.3	184.5	KCNG4	NM_172347.1	KV6.3;KV6.4;MGC4558	voltage-	voltage-	cation
GI_27436995-I	132.7	136.8	143.4	KCNG4	NM_172347.1	KV6.3;KV6.4;MGC4558	voltage-	voltage-	cation
GI_27436997-S	151.7	162	141	KCNA10	NM_005549.2	Kcn1;Kv1.8	intracellula	voltage-	potassium
GI_27436998-S	142.4	194.8	164.9	KCNF1	NM_002236.4	IK8;KH1;KCNF;KV5.1;MGC33316	potassium	voltage-	potassium
GI_27436999-A	127.4	134.8	126.8	KCNH1	NM_002238.2	EAG;EAG1;h-eag;Kv10.1	delayed	voltage-	myoblast
GI_27437000-I	78	78	80.3	KCNH1	NM_172362.1	EAG;EAG1;h-eag;Kv10.1	delayed	voltage-	myoblast
GI_27437002-A	158.4	132.8	153.9	KREMEN2	NM_024507.2	KRM2;MGC10791;MGC16709	oxidoredu	integral to	metabolis
GI_27437005-I	166.9	191.4	163	KREMEN2	NM_145348.1	KRM2;MGC10791;MGC16709	oxidoredu	integral to	metabolis
GI_27437012-A	123.4	135.9	133.9	CAMKK1	NM_172207.1	CAMKKA;MGC34095;DKFZp761M0423			
GI_27437012-I	148.9	169	175.3	CAMKK1	NM_172207.1	CAMKKA;MGC34095;DKFZp761M0423			
GI_27437022-A	286.9	305.8	216	CAMKK2	NM_172215.1	CAMKK;CAMKKB;KIAA0787;MGC15254			
GI_27437029-S	168.6	154.9	232.5	CSF2	NM_000758.2	GMCSF	granulocyt	extracellul	cell
GI_27437039-A	193.1	336.6	356.1	CSF2RA	NM_172249.1	GMR;CD116;CDw116;CSF2RX;CSF2RY;GM	receptor	integral to	antimicrob
GI_27437043-I	104.5	107.5	98.9	CSF3R	NM_156039.2	CD114;GCSFR	receptor	integral to	defense
GI_27437044-A	216.5	253.4	190.1	CSF3R	NM_172313.1	CD114;GCSFR	receptor	integral to	defense
GI_27437048-A	95.5	113.9	96.4	CSF3	NM_172219.1	GCSF;G-CSF;MGC45931	granulocyt	extracellul	positive
GI_27437050-I	103.7	112.9	101.6	CSF3	NM_172220.1	GCSF;G-CSF;MGC45931	granulocyt	extracellul	positive
GI_27475984-S	131.5	129.2	134.5	NEUROD6	NM_022728.2	Atoh2;NEX1M;Math-2	DNA	nucleus	regulation
GI_27477040-S	673	1103.8	639.8	AP2A2	NM_012305.1	HIP9;HYPJ;ADTAB;CLAPA2;KIAA0899;DKF	molecular	coated pit	intracellula
GI_27477044-A	429.2	452.1	375.6	MT	NM_014507.1	MGC47838;bK1191B2.3			
GI_27477048-S	86.2	87.8	87	ASB17	NM_080868.1	Asb-17			intracellula

GI_27477058-S	2557.2	4050.7	3703	FAD104	NM_022763.2	FLJ23399;DKFZp762K137	hematopoi	membran	
GI_27477060-S	112	108.8	92.7	CMYA4	NM_173167.1	UNC45			
GI_27477065-S	123.9	122.3	119.8	SPCX	NM_173168.1				
GI_27477067-S	369.5	426.3	365.7	AFG3L1	NM_001132.1	AFG3			
GI_27477069-S	183.1	183.2	166	BTAF1	NM_003972.1	MOT1;TAF172;TAFII170;TAF(II)170	transcripti	transcripti	regulation
GI_27477073-A	127	150.9	139.2	IL17RB	NM_018725.2	CRL4;EVI27;IL17BR;IL17RH1;MGC5245	interleukin	integral to	defense
GI_27477075-I	99.5	107.3	93.1	IL17RB	NM_172234.1	CRL4;EVI27;IL17BR;IL17RH1;MGC5245	interleukin	integral to	defense
GI_27477077-S	117.2	136.1	123.3	IL17B	NM_014443.2	IL-20;IL-17B;ZCYTO7	cytokine	nucleus	immune
GI_27477078-S	182.1	220.9	181.7	IL17C	NM_013278.3	CX2;IL-21;IL-17C	cytokine	soluble	cell
GI_27477079-I	99	104.7	98.6	IL17E	NM_022789.2	IL25;IL-25;IL-17E	cytokine	membran	biological_
GI_27477080-A	145.3	149.1	139.9	IL17E	NM_172314.1	IL25;IL-25;IL-17E	cytokine	membran	biological_
GI_27477082-A	166.1	192.7	185.7	IL17F	NM_052872.2	ML1;IL24;ML-1;IL-24;IL-26;IL-17F	cytokine		
GI_27477083-I	101.7	112.1	112.9	IL17F	NM_172343.1	ML1;IL24;ML-1;IL-24;IL-26;IL-17F	cytokine		
GI_27477085-S	106.6	117.5	94.2	IL17	NM_002190.2	CTLA8;IL-17;IL-17A	cytokine	extracellul	cell death
GI_27477086-S	203.9	107.7	83.7	IL18R1	NM_003855.2	IL1RRP;IL-1Rrp	receptor	integral to	signal
GI_27477087-S	111.4	115.5	91.1	IL18RAP	NM_003853.2	ACPL	receptor	membran	cell
GI_27477088-I	122.6	125.8	131.3	IL4I1	NM_172374.1	FIG1	amine		electron
GI_27477091-A	115.8	112.6	108.3	IL4	NM_172348.1	BSF1;IL-4	interleukin-	extracellul	chemotaxi
GI_27477093-I	236.8	284.6	249.7	NSD1	NM_022455.3	STO;SOTOS;ARA267;FLJ22263	DNA	nucleus	cell growth
GI_27477094-A	123.3	138.7	133.3	NSD1	NM_172349.1	STO;SOTOS;ARA267;FLJ22263	DNA	nucleus	cell growth
GI_27477096-I	530	687.7	593.6	CGI-85	NM_017635.2	MGC703;FLJ20039;MGC21161			
GI_27477098-A	370.1	314.7	277.4	CGI-85	NM_016028.3	MGC703;FLJ20039;MGC21161			
GI_27477098-I	1261.5	953.7	956.7	CGI-85	NM_016028.3	MGC703;FLJ20039;MGC21161			
GI_27477099-I	92.9	106.6	102.4	SGCD	NM_000337.3	SGD;DAGD;35DAG;CMD1L;MGC22567;SG-		sarcoglyca	muscle
GI_27477100-A	135.1	148.5	143.1	SGCD	NM_172244.1	SGD;DAGD;35DAG;CMD1L;MGC22567;SG-		sarcoglyca	muscle
GI_27477100-I	66.7	79.7	74.9	SGCD	NM_172244.1	SGD;DAGD;35DAG;CMD1L;MGC22567;SG-		sarcoglyca	muscle
GI_27477104-S	90.1	80.6	86.8	BG1	NM_015162.3	BGM;FLJ30320;MGC14352	catalytic		metabolis
GI_27477108-S	263.2	296.9	295.9	ITCH	NM_031483.3	AIF4;AIP4;NAPP1	ubiquitin-	nucleus	ubiquitin
GI_27477110-S	884.5	889.7	816.9	SLU7	NM_006425.3	MGC9280	pre-mRNA	nucleus	mRNA
GI_27477112-S	1035.8	1116.5	850.9	SREBF2	NM_004599.2	SREBP2	RNA	Golgi	lipid
GI_27477116-A	94	111.8	97.5	ABCA9	NM_172386.1	EST640918	nucleotide	membran	transport
GI_27477118-S	170	205.4	172.6	CAMK4	NM_001744.3	CaMK-GR;MGC36771	calcium/ca		protein
GI_27477119-S	2825	2477	2211	CORO1C	NM_014325.2	HCRNN4;coronin-3	cell	kinesin	phagocyto
GI_27477120-I	151.2	162.1	135.8	ICK	NM_014920.2	MRK;LCK2;KIAA0936;MGC46090	protein		protein
GI_27477123-A	97	101.9	92.3	ICK	NM_173041.1	MRK;LCK2;KIAA0936;MGC46090	protein		protein
GI_27477125-S	4084.4	3025	3056.1	KPNA4	NM_002268.3	QIP1;SRP3;IPOA3;MGC12217;MGC26703		importin,	NLS-
GI_27477126-S	422.7	488.7	473.1	KRTHB2	NM_033033.3	HB2;Hb-2	structural	cellular_co	biological_
GI_27477128-S	359.9	302	393.9	MC1R	NM_002386.2	MSH-R;MGC14337	melanocor	integral to	UV
GI_27477130-S	2754	3410.9	3106.1	MRPL17	NM_022061.2	RPL17L;RPML26;MRP-L26	structural	ribosome	protein
GI_27477131-S	404.7	375.3	391.3	PIP3AP	NM_019061.2	3-PAP;FLJ20476;KIAA1682			
GI_27477133-S	136.2	158.7	149.5	NUP210	NM_024923.2	GP210;POM210;FLJ22389;KIAA0906			
GI_27477137-A	205.3	257.8	283.2	ZC3HAV1	NM_024625.3	ZAP;FLB6421;ZC3HDC2;FLJ13288;MGC488			
GI_27477137-I	151.9	176.1	208.6	ZC3HAV1	NM_024625.3	ZAP;FLB6421;ZC3HDC2;FLJ13288;MGC488			
GI_27477259-S	105.1	129.9	110.1	LOC149620	XM_086604.3				

GI_27477322-S	176.6	153	122.7	LOC166867	XM_094142.3	
GI_27477379-S	97.6	98.5	104.5	LOC284968	XM_211707.1	
GI_27477392-S	103.4	98.4	103.8	LOC200373	XM_114222.2	
GI_27477438-S	115.3	150.3	123.7	LOC285205	XM_211805.1	
GI_27477501-S	239.6	271.8	237.5	LOC91181	XM_036740.4	
GI_27477609-S	89	96.6	90.4	LOC285307	XM_211837.1	
GI_27477614-S	140.3	137.8	132.9	LOC285110	XM_211768.1	
GI_27477654-S	240.9	261.3	241.8	LOC285311	XM_209563.1	
GI_27477683-S	104.5	106.8	100.6	LOC92196	XM_043500.3	
GI_27477684-S	746.9	905.2	695	KIAA1728	XM_043492.3	
GI_27477709-S	658.2	427.6	430.7	DKFZp434D0	XM_098238.6	
GI_27477718-S	136.4	134.7	128.7	SFRP2	XM_050625.2	
GI_27477737-S	250.6	274.6	210.6	KIAA1374	XM_028413.6	
GI_27477767-S	426.1	224	137.9	LOC150946	XM_097977.2	
GI_27477792-S	111.4	118.2	119.3	LOC285320	XM_210557.1	
GI_27477860-S	152.7	181.9	181.6	LOC285324	XM_210559.1	
GI_27477864-S	96.6	93.8	82.1	LOC285326	XM_211843.1	
GI_27477986-S	105	132.8	99.5	LOC285141	XM_209489.1	
GI_27478003-S	108	117.9	106.5	LOC151760	XM_098117.3	
GI_27478061-S	105.4	114.6	107.7	DKFZP434B1	XM_046264.6	
GI_27478065-S	141.4	147.4	140.7	LOC285344	XM_211853.1	
GI_27478147-S	304.8	303.4	344.6	LOC138428	XM_059972.6	
GI_27478170-S	265.4	289.5	292.7	LOC131909	XM_067605.3	
GI_27478393-S	337.3	311.8	315.7	LOC285919	XM_212094.1	
GI_27478465-S	76.2	77.4	77.3	LOC255220	XM_171207.2	
GI_27478473-S	95.4	100.2	96.5	KIAA1962	XM_088567.5	
GI_27478680-S	101.4	101.2	103.2	LOC286114	XM_212178.1	
GI_27478728-S	152.1	165.5	151.9	LOC149643	XM_086616.2	
GI_27478738-S	1102.1	706.2	828	LOC286343	XM_210019.1	MGC46502
GI_27478846-S	107.1	116.6	108.5	LOC136242	XM_059830.4	
GI_27478849-S	123.6	134.8	131.1	LOC375748	XM_088578.6	
GI_27478973-S	192.6	224.2	203.7	LOC284623	XM_211557.1	
GI_27479013-S	139.1	136.6	134.1	LOC285694	XM_211983.1	
GI_27479022-S	115.8	126.9	114.2	LOC285697	XM_210642.1	
GI_27479090-S	108.1	112.3	98.7	LOC157813	XM_098828.2	
GI_27479107-S	108.3	104.4	109	LOC286187	XM_209936.1	
GI_27479150-S	90.3	99.4	100.8	SV2C	XM_043493.5	
GI_27479154-S	94.5	87.3	96	LOC285711	XM_211988.1	
GI_27479226-S	1083.6	1608.4	838.6	ZNF36	XM_168302.2	
GI_27479240-S	100.5	87.5	91.8	LOC285995	XM_212123.1	
GI_27479310-S	100.3	93.3	95.5	LOC285721	XM_211995.1	
GI_27479404-S	155.3	151.4	121.6	LOC283553	XM_211086.1	
GI_27479422-S	234.4	252.8	283.9	C14orf35	XM_058661.6	
GI_27479430-S	2774.5	3041.5	2812.3	KIAA1393	XM_050793.4	

GI_27479432-S	131.6	157.1	141.2	LOC161291	XM_090844.2	
GI_27479471-S	389.5	837	543.7	KIAA1130	XM_031104.5	
GI_27479546-S	113.8	106.3	106	LOC283583	XM_211092.1	
GI_27479548-S	93.3	92.2	87.6	LOC283584	XM_211108.1	
GI_27479552-S	98.5	96.6	92.8	LOC283586	XM_211089.1	
GI_27479554-S	107.8	101.5	109.2	LOC283587	XM_211090.1	
GI_27479730-S	150	163.3	155.1	LOC285423	XM_209604.1	
GI_27479781-S	94.4	103.2	88.4	LOC203806	XM_114973.3	
GI_27479816-S	101.4	101.4	97.6	LOC253017	XM_171068.2	
GI_27479851-S	82.8	99.1	82.3	LOC284532	XM_210119.1	
GI_27479896-S	227.3	257.9	227.1	LOC285018	XM_210394.1	
GI_27479970-S	185.4	141.2	136.5	KIAA1604	XM_034594.7	
GI_27480047-S	94.4	90.1	95	LOC255130	XM_173119.2	
GI_27480070-S	95.7	102.7	97.2	LOC254827	XM_173084.2	
GI_27480158-S	210.8	247.4	192	LOC255798	XM_173087.2	
GI_27480483-S	103.9	101.3	102.9	LOC285501	XM_209640.1	
GI_27480510-S	259.9	364.8	326.9	LOC284646	XM_211573.1	
GI_27480565-S	154.3	166	155.8	LOC285509	XM_211923.1	
GI_27480622-S	135.4	142.4	139.8	LOC285510	XM_209643.1	
GI_27480767-S	121.7	125.4	107.8	LOC285299	XM_209554.1	
GI_27480778-S	274.6	321.8	321.9	LOC286224	XM_209959.1	
GI_27480863-S	234.2	238.2	241.7	KIAA0375	XM_048462.4	
GI_27480910-S	2371.5	1999.8	1933.5	LOC286257	XM_209971.1	
GI_27481114-S	223.5	253.5	230.6	LOC285890	XM_212067.1	
GI_27481123-S	1414.9	1220.7	1353.2	KIAA1078	XM_036589.3	
GI_27481171-S	375.8	475.8	432.1	SMYD5	XM_039548.3	
GI_27481242-S	276.7	311.5	293.1	LOC285435	XM_211896.1	
GI_27481296-S	105.6	107.3	103.8	LOC255654	XM_173036.2	
GI_27481390-S	109.9	108.7	96	LOC164045	XM_089318.2	
GI_27481457-S	117.1	115.4	113	LOC127391	XM_059140.3	
GI_27481474-S	101.6	104.9	103.4	LOC285382	XM_211871.1	
GI_27481547-S	967.3	1077.7	618.3	PRICKLE2	XM_093799.2	DKFZp686D143
GI_27481826-S	97.8	93.8	91.2	LOC286076	XM_209889.1	
GI_27481852-S	90.5	105.9	83.6	DKFZp434H2	XM_043863.4	
GI_27481868-S	171.6	191.3	182.2	LOC133923	XM_068602.3	
GI_27481869-S	138.9	167.9	139.2	LOC153441	XM_087671.3	
GI_27481917-S	138.9	162.2	150.4	LOC118461	XM_060969.2	
GI_27481959-S	116.7	128	127.3	LOC153364	XM_087657.4	MGC46734
GI_27482200-S	98.8	98.8	84	LOC142910	XM_084377.3	
GI_27482549-S	183.9	222.4	201.6	LOC283530	XM_211079.1	
GI_27482629-S	92.4	100.3	113.6	DKFZp547H0	XM_085234.2	
GI_27482679-S	160.2	172.8	171.8	LOC283071	XM_208502.1	
GI_27482725-S	92	99.9	94.3	C6orf212	XM_069035.4	
GI_27482800-S	341.4	352.9	339.7	ZNF18	XM_085596.3	

GI_27482884-S	120.1	128.2	125.2	LOC222553	XM_167044.2	
GI_27482991-S	613.2	653.6	552.6	LOC284064	XM_210334.1	
GI_27482999-S	106.1	116.6	101	LOC284067	XM_208990.1	
GI_27483117-S	96.2	102.4	91.8	LOC123722	XM_058721.6	
GI_27483409-S	94.8	105.4	82	FLJ40311	XM_064190.2	
GI_27483466-S	877.8	1103.7	1009.2	LOC283710	XM_211174.1	
GI_27483536-S	98.9	95.7	94.1	LOC283724	XM_208806.1	
GI_27483643-S	200.1	236.4	224.6	LOC285770	XM_209753.1	
GI_27483664-S	95.1	95.9	93.4	LOC285777	XM_212013.1	
GI_27484056-S	786.5	1150.2	1336.8	LOC284120	XM_211339.1	
GI_27484243-S	174.5	190.6	161.9	LOC197135	XM_113825.2	
GI_27484363-S	1025	633.5	582.2	LOC284134	XM_211345.1	
GI_27484425-S	608	533.6	482.8	SYTL3	XM_087804.2	
GI_27484664-S	429.5	485.2	449.5	LOC283780	XM_211197.1	
GI_27484731-S	390.1	461.7	872.3	KIAA1944	XM_062545.5	
GI_27484970-S	99.7	98	88.6	LOC283365	XM_210242.1	
GI_27485028-S	118.7	136	132.4	FLJ35258	XM_209112.1	
GI_27485046-S	484.7	457.3	495.3	LOC126208	XM_058999.7	
GI_27485087-S	110.1	116.4	105.1	LOC284275	XM_211413.1	
GI_27485109-S	163.5	175.5	169.5	LOC283129	XM_208524.1	
GI_27485197-S	114.4	107.6	97.9	KIAA1829	XM_030378.2	
GI_27485201-S	123.3	132.1	115.3	LOC284318	XM_209149.1	
GI_27485203-S	143.7	136.7	145.9	IMUP	XM_085984.4	H2RSP
GI_27485209-S	123.9	129.7	133.2	LOC284321	XM_211432.1	
GI_27485221-S	199.8	266.5	232.7	TIM50L	XM_053074.6	
GI_27485260-S	185	170.9	184.7	LOC284345	XM_209138.1	
GI_27485266-S	120.7	119.1	109.2	LOC126298	XM_065026.2	
GI_27485310-S	314.6	309.5	330.6	ZFP100	XM_046390.5	
GI_27485318-S	335.6	438	375.7	LOC284363	XM_209145.1	
GI_27485347-S	281.6	301.2	323.2	LOC90317	XM_030892.2	
GI_27485351-S	388.1	370.3	347.5	LOC90321	XM_030896.3	
GI_27485378-S	108	122	121.7	LOC284293	XM_209104.1	
GI_27485393-S	174.5	212.9	191.6	MGC41903	XM_058956.6	
GI_27485409-S	215.5	251	218.1	LOC284383	XM_210382.1	
GI_27485419-S	125.7	122.3	148.3	LOC162993	XM_091914.2	
GI_27485472-S	329.7	263.6	223.7	FLJ00012	XM_058426.7	
GI_27485564-S	172.2	206.4	188.6	LOC283403	XM_211028.1	
GI_27485586-S	215	240.1	225.9	KIAA1442	XM_044921.4	
GI_27485636-S	159.1	201.6	171.5	LOC283425	XM_208665.1	
GI_27485880-S	115.2	120	168.8	LOC139067	XM_066457.2	
GI_27486035-S	106.2	191.3	120.7	LOC203569	XM_114723.2	
GI_27486087-S	178.5	221.7	192.9	LOC162073	XM_091331.2	
GI_27486123-S	231.8	223.1	180	KIAA0819	XM_032996.4	
GI_27486196-S	91.2	85.4	91.9	LOC286441	XM_212319.1	

GI_27486209-S	136.9	162.1	134.6	BEAN	XM_085374.2
GI_27486285-S	289.3	339	308	LOC284931	XM_211694.1
GI_27486596-S	170.1	203.1	187	LOC170242	XM_093201.2
GI_27497798-S	164.7	170.1	155.6	LOC148640	XM_086257.2
GI_27497804-S	163.6	166.6	150.7	LOC284527	XM_211509.1
GI_27497918-S	152	171.2	174.1	LOC151363	XM_087182.2
GI_27497943-S	114.4	123.4	114.9	KIAA1486	XM_041126.5
GI_27498044-S	98.9	92.9	102.7	KIAA0935	XM_052620.7
GI_27498253-S	113.4	116.5	99.6	LOC133993	XM_068632.3
GI_27498268-S	101.5	99.2	98	FLJ40584	XM_069189.2
GI_27498358-S	153.5	162.7	149	IRAK1BP1	XM_059729.3
GI_27498382-S	204.2	228.1	228.9	LOC285793	XM_212022.1
GI_27498388-S	150.5	168.5	165.9	LOC168002	XM_094794.2
GI_27498432-S	115.6	115.2	105.7	LOC254751	XM_173173.2
GI_27498465-S	152.4	148.4	126.7	LOC222701	XM_167152.3
GI_27498471-S	224.1	263.7	238.9	ZNF453	XM_167147.2
GI_27498545-S	288.2	442.5	521.9	LOC154467	XM_166346.2
GI_27498554-S	146.7	170.8	151.6	LOC222642	XM_167072.3
GI_27498571-S	528.5	508.1	386	KIAA0240	XM_166479.2
GI_27498864-S	185	204.1	182	BA526D8.4	XM_046861.2
GI_27498920-S	101	112.2	102.6	LOC255022	XM_171370.2
GI_27498926-S	174.2	186.2	127.3	FLJ35908	XM_089747.2
GI_27498946-S	368.9	481.7	417.7	MRF2	XM_084482.3
GI_27499036-S	93.5	93.3	91	LOC283065	XM_210876.1
GI_27499039-S	98.5	113.1	135.5	DKFZp667B0	XM_171410.2
GI_27499073-S	304.2	365.3	337.6	KIAA0298	XM_084529.6
GI_27499130-S	184.9	198.3	186.3	KIAA1201	XM_208530.1
GI_27499140-S	185.3	232.3	207.3	LOC283162	XM_210186.1
GI_27499154-S	147.1	161.4	140.1	LOC283166	XM_210906.1
GI_27499230-S	139.7	166.6	138.3	LOC219527	XM_166856.3
GI_27499430-S	137	156	147.9	LOC283297	XM_208604.1
GI_27499434-S	337.8	476.6	477.5	PPFIBP2	XM_084578.6
GI_27499637-S	102.2	100.2	91.1	LOC283440	XM_211040.1
GI_27499680-S	2814.9	2953	2703.2	GCN1L1	XM_045792.8
GI_27500051-S	109.6	122.2	111	LOC283895	XM_211244.1
GI_27500171-S	200.4	224.4	217.1	KIAA0339	XM_049380.2
GI_27500290-S	88	83.5	88.1	LOC283994	XM_211291.1
GI_27500473-S	182.3	219.6	206.1	LOC284158	XM_209041.1
GI_27500527-S	116	138.4	115	LOC284184	XM_211367.1
GI_27500713-S	100.6	118.1	119.6	LOC284307	XM_209111.1
GI_27500767-S	84.5	95.7	81	LOC284379	XM_209163.1
GI_27500805-S	118.5	130.1	118	LOC126167	XM_058997.5
GI_27500902-S	261.2	305.3	297.5	DKFZp761G1	XM_036218.4
GI_27501092-S	226.9	274.7	250.1	LOC150051	XM_097792.2

GI_27501193-S	115.8	124.5	106.9	LOC91353	XM_018487.3				
GI_27501210-S	108.6	93.2	99.1	LOC284901	XM_209408.1				
GI_27501258-S	442	602.8	547.8	KIAA1093	XM_039385.2				
GI_27501300-S	174.9	214.1	194.7	FLJ20573	XM_033853.2				
GI_27501317-S	111.5	112.7	114	KIAA1202	XM_050478.2				
GI_27501414-S	173.9	189.6	171.9	LOC286478	XM_212326.1				
GI_27501445-S	2382.9	2135.6	1038.8	DENR	NM_003677.2	DRP;DRP1;SMAP-3	translation	cellular_co	intracellula
GI_27501451-S	122.3	131.5	137.3	SPRY3	NM_005840.1	HSPRY3	molecular	membran	histogene
GI_27501455-S	190.5	199.9	184.6	CHDH	NM_018397.1		oxidoredu		electron
GI_27501457-S	929.7	596.4	666.5	CHTF18	NM_022092.1	CHL12;Ctf18;C16orf41;C321D2.4	nucleotide	DNA	DNA
GI_27501463-S	312.1	379	339.7	STK29	NM_003957.1	BRSK2;PEN11B;C11orf7	cAMP-		protein
GI_27502371-I	83.8	91.6	94.4	SPAG8	NM_012436.2	SMP1;BS-84;HSD-1;SPAG3;hSMP-			
GI_27502372-A	113	125.3	117.2	SPAG8	NM_172312.1	SMP1;BS-84;HSD-1;SPAG3;hSMP-			
GI_27502374-I	96.5	87.1	87.8	MEIS2	NM_002399.2	MRG1;MGC2820;HsT18361	transcripti		negative
GI_27502380-A	301.3	402	495.6	MEIS2	NM_172315.1	MRG1;MGC2820;HsT18361	transcripti		negative
GI_27502382-I	109.8	129.8	120.2	MEIS2	NM_172316.1	MRG1;MGC2820;HsT18361	transcripti		negative
GI_27502385-I	97.7	97.3	90.2	NFATC1	NM_172387.1	NFAT2;NFATC;NF-ATC	transcripti	nucleus	transcripti
GI_27502389-S	492.6	609.3	506.9	IL18	NM_001562.2	IGIF;IL-18;IL-1g;IL1F4;MGC12320	cytokine	extracellul	immune
GI_27502392-A	99.9	99.6	97.6	NFATC1	NM_172390.1	NFAT2;NFATC;NF-ATC	transcripti	nucleus	transcripti
GI_27502392-I	119.6	144	127.5	NFATC1	NM_172390.1	NFAT2;NFATC;NF-ATC	transcripti	nucleus	transcripti
GI_27502394-I	98.7	100.5	115.3	IL18BP	NM_005699.2	IL18BPa	signal	soluble	immune
GI_27502399-A	105.4	95.9	94.6	IL18BP	NM_173044.1	IL18BPa	signal	soluble	immune
GI_27502399-I	97.8	112.3	92.7	IL18BP	NM_173044.1	IL18BPa	signal	soluble	immune
GI_27502404-A	2240.6	2331.3	2514.6	MCP	NM_172350.1	TLX;CD46;MIC10;TRA2.10;MGC26544	receptor	integral to	virulence
GI_27502428-S	79.6	85.3	81.2	ABCA10	NM_080282.2	EST698739			
GI_27532981-I	262.6	233.8	254.8	C10orf6	NM_018121.2	FLJ10512;FLJ25012			
GI_27532983-A	409.7	469.3	333.2	MIZ1	NM_173206.1	SIZ2;PIASX-BETA;PIASX-ALPHA	zinc ion	nucleus	
GI_27532983-I	78.1	77.6	78.3	MIZ1	NM_173206.1	SIZ2;PIASX-BETA;PIASX-ALPHA	zinc ion	nucleus	
GI_27544926-S	190.5	229.1	224	ORMDL3	NM_139280.1				
GI_27544938-S	2420.5	2672.8	2394.4	C3orf10	NM_018462.3	MDS027;HSPC300			
GI_27544940-S	129.9	146.1	121.8	MYO1F	NM_012335.2		actin	unconvent	biological_
GI_27545314-S	981.1	978.6	868.2	LOC51204	NM_016360.2				
GI_27545318-S	333.5	378.8	339.8	POU3F1	NM_002699.2	OCT6;OTF6;SCIP	transcripti	nucleus	nerve
GI_27545320-S	5051.4	7964.8	6770.1	C1orf8	NM_004872.3	HSPC001		integral to	
GI_27545321-S	107.8	117.8	103.9	C4BPB	NM_000716.2	C4BP			compleme
GI_27545325-S	386.5	433	380.2	SMARCB1	NM_003073.2	RDT;INI1;SNF5;Snr1;BAF47;Sfh1p;hSNFS;S	tumor	nucleoplas	DNA
GI_27545327-A	207	204.8	191.1	LRRC2	NM_024750.2				
GI_27545327-I	101.4	107	105.6	LRRC2	NM_024750.2				
GI_27545335-S	584.1	538.5	596.3	FLJ10375	NM_018075.2	MGC47890			
GI_27545441-S	96.2	98.3	87.9	NCR1	NM_004829.3	LY94;NKP46;NK-p46	receptor	integral to	killer
GI_27545446-S	2068.8	2579.3	2226.9	SYBL1	NM_005638.3	VAMP7;VAMP-7;TI-VAMP			
GI_27545448-S	754.4	497.2	541.9	TRPC1	NM_003304.3	TRP1;HTRP-1	store-	integral to	calcium
GI_27545449-S	1151.1	1507.5	1385.1	KCTD3	NM_016121.2	NY-REN-45	tumor		
GI_27552756-S	151	162.8	162.7	UGT2B10	NM_001075.2		UDP-	microsom	lipid

GI_27552758-S	149.4	126.2	126.8	RCP9	NM_014478.3	RCP;Crcp;CGRP-RCP	calcitonin	cellular_co	acrosome
GI_27552763-S	633.4	615.1	927.5	NGX6	NM_016446.2				
GI_27552771-S	90	89.6	93.3	NPY2R	NM_000910.2		calcium	integral to	G-protein
GI_27597060-S	371.7	502.5	461.5	C6orf133	NM_015255.1	UBR2;KIAA0349;bA49A4.1;dJ392M17.3	transporte		transport
GI_27597074-S	1005.9	1001.3	724.9	ITGB3BP	NM_014288.3	NRIF3;TAP20;HSU37139	protein C-	cytoplasm	cell
GI_27597077-S	520.8	377	441.1	TYRO3	NM_006293.2	BYK;RSE	transmem	integral to	cell
GI_27597079-S	131.7	152.7	152.3	CACNA1C	NM_000719.3	CaV1.2;CCHL1A1;CACNL1A1	voltage-	voltage-	regulation
GI_27597081-A	110.7	99.4	78.6	HS6ST2	NM_147174.2				
GI_27597081-I	143.2	135.1	147.7	HS6ST2	NM_147174.2				
GI_27597083-S	2938.6	2478.8	2268.3	METAP2	NM_006838.2	p67;MNPEP	methionyl		regulation
GI_27597087-S	160.2	272.8	256.8	CYB561	NM_001915.2		cytochrom	secretory	energy
GI_27597089-S	417	479.7	475.4	SUPT6H	NM_003170.2				
GI_27597093-S	513.3	627.4	494.6	SNF1LK	NM_173354.1	MSK	protein-		protein
GI_27597101-S	146.1	145.4	132.6	PGGT1B	NM_005023.2	BGGI;GGTI	CAAX-	CAAX-	C-terminal
GI_27597103-S	148.4	180.7	164.6	K5B	NM_173352.1				
GI_27734089-S	165.2	140.3	133.4	NAV3	NM_014903.2	POMFIL1;KIAA0938	nucleotide		
GI_27734688-S	126.9	143.5	130.6	FLJ36112	NM_173679.1				
GI_27734690-S	389.7	506.8	456.5	FLJ34047	NM_173669.1				
GI_27734692-S	710.1	603.6	1025.9	C14orf80	NM_173608.1	MGC16771			
GI_27734694-S	97	111.9	76.6	C15orf21	NM_173609.1	FLJ39426			
GI_27734696-A	181.1	214.2	213.9	KCNRG	NM_173605.1				
GI_27734700-S	329.8	406.5	383	FLJ34278	NM_173602.1				
GI_27734702-S	9861.6	12523	10644	FLJ38426	NM_173611.1				
GI_27734704-S	89.3	100.9	93	FLJ34836	NM_173668.1				
GI_27734706-S	327.1	433.3	363.6	FLJ33768	NM_173610.1				
GI_27734708-S	5355.4	6807.6	5701.9	LOC283820	NM_173614.1				
GI_27734712-S	244.7	296.1	258.7	FLJ35894	NM_173616.1				
GI_27734716-S	112.7	128.9	113.6	OPRD1	NM_000911.2	OPRD	delta-	integral to	sensory
GI_27734718-S	129	131.9	122	SLC19A2	NM_006996.1	TC1;THT1;TRMA;THTR1	transporte	integral to	small
GI_27734720-S	358.2	453.8	293.4	PDE8A	NM_002605.1	HsT19550	3',5'-cyclic-	cellular_co	cyclic
GI_27734722-S	138	138.7	137.7	FLJ37396	NM_173671.1				
GI_27734726-S	523.8	473.2	488.3	FLJ90652	NM_173618.1				
GI_27734731-S	201.1	233.5	232.3	FLJ36701	NM_173617.1				
GI_27734733-S	1520.8	1019.2	1003.2	FLJ23825	NM_173620.1				
GI_27734735-S	86.7	90.9	84.4	MGC34761	NM_173619.1				
GI_27734737-S	253.3	268.7	215.9	FLJ36674	NM_173622.1				
GI_27734739-S	156.8	194.5	195	RGMB	NM_173670.1	FLJ90406			
GI_27734741-S	108.3	110.3	107.7	FLJ34790	NM_173621.1				
GI_27734743-S	130.2	160.4	139.1	FLJ40504	NM_173624.1				
GI_27734745-S	229.5	284.9	250.5	FLJ35808	NM_173623.1				
GI_27734747-S	504	509.6	507.1	SLC26A11	NM_173626.1	MGC46523	sulfate	membran	sulfate
GI_27734756-S	97.4	104.6	96.1	FLJ40457	NM_173628.1				
GI_27734760-S	969.1	920.9	953.1	FLJ32440	NM_173685.1				
GI_27734762-S	134.9	147.9	131.4	FLJ25694	NM_173604.1				

GI_27734764-S	126.2	153.9	124.9	FLJ40126	NM_173599.1				
GI_27734768-S	116.7	115.5	118.2	FLJ37587	NM_173597.1				
GI_27734774-S	89.7	81.9	105	FLJ37659	NM_173698.1				
GI_27734776-S	149.4	192.6	168	SLC39A5	NM_173596.1	MGC34778	heavy	membran	heavy
GI_27734778-S	88.2	104.2	96.1	FLJ33977	NM_173666.1				
GI_27734780-S	103.2	107.7	106.6	MGC33889	NM_173699.1				
GI_27734782-S	153.6	171.4	164.9	B4GalNac-T3	NM_173593.1	FLJ40362			
GI_27734786-S	104.2	119.3	98.7	FLJ36102	NM_173590.1				
GI_27734788-S	124.9	152.8	145.9	FLJ90579	NM_173591.1				
GI_27734790-S	90.5	86.9	83.3	FLJ37794	NM_173588.1				
GI_27734794-S	99.4	105.7	113.5	FLJ37543	NM_173667.1				
GI_27734796-S	112.5	103.8	100.9	MGC34821	NM_173586.1		transporte	integral to	transport
GI_27734800-S	90.5	89	86.1	FLJ33790	NM_173583.1				
GI_27734802-S	87.4	88.6	80	FLJ40182	NM_173696.1				
GI_27734804-S	417.8	528.1	489	MGC45840	NM_173584.1		calcium		metabolis
GI_27734806-S	331	348.7	303	FLJ90231	NM_173581.1		beta-	beta-	carbohydr
GI_27734812-S	172.4	214.1	188.6	FLJ40224	NM_173579.1		DNA	nucleus	regulation
GI_27734814-S	95.9	93.4	84	MGC34713	NM_173665.1				
GI_27734816-S	107.1	112.7	110.3	FLJ39058	NM_173580.1				
GI_27734818-S	526.7	647.9	568.8	MGC45541	NM_173577.1				
GI_27734820-S	154.6	180.9	165.9	FLJ90834	NM_173578.1				
GI_27734824-S	99	100.4	96.1	FLJ33610	NM_173697.1				
GI_27734826-S	150.4	173.3	160.4	C10orf48	NM_173576.1	MGC39616	transcripti	nucleus	regulation
GI_27734828-S	113	113.9	124.4	MGC35138	NM_173573.1				
GI_27734832-S	93.3	98.8	101	MGC33414	NM_173574.1		electron		electron
GI_27734834-S	134	122.3	99.6	LOC255313	NM_173571.1				
GI_27734836-S	107.9	113.5	109	C10orf93	NM_173572.1	FLJ25954;bB137A17.3			
GI_27734842-S	191.1	237.8	196.5	FLJ35424	NM_173661.1				
GI_27734844-S	460.3	336.7	555.5	ZDHHC23	NM_173570.1	MGC42530			
GI_27734848-S	216.4	244.7	213.2	MGC34646	NM_173519.1		transporte	intracellula	transport
GI_27734852-S	86.3	79.8	78.3	FLJ36335	NM_173568.1				
GI_27734854-S	120.4	147.3	125.7	LOC222967	NM_173565.1				
GI_27734856-S	578.2	729.9	656.4	MGC50372	NM_173566.1		DNA	nucleus	regulation
GI_27734858-S	90.9	75.3	80.4	LOC285533	NM_173662.1				
GI_27734860-S	222	285.1	261.6	C6orf146	NM_173563.1	MGC43581			
GI_27734864-S	220	288.6	248.5	UNC5CL	NM_173561.1	MGC34763			signal
GI_27734868-S	106.8	114.3	110.1	FLJ25791	NM_173559.1				
GI_27734870-S	118.7	110.1	116.8	RFXDC1	NM_173560.1	MGC33442;dJ955L16.1	DNA	tRNA-	regulation
GI_27734872-S	126.1	124.3	128	RNF152	NM_173557.1	FLJ39176			
GI_27734876-S	1116.4	921.8	1415.2	MGC34695	NM_173555.1		trypsin		proteolysis
GI_27734882-S	229.5	433.8	144.6	FLJ25801	NM_173553.1				
GI_27734884-S	91.4	109.9	95.2	MGC44593	NM_173554.1				
GI_27734886-S	1788.8	1519.1	1518.3	MGC29784	NM_173659.1				
GI_27734888-S	201	217.4	201.9	SAMD6	NM_173551.1	FLJ36928			

GI_27734890-S	154.4	165.3	150.2	FLJ36601	NM_173695.1				
GI_27734896-S	91.3	88	92	FLJ39553	NM_173549.1				
GI_27734902-S	209.6	250.1	215.3	ZNF584	NM_173548.1		nucleic	intracellula	regulation
GI_27734904-S	100.3	86.2	98.1	C2orf13	NM_173545.1	MGC47799			
GI_27734906-S	208.8	248.5	201.5	FLJ90764	NM_173656.1			nucleus	
GI_27734908-S	120.9	151.7	116.3	MGC35097	NM_173546.1				
GI_27734910-S	110.4	104.2	105.9	FLJ32844	NM_173543.1				
GI_27734914-S	207.3	239.3	206.2	C10orf91	NM_173541.1	bA432J24.4	DNA	nucleus	regulation
GI_27734918-S	101.2	93.1	97.6	ZNF596	NM_173539.1		nucleic	intracellula	proteolysis
GI_27734920-S	179	211.8	210.8	FUT11	NM_173540.1	MGC33202	fucosyltra	membran	protein
GI_27734924-S	111.2	112	117.7	FLJ31139	NM_173657.1				
GI_27734926-S	95.8	107.5	89.7	PNPLA1	NM_173676.1	FLJ38755;dJ50J22.1	catalytic		
GI_27734928-S	78	105.9	77.4	FLJ35802	NM_173538.1				
GI_27734934-S	109.7	129.3	116.4	SLC9A9	NM_173653.1	FLJ35613	solute:hyd	integral to	regulation
GI_27734936-S	89.3	69.4	90.2	FLJ35838	NM_173532.1				
GI_27734940-S	87.6	82.1	76.2	FLJ36040	NM_173530.1		nucleic	nucleus	regulation
GI_27734942-S	109.1	115.9	98.8	C9orf84	NM_173521.1	FLJ32779			
GI_27734944-S	79	85.9	86.4	ZNF100	NM_173531.1		nucleic	intracellula	regulation
GI_27734946-S	105.3	98.8	102.9	FLJ38615	NM_173528.1				
GI_27734950-S	167.6	195.9	189.9	C14orf54	NM_173526.1	FLJ36130			
GI_27734952-S	117.7	130.2	108.5	FLJ38964	NM_173527.1		RAS small		protein
GI_27734954-S	128.3	152.6	149.9	DKFZp434C1	NM_173655.1		protein-		protein
GI_27734956-S	185	186.6	174.3	FLJ34780	NM_173651.1				
GI_27734960-S	134.7	146.4	129	MGC34805	NM_173525.1				
GI_27734962-S	150.4	163.1	155.4	FLJ36576	NM_173522.1				
GI_27734964-S	1321.6	941.1	1232.6	C9orf75	NM_173691.1	FLJ90254			
GI_27734968-S	389.8	470.8	432.8	FLJ40852	NM_173677.1				
GI_27734970-S	176.6	201.9	186.8	MGC35463	NM_173520.1				
GI_27734974-S	109.5	100.1	105.3	MGC34824	NM_173652.1				
GI_27734978-S	96.9	113.8	108.1	FLJ40722	NM_173678.1		metallope		proteolysis
GI_27734980-S	96.8	94.8	95.1	FLJ40288	NM_173682.1				
GI_27734982-S	87.9	118.4	109.9	FLJ39106	NM_173629.1				
GI_27734988-S	346.7	391.5	376.3	FLJ90805	NM_173633.1				
GI_27734993-A	106.8	125.7	99.9	SLC22A17	NM_016609.2	BOCT;BOIT;hBOIT	transporte	integral to	transport
GI_27734999-S	79.3	79.4	75.3	FLJ39630	NM_173688.1				
GI_27735001-S	275	324.7	304.3	FLJ34503	NM_173673.1				
GI_27735003-S	83.7	87	83.6	C19orf14	NM_173636.1	FLJ33298;DKFZP434J046			
GI_27735020-S	100	98.6	90.3	FLJ39415	NM_173681.1				
GI_27735026-S	90.8	97.4	77.6	FLJ40235	NM_173635.1				
GI_27735030-S	299.4	354.7	343.4	FLJ35976	NM_173639.1				
GI_27735032-S	121.1	119.9	120.2	DKFZp434P0	NM_173466.1				
GI_27735034-S	232.9	203.9	223.3	SLC25A26	NM_173471.1		binding	mitochond	transport
GI_27735036-S	1506	1362.6	1607.9	LOC93380	NM_173470.1				
GI_27735038-S	2253.1	2444.7	2026.1	LOC119504	NM_173473.1				

GI_27735040-S	137.3	168.6	159.7	MGC40179	NM_173472.1				
GI_27735042-S	107.7	111.1	95	MGC34725	NM_173637.1		binding	mitochond	transport
GI_27735044-S	98.2	91.8	96.2	PPIL6	NM_173672.1	MGC41939;bA425D10.6;dJ919F19.1			protein
GI_27735046-S	424.4	508.1	435.2	MGC48972	NM_173475.1				
GI_27735054-S	120.5	115.6	107.7	LOC126248	NM_173479.1				
GI_27735056-S	139.3	158.1	139.9	FLJ40137	NM_173478.1				cell cycle
GI_27735058-S	120.4	117	119.3	FLJ33655	NM_173641.1		ephrin	membran	
GI_27735060-S	104.8	110.5	106.4	FLJ40906	NM_173640.1		electron	nucleus	electron
GI_27735062-S	93.2	94.6	99.8	FLJ40365	NM_173482.1				
GI_27735064-S	215.7	284.4	246.4	DKFZp547G0	NM_173643.1				
GI_27735068-S	378.8	454	386.1	MGC47816	NM_173642.1				ribosome
GI_27735072-S	86.6	104.4	89.1	FLJ39501	NM_173483.1		monooxyg		electron
GI_27735074-S	263.5	183.8	241	LOC132321	NM_173487.1				
GI_27735076-S	127	131.1	142.9	FLJ37357	NM_173645.1				
GI_27735084-S	122.7	142.5	113.5	PIP5KL1	NM_173492.1	PIPKH;MGC46424;bA203J24.5	1-		
GI_27735086-S	125.7	120.1	113.2	FLJ33860	NM_173644.1				
GI_27735088-S	152.4	194.5	179.7	LSM11	NM_173491.1	FLJ38273	pre-mRNA	small	mRNA
GI_27735090-S	119.3	105.1	98.9	FLJ30296	NM_173495.1		hedgehog	membran	
GI_27735092-S	80.5	83.6	86.7	FLJ39502	NM_173648.1	FLJ26337			
GI_27735094-S	1540.4	1419.8	1145.6	LOC139135	NM_173493.1		signal		signal
GI_27735096-S	146.5	183.7	178.5	FLJ39660	NM_173646.1				
GI_27735098-A	184.4	226.8	219.6	FLJ37306	NM_173497.1	DKFZp761D0614	ubiquitin-	intracellula	ubiquitin
GI_27735098-I	112.6	121.1	127.7	FLJ37306	NM_173497.1	DKFZp761D0614	ubiquitin-	intracellula	ubiquitin
GI_27735102-S	121.9	128.3	115.6	MGC44294	NM_173499.1				
GI_27735104-S	533.8	258.6	117.3	DKFZp434C0	NM_173498.1				
GI_27735106-S	162.4	187	172.5	DNAJC5G	NM_173650.1	FLJ40417;CSP-gamma	chaperone		electron
GI_27735108-S	737.7	322.9	282.3	LOC146174	NM_173501.1				
GI_27735114-S	104.8	107.6	109.5	FLJ40172	NM_173649.1				
GI_27735116-S	223.4	246	228.2	FLJ90661	NM_173502.1		trypsin		proteolysis
GI_27735120-S	88.8	90.4	86.1	LOC147463	NM_173505.1		kinase		
GI_27735122-S	149.8	139	136.4	FLJ37131	NM_173687.1				
GI_27735124-S	134.9	143.5	153.2	FLJ36664	NM_173690.1				
GI_27735126-S	326	301.2	486.3	SLC35F3	NM_173508.1	FLJ37712		membran	
GI_27735128-S	109.3	118.3	113.5	FLJ37118	NM_173507.1				
GI_27735130-S	197.6	215.4	220.4	ALS2CR13	NM_173511.1	FLJ38771			
GI_27735132-S	454.2	505.3	610.9	FLJ33814	NM_173510.1				
GI_27735136-S	129	153.4	133.3	FLJ39822	NM_173512.1		amino	membran	amino
GI_27735138-S	440.5	457.7	351.3	MAGI1	NM_173515.1	FLJ31349	protein		intracellula
GI_27735140-S	115	111	93.6	FLJ33708	NM_173675.1				
GI_27735142-S	239.2	290.7	344.4	DCBLD1	NM_173674.1	MGC46341;dJ94G16.1			cell
GI_27735144-S	141.2	169	133.2	FLJ38464	NM_173689.1				
GI_27735146-S	127.5	114.7	123.9	FLJ35721	NM_173684.1				
GI_27735148-S	306.2	331.3	319.6	FLJ90709	NM_173514.1		amino	membran	amino
GI_27735152-S	341.1	395.8	392.2	VKORC1L1	NM_173517.1				

GI_27735154-S	183.1	223.7	191.8	PNLDC1	NM_173516.1	FLJ40240;dJ195P10.2			
GI_27754147-S	240	276.6	261.8	MGC23270	NM_152646.2				
GI_27754148-S	358.6	401.8	315	GRIPAP1	NM_020137.2				
GI_27754165-S	152.1	169.5	156.5	OR11A1	NM_013937.2	OR11A2;hs6M1-18;dJ994E9.6	olfactory	integral to	olfaction
GI_27754173-S	105.7	105	114.4	NEGR1	NM_173808.1	Ntra;KILON;MGC46680			
GI_27754187-S	202.8	343.6	192.4	MTND6	NM_173714.1		NADH	mitochond	eye
GI_27754191-S	152.7	202.4	152.2	MTND4L	NM_173712.1		NADH	mitochond	mitochond
GI_27754193-S	1505.4	1886.8	1394.3	MTND5	NM_173713.1		NADH	respiratory	eye
GI_27754195-S	28337.5	30496	24679	MTND3	NM_173710.1		NADH	mitochond	mitochond
GI_27754197-S	5856	6962.3	4522.4	MTND4	NM_173711.1		electron	mitochond	eye
GI_27754199-S	2094.7	2047	1264.9	MTND1	NM_173708.1		NADH	mitochond	eye
GI_27754201-S	4932	4886.9	3513.7	MTND2	NM_173709.1		NADH	respiratory	eye
GI_27754203-S	18286.7	19650	15289	MTCO1	NM_173704.1	COI	aa3-type	mitochond	vision
GI_27754205-S	16927.9	19493	14886	MTCO2	NM_173705.1	COII	aa3-type	mitochond	electron
GI_27754207-S	5818	6765.6	4166.4	MTATP6	NM_173702.1	ATP6	hydrogen	proton-	central
GI_27754209-S	113.5	113.7	99.2	MTATP8	NM_173703.1	ATP8	hydrogen	proton-	ATP
GI_27754211-S	134.9	152.7	135.7	NXPH3	NM_007225.1	NPH3	receptor	extracellul	neuropepti
GI_27754764-A	104.5	101.1	87	FXYD1	NM_005031.3	PLM;MGC44983	chloride	integral to	chloride
GI_27754764-I	99.7	109	104.6	FXYD1	NM_005031.3	PLM;MGC44983	chloride	integral to	chloride
GI_27754765-I	122.5	117.2	124.5	FXYD1	NM_021902.2	PLM;MGC44983	chloride	integral to	chloride
GI_27754766-I	222.6	246.8	240.3	FXYD2	NM_021603.2	HOMG2;ATP1G1;MGC12372	sodium/po	sodium/po	small
GI_27754767-A	121.4	121.8	127.1	FXYD2	NM_001680.3	HOMG2;ATP1G1;MGC12372	sodium/po	sodium/po	small
GI_27754767-I	96.8	103.5	103.1	FXYD2	NM_001680.3	HOMG2;ATP1G1;MGC12372	sodium/po	sodium/po	small
GI_27754770-A	93.7	83.9	77.3	PCDH1	NM_002587.3	PC42;PCDH42;MGC45991	cell	intercellula	neurogene
GI_27754770-I	528.6	313.4	273	PCDH1	NM_002587.3	PC42;PCDH42;MGC45991	cell	intercellula	neurogene
GI_27754772-I	161.6	199.4	160	PCDH1	NM_032420.2	PC42;PCDH42;MGC45991	cell	intercellula	neurogene
GI_27754774-S	88.2	93.3	103.5	AFM	NM_001133.2	ALF;ALB2;ALBA	carrier	extracellul	transport
GI_27754777-A	255.9	307.5	275.8	FCN3	NM_173452.1	FCNH;HAKA1;MGC22543	lectin [goid	microfibril	heterophili
GI_27764860-S	101.9	108.9	91.7	MYH6	NM_002471.1	MYHC;MYHCA	structural	muscle	muscle
GI_27764862-S	9782.2	8548.2	7217.5	SLC25A6	NM_001636.1	ANT3;ANT3Y;MGC17525	adenine	mitochond	small
GI_27764864-S	177.9	202.1	192.9	CD1A	NM_001763.1	CD1	protein	integral to	antimicrob
GI_27764866-S	184.3	210.7	204.9	SYP	NM_003179.1		transporte	synaptic	transport
GI_27764872-S	545.2	423.1	424.9	CRLF3	NM_015986.2	CREME9;CYTOR4;MGC20661	receptor		
GI_27764881-S	143.9	104.2	273.7	MLAT4	NM_018192.2	FLJ10718	oxidoredu		protein
GI_27764903-S	99.2	108.2	107.5	FXYD4	NM_173160.1	CHIF	ion	membran	ion
GI_27765075-I	112.2	127.7	125.1	CAPN3	NM_173088.1	p94;CANP3;LGMD2;nCL-	calpain	intracellula	muscle
GI_27765077-A	121.3	145.3	134.3	CAPN3	NM_173089.1	p94;CANP3;LGMD2;nCL-	calpain	intracellula	muscle
GI_27765082-I	131.7	174	114.9	CAST	NM_001750.4	BS-17;MGC9402	endopepti		
GI_27765084-I	474.2	533.6	505.3	CAST	NM_173060.1	BS-17;MGC9402	endopepti		
GI_27765086-A	753	819.9	736.6	CAST	NM_173061.1	BS-17;MGC9402	endopepti		
GI_27765086-I	105.7	109.4	92.5	CAST	NM_173061.1	BS-17;MGC9402	endopepti		
GI_27765088-I	90.2	108.3	95	CAST	NM_173062.1	BS-17;MGC9402	endopepti		
GI_27765092-A	429.5	590	154.2	SIAT1	NM_173217.1	CD75;ST6Gal1;ST6GalI;MGC48859;ST6Gal I	beta-	Golgi	humoral
GI_27765094-I	498.9	561.2	498.4	SIAT1	NM_003032.2	CD75;ST6Gal1;ST6GalI;MGC48859;ST6Gal I	beta-	Golgi	humoral

GI_27765095-A	400.3	511.8	405.4	SIAT4A	NM_173344.1	ST3O;SIATFL;MGC9183;ST3GalIA;Gal-	beta-	Golgi	protein
GI_27765097-I	150.5	171.6	169.5	SIAT4A	NM_003033.2	ST3O;SIATFL;MGC9183;ST3GalIA;Gal-	beta-	Golgi	protein
GI_27765098-S	222.5	322.6	242.9	SIAT4B	NM_006927.2	ST3GALII;Gal-NAc6S;ST3GalA.2	beta-	Golgi	amino
GI_27777631-S	1968.4	1184.7	1279	SLC9A1	NM_003047.2	APNH;NHE1	pH	integral to	small
GI_27777635-S	1235	970.7	712.1	TCF3	NM_003200.1	E2A;ITF1	RNA	nucleus	oncogene
GI_27777654-S	113.7	129.9	116.4	MCF2L	NM_024979.2	DBS;OST;ARHGEF14;FLJ12122;KIAA0362			
GI_27777666-S	150.5	158.7	133.8	SLC30A8	NM_173851.1	ZnT-8	cation	membran	cation
GI_27777668-S	122.2	113.6	122.7	VN1R4	NM_173857.1	V1RL4	receptor	integral to	G-protein
GI_27777672-S	4233	4179.6	3462.3	VN1R2	NM_173856.1	V1RL2	receptor	integral to	G-protein
GI_27777674-S	230.6	251.7	256.5	VN1R5	NM_173858.1	V1RL5	receptor	integral to	G-protein
GI_27804306-S	96.4	136.7	109.5	SDC2	NM_002998.1	HSPG;HSPG1;SYND2	syndecan	proteoglyc	cell
GI_27804312-S	126.5	113.9	108.9	GAL	NM_015973.2	GALN;GLNN;MGC40167			
GI_27804314-S	86.6	93.1	88.7	HOXC12	NM_173860.1	HOX3;HOX3F	transcripti	nucleus	regulation
GI_27881480-S	1707.8	2314.3	2215.8	RAC2	NM_002872.3	Gx;EN-7;HSPC022	GTPase	peripheral	signal
GI_27881481-S	300.6	378.3	383.1	RIG-I	NM_014314.2		nucleotide		
GI_27881483-S	182.5	169.5	170.4	RoXaN	NM_017590.4	FLJ13787;KIAA1031;DKFZp434K0920			
GI_27881485-I	114	131.3	134.2	ZAN	NM_173055.1		cell	integral to	fertilization
GI_27881493-A	105.4	122.3	96.1	ZAN	NM_173059.1		cell	integral to	fertilization
GI_27881504-A	630.4	719.1	807.3	ABCF2	NM_005692.3	ABC28;M-ABC1;HUSSY-	ATP	mitochond	small
GI_27881504-I	167.8	154.4	132.7	ABCF2	NM_005692.3	ABC28;M-ABC1;HUSSY-	ATP	mitochond	small
GI_27881505-I	282.3	361.2	405	ABCF2	NM_007189.1	ABC28;M-ABC1;HUSSY-	ATP	mitochond	small
GI_27883865-S	539.7	595.2	559.4	RIC-8	NM_021932.4				
GI_27885012-S	134.9	149.8	131.7	LOC199675	NM_174918.1				
GI_27886525-A	180.1	221.4	184.8	NFAT5	NM_173215.1	NFATL1;TONEBP;KIAA0827	RNA	nucleus	excretion
GI_27886525-I	1567.4	1830.2	1703.3	NFAT5	NM_173215.1	NFATL1;TONEBP;KIAA0827	RNA	nucleus	excretion
GI_27886528-A	88.2	112.2	95.2	ATP2A1	NM_173201.1	ATP2A;SERCA1	adenosine	smooth	regulation
GI_27886536-A	549.5	931.8	900.2	ATP2A2	NM_001681.2	DD;DAR;ATP2B;SERCA2;MGC45367	calcium-	microsom	epidermal
GI_27886536-I	2358.8	2604.4	1993.6	ATP2A2	NM_001681.2	DD;DAR;ATP2B;SERCA2;MGC45367	calcium-	microsom	epidermal
GI_27886537-I	776.3	1159.9	1159	ATP2A2	NM_170665.2	DD;DAR;ATP2B;SERCA2;MGC45367	calcium-	microsom	epidermal
GI_27886538-A	96.1	98.7	100.5	NFATC2	NM_012340.2	NFAT1;NFATP	transcripti	cytoplasm	regulation
GI_27886540-I	102.4	102	96.6	NFATC2	NM_173091.1	NFAT1;NFATP	transcripti	cytoplasm	regulation
GI_27886542-I	127.8	129.9	108.8	NFATC3	NM_004555.2	NFAT4;NFATX	transcripti	nucleus	regulation
GI_27886554-I	141	145.7	133.7	NFATC3	NM_173163.1	NFAT4;NFATX	transcripti	nucleus	regulation
GI_27886556-S	123.2	130.3	151.7	MSX2	NM_002449.3	FPP;MSH;PFM;CRS2;HOX8;PFM1	DNA	nucleus	skeletal
GI_27886558-A	302	364.9	378.2	NFATC3	NM_173164.1	NFAT4;NFATX	transcripti	nucleus	regulation
GI_27886558-I	318	364.7	345.3	NFATC3	NM_173164.1	NFAT4;NFATX	transcripti	nucleus	regulation
GI_27886565-A	360.7	376.2	278.5	MALT1	NM_173844.1	MLT;MLT1;DKFZp434L132	caspase	intracellula	pathogene
GI_27886567-S	518.2	345.1	293.1	MDA5	NM_022168.2				
GI_27886569-I	122.2	155	159.2	MRPL39	NM_080794.2	L39mt;RPML5;MRP-	structural	mitochond	biological_
GI_27886581-A	1457.6	1511.7	1584	MRPL39	NM_017446.2	L39mt;RPML5;MRP-	structural	mitochond	biological_
GI_27886585-I	92.2	104.7	81.9	PTK2B	NM_173174.1	PKB;PTK;CAKB;FAK2;PYK2;CADTK;FADK2;	focal	cytoskelet	signal
GI_27886587-A	115.6	131	112.6	PTK2B	NM_173175.1	PKB;PTK;CAKB;FAK2;PYK2;CADTK;FADK2;	focal	cytoskelet	signal
GI_27886591-I	156.2	179.7	176.4	PTK2	NM_153831.2	FAK;FADK;FAK1;pp125FAK	focal	cytoskelet	integrin-
GI_27886592-A	526.6	556	675.9	PTK2	NM_005607.3	FAK;FADK;FAK1;pp125FAK	focal	cytoskelet	integrin-

GI_27886594-S	145.2	161.2	155.1	PTK6	NM_005975.2	BRK	non-		protein
GI_27886606-A	195.6	294.3	222.7	PTK7	NM_152881.2	CCK4	transmem	proteoglyc	signal
GI_27886627-S	1581.8	1651.5	1098.2	FLJ20071	NM_017653.2	DMC;SMC;FLJ90130			
GI_27886630-I	87	95.3	85	CD8B1	NM_172099.1	Ly3;CD8B;LYT3;Leu2		integral to	
GI_27886632-A	95.4	117	91.1	CD8B1	NM_172100.1	Ly3;CD8B;LYT3;Leu2		integral to	
GI_27886632-I	127.4	138	133.5	CD8B1	NM_172100.1	Ly3;CD8B;LYT3;Leu2		integral to	
GI_27886634-I	92.5	105.9	96.4	CD8B1	NM_172101.1	Ly3;CD8B;LYT3;Leu2		integral to	
GI_27886640-I	143.2	160.9	142.1	CD8A	NM_001768.4	CD8;MAL;p32;Leu2	T-cell	integral to	
GI_27886641-A	113.3	117.9	96.4	CD8A	NM_171827.1	CD8;MAL;p32;Leu2	T-cell	integral to	
GI_27886643-A	710.1	835.8	1069.1	CDC2	NM_033379.2	CDK1	cyclin-	nucleus	start
GI_27886647-A	83.3	87.5	84.9	KCNH5	NM_172376.1	EAG2;H-EAG2;Kv10.2	voltage-	integral to	cation
GI_27886647-I	86.6	84.6	75.6	KCNH5	NM_172376.1	EAG2;H-EAG2;Kv10.2	voltage-	integral to	cation
GI_27886649-I	1368.3	1474.3	1373.6	KCNH6	NM_030779.2	ERG2;HERG2;Kv11.2	voltage-	integral to	cation
GI_27886650-A	197.9	237.9	215.7	KCNH6	NM_173092.1	ERG2;HERG2;Kv11.2	voltage-	integral to	cation
GI_27886652-I	102.9	100.2	93.9	KCNH7	NM_033272.2	ERG3;HERG3;Kv11.3;MGC45986	voltage-	integral to	cation
GI_27886664-A	105.2	105.1	109.2	KCNH7	NM_173162.1	ERG3;HERG3;Kv11.3;MGC45986	voltage-	integral to	cation
GI_27886664-I	82.2	74.5	79.9	KCNH7	NM_173162.1	ERG3;HERG3;Kv11.3;MGC45986	voltage-	integral to	cation
GI_27886666-S	98.5	109.3	103.9	KCNH8	NM_144633.2	ELK;ELK1;Kv12.1	voltage-	integral to	cation
GI_27886675-I	109.3	101.2	107	KCNIP2	NM_173194.1	KCHIP2;MGC17241;DKFZp566L1246			calcium
GI_27886679-A	111.8	113.9	112.9	KCNIP2	NM_173197.1	KCHIP2;MGC17241;DKFZp566L1246			calcium
GI_27886679-I	316.5	407.3	354.1	KCNIP2	NM_173197.1	KCHIP2;MGC17241;DKFZp566L1246			calcium
GI_27886683-S	183.7	194.9	181.3	KCNIP1	NM_014592.2	VABP;MGC95;KCHIP1	ion		calcium
GI_27894283-S	209.7	242.5	225.2	P2RX1	NM_002558.2	P2X1	ATP-	integral to	small
GI_27894284-I	638.3	312.8	245	PACE4	NM_138325.2	SPC4;PCSK6	subtilase		proteolysis
GI_27894286-A	113.9	113.1	94.6	PHF7	NM_173341.1	HSPC045;HSPC226;NYD-			
GI_27894288-I	136.1	167.9	142.8	PHF7	NM_016483.4	HSPC045;HSPC226;NYD-			
GI_27894289-A	826.9	803.3	637.3	PIGF	NM_002643.2	MGC32646;MGC33136	ethanolam	endoplas	GPI
GI_27894290-I	124.4	143.1	120.7	PIGF	NM_173074.1	MGC32646;MGC33136	ethanolam	endoplas	GPI
GI_27894292-I	161.7	153.2	143.2	PLAGL1	NM_006718.2	ZAC;LOT1;ZAC1	tumor		induction
GI_27894297-A	112.2	107.1	108.6	IL1F7	NM_173203.1	FIL1;FIL1Z;IL1H4;IL-1F7;IL-1H4;IL1RP1;IL-	interleukin-	extracellul	immune
GI_27894301-I	92.9	101.7	94.5	IL1F7	NM_173205.1	FIL1;FIL1Z;IL1H4;IL-1F7;IL-1H4;IL1RP1;IL-	interleukin-	extracellul	immune
GI_27894303-I	186.7	240.5	217.5	IL1F10	NM_032556.4	FKSG75;IL-1HY2;IL1-theta;FIL1-theta	interleukin-	extracellul	immune
GI_27894305-S	929.8	7908.3	22038	IL1B	NM_000576.2	IL-1;IL1F2;IL1-BETA	cytokine	extracellul	negative
GI_27894306-A	132.1	142.2	133	IL1F10	NM_173161.1	FKSG75;IL-1HY2;IL1-theta;FIL1-theta	interleukin-	extracellul	immune
GI_27894308-I	118	120.8	102.5	IL1F5	NM_012275.2	FIL1;FIL1D;IL1L1;IL1HY1;IL1RP3;MGC29840	interleukin-	extracellul	immune
GI_27894309-A	197.2	212.8	219.4	IL1F5	NM_173170.1	FIL1;FIL1D;IL1L1;IL1HY1;IL1RP3;MGC29840	interleukin-	extracellul	immune
GI_27894311-I	91.6	103	92.3	IL1F8	NM_014438.3	FIL1;FIL1H;IL1H2;IL-1F8;IL-1H2;IL1-	interleukin-	extracellul	immune
GI_27894312-A	99.3	95.7	105.1	IL1F8	NM_173178.1	FIL1;FIL1H;IL1H2;IL-1F8;IL-1H2;IL1-	interleukin-	extracellul	immune
GI_27894312-I	144.5	148.7	154.7	IL1F8	NM_173178.1	FIL1;FIL1H;IL1H2;IL-1F8;IL-1H2;IL1-	interleukin-	extracellul	immune
GI_27894314-S	86.1	148.3	119.6	IL1F9	NM_019618.2	IL1E;IL1H1;IL-1F9;IL-1H1;IL1RP2;IL-1RP2;IL-	interleukin-	extracellul	response
GI_27894318-A	106.4	122.4	125.5	IL1RN	NM_173842.1	IRAP;IL1F3;IL1RA;ICIL-1RA;MGC10430	interleukin-	extracellul	inflammat
GI_27894318-I	94.2	114.2	97.5	IL1RN	NM_173842.1	IRAP;IL1F3;IL1RA;ICIL-1RA;MGC10430	interleukin-	extracellul	inflammat
GI_27894320-I	92	88.8	89.7	IL1RN	NM_173843.1	IRAP;IL1F3;IL1RA;ICIL-1RA;MGC10430	interleukin-	extracellul	inflammat
GI_27894322-S	535.8	571.9	618.3	IL1RL1LG	NM_006858.2	MGC1270	receptor	membran	cell-cell

GI_27894323-A	92.4	83	70.7	IL1RL1	NM_016232.4	T1;ST2;DER4;ST2L;ST2V;FIT-1;MGC32623	interleukin	integral to	signal
GI_27894323-I	155.5	172.9	150.5	IL1RL1	NM_016232.4	T1;ST2;DER4;ST2L;ST2V;FIT-1;MGC32623	interleukin	integral to	signal
GI_27894325-I	90.5	83.1	80.3	IL1RL1	NM_173459.1	T1;ST2;DER4;ST2L;ST2V;FIT-1;MGC32623	interleukin	integral to	signal
GI_27894329-S	172	180.9	136	IL1A	NM_000575.3	IL1;IL-1A;IL1F1;IL1-ALPHA	cytokine	extracellul	negative
GI_27894331-S	150.1	399.8	168.6	IL1R1	NM_000877.2	P80;IL1R;IL1RA;CD121A;D2S1473;IL-1R-	interleukin-	integral to	cell
GI_27894332-I	533.1	519	454.2	IL1R2	NM_004633.3	IL1RB;MGC47725	interleukin-	integral to	immune
GI_27894333-A	159	226.2	101.2	IL1R2	NM_173343.1	IL1RB;MGC47725	interleukin-	integral to	immune
GI_27894333-I	102.1	104.4	111.6	IL1R2	NM_173343.1	IL1RB;MGC47725	interleukin-	integral to	immune
GI_27894335-S	96.9	93.6	93.7	IL1RAPL1	NM_014271.2	IL1R8;MRX34;OPHN4;IL1RAPL;TIGIRR-2	receptor	membran	learning
GI_27894336-S	106.2	108.3	115.1	KRT20	NM_019010.1	K20;CK20;KRT21;MGC35423	structural	intermedia	cell shape
GI_27894338-I	96.1	102.2	85	KRT23	NM_015515.3	K23;CK23;HAIK1;MGC26158;DKFZP434G03			
GI_27894340-A	95.2	108.1	97.9	KRT23	NM_173213.1	K23;CK23;HAIK1;MGC26158;DKFZP434G03			
GI_27894340-I	111.6	122.3	123.3	KRT23	NM_173213.1	K23;CK23;HAIK1;MGC26158;DKFZP434G03			
GI_27894342-I	243.8	310.8	272.6	NR4A1	NM_002135.3	HMR;N10;TR3;NP10;GFRP1;NAK-	ligand-		signal
GI_27894345-A	132.4	147.5	149.9	NR4A1	NM_173158.1	HMR;N10;TR3;NP10;GFRP1;NAK-	ligand-		signal
GI_27894345-I	161.2	196.3	183.9	NR4A1	NM_173158.1	HMR;N10;TR3;NP10;GFRP1;NAK-	ligand-		signal
GI_27894352-A	373.8	416.1	357.1	NR4A2	NM_173173.1	NOT;RNR1;HZF-3;NURR1;TINUR	ligand-	nucleus	signal
GI_27894356-I	116.6	113	101.3	NR4A3	NM_173198.1	CHN;TEC;CSMF;NOR1;MINOR	thyroid	nucleus	cell growth
GI_27894358-A	83.3	83.6	96.6	NR4A3	NM_173199.1	CHN;TEC;CSMF;NOR1;MINOR	thyroid	nucleus	cell growth
GI_27894358-I	562.4	697.2	643.3	NR4A3	NM_173199.1	CHN;TEC;CSMF;NOR1;MINOR	thyroid	nucleus	cell growth
GI_27894363-S	97.6	110.6	96.8	GKN1	NM_019617.2	CA11;AMP18;BRICD1	molecular	cellular_co	digestion
GI_27894365-S	357	364.6	282.7	APBB2	NM_173075.1	FE65L;FE65L1;MGC35575	protein C-	membran	protein
GI_27894367-S	511.7	375.5	332.3	NOTCH1	NM_017617.2	hN1;TAN1	tumor	integral to	signal
GI_27894369-S	218.3	243.8	210.4	NOTCH4	NM_004557.2	INT3;NOTCH3	structural	integral to	regulation
GI_27894372-A	303.7	316	338.4	C1D	NM_173177.1	SUNCOR;MGC12261;MGC14659	DNA	nucleus	
GI_27894374-S	110.7	120.4	110.5	CEL	NM_001807.2	BAL;FAP;BSDL;BSSL;CELL;FAPP;LIPA;CEa	serine		cholestero
GI_27894375-S	92.9	93.3	98.6	CHL1	NM_006614.2	CALL;L1CAM2	cell	integral to	cell
GI_27894377-S	104.2	113	106.6	CLIC6	NM_053277.1	CLIC1L	voltage-	membran	chloride
GI_27894379-S	249.9	159.9	163.5	CSEN	NM_013434.3	DREAM;KCHIP3;KCNIP3;MGC18289	transcripti		signal
GI_27894380-S	268.8	324.2	316.4	EFNA2	NM_001405.2	ELF-1;EPLG6;LERK6;HEK7-L	ephrin	membran	cell-cell
GI_27894383-S	417.1	199.7	485.1	FLRT2	NM_013231.2	KIAA0405	receptor	integral to	biological_
GI_27894384-S	299.4	340.7	325.7	FZD5	NM_003468.2	HFZ5	receptor	integral to	establish
GI_27894386-S	239.6	245.4	224.2	HELLS	NM_018063.3	LSH;PASG;SMARCA6;FLJ10339			
GI_27894387-S	6612	8650.7	6844	QP-C	NM_014402.2		ubiquinol-	ubiquinol-	electron
GI_27901802-S	700.1	896.2	777	PSKH1	NM_006742.1		protein	Golgi	protein
GI_27923946-S	103.8	112.1	101.2	VN1R3	NM_174980.1	V1RL3;FKSG46	pheromon	integral to	G-protein
GI_28076868-S	160.5	119.2	93.5	SERPINB4	NM_002974.1	PI11;SCCA2;LEUPIN			
GI_28077090-S	178.8	178.4	171.4	TCF8	NM_030751.2	BZP;ZEB;ZEB1;AREB6;ZFHEP;NIL-	transcripti	nucleus	regulation
GI_28144892-A	380.7	448.8	435.1	CRB3	NM_174881.1	MGC17303			
GI_28144894-I	156.2	188.6	138	CRB3	NM_174882.1	MGC17303			
GI_28144896-A	217.8	280.9	108.9	AK5	NM_174858.1	AK6;MGC33326	adenylate	cytosol	ADP
GI_28144896-I	117.8	123.7	93.4	AK5	NM_174858.1	AK6;MGC33326	adenylate	cytosol	ADP
GI_28144898-I	128	129.8	113	AK5	NM_012093.2	AK6;MGC33326	adenylate	cytosol	ADP
GI_28144900-S	292.1	349	321.2	IL28B	NM_172139.2	IFNL3;IL-28B			

GI_28144902-S	139.9	152.2	135.1	IL23A	NM_016584.2	P19;SGRF;IL-23;IL-23A;IL23P19			
GI_28144903-S	138.4	144.2	146.9	MBD3L2	NM_144614.2				
GI_28144904-S	368.1	445.7	410.1	USH2A	NM_007123.3	US2;USH2	structural	basal	hearing
GI_28144906-I	105.7	114.1	96.4	USH3A	NM_052995.2	USH3			
GI_28144911-A	123.9	127.6	131.8	USH3A	NM_174880.1	USH3			
GI_28144911-I	108.5	113.6	112.7	USH3A	NM_174880.1	USH3			
GI_28144915-S	437.7	443	390.5	F25965	NM_019104.1	MGC9505			
GI_28144919-S	701.6	863.5	835	PEN2	NM_172341.1	MDS033		Golgi	
GI_28173557-S	96.3	112.6	96.7	TA4	NM_175067.1		receptor	integral to	G-protein
GI_28173561-S	92.3	107.5	104.4	TAR3	NM_175057.1	TA3	receptor	integral to	G-protein
GI_28178815-A	2936.9	2913.5	1666.3	IDH3B	NM_174855.1	H-IDHB;MGC903;FLJ11043	isocitrate	mitochond	isocitrate
GI_28178818-I	87.7	101.2	96.6	IDH3B	NM_174856.1	H-IDHB;MGC903;FLJ11043	isocitrate	mitochond	isocitrate
GI_28178824-S	1281.1	1316.9	1543.8	IDH1	NM_005896.2	IDH;IDP;PICD	isocitrate	cytosol	isocitrate
GI_28178831-S	953.9	1469.9	1098	IDH2	NM_002168.2	IDH;IDP;IDHM;ICD-M;mNADP-IDH		mitochond	carbohydr
GI_28178835-S	521.5	604.4	601.8	IDH3A	NM_005530.2		isocitrate	mitochond	carbohydr
GI_28178836-A	870.9	993.9	1080.3	IDH3G	NM_004135.2	H-IDHG	isocitrate		carbohydr
GI_28178837-A	1247.3	1269	1506.3	IDH3G	NM_174869.1	H-IDHG	isocitrate		carbohydr
GI_28178837-I	133.6	165.8	145.8	IDH3G	NM_174869.1	H-IDHG	isocitrate		carbohydr
GI_28178841-I	177.1	156.5	140.1	TGIF	NM_003244.2	HPE4;MGC5066;MGC39747	transcripti	nucleus	developm
GI_28178842-I	278.7	343.1	306	TGIF	NM_170695.2	HPE4;MGC5066;MGC39747	transcripti	nucleus	developm
GI_28178844-I	101.2	120.6	91.7	TGIF	NM_173207.1	HPE4;MGC5066;MGC39747	transcripti	nucleus	developm
GI_28178850-I	312.1	402.5	344.1	TGIF	NM_173209.1	HPE4;MGC5066;MGC39747	transcripti	nucleus	developm
GI_28178854-A	1715.8	1260.9	1174.9	TGIF	NM_173211.1	HPE4;MGC5066;MGC39747	transcripti	nucleus	developm
GI_28178856-I	110.9	132.8	142.4	TGIF	NM_174886.1	HPE4;MGC5066;MGC39747	transcripti	nucleus	developm
GI_28178860-S	133.8	163.4	140.8	IL2	NM_000586.2	IL-2;TCGF	interleukin-	extracellul	cell
GI_28178862-S	116.3	123.4	110.2	OSM	NM_020530.3	MGC20461	cytokine	extracellul	negative
GI_28195383-S	151.8	176.7	176.6	NPTX2	NM_002523.1	NP2;NP-II	lectin [goid	cellular_co	transport
GI_28195387-S	159.1	227.8	150.9	RAB11-FIP4	NM_032932.2	KIAA1821;MGC11316			
GI_28212219-S	108.5	116	107.1	XG	NM_175569.1	PBDX	molecular	integral to	biological_
GI_28212271-S	119.6	120	124.6	C14orf21	NM_174913.1	KIAA2021	RNA	nucleus	regulation
GI_28212273-S	273	333.1	276.5	FLJ35936	NM_173464.1		transcripti	nucleus	regulation
GI_28212275-S	101.8	114.2	104	FLJ35785	NM_173613.1				
GI_28212277-S	91.5	105.4	91.2	FLJ36870	NM_173658.1			nucleus	
GI_28269671-S	174.6	153.9	130.7	SDCCAG8	NM_006642.1	CCCAP;NY-CO-8	tumor		
GI_28269680-S	3905.5	4146.2	3831.2	NDUFA11	NM_175614.1	B14.7	NADH		
GI_28269686-S	121.2	136.3	116.2	ZAR1	NM_175619.1				
GI_28269692-S	91.4	135.1	154.7	XYLT1	NM_022166.1	XT1;XT-I	acetylgluc	membran	glycosami
GI_28269706-S	124.3	108.8	108.6	C14orf27	NM_175060.1		sugar		heterophili
GI_28274681-S	909.4	1191.5	1062.9	ZNF33A	NM_006974.1	KOX31;ZNF33;ZZAPK;FLJ23404;KIAA0065			
GI_28274683-I	98.7	112.9	111.9	TRPM3	NM_020952.1	MLSN2;LTRPC3;FLJ11726;KIAA1616			
GI_28274685-S	201.4	151.2	139.8	ZNF545	NM_133466.1	KIAA1948;MGC45380	nucleic	intracellula	regulation
GI_28274693-S	458.5	315.4	162.8	RASL10B	NM_033315.2	MGC47540;VTS58635	small		small
GI_28274698-S	737.5	554.8	639.9	RAB3IP	NM_022456.2	RABIN3;FLJ22548			
GI_28274700-S	1328.1	1228.2	1280.3	ZNF511	NM_145806.2	MGC30006			

GI_28302128-S	115.1	136.9	109	HBB	NM_000518.4			hemoglobi	
GI_28302129-S	3418.6	3788	1036.1	HBE1	NM_005330.3		oxygen	hemoglobi	oxygen
GI_28302130-S	214.1	295.9	169.5	HBG1	NM_000559.2	HBGA;HBGR	oxygen	hemoglobi	oxygen
GI_28302132-S	237.9	310.8	171.4	HBG2	NM_000184.2			hemoglobi	
GI_28315872-S	93.2	96.9	100	LOC126295	NM_173480.1		nucleic	nucleus	regulation
GI_28316807-S	132.2	150.8	146.4	FLJ39821	NM_173700.1				
GI_28316809-S	223	226.5	221.1	MGC31967	NM_174923.1				
GI_28329413-I	86.1	83.9	76.8	CBFA2T1	NM_004349.2	CDR;ETO;MTG8;AML1T1;ZMYND2;MGC279	transcripti	nucleus	energy
GI_28329415-A	90.4	96.2	87	CBFA2T1	NM_175634.1	CDR;ETO;MTG8;AML1T1;ZMYND2;MGC279	transcripti	nucleus	energy
GI_28329415-I	109	113.7	112.7	CBFA2T1	NM_175634.1	CDR;ETO;MTG8;AML1T1;ZMYND2;MGC279	transcripti	nucleus	energy
GI_28329418-I	239.6	288.7	256	CBFA2T1	NM_175635.1	CDR;ETO;MTG8;AML1T1;ZMYND2;MGC279	transcripti	nucleus	energy
GI_28329421-I	95.1	102.1	93.3	CBFA2T1	NM_175636.1	CDR;ETO;MTG8;AML1T1;ZMYND2;MGC279	transcripti	nucleus	energy
GI_28329424-I	138.8	154.7	121.7	APTX	NM_017692.2	AOA;AOA1;AXA1;EAOH;EOAHA;FHA-			
GI_28329426-A	661	802.8	782.2	APTX	NM_175071.1	AOA;AOA1;AXA1;EAOH;EOAHA;FHA-			
GI_28329438-A	436.3	428.4	379.4	TG737	NM_006531.2	MGC26259;D13S1056E			excretion
GI_28329444-S	117.7	131.5	104.1	KCNV1	NM_014379.2	HNKA;KCNB3;KV2.3;KV8.1	ion	voltage-	potassium
GI_28329446-S	113.8	105.3	103.9	KCNV2	NM_133497.2	Kv8.2;KV11.1	voltage-	voltage-	cation
GI_28372492-S	1311.2	1558.5	899.7	CUL4B	NM_003588.2	KIAA0695	molecular	cellular_co	cell cycle
GI_28372496-S	142.7	169.1	144.1	UBR1	NM_174916.1		structural	ribosome	protein
GI_28372498-S	109.8	105.1	97.1	HUMMLC2B	NM_013292.2	MRLC2;MGC13450	structural	muscle	
GI_28372502-S	138.8	151.7	147.2	K6IRS2	NM_080747.1	KRT6;K6irs;KRT6IRS2		kinesin	
GI_28372504-S	233.6	230.2	259.6	CBX7	NM_175709.1		chromatin	chromatin	chromatin
GI_28372506-S	155.4	183.7	178.1	BASE	NM_173859.1				
GI_28372510-S	94.1	94.2	94.4	ZDHHC22	NM_174976.1	C14orf59			
GI_28372512-S	86.7	94.8	90.5	C14orf39	NM_174978.1				
GI_28372516-S	127.9	153.7	133.8	C8orf15	NM_175076.1				
GI_28372518-S	100.1	100	100.5	C21orf32	NM_175570.1				
GI_28372520-S	121.4	124.9	125.2	HUCEP11	NM_014858.1	KIAA0481		integral to	
GI_28372524-S	133.1	140.6	144.7	BPIL3	NM_174897.1		lipid		
GI_28372526-S	132.2	123	115.6	LOC129530	NM_174898.1		lysozyme		cell wall
GI_28372530-S	138.5	152.9	134.5	PPP4R2	NM_174907.1			centrosom	protein
GI_28372532-S	1072.1	1807.1	1409.9	MGC23909	NM_174909.1				
GI_28372534-S	83.1	83.2	86.2	TCTE3	NM_174910.1				
GI_28372536-S	147.2	133.6	134.6	LOC197322	NM_174917.1		catalytic		metabolis
GI_28372538-S	420.1	611.7	705.7	LOC201895	NM_174921.1				
GI_28372542-S	87.4	93.4	93.5	LOC204474	NM_174924.1		electron	membran	transport
GI_28372544-S	532.6	486.4	435.4	LOC205251	NM_174925.1				
GI_28372546-S	407.4	478.2	361.9	LOC221143	NM_174928.1		N-		DNA
GI_28372550-S	104.1	104.4	105.1	BPIL2	NM_174932.1	dJ149A16.7	lipid		
GI_28372554-S	112.7	119.9	106.2	SCN4B	NM_174934.1				
GI_28372558-S	120.4	133.7	108.1	TCERG1L	NM_174937.1	FLJ38950			
GI_28372560-S	414.2	482.2	557.5	LOC283232	NM_174940.1				
GI_28372562-S	242.6	274.6	235	LOC283431	NM_174942.1				cell cycle
GI_28372566-S	241.4	238.3	218.9	ZNF575	NM_174945.1				

GI_28372568-S	94.1	97	89	LOC131368	NM_175056.1				
GI_28373062-A	83.1	88.1	98.4	KCNIP4	NM_147183.2	CALP;KCHIP4;MGC44947			
GI_28373062-I	89.9	84.5	83.7	KCNIP4	NM_147183.2	CALP;KCHIP4;MGC44947			
GI_28373063-I	152.5	176.4	159.9	KCNIP4	NM_025221.4	CALP;KCHIP4;MGC44947			
GI_28373064-S	93.8	104.1	96.9	KCNQ5	NM_019842.2	Kv7.5	inward	voltage-	synaptic
GI_28373079-S	133.9	289.1	294.5	SIAT9	NM_003896.2	ST3GalV;SIATGM3S	neolactote	integral to	glycosphin
GI_28373083-A	456.6	430.5	494.1	SIAT6	NM_174970.1	ST3N;ST3GALII;ST3GalIII;ST3Gal III	N-	Golgi	protein
GI_28373091-A	764.4	1023.2	1152.9	SIAT7D	NM_175039.1	SIAT3C;ST6GALNAC4;ST6GALNACIV	sialyltransf	soluble	glycolipid
GI_28373095-S	160.9	191.5	168.3	SIAT8A	NM_003034.2	GD3S;SIAT8;ST8SiaI;ST8Sia I	sialyltransf	Golgi	glycosphin
GI_28373096-S	131.2	148.2	137.7	SIAT8B	NM_006011.2	STX;HsT19690;ST8SIA-II	sialyltransf	Golgi	N-glycan
GI_28373098-A	91.6	107.1	107.9	SIAT8D	NM_175052.1	PST;PST1;MGC34450;MGC61459;ST8SIA-	sialyltransf	Golgi	oligosacch
GI_28373098-I	106	102.8	98.3	SIAT8D	NM_175052.1	PST;PST1;MGC34450;MGC61459;ST8SIA-	sialyltransf	Golgi	oligosacch
GI_28373100-S	110	114.4	108.3	SIAT8E	NM_013305.2	ST8SiaV;ST8Sia V	sialyltransf	Golgi	glycosphin
GI_28373114-A	332.8	438.1	371.9	ATP2A3	NM_174958.1	SERCA3	adenosine	endoplas	small
GI_28373118-A	119.3	122.9	116.1	CNTN1	NM_175038.1	F3;GP135	cell	peripheral	cell
GI_28373120-S	200.3	231.8	198.9	CNTN2	NM_005076.2	AXT;TAX;TAX1;TAG-1	cell	integral to	cell
GI_28373121-I	133.2	129.1	131.7	CNTN4	NM_175607.1	AXCAM;BIG-2;CNTN4A;MGC33615			
GI_28373123-I	132.4	147	125.6	CNTN4	NM_175612.1	AXCAM;BIG-2;CNTN4A;MGC33615			
GI_28373125-A	129	131.2	127.8	CNTN4	NM_175613.1	AXCAM;BIG-2;CNTN4A;MGC33615			
GI_28373127-I	100.1	125.4	116.8	CNTN5	NM_014361.2	NB-2;HNB-2s			
GI_28373128-A	90.7	79.9	83.5	CNTN5	NM_175566.1	NB-2;HNB-2s			
GI_28373130-S	91.1	103.9	90.1	CNTN6	NM_014461.2	NB3	ATP	membran	central
GI_28373193-A	2294.1	2292.7	2898.6	ADRM1	NM_175573.1	GP110;MGC29536	tumor	membran	cell
GI_28376641-S	90.5	94.4	91.2	HGNT-IV-H	NM_013244.2	GNTIVH	alpha-1,3-	membran	carbohydr
GI_28376642-S	85.7	82.2	78.7	KLF8	NM_007250.2	BKLF3;DXS741;ZNF741	DNA	nucleus	regulation
GI_28376643-S	598.9	599.3	482.3	GTF2H3	NM_001516.3	BTF2;TFIIH	translation	transcripti	DNA
GI_28376644-S	438.7	710.5	661	MGC10500	NM_031477.2				
GI_28376645-S	1557.2	2098.2	2334.6	HMG1L10	NM_172363.1	bK445C9.3	DNA	chromatin	chromoso
GI_28376647-S	300.8	345.8	302.4	FLJ33590	NM_173821.1				
GI_28376649-S	189.9	222.1	189.3	DKFZp313N0	NM_173826.1				
GI_28376651-S	95.3	108.2	107.2	FLJ25851	NM_174927.1				
GI_28376657-S	143.7	172	166.3	MGC39518	NM_173822.1				
GI_28376659-S	252.4	294	291.9	RABL3	NM_173825.1	MGC23920	small		small
GI_28376663-S	111.9	112	115.4	ANUBL1	NM_174890.1	FLJ40185	molecular		
GI_28376665-S	102.2	93.8	99	MGC39724	NM_174906.1				
GI_28376667-S	435.4	384.4	297	MGC17839	NM_174926.1				
GI_28395019-S	263.5	336.8	295.5	NCR2	NM_004828.2	LY95;NKP44;NK-p44	transmem	integral to	killer
GI_28395034-A	1056.4	1112.5	979.3	CPR8	NM_004748.2	KIAA1254			
GI_28395034-I	80.8	95.3	87.4	CPR8	NM_004748.2	KIAA1254			
GI_28395040-S	104.5	112.8	105.8	NY-REN-7	NM_173663.1	KIAA0752			
GI_28395048-S	316.6	334.3	299	FLJ38991	NM_173827.1			mitochond	signal
GI_28395050-S	127.5	154.7	139.4	FLJ38348	NM_174931.1				
GI_28395052-S	93.4	108.9	86.3	FLJ35487	NM_173820.1				
GI_28411949-A	359.8	289.1	322.1	C14orf130	NM_175748.1	MGC9518;FLJ10483	ubiquitin-		ubiquitin

GI_28411949-I	276.9	374.3	287.2	C14orf130	NM_175748.1	MGC9518;FLJ10483	ubiquitin-		ubiquitin
GI_28416399-I	149.4	169.5	164.2	TJP1	NM_003257.2	ZO-1	protein	septate	intercellula
GI_28416401-A	1396.4	1173.7	1132.3	TJP1	NM_175610.1	ZO-1	protein	septate	intercellula
GI_28416423-A	135.9	160.7	148.8	SLA2	NM_175077.1	SLAP2;SLAP-		membran	intracellula
GI_28416425-A	228.8	249.8	275.6	VIK	NM_024061.2	MGC5521;FLJ23461;MGC10859;MGC16203			
GI_28416425-I	497.6	536.3	751.5	VIK	NM_024061.2	MGC5521;FLJ23461;MGC10859;MGC16203			
GI_28416426-I	1757.3	1251.2	1085.4	VIK	NM_138494.1	MGC5521;FLJ23461;MGC10859;MGC16203			
GI_28416428-S	83.9	98.3	91.5	hIAN2	NM_024711.2	FLJ22690			
GI_28416430-S	265.3	276.3	157.8	HIMAP2	NM_015660.1	IMAP2;MGC24275;DKFZP586D0824	GTP	integral to	
GI_28416432-S	164	215.6	188.8	HIMAP4	NM_018326.2	IAN1;IMAP4;hIAN1;MSTP062;FLJ11110	GTP		
GI_28416433-S	121	122.7	99.4	HIST4H4	NM_175054.2	MGC24116			
GI_28416434-A	619.9	878.1	742.5	ARFGAP1	NM_018209.2	ARF1GAP;MGC39924;HRIHFB2281	protein	Golgi	intracellula
GI_28416437-S	1217.1	1550.7	1089.9	ARFGAP3	NM_014570.3	ARFGAP1	protein	nucleus	intracellula
GI_28416443-I	82.1	87.4	82.7	GRIK1	NM_175611.1	EAA3;EEA3;GLR5;GLUR5	kainate	integral to	central
GI_28416445-A	96.4	98.9	105.4	GRIK1	NM_000830.2	EAA3;EEA3;GLR5;GLUR5	kainate	integral to	central
GI_28416445-I	86.9	92.5	90.1	GRIK1	NM_000830.2	EAA3;EEA3;GLR5;GLUR5	kainate	integral to	central
GI_28416898-A	1137.3	836.5	484	GART	NM_175085.1	AIRS;GARS;PAIS;PGFT;PRGS;GARTF;MGC	phosphori		
GI_28416898-I	818.5	648.3	404.6	GART	NM_175085.1	AIRS;GARS;PAIS;PGFT;PRGS;GARTF;MGC	phosphori		
GI_28416900-I	2178.7	1988.4	1760.8	GART	NM_000819.3	AIRS;GARS;PAIS;PGFT;PRGS;GARTF;MGC	phosphori		
GI_28416901-S	96.5	93.8	87.6	IL1RL2	NM_003854.2	IL1RRP2;IL1R-rp2	interleukin-	integral to	cellular
GI_28416910-A	118.1	126.3	106.5	IL28RA	NM_173065.1	IFNLR;LICR2;IFNLR1;CRF2/12			
GI_28416912-S	183.9	212.2	186.8	IL27	NM_145659.2	P28;IL30;IL-27;IL27p28	protein	extracellul	regulation
GI_28416914-S	163.9	178.3	172.1	IL3	NM_000588.3	IL-3;MCGF;MULTI-CSF	cytokine	extracellul	positive
GI_28416918-I	118	131.2	117.4	P2RX2	NM_170683.2	P2X2	ligand-	integral to	ion
GI_28416920-A	158.6	190.3	164.7	P2RX2	NM_174872.1	P2X2	ligand-	integral to	ion
GI_28416924-S	124.5	114.8	113.6	P2RX3	NM_002559.2	P2X3	ATP-	integral to	small
GI_28416928-A	234.9	223.7	108.3	P2RX4	NM_175567.1	P2X4;P2X4R	ATP-	integral to	small
GI_28416936-A	102	120	156.9	P2RX5	NM_175081.1	P2X5;P2X5R;MGC47755	ion	integral to	small
GI_28416936-I	134	142.5	138.2	P2RX5	NM_175081.1	P2X5;P2X5R;MGC47755	ion	integral to	small
GI_28416938-S	3587.6	3235.5	2276.9	PLS3	NM_005032.3	T-PLASTIN	actin	actin	
GI_28416939-S	1629.8	1563.2	1803.2	SBDS	NM_016038.2	SDS;CGI-97;FLJ10917	molecular		
GI_28416941-S	528.5	636.4	583.8	SNRPD1	NM_006938.2	SMD1;SNRPD;HsT2456	small	small	mRNA
GI_28416942-S	487.7	365.6	280	SSR3	NM_007107.2	TRAPG	signal	microsom	
GI_28416943-S	4436.9	4224	4259.7	SSRP1	NM_003146.2	FACT;T160	DNA	chromatin	regulation
GI_28416944-S	94.9	93.3	91.5	hIAN7	NM_153236.2	MGC27027			
GI_28416947-S	100.1	96.1	98.6	TIGD4	NM_145720.2	MGC43837	DNA	nucleus	metal ion
GI_28416948-S	277.1	361.5	300	IAN4L1	NM_018384.2	IAN4;IAN5;IMAP3;hIAN5;HIMAP3;FLJ11296			
GI_28416950-S	159.8	175.4	168.5	IL3RA	NM_002183.2	IL3R;CD123;IL3RX;IL3RY;IL3RAY;hIL-	interleukin-	integral to	protein
GI_28416951-S	99.5	104.5	107.3	IMAP1	NM_130759.2	HIMAP1;IMAP38			
GI_28416952-S	118.4	129.4	121.6	ACAS2L	NM_032501.2	AceCS2L;MGC33843			
GI_28416954-S	85.4	107.4	94.5	AZU1	NM_001700.3	AZU;HBP;NAZC;AZAMP;CAP37;HUMAZUR	antibacteri	extracellul	chemotaxi
GI_28416955-S	91	107.2	99.6	hIAN6	NM_175571.1	DKFZp667I133			
GI_28416957-S	162.6	176.7	162.1	HPS3	NM_032383.3	SUTAL;FLJ22704			
GI_28460689-I	107.2	98.2	108.1	ADAMTS20	NM_025003.2		zinc ion	extracellul	proteolysis

GI_28460691-S	349.7	408.7	360.8	LOC153328	NM_145282.1		binding	mitochond	transport
GI_28460693-S	107	108.1	102.8	TRAM1L1	NM_152402.1	MGC26568			
GI_28461128-S	795.6	732	779.2	ANKMY2	NM_020319.1	ZMYND20;DKFZP564O043			
GI_28461132-S	175.2	203.2	190.8	TREM5	NM_174892.1		receptor		
GI_28461170-S	1710.4	1665.2	1768.2	SCRN1	NM_014766.2	SES1;KIAA0193	dipeptidas		proteolysis
GI_28461289-S	100.7	116	104.4	TRALPUSH	NM_053002.2	NOPAR;KIAA1635			
GI_28466978-S	100.3	93.6	98.5	ARHGAP15	NM_018460.2	BM046			
GI_28466982-S	6618.4	6898.7	4591.5	LEPREL2	NM_014262.2	GRCB;HSU47926	oxidoredu		protein
GI_28466986-I	575.4	601.9	563.4	MSCP	NM_018579.2	MSC;HT015;PRO1278;PRO1584			
GI_28466988-S	1664.2	1320.9	1059.7	ATP10D	NM_020453.2	ATPVD;KIAA1487	ATP	integral to	cation
GI_28466990-S	121.2	113	121.3	TTBK2	NM_173500.2	TTBK;KIAA0847			
GI_28466996-S	2964.9	2296.2	2519.9	DLG5	NM_004747.2	PDLG;KIAA0583	protein	membran	negative
GI_28466998-I	134.3	152.6	125	ARG99	NM_175861.1				
GI_28467002-I	121.2	136.2	139.3	KIS	NM_175866.1		cAMP-	cytoplasm	peptidyl-
GI_28557676-I	320.8	424.7	350.3	PHF6	NM_032458.1	BFLS;KIAA1823;MGC14797	electron		electron
GI_28557780-S	303.4	781.2	385.2	PRKCH	NM_006255.2	PKCL;PKC-L;PRKCL;MGC5363	protein		protein
GI_28557782-I	109.2	130.4	113.9	RTN4	NM_020532.3	ASY;NOGO;NSP-CL;KIAA0886	protein	endoplas	apoptosis
GI_28558968-A	289.5	374.5	304.3	CRSP3	NM_015979.2	SUR2;CRSP130;CRSP133;DRIP130;DKFZp	transcripti		transcripti
GI_28558968-I	170.5	175.2	152	CRSP3	NM_015979.2	SUR2;CRSP130;CRSP133;DRIP130;DKFZp	transcripti		transcripti
GI_28558970-I	97.4	105.6	109.4	CRSP3	NM_004830.2	SUR2;CRSP130;CRSP133;DRIP130;DKFZp	transcripti		transcripti
GI_28558972-S	100.4	96.5	93.8	CRSP2	NM_004229.2	CSRP;RGR1;EXLM1;CXORF4;CRSP150;DR	transcripti	nucleus	transcripti
GI_28558974-S	233.2	230.4	212.9	CRSP6	NM_004268.3	CRSP77;DRIP80;TRAP80;FLJ10812	transcripti	nucleus	transcripti
GI_28558976-S	112.3	117.7	121.2	CRSP7	NM_004831.2	CRSP70	transcripti	nucleus	transcripti
GI_28558978-S	2218.9	2420.1	2106	CRSP8	NM_004269.2	CRAP34;CRSP34;MGC11274	transcripti		transcripti
GI_28558980-S	344.5	349.8	353.8	CRSP9	NM_004270.3	MED7;CRSP33;MGC12284	transcripti	nucleus	transcripti
GI_28558989-A	198	770.4	312.2	TPO	NM_175722.1	MSA;TPX	peroxidas	integral to	thyroid
GI_28558991-A	99.3	107.3	95.2	GRIK2	NM_021956.2	EAA4;GLR6;GLUR6	kainate	integral to	small
GI_28558992-I	324.9	444.4	357.4	TG737	NM_175605.2	MGC26259;D13S1056E			excretion
GI_28558997-A	14591.1	13043	9502.2	PTBP1	NM_175847.1	PTB;PTB2;PTB3;PTB4;pPTB;HNRPI;PTB-	poly-	nucleoplas	mRNA
GI_28558999-S	110	107.2	95.7	HIST1H2BA	NM_170610.2	STBP;H2BFU;TSH2B;bA317E16.3	DNA	chromoso	nucleoso
GI_28559000-S	3893.1	4983	2355.5	PRDX6	NM_004905.2	PRX;p29;AOP2;1-	phospholi	cytosol	response
GI_28559001-S	91.1	101.9	101.3	ASB14	NM_130387.4	DKFZp313L0121			intracellula
GI_28559002-I	98	110.2	102.5	GRIK2	NM_175768.1	EAA4;GLR6;GLUR6	kainate	integral to	small
GI_28559004-I	111.9	126.4	108	SSX2	NM_003147.4	SSX;HD21;MGC3884;MGC15364;HOM-MEL-			
GI_28559005-A	2708.7	3138	3443.5	SSX2	NM_175698.1	SSX;HD21;MGC3884;MGC15364;HOM-MEL-			
GI_28559007-I	1044	1265.6	1371.5	SSX3	NM_021014.2	MGC14495	tumor		
GI_28559008-A	1703.6	1511.5	1216.9	SSX3	NM_175711.1	MGC14495	tumor		
GI_28559008-I	197.1	213.6	187	SSX3	NM_175711.1	MGC14495	tumor		
GI_28559010-S	761	960.7	1000.1	SSX1	NM_005635.2	SSRC;MGC5162	transcripti	nucleus	cell growth
GI_28559011-I	588.1	488.6	435.5	SSX4	NM_005636.3	MGC12411	tumor	intracellula	regulation
GI_28559012-A	423.6	485.2	491.6	SSX4	NM_175729.1	MGC12411	tumor	intracellula	regulation
GI_28559014-I	88.1	84.4	75	SSX5	NM_021015.3	MGC9494	tumor	intracellula	regulation
GI_28559016-A	563.5	668.9	613.4	SSX5	NM_175723.1	MGC9494	tumor	intracellula	regulation
GI_28559018-S	601.5	789.7	770.8	SSX6	NM_173357.2				

GI_28559030-A	96.9	115.2	103	IL5RA	NM_175728.1	IL5R;CDw125;HSIL5R3;MGC26560	interleukin-	integral to	signal
GI_28559032-S	102.2	106.8	98.4	IL5	NM_000879.2	EDF;TRF;IL-5	interleukin-	extracellul	hypersens
GI_28559038-S	387.7	371.8	307	PPARBP	NM_004774.2	PBP;CRSP1;RB18A;TRIP2;CRSP200;DRIP2	transcripti	obsolete	regulation
GI_28559059-I	90	102.1	108.3	DNMT3B	NM_006892.3	ICF;M.HsaIIIB	DNA	cellular_co	DNA
GI_28559062-A	144.1	163.7	185.3	DNMT3B	NM_175849.1	ICF;M.HsaIIIB	DNA	cellular_co	DNA
GI_28559064-I	124.5	135.3	105.8	DNMT3B	NM_175850.1	ICF;M.HsaIIIB	DNA	cellular_co	DNA
GI_28559066-I	105	91.5	99.1	DNMT3A	NM_022552.3	DNMT3A2;M.HsaIIIA	DNA	nucleus	DNA
GI_28559067-I	92.3	99.2	88	DNMT3A	NM_153759.2	DNMT3A2;M.HsaIIIA	DNA	nucleus	DNA
GI_28559070-A	118	130.2	120.3	DNMT3A	NM_175630.1	DNMT3A2;M.HsaIIIA	DNA	nucleus	DNA
GI_28559070-I	142.3	171.9	166.1	DNMT3A	NM_175630.1	DNMT3A2;M.HsaIIIA	DNA	nucleus	DNA
GI_28559072-I	123.6	144.8	121.8	SMOX	NM_019025.2	PAO;SMO;PAOh1;MGC1010;C20orf16;FLJ2			
GI_28559077-A	2064	2134.4	1036.5	SMOX	NM_175841.1	PAO;SMO;PAOh1;MGC1010;C20orf16;FLJ2			
GI_28559079-I	168.5	189.7	176.2	SMOX	NM_175842.1	PAO;SMO;PAOh1;MGC1010;C20orf16;FLJ2			
GI_28559082-A	840.8	666.3	643.4	CTPS2	NM_019857.3	MGC32997	CTP		pyrimidine
GI_28559082-I	79.4	91.5	76.9	CTPS2	NM_019857.3	MGC32997	CTP		pyrimidine
GI_28559084-I	100.2	100.5	82.4	CTPS2	NM_175859.1	MGC32997	CTP		pyrimidine
GI_28559087-S	125.4	143.1	114.6	LAMA2	NM_000426.2	LAMM	structural	basement	muscle
GI_28559089-S	1086.2	1220.1	1305.5	MLH1	NM_000249.2	FCC2;COCA2;HNPCC;hMLH1;HNPCC2;MG	adenosine	nucleus	mismatch
GI_28565284-A	180.8	234	194.4	USP2	NM_171997.1	USP9;UBP41	cysteine-		deubiquiti
GI_28565284-I	311.9	354.1	346.7	USP2	NM_171997.1	USP9;UBP41	cysteine-		deubiquiti
GI_28570169-S	88	88.3	90.3	OR8B8	NM_012378.1	TPCR85	G-protein	integral to	chemosen
GI_28603817-S	114.1	129.8	119.6	MGC27169	NM_176782.1				
GI_28603839-S	2967.3	2710.5	2498.1	MGC10120	NM_173809.1				
GI_28605122-I	116	132.7	123	PSMD10	NM_002814.2	p28		proteasom	
GI_28605136-A	1582	2059.5	1961.8	PSMD10	NM_170750.1	p28		proteasom	
GI_28605144-S	117	122.4	105.6	GRIK3	NM_000831.2	EAA5;GLR7;GLUR7	glutamate	membran	small
GI_28610146-I	108.4	130.3	118.9	IL6ST	NM_002184.2	CD130;GP130;CDw130;IL6R-beta;GP130-	gp130	integral to	cell
GI_28610148-A	103.8	110	101.9	IL6ST	NM_175767.1	CD130;GP130;CDw130;IL6R-beta;GP130-	gp130	integral to	cell
GI_28610150-S	132.2	139.5	114.1	IL7R	NM_002185.2	CD127;CDW127;IL-7R-alpha	antigen	integral to	regulation
GI_28610152-S	135.7	154	145.5	IL7	NM_000880.2	IL-7	interleukin-	extracellul	positive
GI_28610153-S	700.1	539.4	392.9	IL8	NM_000584.2	K60;NAF;GCP1;IL-8;LECT;LUCT;NAP1;3-	interleukin-	obsolete	negative
GI_28610154-A	272.4	255.7	278.8	CBFA2T2	NM_005093.2	EHT;MTGR1;ZMYND3	transcripti	nucleus	cell
GI_28610155-I	133.9	145.9	145.3	CBFA2T2	NM_175864.1	EHT;MTGR1;ZMYND3	transcripti	nucleus	cell
GI_28626509-S	833.4	353.2	200.1	RCN3	NM_020650.2	RLP49	calcium	endoplas	
GI_28626515-S	377.8	669.9	451.6	PNMA2	NM_007257.3				
GI_28626518-S	149.8	175.4	178.9	PSD	NM_002779.2	TYL;KIAA2011	signal	cellular_co	signal
GI_28626520-S	588.2	831.3	987.8	KIAA1404	NM_021035.1	FLJ11277			
GI_28629867-S	87.6	92.6	87.8	RAG2	NM_000536.1		endonucle	nucleus	DNA
GI_28629870-S	88	105	87	C20orf135	NM_080622.1	dJ591C20.1			
GI_28827773-S	700.6	747.8	651.9	DYRK4	NM_003845.1		protein	cellular_co	protein
GI_28827775-S	107.1	103.6	98.9	LY9	NM_002348.1	hly9;mLY9;CD229;SLAMF3	lymphocyt	integral to	homophili
GI_28827777-S	715	765.1	761.3	SEPN1	NM_020451.1	RSS;SELN;MDRS1;RSMD1	selenium	extracellul	biological_
GI_28827788-S	106.5	126.8	126	NALP13	NM_176810.1	NOD14	sugar		phosphoe
GI_28827796-S	101.6	106.2	98.5	TAS2R38	NM_176817.1	PTC;T2R61			

GI_28830307-S	105.8	109.1	118.6	SULT1C2	NM_006588.2	SULT1C	sulfotransf	cellular_co	biological_
GI_28849872-S	114	126.5	100.3	KIAA1383	NM_019090.1				
GI_28866946-S	171	148.6	145.4	MT1F	NM_005949.1	MT1;MGC32732	zinc ion	cytoplasm	response
GI_28866948-S	95.6	100.5	88	ILT10	NM_024317.2	LILRA5	receptor		
GI_28866959-S	104.7	128.5	111.1	MT1A	NM_005946.1	MT1;MTC;MGC32848	heavy	cytoplasm	heavy
GI_28866965-S	474.7	390.9	715.4	MT1K	NM_176870.1	MT1;MT1M;MGC40498			
GI_28872718-S	486.2	824.4	417.9	BTG2	NM_006763.2	PC3;TIS21	cell cycle		DNA
GI_28872719-A	171.9	200.2	188.8	P2RY2	NM_002564.2	P2U;HP2U;P2U1;P2UR;P2Y2;P2RU1;P2Y2R	receptor	integral to	cell ion
GI_28872721-S	2019.3	2374.9	1797.5	BTG3	NM_006806.3	ANA;TOB5;TOFA;TOB55;MGC8928			negative
GI_28872723-S	141.1	141.7	146.2	BTG4	NM_017589.2	PC3B;MGC33003			
GI_28872724-S	5577.8	6724.9	6174.8	PSMD11	NM_002815.2	S9;p44.5;MGC3844		26S	
GI_28872727-A	3026.6	4035	3258.4	PSMD13	NM_002817.2	p40.5;HSPC027		proteasom	
GI_28872729-I	101	104.3	98.8	PSMD13	NM_175932.1	p40.5;HSPC027		proteasom	
GI_28872731-I	128.3	119.3	100.3	MRPL43	NM_176792.1	bMRP36a;MGC17989;MGC48892	structural		
GI_28872733-I	1842	1940.3	1955.9	MRPL43	NM_032112.2	bMRP36a;MGC17989;MGC48892	structural		
GI_28872735-A	746.5	697.2	796.1	MRPL43	NM_176793.1	bMRP36a;MGC17989;MGC48892	structural		
GI_28872737-I	105.6	111.2	108.7	MRPL43	NM_176794.1	bMRP36a;MGC17989;MGC48892	structural		
GI_28872739-A	1017	1243	1229.3	MRPS11	NM_176805.1	HCC-2;FLJ22512;FLJ23406	structural	ribosome	protein
GI_28872741-S	130.2	145.4	131.6	P2RY1	NM_002563.2	P2Y1	receptor	integral to	G-protein
GI_28872742-I	87.7	94.2	85.2	P2RY2	NM_176071.1	P2U;HP2U;P2U1;P2UR;P2Y2;P2RU1;P2Y2R	receptor	integral to	cell ion
GI_28872744-I	88.1	98.3	89.8	P2RY2	NM_176072.1	P2U;HP2U;P2U1;P2UR;P2Y2;P2RU1;P2Y2R	receptor	integral to	cell ion
GI_28872746-S	107.9	98.1	92.8	P2RY4	NM_002565.2	NRU;P2P;UNR;P2Y4	uridine	integral to	cytosolic
GI_28872747-S	682.8	639	553.8	HIST3H2A	NM_033445.2	MGC3165	DNA	nucleus	nucleoso
GI_28872748-S	100.3	102.7	103.5	HIST3H2BB	NM_175055.2		DNA	chromoso	nucleoso
GI_28872749-I	128.8	129.5	125.3	DUOX1	NM_017434.3	LNOX1;THOX1;NOXEF1			
GI_28872750-A	95.5	93.7	114	DUOX1	NM_175940.1	LNOX1;THOX1;NOXEF1			
GI_28872752-S	230.5	294	271.3	DUOX2	NM_014080.3	LNOX2;THOX2;NOXEF2;P138-TOX	flavin-	membran	electron
GI_28872754-A	136.4	126.3	128.4	FGF14	NM_004115.2	FHF4	growth	extracellul	signal
GI_28872754-I	122.8	126	106.9	FGF14	NM_004115.2	FHF4	growth	extracellul	signal
GI_28872755-I	95.4	80.5	96.2	FGF14	NM_175929.1	FHF4	growth	extracellul	signal
GI_28872757-I	165.1	209.4	149	PRPF4B	NM_003913.3	PR4H;PRP4;PRP4H;PRP4K;KIAA0536	protein	nucleus	RNA
GI_28872758-A	287.4	250.7	189.7	PRPF4B	NM_176800.1	PR4H;PRP4;PRP4H;PRP4K;KIAA0536	protein	nucleus	RNA
GI_28872758-I	91.5	89.3	90.6	PRPF4B	NM_176800.1	PR4H;PRP4;PRP4H;PRP4K;KIAA0536	protein	nucleus	RNA
GI_28872760-A	113.2	124.6	130.3	MTMR1	NM_003828.1		protein		protein
GI_28872762-I	141.2	159.4	159	MTMR1	NM_176789.1		protein		protein
GI_28872764-A	347	430.9	282.4	PSMD12	NM_174871.1	p55		proteasom	
GI_28872775-A	129	145.6	139.2	DNMT2	NM_176086.1	PuMet;M.HsaIIP	DNA	nucleus	DNA
GI_28872779-A	89.5	95.3	88.2	DNMT3L	NM_175867.1	MGC1090	transcripti	nucleus	DNA
GI_28872781-I	191.5	204.1	231.5	CDK5RAP1	NM_016408.2	C42;CGI-05;HSPC167;C20orf34	molecular	cellular_co	brain
GI_28872783-A	1024.8	1050.5	1483.4	CDK5RAP1	NM_016082.3	C42;CGI-05;HSPC167;C20orf34	molecular	cellular_co	brain
GI_28872785-S	1205.9	1822.2	1108.4	CDK5RAP2	NM_018249.3	C48	translation	cytoskelet	brain
GI_28872789-I	334.2	405.1	401.5	CDK5RAP3	NM_176095.1	C53;IC53;HSF-27;MST016;OK/SW-cl.114	neuronal	cellular_co	regulation
GI_28872791-A	2499.8	2117.9	2151.5	CDK5RAP3	NM_176096.1	C53;IC53;HSF-27;MST016;OK/SW-cl.114	neuronal	cellular_co	regulation
GI_28872793-S	187.4	240.7	182.9	CEBPA	NM_004364.2	CEBP;C/EBP-alpha	transcripti	nucleus	energy

GI_28872795-S	14320	12523	15287	CEBPB	NM_005194.2	LAP;CRP2;TCF5;IL6DBP;NF-	transcripti	nucleus	acute-
GI_28872797-S	533.7	847.9	509.8	CEBPD	NM_005195.2	CELF;CRP3;C/EBP-delta;NF-IL6-beta	DNA	nucleus	transcripti
GI_28872799-S	179.6	189.9	190.3	CEBPE	NM_001805.2	CRP1;C/EBP-epsilon	transcripti	nucleus	defense
GI_28872801-S	2553.5	2822.7	2446.2	C1QBP	NM_001212.3	p32;HABP1;gC1qR;GC1QBP;SF2p32;gC1Q-		mitochond	immune
GI_28872802-I	103.5	95.9	89.7	CBFA2T3	NM_005187.4	MTG16;MTGR2;ZMYND4	transcripti		cell
GI_28872804-A	112.7	111.8	105	CBFA2T3	NM_175931.1	MTG16;MTGR2;ZMYND4	transcripti		cell
GI_28872804-I	100.5	102.5	94.4	CBFA2T3	NM_175931.1	MTG16;MTGR2;ZMYND4	transcripti		cell
GI_28872806-S	155.9	209.1	165.8	CBLNL1	NM_080617.3	dJ885A10.1			
GI_28872807-S	127.1	191.6	268.4	GAP43	NM_002045.2	B-50;PP46	calmoduli	membran	response
GI_28872808-S	196.3	223.5	224.2	MATP	NM_016180.2	1A1;AIM1		integral to	melanin
GI_28872811-S	206.3	241.3	182.7	ZCWCC3	NM_015358.1	NXP2;KIAA0136	ATP		
GI_28872813-S	301.3	366.8	306.5	SEMA4G	NM_017893.2	FLJ20590;KIAA1619			
GI_28872862-S	623.6	707.9	811.7	KIAA1194	NM_015455.2	DKFZP564G1964			
GI_28875781-S	866.5	908.4	717.8	DKFZp761C1	NM_022913.1	GPBP			
GI_28875783-S	286.3	299.7	270.4	FLJ13063	NM_024742.1	FLJ00019			
GI_28875785-S	150.1	184.6	161.1	FLJ00007	NM_033449.1				
GI_28875796-S	1432.6	1301.9	1118.4	DKFZP547E1	NM_015607.2				
GI_28875802-S	102.3	146.5	113.4	KIAA1924	NM_153239.2	FLJ36483			
GI_28882025-S	100.5	103.4	91.9	TAS2R39	NM_176881.1		G-protein	integral to	G-protein
GI_28882027-S	119.1	122.7	121.7	TAS2R41	NM_176883.1	T2R59	G-protein	integral to	G-protein
GI_28882030-S	104.8	117	107.9	TAS2R44	NM_176885.1	T2R53			
GI_28882032-S	103.5	109.8	95.6	TAS2R40	NM_176882.1		G-protein	integral to	G-protein
GI_28882034-S	113	115.6	113.5	TAS2R48	NM_176888.1		G-protein	integral to	G-protein
GI_28882036-S	86.6	99.8	92.3	TAS2R43	NM_176884.1	T2R52			
GI_28882038-S	86.1	82.5	94.5	TAS2R50	NM_176890.1	T2R51			
GI_28882040-S	105.7	109.7	102.2	TAS2R46	NM_176887.1	T2R54	G-protein	integral to	G-protein
GI_28882046-S	107.5	109.2	106.8	TAS2R49	NM_176889.1	T2R56			
GI_28882054-S	139.1	172	159.6	NRF1	NM_005011.2	ALPHA-PAL	transcripti	nucleus	energy
GI_28893580-A	128.9	166.1	147.8	LMX1A	NM_177398.1	LMX1;LMX-1;LMX1.1	transcripti	nucleus	regulation
GI_28912911-S	89.9	103	87.2	NKX6-2	NM_177400.1	GTX;NKX6B;NKX6.1;NKX6.2	transcripti	nucleus	regulation
GI_28916690-A	132.8	226.6	194.8	MUC1	NM_002456.3	EMA;PEM;PUM;CD227	actin	cytoskelet	
GI_28916695-A	143.1	162.7	117.1	GTF2IRD2	NM_032203.3	FLJ21423			
GI_28916697-S	344.9	296.9	295.2	LOC63920	NM_022090.2				
GI_28933450-S	263.4	260.3	112	PLXND1	NM_015103.1	PLEXD1;KIAA0620	receptor	membran	developm
GI_28933464-S	524.2	474	379.1	STX12	NM_177424.1	STX13;STX14;MGC51957	protein	membran	intracellula
GI_28951070-S	102.3	125.2	126.4	NOD27	NM_032206.2	FLJ21709			
GI_28973794-S	112.6	125	111.1	TAS2R60	NM_177437.1	T2R60	G-protein	integral to	G-protein
GI_28973798-I	128.2	146.5	169.8	MGC3123	NM_177441.1				
GI_29029527-S	117	98.1	103.2	TRIM42	NM_152616.3	FLJ40097			
GI_29029528-S	2361.4	2455.1	2168.2	TRIM44	NM_017583.3	MC7;DIPB;MGC3490;HSA249128	zinc ion	intracellula	
GI_29029529-I	146.9	174.3	171.2	SULT1C1	NM_176825.1	ST1C1;ST1C2;SULT1C#1;humSULTC2	sulfotransf	cytoplasm	amine
GI_29029531-A	235.1	217.5	141.4	SULT1C1	NM_001056.2	ST1C1;ST1C2;SULT1C#1;humSULTC2	sulfotransf	cytoplasm	amine
GI_29029531-I	205	224.1	167.6	SULT1C1	NM_001056.2	ST1C1;ST1C2;SULT1C#1;humSULTC2	sulfotransf	cytoplasm	amine
GI_29029532-A	142	153.2	137.8	SULT4A1	NM_014351.2	NST;BRSTL1;SULTX3;BR-STL-	sulfotransf	cytosol	steroid

GI_29029533-I	86.8	95	88.8	SULT4A1	NM_176874.1	NST;BRSTL1;SULTX3;BR-STL-	sulfotransf	cytosol	steroid
GI_29029541-I	90.7	94.3	87.4	INADL	NM_005799.2	PATJ			
GI_29029543-I	119.3	134.7	126	INADL	NM_170605.2	PATJ			
GI_29029545-A	108.8	123.5	103.1	INADL	NM_176877.1	PATJ			
GI_29029547-I	92.4	100.8	87.6	INADL	NM_176878.1	PATJ			
GI_29029549-I	181.4	240.2	223.8	CECR1	NM_017424.2		growth	cellular_co	nucleotide
GI_29029551-A	152.1	203.2	161.3	CECR1	NM_177405.1		growth	cellular_co	nucleotide
GI_29029551-I	103	116.5	93.7	CECR1	NM_177405.1		growth	cellular_co	nucleotide
GI_29029553-S	408.9	464	414.9	BBS1	NM_024649.4	BBS2L2;FLJ23590			
GI_29029554-A	168.6	180.4	188.1	BBS7	NM_018190.2	BBS2L1;FLJ10715			vision
GI_29029554-I	128.6	172.7	158.5	BBS7	NM_018190.2	BBS2L1;FLJ10715			vision
GI_29029556-I	258.8	258.3	262.2	BBS7	NM_176824.1	BBS2L1;FLJ10715			vision
GI_29029558-I	2409.1	2639.7	3306.6	CSE1L	NM_001316.2	CAS;CSE1;XPO2	importin-	nuclear	nucleocyto
GI_29029560-A	1170.4	1138.2	1212	CSE1L	NM_177436.1	CAS;CSE1;XPO2	importin-	nuclear	nucleocyto
GI_29029560-I	162.2	155.1	152.3	CSE1L	NM_177436.1	CAS;CSE1;XPO2	importin-	nuclear	nucleocyto
GI_29029562-A	187.7	192.1	179.8	CTMP	NM_053055.2	MGC29636			
GI_29029570-I	105.9	120.1	108.6	CD86	NM_006889.2	B70;B7-2;LAB72;CD28LG2;MGC34413	receptor	integral to	positive
GI_29029571-A	110.8	141.2	126.8	CD86	NM_175862.2	B70;B7-2;LAB72;CD28LG2;MGC34413	receptor	integral to	positive
GI_29029571-I	100.8	104.6	83	CD86	NM_175862.2	B70;B7-2;LAB72;CD28LG2;MGC34413	receptor	integral to	positive
GI_29029588-A	1045.2	1519.2	1249.8	FTSJ1	NM_177434.1	JM23;SPB1;CDLIV	methyltran		rRNA
GI_29029590-I	132.7	141.4	128.5	FTSJ1	NM_177439.1	JM23;SPB1;CDLIV	methyltran		rRNA
GI_29029592-S	231.1	232.8	216.2	EIF2C4	NM_017629.2	AGO4	translation		protein
GI_29029594-S	138.6	123.4	134.5	GRIK4	NM_014619.2	KA1;EAA1;GRIK	kainate	integral to	small
GI_29029596-S	96	92.8	83.5	GRIK5	NM_002088.3	KA2;EAA2			
GI_29029598-S	113.5	122.5	122.3	CYSLTR1	NM_006639.2	HG55;CYSLT1;CYSLTR;CYSLT1R;HMTMF8	leukotrien	membran	cytosolic
GI_29029599-S	167.2	203.1	191.3	CYSLTR2	NM_020377.2	GPCR;HG57;CYSLT2;HPN321;CYSLT2R;hG	leukotrien	integral to	G-protein
GI_29029600-S	1145.1	909.1	1220	DHX37	NM_032656.2	DDX37;MGC2695;MGC4322;KIAA1517;MGC			
GI_29029602-S	499.5	416.1	391.7	P2RY11	NM_002566.3	P2Y11	receptor	integral to	adenylate
GI_29029604-A	122.8	130.1	135.1	P2RY12	NM_176876.1	HORK3;P2Y12;ADPG-	rhodopsin-	integral to	hemostasi
GI_29029606-I	102.3	118.1	107.6	P2RY6	NM_004154.3	P2Y6;MGC15335	G-protein	integral to	G-protein
GI_29029609-A	133.3	198.5	250.6	P2RY6	NM_176797.1	P2Y6;MGC15335	G-protein	integral to	G-protein
GI_29029611-I	104.9	118.7	103.6	P2RY6	NM_176798.1	P2Y6;MGC15335	G-protein	integral to	G-protein
GI_29029613-S	99	111.9	102.6	MAGEA10	NM_021048.3	MAGE10;MGC10599	tumor		
GI_29029614-S	401.1	533.9	406.9	MAGEA11	NM_005366.3	MAGE11;MGC10511	tumor		
GI_29029615-S	1545	161.9	154.9	MAGEA1	NM_004988.3	MAGE1;MGC9326	tumor	plasma	
GI_29029616-I	132.1	138.2	126.5	MAGEA2	NM_005361.2	MAGE2;MAGEA2A	tumor		
GI_29029617-A	181.5	192.2	130.6	MAGEA2	NM_175742.1	MAGE2;MAGEA2A	tumor		
GI_29029619-I	159.9	155.8	149.5	MAGEA2	NM_175743.1	MAGE2;MAGEA2A	tumor		
GI_29029622-S	1892	2135.9	1699	MAGEA3	NM_005362.3	HIP8;HYPD;MAGE3;MGC14613	tumor		
GI_29029623-S	94.2	107.7	99.6	MAGEA4	NM_002362.3	MAGE4;MAGE4A;MAGE4B;MAGE-41;MAGE-	molecular	cellular_co	biological_
GI_29029624-S	114.7	117.8	120.2	MAGEA5	NM_021049.2	MAGE5	molecular	cellular_co	biological_
GI_29029625-A	1656.8	2151.8	1825.9	MAGEA6	NM_005363.2	MAGE6;MAGE3B;MAGE-3b;MGC52297	molecular	cellular_co	biological_
GI_29029626-I	165	186.2	185.1	MAGEA6	NM_175868.1	MAGE6;MAGE3B;MAGE-3b;MGC52297	molecular	cellular_co	biological_
GI_29029628-S	113.7	127.7	119	MAGEA8	NM_005364.3	MAGE8;MGC2182	molecular	cellular_co	biological_

GI_29029631-S	111.2	105	108.3	ALK	NM_004304.3		receptor	integral to	brain
GI_29126184-S	237.9	300.7	284.2	MGC5391	NM_032740.2				
GI_29126186-S	117.7	102.4	109.3	KIAA1984	NM_032874.2	MGC15438;bA216L13.7			
GI_29126188-S	105.6	104.3	96.5	ARHGAP19	NM_032900.2	FLJ00194;MGC14258			
GI_29126221-S	202.2	213.8	231.5	ZSWIM1	NM_080603.2	C20orf162;dJ337O18.5			
GI_29126235-S	90.5	104.4	95.2	PGSF1	NM_174947.2				
GI_29126237-S	20483.9	20423	17389	BTF3	NM_001207.3	NACB;BTF3a;BTF3b;BETA-NAC	RNA	nucleus	transcripti
GI_29126240-S	174.7	207.6	180.1	MTF	NM_177478.1		binding		iron ion
GI_29126244-S	106.4	122.8	117.6	TAS2R45	NM_176886.1	ZG24P	G-protein	integral to	G-protein
GI_29135342-S	11926.5	12162	8876.9	HINT1	NM_005340.2	HINT;PKCI-1;PRKCNH1	protein	cytoskelet	signal
GI_29135352-S	93.9	99.3	99.9	C14orf61	NM_177527.1				
GI_29171294-S	214.8	199.4	140.5	ARHJ	NM_020663.2	TCL;TC10B;RASL7B;FLJ14445	Rho small	cellular_co	small
GI_29171679-S	114.5	124.2	122.4	IL8RA	NM_000634.2	CD128;CXCR1;IL8R1;CMKAR1;IL8RBA;CDw	interleukin-	membran	chemotaxi
GI_29171680-S	110.2	109.5	118.2	IL8RB	NM_001557.2	CXCR2;IL8R2;IL8RA;CMKAR2;CDw128b	interleukin-	cytoplasm	G-protein
GI_29171681-A	100	105.4	93.5	IL9R	NM_002186.2		interleukin-	extracellul	signal
GI_29171681-I	148.5	186	156.6	IL9R	NM_002186.2		interleukin-	extracellul	signal
GI_29171683-I	84.8	99.2	95.1	IL9R	NM_176786.1		interleukin-	extracellul	signal
GI_29171685-A	631.4	605.3	493.1	ILKAP	NM_030768.2	MGC4846;FLJ10181;PP2C-	protein	protein	protein
GI_29171686-I	84.5	95	94.3	ILKAP	NM_176799.1	MGC4846;FLJ10181;PP2C-	protein	protein	protein
GI_29171688-S	126.2	125.3	110.2	ILT7	NM_012276.2	LILRA4	receptor	integral to	immune
GI_29171690-I	1014.8	820.3	725.7	ILVBL	NM_006844.3	AHAS;209L8;ILV2H;MGC1269;MGC19535	protein		protein
GI_29171691-A	924.8	742.7	664.9	ILVBL	NM_176826.1	AHAS;209L8;ILV2H;MGC1269;MGC19535	protein		protein
GI_29171691-I	145.4	153.6	139.9	ILVBL	NM_176826.1	AHAS;209L8;ILV2H;MGC1269;MGC19535	protein		protein
GI_29171701-I	111.6	93.7	93.4	PPA2	NM_176869.1	HSPC124;MGC49850;SID6-306			
GI_29171703-A	1730.2	2170.2	1819.7	MAGED2	NM_014599.4	11B6;BCG1;HCA10;JCL-1;MAGED;MAGE-			
GI_29171703-I	198.8	204.1	207.8	MAGED2	NM_014599.4	11B6;BCG1;HCA10;JCL-1;MAGED;MAGE-			
GI_29171704-I	227	267.8	216.6	MAGED2	NM_177433.1	11B6;BCG1;HCA10;JCL-1;MAGED;MAGE-			
GI_29171706-I	118	122.7	103.3	MAGEB1	NM_002363.3	DAM10;MAGEL1;MAGE-Xp;MGC9322	tumor		
GI_29171708-A	108.5	95.1	93.4	MAGEB1	NM_177404.1	DAM10;MAGEL1;MAGE-Xp;MGC9322	tumor		
GI_29171708-I	104.1	95.8	90.5	MAGEB1	NM_177404.1	DAM10;MAGEL1;MAGE-Xp;MGC9322	tumor		
GI_29171715-S	97.4	111.6	96	MAGEB4	NM_002367.2	MGC33144	tumor		
GI_29171716-I	140.9	156.6	136.8	GPLD1	NM_001503.2	GPIPLD;PIGPLD;GPIPLDM;PIGPLD1;MGC2	phospholi		
GI_29171718-A	95.5	88.4	80.1	GPLD1	NM_177483.1	GPIPLD;PIGPLD;GPIPLDM;PIGPLD1;MGC2	phospholi		
GI_29171718-I	88.3	116.5	102.1	GPLD1	NM_177483.1	GPIPLD;PIGPLD;GPIPLDM;PIGPLD1;MGC2	phospholi		
GI_29171720-I	85.5	88.9	87.5	GPR86	NM_023914.2	GPCR1;GPR94;P2Y13;SP174;FKSG77	receptor	integral to	G-protein
GI_29171722-A	294.6	360.9	335.4	GPR86	NM_176894.1	GPCR1;GPR94;P2Y13;SP174;FKSG77	receptor	integral to	G-protein
GI_29171722-I	117.8	118.7	113.7	GPR86	NM_176894.1	GPCR1;GPR94;P2Y13;SP174;FKSG77	receptor	integral to	G-protein
GI_29171724-S	100.4	99.3	92.1	HIST1H2AA	NM_170745.2	H2AFR;bA317E16.2	DNA	nucleus	nucleoso
GI_29171725-S	100.9	97.9	99.7	PLN	NM_002667.2	PLB	calcium	smooth	calcium
GI_29171726-A	436.7	357.6	475.3	CYP20A1	NM_020674.2	CYP-M;MGC22229			
GI_29171728-S	127.7	144.3	121.7	HIST2H2AB	NM_175065.2		DNA	nucleus	nucleoso
GI_29171729-I	111.5	103.5	116.4	CYP20A1	NM_177538.1	CYP-M;MGC22229			
GI_29171731-S	325.8	382.6	348.8	CPXM	NM_019609.2	CPX1	carboxype		proteolysis
GI_29171732-S	642.9	849.8	852.7	EIF2C1	NM_012199.2	Q99;AGO1;EIF2C;GERP95	translation	eukaryotic	regulation

GI_29171733-S	378	353.9	385.6	EIF2C2	NM_012154.2	Q10;AGO2;MGC3183	translation	cellular_co	protein
GI_29171735-A	269.7	274.7	309.6	PPAP2A	NM_003711.2	PAP2;PAP-2a	protein	membran	germ-cell
GI_29171735-I	193.2	191.7	188.6	PPAP2A	NM_003711.2	PAP2;PAP-2a	protein	membran	germ-cell
GI_29171737-I	121.7	142.8	118.2	PPAP2A	NM_176895.1	PAP2;PAP-2a	protein	membran	germ-cell
GI_29171739-I	154.8	139	143.4	PPAP2B	NM_003713.3	VCIP;Dri42;PAP-2b;PAP2-b;MGC15306	protein	membran	germ-cell
GI_29171741-A	428.3	431.3	253.9	PPAP2B	NM_177414.1	VCIP;Dri42;PAP-2b;PAP2-b;MGC15306	protein	membran	germ-cell
GI_29171744-A	1875.5	1820.7	1906.8	PPAP2C	NM_177526.1	PAP-2c;PAP2-g	protein	membran	
GI_29171746-I	155	177.4	160	PPAP2C	NM_177543.1	PAP-2c;PAP2-g	protein	membran	
GI_29171748-I	452.6	480.6	404.2	PPARD	NM_006238.2	FAAR;NUC1;NUCI;NR1C2;NUCII;PPARB;M	steroid	nucleus	lipid
GI_29171749-A	144.5	165.8	142.9	PPARD	NM_177435.1	FAAR;NUC1;NUCI;NR1C2;NUCII;PPARB;M	steroid	nucleus	lipid
GI_29171749-I	132.2	153.8	154.2	PPARD	NM_177435.1	FAAR;NUC1;NUCI;NR1C2;NUCII;PPARB;M	steroid	nucleus	lipid
GI_29171751-I	1409.8	1230.6	894.5	PPFIA1	NM_003626.2	LIP1;LIP.1;LIPRIN;MGC26800	signal	focal	cell-matrix
GI_29171752-A	266.2	249.5	267.8	PPFIA1	NM_177423.1	LIP1;LIP.1;LIPRIN;MGC26800	signal	focal	cell-matrix
GI_29171752-I	184	161.5	245.1	PPFIA1	NM_177423.1	LIP1;LIP.1;LIPRIN;MGC26800	signal	focal	cell-matrix
GI_29171754-S	93.3	91.7	79.1	PPFIA2	NM_003625.2		cell	focal	cell-matrix
GI_29171756-S	10221.8	10195	7065.4	NPC2	NM_006432.3	HE1;NP-C2;MGC1333	molecular	cellular_co	biological_
GI_29171757-S	134.8	163	140.1	DCSTAMP	NM_030788.2	FIND	phospholi	integral to	lipid
GI_29171760-S	5859.8	5165.2	4308.9	PP	NM_021129.2	PPA1;IOPPP;PPase;SID6-8061	inorganic		phosphate
GI_29171761-S	91.6	88.1	81.9	GSC	NM_173849.2		transcripti	nucleus	gastrulatio
GI_29244580-S	296.3	304.5	272.9	HIP14	NM_015336.1	HIP3;HYPH;ZDHHC17;KIAA0946			
GI_29244922-S	697.1	572.4	360.7	CGI-09	NM_015939.3	MGC5029			
GI_29244923-S	298	361.6	418.3	CHD6	NM_032221.3	CHD5;RIGB;KIAA1335	transporte	membran	transport
GI_29244925-S	115	130.6	118.2	CRN	NM_006587.2	ATC2	serine-	integral to	regulation
GI_29294620-A	181.5	226.6	194.8	TAS1R1	NM_177541.1	TR1;T1R1;GPR70;gm148			
GI_29294622-A	13348.6	14335	12264	SNRPD2	NM_004597.4	SMD2	small	spliceoso	mRNA
GI_29294623-I	185.8	175	158.8	SNRPD2	NM_177542.1	SMD2	small	spliceoso	mRNA
GI_29294626-I	308.4	249.6	257.4	PPFIBP1	NM_003622.2	L2	protein	plasma	cell
GI_29294628-A	120.1	122.8	113.6	PPFIBP1	NM_177444.1	L2	protein	plasma	cell
GI_29294628-I	107.3	118.5	90.6	PPFIBP1	NM_177444.1	L2	protein	plasma	cell
GI_29294634-I	100.4	100.2	101.7	MEST	NM_177524.1	PEG1;MGC8703	epoxide		mesoderm
GI_29294636-A	112.9	121.9	121.9	MEST	NM_177525.1	PEG1;MGC8703	epoxide		mesoderm
GI_29294636-I	106.4	112.5	106.4	MEST	NM_177525.1	PEG1;MGC8703	epoxide		mesoderm
GI_29294638-I	121.6	121.1	119.8	MEST	NM_002402.2	PEG1;MGC8703	epoxide		mesoderm
GI_29294642-A	83.4	92.6	91.5	LYNX1	NM_177458.1	SLURP2;MGC40364			
GI_29294642-I	122.6	124.8	129.9	LYNX1	NM_177458.1	SLURP2;MGC40364			
GI_29294644-I	111	104.1	105.7	LYNX1	NM_177477.1	SLURP2;MGC40364			
GI_29294646-I	139.5	159.4	165.6	EIF2C3	NM_024852.2	AGO3;FLJ12765			
GI_29294648-A	384.7	376.1	436.8	DICER1	NM_030621.2	Dicer;HERNA;KIAA0928	double-	intracellula	RNA
GI_29294648-I	89.3	79	79.6	DICER1	NM_030621.2	Dicer;HERNA;KIAA0928	double-	intracellula	RNA
GI_29294650-I	102.7	103.9	95.8	DICER1	NM_177438.1	Dicer;HERNA;KIAA0928	double-	intracellula	RNA
GI_29294652-I	199.1	219.9	197.6	FTSJ2	NM_177442.1	FJH1	methyltran	nucleus	rRNA
GI_29294654-A	135.8	147.3	126.8	MAGEC3	NM_177456.1	HCA2;MAGE-C3			
GI_29294654-I	80	85.6	82	MAGEC3	NM_177456.1	HCA2;MAGE-C3			
GI_29336036-S	103.5	89.7	97	KIAA1444	NM_032512.1	LU1	protein		intracellula

GI_29336042-S	130.6	114.1	93.6	ATCAY	NM_033064.1	CLAC;BNIP-H;KIAA1872			transport
GI_29336076-S	109.2	105.3	100.8	UNC93A	NM_018974.2	dJ366N23.1;dJ366N23.2			
GI_29336082-S	195.6	289.2	264.5	FLJ12584	NM_025139.2	ARM;KIAA1868			
GI_29337282-I	98.1	86.9	92.6	LYNX1	NM_177476.1	SLURP2;MGC40364			
GI_29337284-S	1978.1	1435	1357.7	CHIC2	NM_012110.2	BTL;MGC21173	molecular	cellular_co	biological_
GI_29337285-A	269.6	354.9	282	EIF2C3	NM_177422.1	AGO3;FLJ12765			
GI_29337287-S	816.6	590.5	558.4	GAS41	NM_006530.2	NUBI-1	DNA	nucleus	oncogene
GI_29337288-S	147.6	151.8	123.8	ABI3	NM_016428.2	NESH			
GI_29337289-S	134.3	155.1	129.8	MAGEB6	NM_173523.2	MAGE-B6;FLJ40242			
GI_29337293-A	625.1	762.4	104.6	MAGED4	NM_177535.1	MAGE1;MAGE-E1;MGC3210;KIAA1859			
GI_29337297-S	104.6	1531.1	98.1	MAGEE1	NM_016249.2	CT10;HCA587;MAGEC2;MGC13377	tumor		
GI_29366811-S	113.4	105.5	103.2	KLK9	NM_012315.1	KLKL3;KLK-L3	trypsin	extracellul	proteolysis
GI_29469068-S	226.3	250.1	233.5	HIPK3	NM_005734.2	PKY;YAK1;DYRK6	protein	cellular_co	protein
GI_29469070-S	469.9	534.7	373.1	RICS	NM_014715.2	GRIT;GC-			
GI_29501806-I	162.5	192.9	163.7	KLC2L	NM_177417.1	KLC2;KLCt;KNS2B			
GI_29501808-S	94	95.4	90.1	FLJ36046	NM_152612.2				
GI_29540530-A	212.7	328.8	182.6	SULT1A1	NM_001055.2	PST;STP;STP1;P-	sulfotransf		amine
GI_29540538-I	174.5	227.4	210.8	SULT1A1	NM_177534.1	PST;STP;STP1;P-	sulfotransf		amine
GI_29540542-I	88.7	91.9	92.3	SULT1A1	NM_177536.1	PST;STP;STP1;P-	sulfotransf		amine
GI_29540544-S	99.8	111.4	111.3	SULT2A1	NM_003167.2	HST;ST2;STD;hSTa;ST2A3;DHEA-ST	sulfotransf		steroid
GI_29540546-A	530.6	787.4	529.9	TRO	NM_177557.1	MAGED3;MAGE-d3;KIAA1114		integral to	embryo
GI_29540554-I	83.8	103.1	92.2	SNRPN	NM_022807.2	SMN;SM-D;HCERN3;SNRNP-N	small	spliceoso	mRNA
GI_29540556-A	1172.5	1283	1075.5	SNRPN	NM_003097.3	SMN;SM-D;HCERN3;SNRNP-N	small	spliceoso	mRNA
GI_29540558-I	243.6	290.8	269.5	GAS2	NM_177553.1	MGC32610		actin	cell growth
GI_29540560-A	101.6	90.2	114.7	GAS2	NM_005256.2	MGC32610		actin	cell growth
GI_29540561-I	98.7	105.2	88	ALEX2	NM_177949.1	MGC8742;KIAA0512;MGC13343			
GI_29540565-A	350.3	397	358.5	ALEX3	NM_177948.1	MGC12199			
GI_29540565-I	220.1	253.6	223.6	ALEX3	NM_177948.1	MGC12199			
GI_29542730-A	332	364.1	376.9	ARL5	NM_177985.1		small		small
GI_29542733-I	201.3	232.7	233.2	ARL5	NM_012097.2		small		small
GI_29543553-I	92.8	112.6	188.6	TRIM9	NM_015163.3	RNF91;SPRING;KIAA0282	zinc ion	intracellula	
GI_29543554-A	107.8	129.2	129.1	TRIM9	NM_052978.2	RNF91;SPRING;KIAA0282	zinc ion	intracellula	
GI_29543554-I	123.5	150.6	209.7	TRIM9	NM_052978.2	RNF91;SPRING;KIAA0282	zinc ion	intracellula	
GI_29544725-I	86	102.9	89.7	DOK5	NM_018431.2	MGC16926;C20orf180	insulin		
GI_29544739-A	96.6	105	94	DOK5	NM_177959.1	MGC16926;C20orf180	insulin		
GI_29544746-S	114.7	110.9	113.6	MYO1A	NM_005379.2	BBMI;MIHC;MYHL	myosin	brush	hearing
GI_29544752-S	145	153.7	144.9	MYO3A	NM_017433.3	DFNB30	protein-	myosin	protein
GI_29550827-S	1414.1	1643.1	1340.7	ACBD3	NM_022735.3	PAP7;GCP60;GOCAP1;GOLPH1			
GI_29550837-I	110.4	116.4	108.4	GOLPH2	NM_016548.2	GP73;PSEC0257		Golgi	
GI_29550849-A	173	200.7	193.5	GOLPH2	NM_177937.1	GP73;PSEC0257		Golgi	
GI_29550849-I	96.9	97.7	93	GOLPH2	NM_177937.1	GP73;PSEC0257		Golgi	
GI_29550859-S	1457.7	1658.5	1587.4	GOLPH3	NM_022130.3	GOPP1;GPP34;FLJ90675			
GI_29550878-A	86.7	91.7	76.2	SULT1A2	NM_001054.2	STP2;HAST4;P-PST;ST1A2;TSPST2	sulfotransf		amine
GI_29550892-I	109.2	103.9	92.7	SULT1A2	NM_177528.1	STP2;HAST4;P-PST;ST1A2;TSPST2	sulfotransf		amine

GI_29550920-A	348	590.3	367.2	SULT1A3	NM_177552.1	STM;HAST;HAST3;M-PST;TL-PST	aryl	cytoplasm	synaptic
GI_29550920-I	109	139.6	95.2	SULT1A3	NM_177552.1	STM;HAST;HAST3;M-PST;TL-PST	aryl	cytoplasm	synaptic
GI_29550927-S	102.1	101.3	93.2	SULT1B1	NM_014465.2	ST1B2;SULT1B2;MGC13356	sulfotransf		biogenic
GI_29553943-S	93.7	107.6	92.9	SALF	NM_172311.1		transcripti	nucleus	transcripti
GI_29553952-S	125.2	171.5	136.4	SULT1E1	NM_005420.2	EST;EST-1;MGC34459	estrone		steroid
GI_29553969-A	402	764.3	951.9	H2AFJ	NM_177925.1	MGC921;FLJ10903	DNA	nucleus	nucleoso
GI_29553969-I	111.6	149.7	144.2	H2AFJ	NM_177925.1	MGC921;FLJ10903	DNA	nucleus	nucleoso
GI_29553976-I	131.3	153	154.3	H2AFJ	NM_018267.2	MGC921;FLJ10903	DNA	nucleus	nucleoso
GI_29553982-S	469.8	722	367.1	HIST2H4	NM_003548.2	H4;H4F2;H4FN			
GI_29557854-A	214.1	231.8	217	PPM1A	NM_177951.1	PP2CA;MGC9201;PP2C-ALPHA	protein	protein	protein
GI_29557854-I	180.8	209.8	222.9	PPM1A	NM_177951.1	PP2CA;MGC9201;PP2C-ALPHA	protein	protein	protein
GI_29557938-I	192.8	222.6	201.2	PPM1A	NM_177952.1	PP2CA;MGC9201;PP2C-ALPHA	protein	protein	protein
GI_29558021-I	639.6	465.1	431.8	PPM1B	NM_177968.1	PP2CB;MGC21657;PP2CBETA;PPC2BETAX	protein	protein	protein
GI_29558098-A	526.1	496.6	425.5	PPM1B	NM_177969.1	PP2CB;MGC21657;PP2CBETA;PPC2BETAX	protein	protein	protein
GI_29558519-S	276.2	327.7	303.4	PPM1D	NM_003620.2	WIP1;PP2C-DELTA	protein	nucleus	DNA
GI_29568085-S	8958.5	7394	6397	SDC1	NM_002997.3	SDC;CD138;SYND1	syndecan	proteoglyc	
GI_29568092-S	10306.4	12416	11554	MRLC2	NM_033546.2	MLC-B	calcium		
GI_29568100-S	954.4	861.1	833.7	ATP5L	NM_006476.3	ATP5JG	hydrogen	mitochond	proton
GI_29568104-S	172.7	198.7	161.2	TMEFF1	NM_003692.2	H7365;C9ORF2	serine	integral to	
GI_29568108-S	173.5	178.7	174.3	DOCK4	NM_014705.2	FLJ34238;KIAA0716		membran	cell growth
GI_29568112-I	110.8	126.7	118.4	MAGI-3	NM_020965.2		kinase		intracellula
GI_29570772-I	406.2	523.7	464.2	PH-4	NM_017732.2	FLJ20262	calcium	endoplas	
GI_29570774-I	192.7	211.7	253.5	DNCL2A	NM_177953.1	BLP;BITH;DNLC2A;HSPC162;MGC15113	microtubul	cytoplasmi	microtubul
GI_29570776-I	304.9	360.4	343.2	DNCL2A	NM_177954.1	BLP;BITH;DNLC2A;HSPC162;MGC15113	microtubul	cytoplasmi	microtubul
GI_29570778-A	3955	4330.6	6419.8	DNCL2A	NM_014183.2	BLP;BITH;DNLC2A;HSPC162;MGC15113	microtubul	cytoplasmi	microtubul
GI_29570779-S	199.3	212.4	184.9	AAK1	NM_014911.2	KIAA1048	ATP		protein
GI_29570781-S	1417.2	1228.3	1514.7	ASXL1	NM_015338.3	KIAA0978		nucleus	regulation
GI_29570783-S	157.8	192.6	172.4	CHRNA4	NM_000744.2	BFNC;NACRA4	nicotinic	nicotinic	small
GI_29570784-S	81	78	91.2	CTCFL	NM_080618.2	BORIS;CTCF-T;dJ579F20.2	DNA	nucleus	regulation
GI_29570786-S	797.4	653	1026.7	CTNNBL1	NM_030877.3	NAP;P14L;C20orf33;FLJ21108;NYD-SP19	DNA	nucleus	regulation
GI_29570787-A	192	222.9	198.3	CSRP2BP	NM_177926.1	CRP2BP;MGC15388;dJ717M23.1	N-	nucleus	
GI_29570787-I	84.1	89.1	86.3	CSRP2BP	NM_177926.1	CRP2BP;MGC15388;dJ717M23.1	N-	nucleus	
GI_29570789-I	761.7	578.6	377.3	CSRP2BP	NM_020536.2	CRP2BP;MGC15388;dJ717M23.1	N-	nucleus	
GI_29570790-I	106.6	102	80.4	CSNK2A1	NM_177559.1	CKII;CK2A1	protein	plasma	protein
GI_29570792-A	1508.5	1333.7	664	CSNK2A1	NM_177560.1	CKII;CK2A1	protein	plasma	protein
GI_29570796-S	206.7	347.9	295.1	PPARGC1A	NM_013261.2	LEM6;PGC1;PGC1A;PPARGC1;PGC-	DNA	nucleus	signal
GI_29570797-S	1046.2	820.1	804.6	PPAT	NM_002703.3	GPAT;ATASE	amidopho		purine
GI_29570799-I	92.7	96.9	86.3	CDH26	NM_177980.1	VR20			
GI_29570801-A	156.4	170.3	159.3	CDH26	NM_021810.3	VR20			
GI_29570801-I	101.1	93.5	95.1	CDH26	NM_021810.3	VR20			
GI_29571103-S	95.2	105.2	89.4	KISS1	NM_002256.2	KiSS-1;MGC39258			cytoskelet
GI_29571105-S	102.7	117.7	107.6	BMP8B	NM_001720.2	OP2;BMP8	cytokine	extracellul	skeletal
GI_29648312-S	717.1	877.5	543.3	LOC57168	NM_020437.3		peptide-		
GI_29648316-I	259.5	270.2	227.5	MT	NM_173467.2	MGC47838;bK1191B2.3			

GI_29648320-S	640.2	583.4	462.2	MGC29875	NM_014388.2	FLJ12704;DJ434O14.5			
GI_29725600-S	106.1	99.4	106.7	MIA2	NM_054024.2	FLJ22404			
GI_29725604-S	164.2	216	304.9	TSPYL4	NM_021648.3	KIAA0721;dJ486I3.2	DNA	nucleus	nucleoso
GI_29725606-I	569.1	719.4	740.9	SMAP-1	NM_018671.2	FLJ10043;IRO039700			
GI_29725621-S	153.5	186.2	117.8	TPCN1	NM_017901.3	TPC1;FLJ20612;KIAA1169			
GI_29725623-S	133.7	143.9	145.7	COL23A1	NM_173465.2	DKFZp434K0621		microfibril	
GI_29725634-S	110.1	132.3	118.8	OTOP1	NM_177998.1				
GI_29727530-S	108	96	104.7	LOC339398	XM_291387.1				
GI_29727545-S	284.2	370.1	348.2	LOC149018	XM_086402.6				
GI_29727605-S	143	153.1	147.5	LOC339951	XM_293656.1				
GI_29727809-S	578.1	685.7	618.2	LOC343069	XM_291395.1				
GI_29727991-S	131.8	150.5	122.7	LOC344620	XM_293514.1				
GI_29728071-S	580.9	466.6	472.7	KIAA0882	XM_093895.6				
GI_29728376-S	151.1	187	169.8	LOC345079	XM_293687.1				
GI_29728513-S	104.5	166	117.3	HES2	XM_290879.1				
GI_29728546-S	249.7	327.8	231.5	KIAA0551	XM_039796.9				
GI_29728788-S	82.2	95.7	84.1	LOC343153	XM_291428.1				
GI_29728998-S	168	178.7	165.7	LOC343170	XM_291436.1				
GI_29729000-S	130.2	141.2	126.5	OR1C1	XM_291437.1				
GI_29729002-S	348.1	430.6	388.2	LOC343171	XM_291438.1				
GI_29729004-S	111.8	121.1	104.6	LOC343172	XM_291439.1				
GI_29729015-S	138.1	148.4	156.5	LOC285047	XM_211749.2				
GI_29729032-S	134.9	146.6	133.1	LOC132946	XM_059617.4				
GI_29729340-S	144.3	141.3	133.9	LOC339744	XM_290994.1				
GI_29729487-S	96.3	99	89.6	LOC339875	XM_295091.1				
GI_29729553-S	173.2	213	194.6	KIAA0232	XM_291106.1				
GI_29729561-S	278.6	242.1	224.4	MGC21874	XM_291105.1				
GI_29729665-S	811.3	742.5	547.3	KIAA1268	XM_291055.1				
GI_29730038-S	126.5	129.9	124.2	LOC127003	XM_059104.4				
GI_29730062-S	107	96.8	94.5	LOC256283	XM_173105.2				
GI_29730133-S	110.3	121.4	109.7	LOC339771	XM_295059.1				
GI_29730274-S	136.4	135.4	130.1	LOC131055	XM_067176.7				
GI_29730298-S	108.5	113.1	111.9	TAS1R3	XM_290905.1				
GI_29730466-S	142	154	147.9	LOC339997	XM_295126.1				
GI_29730519-S	99.1	112.9	106.6	LOC152519	XM_087483.3				
GI_29730668-S	76.7	87.2	77	LOC339902	XM_295097.1				
GI_29731086-S	103	111.2	99.7	LOC339782	XM_295062.1				
GI_29731277-S	338.3	446	360.4	LOC151261	XM_098030.2				
GI_29731394-S	134.1	147.4	130.3	MGC27277	XM_290922.1				
GI_29731560-S	295.6	743.4	427.5	FLJ33674	XM_291074.1				
GI_29731718-S	86.3	114.5	89.7	LOC339793	XM_291017.1				
GI_29731736-S	933.4	857.9	727.1	KIAA1841	XM_087056.4				
GI_29731856-S	102.6	98.9	111.3	LOC344423	XM_293042.1				
GI_29731922-S	185.6	194.6	207.9	FLJ12643	XM_095991.6				

GI_29731964-S	491.5	392.4	307.7	KIAA0804	XM_291080.1
GI_29731972-S	96.6	95.1	107.9	LOC339926	XM_291075.1
GI_29732251-S	91.5	103.8	98.6	LOC339809	XM_291020.1
GI_29732263-S	319.8	333.3	472.9	LOC91373	XM_038063.8
GI_29732373-S	117.8	120.9	97	MGC43306	XM_291304.1
GI_29732565-S	131.5	175.6	132.8	CDGAP	XM_291085.1
GI_29732583-S	165.9	176.7	160.4	LOC285095	XM_211764.2
GI_29732623-S	94.3	85.7	83.9	LOC340477	XM_295257.1
GI_29732655-S	147	143.8	139.5	LOC347169	XM_294534.1
GI_29732833-S	125.4	119.9	129.2	MGC35030	XM_290936.1
GI_29733221-S	113.3	119.1	119.6	DMRTA1	XM_291311.1
GI_29733241-S	170.5	190.4	179	LOC138724	XM_059997.3
GI_29733255-S	124.4	123.6	111.5	FBXO10	XM_291314.1
GI_29733263-S	114.3	97.1	97.3	LOC126661	XM_059061.3
GI_29733317-S	144.4	150.9	152.8	LOC343521	XM_291623.1
GI_29733581-S	287.6	300.8	254.5	KIAA1332	XM_048774.4
GI_29733770-S	84	83.6	73.5	LOC340246	XM_291208.1
GI_29733991-S	94.4	80.8	86.4	LOC340511	XM_295261.1
GI_29733995-S	155.4	180.2	169.8	LOC138805	XM_071099.5
GI_29734032-S	104.1	148.1	117.7	LOC347265	XM_294590.1
GI_29734048-S	131.5	116.4	109.4	LOC347273	XM_294592.1
GI_29734290-S	90	98.1	94.4	LOC286094	XM_212170.2
GI_29734344-S	136.6	169.9	135.5	LOC90987	XM_291262.1
GI_29734346-S	110.4	115.9	98.1	LOC340385	XM_291261.1
GI_29734357-S	126	145.5	141.4	LOC133874	XM_059672.4
GI_29734567-S	171.9	214.3	180.2	LOC340393	XM_291270.1
GI_29734945-S	110.3	120.2	112.3	LOC340286	XM_295200.1
GI_29735169-S	352.8	422.7	405.7	LOC255187	XM_173160.2
GI_29735241-S	178	215.6	202.9	LOC345537	XM_293868.1
GI_29735560-S	143	165.7	137.9	LOC346517	XM_294310.1
GI_29735634-S	103.7	98	99.3	LOC153778	XM_087762.2
GI_29735784-S	187.6	142.8	158.8	LOC90673	XM_033391.8
GI_29735852-S	107.3	115	113.8	TTC6	XM_056434.2
GI_29735919-S	85.4	87.8	77.2	LOC346974	XM_294476.1
GI_29736037-S	170.3	174.9	179	LOC338914	XM_290609.1
GI_29736042-S	112.9	139.6	115.1	LOC338916	XM_294737.1
GI_29736049-S	132.8	130.3	131.9	LOC338918	XM_294743.1
GI_29736110-S	138.4	143.5	171.6	C14orf72	XM_096733.2
GI_29736121-S	87.5	95.4	100.4	LOC338934	XM_290626.1
GI_29736547-S	104.5	115.2	101.7	LOC153630	XM_098406.5
GI_29736621-S	119.7	142.4	144	LOC345651	XM_293924.1
GI_29736784-S	152.1	124.9	118.2	LOC201294	XM_113950.4
GI_29736832-S	90.9	93.5	99.5	LOC283999	XM_211287.2
GI_29736979-S	77.2	94.4	85.7	LOC255275	XM_171855.3

GI_29737062-S	128.8	147.5	155.4	LOC340344	XM_294353.1
GI_29737065-S	90.9	92.7	85.6	LOC154872	XM_098625.2
GI_29737091-S	106.9	108	76.4	LOC340349	XM_295205.1
GI_29737421-S	268.2	256.8	254.3	KIAA1936	XM_056082.6
GI_29738271-S	97.9	83.4	90.6	LOC144762	XM_096676.2
GI_29738554-S	114.3	115.9	119.5	LOC339204	XM_292621.1
GI_29738586-S	142.8	166.3	176.6	LOC339209	XM_294854.1
GI_29739145-S	153.1	161.4	156.7	LOC339230	XM_290771.1
GI_29739147-S	349.1	360	309.9	LOC339231	XM_290777.1
GI_29739184-S	140.5	155	152.3	LOC340149	XM_295169.1
GI_29739190-S	111.8	114.1	105.2	LOC153918	XM_087800.2
GI_29739316-S	91	89.2	103.9	LOC340765	XM_291704.1
GI_29739479-S	96.2	101	84.7	LOC339243	XM_290782.1
GI_29739598-S	112.5	137.2	119.8	LOC118670	XM_058332.3
GI_29739848-S	221.2	287	251.1	LOC339281	XM_294894.1
GI_29740201-S	2017.3	1841.3	1825.5	FLJ14502	XM_031561.6
GI_29740202-S	189.7	199.5	180.5	MAPKBP1	XM_031706.7
GI_29740221-S	285.2	453.6	430.4	FLJ10980	XM_035527.8
GI_29740242-S	771.4	621.2	578.3	LOC145853	XM_096885.6
GI_29740251-S	94	107.3	85.5	LOC338949	XM_294751.1
GI_29740257-S	152.5	171.4	157.9	LOC338951	XM_294750.1
GI_29740609-S	108.6	115.3	117.7	LOC338611	XM_291745.1
GI_29740697-S	82.5	81.8	92	LOC340168	XM_291161.1
GI_29740706-S	108.8	101.9	88	LOC340171	XM_295178.1
GI_29740938-S	291.5	259.9	196	KIAA1136	XM_166110.3
GI_29740943-S	114.6	91.6	97.3	LOC338616	XM_294666.1
GI_29740945-S	94.4	100.4	91.7	LOC338617	XM_291771.1
GI_29741064-S	206.2	237.4	215.6	NUT	XM_171724.3
GI_29741265-S	194.6	201.4	220.3	LOC339321	XM_290831.1
GI_29741281-S	134.3	152	149.5	LOC147975	XM_097351.2
GI_29741414-S	625.4	839.7	777.9	LOC339344	XM_290848.1
GI_29741436-S	279.3	356.5	314.3	LOC147646	XM_085833.3
GI_29741437-S	522.4	521.7	572.7	LOC339352	XM_294910.1
GI_29741463-S	154.2	135.5	109.5	LOC339358	XM_294914.1
GI_29741968-S	105.2	100.5	84	LOC338761	XM_290558.1
GI_29742308-S	95.5	107.7	99.2	LOC341356	XM_292023.1
GI_29742395-S	147.2	172.7	121	LOC340204	XM_291169.1
GI_29742429-S	110.5	130.1	111.8	RGL3	XM_290867.1
GI_29742461-S	116.3	116.5	113.9	LOC340211	XM_291181.1
GI_29742513-S	107.2	103.2	107.3	LOC339375	XM_294922.1
GI_29742584-S	116.6	130	151.2	KIAA1586	XM_166451.2
GI_29742588-S	105.4	119.2	105.8	FLJ21438	XM_029084.5
GI_29742605-S	217.5	261.6	223.1	LOC339377	XM_290866.1
GI_29742698-S	407.5	426.7	333.4	MGC26694	XM_209204.2

GI_29742910-S	128.7	136.3	111.1	LOC342977	XM_292819.1				
GI_29743204-S	100.4	113.9	102.3	LOC338786	XM_294713.1				
GI_29743247-S	84.8	80.1	87.7	LOC341412	XM_292046.1				
GI_29743268-S	458.1	587.6	567.1	OATL1	XM_047025.6				
GI_29743323-S	107	129.8	103.8	LOC347348	XM_293276.1				
GI_29743450-S	122	128.9	134.1	LOC339306	XM_294906.1				
GI_29743461-S	140.6	150	139.6	LOC340527	XM_291321.1				
GI_29743488-S	142.3	158.8	144.3	LOC119679	XM_061611.2				
GI_29743494-S	114	146.8	129.7	LOC119678	XM_061610.2				
GI_29743512-S	388.5	420.6	361.3	NXPH4	XM_290582.1	NPH4	receptor	extracellul	neuropepti
GI_29743632-S	20060	19077	13880	LOC342808	XM_292700.1				
GI_29743707-S	109.2	88.7	102.1	KIAA2022	XM_291326.1				
GI_29743718-S	105.9	123.9	116.9	LOC347359	XM_293293.1				
GI_29743757-S	119.6	133.3	116.7	LOC139793	XM_060054.3				
GI_29743852-S	1614.7	1173.3	1155.8	PRMT3	XM_058460.3		N-	cytoplasm	N-terminal
GI_29743984-S	111.4	115.4	117.5	FLJ34907	XM_290817.1				
GI_29744067-S	115.3	105	98	LOC283420	XM_208667.2				
GI_29744077-S	225.8	231.3	230.2	LOC340542	XM_291335.1				
GI_29744085-S	87	91.4	85.2	LOC340543	XM_291334.1				
GI_29744101-S	113.6	121	104	LOC341461	XM_292098.1				
GI_29744194-S	113.5	133	120.8	LOC343565	XM_293097.1				
GI_29744221-S	124.1	111.6	117.5	LOC340549	XM_293332.1				
GI_29744307-S	116.9	126.2	120.7	LOC143941	XM_084672.2				
GI_29744326-S	98.7	92.7	86.9	LOC338661	XM_290501.1				
GI_29744339-S	94.1	93.5	88.8	LOC338666	XM_294677.1				
GI_29744347-S	125.1	107.1	112.3	LOC338825	XM_294723.1				
GI_29744361-S	190.2	210.3	204.8	KIAA1030	XM_290502.1				
GI_29744402-S	182	171.4	176.3	LOC347423	XM_293341.1				
GI_29744569-S	141.2	153.6	151.4	LOC341511	XM_292109.1				
GI_29744602-S	114.6	127	130.7	KIAA1755	XM_028810.4				
GI_29744642-S	126.9	130.6	132	LOC149738	XM_097725.2				
GI_29744653-S	110.1	122	106.6	LOC339583	XM_295007.1				
GI_29745032-S	139.8	174.4	151.7	LOC338694	XM_294680.1				
GI_29745113-S	174.1	227.9	180	DDN	XM_290598.1				
GI_29745308-S	158.1	189.6	174.7	USP35	XM_290527.1				
GI_29745421-S	103	124.3	100.5	LOC341168	XM_291897.1				
GI_29745452-S	90.8	96.5	86.8	LOC340581	XM_295270.1				
GI_29745490-S	194.1	236.4	211.1	LOC347454	XM_293380.1				
GI_29745634-S	126.8	141.6	122.8	LOC343705	XM_293157.1				
GI_29745744-S	84.8	104	85.8	C21orf54	XM_295017.1				
GI_29745755-S	329.5	231	185.3	LOC150084	XM_086761.3				
GI_29745945-S	122.1	138.5	132.9	KIAA0316	XM_045712.5				
GI_29745993-S	855.6	2290.7	1218.9	KIAA0830	XM_290546.1				
GI_29746068-S	333.7	431.6	389.9	LOC347512	XM_293396.1				

GI_29746157-S	102.4	122.7	115.1	LOC338734	XM_290547.1				
GI_29746244-S	168.5	205	185.3	LOC340595	XM_293405.1				
GI_29746315-S	120.3	135.5	144.8	LOC158957	XM_088726.2				
GI_29746497-S	251	285.3	285.7	LOC338749	XM_294692.1				
GI_29746573-S	93	111.3	102.8	LOC196335	XM_115092.2				
GI_29746633-S	894.2	770.2	896.3	LOC339665	XM_290973.1				
GI_29746781-S	1014.1	1025.3	996.4	KIAA0350	XM_290667.1				
GI_29747011-S	97	110.1	85.4	DKFZP434I2	XM_290684.1				
GI_29747019-S	285.1	338.5	300.8	LOC339065	XM_294794.1				
GI_29747038-S	89.4	89.3	79.8	TNRC9	XM_049037.7				
GI_29747214-S	104.9	128.8	103.9	LOC342355	XM_292503.1				
GI_29747247-S	92.9	99	92.5	LOC342371	XM_292512.1				
GI_29747360-S	1190	2006.5	1650.8	LOC342405	XM_292526.1				
GI_29747408-S	500.9	616.3	545	MGC46336	XM_290712.1				
GI_29747582-S	108.4	121.7	107.1	HYDIN	XM_030075.5				
GI_29747594-S	218.7	252	206.8	LOC283953	XM_208930.2				
GI_29788754-S	98.8	100.9	92	CMT4B2	NM_030962.1	SBF2;MTMR13;KIAA1766			
GI_29788761-S	103	109.1	99.8	DNTT	NM_004088.2	TDT	DNA	nucleus	DNA
GI_29788765-S	102.7	83.4	90	TUBB4Q	NM_020040.2		structural	cytoskelet	microtubul
GI_29788771-S	132.9	140.4	132.3	TNRC4	NM_007185.2	CAGH4;CELF3;ERDA4;BRUNOL1	transcripti		neurogene
GI_29788775-S	121.1	119.8	111.5	XTP7	NM_138568.2	MGC16332			
GI_29788777-A	84.5	88.1	77.3	PRIMA1	NM_178013.1	PRIMA		integral to	neurotran
GI_29788782-I	107.8	109.8	97.5	PRIMA1	NM_178004.1	PRIMA		integral to	neurotran
GI_29788788-S	168.1	201.2	233.3	DCOHM	NM_032151.2	DKFZp566K1946			
GI_29788789-S	146.1	140.1	130.2	HMG2L1	NM_005487.2	THC211630	DNA	nucleus	endosome
GI_29788984-A	189.4	225.7	219.8	SLC24A4	NM_153647.1	NCKX4	symporter	integral to	sodium
GI_29788986-I	439.6	538	507.2	SLC24A4	NM_153648.1	NCKX4	symporter	integral to	sodium
GI_29788995-S	120.2	122.4	138.2	PON3	NM_000940.1		arylestera	extracellul	response
GI_29788999-S	711.5	699.2	512.2	SUCLG2	NM_003848.1	G-BETA			
GI_29789001-S	225.6	231.8	278.6	EVI1	NM_005241.1	PRDM3;MDS1-EVI1	JUN	nucleus	JNK
GI_29789005-S	3675.4	2678.8	2263.4	PLEKHC1	NM_006832.1	MIG2;KIND2;mig-2;UNC112	cell	cytoskelet	regulation
GI_29789007-S	135.7	172.3	156	HYPC	NM_012272.1		protein		mRNA
GI_29789053-S	437.6	595.1	484.4	FCHO1	NM_015122.1	KIAA0290	transferas		metabolis
GI_29789055-A	185.3	194.4	179.9	TRIF	NM_014261.1	TICAM1;PRVTIRB;MGC35334	transmem	membran	
GI_29789057-S	792.3	431.2	417.2	KIBRA	NM_015238.1	KIAA0869			
GI_29789059-S	982.8	661.8	733.2	KIAA0528	NM_014802.1		transporte	membran	transport
GI_29789063-S	218.1	233.4	207.1	SULF1	NM_015170.1	SULF-1;HSULF-1;KIAA1077	sulfuric	Golgi	metabolis
GI_29789067-S	137.4	173.5	154.4	CLONE25003	NM_015381.1	UNQ5208;QLLK5208;bA262A13.1			
GI_29789077-S	89.1	101	98.6	UGT1A10	NM_019075.1	UGT1J	UDP-		
GI_29789087-S	501.6	550	512.4	CCAR1	NM_018237.1	CARP1;CARP-1;FLJ10590;FLJ10839	DNA	nucleus	
GI_29789089-S	2376.7	2738.3	2288.5	TD-60	NM_018715.1	KIAA1470;DKFZp762N0610	DNA	nucleus	regulation
GI_29789101-S	118.7	132.8	151.9	NGEF	NM_019850.1	EPHEXIN			
GI_29789109-S	295.9	537.7	439.9	KIAA1145	NM_020698.1			integral to	
GI_29789111-S	237.9	253.8	208.8	ZNF490	NM_020714.1	KIAA1198	DNA	nucleus	regulation

GI_29789113-S	956.4	892.8	804	TBC1D14	NM_020773.1	KIAA1322			
GI_29789117-S	99.1	106	101.2	KIAA1443	NM_020834.1	HOMEZ	transcripti	nucleus	regulation
GI_29789119-S	106.2	111.2	108.6	PRKWNK3	NM_020922.1	WNK3;KIAA1566	ATP		protein
GI_29789121-S	242.4	208.8	231	CRY2	NM_021117.1	HCRY2;PHLL2;KIAA0658	G-protein		circadian
GI_29789254-A	2172.8	2320.9	2585.2	CMIP	NM_030629.1	KIAA1694			
GI_29789254-I	109	109.6	105.5	CMIP	NM_030629.1	KIAA1694			
GI_29789276-S	94.5	112.3	94.5	GPR123	NM_032422.1	KIAA1828	G-protein	membran	
GI_29789280-S	128.4	144.2	132.7	KIAA1750	NM_033512.1		DNA	nucleus	nucleoso
GI_29789282-S	2144.4	1643.2	1408.4	FLJ12519	NM_032168.1		electron		electron
GI_29789284-S	4356.2	3721.9	5015.8	COMMD7	NM_053041.1	C20orf92;FLJ14987;dJ1085F17.3			
GI_29789286-S	802.2	798.7	701.5	KIAA1754	NM_033397.1	bA127L20.2			
GI_29789292-S	263.8	280.3	298.9	LIP8	NM_053051.1				
GI_29789366-S	254.3	266.8	214.5	FOXP4	NM_138457.1				
GI_29789372-S	150.9	210.2	145.9	LOC92689	NM_138389.1				
GI_29789400-S	651.7	692.7	568.3	LOC92912	NM_173469.1				
GI_29789450-S	102.3	100.5	93.2	CATSPER3	NM_178019.1	CACRC	cation	membran	cation
GI_29824429-A	115.2	103.8	107	TMPRSS6	NM_153019.2	FLJ30744	trypsin	integral to	proteolysis
GI_29824429-I	122.2	143.3	115	TMPRSS6	NM_153019.2	FLJ30744	trypsin	integral to	proteolysis
GI_29825822-S	275.7	315.8	294.7	C17orf28	NM_030630.1	DMC1			
GI_29826278-A	246.7	239.9	149.6	TUB	NM_177972.1			cytoplasm	
GI_29826278-I	134.8	157.6	143.3	TUB	NM_177972.1			cytoplasm	
GI_29826280-I	121.1	124.4	111.6	TUB	NM_003320.3			cytoplasm	
GI_29826281-I	188.2	203.4	188	PPM1G	NM_177983.1	PP2CG;PPP2CG;MGC1675;MGC2870;PP2C	protein	protein	cell cycle
GI_29826283-A	6408.5	6924	6993.5	PPM1G	NM_002707.3	PP2CG;PPP2CG;MGC1675;MGC2870;PP2C	protein	protein	cell cycle
GI_29826284-A	3386.5	3599.2	2848.2	MRPL47	NM_177988.1	NCM1;CGI-204;MGC45403	structural	mitochond	
GI_29826286-I	152	174.5	149.1	MRPL47	NM_020409.2	NCM1;CGI-204;MGC45403	structural	mitochond	
GI_29826288-I	127.8	146.8	107.3	H63	NM_138423.2				
GI_29826290-A	1140.3	1470.3	1237.5	H63	NM_177974.1				
GI_29826292-S	526	541.3	515.1	GORASP1	NM_031899.2	P65;GOLPH5;GRASP65;FLJ23443			
GI_29826293-S	1741.8	1633.3	1098.4	GORASP2	NM_015530.3	p59;GRS2;GOLPH6;GRASP55;FLJ13139;DK	protein		
GI_29826297-S	188.5	186.3	200.6	NDNL2	NM_138704.2	HCA4;MAGEG1			
GI_29826298-A	120	123	109	ARL6	NM_177976.1	MGC32934	small		small
GI_29826298-I	106.2	107.3	95.3	ARL6	NM_177976.1	MGC32934	small		small
GI_29826300-I	82.4	92.4	91.3	ARL6	NM_032146.3	MGC32934	small		small
GI_29826313-S	395.8	417.1	355.8	DDA3	NM_032636.4	MGC1780			
GI_29826314-I	143.7	159	142.8	DUSP15	NM_080611.3	bA243J16.6	protein		protein
GI_29826316-A	108.2	108.2	85.8	DUSP15	NM_177991.1	bA243J16.6	protein		protein
GI_29826316-I	247.4	303.1	263.9	DUSP15	NM_177991.1	bA243J16.6	protein		protein
GI_29826318-A	2005.4	2036.4	2211.9	ADD1	NM_001119.3	ADDA;MGC3339;MGC44427	actin	membran	
GI_29826326-S	386.9	385.3	307.8	GOLPH4	NM_014498.2	P138;GIMPC;GPP130		Golgi	
GI_29826327-S	1046.6	1098	1134.8	GPP34R	NM_018178.3	FLJ10687			
GI_29826328-A	105.1	101.4	90.8	PAK7	NM_177990.1	PAK5;KIAA1264;MGC26232	protein-		protein
GI_29826330-I	122.5	124.2	115.7	PAK7	NM_020341.2	PAK5;KIAA1264;MGC26232	protein-		protein
GI_29826333-S	963.8	814.7	1212.8	PPM1F	NM_014634.2	FEM-2;POPX2;hFEM-			

GI_29826334-S	11535.9	10200	10356	EIF2S2	NM_003908.2	EIF2;EIF2B;MGC8508;EIF2beta	translation	ribosome	protein
GI_29826337-S	117.5	449.9	164.4	IFI30	NM_006332.3	GILT;IP30;IFI-30;MGC32056	oxidoredu	lysosome	immune
GI_29826338-S	101.6	109.1	100.7	SOX2	NM_003106.2	ANOP3;MGC2413	RNA	nucleus	transcripti
GI_29826339-S	5104.6	5667.7	5989.5	ATOX1	NM_004045.2	ATX1;HAH1	copper ion		copper ion
GI_29826340-S	325.8	337.5	338.2	CAMTA2	NM_015099.2	KIAA0909			
GI_29837647-S	132	145.2	128.8	CYP4X1	NM_178033.1	MGC40051	monooxyg		electron
GI_29837653-A	143.8	164.8	176.7	C1orf9	NM_014283.2	CH1			
GI_29837653-I	90.4	96.5	89.9	C1orf9	NM_014283.2	CH1			
GI_29837656-S	91.4	87.8	93.8	FXC1	NM_012192.2	Tim9b;TIM10B;TIMM10B	protein	mitochond	cell-matrix
GI_29837661-S	105	118.2	102.7	PLA2G4D	NM_178034.1	cPLA2delta	phospholi		phospholi
GI_29893546-A	164.2	151.6	145.6	EPB41L4B	NM_018424.1	CG1;EHM2;DKFZp761N1814	structural	cytoskelet	cell shape
GI_29893546-I	136	128.8	111.1	EPB41L4B	NM_018424.1	CG1;EHM2;DKFZp761N1814	structural	cytoskelet	cell shape
GI_29893551-S	366.7	283.7	330.8	TRPM7	NM_017672.2	CHAK;CHAK1;LTRPC7;FLJ20117;TRP-PLIK	cation	integral to	cation
GI_29893554-S	102.4	107.7	95.8	ANGPTL6	NM_031917.2	AGF;ARP5			
GI_29893558-S	127	148.9	129.9	SCN1A	NM_006920.2	NAC1;SCN1;HBSCI;GEFSP2	voltage-	integral to	cation
GI_29893560-S	245.3	349.3	319.8	SNN	NM_003498.3			integral to	response
GI_29893561-S	405.8	472	429	C6orf210	NM_020381.2	bA59I9.3			
GI_29893565-S	203.8	224.6	229	PSCA	NM_005672.2		tumor	plasma	
GI_29893807-S	123.8	155.6	124.6	ARPM2	NM_080431.3	ARPT2;ACTRT2;HARPM2;FLJ25424	structural	actin	
GI_29893810-I	112.7	145.8	111.8	JPH2	NM_020433.3	JP2;JP-2;FLJ40969		integral to	
GI_29893811-A	107.8	101.9	92.2	JPH2	NM_175913.2	JP2;JP-2;FLJ40969		integral to	
GI_29893811-I	131.6	155.1	145.8	JPH2	NM_175913.2	JP2;JP-2;FLJ40969		integral to	
GI_30017464-S	2940.3	3421.7	1844.1	SBP1	NM_178121.1				
GI_30023850-S	2096.2	2136.8	1838.6	USP49	NM_004275.2	TRFP;PRO0213;DKFZp586D2223	protein		regulation
GI_30023852-S	109	113.9	96.1	MTSS1	NM_014751.2	MIM;MIMA;MIMB;KIAA0429	nucleic	actin	transmem
GI_30025025-S	1357.4	2066.4	1403.4	OSTM1	NM_014028.2	GL;GIPN;HSPC019			
GI_30026033-S	1584.4	1955	2044.6	SLC35B2	NM_178148.1	PAPST1;UGTrel4	copper ion		electron
GI_30039687-S	83	78.9	86.2	JCG6	NM_178168.1		olfactory	integral to	olfaction
GI_30039709-S	103.6	105.9	107.2	PTF1A	NM_178161.1	PTF1-p48			
GI_30039713-S	128.8	131.4	118.4	OTOP2	NM_178160.1				
GI_30061484-S	199.3	218.8	213.1	DEFB126	NM_030931.2	C20orf8;DEFB-26;ESP13.2;bA530N10.1	protease	extracellul	xenobiotic
GI_30061486-S	185.4	200.6	173.9	DEFB127	NM_139074.2	DEF-27;DEFB-27;C20orf73;bA530N10.2	antibacteri	cellular_co	xenobiotic
GI_30061487-S	195.1	211.3	208.8	DEFB129	NM_080831.2	DEFB-29;C20orf87;bA530N10.3			xenobiotic
GI_30061488-I	180.4	216.2	196.1	EPB41L1	NM_012156.2	4.1N;KIAA0338;MGC11072	actin	cytoskelet	
GI_30061490-A	296.5	372.9	325.7	EPB41L1	NM_177996.1	4.1N;KIAA0338;MGC11072	actin	cytoskelet	
GI_30061490-I	138.8	133.7	144.7	EPB41L1	NM_177996.1	4.1N;KIAA0338;MGC11072	actin	cytoskelet	
GI_30061493-A	621.3	824.9	730.9	HAP1	NM_177977.1	HLP;HAP2;HIP5;hHLP1		cytoskelet	pathogene
GI_30061495-I	98.7	111.9	103.6	HAP1	NM_003949.2	HLP;HAP2;HIP5;hHLP1		cytoskelet	pathogene
GI_30061497-A	134.3	151.1	134.6	GGTL3	NM_178025.1	GGTL5;D20S101;dJ18C9.2	gamma-	integral to	glutathion
GI_30061497-I	149.1	206.5	186.9	GGTL3	NM_178025.1	GGTL5;D20S101;dJ18C9.2	gamma-	integral to	glutathion
GI_30061499-I	85.8	97.5	95.9	GGTL3	NM_178026.1	GGTL5;D20S101;dJ18C9.2	gamma-	integral to	glutathion
GI_30061503-I	98.9	105	110.4	GCNT2	NM_145649.2	II;IGNT;ULG3;AIGnT;BIGnT;CIGnT;GCNT5;	N-	Golgi	glycosami
GI_30061504-I	128.6	168.2	157.2	GCNT2	NM_001491.2	II;IGNT;ULG3;AIGnT;BIGnT;CIGnT;GCNT5;	N-	Golgi	glycosami
GI_30061505-A	97.4	111.2	117.6	GCNT2	NM_145655.2	II;IGNT;ULG3;AIGnT;BIGnT;CIGnT;GCNT5;	N-	Golgi	glycosami

GI_30061505-I	93.4	101.4	97.2	GCNT2	NM_145655.2	II;IGNT;ULG3;AIGnT;BIGnT;CIGnT;GCNT5;	N-	Golgi	glycosami
GI_30061506-I	112.7	108.3	100.4	PDZK3	NM_178140.1	AIPC;PIN1;PAPIN;PDZD2;KIAA0300	ATP		protein
GI_30061508-A	180.2	231.2	153.8	PDZK3	NM_015022.2	AIPC;PIN1;PAPIN;PDZD2;KIAA0300	ATP		protein
GI_30061555-S	146.3	162.2	134.5	SOX3	NM_005634.2	MRGH;SOXB	DNA	nucleus	central
GI_30061557-A	131	157.2	147.2	SOX5	NM_178010.1	L-SOX5;MGC35153	transcripti	kinesin	transcripti
GI_30061559-I	138.2	139.6	106.3	SOX5	NM_006940.4	L-SOX5;MGC35153	transcripti	kinesin	transcripti
GI_30061560-I	93.3	94.7	89.8	SOX5	NM_152989.2	L-SOX5;MGC35153	transcripti	kinesin	transcripti
GI_30061561-A	98.5	103.8	98.4	GABRB3	NM_021912.2	MGC9051	GABA-A	integral to	small
GI_30061561-I	97.7	113.3	98.6	GABRB3	NM_021912.2	MGC9051	GABA-A	integral to	small
GI_30061562-I	180.8	216.5	196.8	GABRB3	NM_000814.3	MGC9051	GABA-A	integral to	small
GI_30061563-S	360.1	391.1	359.4	GATA5	NM_080473.3	bB379O24.1	transcripti	nucleus	regulation
GI_30061564-A	360.2	361.9	340.2	FLJ10378	NM_178043.1	DKFZp434K245;DKFZp686E0316			
GI_30061564-I	90.8	89.3	87.4	FLJ10378	NM_178043.1	DKFZp434K245;DKFZp686E0316			
GI_30061566-I	288.5	384.8	317.7	FLJ10378	NM_018078.2	DKFZp434K245;DKFZp686E0316			
GI_30061568-I	424	347.7	365	FLJ10378	NM_032239.2	DKFZp434K245;DKFZp686E0316			
GI_30065641-I	426.5	528.3	472	PPP2R4	NM_021131.3	PP2A;PR53;PTPA;MGC2184	protein	soluble	protein
GI_30065644-I	111	116.1	102.6	PPP2R4	NM_178001.1	PP2A;PR53;PTPA;MGC2184	protein	soluble	protein
GI_30065648-A	2836	3290.2	3717.1	PPP2R4	NM_178003.1	PP2A;PR53;PTPA;MGC2184	protein	soluble	protein
GI_30089915-S	374.3	449.9	380	PACS1	NM_018026.2	FLJ10209;KIAA1175			
GI_30089917-I	226.7	272.7	228.9	POLDIP3	NM_032311.3	PDIP46;KIAA1649			
GI_30089918-A	921.7	916.8	858.6	POLDIP3	NM_178136.1	PDIP46;KIAA1649			
GI_30089920-S	185.4	218.4	218.3	FBXO16	NM_172366.2	FBX16			
GI_30089921-A	262.6	205.1	217	FBXO11	NM_012167.1	VIT1;FBX11;FLJ12673;MGC44383;UG063H0	ubiquitin		ubiquitin-
GI_30089921-I	114.5	114.9	99.7	FBXO11	NM_012167.1	VIT1;FBX11;FLJ12673;MGC44383;UG063H0	ubiquitin		ubiquitin-
GI_30089923-I	232.9	205.9	219.1	FBXO11	NM_018693.2	VIT1;FBX11;FLJ12673;MGC44383;UG063H0	ubiquitin		ubiquitin-
GI_30089925-I	989.1	960.3	797.6	FBXO11	NM_025133.3	VIT1;FBX11;FLJ12673;MGC44383;UG063H0	ubiquitin		ubiquitin-
GI_30089927-A	558.7	725	706.5	ASAH1	NM_177924.1	AC;PHP;ASAH;PHP32;FLJ21558;FLJ22079	catalytic		ceramide
GI_30089927-I	369.1	401.4	608.4	ASAH1	NM_177924.1	AC;PHP;ASAH;PHP32;FLJ21558;FLJ22079	catalytic		ceramide
GI_30089929-I	240.3	309.9	254.2	ASAH1	NM_004315.2	AC;PHP;ASAH;PHP32;FLJ21558;FLJ22079	catalytic		ceramide
GI_30089931-A	382.4	361.1	331.7	ASB6	NM_177999.1	MGC1024;FLJ20548			
GI_30089933-I	131.5	140.9	139.1	ASB6	NM_017873.2	MGC1024;FLJ20548			
GI_30089936-A	1200.6	2053.4	1924.5	HSPA5BP1	NM_178031.1	GBP;FLJ20539			
GI_30089938-S	1302.7	2020	1628.5	GOLGA2	NM_004486.3	GM130;MGC20672		Golgi	
GI_30089939-S	1388.3	1398	1546.3	GOLGA3	NM_005895.2	MEA-2;GCP170	transporte	Golgi	intra-Golgi
GI_30089941-A	528.2	661.6	562.4	LHX3	NM_178138.2	M2-LHX3	RNA	nucleus	histogene
GI_30089941-I	116.9	103.5	111.2	LHX3	NM_178138.2	M2-LHX3	RNA	nucleus	histogene
GI_30089942-I	111.4	122.2	106.8	LHX3	NM_014564.2	M2-LHX3	RNA	nucleus	histogene
GI_30089943-I	595.9	599.4	661.3	MGC5178	NM_024044.2	MGC2532;FLJ23439			
GI_30089944-A	3177.9	2819.1	3127.7	MGC5178	NM_178044.1	MGC2532;FLJ23439			
GI_30089946-S	513.7	477.1	432.4	POLDIP2	NM_015584.2	POLD4;PDIP38;DKFZP586F1524			
GI_30089947-S	127.5	119.4	159.9	PPM1E	NM_014906.3	POPX1;PP2CH;KIAA1072	protein	protein	protein
GI_30089951-A	344.7	171.3	220.8	PTP9Q22	NM_152422.3	FLJ37312	protein		protein
GI_30089951-I	147.1	168.1	188.4	PTP9Q22	NM_152422.3	FLJ37312	protein		protein
GI_30089953-S	2019.7	2198	1800.5	H326	NM_015726.2				

GI_30089955-S	328.2	320.5	528	KRT7	NM_005556.2	K7;CK7;SCL;K2C7;MGC3625	structural	kinesin	cytoskelet
GI_30089957-S	2380.9	2279.4	2444.4	MRPS36	NM_033281.4	DC47;MRP-S36;MGC22896	structural	mitochond	protein
GI_30089958-S	98.6	94.3	91.4	ZNRF1	NM_032268.3	NIN283;FLJ14846;MGC15430;DKFZp434E2			
GI_30089959-A	128	149.2	135.2	CDC42BPA	NM_014826.3	MRCK;MRCKA;PK428;FLJ23347;KIAA0451	protein		protein
GI_30089961-I	143.2	178.4	160.7	CDC42BPA	NM_003607.2	MRCK;MRCKA;PK428;FLJ23347;KIAA0451	protein		protein
GI_30089963-S	593.3	435.1	348.4	CDC42EP2	NM_006779.2	CEP2;BORG1			
GI_30089964-S	215.6	239.2	137.4	CDC42EP3	NM_006449.3	UB1;CEP3;BORG2	cytoskelet		signal
GI_30089965-S	633.4	361.2	262.8	CDC42EP5	NM_145057.2	CEP5;Borg3;MGC21945;1700027J19Rik;201	DNA	nucleus	regulation
GI_30089967-A	90.9	108.1	89.8	C20orf41	NM_016434.2	NHL;KIAA1088;bK3184A7.3;DKFZP434C013	helicase	nucleus	oncogene
GI_30089967-I	121	135.1	129.9	C20orf41	NM_016434.2	NHL;KIAA1088;bK3184A7.3;DKFZP434C013	helicase	nucleus	oncogene
GI_30089968-I	168.7	164.4	169.5	C20orf41	NM_032957.2	NHL;KIAA1088;bK3184A7.3;DKFZP434C013	helicase	nucleus	oncogene
GI_30089975-I	98.1	93.5	99	CHRD	NM_177978.1				skeletal
GI_30089977-A	288.2	341.9	317.9	CHRD	NM_177979.1				skeletal
GI_30089990-I	866.6	795.9	727.8	ACP1	NM_004300.2	HAAP;MGC3499	acid	soluble	
GI_30089991-S	90.5	89.4	79	ART5	NM_053017.2	MGC22848	NAD(P)-	membran	protein
GI_30089993-A	144.4	161.1	132.3	ASB7	NM_024708.2	FLJ22551			
GI_30089993-I	103.3	117.1	107.4	ASB7	NM_024708.2	FLJ22551			
GI_30089996-A	2638.4	2636.4	3055.3	BAF53A	NM_177989.1	ACTL6;MGC5382	chromatin	actin	response
GI_30090001-A	3291.6	2671.3	2408.5	ACP1	NM_007099.2	HAAP;MGC3499	acid	soluble	
GI_30102932-A	126.7	156.3	133.5	KIR2DS4	NM_178228.1	PAX;KKA3;KIR1D;NKAT8;cl-39;CD158I	MHC-	integral to	
GI_30102939-S	155.3	188.5	169.8	OTOP3	NM_178233.1				
GI_30102943-S	11068.3	13282	11471	COAS2	NM_178230.1		cyclophilin		protein
GI_30102945-S	177.8	208.1	192.3	ALS2CR14	NM_178231.1				
GI_30141909-S	106.4	116.3	94.6	TNNI3	NM_000363.3	TNNC1		troponin	regulation
GI_30146994-S	136.5	150.1	122.5	CR1L	XM_114735.5				
GI_30147327-S	102	109.4	108.1	LOC152098	XM_087384.7				
GI_30147787-S	97.8	106.9	105.8	LOC344022	XM_292889.2				
GI_30147807-S	103	98.9	99.8	LOC152586	XM_087490.4				
GI_30148114-S	79.4	80	81.8	LOC284555	XM_211518.2				
GI_30148215-S	147.3	166	162	LOC130643	XM_059462.3				
GI_30148267-S	103.7	108.4	106.5	LOC90288	XM_030669.8				
GI_30148318-S	1349.4	883	847	LOC339448	XM_290902.2				
GI_30148676-S	92.9	102.5	98.2	LOC150519	XM_086937.5				
GI_30149001-S	105.6	172	177.5	LOC129607	XM_059368.4				
GI_30149009-S	851	1498.1	940.2	LOC285148	XM_209490.3				
GI_30149745-S	727.3	924.1	758.7	LOC149345	XM_086502.8				
GI_30149753-S	203.9	243.5	194.2	LGR6	XM_097508.8	FLJ14471;VTS20631			
GI_30150161-S	92.6	96.3	88.5	LOC286031	XM_209869.2				
GI_30150520-S	146.9	139.8	143	LOC256686	XM_173012.2				
GI_30150654-S	206.9	292.9	259.5	ZNF406	XM_114619.4				
GI_30151559-S	107.3	110.5	100	C9orf21	XM_114685.3				
GI_30151609-S	316.1	330.1	309.6	DKFZP727G	XM_045308.6				
GI_30151619-S	205.8	234.3	205.6	LOC158125	XM_088492.4				
GI_30152203-S	8406.8	7291.2	5316.6	LOC222901	XM_167275.4				

GI_30152429-S	119.9	133.9	129	FLJ36748	XM_059702.7				
GI_30152488-S	110.8	113.3	108.3	KIAA1889	XM_056298.5				
GI_30152745-S	169.9	171.8	180.4	LOC202051	XM_114430.5				
GI_30153038-S	242.7	305.5	282	C14orf66	XM_058681.6				
GI_30153291-S	81.5	89.6	81	LAMB4	XM_209857.3				
GI_30154059-S	191.4	202.3	157.6	LOC92270	XM_043989.7				
GI_30154219-S	241.5	309.4	279.8	KIAA0346	XM_043272.7				
GI_30154228-S	175	205.2	192.6	LOC124751	XM_064298.4				
GI_30154359-S	184.4	205.6	159.8	LDB3	XM_084376.6	ZASP;CYPHER;ORACLE;PDLIM6;KIAA0613;	protein		electron
GI_30154419-S	97.6	93.6	82.5	LOC119563	XM_061542.6				
GI_30155117-S	144.1	120.9	113.3	LOC342931	XM_292796.2				
GI_30155180-S	118.2	102.9	97	RPEL1	XM_166420.5				
GI_30155334-S	182.5	224.3	221.2	LOC284422	XM_209196.2				
GI_30155379-S	120.4	119.6	120.6	LOC284425	XM_211459.3				
GI_30155904-S	111.9	126.2	107	LOC283804	XM_208847.2				
GI_30156121-S	191.2	206.5	175.6	LOC119774	XM_061676.2				
GI_30156200-S	170.4	179.1	158.2	LOC119694	XM_061626.3				
GI_30156406-S	148.4	149.2	139.5	LOC120364	XM_062025.3				
GI_30156506-S	172.5	208.1	187.1	LOC283159	XM_208543.2				
GI_30156512-S	120.2	133.3	110.9	LOC283160	XM_208541.2				
GI_30156583-S	89.9	109.3	97.5	LOC347376	XM_293312.2				
GI_30156720-S	131.1	156.1	147.1	KIAA1328	XM_029429.5				
GI_30156893-S	105.8	108.7	109	OR5F1	XM_291859.2				
GI_30156895-S	191.1	237.6	206.5	LOC219447	XM_166808.2				
GI_30156899-S	102.6	127.4	109.9	LOC219477	XM_166829.2				
GI_30157437-S	235.4	246.6	267.5	KIAA1542	XM_290536.2				
GI_30157519-S	118	123.3	99.2	LOC139451	XM_066701.4				
GI_30157606-S	158.3	155.1	145.1	LOC338797	XM_290579.2				
GI_30157750-S	216.2	251.6	235.9	LOC284754	XM_211627.2				
GI_30158015-S	92.5	105.4	93.6	KIAA1580	XM_045271.7				
GI_30158339-S	145.7	148.5	141.1	LOC219414	XM_169434.5				
GI_30158524-S	123.3	132.2	128.7	LOC146179	XM_085354.3				
GI_30158785-S	146.8	166.3	148.9	LOC283902	XM_211251.2				
GI_30159652-S	185.3	228.6	199.5	LOC340152	XM_291154.2				
GI_30172563-S	149.1	173.1	126.3	VEGF	NM_003376.3	VEGFA	vascular	soluble	positive
GI_30179898-S	218.6	256.4	208.4	SOX10	NM_006941.3	DOM;WS4;MGC15649	RNA	nucleus	embryoge
GI_30179899-S	107.2	122	108.8	SOX1	NM_005986.2		transcripti	nucleus	establish
GI_30179901-S	740.8	2857.4	1267.8	SOX4	NM_003107.2	EVI16	transcripti	nucleus	regulation
GI_30179902-S	596.3	721.7	621.8	SOX8	NM_014587.2	MGC24837	RNA		central
GI_30179906-A	453.2	607.8	528.1	PILRA	NM_178273.1	FDF03			
GI_30179908-I	84.7	92.6	85.7	PILRA	NM_013439.2	FDF03			
GI_30179910-A	581.1	681	558.3	PILRB	NM_178238.1	FDFACT1;FDFACT2			
GI_30179910-I	115.7	131.6	115.5	PILRB	NM_178238.1	FDFACT1;FDFACT2			
GI_30179912-I	124.5	141.3	129.8	PILRB	NM_175047.2	FDFACT1;FDFACT2			

GI_30179914-I	119.3	139.8	117.1	PILRB	NM_013440.3	FDFACT1;FDFACT2			
GI_30181229-S	101.7	103	98.1	REG1A	NM_002909.3	P19;PSP;PTP;REG;ICRF;PSPS;PSPS1;MGC	lectin [goid		positive
GI_30181230-S	188.4	203	179.7	REG1B	NM_006507.2	REGH;REGL;PSPS2;REGI-BETA	lectin [goid		cell
GI_30181231-S	95.3	102.4	89.2	GPR132	NM_013345.2	G2A	receptor	integral to	G-protein
GI_30181232-S	353.3	393.5	313	LRRN4	NM_002319.2	LRN;LRRN1			neurogene
GI_30181234-S	201.8	236.2	202.9	ZNF165	NM_003447.2	LD65	transcripti	nucleus	regulation
GI_30181235-S	1082.9	927.5	1045.9	CPNE2	NM_152727.4	CPN2;COPN2;MGC16924			
GI_30181237-S	95.5	93.4	82.7	C1orf25	NM_030934.3	MGC57134;bG120K12.3	RNA		tRNA
GI_30181239-I	110.4	129.4	110.4	DCX	NM_178151.1	DC;DBCN;LISX;SCLH;XLIS	microtubul	microtubul	central
GI_30181243-A	300.6	356.5	343.5	DCX	NM_178153.1	DC;DBCN;LISX;SCLH;XLIS	microtubul	microtubul	central
GI_30181245-I	117	127.7	111.4	DCX	NM_000555.2	DC;DBCN;LISX;SCLH;XLIS	microtubul	microtubul	central
GI_30240931-S	1515.5	1053.9	2244.4	EHD1	NM_006795.2	PAST;PAST1;H-PAST;HPAST1	ATP	kinesin	biological_
GI_30240938-S	98.6	103.8	117.9	HCG9	NM_005844.2	HCGIX;HCGIX4;PERB11;HCGIX-4	molecular	cellular_co	biological_
GI_30260186-A	1186.4	1320.7	1494.7	ATPIF1	NM_016311.3	ATPI;MGC1167;MGC8898	enzyme	mitochond	energy
GI_30260187-S	1018.1	1159.3	1015.3	GOLGA5	NM_005113.2	RFG5;ret-II		Golgi	
GI_30260191-I	111.9	134.3	167.2	ATPIF1	NM_178191.1	ATPI;MGC1167;MGC8898	enzyme	mitochond	energy
GI_30260193-S	98.6	99.1	94.5	GOLGA6	NM_018652.2	GLP		kinesin	
GI_30315648-A	117.9	145.4	121.8	MBNL3	NM_133486.1	CHCR;MBLX;MBXL;MBLX39;FLJ11316	nucleic	nucleus	developm
GI_30315648-I	84.5	93.2	80.9	MBNL3	NM_133486.1	CHCR;MBLX;MBXL;MBLX39;FLJ11316	nucleic	nucleus	developm
GI_30315650-S	100.2	99.8	90.5	DMRT3	NM_021240.2	DMRTA3	transcripti	nucleus	sex
GI_30315657-A	186.2	254.5	204.4	SPTBN1	NM_178313.1	SPTB2	actin	spectrin	
GI_30315657-I	105.3	132.4	102	SPTBN1	NM_178313.1	SPTB2	actin	spectrin	
GI_30348953-S	111.6	137.2	116.3	MIB	NM_020774.1		zinc ion		
GI_30348973-S	98.8	91.4	92.9	ARL11	NM_138450.3	ARLTS1;MGC17429			
GI_30348976-S	2185.9	1885.9	3025.1	CBX6	NM_014292.2		chromatin	chromatin	chromatin
GI_30350209-A	90.1	89.7	104.9	APRG1	NM_178343.1				
GI_30350209-I	75.4	81.5	77.9	APRG1	NM_178343.1				
GI_30350213-I	459.4	560.5	502.3	APRG1	NM_178342.1				
GI_30350215-I	88.3	89.6	87.1	APRG1	NM_178344.1				
GI_30387616-S	112.9	108.8	104	APCDD1	NM_153000.3	B7323;DRAPC1			
GI_30387641-S	194.4	221.9	190.2	SPRL4A	NM_178356.1	LEP8			
GI_30387645-S	151.2	160.1	159.6	LEP6	NM_178354.1				
GI_30387647-S	156.8	158.3	140.1	LEP4	NM_178352.1				
GI_30387649-S	243.1	304.4	276.3	LEP5	NM_178353.1				
GI_30387651-S	483.4	608.6	539.7	LEP3	NM_178351.1				
GI_30387653-S	114	131.5	130	LEP1	NM_178348.1				
GI_30387655-S	259.6	365.1	304.2	SPRL2A	NM_178349.1	LEP2			
GI_30409981-S	2153.5	3921.4	2190.4	LAPTM4B	NM_018407.3	LC27;LAPTM4beta		integral to	
GI_30410024-S	120.7	114.6	106.9	FLJ31204	NM_174912.2		amidase		
GI_30410025-S	164	187.7	177	FLJ30507	NM_153010.3				
GI_30410026-S	105.2	117.5	106.6	FLJ90724	NM_153692.2				
GI_30410031-S	127.6	131.5	117.8	PSMAL/GCP_	NM_153696.2		peptidase		proteolysis
GI_30410034-S	246.4	286.2	268.4	SPRL5A	NM_178438.1	LEP18			
GI_30410036-S	113.4	128.9	118.7	SPRL3A	NM_178434.1	LEP15			

GI_30410038-S	149.3	171.2	149.6	LEP13	NM_178431.1				
GI_30410040-S	197.8	250.3	202.2	LEP14	NM_178433.1				
GI_30410042-S	253.4	271.2	253	SPRL1A	NM_178430.1	LEP12			
GI_30410044-S	98.5	115.9	101.2	LEP9	NM_178428.1				
GI_30410046-S	315.9	383.7	352.6	LEP11	NM_178429.1				
GI_30410709-S	376.6	300.9	375.8	SEC15L1	NM_019053.2	EXOC6;SEC15L;Sec15p;FLJ1125;FLJ11251;			
GI_30410711-S	586.8	657.4	629.4	SEC23IP	NM_007190.2	P125;MSTP053	protein	ER-Golgi	Golgi
GI_30410715-A	1235.7	1178.6	917.2	SEC3L1	NM_178237.1	SEC3;EXOC1;Sec3p;BM-102;FLJ10893	protein	kinesin	intracellula
GI_30410717-S	110.2	101.2	98.6	SEC14L3	NM_174975.2	TAP2	transporte	intracellula	transport
GI_30410718-S	117.1	133.4	123.1	SEC14L4	NM_174977.2	TAP3	transporte	intracellula	transport
GI_30410721-I	94.3	85.3	80.4	FUT8	NM_004480.3	MGC26465	glycoprote	Golgi	oligosacch
GI_30410729-A	864.3	1596.5	1706.4	FUT8	NM_178157.1	MGC26465	glycoprote	Golgi	oligosacch
GI_30410773-S	270.1	392.5	850	TBC1D8	NM_007063.2	1;AD3;VRP;HBLP1	GTPase	membran	positive
GI_30410776-I	89.1	96.1	92.6	HYPB	NM_012271.1	HIF1;FLJ22472;KIAA1732			
GI_30410778-A	258.2	283.7	253.2	HYPB	NM_014159.3	HIF1;FLJ22472;KIAA1732			
GI_30410780-A	334.8	373.4	337.1	FLJ12949	NM_178159.1				
GI_30410784-S	121.7	144	181.3	LHX1	NM_005568.2	LIM1;LIM-1	RNA	nucleus	histogene
GI_30410786-S	166.7	213.7	195	LHX4	NM_033343.2	Gsh-4	transcripti	nucleus	regulation
GI_30410787-I	136.2	150	129.6	TUSC3	NM_006765.2	N33;D8S1992;MGC13453	tumor	integral to	electron
GI_30410789-A	1904.2	2188.2	2120.2	TUSC3	NM_178234.1	N33;D8S1992;MGC13453	tumor	integral to	electron
GI_30410791-S	1911.1	2332.2	1836.5	PSME2	NM_002818.2	PA28B;REGbeta;PA28beta	proteasom	26S	immune
GI_30410793-A	1006.3	1137.5	1163.4	PSME3	NM_005789.2	Ki;PA28G;REG-GAMMA;PA28-gamma	proteasom	26S	
GI_30410799-A	979.7	922.2	807.1	APG4B	NM_013325.3	AUTL1;MGC1353;KIAA0943;DKFZp586D182			
GI_30410800-S	105.1	100.3	100.1	FHL5	NM_020482.3	ACT;FLJ33049;dJ393D12.2	catalytic		
GI_30410802-A	91.9	185.6	103.1	CDCP1	NM_178181.1	FLJ22969;MGC31813			
GI_30410802-I	327.4	457.2	371.5	CDCP1	NM_178181.1	FLJ22969;MGC31813			
GI_30410804-I	241.7	1034.7	224.6	CDCP1	NM_022842.3	FLJ22969;MGC31813			
GI_30410845-A	557.1	605.5	500.6	AUTL1	NM_178221.1	AUTL3;APG4-C;FLJ14867;MGC32915			
GI_30425377-S	422.8	450.1	368.9	MGC54289	NM_178454.1				
GI_30425381-S	284.8	310.4	262.6	PTPNS1L2	NM_178460.1	dJ576H24.4			
GI_30425383-S	142.7	159.3	157	C20orf78	NM_178462.1				
GI_30425385-S	106.5	122	109.3	C20orf166	NM_178463.1	FLJ32423;dJ353C17.1			
GI_30425387-S	132.7	162.7	133.8	TSPYL3	NM_178465.1	bA392M18.1	DNA	nucleus	nucleoso
GI_30425389-S	116.7	147.7	122.3	C20orf71	NM_178466.1	SPLUNC3;bA49G10.4	lipid		
GI_30425391-S	86.4	89.7	84.2	HMG4L	NM_178467.1	dJ18C9.3	DNA	chromatin	chromoso
GI_30425393-S	95.8	102.6	93.9	C20orf128	NM_178468.1	dJ614O4.7			
GI_30425399-S	188.7	239.7	212	GPR119	NM_178471.1	GPCR2;hGPCR2	electron	integral to	electron
GI_30425401-S	2828	1757.3	1416.4	C20orf53	NM_178472.1	bA353C18.4			
GI_30425403-S	209	240.9	201.9	C20orf179	NM_178477.1	dJ803K15.1	DNA	nucleus	
GI_30425405-S	87.4	91	87.5	C20orf79	NM_178483.1	dJ1068E13.2	sterol		
GI_30425409-S	99.9	108.8	108.2	R3HDML	NM_178491.1	dJ881L22.3		extracellul	
GI_30425443-S	105.5	127.1	104.2	ANKK1	NM_178510.1	X-kinase	protein-		protein
GI_30425541-S	265.2	252.8	228.4	C17orf31	NM_017575.3	EST1A;SMG-6;KIAA0732			
GI_30425545-S	1460.2	1626.7	1346.2	C14orf11	NM_018453.2	BM036;FLJ20578			

GI_30425552-S	123.2	133.2	115.7	RTN4RL1	NM_178568.1	NgR3;NGRH2;DKFZp547J144	receptor		
GI_30425562-S	267.4	287.5	276.5	RTN4RL2	NM_178570.1	NgR2;NGRH1	receptor		
GI_30466257-S	250.4	293.7	265.6	OSTalpha	NM_152672.2	MGC39807			
GI_30466265-S	2529.9	2548.5	2489.9	MCFD2	NM_139279.2	F5F8D;SDNSF;LMAN1IP	calcium		
GI_30474867-I	1865.6	2082.5	1727.2	SPTLC1	NM_006415.2	HSAN;HSN1;LBC1;LCB1;SPT1;SPTI;HSAN1	serine C-	endoplas	sphingolipi
GI_30474868-I	137.1	137.2	137	RASSF4	NM_032023.3	AD037;MGC44914			neuropepti
GI_30474869-I	674	758.7	1080.8	HRIHFB2122	NM_007032.3	KIAA1662;dJ37E16.4	F-actin	kinesin	actin
GI_30474870-A	359.3	370.5	324.3	SPTLC1	NM_178324.1	HSAN;HSN1;LBC1;LCB1;SPT1;SPTI;HSAN1	serine C-	endoplas	sphingolipi
GI_30474870-I	109.5	112.7	113.3	SPTLC1	NM_178324.1	HSAN;HSN1;LBC1;LCB1;SPT1;SPTI;HSAN1	serine C-	endoplas	sphingolipi
GI_30474872-A	589.2	624.6	634.1	RASSF4	NM_178145.1	AD037;MGC44914			neuropepti
GI_30519882-I	118.9	121.4	115.5	GTF2IRD2	NM_173537.1	FLJ21423			
GI_30520362-S	107.5	109.8	111.5	SLCO6A1	NM_173488.2	OATPY;OATP6A1;MGC26949	transporte	membran	transport
GI_30520372-S	428.5	409.5	282.3	CADPS2	NM_017954.7				
GI_30524927-S	117.1	119.1	119.4	NOD3	NM_178844.1	FLJ00348			
GI_30578409-S	718.6	730.7	445.3	SIMP	NM_178862.1		oligosacch	membran	protein
GI_30581108-I	279	330.2	321.6	HM13	NM_178580.1	H13;SPP;IMP1;PSL3;IMPAS;PSENL3;dJ324	peptidase	integral to	
GI_30581112-I	112	123.4	130.1	HM13	NM_178582.1	H13;SPP;IMP1;PSL3;IMPAS;PSENL3;dJ324	peptidase	integral to	
GI_30581114-A	542	805.5	787	HM13	NM_030789.2	H13;SPP;IMP1;PSL3;IMPAS;PSENL3;dJ324	peptidase	integral to	
GI_30581115-S	121.8	138.8	141	SOX11	NM_003108.3		transcripti	nucleus	neurogene
GI_30581116-I	125.4	154.5	130.7	SOX30	NM_178424.1		RNA	nucleus	spermatog
GI_30581118-A	133.3	132.8	129.2	SOX30	NM_007017.2		RNA	nucleus	spermatog
GI_30581119-S	297.6	308.3	216.3	SOX7	NM_031439.2	MGC10895			
GI_30581133-S	223.3	276.7	244.3	SEC5L1	NM_018303.4	SEC5;EXOC2;Sec5p;FLJ11026	protein	kinesin	intracellula
GI_30581134-S	182.9	174.6	152.1	SMC1L1	NM_006306.2	SMC1;SMCB;SB1.8;DXS423E;KIAA0178;SM	adenosine	mitotic	mitotic
GI_30581136-S	392.6	530	478.7	SMP3	NM_025163.2	FLJ12768;MGC52163			
GI_30581139-A	11239.1	12054	9657.2	PSME1	NM_006263.2	PA28A;IFI5111;MGC8628;REGalpha;PA28al	proteasom	26S	immune
GI_30581140-I	129.1	158.1	147.7	PSME1	NM_176783.1	PA28A;IFI5111;MGC8628;REGalpha;PA28al	proteasom	26S	immune
GI_30581142-I	174.6	206.2	208.9	PSMF1	NM_178578.1	PI31	proteasom	cytosol	ubiquitin-
GI_30581144-A	1579.5	1518.7	914.8	PSMF1	NM_178579.1	PI31	proteasom	cytosol	ubiquitin-
GI_30581147-A	110.7	110.8	117	NR2E3	NM_014249.2	PNR;RNR;ESCS;MGC49976	ligand-	nucleus	photorece
GI_30581147-I	103.9	122.5	104.4	NR2E3	NM_014249.2	PNR;RNR;ESCS;MGC49976	ligand-	nucleus	photorece
GI_30581148-I	96.1	94.4	86	NR2E3	NM_016346.2	PNR;RNR;ESCS;MGC49976	ligand-	nucleus	photorece
GI_30581151-A	100	128.5	107.8	GNRH2	NM_178332.1	GnRH-II;LH-RHII	hormone	soluble	signal
GI_30581154-I	121.6	124.1	107.7	GGTLA4	NM_178311.1	MGC50550;dJ831C21.2	gamma-		
GI_30581156-A	140.8	145.9	142.3	GGTLA4	NM_178312.1	MGC50550;dJ831C21.2	gamma-		
GI_30581158-I	113.7	113.9	110.2	GGTLA4	NM_080920.2	MGC50550;dJ831C21.2	gamma-		
GI_30581159-S	134.2	143.9	124.3	GDAP1L1	NM_024034.3	dJ995J12.1.1			
GI_30581161-S	95.5	131.5	110.8	GHRH	NM_021081.3	GRF;GHRF	receptor	extracellul	G-protein
GI_30581162-S	115.7	115.6	106.4	GPR73L1	NM_144773.2	PKR2;GPRg2;GPR73b;dJ680N4.3	neuropepti	integral to	G-protein
GI_30581163-S	223.9	250.6	230.9	GPR8	NM_005286.2		opioid	integral to	G-protein
GI_30581166-S	2323.6	2699	3683	GSS	NM_000178.2	GSHS;MGC14098	glutathion		amino
GI_30581167-S	98.5	94.9	92	CAPZA3	NM_033328.2	Gsg3;CAPPA3	structural	F-actin	actin
GI_30581168-I	80.6	86.8	79.8	CCR3	NM_001837.2	CKR3;CMKBR3;CC-CKR-3	chemokin	integral to	cytosolic
GI_30581169-A	107.5	106.5	99.7	CCR3	NM_178329.1	CKR3;CMKBR3;CC-CKR-3	chemokin	integral to	cytosolic

GI_30749197-A	898.8	1063.2	1000.3	FBXW5	NM_178226.1	MGC20962;DKFZP434B205			
GI_30794213-S	101.5	107.4	108.4	KIAA1712	NM_030633.1				
GI_30794215-S	419.7	376.5	321.7	TRIM56	NM_030961.1	RNF109;DKFZP667O116	nucleic	intracellula	
GI_30794221-S	808	725.2	1127.6	BTBD6	NM_033271.1	BDPL			
GI_30794245-S	501	530.7	472.4	LOC90736	NM_138362.1				
GI_30794367-I	97.3	103.5	106.7	PB1	NM_018313.2	BAF180			
GI_30794371-A	243.5	263.2	231.8	PB1	NM_018165.2	BAF180			
GI_30794371-I	236.6	279	249.7	PB1	NM_018165.2	BAF180			
GI_30794375-S	103.2	94.7	96.9	DOLPP1	NM_020438.2	LSFR2			
GI_30794471-S	149.2	176.5	149.3	HAPLN4	NM_023002.1	BRAL2;KIAA1926			
GI_30794487-S	100.4	102.8	93.9	KIF27	NM_017576.1	DKFZp434D0917			
GI_30794491-S	395.7	484.9	341.5	FBLP-1	NM_017556.1	FBLP1;MIGFILIN;DKFZp434G171	electron	cytoskelet	electron
GI_30794493-S	105.4	108.1	103.3	ZC3HDC3	NM_015117.1	KIAA0150	nucleic		
GI_30794499-S	1222.2	1823.8	737.8	AOF2	NM_015013.1	BHC110;KIAA0601			electron
GI_30794501-S	101.3	108.4	95.5	ASAHL	NM_014435.1		molecular	cellular_co	biological_
GI_30794503-S	131.9	155	140	ZNF354C	NM_014594.1	KID3	nucleic	nucleus	regulation
GI_30795116-I	96.7	122.2	99.8	FBXO18	NM_032807.3	FBH1;FLJ14590			
GI_30795118-A	2005.6	1993.4	1760.2	FBXO18	NM_178150.1	FBH1;FLJ14590			
GI_30795120-A	310.7	315.9	305.8	FBXW8	NM_012174.1	FBX29;FBXO29;MGC33534	ubiquitin		ubiquitin-
GI_30795122-I	101.2	99.1	85.9	FBXW8	NM_153348.2	FBX29;FBXO29;MGC33534	ubiquitin		ubiquitin-
GI_30795179-I	147.1	170	148	ZFYVE1	NM_021260.1	DFCP1;TAFF1;ZNFN2A1;KIAA1589	zinc ion	Golgi	
GI_30795181-A	824.3	959.7	909.4	ZFYVE1	NM_178441.1	DFCP1;TAFF1;ZNFN2A1;KIAA1589	zinc ion	Golgi	
GI_30795185-A	1929.2	1914.5	1797.9	WDFY1	NM_178350.1	WDF1;FENS-1;ZFYVE17;KIAA1435			
GI_30795187-S	115.6	122.1	106.8	WBSCR19	NM_175064.2	DKFZp434A1014			
GI_30795189-S	189.1	164.8	192.4	WBSCR27	NM_152559.2	MGC40131			
GI_30795191-I	148.3	218.8	179.7	WDFY1	NM_020830.2	WDF1;FENS-1;ZFYVE17;KIAA1435			
GI_30795192-A	1698.6	1393.6	1595.4	10-Sep	NM_178584.1	FLJ11619			
GI_30795194-I	101.1	109.3	99.2	10-Sep	NM_144710.2	FLJ11619			
GI_30795195-S	132.6	152.7	113.9	LHX2	NM_004789.3	LH2;hLhx2	transcripti	nucleus	oncogene
GI_30795197-S	160.6	169	176	LHX5	NM_022363.2		transcripti	nucleus	central
GI_30795198-I	93.6	98	120.4	HTR7	NM_019859.2		serotonin	integral to	circadian
GI_30795200-A	395.9	625.7	691.5	HTR7	NM_000872.3		serotonin	integral to	circadian
GI_30795201-I	241.4	249.6	218.8	HDAC9	NM_178423.1	HD7;HDAC;HDRP;MITR;HDAC7;HDAC7B;H	histone	nucleus	regulation
GI_30795205-S	493.9	564.8	576.1	PPP2R5A	NM_006243.2		protein	protein	signal
GI_30795206-S	259.9	328.5	373.2	PPP2R5B	NM_006244.2		protein	protein	signal
GI_30795207-I	113.2	116.7	111.4	IL19	NM_013371.2	MDA1;NG.1;ZMDA1;IL-10C	cytokine	extracellul	immune
GI_30795209-A	104.1	103.9	114.4	IL19	NM_153758.1	MDA1;NG.1;ZMDA1;IL-10C	cytokine	extracellul	immune
GI_30795209-I	93	83.4	85.3	IL19	NM_153758.1	MDA1;NG.1;ZMDA1;IL-10C	cytokine	extracellul	immune
GI_30795211-S	1214.3	1623.8	1814.3	IMP-3	NM_006547.2	KOC1;VICKZ3	RNA	cytoplasm	RNA
GI_30795213-S	91.9	142.6	103.5	CCR7	NM_001838.2	BLR2;EBI1;CDw197;CMKBR7	chemokin	integral to	cytosolic
GI_30795214-A	84.2	105.5	131	CCRK	NM_012119.2	p42;CDCH			
GI_30795216-I	96.7	99.2	107.9	CCRL1	NM_178445.1	PPR1;CCBP2;CCR10;CCR11;VSHK1;CKR-	chemokin	integral to	chemotaxi
GI_30795218-A	80.1	73.5	80.8	CCRL1	NM_016557.2	PPR1;CCBP2;CCR10;CCR11;VSHK1;CKR-	chemokin	integral to	chemotaxi
GI_30795218-I	151.7	180.7	169.4	CCRL1	NM_016557.2	PPR1;CCBP2;CCR10;CCR11;VSHK1;CKR-	chemokin	integral to	chemotaxi

GI_30795219-S	192.2	203.1	166.3	CRNKL1	NM_016652.3	CRN;HCRN;MSTP021		nucleus	mRNA
GI_30795223-S	328.1	358.1	435.9	TM4SF10	NM_031442.2	BCMP1;MGC32949;DKFZp564E153;DKFZP7			
GI_30795224-S	87.1	263.7	101.2	BM88	NM_016564.2	MGC34326		integral to	
GI_30795226-S	1213.7	1068.2	595.3	HARS2	NM_080820.3	C20orf88;MGC41905;bA379J5.3;bA555E18.1	hydrolase	cytoplasm	D-amino
GI_30795228-S	336	401.9	355.6	HCK	NM_002110.2	JTK9	protein-	peripheral	mesoderm
GI_30795230-S	5017.7	5685.2	8266.3	BASP1	NM_006317.3	CAP23;NAP22;CAP-23;NAP-22;MGC8555	DNA	cytoskelet	regulation
GI_30795232-S	189.4	249	210.5	BICC1	NM_025044.2	FLJ22476			
GI_30795236-A	105	105.4	109.6	ABCA12	NM_015657.3	LI2;ICR2B;DKFZP434G232			
GI_30795236-I	116.7	117.1	116.6	ABCA12	NM_015657.3	LI2;ICR2B;DKFZP434G232			
GI_30795237-I	85.7	106.1	98	ABCA12	NM_173076.2	LI2;ICR2B;DKFZP434G232			
GI_30795239-A	347.2	304.1	350.3	ARNT	NM_178426.1	HIF1B;TANGO;HIF1BETA;HIF-1beta	aryl	nucleus	protein-
GI_30795244-S	121.5	123.6	122.8	GCKR	NM_001486.2	GKRP	enzyme		carbohydr
GI_30795246-S	191.6	242.9	196.7	RNASEL	NM_021133.2	HPC1;RNS4;PRCA1	endoribon	cellular_co	protein
GI_30795247-A	177	237.6	161.8	AUTL2	NM_178270.1	APG4A;MGC43691;dJ889M15.3			
GI_30795249-I	103	94.7	99.4	AUTL2	NM_178271.1	APG4A;MGC43691;dJ889M15.3			
GI_30795253-S	164	181.5	159.7	AUTL4	NM_032885.4	APG4-D;MGC15906			
GI_30795256-I	115.6	133.3	114.4	FBXW5	NM_178225.1	MGC20962;DKFZP434B205			
GI_30840979-S	172.8	207.3	175	NFIA	NM_005595.1	NFI-L;KIAA1439	transcripti	nucleus	DNA
GI_30842823-S	197.4	175.8	158.5	LOC133308	NM_178833.2		solute:hyd	integral to	regulation
GI_30842828-S	113.1	125.6	111.4	PHF12	NM_020889.1	PF1;KIAA1523	DNA		regulation
GI_30911096-S	149.4	167.7	169.1	PUNC	NM_004884.1	HsT18880		plasma	cell
GI_30911100-S	880.2	857.8	814.2	SWAP70	NM_015055.1	SWAP-70;KIAA0640	calcium		
GI_30911102-S	235.8	287.1	246.1	PYGO1	NM_015617.1	DKFZp547G0910	DNA	nucleus	regulation
GI_31077078-A	155.5	181.3	158	C20orf23	NM_017683.1	SNX23;KISC20ORF			
GI_31077196-S	150.1	175.1	148.7	SOX17	NM_022454.2	FLJ22252	DNA	nucleus	regulation
GI_31077197-A	353.7	390.2	425.4	U1SNRNPBP	NM_180699.1	HM-1			
GI_31077201-S	316.5	167	235.6	SOX18	NM_018419.2	HLTS	RNA	nucleus	regulation
GI_31077202-A	165.4	178	166.2	U1SNRNPBP	NM_022717.2	HM-1			
GI_31077203-I	111	134.4	101.8	U1SNRNPBP	NM_007020.2	HM-1			
GI_31077208-A	85.2	81.2	96.9	HNF4A	NM_178850.1	TCF;HNF4;NR2A1;TCF14;NR2A21	RNA	nucleus	pathogene
GI_31077208-I	176.7	202.9	189.1	HNF4A	NM_178850.1	TCF;HNF4;NR2A1;TCF14;NR2A21	RNA	nucleus	pathogene
GI_31077210-A	695.4	1045.8	448.3	HIF1A	NM_181054.1	MOP1;HIF-1alpha;HIF1-ALPHA	RNA	nucleus	response
GI_31077212-I	1313.7	1999.3	748.7	HIF1A	NM_001530.2	MOP1;HIF-1alpha;HIF1-ALPHA	RNA	nucleus	response
GI_31077213-S	174.2	217.8	192.6	HUS1	NM_004507.2				DNA
GI_31077214-S	116.7	137.4	106.2	HUS1B	NM_148959.2				
GI_31083027-S	310.9	352.6	295.4	CCRN4L	NM_012118.2	NOC;CCR4;CCR4L;MGC4120817	transcripti	nucleus	transcripti
GI_31083052-S	129.1	145.5	133	CLN8	NM_018941.2	EPMR		ER-Golgi	neurogene
GI_31083084-A	826.6	1465.8	1201.9	MRPL52	NM_181307.1			extrachro	
GI_31083090-I	215.5	256.8	244.4	GOLGIN-67	NM_181076.1	GOLGA5		Golgi	
GI_31083098-A	957.7	1492	1144.4	GOLGIN-67	NM_181077.1	GOLGA5		Golgi	
GI_31083098-I	102.5	94.8	93.5	GOLGIN-67	NM_181077.1	GOLGA5		Golgi	
GI_31083115-S	684	630.3	631.1	C6orf80	NM_015439.2	CCRL1AP;DKFZp586D0623			
GI_31083125-S	372.1	460.7	413.2	COL9A2	NM_001852.3	MED;EDM2;DJ39G22.4	collagen	microfibril	skeletal
GI_31083135-S	168.5	192.4	169.7	CYP4Z1	NM_178134.2		monooxyg		electron

GI_31083143-A	755.1	439.4	499.7	AXIN1	NM_181050.1	AXIN;MGC52315	GTPase	cytoplasm	oocyte
GI_31083149-I	132.5	151.3	142.9	AXIN1	NM_003502.2	AXIN;MGC52315	GTPase	cytoplasm	oocyte
GI_31083155-S	97.4	100	98.5	IL20RA	NM_014432.2	IL-20R1;ZCYTOR7	receptor	integral to	blood
GI_31083165-S	98.6	98.1	93.6	IL20	NM_018724.2	IL-20;IL10D;ZCYTO10	cytokine	extracellul	immune
GI_31083173-I	194.4	248	241.9	IL21R	NM_181078.1	NILR;MGC10967	receptor	integral to	natural
GI_31083179-I	124.2	116.7	110.8	IL21R	NM_181079.1	NILR;MGC10967	receptor	integral to	natural
GI_31083186-A	273.5	389.3	319.5	IL21R	NM_021798.2	NILR;MGC10967	receptor	integral to	natural
GI_31083186-I	195	247.8	208.3	IL21R	NM_021798.2	NILR;MGC10967	receptor	integral to	natural
GI_31083192-S	117.1	147.8	151.4	ADCY1	NM_021116.1		calcium/ca	integral to	signal
GI_31083201-S	198.9	216.7	159.9	APOBEC3F	NM_145298.3	ARP8	zinc ion		
GI_31083218-A	156.3	188	165.3	NFYA	NM_021705.2	HAP2;CBF-A;CBF-B;NF-YA	transcripti	nucleus	transcripti
GI_31083227-I	102.2	104	102.8	NFYA	NM_002505.3	HAP2;CBF-A;CBF-B;NF-YA	transcripti	nucleus	transcripti
GI_31083242-I	94.4	103.3	94.5	PPP2R5C	NM_178587.1	B56G;MGC23064	protein	protein	signal
GI_31083249-A	694.8	827.3	659.9	PPP2R5C	NM_178588.1	B56G;MGC23064	protein	protein	signal
GI_31083249-I	122.7	120	108.1	PPP2R5C	NM_178588.1	B56G;MGC23064	protein	protein	signal
GI_31083258-I	117.9	108.9	99.8	PPP2R5C	NM_002719.2	B56G;MGC23064	protein	protein	signal
GI_31083266-I	117.7	152.7	146.4	PPP2R5D	NM_006245.2	MGC2134;MGC8949	protein	protein	neurogene
GI_31083287-A	312.4	387.1	417.7	PPP2R5D	NM_180977.1	MGC2134;MGC8949	protein	protein	neurogene
GI_31083295-S	363.5	414.9	415	PPP2R5E	NM_006246.2		protein	protein	signal
GI_31083305-S	77.9	85.4	80.2	FIBL-6	NM_031935.1	FBLN6			
GI_31083314-S	102.5	99.4	104.4	GPR45	NM_007227.3	PSP24A;PSP24(ALPHA)	G-protein	integral to	G-protein
GI_31083343-S	99.4	252.8	443.8	CMKOR1	NM_020311.1	RDC1;GPR159	G-protein	integral to	G-protein
GI_31083366-S	569.4	692.8	669	SEC8L1	NM_021807.2	REC8;SEC8;EXOC4;Sec8p;KIAA1699;MGC2	protein	kinesin	intracellula
GI_31088849-S	192.7	227	203.2	TMSL6	NM_181428.1	TMSB4L;dJ1071L10.1	actin	cytoplasm	cytoskelet
GI_31088851-S	97.8	97.8	98.2	hT2R55	NM_181429.1				
GI_31088867-S	1552.4	1300.3	1535.7	FLJ23476	NM_024640.2	YRDC	molecular		
GI_31317208-A	623.7	574.2	477.8	BTBD3	NM_181443.1	KIAA0952;dJ742J24.1	protein		
GI_31317208-I	98.3	91.2	100.9	BTBD3	NM_181443.1	KIAA0952;dJ742J24.1	protein		
GI_31317210-I	105	114.8	106.5	BTBD3	NM_014962.2	KIAA0952;dJ742J24.1	protein		
GI_31317211-I	1108.9	1247.8	1297.2	ANKFY1	NM_016376.2	ANKHZN;ZFYVE14;KIAA1255	protein		
GI_31317213-I	213.7	246.9	208.6	ARHGAP8	NM_015366.2	PP610;BPGAP1;FLJ20185	GTPase		
GI_31317215-I	82.4	93.1	87.4	ARHGAP8	NM_017701.2	PP610;BPGAP1;FLJ20185	GTPase		
GI_31317217-I	123.6	136.6	120.7	ARHGAP8	NM_181333.1	PP610;BPGAP1;FLJ20185	GTPase		
GI_31317219-I	153	212.2	178.2	ARHGAP8	NM_181334.1	PP610;BPGAP1;FLJ20185	GTPase		
GI_31317221-A	114.5	104.1	104.1	ARHGAP8	NM_181335.1	PP610;BPGAP1;FLJ20185	GTPase		
GI_31317223-S	203.1	349.7	337.3	EDIL3	NM_005711.3	DEL1;MGC26287	integrin		cell
GI_31317225-S	214.1	268.4	196	EFNB1	NM_004429.3	EFL3;EPLG2;LERK2;MGC8782	transmem	soluble	cell
GI_31317226-S	845	824	1548.2	EGR1	NM_001964.2	TIS8;AT225;NGFI-A;ZNF225;KROX-24;ZIF-	DNA	nucleus	regulation
GI_31317227-S	91.3	101.9	85.3	EGR3	NM_004430.2	PILOT	transcripti	nucleus	circadian
GI_31317229-S	103.8	99	102.5	FCER1A	NM_002001.2	FCE1A;FcERI	receptor	integral to	immune
GI_31317230-A	186.8	287	112.8	FKBP7	NM_181342.1	FKBP23;PPIase;MGC9420	cyclophilin	endoplas	protein
GI_31317232-I	103.6	112.2	111.3	FKBP7	NM_016105.2	FKBP23;PPIase;MGC9420	cyclophilin	endoplas	protein
GI_31317233-A	116.3	131.6	124.9	FRAT1	NM_181355.1				oncogene
GI_31317235-I	120.6	116.9	125.3	FRAT1	NM_005479.2				oncogene

GI_31317237-S	489	526.7	578.6	FRAT2	NM_012083.2	MGC10562	molecular	cellular_co	developm
GI_31317238-S	96.7	115.3	102.9	IL22RA1	NM_021258.2	IL22R;CRF2-9	receptor	membran	
GI_31317242-A	149.8	154.1	138	IL22RA2	NM_181310.1	CRF2X;CRF2-10;CRF2-S1;IL-22BP			
GI_31317244-I	88.1	102.2	94	IL22RA2	NM_052962.2	CRF2X;CRF2-10;CRF2-S1;IL-22BP			
GI_31317245-A	181	233.1	190.1	IL24	NM_181339.1	C49A;FISP;MDA7;ST16;IL-24;IL10B;Mob-	tumor	extracellul	apoptosis
GI_31317247-I	181.1	221.2	164.3	IL24	NM_006850.2	C49A;FISP;MDA7;ST16;IL-24;IL10B;Mob-	tumor	extracellul	apoptosis
GI_31317248-A	101.5	110.7	94.9	IL6R	NM_181359.1	CD126;IL6RA;IL-6R-1;IL-6R-alpha	interleukin-	interleukin-	cell growth
GI_31317250-I	126.2	149.7	140.4	IL6R	NM_000565.2	CD126;IL6RA;IL-6R-1;IL-6R-alpha	interleukin-	interleukin-	cell growth
GI_31317251-A	108.4	101.2	107.9	ANKFY1	NM_020740.1	ANKHZN;ZFYVE14;KIAA1255	protein		
GI_31317251-I	104.5	95.5	99.9	ANKFY1	NM_020740.1	ANKHZN;ZFYVE14;KIAA1255	protein		
GI_31317253-S	132	119	113.4	NLGN1	NM_014932.2	KIAA1070;MGC45115	neuroligin	membran	cell
GI_31317254-S	707.6	777.4	771	NLGN2	NM_020795.2	KIAA1366	hydrolase	membran	cell
GI_31317255-A	261.4	108.9	137.3	NLGN4	NM_181332.1	HLNX;HNLX;NLGN;KIAA1260;MGC22376	neuroligin	membran	cell
GI_31317255-I	125.1	140.9	127.6	NLGN4	NM_181332.1	HLNX;HNLX;NLGN;KIAA1260;MGC22376	neuroligin	membran	cell
GI_31317257-I	151.2	167	146.8	NLGN4	NM_020742.2	HLNX;HNLX;NLGN;KIAA1260;MGC22376	neuroligin	membran	cell
GI_31317262-A	436.9	370	401.9	TAZ	NM_181313.1	EFE;BTHS;EFE2;G4.5;CMD3A;XAP-2			heart
GI_31317264-I	725.6	926.4	833.6	TAZ	NM_181314.1	EFE;BTHS;EFE2;G4.5;CMD3A;XAP-2			heart
GI_31317267-A	156.8	182.6	158.3	WDFY3	NM_178583.1	ALFY;ZFYVE25;KIAA0993;MGC16461			
GI_31317267-I	119.7	142.7	126.9	WDFY3	NM_178583.1	ALFY;ZFYVE25;KIAA0993;MGC16461			
GI_31317269-I	133.1	129.6	122.8	WDFY3	NM_178585.1	ALFY;ZFYVE25;KIAA0993;MGC16461			
GI_31317271-I	135.6	166.3	169.6	WDFY3	NM_014991.3	ALFY;ZFYVE25;KIAA0993;MGC16461			
GI_31317273-I	417.1	375.2	368.9	WDR20	NM_181291.1	DMR;FLJ33659;MGC33177;MGC33183			
GI_31317275-A	242.2	260.8	240.1	WDR20	NM_181302.1	DMR;FLJ33659;MGC33177;MGC33183			
GI_31317281-A	108.8	107.5	109	WDR17	NM_181265.1				
GI_31317281-I	93.3	97.2	93.4	WDR17	NM_181265.1				
GI_31317285-A	370.1	555.8	329	WDR21	NM_181341.1	MGC20547;MGC46524;DKFZp434K114			
GI_31317289-A	345.3	337.3	414.5	SMURF1	NM_181349.1		protein	intracellula	ubiquitin
GI_31317291-I	119	123.7	100.9	SMURF1	NM_020429.1		protein	intracellula	ubiquitin
GI_31317293-A	117.4	110.6	109.6	KCNMB2	NM_005832.3	MGC22431	ion	membran	potassium
GI_31317293-I	141	155.2	164.5	KCNMB2	NM_005832.3	MGC22431	ion	membran	potassium
GI_31317294-I	80.1	83.8	70.5	KCNMB2	NM_181361.1	MGC22431	ion	membran	potassium
GI_31317296-I	122.7	152.2	137.4	ID1	NM_181353.1	ID		nucleus	regulation
GI_31317298-A	513.1	1001.2	1097.3	ID1	NM_002165.2	ID		nucleus	regulation
GI_31317300-S	101.5	108.4	111.2	CAPON	NM_014697.1	KIAA0464			
GI_31317302-S	202.5	230.9	208.3	HSPA12B	NM_052970.3	C20orf60;FLJ32150;dJ1009E24.2	ATP		
GI_31317304-S	793.7	832.5	680.4	MPHOSPH1	NM_005791.1	MPP10;MPP10P	cell cycle	nucleolus	M phase
GI_31317306-S	111.8	96	107.9	PCSK9	NM_174936.2	FH3;NARC1;HCHOLA3	subtilase		proteolysis
GI_31317308-S	302.3	389.5	293	PIP5K1C	NM_012398.1	KIAA0589;PIP5Kgamma;PIP5K-GAMMA	1-		
GI_31317310-I	119.5	121.8	131.6	WDR17	NM_170710.2				
GI_31324529-S	128.6	162	152.1	IREM2	NM_181449.1		receptor		
GI_31324542-S	3338.1	2924.6	4123.1	CaMKIINalph	NM_018584.4	PRO1489;MGC22256			
GI_31324576-S	102.8	104.9	103.9	MIRAB13	NM_033386.1	KIAA1668;bA395L14.2	zinc ion	intracellula	vesicle-
GI_31340555-S	131.9	143.3	130.4	cig5	NM_080657.3	vig1			
GI_31340570-S	99.8	101.5	81.9	DACH2	NM_053281.2	FLJ31391		nucleus	cell growth

GI_31340578-S	132.7	142.1	146.1	DKFZp434B2	NM_032263.2	FLJ11667;FLJ23571			
GI_31340581-S	153.7	166.2	156.5	NEUROG2	NM_024019.2	Atoh4;ngn-2;Math4A;MGC46562	DNA	nucleus	regulation
GI_31340617-S	2076.5	2163.5	2030.9	PRKDC	NM_006904.6	p350;DNAPK;DNPK1;HYRC1;XRCC7	protein	nucleus	double-
GI_31340618-S	104.7	118.4	114.4	ZNF70	NM_021916.2	Cos17;MGC48959	transcripti	nucleus	regulation
GI_31340687-S	351.1	370.3	338.7	LOC352909	NM_178837.2				
GI_31340688-S	282.5	326.8	290.8	GATS	NM_178831.2				
GI_31340712-S	291.4	370.9	333.9	LRRTM1	NM_178839.2			integral to	
GI_31340713-S	1990.3	1312.9	202.2	TDE2L	NM_178865.2	TDE2;FKSG84;PRO0899		membran	
GI_31340718-S	95.2	90.8	90.5	MGC51025	NM_178571.2				
GI_31340723-S	276.6	270.4	299.9	CEI	NM_178569.2				
GI_31340828-S	103.1	102.4	97.9	FLJ30435	NM_174950.2				
GI_31340935-S	136.7	160.6	150.8	LGICZ	NM_180990.2	ZAC	extracellul	membran	transport
GI_31341089-S	432.9	527	429.3	PDZK8	NM_173791.2	bA129M16.2	protein		intracellula
GI_31341095-S	477.1	358.2	321.5	LOC128977	NM_173793.2				
GI_31341096-S	324.4	362.3	276.9	FUNDC1	NM_173794.2	MGC51029			
GI_31341099-S	222.2	242.5	213.3	FLJ32096	NM_173795.2				
GI_31341100-S	114.7	105.5	110.1	MGC24125	NM_173796.2				
GI_31341107-S	1191.1	1339.4	1162.4	FLJ38499	NM_173797.2		nucleic		
GI_31341108-S	142.4	178.2	169	LOC170261	NM_173798.2		nucleic	nucleus	regulation
GI_31341110-S	104.6	109.7	99.2	FLJ39873	NM_173799.2				
GI_31341111-S	95.4	102.5	95.6	FLJ90650	NM_173800.2				
GI_31341117-S	90.8	98.2	95.1	MGC50559	NM_173802.2		S-		
GI_31341119-S	121.5	145.6	110.3	IFNT1	NM_176891.2		hematopoi	extracellul	defense
GI_31341122-S	145.5	161.7	154.1	FLJ39599	NM_173803.2				
GI_31341123-S	128	156.3	154.2	FLJ38723	NM_173805.2				
GI_31341127-S	105.7	108.6	89	MGC50721	NM_173806.2				
GI_31341128-S	143.5	155.8	143.3	MGC33370	NM_173807.2				
GI_31341135-S	312.8	331.2	310.4	FLJ32675	NM_173811.2				
GI_31341139-S	87.3	103.2	94	FLJ34154	NM_173813.2				
GI_31341145-S	1945.2	1634.2	1730.4	MGC8902	NM_173638.2		DNA	nucleus	regulation
GI_31341149-S	160	155.3	130.4	FLJ36754	NM_173829.2		nucleic		
GI_31341152-S	145	148.2	140.3	LOC286075	NM_173831.2		nucleic	intracellula	regulation
GI_31341155-S	169.5	196	175.4	FLJ38705	NM_173832.2	FLJ00028	DNA	nucleus	regulation
GI_31341156-S	106.3	111.6	108.1	MGC45780	NM_173833.2				
GI_31341159-S	645.8	780.7	829	MGC21416	NM_173834.2				
GI_31341185-S	93.7	110.3	78.4	SPACA3	NM_173847.2	SLLP1;ALLP17	lysozyme	extracellul	cell wall
GI_31341191-S	121.2	132.1	103.5	OL-64	NM_173850.2		serine		
GI_31341192-S	110.4	124.9	117.5	S100A15	NM_176823.2	S100A7a;S100A7f;S100A7L1	calcium		
GI_31341196-S	1295.5	1104.8	1016.3	KRTCAP2	NM_173852.2	KCP2			
GI_31341197-S	112.4	104	109.5	KRTCAP3	NM_173853.2	KCP3			
GI_31341205-S	87.4	106.2	96.5	LOC283385	NM_173855.2				
GI_31341213-S	144.6	149.6	126.8	LOC200895	NM_176815.2		dihydrofol		nucleotide
GI_31341214-S	102.3	97.6	101.5	KENAE	NM_176816.2				
GI_31341259-S	125.2	113.8	109.7	TMEM16D	NM_178826.2	FLJ34221;FLJ34272;FLJ35277			

GI_31341260-S	105.1	107.5	104.6	OSTbeta	NM_178859.2				
GI_31341282-S	207.3	246.1	212.4	K6IRS3	NM_175068.2	KRT6IRS3			
GI_31341283-S	126	147.3	142.1	INM01	NM_175075.2				
GI_31341302-S	470.5	474.8	379.5	JAZF1	NM_175061.2	DKFZp761K2222		nucleus	cell growth
GI_31341312-S	101.4	92.6	86	K6IRS4	NM_175053.2	KRT5C;KRT6IRS4			
GI_31341313-S	113.5	133.7	121.6	LOC144100	NM_175058.2				
GI_31341319-S	143.8	172.8	141.2	SEZ6	NM_178860.2				
GI_31341340-S	1382.6	913.9	813.7	LOC91942	NM_174889.2				
GI_31341349-S	411.8	502.1	528.9	C14orf79	NM_174891.2				
GI_31341350-S	165.3	201.8	168.5	MGC24133	NM_174896.2				
GI_31341354-S	85.9	81	91.7	FAM9C	NM_174901.2			nucleus	
GI_31341355-S	360.3	267.6	221.5	LOC143458	NM_174902.2				
GI_31341368-S	228.3	270.1	235.7	LOC167127	NM_174914.2		transferas		metabolis
GI_31341376-S	197.2	206.1	181	FLJ36888	NM_178830.2				
GI_31341380-S	154.8	199.6	168.4	LOC201191	NM_174920.2				
GI_31341385-S	520.1	514.8	507.3	PMS2L5	NM_174930.2	PMS7;MGC34222	damaged	cellular_co	mismatch
GI_31341399-S	101.9	108.7	95.5	MGC39681	NM_174939.2				
GI_31341400-S	168.5	252.9	242.5	M160	NM_174941.2	CD163B	protein-	membran	
GI_31341411-S	108.2	109.4	113.3	FLJ25976	NM_174943.2				
GI_31341423-S	120.4	137.4	123.9	AP1S3	NM_178814.2		protein	Golgi	endocytosi
GI_31341424-S	129.5	131.9	133.2	C7orf34	NM_178829.2	ctm-1			
GI_31341428-S	986.3	885.3	761	LEMD2	NM_181336.2	dJ482C21.1		nuclear	
GI_31341468-S	107.4	120.1	109.1	ARL8	NM_178815.2		small		small
GI_31341469-S	607.7	677	624	KCTD13	NM_178863.2	PDIP1;FKSG86;POLDIP1	voltage-	membran	potassium
GI_31341470-S	94	95.8	87	CASC2	NM_178816.2				
GI_31341471-S	105.3	111.4	97	NXF	NM_178864.2		signal		signal
GI_31341477-S	95.8	92.3	91.9	LASS3	NM_178842.2	MGC27091	transcripti	nucleus	regulation
GI_31341566-S	910.8	1130.9	179.4	GJB2	NM_004004.2	HID;KID;PPK;CX26;DFNA3;DFNB1;NSRD1	connexon	connexon	hearing
GI_31341670-S	102.3	122.6	130.6	ZDHHC21	NM_178566.2		zinc ion	integral to	regulation
GI_31341671-S	102.5	118.8	119.5	MGC42638	NM_178567.2		ubiquitin		ubiquitin
GI_31341675-S	95.5	126	110	MGC50831	NM_175924.2		phospholi		lipid
GI_31341683-S	210.1	249.5	297.7	LOC340371	NM_178564.2		ATP		protein
GI_31341688-S	206.3	238.6	211.9	MGC35308	NM_175922.2		DNA	nucleus	regulation
GI_31341689-S	158.5	198.2	176.1	MGC42630	NM_175923.2				
GI_31341691-S	718.5	509.5	444	C10orf83	NM_178832.2	bA548K23.4			
GI_31341698-S	122.9	137.7	123.4	MGC50844	NM_178562.2			integral to	
GI_31341703-S	120.2	122	133.7	FLJ90430	NM_178558.2		electron	nucleus	electron
GI_31341708-S	143.1	149.8	142.6	FLJ37478	NM_178557.2		N-		
GI_31341712-S	94.4	107.2	93.1	MGC35206	NM_178552.2				
GI_31341713-S	184.3	207.3	190.6	MGC44505	NM_178553.2				
GI_31341723-S	94.5	85.7	89.8	MGC42493	NM_178549.2				
GI_31341724-S	132.2	255.3	150.5	MGC48998	NM_178550.2				
GI_31341729-S	481.9	541.3	395.3	ARCH	NM_178547.2				
GI_31341730-S	146.1	144.4	120.4	AP2E	NM_178548.2	MGC49007	transcripti	nucleus	regulation

GI_31341734-S	136.4	132.4	120.6	LOC339456	NM_178545.2				
GI_31341735-S	127.3	134.8	132.6	LOC339483	NM_178546.2				
GI_31341741-S	235.7	264	249.1	ZNF546	NM_178544.2	MGC43537	nucleic	intracellula	regulation
GI_31341752-S	137.2	134.1	123.9	MGC48915	NM_178540.2				
GI_31341753-S	296.8	364.1	339.5	DKFZp762C2	NM_178542.2				
GI_31341765-S	270.4	344.1	374.5	LOC338799	NM_178538.2				
GI_31341766-S	95	91.5	96	TAFA2	NM_178539.2	DKFZp761E1217			
GI_31341771-S	99.8	107	101.4	MGC48935	NM_178536.2		prostaglan		transport
GI_31341776-S	696.9	801.7	699.3	FLJ37940	NM_178534.2				
GI_31341777-S	106.9	128.2	126.3	LOC286103	NM_178535.2				
GI_31341781-S	113.4	121.6	95.2	LOC285671	NM_178532.2				
GI_31341793-S	149.5	170.4	153.1	FLJ40473	NM_178531.2				
GI_31341794-I	126.6	153.7	133.8	C1QTNF3	NM_181435.2	CTRP3;CORS26;FLJ37576		microfibril	
GI_31341799-S	129.8	165.5	201.4	FLJ39485	NM_175920.2				
GI_31341800-S	1116.2	938.7	1016.3	LOC285636	NM_175921.2				
GI_31341814-S	102.6	102.8	90.8	MGC40574	NM_178529.2				
GI_31341815-S	133	135.9	132.6	FLJ38379	NM_178530.2				
GI_31341818-S	124.1	121.7	111.8	MGC43026	NM_178527.2		cation	integral to	cation
GI_31341819-S	96.3	106.1	118.9	FLJ38773	NM_178528.2				
GI_31341824-S	176.4	165.6	175.9	MGC45556	NM_178523.2				
GI_31341825-S	133.7	145.8	140.5	MGC33407	NM_178525.2		N-	actin	DNA
GI_31341830-S	178.3	193.7	177.6	FLJ38792	NM_178520.2				
GI_31341831-S	104	113.9	106.8	FLJ39005	NM_178521.2				
GI_31341836-S	128.8	144.7	128.3	FLJ36878	NM_178518.2				
GI_31341837-S	191.2	232.3	196.6	FLJ39421	NM_178519.2				
GI_31341844-S	279	394.3	391.8	LOC283849	NM_178516.2				
GI_31341845-S	422	517.1	567.9	PIGW	NM_178517.2	Gwt1;FLJ37433			
GI_31341849-S	168.5	177.3	138.7	LOC283487	NM_178514.2				
GI_31341850-S	110.6	115	112.7	FLJ37307	NM_178515.2				
GI_31341857-S	211.9	206	197	FLJ37201	NM_178512.2				
GI_31341858-S	120.1	114.3	108.8	FLJ38690	NM_178513.2				
GI_31341865-S	1548.5	1084.1	1228.6	LOC255783	NM_178511.2				
GI_31341870-S	401	389.3	343.3	FLJ34443	NM_175918.2				
GI_31341871-S	112.8	116.5	129.1	FLJ90723	NM_175919.2				
GI_31341881-S	5061	3699.2	5575.3	MGC57858	NM_178508.2				
GI_31341888-S	1939.1	2317.6	1928.1	NS5ATP13TF	NM_178507.2	MGC52117			
GI_31341894-S	95.1	85.2	80.7	MGC35010	NM_178505.2				
GI_31341899-S	2207.7	2110	2596.3	DTX3	NM_178502.2	RNF154;FLJ34766			
GI_31341900-S	239.5	274.6	262.7	FLJ40542	NM_178503.2				
GI_31341905-S	94.5	95.6	96.4	FLJ40434	NM_178501.2				
GI_31341910-S	444.4	506.1	460.5	MGC39827	NM_178499.2				
GI_31341911-S	264.9	322.8	312.2	PHOSPHO1	NM_178500.2				
GI_31341915-S	100.5	106.7	108.6	FLJ23657	NM_178497.2				
GI_31341916-S	99.5	113.2	105.9	MGC52019	NM_178498.2		transporte	membran	transport

GI_31341922-S	351	500.6	503.1	LOC151963	NM_178496.2				
GI_31341935-S	103.4	99.9	92.7	FLJ40125	NM_178494.2		catalytic	nucleus	regulation
GI_31341936-S	106.9	107.1	95.5	MGC24047	NM_178840.2				
GI_31341942-S	106.6	109.5	121.1	KIAA1892L	NM_178470.2				
GI_31341948-S	107.6	116.9	115.7	MGC52282	NM_178453.2		trypsin		proteolysis
GI_31341949-S	98.8	95.5	98.5	LOC138307	NM_178469.2				
GI_31341954-S	105	95	99.2	ZMYND17	NM_178451.2	FLJ39565			
GI_31341960-S	221.4	272.2	234.8	TIP39	NM_178449.2				
GI_31341961-S	205.4	399.3	528.8	MGC48332	NM_178450.2		electron		electron
GI_31341967-S	330.4	327.7	406.2	LOC89958	NM_178448.2		DNA	nucleus	regulation
GI_31341989-S	440.2	522.3	541	FLJ37818	NM_175916.2				
GI_31341990-S	114	116.7	123.6	FLJ37228	NM_175917.2				
GI_31342038-S	107.5	104.7	112	FLJ39654	NM_175914.2				
GI_31342039-S	225.7	249.5	229.5	FLJ38343	NM_175915.2		DNA	nucleus	regulation
GI_31342074-S	94.5	115.4	96.4	FLJ39582	NM_178315.2				
GI_31342079-S	248.3	223.6	139.4	FLJ39378	NM_178314.2				
GI_31342170-S	113.1	144.1	134.3	C5orf12	NM_178276.2	TPO1	electron	membran	electron
GI_31342210-S	85.2	103.8	85.8	MGC40047	NM_175911.2		olfactory	integral to	G-protein
GI_31342211-S	96.7	100.9	98.9	FLJ39609	NM_175912.2				
GI_31342225-S	108.4	110.7	116.6	MGC33608	NM_175906.2				
GI_31342226-S	487.4	507.7	513.7	MGC45594	NM_175907.2		alcohol		
GI_31342232-S	98.9	123.9	109.6	FLJ40121	NM_175904.2		transporte	membran	transport
GI_31342241-S	104	132.7	109.5	LOC283932	NM_175901.2				
GI_31342242-S	191.6	230.2	184.4	LOC284033	NM_175903.2				
GI_31342253-S	315.5	389.4	353	FIS	NM_175616.2				
GI_31342255-S	889.2	647.2	1472.9	MT1J	NM_175622.2	MT1;MTB	metal ion		
GI_31342257-S	149.8	117.5	129.7	LOC143425	NM_175733.2				
GI_31342258-S	95	95	90.6	LOC201243	NM_175734.2				
GI_31342260-S	155.5	245.5	161.7	FLJ35681	NM_175900.2		DNA	nucleus	regulation
GI_31342325-S	108.8	104.6	106.3	NMNAT3	NM_178177.2	PNAT3;PNAT-3	nucleotidyl		biosynthes
GI_31342330-S	418	513.9	462.4	TREML1	NM_178174.2	TLT1;TLT-1;dJ238O23.3			
GI_31342331-S	98	110.9	110.4	LHFPL1	NM_178175.2				
GI_31342336-S	159.3	174.1	154.4	LOC338328	NM_178172.2		DNA	nucleus	regulation
GI_31342337-S	139.3	154	138.8	LOC339834	NM_178173.2				
GI_31342341-S	139.5	162.4	162.5	NEK8	NM_178170.2	NEK12A	cAMP-		protein
GI_31342342-S	321.2	374	345.5	GSDM	NM_178171.2	FLJ39120			
GI_31342347-S	111.8	116.9	97.4	RASSF3	NM_178169.2	RASSF5			
GI_31342353-S	116.1	123.7	116	ZNF598	NM_178167.2				
GI_31342377-S	197.9	235.2	217.5	SCDR9	NM_178135.2				
GI_31342394-S	330.6	404.3	363.5	TXL-2	NM_178130.2	TXNDC6	nucleoside		electron
GI_31342398-S	101.2	93.5	94	ANGPTL5	NM_178127.2				
GI_31342399-S	101.4	108.4	109	LOC283985	NM_178128.2		oxidoredu		
GI_31342404-S	405	506.2	442.6	TRIM50A	NM_178125.2	TRIM50	zinc ion	intracellula	
GI_31342405-S	2327.8	2666.7	2798.9	LOC162427	NM_178126.2				

GI_31342410-S	263.3	505.4	439.9	SESTD1	NM_178123.2	SOLO;DKFZp434O0515			protein
GI_31342415-S	281.1	209.9	177.1	LOC90529	NM_178122.2				
GI_31342420-S	571.9	445.7	408.7	DLX1	NM_178120.2		transcripti	nucleus	regulation
GI_31342522-S	100.8	99.1	89.3	DSG4	NM_177986.2	LAH;CDGF13;CDHF13	calcium	membran	homophili
GI_31342615-S	776.4	985.7	781.4	PHGDHL1	NM_177967.2	FLJ30548			
GI_31342620-S	121.4	129.6	122.6	LOC157657	NM_177965.2				
GI_31342626-S	107.4	120.7	107.7	SYT12	NM_177963.2	SRG1;SYT11	transporte	membran	transport
GI_31342650-S	115.5	123	117.3	C21orf61	NM_178817.2	B27;FALP		integral to	
GI_31343322-S	137.7	128.9	131.2	LOC283588	NM_175897.2				
GI_31343323-S	94.7	97.7	100.2	LOC283687	NM_175898.2				
GI_31343329-S	101.9	97.8	100.4	LOC152831	NM_175737.2		hydrolase		carbohydr
GI_31343330-S	130.3	219	178.3	RAB37	NM_175738.2		RAS small		small
GI_31343331-S	117.5	129.1	111	FLJ25590	NM_175895.2				
GI_31343332-S	106.9	98.5	162.3	LOC283476	NM_175896.2				
GI_31343337-S	97.5	103.8	105	SERPINA11	NM_175739.2	GCET1			
GI_31343338-S	487.2	488.9	351.5	LOC283241	NM_175893.2				
GI_31343339-S	186.9	163.2	144.3	FLJ33996	NM_175894.2				
GI_31343340-S	87.7	99.1	86.3	FAM9A	NM_174951.2			nucleus	
GI_31343344-S	481.4	466.1	400.2	TRAPPC6B	NM_177452.2				
GI_31343345-S	83.9	91.5	85.8	ANKRD21	NM_174981.2	POTE			
GI_31343346-S	234.8	199.3	180.4	C14orf65	NM_174979.2				
GI_31343353-S	130.8	160	140.5	KRT6E	NM_173086.2		structural	kinesin	cytoskelet
GI_31343354-S	538.4	450.3	529.9	PAQR3	NM_177453.2				
GI_31343355-S	117.1	115.5	114.9	MIST1	NM_177455.2				
GI_31343375-S	323.9	332.5	387.9	DKFZp586M1	NM_178819.2	LPAATZ	acyltransf		metabolis
GI_31343395-S	111.7	117.1	119.3	LOC201164	NM_178836.2				
GI_31343439-S	2882.4	3127.4	2565.1	OLIG3	NM_175747.2	Bhlhb7			
GI_31343457-S	134.2	186	153.1	FBXO36	NM_174899.3				
GI_31343459-S	101.5	108.1	89.1	C6orf165	NM_178823.2	FLJ25974;dJ382I10.1			
GI_31343475-S	1356.8	1242.6	1037.5	GNA13	NM_006572.3	G13;MGC46138	heterotrim	peripheral	cell
GI_31343480-S	153.9	173.5	166.7	LOC222171	NM_175887.2				
GI_31343481-S	113.6	110.9	107.3	FLJ37045	NM_175889.2				
GI_31343485-S	460.4	396.1	393.4	MGC2647	NM_178841.2	MGC14381			
GI_31343491-S	1108.5	1016.1	818.8	LOC152485	NM_178835.2		electron		electron
GI_31343495-S	422	399	396.5	LOC129285	NM_152994.2				
GI_31343498-A	186.2	191.1	179.5	MGC33846	NM_175885.2	FLJ37735	DNA	nucleus	regulation
GI_31343498-I	103.5	110.4	99.4	MGC33846	NM_175885.2	FLJ37735	DNA	nucleus	regulation
GI_31343499-S	103	125.2	124.3	PRPS1L1	NM_175886.2	PRPS3;PRPSL;PRS-III	ribose-	cellular_co	ribonucleo
GI_31343502-S	95.5	104.5	95.9	FLJ14503	NM_152780.2				
GI_31343527-S	111.8	124.3	121.9	MGC48986	NM_175881.2				
GI_31343528-S	360.9	387.9	512.8	FLJ36031	NM_175884.2		DNA	nucleus	regulation
GI_31343531-S	137.5	165.3	149.4	LOC149830	NM_177549.2				
GI_31343532-S	98	113.9	108.6	SLC13A5	NM_177550.2	NACT	transporte	membran	sodium
GI_31343533-S	1860.1	1319	1018.5	LOC143903	NM_178834.2		sugar		

GI_31343534-I	1112.1	1074.8	1078.2	CKLFSF4	NM_178818.2		cytokine	membran	chemotaxi
GI_31343572-S	200.4	201.2	198.2	MGC27345	NM_175880.2				
GI_31343579-S	131.1	118.1	103	MGC57211	NM_175878.2				
GI_31343584-S	114.8	123.6	100.5	C20orf65	NM_176791.2	MGC50820;dJ1028D15.4			
GI_31343587-S	168.9	212.8	172	DEFT1	NM_139127.2				
GI_31343594-S	147.7	175.2	135.6	MGC47869	NM_175874.2				
GI_31343603-S	147.1	185.8	162.3	LOC90768	NM_178838.2				
GI_31343604-S	1134.2	1300	1228.7	LYRIC	NM_178812.2	3D3;AEG1			
GI_31343610-S	280.4	336	302.1	FLJ35119	NM_175871.2				
GI_31343621-S	109.3	109.1	109.3	LOC150759	NM_175853.2				
GI_31343635-S	476.1	388.7	277.9	CHSY2	NM_175856.2				
GI_31343636-S	299	365	346.9	KRTAP8-1	NM_175857.2	KAP8.1		intermedia	
GI_31343637-S	390.9	380.3	364.2	KRTAP11-1	NM_175858.2	KAP11.1		intermedia	
GI_31377467-S	338.3	456.9	391.9	DOCK2	NM_004946.1	KIAA0209	GTPase	cytoplasm	small
GI_31377534-S	842	980.8	923.4	LOC91966	NM_178124.3				
GI_31377537-S	609.1	790.9	722.9	LOC151194	NM_145280.3				
GI_31377542-S	443.9	457.8	456.8	C14orf24	NM_173607.2	FLJ38854	acylphosp		
GI_31377545-S	88.9	97.5	87.4	FLJ40160	NM_173484.2				
GI_31377547-S	180.3	160.3	321.8	PGM2L1	NM_173582.2	BM32A;FLJ32029	intramolec		carbohydr
GI_31377551-S	739.6	907.2	853.5	RAP2A	NM_021033.3	KREV;RAP2;RbBP-30	GTPase	membran	signal
GI_31377552-S	1122.9	1263	1199.7	SFRS3	NM_003017.3	SRP20	RNA	nucleus	mRNA
GI_31377553-S	204	209.6	168.1	EVER2	NM_152468.3	EV2;TMC8;EVIN2;MGC40121			
GI_31377554-S	271	249.7	211.2	MGC46534	NM_153340.2				
GI_31377558-S	149.9	172.1	162.2	MGC14276	NM_153248.2				
GI_31377559-S	168.5	144.1	194.4	C10orf47	NM_153256.2	MGC35403			
GI_31377561-S	136.9	132.1	135.9	FAM29A	NM_017645.3	FLJ20060;KIAA1574			
GI_31377565-S	136.4	161	144.3	FLJ35794	NM_152617.2				
GI_31377567-S	105	112.4	96.9	CEGF3	NM_152753.2	FLJ34743	calcium	membran	blood
GI_31377569-S	178.2	203.1	172.9	C9orf98	NM_152572.2	FLJ32704	ATP		
GI_31377572-S	244.7	216	253	DUSP18	NM_152511.2	DUSP20;LMWDSP20;MGC32658	protein		protein
GI_31377576-S	656.3	822.2	684.8	C10orf13	NM_152429.2	MGC39320	DNA	nucleus	regulation
GI_31377582-S	221.7	211.9	203.4	UBXD3	NM_152376.2	FLJ25429			
GI_31377583-S	84.8	87.7	98.9	MTAC2D1	NM_152332.2	Tac2-N;C14orf47;FLJ36557;c14_5695	transporte	membran	transport
GI_31377584-S	732.9	807.8	920.4	MGC26885	NM_152339.2				
GI_31377586-S	227.7	267.8	234.2	EVC2	NM_147127.2	LBN;LIMBIN	DNA	integral to	regulation
GI_31377588-S	360.7	764	1121.6	SYT11	NM_152280.2	SYT12;KIAA0080;MGC10881;MGC17226	transporte	synaptic	transport
GI_31377590-S	109.5	125.2	106.9	SESN3	NM_144665.2	SEST3;MGC29667		nucleus	cell cycle
GI_31377592-S	93.3	93.8	94.1	FLJ25422	NM_145000.2				
GI_31377594-S	383.3	446.9	464.6	LOC124245	NM_144604.2				
GI_31377596-S	104.8	118.7	115.4	ZBTB8	NM_144621.2	BOZF1;MGC17919			
GI_31377600-S	160.3	170	155.9	C9orf97	NM_139246.3				
GI_31377606-S	1398.8	1217.1	1299	GL004	NM_020194.4				
GI_31377610-S	98.5	100.2	92.8	LOC130940	NM_138803.2				
GI_31377612-S	635.4	718.9	697.4	MYADM	NM_138373.2		transporte	synaptic	transport

GI_31377613-S	136.5	138	113.7	LOC113444	NM_138428.2				
GI_31377615-S	288.5	360.4	291.3	BBAP	NM_138287.2				
GI_31377616-S	129.5	121.9	104.9	FLJ22313	NM_022373.3				
GI_31377617-S	203.9	250.2	217.4	UGT1A8	NM_019076.3	UGT1H	UDP-		metabolis
GI_31377621-S	452.9	511.8	484.9	DEDD2	NM_133328.2	FLAME-3			
GI_31377622-S	123.9	137.4	121.8	MYOZ3	NM_133371.2	CS3;CS-3;FRP3			
GI_31377624-S	760.2	978	890.5	LOC133619	NM_130809.2				
GI_31377625-S	549.8	652	582	DUSP19	NM_080876.2	SKRP1;DUSP17;TS-DSP1	protein		protein
GI_31377626-S	1412.3	1284.9	1064.3	AD24	NM_022451.9	FLJ12820			
GI_31377627-S	147.9	166	155	LOH12CR1	NM_058169.2	LOH1CR12			
GI_31377628-S	261.8	363.2	285.3	CPA5	NM_080385.2		carboxype		proteolysis
GI_31377630-S	107.7	102.9	103.7	GBP5	NM_052942.2		GTPase		immune
GI_31377631-S	328.2	409.8	367.4	LOC117584	NM_057178.2				
GI_31377632-S	90.3	91.2	93.2	TSGA13	NM_052933.2				
GI_31377633-S	197.6	240.3	199.9	GBP4	NM_052941.2	Mpa2	GTPase		immune
GI_31377635-S	139.7	164.2	155.5	RFT1	NM_052859.2			integral to	
GI_31377636-S	257.1	298.6	270.9	MGC21854	NM_052862.2				
GI_31377638-S	97.4	103.2	96.3	SIGLEC10	NM_033130.2	SLG2;SIGLEC-10	lectin [goid	integral to	cell
GI_31377640-S	160	174.5	177.2	SRP	NM_033199.2	URP	adrenocor	extracellul	response
GI_31377641-S	215.7	192.6	169.7	CML66	NM_032869.2	FLJ14991			
GI_31377643-S	528.3	567.5	454.1	FLJ14600	NM_032810.2		nucleotide		
GI_31377647-S	102.3	109.3	107.5	FLJ14397	NM_032779.2				
GI_31377649-S	225.9	328	334.9	FLJ14399	NM_032780.2				
GI_31377651-S	323.7	381	327.9	MGC11332	NM_032718.2		transporte	integral to	transport
GI_31377653-S	147.1	142.1	116.4	MGC16291	NM_032770.2				
GI_31377655-S	1392.5	1345.1	1431.4	MGC11102	NM_032325.2		translation		translation
GI_31377657-S	136.7	155.8	155.1	RNASE7	NM_032572.2		pancreatic	extracellul	xenobiotic
GI_31377662-S	959	906.5	1019.5	SVH	NM_031905.2	MGC3195			
GI_31377664-S	719.7	842.9	780.5	KCTD10	NM_031954.2	MSTP028	voltage-	membran	potassium
GI_31377665-S	578.3	709.8	676.8	MGC12904	NM_031219.2		hydrolase		metabolis
GI_31377666-S	450.8	563.1	567	LONP	NM_031490.2	MGC4840	nucleotide	mitochond	ATP-
GI_31377669-S	96.6	101.3	118	OR12D3	NM_030959.2	hs6M1-27	olfactory	integral to	olfaction
GI_31377680-S	282.5	362.2	340.1	FLJ12975	NM_024809.2				
GI_31377684-S	608.5	551.7	470.8	FLJ23151	NM_024772.2				
GI_31377692-S	369.9	450.7	427.4	FLJ23560	NM_024685.2		ATP		protein
GI_31377694-S	182.3	172	167	FLJ12586	NM_024620.2			nucleus	
GI_31377696-S	1717.2	1744.2	1783.2	FLJ22329	NM_024656.2				lipopolysa
GI_31377698-S	218.8	157.8	154	OGFRL1	NM_024576.2	FLJ21079;dJ331H24.1	receptor	membran	cell growth
GI_31377700-S	415.1	307.3	337.3	FLJ20896	NM_024605.2				
GI_31377702-S	448.5	495.9	462.3	TTC13	NM_024525.2	FLJ22584			
GI_31377704-S	158.4	184.3	149.2	FLJ23047	NM_024548.2				
GI_31377708-S	212.4	264.8	238.8	USP46	NM_022832.2	FLJ12552	cysteine-		ubiquitin-
GI_31377710-S	442.2	385.8	373.4	FLJ22104	NM_022918.2				
GI_31377716-S	143.8	150.7	142.5	EFCBP1	NM_022351.2	NECAB1;STIP-1	calcium		

GI_31377717-S	88.1	101.5	95.7	FLJ21195	NM_022469.2				
GI_31377719-S	306.4	361.6	345.1	PLEKHA1	NM_021622.2	TAPP1			
GI_31377721-S	2646	3003.2	3790.3	PERP	NM_022121.2	THW;KCP1;PIGPC1;KRTCAP1;dJ496H19.1			
GI_31377723-S	1111	1331.5	972	NR2F2	NM_021005.2	ARP1;SVP40;COUPTFB;TFCOUP2;COUP-	ligand-	nucleus	lipid
GI_31377724-S	341.6	252.4	321.1	ZNF462	NM_021224.2	Zfp462;KIAA1803;DKFZP762N2316			
GI_31377726-S	290.6	411	301.3	CTL2	NM_020428.2		choline	integral to	choline
GI_31377729-S	464.5	367.2	341.4	LOC56902	NM_020143.2		nucleic		
GI_31377732-S	422.1	433.3	377.1	RIF1	NM_018372.2	FLJ11269			
GI_31377734-S	267	331	296.2	ERO1LB	NM_019891.2	ERO1-L(BETA)	chaperone	endoplas	protein
GI_31377736-S	130.8	131.2	127	FLJ20716	NM_017938.2				
GI_31377738-S	448.2	537.4	478.7	FLJ11336	NM_018393.2				
GI_31377740-S	1487.4	1484.8	1411.1	SLC41A3	NM_017836.2	FLJ20473;SLC41A1-L2			
GI_31377743-S	3957.3	3670.5	3363	FLJ20397	NM_017802.2				
GI_31377745-S	115.6	107	102.5	FLJ20433	NM_017820.2	FLJ30442			
GI_31377747-S	277.3	262.2	301.4	FLJ20296	NM_017750.2				
GI_31377749-S	1307.9	1363.3	1818.4	C20orf21	NM_017798.2	FLJ20391			
GI_31377751-S	272	379.4	377.4	MPRG	NM_017705.2	PAQR5;FLJ20190		integral to	
GI_31377755-S	173.3	203	190.5	C10orf92	NM_017609.2	bA288G11.4;DKFZp434A1721			
GI_31377757-S	379.3	361.4	339.4	AFTIPHILIN	NM_017657.2	FLJ20080;FLJ23793	calcium		
GI_31377759-S	519	547.5	459.9	LOC51240	NM_016467.3				
GI_31377760-S	102	101.2	106.5	GPR85	NM_018970.3	SREB;SREB2	G-protein	integral to	signal
GI_31377762-S	125.5	140.2	131.1	KLF15	NM_014079.2	KKLF	DNA	nucleus	regulation
GI_31377763-S	204.9	186.5	255.7	ZDHHC2	NM_016353.2	ZNF372	zinc ion	integral to	regulation
GI_31377764-S	281	293.3	299.6	DKFZP564G2	NM_015497.2				
GI_31377766-S	2189.1	2230.6	1035.2	GRINL1A	NM_015532.2	DKFZp586F1918	receptor		
GI_31377769-S	736.6	460.8	709.6	DKFZP434C2	NM_015426.2				
GI_31377771-S	116.4	119.8	114.1	H963	NM_013308.2		rhodopsin-	integral to	G-protein
GI_31377776-S	95.6	113	98.7	NKX2-8	NM_014360.2	NKX2H;NKX2.8;Nkx2-9	RNA	nucleus	oncogene
GI_31377778-S	1604.6	1997.8	1006.5	STK38	NM_007271.2	NDR	protein	nucleus	protein
GI_31377779-S	820.5	747.4	646.5	ZHX1	NM_007222.2		transcripti	nucleus	regulation
GI_31377781-S	863.4	651.6	929.3	PRKCD	NM_006254.2		diacylglyc	membran	protein
GI_31377784-S	155.1	166.3	161.7	NPY5R	NM_006174.2	NPYR5	neuropepti	integral to	G-protein
GI_31377785-S	417.7	498.6	375.4	PITPN	NM_006224.2	VIB1A;PITPNA	phosphati	intracellula	vision
GI_31377786-S	108.7	112.3	112.4	GPR6	NM_005284.2		G-protein	integral to	G-protein
GI_31377787-S	267	235.8	313.2	SIAT10	NM_006100.2	ST3GALVI	sialyltransf	Golgi	amino
GI_31377788-S	164.7	180.3	325.1	GPR37	NM_005302.2	PAELR;EDNRBL	G-protein	integral to	G-protein
GI_31377789-S	104.7	115.5	119.2	GPR41	NM_005304.2		G-protein	integral to	G-protein
GI_31377790-S	130.9	152.2	133.8	CD80	NM_005191.2	LAB7;CD28LG;CD28LG1	receptor	integral to	signal
GI_31377791-S	230.9	252.3	369.9	GPR3	NM_005281.2	ACCA	G-protein	integral to	G-protein
GI_31377792-S	235.7	290	281.2	ET(B)R-LP-2	NM_004767.2		G-protein	integral to	G-protein
GI_31377794-S	924.1	1133	1714.8	CALM1	NM_006888.2	CAMI;PHKD;DD132;CALML2	protein	cytoplasm	G-protein
GI_31377795-S	1509.4	1596	1004	MTMR4	NM_004687.3	ZFYVE11;KIAA0647;FYVE-DSP2	protein		protein
GI_31377797-S	845	899.3	742.8	RABEP1	NM_004703.2	RAB5EP;RABPT5	vesicle	early	endocytosi
GI_31377801-S	1649.3	2022.1	515.9	SEMA3F	NM_004186.2	SEMA4;SEMAK;SEMA-IV;sema IV		extracellul	developm

GI_31377803-S	191.5	195.8	192.7	ZNF345	NM_003419.2	HZF10	transcripti	nucleus	regulation
GI_31377804-S	388.3	431.9	413.3	ZNF45	NM_003425.2		transcripti	nucleus	regulation
GI_31377805-S	121.9	146.5	123.6	PIGR	NM_002644.2		protein	integral to	protein
GI_31377807-S	99	111.1	96.5	TFAP2B	NM_003221.2	CHAR;AP-2B;AP2-B	transcripti	nucleus	regulation
GI_31377808-S	250.9	298.5	276.4	PRKCG	NM_002739.2	PKCC;PKCG;SCA14	protein		protein
GI_31377809-S	523.2	583.5	592.3	NDST2	NM_003635.2	NST2;HSST2;NCST2	heparin N-	Golgi	
GI_31377810-S	451.6	475.9	494.9	LSS	NM_002340.2	OSC	lanosterol		steroid
GI_31377824-S	1198.2	1316.7	1288.9	CL640	NM_015697.3				
GI_31377831-S	102.2	120.2	93.7	PKHD1L1	NM_177531.2	PKHDL1;DKFZp586C1021			
GI_31377836-S	350.4	327.2	247.6	FLJ21901	NM_024622.2	KIAA1800			
GI_31377838-S	151.3	189.1	165.6	ZNF606	NM_025027.2	FLJ14260;KIAA1852	nucleic	intracellula	regulation
GI_31377840-S	546.2	780.9	672.4	FLJ11280	NM_018379.2		DNA	nucleus	regulation
GI_31377842-S	115.4	134.2	116.4	SCN3B	NM_018400.2	SCNB3;HSA243396	voltage-	integral to	sodium
GI_31377845-S	90.9	93.2	88.3	FLJ11142	NM_018338.2				
GI_31377847-S	317.7	400.7	360.7	FLJ10074	NM_017988.2				
GI_31415879-A	153.8	170.2	152.6	PPP1R1B	NM_181505.1	DARPP32;DARPP-32;FLJ20940	protein	cytoplasm	signal
GI_31415879-I	146.3	156.5	163.1	PPP1R1B	NM_181505.1	DARPP32;DARPP-32;FLJ20940	protein	cytoplasm	signal
GI_31415881-S	2333.1	1624.9	1525.1	OIP2	NM_181503.1	RRP43	exonuclea	nucleus	rRNA
GI_31442407-S	328.1	303.9	211.8	SNRK	NM_017719.3	HSNFRK;FLJ20224;KIAA0096	protein-		protein
GI_31442413-S	78.4	88.8	86.2	C7orf9	NM_022150.2	RFRP	G-protein	membran	neuropepti
GI_31442419-S	137.6	169.6	149.8	APXL2	NM_133456.1	KIAA1960			
GI_31442760-S	108.8	105.2	108.9	ACCN5	NM_017419.1	INAC;HINAC	sodium	membran	sodium
GI_31455610-S	128.2	138.4	118.1	ZAP70	NM_001079.2	SRK;STD;ZAP-70	protein-		protein
GI_31455613-S	679.3	833.1	747.5	F-LANa	NM_016041.2	CGI-101;F-LAN-1		integral to	
GI_31541779-S	572.9	748.2	803.8	101F6	NM_007022.3	TSP10	ubiquitin	integral to	cyclin
GI_31541784-S	615.6	655.5	581.7	ABI2	NM_005759.3	ABI-2;ABI2B;AIP-1;AbIBP3;argBPIA	SH3/SH2	cytoplasm	biological_
GI_31541843-S	103.3	97.3	79.5	ACRC	NM_052957.2	NAAR1		nucleus	
GI_31541858-S	1064.1	1110.7	1050.8	ACTR6	NM_022496.2	CDA12;hARP6;hARPX;FLJ13433	structural	actin	
GI_31541901-S	154.9	168.4	149	AMBP	NM_001633.2	HCP;ITI;UTI;ITIL	endopepti		transport
GI_31541940-S	191.5	162.2	171.5	APG-1	NM_014278.2		heat	cytoplasm	heat
GI_31541963-S	801.7	706.8	919	ASL	NM_000048.2		argininosu	cytoplasm	urea cycle
GI_31542090-S	758.2	763.4	679.4	CREB3L4	NM_130898.2	JAL;hJAL;ATCE1;CREB3;CREB4;AIBZIP	DNA	nucleus	regulation
GI_31542152-S	154	156.2	169.5	NPY	NM_000905.2		calcium	cell [goid	regulation
GI_31542183-S	139.2	151.3	132	BARHL1	NM_020064.2		transcripti	nucleus	regulation
GI_31542206-S	128.3	125.5	115	BCNP1	NM_173544.2				
GI_31542212-S	131.2	143	134.4	BXMAS2-10	NM_145016.2	MGC24009			
GI_31542241-S	1066.8	895.5	717.8	C14orf10	NM_017917.2	G4-1;G5pr;FLJ20644	calcium		
GI_31542243-S	172.4	188.3	179.8	LRFN5	NM_152447.2	FLJ30803;C14orf146	DNA	nucleus	
GI_31542245-S	781	673.5	787	C16orf44	NM_024731.2	FLJ12543			
GI_31542247-S	549.8	494.3	398.1	SLC39A11	NM_139177.2	C17orf26	heavy	membran	heavy
GI_31542248-S	641.9	967	971.8	C1GALT2	NM_152692.2	COSMC;HSPC067;C1Gal-	transferas		
GI_31542249-S	104.1	199.8	140.7	C1R	NM_001733.2		compleme		immune
GI_31542254-S	140.7	142.1	133.7	C20orf160	NM_080625.2	dJ310O13.5			
GI_31542256-S	254.6	269	420.2	C20orf172	NM_024918.2	FLJ13346;dJ469A13.2			

GI_31542262-S	174.2	209.7	173.3	C20orf59	NM_022082.2	FLJ23412			
GI_31542267-S	749.1	936.1	581.1	C21orf7	NM_020152.2	TAK1L	transcripti		regulation
GI_31542268-S	113.9	95.7	100.9	C22orf1	NM_001585.2	239AB;FAM1A	molecular	cellular_co	biological_
GI_31542288-S	126.1	133.1	130.7	C7orf16	NM_006658.2	GSBS	protein	soluble	protein
GI_31542289-S	150.1	202.7	173.2	C9	NM_001737.2		hemolysin	membran	compleme
GI_31542290-S	9694.3	11808	10071	CANX	NM_001746.2	CNX	chaperone	endoplas	protein
GI_31542291-S	2668.7	3263.1	3436.8	CCT3	NM_005998.2	Cctg;TRIC5	chaperone	cytosol	protein
GI_31542293-S	81.3	84.8	63	CD2	NM_001767.2	T11;SRBC	receptor	soluble	cell
GI_31542299-S	712	612	533.8	CGI-115	NM_016052.2				
GI_31542304-S	86.1	110.2	104.6	CH25H	NM_003956.2	C25H	steroid	membran	lipid
GI_31542307-S	265.1	378.7	287.7	CHST1	NM_003654.2	C6ST;KS6ST;KSGAL6ST	sulfotransf	integral to	polysacch
GI_31542310-S	116.1	120.7	109.5	CLCNKA	NM_004070.2		voltage-	membran	small
GI_31542314-S	650.7	834.2	795.7	CNOT8	NM_004779.4	CAF1;POP2;CALIF;hCAF1	transcripti	nucleus	negative
GI_31542322-S	1922	2277.8	2234.3	CRIP2	NM_001312.2	CRIP;CRP2;ESP1	zinc ion		
GI_31542324-S	180.4	200.3	199.7	CROT	NM_021151.2	COT	carnitine	peroxisom	fatty acid
GI_31542326-S	91.4	97	104	SLC22A16	NM_033125.2	CT2;OCT6;OKB1;FLIPT2;dJ261K5.1	transporte	integral to	transport
GI_31542479-S	465.8	610.8	598.8	D4ST1	NM_130468.2	HD4ST;D4ST-1;HNK1ST	transferas	integral to	dermatan
GI_31542491-S	811.4	767.9	833.3	DAXX	NM_001350.2	DAP6;BING2	receptor	kinesin	activation
GI_31542492-S	313.8	373.5	361.7	DBP	NM_001352.2	DABP	RNA	nucleus	regulation
GI_31542500-S	285.7	277.3	203.4	DEF6	NM_022047.2	IBP			
GI_31542502-S	4144.7	2906.2	3308.4	DEK	NM_003472.2	D6S231E	specific	nucleus	viral
GI_31542505-S	189.4	225.6	191.5	DHDH	NM_014475.2	HUM2DD	NAD(P)		carbohydr
GI_31542506-S	92.2	94.6	95	DKFZP434A1	NM_032132.2				
GI_31542508-S	526.3	749.3	665.7	ADP-GK	NM_031284.3	DKFZP434B195			
GI_31542510-S	91.1	103.4	96.9	DKFZP434F1	NM_032135.2				
GI_31542512-S	100.5	138.9	117.8	SLC41A2	NM_032148.2	SLC41A1-L1;DKFZP434K0427	cation		cation
GI_31542516-S	171.4	184.4	149.7	DKFZP434N1	NM_032137.2				
GI_31542518-S	728.1	743.7	661.7	DKFZP434N1	NM_030974.2				
GI_31542523-S	2536.6	2819.6	2872.3	DKFZP564K0	NM_030796.2	FLJ20532			
GI_31542525-S	2339.4	2580.9	1670.4	DKFZP564O0	NM_015420.4	HSPC064			
GI_31542527-S	913.5	892	625.6	DKFZP566B1	NM_015509.2				
GI_31542529-S	201.3	209.7	192.8	DKFZp434I09	NM_032269.3				
GI_31542532-S	139.3	163.6	180.2	DKFZp761G0	NM_152542.2		protein	protein	protein
GI_31542536-S	2057.6	1223.8	1306.2	RAM2	NM_018719.2	DKFZp762L0311			
GI_31542542-S	1815.5	2268	2696.1	DNER	NM_139072.2		structural	integral to	
GI_31542584-S	376.8	383.2	351	EDN2	NM_001956.2	ET2	growth	soluble	transmem
GI_31542585-S	431.3	516.1	738	EIF4EBP2	NM_004096.3	4EBP2	translation		regulation
GI_31542586-S	84.1	88.4	87.8	EMX2	NM_004098.2		transcripti	nucleus	regulation
GI_31542589-S	194.8	225.8	204.4	ETV7	NM_016135.2	TEL2;TELB;TEL-2	specific	nucleus	histogene
GI_31542627-S	191.6	242.7	223.8	FBN3	NM_032447.2	KIAA1776	calcium		
GI_31542630-S	120.4	130.7	114.5	FCRH1	NM_052938.3				
GI_31542631-S	2997.9	3779	2792.5	FDFT1	NM_004462.2	DGPT	magnesiu	endoplas	steroid
GI_31542633-S	122.9	160.3	123.3	FILIP1	NM_015687.1	FILIP;KIAA1275			
GI_31542635-S	714.6	822.7	552.9	FKSG32	NM_031307.2		pseudouri		tRNA

GI_31542640-S	300.5	302.2	296.6	TRMT1	NM_018006.2	TRMU;FLJ10140	methyltran	cytoplasm	tRNA
GI_31542644-S	225.8	290	268.8	FLJ10260	NM_018042.2				
GI_31542649-S	220.1	308.7	305.9	FLJ10298	NM_018050.2				
GI_31542657-S	353.8	661.8	412.2	MLSTD1	NM_018099.3	FLJ10462			
GI_31542660-S	295.2	353.5	310.4	FLJ10747	NM_018202.2				
GI_31542662-S	101.3	103.2	95.2	FLJ10884	NM_019079.2				
GI_31542664-S	124.7	144.6	130.6	FLJ11004	NM_018296.2				
GI_31542666-S	134.6	152.4	136.7	FLJ11036	NM_018306.2				
GI_31542670-S	1121.9	1345.6	1270.1	C6orf209	NM_018368.2	FLJ11240;bA810I22.1			
GI_31542672-S	104.2	136.6	126.7	FLJ11749	NM_024591.2		molecular		
GI_31542677-S	683.5	788.9	698.2	FLJ12525	NM_031206.2	dJ475B7.2			
GI_31542679-S	290.6	279.4	374.3	FLJ12785	NM_024855.2		motor	actin	
GI_31542681-S	524.3	505.6	469	QTRTD1	NM_024638.2	FLJ12960	queuine		queuosine
GI_31542685-S	342.1	325.6	328.7	FLJ13263	NM_025125.2				
GI_31542687-S	1166.2	1326.3	1706.7	FLJ13448	NM_025147.2		molecular		
GI_31542688-S	134.2	216.7	236.4	FLJ14054	NM_024563.2				
GI_31542689-S	114.7	134.2	105.2	FLJ14146	NM_024709.2		DNA	nucleus	regulation
GI_31542690-S	119	118.2	108.8	FLJ14281	NM_024920.3		N-		DNA
GI_31542694-S	244.4	179.9	145.8	FLJ14594	NM_032808.2				
GI_31542696-S	309.2	330.9	348.4	FLJ14639	NM_032815.2		DNA	nucleus	regulation
GI_31542698-S	242.7	218.8	221.5	FLJ14981	NM_032868.2				
GI_31542700-S	263.9	319.4	281	AHI1	NM_017651.3	ORF1;FLJ20069			
GI_31542702-S	1307.3	954.8	953.2	FLJ20244	NM_017722.2		S-		tRNA
GI_31542705-S	288	223.4	242.1	FLJ20485	NM_019042.2	KIAA1897	molecular		tRNA
GI_31542706-S	1184.2	1325	629.7	COMMD8	NM_017845.2	FLJ20502			
GI_31542708-S	196	238.5	224.1	TTC12	NM_017868.2	TPARM;FLJ13859;FLJ20535			
GI_31542710-S	142.5	158.3	163.5	C2orf18	NM_017877.2	FLJ20555			
GI_31542712-S	133.8	194	139.1	FLJ20605	NM_017898.3				
GI_31542714-S	1376.4	1596.7	1328.3	FLJ20618	NM_017903.2				
GI_31542717-S	192.5	222.6	151.6	ECHDC3	NM_024693.2	FLJ20909	catalytic		metabolis
GI_31542719-S	777.3	909.1	591.3	FLJ20920	NM_025149.2		catalytic		metabolis
GI_31542721-S	535.7	771.3	574.7	FLJ21127	NM_024549.3				
GI_31542722-S	2143.6	1891.1	1847	FLJ21347	NM_022827.2	FLJ21969			
GI_31542726-S	583.5	168	142.1	FLJ21986	NM_024913.3				
GI_31542728-S	1125	1518.1	769.7	DHX40	NM_024612.3	PAD;DDX40;ARG147;FLJ22060	nucleic		
GI_31542730-S	117.3	122.5	144.4	FLJ22269	NM_032219.2				
GI_31542734-S	419.4	236.1	233.6	FLJ22531	NM_024650.2				
GI_31542737-S	117.4	107.4	101.3	FLJ22593	NM_024703.2				
GI_31542738-S	180.3	228.5	214.4	FLJ22609	NM_022072.2				
GI_31542739-S	106.6	96	95.3	FLJ22655	NM_024730.2		small		small
GI_31542740-S	87.5	103.7	104.2	FLJ22746	NM_024785.2				
GI_31542742-S	118.6	111.7	110.3	FLJ22843	NM_025184.2	FLJ22601;dJ1158H2.1			
GI_31542744-S	2238.5	2293.2	1625.1	FLJ23091	NM_024911.3				
GI_31542746-S	401.9	324.9	354.4	FLJ23841	NM_144589.2		S-		

GI_31542748-S	279.3	336.7	166.2	FLJ25067	NM_152504.2				
GI_31542750-S	477.1	414.8	325.8	FLJ25078	NM_152485.2		nucleic	membran	transport
GI_31542751-S	406.4	285.5	277.9	ZNF533	NM_152520.2	FLJ25270	RNA	nucleus	
GI_31542755-S	955.8	797.8	1042	FLJ30002	NM_152341.2				
GI_31542757-S	125.7	113	122.5	FLJ30046	NM_144595.2				
GI_31542758-S	88	88.6	98.5	FLJ30672	NM_153016.2				
GI_31542759-S	230.3	264.8	229.8	FLJ30707	NM_145019.2				
GI_31542761-S	254.5	218.7	213	FLJ32452	NM_144576.2				
GI_31542769-S	109.1	96.4	99.8	FLJ33718	NM_173660.2				
GI_31542771-S	130.5	142.3	130	ZNF491	NM_152356.2	FLJ34791		nucleus	
GI_31542773-S	554.1	1217	914.3	FLJ35155	NM_152531.3				
GI_31542774-S	347.7	274.9	212.5	FLJ35220	NM_173627.2				
GI_31542776-S	137.5	148.2	122.5	FLJ35867	NM_152455.2		transcripti	nucleus	regulation
GI_31542782-S	190.5	184.4	148.2	FLJ38628	NM_152267.2				
GI_31542788-S	623.1	590.9	693.3	ABHD7	NM_173567.2	EPHXRP;FLJ90341	epoxide		response
GI_31542790-S	88.8	84	83.6	FMO3	NM_006894.3	FMOII;dJ127D3.1	dimethyla	microsom	electron
GI_31542792-S	113.3	121	103.8	FN3K	NM_022158.2		transferas	cellular_co	fructoselys
GI_31542834-S	129.5	209.1	118.9	GAL3ST-4	NM_024637.3	FLJ12116			
GI_31542839-S	561.8	582.3	514.2	GCSH	NM_004483.2	GCE;NKH	aminomet	glycine	glycine
GI_31542844-S	101.4	89.1	91.5	GJA10	NM_030772.2	CX58;CX59	connexon	connexon	cell
GI_31542846-S	109.3	122.4	109.8	GJB1	NM_000166.2	CMTX;CX32;CMTX1	connexon	connexon	small
GI_31542847-S	137.7	160.1	141.1	GJB5	NM_005268.2	CX31.1	connexon	connexon	epidermal
GI_31542848-S	294.6	430.2	374.7	GMPR	NM_006877.2		GMP		response
GI_31542850-S	141.7	154	135.8	GNA14	NM_004297.2		heterotrim	peripheral	signal
GI_31542852-S	148.7	148	150.2	GPR18	NM_005292.2		G-protein	integral to	G-protein
GI_31542855-S	100.6	89.6	97.9	GPR80	NM_080818.2	GPR99	receptor	integral to	G-protein
GI_31542857-S	197.7	128.5	117.3	GPR87	NM_023915.2	GPR95	receptor	integral to	G-protein
GI_31542861-S	765.5	855.9	695	GRWD1	NM_031485.2	GRWD;WDR28			
GI_31542866-S	2185.4	1628.7	2048.3	RRAGC	NM_022157.2	GTR2;RAGC;FLJ13311	small	cytoplasm	transport
GI_31542869-S	102.8	122.5	102.5	GZMH	NM_033423.2	CCP-X;CGL-2;CSP-C;CTLA1;CTSGL2	trypsin	cytoplasm	proteolysis
GI_31542933-S	87.8	73.7	81	HHLA2	NM_007072.2		molecular	cellular_co	biological_
GI_31542934-S	95.7	94.8	96.6	HLF	NM_002126.3		double-	nucleus	transcripti
GI_31542938-S	87.4	76	78.5	HPGD	NM_000860.2	PGDH1;15-PGDH	catalytic		prostaglan
GI_31542940-S	121.9	133.5	120.6	HSD11B2	NM_000196.2	AME;AME1;HSD11K	11-beta-	microsom	glucocorti
GI_31542944-S	1741.6	1906.2	1860.3	HSPC117	NM_014306.2	DJ149A16.6	molecular		
GI_31542945-S	1524.6	2390.3	1116.8	CXXC5	NM_016463.5	HSPC195			
GI_31542979-S	235.8	249.5	171	IFIT4	NM_001549.2	IFI60;ISG60;RIG-G;CIG-49	molecular	cellular_co	immune
GI_31542985-S	88.2	103.4	89.4	ITLN1	NM_017625.2	LFR;HL-1;ITLN;hIntL;FLJ20022			
GI_31542987-S	3555.1	5746.8	4223.1	ITM2B	NM_021999.2	BRI;FBD;ABRI;BRI2;E25B;E3-16;BRICD2B	structural	membran	neurogene
GI_31543016-S	313.6	404	333.7	KIAA0103	NM_014673.2			nucleus	
GI_31543022-S	111	165.3	102.9	KSP37	NM_031950.2				
GI_31543054-S	346.2	409.5	422.8	LGP1	NM_032484.3		molecular	cellular_co	biological_
GI_31543055-S	134.2	129.8	131.9	LILRA3	NM_006865.2	HM31;HM43;ILT6;LIR4;CD85E;LIR-4	antigen	plasma	defense
GI_31543057-S	131.3	144.1	120.7	LILRB5	NM_006840.2	LIR8;CD85C;LIR-8	defense/i		defense

GI_31543059-S	119.6	175.4	135.4	LOC112817	NM_138413.2				
GI_31543061-S	105.1	115.4	89	LOC120224	NM_138788.2				
GI_31543062-S	179.9	155.9	201.9	GLYCTK	NM_145262.2				
GI_31543066-S	108.4	171.3	176.4	LOC146845	NM_145054.2				
GI_31543068-S	289.5	325.7	279.9	LOC148523	NM_144697.2				
GI_31543071-S	127	136	138	LOC161931	NM_139174.2				
GI_31543075-S	304.8	380.8	342.5	C6orf128	NM_145316.2	dJ355M6.2			
GI_31543079-S	3850.2	1403.8	1772.8	RNF149	NM_173647.2	DNAPTP2	peptidase		proteolysis
GI_31543080-S	95.1	143.2	115.5	LOC51161	NM_016210.2				
GI_31543081-S	517.9	708.7	1304.3	LOC51257	NM_016496.3		electron		electron
GI_31543084-S	555.8	837.7	799.3	DHRS6	NM_020139.2	UCPA-OR			
GI_31543086-S	451.7	349	422.6	THAP10	NM_020147.2				
GI_31543087-S	520.6	430.6	366.1	LOC57146	NM_020422.3				
GI_31543088-S	141.7	216.2	153.8	LOC81558	NM_030802.2				
GI_31543090-S	2294.3	1857.9	1655	LOC84549	NM_032509.2		nucleic		
GI_31543092-S	135.7	167.9	132.1	LOC89944	NM_138342.2		beta-	beta-	carbohydr
GI_31543094-S	126.9	143.1	121.8	LOC90050	NM_138344.2				
GI_31543096-S	1574.7	1989.7	1771.6	LRSAM1	NM_138361.2				
GI_31543098-S	142.2	153.5	135.3	LOC92346	NM_139240.2				
GI_31543105-S	292.2	376.4	336.4	LU	NM_005581.2	AU;BCAM;MSK19	blood	integral to	cell
GI_31543135-S	401.1	381	465.1	MAF1	NM_032272.2	DKFZp586G1123			
GI_31543139-S	132.1	118.5	110.4	USHBP1	NM_031941.2	MCC2;AIEBP			
GI_31543141-S	210.2	187.4	169.8	ZNF34	NM_030580.2	KOX32;MGC10520	nucleic	nucleus	regulation
GI_31543143-S	98.3	112.2	97.7	C9orf64	NM_032307.2	MGC10999			
GI_31543145-S	481.2	1055.5	1015.9	MGC11256	NM_024324.2	CRELD2	structural		
GI_31543147-S	131.4	141.2	137.5	MGC11271	NM_024323.3				
GI_31543149-S	686.6	725.1	958.3	MGC11308	NM_032889.2				
GI_31543151-S	2971.2	2679.2	2633	MGC14817	NM_032338.2				
GI_31543152-S	97.4	96.4	99.6	MGC15730	NM_032880.2				
GI_31543154-S	949.7	1116.5	1034.3	MGC15737	NM_032926.2		DNA	nucleus	regulation
GI_31543155-S	108.8	121.5	112.4	MGC15827	NM_032882.2				
GI_31543156-S	114.1	124.2	111.6	MGC15937	NM_080661.2				
GI_31543158-S	233.9	260.6	337.6	MGC16824	NM_020314.3	FLJ21040;DKFZp434B0212			
GI_31543160-S	89.9	98.9	94.2	MGC21621	NM_145015.2				
GI_31543163-S	878.4	560.2	691.8	MGC2655	NM_024339.2				
GI_31543168-S	353.6	425.7	475	MGC2705	NM_032701.2		DNA	nucleus	regulation
GI_31543175-S	542.6	550.3	718.6	C2orf17	NM_024293.2	MGC3035			
GI_31543177-S	348.3	357.6	421	MGC3121	NM_024031.2				
GI_31543178-S	481.6	424.8	593.9	MGC3130	NM_024032.2	FLJ11594			
GI_31543180-S	283.9	612.4	317.9	MGC3265	NM_024028.2				
GI_31543182-S	106.8	121	114.1	MGC34827	NM_152693.2				
GI_31543183-S	114	112.2	100.5	3'HEXO	NM_153332.2	MGC35395	exonuclea	intracellula	
GI_31543187-S	104.1	107.4	105.6	MGC39662	NM_152394.2				
GI_31543190-S	89.9	104.4	100	MGC4248	NM_032333.2				

GI_31543192-S	136.5	140.1	120.9	MGC45438	NM_152459.2				
GI_31543194-S	203.1	220.2	234.4	MGC45866	NM_152259.2				
GI_31543197-S	633.7	521.2	299.2	MGC4796	NM_032017.1	SHIK			
GI_31543199-S	962.1	948.5	1169.3	C7orf21	NM_031434.2	SB144;MGC5442		integral to	
GI_31543200-S	176.6	192.9	180.7	MGC5601	NM_025247.2		acyl-CoA		electron
GI_31543202-S	2249.6	2017.2	2180	MGC8974	NM_052940.3	dJ167A19.4			
GI_31543203-S	112.2	117.6	108.5	MGC9564	NM_080669.2				
GI_31543206-S	2972.8	2376.8	2095.9	MMS19L	NM_022362.2	MET18;MMS19;hMMS19			
GI_31543208-S	162.5	160.6	146.1	MPN	NM_031948.2	CAPH2	trypsin		proteolysis
GI_31543210-S	16969.9	17867	13006	MRCL3	NM_006471.2	MLCB;MRLC3	calcium	muscle	regulation
GI_31543211-S	368.9	542.8	366.2	MST1	NM_020998.2	MSP;HGFL;NF15S2;D3F15S2;DNF15S2	thrombin	cellular_co	proteolysis
GI_31543213-S	1585.6	1004.9	1842.3	MT1X	NM_005952.2	MT1;MT-1l	heavy		heavy
GI_31543214-S	17689.7	13743	27249	MT2A	NM_005953.2	MT2	heavy		copper ion
GI_31543215-S	3060	1210.1	808.4	MYC	NM_002467.2	c-Myc	transcripti	nucleus	iron ion
GI_31543267-S	296	365.4	282.7	MtFMT	NM_139242.2		methyltran	mitochond	protein
GI_31543282-S	102.3	103.7	92.6	NALP14	NM_176822.2	NOD5	binding	membran	transport
GI_31543284-S	1853.3	1503.1	1557.4	NDEL1	NM_030808.2	NUDEL;MITAP1			
GI_31543285-S	150.5	146.6	134.3	NEK9	NM_033116.3	Nek8;NERCC;NERCC1;MGC16714;DKFZp4	protein-		protein
GI_31543287-S	105.4	128.1	109.3	NFAM1	NM_145912.3	CNAIP;FLJ00165		integral to	
GI_31543288-S	108.5	103.9	102.6	NICN1	NM_032316.2	MGC12936			
GI_31543289-S	2621	2661.9	3310.3	NINJ1	NM_004148.2	NIN1;NINJURIN	cell	integral to	cell
GI_31543290-S	916.2	1035.7	773	NIT2	NM_020202.2		hydrolase		nitrogen
GI_31543291-S	147.6	265.5	108.9	NKD2	NM_033120.2				
GI_31543295-S	184.1	226.9	178.7	NPY1R	NM_000909.3	NPYR	neuropepti	integral to	G-protein
GI_31543296-S	1434.5	1034.2	1147.4	NSMAF	NM_003580.2	FAN	receptor	soluble	ceramide
GI_31543298-S	1833.9	1625.9	1912.2	NTE	NM_006702.2	sws	serine		pan-neural
GI_31543300-S	1844.3	1823.8	1736.4	NUDC	NM_006600.2	HNUDC;MNUDC			regulation
GI_31543301-S	96.7	103.6	92.5	NYD-SP17	NM_032600.2				
GI_31543302-S	95.2	87.9	86.4	NYD-SP26	NM_033122.2				
GI_31543304-S	125.2	124.4	118.7	TTLL2	NM_031949.2	C6orf104;NYD-TSPG;dJ366N23.3	tubulin-		protein
GI_31543356-S	618.6	770.7	952.6	OCSP	NM_031945.2			integral to	
GI_31543358-S	451.1	529.8	319.2	ODC-p	NM_052998.2		ornithine	cellular_co	polyamine
GI_31543361-S	1058.4	569.4	940.1	ORF1-FL49	NM_032412.2		rhodopsin-	integral to	G-protein
GI_31543362-S	223.6	275.5	181.7	OVGP1	NM_002557.2	MUC9	hydrolase	extracellul	pregnancy
GI_31543378-S	3150.7	3076.7	4132.4	P5326	NM_031450.2				
GI_31543381-S	167.6	268.1	191	PARVG	NM_022141.3		actin	cytoskelet	cell-matrix
GI_31543382-S	199.9	184	180.9	KCMF1	NM_020122.2	PCMF;ZZZ1;DEBT91;DKFZP434L1021	zinc ion		
GI_31543384-S	188.8	283.6	268.3	PCYT1A	NM_005017.2	CT;CTPCT;PCYT1	choline-	soluble	phospholi
GI_31543388-S	381.5	480.5	446	PDK2	NM_002611.3		[pyruvate	mitochond	glucose
GI_31543389-S	196	204.5	174.3	PDCD1LG2	NM_025239.2	B7DC;Btdc;PDL2;PD-L2;PDCD1L2	molecular	cellular_co	immune
GI_31543390-S	493.4	580.7	460.1	PEG10	NM_015068.2				
GI_31543391-S	112.3	103.1	96.3	PPARGC1B	NM_133263.2	PERC;PGC1B;PGC-1(beta)			
GI_31543395-S	2698.3	4915.4	3868.2	PGAM1	NM_002629.2	PGAMA	bisphosph	cytosol	glycolysis
GI_31543396-S	95.7	95.9	91.5	PGK2	NM_138733.2	PGKB;PGK-2;PGKPS;dJ417L20.2	phosphogl	cytosol	glycolysis

GI_31543398-S	320.8	255.6	335.2	PHCA	NM_018367.3	APHC;FLJ11238	hydrolase	integral to	
GI_31543399-S	910	972.6	883.9	PIAS3	NM_006099.2		transcripti		oncogene
GI_31543400-S	477.3	432	317.5	PIM1	NM_002648.2	PIM	protein	cytoplasm	protein
GI_31543409-S	150.2	173.9	155.3	PLA2G7	NM_005084.2	PAFAH;LDL-PLA2	phospholi	2-acetyl-1-	lipid
GI_31543411-S	181	168.8	141.9	PLEKHF1	NM_024310.2	APPD;MGC4090;PHAFIN1;ZFYVE15	zinc ion		
GI_31543413-S	207	258.3	228	PLEKHF2	NM_024613.2	PHAFIN2;ZFYVE18;FLJ13187	zinc ion		
GI_31543414-S	133.9	124.6	119.4	PLINP-1	NM_052850.2	PRG6;CKBBP2;MGC4667;MGC4758			
GI_31543416-S	3287.7	4277.1	3898.2	PLSCR3	NM_020360.2		calcium	integral to	phospholi
GI_31543418-S	1025.9	839.6	839.5	PNKP	NM_007254.2	PNK	DNA	nucleus	response
GI_31543421-S	143.5	157	130.8	PNMT	NM_002686.2	PENT	phenyleth		catechola
GI_31543422-S	2052.8	2003.2	2321.5	POLE3	NM_017443.3	p17;YBL1;CHRAC17;CHARAC17	epsilon	kinesin	DNA
GI_31543430-S	2083	2888.4	3167.9	PPP1CA	NM_002708.2	PPP1A	protein		protein
GI_31543437-S	116.1	137.3	131.9	PRKACA	NM_002730.2		cAMP-	cAMP-	protein
GI_31543440-S	669.7	967.6	716.2	PRO0659	NM_014138.2				
GI_31543442-S	1386.1	1373.5	752	PRPS2	NM_002765.2	PRSII;PRS II	ribose-		nucleobas
GI_31543449-S	1638.2	819.3	302.8	PTX3	NM_002852.2	TSG-14		extracellul	inflammat
GI_31543450-S	1880.6	2033	1686.5	PX19	NM_013237.2	PRELI;CGI-106			developm
GI_31543451-S	428.1	691	362.1	PXK	NM_017771.2	FLJ20335	ATP		protein
GI_31543534-S	505.8	589.7	582.7	R3HDM	NM_015361.2	KIAA0029			
GI_31543536-S	2687.8	2789.6	2583.2	RAB34	NM_031934.3	RAH;RAB39			
GI_31543538-S	1864.4	2466.5	2166.4	RAB5A	NM_004162.3	RAB5	vesicle	early	endocytosi
GI_31543539-S	105.6	101.6	105.9	RABIF	NM_002871.3	MSS4;RASGFR3;RASGRF3	guanyl-		membran
GI_31543542-S	3126.9	4971.6	5263.9	RAI17	NM_020338.1	Zimp10;FLJ13541;KIAA1224	zinc ion		
GI_31543547-S	1023.9	1214.5	907.5	RBM7	NM_016090.2		RNA	nucleus	meiosis
GI_31543548-S	3936.1	4101.1	3145	REA	NM_007273.3	BAP	receptor	cellular_co	negative
GI_31543551-S	223.7	336.7	292.6	RIT1	NM_006912.2	RIT;RIBB;ROC1	GTP	plasma	signal
GI_31543556-S	559.2	417.4	455	RNU3IP2	NM_004704.2	U3-55K	small	small	rRNA
GI_31543557-S	641.7	611.7	342.6	RPH3AL	NM_006987.2	NOC2	cytoskelet	cytoplasm	exocytosis
GI_31543558-S	227	274.7	204.5	RSHL2	NM_031924.3	RSP3;dJ111C20.1			
GI_31543612-S	628.7	525.5	616.9	SCML1	NM_006746.2		DNA		embryoge
GI_31543618-S	4779.4	5119.3	4890.4	SFRS1	NM_006924.3	ASF;SF2;SRp30a	pre-mRNA	nucleus	mRNA
GI_31543619-S	1318.6	1897.8	1595.6	SGSH	NM_000199.2	HSS;SFMD;MPS3A	catalytic	lysosome	proteoglyc
GI_31543620-S	746.8	738.9	403.2	SH2D2A	NM_003975.2	TSAD;F2771	SH3/SH2	soluble	signal
GI_31543621-S	1140	1467.7	1611.5	ENTPD8	NM_138793.2	SHAPY;SCAN-1			
GI_31543622-S	1030.3	1581	1187.9	SIL1	NM_022464.3	BAP	chaperone	endoplas	intracellula
GI_31543623-S	106.1	104.8	99.7	SLC15A2	NM_021082.2	PEPT2	peptide:hy	integral to	small
GI_31543625-S	146.6	205.2	276.9	SLC1A1	NM_004170.3	EAAC1;EAAT3	L-	membran	L-
GI_31543629-S	4653.5	7708	5969.4	SLC20A1	NM_005415.3	PIT1;GLVR1	sodium:ph	membran	phosphate
GI_31543631-S	348.6	263.4	285.4	SLC25A19	NM_021734.3	DNC;MUP1;MCPHA	binding	mitochond	transport
GI_31543634-S	96.9	104.1	89.6	SLC34A1	NM_003052.2	NPT2;SLC11;NAPI-3;NPTIIa;SLC17A2	sodium-	integral to	phosphate
GI_31543636-S	3391.3	3264.7	3760.3	SLC35A5	NM_017945.2	FLJ20730	nucleotide-	integral to	nucleotide-
GI_31543637-S	5268.2	5434.6	4896.8	SLC38A2	NM_018976.3	ATA2;SAT2;SNAT2;PRO1068;KIAA1382	transcripti	membran	amino
GI_31543639-S	155.3	187.9	167.1	SLC40A1	NM_014585.3	FPN1;HFE4;MTP1;IREG1;SLC11A3	iron ion	mitochond	iron ion
GI_31543640-S	185.1	209	184.6	SLC7A3	NM_032803.3	ATRC3;CAT-3;FLJ14541	amino	integral to	amino

GI_31543646-S	574.2	490.7	418.4	SMC6L1	NM_024624.2	SMC6;FLJ22116			
GI_31543647-S	958.9	1082.6	1178.6	SNRP70	NM_003089.3	RPU1;U1AP;U170K;U1RNP;RNPU1Z	pre-mRNA	ribonucleo	mRNA
GI_31543651-S	2242.8	2137.1	1765.7	SPOP	NM_003563.2	TEF2	protein	nucleus	mRNA
GI_31543652-S	13496.4	18244	14025	SRP14	NM_003134.2	ALURBP	7S RNA	signal	cotranslati
GI_31543654-S	986.4	1167.1	1069.3	SSB	NM_003142.2		ribonucleo	nucleus	tRNA
GI_31543655-S	1052	1547.9	1185.5	STARD3NL	NM_032016.2	MENTHO;MGC3251		integral to	
GI_31543656-S	423	389.9	420	STARD3	NM_006804.2	CAB1;es64;MLN64		cytoplasm	mitochond
GI_31543658-S	204.6	193.1	120.9	STARD8	NM_014725.2	KIAA0189	GTPase		
GI_31543660-S	101.4	107.3	112.9	STARS	NM_139166.2				
GI_31543661-S	297.8	366.2	306.2	STK17B	NM_004226.2	DRAK2	protein	nucleus	induction
GI_31543664-S	847.6	859.5	692.5	STOML1	NM_004809.3	SLP-1;STORP;hUNC-24			
GI_31543665-S	729.4	780.7	629.3	STX5A	NM_003164.2				nonselecti
GI_31543666-S	541.8	387.3	371.3	SUPV3L1	NM_003171.2	SUV3	helicase	mitochond	
GI_31543802-S	119.8	114.2	101.7	TCP11	NM_018679.2	D6S230E			developm
GI_31543803-S	92.1	100.9	82.5	TFPI2	NM_006528.2	PP5;TFPI-2	extracellul	extracellul	blood
GI_31543809-S	1726.6	638.7	370.7	TIE	NM_005424.2	TIE1;JTK14	transmem	integral to	mesoderm
GI_31543810-S	157.8	182.8	155.1	TMG3	NM_024082.2		calcium	extracellul	biological_
GI_31543813-S	19540.3	22859	15648	TMSB10	NM_021103.2		actin	cytoskelet	spermatid
GI_31543814-S	406.6	421.8	514.5	TOE1	NM_025077.2	FLJ13949	nucleic		
GI_31543816-S	1209.6	1267.2	1439.8	TOR3A	NM_022371.2	ADIR;ADIR2;FLJ22345			
GI_31543817-S	128.3	130.9	114.8	TP73L	NM_003722.3	KET;LMS;p51;p63;EEC3;TP63;p73H;p73L;S			induction
GI_31543820-S	1537.3	1577.8	749.6	TPST2	NM_003595.2		protein-	Golgi	peptidyl-
GI_31543822-S	5340.4	5954.2	5061.5	TRAM1	NM_014294.3	TRAM;TRAMP	endoplas	integral to	cotranslati
GI_31543823-S	481.1	709	934	TREM1	NM_018643.2		receptor	plasma	humoral
GI_31543824-S	147.4	157.9	172.9	TSARG2	NM_144644.2	MGC33432			
GI_31543826-A	4703	3673.8	3011.1	TSC22	NM_006022.2	MGC17597	transcripti	nucleus	transcripti
GI_31543826-I	1922.3	1669.2	1053	TSC22	NM_006022.2	MGC17597	transcripti	nucleus	transcripti
GI_31543827-S	109.3	113.7	119.6	TSCOT	NM_033051.2		symporter	integral to	tetracyclin
GI_31543829-S	134.2	154.5	139.6	TSP50	NM_013270.2		trypsin		proteolysis
GI_31543835-S	149.4	175.4	162.5	TXNDC3	NM_016616.2	NME8;SPTRX2;Sptrx-2	nucleoside		electron
GI_31543907-S	1514.8	1788	1869.8	UBP1	NM_014517.2	LBP-1B;LBP-1a	transcripti		viral
GI_31543909-S	841.1	613.2	700	USP1	NM_003368.3		ubiquitin-		deubiquiti
GI_31543911-S	339.1	374.9	361.8	USP20	NM_006676.2	VDU2;KIAA1003	cysteine-	cellular_co	ubiquitin-
GI_31543930-S	179.2	196.8	174.6	VAMP5	NM_006634.2	MYOBREVIN		integral to	nonselecti
GI_31543932-S	263.7	319	280.9	VGLL1	NM_016267.2	TDU;VGL1	transcripti	nucleus	regulation
GI_31543933-S	139	148.7	134.4	VMP	NM_080723.2	p24			
GI_31543935-S	208.6	209.6	216.7	VRK2	NM_006296.2		protein	integral to	protein
GI_31543966-S	435.2	335.2	405.5	XPA	NM_000380.2	XP1;XPAC	damaged	nucleus	nucleotide-
GI_31543977-S	176.7	240.6	237.1	ZHX2	NM_014943.2	KIAA0854	transcripti	nucleus	regulation
GI_31543978-S	83.8	100.6	97.5	ZNF145	NM_006006.3	PLZF	transcripti	nucleus	mesoderm
GI_31543982-S	329.1	369.1	438.9	ZNF289	NM_032389.2	IRZ;Zfp289;FLJ14576	DNA	nucleus	
GI_31543986-S	313.1	337.8	308.3	ZNF350	NM_021632.2	ZFQR;ZBRK1	nucleic	intracellula	regulation
GI_31543988-S	82.3	91.4	87.4	ZNF382	NM_032825.2	KS1;FLJ14686	nucleic	intracellula	regulation
GI_31543989-S	162.8	118.5	176.9	ZNF443	NM_005815.2	ZK1	nucleic	nucleus	induction

GI_31544070-S	151.3	157.8	150.6	ZNF481	NM_020924.2	bioref;KIAA1572	protein	nucleus	regulation
GI_31559770-S	124.6	150	142.5	ODF3	NM_053280.3	SHIPPO1;hSHIPPO			
GI_31559774-S	1060.4	1241.5	1029.4	USP38	NM_032557.4	HP43.8KD;KIAA1891	cysteine-		ubiquitin-
GI_31559779-S	108.2	126.8	106.8	DKFZp547D2	NM_153685.2				
GI_31559780-S	110.4	100.9	97.6	STRC	NM_153700.2	DFNB16			
GI_31559781-S	112.7	111	99.7	FLJ90036	NM_153691.2				
GI_31559782-S	121.3	112.9	116.2	SYCP3	NM_153694.2	COR1;SCP3			
GI_31559784-S	129.3	140.6	143.7	TTL	NM_153712.2	MGC46235	tubulin-		protein
GI_31559785-S	446	544.5	439	PP784	NM_152301.3	MGC9651			
GI_31559786-S	272.8	281.8	331.1	MGC33648	NM_153706.2				
GI_31559787-S	112.9	152.9	115.2	FLJ30277	NM_153008.3		DNA	nucleus	regulation
GI_31559788-S	299.2	383.8	358.7	ODF4	NM_153007.3	OPPO1			
GI_31559820-S	207.4	183.6	145.4	GJE1	NM_181538.1	Cx29	connexon	connexon	cell
GI_31559824-S	107.9	104	98.2	PKD1L3	NM_181536.1		cation	membran	cation
GI_31560860-S	93	108.1	77.5	KAAG1	NM_181337.2	RU2;RU2AS	defense/i	cellular_co	immune
GI_31560862-S	118.6	131.7	120	SYT2	NM_177402.3	SytII	transporte	membran	transport
GI_31560863-S	107.7	130.5	113.1	FLJ36180	NM_178556.3				
GI_31560865-S	257	325.9	276.7	MGC30208	NM_173804.3				
GI_31560866-S	94.9	87.7	76	CESK1	NM_014406.3		ATP		protein
GI_31560867-S	846.3	1478.6	917.6	ITM2C	NM_030926.3	E25;BRI3;E25C;ITM3;BRICD2C;HRPC.1050			
GI_31563329-I	205.1	265.9	232.7	AKAP13	NM_006738.4	BRX;LBC;Ht31;c-lbc;AKAP-	protein	membran	oncogene
GI_31563332-A	1163.2	1226.9	1170.5	AKAP13	NM_144767.3	BRX;LBC;Ht31;c-lbc;AKAP-	protein	membran	oncogene
GI_31563333-I	94.2	102.7	83.9	FOXK2	NM_181430.1	ILF;ILF1;ILF-1	RNA	nucleus	regulation
GI_31563335-A	209.8	240.7	251.7	FOXK2	NM_181431.1	ILF;ILF1;ILF-1	RNA	nucleus	regulation
GI_31563349-A	138.5	153	143.9	PAX3	NM_013942.2	WS1;CDHS;HUP2	transcripti		hearing
GI_31563350-I	107.2	136.8	116.5	PAX3	NM_000438.3	WS1;CDHS;HUP2	transcripti		hearing
GI_31563359-I	182.1	201.4	172.9	MRPL55	NM_181462.1				
GI_31563365-A	402.2	423.1	412.8	MRPL55	NM_181465.1				
GI_31563367-I	97.7	107.2	104.2	KIAA1847	NM_032527.2	FLJ14972;MGC44880;dJ583P15.3	nucleic	intracellula	regulation
GI_31563369-I	81.7	101.6	90.8	KIAA1847	NM_181484.1	FLJ14972;MGC44880;dJ583P15.3	nucleic	intracellula	regulation
GI_31563371-A	683.7	761.1	1156.1	KIAA1847	NM_181485.1	FLJ14972;MGC44880;dJ583P15.3	nucleic	intracellula	regulation
GI_31563373-I	110.5	118.3	125.6	ITGB4BP	NM_181466.1	CAB;EIF6;EIF3A;p27BBP;b(2)gcn	translation	peripheral	translation
GI_31563375-A	5241	4907.7	6301.7	ITGB4BP	NM_181467.1	CAB;EIF6;EIF3A;p27BBP;b(2)gcn	translation	peripheral	translation
GI_31563384-S	102.3	99.7	107	SOX14	NM_004189.2	SOX28	transcripti	chromatin	neurogene
GI_31563385-A	286.8	382.7	317.2	SULT2B1	NM_177973.1	HSST2	sulfotransf	cytoplasm	steroid
GI_31563385-I	294.5	321.1	312.4	SULT2B1	NM_177973.1	HSST2	sulfotransf	cytoplasm	steroid
GI_31563387-I	82.9	89.7	73.3	SULT2B1	NM_004605.2	HSST2	sulfotransf	cytoplasm	steroid
GI_31563411-A	153.9	176.5	167.9	CKLFSF1	NM_181289.1	CKLFH;CKLFH1;CKLFH1a	transporte	membran	transport
GI_31563435-S	98.7	110.8	96.6	CKLFSF2	NM_144673.2	FLJ25732;MGC39436	cytokine	membran	chemotaxi
GI_31563501-S	3181.4	3022.8	3367.3	ACAT1	NM_000019.2	T2;MAT;ACAT;THIL	acetyl-	mitochond	
GI_31563502-A	674.8	789	863.8	ADNP	NM_181442.1	KIAA0784	transcripti	nucleus	regulation
GI_31563504-I	144	152.8	142.6	ADNP	NM_015339.2	KIAA0784	transcripti	nucleus	regulation
GI_31563505-S	134.2	161.6	159.5	AMID	NM_032797.4	PRG3;FLJ14497	disulfide		electron
GI_31563510-S	149.1	145.8	146.7	GTPBP5	NM_015666.2	FLJ10741;MGC29512;dJ1005F21.2	GTP		

GI_31563511-I	121.8	126.3	123	NAT5	NM_181527.1	ARD1;dJ1002M8.1	acyltransf		
GI_31563513-A	5812.1	5423.8	2687.8	NAT5	NM_181528.1	ARD1;dJ1002M8.1	acyltransf		
GI_31563516-S	102.4	110.9	92.5	NTS	NM_006183.3	NN;NT;NT/N;NTS1;NMN-125	peptide	soluble	signal
GI_31563517-A	169	226.4	213.9	MAP1LC3A	NM_181509.1	MAP1ALC3;MAP1BLC3			
GI_31563517-I	123.4	150.5	125.6	MAP1LC3A	NM_181509.1	MAP1ALC3;MAP1BLC3			
GI_31563519-I	134.6	164.6	130.8	MAP1LC3A	NM_032514.2	MAP1ALC3;MAP1BLC3			
GI_31563520-S	418.6	375.2	232.1	MGC10715	NM_024325.4	FLJ39592;MGC20504;dJ734P14.5			
GI_31563522-I	382.9	660.8	546.4	MYL9	NM_006097.3	LC20;MLC2;MRLC1;MYRL2;MGC3505	structural	muscle	regulation
GI_31563523-A	415.6	727.7	559.2	MYL9	NM_181526.1	LC20;MLC2;MRLC1;MYRL2;MGC3505	structural	muscle	regulation
GI_31563525-S	102.1	950.8	173.3	SLC24A3	NM_020689.3	NCKX3	symporter	integral to	sodium
GI_31563527-I	188.8	238.8	204.8	SPINLW1	NM_181502.1	WAP7;EPPIN;WFDC7;EPPIN1;EPPIN2;EPPI	serine		
GI_31563529-A	477.6	580.9	517	SPINLW1	NM_020398.2	WAP7;EPPIN;WFDC7;EPPIN1;EPPIN2;EPPI	serine		
GI_31563529-I	129.9	139	118.5	SPINLW1	NM_020398.2	WAP7;EPPIN;WFDC7;EPPIN1;EPPIN2;EPPI	serine		
GI_31563530-S	1140.7	1060.8	1023.1	STAG2	NM_006603.3	SA2;SA-2		nucleus	meiosis
GI_31563532-S	114.8	115.6	98.2	RAD52B	NM_145654.2	MGC33977	nucleic		
GI_31563533-I	317	295.5	345.1	RFC2	NM_181471.1	A1;RFC40;MGC3665	ATP	DNA	DNA
GI_31563535-A	364	383.5	336.2	RFC2	NM_002914.3	A1;RFC40;MGC3665	ATP	DNA	DNA
GI_31563536-S	569.6	743.8	651.8	CLASP1	NM_015282.1	MAST1;KIAA0622			
GI_31563538-S	282.5	313.5	282	WFDC10A	NM_080753.2	WAP10;C20orf146;dJ688G8.3	serine		
GI_31563539-I	181.9	157	144.8	WFDC10B	NM_172006.2	WAP12			
GI_31563540-A	104.4	103.9	103.9	WFDC10B	NM_172131.2	WAP12			
GI_31563541-S	125.4	144	132	WFDC11	NM_147197.2	WAP11			
GI_31581519-S	325.8	348.7	252.3	C20orf99	NM_033089.4	ZCCHC3;FLJ22115;dJ1103G7.7	nucleic	nucleus	regulation
GI_31581520-S	96.8	101	110.4	MT1E	NM_175617.2	MT1;MTD	heavy		heavy
GI_31581523-S	129	144.5	157.7	COBL	NM_015198.2	KIAA0633			
GI_31581525-S	290.8	386.1	338.6	SSX9	NM_174962.2				
GI_31581528-S	606	747.3	745.7	SSX8	NM_174961.2				
GI_31581540-S	114.8	126.9	118.3	FLJ38973	NM_153689.3				
GI_31581548-S	92.2	95.5	85.4	KRT25B	NM_181539.2			intermedia	
GI_31581550-S	128.9	138.7	133	KRT25C	NM_181537.2			intermedia	
GI_31581551-S	86.9	85.4	89.9	KRT25D	NM_181535.2			intermedia	
GI_31581553-S	131.9	153.8	135	KRT25A	NM_181534.2			intermedia	
GI_31581555-S	137.9	162.2	149	ERAS	NM_181532.2	HRAS2;HRASP	RAS small		protein
GI_31581597-S	99.3	110	112.7	C6orf150	NM_138441.1				
GI_31621295-I	806.6	701.2	714.5	CPR8	NM_020739.1	KIAA1254			
GI_31621298-S	104.7	111.1	106.8	FLJ23059	NM_032234.2				
GI_31621304-S	414.1	488	383	LRPPRC	NM_133259.2	LSFC;GP130;LRP130;CLONE-23970	molecular	cellular_co	biological_
GI_31621308-S	145.2	123.5	130.5	TSLRP	NM_012472.3				
GI_31652216-S	157.6	173.4	152.4	SLC25A16	NM_152707.2	GDA;GDC;ML7;hML7;HGT.1;D10S105E;MG	carrier	mitochond	small
GI_31652217-I	578.1	652	651.7	SURF5	NM_181491.1	MGC48682		soluble	
GI_31652219-A	1453.3	879.7	1035	SURF5	NM_133640.3	MGC48682		soluble	
GI_31652221-I	205.3	204.3	159	MRPL21	NM_181512.1				
GI_31652223-A	5152	4274	3413	MRPL21	NM_181513.1				
GI_31652229-S	121.9	147	120.3	TBX20	NM_020417.1		transcripti	nucleus	regulation

GI_31652231-I	163.6	166.9	151.1	TBX5	NM_181486.1	HOS	RNA		heart
GI_31652237-A	146.2	163.5	175.7	CUTL1	NM_181500.1	CDP;CUX;p75;CASP;COY1;p100;p110;p200	RNA		regulation
GI_31652239-I	146.5	160.7	169.3	CUTL1	NM_181552.1	CDP;CUX;p75;CASP;COY1;p100;p110;p200	RNA		regulation
GI_31652241-A	553.4	467.6	473.4	TCF20	NM_181492.1	AR1;SPBP;KIAA0292	RNA	nucleus	proteolysis
GI_31652243-I	134.9	133.5	129.9	TCF20	NM_005650.1	AR1;SPBP;KIAA0292	RNA	nucleus	proteolysis
GI_31652245-I	539.7	849.3	975.8	TNFRSF19	NM_148957.2	TAJ;TROY;TRADE;TAJ-alpha	tumor	integral to	JNK
GI_31652246-S	704.9	446.5	451.2	STXBP5	NM_139244.2	LGL3			
GI_31652248-S	94.6	144.9	108.1	LBP	NM_004139.2	MGC22233	lipid	integral to	response
GI_31652250-S	334.8	301.7	259.5	LOC51244	NM_016474.3				
GI_31652253-S	118.2	123.1	114.7	MAK	NM_005906.3	dJ417M14.2	ATP		protein
GI_31652254-S	135.4	175.7	125.1	LYG2	NM_175735.3	LYGH	lysozyme		cell wall
GI_31652256-S	522.5	497.8	190.3	MAFB	NM_005461.3	KRML;MGC43127	DNA	nucleus	sensory
GI_31652257-S	203.9	225.7	219.2	MOCS3	NM_014484.3	MGC9252;dJ914P20.3	ligase		Mo-
GI_31652258-S	1088.4	1435	1444.4	MUM1	NM_032853.2	MUM-1;HSPC211;FLJ14868;FLJ22283			
GI_31652260-S	205.3	278.7	422.9	MYBL2	NM_002466.2	BMYB;MGC15600	transcripti	chromatin	anti-
GI_31652261-S	121.4	125.5	105.2	C2F	NM_006331.3		molecular	nucleus	rRNA
GI_31652263-S	288.5	322.9	304.1	C13orf10	NM_022118.3	SE70-2;PRO1777;FLJ20957			
GI_31657091-S	108.2	101.7	123.4	ABCA13	NM_152701.2	FLJ33876;FLJ33951	ATP-	membran	transport
GI_31657093-S	430.9	434	583	ANLN	NM_018685.2	Scraps;ANILLIN	actin		regulation
GI_31657095-A	97.3	99.7	87.1	CKLFSF4	NM_181521.1		cytokine	membran	chemotaxi
GI_31657095-I	138	153.9	155.8	CKLFSF4	NM_181521.1		cytokine	membran	chemotaxi
GI_31657097-I	934.8	845.3	728.1	CKLFSF7	NM_138410.2	FLJ30992	transporte	membran	transport
GI_31657098-A	9143.8	7456.4	6245.2	CKLFSF7	NM_181472.1	FLJ30992	transporte	membran	transport
GI_31657100-A	449.4	416.7	461.9	WDR23	NM_181357.1	GL014;PRO2389			
GI_31657102-I	133.6	139.8	121.8	WDR23	NM_025230.3	GL014;PRO2389			
GI_31657104-I	127.8	141.2	128.5	WFDC8	NM_181510.1	WAP8;C20orf170;dJ461P17.1	serine		
GI_31657106-A	94.7	98.6	101.4	WFDC8	NM_130896.1	WAP8;C20orf170;dJ461P17.1	serine		
GI_31657106-I	92	100.2	88.9	WFDC8	NM_130896.1	WAP8;C20orf170;dJ461P17.1	serine		
GI_31657108-S	291.8	306.9	288.9	ZNF282	NM_003575.1	HUB1	zinc ion	nucleus	regulation
GI_31657110-S	988.3	1157.6	1099.3	ZNF294	NM_015565.1	C21orf10;C21orf98;FLJ11053;KIAA0714			
GI_31657112-S	145.4	146.7	151.9	ZNFN1A1	NM_006060.2	IK1;LYF1;hIk-1;IKAROS;PRO0758;Hs.54452	DNA		mesoderm
GI_31657113-S	230.7	144.1	157.3	ARMC4	NM_018076.2	FLJ10376;FLJ10817;DKFZP434P1735			
GI_31657115-A	648.6	624.1	565.4	KIAA2010	NM_017936.2	MSTP033;FLJ20707			
GI_31657115-I	107.2	105.2	104.1	KIAA2010	NM_017936.2	MSTP033;FLJ20707			
GI_31657116-I	99.5	114.6	98.8	KIAA2010	NM_032560.3	MSTP033;FLJ20707			
GI_31657118-S	101.6	112	106.6	FLJ23598	NM_024783.2		carboxype		proteolysis
GI_31657120-S	222.3	222.6	262.2	HIC2	NM_015094.1	HRG22;KIAA1020	protein	nucleus	regulation
GI_31657122-I	93.1	87.8	85.4	HPS5	NM_181507.1	AIBP63;KIAA1017			
GI_31657124-A	428.2	461.3	451	HPS5	NM_181508.1	AIBP63;KIAA1017			
GI_31657128-S	788.2	617.7	602	PFAS	NM_012393.1	PURL;FGAMS;FGARAT;KIAA0361	ATP	cytoplasm	purine
GI_31657130-S	367.7	449.9	442.8	PI3	NM_002638.2	ESI;WAP3;SKALP;WFDC14;MGC13613	protein	extracellul	copulation
GI_31657133-S	96.3	95.2	77.8	FRK	NM_002031.2	GTK;RAK;PTK5	non-	intracellula	negative
GI_31657134-S	379.9	378.2	410.6	FRS3	NM_006653.3	SNT2;FRS2B;SNT-2;FRS2beta;MGC17167	insulin	peripheral	FGF
GI_31657135-A	91.6	81.7	79.7	FSHR	NM_181446.1	LGR1;ODG1;FSHRO	follicle	integral to	female

GI_31657137-I	203.9	228.6	204	FSHR	NM_000145.2	LGR1;ODG1;FSHRO	follicle	integral to	female
GI_31657139-S	163.9	208.7	179.7	INSRR	NM_014215.1	IRR	transmem	integral to	protein
GI_31657141-S	318.7	361.3	276.8	ITGA1	NM_181501.1	VLA1;CD49a	collagen	integrin	integrin-
GI_31657143-A	2815.1	3186.5	1741.8	ITPA	NM_181493.1	ITPase;C20orf37;dJ794I6.3;HLC14-06-P			
GI_31657146-S	98.9	99.2	98.4	ITR	NM_180989.3				
GI_31711991-S	647.9	699.4	698	DLAT	NM_001931.2	DLTA;PDC-E2	dihydrolip	mitochond	
GI_31712019-S	153.3	160.4	135	SPATA3	NM_139073.2	TSARG1			
GI_31712021-S	340.8	440	341.8	HUMAGCGB	NM_013286.2				
GI_31742475-S	90.8	92.6	93.8	RGS6	NM_004296.3	GAP	GTPase	peripheral	regulation
GI_31742479-I	291.6	253.8	226.2	YWHAB	NM_003404.3	HS1;GW128;KCIP-1	protein		
GI_31742480-A	10013.6	11064	13439	YWHAB	NM_139323.2	HS1;GW128;KCIP-1	protein		
GI_31742481-S	170.3	201.1	179.6	ARSF	NM_004042.3	ASF	arylsulfata		metabolis
GI_31742483-S	539.1	560.6	574.6	EDRF1	NM_015608.2	FLJ21617;DKFZp586F1019			
GI_31742485-S	187.2	276.1	208.4	EGLN3	NM_022073.2	PHD3;HIFPH3;FLJ21620	oxidoredu	nucleus	protein
GI_31742486-S	1023.5	1538.1	1901.8	KIF3B	NM_004798.2	HH0048;KIAA0359	plus-end-	plus-end	anterogra
GI_31742489-S	120.3	129.9	107.2	GABRG1	NM_173536.2	MGC33838	extracellul	integral to	chloride
GI_31742491-S	749	895.1	803	N4BP2	NM_018177.2	B3BP;FLJ10680;KIAA1413	damaged		mismatch
GI_31742495-S	681.9	437	354.2	PP35	NM_181581.1		molecular		
GI_31742497-S	122.6	126.9	138.4	UNC84B	NM_015374.1	SUN2;KIAA0668	microtubul	kinesin	mitotic
GI_31742500-S	2073	2174.7	2014.9	SNX27	NM_030918.4	MY014;KIAA0488;MGC20471	protein		neuropepti
GI_31742502-S	90.6	106.7	75	HIST2H3C	NM_021059.2	H3;H3.2;H3/M;H3F2;H3FM;MGC9629			
GI_31742504-S	114.5	103.2	93.1	KIAA0861	NM_015078.2				
GI_31742506-A	1326.1	1058.2	909	UPP1	NM_003364.2	UP;UPP;UPASE;UDRPASE	uridine		nucleobas
GI_31742506-I	127.1	131.7	132.6	UPP1	NM_003364.2	UP;UPP;UPASE;UDRPASE	uridine		nucleobas
GI_31742507-I	136.4	107.9	115.2	UPP1	NM_181597.1	UP;UPP;UPASE;UDRPASE	uridine		nucleobas
GI_31742512-I	150.6	184.8	165.9	SPG3A	NM_181598.1	FSP1;GBP3;SPG3;AD-FSP	GTPase	nucleus	immune
GI_31742514-A	129.7	127	114.3	FRDA	NM_000144.3	FA;Fxn;X25;FARR;MGC57199;frataxin	iron ion	mitochond	iron ion
GI_31742527-S	212.4	205.2	169.9	SBZF3	NM_020394.2		nucleic	intracellula	regulation
GI_31742529-I	1426.7	1721.2	1748.5	APG16L	NM_030803.5	WDR30;FLJ00045;FLJ10035;FLJ10828;FLJ2			
GI_31742531-S	2066.9	2011.4	2380.3	DIAPH1	NM_005219.2	DRF1;DFNA1;LFHL1;hDIA1	profilin	kinesin	hearing
GI_31742533-S	131.1	133.2	145.9	ETV1	NM_004956.2	ER81	transcripti	nucleus	oncogene
GI_31742535-S	332.6	232.6	169.3	FIGNL1	NM_022116.2		nucleotide		
GI_31745137-S	107	127	110.6	RASA4	NM_006989.3	GAPL;CAPRI;KIAA0538	GTPase		intracellula
GI_31745171-S	96.2	105.5	103.7	C6orf10	NM_006781.2	TSBP			
GI_31745175-S	231.1	249.2	224.6	LOC51252	NM_016490.3				
GI_31745179-S	385	348.8	323	ARNTL2	NM_020183.3	CLIF;MOP9;BMAL2			
GI_31745183-S	81.4	94.2	98.6	FLJ39249	NM_173664.2		GTP		
GI_31745192-I	171.6	190.9	190.5	B7	NM_181613.1				
GI_31747573-S	2349.2	1968.3	1605.5	GTF2H2	NM_001515.2	BTF2;TFIIH;BTF2P44;T-BTF2P44	nucleic	transcripti	response
GI_31747574-S	128.8	140.9	133.1	CLECSF5	NM_013252.2	MDL1;MDL-1	binding	integral to	cellular
GI_31790997-S	88.5	102.1	94.7	KRTAP15-1	NM_181623.1	KAP15.1			
GI_31790999-S	92.2	95	122.1	KRTAP23-1	NM_181624.1	KAP23.1			
GI_31791001-S	147	163.6	149.7	KRTAP13-3	NM_181622.1	KAP13.3			
GI_31791003-S	235.4	283.8	266.1	KRTAP13-4	NM_181600.1	KAP13.4			

GI_31791007-S	106.7	116.2	111.2	KRTAP13-1	NM_181599.1	KAP13.1		intermedia	
GI_31791009-S	111.9	120	119.8	KRTAP21-1	NM_181619.1	KAP21.1			
GI_31791011-S	96.4	95.4	93	KRTAP22-1	NM_181620.1	KAP22.1			
GI_31791013-S	128.6	137.5	126.6	KRTAP20-2	NM_181616.1	KAP20.2			
GI_31791015-S	105.7	113.2	92.6	KRTAP21-2	NM_181617.1	KAP21.2			
GI_31791017-S	136.5	132.4	125.6	KRTAP19-7	NM_181614.1	KAP19.7			
GI_31791019-S	94.3	89.2	96.3	KRTAP20-1	NM_181615.1	KAP20.1			
GI_31791021-S	102.8	99.4	96.5	KRTAP19-5	NM_181611.1	KAP19.5			
GI_31791023-S	138.6	146.9	132	KRTAP19-6	NM_181612.1	KAP19.6			
GI_31791025-S	120.4	113.6	132.7	KRTAP19-3	NM_181609.1	KAP19.3			
GI_31791027-S	83	92.9	75.1	KRTAP19-4	NM_181610.1	KAP19.4			
GI_31791029-S	122	117.5	120.6	KRTAP19-1	NM_181607.1	KAP19.1		intermedia	
GI_31791031-S	96.6	101.6	90.3	KRTAP19-2	NM_181608.1	KAP19.2			
GI_31791033-S	122.7	138.8	140.4	KRTAP6-3	NM_181605.1	KAP6.3			
GI_31791035-S	224.9	251.8	226.6	KRTAP7-1	NM_181606.1	KAP7.1		intermedia	
GI_31791037-S	127.7	136.9	122.2	KRTAP6-1	NM_181602.1	KAP6.1;C21orf103			
GI_31791039-S	116.6	95.5	99.4	KRTAP6-2	NM_181604.1	KAP6.2			
GI_31791046-S	267.7	318.3	268.9	LOC285398	NM_181647.1				
GI_31791048-S	167.1	185.3	162.4	LOC286161	NM_181648.1				
GI_31791050-S	92.9	104	98.9	FLJ25393	NM_181645.1				
GI_31791054-S	129.9	153.8	126.5	LOC128344	NM_181643.1				
GI_31795534-S	187.5	222.3	210.3	RAB36	NM_004914.2		RAB small	Golgi	nonselecti
GI_31795536-I	493.8	537.6	585.9	RFC3	NM_002915.2	RFC38;MGC5276	DNA-	DNA	DNA
GI_31795537-A	329	311.2	326.9	RFC3	NM_181558.1	RFC38;MGC5276	DNA-	DNA	DNA
GI_31795537-I	334.6	365.1	336.2	RFC3	NM_181558.1	RFC38;MGC5276	DNA-	DNA	DNA
GI_31795539-I	235.7	291	271.9	RFC5	NM_181578.1	RFC36;MGC1155	nucleotide	delta-DNA	DNA
GI_31795541-A	771.9	717.8	806.5	RFC5	NM_007370.3	RFC36;MGC1155	nucleotide	delta-DNA	DNA
GI_31795542-S	1504.6	1791.1	1809.8	GMFB	NM_004124.2	GMF	enzyme	intracellula	protein
GI_31795543-S	179.9	199.9	232.1	ORC1L	NM_004153.2	ORC1;PARC1;HSORC1	DNA	nucleus	DNA
GI_31795545-S	201.6	229.5	231.6	SLC13A4	NM_012450.2	SUT1;SUT-1	sodium:su	integral to	sulfate
GI_31795554-A	1537.4	1592.6	1240.9	LOC284018	NM_181655.1				
GI_31795556-I	112.1	106.4	113.9	LOC284018	NM_181656.1				
GI_31795560-S	227.8	259.9	255.7	CPLX4	NM_181654.1	CPXIV			
GI_31795562-S	80.1	83.7	78.8	TPH2	NM_173353.2	NTPH;FLJ37295	monooxyg		metabolis
GI_31795590-S	128.6	148.2	126.8	RGSL1	NM_181572.2		signal		
GI_31880337-S	7278.8	8233.1	6761.6	TUBA6	NM_032704.2	MGC10851;MGC14580			
GI_31880782-S	1803.4	1107.6	1108.2	PELO	NM_015946.4	CGI-17;PRO1770		nucleus	protein
GI_31880793-S	160	186.4	154.3	PON1	NM_000446.3	ESA;PON	arylestera	extracellul	response
GI_31881619-A	2532	2597.6	2102	PPA2	NM_176867.2	HSPC124;MGC49850;SID6-306			
GI_31881629-S	98.1	113.5	98.3	PTGER2	NM_000956.2	EP2	prostaglan	integral to	G-protein
GI_31881646-S	164.8	175.6	146.4	SPTLC2	NM_004863.2	LCB2;SPT2;KIAA0526	serine C-	endoplas	amino
GI_31881686-A	1561.9	1278.9	1303.2	RFC4	NM_181573.1	A1;RFC37;MGC27291	DNA	DNA	DNA
GI_31881692-A	107.1	140	116.5	BTN2A2	NM_181531.1	BTF2;BT2.2			
GI_31881700-I	134.7	142.9	143.6	BTN2A2	NM_006995.3	BTF2;BT2.2			

GI_31881722-S	179.1	305.9	469.7	C14orf137	NM_023112.2	OTB2;OTU2;MGC3102;FLJ21916			
GI_31881739-S	1509.3	1493.3	1505.4	SLC12A9	NM_020246.2	CIP1	cation:chlo	integral to	
GI_31881756-S	3814.5	2801.2	1820	DDAH1	NM_012137.2	DDAH	catalytic		nitric oxide
GI_31881762-S	132	176.3	171.7	DLL4	NM_019074.2	hdelta2	Notch	integral to	circulation
GI_31881769-S	317.8	428.4	369.9	ADAM30	NM_021794.2	svph4	metallope	integral to	proteolysis
GI_31881778-A	1124	1380.3	1642.2	GMPPA	NM_013335.2		nucleotidyl		biosynthes
GI_31881784-S	1754.3	1977.8	2122.8	HPS6	NM_024747.4	FLJ22501;MGC20522			
GI_31881791-S	261.6	293.2	270.9	LTB4R	NM_181657.1	BLTR;P2Y7;GPR16;LTBR1;P2RY7;CMKRL1;	leukotrien	integral to	G-protein
GI_31881797-S	916.8	1192.9	1054.4	MKLN1	NM_013255.2	FLJ11162		cytoplasm	cell-matrix
GI_31881814-S	89.4	105.2	85.6	TITF1	NM_003317.3	BCH;BHC;TEBP;TTF1;NKX2A;TTF-	transcripti	nucleus	regulation
GI_31981491-S	86.7	92.8	90.7	PGR	NM_000926.2	PR;NR3C3	steroid		signal
GI_31982866-S	317.7	289.1	277.5	PINX1	NM_017884.3	LPTL;LPTS;MGC8850;FLJ20565	nucleic	telomere	negative
GI_31982870-S	374.4	261.2	318.5	LOC128439	NM_139016.2		DNA	nucleus	regulation
GI_31982874-S	2715	2828.5	1920.4	LOC134147	NM_138809.2		hydrolase		
GI_31982875-S	91.7	110.8	94	LOC151871	NM_138815.2		DNA	nucleus	
GI_31982877-S	98.4	99.1	98	KIR2DL4	NM_002255.3	103AS;15.212;CD158D;KIR103;KIR103AS	transmem	integral to	cellular
GI_31982879-S	391.6	554.3	518	HMGB1	NM_002128.3	HMG1;HMG3;SBP-1	single-	nuclear	chromoso
GI_31982880-S	141.9	164.6	159.9	FLJ21069	NM_024692.3				
GI_31982882-S	163	212.9	166.8	NKD1	NM_033119.3		lactoylglut		carbohydr
GI_31982883-S	252.7	261.3	235.5	FLJ20813	NM_017961.3				
GI_31982886-S	107.4	125.3	108.8	GATA2	NM_032638.3	NFE1B;MGC2306	transcripti	nucleus	cell growth
GI_31982890-S	4409.7	4678.2	4420.3	SMAP	NM_014267.3	IMAGE145052	molecular	cellular_co	biological_
GI_31982893-S	146.8	228.1	153.6	LOC92691	NM_138390.2				
GI_31982894-S	4714.3	3529.4	3309.2	THAP4	NM_015963.3	CGI-36	DNA		
GI_31982900-S	9632.9	8806.7	7250.9	SCD	NM_005063.3		stearoyl-	endoplas	fatty acid
GI_31982903-S	616	542.6	586.7	LOC129401	NM_138285.2	MP44;NP44;NUP35	porin	mitochond	
GI_31982905-S	194.4	394.5	199.6	FLJ14957	NM_032866.2	KIAA1749			
GI_31982907-S	771.5	401.9	230.4	JDP2	NM_130469.2	JUNDM2	DNA	nucleus	regulation
GI_31982908-S	374.1	410.1	357.7	ZNF394	NM_032164.2	FLJ12298	nucleic	nucleus	regulation
GI_31982910-S	291.2	287.6	271.9	GL009	NM_032492.2				
GI_31982912-S	1200.8	1289.5	1095.3	FKSG44	NM_031904.2			cytoskelet	
GI_31982913-S	4140.8	4632.1	4039.2	FLJ12953	NM_032118.2				
GI_31982914-S	106.4	127.6	99.6	CCDC3	NM_031455.2	DKFZP761F241			
GI_31982916-S	272.2	279.4	235.8	FLJ23042	NM_025157.2				
GI_31982918-S	375.4	432.3	419	ZNF430	NM_025189.2	FLJ13659	nucleic	intracellula	regulation
GI_31982920-S	95.1	95.4	90	FLJ12505	NM_024749.2				
GI_31982926-S	451.6	548.6	478.5	AACS	NM_023928.2	SUR-5;FLJ12389			
GI_31982928-S	446.1	425	457.4	VRK3	NM_016440.2		protein	nucleus	protein
GI_31982934-S	442.1	688.6	719.9	EPM2AIP1	NM_014805.2	FLJ11207;KIAA0766			
GI_31982935-S	713	768.1	391.6	SGPL1	NM_003901.2	SPL;KIAA1252	lyase	endoplas	amino
GI_31982940-S	149.2	189.8	171.6	KIAA0853	NM_015070.2	DKFZp434D1812			
GI_31982942-S	104.4	114.9	107.5	FOXP3	NM_014009.2	JM2;AIID;IPEX;PIDX;XPID;DIETER;SCURFI	transcripti	nucleus	regulation
GI_31982944-S	120.1	117	106	SLC5A10	NM_152351.2	SGLT5;FLJ25217	transporte	membran	transport
GI_31982952-I	576.9	756.3	482.1	MDS010	NM_152305.1	MDSRP;MGC32995			

GI_32129198-S	4326.7	4768	4534.6	CIP29	NM_033082.1	HCC-1;HSPC316;MGC14726	DNA	nucleus	transcripti
GI_32129208-S	683.8	596.8	423.5	RAP2C	NM_021183.3		RAS small		small
GI_32129210-S	116.7	120	115.3	ZNF445	NM_181489.3	ZNF168	nucleic	nucleus	regulation
GI_32129211-S	757	713.6	634.9	ZNF434	NM_017810.2	MGC4179;FLJ20417;FLJ31901			
GI_32129213-S	261.3	319.2	267.3	EFCBP2	NM_019065.2	NECAB2			
GI_32130513-A	1475.2	1378.3	1949.2	NDRG3	NM_022477.2	FLJ13556	catalytic	cytoplasm	spermatog
GI_32130515-S	228.6	279.2	306	SDCCAG1	NM_004713.2	NY-CO-1;FLJ10051	DNA	nucleus	regulation
GI_32130517-S	109.6	127.6	116.1	APOC2	NM_000483.3		lipoprotein	extracellul	lipid
GI_32130524-I	131.2	149.1	139.4	CKLFSF3	NM_144601.2	FLJ31762;MGC51956	transporte	membran	transport
GI_32130525-I	221.4	229.5	210.4	CKLFSF3	NM_181553.1	FLJ31762;MGC51956	transporte	membran	transport
GI_32130529-A	2873.2	3617.4	4689.5	CKLFSF3	NM_181555.1	FLJ31762;MGC51956	transporte	membran	transport
GI_32130531-A	120.1	133.8	122.3	CKLFSF5	NM_138460.2	FLJ37521	transporte	membran	transport
GI_32130532-I	355.2	439.8	376.8	CKLFSF5	NM_181618.1	FLJ37521	transporte	membran	transport
GI_32130534-S	1813	2922.3	2588.6	CKLFSF6	NM_017801.2	PRO2219;FLJ20396	transporte	membran	transport
GI_32130535-S	1284	1092.3	684.9	CKLFSF8	NM_178868.3		cytokine	membran	chemotaxi
GI_32130537-S	128.2	121.8	122.7	CD7	NM_006137.5	GP40;TP41;Tp40;LEU-9	lymphocyt	integral to	calcium
GI_32130538-S	194.5	225.1	200	MAP3K13	NM_004721.3	LZK	protein-	membran	signal
GI_32130539-S	340.4	324.3	339.4	PFTK1	NM_012395.2	KIAA0834;PFTAIRE1	cAMP-	cytoplasm	protein
GI_32140179-S	153.6	166.8	153.7	KRTAP12-1	NM_181686.1	KAP12.1;KRTAP12.1		intermedia	
GI_32140181-S	207.5	251.9	223.1	KRTAP10-10	NM_181688.1	KAP10.10;KRTAP18.10			
GI_32140183-S	187.3	216.6	184.9	KRTAP12-2	NM_181684.1	KAP12.2;KRTAP12.2		intermedia	
GI_32140191-S	110	164.6	138.6	ZFH4	NM_024721.2	ZHF4;FLJ20980	hormone	extracellul	regulation
GI_32140759-S	153.4	155.5	138.5	COL27A1	NM_032888.2	FLJ11895;KIAA1870;MGC11337			
GI_32171174-S	6978.4	6287	4847.6	G10	NM_003910.2	EDG2;EDG-2	transcripti	nucleus	regulation
GI_32171176-S	4454.2	5722.5	5762.2	C6orf49	NM_013397.3	OBTP;DKFZp761H221			
GI_32171179-S	151.7	161.6	149.9	C6orf162	NM_020425.3	dJ102H19.2;DKFZP586E1923			
GI_32171181-S	1105.4	2144.7	460.2	ID3	NM_002167.2	HEIR-1	transcripti	nucleus	developm
GI_32171183-A	613.7	647.9	632.3	C10orf9	NM_181698.1	CFP1;CBCP1			cell cycle
GI_32171183-I	137.7	150.7	148.4	C10orf9	NM_181698.1	CFP1;CBCP1			cell cycle
GI_32171185-S	3510.6	3928	4035.8	BCAP31	NM_005745.5	CDM;BAP31;6C6-AG;DXS1357E	protein	endoplas	intracellula
GI_32171193-S	153.6	172.2	169.7	SPATA12	NM_181727.1	SRG5			
GI_32171195-S	949.4	1132.2	864.2	p30	NM_181716.1				
GI_32171198-S	177.1	219.9	205	LOC338773	NM_181724.1				
GI_32171200-S	491.2	649.1	498	Lrp2bp	NM_181726.1		receptor		
GI_32171202-S	306.1	350.3	307.1	LOC285908	NM_181722.1				
GI_32171204-S	118.7	114.6	99.8	LOC286097	NM_181723.1		calcium	nucleus	regulation
GI_32171208-S	381.1	685.1	435.4	LOC257106	NM_181720.1				
GI_32171210-S	140.7	137.2	123.2	LOC253018	NM_181717.1				
GI_32171214-S	1048.6	926.8	1042.8	TORC2	NM_181715.1				
GI_32171218-S	129.9	149	148.6	C6orf152	NM_181714.1				
GI_32171220-S	122.9	186.5	118.8	GRASP	NM_181711.1		protein		
GI_32171224-S	416.6	463.6	533.5	COQ3	NM_017421.2	bA9819.1	O-	mitochond	ubiquinon
GI_32171232-S	482.7	487.9	385.6	LOC144233	NM_181708.1				
GI_32171235-S	187.4	204.2	197.7	LOC90624	NM_181705.1				

GI_32171239-S	2440.1	2977.1	3318.8	NDUFA2	NM_002488.2	B8	NADH	NADH	energy
GI_32171240-S	170.1	252.9	190.5	PDE4B	NM_002600.2	DPDE4;PDEIVB	cAMP-	insoluble	signal
GI_32171243-S	449.7	599.2	374.1	DKFZP434G1	NM_022742.2	KIAA1793			
GI_32171246-I	1023.8	867.7	625.5	C10orf9	NM_145012.3	CFP1;CBCP1			cell cycle
GI_32171251-S	936.9	1019.5	897.5	QSCN6L1	NM_181701.1	SOXN;DKFZp762A2013			
GI_32171253-S	253.9	256.4	225.4	FLJ10922	NM_018273.2				
GI_32189315-A	494.2	742.3	760	KBTBD4	NM_018095.3	BKLHD4;HSPC252;FLJ10450	protein		
GI_32189353-S	167.4	198	167.6	OPTC	NM_014359.2	OPT	extracellul	extracellul	
GI_32189356-S	150.4	345.7	217.6	MRAS	NM_012219.2	M-RAs;RRAS3;R-RAS3	RAS small	plasma	actin
GI_32189358-S	109.1	95.5	91.7	NR1I3	NM_005122.2	CAR;CAR1;MB67;CAR-BETA	androgen	nucleus	signal
GI_32189359-S	178.4	243.4	197.3	GRAF	NM_015071.2	KIAA0621	Rho	cellular_co	cell growth
GI_32189360-S	96.1	103.3	88.6	SLC4A10	NM_022058.2		inorganic	intracellula	chloride
GI_32189367-S	92	102.3	94.5	IGJ	NM_144646.2	JCH;IGCJ	antigen	extracellul	immune
GI_32189368-S	443.9	388.1	502.2	POLE2	NM_002692.2	DPE2	epsilon	nucleus	DNA
GI_32189370-S	1280.4	1751.7	1489.8	TPARL	NM_018475.2	TMPT27	molecular	membran	
GI_32189374-S	652.7	961	712	SGCB	NM_000232.2	A3b;SGC;LGMD2E		sarcoglyca	muscle
GI_32189375-S	119.3	140.7	111.8	TRIP4	NM_016213.2	HsT17391	transcripti	cytoplasm	transcripti
GI_32189381-S	1379.9	1243.6	758.2	HT007	NM_018480.2				
GI_32189383-S	4497.7	6200.1	5303.3	RPN1	NM_002950.2	RBPH1	oligosacch	endoplas	protein
GI_32189384-I	108.5	106.6	96.8	KBTBD4	NM_016506.3	BKLHD4;HSPC252;FLJ10450	protein		
GI_32189389-S	859.2	1313.4	1381.2	TDG	NM_003211.2		pyrimidine-	nucleoplas	base-
GI_32189393-S	21153.4	23516	17421	ATP5B	NM_001686.2	ATPMB;ATPSB	hydrogen-	proton-	energy
GI_32189397-S	128.5	133.6	135.5	GIF	NM_005142.2		binding	extracellul	transport
GI_32189413-S	264.9	300.9	282.1	SF3A2	NM_007165.3	PRP11;SAP62;SF3a66	small	spliceoso	mRNA
GI_32189414-S	172.6	140.7	103.1	C20orf19	NM_018474.2	HT013;DKFZP586H021			
GI_32189424-S	84.6	88.2	93.4	FLJ25955	NM_178821.1				
GI_32261290-S	163.4	190.6	172.3	FLJ20442	NM_017823.2		protein		protein
GI_32261292-S	4444.2	4097.5	3237	P14	NM_016047.2	SAP14;SF3B14;CGI-	RNA	nucleus	mRNA
GI_32261293-S	1210.1	1213.2	1142.4	PRKRA	NM_003690.3	RAX;PACT	enzyme	intracellula	negative
GI_32261294-S	135.1	118.8	107.9	PRG2	NM_002728.3	MBP;BMPG	lectin [goid	cytoplasm	inflammat
GI_32261296-S	189.3	223.7	166.7	MGC14801	NM_032705.2				
GI_32261298-S	84.4	93.8	95.3	MGC10955	NM_032676.2				
GI_32261299-S	656.3	881.5	1036.4	MGC13010	NM_032687.2				
GI_32261302-S	87.4	103.6	89.8	BAZ2A	NM_013449.2	TIP5;KIAA0314	DNA	kinesin	chromatin
GI_32261305-S	5489.2	5233.7	5074.1	IQGAP1	NM_003870.2	SAR1;p195;KIAA0051;HUMORFA01	GTPase	actin	cell shape
GI_32261308-S	134.8	149.4	141	GPR135	NM_022571.3	PAFR;HUMNPIIY20	platelet	integral to	G-protein
GI_32261311-S	471.4	504.9	582.9	HSPC039	NM_016097.2	PRO2309			
GI_32261312-S	1288.2	1567	1519.9	RBM3	NM_006743.2	IS1-RNPL	RNA		RNA
GI_32261315-S	570.7	721.8	657.9	FLJ14345	NM_024733.2			nucleus	
GI_32261317-S	78.4	91.1	69.5	UNC5B	NM_170744.2	UNC5H2;p53RDL1	receptor		signal
GI_32261319-I	171.8	203.3	195.1	HUMGT198A	NM_013290.3	TBPIP			
GI_32261325-S	1484.2	1488.2	1744	PDPR	NM_017990.3	FLJ10079			
GI_32261328-S	906.1	1282.7	1664.7	TMEM14A	NM_014051.2	PTD011;C6orf73	molecular	integral to	
GI_32261331-S	283.1	326.5	266	SEZ6L	NM_021115.2	KIAA0927		integral to	

GI_32306512-S	103.4	114.5	102.4	PDE4D	NM_006203.2	DPDE3;STRK1	cAMP-	insoluble	
GI_32306514-S	145.2	166.2	164.3	HSPB2	NM_001541.2	MKBP;HSP27;Hs.78846	enzyme	cytosol	heat
GI_32306515-S	94.6	90	87.2	PRO2268	NM_018520.2				
GI_32306516-S	95.1	108.4	101.9	MGC10561	NM_032647.2		chromatin	chromatin	chromatin
GI_32306517-S	118.1	121.7	108.2	ZNF540	NM_152606.2	DKFZp547B0714	nucleic	nucleus	regulation
GI_32306518-S	699.3	790.7	704	MGC10871	NM_031492.2		nucleic		
GI_32306519-S	148.7	155.7	155	FLT1	NM_002019.2	FLT;VEGFR1	vascular	extracellul	transmem
GI_32306535-S	794	914.6	791.5	MTIF3	NM_152912.3		translation		translation
GI_32306537-S	126.4	133.5	133.6	GPM6B	NM_005278.2	M6B	molecular	integral to	neurogene
GI_32306538-S	1245.8	1008.9	1158.7	MGC874	NM_016500.3				
GI_32306540-S	868	756.9	606.3	TRIT1	NM_017646.3	IPT;MOD5;FLJ20061	ATP	cellular_co	tRNA
GI_32306541-S	278.6	310.7	414.8	DKFZP564J0	NM_015459.2				
GI_32306543-S	651.2	834.8	714.3	MGC13005	NM_032685.2				
GI_32307106-A	1039.9	960.6	945.6	WFDC3	NM_181530.1	WAP14;dJ447F3.3	peptidase		
GI_32307108-I	122.5	138.7	122.6	WFDC3	NM_080614.1	WAP14;dJ447F3.3	peptidase		
GI_32307111-S	1762.8	1534.5	1355.6	PPP2R2A	NM_002717.2	MGC52248	protein	protein	signal
GI_32307112-I	113.5	132.1	113.5	PPP2R2B	NM_181674.1	SCA12;MGC24888;PR55-BETA;PP2A-	protein	protein	signal
GI_32307114-I	345.1	396.7	366.8	PPP2R2B	NM_181675.1	SCA12;MGC24888;PR55-BETA;PP2A-	protein	protein	signal
GI_32307116-A	144	173.1	136.4	PPP2R2B	NM_181676.1	SCA12;MGC24888;PR55-BETA;PP2A-	protein	protein	signal
GI_32307118-I	1236.9	1588.3	1329.2	PPP2R2B	NM_181677.1	SCA12;MGC24888;PR55-BETA;PP2A-	protein	protein	signal
GI_32307120-I	78	102.5	90.3	PPP2R2B	NM_181678.1	SCA12;MGC24888;PR55-BETA;PP2A-	protein	protein	signal
GI_32307122-I	93.5	94.2	87.5	PPP2R2B	NM_004576.2	SCA12;MGC24888;PR55-BETA;PP2A-	protein	protein	signal
GI_32307123-A	654.6	816.7	622.2	NCOA3	NM_006534.2	ACTR;AIB1;RAC3;SRC3;pCIP;CTG26;CAGH	transcripti	nucleus	oncogene
GI_32307127-S	858.4	940	848.3	NCOA6	NM_014071.2	NRC;AIB3;ASC2;PRIP;TRBP;RAP250;KIAA0	chromatin	transcripti	transcripti
GI_32307129-A	245.4	250.1	246.1	NFS1	NM_181679.1	NIFS;HUSSY-08	transamin	cytosol	sulfur
GI_32307129-I	250.8	286.6	262.1	NFS1	NM_181679.1	NIFS;HUSSY-08	transamin	cytosol	sulfur
GI_32307131-I	140.7	130.3	165.2	NFS1	NM_021100.3	NIFS;HUSSY-08	transamin	cytosol	sulfur
GI_32307133-S	135.1	161.6	131.6	NKX2-2	NM_002509.2	NKX2B;NKX2.2	transcripti	nucleus	brain
GI_32307134-I	99.8	98.2	101.8	NNAT	NM_005386.2	Peg5;MGC1439	auxiliary		protein-
GI_32307135-A	439.5	543.5	503.6	NNAT	NM_181689.1	Peg5;MGC1439	auxiliary		protein-
GI_32307138-S	202.2	253.8	218.1	PEX26	NM_017929.2	FLJ20695			
GI_32307139-A	129.8	122.8	179.8	PITPNC1	NM_012417.2	RDGBB;RDGBB1;RDGB-BETA	phosphati	cytoplasm	signal
GI_32307141-I	470.7	438.3	791.3	PITPNC1	NM_181671.1	RDGBB;RDGBB1;RDGB-BETA	phosphati	cytoplasm	signal
GI_32307143-S	7228.9	9140.8	5925.4	PLOD	NM_000302.2	LH;LLH;PLOD1	electron	membran	epidermal
GI_32307145-I	103.2	103.9	94.4	OGT	NM_003605.3	HRNT1;FLJ23071;MGC22921;O-GLCNAC	acetylgluc	cytosol	response
GI_32307149-A	1371.1	1354.3	1072.3	OGT	NM_181673.1	HRNT1;FLJ23071;MGC22921;O-GLCNAC	acetylgluc	cytosol	response
GI_32307151-S	167.1	234.8	287.7	OXTR	NM_000916.3	OT-R	oxytocin	endosome	lactation
GI_32307157-S	437.3	457	417.7	CENTG3	NM_031946.3	MRIP-1	small	nucleus	small
GI_32307158-S	230.9	278.7	248.3	CRHR2	NM_001883.2	CRFR2	corticotrop	integral to	G-protein
GI_32307160-S	2292.8	2314	2212.9	CUL1	NM_003592.2		tumor		induction
GI_32307162-A	119.5	122	115	AKT3	NM_181690.1	PKBG;PRKBG;STK-2;RAC-gamma;RAC-PK-	protein		protein
GI_32307162-I	88.3	96.2	88.3	AKT3	NM_181690.1	PKBG;PRKBG;STK-2;RAC-gamma;RAC-PK-	protein		protein
GI_32307164-I	124.8	130.1	122.9	AKT3	NM_005465.3	PKBG;PRKBG;STK-2;RAC-gamma;RAC-PK-	protein		protein
GI_32307165-S	89.1	77.7	84.9	ARHGEF15	NM_173728.2	ARGEF15;FLJ13791;KIAA0915;MGC44868;V			

GI_32307168-A	149.2	167	145.2	DGKH	NM_152910.3	DGKeta;DKFZp761I1510	diacylglyc		protein
GI_32307169-I	105.3	120.4	100.3	DGKH	NM_178009.2	DGKeta;DKFZp761I1510	diacylglyc		protein
GI_32307170-S	349.7	432.2	388.7	DLST	NM_001933.3	DLTS			energy
GI_32307171-S	139	188	155.3	DPT	NM_001937.3	TRAMP	protein	extracellul	cell
GI_32307173-S	857.2	858.5	786.3	KDELR1	NM_006801.2	ERD2;HDEL;PM23;ERD2.1	KDEL	endoplas	intracellula
GI_32307174-S	433.1	481.3	402.2	KIAA1737	NM_033426.2				
GI_32307176-S	102.4	114.5	101	FOXG1B	NM_005249.3	BF1;QIN;FKH2;HFK1;FKHL1;FKHL4;HBF-1	DNA	nucleus	brain
GI_32307179-S	10588.4	12189	11575	CHCHD2	NM_016139.2	C7orf17			
GI_32307180-S	331.1	366.6	248.1	MGC24039	NM_144973.2				
GI_32307182-S	200.8	217.1	354.4	SEMA3C	NM_006379.2	SemE;SEMAE			drug
GI_32307183-S	97.2	126	91.2	SP4	NM_003112.2	HF1B;SPR-1	RNA	nucleus	regulation
GI_32308168-S	118.8	129.4	121.7	ZNF233	NM_181756.1				
GI_32313568-S	309.7	271.5	540.8	AGA	NM_000027.2	AGU	N4-(beta-	lysosome	protein
GI_32313574-A	919.2	733.2	714.6	AUP1	NM_181575.2		molecular		
GI_32313582-I	136.4	140	134.4	AUP1	NM_012103.2		molecular		
GI_32313586-S	128.2	141.6	136.1	CYP39A1	NM_016593.3		oxysterol	microsom	bile acid
GI_32313592-S	233.3	306.7	268.3	GW112	NM_006418.3	GC1			
GI_32313604-A	184.2	231.1	188.3	SPINT1	NM_003710.2	HAI;HAI1	serine	membran	
GI_32313609-S	105.5	174.2	138.7	USP18	NM_017414.2	ISG43;UBP43	ubiquitin-	nucleus	ubiquitin-
GI_32401415-S	207.9	210.8	195.1	FLJ12760	NM_181725.1				
GI_32401419-S	115.6	106.5	107.4	SYNPR	NM_144642.3	SPO;MGC26651	transporte	mitochond	transport
GI_32401423-S	651.9	1176.5	1092.2	MLP	NM_023009.4	F52;MRP;MLP1;MACMARCKS	calmoduli		neurogene
GI_32401432-S	199.7	203.3	183.8	GPR142	NM_181790.1	PGR2	receptor	integral to	G-protein
GI_32401434-S	166.9	195.4	167.6	GPR141	NM_181791.1	PGR13	rhodopsin-	integral to	G-protein
GI_32401436-S	115.1	138.1	126.9	LOC341567	NM_181788.1				
GI_32401438-S	118.2	127.8	120.4	CRG-L2	NM_181789.1				
GI_32401442-S	455.4	465.6	515.8	LOC286148	NM_181787.1				
GI_32401444-S	1014.2	879.5	819.5	SPRED2	NM_181784.1	Spred-2;FLJ21897;FLJ31917			
GI_32401446-S	392.6	451	361.8	LOC283537	NM_181785.1				
GI_32401450-S	157.7	226.6	212.1	FLJ90492	NM_181783.1				
GI_32401452-S	93.2	102.6	97.2	SLC36A2	NM_181776.1	PAT2;TRAMD1	amino	membran	amino
GI_32401458-S	643.5	546.8	534.7	FLJ11088	NM_018318.2	p56			
GI_32401472-S	175.5	226.5	202.8	BTLA	NM_181780.1	BTLA1			
GI_32441270-S	89.2	100.7	95.9	DCDC1	NM_181807.1				intracellula
GI_32441272-S	114	119.5	103.4	BMP8A	NM_181809.1		growth		growth
GI_32441282-I	124.6	125.6	137.7	RALGPS2	NM_152663.2	FLJ10244;FLJ25604	guanyl-		intracellula
GI_32451491-I	90.3	98.3	97.3	C14orf29	NM_181533.3	c14_5314			
GI_32454730-I	84.7	88.8	92.4	WINS1	NM_181739.1	FLJ10583			
GI_32454732-A	283.2	309.9	301.4	WINS1	NM_181740.1	FLJ10583			
GI_32454732-I	127.1	120.5	116.9	WINS1	NM_181740.1	FLJ10583			
GI_32454736-A	342.9	408	358.3	TRIM3	NM_033278.2	BERP;HAC1;RNF22;RNF97	protein C-	kinesin	neurogene
GI_32454738-I	415.5	575.5	469.3	TRIM3	NM_006458.2	BERP;HAC1;RNF22;RNF97	protein C-	kinesin	neurogene
GI_32454740-S	1475.3	2899.9	1238.1	SERPINH1	NM_001235.2	CBP1;CBP2;gp46;HSP47;RA-	collagen	endoplas	response
GI_32454742-S	2895.8	959.3	1063	SESN2	NM_031459.3	HI95;SES2;SEST2;DKFZp761M0212;DKFZp		nucleus	cell cycle

GI_32454743-S	739.7	912.6	687.3	STRN3	NM_014574.2	SG2NA	calmoduli	kinesin	cell cycle
GI_32454745-A	185.4	200.6	188	ORC4L	NM_181741.1	ORC4;ORC4P	DNA	nucleus	DNA
GI_32454751-S	850.1	703.4	624	ORC2L	NM_006190.3	ORC2	DNA	nucleus	DNA
GI_32454752-I	1936.9	1309.2	1071.3	ORC5L	NM_002553.2	ORC5;ORC5P;ORC5T	DNA	nucleus	DNA
GI_32454753-A	238.5	220.5	176.7	ORC5L	NM_181747.1	ORC5;ORC5P;ORC5T	DNA	nucleus	DNA
GI_32454753-I	91.1	94.8	87.4	ORC5L	NM_181747.1	ORC5;ORC5P;ORC5T	DNA	nucleus	DNA
GI_32454755-S	181.6	176.6	177.5	ORC6L	NM_014321.2	ORC6	DNA	nucleus	DNA
GI_32455232-S	123.3	138.1	116.8	LAD1	NM_005558.3	LadA;MGC10355	structural	basement	
GI_32455233-S	315.2	325.8	336.7	LCMT2	NM_014793.3	MGC9534;KIAA0547			
GI_32455234-S	152.5	163.8	133.5	LCN1	NM_002297.2	TP;PMFA;VEGP	cysteine		proteolysis
GI_32455235-S	186.4	223.9	198.1	HELB	NM_033647.2				
GI_32455237-A	2058.3	2206.7	1029.6	HSD11B1	NM_005525.2	HDL;11-DH;HSD11L;MGC13539;11-beta-	11-beta-	microsom	steroid
GI_32455237-I	105.9	107.8	111.3	HSD11B1	NM_005525.2	HDL;11-DH;HSD11L;MGC13539;11-beta-	11-beta-	microsom	steroid
GI_32455240-S	72.4	93.3	89.2	HAPLN3	NM_178232.2	HsT19883	hyaluronic		cell
GI_32455241-S	93	99	101.5	HGFAC	NM_001528.2	HGFA	serine-	extracellul	proteolysis
GI_32455242-S	2726.5	3076.4	3608.6	PPP2R1A	NM_014225.3	MGC786	protein		
GI_32455243-A	236.6	295	301.5	PPP2R1B	NM_181699.1	MGC26454	protein		
GI_32455243-I	135.5	149.9	136.3	PPP2R1B	NM_181699.1	MGC26454	protein		
GI_32455245-I	277.1	336.6	303.6	PPP2R1B	NM_002716.3	MGC26454	protein		
GI_32455247-I	187.5	221.2	187.6	PIK3R1	NM_181523.1	GRB1;p85-ALPHA			
GI_32455249-I	105.1	113.8	100.3	PIK3R1	NM_181524.1	GRB1;p85-ALPHA			
GI_32455251-A	312.7	231.4	466.5	PIK3R1	NM_181504.2	GRB1;p85-ALPHA			
GI_32455251-I	81.2	88	78.5	PIK3R1	NM_181504.2	GRB1;p85-ALPHA			
GI_32455253-A	1419.2	1603.1	1607.4	LASS2	NM_013384.3	L3;SP260;TMSG1;MGC987;FLJ10243	transcripti	nucleus	regulation
GI_32455258-I	2353.4	1961.6	2020	PRDX5	NM_012094.3	PLP;ACR1;B166;PRXV;PMP20;PRDX6;SBBI	electron	peroxisom	respiratory
GI_32455261-A	8220.4	7451.5	7471	PRDX5	NM_181652.1	PLP;ACR1;B166;PRXV;PMP20;PRDX6;SBBI	electron	peroxisom	respiratory
GI_32455265-A	9694.7	14289	11917	PRDX1	NM_181697.1	PAG;PAGA;PAGB;MSP23;NKEFA;TDPX2	peroxidas		skeletal
GI_32455268-S	261.9	264.2	185.2	PKE	NM_173575.2	MGC23665	ATP		protein
GI_32455270-S	355.2	471.3	479.1	POMT2	NM_013382.3		mannosylt	membran	O-linked
GI_32455272-S	134.9	128.3	118	PRKWNK2	NM_006648.3	WNK2;NY-CO-43;SDCCAG43;P/OKcl.13	ATP		protein
GI_32469494-S	175.5	195.5	179.9	TRIK	NM_181840.1	TRESK	ion	membran	potassium
GI_32469500-S	135.8	157.4	160.6	TMC3	NM_181841.1				
GI_32469508-S	179.6	167.4	151.3	C6orf46	NM_181842.1	G10;NG35;D6S59E	protein	nucleus	regulation
GI_32469514-S	496.5	426.4	458.8	NUDT8	NM_181843.1				
GI_32479518-A	210.1	163	199.6	DVL1	NM_181870.1	DVL;MGC54245	signal	cytoplasm	heart
GI_32479520-I	152.9	154.8	150.2	DVL1	NM_004421.2	DVL;MGC54245	signal	cytoplasm	heart
GI_32479522-A	130.9	122.4	134.4	KCNQ1	NM_181797.1	LQT;RWS;WRS;LQT1;KCNA8;KCNA9;Kv1.9	delayed	voltage-	potassium
GI_32479522-I	116.6	110.3	108.9	KCNQ1	NM_181797.1	LQT;RWS;WRS;LQT1;KCNA8;KCNA9;Kv1.9	delayed	voltage-	potassium
GI_32479524-I	159.6	178.5	157.7	KCNQ1	NM_181798.1	LQT;RWS;WRS;LQT1;KCNA8;KCNA9;Kv1.9	delayed	voltage-	potassium
GI_32479526-I	124.3	144.1	144.1	KCNQ1	NM_000218.2	LQT;RWS;WRS;LQT1;KCNA8;KCNA9;Kv1.9	delayed	voltage-	potassium
GI_32481204-A	155.4	164.6	290.3	LAIR2	NM_021270.2				
GI_32481205-S	95.6	87.2	95.4	LCT	NM_002299.2	LAC;LPH	lactase	membran	carbohydr
GI_32481207-I	106.8	127.5	117.7	MAPKAPK2	NM_004759.3		protein	nucleus	MAPKKK
GI_32481208-A	821.7	920.8	750.2	MAPKAPK2	NM_032960.2		protein	nucleus	MAPKKK

GI_32481210-S	131.9	147	130.4	NALP5	NM_153447.2	MATER	ATP		
GI_32481212-S	1024.8	1291.8	1029.2	MK-STYX	NM_016086.2		protein		intracellula
GI_32481214-S	121	121.3	128.9	CD19	NM_001770.3	B4;MGC12802	receptor	integral to	cell
GI_32481215-I	231.5	238	214	COG5	NM_006348.2	GTC90;GOLTC1	protein	membran	intra-Golgi
GI_32481217-A	333.9	256.5	263.4	COG5	NM_181733.1	GTC90;GOLTC1	protein	membran	intra-Golgi
GI_32483356-S	852.6	833.8	700.8	DHRS4	NM_021004.2	SDR-SRL;humNRDR;FLJ11008;SCAD-SRL	electron	peroxisom	carbohydr
GI_32483362-A	290.3	293.6	217	APAF1	NM_181869.1	CED4	caspase	cytosol	neurogene
GI_32483368-A	574.8	575.8	491.9	ORC3L	NM_181837.1	LAT;ORC3;LATHEO	DNA	nucleus	DNA
GI_32483370-A	558	328.9	406.2	GEM	NM_181702.1	KIR;MGC26294	GTP	peripheral	cell growth
GI_32483372-I	143.7	123.8	107.1	GEM	NM_005261.2	KIR;MGC26294	GTP	peripheral	cell growth
GI_32483373-S	1228.5	858.5	457.8	NOL5A	NM_006392.2	NOP56	RNA	nucleolus	ribosome
GI_32483375-S	1728.9	1487.3	1129.6	NYREN18	NM_016118.3	NUB1	molecular	nucleus	biological_
GI_32483376-A	2292.9	2714	2797.4	PRDX3	NM_014098.2	AOP1;MER5;AOP-1;SP-	alkyl	mitochond	peroxidas
GI_32483379-S	141.1	160.5	141.8	ICOS	NM_012092.2	AILIM;MGC39850	receptor	integral to	positive
GI_32483382-I	124.5	149.7	148.2	PKIG	NM_181805.1		cAMP-		negative
GI_32483384-A	604.2	884.1	862.1	PKIG	NM_007066.3		cAMP-		negative
GI_32483385-A	543.8	531.4	479.4	PKIA	NM_181839.1	PRKACN1	cAMP-		negative
GI_32483387-I	146.8	173	157.7	PKIA	NM_006823.2	PRKACN1	cAMP-		negative
GI_32483388-A	96.7	117.1	104.2	PKIB	NM_032471.4	PRKACN2	cAMP-		negative
GI_32483389-I	98.7	97	80.8	PKIB	NM_181794.1	PRKACN2	cAMP-		negative
GI_32483393-A	579.7	505.2	678.6	CLTB	NM_001834.2	LCB	calcium	coated pit	intracellula
GI_32483394-I	93.3	88.1	97.5	CLTB	NM_007097.2	LCB	calcium	coated pit	intracellula
GI_32483395-S	177.3	190.1	172.5	DGKI	NM_004717.2	DGK-IOTA	diacylglyc	cytoplasm	protein
GI_32483396-S	224.5	260.8	221.8	DRD4	NM_000797.2	D4DR	dopamine	integral to	dopamine
GI_32483398-S	976.2	1138.8	1047.4	PAK2	NM_002577.2	PAK65;PAKgamma	protein		negative
GI_32483400-S	106.2	98.4	104.5	PCK1	NM_002591.2	PEPCK1;PEPCKC;MGC22652	phosphoe	cytosol	glucose
GI_32483402-S	101.2	109.8	98.8	PDYN	NM_024411.2	MGC26418	opioid	plasma	neuropepti
GI_32483407-A	476.9	558.4	538.6	GABPB2	NM_016655.2	E4TF1;GABPB;BABPB2;E4TF1B;GABPB1;N	transcripti	nucleus	regulation
GI_32483408-S	191.5	226.8	208.5	GATA1	NM_002049.2	GF1;NFE1;ERYF1	transcripti	nucleus	regulation
GI_32483409-S	108.8	105.1	113.2	GC	NM_000583.2	DBP;VDBG;VDBP	vitamin D	extracellul	vitamin/co
GI_32483411-A	119.4	119.9	116.2	GJA5	NM_181703.1	CX40;MGC11185	connexon	gap	intercellula
GI_32483411-I	121.9	110	108.4	GJA5	NM_181703.1	CX40;MGC11185	connexon	gap	intercellula
GI_32483413-I	88.6	87.4	90.2	GJA5	NM_005266.4	CX40;MGC11185	connexon	gap	intercellula
GI_32483414-S	136.1	133.5	140	GZMB	NM_004131.3	HLP;CCPI;CGL1;CSPB;SECT;CGL-1;CSP-	granzyme	cytoplasm	proteolysis
GI_32483415-S	108.3	117.8	120.4	NEFH	NM_021076.2	NFH;KIAA0845	molecular	neurofilam	neurogene
GI_32484972-I	454.3	457.9	445.7	ADK	NM_001123.2	AK	adenosine		ribonucleo
GI_32484974-A	4261.4	3933	3678.6	ADK	NM_006721.2	AK	adenosine		ribonucleo
GI_32484974-I	201.7	198.5	161.1	ADK	NM_006721.2	AK	adenosine		ribonucleo
GI_32484976-S	96	106.8	87.2	AMOTL2	NM_016201.2	LCCP;KIAA0989			
GI_32484978-S	1152	1350.5	1475.3	AP3B1	NM_003664.3	PE;HPS;HPS2;ADTB3;ADTB3A	protein	Golgi	intracellula
GI_32484980-S	144.2	154.9	134.5	BANK1	NM_017935.2	BANK;FLJ20706	pancreatic	nucleus	metabolis
GI_32484984-S	166.1	201.2	167.9	FS	NM_021996.3	MGC44848;UDP-GalNAc	transferas	membran	glycolipid
GI_32484986-S	383.1	481	399.3	HCA112	NM_018487.2				
GI_32484988-S	1986.3	1702.2	1892.4	MTR3	NM_058219.2				

GI_32484989-S	1952.4	2407.5	3008.3	WSB2	NM_018639.3	SBA2;MGC10210			intracellula
GI_32490556-S	2015.4	1981.6	1455.2	PAPOLA	NM_032632.2	PAP;MGC5378	RNA	cytoplasm	mRNA
GI_32490558-S	5366.5	4633.7	4437.2	LRP10	NM_014045.2	MGC8675;DKFZP564C1940			
GI_32490566-S	146.4	143.2	150.6	GPR100	NM_181885.1	GPCR142	angiotensi	integral to	G-protein
GI_32490571-S	4278.7	3507.4	2704.3	EPB41L3	NM_012307.2	4.1B;DAL1;DAL-1;KIAA0987	actin	cytoskelet	biological_
GI_32490573-A	101.8	117.3	114.8	DMRT2	NM_181872.1		transcripti	nucleus	male
GI_32490578-A	2980.3	2748.2	2446.3	CRA	NM_181873.1				
GI_32490578-I	261.6	272.4	230.6	CRA	NM_181873.1				
GI_32490588-A	123.9	133.3	102.9	PRX	NM_181882.1	CMT4F;KIAA1620	molecular	membran	nerve
GI_32526889-S	317.1	343.7	376.4	FLJ40629	NM_152515.2	MGC39683	DNA	nucleus	regulation
GI_32526891-S	207.6	225.7	196	FLJ25200	NM_144715.2				
GI_32526893-S	136.8	139	130.8	FLJ35834	NM_178827.3				
GI_32526895-A	249.6	285.2	281.3	HSPC056	NM_015396.2	DKFZP434A043			
GI_32526895-I	1162.9	1026.3	1164.8	HSPC056	NM_015396.2	DKFZP434A043			
GI_32526899-S	227.8	264.9	264.7	DCL-1	NM_014880.3	BIMLEC;KIAA0022	sugar	integral to	heterophili
GI_32526900-I	228.3	289.1	234.3	CDV-1	NM_014055.2	CDV1;CDV1R;MGC4027			
GI_32526906-S	76.9	105.8	117.8	FOXQ1	NM_033260.2	HFH1	transcripti	nucleus	regulation
GI_32526910-S	134.3	163.4	179.6	DKFZp434L1	NM_016613.4	AD021;AD036			
GI_32526912-S	98.9	110.9	99.2	FLJ25453	NM_153716.1	HSFY	transcripti	nucleus	regulation
GI_32528262-I	101.5	102.2	96.7	CDK10	NM_003674.2	PISSLRE	cyclin-		negative
GI_32528264-A	1567.7	1458.9	1441.1	CDK10	NM_052987.2	PISSLRE	cyclin-		negative
GI_32528265-I	209.8	256.6	228.2	CDK10	NM_052988.2	PISSLRE	cyclin-		negative
GI_32528267-I	95.6	92.5	94.3	GRM7	NM_181874.1	GLUR7;mGlu7;GPRC1G;MGLUR7	metabotro	integral to	negative
GI_32528269-A	168.9	211.3	193.4	GRM7	NM_181875.1	GLUR7;mGlu7;GPRC1G;MGLUR7	metabotro	integral to	negative
GI_32528269-I	95.1	106.7	91.1	GRM7	NM_181875.1	GLUR7;mGlu7;GPRC1G;MGLUR7	metabotro	integral to	negative
GI_32528272-A	102.5	93.3	91	GRIA3	NM_181894.1	GLUR3;GLURC;GLUR-K3	alpha-	integral to	small
GI_32528272-I	125	133.6	119.2	GRIA3	NM_181894.1	GLUR3;GLURC;GLUR-K3	alpha-	integral to	small
GI_32528277-I	90	102.8	92.4	BACH	NM_181862.1	ACT;ACH1;LACH1;hBACH;CTE-II;MGC1126	acyl-CoA	cytoplasm	lipid
GI_32528281-I	192.4	286.6	375.8	BACH	NM_181864.1	ACT;ACH1;LACH1;hBACH;CTE-II;MGC1126	acyl-CoA	cytoplasm	lipid
GI_32528283-I	102.2	97	98.2	BACH	NM_181865.1	ACT;ACH1;LACH1;hBACH;CTE-II;MGC1126	acyl-CoA	cytoplasm	lipid
GI_32528285-A	4806.8	10179	13094	BACH	NM_181866.1	ACT;ACH1;LACH1;hBACH;CTE-II;MGC1126	acyl-CoA	cytoplasm	lipid
GI_32528285-I	241.5	1169.9	1186.6	BACH	NM_181866.1	ACT;ACH1;LACH1;hBACH;CTE-II;MGC1126	acyl-CoA	cytoplasm	lipid
GI_32528290-I	103.8	107.4	108.7	COVA1	NM_182314.1	APK1;tNOX	protein	cytosol	electron
GI_32528292-A	189.3	238.2	202.4	COVA1	NM_006375.2	APK1;tNOX	protein	cytosol	electron
GI_32528294-I	314.1	207.2	201.6	RPS6KA5	NM_004755.2	MSK1;RLPK;MSPK1;MGC1911	protein	nucleus	DNA
GI_32528296-A	136.8	120.1	110	RPS6KA5	NM_182398.1	MSK1;RLPK;MSPK1;MGC1911	protein	nucleus	DNA
GI_32528296-I	93.7	107.7	91.5	RPS6KA5	NM_182398.1	MSK1;RLPK;MSPK1;MGC1911	protein	nucleus	DNA
GI_32528298-S	485.9	587.7	541.3	BIRC4	NM_001167.2	API3;ILP1;MIHA;XIAP	apoptosis	cytosol	anti-
GI_32528300-S	396.1	455.6	391.9	EPHB4	NM_004444.3	HTK;MYK1;TYRO11	transmem	integral to	histogene
GI_32528302-S	110.2	117.1	94.5	INSM2	NM_032594.2	IA-6;mlt1			
GI_32528304-I	345.3	451.5	493.7	PIP5K2B	NM_003559.3	Pip4k2B;PIP5KIIB	1-	cytoplasm	cell
GI_32528305-S	390.3	384.3	324.4	RFC1	NM_002913.3	A1;RFC;PO-	ATP	DNA	DNA
GI_32528307-S	140	151.5	141.6	SYT8	NM_138567.2	DKFZp434K0322			
GI_32528309-A	113.3	105.4	87	C14orf29	NM_181814.1	c14_5314			

GI_32563526-S	597	468.4	384.4	C10orf28	NM_014472.2	PSORT;GIDRP86			
GI_32567783-S	399.1	483.2	418.7	TBX10	NM_005995.2		RNA	nucleus	embryoge
GI_32698673-S	713.3	586.2	477.7	TRIP8	NM_004241.1	FLJ14374;KIAA1380;DKFZp761F0118	ligand-	intracellula	regulation
GI_32698675-S	1037.4	1310.6	3058.6	LHFPL2	NM_005779.1	KIAA0206			
GI_32698677-S	351.2	399.6	356.3	ZNF213	NM_004220.1	CR53	transcripti	nucleus	regulation
GI_32698685-S	120.1	137.7	123.3	GALNT5	NM_014568.1	GALNAC-T5	UDP-		N-linked
GI_32698687-S	542.5	511.8	500.2	CIT	NM_007174.1	CRIK;STK21;KIAA0949	protein	kinesin	protein
GI_32698689-S	99.5	110.2	109.4	HUMPPA	NM_014603.1		DNA	nucleus	regulation
GI_32698691-S	3750.5	3389.3	3752.5	ZDHHC8	NM_013373.1	ZNF378;ZDHHCL1;KIAA1292		integral to	
GI_32698693-S	1439.2	1027.7	1118.8	KIAA0276	NM_015115.1				
GI_32698695-S	1313.3	921.7	765.5	MAC30	NM_014573.1		molecular	cellular_co	regulation
GI_32698699-S	109.1	132.3	105.5	KIAA1111	NM_015107.1		DNA		regulation
GI_32698701-S	1725.3	1760.2	1610.5	HECTD1	NM_015382.1	KIAA1131	ubiquitin-	intracellula	ubiquitin
GI_32698703-S	178.1	193	208.3	DKFZP434B0	NM_015395.1				
GI_32698709-S	104.9	103.5	99	DKFZP566D1	NM_015391.1				
GI_32698715-S	210	244.1	222.4	HUMRTVLH3	NM_015860.1				
GI_32698717-S	131.7	132.4	121.1	C9orf36	NM_015667.1	DKFZP434B204			
GI_32698727-S	3082.1	2336.9	3181.2	FAM20C	NM_020223.1	DKFZp547D065			
GI_32698729-S	189.1	268.4	209.6	182-FIP	NM_020772.1	KIAA1321			
GI_32698731-S	650.6	706.3	895.6	KIAA1363	NM_020792.1		hydrolase		metabolis
GI_32698733-S	93.1	104.9	97.8	DAZ4	NM_020420.1	pDP1680;pDP1681			
GI_32698735-S	85.9	100	102.3	ARRDC3	NM_020801.1	KIAA1376			sensory
GI_32698737-S	233.5	310.2	266.3	ZNF471	NM_020813.1	ERP1;Z1971;KIAA1396		nucleus	
GI_32698739-S	400.7	367	343.8	SH3MD2	NM_020870.1	POSH;RNF142;SH3RF1;KIAA1494			
GI_32698741-S	140.2	137.8	141.5	KIAA1573	NM_020925.1		electron	membran	electron
GI_32698743-S	235.6	214.2	235.1	USP37	NM_020935.1	KIAA1594	cysteine-		ubiquitin-
GI_32698745-S	200.8	215.1	179	HCN1	NM_021072.1	BCNG1;HAC-2;BCNG-1	voltage-	integral to	cation
GI_32698747-S	167	162	174.2	ZNF248	NM_021045.1	bA162G10.3	nucleic	nucleus	regulation
GI_32698749-S	306.9	371.1	370.7	SR-A1	NM_021228.1				
GI_32698751-S	741.3	938	943.6	C20orf177	NM_022106.1	dJ551D2.5			
GI_32698754-S	140	163	119.5	CPEB4	NM_030627.1	KIAA1673	nucleic		
GI_32698756-S	2453.9	877	180.9	LOC81569	NM_030812.1				
GI_32698758-S	92.6	115.2	97.3	SYT14L	NM_031914.1	yt14r;syt14r;Strep14;CHR14SYT	transporte	membran	transport
GI_32698760-S	162.9	146.1	166.9	ZNF528	NM_032423.1	KIAA1827			
GI_32698762-S	144.3	140.6	126.4	FBXL10	NM_032590.1	CXXC2;PCCX2			
GI_32698764-S	159.3	186.2	161	FGD3	NM_033086.1	ZFYVE5;FLJ00004	zinc ion		
GI_32698766-S	329.6	358.7	332.6	KUB3	NM_033276.1		metallope	DNA-	double-
GI_32698768-S	226.5	157.7	154	FLJ00058	NM_052847.1				
GI_32698770-S	111.6	117.7	133.2	KIAA1893	NM_052899.1				
GI_32698772-S	1162.3	1230.7	694	C8orf13	NM_053279.1	D8S265;DKFZp761G151		kinesin	
GI_32698774-S	135.5	143.1	132.8	ZNF431	NM_133473.1	KIAA1969	nucleic	intracellula	regulation
GI_32698776-S	400.5	409.6	676.4	FLJ34969	NM_152678.1				
GI_32698778-S	169.7	151.9	112.4	MGC45474	NM_152369.2				
GI_32698779-S	90.7	92.4	92.1	CMYA5	NM_153610.2	DKFZp451G182			

GI_32698783-S	182.7	249.4	212.1	GPR120	NM_181745.1	PGR4	receptor	integral to	G-protein
GI_32698785-S	480.3	481.8	429.9	ZNF227	NM_182490.1		nucleic	intracellula	regulation
GI_32698787-S	109.4	132.5	121.8	LOC124773	NM_181707.1				
GI_32698789-S	108.6	111	93.6	LOC346673	NM_182489.1				
GI_32698791-S	102	112.4	105.8	POLN	NM_181808.1	POL4P	DNA-		DNA
GI_32698794-S	215.4	245.8	249.8	LOC169611	NM_182487.1		latrotoxin	membran	
GI_32698814-S	104.4	122.9	106.9	USP12	NM_182488.1	USP12L1	cysteine-	cellular_co	ubiquitin-
GI_32698821-S	848.7	525.4	484.3	LOC90637	NM_182491.1		electron		electron
GI_32698823-S	228.3	256.3	231.2	DKFZp434O	NM_182492.1			membran	
GI_32698825-S	106.6	123.4	101.8	LOC91807	NM_182493.1		ATP		protein
GI_32698827-S	98.7	99.4	91.2	LOC119395	NM_182494.1				
GI_32698829-S	89.5	89.4	84.5	FLJ40089	NM_182496.1				
GI_32698831-S	100	100.5	104.2	FLJ36600	NM_182497.1				
GI_32698834-S	114.4	147.7	141	DKFZp434M2	NM_182499.1				
GI_32698836-S	88	97	89.3	FLJ25143	NM_182500.1				
GI_32698840-S	97.3	107	102.2	DKFZp686L1	NM_182502.1		trypsin		proteolysis
GI_32698844-S	103.3	98	94.9	DEADC1	NM_182503.1	dJ20N2.1;DKFZp686L1118	zinc ion		
GI_32698850-S	225.8	307.5	269.7	FLJ32965	NM_182506.1				
GI_32698852-S	1517.6	1031.4	1678.4	LOC144501	NM_182507.1				
GI_32698854-S	123.7	136.4	129.4	FLJ40919	NM_182508.1				
GI_32698858-S	111.5	114.7	110.7	FLJ32252	NM_182510.1		DNA	nucleus	regulation
GI_32698863-S	366.8	431.8	399.5	MGC52423	NM_182517.1				
GI_32698865-S	250.1	376.1	490.8	Spc24	NM_182513.1	FLJ90806			
GI_32698867-S	98.7	87.1	87.5	C20orf186	NM_182519.1	RY2G5;LPLUNC4;dJ726C3.5	lipid		
GI_32698869-S	109	106.9	97.7	FLJ32011	NM_182516.1				
GI_32698871-S	115.3	130.3	103.1	ZSWIM2	NM_182521.1	ZZZ2;MGC33890	zinc ion		
GI_32698873-S	183.9	218.5	227.4	LOC149469	NM_182518.1				
GI_32698875-S	660.1	641	583.5	MGC61571	NM_182523.1				
GI_32698877-S	203.5	238.6	205.5	FLJ36561	NM_182520.1				
GI_32698879-S	87.6	97.7	86.4	FLJ32770	NM_182525.1				
GI_32698883-S	117.2	114.8	104.6	CABP7	NM_182527.1	MGC57793	calcium		
GI_32698885-S	120.7	130.8	110.9	ZNF595	NM_182524.1		nucleic	intracellula	regulation
GI_32698887-S	97.2	89.2	93.7	THAP5	NM_182529.1				
GI_32698889-S	112.5	94.8	96.6	FLJ33387	NM_182526.1				
GI_32698891-S	158.5	159.3	137.6	FLJ31875	NM_182531.1		nucleic	intracellula	regulation
GI_32698893-S	176.9	170.7	499.3	LOC165257	NM_182528.1				
GI_32698895-S	239.8	295.8	216.5	FLJ31031	NM_182533.1				
GI_32698897-S	211	274.3	244	FLJ25056	NM_182530.1				
GI_32698899-S	117.6	138.7	125.6	LOC200261	NM_182535.1				
GI_32698901-S	104.8	125.6	117.6	LOC199964	NM_182532.1				
GI_32698903-S	128.1	132.5	112.9	HTR3D	NM_182537.1		receptor		
GI_32698905-S	87.8	110.4	89	FLJ23703	NM_182534.1				
GI_32698909-S	125.8	130.3	141.6	MGC33600	NM_182539.1				
GI_32698911-S	149.6	161.9	156.9	LOC203522	NM_182540.1				

GI_32698913-S	170	214.3	181.7	MGC39655	NM_182541.1				
GI_32698915-S	117.2	134.4	135.4	FLJ32682	NM_182542.1				
GI_32698917-S	426.7	437.1	348.2	NOPD1	NM_182543.1	FLJ23743	S-		
GI_32698923-S	119.7	140.4	119.6	MGC40170	NM_182550.1		DNA	nucleus	regulation
GI_32698925-S	94.3	97	87	MGC33530	NM_182546.1				
GI_32698931-S	149.7	155	138.2	LOC282966	NM_182554.1				
GI_32698933-S	95.8	123.7	120.2	UNQ1849	NM_182551.1	FLJ37965	acyltransf		metabolis
GI_32698935-S	362.6	354.1	342.3	BCL9L	NM_182557.1	DLNB11			
GI_32698937-S	446.6	577	763.1	MGC50896	NM_182553.1				
GI_32698939-S	174.1	194.8	157	MGC57341	NM_182559.1		trypsin		proteolysis
GI_32698941-S	331.6	465.3	491.5	LOC283130	NM_182556.1				
GI_32698943-S	84.8	96.7	83.3	FLJ36144	NM_182561.1				
GI_32698945-S	97.6	102.8	99.4	FLJ33810	NM_182558.1				
GI_32698947-S	100.8	104.4	103	GDDR	NM_182536.1				
GI_32698951-S	100	132.8	107.8	FLJ25773	NM_182560.1				
GI_32698955-S	135.7	142.9	162	FLJ39743	NM_182562.1				
GI_32698957-S	123.8	129.5	116.3	FLJ34690	NM_182567.1				
GI_32698959-S	97.9	106.3	99.8	FLJ40319	NM_182564.1				
GI_32698961-S	199.9	172.5	141.1	FLJ37451	NM_182569.1		glyceroph		glycerol
GI_32698963-S	115.9	122.9	122	LOC284013	NM_182566.1				
GI_32698967-S	117.2	131.2	126.6	FLJ36492	NM_182568.1				
GI_32698969-S	186.8	233.6	206.5	FLJ36070	NM_182574.1		DNA	nucleus	
GI_32698971-S	105.6	109	108.4	FLJ25715	NM_182570.1				
GI_32698973-S	178.7	200.1	178.8	MGC39821	NM_182576.1		phospholi		lipid
GI_32698975-S	105.1	125.2	112.2	FLJ30469	NM_182573.1				
GI_32698977-S	102.9	107.4	87.3	FLJ37964	NM_182578.1		catalytic		
GI_32698979-S	127.7	142.9	126.7	MGC34799	NM_182575.1				
GI_32698981-S	820.4	1050.6	891.1	FLJ39035	NM_182580.1			integral to	electron
GI_32698983-S	291.4	361	364.2	C19orf19	NM_182577.1	FLJ40059			
GI_32698985-S	133.5	158.7	136.6	MGC34919	NM_182582.1				
GI_32698987-S	124.2	140.7	130.9	FLJ40343	NM_182579.1				
GI_32698989-S	166.3	193.9	186.3	FLJ33706	NM_182584.1				
GI_32698991-S	223.2	300	252.7	LOC284680	NM_182581.1				
GI_32698993-S	95.4	95.1	93.7	DKFZp451M2	NM_182585.1				
GI_32698995-S	98.1	115.1	105.4	FLJ38374	NM_182583.1				
GI_32698997-S	132.2	143.3	128.7	C2orf21	NM_182587.1	FLJ33496			
GI_32699000-S	94.7	94.1	83.2	FLJ33651	NM_182590.1		DNA	nucleus	regulation
GI_32699002-S	97	116.9	101.3	FLJ33534	NM_182586.1				
GI_32699004-S	124.3	127.4	111.1	FLJ39576	NM_182592.1				
GI_32699006-I	260.4	317.6	292.4	HTR3E	NM_182589.1	5-HT3c1			
GI_32699008-S	373.1	433.9	398.3	DKFZp564N2	NM_182595.1				
GI_32699010-S	119	125.1	105.3	FLJ37673	NM_182591.1				
GI_32699012-S	96.9	112.8	101.7	FLJ36980	NM_182598.1				
GI_32699014-S	266.8	323.5	306	ZNF454	NM_182594.1	FLJ37444	nucleic	nucleus	regulation

GI_32699016-S	122.8	114	121.5	LOC286359	NM_182600.1				
GI_32699018-S	147.4	159.5	144.8	FLJ39575	NM_182597.1				
GI_32699020-S	210.2	228.4	195.8	FLJ36131	NM_182604.1				
GI_32699022-S	117.6	131.2	116.6	FLJ37523	NM_182599.1				
GI_32699025-S	104.5	126.7	118.2	FLJ37874	NM_182603.1		calcium		
GI_32699029-S	139.6	145.3	136.3	FLJ40448	NM_182605.1				
GI_32699032-S	118.9	104.7	97.4	LOC339967	NM_182606.1		trypsin		proteolysis
GI_32699037-S	123.4	151.4	135.2	SAMD7	NM_182610.1	DKFZp686E1583			
GI_32699041-S	99	107.7	100.1	GPR144	NM_182611.1	PGR24	G-protein	integral to	neuropepti
GI_32699044-S	1266.1	1512.9	1301.5	FLJ34283	NM_182612.1				
GI_32699049-S	124.7	211.9	193.4	MGC61550	NM_182616.1				
GI_32699051-S	90.3	122.2	92.5	LOC348158	NM_182617.1		ligase		metabolis
GI_32699053-S	187.6	213.5	178.7	FAM33A	NM_182620.1				
GI_32699055-S	112.5	118.4	116.7	MGC52498	NM_182621.1				
GI_32699057-S	499.8	533.7	509.1	FLJ36766	NM_182623.1				
GI_32699059-S	152.4	175.1	159.7	FLJ40869	NM_182625.1				
GI_32699061-S	109.9	102.2	100.6	FLJ25102	NM_182626.1				
GI_32699063-S	359.4	346.5	353.8	MGC64882	NM_182627.1				
GI_32699065-S	87	94.5	87.2	FLJ40083	NM_182628.1		toxin	extracellul	pathogene
GI_32699069-S	93.5	106.8	100	LOC348840	NM_182631.1				
GI_32699071-S	135.8	145	126.6	FLJ31236	NM_182632.1		neurotran	membran	neurotran
GI_32699073-S	155.4	202.1	181.5	FLJ36166	NM_182634.1				
GI_32699075-S	263.3	246.4	194.9	LOC349236	NM_182635.1				
GI_32699144-S	97.8	93.8	94.5	BAGE5	NM_182484.1				
GI_32699146-S	87.5	91.8	88.6	BAGE4	NM_181704.1				
GI_32699148-S	127.2	115.6	124.6	BAGE3	NM_182481.1				
GI_32699150-S	99.6	94.7	100.7	BAGE2	NM_182482.1				
GI_32813442-A	515.1	643.2	577.7	CTDSP1	NM_182642.1	SCP1;NLIIF			
GI_32813444-S	191.4	203.9	169.3	HKR2	NM_181846.1	ZNF50	DNA	nucleus	regulation
GI_32813446-S	396.1	498.4	476.7	DKFZp686P0	NM_182588.1				
GI_32813448-S	149.1	150.7	144.2	FLJ25037	NM_182596.1				
GI_32880194-S	1162	2123.9	2654.5	M-RIP	NM_015134.1	RHOIP3;KIAA0864			
GI_32880198-S	1037.4	944.3	782.8	MKRN2	NM_014160.3	RNF62;HSPC070	nucleic	intracellula	biological_
GI_32880200-S	112.7	117.8	102.4	SDK1	NM_152744.2	FLJ31425			
GI_32880202-A	200.9	238.9	197.9	CDH24	NM_144985.2	CDH11L;FLJ25193	hydrogen-	membran	homophili
GI_32880205-I	117.8	133	119.1	CDH24	NM_022478.2	CDH11L;FLJ25193	hydrogen-	membran	homophili
GI_32880207-S	228.1	216.9	242	DIAPH3	NM_030932.2	DRF3;DKFZP434C0931	actin	kinesin	cytokinesi
GI_32880228-S	2051.6	2387	2387.5	SELO	NM_031454.1	IMAGE3510317			
GI_32895360-A	98.1	107.9	99.3	LIR9	NM_181879.1	CD85F;ILT11;LILRB7			
GI_32895364-I	114.3	117.6	111.1	LIR9	NM_181986.1	CD85F;ILT11;LILRB7			
GI_32895366-I	97	96.9	92.7	LIR9	NM_021250.2	CD85F;ILT11;LILRB7			
GI_32895367-A	297.9	245.9	157.4	COL8A1	NM_020351.2	MGC9568	collagen	microfibril	cell
GI_32895369-I	100.4	111.2	95	COL8A1	NM_001850.3	MGC9568	collagen	microfibril	cell
GI_32964822-S	195	222.2	205.3	C20orf185	NM_182658.1	RYA3;LPLUNC3;dJ726C3.4	lipid		

GI_32964824-S	95.9	101.7	93.1	C6orf206	NM_152732.2	FLJ30845;MRPS18AL1			
GI_32964828-S	77.4	101.2	90.9	COL24A1	NM_152890.4		extracellul	collagen	cell
GI_32964829-S	150.5	213.1	148.3	COL8A2	NM_005202.1	FECD;PPCD;PPCD2;FLJ00201	collagen	basement	vision
GI_32964831-S	172.7	215.6	205.9	MGC42174	NM_152383.2				
GI_32967253-I	152.4	197.7	174.3	NF2	NM_181825.1	ACN;SCH;BANF	tumor	cytoskelet	negative
GI_32967275-A	1241.9	1335.2	1537	UBE2A	NM_181762.1	UBC2;HHR6A;RAD6A	ubiquitin	nucleus	postreplic
GI_32967277-I	77.7	86.4	77.2	UBE2A	NM_181777.1	UBC2;HHR6A;RAD6A	ubiquitin	nucleus	postreplic
GI_32967281-S	198.8	210.2	191.9	UBE2B	NM_003337.2	HR6B;UBC2;HHR6B;RAD6B;E2-17kDa	ubiquitin	nucleus	postreplic
GI_32967282-I	137.5	141.6	143.7	UBE2C	NM_181799.1	UBCH10;dJ447F3.2	ubiquitin-		cyclin
GI_32967288-I	117	134.8	128.8	UBE2C	NM_181802.1	UBCH10;dJ447F3.2	ubiquitin-		cyclin
GI_32967290-A	1450.8	1180.6	2430.8	UBE2C	NM_181803.1	UBCH10;dJ447F3.2	ubiquitin-		cyclin
GI_32967293-I	137.9	162.2	157.9	C1QTNF6	NM_031910.3	CTRP6;ZACRP6		microfibril	
GI_32967299-A	323.7	1178.3	284.4	C1QTNF6	NM_182486.1	CTRP6;ZACRP6		microfibril	
GI_32967301-I	122.1	145.7	131	CERK	NM_022766.4	LK4;hCERK;FLJ21430;FLJ23239;KIAA1646;			
GI_32967302-A	1168.7	1363.8	1530	CERK	NM_182661.1	LK4;hCERK;FLJ21430;FLJ23239;KIAA1646;			
GI_32967304-I	157.1	202.6	162.9	COQ6	NM_182476.1	CGI-10	monooxyg		ubiquinon
GI_32967306-A	546.4	715.4	570.5	COQ6	NM_182480.1	CGI-10	monooxyg		ubiquinon
GI_32967306-I	136.6	146.8	142	COQ6	NM_182480.1	CGI-10	monooxyg		ubiquinon
GI_32967308-S	112.1	102.1	103.6	EPHA1	NM_005232.2	EPH;EPHT;EPHT1	transmem	integral to	signal
GI_32967310-S	4477.5	3118.3	3302.1	EPHA2	NM_004431.2	ECK	transmem	integral to	signal
GI_32967312-I	90.6	86.2	95.2	EPHA3	NM_005233.3	ETK;HEK;ETK1;HEK4;TYRO4	transmem	integral to	signal
GI_32967313-A	120.5	128.3	122.1	EPHA3	NM_182644.1	ETK;HEK;ETK1;HEK4;TYRO4	transmem	integral to	signal
GI_32967313-I	115.6	128.7	121.7	EPHA3	NM_182644.1	ETK;HEK;ETK1;HEK4;TYRO4	transmem	integral to	signal
GI_32967316-I	168.4	217.1	173.6	EPHA5	NM_004439.3	CEK7;EHK1;HEK7;TYRO4	transmem	integral to	transmem
GI_32967318-A	100.1	94.7	88.7	EPHA5	NM_182472.1	CEK7;EHK1;HEK7;TYRO4	transmem	integral to	transmem
GI_32967320-S	206.9	245.3	213.8	EPHA7	NM_004440.2	EHK3;HEK11	transmem	integral to	transmem
GI_32967513-A	234.4	246	243.2	NF2	NM_181831.1	ACN;SCH;BANF	tumor	cytoskelet	negative
GI_32967585-A	979.9	835	879.3	PPP2R3A	NM_181897.1	PPP2R3	protein		
GI_32967585-I	126.8	144	164.5	PPP2R3A	NM_181897.1	PPP2R3	protein		
GI_32967587-I	92	90.4	78.9	PPP2R2C	NM_020416.2	PR52;IMYPNO;IMYPNO1;MGC33570	protein	protein	signal
GI_32967589-A	117.3	127.9	117.6	PDC	NM_022576.2	PHD;MEKA;PhLP;PhLOP	phospholi	soluble	phototrans
GI_32967590-I	116.9	111.7	114	PDC	NM_002597.3	PHD;MEKA;PhLP;PhLOP	phospholi	soluble	phototrans
GI_32967592-A	136.7	149.2	147.1	PPP2R2C	NM_181876.1	PR52;IMYPNO;IMYPNO1;MGC33570	protein	protein	signal
GI_32967592-I	122	122.4	104.8	PPP2R2C	NM_181876.1	PR52;IMYPNO;IMYPNO1;MGC33570	protein	protein	signal
GI_32967594-I	1245.4	1244.4	1116.4	PPP2R3A	NM_002718.3	PPP2R3	protein		
GI_32967595-I	194.7	222.9	208.6	PKLR	NM_000298.3	PK1;PKL;RPK	pyruvate		glycolysis
GI_32967596-A	101.1	108.9	106.6	PKLR	NM_181871.1	PK1;PKL;RPK	pyruvate		glycolysis
GI_32967596-I	118.6	117.9	101.6	PKLR	NM_181871.1	PK1;PKL;RPK	pyruvate		glycolysis
GI_32967598-A	117	125.7	105.7	ANK3	NM_001149.2		structural	Golgi	cytoskelet
GI_32967598-I	106.7	117.8	79.6	ANK3	NM_001149.2		structural	Golgi	cytoskelet
GI_32967600-I	95.7	96.5	98.9	ANK3	NM_020987.2		structural	Golgi	cytoskelet
GI_32967602-I	132.6	140.3	139.9	BAZ1A	NM_013448.2	ACF1;WALp1;hACF1;WCRF180;DKFZP586	DNA	kinesin	regulation
GI_32967604-A	662	677.1	532.1	BAZ1A	NM_182648.1	ACF1;WALp1;hACF1;WCRF180;DKFZP586	DNA	kinesin	regulation
GI_32967606-S	108.9	111.5	107.2	GPX2	NM_002083.2	GSHPX-GI	glutathion	cytoplasm	peroxidas

GI_32967608-S	321.8	451.2	355.7	SLC13A1	NM_022444.3	NAS1;NaSi-1	transporte	integral to	sulfate
GI_32996732-A	149.3	154.6	135.5	RASSF5	NM_182664.1	RAPL;Maxp1;NORE1;RASSF3;MGC10823			
GI_32996734-I	125.7	115.6	122.6	RASSF5	NM_182665.1	RAPL;Maxp1;NORE1;RASSF3;MGC10823			
GI_32996736-S	201.3	196.7	162.3	TGS	NM_173083.2				
GI_33086946-S	768.4	853.7	955.3	MGC20481	NM_052849.2				
GI_33147079-S	946.5	658.4	649	AMSH-LP	NM_020799.1	AMSH-FP;KIAA1373			
GI_33147083-S	367.1	333.5	341.2	CDAN1	NM_138477.1	CDA1;CDAI;CDA-I;codanin			
GI_33149302-I	186	207.4	180.9	UPK3B	NM_030570.2	P35;UPIIIb;FLJ32198;MGC10902		endoplas	
GI_33149303-A	117.4	106.4	113.2	UPK3B	NM_182683.1	P35;UPIIIb;FLJ32198;MGC10902		endoplas	
GI_33149305-I	101.6	106	103.8	UPK3B	NM_182684.1	P35;UPIIIb;FLJ32198;MGC10902		endoplas	
GI_33149307-S	153	160.4	148.8	UBE2D1	NM_003338.3	SFT;UBCH5;UBC4/5;UBCH5A;E2(17)KB1	ubiquitin		ubiquitin-
GI_33149315-I	93	95.8	107.1	UBE2D3	NM_181889.1	UBC4/5;UBCH5C;MGC5416;MGC43926;E2(	ubiquitin		ubiquitin-
GI_33149321-I	143.9	179.2	139.5	UBE2D3	NM_181892.1	UBC4/5;UBCH5C;MGC5416;MGC43926;E2(	ubiquitin		ubiquitin-
GI_33149323-A	4992.7	4614.3	4396.2	UBE2D3	NM_181893.1	UBC4/5;UBCH5C;MGC5416;MGC43926;E2(	ubiquitin		ubiquitin-
GI_33149325-S	104.3	108.5	99.3	AVPR1A	NM_000706.3	AVPR1	vasopress	endosome	cytosolic
GI_33149330-S	254.7	520.6	168.8	NXN	NM_022463.3	FLJ12614			
GI_33186853-S	349.8	271.1	433.4	TOM1L2	NM_144678.2	FLJ32746	DNA	Golgi	intra-Golgi
GI_33186855-S	98.2	112.9	112.9	GCET2	NM_152785.2	HGAL;GCAT2;MGC40441			
GI_33186881-S	134.5	153.1	141.6	TESSP2	NM_182702.1		trypsin		proteolysis
GI_33186883-S	79.1	91.8	97.3	DDX53	NM_182699.1	CAGE	nucleic		
GI_33186894-S	127.5	132.2	128	SELV	NM_182704.1				
GI_33186900-S	722.6	799.9	773.7	MGC45871	NM_182705.1				
GI_33186904-S	387.3	477.6	448.5	MPRP-1	NM_145243.2		metallope	membran	proteolysis
GI_33186909-A	1531.2	1237.4	1257.7	SCRIB	NM_182706.1	CRIB1;SCRB1;SCRIB1;Vartul;KIAA0147	protein		intracellula
GI_33186909-I	121.2	133.5	119.8	SCRIB	NM_182706.1	CRIB1;SCRB1;SCRIB1;Vartul;KIAA0147	protein		intracellula
GI_33186919-S	112.8	135.4	132.9	DKFZp761B1	NM_173463.2				
GI_33186924-S	219.2	253.1	227	PRKAG2	NM_016203.2	AAKG;WPWS;AAKG2;H91620P	molecular	cellular_co	cholestero
GI_33186926-A	616.6	564.9	413.8	C3orf6	NM_174908.2				
GI_33187364-S	549.9	513.8	557.8	EIF5A2	NM_020390.5	EIF-5A2;eIF5AII	translation		translation
GI_33188426-I	96.6	110.1	109.3	UTY	NM_182659.1	UTY1		nucleus	
GI_33188428-A	108.8	121.3	113.3	UTY	NM_182660.1	UTY1		nucleus	
GI_33188428-I	129.9	161.8	143.4	UTY	NM_182660.1	UTY1		nucleus	
GI_33188430-I	233.4	251.5	229	UTY	NM_007125.3	UTY1		nucleus	
GI_33188434-A	246.9	287.5	254.3	DLC1	NM_024767.2	HP;ARHGAP7;STARD12;FLJ21120;p122-	GTPase	cytoplasm	signal
GI_33188434-I	127.2	123.7	124.9	DLC1	NM_024767.2	HP;ARHGAP7;STARD12;FLJ21120;p122-	GTPase	cytoplasm	signal
GI_33188436-I	120.3	120.9	106.4	DLC1	NM_006094.3	HP;ARHGAP7;STARD12;FLJ21120;p122-	GTPase	cytoplasm	signal
GI_33188438-I	112.3	106.4	106.2	CPEB2	NM_182485.1				
GI_33188442-I	101.2	106.4	92.5	MACF1	NM_033044.2	ACF7;MACF;ABP620;KIAA0465;KIAA1251			
GI_33188444-A	2635.3	2260.5	1546.4	MACF1	NM_012090.3	ACF7;MACF;ABP620;KIAA0465;KIAA1251			
GI_33188444-I	127.3	145.3	132.8	MACF1	NM_012090.3	ACF7;MACF;ABP620;KIAA0465;KIAA1251			
GI_33188446-I	157.3	166.3	250.4	SRPK2	NM_182691.1	SFRSK2	protein	nucleus	RNA
GI_33188448-I	107.1	117.9	106.5	SRPK2	NM_182692.1	SFRSK2	protein	nucleus	RNA
GI_33188453-A	520.3	959.8	720.2	PRDX2	NM_181738.1	PRP;TSA;NKEFB;PRXII;TDPX1;MGC4104	thioredoxi	cytoplasm	killer
GI_33188453-I	95.2	105.6	94.7	PRDX2	NM_181738.1	PRP;TSA;NKEFB;PRXII;TDPX1;MGC4104	thioredoxi	cytoplasm	killer

GI_33188455-I	117.5	125.2	118.8	UBE2D2	NM_181838.1	UBC4;PUBC1;UBC4/5;UBCH5B;E2(17)KB2	ubiquitin		ubiquitin-
GI_33188457-A	502.3	491.3	465.9	UBE2D2	NM_003339.2	UBC4;PUBC1;UBC4/5;UBCH5B;E2(17)KB2	ubiquitin		ubiquitin-
GI_33188458-S	305.9	284.6	297.2	BRAF	NM_004333.2	BRAF1;RAFB1	protein		anti-
GI_33188460-S	193.5	203.3	199.2	GATA4	NM_002052.2		transcripti	nucleus	transcripti
GI_33188462-S	823.3	815.1	599	MRPS9	NM_182640.1	RPMS9			
GI_33188464-S	95.8	109.6	102.1	VIPR2	NM_003382.3		G-protein	integral to	signal
GI_33238871-S	444.8	519.9	453.1	RECQL5	NM_004259.3	RECQ5	DNA		DNA
GI_33239373-S	424.2	425	298.1	MGC3794	NM_152902.2	dJ69E11.3			
GI_33239438-S	365.8	374.5	346.1	SLC25A17	NM_006358.2	PMP34	carrier	peroxisom	small
GI_33239439-S	102.6	97	116.9	ZFY	NM_003411.2		DNA	nucleus	regulation
GI_33239441-I	78.4	96.7	87	SYPL	NM_006754.2	H-SP1	transporte	synaptic	nonselecti
GI_33239442-A	459.8	456.2	461.7	SYPL	NM_182715.1	H-SP1	transporte	synaptic	nonselecti
GI_33239442-I	432.1	547.5	476.5	SYPL	NM_182715.1	H-SP1	transporte	synaptic	nonselecti
GI_33239444-I	138.4	193.8	144.3	EIF3S9	NM_003751.2	PRT1;EIF3-ETA;EIF3-P110;EIF3-P116	translation	eukaryotic	translation
GI_33239446-A	2631.6	2949.7	2540.9	EIF3S9	NM_182712.1	PRT1;EIF3-ETA;EIF3-P110;EIF3-P116	translation	eukaryotic	translation
GI_33239448-S	108.5	143.4	132.7	CYP26B1	NM_019885.2	CYP26A2;P450RAI-2	monooxyg	membran	electron
GI_33239449-I	114.8	128.9	116.7	PCNA	NM_002592.2	MGC8367	proliferatin	delta-DNA	DNA
GI_33239450-A	1685.8	2595.3	1523.8	PCNA	NM_182649.1	MGC8367	proliferatin	delta-DNA	DNA
GI_33239450-I	1182.8	1885.7	1030.3	PCNA	NM_182649.1	MGC8367	proliferatin	delta-DNA	DNA
GI_33285003-S	896.8	945.2	818	ZNF574	NM_022752.2	FLJ22059			
GI_33285005-S	457	432	470.9	C9orf9	NM_018956.3		DNA	nucleus	regulation
GI_33285007-S	224.8	254.7	215.9	GYLTL1B	NM_152312.2	FLJ35207			
GI_33285009-S	204.4	241.7	205.3	FLJ22390	NM_022746.2				
GI_33285012-S	310.2	417	277.6	FLJ12800	NM_022903.2	FLJ13629	DNA	nucleus	regulation
GI_33285014-S	271	257.2	241.4	MGC24976	NM_144598.2				
GI_33286413-A	146	173.5	185.9	HPS1	NM_182639.1	HPS;MGC5277		lysosome	lysosome
GI_33286413-I	400.7	440.9	541.6	HPS1	NM_182639.1	HPS;MGC5277		lysosome	lysosome
GI_33286417-A	6503.9	9420	8758.1	PKM2	NM_002654.3	PK3;PKM;TCB;OIP3;CTHBP;THBP1;MGC39			
GI_33286417-I	1189.7	2092.3	2065.5	PKM2	NM_002654.3	PK3;PKM;TCB;OIP3;CTHBP;THBP1;MGC39			
GI_33286419-I	118.3	140.5	123.6	PKM2	NM_182470.1	PK3;PKM;TCB;OIP3;CTHBP;THBP1;MGC39			
GI_33286423-I	157.5	194.6	172.2	OPRL1	NM_182647.1	OOR;ORL1;KOR-3;NOCIR;MGC34578	G-protein	integral to	G-protein
GI_33286425-A	216.2	185.4	174.6	OPRL1	NM_000913.3	OOR;ORL1;KOR-3;NOCIR;MGC34578	G-protein	integral to	G-protein
GI_33286426-S	107	98.2	96.3	SLC6A4	NM_001045.2	SERT;5-HTT	serotonin	integral to	serotonin
GI_33286427-I	156.1	180.5	180.2	SLC7A8	NM_012244.2	LAT2;LPI-PC1	neutral	integral to	small
GI_33286429-A	133.6	170.4	136.6	SLC7A8	NM_182728.1	LAT2;LPI-PC1	neutral	integral to	small
GI_33286429-I	142.6	177.8	161.1	SLC7A8	NM_182728.1	LAT2;LPI-PC1	neutral	integral to	small
GI_33286433-A	796.5	901.6	708.2	NSFL1C	NM_182483.1	p47;MGC3347;dJ776F14.1			
GI_33286435-I	150.7	161.6	139.4	GGN	NM_152657.3	FLJ35713;MGC33369			
GI_33286437-A	161.8	190.2	185.1	GGN	NM_182477.1	FLJ35713;MGC33369			
GI_33286441-S	306.7	377.2	326.7	FLJ11362	NM_021946.2				
GI_33286443-S	151.8	161.9	121.7	MAML2	NM_032427.1	MAM2;MAM3;MAM-3;MAML3;KIAA1819			
GI_33286445-S	721	759.6	804.4	OGFR	NM_007346.2		opioid	membran	cell growth
GI_33286447-S	475.1	796.5	611.4	PKD2	NM_000297.2	PKD4;APKD2	cytoskelet	voltage-	cation
GI_33300634-S	1303.7	1252.5	1444.2	ZFPL1	NM_006782.2	MCG4;D11S750			

GI_33300636-S	781.5	776.3	625.6	FLJ10036	NM_017975.2				
GI_33300638-S	296.7	292.3	315.3	DKFZp547E0	NM_032276.2				
GI_33300644-S	214.2	268.9	219.1	LOC157740	NM_182753.1				
GI_33300646-S	126.5	134.4	138.2	C8orf5	NM_182754.1				
GI_33300648-S	130.2	155.9	138.3	LOC284467	NM_182759.1				
GI_33300650-S	278.4	251.8	258.8	LOC220929	NM_182755.1				
GI_33300652-S	123.2	129.7	131.3	SPY1	NM_182756.1				
GI_33300654-S	91	102.2	77.8	LOC340069	NM_182761.1				
GI_33300656-S	244.7	223.7	161.7	FLJ38736	NM_182758.1				
GI_33300660-S	107.2	117.6	120.4	7A5	NM_182762.1				
GI_33300662-S	199	239.5	227.5	MGC16202	NM_032373.2				
GI_33300664-I	274.5	331.2	300.1	MUC1	NM_182741.1	EMA;PEM;PUM;CD227	actin	cytoskelet	
GI_33300667-S	87.1	93.4	80.6	PMS2L2	NM_002679.1	PMS4			
GI_33300669-I	484.4	383.1	392.2	MGC15416	NM_138418.2				
GI_33342275-S	109.6	118.8	105.3	FLJ22761	NM_025130.2				
GI_33342277-S	325.6	331	289.8	PP2447	NM_025204.2				
GI_33342279-I	139.5	126.3	107.2	FLJ37306	NM_182765.1	DKFZp761D0614	ubiquitin-	intracellula	ubiquitin
GI_33350927-S	112.8	113.7	120.3	DAB1	NM_021080.3				developm
GI_33350929-S	116	114.5	97.9	C6orf107	NM_017754.2	FLJ20302;dJ349A12.1	NADH	NADH	mitochond
GI_33350931-S	10995.1	10112	9185	DNCH1	NM_001376.2	p22;DHC1;DNCL;DYHC;HL-	adenosine	cytoplasmi	mitosis
GI_33354243-A	171.5	179.5	230.4	NELF	NM_182780.1				
GI_33354243-I	114.6	108	98.8	NELF	NM_182780.1				
GI_33354248-S	91.1	101.7	96.1	DNAJA4	NM_018602.2	PRO1472	chaperone		protein
GI_33354256-S	191.7	261.4	216.7	GPR83	NM_016540.2	GIR;GPR72	G-protein	integral to	G-protein
GI_33354272-S	97.9	89.3	87.6	ZIM2	NM_015363.3		zinc ion	nucleus	regulation
GI_33354274-S	126.4	104.2	91.7	FLJ10521	NM_018125.2				
GI_33354278-S	94.9	93.9	87.5	LSR7	NM_018559.2	AD029;KIAA1704			
GI_33354280-A	306.6	269.9	271.3	SLC6A15	NM_182767.1	V7-3;NTT73;hv7-3;FLJ10316			
GI_33354280-I	313.6	191.6	228.2	SLC6A15	NM_182767.1	V7-3;NTT73;hv7-3;FLJ10316			
GI_33354282-S	207.5	195.5	172.7	DET1	NM_017996.2	FLJ10103			
GI_33354284-S	232.6	300.7	268.8	PEG3	NM_006210.1	PW1;KIAA0287	signal	nucleus	regulation
GI_33356127-I	189.8	186.2	193.6	FLJ22054	NM_024561.3	PRO2435;MGC40612			
GI_33356129-A	119.6	132.1	138.1	FLJ22054	NM_018527.2	PRO2435;MGC40612			
GI_33356129-I	117.3	112.6	128.6	FLJ22054	NM_018527.2	PRO2435;MGC40612			
GI_33356133-S	117.4	115.7	108.8	FLJ25770	NM_178555.2	MGC35086			
GI_33356135-S	359.6	377.3	339.8	FLJ31340	NM_152748.2				
GI_33356137-A	89.2	97.7	89.9	FLJ32940	NM_182766.1	FLJ25438			
GI_33356141-S	448.6	321.8	286.5	C9orf91	NM_153045.2	FLJ38045;DKFZp547P234	binding	mitochond	transport
GI_33356147-S	446.3	364.5	349.8	FMNL1	NM_005892.3	FMNL;FHOD4;KW-			
GI_33356153-A	854.4	890	639.8	UBE2H	NM_182697.1	UBC8;UBCH;UBCH2;E2-20K	ubiquitin		ubiquitin-
GI_33356156-S	149.6	210.4	185.9	ARP10	NM_181773.2				
GI_33356159-S	78.4	78.1	84.1	CCKBR	NM_176875.2	GASR	cholecysto	integral to	phosphati
GI_33356162-S	918.6	991.9	967.2	EIF1AY	NM_004681.2		translation		translation
GI_33356164-S	133.5	182.2	146.3	HOOK3	NM_032410.2	HK3	microtubul	Golgi	Golgi

GI_33356165-S	779.6	831.8	637.4	KIAA1002	NM_014925.2	PR01365			
GI_33356169-S	272.6	301.3	309.6	MYO9B	NM_004145.2	MYR5	myosin	perinuclea	neuropepti
GI_33356171-S	829.6	679.5	804.5	NBS1	NM_002485.3	ATV;NBS;AT-V1;AT-V2;NIBRIN	DNA	nucleus	cell cycle
GI_33356173-S	187.2	219.7	176.1	PNN	NM_002687.2	DRS;SDK3	structural	intermedia	cell
GI_33356175-S	522.5	725.5	590.3	SATB1	NM_002971.2		double-	nucleus	establish
GI_33356176-S	1580	1923.6	1881.5	PTPN11	NM_002834.3	CFC;NS1;SHP2;BPTP3;PTP2C;PTP-	non-		signal
GI_33356178-S	400.3	471.4	441.2	TTF1	NM_007344.2		transcripti	nucleus	transcripti
GI_33356540-A	265.7	359.8	317.4	PLTP	NM_182676.1		lipid	extracellul	lipid
GI_33356542-I	249.9	300.1	289.8	PLTP	NM_006227.2		lipid	extracellul	lipid
GI_33356543-I	155.5	165.5	165.6	PLCB1	NM_182734.1	PLC-I;PI-PLC;PLC-154	phosphoin	cytoplasm	signal
GI_33356545-A	184.3	136.4	158.3	PLCB1	NM_015192.2	PLC-I;PI-PLC;PLC-154	phosphoin	cytoplasm	signal
GI_33356546-S	6764.3	4981.5	6647.1	MCM2	NM_004526.2	BM28;CCNL1;CDCL1;D3S3194;KIAA0030;M	adenosine	chromatin	cell cycle
GI_33356548-S	3664.5	3519.7	4166.9	MCM3	NM_002388.3	HCC5;P1.h;RLFB;MGC1157;P1-MCM3	adenosine	alpha	DNA
GI_33356553-I	129.5	143.2	131.8	FLJ20249	NM_017725.1	DKFZP434F1735	nucleic	intracellula	
GI_33356557-A	176.1	186.7	171.4	AMELX	NM_182681.1	AMG;AIH1;ALGN;AMGL;AMGX	extracellul	extracellul	ossificatio
GI_33356559-S	305	358.9	348.9	JARID1D	NM_004653.2	HY;HYA;SMCY;KIAA0234	DNA	nucleus	regulation
GI_33356561-S	149.1	113.8	286.7	VENTX2	NM_014468.2	NA88A;HPX42B	transcripti	nucleus	regulation
GI_33359209-S	98	104.4	91.9	PKD1L1	NM_138295.2			integral to	
GI_33359210-I	375	457.3	444.4	FLJ36525	NM_182774.1	DKFZp686I0110			
GI_33359212-S	213	250.6	249.1	PKD1	NM_000296.2	PBP		integral to	calcium-
GI_33359216-I	101.4	104	103.5	FLJ36525	NM_182775.1	DKFZp686I0110			
GI_33359218-I	132.3	141.8	128.8	PKD1-like	NM_182686.1	PP791;KIAA1837			
GI_33359220-A	413	535.5	597.7	PKD1-like	NM_024874.3	PP791;KIAA1837			
GI_33359220-I	853	1082	1033.8	PKD1-like	NM_024874.3	PP791;KIAA1837			
GI_33359222-S	123.4	129.2	121.8	ZFD25	NM_016220.2		DNA	nucleus	regulation
GI_33359679-A	168.7	328.3	238.5	EFNA1	NM_182685.1	B61;EFL1;ECKLG;EPLG1;LERK1;TNFAIP4	transmem	membran	cell-cell
GI_33359681-I	138.2	194	160.8	EFNA1	NM_004428.2	B61;EFL1;ECKLG;EPLG1;LERK1;TNFAIP4	transmem	membran	cell-cell
GI_33359683-S	375	454.6	390.8	EFNA3	NM_004952.3	EFL2;EPLG3;LERK3	transmem	membran	cell-cell
GI_33359684-I	347.4	405.4	360.5	EFNA4	NM_005227.2	EFL4;EPLG4;LERK4	transmem	membran	cell-cell
GI_33359685-A	213.3	322.2	276.3	EFNA4	NM_182689.1	EFL4;EPLG4;LERK4	transmem	membran	cell-cell
GI_33359689-S	1975.1	1482.4	2157.9	EFNB2	NM_004093.2	HTKL;EPLG5;Htk-L;LERK5	transmem	integral to	histogene
GI_33359690-A	463	498.3	357.8	UBE2E1	NM_182666.1	UBCH6	ubiquitin		ubiquitin-
GI_33359693-A	2349.5	3079.3	2884.6	UBE2E3	NM_182678.1	UBCH9;UbcM2	ubiquitin		ubiquitin-
GI_33359693-I	90.8	100.3	85.6	UBE2E3	NM_182678.1	UBCH9;UbcM2	ubiquitin		ubiquitin-
GI_33359696-A	287.7	322.2	218.7	UBE2G1	NM_182682.1	UBC7;E217K;UBE2G	ubiquitin		ubiquitin-
GI_33359698-I	622	803.9	706.9	UBE2G1	NM_003342.3	UBC7;E217K;UBE2G	ubiquitin		ubiquitin-
GI_33359699-A	955.1	866.3	612.5	UBE2G2	NM_003343.4	UBC7	ubiquitin		ubiquitin-
GI_33359700-I	129.4	136.5	146.6	UBE2G2	NM_182688.1	UBC7	ubiquitin		ubiquitin-
GI_33383230-A	1271.7	1356.5	1007	ARS2	NM_015908.3	ASR2	molecular	cellular_co	response
GI_33383232-I	94.2	94.7	92.2	ARS2	NM_182800.1	ASR2	molecular	cellular_co	response
GI_33383234-A	328.8	318.7	380.8	MCM10	NM_018518.3	PRO2249			
GI_33383240-A	180.4	200	179.4	PKMYT1	NM_004203.3	MYT1	protein	Golgi	regulation
GI_33386694-A	477.2	405.5	440.9	PBEF1	NM_182790.1	PBEF	cytokine		positive
GI_33386694-I	85.3	96.4	84	PBEF1	NM_182790.1	PBEF	cytokine		positive

GI_33386698-S	259.9	251.9	216.8	TMSL1	NM_182792.1				
GI_33386700-S	878.5	813.2	646.2	TMSL4	NM_182794.1				
GI_33386702-S	178.4	225.1	204.1	TMSL2	NM_182793.1				
GI_33391149-S	90.8	98	93.4	NPM2	NM_182795.1		nucleic	nucleus	regulation
GI_33413399-S	3937	3094.3	3192.4	ESD	NM_001984.1		serine	cytoplasmi	biological_
GI_33413401-A	210.6	233.1	220.2	APOB48R	NM_182804.1		lipoprotein	nucleus	lipid
GI_33413413-S	93.2	85.2	96.9	FRAS1	NM_025074.2	FLJ14927;FLJ22031;KIAA1500	electron		electron
GI_33413424-S	126.3	129.9	135.1	KIAA1582	NM_018996.2	FLJ20015	nucleic		
GI_33413430-A	118.2	125.9	101.2	TLX2	NM_001534.2	Enx;NCX;HOX11L1	molecular	nucleus	regulation
GI_33413430-I	95.7	107.7	97.3	TLX2	NM_001534.2	Enx;NCX;HOX11L1	molecular	nucleus	regulation
GI_33438574-S	147.1	136.9	120.5	ZNF8	NM_021089.1	HF.18	DNA	nucleus	regulation
GI_33438579-S	146.2	191	172.9	FLJ20203	NM_032292.3	FLJ12923;FLJ23040;KIAA1606;DKFZp761I2			
GI_33438581-S	356.6	355	373.2	TROAP	NM_005480.2	TASTIN	cell	cytoplasm	cell
GI_33438585-S	163.4	196.7	167.3	ZNF77	NM_021217.1	pT1	DNA	nucleus	regulation
GI_33438589-S	105.1	110.8	91.4	DMRTC1	NM_033053.1				
GI_33438591-S	98	107.7	101.3	ZNF534	NM_182512.1	KRBO3;FLJ25344	nucleic	intracellula	regulation
GI_33438593-S	241.7	300.2	263.8	HLA-DQB2	NM_182549.1	HLA-DXB	MHC	integral to	immune
GI_33438597-S	103.5	120.9	94.4	MGC48625	NM_182609.1		nucleic	intracellula	regulation
GI_33438599-S	121.7	127.4	118	FLJ39963	NM_182633.1		nucleic	nucleus	regulation
GI_33457296-S	116.6	141.1	120.6	GDF7	NM_182828.1				
GI_33457298-S	130.2	149.8	127.4	TNT	NM_182831.1				
GI_33457300-S	401.3	501.2	453	LOC220032	NM_182833.1				
GI_33457305-S	99.1	88.1	72.9	PLAC4	NM_182832.1				
GI_33457307-S	435.3	534.2	470.9	HNLF	NM_182547.2		protein	membran	intracellula
GI_33457310-S	377.4	397.9	449.3	MGC5987	NM_138476.2				
GI_33457315-S	217.3	221.5	186.6	pp9099	NM_025201.3	PP1628;DKFZp761K2312			
GI_33457321-S	136.1	167.9	155.8	LOC136306	NM_174959.1		transporte	integral to	transport
GI_33457323-S	93.9	86.8	82.1	MGC46496	NM_174952.1				
GI_33457325-S	143.9	180	153.1	GSH1	NM_145657.1	Gsh-1	transcripti	nucleus	regulation
GI_33457327-S	126.2	129.5	119.4	LOC90668	NM_138360.1				
GI_33457329-S	165.2	192	168.9	TTC14	NM_133462.1	FLJ00166;KIAA1980	RNA		
GI_33457331-S	422.4	495.6	495.8	RAVER1	NM_133452.1	KIAA1978	nucleic		
GI_33457333-S	583.4	575.8	527.1	TRIM47	NM_033452.1	GOA;RNF100	zinc ion	intracellula	
GI_33457343-S	439.4	411.5	348.2	COG6	NM_020751.1	COD2;KIAA1134	protein	membran	intracellula
GI_33457347-S	5432	6742.6	6319.8	C19orf10	NM_019107.1	IL25;IL27;SF20;IL-25;IL-			
GI_33457353-S	262.2	336.9	417.9	BAK1	NM_001188.2	BAK;CDN1;BCL2L7	apoptosis	integral to	apoptotic
GI_33457354-S	162.9	177.3	150.4	C6orf151	NM_152551.2	FLJ32234;dJ512B11.2;dJ336K20B.1			
GI_33466360-S	834.7	836.1	1288.7	ARFRP1	NM_003224.2	ARP	small	peripheral	signal
GI_33468964-S	247.1	210.6	197.6	KIAA1143	NM_020696.1				
GI_33469020-S	112.8	113.2	114.4	KIAA1796	NM_032439.1				
GI_33469134-S	561.3	588.3	378.8	FRMD4	NM_018027.2	FLJ10210;KIAA1294;bA295P9.4			
GI_33469136-A	144.3	172.5	137.4	SLC35E2	NM_182838.1	KIAA0447			
GI_33469136-I	151.4	177.8	140.4	SLC35E2	NM_182838.1	KIAA0447			
GI_33469142-S	179.7	176.5	181.6	LRRK1	NM_024652.2	FLJ23119;KIAA1790	protein-	nucleus	protein

GI_33469144-S	97.2	110.5	104.5	LOC158160	NM_182829.1		oxidoredu		metabolis
GI_33469146-I	2281.5	2879	2452	SLC35E2	NM_014854.1	KIAA0447			
GI_33469915-S	1162.2	1058.9	1014.1	MCM3AP	NM_003906.3	GANP;MAP80;KIAA0572	adenosine	nucleus	protein-
GI_33469916-A	654.9	638.5	806.7	MCM4	NM_182746.1	CDC21;CDC54;hCdc21;MGC33310;P1-	adenosine	chromatin	DNA
GI_33469918-I	128.9	118.3	121	MCM4	NM_005914.2	CDC21;CDC54;hCdc21;MGC33310;P1-	adenosine	chromatin	DNA
GI_33469920-S	237	173.1	188.8	MCM6	NM_005915.4	Mis5;P105MCM;MCG40308	DNA	nucleus	cell cycle
GI_33469921-I	130.7	152.6	128.4	MCM7	NM_182776.1	MCM2;CDC47;P85MCM;P1CDC47;PNAS-		chromatin	DNA
GI_33469923-I	96.8	85.9	75.3	MCM8	NM_182802.1	MGC4816;MGC12866;C20orf154;dJ967N21.	DNA		cell cycle
GI_33469925-A	1059.5	1262.4	1113.3	MCM8	NM_032485.4	MGC4816;MGC12866;C20orf154;dJ967N21.	DNA		cell cycle
GI_33469926-S	85	87.4	69	MCMDC1	NM_153255.2	MGC35304;dJ329L24.3	ATP		DNA
GI_33469927-S	86	88.1	75.3	FLJ20097	NM_024553.2	FLJ23581;KIAA1861			
GI_33469928-I	128	145	128.5	FLJ39155	NM_152403.2				
GI_33469936-A	201.8	227.3	194.4	FLJ39155	NM_182801.1				
GI_33469936-I	160.4	192.2	176.1	FLJ39155	NM_182801.1				
GI_33469938-A	429.1	374.3	190.7	PLCB4	NM_182797.1	PI-PLC	phospholi		intracellula
GI_33469940-S	1354.1	1030.8	752.5	POLR1B	NM_019014.2	RPA135;Rpo1-2;FLJ10816;FLJ21921			
GI_33469942-S	98.2	107.7	87.2	FKBP9L	NM_182827.1	MGC20531			
GI_33469944-A	216.2	249.5	282.6	ELMO2	NM_022086.6	CED12;FLJ11656;KIAA1834		membran	phagocyto
GI_33469948-I	118.3	123	124.1	RABGGTA	NM_004581.2		RAB-		vision
GI_33469950-A	850	925.3	985.9	RABGGTA	NM_182836.1		RAB-		vision
GI_33469953-A	695.8	438	390.6	RBM12	NM_152838.2	SWAN;KIAA0765;HRIHFB2091	RNA	nucleus	
GI_33469954-S	250.8	667.1	1018.5	MAOA	NM_000240.2		amine	membran	biogenic
GI_33469957-S	212.5	223.5	218.5	SDS	NM_006843.2	SDH	L-serine		L-serine
GI_33469961-I	154.4	150.6	142.6	SF4	NM_182812.1	RBP;F23858;DKFZp434E2216			
GI_33469963-A	561.9	629	577.8	SF4	NM_172231.2	RBP;F23858;DKFZp434E2216			
GI_33469967-A	7765.4	6957.7	8847.9	MCM7	NM_005916.3	MCM2;CDC47;P85MCM;P1CDC47;PNAS-		chromatin	DNA
GI_33469967-I	92.5	96.7	98.4	MCM7	NM_005916.3	MCM2;CDC47;P85MCM;P1CDC47;PNAS-		chromatin	DNA
GI_33469969-A	294.6	315.5	315.6	AADAT	NM_182662.1	KATII	transamin		
GI_33469969-I	88.9	95.4	94.4	AADAT	NM_182662.1	KATII	transamin		
GI_33469971-I	122.9	114.7	118.8	AADAT	NM_016228.3	KATII	transamin		
GI_33469972-S	494	413.7	404.3	ABHD5	NM_016006.3	CDS;CGI58;IECN2;NCIE2;MGC8731	aminopept		proteolysis
GI_33469973-A	3031.3	2270.8	1569	ATF4	NM_182810.1	CREB2;TXREB;CREB-2;TAXREB67	RNA	nucleus	regulation
GI_33469975-I	254.6	299.7	220	ATF4	NM_001675.2	CREB2;TXREB;CREB-2;TAXREB67	RNA	nucleus	regulation
GI_33469977-A	2069.6	2410.6	2036.5	SCFD1	NM_182835.1	RA410;KIAA0917;STXBP1L2;C14orf163			
GI_33469981-S	97.9	108.1	90.1	BLK	NM_001715.2	MGC10442	protein-	peripheral	protein
GI_33469983-S	1229.2	2093.5	1628.5	ERP70	NM_004911.3	ERP72	protein	endoplas	protein
GI_33469984-S	263.1	296.8	287.8	FKBP9	NM_007270.2	FKBP60;FKBP63;PPIase	cyclophilin	endoplas	protein
GI_33469986-S	342.2	293.5	269.4	HT001	NM_014065.2		nuclease		DNA
GI_33469988-S	179.3	589.3	347.8	NID2	NM_007361.2		collagen	basement	cell
GI_33469990-S	110.8	106.5	100.4	TRIM40	NM_138700.2	RNF35	zinc ion	intracellula	
GI_33504488-S	2395.1	1005.2	282.7	ZD52F10	NM_033317.2				
GI_33504490-S	106.4	132.8	96.4	C10orf81	NM_024889.2	FLJ23537;bA211N11.2	electron		electron
GI_33504570-A	87.2	94.5	84.7	SLIC1	NM_182854.1	MGC35578			
GI_33504570-I	90.4	91.2	85.1	SLIC1	NM_182854.1	MGC35578			

GI_33504572-S	114.6	108.9	107.8	FLJ33915	NM_182613.1	DKFZP434I225			
GI_33504574-S	120.6	135.1	100.9	LOC348174	NM_182619.1				
GI_33519429-A	1749.5	2831.7	1736.4	TXNRD1	NM_182743.1	TR;TR1;TXNR;MGC9145	thioredoxi	cytoplasm	signal
GI_33519435-A	4377.6	3013.1	2323.8	CCNB1IP1	NM_182849.1	HEI10;C14orf18	ligase	extrachro	
GI_33519437-I	121	124.2	122.3	CCNB1IP1	NM_182851.1	HEI10;C14orf18	ligase	extrachro	
GI_33519439-I	98.9	96	88.8	CCNB1IP1	NM_182852.1	HEI10;C14orf18	ligase	extrachro	
GI_33519441-I	113.5	122	118.8	ACCN4	NM_018674.3	ASIC4;BNAC4;MGC17248	sodium	integral to	small
GI_33519443-A	138.6	156.4	154.6	ACCN4	NM_182847.1	ASIC4;BNAC4;MGC17248	sodium	integral to	small
GI_33519445-A	650	2136.2	958.1	NBL1	NM_005380.3	NB;DAN;NO3;MGC8972;D1S1733E	tumor		cell growth
GI_33519446-I	100.1	98.3	94	NBL1	NM_182744.1	NB;DAN;NO3;MGC8972;D1S1733E	tumor		cell growth
GI_33519448-S	91.2	96.1	93.6	NALP10	NM_176821.2	NOD8			
GI_33519449-S	170.1	214	188.1	NALP9	NM_176820.2	NOD6	structural	ribosome	protein
GI_33519451-A	229.3	279.9	220.6	C21orf127	NM_182749.1	N6AMT1;PRED28;MGC19995			
GI_33519453-I	206.1	196.7	163.4	C21orf127	NM_013240.2	N6AMT1;PRED28;MGC19995			
GI_33519454-I	96.4	94.7	86.3	MAT2B	NM_182796.1	TGR;MAT-II;MGC12237;MATIIbeta	transferas		extracellul
GI_33519456-A	1483.3	1429.3	1608.9	MAT2B	NM_013283.3	TGR;MAT-II;MGC12237;MATIIbeta	transferas		extracellul
GI_33519456-I	196.5	188.8	187.8	MAT2B	NM_013283.3	TGR;MAT-II;MGC12237;MATIIbeta	transferas		extracellul
GI_33519457-A	1488.6	1381.5	1396.3	MCL1	NM_182763.1	TM;EAT;MCL1L;MCL1S;MGC1839			apoptotic
GI_33519459-I	383.6	425.8	396.2	MCL1	NM_021960.3	TM;EAT;MCL1L;MCL1S;MGC1839			apoptotic
GI_33519460-S	376.6	457.1	420.8	MGC43690	NM_182552.2				
GI_33519462-S	1775.4	1755.4	1350.1	NDUFA10	NM_004544.2	CI-42KD;MGC5103	NADH	NADH	energy
GI_33519463-S	5008.4	6706.3	5621	NDUFA4	NM_002489.2	MLRQ;CI-MLRQ	NADH	NADH	
GI_33519464-S	1243	1615.3	1680	NDUFA8	NM_014222.2	PGIV;MGC793;CI-19KD;CI-PGIV	NADH	NADH	
GI_33519465-S	2232	2855.5	2773.2	NDUFB2	NM_004546.2	AGGG;CI-AGGG	NADH	NADH	mitochond
GI_33519467-S	6064	6400.5	5168.5	NDUFB5	NM_002492.2	SGDH;CI-SGDH;MGC12314	NADH	NADH	mitochond
GI_33519468-A	1513.6	1898.2	1833.1	NDUFB6	NM_182739.1	CI;B17;MGC13675	NADH	NADH	mitochond
GI_33519471-S	4419.5	4564	4188.9	NDUFB7	NM_004146.4	B18;CI-B18;MGC2480	NADH	NADH	
GI_33519472-S	370.9	393.2	394.1	NDFIP1	NM_030571.2	N4WBP5;MGC10924			
GI_33519473-S	284.8	232.1	237.1	NDP52	NM_005831.3	MGC17318		nucleus	viral life
GI_33519474-S	143.2	157.4	157.7	NDUFS1	NM_005006.5	CI-75Kd;PRO1304;MGC26839	iron-sulfur	NADH	mitochond
GI_33519477-S	610.5	630.1	672.2	EIF1A	NM_001412.2	EIF4C;EIF1AX;eIF-1A;eIF-4C	translation	eukaryotic	translation
GI_33519480-S	110.3	110.5	108.9	NCAM2	NM_004540.2	NCAM21;MGC51008	cell	integral to	neuronal
GI_33519482-S	1148	1054.7	890.1	NCK1	NM_006153.3	NCK;MGC12668;NCKalpha	cytoskelet	cytoplasm	intracellula
GI_33563285-S	1327.4	1704.1	1409.3	VPS39	NM_015289.1	TLP;KIAA0770	small		intracellula
GI_33563295-S	158.5	201.9	170.1	SPACA4	NM_133498.2	SAMP14			
GI_33563339-S	247.2	296	264.5	MYH14	NM_024729.2	NHMCII;FLJ13881;KIAA2034	motor	myosin	
GI_33563375-S	530.5	623.3	396.3	TBC1D16	NM_019020.2	FLJ20748;MGC25062			
GI_33569215-S	105.1	110.3	103	LHX9	NM_020204.2		transcripti	nucleus	regulation
GI_33569217-S	818.8	1014.4	999.8	LYK5	NM_153335.3	STRAD;FLJ90524	protein-		protein
GI_33589813-S	979.1	1184.2	1199.3	C9orf60	NM_006336.2	ZYG			
GI_33589819-S	99.6	117.6	105	PHKG1	NM_006213.2	PHKG	phosphory	phosphory	energy
GI_33589822-S	88.7	88	83.9	PDK4	NM_002612.2		[pyruvate	mitochond	glucose
GI_33589823-S	135.3	154.8	140	CGREF1	NM_006569.2	CGR11	calcium		negative
GI_33589825-S	3513.7	3951.6	3636.3	APG10L	NM_031482.3	FLJ13954;DKFZP586I0418			

GI_33589826-S	755	826.4	816.2	CHRNA5	NM_000745.2		nicotinic	nicotinic	small
GI_33589828-S	4148.1	3090.5	2140.9	CACNA2D4	NM_172364.2			membran	
GI_33589832-S	622.7	597.4	507.8	CHPPR	NM_014637.2	KIAA0009			
GI_33589836-S	156.9	879.7	183.9	ITM2A	NM_004867.2	E25A;BRICD2A		integral to	
GI_33589838-S	121.1	135.4	131.4	TOB2	NM_016272.2	TOB4;TOBL;TROB2;bK223H9;KIAA1663;bK		nucleus	negative
GI_33589842-S	230.9	274.4	243.2	MARK1	NM_018650.2	MARK;KIAA1477	protein	microtubul	regulation
GI_33589844-S	278.2	339.9	330.1	ED1	NM_001399.2	EDA;HED;EDA1;XHED;XLHED	receptor	cytoskelet	ectoderm
GI_33589845-S	271.1	317.9	333.3	TEB4	NM_005885.2	KIAA0597			
GI_33589847-S	149.4	194.2	169.8	TFR2	NM_003227.2	HFE3	transferrin	membran	iron ion
GI_33589849-A	147.5	173.6	159.3	KIR2DL3	NM_014511.2	p58;CL-	receptor	integral to	immune
GI_33589851-S	94.5	100.5	112.4	TG	NM_003235.3		hormone	soluble	signal
GI_33589857-I	386.1	478.8	401.9	SCN1B	NM_001037.2	GEFSP1	voltage-	integral to	sodium
GI_33589858-I	135.3	145	129.4	CREB5	NM_182898.1	CRE-BPA	transcripti	nucleus	transcripti
GI_33589860-S	4496.8	7251.1	5805.2	RAB31	NM_006868.2	Rab22B	RAB small		nonselecti
GI_33591068-S	2509.8	2922.4	2161.8	BLMH	NM_000386.2	BH;BMH	bleomycin	cytoplasm	proteolysis
GI_33598909-I	107.7	102.1	93.2	ACVR1B	NM_020327.2	ALK4;SKR2;ACTRIB;ACVRLK4	transmem	integral to	transmem
GI_33598911-A	168.8	185.5	170.8	ACVR1B	NM_020328.2	ALK4;SKR2;ACTRIB;ACVRLK4	transmem	integral to	transmem
GI_33598911-I	116.1	117.4	117.5	ACVR1B	NM_020328.2	ALK4;SKR2;ACTRIB;ACVRLK4	transmem	integral to	transmem
GI_33598913-I	586.1	567.9	536.8	ACVR1B	NM_004302.3	ALK4;SKR2;ACTRIB;ACVRLK4	transmem	integral to	transmem
GI_33598917-S	85.6	99.7	82.5	CLDN11	NM_005602.4	OSP;OTM	structural	tight	
GI_33598918-A	2825	2669.5	1902.4	SCAMP1	NM_052822.2	SCAMP;SCAMP37	protein	integral to	post-Golgi
GI_33598919-I	183.7	196.8	157.2	SCAMP1	NM_004866.3	SCAMP;SCAMP37	protein	integral to	post-Golgi
GI_33598921-A	194.8	286.4	160.8	SCARA3	NM_182826.1	CSR;APC7;CSR1;MSLR1;MSRL1	scavenger		UV
GI_33598921-I	130.2	154.1	96.3	SCARA3	NM_182826.1	CSR;APC7;CSR1;MSLR1;MSRL1	scavenger		UV
GI_33598923-I	524.1	802.6	583.5	SCARA3	NM_016240.2	CSR;APC7;CSR1;MSLR1;MSRL1	scavenger		UV
GI_33598925-S	4651	4209.7	4610.4	SCARB2	NM_005506.2	CD36L2;HLGP85;LIMPII	receptor	lysosomal	cell
GI_33598932-I	188	208.2	199.6	SCARF1	NM_145351.1	SREC;KIAA0149;MGC47738	scavenger	membran	receptor
GI_33598934-A	130.7	138.7	117.6	SCARF1	NM_145352.1	SREC;KIAA0149;MGC47738	scavenger	membran	receptor
GI_33598936-A	1398.1	912.5	379.6	SCARF2	NM_182895.1	SREC2;SREC-II;SRECRP-1			
GI_33598939-A	440.1	414.6	351.5	PKD1L2	NM_182740.1				
GI_33598941-I	250.1	294.9	240.4	PKD1L2	NM_052892.2				
GI_33598943-S	95.8	107.5	91.3	PKD2L1	NM_016112.2	PCL;PKDL;PKD2L	calcium	integral to	cation
GI_33598945-A	2448.1	2412	2018.7	PLCG1	NM_182811.1	PLC1;PLC-II;PLC148	calcium	cellular_co	intracellula
GI_33598949-S	668.7	497.1	852.4	PODXL	NM_005397.2	PCLP;Gp200		integral to	
GI_33598951-S	493.6	429.5	299.4	POLR3F	NM_006466.2	RPC6;RPC39;MGC13517	DNA-	DNA-	regulation
GI_33598953-S	171.7	179.1	173.3	DKFZp586G0	NM_013386.2				
GI_33598955-I	92.7	104.7	86.5	DKFZp761H0	NM_182896.1				
GI_33598957-A	159.6	163.7	145	DKFZp761H0	NM_144996.2				
GI_33598957-I	99.4	107.8	106	DKFZp761H0	NM_144996.2				
GI_33598959-S	161.6	181.9	172.5	ADRA2B	NM_000682.3	ADRA2L1;ADRARL1;ADRA2RL1	alpha2-	integral to	G-protein
GI_33598961-S	123.7	131	128.2	EPHB3	NM_004443.3	ETK2;HEK2;TYRO6	transmem	integral to	signal
GI_33598962-S	490.5	522.4	558.1	MTMR9	NM_015458.3	MTMR8;C8orf9;LIP-STYX;DKFZp434K171			
GI_33598967-S	234.4	216.2	149	LMO7	NM_005358.3	LOMP;FBX20;FBXO20;KIAA0858	ubiquitin-	cytoplasm	intracellula
GI_33620720-S	465.5	428.5	284	DEXI	NM_014015.3	MYLE			

GI_33620721-I	161.3	186.3	166.4	VGLL2	NM_182645.2	VGL2;VITO1			
GI_33620726-S	787.2	1215	1069.2	TRA2A	NM_013293.2	HSU53209	pre-mRNA	nucleus	mRNA
GI_33620740-S	136.2	145	122.4	KIF3A	NM_007054.3		ATP	kinesin	organelle
GI_33620741-S	232.4	221.2	221.5	FZR1	NM_016263.2	FZR;FZR2;HCDH;HCDH1;KIAA1242	enzyme	anaphase-	ubiquitin-
GI_33620743-A	124.4	135.9	120.9	KIF9	NM_182903.2		ATP	kinesin	microtubul
GI_33620743-I	125	138.5	129.7	KIF9	NM_182903.2		ATP	kinesin	microtubul
GI_33620744-S	277.7	203.6	225.8	PCF11	NM_015885.2	KIAA0824	pre-mRNA	nucleus	mRNA
GI_33620746-S	108.7	124.2	115	MYEF2	NM_016132.2	MEF-2;FLJ11213;HsT18564;KIAA1341	RNA	nucleus	myoblast
GI_33620748-S	193.1	189.9	167.3	KIAA1333	NM_017769.2	FLJ20333	ubiquitin-	intracellula	ubiquitin
GI_33620750-S	256.7	307.3	403.1	PCYOX1	NM_016297.2	PCL1;KIAA0908	lyase	lysosome	prenylated
GI_33620752-S	293.3	329.3	259.9	FLJ10876	NM_018254.2				
GI_33620753-S	172.3	232	206.6	FLJ10404	NM_019057.2	KIAA1931	DNA	nucleus	regulation
GI_33620754-S	1041.3	1004.9	633	FLJ10201	NM_018023.3	FLJ12841;FLJ13308;KIAA1197			
GI_33620756-S	164.7	171.4	172.3	FLJ10324	NM_018059.2	KIAA1849			
GI_33620758-S	423.2	490.7	410.2	DKFZp761O	NM_018409.2				
GI_33620762-S	137.8	158.4	138.9	SBNO1	NM_018183.2	Sno;MOP3;FLJ10701;FLJ10833	nucleic		
GI_33620766-S	1143.6	1806.8	1202.6	SCARB1	NM_005505.3	CLA1;SRB1;CLA-1;SR-BI;CD36L1	transporte	membran	cholestero
GI_33620772-S	1616.2	1269.7	1099.1	KIAA0020	NM_014878.3	XTP5;MGC8749	RNA	nucleus	
GI_33620774-I	89.1	100	91	KTN1	NM_182926.1	CG1;KNT;KIAA0004		endoplas	nonselecti
GI_33620778-S	1101.7	1336.1	1475	LSM4	NM_012321.2	YER112W	small	snRNP U6	mRNA
GI_33624782-I	107.9	115.5	102.2	6-Sep	NM_145799.2	SEP2;KIAA0128;MGC16619;MGC20339	GTP	kinesin	cytokinesi
GI_33624820-A	128.4	177.8	81.5	6-Sep	NM_145802.2	SEP2;KIAA0128;MGC16619;MGC20339	GTP	kinesin	cytokinesi
GI_33624847-I	97.8	90.6	73.3	SYNE2	NM_015180.3	NUA;NUANCE;SYNE-2;KIAA1011;Nesprin-	receptor	kinesin	protein
GI_33624860-I	167.5	175.4	173.7	SYNE2	NM_182910.1	NUA;NUANCE;SYNE-2;KIAA1011;Nesprin-	receptor	kinesin	protein
GI_33624872-A	139.8	162.7	154.1	SYNE2	NM_182913.1	NUA;NUANCE;SYNE-2;KIAA1011;Nesprin-	receptor	kinesin	protein
GI_33624872-I	136.1	158.6	139	SYNE2	NM_182913.1	NUA;NUANCE;SYNE-2;KIAA1011;Nesprin-	receptor	kinesin	protein
GI_33624878-I	94.2	96.3	86.7	SYNE2	NM_182914.1	NUA;NUANCE;SYNE-2;KIAA1011;Nesprin-	receptor	kinesin	protein
GI_33624884-A	94.6	88.2	92.5	ADAMTS9	NM_020249.2	KIAA1312	metallope	extracellul	glycoprote
GI_33624884-I	109.6	108.9	116.3	ADAMTS9	NM_020249.2	KIAA1312	metallope	extracellul	glycoprote
GI_33624895-I	154.5	174.5	225.8	ADAMTS9	NM_182920.1	KIAA1312	metallope	extracellul	glycoprote
GI_33624901-I	97.1	95.2	94.2	ADAMTS9	NM_182921.1	KIAA1312	metallope	extracellul	glycoprote
GI_33624912-S	138.7	146.5	141.9	AQP2	NM_000486.3	AQP-CD;WCH-CD;MGC34501	water	secretory	water
GI_33636688-S	210.1	251.8	221.4	DKFZP586M	NM_031294.2				
GI_33636690-S	230.4	232.4	218.1	TMC7	NM_024847.2	FLJ21240		integral to	
GI_33636694-S	190.2	189.1	151.3	MLF1	NM_022443.2				
GI_33636697-S	162.9	171.2	173	TLK1	NM_012290.3	KIAA0137;PKU-BETA	cAMP-	nucleus	response
GI_33636700-S	596.6	534.5	759	TK2	NM_004614.2		thymidine	mitochond	nucleobas
GI_33636716-S	144.4	219.4	264.7	KIAA1539	NM_025182.2	FLJ11560;bA182N22.6			
GI_33636718-S	813.7	623.6	531.1	TIMM44	NM_006351.2	TIM44	protein	peripheral	mitochond
GI_33636720-S	2899.2	4016	3316.9	PRKAR1A	NM_002734.2	CAR;CNC1;TSE1;PRKAR1	cAMP-	cAMP-	regulation
GI_33636737-I	966.8	811.1	664.3	PRKACB	NM_182948.1		cAMP-	nucleus	signal
GI_33636741-I	832.5	1574	443.7	PLOD2	NM_182943.1		procollage	membran	protein
GI_33636747-S	503.8	513.8	530.9	FLJ21439	NM_025137.2	KIAA1840	DNA	nucleus	carbohydr
GI_33636749-S	243.2	317.6	335.1	E2-230K	NM_022066.2	FLJ12878;KIAA1734	ubiquitin		ubiquitin

GI_33636751-S	119.2	126.2	109.3	FA2H	NM_024306.2	FAAH;FAXDC1	catalytic		electron
GI_33636753-S	132	156.4	171.5	ZNFN1A4	NM_022465.2	EOS;KIAA1782			
GI_33636755-S	95.1	98.7	94.2	MARK4	NM_031417.2	MARKL1;KIAA1860			
GI_33636757-S	428.7	414.6	351.7	RNF146	NM_030963.2	dJ351K20.1;DKFZP434O1427			
GI_33636761-S	194.7	266.2	178.8	ZFYVE19	NM_032850.3	MPFYVE;FLJ14840	zinc ion		electron
GI_33636763-S	201.3	259.9	221.9	FLJ25555	NM_152345.3				
GI_33636765-S	465.9	386.7	188.3	LHPP	NM_022126.2		hydrolase		metabolis
GI_33636767-I	119.7	133.3	121.8	MLL5	NM_182931.1	FLJ10078;FLJ14026;HDCMC04P			
GI_33636770-I	171.5	216.4	199.1	MOBP	NM_182935.1			soluble	neurogene
GI_33667022-S	1180.9	1248.1	1114.5	EIF2B5	NM_003907.1	CLE;CACH;LVWM;EIF-2B;EIF2Bepsilon	translation	cellular_co	amino
GI_33667024-S	276.2	378.7	411.9	ZNF20	NM_021143.1	KOX13	protein	nucleus	regulation
GI_33667026-S	10078.5	11658	8220.6	DC50	NM_031210.3	PD04872	nucleic		
GI_33667027-S	524	605	549.7	IRF2BP2	NM_182972.1				
GI_33667029-S	163	215.6	165.8	ALDRL6	NM_017584.4	MIOX;ALDR6R	aldo-keto	cytoplasm	membran
GI_33667031-S	101	93.1	91.4	COX8-3	NM_182971.1				
GI_33667037-S	175.4	197.3	173.9	STX11	NM_003764.2		SNAP	kinesin	membran
GI_33667039-S	86.7	91.1	86.4	NALP8	NM_176811.2	NOD16			
GI_33667043-S	129.7	113.2	107.9	TARSH	NM_015429.2	NESHBP;FLJ21551;DKFZP586L2024			
GI_33667045-I	133.4	186.8	109.9	NEDD9	NM_006403.2	CASL;HEF1;CAS-L	cell	spindle	mitosis
GI_33667050-S	2748.4	2811.7	3452.5	DP1	NM_005669.3	TB2;D5S346	molecular	integral to	hypersens
GI_33667052-A	99	118.6	92.9	NEDD9	NM_182966.1	CASL;HEF1;CAS-L	cell	spindle	mitosis
GI_33667052-I	96.1	126.7	114.8	NEDD9	NM_182966.1	CASL;HEF1;CAS-L	cell	spindle	mitosis
GI_33667062-S	151.5	163.9	153.1	LOC360200	NM_182973.1		trypsin		proteolysis
GI_33667064-S	106.4	96.4	98.3	GLTDC1	NM_182974.1		transferas		
GI_33667066-S	127.9	164	174.6	HCST	NM_014266.3	DAP10;KAP10;PIK3AP;DKFZP586C1522	SH3/SH2	integral to	humoral
GI_33667071-S	112	106.8	90.2	CMRF-35H	NM_007261.1	IRC1;IRC2;IRp60;CMRF35H;CMRF35H9;CM			
GI_33667073-S	141	158.3	135.7	LOC55908	NM_018687.3				
GI_33667080-S	189.4	225.8	222.5	DKFZP761H1	NM_031297.2				
GI_33667083-S	635.3	659.3	664.6	DNAJC9	NM_015190.3	JDD1;SB73;KIAA0974			
GI_33667098-I	107.9	117	95	C21orf69	NM_182900.1	PRED54			
GI_33667100-I	104.9	122.1	104.5	C11orf17	NM_182901.1	BCA3			
GI_33667102-I	257.1	329.6	289	CLECSF14	NM_182906.1	HML;HML2;CLECSF13	lectin [goid	plasma	heterophili
GI_33667104-I	109.9	108.1	97.6	DOC1	NM_182909.1	GIP90			
GI_33667106-I	103	105.5	95.7	ERG	NM_182918.1		DNA	nucleus	protein
GI_33667110-I	176.1	211.9	216.3	FLT4	NM_182925.1	PCL;VEGFR3	vascular	integral to	transmem
GI_33667114-I	123.7	137.9	124.8	GEFT	NM_182947.1				
GI_33667116-I	149.2	151	168.6	FLJ23471	NM_182924.1				
GI_33695073-S	102.7	107.7	104.9	DDI2	NM_032341.2				
GI_33695083-I	170.9	182	155.9	NNT	NM_012343.2		NAD(P)	mitochond	energy
GI_33695085-A	343.8	545.7	257.1	NNT	NM_182977.1		NAD(P)	mitochond	energy
GI_33695085-I	79.6	103.7	76.8	NNT	NM_182977.1		NAD(P)	mitochond	energy
GI_33695087-S	194.4	222.6	182.7	GPD1	NM_005276.2		glycerol-3-	glycerol-3-	carbohydr
GI_33695089-S	2484.3	2926.8	2821.6	PTOV1	NM_017432.2	DKFZP586I111	ATP	nucleus	tRNA
GI_33695091-I	136.1	142.4	139	OKL38	NM_013370.2				

GI_33695094-S	3768.3	3702.9	3554.9	RAB10	NM_016131.2		GTP		small
GI_33695096-S	100.1	102.2	100.9	GPR35	NM_005301.2		G-protein	integral to	G-protein
GI_33695100-A	133	140.7	117.6	OKL38	NM_182981.1				
GI_33695100-I	94.2	86.6	84	OKL38	NM_182981.1				
GI_33695103-S	98.3	103.1	86.9	GPR65	NM_003608.2	TDAG8;hTDAG8	G-protein	integral to	G-protein
GI_33695106-S	114.1	210.6	107.6	GPR55	NM_005683.2		G-protein	integral to	G-protein
GI_33695108-S	2114	1297.6	1230.7	RAB9P40	NM_005833.2	p40	vesicle	endosome	receptor
GI_33695110-S	285.3	287.6	273.8	PNPT1	NM_033109.2	OLD35;PNPASE;old-35	3'-5'		RNA
GI_33695116-S	292.4	340.6	330	TP53I11	NM_006034.2	PIG11			negative
GI_33695118-S	1005.6	1152.1	1105.1	PAPSS1	NM_005443.3	SK1;PAPSS;ATPSK1	ATP		nucleobas
GI_33695152-I	76.5	81.1	71.9	GNAL	NM_182978.1		heterotrim	peripheral	signal
GI_33695154-I	163.5	212.1	189.6	HPN	NM_182983.1	TMPRSS1	serine-	integral to	cell growth
GI_33695160-I	187.4	216.5	198.6	GRK4	NM_182982.1	GPRK4;GPRK2L	G-protein-		regulation
GI_33859667-S	808.8	842.1	808.7	ZNF364	NM_014455.1	RNF115;CL469780			
GI_33859669-S	131.5	127.7	125.7	CHDC1	NM_015116.1	KIAA1016	sugar		phosphoe
GI_33859677-S	310.9	285.3	288.6	FLJ20557	NM_017879.1		nucleic	nucleus	regulation
GI_33859747-S	279.3	284.3	315	MGC2752	NM_023939.2				
GI_33859754-S	102.6	108.6	123.1	CXXC6	NM_030625.1	LCX;TET1;KIAA1676;bA119F7.1	zinc ion		
GI_33859758-S	331.7	413.5	357.5	JPHL1	NM_032452.1	KIAA1831		integral to	
GI_33859778-S	727	745.6	668.2	MGC33424	NM_153705.2				
GI_33859792-S	2986.8	3283.3	3078.9	MGC35261	NM_173494.1				
GI_33859820-S	709.2	723.6	618.3	MGC40069	NM_182615.1				
GI_33859830-S	3706.7	2454.5	2006.1	RPC62	NM_006468.4	RPC3	DNA-	DNA-	regulation
GI_33859831-S	5952.4	5656.2	4706.8	SPC18	NM_014300.2		peptidase	microsom	proteolysis
GI_33859832-S	2137	2219.1	1841.5	SMBP	NM_020123.2	EP70-P-iso	transporte	integral to	transport
GI_33859834-S	123.1	137.7	125.9	HGF	NM_000601.3	SF;HPTA	hepatocyt	cellular_co	axon
GI_33859836-I	205.1	246.5	216.5	RPP38	NM_183005.1		ribonuclea	nucleolar	tRNA
GI_33859842-I	112.4	129	111.7	SHC1	NM_183001.1	SHC;SHCA	transmem		regulation
GI_33859844-S	112.1	112.6	107.4	ZNF223	NM_013361.2		DNA	nucleus	regulation
GI_33859846-S	204.4	300	261	COX7A3	NM_183003.1	COX7AL2	cytochrom	mitochond	electron
GI_33942062-S	191.2	188.9	390.9	SHREW1	NM_018836.2	MOT8	oxidoredu	integral to	metabolis
GI_33942063-S	893.7	852.7	461.2	SEMA4D	NM_006378.2	CD100;SEMAJ;coll-4;M-sema G;M-sema-G	receptor	integral to	anti-
GI_33942065-S	157.1	191.5	169.7	SENP8	NM_145204.2	DEN1;NEDP1;HsT17512	cysteine-		proteolysis
GI_33942071-S	385.6	457.4	434.6	TNRC5	NM_006586.2	CAG4A;ERDA5			
GI_33942075-S	168.9	161.1	171.5	SLC5A8	NM_145913.2	AIT	transporte	membran	transport
GI_33942079-S	118.9	165.1	144.9	TMC5	NM_024780.3	FLJ13593			
GI_33942082-S	85	87.6	92.7	DUSP21	NM_022076.2	LMWDSP21	protein		protein
GI_33943097-S	726.3	1145	947.7	RAB5B	NM_002868.2		RAB small	membran	
GI_33943098-I	85.6	91.3	86.3	SFTPB	NM_000542.2	SP-B;PSP-B;SFTB3;SFTP3	surfactant	extracellul	respiratory
GI_33943100-S	115.3	104.4	95.5	FLJ32855	NM_182791.1	FLJ23168;MGC34145			
GI_33946268-S	2230.2	1905.3	1991.6	WASL	NM_003941.2	N-WASP;MGC48327	small	actin	actin
GI_33946272-I	118.4	118.1	95.4	PRDM1	NM_001198.2	BLIMP1;PRDI-BF1	tumor	nucleus	cell growth
GI_33946273-A	141.5	139.8	106.2	PRDM1	NM_182907.1	BLIMP1;PRDI-BF1	tumor	nucleus	cell growth
GI_33946273-I	134.7	144.5	123.2	PRDM1	NM_182907.1	BLIMP1;PRDI-BF1	tumor	nucleus	cell growth

GI_33946275-S	1272.3	755.1	637.5	PSCD3	NM_004227.3	GRP1;ARNO3	phosphati	membran	vesicle-
GI_33946276-A	1198.9	1074.4	1030.2	CFL2	NM_021914.5		actin	cytoskelet	
GI_33946276-I	129.9	123.7	126.3	CFL2	NM_021914.5		actin	cytoskelet	
GI_33946277-I	241.8	266.5	217.9	CFL2	NM_138638.1		actin	cytoskelet	
GI_33946279-A	573.7	694.7	608.9	DKFZP434I1	NM_183009.1	MSTP054	nucleic		
GI_33946279-I	350.2	416.4	358.8	DKFZP434I1	NM_183009.1	MSTP054	nucleic		
GI_33946283-I	197.6	160.1	189.8	BIRC3	NM_001165.3	AIP1;API2;MIHC;CIAP2;HAIP1;HIAP1;RNF49	apoptosis	intracellula	anti-
GI_33946284-A	137	114.2	137.6	BIRC3	NM_182962.1	AIP1;API2;MIHC;CIAP2;HAIP1;HIAP1;RNF49	apoptosis	intracellula	anti-
GI_33946286-A	193.6	288.7	238.2	FLJ11383	NM_024938.2	KIAA0435			
GI_33946286-I	166.1	223.1	152.3	FLJ11383	NM_024938.2	KIAA0435			
GI_33946288-I	128.7	147.6	108.5	FLJ11383	NM_014801.2	KIAA0435			
GI_33946290-S	547.8	816.2	620.4	FLJ12443	NM_024830.3		acyltransf		metabolis
GI_33946292-I	85.3	88.8	85.3	FLJ20403	NM_181781.2	MGC61591			
GI_33946294-A	119.7	133.4	122.5	FLJ20403	NM_182975.1	MGC61591			
GI_33946294-I	100.8	109.2	90.9	FLJ20403	NM_182975.1	MGC61591			
GI_33946296-I	118.6	140.9	115.9	FLJ20403	NM_182976.1	MGC61591			
GI_33946298-S	221.2	245.7	226.3	PRPF39	NM_017922.2	FLJ11128;FLJ20666			
GI_33946300-S	241.3	236.4	180.7	FLJ21062	NM_024788.2				
GI_33946307-A	132.4	128.4	117.8	SLC8A3	NM_182936.1	NCX3			
GI_33946307-I	216.7	247.4	227	SLC8A3	NM_182936.1	NCX3			
GI_33946309-I	117.1	110.8	115.4	SLC8A3	NM_033262.3	NCX3			
GI_33946312-I	106.2	109.3	98	NIN	NM_016350.3	KIAA1565			
GI_33946314-I	372	413	346.8	NIN	NM_020921.2	KIAA1565			
GI_33946316-I	139.5	133	141.9	NIN	NM_182944.1	KIAA1565			
GI_33946318-A	132.1	157.9	136.3	NIN	NM_182945.1	KIAA1565			
GI_33946322-S	656.3	718.1	616.1	ARL1	NM_001177.3	ARFL1	enzyme		small
GI_33946323-S	166	165.1	167.4	GNAI1	NM_002069.4	Gi	heterotrim	peripheral	G-protein
GI_33946328-S	5069.9	4454.5	2548.4	RALA	NM_005402.2	RAL;MGC48949	GTP		chemotaxi
GI_33946330-S	251.4	285.5	271.8	SSTR1	NM_001049.2	SRIF-2	somatosta	integral to	negative
GI_33946331-S	1061.8	1211.9	1064.3	WWP1	NM_007013.3	AIP5;Tiul1;hSDRP1;DKFZp434D2111	ubiquitin-	ubiquitin	central
GI_33946332-I	966.9	1298.5	1197.4	ZC3HAV1	NM_020119.3	ZAP;FLB6421;ZC3HDC2;FLJ13288;MGC488			
GI_33946333-S	89.1	90.8	83.9	FLJ23129	NM_024763.2				
GI_33946335-S	108.8	139.2	89.8	ID2	NM_002166.4	ID2A;ID2H;MGC26389		nucleus	developm
GI_34013511-I	95.5	104.6	93.1	TLX2	NM_016170.3	Enx;NCX;HOX11L1	molecular	nucleus	regulation
GI_34013512-S	2334.8	1896.1	1471.3	LSM2	NM_021177.3	G7b;snRNP;C6orf28;YBL026W	pre-mRNA	small	mRNA
GI_34013527-S	340.1	318.5	359	KIAA1196	NM_020713.1		DNA	nucleus	regulation
GI_34013529-S	1600.6	1135	1061.4	TMSL3	NM_183049.1				
GI_34013589-S	940.7	840.7	555	ARHGAP22	NM_021226.2	RhoGAP2			
GI_34098934-S	1664.7	1840.9	1721.4	ATPAF1	NM_022745.1	ATP11;ATP11p;FLJ22351			
GI_34098936-S	383.6	470.9	479	C19orf6	NM_033420.2	ASBABP1;MGC4022;R32184_3			
GI_34098945-S	10705.4	11380	8022.8	NSEP1	NM_004559.2	YB1;BP-8;CSDB;DBPB;YB-1;YBX1;NSEP-	double-	nucleus	response
GI_34098958-S	196.5	370.2	370.6	CYP2U1	NM_183075.1		monooxyg		electron
GI_34098963-S	115.4	124	107.1	DEFB106	NM_152251.2	BD-6;DEFB-6	antibacteri	extracellul	xenobiotic
GI_34098964-S	99.1	91	94.6	LY96	NM_015364.2	MD-2	coreceptor	plasma	antibacteri

GI_34098967-S	99.2	107	96.5	LOC119180	NM_183058.1				
GI_34098969-S	114.9	128.7	117.5	C1orf36	NM_183059.1				
GI_34101266-A	653.8	553.5	607.2	BCKDHB	NM_000056.2	E1B	3-methyl-2-	alpha-	
GI_34101267-S	667.4	496.1	422	KLHL8	NM_020803.3	KIAA1378	protein		
GI_34101271-I	291.7	324.5	392.5	BCKDHB	NM_183050.1	E1B	3-methyl-2-	alpha-	
GI_34101273-I	91	90.2	82.8	FLJ32940	NM_144696.2	FLJ25438			
GI_34101277-A	127.5	138.1	149	MGC10744	NM_183065.1				
GI_34101281-S	201.3	227.5	227.3	SCNN1D	NM_002978.2	ENaCd;SCNED;ENaCdelta	amiloride-	membran	sodium
GI_34101287-S	676.4	647.9	675.8	CPSF2	NM_017437.1	CPSF100;KIAA1367	RNA	nucleoplas	mRNA
GI_34101289-S	104.5	197.9	120.9	FAIM2	NM_012306.2	LFG;NMP35;KIAA0950;LIFEGUARD			
GI_34106705-S	219.5	285.3	236.5	GPC5	NM_004466.3		glypican	proteoglyc	developm
GI_34106706-I	94.4	92.8	85.4	BDNF	NM_170731.2	MGC34632	growth		neurogene
GI_34106707-I	94.6	93.7	91.7	BDNF	NM_170732.2	MGC34632	growth		neurogene
GI_34106708-I	147.2	126.4	120.3	BDNF	NM_170733.2	MGC34632	growth		neurogene
GI_34106709-A	857.5	493.9	372.1	BDNF	NM_170734.2	MGC34632	growth		neurogene
GI_34106709-I	104.9	108.2	96	BDNF	NM_170734.2	MGC34632	growth		neurogene
GI_34106711-I	127.1	139.8	124.5	BDNF	NM_001709.3	MGC34632	growth		neurogene
GI_34147050-S	1586.5	1247.1	994.4	PP1665	NM_030792.4				
GI_34147218-S	1267.7	1950.7	1730.3	C14orf112	NM_016468.3	HSPC203			
GI_34147219-S	181.1	155	179.1	FLJ22965	NM_022101.2				
GI_34147220-S	1403.4	1440.8	672.6	C20orf155	NM_019095.3	GCD10;dJ967N21.6	transferas	integral to	phospholi
GI_34147320-S	812.5	954.7	904.6	IFI35	NM_005533.2	IFP35	transcripti	soluble	immune
GI_34147321-S	310.8	326.7	464.4	SMPDL3A	NM_006714.2	ASM3A;ASML3a;FLJ20177;yR36GH4.1	hydrolase		carbohydr
GI_34147322-S	112.3	114.7	111.7	MYCL1	NM_005376.2	LMYC;MYCL	transcripti	nucleus	cell growth
GI_34147323-S	4125.2	2478.5	1994.7	SERPINE2	NM_006216.2	GDN;PI7;PN1;PNI	serpin	extracellul	developm
GI_34147324-S	5616.1	7191.5	6366.6	CCT5	NM_012073.2	KIAA0098	chaperoni		protein
GI_34147325-S	261.9	312.4	283.5	MCLC	NM_015127.2	KIAA0761			
GI_34147326-S	1242.6	1216.7	1146.7	KIAA0690	NM_015179.2				
GI_34147328-S	854.8	794.2	808.3	DKFZP564O2	NM_015407.3				
GI_34147329-S	1145.8	1122.1	993.8	RRS1	NM_015169.2	KIAA0112	DNA	nucleus	ribosome
GI_34147330-S	705	679.9	457.5	C20orf22	NM_015600.2	dJ965G21.2;DKFZP434P106			
GI_34147331-S	1733.4	1477.8	1330.4	KIAA0409	NM_015324.2				
GI_34147332-S	395.9	413.5	532.1	DKFZP434J0	NM_015671.2				
GI_34147334-S	1086.4	898	1081.6	FLJ20811	NM_019007.2				
GI_34147336-S	458.2	511.6	293.3	ZNF337	NM_015655.2	dJ694B14.1;DKFZp564F1422	DNA	nucleus	regulation
GI_34147337-S	802.4	838.2	907.8	KLP1	NM_020378.2		N-		
GI_34147338-A	172.7	193.1	169.4	NUPL1	NM_014089.2	PRO2463;KIAA0410		nucleus	transport
GI_34147338-I	89.3	101.9	93	NUPL1	NM_014089.2	PRO2463;KIAA0410		nucleus	transport
GI_34147339-S	184.1	208.3	182.1	KIAA1446	NM_020836.2				
GI_34147341-S	355.6	378.2	332.3	KIAA1627	NM_020961.2		DNA	nucleus	regulation
GI_34147342-S	195.7	322.6	215.2	IGSF9	NM_020789.2	Nrt1;KIAA1355			
GI_34147343-S	1829.9	2002.7	1601.5	KIAA1533	NM_020895.2				
GI_34147344-S	2111.4	2859.7	2209.2	KCTD14	NM_023930.2	MGC2376	voltage-	membran	potassium
GI_34147348-S	112.5	138.6	128.3	MGC2474	NM_023931.2				

GI_34147349-S	448.8	496.3	511.5	MGC2601	NM_024042.2	c380A1.2			
GI_34147350-S	122.8	129	135.9	MGC2827	NM_023940.2	MGC4499	small		small
GI_34147351-S	132.7	141.1	132.7	MGC8407	NM_024046.2				
GI_34147352-S	1987.4	1916	1944.1	MGC2803	NM_024038.2		DNA	nucleus	regulation
GI_34147353-S	954.1	960.7	837	C7orf24	NM_024051.2	MGC3077;FLJ11717			
GI_34147354-S	360.9	312	283.3	MGC3101	NM_024043.2	FLJ12582			
GI_34147355-S	583.1	710.7	693.9	MGC2731	NM_024068.2				
GI_34147356-S	451.7	695.2	689.4	MGC2594	NM_024050.2				
GI_34147357-S	775	788	920.6	MGC2747	NM_024104.2				
GI_34147358-S	584.8	646.9	658.2	PDCL3	NM_024065.2	PDCL2;VIAF1;GCPHLP;HTPHLP;MGC3062			phototrans
GI_34147359-S	331.2	475.5	393.2	C9orf16	NM_024112.2	MGC4639;EST00098;FLJ12823	molecular	kinesin	biological_
GI_34147360-S	903.1	987.4	991.4	MGC2749	NM_024069.2				
GI_34147361-S	155.5	179.1	149.9	TRIM48	NM_024114.2	RNF101;MGC4827	zinc ion	intracellula	
GI_34147362-S	5131.9	2665.4	993.1	MGC4504	NM_024111.2				
GI_34147363-S	658	782.8	672	MGC4825	NM_024122.2				
GI_34147364-S	490.7	699.2	533	MGC4707	NM_024113.2	FLJ22210			
GI_34147365-S	533.7	803.9	971.2	MGC1203	NM_024296.2				
GI_34147366-S	2269.5	2388.5	2272	MAPKAP1	NM_024117.2	SIN1;MGC2745	Ras	cellular_co	biological_
GI_34147367-S	855	780.9	694.9	CHCHD7	NM_024300.2	MGC2217			
GI_34147369-S	527.9	528.3	484.3	TNIP2	NM_024309.2	KLIP;FLIP1;ABIN-2;MGC4289			
GI_34147371-S	10725.6	10946	12110	C20orf149	NM_024299.2	MGC2479;FLJ21046;dJ697K14.9	DNA	nucleus	regulation
GI_34147373-S	263.4	288	351.9	MGC4172	NM_024308.2	FLJ22543	oxidoredu		metabolis
GI_34147374-S	927.2	665.5	577.4	C7orf23	NM_024315.2	MGC4175		integral to	
GI_34147375-S	227.6	232.1	241.3	ET	NM_024311.2				
GI_34147376-S	124.9	137.7	135.7	MGC11242	NM_024320.2				
GI_34147377-S	527.2	705.2	1077.3	MGC4294	NM_024314.2				
GI_34147378-S	386.4	299.6	335.4	C1orf35	NM_024319.2	MMTAG2;MGC4174			
GI_34147379-S	428.1	494.7	528.1	C20orf121	NM_024331.2	MGC2470;dJ179M20.3	transporte	intracellula	transport
GI_34147380-S	146.3	123.7	125.6	CYP2R1	NM_024514.2	MGC4663			
GI_34147381-S	272.7	325.2	280.9	MGC4645	NM_024515.2				
GI_34147385-S	945	1071.2	1206.9	PCNT1	NM_024844.2	PCN;PCNT			
GI_34147386-S	115.4	115.7	97.7	EFHD1	NM_025202.2	PP3051;FLJ13612	calcium		
GI_34147387-S	213.6	243.5	224.3	C2orf8	NM_025264.2	MGC2454			
GI_34147388-S	669.9	598.2	541.9	MGC2744	NM_025267.2		ATP		alanyl-
GI_34147389-S	290.4	311	248.1	MGC4659	NM_025268.2				
GI_34147390-S	355.4	483.4	480.7	MGC4093	NM_030578.2				
GI_34147391-S	1672.8	1456.7	1359.2	MGC10471	NM_030818.2				
GI_34147392-S	115.6	111.3	113.2	MGC10731	NM_030907.2		GTP		small
GI_34147394-S	183.2	224.1	215.2	MXD3	NM_031300.2	MAD3;MGC2383			
GI_34147395-S	899.4	733.9	843.9	MGC4293	NM_031304.2			phycobilis	
GI_34147396-S	112.5	125.1	106.3	AKR1CL2	NM_031436.2	LoopADR;MGC10612			
GI_34147397-S	1262.2	1173.4	1259.6	CCM2	NM_031443.2	C7orf22;MGC4067;MGC4607			
GI_34147398-S	1259.8	1089.3	1218.9	C19orf12	NM_031448.2	MGC10922;DKFZP762D096			
GI_34147399-S	1311.8	1309.7	1326.9	C6orf119	NM_031452.2	MGC2560;dJ427A4.2			

GI_34147400-S	126.7	164.9	137.9	RPS6KL1	NM_031464.2	MGC11287	structural		protein
GI_34147401-S	735.7	950.1	787.7	MGC11134	NM_031472.2		transferas		tRNA
GI_34147402-A	181.1	221.1	193.3	CDV-1	NM_031473.2	CDV1;CDV1R;MGC4027			
GI_34147402-I	125	151.3	137	CDV-1	NM_031473.2	CDV1;CDV1R;MGC4027			
GI_34147405-S	135.4	141.2	138.7	KATNAL1	NM_032116.2	MGC2599	nucleotide		
GI_34147407-S	1659.1	1549.6	1547.7	DKFZp586C1	NM_032273.2				
GI_34147410-S	2053	1871.9	1580.3	MGC2714	NM_032299.2				
GI_34147411-S	815.9	820.3	819.3	CHCHD5	NM_032309.2	C2orf9;MGC11104			
GI_34147412-S	608.7	742.4	587.2	MGC11061	NM_032312.2				
GI_34147413-S	1099.1	1022	830.5	C4orf14	NM_032313.2	MGC3232			
GI_34147414-S	792.8	921	647.8	MGC4618	NM_032326.2				
GI_34147419-S	992.2	871.5	891.2	ACBD6	NM_032360.2	MGC2404	acyl-CoA		
GI_34147420-S	838.3	737	783.1	MGC13272	NM_032355.2				
GI_34147421-S	102.6	106.1	106.1	MGC16186	NM_032372.2		metallope		electron
GI_34147422-S	1355.1	1042.3	1058.8	MGC4308	NM_032359.2				
GI_34147424-A	951.6	778.3	670.8	MGC15416	NM_032371.2				
GI_34147425-S	103.3	117.5	103.9	MGC2629	NM_032522.2		protein		
GI_34147426-S	1412.8	1850.6	2123.2	MGC3248	NM_032486.2				
GI_34147427-S	87.8	91.3	84.1	FAPP2	NM_032639.2	MGC3358			
GI_34147428-S	106.2	100.4	100.7	SLC30A2	NM_032513.2	ZNT2;ZnT-2;MGC11303	cation	membran	cation
GI_34147429-S	126.3	137.5	114.8	MGC10701	NM_032658.2				
GI_34147430-S	2901.3	1894.2	2248.9	NIFIE14	NM_032635.2	MGC1936			
GI_34147431-S	120.5	122.4	135.1	MGC4266	NM_032680.2		calcium		
GI_34147433-S	354	377.5	311.2	MGC12760	NM_032723.2				
GI_34147434-S	239.3	235.2	221	USP30	NM_032663.2	FLJ40511;MGC10702	cysteine-		ubiquitin-
GI_34147435-S	137.4	208.4	107.1	C9orf67	NM_032728.2	FLJ14662;MGC12921			
GI_34147439-S	216.8	311.9	246.2	PLCD4	NM_032726.2	MGC12837	calcium		lipid
GI_34147440-S	234.1	291.3	260.1	MGC16075	NM_032761.2				
GI_34147441-S	314.1	230.3	176.6	MGC16121	NM_032762.2				
GI_34147442-S	150.2	145.7	148.4	MGC16153	NM_032764.2				
GI_34147443-S	551.8	719.7	622.2	TRIM52	NM_032765.2	RNF102;MGC16175	zinc ion	intracellula	
GI_34147444-S	510	656.2	611.3	MGC14126	NM_032898.2				
GI_34147445-S	155.1	191.2	173.9	MGC14128	NM_032899.2				
GI_34147446-S	3263.8	3748.6	3284.5	MGC14288	NM_032901.2				
GI_34147447-S	118.6	126.8	122.3	MGC14425	NM_032903.2				
GI_34147448-S	534.9	558.4	692	RTN4IP1	NM_032730.2	NIMP;MGC12934	alcohol		
GI_34147449-S	3973.6	3895	3678.4	MGC14156	NM_032906.2				
GI_34147452-S	261.9	261.5	192.1	LOC87769	NM_033110.1				
GI_34147454-S	511.1	558.5	491.5	RBM18	NM_033117.2	MGC2734	nucleic		
GI_34147455-S	535.8	638.4	701.1	MGC16169	NM_033115.2	HSPC302			
GI_34147457-S	262.5	251.2	272	LOC90355	NM_033211.2				
GI_34147458-S	104.8	106.4	122.9	MGC13138	NM_033410.2		nucleic	intracellula	regulation
GI_34147459-S	700.3	607.9	449	MGC10992	NM_033212.2	MGC13119			
GI_34147460-S	982.8	869.7	1126.1	PP1201	NM_022152.3				

GI_34147461-S	5298.2	4338.3	4295.3	ZPR9	NM_033414.2	MGC2485;MGC17552	RNA	nucleus	
GI_34147462-S	98	128.5	127.3	MGC16309	NM_033413.2	FLJ23553			
GI_34147463-S	110.5	118.9	116.7	C20orf54	NM_033409.2	MGC10698;bA371L19.1		integral to	
GI_34147465-S	2176.1	2534.2	2592.3	FLJ22875	NM_032231.3				
GI_34147466-S	774	753.7	664	BCLP	NM_033504.2	CAC-1			
GI_34147467-S	105.6	238.7	140.2	JM11	NM_033626.2				
GI_34147468-S	3274.1	3102.8	4580.2	WDR34	NM_052844.2	MGC20486;bA216B9.3			
GI_34147469-S	244	251.6	263.6	MGC15396	NM_052855.2				
GI_34147470-S	270.3	313.4	338.5	MGC10485	NM_052875.2		protein	cytosol	intracellula
GI_34147471-S	743.4	1153.9	987.1	MGC20781	NM_052935.2	MGC21375			
GI_34147473-S	179.3	224.3	198.7	MGC16491	NM_052943.2	MGC20845			
GI_34147474-S	101	89.9	81.7	NOSTRIN	NM_052946.2	MGC20702		intracellula	signal
GI_34147475-S	116.5	155.8	117.3	MGC16384	NM_053048.2				
GI_34147476-S	345	397.8	348.6	ZNF307	NM_019110.3	P1P373C6;p373c6.1			
GI_34147477-S	250.5	267.3	282.6	MGC15397	NM_080652.2				
GI_34147481-S	309	262.7	348.3	CDCA5	NM_080668.2	MGC16386			
GI_34147483-S	499.4	273.8	289.3	MGC4562	NM_133375.2		ribonuclea		
GI_34147484-S	346.7	299.8	284.5	PACSIN3	NM_016223.3		cytoskelet	kinesin	endocytosi
GI_34147485-S	1038	756.6	761.9	SAT2	NM_133491.2	SSAT2	N-		
GI_34147486-A	932.3	1228.6	1051.9	C21orf80	NM_133635.2	KIAA0958;DKFZp434E171			
GI_34147489-S	483.7	585.9	495.8	NDUFC2	NM_004549.3	B14.5b	NADH	NADH	
GI_34147490-S	2720.2	2678.9	2578.3	APG3	NM_022488.3	PC3-			
GI_34147491-S	1207.6	1292.7	1272	STX3A	NM_004177.3		protein	kinesin	nonselecti
GI_34147492-S	905.4	1075.8	1037.8	EIF2S1	NM_004094.3	EIF2;EIF-2;EIF2A;EIF-2A;EIF-2alpha	translation	polysome	regulation
GI_34147493-S	5215.9	2916.9	3021.4	MAT2A	NM_005911.3	MATA2;MATII;SAMS2	methionin		one-
GI_34147494-S	113.5	125.7	104.8	SERPINB9	NM_004155.3	PI9;CAP3;CAP-3	protein	cytosol	
GI_34147496-S	91.1	103.3	93.9	MYCN	NM_005378.3	NMYC	transcripti	chromatin	oncogene
GI_34147497-S	393.5	355.9	343.7	FLJ20533	NM_017866.3				
GI_34147499-S	1138.2	1398.9	1147.4	PPP1R2	NM_006241.3	IPP2	type 1		energy
GI_34147501-S	829.2	689.5	501.9	NEK6	NM_014397.3	SID6-1512	protein-		protein
GI_34147502-S	130.3	126.4	138.7	ZNF71	NM_021216.3	EZFIT	DNA	nucleus	regulation
GI_34147505-S	188.2	188	267.9	RPS6KA2	NM_021135.3	RSK;HU-2;RSK3;MAPKAPK1C	protein	nucleus	protein
GI_34147506-S	380	459.1	441.7	FLJ22955	NM_024819.3				
GI_34147508-S	274	207.8	215.3	FKSG28	NM_030929.3	FKSG40;bA108L7.1			
GI_34147509-S	241	282.2	254.4	FLJ21839	NM_021831.3				
GI_34147510-S	119.5	138.5	120.9	C1QTNF2	NM_031908.3	CTRP2;zacrp2	DNA	microfibril	regulation
GI_34147511-S	636.7	623.5	524.5	MYOHD1	NM_025109.3	FLJ22865	ATP	myosin	
GI_34147514-S	2559.8	2189.7	1915.3	PYGO2	NM_138300.2	FLJ33226	DNA	nucleus	regulation
GI_34147515-S	2590.3	1414.9	1139.7	UAP1	NM_003115.3	AgX;AGX1;SPAG2	UDP-N-		UDP-N-
GI_34147516-S	1669.4	1494.4	1268.2	CSNK1A1	NM_001892.3	CK1;HLCDGP1;PRO2975	casein		protein
GI_34147517-S	111.2	134.1	115.4	TOSO	NM_005449.3		apoptosis	nucleus	anti-
GI_34147519-S	221.8	271.9	259.2	STX6	NM_005819.3		vesicle	endosome	nonselecti
GI_34147520-S	528.6	490.3	526.2	NOC4	NM_006067.3	C16orf4	molecular	cytoplasm	
GI_34147521-S	1081.4	1197.3	985.7	CABC1	NM_020247.3		chaperone	mitochond	

GI_34147523-S	259.1	341.6	332.6	SKD3	NM_030813.3		nucleotide		
GI_34147524-S	277.9	207.5	161.3	C20orf55	NM_031424.3	MGC4675;bA371L19.3	DNA	nucleus	regulation
GI_34147525-S	234.7	220.7	225.2	ZNF551	NM_138347.2		nucleic	nucleus	regulation
GI_34147526-S	239.8	266.5	341	LOC90313	NM_138349.2				
GI_34147528-S	647.6	546.5	441	LOC91272	NM_138369.1				
GI_34147531-S	124.7	138.1	130.5	MYLC2PL	NM_138403.2	PLRLC	calcium		
GI_34147533-S	144.6	159.3	164.7	RDH13	NM_138412.2		oxidoredu		metabolis
GI_34147534-S	113.7	103.8	97.6	LOC112937	NM_138416.1		beta-	beta-	carbohydr
GI_34147536-S	2786	3316	2050.1	GRCC10	NM_138425.2				
GI_34147537-S	877.7	2041.6	1997.2	SDSL	NM_138432.2	SDS-RS1	lyase		amino
GI_34147538-S	1764.1	1634.4	1191.4	LOC114926	NM_138436.2				
GI_34147539-S	988.7	1025.8	1084.2	LOC114984	NM_138439.1				
GI_34147541-S	3315.7	3423.2	3488.8	LOC115098	NM_138442.2				
GI_34147542-S	522.4	510.7	490.5	CCDC5	NM_138443.2	HEI-C;HsT1461			
GI_34147543-S	639.6	639.3	813	LOC115509	NM_138447.1		nucleic	intracellula	regulation
GI_34147545-S	125.9	129	120.9	RAB3C	NM_138453.2		GTP		small
GI_34147546-S	1437.5	1135.9	776.4	CTHRC1	NM_138455.2				
GI_34147547-S	1363.7	1898.7	1588.1	C6orf68	NM_138459.2	MGC:7199			
GI_34147548-S	300.6	338.8	333.5	LOC116238	NM_138463.2				
GI_34147549-A	113.5	137.2	126	HSU84971	NM_138490.1	VG5Q;FLJ10283;HUS84971			
GI_34147551-S	1955.4	2614.8	2551.8	EIF5A	NM_001970.3	EIF-5A;EIF5A1	translation	cytoplasm	viral
GI_34147553-S	983.1	1375.4	1118.5	RAB9A	NM_004251.3	RAB9	RAB small	Golgi	nonselecti
GI_34147554-S	212.8	294.2	330.2	MPZL1	NM_003953.3	PZR	protein	integral to	transmem
GI_34147555-S	1214.7	1340.6	1194.9	MADH4	NM_005359.3	JIP;DPC4;SMAD4	transcripti	cytoplasm	SMAD
GI_34147556-S	4945	5458.4	5101	NDUFS2	NM_004550.3		iron-sulfur	NADH	mitochond
GI_34147557-S	99.4	112.8	107.6	LYL1	NM_005583.3		DNA	nucleus	oncogene
GI_34147559-S	12102.3	13007	10750	DDOST	NM_005216.3	OST;OST48;KIAA0115	dolichyl-	endoplas	N-linked
GI_34147560-S	258.6	315	272.4	HSPB7	NM_014424.3	cvHSP	protein C-		regulation
GI_34147561-S	186.5	210.8	125	SMO	NM_005631.3	Gx;SMOH	protein	integral to	cell growth
GI_34147562-S	426.5	411.2	412.7	FLJ11126	NM_018332.3				
GI_34147563-S	136.5	128.9	137.2	SLC1A7	NM_006671.3	AAAT;EAAT5			
GI_34147565-S	113.2	119.5	109.4	SREB3	NM_018969.3		G-protein	integral to	signal
GI_34147566-S	2581.1	2774	2400.9	GUK1	NM_000858.3	GMK	guanylate		GTP
GI_34147567-S	1803.1	1534.6	1401.4	RAP1GDS1	NM_021159.3	GDS1	GTPase	cellular_co	biological_
GI_34147571-S	2761.6	2496.8	673.2	ISG20	NM_002201.4	HEM45	exonuclea	nucleoplas	cell
GI_34147572-S	1127.5	1159.3	1250	SF3A1	NM_005877.3	PRP21;SAP114;SF3A120	pre-mRNA	spliceoso	mRNA
GI_34147573-S	23636	22715	21881	ITGB5	NM_002213.3		cell	integrin	cell-matrix
GI_34147574-S	247.1	252.7	243.4	HTATIP2	NM_006410.3	CC3;TIP30	protein	nucleus	induction
GI_34147575-S	237.6	421.2	199.5	NK4	NM_004221.3		cell	extracellul	cell
GI_34147576-S	101.5	131.9	127.2	RPIP8	NM_006695.3		small		small
GI_34147577-S	225.8	233.9	237.7	NR2F1	NM_005654.3	EAR3;EAR-	ligand-	nucleus	signal
GI_34147578-S	401.9	327.1	356.6	PISD	NM_014338.3	PSSC;DJ858B16;DKFZP566G2246	phosphati		phospholi
GI_34147579-S	2280.2	2659.4	3028	RRAGA	NM_006570.3	RAGA;FIP-1	GTP	peripheral	cell death
GI_34147580-S	1112.4	861.4	934.5	ZSIG11	NM_015926.3	SIG11			

GI_34147581-S	128.7	344.6	298.7	ZAP128	NM_006821.3	PTE2	serine	peroxisom	acyl-CoA
GI_34147582-S	254.3	270.8	264.7	FLJ20291	NM_017748.3				
GI_34147584-S	939	995.1	1032.8	DMAP1	NM_019100.3	DNMAP1;DNMTAP1;FLJ11543;KIAA1425	DNA	kinesin	DNA
GI_34147585-S	4101.6	4916.5	4557.1	ANAPC5	NM_016237.3	APC5;PDL-108	ubiquitin-	anaphase-	mitotic
GI_34147586-S	683.7	778.4	824	MOSPD3	NM_023948.3	CDS3;AF053356_CDS3	structural		
GI_34147587-S	1102.7	549.6	757.7	FLJ20647	NM_017918.3				
GI_34147589-S	127.6	132.3	132.5	LOC56901	NM_020142.3	NUOMS			
GI_34147590-S	1951.6	1389.6	1276.3	PUS1	NM_025215.3		pseudouri	nucleus	tRNA
GI_34147591-S	257	311.7	251.7	MGC3262	NM_024029.3				
GI_34147593-S	2385.4	1990.9	1805.9	MUS81	NM_025128.3	FLJ21012	endonucle	intracellula	DNA
GI_34147595-S	195.1	248.2	267.2	CDCA3	NM_031299.3	GRCC8;TOME-1;MGC2577	molecular	cellular_co	biological_
GI_34147598-S	158.6	167.5	159.5	FCER2	NM_002002.3	CD23;FCE2;CD23A;IGEBF	integrin	integral to	heterophili
GI_34147599-S	5165.6	4035	3616.8	CD99	NM_002414.3	MIC2;MIC2X;MIC2Y	cell	proteoglyc	cell
GI_34147600-S	417.3	415.3	273.5	PGF	NM_002632.3	PLGF;PlGF-2	growth	membran	positive
GI_34147601-S	1916	2138.2	2173.6	ARHGDIA	NM_004309.3	GDIA1;RHOGDI	Rho GDP-	cytoplasm	negative
GI_34147602-S	432.2	422.2	392.1	BCS1L	NM_004328.3	BCS;BCS1;FLNMS;h-	adenosine	respiratory	energy
GI_34147603-S	1681.5	1793.5	1802.3	STX4A	NM_004604.3	p35-2	protein	membran	intracellula
GI_34147604-S	2775.7	2716.9	2470.9	OPTN	NM_021980.3	NRP;FIP2;HIP7;HYPL;GLC1E;TFIIIA-INTP		cytoplasm	pathogene
GI_34147605-S	974.8	1221.5	1110.5	SLC25A10	NM_012140.3	DIC	dicarboxyli	mitochond	dicarboxyli
GI_34147606-S	470	367.9	422.2	CGI-57	NM_015680.3				
GI_34147607-S	2297.6	2923.8	2325	NOSIP	NM_015953.3	CGI-25			
GI_34147608-S	256.9	299.6	266.2	FLJ20519	NM_017860.3				
GI_34147611-S	1091.2	1498.3	1239.3	SUV39H2	NM_024670.3	FLJ23414	methyltran	chromatin	chromatin
GI_34147613-S	967.8	1016	775	OBFC1	NM_024928.3	FLJ22559;bA541N10.2	nucleic		
GI_34147614-S	382.9	445	423.2	FLJ22688	NM_025129.3				
GI_34147615-S	314.1	383.6	392.4	DKFZP434I2	NM_031478.3				
GI_34147616-S	4165.2	4117.3	3503.7	ASC1p100	NM_032204.3	FLJ21588;DKFZp586O0223			
GI_34147617-S	311.4	328.5	315.2	LOC132001	NM_138807.2				
GI_34147618-S	92.5	94.2	96.2	C9orf65	NM_138818.2				
GI_34147619-S	2038.5	1528.9	1057.2	EHD4	NM_139265.2		nucleic	nucleus	
GI_34147620-A	1613.5	1524.8	1488.3	AMPD2	NM_139156.1		AMP	cellular_co	purine
GI_34147620-I	122.5	128.1	135.2	AMPD2	NM_139156.1		AMP	cellular_co	purine
GI_34147622-S	809.4	653.5	661.2	RPA2	NM_002946.3	REPA2	single-	DNA	DNA
GI_34147623-S	2650.4	1959.2	1577.4	SORD	NM_003104.3	SORD1	alcohol		sorbitol
GI_34147624-S	128.9	167.9	176.4	SIX2	NM_016932.3		transcripti	nucleus	embryoge
GI_34147625-S	758.3	561.1	662.7	DUSP22	NM_020185.3	JKAP;JSP1;MKPX	tumor		inactivatio
GI_34147626-S	105.8	97.9	83.3	FLJ12895	NM_023926.3				
GI_34147627-S	1742.6	1059	902.6	HSPBAP1	NM_024610.3	PASS1;FLJ22623			
GI_34147628-S	88.2	92.4	84.1	PROX1	NM_002763.3		specific	nucleus	ectoderm
GI_34147629-S	10511.7	11226	10570	TUFM	NM_003321.3	EFTU;EF-TuMT	translation	mitochond	translation
GI_34147631-S	4585.2	4814.2	4229.8	ZYX	NM_003461.3		cell	focal	cell
GI_34147632-S	426.2	444.6	494.1	PLK1	NM_005030.3	STPK13	protein	nucleus	mitosis
GI_34147633-S	515.1	580.7	539.6	SLC12A4	NM_005072.3	KCC1	potassium	integral to	regulation
GI_34147634-S	720.3	711.9	693.3	CHERP	NM_006387.4	DAN16;SCAF6			pathogene

GI_34147635-S	812.7	938.7	885.4	CBX1	NM_006807.3	CBX;M31;MOD1;HP1-BETA;HP1Hs-beta	chromatin	nucleoplas	chromatin
GI_34147639-S	562.3	562.8	454	FLJ20399	NM_017803.3		double-	intracellula	
GI_34147640-S	391.5	470.8	413.3	ELAC2	NM_018127.4	ELC2;HPC2;FLJ10530			
GI_34147641-S	979.8	982.9	1116.2	MGC10433	NM_024321.3				
GI_34147642-S	228.6	256.1	236.7	FLJ14166	NM_024565.3				
GI_34147643-S	132.7	337.6	128.5	SERPINA5	NM_000624.3	PCI;PAI3;PROCI;PLANH3	serpin		
GI_34147645-S	2334.7	2674.3	2322.3	PLOD3	NM_001084.3	LH3	procollage	membran	protein
GI_34147646-S	2825.6	2153.8	1519.6	FHL1	NM_001449.3	KYO-T;SLIM1	molecular	cellular_co	muscle
GI_34147647-S	311.8	356.9	352.5	PDZK1	NM_002614.3	CAP70;CLAMP;PDZD1	transporte		small
GI_34147648-S	186.2	213.3	177.4	TLE2	NM_003260.3	ESG;ESG2		nucleus	histogene
GI_34147649-S	741.3	830.7	788.5	SLC25A11	NM_003562.3	OGC;SLC20A4	oxoglutara	mitochond	small
GI_34147650-S	501.8	635.7	539.6	MKNK1	NM_003684.3	MNK1	protein		signal
GI_34147651-S	151.8	172.4	174.2	DLK1	NM_003836.3	FA1;ZOG;pG2;PREF1;Pref-1	structural	secretory	developm
GI_34147652-S	233.6	293.1	238.6	NOL3	NM_003946.3	ARC;MYC;NOP;NOP30	apoptosis	cytosol	anti-
GI_34147653-S	3111.7	2164.4	1408.4	SLC3A2	NM_002394.3	4F2;CD98;MDU1;4F2HC;NACAE	amino	integral to	amino
GI_34147654-S	290.7	591.7	694.8	RAB3A	NM_002866.3		RAB small	synaptic	neurotran
GI_34147655-S	88.9	92.5	84.6	SYK	NM_003177.3		protein-		protein
GI_34147656-S	619.3	540	446.4	ZNF76	NM_003427.3	ZNF523;Zfp523;D6S229E	transcripti	nucleus	regulation
GI_34147657-S	2817.2	745.5	524.1	DDIT3	NM_004083.3	CHOP;CEBPZ;CHOP10;GADD153	transcripti	nucleus	response
GI_34147658-S	135.5	171.7	157.1	UCHL1	NM_004181.3	PARK5;PGP9.5	ubiquitin	intracellula	ubiquitin-
GI_34147659-S	467	494.6	434.2	PPP3CC	NM_005605.3	CALNA3		calcineurin	
GI_34147660-S	1609.2	1683.7	1609.1	SFRS4	NM_005626.3	SRP75	pre-mRNA	nucleus	mRNA
GI_34147661-S	529.1	633.2	478.9	TFCP2	NM_005653.3	CP2;LSF;LBP-1C;TFCP2C	DNA		regulation
GI_34147662-S	288.1	359	343.7	HRBL	NM_006076.3	RABR	DNA	mitochond	
GI_34147663-S	2253.3	2748.7	2615.4	TFG	NM_006070.3	TF6	molecular	cellular_co	biological_
GI_34147664-S	165.8	186.6	170.1	RGS14	NM_006480.3		GTPase	peripheral	regulation
GI_34147665-S	2694	2570.1	2379.1	STK25	NM_006374.3	SOK1;YSK1	protein		response
GI_34147667-S	3463.5	2822.1	3532	TFDP1	NM_007111.3	DP1;Dp-1;DRTF1	transcripti	transcripti	regulation
GI_34147668-S	174.3	227.6	224.3	CTXL	NM_014312.3	CTH	antigen	membran	
GI_34147669-S	872.3	1027.3	995.7	SLC39A1	NM_014437.3	ZIP1;ZIRTL	di-, tri-	integral to	di-, tri-
GI_34147670-S	103.2	156.9	127.8	RAB30	NM_014488.3		RAB small	Golgi	protein
GI_34147671-S	607.6	607	654.7	HTATSF1	NM_014500.3	TAT-SF1;dJ196E23.2	transcripti	nucleus	viral
GI_34147672-S	569.7	614.5	636.9	ST6GALNAC	NM_013443.3	ST6GALNACVI	sialyltransf	integral to	glycosphin
GI_34147673-S	727.3	907.1	1182.4	ACAD9	NM_014049.3	ACAD-9;NPD002;MGC14452			
GI_34147674-S	378.2	246.4	195.2	STXBP6	NM_014178.5	amisyn;HSPC156			
GI_34147675-S	891.3	730.3	650.3	CGI-12	NM_015942.3				
GI_34147677-S	4860.2	4241.7	4002	LOC51035	NM_015853.3				
GI_34147678-S	139.3	126.7	127.1	HOOK1	NM_015888.3	HK1			nonselecti
GI_34147679-S	1239.6	1130	793.2	TGFB1I1	NM_015927.3	HIC5;ARA55;HIC-5;TSC-5	protein	focal	negative
GI_34147682-S	1788.2	1961.9	1972	RNPC4	NM_018107.3	FLJ10482	RNA	nucleus	
GI_34147683-S	552.4	665.5	923.5	C10orf3	NM_018131.3	FLJ10540			
GI_34147684-S	163.1	137	158.8	HES6	NM_018645.3		transcripti		regulation
GI_34147685-S	547.4	609	364.2	ABHD6	NM_020676.3				
GI_34147686-S	116.3	114.3	112.3	MGC20741	NM_018561.3		cysteine-		ubiquitin-

GI_34147687-S	256.1	245.1	330.4	FLJ22318	NM_022762.3	DKFZp434K0926			
GI_34147689-S	107.4	132.4	99.2	FLJ22457	NM_024901.3				
GI_34147690-S	185.7	223.6	210	FLJ22582	NM_025045.3				
GI_34147691-S	484.8	570.2	587.1	Lin10	NM_025187.3	FLJ12076			
GI_34147692-S	149.7	163.9	146.2	PLA2G12A	NM_030821.3		calcium-	cellular_co	biological_
GI_34147693-S	8821.3	8560.1	7685.5	FLJ21977	NM_032213.3				
GI_34147695-S	1369.1	1080.2	924.4	C6orf93	NM_032860.3	FLJ14909;dJ468K18.4			
GI_34147697-S	1487.4	1608.8	1285.6	C14orf32	NM_144578.2	MISS;MGC23138;c14_5346			
GI_34147700-S	238.3	218.2	243.1	MGC23280	NM_144683.2		oxidoredu		metabolis
GI_34147701-S	436.1	528.7	509.4	MGC29762	NM_144706.2				
GI_34147703-S	363.1	455.7	562.3	MGC20806	NM_144999.2				
GI_34147704-S	4349.8	4499.3	2295.9	HMGN1	NM_004965.4	HMG14	positive	chromatin	
GI_34147705-S	1379.6	1633.5	1277.7	MGC16703	NM_145042.2		GTP	microtubul	microtubul
GI_34147709-S	91	102.5	78.9	MGC4734	NM_145051.2	FLJ31197			
GI_34147710-S	248.2	182.2	199	C13orf3	NM_145061.2	RAMA1;MGC4832			
GI_34147711-S	942.7	804.5	758.7	C6orf130	NM_145063.2	MGC19570;dJ34B21.3			
GI_34147712-S	499.4	356.7	407	TLE1	NM_005077.3	ESG;ESG1;GRG1		nucleus	histogene
GI_34147713-S	98.8	124.7	106.3	LOC90589	NM_145233.2			nucleus	
GI_34147714-S	109.7	118.4	95.6	CHRDL1	NM_145234.2	CHL;VOPT;NRLN1;dA141H5.1			developm
GI_34147716-S	92.5	77.6	79.8	ZNF31	NM_145238.2	KOX29;ZFP-31	DNA	nucleus	regulation
GI_34147718-S	240.6	290.3	314.5	LOC146542	NM_145271.2	MGC13138	nucleic	intracellula	regulation
GI_34147719-S	137.2	146.7	128.4	C7orf33	NM_145304.2				
GI_34147720-S	95.9	102.2	98.1	LOC220070	NM_145308.2				
GI_34147721-S	154.6	129.6	141.4	ZNF485	NM_145312.2		nucleic	nucleus	regulation
GI_34147722-S	593.8	499.9	847	KIFC2	NM_145754.2		ATP	microtubul	microtubul
GI_34147725-A	2550.6	3493.2	2107.7	SHC1	NM_003029.3	SHC;SHCA	transmem		regulation
GI_34147725-I	147.9	152.3	133.6	SHC1	NM_003029.3	SHC;SHCA	transmem		regulation
GI_34147726-S	183.5	194	176.5	TOB3	NM_031921.3	KIAA1273	nucleotide		
GI_34170263-I	142.9	159.4	156.7	BDNF	NM_170735.3	MGC34632	growth		neurogene
GI_34222089-S	107.2	95.5	86.3	KCNJ13	NM_002242.2	KIR1.4;KIR7.1;MGC33328	voltage-	voltage-	potassium
GI_34222090-S	64.5	71.4	59.7	PIWIL1	NM_004764.2	HIWI;PIWI			female
GI_34222091-S	267.7	322.5	204.7	IFIT2	NM_001547.3	G10P2;IFI54;cig42;IFI-54;GARG-39;ISG-54K	molecular	cellular_co	immune
GI_34222093-S	1235.9	1481.4	1056.3	ELF1	NM_172373.2		transcripti	nucleus	regulation
GI_34222094-S	240.6	449.5	172.9	LTB4DH	NM_012212.2	MGC34943	catalytic	cytoplasm	leukotrien
GI_34222095-S	2050.4	2111.1	1918	UBXD2	NM_014607.2	UBXDC1;KIAA0242	transcripti		regulation
GI_34222096-S	247.3	225.1	251.7	KIAA0089	NM_015141.2		glycerol-3-	glycerol-3-	carbohydr
GI_34222097-S	259.6	292	283	KIAA0759	NM_015305.2				
GI_34222098-S	914.3	1081.7	822.1	KIAA0252	NM_015138.2				
GI_34222099-S	287.7	271.9	219.9	PLCL2	NM_015184.2	PLCE2;KIAA1092	phosphoin		lipid
GI_34222100-S	3672.5	3593.6	3185.7	KIAA1068	NM_015332.2				
GI_34222103-S	147.8	171.5	135.6	C20orf26	NM_015585.2	DKFZP434K156	transporte	membran	transport
GI_34222105-S	154.6	166.4	182.6	SAMD4	NM_015589.2	KIAA1053;DKFZp434H0350			
GI_34222107-S	684.7	966	842.1	STK36	NM_015690.2	FU;KIAA1278;DKFZp434N0223	ATP		protein
GI_34222109-I	243.7	264.4	296.9	MDM1	NM_017440.2				

GI_34222111-S	149.7	132.9	126.3	DKFZp547C1	NM_018712.2				
GI_34222113-S	345.9	471.2	248.6	KIAA1434	NM_019593.2	FLJ11085;MGC26147			
GI_34222114-S	122.7	133.5	135.2	DKFZp566D2	NM_020116.2		calcium		
GI_34222115-S	1705.5	1778.8	1664	TDE2	NM_020755.2	TDE1L;TMS-2;KIAA1253		integral to	
GI_34222116-S	132.9	126.8	114.7	HACE1	NM_020771.2	KIAA1320	ubiquitin-	intracellula	ubiquitin
GI_34222117-S	253.4	296	245.2	WDR35	NM_020779.2	KIAA1336;MGC33196			
GI_34222118-S	100.3	104.3	91	SYT4	NM_020783.2	HsT1192;KIAA1342	transporte	synaptic	transport
GI_34222119-S	1319.2	1396.6	1307.7	ZBTB4	NM_020899.2	KAISO-L1;KIAA1538	protein		
GI_34222120-S	3168	2753.3	2568.9	Nup37	NM_024057.2	MGC5585;FLJ22618	protein	nucleus	intracellula
GI_34222122-S	300	270	287.5	DKFZP566N(	NM_030923.2	DC29			
GI_34222123-S	364.9	428.7	519.5	MGC13183	NM_032358.2				
GI_34222124-S	302.9	369.5	302.3	C9orf59	NM_033387.2	FLJ00024			
GI_34222125-S	528.2	567.7	593	RWDD2	NM_033411.2	MGC13523;dJ747H23.2	acylphosp		
GI_34222126-S	304.9	669.1	262.8	MGC17330	NM_052880.2				
GI_34222128-S	356	360.3	279.4	SSFA2	NM_006751.3	CS1;CS-1;KRAP;SPAG13;KIAA1927		plasma	
GI_34222129-S	1216.1	1473.3	1443.7	RAB18	NM_021252.3		GTP	cellular_co	small
GI_34222130-S	138.7	153.5	139	LOC142937	NM_138470.2				
GI_34222132-S	1957.6	2351.6	2164.7	TXNDC	NM_030755.3	TMX;TXNDC1;DKFZP564E1962	electron		electron
GI_34222134-S	93.3	96.5	99.3	NMU2R	NM_020167.3	FM4	G-protein	integral to	neuropepti
GI_34222135-S	268.2	585.8	413.5	A4GALT	NM_017436.3	P;P1;PK;A14GALT	galactosylt	Golgi	galactosyl
GI_34222136-S	299.1	287.7	297.8	LOC93081	NM_138779.2		catalytic		
GI_34222139-S	1686.6	1396.3	1961.8	SLC17A5	NM_012434.3	SD;AST;NSD;SLD;ISSD;SIASD;SIALIN	hydrogen:	lysosomal	anion
GI_34222140-S	202	240.3	210.9	C19orf22	NM_138774.2	MGC16353			
GI_34222142-S	752.5	796.7	792.3	C9orf12	NM_022755.3	INSP5K2;FLJ13163	kinase		
GI_34222144-S	501.4	404.5	387.4	LOC91689	NM_033318.3				
GI_34222146-S	209.6	245.2	204.5	TGFBRAP1	NM_004257.3	TRAP1;TRAP-1			TGFbeta
GI_34222147-S	98.9	106.2	87.5	C1QTNF7	NM_031911.3	CTRP7;ZACRP7		microfibril	
GI_34222148-S	170.5	218.1	230.4	KBTBD7	NM_032138.3	DKFZP434E2318	protein		
GI_34222150-S	148.9	169.4	151.1	CNN1	NM_001299.3	SMCC;Sm-Calp	actin	cytoskelet	muscle
GI_34222151-S	316.2	376.4	334.6	SLC30A4	NM_013309.3	ZNT4	zinc ion	endosome	zinc ion
GI_34222152-S	118.6	135.2	105.2	VSNL1	NM_003385.3	VILIP;HPCAL3	calcium		central
GI_34222153-S	186.5	214.8	197.5	ZMYND12	NM_032257.3	DKFZp434N2435			
GI_34222154-S	626.2	689.3	613.7	SLC20A2	NM_006749.3	GLVR2;MLVAR;PIT-2;Glvr-2	sodium:ph	membran	small
GI_34222155-S	527	519.8	411	SLC30A3	NM_003459.3	ZNT3	zinc porter	endosome	small
GI_34222156-S	356.4	406.2	366.4	HLC-8	NM_017941.3	FLJ20721			
GI_34222157-S	253.2	309.2	284.6	CD164	NM_006016.3	MGC-24;MUC-24	cell	soluble	negative
GI_34222158-S	468.7	829	1040.9	FLJ10925	NM_018275.3				
GI_34222159-S	931.6	791.7	953.6	ELL2	NM_012081.3		RNA	transcripti	RNA
GI_34222160-S	126.8	154.2	130.4	SPAG4L	NM_080675.3	TSARG4;MGC33594;dJ726C3.1		kinesin	
GI_34222163-S	98.3	92.2	95.4	MGC26768	NM_144634.2		lysozyme	extracellul	cell wall
GI_34222164-S	144.1	126.2	151.3	ZNF502	NM_033210.3	FLJ12515;FLJ14855			
GI_34222165-S	182.5	191.3	181.9	ZDHHC19	NM_144637.2	MGC33345	sugar		
GI_34222166-S	100.8	120.4	106.9	MGC26610	NM_144647.2		calcium		
GI_34222168-S	86.9	89.7	92.3	MGC33371	NM_144664.2				

GI_34222169-S	195.3	234.3	203.3	MGC27019	NM_144705.2			microtubul	microtubul
GI_34222170-S	91.5	93.4	85.5	C10orf82	NM_144661.2	MGC33547			
GI_34222172-S	130.4	159.4	151.8	MGC33630	NM_144668.2				
GI_34222173-S	181.9	187.6	158.5	FLJ32743	NM_145020.2				
GI_34222174-S	330.8	257.1	292.9	MGC22679	NM_144711.2				
GI_34222175-S	213	218.2	216.6	C6orf199	NM_145025.2	MGC26954;dJ70A9.1	ATP		
GI_34222176-S	122.1	149.3	127.7	MGC27016	NM_144979.2		nucleic		
GI_34222178-S	144.7	166.7	133.8	MGC29898	NM_145048.2				
GI_34222179-S	115.4	119.2	98.2	C6orf102	NM_145027.2	MGC33317;dJ137F1.4;dJ188D3.1			
GI_34222180-S	94	103	93.9	LOC127540	NM_145205.2	dJ1007G16.5	DNA	chromatin	regulation
GI_34222181-S	98.2	96.1	102.4	CALR3	NM_145046.2	CRT2;FLJ25355;MGC26577	calcium	endoplas	
GI_34222182-S	200	258.6	204.1	DDIT4L	NM_145244.2	REDD2;Rtp801L			
GI_34222183-S	105.5	108.1	108.2	MGC33182	NM_145203.2		protein-		protein
GI_34222184-S	511.6	499.8	489	LOC133957	NM_145265.2				
GI_34222185-S	94.9	129.4	107.4	FANK1	NM_145235.2				
GI_34222187-S	474.8	383.3	343.6	MOBKL2C	NM_145279.2	MOB3C;MGC26743			
GI_34222188-S	134.5	158.4	131.8	STYX	NM_145251.2		protein		protein
GI_34222189-S	90.3	90.5	90.1	LOC137392	NM_145269.2				
GI_34222190-S	116.8	131.6	121.1	NOXO1	NM_144603.2	P41NOX;P41NOXA;P41NOXB;P41NOXC;M			intracellula
GI_34222191-S	97	108.5	89.6	GALNT15	NM_145292.2				
GI_34222192-S	1257.7	1380.8	1122.2	PRPF4	NM_004697.3	PRP4;HPRP4;Prp4p;HPRP4P	pre-mRNA	spliceoso	RNA
GI_34222193-S	401.4	431.2	336	FLJ10613	NM_019067.3		peptidase	membran	proteolysis
GI_34222195-S	1007	893.3	988.5	FLJ10511	NM_018120.3		metal ion		metal ion
GI_34222196-S	235.2	270.4	245.9	SLC16A7	NM_004731.3	MCT2	pyruvate	membran	pyruvate
GI_34222197-S	804.4	810.7	435.6	C10orf22	NM_032804.4	FLJ14547			
GI_34222198-S	1374.4	937.8	587.9	LRRC5	NM_018103.3	FLJ10470			
GI_34222200-S	142.5	178.2	204.7	MGC10204	NM_153329.2		oxidoredu		metabolis
GI_34222201-S	625	805.1	865.8	ZNF503	NM_032772.3	MGC2555;FLJ45745			
GI_34222202-S	419.2	469.4	456.1	CRI2	NM_153232.2	EID2;EID-2;MGC20452	carboxype		proteolysis
GI_34222204-S	489.8	485.4	384.4	AEBP2	NM_153207.2	MGC17922			
GI_34222205-S	274.2	313.9	270.6	MGC33486	NM_153266.2				
GI_34222206-S	137.5	126.8	126.5	MGC34034	NM_153224.2				
GI_34222207-S	184.7	146.1	263.5	MGC33974	NM_153350.2		receptor		
GI_34222208-S	88.4	93.2	83.4	MGC26143	NM_153243.2				
GI_34222210-S	96.8	92.3	88.7	TCBA1	NM_153355.2	MGC41924			
GI_34222211-S	125.1	129.2	131.1	MGC33653	NM_153346.2				
GI_34222212-S	235	181.1	99.9	EVER1	NM_007267.5	EV1;TMC6;EVIN1;LAK-4P			
GI_34222213-S	299.4	310.8	319	MGC33214	NM_153354.2				
GI_34222214-S	188.3	240.8	216.7	CLDN7	NM_001307.3	CPETRL2;Hs.84359	structural	tight	
GI_34222215-S	339	334.8	268	LNX2	NM_153371.2	MGC46315	protein		intracellula
GI_34222216-I	1678.1	1416.5	1725	GPSN2	NM_138501.3	SC2;TER		integral to	
GI_34222217-S	123.2	134.2	124.4	C10orf46	NM_153810.2	FLJ40409;MGC33215			
GI_34222218-S	887	1000.5	916.9	CBLB	NM_170662.2	RNF56	protein	nucleus	NLS-
GI_34222219-S	453	710.9	836.5	CHPF	NM_024536.4	CSS2;FLJ22678			

GI_34222220-S	4276.9	2683.6	2296	IMP-2	NM_006548.3	IMP2;VICKZ2	RNA	cytoplasm	translation
GI_34222221-S	123.5	107	99.7	EPHX2	NM_001979.3		epoxide	cytoplasm	response
GI_34222222-S	1326	1752	549.1	TPM1	NM_000366.4	CMH3;TMSA	structural	muscle	regulation
GI_34222223-S	115.2	116.7	107.4	UPP2	NM_173355.2	UP2;UPASE2;UDRPASE2	catalytic		nucleoside
GI_34222225-S	312.4	316.2	492	MGC20700	NM_174983.2	PP3501			
GI_34222226-S	93.5	102.3	105.8	C19orf21	NM_173481.2		DNA	nucleus	regulation
GI_34222227-S	109.7	111.5	96.3	MPP7	NM_173496.2	FLJ32798	protein		intracellula
GI_34222229-S	182.4	232.6	198.6	MGC16664	NM_173509.2				
GI_34222230-S	108.3	134.4	115.1	MGC43122	NM_173513.2				
GI_34222231-S	375.8	525.2	414	MGC33365	NM_173552.2				
GI_34222232-S	97.4	105.3	96.5	FGD2	NM_173558.2	ZFYVE4	zinc ion		
GI_34222234-S	860.9	939.6	830.5	MGC29649	NM_173810.3				
GI_34222235-S	108.4	129.4	108.6	LOC283248	NM_173587.2		DNA	nucleus	
GI_34222236-S	464.7	475.9	479.2	MGC26717	NM_173824.2		cysteine-		proteolysis
GI_34222237-S	99.7	104.7	104.9	C6orf182	NM_173830.3	MGC21731;bA487F23.2			
GI_34222238-S	558.3	721.5	582.6	MGC33584	NM_173680.2		DNA	nucleus	regulation
GI_34222239-S	128.5	138.2	129.7	LOC286046	NM_173683.2				
GI_34222240-S	157.7	160.1	144.9	C14orf8	NM_173846.3				
GI_34222241-S	995.3	1126.6	627.2	LOC90410	NM_174887.2				
GI_34222243-S	7187.9	7955.1	6403	ARHC	NM_175744.3	ARH9;RHOC;RHOH9	Rho small		
GI_34222245-I	789.6	811.1	980.2	HRAS	NM_176795.1	HRAS1;RASH1	GTPase	peripheral	chemotaxi
GI_34222247-S	280.8	330.9	310.6	URP2	NM_031471.4	KIND3;MIG2B;MGC10966		cytoskelet	
GI_34222248-S	161.9	151	127.3	FRMD3	NM_174938.3	4.1O;P410;EPB41L4O;MGC20553			
GI_34222251-I	264.2	272.1	284.1	FLJ22222	NM_175902.3				
GI_34222252-S	123.9	139.7	128	DNAJC5B	NM_033105.3	CSP-beta;MGC26226	chaperone	membran	protein
GI_34222253-A	862.1	947.1	903	PH-4	NM_177938.1	FLJ20262	calcium	endoplas	
GI_34222255-S	193.5	212.6	197	DKFZp667B1	NM_177966.3				
GI_34222257-S	813.5	996.9	1108.1	UFD1L	NM_005659.3		ubiquitin-		skeletal
GI_34222259-S	2254.2	2377.7	2026.6	ARD1	NM_003491.2	TE2;DXS707	N-	nucleus	internal
GI_34222260-S	546.9	608.6	508.4	ZNF482	NM_006626.3	ZID;ZBTB6	protein	nucleus	
GI_34222262-S	116	151.4	137.3	KIAA1754L	NM_178495.3				
GI_34222264-S	2771.8	2816.8	2742.1	MCRS1	NM_006337.3	P78;MSP58;ICP22BP		nucleoplas	regulation
GI_34222265-S	102.7	121.8	95.8	MGC41943	NM_178561.3				
GI_34222266-S	228.3	276.1	223.3	STXBP4	NM_178509.3	Synip;MGC50337			
GI_34222267-S	124.6	167.2	161.4	FBXO27	NM_178820.3	FBG5			
GI_34222268-S	99.2	108	110.4	FLJ13057	NM_178439.3	GMCL2			
GI_34222269-S	211.4	205.1	198.3	OXR1	NM_181354.2	FLJ10125			
GI_34222270-S	306.5	346.7	312.5	SFXN2	NM_178858.3		cation	mitochond	cation
GI_34222271-S	845.5	788.3	872	GLUD2	NM_012084.3	GLUDP1	glutamate	mitochond	amino
GI_34222272-S	125.8	141.6	126.8	FLJ33620	NM_178824.3				
GI_34222273-S	274.1	349.5	325.3	OR2H1	NM_030883.3	OR2H6;OR2H8;OR6-2;HS6M1-	olfactory	integral to	olfaction
GI_34222274-S	1032.1	1211.4	1192.1	SSA2	NM_004600.3		ribonucleo	ribonucleo	transcripti
GI_34222276-S	214.2	261.3	227.9	FLJ14001	NM_024677.3				
GI_34222277-S	105	142.7	110.6	FLJ32130	NM_152458.4		nucleic	intracellula	regulation

GI_34222278-S	263.8	318.2	274.7	ARMC2	NM_032131.3	bA787I22.1;DKFZP434P0714			
GI_34222280-S	284.1	361.7	323.6	FLJ35989	NM_152597.3				
GI_34222281-S	264	339.7	313.1	FLJ40342	NM_152347.3		calcium		
GI_34222283-S	135.6	113.3	108.6	FLJ25421	NM_152512.3				
GI_34222285-S	90.6	105.8	93.5	FLJ25534	NM_153234.3				
GI_34222286-S	333.9	315.9	163.3	CYR61	NM_001554.3	CCN1;GIG1;IGFBP10			embryoge
GI_34222287-S	2290.3	2321.9	2913.5	TUBG1	NM_001070.3	TUBG	structural	centrosom	microtubul
GI_34222289-S	329.9	402.1	370.9	GTF2H4	NM_001517.3		transcripti	transcripti	DNA
GI_34222290-S	105.2	101.7	107.2	GRP	NM_002091.3		growth	soluble	signal
GI_34222291-S	468.4	505.2	672.1	THOP1	NM_003249.3		metalloen		proteolysis
GI_34222292-S	321.5	670.9	612.4	GYS1	NM_002103.3	GSY;GYS			glycogen
GI_34222293-S	3326.2	3003.4	2789.1	ATP5D	NM_001687.3		hydrogen-	proton-	proton
GI_34222294-S	303.2	361.8	374.8	TYK2	NM_003331.3	JTK1	non-	cytoskelet	protein
GI_34222295-S	1889.6	2588.2	1898.4	GTF2E2	NM_002095.3	FE;TF2E2;TFIIE-B	general	transcripti	transcripti
GI_34222296-S	487.5	390.3	161.2	FCGRT	NM_004107.3	FCRN	receptor	integral to	pregnancy
GI_34222297-S	165.8	162.2	146.3	PRKCI	NM_002740.3	PKCI;DXS1179E	atypical		protein
GI_34222299-S	437.2	312.2	318.3	EPS8	NM_004447.3		SH3/SH2		EGF
GI_34222300-S	472.7	484.2	434.9	D13S106E	NM_005800.3		cysteine-		ubiquitin-
GI_34222301-S	1371.9	933.8	363.9	SLC1A3	NM_004172.3	EAAT1;GLAST;GLAST1	L-	integral to	L-
GI_34222302-S	304.2	222.9	219.9	TUBGCP3	NM_006322.3	GCP3;Spc98p	structural	centrosom	microtubul
GI_34222303-S	215.1	668.2	1491.7	DHRS3	NM_004753.3	SDR1;Rsdr1;retSDR1	nucleotide	peripheral	fatty acid
GI_34222304-S	527.2	487.1	572.8	DNAJB2	NM_006736.4	HSJ1;HSPF3	co-	nucleus	protein
GI_34222305-S	480.5	419.1	401.2	ZNF263	NM_005741.3	FPM315	transcripti	nucleus	regulation
GI_34222306-S	7170.3	8963.7	6863.9	PARK7	NM_007262.3	DJ1;DJ-1		cytoplasm	RAS
GI_34222307-S	3025	3093.7	4737	TPBG	NM_006670.3	5T4;M6P1;5T4-AG	proteoglyc	integral to	cell
GI_34222308-S	1900.5	2044.5	1847.5	TRAPPC3	NM_014408.3	BET3		Golgi	transport
GI_34222309-S	366.6	465.6	461.2	MYST2	NM_007067.3	HBO1;HBOA	H3/H4	nucleus	DNA
GI_34222311-S	116	124.3	112.1	GAPDS	NM_014364.3	GAPD2;GAPDH-2	glyceralde		glycolysis
GI_34222312-S	466.7	552.3	730.4	GPSM2	NM_013296.3	LGN;Pins	GTPase		G-protein
GI_34222313-S	4725.7	3681.8	3816.4	PRP19	NM_014502.3	PSO4;hPSO4;NMP200	structural		
GI_34222315-S	196.7	239.5	187.7	TMOD3	NM_014547.3	UTMOD	tropomyos	F-actin	
GI_34222316-S	197.9	273	232.4	KIAA0893	NM_014969.3				
GI_34222317-S	557.1	594.8	540.7	CP110	NM_014711.3	KIAA0419	molecular	cellular_co	biological_
GI_34222318-S	872.3	928.1	865.1	DULLARD	NM_015343.3	HSA011916			
GI_34222319-S	2829.5	1994.1	1780	KIAA0063	NM_014876.3			integral to	
GI_34222320-S	1219.7	1752.1	1374.7	RAP1B	NM_015646.3	DKFZP586H0723	RAS small	membran	small
GI_34222322-S	506.2	461.9	557.2	AAAS	NM_015665.3	AAA;GL003;ADRACALA;ADRACALIN;DKFZp	molecular	cellular_co	biological_
GI_34222323-S	1657.7	1931.6	1638.7	CGI-51	NM_015380.3		molecular	cellular_co	biological_
GI_34222324-S	2607.7	3052.1	2599.1	COPB	NM_016451.3	DKFZp761K102	vesicle	Golgi	pathogene
GI_34222325-S	914.8	739.7	717.1	DKFZP564C1	NM_015654.3		N-		
GI_34222326-S	108.9	113.4	118.4	HMP19	NM_015980.3			Golgi	
GI_34222327-S	413.4	532.9	452.7	C14orf122	NM_016049.3	CGI-112	molecular		
GI_34222328-S	1339.2	1001.1	862.8	SLC35F2	NM_017515.3	HSNOV1;FLJ13018			
GI_34222329-S	2621.1	1845.2	1603.2	NOP5/NOP5	NM_015934.3	HSPC120	chaperone	nucleolus	snRNP

GI_34222332-S	1187.3	1484.4	1609.5	FLJ10099	NM_017994.3				
GI_34222333-S	473.2	670.8	563.2	TAPBP-R	NM_018009.3	TAPBPR;FLJ10143			
GI_34222335-S	476	652.4	685.5	FLJ10374	NM_018074.3				
GI_34222336-S	1248.7	1067.6	1453.3	HT021	NM_020685.3				
GI_34222337-S	1416.5	1287.3	1295.6	FLJ11773	NM_021934.3				
GI_34222338-S	100.7	105.2	100.4	LIN28	NM_024674.3	LIN-28;ZCCHC1;FLJ12457	DNA		regulation
GI_34222339-S	600.5	645.7	684.2	FLJ11807	NM_024954.3				
GI_34222340-S	2669.1	3009.6	3440.1	PQLC1	NM_025078.3	FLJ22378			
GI_34222341-S	350.9	490.9	395.6	DKFZP564D1	NM_032124.3		hydrolase		metabolis
GI_34222342-S	91.8	84.2	82.7	DKFZP434L1	NM_032136.3				
GI_34222344-S	211.2	273.1	236.6	GARNL3	NM_032293.3	bA356B19.1;DKFZp761J1523	small		
GI_34222345-S	787.7	1038.4	880.2	DDX49	NM_019070.3	FLJ10432;R27090_2			
GI_34222346-S	264.5	355.2	292.6	ATOH8	NM_032827.3	HATH6;FLJ14708			
GI_34222347-S	511.9	503	445.6	LRP11	NM_032832.3	FLJ14735;bA350J20.3			
GI_34222348-S	92	83.2	89.4	CPXCR1	NM_033048.3				
GI_34222349-S	137.5	151.2	134.8	STK22B	NM_053006.3	DGS-G;TSSK2;SPOGA2;FLJ38613	protein-		protein
GI_34222350-S	4651.1	3480.7	2779.5	SLC7A5	NM_003486.4	E16;CD98;LAT1;MPE16;D16S469E	neutral	integral to	small
GI_34222351-S	1850.5	2143.2	2034.3	C1orf37	NM_138391.3				
GI_34222352-S	388.2	460.9	577.1	SLC25A22	NM_024698.4	GC1;FLJ13044	binding	integral to	transport
GI_34222353-S	314.6	372.6	348.6	HIPK4	NM_144685.3	FLJ32818	protein-		protein
GI_34222354-S	213	198.7	160.2	FLJ11171	NM_018348.4				
GI_34222355-S	2487.5	1714.1	1255	SIAH2	NM_005067.4		transcripti	nucleus	small
GI_34222356-S	309.9	303.9	385.8	C1orf26	NM_017673.4	FLJ20121			
GI_34222357-S	321.1	382.1	384.3	LOC90268	NM_138348.3				
GI_34222359-S	114.3	123.3	97.7	DKFZp434G0	NM_181775.2				
GI_34222360-S	4058.4	4354.8	2882.3	ATP1A1	NM_000701.5		sodium/po	sodium/po	sodium
GI_34222361-S	234.3	293.8	269	LOC148066	NM_181710.2		peptidase		proteolysis
GI_34222363-S	747.8	895	745.4	LOC55971	NM_018842.3	IRTKS			
GI_34222364-S	2525.1	2735.8	2503	DC6	NM_020189.4				
GI_34222365-S	238.3	280.9	246.9	MLPH	NM_024101.4	ln;MELPH;l1Rk3;MGC2771;SLAC2-A;Slac-			
GI_34222368-S	873.7	734.6	726.1	MDS009	NM_020234.3				
GI_34222370-S	123.3	125.5	135.3	WBSCR28	NM_182504.2	MGC26719			
GI_34222372-S	137.5	124.3	108	MGC29671	NM_182538.2				
GI_34222374-S	123.6	131.6	123.1	MGC21830	NM_182563.2				
GI_34222376-S	862.9	1045.1	873	MGC44287	NM_182607.2			membran	
GI_34222377-S	119.2	129	121.5	MGC33835	NM_182548.2				
GI_34222379-S	838.1	1085.2	1012.5	MGC29814	NM_182565.2				
GI_34222380-S	203.7	244.6	331	MGC20579	NM_182614.2				
GI_34222383-S	367	321.5	331.7	FLJ22002	NM_024838.3		ATP		amino
GI_34222384-S	117.8	128.1	123.3	LRRN1	NM_020873.3	KIAA1497			
GI_34222385-S	204.4	252.8	211.9	CRF	NM_006688.3		molecular	microfibril	locomotor
GI_34222388-I	168	154.1	137.4	HTF9C	NM_182984.2	D22S1733E	S-		
GI_34222390-S	442.2	411.9	377.3	ZNF605	NM_183238.1		nucleic	intracellula	regulation
GI_34222392-S	94.6	99.7	101	KSR2	NM_173598.2	FLJ25965	ATP		protein

GI_34222394-S	117.9	150.6	130.4	PR1	NM_183240.1	PR;CACNG5			
GI_34303916-S	738.2	638.8	763.9	FLJ23322	NM_024955.4		disulfide		electron
GI_34303917-S	201.4	234.9	217.7	GPR92	NM_020400.3	GPR93	receptor	integral to	G-protein
GI_34303918-S	147.6	161.1	173.9	ZFYVE27	NM_144588.3	FLJ32919	zinc ion		
GI_34303919-S	400.9	514.2	671.2	LRFN4	NM_024036.3	MGC3103			
GI_34303920-S	89.1	86.3	87.1	PPP3R2	NM_147180.2		calcium		
GI_34303921-S	659.1	631.3	483.1	TRUB1	NM_139169.3		pseudouri		tRNA
GI_34303922-S	170.1	200.1	210.5	RG9MTD2	NM_152292.2	MGC27034			
GI_34303923-S	110.5	102.3	97.9	FLJ32191	NM_144689.3		nucleic	intracellula	regulation
GI_34303924-S	101.3	115.8	105.6	MGC35033	NM_152319.2				
GI_34303925-S	220.1	223.1	227.9	DKFZp727A0	NM_152268.2	MGC14416;MGC19467	ATP		prolyl-
GI_34303927-S	159.3	195.3	167.9	ATP1A3	NM_152296.2	MGC13276	sodium/po	sodium/po	small
GI_34303929-S	1769.8	1643.4	646.9	C14orf31	NM_152330.2	MGC17921;c14_5320		cytoskelet	
GI_34303930-S	126.8	146.6	126.4	MGC20262	NM_152421.2				
GI_34303931-S	106.5	104.1	97.6	MGC35118	NM_152453.2				
GI_34303933-S	96.1	104.9	102.5	C19orf18	NM_152474.2	MGC41906			
GI_34303934-S	264.3	308.3	279.6	MGC33295	NM_152505.2			kinesin	
GI_34303935-S	188.2	196.9	163.1	IBRDC1	NM_152553.2	C6orf172;MGC26996;dJ84N20.1			
GI_34303936-S	131.3	176	180.2	MGC33094	NM_152585.1				
GI_34303938-S	195.1	219.8	197.2	MGC33637	NM_152596.2		nucleic	intracellula	
GI_34303940-S	165.9	206.8	199.9	ZNF567	NM_152603.2	MGC45586	nucleic	nucleus	regulation
GI_34303942-S	105.5	113.5	99.6	C20orf75	NM_152611.2	MGC25027;dJ1056H1.1		integral to	
GI_34303943-S	212.7	239.4	213.9	ZNF515	NM_152629.2	MGC33662			
GI_34303945-S	79	81.7	88.7	MGC26999	NM_152630.2				
GI_34303946-S	113.9	127.1	120.9	MGC26598	NM_152638.2				
GI_34303947-S	115.2	129.5	125.7	MGC34032	NM_152697.2				
GI_34303948-S	274.8	339.4	317.1	SENP5	NM_152699.2	MGC27076	cysteine-		proteolysis
GI_34303949-S	103.3	102.4	93.7	MGC26597	NM_152700.2		kinase		
GI_34303950-S	108.8	118	109.6	MGC26647	NM_152706.2				
GI_34303951-S	1404.5	1888.1	1258.8	ITM1	NM_152713.2	TMC;MGC9042	oligosacch	membran	protein
GI_34303952-S	418.7	368	354.1	ZNF187	NM_152736.2	MGC2815;SRE-ZBP	DNA	nucleus	cell
GI_34303954-S	72.2	69.5	76.9	MGC26989	NM_152763.2				
GI_34303955-S	120.8	132.1	120.4	MGC33510	NM_152765.2				
GI_34303956-S	334.7	507.3	386.8	MGC33212	NM_152773.2				
GI_34303957-S	97.8	101.1	95.1	C14orf48	NM_152777.2	MGC33356;c14_5713			
GI_34303958-S	102.3	106.8	122.5	MGC33329	NM_152782.2				
GI_34303960-S	240.1	219.4	226	NEDD1	NM_152905.2	FLJ35902			
GI_34303961-S	291	298.4	270.2	ZNF548	NM_152909.2	FLJ32932	nucleic	intracellula	regulation
GI_34303962-A	797	1090.2	759.9	MDS010	NM_020231.3	MDSRP;MGC32995			
GI_34303963-A	134.6	134.3	125.7	384D8-2	NM_014551.3	384D8_6;MGC2455;MGC4133;MGC5305;M			
GI_34303963-I	134.3	139	124	384D8-2	NM_014551.3	384D8_6;MGC2455;MGC4133;MGC5305;M			
GI_34303964-S	379.1	382	442.9	TTK	NM_003318.3	ESK;PYT;MPS1L1	protein-	spindle	spindle
GI_34304112-S	110.4	103.9	116.3	BTBD8	NM_183242.1				
GI_34304114-I	99	106.4	94.4	RBPSUH	NM_015874.2	csl;CBF1;KBF2;RBP-			

GI_34304116-S	46826	52889	48372	UBC	NM_021009.2	HMG20	ubiquitin		
GI_34304319-S	1359.2	1558.3	1449.8	MRP63	NM_024026.3	bMRP63;MGC3243	structural		
GI_34304320-A	3186.5	3138.8	2386.9	MRPS21	NM_031901.3	MDS016;RPMS21;MRP-S21			
GI_34304321-S	1650.5	1582.5	1577	MRPL45	NM_032351.3	MGC11321	structural	mitochond	protein
GI_34304323-I	94.7	116	97.6	MRPS12	NM_033362.2	RPS12;RPMS12;RPSM12;MPR-S12;MT-	structural	mitochond	protein
GI_34304324-S	1932.7	1524.2	1346.4	MRPS5	NM_031902.3	MRP-S5	structural	ribosome	protein
GI_34304325-S	3287	2815	2596.8	MRPS6	NM_032476.2	RPMS6;MRP-S6;C21orf101	structural	small	protein
GI_34304330-I	238.9	193	175.5	RNF7	NM_183063.1	SAG;ROC2;CKBBP1	copper ion	cytoplasm	redox
GI_34304332-A	127.2	135.4	119.7	RNF7	NM_183237.1	SAG;ROC2;CKBBP1	copper ion	cytoplasm	redox
GI_34304334-I	287.2	266	300	RNF8	NM_003958.2	KIAA0646			
GI_34304335-A	134.6	138.9	134.7	RNF8	NM_183078.1	KIAA0646			
GI_34304337-S	129.2	179.1	211.9	ABHD3	NM_138340.3	LABH3;MGC11259	catalytic		
GI_34304338-I	172.2	197.8	178.2	ACOX1	NM_004035.4	ACOX;MGC1198;PALMCOX	acyl-CoA	peroxisom	lipid
GI_34304339-A	181.5	230.4	225.2	ACOX1	NM_007292.3	ACOX;MGC1198;PALMCOX	acyl-CoA	peroxisom	lipid
GI_34304339-I	107.1	118.2	114.3	ACOX1	NM_007292.3	ACOX;MGC1198;PALMCOX	acyl-CoA	peroxisom	lipid
GI_34304340-A	537.7	391.3	431.7	PDCD4	NM_014456.3	H731;MGC33046;MGC33047			apoptosis
GI_34304341-I	90.5	88.1	91.5	PDCD4	NM_145341.2	H731;MGC33046;MGC33047			apoptosis
GI_34304342-S	111.3	115	106.5	PPP1R3A	NM_002711.2	PP1G;PPP1R3	type 1		
GI_34304343-A	5014.7	2822.5	1888.7	PSAT1	NM_021154.3	PSA	phosphos		L-serine
GI_34304345-S	5002.8	4666	5158.2	TM4SF7	NM_003271.3	NAG-2;TSPAN-4;TETRASPAN		integral to	protein
GI_34304346-A	333.1	413.7	374	TMPRSS4	NM_183247.1	MT-SP2;TMPRSS3	trypsin	integral to	proteolysis
GI_34304348-I	122.3	115.2	111.5	TMPRSS4	NM_019894.2	MT-SP2;TMPRSS3	trypsin	integral to	proteolysis
GI_34304350-S	120.8	273.3	209.5	BF	NM_001710.3	GBG;CFAB;PBF2	serine-		proteolysis
GI_34304351-S	99.8	95.2	91.1	BGN	NM_001711.3	PGI;DSPG1;PG-S1;SLRR1A	extracellul	extracellul	biological_
GI_34304352-I	108.2	130.6	121.9	SCAPIN1	NM_080672.2	H17739	DNA	nucleus	regulation
GI_34304355-A	100.6	105.1	80.9	SCAPIN1	NM_183246.1	H17739	DNA	nucleus	regulation
GI_34304357-S	343.6	403.1	376.3	NFKBIL2	NM_013432.3	IKBR	transcripti	cytoplasm	
GI_34304359-S	296.7	365	254.2	NPHP3	NM_153240.3	NPH3;FLJ30691;FLJ36696;KIAA2000;DKFZp			
GI_34304361-S	659.8	675.5	678.2	NPHP4	NM_015102.2	SLSN4;KIAA0673			
GI_34304362-S	721.7	588.6	343.3	FADS3	NM_021727.3	CYB5RP;LLCDL3;BC269730_1			
GI_34304364-S	223.8	221.4	278.1	FKBPL	NM_022110.3	NG7;DIR1	molecular	cellular_co	response
GI_34304365-S	122.6	136.8	108.2	FKHL18	NM_004118.3	FREAC10;MGC4544	transcripti	nucleus	circulation
GI_34304366-S	4817	8319.3	5928	FSTL1	NM_007085.3	FRP;FSL1	heparin	extracellul	
GI_34304367-I	114.1	128.2	105.2	DTNBP1	NM_183040.1	SDY;My031;FLJ30031;MGC20210;DKFZP56			
GI_34304371-A	528.6	405.9	411.3	DTNBP1	NM_032122.3	SDY;My031;FLJ30031;MGC20210;DKFZP56			
GI_34304372-S	1271.7	1745.5	1964.9	CCNB1	NM_031966.2	CCNB	cyclin-	nucleus	G2/M
GI_34304373-S	356.9	461.5	397.8	CDK5R1	NM_003885.2	p23;p25;p35;CDK5R;NCK5A;CDK5P35;MGC	cell cycle	cyclin-	regulation
GI_34304375-I	98.4	97.9	105.7	SNX3	NM_152828.2	SDP3;SNX3A;MGC17570		peripheral	endocytosi
GI_34304376-I	119.4	111.3	100.3	HYAL2	NM_033158.2	LUCA2;LuCa-2	hyalurono	lysosome	glycosami
GI_34304378-A	263.9	325.3	296.3	INVS	NM_183245.1	INV;NPH2;NPHP2			
GI_34304380-I	122.2	117	106.6	INVS	NM_014425.2	INV;NPH2;NPHP2			
GI_34304382-S	4436.1	4518	3895.3	USH1G	NM_173477.2	SANS;FLJ33924			
GI_34304384-S	4125.1	5141.6	4615.6	YKT6	NM_006555.3			ER-Golgi	nonselecti
GI_34304385-S	3351.7	3964.2	3614.2	YWHAE	NM_006761.3	MDS;MDCR;KCIP-1;14-3-3E	protein		intracellula

GI_34305287-S	112.7	116	108.9	RNF2	NM_007212.2	DING;BAP-1			
GI_34305288-S	277.2	348.7	310.2	RNF3	NM_006315.3	DONG1;RNF3A;FLJ36550;MGC40413			
GI_34305289-S	676.1	782.1	517.8	RNF4	NM_002938.2	SNURF;RES4-26	antiviral	nucleus	regulation
GI_34305290-S	565.9	716.6	742.4	RNF5	NM_006913.2	RMA1;RING5	protein		
GI_34305292-I	87.5	89.9	91.5	RNF6	NM_183043.1		zinc ion	cellular_co	biological_
GI_34305294-I	78.5	76.7	82	RNF6	NM_183044.1		zinc ion	cellular_co	biological_
GI_34305296-A	118.5	117.1	126	RNF6	NM_183045.1		zinc ion	cellular_co	biological_
GI_34305296-I	93.8	93.8	101.9	RNF6	NM_183045.1		zinc ion	cellular_co	biological_
GI_34305454-S	1355.6	996.1	1002.6	GCC1	NM_024523.5	GCC1P;GCC88;FLJ22035;MGC20706		Golgi	
GI_34305455-S	533.7	692.3	579.3	DRG2	NM_001388.3		GTP		cell growth
GI_34328078-S	425.3	571.1	598.8	PTD015	NM_024684.2	MGC3367;FLJ21035			
GI_34328079-S	683.5	613.4	609.7	LOC90580	NM_138358.2				
GI_34328080-S	625	681	647	MGC29729	NM_152274.2				
GI_34328082-S	148.7	220.2	174.1	SLC10A4	NM_152679.2	MGC29802	bile	membran	sodium
GI_34328898-S	205.4	281.4	207.6	PTPN14	NM_005401.3	PEZ;PTP36	protein	cytoskelet	protein
GI_34328901-A	99.9	105.4	88.4	PTPN6	NM_080548.2	HCP;HCPH;SHP-1;HPTP1C;PTP-1C;SHP-	protein	membran	G-protein
GI_34328901-I	121.4	128.9	109.3	PTPN6	NM_080548.2	HCP;HCPH;SHP-1;HPTP1C;PTP-1C;SHP-	protein	membran	G-protein
GI_34328902-I	240.1	298.9	270.1	PTPN6	NM_080549.2	HCP;HCPH;SHP-1;HPTP1C;PTP-1C;SHP-	protein	membran	G-protein
GI_34328903-A	321.7	285.9	385	PIGN	NM_012327.3	MCD4;MDC4;PIG-N;MGC26427			
GI_34328904-I	99.1	108.7	94.7	PIGN	NM_176787.2	MCD4;MDC4;PIG-N;MGC26427			
GI_34328905-S	1539	1310.2	1042.6	DDX19	NM_007242.3	DBP5	helicase	nuclear	mRNA-
GI_34328906-I	779.5	1107.8	907.1	DNAJB6	NM_058246.3	MRJ;HHDJ1;HSJ-2;MSJ-	heat	cellular_co	biological_
GI_34328907-S	261.1	126	101	DRD5	NM_000798.3	DBDR;DRD1B;DRD1L2;MGC10601	dopamine	integral to	dopamine
GI_34328908-A	5069.1	7153.1	4754.6	DUSP4	NM_001394.4	TYP;HVH2;MKP2;MKP-2	protein	nucleus	MAPKKK
GI_34328908-I	289	439.9	341.4	DUSP4	NM_001394.4	TYP;HVH2;MKP2;MKP-2	protein	nucleus	MAPKKK
GI_34328912-S	254.7	315.6	299.8	WNT7A	NM_004625.3		receptor	extracellul	sex
GI_34328913-I	1095.7	1511.4	1840.8	CD151	NM_004357.3	GP27;SFA1;PETA-3	cell	integral to	cell
GI_34328914-A	10139.6	11819	12041	CD151	NM_139030.2	GP27;SFA1;PETA-3	cell	integral to	cell
GI_34328925-A	255	305.7	274.8	ACRV1	NM_020115.3	SPACA2;D11S4365			developm
GI_34328927-A	2548.4	2100.9	3142.7	IMPDH1	NM_183243.1	IMPD;IMPD1	IMP		GTP
GI_34328929-I	102.8	90.1	91.4	IMPDH1	NM_000883.2	IMPD;IMPD1	IMP		GTP
GI_34328933-S	138	153.6	135.7	NTF5	NM_006179.3	NT4;NT5;NTF4;NT-4/5	growth		
GI_34328934-S	1526.7	1628	1493.2	MRPL13	NM_014078.4	L13;L13mt;RPL13	structural	ribosome	protein
GI_34328935-S	197.3	212.5	243.9	SNRPD3	NM_004175.3	SMD3	small	spliceoso	mRNA
GI_34328936-S	5548.1	5425.6	5406.4	CD63	NM_001780.3	MLA1;ME491;LAMP-3;OMA81H		lysosomal	
GI_34328937-I	249.6	201.9	183.2	CTH	NM_001902.4	MGC9471	cystathioni		cysteine
GI_34328938-A	852.9	429.3	403.6	CTH	NM_153742.3	MGC9471	cystathioni		cysteine
GI_34328939-S	222.9	245.8	205.3	CYCS	NM_018947.4	CYC;HCS	electron	mitochond	induction
GI_34328940-S	153.6	179.2	186.6	TGIF2LX	NM_138960.3	TGIFLX;MGC34726	transcripti	nucleus	regulation
GI_34328942-S	186.2	215.6	195.7	TGIF2LY	NM_139214.2	TGIFLY	transcripti	nucleus	regulation
GI_34328943-S	128.8	129.4	113.5	TMSB4X	NM_021109.2	FX;TB4X;PTMB4;TMSB4	actin	cytoskelet	developm
GI_34328944-S	104.9	112.2	106.6	TMSB4Y	NM_004202.2	TB4Y;MGC26307	actin	cytoskelet	regulation
GI_34330151-S	143.3	153.7	149.7	NUDT13	NM_015901.3	DKFZp586P2219			
GI_34330156-S	175.9	199.8	195.3	LOC113730	NM_138433.2				

GI_34330161-S	120.5	101.6	124.2	OR2H3	NM_007160.2	FAT11;OLFR2	defense/i	integral to	mating
GI_34330167-S	94.7	120.2	103.2	OR6A2	NM_003696.2	I7;OR6A1;OR6A2P;OR11-55	G-protein	integral to	signal
GI_34330189-S	897.3	831.8	765.1	HKR1	NM_181786.2		zinc ion	nucleus	regulation
GI_34330190-S	1741.3	1804.2	2128.2	SLC39A3	NM_144564.3	ZIP3	heavy	membran	heavy
GI_34335114-I	372.7	398.6	368.3	BAX	NM_004324.3				apoptotic
GI_34335124-I	189.4	217.8	209.2	BAX	NM_138764.2				apoptotic
GI_34335126-I	95	86.8	87.4	GCC2	NM_181453.2	GCC185;KIAA0336		Golgi	
GI_34335132-A	124	127.3	108.4	GCC2	NM_014635.3	GCC185;KIAA0336		Golgi	
GI_34335133-A	1048	1349.1	1004.2	SEC13L1	NM_183352.1	SEC13R;D3S1231E	protein		intracellula
GI_34335143-S	5267.3	4986.2	4041.2	RPL36AL	NM_001001.3	RPL36A	structural	ribosome	protein
GI_34335144-I	3750.5	3106.3	2869.2	RPLP0	NM_053275.2	P0;L10E;RPP0;PRLP0	structural	cytosolic	protein
GI_34335149-S	1638.3	2206.9	1706.8	RPS11	NM_001015.3		structural	ribosome	protein
GI_34335150-S	3389.3	3680.9	2443.9	RPS15A	NM_001019.3		structural	cytosolic	protein
GI_34335151-S	19953	18300	14855	RPS16	NM_001020.3		structural	cytosolic	protein
GI_34335176-A	550.3	564.9	531.4	CCL14	NM_032963.2	CC-1;CC-3;CKb1;MCIF;NCC2;SY14;HCC-	signal	extracellul	positive
GI_34335180-A	81.4	77.2	72.3	CCL15	NM_032965.2	LKN1;NCC3;SY15;HCC-2;Lkn-1;MIP-5;NCC-	chemokin	extracellul	chemotaxi
GI_34335180-I	74.5	85.6	69.6	CCL15	NM_032965.2	LKN1;NCC3;SY15;HCC-2;Lkn-1;MIP-5;NCC-	chemokin	extracellul	chemotaxi
GI_34335183-A	140.2	127.8	143.7	BHD	NM_144606.3	FLCL;MGC17998;MGC23445			
GI_34335183-I	431.6	362.6	486.4	BHD	NM_144606.3	FLCL;MGC17998;MGC23445			
GI_34335184-I	832.3	684.7	749.2	BHD	NM_144997.3	FLCL;MGC17998;MGC23445			
GI_34335205-I	101.2	103.5	96	CREM	NM_001881.2	ICER;MGC17881;MGC41893		nucleus	signal
GI_34335229-A	162.7	206.1	161.4	CARD9	NM_052814.2		apoptosis	kinesin	apoptosis
GI_34335230-S	601.8	586.6	641.5	CDC45L	NM_003504.3	CDC45;CDC45L2;PORC-PI-1	cell cycle	nucleus	DNA
GI_34335231-S	1135	2823.7	1421.6	CKB	NM_001823.3	B-CK;CKBB	creatine	cytoplasm	
GI_34335232-S	112.6	120.3	102	CLDN4	NM_001305.3	CPER;CPE-	transmem	tight	pathogene
GI_34335233-I	1136.7	1155.6	1156.3	CNOT7	NM_013354.4	CAF1;hCAF-1	signal	nucleus	carbohydr
GI_34335234-A	412.1	333.9	332.8	CORO2A	NM_052820.2	IR10;WDR2;CLIPINB	protein	kinesin	intracellula
GI_34335235-S	379.5	422	388.2	CPLX1	NM_006651.3	CPX1	vesicle		exocytosis
GI_34335236-S	961.1	1364.6	1080.2	MAGEA12	NM_005367.3	MAGE12	molecular	cellular_co	biological_
GI_34335237-S	163	181.2	146.7	MAGEA2b	NM_153488.3	MAGE2;MAGEA2;MGC16973			
GI_34335238-S	117.2	134.3	129	MAGEA9	NM_005365.4	MAGE9;MGC8421	molecular	cellular_co	biological_
GI_34335239-S	2980.4	2807.3	2982.6	MAGEB2	NM_002364.3	DAM6;MGC26438;MAGE-XP-2	tumor		
GI_34335240-S	1387.3	1474.1	1230.1	MAGEF1	NM_022149.3	MGC19617	sterol		
GI_34335241-S	3393.9	2958.5	3900	MAPKAPK3	NM_004635.3	3PK;MAPKAP3	MAP	nucleus	response
GI_34335242-S	3994.4	4232.7	3938.8	MATR3	NM_018834.3	MGC9105;KIAA0723	structural	nuclear	cell shape
GI_34335243-I	101.1	94.2	95.2	MMP28	NM_032950.2	MM28;MMP25			
GI_34335244-A	132	434.6	100.3	NMNAT2	NM_170706.2	PNAT2;PNAT-			
GI_34335244-I	79.5	74.3	83.7	NMNAT2	NM_170706.2	PNAT2;PNAT-			
GI_34335245-A	2451.4	1908.6	1875	NUP62	NM_012346.3	p62;MGC841;FLJ20822;DKFZp547L134		nuclear	nucleocyto
GI_34335249-S	1263.6	1459.7	1224.6	NXF1	NM_006362.3	TAP;MEX67	RNA	nucleus	nucleocyto
GI_34335250-A	475.5	571.3	608.8	DLGAP4	NM_183006.1	DAP4;SAPAP4;KIAA0964		membran	cell-cell
GI_34335250-I	283.4	333	329.1	DLGAP4	NM_183006.1	DAP4;SAPAP4;KIAA0964		membran	cell-cell
GI_34335252-I	197.5	234.1	217.9	DLGAP4	NM_014902.2	DAP4;SAPAP4;KIAA0964		membran	cell-cell
GI_34335254-S	2609.8	2564.8	2649.4	DCTN2	NM_006400.3	RBP50;DCTN50;DYNAMITIN	motor	kinetochor	mitosis

GI_34335255-S	94.6	106.2	98.6	ADAM7	NM_003817.1	EAPI;GP-83	metalloen	integral to	proteolysis
GI_34335257-S	840.4	1157.1	1636.3	ATP6V0D1	NM_004691.3	P39;VATX;Vma6;ATP6D;ATP6DV;VPATPD	hydrogen	vacuolar	proton
GI_34335259-S	637	525.9	1045	PRIC285	NM_033405.2	FLJ00244;KIAA1769	ribonuclea	nucleus	regulation
GI_34335261-I	149.6	163.7	153	PRKCBP1	NM_183047.1	RACK7;ZMYND8;KIAA1125;MGC31836	DNA		regulation
GI_34335263-A	995.4	1177.4	1493.2	PRKCBP1	NM_183048.1	RACK7;ZMYND8;KIAA1125;MGC31836	DNA		regulation
GI_34335267-S	119.6	130.7	87.1	PRND	NM_012409.2	DPL;PrPLP;DOPPEL;MGC41841;dJ1068H6.			pathogene
GI_34335269-A	13077.9	13795	9511.9	PRNP	NM_183079.1	CJD;PrP;ASCR;PRIP;PrPc;MGC26679;PrP2			virulence
GI_34335271-S	590.9	502.3	427.8	PROCR	NM_006404.3	CCCA;EPCR;CCD41;MGC23024;bA42O4.2	receptor	integral to	inflammat
GI_34335273-I	145.6	157.7	146.6	P2RX7	NM_002562.4	P2X7;MGC20089	ATP-	integral to	small
GI_34335274-A	97.9	108.4	95.5	P2RX7	NM_177427.2	P2X7;MGC20089	ATP-	integral to	small
GI_34335275-S	358.5	357.5	475.7	POPDC3	NM_022361.3	POP3;MGC22671;bA355M14.1	molecular	integral to	biological_
GI_34335276-S	122.1	128.8	118	PPP1R16B	NM_015568.2	TIMAP;ANKRD4;KIAA0823	protein	kinesin	signal
GI_34335277-I	206.5	244.3	185.5	PSMB8	NM_004159.3	LMP7;D6S216;RING10;D6S216E;MGC1491	peptidase	26S	proteolysis
GI_34335278-A	933.8	1184.9	806.8	PSMB8	NM_148919.2	LMP7;D6S216;RING10;D6S216E;MGC1491	peptidase	26S	proteolysis
GI_34335278-I	448.3	495.8	378.3	PSMB8	NM_148919.2	LMP7;D6S216;RING10;D6S216E;MGC1491	peptidase	26S	proteolysis
GI_34335279-S	3357.7	3924.7	3604.6	PSMD7	NM_002811.3	P40;S12;MOV34	translation	proteasom	translation
GI_34335280-S	252.7	337.6	364.8	PSMD9	NM_002813.4	p27;MGC8644	molecular	proteasom	intracellula
GI_34335281-I	108.9	111.9	99.4	OLFM1	NM_014279.2	AMY;NOE1;OlfA;NOELIN			neurogene
GI_34335282-A	89.4	87.2	76.1	OLFM1	NM_058199.2	AMY;NOE1;OlfA;NOELIN			neurogene
GI_34335282-I	117.4	140.5	114.2	OLFM1	NM_058199.2	AMY;NOE1;OlfA;NOELIN			neurogene
GI_34335283-I	86.2	96.4	92.9	OLFM1	NM_006334.2	AMY;NOE1;OlfA;NOELIN			neurogene
GI_34335286-A	1066.1	980.6	1687.3	SLC35C2	NM_173073.2	CGI-			
GI_34335288-I	104.6	111.3	115.8	SLC35C2	NM_173179.2	CGI-			
GI_34335289-S	649.5	842	796.7	SEC22L1	NM_004892.3	ERS-24;SEC22B		endoplas	ER to
GI_34335290-S	1811.5	2026.2	1806.8	TOP3B	NM_003935.3		DNA	nucleus	chromoso
GI_34335291-S	861.9	941.5	813.3	TST	NM_003312.4	RDS;MGC19578	thiosulfate	mitochond	cyanate
GI_34335395-S	320.5	368.7	337.1	BOK	NM_032515.3	BOKL;BCL2L9;MGC4631			induction
GI_34365782-S	144.2	173.5	157.2	CHX10	NM_182894.1	RET1;HOX10	transcripti	nucleus	vision
GI_34365792-S	231.7	251.8	195.9	PRKWNK4	NM_032387.2	WNK4;PHA2B	cAMP-		protein
GI_34365798-S	2342.2	2087.4	1725.2	BET1L	NM_016526.3	GS15;BET1L1;HSPC197			
GI_34398688-S	103.5	111.4	103.2	ADCYAP1R1	NM_001118.3	PACAPR;PACAPRI	receptor	integral to	cell
GI_34419629-S	116.3	114.7	97.2	CD1D	NM_001766.2		class I	integral to	antimicrob
GI_34419632-S	226.8	260.6	225.2	ZNF135	NM_003436.2	ZNF61;pHZ-17	transcripti	nucleus	regulation
GI_34419636-S	100.5	103	96.9	HLA-DOA	NM_002119.2	HLADZ;HLA-DNA;HLA-DZA	class II	plasma	
GI_34419638-S	92	99.1	89.5	ESSPL	NM_183375.1				
GI_34419640-S	102.6	95.3	100.4	OVCH1	NM_183378.1	OVCH			
GI_34419642-S	188.2	197.5	198.7	TESSP1	NM_183379.1				
GI_34419646-S	463	880	396.4	ARRDC4	NM_183376.1				sensory
GI_34419648-S	199.3	214.8	206.3	CYP26C1	NM_183374.1				
GI_34447228-S	363.2	398.8	514.1	STX16	NM_003763.2	SYN16;hsyn16	t-SNARE	Golgi	intra-Golgi
GI_34447230-S	127.9	145.3	117.3	PAPSS2	NM_004670.2	SK2;ATPSK2	ATP		nucleobas
GI_34452172-S	175.9	206.9	148.8	ITGAX	NM_000887.3	CD11C	cell	integrin	histogene
GI_34452680-S	351.9	408.8	451	RNF10	NM_014868.3	RIE2;KIAA0262			
GI_34452682-S	96.3	100.4	95	RNF11	NM_014372.3	CGI-123;SID1669;MGC51169	zinc ion		oncogene

GI_34452683-A	106.4	94.9	100	RNF12	NM_016120.2	RLIM;MGC15161;NY-REN-43			
GI_34452685-I	72.1	81.9	68	RNF12	NM_183353.1	RLIM;MGC15161;NY-REN-43			
GI_34452687-A	148.5	132.3	133.9	RGS11	NM_183337.1	RS11	GTPase	peripheral	regulation
GI_34452689-S	201.6	230.7	205.3	RGS16	NM_002928.2	RGS-R;A28-RGS14;A28-RGS14P	GTPase	peripheral	regulation
GI_34452691-A	1197.8	1048	1159	VPS28	NM_016208.2	MGC60323	protein		intracellula
GI_34452692-I	361.4	422.1	400.8	VPS28	NM_183057.1	MGC60323	protein		intracellula
GI_34452694-I	254.1	283.6	247.7	ACCN1	NM_183377.1	ACCN;BNC1;MDEG;ASIC2;BNaC1;ASIC2a;h	amiloride-	membran	monovale
GI_34452696-A	295.1	353.4	296.1	ACCN1	NM_001094.4	ACCN;BNC1;MDEG;ASIC2;BNaC1;ASIC2a;h	amiloride-	membran	monovale
GI_34452696-I	190.1	229.1	203.8	ACCN1	NM_001094.4	ACCN;BNC1;MDEG;ASIC2;BNaC1;ASIC2a;h	amiloride-	membran	monovale
GI_34452697-S	6775.1	5960.4	4418.3	ACTN4	NM_004924.3	FSGS;FSGS1	actin	actin	invasive
GI_34452698-S	1935.2	2318.8	2122	ACTR3	NM_005721.3	ARP3	structural	Arp2/3	cell
GI_34452699-S	562.7	481	455.7	ABCC4	NM_005845.2	MRP4;MOATB;MOAT-B;EST170205	nucleotide	integral to	transport
GI_34452700-S	138.2	166.3	150.6	ABCG8	NM_022437.2		ATP	integral to	transport
GI_34452701-S	841.3	1057.3	933	ANKH	NM_054027.3	ANK;CMDJ;HANK;MANK;CCAL2;CPPDD	molecular	integral to	phosphate
GI_34452706-I	117.5	132.7	120.3	BRD8	NM_139199.1	P120;SMAP	ligand-	nucleus	cell
GI_34452708-A	505.6	626	655.8	BRD8	NM_183359.1	P120;SMAP	ligand-	nucleus	cell
GI_34452710-A	120.8	121.8	111.5	CADPS	NM_183393.1	CAPS;CAPS1;KIAA1121		cytosol	exocytosis
GI_34452712-I	179	211.3	203.1	CADPS	NM_183394.1	CAPS;CAPS1;KIAA1121		cytosol	exocytosis
GI_34452714-I	100.9	116.2	117.3	CADPS	NM_003716.2	CAPS;CAPS1;KIAA1121		cytosol	exocytosis
GI_34452716-A	973	606.9	583.3	CDC42EP1	NM_007061.3	CEP1;BORG5;MSE55;MGC15316		extracellul	developm
GI_34452718-S	1228	568.2	501.2	CEBPG	NM_001806.2	GPE1BP;IG/EBP-1	transcripti	nucleus	regulation
GI_34452719-S	1905.8	1849.7	1573.3	CRKL	NM_005207.2		protein-		JNK
GI_34452720-S	395.3	423.5	417.3	GABPA	NM_002040.2	NFT2;NRF2;NRF2A;E4TF1A;E4TF1-60	protein	nucleus	transcripti
GI_34452722-S	77.3	91.6	94.6	GABRA4	NM_000809.2		benzodiaz	integral to	gamma-
GI_34452724-S	707.9	772.9	397.5	GALNT4	NM_003774.3	GalNAcT4;GALNAC-T4	polypeptid	Golgi	carbohydr
GI_34452728-I	125.9	162.6	129.6	PAIP1	NM_006451.3	MGC12360	RNA	cytoplasm	translation
GI_34452729-A	2546.6	2414.1	2000.4	PAIP1	NM_183323.1	MGC12360	RNA	cytoplasm	translation
GI_34452731-S	220.2	251	318.6	PREX1	NM_020820.2	KIAA1415	guanyl-	cytosol	intracellula
GI_34452733-I	199.7	220.2	218.7	PXMP4	NM_007238.3	PMP24		peroxisom	
GI_34452735-A	163.5	167.1	169	PXMP4	NM_183397.1	PMP24		peroxisom	
GI_34485705-I	81.1	81.7	78.1	RAB27A	NM_183234.1	GS2;RAM;RAB27;HsT18676	RAB small		protein
GI_34485707-I	76.6	98.7	82.9	RAB27A	NM_004580.3	GS2;RAM;RAB27;HsT18676	RAB small		protein
GI_34485708-I	151.8	185.1	148.5	RAB27A	NM_183235.1	GS2;RAM;RAB27;HsT18676	RAB small		protein
GI_34485710-A	1462.3	1629.9	1485.5	RAB27A	NM_183236.1	GS2;RAM;RAB27;HsT18676	RAB small		protein
GI_34485712-S	2319.8	3380.2	2874.5	RAB11A	NM_004663.3	YL8;MGC1490	RAB small		small
GI_34485713-I	111.2	116.6	114.6	RAB23	NM_016277.3	HSPC137;MGC8900	GTP		small
GI_34485715-A	970.5	599.6	548.5	RAB23	NM_183227.1	HSPC137;MGC8900	GTP		small
GI_34485715-I	94.7	108.1	86.9	RAB23	NM_183227.1	HSPC137;MGC8900	GTP		small
GI_34485717-S	125.9	132.8	114	RAB33A	NM_004794.2	RabS10;MGC1488	RAB small		protein
GI_34485718-S	142.6	153.1	222.7	E2F2	NM_004091.2	E2F-2	protein	transcripti	transcripti
GI_34485719-S	135.8	143.9	147.1	EML5	NM_183387.1	EMAP-2;HuEMAP-2			
GI_34485721-S	1093.4	1090.8	894.2	KPNA3	NM_002267.2	SRP4;IPOA4;hSRP1;SRP1gamma	nuclear	importin,	NLS-
GI_34485723-A	1950.8	2149.4	1607.8	KRAS2	NM_004985.3	KRAS;RASK2;KI-RAS;C-K-RAS;K-RAS2A;K-	GTPase		regulation
GI_34485724-I	153.8	202.5	160.3	KRAS2	NM_033360.2	KRAS;RASK2;KI-RAS;C-K-RAS;K-RAS2A;K-	GTPase		regulation

GI_34485725-S	125.1	157.8	136.3	GCNT1	NM_001490.3	G6NT;C2GNT;NACGT2;NAGCT2;C2GNT-L	beta-1,3-	Golgi	O-linked
GI_34485726-S	105.2	101.5	98.9	HEM1	NM_005337.2			membran	
GI_34485728-S	1130.8	1207.7	986.6	OSBP	NM_002556.2	OSBP1	oxysterol	Golgi	lipid
GI_34485729-S	366.3	377.1	299.2	PRKY	NM_002760.2		protein	nucleus	protein
GI_34486089-S	16978.7	17819	16318	OAZ1	NM_004152.2	OAZ	ornithine		polyamine
GI_34486091-S	113.6	125.6	120.6	ADCY5	NM_183357.1		calcium/ca	integral to	cAMP
GI_34486095-S	1544.1	1569.3	1404	RPL28	NM_000991.3		structural	cytosolic	protein
GI_34486096-S	1463.5	1263.5	1193.9	TEF	NM_003216.2		RNA	nucleus	regulation
GI_34536828-I	216.3	259.7	219.5	C21orf80	NM_015227.2	KIAA0958;DKFZp434E171			
GI_34556190-A	91	99.7	110.6	COH1	NM_181661.1	CHS1;KIAA0532;DKFZp313I0811	metallope	membran	transport
GI_34556190-I	177	205.8	219.7	COH1	NM_181661.1	CHS1;KIAA0532;DKFZp313I0811	metallope	membran	transport
GI_34556206-I	137.2	147.2	152.8	TSC22	NM_183422.1	MGC17597	transcripti	nucleus	transcripti
GI_34577046-I	120	145.2	115.1	BPAG1	NM_183380.1	BPA;BP240;CATX-		basement	cytoskelet
GI_34577050-A	133	128.5	120.8	BPAG1	NM_001723.3	BPA;BP240;CATX-		basement	cytoskelet
GI_34577050-I	110.7	114.8	120.4	BPAG1	NM_001723.3	BPA;BP240;CATX-		basement	cytoskelet
GI_34577051-S	1009.8	3083.6	1522.1	F2RL1	NM_005242.3	PAR2;GPR11	G-protein	Golgi	cytosolic
GI_34577053-S	136.5	247	142.5	F2RL2	NM_004101.2	PAR3	thrombin	integral to	phosphati
GI_34577054-S	436	415.2	461	FBXO30	NM_032145.3	MGC21674	zinc ion		
GI_34577056-S	105.6	103.4	95.6	FLRT1	NM_013280.3		receptor	integral to	biological_
GI_34577058-S	209.6	234.3	187.3	ADFP	NM_001122.2	ADRP;MGC10598		lipid	
GI_34577060-S	126.6	134.8	133.4	ADH1B	NM_000668.3	ADH2	alcohol		ethanol
GI_34577062-S	269.5	261.7	274.2	ADSS	NM_001126.2	ADEH;MGC20404	adenylosu		AMP
GI_34577064-S	130.5	150.6	129	AGTRL1	NM_005161.2	APJ;MGC45246	G-protein	integral to	G-protein
GI_34577067-S	382.1	890.9	125.7	ANGPTL2	NM_012098.2	ARP2;HARP;MGC8889	receptor	kinesin	developm
GI_34577072-A	284.8	340.4	427.8	PTE1	NM_183386.1	hTE;HNAACTE;hACTE-III	acyl-CoA	peroxisom	lipid
GI_34577076-A	151	181.6	180.5	RBL1	NM_183404.1	PRB1;p107;CP107;MGC40006		nucleus	regulation
GI_34577076-I	96.5	96.2	97	RBL1	NM_183404.1	PRB1;p107;CP107;MGC40006		nucleus	regulation
GI_34577078-I	248.4	271.6	297.4	RBL1	NM_002895.2	PRB1;p107;CP107;MGC40006		nucleus	regulation
GI_34577080-S	200	247.8	238.4	RBPSUHL	NM_014276.2	RBP-L	transcripti	nucleus	signal
GI_34577082-A	8692.7	10379	8365.1	RSU1	NM_152724.2	RSP-1;FLJ31034			oncogene
GI_34577084-I	332.1	392	324	RSU1	NM_012425.3	RSP-1;FLJ31034			oncogene
GI_34577085-I	99.5	96.9	90.2	RNF13	NM_007282.3	RZF;MGC13689	peptidase	nucleus	proteolysis
GI_34577092-A	1917.2	2237.3	2301	RNF13	NM_183384.1	RZF;MGC13689	peptidase	nucleus	proteolysis
GI_34577097-A	996.6	1021.5	780	RNF14	NM_183399.1	ARA54;HFB30;HRIHFB2038	transcripti	kinesin	signal
GI_34577101-I	115.4	108.8	123.3	RNF14	NM_183401.1	ARA54;HFB30;HRIHFB2038	transcripti	kinesin	signal
GI_34577103-S	1459.5	1353.2	2056.3	RAB22A	NM_020673.2	MGC16770	GTP		small
GI_34577104-A	572.8	444.1	692.2	RNPC1	NM_183425.1	SEB4B;SEB4D;HSRNASEB;dJ800J21.2	RNA		
GI_34577108-I	109.2	126.3	115.1	ALDOA	NM_000034.2	ALDA;MGC10942;MGC17716;MGC17767	fructose-		fructose
GI_34577109-A	16186.5	17255	13219	ALDOA	NM_184041.1	ALDA;MGC10942;MGC17716;MGC17767	fructose-		fructose
GI_34577109-I	8159.2	10971	8607.5	ALDOA	NM_184041.1	ALDA;MGC10942;MGC17716;MGC17767	fructose-		fructose
GI_34577111-I	125.6	142.4	130.2	ALDOA	NM_184043.1	ALDA;MGC10942;MGC17716;MGC17767	fructose-		fructose
GI_34577117-S	155.8	176.3	154.1	KIAA1117	NM_015018.2	dJ202D23.2			
GI_34577119-S	308.5	306.4	272.9	MTRF1	NM_004294.2	RF1;MTTRF1;MGC47721	translation	mitochond	regulation
GI_34577121-S	2867.4	1899.2	1910.7	NFKB1	NM_003998.2	KBF1;EBP-1;MGC54151;NFKB-p50;NFKB-	transcripti	cytoplasm	response

GI_34577123-S	2541.5	2970.3	1294	PYGB	NM_002862.3	MGC9213	glycogen		glycogen
GI_34594658-S	442.9	426.2	399.4	FLJ39616	NM_016534.2				
GI_34594663-S	104.2	116	103.6	GPSM1	NM_015597.2	AGS3;DKFZP727I051			
GI_34594668-S	904.6	975.4	876.9	HCCA2	NM_053005.2	MOB2			
GI_34732708-I	138.5	155.5	142.9	MECT1	NM_015321.1	TORC1;WAMTP1;FLJ14027;KIAA0616			
GI_34734061-A	96.5	110	109.7	FBLN1	NM_001996.2	FBLN	extracellul	extracellul	
GI_34734061-I	114.4	210.2	111.1	FBLN1	NM_001996.2	FBLN	extracellul	extracellul	
GI_34734063-I	130.5	163.2	145.4	FBLN1	NM_006485.2	FBLN	extracellul	extracellul	
GI_34734065-I	91.2	92.4	97.8	FBLN1	NM_006486.2	FBLN	extracellul	extracellul	
GI_34734067-I	102.5	126.9	121.6	FBLN1	NM_006487.2	FBLN	extracellul	extracellul	
GI_34734069-S	113.1	110.6	111.4	GABRA3	NM_000808.2	MGC33793	benzodiaz	integral to	gamma-
GI_34734070-S	172.4	174.6	172.2	GABRD	NM_000815.2	MGC45284	GABA-A	integral to	small
GI_34734072-I	135.3	157.1	143	SLC22A18	NM_183233.1	HET;ITM;BWR1A;IMPT1;TSSC5;ORCTL2;B	organic	integral to	drug
GI_34734074-A	3527.2	3567	3452.9	SLC22A18	NM_002555.3	HET;ITM;BWR1A;IMPT1;TSSC5;ORCTL2;B	organic	integral to	drug
GI_34734074-I	142	154.8	132.3	SLC22A18	NM_002555.3	HET;ITM;BWR1A;IMPT1;TSSC5;ORCTL2;B	organic	integral to	drug
GI_34734076-S	874	532.4	613.4	FOSL1	NM_005438.2	FRA1;fra-1	transcripti	nucleus	response
GI_34734078-S	526.9	566.2	454.6	FZD6	NM_003506.2	Hfz6	frizzled	integral to	establish
GI_34740324-S	187.5	219.2	156.3	LOC158135	NM_194252.1		tubulin-		protein
GI_34740326-S	333.3	437.9	398.6	LOC91752	NM_194250.1				
GI_34740328-S	3309.1	4325.7	3192.1	hnRNPA3	NM_194247.1				
GI_34740330-I	132.5	156.7	135.2	OTOF	NM_194248.1	DFNB6;DFNB9;NSRD9;FER1L2	vesicle	membran	hearing
GI_34740332-S	157.8	177.9	149.9	GPR151	NM_194251.1	GPCR;PGR7	receptor	integral to	G-protein
GI_34740336-S	98.9	103.7	98.3	CREB3L2	NM_194071.1	BBF2H7;DKFZp586F2423;DKFZp686O1916			
GI_34740338-S	327.7	380.8	338.8	DND1	NM_194249.1	RBMS4;MGC34750	nucleic		
GI_34761063-S	1024.6	1446.4	1107.5	PIK3C3	NM_002647.2		1-	phosphoin	nonselecti
GI_34787408-S	324.1	376.2	522.5	KIAA1219	NM_020336.1				
GI_34787414-S	764.3	809.5	722.1	MGC23401	NM_144982.3	KIAA0546;DKFZp686A0722		intracellula	RNA
GI_34808709-A	292.8	290.7	288.8	SLC19A1	NM_194255.1	CHMD;FOLT;IFC1;REFC;RFC1	folate	membran	folate
GI_34823294-I	149.6	156.9	152.8	SLC19A1	NM_003056.2	CHMD;FOLT;IFC1;REFC;RFC1	folate	membran	folate
GI_34850056-S	122.6	127.4	121.4	HILS1	NM_194072.1				
GI_34850060-S	101.1	102.1	99.5	STMN2	NM_007029.2	SCG10;SGC10;SCGN10	cytoskelet	kinesin	intracellula
GI_34850063-S	859.5	866.3	879.1	NDUFC1	NM_002494.2	KFYI	NADH	NADH	mitochond
GI_34850064-S	103.5	109.7	93.6	TNP1	NM_003284.2	TP1	DNA	chromoso	chromoso
GI_34850073-S	975.8	629.7	864.1	CGI-150	NM_016080.2				
GI_34850075-S	743.5	723.2	848	RAB13	NM_002870.2		RAB small	tight	vesicle-
GI_34878689-A	559.5	415.5	358.6	CIAS1	NM_183395.1	FCU;MWS;FCAS;NALP3;C1orf7;PYPAF1;AII/	apoptosis	cellular_co	induction
GI_34878691-S	573.1	656.7	561	CALCRL	NM_005795.2	CRLR;CGRPR	G-protein	integral to	G-protein
GI_34878692-I	186.5	216.1	188.8	CIAS1	NM_004895.3	FCU;MWS;FCAS;NALP3;C1orf7;PYPAF1;AII/	apoptosis	cellular_co	induction
GI_34878694-I	148.3	174.1	162.2	LKAP	NM_014647.1	KIAA0430;A-362G6.1			
GI_34878696-A	1142.4	1412.6	1318.2	LKAP	NM_019081.2	KIAA0430;A-362G6.1			
GI_34878708-I	136	149.8	136.9	PAX2	NM_003988.2		transcripti	nucleus	axonogen
GI_34878715-A	106.3	112.8	113.9	PAX2	NM_003989.2		transcripti	nucleus	axonogen
GI_34878734-I	100.7	113.4	103.3	FBX30	NM_033182.4	FBG3;MGC14140			
GI_34878748-I	104.1	128	111	FBX30	NM_183412.1	FBG3;MGC14140			

GI_34878752-A	84.1	90.8	85.4	FBX30	NM_183413.1	FBG3;MGC14140			
GI_34878756-A	128.1	134.4	109	FBXO25	NM_012173.3	FBX25;MGC20256;MGC51975	ubiquitin		ubiquitin-
GI_34878776-S	654.3	650.2	671.2	RNF20	NM_019592.5	BRE1A;FLJ11189;FLJ20382;KIAA2779			
GI_34878786-S	255.8	288.8	271.9	RNF25	NM_022453.2	AO7;FLJ13906	ligase		
GI_34878803-S	556.6	662.2	827	RNF26	NM_032015.3	MGC2642	zinc ion	cellular_co	biological_
GI_34878820-I	94.7	99.6	96.8	RNF29	NM_033058.2	MURF-2			
GI_34878851-A	105.1	122.8	100.3	RNF29	NM_184087.1	MURF-2			
GI_34878859-I	132.4	158.9	143	RNF30	NM_032546.2	MURF;MURF-3			
GI_34878869-A	147.5	153.1	150.7	RNF30	NM_187841.1	MURF;MURF-3			
GI_34878876-S	117.2	163.7	117.7	NRN1	NM_016588.2	NRN;MGC44811			
GI_34878895-S	96.7	117.1	96.2	GPR62	NM_080865.2	GPCR8;MGC26943	G-protein	integral to	G-protein
GI_34878901-S	1901.7	1649.7	1649.1	PCM1	NM_006197.2	PTC4		centrosom	
GI_34878903-S	156.9	197.5	165.2	SYCP1	NM_003176.2	SCP1;HOM-TES-14	DNA	synaptone	synapsis
GI_34915989-S	176.4	487.5	194.8	RBPMS2	NM_194272.1				
GI_34915991-S	164	192.9	180.1	MOPT	NM_194270.1	BLOCK27			
GI_34915997-S	272.9	282.6	261.8	FLJ20209	NM_194276.1				
GI_34915999-S	117.1	132.1	120.5	LOC90167	NM_194277.1				
GI_34916001-S	146.4	172.2	164.7	LOC125476	NM_194281.1				
GI_34916003-S	168.6	185.8	178.2	LOC134218	NM_194283.1		RNA	nucleus	electron
GI_34916005-S	106.4	118.8	104	CLDN23	NM_194284.1		structural	tight	regulation
GI_34916007-S	132.8	151.6	141	LOC144747	NM_194286.1				
GI_34916009-S	88.4	91.4	89.4	LOC145497	NM_194287.1				
GI_34916011-S	249.2	259.1	249.4	LOC146712	NM_194288.1				
GI_34916013-S	106.3	189.4	155	LOC152195	NM_194289.1				
GI_34916015-S	94.4	93.4	83.6	DKFZp434I1	NM_194295.1				
GI_34916017-S	122.4	129.4	126.1	LOC153684	NM_194290.1				
GI_34916021-S	95.2	94.9	81.5	LOC221711	NM_194299.1				
GI_34916023-S	4767.4	4590.8	3812	LOC169355	NM_194294.1				
GI_34916025-S	84.8	103.1	88.8	DKFZp434O	NM_194302.1				
GI_34916027-S	254.3	203.2	95.2	SLC16A9	NM_194298.1	C10orf36;FLJ43803			
GI_34916029-S	122.5	120.5	106.1	LOC283031	NM_194304.1				
GI_34916031-S	106.9	105.1	99.4	LOC223075	NM_194300.1				
GI_34916035-S	144.9	204.5	181.4	C10orf39	NM_194303.1	FLJ37857			
GI_34916037-S	81.5	101.4	87.1	LOC284837	NM_194310.1				
GI_34916039-S	98.1	89.9	89.4	LOC283711	NM_194305.1				
GI_34916041-S	363.4	327.3	405.1	LOC339768	NM_194312.1				
GI_34916043-S	108.1	137.3	97	C21orf125	NM_194309.1	PRED49;FLJ38036			
GI_34916045-S	110.4	121.6	112.3	FRBZ1	NM_194314.1		protein		
GI_34916047-S	116.3	144.4	135.9	LOC338769	NM_194311.1				
GI_34916049-S	114.3	117.9	129.3	C9orf48	NM_194313.1	FLJ43884			
GI_34916053-S	120.4	107.6	107	MLR1	NM_153686.4	FLJ30696			
GI_34916054-S	342.5	375.4	353.6	KIRREL	NM_018240.3	NEPH1;FLJ10845			
GI_34916055-I	496.8	696.3	1063	KNS2	NM_005552.3	KLC;KLC1;KNS2A	motor	kinesin	microtubul
GI_34916057-S	318.1	342.2	423.1	KLF4	NM_004235.3	EZF;GKLF	transcripti		mesoderm

GI_34932234-S	106.8	118.2	129	ZNF228	NM_013380.2		DNA	nucleus	regulation
GI_34932413-S	2390.9	2803.6	2601.9	NONO	NM_007363.3	P54;NMT55;NRB54;P54NRB	pre-mRNA	nucleus	mRNA
GI_34932495-S	146.9	164	140.9	BTN3A2	NM_007047.2	BTF4;BT3.2			
GI_34996482-S	144.9	146.6	138.4	DKFZp686L1	NM_194282.1				
GI_34996486-S	2070.3	2001.9	2265.2	HBLD1	NM_194279.1	c14_5557	molecular		
GI_34996490-S	904.6	888.2	925.5	LOC124446	NM_194280.1				
GI_34996518-S	107.9	106.9	110.3	GALIG	NM_194327.1				
GI_34996520-S	137.6	129.7	143.3	ZNF30	NM_194325.1	KOX28;DKFZp686N19164	DNA	nucleus	regulation
GI_34996522-S	159.7	203.3	161.3	MGC52057	NM_194317.1				
GI_34996524-S	380.8	503.9	429.9	ZNF542	NM_194319.1	DKFZp686B2197			
GI_34996526-S	1482.7	1361.7	1210.2	MGC52010	NM_194326.1				
GI_34996530-S	472.1	621.9	740.8	B3GTL	NM_194318.1				
GI_34996532-S	138.7	158.1	136.2	MGC39900	NM_194324.1		actin	cytoplasm	cytoskelet
GI_34996534-S	113.9	117.9	108.6	ZNF169	NM_194320.1	MGC51961	transcripti	nucleus	regulation
GI_35038161-S	374.2	489.4	424.3	RREB1	NM_002955.3	FINB;LZ321;RREB-1	transcripti		RAS
GI_35038527-S	249.7	306.3	298.5	PASK	NM_015148.2	STK37;PASKIN;KIAA0135;DKFZP434O051	ATP		protein
GI_35038563-S	333.6	383.8	238.1	KIAA0922	NM_015196.2	DKFZp586H1322			
GI_35038578-S	753.2	878.8	767.7	LOC157378	NM_194291.1				
GI_35038600-S	186.6	178.7	179.6	DKFZp761A0	NM_194292.1				
GI_35249735-A	199.4	248.1	194	ZNF226	NM_015919.2				
GI_35249735-I	665.1	873.7	598.5	ZNF226	NM_015919.2				
GI_35250685-S	544.5	312.4	263.6	USP36	NM_025090.2	FLJ12851;KIAA1453	cysteine-	nucleus	ubiquitin-
GI_35250772-S	6062.8	6389.1	6698.8	DKFZP564J1	NM_018457.2				
GI_35250828-S	1175	1963	1867.3	COPG	NM_016128.3	COPG1	protein	membran	intracellula
GI_35493718-I	79.5	87.1	84.2	COH1	NM_184042.1	CHS1;KIAA0532;DKFZp313I0811	metallope	membran	transport
GI_35493724-I	137.5	164.1	137.1	COH1	NM_015243.2	CHS1;KIAA0532;DKFZp313I0811	metallope	membran	transport
GI_35493732-I	97.3	108.4	106.7	MOCS2	NM_004531.3	MPTS;MCBPE;MOCO1	catalytic		Mo-
GI_35493763-A	494.2	402.6	344.5	MOCS2	NM_176806.2	MPTS;MCBPE;MOCO1	catalytic		Mo-
GI_35493773-S	87.1	92.6	81.1	RNF18	NM_020358.2		zinc ion	intracellula	
GI_35493781-A	1446.2	1309.2	1248	RNF19	NM_015435.3	DORFIN;DKFZp566B1346	transcripti	centrosom	microtubul
GI_35493781-I	145.4	157.8	165.6	RNF19	NM_015435.3	DORFIN;DKFZp566B1346	transcripti	centrosom	microtubul
GI_35493800-I	162.3	187.3	163.8	RNF19	NM_183419.1	DORFIN;DKFZp566B1346	transcripti	centrosom	microtubul
GI_35493816-I	237.9	262	275.3	RNPC2	NM_184237.1	HCC1;CAPER;CC1.3;CC1.4	pre-mRNA	nucleoplas	RNA
GI_35493837-A	88.4	106.9	99.2	RNPC2	NM_004902.2	HCC1;CAPER;CC1.3;CC1.4	pre-mRNA	nucleoplas	RNA
GI_35493852-I	105.2	107.1	117.4	OTOF	NM_194322.1	DFNB6;DFNB9;NSRD9;FER1L2	vesicle	membran	hearing
GI_35493859-A	288.2	315.2	296.5	OTOF	NM_194323.1	DFNB6;DFNB9;NSRD9;FER1L2	vesicle	membran	hearing
GI_35493877-S	691.7	609.5	578.5	RELB	NM_006509.2	I-REL	transcripti	nucleus	regulation
GI_35493898-S	97.1	105.9	96.4	REM	NM_014012.4	GES;MGC48669	small		small
GI_35493905-S	2405.5	2217.2	895.4	RIN2	NM_018993.2	RASSF4	GTPase		neuropepti
GI_35493915-S	3494.2	5606.9	8250	RPN2	NM_002951.2	RIBIIR;RPN-II	oligosacch	endoplas	protein
GI_35493922-S	577	496.4	642.6	PCNT2	NM_006031.3	KEN;PCN;PCNT;PCNTB;PCTN2;KIAA0402	structural	centrosom	microtubul
GI_35493938-S	160	154.1	146.1	ProSAPiP1	NM_014731.2	KIAA0552		kinesin	
GI_35493944-I	100.4	102.2	94.1	UBE3B	NM_183414.1	DKFZp586K2123;DKFZp686A1051	ubiquitin-	intracellula	ubiquitin
GI_35493951-A	726.1	736.7	565.3	UBE3B	NM_183415.1	DKFZp586K2123;DKFZp686A1051	ubiquitin-	intracellula	ubiquitin

GI_35493986-I	152.5	158.3	148.2	UBE2I	NM_194259.1	P18;UBC9;C358B7.1	ubiquitin	synaptone	ubiquitin-
GI_35493995-A	5785.5	5396.9	5698	UBE2I	NM_194260.1	P18;UBC9;C358B7.1	ubiquitin	synaptone	ubiquitin-
GI_35493995-I	108.9	120.5	121.3	UBE2I	NM_194260.1	P18;UBC9;C358B7.1	ubiquitin	synaptone	ubiquitin-
GI_35494002-I	195.8	230.5	198.8	UBE2I	NM_194261.1	P18;UBC9;C358B7.1	ubiquitin	synaptone	ubiquitin-
GI_36030882-S	673.8	801.7	692.2	RP42	NM_020640.2	SCRO			
GI_36030904-S	657.6	594.3	757.4	KIAA0274	NM_014845.4	SAC3;hSac3;dJ249I4.1			
GI_36030945-S	1184.9	870.2	736.8	LOC90806	NM_144567.2				
GI_36030972-S	413.8	373.8	412.7	UBXD4	NM_181713.3				
GI_36030993-S	496	639.8	514.5	FEM1C	NM_020177.2	FEM1A;KIAA1785;EUROIMAGE686608;EUR			
GI_36031015-S	150.2	145.9	139.9	FLJ10188	NM_018017.2	FLJ35301			
GI_36031099-S	101.2	113.5	108.5	CALML3	NM_005185.2	CLP	calcium		
GI_36054052-S	118.2	131.9	113.5	FABP7	NM_001446.3	MRG;FABPB;B-FABP	intracellula		negative
GI_36054077-S	189.4	211.2	208.8	FDX1	NM_004109.3	ADX;FDX	adrenodox	mitochond	vitamin
GI_36054106-S	94.6	105.9	94.1	BENE	NM_005434.3	MGC4419	transporte	synaptic	transport
GI_36054140-S	124.4	175.6	123.4	EBF	NM_024007.2	COE1;EBF1;OLF1;O/E-1	DNA	nucleus	regulation
GI_36054149-S	272.3	334.2	294.6	RIMS4	NM_182970.2	RIM4;C20orf190;dJ781B1.3			
GI_36054181-S	176.6	224.9	178.4	REG4	NM_032044.2	GISP;RELP;REG-IV	sugar		
GI_36054193-S	630.3	669.6	557.6	ZNF384	NM_133476.2	NP;CIZ;NMP4;CAGH1;TNRC1;CAGH1A			
GI_36287059-A	156.8	175.2	161.7	HTATIP	NM_182709.1	TIP;PLIP;TIP60;cPLA2;HTATIP1	transcripti	nucleus	virulence
GI_36287068-I	140.4	153.7	142.6	HTATIP	NM_182710.1	TIP;PLIP;TIP60;cPLA2;HTATIP1	transcripti	nucleus	virulence
GI_36287109-A	118.1	137.2	121.3	FGFR1OP	NM_194429.1	FOP			positive
GI_36287116-S	366.2	451	477.5	MAN1	NM_014319.3		nucleic	integral to	
GI_36287129-S	219.3	232.3	218.9	MRPS25	NM_022497.3	RPMS25;MRP-	structural	mitochond	protein
GI_36413606-S	99.2	99.5	101.4	ABCB5	NM_178559.3		nucleotide	membran	transport
GI_36949365-S	143.9	154.6	146.7	MSH4	NM_002440.2		DNA	nucleus	meiotic
GI_36950990-S	246.1	238.5	206.2	NR2C2	NM_003298.2	TR4;TAK1;TR2R1;hTAK1	steroid	nucleus	regulation
GI_36951011-S	1336.4	1577	1282.1	GPR1	NM_005279.2		G-protein	integral to	G-protein
GI_36951033-S	126.5	148.8	133.6	GPR78	NM_080819.2		receptor	integral to	G-protein
GI_36951077-S	61.1	70.6	76.5	FUT9	NM_006581.2	Fuc-TIX	fucosyltra	membran	carbohydr
GI_36951095-S	489.7	1587	936	FPR1	NM_002029.3	FPR;FMLP	N-formyl	endosome	activation
GI_36951115-S	131.2	126.9	117.7	ENPEP	NM_001977.2	APA;gp160	glutamyl	integral to	cell
GI_36951139-S	504	555.4	569.8	FKRP	NM_024301.2	MDC1C;LGMD2I;MGC2991;FLJ12576			
GI_36951161-S	104.3	94.8	102	D4S234E	NM_014392.2	P21;NSG1;D4S234		Golgi	
GI_36951195-S	100.9	119.5	115.8	CTNND2	NM_001332.2	GT24;NPRAP	structural	kinesin	cell
GI_37039609-A	264.9	236.9	288	BTRC	NM_003939.2	FWD1;BTRCP;FBW1A;FBXW1A;MGC4643;	ubiquitin	endoplas	ubiquitin-
GI_37039611-I	86.5	99.5	101.1	C9orf72	NM_018325.1	MGC23980			
GI_37039614-A	293.3	351.5	328.9	C9orf72	NM_145005.3	MGC23980			
GI_37039614-I	178.3	160.2	198	C9orf72	NM_145005.3	MGC23980			
GI_37039615-I	102.3	101.3	99.8	BTRC	NM_033637.2	FWD1;BTRCP;FBW1A;FBXW1A;MGC4643;	ubiquitin	endoplas	ubiquitin-
GI_37059722-S	311.3	343.6	289	KIAA0776	NM_015323.2				
GI_37059723-S	429.8	448.4	440	C22orf18	NM_024053.2	Pane1;MGC861			
GI_37059724-S	2408.7	1877.9	2379.5	MGC5576	NM_024056.2				
GI_37059725-S	1107.1	1090.7	957.6	GRPEL1	NM_025196.2	HMGE;FLJ25609	chaperone	mitochond	mitochond
GI_37059727-S	1417.7	1836.7	1740.7	MGC10540	NM_032353.2				

GI_37059728-S	1267.2	1073.5	1085.7	PHF5A	NM_032758.2	INI;MGC1346;SF3b14b;bK223H9.2	molecular		
GI_37059729-S	151.4	144.5	156.2	STAF42	NM_053053.2				
GI_37059730-S	266.1	355.3	346.3	SLC35C1	NM_018389.3	FUCT1;FLJ11320	sugar	Golgi	transport
GI_37059733-S	753.9	748.4	567.7	HADHA	NM_000182.3	GBP;MTPA;LCHAD	3-	mitochond	fatty acid
GI_37059734-S	1204.6	1257.1	950.1	UCHL3	NM_006002.3		ubiquitin	cytoplasm	ubiquitin-
GI_37059735-S	941.5	733.3	845.2	CWF19L1	NM_018294.3	FLJ10998			
GI_37059737-S	235.7	296.6	265.7	LOC120379	NM_138789.2				
GI_37059738-S	255.1	273.3	253.4	LOC123169	NM_138792.2				
GI_37059739-S	201.4	192.2	174.6	LOC128153	NM_138796.2				
GI_37059740-S	146.6	169.9	158.3	ORMDL2	NM_014182.3	HSPC160			
GI_37059741-S	606.3	339.9	260.9	TUBE1	NM_016262.3	TUBE;FLJ22589;dJ142L7.2	structural	pericentrio	centrosom
GI_37059742-S	2314.3	1881.1	1130.8	MKI67IP	NM_032390.3	NIFK;Nopp34	nucleic		
GI_37059743-S	804.8	851	853.4	PIP5K2C	NM_024779.3	FLJ22055	kinase		
GI_37059744-S	330.9	360.7	354.9	FLJ10407	NM_018087.3				
GI_37059745-S	2123.6	1709.3	2016.6	PEX5	NM_000319.3	PXR1;PTS1R	peroxisom	peroxisom	protein-
GI_37059746-S	923.3	1071.2	1141.8	TM9SF1	NM_006405.3	MP70;HMP70	transporte	integral to	transport
GI_37059747-S	672.6	520.9	355.8	MDS006	NM_020233.3				
GI_37059748-S	1741.9	1541.4	1620.8	TBC1D15	NM_022771.3	FLJ12085;DKFZp761D0223			
GI_37059749-S	582.5	704.3	662.3	DKFZP564D1	NM_032042.3				
GI_37059750-S	148.9	173.9	147.3	MGC33367	NM_144602.2				
GI_37059751-S	212.3	208.9	203	THAP6	NM_144721.2	MGC30052	DNA	kinesin	
GI_37059752-S	113.1	112.9	108.4	SUSD3	NM_145006.2	MGC26847			
GI_37059754-S	946.9	663	667.8	LOC90353	NM_145232.2		electron		electron
GI_37059756-S	98.7	95.6	96.6	LOC122258	NM_145248.2				
GI_37059757-S	109.8	136.1	119.4	LOC146853	NM_145272.2		DNA	nucleus	regulation
GI_37059758-S	287	293.5	272.6	TREM4	NM_145273.2				
GI_37059759-S	795	583.9	623.8	MGC33864	NM_152522.2				
GI_37059760-S	142.2	135.8	133.3	MGC33190	NM_152749.2				
GI_37059761-S	1174.2	1666.8	1453.1	MGC40107	NM_152766.2				
GI_37059762-S	189.6	223.7	214.9	STCH	NM_006948.3		adenosine	microsom	
GI_37059763-S	735.5	632.7	610.4	GPHN	NM_020806.3	GPH;GEPH;GPHRYN;KIAA1385	catalytic	cytoskelet	Mo-
GI_37059764-S	3223.5	3140.6	3425.8	UNC50	NM_014044.4	URP;GMH1;UNCL;hGMH1p;DKFZp564G022			
GI_37059766-S	104.6	116.3	106.9	MGC26979	NM_153704.2		molecular		
GI_37059767-S	115.6	124.6	114.6	ENPP6	NM_153343.2	MGC33971	hydrolase		nucleotide
GI_37059768-S	91.5	96.5	85.1	MGC27085	NM_153353.2				
GI_37059769-S	87.3	95.1	96.6	MGC42105	NM_153361.2		protein-		protein
GI_37059770-S	638.3	546.8	544.2	RHPN2	NM_033103.3	p76RBE	protein	intracellula	intracellula
GI_37059771-S	108.7	112.3	97.2	MGC33408	NM_032517.3	bA534G20.1	lysozyme	extracellul	cell wall
GI_37059775-S	650.1	745.5	536	LOC196463	NM_173542.2				
GI_37059776-S	405.8	347.8	398.7	DDX51	NM_175066.2	MGC42193	nucleic	nucleus	regulation
GI_37059777-S	100.9	111.6	112.2	SECP43	NM_017846.3	PRO1902;FLJ20503			
GI_37059778-S	298.8	255.7	266	FLJ20035	NM_017631.3	FLJ10787	ATP		
GI_37059779-S	461.9	541.1	485.9	FIBCD1	NM_032843.3	FLJ14810			
GI_37059780-S	113.9	116.4	99	ZNF183L1	NM_178861.3	MGC26599;bA10G5.1	nucleic		

GI_37059781-S	1288.9	1295.7	1157.1	MPV17	NM_002437.3		molecular	integral to	oxygen
GI_37059782-S	134.2	146.3	128.4	KIAA0980	NM_025176.3	FLJ11792	calcium		
GI_37059783-S	104.5	121.3	121.7	PNLIPRP2	NM_005396.3	PLRP2	triacylglyc	extracellul	triacylglyc
GI_37059784-S	314.3	409.6	304.7	HRB2	NM_007043.5	RIP-1			
GI_37059785-S	228.6	225.5	221	LRRN3	NM_018334.3	NLRR3;NLRR-3;FLJ11129			
GI_37059786-S	1663.1	1553.6	638.9	HCLS1	NM_005335.3	HS1	DNA	DNA-	regulation
GI_37059790-S	464.6	549.3	632.3	FLJ10055	NM_017983.3				
GI_37059791-S	100.2	95	97.7	CCDC7	NM_145023.3	FLJ32762			
GI_37059793-S	167.3	173.3	157.1	C6orf81	NM_145028.3	FLJ25390			
GI_37059794-S	111	111.1	98.7	FLJ25351	NM_152525.3				
GI_37059795-S	152.3	156.2	170	MGC26963	NM_152621.3				
GI_37059796-S	634	708.6	361.7	FLJ38101	NM_153261.3				
GI_37059797-S	3632.8	3399.6	3337.5	THG-1	NM_030935.3		transcripti	nucleus	regulation
GI_37059798-S	93.6	92.3	93.2	DKFZp761N1	NM_181644.2				
GI_37059801-S	207.6	227.1	252.7	MGC41816	NM_016466.4				
GI_37059809-S	120.2	143.7	126.9	LOC285498	NM_194439.1				
GI_37059813-S	130.7	147.1	140.7	ETAA16	NM_019002.2				
GI_37187859-A	96.6	101.9	100.2	CCR6	NM_004367.3	BN-1;CKR6;DCR2;CKRL3;DRY-	chemokin	integral to	cytosolic
GI_37188164-I	90.6	83.6	78	CCR6	NM_031409.2	BN-1;CKR6;DCR2;CKRL3;DRY-	chemokin	integral to	cytosolic
GI_37202113-S	155.1	194.5	170.6	PAPOLB	NM_020144.3	PAPT;TPAP	RNA	nucleus	transcripti
GI_37202115-S	299.5	331.6	276.1	FLJ32110	NM_181646.2				
GI_37202122-S	389.8	374	318.1	NARG2	NM_024611.2	FLJ11896			
GI_37221174-S	661.5	786.6	791.3	PLEKHE1	NM_194449.1	SCOP;KIAA0606	catalytic		
GI_37221176-S	284.9	387.5	292.3	NUDT11	NM_018159.2	DIPP3b;FLJ10628;hDIPP3beta			
GI_37221178-S	740.1	562.8	852.2	ANKRD25	NM_015493.3	FLJ20004;KIAA1518;DKFZp434N161			
GI_37221179-S	225.1	239.4	217.9	KIAA0478	NM_014870.2		DNA	nucleus	regulation
GI_37221186-A	101.9	113.4	97.1	CCM1	NM_194454.1	CAM;KRIT1	small	cytoskelet	small
GI_37221188-A	108.8	109.7	103.1	BTN3A1	NM_194441.1	BTF5;BT3.1			lipid
GI_37221188-I	102.6	102.6	110.4	BTN3A1	NM_194441.1	BTF5;BT3.1			lipid
GI_37537515-S	106.3	115.7	106.4	ZNF138	NM_006524.1	pHZ-32	transcripti	nucleus	developm
GI_37537523-S	1415.8	1081	1558.1	CLDN12	NM_012129.2		structural	tight	
GI_37537547-S	1446.5	1843	1929.9	HSPC268	NM_197964.1				
GI_37537551-S	94.1	112.2	94.8	SOAT	NM_197965.1				
GI_37537553-S	155.1	164.7	138.2	FLJ37538	NM_173564.2				
GI_37537557-S	252.3	235.8	231.4	C9orf90	NM_197956.1	bA379C10.2;DKFZp762G199			
GI_37537682-I	79.3	89.3	87.5	ZNF92	NM_152626.2	TF12;HPF12;FLJ34299	zinc ion	nucleus	regulation
GI_37537683-A	108.9	112.4	107.2	ZNF92	NM_007139.2	TF12;HPF12;FLJ34299	zinc ion	nucleus	regulation
GI_37537685-S	743.9	641.1	485.7	ZNF38	NM_145914.2	Zipro1;NY-REN-21;DKFZp434L134	DNA	nucleus	regulation
GI_37537686-S	1617.3	1625.9	1686.4	ZNF444	NM_018337.2	EZF2;EZF-2;FLJ11137	transcripti	nucleus	regulation
GI_37537688-S	199.6	146.1	178.6	ZNF354A	NM_005649.2	EZNF;HKL1;KID1;KID-1;TCF17	RNA	nucleus	hearing
GI_37537690-S	248.2	225.8	200.7	SPPL3	NM_139015.3	IMP2;PSL4;DKFZP586C1324	peptidase	integral to	
GI_37537693-S	411.8	409.5	388.5	MTMR6	NM_004685.2		protein	cellular_co	protein
GI_37537695-S	154.4	180.3	156.2	MPHOSPH9	NM_022782.2	MPP9;MPP-9;FLJ12954;DKFZp434J034	cell cycle	Golgi	M phase
GI_37537697-S	2973.6	1755.8	1348.2	MGC27005	NM_152582.3				

GI_37537698-S	385.1	253.7	389.1	LOC147965	NM_174905.2				
GI_37537700-S	760.5	857	380.4	KIAA0685	NM_014678.2	dJ579N16.1			
GI_37537702-I	407.8	436.2	339.3	GLRX2	NM_016066.3	GRX2			
GI_37537703-A	384	330.5	361.2	GLRX2	NM_197962.1	GRX2			
GI_37537703-I	183.1	173.1	181.5	GLRX2	NM_197962.1	GRX2			
GI_37537705-A	1057.7	668.7	1081.4	FLJ11196	NM_197958.1		RNA	nucleus	regulation
GI_37537705-I	4743.8	3424.3	5225	FLJ11196	NM_197958.1		RNA	nucleus	regulation
GI_37537707-S	127.4	134.4	129	FLJ14640	NM_032816.2				
GI_37537709-I	2573.7	1300.3	1037.5	FLJ11196	NM_018357.2		RNA	nucleus	regulation
GI_37537711-S	107.5	114.7	97.2	EPB41L4A	NM_022140.2	NBL4;EPB41L4	structural	cytoskelet	biological_
GI_37537713-S	2449.3	2463.2	1748.3	ENTH	NM_014666.2	EPN4;EPNR;Clint;EPSINR;KIAA0171			
GI_37537714-I	1042.6	935.4	758.7	EIF5	NM_001969.3	EIF-5A	GTPase	cytosol	regulation
GI_37537715-A	214	197.1	190.7	EIF5	NM_183004.3	EIF-5A	GTPase	cytosol	regulation
GI_37537715-I	82.9	86.7	80.1	EIF5	NM_183004.3	EIF-5A	GTPase	cytosol	regulation
GI_37537717-S	285.4	292.8	315.1	DCPS	NM_014026.3	HSL1;HINT-5;HSPC015	heat		
GI_37537718-S	383.3	336.5	451.8	DCP2	NM_152624.3	FLJ33245			
GI_37537719-S	2242.3	3163.2	1463.4	CHSY1	NM_014918.3	KIAA0990			
GI_37537720-S	1153.4	1617.9	1450.7	B3GALT6	NM_080605.2	beta3GalT6	galactosylt	membran	protein
GI_37537721-S	137.3	168.7	156.8	AGMAT	NM_024758.3	FLJ23384	arginase	mitochond	arginine
GI_37538133-S	99.6	95.7	96.1	LOC340223	XM_290385.2				
GI_37538135-S	90.1	98.1	82.9	LOC375574	XM_353423.1				
GI_37538137-S	95.5	107.3	107.2	LOC375575	XM_351709.1				
GI_37538141-S	90.9	94.3	83.1	LOC377506	XM_352648.1				
GI_37538155-S	83.7	81.9	83.4	LOC340228	XM_291204.2				
GI_37538165-S	101.3	108.1	104.1	LOC346288	XM_294165.2				
GI_37538171-S	113.5	118.8	121.2	LOC375572	XM_351708.1				
GI_37538173-S	87.8	89.7	84.9	LOC254027	XM_171150.2				
GI_37538174-S	78.4	81.8	77.2	LOC375573	XM_353422.1				
GI_37538197-S	1246.3	1105.5	1293	KIAA1228	XM_036408.5				
GI_37538207-S	84.3	95.2	80.4	LOC375576	XM_353424.1				
GI_37538215-S	210.2	274.7	241.9	LOC375579	XM_351710.1				
GI_37538224-S	133.2	132.5	132	LOC375582	XM_351713.1				
GI_37538226-S	110.5	112.9	109.5	LOC375583	XM_353426.1				
GI_37538244-S	123	141	140.8	LOC377511	XM_352650.1				
GI_37538248-S	93	112.4	105.8	LOC136132	XM_069728.4				
GI_37538256-S	110.2	108.9	106.7	LOC377514	XM_352651.1				
GI_37538268-S	166.6	192.8	181.5	LOC375636	XM_351763.1				
GI_37538329-S	110.4	183.7	125.7	LOC375546	XM_353416.1				
GI_37538331-S	366.2	356.4	329.2	KIAA0415	XM_166527.4				
GI_37538337-S	90.3	99.2	98.3	LOC375548	XM_353417.1				
GI_37538343-S	98.3	95.1	90	LOC375549	XM_351685.1				
GI_37538348-S	2085	2239.4	1477.1	LOC155340	XM_055725.3				
GI_37538350-S	122.6	129.3	118.6	LOC285929	XM_209824.2				
GI_37538362-S	91.3	85.3	86.1	LOC221813	XM_168223.2				

GI_37538364-S	88.1	93.3	94.9	LOC375553	XM_351689.1
GI_37538368-S	91	100.7	97.4	LOC375555	XM_353419.1
GI_37538378-S	123.1	153.3	139	LOC375557	XM_353420.1
GI_37538380-S	327	390.1	348.2	LOC256227	XM_171163.3
GI_37538391-S	957.4	668.4	737.8	LOC375558	XM_351694.1
GI_37538393-S	555.8	468	419.8	LOC222136	XM_166563.2
GI_37538397-S	139.8	136.8	138.7	LOC375559	XM_351695.1
GI_37538413-S	98.8	105.8	98.2	MYO1G	XM_291223.2
GI_37538415-S	115.4	126.5	100.4	KIAA0363	XM_166571.2
GI_37538417-S	103.4	108.8	99.7	LOC375565	XM_351702.1
GI_37538419-S	153.6	200.1	157.3	LOC340290	XM_291214.2
GI_37538421-S	98.6	92.2	78.9	LOC346355	XM_294219.2
GI_37538423-S	110	126.4	111.7	LOC377461	XM_352635.1
GI_37538427-S	111.2	126.5	102.8	LOC377464	XM_352636.1
GI_37538429-S	129	128	135.5	LOC377465	XM_352637.1
GI_37538431-S	102.7	127	108.1	LOC377466	XM_352638.1
GI_37538433-S	103.6	98.3	89.9	LOC377467	XM_352640.1
GI_37538435-S	206.7	255.2	232.7	LOC340265	XM_294249.3
GI_37538454-S	359.5	450.1	237.2	LOC221875	XM_167254.3
GI_37538458-S	88	82.8	91.9	LOC377480	XM_352642.1
GI_37538496-S	90.3	91.9	78.5	KIAA1718	XM_034823.6
GI_37538498-S	112.6	113.4	106.1	LOC375626	XM_351751.1
GI_37538504-S	121.5	128.4	118.9	LOC375632	XM_351759.1
GI_37538517-S	146.8	149.8	143.5	LOC155046	XM_088143.3
GI_37538519-S	116.9	131.1	127.9	LOC346545	XM_294261.2
GI_37538523-S	227.3	267.5	246	LOC375634	XM_353439.1
GI_37538527-S	121.9	110.6	112	LOC377560	XM_352679.1
GI_37538529-S	84.4	85.6	74.8	LOC130075	XM_065555.3
GI_37538531-S	173.6	207.7	173.8	LOC135924	XM_069609.4
GI_37538535-S	87.8	87.4	88	LOC135946	XM_069621.7
GI_37538540-S	72.5	91.9	82.3	LOC346525	XM_294316.3
GI_37538544-S	153.2	179	157.4	LOC135941	XM_069616.4
GI_37538548-S	114	125	103.1	LOC202861	XM_116654.3
GI_37538555-S	82.2	93.7	83.7	LOC340312	XM_294319.2
GI_37538557-S	113.5	108.4	108.7	LOC377585	XM_352694.1
GI_37538559-S	101	90.6	85.9	LOC377586	XM_352695.1
GI_37538563-S	100.4	105.8	107.6	LOC377590	XM_352697.1
GI_37538567-S	100.9	105.1	97.4	LOC377592	XM_352699.1
GI_37538601-S	100.3	106.2	102.4	LOC375594	XM_353428.1
GI_37538603-S	121	137.4	121.7	LOC202802	XM_114560.2
GI_37538617-S	89.1	85.6	75.9	LOC375598	XM_353430.1
GI_37538619-S	84.4	87.3	88.9	LOC375599	XM_353431.1
GI_37538625-S	188.9	189.7	201.7	LOC375602	XM_351729.1
GI_37538629-S	357.6	491.3	497.6	LOC255374	XM_171171.2

GI_37538632-S	222.9	281.7	264.6	LOC375606	XM_351733.1
GI_37538636-S	505.6	597.1	542	MUC3B	XM_168578.3
GI_37538638-S	96.7	115.5	95.5	LOC219612	XM_168585.3
GI_37538640-S	141.9	175.5	147	MUC17	XM_168583.3
GI_37538648-S	93.3	95.4	85.4	LOC222236	XM_168636.3
GI_37538652-S	107.4	119.2	121.7	ZRF1	XM_168590.4
GI_37538654-S	101.3	99.8	91.8	LOC375611	XM_351742.1
GI_37538660-S	738.5	880.1	792.9	IPLA2(GAMM	XM_291241.3
GI_37538664-S	127	134.9	117.4	LOC375613	XM_351744.1
GI_37538667-S	84.8	88.3	93.1	LOC375614	XM_353433.1
GI_37538671-S	105	112.7	112.1	LOC375615	XM_353434.1
GI_37538683-S	166.2	189.2	162.8	LOC375618	XM_353435.1
GI_37538687-S	127.2	257.1	160.7	LOC375620	XM_351747.1
GI_37538693-S	96.5	111.2	95.7	LOC375622	XM_353436.1
GI_37538697-S	88.2	89.7	91.6	LOC375624	XM_353438.1
GI_37538711-S	100.4	93.3	93.5	LOC377522	XM_352658.1
GI_37538713-S	101.3	115	132.8	LOC377523	XM_352659.1
GI_37538715-S	477.6	977.3	801.8	LOC377524	XM_352660.1
GI_37538719-S	355.6	428.1	354.1	LOC377527	XM_352661.1
GI_37538723-S	89.7	90.6	81.6	LOC377530	XM_352662.1
GI_37538725-S	84.4	87.2	74.5	LOC346588	XM_294328.2
GI_37538731-S	108	123.1	102.2	LOC377535	XM_294331.3
GI_37538739-S	117.8	126.7	126.8	LOC377542	XM_352668.1
GI_37538741-S	111.6	152.5	133	LOC285997	XM_209865.2
GI_37538743-S	243.5	295.9	290.7	LOC377544	XM_352669.1
GI_37538745-S	102.8	111.8	100.4	LOC377545	XM_352670.1
GI_37538749-S	112.7	126.8	120.2	LOC377549	XM_352672.1
GI_37538751-S	7359.8	6274.7	5138.9	LOC136143	XM_069734.2
GI_37538753-S	83.9	71.4	83.7	LOC377550	XM_352673.1
GI_37538769-S	86.7	87.2	85.7	LOC377554	XM_352676.1
GI_37538775-S	130	129.4	131.7	LOC377556	XM_352677.1
GI_37538777-S	164.8	154.2	151.6	LOC377557	XM_352678.1
GI_37538781-S	99.7	97.8	91.7	LOC202789	XM_116623.2
GI_37538802-S	127.3	134.3	119	LOC378031	XM_353546.1
GI_37538824-S	76.7	89.9	65.9	LOC340267	XM_295195.2
GI_37538858-S	106.9	116.6	110.7	LOC378054	XM_353836.1
GI_37538916-S	130.9	155.4	142.3	LOC378075	XM_353595.1
GI_37538936-S	217.1	257.7	221.2	LOC340260	XM_294209.3
GI_37538942-S	100.3	108.5	97.5	LOC378217	XM_353718.1
GI_37538976-S	82.4	91.4	85.9	LOC378261	XM_353734.1
GI_37538993-S	116.7	123.3	134	LOC378089	XM_353602.1
GI_37539011-S	255.8	182.4	197.4	LOC378103	XM_353843.1
GI_37539091-S	105.5	99.1	100.8	LOC378135	XM_353637.1
GI_37539093-S	175.6	217.6	192.1	LOC378136	XM_353638.1

GI_37539105-S	486.4	732.8	628.5	LOC378140	XM_353642.1		
GI_37539119-S	97.4	104	93.5	LOC378147	XM_353648.1		
GI_37539139-S	105.1	94.9	92.3	LOC378311	XM_353752.1		
GI_37539180-S	487.2	545.7	399.7	LOC378157	XM_353658.1		
GI_37539232-S	6966.7	6031	4638.1	LOC154995	XM_088103.3		
GI_37539292-S	161.6	189.6	159.1	LOC378201	XM_353702.1		
GI_37539300-S	294.5	309.8	379.2	LOC378204	XM_353706.1		
GI_37539398-S	121.2	138.7	120.2	LOC378396	XM_353806.1		
GI_37539408-S	99	113.5	113	LOC346528	XM_294318.2		
GI_37539440-S	87	96.2	90.5	LOC378421	XM_353822.1		
GI_37539442-S	102.4	103.3	107.3	LOC378422	XM_353869.1		
GI_37539457-S	135.1	152.4	133.8	LOC375186	XM_351420.1		
GI_37539459-S	170.9	145.3	150	LOC130502	XM_059438.4		
GI_37539462-S	94.1	102	77.1	LOC376869	XM_352439.1		
GI_37539464-S	110.9	106.3	93.1	LOC343930	XM_292850.2		
GI_37539470-S	258.4	307.2	274.3	LOC375396	XM_353347.1		
GI_37539472-S	90.3	99	91.7	KIAA1239	XM_049078.3		
GI_37539476-S	165.5	136.2	135.8	MGC19531	XM_352931.1	DKFZp434P1514	catalytic
GI_37539480-S	114.6	125.4	118.7	LOC375002	XM_351278.1		
GI_37539485-S	103.5	109.5	97.8	LOC343263	XM_291485.2		
GI_37539487-S	122.4	159.6	126.2	LOC375004	XM_351280.1		
GI_37539489-S	642.6	619.4	791.2	FLJ14743	XM_042708.7	KIAA1761	
GI_37539490-S	228.1	282.7	248.3	LOC375005	XM_353211.1		
GI_37539492-S	163.5	191.8	170.1	LOC375006	XM_351281.1		
GI_37539505-S	110.7	118.9	108.1	LOC164153	XM_089415.3		
GI_37539508-S	370.4	417.9	392.7	LOC376631	XM_353532.1		
GI_37539523-S	113.7	112.8	105.7	LOC375262	XM_353291.1		
GI_37539525-S	117	127.5	101.9	LOC375263	XM_353292.1		
GI_37539533-S	118.6	127.4	121.6	KCNT1	XM_029962.3		
GI_37539535-S	604.6	502.1	512	DKFZp434G2	XM_351857.1		
GI_37539539-S	3411.2	3139.9	4079.1	LOC375768	XM_353491.1		
GI_37539541-S	125.2	130.5	131.1	LOC138167	XM_070780.4		
GI_37539543-S	85.7	88.9	73	LOC375266	XM_353294.1		
GI_37539545-S	95.5	97.7	96	LOC377827	XM_352807.1		
GI_37539547-S	154.2	288.3	199	LOC376939	XM_352472.1		
GI_37539557-S	105.5	94.8	93.5	LOC284969	XM_210387.2		
GI_37539559-S	103	111.4	101.2	LOC376942	XM_352475.1		
GI_37539565-S	122.2	133.9	109.1	LOC286222	XM_209955.2		
GI_37539569-S	1093.7	1085.4	970	FNBP2	XM_059095.7		
GI_37539573-S	105.4	124.8	116.5	LOC91170	XM_036612.8		
GI_37539575-S	169.1	220	202.2	LOC375050	XM_351319.1		
GI_37539579-S	225	239.6	217	LOC375052	XM_351320.1		
GI_37539581-S	101.9	102.6	92.2	LOC284670	XM_209312.2		
GI_37539583-S	95.7	89.8	94	LOC200125	XM_117190.2		

GI_37539585-S	123.7	139	134.2	LOC375053	XM_353226.1				
GI_37539593-S	126.9	125.9	106.9	LOC343087	XM_291400.2				
GI_37539596-S	158.2	185.1	188.3	LOC343024	XM_291378.2				
GI_37539600-S	114.8	142.8	117	LOC376703	XM_352337.1				
GI_37539604-S	119.4	118	110.5	LOC376705	XM_352338.1				
GI_37539606-S	106.2	106.7	95.8	LOC376706	XM_352339.1				
GI_37539608-S	93.8	89.9	82.5	LOC376707	XM_352340.1				
GI_37539612-S	119.8	143.6	111.8	LOC376709	XM_352342.1				
GI_37539619-S	113.2	134.3	120.8	LOC253662	XM_173063.3				
GI_37539620-S	341.5	412.6	365.2	LOC376864	XM_352436.1				
GI_37539623-S	105.2	127.8	106.5	LOC375743	XM_351834.1				
GI_37539625-S	119.2	115	108.8	LOC138255	XM_059956.3				
GI_37539627-S	93.5	99.2	88.8	LOC138240	XM_059954.3				
GI_37539630-S	97.4	92.4	123	KIAA0367	XM_041018.3				
GI_37539634-S	112.8	134.5	129	LOC347127	XM_294521.2				
GI_37539638-S	230.1	237.3	273.1	FLJ13409	XM_351837.1				
GI_37539651-S	102.7	112.9	112.2	LOC377779	XM_352786.1				
GI_37539655-S	108.9	108.3	92	LOC138972	XM_071201.6				
GI_37539657-S	93.5	99.9	86.2	LOC138932	XM_071173.2				
GI_37539661-S	101.9	93.6	93.2	LOC377781	XM_352787.1				
GI_37539675-S	107.8	96.9	105.3	LOC377789	XM_352789.1				
GI_37539679-S	256.2	343.7	296.1	LOC377792	XM_352791.1				
GI_37539685-S	93.5	99.3	88.2	PDHA2	XM_352954.1	PDHAL	pyruvate	mitochond	glycolysis
GI_37539695-S	131.7	153.2	134.1	KIAA1680	XM_351589.1				
GI_37539697-S	81.8	86.8	88.8	LOC375403	XM_353350.1				
GI_37539709-S	169.9	209.4	189.8	LOC285412	XM_208319.2				
GI_37539711-S	21595.9	20870	19636	LOC375406	XM_351591.1				
GI_37539713-S	207.3	239.2	231	LOC375407	XM_353352.1				
GI_37539715-S	113.9	122.7	117.7	SYNPO2	XM_050219.7				
GI_37539723-S	477.7	554.4	565.1	KIAA1223	XM_048747.8				
GI_37539726-S	138.2	140.6	125.2	LOC375410	XM_351593.1				
GI_37539728-S	89.5	91.2	85.8	LOC375251	XM_087167.4				
GI_37539734-S	1950.7	2380.5	2442.1	RW1	XM_351477.1				
GI_37539736-S	105.7	124.6	108.9	LOC343990	XM_292873.2				
GI_37539746-S	94	102.8	89.8	LOC377175	XM_352555.1				
GI_37539748-S	91.8	85.2	100.6	LOC375252	XM_353288.1				
GI_37539752-S	308.8	314	323.5	LOC375253	XM_353289.1				
GI_37539756-S	180.4	188	148.9	LOC375254	XM_351478.1				
GI_37539764-S	101.1	93.8	101.2	LOC375256	XM_351479.1				
GI_37539770-S	126.9	157.3	124.7	LOC377182	XM_352557.1				
GI_37539776-S	89.9	93.3	80.6	LOC344558	XM_293090.2				
GI_37539782-S	96.4	102	99.3	LOC132556	XM_067904.6				
GI_37539788-S	130.2	160.8	138	LOC129521	XM_065278.2				
GI_37539790-S	196.1	234.2	212.9	LOC377189	XM_352558.1				

GI_37539796-S	111.7	91.8	94.6	LOC376926	XM_352464.1		
GI_37539804-S	101.1	95.3	98.7	LOC376930	XM_352466.1		
GI_37539814-S	200.1	190.2	186	KIAA1350	XM_052597.6		
GI_37539816-S	85.4	102.7	94.1	LOC344988	XM_293671.3		
GI_37539818-S	102.2	113.5	103.4	LOC377199	XM_352560.1		
GI_37539822-S	103.7	109.5	92.7	LOC345013	XM_293658.2		
GI_37539834-S	967.6	1098.9	1084.3	KIAA0310	XM_088459.7		
GI_37539836-S	127.7	139.6	147.2	LOC375769	XM_351859.1		
GI_37539842-S	112.8	111.5	114.1	LOC375771	XM_351860.1		
GI_37539847-S	258.3	307.5	272.4	LOC375772	XM_353493.1		
GI_37539856-S	199.9	215.7	209.1	LOC374943	XM_353194.1		
GI_37539860-S	221.8	259.7	240.8	LOC343133	XM_291419.2		
GI_37539862-S	405.6	539.2	477.9	DNB5	XM_089081.5		
GI_37539864-S	195.8	171.6	164.1	LOC199953	XM_114067.6		
GI_37539870-S	96.7	130.3	98.3	DKFZp434E1	XM_209234.3		
GI_37539873-S	157.4	202.1	175	LOC343066	XM_291392.2		
GI_37539880-S	99.3	112.5	89.9	LOC376564	XM_352291.1		
GI_37539890-S	113.9	126.3	116.2	DKFZp434P0	XM_175125.3		
GI_37539894-S	210.4	268.3	149.1	LOC375762	XM_351854.1		
GI_37539896-S	217	232.9	235.3	LOC375763	XM_353489.1		
GI_37539898-S	150.1	165.7	153.8	LOC375765	XM_353490.1		
GI_37539916-S	116	133.3	116.8	LOC375060	XM_353229.1		
GI_37539931-S	193.3	247.4	223.3	LOC377761	XM_352780.1		
GI_37539940-S	100.6	111.9	102	LOC377766	XM_352781.1		
GI_37539943-S	117.5	112	106.3	LOC375724	XM_351821.1		
GI_37539949-S	130.2	141	126.3	LOC377769	XM_352783.1		
GI_37539969-S	117.9	96.7	97.3	LOC375737	XM_351831.1		
GI_37539984-S	106.4	92.6	94.7	LOC377833	XM_352810.1		
GI_37539986-S	103.8	98.1	88.9	LOC377834	XM_352811.1		
GI_37539989-S	146	165.9	136.2	LOC375776	XM_351867.1		
GI_37539991-S	101.3	117.7	113.4	LOC377837	XM_352813.1		
GI_37539993-S	121.6	124.9	115.5	LOC377838	XM_352814.1		
GI_37539995-S	108.4	114.5	100.6	LOC377839	XM_352815.1		
GI_37540000-S	367.9	391.4	330.3	NOXA1	XM_351868.1	p51NOX;FLJ25475;NY-CO-31;SDCCAG31	tumor
GI_37540022-S	832.7	673.6	515.1	LOC375731	XM_351827.1		
GI_37540034-S	126.2	140.2	121	KIAA1214	XM_291090.2		
GI_37540036-S	111.1	121.2	124.8	LOC148864	XM_086344.4		
GI_37540037-S	79.8	92	79.3	LOC375413	XM_353356.1		
GI_37540039-S	107.7	122.4	110.7	LOC374983	XM_353204.1		
GI_37540041-S	89.9	79.8	90.3	LOC375414	XM_351594.1		
GI_37540045-S	120.9	115.3	113.4	LOC374985	XM_353205.1		
GI_37540047-S	151.4	200.3	166.8	LOC166752	XM_094074.5		
GI_37540051-S	129.1	133.2	128.7	LOC375745	XM_353482.1		
GI_37540053-S	129.6	141.9	149.9	LOC345051	XM_293680.2		

GI_37540055-S	196.9	228.9	223	LOC374987	XM_351264.1
GI_37540058-S	244.7	293.8	258	LOC375416	XM_353357.1
GI_37540060-S	1193.3	713.5	906.4	ELTD1	XM_351265.1
GI_37540066-S	228.5	254.1	241.1	LOC375417	XM_351595.1
GI_37540068-S	349.4	246.3	186.8	LOC148418	XM_086188.7
GI_37540070-S	123.5	232.9	137.6	KIAA1727	XM_034262.7
GI_37540072-S	190.3	143	136.3	MCOLN2	XM_351266.1
GI_37540076-S	2109	2644.7	2306.5	FLJ13815	XM_086186.3
GI_37540081-S	102.5	104.3	97.8	LOC375418	XM_351596.1
GI_37540084-S	97.4	112.4	95.3	LOC374989	XM_353207.1
GI_37540086-S	143.2	157.8	135.4	LOC375419	XM_353358.1
GI_37540092-S	111.9	115.1	103	LOC374990	XM_351267.1
GI_37540095-S	117.1	127.9	133.3	LOC343221	XM_291464.2
GI_37540111-S	92.2	91.6	91.9	LOC152667	XM_087500.7
GI_37540113-S	101.5	108.2	102.6	LOC375779	XM_353494.1
GI_37540117-S	134.4	162.2	141.2	LOC377211	XM_352563.1
GI_37540122-S	112.9	113.8	107.3	LOC377212	XM_352564.1
GI_37540128-S	99	104.4	101.5	LOC377218	XM_352566.1
GI_37540144-S	119.9	122.3	104.9	LOC375784	XM_351876.1
GI_37540243-S	148.4	166	157	LOC375691	XM_353471.1
GI_37540245-S	98.2	106.3	96.7	LOC375692	XM_353472.1
GI_37540247-S	233.2	356.1	264	LOC256280	XM_171224.2
GI_37540251-S	889.5	1581.4	1768.9	FLJ23309	XM_291315.2
GI_37540253-S	355.3	422.9	414.4	KIAA2026	XM_088551.7
GI_37540255-S	248.3	301.2	376.2	RANBP6	XM_039701.4
GI_37540257-S	572.2	782.4	767.5	LOC375693	XM_351798.1
GI_37540261-S	2331.4	2114.6	1573.1	LOC158345	XM_034640.4
GI_37540263-S	115.1	114.7	121.3	LOC375695	XM_351800.1
GI_37540271-S	92	91.1	101.2	LOC375698	XM_353473.1
GI_37540273-S	121.1	131.6	125.1	LOC375699	XM_353474.1
GI_37540275-S	267.6	334.1	282.1	LOC286319	XM_210009.2
GI_37540278-S	84.7	104.5	111.7	LOC375700	XM_351803.1
GI_37540284-S	104.9	109.2	101.5	KIAA1161	XM_351807.1
GI_37540288-S	314.9	398.8	344.6	KIAA1045	XM_048592.3
GI_37540290-S	331.8	414.8	376.7	LOC138729	XM_072554.5
GI_37540292-S	107.5	97.6	103.5	LOC375706	XM_351809.1
GI_37540294-S	81	89.9	78.7	LOC375707	XM_353475.1
GI_37540298-S	294	377.9	326.1	LOC375709	XM_351811.1
GI_37540300-S	114.4	124.6	113.2	LOC347252	XM_294567.2
GI_37540309-S	125.8	161.3	142.9	LOC377721	XM_352765.1
GI_37540311-S	92.3	116.4	100.7	LOC340479	XM_294574.2
GI_37540323-S	197.7	217.3	206.9	LOC340485	XM_294540.2
GI_37540341-S	94.8	98.1	84.6	LOC377730	XM_352770.1
GI_37540345-S	137	132.3	146.3	LOC138715	XM_071061.4

GI_37540349-S	146.7	177.9	153.8	LOC377739	XM_352773.1	
GI_37540351-S	168.3	193.5	172.6	LOC377742	XM_352774.1	
GI_37540355-S	93.9	83.8	86.9	LOC340501	XM_294568.2	
GI_37540365-S	206.6	181.5	175.7	LOC375399	XM_353349.1	
GI_37540369-S	130.1	124.6	132.3	LOC377166	XM_352552.1	
GI_37540377-S	125.9	136.5	128.2	LOC377169	XM_352553.1	
GI_37540379-S	112	132.2	101.3	LOC345378	XM_293802.2	
GI_37540384-S	499.5	358.5	361.7	ODZ3	XM_352956.1	
GI_37540386-S	155.6	139.7	138	FLJ31033	XM_037817.9	
GI_37540388-S	271.5	295	273.3	NEK1	XM_291107.2	KIAA1901;NY-REN-55
GI_37540390-S	105.7	119.9	102.2	LOC375420	XM_351597.1	
GI_37540392-S	149.6	151.7	153.2	LOC375421	XM_353359.1	
GI_37540394-S	115.9	122.1	125.3	LOC375422	XM_353360.1	
GI_37540396-S	1396	958.2	908.1	KIAA1430	XM_087593.7	
GI_37540398-S	103.7	93.5	88.7	LOC285440	XM_209612.2	
GI_37540400-S	109.5	122.4	111	LOC375423	XM_353361.1	
GI_37540402-S	101.5	107	96.6	LOC152663	XM_087499.6	
GI_37540408-S	85.6	82.1	83	LOC375426	XM_353363.1	
GI_37540418-S	128.2	144.8	132.6	LOC285433	XM_210581.2	
GI_37540422-S	145	193.5	157.2	LOC377226	XM_352568.1	
GI_37540424-S	102.8	111.5	94.8	LOC377227	XM_352569.1	
GI_37540426-S	100.1	91.1	100.3	LOC377230	XM_353536.1	
GI_37540428-S	112	106.5	98.6	LOC345156	XM_293715.3	
GI_37540431-S	498.4	641.9	683.9	KIAA0114	XM_353348.1	
GI_37540435-S	190.7	139.3	134.7	KIAA1211	XM_044178.8	
GI_37540437-S	131.9	137.8	118.9	LOC339977	XM_291099.2	
GI_37540447-S	1955.1	1123.8	1306.4	SQV7L	XM_351842.1	
GI_37540449-S	97.9	117.1	101.5	LOC158431	XM_098940.4	
GI_37540451-S	113	111.2	100.8	LOC347262	XM_294584.2	
GI_37540452-S	116.1	139.1	111.2	LOC375749	XM_351844.1	
GI_37540454-S	246.3	300.8	282	KIAA1529	XM_351845.1	
GI_37540458-S	3022.3	3929.9	2005	TXNDC4	XM_088476.6	
GI_37540462-S	149.7	130.7	141.3	LOC375752	XM_353485.1	
GI_37540464-S	101.3	95.9	80	LOC138752	XM_060001.5	
GI_37540466-S	207.3	177.5	139.9	KIAA0368	XM_036708.10	
GI_37540468-S	152.3	133.6	125.6	LOC375753	XM_353486.1	
GI_37540472-S	106.7	141.6	138.5	LOC169834	XM_095965.3	
GI_37540474-S	205.9	227	210.3	KIAA1952	XM_054983.6	
GI_37540478-S	115.8	138.2	126.1	LOC375754	XM_351848.1	
GI_37540487-S	268.8	304.7	293.4	DKFZP434C2	XM_044196.5	
GI_37540489-S	146.7	167.1	164.5	FLJ00001	XM_088525.3	
GI_37540494-S	856.8	835.4	659.2	LOC375757	XM_351851.1	
GI_37540496-S	4644.3	4316.6	3946.9	LRRC8	XM_026998.6	FLJ10337;KIAA1437
GI_37540497-S	172.7	185.9	150.3	LOC375758	XM_353487.1	

GI_37540499-S	259.6	317.3	314.3	LOC375759	XM_351852.1	FLJ35803
GI_37540509-S	133.4	156.4	143.6	LOC340508	XM_295263.2	
GI_37540515-S	105	98.4	105.1	LOC138804	XM_071098.2	
GI_37540517-S	98.3	102.7	99.1	LOC138803	XM_071097.2	
GI_37540519-S	179.3	211.7	202.8	LOC138802	XM_071096.3	
GI_37540521-S	195.2	250.9	215.7	LOC138799	XM_071093.5	
GI_37540525-S	86.3	84.9	93.7	LOC286362	XM_210752.2	
GI_37540527-S	102	111.1	104.6	LOC286365	XM_210755.3	
GI_37540533-S	98.9	102.9	91.3	LOC377808	XM_352796.1	
GI_37540537-S	100.1	113.7	106.2	OR2K2	XM_095961.5	OR2AR1P;HTPCRH06;HSHTPCRH06
GI_37540539-S	91.9	84.3	90	LOC377811	XM_352797.1	
GI_37540541-S	189.8	212.1	196.3	KIAA1958	XM_088566.6	
GI_37540543-S	98.8	105.8	105.3	LOC377812	XM_352798.1	
GI_37540547-S	90.6	106.7	87.1	EGFL5	XM_098838.3	
GI_37540549-S	226	251.7	232.5	LOC347168	XM_294531.3	
GI_37540551-S	235.9	294.7	269.3	OR1J5	XM_294533.2	
GI_37540553-S	474	570	509.1	LOC138882	XM_071151.2	
GI_37540563-S	162.6	178.2	170.2	LOC377819	XM_352801.1	
GI_37540565-S	99.1	111.8	94.8	LOC377820	XM_352802.1	
GI_37540567-S	114.7	135	125.5	LOC377821	XM_352803.1	
GI_37540569-S	139.5	168.9	144.6	LOC286207	XM_209941.3	
GI_37540573-S	276.1	274.5	255.1	LOC377824	XM_352805.1	
GI_37540583-S	215.6	266.8	244.6	LOC132969	XM_068121.2	
GI_37540585-S	114.2	113.4	106.8	HSPX153	XM_352543.1	
GI_37540588-S	7199.4	7221.2	5918.4	LOC375391	XM_353345.1	
GI_37540591-S	279.3	332.7	299	LOC339985	XM_295120.2	
GI_37540593-S	168	172	165.7	LOC345375	XM_293801.3	
GI_37540595-S	83.2	95.1	83.9	KIAA1643	XM_035371.5	
GI_37540597-S	111.7	119.9	112.9	LOC377133	XM_352544.1	
GI_37540600-S	88.3	89.1	87.6	LOC377163	XM_352551.1	
GI_37540604-S	117.6	152.5	134.3	LOC375747	XM_353483.1	
GI_37540606-S	94.4	95.9	96.2	DKFZp434I11	XM_030729.4	
GI_37540610-S	142.3	169	150.5	LOC138652	XM_071013.4	
GI_37540612-S	1252.7	1231.6	1022.8	LOC138649	XM_059987.6	
GI_37540617-S	99.4	107.2	100.3	LOC375392	XM_353346.1	
GI_37540621-S	2856.7	2118	1560.8	C4orf9	XM_035572.8	
GI_37540623-S	123.8	143.4	131.3	LOC345222	XM_293745.2	
GI_37540625-S	182.6	205.3	200.1	LOC377134	XM_352545.1	
GI_37540628-S	84.8	98.8	92.5	LOC255324	XM_171078.4	
GI_37540630-S	170.4	471.8	352.6	KIAA1102	XM_044461.9	
GI_37540632-S	296.1	336.2	311.3	LOC375397	XM_351581.1	
GI_37540634-S	197.3	228.6	172.5	KIAA1458	XM_044434.9	
GI_37540638-S	126.4	155.8	133.1	LOC256165	XM_171080.2	
GI_37540640-S	267.4	307.9	273.9	LOC285429	XM_209607.4	

GI_37540654-S	143.8	203.9	164	KIAA1729	XM_114418.3			
GI_37540659-S	475.9	439.1	445.7	KIAA1345	XM_106386.6			
GI_37540661-S	613.8	642.4	420.5	LOC285550	XM_209656.2			
GI_37540662-S	95.8	90.3	99.3	KIAA1276	XM_039169.2			
GI_37540664-S	116.1	120.2	105.2	LOC375395	XM_351579.1			
GI_37540666-S	463.3	571.2	511.6	GPR125	XM_291111.2			
GI_37540670-S	123.2	124	123.8	LOC377140	XM_352547.1			
GI_37540672-S	84.6	88.7	90	LOC377141	XM_352548.1			
GI_37540680-S	294.2	362.5	314.8	CSN1S2A	XM_352957.1			
GI_37540682-S	109.2	126.6	139.3	LOC375428	XM_351599.1			
GI_37540696-S	397.4	356.2	281.3	RBIG1	XM_352895.1			
GI_37540698-S	111.1	125.3	131.2	LOC374424	XM_350858.1			
GI_37540708-S	162.9	180.8	175.2	RAB39	XM_084662.3			
GI_37540711-S	110.1	114.2	109.9	KIAA1391	XM_040866.4			
GI_37540715-S	123.8	123	108.3	LOC120376	XM_071712.9			
GI_37540717-S	106.2	117.4	97.3	LOC374427	XM_350862.1			
GI_37540721-S	301.2	422.4	384.8	LOC374429	XM_353016.1			
GI_37540723-S	1144.1	1000.2	1004.9	DKFZp547C1	XM_208529.4			
GI_37540730-S	146	179.4	114.6	LOC374430	XM_353017.1			
GI_37540732-S	1401	454.4	285.2	LOC283157	XM_210908.2			
GI_37540735-S	384.3	431.3	380.7	LOC219854	XM_166164.4			
GI_37540736-S	114.3	138.9	135.1	LOC338667	XM_294675.3			
GI_37540740-S	88.9	89.8	72.4	LOC374435	XM_353018.1			
GI_37540742-S	407.6	378.1	531	KIAA0056	XM_166201.3	DNA	nucleus	electron
GI_37540747-S	195	222.8	211.6	KIAA1735	XM_290496.3			
GI_37540765-S	464.2	589.2	606.7	LOC283698	XM_208108.3			
GI_37540767-S	102.7	104.3	96.2	LOC376069	XM_352055.1			
GI_37540771-S	100	103.2	103.8	LOC376072	XM_352056.1			
GI_37540777-S	90.9	101.7	96.9	LOC342167	XM_292394.3			
GI_37540783-S	354.4	459.1	370.2	LOC376074	XM_352058.1			
GI_37540787-S	129.1	157.4	127.9	LOC338662	XM_291838.3			
GI_37540789-S	159	190.3	195.7	LOC219875	XM_166782.4			
GI_37540799-S	90.1	88.7	90.5	LOC219869	XM_166776.2			
GI_37540803-S	112.3	117.5	93.6	LOC376075	XM_352059.1			
GI_37540807-S	255.6	280	238.1	LOC374613	XM_350976.1			
GI_37540809-S	109.4	133.3	123	LOC376077	XM_352062.1			
GI_37540811-S	150.6	185.2	173.1	LOC219865	XM_166767.5			
GI_37540816-S	123.7	108.5	96.2	FLJ20582	XM_090970.6			
GI_37540818-S	196.7	225.7	220.5	LOC376079	XM_352064.1			
GI_37540822-S	107	120.9	118.8	LOC374614	XM_350977.1			
GI_37540824-S	211.6	284.3	227.7	LOC341098	XM_291857.3			
GI_37540826-S	206.9	249.7	237.1	LOC146071	XM_085316.7			
GI_37540827-S	122.6	128.5	107.3	LOC376080	XM_352065.1			
GI_37540832-S	268	221.4	218.5	MGA	XM_031689.7			

GI_37540836-S	104	101	99.7	LOC374616	XM_353083.1				
GI_37540838-S	193.4	230.1	202.5	LOC255189	XM_172929.3				
GI_37540841-S	166.7	163.4	157.8	STARD9	XM_031744.4				
GI_37540846-S	133.2	143.9	128	LOC161823	XM_091156.8				
GI_37540852-S	120.8	130	118.5	LOC90525	XM_032304.4				
GI_37540856-S	81.7	97.5	89.3	KIAA0912	XM_034904.5				
GI_37540860-S	120.9	135.3	121.3	FLJ25756	XM_350984.1				
GI_37540864-S	110.2	124.7	133	LOC145783	XM_085231.7				
GI_37540868-S	235.1	280.4	245.6	LOC145780	XM_096864.2				
GI_37540871-S	322	330.4	315.5	KIAA0295	XM_042833.8				
GI_37540877-S	638.3	795.1	673.8	GLCE	XM_290631.2				
GI_37540879-S	482	629.5	555	LOC374621	XM_353085.1				
GI_37540881-S	99.3	97.2	95.4	LOC123397	XM_063630.5				
GI_37540885-S	109.1	116.1	100.6	LOC196993	XM_116971.5				
GI_37540886-S	104.7	120.9	106.9	LOC196994	XM_116970.2				
GI_37540890-S	222.2	264.4	238.5	LOC196996	XM_113796.3				
GI_37540892-S	184	209.2	191.9	LOC283677	XM_208778.2				
GI_37540898-S	141.5	140.1	119.5	LOC374624	XM_292358.3				
GI_37540911-S	253.5	313.4	284.3	LOC146013	XM_096919.2				
GI_37540913-S	163.2	271.8	185.6	IREB2	XM_039114.4	IRP2;IRP2AD	RNA	cytosol	RNA
GI_37540914-S	161.5	166.1	157	LOC123688	XM_058719.7				
GI_37540915-S	86.3	89.5	87	LOC374628	XM_353086.1				
GI_37540921-S	96.1	118.8	97.1	LOC374631	XM_353087.1				
GI_37540926-S	138.1	248.7	193.8	DKFZp434J0	XM_290645.2				
GI_37540927-S	123.1	153.4	132.5	LOC283726	XM_208809.2				
GI_37540949-S	95.8	97	89.7	LOC374652	XM_353093.1				
GI_37540951-S	113	117.3	109.3	LOC374653	XM_353094.1				
GI_37540955-S	121	123.6	121	LOC254559	XM_172931.4				
GI_37540961-S	121.7	143.3	142.2	MESP2	XM_085261.2				
GI_37540967-S	194.5	216.3	198.9	LOC374657	XM_351011.1				
GI_37540969-S	140.4	151.4	123.9	LOC374658	XM_351012.1				
GI_37540971-S	142.5	152.3	131.9	LOC342132	XM_292384.2				
GI_37540975-S	128.8	146.8	135.4	LOC374660	XM_353095.1				
GI_37540979-S	470	588.5	520.9	LOC374662	XM_353096.1				
GI_37540983-S	92.3	88.6	91.1	LOC342156	XM_292389.3				
GI_37540986-S	158.6	214.7	172.4	DKFZp434P1	XM_115306.5				
GI_37540996-S	100.9	99.7	99.1	LOC219537	XM_166203.4				
GI_37540998-S	104	117.2	106.5	LOC374391	XM_353008.1				
GI_37541000-S	95.2	95.9	92.2	LOC374392	XM_350830.1				
GI_37541002-S	179	206.9	189.8	LOC374393	XM_350831.1				
GI_37541004-S	171.7	214.4	181.5	LOC255649	XM_172860.2				
GI_37541006-S	654.1	945.5	619.1	LOC255714	XM_172861.3				
GI_37541012-S	548.5	618.3	627.5	KIAA1698	XM_290519.2				
GI_37541013-S	1965.9	1960.6	1629.6	LOC374395	XM_350833.1				

GI_37541015-S	97.3	92.3	91.7	LOC374396	XM_350834.1
GI_37541019-S	978.9	996.2	1053.7	LOC144097	XM_290508.2
GI_37541020-S	105.1	136.1	123	HSMDPKIN	XM_290516.3
GI_37541022-S	350.7	407.3	487.5	KIAA0404	XM_290517.2
GI_37541024-S	286.8	355.9	307.5	LOC256676	XM_172852.2
GI_37541026-S	116.7	112.1	99.2	LOC374398	XM_350835.1
GI_37541030-S	189.8	216.7	185.9	LOC374400	XM_350837.1
GI_37541032-S	128.8	142.7	119	LOC374401	XM_350838.1
GI_37541034-S	3534.4	3336.6	3353.4	SF3B2	XM_290506.2
GI_37541036-S	321.6	401.8	355.3	LOC374402	XM_353011.1
GI_37541038-S	255.1	323.1	337.8	LOC254359	XM_170667.3
GI_37541039-S	511.9	596.7	611.3	LOC338692	XM_290509.3
GI_37541042-S	99.7	111.9	102.3	LOC132740	XM_059598.6
GI_37541044-S	98.4	112.7	101.4	LOC374404	XM_350840.1
GI_37541046-S	106.7	113.8	109.6	LOC158490	XM_088585.8
GI_37541062-S	104.2	122.6	105.4	LOC219428	XM_166868.3
GI_37541064-S	110.8	111	114.4	LOC219429	XM_166869.3
GI_37541066-S	93.5	103.1	101.9	LOC219431	XM_166871.2
GI_37541068-S	145.1	173.5	161.9	LOC219432	XM_166872.5
GI_37541070-S	149.8	180.8	163.6	LOC376006	XM_352029.1
GI_37541072-S	192.1	219.5	209.3	LOC219436	XM_166877.6
GI_37541076-S	117.1	111.2	117.9	LOC219449	XM_166809.3
GI_37541079-S	97.4	100.3	96.2	LOC219453	XM_166813.2
GI_37541081-S	96.2	91.4	100.9	LOC219462	XM_166818.2
GI_37541085-S	156.5	168.8	157.2	LOC219464	XM_166820.2
GI_37541087-S	65.6	75.3	63.8	LOC219469	XM_166823.2
GI_37541091-S	128.5	138.2	134.5	LOC219417	XM_166805.4
GI_37541095-S	175.7	184.3	189.8	LOC219484	XM_166835.4
GI_37541097-S	99.3	101.8	99.7	LOC376012	XM_352033.1
GI_37541101-S	84.9	88.9	82	LOC376013	XM_352034.1
GI_37541103-S	131.8	144.3	130.3	LOC338675	XM_291862.2
GI_37541105-S	145.6	151.7	142.2	LOC376015	XM_352035.1
GI_37541107-S	82.6	100.4	95.7	LOC376016	XM_352036.1
GI_37541109-S	100.5	123	123.4	LOC283189	XM_210193.2
GI_37541113-S	121.4	140.5	127.3	LOC283193	XM_210196.3
GI_37541115-S	236	250.4	256	LOC219952	XM_166910.3
GI_37541119-S	107.5	118.2	101.5	LOC219956	XM_166914.3
GI_37541121-S	108	101.9	90.5	LOC219957	XM_166915.3
GI_37541125-S	76.8	74.5	73.6	LOC219965	XM_166923.4
GI_37541131-S	108.1	124.5	104.4	KIAA0937	XM_166213.2
GI_37541135-S	199.4	238.6	222.3	LOC341112	XM_291885.2
GI_37541137-S	199.5	275.9	249.6	LOC376022	XM_352039.1
GI_37541141-S	140.5	159.9	152.8	LOC219982	XM_166899.3
GI_37541149-S	93	93.9	90.1	LOC376024	XM_352040.1

GI_37541153-S	106.5	136.2	131	LOC219986	XM_166903.3				
GI_37541155-S	267.8	277.3	240	LOC376025	XM_352041.1				
GI_37541157-S	104.1	110.6	113.2	LOC339022	XM_294775.2				
GI_37541163-S	135.9	123.3	121.7	LOC341116	XM_291890.3				
GI_37541166-S	69	81.4	74.3	LOC376030	XM_352043.1				
GI_37541173-S	92.6	82.3	79.8	LOC221091	XM_169026.3	MGC61707			
GI_37541176-S	171.5	198.5	174.9	KIAA1394	XM_208522.2				
GI_37541178-S	126.4	128.4	127.8	LOC376035	XM_352045.1				
GI_37541181-S	110.1	122	113.2	LOC376036	XM_352046.1				
GI_37541187-S	3074.5	2986.8	2270.6	LOC374596	XM_350967.1				
GI_37541189-S	132.5	143.5	134.8	LOC374597	XM_350968.1				
GI_37541230-S	95.9	116.9	88.8	LOC374606	XM_353082.1				
GI_37541238-S	99.3	96.1	94.9	LOC374669	XM_351020.1				
GI_37541248-S	169.9	164.2	124.3	LOC374673	XM_353097.1				
GI_37541267-S	321.8	397.1	349.4	DKFZP586P	XM_170681.4				
GI_37541275-S	205.3	241.8	205.9	LOC374410	XM_350844.1				
GI_37541277-S	88.3	105.5	107.7	LOC374411	XM_350845.1				
GI_37541289-S	126.7	131.5	123.3	ODZ4	XM_166254.3				
GI_37541291-S	100.6	121.3	123.4	LOC374416	XM_350850.1				
GI_37541293-S	183.3	207.9	180.7	LOC283226	XM_208554.2				
GI_37541295-S	102.2	127.2	105.8	LOC374417	XM_353014.1				
GI_37541307-S	127.8	144	130.5	LOC376042	XM_352049.1				
GI_37541311-S	159.4	173.3	177.5	LOC341152	XM_291892.2				
GI_37541313-S	87.1	100.7	79.6	MAP6	XM_166256.5				
GI_37541315-S	185.8	219.8	203.7	LOC283219	XM_208568.2				
GI_37541322-S	98.4	107.6	101.6	LOC340968	XM_291786.2				
GI_37541328-S	89	90.6	98.2	LOC374369	XM_352999.1				
GI_37541330-S	119.7	118.7	120.7	LOC374370	XM_353000.1				
GI_37541334-S	102.3	116.6	104.7	LOC374372	XM_350818.1				
GI_37541336-S	89.2	97.3	99.2	LOC374373	XM_350819.1				
GI_37541340-S	147.3	1133.3	146.1	MUC6	XM_290540.2		molecular	cellular_co	response
GI_37541342-S	107.8	135.6	118.6	LOC338731	XM_294688.3				
GI_37541343-S	256.4	313.6	276.8	DKFZp761L1	XM_352003.1				
GI_37541350-S	358.1	440.2	382.7	LOC119749	XM_061656.8				
GI_37541353-S	121.5	121.6	112	LOC374284	XM_352911.1				
GI_37541357-S	98.2	115.3	115.7	LOC374688	XM_351038.1				
GI_37541359-S	107	116.3	101.4	LOC374689	XM_353102.1				
GI_37541361-S	105.3	106.3	103.8	LOC374690	XM_353103.1				
GI_37541363-S	866	793.1	638.2	DKFZP564M	XM_085525.4				
GI_37541367-S	85.5	80.5	92.3	LOC92017	XM_042234.4				
GI_37541369-S	194.4	183.7	151.1	LOC374692	XM_353104.1				
GI_37541381-S	159.8	186.8	192.9	LOC374699	XM_353105.1				
GI_37541385-S	94.8	114.3	96.4	LOC374700	XM_351045.1				
GI_37541387-S	220.7	249.3	206.5	LOC374701	XM_353106.1				

GI_37541389-S	124.9	139.1	133.9	LOC92267	XM_043979.4		
GI_37541395-S	155	161.3	170	LOC374703	XM_351046.1		
GI_37541408-S	84.1	90.6	108.9	HS3ST4	XM_056254.5		
GI_37541410-S	357.7	347.7	325.2	KIAA0556	XM_044632.4		
GI_37541412-S	3299.5	3148.5	2763.3	XPO6	XM_055195.5		
GI_37541417-S	189.3	245.5	188.7	LOC283816	XM_208859.2		
GI_37541419-S	171	199.2	169.5	KIAA0251	XM_352158.1	lyase	amino
GI_37541423-S	108	124.3	118	LOC146110	XM_018432.3		
GI_37541425-S	148.6	162.2	148.6	LOC124274	XM_064062.5		
GI_37541427-S	103.8	119.7	99	LOC342293	XM_292468.3		
GI_37541429-S	126.7	134.6	120	LOC342357	XM_292504.2		
GI_37541433-S	91	91.8	99.1	LOC376316	XM_352161.1		
GI_37541444-S	116.4	134.1	117.5	LOC120146	XM_061890.8		
GI_37541450-S	112.4	112.2	103.5	FAT3	XM_061871.6		
GI_37541452-S	132.9	141.1	122.3	KIAA1731	XM_350854.1		
GI_37541454-S	202	231.8	223.5	LOC374421	XM_350855.1		
GI_37541456-S	117.8	130.9	115.1	LOC374422	XM_350856.1		
GI_37541458-S	79.4	78.5	71.1	LOC374423	XM_350857.1		
GI_37541460-S	90.9	97.1	87.6	LOC341208	XM_291947.3		
GI_37541464-S	82	91.2	87.5	LOC120126	XM_061880.2		
GI_37541466-S	111.1	94.3	93.4	LOC376047	XM_352050.1		
GI_37541470-S	152.7	184.1	174.7	LOC376052	XM_352052.1		
GI_37541474-S	91.6	105.9	84.2	LOC120105	XM_061864.3		
GI_37541478-S	101.8	114.2	105.3	LOC341202	XM_291943.3		
GI_37541480-S	90.2	107	106	LOC376058	XM_352054.1		
GI_37541482-S	223.3	274.1	248.8	LOC120082	XM_061849.7		
GI_37541488-S	123	158.1	138.1	LOC374734	XM_353115.1		
GI_37541492-S	94.6	92.4	83.3	KIAA1005	XM_051197.6		
GI_37541493-S	911.7	1143.9	1215.4	FTO	XM_051200.5		
GI_37541506-S	938.2	941.7	866.3	DKFZP434K0	XM_166276.4		
GI_37541508-S	160.9	199.1	180	LOC374738	XM_351072.1		
GI_37541510-S	78.1	88.4	85	LOC374739	XM_351073.1		
GI_37541512-S	111.7	105.9	110.2	LOC374740	XM_353120.1		
GI_37541514-S	106.4	117.4	124	LOC146212	XM_085367.4		
GI_37541516-S	221.8	295.3	297.3	KIAA1464	XM_043069.5		
GI_37541518-S	104.3	110.4	118.7	ZFP90	XM_085375.7		
GI_37541526-S	230.2	278.7	243.4	LOC92154	XM_208937.4		
GI_37541528-S	130.7	135.8	131	LOC374743	XM_351076.1		
GI_37541530-S	112.1	107.1	90.3	FLJ14665	XM_351077.1		
GI_37541532-S	325.3	352.6	359.5	KIAA0931	XM_041191.5		
GI_37541534-S	119.6	122.1	110.7	LOC376351	XM_352179.1		
GI_37541536-S	184.1	230.2	189.7	LOC376353	XM_352180.1		
GI_37541538-S	243.2	235.9	225	LOC146206	XM_085383.5		
GI_37541540-S	97.7	101.8	92.1	LOC376355	XM_352181.1		

GI_37541551-S	14234.2	12628	10889	LOC376348	XM_352178.1
GI_37541554-S	100.9	104.4	101.9	SNAI3	XM_351083.1
GI_37541558-S	177.2	212.1	202.7	LOC374754	XM_351085.1
GI_37541560-S	103.8	108.1	97.8	LOC374755	XM_353126.1
GI_37541568-S	144	150	137.1	KIAA1858	XM_040592.4
GI_37541570-S	327.7	298.3	286.4	LOC348180	XM_352185.1
GI_37541572-S	133	139.6	124.3	LOC376362	XM_352186.1
GI_37541581-S	103.3	112.6	96.7	MUC5B	XM_039877.8
GI_37541583-S	98.4	113.7	99	LOC374374	XM_353002.1
GI_37541588-S	253.6	321.9	291.3	CNGA4	XM_290552.2
GI_37541590-S	94.8	90.9	92.2	LOC196337	XM_113696.2
GI_37541606-S	99.7	87	102.2	LOC374380	XM_353004.1
GI_37541611-S	98.1	115.5	112.9	LOC374381	XM_350825.1
GI_37541613-S	81.4	88.8	95.7	LOC374382	XM_353005.1
GI_37541615-S	85.7	95.6	89.5	LOC374383	XM_350826.1
GI_37541617-S	163.2	198.3	163.8	FLJ39441	XM_084736.7
GI_37541618-S	110.9	97.6	113.6	LOC203859	XM_115009.4
GI_37541622-S	117.5	128.5	127.7	LOC196296	XM_113688.3
GI_37541624-S	137.1	143.3	123.4	G2	XM_039515.10
GI_37541626-S	84.2	93.7	82.4	LOC374385	XM_353006.1
GI_37541628-S	124.8	118.3	119.5	LOC374386	XM_353007.1
GI_37541632-S	178.9	204.2	197	LRP4	XM_035037.3
GI_37541634-S	964.9	1137.4	940.5	NUP160	XM_113678.4
GI_37541640-S	99.2	103.5	95.6	LOC283257	XM_208060.2
GI_37541642-S	232	300.5	260.5	MRGE	XM_171536.4
GI_37541647-S	106.3	104.5	104.4	LOC340977	XM_291793.3
GI_37541657-S	120.4	133.5	119.3	LOC143496	XM_089858.6
GI_37541659-S	97.3	110.4	105.5	LOC119775	XM_061677.2
GI_37541661-S	205.9	245	209.3	LOC375962	XM_352007.1
GI_37541665-S	222.3	264.7	244.5	LOC143502	XM_089863.4
GI_37541667-S	190.7	245.5	214.3	LOC375963	XM_352008.1
GI_37541669-S	106.4	88.6	100.8	LOC119696	XM_061628.3
GI_37541671-S	139	161.1	153.7	LOC119691	XM_061623.2
GI_37541673-S	128.7	153.5	142.8	LOC119689	XM_061621.2
GI_37541675-S	155.1	178.2	157	LOC119687	XM_061619.2
GI_37541679-S	159.6	165.5	171.2	LOC119684	XM_061616.2
GI_37541681-S	99.9	111.7	102.4	LOC283110	XM_210180.2
GI_37541683-S	384.8	432.3	411.2	LOC283111	XM_210181.4
GI_37541689-S	156.9	167	155.3	LOC340980	XM_291806.2
GI_37541691-S	106.1	105.4	97.3	LOC375969	XM_352009.1
GI_37541693-S	140.5	148	125.8	LOC375970	XM_352010.1
GI_37541695-S	92.9	103	96.3	LOC375971	XM_352011.1
GI_37541697-S	143.3	162.2	139.3	LOC375972	XM_352012.1
GI_37541699-S	134.8	154.3	143.5	LOC375973	XM_352013.1

GI_37541701-S	371.6	450.2	398.4	LOC375974	XM_352014.1	
GI_37541703-S	110.4	115.8	106.6	LOC375975	XM_352015.1	
GI_37541705-S	143.4	165.4	166.1	LOC375976	XM_352016.1	
GI_37541707-S	136.2	137.9	136.4	LOC375977	XM_352017.1	
GI_37541709-S	100.3	104.5	97.8	LOC338751	XM_291977.2	
GI_37541711-S	94.6	100.9	103.6	LOC120793	XM_062269.8	
GI_37541713-S	101	94.6	82.7	LOC120796	XM_062272.9	
GI_37541715-S	475.1	567.5	471.6	LOC338755	XM_291980.3	
GI_37541721-S	151.8	193.6	163.2	OR10A3	XM_291986.3	
GI_37541723-S	85.7	94.7	90.2	LOC283102	XM_210177.3	
GI_37541725-S	107.6	94.5	85	LOC119593	XM_061562.6	
GI_37541727-S	100.5	94.1	88.1	LOC338750	XM_291974.2	
GI_37541733-S	106.8	107.8	99.3	LOC340990	XM_291816.2	
GI_37541737-S	108.8	116.3	99.3	LOC120237	XM_061930.6	
GI_37541754-S	91.1	104.6	88.9	LOC219638	XM_169258.4	
GI_37541758-S	88.8	77	95.1	LOC119764	XM_061666.2	
GI_37541760-S	197.3	241.9	232	LOC256148	XM_171490.2	
GI_37541762-S	265.2	343.1	305.4	LOC256144	XM_171489.4	
GI_37541768-S	125.2	148.4	129.8	LOC375995	XM_352022.1	
GI_37541770-S	130.7	119.8	119.2	LOC375996	XM_352023.1	
GI_37541772-S	78.8	88.5	84.6	LOC120824	XM_062300.3	
GI_37541776-S	147.7	168.3	134.1	LOC283117	XM_210184.3	
GI_37541778-S	119.6	128.6	124.9	LOC196346	XM_115100.2	
GI_37541782-S	106.3	101.1	93.2	LOC375998	XM_352024.1	
GI_37541784-S	95.8	104.5	116.8	LOC375999	XM_352025.1	
GI_37541786-S	304.1	388.9	364.5	LOC283092	XM_210168.3	
GI_37541788-S	107.7	123.8	124.7	LOC283093	XM_210169.2	
GI_37541790-S	225.6	257.9	228.8	LOC376000	XM_352026.1	
GI_37541792-S	108.5	112.5	117.1	LOC146439	XM_085463.3	
GI_37541794-S	125.7	144.3	129.3	LOC197350	XM_113871.4	
GI_37541798-S	67.4	87.6	67.5	LOC374686	XM_353101.1	
GI_37541800-S	114.2	118.8	109.1	SRL	XM_064152.5	
GI_37541802-S	170	201.6	179.1	LOC342346	XM_296817.3	
GI_37541804-S	92.1	108.9	93.3	MGRN1	XM_048119.8	GP2B;CD41B;ITGA2B;RNF156;KIAA0544
GI_37541806-S	176.5	162.8	147.3	LOC196483	XM_016909.7	
GI_37541810-S	116.7	116.3	116.7	KIAA0557	XM_085507.3	
GI_37541812-S	95.8	99.9	96.6	KIAA0420	XM_032693.2	
GI_37541815-S	206.7	263.3	301.7	LOC374751	XM_353124.1	
GI_37541817-S	94.7	77.4	84.1	LOC374752	XM_353125.1	
GI_37541821-S	92.6	90.5	92.2	LOC376361	XM_352184.1	
GI_37541823-S	262.3	261.5	267.8	LOC374731	XM_353113.1	
GI_37541833-S	327.3	333.8	263.1	LOC374744	XM_351078.1	
GI_37541841-S	1227.7	1239.4	1105	FLJ12270	XM_290704.2	
GI_37541843-S	326	399.8	363.8	LOC374746	XM_351081.1	

GI_37541845-S	249.3	220	326.5	LOC374747	XM_351082.1	
GI_37541847-S	139.7	161.8	155.7	LOC374748	XM_353121.1	
GI_37541851-S	147.4	178.8	171.4	LOC146167	XM_085347.2	
GI_37541855-S	103.3	101.1	110.5	LOC123855	XM_063871.4	
GI_37541857-S	229.2	268.8	234.6	LOC374750	XM_353123.1	
GI_37541859-S	107	105.6	112	LOC342409	XM_292527.2	
GI_37541867-S	110.6	112.8	103.4	LOC376357	XM_352182.1	
GI_37541874-S	215.3	242.7	202.1	FLJ11183	XM_352898.1	
GI_37541876-S	77.4	82.5	84.5	LOC338757	XM_291991.2	
GI_37541878-S	116.1	136.8	134.5	LOC374462	XM_350882.1	
GI_37541880-S	102.7	107.6	100	LOC144448	XM_084868.6	
GI_37541888-S	103.5	111.1	111	LOC374464	XM_353031.1	
GI_37541896-S	112.6	96.8	106.1	LOC374466	XM_353032.1	
GI_37541900-S	89.2	94.6	98.8	LOC374468	XM_353033.1	
GI_37541910-S	109.2	133.7	104.2	FLJ38508	XM_090294.4	
GI_37541916-S	1004.7	856.7	925.6	KIAA1033	XM_035313.6	
GI_37541920-S	163.1	206.9	176.8	KIAA0789	XM_033113.3	
GI_37541922-S	117.9	123.1	120.9	LOC283892	XM_211246.2	
GI_37541926-S	128.1	132.4	128.5	LOC338756	XM_291989.2	
GI_37541937-S	3735.6	3643	2871.4	LOC376141	XM_352085.1	
GI_37541941-S	2360.4	2859.6	2201.3	LOC376142	XM_352086.1	
GI_37541953-S	176.8	203.4	237.7	LOC339088	XM_290702.2	
GI_37541954-S	134.2	139.5	112.2	LOC376145	XM_352087.1	
GI_37541958-S	107.5	109.1	109.1	LOC121456	XM_062645.3	
GI_37541960-S	235.6	322.3	274.9	LOC374716	XM_353107.1	
GI_37541966-S	215.9	278.3	250.9	LOC374718	XM_353109.1	
GI_37541968-S	103.2	117.7	107.4	LOC283350	XM_208635.2	
GI_37541974-S	126.9	116.7	112.3	LOC376148	XM_352089.1	
GI_37541982-S	124.9	128.3	128	LOC374720	XM_351063.1	
GI_37541986-S	449.5	548.4	506	LOC374721	XM_351064.1	
GI_37541988-S	125	128.2	109.6	ASCL4	XM_062690.3	HASH4
GI_37541994-S	135	163.7	147.7	LOC146489	XM_047734.8	
GI_37541996-S	104.3	115.5	99.3	LOC374722	XM_353111.1	
GI_37541998-S	85.6	87.2	85.8	LOC283957	XM_208142.2	
GI_37542000-S	177.3	271.2	211.1	LOC374723	XM_351066.1	
GI_37542004-S	190.2	247.1	214.3	LOC374725	XM_351068.1	
GI_37542014-S	103.6	105.5	116.7	KIAA0326	XM_034819.4	
GI_37542018-S	126.2	112.7	118.8	LOC376322	XM_352165.1	
GI_37542022-S	98.2	106.6	101.3	LOC124411	XM_058804.5	
GI_37542024-S	85.7	93.4	85	LOC376324	XM_352166.1	
GI_37542034-S	156.1	174.9	163.8	LOC339133	XM_292573.3	
GI_37542036-S	82.6	94.2	86.5	LOC124149	XM_064003.6	
GI_37542038-S	93.4	110.3	97.3	LOC374733	XM_351071.1	
GI_37542040-S	165.8	154.7	145	LOC376343	XM_352175.1	

GI_37542174-S	1003.9	1332.8	709.7	RAB26	XM_352913.1	V46133	GTP	cellular_co	protein
GI_37542183-S	194.7	155.4	223	LOC339123	XM_290722.2				
GI_37542187-S	108.7	122.6	114.7	LOC374683	XM_351034.1				
GI_37542189-S	221.3	252.6	233.9	CRAMP1L	XM_034570.5				
GI_37542191-S	275.6	336.4	324.4	LOC283871	XM_208887.2				
GI_37542192-S	123.6	116.3	100	LOC374684	XM_353099.1				
GI_37542195-S	204.7	199.2	191.3	KIAA1171	XM_351035.1				
GI_37542198-S	115.8	133.9	124.1	FLJ36208	XM_208927.3				
GI_37542202-S	160.7	190	175	LOC376295	XM_352153.1				
GI_37542206-S	102.8	122.3	101.3	LOC376298	XM_352154.1				
GI_37542208-S	199.2	204.9	195.5	LOC376299	XM_352155.1				
GI_37542210-S	302.1	380	312.3	LOC342460	XM_292562.3				
GI_37542212-S	94.5	105.3	91.3	LOC376301	XM_352156.1				
GI_37542221-S	117.3	123.4	113.8	LOC374729	XM_351069.1				
GI_37542223-S	212.4	243.5	199.1	LOC374730	XM_351070.1				
GI_37542225-S	96.4	108	101.7	LOC376332	XM_352171.1				
GI_37542230-S	101.8	110.5	104.5	LOC376333	XM_352172.1				
GI_37542232-S	214	236.4	221.2	LOC376336	XM_352173.1				
GI_37542474-S	110.4	103.8	95.6	LOC374820	XM_353147.1				
GI_37542476-S	95.7	104	97.7	LOC374821	XM_353148.1				
GI_37542480-S	335.2	353.7	305.6	LOC374822	XM_353149.1				
GI_37542482-S	156.6	173.2	162.8	LOC374823	XM_351143.1				
GI_37542486-S	312.8	335.5	367	LOC283989	XM_208944.4				
GI_37542491-S	576.4	633.6	645.4	KIAA1753	XM_036115.4				
GI_37542499-S	355.3	445.8	378.2	LOC374827	XM_353152.1				
GI_37542501-S	320.5	296.9	255.7	LOC125061	XM_058889.5				
GI_37542503-S	125.5	126	119.7	LOC374828	XM_353153.1				
GI_37542511-S	94.5	119.7	106.9	LOC376418	XM_352215.1				
GI_37542515-S	202.1	216.4	205.1	LOC376422	XM_352217.1				
GI_37542517-S	109.9	100.4	100.6	KIAA1917	XM_290732.3				
GI_37542666-S	125.7	138.8	117.8	LOC374833	XM_351147.1				
GI_37542672-S	1310	1415.2	1330.2	LOC284207	XM_209073.3				
GI_37542851-S	169.4	155.9	109.9	POU6F1	XM_352901.1				
GI_37542857-S	86.1	96.1	80.9	LOC144245	XM_047770.6				
GI_37542859-S	1864.7	1756.1	1630.5	DKFZp313M	XM_113743.4				
GI_37542863-S	240.4	276.4	233.1	LOC374450	XM_353025.1				
GI_37542865-S	96.1	100.8	89	LOC374451	XM_353026.1				
GI_37542881-S	171.9	214.5	190.1	LOC283389	XM_211009.3				
GI_37542883-S	143	160.3	150.7	LOC255411	XM_170708.3				
GI_37542884-S	125.1	151.2	109.9	KIAA1602	XM_035497.10				
GI_37542886-S	105.7	103.9	100.7	LOC121006	XM_290556.3				
GI_37542888-S	240	306.6	260.8	LOC374453	XM_353027.1				
GI_37542896-S	106.8	124.7	100.1	LOC374455	XM_353028.1				
GI_37542906-S	164.3	176.7	170.6	KIAA0286	XM_043118.5				

GI_37542910-S	243.1	292.9	249	LOC256176	XM_172889.4
GI_37542911-S	116.7	125.1	112.3	LOC374457	XM_350879.1
GI_37542913-S	108.6	111.5	130.9	KIAA1040	XM_051091.9
GI_37542914-S	130.7	137.2	127.6	LOC374458	XM_350880.1
GI_37542922-S	94	94.9	99.4	LOC115749	XM_056680.5
GI_37542926-S	105.1	89.6	81.4	LOC374460	XM_353029.1
GI_37542930-S	96.1	95.9	96.9	LOC374461	XM_353030.1
GI_37542932-S	132.6	138.9	116.8	GRIP1	XM_290559.3
GI_37542940-S	90.3	88.8	87.5	LOC121216	XM_062520.2
GI_37542946-S	92.1	114.9	83.2	LOC283464	XM_290597.2
GI_37542949-S	113.8	120.4	107.9	LOC341568	XM_292136.2
GI_37542951-S	169.3	200.8	173.1	LOC376114	XM_352074.1
GI_37542957-S	121.2	114.8	119.4	LOC341404	XM_292056.3
GI_37542961-S	128.7	130.6	110.4	LOC376116	XM_352075.1
GI_37542963-S	129.9	144.9	135.6	LOC121360	XM_062594.2
GI_37542965-S	109.5	121.4	116.2	LOC121364	XM_062598.3
GI_37542967-S	110	113.8	100.5	LOC254783	XM_171578.3
GI_37542969-S	110.5	153.9	122.8	LOC254786	XM_171581.3
GI_37542971-S	195.4	233.3	211	LOC376118	XM_352076.1
GI_37542975-S	105.1	113.2	97.8	LOC341416	XM_292049.3
GI_37542977-S	148.8	182.2	185.7	LOC341418	XM_292051.3
GI_37542979-S	108.5	124.2	115.2	LOC121130	XM_062468.4
GI_37542981-S	331.3	376.6	522.2	LOC283377	XM_208647.2
GI_37542986-S	118.9	134.7	116.9	LOC376125	XM_352078.1
GI_37542990-S	92.1	98.3	91.3	KIAA1157	XM_051093.3
GI_37542993-S	144	170.2	165.2	LOC376128	XM_352079.1
GI_37542995-S	989.7	1131.7	842.7	LOC341315	XM_292012.3
GI_37542999-S	106.7	127.3	109.8	LOC341333	XM_296117.2
GI_37543001-S	107.5	102.1	87.4	LOC376132	XM_352080.1
GI_37543003-S	105.4	121.5	107.1	LOC376133	XM_352081.1
GI_37543009-S	5040.2	4554.6	3592.1	LOC376138	XM_352084.1
GI_37543181-S	137	147.2	132	LOC376167	XM_352100.1
GI_37543220-S	166.4	182.9	230.1	LOC144404	XM_084852.8
GI_37543222-S	378.3	473.7	478.1	KIAA1076	XM_037523.8
GI_37543269-S	79.6	106.1	90.6	LOC374761	XM_353129.1
GI_37543271-S	1770.8	1282.7	1089.6	KIAA0397	XM_029438.4
GI_37543272-S	111.4	110.4	122.1	LOC201130	XM_113900.2
GI_37543280-S	97.8	106.3	96.3	LOC374763	XM_351092.1
GI_37543282-S	241.4	291.9	242.8	LOC374764	XM_353130.1
GI_37543284-S	256.3	233.7	202	KIAA1871	XM_290737.2
GI_37543286-S	321.1	468.2	220.7	LOC374765	XM_351093.1
GI_37543288-S	139.1	167.8	135.3	KIAA0523	XM_041964.8
GI_37543291-S	290.9	275.2	313.3	LOC374767	XM_353131.1
GI_37543293-S	538.3	541.7	440	MGC49942	XM_351095.1

GI_37543295-S	133.4	166.4	141.9	LOC201232	XM_115484.3				
GI_37543318-S	118.5	151.7	118.9	LOC146754	XM_085578.4				
GI_37543322-S	124.8	111.9	108.8	MYH10	XM_290747.3	NMMHCB	actin	kinesin	cytokinesi
GI_37543324-S	126.1	157.7	143.7	LOC374769	XM_351098.1				
GI_37543328-S	186.6	208	189.6	LOC201140	XM_113912.2				
GI_37543348-S	85.7	86.9	78.8	LOC374770	XM_351100.1				
GI_37543352-S	111.2	106.1	104	LOC146822	XM_085606.2				
GI_37543356-S	107.1	116.7	110.6	LOC374773	XM_353132.1				
GI_37543359-S	140.8	150	146.4	KIAA0565	XM_351103.1				
GI_37543367-S	285.3	337	334.7	LOC339237	XM_290780.2				
GI_37543372-S	125.8	129.8	123.2	LOC376365	XM_352187.1				
GI_37543390-S	90.3	86.5	79.9	LOC376366	XM_352188.1				
GI_37543394-S	144	175.6	176.6	KIAA1039	XM_352189.1				
GI_37543396-S	161.3	186.1	155.4	LOC124976	XM_058879.7				
GI_37543398-S	124.6	118.6	103.2	LOC376368	XM_352190.1				
GI_37543403-S	111.3	103.7	105	LOC376371	XM_352191.1				
GI_37543439-S	105.6	110.2	105.9	C17orf36	XM_085689.5				
GI_37543441-S	218.5	253.3	225.7	LOC376372	XM_352192.1				
GI_37543443-S	119.8	146.1	126.5	LOC376374	XM_352193.1				
GI_37543449-S	106.5	108.2	102	KIAA1349	XM_047617.5				
GI_37543453-S	95.1	112.2	91.5	LOC96597	XM_039922.3				
GI_37543681-S	178.7	198.9	208.3	LOC341392	XM_292035.2				
GI_37543683-S	87.7	99.7	84.8	LOC338759	XM_290555.2				
GI_37543685-S	120.1	131.3	124.1	LOC360030	XM_350866.1				
GI_37543687-S	92.5	120.1	107.7	KRT10	XM_352919.1	K10;KPP	structural	intermedia	epidermal
GI_37543691-S	95.6	95.7	93.2	LOC283321	XM_208612.2				
GI_37543694-S	156.8	196.2	187.3	LOC374437	XM_353020.1				
GI_37543701-S	99.6	96.5	113.4	KIAA1501	XM_290799.3				
GI_37543705-S	104.6	108.7	100.9	KIAA1684	XM_290806.2				
GI_37543709-S	100.1	98.1	97	LOC374799	XM_351127.1				
GI_37543713-S	126.4	154.9	119.2	LOC342667	XM_292673.3				
GI_37543738-S	100.2	105	99.3	LOC201181	XM_113916.4				
GI_37543748-S	246.5	271.8	407.5	KIAA1467	XM_350874.1				
GI_37543750-S	128.6	130.2	119.8	LOC376401	XM_352207.1				
GI_37543752-S	105.3	116.5	104.7	LOC342669	XM_292674.2				
GI_37543754-S	96.9	97.8	105.3	LOC338821	XM_292093.2				
GI_37543758-S	103.3	144	121.7	LOC374446	XM_353021.1				
GI_37543760-S	116.7	116.3	126.5	LOC376404	XM_352208.1				
GI_37543768-S	208.7	215.1	218	LOC374448	XM_353023.1				
GI_37543771-S	124.3	137.3	125.4	LOC341371	XM_292029.3				
GI_37543773-S	191.4	223	206.5	LOC341346	XM_292021.2				
GI_37543775-S	715.6	682.1	794	KIAA1340	XM_044836.8				
GI_37543779-S	338.8	373.6	353.9	LOC196394	XM_113708.3				
GI_37543804-S	95.2	101.2	89.1	LOC341370	XM_292027.2				

GI_37543806-S	15022	18886	16059	LOC376101	XM_352070.1
GI_37543808-S	100.6	95.9	74.8	LOC376102	XM_352071.1
GI_37543816-S	113	137.4	124.4	LOC341359	XM_292025.3
GI_37543871-S	122.2	144	109.7	DNAH10	XM_113706.4
GI_37543873-S	245.7	297	291.6	LOC374483	XM_350891.1
GI_37543875-S	97.1	122.1	102.3	DKFZp761O2	XM_044062.7
GI_37543878-S	136	137.8	182	LOC253934	XM_172887.2
GI_37543880-S	104.7	113.9	111.4	KIAA0318	XM_044334.4
GI_37543890-S	114.9	121.9	113.8	KIAA1786	XM_038436.9
GI_37543892-S	125.2	130.6	111.8	KIAA1906	XM_055095.3
GI_37543896-S	108.2	105.5	106.6	LOC376159	XM_352095.1
GI_37543898-S	112.6	120.2	105.3	LOC160348	XM_090235.2
GI_37543902-S	108.8	115.1	107.4	LOC338792	XM_292064.2
GI_37543906-S	139.4	146.7	200.7	LOC376163	XM_352098.1
GI_37543909-S	106.1	104.2	97.6	LOC376164	XM_352099.1
GI_37543961-S	176.7	212.4	182	LOC374436	XM_353019.1
GI_37543967-S	154.5	191.4	177.5	LOC376084	XM_352067.1
GI_37543969-S	2900.6	4427.8	2789.2	LOC376086	XM_352068.1
GI_37544001-S	381	465.6	419.6	KIAA0553	XM_290758.2
GI_37544003-S	113.7	120.2	114.4	FLJ35848	XM_290755.2
GI_37544007-S	149.2	166.1	171	LOC146909	XM_085634.4
GI_37544009-S	145.8	143	151.8	LOC374804	XM_353142.1
GI_37544011-S	166.4	168.7	153.1	LOC374805	XM_351130.1
GI_37544019-S	294.3	346.3	293.1	LOC374807	XM_351132.1
GI_37544031-S	141.2	154.9	148	LOC253962	XM_172968.3
GI_37544033-S	855.1	960.3	729.4	LOC374811	XM_351136.1
GI_37544037-S	205.5	241.4	209.4	LOC342600	XM_292624.2
GI_37544046-S	102.3	113.1	97.3	LOC374816	XM_353145.1
GI_37544053-S	114.6	141.5	117.1	LOC374817	XM_353146.1
GI_37544055-S	222.4	252.9	224	LOC284021	XM_211305.4
GI_37544061-S	112.9	110.8	108	LOC376406	XM_352210.1
GI_37544063-S	122	143.2	127.3	DKFZp761G2	XM_046017.6
GI_37544071-S	95.3	102.1	100.8	LOC376409	XM_352211.1
GI_37544075-S	121.3	128.8	117.4	LOC124667	XM_064257.5
GI_37544079-S	103.5	112.2	99.7	OR4D1	XM_292627.3
GI_37544081-S	104.8	102	92.1	LOC124538	XM_064177.3
GI_37544110-S	737.6	638.9	514.2	LOC121642	XM_058581.9
GI_37544111-S	90.7	108	94.2	LOC374473	XM_353035.1
GI_37544113-S	112.5	106.3	110.4	FOXN4	XM_062735.6
GI_37544115-S	95.7	87.1	84	LOC374474	XM_353036.1
GI_37544117-S	89	101.2	93.5	CUTL2	XM_027045.9
GI_37544121-S	132.2	130.7	121.7	LOC374476	XM_353037.1
GI_37544123-S	110.8	124.4	97.7	LOC374477	XM_353038.1
GI_37544127-S	93.6	96.3	97.3	LOC374478	XM_353039.1

GI_37544129-S	96	117.8	104.2	LOC374479	XM_350889.1
GI_37544131-S	121.1	142.6	125.5	LOC92558	XM_045787.8
GI_37544141-S	367.9	391.2	294.5	LOC376156	XM_352094.1
GI_37544434-S	135.2	144.6	116.2	LOC374784	XM_351113.1
GI_37544436-S	1812.7	1110.9	1434.1	LOC374785	XM_353135.1
GI_37544450-S	109.4	123	115.1	LOC374787	XM_353136.1
GI_37544460-S	298.1	364.3	313.4	LOC124842	XM_064333.4
GI_37544490-S	93	103.9	92.8	LOC376396	XM_352203.1
GI_37544494-S	110.4	139.2	110.8	LOC376400	XM_352205.1
GI_37544497-S	112.4	127.7	109.7	MYO1D	XM_050041.8
GI_37544565-S	311.9	375.6	333.2	KIAA1554	XM_290768.2
GI_37544571-S	96.4	121.4	112.9	LOC146701	XM_097065.5
GI_37544574-S	120	144.2	121.8	LOC374832	XM_353156.1
GI_37544576-S	189.4	240.1	220.6	LOC339226	XM_294867.3
GI_37544578-S	113.2	112.5	104.4	KIAA1447	XM_351146.1
GI_37544582-S	119.9	114.2	107.8	AZI1	XM_045581.7
GI_37544593-S	134.1	179.9	160.8	LOC374758	XM_351089.1
GI_37544650-S	91.6	102.7	94.5	LOC374778	XM_353134.1
GI_37544652-S	99.5	97.5	106.7	LOC374779	XM_351106.1
GI_37544656-S	93.8	91.1	85.9	LOC256223	XM_170840.2
GI_37544658-S	109.3	101	96.8	LOC374781	XM_351110.1
GI_37544666-S	97	89.3	85.1	KIAA0918	XM_054869.3
GI_37544667-S	3631	4355.6	4149.7	USP22	XM_042698.6
GI_37544669-S	95.5	106.2	97.4	LOC374511	XM_353050.1
GI_37544673-S	84.1	83.7	88.8	LOC374512	XM_353051.1
GI_37544677-S	92.2	90.5	82.9	LOC374513	XM_353052.1
GI_37544681-S	89.6	95.7	98.7	LOC196541	XM_116936.2
GI_37544683-S	113	104.3	91.9	LOC376385	XM_352199.1
GI_37544685-S	146.7	174.7	154.9	FLJ40176	XM_062871.4
GI_37544691-S	132.4	160.1	138	LOC144920	XM_096688.4
GI_37544694-S	315.7	306.1	360.7	LOC374514	XM_350908.1
GI_37544698-S	100.4	104.6	91.1	MYR8	XM_028522.3
GI_37544714-S	235.9	287	239.7	LOC376220	XM_352115.1
GI_37544717-S	102.2	86.6	91.2	LOC121952	XM_062872.3
GI_37544742-S	103.8	117.9	103.4	LOC341604	XM_296315.3
GI_37544744-S	92.2	105.9	104.6	LOC122335	XM_063084.2
GI_37544774-S	124.5	143.3	135.7	LOC339253	XM_290786.2
GI_37544910-S	253.4	327.6	265.7	LOC376225	XM_352118.1
GI_37544934-S	629.3	427.5	367.6	LOC284942	XM_209415.3
GI_37544963-S	457	528.6	508	LOC374841	XM_353161.1
GI_37544988-S	314.2	366.6	314.1	LOC374843	XM_351156.1
GI_37544990-S	373.2	352	330.2	LOC374845	XM_351157.1
GI_37545002-S	109.5	118	110.2	LOC374851	XM_353162.1
GI_37545048-S	132.9	199.3	154.6	FLJ10312	XM_352921.1

GI_37545052-S	85.6	86.8	100.7	LOC374852	XM_351159.1
GI_37545056-S	212.2	252.9	262	LOC201475	XM_113967.3
GI_37545060-S	1167.5	1024.9	606.3	KIAA0802	XM_031357.5
GI_37545064-S	95.6	102.5	95.4	LOC374856	XM_353163.1
GI_37545066-S	172	207.3	177	LOC284232	XM_209076.3
GI_37545068-S	136.9	188.8	151.1	LOC374858	XM_353164.1
GI_37545070-S	117	123.4	122.7	LOC374860	XM_351161.1
GI_37545082-S	103.3	92.1	105.1	LOC376435	XM_352224.1
GI_37545084-S	107.2	117.5	123.1	LOC339291	XM_292678.2
GI_37545110-S	99.5	100.7	90.4	LOC342850	XM_292717.3
GI_37545112-S	164.2	135.1	118	Spir-1	XM_290818.2
GI_37545266-S	193.4	206.4	226.4	LOC374868	XM_351168.1
GI_37545268-S	301.8	304.6	354.1	LOC374869	XM_353166.1
GI_37545270-S	174.2	217.9	207.2	LOC374870	XM_353167.1
GI_37545279-S	92.4	97.4	103.9	LOC376473	XM_352235.1
GI_37545281-S	80.8	78.2	86.1	LOC147294	XM_091727.7
GI_37545349-S	92.3	99.2	95.6	LOC374489	XM_350896.1
GI_37545351-S	13644.6	12032	10178	LOC374490	XM_350897.1
GI_37545353-S	111.4	123.8	107.2	LOC374491	XM_350898.1
GI_37545358-S	134.9	174.2	136.2	LOC254109	XM_172905.3
GI_37545360-S	131.1	137.3	150.3	KIAA0774	XM_166270.2
GI_37545362-S	101	122.7	105.2	LOC374493	XM_353043.1
GI_37545368-S	97.4	116.3	110.5	LOC374495	XM_350900.1
GI_37545370-S	99.2	105.1	111	DKFZp686J0	XM_292193.2
GI_37545373-S	534.2	573.7	463.8	KIAA0564	XM_038664.7
GI_37545376-S	355.4	381.7	306.4	LOC253512	XM_170736.3
GI_37545377-S	122	118.9	120.2	LOC220416	XM_166971.3
GI_37545383-S	193.8	198.2	189.6	LOC374496	XM_350901.1
GI_37545408-S	132.9	145.1	129.3	LOC374497	XM_353044.1
GI_37545414-S	102.9	110.9	106.5	LOC341676	XM_292160.3
GI_37545449-S	92.3	86.1	104.2	LOC374504	XM_353045.1
GI_37545451-S	102.2	104.4	99.2	LOC374505	XM_353046.1
GI_37545455-S	136.2	165.6	134.9	LOC374508	XM_353047.1
GI_37545457-S	115.4	129.9	115.3	LOC374509	XM_353048.1
GI_37545459-S	125	117.4	137.8	AK000009	XM_085023.5
GI_37545463-S	118.1	119.8	100.9	LOC374510	XM_353049.1
GI_37545486-S	133.6	140.8	123.3	LOC376171	XM_352101.1
GI_37545498-S	145.7	145.3	154.9	LOC376174	XM_352104.1
GI_37545504-S	120.5	110.9	94.7	LOC376183	XM_352105.1
GI_37545508-S	101.7	125.1	119	LOC376191	XM_352106.1
GI_37545524-S	118.1	126.1	109.1	LOC341651	XM_292197.3
GI_37545530-S	120.9	128.8	113.8	LOC283514	XM_210264.3
GI_37545556-S	184.5	244.7	224.9	LOC121981	XM_062890.2
GI_37545558-S	139.2	177.2	146.8	LOC376201	XM_352109.1

GI_37545568-S	95.6	90.6	81.6	LOC122134	XM_062966.2
GI_37545572-S	121.7	113.6	122.1	LOC341720	XM_292184.2
GI_37545574-S	118.1	137.4	124.5	LOC376210	XM_352112.1
GI_37545578-S	491	637.4	589.1	NDFIP2	XM_041162.3
GI_37545580-S	88.2	87.3	88.4	KIAA1910	XM_055514.2
GI_37545618-S	2164.3	2396	1615.8	KIAA1695	XM_352922.1
GI_37545625-S	256.7	156.7	163.5	TAF4B	XM_290809.2
GI_37545631-S	109.5	127.8	110	LOC374864	XM_351164.1
GI_37545635-S	148.7	156.3	145.6	LOC147354	XM_085777.2
GI_37545637-S	94	96.9	85.4	KIAA1713	XM_290811.2
GI_37545641-S	142.6	136.5	120.2	LOC374865	XM_353165.1
GI_37545645-S	123.1	122.4	117.6	LOC284260	XM_211408.2
GI_37545679-S	248.6	267.9	236.7	KIAA1632	XM_038864.4
GI_37545685-S	119.5	138.9	138.5	LOC201501	XM_113971.2
GI_37545687-S	127.2	133	103.1	MYO5B	XM_351166.1
GI_37545693-S	212.8	242.9	230.1	LOC147468	XM_091809.2
GI_37545699-S	174	193	166.3	LOC376453	XM_352228.1
GI_37545842-S	119	148.2	150.9	ATP11A	XM_085028.3
GI_37545846-S	96.7	111.1	92.9	LOC376222	XM_352116.1
GI_37545854-S	82.9	85.7	78	LOC125595	XM_064689.5
GI_37545856-S	128.7	146	113.6	LOC376469	XM_352232.1
GI_37545859-S	307	290.9	209.8	LOC374516	XM_353055.1
GI_37545861-S	93.7	100.2	105.5	LOC376224	XM_352117.1
GI_37545866-S	118.1	109.4	114	LOC374867	XM_351167.1
GI_37545870-S	672.5	731.5	634.2	LOC125704	XM_058931.6
GI_37545871-S	150.5	160.4	149.7	LOC376464	XM_352229.1
GI_37545877-S	105.9	100.5	98.4	LOC342784	XM_292707.2
GI_37545889-S	100.6	113.7	101.6	LOC374521	XM_353056.1
GI_37545891-S	2057.8	1386.2	1474.1	DKFZP564O	XM_033371.3
GI_37545893-S	98.1	98	98.1	ZFHX2	XM_033370.9
GI_37545897-S	119.2	121.7	115.8	LOC374540	XM_353058.1
GI_37545901-S	108.7	100.5	109.4	LOC374542	XM_350929.1
GI_37545907-S	281.6	357.3	304.7	LOC374543	XM_353060.1
GI_37545909-S	228.8	265.1	224	LOC374544	XM_350930.1
GI_37545911-S	393.9	463.7	432.2	DKFZP434I1	XM_113763.4
GI_37545913-S	365.8	430	389.9	LOC374545	XM_350931.1
GI_37545915-S	109.1	91.3	103.7	LOC374546	XM_353061.1
GI_37545917-S	96.1	114.6	104.2	LOC374547	XM_353062.1
GI_37545919-S	194.5	247.4	209.5	LOC374548	XM_353063.1
GI_37545925-S	100	98.8	92.2	LOC253970	XM_172910.3
GI_37545927-S	123.6	122.9	118.8	C14orf25	XM_350932.1
GI_37545931-S	220.3	201.1	178.4	C14orf28	XM_071793.5
GI_37545932-S	90.5	100.2	93.3	KIAA1596	XM_048128.7
GI_37545936-S	220	253.7	234.9	KIAA1344	XM_051699.3

GI_37545938-S	92.9	95.1	94.5	DKFZp762F0	XM_290615.2			
GI_37545942-S	127.4	170.2	139	DDHD1	XM_051692.3		metal ion	lipid
GI_37545946-S	127.5	130.5	129.6	LOC145414	XM_085138.3			
GI_37545948-S	111.2	97.6	104	LOC341880	XM_292260.2			
GI_37545950-S	141.4	170.4	169.6	LOC374553	XM_353066.1			
GI_37545954-S	101.4	119	109.4	KIAA0227	XM_027236.2			
GI_37545956-S	136.7	275.2	413.1	MAP3K9	XM_027237.6			
GI_37545958-S	571.3	855.6	765.8	S164	XM_027330.11			
GI_37545960-S	89.7	95	92.9	C14orf42	XM_090885.3			
GI_37545966-S	1145.8	1070.7	1044.5	ZAP3	XM_085151.7			
GI_37545970-S	133.5	130.4	123.1	DKFZP434P0	XM_041116.5			
GI_37545972-S	98.2	105	93.3	LOC283578	XM_208746.2			
GI_37545976-S	130.2	135.4	135.3	LOC374557	XM_353068.1			
GI_37545978-S	84.6	88	87.4	LOC374558	XM_353069.1			
GI_37545980-S	647.2	491.7	427.6	TTC7L1	XM_085175.3			
GI_37545982-S	464.4	363.2	228.3	KIAA1509	XM_029353.2			
GI_37545986-S	1306.6	940.1	1263.5	C14orf109	XM_058628.5			
GI_37545987-S	83.8	99	84.5	LOC374561	XM_350939.1			
GI_37545989-S	93	96.5	96.4	KIAA1409	XM_028395.2	FLJ43337		
GI_37545993-S	119.8	128.9	118.6	LOC256394	XM_170754.3			
GI_37545995-S	113.2	142.2	118.3	LOC374564	XM_353071.1			
GI_37545997-S	135	155.3	137.8	LOC374565	XM_353072.1			
GI_37545999-S	188.3	239.5	198.7	C14orf68	XM_208731.2			
GI_37546002-S	94.9	92.5	91.9	LOC374566	XM_353073.1			
GI_37546004-S	160.4	158.4	135.6	LOC374567	XM_353074.1			
GI_37546007-S	146	172	166.4	LOC283604	XM_211088.2			
GI_37546008-S	111.9	131.3	118.9	C14orf73	XM_040910.4			
GI_37546012-S	229.6	283.6	247.2	LOC374569	XM_350943.1			
GI_37546014-S	121.8	115.7	108.8	KIF26A	XM_050278.7			
GI_37546018-S	1698.6	1760.6	2073.8	KIAA0284	XM_208766.2			
GI_37546020-S	300.4	304.4	341.2	LOC374571	XM_350945.1			
GI_37546022-S	169.9	176.2	207.2	C14orf78	XM_290629.2			
GI_37546026-S	99.8	126.2	93.3	LOC374572	XM_350946.1			
GI_37546028-S	122.3	135	120.5	LOC374573	XM_350947.1			
GI_37546036-S	106.5	127.8	102.3	LOC376226	XM_352119.1			
GI_37546040-S	109.5	124.3	102.8	LOC283621	XM_210282.3			
GI_37546044-S	135.8	154.6	132.5	LOC122740	XM_063308.3			
GI_37546046-S	135.4	138.1	129.4	LOC122748	XM_063315.2			
GI_37546048-S	104.7	113.5	110.6	LOC123103	XM_063481.2			
GI_37546050-S	103.7	118.9	93.7	LOC338879	XM_292225.2			
GI_37546052-S	94.6	98.7	94.1	LOC376227	XM_352120.1			
GI_37546054-S	145.4	163.6	146.3	LOC341799	XM_292227.2			
GI_37546056-S	192.7	227	203.6	LOC376229	XM_352121.1			
GI_37546058-S	137.1	154.2	129.3	LOC122706	XM_063287.6			

GI_37546066-S	120.8	133.4	126.4	LOC376247	XM_352133.1	
GI_37546086-S	137.4	158.2	147.1	LOC376263	XM_352136.1	
GI_37546090-S	122.4	127	129.7	KIAA0599	XM_085127.7	
GI_37546094-S	150.5	162.1	153.2	LOC122438	XM_063138.2	
GI_37546100-S	121.8	137.7	119.4	LOC341912	XM_292301.2	
GI_37546102-S	181.7	239.4	203.4	LOC376279	XM_352142.1	
GI_37546110-S	120.1	141.7	113.8	LOC376283	XM_352144.1	
GI_37546112-S	100.9	116.7	103.7	LOC122423	XM_063123.4	
GI_37546114-S	138.6	156.1	138.5	LOC376284	XM_352145.1	
GI_37546116-S	94.5	102.8	97.4	LOC376285	XM_352146.1	
GI_37546131-S	84.5	84.1	81.6	LOC375805	XM_351892.1	
GI_37546137-S	120.3	147	136.8	PPP1R3F	XM_351895.1	
GI_37546139-S	113.8	129.3	98.5	LOC286408	XM_210035.2	
GI_37546148-S	113.9	135	125.7	LOC377882	XM_352833.1	
GI_37546152-S	108.7	117.5	112.6	LOC347344	XM_293284.2	
GI_37546154-S	107	111.5	108.1	ZNF21	XM_092995.3	
GI_37546156-S	121.5	125.5	110.4	LOC377886	XM_352834.1	
GI_37546160-S	371.7	412	356.2	LOC377887	XM_352835.1	
GI_37546163-S	120.9	124.1	120.5	LOC375807	XM_353505.1	
GI_37546165-S	179.8	238.4	208.9	KIAA0522	XM_291345.2	
GI_37546167-S	148	147.4	155	LOC375808	XM_351905.1	
GI_37546173-S	173.7	204.1	192.3	LOC375809	XM_351906.1	
GI_37546177-S	99	118	110.5	LOC375811	XM_353506.1	
GI_37546183-S	89.6	90.5	82.5	LOC377893	XM_352840.1	
GI_37546189-S	95	102.3	91.3	LOC377895	XM_352841.1	
GI_37546196-S	146.9	189.6	164	LOC139189	XM_066534.2	
GI_37546200-S	164.9	214	183.3	LOC377888	XM_352836.1	
GI_37546202-S	130.4	137.3	115.9	LOC377889	XM_352837.1	
GI_37546204-S	117.1	136.8	130	LOC340602	XM_291352.2	MGC47837
GI_37546205-S	99.6	105.3	87.9	LOC347549	XM_293416.2	
GI_37546214-S	404.6	523.6	447	CYLC1	XM_088636.4	
GI_37546216-S	178.3	201	187.1	LOC340562	XM_291339.2	
GI_37546220-S	100.5	129	118.8	PCDH19	XM_033173.7	
GI_37546222-S	111.9	108.9	125.6	LOC375818	XM_351913.1	
GI_37546224-S	112.7	111.3	107.3	LOC375819	XM_353510.1	
GI_37546226-S	91.6	92.8	94.9	KIAA1789	XM_040486.3	
GI_37546229-S	126.9	141.4	127.8	FLJ10097	XM_043653.6	
GI_37546231-S	94.2	108.9	103.3	LOC158983	XM_088735.3	
GI_37546232-S	104.2	109.7	119.6	LOC286436	XM_210048.2	
GI_37546234-S	132.8	144.8	105.9	LOC139231	XM_060020.5	
GI_37546237-S	132.1	166.4	164.8	LOC92129	XM_351915.1	
GI_37546245-S	196.8	219.8	201.6	LOC139302	XM_066621.3	
GI_37546249-S	166.3	216.1	188.4	LOC286453	XM_210054.2	
GI_37546258-S	163.8	154.5	133.1	LOC347393	XM_293320.3	

GI_37546264-S	122.1	128.9	127.9	KIAA1817	XM_042978.2				
GI_37546267-S	248.6	283	264.3	LOC158835	XM_088683.2				
GI_37546271-S	89	86.5	73.7	LOC158833	XM_088691.3				
GI_37546273-S	315.9	414.9	342.7	LOC347517	XM_293398.2				
GI_37546275-S	164.4	182.9	163.5	LOC158825	XM_088686.4				
GI_37546288-S	95.3	101.7	99.2	LOC139886	XM_066946.3				
GI_37546291-S	227.5	196.4	204.4	LOC286449	XM_212321.2				
GI_37546293-S	116.3	124.3	123.7	LOC340554	XM_293334.2				
GI_37546299-S	115.2	119.4	95.3	LOC377909	XM_352843.1				
GI_37546303-S	105.3	112.5	102.1	LOC377911	XM_352844.1				
GI_37546305-S	130.5	119.9	114.9	LOC139562	XM_066765.3				
GI_37546306-S	212.5	263	253.9	LOC377913	XM_352845.1				
GI_37546309-S	171.9	208.7	174.5	KIAA2001	XM_291322.2				
GI_37546313-S	122.2	130.7	108.4	LOC340529	XM_291328.2				
GI_37546317-S	378.6	390.8	272.4	LOC377917	XM_352848.1				
GI_37546335-S	1375.7	1118.5	1124.8	LOC375833	XM_351929.1				
GI_37546337-S	3305.4	3254.5	3194.3	LOC375834	XM_351930.1				
GI_37546339-S	119.7	117.6	107.8	ZNF275	XM_351933.1				
GI_37546343-S	176.6	188.5	172.5	LOC139046	XM_066443.5				
GI_37546350-S	581.7	858.3	714.1	DXS1283E	XM_047871.6	GS2	catalytic	cellular_co	biological_
GI_37546356-S	106	102.4	113.3	LOC375796	XM_351887.1				
GI_37546360-S	71.4	81.9	81.4	LOC375797	XM_353502.1				
GI_37546364-S	316.2	294.1	339.4	LOC220895	XM_165534.4				
GI_37546368-S	112.6	120.5	110.8	LOC139420	XM_066685.3				
GI_37546372-S	97.2	100.6	98.9	LOC377856	XM_352829.1				
GI_37546376-S	87.1	85.3	78.4	LOC92552	XM_045705.5				
GI_37546381-S	109.6	109.3	113.4	KIAA1677	XM_040383.6				
GI_37546382-S	142.7	160.9	159.5	LOC347438	XM_293352.3				
GI_37546384-S	108.8	125.2	122.4	LOC170067	XM_093087.3				
GI_37546389-S	102.2	100.2	97.4	LOC347541	XM_293407.2				
GI_37546394-S	131.5	132.7	131.5	LOC347442	XM_293354.3				
GI_37546396-S	82.2	83.6	90	LOC139425	XM_066690.3				
GI_37546398-S	123.4	132.7	114.7	LOC139431	XM_066695.3				
GI_37546400-S	350.6	433.5	397.4	LOC377862	XM_352830.1				
GI_37546402-S	98.9	98.8	99.4	LOC340571	XM_293360.3				
GI_37546411-S	94.9	91.3	88.3	FLJ12649	XM_291344.2				
GI_37546413-S	119	148.3	130.1	LOC375825	XM_353512.1				
GI_37546415-S	120.5	109.6	112.5	LOC375826	XM_351923.1				
GI_37546417-S	112.2	117.9	113.5	LOC347487	XM_298053.2				
GI_37546419-S	94.4	109.2	98.5	LOC375828	XM_353513.1				
GI_37546429-S	99.1	93.5	87.9	LOC377963	XM_352861.1				
GI_37546435-S	99.5	101.9	102.2	LOC347468	XM_293366.3				
GI_37546437-S	104.3	120.5	94.5	LOC347475	XM_298045.2				
GI_37546442-S	349.2	539.9	424.8	LOC377970	XM_352863.1				

GI_37546444-S	86.8	89	76.1	LOC377972	XM_352864.1
GI_37546449-S	103.3	105	94	LOC377975	XM_352865.1
GI_37546456-S	350.3	353.3	295.4	LOC375832	XM_351927.1
GI_37546461-S	143.2	169.6	154.6	LOC347527	XM_293401.2
GI_37546464-S	178.6	219.9	191.7	H2AFB	XM_352873.1
GI_37546471-S	122.3	144.1	126.6	LOC203510	XM_115897.2
GI_37546474-S	173	221.4	195.5	LOC375835	XM_351934.1
GI_37546480-S	127.1	134.4	117.9	LOC377980	XM_352869.1
GI_37546482-S	105.6	124.6	114.6	LOC139735	XM_066859.2
GI_37546496-S	776.8	809.6	607.8	LOC286528	XM_210501.3
GI_37546507-S	99.4	95.7	94.9	LOC255766	XM_172794.2
GI_37546509-S	107.5	122.4	101.8	KIAA1210	XM_172801.2
GI_37546511-S	102.6	113.3	92.9	LOC158796	XM_088677.2
GI_37546515-S	521.3	690.6	538.7	THOC2	XM_047325.6
GI_37546517-S	120.3	130	112.5	LOC375822	XM_351919.1
GI_37546519-S	276.1	332.9	324.4	LOC377950	XM_352856.1
GI_37546521-S	255.7	291	294.1	LOC377952	XM_352857.1
GI_37546529-S	137	161	154.8	LOC377955	XM_352858.1
GI_37546535-S	1065.8	1839.5	2286.2	LOC377960	XM_352860.1
GI_37546538-S	127.3	115	117.4	LOC375836	XM_351938.1
GI_37546550-S	103.9	107.6	100	LOC338829	XM_292122.3
GI_37546554-S	104.5	110.5	112.5	LOC377990	XM_352876.1
GI_37546557-S	125.2	121.4	114	LOC377991	XM_352877.1
GI_37546565-S	91.3	107.3	90.1	LOC375800	XM_353504.1
GI_37546575-S	106.9	116.9	101.3	HYPM	XM_048235.2
GI_37546580-S	122.4	118	112.8	LOC347411	XM_293325.2
GI_37546582-S	136.9	156.9	144.6	LOC377870	XM_352832.1
GI_37546588-S	104.9	122.9	102.1	LOC375817	XM_351912.1
GI_37546613-S	116	131	106.6	LOC375847	XM_353522.1
GI_37546619-S	262.2	311.4	256.7	CYorf15A	XM_351950.1
GI_37546626-S	94.9	90.8	97.2	LOC375845	XM_351948.1
GI_37546632-S	93.7	95.7	101.5	LOC286561	XM_210515.2
GI_37546637-S	254.7	294.8	265.1	LOC375843	XM_293449.2
GI_37546639-S	113.1	112.5	106.8	LOC375844	XM_351945.1
GI_37546649-S	99.8	117.9	104.1	LOC347596	XM_293460.3
GI_37546653-S	105.5	120.5	111.2	LOC140103	XM_067076.2
GI_37546658-S	103.7	115.6	111.9	LOC375849	XM_351954.1
GI_37546662-S	188.1	276.6	214.7	LOC375851	XM_353524.1
GI_37546668-S	80.5	76.1	80.6	LOC159184	XM_010658.8
GI_37546705-S	400.1	482.5	305.6	LOC375786	XM_353496.1
GI_37546711-S	115	129.8	124.8	LOC375787	XM_353497.1
GI_37546713-S	77.7	79.4	78	LOC377850	XM_352825.1
GI_37546716-S	165.6	139.6	126.2	LOC375788	XM_351882.1
GI_37546720-S	96.2	95.6	99.2	LOC377851	XM_352826.1

GI_37546726-S	85.6	92.6	96.3	KIAA1751	XM_351884.1		
GI_37546728-S	135.3	148.4	152	LOC339457	XM_353498.1		
GI_37546731-S	2425.3	3056.7	3438.4	LOC375790	XM_351885.1		
GI_37546739-S	124.4	112.2	110.5	KIAA1107	XM_034086.3		
GI_37546741-S	134.7	175.6	162.9	LOC374993	XM_351272.1		
GI_37546745-S	127.2	129.7	112.9	LOC374994	XM_353208.1		
GI_37546747-S	100.3	94.4	90.4	LOC374995	XM_353209.1		
GI_37546761-S	236.8	284.1	238.7	LOC126598	XM_060087.8		
GI_37546763-S	103.2	130	119.6	LOC376619	XM_352309.1		
GI_37546765-S	89.6	82.8	79.2	LOC163404	XM_088864.4		
GI_37546767-S	86.3	82.1	89	LOC376622	XM_352310.1		
GI_37546772-S	91.1	101.7	106.9	LOC374997	XM_353210.1		
GI_37546774-S	84.6	98.3	96.5	FLJ25070	XM_351275.1	FLJ20008;KIAA1839	nucleic
GI_37546776-S	160.7	180.6	156.1	LOC126987	XM_060278.3		
GI_37546785-S	168.3	184.6	162.3	CROCC	XM_351240.1		
GI_37546787-S	128.6	127.2	122.4	LOC376576	XM_352295.1		
GI_37546790-S	109.7	122.7	116.2	LOC343169	XM_291435.2		
GI_37546792-S	107.1	134.6	116.9	LOC376737	XM_352351.1		
GI_37546794-S	112.8	122.3	121.3	LOC127614	XM_060569.2		
GI_37546796-S	203.1	216.7	188.4	LOC284535	XM_210122.3		
GI_37546798-S	112.3	121.3	120.9	LOC127608	XM_060563.7		
GI_37546804-S	88.4	112	85.7	LOC376739	XM_352352.1		
GI_37546808-S	97.1	98.2	90.1	OR2T1	XM_060316.3		
GI_37546816-S	209.1	210.6	181.4	LOC375024	XM_353218.1		
GI_37546818-S	98.8	105.5	104.5	LOC199882	XM_114047.2		
GI_37546822-S	149.3	174.2	185.5	LOC375025	XM_351295.1		
GI_37546824-S	109.3	118.1	101.8	FLJ36032	XM_351296.1		
GI_37546828-S	107.3	99.8	98.8	LOC375026	XM_351297.1		
GI_37546836-S	101.1	106.8	98.3	LOC126637	XM_060104.4		
GI_37546837-S	91.5	107.6	94.9	LOC376659	XM_352326.1		
GI_37546846-S	244.7	315.7	302.9	KIAA1240	XM_039676.4		
GI_37546848-S	107.2	100.9	95.2	LOC375188	XM_351422.1		
GI_37546854-S	111.9	116.7	101.5	LOC375191	XM_353278.1		
GI_37546856-S	98.4	104.3	101.3	KIAA0953	XM_039733.3		
GI_37546860-S	138.2	138.3	129.4	LOC375193	XM_351426.1		
GI_37546862-S	100.2	97.2	97.3	LOC130106	XM_059399.3		
GI_37546863-S	381	352.4	335.7	SLB	XM_114272.2		
GI_37546867-S	2342.6	1814.3	1388.5	KIAA0007	XM_087089.3		
GI_37546881-S	241.7	281.8	256.6	KIAA1414	XM_042685.3		
GI_37546886-S	116.9	154.8	120.8	LOC344387	XM_293029.2		
GI_37546888-S	114	118.3	100.3	LOC375197	XM_351431.1		
GI_37546892-S	143.7	163.3	140.7	LOC91461	XM_038576.6		
GI_37546893-S	955.6	953.2	789.6	MTA3	XM_038567.6		
GI_37546895-S	125.9	111.3	101.6	LOC375198	XM_351432.1		

GI_37546901-S	122.1	107.4	102.3	KIAA2028	XM_059415.4		actin	cytoskelet
GI_37546902-S	87.9	85.6	88.3	LOC375201	XM_353279.1			
GI_37546904-S	101.8	103.5	106.6	LOC151111	XM_087097.2			
GI_37546906-S	180.5	213.6	190.1	LOC375202	XM_353280.1			
GI_37546908-S	286.6	326	308.6	LOC375203	XM_351435.1			
GI_37546910-S	136.1	150.5	155.5	LOC375204	XM_353281.1			
GI_37546913-S	94.9	96.1	102	LOC375205	XM_351436.1			
GI_37546917-S	105.1	122.1	110	LOC344403	XM_293032.3			
GI_37546921-S	605.2	628.5	390.7	LOC339804	XM_291016.2			
GI_37546924-S	135.7	123.9	127.3	FLJ13305	XM_291019.2			
GI_37546926-S	24634.6	22421	16069	LOC375207	XM_351437.1			
GI_37546934-S	88.3	102.2	95.8	LOC285002	XM_353282.1			
GI_37546938-S	806	731.9	927.1	SEC15B	XM_039570.5			
GI_37546944-S	483	632	585.8	MGC22014	XM_351441.1			
GI_37546946-S	407.5	468.2	431.5	LOC375211	XM_351442.1			
GI_37546948-S	99.7	110.9	110.1	LOC375212	XM_351443.1			
GI_37546950-S	325.3	208.3	341.3	LOC257200	XM_171008.2			
GI_37546953-S	173.1	224	194.5	LOC375213	XM_351444.1			
GI_37546955-S	103.2	108.4	139.9	FLJ23529	XM_049952.2			
GI_37546957-S	221.5	188.4	149	LOC129293	XM_059341.4			
GI_37546959-S	224.8	230.9	239.8	LOC375215	XM_351445.1			
GI_37546969-S	152.7	180.2	180.6	LOC115281	XM_036448.7			
GI_37546973-S	99	99.6	98.3	LOC344165	XM_292957.2			
GI_37546978-S	4486.8	4677.6	3335	LOC376872	XM_352441.1			
GI_37546980-S	173.2	195.1	177.7	LOC376873	XM_352442.1			
GI_37546982-S	275.5	354	327.4	LOC376874	XM_352443.1			
GI_37546984-S	83.9	97.9	89.7	LOC130482	XM_065743.6			
GI_37546986-S	105.7	115.9	103.4	LOC376875	XM_352444.1			
GI_37546996-S	173.6	208.8	194.3	LOC344382	XM_293026.3			
GI_37547004-S	134.8	124.7	119.2	LOC376891	XM_352450.1			
GI_37547008-S	190.6	210.7	196.4	LOC129656	XM_065332.7			
GI_37547010-S	97	110.6	91.2	LOC376892	XM_352451.1			
GI_37547012-S	497.5	711.9	619.5	PSME4	XM_040158.5	PA200;KIAA0077		
GI_37547014-S	126.7	141	142	LOC344405	XM_293034.2			
GI_37547028-S	183.6	230.2	222.9	LOC344167	XM_292958.3			
GI_37547034-S	338.1	431.2	352.7	LOC374968	XM_351247.1			
GI_37547042-S	296	399.8	355.4	PRNPIP	XM_290941.2			
GI_37547044-S	261.7	309.7	246	LOC339541	XM_294997.2			
GI_37547050-S	134.2	143.1	136.5	KIAA1511	XM_046581.6			
GI_37547052-S	132.8	149.3	141.2	DKFZP564I1	XM_032397.3			
GI_37547053-S	114.6	118	111	LOC374973	XM_351251.1			
GI_37547060-S	151.2	178.2	158.5	DMRTA2	XM_027162.2			
GI_37547062-S	117.9	141.4	125.2	LOC284546	XM_209252.2			
GI_37547063-S	107.9	119.6	117.6	C1orf34	XM_027172.2			

GI_37547065-S	441.8	527.5	605.9	KIAA1836	XM_114087.4
GI_37547067-S	422.3	399.9	334.4	KIAA0191	XM_038288.8
GI_37547069-S	88.7	89.7	88.9	LOC374975	XM_351253.1
GI_37547073-S	138.2	136	137.1	LOC374976	XM_351254.1
GI_37547075-S	145.1	157.8	139.7	LOC374977	XM_351255.1
GI_37547077-S	970.3	949.9	888.5	USP24	XM_165973.4
GI_37547079-S	119.2	119.4	105.1	LOC374978	XM_351256.1
GI_37547083-S	119.4	139.8	114.8	KIAA1915	XM_055481.6
GI_37547085-S	106.1	124.1	110.6	KIAA1799	XM_351258.1
GI_37547087-S	115.9	112	117.1	LOC284671	XM_209313.3
GI_37547093-S	129.1	149.2	126.5	INPP5B	XM_290919.2
GI_37547099-S	94.7	89.6	98.5	LOC128208	XM_060880.9
GI_37547101-S	108.7	124.3	117.8	LOC128192	XM_060887.2
GI_37547103-S	110.5	107.9	111.8	LOC200010	XM_117174.3
GI_37547107-S	722.7	750.8	617.3	LOC376601	XM_352304.1
GI_37547115-S	129.8	145.1	127.9	LOC376607	XM_352306.1
GI_37547117-S	96.6	102.6	89.6	LOC376609	XM_352307.1
GI_37547125-S	3435.9	5367.5	711.1	D2S448	XM_056455.3
GI_37547129-S	168.8	191.5	198.3	LOC376863	XM_352435.1
GI_37547136-S	107.9	119.9	115.5	LOC375014	XM_353213.1
GI_37547138-S	132.4	147.6	140.6	LOC375182	XM_353276.1
GI_37547147-S	131.7	125.1	125.9	LOC285016	XM_211736.4
GI_37547148-S	123.2	114.7	113.3	LOC200491	XM_117239.5
GI_37547151-S	152.3	162.1	136.3	LOC375180	XM_353275.1
GI_37547153-S	112.1	100.7	102.6	LOC376651	XM_352323.1
GI_37547158-S	111.9	123.9	116.1	LOC200493	XM_115715.4
GI_37547173-S	146.9	155.6	131.8	NFASC	XM_046808.10
GI_37547175-S	342.6	392.3	383.8	KIAA0472	XM_290898.2
GI_37547177-S	119.5	108.8	91.5	LOC93273	XM_351317.1
GI_37547182-S	98.8	101.2	93.2	LOC344065	XM_292895.2
GI_37547184-S	114.2	128.7	123.9	LOC375241	XM_353286.1
GI_37547198-S	86.7	97	87.5	LOC150763	XM_086996.3
GI_37547210-S	104.7	107.3	96.6	LOC375249	XM_351475.1
GI_37547214-S	120.1	104.5	90.5	LOC205272	XM_115760.3
GI_37547218-S	89.2	75.8	89.5	LOC129870	XM_065445.2
GI_37547222-S	92.6	100.1	97.4	MRF-1	XM_049068.6
GI_37547226-S	105.3	101.2	94.6	LOC374935	XM_351222.1
GI_37547228-S	259.2	307.3	300.8	LOC284591	XM_211529.3
GI_37547229-S	80.3	86.5	76.9	LOC376555	XM_352285.1
GI_37547236-S	121.1	106.4	96.6	LOC376934	XM_352469.1
GI_37547250-S	129.9	147.8	140.5	LOC376917	XM_352461.1
GI_37547259-S	162.6	171.3	127.8	LOC374963	XM_351244.1
GI_37547270-S	155.8	183.4	149.8	LOC376583	XM_352298.1
GI_37547272-S	1559.7	2423.6	1767.8	LOC376584	XM_352299.1

GI_37547280-S	277.2	148.6	155.9	EGFL3	XM_031401.6
GI_37547282-S	88.7	98.7	102.8	LOC374940	XM_353191.1
GI_37547284-S	556.8	491.2	399.7	LOC374941	XM_353192.1
GI_37547286-S	147.3	151.6	162	LOC376559	XM_352288.1
GI_37547296-S	106.4	122.9	91.7	LOC374938	XM_351227.1
GI_37547301-S	348.4	273.5	245.3	LOC375062	XM_351327.1
GI_37547314-S	158.5	178.3	167.1	LOC375277	XM_351498.1
GI_37547316-S	110.2	111.3	107.5	LOC375278	XM_353297.1
GI_37547327-S	199.4	232.1	198.7	LOC375282	XM_353298.1
GI_37547331-S	98.1	100.4	106.2	LOC344147	XM_292942.2
GI_37547335-S	98.4	108.9	97.4	KIAA1679	XM_046570.4
GI_37547337-S	416.7	632.6	522.2	LOC150498	XM_086931.5
GI_37547343-S	132.3	131.1	124.6	PGR6	XM_293092.2
GI_37547347-S	2296.8	3421.6	3058.2	LOC129439	XM_065237.5
GI_37547351-S	91.1	97.8	91.7	LOC376957	XM_352480.1
GI_37547365-S	138	173.4	150.7	LOC376963	XM_352484.1
GI_37547393-S	93.5	123.7	112.3	LOC339760	XM_295058.2
GI_37547395-S	87.8	83.4	80.8	LOC375267	XM_353295.1
GI_37547399-S	110.4	108	99.2	LOC375268	XM_353296.1
GI_37547401-S	116.8	101.5	101.6	LOC375269	XM_351489.1
GI_37547404-S	115.3	137.6	121.1	LOC375270	XM_351490.1
GI_37547418-S	160.4	204.7	196.1	LOC339761	XM_291005.2
GI_37547420-S	178.4	207	182.3	LOC376946	XM_352476.1
GI_37547422-S	209.9	229.9	204.7	LOC285101	XM_210411.3
GI_37547468-S	349.3	303.1	294.5	FLJ37034	XM_352945.1
GI_37547470-S	150.4	151.5	146.2	LOC375314	XM_351522.1
GI_37547472-S	100.7	118.9	105.3	LOC339766	XM_291007.2
GI_37547476-S	116.8	109.7	103.6	LOC375315	XM_353311.1
GI_37547484-S	167.9	177.3	179.1	LOC151174	XM_351524.1
GI_37547486-S	198.4	206.9	179.1	LOC151507	XM_087225.3
GI_37547488-S	141.9	171	153.9	LOC339767	XM_292989.3
GI_37547492-S	128.7	142.4	121.5	LOC377008	XM_352497.1
GI_37547499-S	93.7	97.8	104.2	LOC375037	XM_351307.1
GI_37547503-S	119.5	143.1	145.5	KIAA2025	XM_086409.5
GI_37547505-S	425	494.2	453.7	TNN	XM_040527.5
GI_37547507-S	108.1	112.2	116.6	LOC375038	XM_353221.1
GI_37547509-S	346	434.7	388.6	ASTN	XM_045113.3
GI_37547514-S	95.7	108	92	LOC375041	XM_353222.1
GI_37547516-S	112.5	124.6	113.9	LOC376675	XM_352330.1
GI_37547518-S	444.4	410.9	332.5	LOC376679	XM_352331.1
GI_37547520-S	89.5	99.3	86.7	LOC376681	XM_352332.1
GI_37547528-S	129.6	147.8	140.4	LOC376686	XM_352333.1
GI_37547539-S	928.1	929.9	812.2	KIDINS220	XM_291015.2
GI_37547541-S	171.2	231	197.3	LOC375183	XM_353277.1

GI_37547937-S	115.2	117.3	111.1	LOC374967	XM_353200.1				
GI_37547939-S	93	90.7	83.3	LOC149086	XM_097580.3				
GI_37548017-S	141.5	177.4	150.4	LOC127550	XM_060537.8				
GI_37548193-S	101.6	105.9	100.8	LOC90719	XM_033704.3				
GI_37548194-S	158.2	168.8	173.7	LOC376587	XM_352301.1				
GI_37548197-S	132.3	158.8	161	LOC374942	XM_353193.1				
GI_37548199-S	130.2	128.1	131.3	LOC376563	XM_352290.1				
GI_37548317-S	91	81.5	81.5	LOC126772	XM_060171.3				
GI_37548519-S	80.9	90.9	84.3	LOC347813	XM_351322.1				
GI_37548521-S	103.3	112.1	100.2	LOC127602	XM_059166.6				
GI_37548529-S	217.9	247.8	223.3	KIAA1639	XM_290923.2				
GI_37548531-S	291.1	269	287	LOC149603	XM_047499.5				
GI_37548535-S	266.6	315.8	272.1	LOC375059	XM_353228.1				
GI_37548537-S	117.7	129.5	117.1	LOC376711	XM_352343.1				
GI_37548547-S	167.6	188.1	167.4	LOC376716	XM_352345.1				
GI_37548549-S	189.9	235	195.8	LOC376718	XM_352346.1				
GI_37548551-S	489.5	511.9	419.9	LOC343363	XM_291533.2				
GI_37548608-S	106.3	116.3	102.8	LOC374960	XM_351241.1				
GI_37548610-S	152.8	184.1	155.2	LOC254897	XM_170950.2				
GI_37548613-S	103.9	95.9	92.8	KIF17	XM_027915.8	KIF3X;KIF17B;KIAA1405	ATP	microtubul	intracellula
GI_37548619-S	275	329.6	304.9	LOC127309	XM_059132.3				
GI_37548623-S	107	114.3	99.8	LOC376578	XM_352297.1				
GI_37548625-S	100.8	112.4	104	LOC163933	XM_089243.7				
GI_37548627-S	91.8	99.8	93.5	LOC343381	XM_291543.2				
GI_37548628-S	2580.7	4244.8	3603.6	LOC343384	XM_291544.2				
GI_37548655-S	334.2	507	323.8	DKFZP586L1	XM_034000.6				
GI_37548657-S	150.7	190.7	194.7	LOC149297	XM_097622.6				
GI_37548660-S	106.2	119.1	110.5	LOC92235	XM_043739.3				
GI_37548664-S	103	105.8	103.3	LOC375036	XM_353220.1				
GI_37548666-S	95.6	102.5	91.1	LOC149281	XM_089281.2				
GI_37548754-S	293.3	353.3	294.4	LOC375042	XM_351309.1				
GI_37548756-S	122	134.6	120.6	LOC375043	XM_353223.1				
GI_37548758-S	94.5	87.2	87.2	LOC343450	XM_291574.2				
GI_37548762-S	437.1	453.3	515.8	LOC375044	XM_351311.1				
GI_37548764-S	99.6	87.8	102.4	LOC375045	XM_353224.1				
GI_37548766-S	352	423.9	400.1	LOC375046	XM_351313.1				
GI_37548772-S	233.6	249.8	227.2	LOC375049	XM_351316.1				
GI_37548774-S	326.5	445.4	345.1	PPFIA4	XM_046751.4				
GI_37548778-S	94.8	86.9	96.8	LOC164036	XM_089307.4				
GI_37548786-S	95.2	87.3	85.1	LOC339521	XM_291577.2				
GI_37548898-S	98.7	106.7	101.1	LOC343466	XM_291580.2				
GI_37548900-S	243.8	296.5	261.7	LOC343472	XM_291583.3				
GI_37549240-S	98.1	118.3	95.5	LOC374295	XM_352938.1				
GI_37549242-S	99.3	93.2	114.8	LOC148766	XM_086308.2				

GI_37549244-S	200.3	244.7	220.4	LOC375008	XM_353212.1				
GI_37549246-S	1331.9	5516.5	2401	PTGFRN	XM_040709.4	FPRP;EWI-F;CD9P-1;SMAP-	protein	integral to	negative
GI_37549250-S	107.5	100.2	90.7	LOC343505	XM_291607.3				
GI_37549297-S	273.7	228.1	278.7	DOCK10	XM_352946.1				
GI_37549303-S	172.8	194.8	159.7	DKFZP434D1	XM_114297.4				
GI_37549309-S	237.1	300.6	287.7	LOC375291	XM_351505.1				
GI_37549311-S	139	124.5	114.2	LOC129881	XM_059384.7				
GI_37549314-S	88.8	94.4	87.3	LOC375292	XM_351506.1				
GI_37549316-S	290.8	204.9	218.7	LOC375293	XM_353303.1				
GI_37549324-S	99.6	118.9	99.2	LOC375296	XM_351507.1				
GI_37549326-S	324.4	395.3	344.6	LOC375297	XM_351508.1				
GI_37549328-S	97.2	101.2	101	LOC375298	XM_353305.1				
GI_37549330-S	127.4	129.7	118	LOC151242	XM_087137.5				
GI_37549332-S	166.5	203.7	172.5	LOC375299	XM_351509.1				
GI_37549338-S	647.3	803.1	509.4	MYO1B	XM_290989.2	myr1	actin	myosin	
GI_37549340-S	92.2	90.4	86.7	LOC375300	XM_353306.1				
GI_37549342-S	1489.4	1576.1	1192.7	KIAA1265	XM_047707.5				
GI_37549344-S	120.3	127.6	119.2	LOC375301	XM_351511.1				
GI_37549346-S	100.9	102.3	96.7	LOC375302	XM_353307.1				
GI_37549350-S	187.9	227	196.4	FLJ39061	XM_092342.4				
GI_37549357-S	91	89	93.4	LOC375303	XM_351512.1				
GI_37549373-S	110.9	118.4	101.6	IHH	XM_050846.5				
GI_37549375-S	114.6	116.3	116.5	LOC375308	XM_351515.1				
GI_37549379-S	127	142.4	122.2	LOC375309	XM_351516.1				
GI_37549381-S	131.3	182.8	215	LOC130612	XM_059461.6				
GI_37549382-S	212.7	205.9	248.4	KIAA0657	XM_051017.3				
GI_37549388-S	112.9	112.2	97.7	LOC375311	XM_353310.1				
GI_37549390-S	91.2	82.9	86.1	LOC375312	XM_351519.1				
GI_37549392-S	126.3	134.5	114.6	LOC375313	XM_351520.1				
GI_37549394-S	104.8	113.4	97.1	LOC344332	XM_293018.2				
GI_37549396-S	3196.2	3880.9	3059.7	LOC376965	XM_352485.1				
GI_37549400-S	396.7	651	509.2	LOC344178	XM_292963.2				
GI_37549404-S	106.3	108	110.1	LOC376970	XM_352486.1				
GI_37549409-S	106.5	111.3	113.8	LOC344191	XM_292968.2				
GI_37549413-S	133.6	215.5	153.2	LOC150739	XM_092267.2				
GI_37549417-S	104.9	115.6	96.1	LOC376975	XM_352487.1				
GI_37549445-S	102.2	116.5	102.9	LOC130429	XM_065722.2				
GI_37549449-S	166.7	154.2	160.1	LOC200595	XM_115769.2				
GI_37549451-S	144.4	159	134.6	LOC376992	XM_352490.1				
GI_37549455-S	121.5	122.5	132.7	KIAA1399	XM_046685.7				
GI_37549460-S	107.5	101.2	97.8	LOC130600	XM_065796.2				
GI_37549466-S	99.2	129.8	109.4	LOC377005	XM_352494.1				
GI_37549470-S	150.7	128.2	153.4	FLJ10157	XM_352939.1				
GI_37549482-S	98.9	105.4	101.6	LOC375066	XM_353231.1				

GI_37549488-S	261.9	322.6	266.2	LOC339529	XM_294993.2				
GI_37549490-S	87.3	82.3	91.6	LOC343484	XM_295598.2				
GI_37549492-S	102.2	97.1	115.7	LOC200159	XM_114129.3				
GI_37549498-S	106.7	118.9	101.3	LOC376727	XM_352348.1				
GI_37549504-S	108.7	112.9	116.7	LOC376735	XM_352349.1				
GI_37549519-S	117	147.6	146.6	LOC126755	XM_059074.2				
GI_37549523-S	128.7	136.3	115.4	LOC374952	XM_351232.1				
GI_37549525-S	128.2	150.7	134.4	KIAA1937	XM_057107.4				
GI_37549529-S	260.7	302.9	281.8	LOC374953	XM_351233.1				
GI_37549531-S	22129.8	20418	16759	LOC374954	XM_351234.1				
GI_37549535-S	101.2	117.7	106.5	KIAA1026	XM_048825.8				
GI_37549539-S	137.1	152	166.7	KIAA0842	XM_290944.2				
GI_37549550-S	248.5	305.6	268.9	LOC285192	XM_351525.1				
GI_37549554-S	109.2	113.5	97.8	LOC285188	XM_209505.2				
GI_37549556-S	129.8	173.8	175.8	FLJ00133	XM_059482.6				
GI_37549558-S	248.2	344.2	271.9	LOC344525	XM_297687.3				
GI_37549560-S	250.7	278.5	262.6	LOC375319	XM_353313.1				
GI_37549566-S	118.3	130.4	130.7	LOC150681	XM_092241.7				
GI_37549568-S	134.8	153.3	131	LOC377010	XM_352499.1				
GI_37549570-S	160.1	210	179.3	LOC377011	XM_352500.1				
GI_37549572-S	90.7	80.1	87	LOC377012	XM_352501.1				
GI_37549574-S	75.8	70.2	80.9	LOC377013	XM_352502.1				
GI_37549590-S	140.8	162.1	159.5	LOC374931	XM_353188.1				
GI_37549609-S	145.2	172.7	143.3	LOC374936	XM_351223.1				
GI_37549618-S	122.5	139	139.1	LOC339453	XM_294960.2				
GI_37549620-S	122.8	140.4	124.5	LOC376558	XM_352287.1				
GI_37549625-S	154.7	179.8	145.3	LOC343531	XM_291627.2				
GI_37549631-S	129.9	142.4	138.6	KIAA1922	XM_057040.2				
GI_37549642-S	84.1	91	85.1	LOC376645	XM_352317.1				
GI_37549647-S	74	73.9	78.2	LOC375019	XM_353215.1				
GI_37549664-S	166.1	202.2	198.9	MGC34132	XM_291029.3				
GI_37549667-S	99.7	105.8	96.3	GRSP1	XM_114303.2				
GI_37549669-S	381.4	678	413.6	LOC375351	XM_351558.1				
GI_37549671-S	102.4	116.2	103.3	SEMACAP3	XM_041363.10				
GI_37549673-S	102.2	114.2	101.1	CNTN3	XM_039627.8				
GI_37549679-S	104	100.2	104.3	LOC376748	XM_352361.1				
GI_37549681-S	432.2	512.1	371.7	LOC285296	XM_208312.2				
GI_37549687-S	85.1	102.5	87	ROBO2	XM_031246.8				
GI_37549691-S	83.2	86.4	73.5	LOC375357	XM_351563.1				
GI_37549693-S	99.2	95.2	98.9	LOC344709	XM_298233.3				
GI_37549705-S	101.6	83.5	92.5	LOC377065	XM_352519.1				
GI_37549711-S	133.7	139	120.9	LOC339495	XM_290926.2				
GI_37549742-S	117.8	128.5	130.3	LOC375029	XM_351299.1				
GI_37549744-S	275.6	298	268.7	ATP8B2	XM_290875.2	ATPID;KIAA1137;DKFZp434M0219	magnesiu	integral to	cation

GI_37549750-S	88	88.2	87	KIAA0446	XM_044155.2		transporte	mitochond	transport
GI_37549754-S	160.1	173.6	153.9	LOC375033	XM_351303.1				
GI_37549760-S	225.6	465.2	150.7	VANGL2	XM_049695.5				
GI_37549762-S	109.1	108.8	112.1	LOC257177	XM_170909.2				
GI_37549764-S	382.9	464.6	413.7	LOC343052	XM_295309.2				
GI_37549769-S	367.9	465.2	367.9	LOC92312	XM_044166.6				
GI_37549771-S	201.9	249.7	204.6	LOC164118	XM_089384.7				
GI_37549775-S	111.2	123.6	122.8	LOC128360	XM_060945.2				
GI_37549777-S	118.6	127.8	115.3	LOC343406	XM_291548.2				
GI_37549779-S	151.2	175.6	164	LOC376663	XM_352327.1				
GI_37549781-S	162.2	191.2	179.3	LOC128366	XM_060951.3				
GI_37549785-S	152.6	178.6	175.7	LOC128370	XM_060955.3				
GI_37549793-S	101.6	99.8	97.3	LOC127385	XM_060458.4				
GI_37549795-S	131.2	165.5	161.2	LOC339511	XM_291568.2				
GI_37549797-S	93.2	95.3	101	LOC343413	XM_291569.2				
GI_37549799-S	233.5	283.5	251.4	LOC376666	XM_352329.1				
GI_37549804-S	96.7	101.4	98.2	LOC376699	XM_352336.1				
GI_37549827-S	1184.9	938.6	858.4	LOC376751	XM_352363.1				
GI_37549837-S	226.1	259.3	226.4	LOC376752	XM_352364.1				
GI_37549839-S	94.8	111.6	88.9	LOC376753	XM_352365.1				
GI_37549841-S	145.8	167.4	141	LOC376754	XM_352366.1				
GI_37549862-S	91.4	99.3	98.3	LOC376764	XM_352375.1				
GI_37549867-S	100.9	110.5	110.3	KIAA1909	XM_291137.2	FLJ43173			
GI_37549871-S	88.2	101.4	86.8	LOC375430	XM_351603.1				
GI_37549873-S	520.7	625.1	528.8	LOC375431	XM_353364.1				
GI_37549875-S	99.7	110.8	106.3	LOC375432	XM_353365.1				
GI_37549879-S	116.4	112.2	121.1	LOC375435	XM_353367.1				
GI_37549884-S	114.7	105.6	119.1	LOC340094	XM_295155.2				
GI_37549886-S	2089.4	1847.3	1855	KIAA0947	XM_029101.6				
GI_37549888-S	113.6	129.7	125.2	LOC134111	XM_059689.3				
GI_37549894-S	113.5	115	96.8	LOC375438	XM_353369.1				
GI_37549896-S	106.3	107.4	91.5	LOC377233	XM_352571.1				
GI_37549900-S	122.6	127.3	127	LOC340024	XM_291120.3				
GI_37549904-S	91.4	101.6	92.1	LOC345711	XM_293937.3				
GI_37549908-S	102	99.3	103	LOC340096	XM_293943.2				
GI_37549910-S	184.8	229.9	212.5	LOC348938	XM_351632.1				
GI_37549912-S	115.6	109.7	104	LOC375478	XM_351633.1				
GI_37549914-S	79.3	98.2	86.7	KIAA1935	XM_087672.2				
GI_37549920-S	144.2	166.3	149	LOC285588	XM_209668.2				
GI_37549924-S	103.3	106.8	98.7	LOC375480	XM_353389.1				
GI_37549926-S	202.5	226.8	222.5	LOC375481	XM_353390.1				
GI_37549928-S	107.4	107.7	120.4	LOC375482	XM_351635.1				
GI_37549934-S	106.9	117.4	104.5	KIAA1976	XM_030300.5				
GI_37549941-S	109.9	106.6	99.5	LOC134541	XM_068903.3				

GI_37549943-S	92.5	89.5	90	LOC345630	XM_293903.2
GI_37549949-S	100.3	100.1	95.7	LOC377323	XM_352593.1
GI_37549951-S	161.6	181.4	173.2	LOC377324	XM_352594.1
GI_37549957-S	172.5	192.8	180.4	LOC375458	XM_353375.1
GI_37549959-S	2363.5	2891.1	2265.7	LOC375459	XM_351625.1
GI_37549971-S	355.5	367.8	302.6	KIAA1311	XM_291128.2
GI_37549973-S	106.1	97.6	99.8	LOC375475	XM_351631.1
GI_37549975-S	167.7	223.8	199.4	LOC340075	XM_291139.2
GI_37549977-S	149.8	177.2	152.2	LOC375476	XM_353387.1
GI_37549979-S	145	162.6	141.2	LOC375477	XM_353388.1
GI_37549985-S	130.4	129.6	134.5	KIAA1317	XM_098368.4
GI_37549991-S	97.8	126.4	119.9	LOC345611	XM_293893.2
GI_37549993-S	256.6	287.9	265.8	LOC377315	XM_352590.1
GI_37549999-S	113.9	115.9	108	LOC375322	XM_353316.1
GI_37550005-S	151.7	150	144	LOC375325	XM_353318.1
GI_37550007-S	628	817.8	966.4	KIAA0121	XM_052386.3
GI_37550009-S	143.5	185.4	140.7	TIP120B	XM_351535.1
GI_37550011-S	121.3	115.2	103.4	KIAA1719	XM_042936.4
GI_37550015-S	896.7	799.9	628.6	KIAA0379	XM_042860.8
GI_37550019-S	110	128.6	121.9	LOC375328	XM_351538.1
GI_37550023-S	105.4	103.8	108.4	LOC375329	XM_351539.1
GI_37550025-S	136.5	152	133.2	LOC131405	XM_067369.3
GI_37550027-S	185.3	203.4	185.2	LOC375330	XM_353319.1
GI_37550029-S	123.9	126.9	109	KIAA0527	XM_171054.2
GI_37550031-S	296.8	251.5	310.2	CLASP2	XM_291057.3
GI_37550035-S	93.3	93.3	92.3	KIAA1765	XM_047355.6
GI_37550037-S	197.2	251.3	225.8	KIAA0342	XM_047357.4
GI_37550039-S	143.7	158.4	151.8	LOC375332	XM_351541.1
GI_37550041-S	93.4	94.1	93.3	LOC375333	XM_351542.1
GI_37550045-S	265.2	313.8	275.1	MGC50836	XM_171060.4
GI_37550049-S	179.3	211.3	222.8	DKFZp434E1	XM_043624.5
GI_37550053-S	95.5	94.6	92.3	LOC339903	XM_291063.2
GI_37550054-S	90.3	103.4	115.2	LOC375337	XM_351544.1
GI_37550058-S	105.5	125.5	114.8	LOC285346	XM_209579.2
GI_37550069-S	1075.1	1524.2	1391.8	LOC375340	XM_351549.1
GI_37550075-S	104	119.2	115.9	LOC375342	XM_351551.1
GI_37550079-S	176.3	214.9	185	LOC375344	XM_353321.1
GI_37550081-S	126.6	139.7	125.4	LOC375345	XM_351553.1
GI_37550095-S	96.1	81.8	81.7	LOC132203	XM_059578.4
GI_37550101-S	123.4	132.1	128.9	LOC377024	XM_352507.1
GI_37550107-S	90.5	97.2	79.6	LOC377026	XM_352508.1
GI_37550109-S	142.2	166	137	LOC377027	XM_352509.1
GI_37550111-S	118	141	133.9	LOC377028	XM_352510.1
GI_37550121-S	95.2	84.4	94.4	LOC131572	XM_067448.2

GI_37550123-S	95.6	84.2	94.8	LOC339896	XM_291059.2
GI_37550133-S	98.9	90.3	88.9	LOC344682	XM_293542.3
GI_37550135-S	145.9	156.2	164.7	LOC377047	XM_352512.1
GI_37550137-S	104.2	114.6	108.9	LOC377050	XM_352513.1
GI_37550139-S	118.7	137.5	135.9	LOC285405	XM_210576.3
GI_37550143-S	5599.5	7440.9	6150	LOC131691	XM_067503.2
GI_37550145-S	117.6	119.1	115.5	LOC377053	XM_352514.1
GI_37550151-S	104.1	106	112.3	LOC377055	XM_352516.1
GI_37550155-S	221.2	246	184.9	LOC375460	XM_351626.1
GI_37550164-S	104.8	120.3	123.1	LOC255338	XM_171105.5
GI_37550176-S	128.8	211.9	150.5	KIAA1281	XM_114432.5
GI_37550177-S	170.8	215.7	203	LOC153274	XM_087642.2
GI_37550181-S	223.7	247.4	225.9	LOC375465	XM_351628.1
GI_37550185-S	152.5	171.3	147.4	LOC375467	XM_353380.1
GI_37550187-S	338.8	278.6	220.3	LOC375468	XM_351629.1
GI_37550189-S	169.5	120.9	114.2	8-Sep	XM_034872.7
GI_37550191-S	208.6	302.7	259.8	SEC24A	XM_094581.4
GI_37550193-S	110.8	114.4	103	LOC375469	XM_353381.1
GI_37550195-S	240.4	267	235.2	LOC375470	XM_353382.1
GI_37550197-S	140.9	171	171.7	LOC375471	XM_353383.1
GI_37550199-S	101	112.7	110.2	LOC375472	XM_353384.1
GI_37550208-S	170.5	191.2	188	LOC345754	XM_293958.2
GI_37550226-S	875.8	1072.7	731	LOC377296	XM_352588.1
GI_37550230-S	196.3	232.2	212.3	PRDM6	XM_049619.6
GI_37550242-S	102.8	89.5	88.5	LOC255812	XM_171032.4
GI_37550246-S	451.4	495.8	533	KIAA0794	XM_087353.6
GI_37550254-S	2132	1678.5	2183.2	KIAA0226	XM_032901.6
GI_37550260-S	93.1	92.1	82.6	LOC285253	XM_210543.4
GI_37550262-S	178.6	173.1	185	LOC200933	XM_117294.5
GI_37550263-S	256.6	306.5	266.6	LOC377129	XM_352540.1
GI_37550266-S	159.6	175.3	178	LOC285280	XM_209550.3
GI_37550268-S	133.4	144.5	133	LOC285303	XM_209559.2
GI_37550274-S	97.4	128.5	116.9	LOC345643	XM_293918.2
GI_37550278-S	235.8	275.8	293.7	MAP3K1	XM_042066.8
GI_37550282-S	156.8	158.3	136.2	KIAA1577	XM_035299.3
GI_37550284-S	211.4	276.6	243.7	LOC133995	XM_059682.2
GI_37550302-S	97.3	96.7	95.8	LOC377256	XM_352576.1
GI_37550304-S	773.1	919.2	822.6	LOC345645	XM_293923.2
GI_37550312-S	116.7	135.8	106.9	LOC377262	XM_352578.1
GI_37550314-S	135.4	146.3	120.8	LOC345659	XM_293927.2
GI_37550322-S	128.7	138.9	129.5	LOC374299	XM_352960.1
GI_37550328-S	92.4	93.4	109.3	LOC375439	XM_351606.1
GI_37550334-S	187.3	235.6	226.7	LOC375442	XM_353370.1
GI_37550336-S	120.2	136.7	116.5	LOC345557	XM_293875.2

GI_37550343-S	169.3	193.1	182.6	LOC375445	XM_353371.1	
GI_37550351-S	127.7	144.3	126.2	KIAA1999	XM_114447.5	
GI_37550356-S	1600.8	695.3	682.7	RGNEF	XM_352962.1	
GI_37550358-S	269.4	227.6	230.7	LOC115548	XM_291142.3	
GI_37550361-S	104.5	106.6	86.5	KIAA0888	XM_032571.3	
GI_37550363-S	94.4	90.6	91.5	FLJ40191	XM_293911.2	
GI_37550371-S	132.3	140.3	132.8	LOC375457	XM_353374.1	
GI_37550377-S	106.3	120.7	120.5	LOC116068	XM_351624.1	
GI_37550379-S	82.7	81.3	80	LOC377271	XM_352582.1	
GI_37550381-S	102.3	109.9	100.7	LOC377272	XM_352583.1	
GI_37550389-S	151.8	151.2	145.9	LOC377277	XM_352584.1	
GI_37550391-S	112.5	138.3	124.6	LOC345778	XM_293971.2	
GI_37550393-S	2280.5	2843.5	2275.5	LOC134478	XM_068864.5	
GI_37550395-S	113	150.1	147.7	LOC167555	XM_094565.4	
GI_37550397-S	149.8	164.9	153.2	LOC340120	XM_293976.3	
GI_37550399-S	121	120.3	101.4	LOC377283	XM_352585.1	
GI_37550406-S	99.7	115.3	125.1	LOC345462	XM_293828.2	
GI_37550409-S	187.5	245.7	224.9	LOC285679	XM_209719.3	
GI_37550411-S	112.9	113	101.8	LOC375485	XM_351644.1	
GI_37550419-S	175.6	212.1	182.3	LOC285647	XM_209700.4	
GI_37550421-S	90.1	102.6	86.7	N4BP3	XM_038920.6	
GI_37550426-S	196.1	239.6	210.7	LOC134082	XM_068681.4	
GI_37550428-S	106	104.5	99.7	LOC134083	XM_068682.4	
GI_37550430-S	107.6	103.9	98.5	LOC377336	XM_352598.1	
GI_37550436-S	144.1	174.2	150.2	LOC285659	XM_210637.3	
GI_37550443-S	141.2	159	137.4	LOC377266	XM_352579.1	
GI_37550457-S	100.3	101.3	96.2	LOC253220	XM_172831.2	
GI_37550459-S	116.5	100.2	98	LOC374329	XM_352983.1	
GI_37550463-S	117	128.5	124.5	LOC170370	XM_096317.7	
GI_37550467-S	299.9	360.8	326.7	DRG11	XM_060970.9	
GI_37550469-S	81.3	81.3	78.3	KIAA1768	XM_113594.2	
GI_37550480-S	132.5	160.3	134.8	LOC374364	XM_352997.1	
GI_37550482-S	162.8	164.4	132.6	KIAA1674	XM_290462.3	
GI_37550488-S	654.9	530.3	531.7	MGC11349	XM_352951.1	FLJ13861
GI_37550494-S	122.3	131.6	128.5	LOC255025	XM_173083.4	
GI_37550501-S	94.5	98.4	97.2	LOC344595	XM_298151.2	
GI_37550503-S	165.6	174.6	192.4	KIAA1000	XM_036988.9	
GI_37550507-S	120.6	126.2	140.3	TMPRSS7	XM_293599.3	
GI_37550509-S	102.7	104.3	113.7	LOC285335	XM_210562.3	
GI_37550513-S	100.1	106.8	94.2	AAT1	XM_291086.2	
GI_37550514-S	168	160.8	177.3	LOC375362	XM_353325.1	
GI_37550516-S	88.2	97.8	92.7	LOC116064	XM_057296.2	
GI_37550518-S	97.3	105.2	104.3	KIAA1006	XM_045911.7	
GI_37550520-S	617	528.3	529.7	LOC131076	XM_059492.5	

GI_37550522-S	149.1	158.9	139.7	SEMA5B	XM_032249.5	SemG;SEMAG;FLJ10372;KIAA1445	receptor	membran	developm
GI_37550526-S	925.9	2399.8	1004.6	KIAA1237	XM_087386.5				
GI_37550530-S	104.5	123.6	116.6	LOC375363	XM_353326.1				
GI_37550532-S	178.5	252.1	193.2	LOC200810	XM_114301.4				
GI_37550534-S	294.4	314.9	352.8	TRXR3	XM_051264.11				
GI_37550536-S	250.6	246.7	243.5	LOC339122	XM_290714.2				
GI_37550538-S	300.1	325.8	262.1	KIAA0779	XM_098229.9				
GI_37550539-S	127.5	147.8	146.2	LOC285407	XM_209597.3				
GI_37550540-S	93.4	93.7	81.7	LOC339944	XM_291088.3				
GI_37550544-S	108.4	133.3	122.8	LOC375365	XM_353328.1				
GI_37550550-S	230.4	289.4	252.9	CHR3SYT	XM_291067.2				
GI_37550552-S	232.7	263.7	254.1	LOC375366	XM_353329.1				
GI_37550554-S	612.3	565	449.6	FLJ35036	XM_172341.3				
GI_37550558-S	1247.3	880.8	859.7	SR140	XM_031553.8				
GI_37550560-S	114.6	141.3	132	LOC375367	XM_353330.1				
GI_37550566-S	104	104.9	95.1	LOC375370	XM_351569.1				
GI_37550568-S	168.8	183.8	152.5	LOC339899	XM_295096.2				
GI_37550573-S	132.5	136.7	132.5	LOC375371	XM_353332.1				
GI_37550577-S	115	117.4	111.5	LOC375373	XM_353334.1				
GI_37550579-S	112.4	111.1	104.6	LOC375374	XM_353335.1				
GI_37550581-S	118	117.6	103.7	LOC344752	XM_293577.2				
GI_37550583-S	101.2	101	92.2	PGR10	XM_293580.2				
GI_37550591-S	108.2	116.6	114.8	LOC375377	XM_351571.1				
GI_37550593-S	369	364.6	322.6	LOC375378	XM_353337.1				
GI_37550598-S	99.6	94.3	96	LOC344657	XM_293529.2				
GI_37550600-S	115.2	114.6	109.6	KIAA1613	XM_035946.7				
GI_37550602-S	15942.7	11084	7777.9	LOC200916	XM_114317.6				
GI_37550603-S	95.4	107.4	99.8	LOC375380	XM_351572.1				
GI_37550607-S	94	85.4	82.1	DKFZp434A1	XM_291028.2				
GI_37550609-S	603.8	627.5	539.9	ATP11B	XM_087254.3				
GI_37550613-S	148.3	152.7	138.1	LOC285248	XM_211816.3				
GI_37550615-S	176.6	211.9	193.2	LOC375383	XM_353338.1				
GI_37550623-S	115	122.3	124.8	DKFZp761I10	XM_039929.9				
GI_37550627-S	86.9	88.4	80.9	LOC254808	XM_353341.1				
GI_37550629-S	170.6	173.4	148.3	LOC200959	XM_116036.4				
GI_37550631-S	75.3	87.9	91.9	LOC377070	XM_352521.1				
GI_37550637-S	99.3	103.4	100	LOC377072	XM_352522.1				
GI_37550647-S	149.7	170.1	140.9	LOC377077	XM_352525.1				
GI_37550657-S	95.9	98.9	80.1	LOC377083	XM_352528.1				
GI_37550663-S	465.7	586.9	506.2	LOC166348	XM_093813.5				
GI_37550669-S	154.3	174	162.9	LOC131873	XM_067585.8				
GI_37550673-S	176.8	231	207.5	LOC377094	XM_352531.1				
GI_37550681-S	121.2	99.2	100.8	LOC377102	XM_352533.1				
GI_37550687-S	98	86.7	88.1	LOC344760	XM_293581.2				

GI_37550691-S	179.7	191.1	179	LOC90133	XM_029323.3
GI_37550693-S	103.8	104.1	105.6	LOC131149	XM_067228.6
GI_37550711-S	101.9	115.1	107.2	LOC90113	XM_291077.2
GI_37550713-S	92.8	100.5	88.7	LOC377120	XM_352537.1
GI_37550722-S	109.1	119.4	94.9	LOC377124	XM_352539.1
GI_37550724-S	304.8	380.7	337.5	LOC285388	XM_208316.2
GI_37550761-S	221.3	288.5	261.5	FLJ22529	XM_352890.1
GI_37550763-S	98.2	103.4	101.1	LOC374340	XM_350795.1
GI_37550765-S	146.2	156.9	138.6	PLAC9	XM_166090.4
GI_37550766-S	245.7	298.6	264.5	NRG3	XM_166086.4
GI_37550771-S	76.1	88.6	89.4	KIAA1975	XM_208476.2
GI_37550777-S	81.9	83.5	80.5	LOC374344	XM_350798.1
GI_37550779-S	145.1	153.8	150.9	LOC374345	XM_352989.1
GI_37550783-S	104.8	117.6	103.9	KIAA0608	XM_051081.9
GI_37550785-S	89.9	89.1	79	LOC374347	XM_352990.1
GI_37550787-S	82.4	84.1	77.1	LOC142827	XM_084357.2
GI_37550789-S	111.8	91	100.9	LOC374348	XM_352991.1
GI_37550791-S	94.7	92	92.3	LOC374349	XM_350800.1
GI_37550793-S	25033.6	24444	19009	LOC374351	XM_350801.1
GI_37550797-S	311.4	332.8	306	LOC90271	XM_030445.6
GI_37550803-S	340.7	357	410.6	MGC11279	XM_350802.1
GI_37550805-S	292.5	385.9	309.3	LOC90470	XM_031975.5
GI_37550816-S	97.7	94.5	116.5	LOC374353	XM_352993.1
GI_37550830-S	213.3	222.5	220.6	LOC119548	XM_058404.4
GI_37550831-S	326.6	236.3	192.8	HSPA12A	XM_048898.5
GI_37550839-S	182.8	219.3	222.9	LOC196051	XM_113641.3
GI_37550842-S	434.5	520.3	493.3	LOC374359	XM_352996.1
GI_37550844-S	150.6	161.4	148.2	LOC375914	XM_351980.1
GI_37550861-S	105.5	115.6	107.9	LOC340749	XM_291698.2
GI_37550868-S	89.1	111.5	94.8	LOC118934	XM_061222.3
GI_37550870-S	101.5	105.3	95.8	LOC340654	XM_291663.2
GI_37550872-S	926.6	1429.5	1088.5	LOC375930	XM_351988.1
GI_37550874-S	119.1	121.4	115.9	LOC375931	XM_351989.1
GI_37550882-S	240.7	375	322.7	LOC375936	XM_351991.1
GI_37550888-S	102.8	103	95.4	LOC375939	XM_351994.1
GI_37550959-S	127	151.7	127.5	LOC283029	XM_210856.2
GI_37550961-S	112.6	126.3	111	LOC283034	XM_210860.2
GI_37550963-S	97.9	98.5	96	LOC374319	XM_352980.1
GI_37550967-S	1545	1229.9	1363.3	LOC374320	XM_350780.1
GI_37550975-S	165.5	189.5	182	LOC375887	XM_351971.1
GI_37550984-S	115.6	115.9	103.9	LOC374360	XM_350808.1
GI_37550986-S	80.7	97.7	88.6	LOC374361	XM_350809.1
GI_37550988-S	212.8	257.5	246.5	FLJ32938	XM_061055.8
GI_37551001-S	235.7	278.5	217.4	LOC253436	XM_172825.5

GI_37551003-S	78	81.1	69.5	LOC340784	XM_291716.3		
GI_37551007-S	107.4	80.9	92.8	LOC375941	XM_351996.1		
GI_37551009-S	106.8	107.4	102.9	LOC119587	XM_058409.5	carboxype	proteolysis
GI_37551016-S	110.6	112.2	110.9	KIAA0217	XM_040265.6		
GI_37551018-S	90.5	92.9	82.7	LOC374305	XM_350772.1		
GI_37551027-S	191.1	225.2	215.8	DKFZP434N1	XM_166138.5		
GI_37551029-S	2137	2246.4	2140.9	LOC221061	XM_167709.2		
GI_37551030-S	89.5	95.4	99	ITGA8	XM_167711.2		
GI_37551032-S	90.1	101.1	86	ST8SIA-VI	XM_291725.2		
GI_37551034-S	100.3	107	97.3	LOC340843	XM_291726.2		
GI_37551040-S	114.8	121.7	123	TAF3	XM_291729.2		
GI_37551046-S	130.4	127.2	139.4	LOC375861	XM_351961.1		
GI_37551048-S	105.8	107.6	102.8	LOC375863	XM_351962.1		
GI_37551050-S	145.9	163.1	161	LOC375866	XM_351963.1		
GI_37551060-S	86.6	106	86.3	LOC375946	XM_351999.1		
GI_37551086-S	243.4	272.1	220.5	DKFZp451A1	XM_352963.1		
GI_37551090-S	108.1	104.8	107.8	LOC375520	XM_351667.1		
GI_37551092-S	254.8	311.8	288.5	LOC375521	XM_351668.1		
GI_37551094-S	105.4	121.4	112.4	LOC375522	XM_353403.1		
GI_37551096-S	136.5	125.5	129.7	LOC375523	XM_351669.1		
GI_37551098-S	762.6	726.1	465.8	AIM1	XM_166300.2		
GI_37551106-S	127.6	147.2	128.6	LOC221261	XM_168053.4		
GI_37551107-S	115.7	111.2	106.8	LOC221262	XM_168055.3		
GI_37551109-S	97.4	108.5	88.3	LOC375525	XM_353405.1		
GI_37551122-S	101.9	95.9	89.7	LOC375527	XM_351671.1		
GI_37551124-S	203.5	173.9	135.4	LOC375528	XM_351672.1		
GI_37551126-S	105.9	98.2	99.7	LOC375529	XM_351673.1		
GI_37551128-S	127.3	134.5	122.4	LOC375530	XM_351674.1		
GI_37551130-S	236.6	296.8	225.9	KIAA1798	XM_027074.5		
GI_37551135-S	658.8	413.9	415.4	LOC375531	XM_353406.1		
GI_37551137-S	127.5	145.8	117.5	LOC345930	XM_294019.2		
GI_37551139-S	963	2060.8	1586.5	PRO2013	XM_351675.1		
GI_37551141-S	95.9	105.4	93.1	LOC340148	XM_295166.2		
GI_37551144-S	183.4	181.9	174	LOC285741	XM_209741.2		
GI_37551146-S	144.2	147.6	138.9	LOC375533	XM_351677.1		
GI_37551148-S	144.5	152.3	147.6	LOC375534	XM_351678.1		
GI_37551150-S	126	123.9	139.2	LOC375535	XM_353407.1		
GI_37551154-S	102.8	115.6	89.6	LOC375537	XM_353408.1		
GI_37551156-S	140	169.3	161.1	LOC375538	XM_353409.1		
GI_37551160-S	141.8	152.1	127.7	KIAA1553	XM_166320.3		
GI_37551186-S	119	151.3	127	LOC340146	XM_294017.3		
GI_37551208-S	113	121.2	113.6	LOC374334	XM_352985.1		
GI_37551214-S	125.4	137.4	120.1	DNA2L	XM_166103.3		
GI_37551218-S	163.1	210.8	204.3	LOC374336	XM_352986.1		

GI_37551220-S	530.5	833.2	725.9	KIAA0913	XM_044347.4
GI_37551222-S	150.7	167.2	164.4	LOC374337	XM_352987.1
GI_37551224-S	130.5	143.5	131.7	LOC374338	XM_352988.1
GI_37551258-S	76.5	78.4	67.5	LOC375910	XM_351978.1
GI_37551260-S	111	100.6	98.3	LOC338599	XM_291741.3
GI_37551266-S	152.9	193.1	151.7	LOC375911	XM_351979.1
GI_37551273-S	98.8	104.4	111.7	LOC221766	XM_168101.4
GI_37551274-S	2793.2	2138.7	1903.5	LOC375489	XM_353393.1
GI_37551277-S	96.5	99.7	94.6	LOC377339	XM_352599.1
GI_37551279-S	91.1	112.3	111.3	LOC377340	XM_352600.1
GI_37551281-S	358.7	440.6	403	DKFZP434F0	XM_291159.2
GI_37551290-S	162.5	194.7	181.3	LOC340895	XM_295865.2
GI_37551292-S	115.1	108.8	106.4	LOC374306	XM_352976.1
GI_37551300-S	138	153.1	148.6	LOC374308	XM_350775.1
GI_37551306-S	216.5	277.7	245.4	KIAA1462	XM_166132.2
GI_37551308-S	231.9	266	251.2	LOC143110	XM_083843.4
GI_37551310-S	93.1	92.7	97.1	LOC374311	XM_352978.1
GI_37551314-S	103.4	95.3	102.4	LOC340947	XM_291763.2
GI_37551324-S	101	118.2	92.9	LOC220998	XM_166720.4
GI_37551328-S	82.9	90.6	83.5	LOC340900	XM_291767.2
GI_37551330-S	152.6	151.2	185	LOC220213	XM_166659.3
GI_37551334-S	92.5	89	76	LOC375871	XM_351965.1
GI_37551336-S	106.8	105.6	96.6	LOC340913	XM_291770.3
GI_37551346-S	245.3	304.3	268.7	LOC375880	XM_351967.1
GI_37551348-S	99.2	116.3	107.2	ZNF37A	XM_035863.5
GI_37551350-S	102.3	109	84.5	LOC375881	XM_351968.1
GI_37551361-S	94.4	87.7	81	LOC375515	XM_353401.1
GI_37551363-S	93.7	98.4	89.1	LOC154288	XM_087901.2
GI_37551369-S	94	101.7	84.4	LOC375518	XM_353402.1
GI_37551374-S	90.1	88.8	88.5	ZNF292	XM_048070.2
GI_37551378-S	125.7	122.2	109.4	C6orf163	XM_116497.3
GI_37551403-S	147.3	134.3	113.6	ACY1L2	XM_072402.5
GI_37551407-S	118.4	127.2	124.5	LOC374362	XM_350810.1
GI_37551411-S	174	203.6	177.4	LOC338623	XM_291782.3
GI_37551767-S	1713	1805.3	2042.5	KIAA1423	XM_029703.2
GI_37551769-S	154.7	189.3	172.4	LOC375539	XM_353410.1
GI_37551771-S	109.9	112	102.7	LOC375540	XM_353411.1
GI_37551773-S	92.7	91.6	77.9	LOC375541	XM_353412.1
GI_37551775-S	130.7	133	132.7	FNDC1	XM_027658.6
GI_37551783-S	90.8	113.1	97.1	QKI	XM_037438.6
GI_37551868-S	170.3	194.1	170.7	MGC35045	XM_352924.1
GI_37551870-S	84.5	78.4	79.8	LOC374893	XM_351186.1
GI_37551872-S	349	409.6	396.9	LOC342865	XM_292785.3
GI_37551878-S	106.6	116	105.7	LOC374896	XM_353179.1

GI_37551880-S	114	106.8	91.2	FLJ13072	XM_117117.3	
GI_37551881-S	109.7	106.4	113.8	LOC126374	XM_059037.4	
GI_37551883-S	101.4	110.9	94.1	FLJ30663	XM_086046.2	
GI_37551886-S	126	112.8	116	LOC374898	XM_351188.1	
GI_37551888-S	130.2	132.7	138.8	LOC342892	XM_292740.2	
GI_37551890-S	185	166.8	139.1	LOC374899	XM_351189.1	
GI_37551894-S	107.8	99.1	100.9	LOC284409	XM_211447.2	
GI_37551895-S	1831.7	1947	1640.9	KIAA0545	XM_032278.8	
GI_37551901-S	170.2	182.5	145.9	LOC374902	XM_353180.1	
GI_37551903-S	131.3	143.3	122.4	LOC342897	XM_292745.2	
GI_37551907-S	175.9	138.7	125.2	KIAA1484	XM_290842.2	
GI_37551909-S	261.7	274.4	280.2	FLJ10211	XM_290820.2	
GI_37551911-S	867.7	744.7	627.5	CLG	XM_290828.2	FLJ00018;FLJ22458
GI_37551912-S	98	110.7	107.7	LOC148003	XM_086001.3	
GI_37551915-S	230.8	251	248.2	LOC374903	XM_353181.1	
GI_37551917-S	112.6	116.9	102.7	LOC163131	XM_092019.4	
GI_37551919-S	102.5	104.4	97.7	LOC284323	XM_209140.3	
GI_37551924-S	104.4	103.6	99	LOC374908	XM_353182.1	
GI_37551930-S	193.8	237.8	197.6	EGFL4	XM_290821.2	
GI_37551932-S	109.6	116.5	103.4	LOC374910	XM_351198.1	
GI_37551941-S	208.3	238.3	249.9	LOC284347	XM_209120.4	
GI_37551946-S	115.2	109.5	104.4	ZNF229	XM_351202.1	
GI_37551948-S	98.1	102.3	84.9	LOC147711	XM_085851.3	
GI_37551950-S	149.6	198.3	153.4	LOC147710	XM_097278.4	
GI_37551951-S	103.3	111.2	104.9	LOC374914	XM_351203.1	
GI_37551963-S	141.8	294.1	161.4	LOC374917	XM_353186.1	
GI_37551965-S	279.9	357.1	318.2	LOC147920	XM_085932.6	
GI_37551969-S	99.8	114.2	86.4	LOC374919	XM_351206.1	
GI_37551971-S	111.9	140.6	126.8	MRG2	XM_085929.8	
GI_37551979-S	159.5	270.5	215	KIAA1883	XM_055866.5	
GI_37551981-S	470.8	575.9	516.9	KIAA1205	XM_046305.3	
GI_37551986-S	109.9	108.4	111.8	DKFZp761A1	XM_292778.2	
GI_37551988-S	101.7	94.9	87	LOC342918	XM_292779.3	
GI_37551990-S	331	655.9	380.8	LOC284367	XM_290822.2	
GI_37551992-S	85.8	94.3	86.4	LOC339351	XM_292784.2	
GI_37551994-S	263.7	297.8	289.1	LOC147645	XM_085831.7	
GI_37551996-S	149.3	191.8	165.9	LOC147650	XM_085824.5	
GI_37552000-S	143	160.8	147.4	LOC284371	XM_209155.2	
GI_37552006-S	141	145.1	127.7	LOC374923	XM_351211.1	
GI_37552008-S	115.3	124.4	128.3	LOC162966	XM_091888.8	
GI_37552010-S	99.6	108.7	107	ZNF28	XM_209154.2	
GI_37552012-S	178	211.6	203.8	LOC90333	XM_030958.7	
GI_37552022-S	147.6	174.7	150.2	LOC284417	XM_209187.2	
GI_37552024-S	151.8	220.1	258.1	LOC374926	XM_351215.1	

GI_37552028-S	96.8	105.3	97.5	LOC147670	XM_097265.7	
GI_37552029-S	117.3	120.8	129.3	DKFZp434H0	XM_064865.4	
GI_37552031-S	417.8	475.1	457.4	ZNF17	XM_091895.6	HPF3;KOX10
GI_37552033-S	118.7	127.4	111.7	LOC374927	XM_351216.1	
GI_37552041-S	121.3	135.2	125.8	KIAA1956	XM_085836.7	
GI_37552048-S	118.2	143	128.9	LOC376511	XM_352258.1	
GI_37552052-S	189.8	214.7	186.4	LOC126235	XM_065006.3	
GI_37552056-S	103	107.8	101.8	LOC376514	XM_352260.1	
GI_37552068-S	119	123	116	LOC376517	XM_352262.1	
GI_37552072-S	140.9	159.2	151.6	LOC339324	XM_290838.2	
GI_37552074-S	113.9	131	118	LOC376519	XM_352263.1	
GI_37552076-S	98.6	98.5	93.1	LOC376520	XM_352264.1	
GI_37552078-S	303.9	371.8	310	DKFZp434H2	XM_290829.2	
GI_37552082-S	408.6	520.3	450.2	LOC376527	XM_352267.1	
GI_37552088-S	108.2	110.2	110.1	LOC376528	XM_352268.1	
GI_37552090-S	109.3	111.4	110.3	LOC284352	XM_113978.4	
GI_37552094-S	168.2	184.8	178.2	LOC376532	XM_352271.1	
GI_37552096-S	78.5	92.4	80.6	LOC339346	XM_292769.2	
GI_37552098-S	150.8	153.2	140.1	LOC376534	XM_352272.1	
GI_37552100-S	89.4	92.6	85.4	C19orf7	XM_028253.3	
GI_37552104-S	114.8	94.2	103.9	LOC376539	XM_352276.1	
GI_37552115-S	91.6	85.7	90.6	LOC376544	XM_352279.1	
GI_37552117-S	94.6	95.8	93.5	LOC91664	XM_039908.2	
GI_37552121-S	122.6	131.7	124.7	LOC89887	XM_058964.5	
GI_37552125-S	131	134.4	117.1	LOC90485	XM_032059.2	
GI_37552127-S	90.8	92.7	85.5	LOC342939	XM_292729.2	
GI_37552135-S	540.3	501.5	657.2	KIFC1	XM_352965.1	
GI_37552139-S	112.1	126.2	108.4	LOC375491	XM_351648.1	
GI_37552143-S	130.3	157.2	135.2	LOC375492	XM_353394.1	
GI_37552147-S	148.3	169.7	156.5	LOC375493	XM_353395.1	
GI_37552150-S	393.1	415.7	310.5	LOC154165	XM_087859.4	
GI_37552160-S	112.3	129.6	124.9	LOC346157	XM_294077.2	
GI_37552162-S	128.2	172.3	129	ZNF311	XM_212581.2	
GI_37552164-S	148.6	164	156	LOC346171	XM_294093.2	
GI_37552166-S	166.2	195.5	176	LOC375501	XM_353396.1	
GI_37552173-S	117.5	129.8	126.8	LOC375502	XM_351655.1	
GI_37552180-S	82.7	87.3	86	KIAA1246	XM_166372.2	
GI_37552181-S	240.4	273.4	252.3	LOC221442	XM_166432.4	
GI_37552185-S	486.7	496	391.9	LOC375506	XM_351658.1	
GI_37552187-S	122.6	133.1	110.1	LOC375507	XM_351659.1	
GI_37552191-S	106.2	116.6	96.2	LOC375508	XM_353398.1	
GI_37552193-S	121.4	110.3	108.5	TTBK1	XM_166453.4	
GI_37552195-S	182.7	221.7	203.7	LOC375509	XM_351660.1	
GI_37552197-S	122.1	134.9	134	LOC375510	XM_353399.1	

GI_37552201-S	211.8	214.5	171.9	AARSL	XM_291190.2	KIAA1270;bA444E17.1	ATP		alanyl-
GI_37552205-S	235.4	287	260.5	LOC375511	XM_351661.1				
GI_37552209-S	125.8	142.7	131.6	LOC375512	XM_353400.1				
GI_37552211-S	89.3	82.3	80.4	C6orf143	XM_294139.2				
GI_37552220-S	104.8	107.4	103	IBRDC2	XM_172581.3	p53RFP;bA528A10.3	electron		electron
GI_37552234-S	95.4	91.9	92.1	C6orf194	XM_167149.3				
GI_37552235-S	94.7	100.8	104	ZNF452	XM_166375.3				
GI_37552272-S	224.9	250.8	207.9	LOC346217	XM_294117.3				
GI_37552286-S	80.5	67.6	82.4	LOC375542	XM_353413.1				
GI_37552310-S	583.1	669.9	769.2	LOC91978	XM_042012.4				
GI_37552312-S	151	180.3	119.4	GRIN3B	XM_290850.3				
GI_37552316-S	1249.9	1357	2298.1	MIDN	XM_028067.6				
GI_37552318-S	128	122.5	128.8	LOC339366	XM_294919.2				
GI_37552320-S	734.7	963.8	1023.9	LOC126435	XM_059047.4				
GI_37552322-S	358.9	445.5	402	ATP8B3	XM_086103.4	ATPIK	ATP	integral to	cation
GI_37552328-S	94.6	83.3	88	KIAA1086	XM_047610.2				
GI_37552330-S	104.5	108.7	106	LOC374873	XM_353170.1				
GI_37552332-S	241.5	266.4	229.8	KIAA1981	XM_114000.2				
GI_37552337-S	113.1	125.4	124.4	LOC342959	XM_292803.2				
GI_37552339-S	1428	1811.3	1653.8	KIAA0876	XM_290852.2				
GI_37552341-S	119	125.4	122.2	LOC374874	XM_353171.1				
GI_37552345-S	237.5	200.3	229.4	LOC374876	XM_353172.1				
GI_37552347-S	285.8	346.9	331.6	GPR108	XM_290854.2				
GI_37552352-S	369	438.7	395.7	LOC376475	XM_352236.1				
GI_37552356-S	199	229.1	203.9	KIAA1193	XM_041843.3		DNA	nucleus	
GI_37552360-S	104.5	87.7	83.6	LOC376480	XM_352239.1				
GI_37552366-S	88.4	119.7	107.8	KIAA1881	XM_170901.2				
GI_37552369-S	119.7	130.6	117.4	LOC376483	XM_352242.1				
GI_37552372-S	3297.3	3080.7	4093.9	KIAA0062	XM_046677.7				
GI_37552374-S	164.2	180	187.3	LOC375653	XM_353449.1				
GI_37552376-S	92.3	89.7	95.9	LOC375654	XM_353450.1				
GI_37552378-S	119.5	121.8	118.9	LOC375655	XM_353451.1				
GI_37552380-S	229.6	252.2	313.1	CDCA2	XM_351774.1	FLJ25804			
GI_37552382-S	196.9	223.9	208.7	LOC375656	XM_351775.1				
GI_37552384-S	178.7	188.3	146.3	LOC375657	XM_351776.1				
GI_37552386-S	106.4	106.2	97.1	LOC375658	XM_353452.1				
GI_37552388-S	417.3	471.9	502.2	LOC203069	XM_114618.3				
GI_37552390-S	353.1	444.9	423.6	LOC137814	XM_070619.6				
GI_37552392-S	112.8	120.6	123.8	LOC377637	XM_352724.1				
GI_37552398-S	265.6	295.1	271.8	LOC346848	XM_294438.3				
GI_37552401-S	9760.4	4976.8	3295	LOC375662	XM_351780.1				
GI_37552407-S	166.4	185	174.4	LOC377649	XM_352730.1				
GI_37552415-S	325.9	416.1	327.3	LOC375684	XM_353468.1				
GI_37552417-S	107.5	98.6	98.2	LOC375685	XM_353469.1				

GI_37552419-S	99.4	112.2	97.3	LOC286080	XM_212162.2
GI_37552421-S	507.7	556.1	592.5	GRINA	XM_291268.3
GI_37552425-S	128.2	171.3	155.4	OPLAH	XM_291266.3
GI_37552427-S	109.6	108.6	101.8	KIAA1875	XM_291269.2
GI_37552429-S	93.9	83.6	89.4	LOC377707	XM_352752.1
GI_37552431-S	100.8	103.2	90.6	LOC377708	XM_352753.1
GI_37552433-S	178.5	174.8	139.9	LOC377709	XM_352754.1
GI_37552435-S	197	234.9	224.1	LOC377710	XM_352755.1
GI_37552437-S	97.9	112.7	108.5	LOC377711	XM_352756.1
GI_37552442-S	138.2	147.4	110.4	LOC375638	XM_353442.1
GI_37552464-S	152	191.5	183.8	LOC346910	XM_294456.2
GI_37552466-S	117.2	111.7	125.2	LOC377609	XM_352709.1
GI_37552468-S	110.9	146.3	120.5	LOC377610	XM_352710.1
GI_37552470-S	123.3	139	126.7	LOC340372	XM_294407.2
GI_37552472-S	356.7	461.9	386.8	LOC286088	XM_209893.3
GI_37552474-S	81.7	94.3	83.5	LOC377614	XM_352711.1
GI_37552476-S	128.8	126.4	125.9	LOC377616	XM_352712.1
GI_37552478-S	136.3	158.2	155	LOC377618	XM_352713.1
GI_37552480-S	99.9	103.8	88.9	LOC377619	XM_352714.1
GI_37552485-S	268.4	229.7	261	KIAA0870	XM_088315.4
GI_37552486-S	151.4	183.9	198	KIAA1126	XM_050325.4
GI_37552498-S	119.2	129.7	116.7	LOC374879	XM_351175.1
GI_37552500-S	98.2	100.9	108.5	LOC374880	XM_351176.1
GI_37552502-S	118.1	110	102.6	LOC147740	XM_085870.2
GI_37552513-S	81.1	87.5	89.5	LOC342970	XM_292810.2
GI_37552517-S	87.8	89.9	82	DKFZp434I16	XM_032812.2
GI_37552519-S	228.4	214.7	211.6	LOC342972	XM_292813.2
GI_37552523-S	484	331.2	358.2	LOC374883	XM_351179.1
GI_37552529-S	102.2	107.8	96.9	LOC342979	XM_292820.2
GI_37552533-S	226.5	252.2	264.1	LOC113230	XM_053966.7
GI_37552537-S	102.8	107.8	101.3	LOC374886	XM_351181.1
GI_37552539-S	3707.4	4928	4266.4	LOC284434	XM_211460.2
GI_37552541-S	1307.5	1670.6	1134.6	SIN3B	XM_050561.7
GI_37552543-S	102.6	96.9	89.5	KIAA1032	XM_038604.5
GI_37552547-S	148.2	220.3	230.1	KIAA0561	XM_038150.3
GI_37552549-S	139.9	149.6	143.8	KIAA1683	XM_351182.1
GI_37552553-S	827.7	795.2	868.5	KIAA0892	XM_048457.3
GI_37552558-S	99.6	111.4	106.3	LOC163233	XM_290865.2
GI_37552560-S	214.7	244.7	204.8	LOC148203	XM_086095.4
GI_37552572-S	836	1071.4	913.5	KIAA1473	XM_047550.3
GI_37552575-S	227.5	282.4	245.1	LOC376486	XM_352243.1
GI_37552580-S	96.7	119.2	109.9	LOC125962	XM_064883.9
GI_37552582-S	157.9	174.4	153.7	MTMR7	XM_044727.5
GI_37552586-S	103.1	103.9	92	LOC375650	XM_353446.1

GI_37552588-S	148.8	168.6	158.7	LOC125958	XM_064879.5				
GI_37552590-S	95.6	90.2	91.7	LOC375651	XM_353447.1				
GI_37552593-S	97.9	93.5	86.7	LOC375652	XM_353448.1				
GI_37552595-S	110.9	139.2	117.9	LOC342967	XM_292817.2				
GI_37552597-S	284.7	300.7	270.8	LOC342969	XM_292824.3				
GI_37552599-S	102.2	97.3	101.7	LOC346708	XM_294383.3				
GI_37552603-S	222.4	261.9	246.6	LOC377632	XM_352722.1				
GI_37552605-S	114.5	138.4	120	LOC376492	XM_352247.1				
GI_37552609-S	167.4	194.5	179.9	HSZFP36	XM_290868.2				
GI_37552613-S	171.8	178.4	164.6	LOC376494	XM_352249.1				
GI_37552615-S	149.6	157.5	153.5	LOC376495	XM_352250.1				
GI_37552617-S	134.2	139	144	LOC126370	XM_065050.2				
GI_37552625-S	117.3	121.3	121.9	LOC376497	XM_352251.1				
GI_37552629-S	128.5	121	111.9	ZNF90	XM_352252.1				
GI_37552634-S	150.3	161.6	147.2	LOC342991	XM_292832.3				
GI_37552642-S	75.5	105.3	87.7	LOC126502	XM_065124.5				
GI_37552646-S	99.1	107.6	101.4	LOC253342	XM_171973.3				
GI_37552650-S	77.7	96.7	88.3	LOC376507	XM_352255.1				
GI_37552665-S	2600.3	3859.6	1485.9	DKFZp761P0	XM_291277.2				
GI_37552667-S	135.9	154.8	139.5	LOC375645	XM_353444.1				
GI_37552671-S	95.3	86.2	86.6	LOC203076	XM_114621.3				
GI_37552675-S	111.5	129.3	113.8	LOC375647	XM_353445.1				
GI_37552677-S	129.4	140.1	120.2	LOC375648	XM_351772.1				
GI_37552685-S	156	186.9	166.7	LOC377625	XM_352719.1				
GI_37552689-S	117.6	120.5	109.8	LOC377626	XM_352720.1				
GI_37552699-S	200.5	194.9	230.9	KIAA1764	XM_045086.4				
GI_37552850-S	93.6	94	84.3	LOC375104	XM_353245.1				
GI_37552854-S	152.8	161.1	171	KIAA1510	XM_028834.5		structural	microfibril	cell
GI_37552857-S	292.4	350.5	299.1	LOC149659	XM_086622.2				
GI_37552860-S	288.8	340.9	315.5	LOC200213	XM_114156.3				
GI_37552864-S	319.7	333.7	564.9	LOC375105	XM_353246.1				
GI_37552867-S	245.3	296.8	278.6	DNAJC5	XM_028966.7	CSP;FLJ00118;FLJ13070;DKFZP434N1429			
GI_37552872-S	270.8	325.6	292.5	LOC376797	XM_352394.1				
GI_37555865-S	124.4	153.8	129.4	LOC340450	XM_295252.2				
GI_37555866-S	110.8	124.5	113.3	LOC375675	XM_353461.1				
GI_37555868-S	135.9	141.6	141.2	LOC375676	XM_351787.1				
GI_37555870-S	151.5	145.2	153.1	LOC286151	XM_209918.2				
GI_37555873-S	648.2	526.3	507.8	LOC346887	XM_294450.2				
GI_37555875-S	83.2	102.2	88.6	COL14A1	XM_044622.4				
GI_37555876-S	129.2	162.8	142	LOC375678	XM_353462.1				
GI_37555878-S	146.5	147.4	139.1	LOC375679	XM_353463.1				
GI_37555887-S	1604.7	1499.9	1143.2	KIAA0143	XM_035825.4				
GI_37555889-S	399	492.4	436	LOC375683	XM_353467.1				
GI_37555891-S	316.7	317	281.3	LOC377678	XM_352744.1				

GI_37555895-S	134.9	138.8	133.9	DKFZp762C1	XM_095568.6				
GI_37555903-S	123.9	126.9	116.5	LOC377685	XM_352746.1				
GI_37555905-S	111.5	118.4	107.6	LOC377686	XM_352747.1				
GI_37555909-S	84.9	89.6	82.6	KCNS2	XM_043106.4	KV9.2	voltage-	voltage-	cation
GI_37555914-S	102.8	110.3	118.3	LOC377696	XM_352749.1				
GI_37555920-S	110.3	138.7	125.4	LOC377697	XM_352750.1				
GI_37555922-S	134.4	146.2	127.5	LOC340359	XM_294387.2				
GI_37555926-S	112	116.5	119.2	LOC137202	XM_070277.5				
GI_37555931-S	95.6	118.9	96.9	LOC375096	XM_351367.1				
GI_37555934-S	1110.3	505.1	604.3	LOC375097	XM_353241.1				
GI_37555937-S	102.9	129	117	LOC375098	XM_351368.1				
GI_37555939-S	403.1	466.3	440.4	C20orf142	XM_351369.1				
GI_37555941-S	86.5	83.8	83.8	LOC200226	XM_114158.2				
GI_37555943-S	202.8	193.5	266.8	LOC128499	XM_059256.5				
GI_37555948-S	410.8	555.6	638.8	SLC9A8	XM_030524.3	NHE8;KIAA0939	sodium:hy	integral to	sodium
GI_37555950-S	135.1	136.4	124.7	LOC200230	XM_114166.3				
GI_37555952-S	83	82.6	79.4	PARD6B	XM_030559.2				
GI_37555955-S	160.4	183.1	168.1	C20orf106	XM_351371.1				
GI_37555957-S	167.5	167.5	149.7	LOC375101	XM_351372.1				
GI_37555961-S	105	113.3	103.6	PPP4R1L	XM_086650.5				
GI_37555965-S	78.7	85	89.2	C20orf174	XM_066058.3				
GI_37555969-S	150.2	177.5	146.6	LOC343574	XM_293104.2				
GI_37555971-S	104.9	106.2	91.3	LOC343578	XM_293123.2				
GI_37555973-S	130.7	144.3	120.5	C20orf130	XM_029741.3				
GI_37555975-S	163	176.1	154.3	LOC376788	XM_352388.1				
GI_37555977-S	105.1	116.8	108.1	LOC343593	XM_293106.2				
GI_37555981-S	113.8	115.8	111.1	LOC376793	XM_352391.1				
GI_37555984-S	83.5	85.5	84.8	LOC343629	XM_293121.2				
GI_37555986-S	321.3	418	369.5	LOC376795	XM_352392.1				
GI_37555988-S	116.2	146.4	134.8	LOC128629	XM_066069.2				
GI_37555995-S	371.1	365.4	346.7	KIAA0146	XM_291253.3				
GI_37555997-S	95.2	101	113.7	LOC375663	XM_353455.1				
GI_37555999-S	123.1	134.4	139	LOC375664	XM_353456.1				
GI_37556001-S	104.8	126.5	118.2	LOC157708	XM_088367.2				
GI_37556003-S	105.7	115.3	104.5	LOC375665	XM_351781.1				
GI_37556007-S	86.2	97.2	90.7	LOC375668	XM_351783.1				
GI_37556009-S	191	200.8	231.9	LOC137886	XM_059929.4				
GI_37556011-S	151.6	163.2	146.9	LOC375669	XM_353458.1				
GI_37556013-S	118.6	139.3	120.2	KIAA1416	XM_098762.9				
GI_37556017-S	114.2	116.4	109	LOC375670	XM_351784.1				
GI_37556019-S	101	101.2	94.6	LOC375671	XM_353459.1				
GI_37556021-S	86.7	92.7	83.3	LOC375672	XM_353460.1				
GI_37556023-S	19793.6	18715	14196	LOC157552	XM_013127.5				
GI_37556025-S	91	103.5	105.3	LOC375673	XM_351785.1				

GI_37556027-S	119.8	96.1	116	LOC375674	XM_351786.1
GI_37556031-S	91.8	89.8	97.8	LOC377651	XM_352731.1
GI_37556035-S	440.7	439.9	328.1	LOC377653	XM_352732.1
GI_37556037-S	92.4	106.9	79.9	LOC377654	XM_352733.1
GI_37556039-S	98.8	94.1	81.3	LOC377655	XM_352734.1
GI_37556045-S	99.4	96.1	98	LOC377658	XM_352737.1
GI_37556049-S	108	104.7	102	LOC377662	XM_352738.1
GI_37556053-S	2939	2689.8	2111.3	LOC286157	XM_209920.3
GI_37556059-S	87.5	96	83.4	LOC377672	XM_353538.1
GI_37556063-S	128.7	128.2	122.4	LOC377675	XM_352742.1
GI_37556065-S	376.2	471.4	418.5	LOC284759	XM_209363.2
GI_37556067-S	178.2	214.4	175.1	LOC375083	XM_353235.1
GI_37556071-S	164.5	174.5	153.3	LOC375084	XM_351359.1
GI_37556073-S	166	170.8	158.7	C20orf194	XM_045421.2
GI_37556080-S	120.8	118.7	126	LOC128710	XM_059267.5
GI_37556082-S	95.9	98.6	83.2	C20orf50	XM_046437.4
GI_37556084-S	1845.6	1411.4	778.6	LOC375088	XM_353238.1
GI_37556086-S	117.7	113.4	103.8	LOC375089	XM_353239.1
GI_37556088-S	162.4	181.5	154.4	KIAA1272	XM_046600.9
GI_37556090-S	135	154.4	153.7	LOC149913	XM_097753.4
GI_37556092-S	107.8	117.9	119.2	LOC375090	XM_351361.1
GI_37556098-S	168.5	208.7	175.3	LOC376765	XM_352378.1
GI_37556100-S	116.4	128.2	117.6	LOC343637	XM_297816.3
GI_37556106-S	124	135.6	132.9	C20orf82	XM_097736.4
GI_37556110-S	93.8	95.7	77.1	LOC376772	XM_352381.1
GI_37556112-S	378.9	464.8	417.2	LOC376775	XM_353533.1
GI_37556114-S	99.4	99.1	109.6	LOC376777	XM_352383.1
GI_37556116-S	300.3	320.8	332.9	KIAA0725	XM_291291.2
GI_37556129-S	79.4	78.8	76.5	LOC340441	XM_294480.2
GI_37556875-S	97.8	107.9	90.3	LOC375092	XM_351363.1
GI_37556880-S	179.8	207.3	202	LOC375093	XM_351364.1
GI_37556886-S	286.8	372.4	346.4	LOC375094	XM_351365.1
GI_37556892-S	122.4	141.5	123	LOC375095	XM_351366.1
GI_37556898-S	96.3	88.6	98.1	LOC343702	XM_293160.3
GI_37556901-S	342.6	441.5	356.6	LOC376780	XM_352385.1
GI_37558299-S	100.8	97.2	97.6	LOC375110	XM_353248.1
GI_37558305-S	117.4	126.9	113.9	LOC375112	XM_353250.1
GI_37558319-S	185.8	185.2	166.4	LOC375114	XM_351376.1
GI_37558322-S	174.7	187.2	172.7	LOC375115	XM_353252.1
GI_37558325-S	97	102.9	90.9	LOC375116	XM_353253.1
GI_37558330-S	125	133.1	118.3	LOC375117	XM_353254.1
GI_37558992-S	297.4	336.7	300.4	LOC200292	XM_117213.2
GI_37558995-S	260.4	289.4	244.4	LOC375122	XM_353256.1
GI_37559272-S	105.4	103.9	97.9	LOC375118	XM_351378.1

GI_37559275-S	126.5	121.4	141.1	C21orf25	XM_032945.4	MGC71445;DKFZP586F0422
GI_37559278-S	97.6	109.1	100.9	LOC375119	XM_351379.1	
GI_37559281-S	162.4	180.5	166.4	LOC375120	XM_353255.1	
GI_37559466-S	138.7	151.8	138.8	LOC128939	XM_066243.2	
GI_37559469-S	83.3	88.9	79.9	LOC376798	XM_352396.1	
GI_37559950-S	655.6	760	690.3	MICAL3	XM_032997.4	
GI_37559964-S	104.5	109.7	100.7	LOC375128	XM_353257.1	
GI_37559973-S	132.6	151.3	145	LOC375131	XM_353258.1	
GI_37559987-S	108.6	155.5	200.3	KIAA1666	XM_351388.1	
GI_37559996-S	96.6	104.6	99.5	LOC376807	XM_352399.1	
GI_37560002-S	109.8	99.2	100	CECR2	XM_352401.1	
GI_37560012-S	97.6	104.2	92.3	LOC343830	XM_293220.3	
GI_37560015-S	288.8	362.9	314.9	LOC376811	XM_352403.1	
GI_37563586-S	118.5	130.4	139.7	LOC375141	XM_351393.1	
GI_37563604-S	1410.6	1094.3	1065.5	LOC150223	XM_097886.5	
GI_37563608-S	121.1	147.1	140.1	LOC375157	XM_351406.1	
GI_37563614-S	98.9	99.8	116.8	LOC129039	XM_059329.7	
GI_37563621-S	138.2	170.1	149.5	LOC284890	XM_208261.2	
GI_37563628-S	79.4	95.5	84.3	LOC375161	XM_353263.1	
GI_37563633-S	105.1	103.1	96.2	KIAA1941	XM_059318.5	
GI_37563637-S	166	210	178.2	LOC255349	XM_170994.2	
GI_37563645-S	174.8	205.3	199.8	LOC375162	XM_353264.1	
GI_37563648-S	88.4	94.9	86.3	LOC375163	XM_353265.1	
GI_37563655-S	193.7	237.6	230.4	LOC200312	XM_117224.6	
GI_37563661-S	193.9	208.7	205.4	KIAA0542	XM_038520.7	
GI_37563666-S	100	93.2	87.4	LOC150297	XM_086894.3	
GI_37563669-S	97.6	96.9	99.1	LOC375165	XM_353266.1	
GI_37563678-S	302.6	372.4	338.7	KIAA1904	XM_056282.2	
GI_37563681-S	115.9	137.1	132.3	LOC375167	XM_351413.1	
GI_37563692-S	111	105.3	107.6	LOC200321	XM_114200.3	
GI_37563696-S	143.7	137.5	126.4	MGC40042	XM_351415.1	
GI_37563699-S	179.2	227.2	170.4	LOC150368	XM_086826.4	
GI_37563702-S	323.6	265.1	254.1	LOC375172	XM_351416.1	
GI_37563711-S	130.8	97.5	216.7	LOC376816	XM_352408.1	
GI_37563726-S	126.5	147.7	134.5	LOC376823	XM_352411.1	
GI_37563733-S	80.1	80	93.1	LOC376836	XM_352422.1	
GI_37563738-S	443.3	513.7	455.9	KIAA0376	XM_037759.5	
GI_37563748-S	101	99.4	99.3	LOC376839	XM_352423.1	
GI_37563751-S	221	257.6	225.5	FLJ12747	XM_290972.2	
GI_37563764-S	154.7	162.6	144.3	LOC376854	XM_352428.1	
GI_37564256-S	650.7	1220.6	800.1	KIAA0930	XM_047214.6	
GI_37564508-S	116.5	125	113.1	LOC150383	XM_086905.5	
GI_37564513-S	97.4	100.7	94.1	LOC375174	XM_353270.1	
GI_37564517-S	106.6	105.3	109.6	LOC375175	XM_353271.1	

GI_37564595-S	103	98.8	93.5	LOC375176	XM_353272.1				
GI_37564605-S	108.5	123.3	107.7	LOC376856	XM_352429.1				
GI_37564608-S	117.3	140.2	113.5	LOC376857	XM_352430.1				
GI_37564791-S	193.8	249.5	219.1	SHANK3	XM_037493.2				
GI_37564886-S	148.9	146.5	136.5	LOC164714	XM_104657.3				
GI_37564923-S	113.8	113.6	114.4	LOC284943	XM_209417.2				
GI_37574041-S	146.2	181.6	158	AGXT2L1	NM_031279.2		transamin		
GI_37574045-S	291.1	303.5	290.6	LOC197336	NM_145294.3				
GI_37574156-I	509.9	618.3	384.2	ALG2	NM_197973.1	CDGIi;hALPG2;FLJ14511			
GI_37574600-S	332	272	265.1	ZNF232	NM_014519.2		transcripti	nucleus	regulation
GI_37574602-S	184.8	194.8	210.1	ZNF256	NM_005773.2	BMZF3;BMZF-3	transcripti	nucleus	developm
GI_37574605-A	1048.5	1042.4	798.6	ZNF198	NM_197968.1	FIM;MYM;RAMP;SCLL	protein		
GI_37574607-I	143.2	171.6	149.8	ZNF189	NM_197977.1		transcripti	nucleus	negative
GI_37574611-S	1580.8	1576.6	1439.9	SBF1	NM_002972.1	MTMR5	protein	integral to	protein
GI_37574613-A	1583.7	1846.3	1448.8	NME7	NM_197972.1		nucleoside		GTP
GI_37574615-S	92.3	96.2	83.3	NUDT12	NM_031438.2	DKFZP761I172			
GI_37574617-A	85.5	101.1	87.8	HEMGN	NM_197978.1	EDAG;EDAG-1			
GI_37574619-S	153	183.2	167.3	GP6	NM_016363.3	GPIV;GPVI	collagen	integral to	enzyme
GI_37574621-I	90.3	84	95.3	HEMGN	NM_018437.3	EDAG;EDAG-1			
GI_37574623-I	125.6	127.3	138.1	BTNL3	NM_197975.1	BTNLR	receptor		lipid
GI_37574625-A	121	144.7	126.3	BTNL3	NM_006707.2	BTNLR	receptor		lipid
GI_37574625-I	341.4	419.4	392	BTNL3	NM_006707.2	BTNLR	receptor		lipid
GI_37574627-A	321.5	442.4	308.8	BTN3A3	NM_197974.1	BTF3			
GI_37574688-S	109.8	120.4	105.2	LOC286101	XM_209902.2				
GI_37574699-S	465.3	771.4	521.1	LOC92755	XM_047083.5				
GI_37574707-S	108.7	112	100	LOC377641	XM_352726.1				
GI_37574713-S	182.7	214.2	186.5	KIAA1543	XM_048362.7				
GI_37574716-S	1881.8	2263.2	2424.4	TRAPPC5	XM_058961.4				
GI_37574717-S	123.2	115.7	112.4	LOC374878	XM_353174.1				
GI_37574725-I	112.7	113.1	118.8	BID	NM_197966.1	MGC15319;MGC42355	death	cytosol	apoptotic
GI_37574727-A	832.9	733.9	435.2	BID	NM_197967.1	MGC15319;MGC42355	death	cytosol	apoptotic
GI_37574729-I	123	125.7	128.3	BOLL	NM_033030.3	BOULE	nucleic		
GI_37574730-A	115.1	127.8	116.9	BOLL	NM_197970.1	BOULE	nucleic		
GI_37574730-I	97.8	96.6	83.3	BOLL	NM_197970.1	BOULE	nucleic		
GI_37577088-I	101.3	100.3	95.7	DPP8	NM_197960.1	FLJ14920;FLJ20283;MGC26191			
GI_37577092-A	923	1264.6	1139.4	DPP8	NM_017743.3	FLJ14920;FLJ20283;MGC26191			
GI_37577100-A	779.1	393.8	459.4	DTNB	NM_033148.2	MGC17163;MGC57126	protein	cytoskelet	
GI_37577102-S	194.8	256.6	217.2	CLEC1	NM_016511.2	MGC34328	transmem	intracellula	defense
GI_37577106-S	115.9	116.2	117.3	CLECSF2	NM_005127.2	AICL;IFNRG1;HP10085	lectin [goid	integral to	antimicrob
GI_37577111-A	168.3	196.5	153.5	PAX8	NM_013992.2		thyroid-	nucleus	embryoge
GI_37577112-I	247.8	316.2	269.5	PAX8	NM_003466.2		thyroid-	nucleus	embryoge
GI_37577116-A	120.5	162.2	113.1	CLECSF6	NM_194448.1	DCIR;LLIR;DDB27;HDCGC13P	transmem	integral to	cell
GI_37577120-S	79.1	88	71.2	CLECSF8	NM_080387.4	Mpcl;CLEC-6;MGC40078	sugar		heterophili
GI_37577121-I	752	581.5	962.7	UBE2J1	NM_016021.2	Ubc6p;CGI-	ubiquitin		ubiquitin

GI_37577127-I	154.8	181.6	152.3	UBE2J2	NM_194316.1	NCUBE2;PRO2121			
GI_37577129-A	393.6	452.4	416.1	UBE2J2	NM_194457.1	NCUBE2;PRO2121			
GI_37577131-I	127.3	142.9	110.7	UBE2J2	NM_194458.1	NCUBE2;PRO2121			
GI_37577133-S	2325.7	2630.2	2239.5	UBE2M	NM_003969.2	UBC12;hUbc12;UBC-RS2	ubiquitin		protein
GI_37577134-S	911.7	1027.1	1038.1	UBE2N	NM_003348.3	UBC13;MGC8489;UbcH-ben	ubiquitin		regulation
GI_37577141-A	168.2	185.4	170.9	MAX	NM_197957.1	MGC10775;MGC11225;MGC18164;MGC346	transcripti		oncogene
GI_37577141-I	176.6	210.5	196.2	MAX	NM_197957.1	MGC10775;MGC11225;MGC18164;MGC346	transcripti		oncogene
GI_37577147-A	394.1	427.2	368.8	NCKIPSD	NM_184231.1	DIP1;ORF1;WISH;AF3P21;SPIN90;WASLBP	cytoskelet	intermedia	NLS-
GI_37577150-S	442.7	516.4	507.4	APEG1	NM_005876.3	SPEG;KIAA1297;MGC12676	ATP	nucleus	negative
GI_37577152-S	104.3	119.2	93.8	ATP1A4	NM_144699.1	ATP1AL2;MGC25056	monovale	integral to	sodium
GI_37577154-S	1087.2	1406.3	1728.3	ATP6AP1	NM_001183.3	16A;CF2;ORF;Ac45;XAP3;XAP-	adenosine	vacuolar	proton
GI_37577155-S	156.4	148.4	154.2	CA5B	NM_007220.2	MGC39962	carbonate	mitochond	one-
GI_37577156-S	131.3	134.8	100.7	CAPN5	NM_004055.3	HTRA3;nCL-3	calpain	intracellula	signal
GI_37577158-S	106.9	124.9	100.5	CASR	NM_000388.2	FHH;HHC;HHC1;NSHPT;PCAR1;GPRC2A	G-protein	integral to	calcium
GI_37577160-S	89.5	97.4	82.1	CCBP2	NM_001296.3	D6;CCR9;CCR10;CMKBR9	chemokin	integral to	chemotaxi
GI_37577161-I	102	101	122.4	EPIM	NM_194356.1	STX2A;STX2B;STX2C;MGC51014	protein	microsom	ectoderm
GI_37577163-A	211.7	149.7	139.9	LIAS	NM_194451.1	LAS;LIP1;HUSSY-01;MGC23245	lipoate	mitochond	lipoate
GI_37577165-I	425.3	310	247.7	LIAS	NM_006859.2	LAS;LIP1;HUSSY-01;MGC23245	lipoate	mitochond	lipoate
GI_37577167-S	357.1	294.1	336.9	LOC345667	NM_197941.1				
GI_37577171-A	136.2	163	134.3	RNASE4	NM_194431.1	RNS4;MGC9306	pancreatic	cellular_co	mRNA
GI_37577171-I	117.3	130.2	119.9	RNASE4	NM_194431.1	RNS4;MGC9306	pancreatic	cellular_co	mRNA
GI_37577182-A	730.4	816.9	586	RNF38	NM_194331.1	FLJ21343			
GI_37577286-A	549.5	595.1	619.2	EPIM	NM_001980.2	STX2A;STX2B;STX2C;MGC51014	protein	microsom	ectoderm
GI_37588847-I	235.3	237	170.8	VAPA	NM_003574.4	VAP-A;VAP33;VAP-33;MGC3745;hVAP-33	structural	kinesin	membran
GI_37588849-A	138.1	139	131	VAPA	NM_194434.1	VAP-A;VAP33;VAP-33;MGC3745;hVAP-33	structural	kinesin	membran
GI_37588852-A	523.6	201	209	VIP	NM_194435.1	PHM27;MGC13587	neuropepti	soluble	positive
GI_37588854-A	818.4	895.5	987.5	RNF40	NM_014771.2	BRE1B;RBP95;STARING;KIAA0661;MGC13			
GI_37588855-I	106.8	113.3	126.5	RNF40	NM_194352.1	BRE1B;RBP95;STARING;KIAA0661;MGC13			
GI_37588858-I	125.4	134.1	138.5	RNF41	NM_194358.1	SBBI03;MGC45228			
GI_37588860-A	509	465.3	478	RNF41	NM_194359.1	SBBI03;MGC45228			
GI_37588864-A	739.9	860.8	889.1	RNF121	NM_194452.1	FLJ11099			
GI_37588868-S	569.7	768.4	701.6	RNF123	NM_022064.2	FLJ12565			
GI_37588870-A	141.2	212.9	160.5	RNF128	NM_024539.3	GRAIL;FLJ23516			
GI_37588870-I	102.2	112	90.1	RNF128	NM_024539.3	GRAIL;FLJ23516			
GI_37588872-I	108.5	126.8	110.7	RNF128	NM_194463.1	GRAIL;FLJ23516			
GI_37594438-S	355.9	535.5	587.4	ZNF175	NM_007147.2	OTK18	transcripti	nucleus	regulation
GI_37594439-S	2070.1	2468.4	2361.4	ZNHIT1	NM_006349.2	CG1I;ZNFN4A1	cyclin-		
GI_37594440-S	254.9	294.7	267.8	ZNF136	NM_003437.2	pHZ-20	transcripti	nucleus	negative
GI_37594441-S	188.8	199	167.7	ZNF140	NM_003440.2	pHZ-39	transcripti	nucleus	regulation
GI_37594443-S	180.2	222	191.2	ZMYND10	NM_015896.2	BLU;FLU			
GI_37594445-S	555.8	571.2	656	ZMYND19	NM_138462.2	MIZIP			
GI_37594446-A	909	1096.5	1180	ZDHHC16	NM_198045.1	APH2;MGC2993			
GI_37594448-I	152.4	157.5	165.6	ZDHHC16	NM_198046.1	APH2;MGC2993			
GI_37594456-A	1055	1061.6	1086.2	NUDT9	NM_198038.1	NUDT10;MGC3037	calcium	intracellula	cation

GI_37594460-A	352.2	368.5	295	NUDT6	NM_198041.1	gfg;bFGF;FGF-2;gfg-1;ASFGF2;FGF-	growth	cellular_co	biological_
GI_37594460-I	441.8	573.1	493.7	NUDT6	NM_198041.1	gfg;bFGF;FGF-2;gfg-1;ASFGF2;FGF-	growth	cellular_co	biological_
GI_37594463-S	2870.1	3346.5	3273	NUDT5	NM_014142.2	YSA1H;hYSAH1	protein	intracellula	ADP
GI_37594465-I	227.8	237.8	193.2	NUDT6	NM_007083.3	gfg;bFGF;FGF-2;gfg-1;ASFGF2;FGF-	growth	cellular_co	biological_
GI_37594466-S	794.9	860.7	1323	NUDT14	NM_177533.2	UGPP			
GI_37594468-A	435	552	627.5	HIBCH	NM_198047.1	HIBYL-COA-H	3-		metabolis
GI_37595527-I	162.2	174.6	177.5	PHC2	NM_198040.1	EDR2;HPH2	protein	nucleus	
GI_37595529-A	2373.7	2048.6	2129.8	PHC2	NM_004427.2	EDR2;HPH2	protein	nucleus	
GI_37595529-I	154.4	155	135.3	PHC2	NM_004427.2	EDR2;HPH2	protein	nucleus	
GI_37595531-I	125	144.5	129.9	PHEMX	NM_139022.2	PHMX;TSSC6;MGC22455	tumor	integral to	biological_
GI_37595532-A	582.1	749.8	566.1	PHEMX	NM_139024.2	PHMX;TSSC6;MGC22455	tumor	integral to	biological_
GI_37595534-S	364.3	457.9	510.5	RNF103	NM_005667.2	KF1;hkf-1;ZFP103;MGC41857			central
GI_37595535-S	341.6	395.7	376.7	RNF32	NM_030936.2	FKSG33;DKFZp434C135			
GI_37595536-A	2029.7	2210.6	2089	RNF34	NM_025126.2	RFI;RIFF;FLJ21786	electron		electron
GI_37595538-I	100.2	117.2	126.2	RNF34	NM_194271.1	RFI;RIFF;FLJ21786	electron		electron
GI_37595540-A	113.4	125.3	110	RNF36	NM_080745.2	Trif			
GI_37595542-I	119.6	134.1	120.4	RNF36	NM_182985.2	Trif			
GI_37595544-S	971.5	570.6	416.4	PCTK2	NM_002595.2	PCTAIRE2	protein		protein
GI_37595546-S	131.8	177.1	142.4	PDK1	NM_002610.3		[pyruvate	mitochond	small
GI_37595547-S	130.3	159.9	147.7	PEPP3	NM_014935.2	KIAA0969			
GI_37595549-I	182.5	229.2	197.5	PKNOX1	NM_004571.3	PREP1	specific		
GI_37595550-A	325.2	354.4	308.2	PKNOX1	NM_197976.1	PREP1	specific		
GI_37595552-S	160.3	169.6	157.6	RNF111	NM_017610.6	ARK;FLJ38008;DKFZp761D081;DKFZp313E			
GI_37595554-S	101.1	91.1	90.8	RNF125	NM_017831.2	FLJ20456;MGC21737			
GI_37595556-S	522.8	763.4	751.4	ATP1B1	NM_001677.2	ATP1B	sodium/po	sodium/po	small
GI_37595557-I	248.4	259.7	178.7	BTN3A1	NM_007048.3	BTF5;BT3.1			lipid
GI_37595559-S	94.1	114.5	94	DNALI1	NM_003462.3	P28;hp28	axonemal	axonemal	fertilization
GI_37595561-S	292.4	366.9	334.3	NFATC4	NM_004554.3	NFAT3;NF-ATc4	transcripti	nucleus	transcripti
GI_37595562-S	263.3	299.3	294.2	OLR1	NM_002543.2	LOX1;SCARE1	LDL	membran	proteolysis
GI_37595563-A	190.8	249.5	221.6	CD3Z	NM_000734.2	CD3H;CD3Q;TCRZ;CD3-ZETA	T-cell	integral to	cellular
GI_37595566-S	3651.1	2968.1	2844.1	RNF110	NM_007144.2	MEL-18;ZNF144;MGC10545	transcripti	nucleus	regulation
GI_37595567-S	91.5	130.5	92.4	SALL4	NM_020436.2	DRRS;HSAL4;dJ1112F19.1	DNA	nucleus	regulation
GI_37595568-S	6338.3	4380.8	3623.2	SCGF	NM_002975.2	P47;LSLCL;CLECSF3	stem cell	extracellul	positive
GI_37595749-I	112.9	130.8	118.5	LBR	NM_002296.2	PHA;LMN2R;MGC9041;PRO0650	lamin/chro	integral to	
GI_37595751-A	2850.8	2458	2917.7	LBR	NM_194442.1	PHA;LMN2R;MGC9041;PRO0650	lamin/chro	integral to	
GI_37595751-I	92.8	100.6	105.9	LBR	NM_194442.1	PHA;LMN2R;MGC9041;PRO0650	lamin/chro	integral to	
GI_37595753-I	122.5	121.6	108.5	LDHD	NM_153486.2	MGC57726			electron
GI_37595755-A	177.4	207	194.4	LDHD	NM_194436.1	MGC57726			electron
GI_37596296-S	195.4	226.3	190.3	CDKL1	NM_004196.3	p42;KKIALRE	cyclin-		protein
GI_37596298-S	234.8	276.1	243.6	HOXA2	NM_006735.3		transcripti	nucleus	regulation
GI_37620158-S	187.6	194.7	236.2	KIAA0625	NM_015046.4	AOA2;SETX;SCAR1			
GI_37620162-I	267.4	343.9	260.3	MASK	NM_020690.3	FLJ10042;FLJ11979;FLJ14127;FLJ20288;KI			
GI_37620164-S	1466.3	1062.8	1032.2	FLJ20360	NM_017782.2				
GI_37620168-S	111	119.4	109.9	GPR126	NM_020455.3	VIGR;FLJ14937;DKFZp564D0462	G-protein	membran	neuropepti

GI_37620170-S	194.4	160	130.5	AKNA	NM_030767.2				
GI_37620172-S	91.5	93.4	88.1	FLJ11457	NM_024753.2				
GI_37620174-S	112	119.6	109.9	CMYA3	NM_152381.2				
GI_37620176-I	145	146.3	153.5	EB-1	NM_152788.2	AIDA;MGC26087			
GI_37620180-S	451.1	517.4	434.3	DKFZP564G	NM_015601.2	KIAA1593	ubiquitin-	intracellula	ubiquitin
GI_37620203-S	219.6	254.3	246.3	OR2C3	NM_198074.1	OR2C4;OR2C5P;OST742	olfactory	integral to	perception
GI_37620205-S	1282.9	1255.1	1040.2	gm117	NM_198077.1				
GI_37620211-S	81.3	89.3	86.4	SCML4	NM_198081.1	dJ47M23.1			
GI_37620213-S	106.9	127.1	119.2	C21orf121	NM_198078.1	PRED87			
GI_37620215-S	1635.5	2008.4	1539.4	LOC253827	NM_198080.1				
GI_37620217-S	120.9	142.5	137	LOC284001	NM_198082.1				
GI_37622340-I	112	111.5	106.4	ZNF42	NM_198055.1	MZF1;MZF-1;MZF1B	transcripti	nucleus	regulation
GI_37622342-A	891.8	1123	847.4	ZNF266	NM_198058.1	HZF1	DNA	nucleus	developm
GI_37622344-A	689.8	850.5	815.3	ZNF42	NM_003422.2	MZF1;MZF-1;MZF1B	transcripti	nucleus	regulation
GI_37622348-I	111.6	110.3	94.9	ZNF266	NM_006631.2	HZF1	DNA	nucleus	developm
GI_37622350-S	814.2	988.8	831.8	NUDT3	NM_006703.2	DIPP	diphospho		diadenosi
GI_37622351-S	162.5	157.9	149.6	ITLN2	NM_080878.2	HL-2	lectin [goid		heterophili
GI_37622352-S	114.7	157.7	105.6	NME5	NM_003551.2	NM23H5;NM23-H5	nucleoside	cellular_co	nucleoside
GI_37622353-S	1799.4	1084.7	214.2	INHBE	NM_031479.3	MGC4638;activin	hormone	extracellul	cell growth
GI_37622354-S	411.2	586	423.9	BLZF1	NM_003666.2	JEM1;JEM-1;GOLGIN-45	RNA	nucleus	regulation
GI_37622886-A	1070.8	1199.3	1261.5	CES2	NM_198061.1	iCE;CE-2	carboxyles	endoplas	catabolis
GI_37622888-S	1108.9	1300.9	1215.7	CHP	NM_007236.3	SLC9A1BP	potassium		small
GI_37622889-A	93	111.3	97.5	PLAGL1	NM_002656.2	ZAC;LOT1;ZAC1	tumor		induction
GI_37622891-A	1309.4	1106.2	987	RNF126	NM_017876.3	MGC1022;FLJ20552;MGC14317			
GI_37622893-I	275.3	279	282.7	RNF126	NM_194460.1	MGC1022;FLJ20552;MGC14317			
GI_37622895-S	101.2	122	121.2	RNF127	NM_024778.3	FLJ22612			
GI_37622897-S	106.6	116.7	104.8	RNF129	NM_152620.2	FLJ35882	zinc ion	intracellula	
GI_37622898-S	282	249.8	288.3	RNF137	NM_018073.5	SS-56;FLJ10369	zinc ion	intracellula	
GI_37622900-A	2048.7	847.9	421.7	DSIPI	NM_004089.2	DIP;GILZ;TSC-22R	transcripti	nucleus	regulation
GI_37622900-I	184.5	133.4	122.5	DSIPI	NM_004089.2	DIP;GILZ;TSC-22R	transcripti	nucleus	regulation
GI_37622902-I	132.9	158.9	143.2	DSIPI	NM_198057.1	DIP;GILZ;TSC-22R	transcripti	nucleus	regulation
GI_37622904-S	380.9	493.7	726.3	PPP1R3D	NM_006242.3	PPP1R6	protein		glycogen
GI_37622905-A	104.1	100.4	91.9	SCN5A	NM_000335.3	HB1;HB2;HH1;IVF;LQT3;Nav1.5	sodium	voltage-	sodium
GI_37622908-I	97	109	96.6	USH3A	NM_174878.2	USH3			
GI_37622909-S	122	138.7	107.6	CHRM1	NM_000738.2	M1;HM1;MGC30125	muscarini	membran	phosphati
GI_37655156-S	1431.9	1292.8	711.3	COPEB	NM_001300.3	GBF;ZF9;BCD1;CPBP;KLF6;PAC1;ST12			
GI_37655158-A	1436.4	1690.2	1769.7	COX15	NM_004376.3		cytochrom	mitochond	respiratory
GI_37655159-I	399.7	586.3	504.9	COX15	NM_078470.2		cytochrom	mitochond	respiratory
GI_37655164-S	551.7	538.4	594.7	RNF134	NM_032154.3	MBLR;MGC15678;MGC17541			
GI_37655166-I	192.8	178	176.6	RNF135	NM_032322.3	MGC13061			
GI_37655168-A	140	127	131.2	RNF135	NM_197939.1	MGC13061			
GI_37655170-I	96.4	112	109.8	ZNF155	NM_003445.2	pHZ-96	transcripti	nucleus	regulation
GI_37655172-A	326.4	372.5	328.9	ZNF155	NM_198089.1	pHZ-96	transcripti	nucleus	regulation
GI_37655174-S	850.3	588	467.5	ZNF26	NM_019591.2	KOX20;FLJ20755	DNA	nucleus	regulation

GI_37655176-S	101.1	109.4	95.8	ZNF415	NM_018355.2	FLJ11191	nucleic	intracellula	regulation
GI_37655178-S	168.5	196.3	171.4	AP3B2	NM_004644.3	NAPTB	vesicle	secretory	post-Golgi
GI_37655179-S	1867.2	1816.9	2702.6	DUSP3	NM_004090.2	VHR	protein		protein
GI_37655180-S	156.4	136.4	168.4	TCEB3BP1	NM_020695.2	EloA-BP1;KIAA1138	exonuclea	intracellula	regulation
GI_37655182-S	14866.6	9611.6	10921	NDRG1	NM_006096.2	GC4;RTP;DRG1;NDR1;NMSL;TDD5;CAP43;	tumor	nucleus	response
GI_37674208-S	4626.7	4627	4431.6	WDR18	NM_024100.2	MGC2436;R32184_1			
GI_37674209-S	378.2	402.5	355.8	SSH2	NM_033389.2	SSH-2;KIAA1725			
GI_37674228-S	115.6	145.6	139.6	KIAA0514	NM_014696.2	MGC15171			
GI_37674229-S	163	141.1	121	C9orf61	NM_004816.2	X123			
GI_37674231-S	507.6	435.4	285	HOZFP	NM_152995.3		transcripti	nucleus	regulation
GI_37674282-S	202.8	245.6	236.5	C7orf28A	NM_015622.4	CGI-43;H_DJ1163J12.2			
GI_37674288-S	3120.1	3314.5	3018.7	C7orf28B	NM_198097.1	MGC19819;DKFZP586I1023;H_NH0577018.			
GI_37675267-A	252.7	233.5	263.4	ZNF200	NM_198087.1		molecular	nucleus	regulation
GI_37675271-A	123.5	125.5	127.4	ZFP29	NM_017894.2	FLJ20595	transcripti	nucleus	regulation
GI_37675271-I	104.2	106.9	111	ZFP29	NM_017894.2	FLJ20595	transcripti	nucleus	regulation
GI_37675272-I	99.8	112.3	109.4	ZNF200	NM_003454.2		molecular	nucleus	regulation
GI_37675274-I	108.9	123.5	102.6	ZFP29	NM_181877.2	FLJ20595	transcripti	nucleus	regulation
GI_37675275-S	569.3	720.5	530	NME4	NM_005009.2	NM23H4;nm23-H4	nucleoside	mitochond	nucleoside
GI_37675276-S	108.6	123.1	98.3	RNF148	NM_198085.1	MGC35222	peptidase		proteolysis
GI_37675278-I	141.4	120.7	114.2	JUB	NM_032876.4	MGC15563	transporte	membran	transport
GI_37675279-A	1456.4	886.6	585.4	JUB	NM_198086.1	MGC15563	transporte	membran	transport
GI_37675279-I	139.8	129	114.7	JUB	NM_198086.1	MGC15563	transporte	membran	transport
GI_37675281-S	754.9	935.1	749.5	DECR2	NM_020664.3	PDCR	oxidoredu		metabolis
GI_37675282-S	96.7	101.5	91.6	AP4E1	NM_007347.2			secretory	nonselecti
GI_37675386-A	104.4	98.7	91.1	CLECSF12	NM_197954.1	BGR;DECTIN1			
GI_37675386-I	100.3	93.6	85	CLECSF12	NM_197954.1	BGR;DECTIN1			
GI_37693520-S	854.8	826	735.4	DHRS4L2	NM_198083.1	MGC905			
GI_37693523-S	527.4	471.4	538.2	ZFHX1B	NM_014795.2	SIP1;SIP-1;SMADIP1;KIAA0569	transcripti	nucleus	regulation
GI_37693524-A	344.7	427.3	338.7	ZNF189	NM_003452.2		transcripti	nucleus	negative
GI_37693992-S	405.8	551.1	513.4	NME3	NM_002513.2	DR-nm23	nucleoside		induction
GI_37693994-S	448.3	583.1	532.5	KLF13	NM_015995.2	BTEB3;FKLF2;NSLP1;RFLAT1;RFLAT-1	RNA	nucleus	transcripti
GI_37693998-S	90.3	81.5	73.8	CKTSF1B1	NM_013372.4	DRM;IHG-2;GREMLIN	protein	extracellul	developm
GI_37694060-A	250.3	303.6	280.4	AQP1	NM_000385.3	CO;CHIP28;AQP-CHIP;MGC26324	water	integral to	water
GI_37694061-I	184.6	237.8	203.7	AQP1	NM_198098.1	CO;CHIP28;AQP-CHIP;MGC26324	water	integral to	water
GI_37694063-I	192.9	164	149.6	EBAG9	NM_004215.3	EB9;RCAS1	apoptotic	kinesin	apoptosis
GI_37694064-A	1463.9	1224.3	1161.2	EBAG9	NM_198120.1	EB9;RCAS1	apoptotic	kinesin	apoptosis
GI_37694064-I	128	125	126.2	EBAG9	NM_198120.1	EB9;RCAS1	apoptotic	kinesin	apoptosis
GI_37694066-A	127.8	269.3	447	NMES1	NM_197955.1	FOAP-11;FLJ22645;MGC32925			
GI_37694068-I	105.7	108.3	116.1	NMES1	NM_032413.2	FOAP-11;FLJ22645;MGC32925			
GI_37700248-S	113.2	114.5	104.9	LOC253012	NM_198151.1				
GI_37700251-S	96.1	83.5	83.5	URP	NM_198152.1				
GI_37700253-S	84.8	87.5	99.8	LOC285852	NM_198153.1				
GI_37700255-S	161.4	200.9	162.5	LOC339168	NM_198154.1				
GI_37704380-S	18423.5	20075	14032	B2M	NM_004048.2		amyloid		antigen

GI_37704381-A	137.7	150.5	130	DEFB119	NM_153289.2	DEFB-19;DEFB-20;DEFB120			xenobiotic
GI_37704385-S	103.8	125.6	120.9	RYR3	NM_001036.2		calcium-	membran	calcium
GI_37704387-S	2316.7	2038.8	2330.6	SOX9	NM_000346.2	CMD1;SRA1;CMPD1	RNA	nucleus	cartilage
GI_38016126-S	81.2	82.5	61.9	KIAA0117	NM_015014.1		DNA	intracellula	biological_
GI_38016130-S	377.8	679.1	306	GSTO2	NM_183239.1		glutathion	cytoplasm	metabolis
GI_38016132-S	129.7	137.3	126.8	FLJ40113	NM_198079.1				
GI_38016136-S	113.4	122.2	120.8	GPR103	NM_198179.1	AQ27;SP9155	neuropepti	integral to	electron
GI_38016139-S	91.1	97.5	98.6	P518	NM_198180.1	QRFP			
GI_38016155-S	99.4	95.6	102.2	FLJ11331	NM_018392.3				
GI_38016157-S	140.3	151.2	136.2	LOC91431	NM_138698.2				
GI_38016179-S	116.8	124.5	106.6	FAM13C1	NM_198215.1	MGC33233			
GI_38016201-S	488	440.6	514.9	SATB2	NM_015265.1	FLJ21474;KIAA1034			
GI_38016203-S	76.7	79.4	85.4	CBWD2	NM_172003.2				
GI_38016902-S	879.2	957.4	891.3	XTP2	NM_015172.2	BAT2-iso;KIAA1096			
GI_38016903-S	133.3	154.8	128.5	TSRC1	NM_019032.2	DKFZP434K1772			
GI_38016906-A	98.9	225.2	137.4	STOM	NM_198194.1	BND7;EPB7;EPB72		cytoskelet	
GI_38016908-S	108.9	108.4	100.5	TCF1	NM_000545.3	HNF1;LFB1;HNF1A;MODY3	RNA	nucleus	regulation
GI_38016910-I	139.7	173.7	147.2	STOM	NM_004099.4	BND7;EPB7;EPB72		cytoskelet	
GI_38016912-S	3939.4	4402	4075.5	SFRS9	NM_003769.2	SRp30c	pre-mRNA	nucleus	mRNA
GI_38016913-S	196.8	269.4	232.9	SAMHD1	NM_015474.2	DCIP;MOP-5;SBBI88;DKFZP564A032	GTPase	intracellula	response
GI_38016915-A	181.2	137.8	89.7	SDCBP2	NM_015685.3	ST-2;SITAC18	protein		intracellula
GI_38016915-I	333.7	421.5	376.8	SDCBP2	NM_015685.3	ST-2;SITAC18	protein		intracellula
GI_38016917-I	95.4	113.2	95.7	RSN	NM_002956.2	CLIP;CLIP1;CYLN1;CLIP170;CLIP-170	microtubul	endosome	nonselecti
GI_38016918-S	741.2	762.4	636.2	PRO0149	NM_014117.2				
GI_38016920-S	1640.7	1512.2	1344.8	RAB35	NM_006861.4	RAY;H-ray;RAB1C	RAB small		small
GI_38016921-A	472.4	566.5	596.4	POP5	NM_198202.1	RPP2;RPP20;HSPC004			
GI_38016923-S	512	489.9	433.8	PRKAB1	NM_006253.4	ampk;HAMPKb			signal
GI_38016925-I	95.1	103	93.3	POP5	NM_198201.1	RPP2;RPP20;HSPC004			
GI_38016927-S	105.8	113.2	97.4	PLA2G1B	NM_000928.2	PLA2;PLA2A;PPLA2	phospholi		actin
GI_38016928-S	5659.5	5303.9	5423.3	PBP	NM_002567.2	RKIP	phosphati		
GI_38016929-A	123.4	171.1	128	OASL	NM_198213.1	TRIP14;p59OASL	double-	nucleolus	immune
GI_38016931-S	151.4	135.6	110.7	PARG1	NM_004815.2		Rho		Rho
GI_38016933-I	371.4	430.7	385.7	OASL	NM_003733.2	TRIP14;p59OASL	double-	nucleolus	immune
GI_38016936-S	124.4	129.9	156.2	KPI2	NM_014916.2	cprk;KPI-2;KIAA1079	protein-		protein
GI_38016938-S	100.7	117.4	100.6	HPD	NM_002150.2	PPD	4-		tyrosine
GI_38016939-S	913	973.9	1260.2	HSRG1	NM_014940.2	KIAA0872	molecular		
GI_38016940-S	145.6	226	222.3	HSPB8	NM_014365.2	H11;E2IG1;HSP22	protein	cellular_co	biological_
GI_38016941-I	234.1	272.6	228.4	GSN	NM_000177.3		barbed-	extracellul	actin
GI_38016942-S	467.3	544.6	514.8	FLJ14466	NM_032790.2				
GI_38016944-S	383	336.2	333.8	DEAF1	NM_021008.2	SPN;NUDR;ZMYND5	transcripti	nucleus	germ-cell
GI_38016946-S	136.5	171.4	195.3	C5	NM_001735.2		antibacteri	membran	response
GI_38016948-A	522.5	624.2	540.7	ASTN2	NM_198188.1	KIAA0634			
GI_38016948-I	161.1	199.9	190.5	ASTN2	NM_198188.1	KIAA0634			
GI_38016954-I	108.8	118.5	102.8	ASTN2	NM_014010.2	KIAA0634			

GI_38016956-S	205.1	224	241.4	ARHF	NM_019034.2	RIF;FLJ20247			
GI_38026848-I	92	103	100.6	ABHD2	NM_007011.4	HS1-2;LABH2;PHPS1-2;MGC26249	catalytic	integral to	biological_
GI_38026872-A	141.5	143.9	121.1	ABHD2	NM_152924.2	HS1-2;LABH2;PHPS1-2;MGC26249	catalytic	integral to	biological_
GI_38026891-S	336.2	349.3	399	ALG6	NM_013339.2		oligosacch	endoplas	N-linked
GI_38026914-A	462.5	555.1	503.9	ARHGEF11	NM_014784.2	GTRAP48;KIAA0380;PDZ-RHOGEF	signal		intracellula
GI_38026933-I	116.5	127.5	117.4	ARHGEF11	NM_198236.1	GTRAP48;KIAA0380;PDZ-RHOGEF	signal		intracellula
GI_38026942-A	101.7	123.5	115.3	C21orf107	NM_018963.3	N143;WDR9;FLJ11315			
GI_38026942-I	164.6	171.5	182	C21orf107	NM_018963.3	N143;WDR9;FLJ11315			
GI_38026951-I	120	133.9	143.3	C21orf107	NM_033656.2	N143;WDR9;FLJ11315			
GI_38026959-A	2434.3	2353.8	2296.8	C21orf33	NM_198155.1	ES1;HES1;KNPH;KNPI;GT335;KNP-	molecular	mitochond	
GI_38026968-I	610.4	589.6	602.3	C21orf33	NM_004649.4	ES1;HES1;KNPH;KNPI;GT335;KNP-	molecular	mitochond	
GI_38027922-S	2757.7	2654.6	2464.6	COPS5	NM_006837.2	JAB1;SGN5;MOV-34;MGC3149	translation	eukaryotic	protein
GI_38027945-S	413.8	462.9	480.1	COPS6	NM_006833.4	MOV34-34KD	translation		translation
GI_38044105-S	191.1	214.7	237.9	OVTN	NM_198185.1				
GI_38044107-S	95.3	110.3	113	OSTN	NM_198184.1				
GI_38044109-S	169.7	179.2	143.4	LOC374676	NM_198181.1				
GI_38044111-A	113.1	122.5	125.5	RSN	NM_198240.1	CLIP;CLIP1;CYLN1;CLIP170;CLIP-170	microtubul	endosome	nonselecti
GI_38044113-I	137	122.1	109.7	SDCBP2	NM_080489.2	ST-2;SITAC18	protein		intracellula
GI_38044279-S	266.7	290.6	286.7	SEDL	NM_014563.2	SEDT	intracellula	Golgi	nonselecti
GI_38044281-A	1426.3	656.9	1106.6	NAV2	NM_145117.2	HELAD1;RAINB1;POMFIL2;FLJ10633;FLJ11			
GI_38044283-I	178.2	228.2	188.4	NAV2	NM_182964.3	HELAD1;RAINB1;POMFIL2;FLJ10633;FLJ11			
GI_38044285-S	98.6	97.5	103.6	ZNF547	NM_173631.2	FLJ31100	nucleic	intracellula	regulation
GI_38044287-A	1609.9	2386.6	1897.6	GSN	NM_198252.1		barbed-	extracellul	actin
GI_38044287-I	168.3	215.8	171.8	GSN	NM_198252.1		barbed-	extracellul	actin
GI_38044289-S	558.3	349	318	ZCCHC8	NM_017612.2	DKFZp434E2220	DNA	nucleus	regulation
GI_38045884-S	158	165.1	284	CSMD2	NM_052896.2	KIAA1884			
GI_38045885-A	184.7	149.8	131.5	CSMD3	NM_052900.2	KIAA1894			
GI_38045889-I	117.9	138.4	128.7	CSMD3	NM_198124.1	KIAA1894			
GI_38045893-A	203.1	223.6	216.5	ELKS	NM_178038.1	ERC1;RAB6IP2;KIAA1081;MGC12974			
GI_38045897-I	113.5	106.5	98.6	ELKS	NM_178040.1	ERC1;RAB6IP2;KIAA1081;MGC12974			
GI_38045900-I	182.4	185.4	161.1	TFCP2L2	NM_014552.2	MGR;GRHL1;LBP-32			
GI_38045902-A	90.9	85.3	95.6	TFCP2L2	NM_198182.1	MGR;GRHL1;LBP-32			
GI_38045904-I	152	145.9	148.2	VHL	NM_000551.2	RCA1;HRCA1	transcripti	cytosol	negative
GI_38045905-A	307.4	323.6	264.7	VHL	NM_198156.1	RCA1;HRCA1	transcripti	cytosol	negative
GI_38045907-A	187	231.7	344.9	LAMA3	NM_000227.2	E170;LOCS;LAMNA	structural	basement	epidermal
GI_38045907-I	105.6	114.3	118.3	LAMA3	NM_000227.2	E170;LOCS;LAMNA	structural	basement	epidermal
GI_38045909-I	369.8	406	377	LAMA3	NM_198129.1	E170;LOCS;LAMNA	structural	basement	epidermal
GI_38045911-A	7082	8195.3	7242.3	NME1	NM_000269.2	AWD;GAAD;NM23;NDPKA;NM23-H1	nucleoside	nucleus	negative
GI_38045912-I	253.8	295.6	248	NME1	NM_198175.1	AWD;GAAD;NM23;NDPKA;NM23-H1	nucleoside	nucleus	negative
GI_38045914-S	2343.4	3422.4	3941.6	PAPPA	NM_002581.3	PAPA;PAPP-A;ASBABP2;IGFBP-4ase	metallope	membran	pregnancy
GI_38045916-A	360.1	456.4	405	PIGO	NM_152850.2	MGC3079;FLJ00135;MGC20536;DKFZp434	molecular	endoplas	GPI
GI_38045918-S	160.2	210.5	179.3	HIP1	NM_005338.4		structural	cytoskelet	cell shape
GI_38045920-S	859.7	684.7	483.4	HNT	NM_016522.2	NTM;MGC60329	cell	integral to	neuronal
GI_38045927-A	261.2	342.6	291.2	RAPSN	NM_032645.3	MGC3597		cytoskelet	synaptic

GI_38045929-I	98.7	94.6	93.7	RAPSN	NM_005055.3	MGC3597		cytoskelet	synaptic
GI_38045930-S	179.5	225.7	172.4	RNF122	NM_024787.2	FLJ12526			
GI_38045932-I	99.5	91.6	90.8	RNF138	NM_016271.3	HSD-4;STRIN;MGC8758			
GI_38045933-A	363.7	367.6	292.3	RNF138	NM_198128.1	HSD-4;STRIN;MGC8758			
GI_38045935-S	93.5	90.4	82	RNF139	NM_007218.3	RCA1;TRC8;HRCA1;MGC31961	receptor	integral to	signal
GI_38045936-S	213	239	230	RNF141	NM_016422.3	ZFP26;ZNF230;MGC8715			
GI_38045937-S	2341.9	3282.2	1947.3	RNF144	NM_014746.2	KIAA0161;UBCE7IP4		nucleus	
GI_38045939-S	515.3	512.6	583.1	RNF31	NM_017999.3	ZIBRA;FLJ10111;FLJ23501;MGC19975			
GI_38045945-A	1069.6	1350.1	977.8	UBE1C	NM_198197.1	UBA3;hUba3;MGC22384;DKFZp566J164	ubiquitin-		proteolysis
GI_38045947-S	429.8	772.9	599.3	UBE1L	NM_003335.2	D8;UBE2;MGC12713	ubiquitin		protein
GI_38045949-S	543.9	657.1	497.5	UBE2Q	NM_017582.5	NICE-5;PRO3094	ubiquitin-		ubiquitin
GI_38045950-S	219.8	260	243.5	ZNF10	NM_015394.4	KOX1;MGC26561	RNA		regulation
GI_38045951-S	563.3	713.7	663.3	ZNF14	NM_021030.2	KOX6;GIOT-4	DNA	nucleus	regulation
GI_38045953-S	613.1	600.4	606.5	ZNF16	NM_006958.2	KOX9	DNA	nucleus	regulation
GI_38045955-S	109.4	112	100.9	ZNF19	NM_006961.2	KOX12;MGC51021	transcripti	nucleus	regulation
GI_38045964-A	119	138.9	117.4	ZNFN1A3	NM_183231.1	AIOLOS	transcripti	nucleus	mesoderm
GI_38049008-I	104	116.5	123.3	SOM	NM_198173.1	GRHL3;MGC46624			
GI_38049010-A	99	99.4	86.1	SOM	NM_198174.1	GRHL3;MGC46624			
GI_38049013-A	111.8	108.7	101.4	SEMG1	NM_198139.1	SGI;SEMG;MGC14719		extracellul	inseminati
GI_38049015-S	82	80.2	77.4	SEMG2	NM_003008.2	SGII		extracellul	
GI_38093638-S	119.5	133.3	123.2	LMOD3	NM_198271.1				
GI_38093640-S	1371.8	1180.2	1428.1	DKFZP566G1	NM_198272.1				protein
GI_38093642-S	162.2	197	144.5	SMYD1	NM_198274.1	BOP;ZMYND18	DNA	nucleus	regulation
GI_38093644-S	107.7	108.5	91.8	LOC196264	NM_198275.1				
GI_38093646-S	530.8	609.2	586.8	TMEM17	NM_198276.1	FLJ34583			
GI_38093648-S	450.8	701.4	803.9	SLC37A2	NM_198277.1	FLJ00171			
GI_38093650-S	153	168.9	151.8	LOC255743	NM_198278.1				
GI_38093652-S	133.8	131.5	125.6	LOC256643	NM_198279.1				
GI_38093654-S	171	212.4	179.9	LOC284612	NM_198280.1				
GI_38093656-S	293.8	351.8	297.8	LOC285513	NM_198281.1				
GI_38093658-S	186.9	212.4	173	LOC340061	NM_198282.1				
GI_38093660-S	114.4	122.4	112.8	EGFL11	NM_198283.1	dJ1018A4.2			
GI_38093662-S	133.3	280.7	130.3	LOC349136	NM_198285.1				
GI_38093664-S	460.9	568.2	558.2	LOC349114	NM_198284.1				
GI_38142463-S	1168.5	826.6	645.6	ABC1	NM_022070.3	FLJ22087			
GI_38146000-S	262.6	304	300.5	ASXL2	NM_018263.2	ASXH2;FLJ10898;KIAA1685			
GI_38146007-A	675.4	918.9	1025.7	TTC8	NM_198310.1	BBS8			
GI_38146009-A	95.2	105	91.9	HTR3E	NM_198313.1	5-HT3c1			
GI_38146009-I	100.7	112.1	103.2	HTR3E	NM_198313.1	5-HT3c1			
GI_38146093-S	689.6	696.5	845.7	THRAP5	NM_005481.2	DRIP92;TRAP95	transcripti	nucleus	transcripti
GI_38146097-S	246.5	227	325.8	SPP1	NM_000582.2	OPN;BNSP;BSPI;ETA-1		extracellul	ossificatio
GI_38146100-S	753.5	624.2	518.7	RPC5	NM_018119.2	FLJ10509	DNA-	nucleus	transcripti
GI_38146101-S	498.7	445.2	434.6	POLL	NM_013274.2	BETA-N;POL-KAPPA			
GI_38146102-S	137.8	199.8	183.1	MGC2641	NM_032631.2		DNA	nucleus	regulation

GI_38146105-S	1006.4	957.9	1008.6	FLJ11856	NM_024531.3	GPCR;PAR1;GPCR41			
GI_38146106-A	1382.8	1776.7	1896.9	FLJ11021	NM_023012.3				
GI_38146110-S	891	736.9	729.3	FLJ10496	NM_018114.3				
GI_38146114-S	982	1007.2	1152.7	FHX	NM_018416.2		transcripti	nucleus	regulation
GI_38146115-I	108.6	119.1	113.6	C1orf2	NM_006589.2	COTE1;cote 1			
GI_38146117-A	1598.1	1622.4	2113.3	C1orf2	NM_198264.1	COTE1;cote 1			
GI_38148698-S	2627.9	2784.1	2560.9	SEC6L1	NM_007277.3	SEC6;EXOC3;Sec6p	protein	kinesin	intracellula
GI_38149839-A	195.9	245.2	179.2	SEC31L2	NM_015490.3	SEC31B-1;DKFZP434M183			
GI_38149839-I	286.6	339.3	292.4	SEC31L2	NM_015490.3	SEC31B-1;DKFZP434M183			
GI_38149909-I	239.7	291.6	265	SEC31L2	NM_198138.1	SEC31B-1;DKFZP434M183			
GI_38149917-I	1025.7	1274.2	864.8	SNRPB2	NM_003092.3	MGC24807;MGC45309	pre-mRNA	snRNP U2	mRNA
GI_38149980-A	904.8	907.1	459.7	SNRPB2	NM_198220.1	MGC24807;MGC45309	pre-mRNA	snRNP U2	mRNA
GI_38149990-I	4124.1	3752.8	2107.6	SNRPB	NM_003091.3	COD;SNRPB1;snRNP-B;SmB/SmB'	small	spliceoso	mRNA
GI_38150006-A	6710	5287.1	3383.5	SNRPB	NM_198216.1	COD;SNRPB1;snRNP-B;SmB/SmB'	small	spliceoso	mRNA
GI_38156696-A	276.9	361.4	308	MITF	NM_198158.1	WS2A	DNA	nucleus	hearing
GI_38156698-I	224	256.8	236.5	MITF	NM_198159.1	WS2A	DNA	nucleus	hearing
GI_38156700-I	95.2	108.9	103.3	MITF	NM_006722.1	WS2A	DNA	nucleus	hearing
GI_38157975-I	141.8	150.6	137.8	UBE2L3	NM_198157.1	E2-F1;L-UBC;UBCH7;UbcM4	ubiquitin	ubiquitin	ubiquitin-
GI_38157977-A	1487.1	1518.8	1394.2	UBE2L3	NM_003347.2	E2-F1;L-UBC;UBCH7;UbcM4	ubiquitin	ubiquitin	ubiquitin-
GI_38157980-A	400.2	414.3	329.2	UBE2L6	NM_004223.3	RIG-B;UBCH8;MGC40331	ubiquitin		protein
GI_38157980-I	929.9	983.3	715	UBE2L6	NM_004223.3	RIG-B;UBCH8;MGC40331	ubiquitin		protein
GI_38157985-I	128.2	146.4	135.9	UBE2L6	NM_198183.1	RIG-B;UBCH8;MGC40331	ubiquitin		protein
GI_38158004-A	134.3	144.4	140.6	TYROBP	NM_198125.1	DAP12;KARAP;PLOSL	receptor	integral to	cellular
GI_38158008-A	99.1	99.8	99	CIDEA	NM_001279.2	CIDE-A	apoptosis	intracellula	DNA
GI_38158010-I	110	109	96.1	CIDEA	NM_198289.1	CIDE-A	apoptosis	intracellula	DNA
GI_38158012-S	100.5	95.3	89.8	MAMDC1	NM_182830.2	MDGA2;c14_5286		membran	
GI_38158014-S	131.3	132.9	120.5	MAML3	NM_018717.2	GDN;MAM2;CAGH3;ERDA3;MAM-	transcripti	nucleus	neurogene
GI_38158017-S	173.8	158.2	163.7	CEP1	NM_007018.3	FAN;CEP110	RNA	nucleus	
GI_38158019-I	107.8	121.7	108.4	DHX34	NM_194428.1	HRH1;DDX34;KIAA0134	ATP		
GI_38158021-A	377.9	282.6	306.3	DHX34	NM_014681.3	HRH1;DDX34;KIAA0134	ATP		
GI_38158027-S	157	169.4	159.9	GPR54	NM_032551.2	AXOR12;HOT7T175	receptor	integral to	G-protein
GI_38158029-S	6543.9	5421.9	4632.1	SFRS6	NM_006275.4	B52;SRP55;MGC5045	pre-mRNA	nucleus	mRNA
GI_38175820-S	122.3	123.2	111.7	DKFZp434B1	NM_178275.3				
GI_38176148-S	78.3	76.5	71.5	GUCA2A	NM_033553.2	GUCA2;STARA;GUANYLIN	peptide	extracellul	signal
GI_38176150-S	221.1	218.3	216.6	KIAA1715	NM_030650.1	Ul;LNP;ulnaless			
GI_38176152-S	98	98.9	101.3	NODAL	NM_018055.3		cytokine		developm
GI_38176153-S	331.1	327.5	388.9	UNC13B	NM_006377.2	UNC13;MUNC13;Unc13h2;hmunc13	receptor	Golgi	induction
GI_38176155-S	321.7	382.6	355.4	SARA2	NM_016103.2	CMRD;SAR1B	small	Golgi	small
GI_38176156-S	566	512.2	834.4	SPATA2	NM_006038.2	PD1;KIAA0757	molecular	cytoplasm	spermatog
GI_38176157-S	1412.3	1335.5	1215.1	CCNK	NM_003858.2	CPR4;MGC9113			regulation
GI_38176159-S	152.3	170.2	160.2	CHRM5	NM_012125.2	HM5;MGC41838	molecular	integral to	phosphati
GI_38176162-S	821	801.2	688	RNF130	NM_018434.4	GP;G1RZFP;GOLIATH	peptidase		proteolysis
GI_38176282-I	100.8	106.1	117.5	ASB7	NM_198243.1	FLJ22551			
GI_38176284-S	610.9	940.8	1041.3	AYP1	NM_032193.2	FLJ20974;MGC22934			

GI_38176288-I	99	109.3	106.5	CABP1	NM_031205.2	CALBRAIN;HCALB_BR	enzyme		
GI_38176289-A	342.7	369.2	358.4	CABP1	NM_004276.3	CALBRAIN;HCALB_BR	enzyme		
GI_38176290-I	709.8	618.5	431.1	CAV2	NM_001233.3	CAV;MGC12294	tumor	integral to	
GI_38176291-A	1258	833.5	592.6	CAV2	NM_198212.1	CAV;MGC12294	tumor	integral to	
GI_38176293-S	259.5	414.6	159.3	LOC348094	NM_182703.2				
GI_38176295-I	175	190	161.5	LASS1	NM_198207.1	LAG1;UOG1			
GI_38176298-S	354.7	418.7	372.8	MPN2	NM_183062.2				
GI_38176299-S	104.4	121.3	100.6	NES	NM_006617.1	FLJ21841	structural	intermedia	cell shape
GI_38176301-S	2525.8	2160.2	2006.7	ALG5	NM_013338.3	bA421P11.2	oligosacch	endoplas	protein
GI_38194223-S	244	299.8	265.7	GPR25	NM_005298.2		G-protein	integral to	G-protein
GI_38194225-S	116.3	152.2	133.3	SLC6A3	NM_001044.2	DAT;DAT1	dopamine	integral to	small
GI_38194228-S	765.6	1000.9	871.1	LOC339451	NM_198317.1		protein		
GI_38195079-I	133	132.3	212.8	LOH11CR2A	NM_014622.3	BCSC-1	tumor		
GI_38195081-A	140.2	149.6	267.1	LOH11CR2A	NM_198315.1	BCSC-1	tumor		
GI_38195081-I	179.3	216	587	LOH11CR2A	NM_198315.1	BCSC-1	tumor		
GI_38195083-I	232.1	154.7	152.5	HRMT1L2	NM_198319.1	ANM1;HCP1;IR1B4;PRMT1	N-	cytoplasm	protein
GI_38195085-S	7974.3	9534.6	8133.4	LOC63929	NM_022098.2				
GI_38195086-A	3516.8	3743.9	3345.1	HRMT1L2	NM_198318.1	ANM1;HCP1;IR1B4;PRMT1	N-	cytoplasm	protein
GI_38198662-S	227.4	255.2	242.8	KCTD8	NM_198353.1				
GI_38198666-S	143	172	126.7	SLC23A3	NM_144712.2	SVCT3;Yspl1;FLJ31168	transporte	membran	transport
GI_38201610-I	188.3	211	185.1	TCFL4	NM_170607.2	MLX;MAD7;MXD7	transcripti	cytoplasm	regulation
GI_38201613-A	337.2	401.2	418	TCFL4	NM_198205.1	MLX;MAD7;MXD7	transcripti	cytoplasm	regulation
GI_38201615-I	100.1	115.7	108.1	RHOBTB1	NM_014836.3	KIAA0740;MGC33059;MGC33841	small		small
GI_38201616-A	113.3	114.1	116.4	RHOBTB1	NM_198225.1	KIAA0740;MGC33059;MGC33841	small		small
GI_38201616-I	96.6	101.3	99.6	RHOBTB1	NM_198225.1	KIAA0740;MGC33059;MGC33841	small		small
GI_38201618-A	1461.8	1552.9	1305.7	EIF4G1	NM_004953.2	p220;EIF4G	translation	eukaryotic	regulation
GI_38201618-I	170.9	208.9	192.2	EIF4G1	NM_004953.2	p220;EIF4G	translation	eukaryotic	regulation
GI_38201620-I	110.7	98.6	95.2	EIF4G1	NM_182917.2	p220;EIF4G	translation	eukaryotic	regulation
GI_38201629-I	78.5	72.7	73.5	ST7L	NM_198327.1	ST7R;STLR;FLJ11657;FLJ20284			
GI_38201636-A	264	256.3	178	ST7L	NM_138729.2	ST7R;STLR;FLJ11657;FLJ20284			
GI_38201636-I	272.3	274.1	225.3	ST7L	NM_138729.2	ST7R;STLR;FLJ11657;FLJ20284			
GI_38201637-A	119.5	139.6	112.6	HIPK1	NM_152696.3	Myak;Nbak2;KIAA0630;MGC26642;MGC334			
GI_38201637-I	110.1	133.2	116.2	HIPK1	NM_152696.3	Myak;Nbak2;KIAA0630;MGC26642;MGC334			
GI_38201641-I	88.8	93.1	93.2	HIPK1	NM_198269.1	Myak;Nbak2;KIAA0630;MGC26642;MGC334			
GI_38201643-I	87.9	97	79	HIPK1	NM_181358.1	Myak;Nbak2;KIAA0630;MGC26642;MGC334			
GI_38201648-A	1205.9	1027.1	970.9	E2F6	NM_198257.1	E2F-6	transcripti	transcripti	negative
GI_38201654-I	143.9	148.4	128.1	ING3	NM_019071.2	p47ING3;FLJ20089	DNA		regulation
GI_38201658-A	188.1	206.5	226.8	ING3	NM_198267.1	p47ING3;FLJ20089	DNA		regulation
GI_38201658-I	109.1	99.4	113.2	ING3	NM_198267.1	p47ING3;FLJ20089	DNA		regulation
GI_38201660-I	92.3	108.1	108.1	ING1	NM_005537.3	p33ING1	tumor		negative
GI_38201662-A	280.4	418.9	380.7	ING1	NM_198217.1	p33ING1	tumor		negative
GI_38201662-I	89.9	87.6	84.3	ING1	NM_198217.1	p33ING1	tumor		negative
GI_38201666-I	96.9	114.4	99.6	ING1	NM_198219.1	p33ING1	tumor		negative
GI_38201668-S	121.1	120.7	111.6	ING2	NM_058171.2	ING1-like			

GI_38201669-A	150.6	160.9	145.4	ING4	NM_016162.2	my036;p29ING4;MGC12557	DNA		regulation
GI_38201671-I	143.8	164.9	133.1	ING4	NM_198287.1	my036;p29ING4;MGC12557	DNA		regulation
GI_38201673-S	531.7	367.3	387.7	ING5	NM_032329.4	p28ING5;FLJ23842	DNA		regulation
GI_38201674-S	894.9	849.1	2026.8	SDC4	NM_002999.2	SYND4;MGC22217	cytoskelet	proteoglyc	biological_
GI_38201676-S	423.4	450.9	447.7	SDCCAG33	NM_005786.3	NY-CO-33	tumor	nucleus	regulation
GI_38201678-I	94.8	100.7	97.5	SPO11	NM_012444.2	MGC39953	DNA	nucleus	meiotic
GI_38201679-A	87.4	107	99.3	SPO11	NM_198265.1	MGC39953	DNA	nucleus	meiotic
GI_38201681-I	75.2	85.4	82.5	RNASE1	NM_198232.1	RIB1;RNS1;MGC12408	pancreatic	extracellul	
GI_38201687-A	97.5	90.5	82.9	RNASE1	NM_002933.3	RIB1;RNS1;MGC12408	pancreatic	extracellul	
GI_38201688-S	4178.6	2918.9	4527.9	RANGAP1	NM_002883.2	Fug1;KIAA1835;MGC20266	Ran	nuclear	signal
GI_38201689-S	626.7	671.2	559.2	RAP2B	NM_002886.2	MGC20484	GTP		signal
GI_38201691-S	1565.3	1358.3	1489.4	RASA3	NM_007368.2	GAPIII;MGC46517;MGC47588;GAP1IP4BP	GTPase	plasma	signal
GI_38201693-S	691.2	2296.9	760.1	RGS4	NM_005613.3	RGP4;MGC2124;MGC60244	GTPase	peripheral	regulation
GI_38201694-S	146.8	155.3	134.5	RLBP1	NM_000326.3	CRALBP;MGC3663	binding	soluble	vitamin A
GI_38201695-S	233.3	211.7	212.1	RTTN	NM_173630.2	FLJ26356;FLJ39085;DKFZP434G145			
GI_38201699-A	142.4	147.1	151.9	TERT	NM_198254.1	TP2;TRT;EST2;TCS1;hEST2	telomeras	telomere	telomere
GI_38201703-S	296.3	310.4	386.1	C9orf86	NM_024718.2	pp8875;FLJ10101;FLJ13045;bA216L13.9	GTP		protein
GI_38201705-S	307.4	373.3	391.6	FLJ20073	NM_017654.2	KIAA2004			
GI_38201709-I	134.3	148.7	127.4	DDX17	NM_006386.3	P72;RH70	RNA	nucleus	RNA
GI_38201711-A	6831.2	5311.6	4280.2	DDX17	NM_030881.2	P72;RH70	RNA	nucleus	RNA
GI_38201711-I	152.1	197.4	155.6	DDX17	NM_030881.2	P72;RH70	RNA	nucleus	RNA
GI_38201712-S	1254.4	1052.7	550.2	EFNB3	NM_001406.3	EFL6;EPLG8;LERK8	transmem	integral to	neurogene
GI_38201713-S	212.5	194.9	212.9	ELAVL1	NM_001419.2	HUR;Hua;MelG;ELAV1	mRNA 3'		RNA
GI_38201715-A	131.9	150.9	135.7	ELF5	NM_001422.2	ESE2	transcripti		transcripti
GI_38201715-I	188.6	204.9	197.7	ELF5	NM_001422.2	ESE2	transcripti		transcripti
GI_38201716-I	109.1	126.1	120	ELF5	NM_198381.1	ESE2	transcripti		transcripti
GI_38202203-S	1643.5	1436	1360.7	ZFR	NM_016107.3		RNA	nucleus	
GI_38202204-S	372.3	469.4	510.7	ZFYVE26	NM_015346.2	KIAA0321	zinc ion		
GI_38202206-S	90.1	106.9	85.4	MAOB	NM_000898.3	MGC26382	amine	mitochond	electron
GI_38202208-S	235.3	309.8	259.9	MBD5	NM_018328.3	FLJ11113;FLJ30517;KIAA1461	DNA		
GI_38202210-S	431.9	505.7	760	MGC4170	NM_024312.3	DKFZp762B226		membran	cell
GI_38202212-S	264.8	312.4	297.8	SEC10L1	NM_006544.2	EXOC5;SEC10;SEC10P;PRO1912;MGC476	protein	kinesin	post-Golgi
GI_38202213-S	220.8	268	236.1	SEC23A	NM_006364.2	MGC26267	protein	COPII	vesicle-
GI_38202215-I	113.8	135.3	125.2	SRC	NM_005417.3	ASV;SRC1;c-SRC;p60-Src	protein-		signal
GI_38202216-A	459.2	562.3	500.1	SRC	NM_198291.1	ASV;SRC1;c-SRC;p60-Src	protein-		signal
GI_38202216-I	205.2	220.8	192.4	SRC	NM_198291.1	ASV;SRC1;c-SRC;p60-Src	protein-		signal
GI_38202218-S	892.6	876	633.4	FLJ12178	NM_025134.2	KIAA0308	ATP		
GI_38202220-A	132.6	308.9	284.3	FLRT3	NM_013281.2		cell	integral to	signal
GI_38202221-I	127.3	145	124.4	FLRT3	NM_198391.1		cell	integral to	signal
GI_38202223-S	85	98.2	91.2	DLGAP2	NM_004745.3	DAP2;SAPAP2	protein	neurofilam	cell-cell
GI_38202225-S	326	395.9	398.7	ZZEF1	NM_015113.2	ZZZ4;FLJ10821;KIAA0399	zinc ion		
GI_38202227-S	1106.5	1484.7	2072.1	SCAP2	NM_003930.3	PRAP;RA70;SAPS;SKAP55R;MGC10411;M	SH3/SH2		protein
GI_38202228-I	104.4	104.1	96.3	SIAT8D	NM_005668.3	PST;PST1;MGC34450;MGC61459;ST8SIA-	sialyltransf	Golgi	oligosacch
GI_38202231-A	181.5	610.5	2260.4	T1A-2	NM_198389.1	GP36;HT1A-1		integral to	

GI_38202233-S	182.2	143.3	136.7	T2BP	NM_052864.2	TIFA;MGC20791			
GI_38202236-A	109.8	104.2	91.8	TCF21	NM_003206.2	POD1	RNA	nucleus	mesoderm
GI_38202236-I	541.7	624.5	584.4	TCF21	NM_003206.2	POD1	RNA	nucleus	mesoderm
GI_38202238-I	129.6	123.5	122.8	TCF21	NM_198392.1	POD1	RNA	nucleus	mesoderm
GI_38202240-I	95.4	117	102.1	WISP3	NM_198239.1	PPD;CCN6;LIBC;PPAC		soluble	oncogene
GI_38202242-S	5072.3	5322.8	5115.4	YARS	NM_003680.2	YRS;YTS;tyrRS	interleukin-	soluble	tyrosyl-
GI_38202243-S	104.3	112.4	94.4	SLC25A27	NM_004277.2	UCP4;FLJ33552	uncouplin	mitochond	energy
GI_38202245-S	91.9	106.1	92.6	SNPH	NM_014723.2	KIAA0374;MGC46096;bA314N13.5	syntaxin-1	kinesin	neurotran
GI_38202247-S	2226.4	2012.5	1870.4	STAT2	NM_005419.2	P113;ISGF-3;STAT113;MGC59816	hematopoi	nucleus	JAK-STAT
GI_38202248-S	506	536.7	497.8	SUHW2	NM_080764.2	5'OY11.1	DNA	nucleus	regulation
GI_38202249-S	1159.1	1439.5	1623.6	SUMF1	NM_182760.2	FGE	molecular	endoplas	glycosami
GI_38202253-S	1467.7	1690.2	1288.8	PDAP1	NM_014891.4	PAP;PAP1;HASPP28			signal
GI_38202254-S	4038	3898.5	3156.4	TARS	NM_152295.3	ThrRS;MGC9344	ATP	soluble	protein
GI_38202256-A	4277.6	4676.7	4325.1	G2AN	NM_198334.1	KIAA0088	hydrolase		carbohydr
GI_38229312-I	118.1	105.6	105.2	CMIP	NM_198390.1	KIAA1694			
GI_38230497-S	134.5	165.5	148.2	SACS	NM_014363.3	ARSACS;FLJ33280;KIAA0730	chaperone	cellular_co	protein
GI_38257138-S	109	122.8	110.7	PRKAR1B	NM_002735.1	PRKAR1	cAMP-	cAMP-	protein
GI_38257140-S	2765.2	2538.2	2591.7	MAPK3	NM_002746.1	ERK1;PRKM3;P44ERK1;P44MAPK	protein	cellular_co	chemotaxi
GI_38257143-S	109	121.6	113.9	KCTD4	NM_198404.1	bA321C24.3	voltage-	membran	potassium
GI_38257145-S	407.9	434	693.1	LOC157567	NM_198401.1				
GI_38257147-S	99.1	94.4	86.4	PAQR10	NM_198403.1		lysin	integral to	cytolysis
GI_38257150-I	93.3	97.7	95.3	NEDD4	NM_198400.1	KIAA0093	ubiquitin-	intracellula	small
GI_38257154-A	560.8	508	576.9	NEDD4	NM_006154.1	KIAA0093	ubiquitin-	intracellula	small
GI_38257154-I	124.3	136.9	123.2	NEDD4	NM_006154.1	KIAA0093	ubiquitin-	intracellula	small
GI_38257156-S	601.9	735.3	788.5	OSTF1	NM_012383.3	OSF;SH3P2;bA235O14.1	protein	intracellula	ossificatio
GI_38261959-S	82.5	93.7	88.1	FLJ31196	NM_152908.2		drug	membran	multidrug
GI_38261961-S	445.7	506.4	462.4	ATF7IP	NM_018179.3	MCAF;p621;FLJ10139;FLJ10688	protein	nucleus	DNA
GI_38261963-S	892	797.4	611.2	ATF1	NM_005171.2	TREB36	transcripti	nucleus	regulation
GI_38261964-A	95.7	93.4	95.2	ARPP-21	NM_198399.1		molecular	cellular_co	biological_
GI_38261964-I	103	107.8	100.9	ARPP-21	NM_198399.1		molecular	cellular_co	biological_
GI_38261966-S	99.5	104.8	97.2	ASB15	NM_080928.2	Asb-15			intracellula
GI_38261968-S	1153.7	823.3	706.6	APG12L	NM_004707.2	APG12;HAPG12	protein	cytoplasm	autophagy
GI_38261970-I	101.3	96.4	95.5	ARPP-21	NM_016300.3		molecular	cellular_co	biological_
GI_38261972-S	2556.9	2362.2	2305	ADIPOR2	NM_024551.2	MGC4640;FLJ21432	receptor	integral to	fatty acid
GI_38327028-S	2364.4	2872.6	2728.8	UBE4A	NM_004788.2	E4;UFD2;KIAA0126	ubiquitin	ubiquitin	ubiquitin-
GI_38327030-A	351.5	432.7	363.1	UBE1DC1	NM_024818.2	FLJ23251	catalytic		L-serine
GI_38327031-I	165.4	175.5	168.1	UBE1DC1	NM_198329.1	FLJ23251	catalytic		L-serine
GI_38327033-S	545.3	776	720.1	UBE4B	NM_006048.2	E4;686;UFD2;HDNB1;KIAA0684	ubiquitin	ubiquitin	response
GI_38327035-S	1353.4	1434.5	2240.3	HAGH	NM_005326.3	GLO2;GLXII;HAGH1	hydroxyac		
GI_38327036-S	370.3	448.2	454.3	HCN3	NM_020897.1	KIAA1535	cation	integral to	cation
GI_38327038-I	489.8	464.7	545	HSPA4	NM_002154.3	RY;APG-2;hsp70;hsp70RY	molecular		
GI_38327040-A	336.9	407.5	387.5	HSPA4	NM_198431.1	RY;APG-2;hsp70;hsp70RY	molecular		
GI_38327514-S	120.5	119.1	109.1	BCL6B	NM_181844.2	BAZF;ZNF62	protein	nucleus	regulation
GI_38327515-A	118.2	133.8	142.4	KBTBD3	NM_152433.2	BKLHD3;FLJ30685	protein		

GI_38327517-I	155	156.4	164.1	KBTBD3	NM_198439.1	BKLHD3;FLJ30685	protein		
GI_38327519-S	85.3	90.4	91.7	BMPER	NM_133468.2	CV2;CV-2	calcium	extracellul	
GI_38327520-S	102.2	95.7	89.1	ANGPTL1	NM_004673.3	ANG3;ARP1;AngY;ANGPT3;UNQ162	receptor		
GI_38327521-S	671.9	935.5	247.6	ANKRD1	NM_014391.2	ALRP;CARP;C-193;CVARP;MCARP	DNA	nucleus	defense
GI_38327523-S	110	113.7	113.2	ATOH7	NM_145178.2	Math5			
GI_38327524-I	103	118.7	119.2	CPM	NM_001874.2		carboxype	peripheral	embryoge
GI_38327525-A	231.4	288.3	260.5	CPM	NM_198320.1		carboxype	peripheral	embryoge
GI_38327528-I	154.2	180.9	157.7	INSIG1	NM_198336.1	CL-6;MGC1405	DNA	nucleus	metabolis
GI_38327530-A	486.3	1196.3	1073.5	INSIG1	NM_198337.1	CL-6;MGC1405	DNA	nucleus	metabolis
GI_38327532-S	691.5	1288.4	770.4	INSIG2	NM_016133.2	MGC26273			
GI_38327534-S	109.4	121.1	110.2	INSL3	NM_005543.2	RLF;RLNL	insulin	soluble	spermatog
GI_38327536-S	1417.4	1213.9	1026.4	INPP5A	NM_005539.2	5PTASE	inositol-	membran	cell
GI_38327538-S	799.9	630.9	601.7	INPP5E	NM_019892.2	PPI5PIV			
GI_38327540-I	107.7	104.9	104.1	INPP5F	NM_014937.2	SAC2;hSAC2;MSTPO47;KIAA0966;MGC597			
GI_38327541-I	168.1	154.8	163.6	INPP5F	NM_198330.1	SAC2;hSAC2;MSTPO47;KIAA0966;MGC597			
GI_38327543-A	171.5	179.2	132.2	INPP5F	NM_198331.1	SAC2;hSAC2;MSTPO47;KIAA0966;MGC597			
GI_38327543-I	419.6	473.7	350.1	INPP5F	NM_198331.1	SAC2;hSAC2;MSTPO47;KIAA0966;MGC597			
GI_38327545-S	442.4	555.5	499	P2RXL1	NM_005446.2	P2X6;P2XM;P2RX6	channel/p	integral to	small
GI_38327546-I	107	97.3	108.5	P2RY10	NM_014499.2	P2Y10	rhodopsin-	integral to	G-protein
GI_38327547-A	98.2	84.4	85.9	P2RY10	NM_198333.1	P2Y10	rhodopsin-	integral to	G-protein
GI_38327549-S	88.8	95.4	88.8	P2RY5	NM_005767.3	P2Y5	rhodopsin-	integral to	G-protein
GI_38327551-A	7339.8	7618.2	6590.1	G3BP	NM_198395.1	'HDH VIII'	ATP	cytoplasm	RAS
GI_38327553-S	123.4	122.9	121.8	GABRA1	NM_000806.3		GABA-A	integral to	gamma-
GI_38327555-S	115	127.1	118.2	GALNT9	NM_021808.2	GALNAC-T9	polypeptid	membran	O-linked
GI_38327557-S	114.4	102.4	100.3	GBP2	NM_004120.3		GTP		immune
GI_38327559-S	1077	963.1	619.3	STK35	NM_080836.2	CLIK1	cAMP-		protein
GI_38327560-S	2113.5	1819.1	2585.5	STK4	NM_006282.2	KRS2;MST1	protein		heat
GI_38327571-A	920	939.5	1227.3	STK6	NM_198437.1	AIK;ARK1;AURA;BTAK;STK15;MGC34538	protein	spindle	oncogene
GI_38327597-I	357	539.7	540.3	RGS12	NM_002926.2		GTPase	peripheral	regulation
GI_38327598-I	108.3	101.2	96.8	RGS12	NM_198227.1		GTPase	peripheral	regulation
GI_38327602-I	108.2	112.7	104.2	RGS12	NM_198230.1		GTPase	peripheral	regulation
GI_38327606-I	129.5	126.3	132.6	RGS12	NM_198432.1		GTPase	peripheral	regulation
GI_38327608-I	104.5	112.8	108.7	RGS12	NM_198587.1		GTPase	peripheral	regulation
GI_38327613-A	4518.8	4694.3	5706.4	SDBCAG84	NM_015966.2	CGI-54;PRO0989;C20orf47;NY-BR-84			
GI_38327616-S	243	307.2	267.3	SLAMF6	NM_052931.3	KALI;NTBA;KALIb;Ly108;NTB-A;SF2000	receptor		
GI_38327617-A	200.1	164.5	158.9	TEX14	NM_031272.2		protein-		protein
GI_38327619-I	84.6	96.4	95.4	TEX14	NM_198393.1		protein-		protein
GI_38327621-S	356	600.1	343	TLE4	NM_007005.3	ESG;ESG4;BCE-1;E(spl)	molecular	nucleus	signal
GI_38327624-A	1768.6	2036.4	1935.7	CS	NM_004077.2		citrate (Si)-	mitochond	tricarboxyli
GI_38327626-I	123.3	140	139.4	CS	NM_198324.1		citrate (Si)-	mitochond	tricarboxyli
GI_38327628-I	256.5	224.7	191.8	C9orf85	NM_182505.3	MGC61599	DNA	nucleus	regulation
GI_38327629-A	878.8	1085.6	901.5	C9orf85	NM_198394.1	MGC61599	DNA	nucleus	regulation
GI_38327631-A	987.2	2611.4	1620.6	DDR1	NM_001954.3	CAK;DDR;NEP;PTK3;RTK6;TRKE;CD167;E	transmem	integral to	cell
GI_38327631-I	87.1	92.2	93	DDR1	NM_001954.3	CAK;DDR;NEP;PTK3;RTK6;TRKE;CD167;E	transmem	integral to	cell

GI_38327633-S	2632.2	2360.5	2059.7	DDX18	NM_006773.3	MrDb	ATP		
GI_38327635-S	1227.6	1255	1378.3	C14orf4	NM_024496.2	KIAA1865	electron	nucleus	electron
GI_38327636-S	134.1	149.7	138.7	CALML5	NM_017422.3	CLSP	calcium		epidermal
GI_38327637-S	651.7	919.8	763.5	CREB3	NM_006368.4	LZIP;LUMAN;MGC15333;MGC19782	translation	nucleus	transcripti
GI_38327638-S	328.4	441.2	367	CRX	NM_000554.2	CRD;CORD2	transcripti	nucleus	vision
GI_38327639-S	382.3	522.3	357.7	CTSO	NM_001334.2	CTSO1	cysteine-		proteolysis
GI_38327640-S	104.1	113.6	110.6	DLX3	NM_005220.2	TDO	transcripti	nucleus	skeletal
GI_38327641-S	241.3	234.5	274.3	FLJ20195	NM_017706.3	FLJ21702			
GI_38327643-S	189.2	218.9	215.4	KIAA1609	NM_020947.2	MGC25024			
GI_38327648-S	94	100.7	93.3	ZP3	NM_007155.4	ZPC;ZP3A;ZP3B;HUMZP3;ZP3-372;ZP3-424	receptor	extracellul	
GI_38327653-S	337.2	434	402.5	CHRNE	NM_000080.2	ACHRE	cation	nicotinic	synaptic
GI_38327656-I	82.9	239	89.8	SULF2	NM_018837.2	HSULF-2;KIAA1247	sulfuric	Golgi	amino
GI_38327657-A	281.9	4861.8	365.8	SULF2	NM_198596.1	HSULF-2;KIAA1247	sulfuric	Golgi	amino
GI_38348182-S	115.3	120.5	105.3	HLXB9	NM_005515.2	HB9;SCRA1;HOXHB9	RNA	nucleus	humoral
GI_38348195-S	100.1	116.3	87.1	FLJ43842	NM_198440.1	MGC71803			
GI_38348197-S	119	125.6	115	FLJ40296	NM_198441.1		DNA	nucleus	regulation
GI_38348199-S	116.9	114.2	104	FLJ45651	NM_198442.1				
GI_38348201-S	206.2	243.6	233.6	UNQ2446	NM_198443.1				
GI_38348203-S	102.9	112.8	109.8	UNQ9366	NM_198444.1				
GI_38348205-S	95.7	118.7	92	FLJ45909	NM_198445.1				
GI_38348207-S	3679.4	5055.6	4747.3	FLJ45459	NM_198446.1				
GI_38348210-S	90.1	93.1	86.5	FLJ42654	NM_198447.1	MGC62027			
GI_38348212-S	191.9	157.5	133.1	UNQ429	NM_198448.1				
GI_38348214-S	150.2	154	130.7	MGC71745	NM_198449.1				
GI_38348216-S	168.7	212.8	176.1	UNQ8193	NM_198450.1				
GI_38348218-S	160.8	158.5	135.7	MGC21658	NM_198451.1				
GI_38348220-S	240	268.9	184.2	MGC45419	NM_198452.1		ATP		protein
GI_38348231-S	117.8	151.6	124.2	DUSP7	NM_001947.1	MKPX;MKP-X;PYST2	protein	cytoplasm	MAPKKK
GI_38348235-S	368	414.2	408.2	ZNF497	NM_198458.1	FLJ44773			
GI_38348237-S	122.7	122.9	119.9	FLJ37099	NM_198459.1	dJ1156J9.1;DKFZp686G0351;DKFZp779P11			
GI_38348239-S	125.8	147.6	128.3	DKFZp686G0	NM_198460.1		GTPase		immune
GI_38348241-S	111.3	147.6	169.8	FLJ45273	NM_198461.1				
GI_38348243-S	175.1	188.5	176.8	FLJ42117	NM_198463.1	FLJ42930			
GI_38348247-S	126.8	135.6	120	UNQ9391	NM_198464.1				
GI_38348249-S	147.2	159.1	142.6	DKFZp686A1	NM_198465.1		small		protein
GI_38348251-S	106.3	99.6	100.1	FLJ37183	NM_198466.1				
GI_38348253-S	282.6	304.2	295.8	FLJ42526	NM_198467.1	FLJ45813;MGC71764			
GI_38348255-S	175.7	173.1	158	C6orf167	NM_198468.1	FLJ46180;dJ39B17.2			
GI_38348257-S	115	132.7	112.2	FLJ46909	NM_198469.1				
GI_38348259-S	150.4	179.7	170.6	FLJ46061	NM_198471.1		DNA	nucleus	regulation
GI_38348261-S	375.1	430	343.9	FLJ26016	NM_198472.1				
GI_38348263-S	222.4	271	239.9	UNQ564	NM_198474.1				
GI_38348265-S	199.5	254.3	222	MGC34829	NM_198475.1				
GI_38348267-S	1057.5	890.4	848	FLJ41131	NM_198476.1				

GI_38348269-S	277.9	377.1	299	UNQ473	NM_198477.1				
GI_38348271-S	132.1	142.7	130.5	FLJ33600	NM_198478.1				
GI_38348273-S	113.2	129	112.1	FLJ40321	NM_198479.1		transcripti	nucleus	regulation
GI_38348275-S	337.2	419.6	377.9	FLJ33710	NM_198480.1	FLJ39372		nucleus	
GI_38348277-S	85.2	98	80.7	UNQ3033	NM_198481.1				
GI_38348279-A	121	120.6	121.6	LOC284948	NM_198482.1				intracellula
GI_38348281-S	239.6	293.2	267.4	FLJ46536	NM_198483.1				
GI_38348283-S	152.9	137.5	130.9	FLJ45246	NM_198484.1				
GI_38348285-S	88	101	102.5	FLJ41238	NM_198485.1	FLJ43694			
GI_38348287-S	1146.1	1153.3	1015.6	RPL7L1	NM_198486.1	MGC62004;dJ475N16.4			
GI_38348289-S	168.6	184.2	139	FLJ46072	NM_198488.1				
GI_38348291-S	133.4	187.2	180.1	DLNB14	NM_198489.1				
GI_38348293-S	117.2	135.7	111.7	FLJ44299	NM_198491.1				
GI_38348295-S	124.2	155.8	139.9	UNQ431	NM_198492.1				
GI_38348297-S	108.1	128.6	115.5	FLJ45235	NM_198493.1				
GI_38348299-S	133.4	143.5	130.8	FLJ16030	NM_198494.1				
GI_38348301-S	105	170.2	102.4	FLJ43692	NM_198495.1				
GI_38348303-S	130.8	159	136.5	AMACO	NM_198496.1	FLJ16213;FLJ45857			
GI_38348309-S	173	207.5	175.1	MGC50104	NM_198498.1				
GI_38348311-S	98.2	100.8	99.1	FLJ46156	NM_198499.1				
GI_38348315-S	91.9	97.2	91.6	FLJ42461	NM_198501.1				
GI_38348319-S	96.7	103.6	100.7	FLJ43826	NM_198502.1				
GI_38348321-S	411.9	550	605.3	UNQ1912	NM_198507.1	MGC17345			
GI_38348323-S	87.2	113.9	99	PAQR9	NM_198504.1	FLJ41938			
GI_38348327-S	145	181.4	135	FLJ44691	NM_198506.1				
GI_38348329-S	98.4	99.9	95.6	FLJ42925	NM_198511.1				
GI_38348331-S	111.2	102.1	109.4	FLJ44186	NM_198508.1				
GI_38348335-S	259	315.4	303.3	UNQ6369	NM_198510.1				
GI_38348337-S	148.1	235.6	168	MGC71806	NM_198516.1				
GI_38348339-S	88	93	95.4	FLJ25989	NM_198512.1				
GI_38348341-S	109.7	110.9	116.9	MGC12965	NM_198519.1				
GI_38348343-S	128.7	124.2	120.9	MGC35062	NM_198515.1				
GI_38348345-S	101.7	109.4	109.6	FLJ25323	NM_198521.1		DNA	nucleus	regulation
GI_38348347-S	100.4	104.2	95.3	FLJ00332	NM_198517.1	MGC46488			
GI_38348349-S	237.2	252.7	179	LOC374654	NM_198525.1	UNQ340			
GI_38348351-S	84	80	88.9	FLJ44112	NM_198520.1				
GI_38348353-S	131.3	161.2	140.3	FLJ46247	NM_198529.1	DKFZp434G2420			
GI_38348355-S	124.4	120.9	106.7	LOC161577	NM_198524.1	MGC40181			
GI_38348359-S	1021	888.4	932.3	MGC45386	NM_198527.1		catalytic		
GI_38348363-S	2720.1	3809	3361	FLJ46603	NM_198530.1				
GI_38348365-S	902.7	1525.2	1041.5	UNQ698	NM_198538.1				
GI_38348367-S	166.9	194.1	192.4	FLJ45778	NM_198532.1				
GI_38348369-S	159.3	171.8	156.8	UNQ644	NM_198541.1				
GI_38348371-S	157.4	155.3	130.1	FLJ44968	NM_198537.1				

GI_38348377-S	143.1	164.5	144.9	LOC148872	NM_198543.1	MGC35434			
GI_38348381-S	105.3	105.1	108.8	LOC374955	NM_198546.1		calcium		
GI_38348383-S	227.1	256.6	256.4	FLJ35093	NM_198549.1	DKFZp686M07166			
GI_38348385-S	178.2	219.8	200.1	FLJ36760	NM_198550.1			nucleus	
GI_38348387-S	119.1	121.6	111.4	UNQ6077	NM_198551.1				
GI_38348389-S	713.4	568.7	439.5	MGC15887	NM_198552.1		DNA	nucleus	regulation
GI_38348391-S	92.2	93.4	96.4	FLJ30851	NM_198553.1				
GI_38348393-S	88.4	102.8	91.8	FLJ45645	NM_198557.1				
GI_38348395-S	180	201.2	178.5	MGC50811	NM_198559.1				
GI_38348397-S	120.9	127.8	114.9	LOC375323	NM_198560.1				
GI_38348399-S	184.7	199.6	166.8	FLJ43654	NM_198562.1	MGC61663;MGC62079			
GI_38348401-S	111.6	123	130.5	MGC52022	NM_198563.1				
GI_38348403-S	128.9	125.9	122.2	FLJ44290	NM_198564.1				
GI_38348405-S	120.2	260.4	277.1	UNQ3030	NM_198565.1	MGC50789			
GI_38348407-S	288.7	208.7	214.5	FLJ32363	NM_198566.1	MGC46448			
GI_38348409-S	243.1	348	315.7	FLJ44216	NM_198567.1	MGC33586;MGC40402			
GI_38348411-S	82.5	80.4	78.6	GJB7	NM_198568.1	CX25;MGC71746;bA136M9.1;connexin25	connexon	connexon	cell
GI_38348413-S	94.4	97	86.6	UNQ739	NM_198570.1				
GI_38348415-S	208.9	231.9	171.1	FLJ39237	NM_198571.1	DKFZp547K159			
GI_38348417-S	157.2	195.1	153.5	MGC61633	NM_198572.1				
GI_38348419-S	109.3	122.2	108.1	UNQ470	NM_198573.1				
GI_38348427-S	95.2	100.3	95.7	FLJ46361	NM_198577.1				
GI_38348429-S	115.9	106	105.9	FLJ45829	NM_198578.1				
GI_38348431-S	125	128.2	106	FLJ41410	NM_198581.1	FLJ45877;KIAA2035			
GI_38348433-S	93.1	92.1	90.3	FLJ43374	NM_198582.1				
GI_38348435-S	152.2	149.3	152.1	CA13	NM_198584.1	CAXIII;FLJ37995;MGC59868	carbonate		one-
GI_38348437-S	89.9	137.2	104.8	UNQ2492	NM_198585.1				
GI_38348726-I	100.3	117.3	115.8	THADA	NM_022065.3	GITA;FLJ21877;FLJ44016;FLJ44876;KIAA17			
GI_38348728-S	262.5	314.2	290	C9orf93	NM_173550.2	FLJ39267;FLJ46740;bA778P13.1			
GI_38348730-S	137.9	166.9	146.9	FLJ20506	NM_017848.3	CXorf17			
GI_38348732-A	466.1	789.6	757.2	THADA	NM_198554.1	GITA;FLJ21877;FLJ44016;FLJ44876;KIAA17			
GI_38371736-S	142.9	171.6	142.1	KRTAP12-3	NM_198697.1	KRTAP12.3			
GI_38371738-S	584.4	429.8	303.8	RAB15	NM_198686.1		RAS small		small
GI_38371743-S	125.6	168.6	142.7	KRTAP12-4	NM_198698.1	KRTAP12.4			
GI_38372900-S	505.6	534.1	643.9	SP1	NM_138473.2		RNA	nucleus	regulation
GI_38372908-S	1379.9	1149.5	1209.9	C5orf7	NM_016604.2	5qNCA;KIAA1082			
GI_38372910-S	121.9	150.6	148.8	DUSP16	NM_030640.1	MKP7;MKP-7;KIAA1700			
GI_38372914-S	108	159.5	114.6	C21orf63	NM_058187.3	B18;SUE21;PRED34	lectin [goid	integral to	heterophili
GI_38372916-A	311.4	409.5	348.6	C1QTNF1	NM_198593.1	GIP;CTRP1;ZSIG37;FLJ90694		microfibril	
GI_38372916-I	128.4	129.7	117.5	C1QTNF1	NM_198593.1	GIP;CTRP1;ZSIG37;FLJ90694		microfibril	
GI_38372918-I	194.8	232.1	222	BSG	NM_001728.2	M6;OK;5F7;TCSF;CD147;EMMPRIN	signal	peripheral	cell
GI_38372922-A	2952.7	3833.5	2851.5	BSG	NM_198591.1	M6;OK;5F7;TCSF;CD147;EMMPRIN	signal	peripheral	cell
GI_38372928-S	449.4	584.9	187.1	BOC	NM_033254.2				
GI_38372929-S	1143.2	1410.6	1402	BCKDHA	NM_000709.2	MSUD1	3-methyl-2	alpha-	metabolis

GI_38372930-A	94.1	92.4	96.8	BCAN	NM_198427.1	BEHAB;CSPG7;MGC13038	sugar		cell
GI_38372930-I	167.5	184.8	175.4	BCAN	NM_198427.1	BEHAB;CSPG7;MGC13038	sugar		cell
GI_38372934-I	102.5	114.3	100.3	BCAN	NM_021948.3	BEHAB;CSPG7;MGC13038	sugar		cell
GI_38372936-A	6983.3	7593.9	7240.1	BC-2	NM_014453.2		molecular		
GI_38372937-S	114.9	132.1	119.8	ATP8A2	NM_016529.3	IB;ATP;ML-1;ATPIB;DKFZP434B1913	tumor	integral to	negative
GI_38372939-S	201.5	251.6	195	AZGP1	NM_001185.2	ZAG;ZA2G	plasma	soluble	immune
GI_38373667-S	148.9	149.4	144.3	P2RY8	NM_178129.3	P2Y8;MGC50878	rhodopsin-	integral to	G-protein
GI_38373668-I	127.2	172.9	120	SEC24C	NM_004922.2	KIAA0079	actin	Golgi	ER to
GI_38373670-A	2713.5	3121.2	3102.7	SEC24C	NM_198597.1	KIAA0079	actin	Golgi	ER to
GI_38373672-S	114.9	132.9	133.4	SYCP2	NM_014258.2	SCP2	DNA	synaptone	synaptone
GI_38373674-A	1300.5	1125	1307.4	RAPGEF1	NM_005312.2	C3G;GRF2	guanyl-		transmem
GI_38373674-I	93.9	96.6	90.5	RAPGEF1	NM_005312.2	C3G;GRF2	guanyl-		transmem
GI_38373676-I	105.3	116.9	113.3	RAPGEF1	NM_198679.1	C3G;GRF2	guanyl-		transmem
GI_38373678-A	96.1	101.6	89.3	GYPE	NM_002102.2	GPE	blood	integral to	
GI_38373678-I	86.8	98.9	98.4	GYPE	NM_002102.2	GPE	blood	integral to	
GI_38373679-I	95.8	123.3	114.5	GYPE	NM_198682.1	GPE	blood	integral to	
GI_38373681-A	376.4	439.6	383.9	KIAA0720	NM_020631.2				
GI_38373681-I	120.7	114	115.4	KIAA0720	NM_020631.2				
GI_38373683-I	96.3	109.8	90.9	KIAA0720	NM_198681.1				
GI_38373685-S	172.2	178.5	163.4	ACADSB	NM_001609.2	ACAD7;SBCAD;2-MEBCAD	acyl-CoA	mitochond	fatty acid
GI_38373686-S	360	462.6	424.1	AP1G1	NM_001128.4	ADTG;CLAPG1;MGC18255	vesicle	clathrin	intracellula
GI_38373687-A	119.4	132.3	114	AQP4	NM_001650.3	MIWC;HMIWC2	water	integral to	small
GI_38373687-I	91.6	92.1	83	AQP4	NM_001650.3	MIWC;HMIWC2	water	integral to	small
GI_38373688-I	121.1	114.4	109.7	AQP4	NM_004028.2	MIWC;HMIWC2	water	integral to	small
GI_38373689-S	908.7	1046.5	1045.1	COPS4	NM_016129.2	MGC10899;MGC15160			
GI_38373691-S	969	1070.4	987.2	H3F3B	NM_005324.3	H3.3B	DNA	chromoso	nucleoso
GI_38373692-S	496.4	502.1	453.6	SP3	NM_003111.1	SPR-2	DNA	nucleus	regulation
GI_38373694-S	568	362.4	238.4	WASPIP	NM_003387.3	WIP;PRPL-2	profilin	actin	actin
GI_38424072-S	290.9	362.6	314.3	PHLDB1	NM_015157.1	LL5A;FLJ00141;KIAA0638			
GI_38424080-A	440.9	415.2	426.8	SCDR10	NM_198704.1				
GI_38454187-S	151.4	146	148.1	FLJ11016	NM_018301.2	FLJ13670			
GI_38454193-S	1078	1143.3	987.7	76P	NM_014444.2		structural	centrosom	microtubul
GI_38454321-S	153.2	182.3	157.5	AMIGO3	NM_198722.1				
GI_38454323-S	488	641.7	564.4	CYGB	NM_134268.3	HGB;STAP	globin	cytoplasm	oxygen
GI_38454325-S	129.4	145.6	115.8	CD38	NM_001775.2		catalytic	integral to	induction
GI_38454327-S	1536	2267.3	2807	CDK5	NM_004935.2	PSSALRE	cyclin-		cell
GI_38455384-S	117.9	199.9	122.2	LAMP3	NM_014398.2	LAMP;DCLAMP;TSC403;DC-LAMP		lysosomal	oncogene
GI_38455386-S	82.7	94.6	83.4	ENPP5	NM_021572.4		hydrolase		nucleotide
GI_38455387-S	106.5	124	103.1	FRZB	NM_001463.2	FRP-3;FRZB1;SFRP3;FRZB-PEN	transmem	membran	skeletal
GI_38455389-S	121.4	139.1	128.2	RASL12	NM_016563.2	RIS	small		small
GI_38455390-S	1026.8	718.5	950.7	RNASEH2A	NM_006397.2	RNHL;RNHIA;RNASEHI	ribonuclea		DNA
GI_38455392-S	660.8	701.7	762.7	NTHL1	NM_002528.4	NTH1;OCTS3	DNA-	nucleus	base-
GI_38455393-S	3206.5	2939.4	1962	POLE4	NM_019896.2	p12	epsilon	nucleus	
GI_38455395-S	153.8	183.1	169.7	NEUROG1	NM_006161.2	AKA;ngn1;Math4C;NEUROD3	transcripti	nucleus	regulation

GI_38455397-S	109.2	120.2	107	NKIR	NM_139018.2	IREM1			
GI_38455399-S	335.4	332.7	218.5	MADH5	NM_005903.4	JV5-1;SMAD5	receptor	integral to	TGFbeta
GI_38455401-S	205	246.5	228.3	LCN2	NM_005564.2	NGAL	binding	soluble	transport
GI_38455403-S	138.5	131.1	143.3	KLF1	NM_006563.2	EKLF	transcripti	nucleus	histogene
GI_38455404-S	85	92.2	98.4	KNG	NM_000893.2		cysteine	cellular_co	neuropepti
GI_38455405-S	132.5	141.7	130.5	INDO	NM_002164.3	IDO;CD107B	electron		tryptophan
GI_38455406-S	120.5	126.9	125.3	JTB	NM_006694.2	PAR;hJT;HJTB;B PAR		membran	oncogene
GI_38455407-S	321	279.9	250.9	HRASLS	NM_020386.2	A-C1;H-REV107			
GI_38455408-S	1103.5	1588.2	1381.5	HKE2	NM_014260.2	KE-2;H2-KE2	chaperone	prefoldin	protein
GI_38455409-I	207.1	253	231.3	GHSR	NM_198407.1		G-protein	integral to	G-protein
GI_38455411-S	398.4	278.6	249.7	GAJ	NM_032117.2	MND1			
GI_38455412-S	106.5	152.9	87.1	FPRL2	NM_002030.3	FMLPY;FPRH1;FPRH2;RMLP-R-I	N-formyl	integral to	cell
GI_38455414-S	110.2	112.7	99.6	FLJ21736	NM_024922.3		hydrolase		
GI_38455415-S	300.2	237.8	234.7	FLT3LG	NM_001459.2		receptor	soluble	positive
GI_38455417-S	100.8	117.3	96.5	FAM3D	NM_138805.2	EF7	cytokine	extracellul	negative
GI_38455418-S	204.8	244.7	216.3	ESX1L	NM_153448.2	ESXR1	transcripti	nucleus	regulation
GI_38455419-S	494.5	640	562.6	DSCR1L2	NM_013441.2	RCN3;MCIP3;hRCN3	RNA		embryoge
GI_38455420-S	116.7	108.7	99.1	CRL3	NM_139017.3	GPL;GLMR;GLM-R	receptor		
GI_38455423-S	101.2	130	95.9	CLDN2	NM_020384.2		structural	tight	
GI_38455424-S	269.7	307.1	252.8	CHRNB3	NM_000749.2		nicotinic	nicotinic	synaptic
GI_38455425-S	146	156.5	183.4	CITED4	NM_133467.2		DNA	nucleus	regulation
GI_38455426-S	7823.4	7852.9	6372.9	CCT4	NM_006430.2	SRB;Cctd	chaperone	cytoplasm	protein
GI_38455428-S	223.5	282.4	258.2	BCMP11	NM_176813.3	HAG3;hAG-3			
GI_38488691-S	106.3	91.7	102.3	KIAA1985	NM_024577.2	CMT4C;CMTND;FLJ13605			
GI_38488711-S	190.9	208.9	286.7	DKFZp761P1	NM_152906.2				
GI_38488717-S	211	230.9	225.5	FLJ20309	NM_017759.2				
GI_38488719-S	372.7	287.6	226.2	DGCR8	NM_022720.4	Gy1;FLJ21774;FLJ21886;FLJ22127	double-	intracellula	
GI_38488723-S	123.3	143.2	124.6	TFF2	NM_005423.2	SP;SML1			defense
GI_38488726-S	792.9	774	849.2	MGC12197	NM_016625.2				
GI_38488756-S	141	170.7	156.7	ATP5L2	NM_198822.1	ATP5K2;dJ222E13.5			
GI_38488766-S	234.7	278.4	279.3	LOC375449	NM_198828.1				
GI_38490530-S	1643.4	1673.2	1194	SFRS14	NM_014884.1	KIAA0365			
GI_38490536-S	109.7	136.2	113.9	MGC9726	NM_177403.3	RAB7;MGC16212	small		small
GI_38490555-S	2621.3	1535.7	1930.3	FLJ20847	NM_017966.3				
GI_38490687-S	119.2	134.6	135.1	IGSF10	NM_178822.3	FLJ25972	vascular		protein
GI_38492354-S	126.2	133.4	130.6	PDHA2	NM_005390.3	PDHAL	pyruvate	mitochond	glycolysis
GI_38492355-S	566.2	448.7	526.4	POLD3	NM_006591.1	P66;P68;KIAA0039	delta DNA	delta DNA	DNA
GI_38492357-S	658.4	665	649.4	KIAA0632	NM_015545.2				
GI_38502311-S	109.2	122.3	96.6	LOC283514	NM_198849.1				
GI_38502313-S	130	126	105.1	LOC348645	NM_198851.1				
GI_38502315-I	182.1	209.3	187.8	ZPBP2	NM_198844.1	ZPBPL;MGC41930			
GI_38502317-S	92	95.6	82.6	LOC284345	NM_198850.1				
GI_38502320-S	89.1	90.1	86	FLJ40411	NM_198852.1				
GI_38502322-S	477.6	437.1	522.7	C9orf10OS	NM_198841.1	FLJ31534			

GI_38504662-S	108.4	119	110.9	SIGLEC6	NM_001245.2	CD33L;OBBP1;CD33L1;SIGLEC-6	lectin [goid	membran	cell-cell
GI_38504666-I	139	160.7	137.3	SFTPB	NM_198843.1	SP-B;PSP-B;SFTB3;SFTP3	surfactant	extracellul	respiratory
GI_38504670-S	116	127.3	98.3	SCRN3	NM_024583.2	SES3;FLJ23142	dipeptidas		proteolysis
GI_38504672-S	1154.1	930.2	1255.4	SERPINB8	NM_002640.3	PI8;CAP2	protein	cytosol	
GI_38505154-A	2277	2149.3	2776.2	TCEA2	NM_003195.4	TFIIS	transcripti	transcripti	transcripti
GI_38505155-I	110.6	119.4	109.3	TCEA2	NM_198723.1	TFIIS	transcripti	transcripti	transcripti
GI_38505157-S	151.3	168.5	154.8	TCF15	NM_004609.2	EC2;PARAXIS	RNA	nucleus	mesoderm
GI_38505158-S	329.4	295	262.6	TCFL5	NM_006602.2	CHA;E2BP-1;MGC46135	transcripti	nucleus	spermatog
GI_38505160-S	92	97	91.1	TDRD1	NM_198795.1	FLJ21082	nucleic		
GI_38505162-I	206.3	157.9	106.7	RAC1	NM_018890.2	TC-25;p21-Rac1	GTPase	peripheral	response
GI_38505163-A	10907.2	9981.5	9348.1	RAC1	NM_006908.3	TC-25;p21-Rac1	GTPase	peripheral	response
GI_38505164-I	132	151.9	147.3	RAC1	NM_198829.1	TC-25;p21-Rac1	GTPase	peripheral	response
GI_38505166-S	312.8	465.1	485.5	RARG	NM_000966.3	RARC;NR1B3	retinoic		developm
GI_38505169-S	192.6	206	201.8	RASGRF2	NM_006909.1	GRF2;RAS-GRF2	guanyl-		activation
GI_38505179-I	99.1	91.4	93.6	PTGER3	NM_198715.1	EP3;MGC27302	prostaglan	nuclear	G-protein
GI_38505185-I	101.9	123.6	103.6	PTGER3	NM_198718.1	EP3;MGC27302	prostaglan	nuclear	G-protein
GI_38505187-I	101.1	94.2	95.6	PTGER3	NM_198719.1	EP3;MGC27302	prostaglan	nuclear	G-protein
GI_38505189-I	103.8	96.4	99.4	PTGER3	NM_198720.1	EP3;MGC27302	prostaglan	nuclear	G-protein
GI_38505191-S	131.7	131.3	124.3	PTGDR	NM_000953.2	DP;MGC49004	rhodopsin-	integral to	G-protein
GI_38505192-S	285.5	333.7	294.6	PTGDS	NM_000954.5	PDS;PGD2;PGDS;PGDS2	prostaglan	membran	transport
GI_38505193-S	142.2	154.3	150.5	PTGER1	NM_000955.2	EP1	prostaglan	integral to	G-protein
GI_38505195-S	190.7	302.2	1310	PTGES	NM_004878.3	PGES;PIG12;PP102;PP1294;MGST-		membran	prostaglan
GI_38505196-S	127.7	136.6	117.1	PTGER4	NM_000958.2	EP4;EP4R	prostaglan	integral to	G-protein
GI_38505200-S	214.4	247.8	165.6	PCTK3	NM_002596.1	PCTAIRE;PCTAIRE3	protein	cellular_co	protein
GI_38505202-S	84.2	93	95.4	PLDN	NM_012388.2	PA;PALLID	syntaxin-	cellular_co	synaptic
GI_38505203-S	119.3	117.3	95.4	PRRX2	NM_016307.3	PMX2;PRX2;MGC19843	transcripti	nuclear	regulation
GI_38505204-S	469.4	582.6	467	PTEN	NM_000314.2	BZS;MHAM;TEP1;MMAC1;PTEN1;MGC1122	inositol/ph	cytoplasm	regulation
GI_38505206-S	233.9	198.2	222.9	FLJ22624	NM_024808.2				
GI_38505208-S	550.9	541.9	582.9	FLJ22794	NM_022074.2	KIAA1895			
GI_38505212-S	188.4	189.3	172.1	FLJ21940	NM_022828.2	FLJ10053;DKFZp564A186			
GI_38505214-S	169.4	169.6	153.4	FLJ21941	NM_025040.2				
GI_38505216-S	97.5	104.8	96.4	FLJ21963	NM_024560.2		catalytic		metabolis
GI_38505217-S	1203.7	931.2	491.1	FLJ12592	NM_032169.3		acyl-CoA		electron
GI_38505219-S	94.1	128.5	98.2	FLJ20581	NM_017888.2		catalytic		metabolis
GI_38505221-S	1266.5	1789.5	1320.3	FLJ20793	NM_019022.3	KIAA1830	calcium		electron
GI_38505223-S	340	300.7	303	METTL4	NM_022840.2	HsT661;FLJ23017			
GI_38505225-S	140.2	140.3	140.1	FLJ23311	NM_024680.2				
GI_38505264-S	573.6	559.3	623	DNCLI2	NM_006141.2	LIC2	adenosine	cytoplasmi	microtubul
GI_38505265-S	2098.9	1435.1	1932.5	DNTTIP1	NM_052951.2	Tdif1;C20orf167;dJ447F3.4		nucleus	
GI_38505291-I	91.2	91.1	90	CACNA1G	NM_198396.1	NBR13;Ca(V)T.1	low	voltage-	small
GI_38505293-I	108.8	132.7	127	CACNA1G	NM_198397.1	NBR13;Ca(V)T.1	low	voltage-	small
GI_38524584-S	3240.5	3313.6	3162.2	NDUFS7	NM_024407.3	PSST;FLJ45860;FLJ46880	NADH		mitochond
GI_38524586-S	178.5	182.6	167.2	FLJ43855	NM_198857.1				
GI_38524588-S	462	728.3	312.6	FLJ43070	NM_152286.2	FLJ31318;FLJ44279			

GI_38524590-S	97.2	92	85.8	IMP5	NM_175882.1		peptidase		proteolysis
GI_38524593-S	1335.7	1335.9	1106.4	TIPARP	NM_015508.2	DDF1;DKFZP434J214;DKFZp686N0351	nucleic		
GI_38524599-S	262.5	288.8	251.1	FLJ14011	NM_022103.2			nucleus	
GI_38524611-S	424.2	530.3	452	TRIM50C	NM_198853.1		zinc ion	intracellula	
GI_38524613-S	137.8	134.6	132.2	MGC4728	NM_198542.1				
GI_38524615-S	764.2	487.4	396.4	SLC27A1	NM_198580.1	FATP;FATP1;MGC71751	catalytic		metabolis
GI_38524617-S	731.8	855.1	612.5	FMNL2	NM_052905.1	FHOD2;KIAA1902	actin	nucleus	cytokinesi
GI_38524619-S	448.9	495.4	299.5	PRICKLE2	NM_198859.1	DKFZp686D143			
GI_38524621-S	1118.8	1104.4	996.1	FNBP1	NM_015033.1	FBP17;KIAA0554	DNA	nucleus	regulation
GI_38564321-S	133.7	161.1	142	ZNF154	NM_003444.1	pHZ-92	transcripti	nucleus	regulation
GI_38564323-S	275.8	246.9	250.6	NME6	NM_005793.3	NM23-H6;IPIA-ALPHA	nucleoside	cellular_co	GTP
GI_38564324-S	212.1	254	217.2	FLJ40243	NM_173489.2				
GI_38564326-S	113	107.8	106	THAP9	NM_024672.2	FLJ23320;FLJ34093			
GI_38566701-S	176.4	136.3	180.1	ZNF285	NM_152354.2	FLJ30747		nucleus	
GI_38568177-S	207.4	214.4	213.7	KIAA0467	NM_015284.1	FLJ23425	copper,		superoxid
GI_38569232-S	92.1	96.1	87.7	INSL5	NM_005478.3	PRO182;UNQ156	hormone	extracellul	physiologi
GI_38569393-S	879.1	872.1	790.2	IKBKAP	NM_003640.2	FD;DYS;IKAP	phosphory		protein
GI_38569395-S	98.6	121.8	94.6	INSL6	NM_007179.2	RIF1	hormone	extracellul	physiologi
GI_38569397-S	545	414.7	250.6	ITGA10	NM_003637.3		collagen	integrin	cell-matrix
GI_38569399-S	331.4	455.1	623.3	ITPKB	NM_002221.2	IP3K;IP3K-B	inositol-		signal
GI_38569401-S	884.8	1264.5	1137.9	ARFIP2	NM_012402.2	POR1	GTP		small
GI_38569402-S	717.8	1011.6	891.6	ARL3	NM_004311.2	ARFL3	GTP		small
GI_38569403-S	1413.9	1745.5	1278.2	ARL7	NM_005737.3	LAK	small	nucleus	small
GI_38569406-I	115.5	102.1	115.5	ARSB	NM_198709.1	ASB;G4S;MPS6	arylsulfata	lysosome	lysosomal
GI_38569412-I	85.1	84	72.4	APBA2BP	NM_031231.2	NIP1;XB51;EFCBP3;NECAB3;SYTIP2;dJ63M	calcium	endoplas	protein
GI_38569414-I	428.5	444.8	619.8	APBA2BP	NM_031232.2	NIP1;XB51;EFCBP3;NECAB3;SYTIP2;dJ63M	calcium	endoplas	protein
GI_38569416-S	275.7	321.9	260.9	AARSL	NM_020745.1	KIAA1270;bA444E17.1	ATP		alanyl-
GI_38569418-S	93	98.7	95.8	AAT1	NM_033364.2				
GI_38569420-S	3323.2	3879.8	3443.8	ACLY	NM_001096.2	ATPCL;CLATP	ATP	citrate	ATP
GI_38569424-S	107.4	109	115.3	ALAD	NM_000031.3	ALADH;MGC5057	porphobili		heme
GI_38569425-S	143.7	152.1	107.2	ANKRD5	NM_022096.4	FLJ21669;dJ839B4.6	calcium		
GI_38569429-S	194.8	409.6	149.5	ATF7IP2	NM_024997.2	FLJ12668			
GI_38569431-A	172.3	198.4	197.6	B1	NM_014451.2	PTHB1			
GI_38569433-I	95.1	117.8	91.1	B1	NM_198428.1	PTHB1			
GI_38569437-S	304.8	381.1	315	BCAS4	NM_017843.2	BHLHB4;FLJ20495			cell growth
GI_38569441-S	1241.9	1360.3	866.4	BCAT1	NM_005504.3	BCT1;ECA39;MECA39	branched-	cytosol	branched
GI_38569442-I	236.5	252.9	232.9	BMPR2	NM_001204.4	BMR2;PPH1;BMPR3;BRK-3;T-ALK;BMPR-II	protein	integral to	transmem
GI_38569443-A	283.4	323.4	291.1	BMPR2	NM_033346.2	BMR2;PPH1;BMPR3;BRK-3;T-ALK;BMPR-II	protein	integral to	transmem
GI_38569444-S	293.6	324.8	300.9	ZNF211	NM_006385.2	ZNF-25;ZNFC25;C2H2-25;CH2H2-25	transcripti	nucleus	regulation
GI_38569448-S	102.4	106.5	110.5	XCL2	NM_003175.2	SCM1B;SCYC2;SCM-1b	chemokin	soluble	circulation
GI_38569451-S	173.7	208.7	200.2	VCIP135	NM_025054.3	FLJ23132;KIAA1850			
GI_38569452-I	175.9	222.8	164.5	STARD5	NM_030574.2	MGC10327	cholestero		lipid
GI_38569454-S	102.2	90.2	96.8	SLC9A2	NM_003048.3	NHE2	sodium:hy	integral to	sodium
GI_38569455-A	148.7	177.8	152.1	STARD5	NM_181900.2	MGC10327	cholestero		lipid

GI_38569458-S	98.6	106	97.7	SLC6A7	NM_014228.2	PROT	neurotran	membran	L-proline
GI_38569459-S	140	180.7	173.9	SIK2	NM_015191.1	KIAA0781;DKFZp434K1115	protein-		protein
GI_38569461-S	178.7	250.8	219.1	SLC12A2	NM_001046.2	BSC;BSC2;NKCC1	sodium:ch	membran	small
GI_38569462-S	560.1	635.4	502.9	RRAS2	NM_012250.3	TC21	RAS small	endoplas	oncogene
GI_38569463-S	295.5	272.4	295.2	SASH1	NM_015278.2	KIAA0790;dJ323M4.1	DNA	nucleus	negative
GI_38569465-S	224.6	248.3	205.3	ROD1	NM_005156.3		RNA		embryoge
GI_38569467-S	987	816.2	748.7	RPF1	NM_025065.5	FLJ12475			
GI_38569468-S	532.3	549.2	374.6	RAI16	NM_022749.4	FLJ21801			
GI_38569470-S	2739.9	2793.7	2681.8	MUF1	NM_006369.3				
GI_38569472-S	1945.2	2484.9	2640.2	NDUFB1	NM_004545.3	MNLL;CI-SGDH	NADH	NADH	
GI_38569474-S	282.6	337.5	272	MTX1	NM_002455.2	MTX;MTXN		integral to	
GI_38569478-S	114.9	100.1	108.2	KRTAP13-2	NM_181621.2	KAP13-2			
GI_38569479-S	114.4	112.2	105.4	MRTF-B	NM_014048.3	MKL2;NPD001;KIAA1243			
GI_38569481-S	616.1	1504.7	1088.7	KIAA1324	NM_020775.2				
GI_38569483-S	346.7	282.3	442.1	KIF21A	NM_017641.2	FEOM1;CFEOM1;FLJ20052;KIAA1708	ATP	kinesin	microtubul
GI_38569485-S	515.8	520	454.6	KIAA1190	NM_145166.2	DKFZp434N0615	DNA	nucleus	regulation
GI_38569486-S	132.7	144	139.5	KIAA1244	NM_020340.2				
GI_38569492-S	545.8	540.5	482.1	KCNH3	NM_012284.1	BEC1;ELK2;Kv12.2;KIAA1282	voltage-	voltage-	potassium
GI_38569498-S	189.4	218.7	197.9	DPCR1	NM_080870.2	PBLT			
GI_38569501-I	1306.3	1385.6	1177.5	DKFZP434I1	NM_015496.3	MSTP054	nucleic		
GI_38569502-I	382	455.5	333.4	DDX52	NM_152300.2	ROK1	ATP	nucleus	
GI_38569504-A	454.1	464.1	338.6	DDX52	NM_007010.2	ROK1	ATP	nucleus	
GI_38569506-S	203	205.6	194.2	DACT1	NM_016651.4	DPR1;FRODO;HDPR1;DAPPER;THYEX3;D		kinesin	
GI_38570041-S	102.6	105.8	104	CLDN5	NM_003277.2	AWAL;BEC1;TMVCF;CPETRL1	structural	tight	
GI_38570051-S	293	356.4	306.7	C14orf49	NM_152592.2	FLJ25605;c14_5734			
GI_38570053-S	286.2	254.8	275.4	C6orf149	NM_020408.3	CGI-203			
GI_38570057-S	96.9	112.2	104.2	C6orf97	NM_025059.2	FLJ23305;bA282P11.1			
GI_38570061-S	260.9	270.2	270	C7orf20	NM_015949.2	CGI-20			
GI_38570063-S	105.1	115.6	104	C7orf31	NM_138811.3				
GI_38570067-S	135.1	164.7	155.7	C8orf2	NM_007175.4		molecular	cellular_co	biological_
GI_38570070-A	95.8	115.2	99.8	CLDN10	NM_006984.3	OSP-L;CPETRL3		tight	cell
GI_38570070-I	86.5	93	103.8	CLDN10	NM_006984.3	OSP-L;CPETRL3		tight	cell
GI_38570071-I	82.7	81.8	75.1	CLDN10	NM_182848.2	OSP-L;CPETRL3		tight	cell
GI_38570072-A	98.5	106.3	98.6	COL25A1	NM_032518.2		DNA	microfibril	regulation
GI_38570074-I	116.8	114.9	107.6	COL25A1	NM_198721.1		DNA	microfibril	regulation
GI_38570080-I	85.7	95.9	82.1	CUGBP1	NM_198700.1	CUGBP;NAB50;CUG-BP;hNab50;BRUNOL2	RNA	nucleus	mRNA
GI_38570082-A	176.7	216.8	195.2	CUGBP1	NM_006560.2	CUGBP;NAB50;CUG-BP;hNab50;BRUNOL2	RNA	nucleus	mRNA
GI_38570087-S	326.8	363.7	282.6	CDC40	NM_015891.2	EHB3;PRP17;PRPF17;FLJ10564		spliceoso	mRNA
GI_38570088-S	119.9	138.9	119.7	CHC1L	NM_001268.2		Ran		chromoso
GI_38570089-S	369.8	414.9	408.1	CIAO1	NM_004804.2			nucleus	positive
GI_38570090-S	1283	1985.6	1972.7	CNP	NM_033133.3	CNP1	2',3'-cyclic-	membran	synaptic
GI_38570092-S	103.6	111.3	102	FLJ20160	NM_017694.2				
GI_38570094-S	153.8	201.8	168.1	FLJ20202	NM_017709.2				
GI_38570096-S	1311.9	1633.3	1559.3	FLJ20259	NM_017730.2		DNA	nucleus	regulation

GI_38570100-A	118.5	153	127.2	FLJ20298	NM_017752.2		transporte	membran	transport
GI_38570102-I	84.1	110.7	101.6	FLJ20298	NM_198881.1		transporte	membran	transport
GI_38570104-S	132.5	135.1	100.7	RAIN	NM_017805.2	FLJ20401			
GI_38570106-S	171.2	196.6	193.5	FLJ23588	NM_022785.2	DJBP;HSCBCIP1;KIAA1672;dJ185D5.1	calcium		
GI_38570110-S	213.5	244.7	239.2	FLJ25005	NM_152334.2		ATP		threonyl-
GI_38570112-S	96.7	101.9	102.2	RASGEF2	NM_152643.3	C10orf23;FLJ25027	guanyl-		intracellula
GI_38570114-S	807.1	1065	941.2	FLJ25476	NM_152493.2				
GI_38570116-S	120.5	112.3	122.7	ZNF569	NM_152484.2	FLJ32053		nucleus	
GI_38570118-S	214.5	308.3	296.4	FLJ38451	NM_175872.3			nucleus	
GI_38570120-S	507	430.9	411.8	FLJ10546	NM_018133.2				
GI_38570130-S	101.1	94.7	92.6	HIST1H2AG	NM_021064.3	H2A/p;H2AFP;H2A.1b;pH2A/f			
GI_38570131-S	525.1	674.6	589.2	HRB	NM_004504.3	RAB;RIP	RNA	nuclear	mRNA-
GI_38570133-S	396.5	421.6	309.2	MAP4K5	NM_006575.3	KHS;GCKR;KHS1;MAPKKKK5	protein	cytoplasm	activation
GI_38570136-S	158.6	150.4	153.1	MCOLN3	NM_018298.9	FLJ11006			
GI_38570137-S	514.9	528	680.6	MGC15677	NM_032878.2				
GI_38570141-S	139.6	178.9	158.2	MPP5	NM_022474.2	PALS1;FLJ12615	protein	membran	intracellula
GI_38570143-S	99.9	102.3	98.7	SLC12A5	NM_020708.3	KCC2;KIAA1176	cation:chlo	integral to	chloride
GI_38570144-S	103.1	97.6	101.5	SPATS1	NM_145026.2	SRSP1;SPATA8;FLJ25442			
GI_38570145-S	118.6	125.3	123.7	SYT7	NM_004200.2	SYT-VII	calcium-	synaptic	exocytosis
GI_38570147-A	556.1	581.9	584	KIAA1259	NM_032196.3	FLJ21124			
GI_38570148-S	462	422	317.1	KIAA1280	NM_015691.2	BM042			
GI_38570150-I	3878.8	3423.9	3310.4	TAF9	NM_003187.3	TAF2G;CGI-	protein C-	transcripti	transcripti
GI_38570151-A	2902.9	2789	2388.1	TAF9	NM_016283.3	TAF2G;CGI-	protein C-	transcripti	transcripti
GI_38570151-I	534	652.4	493.4	TAF9	NM_016283.3	TAF2G;CGI-	protein C-	transcripti	transcripti
GI_38570152-S	102.1	114.3	95.5	TEAD1	NM_021961.2	TCF13;TEF-1	DNA	nucleus	regulation
GI_38570153-S	177.5	183.8	174	JAZ	NM_012279.2		double-	nucleolus	cell growth
GI_38570154-S	90.2	102.7	99.9	LRRC4	NM_022143.3	NAG14;NGL-1			
GI_38570155-S	695.2	801	730.9	NT5C2L1	NM_152729.2	HT023;C6orf200;MGC24302;dJ486I3.1;dJ48			
GI_38570157-S	122.4	145.8	122.1	OVOL1	NM_004561.2	HOVO1	transcripti	nucleus	regulation
GI_38570159-S	704.2	691	557.5	XPO4	NM_022459.3	FLJ13046;KIAA1721	protein	nucleus	intracellula
GI_38604072-S	164.8	149.4	139.9	FLJ13231	NM_023073.2	FLJ21126			
GI_38605731-A	203.1	222	159.8	NUP43	NM_024647.4	p42;FLJ13287;bA350J20.1	protein	nucleus	intracellula
GI_38605732-I	196.8	227.9	208.8	NUP43	NM_198887.1	p42;FLJ13287;bA350J20.1	protein	nucleus	intracellula
GI_38605734-S	372.1	471.7	372.9	FLJ10849	NM_018243.2				
GI_38638697-S	2891.6	10037	8151.8	KIAA1199	NM_018689.1	IR2155535			
GI_38678523-S	117.4	123.2	118.8	OPN5	NM_181744.1	PGR12;GPR136;TMEM13;dJ402H5.1	receptor	integral to	G-protein
GI_38678527-S	181.9	226.7	201.2	HFL-EDDG1	NM_006553.2				
GI_38678531-S	92.1	114.5	92.1	MGC39581	NM_152784.2				
GI_38678533-S	146	173.4	164.9	MGC27466	NM_152373.2		nucleic	intracellula	regulation
GI_38679883-I	88.9	100.1	94.3	SRI	NM_198901.1	SCN	calcium	cytoplasm	regulation
GI_38679885-S	436.8	438.3	438.2	SSB3	NM_080861.3				
GI_38679886-A	4093.6	3932.1	3967.3	SRI	NM_003130.2	SCN	calcium	cytoplasm	regulation
GI_38679887-I	130.7	135.5	117.6	RAB6A	NM_198896.1	RAB6	RAB small	Golgi	nonselecti
GI_38679889-S	112.1	111.1	97.3	SLCO4C1	NM_180991.4	OATPX;OATP-H;OATP-			

GI_38679891-S	144.3	174	165.3	PIN4	NM_006223.2	EPVH;PAR14	peptidyl-	mitochond	protein
GI_38679893-A	431.8	508.2	455.5	RAB6A	NM_002869.4	RAB6	RAB small	Golgi	nonselecti
GI_38679894-S	3753.9	4817.6	3509	TXNDC7	NM_005742.2	P5	protein	endoplas	protein
GI_38679895-S	459.4	463.7	526.5	PHIP	NM_017934.4	ndrp;WDR11;FLJ20705			
GI_38679896-S	126.6	137.8	139.1	BTBD14B	NM_052876.2	NAC1	protein		
GI_38679897-S	105.5	113.5	106.2	OR3A2	NM_002551.2	OR228;OLFRA04;OR17-228	receptor	integral to	chemosen
GI_38679899-S	138.6	166.2	155.1	LOC91056	NM_138368.2	DKFZp761E198			
GI_38679901-S	4082	3506.7	1536.3	LOC93109	NM_138399.2				
GI_38679903-S	138.9	139.2	132.2	ARL10B	NM_138795.2	FLJ45195	small		small
GI_38679904-S	257.7	241.1	234.1	LOC201292	NM_173547.2				
GI_38679906-S	1877	2173.5	3579.4	LOC127262	NM_182752.2		transporte		transport
GI_38679908-S	625.4	578.9	485.6	HT008	NM_018469.3	KIAA1738	sugar		phosphoe
GI_38679910-S	1675.6	1782.9	1221.1	HSPC132	NM_016399.2				
GI_38679911-S	125.7	136.3	162.1	HSPC109	NM_016390.2	DKFZP566D143			
GI_38679913-S	231.8	220.5	179	FLJ13089	NM_024953.2				
GI_38679925-S	441.2	595.1	420.3	CEECAM1	NM_016174.3	CerCAM	cell	integral to	leukocyte
GI_38679945-S	209.5	213.7	184.6	ABAT	NM_020686.3	GABAT;NPD009;GABA-AT	4-	mitochond	amino
GI_38679949-S	100.2	112.2	90.7	ABAT	NM_000663.2	GABAT;NPD009;GABA-AT	4-	mitochond	amino
GI_38679953-A	2831.9	2594.4	2500.7	ABR	NM_001092.3	MDB	GTPase		small
GI_38679953-I	121	109.1	107.1	ABR	NM_001092.3	MDB	GTPase		small
GI_38679956-I	109	100.9	112.5	ABR	NM_021962.2	MDB	GTPase		small
GI_38679976-I	85.5	80.9	83.5	ACACA	NM_198839.1	ACC;ACAC;ACC1;ACCA	acetyl-	biotin	biotin
GI_38679979-A	1431.6	1510.9	820.3	ACACA	NM_000664.3	ACC;ACAC;ACC1;ACCA	acetyl-	biotin	biotin
GI_38683796-S	566	654.8	646.2	ANKS1	NM_015245.1	KIAA0229	DNA	nucleus	regulation
GI_38683798-S	796.6	780.9	679.5	ANKRD13	NM_033121.1	NY-REN-25			
GI_38683806-S	356.4	432.1	329.9	ANKRD17	NM_032217.3	GTAR;FLJ22206;KIAA0697;NY-BR-16			
GI_38683837-S	2036.2	1716.5	1447.7	CD47	NM_001777.2	IAP;OA3;MER6	plasma	proteoglyc	integrin-
GI_38683838-S	94	102.7	99	CD96	NM_005816.3	TACTILE;MGC22596	defense/i	integral to	cell
GI_38683841-S	978.6	1136.9	991.9	CDC26	NM_139286.3	C9orf17			
GI_38683842-S	2436.5	1944.1	1711.6	C6orf108	NM_006443.2	RCL;dJ330M21.3		nucleus	cell
GI_38683843-I	104.2	105.2	94.8	CNR1	NM_016083.3	CB1;CNR;CB-R;CB1A;CANN6;CB1K5	cannabino	integral to	G-protein
GI_38683845-S	543.1	416.2	502.8	CPNE8	NM_153634.2				
GI_38683846-S	134.6	160	146.7	FGF11	NM_004112.2	FHF3;MGC45269	growth	extracellul	signal
GI_38683847-S	1348.2	1707	1733.1	FIBP	NM_004214.4	FGFIBP;FIBP-1	protein	membran	FGF
GI_38683850-S	126.6	163.8	133.8	FLJ11220	NM_018364.2				
GI_38683852-S	177.1	223	217.1	FLJ13946	NM_152275.2				
GI_38683854-S	1022.9	925.6	962.1	FLJ20758	NM_017952.4				
GI_38683856-S	109	108.4	103.2	ICEBERG	NM_021571.2		cysteine	intracellula	apoptosis
GI_38683857-I	111.1	123.4	107.3	IRF5	NM_002200.3		RNA	nucleus	cell growth
GI_38683858-A	156	161.2	151.8	IRF5	NM_032643.3		RNA	nucleus	cell growth
GI_38683859-S	109	111.6	103.2	IRS2	NM_003749.2		signal		positive
GI_38683861-S	287.7	381.9	307.4	RAC3	NM_005052.2		GTPase		intracellula
GI_38683862-I	80.7	79.1	72.8	RBBP6	NM_006910.4	MY038;RBQ-1;DKFZp761B2423	protein		regulation
GI_38683864-A	237.4	239.1	204.3	RBBP6	NM_032626.5	MY038;RBQ-1;DKFZp761B2423	protein		regulation

GI_38683864-I	111.9	130.5	119.7	RBBP6	NM_032626.5	MY038;RBQ-1;DKFZp761B2423	protein		regulation
GI_38683865-S	2905.8	1675.2	1296.3	RNASET2	NM_003730.3	FLJ10907;RNASE6PL;bA514O12.3	ribonuclea	extracellul	RNA
GI_38683866-S	21109.7	18453	15348	RPL36A	NM_021029.3	L44L;RPL44			
GI_38683867-A	133.5	149.9	171.4	APG16L	NM_017974.2	WDR30;FLJ00045;FLJ10035;FLJ10828;FLJ2			
GI_38707980-S	183.8	227.8	184.7	CAPN12	NM_144691.2	MGC20576			
GI_38708010-S	120.7	141.4	103.7	MGC45477	NM_198924.1				
GI_38708168-S	502	478.3	388.5	SNX25	NM_031953.2	SBBI31;MSTP043;FLJ23161			
GI_38708298-S	93.6	98.6	95.9	SLC29A2	NM_001532.2	ENT2;DER12;HNP36	nucleoside	nucleolus	nucleoside
GI_38708308-S	198.4	211.4	208	PNAS-4	NM_016076.2	CGI-146			
GI_38708312-A	394.2	532.1	577.2	LOC253982	NM_181718.3				
GI_38708316-I	141.5	169	144.8	LOC253982	NM_198907.1				
GI_38708320-I	204.8	163.6	196.6	KIAA1259	NM_017553.1	FLJ21124			
GI_38708325-S	1003.5	712.1	505.6	CSNK2A2	NM_001896.2	CK2A2;CSNK2A1	protein		spermatid
GI_38787903-A	236.2	283.3	258.3	BMP2K	NM_017593.3	BIKE;HRIHFB2017;DKFZp434K0614;DKFZp	cAMP-	nucleus	protein
GI_38787934-I	121.5	113.1	120.3	BMP2K	NM_198892.1	BIKE;HRIHFB2017;DKFZp434K0614;DKFZp	cAMP-	nucleus	protein
GI_38787940-I	113	113.3	107	TENC1	NM_015319.2	C1TEN;C1-TEN;KIAA1075			intracellula
GI_38787956-A	200.1	179.5	145.7	TENC1	NM_170754.2	C1TEN;C1-TEN;KIAA1075			intracellula
GI_38787956-I	98.8	112	97	TENC1	NM_170754.2	C1TEN;C1-TEN;KIAA1075			intracellula
GI_38787975-S	2253.4	2294.1	2279.7	TM4SF8	NM_005724.4	TM4-A;TSPAN-3	cell	integral to	mystery
GI_38787996-I	162.2	193.5	180.2	TREX1	NM_033627.3	DRN3;ATRIP;FLJ12343;DKFZp434J0310	3'-5'		DNA
GI_38788009-S	780.7	815.9	779.1	SART1	NM_005146.3	Ara1;HOMS1;MGC2038;SART1259	tumor	cytosol	
GI_38788093-I	107.2	108.7	103.7	3-Sep	NM_019106.4	SEP3;bK250D10.3			
GI_38788107-S	2812	2656.1	2453.6	SGTA	NM_003021.3	SGT	protein	cellular_co	biological_
GI_38788121-S	8407.7	7624.6	6773.9	SPUVE	NM_007173.3	ZSIG13;MGC5107;PRSS23-PENDING	trypsin		proteolysis
GI_38788134-A	229.8	274.1	244.7	GABRG2	NM_000816.2	CAE2;ECA2;GEFSP3	benzodiaz	integral to	gamma-
GI_38788154-I	90.9	98.7	100.5	GABRG2	NM_198904.1	CAE2;ECA2;GEFSP3	benzodiaz	integral to	gamma-
GI_38788159-I	167.7	186	173.1	GALNT10	NM_198321.2	FLJ00205;FLJ11715;GalNAcT10;DKFZp586			
GI_38788170-A	313.4	370.1	406.5	GALNT10	NM_017540.3	FLJ00205;FLJ11715;GalNAcT10;DKFZp586			
GI_38788170-I	114.7	142	119.8	GALNT10	NM_017540.3	FLJ00205;FLJ11715;GalNAcT10;DKFZp586			
GI_38788179-S	124.5	132.8	112.9	EAF1	NM_033083.5				
GI_38788192-S	109	123.7	108.8	EDG3	NM_005226.2	LPB3;S1P3;EDG-3;FLJ37523;MGC71696	lipid	integral to	cytosolic
GI_38788218-S	1290.5	2112.5	1087.8	MGC51082	NM_182498.2		DNA	nucleus	regulation
GI_38788229-S	1293.8	1338.3	1401.2	MRPL48	NM_016055.3	CGI-118;MGC13323	structural	ribosome	protein
GI_38788259-A	173.4	200	163.3	FALZ	NM_004459.5	BPTF;FAC1;NURF301		cytoplasm	neurogene
GI_38788259-I	176.4	185.7	180.7	FALZ	NM_004459.5	BPTF;FAC1;NURF301		cytoplasm	neurogene
GI_38788273-I	250.8	321.1	296.1	FALZ	NM_182641.2	BPTF;FAC1;NURF301		cytoplasm	neurogene
GI_38788287-S	194.8	228.9	240.6	ZNF160	NM_033288.2	F11;HZF5;KR18;:KR18;HKr18;FLJ00032;KIA	DNA	nucleus	regulation
GI_38788301-I	118.2	119.2	127.2	ZNF160	NM_198893.1	F11;HZF5;KR18;:KR18;HKr18;FLJ00032;KIA	DNA	nucleus	regulation
GI_38788307-S	961.4	924	1021.1	GNE	NM_005476.3	NM;DMRV;IBM2;Uae1;GLCNE	UDP-N-	cytoplasm	N-
GI_38788318-S	169.1	172	167.9	GNL1	NM_005275.2	HSR1	GTP		signal
GI_38788332-S	294.8	362.8	351.6	HBXAP	NM_016578.3	RSF1;XAP8;p325	DNA		regulation
GI_38788352-S	3835	4577.7	4546.2	HBXIP	NM_006402.2	XIP	antiviral		viral
GI_38788371-S	1339.7	1412.6	1308.7	AQR	NM_014691.1	KIAA0560			
GI_38788379-S	186.2	196.5	215.7	DHTKD1	NM_018706.4	MGC3090;KIAA1630;DKFZP762M115	oxidoredu		metabolis

GI_38788404-S	268.6	362.2	292.1	HD	NM_002111.4	IT15	microtubul	soluble	induction
GI_38788415-S	429.9	178.7	237.8	LAMA1	NM_005559.2	LAMA	extracellul	basal	cell-matrix
GI_38788425-S	256.4	239.3	244.4	NOG	NM_005450.2	SYM1;SYNS1		extracellul	skeletal
GI_38788444-S	146	167.4	139.7	OTC	NM_000531.3	OCTD	ornithine	ornithine	'de novo'
GI_38788468-S	124.4	152.5	130	PCDH18	NM_019035.2	PCDH68L;KIAA1562;DKFZP434B0923	carboxype	membran	homophili
GI_38788480-S	402.9	487.8	386.7	PROSC	NM_007198.2		molecular	cytoplasm	biological_
GI_38888174-S	118.7	117.9	110.3	SFTPA1	NM_005411.3	PSAP;PSPA;SP-A;SFTP1;SP-A1;COLEC4	apolipopro	extracellul	
GI_39204546-S	291.7	364.2	308.1	TSARG6	NM_153614.2	TSARG5;FLJ46748			
GI_39540511-S	420.7	561.2	478.5	DNAJC14	NM_032364.4	DNAJ;HDJ3;LIP6;DRIP78	chaperone		protein
GI_39545574-I	94.1	90.4	93.7	LOC55924	NM_198926.1		DNA	nucleus	regulation
GI_39545576-S	810	856.8	809.6	LOC51320	NM_016626.2				
GI_39545578-A	121.4	124.4	127.6	LOC55924	NM_019099.3		DNA	nucleus	regulation
GI_39545579-S	772.7	619	702.8	LOC51185	NM_016302.2		ATP-		ATP-
GI_39573706-S	220.8	233.6	211.4	DKFZp434K1	NM_182905.1				
GI_39573712-S	101	112.2	113	ALS2CR17	NM_198945.1				
GI_39573715-S	121.4	132.5	114.1	LCN6	NM_198946.1	UNQ643			
GI_39573717-S	116	150.7	156.7	CANP	NM_198947.1				
GI_39573729-S	834.4	914.3	660.9	MGC52000	NM_198943.1				
GI_39652617-S	497.9	464.8	461.4	TTC4	NM_004623.2	MGC5097	tumor		oncogene
GI_39652623-S	193.3	223.5	240.2	ESPL1	NM_012291.3	ESP1;SEPARIN;KIAA0165	protein	centrosom	mitotic
GI_39653312-S	92.5	85.6	89.3	FLJ46154	NM_198462.1	KIAA1493			intracellula
GI_39653314-S	135.5	138.1	193.8	DUFD1	NM_138419.2				
GI_39653316-S	157.9	171.4	155.9	JMJD2D	NM_018039.2		DNA	nucleus	regulation
GI_39653318-S	94.9	81.9	91.5	DKFZp434B0	NM_013377.2	PDZRN4			
GI_39653320-I	79.8	82.6	76.9	CGI-72	NM_024878.1	FLJ13649;FLJ21615;MGC64923			
GI_39653322-I	147.9	179.4	158.7	CGI-72	NM_032205.2	FLJ13649;FLJ21615;MGC64923			
GI_39725631-I	3688.1	4985.1	2084.3	TPM3	NM_153649.2	TRK;NEM1			
GI_39725632-S	1641.4	1400.8	1000.4	KIAA0116	NM_015004.2	RRP42	exonuclea	nucleus	rRNA
GI_39725633-S	975.9	1123.8	1053.1	LARP	NM_015315.2	KIAA0731;MGC19556			electron
GI_39725635-S	1840	2766.3	2425.4	HSGP25L2G	NM_017510.3		protein	endoplas	intracellula
GI_39725639-I	693.3	602.9	534.3	FLJ20542	NM_017871.3	FLJ13294			
GI_39725640-S	1009.8	972.6	915.6	C6orf166	NM_018064.2	FLJ10342;dJ486L4.2			
GI_39725642-S	579.6	587	606.7	SELB	NM_021937.2	EFSEC;EEFSEC	GTP	cytoplasm	translation
GI_39725643-A	343.8	688.6	284.6	MR-1	NM_022572.2	BRP17;FKSG19;TAHCCP2;KIAA1184;MGC3			
GI_39725643-I	148	168.6	146.8	MR-1	NM_022572.2	BRP17;FKSG19;TAHCCP2;KIAA1184;MGC3			
GI_39725645-I	119.1	123.7	117.3	STAG3	NM_024070.2	MGC2463		synaptone	synaptone
GI_39725646-S	1914.4	1691	1652.3	ALG8	NM_024079.2	MGC2840	transferas	endoplas	
GI_39725648-S	589.4	727.4	755.5	MGC4606	NM_024516.2				
GI_39725649-S	1419.5	1343.1	1434.3	MGC2408	NM_032331.2		S-		
GI_39725650-S	681.3	509.4	585.7	MGC4238	NM_032332.2				
GI_39725651-S	89.1	107.4	104.7	MGC3047	NM_032348.2				
GI_39725652-S	321.6	458.7	571.6	SDOS	NM_032349.2	MGC11275			
GI_39725653-S	109.9	132.6	121.3	MGC2562	NM_032374.2				
GI_39725654-S	1732.4	1845.6	1883.2	AKT1S1	NM_032375.2	Lobe;PRAS40;MGC2865			

GI_39725655-S	1381.8	1268.5	1245.1	MGC4251	NM_032376.2				
GI_39725656-S	1040.9	1198	1097.6	MGC4549	NM_032377.2				
GI_39725657-S	882.3	715.3	705.7	MGC13125	NM_032725.2				
GI_39725658-S	169.5	212.1	198.5	INA	NM_032727.2	NEF5;NF-66;TXBP-1;MGC12702	structural	neurofilam	
GI_39725659-S	513.5	621	566.7	MGC4126	NM_032773.2				
GI_39725660-S	203.1	217.4	168.5	MGC13159	NM_032927.2				
GI_39725661-S	1014	1028.9	779.5	MGC14141	NM_032928.2				
GI_39725662-S	675.4	663.2	303.3	C6orf11	NM_005452.4	BING4	molecular	cellular_co	biological_
GI_39725663-S	733.6	845.9	968.2	T54	NM_015698.3				
GI_39725664-S	92.3	104.1	98	MGC14289	NM_080660.2				
GI_39725665-S	106.8	114.7	108.6	PEX11G	NM_080662.2	MGC4281			
GI_39725666-S	425.9	548.5	430.5	SLC35A4	NM_080670.2	MGC2541			
GI_39725667-S	407.2	836.5	450	HTR1D	NM_000864.3	HTRL;RDC4;HT1DA;HTR1DA	serotonin	integral to	G-protein
GI_39725669-S	150.3	174.3	167.2	MPZ	NM_000530.3	P0;CHM;DSS;MPP;CMT1B;CMT2I;CMT2J;C	structural	integral to	homophili
GI_39725670-S	320	353.2	334.2	AP3S2	NM_005829.3	AP3S3;sigma3b;FLJ35955	protein	Golgi	intracellula
GI_39725671-S	600.9	572.4	730.1	SCLY	NM_016510.3	SCL	selenocyst	cytosol	amino
GI_39725672-S	5389.1	4369.6	6526	CLCN7	NM_001287.3	CLC7;CLC-7;OPTA2	chloride	membran	small
GI_39725673-S	699.3	587.3	652.8	VEGFB	NM_003377.3	VRF;VEGFL	vascular	membran	positive
GI_39725674-S	750.3	801.7	842.1	NMT1	NM_021079.3	NMT	catalytic		protein-
GI_39725675-S	987.1	1459.2	1905.6	DOC-1R	NM_005851.3		tumor		
GI_39725676-S	286	378	302.5	NUCB1	NM_006184.3	NUC	DNA	Golgi	
GI_39725677-S	529.8	636.8	543.1	SNAPAP	NM_012437.3	SNAPIN	SNARE	secretory	intracellula
GI_39725678-S	820.9	657.1	874.5	BM039	NM_018455.3				
GI_39725679-S	2013.8	2586.3	2247.4	TOMM22	NM_020243.3	TOM22	receptor	mitochond	mitochond
GI_39725680-S	193	234.1	223.9	CLDN6	NM_021195.3		structural	tight	
GI_39725681-S	115.2	106.2	97.1	STRAIT1149	NM_021242.3	FLJ10386			
GI_39725682-S	566.5	492.4	457.4	FLJ23441	NM_024678.3		aspartate-	intracellula	aspartyl-
GI_39725684-S	238.3	236.5	234.6	FLJ12528	NM_025150.3				
GI_39725686-S	140.2	158.2	131	LDB1	NM_003893.3	NLI;CLIM2	transcripti	nucleus	developm
GI_39725687-S	2224.2	2517.8	2220.3	NDUFA9	NM_005002.3	NDUFS2L	NADH	mitochond	sodium
GI_39725688-S	5573.4	5979	5894.7	TUBB2	NM_006088.3		structural	cytoskelet	microtubul
GI_39725690-S	817.2	714.7	719.9	SPUF	NM_013349.3				electron
GI_39725691-S	97.2	104.2	106.2	GTSE1	NM_016426.3	B99;GTSE-1	molecular	cytoplasmi	G2 phase
GI_39725692-S	1211.9	1393.6	1127.9	FLJ10420	NM_018090.3				
GI_39725693-S	569.4	649.4	722.3	BIN3	NM_018688.3			kinesin	endocytosi
GI_39725694-S	377.6	368.7	361.9	CRIP1	NM_001311.3	CRHP;CRIP;CRP1	zinc ion	cytoplasm	cell
GI_39725695-S	484.6	530.2	623.5	L3MBTL2	NM_031488.3	dJ756G23.3;H-l(3)mbt-l;DKFZP761I141	transcripti	nucleus	regulation
GI_39725696-S	229.8	238.9	221.8	SCGB1A1	NM_003357.3	UGB;CC10;CC16;CCSP	cytokine		embryo
GI_39725697-S	100	116.3	110.7	LOC51063	NM_015916.3				
GI_39725699-S	2871.2	3153.4	2856.5	RRP4	NM_014285.4		7S RNA	exosome	rRNA
GI_39725700-S	1472.2	2033.3	1548.4	HIP-55	NM_014063.4	SH3P7	enzyme	intracellula	activation
GI_39725701-S	109.5	107	104.4	FLJ32416	NM_144616.2	JP-45	DNA	nucleus	regulation
GI_39725704-S	815.7	969.2	1004.6	FLJ13479	NM_024706.3			nucleus	
GI_39725705-S	4652.7	3621.4	3841.4	TNFSF5IP1	NM_020232.3	HCCA3;CLAST3;MDS003;HsT1707;MGC150			

GI_39725706-S	1359.1	1414.5	1173.9	BMI1	NM_005180.5	RNF51;MGC12685		nucleus	segment
GI_39725709-S	155.5	195.7	166.3	LOC90925	NM_175870.3				
GI_39725710-S	92.2	94.2	86.3	MGC4701	NM_024511.3	IT1			
GI_39725712-S	905.1	958.3	832	PFKM	NM_000289.3	MGC8699	phosphofr	6-	regulation
GI_39725713-S	2204.5	1863.4	2129.9	ALG3	NM_005787.3	CDGS4;Not56;NOT56L;D16Ertd36e	transferas	endoplas	protein
GI_39725714-S	5430.7	4690.1	4344.6	ATIC	NM_004044.4	PURH;AICARFT;IMPCHASE	phosphori		nucleobas
GI_39725715-S	938.7	1114	759.6	SNRPA	NM_004596.3		small	snRNP U1	
GI_39725933-S	136.2	133.7	93.2	SERPINF1	NM_002615.3	PEDF;EPC-1	serpin		histogene
GI_39725935-S	328	332	304.6	STX18	NM_016930.2		protein	kinesin	nonselecti
GI_39725936-S	100.6	90.4	90.7	PGM5	NM_021965.2	PGMRP	structural	cell-cell	cell shape
GI_39725937-S	157.8	162.1	151.6	RPC155	NM_007055.2	RPC1	DNA-	nucleus	transcripti
GI_39725939-S	113.6	140	125.5	OPRK1	NM_000912.2	KOR;OPRK	kappa-	integral to	G-protein
GI_39725941-S	1536.6	1170.9	938.6	PEO1	NM_021830.3	PEO;TWINL;C10orf2;FLJ21832	helicase		
GI_39725945-S	163.4	194.4	136.1	NINJ2	NM_016533.4		cell	integral to	neuronal
GI_39725947-S	422.3	444.8	429.6	MIZF	NM_015517.3	HiNF-P;DKFZP434F162			
GI_39725949-S	446.7	437.5	437.3	IPO11	NM_016338.3	RanBP11	protein	nuclear	protein-
GI_39725951-S	285	335	316.1	HSU84971	NM_018046.2	VG5Q;FLJ10283;HUS84971	nucleic	intracellula	
GI_39725953-S	199	183.4	181.2	FLJ11149	NM_018339.3	RFK	riboflavin		vitamin B2
GI_39725954-S	209.9	247.2	210	FLJ21613	NM_024635.2	FLJ22643			
GI_39725956-I	122.4	132.3	96.9	DZIP1	NM_198968.1	DZIP;KIAA0996			
GI_39725958-A	391.1	417	339.7	DZIP1	NM_014934.2	DZIP;KIAA0996			
GI_39725959-S	104.6	113.8	105	DKFZp451J0	NM_175852.3				
GI_39752638-S	535.2	643.1	658.9	FLJ22374	NM_032222.1				
GI_39752644-S	2655.8	2506.7	2761.9	FLJ10326	NM_018060.2		ATP		isoleucyl-
GI_39752662-S	111.5	126.3	116.4	LENG9	NM_198988.1				
GI_39752666-S	94.4	99.9	98.9	DLEU7	NM_198989.1				
GI_39752670-S	149.9	145.1	136.5	SYT10	NM_198992.1				
GI_39752672-S	294.1	361.5	312.5	24b2/STAC2	NM_198993.1				
GI_39752674-S	137.7	158.2	133.1	TGM6	NM_198994.1				
GI_39752676-S	105.6	106.1	117.3	LOC374864	NM_198995.1				
GI_39752678-S	101.5	95.3	89.4	LOC375108	NM_198996.1				
GI_39752682-A	84.8	99.5	90.5	PRES	NM_198999.1	SLC26A5	motor	membran	sulfate
GI_39752684-S	82.1	79	78.6	LHFPL3	NM_199000.1				
GI_39752686-S	182	208.1	209.5	MGC59937	NM_199001.1				
GI_39753951-S	2788.2	3071.8	2872.4	NDUFAB1	NM_005003.2	ACP;SDAP	NADH	NADH	fatty acid
GI_39753952-S	563.8	425.6	419.7	LOC168850	NM_176814.3				
GI_39753954-S	689.7	927.9	948.4	MIR16	NM_016641.3				
GI_39753955-S	149.1	207.5	183.3	KRT6L	NM_175834.2			intermedia	
GI_39753956-S	807.5	982	1072.1	LAP1B	NM_015602.2	MGC3413;DKFZP586G011			
GI_39753958-S	482.6	654.7	566.5	KCTD9	NM_017634.2	FLJ20038			
GI_39753960-S	1353.8	1304.1	2108.3	IQGAP3	NM_178229.3	MGC1947;MGC10170;MGC10831	Ras		small
GI_39753962-S	107.4	117.3	114.8	GPB5	NM_145171.2		hormone	extracellul	
GI_39753964-S	784.8	1034.1	964.1	HIAT1	NM_033055.2	DKFZP564L0864	transporte	integral to	transport
GI_39753966-S	107.6	114.4	107.8	CSPG5	NM_006574.2	NGC	chondroiti	proteoglyc	

GI_39753967-S	107.3	109.7	107.6	FLJ46354	NM_198547.1				
GI_39753969-S	142.7	163	165.2	CAMP	NM_004345.3	LL37;CAP18;FALL39;FALL-39	antimicrob	extracellul	defense
GI_39777581-S	113.5	137.5	109.3	DHX57	NM_144995.2	FLJ32861	nucleic		
GI_39777585-I	90.6	100	97.6	DHX57	NM_198963.1	FLJ32861	nucleic		
GI_39777587-I	218.8	279.6	241.6	NOL6	NM_022917.4	NRAP;FLJ21959;MGC14896;MGC14921;MG			
GI_39777589-A	466.5	540.4	467.7	NOL6	NM_139235.3	NRAP;FLJ21959;MGC14896;MGC14921;MG			
GI_39777590-S	132.6	158.2	147.4	SLC13A3	NM_022829.3	NADC3;SDCT2	transporte	integral to	sodium
GI_39777591-S	126	133.1	95.8	SLC2A10	NM_030777.3	GLUT10	transporte	integral to	glucose
GI_39777592-S	290	272.3	293	SLC2A4RG	NM_020062.3	GEF;HDBP1	transcripti	nucleus	regulation
GI_39777593-S	492.9	309.5	336.2	SLCO4A1	NM_016354.3	POAT;OATP1;OATP-	transporte	integral to	ion
GI_39777595-S	744.8	807	574.2	TGIF2	NM_021809.4		transcripti	nucleus	regulation
GI_39777598-I	868	1169.4	1212.4	TGM2	NM_198951.1	TGC	acyltransf	cellular_co	protein
GI_39777600-S	176.1	199.1	190.4	TGM3	NM_003245.2	TGE;TGX	acyltransf		protein
GI_39777602-S	269.4	218.2	192.4	ARHGEF1	NM_004706.3	GEF1;LBCL2;SUB1.5;P115-RHOGEF	Rho	cytoplasm	Rho
GI_39777607-A	2764.3	3300.4	3898.3	SEMA4B	NM_020210.2	SemC;SEMAC;KIAA1745	receptor	integral to	developm
GI_39777609-I	160.2	185.3	176.8	SEMA4B	NM_198925.1	SemC;SEMAC;KIAA1745	receptor	integral to	developm
GI_39777611-A	349.3	459.8	558.8	SS18L1	NM_015558.3	CREST;KIAA0693;MGC26711			
GI_39777613-I	124.3	129.3	121.2	SS18L1	NM_198935.1	CREST;KIAA0693;MGC26711			
GI_39777615-A	1208.9	1109.4	1128.1	SNX14	NM_020468.2	RGS-PX2;MGC13217	protein		intracellula
GI_39777616-I	105.7	125.9	118	SNX14	NM_153816.2	RGS-PX2;MGC13217	protein		intracellula
GI_39777617-I	204	210.9	156	SYNGR1	NM_004711.3	MGC:1939	transporte	synaptic	transport
GI_39777618-I	225.3	308.2	198.3	SYNGR1	NM_145731.2	MGC:1939	transporte	synaptic	transport
GI_39780551-S	1086.4	1061.6	1368.4	FLJ10305	NM_018052.3				
GI_39780570-S	500.1	516.6	422	FLJ10504	NM_018116.2	LST005			
GI_39780587-S	338.2	321.2	293.5	FLJ10534	NM_018128.4	KIAA1401			
GI_39780596-S	124.8	130.9	125.3	FLJ10781	NM_018215.2				
GI_39811997-A	679.5	723.9	710	AES	NM_001130.5	GRG;ESP1;AES-1/AES-2		nucleus	histogene
GI_39812018-I	132.6	143.2	134.1	AES	NM_198969.1	GRG;ESP1;AES-1/AES-2		nucleus	histogene
GI_39812034-S	117.3	129.7	129.3	ARRB2	NM_004313.3	ARB2;ARR2		cytoplasm	sensory
GI_39812062-S	2064.1	2803.4	2628.9	MRPL28	NM_006428.3	p15;MAAT1;MGC8499	tumor		
GI_39812071-S	799.6	802.7	363.8	MRPS26	NM_030811.3	GI008;RPMS13;MRP-S13;MRP-S26;NY-BR-			
GI_39812087-A	1117.4	1607.1	2056.2	TDE1	NM_006811.2	TDE;TMS-1;DIFF33;SBBI99		integral to	
GI_39812105-I	168.3	224.7	326.3	TDE1	NM_198941.1	TDE;TMS-1;DIFF33;SBBI99		integral to	
GI_39812114-S	157.3	178	183.4	ACTR8	NM_022899.3	ARP8;FLJ12934;FLJ22579			
GI_39812132-S	123	121	111.9	ANKRD2	NM_020349.2	AARP			
GI_39812180-S	106.9	124.3	110.5	MGAT5B	NM_144677.2	GnT-IX;GnT-VB;FLJ25132			
GI_39812196-I	94.6	112.1	95.3	MGAT5B	NM_198955.1	GnT-IX;GnT-VB;FLJ25132			
GI_39812204-S	885.9	892.4	731.2	KIAA0999	NM_025164.3	FLJ12240	ATP		protein
GI_39812228-S	145.2	159.7	139.7	KPNA5	NM_002269.2	SRP6;IPOA6	protein	importin,	NLS-
GI_39812261-S	108.9	114.8	96.7	HIST1H3D	NM_003530.3	H3/b;H3FB	DNA	chromoso	nucleoso
GI_39812281-S	8322.8	5532.6	5570.9	HSPA9B	NM_004134.4	CSA;MOT;MOT2;GRP75;HSPA9;PBP74;mot-	ATP	cytoplasm	
GI_39812319-S	231.7	188.5	174.9	LRRC16	NM_017640.2	FLJ20048;dJ501N12.1			
GI_39812335-S	7996.2	9139.3	8945.9	NDUFS6	NM_004553.2		iron-sulfur	NADH	mitochond
GI_39812354-S	122.7	127.8	120.7	OR7C1	NM_198944.1	OR7C4;OR19-5;TPCR86;HSTPCR86P;CIT-	G-protein		physiologi

GI_39812361-S	1804.6	2396	2740.7	PSMD8	NM_002812.3	S14;p31;HIP6;HYPF;Nin1p;MGC1660		proteasom	regulation
GI_39812377-S	443.9	424.7	407.8	RANBP9	NM_005493.2	RANBPM	RAN	microtubul	microtubul
GI_39812393-S	991.3	902.9	813.9	REPS1	NM_031922.2	RALBP1	calcium		
GI_39812410-S	36099	34618	30543	RPS4X	NM_001007.3	CCG2;SCAR;SCR10;DXS306	structural	cytosolic	protein
GI_39812427-S	1283.7	1997.5	1130.7	SC65	NM_006455.2	NOL55		nuclear	synaptone
GI_39812446-S	90.9	103.9	102	SRD5A2	NM_000348.2		electron	microsom	androgen
GI_39812452-S	1390.2	1414.7	1200.5	SURF6	NM_006753.3	FLJ30322	RNA	nucleolus	
GI_39812473-S	251.1	662	1132.3	TFAP2C	NM_003222.3	ERF1;AP2-GAMMA	transcripti	nucleus	oncogene
GI_39812483-A	1657.5	1891.7	2636	TH1L	NM_016397.2	TH1;NELF-C;NELF-D;HSPC130			
GI_39812491-I	3032.8	3117.6	4547.1	TH1L	NM_198976.1	TH1;NELF-C;NELF-D;HSPC130			
GI_39812495-A	99.5	105.6	89.6	SP8	NM_182700.2	BTD	DNA	nucleus	
GI_39812500-I	150	169.3	152.1	SP8	NM_198956.1	BTD	DNA	nucleus	
GI_39841070-S	195.9	206	212.7	ZNF322B	NM_199005.1	ZNF322			
GI_39841072-S	1001	986.8	816.2	FLJ10379	NM_018079.3		RNA		
GI_39930312-S	218.5	215.2	220.1	IRLB	NM_005848.1		DNA	nucleus	regulation
GI_39930314-S	450.6	533.5	461.5	NXPH4	NM_007224.1	NPH4	receptor	extracellul	neuropepti
GI_39930340-S	612.3	465.3	318.1	KIAA0970	NM_014923.2				
GI_39930342-S	440.6	457.6	397.1	KIAA0779	NM_015008.1			integral to	
GI_39930344-S	169.7	187.2	159.6	KIAA0251	NM_015027.1		lyase		amino
GI_39930346-S	84.7	106.4	91.9	PIP5K3	NM_015040.1	p235;PIP5K;PIKfyve;KIAA0981;MGC40423	kinase		intracellula
GI_39930348-S	2006.8	1770.4	1306.4	KIAA0746	NM_015187.1				
GI_39930350-S	193.7	174.7	142.4	KIAA1010	NM_015221.1	TUBA	guanyl-		endocytosi
GI_39930352-S	1474.3	1448.3	1226.9	KIAA0052	NM_015360.2		nucleic	nucleus	
GI_39930354-S	776	1228.3	907.7	DPCD	NM_015448.1	DKFZP566F084			
GI_39930360-S	1663.4	1606.6	1988.8	DKFZP434C1	NM_015518.1		protein-		protein
GI_39930366-S	172.6	226	179.6	SEMA5B	NM_018987.1	SemG;SEMAG;FLJ10372;KIAA1445	receptor	membran	developm
GI_39930374-S	167	192.3	143.1	ENAH	NM_018212.2	NDPP1;FLJ10773			
GI_39930376-S	96.1	115.5	100.1	KIAA1164	NM_019092.1		ATP		proteolysis
GI_39930378-S	533.8	481.6	432.7	LRRC8	NM_019594.1	FLJ10337;KIAA1437			
GI_39930382-S	375.9	473.9	430.9	BARHL2	NM_020063.1		DNA	nucleus	regulation
GI_39930384-S	199.4	350	225.9	KIAA1217	NM_019590.1	DKFZP761L0424			
GI_39930390-S	494.7	747.3	570.9	KIAA1463	NM_020849.1		catalytic		metabolis
GI_39930392-S	368.3	313.2	318.1	C9orf102	NM_020207.1		helicase		
GI_39930394-S	233.9	377.2	318.9	KIAA1618	NM_020954.1		transcripti	intracellula	regulation
GI_39930396-S	231	253	223.8	KIAA1387	NM_020463.1				
GI_39930398-S	378.9	482.2	875.2	C20orf110	NM_021202.1	PINH;FLJ21759;FLJ23500;dJ1181N3.1;DKF		microfibril	
GI_39930400-S	123.4	136	120.7	KIAA1465	NM_020851.1				
GI_39930402-S	278.7	341.7	309.3	LGR6	NM_021636.1	FLJ14471;VTS20631			
GI_39930458-S	733.5	1032.3	839.3	IRX3	NM_024336.1	IRX-1	transcripti	nucleus	regulation
GI_39930462-S	137.7	140.3	123.1	KIAA1701	NM_030639.1				
GI_39930468-S	1016.6	670.4	549.8	BXDC1	NM_032194.1	FLJ21087;bA397G5.4		nucleus	
GI_39930470-S	295	282	284	FLJ22789	NM_032230.1				
GI_39930472-S	315.5	248.6	326	MLR2	NM_032440.1	LCOR;KIAA1795	DNA	nucleus	regulation
GI_39930474-S	375.3	339.1	400.3	IRX2	NM_033267.1		transcripti	nucleus	regulation

GI_39930478-S	172.1	347.6	295.9	DIXDC1	NM_033425.1	KIAA1735	signal	intracellula	frizzled
GI_39930482-S	126	159.3	134.5	IMAGE:42153	NM_052878.1				
GI_39930484-S	510.1	465.9	455.6	MCSC	NM_052901.1	KIAA1896	binding	mitochond	transport
GI_39930510-S	687.3	394.7	239.1	FLJ30681	NM_133459.1	KIAA1983	calcium		
GI_39930516-S	172.7	184.5	219.2	LOC90378	NM_138352.1				
GI_39930520-S	1888.8	3856.6	3030.2	LOC114990	NM_138440.1				
GI_39930522-S	134.6	159.3	162.4	LOC144097	NM_138471.1				
GI_39930526-S	3595.5	2566.5	1726.8	TNNT1	NM_003283.3	ANM	tropomyos		regulation
GI_39930528-S	208	254.9	238.4	UPA	NM_145202.2				
GI_39930530-S	289.4	333.1	305.9	MGC34132	NM_173654.1				
GI_39930532-S	290.7	327.5	285.4	MGC19531	NM_005167.4	DKFZp434P1514	catalytic		
GI_39930536-S	134.1	192.9	141	HMGCS1	NM_002130.3	HMGCS	hydroxym	soluble	lipid
GI_39930540-S	918.6	834.5	832	LOC286257	NM_183241.1				
GI_39930546-S	271.2	306	263.1	FLJ39441	NM_194285.1				
GI_39930568-S	141.9	153.4	191.3	LOC116236	NM_198147.1				
GI_39930570-S	169.9	204.5	210.1	DKFZp761L1	NM_198075.1				
GI_39930572-S	227	277.5	242.5	LOC119587	NM_198148.1		carboxype		proteolysis
GI_39930574-S	96.4	122.9	108.3	C1orf40	NM_198149.1				
GI_39930576-S	6443	7705.9	7070.4	DKFZp313G1	NM_198150.1		sulfuric		metabolis
GI_39930584-S	165.2	179.2	173.7	ZNF600	NM_198457.1	KR-ZNF1;DKFZp686F06123		nucleus	
GI_39930586-S	118.7	120.4	119.5	ZNF568	NM_198539.1	FLJ35804;DKFZp686B0797	nucleic	nucleus	regulation
GI_39930590-S	219.7	283.2	243.8	GANC	NM_198141.1		hydrolase		carbohydr
GI_39930600-S	893.6	781.3	957.1	SPATA11	NM_032306.2	UNQ6002;MGC10974			
GI_39930601-S	128	145.5	133.5	TRF3	NM_199047.1				
GI_39930603-S	174.2	179.2	153.9	SOS2	NM_006939.1		guanyl-	cellular_co	small
GI_39930609-I	168.5	196	179.2	SCN1B	NM_199037.1	GEFSP1	voltage-	integral to	sodium
GI_39930611-I	2583	4326.5	2951.3	KLHL5	NM_199039.1		actin	cytoskelet	actin
GI_39932584-S	90.4	90.1	73.2	C10orf24	NM_152709.2	FLJ25162			
GI_39932586-S	113.9	130.3	131.4	C14orf101	NM_017799.2	FLJ20392		integral to	
GI_39932588-S	367.9	223.7	189.2	ARHGAP18	NM_033515.2	MacGAP;bA307O14.2			
GI_39979625-S	99	120	129.5	FLJ13646	NM_024584.2		structural	microtubul	microtubul
GI_39979635-S	546.1	564.4	595.4	NOL8	NM_017948.3	Nop132;C9orf34;FLJ20736			
GI_39979637-S	160.3	177.6	152.6	DBCCR1L	NM_199051.1				
GI_39995057-I	149.4	170.5	154.4	CASP2	NM_001224.3	ICH1;NEDD2;CASP-2;ICH-1L;ICH-1L/1S	caspase-2		apoptotic
GI_39995062-A	192.5	181.8	242.6	CASP2	NM_032984.2	ICH1;NEDD2;CASP-2;ICH-1L;ICH-1L/1S	caspase-2		apoptotic
GI_39995063-S	219.9	291.8	270.9	PANX1	NM_015368.3	MRS1;UNQ2529;MGC21309		gap	
GI_39995065-S	105.3	121	109.7	PANX2	NM_052839.2	hPANX2		gap	
GI_39995066-S	107.1	106.6	97.7	PANX3	NM_052959.2			gap	
GI_39995067-I	119.2	118.6	114.8	EXO1	NM_130398.2	HEX1;hExoI	ribonuclea		mismatch
GI_39995068-A	590.8	524.1	616.2	EXO1	NM_003686.3	HEX1;hExoI	ribonuclea		mismatch
GI_39995072-S	3167.9	3805.9	2230.2	CDC37	NM_007065.3	P50CDC37	protein		protein
GI_39995073-A	305.3	316.4	388.9	CDKN2D	NM_079421.2	p19;INK4D;p19-INK4D	cyclin-	cytoplasm	cell cycle
GI_39995074-I	120.1	130.3	131.4	CDKN2D	NM_001800.3	p19;INK4D;p19-INK4D	cyclin-	cytoplasm	cell cycle
GI_39995075-S	1109.1	1158.6	973.4	FLJ12716	NM_021942.4				

GI_39995079-S	325	318.7	317.7	FLJ13725	NM_024519.2	KIAA1930			
GI_39995081-S	5371.2	5357.8	3559.7	FLJ20303	NM_017755.4				
GI_39995083-S	892.8	1277.1	1130.3	FLJ21919	NM_023015.3				
GI_39995085-S	269.9	263	301.3	NCKX6	NM_024959.2	FLJ22233		integral to	
GI_39995087-S	303.7	392.7	330.8	PTHLH	NM_002820.2	HHM;PLP;PTHR;PTHRP;MGC14611	cAMP	perinuclea	epidermal
GI_39995094-S	115.5	150.2	174.7	PTGFR	NM_000959.2	FP;MGC46203	prostaglan	integral to	parturition
GI_39995095-S	288.1	379.6	317.6	PTGIR	NM_000960.3	IP;PRIPR	prostaglan	integral to	G-protein
GI_39995096-S	244.8	194.9	133.6	PTHR1	NM_000316.2	PTHR	parathyroi	cytoplasm	G-protein
GI_39995097-S	129.1	141.2	138.8	PTHR2	NM_005048.2		parathyroi	integral to	G-protein
GI_39995098-S	123.8	127.7	119.6	PTH	NM_000315.2		cAMP	soluble	induction
GI_39995106-A	204.7	239.3	247.4	FASTK	NM_033015.2	FAST;FLJ13079	protein		induction
GI_39995108-S	298.7	272	171.4	GM2A	NM_000405.3	SAP-3	sphingolipi	lysosome	glycosphin
GI_39995110-S	124	185.3	136.4	GSTM3	NM_000849.3	GST5;GSTB;GTM3;GSTM3-	glutathion		establish
GI_40018613-S	202.5	281.2	284.5	DRE1	NM_017644.2	FLJ20059;FLJ22673			
GI_40018619-S	732.4	722.1	641.4	KIAA1055	NM_015079.2	FLJ20166	nucleic	intracellula	regulation
GI_40018625-S	684.5	794.8	676.5	MOBKL2A	NM_130807.2	moblak			
GI_40018626-I	187.5	190	197.2	MKNK2	NM_199054.1	MNK2;GPRK7	G-protein-		protein
GI_40018628-S	118.5	124.8	110.2	KIAA1033	NM_015275.1				
GI_40018630-A	544.6	520.1	404.1	MKNK2	NM_017572.2	MNK2;GPRK7	G-protein-		protein
GI_40018632-S	1840	2817.6	2154.2	IDI1	NM_004508.2		isopenten	peroxisom	isoprenoid
GI_40018634-S	1690	1250.8	877.9	FTHFSDC1	NM_015440.3	FLJ21145;DKFZp586G1517	formate-		folic acid
GI_40018637-S	788.8	835.9	1479.3	C21orf25	NM_199050.1	MGC71445;DKFZP586F0422			
GI_40018639-S	310.6	331.6	303.7	HRPT2	NM_024529.3	HPT-JT;C1orf28;FLJ23316			
GI_40018643-A	97.8	95	101.2	C14orf118	NM_017972.2	FLJ10033;FLJ20689			
GI_40018645-I	139.8	154.7	160.2	C14orf118	NM_017926.2	FLJ10033;FLJ20689			
GI_40018647-S	5087.7	4455.9	5041.7	AP3D1	NM_003938.4	ADTD	vesicle	Golgi	eye
GI_40068036-S	97	98.4	98.3	SIT	NM_014450.2		SH3/SH2	integral to	signal
GI_40068037-S	112.2	137	100.7	LOC51760	NM_016524.2		transporte	membran	transport
GI_40068041-S	184.9	197.2	163	HSJ001348	NM_017527.2				
GI_40068043-S	445.8	416.9	274.9	KIAA1495	NM_020871.2				
GI_40068048-S	271.5	348.2	367.1	CNNM3	NM_017623.3	ACDP3;FLJ20018			
GI_40068050-I	169.3	159.6	150.3	CNNM2	NM_199077.1	ACDP2;FLJ20064			
GI_40068058-S	290.1	326.3	235	CIR	NM_004882.3		transcripti		electron
GI_40068060-S	244.3	258.6	261.9	C6orf139	NM_018132.2	FLJ10545			
GI_40068062-S	246.8	257.8	221.7	C6orf197	NM_017772.2	FLJ20337;dJ744I24.2			
GI_40068064-A	161.9	184.3	163	C21orf58	NM_058180.2				
GI_40068066-I	90.8	96.7	88.8	C21orf58	NM_199071.1				
GI_40068460-S	1229.6	1154	1341	PTK9L	NM_007284.3	A6RP	actin	intracellula	
GI_40068461-I	152.3	176.6	161.5	ARID1B	NM_175863.2	6A3-	molecular	cellular_co	biological_
GI_40068463-A	301.1	330.7	296	ARID1B	NM_020732.2	6A3-	molecular	cellular_co	biological_
GI_40068465-I	175	209.2	197.6	ARID1B	NM_017519.1	6A3-	molecular	cellular_co	biological_
GI_40068467-S	415.1	492	535.2	PTGES2	NM_025072.4	GBF1;PGES2;C9orf15;FLJ14038;MGC11289	electron		electron
GI_40068474-S	1429.3	1566.7	1719.8	PTK9	NM_002822.3	A6;MGC23788;MGC41876	protein-	intracellula	protein
GI_40068478-S	290.2	248	256	FLJ22578	NM_024864.3		RNA		RNA

GI_40068480-I	754	757	742.5	FLJ23027	NM_032233.2				
GI_40068482-I	171.2	195.7	208.4	FLJ23027	NM_199123.1				
GI_40068484-S	290.8	530.7	399.5	WARP	NM_022834.3	FLJ22215;DKFZp761O051			
GI_40068494-S	169.8	209.5	199.9	MGC20983	NM_145045.3	FLJ31801			
GI_40068496-S	546.8	596.7	536.1	MGC5297	NM_024091.2	FLJ23274			
GI_40068498-S	387.6	399.8	340.5	THAP1	NM_018105.2	FLJ10477;MGC33014	DNA		
GI_40068503-S	6308.9	6030.3	5483.7	RARS	NM_002887.3	ArgRS;MGC8641	ATP	soluble	arginyl-
GI_40068504-S	1776.1	3135.2	3291.3	BSCL2	NM_032667.4	SPG17;GNG3LG;SEIPIN;MGC4694			
GI_40068508-S	191.4	249.2	201	DOCK11	NM_144658.2	FLJ32122			
GI_40068510-S	288.1	278.3	214.3	ERCC2	NM_000400.2	EM9;MAG;XPD	DNA	transcripti	nucleotide-
GI_40068511-S	980.1	607.8	242	FUCA2	NM_032020.3	MGC1314;dJ20N2.5	alpha-L-		carbohydr
GI_40068514-S	98.3	122.7	100.9	KIAA1409	NM_020818.1	FLJ43337			
GI_40068516-S	595.1	600.9	514	KIN	NM_012311.2	BTCD;KIN17	DNA	nucleus	
GI_40068517-S	800.6	1037.2	1039.6	PGD	NM_002631.2	6PGD	electron		pentose-
GI_40068519-I	149.3	166	134.7	PRO1853	NM_144736.2				
GI_40217610-S	324.8	356.4	283.9	DOCK6	NM_020812.1	KIAA1395	peroxidas		response
GI_40217621-S	106.3	113.5	110.4	VAX1	NM_199131.1				
GI_40217625-S	355.2	511.6	534.4	LOC134145	NM_199133.1				
GI_40217627-S	124	136.3	101.4	LOC283970	NM_199134.1				
GI_40217629-S	84.2	78.5	93.3	MGC72075	NM_199136.1				
GI_40217782-S	249.7	239.9	243.9	USP28	NM_020886.2	KIAA1515			
GI_40217785-I	332.4	331.9	342.5	LRRC1	NM_018214.3	LANO;FLJ10775;FLJ11834;dJ523E19.1			
GI_40217787-S	153.8	187.7	171.8	FLJ35630	NM_152618.2		ATP		protein
GI_40217789-S	504.8	533	464.6	ZNF512	NM_032434.2	KIAA1805			
GI_40217793-S	187.5	217	188.6	FLJ23861	NM_152519.2				
GI_40217795-S	406.7	273	336.2	FLJ23749	NM_152271.2		ATP-		ATP-
GI_40217797-S	221.4	261.4	223.8	ZNF585A	NM_152655.2	FLJ23765	nucleic	intracellula	regulation
GI_40217800-I	113.1	114.9	112.3	FLJ23554	NM_199124.1				
GI_40217802-S	193.4	246.7	218.1	FLJ23420	NM_025061.3				
GI_40217804-S	137.6	143.6	146.7	FLJ23323	NM_024654.3				
GI_40217806-S	103.7	93.8	101.1	FERD3L	NM_152898.2	NATO3;NTWIST;N-TWIST			
GI_40217807-S	155.4	176.2	172.2	Eu-HMTase1	NM_024757.3	FLJ12879;KIAA1876	methyltran	nucleus	chromatin
GI_40217811-A	1028.8	1078.8	1198.7	TBRG4	NM_004749.2	CPR2;KIAA0948			cell cycle
GI_40217811-I	192	244.4	254.8	TBRG4	NM_004749.2	CPR2;KIAA0948			cell cycle
GI_40217814-I	157.7	181.6	159	DDO	NM_003649.2	DASOX;DDO-1;DDO-2	D-	peroxisom	aspartate
GI_40217816-S	123.6	136.4	125.3	SLITRK1	NM_052910.1	KIAA1910			
GI_40217818-S	94.1	88	93.6	SLITRK2	NM_032539.2	CXorf2;SLITL1;KIAA1854	DNA	nucleus	regulation
GI_40217819-S	106.2	112.4	98.7	SLITRK3	NM_014926.2	KIAA0848			
GI_40217821-S	115.5	128.2	136.2	SLITRK4	NM_173078.2	DKFZp547M2010			
GI_40217822-S	103.4	106.6	98.4	SLITRK5	NM_015567.1	KIAA0918			
GI_40217824-S	97	88.6	152.1	SLITRK6	NM_032229.2	FLJ22774;DKFZp564O1278			
GI_40217826-A	190.9	200.9	173.3	DDO	NM_004032.2	DASOX;DDO-1;DDO-2	D-	peroxisom	aspartate
GI_40217828-S	429.8	499.1	470.4	GPR68	NM_003485.2	OGR1	G-protein	integral to	G-protein
GI_40217830-A	111.4	1113.9	830	GPRC5C	NM_022036.2	RAIG3;RAIG-3	G-protein	integral to	G-protein

GI_40217837-A	451.2	425.1	417.8	WDR4	NM_033661.3		molecular	cellular_co	biological_
GI_40217837-I	1409.4	1226.8	1214.7	WDR4	NM_033661.3		molecular	cellular_co	biological_
GI_40217838-S	314.8	363.5	338.8	FMNL3	NM_175736.3	WBP3;FHOD3;MGC45819;DKFZp762B245	actin		cytokinesi
GI_40217842-S	128.2	130.7	129.3	COMP	NM_000095.2	MED;EDM1;EPD1;PSACH	extracellul	extracellul	skeletal
GI_40217844-S	185.4	253.3	210.5	ITGAV	NM_002210.2	CD51;MSK8;VNRA	cell	integrin	cell
GI_40217845-S	1423.2	998.2	765.4	XPOT	NM_007235.3	XPO3	tRNA	exportin	nucleocyto
GI_40217846-S	3077.7	3406.6	3075.4	U5-200KD	NM_014014.2	KIAA0788	hydrolase	spliceoso	mRNA
GI_40217848-S	210.6	258.7	224.9	ZNF46	NM_006977.2	KUP	transcripti	nucleus	regulation
GI_40217850-S	171.4	206.2	177.9	KRT19	NM_002276.3	K19;CK19;K1CS;MGC15366	structural	intermedia	
GI_40254414-S	109.1	126.5	119.6	GUCA1A	NM_000409.2	GCAP;GUCA;GCAP1;GUCA1	calcium		vision
GI_40254417-S	645.3	1099.9	962.8	SMPD1	NM_000543.2	ASM;NPD	sphingom	lysosome	sphingom
GI_40254421-S	216.3	268	310.5	NOS3	NM_000603.2	eNOS;ECNOS	nitric-	cytoplasm	amino
GI_40254423-S	157.2	170.2	156	PHEX	NM_000444.2	HYP;PEX;XLH;HPDR;HYP1;HPDR1	zinc ion	integral to	proteolysis
GI_40254425-S	115.9	135.1	123.7	NPR1	NM_000906.2	ANPa;NPRA;ANPRA;GUC2A	receptor	integral to	regulation
GI_40254427-S	79.9	106.1	82.5	SLC11A1	NM_000578.2	LSH;NRAMP;NRAMP1	transporte	membran	response
GI_40254429-S	82.9	96.3	90.6	PRL	NM_000948.2		prolactin	soluble	hemocyte
GI_40254430-S	239.2	275.3	265.5	HTR2B	NM_000867.2	5-HT2B;5-HT(2B)	serotonin	integral to	G-protein
GI_40254432-S	95.3	117.5	91.2	SST	NM_001048.2	SMST	peptide	extracellul	induction
GI_40254433-S	108.2	127.2	111.4	PDE3B	NM_000922.2		cGMP-	membran	signal
GI_40254435-S	162.6	193.2	196.3	PRLR	NM_000949.2		prolactin		embryo
GI_40254436-S	211.1	257.3	224.4	C16orf3	NM_001214.2		molecular	cellular_co	biological_
GI_40254440-S	111.5	113.4	98	NDST1	NM_001543.2	HSST;NST1	heparin N-	Golgi	heparan
GI_40254443-S	750.3	782.9	531.3	SIAH1	NM_003031.2			nucleus	axon
GI_40254445-S	124.9	131.1	121.8	CUL5	NM_003478.2	VACM1;VACM-1	calcium		induction
GI_40254447-S	266.2	329.2	277.8	PIK3R3	NM_003629.2	p55-GAMMA	1-	phosphoin	insulin
GI_40254449-S	1403.6	3539.8	915	IFITM1	NM_003641.2	9-27;CD225;IFI17;LEU13	receptor	integral to	negative
GI_40254451-S	251.8	314.7	237.9	NRP1	NM_003873.2	NRP;VEGF165R	vascular	integral to	axon
GI_40254453-S	129.8	153.3	147.6	ATP1B2	NM_001678.2	AMOG	sodium/po	integral to	small
GI_40254455-S	103.7	110.2	106.7	ATP2B4	NM_001684.2	PMCA4;ATP2B2	calcium-	integral to	small
GI_40254457-S	425.3	408.4	354.2	SLC31A1	NM_001859.2	CTR1;COPT1	copper ion	integral to	copper ion
GI_40254458-S	103.4	98.1	106.1	HAPLN1	NM_001884.2	CRTL1	hyaluronic	extracellul	cell
GI_40254459-S	638.3	898.7	878	CTNNB1	NM_001904.2	CTNNB	tumor	cytoskelet	oncogene
GI_40254460-S	124.7	139.7	131.2	GLRA2	NM_002063.2	GLR	glycine-	integral to	small
GI_40254461-S	126.4	145.7	130.9	GNAQ	NM_002072.2	G-ALPHA-q	heterotrim	heterotrim	phospholi
GI_40254463-S	308.7	392.4	337.5	LEPR	NM_002303.2	OBR	transmem	integral to	energy
GI_40254465-S	1126.3	1113.2	844.4	NCBP1	NM_002486.2	NCBP;CBP80	RNA	nucleoplas	binding to
GI_40254468-S	462.7	592.8	511.2	SLC7A1	NM_003045.2	ERR;ATRC1;CAT-1;HCAT1;REC1L	basic	integral to	small
GI_40254469-S	393	702.3	386.2	SPN	NM_003123.2	LSN;CD43;GPL115	binding	membran	negative
GI_40254470-S	119.9	137.7	131.6	UGT8	NM_003360.2	CGT	UDP-	microsom	peripheral
GI_40254472-S	479.4	541.3	482.6	VLDLR	NM_003383.2		low-	plasma	memory
GI_40254474-S	291.1	367.5	304.2	HNF4G	NM_004133.3	NR2A2	transcripti	nucleus	regulation
GI_40254476-S	2008.3	1789.5	1874.9	DRG1	NM_004147.2	DRG;NEDD3	transcripti		transcripti
GI_40254477-S	209.5	213.3	216.2	SLC1A2	NM_004171.2	EAAT2;GLT-1	L-	integral to	L-
GI_40254479-S	135.8	152	143.7	GFI1B	NM_004188.2		specific		G1-

GI_40254481-S	141.2	130.7	103.3	AMY1A	NM_004038.2	AMY1	alpha-		carbohydr
GI_40254803-S	116.2	117	118.4	FLJ35784	NM_198534.1				
GI_40254807-S	122.3	125.4	123.5	PRF1	NM_005041.2	P1;PFP;HPLH2	channel-	cytosol	programm
GI_40254809-S	171.3	182.6	170	NR1D2	NM_005126.2	RVR;BD73;HZF2;EAR-1r;Hs.37288	ligand-	nucleus	signal
GI_40254811-S	253.9	269.7	264.3	DOCK3	NM_004947.2	MOCA;KIAA0299			
GI_40254812-S	112	117.5	107.1	GUCA1C	NM_005459.2	GCAP3	calcium		vision
GI_40254814-S	222.3	301.3	256.5	GYS2	NM_021957.2		glycogen		glycogen
GI_40254815-S	3708.9	5139.7	4784.2	HSPCA	NM_005348.2	HSPN;LAP2;HSP86;HSPC1;Hsp89;Hsp90;H	ATP	cytoplasm	biological_
GI_40254817-S	178.4	232.5	186.2	SKIL	NM_005414.2	SNO	TGFbeta	nucleus	oncogene
GI_40254818-S	249.3	307.4	261.5	KRN1	NM_005553.2			cytoskelet	epidermal
GI_40254820-S	157.1	181	162.4	PRKAB2	NM_005399.2				signal
GI_40254821-S	741.2	736.5	618.5	MEF2D	NM_005920.2		transcripti	nucleus	muscle
GI_40254822-S	235.8	303.9	181.1	INPP5D	NM_005541.2	SHIP	inositol-		phosphate
GI_40254824-S	115.9	130.2	135.9	PPYR1	NM_005972.2	Y4;PP1;NPY4R	G-protein	integral to	G-protein
GI_40254826-S	16437.9	16842	13789	NACA	NM_005594.2			nascent	nascent
GI_40254828-S	96.2	113.8	117.6	MTHFR	NM_005957.2		methylene		amino
GI_40254830-S	302.2	355.9	276.4	PRKAA1	NM_006251.2		protein		protein
GI_40254832-S	111.2	109.7	111.8	HTR3B	NM_006028.2	5-HT3B	serotonin-	membran	small
GI_40254835-S	94.7	95.7	88.5	PENK	NM_006211.2		neuropepti	soluble	signal
GI_40254836-S	84.3	85.7	87.6	GJB6	NM_006783.2	ED2;EDH;HED;CX30;DFNA3	connexon	connexon	hearing
GI_40254838-S	324.6	376.8	347.2	PROP1	NM_006261.2		RNA	nucleus	central
GI_40254839-S	5581	5737.1	4916	SFRS5	NM_006925.2	HRS;SRP40	pre-mRNA	nucleus	mRNA
GI_40254840-S	161.1	200	189.3	MAN1A2	NM_006699.2	MAN1B	mannosyl-	Golgi	N-glycan
GI_40254841-S	328.4	351	282.1	CENTB2	NM_012287.3	ACAP2;CNT-B2;KIAA0041	GTPase	nucleus	
GI_40254843-S	139.7	179.2	162.1	RIPK3	NM_006871.2	RIP3	protein		induction
GI_40254845-S	116	126.5	118.4	TFPI	NM_006287.3	EPI;LACI	endopepti		blood
GI_40254846-S	535.4	686.7	1011.9	UBL3	NM_007106.2	HCG-1;PNSC1;DKFZP434K151			
GI_40254847-S	1897	2316.4	2230.7	MTCH2	NM_014342.2	HSPC032	binding	mitochond	transport
GI_40254848-S	595.4	580.7	521.6	SF3B3	NM_012426.2	RSE1;SAP130;SF3B130;KIAA0017	pre-mRNA	spliceoso	mRNA
GI_40254852-S	150.9	153.5	164.5	UBL4	NM_014235.2	GDX;DXS254E	small		protein
GI_40254853-S	285.4	381.6	228.3	KIAA0773	NM_014690.2				
GI_40254856-S	311.5	431	466.7	KIAA1036	NM_014909.2				
GI_40254857-S	362.6	492.3	389.6	DZIP3	NM_014648.2	KIAA0675			
GI_40254858-S	3016.4	2399.8	2626	KIAA0664	NM_015229.2		translation		protein
GI_40254862-S	166.8	182.1	175.6	CDK11	NM_015076.2	KIAA1028;bA346C16.3	ATP		protein
GI_40254863-S	102.1	144.5	84.9	DKFZP586A0	NM_014033.2		S-		
GI_40254865-S	668.2	729.4	807.1	DKFZP564O1	NM_014043.2		molecular		
GI_40254867-S	1340.9	1236.5	1071.6	ZZZ3	NM_015534.3	DKFZP564I052	DNA	nucleus	
GI_40254868-S	1323	1673.6	1684.6	PRPF31	NM_015629.2	RP11;PRP31;NY-BR-99;DKFZp566J153			
GI_40254870-S	92.9	102.5	103.6	DESC1	NM_014058.2		trypsin	integral to	proteolysis
GI_40254872-S	248.2	364.4	226.1	HSPC049	NM_014149.2				
GI_40254874-S	1789.9	2067.1	1967.6	VDRIP	NM_014166.2	DRIP36;HSPC126	RNA	mediator	transcripti
GI_40254875-S	3112	3323.5	3544.9	LOC51248	NM_016484.3		protein		intracellula
GI_40254876-S	92.7	99.2	106.8	ZNF571	NM_016536.2	HSPC059	nucleic	nucleus	regulation

GI_40254878-S	112.5	120.3	109.1	CGI-77	NM_016023.2				
GI_40254881-S	271.6	370	277.5	C21orf91	NM_017447.2	YG81;C21orf38			
GI_40254883-S	188.9	261.2	255.2	SSH1	NM_018984.2	SSH-1;KIAA1298			
GI_40254885-S	221.3	252.7	241.8	CXorf9	NM_018990.2	SLY;753P9			
GI_40254886-S	141.9	138.5	135.9	1-Sep	NM_019001.2	XRN1;DKFZp434P0721	nuclease	cytoplasm	RNA
GI_40254888-S	129.2	139.8	119.8	FLJ10895	NM_019084.2			nucleus	regulation
GI_40254890-S	118.1	120.7	131.8	FLJ20674	NM_019086.2				
GI_40254892-S	634	536.8	537.9	FLJ11273	NM_018374.2				
GI_40254894-S	986.7	833.5	960.6	FLJ10349	NM_018066.2		ATP		
GI_40254896-S	851	712.1	561.3	DKFZp434K1	NM_017606.2				
GI_40254897-S	161.2	188.1	165.9	FLJ20032	NM_017628.2				
GI_40254903-S	119.1	117.1	101.1	FLJ20321	NM_017766.2				
GI_40254905-S	163.5	179.7	164	ELOVL2	NM_017770.2	Ssc2;FLJ20334		endoplas	fatty acid
GI_40254907-S	121.6	121.1	118.8	C21orf55	NM_017833.2	C21orf78;FLJ20461	chaperone		
GI_40254909-S	2623.5	2077.8	1762.4	FLJ20527	NM_017863.2				
GI_40254910-S	866.8	777.8	524.9	C20orf27	NM_017874.2	FLJ20550			
GI_40254914-S	118.3	127.6	140.2	C13orf11	NM_017905.2	FLJ20623			
GI_40254916-S	169.7	218	184.4	FLJ10060	NM_017986.2	GPCR;PAR2;GPCR42			
GI_40254918-S	451.9	442	232.9	FLJ10726	NM_018195.2				
GI_40254920-S	80.2	80.3	88.2	FLJ11155	NM_018342.2				
GI_40254922-S	280.6	356.8	328.7	LIN7C	NM_018362.2	VELI3;LIN-7C;MALS-3;LIN-7-C;FLJ11215	protein		intracellula
GI_40254923-S	2206.1	3159.8	3253.7	PRO1855	NM_018509.2				
GI_40254925-S	399.9	535.9	501.9	GNG12	NM_018841.2		signal	heterotrim	signal
GI_40254927-S	208.7	328	197.8	SLC39A9	NM_018375.2	FLJ11274	metal ion	membran	metal ion
GI_40254929-S	268.1	292.1	303.4	KBRAS1	NM_020345.2		small	cellular_co	NIK-I-
GI_40254930-S	346.4	370.3	431.8	FLJ10706	NM_018186.2		cysteine-		proteolysis
GI_40254932-S	427.4	357.1	372.4	PHTF2	NM_020432.2	DKFZP564F013			
GI_40254935-S	79.1	95.3	84.5	AD026	NM_020683.3	bA552M11.5			
GI_40254937-S	280.7	314.9	322.7	ADCK1	NM_020421.2	FLJ39600			
GI_40254939-S	118	118.8	120.8	ZNF530	NM_020880.2	KIAA1508		nucleus	
GI_40254942-S	162.6	190.6	173.2	KIAA1560	NM_020918.2	GPAM;MGC26846	acyltransf	mitochond	metabolis
GI_40254944-S	156.3	186.1	150.3	ZNF295	NM_020727.2	KIAA1227	protein	nucleus	regulation
GI_40254948-S	104.7	124.1	120.8	EPB41L5	NM_020909.2	BE37;FLJ12957;KIAA1548		cytoskelet	
GI_40254950-S	1645.5	2503.8	2709.8	TRAPPC1	NM_021210.2	BET5;MUM2		Golgi	transport
GI_40254951-S	208.8	242.2	219.6	HPSE2	NM_021828.2	HPA2;HPR2			
GI_40254954-S	207.3	265	269.5	FLJ23360	NM_023076.2				
GI_40254956-S	261.8	249	218.3	FLJ13171	NM_023923.2		binding	mitochond	transport
GI_40254958-S	399.6	465.5	540.1	FLJ22169	NM_024085.2	MGD3208			
GI_40254960-S	388.1	475.8	421.6	MGC3067	NM_024295.3	PRO2577;FLJ13784			
GI_40254961-S	385.4	429.5	412.1	FLJ23548	NM_024590.2				
GI_40254963-S	205	231.9	211.5	TIRP	NM_021649.2	TRAM;TICAM2;TICAM-2	transmem	membran	
GI_40254964-S	213.2	212	190.9	FLJ11753	NM_024659.2	PRO0159			
GI_40254966-S	104.9	100.9	109.2	FLJ21924	NM_024774.2				
GI_40254968-S	265.3	377.5	340.8	FLJ22494	NM_024815.2				

GI_40254970-S	217.6	281.3	231.1	FLJ23447	NM_024825.2				
GI_40254972-S	210.3	240.8	207.6	FLJ14213	NM_024841.2				
GI_40254974-S	126.7	144.9	106.6	ITPKC	NM_025194.2		inositol-		
GI_40254975-S	152.2	159.7	183.6	SGPP1	NM_030791.2	SPPase1	hydrolase	integral to	
GI_40254976-S	402.1	351	182.9	C9orf45	NM_030814.3	GL012;FLJ22161			
GI_40254977-S	640.6	632.6	548.8	FIP1L1	NM_030917.2	Rhe;DKFZp586K0717			
GI_40254979-S	381.4	326.5	284	LAT1-3TM	NM_031211.2				
GI_40254981-S	563.4	863.8	635.2	C10orf45	NM_031453.2	FLJ45505;MGC11034			
GI_40254983-S	145.8	169.1	135.1	MLSTD2	NM_032228.3	FLJ22728			
GI_40254984-S	196.7	178.8	176.8	MGC10854	NM_032300.2				
GI_40254985-S	630.4	624.8	551.9	C9orf99	NM_032303.2	MGC10940	sterol		metabolis
GI_40254987-S	1850.5	2371	2432.9	MGC14151	NM_032356.3		pre-mRNA	small	mRNA
GI_40254989-S	351.5	294.2	346.7	HH114	NM_032499.3	MGC11326			
GI_40254990-S	100.9	105.8	101.4	PARD6G	NM_032510.2	PAR-6G;PAR6gamma	protein	tight	intracellula
GI_40254993-S	79.9	90.5	80.2	HSH2	NM_032855.2	ALX;FLJ14886			intracellula
GI_40254994-S	234.5	239.6	208	SERAC1	NM_032861.2	FLJ14917	catalytic		
GI_40254998-S	234.2	274.3	202.8	MGC11386	NM_032933.3				
GI_40255000-S	632	527.6	259.5	LOC88523	NM_033111.2				
GI_40255002-S	174.8	166.5	145.7	MGC16733	NM_033547.2				
GI_40255004-S	307.1	149.5	291.7	PLXDC2	NM_032812.7	TEM7R;FLJ14623			
GI_40255006-S	89.3	102.1	87.1	MRGX2	NM_054030.2		receptor	integral to	G-protein
GI_40255007-S	183.4	221.8	196.2	LRRC15	NM_130830.2	LIB		integral to	
GI_40255010-S	456.6	522	428.2	SLC35E1	NM_024881.3	FLJ14251			
GI_40255011-S	141.2	227.9	189.2	KCTD12	NM_138444.2	C13orf2;KIAA1778	voltage-	membran	potassium
GI_40255012-S	69.9	74.4	67.2	CEACAM6	NM_002483.3	NCA;CEAL;CD66c		integral to	signal
GI_40255014-S	98	102	102.8	PRTFDC1	NM_020200.5	HHGP	hypoxanth	cytoplasm	purine
GI_40255015-S	468.9	481.1	414.3	LOC92979	NM_138396.3				
GI_40255019-S	1758.6	1356.5	1552	FLJ11730	NM_022756.3	CDABP0189			
GI_40255021-S	111.7	148.2	118.2	UBL1	NM_003352.3	GMP1;PIC1;SMT3;SMT3C;SMT3H3;SUMO-	ubiquitin	nuclear	small
GI_40255022-S	551.8	595	470	FLJ21125	NM_024627.4				
GI_40255024-S	522.7	409.5	478.2	RIPK2	NM_003821.4	RICK;RIP2;CARD3;CARDIAK	protein	intracellula	signal
GI_40255027-S	79.6	76.9	74.5	TMG4	NM_024081.4		calcium	extracellul	biological_
GI_40255028-S	135.2	166.8	145.7	LOC90693	NM_138771.2				
GI_40255030-S	584.6	644.9	623.3	FLJ12150	NM_024736.4				
GI_40255032-S	560.3	587.4	469.8	SP192	NM_021639.3				
GI_40255033-S	253.5	191.1	173.3	MIPOL1	NM_138731.2		tubulin-		chaperoni
GI_40255036-S	182.8	197.3	183.5	CAS1	NM_022900.3	C7ORF12;FLJ21213;FLJ21879			
GI_40255038-S	137.1	148.1	139.7	FLJ10808	NM_018227.3		ubiquitin		ubiquitin
GI_40255040-S	1922.3	3165.1	2276.9	TMP21	NM_006827.4	P24(DELTA)	vesicle	microsom	ER to
GI_40255042-S	222.1	278.6	297	GLB1L	NM_024506.3	MGC10771	beta-	beta-	carbohydr
GI_40255044-S	265.4	322.9	296.3	C14orf103	NM_018036.4	FLJ10242			
GI_40255046-S	284.8	320.6	312.6	FLJ21019	NM_024927.3				
GI_40255048-S	443.8	499.5	495.6	C9orf55	NM_017925.3	FLJ20686			
GI_40255050-S	266.9	293.8	364.8	FLJ12770	NM_032174.3		voltage-	mitochond	anion

GI_40255051-S	90.4	90.8	84.7	FLJ22527	NM_024726.3				
GI_40255053-S	625.8	427.1	268	MGC11324	NM_032717.3		acyltransf		metabolis
GI_40255056-S	233.7	627.3	430.3	MGC29643	NM_144586.3				
GI_40255059-S	386.1	506.8	412.9	FLJ32499	NM_144607.2		serine	extracellul	electron
GI_40255061-S	696.3	1009.5	950	MGC32124	NM_144611.2				electron
GI_40255064-S	131.1	103.4	101.3	FLJ30294	NM_144632.2				
GI_40255066-S	9704.3	10534	9130.6	FLJ31952	NM_144682.2				
GI_40255068-S	369.5	457.3	412.3	FLJ32658	NM_144688.2				
GI_40255072-S	140.9	127.1	111.2	MGC34923	NM_144717.2		receptor		
GI_40255074-S	184.3	215	217.7	LOC152185	NM_144718.2				
GI_40255077-S	87.4	96.1	91.3	FLJ25439	NM_144725.2				
GI_40255079-S	103.1	556	90.8	FLJ30058	NM_144967.2				
GI_40255081-S	359.6	360.3	365.6	LZIC	NM_032368.3	MGC15436			
GI_40255082-S	112.9	111.5	113.2	ADMP	NM_145035.2				
GI_40255084-S	218	261.1	227.4	MGC20470	NM_145053.2				
GI_40255086-S	106.7	115.5	95.5	LOC118491	NM_145170.2				
GI_40255088-S	212.7	264.3	237.4	PP3856	NM_145201.3				
GI_40255090-S	192.5	185	169.6	C10orf78	NM_145247.3	bA373N18.1			
GI_40255093-S	311.6	327	319.1	LOC159090	NM_145284.3				
GI_40255095-S	103	110.4	107.8	ZNF509	NM_145291.2				
GI_40255097-S	108.1	118.1	113.6	MUC15	NM_145650.2				
GI_40255100-S	387.3	401.5	329.7	SLC39A13	NM_152264.2	FLJ25785	heavy	membran	heavy
GI_40255102-S	283.7	396.7	333.1	ZNF488	NM_153034.2	FLJ32104	DNA	nucleus	regulation
GI_40255103-S	320.7	367.4	318.8	FLJ39369	NM_152363.2			nuclear	
GI_40255105-S	112	130.6	125	FLJ35961	NM_152372.2				
GI_40255107-S	415.3	404.7	303.5	FLJ30596	NM_153013.2				
GI_40255108-S	1338.3	970.4	849	GRPEL2	NM_152407.2	FLJ23713;FLJ33918;Mt-			
GI_40255110-S	225.7	266.7	261.6	FLJ37562	NM_152409.2		DNA	nucleus	regulation
GI_40255112-S	164.5	192.7	170.4	MGC35285	NM_152428.2		protein		intracellula
GI_40255114-S	421.7	462.5	383.1	FLJ31821	NM_153029.2				
GI_40255116-S	368.5	411.3	365.2	FLJ31413	NM_152557.2				
GI_40255122-S	111.5	142.4	123.6	MGC33948	NM_152587.2				
GI_40255124-S	126.7	159.4	138.1	FLJ35382	NM_152608.2				
GI_40255126-S	102.5	104.4	106.8	FLJ35954	NM_152622.2		DNA	nucleus	
GI_40255128-S	144.5	185	129.3	MGC9712	NM_152689.2				
GI_40255132-S	87.6	108	87.3	FLJ23834	NM_152750.2		calcium	membran	homophili
GI_40255134-S	733.5	889.3	791.9	FLJ31657	NM_152758.2				
GI_40255136-S	109.2	97.3	104.1	MGC35140	NM_152759.3				
GI_40255138-S	1349	1001.8	1027	MGC25181	NM_152783.2				electron
GI_40255140-S	311.5	1843.1	1358.6	ChGn	NM_018371.3	FLJ11264;beta4GalNAcT			
GI_40255142-S	153.5	172.2	148.9	C6orf60	NM_024581.3	FLJ13942			
GI_40255144-S	186.5	232.7	213.2	ZNF555	NM_152791.3	MGC26707	nucleic	nucleus	regulation
GI_40255146-S	230.8	308.9	254	GPR155	NM_152529.3	DEP.7;PGR22;DEPDC3;FLJ31819	molecular	integral to	intracellula
GI_40255148-S	223.2	281.8	247.2	ARHGEF19	NM_153213.2	FLJ33962			

GI_40255150-S	498.5	440.2	378.1	ZNF550	NM_153231.2	MGC41917	nucleic	nucleus	regulation
GI_40255152-S	533.5	777.9	547.7	KCTD6	NM_153331.2	MGC27385	voltage-	membran	potassium
GI_40255154-S	178	197.1	182.2	FLJ35880	NM_153264.2				
GI_40255156-S	481	1316.1	983.9	FLJ90440	NM_153377.3				
GI_40255159-S	374.4	685.7	788.2	MGC20446	NM_153611.2			integral to	electron
GI_40255160-S	140.2	171.7	149.4	SLC29A3	NM_018344.3	ENT3;FLJ11160	nucleoside	membran	transport
GI_40255162-S	363.7	438.3	375.4	KIAA2024	NM_172070.2	FLJ37422;DKFZp434P117			
GI_40255164-S	109.1	114.8	105.8	LOC317671	NM_173362.2		oxidoredu		electron
GI_40255165-S	117.1	132.4	122.4	FLJ34512	NM_173476.2				
GI_40255167-S	100.1	92.6	83.8	C20orf17	NM_173485.2	OVC10-2;FLJ33887	transcripti	nucleus	regulation
GI_40255169-S	160.8	201.8	170.3	MGC42718	NM_173506.3				
GI_40255171-S	251.1	281	260.4	FLJ25692	NM_173518.2				
GI_40255173-S	97	96.7	98.1	C10orf64	NM_173524.2				
GI_40255175-S	119.9	105.8	96.7	MGC33382	NM_173529.3				
GI_40255177-S	93.4	100.4	100.2	TDRD5	NM_173533.2	FLJ34823	nucleic		
GI_40255179-S	86.8	95.4	94.4	MGC34732	NM_173556.2				
GI_40255181-S	355.4	386.8	442.7	C6orf69	NM_173562.3	MGC14254;dJ108K11.3	molecular	cellular_co	biological_
GI_40255183-S	134.1	149.5	155.4	FLJ32949	NM_173812.3				
GI_40255185-S	277.3	308.6	285.3	FLJ37464	NM_173815.3		hydrolase		
GI_40255187-S	191.6	192.7	183.3	FLJ38288	NM_173632.2				
GI_40255189-S	206.8	248.5	241.8	C5orf16	NM_173828.3	FLJ90583	DNA	nucleus	regulation
GI_40255191-S	127.8	128.4	131.4	LOC138046	NM_173848.3		nucleic		
GI_40255193-S	146.9	173.6	168.9	SLC41A1	NM_173854.3	MgtE	cation		cation
GI_40255195-S	94.3	109.9	98.1	NSE2	NM_174911.3	BCMP101			
GI_40255196-S	136.4	147.8	129.3	RASGEF1C	NM_175062.2		guanyl-		small
GI_40255200-S	101.1	102	105.5	MGC35023	NM_175877.3				
GI_40255202-S	93.8	104.6	101.7	FLJ37266	NM_175892.3				
GI_40255204-S	129.8	119.2	121.7	LOC284296	NM_175908.3				
GI_40255206-S	301.2	240.5	292.4	TRA16	NM_176880.3		receptor		
GI_40255207-S	201.4	250.2	221.4	KIAA1946	NM_177454.2				
GI_40255209-S	561.5	958.4	410.2	LOC130576	NM_177964.3		receptor	nucleus	regulation
GI_40255211-S	185.5	247.5	239.2	LRRTM4	NM_024993.3	FLJ12568		integral to	
GI_40255213-S	140.8	149.4	145.2	LOC147111	NM_178493.3				
GI_40255215-S	88.6	86.3	86.9	LRRTM3	NM_178011.2			integral to	
GI_40255217-S	88.2	97.2	91.3	MGC35555	NM_178565.3				
GI_40255219-S	96.1	103	105.9	LOC123872	NM_178452.3				
GI_40255222-S	108.8	105.1	102.3	FLJ40427	NM_178504.3		microtubul	dynein	microtubul
GI_40255224-S	2020.6	1557.7	1069.9	FLJ12892	NM_022757.3	DKFZp434L1050	copper ion		electron
GI_40255226-S	163	185.1	159.8	C9orf79	NM_178828.3	FLJ35866			
GI_40255228-S	196.7	270.5	225.4	DKFZp564K1	NM_032121.3	PRO0756;FLJ14726			
GI_40255230-S	146.2	152.9	131.6	CUZD1	NM_022034.3	ERG-1;UO-44		integral to	
GI_40255231-S	92.1	100.7	89.5	ZNF493	NM_175910.4	FLJ36504		nucleus	
GI_40255233-S	111.2	134.5	126.7	FLJ23033	NM_024686.3		tubulin-		protein
GI_40255235-S	609.9	552.9	583.9	ZNF281	NM_012482.3	ZBP-99;ZNP-99	specific	DNA-	negative

GI_40255236-S	261.7	263.6	251.8	MTB	NM_017760.4	FLJ20311			
GI_40255239-S	869	1100.6	1235.2	FLJ10276	NM_018045.4				
GI_40255241-S	5297.7	5919.9	5124.3	SOD1	NM_000454.3	ALS;ALS1;IPOA	copper,	cytoplasm	response
GI_40255242-S	251.1	246.8	232.7	RBM17	NM_032905.3	SPF45;MGC14439	nucleic	intracellula	mRNA
GI_40255243-S	1204	1683.5	1392.2	KIAA0101	NM_014736.3	NS5ATP9			
GI_40255244-S	119	110.2	88	GPR51	NM_005458.5	HG20;GABBR2;GPRC3B;GABABR2	GABA-B	kinesin	negative
GI_40255246-S	527.8	452.6	591.3	FLJ13119	NM_024580.3		GTP		translation
GI_40255248-S	530.5	686.5	680	FLJ14566	NM_032806.4				
GI_40255249-S	274.7	347.8	286.5	RTN4R	NM_023004.4	NGR;NOGOR	receptor	membran	axonogen
GI_40255250-S	1377.5	1098.4	1331.6	MGC21688	NM_144635.3				
GI_40255252-S	256.4	262.8	299.6	FLJ12687	NM_024917.4		S-	mitochond	transport
GI_40255253-S	689.6	848.7	780.9	SCFD2	NM_152540.3	FLJ39514;STXBP1L1	protein		protein
GI_40255256-S	116.4	121.3	107	LOC144347	NM_181709.2				
GI_40255258-S	99.8	119.8	119.2	TG1019	NM_148962.3	GPCR	receptor	integral to	G-protein
GI_40255259-S	278.2	538.4	445.9	FLJ20701	NM_017933.3				
GI_40255261-S	410.7	460.2	409.7	SMAP-5	NM_030799.5	SB140;FLJ30014			
GI_40255262-S	787.2	1215.2	971.9	CGI-109	NM_181836.3				
GI_40255263-S	182.7	224.9	201.1	CBLN2	NM_182511.2				
GI_40255264-S	85	83.3	71.7	FLJ25161	NM_182522.2				
GI_40255265-S	103.9	116.5	103.7	FLJ33779	NM_182572.2				
GI_40255267-S	697	795.2	859.6	DKFZp686O1	NM_182608.2				
GI_40255269-S	136.2	134.2	128.5	C-P4H{alpha}	NM_182904.2		oxidoredu		protein
GI_40255270-S	125.4	127.1	122.2	PRKCB1	NM_002738.4	PKCB;PRKCB;PRKCB2	protein	cytoplasm	protein
GI_40255271-S	359.6	437.8	374.4	CMYA1	NM_194293.2	DKFZp451D042			
GI_40255273-S	107.6	147.1	125.7	LOC374946	NM_198545.2	UNQ3119			
GI_40255275-S	326.8	344.5	422	T1	NM_031466.3	MGC4737;MGC4769;KIAA1882			
GI_40255277-S	114.3	138.1	135.3	RP1L1	NM_178857.4				
GI_40255279-S	585.5	667.9	423.9	LOC116228	NM_198076.2				
GI_40255282-S	123.2	101.8	113.5	NHLRC1	NM_198586.2	EPM2A;EPM2B;bA204B7.2			
GI_40255306-S	241.4	319.4	280.7	PDE7B	NM_018945.2		cAMP-		synaptic
GI_40255309-S	3931.2	2819.6	2958.9	UBN1	NM_016936.2		transcripti	nucleus	regulation
GI_40255312-S	326.9	373.7	352.5	P38IP	NM_017569.2	C13			
GI_40255313-S	90.8	85.5	95.2	OBSCN	NM_052843.1	UNC89;KIAA1556	ATP		tRNA
GI_40255315-S	114.5	122.3	109.3	SCN4A	NM_000334.3	HYPP;HYKPP;NAC1A;hNa(V)1.4	voltage-	voltage-	sodium
GI_40288186-A	3776.8	3196.3	2428.1	PDLIM2	NM_198042.2	FLJ34715			
GI_40288186-I	167	208.1	178.8	PDLIM2	NM_198042.2	FLJ34715			
GI_40288187-I	126.8	121.4	123.2	PDLIM2	NM_176871.2	FLJ34715			
GI_40288188-I	422.2	503.9	458.2	PDLIM2	NM_021630.4	FLJ34715			
GI_40288189-S	175.4	188.1	161.9	ITIH4	NM_002218.3	H4P;IHRP;PK120;ITIHL1	endopepti		acute-
GI_40288190-S	125.3	149.3	122.2	HSXIAPAF1	NM_017523.2	XAF1	zinc ion		
GI_40288196-S	463.1	988.2	799.7	GATA6	NM_005257.3		transcripti	nucleus	muscle
GI_40288200-S	194.6	184.9	223.7	FLJ33008	NM_152449.2				
GI_40288202-S	100.9	101.6	89.7	FLJ25477	NM_152704.2				
GI_40288273-S	969.9	968.9	910.2	NUDT1	NM_002452.3	MTH1	GTPase		DNA

GI_40288287-S	5876.4	4670.1	5469.1	CARM1	NM_199141.1	PRMT4	methyltran		
GI_40288289-S	112	440.3	272.3	CLIC3	NM_004669.2		chloride	membran	small
GI_40288292-S	102.1	155.1	839.5	THBD	NM_000361.2	TM;THRM;CD141	calcium	integral to	blood
GI_40316836-S	129.7	157.8	146.8	ATP8B2	NM_020452.1	ATPID;KIAA1137;DKFZp434M0219	magnesiu	integral to	cation
GI_40316838-S	368.5	372.4	313.3	ATP11C	NM_173694.2	ATPIG;ATPIQ;FLJ34233	magnesiu	integral to	cation
GI_40316842-S	130.6	132.7	121.6	C21orf123	NM_199175.1	PRED80			
GI_40316908-S	108.7	117.2	112.6	TBX22	NM_016954.2	CPX;TBXX;dJ795G23.1	transcripti	nucleus	regulation
GI_40316911-S	160.4	207.9	134.2	SAA1	NM_000331.2	SAA;PIG4;TP53I4	high-		inflammat
GI_40316913-I	267.5	335.3	301.3	PITX2	NM_000325.4	RS;RGS;ARP1;Brx1;IDG2;IGDS;IHG2;PTX2;	transcripti	nucleus	determinat
GI_40316914-S	641.5	781	568.5	RNPEP	NM_020216.3	DKFZP547H084	metallope		proteolysis
GI_40316916-S	115.2	131.5	116.1	PCSK4	NM_017573.2	PC4;SPC5;MGC34749;DKFZp434B217	subtilase	extracellul	electron
GI_40316917-S	181.6	134.5	162.7	MGC22960	NM_199044.2				
GI_40316919-S	225.4	304.2	236.1	LOC223082	NM_147128.3	ZNRF2			
GI_40316920-S	265.9	285.9	301.1	HTPAP	NM_032483.2				
GI_40316921-S	328.8	466.2	522.3	KBRAS2	NM_017595.4	DKFZP434N1526			
GI_40316922-I	107.5	135.1	103.5	CXCL12	NM_000609.3	PBSF;SDF1;SDF1A;SDF1B;TPAR1;SCYB12;	chemokin	extracellul	regulation
GI_40316923-I	130.6	145.2	129	CXCL12	NM_199168.1	PBSF;SDF1;SDF1A;SDF1B;TPAR1;SCYB12;	chemokin	extracellul	regulation
GI_40316925-I	86.7	91.6	93.8	CLUL1	NM_199167.1	RA337M			cell death
GI_40316927-S	161.3	166.1	174.8	CACNB3	NM_000725.2	CACNLB3	voltage-	voltage-	small
GI_40316929-A	85	88.5	86.1	CLUL1	NM_014410.4	RA337M			cell death
GI_40316934-S	833.3	890.6	780.5	ALS2	NM_020919.2	ALSJ;PLSJ;IAHSP;KIAA1563	Rho	early	endosome
GI_40316936-S	332.9	410.6	380.7	ALOX15	NM_001140.3		lipoxygena	plasma	lipid
GI_40316940-S	643	634.3	476.5	AIG1	NM_016108.2	AIG-1;FLJ10485;dJ95L4.1			
GI_40316942-S	593.1	439.7	421.8	ALAS1	NM_000688.4	ALAS;ALASH	acyltransf	mitochond	heme
GI_40316943-I	237.7	295.7	261.8	ADSSL1	NM_199165.1	FLJ38602	adenylosu		purine
GI_40316945-I	235	294.8	253.3	ADPRHL1	NM_199162.1	ARH2	hydrolase		
GI_40316947-A	102.2	111.8	105.6	ADSSL1	NM_152328.3	FLJ38602	adenylosu		purine
GI_40316948-A	115.3	124	123.8	ADPRHL1	NM_138430.3	ARH2	hydrolase		
GI_40316949-S	198.2	248.6	215.1	ABLIM2	NM_032432.2	KIAA1808			
GI_40316951-S	94.3	95.7	103.6	ADAM32	NM_145004.4		metalloen		integrin-
GI_40317613-A	1378.2	1146.4	1086.9	MRRF	NM_138777.2	RRF;MRFF;MTRRF			
GI_40317614-A	2373.2	2754.9	4815.7	TMEPAI	NM_020182.3	STAG1;PMEPA1	molecular	integral to	androgen
GI_40317619-I	150.9	175.7	142.3	TMEPAI	NM_199171.1	STAG1;PMEPA1	molecular	integral to	androgen
GI_40317621-I	154.5	129.7	140	MRRF	NM_199176.1	RRF;MRFF;MTRRF			
GI_40317625-S	1010.6	8760.1	2239	THBS1	NM_003246.2	TSP;THBS;TSP1	endopepti	extracellul	blood
GI_40317627-S	1492	2896.6	1512.8	THBS2	NM_003247.2	TSP2	heparin	extracellul	cell
GI_40317629-S	282.1	390.3	277.2	THBS3	NM_007112.3	TSP3	heparin	extracellul	cell-matrix
GI_40317630-S	561.8	471.9	1177.9	ZHX3	NM_015035.2	TIX1;KIAA0395	transcripti	nucleus	regulation
GI_40317631-S	661.4	524.8	624.7	NUDT4	NM_019094.3	DIPP2;HDCMB47P;KIAA0487;DIPP2beta;DI	diphospho		cyclic
GI_40353201-S	324.5	367.7	352.2	DKFZp761A0	NM_017602.2				
GI_40353202-S	465.7	428.6	374.5	C15orf17	NM_020447.2	FLJ00005			
GI_40353203-I	109.5	130.2	112.2	SPTBN4	NM_020971.1	QV;SPTBN3;KIAA1642			
GI_40353205-S	239.4	221.5	231.1	C6orf106	NM_022758.3	FLJ22195;dJ391O22.4			
GI_40353206-S	2784.5	1974.4	2176.5	C20orf20	NM_018270.3	MRGBP;FLJ10914			

GI_40353209-S	803.8	905.3	980.4	FLJ20308	NM_017758.2				
GI_40353211-S	104.9	109.4	103.7	C17orf1A	NM_031456.2	HREP;SM25H2;SM2SH2;C17ORF1			
GI_40353238-S	123	131	116.6	TESSP5	NM_199183.1				
GI_40353240-S	107.7	120	99.9	FLJ46111	NM_198473.1				
GI_40353242-S	352.1	428.7	412.6	FLJ44670	NM_199181.1				
GI_40353726-S	124.7	138.3	154.3	SYNPO	NM_007286.3				
GI_40353730-S	784.6	952	898.4	PAN3	NM_175854.4				
GI_40353732-S	17702.7	15447	11191	NPM1	NM_002520.4	B23;NPM		nucleolus	
GI_40353737-S	336.4	374	295.3	LOC113251	NM_052879.3		nucleic		
GI_40353741-I	216.7	246.3	220.2	KIRREL2	NM_199180.1	NLG1;NEPH3;MGC15718;DKFZP564A1164			
GI_40353745-A	95.5	93.8	99.8	KIRREL2	NM_032123.4	NLG1;NEPH3;MGC15718;DKFZP564A1164			
GI_40353747-I	380.1	406	372.2	GGTL4	NM_199127.1		gamma-	cellular_co	glutathion
GI_40353749-S	2149.1	2239.2	1961.4	IMAA	NM_199182.1	MMAA			
GI_40353751-A	205.4	247.6	255.9	GGTL4	NM_080839.4		gamma-	cellular_co	glutathion
GI_40353752-S	893.1	956.3	707.1	FLJ25222	NM_199163.2				
GI_40353762-S	616.1	709	725.7	BRE	NM_004899.3				signal
GI_40353763-I	140.7	163.3	151	BPGM	NM_199186.1		bisphosph		respiratory
GI_40353765-S	172.1	190.7	178.5	BPNT1	NM_006085.3	PIP	3'(2'),5'-		nucleobas
GI_40353767-A	177.6	215.2	209.4	BPGM	NM_001724.3		bisphosph		respiratory
GI_40353768-S	162.9	200.4	162.9	BNF1	NM_015424.3	FKSG37;DKFZp586N2124			
GI_40353770-S	2387	2199.1	1902.3	BOP1	NM_015201.3	KIAA0124		nucleus	
GI_40353771-S	1400	1686.5	1787.1	BLVRA	NM_000712.3	BLVR;BVRA	biliverdin		electron
GI_40353772-S	1000.3	1209.2	1070.6	BIA2	NM_015431.2	DKFZp434C091			
GI_40353774-S	125.4	133.7	115.2	BLNK	NM_013314.2	Ly57;SLP65;BLNK-s;SLP-65	transmem	cytoplasm	hemocyte
GI_40354191-S	1592.6	1519.5	1144	KRT10	NM_000421.2	K10;KPP	structural	intermedia	epidermal
GI_40354193-A	2681.2	4586.6	2437.8	KRT18	NM_000224.2	K18;CYK18	structural	intermedia	embryoge
GI_40354194-I	262	326	241.7	KRT18	NM_199187.1	K18;CYK18	structural	intermedia	embryoge
GI_40354196-S	2361.8	2597.1	1870.3	THAP11	NM_020457.2	CTG-B43a;CTG-B45d;HRIHFB2206	DNA	nucleus	
GI_40354198-S	90.6	101.7	101.6	TNFSF18	NM_005092.2	TL6;AITRL;GITRL;hGITRL	receptor	integral to	anti-
GI_40354199-S	739	609.6	904.2	TPX2	NM_012112.4	DIL2;P100;DIL-	GTP	spindle	mitosis
GI_40354200-I	114.1	118.9	103.5	C6orf108	NM_199184.1	RCL;dJ330M21.3		nucleus	cell
GI_40354203-S	97.7	104.3	91.9	CCL3L1	NM_021006.3	LD78;464.2;SCYA3L;SCYA3L1;LD78BETA;M	cytokine	extracellul	response
GI_40354204-S	220.5	253.3	230.2	ALDOB	NM_000035.2		fructose-	cytoplasm	fructose
GI_40354206-S	109.9	130	124.8	KIAA1772	NM_024935.2	FLJ13687			
GI_40354208-S	379.6	425.4	363.9	IDUA	NM_000203.2	IDA;MPS1	L-	lysosome	disacchari
GI_40354209-S	92.4	100.7	77.7	ORAOV2	NM_018043.4	TAOS2;TMEM16A;FLJ10261			
GI_40354211-S	136.3	117.9	109.1	PIP3-E	NM_015553.1	IPCEF1;KIAA0403	peroxidas	cytoplasm	oxygen
GI_40354213-S	101.9	106.6	100.5	RBP2	NM_004164.2	CRBP2;RBPC2;CRBPII;CRABP-II	retinoid		vitamin A
GI_40354215-S	1043.9	1315.9	1373.6	SIX5	NM_175875.3	DMAHP			
GI_40385863-S	178.6	203.2	174.8	KIF17	NM_020816.1	KIF3X;KIF17B;KIAA1405	ATP	microtubul	intracellula
GI_40385866-S	134.5	146.9	121	MAP1D	NM_199227.1				
GI_40385872-S	143.3	167.1	141.3	LOC285601	NM_199243.1				
GI_40445386-S	172.6	205	190	FOXD4b	NM_199244.1		transcripti	nucleus	regulation
GI_40445400-S	338.6	285.9	305.1	C2orf22	NM_152391.2	MGC33602			

GI_40538725-I	112.6	131.3	119.3	SPRY1	NM_005841.1	hSPRY1		membran	histogene
GI_40538727-S	525.4	464.3	719.3	PLEKHM1	NM_014798.1	B2;AP162;KIAA0356			intracellula
GI_40538729-S	684.9	654.2	611.7	CAMSAP1	NM_015447.1	PRO2405;FLJ31228;DKFZP434F195;DKFZp			
GI_40538735-S	252.4	316.1	309.8	RANBP10	NM_020850.1	KIAA1464			
GI_40538737-S	114.3	120	107.3	ZNF273	NM_021148.1	HZF9	DNA	nucleus	regulation
GI_40538771-S	268.8	258.8	212.7	LOC90826	NM_138364.2				
GI_40538773-S	343.3	458.8	334.9	WDR26	NM_025160.3	FLJ21016			
GI_40538783-S	137.6	124.8	125.7	IBRDC2	NM_182757.1	p53RFP;bA528A10.3	electron		electron
GI_40538787-S	153	159	122.9	NLGN4Y	NM_014893.2	KIAA0951	neuroligin	membran	cell
GI_40538790-S	118.1	111.1	99.7	ICOSL	NM_015259.2	B7H2;GL50;B7-H2;B7RP1;LICOS;B7RP-	defense/i	integral to	immune
GI_40538791-S	1516.2	1488.2	1255.2	CGI-37	NM_016101.2	HSPC031			
GI_40538792-S	268	299.4	282.4	C6orf18	NM_019052.2	HCR;SBP			
GI_40538793-S	252.5	309.2	312.5	DKFZP434L0	NM_022778.2	FLJ13976;FLJ22000;DKFZp434P232			
GI_40538795-S	140.5	213	151.1	FLJ10916	NM_018271.2				
GI_40538798-S	154	178.1	169.4	C1orf6	NM_020131.3	A1U;UBIN			
GI_40538800-S	3268.9	3225.8	4192.1	KIAA1913	NM_052913.2				
GI_40538801-S	141.3	153.5	130.1	MAMDC2	NM_153267.3	MGC21981		membran	
GI_40538803-S	475.5	564.7	515.2	GPR97	NM_170776.3	Pb99;GPR-97	G-protein	membran	neuropepti
GI_40538805-S	126.6	148.1	121.3	FLJ10213	NM_018029.3				
GI_40538807-S	107.9	105.5	92.9	COXVIB2	NM_144613.3	FLJ32865	DNA	nucleus	regulation
GI_40538808-S	903.8	926.1	1006.3	C40	NM_017546.3		molecular	cellular_co	cell
GI_40538810-S	152.1	197.8	206.2	C21orf4	NM_006134.4		molecular	integral to	biological_
GI_40538879-S	359.9	460.5	454.2	AQP12	NM_198998.1				
GI_40548321-S	480.6	392.8	503.2	LOC201176	NM_199282.1	FLJ43547			
GI_40548323-S	112.8	114.2	102.1	LOC165186	NM_199280.1				
GI_40548325-S	120.9	152.1	132.2	LOC338759	NM_199286.1				
GI_40548365-S	330.7	346.5	346.6	ZNF322A	NM_024639.2	ZNF322;ZNF489;FLJ23393;bA457M11.3			
GI_40548370-S	120.3	127.2	98.8	TIEG2	NM_003597.4	FKLF;FKLF1;KLF11	transcripti	nucleus	negative
GI_40548371-S	714.5	748.2	707	TTC15	NM_016030.5	CGI-87			
GI_40548373-A	102.9	106.8	103.2	TCL1B	NM_004918.2	TML1			oncogene
GI_40548374-I	106.9	113	121.3	TCL1B	NM_199206.1	TML1			oncogene
GI_40548376-S	123.6	139.3	121.4	Shax3	NM_152284.2	CHMP4C;MGC22825	molecular		
GI_40548379-S	2228.7	1897.7	2061.7	RNASEH1	NM_002936.3	H1RNA	ribonuclea		RNA
GI_40548380-S	1267.8	1090.8	1142.6	NAGLU	NM_000263.2	NAG;MPS3B	alpha-N-	lysosome	neurogene
GI_40548381-I	193.9	204.5	198.4	MGC13170	NM_199249.1				
GI_40548385-S	819.7	1043	782.7	RAB8A	NM_005370.4	MEL;RAB8	GTP		oncogene
GI_40548386-S	373.5	550.1	570.4	LOC129642	NM_138799.2				
GI_40548388-I	94.4	112.1	100.8	DKK3	NM_015881.4	REIC		extracellul	embryoge
GI_40548390-S	718	630.5	670.8	TMEM18	NM_152834.2	DKFZp434C1714			
GI_40548392-A	1556.3	1427.7	733.7	DKK3	NM_013253.3	REIC		extracellul	embryoge
GI_40548392-I	153.5	159.1	140.1	DKK3	NM_013253.3	REIC		extracellul	embryoge
GI_40548396-I	210	261.1	220.5	DHRS9	NM_199204.1	RDHL;RETSDR8;3alpha-HSD			
GI_40548398-A	11184.1	8866	12133	DHRS2	NM_005794.2	HEP27	alcohol	nucleus	carbohydr
GI_40548399-S	239.9	321.6	299.9	DHRS9	NM_005771.3	RDHL;RETSDR8;3alpha-HSD			

GI_40548400-S	645.4	540.6	544.6	DELGEF	NM_012139.2		Ran	cytoplasm	signal
GI_40548401-I	16567	15481	18845	DHRS2	NM_182908.3	HEP27	alcohol	nucleus	carbohydr
GI_40548402-S	603.7	557.8	466.5	DCP1B	NM_152640.3	hDcp1b;FLJ31638			
GI_40548404-S	122	125.9	126.7	DCAL1	NM_172004.2			integral to	
GI_40548405-S	2564.5	4071.3	2750.1	DC2	NM_021227.2				
GI_40548406-A	513.6	591.4	602.5	DBC-1	NM_021174.4	DBC1;KIAA1967			
GI_40548407-I	155.9	190	160.7	DBC-1	NM_199205.1	DBC1;KIAA1967			
GI_40548409-S	5593.3	6562.5	4702.2	DAP13	NM_018838.3				
GI_40548412-I	234.1	240.1	181.3	D2LIC	NM_016008.2	LIC3;CGI-60;DKFZP564A033			
GI_40548414-S	407.3	764.8	154.2	DAAM2	NM_015345.2	KIAA0381	actin		cytokinesi
GI_40548417-A	296.7	361.4	267.8	D2LIC	NM_015522.2	LIC3;CGI-60;DKFZP564A033			
GI_40548417-I	103.8	97.1	97.2	D2LIC	NM_015522.2	LIC3;CGI-60;DKFZP564A033			
GI_40548418-A	210.1	143.6	176.2	COLEC11	NM_024027.3	MGC3279	sugar	nucleus	regulation
GI_40548419-I	104.5	102.9	106.1	COLEC11	NM_199235.1	MGC3279	sugar	nucleus	regulation
GI_40548421-S	583.8	584.6	477.6	C14orf123	NM_014169.2	Shax2;CHMP4A;CHMP4B;HSPC134	molecular		
GI_40548424-I	115.7	102.5	106.4	ALLC	NM_199232.1	ALC			
GI_40549393-S	129.1	152.8	138.7	ADPRH	NM_001125.2	ARH1	ADPribosy		protein
GI_40549398-S	1670.2	1731.5	2705.5	C20orf178	NM_176812.3	Shax1;CHMP4A;CHMP4B;dJ553F4.4	molecular		
GI_40549399-A	4358.7	4143.1	2605.1	CSNK1E	NM_001894.4	HCKIE;MGC10398	casein		protein
GI_40549399-I	148.2	173.4	177.2	CSNK1E	NM_001894.4	HCKIE;MGC10398	casein		protein
GI_40549401-A	82.7	87.5	83.2	GDNF	NM_000514.2	ATF1;ATF2	receptor	nucleus	anti-
GI_40549410-I	112.2	117.9	102.9	GDNF	NM_199231.1	ATF1;ATF2	receptor	nucleus	anti-
GI_40549416-S	233.3	309.2	275.8	LHX6	NM_014368.2	LHX6.1	transcripti	nucleus	brain
GI_40549417-S	131.7	141.5	127.7	LPO	NM_006151.1	SPO	peroxidas	soluble	peroxidas
GI_40549419-S	120.9	124.1	127.9	THBS4	NM_003248.3	TSP4	heparin	extracellul	substrate-
GI_40549420-S	199.5	239.5	198.4	THEG	NM_016585.3	MGC26138			protein
GI_40549423-S	660.5	769.5	645.6	THEM2	NM_018473.2	HT012;MGC4961;PNAS-27	catalytic		
GI_40549424-I	116.9	114	114.9	TPIP	NM_199254.1				
GI_40549426-I	101.2	95.3	97.3	TPIP	NM_199255.1				
GI_40549430-S	296.9	284.4	295.5	TPTE	NM_013315.2	PTEN2	protein	integral to	signal
GI_40549443-I	129.6	159.6	137.8	VAMP1	NM_016830.2	SYB1;VAMP-1		synaptic	nonselecti
GI_40549445-I	127	154.4	132.5	VAMP1	NM_199245.1	SYB1;VAMP-1		synaptic	nonselecti
GI_40549447-S	105.4	101.6	93	VAV2	NM_003371.2		guanyl-		signal
GI_40549449-S	126	138.8	122.2	XEDAR	NM_021783.2	EDAA2R;EDA-A2R	tumor	integral to	epidermal
GI_40549450-S	85.2	101.3	98.2	XLKD1	NM_006691.2	HAR;LYVE1;LYVE-1	receptor	membran	response
GI_40549452-S	199.1	192.6	208.3	ZBTB7	NM_015898.2	LRF;FBI1;FBI-1	protein	nucleus	regulation
GI_40549453-S	127.5	155	138.7	HTLF	NM_002158.2	FOXN2	transcripti	nucleus	invasive
GI_40549455-S	732.7	694	513.2	NHS	NM_198270.2				
GI_40549456-A	96.5	99.9	102.9	SYT15	NM_031912.3	sytXV;CHR10SYT	transporte	integral to	transport
GI_40549457-I	489.5	485.3	430.1	SYT15	NM_181519.2	sytXV;CHR10SYT	transporte	integral to	transport
GI_40549458-S	119.5	145.9	134.3	YPEL1	NM_013313.3	FKSG3		nucleus	
GI_40556268-S	92.8	99.2	92.2	C19orf15	NM_021185.3	FLJ46353;DKFZP434A1022			
GI_40556270-S	430	376	361.7	LOC134492	NM_145266.4				
GI_40556360-S	102.1	103.1	99.4	LOC56964	NM_020212.1				

GI_40556362-S	1060.6	752.3	693.7	NT5C3	NM_016489.1	PN-I;PSN1;UMPH;UMPH1;P5'N-1;cN-III	transcripti		regulation
GI_40556369-S	106.5	103.4	96.2	PHF15	NM_015288.4	JADE2;KIAA0239	DNA		regulation
GI_40556371-S	116.6	120.3	123.4	ANKRD12	NM_015208.2	GAC-1;FLJ20053;KIAA0874			
GI_40556373-S	127.8	151.7	122.1	SARG	NM_023938.3	MGC2742;MGC4309			
GI_40556374-S	5075.7	5085.3	2275	AMIGO2	NM_181847.2	ALI1;DEGA		integral to	
GI_40556375-S	111.4	115	116.9	N-PAC	NM_032569.2	BM045;HIBDL	DNA	nucleus	pentose-
GI_40556377-S	422.7	438.4	372.2	FLJ25070	NM_017619.2	FLJ20008;KIAA1839	nucleic		
GI_40556387-S	167.8	254.5	120.7	SCNN1A	NM_001038.3	ENaCa;SCNEA;SCNN1;ENaCalpha	amiloride-	membran	sodium
GI_40556388-I	97.3	106.3	107.5	ZPBP2	NM_199321.1	ZPBPL;MGC41930			
GI_40556392-I	246	206.3	186	JADE1	NM_199320.1	FLJ22479;KIAA1807	DNA		regulation
GI_40786390-S	4003.9	2804.7	2611.1	DNAJA3	NM_005147.3	TID1;hTid-1	chaperone	membran	cell growth
GI_40786393-S	189.6	165.9	147.8	DKFZp434N0	NM_199336.1		catalytic		metabolis
GI_40786395-S	90.3	90.7	92.6	FLJ35171	NM_199338.1				
GI_40786399-S	104.9	109.9	93.8	FLJ34306	NM_199340.1				
GI_40786401-S	2301.4	2219.9	1906.1	LOC374395	NM_199337.1				
GI_40786403-S	699.8	793.3	668.8	LOC374969	NM_199342.1				
GI_40786405-S	110	116.7	109.5	LOC374768	NM_199339.1				
GI_40786407-S	149.7	179.2	160	LOC375035	NM_199344.1	UNQ512;dJ747L4.C1.2			
GI_40786409-S	153.8	143.3	130.3	LOC374920	NM_199341.1	MGC50339			
GI_40786413-S	176.2	230.4	193.7	FLJ90637	NM_199343.1				
GI_40786415-S	108.3	113.9	106.7	LOC375616	NM_199349.1				
GI_40786417-S	119.3	133.8	119.2	PFN4	NM_199346.1				
GI_40786419-S	386	507.3	452.9	C1orf32	NM_199351.1				
GI_40786421-S	104.3	114.4	110.4	LOC375418	NM_199348.1				
GI_40786425-S	136	133.6	138.2	LOC375759	NM_199350.1	FLJ35803			
GI_40786429-S	135.1	151.4	139.4	LOC387601	NM_199352.1				
GI_40786533-S	248.5	362.5	310	LOC375133	NM_199345.1				
GI_40786537-S	158.5	185.2	176.9	FOXD4L3	NM_199358.1				
GI_40786545-S	113.4	118.9	107.4	TH	NM_000360.2	TYH	tyrosine 3-		catechola
GI_40786546-S	2787.4	1922	2123.3	ANKRD11	NM_013275.3	T13;LZ16			
GI_40787998-S	756.4	1024.7	873.5	SSBP2	NM_012446.2	HSPC116	DNA	nucleus	regulation
GI_40788000-I	132.7	148.1	129.6	SPRY1	NM_199327.1	hSPRY1		membran	histogene
GI_40788002-S	1624.5	2218.9	1960.4	PSME4	NM_014614.1	PA200;KIAA0077			
GI_40788008-S	6676.6	3431.6	1748.7	SLC43A3	NM_017611.2	EEG1;FOAP-13;PRO1659;SEEEG-			
GI_40788009-S	2426.1	1481	1880	DAF	NM_000574.2	CR;TC;CD55		soluble	
GI_40788010-I	82.8	77.3	74.3	CLDN8	NM_199328.1		structural	tight	
GI_40788012-S	186.7	194.9	199.1	CTF1	NM_001330.2	CT1;CT-1	leukemia	extracellul	positive
GI_40788013-A	116.9	129.2	117.4	CLDN8	NM_012132.3		structural	tight	
GI_40788014-S	131.3	126.6	125.1	CARD12	NM_021209.3	CLAN;IPAF;CLAN1;CLANA;CLANB;CLANC;	ATP	intracellula	apoptosis
GI_40788016-S	917.4	1252.5	1245.8	C8FW	NM_025195.2	GIG2;SKIP1	protein	cytoplasm	cell
GI_40788017-I	88.9	95.9	84.7	ARHGAP11A	NM_199357.1	KIAA0013;MGC70740			
GI_40788019-S	496.6	337.8	359.3	C1orf21	NM_030806.2				
GI_40788020-I	128.5	124.3	107.6	ARHGAP11A	NM_014783.2	KIAA0013;MGC70740			
GI_40789088-S	3668.2	3585	2842.3	NTAN1	NM_173474.2		hydrolase		

GI_40789101-S	223.9	274.6	257.2	LOC220686	NM_199283.2				
GI_40789228-S	251.6	347.1	325.5	SFRS15	NM_020706.1	SRA4;KIAA1172;DKFZP434E098	RNA		
GI_40789232-S	1901.2	1816.8	1787.8	DKFZP434K0	NM_020312.1				
GI_40789255-S	1512.8	1564.6	1056.5	SRP72	NM_006947.2			signal	
GI_40789258-S	202.6	224.4	230.4	TDRD4	NM_019038.2	FLJ11045	nucleic		
GI_40789260-S	101.1	100.7	85.1	SLC16A6	NM_004694.2	MCT6	monocarb	membran	monocarb
GI_40789262-S	104.7	99.5	109.9	TMOD2	NM_014548.2	NTMOD	tropomyos	F-actin	cell shape
GI_40789263-S	3140.3	3023.6	2765.8	MGC11257	NM_032350.3				
GI_40789264-S	92.4	128	105	FLJ25045	NM_178537.3		DNA	nucleus	regulation
GI_40789266-S	117.8	119.9	114.2	FLJ12684	NM_024534.2				
GI_40789269-S	253	205.1	172.7	ZNF573	NM_152360.2	FLJ30921		nucleus	
GI_40789305-I	103.8	118.9	106.1	ZNF365	NM_199451.1	KIAA0844			
GI_40789307-I	163.3	176.1	143.2	ZNF365	NM_199452.1	KIAA0844			
GI_40789309-I	115	123.1	126.2	ZNF365	NM_199450.1	KIAA0844			
GI_40795664-S	396.4	482.3	511.1	USP4	NM_003363.2	UNP	lysosomal	cytoplasm	deubiquiti
GI_40795668-S	128.4	145.9	133.3	SLC38A3	NM_006841.3	G17;SN1	amino	integral to	acidic
GI_40795669-S	2789.6	3058	3118.9	PL6	NM_007024.4		guanyl-	integral to	signal
GI_40795670-S	408.3	344.7	334.4	FLJ37970	NM_032251.3	BRLZ;FLJ00354;DKFZp434G0920			
GI_40795672-S	101.8	112.6	99.1	FLJ25530	NM_152722.3	HEPN1	DNA	nucleus	regulation
GI_40804463-S	107.6	113.6	115.2	C20orf103	NM_012261.2			integral to	
GI_40804464-S	192.7	207.2	176.4	C20orf104	NM_016436.3	NZF;TZP;GLEA2;HCA58	DNA	nucleus	regulation
GI_40804465-S	89.4	80.2	89.2	C20orf10	NM_014477.2	CLG01;TP53TG5	molecular	perinuclea	intracellula
GI_40804466-S	928.6	948.1	1285.7	C20orf11	NM_017896.2	TWA1		kinesin	
GI_40804467-I	178.4	224.1	204.2	CACNB1	NM_000723.3	CAB1;CCHLB1;CACNLB1;MGC41896	voltage-	voltage-	small
GI_40804469-I	152.4	170.6	160.2	CACNB1	NM_199247.1	CAB1;CCHLB1;CACNLB1;MGC41896	voltage-	voltage-	small
GI_40804741-S	1211	1222.7	1311.6	FLJ11806	NM_024824.2	NY-REN-37			
GI_40804743-S	341	438.7	401.7	SEMA4C	NM_017789.3	SEMAI;Semaf;Semacl1;FLJ20369;KIAA1739;	receptor	membran	developm
GI_40804747-S	160.6	145.7	115.4	LIMS2	NM_017980.2	PINCH-2;FLJ10044			
GI_40804749-S	172	175.5	193	PAXIP1L	NM_007349.2	PTIP;TNRC2;CAGF28;CAGF29		intracellula	
GI_40804753-S	170.8	155.9	140.9	RTN2	NM_005619.2	NSP2;NSPL1	molecular	endoplas	signal
GI_40804754-S	117.1	131.8	126	LOC283439	NM_199460.1				
GI_40804758-S	123.4	131.4	135.9	C10orf71	NM_199459.1	FLJ45913	transporte	membran	transport
GI_40804760-S	167.9	191.9	184.9	NANOS1	NM_199461.1				
GI_40804767-S	222.5	250.5	243.6	EFO1	NM_052911.1	KIAA1911			
GI_40804769-I	132.8	143	130	TEPP	NM_199046.1				
GI_40805101-S	129.9	120.3	102.5	ZFP276	NM_152287.2	ZNF477;MGC45417			
GI_40805103-S	285.4	336.2	372.7	TOPORS	NM_005802.2	LUN;TP53BPL	DNA	nucleus	regulation
GI_40805105-S	123.8	143.5	134.2	FUT10	NM_032664.3	MGC11141			
GI_40805107-S	476.9	665.2	599.2	NID67	NM_032947.3				
GI_40805821-S	2310.3	3368	3022.6	COPE	NM_007263.3	FLJ13241;epsilon-COP	protein	membran	nonselecti
GI_40805822-S	156.4	135.2	750.2	COL22A1	NM_152888.1		structural	microfibril	cell
GI_40805828-A	3111.2	3283.5	3527.7	COPS8	NM_006710.4	COP9;CSN8;SGN8;MGC1297		nucleus	
GI_40805829-I	115	115.5	104.6	COPS8	NM_198189.2	COP9;CSN8;SGN8;MGC1297		nucleus	
GI_40805830-S	834.7	1071.9	805	CCNG1	NM_004060.3	CCNG	cyclin-	nucleus	regulation

GI_40805833-S	306.2	290.1	223.3	CCRL2	NM_003965.3	HCR;CKRX;CRAM-A;CRAM-B	chemokin	integral to	chemotaxi
GI_40805834-S	1436.6	1474.6	1271.6	CNO	NM_018366.2	FLJ11230			
GI_40805835-S	118.6	138	109.5	CYP2D6	NM_000106.3	CPD6;CYP2D;CYP2D@;CYP2DL1;P450C2D	cytochrom		
GI_40805838-S	150.1	177.9	150.8	PRAC	NM_032391.2	MGC32520		nucleus	
GI_40805839-A	1397.1	1718.7	1497.8	PRCP	NM_005040.2	PCP;HUMPCP;MGC2202	serine	lysosome	proteolysis
GI_40805840-I	112.7	118.6	106.8	PRCP	NM_199418.1	PCP;HUMPCP;MGC2202	serine	lysosome	proteolysis
GI_40805842-S	159.2	161.7	154.3	PCAF	NM_003884.3	CAF;P/CAF	histone	nucleus	protein
GI_40805844-S	453.9	386.4	437	POLQ	NM_006596.3	POLH;PRO0327	DNA-	nucleoplas	DNA
GI_40805848-A	134.4	149.8	153.2	PTPRE	NM_130435.2	PTPE;HPTPE;R-PTP-EPSILON	transmem	soluble	protein
GI_40805848-I	101.7	98.9	89.4	PTPRE	NM_130435.2	PTPE;HPTPE;R-PTP-EPSILON	transmem	soluble	protein
GI_40805849-I	143.9	178.1	171.6	PTPRE	NM_006504.3	PTPE;HPTPE;R-PTP-EPSILON	transmem	soluble	protein
GI_40805850-S	653.2	578.2	360.8	THSD1	NM_018676.2	TMTSP;UNQ3010;MGC74971	defense/i	cell	
GI_40805853-S	125.5	133.5	115.6	THSD3	NM_182509.2		molecular	extrachro	
GI_40805855-I	82.6	90.7	85.4	THSD3	NM_199265.1		molecular	extrachro	
GI_40805859-S	3636	3086.7	4986.8	TPD52L2	NM_003288.2	D54;hD54		kinesin	cell
GI_40805871-S	348.2	443	363.1	THPO	NM_000460.2	ML;TPO;MGDF;MKCSF;MPLLG	growth	extracellul	developm
GI_40806158-I	658.8	798.5	659.3	THRA	NM_003250.4	AR7;EAR7;ERBA;ERBA1;NR1A1;THRA1;TH	thyroid	nucleus	transcripti
GI_40806159-I	122.3	114.3	99.1	THRA	NM_199334.1	AR7;EAR7;ERBA;ERBA1;NR1A1;THRA1;TH	thyroid	nucleus	transcripti
GI_40806161-S	88.7	85.1	95.6	THRB	NM_000461.2	GRTH;THR1;ERBA2;NR1A2;THRB1;THRB2;	thyroid	nucleus	transcripti
GI_40806163-I	138.6	149.8	142.7	UBE2V1	NM_021988.3	CIR1;UEV1;CROC1;UEV-1;UEV1A;CROC-1	ubiquitin		protein
GI_40806165-A	6747.5	7236.3	6885.3	UBE2V1	NM_022442.3	CIR1;UEV1;CROC1;UEV-1;UEV1A;CROC-1	ubiquitin		protein
GI_40806168-S	121.4	138.2	140.4	SPG4	NM_014946.3	FSP2;ADPSP;SPAST;KIAA1083	adenosine	nucleus	
GI_40806171-I	1457.1	1817.1	1844	SPG7	NM_003119.2	CAR;PGN;CMAR	adenosine	integral to	proteolysis
GI_40806172-I	129.2	121.4	127	SPG7	NM_199367.1	CAR;PGN;CMAR	adenosine	integral to	proteolysis
GI_40806174-S	104.1	102.6	112.3	DGKQ	NM_001347.2	DAGK;DAGK4;DAGK7	diacylglyc		neuropepti
GI_40806177-A	143.6	213.3	154.2	DSC2	NM_024422.2	DG2;DSC3;CDHF2;DGII/III	cell	cytoskelet	cell
GI_40806178-I	176.7	204.8	195.5	DustyPK	NM_015375.1	HDCMD38P;KIAA0472			
GI_40806182-S	1633.6	1196.7	1332	FLJ10514	NM_018122.3		aspartate-	cytoplasm	aspartyl-
GI_40806183-S	838.3	797.2	448.5	FLJ13149	NM_021826.4				
GI_40806184-A	106.9	119.5	95.5	ADAMTS18	NM_139054.2	ADAMTS21	metalloen	extracellul	proteolysis
GI_40806186-I	154.5	102.5	90.7	ADAMTS18	NM_199355.1	ADAMTS21	metalloen	extracellul	proteolysis
GI_40806188-S	228.7	230.3	170.4	HK2	NM_000189.4	HKII;HXK2	hexokinas	mitochond	glucose
GI_40806189-I	187.1	213.6	204.6	Kua-UEV	NM_199203.1	CROC-1B			
GI_40806191-I	237	357.3	378.7	Kua-UEV	NM_003349.4	CROC-1B			
GI_40806192-S	627.3	840.5	908	Kua	NM_199129.1				
GI_40806194-S	295.7	299.6	282.4	UBCE7IP5	NM_014948.2	RNF37		nucleus	
GI_40806197-S	177.2	158.2	182.8	SPG20	NM_015087.3	SPARTIN;TAHCCP1;KIAA0610			
GI_40806198-A	102.5	115.1	109.9	MAP2K7	NM_145185.2	MKK7;Jnkk2;MAPKK7;PRKMK7	MAP		response
GI_40806198-I	115.7	122.9	111.8	MAP2K7	NM_145185.2	MKK7;Jnkk2;MAPKK7;PRKMK7	MAP		response
GI_40806199-S	94.4	100.9	101.8	MTL5	NM_004923.2	MTLT;TESMIN	heavy		metal ion
GI_40806201-S	6976.1	8522.6	6767.3	NDUFB4	NM_004547.4	B15;CI-B15;MGC5105	NADH	NADH	mitochond
GI_40806202-S	2636.9	2952.2	4236.3	NEU1	NM_000434.2	NEU;SIAL1	exo-alpha-	lysosome	carbohydr
GI_40806203-S	100.1	118.9	101.1	WFIKKNRP	NM_175575.4		serine-		
GI_40806208-I	306	429.8	517.9	WWP2	NM_199423.1	AIP2	ubiquitin-	ubiquitin	protein

GI_40806210-I	111.7	131.1	113.9	WWP2	NM_199424.1	AIP2	ubiquitin-	ubiquitin	protein
GI_40806212-S	518	524.1	601.1	VAPB	NM_004738.3	VAP-B;VAP-C;VAMP-B;VAMP-C	structural	kinesin	nonselecti
GI_40806213-S	118.3	121	109.4	VIAAT	NM_080552.2	VGAT	amino	membran	amino
GI_40806214-I	91.6	102.2	87.1	VSX1	NM_014588.4	PPD;KTCN;PPCD;RINX	transcripti	nucleus	vision
GI_40806215-I	165.4	192.4	187.2	VSX1	NM_199425.1	PPD;KTCN;PPCD;RINX	transcripti	nucleus	vision
GI_40806217-S	744.2	663.3	886.9	THY28	NM_014174.2	MY105;MDS012;HSPC144;MGC12187			
GI_40806222-A	712.4	804.1	868.7	ZFP64	NM_018197.2	ZNF338			
GI_40806224-I	145.7	133.9	143.6	ZFP64	NM_022088.4	ZNF338			
GI_40806228-I	805.7	778.5	574.3	ZFP64	NM_199427.1	ZNF338			
GI_40807350-S	273.8	171.5	250.4	SLC36A4	NM_152313.2	PAT4;FLJ38932	amino	membran	amino
GI_40807356-S	107	112.8	120.1	SLC27A4	NM_005094.2	FATP4	fatty acid		fatty acid
GI_40807361-S	2784.3	3194.2	3027.3	RAB7	NM_004637.5	PSN;CMT2B;PRO2706	RAB small	late	endocytosi
GI_40807362-S	103	110.1	97.2	RDH-E2	NM_138969.2	FLJ33105	oxidoredu		metabolis
GI_40807365-S	2440.9	2442	2468.3	PP3111	NM_022156.3				
GI_40807367-I	128.8	134.2	119.2	KCNRG	NM_199464.1				
GI_40807441-S	1458.5	1585.3	2069.4	PRC1	NM_003981.2	MGC1671;MGC3669		spindle	mitotic
GI_40807446-S	997.7	1101.4	1090.8	PRCC	NM_005973.4	TPRC;RCCP1;MGC4723;MGC17178	molecular	cellular_co	cell growth
GI_40807451-S	1080.3	888	764.5	PPRC1	NM_015062.3	PRC;KIAA0595;MGC74642	nucleic		
GI_40807453-S	517.4	598.9	316.2	ZNF133	NM_003434.3	pHZ-13	transcripti	nucleus	regulation
GI_40807454-S	779.7	942.4	1082.1	ZNF217	NM_006526.2	ZABC1	transcripti	nucleus	transcripti
GI_40807455-S	2661.7	2438.3	3332.8	ZNF313	NM_018683.3	RNF114			
GI_40807456-A	105.1	115.9	105.1	ZNF334	NM_018102.3				
GI_40807458-I	97.3	99.5	96.9	ZNF334	NM_199441.1				
GI_40807460-S	142.3	160.8	167.8	ZNF335	NM_022095.3	NIF1	DNA	nucleus	regulation
GI_40807461-S	158.1	165.8	107.7	ZNF336	NM_022482.3	GZF1	protein	nucleus	regulation
GI_40807464-S	114.6	118.1	112.6	ZNF341	NM_032819.3		DNA	nucleus	regulation
GI_40807466-S	111.6	90.7	89	TNNC2	NM_003279.2		calcium	troponin	regulation
GI_40807467-S	3116.8	3395.1	4432.2	TOMM34	NM_006809.4	TOM34;HTOM34P	signal	mitochond	mitochond
GI_40807468-S	386.1	258.8	353.8	TRIP	NM_005879.2	TRAIP			induction
GI_40807470-S	494.9	638.4	560.6	TTF2	NM_003594.3	HuF2	Pol II	transcripti	transcripti
GI_40807473-S	99.7	127.7	114.8	ORM2	NM_000608.2	AGP2;AGP-B;AGP-B'	acute-	extracellul	acute-
GI_40807474-S	130.2	135.6	124.7	PRAM-1	NM_032152.3	MGC39864			
GI_40807476-I	268.4	264.4	205.6	RAI1	NM_030665.3	SMS;SMCR;KIAA1820;MGC12824;DKFZP43			
GI_40807478-S	111.2	116.3	120.2	SOCS4	NM_080867.2	SOCS7	DNA	nucleus	intracellula
GI_40807479-I	111.6	133.2	115	SOCS4	NM_199421.1	SOCS7	DNA	nucleus	intracellula
GI_40807481-S	89.3	99.8	89.4	C20orf114	NM_033197.2	LPLUNC1;MGC14597	lipid		
GI_40807483-S	1404.2	1295	1522.8	C20orf126	NM_030815.2	PDRG			
GI_40807484-S	1493.2	1294.5	1788.4	C20orf14	NM_012469.2	TOM;ANT-1	pre-mRNA	spliceoso	spliceoso
GI_40807486-S	183.2	172.5	179.3	NEURL2	NM_080749.2				intracellula
GI_40807487-S	178.8	204.8	188	C20orf165	NM_080608.3	dJ337O18.8		integral to	
GI_40807488-S	233.3	444.1	160.7	EMR1	NM_001974.3		G-protein	integral to	G-protein
GI_40807492-S	813.6	828.3	711.4	FBXO34	NM_017943.2	CGI-301;FLJ20725;DKFZp547C162	molecular		
GI_40807494-A	98.6	110.2	90.2	HSHIN1	NM_017493.4	HIN1;KIAA1046;DKFZp434I0721	molecular	cellular_co	biological_
GI_40807495-I	1124.5	851.8	623.6	HSHIN1	NM_199324.1	HIN1;KIAA1046;DKFZp434I0721	molecular	cellular_co	biological_

GI_40807499-S	276.3	311.3	270.8	AB026190	NM_014458.3			actin	cytoskelet
GI_40807503-I	128.5	147.6	138.5	AFAP	NM_198595.1	AFAP-110			
GI_40807505-A	510.9	691.3	627.3	AFAP	NM_021638.3	AFAP-110			
GI_41053624-S	163.9	213.1	161.9	MMAB	NM_052845.2	ATR;MGC20496	transferas	mitochond	
GI_41054803-S	164.9	187.5	462.1	MGC15882	NM_032884.2		DNA	nucleus	regulation
GI_41054843-S	158.7	180.7	187.7	DNAJB12	NM_017626.2	FLJ20027	chaperone	integral to	protein
GI_41054845-S	255.3	245	255.5	FLJ12969	NM_022838.2	FLJ13382	ATP		
GI_41055004-S	1309.7	1331.3	1043.5	TTC17	NM_018259.3	FLJ10890			
GI_41055203-A	932.8	996.3	1141.6	KNS2	NM_182923.2	KLC;KLC1;KNS2A	motor	kinesin	microtubul
GI_41055203-I	180.8	227.1	209.2	KNS2	NM_182923.2	KLC;KLC1;KNS2A	motor	kinesin	microtubul
GI_41055952-S	156.3	173.1	160.6	USP40	NM_018218.1	FLJ10785	cysteine-		ubiquitin-
GI_41055988-S	311.7	353	382.4	HSMPP8	NM_017520.2		molecular	cytoplasm	cell cycle
GI_41056186-S	653	731.5	631.9	USP34	NM_014709.2	KIAA0570;KIAA0729	cysteine-		ubiquitin-
GI_41056258-I	124.3	104	99.4	SLC43A3	NM_199329.1	EEG1;FOAP-13;PRO1659;SEEEG-			
GI_41057795-S	135.1	157.2	131.5	LOC389804	XM_374308.1				
GI_41057810-S	120.7	136.5	127	LOC389806	XM_374309.1				
GI_41057820-S	245.8	300.5	283.8	LOC388663	XM_373857.1				
GI_41058250-S	96.3	100.6	102.3	LOC390995	XM_372758.1				
GI_41058258-S	107	112.8	93.8	LOC390999	XM_372760.1				
GI_41058279-S	107.8	110.9	117.7	LOC388644	XM_373850.1				
GI_41103619-S	147.6	139.4	132.4	NY-SAR-41	XM_371270.1				
GI_41103645-S	120.2	117.8	110.7	LOC391062	XM_372785.1				
GI_41104564-S	127.2	138.6	133.6	OR2M4	XM_371358.1				
GI_41104585-S	138.9	168.2	166.9	LOC391191	XM_372822.1				
GI_41104601-S	239.9	294.2	257.9	LOC391195	XM_372826.1				
GI_41106713-S	168.6	181.1	175	LOC388699	XM_371314.1				
GI_41107411-S	130.6	155.5	134.1	LOC388623	XM_373840.1				
GI_41107446-S	87.7	97.2	91.4	LOC388632	XM_371252.1				
GI_41107456-S	241.9	257.5	251.4	LOC388635	XM_373844.1				
GI_41107468-S	296.4	230.5	155.4	KIAA1579	XM_371258.1				
GI_41107475-S	108.2	113.7	104.1	DKFZp547I04	XM_371259.1				
GI_41107500-S	116.5	126	114.9	LOC391092	XM_372792.1				
GI_41107683-S	97.2	100.9	92.4	LOC388609	XM_373832.1				
GI_41107685-S	109.7	114.7	85.8	CATSPER4	XM_371237.1				
GI_41107691-S	125.8	143.7	125.9	LOC388612	XM_373833.1				
GI_41107699-S	27061.2	22148	18917	LOC391023	XM_372773.1				
GI_41107701-S	128.6	164.9	142.2	DJ159A19.3	XM_372774.1				
GI_41109026-S	169.3	190.3	187.1	LOC388614	XM_373835.1				
GI_41109030-S	132.3	131.6	127.5	LOC388615	XM_373836.1				
GI_41110098-S	84.2	76.5	91	LOC388746	XM_373890.1				
GI_41111276-S	168.7	193.8	176.9	LOC388601	XM_373828.1				
GI_41112871-S	270.6	330.8	301.8	LOC388725	XM_371334.1				
GI_41113031-S	101.2	109.8	105	LOC388646	XM_371265.1				
GI_41114101-S	99.4	125.7	106.2	LOC339077	XM_294802.4				

GI_41114103-S	104.6	113.2	101.5	LOC388758	XM_373898.1
GI_41114495-S	158.1	191.2	187.4	LOC388594	XM_371221.1
GI_41114528-S	251	288.8	267.8	LOC391005	XM_372765.1
GI_41114575-S	116.8	135.1	124.1	LOC374947	XM_291625.3
GI_41114579-S	98.7	88.1	76.6	LOC391001	XM_372761.1
GI_41114582-S	140.2	166.3	159.1	LOC391002	XM_372762.1
GI_41115071-S	115.8	131	115.4	LOC388580	XM_373818.1
GI_41115343-S	99.4	96.8	91.6	LOC391012	XM_372768.1
GI_41115452-S	143.1	166.5	150	LOC388673	XM_371291.1
GI_41116237-S	115.9	116.6	107.7	LOC391027	XM_372776.1
GI_41117239-S	106.3	97.8	99.5	LOC391201	XM_372833.1
GI_41117409-S	2179.9	2084.8	2173.3	S100A13	XM_371380.1
GI_41117712-S	134.4	125.8	126.4	LOC388926	XM_371477.1
GI_41117724-S	109.7	119.5	111.1	LOC391353	XM_372917.1
GI_41118748-S	115.6	112.5	100.4	LOC389025	XM_374004.1
GI_41118759-S	328.6	372.2	358.9	LOC389028	XM_374006.1
GI_41118768-S	128.2	141	115.7	LOC391427	XM_372952.1
GI_41118879-S	530.1	270.1	238	LOC388922	XM_371476.1
GI_41119889-S	98	105.8	93.2	LOC391419	XM_372946.1
GI_41120019-S	211.8	255	233.7	LOC389089	XM_374029.1
GI_41123791-S	96.2	100.1	92.9	LOC388929	XM_371480.1
GI_41123794-S	233.1	261.6	262.8	LOC388930	XM_373975.1
GI_41123815-S	99.1	116	118.6	LOC388934	XM_373977.1
GI_41124044-S	103.5	104.9	89.4	LOC391342	XM_372910.1
GI_41124491-S	102.1	107.5	95.3	LOC389005	XM_371537.1
GI_41124889-S	507	627.1	556.4	LOC391403	XM_372940.1
GI_41125701-S	428.8	523.8	474.5	LOC389038	XM_374011.1
GI_41125704-S	114.4	135.6	130.5	LOC389039	XM_371561.1
GI_41125747-S	127.1	161.5	134.8	LOC389050	XM_374014.1
GI_41125793-S	107.7	125.6	105	LOC391446	XM_372959.1
GI_41126366-S	103.1	94.4	103.9	LOC389032	XM_374009.1
GI_41126929-S	138.1	157.5	127.2	LOC391493	XM_372974.1
GI_41133988-S	93.7	104.8	101.6	LOC389055	XM_374016.1
GI_41144256-S	624.3	758.7	577.8	FLJ10707	XM_371614.1
GI_41144279-S	110.8	117.9	122.9	LOC389096	XM_371618.1
GI_41144284-S	85.7	179	101.7	FGD5	XM_371619.1
GI_41144322-S	144.6	166	164.3	LOC389102	XM_371623.1
GI_41144338-S	122.1	122	116.5	LOC389105	XM_374037.1
GI_41144364-S	141.6	147.3	143.3	LOC389111	XM_371629.1
GI_41144864-S	517.5	661.7	576.1	LOC389188	XM_374070.1
GI_41144869-S	187.7	210.5	212.7	LOC389189	XM_374071.1
GI_41144883-S	109.6	100.4	98.7	LOC389192	XM_371684.1
GI_41146521-S	94	85.3	85.9	LOC389138	XM_371656.1
GI_41146525-S	89.2	96.3	96.7	LOC389139	XM_374045.1

GI_41146530-S	13195.2	13174	10591	LOC389141	XM_371658.1
GI_41146541-S	90.3	95.9	85.1	LOC389142	XM_374046.1
GI_41146558-S	117.4	124.5	122.3	LOC255330	XM_371662.1
GI_41146599-S	119.6	142.9	117.2	LOC389159	XM_374055.1
GI_41146605-S	100.4	102.6	96.5	LOC389161	XM_374057.1
GI_41146621-S	111.4	109.5	104.1	LOC389170	XM_371674.1
GI_41146631-S	90	104.2	87.6	LOC389173	XM_371677.1
GI_41146633-S	97.4	91.4	89.9	LOC389174	XM_371678.1
GI_41146646-S	124.4	113.5	105.7	LOC389180	XM_371682.1
GI_41146652-S	128.9	147.1	147.4	LOC389184	XM_374066.1
GI_41146696-S	121.2	140.1	132.1	LOC389230	XM_374088.1
GI_41146703-S	120.5	129.3	116	LOC389232	XM_374090.1
GI_41146705-S	201.8	231.3	218.7	LOC389233	XM_374091.1
GI_41146709-S	139.9	142.8	136.3	LOC389234	XM_374092.1
GI_41146716-S	96	94.1	93.2	LOC389237	XM_374094.1
GI_41146730-S	122.3	123.1	118.4	LOC391711	XM_373037.1
GI_41146732-S	206.5	215.5	178.7	LOC391712	XM_373038.1
GI_41146752-S	105.4	117.3	98.8	LOC389242	XM_374095.1
GI_41146762-S	117.3	135.5	128.1	LOC389246	XM_371718.1
GI_41146772-S	145	158.6	124.4	LOC389250	XM_374101.1
GI_41146786-S	107.1	114.3	114.5	LOC391723	XM_373043.1
GI_41146796-S	187.1	222.4	200.7	LOC391728	XM_374368.1
GI_41146798-S	138.9	149.1	128.2	LOC391729	XM_374369.1
GI_41146809-S	84.1	88.8	83.4	LOC391654	XM_373026.1
GI_41146823-S	143.9	156	143.5	LOC389197	XM_371687.1
GI_41146825-S	126.3	143.9	126.6	LOC389198	XM_374076.1
GI_41146841-S	133.5	128	125.8	LOC389206	XM_371693.1
GI_41146856-S	315.1	405.2	355	LOC389201	XM_374077.1
GI_41146861-S	106	138.9	122.7	LOC285548	XM_374078.1
GI_41146898-S	118.8	110	106.6	LOC389209	XM_374081.1
GI_41146916-S	154.3	181.2	171.2	LOC389262	XM_374106.1
GI_41146927-S	256.7	340.3	289.3	LOC389268	XM_374110.1
GI_41146929-S	84.2	83.9	85.1	LOC389269	XM_374111.1
GI_41146931-S	106.9	100.4	99.2	LOC389340	XM_374147.1
GI_41146946-S	134.6	154.1	134.5	LOC389343	XM_374148.1
GI_41146960-S	195.1	240.6	217.5	LOC391844	XM_373098.1
GI_41146964-S	164.8	161.8	146.6	LOC391847	XM_373099.1
GI_41146980-S	125.4	135.9	125.1	LOC389310	XM_374130.1
GI_41147023-S	175.5	158.3	154.5	LOC389316	XM_374132.1
GI_41147030-S	107.4	116.5	112.5	LOC389319	XM_374134.1
GI_41147036-S	82.9	88.5	90.7	LOC389321	XM_371769.1
GI_41147060-S	108.2	111.6	98.8	LOC389332	XM_374141.1
GI_41147065-S	98.3	91.1	88	LOC389334	XM_374143.1
GI_41147107-S	167.7	177.9	169.3	LOC389279	XM_371729.1

GI_41147113-S	136.9	143.3	121.6	LOC389282	XM_371732.1
GI_41147167-S	103.2	107.7	104.1	LOC391767	XM_373078.1
GI_41147169-S	159.5	159.1	154.6	LOC391769	XM_373079.1
GI_41147171-S	157.4	170.6	160.2	LOC391770	XM_373080.1
GI_41147177-S	117.9	137.1	129.1	LOC389301	XM_371754.1
GI_41147197-S	115.5	121.2	127.5	LOC389306	XM_374127.1
GI_41147203-S	118.6	107.4	111.6	LOC389308	XM_371758.1
GI_41147213-S	192.8	216	202.6	LOC391802	XM_373091.1
GI_41147217-S	96.5	93.6	107.9	LOC391807	XM_373092.1
GI_41147230-S	94.9	103.9	96.4	LOC389351	XM_371790.1
GI_41147232-S	184.8	220.6	208.9	LOC202404	XM_114481.6
GI_41147237-S	93.7	99.8	94.1	LOC389353	XM_374152.1
GI_41147247-S	114.2	96.3	108.9	LOC391859	XM_373106.1
GI_41147265-S	106.5	109	91.8	LOC391794	XM_373088.1
GI_41147292-S	105.2	94.8	94.2	LOC389357	XM_374154.1
GI_41147294-S	140.1	168.3	144	LOC389358	XM_374155.1
GI_41147296-S	555.2	690.8	606.3	LOC389359	XM_374156.1
GI_41147298-S	93.6	110.6	111.9	LOC389360	XM_374157.1
GI_41147300-S	87	89.6	82.4	LOC389361	XM_374158.1
GI_41147306-S	129.5	132.1	125.4	LOC389364	XM_371796.1
GI_41147315-S	120.6	118.4	110.4	LOC389403	XM_374172.1
GI_41147328-S	168.2	174.5	161.1	LOC389411	XM_374174.1
GI_41147340-S	223.5	319.5	287.4	LOC389414	XM_374176.1
GI_41147342-S	147.6	144.9	135.3	LOC389415	XM_374177.1
GI_41147351-S	163.9	196.8	165.7	LOC389450	XM_374194.1
GI_41147355-S	153.9	123.5	119.1	LOC389438	XM_374186.1
GI_41147357-S	161.8	190.1	161.9	LOC389439	XM_374187.1
GI_41147365-S	164.4	195.3	174.2	LOC389443	XM_374191.1
GI_41147367-S	103.5	118.7	109.1	LOC389444	XM_371856.1
GI_41147373-S	130.6	151.1	131.6	LOC389447	XM_374192.1
GI_41147381-S	88.4	97.1	92.1	LOC389449	XM_374193.1
GI_41147425-S	285.3	352.8	330.8	LOC389455	XM_374198.1
GI_41147464-S	116.3	119	119.1	LOC392160	XM_374370.1
GI_41147534-S	112.1	109.2	99.4	LOC392164	XM_373224.1
GI_41147544-S	98.9	103.2	97.3	LOC389456	XM_374199.1
GI_41147546-S	414.1	433.1	407.7	LOC389562	XM_374236.1
GI_41147787-S	109	122.4	127.9	LOC392657	XM_374721.1
GI_41147791-S	359.5	456.2	396.8	LOC392660	XM_374427.1
GI_41147807-S	92.1	105.1	88.8	LOC392668	XM_374434.1
GI_41147813-S	135	157.3	149.2	LOC392670	XM_374437.1
GI_41147857-S	152	187.7	191.4	LOC392862	XM_374600.1
GI_41147867-S	258.1	279.4	261.6	LOC392888	XM_374605.1
GI_41147873-S	149.5	157.2	151.9	MGC26484	XM_374608.1
GI_41147897-S	141.1	161.4	149.2	LOC392702	XM_374730.1

GI_41147939-S	188.5	221.8	187.9	LOC392726	XM_374734.1
GI_41148005-S	85.1	108	91.8	PPP1R9A	XM_374491.1
GI_41148031-S	126.6	121.3	121	LOC392762	XM_374501.1
GI_41148131-S	106.8	108.7	108.4	LOC392791	XM_374752.1
GI_41148163-S	120.6	159.3	123.6	KIAA1277	XM_374538.1
GI_41148256-S	112.5	102.2	108.9	LOC392842	XM_374585.1
GI_41148258-S	89.7	95	81.9	LOC392843	XM_374586.1
GI_41148268-S	111.3	110.8	104.5	LOC392964	XM_374636.1
GI_41148288-S	130.1	147.6	132.3	LOC392979	XM_374646.1
GI_41148302-S	161.5	191	174.2	LOC392993	XM_374653.1
GI_41148356-S	141.1	157.4	147.8	LOC393037	XM_374680.1
GI_41148360-S	139.9	160.9	131.4	LOC393045	XM_374682.1
GI_41148370-S	91.7	90.5	78.8	LOC393051	XM_374687.1
GI_41148384-S	198	249.9	209.3	LOC393062	XM_374694.1
GI_41148406-S	132.9	126.8	180.4	LOC392848	XM_374589.1
GI_41148408-S	161.1	182.7	156.3	LOC392849	XM_374761.1
GI_41148412-S	119.7	123.3	124.9	LOC392851	XM_374591.1
GI_41148418-S	129.9	141.2	133	LOC393076	XM_374763.1
GI_41148428-S	107.8	113.2	102.8	LOC389639	XM_374258.1
GI_41148453-S	140.4	165.6	134.5	LOC392208	XM_373246.1
GI_41148459-S	89.1	117.3	103.5	LOC389654	XM_374267.1
GI_41148469-S	104.9	124.5	115.1	LOC389694	XM_372062.1
GI_41148475-S	121.4	134.1	113.5	LOC389697	XM_372063.1
GI_41148493-S	121.1	136.8	122.1	LOC389609	XM_374244.1
GI_41148521-S	233.8	259.2	252	LOC392177	XM_374371.1
GI_41148533-S	121.6	120.8	111.7	LOC389690	XM_372060.1
GI_41148591-S	108.4	115.1	107.3	LOC389626	XM_372026.1
GI_41148593-S	123.2	109.7	105.8	LOC389627	XM_372027.1
GI_41148634-S	117	114.7	112.9	LOC389647	XM_374263.1
GI_41148662-S	134.6	158.4	131.6	LOC389684	XM_374278.1
GI_41148670-S	408.2	510.8	464.8	LOC389687	XM_374281.1
GI_41148687-S	116.1	128.5	115.8	LOC392262	XM_373263.1
GI_41148721-S	113	127.4	119.2	LOC389666	XM_374272.1
GI_41148766-S	108.3	123.8	115.1	LOC389651	XM_372039.1
GI_41148781-S	143.5	160.2	140.2	LOC389763	XM_372120.1
GI_41148787-S	92.6	91.3	92.6	LOC389766	XM_372123.1
GI_41148795-S	101.4	118.7	98.7	LOC389768	XM_372125.1
GI_41148815-S	128.6	129.9	127.5	LOC389796	XM_372148.1
GI_41148823-S	88.1	93.4	84.5	LOC392396	XM_373320.1
GI_41148833-S	115.1	111.1	109.9	LOC389727	XM_372092.1
GI_41148849-S	573.6	618.5	555.6	LOC389739	XM_372100.1
GI_41148989-S	102	113.4	94.4	LOC389720	XM_374294.1
GI_41148998-S	96.7	88.9	90.9	LOC392285	XM_373275.1
GI_41149002-S	85.1	107.4	80.4	LOC392288	XM_373277.1

GI_41149014-S	94.7	105.5	101.8	LOC392299	XM_373283.1
GI_41149016-S	97.6	97	77.7	LOC392300	XM_373284.1
GI_41149020-S	95.1	102.7	94.2	LOC392308	XM_373288.1
GI_41149035-S	159.1	168.8	159.6	LOC389778	XM_374301.1
GI_41149048-S	105.3	110.2	113.4	LOC389783	XM_374303.1
GI_41149074-S	102.8	92.7	79.9	LOC389775	XM_374299.1
GI_41149110-S	118.2	114.5	105.5	LOC387695	XM_370566.1
GI_41149128-S	141.2	157.4	147.1	LOC387702	XM_370570.1
GI_41149184-S	100.8	98.4	101.7	LOC389993	XM_372324.1
GI_41149227-S	177.7	189.2	166.7	LOC390010	XM_372331.1
GI_41149233-S	207.1	253.5	221.3	LOC387717	XM_373478.1
GI_41149237-S	117.8	113.2	103.8	LOC390009	XM_372330.1
GI_41149241-S	442.4	587.1	535	LOC387630	XM_373444.1
GI_41149249-S	229.1	288.5	265	LOC389931	XM_374349.1
GI_41149304-S	136.7	151.7	147.1	LOC387683	XM_373461.1
GI_41149320-S	93.9	93.2	86.9	LOC387688	XM_370562.1
GI_41149324-S	100.9	109	91.6	LOC387690	XM_373466.1
GI_41149334-S	213.2	228.3	205.3	LOC389972	XM_372314.1
GI_41149336-S	480.5	460.2	322.9	LOC389974	XM_372315.1
GI_41149340-S	98.3	106.1	94.7	LOC389978	XM_372316.1
GI_41149348-S	86.3	92.9	92	LOC387636	XM_373448.1
GI_41149356-S	143.1	144.8	132.4	LOC387640	XM_370534.1
GI_41149361-S	273.7	362.2	307.1	LOC387643	XM_370537.1
GI_41149389-S	101.4	106.4	97.6	LOC387654	XM_373453.1
GI_41149411-S	115.7	122.5	133	LOC387722	XM_373479.1
GI_41149413-S	122	108.6	105.1	LOC387723	XM_370586.1
GI_41149433-S	143.7	133.3	133.1	PLET1	XM_370657.1
GI_41149437-S	102.3	96.5	97.8	LOC387811	XM_370658.1
GI_41149444-S	221.3	258.9	228.7	LOC387814	XM_373515.1
GI_41149461-S	309	367.8	323.6	LOC387817	XM_373516.1
GI_41149467-S	269.3	346.4	281.5	LOC387821	XM_373518.1
GI_41149469-S	98.1	112.6	101.4	LOC387822	XM_370666.1
GI_41149479-S	110.2	100.7	111.1	LOC390253	XM_372431.1
GI_41149489-S	137.8	153.2	140.3	LOC390264	XM_372436.1
GI_41149491-S	102.2	115.5	96.7	LOC390265	XM_372437.1
GI_41149503-S	89.1	84.3	87.7	LOC390275	XM_372443.1
GI_41149547-S	93.9	80.2	75	LOC387787	XM_370636.1
GI_41149557-S	631.9	630.4	456.8	LOC387791	XM_370639.1
GI_41149571-S	116.9	132.4	107.5	LOC387796	XM_373511.1
GI_41149594-S	91.5	116.8	99.8	LOC387736	XM_373483.1
GI_41149596-S	91.4	104.6	107.5	LOC387737	XM_373484.1
GI_41149603-S	149.9	174.2	166.2	LOC387739	XM_373485.1
GI_41149613-S	86	97.2	90.7	LOC387800	XM_370644.1
GI_41149627-S	4706.1	6660.7	5726.1	LOC387805	XM_370649.1

GI_41149631-S	209.5	235.4	215.9	LOC390231	XM_372423.1
GI_41149660-S	107.5	113	106.9	LOC387746	XM_373489.1
GI_41149668-S	322.4	307.4	257.7	LOC387749	XM_370606.1
GI_41149683-S	112.5	128.5	101.9	LOC387871	XM_373539.1
GI_41149693-S	101.8	107.4	99	LOC387872	XM_373540.1
GI_41149730-S	177.1	151	127.9	LOC390353	XM_372474.1
GI_41149769-S	107.6	119.2	104.8	LOC387861	XM_370695.1
GI_41149771-S	150.3	168	155.6	LOC387898	XM_373556.1
GI_41149781-S	150.2	168.2	151.7	LOC283314	XM_373522.1
GI_41149799-S	151.9	179.5	164.1	LOC387833	XM_373524.1
GI_41149808-S	145.8	163.7	158.5	LOC387836	XM_370678.1
GI_41149815-S	101.3	113.8	103.8	LOC387838	XM_373525.1
GI_41149833-S	239	285.3	259.1	LOC387895	XM_373553.1
GI_41149841-S	185.1	222.1	191.8	LOC387896	XM_373554.1
GI_41149843-S	88.7	102.4	91	LOC387897	XM_373555.1
GI_41149851-S	119.8	133	125	LOC390369	XM_372482.1
GI_41149855-S	100.5	112.2	97.2	LOC387825	XM_370668.1
GI_41149880-S	144.4	156	133.5	LOC387886	XM_373548.1
GI_41149904-S	107.8	106.2	106.4	LOC387941	XM_373572.1
GI_41149918-S	101.6	100.7	104.3	LOC387946	XM_373575.1
GI_41149935-S	154.9	148.5	140.2	LOC387948	XM_373577.1
GI_41149939-S	100.8	97.6	105	LOC387950	XM_373578.1
GI_41149957-S	1093.5	1244.4	1343	HELSNF1	XM_370738.1
GI_41150010-S	166.3	193.5	159.3	LOC388107	XM_370849.1
GI_41150014-S	151.1	168.2	143.1	LOC388109	XM_370851.1
GI_41150026-S	97.7	118.4	102.1	LOC388114	XM_373626.1
GI_41150032-S	89.3	83.9	88.7	LOC388116	XM_370856.1
GI_41150052-S	146.8	159.4	160	LOC388170	XM_373646.1
GI_41150062-S	137.4	152.8	133.3	LOC390550	XM_374354.1
GI_41150072-S	105.3	108.8	101.1	LOC390547	XM_372553.1
GI_41150092-S	211.8	267.2	227	LOC390644	XM_372593.1
GI_41150100-S	179.2	217.7	208.6	LOC390649	XM_372597.1
GI_41150104-S	105.5	123.2	108.9	LOC390651	XM_372599.1
GI_41150129-S	103.9	107.9	99.5	LOC390530	XM_372543.1
GI_41150137-S	106	108.7	108.1	LOC390537	XM_372547.1
GI_41150141-S	106.5	112	118.4	LOC388077	XM_370834.1
GI_41150145-S	142.9	123.9	110.4	LOC388079	XM_370836.1
GI_41150147-S	129.3	152.8	132.1	LOC390538	XM_372548.1
GI_41150177-S	114.4	133.4	110.9	LOC390625	XM_372586.1
GI_41150239-S	81.4	84.4	82.9	LOC388216	XM_373667.1
GI_41150280-S	96.9	97.2	99.3	LOC388277	XM_373686.1
GI_41150284-S	690.1	807.2	694.6	LOC388278	XM_373687.1
GI_41150286-S	150.7	163.3	161.9	LOC388273	XM_373683.1
GI_41150288-S	92	109.5	112.3	LOC388274	XM_373684.1

GI_41150315-S	95.3	106.6	91.7	LOC390751	XM_374358.1
GI_41150317-S	108.7	101.9	105	LOC388205	XM_370930.1
GI_41150319-S	286.9	328.9	307	LOC388206	XM_373660.1
GI_41150323-S	107.9	97.6	83.4	FLJ39639	XM_370932.1
GI_41150361-S	435.7	535	482.1	LOC388291	XM_373692.1
GI_41150381-S	103.5	97.6	93.1	LOC388300	XM_373695.1
GI_41150385-S	115.1	110.3	116.6	LOC388302	XM_373697.1
GI_41150409-S	101.6	121	118.8	LOC388243	XM_370966.1
GI_41150435-S	93.1	103.8	91.8	LOC388258	XM_370974.1
GI_41150451-S	451	485.4	425.4	LOC390690	XM_372617.1
GI_41150461-S	81.3	88	83.9	LOC390697	XM_372622.1
GI_41150483-S	230.7	226	203.4	LOC388272	XM_370981.1
GI_41150491-S	83.1	85.4	88.8	LOC388198	XM_373655.1
GI_41150493-S	267.2	282.4	261.3	LOC388199	XM_370924.1
GI_41150497-S	1097.4	1189	926.7	LOC283951	XM_370925.1
GI_41150499-S	121.4	125	125.3	LOC388201	XM_373657.1
GI_41150548-S	112.6	112.2	107.2	LOC388418	XM_373748.1
GI_41150565-S	86.6	109.9	85.9	LOC388422	XM_373751.1
GI_41150571-S	114.4	116.2	115.3	LOC390812	XM_372679.1
GI_41150577-S	132.7	167.8	144.1	LOC390816	XM_372682.1
GI_41150585-S	146.2	147.2	170.8	LOC388434	XM_373761.1
GI_41150590-S	136.1	136.7	108.5	LOC388318	XM_373707.1
GI_41150622-S	104.3	103.7	98.5	LOC388329	XM_371012.1
GI_41150630-S	98.6	93.6	92.1	LOC388332	XM_371013.1
GI_41150636-S	102.9	110	101.2	LOC388334	XM_373713.1
GI_41150642-S	99.4	124.2	97.6	LOC388336	XM_371017.1
GI_41150677-S	162.4	195.6	165.6	LOC388348	XM_373718.1
GI_41150705-S	470.6	489.8	289.8	LOC388380	XM_373728.1
GI_41150726-S	969	1128.5	1147.7	KIAA0100	XM_371036.1
GI_41150732-S	92.9	102.2	95.4	LOC388366	XM_373724.1
GI_41150754-S	129.1	114	123.3	LOC390788	XM_372666.1
GI_41150760-S	100.9	105.5	110	FLJ20753	XM_371082.1
GI_41150766-S	213	260.4	212	LOC388426	XM_373754.1
GI_41150770-S	114.7	112.3	104.4	LOC388428	XM_371083.1
GI_41150780-S	143.1	147.9	132	LOC388431	XM_373758.1
GI_41150782-S	700.9	676	666	LOC339229	XM_371085.1
GI_41150784-S	132.6	139.2	120.2	LOC388314	XM_373705.1
GI_41150794-S	175.6	161.6	166.3	LOC388353	XM_371028.1
GI_41150802-S	174	200.5	161.3	LOC388357	XM_371032.1
GI_41150868-S	90.8	98.4	89.9	LOC388456	XM_373771.1
GI_41150880-S	101.7	141.9	114.9	LOC388461	XM_373773.1
GI_41150902-S	283.3	350.2	329.3	LOC390821	XM_374359.1
GI_41150914-S	199.8	237.1	223.4	LOC388484	XM_373783.1
GI_41150926-S	148.4	159.4	149.9	LOC390870	XM_374361.1

GI_41150934-S	242.4	276.8	248	LOC390864	XM_372697.1
GI_41150942-S	94.7	102.4	94.2	LOC388478	XM_371118.1
GI_41150946-S	99.1	118	98.3	LOC388481	XM_373780.1
GI_41150950-S	176.8	225.7	199.8	LOC390861	XM_372696.1
GI_41150958-S	101.4	110.3	98.3	LOC388527	XM_373799.1
GI_41150960-S	104.1	106.4	94.7	LOC388528	XM_373800.1
GI_41150966-S	182.8	207.6	175.1	LOC147991	XM_371158.1
GI_41150981-S	108.6	124.4	116.6	LOC388535	XM_373803.1
GI_41150990-S	89.9	99.3	90.8	NYD-SP11	XM_371164.1
GI_41150993-S	96.5	102.9	84	LOC388538	XM_371165.1
GI_41151023-S	225.5	243.7	221.6	LOC388488	XM_371122.1
GI_41151028-S	191.9	236.4	222.4	LOC388489	XM_373786.1
GI_41151030-S	90.4	92.5	87.4	LOC388490	XM_373787.1
GI_41151032-S	118.6	117.6	116.5	LOC388491	XM_371125.1
GI_41151055-S	100.9	90	99.4	LOC390875	XM_372703.1
GI_41151057-S	3585	2796.3	2220.5	LOC390876	XM_372704.1
GI_41151072-S	326.2	323.8	303.5	LOC388504	XM_373793.1
GI_41151092-S	102.9	111.6	104	LOC388509	XM_371142.1
GI_41151115-S	101.3	107.9	92.3	LOC388516	XM_373796.1
GI_41151119-S	124.3	125.6	133.2	LOC388517	XM_371147.1
GI_41151129-S	133.9	146.4	140.9	LOC388519	XM_371151.1
GI_41151136-S	96.7	102.4	98.8	LOC388521	XM_371153.1
GI_41151168-S	120.5	136.4	144.1	LOC390892	XM_372712.1
GI_41151174-S	96.2	96.3	92.9	LOC390895	XM_372715.1
GI_41151204-S	167.4	168.9	154.4	LOC284739	XM_373924.1
GI_41151210-S	111.6	117.7	118.5	LOC391262	XM_372874.1
GI_41151223-S	140.2	168	147	LOC388798	XM_373915.1
GI_41151232-S	151.5	162.6	151.5	LOC388800	XM_373916.1
GI_41151236-S	204.1	252	215.2	LOC388801	XM_373917.1
GI_41151269-S	120.1	121.5	110.2	LOC388785	XM_373905.1
GI_41151273-S	120	117.1	110.5	LOC388787	XM_373907.1
GI_41151279-S	109.4	113	108.1	LOC388790	XM_373909.1
GI_41151281-S	118	127.3	131	LOC388791	XM_373910.1
GI_41151283-S	117.3	142.9	122.2	LOC388792	XM_373911.1
GI_41151295-S	327.3	416.1	367.3	LOC388793	XM_373913.1
GI_41151312-S	172.8	155.4	154.1	LOC388815	XM_373927.1
GI_41151326-S	118.7	131.2	103.1	LOC388823	XM_373931.1
GI_41151334-S	96.2	105	93.1	LOC391268	XM_372875.1
GI_41151336-S	94.1	89.6	77.5	LOC391269	XM_372876.1
GI_41151340-S	11245.5	10539	8909.4	LOC391282	XM_372878.1
GI_41151346-S	101.7	104.6	99.8	LOC388831	XM_373938.1
GI_41151350-S	202.1	255.5	222.3	LOC388833	XM_373940.1
GI_41151354-S	115.7	130.3	124.8	C21orf57	XM_372879.1
GI_41151358-S	109.9	117	108.9	LOC388827	XM_371415.1

GI_41151366-S	126.9	154.5	139.8	LOC388840	XM_371421.1				
GI_41151368-S	101.1	90.7	100.9	LOC388843	XM_373943.1				
GI_41151378-S	105.8	97.9	90.7	LOC388847	XM_371424.1				
GI_41151441-S	109.6	107.4	113.7	LOC388911	XM_373965.1				
GI_41151454-S	115.1	117.6	112.7	LOC388916	XM_373969.1				
GI_41151474-S	2761.1	3230.6	2425.1	PLXNB2	XM_371474.1				
GI_41151506-S	112.6	117.1	105.9	LOC392462	XM_373345.1				
GI_41151532-S	99.7	94.3	95.9	LOC392468	XM_373350.1				
GI_41151590-S	112.7	115	112	MGC17403	XM_372198.1				
GI_41151616-S	84.8	84.7	77.4	LOC392426	XM_373339.1				
GI_41151626-S	174.2	196.2	192.2	LOC389887	XM_372247.1				
GI_41151637-S	108.8	109.1	94.2	LOC389892	XM_372254.1				
GI_41151643-S	103	86.4	86	LOC389896	XM_374339.1				
GI_41151653-S	111.7	95.3	105.6	LOC392546	XM_373372.1				
GI_41151663-S	104.6	101.3	101.7	LOC389899	XM_372258.1				
GI_41151697-S	99.2	95.1	78.2	LOC392533	XM_373368.1				
GI_41151725-S	113.9	142.1	125.1	LOC392570	XM_373388.1				
GI_41151743-S	96.4	99.2	96.2	LOC392597	XM_373399.1				
GI_41151752-S	110.2	121.6	117.5	LOC392583	XM_374379.1				
GI_41151754-S	265.5	308.8	319.9	LOC392584	XM_373397.1				
GI_41151802-S	161.9	156.1	177.7	LOC389830	XM_372186.1				
GI_41151809-S	185.3	214	167.3	LOC389833	XM_372191.1				
GI_41151823-S	87.9	116.3	95.7	MGC13275	XM_372194.1				
GI_41152057-S	176.3	202.4	187.3	SLCO2B1	NM_007256.2	OATPB;OATP-	transporte	integral to	ion
GI_41152068-S	112.1	119.9	106.6	ZNF-kaiso	NM_006777.3	WUGSC:H_DJ525N14.1	protein	nucleus	intracellula
GI_41152069-S	119.1	116.4	113.9	ZNF75	NM_007131.2	D8C6	zinc ion	nucleus	regulation
GI_41152071-S	801	817.9	714.9	ZDHHC5	NM_015457.2	ZNF375;KIAA1748;DKFZP586K0524	zinc ion	integral to	regulation
GI_41152073-I	106.7	126.8	103.2	URB	NM_199511.1	SSG1			
GI_41152077-S	90.3	92.8	86.8	TUBB1	NM_030773.2	dJ543J19.4	GTP	microtubul	microtubul
GI_41152082-S	1032.9	864.8	816.3	TIM14	NM_145261.2				
GI_41152085-S	6101.4	5333.1	5647.6	SERPINB6	NM_004568.4	CAP;PI6;PTI	protein	cytosol	
GI_41152087-S	163.7	239.3	201.3	PLXNB1	NM_002673.3	SEP;PLXN5;KIAA0407;PLEXIN-B1	receptor	integral to	signal
GI_41152088-S	672.2	670.5	650.7	LOC284058	NM_015443.2	DKFZP727C091			
GI_41152089-S	91.6	101	90.5	MAP17	NM_005764.3	DD96		integral to	oncogene
GI_41152092-I	160.8	175.7	161	KIAA1221	NM_201269.1	BM-			
GI_41152096-S	1933.3	2700.2	2221.9	DXYS155E	NM_005088.2	XE7;XE7Y;MGC39904	DNA	membran	regulation
GI_41152102-S	732.4	666.9	779.2	C16orf40	NM_058192.2	RLUCL;MGC19600	pseudouri		
GI_41152103-S	179.5	179.3	193.3	C10orf26	NM_017787.3	FLJ20154;FLJ20367			
GI_41152105-S	1051.2	1313.9	988.5	BMSC-UbP	NM_032907.3	MGC14421		membran	protein
GI_41152108-S	120.4	126.2	115.9	BGLAP	NM_199173.2	BGP	structural	extracellul	skeletal
GI_41152109-S	101.3	119.3	103.8	ADM2	NM_024866.2	AM2;FLJ21135			
GI_41152111-S	104.2	114.6	104.9	AFAR3	NM_201252.1	AKR7A4			
GI_41152113-S	92.9	113.7	96.6	AKR7A3	NM_012067.2	AFAR2	aldo-keto	cytosol	aldehyde
GI_41152145-S	141.9	153.9	143.2	HM74a	NM_177551.3	HM74b	rhodopsin-	integral to	G-protein

GI_41152234-S	137	129.2	125.7	USP51	NM_201286.1				
GI_41152236-S	667	509.8	436.9	MUTED	NM_201280.1	MU;dJ303A1.3;dJ511E16.2			
GI_41152252-S	2901.9	2873	2352.7	GLI4	NM_138465.3	HKR4	DNA	nucleus	biological_
GI_41152505-S	1209.3	4812.5	2217.4	PTGFRN	NM_020440.2	FPRP;EWI-F;CD9P-1;SMAP-	protein	integral to	negative
GI_41187875-S	98.5	112.8	126.6	PLXNA2	XM_372810.1				
GI_41187884-S	114.1	132.5	124.9	LOC391164	XM_372814.1				
GI_41188084-S	87.8	101.7	98.2	LOC388715	XM_373875.1				
GI_41188092-S	154.8	177.4	155.2	LOC388717	XM_373877.1				
GI_41188100-S	100.5	119.8	112.8	LOC388718	XM_371329.1				
GI_41188259-S	116.5	120.6	127.1	LOC388604	XM_373831.1				
GI_41188447-S	97.7	110	112.7	LOC388726	XM_371335.1				
GI_41188450-S	633.5	1136.7	718.2	LOC388727	XM_373881.1				
GI_41188793-S	136.7	110.3	106.9	LOC388706	XM_373870.1				
GI_41188811-S	152.4	167.2	157.2	LOC388709	XM_373871.1				
GI_41188817-S	96	113.1	108.4	LOC391109	XM_372797.1				
GI_41188832-S	101.4	104.2	102.3	LOC391122	XM_372801.1				
GI_41190370-S	524.6	628.4	506.4	LOC388940	XM_373980.1				
GI_41190399-S	71.7	95	93	LOC388947	XM_373984.1				
GI_41190411-S	268.8	326.8	286.3	LOC388950	XM_371493.1				
GI_41190413-S	118.7	113.2	114.3	LOC388951	XM_371494.1				
GI_41190418-S	864.4	844	728.5	LOC388952	XM_373986.1				
GI_41190460-S	101.9	109.9	99.9	LOC388960	XM_371500.1				
GI_41190479-S	484.6	612.4	588	LOC388967	XM_373992.1				
GI_41190543-S	138.7	162.2	134.2	LOC391392	XM_372933.1				
GI_41190797-S	111.1	113.2	94	UNQ2430	XM_371540.1				
GI_41190805-S	112.9	108.9	90.9	LOC391407	XM_372942.1				
GI_41191410-S	604.3	615.5	488.5	LOC375295	XM_374020.1				
GI_41191505-S	101.2	95.8	90	LOC391456	XM_372965.1				
GI_41193262-S	108.5	121.1	126.2	LOC389118	XM_371639.1				
GI_41193290-S	102.4	119.9	110.5	LOC391509	XM_372984.1				
GI_41193302-S	96.6	102.7	86.9	LOC391532	XM_372988.1				
GI_41194212-S	104.7	105.9	93.6	LOC389186	XM_374068.1				
GI_41194251-S	107.1	110.3	119.2	LOC391594	XM_373004.1				
GI_41195115-S	79.3	84	79.6	LOC391701	XM_373033.1				
GI_41195532-S	102.3	104.2	109.9	LOC391733	XM_373053.1				
GI_41196201-S	114.4	118.9	108.2	LOC389426	XM_374181.1				
GI_41197088-S	98.5	94.9	85	HLA-DQA1	XM_371812.1	DQA1;HLA-DQ;CELIAC1;HLA-DQA	class II	integral to	pathogene
GI_41197090-S	130.2	133.9	129.4	LOC389380	XM_374164.1				
GI_41197095-S	125.5	150.9	131.2	LOC389381	XM_374165.1				
GI_41197099-S	138.4	139.1	126	LOC389383	XM_371815.1				
GI_41197105-S	238.7	298.2	288.1	LOC389385	XM_371817.1				
GI_41197110-S	2797.8	2215.6	1436.5	LOC389387	XM_371819.1				
GI_41197134-S	299.5	377.4	349.4	LOC389393	XM_374169.1				
GI_41197144-S	340	400.8	371.1	LOC389396	XM_371825.1				

GI_41197149-S	123.3	134.6	125.6	LOC389399	XM_374171.1
GI_41197153-S	110.2	117.4	119.5	LOC389400	XM_371826.1
GI_41199227-S	143.1	163.5	162.5	LOC389556	XM_374232.1
GI_41199294-S	82.7	84.6	91.3	LOC392084	XM_373180.1
GI_41199582-S	430.1	531.3	471.5	LOC389816	XM_372161.1
GI_41199585-S	113.3	132.9	108.6	LOC389817	XM_372162.1
GI_41200333-S	92.3	110	114.9	LOC387776	XM_373502.1
GI_41200338-S	98.8	86.3	90.3	LOC387777	XM_373503.1
GI_41200362-S	233.1	302.2	248.8	LOC387783	XM_373505.1
GI_41200377-S	93.1	81.7	88.2	LOC390137	XM_372384.1
GI_41200379-S	131.9	168.6	150	LOC390138	XM_372385.1
GI_41200391-S	96	102.3	95.9	OR5L2	XM_372387.1
GI_41200394-S	103.8	106.8	101.3	LOC390144	XM_372388.1
GI_41200409-S	110.9	118.3	108.1	LOC390152	XM_372391.1
GI_41200424-S	106.7	122.8	112.4	LOC390157	XM_372395.1
GI_41200427-S	139.8	127.6	122.8	LOC390158	XM_372396.1
GI_41200431-S	143.2	160.5	144	LOC390162	XM_372397.1
GI_41200448-S	159.3	194.2	164.9	LOC390169	XM_372402.1
GI_41200470-S	99.3	103.6	99.9	LOC390186	XM_372406.1
GI_41200477-S	91.8	110.9	96.4	LOC390191	XM_372409.1
GI_41200489-S	91.5	102.2	87.2	LOC390195	XM_372411.1
GI_41200497-S	96.6	114	99.8	LOC390199	XM_372413.1
GI_41200501-S	103.2	90.6	92.5	LOC390204	XM_372415.1
GI_41200870-S	255.3	289.2	265.1	LOC387757	XM_373492.1
GI_41200889-S	146.3	171.1	149	LOC387760	XM_373494.1
GI_41200900-S	89.2	113.8	95.9	LOC387762	XM_373496.1
GI_41200910-S	156	205.3	190	LOC387765	XM_373499.1
GI_41200912-S	306.3	364.5	353.1	FLJ20294	XM_370618.1
GI_41200935-S	101.8	120.8	112	LOC390034	XM_372346.1
GI_41200947-S	114.4	147.2	126.9	LOC390039	XM_372350.1
GI_41200959-S	109.2	108.3	106.9	LOC390054	XM_372352.1
GI_41200962-S	86.8	85.1	85.6	LOC390058	XM_372353.1
GI_41200965-S	91.3	103.8	94.7	LOC390059	XM_372354.1
GI_41200969-S	82.6	90.1	85.6	LOC390063	XM_372356.1
GI_41200974-S	117.4	115.8	121.5	LOC390065	XM_372358.1
GI_41200976-S	645.3	779.6	683.8	LOC390066	XM_372359.1
GI_41200979-S	152.2	166	161.1	LOC390067	XM_372360.1
GI_41200985-S	127.6	130.4	125.3	LOC390073	XM_372362.1
GI_41200997-S	116.1	103.6	117.7	LOC390079	XM_372367.1
GI_41201006-S	145.1	159.1	144.1	LOC390084	XM_372371.1
GI_41201018-S	114.7	112.7	94	LOC390093	XM_372373.1
GI_41201031-S	120.3	133.2	125.8	LOC390110	XM_372375.1
GI_41201035-S	342	350.7	305.8	LOC390113	XM_372376.1
GI_41201706-S	122.4	117.1	105.7	LOC387863	XM_373534.1

GI_41201711-S	133.1	157.1	150	FLJ34236	XM_370696.1
GI_41201751-S	113.1	121.7	122.4	LOC390310	XM_372456.1
GI_41201767-S	114.1	116	128	LOC390323	XM_372460.1
GI_41201774-S	100.3	101.4	100.4	LOC390326	XM_372463.1
GI_41201777-S	138.7	154	129.9	LOC390327	XM_372464.1
GI_41201795-S	150.4	148.1	151.7	LOC390343	XM_372470.1
GI_41202045-S	9338.8	9273.8	7311.4	LOC387845	XM_370684.1
GI_41202063-S	188.5	191.5	156.7	LOC387849	XM_370686.1
GI_41202068-S	114.8	118.5	98.1	LOC387850	XM_370687.1
GI_41202077-S	98.9	105.6	96.8	LOC390288	XM_372449.1
GI_41202079-S	91.4	106.7	98.5	LOC390290	XM_372450.1
GI_41202572-S	105.8	100.3	107.5	LOC387901	XM_373557.1
GI_41202576-S	83.7	96.5	91.7	LOC387903	XM_373558.1
GI_41202581-S	116.3	123.8	101.7	LOC387905	XM_373559.1
GI_41202591-S	105.4	91.7	89.2	LOC387910	XM_373560.1
GI_41202601-S	330.7	419.3	384.4	LOC387914	XM_370718.1
GI_41202613-S	82.5	93.6	88.9	LOC387918	XM_373563.1
GI_41202624-S	78.9	77.6	85.4	LOC387922	XM_370723.1
GI_41202645-S	150.3	165.9	159.4	LOC387927	XM_370726.1
GI_41202691-S	115.5	124	118	LOC390377	XM_372486.1
GI_41202705-S	89	98.9	100.7	LOC390393	XM_372491.1
GI_41203719-S	110.5	131.5	123.1	LOC387993	XM_373595.1
GI_41203727-S	174.2	189.9	166.1	LOC387994	XM_373596.1
GI_41203742-S	105.1	109.3	102.5	PAPLN	XM_370765.1
GI_41203785-S	188	223.6	190.9	LOC388006	XM_373602.1
GI_41203788-S	161.6	189.8	175.7	C14orf86	XM_373603.1
GI_41203790-S	152.4	187.3	168.8	LOC388007	XM_370772.1
GI_41203818-S	206.4	245.8	243.2	LOC388017	XM_373609.1
GI_41203826-S	349.1	449.9	374.1	LOC388019	XM_373611.1
GI_41203834-S	116.9	107.3	110.7	LOC388021	XM_370778.1
GI_41203856-S	99.1	103.4	94.4	C14orf81	XM_370785.1
GI_41203866-S	186.5	204.6	167.8	LOC390431	XM_372501.1
GI_41203872-S	115.5	142.1	155.3	LOC390432	XM_372502.1
GI_41203875-S	88.1	89.5	87.3	LOC390433	XM_372503.1
GI_41203882-S	145	173.3	157.4	LOC390439	XM_372506.1
GI_41203885-S	223.3	283.2	233.5	LOC390442	XM_372507.1
GI_41203897-S	107.8	113.6	114.1	LOC390468	XM_372522.1
GI_41203903-S	103.4	115.3	120.1	LOC390485	XM_372525.1
GI_41204880-S	198.5	221.6	208.2	LOC388118	XM_370858.1
GI_41204903-S	170.5	242	188.7	ATP8B4	XM_370863.1
GI_41204905-S	172.6	156.3	98.7	LOC388121	XM_370864.1
GI_41204912-S	83.4	91.5	87.9	LOC388123	XM_373628.1
GI_41204930-S	122.2	131.7	113.1	LOC388125	XM_370868.1
GI_41204932-S	97.1	97.5	94.8	LOC388126	XM_373630.1

GI_41204956-S	124.5	146	121.8	LOC388134	XM_373633.1
GI_41204969-S	97.7	105	110.8	LOC388136	XM_373634.1
GI_41204979-S	900.1	1172.8	673.1	KIAA2002	XM_370878.1
GI_41204983-S	151.7	176.4	158.5	LOC388141	XM_373637.1
GI_41205014-S	115.2	126.8	121.5	LOC390558	XM_372559.1
GI_41205021-S	110.2	119.1	114	LOC390564	XM_372562.1
GI_41205031-S	187.5	230.6	224.1	LOC390568	XM_374356.1
GI_41205033-S	97.1	94.2	90.9	LOC390569	XM_372565.1
GI_41205035-S	145	155.1	135.6	LOC390570	XM_372566.1
GI_41205051-S	129.1	136	122	LOC390594	XM_372573.1
GI_41205056-S	98.8	104	102.6	LOC390596	XM_372575.1
GI_41205075-S	99.5	100.8	99.2	LOC390613	XM_372583.1
GI_41205080-S	119.9	136.7	120.4	LOC390623	XM_372585.1
GI_41205607-S	106	122.4	112.5	LOC388175	XM_370906.1
GI_41205617-S	104.2	107.5	120.2	LOC388177	XM_370909.1
GI_41205627-S	142	138.4	136.6	LOC390633	XM_372588.1
GI_41205631-S	105.8	131	119.6	LOC390638	XM_372591.1
GI_41206115-S	153.7	163.9	152.1	ERN2	XM_370947.1
GI_41206117-S	145.5	204.7	173.7	LOC388227	XM_373670.1
GI_41206133-S	116.1	128	110.6	LOC388231	XM_373671.1
GI_41206146-S	103.8	118.1	114	LOC390680	XM_372611.1
GI_41206154-S	112.1	118.5	104.7	LOC390683	XM_372614.1
GI_41206406-S	287.3	245.7	207.3	LOC388279	XM_373688.1
GI_41206408-S	121.4	116.2	129.2	LOC388281	XM_373689.1
GI_41206439-S	90.6	93.7	81.3	LOC388288	XM_370986.1
GI_41206445-S	199.3	250.4	230.2	LOC388289	XM_370987.1
GI_41206449-S	121.7	139.9	133.2	LOC390732	XM_372639.1
GI_41206830-S	110.3	127.1	115.4	LOC390792	XM_372669.1
GI_41207734-S	101.6	98.3	105.1	LOC390845	XM_372692.1
GI_41208718-S	197.5	192.3	146.8	ZNF283	XM_371174.1
GI_41208736-S	195.8	246.7	210.5	LOC388550	XM_371176.1
GI_41208742-S	115.4	134.4	130.4	LOC388552	XM_371178.1
GI_41208805-S	111.3	107.2	109	LOC162967	XM_371190.1
GI_41208814-S	97.8	88.9	86.5	LOC388561	XM_371192.1
GI_41208825-S	152.4	174.2	171.3	LOC388563	XM_373811.1
GI_41208836-S	117	128.5	130.8	LOC388565	XM_371197.1
GI_41208856-S	98.5	86.6	83	LOC388567	XM_371200.1
GI_41208888-S	87.1	74.6	85.8	LOC390939	XM_372731.1
GI_41208923-S	155.1	176.6	148.6	LOC390971	XM_372746.1
GI_41208928-S	90.9	107.4	86.6	LOC390974	XM_372748.1
GI_41208930-S	120.7	135.3	134	LOC390975	XM_372749.1
GI_41208933-S	134.2	116.9	114.7	LOC390976	XM_372750.1
GI_41208936-S	92.3	109.2	100.6	LOC390977	XM_372751.1
GI_41208941-S	126.9	132.2	132.8	LOC390980	XM_372753.1

GI_41209284-S	392.8	464.9	414.1	LOC391241	XM_372864.1				
GI_41209794-S	153.4	197.5	296	LOC150221	XM_036942.3				
GI_41209810-S	106.4	119.3	106.3	LOC388885	XM_373949.1				
GI_41209837-S	108.8	100.2	99.2	LOC388890	XM_373953.1				
GI_41209858-S	84.8	89.4	79.1	LOC388897	XM_373957.1				
GI_41209895-S	227.3	250.9	230.7	LOC391304	XM_372892.1				
GI_41209901-S	139	151.1	141.8	LOC391306	XM_372894.1				
GI_41209910-S	143.2	188.9	155.7	LOC391328	XM_372901.1				
GI_41210305-S	97.2	118.9	101.3	LOC392517	XM_373362.1				
GI_41222100-S	1515.8	1754.5	2234.1	KIAA0877	XM_371891.1				
GI_41222114-S	413.8	349.4	269.5	DKFZp761I21	XM_371897.1				
GI_41222645-S	146.6	167.1	157.4	LOC389790	XM_372141.1				
GI_41222683-S	237.9	311.2	297.6	LOC392379	XM_373309.1				
GI_41222688-S	148.7	159.7	149.8	LOC392382	XM_373311.1				
GI_41222707-S	141.1	156.5	141.7	LOC392389	XM_373314.1				
GI_41222827-S	275	360.5	281	LOC388399	XM_371066.1				
GI_41222833-S	91.2	104.6	98.2	LOC388402	XM_371069.1				
GI_41222839-S	94.2	123.1	103.4	LOC388403	XM_371070.1				
GI_41222851-S	671.9	662.6	829.5	DKFZP564D1	XM_371074.1				
GI_41281366-S	450.2	697.3	878.4	EXTL3	NM_001440.2	REG;RPR;EXTR1;KIAA0519	tumor	endoplas	cell growth
GI_41281370-S	1853.5	1521.3	1260.3	FDPS	NM_002004.2	FPS	geranyltra		cholestero
GI_41281375-S	517.1	565.7	597.5	USP8	NM_005154.2	UBPY;HumORF8;KIAA0055	ubiquitin-		deubiquiti
GI_41281383-S	8488.5	8114.8	5612	NEDD5	NM_004404.2	DIFF6;SEPT2;hNedd5;KIAA0158	GTPase	contractile	cytokinesi
GI_41281385-S	124	170.5	113.7	HA-1	NM_012292.1	HLA-HA1;KIAA0223			intracellula
GI_41281388-S	279.1	185.4	97.5	NRCAM	NM_005010.2	KIAA0343	tumor	integral to	cell
GI_41281392-S	397.4	497	452	SETDB1	NM_012432.2	ESET;KG1T;KIAA0067	methyltran	kinesin	oncogene
GI_41281397-S	730.8	812.4	735.7	SHOC2	NM_007373.2	SOC2;SUR8;SOC-2;SUR-	molecular	cytoplasm	FGF
GI_41281402-S	89.5	87.1	75.8	RAPGEF5	NM_012294.2	GFR;REPAC;MR-GEF;KIAA0277	guanyl-	nucleus	small
GI_41281407-S	849.2	991.1	724.9	SH2BP1	NM_014633.2	TSBP;p150TSP;KIAA0155	DNA	nucleus	regulation
GI_41281417-S	1694.9	1486	1209.7	MICAL2	NM_014632.2	KIAA0750	monooxyg		electron
GI_41281419-S	391.8	321.5	446.1	KIAA0377	NM_014659.2		acid		
GI_41281422-S	1300.9	1463.4	1125.8	KIAA0372	NM_014639.2				protein
GI_41281428-S	4720.7	5257.1	5192	BZW1	NM_014670.2	BZAP45;KIAA0005			
GI_41281432-S	222.7	269	230.2	ECE2	NM_014693.2	KIAA0604	zinc ion	integral to	regulation
GI_41281436-S	1757.3	1629.7	1629.8	KIAA0095	NM_014669.2	MGC21106			
GI_41281440-S	151.4	176.9	182.2	KIAA0296	NM_014699.2		DNA	nucleus	regulation
GI_41281443-S	146.4	132.4	119	RIMS2	NM_014677.2	OBOE;RIM2;RAB3IP3;KIAA0751	protein		intracellula
GI_41281446-S	343.1	433.1	347.4	KIAA0590	NM_014714.2				
GI_41281449-S	286.4	340.6	314.7	KIAA0605	NM_014694.2				
GI_41281452-S	444.9	466.6	446.8	SLK	NM_014720.2	KIAA0204	nuclease		nucleotide-
GI_41281455-S	336.3	376.4	329.8	Rab11-FIP3	NM_014700.2	KIAA0665	calcium		
GI_41281456-S	249.7	322.5	303.4	KIAA0247	NM_014734.2			integral to	
GI_41281459-S	238.1	285.2	227.9	CENTB1	NM_014716.2	ACAP1;KIAA0050	phospholi	nucleus	intracellula
GI_41281461-S	289.5	367	382.1	KIAA0652	NM_014741.2				

GI_41281465-S	119.4	117.3	109.4	ZFYVE16	NM_014733.2	ENDOFIN;KIAA0305	zinc ion		
GI_41281468-S	287.3	303.2	309.6	KIAA0586	NM_014749.2				
GI_41281472-S	234.3	257	276.9	KIAA0195	NM_014738.2		ATP	membran	cation
GI_41281475-S	98.8	100.6	93.4	PHYHIP	NM_014759.2	PAHX-AP;KIAA0273			
GI_41281478-S	1588.6	1807.8	2308.9	TM9SF4	NM_014742.2	KIAA0255	transporte	integral to	transport
GI_41281480-S	1368	1874.7	2430.7	DAZAP2	NM_014764.2	MGC766;KIAA0058;MGC14319	transporte	membran	transport
GI_41281482-S	2045.4	1896.6	1914.5	BMS1L	NM_014753.2	KIAA0187	ATP	nucleus	ribosome
GI_41281484-S	536.8	412.9	425	KIAA0141	NM_014773.2				
GI_41281488-S	2120.2	2044.7	1899.6	KIAA0174	NM_014761.2				
GI_41281490-S	759.8	806.2	995.1	MELK	NM_014791.2	KIAA0175	protein-		protein
GI_41281493-S	252.7	313.3	268.5	CENTG1	NM_014770.2	PIKE;AGAP2;GGAP2;KIAA0167	GTPase	nucleus	signal
GI_41281495-S	232.1	226.9	199.9	THRAP4	NM_014815.2	DRIP100;TRAP100;KIAA0130	ATP	mediator	regulation
GI_41281508-S	139.7	121	114.3	SV2B	NM_014848.2	HsT19680;KIAA0735	transporte	integral to	transport
GI_41281511-S	2470.9	2164.2	1891.1	PJA2	NM_014819.2	RNF131;KIAA0438;Neurodap1	N-		DNA
GI_41281514-S	353.5	645.9	425	ARNT2	NM_014862.2	KIAA0307	aryl	nucleus	response
GI_41281517-S	1860.8	2233.1	2357.1	KIAA0196	NM_014846.2				
GI_41281520-S	856.1	1056.3	1020.9	CNAP1	NM_014865.2	KIAA0159	histone	nucleus	mitotic
GI_41281526-S	634.4	767.4	644.6	USP52	NM_014871.2	PAN2;KIAA0710	exonuclea	intracellula	ubiquitin-
GI_41281529-S	1796.6	2223.7	2565.2	FAM20B	NM_014864.2	KIAA0475			
GI_41281534-S	90.8	84.2	91.3	GPR105	NM_014879.2	KIAA0001	rhodopsin-	integral to	G-protein
GI_41281538-S	1783.1	1603.8	892.6	RHOBTB3	NM_014899.2	KIAA0878	Rho small	intracellula	biological_
GI_41281541-S	381	240.5	265.1	COBLL1	NM_014900.2	KIAA0977			
GI_41281547-S	830.4	1010.8	1324.9	TMEM15	NM_014908.2	KIAA1094		integral to	
GI_41281554-S	179.1	165.9	215	CENTG2	NM_014914.2	AGAP1;GGAP1;KIAA1099	small	nucleus	small
GI_41281556-S	587.1	720.9	727.4	LPHN1	NM_014921.2	LEC2;CIRL1;FLJ11939;KIAA0821	sugar	integral to	neuropepti
GI_41281560-S	6053.8	6946.3	6336	CLSTN1	NM_014944.2	CSTN1;KIAA0911	calcium	integral to	homophili
GI_41281563-S	213.8	240.9	233	KIAA0982	NM_014023.2				
GI_41281570-S	213.9	159.8	177.3	SSX2IP	NM_014021.2	ADIP;KIAA0923			
GI_41281572-S	550.6	625.2	772.2	BAHD1	NM_014952.2	KIAA0945	DNA		
GI_41281576-S	161.7	188.5	196.6	RIPX	NM_014961.2	KIAA0871			
GI_41281578-S	530.8	603.8	487.1	SACM1L	NM_014016.2	SAC1;KIAA0851			
GI_41281582-S	123.3	138.4	135.4	KIAA0433	NM_015216.2		acid		
GI_41281590-S	861.7	780.5	963.3	MBNL1	NM_021038.2	EXP;MBNL;EXP35;EXP40;EXP42;KIAA0428	RNA	nucleus	
GI_41281598-S	321.7	383.3	347.1	SMA4	NM_021652.1		molecular	cellular_co	carbohydr
GI_41281602-S	113	112.8	111.2	IMUP	NM_033520.1	H2RSP			
GI_41281611-S	989.7	761.7	705	C13orf8	NM_032436.1	FLJ90413;KIAA1802			
GI_41281652-I	171.5	200.5	187.4	GTPBP3	NM_133644.1	MSS1;MTGP1;THDF1;GTPBG3;FLJ14700	GTPase		tRNA
GI_41281667-S	420.7	440.2	424.4	SP2	NM_003110.4	KIAA0048	RNA		regulation
GI_41281671-I	93.8	101.3	97.2	TSAP6	NM_138637.1	FLJ10829			
GI_41281674-I	160.2	176.9	177.6	MPPE1	NM_138608.1	FLJ11585			
GI_41281682-I	102.6	107.6	103.3	DAB2IP	NM_138709.1	AF9Q34;DIP1/2;KIAA1743			
GI_41281684-I	119	125.3	113.5	GNAO1	NM_138736.1	GNAO;G-ALPHA-o	heterotrim	peripheral	axon
GI_41281694-S	100.4	95.4	102.5	OLIG1	NM_138983.1	BHLHB6	DNA	nucleus	regulation
GI_41281708-I	135.6	166.3	143.9	TA-NFKBH	NM_139239.1	MGC11314			

GI_41281711-I	142.8	166.5	161	PQBP1	NM_144494.1	SHS;MRX55;NPW38	transcripti	nucleus	regulation
GI_41281724-I	160.4	167.5	164	PJA1	NM_145119.1	RNF70;FLJ11830	ligase		
GI_41281739-I	80.5	87.1	78.4	COG4	NM_145818.1	COD1;DKFZp586E1519			
GI_41281748-I	157.9	417.5	219.2	ZNF323	NM_145909.1	FLJ23407	transcripti	nucleus	regulation
GI_41281752-I	128.4	150.3	140.5	NEK11	NM_145910.1	FLJ23495	protein-		protein
GI_41281777-I	171.5	202.2	175.8	ZNF268	NM_152943.1	HZF3	transcripti	nucleus	developm
GI_41281781-I	165.4	182.1	165.4	SPPL2B	NM_152988.1	IMP4;PSL1;KIAA1532	peptidase	integral to	proteolysis
GI_41281787-I	117.7	136.2	115.5	MINA	NM_153182.1	MDIG;MINA53;FLJ14393			
GI_41281793-I	114.5	113.6	112.4	PMCHL2	NM_153381.1		molecular	cellular_co	synaptic
GI_41281797-I	165.6	178.8	149.8	MAP3K7IP1	NM_153497.1	TAB1	transformi		activation
GI_41281804-I	105.2	110.9	109.7	RGS20	NM_170587.1	RGSZ1;ZGAP1	protein	peripheral	regulation
GI_41281807-I	217.2	258.6	235.4	USH1C	NM_153676.1	AIE-75;DFNB18;PDZ-45;PDZ-	protein	cellular_co	intracellula
GI_41281816-I	208.6	248.2	242	EIF2B4	NM_172195.1	EIF2B;EIF-2B;EIF2Bdelta;DKFZP586J0119	translation	eukaryotic	translation
GI_41281820-I	373.9	472	422.3	SH2D3C	NM_170600.1	CHAT;NSP3	SH3/SH2		JNK
GI_41281830-I	99.1	98.2	88.4	NPAS3	NM_173159.1	MOP6			
GI_41281845-I	102.5	101.5	94.6	CLCN3	NM_173872.1	CLC3	voltage-	integral to	small
GI_41281873-I	918.2	616.2	666.2	ELYS	NM_175865.1	TMBS62;DKFZp434N093	structural	microtubul	microtubul
GI_41281881-I	94.3	100.4	93.3	ADAMTS20	NM_175851.1		zinc ion	extracellul	proteolysis
GI_41281884-S	6528.3	7140.3	7089.1	HSPC051	NM_013387.2	UCRC;HSPC119			
GI_41281894-I	125.6	141.1	131.2	LMX1A	NM_177399.1	LMX1;LMX-1;LMX1.1	transcripti	nucleus	regulation
GI_41281901-I	104.8	108.8	114.9	STARD13	NM_178008.1	DLC2;GT650;4902678	GTPase		
GI_41281906-I	150.9	168.1	173.1	STARD13	NM_178007.1	DLC2;GT650;4902678	GTPase		
GI_41281910-I	125.8	124	109.4	C3orf6	NM_178335.1				
GI_41281932-I	137.4	134.3	139.5	PACE-1	NM_181093.1	PACE1	ATP		protein
GI_41281936-I	570.3	805.7	382.1	NCAM1	NM_181351.1	CD56;NCAM;MSK39	cell	integral to	synaptic
GI_41281950-I	381.1	401.5	366.8	SUPT3H	NM_181356.1	SPT3;SPT3L	RNA	transcripti	regulation
GI_41281953-S	5251.8	3021.2	3626.1	GNPDA1	NM_005471.3	GPI;HLN;GNPI;GNPDA;KIAA0060	glucosami		glucosami
GI_41281973-I	126.4	121.1	125.8	TSAP6	NM_182915.1	FLJ10829			
GI_41281980-I	2100.2	1700.4	1794.6	TRIF	NM_182919.1	TICAM1;PRVTIRB;MGC35334	transmem	membran	
GI_41281983-I	128.6	129.4	142	TSGA10	NM_182911.1		porin	mitochond	
GI_41281986-I	109.4	96.9	117.2	SYNE1	NM_182961.1	8B;CPG2;MYNE1;MYNE-1;SYNE-1;SYNE-	lamin	nuclear	Golgi
GI_41281989-I	581.5	481	424.8	TRNT1	NM_182916.1	CCA1;MtCCA;CGI-47	nucleotide	mitochond	tRNA
GI_41281992-I	134.3	149.8	143.6	SOC	NM_183008.1				
GI_41281995-I	228.9	236.2	233	FLJ20718	NM_182922.1				
GI_41282001-I	120.6	116.6	122.7	SPHK1	NM_182965.1	SPHK	diacylglyc	cytosol	sphingosin
GI_41282018-I	99.4	93.3	94.8	NRAP	NM_198060.1		structural	actin	actin
GI_41282073-I	97.9	110.3	100.7	HTR4	NM_199453.1		serotonin	integral to	G-protein
GI_41282212-S	81.1	80.2	84.8	UGT1A7	NM_019077.2	UGT1G	UDP-	extracellul	metabolis
GI_41282220-S	367.7	409.8	306.7	PPP1R15B	NM_032833.2	FLJ14744			
GI_41282228-S	118.6	125.7	119.4	UGT1A3	NM_019093.2	UGT1C	UDP-	microsom	metabolis
GI_41282232-S	187	214.3	175.8	DEPDC1	NM_017779.3	DEP.8;SDP35;FLJ20354			intracellula
GI_41282244-I	117.7	141.8	129.1	CASC2	NM_201377.1				
GI_41282247-S	1433.9	1389.6	1116.6	ZBED1	NM_004729.2	TRAMP;KIAA0785	transposa	nuclear	
GI_41322907-I	143.9	152.8	128.7	PLEC1	NM_201379.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet

GI_41322909-I	184.5	220.2	175.6	PLEC1	NM_201381.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet
GI_41322911-I	111.1	134.2	124.6	PLEC1	NM_201378.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet
GI_41322913-I	137.7	148.3	160.1	PLEC1	NM_201383.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet
GI_41322915-I	100	108.6	99.1	PLEC1	NM_201380.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet
GI_41322918-I	296.1	344.4	319.9	PLEC1	NM_201382.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet
GI_41322922-I	90.2	103.4	91.1	PLEC1	NM_201384.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet
GI_41327153-S	525.7	633.8	585.3	OBRGRP	NM_017526.2		molecular	integral to	biological_
GI_41327154-S	186.2	220.2	204.1	EPAS1	NM_001430.3	MOP2;HIF2A	transcripti	nucleus	signal
GI_41327157-S	148.9	1972.8	143.1	ARHGAP4	NM_001666.2	C1;RGC1;RhoGAP4;KIAA0131	SH3/SH2	peripheral	regulation
GI_41327682-S	117.1	110	100.2	CORT	NM_001302.2	CST-14;CST-17;CST-29;MGC32686	neuropepti	soluble	G-protein
GI_41327684-S	362.6	453.3	483.6	C20orf44	NM_018244.3	BFZB			
GI_41327690-I	153	182.6	182.8	C20orf23	NM_024704.3	SNX23;KISC20ORF			
GI_41327692-S	2648.2	3828.9	4159.7	C20orf24	NM_018840.2	RIP5;PNAS-11			
GI_41327699-S	188.8	167.7	171.2	CORT	NM_198544.2	CST-14;CST-17;CST-29;MGC32686	neuropepti	soluble	G-protein
GI_41327706-S	126.6	123.9	130.1	CRB1	NM_012076.2	RP12	calcium		establish
GI_41327709-A	944.7	1148.8	971.5	CRK	NM_005206.3	CRKII	SH3/SH2	cytoplasm	actin
GI_41327711-I	317.3	338.5	287.9	CRK	NM_016823.2	CRKII	SH3/SH2	cytoplasm	actin
GI_41327713-S	2027.6	2525	1173.1	C20orf3	NM_020531.2	BSCv;APMAP;C20ORF2	molecular	integral to	biological_
GI_41327714-S	172.2	183.7	214.6	C20orf64	NM_033550.3	PRPK;Nori-2;Nori-2p	protein-	nucleus	protein
GI_41327716-S	176.5	213.7	267.4	C20orf67	NM_022104.3	PCIF1			
GI_41327717-S	16129	4429.8	3035.1	C20orf97	NM_021158.3	NIPK;SINK;TRB3;SKIP3;TRIB3	ATP		protein
GI_41327718-S	106.2	117.7	115.8	CAMK1G	NM_020439.2	VWS1;CLICKIII;dJ272L16.1	ATP		protein
GI_41327719-S	213.6	255.7	243.1	CAP2	NM_006366.2			membran	establish
GI_41327720-S	211.3	208.9	217.6	CAPN7	NM_014296.2	PALBH;CALPAIN7	calpain	intracellula	proteolysis
GI_41327721-S	459.9	536	465.1	CAPZA2	NM_006136.2	CAPZ;CAPPA2	actin	F-actin	cell
GI_41327725-S	267.7	315	273.2	CHRNB1	NM_000747.2	ACHRB;CHRNB	acetylcholi	integral to	synaptic
GI_41327727-S	183.9	253.9	232.5	CLTC	NM_004859.2	CLH-17;CLTCL2;KIAA0034	structural	coated pit	intracellula
GI_41327728-S	710.7	903.5	799.6	CNN2	NM_004368.2		actin	cytoskelet	cytoskelet
GI_41327731-I	106	122.5	113.4	EGFR	NM_201282.1	ERBB;ERBB1	epidermal	endosome	EGF
GI_41327733-I	90.7	100.2	90.2	EGFR	NM_201283.1	ERBB;ERBB1	epidermal	endosome	EGF
GI_41327735-I	304.9	383.6	331.7	EGFR	NM_201284.1	ERBB;ERBB1	epidermal	endosome	EGF
GI_41327737-I	264.7	217.5	235	EGFR	NM_005228.3	ERBB;ERBB1	epidermal	endosome	EGF
GI_41327738-I	214.2	252.8	230.8	EPN2	NM_014964.3	EHB21;KIAA1065			
GI_41327739-A	276.8	247.3	230.5	EPN2	NM_148921.2	EHB21;KIAA1065			
GI_41327740-S	957.4	1067.3	1384.2	ETHE1	NM_014297.3	HSCO;YF13H12			
GI_41327742-S	107.1	117.4	112.6	KCNJ12	NM_021012.3	IRK2;hIRK;KCNJN1;Kir2.2;Kir2.2v	inward	membran	potassium
GI_41327743-S	164.2	180.9	177.5	KIF1A	NM_004321.4	ATSV;UNC104;HUNC-104	motor	kinesin	anterogra
GI_41327744-S	606.3	522.1	588.2	KNTC1	NM_014708.3	ROD;KIAA0166	protein	kinetochor	mitotic
GI_41327747-S	573.4	694.8	653.4	ANAPC2	NM_013366.3	APC2	ubiquitin-		cyclin
GI_41327748-S	760.7	670	505	ANAPC4	NM_013367.2	APC4	ubiquitin-	anaphase-	mitotic
GI_41327750-S	108.5	116.6	106.4	ANGPTL3	NM_014495.2	ANGPT5		kinesin	
GI_41327751-S	107.3	116.6	105	ANKRD23	NM_144994.6	DARP;MARP3;FLJ32449			
GI_41327753-S	122.6	272.2	246.3	ANKRD3	NM_020639.2	DIK;PKK;RIP4;ANKK2	protein-		protein
GI_41327755-S	116.2	109.8	95	ADAMTS4	NM_005099.3	ADMP-1;ADAMTS-2;ADAMTS-4;KIAA0688	metallope	extracellul	proteolysis

GI_41327757-S	282.4	309.8	242.7	ADCY7	NM_001114.2	KIAA0037	calcium/ca	integral to	signal
GI_41327758-S	10609.3	11546	8585	ATP5O	NM_001697.2	ATPO;OSCP	hydrogen-	proton-	proton
GI_41327759-S	330.5	386.5	393	ATP9B	NM_198531.3	NEO1L;ATPIIB;ATPASEP;FLJ46612;HUSSY-	ATP	integral to	aminopho
GI_41327761-S	207.1	230.3	195.2	ABCA8	NM_007168.2	KIAA0822	nucleotide	membran	transport
GI_41327762-S	203.7	234	245.8	AGPAT3	NM_020132.3	MGC4604;LPAAT-GAMMA1			
GI_41327763-S	3964.5	3928.1	4629.2	AKR7A2	NM_003689.2	AFAR;AKR7;AFAR1;AFB1-AR1	aldehyde	Golgi	aldehyde
GI_41327765-A	828.5	629.2	491.1	ALEX2	NM_014782.4	MGC8742;KIAA0512;MGC13343			
GI_41327766-S	735.7	807.6	602.5	ARF4L	NM_001661.2	ARL6	ARF small	nucleus	protein
GI_41327768-S	729.4	851.1	659.4	ARHGEF18	NM_015318.2	KIAA0521;MGC15913			
GI_41327770-S	963.9	1197.2	1239	DDX23	NM_004818.2	prp28;MGC8416;U5-100K	ATP	nucleus	mRNA
GI_41327772-S	735.1	857.9	820.2	DDX46	NM_014829.2	MGC9936;FLJ25329;KIAA0801	nucleic	nucleus	regulation
GI_41327774-S	3160.3	3912.6	2756.4	DDX47	NM_016355.3	E4-			
GI_41327778-S	799.4	772	745.3	DDX55	NM_020936.1	KIAA1595;MGC33209	nucleic		
GI_41327784-I	188.4	228.6	212.3	DKFZP564J0	NM_199073.1	MGC10527		nucleus	
GI_41327786-I	89.2	108.8	93.3	DKFZP564J0	NM_199074.1	MGC10527		nucleus	
GI_41327788-I	167.8	185.5	161.5	DKFZP564J0	NM_199417.1	MGC10527		nucleus	
GI_41349433-S	159.8	175.6	170.1	BAAT	NM_001701.2	BAT;BACAT	acyltransf	cytosol	glycine
GI_41349434-S	213.4	227.7	218.9	BET1	NM_005868.3	hbet1	protein	Golgi	ER to
GI_41349435-S	1006.9	799.3	706.2	BIRC2	NM_001166.3	API1;MIHB;CIAP1;HIAP2;RNF48	apoptosis	intracellula	cell
GI_41349436-S	344.8	487.5	451.6	BMPR1A	NM_004329.2	ALK3;ACVRLK3	cAMP-	integral to	transformi
GI_41349438-I	186.7	232.7	153.7	SEC31L1	NM_014933.2	ABP125;ABP130;SEC31A;HSPC275;HSPC3			
GI_41349440-A	2292.4	2787	1673	SEC31L1	NM_016211.2	ABP125;ABP130;SEC31A;HSPC275;HSPC3			
GI_41349442-S	88.1	95.6	99.2	SLICK	NM_198503.2	SLO2.1			
GI_41349444-A	916.6	1273.9	1449.3	SOCS5	NM_014011.4	CIS6;CISH6;Cish5;SOCS-5;KIAA0671	protein	cytoplasm	JAK-STAT
GI_41349444-I	322	381.8	331.3	SOCS5	NM_014011.4	CIS6;CISH6;Cish5;SOCS-5;KIAA0671	protein	cytoplasm	JAK-STAT
GI_41349445-I	94.6	98.4	85.2	SOCS5	NM_144949.2	CIS6;CISH6;Cish5;SOCS-5;KIAA0671	protein	cytoplasm	JAK-STAT
GI_41349447-S	301.5	368.5	320.3	PREB	NM_013388.4	SEC12;MGC3467	transcripti	nucleus	regulation
GI_41349448-A	1155.5	1297.3	1318.4	PREI3	NM_015387.2	2C4D;CGI-95;MGC12264;MOB1;MOB3			
GI_41349450-I	112.2	110.3	104.9	PREI3	NM_199482.1	2C4D;CGI-95;MGC12264;MOB1;MOB3			
GI_41349452-S	99.1	113.5	96.8	PRELP	NM_002725.3	SLRR2A;MGC45323	extracellul	extracellul	skeletal
GI_41349455-S	860.2	1241.4	1233.1	PREP	NM_002726.3	PE;PEP;MGC16060	prolyl	cytoplasm	proteolysis
GI_41349457-S	269	283	249	PRDM10	NM_020228.2	KIAA1231;PFM7	DNA	nucleus	regulation
GI_41349465-S	227.3	320.5	285.8	PRDM11	NM_020229.2	PFM8			
GI_41349467-S	139.6	161.9	141.7	PRDM13	NM_021620.2	MU-MB-20.220;PFM10	DNA	nucleus	regulation
GI_41349469-S	84.7	103.5	102.6	PRDM16	NM_022114.2	MEL1;KIAA1675;PFM13	transcripti	nucleus	regulation
GI_41349473-S	1975.1	1453.8	1449.4	PRDM4	NM_012406.3	PFM1;MGC45046	RNA	nucleus	signal
GI_41349475-S	101.2	96.5	99.4	PRDM5	NM_018699.2	PFM2	DNA	nucleus	regulation
GI_41349477-S	176	219.2	196.9	PRDM7	NM_052996.2	PFM4	DNA	nucleus	regulation
GI_41349481-S	255.1	318	300	PRB1	NM_005039.2	PM;PMF;PMS		extracellul	
GI_41349487-S	230.5	263.2	239.3	PRB3	NM_006249.3	G1;PRG			
GI_41349489-S	199.6	256.8	233.8	PRB4	NM_002723.3	Po	rhodopsin-	integral to	G-protein
GI_41349490-I	164.2	175.4	156.7	PR48	NM_199326.1	B";PP2A;NY-REN-8	protein	nucleus	cell cycle
GI_41349492-A	702.5	421.4	493.1	PR48	NM_013239.3	B";PP2A;NY-REN-8	protein	nucleus	cell cycle
GI_41349493-S	744.5	625.8	736.9	PRIM1	NM_000946.2	p49;MGC12308	DNA	alpha	DNA

GI_41349494-S	846.9	769.5	834.1	PRIM2A	NM_000947.2	p58;PRIM2;MGC75142	DNA	alpha	DNA
GI_41349496-S	161	170.5	163.1	PDP2	NM_020786.1	KIAA1348	protein	mitochond	protein
GI_41349498-S	115.4	121.1	110.5	PLP1	NM_000533.3	PLP;PMD;MMPL;SPG2;PLP/DM20	structural	integral to	nerve
GI_41349503-S	184.9	190.5	164	GPR146	NM_138445.2	PGR8	rhodopsin-	integral to	G-protein
GI_41349504-S	605.9	673.3	838.4	MGC19780	NM_144988.2				
GI_41349679-S	319.9	431.8	387.7	FLJ25224	NM_182495.3				
GI_41349931-S	133	144	131.1	DUB3	NM_201402.1				
GI_41350194-S	1108.6	1357	1140.2	RB1CC1	NM_014781.3	CC1;DRAGOU14;KIAA0203			
GI_41350195-S	4677.2	5671.4	3897.4	RAB1A	NM_004161.3	RAB1;DKFZP564B163	RAB small	Golgi	vesicle-
GI_41350196-S	303.9	420.8	342.4	FATE	NM_033085.2			integral to	
GI_41350197-S	385.4	393.6	453.7	FGIF	NM_017704.2	FLJ20189			
GI_41350199-S	111.9	123.8	124.1	EAF2	NM_018456.4	BM040;TRAITS			
GI_41350200-S	530.6	602.6	561.7	EPN1	NM_013333.2			coated	endocytosi
GI_41350202-S	109.7	126.8	106.9	DAT1	NM_018640.3				
GI_41350203-S	1745.7	1355.7	1616.6	DCXR	NM_016286.2	DCR;P34H;KIDCR	oxidoredu		metabolis
GI_41350204-S	1274.3	1795.1	1451.1	CRIPT	NM_014171.3	HSPC139			
GI_41350205-S	174.9	195	199.4	CNNM4	NM_020184.2	ACDP4;KIAA1592			
GI_41350207-S	159.2	222	181.3	CASC1	NM_018272.2	LAS1;FLJ10921			
GI_41350209-S	102.2	114.9	95.7	BCDO2	NM_031938.2	B-DIOX-II	oxidoredu		
GI_41350211-S	699	822.8	807	BRD7	NM_013263.2	BP75;NAG4;CELTIX1		cytoplasm	
GI_41350213-S	97.3	108.6	89.2	ASPN	NM_017680.3	PLAP1;SLRR1C;FLJ20129		extracellul	
GI_41350215-S	695.6	822.8	1022.1	ALG1	NM_019109.3	HMAT1;HMT-1	mannosylt	endoplas	lipopolysa
GI_41350303-I	97.9	104.8	102.8	NRXN3	NM_004796.3	KIAA0743	receptor	integral to	axon
GI_41350304-A	125.6	138.4	124.6	NRXN3	NM_138970.2	KIAA0743	receptor	integral to	axon
GI_41350306-I	369.5	487.2	417	NALP1	NM_014922.3	CARD7;DEFCAP;PP1044;KIAA0926;DEFCA			
GI_41350309-A	182.1	187.1	147.6	NALP1	NM_033007.2	CARD7;DEFCAP;PP1044;KIAA0926;DEFCA			
GI_41350315-I	130.2	134.4	127.5	MTMR2	NM_201278.1	CMT4B;CMT4B1;KIAA1073	protein	cellular_co	protein
GI_41350319-I	95.8	94.5	92.2	MAGED2	NM_201222.1	11B6;BCG1;HCA10;JCL-1;MAGED;MAGE-			
GI_41350321-S	371.4	434.8	337.3	MAML1	NM_014757.3	Mam1;Mam-1;KIAA0200			
GI_41350322-I	1273.7	1842.8	1266.9	MAPK8IP3	NM_033392.3	JIP3;SYD2;JSAP1;FLJ00027;KIAA1066	kinesin	kinesin	vesicle-
GI_41350324-A	93.5	93.8	89.1	MAPK8IP3	NM_015133.2	JIP3;SYD2;JSAP1;FLJ00027;KIAA1066	kinesin	kinesin	vesicle-
GI_41350325-S	1924	2536.5	2587.2	MBTPS1	NM_003791.2	S1P;PCSK8;SKI-1;KIAA0091	serine-	endoplas	proteolysis
GI_41350328-S	315	330.1	359.6	MFN2	NM_014874.2	MARF;CPRP1;KIAA0214			
GI_41350329-S	240.8	188.5	149.5	MOBKL2B	NM_024761.3	MOB3B;FLJ13204;MGC32960			
GI_41350331-S	195.4	222.8	203.8	MOB	NM_147156.3	MGC17342			
GI_41350332-S	2161.6	2171.2	2405.3	TBCD	NM_005993.3	KIAA0988	co-	microtubul	beta-
GI_41350334-S	89.1	101.1	113.2	TCEA3	NM_003196.1	TFIIS.H	transcripti	nucleus	transcripti
GI_41350336-S	87.2	81.9	87.3	TLR1	NM_003263.3	TIL;rsc786;KIAA0012;DKFZp547I0610;DKFZ	antibacteri	integral to	signal
GI_41351543-I	102.7	101.7	106.8	CREB5	NM_182899.2	CRE-BPA	transcripti	nucleus	transcripti
GI_41352060-I	190.9	230.9	234.6	PITRM1	NM_014889.2	MP1;hMP1;KIAA1104	pitrilysin		proteolysis
GI_41352062-S	4305.9	6027.6	4960.6	PFKP	NM_002627.3	PFKF;PFK-C	magnesiu	6-	glycolysis
GI_41352689-S	365.2	348.4	368.8	LARS2	NM_015340.3	LEURS;KIAA0028;MGC26121	ATP	mitochond	leucyl-
GI_41352690-S	1209.4	1844.3	1478.3	LAPTM4A	NM_014713.3	MBNT;Mtrp;LAPTM4;HUMORF13;KIAA0108		integral to	transport
GI_41352692-S	237.9	311.8	252.3	IREB2	NM_004136.1	IRP2;IRP2AD	RNA	cytosol	RNA

GI_41352694-S	114.3	105.6	127.3	FGF2	NM_002006.3	BFGF;FGFB;HBGH-2	fibroblast	extracellul	activation
GI_41352696-S	187.3	220.5	208.6	FSHPRH1	NM_006733.2	CENPI;LRPR1			female
GI_41352698-S	328.3	388.6	331.9	WARS2	NM_015836.2	TrpRS	tryptophan-	soluble	protein
GI_41352701-S	2301.9	2049.3	2247.7	DPH2L2	NM_001384.3	DPH2			
GI_41352704-S	237.1	238.5	250.9	KIF3C	NM_002254.5		motor	kinesin	nonselecti
GI_41352706-S	112.4	130.2	103.3	OCLM	NM_022375.2	TISR			mechanos
GI_41352707-I	401.8	467.5	444.2	ARGBP2	NM_021069.2	KIAA0777	cytoskelet	actin	
GI_41352708-A	430.2	631.1	336.3	ARGBP2	NM_003603.3	KIAA0777	cytoskelet	actin	
GI_41352708-I	148.9	152.4	131.1	ARGBP2	NM_003603.3	KIAA0777	cytoskelet	actin	
GI_41352711-S	554.5	646.4	710.5	IKBKB	NM_001556.1	IKK2;IKKB;NFKBIKB;IKK-beta	ATP	cytoplasm	protein
GI_41352713-S	86.4	78.6	89.7	MYT1	NM_004535.2	MTF1;MYTI;PLPB1	zinc ion	nucleus	transcripti
GI_41352714-S	3413.2	3358.7	3188.2	VPS35	NM_018206.3	MEM3;FLJ10752;FLJ13588;FLJ20388;DKFZ	protein	cytosol	intracellula
GI_41352715-S	121.1	116.3	112.4	D21S2056E	NM_003683.4	NNP-1;NOP52		nucleus	
GI_41352716-S	564.1	619.7	533.5	DD5	NM_015902.4	EDD;HYD;KIAA0896	ubiquitin	soluble	ubiquitin-
GI_41352717-S	130.4	139.7	106.8	DTX1	NM_004416.2		transcripti	cytoplasm	cell
GI_41352719-S	96.6	105.5	94.9	DLX5	NM_005221.4		transcripti	nucleus	skeletal
GI_41352720-S	119.2	125.5	126.6	SLC36A1	NM_078483.2	PAT1;LYAAT1	amino	membran	amino
GI_41387215-S	537.5	621.5	606.5	RGS5	NM_003617.2	MSTP032	GTPase	peripheral	regulation
GI_41393186-S	122.6	141	141	NOXA1	NM_006647.1	p51NOX;FLJ25475;NY-CO-31;SDCCAG31	tumor		
GI_41393543-S	112.1	128.3	113.3	TSP-NY	NM_032573.3	aaa			
GI_41393544-A	606.7	852.5	817.8	RAB5C	NM_004583.2	RABL;RAB5CL	RAB small		small
GI_41393546-S	870.6	877.1	721.1	NAG	NM_015909.2	DKFZP586G1219	molecular	ribosome	oncogene
GI_41393548-S	94.6	108.6	90.3	NUDT10	NM_153183.1	DIPP3a;hDIPP3alpha	hydrolase		
GI_41393550-S	492.1	631.3	603.5	NADSYN1	NM_018161.4	FLJ10631	ATP		nitrogen
GI_41393552-S	520.1	368.7	155.4	MGLL	NM_007283.4	MGL;HU-K5	lysophosp		lipid
GI_41393555-S	91.7	110.1	111	MANEA	NM_024641.2	FLJ12838			
GI_41393557-S	263.7	335.6	305.4	LUC7L	NM_018032.3	SR+89;LUC7B1;FLJ10231;LUC7-LIKE			
GI_41393558-I	247.4	325.6	145.3	KIF1B	NM_183416.2	KLP;CMT2;CMT2A;HMSNII;KIAA0591;KIAA1			
GI_41393560-S	1077.4	1234.6	1159.9	LAP3	NM_015907.2	LAP;PEPS;LAPEP	zinc ion	cytoplasm	proteolysis
GI_41393562-I	95.2	96.1	96.1	KIF1B	NM_015074.2	KLP;CMT2;CMT2A;HMSNII;KIAA0591;KIAA1			
GI_41393564-S	212.9	185.4	285.7	ITPK1	NM_014216.3	ITRPK1	catalytic		signal
GI_41393565-S	650	633.5	521.7	HIBADH	NM_152740.2	MGC40361	phosphogl	mitochond	pentose-
GI_41393566-S	91.8	85.3	82.5	IL22	NM_020525.4	IL21;TIFa;IL-21;IL-22;ILTIF;IL-TIF;IL-	cytokine	extracellul	immune
GI_41393567-S	1431.3	1745	1644.2	HEBP2	NM_014320.2	SOUL;C6orf34			
GI_41393568-S	93	118.9	106.2	HBP17	NM_005130.2	FGFBP;FGFBP1	heparin	extracellul	negative
GI_41393569-S	129.3	129.6	136.9	HDAC10	NM_032019.4	DKFZP761B039	hydrolase	nucleus	regulation
GI_41393571-S	1225.9	1175.3	1604.2	GMNN	NM_015895.3	Gem			negative
GI_41393572-S	489.8	547.2	509.1	GIT1	NM_014030.2		ARF	nucleus	regulation
GI_41393574-S	99	103.1	107.9	GK2	NM_033214.2	GKP2;GKTA	ATP	mitochond	carbohydr
GI_41393576-S	1457.8	1701.2	1309	GEMIN6	NM_024775.9	FLJ23459	pre-mRNA	spliceoso	spliceoso
GI_41393578-S	123	130.5	117.2	GIPC2	NM_017655.4	SEMCAP2;FLJ20075	protein		intracellula
GI_41393580-S	133.1	142.7	114.8	ETS1	NM_005238.2		RNA	nucleus	negative
GI_41393581-S	654.1	405.2	274.1	EGFL7	NM_016215.3	ZNEU1	calcium		
GI_41393584-S	115.2	109.8	110.2	DNASE1L2	NM_001374.2	DNAS1L2	deoxyribo		DNA

GI_41393585-A	294.2	450.7	273.7	DGKA	NM_001345.4	DAGK1;MGC12821;MGC42356;DGK-alpha	diacylglyc		intracellula
GI_41393588-S	137.3	133.4	181.9	ASAM	NM_024769.2	CLMP;FLJ22415			
GI_41393589-S	384.6	406.8	373.4	ASK	NM_006716.3	DBF4	enzyme	intracellula	G1/S
GI_41393590-S	1059.2	1210.9	1213.8	API5	NM_006595.2	AAC-11;API5L1	apoptosis		anti-
GI_41393591-S	1200.2	863.2	999.9	ADCK2	NM_052853.3	AARF;MGC20727			
GI_41393592-S	145.9	167.6	169.9	ADCK5	NM_174922.3	FLJ35454			
GI_41393594-S	195.8	187.9	209.4	CSMD1	NM_033225.3	KIAA1890	hydrolase		carbohydr
GI_41393596-S	298.9	354.9	306.8	CSAD	NM_015989.3	CSD;PCAP			
GI_41393600-A	347.9	1008.7	665.8	C1S	NM_001734.2		compleme		compleme
GI_41393601-I	109.5	160.1	131.4	C1S	NM_201442.1		compleme		compleme
GI_41393603-I	382.5	482.5	431.3	RTN3	NM_201429.1	ASYIP;NSPL2;NSPLII	molecular	endoplas	
GI_41393607-I	103.5	96.2	104.1	RTN3	NM_201428.1	ASYIP;NSPL2;NSPLII	molecular	endoplas	
GI_41393609-I	114.4	111.9	109.2	RASSF6	NM_201431.1				
GI_41393611-A	1824	1455.3	1434.8	RTN3	NM_006054.2	ASYIP;NSPL2;NSPLII	molecular	endoplas	
GI_41393612-A	127.2	139.7	124.9	RASSF6	NM_177532.3				
GI_41393613-I	293.5	368.2	309.2	RAB5C	NM_201434.1	RABL;RAB5CL	RAB small		small
GI_41393615-S	112.7	118.4	105.1	RAD9B	NM_152442.2	FLJ40346			
GI_41399283-A	7263.8	6876.1	6800.1	HSPD1	NM_002156.4	CPN60;GROEL;HSP60;SPG13;HuCHA60	ATP	mitochond	protein
GI_41399284-I	91.7	93.8	91.8	HSPD1	NM_199440.1	CPN60;GROEL;HSP60;SPG13;HuCHA60	ATP	mitochond	protein
GI_41406049-S	218.5	254.4	229.3	DOK2	NM_003974.2	p56DOK;p56dok-2	protein		cell
GI_41406053-S	2949.4	3031.2	3468.8	APP	NM_000484.2	AAA;AD1;PN2;ABPP;APPI;CVAP;ABETA;Pre	serine-	Golgi	copper ion
GI_41406060-I	125.8	116.1	124.6	MOBKL2C	NM_201403.1	MOB3C;MGC26743			
GI_41406062-S	194.1	225.3	193.2	MOBKL1A	NM_173468.2	MOB4A;MGC33910			
GI_41406063-S	1042.1	996.3	1398.9	MYH10	NM_005964.1	NMMHCB	actin	kinesin	cytokinesi
GI_41406065-A	1369.5	1960.2	1979.7	H2AV	NM_012412.3	MGC1947;MGC10170;MGC10831			
GI_41406065-I	2596.2	2703.1	2872.1	H2AV	NM_012412.3	MGC1947;MGC10170;MGC10831			
GI_41406075-A	129.8	150.5	150.9	GAS7	NM_003644.2	MGC1348;KIAA0394	transcripti	kinesin	cell cycle
GI_41406075-I	208.5	222.7	197.3	GAS7	NM_003644.2	MGC1348;KIAA0394	transcripti	kinesin	cell cycle
GI_41406077-I	143.5	175.7	179.4	GAS7	NM_201432.1	MGC1348;KIAA0394	transcripti	kinesin	cell cycle
GI_41406079-I	100.1	107.7	93.1	GAS7	NM_201433.1	MGC1348;KIAA0394	transcripti	kinesin	cell cycle
GI_41406081-I	116.8	137.3	133.5	GPX1	NM_201397.1	GSHPX1;MGC14399	glutathion		peroxidas
GI_41406085-S	98.2	117.4	101.2	SEMA3D	NM_152754.2	coll-2;Sema-Z2;MGC39708			developm
GI_41406088-S	438.8	543.1	576.2	SOX13	NM_005686.2	ICA12;Sox-13	transcripti	nucleus	embryoge
GI_41406090-S	121.8	165	138	SPG6	NM_144599.3	FSP3;NIPA1;MGC35570			
GI_41406092-I	217.7	400.9	248.1	JDP1	NM_021800.2		chaperone		protein
GI_41406093-I	167.1	237.2	167.3	JDP1	NM_201262.1		chaperone		protein
GI_41406095-S	333.6	361.7	308.6	DHX38	NM_014003.3	DDX38;PRP16;PRPF16;KIAA0224	nucleic	nucleus	mRNA
GI_41406096-S	1017.3	1124.1	951.8	DVL3	NM_004423.3	KIAA0208			heart
GI_41462405-S	104.5	125.9	121	FLJ26056	NM_201401.2				
GI_41462411-S	125.6	143.8	132	FLJ40217	NM_201520.1		binding	membran	transport
GI_41529827-S	342.3	418.2	396.6	SLC30A7	NM_133496.3	ZNT7;ZnTL2	cation	membran	cation
GI_41529828-S	307.2	279.1	307.4	MGC19604	NM_080665.3				
GI_41529833-S	158.2	178.3	173.1	C6orf170	NM_152730.3	FLJ30899;dJ310J6.1			
GI_41582235-S	111	102.9	104.7	LOC200030	NM_183372.2				

GI_41582237-A	87.2	86.9	80.7	ISLR	NM_005545.3	HsT17563	protein		cell
GI_41582238-I	267.9	289.9	287.5	ISLR	NM_201526.1	HsT17563	protein		cell
GI_41584199-S	469.1	1698.6	2027.2	GPR56	NM_005682.4	TM7LN4;TM7XN1	G-protein	membran	G-protein
GI_41584203-S	2171.3	2509.7	2414.1	GNPNAT1	NM_198066.2	GNPNAT;Gpnat1;FLJ10607	N-		
GI_41584204-S	2144.3	1956.4	1396.4	GMDS	NM_001500.2	GMD	GDP-		carbohydr
GI_41584205-S	87.5	87.5	88.3	GNGT1	NM_021955.2	GNG1	heterotrim	peripheral	signal
GI_41680634-S	273.1	344.1	300.8	LOC200008	NM_201546.1		oxidoredu		electron
GI_41680643-S	80	78.9	84.5	C4orf11	NM_201547.1				
GI_41680687-S	136.4	158.1	142.8	RP26	NM_201548.1	CERKL			
GI_41680693-S	129.9	167.8	163.2	HRLRRP	NM_201550.1				
GI_41871954-I	89.9	95	92.2	KNSL8	NM_201522.1	bA387M24.3			
GI_41871964-I	95.9	99.8	101.8	KNSL8	NM_138343.2	bA387M24.3			
GI_41872338-I	144.3	162.1	156.4	PPHLN1	NM_201438.1	HSPC206;HSPC232;MGC48786			
GI_41872353-I	189.4	245.1	181.9	PPHLN1	NM_016488.4	HSPC206;HSPC232;MGC48786			
GI_41872373-S	553	620.3	542.9	PLK3	NM_004073.2	CNK;FNK;PRK	protein		protein
GI_41872388-S	406.2	419.2	366	PP591	NM_025207.3	MGC31803;MGC40255			
GI_41872408-S	104.7	113.7	108.7	PPBP	NM_002704.2	PBP;TC1;TC2;TGB;LDGF;MDGF;TGB1;B-	glucose	extracellul	glucose
GI_41872428-S	680.1	931.5	975.2	TRPC4AP	NM_015638.2	TRUSS;TRRP4AP;C20orf188	peptide	endoplas	peptide
GI_41872447-A	246	268.2	241.6	ELK4	NM_001973.2	SAP1	transcripti	nucleus	transcripti
GI_41872447-I	286	340.4	316.8	ELK4	NM_001973.2	SAP1	transcripti	nucleus	transcripti
GI_41872461-I	96.6	89.1	78	ELK4	NM_021795.2	SAP1	transcripti	nucleus	transcripti
GI_41872473-S	312	460.5	361.2	ETV6	NM_001987.3	TEL	transcripti	nucleus	oncogene
GI_41872487-I	112.4	105.2	103.9	DGKA	NM_201444.2	DAGK1;MGC12821;MGC42356;DGK-alpha	diacylglyc		intracellula
GI_41872493-I	131.8	121.3	112.7	DGKA	NM_201445.1	DAGK1;MGC12821;MGC42356;DGK-alpha	diacylglyc		intracellula
GI_41872506-A	289.3	333.6	350.9	DGKZ	NM_003646.2	DAGK5;DAGK6;DGK-ZETA;hDGKzeta	diacylglyc	nucleus	signal
GI_41872526-I	87.5	97.8	78.7	DGKZ	NM_201533.1	DAGK5;DAGK6;DGK-ZETA;hDGKzeta	diacylglyc	nucleus	signal
GI_41872532-A	214.2	291.8	293.1	NRP2	NM_003872.2	NPN2;PRO2714;VEGF165R2;NP2	vascular	membran	axon
GI_41872532-I	162.6	198	168.8	NRP2	NM_003872.2	NPN2;PRO2714;VEGF165R2;NP2	vascular	membran	axon
GI_41872543-I	138	159.8	165	NRP2	NM_018534.3	NPN2;PRO2714;VEGF165R2;NP2	vascular	membran	axon
GI_41872556-I	162.6	184.2	225.4	NRP2	NM_201264.1	NPN2;PRO2714;VEGF165R2;NP2	vascular	membran	axon
GI_41872576-S	1258.8	2209	3016.8	RAFTLIN	NM_015150.1	KIAA0084			
GI_41872582-S	296.3	318.9	277.3	ROCK2	NM_004850.3	KIAA0619	protein	intracellula	cytokinesi
GI_41872597-S	2923.3	2565.8	2804.9	CPNE3	NM_003909.2	CPN3;PRO1071;KIAA0636	transporte		vesicle-
GI_41872613-S	126	120.3	115	CXCL5	NM_002994.3	SCYB5;ENA-78	chemokin	extracellul	positive
GI_41872630-S	9261.7	9837.1	8514.7	FASN	NM_004104.4	FAS;OA-519;MGC14367;MGC15706	alcohol		fatty acid
GI_41872645-S	577	724.2	652.2	KIAA0076	NM_014780.3	CUL7			
GI_41872659-S	378.8	342.4	411.4	MRPL2	NM_015950.3	CGI-22;RPML14;MRP-L14	structural	ribosome	protein
GI_41872679-S	427.5	476.7	388.3	PPAN	NM_020230.3	SSF1;MGC14226;MGC45852	DNA	nucleus	mRNA
GI_41872688-S	331.3	392.6	384.5	PPFIA3	NM_003660.2	LPNA3;KIAA0654			
GI_41872702-S	153.5	191.6	223.8	SLC9A8	NM_015266.1	NHE8;KIAA0939	sodium:hy	integral to	sodium
GI_41872708-A	81.9	90.4	77.7	ZCCHC2	NM_017742.3	FLJ20281;KIAA1744;MGC13269;DKFZp451A			
GI_42403569-I	101.7	124.8	97.3	FHL2	NM_201557.1	DRAL;SLIM3		nucleus	oncogene
GI_42403574-I	232.2	284	267.3	FHL2	NM_201555.1	DRAL;SLIM3		nucleus	oncogene
GI_42403584-A	4266.9	5794	4666	FHL2	NM_001450.3	DRAL;SLIM3		nucleus	oncogene

GI_42415470-S	119.9	130.6	131.2	DXS1283E	NM_004650.1	GS2	catalytic	cellular_co	biological_
GI_42415487-S	133.3	148.9	139.7	LOC284861	NM_201565.1				
GI_42415489-S	102.3	98.7	110.7	TRIM46	NM_025058.2	FLJ23229	zinc ion	intracellula	
GI_42415491-S	92.6	96.6	100.3	C14orf106	NM_018353.3	FLJ11186;KIAA1903;HSA242977			
GI_42415493-S	126.2	166.5	145.5	IRX5	NM_005853.3	IRX-2a	transcripti	nucleus	regulation
GI_42415495-S	190.7	234.2	223.1	SLC16A14	NM_152527.3	FLJ30794			
GI_42415498-S	149.5	174.9	163.2	CRTAC1	NM_018058.2	ASPIC1;CEP-68;FLJ10320			
GI_42415502-S	148.6	151.2	157.3	USP31	NM_020718.2	KIAA1203	cysteine-		ubiquitin-
GI_42415526-S	124.9	143.4	116.5	MAFA	NM_201589.1	hMafA;RIPE3b1			
GI_42415528-I	117.2	118.4	115.5	SLC4A3	NM_201574.1	AE3;SLC2C	inorganic	membran	small
GI_42415530-I	78.2	76.8	86.4	C10orf94	NM_201564.1	bA108K14.6			
GI_42415532-S	111.9	121.6	123	FCGR2C	NM_201563.1		receptor	integral to	signal
GI_42475554-S	241.3	286.5	273.1	SLC16A13	NM_201566.1				
GI_42475556-S	10249.8	12493	11205	SERF2	NM_005770.3	FAM2C;4F5REL;H4F5rel;HsT17089			pathogene
GI_42475557-I	98.5	102.6	99.6	C1orf16	NM_173156.1	EST1C;SMG-7;KIAA0250			
GI_42475939-A	1596.3	1333.6	1413.9	ZNF261	NM_005096.2	MYM;XFIM;DXS6673E;KIAA0385;ZNF198L2	DNA	integral to	developm
GI_42475940-I	124.2	131.5	132.4	ZNF261	NM_201599.1	MYM;XFIM;DXS6673E;KIAA0385;ZNF198L2	DNA	integral to	developm
GI_42475964-S	995.9	655.2	303.5	AF038169	NM_013310.2				
GI_42475969-S	743.6	747.8	618.9	7h3	NM_033025.4	FLJ13511			
GI_42476001-S	104.2	100.4	84.9	FLJ35107	NM_182629.2				
GI_42476002-S	111.8	107.6	98	FLJ36198	NM_173801.3				
GI_42476004-S	188.9	198	192.2	FLJ32569	NM_152491.2		metallope		proteolysis
GI_42476006-S	141.4	149.8	135.2	FLJ34922	NM_152270.2				
GI_42476008-S	136.6	155	136.8	FLJ30678	NM_144657.2		transcripti	nucleus	regulation
GI_42476012-S	315.2	383.8	370.5	FLJ25621	NM_198514.2	FLJ20147;FLJ33312;MGC45492;DKFZp779F	electron		electron
GI_42476014-S	106.3	114.2	115.5	FLJ22662	NM_024829.2				
GI_42476016-S	411.3	689.6	746.9	FLJ23751	NM_152282.2				
GI_42476017-S	3266.3	3158.2	3651.8	C19orf24	NM_017914.2	FLJ20640			
GI_42476019-S	88.1	89.1	95.8	FLJ21934	NM_024743.2		transferas		metabolis
GI_42476021-S	367.3	346	301	FLJ20272	NM_017735.3				
GI_42476023-S	1201.6	1153.3	1525.8	FLJ20274	NM_017736.2				
GI_42476025-S	243.6	252.4	298.1	FLJ11526	NM_024632.2				
GI_42476026-S	463.9	332.4	235.6	FLJ20095	NM_017666.2				
GI_42476027-S	982.1	826.8	847.5	FLJ10709	NM_018188.2		nucleotide		
GI_42476029-S	1006	1037	948.1	FLJ10826	NM_018233.2		oxidoredu		protein
GI_42476031-S	613.8	677.9	690.2	FLJ10587	NM_018149.3				
GI_42476034-S	96.1	100.7	82.9	FAM20A	NM_017565.2	DKFZp434F2322			
GI_42476040-S	1831.2	1814.9	1773.2	DC13	NM_020188.2				
GI_42476060-S	407.2	472.4	381.7	C4orf8	NM_003704.2	RES4-22	DNA	nucleus	regulation
GI_42476062-S	1401.6	856.7	853	C6orf145	NM_183373.2				
GI_42476063-S	88.1	111.4	89.2	C20orf58	NM_152864.2	bA261N11.2			
GI_42476067-S	7432.9	7673.4	4259	C20orf30	NM_014145.3	HSPC274			
GI_42476071-S	397.9	505.9	389.8	C14orf159	NM_024952.4	FLJ12618;FLJ20950;FLJ39975;C14orf160	GTP	signal	protein
GI_42476073-A	1235.7	1171.3	916.5	C1orf16	NM_014837.3	EST1C;SMG-7;KIAA0250			

GI_42476075-S	715.7	765.5	728.8	KIAA1012	NM_014939.2	HsT2706	intracellula	Golgi cis-	ER to
GI_42476079-S	83	91.6	87	IMPK	NM_152230.2	IPMK	inositol-		
GI_42476100-I	100.5	117.2	105.3	GTF2A1	NM_201595.1	TF2A1;TFIIA	RNA	transcripti	transcripti
GI_42476103-A	97.9	106.1	101.1	GTF2A1	NM_015859.2	TF2A1;TFIIA	RNA	transcripti	transcripti
GI_42476106-A	129.4	107.6	99.5	GPM6A	NM_005277.3	M6A;GPM6		integral to	
GI_42476107-I	104.8	106.6	98.9	GPM6A	NM_201591.1	M6A;GPM6		integral to	
GI_42476109-S	1569.9	1547.6	1579.7	GNPTAG	NM_032520.3	CAB56184;c316G12.3			
GI_42476110-S	137.9	152.6	159.9	GNA12	NM_007353.2	RMP;NNX3	heterotrim	membran	cell growth
GI_42476117-S	118.9	128.7	124.8	FYB	NM_001465.3	ADAP;PRO0823;SLAP-130	protein	nucleus	NLS-
GI_42476119-S	460.7	575.7	666.5	FNTB	NM_002028.3	FPTB;MGC31935	protein	cytoplasm	C-terminal
GI_42476122-S	1335.8	1279.1	1779.9	RUSC1	NM_014328.2	NESCA	SH3/SH2		
GI_42476126-S	770.1	690.5	782.1	RPC2	NM_018082.3	FLJ10388	DNA-	nucleus	transcripti
GI_42476128-S	103.5	123	107.7	RRP22	NM_006477.2		small		small
GI_42476129-S	760.1	613.1	671.2	RAP80	NM_016290.3				
GI_42476152-S	92.2	144.1	92.5	PTN	NM_002825.5	HARP;HBNF;HBGF8;NEGF1	protein	extracellul	transmem
GI_42476153-S	844.5	814	1317.9	PTPLB	NM_198402.2				
GI_42476154-S	1198.3	1596.9	1456.3	PTMS	NM_002824.3			nucleus	DNA
GI_42476156-S	442.7	548.1	517.5	PRKCL1	NM_002741.2	DBK;PKN;PRK1	protein	intracellula	activation
GI_42476158-S	107.9	106.9	95.2	PSG3	NM_021016.2				
GI_42476159-S	151.1	166.8	148	PPY	NM_002722.2	PNP	receptor	soluble	protein
GI_42476160-S	2125.9	2397.2	2753	PPP1R16A	NM_032902.5	MYPT3;MGC14333		kinesin	
GI_42476161-S	124.8	129.9	123.4	PPP1R3C	NM_005398.3	PPP1R5	protein		
GI_42476163-S	957.1	812.6	764.9	POU2F1	NM_002697.2	OCT1;OTF1	transcripti	nucleus	regulation
GI_42476165-S	2590	1677.2	833.1	PYGL	NM_002863.2		glycogen		glycogen
GI_42476168-S	406.2	462	479.4	PD2	NM_019088.2	F23149_1;FLJ11123			
GI_42476171-S	3005.9	3053	2454.3	NIPA2	NM_030922.3	MGC5466	copper,		superoxid
GI_42476173-S	126.2	149.7	165.3	NAPE-PLD	NM_198990.2				
GI_42476174-S	1057.2	930.4	748.8	NCOA7	NM_181782.2	ERAP140;dJ187J11.3			cell wall
GI_42476188-S	103.6	115.7	98.3	MPRA	NM_178422.3		receptor	integral to	
GI_42476189-S	97.2	85.3	75.8	MYH2	NM_017534.2	MYH2A;MYHSA2;MYHas8;MyHC-2A;MyHC-	muscle	striated	striated
GI_42476191-S	308.4	538.9	439.7	MGC8685	NM_178012.3	DKFZp566F223	GTP	microtubul	microtubul
GI_42476192-S	5008.4	6602.7	5988.4	MGC8721	NM_016127.4	XTP3;FOAP-7;HSPC035;FLJ22274			
GI_42476196-S	163.7	161.9	162.5	MGC71999	NM_199290.2				
GI_42476197-S	146.3	166.3	163.2	MGC15407	NM_080667.3				
GI_42476199-S	117.8	129.8	110.5	MBD6	NM_052897.2	KIAA1887	DNA		
GI_42476202-S	1462	4528	3702.4	MADH3	NM_005902.2	SMAD3;JV15-2;HsT17436	tumor	intracellula	transformi
GI_42476203-S	271.9	432.6	327.1	LOC90139	NM_130783.2	TSPAN			
GI_42476205-S	113.6	172.2	156	LOC51308	NM_016606.2	SGC32445			
GI_42476207-S	1641.7	1494.9	1383.8	LOC51321	NM_016627.2		metallope		proteolysis
GI_42476209-S	711.6	687.4	214.3	LOC255104	NM_181719.2				
GI_42476211-S	99.6	122.4	109.1	LOC134285	NM_173490.4				
GI_42476213-S	275.5	302.2	261.9	LOC120526	NM_181706.3				
GI_42476215-S	673.5	896.6	712.3	LOC119710	NM_138787.2				
GI_42476268-S	126	145.5	106.7	ZXDA	NM_007156.2		DNA	nucleus	biological_

GI_42476270-S	230.3	308.7	267.5	ZFP42	NM_174900.2	REX1			
GI_42476271-S	109.1	184.1	127.8	ZNF513	NM_144631.3	FLJ32203			
GI_42476278-S	9802.5	10056	8465.4	VKORC1	NM_024006.3	VKOR;MST134;MST576;UNQ308;VKCFD2;			
GI_42476280-S	5862	6112.3	5624.3	VDAC2	NM_003375.2		voltage-	mitochond	anion
GI_42476283-S	4142.5	5663.6	4746.7	UBL5	NM_024292.2	HUB1	molecular	cytoplasm	biological_
GI_42476295-S	1839.9	2677.8	1467.9	TPM2	NM_003289.2	DA1;TMSB;AMCD1	structural	muscle	muscle
GI_42476298-S	271.3	331.2	325.7	TNRC15	NM_015575.2	GIGYF2;KIAA0642			
GI_42476300-S	275.1	327.1	275.5	TOMM70A	NM_014820.2			mitochond	
GI_42476304-S	922.4	1140.7	969.1	TMEM4	NM_014255.3	MSAP;ZSIG9;HP10390		integral to	
GI_42476317-S	120.6	131.9	129.3	SLRN	NM_181506.3				
GI_42476319-S	161	273.7	187.5	SUSD1	NM_022486.2	DKFZP761E1824			
GI_42476321-S	252.2	349.2	286	SLC36A3	NM_181774.2	PAT3;TRAMD2;tramdorin2	amino	membran	amino
GI_42476323-S	430.3	470.2	351.5	SLC43A1	NM_003627.4	LAT3;PB39;POV1;R00504			oncogene
GI_42476324-S	82.4	84.7	81.3	SLC18A2	NM_003054.2	SVAT;SVMT;VAT2;VMAT2	monoamin	secretory	monoamin
GI_42476327-S	237.9	310.5	250.4	SHD	NM_020209.2				intracellula
GI_42476329-S	95.4	91.5	96.3	SFTPD	NM_003019.3	SP-D;SFTP4;COLEC7	lectin [goid	kinesin	antimicrob
GI_42476331-S	17145.9	23364	23736	SH3BGRL3	NM_031286.2	TIP-B1		nucleus	
GI_42476334-S	102.1	115.3	109.1	SFTPC	NM_003018.2	SP-C;PSP-C;SFTP2	surfactant	extracellul	respiratory
GI_42476336-I	158.2	145.7	147.2	SB153	NM_201400.1	MGC19636			
GI_42490739-S	146.5	158.8	146.6	MICL	NM_138337.3	CLL-1	lectin [goid		heterophili
GI_42490743-I	131.7	148.3	153.5	MICL	NM_201625.1	CLL-1	lectin [goid		heterophili
GI_42490745-A	1333.3	1107.1	1529.3	MED8	NM_052877.2	ARC32;MGC17544;MGC19641	receptor	nucleus	regulation
GI_42490746-I	861	918.1	801.1	MED8	NM_201542.1	ARC32;MGC17544;MGC19641	receptor	nucleus	regulation
GI_42490748-S	437.1	393.5	246.7	ABCB7	NM_004299.3	ABC7;ASAT;Atm1p;EST140535	heme	mitochond	small
GI_42490752-S	150.6	243.1	193.3	TEAD3	NM_003214.2	TEF5;TEAD5;TEF-5;DTEF-1;ETFR-1	RNA	nucleus	pregnancy
GI_42490754-S	172.2	210.7	185.5	TSHB	NM_000549.2	TSH-BETA	peptide	extracellul	G-protein
GI_42490755-S	287.8	366.7	317.4	GNS	NM_002076.2	G6S;MGC21274	N-	lysosome	glycosami
GI_42490756-S	389.8	383	417.8	GOLGA1	NM_002077.2	MGC33154;golgin-97		Golgi	
GI_42490757-S	143.7	150.5	149.3	CDC25A	NM_001789.2		prenylated	intracellula	regulation
GI_42490763-S	766.5	753.6	560.6	ELOVL1	NM_022821.2	Ssc1;CGI-88		endoplas	fatty acid
GI_42490765-S	467.1	615.2	558.7	SP6	NM_199262.2	KLF14			
GI_42491353-I	192.3	211.3	196.5	LOC284948	NM_201594.1				intracellula
GI_42491357-I	117.8	113.4	115.3	PSK-1	NM_201575.1				
GI_42491361-I	110.6	112.6	119.3	IKIP	NM_201612.1	FLJ31051			
GI_42491369-S	131.5	156.8	141.1	FLJ43806	NM_201628.1				
GI_42516554-S	125.4	113.4	98.9	pknbeta	NM_013355.3		protein	Golgi	protein
GI_42516559-S	422.6	543.5	707.9	ZDHHC12	NM_032799.4	ZNF400;FLJ14524;MGC13153;MGC54050		integral to	
GI_42516560-I	94.3	82.7	92.6	USP33	NM_201626.1	VDU1;KIAA1097;MGC16868	cysteine-		ubiquitin
GI_42516562-S	644.7	784.2	748	UXS1	NM_025076.2	FLJ23591	catalytic		nucleotide-
GI_42516568-S	5468.8	3660.6	3237.6	TRIP10	NM_004240.2	CIP4	protein		actin
GI_42516569-S	177.6	184.5	172.4	TXNDC2	NM_032243.4	SPTRX;MGC35026;DKFZp434H0311	electron		electron
GI_42516571-S	896.2	1094.6	1346.8	TRIM41	NM_033549.3	MGC1127;MGC31991			
GI_42516575-S	6486.6	7236.9	6859.3	C14orf87	NM_016417.2	FLB4739;PR01238			
GI_42518066-S	333.1	353.6	304	TNPO3	NM_012470.2	IPO12;MTR10A;TRN-SR;TRN-SR2	receptor	transportin	nucleocyto

GI_42518067-S	154.1	200.6	226.6	TGOLN2	NM_006464.2	TGN38;TGN46;TGN48;TGN51;TTGN2;MGC		Golgi-	
GI_42518069-S	526	965.1	1018.8	TJP2	NM_004817.2	ZO2;X104;ZO-2;MGC26306	membran	tight	intracellula
GI_42518071-I	105.8	92.4	91.1	TGM5	NM_201631.1	TGX;TGM6;TGMX	protein-		epidermal
GI_42518075-S	849.7	810	1022.6	TEX261	NM_144582.2	MGC32043			
GI_42518079-S	193.4	289	268.2	TCF7	NM_003202.2	TCF-1;MGC47735	RNA	nucleus	regulation
GI_42518081-I	220.5	168.5	128	TBXA2R	NM_201636.1		thromboxa	integral to	respiratory
GI_42518083-I	181.1	229.2	204	TBXA2R	NM_001060.3		thromboxa	integral to	respiratory
GI_42519906-I	172.2	201.6	187.7	GLYAT	NM_005838.2	CAT;GAT;ACGNAT	acyltransf	mitochond	response
GI_42519908-I	82.2	93.8	89.9	GLYAT	NM_201648.1	CAT;GAT;ACGNAT	acyltransf	mitochond	response
GI_42519910-S	2842	3079.4	2232.1	STAMBP	NM_006463.3	AMSH		nucleus	JAK-STAT
GI_42519913-S	476.3	547.7	433.8	STAT5B	NM_012448.3	STAT5	transcripti	nucleus	JAK-STAT
GI_42519914-A	275.4	260	233.8	FOXO3A	NM_001455.2	AF6q21;FKHRL1;FKHRL1P2;MGC12739;MG	transcripti	cytoplasm	induction
GI_42519915-I	132.1	108.8	107.3	FOXO3A	NM_201559.1	AF6q21;FKHRL1;FKHRL1P2;MGC12739;MG	transcripti	cytoplasm	induction
GI_42542378-S	2587.1	2966.6	2767.9	SRRM1	NM_005839.2	160-KD;POP101;SRM160;MGC39488	pre-mRNA	nucleus	mRNA
GI_42542380-I	605.3	755.8	685.3	SLC28A1	NM_004213.3	CNT1;HCNT1	nucleoside	membran	nucleoside
GI_42542382-I	114	115.2	102.7	SLC28A1	NM_201651.1	CNT1;HCNT1	nucleoside	membran	nucleoside
GI_42542384-S	161.7	230.4	180.5	SILV	NM_006928.3	SI;SIL;ME20;gp100;PMEL17;D12S53E	tumor	integral to	melanin
GI_42542385-S	92.5	99.3	92	SLC22A9	NM_080866.2	OAT4;ust3;HOAT4;UST3H			
GI_42542387-S	2563.3	1629.8	1471.1	SFXN4	NM_178867.3	BCRM1	cation	membran	cation
GI_42542389-S	131.6	150.3	134.9	CD209L	NM_014257.3	LSIGN;DCSIGNR;HP10347;DC-SIGN2;DC-		integral to	
GI_42542391-S	1817.3	1523	1059.8	CEBPZ	NM_005760.2	CBF2;HSP-CBF	transcripti	nucleus	transcripti
GI_42542393-S	438.8	591.6	608.3	C3F	NM_005768.5				
GI_42542397-A	87.6	99.6	97.3	CHIA	NM_021797.2	ECF-L;AMCase;TSA1902	chitin	extracellul	carbohydr
GI_42542399-I	99.8	110.8	96.9	CHIA	NM_201653.1	ECF-L;AMCase;TSA1902	chitin	extracellul	carbohydr
GI_42542401-A	807.3	844.6	774.2	B7	NM_006992.2				
GI_42542402-S	1437.8	1392.3	1546.6	CGI-01	NM_015935.3	KIAA0859	S-		
GI_42543993-S	101.2	90.9	101.6	ZNF539	NM_203282.1				
GI_42544116-I	112.9	133.5	130.9	HSRTSBETA	NM_202758.1	RTS			
GI_42544118-A	172.5	254.9	220	HSRTSBETA	NM_017512.2	RTS			
GI_42544120-S	493.4	544.2	562.4	VPS13C	NM_017684.3	FLJ10381;FLJ20136;KIAA1421			
GI_42544126-I	149.5	159.2	132.6	SF1	NM_201997.1	ZFM1;ZNF162;D11S636	transcripti	nucleus	regulation
GI_42544128-S	118.3	136.7	144.6	SCAMP5	NM_138967.2	MGC24969			
GI_42544131-A	156.7	132.3	88.6	SAH	NM_005622.2	SA	catalytic		regulation
GI_42544133-I	241.6	233.2	207.1	SAH	NM_202000.1	SA	catalytic		regulation
GI_42544135-S	624.4	883.1	546.2	RRM2B	NM_015713.3	P53R2;MGC42116	ribonucleo		response
GI_42544137-S	2467.2	1879.5	1411.8	RRP46	NM_020158.2	MGC12901	exonuclea	nucleolus	rRNA
GI_42544150-S	666.9	686.1	648.8	MGC4268	NM_031445.2				
GI_42544152-S	162.1	168.5	156.9	LTK	NM_002344.2	TYK1	protein-	soluble	protein
GI_42544154-S	410	473.1	448.7	MED6	NM_005466.2	NY-REN-28	RNA	nucleus	regulation
GI_42544158-S	1492.2	2040.5	2316.9	HSPH1	NM_006644.2	HSP105A;HSP105B;KIAA0201;NY-CO-25	heat	cytoplasm	heat
GI_42544162-S	182.7	345.8	171.9	FREB	NM_032738.3	FCRL;MGC4595			
GI_42544164-A	1231.7	1273.9	1798.3	FOXM1	NM_021953.2	MPP2;HFH11;HNF-3;INS-1;MPP-	RNA	nucleus	response
GI_42544166-I	78.7	84.4	79.4	FOXM1	NM_202002.1	MPP2;HFH11;HNF-3;INS-1;MPP-	RNA	nucleus	response
GI_42544168-I	176.1	174	140.6	ERCC1	NM_202001.1	UV20	endodeox	nucleus	nucleotide-

GI_42544170-A	1050.8	1100.7	1100.1	ERCC1	NM_001983.2	UV20	endodeox	nucleus	nucleotide-
GI_42544171-I	122.9	120.5	123	ELF2	NM_201999.1	EU32;NERF;NERF-2;NERF-1A;NERF-1B	transcripti	nucleus	regulation
GI_42544173-S	2564.9	2451.7	2999.8	DTYMK	NM_012145.2	CDC8;TMPK;TYMK	thymidylat		cell cycle
GI_42544175-A	628	668.8	392.1	ELF2	NM_006874.2	EU32;NERF;NERF-2;NERF-1A;NERF-1B	transcripti	nucleus	regulation
GI_42544176-S	78.2	76.1	63.8	CR2	NM_001877.2	C3DR;CD21	compleme	integral to	compleme
GI_42544178-S	254.5	281.7	256.6	CIZ1	NM_012127.2	LSFR1;ZNF356	zinc ion	nucleus	regulation
GI_42544180-A	88.8	96.7	89.6	BMX	NM_001721.4	ETK;PSCTK2;PSCTK3	protein-		mesoderm
GI_42544181-I	125.7	125.8	108.2	BMX	NM_203281.1	ETK;PSCTK2;PSCTK3	protein-		mesoderm
GI_42544183-S	128.2	143.5	126.8	APOBEC2	NM_006789.2	ARP1;ARCD1	cytidine		RNA
GI_42544184-A	407	416.7	354.8	LGALS8	NM_006499.3	Gal-8;PCTA-1;Po66-CBP	lectin [goid	extracellul	oncogene
GI_42544188-I	103.9	101.9	93.6	FGL1	NM_004467.3	HFREP1;HP-041;LFIRE1;MGC12455	fibrinogen	fibrinogen	
GI_42544190-I	128.9	143.9	142.9	LGALS8	NM_201544.1	Gal-8;PCTA-1;Po66-CBP	lectin [goid	extracellul	oncogene
GI_42544192-I	120.1	133.9	127.3	LGALS8	NM_201545.1	Gal-8;PCTA-1;Po66-CBP	lectin [goid	extracellul	oncogene
GI_42544194-I	290.3	234.8	222.8	DIABLO	NM_138930.2	SMAC;SMAC3;DIABLO-		mitochond	caspase
GI_42544195-I	596.7	693.2	619.8	DIABLO	NM_019887.3	SMAC;SMAC3;DIABLO-		mitochond	caspase
GI_42544196-A	566.6	619.6	602.4	DIABLO	NM_138929.2	SMAC;SMAC3;DIABLO-		mitochond	caspase
GI_42544197-A	107.7	112.7	107.4	FGL1	NM_147203.2	HFREP1;HP-041;LFIRE1;MGC12455	fibrinogen	fibrinogen	
GI_42544197-I	114.4	122.2	105.5	FGL1	NM_147203.2	HFREP1;HP-041;LFIRE1;MGC12455	fibrinogen	fibrinogen	
GI_42544203-I	83.2	78.8	77	TSLP	NM_033035.3				
GI_42544204-A	90.7	113.7	133.7	TSLP	NM_138551.2				
GI_42544204-I	199.5	214	194	TSLP	NM_138551.2				
GI_42544205-S	481.1	621.8	780.6	VAMP3	NM_004781.3	CEB		synaptoso	vesicle
GI_42544206-A	105.7	105	110.3	VAMP4	NM_003762.2	VAMP24		endosome	protein
GI_42544208-I	277.7	230.2	211	VAMP4	NM_201994.1	VAMP24		endosome	protein
GI_42544214-S	149.9	144.7	111.9	NDRG2	NM_016250.2	SYLD;KIAA1248	molecular	cytosol	cell
GI_42544225-S	620.4	825.7	792.2	VPS18	NM_020857.2	KIAA1475	protein	membran	intracellula
GI_42544226-S	546.1	526.7	621.3	VPS33A	NM_022916.3	FLJ22395;FLJ23187	protein	membran	protein
GI_42544227-S	95	94.7	93.2	TNFRSF10D	NM_003840.3	DCR2;TRUNDD;TRAILR4	transmem	integral to	anti-
GI_42544228-I	107	109.6	102.9	TRAF2	NM_021138.3	TRAP;TRAP3;MGC:45012	signal		signal
GI_42544229-S	560.9	533.2	487.1	TULP3	NM_003324.3	TUBL3;MGC45295			
GI_42544230-S	152.4	186.3	172.7	LRRN5	NM_006338.2	GAC1;LRANK1	receptor	integral to	cell
GI_42544232-I	118.8	125.7	103.4	LRRN5	NM_201630.1	GAC1;LRANK1	receptor	integral to	cell
GI_42544234-S	8545.9	7550.5	7581.6	ACP33	NM_016630.3	MAST;GL010;SPG21;BM-019	catalytic		
GI_42544235-S	106.6	103.7	93.7	B3GNT4	NM_030765.2	B3GN-T4;beta3Gn-T4	galactosylt	membran	protein
GI_42544236-S	284	313.4	294.4	CNOT3	NM_014516.2	NOT3;LENG2;NOT3H;KIAA0691			
GI_42544237-S	189.1	190.3	176.4	DCAMKL1	NM_004734.2	DCLK;KIAA0369	protein	integral to	protein
GI_42544238-S	109.9	133.3	95.3	DF	NM_001928.2	ADN	compleme		compleme
GI_42544240-S	445.2	576.6	487	IRX6	NM_024335.2	IRX7;IRX-3	transcripti	nucleus	regulation
GI_42544242-S	200.5	210.7	217.4	DNM3	NM_015569.2	Dyna III;KIAA0820	dynamin		endocytosi
GI_42544244-S	149.1	159.8	149	OTOS	NM_148961.3	OTOSP			
GI_42544245-S	1035.6	1317.8	1511.4	SEPW1	NM_003009.2	selW	selenium	cellular_co	biological_
GI_42544246-S	405.6	501.3	415.1	WDR5B	NM_019069.3	FLJ11287;MGC49879	signal	heterotrim	G-protein
GI_42558242-S	104.1	117.4	110.3	LOC340351	NM_178563.1		carboxype		proteolysis
GI_42558244-S	633.1	728.8	854.3	GMRP-1	NM_032320.4	MGC13007	ion		

GI_42558249-I	1540.1	1945.8	1699.4	M11S1	NM_005898.3	GPIAP1		integral to	
GI_42558251-S	324.8	376.2	348.2	LOC118487	NM_203298.1				
GI_42558253-S	107.2	100.3	95.4	MGC41945	NM_203299.1		DNA	nucleus	regulation
GI_42558255-S	382	442.3	600.1	LOC147727	NM_203300.1				
GI_42558257-S	414.7	529.2	491.9	FBXO33	NM_203301.1	c14_5247			
GI_42558259-S	81.4	76.8	74.9	LOC389874	NM_203303.1		nucleic		
GI_42558261-S	228.2	263	235.6	RKHD1	NM_203304.1	Tino;KIAA2031;OK/SW-cl.4	nucleic		
GI_42558263-S	211.6	227	355.3	MGC50853	NM_203305.1				
GI_42558265-S	105.7	119.3	100.3	MGC34774	NM_203308.1				
GI_42558267-S	295.5	352.5	365.7	MGC39606	NM_203306.1				
GI_42558269-S	131.4	132.1	127.9	MGC48595	NM_203309.1				
GI_42558278-S	87.1	90.5	76.1	TUBB8-pendi	NM_177987.1		GTP	microtubul	microtubul
GI_42558280-S	625	722.6	598.5	LOC220869	NM_201453.1				
GI_42560226-I	4210.2	2441.3	2667.6	RBPSUH	NM_005349.2	csl;CBF1;KBF2;RBP-	tyrosine-	nucleus	DNA
GI_42560228-A	1733.3	1368.2	1162.4	RBPSUH	NM_015874.3	csl;CBF1;KBF2;RBP-	tyrosine-	nucleus	DNA
GI_42560230-I	248.7	264.8	250.7	PVRL1	NM_203285.1	ED4;PRR;HIgR;HVEC;PRR1;PVRR;CD111;P	coreceptor	membran	virulence
GI_42560232-I	105.3	113.6	137.4	PVRL1	NM_203286.1	ED4;PRR;HIgR;HVEC;PRR1;PVRR;CD111;P	coreceptor	membran	virulence
GI_42560234-S	109.7	105.7	105.4	PSG4	NM_002780.2	PSG9	plasma	extracellul	pregnancy
GI_42560236-I	115.7	119.5	109.7	PVRL1	NM_002855.3	ED4;PRR;HIgR;HVEC;PRR1;PVRR;CD111;P	coreceptor	membran	virulence
GI_42560238-S	2001.2	2185.6	2054.2	PRKAG1	NM_002733.2	MGC8666	cAMP-		protein
GI_42560239-I	162.8	199.1	183.1	PSG11	NM_002785.2	PSG13;PSG14;MGC22484	plasma	extracellul	pregnancy
GI_42560241-I	94.4	88.3	91.8	POU5F1	NM_203289.1	OCT3;OTF3;OTF4;Oct4;MGC22487	transcripti	nucleus	embryoge
GI_42560243-S	110.1	107.5	103.5	PPIG	NM_004792.2	CYP;SRCyp;CARS-Cyp	cyclophilin	nucleoplas	mRNA
GI_42560245-I	2347.5	2137.8	1882.7	POLR1C	NM_203290.1	RPA5;RPA39;RPA40;RPAC1	DNA-	RNA	transcripti
GI_42560247-A	91.4	97.3	98.7	POU5F1	NM_002701.2	OCT3;OTF3;OTF4;Oct4;MGC22487	transcripti	nucleus	embryoge
GI_42560249-A	546.1	539.8	476.1	POLR1C	NM_004875.2	RPA5;RPA39;RPA40;RPAC1	DNA-	RNA	transcripti
GI_42600568-S	931	952.3	794.6	LOC389903	NM_203311.1		DNA	nucleus	regulation
GI_42627874-S	165.6	168.6	147.8	CDON	NM_016952.2	CDO;ORCAM	tumor		cell
GI_42627890-S	111.7	111.4	105.9	MGC35402	NM_203307.1	FLJ39509			
GI_42655578-S	226.6	297.9	249.4	LOC400768	XM_378883.1				
GI_42655584-S	102.6	90	85.9	LOC388665	XM_371281.2				
GI_42655585-S	130.5	138.6	134.7	LOC388666	XM_371283.2				
GI_42655592-S	479.1	510.2	519.7	IKBKE	XM_375834.1				
GI_42655597-S	105.6	101.3	108.1	LOC388732	XM_373884.2				
GI_42655599-S	430.6	345.5	431	LOC400802	XM_378933.1				
GI_42655601-S	107.3	108.3	109.6	LOC400803	XM_378934.1				
GI_42655604-S	137.7	166	144.5	LOC388734	XM_371340.2				
GI_42655626-S	155.3	181.7	160.8	LOC400733	XM_378835.1				
GI_42655642-S	92.2	92.9	84.5	LOC401938	XM_377563.1				
GI_42655658-S	134.5	149.2	128.8	LOC401953	XM_377593.1				
GI_42655662-S	150	194.9	168.1	LOC388649	XM_371268.2				
GI_42655666-S	351.6	450.6	385	LOC400763	XM_378879.1				
GI_42655672-S	169.6	188.1	162.6	LOC163404	XM_375754.1				
GI_42655676-S	136.2	145.8	136.9	LOC400766	XM_375756.1				

GI_42655683-S	1022.1	523	575.6	NTNG1	XM_375762.1	structural	extracellul	axonogen
GI_42655687-S	308.8	365.2	315.8	LOC400741	XM_378841.1			
GI_42655689-S	141.7	170.3	149.3	LOC400742	XM_378842.1			
GI_42655693-S	100.5	92	95.6	LOC400743	XM_378843.1			
GI_42655700-S	230.9	273.9	251.9	LOC401991	XM_377635.1			
GI_42655722-S	165.3	172.1	155.3	LOC400785	XM_375803.1			
GI_42655724-S	83.4	96.2	85.1	LOC400786	XM_378901.1			
GI_42655735-S	94.6	98.9	91.3	LOC339442	XM_378855.1			
GI_42655745-S	97.7	104	108.9	LOC400751	XM_378859.1			
GI_42655748-S	275.8	347.8	297.9	LOC149478	XM_378860.1			
GI_42655750-S	491.5	622.3	606.2	FLJ21156	XM_371246.2			
GI_42655751-S	241.1	291.1	266.8	LOC400752	XM_378861.1			
GI_42655756-S	135.5	156.6	146.7	LOC400753	XM_378862.1			
GI_42655764-S	117.9	110.7	108.6	LOC388630	XM_371250.2			
GI_42655775-S	121.9	142.1	132.2	LOC400754	XM_375732.1			
GI_42655777-S	227.9	296.1	261.9	LOC400756	XM_378865.1			
GI_42655779-S	98.7	113.7	94.9	LOC199899	XM_378866.1			
GI_42655787-S	97	108.8	104.6	LOC339468	XM_373847.2			
GI_42655803-S	105.2	108.4	89.1	LOC388681	XM_371299.2			
GI_42655807-S	321.1	394	347.7	LOC401964	XM_377601.1			
GI_42655811-S	140.2	185.7	171	LOC388689	XM_371306.2			
GI_42655813-S	822.7	779.3	592.9	LOC388690	XM_373865.2			
GI_42655820-S	314.4	400.7	355	LOC400801	XM_378930.1			
GI_42655832-S	261.4	281.9	263	LOC400747	XM_375707.1			
GI_42655836-S	103.6	99.4	91.6	LOC401945	XM_377579.1			
GI_42655845-S	121.2	139.8	125.7	KIAA0450	XM_371214.2			
GI_42655847-S	128	124.8	131	LOC388586	XM_373821.2			
GI_42655848-S	122.8	110.3	97.3	LOC115110	XM_378828.1			
GI_42655850-S	94.4	91.2	85.7	LOC401936	XM_377556.1			
GI_42655858-S	152.4	139.3	145.2	dJ383J4.3	XM_371328.2			
GI_42655861-S	213.2	252.8	221.9	KIAA0492	XM_378914.1			
GI_42655865-S	126.3	142.8	120.9	LOC400796	XM_378917.1			
GI_42655881-S	141.6	170.1	154	LOC401976	XM_377618.1			
GI_42655883-S	112.5	115.6	96.7	LOC400748	XM_378852.1			
GI_42655888-S	80.7	86.4	83.1	LOC284551	XM_375713.1			
GI_42655890-S	703.8	830.1	627.1	LOC400749	XM_375714.1			
GI_42655896-S	1594.9	861.2	565.7	LOC85028	XM_378848.1			
GI_42655900-S	134.6	135.7	122	LOC401947	XM_377583.1			
GI_42655902-S	111.6	119.8	100.6	LOC400732	XM_378831.1			
GI_42655923-S	212.8	207.2	175.6	LOC400810	XM_375850.1			
GI_42655933-S	120.2	141.5	106.2	KIAA0459	XM_375697.1			
GI_42655935-S	1126.1	460.2	595.6	LOC400745	XM_375698.1			
GI_42655949-S	247.1	335.2	282.3	LOC284688	XM_378912.1			
GI_42655951-S	212.6	237.2	213.2	LOC401974	XM_377613.1			

GI_42655953-S	195.8	232.3	209.2	LOC391130	XM_372803.2
GI_42655957-S	80.7	91.2	84	LOC400800	XM_378925.1
GI_42655967-S	96.1	86.9	105.8	LOC400759	XM_375746.1
GI_42655973-S	110.9	105.5	106.4	LOC149351	XM_378876.1
GI_42655977-S	99.7	101	95.6	LOC284475	XM_378886.1
GI_42655979-S	150.3	200.6	177.5	TBX15	XM_371284.2
GI_42655983-S	838	737.7	643.3	FLJ10359	XM_375853.1
GI_42655985-S	100.3	92.1	94.8	LOC388754	XM_371351.2
GI_42655988-S	218.3	144.8	142.2	FMN2	XM_371352.2
GI_42655994-S	110.9	111.7	100.3	LOC149134	XM_378945.1
GI_42655996-S	115.7	123.3	95.4	LOC400812	XM_378946.1
GI_42656002-S	98	108.8	96.8	LOC401990	XM_377633.1
GI_42656011-S	214.9	229.9	209.4	LOC400738	XM_378837.1
GI_42656018-S	147.7	162.4	159.7	LOC401939	XM_377565.1
GI_42656020-S	108.8	118.8	104	LOC401940	XM_377566.1
GI_42656047-S	126.1	118.7	117.2	LOC254099	XM_378822.1
GI_42656051-S	96.8	104.5	96.5	LOC401934	XM_377555.1
GI_42656055-S	105.2	111.4	110.6	LOC400729	XM_378824.1
GI_42656064-S	111.1	136	112.4	LOC400739	XM_378838.1
GI_42656066-S	116.2	127.1	106.7	LOC388597	XM_373827.2
GI_42656068-S	362.4	361.3	288.3	LOC400775	XM_378892.1
GI_42656072-S	175.8	231	219	LOC400776	XM_375779.1
GI_42656074-S	118.8	126	101.8	LOC388674	XM_371292.2
GI_42656084-S	95.5	87.8	92.6	LOC401995	XM_377649.1
GI_42656096-S	87.2	87.5	80.7	LOC400823	XM_375882.1
GI_42656099-S	121.1	111.6	102.2	LOC388775	XM_301210.3
GI_42656103-S	127.8	120.1	118.7	LOC400771	XM_378890.1
GI_42656107-S	176.9	180.9	175	LOC388618	XM_371241.2
GI_42656112-S	123.6	119.3	116.9	LOC400782	XM_378898.1
GI_42656118-S	144.8	150	150.4	LOC126669	XM_375809.1
GI_42656120-S	242.6	298.2	268.6	LOC400787	XM_375810.1
GI_42656126-S	227.6	269.5	253.8	LOC400789	XM_378903.1
GI_42656130-S	96.6	102.3	93	LOC400790	XM_375814.1
GI_42656138-S	128.5	142.2	140.9	LOC400792	XM_375816.1
GI_42656157-S	119.4	121.4	113.3	LOC400826	XM_375897.1
GI_42656181-S	291.1	376.7	325.9	LOC402008	XM_377666.1
GI_42656187-S	552.9	664.4	623.4	LOC400829	XM_378955.1
GI_42656189-S	124.6	132.4	119.7	LOC400945	XM_379078.1
GI_42656192-S	200.8	215.7	220.6	LOC400946	XM_379079.1
GI_42656195-S	150.2	169.7	163.5	LOC400947	XM_379080.1
GI_42656198-S	116.6	105.9	100.9	LOC402068	XM_377732.1
GI_42656202-S	73.8	77.2	67.2	LOC400997	XM_379122.1
GI_42656206-S	263.6	236.4	222	LOC400999	XM_379123.1
GI_42656225-S	104.8	101.3	109.4	LOC400990	XM_379113.1

GI_42656234-S	101.3	103.7	90.7	LOC400991	XM_376108.1
GI_42656238-S	99.8	98.4	93.1	LOC150568	XM_379117.1
GI_42656242-S	90.9	98.8	88	LOC285000	XM_379119.1
GI_42656258-S	145.7	169.9	149.3	LOC401040	XM_376191.1
GI_42656260-S	80.3	77.6	73	LOC401041	XM_379166.1
GI_42656266-S	365.7	495.3	483.8	LOC391356	XM_372919.2
GI_42656280-S	111.4	118.3	103.4	LOC388939	XM_371488.2
GI_42656282-S	370.6	457.4	417.4	LOC285043	XM_379085.1
GI_42656284-S	142.5	168.8	154.8	LOC285045	XM_379086.1
GI_42656292-S	127.5	117.1	124.2	LOC388942	XM_373981.2
GI_42656293-S	113.1	109.5	95.2	LOC400950	XM_376049.1
GI_42656299-S	125.2	133.7	132.4	LOC400951	XM_379089.1
GI_42656301-S	158.5	167.9	160.4	LOC400952	XM_376051.1
GI_42656305-S	97.4	121.3	105.4	LOC400953	XM_379094.1
GI_42656311-S	90.2	103.2	102.2	LOC400955	XM_379096.1
GI_42656313-S	96.9	117.2	109.6	LOC400957	XM_379097.1
GI_42656315-S	213.2	239.4	191.6	LOC339803	XM_379098.1
GI_42656324-S	139.3	158.6	144.9	LOC400958	XM_379100.1
GI_42656331-S	355.5	420.6	362.9	LOC388957	XM_371497.2
GI_42656335-S	125.4	110.8	110.7	LOC400961	XM_376062.1
GI_42656342-S	168.1	198.4	184.5	LOC400962	XM_376068.1
GI_42656345-S	290.8	389.1	328.1	LOC400964	XM_379106.1
GI_42656348-S	593.1	729.6	779.6	LOC388969	XM_371506.2
GI_42656349-S	86.1	103.3	97.5	LOC400965	XM_376072.1
GI_42656351-S	168.1	181.1	160.8	LOC400967	XM_376073.1
GI_42656353-S	217.9	283.2	254.1	LOC400968	XM_376074.1
GI_42656357-S	119.6	112.7	116.5	LOC388976	XM_371515.2
GI_42656361-S	169.6	195.5	194.3	TTC7	XM_372927.2
GI_42656365-S	142.2	177	144.7	KIAA1940	XM_377742.1
GI_42656370-S	116.4	106	108.2	LOC402066	XM_377725.1
GI_42656372-S	204.7	266.3	233.9	LOC400937	XM_379068.1
GI_42656376-S	220.2	274	223	LOC391343	XM_372911.2
GI_42656385-S	79.1	82.6	78	LOC400984	XM_376097.1
GI_42656389-S	89.6	94.1	89.8	LOC400986	XM_376100.1
GI_42656395-S	134.5	144.6	130.3	LOC285033	XM_379111.1
GI_42656398-S	113.2	108.5	111.3	LOC375247	XM_351473.3
GI_42656400-S	109.8	111.9	111.6	LOC402090	XM_377754.1
GI_42656402-S	73.6	81.9	69.1	LOC391408	XM_352463.2
GI_42656416-S	270.2	294.2	277.2	LOC401044	XM_379169.1
GI_42656418-S	91.3	89.6	83.9	LOC401045	XM_376195.1
GI_42656435-S	106	96.5	97.5	LOC389047	XM_371568.2
GI_42656442-S	140.2	156.8	139.2	LOC401013	XM_376142.1
GI_42656450-S	91.8	97.6	87.9	LOC401014	XM_379141.1
GI_42656454-S	129.8	157.1	135.8	LOC402107	XM_377771.1

GI_42656461-S	141.9	167.5	142.6	LOC151121	XM_379133.1
GI_42656463-S	163.3	189.1	160.6	LOC401002	XM_376125.1
GI_42656465-S	94.6	103.6	84.9	LOC401003	XM_376126.1
GI_42656472-S	167.4	225.5	191.3	LOC344227	XM_292982.4
GI_42656479-S	107.4	100.7	91.6	LOC93463	XM_376186.1
GI_42656483-S	105.7	136.8	104.8	LOC401038	XM_379163.1
GI_42656489-S	147.7	145.3	138.5	DKFZP586K1	XM_376189.1
GI_42656493-S	114.9	122.1	120.3	LOC400940	XM_376031.1
GI_42656495-S	121.4	128.2	120.6	LOC400941	XM_376032.1
GI_42656498-S	98.5	98.3	97	LOC386597	XM_379073.1
GI_42656500-S	155.2	165	157.7	LOC339788	XM_379074.1
GI_42656509-S	120.1	119.3	118.8	LOC400943	XM_376034.1
GI_42656511-S	135.5	164.2	141.3	FAM10A3	XM_015334.6
GI_42656513-S	366	428	412.2	LOC400944	XM_379077.1
GI_42656521-S	131.3	187.3	114.8	KIAA1189	XM_371576.2
GI_42656533-S	93.5	104.2	96.9	LOC401020	XM_379145.1
GI_42656535-S	102.7	125.6	108.9	LOC401021	XM_379146.1
GI_42656537-S	149.2	175.9	165.5	LOC401022	XM_379147.1
GI_42656544-S	116.9	118.7	105.8	LOC401025	XM_379149.1
GI_42656546-S	119	115	104.7	FLJ25415	XM_371586.2
GI_42656547-S	362.5	425	399.4	LOC401026	XM_376160.1
GI_42656554-S	146.3	155.7	125.8	LOC401028	XM_376162.1
GI_42656560-S	155.7	141.7	136.9	KIAA1571	XM_371590.2
GI_42656574-S	216.6	265	252.5	LOC151300	XM_379154.1
GI_42656581-S	119.9	125.7	113.9	LOC401032	XM_379156.1
GI_42656583-S	101.9	93.5	92	CUL3	XM_376176.1
GI_42656589-S	187.4	216.1	195	LOC401033	XM_379158.1
GI_42656591-S	97.3	98	89.5	LOC151484	XM_379159.1
GI_42656593-S	133.5	143.9	132.8	LOC401034	XM_376179.1
GI_42656595-S	135.5	173	137.8	LOC401035	XM_376180.1
GI_42656598-S	123.7	148	127.9	KIF5C	XM_377774.1
GI_42656602-S	108.6	119.5	122.7	LOC402110	XM_377778.1
GI_42656611-S	339.4	421.2	372.9	LOC389090	XM_371606.2
GI_42656629-S	779.6	822.2	573.3	LOC402100	XM_377761.1
GI_42656635-S	105.3	100.6	98.1	LOC401072	XM_376243.1
GI_42656637-S	169.3	199.2	179.6	LOC401073	XM_379197.1
GI_42656639-S	104.7	116.5	113.5	LOC285286	XM_379198.1
GI_42656647-S	295.4	348.2	301.5	LOC401074	XM_376247.1
GI_42656649-S	160.2	145	153.7	LOC401075	XM_376248.1
GI_42656656-S	113.4	140.4	122.9	LOC401078	XM_379200.1
GI_42656658-S	107	95.9	95	LOC391544	XM_372993.2
GI_42656660-S	318.7	298.6	306.8	LOC401048	XM_379171.1
GI_42656664-S	106.8	124	106.5	LOC401049	XM_379172.1
GI_42656668-S	88.5	87	88	LOC401051	XM_379174.1

GI_42656670-S	344.3	452.7	399.3	LOC401052	XM_379175.1
GI_42656673-S	603.4	700.6	806.6	KIAA0218	XM_376203.1
GI_42656675-S	130.1	153.1	153.7	LOC401053	XM_379177.1
GI_42656686-S	97.4	105.6	105.2	LOC152274	XM_379179.1
GI_42656698-S	172.1	219.6	183.9	LOC401056	XM_379180.1
GI_42656700-S	124.4	140.2	141.8	LOC401057	XM_379181.1
GI_42656702-S	111	103.6	99	LOC401058	XM_379182.1
GI_42656706-S	144.7	136.4	170.5	LOC401059	XM_379184.1
GI_42656719-S	91.7	90.2	88.9	LOC401061	XM_379189.1
GI_42656724-S	161.6	159.3	151.2	LOC401062	XM_379190.1
GI_42656726-S	85.2	105.6	87.2	LOC401063	XM_376225.1
GI_42656730-S	156.2	154.3	126.7	LOC401064	XM_376227.1
GI_42656742-S	188.4	189.5	191.1	LOC285331	XM_376238.1
GI_42656747-S	134.5	160.6	138.2	LOC285401	XM_379195.1
GI_42656749-S	85.3	102.2	85.2	LOC401070	XM_376241.1
GI_42656753-S	95.9	109.6	96.9	LOC402123	XM_377797.1
GI_42656758-S	162.8	205.5	175.6	LOC401107	XM_379244.1
GI_42656760-S	130.7	157.8	144.4	LOC401109	XM_376292.1
GI_42656765-S	185.6	196.9	179.7	LOC220729	XM_049575.11
GI_42656771-S	97.3	91.4	94.8	LOC401106	XM_379243.1
GI_42656783-S	132.3	133.7	133.4	LOC152225	XM_379204.1
GI_42656787-S	152.6	187.2	172.2	LOC151658	XM_379205.1
GI_42656794-S	369.7	468.2	431.1	LOC401082	XM_376257.1
GI_42656796-S	83.9	77.7	74.4	LOC401083	XM_376258.1
GI_42656799-S	102.9	88.9	90.1	LOC285194	XM_379207.1
GI_42656819-S	131	153.8	145.8	LOC401086	XM_379213.1
GI_42656821-S	124.1	124.6	117.8	LOC389147	XM_371663.2
GI_42656822-S	109.8	112.1	95.8	KIAA1257	XM_371664.2
GI_42656823-S	118.7	134.4	119.9	LOC401087	XM_376267.1
GI_42656826-S	132.6	149.4	130.1	LOC339942	XM_379214.1
GI_42656828-S	106.2	111.4	103.1	LOC132241	XM_379215.1
GI_42656854-S	127.1	260.1	312.7	LOC401093	XM_379228.1
GI_42656857-S	3870.3	3864.6	3226.9	LOC389168	XM_371672.2
GI_42656866-S	94.2	98.6	88.1	LOC401097	XM_376281.1
GI_42656872-S	142.9	155	132.5	LOC401099	XM_379233.1
GI_42656874-S	107.1	120.9	103	LOC93556	XM_376284.1
GI_42656878-S	230	275	262	LOC401100	XM_376287.1
GI_42656881-S	109	110.6	132.8	LOC401101	XM_379234.1
GI_42656883-S	161.6	173.9	158.3	LOC401103	XM_379235.1
GI_42656889-S	110.1	126	116.5	LOC389185	XM_374067.2
GI_42656890-S	147.1	151.5	131.2	LOC401104	XM_379240.1
GI_42656892-S	123.7	139.2	130.6	LOC401105	XM_376290.1
GI_42656896-S	98.6	98.7	107.3	OR5K1	XM_372997.2
GI_42656900-S	149.3	180.2	165.4	LOC402136	XM_377811.1

GI_42656902-S	98.1	88.7	94.2	LOC402141	XM_377815.1
GI_42656906-S	96.7	99.4	98.4	LOC402148	XM_377818.1
GI_42656910-S	290.2	300.5	269.7	LOC402152	XM_377820.1
GI_42656912-S	97.7	117.5	118.1	LOC402155	XM_377823.1
GI_42656916-S	102.3	105	100.7	LOC389205	XM_371692.2
GI_42656931-S	125.6	131.8	123.5	LOC401144	XM_379271.1
GI_42656935-S	111.5	120.1	105.1	LOC285556	XM_373030.2
GI_42656939-S	109	102.2	90.3	LOC401147	XM_376334.1
GI_42656946-S	139	163.2	160.2	LOC401150	XM_376338.1
GI_42656948-S	136.1	104	119	LOC401151	XM_379274.1
GI_42656955-S	429.6	472.2	456	LOC389221	XM_371705.2
GI_42656959-S	183.9	208.1	219.7	LOC401154	XM_376342.1
GI_42656961-S	453.2	374.6	417.4	KIAA1109	XM_371706.2
GI_42656964-S	416	543.7	465.5	LOC401155	XM_379276.1
GI_42656977-S	87.1	88	86.9	LOC401156	XM_379278.1
GI_42656991-S	111.2	104.3	90.9	LOC401159	XM_379287.1
GI_42656993-S	140	147.7	139.8	LOC340017	XM_379288.1
GI_42656995-S	238.3	254.8	247.8	LOC201725	XM_376349.1
GI_42657007-S	779.7	488.1	439.8	LOC401135	XM_379268.1
GI_42657010-S	107.1	111.1	104.7	LOC389208	XM_371695.2
GI_42657014-S	128.6	123.5	127.7	LOC401160	XM_376353.1
GI_42657022-S	123.8	115.3	122.4	LOC389247	XM_374099.2
GI_42657024-S	256.2	331.9	284.4	LOC401163	XM_379294.1
GI_42657027-S	102.6	106.4	95.5	LOC285441	XM_379295.1
GI_42657029-S	102.9	107.5	87.3	LOC401164	XM_379298.1
GI_42657032-S	134	154.9	137.9	LOC401165	XM_379299.1
GI_42657041-S	4932.3	4858.2	3516.4	LOC402176	XM_377841.1
GI_42657043-S	108.5	114.8	100.9	LOC401112	XM_379248.1
GI_42657045-S	97.4	99.9	82.5	LOC401113	XM_379249.1
GI_42657047-S	115.7	121.5	108.4	LOC401114	XM_376299.1
GI_42657060-S	252	302.7	234.9	LOC401118	XM_376301.1
GI_42657062-S	85.9	98.9	78.2	LOC285484	XM_376303.1
GI_42657067-S	101.9	114.4	96.8	LOC401119	XM_379255.1
GI_42657071-S	111.4	154.6	134	LOC401117	XM_379252.1
GI_42657075-S	114.6	104.2	114.7	FLJ13105	XM_376325.1
GI_42657079-S	101.8	101.2	110.4	LOC401129	XM_379265.1
GI_42657088-S	206.6	218.6	183.8	LOC401130	XM_376317.1
GI_42657091-S	104.1	99.6	100.2	LOC401120	XM_379256.1
GI_42657095-S	110	116.3	104.6	LOC401122	XM_376306.1
GI_42657105-S	76.6	78.2	78.1	LOC285547	XM_379258.1
GI_42657107-S	73.5	133.4	91.2	LOC152742	XM_379260.1
GI_42657116-S	174.7	159.7	144.1	ZCCHC4	XM_376310.1
GI_42657118-S	2654.4	2311.8	1481.6	LOC389203	XM_371691.2
GI_42657137-S	95.2	88.2	89	LOC401137	XM_376322.1

GI_42657147-S	77.7	70.4	77.2	LOC401166	XM_376364.1
GI_42657153-S	149.1	165.9	152.5	LOC401168	XM_379303.1
GI_42657158-S	155.5	161.3	154.4	LOC401169	XM_379306.1
GI_42657165-S	157	189.9	171.5	LOC401171	XM_379309.1
GI_42657172-S	99.5	110.5	111.1	LOC401172	XM_376370.1
GI_42657175-S	84.2	100.7	97.6	LOC401173	XM_379313.1
GI_42657177-S	103.7	97.7	99.9	LOC401174	XM_376371.1
GI_42657179-S	106	109.7	117.6	LOC134121	XM_376372.1
GI_42657181-S	149	174.5	157.2	LOC389271	XM_374113.2
GI_42657189-S	92.8	101.3	85	LOC401177	XM_379320.1
GI_42657192-S	114.2	130.3	131.3	LOC285626	XM_379371.1
GI_42657195-S	120.6	135	126.6	LOC285629	XM_376440.1
GI_42657197-S	102.9	115	94.2	LOC401216	XM_379372.1
GI_42657205-S	97.3	100.3	89.8	LOC257358	XM_379373.1
GI_42657207-S	189.2	243.4	230.7	LOC401217	XM_376443.1
GI_42657212-S	885	961.5	822	LOC401219	XM_379377.1
GI_42657216-S	118.6	140.4	120.2	LOC401221	XM_376447.1
GI_42657218-S	282.6	310.8	306.2	LOC389348	XM_374151.2
GI_42657219-S	127	125.6	112.6	LOC402235	XM_377918.1
GI_42657221-S	142.6	168	146	LOC402237	XM_377919.1
GI_42657223-S	100.4	87.8	94	LOC402238	XM_377920.1
GI_42657225-S	177.7	174.7	237.8	LOC401201	XM_379343.1
GI_42657229-S	181.9	227.2	199.2	LOC401202	XM_376412.1
GI_42657246-S	116.8	113.6	126.3	LOC153218	XM_376433.1
GI_42657252-S	150.3	173.6	161.8	LOC134466	XM_376436.1
GI_42657260-S	127.5	129.3	114.9	LOC402231	XM_377911.1
GI_42657279-S	98.5	91.1	98.5	LOC401208	XM_376427.1
GI_42657284-S	218.7	272.7	269.5	LOC340074	XM_379355.1
GI_42657286-S	456.4	566.5	471.1	LOC401210	XM_379359.1
GI_42657308-S	373.4	415.6	345.3	FLJ23563	XM_371740.2
GI_42657314-S	87.9	94.7	81.6	LOC401191	XM_376387.1
GI_42657316-S	106.9	110.6	102.1	LOC402214	XM_377896.1
GI_42657320-S	92.5	104.7	97.5	LOC340107	XM_379321.1
GI_42657324-S	99.7	99.4	89.4	LOC401178	XM_379323.1
GI_42657326-S	320.5	383.2	355.9	LOC340113	XM_379324.1
GI_42657330-S	106.1	114.7	110.6	LOC401180	XM_379325.1
GI_42657332-S	99.3	108.2	95.5	LOC401181	XM_379326.1
GI_42657334-S	160.1	169.1	135.2	LOC401182	XM_379327.1
GI_42657336-S	100.9	116.4	104.8	LOC401183	XM_376379.1
GI_42657338-S	131	167.3	150.9	LOC401184	XM_379328.1
GI_42657342-S	159	171.1	170	LOC389289	XM_371738.2
GI_42657343-S	117.4	134.4	129.5	LOC401185	XM_379331.1
GI_42657377-S	116.8	99.6	108.6	LOC401197	XM_376403.1
GI_42657380-S	271.1	263	223.9	LOC389302	XM_374125.2

GI_42657383-S	106.8	103.1	96.7	RGNEF	XM_376405.1
GI_42657403-S	97	91.7	100.6	LOC401223	XM_376453.1
GI_42657405-S	105.3	113.9	102	LOC401224	XM_376454.1
GI_42657410-S	153.1	184	161.9	LOC401226	XM_379382.1
GI_42657439-S	142.8	170.4	156.3	LOC401270	XM_376522.1
GI_42657442-S	656.2	583.4	627.2	ZNF450	XM_376525.1
GI_42657446-S	82.3	80.8	83.3	LOC401271	XM_376527.1
GI_42657448-S	98.2	96.8	109.3	LOC285758	XM_379430.1
GI_42657462-S	121.2	101.7	97.9	LOC285735	XM_379433.1
GI_42657464-S	306.4	385.8	336.6	LOC284397	XM_209180.4
GI_42657465-S	287.3	379	309.5	LOC401274	XM_376536.1
GI_42657467-S	118.6	123	122.7	LOC154092	XM_379434.1
GI_42657477-S	222.3	273.1	233.1	LOC153910	XM_379437.1
GI_42657479-S	139.7	138.7	127.9	LOC285740	XM_379438.1
GI_42657484-S	107.9	117.2	112.9	LOC401277	XM_379439.1
GI_42657486-S	123.2	150.2	127.6	LOC401278	XM_376541.1
GI_42657490-S	105.5	105.9	98.8	LOC401279	XM_379441.1
GI_42657496-S	169	186.9	175.6	LOC401229	XM_376461.1
GI_42657498-S	119.7	132.9	126.9	LOC285766	XM_379384.1
GI_42657500-S	133.2	147.1	138.9	LOC285768	XM_379386.1
GI_42657502-S	106.4	105.7	116.3	LOC401230	XM_379391.1
GI_42657504-S	169.5	191.5	167.6	LOC401231	XM_379392.1
GI_42657508-S	211.4	255.7	227.7	MGC39372	XM_376463.1
GI_42657510-S	163.2	180.3	171.5	LOC401232	XM_379393.1
GI_42657528-S	127.8	104.7	89.1	ANKRD6	XM_376519.1
GI_42657536-S	184	205.7	186.5	LOC401287	XM_379458.1
GI_42657540-S	280.7	323.4	311.3	LOC401288	XM_376557.1
GI_42657549-S	18306.1	16828	12458	LOC389445	XM_371857.2
GI_42657555-S	112.3	125.6	110.5	LOC401283	XM_379453.1
GI_42657559-S	95.8	117.4	98.4	LOC401284	XM_379454.1
GI_42657565-S	155	180.2	163.3	LOC401289	XM_379459.1
GI_42657567-S	127.5	135.1	128.4	LOC401290	XM_379460.1
GI_42657572-S	107.7	111.7	100	LOC401234	XM_379395.1
GI_42657575-S	195.4	202.7	226.3	LOC221710	XM_379396.1
GI_42657577-S	170.2	200.5	194.6	LOC401236	XM_376469.1
GI_42657580-S	608.8	1372.7	1182.6	LOC401237	XM_379398.1
GI_42657582-S	108.4	107.6	97.3	LOC401238	XM_376471.1
GI_42657584-S	95.9	94.7	98.4	LOC401239	XM_376472.1
GI_42657607-S	379.7	314.8	306.4	LOC401245	XM_379404.1
GI_42657624-S	224.5	238.8	199.5	LOC401253	XM_376491.1
GI_42657630-S	208.4	246.1	213	LOC401256	XM_379409.1
GI_42657632-S	305.6	368.4	331	LOC401257	XM_379410.1
GI_42657636-S	95.1	118.9	111	LOC401258	XM_379411.1
GI_42657639-S	105.1	113.4	113.1	LOC401259	XM_376498.1

GI_42657641-S	110.1	163.5	96.3	LOC401260	XM_376499.1
GI_42657645-S	96.7	105.9	98.2	LOC401261	XM_379413.1
GI_42657651-S	235.1	275.4	244.3	C6orf110	XM_371822.2
GI_42657661-S	425.3	432.3	364.8	LOC401264	XM_379417.1
GI_42657663-S	166.8	197.4	179	LOC401265	XM_376508.1
GI_42657667-S	175.8	214.4	204.5	LOC401291	XM_379461.1
GI_42657669-S	133.4	154.9	135.7	LOC401292	XM_379462.1
GI_42657671-S	99.8	106.1	103.3	LOC401293	XM_376558.1
GI_42657673-S	108.8	119.8	113	LOC401294	XM_379463.1
GI_42657675-S	149.5	176	167.4	LOC401295	XM_376560.1
GI_42657802-S	98.5	109.2	99	LOC389605	XM_374242.2
GI_42657830-S	94.2	96.2	90	USP42	XM_376571.1
GI_42657967-S	340.9	326.1	300.8	LOC401428	XM_376715.1
GI_42657971-S	451.2	549.7	521.3	KIAA1862	XM_044212.5
GI_42657986-S	493.1	652.7	605.2	LOC155036	XM_376722.1
GI_42658099-S	82.4	91.4	72.8	LOC401401	XM_376668.1
GI_42658141-S	134.7	173.8	146.9	LOC392736	XM_374481.2
GI_42658151-S	92.9	89.9	84.1	LOC402290	XM_377959.1
GI_42658173-S	1663.7	1757.5	1750	UNC84A	XM_379766.1
GI_42658179-S	213.8	230.9	217.5	LOC392617	XM_374386.2
GI_42658193-S	83	99.7	88.3	LOC402452	XM_379775.1
GI_42658197-S	387	385	417.4	LOC402454	XM_379776.1
GI_42658199-S	86.7	99.8	102.7	LOC402455	XM_374713.2
GI_42658205-S	106.1	107.8	98.6	LOC402458	XM_379781.1
GI_42658222-S	104.7	105.3	99.3	KIAA0960	XM_374404.2
GI_42658224-S	133	158.1	159.6	LOC392634	XM_374405.2
GI_42658226-S	218.5	259.5	224.8	LOC392636	XM_374406.2
GI_42658228-S	154.2	151.6	145.1	LOC402463	XM_380089.1
GI_42658230-S	1156.5	982.4	1035.4	LOC402464	XM_379792.1
GI_42658236-S	98.3	103.4	90.1	LOC402466	XM_380091.1
GI_42658240-S	131.4	156.8	154.1	LOC402469	XM_379797.1
GI_42658244-S	247.8	297.2	264.3	LOC285941	XM_380092.1
GI_42658248-S	91.8	108.1	106.6	LOC402471	XM_380094.1
GI_42658251-S	333.8	368	348.8	LOC402472	XM_380095.1
GI_42658255-S	129.6	125.2	120.9	LOC402473	XM_380096.1
GI_42658263-S	113.1	131.1	124.4	LOC89231	XM_379802.1
GI_42658265-S	134.6	138.5	134.6	LOC402476	XM_380099.1
GI_42658267-S	104.2	130.6	106.2	LOC402477	XM_379803.1
GI_42658274-S	119.9	136.6	119.7	LOC402480	XM_380100.1
GI_42658276-S	185.5	236	218.2	LOC402481	XM_379809.1
GI_42658279-S	100.2	122.6	122.2	LOC392887	XM_374604.2
GI_42658281-S	92.9	124	106.6	LOC402482	XM_379812.1
GI_42658283-S	112.5	112.8	113.9	LOC392661	XM_374428.2
GI_42658285-S	129.9	137.5	132.1	LOC402483	XM_380103.1

GI_42658289-S	94.3	119.7	101.5	LOC402485	XM_380104.1
GI_42658295-S	472	566.5	456.5	LOC402488	XM_379818.1
GI_42658301-S	1046.7	491.8	401.2	LOC285958	XM_380105.1
GI_42658308-S	113.9	111.1	114.8	LOC402493	XM_380106.1
GI_42658310-S	99.9	103	100.9	LOC402494	XM_379827.1
GI_42658312-S	404.6	485	419.6	LOC136288	XM_374435.2
GI_42658313-S	451.7	409	704	LOC402495	XM_379830.1
GI_42658326-S	81.5	101	90	LOC402504	XM_380107.1
GI_42658332-S	103.7	104.7	101.5	LOC402507	XM_380109.1
GI_42658342-S	121.8	152.4	120.8	LOC402512	XM_380111.1
GI_42658346-S	83.8	116.6	91.3	LOC402633	XM_379986.1
GI_42658358-S	104.5	114.4	110.4	LOC402639	XM_379993.1
GI_42658368-S	102.8	111.8	106.3	LOC402644	XM_379998.1
GI_42658370-S	88.1	90.4	81.9	LOC402645	XM_379999.1
GI_42658380-S	110.9	122.3	111.4	LOC402517	XM_379844.1
GI_42658384-S	120.2	126.9	129.1	LOC402519	XM_379846.1
GI_42658386-S	112	112.8	126.2	LOC402520	XM_379847.1
GI_42658402-S	134.4	146.5	136.7	LOC402528	XM_380115.1
GI_42658412-S	110.7	122.4	118.8	LOC402534	XM_380118.1
GI_42658426-S	108.9	118.7	108.7	LOC402541	XM_379860.1
GI_42658440-S	656.8	652.7	511.2	WBSCR24	XM_379866.1
GI_42658446-S	149.6	164.5	156.9	LOC402663	XM_380007.1
GI_42658452-S	95.1	95.5	102.2	LOC402668	XM_380010.1
GI_42658454-S	130.3	141.8	124.3	LOC402669	XM_380011.1
GI_42658480-S	232.8	263.4	255	LOC402557	XM_380126.1
GI_42658482-S	279.5	290.2	289.1	LOC402558	XM_379879.1
GI_42658486-S	108.6	128.7	130.2	LOC402559	XM_379881.1
GI_42658488-S	222.8	237.8	201.6	LOC402560	XM_380127.1
GI_42658496-S	235.8	264.9	246	LOC402563	XM_380128.1
GI_42658501-S	86.4	92.5	89.9	LOC402565	XM_379887.1
GI_42658506-S	162.9	200.6	169.6	FLJ34048	XM_380131.1
GI_42658518-S	127.3	124.1	99.3	LOC285989	XM_379896.1
GI_42658520-S	138.9	138.4	139.6	LOC402571	XM_379897.1
GI_42658525-S	2227.6	2570.2	2599.9	LOC392758	XM_374498.2
GI_42658538-S	532.1	603.7	521.7	DKFZP434A	XM_380018.1
GI_42658544-S	132.6	145.9	132.4	LOC402677	XM_380021.1
GI_42658546-S	91.4	100.1	105.8	LOC402679	XM_380022.1
GI_42658560-S	209.7	215.8	234.9	LOC402577	XM_379906.1
GI_42658564-S	794.8	977.1	751	LOC402578	XM_380135.1
GI_42658570-S	121.4	134.2	114.9	LOC402581	XM_379910.1
GI_42658576-S	114.7	109	124	LOC340340	XM_380137.1
GI_42658582-S	2117.7	2323.3	2149.5	LOC402587	XM_380139.1
GI_42658584-S	361.6	411.4	414.4	LOC286009	XM_379914.1
GI_42658588-S	87.2	97.2	98.8	LOC402588	XM_379917.1

GI_42658596-S	100.2	103	96.6	LOC402592	XM_380143.1
GI_42658602-S	105.4	120.4	116.8	LOC346653	XM_379921.1
GI_42658606-S	150.8	106.7	129.8	KIAA1170	XM_379923.1
GI_42658612-S	255.1	289.3	275.5	LOC392988	XM_374650.2
GI_42658616-S	101	108.8	100.7	LOC402597	XM_380147.1
GI_42658618-S	287.7	345.9	298.3	KIAA1466	XM_374529.2
GI_42658619-S	1189.9	1091.1	1283.9	NUP205	XM_374530.2
GI_42658623-S	114.4	136.6	127.2	LOC155006	XM_379931.1
GI_42658625-S	418.7	674.1	800.9	KIAA1549	XM_379932.1
GI_42658627-S	169.1	210.9	183.4	FLJ25778	XM_379933.1
GI_42658629-S	230.1	257	270	LOC402599	XM_380149.1
GI_42658637-S	93.3	108.2	87.8	LOC402603	XM_380150.1
GI_42658639-S	1066	871.9	700.8	LCHN	XM_379938.1
GI_42658643-S	90.9	102.4	93.8	LOC93432	XM_379940.1
GI_42658645-S	3326.7	2712.8	2663.3	LOC402617	XM_380151.1
GI_42658653-S	287.5	322.4	292	FLJ43692	XM_379959.1
GI_42658659-S	86.4	86.3	86.6	FLJ45737	XM_379965.1
GI_42658661-S	117.8	134.5	108.9	LOC402621	XM_379966.1
GI_42658663-S	426.2	507.7	481.7	KIAA0543	XM_379967.1
GI_42658665-S	223.1	254.8	242.5	C7orf32	XM_379968.1
GI_42658667-S	166.5	192.4	173.3	LOC90520	XM_380152.1
GI_42658669-S	250	290.2	259.6	LOC402622	XM_380153.1
GI_42658671-S	118.8	135.8	120.8	LOC402624	XM_379970.1
GI_42658673-S	100.1	179.1	103.7	LOC285972	XM_380154.1
GI_42658675-S	286.3	402.2	366.2	CSGlcA-T	XM_379974.1
GI_42658679-S	97.8	114.7	101.5	LOC402626	XM_380155.1
GI_42658683-S	123.7	137.5	109.7	LOC402628	XM_379976.1
GI_42658685-S	142.1	161.2	128.7	LOC402629	XM_379977.1
GI_42658687-S	342.4	385.5	390.4	LOC393073	XM_374702.2
GI_42658689-S	110.7	113.5	105.9	LOC402630	XM_380157.1
GI_42658709-S	6447.7	6299.7	5378.5	LOC402694	XM_380042.1
GI_42658711-S	105.4	120	105.4	LOC402695	XM_380044.1
GI_42658719-S	111.2	129.6	116.7	LOC402707	XM_380055.1
GI_42658723-S	109.4	112.5	91.2	LOC402709	XM_380057.1
GI_42658725-S	169.7	210.7	188.5	LOC402710	XM_380059.1
GI_42658745-S	102.2	130.5	115.1	LOC402720	XM_380077.1
GI_42658749-S	108.4	126.7	113.2	LOC402632	XM_380159.1
GI_42658751-S	90.8	86.1	89	LOC285888	XM_379979.1
GI_42658753-S	160.2	177	164.1	LOC155435	XM_379980.1
GI_42658755-S	93.8	111	97.2	LOC285889	XM_380160.1
GI_42658757-S	222.1	207.5	177.9	LOC392850	XM_374590.2
GI_42658761-S	91.8	87.5	83.2	LOC392852	XM_374592.2
GI_42658762-S	79.4	86.8	75.4	LOC154822	XM_380162.1
GI_42658769-S	2213.5	1839.8	1925.7	LOC401457	XM_376761.1

GI_42658782-S	2027.1	2569.4	2073.4	LOC401483	XM_376800.1
GI_42658785-S	114.7	125.1	106.3	LOC401484	XM_376801.1
GI_42658797-S	94	102.3	87.3	LOC389607	XM_372010.2
GI_42658801-S	97.6	105.2	107.6	LOC401442	XM_379543.1
GI_42658807-S	79.5	70.5	81.5	LOC401445	XM_379547.1
GI_42658811-S	139.6	151.5	147.3	LOC401446	XM_379548.1
GI_42658837-S	165.9	189.3	178.1	LOC401479	XM_376797.1
GI_42658843-S	140.9	144.7	154.5	LOC389689	XM_374283.2
GI_42658845-S	224.8	271.5	247	LOC401480	XM_379608.1
GI_42658853-S	194.2	210	210	LOC389632	XM_374251.2
GI_42658863-S	98.9	104.1	101.2	LOC401456	XM_379562.1
GI_42658866-S	539.5	730.9	402.6	MTSG1	XM_372031.2
GI_42658872-S	156.9	151.1	141	LOC349196	XM_379551.1
GI_42658875-S	93.6	91	94.6	LOC389628	XM_374249.2
GI_42658877-S	122.4	141.9	129.5	LOC401449	XM_379552.1
GI_42658879-S	114.2	124.3	111.6	LOC401450	XM_376746.1
GI_42658881-S	104.6	108.1	94	LOC389622	XM_372024.2
GI_42658882-S	163.1	193.5	161.9	LOC401451	XM_379553.1
GI_42658884-S	324.1	398.3	351.1	LOC157273	XM_379554.1
GI_42658887-S	134.1	144.5	141	LOC401452	XM_376750.1
GI_42658896-S	98.5	103.7	88.8	LOC401485	XM_376809.1
GI_42658900-S	92.6	92.4	83.2	LOC389295	XM_374123.2
GI_42658907-S	89.7	95.7	94.4	LOC401468	XM_376785.1
GI_42658911-S	2690.8	3029.5	2382.6	LOC401470	XM_376787.1
GI_42658913-S	212.9	266	234.1	LOC286144	XM_379592.1
GI_42658917-S	97.8	129.2	111.2	LOC392255	XM_373260.2
GI_42658923-S	168	225.9	191.7	LOC401472	XM_376791.1
GI_42658925-S	171	183.4	176.6	LOC401473	XM_379596.1
GI_42658927-S	137.5	163	141.5	FLJ10489	XM_379597.1
GI_42658937-S	121.8	120.2	122.6	LOC401476	XM_379603.1
GI_42658939-S	80.4	82.3	76.4	LOC401477	XM_379605.1
GI_42658946-S	126	143.4	136.2	LOC401459	XM_376771.1
GI_42658949-S	108	107	106.9	LOC389659	XM_374270.2
GI_42658950-S	136	149.5	142.7	LOC401460	XM_376774.1
GI_42658952-S	131	155.2	133	LOC286177	XM_379582.1
GI_42658956-S	106.6	92	90	TOX	XM_376776.1
GI_42658960-S	89.8	95.6	81.7	LOC401462	XM_379583.1
GI_42658964-S	95.2	89.7	88.6	LOC286186	XM_379586.1
GI_42658975-S	158.9	173	159.6	SLC10A5	XM_376781.1
GI_42658984-S	157.8	151.8	143.8	LOC402343	XM_378035.1
GI_42658989-S	90.9	93.5	87.4	LOC389649	XM_372037.2
GI_42658991-S	145.1	169.4	183.4	FLJ32731	XM_372038.2
GI_42658994-S	165.5	167.5	156.2	LOC401557	XM_379676.1
GI_42658996-S	168.3	190.2	174.2	C9orf62	XM_376924.1

GI_42658998-S	128.4	165.9	143.8	LOC401558	XM_379677.1
GI_42659002-S	670.7	637.7	929	LOC90120	XM_379680.1
GI_42659006-S	111	127.4	104.4	LOC402381	XM_378089.1
GI_42659008-S	182.5	248.3	196.7	LOC402382	XM_378090.1
GI_42659027-S	92.7	91.2	80.3	LOC401535	XM_376885.1
GI_42659031-S	590.1	443.6	464.1	LOC401536	XM_379645.1
GI_42659033-S	220.7	210.8	182.7	LOC401537	XM_376888.1
GI_42659039-S	273.1	259.5	275.5	LOC401560	XM_376925.1
GI_42659043-S	105.2	107.4	96.8	LOC401561	XM_379682.1
GI_42659048-S	125.9	160.8	141.3	LOC401562	XM_376930.1
GI_42659050-S	104.8	126.9	104.3	LOC401563	XM_376931.1
GI_42659054-S	2474.8	2812.2	2424.4	FUBP3	XM_376917.1
GI_42659063-S	125	143.1	118.4	LOC401508	XM_376840.1
GI_42659069-S	92.3	95.5	88.9	LOC402366	XM_378063.1
GI_42659078-S	107.5	104.4	101.7	LOC402367	XM_378064.1
GI_42659088-S	88.2	103.8	90.9	LOC401518	XM_379638.1
GI_42659101-S	116.4	115.5	123.9	LOC389749	XM_372109.2
GI_42659113-S	384.6	475.1	409.4	LOC401528	XM_379642.1
GI_42659115-S	117.7	117.6	108.1	LOC401529	XM_376872.1
GI_42659123-S	101.7	111.2	102.5	LOC401565	XM_376939.1
GI_42659130-S	122.2	142.8	128	LOC375719	XM_372110.2
GI_42659132-S	149.4	172.6	154	LOC401539	XM_379648.1
GI_42659140-S	157.3	154.5	160.5	LOC401568	XM_376950.1
GI_42659142-S	196.2	221.8	205.2	LOC286238	XM_379684.1
GI_42659144-S	115.8	126.5	117.6	LOC401487	XM_376814.1
GI_42659148-S	136.3	146.5	125.4	LOC401488	XM_379617.1
GI_42659154-S	114.5	131.6	131.5	LOC401491	XM_379622.1
GI_42659164-S	116.3	125.4	115.1	LOC401492	XM_379623.1
GI_42659167-S	99.8	103.8	90	LOC401494	XM_376819.1
GI_42659169-S	134.5	132.8	120.4	LOC401495	XM_379625.1
GI_42659172-S	191	209.3	205	C9orf14	XM_376821.1
GI_42659176-S	111.8	125.2	101.1	LOC401497	XM_376822.1
GI_42659178-S	105.6	121.1	101.4	LOC401498	XM_376824.1
GI_42659182-S	958.7	631.4	676.3	LOC401500	XM_379629.1
GI_42659193-S	337.3	416.5	379	KIAA0258	XM_376830.1
GI_42659195-S	225.5	266.2	231.6	LOC401503	XM_379630.1
GI_42659199-S	222.1	277.6	224.7	LOC158376	XM_379632.1
GI_42659207-S	7332.4	6656.3	6220.9	LOC401505	XM_376833.1
GI_42659210-S	130.2	150.4	147.5	LOC401506	XM_379635.1
GI_42659216-S	152.7	167.5	148.5	LOC402357	XM_378052.1
GI_42659220-S	98.5	92.6	85.9	FLJ10232	XM_378199.1
GI_42659222-S	97.2	109.3	99.7	LOC401543	XM_379656.1
GI_42659238-S	290.8	376.2	349.6	LOC401547	XM_376900.1
GI_42659240-S	102.9	122.7	94.9	LOC389785	XM_372137.2

GI_42659246-S	124	156.4	149.9	LOC286333	XM_379665.1
GI_42659248-S	576.4	479.4	532.5	KIAA0674	XM_376903.1
GI_42659254-S	143	143.4	124.7	LOC401550	XM_379667.1
GI_42659257-S	120.6	119.7	124.2	LOC389789	XM_372140.2
GI_42659267-S	138.9	187.7	154.2	LOC401552	XM_379668.1
GI_42659275-S	283.2	335.4	305.8	LOC389794	XM_374306.2
GI_42659277-S	714.4	669.5	683.5	LOC401553	XM_379671.1
GI_42659279-S	95.1	94.4	87.3	LOC401554	XM_379672.1
GI_42659293-S	121	132.1	102.8	LOC402377	XM_378080.1
GI_42659301-S	229.4	346	306	LOC389772	XM_372128.2
GI_42659317-S	98.3	99.6	110.2	LOC399763	XM_374803.1
GI_42659320-S	119.8	154.7	136.5	LOC170371	XM_378226.1
GI_42659322-S	103.9	105.2	97.4	LOC387726	XM_373481.2
GI_42659325-S	98.7	109.6	107.9	LOC399832	XM_378259.1
GI_42659327-S	174.3	201.2	183.1	LOC399833	XM_378260.1
GI_42659332-S	123.2	122.7	111.6	LOC399827	XM_378255.1
GI_42659341-S	126.1	169.5	166	LOC387694	XM_370565.2
GI_42659345-S	99.3	98.8	86.9	LOC170425	XM_378240.1
GI_42659368-S	1172.5	1021.5	753.7	PDCD11	XM_374829.1
GI_42659379-S	110	108.2	103.9	LOC399810	XM_374832.1
GI_42659381-S	256.8	338.9	286.3	LOC143188	XM_378251.1
GI_42659388-S	94.3	105.9	99.8	LOC387712	XM_370577.2
GI_42659391-S	105	117.9	116.1	LOC401647	XM_377129.1
GI_42659395-S	130.6	147.9	138.3	LOC387673	XM_370555.2
GI_42659399-S	132.4	156.5	133.1	LOC399747	XM_374787.1
GI_42659406-S	88.1	91	88.9	LOC389959	XM_372312.2
GI_42659420-S	183.4	159.1	147.5	LOC399818	XM_374839.1
GI_42659431-S	173.8	167.4	155.6	LOC399815	XM_374836.1
GI_42659437-S	116.6	122	128.3	LOC399706	XM_378200.1
GI_42659439-S	84.5	80.7	90.5	LOC282980	XM_378201.1
GI_42659443-S	195.6	256.8	222	LOC399708	XM_378203.1
GI_42659454-S	95.3	101.7	100.1	LOC399716	XM_374767.1
GI_42659459-S	102.7	100.9	94.2	LOC399717	XM_378210.1
GI_42659461-S	100.9	105.6	101.1	LOC254312	XM_378211.1
GI_42659463-S	394.4	385.4	377.6	USP6NL	XM_374768.1
GI_42659465-S	121.5	135.8	123.8	LOC399718	XM_374769.1
GI_42659468-S	116.9	115.8	115.6	LOC399719	XM_374770.1
GI_42659493-S	112.1	121.8	113.2	LOC399841	XM_374854.1
GI_42659497-S	120.5	143	129	LOC399768	XM_378228.1
GI_42659502-S	204.2	269.4	235.8	LOC283025	XM_378230.1
GI_42659511-S	215.6	236.7	232.1	LOC219690	XM_378232.1
GI_42659524-S	294.5	363.3	303	LOC399786	XM_378236.1
GI_42659526-S	249	269.4	327.5	LOC283050	XM_378238.1
GI_42659530-S	1411.5	1430.7	1262.3	LOC399788	XM_374817.1

GI_42659532-S	125.2	141	120.6	LOC401644	XM_377117.1
GI_42659538-S	112.2	105	109.3	LOC387635	XM_370532.2
GI_42659544-S	206.9	257.1	273.2	ANKRD26	XM_374779.1
GI_42659549-S	280.3	255.5	225.3	LOC220906	XM_374781.1
GI_42659552-S	135.7	118.3	113.1	LOC387647	XM_373451.2
GI_42659560-S	89.8	90.4	104.6	LOC399737	XM_378219.1
GI_42659564-S	98.8	102.2	76.5	LOC387655	XM_370545.2
GI_42659567-S	126.2	121.1	116.3	LOC401638	XM_377109.1
GI_42659569-S	134	157.2	140	LOC401639	XM_377110.1
GI_42659571-S	186.4	208.4	179.4	LOC387720	XM_370584.2
GI_42659577-S	157.7	192.1	172.7	KIAA1377	XM_374927.1
GI_42659581-S	258.1	219.8	237.3	DNCH2	XM_370652.2
GI_42659583-S	96.9	94.4	96.7	KIAA1826	XM_370653.2
GI_42659588-S	122.5	127.6	113	LOC399948	XM_374932.1
GI_42659594-S	109.7	123.4	110.5	LOC399951	XM_378309.1
GI_42659596-S	101.1	107	110.4	LOC399954	XM_378311.1
GI_42659598-S	105.3	120.4	103.2	LOC283143	XM_378312.1
GI_42659606-S	185.1	204.5	189.5	LOC399955	XM_378313.1
GI_42659610-S	176.7	212.7	201.1	LOC399957	XM_374937.1
GI_42659614-S	2055.2	1212.6	591.8	LOC399959	XM_378316.1
GI_42659619-S	215.8	247.3	232.2	LOC399961	XM_378317.1
GI_42659621-S	119.8	129.4	119.7	LOC390271	XM_372441.2
GI_42659626-S	195	222.8	206.2	LOC399968	XM_374945.1
GI_42659631-S	868	1043.6	927.5	LOC399972	XM_378321.1
GI_42659634-S	158.5	161.9	146.6	LOC399975	XM_374948.1
GI_42659638-S	1381.2	1636.9	1652	LOC399979	XM_374949.1
GI_42659640-S	113.9	110.7	111.5	LOC399980	XM_378326.1
GI_42659644-S	215.2	245	222.5	LOC283177	XM_378327.1
GI_42659655-S	95.7	119	99.3	LOC399898	XM_374885.1
GI_42659661-S	121.3	141.6	124.2	MPEG1	XM_166227.4
GI_42659668-S	135.6	148	153.1	LOC399900	XM_374890.1
GI_42659673-S	107.9	117.3	109.5	LOC399904	XM_374893.1
GI_42659675-S	222.5	306.1	275.6	LOC387779	XM_370632.2
GI_42659678-S	371.4	532.9	487.4	LOC399909	XM_374898.1
GI_42659685-S	229	375.7	317.6	LOC399912	XM_378297.1
GI_42659687-S	114.1	125.7	120.7	LOC399913	XM_374899.1
GI_42659693-S	119.9	133.4	115.6	LOC387785	XM_373507.2
GI_42659694-S	394.9	406.8	346.4	LOC399917	XM_374902.1
GI_42659696-S	113.6	116.8	117.5	LOC390217	XM_372420.2
GI_42659698-S	144	139	137	LOC390148	XM_372389.2
GI_42659700-S	114.7	110.9	117.4	LOC401687	XM_377200.1
GI_42659708-S	74.6	95.7	76.4	LOC401694	XM_377218.1
GI_42659716-S	97.1	121.7	100.3	LOC399920	XM_378300.1
GI_42659718-S	105	105.2	93.5	LOC399921	XM_374904.1

GI_42659720-S	158.8	138.8	140.3	LOC399922	XM_374905.1
GI_42659724-S	99.4	111.1	93	LOC399924	XM_378301.1
GI_42659728-S	1061.6	1040	710	KIAA0280	XM_370635.2
GI_42659730-S	206	264.2	225.9	LOC399925	XM_374909.1
GI_42659734-S	13314.1	13205	9489.2	LOC399927	XM_374911.1
GI_42659736-S	359	423.2	423.2	XRRA1	XM_374912.1
GI_42659738-S	106.9	98.6	94.4	LOC387789	XM_373509.2
GI_42659741-S	107.8	115.1	107.9	LOC283214	XM_378303.1
GI_42659743-S	88.4	98.6	88.4	LOC399930	XM_378304.1
GI_42659749-S	96.1	116	90.2	LOC399933	XM_378305.1
GI_42659777-S	105.3	106.2	107.9	LOC399940	XM_374920.1
GI_42659789-S	142.5	161.9	158.6	LOC399851	XM_378266.1
GI_42659791-S	104.2	107.4	104.8	LOC387743	XM_373488.2
GI_42659797-S	364.1	446.9	384.9	LOC387750	XM_370607.2
GI_42659804-S	115.7	128.7	91.9	LOC399865	XM_378271.1
GI_42659806-S	194.6	229.2	233.7	LOC399866	XM_378272.1
GI_42659808-S	100.5	105.7	94.9	LOC399867	XM_378273.1
GI_42659810-S	96.3	104.3	101.4	LOC387755	XM_370613.2
GI_42659814-S	118.2	115.9	100.9	LOC399872	XM_378276.1
GI_42659822-S	111.5	128.9	129.7	LOC399875	XM_378279.1
GI_42659824-S	117.4	126.4	118.2	LOC399876	XM_378280.1
GI_42659833-S	110.2	119.2	111.7	LOC399879	XM_378283.1
GI_42659836-S	323	448.3	258.3	LOC387763	XM_373497.2
GI_42659838-S	80.3	93.2	88.3	LOC399884	XM_378286.1
GI_42659840-S	120.3	119.4	120.2	LOC399886	XM_378288.1
GI_42659842-S	945.2	1041.6	932.9	DKFZp779M(	XM_374877.1
GI_42659844-S	731.5	749	636.7	LOC114971	XM_374879.1
GI_42659846-S	104.9	107.7	108.5	LOC399888	XM_374880.1
GI_42659851-S	95.8	90.1	112.6	LOC399892	XM_374882.1
GI_42659855-S	107.9	124.7	118.4	LOC401660	XM_377147.1
GI_42659867-S	155.7	166.1	158.8	LOC390046	XM_372351.2
GI_42659871-S	111.6	137.6	115	LOC401667	XM_377159.1
GI_42659875-S	117.5	138.5	139.4	LOC401675	XM_377179.1
GI_42659883-S	180.9	204.5	210	LOC401681	XM_377189.1
GI_42659894-S	98.3	102.5	94.7	LOC256021	XM_378372.1
GI_42659896-S	164.5	202.6	196.4	LOC338809	XM_378374.1
GI_42659922-S	107.1	111	88.9	LOC400023	XM_374972.1
GI_42659925-S	92.3	101.3	97.3	LOC400025	XM_374973.1
GI_42659928-S	630.8	877.6	917.2	LOC400027	XM_378350.1
GI_42659930-S	546.8	740.2	816.9	ARID2	XM_370690.2
GI_42659933-S	101.8	111.7	113.2	LOC400030	XM_378353.1
GI_42659938-S	120.6	145.3	122.3	LOC387856	XM_370691.2
GI_42659944-S	100.7	124.2	123.1	LOC283332	XM_378355.1
GI_42659948-S	101.9	113.3	110.9	LOC283400	XM_378356.1

GI_42659957-S	132.8	140.7	127.6	LOC400043	XM_378360.1
GI_42659974-S	192.6	152.9	142.8	LOC400047	XM_378363.1
GI_42659979-S	123.2	120.5	131.9	LOC400050	XM_378365.1
GI_42659981-S	107.1	115.7	104.6	LOC400051	XM_378366.1
GI_42659988-S	268.9	322.3	283.9	LOC401716	XM_377262.1
GI_42659994-S	128.1	129.6	130	LOC400092	XM_378398.1
GI_42659999-S	98.4	99.3	90.5	LOC399993	XM_378336.1
GI_42660011-S	78.9	85.6	89.2	LOC400002	XM_378339.1
GI_42660017-S	394.6	476.4	354.4	LOC400006	XM_378342.1
GI_42660032-S	306.5	375.4	329.1	LOC196415	XM_378346.1
GI_42660034-S	1013.6	1209.6	1058.6	LOC144363	XM_370685.2
GI_42660046-S	94.2	97.4	93.8	LOC400082	XM_375004.1
GI_42660048-S	124.4	133.1	130.1	LOC400083	XM_375005.1
GI_42660055-S	101.4	99.2	101.7	LOC400084	XM_378389.1
GI_42660057-S	156.3	180.1	183.3	LOC144678	XM_378390.1
GI_42660063-S	100.6	101.6	88.9	LOC400088	XM_378393.1
GI_42660065-S	95.7	110.7	94.1	LOC116437	XM_378394.1
GI_42660071-S	107.3	124.8	114.6	KIAA1110	XM_370667.2
GI_42660072-S	110.9	124.5	117.2	LOC399982	XM_378328.1
GI_42660076-S	91.9	116.1	105.3	LOC399984	XM_378330.1
GI_42660078-S	145.4	177.8	160.8	LOC399986	XM_378331.1
GI_42660080-S	108.3	114.1	108.9	LOC399987	XM_378332.1
GI_42660082-S	82.9	88.4	89.2	LOC399990	XM_374952.1
GI_42660098-S	226.5	271.3	242.5	KIAA1853	XM_375000.1
GI_42660100-S	109.3	122.6	116	LOC144742	XM_378388.1
GI_42660112-S	118.9	117.5	114.4	LOC144776	XM_375033.1
GI_42660116-S	142.9	174.4	155.7	LOC400154	XM_378428.1
GI_42660129-S	277.1	282.7	298.8	LOC387945	XM_370732.2
GI_42660137-S	112.6	99.7	105	LOC400099	XM_378399.1
GI_42660139-S	3733	3733.9	2589	LOC387902	XM_370710.2
GI_42660142-S	25312.6	25818	19936	LOC387908	XM_370714.2
GI_42660143-S	125.2	141	125.4	LOC400108	XM_378404.1
GI_42660151-S	139.2	178	144	LOC387915	XM_373561.2
GI_42660159-S	190	187.7	168.2	LOC400121	XM_375018.1
GI_42660164-S	136.8	158.5	133.5	LOC400123	XM_378411.1
GI_42660166-S	93.9	106.3	93.6	LOC400125	XM_378412.1
GI_42660173-S	122.5	134.7	122	LOC400131	XM_378414.1
GI_42660175-S	153.9	167.9	154.1	LOC400132	XM_375023.1
GI_42660188-S	108	119.5	111.7	LOC144766	XM_378419.1
GI_42660193-S	182.2	209.4	171.9	LOC387934	XM_370729.2
GI_42660196-S	198.2	233.3	214.1	LOC400145	XM_375031.1
GI_42660198-S	468.6	460.1	426.3	TBC1D4	XM_375032.1
GI_42660207-S	77.2	92.6	84.7	LOC400161	XM_378434.1
GI_42660209-S	108.6	101.8	105.5	LOC400163	XM_378436.1

GI_42660213-S	231.8	256.4	227.2	LOC400165	XM_375038.1
GI_42660215-S	104.5	80.5	92.5	LOC387949	XM_370733.2
GI_42660217-S	98	113.6	101.8	LOC400167	XM_378439.1
GI_42660219-S	146.4	167.1	151.1	LOC400169	XM_375039.1
GI_42660221-S	127.9	133.8	128.5	LOC401740	XM_377305.1
GI_42660224-S	145	176.7	155.1	LOC400171	XM_378441.1
GI_42660228-S	148.9	156.8	153.3	LOC400172	XM_375041.1
GI_42660230-S	596.1	273	1299	DKFZP434B	XM_375042.1
GI_42660245-S	149.2	198.9	159.8	KIAA1305	XM_370756.2
GI_42660251-S	127	121.2	106.1	LOC387982	XM_370760.2
GI_42660254-S	427.8	337.4	443.8	LOC387984	XM_170749.7
GI_42660260-S	89.7	109.1	90.6	LOC400207	XM_375076.1
GI_42660264-S	114.4	97	105	LOC400208	XM_378453.1
GI_42660266-S	112.1	126.6	103.1	LOC283547	XM_378454.1
GI_42660274-S	92.8	99.1	94	LOC283551	XM_378455.1
GI_42660276-S	111.7	129.4	120.9	LOC400212	XM_378456.1
GI_42660279-S	93.1	99.4	80.8	LOC400213	XM_378457.1
GI_42660285-S	411.4	459	369.1	KIAA0831	XM_375080.1
GI_42660287-S	339.8	199.5	242.6	LOC400214	XM_375081.1
GI_42660289-S	138.7	154.7	145.6	LOC400216	XM_378460.1
GI_42660295-S	70.9	66	85.2	LOC400219	XM_375084.1
GI_42660301-S	76.6	95.2	75.1	ZBTB1	XM_375086.1
GI_42660303-S	169.3	174.9	208.7	PLEKHH1	XM_375087.1
GI_42660305-S	121.2	130.3	121.3	LOC400223	XM_375088.1
GI_42660310-S	84.2	105.9	105.3	LOC400224	XM_375090.1
GI_42660325-S	260.3	356.8	294.6	LOC400231	XM_378467.1
GI_42660329-S	170.4	185.5	185.4	LOC400234	XM_378470.1
GI_42660334-S	224.9	253.2	249.3	LOC400236	XM_378472.1
GI_42660336-S	137.9	148.9	131.5	LOC400238	XM_378473.1
GI_42660339-S	187.9	174.6	153.7	LOC400239	XM_375101.1
GI_42660343-S	189.1	205.4	157.1	LOC400242	XM_378476.1
GI_42660347-S	181.5	208.9	194.5	LOC388009	XM_373604.2
GI_42660350-S	126.7	135.1	121.1	LOC400249	XM_378482.1
GI_42660360-S	115.5	145.2	132.2	LOC145216	XM_378487.1
GI_42660363-S	88.9	100.5	97.5	LOC374569	XM_370777.2
GI_42660369-S	104.7	106.2	105.1	LOC400258	XM_375108.1
GI_42660371-S	435.6	494.7	525.3	LOC388022	XM_370779.2
GI_42660386-S	139.9	186.4	168.9	LOC401766	XM_377337.1
GI_42660388-S	129.3	156.3	157.5	KIAA0323	XM_377338.1
GI_42660390-S	85.4	86.4	84.7	LOC401778	XM_377343.1
GI_42660392-S	125.9	131.7	117.1	KIAA0602	XM_377355.1
GI_42660398-S	170.6	297.7	169.4	LOC283697	XM_373624.2
GI_42660407-S	147.3	138.8	142.6	LOC390561	XM_372560.2
GI_42660413-S	170.4	207	202.8	LOC388104	XM_370848.2

GI_42660416-S	110.7	112.8	104.1	LOC400350	XM_378506.1
GI_42660428-S	111.6	128.1	124.8	LOC145845	XM_378507.1
GI_42660430-S	132.8	166.1	150.6	LOC400359	XM_375190.1
GI_42660432-S	97.7	93.6	98.2	LOC400360	XM_375191.1
GI_42660434-S	110.3	97.4	87.6	LOC388113	XM_373625.2
GI_42660445-S	285.9	307.5	243.2	LOC400368	XM_378511.1
GI_42660448-S	108.1	120.2	111.2	LOC400369	XM_378512.1
GI_42660461-S	115	146.9	104.6	LOC283663	XM_378514.1
GI_42660475-S	168	187.9	172.8	LOC400382	XM_375210.1
GI_42660477-S	166.4	178.3	170.6	MGC4809	XM_370870.2
GI_42660481-S	244.9	333.4	285	LOC388131	XM_373632.2
GI_42660495-S	100.7	108.4	100.6	LOC283731	XM_378525.1
GI_42660501-S	181.7	214.2	160.7	LOC400398	XM_378528.1
GI_42660505-S	103.6	102.6	99.7	LOC388140	XM_373636.2
GI_42660507-S	110.9	137.5	116.9	LOC253044	XM_378532.1
GI_42660509-S	213.2	279.4	247.2	LOC390611	XM_372581.2
GI_42660513-S	134	110	107.5	LOC390616	XM_372584.2
GI_42660518-S	85.5	112.7	90.3	LOC400411	XM_378535.1
GI_42660520-S	127.7	125.4	113.5	MESDC2	XM_370880.2
GI_42660535-S	126.3	141.6	131.2	LOC401812	XM_377377.1
GI_42660537-S	104.5	109.8	103.1	LOC390575	XM_372568.2
GI_42660541-S	95.9	92.8	90	LOC401819	XM_377388.1
GI_42660543-S	231.8	262	237.7	LOC401820	XM_377390.1
GI_42660551-S	329.4	489.8	406.8	LOC388165	XM_370897.2
GI_42660553-S	152.2	153.4	140.9	LOC400435	XM_375246.1
GI_42660569-S	174.5	243.6	218.8	LOC283761	XM_378542.1
GI_42660572-S	185.5	202.7	199.7	MGC14386	XM_370908.2
GI_42660574-S	137.2	174.5	135.7	LOC400451	XM_375260.1
GI_42660578-S	109.9	101.5	96.7	LOC400454	XM_375263.1
GI_42660580-S	95.2	112.8	82.4	LOC283682	XM_378544.1
GI_42660582-S	99	100.8	97.8	LOC400456	XM_378545.1
GI_42660584-S	144.7	172.3	141.5	LOC145820	XM_378546.1
GI_42660586-S	126.4	115.4	107.1	LOC388179	XM_373649.2
GI_42660587-S	95.9	93	93	LOC388181	XM_370910.2
GI_42660598-S	87.9	102.2	84.7	LOC145814	XM_372592.2
GI_42660600-S	162.5	192.1	150.4	LOC400461	XM_375266.1
GI_42660606-S	184.3	225.3	250.7	LOC400464	XM_375268.1
GI_42660608-S	132.7	148.1	129.9	LOC400465	XM_375269.1
GI_42660610-S	188.8	206.8	184.4	LOC400296	XM_375145.1
GI_42660614-S	111.8	112.5	96	LOC400298	XM_375147.1
GI_42660619-S	82.9	94.4	92.1	LOC400301	XM_375150.1
GI_42660621-S	186.7	229	184.1	LOC400302	XM_378493.1
GI_42660627-S	127.6	125.8	127.8	LOC400307	XM_378494.1
GI_42660629-S	250.6	319.2	262	DKFZP547L1	XM_375153.1

GI_42660632-S	106.6	120.7	121	LOC400309	XM_375154.1
GI_42660635-S	195.9	243.3	215.7	LOC388073	XM_373616.2
GI_42660640-S	193.8	231.6	214	LOC400314	XM_378496.1
GI_42660646-S	165.9	157.9	167.6	LOC388158	XM_373641.2
GI_42660656-S	107.9	106.2	108.2	LOC400431	XM_375242.1
GI_42660660-S	103.3	111.6	101.2	LOC401824	XM_377394.1
GI_42660666-S	152.8	156.1	150.3	LOC400320	XM_375163.1
GI_42660673-S	97	99.8	93.7	LOC401806	XM_377369.1
GI_42660677-S	181.9	233.5	184.8	LOC400336	XM_375170.1
GI_42660706-S	96.8	111.7	92.4	LOC400499	XM_375302.1
GI_42660720-S	112	123.1	126.6	LOC400505	XM_378567.1
GI_42660736-S	105	113.4	115.3	LOC146177	XM_370944.2
GI_42660740-S	122.8	128.2	124.9	LOC390684	XM_372615.2
GI_42660747-S	253	341.7	289.7	LOC283887	XM_375316.1
GI_42660751-S	146.1	145.9	139.2	LOC400512	XM_378573.1
GI_42660771-S	113.6	111.8	105.8	LOC400537	XM_375357.1
GI_42660776-S	152.9	172.9	173.4	LOC400538	XM_378601.1
GI_42660794-S	382.7	534.7	499.2	LOC388284	XM_370984.2
GI_42660799-S	178.9	214	210.6	LOC400542	XM_375363.1
GI_42660801-S	109.3	125.4	111.9	LOC400543	XM_375364.1
GI_42660803-S	500.6	830.5	622.5	LOC400544	XM_378609.1
GI_42660811-S	134.4	149.3	131.5	LOC401858	XM_377439.1
GI_42660817-S	127.7	121.9	110.2	LOC400535	XM_378594.1
GI_42660821-S	395.1	458.8	410.5	LOC400555	XM_375379.1
GI_42660823-S	987.9	1181.5	1062.6	MGC23284	XM_378628.1
GI_42660828-S	108.2	113.7	91.7	LOC400556	XM_378629.1
GI_42660832-S	667.9	777	711.2	LOC400558	XM_378631.1
GI_42660836-S	115.7	116.7	112.2	LOC400560	XM_378632.1
GI_42660838-S	102.1	109.6	125.5	LOC400561	XM_378633.1
GI_42660843-S	101.3	110.7	108.7	LOC400563	XM_375384.1
GI_42660850-S	259	346.4	241.1	LOC400565	XM_378637.1
GI_42660854-S	188.4	224.9	185.5	LOC146443	XM_378558.1
GI_42660858-S	191.4	209.7	199.6	KIAA1987	XM_375298.1
GI_42660870-S	116.8	100.8	100.9	LOC400496	XM_378562.1
GI_42660876-S	208.1	230.1	220.9	LOC400550	XM_378620.1
GI_42660878-S	95.7	102.9	96.1	LOC400551	XM_378621.1
GI_42660888-S	128.1	184.3	156.9	LOC400531	XM_378586.1
GI_42660890-S	133.6	132.8	127.5	LOC400532	XM_378588.1
GI_42660894-S	120.7	115.4	128.5	LOC146481	XM_375353.1
GI_42660903-S	227.9	279.4	250.2	LOC388295	XM_373693.2
GI_42660906-S	102.6	132.5	128.5	LOC400547	XM_375373.1
GI_42660914-S	101.2	97.5	100.2	LOC400548	XM_378617.1
GI_42660918-S	130.5	131.9	137.1	LOC401860	XM_377445.1
GI_42660922-S	93.7	96.5	88.1	LOC401862	XM_377447.1

GI_42660932-S	188.1	222.5	192.6	LOC400516	XM_378576.1
GI_42660934-S	301.1	401.3	289.5	LOC400517	XM_378577.1
GI_42660936-S	115.3	157.2	110.9	LOC400518	XM_378578.1
GI_42660948-S	91.1	91.7	89.8	LOC400521	XM_375331.1
GI_42660952-S	104	102.7	96.6	LOC400522	XM_378579.1
GI_42660954-S	255.6	294.2	279.6	LOC283901	XM_375334.1
GI_42660956-S	2207	2387.9	1967.8	KIAA0220	XM_290670.4
GI_42660961-S	124.4	132.2	123.2	LOC400523	XM_378582.1
GI_42660981-S	208.4	173.5	156	LOC400528	XM_375349.1
GI_42660985-S	174.5	200	188.1	LOC401841	XM_377423.1
GI_42660987-S	138.5	157.6	149.5	LOC401842	XM_377424.1
GI_42660996-S	101.4	107.8	103	LOC400479	XM_375282.1
GI_42661000-S	134.2	157.3	139.3	LOC388197	XM_373654.2
GI_42661009-S	159.3	208.9	163.7	LOC400492	XM_375292.1
GI_42661014-S	77	77.2	70.1	LOC401828	XM_377408.1
GI_42661029-S	328.6	426.2	361.5	LOC400618	XM_378700.1
GI_42661031-S	120.2	104.7	103.2	LOC146795	XM_378701.1
GI_42661033-S	115.9	199.3	171.3	LOC400619	XM_378703.1
GI_42661035-S	132.5	125.3	130.9	LOC400620	XM_378705.1
GI_42661042-S	145.6	270.3	371.1	LOC400621	XM_378706.1
GI_42661044-S	110.8	110.9	104.6	LOC400622	XM_375491.1
GI_42661046-S	91.5	100.6	88.5	LOC400623	XM_378708.1
GI_42661057-S	101.5	101.4	99.4	LOC146713	XM_378712.1
GI_42661060-S	300.8	214.8	167	LOC400629	XM_375502.1
GI_42661065-S	139.5	147.1	139.1	LOC284009	XM_378642.1
GI_42661069-S	260.3	297.1	299.4	LOC400568	XM_378643.1
GI_42661071-S	151.8	168	127.4	LOC400569	XM_375392.1
GI_42661075-S	108.5	126.9	114.4	LOC388325	XM_371007.2
GI_42661079-S	224.4	234.8	234.5	LOC388327	XM_371009.2
GI_42661084-S	190	180.6	189.3	LOC400571	XM_378646.1
GI_42661092-S	166.9	209.7	183.4	LOC146850	XM_375404.1
GI_42661094-S	96.8	123.7	102.2	LOC400572	XM_378648.1
GI_42661096-S	101.8	124	112.2	USP43	XM_371015.2
GI_42661105-S	136.2	136.4	120.1	LOC400574	XM_375410.1
GI_42661107-S	133.9	156.6	138.7	LOC400575	XM_378650.1
GI_42661110-S	94.1	120.8	95.6	LOC400576	XM_375412.1
GI_42661114-S	100	110.3	99.2	LOC388341	XM_371020.2
GI_42661116-S	85.1	89.3	89.3	LOC390766	XM_372658.2
GI_42661141-S	123.4	141	123.1	NAP4	XM_371052.2
GI_42661147-S	899.6	1108.3	982.1	LOC388382	XM_371054.2
GI_42661149-S	380.2	457.8	401.8	LOC388384	XM_373730.2
GI_42661150-S	104.9	116.3	100.4	KRTAP4-9	XM_373731.2
GI_42661155-S	194.2	211.9	181.5	LOC400597	XM_375453.1
GI_42661157-S	318.9	375.3	323.1	LOC400598	XM_378676.1

GI_42661159-S	99.9	110.4	98.2	LOC388387	XM_373733.2
GI_42661163-S	109	116	114.3	LOC388388	XM_373734.2
GI_42661167-S	222.5	295.7	239.8	LOC400600	XM_378678.1
GI_42661174-S	204.7	240	249.6	LOC201175	XM_371057.2
GI_42661175-S	101.3	105.4	109.6	LOC147080	XM_378680.1
GI_42661184-S	2145.6	2520.7	2143.4	KIAA0924	XM_375471.1
GI_42661187-S	119.6	128.8	139.8	LOC400603	XM_378683.1
GI_42661189-S	101.1	108.4	102.1	LOC400604	XM_378684.1
GI_42661191-S	112.5	110.6	101.3	LOC400605	XM_378685.1
GI_42661198-S	96.3	104	92.5	LOC339210	XM_378687.1
GI_42661202-S	329.4	392.9	317.4	LOC400608	XM_375475.1
GI_42661209-S	160.8	107.8	101.1	LOC400610	XM_375478.1
GI_42661213-S	88	85.4	76.7	LOC400612	XM_378692.1
GI_42661216-S	85.1	89.4	85.5	LOC400613	XM_375482.1
GI_42661220-S	122	135.7	117.1	LOC400614	XM_378693.1
GI_42661225-S	1654.3	2602.5	2370.7	LOC146784	XM_378694.1
GI_42661231-S	260.3	307.6	264.4	LOC401884	XM_377476.1
GI_42661235-S	309.4	317.3	226.8	LOC401886	XM_377480.1
GI_42661241-S	120.7	172.6	138.3	LOC400588	XM_378664.1
GI_42661251-S	139.2	159.2	138.5	LOC147004	XM_378667.1
GI_42661253-S	177	209	184.8	LOC400591	XM_375436.1
GI_42661257-S	194.9	203.8	149.8	MGC19764	XM_371039.2
GI_42661270-S	123.6	133.1	113.7	LOC388425	XM_373753.2
GI_42661274-S	102.5	100.9	106.5	AATK	XM_375495.1
GI_42661276-S	514.9	618.7	571.1	LOC400628	XM_375496.1
GI_42661292-S	1714.4	1612.7	1328.8	LOC400586	XM_375424.1
GI_42661295-S	3016.4	3066.6	2130.6	LOC400587	XM_375426.1
GI_42661299-S	196.9	265.5	244.2	LOC388358	XM_373721.2
GI_42661300-S	99.4	120.5	103.9	LOC400567	XM_378639.1
GI_42661305-S	177	196.8	184.8	LOC284100	XM_375443.1
GI_42661312-S	155.8	148.7	137.4	LOC388438	XM_371089.2
GI_42661314-S	109.4	114.9	106.5	LOC400630	XM_378724.1
GI_42661316-S	230.9	296.8	258.7	LOC388440	XM_371092.2
GI_42661335-S	171.4	217.3	164.7	LOC400638	XM_378730.1
GI_42661337-S	88.8	109.2	102.2	LOC388457	XM_371105.2
GI_42661344-S	192.4	225.3	175.6	LOC400642	XM_378735.1
GI_42661348-S	163.5	314.2	632.1	LOC400643	XM_378738.1
GI_42661353-S	150.8	163	170.2	LOC162835	XM_091830.7
GI_42661356-S	104.5	116.6	115.8	LOC284230	XM_208185.3
GI_42661360-S	233.3	283.2	234.9	LOC400644	XM_378741.1
GI_42661364-S	131.5	145.3	133.5	LOC401891	XM_377488.1
GI_42661366-S	117.1	122.8	100.1	LOC400662	XM_378760.1
GI_42661368-S	112.4	108.3	107.1	LOC284240	XM_378763.1
GI_42661374-S	100.1	96.7	96.3	LOC388471	XM_371113.2

GI_42661380-S	334.9	440.8	366.3	LOC400647	XM_378743.1
GI_42661387-S	92.5	90.1	82.1	LOC400648	XM_378745.1
GI_42661389-S	399.8	578.6	444	LOC400649	XM_378746.1
GI_42661395-S	90.8	95.2	93.1	LOC400650	XM_375537.1
GI_42661401-S	144.4	147.4	122.7	LOC400651	XM_378747.1
GI_42661405-S	108.8	98.6	79.9	LOC284274	XM_378756.1
GI_42661409-S	89.6	94.2	87.6	LOC400659	XM_378757.1
GI_42661413-S	113.4	132.6	95.8	LOC400661	XM_375545.1
GI_42661417-S	488	585.2	547.7	LOC400653	XM_378750.1
GI_42661421-S	130	139.2	111.1	LOC400655	XM_378753.1
GI_42661423-S	197.9	224.3	203.1	LOC400656	XM_378754.1
GI_42661554-S	145.4	133.9	173.7	MGC9913	XM_378178.1
GI_42661564-S	108.6	128.2	100.2	LOC339316	XM_378791.1
GI_42661568-S	123.1	145.8	128.5	LOC400684	XM_378793.1
GI_42661576-S	101.3	102.2	98.4	FLJ21369	XM_375599.1
GI_42661581-S	174.6	184.6	192.5	LOC284402	XM_378794.1
GI_42661584-S	151.1	170.1	149.3	LOC400685	XM_378795.1
GI_42661586-S	154	163.7	140.4	LOC400686	XM_378796.1
GI_42661599-S	127.7	117.9	101.3	LOC400690	XM_378798.1
GI_42661601-S	100.4	114.6	111.6	LOC388536	XM_371163.2
GI_42661614-S	188	193.7	159.6	LOC400693	XM_375609.1
GI_42661616-S	100.1	102.8	113.6	LOC400694	XM_378800.1
GI_42661618-S	158.8	177.7	158.5	LOC400695	XM_378801.1
GI_42661624-S	97.6	90.9	86.3	SYCN	XM_371167.2
GI_42661629-S	190.9	225.9	190.5	LOC400696	XM_375614.1
GI_42661634-S	97.8	105.5	93.3	LOC400700	XM_378804.1
GI_42661636-S	97.6	97.7	89.5	LOC400701	XM_378805.1
GI_42661638-S	282.5	344.4	319.3	LOC400702	XM_378806.1
GI_42661645-S	274.3	355.9	300.8	LOC400704	XM_378807.1
GI_42661655-S	87.9	101.2	92.3	NANOS2	XM_371181.2
GI_42661658-S	120.5	127.9	118.8	DKFZp434J0	XM_375629.1
GI_42661660-S	204.1	263.7	209.2	KIAA1183	XM_371184.2
GI_42661663-S	102.2	105.3	86.9	LOC400707	XM_375631.1
GI_42661667-S	171.1	186.6	180.4	SLC8A2	XM_375633.1
GI_42661669-S	507.3	558.7	442.2	LOC199800	XM_373810.2
GI_42661677-S	103.8	128.2	103.9	MGC45922	XM_371187.2
GI_42661690-S	143.6	153.1	144.2	LOC400713	XM_375638.1
GI_42661704-S	93.8	79.1	89.6	ZNF525	XM_375646.1
GI_42661716-S	104.7	109	105.2	LOC400717	XM_375655.1
GI_42661719-S	155.7	166.9	142	LOC400718	XM_375656.1
GI_42661725-S	117.9	107.2	102.5	LOC388566	XM_371198.2
GI_42661739-S	97.3	92.3	90.2	LOC401911	XM_377527.1
GI_42661743-S	110.2	98.8	97.7	LOC401915	XM_377529.1
GI_42661752-S	177.5	210.7	180.3	LOC401919	XM_377533.1

GI_42661754-S	91.3	94.9	94.4	LOC401922	XM_377537.1
GI_42661761-S	90.4	92.4	80.6	LOC401932	XM_377553.1
GI_42661763-S	81.3	105.3	90.3	LOC401933	XM_377554.1
GI_42661835-S	113.5	108.2	102	LOC400663	XM_375548.1
GI_42661847-S	132.8	132.7	121.2	LOC400667	XM_378765.1
GI_42661849-S	128.7	151.4	146.5	LOC400668	XM_375552.1
GI_42661854-S	124.7	129.7	125.5	LOC400669	XM_378766.1
GI_42661865-S	178.7	202.3	198	NY-REN-24	XM_375557.1
GI_42661879-S	105.8	117	108.6	LOC401895	XM_377500.1
GI_42661883-S	95.3	126.9	102.5	EMR4	XM_377506.1
GI_42661954-S	215.4	250.6	242.9	FLJ38149	XM_375563.1
GI_42661956-S	233	310.5	289.8	LOC284385	XM_378777.1
GI_42661972-S	362.7	302.3	349.1	DKFZp434I16	XM_375569.1
GI_42661974-S	107.5	128.2	107.4	FLJ14959	XM_371139.2
GI_42661975-S	127.3	117.7	123.9	LOC388507	XM_371140.2
GI_42661991-S	101.9	101.8	95.6	LOC126536	XM_378780.1
GI_42662010-S	130.9	139	136.1	LOC400680	XM_378783.1
GI_42662014-S	173.6	176.4	190	LOC400681	XM_375589.1
GI_42662016-S	198.9	242.3	240.4	LOC400682	XM_375590.1
GI_42662032-S	152.3	127.8	125.4	LOC401896	XM_377511.1
GI_42662043-S	495.3	478.7	379.5	LOC401900	XM_377516.1
GI_42662080-S	201.8	230.8	197.1	LOC388806	XM_373921.2
GI_42662083-S	208.5	229.6	210	LOC400852	XM_378993.1
GI_42662088-S	96	92.6	80.8	LOC400854	XM_375925.1
GI_42662092-S	136.1	161.3	170.6	LOC400855	XM_375928.1
GI_42662213-S	167.8	192.8	190.1	LOC400844	XM_378977.1
GI_42662217-S	214.2	235.9	221.7	LOC400845	XM_378978.1
GI_42662221-S	137.5	137	136.8	LOC149692	XM_375917.1
GI_42662227-S	115	153.5	125.4	LOC400847	XM_378982.1
GI_42662229-S	121.7	126.3	131.7	LOC284749	XM_378983.1
GI_42662244-S	110.6	111.9	112.3	LOC400849	XM_378988.1
GI_42662248-S	101.9	115.9	102	LOC400830	XM_375902.1
GI_42662256-S	99.7	88.8	80.2	LOC400832	XM_378957.1
GI_42662258-S	146.1	175.7	159.6	LOC388779	XM_373903.2
GI_42662266-S	4359.2	5302	4114	LOC388783	XM_371390.2
GI_42662267-S	99.6	108.1	100.5	LOC400835	XM_378961.1
GI_42662273-S	103.4	114.4	102.1	LOC284788	XM_378969.1
GI_42662276-S	114.6	110.1	114.6	LOC400839	XM_378970.1
GI_42662278-S	104.2	103.8	118.3	LOC284798	XM_378971.1
GI_42662288-S	108.5	103.2	101.7	LOC400841	XM_378974.1
GI_42662293-S	142.5	151.2	139.4	MYH7B	XM_371398.2
GI_42662295-S	314.5	348	491.1	LOC400843	XM_378976.1
GI_42662309-S	115.8	107	105.8	LOC388813	XM_373925.2
GI_42662311-S	155.2	176.5	154.6	LOC400860	XM_375934.1

GI_42662313-S	90.1	89.5	93	LOC284825	XM_375935.1
GI_42662318-S	95.1	105.9	99	LOC400861	XM_379002.1
GI_42662323-S	99	113.7	104.3	LOC400863	XM_379004.1
GI_42662326-S	101.9	111.8	87.1	LOC400865	XM_379006.1
GI_42662329-S	94.8	94.3	94.3	LOC388824	XM_373932.2
GI_42662331-S	99.5	102.1	90.6	LOC400866	XM_379009.1
GI_42662333-S	103.6	114.2	99.9	LOC400867	XM_375941.1
GI_42662335-S	100.8	107.3	97.5	LOC284835	XM_379011.1
GI_42662337-S	100.7	124.9	94.5	LOC402027	XM_377687.1
GI_42662339-S	122.3	138.7	111.6	LOC400869	XM_379014.1
GI_42662343-S	93.6	98	88.3	LOC400871	XM_379016.1
GI_42662345-S	184.1	212.9	197.2	LOC400872	XM_379017.1
GI_42662347-S	136.4	154.4	150.2	LOC400873	XM_379018.1
GI_42662349-S	161.2	182.1	166.1	LOC400874	XM_379020.1
GI_42662353-S	103.4	95.4	82.8	LOC400875	XM_379022.1
GI_42662355-S	112.7	123.7	113.1	LOC400876	XM_379023.1
GI_42662363-S	125.4	141.1	132.9	LOC388832	XM_373939.2
GI_42662368-S	403.7	475.7	440.1	LOC402030	XM_377690.1
GI_42662370-S	134.2	147.6	137.5	LOC402032	XM_377691.1
GI_42662372-S	413.1	440	348.6	PRDM15	XM_371414.2
GI_42662379-S	91.8	111.4	101	LOC400880	XM_379030.1
GI_42662398-S	120.4	134.3	126.8	LOC388849	XM_373945.2
GI_42662399-S	119.1	118.2	132.4	LOC400889	XM_375958.1
GI_42662415-S	180	219.9	190.6	LOC400890	XM_379036.1
GI_42662421-S	118.4	119.5	117.1	LOC400893	XM_375965.1
GI_42662431-S	113.9	120.8	110.9	LOC400917	XM_375996.1
GI_42662435-S	2802.9	2859.1	3289.8	MGC1842	XM_371459.2
GI_42662437-S	121.2	138.1	100.1	LOC388886	XM_371460.2
GI_42662440-S	93.1	96.3	99.4	LOC400919	XM_379040.1
GI_42662444-S	118.4	130.2	113.3	LOC400920	XM_379041.1
GI_42662448-S	95.6	94.3	97.8	LOC400921	XM_376001.1
GI_42662456-S	203.5	242.3	220	LOC400924	XM_376003.1
GI_42662463-S	100.9	102.1	99.2	LOC91464	XM_376008.1
GI_42662472-S	106	118.4	93	LOC400927	XM_376010.1
GI_42662478-S	155.2	165	146.3	LOC388906	XM_371469.2
GI_42662480-S	123	119.9	117.8	LOC400929	XM_379055.1
GI_42662492-S	148.9	168	149	LOC402056	XM_377715.1
GI_42662494-S	82.4	91.8	98.6	LOC402057	XM_377716.1
GI_42662498-S	129.4	133.9	124.5	LOC150356	XM_377720.1
GI_42662500-S	170.8	551.5	155.3	KIAA1644	XM_376018.1
GI_42662503-S	370.9	435.3	378.5	LOC400930	XM_376019.1
GI_42662505-S	119.8	156.1	128.1	LOC400931	XM_376020.1
GI_42662514-S	114.4	123.3	113.3	LOC284933	XM_379064.1
GI_42662516-S	116.6	126.4	108.7	LOC402064	XM_377721.1

GI_42662518-S	95.4	95.1	86.8	LOC400933	XM_379065.1
GI_42662520-S	226.3	264.7	231.7	LOC400934	XM_376022.1
GI_42662524-S	159	200	230.9	LOC388918	XM_373971.2
GI_42662533-S	120.5	157.7	150.3	LOC401615	XM_379721.1
GI_42662536-S	269	272.3	210.6	LOC389848	XM_372204.2
GI_42662537-S	97.7	99.8	91.7	LOC401585	XM_379702.1
GI_42662541-S	92.2	97.7	92.9	LOC401587	XM_379703.1
GI_42662543-S	147.4	144.5	154	LOC401588	XM_379704.1
GI_42662567-S	81.6	81.4	81.4	LOC401590	XM_377002.1
GI_42662569-S	90.5	122.8	94.3	LOC402402	XM_378113.1
GI_42662571-S	110.6	151.3	151	LOC402403	XM_378116.1
GI_42662576-S	76.1	90.8	81.4	LOC401602	XM_377024.1
GI_42662580-S	163.4	178.5	159.8	LOC401604	XM_377026.1
GI_42662586-S	93.9	106.2	100.5	LOC401607	XM_379717.1
GI_42662591-S	199.6	246.7	222.6	LOC401610	XM_377031.1
GI_42662606-S	119.1	126.4	125.3	LOC402415	XM_378125.1
GI_42662616-S	170.4	195.9	195.2	LOC389865	XM_374329.2
GI_42662617-S	114.1	135.6	119.4	LOC389866	XM_372227.2
GI_42662621-S	291.1	315.7	313.6	LOC401595	XM_377019.1
GI_42662625-S	100.9	111	108.7	LOC392490	XM_373356.2
GI_42662627-S	103.1	112.1	121	FLJ20105	XM_372231.2
GI_42662629-S	241.4	279.5	254	LOC389873	XM_372233.2
GI_42662630-S	136.9	134.7	125.1	LOC401597	XM_379715.1
GI_42662641-S	3532	3253.2	2464.6	LOC203547	XM_377060.1
GI_42662643-S	85.1	83.1	78.7	LOC401620	XM_377062.1
GI_42662647-S	168	166.9	174.5	LOC402429	XM_378143.1
GI_42662651-S	171.9	187	185.3	LOC401579	XM_379696.1
GI_42662654-S	141.5	148.3	133.7	LOC389839	XM_372197.2
GI_42662662-S	116.5	136.6	123.4	LOC401582	XM_379697.1
GI_42662676-S	95.4	102.5	100.8	LOC401583	XM_379699.1
GI_42662678-S	138.6	153.8	147.4	LOC401618	XM_377041.1
GI_42662683-S	109.2	101.4	96.8	LOC389889	XM_374336.2
GI_42662684-S	128.7	142.5	122	RAC4	XM_210062.4
GI_42662685-S	104.9	98.5	97.7	LOC286411	XM_379728.1
GI_42662702-S	118.5	139.9	131.3	LOC401621	XM_379730.1
GI_42662714-S	106	119.4	115.1	LOC401616	XM_379722.1
GI_42662716-S	106.1	115.5	122.3	LOC401617	XM_379723.1
GI_42662721-S	196.6	208.2	199	LOC401625	XM_377076.1
GI_42662730-S	102.6	108.4	97.7	LOC401584	XM_376986.1
GI_42662732-S	104.4	108.1	112.7	LOC402414	XM_378124.1
GI_42662742-S	87.6	97.3	84.5	LOC402437	XM_378158.1
GI_42662756-S	102.4	104.7	93	LOC402433	XM_379761.1
GI_42662760-S	106.6	118.2	111.2	LOC401627	XM_377087.1
GI_42662766-S	115.6	107.7	109	LOC389828	XM_372181.2

GI_42662773-S	110.6	131.3	122.2	LOC401571	XM_379686.1				
GI_42662775-S	110.7	120.8	113.4	LOC401572	XM_376968.1				
GI_42662779-S	202.1	249.5	216.3	LOC401573	XM_379688.1				
GI_42662787-S	99.2	111.5	97.4	LOC401574	XM_379692.1				
GI_42714610-S	195.8	221.8	216.4	UNQ2541	NM_203347.1				
GI_42714663-I	88.4	93.8	86	PSG11	NM_203287.1	PSG13;PSG14;MGC22484	plasma	extracellul	pregnancy
GI_42716274-S	1263.8	1252.6	1126.3	KIAA1007	NM_016284.3	AD-005			
GI_42716276-S	265.1	268.4	221.9	KIAA0285	NM_014807.3	DLNB23			
GI_42716278-A	10337.1	11497	8969.2	HDLBP	NM_005336.2	HBP;VGL	lipid	nucleus	cholestero
GI_42716279-I	171	198.2	155.8	HDLBP	NM_203346.1	HBP;VGL	lipid	nucleus	cholestero
GI_42716281-S	970.1	811.7	715.2	GTL3	NM_013242.2				developm
GI_42716282-S	1130.7	1865.2	1707.6	FLJ13154	NM_024598.2				
GI_42716284-S	162.8	144.5	150.9	FOXL2	NM_023067.2	BPES;PFRK;BPES1;PINTO	transcripti	nucleus	regulation
GI_42716285-S	254.7	225.1	156.2	FANCF	NM_022725.2	FAF	molecular	nucleus	DNA
GI_42716286-S	471.9	503.7	423.2	FLJ10904	NM_018268.2	MSTP048			
GI_42716292-S	410.1	558.3	536.8	EMP2	NM_001424.3	XMP;MGC9056		integral to	cell death
GI_42716294-S	522.9	704.1	586.9	DKFZp761B1	NM_032288.4				
GI_42716296-S	1313.7	3276.9	2464.2	CLU	NM_001831.2	CLI;APOJ;SGP2;SGP-2;SP-	plasma		compleme
GI_42716300-S	6103	8395.5	6753.9	CD59	NM_000611.4	MIN1;MIN2;MIN3;MIC11;MSK21;MGC2354;P	lymphocyt	membran	blood
GI_42716303-S	261.1	293.6	282	C11orf5	NM_014205.2	FON;ZNHIT2			
GI_42716304-I	161.1	151.2	138.8	AZ2	NM_203326.1	NAP1;FLJ21939			
GI_42716306-S	96.7	101.2	112.5	BTBD14A	NM_144653.3	BTBD14;MGC23427	protein		
GI_42716307-I	316	342.6	275.6	AZ2	NM_022461.2	NAP1;FLJ21939			
GI_42716308-S	167.5	173.2	152.5	ASCL2	NM_005170.2	ASH2;HASH2;MASH2	transcripti	nucleus	peripheral
GI_42716309-S	129.5	166.5	155.3	ARHB	NM_004040.2	ARH6;RHOB;RHOH6	Rho small	peripheral	Rho
GI_42716310-S	649.1	502.2	572.3	ARNTL	NM_001178.3	TIC;JAP3;MOP3;BMAL1;MGC47515	signal	nucleus	circadian
GI_42716312-S	475.2	566.1	447.2	ANG	NM_001145.2	RNASE5	pancreatic		RNA
GI_42717993-A	318	396.2	388.4	DTNA	NM_001392.3	DTN;DRP3;D18S892E	protein	kinesin	striated
GI_42717993-I	353.3	407.7	383.4	DTNA	NM_001392.3	DTN;DRP3;D18S892E	protein	kinesin	striated
GI_42718002-I	149.6	189.8	230.4	DTNA	NM_001391.3	DTN;DRP3;D18S892E	protein	kinesin	striated
GI_42718008-S	146	187.8	163.1	CCR4	NM_005508.3	CKR4;k5-5;CMKBR4;ChemR13;CC-CKR-	chemokin	integral to	cytosolic
GI_42718009-S	107	89.5	96.4	CIB3	NM_054113.2	KIP3	calcium		
GI_42718010-S	107.6	108.1	117.6	CNGA2	NM_005140.1	CNCA;CNG2;CNCA1;OCNC1;OCNCa;OCNC	ion	intracellula	perception
GI_42718012-A	1484	1410.1	1459.9	RBBP8	NM_002894.2	RIM;CTIP		kinesin	cell cycle
GI_42718016-I	101	98.5	100.7	RBBP8	NM_203292.1	RIM;CTIP		kinesin	cell cycle
GI_42718018-S	510.4	424	439.6	RNF44	NM_014901.4	KIAA1100			
GI_42718019-S	843.1	547.5	615.7	RP9	NM_203288.1	PAP-1	nucleic	nucleus	visual
GI_42733591-S	134.3	163.8	146.2	MGC50722	NM_203348.1				
GI_42733607-S	98.5	107.8	101.2	ZNF124	NM_003431.2	HZF16	DNA	nucleus	regulation
GI_42733609-S	124.2	169.2	161	ZNF132	NM_003433.2	pHZ-12	transcripti	nucleus	regulation
GI_42734299-S	88.7	99.2	87.5	ZNF272	NM_006635.1	HZF8	DNA	nucleus	regulation
GI_42734303-S	142.7	167.3	151	MUC6	NM_005961.1		molecular	cellular_co	response
GI_42734305-S	770.8	628.7	381.4	IQCB1	NM_014642.2	KIAA0036			
GI_42734307-S	938.8	573	641	SLC35D2	NM_007001.1	SQV7L;UGTrel8	nucleotide-	cellular_co	biological_

GI_42734309-S	272.9	279.4	262.9	KIAA0140	NM_014661.2	bA12J10.2	S-		carbohydr
GI_42734313-S	546.3	643.3	490.2	KIAA0669	NM_014779.2		transcripti		regulation
GI_42734318-S	348.2	304	305.1	DCLRE1A	NM_014881.2	PSO2;SNM1;KIAA0086			
GI_42734322-S	786.5	945.7	851.6	KIAA0913	NM_015037.1				
GI_42734324-S	240.6	272.4	242.8	KIAA0261	NM_015045.1	FOE			
GI_42734326-S	616	346.4	418.5	GARNL4	NM_015085.1	KIAA1039			
GI_42734330-S	1073.9	1062.8	1065.4	DNAJC13	NM_015268.1	RME8;KIAA0678	ATP		tRNA
GI_42734332-S	156	172.4	174.4	VPS13D	NM_015378.1	FLJ10619;KIAA0453			
GI_42734334-S	849.4	1174.5	977.9	DKFZP564F0	NM_015475.1				
GI_42734336-S	323.2	374.1	350	DKFZp434K0	NM_019085.1	MGC50505			
GI_42734338-S	220	217.8	234.7	FLJ10719	NM_018193.1	KIAA1794			
GI_42734342-S	174.2	193.9	164.9	KIAA1271	NM_020746.1				
GI_42734346-S	142.3	154.9	156	KIAA1641	NM_020970.1	FLJ21281			
GI_42734348-S	536.8	579.4	683.6	SDS3	NM_022491.1	FLJ00052			
GI_42734354-S	308.5	286.2	273.3	MGC11349	NM_025112.2	FLJ13861			
GI_42734355-S	556.5	635.9	612.3	DKFZp547D1	NM_032282.1				
GI_42734357-S	130	146.5	135.5	KIAA1822	NM_032425.1				
GI_42734359-S	204.9	244.2	234.5	FLJ14743	NM_033088.1	KIAA1761			
GI_42734361-S	871.3	847.1	737.4	DOCK7	NM_033407.1	KIAA1771			
GI_42734363-S	98.6	101	89	KIAA1909	NM_052909.1	FLJ43173			
GI_42734367-S	497	493.2	434.8	MGC14798	NM_080650.2				
GI_42734372-S	495.1	650.7	837.1	KIAA1944	NM_133448.1				
GI_42734374-S	194.3	200.6	157.3	KIAA1977	NM_133450.1	FLJ32345;FLJ32767			
GI_42734376-S	592.4	699.6	685.8	CHD1L	NM_004284.2	CHDL;FLJ22530	ATP		
GI_42734378-S	94.4	80.3	85.2	MGC33488	NM_138350.2		DNA		
GI_42734380-S	229	219	208.2	LOC127253	NM_138467.1	FLJ40918			
GI_42734382-S	209.1	223.9	222.5	LOC148898	NM_138479.1				
GI_42734384-S	260.4	238.3	165.2	PWWP2	NM_138499.1	bA432J24.1			
GI_42734386-S	883.9	859.9	661.4	LOC199692	NM_145295.2		nucleic	intracellula	regulation
GI_42734387-S	592.6	636.8	572.8	C14orf75	NM_153046.1	FLJ36164;DKFZp434N0820	nucleic		
GI_42734389-S	110.9	106.5	108.9	FLJ40298	NM_173486.1				
GI_42734392-S	96.9	101.6	92.7	LOC283150	NM_181721.1		transcripti	nucleus	regulation
GI_42734394-S	129.8	133.7	131	DKFZp547K1	NM_198526.1	FLJ37393	electron		electron
GI_42734396-S	209.4	195	151.4	C6orf157	NM_198920.1	H10BH;DKFZp434A1520			
GI_42734400-S	123.7	127.2	102.6	C14orf20	NM_174944.2	c14_5117	ATP		protein
GI_42734423-S	1132.5	1271.4	1176.8	PSMD14	NM_005805.2	PAD1;POH1;rpn11		26S	ubiquitin-
GI_42734426-S	191.1	215.3	182.7	NAB2	NM_005967.2	MADER	transcripti		neurogene
GI_42734427-S	167.9	157.7	135.1	SPRR2B	NM_006945.2		structural	cytoplasm	epidermal
GI_42734429-S	138.6	149.7	145.4	PTRF	NM_012232.2	FKSG13			
GI_42734431-S	382.7	385.6	292.1	NLK	NM_016231.2		protein	nucleus	protein
GI_42734433-S	154.4	223.6	229.4	FLJ22353	NM_024587.2				
GI_42734435-S	2875.3	2555.4	2481	EFHD2	NM_024329.4	MGC4342	calcium		
GI_42734437-S	1049.7	1231.6	949.6	BM-009	NM_016623.3				
GI_42734442-S	170.7	188.7	172.2	DKKL1-pendi	NM_014419.3	SGY;SGY1;SGY-1	signal	extracellul	embryoge

GI_42734502-I	84.7	88.1	89.4	M11S1	NM_203364.1	GPIAP1		integral to	
GI_42734506-S	509.2	658.2	364.5	RAB26	NM_014353.3	V46133	GTP	cellular_co	protein
GI_42740889-S	159.5	251.1	189.4	SLC12A8	NM_024628.4	CCC9;FLJ23188	amino	membran	amino
GI_42740890-S	3282.9	3467.5	3620.2	SF3B5	NM_031287.2	SF3b10;MGC3133		spliceoso	mRNA
GI_42740891-I	103	99.3	100.8	RAPH1	NM_025252.2	RMO1;ALS2CR9;ALS2CR18;KIAA1681;RalG		cytoskelet	neuropepti
GI_42740892-I	119	126	114.6	RAPH1	NM_203365.1	RMO1;ALS2CR9;ALS2CR18;KIAA1681;RalG		cytoskelet	neuropepti
GI_42740896-A	101.5	97.3	88.2	MGEA6	NM_005930.2	MEA6;MGEA;CTAGE-5A	enzyme	kinesin	
GI_42740900-I	131.3	108.9	96.3	MGEA6	NM_203356.1	MEA6;MGEA;CTAGE-5A	enzyme	kinesin	
GI_42740902-S	231.6	233.2	220.9	MGC61716	NM_182501.2				
GI_42740904-I	94	88.2	93.7	MGEA6	NM_203354.1	MEA6;MGEA;CTAGE-5A	enzyme	kinesin	
GI_42741647-S	6272.1	7017.4	5823.4	15-Sep	NM_004261.3		selenium		
GI_42741651-I	122.3	123.8	125.1	SERTAD3	NM_203344.1	RBT1			
GI_42741653-S	2293	2603.5	2557.9	TARDBP	NM_007375.3	TDP-43	microtubul	nucleus	mitosis
GI_42741654-S	233.8	216.9	186.6	MET	NM_000245.2	HGFR;RCCP2	hepatocyt	integral to	oncogene
GI_42741656-A	273.9	370.9	378.9	TIAF1	NM_004740.3	MAJN		perinuclea	anti-
GI_42741657-S	102.8	121.6	111.1	TNP2	NM_005425.4		DNA	chromoso	DNA
GI_42741658-S	113.4	118.9	122.3	ABCB1	NM_000927.3	CLCS;MDR1;P-	ATP	integral to	drug
GI_42741662-S	427.3	477.8	467.4	CCBL1	NM_004059.3	MGC29624	transamin	cytosol	amino
GI_42741664-S	393.9	501.6	447.9	CDK5R2	NM_003936.3	P39;NCK5AI;p39nck5ai	cell cycle	cyclin-	regulation
GI_42741665-S	258.1	293.5	261.2	CDK6	NM_001259.4	PLSTIRE;MGC59692	cell cycle		G1 phase
GI_42741666-S	272.2	317.6	298.1	GALNT13	NM_052917.1	KIAA1918;GalNAc-T13			
GI_42741668-S	123.2	106.1	94.9	KBTBD10	NM_006063.2	SARCOSIN	protein	cytoskelet	striated
GI_42741670-S	202.1	215.3	255.4	NAT1	NM_000662.4	AAC1	arylamine		
GI_42741672-S	914.5	1044.1	898.9	SAS	NM_005981.3			membran	positive
GI_42741673-S	7102.2	6805.4	5866.7	PDLIM7	NM_005451.3	ENIGMA			receptor
GI_42741678-S	186.1	224.6	228	ATP6V0A2	NM_012463.2	a2;TJ6;J6B7;Stv1;TJ6M;TJ6s;Vph1;ATP6a2;			immune
GI_42741680-S	284.8	230.5	198.1	ATP6V1E2	NM_080653.3	VMA4;ATP6E1;ATP6EL2;MGC9341;ATP6V1	hydrogen-	proton-	ATP
GI_42741681-S	2078.1	1881.9	1208.4	ZNF265	NM_005455.3	ZIS;ZIS1;ZIS2	RNA	nucleus	RNA
GI_42761478-S	127.5	128.4	126.3	FLJ35709	NM_173589.2				
GI_42764629-S	272.1	343.4	299	THRSP	NM_003251.2	S14;SPOT14;MGC21659		nucleus	lipid
GI_42764682-I	92.1	95.5	87.1	DUSP6	NM_001946.2	MKP3;PYST1	phosphopr	soluble	inactivatio
GI_42764686-A	100.4	108.8	104.8	DUSP6	NM_022652.2	MKP3;PYST1	phosphopr	soluble	inactivatio
GI_42766421-S	95.5	94.6	91.7	LOC387758	NM_203371.1	MGC24932			
GI_42766423-S	280.3	298.3	286	LOC389119	NM_203370.1	MGC20416			
GI_42766427-S	301	266.5	253.7	FLJ20232	NM_019008.4	HSU79252;dJ1104E15.3	molecular	cellular_co	biological_
GI_42789379-S	1292.6	1755	1669.9	SELT	NM_016275.3		selenium	cellular_co	selenocyst
GI_42789728-S	104.9	114.2	107.5	LRMP	NM_006152.2	JAW1		endoplas	vesicle
GI_42794008-S	2200.7	2311.7	2293.3	DPAGT1	NM_001382.2	GPT;ALG7;DGPT;G1PT;UAGT;UGAT;DPAG	UDP-N-	endoplas	lipid
GI_42794262-S	196.8	173.9	194.9	LOC389677	NM_203390.1	MGC:33837			
GI_42794264-S	411.8	459.3	387.6	MRGD	NM_198923.2		receptor	integral to	G-protein
GI_42794268-S	141.5	161.5	149.7	LOC284123	NM_203392.1	MGC35151			
GI_42794270-S	144.1	169.5	149.6	DEHAL1	NM_203395.1				
GI_42794272-S	1155	1436.9	1152.8	LOC283807	NM_203373.1	MGC75496			
GI_42794274-S	113.1	130.7	133.8	MGC71805	NM_203381.1				

GI_42794609-S	1154.2	1048.7	1097.7	RNH	NM_002939.3	RAI;MGC4569;MGC18200;MGC54054	ribonuclea		RNA
GI_42794610-S	1321.9	1231.9	858.3	PGLS	NM_012088.2	6PGL	6-		pentose-
GI_42794611-S	100.1	87	97.4	MYEOV	NM_138768.2	OCIM	nucleic		
GI_42794613-S	129.7	133	129.7	LOC389458	NM_203393.1	MGC:35170			
GI_42794615-S	142.1	157.1	161.7	LOC284912	NM_203375.1	MGC3170			
GI_42794617-S	141.4	157.6	140.6	LOC388730	NM_203376.1	MGC75217			
GI_42794619-S	180.3	259.5	340	HYPE	NM_007076.2	MGC5623;UNQ3041	protein		pathogene
GI_42794621-S	263.7	229.4	268.2	LOC147808	NM_203374.1	MGC75238			
GI_42794623-S	259.9	305.1	302.3	C20orf141	NM_080739.2	MGC26144;dJ860F19.4			
GI_42794624-S	290.6	281.8	281.1	AMACR	NM_014324.4	RACE	alpha-	peroxisom	metabolis
GI_42794751-S	82.9	85.3	94.5	ACSL3	NM_004457.3	ACS3;FACL3;PRO2194	fatty-acyl-		fatty acid
GI_42794755-S	288	339	258.3	ACSL5	NM_016234.3	ACS2;ACS5;FACL5	long-chain-		fatty acid
GI_42794757-I	105.4	108.5	106.2	ACSL5	NM_203379.1	ACS2;ACS5;FACL5	long-chain-		fatty acid
GI_42794759-I	93.5	106.6	105	ACSL5	NM_203380.1	ACS2;ACS5;FACL5	long-chain-		fatty acid
GI_42794761-S	208.9	179.1	204	GK	NM_000167.3	GKD	ATP	mitochond	carbohydr
GI_42794764-A	315.8	397.9	455.6	MAP3K3	NM_002401.3	MEKK3;MAPKKK3	MAP		MAPKKK
GI_42794766-I	105.2	111.1	113.2	MAP3K3	NM_203351.1	MEKK3;MAPKKK3	MAP		MAPKKK
GI_42794768-S	953.9	762.7	887.5	PAK1	NM_002576.3	PAKalpha	protein		JNK
GI_42794770-A	3308.8	5270.2	3962.5	TXNDC5	NM_030810.2	UNQ364;EndoPDI;MGC3178;FLJ21353;FLJ9	electron	endoplas	electron
GI_42794774-I	172.7	181	134.3	TXNDC5	NM_022085.3	UNQ364;EndoPDI;MGC3178;FLJ21353;FLJ9	electron	endoplas	electron
GI_42794776-S	1495.7	1391.9	1792.9	ARL2BP	NM_012106.3	BART1	small		signal
GI_42794777-I	107.3	115.8	113.7	MYO18A	NM_078471.3	MYSPDZ			
GI_42821106-S	105.2	117.3	108.6	BGALT15	NM_198540.2		transferas	membran	protein
GI_42821107-S	112.9	114.6	108.3	LOC388394	NM_203400.1	MGC43894			
GI_42821109-S	184.5	187.9	177.5	LOC340602	NM_203407.1	MGC47837			
GI_42821113-S	95.5	106.3	89.6	LOC158724	NM_203408.1	MGC27003			
GI_42822875-S	257.8	186.4	203.2	LOC286343	NM_203403.1	MGC46502			
GI_42822877-S	88.5	96.6	94.3	LOC388818	NM_203405.1	MGC71787			
GI_42822879-S	607.8	485.3	505.8	LOC153364	NM_203406.1	MGC46734			
GI_42822881-S	723.5	873	728.8	LOC161247	NM_203402.1	MGC46490			
GI_42822885-S	134.8	133.8	113	HSPA6	NM_002155.3		heat		heat
GI_42822886-S	114.1	119.5	107.2	FY	NM_002036.2	GPD;DARC;CCBP1	transmem	integral to	G-protein
GI_42822888-S	153.9	142.3	170	DKFZP572C1	NM_033160.3			nucleus	
GI_42822890-S	321.7	436.7	570	C17orf37	NM_032339.3	C35;ORB3;XTP4;MGC14832			
GI_44662802-S	83.8	92.1	109.3	LOC389199	NM_203423.1	MGC35057			
GI_44662806-S	94.1	102.5	97.5	LOC388407	NM_203425.1				
GI_44662812-S	241.9	277.9	255.5	LOC92162	NM_203411.1	MGC71744			
GI_44662814-S	1212.2	1999.3	1766.7	LOC286016	NM_203419.1				
GI_44662816-S	124.4	118.9	130.7	LOC389123	NM_203424.1	MGC50809			
GI_44662818-S	123.5	133.5	117.1	LOC164153	NM_203412.1				
GI_44662820-S	246.8	220.9	110.1	LOC221091	NM_203422.1	MGC61707			
GI_44662822-S	120.2	105.7	109.8	HFE2	NM_145277.3	JH;RGMC;HFE2A			
GI_44662824-S	5149.4	6566.3	7858.9	KIAA0152	NM_014730.2			integral to	
GI_44662825-I	283.4	348.5	325.9	DERP6	NM_203414.1	HSPC002			

GI_44662829-A	457.1	394.4	410	DERP6	NM_015362.3	HSPC002			
GI_44662831-I	205.2	279	230.8	DERP6	NM_203413.1	HSPC002			
GI_44662835-S	347.9	324.8	278.3	BCAR1	NM_014567.2	CAS;CRKAS;P130CAS	signal	cytoplasm	cell
GI_44662837-S	195.5	200.6	135.6	AMT	NM_000481.2	GCE;NKH;GCST	aminomet	glycine	glycine
GI_44680104-I	115	114.4	100.3	CALD1	NM_033138.2	CDM;NAG22;MGC21352;H-CAD;L-CAD	tropomyos	cytoskelet	muscle
GI_44680111-S	4331.8	2046.2	1388.1	DSCR1	NM_004414.5	CSP1;DSC1;RCN1;MCIP1;ADAPT78	DNA	nucleus	central
GI_44680112-S	2726.4	2294.9	2115.5	DSCR2	NM_003720.2	C21LRP;LRPC21		membran	
GI_44680115-A	134.4	561.1	178.4	DSCR8	NM_032589.2	MMA-1;MTAG2;C21orf65	molecular	cellular_co	biological_
GI_44680118-I	114.1	103.2	100.7	DSCR8	NM_203429.1	MMA-1;MTAG2;C21orf65	molecular	cellular_co	biological_
GI_44680120-I	187.6	164.3	125	TRIM7	NM_033342.2	GNIP;RNF90	zinc ion	intracellula	
GI_44680127-I	91.2	96.5	100	TRIM7	NM_203296.1	GNIP;RNF90	zinc ion	intracellula	
GI_44680129-I	113.6	106.9	106.4	TRIM7	NM_203297.1	GNIP;RNF90	zinc ion	intracellula	
GI_44680131-S	794.1	847.8	1005.8	B3GNT5	NM_032047.3	B3GN-T5;beta3Gn-T5	galactosylt	membran	protein
GI_44680132-I	89.2	93.8	94.1	BDH	NM_203315.1	MGC2723;MGC4347;MGC9788	3-	mitochond	metabolis
GI_44680134-A	175	255.1	410.3	BDH	NM_004051.3	MGC2723;MGC4347;MGC9788	3-	mitochond	metabolis
GI_44680135-I	111.3	121.8	117.6	BDH	NM_203314.1	MGC2723;MGC4347;MGC9788	3-	mitochond	metabolis
GI_44680137-S	87.6	95.7	90.4	BHLHB5	NM_152414.3	Beta3;CAGL85;TNRC20			
GI_44680138-S	110.9	122.4	102.1	BIRC8	NM_033341.3	ILP2;ILP-2;hILP2	apoptosis	intracellula	anti-
GI_44680142-A	260	309.9	273.1	SLC23A1	NM_152685.2	SVCT1;YSPL3;SLC23A2;MGC22361	nucleobas	integral to	nucleobas
GI_44680142-I	105.5	107.4	94.9	SLC23A1	NM_152685.2	SVCT1;YSPL3;SLC23A2;MGC22361	nucleobas	integral to	nucleobas
GI_44680144-I	269.3	279.2	248.2	SLC23A1	NM_005847.3	SVCT1;YSPL3;SLC23A2;MGC22361	nucleobas	integral to	nucleobas
GI_44680146-A	94.8	123.5	105.3	SLC23A2	NM_005116.5	NBTL1;SVCT2;YSPL2;SLC23A1;KIAA0238	nucleobas	integral to	nucleobas
GI_44680147-I	144	135.4	143.3	SLC23A2	NM_203327.1	NBTL1;SVCT2;YSPL2;SLC23A1;KIAA0238	nucleobas	integral to	nucleobas
GI_44680149-S	114.4	134.4	127.5	CLDN9	NM_020982.2		structural	tight	
GI_44680150-S	9380.7	8925	9632.9	CRI1	NM_014335.2	EID1;EID-1;PTD014;C15orf3;PNAS-	protein	cellular_co	biological_
GI_44680151-S	474.4	643.7	501.3	FOSL2	NM_005253.3	FRA2;FLJ23306	transcripti	nucleus	cell death
GI_44680152-S	797.6	508.1	337.5	LOC388152	NM_203426.1	MGC60197			
GI_44680155-S	283	347.2	321.9	ALG10	NM_032834.2	FLJ14751	transferas		
GI_44680157-S	294.8	368.3	320.8	PURB	NM_033224.3	PURBETA			
GI_44680158-S	193	476.2	275.7	RaLP	NM_203349.2	MGC34023			intracellula
GI_44681483-S	285	340.1	359.3	CDCA2	NM_152562.2	FLJ25804			
GI_44681485-S	420.8	368	434.7	LOC389792	NM_203434.1	MGC70833			
GI_44771157-S	205	1987.8	983.8	IFI27	NM_005532.2	P27;ISG12	molecular	integral to	immune
GI_44771172-S	172.1	185	179.7	GPR116	NM_015234.3	KIAA0758;DKFZp564O1923	G-protein	membran	neuropepti
GI_44771179-S	1620.7	1204	1714.2	NACSIN	NM_015252.2	KIAA0903	ubiquitin		ubiquitin
GI_44771197-S	387.1	293.7	305.1	PRMT3	NM_005788.1		N-	cytoplasm	N-terminal
GI_44771200-S	407.7	503	475.7	KIAA1698	NM_030628.1				
GI_44771205-S	91.8	93.7	93.9	ASCL4	NM_203436.1	HASH4			
GI_44771210-S	252.6	260.4	213.8	THRAP2	NM_015335.1	KIAA1025;TRAP240L;PROSIT240			
GI_44829053-S	474.7	518.9	490	E2F4	NM_001950.3	E2F-4	transcripti	transcripti	regulation
GI_44888813-S	299.6	278.6	322.6	MGC21881	NM_203448.1				
GI_44888815-S	96.5	80.8	82.7	FLJ20444	NM_203449.1				
GI_44888817-S	398.7	513.7	304.1	KIAA0934	NM_014974.1		catalytic		metabolis
GI_44888819-S	223.5	223.6	195.8	KIAA0423	NM_015091.1		binding	mitochond	transport

GI_44888824-S	89.5	105	91.2	LOC400120	NM_203451.1	MGC33996			
GI_44888826-S	348.4	425.6	385.3	MGC39545	NM_203452.1				
GI_44888828-S	610.1	617.4	716.3	LOC403313	NM_203453.1	MGC15483			
GI_44888830-S	244.6	298.5	274.8	MGC26594	NM_203454.1	FLJ25691			
GI_44888832-S	128.5	117.9	118.3	PDZK6	NM_015693.2	PDZD6;KIAA1284	protein		intracellula
GI_44888834-S	100.7	107.6	105.2	ATP8B3	NM_138813.1	ATPIK	ATP	integral to	cation
GI_44889413-S	968.2	956.9	945.1	USP32	NM_032582.3	USP10;NY-REN-60	cysteine-		ubiquitin-
GI_44889474-S	701.2	843.4	741.2	RAB6IP1	NM_015213.2	KIAA1091			
GI_44889476-I	137.8	158.6	147.1	SYNJ1	NM_203446.1	INPP5G	inositol-	secretory	synaptic
GI_44889478-S	111.5	129	119.7	GJC1	NM_152219.2	GJA11;CX31.9	connexon	connexon	cell
GI_44889480-S	572.8	636.5	422.4	MYO1B	NM_012223.2	myr1	actin	myosin	
GI_44889482-S	93.4	116.9	93.3	CDR1	NM_004065.2	CDR;CDR34;CDR62A			cell growth
GI_44889959-S	78.4	84.7	69.2	DOCK8	NM_203447.1	FLJ00026;FLJ00152			
GI_44889961-A	839.1	964.3	1103.9	STMN1	NM_005563.3	Lag;SMN;OP18;PP17;PP19;PR22;LAP18	signal	cytosol	cell growth
GI_44890049-I	124.2	123.6	121.2	STMN1	NM_203399.1	Lag;SMN;OP18;PP17;PP19;PR22;LAP18	signal	cytosol	cell growth
GI_44890051-I	113.3	113.7	127.6	STMN1	NM_203401.1	Lag;SMN;OP18;PP17;PP19;PR22;LAP18	signal	cytosol	cell growth
GI_44890053-S	254.5	209.1	196.7	STK33	NM_030906.2		protein-		protein
GI_44890054-S	174	208.1	195.2	SSTR2	NM_001050.2		somatosta	integral to	negative
GI_44890055-S	132.3	162.7	144.3	SSTR3	NM_001051.2		somatosta	integral to	induction
GI_44890057-S	257.8	328.1	277.9	ACDC	NM_004797.2	APM1;APM-1;GBP28;ACRP30;ADIPOQ	hormone	microfibril	energy
GI_44890058-S	132.4	140.1	145.6	IVL	NM_005547.2		structural	cytosol	
GI_44890060-S	3792.1	6433.2	4233.7	PPIB	NM_000942.4	CYPB;SCYLP;CYP-S1;MGC2224;MGC14109	chaperone	endoplas	protein
GI_44890061-S	665	596.4	556	C14orf43	NM_194278.2	c14_5541	DNA	nucleus	
GI_44890063-S	113.7	118.7	119.7	INSM1	NM_002196.2	IA1;IA-1	DNA	nucleus	regulation
GI_44890064-S	1280.6	817.5	677.1	C2orf3	NM_003203.3	GCF;TCF9;DNABF	RNA	nucleus	regulation
GI_44890066-S	660.2	398	376.1	JUN	NM_002228.3	AP1	RNA	nuclear	regulation
GI_44890067-S	585.4	541.8	415.1	ZNF262	NM_005095.2	MYM;CDIR;KIAA0425;ZNF198L3	DNA	extracellul	developm
GI_44890236-A	403.1	660.9	187.4	CALD1	NM_033140.2	CDM;NAG22;MGC21352;H-CAD;L-CAD	tropomyos	cytoskelet	muscle
GI_44917602-S	124	133.9	139.7	ZNF305	NM_014724.2	ZFP96;ZNF29K1;KIAA0426;dJ29K1.2	transcripti	nucleus	regulation
GI_44917603-S	857.1	502.4	569.9	SRGAP1	NM_020762.1	ARHGAP13;KIAA1304			
GI_44917605-S	221.1	209.2	178.4	NAPB	NM_022080.1	SNAP-BETA	intracellula	Golgi	intracellula
GI_44917607-S	289.8	401.3	436.9	MGRN1	NM_015246.1	GP2B;CD41B;ITGA2B;RNF156;KIAA0544			
GI_44917609-S	265.5	301.8	271.1	KIAA1510	NM_020882.1		structural	microfibril	cell
GI_44917611-S	340.4	312.5	324.2	KIF1C	NM_006612.3	LTXS1;KIAA0706	adenosine	Golgi	retrograde
GI_44917612-S	115.2	127	116	LOC163782	NM_181712.2				
GI_44917616-S	466.8	489.4	625	N2N	NM_203458.1				
GI_44917618-S	252.1	320.4	277.9	KIAA0265	NM_014997.1				
GI_44921601-S	749.9	730	818.8	ZNF524	NM_153219.2	MGC23143	DNA	nucleus	regulation
GI_44921602-S	3021.4	3122.6	2642.8	ZNF358	NM_018083.2	ZFEND;FLJ10390	DNA	nucleus	regulation
GI_44921604-S	131.4	165	135.2	TBX2	NM_005994.3	FLJ10169	DNA	nucleus	regulation
GI_44921605-A	127.9	139.4	116.7	SYNJ1	NM_003895.2	INPP5G	inositol-	secretory	synaptic
GI_44921609-S	110.4	123.4	125	LOC134548	NM_175873.3				
GI_44921611-S	97.9	111.2	108.4	JUNB	NM_002229.2		transcripti	chromatin	regulation
GI_44921612-S	107.5	110	105.4	KIP2	NM_006383.2		protein		

GI_44921613-S	82.7	73.6	89.9	GPR73	NM_138964.2	ZAQ;PKR1;GPR73a	rhodopsin-	integral to	G-protein
GI_44921614-S	125	132.2	141.6	EXOC8	NM_175876.2	EXO84;SEC84;Exo84p			
GI_44955890-I	219.3	228.7	224.2	ARFD1	NM_001656.3	ARD1;RNF46;TRIM23	GTPase	intracellula	small
GI_44955904-A	97	99.7	89.4	ARFD1	NM_033228.2	ARD1;RNF46;TRIM23	GTPase	intracellula	small
GI_44955909-S	1250.3	1100.1	1675.4	E2F7	NM_203394.1				
GI_44955913-S	122.3	127.3	113.1	EDG4	NM_004720.4	LPA2;EDG-4	lipid	integral to	cytosolic
GI_44955920-S	264	213.6	191.1	ELK3	NM_005230.2	ERP;NET;SAP2	transcripti	nucleus	signal
GI_44955925-S	432.7	639.2	491.2	KIAA0182	NM_014615.1				
GI_44955928-S	1235	1153	1288.9	KIAA1078	NM_203459.1				
GI_44955932-I	1572.6	1841.5	1741	UBQLN1	NM_013438.3	DA41;DSK2;XDRP1;PLIC-1			
GI_45006902-S	159.9	178.2	180.8	MEIS1	NM_002398.2		RNA	nucleus	oncogene
GI_45006928-S	121.9	132.7	108.5	MYCL2	NM_005377.2		transcripti	nucleus	regulation
GI_45006950-S	387.9	370.3	331.2	DHODH	NM_001361.2	DHOdehase	dihydrooro	membran	'de novo'
GI_45006969-S	748.6	848.3	616.2	DR1	NM_001938.2	NC2;NC2-BETA	transcripti	nucleus	negative
GI_45006985-S	1530.7	1306	1104.1	SCYE1	NM_004757.2	p43;EMAP2;EMAP-2;EMAPII;EMAP II;EMAP-	cytokine	extracellul	tRNA
GI_45007001-S	1040.4	946.6	745.3	LOC253782	NM_203463.1				
GI_45007006-S	180.1	224.3	131.5	OAS3	NM_006187.2	p100	antiviral	microsom	nucleobas
GI_45007020-S	80.1	95.4	81	TEX12	NM_031275.3				
GI_45007036-S	108.7	122.1	128.7	WASF2	NM_006990.2	SCAR2;WAVE2;dJ393P12.2	actin	actin	actin
GI_4501840-S	16506.2	9915.2	8606.7	AARS	NM_001605.1		tRNA	soluble	alanyl-
GI_4501844-S	84.5	96.5	82.1	AANAT	NM_001088.1	SNAT;AA-NAT	aralkylami		circadian
GI_4501848-S	120.4	127.2	111.8	ABCA3	NM_001089.1	ABC3;ABC-C;LBM180;EST111653	ATP	integral to	drug
GI_4501850-S	177.5	189.3	164.3	ABP1	NM_001091.1	DAO;AOC1	amine	peroxisom	metabolis
GI_4501854-S	123.7	133.3	104.8	ACACB	NM_001093.1	ACC2;ACCB;HACC275	acetyl-	biotin	biotin
GI_4501856-S	116.2	113.8	109.7	ACADL	NM_001608.1	LCAD;ACAD4	long-chain-	mitochond	electron
GI_4501866-S	835.2	1172.8	1128.4	ACO2	NM_001098.1		aconitate	mitochond	citrate
GI_4501868-S	955.6	1673.6	1442.2	ACOX2	NM_003500.1	BCOX;BRCOX;BRCACOX	acyl-CoA	peroxisom	bile acid
GI_4501870-S	316	317.8	276	ACOX3	NM_003501.1		acyl-CoA	peroxisom	bile acid
GI_4501876-S	117.2	118.5	109	ACR	NM_001097.1		acrosin		acrosome
GI_4501882-S	5137.1	4689.5	3434.6	ACTA2	NM_001613.1	ACTSA	structural	actin	muscle
GI_4501892-S	95.8	134.3	93.6	ACTN2	NM_001103.1		structural	actin	
GI_4501900-S	979	1389.5	1311.2	ACY1	NM_000666.1	ACYLASE	aminoacyl	cytosol	amino
GI_4501912-S	214.2	138.3	231.8	ADAM23	NM_003812.1	MDC3	integrin	integral to	central
GI_4501914-S	957.5	1585.4	902.9	ADAM9	NM_003816.1	MCMP;MDC9;Mltng;KIAA0021	integrin	integral to	protein
GI_4501944-S	120.1	119.1	111.4	ADM	NM_001124.1	AM	receptor	soluble	progester
GI_4501946-S	349.2	469.3	292.4	ADORA1	NM_000674.1	RDC7	adenosine	integral to	phagocyto
GI_4501960-I	97.5	110.3	91.3	ADRA1A	NM_000680.1	ADRA1C;ADRA1L1	alpha1-	integral to	protein
GI_4501988-S	98.9	113.1	82.2	AFP	NM_001134.1	FETA;HPAFP	plasma	extracellul	immune
GI_4501990-A	124.4	147.6	137.9	AGC1	NM_001135.1	CSPG1;MSK16;CSPGCP	chondroiti	extracellul	heterophili
GI_4501992-S	516.2	543	408.1	AGPS	NM_003659.1	ADAS;ADPS;ADAP-S;ADHAPS;ALDHPSY	alkylglycer	peroxisom	lipid
GI_4501994-I	96.8	96.4	79	AGRP	NM_001138.1	ART;AGRT;ASIP2	neuropepti		neuropepti
GI_4502004-S	118.2	118	116.8	AHSG	NM_001622.1	AHS;HSGA;FETUA	proteoglyc	soluble	ossificatio
GI_4502008-S	1113.9	1223.8	1209.1	AIP	NM_003977.1	ARA9;XAP2;FKBP37	transcripti	cytoplasm	protein
GI_4502010-S	403.8	490.5	420.3	AK1	NM_000476.1		adenylate	cytosol	ATP

GI_4502028-S	333.6	199.7	209.4	ALCAM	NM_001627.1	MEMD;CD166	receptor	membran	cell
GI_4502040-S	132.6	298.2	1471.9	ALDH1A3	NM_000693.1	ALDH6;RALDH3;ALDH1A6	aldehyde		alcohol
GI_4502042-S	1600.2	1641.6	1259.8	ALDH3B1	NM_000694.1	ALDH4;ALDH7	aldehyde		alcohol
GI_4502050-S	175	221.6	191.8	ALOX12	NM_000697.1	LOG12	arachidon		fatty acid
GI_4502052-S	170	200.6	185.3	ALOX12B	NM_001139.1	12R-LOX	arachidon		epidermal
GI_4502056-S	194.3	236.7	199	ALOX5	NM_000698.1	LOG5	arachidon		leukotrien
GI_4502072-S	318.7	370.6	339.7	AMELY	NM_001143.1	AMGL;AMGY	extracellul	extracellul	developm
GI_4502078-S	372.1	493.2	616.8	AMPD3	NM_000480.1		AMP		AMP
GI_4502094-S	2463.3	2351.2	2346.3	ANPEP	NM_001150.1	CD13;LAP1;PEPN;gp150	aminopept	proteoglyc	pathogene
GI_4502096-S	1095.1	886.5	1152.3	SLC25A4	NM_001151.1	T1;ANT;ANT1;PEO2;PEO3	adenine	mitochond	mitochond
GI_4502098-S	6759.7	7276.8	5492.9	SLC25A5	NM_001152.1	T2;T3;ANT2	adenine	mitochond	small
GI_4502100-S	6348.4	4957.9	5673.9	ANXA1	NM_000700.1	ANX1;LPC1	phospholi		lipid
GI_4502102-S	177.3	195.6	177.4	ANXA9	NM_003568.1	ANX31	phospholi		
GI_4502112-S	364.3	853.7	380.4	ANXA8	NM_001630.1	ANX8	phospholi		oncogene
GI_4502114-S	126.2	136.5	117.3	AOAH	NM_001637.1		catalytic	integral to	lipid
GI_4502144-S	891.7	959.8	940.2	BIRC5	NM_001168.1	API4;EPR-1;SURVIVIN	apoptosis	spindle	G2/M
GI_4502146-S	1772.6	1604.6	2809.8	APLP2	NM_001642.1	APPH;APPL2;CDEBP			
GI_4502148-S	78.2	84.7	75.6	APOA2	NM_001643.1		high-		lipid
GI_4502152-S	103.5	101.7	94	APOB	NM_000384.1	FLDB	low-	microsom	circulation
GI_4502160-S	104	109.4	106.4	APOC4	NM_001646.1		apolipopro		lipid
GI_4502162-S	127.2	150.2	153.9	APOD	NM_001647.1		high-	extracellul	lipid
GI_4502164-S	100.8	91.2	91.6	APOF	NM_001638.1		cholestero	integral to	lipid
GI_4502170-S	2529.5	2863.2	2670.4	APRT	NM_000485.1	AMP	adenine		nucleoside
GI_4502182-S	114.6	110.4	110.2	AQP5	NM_001651.1		water	integral to	water
GI_4502186-S	130.9	125.4	125.1	AQP7	NM_001170.1	AQP9;AQP7L;AQPap	glycerol	integral to	glycerol
GI_4502192-S	427.2	539.6	560.9	ARAF1	NM_001654.1	PKS2;A-RAF;RAFA1	protein	cellular_co	oncogene
GI_4502202-S	572.1	732.2	864.9	ARF3	NM_001659.1		GTPase	Golgi	nonselecti
GI_4502218-S	1862.2	1512.7	1953.7	ARHG	NM_001665.1		Rho small		Rho
GI_4502220-S	92.3	98.7	101.1	ARHGAP5	NM_001173.1	P190-B;RHOGAP5	GTPase	peripheral	Rho
GI_4502224-S	193.9	217.1	205.4	ARHGDIG	NM_001176.1		Rho GDP-	peripheral	negative
GI_4502228-S	8847.1	6644.5	10273	ARL2	NM_001667.1	ARFL2	GTPase		tubulin
GI_4502238-A	107.4	123.3	121.4	ARSD	NM_001669.1		arylsulfata		
GI_4502238-I	119.4	151.3	125.8	ARSD	NM_001669.1		arylsulfata		
GI_4502240-S	174.1	235.9	171.1	ARSE	NM_000047.1	CDPX;CDPX1;CDPXR	arylsulfata		skeletal
GI_4502246-S	111.5	132.5	131	ARVCF	NM_001670.1		structural	kinesin	cell
GI_4502248-S	1527.8	1855.7	1224	DDEF2	NM_003887.1	PAP;PAG3;SHAG1;KIAA0400;Pap-alpha	enzyme	nucleus	nonselecti
GI_4502260-S	134.4	143.7	130.4	SERPINC1	NM_000488.1	AT3;ATIII	serine		
GI_4502262-A	117.1	104.5	105.6	ATF3	NM_001674.1		transcripti	nucleus	regulation
GI_4502270-S	111.8	115.9	118.3	ATP1A2	NM_000702.1	FHM2;MHP2	sodium/po	sodium/po	sodium
GI_4502280-S	3944.4	3929	3674.4	ATP1B3	NM_001679.1	FLJ29027	sodium/po	sodium/po	small
GI_4502286-S	567.8	344.6	459.5	ATP2B1	NM_001682.1	PMCA1	calcium-	integral to	small
GI_4502290-S	89.3	104.2	97.9	ATP4A	NM_000704.1	ATP6A	hydrogen/	integral to	small
GI_4502300-S	5063	6849.1	5736.8	ATP5G3	NM_001689.1		hydrogen-	proton-	energy
GI_4502320-S	178.5	180.1	167.7	ATP7A	NM_000052.1	MK;MNK;OHS	copper-	Golgi	copper ion

GI_4502322-S	287.9	307.7	322.4	ATP7B	NM_000053.1	WND	copper-	Golgi	copper ion
GI_4502326-S	455.6	521	837.9	AUH	NM_001698.1		mRNA 3'	mitochond	mRNA
GI_4502352-S	892	756.2	423.4	BACH1	NM_001186.1		transcripti	nucleus	regulation
GI_4502354-S	162.4	172.5	178.5	BAI1	NM_001702.1		protein	intercellula	axonogen
GI_4502356-S	296.6	447.9	335.3	BAI2	NM_001703.1		tumor	integral to	neuropepti
GI_4502358-S	80.2	91.1	75.1	BAI3	NM_001704.1	KIAA0550	tumor	integral to	neuropepti
GI_4502368-S	108.8	228.8	171.9	BBOX1	NM_003986.1	BBH;BBOX;G-BBH;gamma-BBH	gamma-		carnitine
GI_4502370-S	5744.3	4141.7	4086.2	BCAR3	NM_003567.1	NSP2;SH2D3B	guanyl-		drug
GI_4502372-S	152.4	165.6	144.6	BCAS1	NM_003657.1	AIBC1;NABC1			oncogene
GI_4502374-S	1355.4	791.8	1296.5	BCAT2	NM_001190.1	BCAM;BCT2	branched-	mitochond	branched
GI_4502386-S	88.4	96.3	92.2	OPN1SW	NM_001708.1	BCP;CBT	opsin	integral to	vision
GI_4502406-S	194.9	252.4	215.9	BHMT	NM_001713.1		homocyst		
GI_4502408-S	142.7	146.9	135.1	BICD1	NM_001714.1		structural	Golgi	RNA
GI_4502418-S	992.1	665.5	678.6	BLVRB	NM_000713.1	FLR;BVRB	biliverdin		
GI_4502426-S	110.7	115	99.9	BMP7	NM_001719.1	OP-1			skeletal
GI_4502430-S	95.6	99.4	87.6	BMPR1B	NM_001203.1	ALK6;ALK-6	transmem	integral to	transmem
GI_4502436-S	911.1	796.6	782.2	POLR3D	NM_001722.1	RPC4;BN51T;TSBN51	DNA-	nucleus	regulation
GI_4502446-S	139.7	179.8	147.1	BPI	NM_001725.1		Gram-	integral to	immune
GI_4502450-S	111	119.7	110.9	BRCA2	NM_000059.1	FAD;FAD1;FANCB;FANCD1	tumor	secretory	establish
GI_4502452-S	110.6	115.8	105.7	BRDT	NM_001726.1	BRD6	protein	nucleus	
GI_4502454-S	201.5	263.6	235.3	BRS3	NM_001727.1		bombesin	integral to	adult
GI_4502460-S	94.9	109.4	96.8	BTC	NM_001729.1		epidermal	soluble	positive
GI_4502466-S	98.4	116.9	96.2	BTF3L1	NM_001208.1	OPG;OCIF;HUMBTFB;TNFRSF11B	transcripti	nucleus	regulation
GI_4502472-S	5478.9	4414.5	4363.9	BTG1	NM_001731.1		cell cycle		negative
GI_4502474-S	135.7	169.5	146	BTN1A1	NM_001732.1	BT;BTN	receptor	integral to	
GI_4502484-S	446.3	588.9	513	C11orf8	NM_001584.1	239FB;FAM1B;D11S302E;Hs.46638	hydrolase		neurogene
GI_4502508-S	360.9	295.5	254.3	C5R1	NM_001736.1	C5A;C5AR;CD88	C5a	integral to	activation
GI_4502516-S	124.4	131.1	118.6	CA1	NM_001738.1		carbonate	cytoplasm	one-
GI_4502520-S	97.3	85.4	92	CA5A	NM_001739.1	CA5;CAV;CAVA	carbonate	mitochond	one-
GI_4502522-S	95.8	100.5	85.3	CACNA1B	NM_000718.1	CACNN;CACNL1A5	voltage-	voltage-	small
GI_4502526-S	302.5	332.2	279.8	CACNA1D	NM_000720.1	CCHL1A2;CACNL1A2	dihydropyr	voltage-	small
GI_4502528-S	246.3	277.9	270.2	CACNA1E	NM_000721.1	Cav2.3;CACNL1A6	voltage-	voltage-	small
GI_4502536-S	136.2	118.8	119.6	CACNB4	NM_000726.1		voltage-	voltage-	small
GI_4502544-S	223	268.4	238.1	CALCA	NM_001741.1	CT;KC;CGRP;CALC1;CGRP1;CGRP-I	receptor	soluble	regulation
GI_4502546-S	138.1	161.5	140.5	CALCR	NM_001742.1	CRT;CTR;CTR1	calcitonin	integral to	phosphati
GI_4502560-S	3046.6	1531.2	606.6	CAPG	NM_001747.1	MCP;AFCP	barbed-	F-actin	response
GI_4502564-S	2621	3844.2	4738.6	CAPNS1	NM_001749.1	30K;CANP;CDPS;CANPS;CAPN4	calpain		positive
GI_4502566-S	393.2	559.6	549.4	CASK	NM_003688.1	LIN2	membran	actin	cell
GI_4502598-S	313.3	406.9	395.2	CBR1	NM_001757.1	CBR	carbonyl	cytosol	metabolis
GI_4502602-S	80.2	80.7	86.4	CBX4	NM_003655.1	PC2;hPC2	transcripti	chromatin	negative
GI_4502606-S	127	151.1	144.3	CCKAR	NM_000730.1		cholecysto	integral to	cytosolic
GI_4502620-S	216.4	243.2	306.7	CCNF	NM_001761.1	FBX1;FBXO1	cyclin-	nucleus	regulation
GI_4502630-S	245.9	195.9	381.5	CCR1	NM_001295.1	CKR-1;HM145;CMKBR1;MIP1aR	chemokin	integral to	cytosolic
GI_4502638-S	128.2	132.8	118.4	CCR5	NM_000579.1	CKR5;CD195;CKR-5;CCCKR5;CMKBR5;CC-	chemokin	endosome	phosphati

GI_4502644-S	100.1	106.2	99.4	CD1B	NM_001764.1	CD1		endosome	antimicrob
GI_4502646-S	279.8	305.3	270.5	CD1C	NM_001765.1	CD1		integral to	antimicrob
GI_4502650-S	1072.7	330.5	263.6	CD22	NM_001771.1	SIGLEC-2	cell	integral to	cell
GI_4502654-S	1250.1	943.1	294.5	CD33	NM_001772.1	p67;SIGLEC-3	receptor	integral to	negative
GI_4502658-S	227.9	287.3	253.1	SIGLEC5	NM_003830.1	OBBP2;CD33L2;OB-BP2;SIGLEC-5	lectin [goid	integral to	cell
GI_4502660-S	142.5	172.1	129.2	CD34	NM_001773.1		lymphocyt	integral to	cell
GI_4502662-S	92.8	89.2	76.8	CD37	NM_001774.1	GP52-40		integral to	N-linked
GI_4502668-S	142.9	279.2	172	CD3D	NM_000732.1	T3D;CD3-DELTA	T-cell	integral to	cell
GI_4502670-S	95.8	112.4	105.1	CD3E	NM_000733.1	T3E;TCRE	T-cell	integral to	signal
GI_4502676-S	1181.9	1352.5	1355.6	CD58	NM_001779.1	LFA3	cell	membran	cell
GI_4502680-S	97.7	97.5	97	CD69	NM_001781.1		transmem	integral to	defense
GI_4502682-S	174.6	228.8	199	CD72	NM_001782.1	LYB2	receptor	integral to	cell
GI_4502684-I	118	115.1	98.7	CD79A	NM_001783.1	IGA;MB-1	transmem	integral to	defense
GI_4502686-S	132.8	160	145.7	CD84	NM_003874.1	LY9B;hCD84;mCD84;SLAMF5	lymphocyt	integral to	homophili
GI_4502744-S	382.7	422.3	357.7	CDK8	NM_001260.1	K35	cell cycle		regulation
GI_4502754-S	94.4	94.3	88.4	CDO1	NM_001801.1		electron		
GI_4502760-S	87.3	113.2	93.6	CDW52	NM_001803.1	CD52	lymphocyt	membran	
GI_4502762-S	109.6	124.6	95.8	CDX1	NM_001804.1		transcripti	nucleus	histogene
GI_4502778-S	220.3	255.8	271.9	CENPC1	NM_001812.1	CENPC	DNA	kinetochor	chromoso
GI_4502780-S	291.3	305.3	236.2	CENPE	NM_001813.1	KIF10	kinetochor	kinetochor	mitotic
GI_4502792-S	124.6	139.5	118	CEACAM3	NM_001815.1	CGM1;CD66D	tumor	integral to	
GI_4502796-S	115.1	112	113.6	CEACAM4	NM_001817.1	CGM7	tumor	membran	
GI_4502798-S	169	195.2	185.6	CHAD	NM_001267.1	SLRR4A	extracellul	extracellul	regulation
GI_4502806-S	259.2	255.2	228.7	CHGB	NM_001819.1	SCG1	peptide	extracellul	regulation
GI_4502808-S	157.3	189.8	162	CHIT1	NM_003465.1	CHIT	chitinase	extracellul	response
GI_4502810-S	174.3	199.1	187.7	CHML	NM_001821.1	REP2	Rab	Rab-	visual
GI_4502816-S	117	124.7	113.9	CHRM2	NM_000739.1	HM2	muscarini	integral to	muscarini
GI_4502818-S	174.2	201.2	166.5	CHRM3	NM_000740.1	HM3	muscarini	integral to	phosphati
GI_4502820-S	95.8	96.2	89.7	CHRM4	NM_000741.1	HM4	muscarini	integral to	acetyl
GI_4502822-S	106.7	114.2	107.4	CHRNA2	NM_000742.1		nicotinic	nicotinic	synaptic
GI_4502832-S	122.8	126.8	130.7	CHRNB2	NM_000748.1	EFNL3	nicotinic	nicotinic	small
GI_4502836-S	116.4	119.9	117.5	CHRNB4	NM_000750.1		acetylcholi	nicotinic	synaptic
GI_4502838-S	286.8	318.3	217.2	CHS1	NM_000081.1	CHS;LYST			
GI_4502844-S	113.2	150.6	113.8	CILP	NM_003613.1	HsT18872	phosphopr	extracellul	nucleobas
GI_4502846-S	3044.5	3277.1	2803.4	CIRBP	NM_001280.1	CIRP	RNA	nucleus	response
GI_4502848-S	1041.6	1236	1421.2	CKAP1	NM_001281.1	CG22;TBCB;CKAPI	chaperone	microtubul	microtubul
GI_4502854-S	199.6	246.9	215.9	CKMT2	NM_001825.1	SMTCK	creatine	mitochond	muscle
GI_4502856-S	6230.7	4438.2	5814.7	CKS1B	NM_001826.1	CKS1;ckshs1	cyclin-		regulation
GI_4502858-S	1534.9	1586.8	1741.5	CKS2	NM_001827.1	CKSHS2	cyclin-		regulation
GI_4502860-S	3893.4	3740.2	2740.4	AP3S1	NM_001284.1	CLAPS3;Sigma3A	vesicle	Golgi-	insulin
GI_4502864-S	147.9	151.5	140.4	CLCA1	NM_001285.1	CaCC	chloride	integral to	small
GI_4502866-S	505.8	616	551.8	CLCN1	NM_000083.1	CLC1	voltage-	integral to	small
GI_4502868-I	489.3	501.6	480.5	CLCN3	NM_001829.1	CLC3	voltage-	integral to	small
GI_4502872-I	110.8	131.8	116.6	CLCN6	NM_001286.1	CLC-6;KIAA0046	chloride	membran	small

GI_4502882-I	149.2	144.9	132.1	CLK2	NM_003993.1		protein	nucleus	protein
GI_4502884-I	273.6	286.5	263.7	CLK3	NM_003992.1		protein	nucleus	protein
GI_4502888-S	506.9	515.3	533.3	CLN3	NM_000086.1	BTS	chaperone	mitochond	protein
GI_4502890-S	3714.7	3728.4	3014.4	CLNS1A	NM_001293.1	CLCI;ICln;CLNS1B	auxiliary	plasma	vision
GI_4502892-S	106.1	96.9	94.5	CSRP3	NM_003476.1	CLP;MLP;CRP3;LMO4;CMD1M		nucleus	myogenes
GI_4502896-S	710.1	931.7	928.9	CLPTM1	NM_001294.1			integral to	developm
GI_4502898-A	4518.9	4312.3	4117.3	CLTA	NM_001833.1	LCA	calcium	coated pit	intracellula
GI_4502902-A	195.8	167.6	147.1	CLTCL1	NM_001835.1	CLTD;CLH22;CLTCL	signal	coated pit	receptor
GI_4502914-S	95.1	98.6	92.6	CNGA1	NM_000087.1	CNCG;CNG1;CNCG1;RCNC1;RCNCa;RCN	ligand-	integral to	vision
GI_4502916-S	97	98.8	92.4	CNGA3	NM_001298.1	CNG3;ACHM2;CCNC1;CCNCa;CNCG3;CCN	ligand-	membran	vision
GI_4502918-S	106.5	111.6	91.8	CNGB1	NM_001297.1	GAR1;GARP;CNCG2;RCNC2;RCNCb;CNCG	ligand-	membran	vision
GI_4502922-S	3836.2	5166	3235.4	CNN3	NM_001839.1		tropomyos	cellular_co	smooth
GI_4502928-S	80.2	95.6	88.4	CNR2	NM_001841.1	CB2;CX5	cannabino	integral to	G-protein
GI_4502996-S	388.6	522.8	468.5	CPA1	NM_001868.1	CPA	carboxype		proteolysis
GI_4502998-S	94.2	102.4	93	CPA2	NM_001869.1		carboxype		vacuolar
GI_4503000-S	95	105.6	88.9	CPA3	NM_001870.1		carboxype	secretory	proteolysis
GI_4503002-S	115.4	128.8	114.5	CPB1	NM_001871.1	PASP;PCPB	carboxype		proteolysis
GI_4503008-S	821.8	813.9	409.6	CPE	NM_001873.1		carboxype	peripheral	neuropepti
GI_4503010-S	136.4	158.4	155.5	CPN1	NM_001308.1	CPN;SCPN	metallocar	extracellul	proteolysis
GI_4503020-S	117	131	119.3	CPT1A	NM_001876.1	CPT1;CPT1-L;L-CPT1	carnitine	integral to	fatty acid
GI_4503022-S	649.8	845.7	909.1	CPT2	NM_000098.1	CPT1;CPTASE	acyltransf	mitochond	fatty acid
GI_4503024-S	106.9	188.9	108	CPZ	NM_003652.1		metallocar		proteolysis
GI_4503036-S	883.1	1211.8	1144.7	CREG	NM_003851.1	CREG1	transcripti		regulation
GI_4503040-S	139.9	134	110.2	CRH	NM_000756.1	CRF	hormone	soluble	learning
GI_4503056-S	106.2	109.2	93.8	CRYAB	NM_001885.1	CRYA2;CTPP2	chaperone	cytoplasm	vision
GI_4503058-S	126	133.4	119.2	CRYBA4	NM_001886.1		structural		vision
GI_4503062-S	322	422.4	346.6	CRYBB2	NM_000496.1	CCA2;CRYB2;CRYB2A;D22S665	structural		vision
GI_4503064-S	91.9	97.4	96.3	CRYM	NM_001888.1	THBP;DFNA40	ornithine		vision
GI_4503068-I	168.1	198.2	205.1	MAPK14	NM_001315.1	RK;p38;EXIP;Mxi2;CSBP1;CSBP2;CSPB1;P	MAP	cytoplasm	chemotaxi
GI_4503084-S	137.3	191.1	158.7	CSN1S1	NM_001890.1	CASA;CSN1			digestion
GI_4503086-S	180.5	199.1	167.8	CSN2	NM_001891.1	CASB	milk		calcium
GI_4503100-S	473.1	576.8	606.8	CSRP2	NM_001321.1	CRP2;LMO5	molecular	nucleus	muscle
GI_4503118-S	108.4	115.1	106.9	CTAG1	NM_001327.1	CTAG;ESO1;LAGE2B;NY-ESO-1	tumor		
GI_4503122-S	15921	15377	6584.7	CTGF	NM_001901.1	CCN2;NOV2;IGFBP8	insulin-like	extracellul	epidermal
GI_4503126-S	476.8	664.9	732.3	CTNNA1	NM_001903.1	CAP102	cell	cytoskelet	cell
GI_4503128-S	2240.7	2443.2	1755.7	CTNNAL1	NM_003798.1	CLLP;alpha-CATU			apoptosis
GI_4503132-S	804.4	658.5	722.2	CTPS	NM_001905.1		CTP		drug
GI_4503134-S	121.6	126.8	108.7	CTRB1	NM_001906.1	CTRB	trypsin	extracellul	proteolysis
GI_4503136-S	112.2	133	115.3	CTRL	NM_001907.1	CTRL1		extracellul	proteolysis
GI_4503164-S	118.5	118.2	114.3	CUL3	NM_003590.1				
GI_4503174-S	192.9	159.6	153.3	CXCR4	NM_003467.1	HM89;LAP3;NPYR;WHIM;LESTR;NPY3R;fus	chemokin	cytoplasm	activation
GI_4503176-S	166.7	210.7	183	CXorf2	NM_001586.1	TEX28	molecular	integral to	biological_
GI_4503178-S	148.2	134.6	129.8	OFD1	NM_003611.1	71-7A;CXORF5	molecular	kinesin	biological_
GI_4503180-S	1574.3	2190	2414.5	CXX1	NM_003928.1		molecular	membran	biological_

GI_4503182-S	376.3	399.1	374.6	CYB5	NM_001914.1		cytochrom	microsom	energy
GI_4503188-S	266.9	323.4	265.6	CYP11A1	NM_000781.1	CYP11A;P450SCC	cytochrom	membran	androgen
GI_4503218-S	132	149.6	137.2	CYP2C19	NM_000769.1	CPCJ;CYP2C;P450C2C;P450IIC19	monooxyg	microsom	electron
GI_4503240-S	218.3	239.1	216.9	CYP4F3	NM_000896.1	CPF3;CYP4F;LTB4H	monooxyg	membran	leukotrien
GI_4503250-S	1244.1	772.6	752.6	DAB2	NM_001343.1	DOC2;DOC-2	tumor	nucleus	cell
GI_4503252-S	5558.5	5588.8	4210	DAD1	NM_001344.1		apoptosis	microsom	anti-
GI_4503264-S	562.6	574.2	642.4	DBT	NM_001918.1	MSUD2;BCATE2	acyltransf	alpha-	metabolis
GI_4503266-S	1522.9	923.4	1051.1	DCI	NM_001919.1		dodeceno	mitochond	fatty acid
GI_4503268-S	596.9	638	690.2	DCK	NM_000788.1		deoxycytid	nucleus	pyrimidine
GI_4503276-S	1026	1112.9	939.3	DCTD	NM_001921.1		dCMP		pyrimidine
GI_4503280-S	152.5	197.1	156.1	DDC	NM_000790.1	AADC	aromatic-L-		catechola
GI_4503298-S	2891	3945.2	5273.7	BHLHB2	NM_003670.1	DEC1;Stra14	transcripti	nucleus	regulation
GI_4503300-S	2496.2	2990.6	3124.1	DECR1	NM_001359.1	DECR;NADPH	2,4-	mitochond	metabolis
GI_4503302-S	99.1	107.1	99.2	DEFA4	NM_001925.1	HP4;DEF4;HP-4;HNP-4	calcium	extracellul	xenobiotic
GI_4503312-S	103.2	104.4	98.1	DGKE	NM_003647.1	DGK;DAGK6	diacylglyc		phospholi
GI_4503314-S	155.4	199.7	182	DGKG	NM_001346.1	DAGK3;DGK-GAMMA	diacylglyc		signal
GI_4503320-S	1194	1355	1238.8	DHCR7	NM_001360.1	SLOS	cholestero	integral to	cholestero
GI_4503334-S	106.8	107.5	117.4	DIO3	NM_001362.1	D3;5DIII;TXDI3;DIOIII	thyroxine	cellular_co	biological_
GI_4503348-S	355.4	588.6	384.5	DNASE2	NM_001375.1	DNL;DNL2	deoxyribo	lysosome	DNA
GI_4503350-S	4172.2	3690.5	3819.8	DNMT1	NM_001379.1	DNMT;MCMT;CXXC9	DNA	nucleus	DNA
GI_4503352-S	103.7	116.6	101	DOC2A	NM_003586.1		binding	secretory	synaptic
GI_4503354-S	558.5	506.5	693.9	DOCK1	NM_001380.1	DOCK180	GTPase	cytoplasm	small
GI_4503360-S	150.6	163.4	153.8	DPH2L1	NM_001383.1	DPH2L;OVCA1			protein
GI_4503362-S	2781.7	3180	2742.6	DPM1	NM_003859.1	MPDS	dolichyl-	endoplas	protein
GI_4503374-S	140	154.5	119.9	DPYS	NM_001385.1	DHP;DHPase	dihydropyr		response
GI_4503392-S	108.4	106.2	106.6	DRP2	NM_001939.1		structural	cytoskelet	central
GI_4503400-S	94.2	95.8	87.9	DSG1	NM_001942.1	DG1;DSG;CDHF4	cell	cytoskelet	cell
GI_4503402-S	376.4	454.2	363.2	DSG2	NM_001943.1	HDGC;CDHF5	cell	cytoskelet	homophili
GI_4503404-S	94.4	112	99	DSG3	NM_001944.1	PVA;CDHF6	cell	cytoskelet	homophili
GI_4503412-S	1380.6	955.1	1189.4	DTR	NM_001945.1	DTS;HBEGF;HEGFL	epidermal	extracellul	positive
GI_4503414-S	1001.5	1062.5	921.1	DUSP11	NM_003584.1	PIR1	RNA	nucleus	RNA
GI_4503420-S	155.9	198.2	169.1	DUSP9	NM_001395.1	MKP4;MKP-4	protein	cytoplasm	JNK
GI_4503428-S	903.4	841.8	720.3	DYRK3	NM_003582.1		protein		protein
GI_4503442-S	199.9	249.5	353.1	ECE1	NM_001397.1	ECE	metalloen	integral to	cell-cell
GI_4503446-S	2423	2819.3	2440	ECH1	NM_001398.1	HPXEL	enoyl-CoA	peroxisom	fatty acid
GI_4503458-S	105.3	115.4	123.3	EDG6	NM_003775.1	LPC1;SLP4	lipid	integral to	cytosolic
GI_4503464-S	616	668.6	361.9	EDNRA	NM_001957.1	ETA;ETRA	endothelin	integral to	phosphati
GI_4503466-A	420.8	525.5	475.2	EDNRB	NM_003991.1	ETB;ETRB;HSCR;ABCDS;HSCR2	endothelin	integral to	negative
GI_4503466-I	87.6	101.6	99.7	EDNRB	NM_003991.1	ETB;ETRB;HSCR;ABCDS;HSCR2	endothelin	integral to	negative
GI_4503468-S	116.1	139.3	124.8	EEA1	NM_003566.1	ZFYVE2	phosphati	peripheral	nonselecti
GI_4503486-S	111.2	119.6	113.9	EFNA5	NM_001962.1	AF1;EFL5;RAGS;EPLG7;LERK7	GPI-linked	membran	neurogene
GI_4503494-S	93.9	87.8	91.6	EGR4	NM_001965.1	NGFIC;NGFI-C;PAT133	DNA	nucleus	positive
GI_4503496-S	109.8	126	133.8	EHHADH	NM_001966.1	LBP;LBFP;PBFE	3-	peroxisom	energy
GI_4503502-S	1991.1	2425	2105.5	EIF2B1	NM_001414.1	EIF2B;EIF-2B;EIF2BA;EIF-2Balpha	translation	eukaryotic	translation

GI_4503508-S	2508	2386.7	2262.4	EIF3S10	NM_003750.1	P167;EIF3A;KIAA0139;eIF3-p170;eIF3-theta	translation	eukaryotic	regulation
GI_4503510-S	490.5	574.1	323.1	EIF3S1	NM_003758.1	eIF3-p35;eIF3-alpha	translation	eukaryotic	regulation
GI_4503512-S	2931.3	3456.9	3208.6	EIF3S2	NM_003757.1	TRIP1;TRIP-1;eIF3-p36;eIF3-beta	translation	eukaryotic	regulation
GI_4503514-S	4976.4	5223.8	3715.5	EIF3S3	NM_003756.1	eIF3-p40;eIF3-gamma	translation	eukaryotic	regulation
GI_4503516-S	6903.7	6758.4	6727.6	EIF3S4	NM_003755.1	EIF3-P42;eIF3-p44;eIF3-delta	translation		regulation
GI_4503518-S	8993.5	8230.7	6642.2	EIF3S5	NM_003754.1	eIF3-p47	translation	eukaryotic	regulation
GI_4503520-S	10070.4	9241.3	7786.5	EIF3S6	NM_001568.1	INT6;eIF3e;EIF3-P48;eIF3-p46	translation	eukaryotic	cell growth
GI_4503528-S	10777	11072	10089	EIF4A1	NM_001416.1	DDX2A;EIF4A;EIF-4A	helicase	eukaryotic	binding to
GI_4503532-S	936.5	912.1	664.4	EIF4B	NM_001417.1	EIF-4B	translation	eukaryotic	regulation
GI_4503534-S	579.4	721.7	606.5	EIF4E	NM_001968.1	EIF-4E;EIF4EL1	mRNA	cytoplasm	binding to
GI_4503536-S	254	316.6	302.6	EIF4EBP3	NM_003732.1	4E-BP3			
GI_4503538-S	7131.8	7441.5	6485.6	EIF4G2	NM_001418.1	p97;DAP5;NAT1	translation	eukaryotic	cell cycle
GI_4503548-S	227.2	274.1	264.6	ELA2	NM_001972.1	NE	macropha		proteolysis
GI_4503554-S	575.3	392.6	524.4	ELF4	NM_001421.1	MEF;ELFR	transcripti		transcripti
GI_4503558-S	1330.1	956.5	1023.2	EMP1	NM_001423.1	TMP;CL-20		integral to	epidermal
GI_4503562-S	3365.9	2788.3	3369.8	EMP3	NM_001425.1	YMP		integral to	negative
GI_4503578-S	600	395.8	439.4	EPB41L2	NM_001431.1	4.1-G	structural	spectrin	cell shape
GI_4503580-S	439.3	530.7	479.2	EPB49	NM_001978.1	DMT;DEMATIN	actin	actin	cell shape
GI_4503588-S	110.3	114.5	112.3	EPO	NM_000799.1	EP	erythropoi	extracellul	response
GI_4503592-S	673.6	658.1	545	EPS15	NM_001981.1	AF1P;AF-1P;MLLT5	calcium		EGF
GI_4503594-S	105.6	95.1	87.7	EPX	NM_000502.1	EPO;EPP;EPX-PEN	peroxidas		peroxidas
GI_4503596-S	277.2	331.6	314.9	ERBB3	NM_001982.1	HER3	transmem	integral to	protein
GI_4503600-S	677.3	876.3	888.8	ERCC5	NM_000123.1	XPG;UVDR;XPGC;ERCM2	endodeox	nucleus	nucleotide-
GI_4503602-S	105	116	95.3	ESR1	NM_000125.1	ER;ESR;Era;ESRA;NR3A1	steroid	membran	transcripti
GI_4503606-S	2904	3139	2671.4	ETFA	NM_000126.1	EMA;GA2;MADD	electron	mitochond	electron
GI_4503608-S	1173.5	1470	1326.9	ETFB	NM_001985.1	MADD	electron	mitochond	electron
GI_4503612-S	313.9	409.8	347.1	EVPL	NM_001988.1	EVPK	structural	plasmode	epidermal
GI_4503638-S	523.7	554.7	475.6	F2RL3	NM_003950.1	PAR4	thrombin	integral to	G-protein
GI_4503650-S	527	361	580.3	ACSL1	NM_001995.1	ACS1;LACS;FACL1;FACL2;LACS1;LACS2	long-chain-		fatty acid
GI_4503654-S	272.6	299.7	280	FANCA	NM_000135.1	FA;FA1;FAA;FAH;FA-H;FACA;FANCH		cytoplasm	DNA
GI_4503656-S	110.9	117.7	102.1	FOXH1	NM_003923.1	FAST1;FAST-1	transcripti	nucleus	signal
GI_4503664-S	185.1	160.4	130	FBLN2	NM_001998.1		extracellul	extracellul	
GI_4503680-S	264.9	254.4	207.1	FCGBP	NM_003890.1	FC(GAMMA)BP	protein		immune
GI_4503690-S	128.6	130.8	128.4	FGF16	NM_003868.1		growth	extracellul	response
GI_4503692-S	131.2	141.9	123.2	FGF17	NM_003867.1	FGF-13	growth	extracellul	signal
GI_4503694-I	135.9	151.1	159.5	FGF18	NM_003862.1	ZFGF5;FGF-18	growth	extracellul	positive
GI_4503700-S	90.8	99.5	84.8	FGF4	NM_002007.1	HST;KFGF;HST-1;HSTF1;K-FGF;HBGF-4	growth	extracellul	positive
GI_4503706-S	91.5	105.9	86.5	FGF9	NM_002010.1	GAF;HBFG-9	growth	extracellul	signal
GI_4503718-S	171	195.2	186.4	FHIT	NM_002012.1	FRA3B;AP3Aase	catalytic		nucleotide
GI_4503732-S	91	104.2	112.4	FOXF1	NM_001451.1	FKHL5;FREAC1	protein	transcripti	regulation
GI_4503734-S	448.1	486.6	684.9	FOXC1	NM_001453.1	ARA;IGDA;IHG1;FKHL7;IRID1;FREAC3	DNA	nucleus	vision
GI_4503744-S	23904.3	24993	21057	FLNA	NM_001456.1	FLN;FMD;MNS;ABPX;FLN1;NHBP;OPD1;OP	actin	actin	actin
GI_4503746-S	2949.3	2787.5	2957.5	FLNB	NM_001457.1	FH1;TAP;TABP;FLN1L;ABP-278	membran	actin	actin
GI_4503752-A	106.2	101.2	95.5	FLT4	NM_002020.1	PCL;VEGFR3	vascular	integral to	transmem

GI_4503752-I	722	822.7	887.1	FLT4	NM_002020.1	PCL;VEGFR3	vascular	integral to	transmem
GI_4503754-S	260	380.3	295.2	FMO1	NM_002021.1		monooxyg	microsom	electron
GI_4503756-S	88.8	91.8	79.3	FMO2	NM_001460.1		monooxyg	microsom	electron
GI_4503758-S	308.9	379.2	362.1	FMO4	NM_002022.1	FMO2	dimethyla	microsom	xenobiotic
GI_4503760-S	128.8	163	137.6	FMO5	NM_001461.1		dimethyla	microsom	electron
GI_4503764-S	348.7	459.7	448.4	FMR1	NM_002024.1	FMRP;FRAXA	mRNA	polysome	
GI_4503766-S	108.9	94.7	92	FMR2	NM_002025.1	MRX2;OX19;FRAXE			brain
GI_4503768-S	128.9	140.2	130.5	NPFF	NM_003717.1	FMRFAL	receptor	soluble	neuropepti
GI_4503770-S	3275.9	2530.1	1967.2	FNTA	NM_002027.1	FPTA;PGGT1A	protein	cytoplasm	C-terminal
GI_4503776-S	85.3	91.6	87.2	FPGT	NM_003838.1	GFPP	catalytic	cytoplasm	fucose
GI_4503780-S	114.9	122.9	111.4	FPRL1	NM_001462.1	ALXR;HM63;FMLPX;FPR2A;FPRH1;FPRH2;	N-formyl	integral to	chemotaxi
GI_4503790-S	98.7	97.3	94.7	FSHB	NM_000510.1		hormone	soluble	female
GI_4503794-S	4554	4522.4	3579.4	FTH1	NM_002032.1	FTH;FTHL6	iron ion	ferritin	intracellula
GI_4503804-S	277.8	223.9	180.3	FUT1	NM_000148.1	H;HH	blood	Golgi	carbohydr
GI_4503806-S	104	119.3	106.4	FUT2	NM_000511.1	SE	fucosyltra	membran	carbohydr
GI_4503808-S	105.1	122.7	109.7	FUT3	NM_000149.1	LE;Les	fucosyltra	Golgi	carbohydr
GI_4503810-S	238.1	198.2	226.7	FUT4	NM_002033.1	FCT3A;FUC-TIV	fucosyltra	Golgi	carbohydr
GI_4503812-S	120.3	125	111.5	FUT5	NM_002034.1	FUC-TV	fucosyltra	Golgi	carbohydr
GI_4503814-S	769.2	917.6	935.5	FUT6	NM_000150.1		fucosyltra	Golgi	protein
GI_4503816-S	829.5	716.2	845.7	FVT1	NM_002035.1		oxidoredu	extracellul	oncogene
GI_4503824-S	237	213	365.1	FZD1	NM_003505.1		transmem	integral to	G-protein
GI_4503832-S	129.3	240.6	227.1	FZD7	NM_003507.1	FzE3	frizzled	integral to	frizzled
GI_4503834-S	97.3	169.2	172.6	FZD9	NM_003508.1	FZD3	frizzled	integral to	frizzled
GI_4503850-S	133	153.5	149.7	GAB1	NM_002039.1		SH3/SH2		insulin
GI_4503864-A	107.9	134.7	112.5	GABRB2	NM_000813.1		GABA-A	integral to	gamma-
GI_4503870-S	125.5	125.2	114.3	GABRR2	NM_002043.1		GABA-A	integral to	small
GI_4503872-I	98.4	86.5	95.2	GAD1	NM_000817.1	GAD;GAD25;GAD67			glutamate
GI_4503874-S	87.4	84.6	84.5	GAD2	NM_000818.1	GAD65			glutamate
GI_4503876-S	257.3	111.1	104.5	GAGE1	NM_001468.1		tumor		cellular
GI_4503878-S	7016.8	2546.7	2514.3	GAGE2	NM_001472.1		molecular	cellular_co	biological_
GI_4503882-S	6913.5	2476	2327.6	GAGE4	NM_001474.1		tumor		
GI_4503884-S	2175	1423.8	1398.9	GAGE5	NM_001475.1		tumor		
GI_4503886-S	9712.8	3751.3	3211.4	GAGE6	NM_001476.1		tumor		
GI_4503888-S	6691.1	2396.7	2356.7	GAGE7B	NM_001477.1		molecular	cellular_co	biological_
GI_4503894-S	2536.7	2267.8	2930	GALK1	NM_000154.1	GK1;GALK	galactokin	cytoplasm	galactose
GI_4503896-S	450.3	512.4	496.7	GALK2	NM_002044.1	GK2	galactokin	cytoplasm	carbohydr
GI_4503906-S	182.5	200	166.9	GALR3	NM_003614.1		galanin	integral to	negative
GI_4503916-S	389.8	385.4	279.4	GAS8	NM_001481.1	GAS11	molecular	kinesin	negative
GI_4503918-S	100.6	156.3	140.7	GAS1	NM_002048.1		molecular	integral to	cell cycle
GI_4503928-S	389.6	488.4	550.4	GATA3	NM_002051.1	HDR;MGC5445	transcripti		embryoge
GI_4503932-S	106.5	116.8	120.3	GATM	NM_001482.1	AGAT	glycine	cytosol	creatine
GI_4503934-S	319.9	395.5	521.1	GBA	NM_000157.1	GBA1;GLUC		lysosome	
GI_4503936-S	1593.1	1630.2	1323.6	GBAS	NM_001483.1	NIPSNAP2	folic acid	membran	metabolis
GI_4503938-S	190.6	227.9	133.1	GBP1	NM_002053.1		GTP		immune

GI_4503942-I	237.7	269.8	276.9	GCDH	NM_000159.1	ACAD5	glutaryl-	mitochond	electron
GI_4503946-S	149.5	174.1	160.9	GCGR	NM_000160.1	GGR	glucagon	integral to	regulation
GI_4503948-S	243.1	316.3	336.5	GCH1	NM_000161.1	GCH;DYT5;GTPCH1	GTP		nitric oxide
GI_4503954-S	1658.8	1685.2	1938.4	GCN5L1	NM_001487.1		molecular	cellular_co	biological_
GI_4503964-S	163.3	195.3	165.5	OPN1MW	NM_000513.1	CBD;DCB;GCP;CBBM	green-	integral to	vision
GI_4503970-S	584.4	592.8	688.9	GDI1	NM_001493.1	GDIL;MRX41;MRX48;OPHN2;XAP-	GDP-		nonselecti
GI_4503976-S	138.7	149.3	124	GENX-3414	NM_003943.1	GENEX3414	catalytic	membran	muscle
GI_4503980-S	486.9	513.6	419.1	GFPT1	NM_002056.1	GFA;GFAT;GFPT;GFAT1	glutamine-	cytoplasm	energy
GI_4503986-S	1100.1	1334.1	1127.1	GGH	NM_003878.1	GH	exopeptid	lysosome	
GI_4503992-S	174.6	167.8	160	GHR	NM_000163.1		growth	integral to	growth
GI_4503996-S	342.5	424.7	367.9	GHRHR	NM_000823.1	GHRFR	G-protein	integral to	adenylate
GI_4504002-S	124.3	141.6	139.6	GJA4	NM_002060.1	CX37	connexon	gap	intercellula
GI_4504008-S	609.9	969.4	746.3	GLA	NM_000169.1	GALA	hydrolase	lysosome	carbohydr
GI_4504010-S	353	741	423	GCLM	NM_002061.1	GLCLR	glutamate-		cysteine
GI_4504012-S	152.3	136.1	114.8	GLDC	NM_000170.1	GCE;NKH;GCSP;HYGN1	glycine	mitochond	glycine
GI_4504018-S	246.8	302.9	271.4	GLRA1	NM_000171.1	STHE	glycine-	integral to	small
GI_4504024-S	202.6	260.6	228.4	GLRX	NM_002064.1	GRX	glutaredox		electron
GI_4504032-S	132.7	137.6	127.1	GML	NM_002066.1	LY6DL	GPI-	plasma	DNA
GI_4504034-S	3492.7	3116	3175.7	GMPS	NM_003875.1		GMP		purine
GI_4504036-S	3788.3	4470.4	4619.8	GNA11	NM_002067.1	GNA-11	heterotrim	peripheral	signal
GI_4504038-S	204.7	225.5	215.4	GNA15	NM_002068.1	GNA16	heterotrim	peripheral	phospholi
GI_4504040-S	2285.3	3006.2	2879.5	GNAI2	NM_002070.1	GIP;GNAI2B	heterotrim	peripheral	negative
GI_4504042-A	184.6	213.8	192.7	GNAL	NM_002071.1		heterotrim	peripheral	signal
GI_4504042-I	97.8	87.2	97.1	GNAL	NM_002071.1		heterotrim	peripheral	signal
GI_4504058-S	154.8	190	169	GNRHR	NM_000406.1	GRHR;LHRHR	gonadotro	integral to	G-protein
GI_4504066-S	4322.7	2157.9	1933.5	GOT1	NM_002079.1		aspartate	cytosol	aspartate
GI_4504068-S	2676.4	3361.1	3441.8	GOT2	NM_002080.1		aspartate	mitochond	aspartate
GI_4504074-S	131.2	136.6	135.8	GP2	NM_001502.1	ZAP75		secretory	
GI_4504076-S	128.8	131.8	124.8	GP9	NM_000174.1	CD42a	cell	integral to	blood
GI_4504080-S	448	549.4	570.3	GPC1	NM_002081.1		glypican	proteoglyc	developm
GI_4504084-S	172	224.2	209.8	GPD2	NM_000408.1	GDH2	glycerol-3-	glycerol-3-	glucose
GI_4504090-S	135.7	137.7	116.2	GPR30	NM_001505.1	FEG-1;CMKRL2;GPCR-Br	G-protein	integral to	G-protein
GI_4504092-S	154.3	186.7	174.2	GPR32	NM_001506.1		G-protein	integral to	G-protein
GI_4504094-S	93.3	101.1	93.7	GPR38	NM_001507.1	MTLR1	G-protein	integral to	G-protein
GI_4504096-S	130.1	128.8	143	GPR39	NM_001508.1		G-protein	integral to	G-protein
GI_4504098-S	111.1	125.8	108.5	CXCR3	NM_001504.1	GPR9;IP10;MigR;CD183;Mig-R;CKR-	chemokin	cytoplasm	cytosolic
GI_4504100-S	125.2	142.2	129.2	GRK6	NM_002082.1	GPRK6	G-protein-		regulation
GI_4504106-S	4546.7	4431.4	4622.5	GPX4	NM_002085.1	snGPx	glutathion	mitochond	phospholi
GI_4504130-S	92.2	110.9	100.7	GRIN2D	NM_000836.1	EB11;NMDAR2D	N-methyl-	integral to	signal
GI_4504132-S	765.7	992.5	463.9	NR3C1	NM_000176.1	GR;GCR;GRL	glucocorti	mitochond	transcripti
GI_4504136-S	215	229.1	217.3	GRM2	NM_000839.1	GLUR2;mGlu2;GPRC1B;MGLUR2	metabotro	integral to	negative
GI_4504138-S	80.8	93.1	83.4	GRM3	NM_000840.1	GLUR3;mGlu3;GPRC1C;MGLUR3	metabotro	integral to	negative
GI_4504140-S	734.3	931.8	792.4	GRM4	NM_000841.1	mGlu4;GPRC1D;MGLUR4	metabotro	integral to	negative
GI_4504142-S	93.6	102.3	78.8	GRM5	NM_000842.1	mGlu5;GPRC1E;MGLUR5;MGLUR5A;MGLU	metabotro	integral to	metabotro

GI_4504148-S	105.5	100.3	94	GRM8	NM_000845.1	GLUR8;mGlu8;GPRC1H;MGLUR8	metabotro	integral to	negative
GI_4504150-S	6195.8	5146.6	4838	GRN	NM_002087.1	PEPI;PCDGF	growth	extracellul	positive
GI_4504152-S	200.1	214.6	196.7	CXCL1	NM_001511.1	GRO1;GROa;MGSA;NAP-3;SCYB1;MGSA-a	cytokine	soluble	pan-neural
GI_4504154-S	95.4	102.9	96.2	CXCL2	NM_002089.1	GRO2;GROb;MIP2;MIP2A;SCYB2;MGSA-	cytokine	soluble	chemotaxi
GI_4504156-S	153.1	138.3	124.3	CXCL3	NM_002090.1	GRO3;GROg;MIP2B;SCYB3;MIP-2b;CINC-	cytokine	extracellul	G-protein
GI_4504160-S	1967.2	1788.7	1602.4	GRSF1	NM_002092.1		mRNA	cytoplasm	mRNA
GI_4504166-S	5232.1	5146.3	4307.9	GSPT1	NM_002094.1	GST1;ETF3A;eRF3a	GTPase	nucleus	G1/S
GI_4504184-S	438.7	615.7	600	GSTT1	NM_000853.1		glutathion		response
GI_4504190-S	2050.2	1645.3	2015	MSH6	NM_000179.1	GTBP;HNPCC5	DNA	nucleus	mismatch
GI_4504196-S	782.7	792.5	762	GTF2F1	NM_002096.1	BTF4;RAP74;TF2F1;TFIIF	protein	transcripti	transcripti
GI_4504204-S	2133.5	1873.3	1975	GTF3C2	NM_001521.1	KIAA0011;TFIIIC110;TFIIIC-BETA	RNA	transcripti	transcripti
GI_4504210-S	164.6	232	176.1	GUCY1A2	NM_000855.1	GC-SA2;GUC1A2	guanylate	guanylate	signal
GI_4504212-S	246.1	316.8	261.8	GUCY1A3	NM_000856.1	GUCA3;GC-SA3;GUC1A3;GUCSA3	receptor	guanylate	nitric oxide
GI_4504214-S	176.9	281.1	239.9	GUCY1B3	NM_000857.1	GUCB3;GC-SB3;GUC1B3;GUCSB3;GC-S-	receptor	guanylate	nitric oxide
GI_4504216-S	125.2	129.2	118.4	GUCY2D	NM_000180.1	LCA;LCA1;CORD6;GUC2D;retGC;GUC1A4;	receptor	membran	receptor
GI_4504218-S	86.4	116.2	94.6	GUCY2F	NM_001522.1	GC-F;GUC2F;GUC2DL;RETGC-2;ROS-GC2	receptor	nuclear	receptor
GI_4504222-S	1434.8	1288.4	1456.8	GUSB	NM_000181.1	MPS7	beta-	lysosome	glycosami
GI_4504234-S	104.7	143.3	141.8	GZMK	NM_002104.1	PRSS;TRYP2	serine-	cytoplasm	proteolysis
GI_4504236-S	133.5	170.5	157.6	SEMA7A	NM_003612.1	CD108;SEMAL;CDw108;SEMAK1;H-Sema-		peripheral	immune
GI_4504252-S	2584.4	3286.6	4178.3	H2AFX	NM_002105.1	H2AX;H2A.X;H2A/X	DNA	chromoso	nucleoso
GI_4504326-S	1356.9	1390	1231	HADHB	NM_000183.1	HADH	acetyl-	mitochond	fatty acid
GI_4504334-S	94.6	104.9	99.8	HAPIP	NM_003947.1	duo;HS.8004	guanyl-		vesicle-
GI_4504338-S	118.4	123.7	108.7	HAS1	NM_001523.1	HAS	transferas	extracellul	glycosami
GI_4504340-S	640.3	717	811.8	HAT1	NM_003642.1		histone	nucleus	internal
GI_4504364-S	279.9	341	289.4	HDC	NM_002112.1		histidine		histidine
GI_4504366-S	213.6	239.2	196.2	HESX1	NM_003865.1	RPX	DNA	nucleus	brain
GI_4504374-S	112	119.2	115.4	HF1	NM_000186.1	HF;CFH;HUS;FHL1	compleme	extracellul	compleme
GI_4504380-S	109.5	111.6	99	HGD	NM_000187.1	AKU;HGO	homogenti		tyrosine
GI_4504388-S	263.7	221.1	231.8	HIVEP1	NM_002114.1	MBP-1;ZNF40;PRDII-BF1	transcripti	nucleus	regulation
GI_4504390-A	7776.5	6788.7	6649.6	HK1	NM_000188.1	HKI;HXK1	hexokinas	membran	glycolysis
GI_4504390-I	129.4	137.6	134.5	HK1	NM_000188.1	HKI;HXK1	hexokinas	membran	glycolysis
GI_4504394-S	73.7	75.2	70.6	HK3	NM_002115.1	HXK3;HKIII	hexokinas	membran	glycolysis
GI_4504410-S	101.6	107.8	108	HLA-DRB1	NM_002124.1	HLA-DR1B	class II	integral to	pathogene
GI_4504416-S	344.9	545.9	339.4	MR1	NM_001531.1	HLALS	class I		immune
GI_4504426-S	344.1	360.8	290.7	HMGCL	NM_000191.1	HL	hydroxym	mitochond	amino
GI_4504436-S	598.4	631.4	512.3	HMOX1	NM_002133.1	HO-1;bK286B10	heme	microsom	heme
GI_4504444-A	14398.7	12432	9917.1	HNRPA1	NM_002136.1	HNRNPA1	heterogen	nucleoplas	RNA-
GI_4504450-S	3898.1	3525.8	2501.9	RBMX	NM_002139.1	HNRPG;hnRNP-G	RNA	heterogen	biological_
GI_4504480-A	104.9	110.9	104.9	HPN	NM_002151.1	TMPRSS1	serine-	integral to	cell growth
GI_4504482-S	867.6	958.6	839.5	HPRT1	NM_000194.1	HPRT;HGPRT	hypoxanth	cytoplasm	purine
GI_4504486-S	144.5	141.7	132.8	HRC	NM_002152.1		calcium	smooth	muscle
GI_4504492-S	128.5	111.8	112.8	HRK	NM_003806.1	DP5;HARAKIRI	apoptosis		negative
GI_4504494-S	1952.2	1536.9	1225.1	HRMT1L1	NM_001535.1	PRMT2	signal	nucleus	protein
GI_4504500-S	110.9	114.1	102.5	HSD17B1	NM_000413.1	HSD17;EDHB17;EDH17B2	catalytic	cytoplasm	estrogen

GI_4504502-S	195	198.9	222.4	HSD17B2	NM_002153.1	HSD17;EDH17B2	estradiol	endoplas	estrogen
GI_4504504-S	548.6	683.4	787	HSD17B4	NM_000414.1		estradiol	peroxisom	steroid
GI_4504506-S	188.1	216	188.4	HSD3B1	NM_000862.1	HSD3B;HSDB3	steroid	endoplas	steroid
GI_4504508-S	113.8	126.7	110.9	HSD3B2	NM_000198.1	HSDB;HSDB3	steroid	endoplas	steroid
GI_4504510-S	1997.3	3307.4	2628.1	DNAJA1	NM_001539.1	HDJ2;HSDJ;HSJ2;HSPF4	heat		heat
GI_4504522-S	6290.3	7993.1	7861.5	HSPE1	NM_002157.1	CPN10;GROES;HSP10	co-	mitochond	protein
GI_4504530-S	113.3	125.7	115.7	HTR1A	NM_000524.1	ADRBRL1;ADRB2RL1	serotonin	integral to	positive
GI_4504532-S	115.9	130.5	105.4	HTR1B	NM_000863.1	S12;HTR1D2;HTR1DB	serotonin	integral to	G-protein
GI_4504536-S	119.2	120.6	120.5	HTR1E	NM_000865.1		serotonin	integral to	G-protein
GI_4504540-S	85.6	80	83.9	HTR2C	NM_000868.1	HTR1C	serotonin	integral to	serotonin
GI_4504542-S	151.4	197.7	180.8	HTR3A	NM_000869.1	HTR3	serotonin-	integral to	small
GI_4504544-S	106.1	112.2	94.9	HTR6	NM_000871.1		histamine	integral to	G-protein
GI_4504548-S	434.8	350.3	637.6	TNC	NM_002160.1	TN;HXB	binding	extracellul	cell
GI_4504566-S	131.9	168.1	158.4	ICSBP1	NM_002163.1	IRF8;ICSBP;IRF-8	RNA	nucleus	immune
GI_4504578-S	147.1	285.2	203.9	IF	NM_000204.1	FI	compleme	membran	compleme
GI_4504584-S	171.4	247.1	210.4	IFIT1	NM_001548.1	G10P1;IFI56;IFI-56;IFNAI1;RNM561;GARG-	molecular	cytoplasm	immune
GI_4504588-S	102.9	97.5	87.9	IFNA10	NM_002171.1		interferon-	extracellul	defense
GI_4504590-S	83	90.3	94.9	IFNA14	NM_002172.1		hematopoi	extracellul	defense
GI_4504592-S	95.8	97.4	91.7	IFNA16	NM_002173.1		interferon-	extracellul	defense
GI_4504594-S	99.4	100.9	98.4	IFNA21	NM_002175.1		hematopoi	extracellul	defense
GI_4504596-S	95.5	100.6	83.9	IFNA5	NM_002169.1	INFA5	hematopoi	extracellul	defense
GI_4504598-S	144.3	145.1	153.9	IFNA8	NM_002170.1		hematopoi	extracellul	defense
GI_4504602-S	124.6	123.1	109.3	IFNB1	NM_002176.1	IFB;IFF;IFNB	interferon-	extracellul	response
GI_4504604-S	109.3	109.2	95.6	IFNW1	NM_002177.1		interferon-	extracellul	response
GI_4504606-S	1287.1	794.2	541.6	IFRD1	NM_001550.1	PC4;TIS7			myoblast
GI_4504610-S	930.1	1181.7	1204.9	IGF2R	NM_000876.1	MPRI;CD222;CIMPR;M6P-R	insulin-like	lysosome	receptor
GI_4504614-S	105.6	105.7	106.2	IGFBP1	NM_000596.1	IBP1;IGF-BP25	insulin-like	extracellul	signal
GI_4504618-S	2357.3	5996.6	2930.4	IGFBP7	NM_001553.1	PSF;FSTL2;MAC25;IGFBP-7	insulin-like	extracellul	negative
GI_4504622-S	601.6	650.5	718.3	IGHMBP2	NM_002180.1	HCSA;CATF1;SMARD1;SMUBP2	DNA	nucleus	single-
GI_4504626-S	155.8	173.9	166.5	IGSF3	NM_001542.1	V8;EWI-3		membran	
GI_4504688-S	14880.1	11505	9198.2	IMPDH2	NM_000884.1	IMPD2	IMP		purine
GI_4504692-S	135.3	157.6	135.8	INE1	NM_003669.1		molecular	cellular_co	biological_
GI_4504694-S	263.8	267.7	289.8	ING1L	NM_001564.1	p33ING2	chromatin	chromoso	signal
GI_4504698-S	585.8	2825.2	1332.8	INHBA	NM_002192.1	EDF;FRP	transformi	extracellul	cell growth
GI_4504700-S	160	155.2	164	CXCL10	NM_001565.1	C7;IFI10;INP10;IP-10;crg-2;mob-	chemokin	soluble	positive
GI_4504704-I	128	131.4	119.5	INPP4A	NM_001566.1	INPP4			signal
GI_4504706-S	271.3	290.3	233.9	INPP4B	NM_003866.1		inositol-		signal
GI_4504710-S	113.6	141.5	109.3	INSL4	NM_002195.1	EPIL;PLACENTIN	insulin-like	soluble	pregnancy
GI_4504720-S	2284	1247.8	1036.9	IRF1	NM_002198.1	MAR;IRF-1	transcripti	nucleus	oncogene
GI_4504724-S	555.2	644.9	805.8	IRF3	NM_001571.1		transcripti	nucleus	transcripti
GI_4504732-S	77.8	86.1	92.9	IRS4	NM_003604.1	IRS-4;PY160	SH3/SH2	peripheral	signal
GI_4504736-S	170.1	151.1	199.7	ISL1	NM_002202.1	Isl-1	RNA	nucleus	energy
GI_4504738-S	368.3	412.3	337.7	CXorf12	NM_003492.1	ITBA1;DXS9878E	molecular	cellular_co	biological_
GI_4504746-I	279.3	312.2	316.3	ITGA3	NM_002204.1	VL3A;CD49C;GAPB3;MSK18;VCA-	cell	integrin	cell-matrix

GI_4504750-S	661.1	1444.6	1238.9	ITGA5	NM_002205.1	FNRA;CD49e;VLA5A	cell	integrin	cell
GI_4504752-S	111.7	120	128.1	ITGA7	NM_002206.1		cell	integrin	homophili
GI_4504756-S	114.7	115.9	104.4	ITGAL	NM_002209.1	CD11A;LFA-1;LFA1A	cell	integrin	cell
GI_4504776-S	94	108.4	97.5	ITGB7	NM_000889.1		cell	integrin	cell
GI_4504778-S	99.2	129.7	134.7	ITGB8	NM_002214.1		cell	integrin	cell
GI_4504780-S	154.6	157.4	142.8	ITIH1	NM_002215.1	H1P;ITIH;IATIH	serine		
GI_4504782-S	99.4	103.8	89.9	ITIH2	NM_002216.1	H2P	endopepti		
GI_4504788-S	616	441.6	764.4	ITPKA	NM_002220.1		inositol-		signal
GI_4504792-S	241.6	309.5	255.3	ITPR2	NM_002223.1	IP3R2	inositol-	integral to	small
GI_4504794-S	8972.2	5677.5	6976.4	ITPR3	NM_002224.1	IP3R3	inositol-	brush	small
GI_4504796-S	121.9	132.2	118.1	ITSN1	NM_003024.1	ITSN;SH3D1A;SH3P17	calcium	kinesin	synaptic
GI_4504802-S	834.4	898.5	880.9	JAK1	NM_002227.1	JAK1A	protein-	peripheral	protein
GI_4504810-I	113.1	217.1	212.7	JUP	NM_002230.1	DP3;PDGB;PKGB;DPIII	cytoskelet	soluble	cell
GI_4504848-S	89.9	91.3	91.2	KCNK3	NM_002246.1	OAT1;TASK;TBAK1;TASK-1	potassium	integral to	potassium
GI_4504864-S	3203.3	3485.9	2747.6	KHSRP	NM_003685.1	FBP2;KSRP;FUBP2	pre-mRNA	nucleus	mRNA
GI_4504878-S	104.9	103.8	89.3	KLRB1	NM_002258.1	NKR;CD161;NKR-P1;NKRP1A;NKR-P1A	lectin [goid	plasma	cell
GI_4504884-I	165.8	154.7	162.3	KLRC3	NM_002261.1	NKG2E;NKG2-E	transmem	integral to	cellular
GI_4504890-S	175.9	208.9	186.2	KMO	NM_003679.1		kynurenin		metabolis
GI_4504894-S	1174.8	1306.5	1452	KPNA1	NM_002264.1	RCH2;SRP1;IPOA5;NPI-1	nuclear	importin,	regulation
GI_4504896-S	3537.7	4387.7	4859.1	KPNA2	NM_002266.1	QIP2;RCH1;IPOA1;SRP1alpha	nuclear	importin,	spindle
GI_4504918-S	1834.9	4930.3	2983	KRT8	NM_002273.1	K8;KO;CK8;CYK8;K2C8;CARD2	structural	kinesin	cytoskelet
GI_4504936-S	147	111.2	142.4	KYNU	NM_003937.1		peptidase		tryptophan
GI_4504938-S	122.6	117.5	116.2	LAF4	NM_002285.1	MLLT2-like	transcripti	nucleus	oncogene
GI_4504946-S	106.7	136.7	114.4	LALBA	NM_002289.1		antimicrob	extracellul	induction
GI_4504950-S	2221.7	3620.3	1348.4	LAMB1	NM_002291.1		structural	basement	cell
GI_4504956-A	745.3	1017.1	838.7	LAMP2	NM_002294.1	LAMPB;CD107b		lysosomal	
GI_4504956-I	1174	1613.1	1297.5	LAMP2	NM_002294.1	LAMPB;CD107b		lysosomal	
GI_4504970-S	397.3	150.4	217.8	LDB2	NM_001290.1	LDB1;CLIM1	transcripti	nucleus	
GI_4504976-S	88.8	93.2	93.9	LECT2	NM_002302.1	chm2;chm-II		extracellul	chemotaxi
GI_4504982-S	351	401.6	449	LGALS3	NM_002306.1	GAL3;MAC2;CBP35;GALBP;LGALS2	lectin [goid	nucleus	heterophili
GI_4504984-S	103.9	139.5	119.7	LGALS7	NM_002307.1	GAL7;PIG1;TP53I1	lectin [goid	extracellul	cell growth
GI_4505004-S	201.6	262.1	213.5	LMO1	NM_002315.1	TTG1;RBTN1;RHOM1	transcripti		developm
GI_4505006-S	138.4	129.8	118.4	LMX1B	NM_002316.1	NPS1;LMX1.2	transcripti	nucleus	regulation
GI_4505010-S	13890.7	17584	19108	LOXL2	NM_002318.1	WS9-14	electron	membran	aging
GI_4505014-S	292.3	250.7	141	LRP3	NM_002333.1		LDL	integral to	receptor
GI_4505016-S	189.6	225.1	211.9	LRP6	NM_002336.1		LDL	integral to	
GI_4505018-S	536.9	794.1	334.6	LRP5	NM_002335.1	HBM;LR3;OPS;LRP7;OPPG;BMND1;VBCH2	LDL	integral to	positive
GI_4505020-S	1027.1	1309.9	1261.7	LRPAP1	NM_002337.1	RAP;MRAP;A2RAP;HBP44;A2MRAP	asialoglyc	integral to	vesicle-
GI_4505028-S	5099	4487	4093.5	LTA4H	NM_000895.1		leukotrien		leukotrien
GI_4505036-S	951.8	666.6	724.5	LTBP4	NM_003573.1	LTBP-4	protein	extracellul	
GI_4505038-S	1300	1527.6	1511.5	LTBR	NM_002342.1	CD18;TNFCR;TNFR-RP;TNFRSF3;TNFR2-	receptor	integral to	signal
GI_4505042-S	245.3	227.6	136.9	LTF	NM_002343.1	HLF2	serine-	extracellul	humoral
GI_4505048-S	1359.3	1683.4	1641.1	LY6E	NM_002346.1	RIGE;SCA2;RIG-E;SCA-2;TSA-1		membran	defense
GI_4505050-S	106.4	111.6	102.7	LY6H	NM_002347.1	NMLY6		membran	histogene

GI_4505052-S	105.4	115.1	100.7	LY75	NM_002349.1	DEC-205;GP200-MR6	defense/i	integral to	immune
GI_4505054-S	342.1	349.9	349.3	LYN	NM_002350.1	JTK8	protein-	peripheral	protein
GI_4505056-S	122.6	111.9	104.2	TACSTD2	NM_002353.1	M1S1;EGP-1;GA733;TROP2;GA733-1	receptor	membran	vision
GI_4505058-S	93.6	109.6	102.6	TACSTD1	NM_002354.1	EGP;KSA;M4S1;MK-	lymphocyt	plasma	
GI_4505064-S	912.3	370	572.9	MAD1L1	NM_003550.1	MAD1;PIG9;HsMAD1;TP53I9;TXBP181		centrosom	mitotic
GI_4505068-S	148.2	157.6	138.3	MAD	NM_002357.1	MXD1	transcripti	nucleus	developm
GI_4505072-S	1862.7	2094.7	2555.9	MAFG	NM_002359.1		transcripti	chromatin	transcripti
GI_4505074-S	276.3	364.7	319.7	MAFK	NM_002360.1	P18;NFE2U	transcripti	chromatin	regulation
GI_4505088-S	195	242.9	195.9	MAGP2	NM_003480.1	MP25	extracellul	extracellul	
GI_4505120-S	2392.2	2440.9	1931.7	MBD4	NM_003925.1	MED1	satellite	nucleus	DNA
GI_4505122-S	221.8	268.8	231.9	MBP	NM_002385.1		structural	nucleus	nerve
GI_4505126-S	242.2	310.1	267.2	MC2R	NM_000529.1	ACTHR	adrenocor	integral to	G-protein
GI_4505128-S	123.4	145	134.5	MCC	NM_002387.1		tumor		signal
GI_4505136-I	109.3	133.3	101.5	MDM2	NM_002392.1	hdm2			negative
GI_4505138-S	335.3	387.7	325.8	MDM4	NM_002393.1	MDMX		nucleus	negative
GI_4505148-S	806.5	534.8	810.9	SERPINB7	NM_003784.1	MEGSIN	serpin		
GI_4505168-S	80.2	95.5	84.9	SCGB2A2	NM_002411.1	MGB1;UGB2	steroid	cellular_co	biological_
GI_4505170-S	103.8	118.1	103.8	SCGB2A1	NM_002407.1	LPHC;MGB2;UGB3	androgen	cellular_co	biological_
GI_4505174-I	145.1	169.4	157.7	KITLG	NM_000899.1	SF;MGF;SCF;KL-1;Kitl	stem cell	integral to	histogene
GI_4505176-S	309.4	310.8	648.7	MGMT	NM_002412.1		DNA-	nucleus	DNA
GI_4505178-S	198.9	246.2	182.1	MGP	NM_000900.1	NTI;MGLAP	structural	extracellul	ossificatio
GI_4505184-S	14686.7	16736	12028	MIF	NM_002415.1	GIF;GLIF;MMIF	cytokine	extracellul	immune
GI_4505186-S	123	123.8	113.5	CXCL9	NM_002416.1	CMK;MIG;Humig;SCYB9;crg-10	cytokine	extracellul	chemotaxi
GI_4505196-S	140.5	154.3	138.4	MLL2	NM_003482.1	ALR	transcripti	nucleus	oncogene
GI_4505198-S	171.4	110.2	146.8	NR3C2	NM_000901.1	MR;MCR;MLR	steroid	nucleus	sodium
GI_4505204-S	118.1	115.8	113.4	MMP10	NM_002425.1	SL-2;STMY2	zinc ion	extracellul	proteolysis
GI_4505206-S	121.8	119.5	114.4	MMP12	NM_002426.1	HME;MME	macropha	extracellul	proteolysis
GI_4505220-S	117.4	138.9	120.6	MMP8	NM_002424.1	HNC;CLG1;PMNL-CL	neutrophil	extracellul	proteolysis
GI_4505222-S	125.4	160.2	128.5	MN1	NM_002430.1	MGCR;MGCR1;MGCR1-PEN	molecular	cellular_co	cell growth
GI_4505224-S	1093.4	1061.8	810	MNAT1	NM_002431.1	MAT1;RNF66	zinc ion	nucleus	regulation
GI_4505226-S	77.9	76.3	70.1	MNDA	NM_002432.1		DNA	nucleus	cellular
GI_4505230-S	387.7	429.9	416.7	MPDZ	NM_003829.1	MUPP1	protein		intracellula
GI_4505232-S	1077.4	906.3	884.4	MPG	NM_002434.1	AAG;MDG;APNG	damaged	nucleoplas	DNA
GI_4505234-S	458.7	612.8	448.6	MPI	NM_002435.1	PMI;PMI1	mannose-		mannose
GI_4505244-S	116.4	110	101.1	MRC1	NM_002438.1		mannose	integral to	receptor
GI_4505248-S	1232	1454	1395.4	MSH3	NM_002439.1		damaged		mismatch
GI_4505256-S	3492.9	3852.4	3058.6	MSN	NM_002444.1		structural	cytoskelet	cell
GI_4505264-S	125.3	161	132.3	MST1R	NM_002447.1	RON;CDw136	macropha	integral to	positive
GI_4505266-S	1092	1127.4	259.6	MSX1	NM_002448.1	HOX7;HYD1	transcripti	nucleus	skeletal
GI_4505276-S	866.5	732.2	639	MTIF2	NM_002453.1		translation	mitochond	regulation
GI_4505278-A	1158	1070.5	910.9	MTRR	NM_002454.1	MSR	electron	mitochond	amino
GI_4505278-I	125.1	123.2	118	MTRR	NM_002454.1	MSR	electron	mitochond	amino
GI_4505284-S	109	118.8	97.3	MUC2	NM_002457.1			secretory	
GI_4505286-S	113	116.6	111	IRF4	NM_002460.1	MUM1;LSIRF	RNA	nucleus	oncogene

GI_4505288-S	220	215.7	198.6	MVD	NM_002461.1	MPD	diphospho		isoprenoid
GI_4505294-S	176.3	191.3	160.4	MYBPC1	NM_002465.1	MYBPCC;MYBPCS	structural	striated	striated
GI_4505298-S	164.6	173.5	178.5	MYF6	NM_002469.1	MRF4;HERCULIN	transcripti	nucleus	myogenes
GI_4505300-S	112.3	95.6	103.6	MYH8	NM_002472.1	MyHC-pn;MyHC-peri	structural	muscle	striated
GI_4505304-S	316.3	395.5	281.9	MYL5	NM_002477.1		structural	muscle	regulation
GI_4505306-S	252.1	249.6	248	MYO7A	NM_000260.1	DFNB2;MYU7A;NSRD2;USH1B;DFNA11	myosin	kinesin	hearing
GI_4505312-S	99.9	115.4	99.7	MYOM1	NM_003803.1	SKELEMIN	structural	striated	muscle
GI_4505314-S	157.2	210	115.4	MYOM2	NM_003970.1	TTNAP	structural	striated	muscle
GI_4505316-S	405.6	406.1	365.3	PPP1R12A	NM_002480.1	MBS;MYPT1	signal	actin	regulation
GI_4505324-S	715	661.4	809.5	SSNA1	NM_003731.1	N14;NA14		kinesin	
GI_4505328-S	2391.7	3209.8	4188.9	NAPA	NM_003827.1	SNAPA;ALPHASNAP;alpha SNAP	intracellula	inter-Golgi	intra-Golgi
GI_4505330-S	254.7	313	311.1	NAPG	NM_003826.1	GAMMASNAP	intracellula	inter-Golgi	intra-Golgi
GI_4505336-S	1835.7	1786.3	1594.2	NUBP1	NM_002484.1	NBP;NBP1	nucleotide		septin
GI_4505346-S	158.7	158.6	135	NCK2	NM_003581.1	GRB4;NCKbeta	cytoskelet	cytoplasm	regulation
GI_4505360-S	143	209.4	182.4	NDUFB3	NM_002491.1	B12	NADH	NADH	mitochond
GI_4505368-S	2982	3176.7	2307.4	NDUFS4	NM_002495.1	AQDQ	NADH	NADH	mitochond
GI_4505370-S	6789.3	7176.6	7949.7	NDUFS8	NM_002496.1	TYKY	iron-sulfur	NADH	mitochond
GI_4505372-S	151.7	159.1	176.2	NEK2	NM_002497.1	NLK1;HsPK21;HsPK 21	protein	centrosom	regulation
GI_4505374-S	145.8	177.1	212.9	NEO1	NM_002499.1	NGN;HsT17534	tumor	integral to	cell
GI_4505376-S	101.1	110.8	97.7	NEUROD1	NM_002500.1	BETA2;BHF-1;NIDDM;NeuroD	RNA	nucleus	regulation
GI_4505378-S	1204.6	1579.7	1218.8	NFE2L1	NM_003204.1	NRF1;TCF11;LCR-F1;FLJ00380	transcripti	nucleus	heme
GI_4505380-S	120.2	145.2	118.9	NFIX	NM_002501.1	NF1A	transcripti	nucleus	transcripti
GI_4505390-S	112.8	158.9	112.9	NGFB	NM_002506.1	NGF	signal		developm
GI_4505392-S	136	127.1	132.2	NGFR	NM_002507.1	TNFRSF16;p75(NTR)	transmem	integral to	neurogene
GI_4505394-S	229	198	139.9	NID	NM_002508.1	NID1;ENTACTIN	extracellul	basement	cell-matrix
GI_4505396-S	1052.8	775.6	478.1	MAP3K14	NM_003954.1	HS;NIK;HSNIK;FTDCR1B	protein		protein
GI_4505398-S	2001	2488.1	2218.2	NIPSNAP1	NM_003634.1		folic acid		metabolis
GI_4505404-S	674.7	496.2	243.6	GPNMB	NM_002510.1	NMB		integral to	negative
GI_4505406-S	91.7	101.3	93.3	NMBR	NM_002511.1		bombesin	integral to	G-protein
GI_4505408-S	5166.7	4619.7	4104.1	NME2	NM_002512.1	puf;NDPKB;NM23B;NM23-H2	nucleoside	nucleus	negative
GI_4505414-S	659.8	1041.8	850.5	NQO1	NM_000903.1	DTD;QR1;DHQU;DIA4;NMOR1;NMORI	NAD(P)H	cytoplasm	nitric oxide
GI_4505416-S	436.5	457.8	540	NQO2	NM_000904.1	QR2;DHQV;NMOR2	NADPH		electron
GI_4505420-S	136.5	159.1	154.1	NOL4	NM_003787.1	NOLP;HRIHFB2255	RNA	nucleolus	
GI_4505430-S	372.9	385.8	399.5	NPAT	NM_002519.1	E14			
GI_4505432-S	89.5	94.8	93.7	NPPB	NM_002521.1	BNP	diuretic	extracellul	fluid
GI_4505436-I	266.2	318.3	304.8	NPR2	NM_000907.1	NPRB;ANPRB;GUC2B;NPRBi	transmem	integral to	regulation
GI_4505442-S	109	122.4	111.2	NPTX1	NM_002522.1	NP1			transport
GI_4505452-S	2281.2	2448.2	1832.4	NRD1	NM_002525.1		metalloen		neuromus
GI_4505454-S	370.3	482.5	728.1	NRIP1	NM_003489.1	RIP140	transcripti	nucleus	transcripti
GI_4505460-S	528.9	546.6	456.2	ENC1	NM_003633.1	NRPB;CCL28;ENC-1;PIG10;TP53I10	actin	cytoskelet	developm
GI_4505462-S	712.4	480.5	602.2	CNTNAP1	NM_003632.1	P190;CASPR;NRXN4;CNTNAP	SH3/SH2	integral to	signal
GI_4505466-S	106.9	120.1	93.1	NT5E	NM_002526.1	eN;NT5;NTE;eNT;CD73;E5NT	5'-	membran	DNA
GI_4505474-S	115	117	116	NTRK3	NM_002530.1	TRKC	neurotrop	integral to	transmem
GI_4505476-S	119.4	114.5	162.1	NTSR1	NM_002531.1	NTR	G-protein	Golgi	G-protein

GI_4505484-I	116.6	127.8	111.2	OAS2	NM_002535.1	P69	antiviral	membran	nucleobas
GI_4505488-S	5337	3411.6	4199.8	ODC1	NM_002539.1		ornithine	cellular_co	polyamine
GI_4505492-S	285.9	346.1	342.8	OGDH	NM_002541.1	E1k		oxoglutara	energy
GI_4505506-S	113.7	120.5	123.4	OPHN1	NM_002547.1	OPN1	Rho		substrate-
GI_4505514-S	101.2	117.6	93.2	OPRM1	NM_000914.1	OPRM;MOR-1	mu-opioid	Golgi	negative
GI_4505516-S	139.8	162	139.1	OR1D2	NM_002548.1	OLFR1;OR17-4	olfactory	integral to	olfaction
GI_4505518-S	91.8	88.1	91.4	OR3A1	NM_002550.1	OR40;OLFRA03;OR17-40	olfactory	integral to	signal
GI_4505540-S	2540.2	2770.7	1884.2	VDP	NM_003715.1	TAP;P115	vesicle	Golgi	nonselecti
GI_4505564-S	1600	2844.8	1511.5	P4HA1	NM_000917.1	P4HA	procollage	endoplas	protein
GI_4505574-S	17759.6	21137	14802	PABPC1	NM_002568.1	PAB1;PABP;PABP1;PABPL1	poly(A)	cytoplasm	mRNA
GI_4505582-S	701.6	1158.6	353.6	PAEP	NM_002571.1	GdA;GdS;PEP;PP14	transporte		developm
GI_4505584-S	112.6	145.2	127.5	PAFAH1B2	NM_002572.1		1-alkyl-2-	soluble	lipid
GI_4505594-S	93.6	121.1	175.3	SERPINB2	NM_002575.1	PAI;PAI2;PLANH2;HsT1201	enzyme		anti-
GI_4505600-S	224.2	276.6	252.4	PAK3	NM_002578.1	MRX30;OPHN3;PAK3beta	protein		protein
GI_4505608-S	489.8	608.5	535	PARG	NM_003631.1		poly(ADP-	cytoplasm	
GI_4505610-S	990.4	1006.8	1017.7	PARN	NM_002582.1	DAN	nuclease	cytoplasm	RNA
GI_4505612-S	816	744.5	391.1	PAWR	NM_002583.1	PAR4;par-4	transcripti	cytoplasm	negative
GI_4505614-A	452.3	395.3	359	PAX6	NM_000280.1	AN;AN2;MGDA;WAGR;D11S812E	transcripti	nucleus	eye
GI_4505622-S	97.6	130.9	121	PBX1	NM_002585.1		transcripti	nucleus	transcripti
GI_4505650-S	225.1	269.1	383.3	PCYT2	NM_002861.1	ET	ethanolam	cellular_co	phospholi
GI_4505656-S	120.8	111.2	107	PDE2A	NM_002599.1		cGMP-	membran	signal
GI_4505664-S	131.1	145.8	138.3	PDE4C	NM_000923.1	DPDE1	cAMP-		
GI_4505668-S	95.1	120.5	90.2	PDE6B	NM_000283.1	PDEB;CSNB3	cGMP-	membran	phototrans
GI_4505670-S	814.8	861.4	820.2	PDE6D	NM_002601.1	PDED	3',5'-cyclic-	peripheral	vision
GI_4505672-S	196.6	339.7	315.8	PDE6G	NM_002602.1	PDEG	enzyme	nucleus	vision
GI_4505674-S	98.3	96.3	95.1	PDE9A	NM_002606.1	HSPDE9A2	3',5'-cyclic-		signal
GI_4505680-I	262.2	300.2	277.1	PDGFB	NM_002608.1	SIS;SSV;PDGF2;c-sis	platelet-	membran	response
GI_4505684-S	3331.7	3186	2507.6	PDHA1	NM_000284.1	PDHA;PHE1A;PDHCE1A	pyruvate	mitochond	acetyl-
GI_4505686-S	3676.3	4653.5	4434.3	PDHB	NM_000925.1	PHE1B	pyruvate	mitochond	glucose
GI_4505694-S	307.5	343.4	362.3	PDPK1	NM_002613.1	PDK1;PRO0461	3-		insulin
GI_4505696-S	818.9	1061	794.9	SLC26A4	NM_000441.1	PDS;DFNB4	iodide	integral to	inorganic
GI_4505698-S	643.1	801	989.2	PDHX	NM_003477.1	E3BP;OPDX;PDX1;proX;DLDBP	electron	pyruvate	metabolis
GI_4505712-S	389.2	440	339.3	PER1	NM_002616.1	PER;RIGUI	signal	nucleus	entrainme
GI_4505716-S	298.4	287.3	275.3	PEX11A	NM_003847.1	PEX11-ALPHA		integral to	peroxisom
GI_4505718-S	663.1	713.1	873.4	PEX11B	NM_003846.1	PEX11-BETA		integral to	peroxisom
GI_4505720-S	232.3	207.1	188.6	PEX12	NM_000286.1		protein	integral to	protein-
GI_4505722-S	247.8	317.7	284.3	PEX13	NM_002618.1	ZWS;NALD	protein	integral to	intracellula
GI_4505724-S	240.9	234.1	219.6	PEX1	NM_000466.1	ZWS1	peroxisom	peroxisom	peroxisom
GI_4505726-S	305.6	276.4	270	PEX3	NM_003630.1			integral to	peroxisom
GI_4505730-S	512	543.2	356.5	PEX7	NM_000288.1	PTS2R;RCDP1	peroxisom	peroxisom	protein-
GI_4505732-S	210.9	225.4	238.9	PF4	NM_002619.1	CXCL4;SCYB4	chemokin	extracellul	chemotaxi
GI_4505734-S	87.5	83.2	71.4	PF4V1	NM_002620.1	PF4A;CXCL4V1;PF4-ALT;SCYB4V1	chemokin	extracellul	immune
GI_4505736-S	123	128.2	122.6	PFC	NM_002621.1	BFD;PFD;PROPERDIN	antibacteri	extracellul	immune
GI_4505744-S	114.8	131.3	121.2	PFKFB1	NM_002625.1	PFRX	fructose-		fructose

GI_4505754-S	106.4	119.7	92.4	PGAM2	NM_000290.1	PGAMM	phosphogl		striated
GI_4505756-S	104.8	116.4	106.8	PGC	NM_002630.1		aspartic-	extracellul	proteolysis
GI_4505774-I	5048.8	5363.9	3777.3	SLC25A3	NM_002635.1	PHC	phosphate	mitochond	small
GI_4505778-S	313.1	321.5	261.8	PHKA1	NM_002637.1	PHKA	phosphory		glycogen
GI_4505780-S	379.2	395.3	344	PHKA2	NM_000292.1	PHK;PYK;XLG;PYKL;XLG2	phosphory	phosphory	energy
GI_4505782-S	265.3	324.6	298.8	PHKB	NM_000293.1		phosphory		glycogen
GI_4505784-S	169.3	175.6	195.4	PHKG2	NM_000294.1		phosphory		glycogen
GI_4505788-S	486.8	753.5	567.5	SERPINB5	NM_002639.1	PI5;maspin	serpin		cell
GI_4505798-S	149.6	191.6	190.2	PIK3C2A	NM_002645.1	CPK;PI3-K-C2A;PI3-K-C2(ALPHA)	1-	phosphoin	phosphati
GI_4505806-A	2953.8	2972.6	2515.5	PIK4CA	NM_002650.1	pi4K230;PI4K-ALPHA	1-	Golgi	phosphati
GI_4505806-I	118.3	130.2	127.6	PIK4CA	NM_002650.1	pi4K230;PI4K-ALPHA	1-	Golgi	phosphati
GI_4505808-S	454.9	438.2	409.1	PIK4CB	NM_002651.1	PI4Kbeta;PI4K-BETA	1-	endosome	phosphati
GI_4505812-S	4377.3	4441	4154.4	DNCL1	NM_003746.1	LC8;PIN;DLC1;DLC8;hdlc1	enzyme	cytoplasmi	nitric oxide
GI_4505814-S	681.2	632.4	617.9	PIP5K1A	NM_003557.1		1-		glyceroph
GI_4505816-S	83.6	86.8	100.4	PIP5K1B	NM_003558.1	MSS4;STM7	1-		
GI_4505820-S	85.3	91.5	97.8	PIP	NM_002652.1	GP17;GCDFP-15	actin	extracellul	biological_
GI_4505822-S	262.6	421.5	231.3	PIR	NM_003662.1		transcripti	nucleus	transcripti
GI_4505836-S	482.4	471.6	454	STK16	NM_003691.1	KRCT;MPSK;TSF1;PKL12	protein		protein
GI_4505840-S	104.4	111.2	106.3	PKP1	NM_000299.1	B6P	signal	intermedia	signal
GI_4505844-S	443.2	443.1	391.7	PLA2G10	NM_003561.1	SPLA2;GXPLA2;GXSPLA2	secreted	extracellul	lipid
GI_4505850-S	138.4	138.4	115.3	PLA2G4C	NM_003706.1	cPLA2-gamma	calcium-	membran	phospholi
GI_4505852-S	112.4	153.3	122.4	PLA2G5	NM_000929.1		calcium-	extracellul	phospholi
GI_4505854-S	219	228.7	252.1	PLAG1	NM_002655.1	PSA;SGPA	transcripti		
GI_4505862-S	33363.1	30879	24621	PLAU	NM_002658.1	UPA;URK	u-	extracellul	cell growth
GI_4505864-S	753.6	710.6	1082.8	PLAUR	NM_002659.1	CD87;UPAR;URKR	GPI-	plasma	chemotaxi
GI_4505870-S	140.3	146.8	93	PLCG2	NM_002661.1		phospholi		phospholi
GI_4505872-S	823.3	851.4	572.3	PLD1	NM_002662.1		phospholi	membran	small
GI_4505876-A	3087.2	3393	4554.8	PLEC1	NM_000445.1	PCN;EBS1;EBSO;PLTN	structural	intermedia	cytoskelet
GI_4505878-S	411.1	532.2	438.9	PLEK	NM_002664.1	P47	calcium		intracellula
GI_4505880-S	90	96.4	91.1	PLG	NM_000301.1		plasmin	nucleus	negative
GI_4505884-S	357.6	423.6	380	PLIN	NM_002666.1		lipid	lipid	lipid
GI_4505888-A	4442.3	6955	4823.4	PLOD2	NM_000935.1		procollage	membran	protein
GI_4505892-S	3067.4	2594.6	3156.9	PLP2	NM_002668.1	A4;A4-LSB	ion	endoplas	ion
GI_4505894-S	3020.4	2538	2263.7	PLRG1	NM_002669.1	PRL1	transcripti	nucleus	nuclear
GI_4505896-S	390.1	326.2	331.6	PLS1	NM_002670.1	I-PLASTIN	actin	brush	
GI_4505898-S	100.6	102.6	93.1	PMCH	NM_002674.1	MCH	neuropepti	extracellul	signal
GI_4505900-S	568.4	494.6	552.1	C17orf35	NM_003876.1	PM1;PMI	G-protein	integral to	signal
GI_4505904-S	534.8	538.7	523.1	PMM1	NM_002676.1		phosphom	cytoplasm	mannose
GI_4505916-S	2082.8	1768.3	1845.4	PMSCL2	NM_002685.1	PMSCL;PM-Scl	protein	nucleolus	rRNA
GI_4505924-S	185.7	200.8	187.8	PNR	NM_003967.1		G-protein	integral to	synaptic
GI_4505930-S	587.1	673.9	648.2	POLB	NM_002690.1		beta DNA	nucleus	DNA
GI_4505932-S	635.1	601	652.6	POLD1	NM_002691.1	POLD	delta DNA	nucleus	response
GI_4505936-S	1228	1298	1359.9	POLG	NM_002693.1	PEO;POLG1;POLGA	gamma	gamma	DNA
GI_4505940-S	1384	1452.3	1414	POLR2B	NM_000938.1	RPB2;POL2RB;hsRPB2;hRPB140	DNA	DNA-	transcripti

GI_4505946-S	3247.6	3135.1	3171.1	POLR2G	NM_002696.1	RPB7;hRPB19;hsRPB7	DNA-	DNA-	transcripti
GI_4505948-S	114.2	102.3	112.5	POMC	NM_000939.1	MSH;POC;ACTH;CLIP	receptor	soluble	energy
GI_4505952-S	3251.9	4573.9	4609.9	PON2	NM_000305.1		arylestera	extracellul	
GI_4505954-S	98.2	99.5	91.5	POU1F1	NM_000306.1	PIT1;GHF-1	transcripti	nucleus	negative
GI_4505958-S	634.7	636	619	POU2F2	NM_002698.1	OCT2;OTF2	transcripti		humoral
GI_4505962-S	96.4	97.9	82.4	POU3F4	NM_000307.1	BRN4;DFN3;OTF9;BRAIN-4	transcripti	nucleus	hearing
GI_4505964-S	97.7	100	102.1	POU4F3	NM_002700.1	BRN3C;DFNA15	DNA	nucleus	eye
GI_4505988-S	8781.8	6845.7	10507	PPGB	NM_000308.1	GSL;CTSA;GLB2;NGBE;PPCA	carboxype	lysosome	intracellula
GI_4506004-S	1071.7	1223	1094.2	PPP1CB	NM_002709.1	PPP1CD	protein		cytokinesi
GI_4506006-S	6524.8	5864.9	4985.8	PPP1CC	NM_002710.1	PPP1G	protein		cytokinesi
GI_4506012-S	1078	1265.6	852	PPP1R7	NM_002712.1	SDS22	protein	cytoplasm	
GI_4506016-S	6001.9	6625	6089.2	PPP2CA	NM_002715.1	PP2CA	protein	protein	oncogene
GI_4506026-S	2469.8	2969.7	2980	PPP4C	NM_002720.1	PP4;PPX	NF-	centrosom	microtubul
GI_4506030-S	1905.5	2181.5	2351.3	PPT1	NM_000310.1	PPT;CLN1;INCL	palmitoyl-	lysosome	neurogene
GI_4506056-A	259.3	237.8	205.6	PRKACB	NM_002731.1		cAMP-	nucleus	signal
GI_4506056-I	243.1	306.8	255.4	PRKACB	NM_002731.1		cAMP-	nucleus	signal
GI_4506064-S	245.7	190.3	230.2	PRKAR2B	NM_002736.1	PRKAR2;RII-BETA	cAMP-	cAMP-	intracellula
GI_4506066-S	246.3	271.5	232.9	PRKCA	NM_002737.1	PKCA	protein	peripheral	induction
GI_4506074-S	236	271.2	281	PRKCM	NM_002742.1	PKD;PKCM;PKC-MU	atypical	cytosol	protein
GI_4506076-S	1527.7	1427.1	1410.2	PRKCSH	NM_002743.1	PCLD;G19P1;AGE-R2	calcium	intracellula	protein
GI_4506102-S	96.4	95.2	96.7	PRKR	NM_002759.1	PKR;EIF2AK1	eukaryotic	intracellula	negative
GI_4506108-S	101	98.4	93.3	PRM1	NM_002761.1		DNA	nucleoplas	DNA
GI_4506110-S	93.7	102.5	97.3	PRM2	NM_002762.1		DNA	nucleoplas	DNA
GI_4506114-S	112.1	114.3	102.5	PROC	NM_000312.1		protein C	extracellul	proteolysis
GI_4506116-S	1021	455.5	333.7	PROS1	NM_000313.1	PSA;PROS	endopepti	extracellul	blood
GI_4506120-S	98.8	103.9	106	PROZ	NM_003891.1	PZ	protein	extracellul	proteolysis
GI_4506130-S	1983.9	1681.2	1788.4	PRPSAP1	NM_002766.1	PAP39	enzyme		nucleobas
GI_4506134-S	506.2	497.4	434.3	PRRG1	NM_000950.1	PRGP1	calcium	extracellul	
GI_4506136-S	127.5	171.9	151	PRRG2	NM_000951.1	PRGP2	calcium	extracellul	regulation
GI_4506138-S	1108.8	1270	1675.9	PCOLN3	NM_002768.1	PRSM1;KIAA0047	metallope		
GI_4506150-S	104	118.7	115.7	PRSS7	NM_002772.1	ENTK	trypsin	brush	proteolysis
GI_4506176-S	485.5	570.5	488.7	PSG7	NM_002783.1		plasma	extracellul	pregnancy
GI_4506264-S	145.5	452.8	617.7	PTGS2	NM_000963.1	COX2;COX-2;PHS-2;PGG/HS;PGHS-2;hCox-	prostaglan	membran	physiologi
GI_4506312-S	188.4	160.3	209.4	PTPRH	NM_002842.1	SAP-1	transmem	integral to	protein
GI_4506328-S	123.4	125.7	111.9	PTPRZ1	NM_002851.1	PTPZ;HPTPZ;PTP18;PTPRZ;RPTPB	transmem	integral to	central
GI_4506330-S	1350.1	1972.1	2247.4	PTS	NM_000317.1	PTPS	6-		tetrahydro
GI_4506334-S	89.1	94.1	93.2	PVALB	NM_002854.1	D22S749	calcium		muscle
GI_4506338-S	700.9	729.8	870.8	PXF	NM_002857.1				
GI_4506342-S	1551.8	1675.8	1586.2	PXMP3	NM_000318.1	PAF1;PEX2;PAF-1;PMP35;RNF72		integral to	protein-
GI_4506344-S	499.8	391.5	241.6	PXN	NM_002859.1	FLJ23042	protein	microtubul	signal
GI_4506354-S	114.5	116.2	108.1	PZP	NM_002864.1		serine	cellular_co	pregnancy
GI_4506358-S	333.2	398.6	366.4	QDPR	NM_000320.1	DHPR;PKU2	6,7-		dihydrobio
GI_4506364-S	524.5	637	523.2	RAB2	NM_002865.1	RAB2A	RAB small	Golgi	ER to
GI_4506374-S	932.4	827.6	926.6	RAB7L1	NM_003929.1		RAB small		small

GI_4506382-I	83	84.9	86.4	RAD17	NM_002873.1	R24L;Rad24;HRAD17;RAD17Sp		nucleus	DNA
GI_4506400-S	577.3	634.1	540.6	RAF1	NM_002880.1		protein	mitochond	protein
GI_4506404-S	140.4	164.9	153.1	RALB	NM_002881.1		GTP		signal
GI_4506408-I	755.9	718.5	724	RANBP3	NM_003624.1	DKFZp586I1520	RAN	nucleus	
GI_4506412-S	954.6	875.3	710.8	RAP1A	NM_002884.1	KREV1;KREV-1;SMGP21	GTPase		signal
GI_4506414-S	173.5	196.1	179.1	RAP1GA1	NM_002885.1	RAP1GAP;KIAA0474	GTPase	membran	signal
GI_4506418-S	1393.7	1241.6	909.5	RARA	NM_000964.1	RAR;NR1B1	retinoic	nucleus	oncogene
GI_4506424-S	99.8	90	92.9	RARRES1	NM_002888.1	TIG1		integral to	negative
GI_4506430-I	126.1	116.9	98.5	RASA1	NM_002890.1	GAP;PKWS;RASA;CMAVM;RASGAP;p120G	Ras		cell growth
GI_4506434-S	451.2	577.4	524.7	RB1	NM_000321.1	RB	tumor	chromatin	cell cycle
GI_4506444-S	2057.5	1944.1	1915.9	RBM4	NM_002896.1	LARK	RNA		RNA
GI_4506448-S	257.9	325.7	228.8	RBMS2	NM_002898.1	SCR3	RNA		RNA
GI_4506452-S	105.8	108	97.2	RBP3	NM_002900.1	IRBP;RBPI;D10S64;D10S65;D10S66	retinoid	extracellul	vision
GI_4506454-S	4166.1	5241	3399.3	RCN1	NM_002901.1	RCN	calcium	endoplas	
GI_4506456-S	1858.2	2603.7	2272.2	RCN2	NM_002902.1	E6BP;ERC55;ERC-55	protein	endoplas	
GI_4506458-S	323.2	427	394.5	RCV1	NM_002903.1		calcium		vision
GI_4506462-S	411.9	414.9	333.8	RDH5	NM_002905.1	RDH1	retinol	membran	vision
GI_4506472-S	157.9	170.3	184.8	REL	NM_002908.1	C-Rel	transcripti	nucleus	transcripti
GI_4506482-S	187.5	197.6	226.1	REV3L	NM_002912.1	POLZ;REV3	zeta DNA	zeta DNA	DNA
GI_4506516-S	214.4	338	287.1	RGS2	NM_002923.1	G0S8	GTPase	peripheral	regulation
GI_4506520-S	125.4	118	113.7	RGS9	NM_003835.1	PERRS;RGS9L	GTPase	peripheral	regulation
GI_4506522-S	161.2	187	171	RHAG	NM_000324.1	RH2;RH50A	blood	integral to	protein
GI_4506524-S	276.3	306.5	233.4	RHBDL1	NM_003961.1	RRP;RHBDL	serine-	membran	signal
GI_4506528-S	181.6	196.5	176.7	RHOK	NM_002929.1	RK;GRK1;GPRK1	G-protein-		rhodopsin
GI_4506532-S	93.9	114.4	97.3	RIT2	NM_002930.1	RIN;RIBA;ROC2	GTPase	plasma	synaptic
GI_4506558-S	1565.3	1394.8	1217.7	ABCE1	NM_002940.1	RLI;OABP;ABC38;RNS4I;RNASELI	ribonuclea	membran	response
GI_4506562-S	779.3	968	1092.5	RNGTT	NM_003800.1	HCE;HCE1;hCAP;CAP1A	mRNA	nucleus	mRNA
GI_4506566-S	1078.6	899.8	960	RNMT	NM_003799.1	MET;RG7MT1;KIAA0398	mRNA	nucleus	mRNA
GI_4506580-S	278.9	237.7	279.2	RPGR	NM_000328.1	CRD;RP3;COD1;PCDX;RP15	protein	Golgi	vision
GI_4506588-S	811.8	973.1	704.8	RTCD1	NM_003729.1	RPC	RNA-3'-	nucleoplas	assembly
GI_4506590-S	96.3	108.6	109.3	RPE65	NM_000329.1	LCA2;RP20	protein		vitamin A
GI_4506734-S	426.5	426.3	593	RPS6KA4	NM_003942.1	MSK2;RSKB;RSK-B	protein	nucleus	protein
GI_4506736-S	102.9	108.9	120.5	RPS6KB1	NM_003161.1	S6K1;STK14A	protein		signal
GI_4506738-S	334.2	385.5	410.8	RPS6KB2	NM_003952.1	p70S6Kb;P70-BETA	protein		protein
GI_4506742-S	23202.7	21050	16409	RPS8	NM_001012.1		structural	cytosolic	protein
GI_4506752-S	3310	3233.6	2943.3	RUVBL1	NM_003707.1	ECP54;TIP49;NMP238	DNA	nucleus	recombina
GI_4506756-S	88.1	100.2	83.6	RYR2	NM_001035.1	VTSIP	calcium-	integral to	regulation
GI_4506760-S	6531.4	9755.8	7897.4	S100A10	NM_002966.1	42C;P11;p10;GP11;ANX2L;CAL1L;CLP11;Ca	receptor		signal
GI_4506762-S	159.4	223.3	132.9	S100A3	NM_002960.1	S100E	calcium		
GI_4506766-S	119	122.4	112	S100A5	NM_002962.1	S100D	calcium		
GI_4506782-S	824.2	747.1	606.1	SAP30	NM_003864.1		transcripti	histone	
GI_4506788-S	2628.6	1518.7	1773.3	SAT	NM_002970.1	SSAT	diamine N-		
GI_4506792-S	394.5	357.6	561.4	SCA1	NM_000332.1	ATX1;D6S504E		cytoplasm	
GI_4506794-S	2217	1869.9	1589.1	SCA2	NM_002973.1	ATX2;TNRC13	molecular	cytoplasm	pathogene

GI_4506796-S	95	103.6	84.8	SCA7	NM_000333.1	OPCA3;ADCAII	molecular	nucleus	nuclear
GI_4506810-S	147.4	180.6	165.4	SCN7A	NM_002976.1	SCN6A	voltage-	voltage-	sodium
GI_4506812-S	197.8	227.1	206.9	SCN9A	NM_002977.1	PN1;NE-NA	voltage-	voltage-	sodium
GI_4506816-S	301.4	376.2	340.7	SCNN1B	NM_000336.1	ENaCb;SCNEB;ENaCbeta	amiloride-	membran	sodium
GI_4506820-S	130.4	140.8	121.8	SCNN1G	NM_001039.1	PHA1;ENaCg;SCNEG;ENaCgamma	sodium	integral to	sodium
GI_4506824-S	100.6	100.1	87.3	SCTR	NM_002980.1	SR	secretin	integral to	G-protein
GI_4506832-S	216.1	294.5	264.4	CCL1	NM_002981.1	P500;SISe;TCA3;I-309;SCYA1	chemokin	extracellul	viral life
GI_4506842-S	85.4	133.4	96.6	CCL3	NM_002983.1	MIP1A;SCYA3;LD78ALPHA;MIP-1-alpha	chemokin	soluble	regulation
GI_4506844-S	238.6	272.9	250.5	CCL4	NM_002984.1	ACT2;LAG1;Act-	cytokine	extracellul	viral
GI_4506850-S	113.4	115.6	104.3	CXCL6	NM_002993.1	GCP2;CKA-3;GCP-2;SCYB6	chemokin		chemotaxi
GI_4506852-S	142.8	158.6	145.4	XCL1	NM_002995.1	LTN;ATAC;LPTN;SCM1;SCM-1;SCYC1;SCM-	cytokine	extracellul	chemotaxi
GI_4506856-S	88.1	97.4	84.4	CX3CL1	NM_002996.1	NTN;NTT;CXC3;CXC3C;SCYD1;ABCD-	chemokin	integral to	chemotaxi
GI_4506864-S	2599.4	2720.5	2269.7	SDHD	NM_003002.1	PGL;CBT1;PGL1;SDH4	electron	mitochond	tricarboxyli
GI_4506866-S	572.5	706.9	588.2	SEC14L1	NM_003003.1	SEC14L	binding	membran	nonselecti
GI_4506868-S	99.4	113.7	94.5	SECTM1	NM_003004.1	K12	cytokine	Golgi	mesoderm
GI_4506870-S	93.3	109.5	105.5	SELE	NM_000450.1	ELAM;ESEL;CD62E;ELAM1;LECAM2	cell	integral to	inflammat
GI_4506880-S	440.8	139.8	263.2	SEMA5A	NM_003966.1	semF;SEMAF	receptor	integral to	cell
GI_4506890-S	5540	5515.1	4522.2	SET	NM_003011.1	2PP2A;IGAAD;I2PP2A;PHAPII;TAF-IBETA	protein	nucleus	nucleoso
GI_4506898-S	5042	7152	6184.5	SFRS2	NM_003016.1	SC35;PR264;SC-35;SRp30b	pre-mRNA	nucleus	mRNA
GI_4506910-S	85.6	93.4	73	SGCA	NM_000023.1	A2;ADL;DAG2;DMDA2;50-		dystrophin-	muscle
GI_4506916-S	1513.9	7487.9	3595.1	SGNE1	NM_003020.1	P7B2	GTP	secretory	neuropepti
GI_4506922-S	129.7	110.7	118.7	SH2D1A	NM_002351.1	LYP;SAP;XLP;DSHP;EBVS;IMD5;XLPD;MTC	SH3/SH2	cytoplasm	cellular
GI_4506924-S	825.6	1279.1	1071	SH3BGRL	NM_003022.1	SH3BGR	SH3/SH2		
GI_4506928-S	360.3	405.2	416.6	SH3GL1	NM_003025.1	EEN;CNSA1;SH3P8;SH3D2B		kinesin	central
GI_4506930-S	118.3	123.3	109.5	SH3GL2	NM_003026.1	CNSA2;SH3P4;EEN-B1;SH3D2A		kinesin	central
GI_4506934-S	193.9	223.2	234.6	SHB	NM_003028.1		SH3/SH2		intracellula
GI_4506944-S	95.7	89.5	86.8	SI	NM_001041.1		catalytic	brush	carbohydr
GI_4506958-S	113.2	120.1	109.8	SIL	NM_003035.1				cell
GI_4506960-S	197.3	197.7	153.2	SIP1	NM_003616.1	GEMIN2	pre-mRNA	spliceoso	mRNA
GI_4506966-S	211.2	233.9	230.8	SKI	NM_003036.1	SKV	molecular	kinesin	cell growth
GI_4506968-S	82.4	91.5	80.5	SLAMF1	NM_003037.1	SLAM;CDw150	antigen	integral to	positive
GI_4506970-S	98.6	102.1	84.8	SLC10A1	NM_003049.1	NTCP;NTCP1	bile	integral to	small
GI_4506972-S	116.6	140	122.6	SLC10A2	NM_000452.1	ASBT;ISBT;NTCP2	bile	integral to	small
GI_4506976-S	101.3	99.4	102	SLC12A3	NM_000339.1	TSC;NCCT	sodium:ch	membran	small
GI_4506978-S	194	224	204.5	SLC13A2	NM_003984.1	NADC1;NaDC-1	low affinity	membran	small
GI_4506986-S	283.4	354.1	313.4	SLC18A1	NM_003053.1	CGAT;VAT1;VMAT1			
GI_4506990-S	159.9	196.4	190.5	SLC18A3	NM_003055.1	VACHT	acetylcholi	secretory	acetylcholi
GI_4507010-S	96.3	112.4	99.2	SLC2A4	NM_001042.1	GLUT4	glucose	membran	glucose
GI_4507012-S	132.3	169.3	144.3	SLC2A5	NM_003039.1	GLUT5	fructose	integral to	fructose
GI_4507016-S	202.4	307.6	247.5	SLC31A2	NM_001860.1	CTR2;COPT2;SLC13A2	copper ion	integral to	copper ion
GI_4507020-S	102.8	109.6	81.2	SLC4A1	NM_000342.1	DI;AE1;WD1;BND3;EPB3;CD233;EMPB3;RT	anion	integral to	cell ion
GI_4507024-S	98.3	94.8	121	SLC4A4	NM_003759.1	KNBC;NBC1;NBC2;pNBC;HNBC1;hhNMC;S	sodium:bi	integral to	small
GI_4507030-S	124.8	144.6	129.1	SLC5A1	NM_000343.1	NAGT;SGLT1;D22S675	glucose:s	integral to	sugar
GI_4507032-S	349.8	454.1	419.4	SLC5A2	NM_003041.1	SGLT2	low-affinity	integral to	small

GI_4507034-S	110.9	118.6	108	SLC5A5	NM_000453.1	NIS	iodide	integral to	small
GI_4507038-S	165.6	173.1	141.9	SLC6A1	NM_003042.1	GAT1;GABATR;GABATHG	gamma-	integral to	small
GI_4507044-S	247.1	294.3	266.9	SLC6A6	NM_003043.1	TAUT	taurine:so	integral to	small
GI_4507048-S	82.1	88.9	80.4	SLC7A2	NM_003046.1	ATRC2;CAT-2;HCAT2	basic	membran	small
GI_4507052-S	335.7	363.6	454.4	SLC7A6	NM_003983.1				
GI_4507060-S	147	178.8	169	SLIT1	NM_003061.1	MEGF4;SLIL1;SLIT3;Slit-1	protein	cellular_co	brain
GI_4507062-S	173.6	222.7	198.7	SLN	NM_003063.1	MGC12301		smooth	small
GI_4507094-S	274.4	294.5	292.3	SMPD2	NM_003080.1	NSMASE	sphingom	integral to	sphingom
GI_4507102-S	419.3	401.9	433.4	SNAPC2	NM_003083.1	SNAP45;PTFdelta	transcripti	nucleus	snRNA
GI_4507104-S	521.6	654.7	613.8	SNAPC3	NM_003084.1	SNAP50;PTFbeta	DNA	nucleus	snRNA
GI_4507106-S	1524.9	1520.5	1127.1	SNAPC4	NM_003086.1	SNAP190;FLJ13451;PTFalpha	DNA	nucleus	snRNA
GI_4507112-S	206.5	231.1	202.3	SNCG	NM_003087.1	SR;BCSG1		cytoplasm	oncogene
GI_4507114-S	285.7	304.2	307.3	FSCN1	NM_003088.1	SNL;p55	actin	actin	actin
GI_4507120-S	1234.7	1290.7	1021	SNRPA1	NM_003090.1		small	snRNP U2	mRNA
GI_4507126-S	1311.1	1271.5	1201.1	SNRPC	NM_003093.1		small	snRNP U1	mRNA
GI_4507128-S	3620.9	3465.7	2867.2	SNRPE	NM_003094.1	SME	small	spliceoso	mRNA
GI_4507130-S	2378	2477.3	2423.5	SNRPF	NM_003095.1	SMF	small	spliceoso	mRNA
GI_4507150-S	197.7	488.1	207.4	SOD3	NM_003102.1		superoxid	extracellul	superoxid
GI_4507170-S	31108.4	58234	36399	SPARC	NM_003118.1	ON	collagen	extracellul	ossificatio
GI_4507174-S	296.9	378.6	327.7	SPI1	NM_003120.1	OF;PU.1	transcripti	nucleus	negative
GI_4507176-S	317.1	308	295.8	SPIB	NM_003121.1	SPI-B	RNA	cytoplasm	regulation
GI_4507186-S	206.9	232.9	219.3	SPRR1B	NM_003125.1	SPRR1;GADD33;CORNIFIN	structural	intermedia	epidermal
GI_4507188-S	120.4	114.3	110.4	SPTA1	NM_003126.1	EL2	actin	spectrin	actin
GI_4507190-S	265.5	448.6	327.1	SPTAN1	NM_003127.1	(ALPHA)II-SPECTRIN	actin	spectrin	cell shape
GI_4507194-I	104	114.5	99.4	SPTBN1	NM_003128.1	SPTB2	actin	spectrin	
GI_4507200-S	374	421.6	586	SRD5A1	NM_001047.1		electron	microsom	sex
GI_4507204-S	2106.4	1797.4	1533.6	SRF	NM_003131.1		RNA	nucleus	signal
GI_4507208-S	10955.2	11926	11650	SRM	NM_003132.1	SPS1;SRML1	spermidin		spermidin
GI_4507212-S	1095.4	1237.6	1078.3	SRP19	NM_003135.1		7S RNA	signal	cotranslati
GI_4507216-S	5073.5	6054.6	4894.5	SRP9	NM_003133.1	ALURBP	RNA	signal	regulation
GI_4507224-S	113.8	113.1	102.1	SRY	NM_003140.1	TDF;TDY	DNA	nucleus	sex
GI_4507230-S	3470	3520.9	3201.4	SSBP1	NM_003143.1	SSBP	single-	mitochond	DNA
GI_4507232-S	142.5	162	119.5	SOCS1	NM_003745.1	JAB;CIS1;SSI1;TIP3;CISH1;SSI-1;SOCS-1	protein	cytoplasm	JAK-STAT
GI_4507246-S	169.9	140.9	150.2	STAC	NM_003149.1			soluble	intracellula
GI_4507250-S	94.7	96.9	87.3	STAR	NM_000349.1	STARD1	cholestero	mitochond	steroid
GI_4507260-S	102.8	93.7	82.4	STATH	NM_003154.1	STR	protein	extracellul	ossificatio
GI_4507264-S	7529.7	5914.8	9139.6	STC1	NM_003155.1	STC	glycopepti	extracellul	response
GI_4507266-S	229.6	474.8	252	STC2	NM_003714.1	STC-2;STCRP	glycopepti	extracellul	response
GI_4507272-S	458.3	505.7	422.2	AURKC	NM_003160.1	AIE2;AIK3;STK13	protein	centrosom	cytokinesi
GI_4507276-S	130.5	129.6	123.5	NEK4	NM_003157.1	NRK2;STK2	protein	nucleus	protein
GI_4507280-S	119.7	142.9	127.3	CDKL5	NM_003159.1	STK9	protein		protein
GI_4507282-S	134.1	160	145.8	STRN	NM_003162.1	SG2NA	calmoduli	kinesin	biological_
GI_4507284-S	1294.3	1267.7	1387.3	STX10	NM_003765.1	SYN10;hsyn10	protein	Golgi	intracellula
GI_4507294-S	283.7	267.5	280.4	STX7	NM_003569.1		vesicle	endosome	post-Golgi

GI_4507296-S	539.9	621.5	530.5	STXBP1	NM_003165.1	UNC18;hUNC18;MUNC18-1		insoluble	Golgi to
GI_4507308-A	323.9	310.9	245.3	SUPT3H	NM_003599.1	SPT3;SPT3L	RNA	transcripti	regulation
GI_4507310-S	911	1188.8	842.5	SUPT4H1	NM_003168.1	SPT4H;SUPT4H	transcripti	nucleus	chromatin
GI_4507320-S	309.7	386	367	SUV39H1	NM_003173.1	SUV39H	methyltran	nuclear	establish
GI_4507336-S	149.2	170.5	144.5	SYT5	NM_003180.1		transporte	synaptic	synaptic
GI_4507344-S	176.8	199.7	183.3	TACR2	NM_001057.1	SKR;NK2R;NKNAR;TAC2R	tachykinin	integral to	tachykinin
GI_4507356-S	3888.5	5560.8	4758	TAGLN2	NM_003564.1	HA1756;KIAA0120			muscle
GI_4507362-S	293.3	392.5	351.4	TAL1	NM_003189.1	SCL;TCL5	DNA		oncogene
GI_4507368-S	149.5	152.4	160	TAT	NM_000353.1				
GI_4507372-S	539.6	710.1	681.2	TBCC	NM_003192.1	CFC	co-	microtubul	post-
GI_4507388-S	827.1	908.4	835.9	TCEB3	NM_003198.1	SIII;TCEB3A	protein	nucleus	regulation
GI_4507396-A	188.6	219.7	206.9	TCF2	NM_000458.1	HNF2;LFB3;HNF1B;MODY5;VHNF1;HNF1be	DNA	nucleus	regulation
GI_4507396-I	117.3	137.5	115.6	TCF2	NM_000458.1	HNF2;LFB3;HNF1B;MODY5;VHNF1;HNF1be	DNA	nucleus	regulation
GI_4507398-S	212.6	202.7	181.7	TCF4	NM_003199.1	E2-2;ITF2;SEF2;SEF2-1;SEF2-1B	RNA	nucleus	regulation
GI_4507400-I	2227.8	1755	1759.6	TFAM	NM_003201.1	TCF6;MtTF1;mtTFA;TCF6L2	transcripti	mitochond	transcripti
GI_4507410-S	905.8	790.2	745	TCOF1	NM_000356.1	MFD1;treacle	transporte	nucleolus	nucleocyto
GI_4507424-S	106.9	99.4	90.7	TDGF1	NM_003212.1	CR;CRGF;CRIPTO	receptor		signal
GI_4507426-S	1595.8	939.8	959	TEAD4	NM_003213.1	RTEF1;TEF-3;EFTR-2;RTEF-1;TEFR-	RNA		muscle
GI_4507428-S	109.4	130.9	102.8	TEC	NM_003215.1	PSCTK4	non-		protein
GI_4507432-S	9576.5	8810.2	9459.2	TEGT	NM_003217.1	BI-1		insoluble	apoptosis
GI_4507440-S	117.4	129.6	114.7	TFAP2A	NM_003220.1	AP-2;AP2TF;TFAP2	RNA	nucleus	ectoderm
GI_4507446-S	197.7	214.7	209.4	TFAP4	NM_003223.1	AP-4	RNA	nucleus	regulation
GI_4507450-S	246.1	295.9	266.6	TFF1	NM_003225.1	pS2;BCEI;HPS2;pNR-2;D21S21	growth		cell growth
GI_4507452-S	126	135.6	127.9	TFF3	NM_003226.1	ITF;HITF		extracellul	defense
GI_4507456-S	2811.2	4756.1	4425.7	TFRC	NM_003234.1	TFR;CD71;TRFR	transferrin	endosome	iron ion
GI_4507460-S	642.1	1326.7	1799.3	TGFA	NM_003236.1		protein-	soluble	cell
GI_4507462-S	184.9	262.7	224.3	TGFB2	NM_003238.1		transformi	extracellul	signal
GI_4507464-S	475	697.4	556.9	TGFB3	NM_003239.1		transformi		histogene
GI_4507466-S	8779.7	7520.6	6295.5	TGFBI	NM_000358.1	CSD;CDB1;CDG2;CSD1;CSD2;CSD3;LCD1;	integrin	extracellul	negative
GI_4507470-S	569.6	545	634.9	TGFBR3	NM_003243.1		glycosami	integral to	TGFbeta
GI_4507474-S	121.5	131	119.7	TGM1	NM_000359.1	LI;LI1;TGK;ICR2;TGASE	protein-	membran	protein
GI_4507478-S	192.3	237.7	206.3	TGM4	NM_003241.1	TGP	acyltransf	cellular_co	peptide
GI_4507500-S	363.9	470.6	434.7	TIAM1	NM_003253.1		Rho		oncogene
GI_4507506-S	700.5	624.5	850.4	TIMELESS	NM_003920.1	TIM;TIM1;hTIM	protein	nucleus	response
GI_4507508-S	9850.6	11188	9562.2	TIMP1	NM_003254.1	EPA;EPO;HCI;CLGI;TIMP	metalloen	extracellul	positive
GI_4507514-S	237.6	280.1	246.1	TIMP4	NM_003256.1		metalloen	extracellul	biological_
GI_4507518-S	1509.3	2024.3	1737.1	TK1	NM_003258.1		thymidine	cytoplasm	nucleobas
GI_4507520-S	8270.3	8762.3	9084.6	TKT	NM_001064.1	TKT1	transketol		
GI_4507544-S	849.5	878.4	922.8	TM7SF1	NM_003272.1			membran	
GI_4507546-S	303.9	301	261.9	TM7SF2	NM_003273.1	ANG1	molecular	cellular_co	biological_
GI_4507552-S	135.1	164	159.1	TMOD1	NM_003275.1	TMOD;ETMOD;D9S57E	tropomyos	cytoskelet	cytoskelet
GI_4507554-S	341.2	375.3	378.6	TMPO	NM_003276.1	TP;LAP2	lamin/chro	nuclear	
GI_4507556-S	162.6	189.5	169.1	TNA	NM_003278.1	TN	lectin [goid	extracellul	skeletal
GI_4507610-S	98.6	110.3	93.9	TNK1	NM_003985.1		non-		protein

GI_4507612-S	203.1	239.1	226.9	TNKS	NM_003747.1	TIN1;PARPL;TINF1;TNKS1	NAD ADP-	telomere	telomeras
GI_4507614-S	111.7	112.7	106.8	TNNC1	NM_003280.1	TNC;TNNC	calcium		regulation
GI_4507620-S	95.9	85.5	93.6	TNNI2	NM_003282.1	DA2B;FSSV;AMCD2B	actin		regulation
GI_4507626-S	249.6	313.6	286.1	TNNT2	NM_000364.1	CMH2;CMD1D		troponin	regulation
GI_4507630-S	88.3	91.5	90.2	TNR	NM_003285.1		extracellul	extracellul	axon
GI_4507640-S	471.9	509.1	270.8	TPD52L1	NM_003287.1	D53			oncogene
GI_4507650-S	4973.3	6580.7	5140.3	TPM4	NM_003290.1		structural	muscle	muscle
GI_4507652-S	121.4	113.7	107.3	TPMT	NM_000367.1				
GI_4507656-S	158	158.5	138.3	TPP2	NM_003291.1		tripeptidyl-	cytoplasm	proteolysis
GI_4507658-S	1130.3	1404.8	1289.7	TPR	NM_003292.1			nuclear	protein-
GI_4507668-S	24187.9	22986	19946	TPT1	NM_003295.1	HRF;p02;TCTP	molecular	cytoplasm	
GI_4507670-S	107.2	118.8	101.4	CRISP2	NM_003296.1	TPX1;TSP1;GAPDL5;CRISP-2		extracellul	
GI_4507672-S	277.9	310.7	225.3	NR2C1	NM_003297.1	TR2;TR2-11	steroid	nucleus	regulation
GI_4507676-S	3911.5	6535.8	4408.5	TRA1	NM_003299.1	ECGP;GP96;GRP94	heat	endoplas	response
GI_4507680-S	79.7	79.4	73.1	TRHR	NM_003301.1		thyrotropin-	integral to	G-protein
GI_4507686-S	139.5	140.7	130.4	TRPC3	NM_003305.1	TRP3	store-	integral to	phototrans
GI_4507688-S	288.7	346.1	303.1	TRPM2	NM_003307.1	KNP3;EREG1;TRPC7;LTRPC2	calcium	integral to	calcium
GI_4507690-S	1330.3	1444.5	1513.6	TRRAP	NM_003496.1	TR-AP;PAF400			oncogene
GI_4507700-S	111.1	120.4	116.5	TSHR	NM_000369.1	LGR3	thyroid-	integral to	positive
GI_4507702-S	540.5	624.2	514.1	TSSC1	NM_003310.1		tumor		
GI_4507710-S	1275.7	1406.1	1322.3	TTC1	NM_003314.1	TPR1	protein		protein
GI_4507712-S	2901.1	2677.8	2484.9	DNAJC7	NM_003315.1	TPR2;TTC2;DANJC7	protein		protein
GI_4507722-S	101.4	96.8	96.4	TTPA	NM_000370.1	AVED;TTP1	tocopherol	cytosol	small
GI_4507724-S	160.8	162.7	142.2	TTR	NM_000371.1	PALB;TBPA;HsT2651	thyroid	extracellul	small
GI_4507728-S	642.1	1395.9	1208.8	TUBB	NM_001069.1		structural	cytoskelet	
GI_4507736-S	114.3	114.8	111.3	TULP2	NM_003323.1	TUBL2			vision
GI_4507742-S	91.4	81.1	94.7	TXK	NM_003328.1	RLK;TKL;BTKL;PTK4;PSCTK5	non-	cytoplasm	protein
GI_4507744-S	10247.9	11745	9793	TXN	NM_003329.1	TRX	thioredoxi		cell
GI_4507750-S	1666.5	1951.5	1810.3	TYMS	NM_001071.1	TS;TMS;TSase;HsT422	methyltran		deoxyribo
GI_4507756-S	222	257.4	237.9	TYRP1	NM_000550.1	TRP;CAS2;CATB;GP75;TYRP;b-PROTEIN	monooxyg	integral to	melanin
GI_4507810-S	873.4	816.4	600.4	UGCG	NM_003358.1	GCS	ceramide	endoplas	glucosylce
GI_4507812-S	836.5	1215.3	918.3	UGDH	NM_003359.1	UDPGDH	UDP-		UDP-
GI_4507814-S	153.8	186.1	170.1	UGT1A6	NM_001072.1	GNT1;HLUGP;UGT1F;HLUGP1;MGC29860	glucurono	microsom	xenobiotic
GI_4507818-S	170.7	213.4	195.7	UGT2B15	NM_001076.1	UGT2B8	UDP-	microsom	steroid
GI_4507820-S	95.3	98.1	99.3	UGT2B17	NM_001077.1		UDP-	microsom	steroid
GI_4507822-S	109	113.9	104.9	UGT2B11	NM_001073.1		UDP-	microsom	estrogen
GI_4507824-S	114.8	110	110.3	UGT2B7	NM_001074.1	UGT2B9	UDP-	microsom	lipid
GI_4507828-S	127.8	151.4	148.5	KLF7	NM_003709.1	UKLF	zinc ion		regulation
GI_4507830-S	1304.3	1607.8	1820.3	ULK1	NM_003565.1	UNC51	protein		protein
GI_4507832-S	177.3	210.4	183.8	UMOD	NM_003361.1	FJHN;HNFJ;MCKD2;ADMCKD2	GPI-	peripheral	negative
GI_4507834-S	152.2	157.9	154.2	UMPS	NM_000373.1	OPRT	orotate		UMP
GI_4507840-S	2542.7	2649.9	3199.7	UQCRC1	NM_003365.1	D3S3191	ubiquinol-	mitochond	oxidative
GI_4507842-S	3279	3924.4	2627.1	UQCRC2	NM_003366.1		ubiquinol-	mitochond	oxidative
GI_4507846-S	407.1	493.3	443.6	USF2	NM_003367.1	FIP	RNA	nucleus	regulation

GI_4507848-S	340.8	331.8	381.8	USP13	NM_003940.1	ISOT3;IsoT-3	ubiquitin-		deubiquiti
GI_4507854-S	114.5	129	148.6	USP5	NM_003481.1	ISOT	ubiquitin	26S	deubiquiti
GI_4507856-S	543.4	596.5	523.5	USP7	NM_003470.1	TEF1;HAUSP	ubiquitin-	nucleus	deubiquiti
GI_4507858-S	732.2	962.9	835.3	UTF1	NM_003577.1		RNA	nucleus	regulation
GI_4507868-S	7596.4	7881	7052.7	VASP	NM_003370.1		actin	focal	cell
GI_4507878-S	5031.2	5077.6	4752.4	VDAC1	NM_003374.1	PORIN;PORIN-31-HL	apoptogen	mitochond	apoptotic
GI_4507882-S	335.5	357.2	422.8	VDR	NM_000376.1	NR1I1	vitamin D3	nucleus	signal
GI_4507894-S	23083.4	19971	15309	VIM	NM_003380.1				
GI_4507902-S	379.7	348.4	353.2	VRK1	NM_003384.1		protein		protein
GI_4507908-S	256.3	330.6	289.5	WAS	NM_000377.1	THC;IMD2;WASP	small	actin	actin
GI_4507912-S	696.6	654.5	551.2	WASF1	NM_003931.1	WAVE;SCAR1;WAVE1;KIAA0269	actin	cytoskelet	cell
GI_4507926-S	94.5	98.6	87.8	WNT2	NM_003391.1	IRP;INT1L1	extracellul	extracellul	developm
GI_4507960-S	781.7	796.3	773.1	ZFP36	NM_003407.1	TTP;GOS24;TIS11;NUP475	single-	nucleus	mRNA
GI_4507962-S	231.8	308.1	288.6	ZFP37	NM_003408.1		zinc ion	nucleus	regulation
GI_4507964-S	152.8	158	138	ZFX	NM_003410.1		DNA	nucleus	regulation
GI_4507982-S	410.2	354.4	391.4	ZNF134	NM_003435.1	pHZ-15	transcripti	nucleus	regulation
GI_4507988-S	140.1	160	169.4	ZNF137	NM_003438.1	pHZ-30	transcripti	nucleus	regulation
GI_4507992-S	104.5	106.7	108.9	ZNF141	NM_003441.1	D4S90;pHZ-44	specific	nucleus	embryoge
GI_4507996-S	477.1	529.5	538.3	ZNF151	NM_003443.1	MIZ1;pHZ-67	protein	nucleus	oncogene
GI_4508006-S	131.1	131.5	132.4	ZNF174	NM_003450.1		protein	nucleus	negative
GI_4508008-S	139.8	134	114.8	ZNF177	NM_003451.1		DNA	nucleus	negative
GI_4508014-S	196.3	161.4	161.1	ZNF205	NM_003456.1	ZNF210	zinc ion	nucleus	regulation
GI_4508016-S	3256.8	3465.3	3008.3	ZNF207	NM_003457.1		zinc ion	nucleus	regulation
GI_4508018-S	133.2	142.1	128.2	BSN	NM_003458.1	ZNF231	structural	cytoskelet	synaptic
GI_4508020-S	1140.6	1128.6	1025.7	ZNF259	NM_003904.1	ZPR1	protein	nucleolus	signal
GI_4508026-S	95	77.4	77.2	ZNF43	NM_003423.1	HTF6;KOX27;ZNF39L1	DNA	nucleus	regulation
GI_4508030-S	238.3	272.3	249.9	ZNF74	NM_003426.1	Cos52;ZNF520;Zfp520	RNA	nucleus	regulation
GI_4508034-S	447	424.7	400.5	ZNF7	NM_003416.1	KOX4;HF.16	DNA	nucleus	developm
GI_4508036-S	392.3	342.2	254.6	ZNF84	NM_003428.1	HPF2	zinc ion	nucleus	regulation
GI_4508038-S	94.5	84.4	101.8	ZNF85	NM_003429.1	HPF4;HTF1	transcripti	nucleus	
GI_4508040-S	15225.8	16572	13401	ZNF91	NM_003430.1	HPF7;HTF10	zinc ion	nucleus	regulation
GI_4508044-S	100	108.1	98.9	ZP2	NM_003460.1	ZPA	coreceptor	extracellul	binding of
GI_45120095-S	115.8	119	116.1	BRODL	NM_153252.2	FLJ38568			
GI_45120103-S	142.4	150.3	133.8	MGC70870	NM_203481.1				
GI_45120110-S	551.1	508.4	573.7	KBTBD2	NM_015483.1	BKLHD1	protein		
GI_45120112-S	93.5	97.7	80.4	DDHD1	NM_030637.1		metal ion		lipid
GI_45120114-S	700.7	415	311.6	DKFZP434H1	NM_015492.3				
GI_45120116-S	748	972.6	914.1	KIAA0256	NM_014701.1		structural	ribosome	protein
GI_45120118-S	159.8	176.3	174.3	SAST	NM_014975.1	SAST170;KIAA0973	protein		protein
GI_45120120-S	236	282.1	255	KIAA2028	NM_172069.1		actin	cytoskelet	
GI_45237192-S	825.2	1092.3	1385.5	KIAA0446	NM_014655.1		transporte	mitochond	transport
GI_45237196-S	348.7	399.9	373.5	CLG	NM_022835.1	FLJ00018;FLJ22458			
GI_45237199-S	108	161.7	124.8	SIPA1L2	NM_020808.1	KIAA1389	protein		intracellula
GI_45237201-S	122.5	125.8	126.5	KIAA1456	NM_020844.1		S-		

GI_45238579-S	306	326.1	360.7	FBXO13	NM_022824.1	DKFZp434C1715			
GI_45238844-S	338.3	412.2	366.3	UCN3	NM_053049.2	SCP;SPC;UCNIII	hormone		
GI_45238846-S	217.5	246.2	233.3	SFN	NM_006142.3		protein	extracellul	negative
GI_45238847-S	1631.2	1796.6	1522.1	PPP3R1	NM_000945.3	CNB;CNB1;CALNB1	calcium	calcineurin	biological_
GI_45238848-S	4784	5783.7	4157.7	PABPC3	NM_030979.2	PABP3;PABPL3	poly(A)	cytoplasm	mRNA
GI_45238850-I	151.3	172.2	152.8	MGC70863	NM_203477.1				
GI_45238852-I	161.6	150.8	149.6	MGC70863	NM_203302.2				
GI_45238853-S	302.1	362.4	311.1	MGC20410	NM_138456.3				
GI_45238855-S	162.1	168.4	155.2	LOC150236	NM_131915.2				
GI_45238856-S	362.1	410.9	441.4	LOC114928	NM_138437.2				
GI_45238857-S	186.4	237.1	233.3	DKFZp686L2	NM_019045.3	MGC26781			
GI_45238859-S	363.7	348.3	363.4	C9orf42	NM_138333.2	MGC17347			
GI_45243468-S	105.6	107.7	92.4	RNASE2	NM_002934.2	EDN;RNS2	ribonuclea	secretory	RNA
GI_45243500-S	3202.1	3179.5	2582.2	BCL2L13	NM_015367.2	MIL1;BCL-RAMBO	caspase	mitochond	caspase
GI_45243506-S	107.4	111.8	108.1	RNASE3	NM_002935.2	ECP;RNS3	ribonuclea	secretory	RNA
GI_45243513-A	1312.1	864.1	1198.2	ABCB9	NM_019624.2	TAPL;KIAA1520;EST122234	ATP	lysosome	small
GI_45243519-I	201.2	180.3	216.5	ABCB9	NM_019625.2	TAPL;KIAA1520;EST122234	ATP	lysosome	small
GI_45243523-I	239.6	294.1	270.7	ABCB9	NM_203444.1	TAPL;KIAA1520;EST122234	ATP	lysosome	small
GI_45243529-S	81.5	92.4	80	FLJ35775	NM_152418.2				
GI_45243533-I	210.5	222.5	202.6	PCDH9	NM_203487.1		calcium	membran	homophili
GI_45243537-A	95.1	94.7	88.9	PCDH9	NM_020403.3		calcium	membran	homophili
GI_45243546-I	102.6	81.3	97.9	ACYP1	NM_203488.1	ACYPE	acylphosp		phosphate
GI_45243550-S	179	183.9	178.3	DLL3	NM_016941.2	SCDO1	Notch	integral to	skeletal
GI_45243553-S	141.6	145.8	137.4	DKFZP566K	NM_015605.4		protein-		protein
GI_45267816-S	249.1	284.7	276.5	CEAL1	NM_020219.2	DKFZp547N157	DNA	nucleus	regulation
GI_45267827-S	93.6	102.5	99.7	FLJ23865	NM_203498.1				
GI_45267831-S	558.1	562.9	607.6	KIAA0971	NM_014929.2				
GI_45267834-S	186.9	239.2	215.4	USP50	NM_203494.1				
GI_45267838-S	582	702	693.8	KIAA1193	NM_017550.1		DNA	nucleus	
GI_45269132-S	100.2	95.3	100.1	GCM1	NM_003643.2	GCMA;hGCMa	DNA	nucleus	embryoge
GI_45269134-S	91.4	99.8	92.7	GP1BA	NM_000173.2	BSS;GP1B;CD42b;MGC34595	thrombin	integral to	blood
GI_45269136-I	100.7	99.8	101.1	MFN1	NM_033540.2	FLJ20693;MGC41806	GTPase	integral to	biological_
GI_45269138-A	1238.6	1586.7	1420.1	MFN1	NM_017927.2	FLJ20693;MGC41806	GTPase	integral to	biological_
GI_45269140-S	105	99.3	95.3	MMRN1	NM_007351.2	ECM;MMRN;GPIa*;EMILIN4		kinesin	blood
GI_45269142-S	191.6	255.9	199.6	CDH3	NM_001793.3	CDHP;HJMD;PCAD	cell	integral to	cell
GI_45269143-A	523.8	569.8	521.1	KEAP1	NM_012289.3	INrf2;MGC1114;MGC4407;MGC9454;KIAA01	protein		regulation
GI_45269144-I	301.1	369.7	328.2	KEAP1	NM_203500.1	INrf2;MGC1114;MGC4407;MGC9454;KIAA01	protein		regulation
GI_45269146-S	104.8	113.3	104	NELL1	NM_006157.2	NRP1;IDH3GL	structural		neurogene
GI_45269147-S	103.2	121	119.6	PMP2	NM_002677.3	P2;MP2;FABP8	lipid	cytoplasm	lipid
GI_45269148-S	128	216.2	96.7	QPRT	NM_014298.3	QPRTase	nicotinate-		synaptic
GI_45269150-S	121.2	122.2	103.6	RAPGEF3	NM_006105.3	EPAC;bcm910;MGC21410;CAMP-GEFI	guanyl-	cAMP-	signal
GI_45269153-S	1916.3	2297.5	644.1	S100A2	NM_005978.3	CAN19;S100L	calcium	cellular_co	biological_
GI_45269154-S	321.8	454.8	426.6	SEPHS1	NM_012247.3	SPS;SELD;SPS1;MGC4980	GTP		protein
GI_45269155-S	176.7	201.2	123	SUHW1	NM_080740.3	3'OY11.1	DNA	nucleus	regulation

GI_45331203-S	250.7	284.5	271.1	MAP4K1	NM_007181.3	HPK1	protein		activation
GI_45331210-S	420.2	539.1	427.9	FLJ00060	NM_033206.1				
GI_45331212-S	357.9	475.6	663.5	RANBP6	NM_012416.1				
GI_45331214-S	620.8	676.1	555.1	LZTS2	NM_032429.1	LAPSER1;KIAA1813	copper,		superoxid
GI_45331216-S	258.3	230.7	210.1	ZNF526	NM_133444.1	MGC4267;KIAA1951			
GI_45333882-S	6588	8131.4	7209.5	KBTBD6	NM_152903.3	DKFZp547E1912	protein		
GI_45333897-S	247.5	438.7	266.4	FLJ90022	NM_153690.4				
GI_45333908-I	108.1	132.7	113	COMMD6	NM_203497.1	Acrg			
GI_45333915-S	141.8	141.8	144.3	C20orf85	NM_178456.2	bA196N14.1			
GI_45333920-S	475.7	528.3	496.5	ASB8	NM_024095.3	MGC5540;PP14212;FLJ21255			intracellula
GI_45356148-S	436.1	445.5	536.7	FBXO23	NM_130465.1	FBX23;MGC14859	ubiquitin	ubiquitin	ubiquitin-
GI_45356150-S	346.3	318.6	408.8	KIAA0056	NM_015261.1		DNA	nucleus	electron
GI_45356742-S	136.5	125.5	126.1	SET8	NM_020382.3	SET07			
GI_45359830-A	98.2	98.3	95.9	CACNB2	NM_000724.2	MYSB;CACNLB2	voltage-	voltage-	neuromus
GI_45359833-I	111.6	120.1	107	CACNB2	NM_201570.1	MYSB;CACNLB2	voltage-	voltage-	neuromus
GI_45359839-I	122.3	120.9	107.9	CACNB2	NM_201590.1	MYSB;CACNLB2	voltage-	voltage-	neuromus
GI_45359844-S	874.2	1014.7	930.1	G3BP2	NM_012297.3		protein	cytoplasm	cytoplasmi
GI_45359851-S	534.1	392.4	406.7	GCLC	NM_001498.2	GCS;GLCL;GLCLC	glutamate-		glutamate
GI_45359854-S	871.9	860.8	933.4	GOLGA4	NM_002078.3	GCP2;GOLG;p230;golgin 245		peripheral	vesicle-
GI_45359857-S	2170.4	2386	2614.1	GRB2	NM_002086.3	ASH;Grb3-3;EGFRBP-GRB2	SH3/SH2		epidermal
GI_45359860-S	3384.7	5182.9	4488.5	POLR2L	NM_021128.3	RPB10;RPABC5;RPB7.6;hRPB7.6;hsRPB10	DNA-	DNA-	regulation
GI_45359861-S	2920.5	3686.7	2569	PSMA2	NM_002787.3	MU;HC3;PSC2;PMSA2	peptidase	26S	ubiquitin-
GI_45359864-S	111.2	112	106.2	MMP20	NM_004771.3	MMP-20	zinc ion	extracellul	proteolysis
GI_45359866-S	128.3	155	230.9	NAP1L3	NM_004538.3	MB20;NPL3;MGC26312	DNA	chromatin	nucleoso
GI_45359869-S	104.1	110.4	92.9	NTF3	NM_002527.3	NT3;HDNF;NGF-2	receptor		anti-
GI_45387924-S	164.2	170.2	173	UNQ430	NM_205545.1				
GI_45387928-S	165.3	200.4	180.2	ALS2CR16	NM_205543.1				
GI_45387944-S	112.8	128.8	117	KIAA1228	NM_020728.1				
GI_45387946-S	233.1	303	222.7	MGC9718	NM_021061.1		DNA	nucleus	regulation
GI_45387948-S	1004.3	1133	891.9	KIAA1972	NM_133368.1				
GI_45387950-S	241	258.3	226.3	MGC3040	NM_023943.1		transporte	membran	transport
GI_45387954-S	2550.4	2840.4	2283.7	QIL1	NM_205767.1				
GI_45387956-S	77.3	72.3	75.7	CD164L1	NM_020404.2	TEM1	sugar	extracellul	biological_
GI_45387957-S	1069.8	870.5	719.9	KIAA0649	NM_014811.3				
GI_45433494-S	156.9	193.3	154.8	ARHGAP20	NM_020809.1	KIAA1391			neuropepti
GI_45433498-S	412.6	453.8	460.3	ZDHHC18	NM_032283.1	DKFZp667O2416	zinc ion	integral to	regulation
GI_45433500-S	130	154.7	121.5	EMILIN3	NM_052846.1	EMILIN5;C20orf130;dJ620E11.4;DKFZp434A		extracellul	
GI_45433512-S	434.6	415.5	336.9	LOC93622	NM_138699.2		DNA	nucleus	regulation
GI_45433538-S	1407.4	1730.7	1666.8	TIMM23	NM_006327.2	TIM23	protein	mitochond	mitochond
GI_45433541-S	125.9	132.4	125.4	R30953_1	NM_019612.2				
GI_45433544-S	329.8	355.2	351.1	KIAA0460	NM_015203.2				
GI_45433545-S	120.5	147.6	136.4	KCNS2	NM_020697.2	KV9.2	voltage-	voltage-	cation
GI_45433546-S	156.9	157.9	155.1	CASKIN2	NM_020753.2	FLJ21609;KIAA1139			
GI_45433547-S	137.1	132.6	131.7	SLC16A10	NM_018593.3	TAT1;PRO0813			

GI_45433549-S	189.2	211.8	222	DSCR9	NM_148675.2		molecular	cellular_co	biological_
GI_45433550-S	67.5	75.1	72.9	AKAP28	NM_178813.4		kinase		
GI_45433551-S	135.7	177.7	158.6	GPR133	NM_198827.2	PGR25;DKFZp434B1272	G-protein	membran	neuropepti
GI_45433553-S	168.5	129.6	127	FLJ37078	NM_153043.3	FLJ35271	DNA	nucleus	regulation
GI_45439300-A	200.2	221	195.6	ZNF238	NM_006352.3	RP58;TAZ-1;C2H2-171	protein	nuclear	chromoso
GI_45439301-I	97.9	89.2	89.4	ZNF238	NM_205768.1	RP58;TAZ-1;C2H2-171	protein	nuclear	chromoso
GI_45439305-S	4592.3	4580.5	3948.3	DARS	NM_001349.2		aspartate-	soluble	aspartyl-
GI_45439310-I	689.2	407.7	312.6	PPIA	NM_203430.1	CYPA;CYPH;MGC12404	protein		viral
GI_45439315-I	325.3	389.6	234.4	PPIE	NM_203456.1	CYP-33;MGC3736	cyclophilin	nucleus	protein
GI_45439319-S	898.7	1563.9	1205.5	PPIC	NM_000943.4	CYPC;MGC3673	cyclospori	cytoplasm	signal
GI_45439320-S	689.6	853.3	630	PPID	NM_005038.2	CYPD;CYP-40;MGC33096	cyclophilin		protein
GI_45439321-S	1152.6	1149.2	1378.3	PPIF	NM_005729.3	CYP3	peptidyl-	mitochond	protein
GI_45439322-S	906.1	1015.9	908.1	PPIH	NM_006347.3	CYPH;CYP-20;MGC5016;USA-CYP;SnuCyp-	cyclophilin	spliceoso	snRNP
GI_45439323-A	136.9	154.8	140.4	PPL13	NM_020129.2	MGC22235;CLC2;LGALS14	lectin [goid		
GI_45439324-I	98	114.8	116.3	PPL13	NM_203471.1	MGC22235;CLC2;LGALS14	lectin [goid		
GI_45439326-S	147.2	132.5	97.3	PPL	NM_002705.3	KIAA0568	structural	cytoskelet	cell shape
GI_45439328-S	220.7	565.8	803.5	PPN	NM_022825.2	MG61;PORC;MGC29687			
GI_45439340-S	269.2	228.9	270.1	PPOX	NM_000309.2	VP;PPO;MGC8485	protoporp	mitochond	heme
GI_45439341-A	368.2	394.3	376.9	PPIL5	NM_152329.3	LRR-1;4-1BBLRR;MGC20689			
GI_45439343-I	126.1	133.6	135	PPIL5	NM_203466.1	LRR-1;4-1BBLRR;MGC20689			
GI_45439347-I	3085.2	3394.9	3046.8	SELS	NM_018445.4	SBBI8;MGC2553;AD-015		integral to	
GI_45439348-I	191.3	186.7	156.2	SELS	NM_203472.1	SBBI8;MGC2553;AD-015		integral to	
GI_45439350-S	1070.3	1822.8	1392.3	SEPX1	NM_016332.2	SELR;SELX;MGC3344;HSPC270	molecular	cellular_co	biological_
GI_45439351-S	132.9	155.5	137.4	SOCS3	NM_003955.3	CIS3;Cish3;SSI-3;SOCS-3;MGC71791	protein		JAK-STAT
GI_45439353-S	5709.5	3621.9	3441	TCEA1	NM_006756.2	SII;TCEA;TF2S;GTF2S;TFIIS	general	nucleus	regulation
GI_45439356-S	219.7	252	218.7	TCEB3B	NM_016427.2	HsT832;TCEB3L;elongin A2	transcripti	nucleus	transcripti
GI_45439358-S	374.4	427.5	317.2	TRIO	NM_007118.2		protein	peripheral	transmem
GI_45439360-S	102.6	92	81.9	CALCB	NM_000728.3	CALC2;CGRP2;CGRP-II	neuropepti	soluble	calcium
GI_45439361-S	256.7	377.7	368.6	DOCK5	NM_024940.4				
GI_45439363-S	169.4	199.5	186.2	EPHA4	NM_004438.3	SEK;HEK8;TYRO1	transmem	integral to	signal
GI_45439364-S	196.9	206.6	219.2	FLJ22529	NM_024789.2				
GI_45439366-S	454	565.9	469.1	GJA12	NM_020435.2	Cx47;CX46.6	connexon	integral to	cell
GI_45439368-S	533.7	586.7	422.2	IER5	NM_016545.3	SBBI48			
GI_45439369-S	162.9	192.4	164.3	KIAA1361	NM_020791.1	MARKK;FLJ14314	ATP		protein
GI_45439371-S	105.6	120.9	122.5	WNT4	NM_030761.3	WNT-4	extracellul	extracellul	developm
GI_45446739-S	193.7	232.2	230.9	ABCA2	NM_001606.3	ABC2	ATP	integral to	small
GI_45446741-S	93.5	102.2	188.5	AKR1C2	NM_001354.4	DD;DD2;BABP;DDH2;HBAB;HAKRD;MCDR2	bile acid		canalicular
GI_45446742-S	1567.3	1564.4	1282.1	DDX42	NM_007372.2	RHELP;RNAHP;SF3b125	nucleic		
GI_45446748-S	132.8	144.7	131.2	KIF5A	NM_004984.2	NKHC;MY050;SPG10;D12S1889	adenosine	kinesin	microtubul
GI_45446750-S	108.9	130.6	124.9	MAGEB3	NM_002365.3		tumor	nucleus	regulation
GI_45446751-S	78.8	85.9	92.9	AQP8	NM_001169.2		water	integral to	water
GI_45446753-S	97.4	99.3	101.5	CAPN11	NM_007058.2		calpain	intracellula	proteolysis
GI_45447089-I	127.8	169.4	154.1	GMPPA	NM_205847.1		nucleotidyl		biosynthes
GI_45504345-S	77.5	88.3	88.5	OR2K2	NM_205859.1	OR2AR1P;HTPCRH06;HSHTPCRH06			

GI_45504347-S	155.4	172.2	159.5	FBI4	NM_205857.1				
GI_45504350-S	229.3	262.1	241.7	UNQ1940	NM_205855.1				
GI_45504352-S	94	94.9	89.4	LOC389852	NM_205856.1	UNQ6288;dJ54B20.3			
GI_45504354-S	238.9	270.7	249.2	MUSTN1	NM_205853.1	Mustang			
GI_45504356-S	108.6	113.9	111.2	UNQ541	NM_205854.1				
GI_45504360-S	145.9	153.1	148.9	UNQ5782	NM_205852.1				
GI_45504362-S	198	222.3	209.4	FLJ35700	NM_205851.1				
GI_45504368-S	118.3	139.9	120.4	SLC24A5	NM_205850.1	JSX;NCKX5			
GI_45504370-S	99	106.9	108.1	FAM9B	NM_205849.1				
GI_45504375-S	126.2	143.7	141.9	SYT6	NM_205848.1				
GI_45504379-S	252.2	281.5	278.4	JMJD2B	NM_015015.1	KIAA0876	DNA	nucleus	regulation
GI_45504385-S	194.3	248.2	222.6	OR2B6	NM_012367.1	OR2B1;OR2B5;OR2B1P;OR2B6P;OR5-	olfactory	integral to	G-protein
GI_45504399-S	229.3	214.9	196.4	FLJ20509	NM_017851.2				
GI_45505128-S	287.4	355	360.3	TAO1	NM_004783.2	PSK;TAO2;KIAA0881	protein	cytoplasmi	protein
GI_45505129-S	283.5	347.2	314.3	TAO1	NM_016151.2	PSK;TAO2;KIAA0881	protein	cytoplasmi	protein
GI_45505131-S	147.7	144.4	563.6	SPINK1	NM_003122.2	PCTT;PSTI;TATI	endopepti		
GI_45505133-S	158.5	182.3	171.8	SENP1	NM_014554.2		endopepti	nucleus	proteolysis
GI_45505136-S	155.8	165.4	138.2	PODN	NM_153703.3	PCAN;SLRR5A;MGC24995			
GI_45505138-S	334.4	389.8	365	PIK3AP1	NM_152309.2	BCAP;FLJ35564	kinase		
GI_45505140-S	93.4	113.8	99.8	NPR3	NM_000908.2	NPRC;ANPRC	receptor	integral to	skeletal
GI_45505141-A	119.4	114.1	91.4	NR5A2	NM_003822.3	B1F;CPF;FTF;B1F2;HB1F;LRH-1;FTZ-	transcripti	nucleus	pathogene
GI_45505142-S	119.2	1178.8	466.8	NMB	NM_021077.3	MGC2277;MGC3936;MGC17211	peptide	soluble	signal
GI_45505146-S	455.6	388	398.5	NJMU-R1	NM_022344.2		molecular	cellular_co	spermatog
GI_45505148-A	272.4	278.4	279.8	NFIC	NM_005597.2	CTF;NFI;CTF5;NF-I;MGC20153	transcripti	nucleus	transcripti
GI_45505150-I	122.4	148.6	135	NFIC	NM_205843.1	CTF;NFI;CTF5;NF-I;MGC20153	transcripti	nucleus	transcripti
GI_45505152-S	5703.7	5039.1	5124.1	NCKAP1	NM_013436.3	NAP1;NAP125;MGC8981;KIAA0587		integral to	central
GI_45505153-A	308.2	293.3	266.7	MGC21644	NM_138492.4				
GI_45505153-I	152.5	166.8	156.8	MGC21644	NM_138492.4				
GI_45505154-S	997.5	1164.2	1077.4	MOKA	NM_030793.3	SP329	receptor		
GI_45505158-S	77.4	78.6	69.1	MGC21394	NM_205841.1	UNQ844			
GI_45505160-I	111.5	134.7	111.3	LST1	NM_205837.1	B144;LST-1;D6S49E	defense/i	integral to	cellular
GI_45505162-A	296.1	383.9	373	LISCH7	NM_015925.4	MGC10659;MGC48312	receptor		metabolis
GI_45505166-S	181	268.7	202.7	IGSF1	NM_001555.2	IGCD1;IGDC1;INHBP;KIAA0364;MGC75490	cell	integral to	cell
GI_45505170-S	93.4	116.5	119.8	FLJ33207	NM_178554.3				
GI_45505172-A	506.3	1075.2	515.7	GALNAC4S-6	NM_015892.2	BRAG;KIAA0598;MGC34346	sulfotransf	integral to	hexose
GI_45505174-S	185.6	203.8	183.3	ECG2	NM_032566.2	ECRG2	serine-		
GI_45505175-S	3546.9	3185.4	1898.6	DPYSL3	NM_001387.2	DRP3;ULIP;CRMP4;DRP-3;CRMP-4	dihydropyr		nucleobas
GI_45505176-A	123.8	128.6	123.8	CTAG3	NM_175745.3	CAGE1;FLJ40441;bA69L16.7			
GI_45505177-I	97.3	117.2	105.9	CTAG3	NM_205864.1	CAGE1;FLJ40441;bA69L16.7			
GI_45505179-S	583.6	585	622.8	CAB2	NM_033419.3	PP1498;AGLA546;MGC9753			
GI_45505181-I	106.5	116.7	104.2	ALS2CR19	NM_152526.3	PAR3B;PAR3L;MGC16131;PAR3beta	protein	tight	cell cycle
GI_45544621-S	120	122.4	127.7	MRVLDC3	NM_052858.2	MARVD3	ATP	membran	protein
GI_45545404-I	92.5	106.3	98.8	NR5A2	NM_205860.1	B1F;CPF;FTF;B1F2;HB1F;LRH-1;FTZ-	transcripti	nucleus	pathogene
GI_45545408-I	131.3	135.2	113.6	MOKA	NM_205836.1	SP329	receptor		

GI_45545416-S	153	183.5	166.2	MOG	NM_002433.2	MGC26137		integral to	central
GI_45545420-S	103.9	103.4	97.7	LOC339221	NM_178543.3	MGC50179;ALK-SMase	hydrolase		nucleotide
GI_45545422-I	109.1	95.6	92.7	MGC21644	NM_182960.2				
GI_45545423-I	115	105.6	105.4	LISCH7	NM_205834.1	MGC10659;MGC48312	receptor		metabolis
GI_45545425-S	88.6	94.5	91.9	GIPR	NM_000164.2		transmem	integral to	adenylate
GI_45545426-I	91.4	83.6	81.7	ESRRG	NM_206594.1	ERR3;NR3B3	transcripti	nucleus	regulation
GI_45545430-A	280.9	298.5	209.3	EGFL9	NM_023932.2	MGC2487	calcium		
GI_45545432-A	101	101.3	92.9	ESRRG	NM_001438.2	ERR3;NR3B3	transcripti	nucleus	regulation
GI_45545436-I	277.5	132.3	108.4	CLYBL	NM_206808.1	CLB;bA134O15.1	malate		tricarboxyli
GI_45545438-A	164.4	197.8	178.1	ALS2CR19	NM_057177.4	PAR3B;PAR3L;MGC16131;PAR3beta	protein	tight	cell cycle
GI_45545438-I	114.6	124.4	122.4	ALS2CR19	NM_057177.4	PAR3B;PAR3L;MGC16131;PAR3beta	protein	tight	cell cycle
GI_4557009-S	228.6	298.4	228	ACP2	NM_001610.1		acid	lysosomal	
GI_4557013-S	678.5	1269.4	1532.2	CAT	NM_001752.1		catalase	peroxisom	response
GI_4557017-S	275.7	483.7	292.3	CHI3L1	NM_001276.1	GP39;YKL40;HC-gp39;HCGP-3P	extracellul	extracellul	metabolis
GI_4557023-S	86.9	82.8	87.5	FOXJ1	NM_001454.1	HFH4;HFH-4;FKHL13	DNA	nucleus	spermatog
GI_4557025-S	295.4	354.1	309.3	HERC1	NM_003922.1	p532;p619	ARF	Golgi	nonselecti
GI_4557033-S	121.2	124.5	140.7	MLN	NM_002418.1		receptor	soluble	G-protein
GI_4557039-S	358.2	415.9	382.4	OSMR	NM_003999.1	OSMRB	oncostatin-	oncostatin-	cell
GI_4557041-S	231.2	308.1	258.7	PALM	NM_002579.1	KIAA0270		cytoplasmi	regulation
GI_4557045-S	93.2	109.1	84.9	SLC6A2	NM_001043.1	NET;NAT1;NET1;SLC6A5	noradrenal	membran	small
GI_4557226-S	86.2	93.9	86.1	AADAC	NM_001086.1	DAC	catalytic	microsom	metabolis
GI_4557228-S	576.5	584.6	714.2	AAMP	NM_001087.1		heparin		cell
GI_4557232-S	192.3	231.4	249.3	ACADS	NM_000017.1	SCAD;ACAD3	acyl-CoA	mitochond	fatty acid
GI_4557234-S	10738.2	12620	11646	ACADVL	NM_000018.1	ACAD6;LCACD;VLCAD	long-chain-	mitochond	fatty acid
GI_4557240-S	144.3	170.1	155.3	ACTN3	NM_001104.1		structural	actin	
GI_4557242-S	125.7	116.9	94.8	ACVRL1	NM_000020.1	HHT;ALK1;HHT2;ORW2;SKR3;ALK-	transmem	integral to	TGFbeta
GI_4557248-S	1087	1217.3	574	ADA	NM_000022.1		adenosine		adenosine
GI_4557250-S	423.8	732.5	477.8	ADAM10	NM_001110.1	kuz;MADM;HsT18717;kuzbanian	metallope	integral to	cell-cell
GI_4557252-S	182.4	207.9	181.8	ADAM8	NM_001109.1	MS2;CD156	metallope	proteoglyc	proteolysis
GI_4557256-S	113.7	108.1	101.8	ADCY8	NM_001115.1	ADCY3;HBAC1	calcium/ca	membran	learning
GI_4557258-S	296.1	256.8	251.4	ADCY9	NM_001116.1		adenylate	integral to	signal
GI_4557264-S	106.5	105.5	99.5	ADRB1	NM_000684.1	RHR;B1AR;ADRB1R	beta1-	integral to	adenylate
GI_4557266-S	132	141	137.4	ADRB3	NM_000025.1		beta3-	integral to	energy
GI_4557268-S	5985.5	6135.6	5677.2	ADSL	NM_000026.1		adenylosu		purine
GI_4557274-I	129.5	138.1	132.7	AGL	NM_000028.1	GDE	glycogen	debranchi	glycogen
GI_4557276-I	115.7	126.5	126.9	AGL	NM_000642.1	GDE	glycogen	debranchi	glycogen
GI_4557280-A	248.3	340.4	316.3	AGL	NM_000644.1	GDE	glycogen	debranchi	glycogen
GI_4557282-I	111.9	124.9	100.1	AGL	NM_000645.1	GDE	glycogen	debranchi	glycogen
GI_4557284-I	103.3	104.6	103.2	AGL	NM_000646.1	GDE	glycogen	debranchi	glycogen
GI_4557286-S	152.1	136.1	114.9	AGT	NM_000029.1	ANHU;SERPINA8	hormone	soluble	regulation
GI_4557288-S	121.7	132.7	123.7	AGXT	NM_000030.1	AGT;SPT;AGT1;SPAT;TLH6;AGXT1	alanine-	peroxisom	
GI_4557290-I	4569.6	4991.9	4326.6	AIRE	NM_000383.1	APS1;APSI;PGA1;APECED	transcripti	cytoplasm	immune
GI_4557294-A	225.3	316	259.9	AIRE	NM_000659.1	APS1;APSI;PGA1;APECED	transcripti	cytoplasm	immune
GI_4557298-S	129.7	151	135.6	ALAS2	NM_000032.1	ASB;ANH1			heme

GI_4557302-S	208	251	266.9	ALDH3A2	NM_000382.1	SLS;FALDH;ALDH10	aldehyde	microsom	epidermal
GI_4557308-S	152.3	177.3	130.4	ALOX15B	NM_001141.1		lipoxygena		fatty acid
GI_4557310-S	89.9	92.5	88.6	AMPD1	NM_000036.1	MADA	AMP		adenylate
GI_4557314-S	118.3	116.6	108.8	ANGPT2	NM_001147.1	ANG2	receptor	kinesin	cell growth
GI_4557320-S	119.4	123.6	102.6	APOA1	NM_000039.1		high-		cholestero
GI_4557322-S	89.5	96.3	98.7	APOC3	NM_000040.1		apolipopro		lipid
GI_4557324-S	185.2	474.4	167.9	APOE	NM_000041.1		lipid		cholestero
GI_4557326-S	98.1	106.8	85.7	APOH	NM_000042.1	BG;B2G1	defense/i		
GI_4557328-S	105.7	113.4	99.7	TNFSF6	NM_000639.1	FASL;CD178;CD95L;APT1LG1	receptor	extracellul	induction
GI_4557332-I	183.8	227.8	252.2	ARSB	NM_000046.1	ASB;G4S;MPS6	arylsulfata	lysosome	lysosomal
GI_4557334-S	94.7	90	102.2	ASPA	NM_000049.1	ASP;ACY2	aminoacyl		aspartate
GI_4557338-S	107.7	98.7	93.8	ATP4B	NM_000705.1	ATP6B	hydrogen/	integral to	sodium
GI_4557342-S	1670.2	1980.4	2238.2	ALDH7A1	NM_001182.1	ATQ1	aldehyde	cellular_co	hearing
GI_4557346-S	91	91	77	BAGE	NM_001187.1	BAGE1	tumor		
GI_4557348-S	238.2	162.5	203.5	BARD1	NM_000465.1		tumor	nucleus	
GI_4557350-S	95.1	93.9	111.1	BCHE	NM_000055.1	E1;CHE1	cholineste		
GI_4557354-I	283.6	157.4	158.5	BCL2	NM_000633.1	Bcl-2	apoptosis	mitochond	negative
GI_4557356-I	101.9	110	114.5	BCL2	NM_000657.1	Bcl-2	apoptosis	mitochond	negative
GI_4557364-S	233.4	215.1	215.7	BLM	NM_000057.1	BS;RECQ2;RECQL2;RECQL3	helicase	nucleus	DNA
GI_4557368-S	114.4	121.7	114.9	BMP2	NM_001200.1	BMP2A	receptor	extracellul	skeletal
GI_4557370-S	126.6	144.4	131.1	BMP3	NM_001201.1		receptor		skeletal
GI_4557372-S	242.1	304	274	BTD	NM_000060.1		biotin		epidermal
GI_4557374-S	2564.7	5695.9	4604	BTEB1	NM_001206.1	BTEB;KLF9	transcripti	nucleus	regulation
GI_4557376-S	117.8	144.8	107.9	BTK	NM_000061.1	AT;ATK;BPK;XLA;IMD1;AGMX1;PSCTK1	protein-	cytoplasm	induction
GI_4557378-S	253.7	249.7	204.1	SERPING1	NM_000062.1	C1IN;C1NH;HAE1;HAE2;C1-INH	serpin	extracellul	circulation
GI_4557380-S	77.9	87.6	77.3	C1orf1	NM_001213.1				
GI_4557384-S	118.2	388.8	317.8	C3	NM_000064.1	ASP	receptor	extracellul	G-protein
GI_4557388-S	134.5	151	129.7	C8A	NM_000562.1		compleme	membran	response
GI_4557390-S	164.7	203.6	171.4	C8B	NM_000066.1		compleme	membran	response
GI_4557392-S	112.3	109.7	115.1	C8G	NM_000606.1	C8C	compleme	membran	compleme
GI_4557394-S	102	95.6	131.5	CA2	NM_000067.1	CA-II	carbonate	cytoplasm	one-
GI_4557396-S	115.9	110.7	116.8	CA6	NM_001215.1	GUSTIN	carbonate		one-
GI_4557400-S	90.1	92.3	88.8	CACNA1S	NM_000069.1	MHS5;HOKPP;hypoPP;CCHL1A3;CACNL1A	dihydropyr	voltage-	small
GI_4557408-S	113.1	115.2	114.5	CASQ2	NM_001232.1		calcium	smooth	heart
GI_4557414-S	507	463.9	411.9	CBS	NM_000071.1	HIP4	cystathioni	cytoplasm	cysteine
GI_4557416-S	105.6	98.9	106.8	CD14	NM_000591.1		peptidogly	plasma	phagocyto
GI_4557418-S	157.7	180.6	150.3	CD36	NM_000072.1	FAT;GP4;GP3B;GPIV;SCARB3	cell	membran	fatty acid
GI_4557420-S	228.8	291	279.4	ENTPD2	NM_001246.1	CD39L1;NTPDase-2	adenosine	integral to	
GI_4557422-S	932.8	896.4	735.7	ENTPD6	NM_001247.1	CD39L2;IL6ST2;IL-6SAG;NTPDase-	adenosine	Golgi	
GI_4557424-S	107.2	104.3	95.7	ENTPD3	NM_001248.1	HB6;CD39L3;NTPDase-3	adenosine	integral to	
GI_4557426-S	136.5	144.4	137.8	ENTPD5	NM_001249.1	PCPH;CD39L4;NTPDase-5	adenosine	endoplas	
GI_4557428-S	142	156	143.8	CD3G	NM_000073.1	T3G;CD3-GAMMA	T-cell	integral to	cellular
GI_4557432-S	123.5	139.9	113	TNFSF5	NM_000074.1	IGM;IMD3;TRAP;gp39;CD154;CD40L;HIGM1	receptor	integral to	immune
GI_4557434-S	251	260.3	235.2	CD68	NM_001251.1	SCARD1		lysosome	

GI_4557436-S	4959.6	4967.7	5088.5	CDC20	NM_001255.1	p55CDC		spindle	cell cycle
GI_4557438-S	165.5	201.1	177.2	CDK3	NM_001258.1		cyclin-		oncogene
GI_4557440-S	201.2	168.5	138.4	CDKN1C	NM_000076.1	BWS;WBS;p57;BWCR;KIP2	cyclin-	nucleus	cell cycle
GI_4557442-S	244.2	284.2	255.6	CETP	NM_000078.1		catalytic		cholestero
GI_4557446-S	593.5	588.2	595.5	CHD1	NM_001270.1		ATP	chromatin	chromoso
GI_4557448-S	178.4	172.8	169.4	CHD2	NM_001271.1		ATP	nucleus	chromoso
GI_4557452-S	448.6	769.5	616.2	CHD4	NM_001273.1	Mi2-BETA	ATP	chromatin	chromoso
GI_4557454-S	167	146.4	146.8	CHK	NM_001277.1	CKI	choline		lipid
GI_4557456-S	118.8	131.1	133.1	CHRNA1	NM_000079.1	ACHRA;CHRNA	ion	nicotinic	small
GI_4557460-S	124.3	132	127.8	CHRND	NM_000751.1	ACHRD	nicotinic	nicotinic	small
GI_4557466-S	353.2	287.8	257.4	CKN1	NM_000082.1	CSA;ERCC8	RNA		DNA
GI_4557468-S	880.3	1157.1	1052.8	AP2B1	NM_001282.1	ADTB2;CLAPB1;AP2-BETA	vesicle	clathrin	nonselecti
GI_4557472-S	98.8	96.9	93.9	CLCN5	NM_000084.1	XRN;CLC5;XLRH;CLCK2;DENTS;NPHL2;hC	chloride	integral to	small
GI_4557474-S	165.3	191.5	188.3	CLCNKB	NM_000085.1	CLCKB	voltage-	membran	small
GI_4557476-A	541.8	650.7	552.2	CLK2	NM_001291.1		protein	nucleus	protein
GI_4557478-A	815.9	772.8	673.2	CLK3	NM_001292.1		protein	nucleus	protein
GI_4557480-S	100.9	112.5	99.7	ABCC2	NM_000392.1	DJS;MRP2;cMRP;ABC30;CMOAT	organic	membran	small
GI_4557484-S	86.1	90.9	80.2	CP	NM_000096.1		ferroxidas	extracellul	iron ion
GI_4557490-S	537.3	716.3	917.3	CSTF1	NM_001324.1		RNA	nucleus	mRNA
GI_4557492-S	1022.8	843.1	891.6	CSTF2	NM_001325.1		RNA	nucleus	mRNA
GI_4557494-S	513.4	474.4	284.5	CSTF3	NM_001326.1		RNA	nucleus	mRNA
GI_4557496-S	96.9	113.4	103.2	CTBP1	NM_001328.1		protein C-	nucleus	viral
GI_4557498-A	1203.5	1171.7	982.4	CTBP2	NM_001329.1		tumor		viral
GI_4557498-I	185.6	212	178.1	CTBP2	NM_001329.1		tumor		viral
GI_4557504-S	104.7	108.4	98.4	CYBA	NM_000101.1		cytochrom	membran	superoxid
GI_4557508-S	155.7	171.1	159.8	CYLC2	NM_001340.1		structural	cytoskelet	cell shape
GI_4557510-S	342	438.8	389.7	DAPK3	NM_001348.1	ZIP;ZIPK	protein	nucleus	induction
GI_4557514-S	569.6	578.4	535.4	DDB2	NM_000107.1		damaged	nucleus	pyrimidine-
GI_4557516-S	1682.6	1848.5	1732.6	DHX15	NM_001358.1	DBP1;HRH2;DDX15;PRP43;PrPp43p	RNA	nucleus	mRNA
GI_4557521-S	97.7	84.2	91.6	DIO1	NM_000792.2	TXDI1	thyroxine	integral to	thyroid
GI_4557526-S	111.3	102.6	98.3	DLG2	NM_001364.1	PSD-93	guanylate	plasma	intracellula
GI_4557528-S	189.6	210.7	185.3	DLG4	NM_001365.1	PSD95;SAP90	protein C-		learning
GI_4557534-S	140.1	169	134.3	SLC26A3	NM_000111.1	CLD;DRA	transcripti	integral to	anion
GI_4557538-S	228.5	340.6	337.7	SLC26A2	NM_000112.1	DTD;EDM4;DTDST;D5S1708	sulfate	membran	sulfate
GI_4557540-S	381	475.8	473.8	DYT1	NM_000113.1	DQ2;TOR1A	endopepti	cytoplasm	heat
GI_4557542-S	217.8	281.2	159.6	ECM2	NM_001393.1		integrin	extracellul	cell-matrix
GI_4557544-S	86.7	93	94.5	EDN3	NM_000114.1	ET3	receptor	soluble	circulation
GI_4557546-A	488.6	667	583.1	EDNRB	NM_000115.1	ETB;ETRB;HSCR;ABCDS;HSCR2	endothelin	integral to	negative
GI_4557546-I	98.6	101.8	89.3	EDNRB	NM_000115.1	ETB;ETRB;HSCR;ABCDS;HSCR2	endothelin	integral to	negative
GI_4557552-S	3412.8	2587.1	2145.2	EMD	NM_000117.1	STA;EDMD		nuclear	nonselecti
GI_4557554-S	540.3	524.8	283.8	ENG	NM_000118.1	END;ORW;HHT1;ORW1;CD105	protein	integral to	circulation
GI_4557556-S	278.3	333	355.4	EP300	NM_001429.1	p300	protein C-	nucleus	signal
GI_4557558-S	195.7	230.9	205.8	EPB42	NM_000119.1	PA	ATP	peripheral	cell shape
GI_4557560-S	201.6	289.5	249.5	EPHX1	NM_000120.2	MEH;EPHX;EPOX	epoxide	microsom	response

GI_4557561-S	134.8	134.1	155.3	EPOR	NM_000121.2		erythropoi	integral to	signal
GI_4557562-S	606.5	709.3	721.6	ERCC3	NM_000122.1	XPB;BTF2;GTF2H;RAD25;TFIIH	DNA	nucleus	nucleotide-
GI_4557564-S	209.7	276.5	238.6	ERCC6	NM_000124.1	CSB;CKN2;COFS;RAD26	DNA	nucleus	DNA
GI_4557566-S	119.6	134	126.3	EREG	NM_001432.1	ER	epidermal	extracellul	EGF
GI_4557568-S	121.4	142.4	122.3	ERN1	NM_001433.1	IRE1;IRE1P	endoribon	endoplas	protein
GI_4557570-S	1014.5	2747.6	2381.6	EXT1	NM_000127.1	EXT	tumor	endoplas	glycosami
GI_4557572-S	754.8	1154.5	1080.3	EXT2	NM_000401.1		tumor	endoplas	glycosami
GI_4557574-S	111.3	117.4	114.1	FAAH	NM_001441.1		amidase	insoluble	fatty acid
GI_4557576-S	172.5	204.3	174.2	FABP1	NM_001443.1	FABPL;L-FABP	lipid	cytoplasm	fatty acid
GI_4557578-S	116.4	118.7	120.7	FABP4	NM_001442.1	A-FABP	fatty acid	soluble	transport
GI_4557580-S	288.8	591.2	359.2	FABP5	NM_001444.1	EFABP;E-FABP;PAFABP;PA-FABP	lipid	cytoplasm	epidermal
GI_4557582-S	227.7	271.3	177.4	FABP6	NM_001445.1	ILBP;I-15P;ILBP3;ILLBP;I-BABP	lipid	cytoplasm	negative
GI_4557586-S	1618.4	3153.7	2561.5	FAH	NM_000137.1		fumarylac		tyrosine
GI_4557588-S	697.5	497.7	384.4	FANCC	NM_000136.1	FA3;FAC;FACC		cytoplasm	DNA
GI_4557592-S	383.8	505.4	468.3	FECH	NM_000140.1	EPP;FCE	ferrochelat	mitochond	heme
GI_4557594-S	1067.6	762	1277.9	FOXF2	NM_001452.1	FKHL6;FREAC2	RNA	transcripti	transcripti
GI_4557596-S	113	98.6	109.6	FLNC	NM_001458.1	ABPA;ABPL;FLN2;ABP-280;ABP280A	actin	actin	
GI_4557598-S	135	171.6	142.9	G6PC	NM_000151.1	G6PT;GSD1a	glucose-6-	microsom	glycogen
GI_4557600-S	128	122.3	127.4	GABRA2	NM_000807.1		benzodiaz	integral to	gamma-
GI_4557606-S	223	262.3	238	GABRA6	NM_000811.1		benzodiaz	integral to	small
GI_4557612-S	129.8	133.9	121.9	GALC	NM_000153.1		galactosyl	lysosome	carbohydr
GI_4557616-S	6157.7	5731.1	3130	GAS6	NM_000820.1	AXSF;AXLLG	receptor	extracellul	signal
GI_4557618-S	1200.8	1620.2	1100.7	GBE1	NM_000158.1	GBE	1,4-alpha-		glycogen
GI_4557626-S	117.8	119.9	139.6	GLE1L	NM_001499.1			nuclear	mRNA-
GI_4557628-I	113	106.7	98.5	GPX5	NM_001509.1		glutathion	extracellul	response
GI_4557630-S	114.7	106.4	104	GRIA4	NM_000829.1	GLUR4;GLURD	inotropic	integral to	small
GI_4557632-S	97.9	103.2	103.3	GRID2	NM_001510.1		glutamate	integral to	small
GI_4557634-S	149	171.7	143.7	HCRT	NM_001524.1	OX;PPOX		synaptic	synaptic
GI_4557636-S	234.9	264.4	252.2	HCRTR1	NM_001525.1	OX1R	G-protein	integral to	neuropepti
GI_4557640-S	2589.6	2666.3	2249.7	HDAC2	NM_001527.1	RPD3;YAF1	histone	nucleus	regulation
GI_4557642-S	636.3	1375.6	1073.4	HMGCR	NM_000859.1		hydroxym	endoplas	gonad
GI_4557644-S	1263.3	1631.6	1821.1	HNRPL	NM_001533.1	hnRNP-L	heterogen	nucleoplas	RNA
GI_4557646-S	2460.6	3669.2	3132.3	HSBP1	NM_001537.1		transcripti	nucleus	heat
GI_4557648-S	104.4	94.1	96.9	HSD17B3	NM_000197.1	EDH17B3	estradiol	microsom	male
GI_4557650-S	593.2	739.5	633.4	HSF4	NM_001538.1	CTM	transcripti	nucleus	heat
GI_4557652-S	120.3	87.2	92.9	HTN3	NM_000200.1	HIS2;HTN2;HTN5	antifungal	extracellul	ossificatio
GI_4557654-S	122.6	130.3	130.7	IAPP	NM_000415.1	DAP;IAP;AMYLIN	receptor	soluble	pathogene
GI_4557656-S	1085.8	1034.8	824.5	ICT1	NM_001545.1	DS-1	translation	cellular_co	biological_
GI_4557662-S	840.4	799.8	666.8	IGBP1	NM_001551.1		protein	cytoplasm	response
GI_4557666-S	107.3	117	104.8	IL2RA	NM_000417.1	CD25;IL2R;TCGFR	interleukin-	plasma	cell
GI_4557668-S	2431.7	2479.6	3231.6	IL4R	NM_000418.1	CD124;IL4RA	interleukin-	integral to	signal
GI_4557670-S	366.1	407.1	347.2	INS	NM_000207.1		insulin	extracellul	glucose
GI_4557672-S	142.5	168.2	164.8	IPF1	NM_000209.1	IUF1;PDX1;IDX-1;MODY4;PDX-1;STF-1	RNA	nucleus	histogene
GI_4557674-S	125.9	123	110.2	ITGA6	NM_000210.1	CD49f	cell	integrin	cell-

GI_4557676-S	126.7	149.4	164.8	ITGB3	NM_000212.1	CD61;GP3A;GPIIIa	cell	integrin	blood
GI_4557678-S	537.7	687.7	347.4	JAG1	NM_000214.1	AGS;AHD;AWS;HJ1;JAGL1			
GI_4557680-S	119.4	131.3	118.5	JAK3	NM_000215.1	JAKL;LJAK	protein-		mesoderm
GI_4557682-S	1086.1	711.3	976	KAL1	NM_000216.1	HHA;KAL;KMS;ADMLX;KALIG-1	extracellul	extracellul	axon
GI_4557684-S	115.1	117	108.2	KCNA1	NM_000217.1	EA1;MK1;AEMK;HUK1;MBK1;RBK1;KV1.1	potassium	voltage-	potassium
GI_4557686-S	133	145.4	140	KCNE1	NM_000219.1	ISK;JLNS;LQT5;MinK	potassium	voltage-	potassium
GI_4557692-A	115	113.6	112.2	KHK	NM_000221.1		ketohexok		
GI_4557692-I	178	203.2	210.2	KHK	NM_000221.1		ketohexok		
GI_4557694-S	78.1	162.5	139.3	KIT	NM_000222.1	PBT;SCFR;CD117	protein-	integral to	oncogene
GI_4557698-S	104.8	117.4	101.2	KRT12	NM_000223.1	K12	structural	intermedia	vision
GI_4557700-S	111.3	146.7	106.5	KRT17	NM_000422.1	PC;K17;PC2;PCHC1	structural	intermedia	epidermal
GI_4557702-S	235.5	287.8	244.6	KRT2A	NM_000423.1	KRTE;KRT2E	structural	intermedia	epidermal
GI_4557704-S	177.5	207.3	199.3	KRT9	NM_000226.1	K9;EPPK	structural	intermedia	epidermal
GI_4557712-S	17963.1	7793.6	7407.3	LAMB3	NM_000228.1	LAMNB1	structural	laminin-5	epidermal
GI_4557714-S	148.5	165.3	163.4	LEP	NM_000230.1	OB;OBS	hormone	extracellul	energy
GI_4557716-S	154.1	177.5	161.4	LHCGR	NM_000233.1	LHR;LCGR;LGR2	internaliza	endosome	male
GI_4557718-S	407.5	403	478.4	LIG1	NM_000234.1		DNA	nucleus	embryoge
GI_4557720-S	1266.2	1497.9	1692.1	LIPA	NM_000235.1	LAL;CESD	lipoprotein	lysosome	N-linked
GI_4557722-S	106.2	120.1	121.8	LIPC	NM_000236.1	HL;HTGL;LIPH	triacylglyc		N-linked
GI_4557724-S	114.2	103.2	99.9	LOR	NM_000427.1		structural	insoluble	cell shape
GI_4557726-S	100.5	103.6	96.3	LPL	NM_000237.1	LIPD	heparin	extracellul	fatty acid
GI_4557730-S	1870.3	2719.4	2465.9	LTBP1	NM_000627.1		protein		
GI_4557732-S	670.9	575.4	500.7	LTBP2	NM_000428.1	LTBP3	protein	extracellul	protein
GI_4557736-S	116.2	125.6	113.7	MAT1A	NM_000429.1	MAT;SAMS;MATA1;SAMS1	methionin		amino
GI_4557738-S	82.2	91.1	87	MBL2	NM_000242.1	MBL;MBP;MBP1;COLEC1	mannose	membran	compleme
GI_4557742-S	78.7	101.3	89.3	MEFV	NM_000243.1	FMF;MEF;TRIM20	actin	microtubul	inflammat
GI_4557748-S	101	135.9	103.8	MHC2TA	NM_000246.1	C2TA;CIITA	RNA	nucleus	perception
GI_4557750-S	561.8	754.5	604.9	MICA	NM_000247.1		protein		cell
GI_4557758-S	126.3	174	171.6	MPO	NM_000250.1		peroxidas	lysosome	anti-
GI_4557760-S	156.4	176.9	171.4	MSH2	NM_000251.1	FCC1;COCA1;HNPCC;HNPCC1	damaged	nucleus	mismatch
GI_4557762-S	88.9	104.4	85.1	MTP	NM_000253.1		binding	microsom	lipid
GI_4557764-S	459.2	410.7	477.1	MTR	NM_000254.1		homocyst	intracellula	central
GI_4557766-S	808.6	886.3	772.6	MUT	NM_000255.1	MCM	methylmal	mitochond	metabolis
GI_4557768-S	190.3	228.3	179.6	MVK	NM_000431.1	MVLK	mevalonat	peroxisom	isoprenoid
GI_4557772-S	130.3	135	121.7	MYH7	NM_000257.1	CMH1;MYHCB	structural	muscle	striated
GI_4557774-S	131	152.5	151.3	MYL2	NM_000432.1	MLC2	structural	cytoskelet	regulation
GI_4557776-S	174.5	178.4	183.4	MYL3	NM_000258.1	VLC1;MLC1V	structural	muscle	muscle
GI_4557778-S	90.8	99.2	88	MYOC	NM_000261.1	GPOA;JOAG;TIGR;GLC1A	structural	cilium	morphoge
GI_4557780-S	216.5	198	236.7	NAGA	NM_000262.1	GALB;D22S674	alpha-N-	lysosome	carbohydr
GI_4557782-S	130.4	159.9	105.1	NAT2	NM_000015.1	AAC2	arylamine		metabolis
GI_4557784-S	178.7	206.7	190.8	NCF1	NM_000265.1	NOXO2;p47phox	GTPase	cytosol	superoxid
GI_4557786-S	207.8	334.4	140.2	NCF2	NM_000433.1	NOXA2;P67PHOX;P67-PHOX	electron	cytosol	superoxid
GI_4557788-S	100.4	100.4	82	NDP	NM_000266.1	ND	growth	extracellul	vacuole
GI_4557792-S	125.4	150.7	129	NF1	NM_000267.1	WSS;NFNS;VRNF	Ras	cytoplasm	negative

GI_4557798-S	105	229.6	144.5	NOTCH3	NM_000435.1	CASIL;CADASIL		integral to	embryoge
GI_4557800-S	1179	648.4	1153.1	NP	NM_000270.1	PNP	purine-		DNA
GI_4557802-S	9092.8	4204	5584.6	NPC1	NM_000271.1	NPC	intracellula	lysosome	intracellula
GI_4557804-S	125.2	123.4	123.7	NPHP1	NM_000272.1	NPH1;SLSN1	protein	kinesin	excretion
GI_4557806-S	142.2	166.2	147.8	GPR143	NM_000273.1	OA1	G-protein	membran	eye
GI_4557808-S	1956.2	2430.6	2504.2	OAT	NM_000274.1	HOGA	ornithine-	mitochond	ornithine
GI_4557810-S	152.4	166.2	177.5	OCA2	NM_000275.1	P;PED;BOCA;D15S12	L-tyrosine	integral to	eye
GI_4557816-S	211.7	262.9	360.3	OXCT	NM_000436.1	SCOT;OXCT1	3-oxoacid	mitochond	succinyl-
GI_4557818-S	84.6	87.1	77.6	PAH	NM_000277.1	PKU;PKU1	phenylala		amino
GI_4557830-S	675.9	628.4	680.6	PCBD	NM_000281.1	PCD;DCOH	4-alpha-	cytoplasm	L-
GI_4557832-S	726.6	473.5	589.2	PCCA	NM_000282.1		biotin	mitochond	fatty acid
GI_4557834-S	2242.2	2317.2	2535.8	PEPD	NM_000285.1	MGC10905;PROLIDASE	metallocar		proteolysis
GI_4557838-S	1200.3	1323.4	1495.9	PMM2	NM_000303.1	CDG1;CDGS	phosphom	cytoplasm	GDP-
GI_4557840-S	98.7	120.7	95.1	RAG1	NM_000448.1	RNF74	DNA	nucleus	hemocyte
GI_4557844-S	296.9	405.7	402.8	RRM2	NM_001034.1	R2	ribonucleo	cytoplasm	DNA
GI_4557846-S	95.2	91.6	89.2	SGCG	NM_000231.1	A4;MAM;DMDA;SCG3;TYPE;DAGA4;DMDA1		sarcoglyca	muscle
GI_4557848-S	129.4	154.5	140.7	SLC12A1	NM_000338.1	BSC1;NKCC2	sodium:ch	integral to	small
GI_4557850-S	96.7	99.8	94	SLC2A2	NM_000340.1	GLUT2	glucose	membran	glucose
GI_4557862-S	122.2	143.3	118.9	SSTR4	NM_001052.1		somatosta	integral to	negative
GI_4557864-S	131.1	142.1	127.1	SSTR5	NM_001053.1		somatosta	integral to	negative
GI_4557866-S	143.2	192.2	161.6	SUOX	NM_000456.1		sulfite	mitochond	methionin
GI_4557868-S	160.2	162.5	147.7	TEK	NM_000459.1	TIE2;VMCM;TIE-2;VMCM1;CD202B	transmem	integral to	transmem
GI_4557872-S	3247.8	3718.4	3460.6	UROS	NM_000375.1		uroporphy		uroporphy
GI_4557874-S	369.9	277.7	291.9	DPYD	NM_000110.2	DHP;DPD			
GI_4557875-S	157.5	293.3	169.1	ABCA4	NM_000350.1	FFM;RMP;ABCR;RP19;STGD;ABC10;STGD	ATP	membran	phototrans
GI_4557877-S	337.6	440.6	353.1	ICAM1	NM_000201.1	BB2;CD54	transmem	proteoglyc	cell-cell
GI_4557879-S	1650.5	1479.2	1285.5	IFNGR1	NM_000416.1	CD119;IFNGR	interferon-	integral to	resistance
GI_4557881-S	130.2	151.3	135.2	IL2RG	NM_000206.1	IMD4;CD132;SCIDX;SCIDX1	interleukin-	integral to	signal
GI_4557883-S	107.4	121.8	120.5	INSR	NM_000208.1		transmem	integral to	cell growth
GI_4557885-S	150.9	118.6	103.1	ITGB2	NM_000211.1	LAD;CD18;MF17;LCAMB;LFA-1	cell	integrin	integrin-
GI_4557891-S	276.8	290.1	258.4	LCAT	NM_000229.1		acyltransf	extracellul	lipid
GI_4557893-S	78.8	83.5	78.3	LYZ	NM_000239.1		lysozyme	extracellul	antimicrob
GI_4557895-S	202.1	202.2	239.7	MTM1	NM_000252.1	CNM;MTMX;XLMTM	protein	cellular_co	cell growth
GI_45580687-S	167.7	190.9	177	C7	NM_000587.2		compleme	membran	response
GI_45580689-S	94.2	103.6	92.4	CLECSF7	NM_130441.2	DLEC;HECL;BDCA2;CLECSF11	sugar		heterophili
GI_45580690-S	8625.2	17294	2475.3	COL4A1	NM_001845.3		collagen	collagen	regulation
GI_45580693-S	1276.2	1815	1992.1	LOC284361	NM_175063.3	INM02;AAAS764;MGC33203			
GI_45580697-A	90.6	112.9	113.5	EDG2	NM_001401.3	LPA1;edg-2;vzg-1;Gpcr26;Mrec1.3;rec.1.3	G-protein	integral to	cytosolic
GI_45580699-S	115.9	179.9	127.6	ENTPD1	NM_001776.3	CD39;ATPDase;NTPDase-1	adenosine	membran	blood
GI_45580703-S	97.3	111.1	100.3	FLJ39647	NM_173625.3	MGC34759			
GI_45580705-S	99.2	106.3	107.6	FOXD4L1	NM_012184.3	bA395L14.1	transcripti	nucleus	regulation
GI_45580706-S	110.7	108.6	100.4	HS6ST3	NM_153456.2		transferas		
GI_45580708-S	149.2	175.2	162.1	UNC93B1	NM_030930.2	UNC93;UNC93B			
GI_45580710-I	147.2	187.9	158.4	BAT1	NM_004640.4	D6S81E	ATP-	nucleus	

GI_45580711-A	2693.5	3864.8	2897.7	BAT1	NM_080598.3	D6S81E	ATP-	nucleus	
GI_45580714-A	250.2	239.5	187.6	OSCAR	NM_133168.2	PIGR3;MGC33613	receptor		
GI_45580720-S	129.9	129.7	115.2	HOXB4	NM_024015.3	HOX2;HOX2F;HOX-2.6	transcripti	nucleus	regulation
GI_45580721-S	98.3	111.2	98.3	HOXC8	NM_022658.3	HOX3;HOX3A	transcripti	nucleus	regulation
GI_45580722-S	92.3	112.5	90	HPR	NM_020995.3		plasma		proteolysis
GI_45580724-S	128.2	140.1	120.9	GDA	NM_004293.2	CYPIN;GUANASE;NEDASIN;KIAA1258	guanine	intracellula	nucleobas
GI_45580725-S	124.3	130.4	96.2	GNAZ	NM_002073.2		heterotrim	nuclear	G-protein
GI_45580726-S	112.8	172.9	174.5	MAP1A	NM_002373.4	MAP1L;MTAP1A	structural	microtubul	cell shape
GI_45580729-S	535.3	440.3	354.6	NRPS998	NM_181806.2		catalytic		electron
GI_45580741-S	922.8	1218.1	1011.7	DHDDS	NM_024887.2	DS;CIT;HDS;FLJ13102	transferas		metabolis
GI_45580743-I	85.7	98.3	127.1	ADD3	NM_016824.2	ADDL	structural	membran	
GI_45580744-I	100.9	104	94.4	CLYBL	NM_138280.3	CLB;bA134O15.1	malate		tricarboxyli
GI_45592948-S	89	91	94.8	UNQ9372	NM_206832.1				
GI_45592951-S	441.1	404.7	458.6	DESR1	NM_206831.1				
GI_45592953-S	2502.3	4643.2	6646.8	CTXN1	NM_206833.1	CTXN;FLJ25968			
GI_45592958-S	136.8	162.2	143.5	LDB3	NM_007078.1	ZASP;CYPHER;ORACLE;PDLIM6;KIAA0613;	protein		electron
GI_45592960-S	159.1	180.5	184.5	C20orf70	NM_080574.1	SPLUNC2;bA49G10.1	lipid		
GI_45592962-S	282.6	360.6	305	RASL11A	NM_206827.1				
GI_45593129-S	2453.4	1919	1403.5	NS	NM_014366.4	E2IG3;MGC800			
GI_45593137-S	307.9	344.2	328	LRRC25	NM_145256.2	MAPA			
GI_45593139-S	1398	982.6	1030.3	GTPBP2	NM_019096.3	MGC74725	GTPase		small
GI_45593141-S	121.3	128.2	120	KBTBD5	NM_152393.2	SRYP;FLJ32015	protein		DNA
GI_45593143-S	129.2	132.1	123.4	GBX2	NM_001485.2		transcripti	nucleus	histogene
GI_45593145-S	106.1	112.8	102.8	GFRA3	NM_001496.3		GPI-	peripheral	peripheral
GI_45593146-I	132.6	127.5	117.3	EGFL9	NM_206539.1	MGC2487	calcium		
GI_45593148-A	524.5	1047	438	ADD3	NM_019903.2	ADDL	structural	membran	
GI_4559405-S	92	97.4	100.4	C6	NM_000065.1		compleme	membran	response
GI_4559407-S	412.4	515.3	447	CSF2RB	NM_000395.1	CD131;IL3RB;IL5RB;CDw131	receptor	granulocyt	respiratory
GI_45594239-S	120.9	156	130.5	LSAMP	NM_002338.2	LAMP	cell	peripheral	neurogene
GI_45594308-S	131.4	146.9	156.5	MAP7	NM_003980.3	EMAP115;E-MAP-115	structural	microtubul	establish
GI_45594309-S	102.6	112.2	102.4	OR5V1	NM_030876.4	6M1-21;hs6M1-21	olfactory	integral to	perception
GI_45594311-S	978.5	972.4	914.8	RFWD1	NM_032271.2	TRAF7;RNF119;DKFZp586I021	zinc ion		
GI_45594507-S	107.9	113	97.8	LOC390511	NM_206838.1				
GI_45594662-S	195	204.9	204	MMP15	NM_002428.2	MTMMP2;SMCP-2;MT2-MMP	enzyme	extracellul	protein
GI_45597173-S	258.8	296.7	245.8	NFYB	NM_006166.3	HAP3;CBF-A;CBF-B;NF-YB	transcripti	nucleus	regulation
GI_45597457-S	126.6	116.3	123.9	KRT1B	NM_175078.1			intermedia	
GI_45597461-S	118.7	115.3	125.4	C6orf201	NM_206834.1	MGC87625			
GI_45598368-S	97.8	112.7	86.3	EMX1	NM_004097.1		transcripti	nucleus	developm
GI_45598382-S	1076.7	703.9	553.1	C20orf42	NM_017671.3	URP1;KIND1;DTGCU2;FLJ20116	protein	cytoskelet	cell
GI_45643116-S	694.8	671.7	603.9	TLK2	NM_006852.2	MGC44450;PKU-ALPHA	ATP	cellular_co	protein
GI_45643118-A	1551.8	1606.6	2157.9	PECI	NM_006117.2	DRS1;ACBD2;HCA88	acyl-CoA	peroxisom	fatty acid
GI_45643120-I	76.7	86.7	81.8	PECI	NM_206836.1	DRS1;ACBD2;HCA88	acyl-CoA	peroxisom	fatty acid
GI_45643122-S	203.7	194.8	193.7	NVL	NM_002533.2		ATP	nucleus	
GI_45643130-I	136.7	181.9	200.2	NOR1	NM_206837.1	MGC26685			

GI_45643132-I	140.8	166.5	153.8	NOR1	NM_145047.3	MGC26685			
GI_45643134-I	130.4	142.5	127.5	MORF4L1	NM_206839.1	MRG15;HsT17725;MGC10631;MORFRG15	chromatin	chromatin	chromatin
GI_45643136-A	8011	10190	9549.1	MORF4L1	NM_006791.2	MRG15;HsT17725;MGC10631;MORFRG15	chromatin	chromatin	chromatin
GI_45643137-S	91.2	92.6	95	KLHL13	NM_033495.2	FLJ10262;KIAA1309;MGC74791	protein		
GI_45643139-S	117.9	119.5	124.4	LGI3	NM_139278.2		transporte		transport
GI_4580414-S	123.7	144.6	122.1	ALDH3B2	NM_000695.2	ALDH8	aldehyde		alcohol
GI_4580418-S	99.8	109.8	102.1	SERPINA6	NM_001756.2	CBG	serpin		transport
GI_4580419-A	87.5	96.4	97.6	KITLG	NM_003994.2	SF;MGF;SCF;KL-1;Kitl	stem cell	integral to	histogene
GI_4580421-A	312.4	396.9	436.6	NPR2	NM_003995.2	NPRB;ANPRB;GUC2B;NPRBi	transmem	integral to	regulation
GI_4585642-S	194.5	179.8	181.7	ZNF264	NM_003417.1				
GI_4585709-I	118.5	135.6	118.7	ADAM11	NM_002390.2	MDC	integrin	integral to	integrin-
GI_4585711-S	107.1	102.6	104	NTRK1	NM_002529.2	MTC;TRK;TRKA	neurotrop	integral to	transmem
GI_4585861-S	335.9	328.3	351.6	CENPA	NM_001809.2		chromatin	centromer	chromoso
GI_4585863-S	100.8	98.2	86	PDE6A	NM_000440.1	PDEA;CGPR-A	cGMP-		vision
GI_4585865-S	710	746.4	623	TCF12	NM_003205.2	HEB;HTF4;HsT17266	RNA	nucleus	muscle
GI_4753158-S	3213.5	3426.6	2731.5	GTF3A	NM_002097.1	AP2;TFIIIA	RNA	nucleus	rRNA
GI_4753160-S	278.2	437.1	431.2	GTF3C1	NM_001520.1	TFIIIC;TFIIIC220;TFIIICalpha	RNA	transcripti	tRNA
GI_4755127-I	261.3	324.4	280.9	ATF3	NM_004024.2		transcripti	nucleus	regulation
GI_4755130-S	84.4	92.1	86.1	CCK	NM_000729.2		hormone	soluble	signal
GI_4755133-S	2301.7	4073.1	1798.1	DOK1	NM_001381.2	P62DOK	protein		transmem
GI_4755135-S	430.6	326	127	FBN2	NM_001999.2	CCA	extracellul	extracellul	embryoge
GI_4755136-S	80.5	86.3	82.1	GJA1	NM_000165.2	ODD;CX43;ODDD;ODOD;SDTY3;DFNB38	ion	connexon	heart
GI_4755138-S	375.5	346.2	254.8	INPP1	NM_002194.2		inositol-		phosphate
GI_4755139-A	96.2	92.2	81.2	INPP4A	NM_004027.1	INPP4			signal
GI_4755139-I	157.6	169.9	152.3	INPP4A	NM_004027.1	INPP4			signal
GI_4755141-S	1991.3	1916	1630	INPPL1	NM_001567.2	SHIP2	inositol/ph		phosphate
GI_4755143-S	4732.7	2967.1	3946.5	IRAK1	NM_001569.2	IRAK;pelle	NF-		protein
GI_4755144-S	209.3	232.6	223.9	IRF2	NM_002199.2	IRF-2	RNA	nucleus	oncogene
GI_4755145-S	104.1	123.6	108.5	AEBP1	NM_001129.2	ACLP	carboxype	cytoplasm	muscle
GI_4757701-S	2122.6	3234.3	2800.2	EIF4EL3	NM_004846.1	4EHP;IF4E;4E-LP	mRNA	cytoplasm	regulation
GI_4757715-S	1204.5	1258.7	1192.6	SPAG7	NM_004890.1	ACRP;FSA-1;MGC20134	nucleic		
GI_4757725-S	177.1	208.5	190.8	MLLT10	NM_004641.1	AF10	DNA	nucleus	cell growth
GI_4757733-S	280.3	584.9	617.5	AIM2	NM_004833.1		tumor		immune
GI_4757753-S	84.8	77.6	83.5	ANXA13	NM_004306.1	ISA;ANX13	calcium-	plasma	cell
GI_4757755-S	13236.9	21215	11834	ANXA2	NM_004039.1	ANX2;LIP2;LPC2;CAL1H;LPC2D;ANX2L4	phospholi	soluble	skeletal
GI_4757769-S	122.2	111.7	112.9	ARHH	NM_004310.1	TTF;RHOH	Rho small		oncogene
GI_4757771-S	121.5	118.9	110.4	ARHI	NM_004675.1	NOEY2	small		small
GI_4757775-S	107.1	108.9	101.6	ARR3	NM_004312.1	ARRX		soluble	vision
GI_4757783-S	97.5	85.2	89.6	ART1	NM_004314.1	RT6;ART2	NAD ADP-	integral to	protein
GI_4757787-S	143.4	205	153.2	ASCL1	NM_004316.1	ASH1;HASH1;MASH1	transcripti	nucleus	oncogene
GI_4757789-S	1240.2	1227.4	1412	ASH2L	NM_004674.1	ASH2L1;ASH2L2	RNA	nucleus	regulation
GI_4757791-S	146.9	141.5	154.2	ASMT	NM_004043.1	ASMTY;HIOMT;HIOMTY	O-		protein
GI_4757793-S	460.8	701.2	625.9	ASMTL	NM_004192.1	ASTML;ASMTLX	acetylsero	cellular_co	melatonin
GI_4757795-S	397.3	502	570.4	ASNA1	NM_004317.1	ARSA1;ARSA-I	arsenite	soluble	nucleocyto

GI_4757797-S	301.3	212.4	175.5	APG5L	NM_004849.1	ASP;APG5;hAPG5		cytoplasm	apoptosis
GI_4757805-S	427.8	384.2	405.9	C16orf7	NM_004913.1	ATP-BL	transporte		ATP
GI_4757807-S	212.5	238.9	222.8	ATP2B2	NM_001683.1	PMCA2	adenosine	integral to	small
GI_4757811-S	2056.1	2882.7	2813.1	ATP5J2	NM_004889.1	ATP5JL;F1Fo-ATPase	hydrogen	mitochond	proton
GI_4757823-S	80.2	85.8	82.4	AXIN2	NM_004655.1	AXIL	tumor	intracellula	signal
GI_4757845-S	175.4	200.5	194.1	BCL9	NM_004326.1	LGS		nucleus	oncogene
GI_4757849-S	128.7	164.3	168	ABCG2	NM_004827.1	MRX;MXR;ABCP;BCRP;BMDP;MXR1;ABC1	xenobiotic-	integral to	drug
GI_4757855-S	900.6	1026.7	852.2	BNIP2	NM_004330.1	NIP2;BNIP-2	apoptosis		anti-
GI_4757859-S	730.9	833.5	715.9	BNIP3L	NM_004331.1	NIX;BNIP3a	tumor	integral to	negative
GI_4757861-S	219	205.9	260.9	BPHL	NM_004332.1	MCNAA	hydrolase		amino
GI_4757863-S	109.1	115.1	116.5	VCY2	NM_004678.1	BPY2			fertilization
GI_4757865-S	331	365.7	365.6	BRPF1	NM_004634.1	BR140	transcripti	nucleus	regulation
GI_4757873-S	321.7	379.6	368.2	BST1	NM_004334.1	CD157	GPI-	peripheral	humoral
GI_4757877-S	402.8	404.2	521.4	BUB1	NM_004336.1		protein	kinetochor	mitotic
GI_4757879-S	5410.1	5621.8	5776.3	BUB3	NM_004725.1	BUB3L		kinetochor	mitotic
GI_4757883-S	112.3	122.4	119.4	C18orf1	NM_004338.1		molecular	integral to	biological_
GI_4757889-S	283	280.4	260.4	C8orf1	NM_004337.1	hT41	molecular	cellular_co	germ-cell
GI_4757893-S	119	126.9	125.7	CACNA2D1	NM_000722.1	CACNA2;CACNL2A	dihydropyr	voltage-	small
GI_4757897-S	96.2	109.5	107.7	CALB3	NM_004057.1	CABP1;CABP9K	calcium		
GI_4757901-S	1728.6	2914.4	3868.1	CETN2	NM_004344.1	CALT;CEN2	calcium	centrosom	cytokinesi
GI_4757909-S	256.8	309.9	281.2	CART	NM_004291.1			extracellul	signal
GI_4757913-S	163.5	177.9	161.5	CASP5	NM_004347.1	ICH-3;ICEREL-III;ICE(rel)III	cysteine-	intracellula	proteolysis
GI_4757917-S	1474.1	4535.1	3188.9	RUNX3	NM_004350.1	AML2;CBFA3;PEBP2aC	ATP	nucleus	transcripti
GI_4757921-S	333.5	389.9	381	CBLN1	NM_004352.1			membran	synaptic
GI_4757935-S	201.9	328.1	278.9	CCNG2	NM_004354.1		cyclin-		cell cycle
GI_4757937-A	80.2	78.8	79.8	CCR2	NM_000648.1	CKR2;CCR2A;CCR2B;CKR2A;CKR2B;CMKB	chemokin	soluble	negative
GI_4757937-I	94.4	91.2	98	CCR2	NM_000648.1	CKR2;CCR2A;CCR2B;CKR2A;CKR2B;CMKB	chemokin	soluble	negative
GI_4757973-S	93.7	88.4	83	CETN1	NM_004066.1	CEN1;CETN	calcium	centrosom	centrosom
GI_4757975-S	102.8	90.9	88.4	CETN3	NM_004365.1	CEN3	calcium	centriole	centrosom
GI_4757979-S	260	332	303.3	CHN2	NM_004067.1	ARHGAP3;RHOGAP3	SH3/SH2		intracellula
GI_4757997-S	109.1	116.2	110.9	CLCA3	NM_004921.1		transporte	extracellul	small
GI_4758003-S	144.7	141.1	237.7	CLGN	NM_004362.1		chaperone	integral to	fertilization
GI_4758007-S	1379.8	1284.9	1277	CLK1	NM_004071.1	CLK;STY	protein	nucleus	regulation
GI_4758013-S	126.6	129.3	134.8	CMKLR1	NM_004072.1	DEZ;ChemR23	chemokin	integral to	chemotaxi
GI_4758021-S	128.2	177.2	252.7	COCH	NM_004086.1	DFNA9;DFNA31;COCH5B2;COCH-5B2			hearing
GI_4758023-S	322.9	317.8	359.5	COIL	NM_004645.1	CLN80;p80-coilin	DNA	nucleus	regulation
GI_4758031-S	1611.1	2576.9	2244.3	COPB2	NM_004766.1	beta'-COP	protein	cytosol	exocytosis
GI_4758043-S	6358.9	7508	6849.4	COX8	NM_004074.1	COX VIII	cytochrom	mitochond	energy
GI_4758051-S	276.1	308.1	296.6	CRABP1	NM_004378.1	RBP5;CRABP;CRABPI;CRABP-I	retinoid	cytoplasm	signal
GI_4758055-S	648.3	689.4	632.5	CREBBP	NM_004380.1	CBP;RTS;RSTS	transcripti	cytoplasm	regulation
GI_4758069-S	110.3	147.9	135.4	GPR44	NM_004778.1	CRTH2	G-protein	integral to	G-protein
GI_4758077-S	1369.7	1257	1229.8	CSK	NM_004383.1		protein C-	cytoplasm	protein
GI_4758079-S	657.8	602.6	405.3	CSNK1G3	NM_004384.1		protein		signal
GI_4758083-S	305.2	393.8	346.3	CSPG3	NM_004386.1	NCAN	chondroiti		cell

GI_4758085-S	11254.5	7132.5	6389.9	CSRP1	NM_004078.1	CRP;CRP1;CSRP;D1S181E	zinc ion	nucleus	
GI_4758087-S	116.1	106.7	107.6	CST	NM_004861.1	GAL3ST1	sulfotransf	membran	N-linked
GI_4758089-S	222	230.9	210.7	NKX2-5	NM_004387.1	CSX;CSX1;NKX2E;NKX2.5	transcripti	nucleus	heart
GI_4758091-S	497.6	516.7	460.3	CTBS	NM_004388.1	CTB	hydrolase	lysosome	carbohydr
GI_4758099-S	107.7	105.1	96.7	CXorf1	NM_004709.1		molecular	cellular_co	biological_
GI_4758115-S	795	1142.6	1578	DAG1	NM_004393.1	A3a;DAG;AGRNR	laminin	extracellul	muscle
GI_4758119-S	5843.6	4677.9	7047.2	DAP	NM_004394.1				induction
GI_4758135-A	674.4	532.7	558.9	DDX11	NM_004399.1	CHL1;KRG2;CHLR1;MGC9335	helicase	nucleolus	mitotic
GI_4758147-S	986	848	678.8	DFFA	NM_004401.1	DFF1;ICAD;DFF-45	caspase-	cytosol	DNA
GI_4758149-S	272.5	242	224.2	DFFB	NM_004402.1	CAD;CPAN;DFF2;DFF40;DFF-40	caspase-	cytosol	DNA
GI_4758153-S	6070.5	4580.1	4242.8	DFNA5	NM_004403.1	ICERE-1			hearing
GI_4758161-S	226.9	325.5	235	DLG1	NM_004087.1	hdlg;SAP97	cytoskelet	cytoplasm	cell shape
GI_4758169-A	246.9	757.5	645.9	DMBT1	NM_004406.1	GP340	tumor		
GI_4758171-S	101.3	118.2	102	DMP1	NM_004407.1		integrin	extracellul	ossificatio
GI_4758173-S	457.1	390.6	310.6	DMPK	NM_004409.1	DM;DM1;DMK	protein	kinesin	muscle
GI_4758175-A	96.2	103.7	96.6	DNAH9	NM_004662.1	DYH9;HL20;DNAL1;DNEL1;HL-	adenosine	cytoskelet	spermatog
GI_4758175-I	190.8	235.4	204.1	DNAH9	NM_004662.1	DYH9;HL20;DNAL1;DNEL1;HL-	adenosine	cytoskelet	spermatog
GI_4758177-S	93.4	112.1	97.5	DNCI1	NM_004411.1	DNCIC1	motor	cytoplasmi	microtubul
GI_4758181-S	255.1	387.3	357.6	DNM1	NM_004408.1	DNM	GTP	coated pit	receptor
GI_4758189-S	105.1	107.9	93.2	DPEP1	NM_004413.1	MDP;RDP	membran	peripheral	proteolysis
GI_4758191-S	492.1	548.6	510	STK17A	NM_004760.1	DRAK1	protein	nucleus	induction
GI_4758199-S	264.2	330.2	274	DSP	NM_004415.1	DPI;DPII;KPPS2;PPKS2	structural	intermedia	epidermal
GI_4758211-S	131	161.9	129.8	DUSP8	NM_004420.1	HB5;HVH8;HVH-5	protein	nucleus	inactivatio
GI_4758215-S	459.1	484.1	445	DVL2	NM_004422.1		signal	cytoplasm	imaginal
GI_4758219-S	4498.2	3426.8	3725.6	DXS9928E	NM_004699.1	9F;XAP5;HXC-26		nucleus	
GI_4758231-S	154.1	210.7	175.8	ECEL1	NM_004826.1	XCE;ECEX	metallope	integral to	neuropepti
GI_4758239-S	373.1	459.8	428.9	EDG5	NM_004230.1	H218;LPB2;S1P2;AGR16;EDG-5;Gpcr13	lipid	integral to	activation
GI_4758261-S	199.4	242.6	217.9	ELAVL2	NM_004432.1	HUB;HELN1;HEL-N1	mRNA 3'		regulation
GI_4758267-S	186.3	163.1	141.6	EML1	NM_004434.1	EMAP;ELP79;EMAPL;HuEMAP		microtubul	vision
GI_4758269-S	1588.2	1282.8	2056.7	ENDOG	NM_004435.1		endonucle	mitochond	DNA
GI_4758271-S	210.3	228.2	247	ENSA	NM_004436.1		ion		response
GI_4758273-S	362.7	387.4	335.7	EPB41	NM_004437.1	HE;EL1;4.1R	structural	spectrin	circulation
GI_4758291-S	203.8	728.7	343.6	EPHB6	NM_004445.1	HEP	ephrin	integral to	transmem
GI_4758293-S	5034.3	4223.7	3720.9	EPRS	NM_004446.1	PARS;QARS;QPRS	ATP	soluble	glutamyl-
GI_4758297-S	154.3	178.2	157.1	ERBB2	NM_004448.1	NEU;NGL;HER2;TKR1;HER-2	Neu/ErbB-		enzyme
GI_4758301-S	4021.7	5353.4	4402.1	ERH	NM_004450.1	DROER	molecular		pyrimidine
GI_4758311-S	499.4	533.6	389.4	ETFDH	NM_004453.1	MADD;ETFQO	electron	mitochond	electron
GI_4758313-S	1534.8	1075.6	1211.3	IER2	NM_004907.1	ETR101			
GI_4758315-S	3626.7	2433.4	3062.2	ETV5	NM_004454.1	ERM	DNA	nucleus	regulation
GI_4758317-S	117.5	125.4	109.5	EXTL1	NM_004455.1	EXTL	tumor	endoplas	skeletal
GI_4758331-A	536.1	612	600.2	ACSL4	NM_004458.1	ACS4;FACL4;LACS4;MRX63	long-chain-		learning
GI_4758339-S	3517.3	3157	2811.4	FARSLA	NM_004461.1	FRSA;CML33;FARSL;PheHA	phenylala	soluble	pathogene
GI_4758343-S	140.6	141.2	141.1	FCER1G	NM_004106.1		receptor	integral to	immune
GI_4758359-S	95.9	109.8	96.4	FGF10	NM_004465.1		fibroblast	extracellul	histogene

GI_4758373-S	927.6	1131.1	589.8	FHL3	NM_004468.1	SLIM2			muscle
GI_4758387-S	122.9	151.9	134.9	FOXD2	NM_004474.1	FKHL17;FREAC9	transcripti	nucleus	regulation
GI_4758391-S	6444.8	4441.5	2804.6	FOXD1	NM_004472.1	FKHL8;FREAC4	DNA	nucleus	regulation
GI_4758393-S	4559.6	4713.4	5761.7	FLOT2	NM_004475.1	ESA;ECS1;ESA1;ECS-1;M17S1	cell	plasma	epidermal
GI_4758395-S	122.4	122.1	109.1	FLT3	NM_004119.1	FLK2;STK1;CD135	vascular	integral to	transmem
GI_4758397-S	126.4	132.1	128.2	FOLH1	NM_004476.1	PSM;FOLH;GCP2;PSMA;NAALAD1;NAALAd	catalytic	membran	proteolysis
GI_4758403-S	2879.3	2512.6	2540.1	FRG1	NM_004477.1	FSG1			pathogene
GI_4758405-S	152	175.4	160.4	FUT7	NM_004479.1		fucosyltra	Golgi	protein
GI_4758415-S	938.3	906.2	1001.1	GBF1	NM_004193.1	KIAA0248	ARF	Golgi	retrograde
GI_4758419-S	87.5	90.8	77.2	GCM2	NM_004752.1	GCMB;hGCMb	DNA	nucleus	developm
GI_4758421-S	207.3	261.4	223	GCNT3	NM_004751.1	GnT-M;C2/4GnT;C2GnT-M	N-	membran	O-linked
GI_4758431-S	259.7	300.9	270.3	GGTLA1	NM_004121.1	GGT5;GGT-REL;DKFZP566O011	gamma-	integral to	glutathion
GI_4758433-A	137.6	154.8	146.8	GHSR	NM_004122.1		G-protein	integral to	G-protein
GI_4758433-I	302.6	356	306.9	GHSR	NM_004122.1		G-protein	integral to	G-protein
GI_4758435-S	318.3	409.9	366.3	GIP	NM_004123.1		peptide	soluble	energy
GI_4758437-S	90.5	90.1	98.9	GLP2R	NM_004246.1		G-protein	integral to	positive
GI_4758439-S	116.4	217	90.8	GMFG	NM_004877.1	GMF-GAMMA	enzyme	intracellula	protein
GI_4758453-S	1437.7	2014.2	1749.9	GOLGB1	NM_004487.1	GCP;GCP372;GIANTIN		Golgi	Golgi
GI_4758455-S	1181.8	1299.8	1188.7	GOSR1	NM_004871.1	P28;GS28;GOS28;GOS28/P28	v-SNARE	ER-Golgi	intra-Golgi
GI_4758459-S	94.9	96	93.9	GP5	NM_004488.1	CD42d	cell	integral to	blood
GI_4758467-S	144.6	172.1	158.3	GPR50	NM_004224.1	H9	G-protein	integral to	G-protein
GI_4758473-S	498	567.3	524.2	GPR10	NM_004248.1	GR3;PrRPR	neuropepti	integral to	pregnancy
GI_4758477-S	223.1	209.3	231.2	GRB14	NM_004490.1		SH3/SH2		signal
GI_4758479-S	126	142.6	125.2	GRIA2	NM_000826.1	GLUR2;GLURB;HBGR2	glutamate	plasma	synaptic
GI_4758483-S	5583.3	4682	4020.7	GSTO1	NM_004832.1	P28;GSTTLp28	glutathion	cytoplasm	glutathion
GI_4758485-S	2255	2368.6	2138.5	GTF2A2	NM_004492.1	TFIIA			
GI_4758487-S	3067.4	3270	3433.2	GTF2F2	NM_004128.1	BTF4;RAP30;TFIIF			
GI_4758497-S	161.9	176.9	180.8	H6PD	NM_004285.1	GDH;G6PDH	glucose-6-	endoplas	pentose-
GI_4758499-A	551.2	663.6	522.6	CREB5	NM_004904.1	CRE-BPA	transcripti	nucleus	transcripti
GI_4758499-I	86	83.6	85.9	CREB5	NM_004904.1	CRE-BPA	transcripti	nucleus	transcripti
GI_4758503-S	1631.8	2059.8	2761.8	HADH2	NM_004493.1	ERAB;MHBD;17b-HSD10	7-alpha-	cytoplasm	lipid
GI_4758505-S	207.7	218.4	197.7	HAND1	NM_004821.1	Hxt;eHand;Thing1	transcripti	nucleus	heart
GI_4758507-S	110.7	134.1	113.3	HAT	NM_004262.1		peptidase	extracellul	respiratory
GI_4758513-S	106.1	110.7	98.3	ZNF254	NM_004876.1	BMZF-5;ZNF91L;HD-ZNF1	DNA	nucleus	negative
GI_4758515-S	6858.5	6468.4	6687.3	HDGF	NM_004494.1	HMG1L2	heparin	extracellul	signal
GI_4758525-I	123.7	123.1	110.1	NRG1	NM_004495.1	GGF;HGL;HRG;NDF;ARIA;GGF2;HRGA;SM			
GI_4758547-S	125.6	255	281.1	HOMER2	NM_004839.1	CPD;ACPD;Vesl-2;Cupidin;HOMER-			metabotro
GI_4758555-S	875.9	1025.9	969.1	PRPF3	NM_004698.1	PRP3;RP18;HPRP3;Prp3p;HPRP3P	pre-mRNA	ribonucleo	mRNA
GI_4758559-S	747.9	675.5	652.2	HPRP8BP	NM_004814.1	SPF38;PRPF8BP	pre-mRNA	snRNP U5	RNA
GI_4758563-S	109.5	130.5	131.6	USP6	NM_004505.1	HRP1;TRE2;TRE-2;TRE17			
GI_4758565-S	193.7	238.5	211.8	HS6ST1	NM_004807.1	HS6ST	sulfotransf	integral to	heparan
GI_4758579-S	144.4	321.5	213.9	C1orf38	NM_004848.1	ICB-1			cell
GI_4758589-S	107.2	101.1	100.5	IGSF2	NM_004258.1	V7;CD101	plasma	integral to	cell
GI_4758605-S	6134.4	6717	6537.6	ILK	NM_004517.1	P59	protein	peripheral	integrin-

GI_4758613-S	568.5	603.9	572.3	ITGBL1	NM_004791.1	OSCP;TIED	cell	integrin	cell
GI_4758617-S	333.3	387.4	347.8	K6HF	NM_004693.1		structural	intermedia	
GI_4758623-S	127.8	147.1	140.9	KCNK6	NM_004823.1	TOSS;KCNK8;TWIK2;TWIK-2;FLJ12282	inward	voltage-	potassium
GI_4758643-S	926.2	881.2	856.7	KIF2	NM_004520.1	HK2	adenosine	cytoskelet	microtubul
GI_4758647-S	540.5	678.2	527.2	KIF5B	NM_004521.1	KNS;KINH;KNS1;UKHC;U-KHC	microtubul	kinesin	microtubul
GI_4758661-S	283.3	347	356.2	LYSAL1	NM_004901.1	LAP70;LALP70;KIAA0392	apyrase	lysosome	nucleobas
GI_4758669-S	1357.2	3070.7	1079.4	LPXN	NM_004811.1	LDPL		cytoplasm	cell
GI_4758675-S	112.6	136.7	115.8	LIPF	NM_004190.1	HGL;HLAL	triacylglyc	cellular_co	triacylglyc
GI_4758679-S	242.5	334.8	261.7	LLGL2	NM_004524.1	HGL			
GI_4758683-S	97.9	97.7	90.9	LRAT	NM_004744.1		acyltransf		
GI_4758685-S	720.1	678.6	374.8	LRP1	NM_002332.1	APR;LRP;A2MR;CD91;APOER	lipoprotein	coated pit	pathogene
GI_4758689-S	894.9	841.6	695.1	LRRFIP1	NM_004735.1	GCF2;TRIP;GCF-2;FLAP-1;HUFI-	double-	cytoskelet	regulation
GI_4758697-S	1420.6	1621.8	2263.4	MAN2A1	NM_002372.1	MANA2	mannosyl-	Golgi	glycoprote
GI_4758703-S	145.1	136.2	169.3	MFHAS1	NM_004225.1	MASL1	small	nucleus	oncogene
GI_4758707-S	120.3	144	135	LY86	NM_004271.1	MD-1;dJ80N2.1	signal	plasma	humoral
GI_4758711-S	109.5	122	113	MGAM	NM_004668.1	MG;MGA	catalytic	integral to	starch
GI_4758719-S	637.3	649.7	728.9	MLLT3	NM_004529.1	AF9	translation	nucleus	oncogene
GI_4758727-S	170.1	195.3	186.8	MMPL1	NM_004142.1	MMP20	metallope	extracellul	proteolysis
GI_4758733-S	3113.8	3034.2	2865.5	PMPCB	NM_004279.1	MPPB;MPP11;MPPP52	peptidase	mitochond	proteolysis
GI_4758747-S	164.6	181.6	166.4	MYBPC2	NM_004533.1	MYBPC;MYBPCF	structural	striated	striated
GI_4758751-S	259	316.7	267.4	BIRC1	NM_004536.1	NAIP	apoptosis	intracellula	anti-
GI_4758765-S	99.6	113.4	82.9	NDST3	NM_004784.1		heparin N-		protein
GI_4758771-S	583.2	695.5	675.6	NDUFA3	NM_004542.1	B9	NADH	NADH	
GI_4758773-S	1632.5	2369.5	1915.7	NDUFB10	NM_004548.1	PDSW	NADH	NADH	
GI_4758787-S	2049.4	2205.8	1942.9	NDUFS3	NM_004551.1		iron-sulfur	NADH	mitochond
GI_4758789-S	3120.4	4057.4	3576.3	NDUFS5	NM_004552.1		NADH	NADH	mitochond
GI_4758797-S	108.2	104.3	119	DPF1	NM_004647.1	NEUD4;neuro-d4	DNA	nucleus	induction
GI_4758805-S	581.2	393.4	338.1	NFKBIE	NM_004556.1	IKBE	transcripti	cytoplasm	
GI_4758813-S	375.4	491.9	377.7	NMI	NM_004688.1		transcripti	cytoplasm	JAK-STAT
GI_4758815-S	1274.2	1226.2	914.9	NMT2	NM_004808.1		catalytic		protein-
GI_4758819-I	119.7	102.8	107.5	GPR74	NM_004885.1	NPFF2;NPGPR	G-protein	integral to	perception
GI_4758821-S	94.7	100.3	98.5	NPHS1	NM_004646.1	CNF;NPHN	cell	integral to	excretion
GI_4758825-S	102.8	100.6	94.7	NRTN	NM_004558.1	NTN	receptor		transmem
GI_4758839-S	126.3	134.1	124.7	NTN1	NM_004822.1	NTN1L	structural	soluble	oncogene
GI_4758847-S	106.4	107.4	111.8	ONECUT2	NM_004852.1	OC2;OC-2	RNA	nucleus	histogene
GI_4758851-S	241.6	273.8	264.2	SLC22A13	NM_004256.1	OCTL1;OCTL3;ORCTL3	organic	membran	small
GI_4758859-S	391.5	371.6	326.8	NOLC1	NM_004741.1	P130;NOPP130;NOPP140;KIAA0035	GTP	nucleolus	rRNA
GI_4758865-S	673.5	1295.8	813.6	C5orf13	NM_004772.1	P311;PTZ17;D4S114;PRO1873			
GI_4758867-S	1939.8	2072.8	1741.6	P4HA2	NM_004199.1		procollage	endoplas	protein
GI_4758873-S	2159.9	3124.7	2164.1	TM9SF2	NM_004800.1	P76	transporte	endosome	small
GI_4758875-S	457.9	497.9	436.4	PABPN1	NM_004643.1	OPMD;PAB2;PABP2	RNA	nucleus	RNA
GI_4758877-S	206.9	219.6	218.1	PAFAH2	NM_000437.2	HSD-PLA2	phospholi	soluble	lipid
GI_4758883-I	114.2	127.9	119.9	PARK2	NM_004562.1	PDJ;PRKN;AR-JP	ubiquitin-		central
GI_4758885-S	3890.3	2682.4	1307.6	PCK2	NM_004563.1	PEPCK;PEPCK2	phosphoe	mitochond	glucose

GI_4758893-S	572	620.2	467.1	PET112L	NM_004564.1	PET112	translation	mitochond	protein
GI_4758895-S	455.8	492.8	484.3	PEX14	NM_004565.1	NAPP2		integral to	
GI_4758897-A	1150.2	928.2	1031.8	PEX16	NM_004813.1			integral to	peroxisom
GI_4758897-I	1678.8	1440	1661	PEX16	NM_004813.1			integral to	peroxisom
GI_4758899-S	122.3	124.7	108.6	PFKFB3	NM_004566.1	IPFK2	fructose-	cellular_co	fructose
GI_4758907-I	200.5	217.7	176.8	MIZ1	NM_004671.1	SIZ2;PIASX-BETA;PIASX-ALPHA	zinc ion	nucleus	
GI_4758913-S	1824.7	3980.4	3080.4	LITAF	NM_004862.1	PIG7;CMT1C;SIMPLE;TP53I7;FLJ38636	RNA	nucleus	regulation
GI_4758925-S	231	295.8	259.2	PITPNM1	NM_004910.1	NIR2;RDGB;DRES9;RDGB1;PITPNM;RDGB	phosphati	intracellula	phototrans
GI_4758931-S	146.9	154.8	127.3	PKP2	NM_004572.1		structural	cytoskelet	cell-cell
GI_4758935-S	22246.6	15648	10315	GDF15	NM_004864.1	PDF;MIC1;PLAB;MIC-1;NAG-1;PTGFB;GDF-	cytokine	extracellul	transformi
GI_4758937-S	128.5	139.8	121	PLCB2	NM_004573.1		phospholi		phosphati
GI_4758939-S	1274.7	1390.8	1179.5	C14orf2	NM_004894.1	MP68;PLPM		mitochond	
GI_4758943-S	117.3	142.7	114.2	REPS2	NM_004726.1	POB1	calcium		EGF
GI_4758947-S	100.2	102.5	102.2	POU4F2	NM_004575.1	BRN3B;BRN3.2;Brn-3b	transcripti		eye
GI_4758951-S	2312.5	2656.6	2717.9	PPP2CB	NM_004156.1	PP2CB	protein		protein
GI_4758955-S	567.2	217.3	142.4	BZRAP1	NM_004758.1	PRAX-1;KIAA0612	receptor	mitochond	biological_
GI_4758957-S	226.4	265.9	273.2	PRKAR2A	NM_004157.1	PRKAR2	cAMP-	cytoplasm	intracellula
GI_4758981-S	152.4	178.7	156	PYY	NM_004160.1		peptide	soluble	regulation
GI_4758985-S	130.4	147.4	141.2	RAB11B	NM_004218.1	H-YPT3	RAB small		small
GI_4758993-S	115.6	112.3	102.9	RAB28	NM_004249.1		RAB small		
GI_4759025-S	155.4	222.4	138.8	RASAL1	NM_004658.1	RASAL	Ras		signal
GI_4759029-S	173.4	207.1	210.4	RECQL4	NM_004260.1	RTS;RECQ4	DNA	nucleus	DNA
GI_4759033-S	1474.8	1513.8	1179.9	ETF1	NM_004730.1	ERF;RF1;ERF1;TB3-1;D5S1995;SUP45L1	translation	cytoplasm	regulation
GI_4759039-S	256.3	260.2	374.5	RIN1	NM_004292.1		protein	peripheral	signal
GI_4759049-S	215.9	295.2	287.7	RPS6KA3	NM_004586.1	RSK;HU-2;HU-3;RSK2;MRX19;ISPK-	protein		central
GI_4759053-S	133	162.7	131.9	RRAD	NM_004165.1	RAD;RAD1;REM3	small		small
GI_4759055-S	253	340.2	200.1	RRBP1	NM_004587.1	ES130;ES/130	extracellul	ribosome	protein
GI_4759057-S	115.8	130.8	121.5	SH3BP5	NM_004844.1	SAB	SH3/SH2	cytoplasm	signal
GI_4759059-I	701	767.8	769.9	MADHIP	NM_004799.1	SARA;ZFYVE9	serine-	cytoplasm	SMAD
GI_4759061-A	1565.6	1398.6	1638.4	GPSN2	NM_004868.1	SC2;TER		integral to	
GI_4759067-S	1457.9	1649.8	1320.8	SCO1	NM_004589.1	SCOD1	chaperone	mitochond	cytochrom
GI_4759075-S	164.7	253.8	114.6	CCL20	NM_004591.1	CKb4;LARC;ST38;MIP3A;MIP-3a;SCYA20	chemokin	extracellul	chemotaxi
GI_4759079-S	2131.7	2359.3	2479.5	SDHA	NM_004168.1	FP;SDH2;SDHF	electron	mitochond	aerobic
GI_4759091-S	202	284.6	167.2	SEMA3B	NM_004636.1	SemA;SEMA5;SEMAA;semaV;LUCA-1		endoplas	axon
GI_4759097-S	1364.2	1310.1	1195.9	SFRS10	NM_004593.1	TRA2B;SRFS10;TRA2-BETA;Htra2-beta	pre-mRNA	nucleus	RNA
GI_4759109-S	886.2	942.9	937	MPDU1	NM_004870.1	SL15;Lec35			
GI_4759111-S	941.4	1273.7	1473.8	SLC16A3	NM_004207.1	MCT3;MCT4	monocarb	membran	monocarb
GI_4759113-S	135.4	186.5	90.9	SLC16A4	NM_004696.1	MCT4	monocarb	membran	monocarb
GI_4759127-S	217.6	226.3	221.3	SLC24A1	NM_004727.1	NCKX;RODX;NCKX1;HsT17412;KIAA0702	calcium,	integral to	small
GI_4759131-S	90.6	84.7	94.4	SLC28A2	NM_004212.1	CNT2;HCNT2;SPNT1;HsT17153	purine	membran	purine
GI_4759133-S	107.9	111.6	103.1	SLC4A8	NM_004858.1	NBC3	inorganic	membran	anion
GI_4759135-S	156.3	188.1	167.6	SLC6A5	NM_004211.1	GLYT2	glycine:so	integral to	small
GI_4759137-S	193.9	235.6	197.7	SLC7A4	NM_004173.1	CAT4;CAT-4;HCAT3	basic	integral to	small
GI_4759139-S	457.8	739.1	663.1	SLC9A3R1	NM_004252.1	EBP50;NHERF	protein	actin	protein

GI_4759141-S	484	550.6	444.4	SLC9A3R2	NM_004785.1	SIP1;OCTS2;SIP-1;TKA-	protein	plasma	protein
GI_4759143-S	190.8	247.9	153.7	SLC9A5	NM_004594.1	NHE5	sodium:hy	integral to	small
GI_4759145-S	129.9	133.8	175.7	SLIT2	NM_004787.1	Slit-2	protein	extracellul	motor
GI_4759171-S	231.2	240.6	223.3	SFRS2IP	NM_004719.1	SIP1;CASP11;SRRP129	pre-mRNA	DNA-	mRNA
GI_4759175-I	182.1	228.2	196	STAU	NM_004602.1		double-	microtubul	
GI_4759177-S	2078.6	1660.3	2445.9	AURKB	NM_004217.1	AIK2;AIM1;ARK2;AurB;IPL1;AIM-1;STK12	protein		cell cycle
GI_4759179-A	605.7	616.9	490.4	STK19	NM_004197.1	G11;RP1;D6S60;D6S60E;HLA-RP1	protein	nucleus	protein
GI_4759181-S	4679.2	4453.8	5080.1	STX1A	NM_004603.1	STX1;HPC-1;p35-1	protein	kinesin	nonselecti
GI_4759187-S	1756.2	2224.4	1886.9	STX8	NM_004853.1	CARB		kinesin	nonselecti
GI_4759195-S	161.2	172.9	157.8	SYMPK	NM_004819.1	SPK;SYM			
GI_4759211-S	4119.5	3989.7	3600.6	TBCA	NM_004607.1		co-	cytoskelet	post-
GI_4759215-S	733.6	736	690	TCEAL1	NM_004780.1	P21;SIIR;pp21	RNA	nucleus	negative
GI_4759221-S	143.9	138.6	141.7	TCP10	NM_004610.1			cytosol	
GI_4759225-S	136.2	187.5	148.2	TGFBR1	NM_004612.1	ALK-5;ACVRLK4	type I	integral to	TGFbeta
GI_4759229-A	123.3	199.7	115.1	TGM5	NM_004245.1	TGX;TGM6;TGMX	protein-		epidermal
GI_4759247-S	88.6	89.9	85.5	TPH1	NM_004179.1	TPH;TPRH	iron ion		tryptophan
GI_4759255-S	2142.4	1994.8	1721.8	TRAG3	NM_004909.1		DNA	nucleus	drug
GI_4759263-S	1463.3	1911.8	1394.3	TRIP15	NM_004236.1	CSN2;SGN2;ALIEN;COPS2;COPS2-	protein	signaloso	signal
GI_4759273-S	272.3	327.7	257.8	TXNL	NM_004786.1	Txl;TRP32	thioredoxi	cytoplasm	protein-
GI_4759279-S	134.5	165.6	157.5	U5-116KD	NM_004247.1	KIAA0031	GTPase	spliceoso	mRNA
GI_4759303-S	525.6	824.9	865.9	VCY	NM_004679.1	BPY1;VCY1	DNA	nucleus	regulation
GI_4759305-S	132.7	150.3	128	LIN7A	NM_004664.1	LIN7;VELI1;LIN-7A;MALS-1;TIP-33	protein		exocytosis
GI_4759309-S	163.2	149.9	131.8	VMD2	NM_004183.1	BMD;BEST	molecular	integral to	vision
GI_4759311-S	141.4	145.2	157.1	VNN1	NM_004666.1	Tiff66	hydrolase		cell
GI_4759329-S	76.5	84.1	84.7	XKRY	NM_004677.1			integral to	fertilization
GI_4759335-S	507.3	407.6	554.9	FANCG	NM_004629.1	FAG;XRCC9	tumor	nucleus	cell cycle
GI_4809272-S	1791.4	1740.1	1682.6	ANXA4	NM_001153.2	ANX4	phospholi		
GI_4809273-S	9209.9	7635.1	8867.3	ANXA5	NM_001154.2	PP4;ANX5;ENX2	phospholi		blood
GI_4809275-A	403.9	701.6	144.7	ANXA6	NM_004033.1	ANX6;CBP68	phospholi		
GI_4809277-A	2475.4	2365.8	616.3	ANXA7	NM_001156.2	SNX;ANX7	phospholi		
GI_4809278-I	113.9	140.8	127.6	ANXA7	NM_004034.1	SNX;ANX7	phospholi		
GI_4809281-S	314.1	517.3	597	BMP6	NM_001718.2	VGR;VGR1	cytokine		skeletal
GI_4809282-S	89.9	105.3	81.9	HAL	NM_002108.2	HIS;HSTD	histidine	cytosol	histidine
GI_4809285-A	111.3	112.6	85.6	IRF7	NM_004030.1	IRF7A	specific	cytoplasm	response
GI_4809289-S	348.3	684.9	563.1	GALGT	NM_001478.2	GALNACT	(N-	Golgi	glycosphin
GI_4826642-S	741.4	634.3	394.5	ANXA3	NM_005139.1	ANX3	calcium-	cytoplasm	
GI_4826650-S	102.4	106.9	102	C21orf2	NM_004928.1	A2;YF5	molecular	cellular_co	biological_
GI_4826652-S	318.3	250.1	219.6	C21orf5	NM_005128.1	pad-1;KIAA0933	molecular	cellular_co	developm
GI_4826658-S	1435.4	2131.5	1538.2	CAPZB	NM_004930.1	CAPB;CAPZ;CAPPB	actin	F-actin	
GI_4826664-S	368.7	464.5	389.1	CCS	NM_005125.1		intracellula	obsolete	intracellula
GI_4826681-S	915	984	1061.4	CTNS	NM_004937.1	CTNS-LSB	L-cystine	lysosomal	L-cystine
GI_4826683-S	136.7	361	138.4	DAPK1	NM_004938.1	DAPK	calmoduli		induction
GI_4826685-S	4091	4279.2	3918.4	DDX1	NM_004939.1	DBP-RB	RNA	cellular_co	ribosome
GI_4826689-S	481.4	579.1	555.2	DHX8	NM_004941.1	DDX8;HRH1;PRP22	ATP	spliceoso	RNA

GI_4826693-S	389.3	452.2	566.8	DGCR2	NM_005137.1	IDD;LAN;DGS-C;SEZ-12;KIAA0163	lectin [goid	integral to	histogene
GI_4826697-S	113.2	146.1	124.1	DNASE1L3	NM_004944.1	LSD;DNAS1L3	deoxyribo	nucleus	DNA
GI_4826699-S	398.5	515.4	573.1	DNM2	NM_004945.1	DYNII	microtubul		G2/M
GI_4826713-S	168.9	173.9	173.9	ENDOGL1	NM_005107.1	ENGL;ENGL-B;ENGL-a;ENDOGL2			
GI_4826715-S	263.7	311.4	218.5	SLC29A1	NM_004955.1	ENT1	nucleoside	membran	nucleoside
GI_4826733-S	3641.8	3206.9	2757.7	FUS	NM_004960.1	TLS;FUS1	RNA	nucleus	cell growth
GI_4826735-S	4936.3	4953.2	3787.8	FXR1	NM_005087.1		RNA	polysome	nucleocyto
GI_4826741-S	4150.1	5508.5	7302.4	GFPT2	NM_005110.1	GFAT2	glutamine-	cytoplasm	energy
GI_4826745-S	116.3	120.1	117.4	GNG7	NM_005145.1		heterotrim	peripheral	regulation
GI_4826751-S	110	129.3	117.4	GUCY2C	NM_004963.1	STAR;GUC2C	guanylate	brush	receptor
GI_4826761-S	117	126.3	114.1	HP	NM_005143.1		plasma		defense
GI_4826763-S	148.1	180.6	184.4	HS3ST1	NM_005114.1	3OST;3OST1	sulfotransf	Golgi	proteolysis
GI_4826767-A	236.6	311	450	ICA1	NM_004968.1	ICA69;ICAp69		cytoplasm	
GI_4826769-S	357.6	468.9	447	IDE	NM_004969.1		insulysin	soluble	sex
GI_4826771-S	99.7	100.2	96.3	IGFALS	NM_004970.1	ALS			
GI_4826773-S	705.6	1219.5	1218.7	G1P2	NM_005101.1	UCRP;IFI15;ISG15	protein	extracellul	immune
GI_4826779-S	200.9	230.2	227.9	SLC12A6	NM_005135.1	KCC3;ACCPN;KCC3A;KCC3B;DKFZP434D2	potassium	integral to	small
GI_4826797-A	170.6	186.9	146.1	KCNJ4	NM_004981.1	HIR;HRK1;HIRK2;Kir2.3	inward	voltage-	potassium
GI_4826797-I	97.2	85.8	86.7	KCNJ4	NM_004981.1	HIR;HRK1;HIRK2;Kir2.3	inward	voltage-	potassium
GI_4826813-A	1471.4	1614.3	1307.1	KTN1	NM_004986.1	CG1;KNT;KIAA0004		endoplas	nonselecti
GI_4826815-S	96.9	86.8	86.5	LGI1	NM_005097.1	EPT;IB1099	tumor		neurogene
GI_4826827-S	117.6	111.2	104.5	MDS1	NM_004991.1	PRDM3;MDS1-EVI1	transcripti		
GI_4826835-S	5049.2	352.9	158.6	MMP9	NM_004994.1	GELB;CLG4B	collagenas	extracellul	proteolysis
GI_4826841-S	111	128.5	103.3	MYBPH	NM_004997.1		structural	cytoskelet	regulation
GI_4826843-S	165.3	193.5	173.4	MYO1E	NM_004998.1	MYO1C	myosin	myosin	
GI_4826845-S	488.6	631.6	588	MYO6	NM_004999.1				
GI_4826849-S	522	704	656.2	NDUFA7	NM_005001.1	B14.5a	NADH	NADH	
GI_4826853-S	2046.1	2268.8	1751.3	NDUFB8	NM_005004.1	ASHI	NADH	NADH	mitochond
GI_4826859-S	1832.6	1841.1	1432.1	NHP2L1	NM_005008.1	NHPX;OTK27	RNA	nucleolus	regulation
GI_4826867-S	472.9	1303.6	890.4	ROR1	NM_005012.1	NTRKR1;dJ537F10.1	transmem	cytoplasm	transmem
GI_4826869-S	477.7	545	460.8	NUCB2	NM_005013.1	NEFA	calcium	cytosol	
GI_4826875-S	167.6	210.6	172.1	OMD	NM_005014.1	SLRR2C	cell	extracellul	cell
GI_4826879-S	2415.8	2189.8	1856.4	OXA1L	NM_005015.1			mitochond	aerobic
GI_4826881-S	1001.6	730.1	679.1	THOC1	NM_005131.1	P84;HPR1	structural	nucleus	RNA
GI_4826889-S	263.3	335.7	289.1	PDCD1	NM_005018.1	PD1;SLEB2;hPD-l	signal	integral to	humoral
GI_4826893-S	97.5	93.6	91.1	PDE1C	NM_005020.1	Hcam3	calmoduli		signal
GI_4826901-S	101.1	109.2	111.4	SERPINB10	NM_005024.1	PI10;bomapin	protein		
GI_4826903-S	907.4	236.6	137.3	SERPINI1	NM_005025.1	PI12;neuroserpin	serpin		peripheral
GI_4826907-S	250.4	290	289.9	PIK3R2	NM_005027.1	P85B;p85-BETA	1-	phosphoin	intracellula
GI_4826913-S	440.2	552.5	506.4	PLA2G4B	NM_005090.1	HsT16992;cPLA2-beta	calcium-		phospholi
GI_4826921-S	1031.3	989.7	1028.4	PMSCL1	NM_005033.1		exonuclea	nucleolus	rRNA
GI_4826933-S	1207.2	1363	1152.5	PPP4R1	NM_005134.1	PP4R1			
GI_4826943-S	98.9	104.6	96.5	PRH2	NM_005042.1	Pr		extracellul	
GI_4826947-S	285.3	299.4	275.1	PRKX	NM_005044.1	PKX1	cAMP-		protein

GI_4826955-S	995.3	791.9	657.3	PWP2H	NM_005049.1	PWP2;EHOC-17	signal		signal
GI_4826959-S	7795.9	7441.3	6736.6	QARS	NM_005051.1	GLNRS	glutamine-	soluble	glutaminyl-
GI_4826967-S	1172.1	1531.9	1480.8	JARID1A	NM_005056.1	RBP2;RBBP2	protein	nucleus	transcripti
GI_4826969-S	170.1	191.5	197.3	RBBP5	NM_005057.1	RBQ3		nucleus	
GI_4826973-S	163.7	179.5	193.4	RBMY1A1	NM_005058.1	RBM1;RBM2;RBMY;YRRM1;YRRM2	RNA	nucleus	RNA
GI_4826975-S	570.8	621.1	662.7	RCE1	NM_005133.1	FACE2;RCE1A;RCE1B;hRCE1;FACE-2	prenyl-	endoplas	proteolysis
GI_4826979-S	168.4	211.7	173	NR1H4	NM_005123.1	BAR;FXR;HRR1;HRR-1;RIP14	transcripti	nucleus	bile acid
GI_4826991-S	1133.2	1094.6	1188.2	SCO2	NM_005138.1	SCO1L	copper ion	mitochond	electron
GI_4826997-S	720.8	597.1	464.9	SFPQ	NM_005066.1	PSF;POMP100	pre-mRNA	nucleus	mRNA
GI_4827007-S	108.3	97.2	106	SLC15A1	NM_005073.1	PEPT1;HPECT1;HPEPT1	peptide:hy	membran	small
GI_4827009-S	86.1	85.1	74.8	SLC17A1	NM_005074.1	NPT1;NAPI-1	sodium-	membran	phosphate
GI_4827011-S	91.3	98.6	99.2	SLC1A6	NM_005071.1	EAAT4	glutamate/	membran	L-
GI_4827015-A	154.1	202.9	216.5	SLC4A3	NM_005070.1	AE3;SLC2C	inorganic	membran	small
GI_4827023-S	196.7	239.3	241.4	TBX19	NM_005149.1	TPIT;TBS19;dJ747L4.1	RNA	nucleus	embryoge
GI_4827029-S	250.5	312.2	329.6	TLE3	NM_005078.1	ESG;ESG3;HsT18976;KIAA1547		nucleus	histogene
GI_4827035-S	218.6	282.9	220.2	PGLYRP1	NM_005091.1	PGRP;TAG7;PGRPS;PGLYRP;PGRP-	bacterial	extracellul	immune
GI_4827037-S	113.6	118.5	117	TPD52	NM_005079.1	D52;N8L;hD52		kinesin	embryoge
GI_4827039-S	142.5	143.4	122.6	THRAP3	NM_005119.1	TRAP150	transcripti	nucleus	regulation
GI_4827041-S	167.1	183.1	140	TNRC11	NM_005120.1	HOPA;OPA1;CAGH45;TRAP230;KIAA0192	transcripti	nucleus	regulation
GI_4827043-S	167.6	221.2	179.5	THRAP1	NM_005121.1	TRAP240;KIAA0593	transcripti	nucleus	regulation
GI_4827045-S	109	113.6	109.8	U2AF1L2	NM_005089.1	U2AF1RS2;U2AF1-RS2	pre-mRNA	ribonucleo	mRNA
GI_4827062-S	460.7	371.2	537.1	ZNF142	NM_005081.1				
GI_4827070-S	4314.3	3755.4	3218.9	ZNF9	NM_003418.1	DM2;CNBP;CNBP1;PROMM	transcripti		cholestero
GI_4885060-S	371.7	469.3	490	AKT1	NM_005163.1	PKB;RAC;PRKBA;RAC-ALPHA	receptor	nucleus	response
GI_4885062-S	5143.1	4725.9	2287.7	ALDOC	NM_005165.1	ALDC	fructose-		fructose
GI_4885070-S	219.5	258.1	236.7	PHOX2A	NM_005169.1	ARIX;FEOM2;NCAM2;PMX2A;CFEOM2	transcripti	nucleus	neurotran
GI_4885074-S	100.6	119.9	105.8	ATOH1	NM_005172.1	ATH1;HATH1;MATH-1	transcripti	nucleus	central
GI_4885078-S	6217.6	6628.9	5840.7	ATP5C1	NM_005174.1	ATP5C;ATP5CL1	hydrogen-	proton-	energy
GI_4885080-S	2361.2	3442.8	2896	ATP5G1	NM_005175.1	ATP5G	hydrogen-	proton-	proton
GI_4885096-S	144.8	168.8	150.5	BMP15	NM_005448.1	GDF9B	cytokine	extracellul	female
GI_4885100-S	159.8	181.4	166.2	CA7	NM_005182.1		carbonate		one-
GI_4885102-S	88.7	115.6	98.1	CACNA1F	NM_005183.1	CSNB2;CSNBX2	voltage-	voltage-	vision
GI_4885104-S	418.9	437.2	466.2	CHAF1B	NM_005441.1	CAF1;MPP7;CAF-	histone-	chromatin	DNA
GI_4885106-S	211.1	237.3	230.8	CHAF1A	NM_005483.1	CAF1;CAF-1;CAF1B;CAF1P150	histone-	chromatin	DNA
GI_4885108-S	337.9	396.2	348.3	CALM3	NM_005184.1	PHKD;PHKD3	calcium		
GI_4885116-S	98.2	92.9	97.7	CBL	NM_005188.1	CBL2;C-CBL;RNF55	transcripti	nucleus	oncogene
GI_4885126-S	129.2	122.5	118.9	CDX4	NM_005193.1		transcripti	nucleus	regulation
GI_4885134-S	140.9	143.8	144.5	CER1	NM_005454.1		molecular	cellular_co	biological_
GI_4885136-S	301.8	293.8	204	CHES1	NM_005197.1	FOXN3	cell cycle	nucleus	DNA
GI_4885160-S	117.3	123.1	129.4	CSN3	NM_005212.1	CSN10	molecular	extracellul	physiologi
GI_4885168-S	190.7	191.8	172.4	GJA7	NM_005497.1	CX45	connexon	gap	intercellula
GI_4885170-S	194.3	246.9	280.2	CXorf6	NM_005491.1	CG1;F18	molecular	cellular_co	biological_
GI_4885172-S	381.7	320.7	298.5	CCDC6	NM_005436.1	H4;PTC;TPC;TST1;D10S170	structural		cell growth
GI_4885174-S	123	98.2	120.8	DCC	NM_005215.1	CRC18;CRCR1	transmem	peripheral	axonogen

GI_4885192-S	325.5	355	506.5	ARID3A	NM_005224.1	DRIL1;BRIGHT;E2FBP1	transcripti	nucleus	regulation
GI_4885214-S	114.2	120	115.2	ERBB4	NM_005235.1	HER4	transmem	integral to	oncogene
GI_4885216-S	179.8	190	177.7	ERCC4	NM_005236.1	XPF;RAD1	endodeox	nucleus	nucleotide-
GI_4885224-I	3822.1	3702.9	2864.1	EWSR1	NM_005243.1	EWS	RNA		oncogene
GI_4885228-S	1070.9	1563.4	1297.2	FAT	NM_005245.1	ME5;CDHF7	tumor	integral to	embryoge
GI_4885230-S	279.1	253.3	238.5	FER	NM_005246.1	TYK3	protein-	nucleus	protein
GI_4885234-S	114.8	110.2	121.2	FGR	NM_005248.1	SRC2;c-fgr;p55c-fgr	protein-		response
GI_4885236-S	226.1	324.2	265.1	FOXC2	NM_005251.1	MFH1;MFH-1;FKHL14	transcripti	nucleus	mesoderm
GI_4885250-S	2813.2	2844.9	2617.4	GAK	NM_005255.1		protein	endoplas	regulation
GI_4885258-S	206.1	240.1	219.9	GDF8	NM_005259.1	MSTN	growth		TGFbeta
GI_4885264-S	121.4	150	113	GFER	NM_005262.1	ALR;HSS;ERV1;HPO1;HPO2;HERV1	molecular	cellular_co	spermatog
GI_4885266-S	227.6	207.1	244.2	GFI1	NM_005263.1	ZNF163	RNA	nucleus	G1/S-
GI_4885270-A	203.6	232.2	157.2	GGT1	NM_005265.1	GGT;GTG;CD224;D22S672;D22S732	gamma-	membran	amino
GI_4885278-S	107.8	125.6	119.7	GLI	NM_005269.1	GLI1	RNA	nucleus	oncogene
GI_4885280-S	2062.8	1745	2295.9	GLUD1	NM_005271.1	GDH;GLUD	glutamate	mitochond	glutamate
GI_4885286-S	509.9	495.8	456	GNG5	NM_005274.1		heterotrim	heterotrim	G-protein
GI_4885294-S	108.8	134.6	133.5	GPR12	NM_005288.1	GPCR21	G-protein	integral to	G-protein
GI_4885298-S	117.4	123.3	123	GPR15	NM_005290.1		G-protein	integral to	G-protein
GI_4885300-S	109	118.8	102.9	GPR17	NM_005291.1		chemokin	integral to	G-protein
GI_4885304-S	158.1	195.1	159.4	GPR20	NM_005293.1		G-protein	integral to	G-protein
GI_4885306-S	112.7	137.5	117.5	GPR21	NM_005294.1		G-protein	integral to	G-protein
GI_4885308-S	108	114	113	GPR22	NM_005295.1		G-protein	integral to	G-protein
GI_4885310-S	127.9	133.5	131	GPR23	NM_005296.1	P2Y9;P2Y5-LIKE	G-protein	integral to	G-protein
GI_4885316-S	102.3	100.9	99.3	GPR31	NM_005299.1		G-protein	integral to	G-protein
GI_4885326-S	109.7	122	109.1	GPR40	NM_005303.1		G-protein	integral to	G-protein
GI_4885330-S	100	120.7	104.3	GPR42	NM_005305.1		G-protein	integral to	G-protein
GI_4885332-S	122.4	131.3	119.4	GPR43	NM_005306.1	FFA2R	G-protein	integral to	G-protein
GI_4885334-S	99.5	108.4	108.8	GPR4	NM_005282.1		G-protein	integral to	G-protein
GI_4885338-S	498.5	568.7	482.2	XCR1	NM_005283.1	GPR5;CCXCR1	chemokin	integral to	cytosolic
GI_4885342-S	227.7	281.3	247.8	GPR7	NM_005285.1		opioid	integral to	G-protein
GI_4885346-A	175.7	221.4	207.9	GRK4	NM_005307.1	GPRK4;GPRK2L	G-protein-		regulation
GI_4885348-S	504.9	513.3	671.4	GRK5	NM_005308.1	GPRK5	G-protein-	soluble	regulation
GI_4885350-S	84.5	85.3	86	GPT	NM_005309.1	AAT1;ALT1;GPT1	transamin	soluble	amino
GI_4885354-S	156.8	165.4	153.7	GRB7	NM_005310.1		SH3/SH2		EGF
GI_4885360-S	160.6	196.3	180.2	GRPR	NM_005314.1		peptide	integral to	G-protein
GI_4885362-S	78.6	81.2	85.2	GSCL	NM_005315.1		DNA	nucleus	embryoge
GI_4885386-S	684.1	707	577	HADHSC	NM_005327.1	SCHAD	3-	mitochond	
GI_4885390-S	959.5	1077.3	151.9	HAS2	NM_005328.1		transferas	integral to	
GI_4885400-S	1300.5	1387.6	1361.4	HCCS	NM_005333.1	CCHL	holocytoch	mitochond	electron
GI_4885402-S	507	622.8	573.5	HCFC1	NM_005334.1	HCF1;HFC1;HCF-1	transcripti	nucleus	transcripti
GI_4885406-S	91.5	95.4	93.4	HCN4	NM_005477.1		cation	integral to	cation
GI_4885418-S	821.7	673.7	573	HKR3	NM_005341.1		transcripti	nucleus	regulation
GI_4885420-S	688.4	2314.4	1135.2	HMGB3	NM_005342.1	HMG4;HMG2A	DNA	chromatin	developm
GI_4885424-A	314	361	470.7	HRAS	NM_005343.1	HRAS1;RASH1	GTPase	peripheral	chemotaxi

GI_4885440-S	239.6	264.6	238.2	SLC17A4	NM_005495.1	KAIA2138	sodium:ph	membran	sodium
GI_4885454-S	2185.9	2365.5	2172.6	LNK	NM_005475.1				intracellula
GI_4885476-S	95.2	123.2	101.9	MB	NM_005368.1	PVALB;MGC13548	electron		oxygen
GI_4885486-S	759.6	1165.2	1118.5	MLF2	NM_005439.1		molecular	nucleus	biological_
GI_4885488-S	137.4	143.8	131.4	MOS	NM_005372.1	MSV	protein		protein
GI_4885490-S	303.9	393.4	336.2	MPL	NM_005373.1	MPLV;TPOR;C-MPL;CD110	transmem	integral to	cell
GI_4885496-S	122.6	121.4	107.5	MYB	NM_005375.1				
GI_4885506-S	129.7	130.5	119.1	NAALADL1	NM_005468.1	I100;NAALADASEL	aminopept	integral to	proteolysis
GI_4885510-S	1172.6	1119.2	1073.1	NCL	NM_005381.1	C23	RNA	nucleolus	
GI_4885512-S	204.4	282.9	251.5	NEF3	NM_005382.1	NFM;NEFM;NF-M	structural	neurofilam	
GI_4885514-S	138.8	153.4	122.7	NEU2	NM_005383.1	SIAL2	catalytic	cytoplasm	carbohydr
GI_4885516-S	1559.7	1888.1	1334.7	NFIL3	NM_005384.1	E4BP4;IL3BP1;NFIL3A;NF-IL3A	transcripti	nucleus	transcripti
GI_4885524-S	117.2	130.8	115.9	SH2D3A	NM_005490.1	NSP1	SH3/SH2		JNK
GI_4885526-A	104.8	105.7	103.6	SH2D3C	NM_005489.1	CHAT;NSP3	SH3/SH2		JNK
GI_4885538-S	2260.1	2355.9	2503.6	PCMT1	NM_005389.1		protein-L-	endoplas	protein
GI_4885544-S	221	332.7	301.7	PDK3	NM_005391.1		[pyruvate	mitochond	glucose
GI_4885552-S	313.3	261.7	255.5	PMS2L9	NM_005395.1	PMSR3	nucleic	intracellula	regulation
GI_4885562-S	119.8	125.1	104.4	PRKCE	NM_005400.1	PKCE	protein	peripheral	induction
GI_4885578-S	176.1	196.3	182.7	RQCD1	NM_005444.1	RCD1;CNOT9;RCD1+			sex
GI_4885582-S	151.5	144.6	150	ROCK1	NM_005406.1	P160ROCK	protein	intracellula	actin
GI_4885584-S	6030.4	5346.9	6269.2	SAE1	NM_005500.1	AOS1;SUA1;HSPC140	ubiquitin-		small
GI_4885590-S	90.1	100.1	92	SEPP1	NM_005410.1	SeP	selenium		response
GI_4885596-S	150.7	193	167.9	SIX3	NM_005413.1	HPE2	transcripti	nucleus	brain
GI_4885602-S	161.8	138.9	127.3	SNCAIP	NM_005460.1	SYPH1	protein	kinesin	pathogene
GI_4885606-S	126.5	157.2	137.5	SPRR3	NM_005416.1		structural		
GI_4885610-S	92.2	91.8	86.3	ABI1	NM_005470.1	E3B1;NAP1;ABI-1	cytoskelet	cytosol	transmem
GI_4885618-S	110	116.4	102.4	TAL2	NM_005421.1		protein		oncogene
GI_4885626-S	102.6	96.9	106.9	TECTA	NM_005422.1	DFNA8;DFNA12;DFNB21	extracellul	extracellul	hearing
GI_4885636-S	1106.4	1155	1538.7	TOM1	NM_005488.1			endosome	nonselecti
GI_4885638-S	337.4	394.9	306.6	TOM1L1	NM_005486.1	SRCASM	protein	endosome	nonselecti
GI_4885642-S	665.8	734.5	711.7	TP53BP2	NM_005426.1	53BP2;ASPP2;PPP1R13A	SH3/SH2	cytoplasm	regulation
GI_4885644-S	477.2	608.4	556.1	TP73	NM_005427.1	P73	transcripti	nucleus	DNA
GI_4885648-S	1037.6	941.5	901.8	UBA2	NM_005499.1	SAE2	ubiquitin-		small
GI_4885656-S	243.2	270.1	245.6	XRCC2	NM_005431.1		DNA	nucleus	meiosis
GI_4895106-S	263.8	296.2	272.4	AVPR2	NM_000054.2	DI1;DIR;NDI;V2R;ADHR	vasopress	endosome	hemostasi
GI_4996892-S	206	220.7	208.3	HSPB1	NM_001540.2	HSP27;HSP28;Hsp25;HS.76067	heat	cytoplasm	regulation
GI_5016087-S	117	114.4	112.6	ACTA1	NM_001100.2	ACTA;ASMA;NEM1;NEM2	structural	actin	muscle
GI_5016088-S	38652.8	45115	41703	ACTB	NM_001101.2		structural	actin	cell
GI_5016089-S	83.5	93.4	90.3	NR0B1	NM_000475.2	AHC;AHX;GTD;HHG;AHCH;DAX1;NROB1	ligand-	nucleus	sex
GI_5016091-S	2338.3	3116.2	2737.4	AHR	NM_001621.2		ligand-	nucleus	cell cycle
GI_5016092-S	1253.9	1199.9	1210.3	DLD	NM_000108.2	E3;LAD;DLDH;PHE3	dihydrolip	mitochond	energy
GI_5016093-S	88.8	113.3	86	FMOD	NM_002023.2	SLRR2E	protein	extracellul	TGFbeta
GI_5031560-S	222.1	265.8	213.1	GPA33	NM_005814.1	A33	receptor	proteoglyc	
GI_5031564-S	112.6	112.6	105.2	C4orf6	NM_005750.1	aC1			neurogene

GI_5031570-S	705.2	1091.6	966.6	ACTR2	NM_005722.1	ARP2	structural	Arp2/3	cell
GI_5031586-S	233.8	235.9	230.8	APC2	NM_005883.1	APCL	beta-	extracellul	signal
GI_5031602-S	382.4	266.3	261.4	ARL4	NM_005738.1		small	nucleus	small
GI_5031608-S	613.6	811.8	667.2	BCKDK	NM_005881.1			alpha-	
GI_5031614-S	127.8	125.8	116.5	ZNF255	NM_005774.1				
GI_5031632-S	348.9	419.7	281	FARP1	NM_005766.1	CDEP;p63RhoGEF	Rho	cytoskelet	
GI_5031634-S	6477.4	10471	9569.9	CFL1	NM_005507.1	CFL	actin	cytoskelet	Rho
GI_5031636-S	155.5	178.1	157.4	CLECSF1	NM_005752.1		lectin [goid	extracellul	skeletal
GI_5031638-S	2450.7	2781.9	2373.7	CNIH	NM_005776.1	CNIL;TGAM77		integral to	signal
GI_5031644-S	1389.7	2600	2664.3	COX17	NM_005694.1		intracellula	mitochond	copper ion
GI_5031650-S	434.8	398.3	405.6	D8S2298E	NM_005671.1	REP8			fertilization
GI_5031652-S	291.3	342.5	305.1	BCAS2	NM_005872.1	DAM1	pre-mRNA	spliceoso	RNA
GI_5031654-S	86.7	90.7	92.2	DSCR4	NM_005867.1	DCRB;DSCRB	molecular	cellular_co	biological_
GI_5031666-S	803.6	897.4	728.3	DNAL4	NM_005740.1	dJ327J16	microtubul	dynein	microtubul
GI_5031672-S	83.8	86.9	82.3	IGSF6	NM_005849.1	DORA	transmem	integral to	cell
GI_5031694-S	92	89.5	83.8	HFL3	NM_005666.1	FHR2		extracellul	
GI_5031696-S	180.5	177.6	121.9	ATP8B1	NM_005603.1	BRIC;FIC1;PFIC;ATPIC;PFIC1	ATP	integral to	bile acid
GI_5031700-S	277.9	396.1	592.6	FSTL3	NM_005860.1	FLRG;FSRP		extracellul	oncogene
GI_5031704-S	300.9	236.3	278.5	RGS19	NM_005873.1	GAIP;RGSGAIP	GTPase	heterotrim	small
GI_5031706-S	103.4	114.8	102.6	GARP	NM_005512.1	D11S833E		integral to	
GI_5031710-S	5451	3687.8	3807.1	GC20	NM_005875.1		translation		regulation
GI_5031714-S	1863.9	1899.5	2022.7	RGS19IP1	NM_005716.1	NIP;GIPC;IIP-1;TIP-	protein	soluble	G-protein
GI_5031716-I	310.9	400.5	357.8	COL4A3BP	NM_005713.1	GPBP;CERTL;STARD11	protein	kinesin	protein
GI_5031720-S	113.9	124.2	107.3	GPR52	NM_005684.1		G-protein	integral to	G-protein
GI_5031726-S	377	399.1	436.3	GTF2E1	NM_005513.1	FE;TFIIE-A			
GI_5031728-S	1011.3	1049.1	1056.2	HAN11	NM_005828.1	AN11		cytoplasm	signal
GI_5031732-S	136.8	149.2	138.9	GPR64	NM_005756.1	HE6;TM7LN2	G-protein	integral to	G-protein
GI_5031734-S	193	221.2	171.9	CHST4	NM_005769.1	LSST	sulfotransf		protein
GI_5031738-S	133.7	152.8	139.8	HHLA1	NM_005712.1	PLA2L			
GI_5031748-S	5439.8	6051.9	5511	HMGN2	NM_005517.1	HMG17;MGC5629			
GI_5031750-S	192	229.2	203.8	HMGCS2	NM_005518.1		hydroxym	mitochond	cholestero
GI_5031752-S	1165.3	1130.6	1074	HNRPH1	NM_005520.1	HNRPH;hnRNPH	poly(U)	ribonucleo	RNA
GI_5031766-S	392.7	304.5	345.5	HSF1	NM_005526.1	HSTF1	transcripti	nucleus	heat
GI_5031770-S	345.7	387.1	366	DNAJC4	NM_005528.1	HSPF2;MCG18;DANJC4	heat	integral to	protein
GI_5031774-S	277.7	272.5	261.7	CTDSPL	NM_005808.1	SCP3;HYA22;C3orf8	molecular	nucleus	biological_
GI_5031778-S	1947.1	1598.7	1274.8	IFI16	NM_005531.1	IFNGIP1			
GI_5031782-S	2551.9	2915.5	2781.3	IFNGR2	NM_005534.1	AF-1;IFGR2;IFNGT1	interferon-	integral to	resistance
GI_5031784-I	198.8	231.5	203.8	IL12RB1	NM_005535.1	IL12RB;MGC34454;IL-12R-BETA1	interleukin	integral to	positive
GI_5031804-S	952	662.6	506.8	IRS1	NM_005544.1	HIRS-1	transmem	cytoplasm	signal
GI_5031814-S	1764	1915	1558.6	KARS	NM_005548.1	KIAA0070	lysine-	soluble	protein
GI_5031816-S	1153.2	923.5	919.7	KATNB1	NM_005886.1	KAT	microtubul	centrosom	microtubul
GI_5031846-I	1295.3	1492	1274.2	LAMC2	NM_005562.1	EBR2;BM600;EBR2A;LAMB2T;LAMNB2;KAL	heparin	laminin-5	epidermal
GI_5031856-S	14526.2	19711	17877	LDHA	NM_005566.1	LDH1	L-lactate	cytosol	glycolysis
GI_5031858-S	834.8	572.2	462	DLEU1	NM_005887.1	BCMS;LEU1;XTP6	tumor		cell growth

GI_5031864-S	379.2	415.9	393.1	LHFP	NM_005780.1		DNA		
GI_5031880-S	154.7	279.2	265	LNPEP	NM_005575.1	CAP;IRAP;PLAP	metallope	integral to	pregnancy
GI_5031882-S	724.2	1081.2	568.7	LOXL1	NM_005576.1	LOXL	electron	extracellul	protein
GI_5031884-S	93.3	108.2	110.8	LPA	NM_005577.1	LP;AK38	apolipopro		pathogene
GI_5031886-S	467.9	481.5	421.4	LPP	NM_005578.1		molecular	cellular_co	biological_
GI_5031892-S	350.8	524.7	251.8	NR1H3	NM_005693.1	LXRA;LXR-a;RLD-1	ligand-	nucleus	regulation
GI_5031894-S	152.3	193.9	153.5	LY64	NM_005582.1	CD180;RP105	protein	integral to	immune
GI_5031906-S	196.5	197.6	190	MEF2A	NM_005587.1	ADCAD1;RSRFC4;RSRFC9	transcripti	nucleus	muscle
GI_5031908-S	103.6	112.8	109.6	MEP1A	NM_005588.1	PPHA	meprin A	microvillus	digestion
GI_5031910-S	94.7	99	93.3	LILRB2	NM_005874.1	ILT4;LIR2;CD85D;LIR-2;MIR10;MIR-10	defense/i	membran	cell
GI_5031912-S	103.2	126.5	112.2	MLANA	NM_005511.1	MART1;MART-1	tumor	integral to	
GI_5031918-S	413.1	384.4	499.3	MPHOSPH6	NM_005792.1	MPP;MPP6;MPP-6	cell cycle	nucleus	M phase
GI_5031924-S	111.8	124.8	109.9	PRG4	NM_005807.1	MSF;SZP;CACP;JCAP	proteoglyc	extracellul	cell
GI_5031926-S	194.6	224.9	218	MUSK	NM_005592.1		transmem	microtubul	transmem
GI_5031928-S	152.7	182.6	152.7	MYF5	NM_005593.1		RNA	nucleus	myogenes
GI_5031940-S	924.3	571.6	293.4	NFIB	NM_005596.1	NFIB2;NFIB3;NFI-RED	transcripti	nucleus	DNA
GI_5031944-S	119.8	109.2	124.4	NHLH2	NM_005599.1	HEN2;NSCL2	DNA		central
GI_5031946-S	1968.5	1836	1751.3	NIT1	NM_005600.1		nitrilase		nitrogen
GI_5031954-S	109.3	120.9	117.7	SLC17A2	NM_005835.1	NPT3	sodium:ph	membran	sodium
GI_5031956-A	966.1	826.1	855.7	PQBP1	NM_005710.1	SHS;MRX55;NPW38	transcripti	nucleus	regulation
GI_5031958-S	1068.8	887.2	704.3	SDCCAG10	NM_005869.1	NY-CO-10	cyclophilin		protein
GI_5031962-S	1349.4	1455	2120.5	STUB1	NM_005861.1	CHIP;HSPABP2;NY-CO-7;SDCCAG7		cytoplasm	protein
GI_5031970-S	1801	4482.3	495.8	LRRC17	NM_005824.1	P37NB			oncogene
GI_5031976-I	1630.2	1187.3	1284.4	PBEF1	NM_005746.1	PBEF	cytokine		positive
GI_5031982-S	85.5	90.7	80.2	POU3F2	NM_005604.1	BRN2;OCT7;OTF7;POUF3	transcripti	nucleus	regulation
GI_5031984-S	1879.2	1817.3	1764.9	NUTF2	NM_005796.1	NTF2;PP15	transporte	nuclear	nucleocyto
GI_5032004-S	190.5	237.9	202.5	PTPRCAP	NM_005608.1	LPAP;CD45-AP	antimicrob	integral to	
GI_5032008-S	185	197.9	185.4	PYGM	NM_005609.1		glycogen		glycogen
GI_5032012-S	425.3	880.5	740	KIF20A	NM_005733.1	RAB6KIFL	vesicle	Golgi	vesicle-
GI_5032018-S	107.1	137.4	375.2	RAMP1	NM_005855.1		protein	integral to	regulation
GI_5032020-S	159	203.5	169	RAMP2	NM_005854.1		receptor	coated pit	protein
GI_5032022-S	125.3	141.9	123.3	RAMP3	NM_005856.1		receptor	coated	protein
GI_5032026-S	732.9	911.5	804.6	RBBP4	NM_005610.1	RBAP48		nucleus	negative
GI_5032030-S	1317.9	1686.4	1387.3	RBM5	NM_005778.1	G15;RMB5;LUCA15	RNA	nucleus	RNA
GI_5032032-S	409.3	487.1	322.9	RBM6	NM_005777.1	3G2;g16;DEF3;DEF-3;NY-LU-12	RNA	nucleus	RNA
GI_5032046-S	1273.3	1400.8	1571.1	POP7	NM_005837.1	RPP2;RPP20	ribonuclea	nucleolar	tRNA
GI_5032056-S	3426.7	4349.3	3817.9	S100A11	NM_005620.1	MLN70;S100C	calcium	cytoplasm	negative
GI_5032058-S	234.2	289.1	257.5	S100A12	NM_005621.1	p6;CGRP;MRP6;CAAF1;ENRAGE	calcium	insoluble	inflammat
GI_5032062-S	260.6	238.1	268.2	STAG1	NM_005862.1	SA-1	DNA	nucleus	chromoso
GI_5032082-S	1895.3	1720.3	1925	SDCBP	NM_005625.1	ST1;SYCL;MDA-9;TACIP18;SYNTENIN	cytoskelet	secretory	protein-
GI_5032092-S	11097.7	6362.7	3469.6	SLC1A5	NM_005628.1	R16;AAAT;ATBO;M7V1;RDRC;ASCT2;M7VS	neutral	membran	neutral
GI_5032094-S	149.1	295	136.5	SLCO2A1	NM_005630.1	PGT;OATP2A1;SLC21A2	lipid	membran	lipid
GI_5032096-S	355	392.8	262.4	SLC6A8	NM_005629.1	CT1;CRTR	creatine:s	integral to	small
GI_5032100-S	438.9	478.8	605.7	ABCC5	NM_005688.1	MRP5;SMRP;ABC33;MOATC;MOAT-	organic	membran	small

GI_5032104-S	113.9	122.5	121.4	SOLH	NM_005632.1		calpain	intracellula	proteolysis
GI_5032124-S	439	546.3	281.6	SS18	NM_005637.1	SYT;SSXT	transcripti	nucleus	cell growth
GI_5032138-S	106.1	117.3	112.3	SYT1	NM_005639.1	P65;SYT;SVP65	phospholi	secretory	synaptic
GI_5032164-S	194.4	268	128.5	TDO2	NM_005651.1	TDO;TPH2;TRPO	tryptophan		neurotran
GI_5032176-S	522.2	594.2	474.6	TIEG	NM_005655.1	EGRA;KLF10;TIEG1	transcripti	nucleus	negative
GI_5032180-S	642.5	729.1	806.7	TIMM17B	NM_005834.1	JM3;TIM17B;DXS9822	protein	mitochond	mitochond
GI_5032188-S	1000	1418.4	1262.1	TP53BP1	NM_005657.1	p202;53BP1	P-element	nucleoplas	positive
GI_5032210-S	317.7	393.7	346.1	SLC35A2	NM_005660.1	UGT;UGAT;UGT1;UGT2;UGTL;UGALT	UDP-	Golgi	UDP-
GI_5032212-S	1414.6	1871.8	1776.6	SLC35B1	NM_005827.1	UGTREL1	UDP-	microsom	small
GI_5032214-S	281.8	342.3	234.6	UK114	NM_005836.1	PSP;P14.5		cytoplasm	regulation
GI_5032218-S	602.7	557.9	468.5	UST	NM_005715.1		sulfotransf	integral to	protein
GI_5032222-S	120.6	122.6	116	PLXNC1	NM_005761.1	VESPR;PLXN-C1	receptor	integral to	cell
GI_5032234-S	79.7	143.1	88.4	DSCR1L1	NM_005822.1	CSP2;RCN2;MCIP2;hRCN2;ZAKI-4			
GI_5032242-S	96.6	96.2	93.3	MKRN3	NM_005664.1	D15S9;RNF63;ZFP127;ZNF127	ribonucleo	ribonucleo	
GI_5032244-S	262.1	188.5	299.8	ZNF239	NM_005674.1	MOK2;HOK-2	RNA	nucleolus	transcripti
GI_5032280-I	111.9	122.8	116.5	DMD	NM_000109.2	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5032282-I	126.4	148.2	136.9	DMD	NM_004006.1	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5032290-I	79.3	84.3	82.7	DMD	NM_004012.1	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5032294-I	121	133.1	121.6	DMD	NM_004014.1	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5032304-A	83.1	92	84.4	DMD	NM_004019.1	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5032304-I	190.1	220.2	206.8	DMD	NM_004019.1	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5032314-A	101.9	119.2	111.2	DMD	NM_004010.1	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5032314-I	109.7	108.5	102.1	DMD	NM_004010.1	BMD;DXS142;DXS164;DXS206;DXS230;DX	structural	peripheral	muscle
GI_5123452-S	180.4	193.6	176.4	GDF5	NM_000557.2	LAP4;CDMP1	protein		TGFbeta
GI_51470882-S	106.9	121.2	113	LOC283247	XM_208058.5				
GI_5174384-S	275.8	266.6	231.5	ALKBH	NM_006020.1	ABH;alkB;hABH			DNA
GI_5174386-S	174.2	198.2	168.6	PROM1	NM_006017.1	AC133;CD133;PROML1		integral to	vision
GI_5174388-S	688.1	729.1	675.3	ACAT2	NM_005891.1		transferas	cytoplasm	lipid
GI_5174392-S	2785.6	6272.5	4954.2	ARMET	NM_006010.1	ARP			oncogene
GI_5174402-S	193.5	214.9	217.3	CACNA2D2	NM_006030.1	CACNA2D;gene 26;KIAA0558		membran	
GI_5174408-S	658.8	778	891.2	CD2BP2	NM_006110.1			cytoplasm	antimicrob
GI_5174410-S	119.6	106.7	97.6	CD5L	NM_005894.1	SP-ALPHA	protein-	membran	cellular
GI_5174418-S	1544.3	1677.7	1508.5	CLPP	NM_006012.1		peptidase	mitochond	proteolysis
GI_5174422-S	2605.7	3111.9	2644.7	C10orf7	NM_006023.1	D123			cell cycle
GI_5174424-S	751.6	750.8	834.5	DSCR3	NM_006052.1	DCRA;DSCRA			
GI_5174428-S	1015.2	1515.7	1321.3	ACAA2	NM_006111.1	DSAEC	3-oxoacyl-	mitochond	fatty acid
GI_5174444-S	1759.5	2098	2043.5	LANCL1	NM_006055.1	p40;GPR69A	G-protein	integral to	G-protein
GI_5174456-S	473.5	453	544.7	KNTC2	NM_006101.1	HEC;HEC1		centromer	mitotic
GI_5174460-S	140.9	184.4	161.2	HM74	NM_006018.1	PUMAG	G-protein	integral to	G-protein
GI_5174462-S	133.5	136.6	120.9	HS3ST2	NM_006043.1	30ST2;3OST2	sulfotransf	integral to	
GI_5174464-S	5606.3	3081.8	3887.1	HS3ST3A1	NM_006042.1	30ST3A1;3OST3A1	sulfotransf	integral to	
GI_5174466-S	104.8	112	104.5	HS3ST3B1	NM_006041.1	30ST3B1;3OST3B1	heparin-	integral to	heparan
GI_5174472-S	277.6	333.3	285.9	IPP	NM_005897.1		actin	actin	
GI_5174476-S	12652.2	14277	11581	K-ALPHA-1	NM_006082.1		structural	microtubul	microtubul

GI_5174484-S	1095	1206.1	675.2	MRC2	NM_006039.1	UPARAP;ENDO180;KIAA0709	sugar		transport
GI_5174494-S	149.2	193.7	178.1	DLEU2	NM_006021.1	LEU2;BCMSUN	tumor		cell growth
GI_5174496-S	296.8	1393.8	746.7	LIPG	NM_006033.1	EL;EDL	phospholi		lipid
GI_5174508-S	976.3	744.6	852.9	MADH1	NM_005900.1	BSP1;JV4-	transcripti	integral to	transformi
GI_5174516-S	541.9	555.3	588.5	MADH7	NM_005904.1	MADH8;SMAD7	inhibitory	intracellula	TGFbeta
GI_5174532-S	84.7	85.2	76.4	MC4R	NM_005912.1		melanocor	integral to	physiologi
GI_5174534-S	122.9	130.3	113.8	MC5R	NM_005913.1		melanocor	integral to	G-protein
GI_5174542-S	144.2	211.7	187	MEF2B	NM_005919.1	RSRFR2	transcripti	nucleus	muscle
GI_5174550-S	111	137.6	117.8	MEP1B	NM_005925.1		zinc ion	extracellul	digestion
GI_5174552-S	906.7	935.4	817.2	MFAP1	NM_005926.1		extracellul	extracellul	
GI_5174556-S	4896.5	4557	2799.7	MFGE8	NM_005928.1	BA46;EDIL1;OAcGD3S;HsT19888	milk	lipid	cell
GI_5174566-S	495.8	585.4	670.1	MIPEP	NM_005932.1	MIP;HMIP	metalloen	mitochond	mitochond
GI_5174568-S	143.7	180.5	158.7	MLL	NM_005933.1	HRX;TRX1;ALL-1;CXXC7;HTRX1	RNA	nucleus	oncogene
GI_5174572-S	611.1	674.7	451.9	MLLT2	NM_005935.1	AF4;AF-4	transcripti	nucleus	oncogene
GI_5174574-S	171.1	193.7	182.8	MLLT4	NM_005936.1	AF6;AF-6;AFADIN	protein C-	intercellula	cell
GI_5174576-S	149	191.8	173.1	MLLT6	NM_005937.1	AF17			regulation
GI_5174578-S	140.7	142.9	149.5	MLLT7	NM_005938.1	AFX;AFX1;FOXO4	transcripti	nucleus	cell cycle
GI_5174588-S	344.7	425.2	367.4	MTF1	NM_005955.1	MTF-1	DNA	nucleus	response
GI_5174616-S	251.8	268.1	229.2	CARD4	NM_006092.1	NOD1	caspase	intracellula	signal
GI_5174618-S	87.3	104.5	106.8	OA48-18	NM_006107.1				response
GI_5174632-S	116.8	113.5	95.6	PKDREJ	NM_006071.1		cation	membran	acrosome
GI_5174662-S	109.7	95.2	98.2	S100P	NM_005980.1		protein		
GI_5174668-S	178	210.9	189.2	SCML2	NM_006089.1		DNA		embryoge
GI_5174672-S	217.1	170.4	169.8	SEMA3A	NM_006080.1	SemD;SEMA1;SEMAD;SEMAL;coll-1;Hsema-		extracellul	developm
GI_5174674-S	91.9	91.5	99.4	CRISP3	NM_006061.1	Aeg2;CRS3;SGP28;CRISP-3;dJ442L6.3	molecular	intracellula	biological_
GI_5174678-S	625.3	782.6	765.9	SIRPB1	NM_006065.1	SIRP-BETA-1		integral to	cell
GI_5174680-S	129.2	151.6	129.3	SIX1	NM_005982.1		transcripti	nucleus	muscle
GI_5174688-S	272.5	264.1	257.1	SNAPC5	NM_006049.1	SNAP19	transcripti	nucleus	transcripti
GI_5174692-S	343	448.6	415.7	SPRR2A	NM_005988.1		structural	cytoplasm	keratinocy
GI_5174694-S	101.9	116.9	95.7	AKR1D1	NM_005989.1	SRD5B1;3o5bred	electron		digestion
GI_5174700-S	934.3	1000.3	694.8	STK10	NM_005990.1	LOK;PRO2729	protein		protein
GI_5174702-I	510.5	458.3	484.4	MAP3K7IP1	NM_006116.1	TAB1	TGFbeta		activation
GI_5174710-I	111.2	118.6	107.2	TBX1	NM_005992.1	DGS;TGA;CAFS;CTHM;DGCR;DORV;VCFS;	RNA	nucleus	heart
GI_5174714-S	3358	2930.2	2947.7	TCFL1	NM_005997.1	YL1;YL-1	RNA	nucleus	negative
GI_5174722-S	727.8	866.7	918.9	TOMM40	NM_006114.1	TOM40;PEREC1;C19orf1;PER-	protein	mitochond	anion
GI_5174724-S	127.3	136.8	124.4	TRDN	NM_006073.1	TDN;TRISK;TRISK51		sarcoplas	muscle
GI_5174736-S	1650.6	2501.4	2193.2	TUBB4	NM_006086.1		structural	cytoskelet	microtubul
GI_5174742-S	5100.6	5567.2	5410.6	UQCRFS1	NM_006003.1	RIS1	ubiquinol-	ubiquinol-	electron
GI_5174744-S	4145.8	4513.1	3468.6	UQCRH	NM_006004.1		ubiquinol-	mitochond	oxidative
GI_5174754-S	2690	3604.8	2416.7	ZNF216	NM_006007.1	ZA20D2	zinc ion	cellular_co	biological_
GI_5174761-S	120.1	130.8	137.6	MT3	NM_005954.1	GIF;GIFB;GRIF	heavy	synaptic	metal ion
GI_5174773-S	109.3	122.7	96.1	APOA4	NM_000482.2		apolipopro		lipid
GI_5174774-S	153.4	198.8	162.1	APOC1	NM_001645.2		lipid	extracellul	lipid
GI_5209326-S	566.8	655.3	504.6	AMD1	NM_001634.3	AMD;ADOMETDC	lyase	cellular_co	spermine

GI_5231299-S	110	112.4	106.4	ELAVL3	NM_001420.2	HUC;PLE21	mRNA 3'		neurogene
GI_5292160-A	2134.4	2505.4	2265.1	PSMD4	NM_002810.1	AF;ASF;S5A;AF-1;MCB1;Rpn10;pUB-R5		26S	
GI_5360207-A	1151.6	1347.5	1191.2	IDS	NM_006123.1	MPS2;SIDS	iduronate-	lysosome	
GI_5360207-I	207.3	247	223.6	IDS	NM_006123.1	MPS2;SIDS	iduronate-	lysosome	
GI_5360209-S	730	1084.2	875.6	PVRL2	NM_002856.1	HVEB;PRR2;CD112;PVRR2	coreceptor	plasma	virulence
GI_5360211-I	99.7	100.2	99.8	GAS7	NM_005890.1	MGC1348;KIAA0394	transcripti	kinesin	cell cycle
GI_5360213-S	88.4	90.6	94.6	GPC3	NM_004484.2	SGB;DGSX;SDYS;SGBS;SGBS1	glypican	proteoglyc	cell growth
GI_5360215-I	337.5	699.6	603.8	IDS	NM_000202.2	MPS2;SIDS	iduronate-	lysosome	
GI_5453548-S	3101.3	3171.4	2386.3	PRDX4	NM_006406.1	AOE37-2	thioredoxi		I-kappaB
GI_5453556-S	1967.4	1912	1699.1	ARIH2	NM_006321.1	ARI2;TRIAD1	zinc ion	kinesin	developm
GI_5453558-S	2254	2629.9	2515.5	ATP5H	NM_006356.1	ATPQ;ATP5JD	hydrogen	mitochond	proton
GI_5453564-A	287.9	287.1	311.7	BAIAP2	NM_006340.1	BAP2;IRSP53	protein C-	cytoplasm	insulin
GI_5453564-I	1039.1	1050.4	1004.7	BAIAP2	NM_006340.1	BAP2;IRSP53	protein C-	cytoplasm	insulin
GI_5453566-S	1537.2	1581.3	1507.2	CFDP1	NM_006324.1	p97;BCNT;CP27			
GI_5453572-S	134.1	165.4	222.5	ARFGEF2	NM_006420.1	BIG2;dJ1164I10.1	guanyl-		exocytosis
GI_5453576-S	88.4	98.5	88.7	CXCL13	NM_006419.1	BLC;BCA1;ANGIE;BCA-	chemokin	soluble	cytosolic
GI_5453580-S	89.9	92.1	92.6	CDRT1	NM_006382.1	HREP;SM25H2			
GI_5453590-S	372.7	305.3	408.3	SMC2L1	NM_006444.1	CAPE;CAP-E;hCAP-E	ATP	membran	mitotic
GI_5453596-S	303	387.8	354	CAPZA1	NM_006135.1	CAPZ;CAZ1;CAPPA1	actin	F-actin	cell
GI_5453602-S	7424.4	9142.5	8533	CCT2	NM_006431.1	CCTB	chaperone	cytoplasm	regulation
GI_5453606-S	8992.1	8852.5	7939.7	CCT7	NM_006429.1	Ccth;Nip7-1	chaperone	cytoplasm	protein
GI_5453610-S	108	113.8	110.1	CD28	NM_006139.1	Tp44	defense/i	integral to	viral
GI_5453622-S	272.5	292	265.7	CNK1	NM_006314.1	CNK;KSR	protein	intercellula	transmem
GI_5453624-S	202.7	252.9	211.6	CROC4	NM_006365.1				
GI_5453630-S	5446.9	6704.6	6892.9	DDT	NM_001355.2		dopachro		melanin
GI_5453631-S	1307.9	1330	1650	SPAG5	NM_006461.1	MAP126;DEEPEST;hMAP126			
GI_5453637-S	579.1	398.9	367.4	ARID3B	NM_006465.1	BDP;DRIL2	DNA	nucleus	biological_
GI_5453639-S	3907.9	4653.1	3872.5	SHFM1	NM_006304.1	ECD;DSS1;SEM1;SHFD1;SHSF1;Shfdg1	protein	cellular_co	cell cycle
GI_5453661-S	354.6	503.7	458	GCS1	NM_006302.1		glucosidas	integral to	N-linked
GI_5453665-S	67.1	67.3	68.7	GPR19	NM_006143.1		G-protein	integral to	G-protein
GI_5453667-S	1447.2	1581.9	1779.1	APG7L	NM_006395.1	GSA7	ubiquitin	cytoplasm	membran
GI_5453673-S	93	92.4	91.6	GYG2	NM_003918.1	GN2;GN-2	glycogenin	soluble	glycogen
GI_5453681-S	1020.9	1469.3	1209.1	HIS1	NM_006460.1	CLP1;MAQ1;HEXIM1	DNA	nucleus	regulation
GI_5453683-A	97.8	98.6	100.4	CLECSF13	NM_006344.1	HML;HML2	lectin [goid	plasma	heterophili
GI_5453687-S	97.3	116.2	100.5	HSPB3	NM_006308.1	HSPL27	heat		
GI_5453689-S	908.2	913.1	1046.9	DNAJB1	NM_006145.1	HSPF1	heat		heat
GI_5453709-S	5318.5	4870.8	4472.8	LASP1	NM_006148.1	MLN50	SH3/SH2		
GI_5453713-S	993.4	1323.5	1014.6	LIM	NM_006457.1	ENH	protein		signal
GI_5453725-I	98	104.1	96.9	LRRFIP2	NM_006309.1	HUFI-2;FLJ20248			
GI_5453735-S	104.6	106.3	248.1	MAF	NM_005360.2		RNA	chromatin	transcripti
GI_5453737-S	286.2	144.6	112.7	MERTK	NM_006343.1	mer;C-MER	transmem	soluble	protein
GI_5453745-S	538.5	622.1	588.9	MTHFS	NM_006441.1	HsT19268			
GI_5453751-S	96	108.5	98.3	SLC34A2	NM_006424.1	NPTIIb;NAPI-3B	sodium-	membran	phosphate
GI_5453755-S	178.3	223.7	198.4	NCYM	NM_006316.1				

GI_5453757-S	122.2	139.7	129.2	NEBL	NM_006393.1		regulation	actin	muscle
GI_5453759-S	8234.2	9813.8	8869.6	NEDD8	NM_006156.1	Nedd-8	ubiquitin	nucleus	proteolysis
GI_5453761-S	274.7	316.6	386.7	NEFL	NM_006158.1	NFL;NF68;CMT1F;CMT2E	structural	neurofilam	
GI_5453765-S	162	168.6	184.7	NELL2	NM_006159.1	NRP2	structural	extracellul	cell
GI_5453773-S	140.7	208.5	160.5	NFE2	NM_006163.1	p45;NF-E2	transcripti	nucleus	hemostasi
GI_5453787-S	115.8	123.1	101.9	NKX6-1	NM_006168.1	NKX6A;NKX6.1	transcripti	nucleus	histogene
GI_5453789-S	6726.8	9264.7	4530.1	NNMT	NM_006169.1				
GI_5453791-S	358.6	381.2	323.3	NOL1	NM_006170.1	p120;NOP120	DNA	nucleolus	positive
GI_5453799-S	206.1	199.1	172.5	NRGN	NM_006176.1	RC3;hng	calmoduli		signal
GI_5453801-S	150.7	161.5	167.4	NRL	NM_006177.1	RP27;D14S46E	specific	nucleus	regulation
GI_5453809-S	106.8	111.2	105.3	NTN2L	NM_006181.1		structural	cellular_co	axon
GI_5453813-S	1087.6	956.2	599.7	DDR2	NM_006182.1	TKT;NTRKR3;TYRO10	transmem	integral to	cell
GI_5453819-S	164	197	187.6	NUMA1	NM_006185.1	NUMA	structural	spindle	nuclear
GI_5453827-S	93.9	78.7	82.1	OMP	NM_006189.1			cytoplasm	olfaction
GI_5453833-S	103.2	113.2	102.1	POSTN	NM_006475.1	PN;OSF-2;periostin	cell	extracellul	skeletal
GI_5453837-S	553.8	764.2	598.7	SSSCA1	NM_006396.1	p27			mitosis
GI_5453841-S	6063.1	5258.6	5649.4	PA2G4	NM_006191.1		methionyl	nucleus	cell cycle
GI_5453849-S	120.3	127	122.4	PAX4	NM_006193.1		DNA	nucleus	histogene
GI_5453857-S	93.4	80.8	70.7	PCP4	NM_006198.1	PEP-19			central
GI_5453861-S	334.2	316.1	275.1	PDE4A	NM_006202.1	DPDE2	cAMP-	insoluble	signal
GI_5453867-S	89.9	92	84.9	PDE6H	NM_006205.1		cGMP-	nucleus	vision
GI_5453871-S	352.5	805.6	267.3	PDGFRL	NM_006207.1	PDGRL;PRLTS	platelet		
GI_5453877-S	106.3	101.3	111.4	PFKFB2	NM_006212.1		6-		fructose
GI_5453889-S	97.6	100.4	90	PIBF1	NM_006346.1				
GI_5453891-S	280.7	389.1	292	PIK3CA	NM_006218.1		phosphati	phosphoin	oncogene
GI_5453893-S	306.6	351.7	323.2	PIK3CB	NM_006219.1	PIK3C1;p110-BETA	1-	phosphoin	activation
GI_5453897-S	2560.6	2916.6	3200.3	PIN1	NM_006221.1	DOD	peptidyl-	nucleus	regulation
GI_5453899-S	121.1	149.3	129.5	PIN1L	NM_006222.1		molecular	cellular_co	biological_
GI_5453909-S	201.7	218.5	211.1	PLCD1	NM_006225.1		phospholi		phosphati
GI_5453911-S	93.5	93.8	108	PLCL1	NM_006226.1	PLCE;PLCL;PLC-L;PLDL1	phospholi		intracellula
GI_5453915-S	4556.8	5223.7	4032.3	PGRMC2	NM_006320.1	DG6;PMBP	steroid	integral to	
GI_5453919-S	115.9	135	129.3	PNLIPRP1	NM_006229.1	PLRP1	triacylglyc	extracellul	
GI_5453923-S	5050.6	4119	3752	POLD2	NM_006230.1		eta DNA	nucleus	DNA
GI_5453925-S	157.4	196.7	201.7	POLE	NM_006231.1	POLE1;FLJ21434	DNA	nucleus	DNA
GI_5453933-S	190.3	231.2	196.8	POU2AF1	NM_006235.1	BOB1;OBF1;OCAB;OBF-1	transcripti	nucleus	humoral
GI_5453935-S	104.4	97.7	91.2	POU3F3	NM_006236.1	BRN1;OTF8	transcripti	nucleus	central
GI_5453959-S	1113.1	1517.8	1545.3	RABAC1	NM_006423.1	PRA1;YIP3			nonselecti
GI_5453965-S	115	134.4	117.1	PRKAA2	NM_006252.1	AMPK;PRKAA	protein		protein
GI_5453973-S	287.9	320.9	275.9	PRKCL2	NM_006256.1	PRK2	protein	intracellula	protein
GI_5453975-S	112.9	138	127.8	PRKCQ	NM_006257.1		protein-	intracellula	protein
GI_5453977-S	86.7	99.7	84.8	PRKG2	NM_006259.1	PRKGR2	protein		protein
GI_5453993-S	2798.2	2376.8	2605.9	RAD21	NM_006265.1	HR21;MCD1;NXP1;SCC1;hHR21;HRAD21;KI	calcium	nucleus	meiotic
GI_5453997-S	826.1	866.7	636.5	IPO7	NM_006391.1	RANBP7	small	nuclear	nucleocyto
GI_5453999-S	216.3	233	186	IPO8	NM_006390.1	RANBP8	RAN	nuclear	signal

GI_5454007-S	99.3	100.3	90.1	RIG	NM_006394.1				
GI_5454015-S	99.9	91.6	83.4	RP1	NM_006269.1	ORP1	molecular		phototrans
GI_5454017-S	109.3	102.4	107.4	RPC32	NM_006467.1	RPC7	DNA-	transcripti	regulation
GI_5454025-A	437	443.3	449.4	RPP38	NM_006414.1		ribonuclea	nucleolar	tRNA
GI_5454031-S	105.5	104.1	107.5	S100A1	NM_006271.1	S100;S100A	calcium		cell shape
GI_5454033-S	147.3	146.4	137	S100B	NM_006272.1	NEF;S100	calcium	extracellul	axonogen
GI_5454045-S	996.8	1010.7	904.2	SEC24B	NM_006323.1	SEC24	vesicle	COPII	vesicle-
GI_5454055-A	89.3	90.7	94.9	SORBS1	NM_006434.1	CAP;SH3D5;SORB1;SH3P12;ponsin;FLJ124	cytoskelet	cell-cell	cell-matrix
GI_5454057-S	295.1	233.3	233.7	SIAT4C	NM_006278.1	STZ;SAT3;CGS23;SIAT4;NANTA3;FLJ11867	beta-		
GI_5454063-S	1221.4	1500.8	1523.8	RBM14	NM_006328.1	SIP;COAA;SYTIP1	nucleic		
GI_5454069-S	269.2	255.2	311.3	SLC9A6	NM_006359.1	NHE6;KIAA0267	sodium:hy	integral to	small
GI_5454073-S	1754.9	1571.8	1761.7	NCOR2	NM_006312.1	SMRT;CTG26;SMRTE;TRAC1;TNRC14;TRA	transcripti	kinesin	regulation
GI_5454079-S	238.1	272.5	265.6	HMG20B	NM_006339.1	SOXL;HMGX2;BRAF25;BRAF35;SMARCE1r	DNA		chromatin
GI_5454087-S	8435.3	7074.7	6485.4	ANP32B	NM_006401.1	APRIL;SSP29;PHAPI2			oncogene
GI_5454089-S	1602	2086.7	1499.7	SSR4	NM_006280.1	TRAPD	calcium	endoplas	intracellula
GI_5454091-S	113	133.7	103.9	SIAT7B	NM_006456.1	IV;III;STHM;SIAT7;ST6GalNAII;ST6GalNA II	sialyltransf	Golgi	protein
GI_5454093-S	1120.1	931	435.1	STK3	NM_006281.1	KRS1;MST2	protein	cytoplasm	heat
GI_5454099-S	1846.6	1689.7	1215.4	TACC1	NM_006283.1	Ga55;KIAA1103		kinesin	oncogene
GI_5454101-S	365.1	460.8	452.5	TACC3	NM_006342.1	ERIC1		kinesin	cell growth
GI_5454109-S	282.2	338.6	389	TESK1	NM_006285.1		protein		spermatog
GI_5454111-S	377	358.3	315.5	TFDP2	NM_006286.1	DP2;Dp-2	transcripti		oncogene
GI_5454119-S	132.8	172.2	148.3	TIMM17A	NM_006335.1	TIM17;TIM17A	protein	mitochond	mitochond
GI_5454143-S	126.5	174.7	114.2	UBD	NM_006398.1	FAT10	polyubiquit		proteolysis
GI_5454155-S	923.6	1139.9	1006.7	USP16	NM_006447.1	Ubp-M	ubiquitin-	cytoplasm	deubiquiti
GI_5454157-S	2253.6	2399.1	1790.5	VARS2	NM_006295.1	G7A	ATP	intracellula	translation
GI_5454161-S	5566.9	5320.9	1721.8	TXNIP	NM_006472.1	THIF;VDUP1;HHCPA78;EST01027	molecular	cellular_co	sensory
GI_5454165-S	690.6	647.1	721.6	VTI1B	NM_006370.1	VTI1;VTI2;VTI1L	receptor		nonselecti
GI_5454171-S	584.5	501	607.8	XRCC1	NM_006297.1	RCC	DNA	nucleus	single
GI_5454177-S	87.8	104.7	89.7	ZNF192	NM_006298.1	LD5-1	protein	nucleus	regulation
GI_5454181-S	107.3	89.7	89.2	ZNF230	NM_006300.1	FDZF2	DNA	nucleus	regulation
GI_5540099-S	340.3	282.8	385.3	MAN2A2	NM_006122.1	MANA2X;PRO2198;HsT19662	mannosyl-	Golgi	carbohydr
GI_5579451-S	92.8	90.9	84.3	CALB1	NM_004929.2	CALB	protein		
GI_5579457-S	15332.1	14301	13984	EIF3S8	NM_003752.2	eIF3-p110	translation	eukaryotic	regulation
GI_5579480-S	128.1	127.7	122.1	ARHN	NM_005440.2	RHO7;RhoN;Rnd2	GTPase		signal
GI_5597012-S	6759.5	5582.4	5702.5	CLN2	NM_000391.2	TPP1;LINCL;TPP I;TPP-I	peptidase	lysosome	proteolysis
GI_5670341-I	176.5	196.5	185.8	KHK	NM_006488.1		ketohexok		
GI_5713320-S	209.2	231.5	224.7	SELL	NM_000655.2	TQ1;LAM1;LNHR;LSEL;CD62L;LAM-	selectin	integral to	cell
GI_5729727-S	93.1	106.7	97.9	ALX3	NM_006492.1		transcripti	nucleus	regulation
GI_5729737-S	659.8	688.4	819.3	BLCAP	NM_006698.1	BC10	molecular	integral to	biological_
GI_5729741-S	577.1	671.6	628.3	AP4B1	NM_006594.1	BETA-4	vesicle	secretory	nonselecti
GI_5729745-S	166.7	178	155	BS69	NM_006624.1	ZMYND11;PRKCBP1L1	transcripti	nucleus	cell
GI_5729757-S	107.8	134.3	118	CAPN9	NM_006615.1	GC36;nCL-4;CALPAIN9	calpain	intracellula	digestion
GI_5729760-S	141.7	172.8	186.4	CCT6B	NM_006584.1	Cctz2;CCTZ-2;TSA303	protein		protein
GI_5729764-S	485.3	466	414.3	CGRRF1	NM_006568.1	CGR19			negative

GI_5729771-S	823.9	987.6	872.7	CLN5	NM_006493.1	NCL		lysosome	cell growth
GI_5729789-S	1424.1	1246.4	1449.3	CTCF	NM_006565.1		transcripti	nucleus	negative
GI_5729795-S	79	90.7	83.7	CYP46A1	NM_006668.1	CP46;CYP46	steroid	microsom	cholestero
GI_5729807-S	98.1	113	97	CD226	NM_006566.1	PTA1;DNAM1;DNAM-1;TLiSA1	cell	integral to	cell
GI_5729809-S	242.5	372.5	412.7	EBP	NM_006579.1	CPX;CHO2;CPXD;CDPX2	steroid	endoplas	cholestero
GI_5729811-S	645	812.2	739.6	ELL	NM_006532.1	Men;ELL1	positive	nucleus	RNA
GI_5729813-S	158.4	187.7	157.8	ERF	NM_006494.1	PE-2	ligand-	nucleus	regulation
GI_5729815-S	132.7	119.5	99.9	CUGBP2	NM_006561.1	Etr-3;NAPOR;BRUNOL3;NAPOR-2	RNA		regulation
GI_5729819-S	666.4	770.9	763.6	FARS1	NM_006567.1	dJ236A3.1	phenylala	soluble	tRNA
GI_5729825-S	140	159.6	159.1	FHR-4	NM_006684.1	FHR4	apolipopro		
GI_5729827-S	473.9	708.4	611.6	FLN29	NM_006700.1				
GI_5729829-S	116.3	104.5	101.7	FSBP	NM_006550.1				
GI_5729839-S	2149	2153.9	2817.3	TUBGCP2	NM_006659.1	GCP2;Spc97p		microtubul	microtubul
GI_5729841-S	5838.5	5945.2	3876.1	GLO1	NM_006708.1	GLYI	lactoylglut		carbohydr
GI_5729843-S	146.8	173.9	163.9	GLRA3	NM_006529.1		extracellul	integral to	chloride
GI_5729849-S	1053.4	1165	908.4	GNAI3	NM_006496.1		heterotrim	peripheral	negative
GI_5729857-S	160.9	221.4	196.7	NCOA2	NM_006540.1	TIF2;GRIP1;NCoA-2	transcripti	nucleus	regulation
GI_5729867-S	824.3	899.8	930	HERC2	NM_004667.2	jdf2;p528;D15F37S1;KIAA0393	ubiquitin-	intracellula	ubiquitin
GI_5729868-S	101	84	98.1	HHCM	NM_006543.1	hhc(M)			oncogene
GI_5729870-S	90.9	106.2	110.2	HIC1	NM_006497.1		protein	nucleus	cell growth
GI_5729886-S	108.6	133.5	101.2	IQGAP2	NM_006633.1		GTPase	actin	signal
GI_5729898-S	77.4	92.8	75.5	KLRA1	NM_006611.1	Ly49;LY49L	lectin [goid	plasma	cell
GI_5729902-S	110.6	123.4	113.7	LGALS2	NM_006498.1		sugar	soluble	heterophili
GI_5729906-S	96.1	95.7	94	SCGB1D1	NM_006552.1	LIPA;LPHA		extracellul	
GI_5729917-S	138.9	175.1	174	MCAM	NM_006500.1	CD146;MUC18	tumor	integral to	embryoge
GI_5729919-S	158.1	158.6	145.4	ME3	NM_006680.1		malate	mitochond	pyruvate
GI_5729924-S	193.7	641.4	173.7	MIA	NM_006533.1	CD-RAP	growth	extracellul	cell
GI_5729930-A	236.2	252.1	217.1	MOBP	NM_006501.1			soluble	neurogene
GI_5729936-S	1519.8	1366.1	1224.4	MTX2	NM_006554.1		protein	mitochond	mitochond
GI_5729938-S	2688.4	2107.2	2036.7	CPSF4	NM_006693.1	NAR;NEB1;CPSF30	RNA	nucleus	mRNA
GI_5729946-S	144.8	154.6	130.4	NMU	NM_006681.1		receptor		G-protein
GI_5729959-S	101.9	121.7	99.1	OR5I1	NM_006637.1	OLF1;HSOlf1	receptor	integral to	signal
GI_5729965-S	191.3	363.8	193.7	HCP5	NM_006674.1	P5-1;D6S2650E	defense/i	cellular_co	biological_
GI_5729971-S	102.5	133.6	126.3	PDE10A	NM_006661.1		3',5'-cyclic-		signal
GI_5729975-S	352.9	589.8	437.7	PHTF1	NM_006608.1	PHTF	transcripti	nucleus	transcripti
GI_5729981-S	161.1	179.2	160.5	POLH	NM_006502.1	XPV;XP-V;RAD30A	eta DNA	nucleoplas	regulation
GI_5729985-S	1124.1	1382.3	1480.8	POP4	NM_006627.1	RPP29	ribonuclea	ribonuclea	tRNA
GI_5730000-S	810.8	698.8	476.3	RAI	NM_006663.1	IASPP;PPP1R13L	transcripti	nucleus	regulation
GI_5730010-S	172.9	174.8	158.7	RFPL2	NM_006605.1	RNF79	protein		
GI_5730012-S	208.6	247.2	213	RFPL3	NM_006604.1		antisense		
GI_5730016-S	993.4	967.7	911.8	RPP40	NM_006638.1	bA428J1.3	ribonuclea	nucleolar	tRNA
GI_5730018-S	121.2	125.5	127	RRH	NM_006583.1		G-protein	integral to	vision
GI_5730020-S	144.1	171.2	165.9	RSC1A1	NM_006511.1	RS1	ion		small
GI_5730022-S	2119.6	2154.6	1995.1	RUVBL2	NM_006666.1	ECP51;TIP48;CGI-46;TIP49B	ATP	cytosol	protein

GI_5730024-S	1779.5	1527	1469.8	USP39	NM_006590.1	SAD1;CGI-21	pre-mRNA	nucleus	mRNA
GI_5730026-S	5274.8	5171.3	4405.3	KHDRBS1	NM_006559.1	p62;Sam68	mRNA		G1/S
GI_5730032-S	108.4	117.6	116.9	SCN10A	NM_006514.1	hPN3	voltage-	voltage-	sodium
GI_5730038-S	751.4	922.9	647.6	SETMAR	NM_006515.1		transposa		
GI_5730042-S	330.9	991.7	128.2	SLC12A7	NM_006598.1	KCC4;DKFZP434F076	potassium	integral to	small
GI_5730044-S	178.9	197.8	275.3	SLC16A2	NM_006517.1	MCT8;XPCT;DXS128;DXS128E	monocarb	membran	monocarb
GI_5730046-S	92.2	120	96.7	SLC17A3	NM_006632.1	NPT4	sodium:ph	membran	sodium
GI_5730050-S	339.8	708.2	444.5	SLC2A1	NM_006516.1	GLUT;GLUT1	glucose	membran	glucose
GI_5730054-S	2731.3	6975	1265.6	PLK2	NM_006622.1	SNK	ATP		cell cycle
GI_5730060-S	229.1	278	238.5	SPBPBP	NM_006692.1		transcripti	nucleus	respiratory
GI_5730062-S	231.1	403.5	307.3	SPHAR	NM_006542.1				DNA
GI_5730064-S	130.9	148.1	157.6	SPIN	NM_006717.1		cell cycle		gametoge
GI_5730066-S	177.5	211.9	193.2	SRCAP	NM_006662.1	KIAA0309	histone	nucleus	regulation
GI_5730072-S	464	229.3	374	KHDRBS3	NM_006558.1	Etle;SALP;SLM2;SLM-2;T-STAR;etoile	protein	nucleus	spermatog
GI_5730074-S	127.6	140.6	117.9	FGL2	NM_006682.1	T49;pT49		fibrinogen	
GI_5730084-S	1440.6	1591.5	1398	TCTEL1	NM_006519.1	CW-1;tctex-1	microtubul	cytoplasmi	biological_
GI_5730086-S	686.4	766.9	801.2	TCTE1L	NM_006520.1	TCTEX1L	molecular	cellular_co	biological_
GI_5730103-S	110.3	108.2	97.2	TXNL2	NM_006541.1	PICOT	electron		electron
GI_5730105-S	95.7	102.5	101.8	CXCR6	NM_006564.1	BONZO;STRL33;TYMSTR	coreceptor	integral to	viral
GI_5730109-S	1944.7	1851.2	1469.3	USP3	NM_006537.1		ubiquitin-		deubiquiti
GI_5802969-S	899.8	760.2	720.1	AFG3L2	NM_006796.1		adenosine	integral to	proteolysis
GI_5802975-S	442.8	596.2	594.6	APM2	NM_006829.1		molecular	cellular_co	biological_
GI_5802979-S	144.6	157.7	162.1	ATF7	NM_006856.1	ATFA	transcripti	nucleus	regulation
GI_5802981-S	144.9	183.2	163.4	PNRC1	NM_006813.1	B4-2;PRR2;PROL2	protein	nucleus	
GI_5802983-S	2599.8	2759.8	3512.4	B3GNT6	NM_006876.1	IGAT;IGNT;BETA3GNTI	acetylgluc	Golgi	oligosacch
GI_5802993-S	253.5	316.3	268.2	CD6	NM_006725.1	TP120	lymphocyt	integral to	immune
GI_5803001-S	111.1	110.5	112.1	CLCN2	NM_004366.2	CLC2;ECA3;EGI3;EGMA;CIC-2	voltage-	membran	small
GI_5803004-S	1035.5	1023	1071.9	DIPA	NM_006848.1		molecular	kinesin	virulence
GI_5803006-S	637.8	606.6	473	DNASE1L1	NM_006730.1	XIB;DNL1L;DNAS1L1	deoxyribo		DNA
GI_5803014-S	380.9	368.7	366.8	FCMD	NM_006731.1	FKTN;fukutin		extracellul	muscle
GI_5803016-S	410.3	590.9	709.2	FOSB	NM_006732.1	GOS3;GOSB	transcripti	nucleus	behavior
GI_5803022-S	954.4	1159	1104.5	LMAN2	NM_006816.1	GP36B;VIP36;C5orf8	lectin [goid	Golgi	intracellula
GI_5803024-S	169.1	179	167.3	GPR75	NM_006794.1	GPR-chr2;WI-31133	G-protein	integral to	vision
GI_5803026-S	106.9	105.4	99.6	C1orf29	NM_006820.1	GS3686			
GI_5803028-S	536.3	610.5	666.2	HEAB	NM_006831.1	CLP1;hClp1	GTP	nucleus	mRNA
GI_5803051-S	121.4	139.2	118.8	KIR3DL2	NM_006737.1	CL-5;NKAT4;CD158K;NKAT4A;NKAT4B	MHC-	integral to	cellular
GI_5803055-S	127.8	128.5	150.2	LAPTM5	NM_006762.1			lysosome	
GI_5803059-S	85	109.9	108.5	LILRB3	NM_006864.1	HL9;ILT5;LIR3;CD85A;LIR-3	defense/i	integral to	defense
GI_5803065-S	104.2	98.1	107.5	LILRA1	NM_006863.1	LIR6;CD85I;LIR-6	antigen	integral to	defense
GI_5803067-S	97.5	101.9	96.6	LILRA2	NM_006866.1	ILT1;LIR7;CD85H;LIR-7	antigen	integral to	defense
GI_5803073-S	1565.9	1643.4	1665.4	LZTR1	NM_006767.1	TCFL2;LZTR-1	transcripti		embryoge
GI_5803087-I	189.7	206.6	179.9	MAP3K4	NM_005922.1	MTK1;MEKK4;MAPKKK4;KIAA0213	MAP		activation
GI_5803097-S	1035.2	955.5	812.4	MYST3	NM_006766.1	MOZ;ZNF220;RUNXBP2	DNA	nucleus	DNA
GI_5803105-S	112.9	122.6	121.2	TTID	NM_006790.1	MYOT	structural	actin	muscle

GI_5803108-S	577	711.1	727.8	OS-9	NM_006812.1				soluble	cell growth
GI_5803110-S	5368.3	5963	6443.4	EBNA1BP2	NM_006824.1	P40;EBP2;NOBP			kinesin	ribosome
GI_5803114-S	1489.2	1679	1342.5	IMMT	NM_006839.1	HMP;P87;P89;P87/89;MITOFILIN		molecular	mitochond	biological_
GI_5803118-S	105.2	86.2	94.5	PDIP	NM_006849.1	PDI;PDA2;PDIR;PDIA2		protein	endoplas	protein-ER
GI_5803120-S	1336.9	1244.1	977.8	PDIR	NM_006810.1			protein	endoplas	response
GI_5803124-S	121.3	137.9	111.3	PIM2	NM_006875.1			protein		male
GI_5803140-S	767.8	1569.5	1672	RBPMS	NM_006867.1	HERMES		RNA		RNA
GI_5803150-S	1481.8	3098.9	1245.2	GLIPR1	NM_006851.1	GLIPR;RTVP1			extracellul	pathogene
GI_5803162-S	180	192.7	198.9	RAB40B	NM_006822.1	RAR;SEC4L		GTP		protein
GI_5803166-S	1702.2	1790.2	1885.2	SF3A3	NM_006802.1	PRP9;SAP61;SF3a60		pre-mRNA	spliceoso	mRNA
GI_5803170-S	93	103.6	98.5	SLA	NM_006748.1	SLA1;SLAP		SH3/SH2		intracellula
GI_5803174-S	138.3	155.4	137.9	SMA3	NM_006780.1	b55C20.2		hydrolase		skeletal
GI_5803180-S	976.2	1203.7	1306.4	STIP1	NM_006819.1	HOP;P60;STI1L;IEF-SSP-3521			Golgi	response
GI_5803186-S	5065.3	6458.1	7190.1	TALDO1	NM_006755.1	TAL;TAL-H;TALDOR		transaldol	cytoplasm	carbohydr
GI_5803202-S	365.1	449.3	404.5	TNNT3	NM_006757.1	DA2B;FSSV;AMCD2B		tropomyos	troponin	regulation
GI_5803206-S	5751	4669.5	4630.2	U2AF1	NM_006758.1	RN;U2AF35;U2AFBP;RNU2AF1		pre-mRNA	Cajal body	mRNA
GI_5803212-S	127.6	127.8	131.3	UGT2A1	NM_006798.1			UDP-	microsom	perception
GI_5803214-S	201.9	250.2	213	UPK2	NM_006760.1				integral to	developm
GI_5803218-S	145.1	165.7	149.6	SPINK5	NM_006846.1	LEKTI;LETKI;VAKTI		serine	extracellul	antimicrob
GI_5803220-S	164.5	146.9	144	WDR3	NM_006784.1				nucleus	
GI_5870890-I	585.9	601.1	542.5	CRA	NM_006697.1					
GI_5881412-S	103.4	111.6	112	ELN	NM_000501.1	WS;WBS;SVAS		extracellul	extracellul	respiratory
GI_5901887-S	99.1	102.2	98.8	ADAMTS5	NM_007038.1	ADMP-2;ADAMTS11		integrin	extracellul	proteolysis
GI_5901891-S	477.6	341.4	428.5	WDHD1	NM_007086.1	AND-1		DNA	nucleoplas	regulation
GI_5901909-S	93.4	98.1	98.2	CD160	NM_007053.1	NK1;BY55;NK28		MHC-	integral to	cell
GI_5901913-S	94.8	102.1	96.5	RAPGEF4	NM_007023.1	CGEF2;EPAC2;CAMP-GEFII		guanyl-	cAMP-	G-protein
GI_5901917-S	106	106.5	101.1	CART1	NM_006982.1			transcripti	nucleus	brain
GI_5901925-S	2173.3	2529.1	2027.5	CPSF5	NM_007006.1	CFIM25		RNA	nucleus	mRNA
GI_5901927-S	231.5	201.8	132.7	CPSF6	NM_007007.1	CFIM;CFIM68;HPBRII-4;HPBRII-7		RNA	nucleus	mRNA
GI_5901929-S	101.3	94.2	93.4	CEACAM7	NM_006890.1	CGM2		tumor	integral to	
GI_5901931-S	105.8	107.8	113.6	LECT1	NM_007015.1	CHM1;CHM-I;BRICD3		molecular	basement	proteoglyc
GI_5901935-S	910.4	1553.3	969.1	SLC39A7	NM_006979.1	KE4;HKE4;RING5;H2-		heavy	integral to	heavy
GI_5901937-S	398.5	537.3	332	C10orf10	NM_007021.1	FIG;DEPP		DNA	nucleus	regulation
GI_5901943-S	96	116.3	103.5	EMILIN1	NM_007046.1	gp115;EMILIN;EMILIN-1;DKFZP586M121		extracellul	extracellul	cell
GI_5901965-S	169.1	215	174.5	HHLA3	NM_007071.1					
GI_5901969-S	205.2	250	225.8	HNMT	NM_006895.1					
GI_5901975-S	2003.3	3184.9	1356.5	HRASLS3	NM_007069.1	HREV107;HREV107-3;H-REV107-1		molecular	cellular_co	biological_
GI_5901979-S	419.8	587.5	434.2	HSF2BP	NM_007031.1					spermatog
GI_5901987-S	1135.1	1123.1	1109.9	JM5	NM_007075.1					
GI_5901993-S	743.4	806.7	1121.8	KPTN	NM_007059.1		2.00E+04	actin	microtubul	actin
GI_5901997-S	1103.2	878.2	782	LSM6	NM_007080.1	YDR378C		small	small	mRNA
GI_5902001-S	1701.8	1869	1380.9	DUSP14	NM_007026.1	MKP6;MKP-L		protein		protein
GI_5902003-S	179.2	199.5	154.1	MMP23B	NM_006983.1	MIFR;MMP22;MIFR-1				
GI_5902011-S	454.5	490.3	472.5	MYO9A	NM_006901.1	FLJ11061			actin	vision

GI_5902013-S	4008.5	4213.7	3603	NPIP	NM_006985.1				
GI_5902015-A	10471.5	9553.3	8594.6	RTN4	NM_007008.1	ASY;NOGO;NSP-CL;KIAA0886	protein	endoplas	apoptosis
GI_5902015-I	99	95.9	89.2	RTN4	NM_007008.1	ASY;NOGO;NSP-CL;KIAA0886	protein	endoplas	apoptosis
GI_5902017-S	120.7	124.9	134	p25	NM_007030.1	p24	DNA	nucleus	regulation
GI_5902033-S	2068	1803.8	1853.6	PWP1	NM_007062.1	IEF-SSP-9502		nucleus	transcripti
GI_5902039-S	535.9	495.7	421.8	RABL2B	NM_007081.1		RAB small		small
GI_5902059-S	161.9	186.3	172.2	RP2	NM_006915.1		chaperone		beta-
GI_5902065-S	391.9	459.9	396.8	RPP14	NM_007042.1		RNA	nucleus	tRNA
GI_5902071-S	112.8	125.3	110.2	SERPINB3	NM_006919.1	SCC;T4-A;SCCA1;HsT1196;SCCA-PD	serine-		
GI_5902089-S	513.9	697.6	875.9	SLC2A3	NM_006931.1	GLUT3	glucose	integral to	glucose
GI_5902091-S	129.4	123.7	117.5	SLC5A3	NM_006933.1	SMIT;SMIT2	myo-	integral to	small
GI_5902093-S	180.7	219.3	202.6	SLC6A9	NM_006934.1	GLYT1	glycine:so	membran	small
GI_5902095-S	2976.2	2773.4	3138.6	SMT3H1	NM_006936.1	SMT3A;SUMO-3		kinetochor	
GI_5902105-S	229.2	277.4	229.2	SOX15	NM_006942.1	SOX20;SOX26;SOX27	RNA	nucleus	male
GI_5902107-S	124.4	150.2	116.9	SOX21	NM_007084.1	SOX25	RNA	nucleus	establish
GI_5902115-S	156	203.7	155.9	ZPBP	NM_007009.1	SP38;ZPBP1		extracellul	
GI_5902117-S	148.3	133.9	118.2	SPP2	NM_006944.1	SPP24	endopepti	extracellul	skeletal
GI_5902121-S	2297.6	1738.5	1135.1	SPTBN2	NM_006946.1		actin	spectrin	cell shape
GI_5902127-S	368.9	460.2	349.4	STXBP2	NM_006949.1	UNC18B;UNC18-2;MUNC18-2	protein	cellular_co	protein
GI_5902129-S	253.5	237.1	218.2	SFRS16	NM_007056.1	CLASP;SWAP2	DNA	nucleus	regulation
GI_5902133-S	106.9	121	111.3	CORO1A	NM_007074.1	p57;TACO;CLABP;HCORO1;CLIPINA;Clabp	actin	lysosomal	transport
GI_5902139-S	99.6	89.1	91.7	TRAD	NM_007064.1	DUET	protein	actin	protein
GI_5902151-S	230.8	263.6	243.5	UPK3A	NM_006953.1	UPK3		integral to	
GI_5902157-S	632.8	517.8	510.8	ZNF183	NM_006978.1	RNF113	nucleic		developm
GI_5902159-S	88.9	113.4	144.7	ZNF22	NM_006963.1	KOX15;HKR-T1;ZNF422;Zfp422	zinc ion	nucleus	regulation
GI_5902161-S	137.3	158.1	160.8	ZNF24	NM_006965.1	KOX17;RSG-A;ZNF191	DNA	nucleus	regulation
GI_5902723-S	344.8	461.8	392.5	NOVA2	NM_002516.1	ANOVA;NOVA3	RNA	nucleus	
GI_5902807-I	119.8	133.6	119.5	BMP1	NM_006128.1	TLD	metallope	extracellul	cartilage
GI_5902809-I	1642.9	2126.4	1147.6	BMP1	NM_006129.2	TLD	metallope	extracellul	cartilage
GI_5902810-A	282.9	746.3	363	BMP1	NM_006130.1	TLD	metallope	extracellul	cartilage
GI_5902812-I	344.9	435.4	382.1	BMP1	NM_006131.1	TLD	metallope	extracellul	cartilage
GI_5902814-I	87.5	111	106.7	BMP1	NM_006132.1	TLD	metallope	extracellul	cartilage
GI_5921994-A	102.6	107.3	109.4	APOBEC1	NM_005889.1	BEDP;CDAR1	cytidine		mRNA
GI_5921996-S	823.5	1251.8	1137.6	CALR	NM_004343.2	RO;SSA;cC1qR	transcripti	endoplas	regulation
GI_5921997-S	94.6	90.7	100.4	CRHBP	NM_001882.2	CRFBP;CRF-BP	protein	soluble	learning
GI_5921998-A	324.4	385.3	363.4	DYRK1B	NM_006483.1	MIRK	protein	nucleus	protein
GI_5922002-A	249	375.6	384.3	DYRK2	NM_003583.2		protein	cytoplasm	protein
GI_5922003-I	119.7	130.3	115.1	DYRK2	NM_006482.1		protein	cytoplasm	protein
GI_5922005-S	95.4	112.9	100.8	F2	NM_000506.2	PT	thrombin	soluble	tyrosine
GI_5922012-S	2354.8	1843.1	1444.8	FZD2	NM_001466.2		receptor	integral to	establish
GI_6005714-S	94.4	106.3	98.3	SLC6A14	NM_007231.1	OBX;ATB(0+)	amino	integral to	small
GI_6005716-S	744.4	711.1	567.8	ATP5I	NM_007100.1	ATP5K	hydrogen	mitochond	proton
GI_6005718-S	123.2	126.9	121.2	C14orf1	NM_007176.1		molecular	integral to	biological_
GI_6005726-S	8818.6	8428	6708.7	CCT8	NM_006585.1				

GI_6005732-S	1122.2	1392.5	952.9	PICALM	NM_007166.1	LAP;CALM;CLTH			vesicle-
GI_6005759-S	270.8	300.3	394.3	TUSC2	NM_007275.1	PAP;FUS1;PDAP2;C3orf11			cell
GI_6005763-S	7887.5	10402	9809.1	GABARAP	NM_007278.1	MM46	tubulin	plasma	protein
GI_6005771-S	302.8	252	206.1	GPR	NM_007223.1		G-protein	integral to	G-protein
GI_6005773-S	130.7	148.9	136.9	GUCA2B	NM_007102.1	UGN;GCAP-II	calcium		excretion
GI_6005781-S	211	240.5	230.4	HRH3	NM_007232.1	HH3R;GPCR97	histamine	integral to	G-protein
GI_6005783-S	1076.8	1167.5	1189	HSGT1	NM_007265.1		transcripti		regulation
GI_6005787-S	674.5	970	798.7	NISCH	NM_007184.1	I-1;IRAS;KIAA0975			electron
GI_6005791-S	189.2	215.4	187.1	IRAK3	NM_007199.1	IRAK-M	receptor		protein
GI_6005793-S	504.2	747.5	651.6	JM4	NM_007213.1				
GI_6005801-S	335.9	333.1	239.9	PROL4	NM_007244.1	LPRP;PRR4	DNA	extracellul	physiologi
GI_6005807-A	2485.5	2493.7	2598.9	MAN1B1	NM_007230.1	MANA-ER;DKFZP434I213	mannosyl-	membran	oligosacch
GI_6005825-S	3051.4	3158.4	2403.9	PACSIN2	NM_007229.1		vesicle	kinesin	actin
GI_6005829-S	221.3	230.7	254.2	PKP3	NM_007183.1		cell	cytoskelet	cell
GI_6005831-S	711.9	683.8	745.8	PMF1	NM_007221.1		transcripti	transcripti	transcripti
GI_6005837-S	447	459.9	336.8	POLG2	NM_007215.1	HP55;POLB;POLGB;MTPOLB	gamma	mitochond	DNA
GI_6005847-S	93.6	91.8	70.1	POLI	NM_007195.1	RAD30B	iota DNA	nucleoplas	DNA
GI_6005855-S	135.6	137.6	143	POU6F2	NM_007252.1	RPF-1	transcripti	nucleus	ganglion
GI_6005869-S	107.8	123.3	123.7	SCRG1	NM_007281.1	SCRG-1		extracellul	neurogene
GI_6005873-S	182.4	178.3	180.8	SLMAP	NM_007159.1	SLAP;KIAA1601		smooth	muscle
GI_6005877-S	201	227.8	194.1	SLC22A1LS	NM_007105.1	BWR1B;BWSCR1B;ORCTL2S;p27-BWR1B	molecular	cellular_co	biological_
GI_6005885-S	195.2	227.2	221.8	STXBP3	NM_007269.1	PSP;MUNC18C;UNC-18C;MUNC18-3	protein	cellular_co	protein
GI_6005889-S	5309.3	5503.3	6040.9	TCEB2	NM_007108.1	SIII	protein	nucleus	RNA
GI_6005891-S	166.2	171.4	168.2	TCF19	NM_007109.1	SC1	transcripti	nucleus	regulation
GI_6005895-S	149.3	155.1	167	TESK2	NM_007170.1		protein	nucleus	spermatog
GI_6005903-S	250.9	305.8	255.7	TMF1	NM_007114.1	ARA160	transcripti	kinesin	regulation
GI_6005909-S	218.1	274.1	206.1	TP53AP1	NM_007233.1	TP53TG1	signal		response
GI_6005913-S	97.4	104.7	105.8	TREH	NM_007180.1	TRE;TREA	alpha,alph	plasma	trehalose
GI_6005919-S	127.1	145.7	150.2	TRH	NM_007117.1		thyrotropin-	soluble	signal
GI_6005923-S	172.9	202.7	176	TU3A	NM_007177.1	DRR1			
GI_6005925-S	195.8	235	179.3	U2AF2	NM_007279.1	U2AF65	pre-mRNA	nucleus	mRNA
GI_6005929-S	155.3	181.3	163.7	UGT1A4	NM_007120.1	UGT1D;HUG-BR2	glucurono	microsom	metabolis
GI_6005937-S	109	116	113.1	UTRN	NM_007124.1	DRP;DMDL;DRP1	actin	cytoskelet	muscle
GI_6005943-S	87.1	85.7	84.2	VIL1	NM_007127.1	VIL;D2S1471	actin	F-actin	protein
GI_6005951-S	1001.5	1294.4	960.4	B4GALT7	NM_007255.1	XGPT1;XGALT1;XGALT-1;B4GAL-	galactosylt	integral to	proteoglyc
GI_6005955-S	1415.6	1226.1	1229	DUSP12	NM_007240.1	YVH1;DUSP1	zinc ion		cell growth
GI_6005957-S	167.4	199.9	174.3	Z39IG	NM_007268.1				
GI_6005965-S	243.4	215	200.7	ZNF146	NM_007145.1	OZF	heparin	nucleus	regulation
GI_6005967-S	750.9	743.6	764.5	ZNF161	NM_007146.1	DB1	specific	nucleus	cellular
GI_6005971-S	415.9	384.2	1064.5	ZNF185	NM_007150.1		zinc ion		
GI_6005973-S	494.7	512.9	455.6	ZNF195	NM_007152.1		zinc ion	nucleus	regulation
GI_6005975-S	101.9	102.1	95.1	ZNF208	NM_007153.1	PMIDP	zinc ion	nucleus	regulation
GI_6005977-I	106.9	123.6	115.9	ZNF258	NM_007167.1	MYM;ZNF198L4	DNA		developm
GI_6005981-S	123.1	125.1	121.5	ZNF80	NM_007136.1	pT17	transcripti	nucleus	regulation

GI_6005991-S	6746.2	10252	8142.5	CALU	NM_001219.2		calcium	Golgi	
GI_6005992-I	94.3	87.1	77.5	CLTA	NM_007096.1	LCA	calcium	coated pit	intracellula
GI_6005996-S	90.8	94.4	101.7	DOC2B	NM_003585.1		calcium-	membran	transport
GI_6005998-S	333.7	383	332.2	DRPLA	NM_001940.2	B37;NOD;ATN1	protein	cytoplasm	central
GI_6005999-S	103.1	93.8	86.2	GAS	NM_000805.2	GAST	peptide	soluble	smooth
GI_6006000-S	105.9	138.2	107.2	GPX3	NM_002084.2		glutathion	soluble	response
GI_6006002-S	110.1	114.8	98.8	GRIN2A	NM_000833.2	NR2A;NMDAR2A	N-methyl-	integral to	learning
GI_6006003-S	107.9	104.3	99.7	GRIN2B	NM_000834.2	NR2B;hNR3;NMDAR2B	N-methyl-	integral to	learning
GI_6006004-S	109.8	114.6	107.1	GRIN2C	NM_000835.2	NR2C;NMDAR2C	N-methyl-	integral to	small
GI_6006005-S	179	212.4	184.6	GRM1	NM_000838.2	GRM1A;mGlu1;GPRC1A;MGLUR1;MGLUR1	metabotro	integral to	G-protein
GI_6006006-S	134.4	161	139.8	GRM6	NM_000843.2	mGlu6;GPRC1F;MGLUR6	metabotro	integral to	metabotro
GI_6006008-S	2416.7	3464.9	3219.2	ITGA2	NM_002203.2	BR;CD49B;VLAA2	collagen	integrin	blood
GI_6006009-S	285.8	428.5	344	ITGA2B	NM_000419.2	GTA;CD41;GP2B;CD41B;GPIIb	calcium-	integral to	cell
GI_6006010-A	4263.9	4076.5	4075	ITGA3	NM_005501.1	VL3A;CD49C;GAPB3;MSK18;VCA-	cell	integrin	cell-matrix
GI_6006013-S	87	90.1	91.7	ITGAM	NM_000632.2	CR3A;MO1A;CD11B;MAC-1;MAC1A	cell	integrin	cell
GI_6006015-S	14644.3	16372	17160	LGALS1	NM_002305.2	GBP	galactose		apoptosis
GI_6006016-S	2130	3102.6	1190.6	LGALS3BP	NM_005567.2	90K;MAC-2-BP	scavenger	membran	cellular
GI_6006017-S	104.6	112.2	104.3	LGALS4	NM_006149.2	GAL4	lectin [goid	cytosol	cell
GI_6006018-S	558.7	648.3	1046.6	LIF	NM_002309.2	CDF;HILDA;D-FACTOR	leukemia	extracellul	positive
GI_6006019-S	1768.7	1275.8	1931.5	MAD2L2	NM_006341.2	REV7;MAD2B			mitotic
GI_6006021-S	1647.5	1331.3	1126.6	MAGOH	NM_002370.2		molecular	nucleus	sex
GI_6006022-S	760	867.1	784.1	MAS1	NM_002377.2	MAS	angiotensi	integral to	G-protein
GI_6006024-S	458.2	628.5	705.9	MPP1	NM_002436.2	PEMP;EMP55;DXS552;DXS552E	guanylate	membran	signal
GI_6006025-S	91.1	82.3	86.9	MTAP	NM_002451.2	MSAP	phosphory		nucleobas
GI_6006027-S	570.3	660.3	828.8	NRAS	NM_002524.2	N-ras;NRAS1	GTPase		oncogene
GI_6006029-S	1478.8	1408.2	1252	TBCE	NM_003193.2	HRD;KCS;KCS1;pac2	co-	microtubul	beta-
GI_6006032-S	69.5	204.7	154.5	ITGA4	NM_000885.2	CD49D	cell	integrin	cell
GI_6006037-S	105.5	110.1	103.8	HCRTR2	NM_001526.2	OX2R	neuropepti	integral to	neuropepti
GI_6006038-S	257	265.5	230.5	MAPK12	NM_002969.2	ERK3;ERK6;SAPK3;PRKM12;SAPK-	MAP	cytoplasm	DNA
GI_6006040-S	213.4	320.5	254.9	SLC25A20	NM_000387.2	CAC;CACT	lipid	mitochond	transport
GI_6007850-S	752.5	862.7	817.1	ITGAE	NM_002208.3	CD103;HUMINAE	cell	integrin	leukocyte
GI_6031156-S	93.3	97.2	91.4	ADORA3	NM_000677.2	A3AR	adenosine	integral to	regulation
GI_6031157-S	91.3	92.6	98.3	AGTRL2	NM_005162.2				
GI_6031161-A	315	1531.9	4591.5	CALB2	NM_007088.1	CAL2	calcium		
GI_6031163-S	117.6	150.7	115.6	EGF	NM_001963.2	URG	epidermal	integral to	activation
GI_6031164-S	528	1216.8	783	F2R	NM_001992.2	TR;CF2R;PAR1	thrombin	Golgi	tyrosine
GI_6031165-S	101.3	102.3	80.4	GALR1	NM_001480.2	GALNR;GALNR1	galanin	integral to	negative
GI_6031166-S	819.5	1199.6	1166.2	GPAA1	NM_003801.2	GAA1;hGAA1	GPI-	plasma	protein
GI_6031167-S	249.4	323.8	289.7	IVD	NM_002225.2	ACAD2	isovaleryl-	mitochond	electron
GI_6031177-A	300.8	378.9	347.6	MDM2	NM_006882.1	hdm2			negative
GI_6031179-A	855.3	747.1	814.4	MAP3K4	NM_006724.1	MTK1;MEKK4;MAPKKK4;KIAA0213	MAP		activation
GI_6031182-S	522.9	717.8	781.3	MGAT1	NM_002406.2	MGAT;GLCT1;GLYT1;GNT-1;GNT-	acetylgluc	Golgi	aminoglyc
GI_6031185-S	117	128.6	128.1	MGAT5	NM_002410.2	GNT-V	transferas	Golgi	N-linked
GI_6031188-A	152.5	152.2	159.9	NOVA1	NM_006491.1	Nova-1	RNA	nucleus	locomotor

GI_6031188-I	103.1	102	105.1	NOVA1	NM_006491.1	Nova-1	RNA	nucleus	locomotor
GI_6031190-S	1751.5	1861.1	1727.5	PHB	NM_002634.2		tumor		cell growth
GI_6031191-A	7771.4	7465.9	5869.8	SLC25A3	NM_005888.1	PHC	phosphate	mitochond	small
GI_6031191-I	131.4	124.2	122	SLC25A3	NM_005888.1	PHC	phosphate	mitochond	small
GI_6031195-S	627.9	548.3	937.5	PLAGL2	NM_002657.2		transcripti	nucleus	regulation
GI_6031196-S	155.7	185.1	161	SELP	NM_003005.2	CD62;GRMP;PSEL;CD62P;GMP140;PADGE	selectin	secretory	defense
GI_6031197-S	144.5	162.4	153.9	SELPLG	NM_003006.2	CD162;PSGL1;PSGL-1	bacterial	integral to	cell
GI_6031198-A	162	190.4	171.2	SHOX2	NM_003030.2	OG12;SHOT;OG12X;OGI2X	transcripti	nucleus	heart
GI_6031198-I	69.4	80.2	76.8	SHOX2	NM_003030.2	OG12;SHOT;OG12X;OGI2X	transcripti	nucleus	heart
GI_6031199-I	88.6	80.9	93.3	SHOX2	NM_006884.1	OG12;SHOT;OG12X;OGI2X	transcripti	nucleus	heart
GI_6031201-I	146.7	153.5	132.1	SHOX	NM_000451.2	SS;GCFX;PHOG;SHOXY	transcripti	nucleus	skeletal
GI_6031202-A	111.7	110.3	106.1	SHOX	NM_006883.1	SS;GCFX;PHOG;SHOXY	transcripti	nucleus	skeletal
GI_6031202-I	214.4	267.4	254	SHOX	NM_006883.1	SS;GCFX;PHOG;SHOXY	transcripti	nucleus	skeletal
GI_6031204-I	150.7	186.1	152	TCF2	NM_006481.1	HNF2;LFB3;HNF1B;MODY5;VHNF1;HNF1be	DNA	nucleus	regulation
GI_6031206-S	2285.5	2148.6	2324.3	PAFAH1B1	NM_000430.2	LIS1;MDCR;PAFAH	plasma	cytoplasm	lipid
GI_6031207-S	126.9	137	120.5	GABRA5	NM_000810.2		transporte	integral to	small
GI_6041664-S	3138.1	2256	2540.6	AGPAT2	NM_006412.2	BSCL;BSCL1;LPAAB;LPAAT-beta	lysophosp	integral to	phosphati
GI_6041666-S	125.3	119.3	87.9	DCT	NM_001922.2	TYRP2	copper ion	integral to	epidermal
GI_6042194-S	403.1	548.1	444.5	SLC33A1	NM_004733.2	AT1;AT-1;ACATN	acetyl-	endoplas	small
GI_6042195-S	229.4	360.6	323.4	CTSF	NM_003793.2	CATSF	lysosomal	lysosome	proteolysis
GI_6042197-S	111.2	163.9	167.7	LIFR	NM_002310.2	SWS;SJS2;STWS	leukemia	integral to	cell
GI_6042199-I	182.6	142.4	166.4	MME	NM_007287.1	NEP;CD10;CALLA	metallope	integral to	proteolysis
GI_6042201-A	12133.4	2580.3	4529.4	MME	NM_007288.1	NEP;CD10;CALLA	metallope	integral to	proteolysis
GI_6042203-I	225	197.1	185.2	MME	NM_007289.1	NEP;CD10;CALLA	metallope	integral to	proteolysis
GI_6042205-I	178.1	103.2	115.6	MME	NM_000902.2	NEP;CD10;CALLA	metallope	integral to	proteolysis
GI_6042206-S	1330.5	1433.9	1285.5	RAN	NM_006325.2	TC4;ARA24	RAN small	nuclear	mitotic
GI_6138970-S	665.3	574.1	246.5	ACP5	NM_001611.2	TRAP	acid	integral to	
GI_6138971-S	138.7	149.1	150.6	ADRBK1	NM_001619.2	GRK2;BARK1;BETA-ARK1	protein	soluble	signal
GI_6138972-S	217.6	253.7	240	ADRBK2	NM_005160.2	GRK3;BARK2	protein		signal
GI_6138973-S	174.9	156.7	110.9	AMH	NM_000479.2	MIF;MIS	glycopepti	extracellul	sex
GI_6138974-S	415.6	334.9	333.7	TIMM8A	NM_004085.2	DDP;MTS;DDP1;DFN1;MGC12262	protein	mitochond	neurogene
GI_6226959-S	106.5	95.9	92.7	A2M	NM_000014.3		protein		intracellula
GI_6274549-S	6969	6630.3	6196.2	NDUFB9	NM_005005.1	B22;UQOR22	NADH	mitochond	hearing
GI_6382056-I	130	145.9	151.6	ABL1	NM_005157.2	ABL;JTK7;p150;c-ABL;v-abl	protein-	nucleus	S-specific
GI_6382057-A	665.8	749.2	689.1	ABL1	NM_007313.1	ABL;JTK7;p150;c-ABL;v-abl	protein-	nucleus	S-specific
GI_6382057-I	113	137.3	119.3	ABL1	NM_007313.1	ABL;JTK7;p150;c-ABL;v-abl	protein-	nucleus	S-specific
GI_6382059-A	249.2	209	214	ABL2	NM_005158.2	ARG;ABLL	protein	cytoplasm	signal
GI_6382059-I	145	166	163.2	ABL2	NM_005158.2	ARG;ABLL	protein	cytoplasm	signal
GI_6382061-I	98.9	114.5	96.5	ABL2	NM_007314.1	ARG;ABLL	protein	cytoplasm	signal
GI_6382063-S	200.1	236.6	311.8	ACPP	NM_001099.2	PAP	protein	extracellul	regulation
GI_6382069-S	245.2	284.1	203.8	CRABP2	NM_001878.2	RBP6;CRABP-II	retinoid		epidermal
GI_6382070-A	344.2	272	302.1	DIAPH2	NM_007309.1	DIA;POF;DIA2;POF2	receptor	kinesin	cytokinesi
GI_6382070-I	290.2	251.8	249.9	DIAPH2	NM_007309.1	DIA;POF;DIA2;POF2	receptor	kinesin	cytokinesi
GI_6382072-S	157.2	281.2	189.6	GCHFR	NM_005258.2	GFRP;HsT16933			nitric oxide

GI_6382077-S	2845.1	3012	2628.6	RANBP1	NM_002882.2		RAN		signal
GI_6382080-S	88.5	85.3	90.4	RASGRP1	NM_005739.2	V;RASGRP;CALDAG-GEFI	lipid	membran	RAS
GI_6453816-S	106.5	106.3	93.8	IGF2	NM_000612.2				
GI_6453817-S	649.5	577.9	870.1	KIF22	NM_007317.1	KID;OBP;KNSL4;OBP-1;OBP-2	microtubul	kinetochor	mitosis
GI_6466447-S	4330.6	5663.2	2631.1	DSTN	NM_006870.2	ADF;ACTDP	actin	intracellula	actin
GI_6466448-S	184.5	230.6	198.4	ADMR	NM_007264.2	AMR;7TMR;hrhAMR	transmem	integral to	cell
GI_6466449-A	5605.5	6069.7	3460.5	COMT	NM_007310.1		O-	microsom	catechola
GI_6466451-I	838	901.6	515.3	COMT	NM_000754.2		O-	microsom	catechola
GI_6466452-S	571.2	645.2	564.5	MAD2L1	NM_002358.2	MAD2;HSMAD2		kinetochor	mitotic
GI_6466453-S	218.5	261.3	224.6	SNCB	NM_003085.2		phospholi	cytoplasm	
GI_6466461-A	193.2	224	225.8	RANBP3	NM_007320.1	DKFZp586I1520	RAN	nucleus	
GI_6466463-I	105.5	109.4	96.2	RANBP3	NM_007321.1	DKFZp586I1520	RAN	nucleus	
GI_6552300-I	144.6	153.6	128.4	BRCA1	NM_007295.1	PSCP;RNF53	protein	transcripti	regulation
GI_6552306-A	273.3	193.7	249.8	BRCA1	NM_007298.1	PSCP;RNF53	protein	transcripti	regulation
GI_6552322-I	110.1	103.4	89.2	BRCA1	NM_007306.1	PSCP;RNF53	protein	transcripti	regulation
GI_6552326-A	873.8	1165.8	1302.1	DIA1	NM_000398.3		cytochrom	hemoglobi	iron ion
GI_6552327-I	211.1	242.8	220.2	DIA1	NM_007326.1		cytochrom	hemoglobi	iron ion
GI_6552331-S	5499.2	2549.7	3397.4	FLOT1	NM_005803.2			caveola	
GI_6552332-S	334.7	613.9	807.5	FOS	NM_005252.2		specific	nucleus	DNA
GI_6552333-S	104.9	94	97.4	GRIA1	NM_000827.2	GLUH1;GLUR1;GLURA;HBGR1	alpha-	integral to	synaptic
GI_6552334-S	3091.4	3713.9	2593.1	GSTP1	NM_000852.2	PI;DFN7;GST3;FAEES3	glutathion		central
GI_6552335-S	948.1	956.8	796.9	PABPC4	NM_003819.2	APP1;APP-1;IPABP;PABP4	poly(A)	cytoplasm	response
GI_6552336-A	135.3	141	141.6	MADHIP	NM_007323.1	SARA;ZFYVE9	serine-	cytoplasm	SMAD
GI_6552336-I	279.4	362.3	302.4	MADHIP	NM_007323.1	SARA;ZFYVE9	serine-	cytoplasm	SMAD
GI_6552340-S	1771	2686.9	1893.2	SSR1	NM_003144.2	TRAPA	signal	integral to	cotranslati
GI_6552341-S	9298.3	14341	10875	SSR2	NM_003145.2	TLAP;TRAPB	signal	integral to	cotranslati
GI_6563384-S	321.7	343.2	264	PRKCN	NM_005813.2	EPK2;PKC-NU	protein		protein
GI_6594682-I	134.4	125.6	144	WHSC1	NM_007331.1	NSD2;TRX5;MMSET;REIIBP;KIAA1090			embryoge
GI_6598316-S	390.6	592.8	668.5	ACAA1	NM_001607.2	ACAA;THIO;PTHIO		peroxisom	energy
GI_6598317-A	133.1	159	145.9	AGRP	NM_007316.1	ART;AGRT;ASIP2	neuropepti		neuropepti
GI_6598319-S	353.9	349.2	359.7	AOX1	NM_001159.2	AO;AOH1	aldehyde		oxygen
GI_6598321-S	333.4	313.1	410.7	FXR2	NM_004860.2	FMR1L2	RNA	polysome	pathogene
GI_6598322-S	2614	2679.6	2139.1	GDI2	NM_001494.2	RABGDIB	RAB GDP-		nonselecti
GI_6598326-S	353.9	435.7	358.2	TSTA3	NM_003313.2	FX;P35B	catalytic		nucleotide-
GI_6601589-S	130.3	157.2	144.2	TRPA1	NM_007332.1	ANKTM1	channel/p	membran	ion
GI_6631076-S	2159.2	1903.4	1737.7	BAG5	NM_004873.1	BAG-5;KIAA0873	protein		protein
GI_6631089-S	89.8	89.3	77.7	IMPG1	NM_001563.2	IPM150	extracellul	extracellul	vision
GI_6631092-S	1006.7	1209.5	871.4	MAN2C1	NM_006715.1	MANA;MANA1;MAN6A8	alpha-		carbohydr
GI_6631099-S	443.9	561.3	552.9	NKTR	NM_005385.2		peptidyl-	plasma	protein
GI_6631101-I	172.4	199.7	188.1	PCDH8	NM_002590.2	PAPC;ARCADLIN	calcium-	integral to	cell-cell
GI_6631103-S	1795.3	2199.6	1725.9	EI24	NM_004879.2	PIG8;TP53I8			induction
GI_6631114-S	569.6	562.4	508.3	POLS	NM_006999.2	POLK;TRF4;LAK-1;TRF4-1	DNA	nucleus	DNA
GI_6633803-S	206.3	259.9	201.5	HBD	NM_000519.2		globin	hemoglobi	oxygen
GI_6633805-S	180.9	215.3	199.7	HBZ	NM_005332.2		oxygen	hemoglobi	oxygen

GI_6633806-S	106.5	116.3	111.4	LMO2	NM_005574.2	TTG2;RBTN2;RHOM2;RBTNL1		nucleus	oncogene
GI_6671584-S	588.5	675.6	686.1	ATF6	NM_007348.1		RNA	nuclear	unfolded
GI_6671590-S	101.7	106.7	102.8	ATP5G2	NM_005176.3		hydrogen-	proton-	proton
GI_6677700-A	247.9	274.5	241.6	GPR161	NM_007369.1	RE2			
GI_6677700-I	174.9	232.8	210.7	GPR161	NM_007369.1	RE2			
GI_6677928-S	159.5	200.9	197.6	SH3BGR	NM_007341.1	SH3GBR;21-GARP	SH3/SH2		protein
GI_6677978-S	104.3	114.8	104.6	SIX6	NM_007374.1	Six9;OPTX2	transcripti	nucleus	vision
GI_6678648-S	333.1	453	401.3	KRTHA6	NM_003771.3	HA6;hHa6	structural	kinesin	biological_
GI_6678675-S	934.2	883	651	COG2	NM_007357.1	LDLC	protein	Golgi	oligosacch
GI_6678763-S	390.8	441.1	376.1	M96	NM_007358.1	MTF2	DNA	nucleus	regulation
GI_6679051-S	143.4	135.4	127.3	KLRK1	NM_007360.1	KLR;NKG2D;NKG2-D;D12S2489E	receptor	integral to	signal
GI_6679073-S	638.2	611.5	413.2	NUPL2	NM_007342.1	CG1;hCG1;NLP-1;NLP_1	nuclear	nucleus	protein-
GI_6679187-S	107.7	103.8	96.6	PROL3	NM_006685.2	P-B;PRL3	molecular	cellular_co	biological_
GI_6679188-S	7320.5	6787.7	6034.2	P24B	NM_007364.1		protein	Golgi	intracellula
GI_6679302-S	2665.4	1904.5	1751.3	PHLDA1	NM_007350.1	TDAG51;DT1P1B11		nucleus	
GI_6679624-S	87.7	104.4	89.1	ELA3B	NM_007352.1		pancreatic	extracellul	cholestero
GI_6680080-S	113	127.3	123.1	GR6	NM_007354.1				oncogene
GI_6680470-I	274.9	330.5	289.4	AIF1	NM_004847.2	IBA1;AIF-1;IRT-1		nucleus	cell cycle
GI_6715560-S	140.3	172.6	145.3	ABCC6	NM_001171.2	ARA;PXE;MLP1;MRP6;ABC34;MOATE;EST3	ATP	membran	drug
GI_6715585-S	118.1	130.9	124.5	AKT2	NM_001626.2	PRKBB;PKBBETA;RAC-BETA	protein		protein
GI_6715587-S	1521.2	1067	504.7	BAG2	NM_004282.2	BAG-2	protein		protein
GI_6715588-S	905.5	795.1	906.5	BIG1	NM_006421.2	P200;ARFGEP1;DKFZP434L057	guanyl-		exocytosis
GI_6715592-A	183.5	212.9	189.2	DLEC1	NM_007336.1	F56;DLC1	tumor		negative
GI_6715598-S	162.4	188.5	160.5	GDF9	NM_005260.2		growth	extracellul	TGFbeta
GI_6715601-A	312.8	398.7	338.9	GPX5	NM_003996.2		glutathion	extracellul	response
GI_6715608-S	496.1	612.5	574	MAPK4	NM_002747.2	ERK3;PRKM4;p63MAPK;ERK3-RELATED	MAP		protein
GI_6715609-S	114.1	104.8	108.7	TULP1	NM_003322.2	RP14;TUBL1			vision
GI_6755759-S	158.8	164.8	149.1	TDRKH	NM_006862.2	TDRD2	nucleic		
GI_6806880-A	324	419.3	350	AOC2	NM_001158.2	RAO;DAO2	amine		biogenic
GI_6806881-I	117.9	126.7	111.9	AOC2	NM_009590.1	RAO;DAO2	amine		biogenic
GI_6806883-S	104.2	111.3	100.2	AOC3	NM_003734.2	HPAO;VAP1;VAP-1	amine	integral to	amine
GI_6806884-I	334.5	449.1	392.3	ARSD	NM_009589.1		arylsulfata		
GI_6806888-S	1025.5	691.9	688.2	HSF2	NM_004506.2		transcripti	nucleus	heat
GI_6806889-I	281.6	359.3	315.5	LGALS9	NM_009587.1		galactose		heterophili
GI_6806891-A	362.1	438.2	396.6	LGALS9	NM_002308.2		galactose		heterophili
GI_6806892-S	125.4	143.8	129.9	LTA	NM_000595.2	LT;TNFB;TNFSF1	receptor	membran	induction
GI_6806894-S	164.9	160	187.5	PKP4	NM_003628.2	p0071	structural	kinesin	cell
GI_6806896-I	87.2	81.2	90.8	SNCA	NM_000345.2	PD1;NACP;PARK1	structural	cytoplasm	anti-
GI_6806897-A	230.7	274	255.8	SNCA	NM_007308.1	PD1;NACP;PARK1	structural	cytoplasm	anti-
GI_6806899-S	778.3	1060.9	660.6	SQLE	NM_003129.2		squalene	microsom	electron
GI_6806912-S	646.4	609.3	620.6	CENTA1	NM_006869.1	GCS1L;p42IP4	phospholi	nucleus	cell
GI_6806918-S	169.9	206.3	172.1	LRP2	NM_004525.1	gp330	LDL	lysosome	receptor
GI_6806920-S	126.2	147.9	142.2	SLC9A3	NM_004174.1	NHE3	sodium:hy	integral to	sodium
GI_6857798-S	613.1	655.5	579.4	PGRMC1	NM_006667.2	MPR;HPR6.6	steroid	microsom	electron

GI_6857817-S	1500.7	1278.3	1113	NPM3	NM_006993.1		nucleic	nucleus	
GI_6912241-S	200.5	243.3	221.4	APPL	NM_012096.1	DIP13alpha	protein	cytoplasm	signal
GI_6912245-S	723.1	578.7	498	ASE-1	NM_012099.1	CAST	antisense	nucleolus	rRNA
GI_6912247-S	636.5	552.8	670.6	DNPEP	NM_012100.1	DAP;ASPEP	aminopept	cytoplasm	peptide
GI_6912269-S	216.3	242.9	240.6	BP75	NM_012107.1				
GI_6912271-S	99.8	89.6	82.8	BRDG1	NM_012108.1	STAP1;STAP-1			membran
GI_6912273-S	283.1	487.4	227.3	C19orf4	NM_012109.1	BSMAP		integral to	
GI_6912277-S	3324	3679.8	2614.7	COMMD3	NM_012071.1	BUP;C10orf8			
GI_6912279-S	4014.5	5372.7	4286.4	AHSA1	NM_012111.1	p38;AHA1;C14orf3			
GI_6912283-S	162.4	214.8	183.5	CA14	NM_012113.1		carbonate	integral to	one-
GI_6912285-S	89.4	98.6	102.8	CASP14	NM_012114.1	MICE	caspase		epidermal
GI_6912291-S	417.1	562.7	440.7	CBX5	NM_012117.1	HP1;HP1-ALPHA;HP1Hs-alpha	lamin/chro	nuclear	chromatin
GI_6912299-A	831.2	606.3	670.9	MTO1	NM_012123.1	CGI-02	molecular		electron
GI_6912301-S	2833.8	1885.7	1989.6	C16orf35	NM_012075.1	-14;CGTHBA	molecular	cellular_co	biological_
GI_6912303-S	361.8	398.2	343.8	CHORDC1	NM_012124.1	CHP1	molecular	cellular_co	biological_
GI_6912305-A	136	156.4	135	CHST5	NM_012126.1	FLJ22167	sulfotransf	integral to	protein
GI_6912305-I	162.1	188.9	167.8	CHST5	NM_012126.1	FLJ22167	sulfotransf	integral to	protein
GI_6912315-S	101.5	104.8	92.3	CLDN17	NM_012131.1		structural	tight	
GI_6912319-S	432.6	458.8	452.4	COPG2	NM_012133.1	2-COP;FLJ11781	vesicle		nonselecti
GI_6912323-S	91.2	101	95.9	LMOD1	NM_012134.1	1D;D1;64kD;SM-LMOD	tropomyos	cytoskelet	pathogene
GI_6912325-S	108.4	97.3	105.9	D6S2654E	NM_012135.1	X5L			
GI_6912343-S	213.5	198.8	196.9	DUX3	NM_012148.1				
GI_6912345-S	618.7	508	599.5	FAM16AX	NM_012080.1	GS1;DXF68S1E	molecular	cellular_co	metabolis
GI_6912347-S	222.2	134	148	EDG7	NM_012152.1	GPCR;Edg-7;LP-A3;HOFNH30;RP4-678I3	lipid	integral to	cytosolic
GI_6912355-S	588.4	1563.5	1009.2	EML2	NM_012155.1	ELP70;EMAP2;EMAP-2		microtubul	hearing
GI_6912361-S	112.8	140.2	122.8	FBXW3	NM_012165.1	FBW3	ubiquitin-		ubiquitin-
GI_6912371-S	105.9	105.7	95.3	FOXD3	NM_012183.1	HFH2;Genesis	transcripti	nucleus	regulation
GI_6912379-S	222.9	213.7	239.4	FUS2	NM_012191.1	FUS-2	acyltransf		cell growth
GI_6912389-S	335.3	437.1	376.3	GLG1	NM_012201.1	CFR-1;ESL-1;MG160;MG-160	receptor	Golgi	
GI_6912393-S	106.8	112	99.3	GNG3	NM_012202.1		heterotrim	heterotrim	activation
GI_6912395-S	5019.8	4672.4	4411.4	GRHPR	NM_012203.1	GLXR	electron		excretion
GI_6912397-S	470	510.8	395.1	GTF3C3	NM_012086.1	TFIIIC102;TFIIICgamma;TFiiiC2-102	RNA	transcripti	transcripti
GI_6912399-S	437.3	449.6	409.6	GTF3C4	NM_012204.1	TFIII90;TFIIIC90;TFiiiC2-90;TFIIICdelta	H3/H4	transcripti	transcripti
GI_6912401-S	1788.4	1864.5	1884.2	GTF3C5	NM_012087.1	TFIIIC63;TFiiiC2-63;TFIIICepsilon	RNA	transcripti	transcripti
GI_6912405-S	318.4	405.2	358	HAAO	NM_012205.1	HAO;3-HAO	quinolinat		
GI_6912407-S	104.9	116.6	108.4	HAVCR1	NM_012206.1	KIM1;TIM1;HAVCR;KIM-1;TIM-			
GI_6912413-S	101.8	132.3	94.7	HEY2	NM_012259.1	GRL;HERP1	DNA		histogene
GI_6912417-S	1608.3	1498.5	1431.4	HPCL2	NM_012260.1		magnesiu	peroxisom	lipid
GI_6912427-S	256.9	310.8	245.7	HYAL4	NM_012269.1		hyalurono		glycosami
GI_6912437-S	113.1	110.8	102.3	ITGB1BP2	NM_012278.1	CHORDC3;ITGB1BP;MELUSIN;MSTP015	protein	peripheral	muscle
GI_6912443-S	106.5	98.9	88.2	KCNG2	NM_012283.1	KCNF2;KV6.2	delayed	voltage-	potassium
GI_6912445-S	426	511.6	458.9	KCNH4	NM_012285.1	BEC2;ELK1;Kv12.3	voltage-	voltage-	potassium
GI_6912447-S	2203.6	3449.9	3166.1	MORF4L2	NM_012286.1	MRGX;MORFL2;KIAA0026	molecular	nucleus	regulation
GI_6912449-S	1204.1	1652.4	1335.7	TRAM2	NM_012288.1				

GI_6912463-S	493.5	476.5	802.1	LPHN2	NM_012302.1	LEC1;LPHH1;KIAA0786			
GI_6912471-S	172.4	195.6	175.5	KIR2DS2	NM_012312.1	CL-49;NKAT5;p50.2;CD158J;183ACTI			
GI_6912473-S	89	100.7	84.8	KIR2DS3	NM_012313.1	NKAT7	MHC-	integral to	cellular
GI_6912481-S	382.7	400.9	379	LETM1	NM_012318.1		calcium	integral to	signal
GI_6912487-S	2241.4	2231.3	1953.9	LSM5	NM_012322.1	YER146W	RNA	small	mRNA
GI_6912493-S	2948.9	3772.2	4957.3	MAPRE1	NM_012325.1	EB1	protein C-		oncogene
GI_6912497-S	749.2	789.2	938.5	MLYCD	NM_012213.1	MCD;hMCD	methylmal	peroxisom	acyl-CoA
GI_6912501-S	84.7	80.5	78.6	MGAT4A	NM_012214.1	GNT-IV;GnT-Iva	alpha-1,3-	membran	N-glycan
GI_6912505-S	140	140.4	127.3	MIP	NM_012064.1	AQP0;LIM1;MP26;MIP26	transporte	gap	cell-cell
GI_6912507-S	442.9	1406.4	1717.7	MMD	NM_012329.1	MMA	receptor	membran	cytolysis
GI_6912511-S	149.1	148.9	141.1	MYST4	NM_012330.1	qkf;MORF;MOZ2;KIAA0383;querkopf	histone	nucleus	regulation
GI_6912517-S	681.5	626	745.2	ACATE2	NM_012332.1	CGI-16;MT-ACT48	catalytic	mitochond	lipid
GI_6912519-S	870.5	606.2	673.4	MUTYH	NM_012222.1	MYH	endonucle	nucleus	mismatch
GI_6912525-S	251.5	193.6	213.5	NESG1	NM_012337.1			soluble	
GI_6912531-S	2721	2508	2674.6	GTPBP4	NM_012341.1	NGB;CRFG;FLJ10686;FLJ10690	GTP	nucleus	
GI_6912533-S	155.4	459.4	394	BAMBI	NM_012342.1	NMA		integral to	oncogene
GI_6912539-S	3650.5	3558.1	4160.6	NUBP2	NM_012225.1	CFD1	nucleotide		
GI_6912541-S	307.8	269.8	251	NUFIP1	NM_012345.1	NUFIP	protein	nucleus	RNA
GI_6912549-S	96.6	88.7	98.7	OR10J1	NM_012351.1	HGMP07J;HSHGMP07J	G-protein	integral to	chemosen
GI_6912551-S	140	155.8	147.9	OR1A2	NM_012352.1	OR17-6	olfactory	integral to	olfaction
GI_6912553-S	207.1	254.3	246.3	OR1F1	NM_012360.1	OLFMF;OR1F4;OR1F5;OR1F6;OR1F7;OR1	receptor	integral to	signal
GI_6912555-S	159.7	178.2	160	OR2C1	NM_012368.1	OLFmf3;OR2C2P	olfactory	integral to	perception
GI_6912557-S	373.6	436.5	416.4	OR2F1	NM_012369.1	OLF3;OR2F3;OR2F4;OR2F5;OR2F3P;OR14-	receptor	integral to	signal
GI_6912559-S	329.9	454.1	394	OR52A1	NM_012375.1	HPFH1OR	transmem	integral to	olfaction
GI_6912569-S	392.9	406.5	97.9	P8	NM_012385.1	COM1	molecular	nucleus	induction
GI_6912575-S	134.8	275.7	195.1	PADI4	NM_012387.1	PAD;PDI4;PDI5;PADI5	protein-		protein
GI_6912577-S	331.9	380.1	321.8	PROL5	NM_012390.1	PBI;P-B1;PRL5		extracellul	
GI_6912579-S	98.3	100.5	91.7	SPDEF	NM_012391.1	PDEF;bA375E1.3	protein	nucleus	developm
GI_6912581-S	840.5	1017.9	1044.3	PEF	NM_012392.1	PEFLIN	calcium		
GI_6912587-S	1275.7	988.6	1006	PGPL	NM_012227.1		GTP		
GI_6912589-S	765.3	788.3	802.7	PHLDA3	NM_012396.1	TIH1			embryoge
GI_6912603-S	122	142.6	115.4	ANP32C	NM_012403.1	PP32R1			oncogene
GI_6912611-A	318.7	381.7	424.2	PSK-1	NM_012410.1				
GI_6912625-S	115.9	121.1	110.2	FSCN2	NM_012418.1	RFSN;RP30	actin	actin	vision
GI_6912629-S	237.5	206.4	185.3	IFIT5	NM_012420.1	RI58	molecular	cellular_co	immune
GI_6912631-S	449.9	565.7	378.1	RLF	NM_012421.1		zinc ion	nucleus	regulation
GI_6912641-S	371.3	349.6	320	SCMH1	NM_012236.1	Scml3	DNA		embryoge
GI_6912645-I	140.8	160.8	154.3	SDFR1	NM_012428.1	GP55;GP65			
GI_6912649-S	302.9	364.7	363.6	SEMA3E	NM_012431.1				
GI_6912653-S	1189.2	1802.6	1594.8	SF3B1	NM_012433.1	PRP10;SAP155;SF3B155	pre-mRNA	spliceoso	mRNA
GI_6912661-S	128.3	154.1	152.3	SIRT4	NM_012240.1	SIR2L4	NAD ADP-	chromatin	chromatin
GI_6912667-S	322.3	333.2	342.6	SLC35A3	NM_012243.1		UDP-N-	Golgi	UDP-N-
GI_6912681-S	90	88	75.3	SPON2	NM_012445.1	DIL1;DIL-1;Mindin;M-spondin	structural	extracellul	axon
GI_6912685-I	138.8	178.6	149.1	STAG3	NM_012447.1	MGC2463		synaptone	synaptone

GI_6912695-S	164.2	207.5	176.8	ARHQ	NM_012249.1	TC10;TC10A;RASL7A	Rho small	plasma	small
GI_6912699-A	431.9	380.6	382.5	TFAM	NM_012251.1	TCF6;MtTF1;mtTFA;TCF6L2	transcripti	mitochond	transcripti
GI_6912701-S	163.9	189.3	188.9	TFEC	NM_012252.1	TCFEC;TFECL	transcripti	nucleus	
GI_6912705-S	158.8	250.5	126.1	TIC	NM_012455.1	EFA6B			
GI_6912707-S	1446	1267.1	1348.9	TIMM10	NM_012456.1	TIM10;TIM10A	zinc ion	mitochond	mitochond
GI_6912711-S	2160.2	3845.7	3070	TIMM8B	NM_012459.1	DDP2;TIM8B	zinc ion	mitochond	mitochond
GI_6912715-S	1390	1274.7	1494.9	TINF2	NM_012461.1	TIN2	protein	telomere	telomeras
GI_6912727-S	196.3	247.1	221.3	TPSG1	NM_012467.1	TMT;PRSS31	serine-	integral to	proteolysis
GI_6912735-S	129.1	165.3	144.7	TRPC5	NM_012471.1	TRP5	store-	integral to	calcium
GI_6912747-S	90.2	95.9	97.4	ZNF73	NM_012480.1				
GI_6981363-S	378.5	490.5	400.2	PLA2G6	NM_003560.1	iPLA2	phospholi	membran	phospholi
GI_6995993-I	113.7	111.3	111.3	AGC1	NM_013227.1	CSPG1;MSK16;CSPGCP	chondroiti	extracellul	heterophili
GI_6995995-S	106.7	116	113.1	CFTR	NM_000492.2	CF;MRP7;ABC35;ABCC7	ATP-	membran	respiratory
GI_6995997-S	7521.4	8877.5	7539.4	ARF1	NM_001658.2		GTPase	Golgi	small
GI_6995998-S	4210.6	5305	4126.5	ARF4	NM_001660.2		ARF small	Golgi	small
GI_6995999-S	626.4	715.4	757.5	ARF5	NM_001662.2		ARF small	Golgi	small
GI_6996000-S	137.1	148.1	130.6	ARF6	NM_001663.2		ARF small	Golgi	nonselecti
GI_6996001-S	198.9	260.7	225.9	CA3	NM_005181.2	CAIII	carbonate	cytoplasm	one-
GI_6996002-S	4384.6	5396.5	3960.9	COPA	NM_004371.2	HEP-COP	vesicle	coated	ER to
GI_6996003-S	303.8	234.3	292.6	DLX2	NM_004405.2	TES1;TES-1	transcripti	nucleus	brain
GI_6996006-A	265.6	350.1	325.6	DNM1L	NM_012063.1	DLP1;DRP1;DVLP;VPS1;DYMPLE;HDYNIV	GTPase	Golgi cis-	mitochond
GI_6996009-S	21952.4	18465	14004	GARS	NM_002047.1	CMT2D;SMAD1	glycine-	soluble	protein
GI_6996012-S	159.8	110.9	97.7	GZMA	NM_006144.2	HFSP;CTLA3	granzyme		immune
GI_6996015-A	123.5	122.8	109.5	LTB	NM_009588.1	p33;TNFC;TNFSF3	receptor	integral to	signal
GI_6996017-S	397.2	357.4	230.1	MSC	NM_005098.2	ABF1;MYOR;ABF-1	transcripti	nucleus	transcripti
GI_6996020-S	160.8	200.1	173.1	CYBB	NM_000397.2	CGD;NOX2;GP91-1;GP91PHOX;GP91-	cytochrom	integral to	energy
GI_6996927-S	1132.6	1464.8	1375.6	MORF4	NM_006792.2	CSR;SEN;CSRB;SEN1	transcripti	nucleus	aging
GI_6997248-S	205.8	243.7	243	SALL1	NM_002968.1	TBS;HSAL1	DNA	nucleus	embryoge
GI_7019332-S	333.4	393.1	526.3	NRBP	NM_013392.1	MADM;BCON3;MUDPNP	SH3/SH2	nucleus	signal
GI_7019334-S	352.3	369.7	189.2	C11orf9	NM_013279.1	KIAA0954;MGC10781			
GI_7019336-S	398.6	306.1	304.3	C16orf5	NM_013399.1		molecular	nucleus	biological_
GI_7019340-S	745	946.5	1457.3	CARKL	NM_013276.1		kinase		carbohydr
GI_7019342-S	119.6	173.3	347	CD24	NM_013230.1	CD24A		plasma	humoral
GI_7019356-A	148.1	139.4	121.2	CRYBA2	NM_005209.1		structural	cellular_co	biological_
GI_7019370-S	514.9	496.9	517.6	TFPT	NM_013342.1	FB1;amida	nuclear	nucleus	induction
GI_7019372-S	3007	2386.8	2151.5	FEZ2	NM_005102.1	HUM3CL	cell		axon
GI_7019374-S	561.7	774.5	676.3	FHOD1	NM_013241.1	FHOS	actin	kinesin	cytokinesi
GI_7019404-S	153.1	181.2	133	HCF-2	NM_013320.1	HCF2	RNA	membran	viral life
GI_7019408-S	477.8	446.5	354.1	HIG2	NM_013332.1		molecular	integral to	response
GI_7019410-S	237.7	297.8	285.3	HOOK2	NM_013312.1	HK2			endocytosi
GI_7019418-S	2979.5	2633.8	2708.9	HUMAUANTI	NM_013285.1		GTPase	nucleus	biological_
GI_7019440-S	188	254.6	209.1	KIR3DL1	NM_013289.1	KIR;CL-2;NKB1;AMB11;CL-			
GI_7019446-S	116.4	124.5	91.5	LLT1	NM_013269.1		transmem	membran	cell
GI_7019450-S	111.9	125	113.7	PNMA3	NM_013364.1	MA3;MA5	nucleic		

GI_7019452-S	1719.9	2125.9	1485.2	DNAJD1	NM_013238.1	MCJ			
GI_7019466-S	582.6	619.6	562.8	CNOT4	NM_013316.1	NOT4;NOT4H;CLONE243			
GI_7019468-S	93.2	90.3	96.3	NPC1L1	NM_013389.1		hedgehog	integral to	sterol
GI_7019492-S	269.7	294.7	267.6	POLM	NM_013284.1	Tdt-N;POL-IOTA;Pol iota	eta DNA	intracellula	DNA
GI_7019510-S	975	782.6	905.4	DPP7	NM_013379.1	QPP;DPP2;DPPII	serine-	lysosome	proteolysis
GI_7019520-S	2424.8	2328.8	1699.1	SART2	NM_013352.1		tumor	endoplas	
GI_7019524-S	367.8	446.3	512.1	SERTAD1	NM_013376.1	SEI1;TRIP-Br1			regulation
GI_7019528-S	114.2	116.5	104.4	SLC16A8	NM_013356.1	MCT3	lactate	membran	lactate
GI_7019542-S	1687.1	941.1	1156.8	STK39	NM_013233.1	DCHT;SPAK	protein-	cytoplasm	response
GI_7019548-S	109.3	135.3	124	TBX21	NM_013351.1	T-PET;T-bet;TBLYM	transcripti	nucleus	regulation
GI_7019550-S	1059.1	745.5	919.2	TERE1	NM_013319.1			membran	
GI_7019552-S	1445.7	1408.9	1288	TIMM22	NM_013337.1	TEX4;TIM22	protein	mitochond	intracellula
GI_7019554-S	272.8	424.1	496.5	TMEM2	NM_013390.1			integral to	
GI_7019556-S	144.2	165.2	152.5	TMOD4	NM_013353.1	Sk-Tmod	tropomyos	F-actin	muscle
GI_7019560-S	185.8	174.4	188.6	TRHDE	NM_013381.1	PAP-II	aminopept	integral to	sterol
GI_7019566-S	110.7	123	101.4	VPREB3	NM_013378.1	8HS20		endoplas	
GI_7019570-S	96.8	102.2	98.3	CTNNA3	NM_013266.1	VR22;MGC26194			
GI_7019572-S	1308.9	1191.2	1121.6	STRN4	NM_013403.1	ZIN;zinedin	structural	kinesin	synaptic
GI_7019576-S	171.5	202.3	171.7	TAC3	NM_013251.1	NKB;NKNB;ZNEUROK1	tachykinin	soluble	tachykinin
GI_7019578-S	395.5	432.8	377.2	ZNF180	NM_013256.1	HHZ168	DNA	nucleus	regulation
GI_7019580-S	82.7	96.3	80.1	ZNF214	NM_013249.1	BAZ1	zinc ion	nucleus	regulation
GI_7019582-S	89.2	85.4	86.5	ZNF215	NM_013250.1	BAZ2			
GI_7019584-S	123.4	148.5	133.3	ZNF221	NM_013359.1		DNA	nucleus	regulation
GI_7019586-S	240.3	203	181.4	ZNF222	NM_013360.1		DNA	nucleus	regulation
GI_7019590-S	95.1	111.4	91.4	ZNF224	NM_013398.1	BMZF2;ZNF255	DNA	nucleus	regulation
GI_7019592-S	130.1	151.9	124.9	ZNF225	NM_013362.1		DNA	nucleus	regulation
GI_7106298-S	1487.5	1677.4	1423.2	E46L	NM_013236.1	DKFZP586H2219	molecular	cellular_co	biological_
GI_7106370-S	110.7	129.3	114	LOH3CR2A	NM_013343.1	NAG7;NAG-7			
GI_7108334-S	330.1	325.2	301.6	CBR3	NM_001236.2		carbonyl	cytosol	metabolis
GI_7108339-A	1422	1505.3	1573.6	DHPS	NM_013407.1		deoxyhypu		positive
GI_7108341-I	1548	1626.4	1742.5	DHPS	NM_001930.2		deoxyhypu		positive
GI_7108342-S	573.3	1103	1431.1	DUSP1	NM_004417.2	HVH1;CL100;MKP-1;PTPN10	non-		response
GI_7108343-A	248.9	315.3	266.5	GNLY	NM_006433.2	519;LAG2;NKG5;LAG-2;D2S69E;TLA519	antifungal	extracellul	cellular
GI_7108343-I	118.3	126	124.6	GNLY	NM_006433.2	519;LAG2;NKG5;LAG-2;D2S69E;TLA519	antifungal	extracellul	cellular
GI_7108345-I	124.2	117.9	113.7	GNLY	NM_012483.1	519;LAG2;NKG5;LAG-2;D2S69E;TLA519	antifungal	extracellul	cellular
GI_7108347-S	127.8	143.4	137.7	GZMM	NM_005317.2	MET1;LMET1	serine-		proteolysis
GI_7108350-A	382.3	420.4	400.9	HMMR	NM_012485.1	RHAMM	hyaluronic		oncogene
GI_7108353-S	162.1	161.2	181	KLRC2	NM_002260.2	NKG2C;NKG2-C	transmem	integral to	cellular
GI_7108354-S	2084.6	1256.2	1567.7	LMO4	NM_006769.2		transcripti	nucleus	embryoge
GI_7108357-A	134.4	175	146.7	MSLN	NM_005823.2	MPF;SMR;CAK1			
GI_7108359-A	822.4	780	1087.5	PSEN2	NM_012486.1	AD4;PS2;AD3L;STM2		integral to	apoptotic
GI_7108361-A	150.6	184.5	144.3	SIM2	NM_009586.1	SIM	DNA	nucleus	embryoge
GI_7108361-I	79.1	96	93.1	SIM2	NM_009586.1	SIM	DNA	nucleus	embryoge
GI_7108363-I	173.7	222.9	184.9	SIM2	NM_005069.2	SIM	DNA	nucleus	embryoge

GI_7108366-S	112.3	102.2	103.3	VAV1	NM_005428.2	VAV	transcripti	nucleus	oncogene
GI_7110592-S	434.2	445.5	219.2	FLI1	NM_002017.2	EWSR2;SIC-1	DNA	nucleus	hemostasi
GI_7110640-S	378.1	466.4	411.6	PLD3	NM_012268.1	HU-K4	phospholi		virulence
GI_7110678-S	139.1	163.3	191.4	OSRF	NM_012382.1				
GI_7110696-S	1422.1	1900.2	1616.1	PRKCABP	NM_012407.1	PICK1;dJ1039K5	protein C-	presynapti	ion
GI_7110714-S	260.6	314.1	303.8	SEC14L2	NM_012429.1	SPF;TAP;C22orf6;KIAA1186;KIAA1658	tocopherol	cytoplasm	transport
GI_7110718-S	132.3	147.3	123.1	DKK1	NM_012242.1	SK;DKK-1	growth		developm
GI_7110726-S	112.4	111	115	TKTL1	NM_012253.1	TKR;TKT2	transketol		thiamin
GI_7110734-S	100.5	129	114.4	VAX2	NM_012476.1	DRES93	transcripti	nucleus	ectoderm
GI_7242166-S	99.6	107.6	90.4	PAX9	NM_006194.1		DNA	nucleus	regulation
GI_7242221-A	591.2	1196.8	308.7	FST	NM_013409.1	FS	activin	extracellul	developm
GI_7242223-I	103.3	150.5	93.3	FST	NM_006350.2	FS	activin	extracellul	developm
GI_7262293-S	176	223.9	183	ARSA	NM_000487.3	MLD	arylsulfata	lysosome	sphingolipi
GI_7262372-S	135.2	270.2	142.3	BST2	NM_004335.2			integral to	humoral
GI_7262376-S	295.4	310.8	354.3	DHFR	NM_000791.2		dihydrofol	cellular_co	glycine
GI_7262380-S	371.5	547.6	526.3	SERPIND1	NM_000185.2	HC2;LS2;HCF2;HLS2;HC-II;D22S673	endopepti		chemotaxi
GI_7262382-I	174.8	219.3	188	KLRC1	NM_002259.2	NKG2;NKG2A;CD159A;NKG2-A;NKG2-B	transmem	integral to	cell
GI_7262383-A	107.7	121.4	112	KLRC1	NM_007328.1	NKG2;NKG2A;CD159A;NKG2-A;NKG2-B	transmem	integral to	cell
GI_7262385-A	123.4	121.2	126.8	KLRC3	NM_007333.1	NKG2E;NKG2-E	transmem	integral to	cellular
GI_7262385-I	72.8	81.5	95	KLRC3	NM_007333.1	NKG2E;NKG2-E	transmem	integral to	cellular
GI_7262387-S	10663.3	9250.6	7845.3	NARS	NM_004539.2	ASNRS	asparagin	soluble	protein
GI_7262388-S	765.3	3450.5	192	PCOLCE	NM_002593.2	PCPE	collagen		cell growth
GI_7262389-S	124.7	115.3	116.4	RHO	NM_000539.2	RP4;OPN2	G-protein	integral to	rhodopsin
GI_7262392-S	117.4	157.6	122.3	ABCD1	NM_000033.2	ALD;AMN;ALDP;ABC42	nucleotide	integral to	peroxisom
GI_7304922-S	237.9	309.2	268.3	BAZ2B	NM_013450.1	DKFZP434H071	DNA	kinesin	regulation
GI_7305204-S	373.7	398.9	468.1	KIF4A	NM_012310.2	KIF4;KIF4-G1;HSA271784	microtubul	spindle	anterogra
GI_7305450-S	86.3	98.3	89.3	RAX	NM_013435.1	RX	RNA	nucleus	vision
GI_7305502-S	2370.9	1920.9	1559.1	STOML2	NM_013442.1	SLP-2;HSPC108	receptor	peripheral	
GI_7305624-S	756.1	192	640.3	VCX	NM_013452.1	VCX-B1;VCX10R;VCX-10r			spermatog
GI_7330334-S	4396.4	4691.5	3216.2	CLIC4	NM_013943.1	H1;huH1;P64H1;CLIC4L;DKFZP566G223	chloride	membran	chloride
GI_7330336-S	114.1	119	110.8	OR10H2	NM_013939.1		olfactory	integral to	olfaction
GI_7330338-S	89.2	95.2	81	OR10H3	NM_013938.1		olfactory	integral to	olfaction
GI_7363438-S	95.9	100.5	85.9	OR10H1	NM_013940.1		olfactory	integral to	olfaction
GI_7382453-S	112.5	118.1	122.8	CHRNG	NM_005199.3	ACHRG	muscarini	integral to	small
GI_7382457-S	195.4	241.5	210.6	PRTN3	NM_002777.2	MBT;P29;ACPA;AGP7;PR-3	serine-	cellular_co	positive
GI_7382459-S	180.9	206.5	193.5	SHBG	NM_001040.2	ABP	androgen		
GI_7382475-S	577.6	701.1	465.7	ADAT1	NM_012091.2	HADAT1	tRNA		tRNA
GI_7382476-I	133.7	136.9	137	ARHGAP6	NM_001174.2	RHOGAP6	SH3/SH2	actin	Rho
GI_7382477-A	98.5	109.9	104.5	ARHGAP6	NM_013422.1	RHOGAP6	SH3/SH2	actin	Rho
GI_7382479-I	116.9	126.2	116.9	ARHGAP6	NM_013423.1	RHOGAP6	SH3/SH2	actin	Rho
GI_7382485-S	505.3	691.9	587.7	CCNC	NM_005190.2		cyclin-	nucleus	regulation
GI_7382489-S	438.3	500.3	437.7	DGAT1	NM_012079.2	DGAT;ARGP1	diacylglyc	endoplas	triacylglyc
GI_7382490-S	4423.7	1027.7	1111	LCP1	NM_002298.2	CP64;PLS2;LC64P;L-PLASTIN	actin	cytosol	biological_
GI_7382491-S	79.3	81.2	80.5	LCP2	NM_005565.2	SLP76;SLP-76	protein		transmem

GI_7382492-I	459.7	558.4	493.1	NCF4	NM_013416.1	NCF;P40PHOX	electron	cytosol	defense
GI_7382494-A	100.5	94.3	92.2	NCF4	NM_000631.2	NCF;P40PHOX	electron	cytosol	defense
GI_7382494-I	139.6	155.5	121	NCF4	NM_000631.2	NCF;P40PHOX	electron	cytosol	defense
GI_7382497-S	554.6	544.3	535.2	PAK4	NM_005884.2		protein	Golgi	cell
GI_7427516-S	112.9	114.1	105.1	HSPG2	NM_005529.2	PLC;SJA;SJS;SJS1	heparin	basement	
GI_7524013-S	108.2	104.3	86	PSG6	NM_002782.3	PSG10	plasma	extracellul	pregnancy
GI_7524347-A	307.6	225	204	BNIP1	NM_013978.1	NIP1	apoptosis	integral to	anti-
GI_7524353-S	481	501	451.3	DDAH2	NM_013974.1	G6a;NG30;DDAHII	catalytic		nitric oxide
GI_7524358-A	779.1	965.5	854.4	PAX7	NM_013945.1	HUP1	transcripti	nucleus	anti-
GI_7549792-A	1152.9	1054.3	1027.2	TBL2	NM_012453.1	WBSCR13;WS-betaTRP;DKFZP43N024	molecular	cellular_co	biological_
GI_7549801-S	1343.3	1979.2	2039.8	BAG1	NM_004323.2		apoptosis	cytoplasm	anti-
GI_7549802-I	89.9	92.1	100.4	DIO2	NM_013989.1	SelY;TXDI2	selenium	integral to	thyroid
GI_7549804-A	105.7	114.7	112.4	DIO2	NM_000793.2	SelY;TXDI2	selenium	integral to	thyroid
GI_7549806-S	458	553.6	481.4	FBXW2	NM_012164.2	FBW2	ubiquitin		proteolysis
GI_7549807-S	2480.7	2312.6	1593.6	DNAJA2	NM_005880.2	CPR3;DNAJ;DNJ3;HIRIP4;PRO3015			positive
GI_7549810-S	97.8	120.7	117	PPARA	NM_005036.2	PPAR;NR1C1;hPPAR	peroxisom	nucleus	fatty acid
GI_7549812-I	100.4	88.8	90.9	PSEN1	NM_007318.1	AD3;FAD;PS1;S182		integral to	chromoso
GI_7549814-A	476	597.4	489.5	PSEN1	NM_007319.1	AD3;FAD;PS1;S182		integral to	chromoso
GI_7549814-I	140	184.2	157.8	PSEN1	NM_007319.1	AD3;FAD;PS1;S182		integral to	chromoso
GI_7549816-I	212.2	240.5	203.4	RABL2A	NM_013412.1		RAB small		small
GI_7549818-A	563.4	470.4	379.2	RABL2A	NM_007082.2		RAB small		small
GI_7656842-A	745.8	1505.1	608.8	GRCA	NM_014449.1				
GI_7656848-S	427.2	511.9	557.5	ACAD8	NM_014384.1	ACAD-8	acyl-CoA	mitochond	lipid
GI_7656858-S	123.1	124.8	121.5	AD7C-NTP	NM_014486.1			integral to	central
GI_7656860-S	152.2	159.6	142.6	ADAM18	NM_014237.1	ADAM27;tMDCIII	metallope	integral to	spermatog
GI_7656862-I	83.7	85.4	76.3	ADAM28	NM_014265.1	MDCL;ADAM23;MDC-Lm;MDC-Ls;eMDCII	metallope	integral to	spermatog
GI_7656866-I	116.3	109.8	134.2	ADAMTS2	NM_014244.1	NPI;PCINP;PCPNI;hPCPNI;ADAM-	collagenas	extracellul	collagen
GI_7656870-S	1057.9	840	779.2	ZNF544	NM_014480.1		nucleic	nucleus	regulation
GI_7656878-S	112.3	138.1	117.1	AF5Q31	NM_014423.1	MCEF	transcripti		oncogene
GI_7656882-S	642.8	402.8	136.5	PDLIM3	NM_014476.1	ALP			
GI_7656889-A	1445.7	1422.4	1134	REPIN1	NM_014374.1	AP4;RIP60;ZNF464;Zfp464	DNA	nuclear	DNA
GI_7656889-I	119.5	130.4	122.2	REPIN1	NM_014374.1	AP4;RIP60;ZNF464;Zfp464	DNA	nuclear	DNA
GI_7656907-S	125.7	116.8	91.9	ASML3B	NM_014474.1				
GI_7656909-S	2250.1	3088.7	2294.2	ATP2C1	NM_014382.1	HHD;BCPM;PMR1;SPCA1;hSPCA1;ATP2C1	adenosine	integral to	epidermal
GI_7656927-S	134.8	129.4	112.8	BMP10	NM_014482.1		cytokine	extracellul	cell growth
GI_7656933-S	2495.5	2393.3	1953.3	C11orf10	NM_014206.1				
GI_7656945-S	1367.7	1449.8	1147.4	SLC30A9	NM_006345.2	HUEL;ZNT9;C4orf1	cation	membran	cation
GI_7656949-I	93.5	100.1	102.4	CACNG5	NM_014404.1		ion	membran	small
GI_7656951-S	121.9	123.2	119.3	SIP	NM_014412.1	CACYBP	cyclin-		
GI_7656966-S	186.2	251.3	213.8	CELSR1	NM_014246.1	ME2;FMI2;CDHF9;HFMI2	transmem	integral to	central
GI_7656970-S	677.4	557.8	655.2	PFAAP5	NM_014887.1	CG005	molecular	cellular_co	biological_
GI_7656974-S	1924.7	1706.7	1867.8	CXXC1	NM_014593.1	CGBP;PCCX1;PHF18;hCGBP;HsT2645	transcripti	kinesin	regulation
GI_7656978-S	316.1	389.4	362.2	CIDEB	NM_014430.1		apoptosis	intracellula	DNA
GI_7656980-I	1039.2	829.8	605.4	CLDN15	NM_014343.1	MGC19536			

GI_7656994-S	2577.9	1943.7	2506.8	CARHSP1	NM_014316.1	CRHSP-24	signal	cytoplasm	intracellula
GI_7656998-S	105.2	114.3	111.9	CTNNA2	NM_004389.1	CAPR;CTNR;CAP-R	structural	cytoskelet	cell
GI_7657006-S	172.6	181.9	181.5	DAPP1	NM_014395.1	BAM32	phospholi		signal
GI_7657008-S	112.7	113.9	140.4	DBC1	NM_014618.1	FAM5A;DBCCR1	tumor		oncogene
GI_7657020-S	105.7	129.4	109.4	DKFZP434P2	NM_014549.1	UNQ2565	DNA	nucleus	regulation
GI_7657022-S	130.6	126.2	107.9	DKK2	NM_014421.1	DKK-2		extracellul	
GI_7657024-S	113.6	114.4	99.1	DKK4	NM_014420.1	DKK-4;hdkk-4	molecular	cellular_co	developm
GI_7657032-S	625.4	569	418.4	NT5C	NM_014595.1	DNT;cdN;DNT1;P5N2;PN-I;PN-	transcripti	nucleus	regulation
GI_7657034-S	640.1	566.8	453.2	APC10	NM_014885.1	DOC1;DKFZP564L0562;ANAPC10-	ubiquitin-	anaphase-	mitotic
GI_7657036-A	168.9	181.9	158.2	DOC1	NM_014890.1	GIP90			
GI_7657036-I	90.8	91.8	82.2	DOC1	NM_014890.1	GIP90			
GI_7657040-S	132.4	138.3	143.7	DRIM	NM_014503.1				negative
GI_7657043-S	9472.9	9059.6	7718.3	NGFRAP1	NM_014380.1	Bex;BEX3;NADE;HGR74;DXS6984E			developm
GI_7657045-S	1728.6	1933.9	1788.7	UBE2S	NM_014501.1	E2-EPF	ubiquitin		protein
GI_7657055-S	168.2	305.4	288.6	EHD3	NM_014600.1		nucleic	kinesin	
GI_7657057-S	3122.9	2531	2049.9	EIF2B2	NM_014239.1	EIF2B;EIF-2Bbeta	translation	eukaryotic	translation
GI_7657065-A	236.2	283.4	267.1	ERG	NM_004449.2		DNA	nucleus	protein
GI_7657068-S	1118.3	1443.6	649.2	ERO1L	NM_014584.1		calcium	microsom	response
GI_7657070-S	244.1	182.6	166.2	OPN3	NM_014322.1	ERO;ECPN;NMO-1;PANOPSIN	G-protein	integral to	G-protein
GI_7657074-S	328	161.8	162.6	EVI2A	NM_014210.1	EVDA;EVI2	transmem	integral to	cell
GI_7657091-S	155.2	171.4	143.4	IL1F6	NM_014440.1	FIL1E;IL1(EPSILON);FIL1(EPSILON)			
GI_7657101-S	517.1	497.7	537.8	FRAG1	NM_014489.1		tumor	integral to	
GI_7657105-S	135	149.1	145.5	GABRP	NM_014211.1		GABA-A	integral to	ion
GI_7657121-S	2136.7	1787.9	1450.2	GEMIN4	NM_015721.1	HHRF-1;DKFZP434B131;DKFZP434D174	small	nucleolus	ribosome
GI_7657123-S	375.9	373.6	342.2	TNFAIP8	NM_014350.1	GG2-1;SCC-S2;MDC-3.13			anti-
GI_7657125-S	109.4	127.4	108	PLA2G3	NM_015715.1	GIII-SPLA2	calcium-	extracellul	phospholi
GI_7657127-S	152.8	171.7	158.5	GLTSCR1	NM_015711.1		tumor		
GI_7657133-S	1763.9	1639.7	1678.9	GNPAT	NM_014236.1	DAPAT;DAP-AT;DHAPAT	acyltransf	peroxisom	fatty acid
GI_7657135-S	741.3	394.8	191.4	GPR160	NM_014373.1	GPCR1;GPCR150	receptor	integral to	G-protein
GI_7657141-S	160.8	171.8	156.1	GPR58	NM_014626.1		G-protein	integral to	G-protein
GI_7657151-S	205	201.6	226.8	HERC3	NM_014606.1				
GI_7657155-S	92.4	100.5	80.7	C6orf54	NM_014354.1	HGC6.1.1	molecular	cellular_co	biological_
GI_7657157-S	101.5	96.2	84.7	C6orf123	NM_014356.1	HGC6.2;dJ431P23.4	molecular	cellular_co	biological_
GI_7657177-S	1553	1393.1	1092.7	TMEM5	NM_014254.1	HP10481		integral to	
GI_7657183-S	346.3	361.6	410.2	ZNF318	NM_014345.1	ZFP318;HRIHFB2436	RNA	nucleus	
GI_7657185-S	95.2	110.2	95.5	HS322B1A	NM_015371.1				
GI_7657193-S	97.2	94.8	87.3	HS747E2A	NM_015370.1				
GI_7657197-S	3199.7	2211.8	1954.6	HSA9761	NM_014473.1		S-		mRNA
GI_7657203-S	845.6	861.8	795.9	HSU15552	NM_014597.1				
GI_7657209-S	344.3	450	360.2	ARFIP1	NM_014447.1	HSU52521			
GI_7657213-S	94.4	112.3	108.9	HUNK	NM_014586.1		protein		signal
GI_7657217-A	133.1	146	141.1	BRD4	NM_014299.1	CAP;MCAP;HUNKI			
GI_7657217-I	158.5	205.8	193.7	BRD4	NM_014299.1	CAP;MCAP;HUNKI			
GI_7657235-S	263.9	341.7	329.1	IMPA2	NM_014214.1		inositol-		phosphate

GI_7657241-S	122.6	131.1	120.8	FETUB	NM_014375.1	16G2;Gugu;IRL685	cysteine	extracellul	biological_
GI_7657256-S	4111.9	4579.5	3611.1	TOMM20	NM_014765.1	MAS20;MOM19;TOM20;KIAA0016	protein	mitochond	mitochond
GI_7657258-S	113.9	132.7	102.7	KIAA0040	NM_014656.1				
GI_7657260-S	921.7	787	670.1	PDZGEF1	NM_014247.1				
GI_7657268-I	228.8	222.2	267.1	APRIN	NM_015032.1	AS3;CG008;FLJ23236;KIAA0979	ATP	nucleus	negative
GI_7657270-S	80.8	96.1	81.2	KIR2DL1	NM_014218.1	47.11;CL-42;NKAT1;P58.1;CD158A	receptor	integral to	immune
GI_7657272-S	123.1	129	122.2	KIR2DL2	NM_014219.1	CL-43;NKAT6;p58.2;CD158B1	receptor	integral to	
GI_7657276-S	143.9	116.3	138.7	KIR2DS1	NM_014512.1	p50.1;CD158H;EB6ActI;EB6ActII	transmem	integral to	immune
GI_7657278-S	171.2	195.1	188.7	KIR2DS5	NM_014513.1	NKAT9;CD158G	receptor	integral to	immune
GI_7657280-S	89.5	95.3	87.7	KIR3DS1	NM_014514.1	NKAT10;CD158E2			
GI_7657290-S	113.1	119.1	116.9	CD207	NM_015717.1	LANGERIN	internaliza	endocytoti	heterophili
GI_7657298-S	197.4	232.7	219	TFCP2L1	NM_014553.1	CRTR1;LBP-9	transcripti		pregnancy
GI_7657300-S	2063.9	1772.3	1467.7	KLHDC2	NM_014315.1	LCP;HCLP-1			
GI_7657306-S	216	218.8	229.8	LIMD1	NM_014240.1		protein	nuclear	cell growth
GI_7657312-S	3018.3	3250.7	2476.7	LSM1	NM_014462.1	CASM;YJL124C	pre-mRNA	small	mRNA
GI_7657314-S	2098.3	2367.2	2471.5	LSM3	NM_014463.1	SMX4;USS2;YLR438C	pre-mRNA	small	mRNA
GI_7657325-S	509.2	603.1	678.3	MEA	NM_014623.1	HYS			male
GI_7657330-A	96.4	96.5	84.2	ITGB1BP3	NM_014446.1	MIBP	protein	peripheral	myoblast
GI_7657332-S	178.5	204.7	188.8	CLECSF9	NM_014358.1	MINCLE	lectin [goid		antimicrob
GI_7657336-S	281.6	347.4	308.4	MLH3	NM_014381.1	HNPCC;S240II117	satellite	cellular_co	mismatch
GI_7657340-S	148.7	170.2	147.9	MORC	NM_014429.1		ATP	nucleus	spermatog
GI_7657344-S	10545.6	9004.2	9123.6	MTCH1	NM_014341.1	PSAP;CGI-64			
GI_7657348-S	609.3	621.9	592.9	MTCP1	NM_014221.1	C6.1B			oncogene
GI_7657350-S	1432.1	1313.7	1070.9	MYBBP1A	NM_014520.1	P160;PAP2	transcripti	nucleolus	regulation
GI_7657354-S	325.8	277.1	311.3	AKAP8L	NM_014371.1	HAP95;NAKAP95	DEAD/H-	nucleus	biological_
GI_7657384-S	2729.2	2454.3	2088.7	CNOT2	NM_014515.1	NOT2;CDC36;NOT2H;HSPC131			
GI_7657392-S	389.2	408.5	451.8	NR1	NM_014434.1		flavin-	cytoplasm	oncogene
GI_7657404-S	111.7	116	115.2	OBP2A	NM_014582.1	OBP;hOBPIIa;hOBPIIa(alpha)	odorant	cellular_co	chemosen
GI_7657406-S	135.8	168.2	170.6	OBP2B	NM_014581.1	hOBPIIb	odorant	cellular_co	chemosen
GI_7657408-S	102.2	112.7	117.3	POU2F3	NM_014352.1	OCT11;PLA-1;Epoc-1;Skn-1a	transcripti	nucleus	epidermal
GI_7657410-S	94.9	82.6	89.5	ODZ1	NM_014253.1	TNM;ODZ3;TNM1;TEN-M1	heparin	extracellul	negative
GI_7657420-S	131.7	152	149.1	OR1A1	NM_014565.1	OR17-7	olfactory	integral to	olfaction
GI_7657422-S	169.7	198.2	183.8	OR1D5	NM_014566.1	OR17-31	olfactory	integral to	olfaction
GI_7657430-S	7431.7	8741.8	7292.1	SND1	NM_014390.1	p100	transcripti	nucleus	
GI_7657432-S	131.4	151.3	145	P101-PI3K	NM_014308.1				
GI_7657436-S	267.6	455.3	276.3	SESN1	NM_014454.1	PA26;SEST1		nucleus	cell cycle
GI_7657442-A	71.4	76.9	80.3	PCDH11X	NM_014522.1	PCDHX;PCDH-X;PCDH11	cell	integral to	
GI_7657442-I	83.2	85.5	83.8	PCDH11X	NM_014522.1	PCDHX;PCDH-X;PCDH11	cell	integral to	
GI_7657452-S	198.5	726.8	322.5	SPINK4	NM_014471.1	PEC-60	serine		
GI_7657456-S	117.5	117	101	PGDS	NM_014485.1		prostaglan	cytoplasm	locomotor
GI_7657458-S	100.9	110.9	95	PKD2L2	NM_014386.1		cation	kinesin	cation
GI_7657460-S	198	224.1	201.6	PLA2G2E	NM_014589.1		secreted	extracellul	phospholi
GI_7657464-S	856.4	820.7	1075.9	PODLX2	NM_015720.1		glycosami	integral to	
GI_7657468-S	90.4	95.7	80.7	POM121L1	NM_014348.1				

GI_7657477-S	111.6	134.3	115.1	RDH8	NM_015725.1	PRRDH	retinol	integral to	vision
GI_7657479-S	4096.1	4063.1	3943	GHITM	NM_014394.1	DERP2;My021;PTD010;HSPC282		integral to	
GI_7657495-S	794.4	650.4	696	RABGEF1	NM_014504.1	RABEX5;rabex-5	zinc ion		
GI_7657497-S	1230.6	2009.8	1480.8	RAGE	NM_014226.1	MOK;RAGE1	protein	cytoplasm	protein
GI_7657503-S	147.5	214.1	94.3	RBM9	NM_014309.1	RTA;HRNBP2	transcripti	nucleus	RNA
GI_7657505-S	223.2	194.7	178.9	RBMS3	NM_014483.1		RNA		
GI_7657525-S	77.1	87.3	72.2	RPS6KA6	NM_014496.1	RSK4	protein		central
GI_7657539-S	547.2	622.2	635.9	SCHIP1	NM_014575.1	SCHIP-1		cytoplasm	
GI_7657541-S	223.3	250.7	231.3	SCN11A	NM_014139.1	NAV1.9;SCN12A	voltage-	integral to	drug
GI_7657543-S	118.6	139.6	137.9	SCN8A	NM_014191.1	MED	voltage-	voltage-	sodium
GI_7657561-S	1971.1	2251	2304.1	SH3BP4	NM_014521.1	BOG25	signal	nucleus	endocytosi
GI_7657569-I	108.7	111.3	106.4	SIGLEC7	NM_014385.1	p75;QA79;AIRM1;SIGLEC-7;p75/AIRM1	lectin [goid	integral to	cell
GI_7657571-S	576.1	733.1	637	SIGLEC8	NM_014442.1	SAF2;SIGLEC-8;SIGLEC8L	lectin [goid	integral to	signal
GI_7657580-S	941	921.9	1289.4	SLC25A13	NM_014251.1	CTLN2;CITRIN;ARALAR2	carrier	mitochond	small
GI_7657584-S	453.6	427.2	437.3	SLC25A15	NM_014252.1	HHH;ORNT1;D13S327	L-ornithine	mitochond	mitochond
GI_7657586-S	133.7	125.8	129	SLC6A11	NM_014229.1	GAT3;GAT-3	betaine/G	integral to	neurotran
GI_7657590-S	112.4	114.6	91.8	SLC7A9	NM_014270.1	CSNU3	amino	integral to	small
GI_7657596-S	1699.9	1814.7	2010.1	SMUG1	NM_014311.1		uracil DNA		DNA
GI_7657610-S	1772	1990	2284.2	DNAJC8	NM_014280.1	SPF31	chaperone		
GI_7657614-S	212.2	235.8	218.1	NPHS2	NM_014625.1	PDCN;SRN1		integral to	excretion
GI_7657618-S	283.9	528.9	241.7	SRPUL	NM_014467.1				oncogene
GI_7657624-S	184.5	284.4	303.9	STAU2	NM_014393.1	39K2;39K3	double-		
GI_7657628-S	121.8	125	134.2	STK23	NM_014370.1	MSSK1	cAMP-	cellular_co	protein
GI_7657640-S	796.9	679.1	592.7	TGDS	NM_014305.1	TDPGD	dTDP-		nucleotide-
GI_7657644-S	106.7	112.5	106.8	TINAG	NM_014464.1	TIN1;TIN2;TIN-AG	nucleotide	basement	Malpighia
GI_7657658-S	118.1	119.6	124.7	TRPS1	NM_014112.1	GC79	zinc ion	nucleus	NLS-
GI_7657664-S	102.6	103.2	101	TZFP	NM_014383.1	FAXF;FAZF	transcripti	nucleus	negative
GI_7657670-S	300.2	351.4	342.6	UBTF	NM_014233.1	UBF;NOR-90	RNA	nucleolus	regulation
GI_7657674-S	240.5	287.8	252.1	VAMP2	NM_014232.1	SYB2;VAMP-2		secretory	nonselecti
GI_7657692-S	209.7	223.7	211.6	ZNF324	NM_014347.1	ZF5128	DNA	nucleus	regulation
GI_7657698-S	103.9	121	101.2	SLC39A2	NM_014579.1	ZIP2	zinc ion	integral to	zinc ion
GI_7657702-S	165.3	153.6	137.6	ZNF-U69274	NM_014415.1		protein	aspartate	'de novo'
GI_7657706-S	228.2	208.5	241.2	ZNF237	NM_014242.1	HSPC050;ZNF198L1			
GI_7661527-S	854.8	742	702.3	AD-003	NM_014064.1		S-		
GI_7661531-S	1398.8	1201.7	866.4	NOB1P	NM_014062.1	ART-4			
GI_7661537-S	10168.6	7357.5	9125.5	BRI3	NM_015379.1	I3		integral to	
GI_7661547-S	3589.2	3845.7	3382.2	CL25022	NM_015702.1				
GI_7661555-S	723.6	795.4	878.8	TRUB2	NM_015679.1	CLONE24922	pseudouri		RNA
GI_7661563-S	200.9	230.9	124	TTLL3	NM_015644.1	HOTTL;DKFZP434B103	tubulin-		protein
GI_7661565-S	336.8	328.1	272.3	DKFZP434B1	NM_015434.1				
GI_7661567-S	492.6	842.5	770	PGM3	NM_015599.1	AGM1;PAGM;DKFZP434B187	phosphoa	cellular_co	carbohydr
GI_7661579-I	1357.3	1391	1583	DKFZP434J1	NM_015610.1	CGI-50;FLJ12979;FLJ14217			
GI_7661585-S	176.6	190.5	173	DKFZP434O(	NM_015594.1				
GI_7661591-S	352.7	487.2	487.1	ASF1A	NM_014034.1	CIA;DKFZP547E2110			

GI_7661597-S	3737.7	2845.9	4014.4	DNAPTP6	NM_015535.1	DKFZp564A2416			
GI_7661599-S	400.3	497.6	515.7	DKFZP564B1	NM_015582.1	MGC8471			
GI_7661601-S	834.6	968.5	866.6	DKFZP564B1	NM_015415.1		molecular		
GI_7661605-S	872.3	960.6	830.3	DKFZP564C1	NM_015658.1		molecular	nucleus	
GI_7661615-S	671.9	1117.8	226.3	DKFZP564K1	NM_015544.1				
GI_7661617-S	746.3	689.1	671.2	DKFZP564K2	NM_015421.1				
GI_7661619-S	1640.7	1828.3	1922.8	HIG1	NM_014056.1	DKFZP564K247			
GI_7661621-S	427.3	536.7	525	DKFZP564M(	NM_014042.1				
GI_7661625-S	5079.3	5307.5	4782.4	PAI-RBP1	NM_015640.1	CGI-55;DKFZp564M2423	DNA	nucleus	regulation
GI_7661631-S	503.5	604.7	515.7	DKFZP564O(	NM_015393.1				
GI_7661635-S	378.6	397.6	378.6	P29	NM_015484.1	DKFZP564O2082	protein	nucleus	biological_
GI_7661645-S	5457.1	5453.9	4950.9	DKFZP566E1	NM_015523.1	SFN;CGI-114	3'-5'	mitochond	nucleotide
GI_7661651-S	418	402.2	524.1	ZNF288	NM_015642.1	HOF;DPZF;ODA-8S;DKFZp566F123	protein	nucleus	regulation
GI_7661667-S	226.8	285.2	308.3	E2IG4	NM_015516.1	DKFZP586E011			
GI_7661669-S	166.4	210.8	156.3	SH3YL1	NM_015677.1	Ray;DKFZP586F1318			
GI_7661685-S	194.9	210.5	184	POLR1A	NM_015425.1	RPA1;RPO1-4;FLJ21915;DKFZP586M0122	DNA-	nucleus	transcripti
GI_7661687-S	105.4	120.7	114.9	DKFZP586M(	NM_015583.1				
GI_7661689-S	242.2	210.1	262.8	CCDC9	NM_015603.1	DKFZP586M1019			
GI_7661691-S	1381.2	4286	3230.8	DKFZP586N(	NM_015400.1	HSPC193			
GI_7661695-S	2454.6	2893.5	2848.9	FAM32A	NM_014077.1	DKFZP586O0120			
GI_7661699-I	109.5	118.8	109.6	SORBS1	NM_015385.1	CAP;SH3D5;SORB1;SH3P12;ponsin;FLJ124	cytoskelet	cell-cell	cell-matrix
GI_7661707-S	144.7	156.9	180.7	FLVCR	NM_014053.1		transporte	integral to	small
GI_7661713-S	1601.4	1878.5	1992.9	FAM3C	NM_014888.1	GS3786	cytokine	extracellul	biological_
GI_7661719-S	1338.4	1240.2	1203.1	HIRIP5	NM_015700.1	Nfu;CGI-33			
GI_7661723-S	105.1	105	106.5	HSN44A4A	NM_015372.1				
GI_7661727-S	1711.7	2387.2	2080.8	MAPBPIP	NM_014017.1	HSPC003		Golgi	
GI_7661731-S	1835.3	2476.9	2776.2	HSPC009	NM_014019.1				
GI_7661741-S	1739.6	1953.2	1629.7	HSPC023	NM_014047.1				
GI_7661743-S	1271.9	1371.6	832.1	BZW2	NM_014038.1	HSPC028			
GI_7661745-S	6818.4	7816.2	6780.5	SPC12	NM_014041.1	HSPC033	peptidase	microsom	proteolysis
GI_7661749-S	177.2	208.9	189.1	HSPC047	NM_014147.1				
GI_7661751-S	121.4	136.7	132.7	HSPC048	NM_014148.1				
GI_7661757-S	93.4	99.7	83	C14orf110	NM_014151.1				
GI_7661759-S	114.3	117	110.7	HSPC054	NM_014152.1				
GI_7661763-I	181.7	218.8	227.5	HSPC056	NM_014154.1	DKFZP434A043			
GI_7661765-S	150.4	181.6	148.8	HSPC063	NM_014155.1				
GI_7661779-S	300.3	370.1	335.4	HSPC072	NM_014162.1				
GI_7661781-S	147.4	168.2	150.5	HSPC073	NM_014163.1				
GI_7661785-S	761	622.8	604.6	C6orf66	NM_014165.1	My013;HSPC125;bA22L21.1			
GI_7661789-S	1761	1469.7	1276	HSPC128	NM_014167.1				
GI_7661791-S	3409.5	3131.8	2248.5	HSPC133	NM_014168.1		N-		DNA
GI_7661795-S	601.4	723.7	573.5	HSPC135	NM_014170.1				
GI_7661801-S	1687.2	2232.5	2008.3	HSPC142	NM_014173.1				
GI_7661807-S	524	610.1	710.7	HSPC150	NM_014176.1		ubiquitin		ubiquitin

GI_7661809-S	1809.7	2008.1	1693.5	HSPC154	NM_014177.1				
GI_7661813-S	780.4	805.9	1204.8	HSPC157	NM_014179.1				
GI_7661817-S	210.6	146.1	112.3	HSPC159	NM_014181.1		lectin [goid		
GI_7661823-S	2588.1	2427.3	2327.6	HSPC163	NM_014184.1				
GI_7661825-A	465.6	391.7	392.5	RANGNRF	NM_014185.1	MOG1;HSPC165;HSPC236			
GI_7661827-S	617.4	716.6	773.5	COMMD9	NM_014186.1	HSPC166			
GI_7661829-S	303.4	365.5	379.1	HSPC171	NM_014187.1				
GI_7661831-S	5770.5	4958.5	4027.2	HSPC182	NM_014188.1	FLJ13048			
GI_7661835-S	324.9	381.1	338.1	ATP5S	NM_015684.1	ATPW;HSU79253			
GI_7661843-S	220.1	271.1	264.1	JM1	NM_014008.1				
GI_7661855-S	754	728.9	589.2	KIAA0010	NM_014671.1				
GI_7661859-S	540.1	470.4	563.7	LRRC14	NM_014665.1	KIAA0014			
GI_7661869-S	1433.1	1329.2	630.1	HERPUD1	NM_014685.1	SUP;HERP;Mif1;KIAA0025	molecular	endoplas	response
GI_7661877-S	330.1	295.7	393.8	KIF14	NM_014875.1				
GI_7661881-S	117.9	121.2	90.9	KIAA0053	NM_014882.1				
GI_7661883-S	252.6	348	281.2	HELZ	NM_014877.1				
GI_7661891-S	143.3	131.9	125.8	RCOR	NM_015156.1	COREST;KIAA0071	DNA	nucleus	
GI_7661895-S	83.3	91.4	74.5	KIAA0087	NM_014769.1				
GI_7661899-S	1477.9	938.4	1051.7	KIAA0092	NM_014679.1				
GI_7661907-S	2611	3126.2	2914.3	KIAA0102	NM_014752.1		peptidase	microsom	
GI_7661913-S	2734.4	3686.4	3430.4	p44S10	NM_014814.1	KIAA0107	ATPase	proteasom	ATP-
GI_7661917-S	1891.9	1834.4	1737.9	MAD2L1BP	NM_014628.1	CMT2;KIAA0110;dJ261G23.1			
GI_7661921-S	595.5	600.4	574.6	RAB21	NM_014999.1	KIAA0118	GTP		small
GI_7661925-S	660.7	449.1	536.9	TRIP-Br2	NM_014755.1				
GI_7661931-S	453	466.8	408	KIAA0133	NM_014777.1				
GI_7661935-S	1555.7	1511	1500.8	SAFB2	NM_014649.1				
GI_7661941-S	548.5	653.9	639	NICE-4	NM_014847.1	KIAA0144			
GI_7661945-S	284.4	339.9	294.9	IKBKE	NM_014002.1				
GI_7661957-S	2284.8	2755.6	2084.5	BTF	NM_014739.1				
GI_7661963-I	105.5	113.4	109.5	RASSF2	NM_014737.1	KIAA0168			neuropepti
GI_7661965-S	582.7	488.6	582.7	MDC1	NM_014641.1				
GI_7661969-S	115.6	134.8	123.8	TTLL4	NM_014640.1	KIAA0173	tubulin-		protein
GI_7661995-S	514.2	628.3	529.2	KIAA0205	NM_014873.1				
GI_7661997-S	249	226.7	222.9	TBC1D5	NM_014744.1	KIAA0210	GTPase		
GI_7661999-S	122.7	127.9	125.8	KIAA0211	NM_014630.1				
GI_7662001-S	2064.9	2503.6	2575.7	EDEM1	NM_014674.1				
GI_7662009-S	141.5	123.9	103.1	KIAA0222	NM_014643.1				
GI_7662013-S	2159	1789.4	1839.3	KIAA0233	NM_014745.1				
GI_7662015-S	186.1	259.9	173.8	RIMS3	NM_014747.1				
GI_7662017-S	294.8	277.4	277.2	PHF3	NM_015153.1	KIAA0244	DNA		transcripti
GI_7662035-S	91.2	94.6	84	SPOCK2	NM_014767.1	testican-2	calcium	extracellul	synaptoge
GI_7662041-S	521.6	427.8	397.2	ARHGEF10	NM_014629.1	GEF10;KIAA0294			
GI_7662045-S	260.6	239.9	201.3	MLL4	NM_014727.1	HRX2;MLL2;TRX2;WBP7;KIAA0304	zinc ion	nucleus	chromatin-
GI_7662051-S	540.2	698.3	689	KIAA0317	NM_014821.1		ubiquitin-	intracellula	ubiquitin

GI_7662053-S	94.1	104.9	107.2	KIAA0319	NM_014809.1				
GI_7662057-S	201.6	202.7	224.1	KIAA0329	NM_014844.1				
GI_7662069-S	150.6	134.2	121.9	RALGPS1A	NM_014636.1				
GI_7662071-S	175.8	211.8	194.6	KIAA0352	NM_014830.1				
GI_7662073-S	369.4	464.6	556.8	ZBTB5	NM_014872.1		protein		
GI_7662075-S	1287.2	1376.5	903.6	KIAA0355	NM_014686.1				
GI_7662079-S	388.7	351.8	327.8	KIAA0373	NM_014684.1				
GI_7662087-S	232.9	226.6	225.9	ARHGEF12	NM_015313.1	LARG;PRO2792;KIAA0382	signal		intracellula
GI_7662091-S	129.5	152.2	141.2	KIAA0390	NM_014717.1				
GI_7662093-S	140.2	150.5	140.4	KIAA0391	NM_014672.1				
GI_7662095-S	128	161.9	143.5	KIAA0408	NM_014702.1				
GI_7662099-S	189.5	211.8	221.7	ZNF297B	NM_014007.1	ZNF-X	protein	nucleus	regulation
GI_7662101-S	114.9	132.1	128.4	LRRTM2	NM_015564.1				
GI_7662103-S	233.5	288.3	237.1	FISH	NM_014631.1				
GI_7662107-S	763	649.2	500.6	ARHGEF9	NM_015185.1				
GI_7662111-S	281.3	324.3	221.3	KIAA0427	NM_014772.1		RNA	nucleus	protein
GI_7662115-S	199.6	256.6	223.2	KIAA0431	NM_015251.1				
GI_7662121-S	170.3	196.2	289.7	SETBP1	NM_015559.1	SEB;KIAA0437	transporte	membran	transport
GI_7662125-S	2952.6	2997.7	2416.2	SIPA1L1	NM_015556.1	E6TP1;KIAA0440	protein		
GI_7662127-S	491.1	438.6	455.8	ZNF450	NM_014797.1				
GI_7662129-S	84.3	98.7	93.5	GASP	NM_014710.1				
GI_7662137-S	824.1	1734.8	1396.5	SDC3	NM_014654.1				
GI_7662139-S	399.7	348.4	465.3	KIAA0469	NM_014851.1				
GI_7662141-S	481.5	475.6	403.4	KAB	NM_014812.1	KIAA0470			
GI_7662143-S	163.7	173.3	156.7	HHL	NM_014857.1	KIAA0471			
GI_7662145-S	102.9	96.1	100.5	DNAJC6	NM_014787.1				
GI_7662151-S	1225.5	1190.4	1250.5	KIAA0476	NM_014856.1				
GI_7662157-S	691.6	762.5	641.7	KIAA0483	NM_015176.1				
GI_7662159-S	1493.9	1820	2081.1	KIAA0494	NM_014774.1				
GI_7662163-S	213.3	247.6	196.6	KIAA0513	NM_014732.1				
GI_7662167-S	119.8	130.3	118.1	ST18	NM_014682.1	ZNF387;KIAA0535	transcripti	nucleus	regulation
GI_7662169-S	687.1	679.2	613.5	ARK5	NM_014840.1				
GI_7662177-S	107.9	100.6	96.4	KIAA0555	NM_014790.1				
GI_7662179-S	279.8	338.1	286.2	KIAA0562	NM_014704.1				
GI_7662181-S	93.2	103.9	82	KIAA0563	NM_014834.1				
GI_7662195-I	112.3	126.9	120.9	GALNAC4S-6	NM_014863.1	BRAG;KIAA0598;MGC34346			
GI_7662203-S	609.3	555.9	596.3	N4BP1	NM_014664.1				
GI_7662213-S	1216.8	1467.5	1206.5	KIAA0628	NM_014789.1				
GI_7662215-S	404.8	291.2	328.4	KIAA0635	NM_014645.1				
GI_7662217-S	438	399.3	371.1	ZBED4	NM_014838.1				
GI_7662219-S	206	239.9	238	KIAA0644	NM_014817.1				
GI_7662221-S	165.2	180.9	182	KIAA0645	NM_014662.1				
GI_7662227-S	71.4	71.2	101.4	SNAP91	NM_014841.1				
GI_7662231-S	2588.9	2702.5	2589	KIAA0663	NM_014827.1		nucleic		

GI_7662237-S	667.1	790.9	673.2	ACINUS	NM_014977.1	ACN;KIAA0670	ATPase	nucleus	erythrocyt
GI_7662241-S	170.1	136.3	110.8	KIAA0672	NM_014859.1				
GI_7662245-S	264.6	258.9	230.2	JMJD2A	NM_014663.1	JMJD2;KIAA0677	DNA		regulation
GI_7662247-S	367.7	465.6	361.4	C6orf56	NM_014721.1				
GI_7662255-S	239.5	284	210.7	KIAA0703	NM_014861.1				
GI_7662259-S	98.6	83	78.6	KIAA0711	NM_014867.1				
GI_7662265-S	218.2	246.4	251.9	IPO13	NM_014652.1	IMP13;RANBP13;KIAA0724	protein	nuclear	protein-
GI_7662267-S	161.8	233.5	186.1	CLSTN3	NM_014718.1	CSTN3;KIAA0726	calcium	integral to	homophili
GI_7662271-S	426	500.5	406.8	SV2A	NM_014849.1	SV2;KIAA0736	transporte	integral to	transport
GI_7662273-S	387.9	394.7	366.1	C14orf92	NM_014828.1				
GI_7662275-S	252.9	311.7	308.3	KIAA0738	NM_014719.1				
GI_7662279-I	198	143.7	153.6	HDAC9	NM_014707.1	HD7;HDAC;HDRP;MITR;HDAC7;HDAC7B;H	histone	nucleus	regulation
GI_7662281-S	125.8	128	113.3	KIAA0748	NM_014796.1				
GI_7662287-S	256.6	258.3	227	KIAA0753	NM_014804.1				
GI_7662289-S	150.5	210.1	155.5	KIAA0763	NM_014869.1				
GI_7662291-S	154.6	174.9	162.8	STAF65(gam	NM_014860.1				
GI_7662295-S	1123.5	757.8	663.5	KIAA0769	NM_014824.1				
GI_7662301-S	372.9	428.3	372.3	ProSAPiP2	NM_014726.1				
GI_7662303-S	204.8	194.4	160.6	PHF14	NM_014660.1				
GI_7662307-S	495.4	523.5	509	KIAA0792	NM_014698.1				
GI_7662309-S	130.1	141	137.2	FARP2	NM_014808.1				
GI_7662311-S	603.8	542.8	453.9	SENP6	NM_015571.1	SSP1;SUSP1;KIAA0797	cysteine-		proteolysis
GI_7662313-S	349.3	411.8	423	ZNF432	NM_014650.1		DNA	nucleus	regulation
GI_7662315-S	185.4	177.7	204.9	VprBP	NM_014703.1				
GI_7662319-S	211.9	197.8	179.1	LRIG2	NM_014813.1				
GI_7662329-S	401.6	457.1	386.9	ABLIM3	NM_014945.1		actin		cytoskelet
GI_7662333-A	102.5	112.6	102.3	RASGRP3	NM_015376.1	GRP3;KIAA0846	guanyl-		small
GI_7662339-S	1504.6	1218	1388.4	KIAA0852	NM_014941.1				
GI_7662345-S	499.4	523.5	464	KIAA0863	NM_014913.1				
GI_7662347-S	465	755.1	491.8	MONDOA	NM_014938.1	MIR;KIAA0867			
GI_7662357-S	165.3	244.2	246.5	ENPP4	NM_014936.1				
GI_7662367-S	85.2	99.2	96.3	CNK2	NM_014927.1	KIAA0902	binding	mitochond	transport
GI_7662371-S	1007.6	1006.8	884.8	KIAA0907	NM_014949.1				
GI_7662375-S	322.7	361.6	333.2	FAM13A1	NM_014883.1				
GI_7662391-S	119.7	107.3	102.8	CPEB3	NM_014912.1	KIAA0940	nucleic		
GI_7662393-S	523.5	427.4	457.7	Rab11-FIP2	NM_014904.1	nRip11;KIAA0941			
GI_7662395-S	480.1	664.5	567.2	EFA6R	NM_015310.1	HCA67;KIAA0942			
GI_7662403-S	108.7	107.1	94.4	CARD8	NM_014959.1	DACAR;NDPP1;TUCAN;CARDINAL;KIAA095	apoptosis	nucleus	apoptosis
GI_7662407-S	171.8	212.7	175.2	ZFP30	NM_014898.1				
GI_7662409-S	236.7	280.9	270.9	KIAA0963	NM_014963.1				
GI_7662415-S	480.4	611.6	572	FRMPD1	NM_014907.1	FRMD2;KIAA0967	protein	cytoskelet	intracellula
GI_7662423-S	146.9	174.2	165.1	KIAA0972	NM_014930.1				
GI_7662425-S	126.4	124.4	123.1	KIAA0976	NM_014917.1				
GI_7662431-S	170	184.3	173.9	RPH3A	NM_014954.1	KIAA0985;rabphilin	protein	membran	intracellula

GI_7662439-S	3694.3	4202.3	3918.8	KIAA1001	NM_014960.1	ARSG	sulfuric		metabolis
GI_7662445-S	263.9	305.8	317.2	C6orf84	NM_014895.1				
GI_7662449-S	756.3	687.8	587.3	KIAA1018	NM_014967.1				
GI_7662451-S	444.3	687	534.2	AGTPBP1	NM_015239.1	NNA1;KIAA1035	carboxype		proteolysis
GI_7662455-S	1604.9	1502.9	1343.6	KIAA1041	NM_014947.1				
GI_7662457-S	629.7	735.3	600.9	OIP106	NM_014965.1		protein	kinesin	protein
GI_7662463-S	423.5	388.6	391	KIAA1052	NM_014956.1				
GI_7662465-S	122.7	151.8	116	ZNF409	NM_014894.1				
GI_7662473-S	240.3	252.3	255.3	KIAA1074	NM_014915.1				
GI_7662479-S	100.1	106.1	101.1	KIAA1084	NM_014910.1				
GI_7662489-S	324	354.1	368.5	KIAA1115	NM_014931.1				
GI_7662491-S	370	426.2	410.8	RBM16	NM_014892.1				
GI_7662501-S	2746.2	3609.3	2956	MCTS1	NM_014060.1	MCT-1	RNA		positive
GI_7662509-S	736.8	895.2	777	LEPROTL1	NM_015344.1	my047		integral to	
GI_7662517-S	129.1	154.6	135	SLC6A16	NM_014037.1	NTT5	neurotran	intracellula	neurotran
GI_7662519-S	146.5	152.9	149.9	PRO0038	NM_014113.1				
GI_7662525-S	177.5	211.2	178.6	PRO0132	NM_014116.1				
GI_7662529-S	92.5	95.7	91.5	PRO0159	NM_014118.1				
GI_7662535-S	101.5	101.2	103.5	PRO0233	NM_014121.1				
GI_7662545-S	292	377.5	327.6	PRO0327	NM_014125.1				
GI_7662547-S	91.1	93	82	PRO0365	NM_014126.1				
GI_7662551-S	148.3	164.9	152.2	PRO0456	NM_014127.1				
GI_7662559-S	91.1	94.5	89	PRO0478	NM_014129.1				
GI_7662573-S	100.9	110.7	90.6	PRO0618	NM_014133.1				
GI_7662575-S	127.5	134	138	PRO0628	NM_014134.1				
GI_7662577-S	139.8	165.3	162.5	PRO0641	NM_014135.1				
GI_7662610-S	102.9	106.7	91.5	PRO1768	NM_014099.1				
GI_7662620-S	88.9	91.5	85.9	PRO1880	NM_014104.1				
GI_7662624-S	479.7	637.5	569.2	PRO1914	NM_014106.1				
GI_7662634-S	89.6	96.3	86.2	PRO2086	NM_014111.1				
GI_7662646-S	499.2	513.3	507.2	PTDSS1	NM_014754.1	PSSA;KIAA0024			
GI_7662650-S	124.7	142.7	125.7	RGC32	NM_014059.1		cell cycle	cytoplasm	regulation
GI_7662654-S	271.8	208	230	SNX24	NM_014035.1	SBBI31	protein		intracellula
GI_7662658-S	321.9	855.9	523.8	SEC24D	NM_014822.1	KIAA0755			
GI_7662660-S	374.3	482.2	445.5	PSORS1C1	NM_014068.1	SEEK1;C6orf16	copper,		pathogene
GI_7662662-S	124.2	154.3	116.6	C11orf21	NM_014144.1				
GI_7662664-S	332.2	397.2	362.7	PSORS1C2	NM_014069.1	SPR1;C6orf17	molecular	cellular_co	biological_
GI_7662666-S	277.9	332.7	308.5	C6orf15	NM_014070.1	STG	molecular	cellular_co	biological_
GI_7662670-S	490.6	581	573.4	TED	NM_015686.1		transmem	integral to	developm
GI_7662674-I	143.4	138.8	151.4	TP53TG3	NM_015369.1	TP53TG3A			
GI_7669471-I	218.4	290.2	247.1	ADAR	NM_001111.2	DSH;ADAR1;DRADA;DSRAD	double-	nucleus	antimicrob
GI_7669474-A	3002.5	2919.3	2860.9	ADAR	NM_015841.1	DSH;ADAR1;DRADA;DSRAD	double-	nucleus	antimicrob
GI_7669476-I	152.9	163.6	152.6	ADARB1	NM_015833.1	RED1;ADAR2;DRABA2;DRADA2	adenosine	nucleus	RNA
GI_7669478-A	264.5	312.3	282.6	ADARB1	NM_015834.1	RED1;ADAR2;DRABA2;DRADA2	adenosine	nucleus	RNA

GI_7669480-S	4634.1	5460.7	3014.6	BNIP3	NM_004052.2	NIP3	apoptosis	mitochond	anti-
GI_7669488-S	490.8	398.6	418.7	ECGF1	NM_001953.2	TP;PDECGF;hPD-ECGF	thymidine	soluble	pyrimidine
GI_7669489-A	958.8	973.2	888.7	EWSR1	NM_013986.1	EWS	RNA		oncogene
GI_7669491-S	24576.8	30700	24231	GAPD	NM_002046.2	G3PD;GAPDH	glyceralde	cytoplasm	glycolysis
GI_7669493-A	186.8	212.7	222.5	GCDH	NM_013976.1	ACAD5	glutaryl-	mitochond	electron
GI_7669495-S	127.8	147.8	122.3	GSTT2	NM_000854.2		glutathion		
GI_7669496-S	2089.9	2393.7	1821.7	JWA	NM_006407.2	jmx;DERP11;HSPC127;GTRAP3-18			
GI_7669497-I	119.8	109.3	114.5	KLRD1	NM_002262.2	CD94	transmem	integral to	cell
GI_7669498-A	95.5	97.7	96.6	KLRD1	NM_007334.1	CD94	transmem	integral to	cell
GI_7669500-S	7549	8030	7939.2	LAMP1	NM_005561.2	LAMPA;CD107a;LGP120		membran	
GI_7669502-I	2237	2758.1	2381.2	LAMP2	NM_013995.1	LAMPB;CD107b		lysosomal	
GI_7669505-S	106	108.3	105.8	MYH1	NM_005963.2	MYHa;MYHSA1;MyHC-2X/D	muscle	muscle	striated
GI_7669507-A	193.9	209.3	203.4	NOX1	NM_013954.1	MOX1;NOH1;NOH-1;GP91-2	superoxid	integral to	proton
GI_7669517-I	102.3	98.9	103.4	NRG1	NM_013959.1	GGF;HGL;HRG;NDF;ARIA;GGF2;HRGA;SM			
GI_7669519-I	91.8	103	92.8	NRG1	NM_013960.1	GGF;HGL;HRG;NDF;ARIA;GGF2;HRGA;SM			
GI_7669521-A	166.9	232.1	220.9	NRG1	NM_013961.1	GGF;HGL;HRG;NDF;ARIA;GGF2;HRGA;SM			
GI_7669523-I	108.2	89.1	87.4	NRG1	NM_013962.1	GGF;HGL;HRG;NDF;ARIA;GGF2;HRGA;SM			
GI_7669535-A	112.6	100	115.9	NRG2	NM_013985.1	NTAK;Don-1	receptor	integral to	anti-
GI_7669539-A	168.4	185	157.2	PARK2	NM_013988.1	PDJ;PRKN;AR-JP	ubiquitin-		central
GI_7669544-I	198.8	250.6	233.9	TACR1	NM_001058.2	SPR;NK1R;NKIR;TAC1R	tachykinin	integral to	tachykinin
GI_7669545-A	99.4	101.6	89.9	TACR1	NM_015727.1	SPR;NK1R;NKIR;TAC1R	tachykinin	integral to	tachykinin
GI_7669545-I	88.3	109.4	89.8	TACR1	NM_015727.1	SPR;NK1R;NKIR;TAC1R	tachykinin	integral to	tachykinin
GI_7669547-S	94.9	96.1	85.2	TACR3	NM_001059.1	NK3R;TAC3RL	tachykinin	integral to	tachykinin
GI_7669549-I	103.1	100.3	93.6	VCL	NM_014000.1		structural	cytoskelet	cell shape
GI_7669551-A	3522.5	3037.5	1864.7	VCL	NM_003373.2		structural	cytoskelet	cell shape
GI_7669552-S	704.3	1433.7	1401.1	VCP	NM_007126.2	p97;TERA	nucleotide	Golgi	transport
GI_7669553-S	235.5	278.7	249.3	AMMECR1	NM_015365.1	AMMERC1	molecular	cellular_co	biological_
GI_7705267-S	1221.9	1321.6	1211.9	FAM8A1	NM_016255.1	AHCP	DNA	nucleus	regulation
GI_7705283-S	288.2	263.3	272	ANAPC7	NM_016238.1	APC7		anaphase-	regulation
GI_7705287-A	604.2	731.2	799.9	APRIN	NM_015928.1	AS3;CG008;FLJ23236;KIAA0979	ATP	nucleus	negative
GI_7705287-I	74.1	78.8	66.8	APRIN	NM_015928.1	AS3;CG008;FLJ23236;KIAA0979	ATP	nucleus	negative
GI_7705295-A	145.8	173.1	168.7	BIN2	NM_016187.1	BRAP-1			
GI_7705299-S	402.4	375.7	371.8	BM-002	NM_016617.1				
GI_7705301-S	97.2	113.8	107.1	KIAA1221	NM_016620.1	BM-			
GI_7705307-S	110.6	107.2	113.5	GDF2	NM_016204.1	BMP9;BMP-9	cytokine	extracellul	cell growth
GI_7705311-I	126.8	118.6	126.4	CABP2	NM_016366.1		calcium		signal
GI_7705315-S	94.2	115.1	89	GPR2	NM_016602.1	CCR10	G-protein	integral to	G-protein
GI_7705317-S	231.4	228	326.4	GULP1	NM_016315.1	CED6;GULP;CED-6	signal		phagocyto
GI_7705321-I	116.2	125.3	113.2	C1orf9	NM_016227.1	CH1			
GI_7705327-S	102.9	105	94.6	CML2	NM_016347.1		N-		
GI_7705329-S	978.3	1045.9	1028	COPS7A	NM_016319.1				
GI_7705343-S	343.6	328.6	341.5	POLK	NM_016218.1	DINP;POLQ;DINB1			mutagene
GI_7705345-S	406.5	435.6	437.5	KIAA0683	NM_016111.1	DKFZp434A073			
GI_7705347-S	492.9	480	537	MPHOSPH1	NM_016195.1	MPP1;KRMP1;MPP-1;DKFZP434B0435	cell cycle	kinesin	M phase

GI_7705364-A	171.6	239.6	232.8	RBM19	NM_016196.1	NPO;KIAA0682;DKFZp586F1023	nucleic		
GI_7705364-I	288.5	329.6	342.8	RBM19	NM_016196.1	NPO;KIAA0682;DKFZp586F1023	nucleic		
GI_7705372-S	2377.1	2806	2127.2	EPLIN	NM_016357.1	SREBP3		focal	
GI_7705378-S	1248.8	377.4	329.3	GAGE8	NM_012196.1		tumor		cellular
GI_7705380-S	2003.1	2187.6	2359.5	UBADC1	NM_016172.1	GBDR1			
GI_7705386-I	123.5	139.8	122.5	GTF2IRD1	NM_016328.1	GTF3;RBAP2;CREAM1;MUSTRD1;WBSCR1	transcripti	nucleus	regulation
GI_7705388-S	147.4	185.8	148.1	H-plk	NM_015852.1		molecular	nucleus	biological_
GI_7705392-S	250.4	296.4	265	HAO2	NM_016527.1	HAOX2	(S)-2-	peroxisom	electron
GI_7705396-S	344.8	333.6	324.7	VPS54	NM_016516.1	HCC8;SLP-8p;VPS54L			
GI_7705400-S	1081.2	1115.9	1031.5	HDCMA18P	NM_016648.1	DKFZP564K112			
GI_7705408-S	114.1	129.1	100.1	HEMK	NM_016173.1		N-		DNA
GI_7705410-S	1604	1968	1513.9	HGRG8	NM_016258.1		tumor		humoral
GI_7705416-S	269.9	315.1	273	HP1-BP74	NM_016287.1	HP1BP3	DNA	nucleus	nucleoso
GI_7705420-S	658.8	780.7	642.5	HSD17B7	NM_016371.1	PRAP	estradiol		
GI_7705430-S	1892.9	1898	1622.2	HSPC016	NM_015933.1				
GI_7705432-S	12640	11041	9290	EIF3S6IP	NM_016091.1	HSPC021;HSPC025	translation		protein
GI_7705458-S	201.1	219.5	201.8	HSPC121	NM_016395.1	B-IND1	GTPase		NIK-I-
GI_7705460-S	263.8	288.8	284.2	HSPC129	NM_016396.1	HSPC058			
GI_7705474-S	1293.7	1307.1	1154.7	HSPC148	NM_016403.1				
GI_7705476-S	9526.7	10087	9070	HSPC152	NM_016404.1				
GI_7705480-S	1614.6	1727.7	1611.4	HSPC155	NM_016406.1		ubiquitin		ubiquitin
GI_7705482-S	2838.1	3166.3	3309.6	C20orf43	NM_016407.1	CDAO5;HSPC164			
GI_7705544-S	160.1	177.8	162.5	HUMCYT2A	NM_015848.1		structural	kinesin	cytoskelet
GI_7705552-S	255.8	338.8	291.9	IHPK2	NM_016291.1	IP6K2;DKFZP586M0617	polyphosp		
GI_7705554-S	131	146.7	144.5	IRX4	NM_016358.1		transcripti	nucleus	heart
GI_7705567-I	148.9	179.3	149.8	KIR2DL3	NM_015868.1	p58;CL-	receptor	integral to	immune
GI_7705573-S	96.7	100.1	91.6	KLRF1	NM_016523.1		transmem	integral to	cell
GI_7705575-S	709.2	714.8	826.2	RAMP	NM_016448.1	L2DTL			
GI_7705579-A	2112.2	2107.7	2344.1	LCMT1	NM_016309.1	LCMT;CGI-68	S-		protein
GI_7705581-S	101.6	113	95.7	GLULD1	NM_016571.1	LGS	glutamate-		nitrogen
GI_7705589-S	773.8	856.6	650.8	CGI-121	NM_016058.1				
GI_7705591-S	115	121.5	106.9	CGI-125	NM_016060.1			nucleus	regulation
GI_7705601-S	1125.7	1161	1043.1	ASCC1	NM_015947.1	CGI-18;ASC1p50	nucleic		
GI_7705605-S	2507.1	2104.2	1963.2	RRP40	NM_016042.1		exonuclea	nuclear	rRNA
GI_7705607-S	1308.7	1114.9	1138.9	CGI-105	NM_016044.1		catalytic		metabolis
GI_7705609-S	237.3	198.7	216.5	C20orf45	NM_016045.1	dJ543J19.5			
GI_7705613-S	595.9	430.9	541.6	CGI-111	NM_016048.1		catalytic		metabolis
GI_7705621-S	1351.2	1392.6	1391.7	CGI-116	NM_016053.1				
GI_7705623-S	3265.9	2294.1	1723.6	C6orf74	NM_016063.1	CGI-130;NS5ATP2;dJ167O5.2			
GI_7705629-S	1835.1	1782	1576.8	MRPS18C	NM_016067.1	CGI-134;FLJ11146;FLJ22967;MRPS18-	structural	ribosome	protein
GI_7705631-S	3644.2	4832.5	5681.7	TTC11	NM_016068.1	Fis1;CGI-135			
GI_7705637-S	347	422.1	412.4	CGI-143	NM_016074.1		transcripti		
GI_7705639-S	476.1	514.1	460.1	C13orf9	NM_016075.1	CGI-145			
GI_7705643-S	109.7	99.5	98.9	FAM18B	NM_016078.1	CGI-148;YDR084C		integral to	

GI_7705647-S	101.2	128.9	102.9	ELA2B	NM_015849.1		pancreatic	extracellul	proteolysis
GI_7705655-S	219.9	267.4	258.2	LOC51036	NM_015854.1		retinoic	nucleus	regulation
GI_7705663-S	270	321.9	300.5	ZFP67	NM_015872.1	c-Krox;hcKrox	specific		ectoderm
GI_7705667-S	102.8	96.2	100.7	SIAT8C	NM_015879.1	ST8SiaIII;ST8Sia III	sialyltransf	Golgi	oligosacch
GI_7705673-S	103.6	105.1	89.8	LOC51049	NM_015883.1				
GI_7705675-S	104.4	106.8	103.7	PI15	NM_015886.1	P24TI;P25TI	endopepti	extracellul	biological_
GI_7705679-S	92.6	93.2	82.6	PRH	NM_015893.1		peptide		
GI_7705683-S	449	395.8	418.7	LOC51054	NM_015899.1				
GI_7705703-S	1513.3	1426.6	1357.4	LOC51064	NM_015917.1	GSTK1	glutathion	mitochond	
GI_7705707-S	90.4	107.6	109.6	LOC51066	NM_015931.1		electron		electron
GI_7705709-S	539.8	610.8	541.7	CGI-04	NM_015936.1		ATP		tyrosyl-
GI_7705717-S	2978.5	3237.4	2801.4	CGI-26	NM_015954.1		deoxyribo		
GI_7705723-S	793.3	869.7	796.3	MMRP19	NM_015957.1				
GI_7705725-S	1694.1	1944.7	1782.3	TMX2	NM_015959.1	CGI-31	electron	nucleus	electron
GI_7705727-S	677.3	564.9	554.3	CGI-32	NM_015960.1				
GI_7705729-S	300.4	282	245.9	C14orf111	NM_015962.1	CGI-35			
GI_7705739-S	5939.6	3846.3	3028.7	POLR1D	NM_015972.1	RPA9;RPA16;RPAC2;RPO1-3	DNA-	nucleus	transcripti
GI_7705743-S	280.2	222.5	172.6	CRYL1	NM_015974.1		oxidoredu		fatty acid
GI_7705747-S	86	93.2	84.8	TNNI3K	NM_015978.1	CARK	protein-		protein
GI_7705750-S	153.9	177.1	167.7	YBX2	NM_015982.1	MSY2;MGC45104	RNA	cytoplasm	translation
GI_7705752-S	173.3	196.4	174	C1QA	NM_015991.1		compleme	compleme	compleme
GI_7705754-S	191.5	241.2	212.5	TM4SF11	NM_015993.1	PLLP;PMLP			
GI_7705756-S	899.1	1513.8	1054.9	CGI-40	NM_015996.1				
GI_7705764-S	866.5	793.7	878.8	CGI-48	NM_016001.1		DNA	nucleus	regulation
GI_7705766-S	478.1	390.4	340.8	CGI-49	NM_016002.1				
GI_7705768-S	469.7	532.2	597	C20orf9	NM_016004.1	NGD5;CGI-53;dJ1028D15.1			
GI_7705774-S	181	191.5	159.3	CGI-62	NM_016010.1				
GI_7705776-S	1124.4	1099.9	825.9	CGI-63	NM_016011.1	NRBF1	alcohol		
GI_7705778-S	638.2	924	729.4	NDUFAF1	NM_016013.1	CGI65;CIA30;CGI-65	chaperone	mitochond	
GI_7705780-S	238.4	294.6	269.9	C9orf77	NM_016014.1	CGI-67	catalytic		
GI_7705784-S	745	635.1	477.5	TFB1M	NM_016020.1	CGI75;mtTFB;CGI-75	rRNA		rRNA
GI_7705786-S	1991	2175.5	1867.7	APH-1A	NM_016022.1	APH1A;CGI-78		Golgi	
GI_7705792-S	987.5	761.4	845.5	LACTB2	NM_016027.1	CGI-83			
GI_7705800-S	99.8	109.8	104.1	ZDHHC9	NM_016032.1	CGI-89;ZNF379	zinc ion	integral to	regulation
GI_7705802-S	1341.7	1565.3	1180.5	CGI-90	NM_016033.1				
GI_7705806-S	539.2	557.1	611.5	COQ4	NM_016035.1	CGI-92			ubiquinon
GI_7705808-S	1896.7	2534	2154	CGI-94	NM_016037.1			nucleus	rRNA
GI_7705814-S	100.8	95.1	81	COMMD2	NM_016094.1	HSPC042;MGC57611			
GI_7705816-S	2024.7	2102	1756	LOC51123	NM_016096.1				
GI_7705820-S	1484.4	1624.1	1541.2	GOLGA7	NM_016099.1	GCP16;HSPC041;GOLGA3AP1			
GI_7705824-S	190	250.8	201.3	TRIM17	NM_016102.1	RBCC;terf;RNF16	zinc ion	intracellula	biological_
GI_7705832-S	777.5	958.7	666.2	PHF11	NM_016119.1	APY;BCAP;IGEL;IGER;IGHER;NYREN34;NY-	DNA	nucleus	regulation
GI_7705838-S	198.3	203.4	198.1	NY-REN-58	NM_016122.1				
GI_7705840-S	183.3	185.4	184.4	IRAK4	NM_016123.1	REN64;NY-REN-64	tumor		protein

GI_7705852-S	374.3	392.3	347.6	DNCLI1	NM_016141.1		small		small
GI_7705854-S	2411.6	2446.4	2070	HSD17B12	NM_016142.1	KAR	oxidoredu		metabolis
GI_7705856-S	260.5	282.5	242	LOC51145	NM_016158.1		DNA	integral to	regulation
GI_7705858-S	148.6	160.7	154.2	alpha4GnT	NM_016161.1		acetylgluc	Golgi	O-linked
GI_7705864-S	115	118.3	109.9	LOC51149	NM_016175.1				
GI_7705870-S	91.3	99.6	94.7	LOC51152	NM_016181.1				
GI_7705876-S	4197	5686.2	4302.8	HN1	NM_016185.1				
GI_7705878-S	96	111.9	119.8	SERPINA10	NM_016186.1	PZI;ZPI;CENTERIN	serpin		
GI_7705880-S	3060.9	3225.9	3715.8	ZNF580	NM_016202.1		DNA	nucleus	regulation
GI_7705882-S	144.1	153.2	146.3	LOC51159	NM_016206.1				
GI_7705890-S	317.7	344.3	337.4	DBR1	NM_016216.1		hydrolase		
GI_7705904-S	1088	1070.5	649.6	DHRS8	NM_016245.1	PAN1B;RETSDR2	oxidoredu		metabolis
GI_7705906-S	139.9	143.7	116.1	DHRS10	NM_016246.1	retSDR3	oxidoredu		metabolis
GI_7705908-S	473.2	590.7	556.5	NAGPA	NM_016256.1	UCE;APAA	N-	integral to	lysosome
GI_7705910-S	104.2	98.9	99.1	ZNFN1A2	NM_016260.1	HELIOS;ZNF1A2			
GI_7705912-S	244.1	300.9	271.7	TUBD1	NM_016261.1	TUBD	structural	centriole	microtubul
GI_7705930-S	138.2	209.9	127.9	CEB1	NM_016323.1		ubiquitin-	intracellula	regulation
GI_7705934-S	136.9	145.4	127.9	ANC_2H01	NM_016331.1	ZASC1			
GI_7705938-S	529.8	665.6	558.3	RAPGEFL1	NM_016339.1	Link-GEFII	guanyl-	membran	G-protein
GI_7705942-A	131.5	483.5	315.7	C5orf4	NM_016348.1	FLJ13758			
GI_7705942-I	270.9	332.4	305	C5orf4	NM_016348.1	FLJ13758			
GI_7705944-S	131.5	113.9	101.8	LOC51198	NM_016349.1				
GI_7705950-I	775.5	790.4	1086.6	NUSAP1	NM_016359.1	LNP;ANKT;SAPL;BM037;Q0310;FLJ13421;P			
GI_7705960-S	101.8	101.9	103.8	CLDN18	NM_016369.1		structural	tight	
GI_7705962-S	119.1	113.5	118.3	RAB9B	NM_016370.1	RAB9L	GTP	Golgi	small
GI_7705964-S	662.7	738.7	726	TPRA40	NM_016372.1		G-protein	integral to	aging
GI_7705968-S	86.8	92.9	92	LOC51212	NM_016380.1				
GI_7705970-S	135.9	164.9	163.5	HOM-TES-85	NM_016383.1				
GI_7705972-S	101.6	112	113.7	IGF2AS	NM_016412.1	PEG8	DNA	nucleus	regulation
GI_7705974-S	215.7	230.3	216.2	ZNF219	NM_016423.1	ZFP219	transcripti	nucleus	transcripti
GI_7705982-S	367.3	541.4	392.3	COPZ2	NM_016429.1		protein	Golgi cis-	intracellula
GI_7705994-S	120.5	138.4	119.9	LOC51233	NM_016449.1				
GI_7706060-S	99.7	110.4	119.6	CLEC2	NM_016509.1		transmem	integral to	defense
GI_7706064-S	101	113	104.5	PIPOX	NM_016518.1	LPIPOX	sarcosine	peroxisom	tetrahydrof
GI_7706082-S	529.4	876	635.6	C1RL	NM_016546.1	C1RL1;C1r-LP	trypsin		proteolysis
GI_7706086-I	122	132.4	114.3	ANKMY1	NM_016552.1	ZMYND13;FLJ20499			
GI_7706090-S	857.4	978.7	1109.7	BFAR	NM_016561.1	BAR;RNF47	apoptosis	membran	anti-
GI_7706098-S	426.5	564.5	443.2	E2IG2	NM_016565.1				
GI_7706102-S	160.3	161.8	154.8	SALPR	NM_016568.1		G-protein	integral to	G-protein
GI_7706104-S	611.9	775.9	695.3	PTX1	NM_016570.1	CDA14;cd002			
GI_7706106-S	250.9	294.9	330.5	GMIP	NM_016573.1		oxidoredu		metabolis
GI_7706110-S	804.6	602.8	317.9	8D6A	NM_016579.1	8D6			positive
GI_7706116-S	111.8	122.1	97.2	SLC15A3	NM_016582.1	PHT2;PTR3;hPTR3	transporte	membran	oligopepti
GI_7706124-S	5623.3	6386.3	5262.1	C3orf1	NM_016589.1		protein	mitochond	protein

GI_7706126-S	130.2	127	115.8	C2GNT3	NM_016591.1		N-	membran	O-linked
GI_7706130-S	298	396.8	304.6	FKBP11	NM_016594.1	FKBP19	cyclophilin		protein
GI_7706132-S	646.3	751	637.8	ZDHHC3	NM_016598.1	GODZ;ZNF373	zinc ion	Golgi	regulation
GI_7706136-S	320.5	297.3	292.5	C5orf5	NM_016603.1	N61;KHCHP	GTPase		
GI_7706138-S	2458	2167	2223.7	C5orf6	NM_016605.1			nucleus	
GI_7706142-S	804.9	621.5	640.3	ALEX1	NM_016608.1				
GI_7706149-A	1726	1446.6	1357.4	MSCP	NM_016612.1	MSC;HT015;PRO1278;PRO1584			
GI_7706155-S	348.9	401.9	226	LOC51315	NM_016618.1				
GI_7706157-S	137.7	257.7	121.5	PLAC8	NM_016619.1	C15			
GI_7706177-S	139.5	169.4	153.3	LOC51326	NM_016632.1				
GI_7706179-S	218.4	251.5	241.9	ERAF	NM_016633.1	AHSP;EDRF	chaperone	hemoglobi	hemopoie
GI_7706183-I	1669.7	1657.7	1533.2	ARL6IP4	NM_016638.1	SR-25;SRp25		nucleus	RNA
GI_7706185-S	2153.7	1383.5	1812.8	TNFRSF12A	NM_016639.1	FN14;TWEAKR	receptor	integral to	cell
GI_7706189-S	403.4	511.4	405.8	SPTBN5	NM_016642.1	BSPECV;HUSPECV;HUBSPECV	actin	spectrin	actin
GI_7706191-S	126.5	158.1	136.8	LOC51333	NM_016643.1				
GI_7706193-S	452.4	515.9	443.7	LOC51334	NM_016644.1				
GI_7706195-S	3248.9	2345.2	2395.3	NEUGRIN	NM_016645.1		molecular	nucleus	neuron
GI_7706197-S	92.6	104.3	88.4	LOC51336	NM_016646.1				
GI_7706199-S	1986.5	1905.6	2745.8	LOC51337	NM_016647.1				
GI_7706243-S	6045.7	5565.4	6736.8	C6orf82	NM_015921.1	CUTA			
GI_7706261-S	1581.6	2112.2	2332.3	ATP6V1H	NM_015941.1	SFD;VMA13;CGI-11;SFDbeta;SFDalpha			
GI_7706269-S	2953.5	2773.6	2367.8	RWDD1	NM_015952.1	PTD013			
GI_7706271-S	3059.6	2239.7	1717.1	CGI-30	NM_015958.1				
GI_7706275-A	226.2	256.7	150.7	CGI-38	NM_015964.1				
GI_7706293-A	1240.2	1356.4	1501.5	DKFZP434J1	NM_016003.1	CGI-50;FLJ12979;FLJ14217			
GI_7706293-I	89.3	94.9	95.6	DKFZP434J1	NM_016003.1	CGI-50;FLJ12979;FLJ14217			
GI_7706305-S	3944.2	3660.1	3827.7	CGI-69	NM_016016.1		binding	mitochond	transport
GI_7706309-S	161	156.9	201.1	LUC7L2	NM_016019.1	CGI-59;CGI-74			
GI_7706315-S	882.5	1065.8	952	CGI-79	NM_016024.1		RNA		
GI_7706317-S	1927.4	2195	1366.2	DHRS7	NM_016029.1	retDSR4;retSDR4	oxidoredu		metabolis
GI_7706321-S	3034.2	3042.9	2779.8	C14orf166	NM_016039.1	CGI-99			
GI_7706334-S	835.9	964	887.5	CGI-119	NM_016056.1				
GI_7706336-S	1472.9	1924.3	1818.9	COPZ1	NM_016057.1	COPZ;CGI-120	protein	membran	intracellula
GI_7706340-S	1912.5	1681.8	1494.9	CGI-127	NM_016061.1				
GI_7706342-S	2544.4	2726.9	3172.7	CGI-128	NM_016062.1				
GI_7706350-S	1334	1425.2	1039.8	CGI-147	NM_016077.1			integral to	
GI_7706352-S	872	1073.2	1121.1	VPS24	NM_016079.1	25.1;NEDF;CGI-149	molecular		
GI_7706366-S	832.4	913.3	1249.6	Pfs2	NM_016095.1	HSPC037		nucleus	DNA
GI_7706368-S	1170.1	906.8	1082	BRP44L	NM_016098.1	CGI-129;dJ68L15.3	molecular		
GI_7706378-A	133.5	136	150.1	ASB4	NM_016116.1	ASB-4			
GI_7706378-I	94.8	99.3	98.1	ASB4	NM_016116.1	ASB-4			
GI_7706382-S	637.1	642.8	722.4	LOC51668	NM_016126.1				
GI_7706422-S	1754.1	1580	1354.8	LSM7	NM_016199.1	YNL147W	pre-mRNA	small	mRNA
GI_7706428-S	1894.5	1809.6	2159.7	LOC51693	NM_016209.1				

GI_7706434-S	1175.7	998.6	906.4	HECA	NM_016217.1	HDC;HDCL;hHDC;dJ225E12.1	electron	nucleus	electron
GI_7706436-I	121.6	165.9	142.3	MAN1B1	NM_016219.1	MANA-ER;DKFZP434I213	mannosyl-	membran	oligosacch
GI_7706442-S	163.4	369.3	567.4	CYB5R2	NM_016229.1	B5R.2			
GI_7706446-S	119.7	247.6	138.7	PADI3	NM_016233.1	PDI3	protein-		protein
GI_7706450-S	254.1	290.7	268.9	GPRC5B	NM_016235.1	RAIG2;RAIG-2	metabotro	membran	
GI_7706454-S	853.3	754.9	617.2	CYB5R1	NM_016243.1	B5R.1	oxidoredu		electron
GI_7706462-S	97.5	98.2	100.4	ZNF44	NM_016264.1	KOX7;ZNF58;GIOT-2;ZNF58 withdrawn	DNA	nucleus	regulation
GI_7706464-S	245.9	272.5	252.8	ZNF325	NM_016265.1	GIOT-3	DNA	nucleus	regulation
GI_7706468-S	1012.3	475.8	502.2	KLF2	NM_016270.1	LKLF	transcripti	nucleus	regulation
GI_7706474-S	88.6	95.4	84.4	CES4	NM_016280.1	CESR;PCE-3	carboxyles	endoplas	xenobiotic
GI_7706484-S	1583.8	1215.4	1178.7	TRAP1	NM_016292.1	HSP75	protein	mitochond	heat
GI_7706492-S	98.4	102	97.3	LOC51725	NM_016298.1		zinc ion		
GI_7706496-S	345.5	477.3	437.1	UMP-CMPK	NM_016308.1		uridine	cytoplasm	pyrimidine
GI_7706508-S	153.8	203.6	142.2	UPB1	NM_016327.1	BUP1	beta-		nitrogen
GI_7706512-S	378.4	432.3	328.8	RAPGEF6	NM_016340.1	PDZGEF2;PDZ-GEF2;RA-GEF-2	protein	plasma	small
GI_7706518-S	86.2	89.4	92.7	GHRL	NM_016362.1	MTLRP	growth	soluble	G-protein
GI_7706528-S	129.4	147.9	128.6	CD244	NM_016382.1	2B4;NAIL;Nmrk;NKR2B4;SLAMF4	protein	integral to	cellular
GI_7706548-S	462	512.6	541.6	CRK7	NM_016507.1	CRKRS;KIAA0904	ATP	nucleus	protein
GI_7706556-A	2218.4	2272.2	2325.5	C9orf78	NM_016520.1	HSPC220			
GI_7706562-S	191.1	213.9	147.7	RAB8B	NM_016530.1		GTP	cellular_co	small
GI_7706566-S	273	337.1	284.1	GNG13	NM_016541.1	h2-35	signal	heterotrim	G-protein
GI_7706570-A	152.2	151.9	129.3	SIGLEC7	NM_016543.1	p75;QA79;AIRM1;SIGLEC-7;p75/AIRM1	lectin [goid	integral to	cell
GI_7706572-I	105.9	116	112.5	Cab45	NM_016547.1				
GI_7706574-S	2245.2	3369.3	3252.9	TM7SF3	NM_016551.1			integral to	
GI_7706576-A	130.9	130.7	116.2	HUMGT198A	NM_016556.1	TBPIP			
GI_7706588-I	216.9	250.1	219.2	GNAS	NM_016592.1	AHO;GSA;GSP;POH;GPSA;NESP;GNAS1;P	heterotrim	peripheral	Golgi to
GI_7706600-A	250.8	227.7	265	ZAK	NM_016653.1	MLTK;mlklak			
GI_7706600-I	165.3	135.7	165.6	ZAK	NM_016653.1	MLTK;mlklak			
GI_7706602-S	209.8	182.7	171.6	LW-1	NM_016153.1		transcripti	nucleus	regulation
GI_7706610-S	470.3	543.1	422.4	MBIP	NM_016586.1		protein		inactivatio
GI_7706634-S	96.4	121.1	97.7	C1orf10	NM_016190.1	PDRC1	calcium		
GI_7706636-S	443.5	545.9	459	PIAS1	NM_016166.1	GBP;DDXBP1;GU/RH-II	ATP	nucleus	JAK-STAT
GI_7706642-S	218.4	242	239	PLEK2	NM_016445.1			membran	actin
GI_7706644-S	792.1	975.2	806.1	PME-1	NM_016147.1		protein		protein
GI_7706660-S	158.7	181.1	164	PLA1A	NM_015900.1	PSPLA1;PS-PLA1	phospholi		phosphati
GI_7706664-S	4923.2	5112.2	4932.7	PTD008	NM_016145.1		molecular	integral to	
GI_7706666-S	2300	3165.1	3001.2	TRAPPC4	NM_016146.1	SBDN;TRS23;PTD009;CGI-104;HSPC172	protein	Golgi	vesicle-
GI_7706670-S	123.1	138.5	105.3	PEX5R	NM_016559.1	PXR2B			
GI_7706674-S	389	463.6	282.4	RAB6B	NM_016577.1		GTP	Golgi	retrograde
GI_7706676-S	126.9	189.1	143.7	SLC14A1	NM_015865.1	JK;UT1;UTE;RACH1;UT-B1;HsT1341	urea	integral to	urea
GI_7706680-S	307.8	278.3	256.5	REV1L	NM_016316.1	REV1	DNA	intracellula	mutagene
GI_7706682-S	101.6	106.7	86	RHCG	NM_016321.1	RHGK	transporte	integral to	cell growth
GI_7706686-S	333.6	451.9	307.7	EVL	NM_016337.1	RNB6	cytoskelet	cytoplasm	actin
GI_7706688-S	173.3	190.4	187.1	SFMBT1	NM_016329.1	RU1;SFMBT;DKFZp434L243			

GI_7706690-S	106.2	90.6	91.4	DCDC2	NM_016356.1	RU2;KIAA1154	tumor		cellular
GI_7706692-S	166.7	211.9	183.5	MBTPS2	NM_015884.1	S2P	metalloen	integral to	cholestero
GI_7706703-S	251	261.2	237.4	SH120	NM_016334.1	GPR89-PENDING	receptor		
GI_7706709-S	2892.6	2400	2888.3	SIRT6	NM_016539.1	SIR2L6	DNA	chromatin	chromatin
GI_7706711-S	882.6	967.5	1291.8	SIRT7	NM_016538.1	SIR2L7	DNA	chromatin	chromatin
GI_7706713-S	255.1	293.9	286	SLCO3A1	NM_013272.2	OATP-D;OATP3A1;SLC21A11	transporte	integral to	ion
GI_7706716-S	92.3	96.1	89.8	IMPG2	NM_016247.1	IPM200;SPACRCAN	extracellul	extracellul	vision
GI_7706726-S	173.2	167.5	171.7	ZNF589	NM_016089.1	SZF1	nucleic	intracellula	regulation
GI_7706742-A	703.1	691.2	757.5	TP53TG3	NM_016212.1	TP53TG3A			
GI_7706744-S	142.1	154.6	131.6	TRIM	NM_016388.1	HSPC062	transmem	integral to	cellular
GI_7706746-S	88.2	85.3	85.9	TRPC4	NM_016179.1	TRP4;HTRP4	store-		calcium
GI_7706748-S	2939.4	1984.1	1657	TU12B1-TY	NM_016575.1				
GI_7706750-S	1027.4	1341.3	1077	TUBG2	NM_016437.1		structural	microtubul	microtubul
GI_7706752-S	955.7	1258.2	858.9	UCHL5	NM_015984.1	UCH37;CGI-70	ubiquitin	cytosol	ubiquitin-
GI_7706758-S	524.7	146.9	418.7	VCX-2r	NM_016378.1	VCXB	molecular	cellular_co	biological_
GI_7706760-S	305.6	116.3	252.7	VCX-8r	NM_016379.1	VCX-A	molecular	cellular_co	biological_
GI_7706762-S	402	521	439.5	VILL	NM_015873.1		structural	actin	cytoskelet
GI_7706780-I	652.9	584	477.1	ZNF226	NM_016444.1				
GI_7710049-S	144.9	173.4	165.7	OAZ3	NM_016178.1	OAZ-t	ornithine		spermatog
GI_7710111-I	182.1	226.4	200.3	ACHE	NM_015831.1	YT	acetylcholi	peripheral	neurotran
GI_7710118-S	224	275.1	232.1	EN1	NM_001426.2		transcripti	nucleus	skeletal
GI_7710120-S	94	98.7	95.3	EN2	NM_001427.2		transcripti	nucleus	developm
GI_7710123-S	119.8	128.1	129.3	KLRC4	NM_013431.1	NKG2F;NKG2-F	receptor	integral to	cellular
GI_7710125-I	367.7	426.9	429.9	LIG3	NM_013975.1		DNA	nucleus	meiotic
GI_7710127-A	229.5	278.5	242.7	LIG3	NM_002311.2		DNA	nucleus	meiotic
GI_7710127-I	109.8	123.3	118.9	LIG3	NM_002311.2		DNA	nucleus	meiotic
GI_7710128-S	206.4	282.1	270.2	LMO6	NM_006150.3		molecular	cellular_co	biological_
GI_7710148-S	232.7	206.7	195.6	MECP2	NM_004992.2	RTS;RTT;PPMX;MRX16;MRX79	transcripti	nucleus	negative
GI_7710155-S	4476.1	4038.2	2808.7	WARS	NM_004184.2	IFI53;IFP53;GAMMA-2	ATP	soluble	tryptophan
GI_7710156-A	298.1	362.7	337	ACHE	NM_000665.2	YT	acetylcholi	peripheral	neurotran
GI_7770071-I	115.1	129.2	108.2	IARS	NM_013417.1	ILRS	ATP	soluble	protein
GI_7770073-A	10004.2	7981.4	6722.8	IARS	NM_002161.2	ILRS	ATP	soluble	protein
GI_7770078-A	102.6	106.9	103.8	TAC1	NM_013998.1	NK2;NKNA;TAC2;Hs.2563	tachykinin	extracellul	inseminati
GI_8051576-A	111.7	186.6	577.4	ABCG1	NM_016818.1	ABC8;WHITE1	L-	membran	small
GI_8051578-S	365	523.3	392.4	AK3	NM_013410.1	AK4	adenylate	mitochond	nucleobas
GI_8051583-S	117.5	132.2	118.8	FCN1	NM_002003.2	FCNM	lectin [goid		opsinizatio
GI_8051585-A	86.3	89.3	85	FCN2	NM_015837.1	P35;FCNL;EBP-37	lectin [goid	microfibril	opsinizatio
GI_8051589-I	303.4	368.3	323.6	FCN2	NM_015839.1	P35;FCNL;EBP-37	lectin [goid	microfibril	opsinizatio
GI_8051600-S	104.2	115	100.2	GALR2	NM_003857.2	GALNR2	galanin	integral to	cytosolic
GI_8051601-S	417.4	851.4	562.3	GPC6	NM_005708.2		glypican	membran	cell growth
GI_8051602-S	147.9	173.7	159.5	GYPA	NM_002099.2	MN;GPA;MNS	blood	membran	invasive
GI_8051603-S	155.3	179.1	162.8	GYPB	NM_002100.2	SS;MNS	blood	integral to	
GI_8051607-S	137.5	162.4	144.7	HMOX2	NM_002134.2	HO-2	heme	microsom	heme
GI_8051609-S	901.6	1186.2	818.5	KDELR2	NM_006854.2	ELP-1;ERD2.2	KDEL	Golgi	intracellula

GI_8051610-A	554.4	704.9	406.5	KDELR3	NM_016657.1	ERD2L3	protein	endoplas	intracellula
GI_8051610-I	230.2	241.1	223.9	KDELR3	NM_016657.1	ERD2L3	protein	endoplas	intracellula
GI_8051612-I	541.6	692	389.5	KDELR3	NM_006855.2	ERD2L3	protein	endoplas	intracellula
GI_8051613-S	1465.7	2800.8	2917.5	LDLR	NM_000527.2	FH;FHC	lipoprotein	coated pit	endocytosi
GI_8051614-A	3069	3763.8	6920.8	LIMK1	NM_016735.1	LIMK	protein	cytoplasm	actin
GI_8051616-I	140.8	153.3	143.9	LIMK1	NM_002314.2	LIMK	protein	cytoplasm	actin
GI_8051617-I	109.2	105.6	103.3	LIMK2	NM_016733.1				
GI_8051619-A	431.5	460	361.9	LIMK2	NM_005569.2				
GI_8051619-I	142.1	165.4	148.1	LIMK2	NM_005569.2				
GI_8051620-I	249.7	328.5	161	OAS1	NM_016816.1	OIAS;IFI-4;OIASI	antiviral	cytoplasm	nucleobas
GI_8051622-A	194.1	262.5	129.3	OAS1	NM_002534.1	OIAS;IFI-4;OIASI	antiviral	cytoplasm	nucleobas
GI_8051622-I	1015.7	1211.3	1102	OAS1	NM_002534.1	OIAS;IFI-4;OIASI	antiviral	cytoplasm	nucleobas
GI_8051624-A	117.8	130.5	116.5	OAS2	NM_016817.1	P69	antiviral	membran	nucleobas
GI_8051624-I	131.5	166	113.8	OAS2	NM_016817.1	P69	antiviral	membran	nucleobas
GI_8051626-I	112.3	111.3	117.5	RRAGB	NM_016656.1	RAGB	GTP	cytoplasm	signal
GI_8051628-A	188.2	206.9	204.9	RRAGB	NM_006064.2	RAGB	GTP	cytoplasm	signal
GI_8051632-S	119.8	152.8	139.8	RARRES2	NM_002889.2	TIG2;HP10433	molecular	cellular_co	retinoid
GI_8051633-S	154.6	409.9	182.8	RARRES3	NM_004585.2	RIG1;TIG3	tumor		negative
GI_8051634-S	2039	2051.8	1860.4	XPO1	NM_003400.2	CRM1	protein	nuclear	nucleocyto
GI_8392890-S	82.5	100.1	95.2	ALB	NM_000477.3	PRO0883	transporte	extracellul	transport
GI_8393008-S	795.3	880.2	860.7	C11orf2	NM_013265.2	ANG2	molecular	integral to	biological_
GI_8393012-S	390.5	428.5	308.4	C21orf18	NM_017438.1				
GI_8393017-S	993.2	1133.6	520	C21orf6	NM_016940.1	GL011	acylphosp	cellular_co	biological_
GI_8393146-S	82.6	88.4	88.8	CLIC5	NM_016929.1	CLIC5B	chloride	insoluble	pregnancy
GI_8393249-S	105.5	104.1	102.2	1-Dec	NM_017418.1	CTS9	tumor		negative
GI_8393258-S	2952.7	2470.6	2198.8	TFIP11	NM_012143.1	TIP39;DKFZP434B194	nucleic	nucleus	ossificatio
GI_8393298-S	990.3	1521.2	622.1	EFEMP2	NM_016938.1	UPH1;FBLN4	extracellul	basement	blood
GI_8393364-S	67.3	84.2	83.5	BCMO1	NM_017429.1	BCO;BCDO;BCMO;BCDO1;FLJ10730	oxidoredu		
GI_8393383-S	8643.2	5522	4987	C6orf48	NM_016947.1	G8;D6S57	major		
GI_8393411-S	99.8	95.9	89.5	GALNT8	NM_017417.1	GALNAC-T8	polypeptid	membran	RNA
GI_8393506-S	121	142.1	137.5	GUCY1B2	NM_004129.1	GC-SB2	guanylate		intracellula
GI_8393515-S	537.7	671	688.5	H105E3	NM_015922.1	NSDHL	3-beta-		cholestero
GI_8393566-S	114.7	110	101.2	SPOCK3	NM_016950.1	TES-3;HSAJ1454;testican-3	metalloen	extracellul	
GI_8393607-S	421.3	564.3	522.8	IMPA1	NM_005536.2	IMPA	inositol-		phosphati
GI_8393671-S	231	193.4	160.5	KLHL3	NM_017415.1	KIAA1129			
GI_8393712-A	195.2	191.6	165.5	SLA/LP	NM_016955.1		tRNA		
GI_8393994-S	108.8	113.2	109.5	POLA	NM_016937.1		eta DNA	nucleus	DNA
GI_8394043-S	184.8	230.7	210.1	PRKAG3	NM_017431.1		SNF1A/A		protein
GI_8394276-S	156.5	135.3	140.7	SIX4	NM_017420.1	AREC3	transcripti	nucleus	embryoge
GI_8394394-S	331.5	416.6	356.4	TAS2R16	NM_016945.1	T2R16	taste	integral to	taste [goid
GI_8394397-S	95.9	98.9	106.9	TAS2R3	NM_016943.1	T2R3	taste	integral to	taste [goid
GI_8394401-S	143.7	166.2	150.2	TAS2R4	NM_016944.1	T2R4	taste	integral to	taste [goid
GI_8394416-S	327.3	223.2	400.9	PARD6A	NM_016948.1	PAR-6;TAX40;PAR-6A;TIP-40;PAR6alpha	transcripti	tight	viral life
GI_8400709-S	515.8	785.2	524.7	HES1	NM_005524.2	HHL;HRY;HES-1;FLJ20408	DNA	nucleus	neurogene

GI_8400712-I	189.7	207	188.1	MAPT	NM_016835.1	TAU;MSTD;PPND;DDPAC;MAPTL;MTBT1;M	structural	microtubul	microtubul
GI_8400714-A	94.9	117.3	112.7	MAPT	NM_016841.1	TAU;MSTD;PPND;DDPAC;MAPTL;MTBT1;M	structural	microtubul	microtubul
GI_8400716-S	95.6	83.1	92.4	NEB	NM_004543.2	NEM2	structural	actin	muscle
GI_8400721-A	2062.8	1870.4	1323.9	RBMS1	NM_016838.1	YC1;SCR2;MSSP-1;MSSP-2;MSSP-3	double-		RNA
GI_8400723-I	89	79.7	82.4	RBMS1	NM_016839.1	YC1;SCR2;MSSP-1;MSSP-2;MSSP-3	double-		RNA
GI_8400726-S	109.2	116.8	96.9	RBP1	NM_002899.2	CRBP;RBPC;CRBP1;CRABP-I	retinoid		vitamin A
GI_8400727-S	134.3	125	112.3	RBP4	NM_006744.2		retinoid	extracellul	
GI_8400731-S	322	1336.7	3733.3	SFRP1	NM_003012.2	FRP;FRP1;FrzA;FRP-1;SARP2	transmem	membran	anti-
GI_8400733-S	159.2	191	168.5	SFRP4	NM_003014.2	FRP-4;FRPHE	transmem	membran	embryo
GI_8400734-S	166.7	207.5	181.7	SFRP5	NM_003015.2	SARP3	transmem	membran	establish
GI_8400737-S	395.4	467.3	368.6	TP53	NM_000546.2	P53;TRP53	nuclease	nucleus	induction
GI_8567387-S	375.4	406	391.5	PER3	NM_016831.1		signal	nucleus	regulation
GI_8659554-S	4207.9	7301.6	4337.4	ACO1	NM_002197.1	IRP1;IREB1;IREBP	aconitate	cytoplasm	tricarboxyli
GI_8659566-S	120.7	123.9	115.2	KERA	NM_007035.2	CNA2;SLRR2B	molecular	extracellul	eye
GI_8670537-A	317.4	269.9	292.2	OGG1	NM_016827.1	HMMH;MUTM;OGH1;HOGG1	purine-	nucleoplas	base-
GI_8670543-A	686.1	892	1160.2	PSCD1	NM_017456.1	B2-1;SEC7;D17S811E;CYTOHESIN-1	ARF	kinesin	vesicle-
GI_8670549-S	148	244.5	311.3	PSCD4	NM_013385.2	CYT4;DJ63G5.1;CYTOHESIN-4	ARF		
GI_8670550-S	107.8	128.9	95.3	PSCDBP	NM_004288.2	HE;B3-1;CYBR	protein		intracellula
GI_8850216-S	88.1	94.8	85.8	HNRNPG-T	NM_014469.2	HNRPGT	nucleic	ribonucleo	regulation
GI_8850230-S	199.9	237	198.2	MYCBP	NM_012333.2	AMY-1	transcripti	mitochond	regulation
GI_8850235-S	93.6	98	89.8	UGT1A1	NM_000463.1	GNT1;UGT1;UGT1A;UGT1A5	UDP-	microsom	bilirubin
GI_8922068-S	205	247.5	218.3	C5orf3	NM_018691.1	133K02	purine	cellular_co	biological_
GI_8922070-S	135.4	160.3	138.1	LOC55565	NM_017530.1				
GI_8922074-S	2056.9	1764.6	2305	ACK1	NM_005781.2	ACK	GTPase	cytoplasm	small
GI_8922076-S	151.4	188.4	166	ADARB2	NM_018702.1	RED2;ADAR3;hRED2	double-	intracellula	RNA
GI_8922080-S	120	143.9	128.6	ASH1L	NM_018489.1	ASH1;ASH1L1;huASH1;KIAA1420	RNA	tight	positive
GI_8922084-S	570.6	471.6	702.4	SLC35E3	NM_018656.1	BLOV1			
GI_8922103-S	208.4	224.8	189.2	BM045	NM_018459.1				
GI_8922107-S	111	409.9	82.2	C17	NM_018659.1		receptor	soluble	signal
GI_8922115-S	138.3	175.9	124	C9orf7	NM_017586.1	D9S2135			
GI_8922121-S	183.4	219.4	169.9	ELAC1	NM_018696.1	D29			
GI_8922125-S	336	198.3	162.4	DKFZp434C0	NM_017577.1				
GI_8922127-S	98.6	93.8	92.3	DKFZp434C0	NM_017598.1				
GI_8922129-I	95.1	93.2	110.1	EGLN2	NM_017555.1	EIT6;PHD1;HIFPH1;DKFZp434E026			
GI_8922137-S	230.4	288	251.7	DKFZp434H2	NM_017559.1				
GI_8922152-S	94.4	103.8	97.5	DKFZp547G1	NM_018705.1				
GI_8922154-S	89.9	95.1	81.9	ZNT8	NM_018713.1	DKFZp547M236	cation	membran	cation
GI_8922158-S	140.3	145.5	128.4	DKFZp566H0	NM_017535.1				
GI_8922171-S	1098.2	1535	1199.5	DKFZp761K1	NM_018422.1				
GI_8922174-S	94.6	118.3	105.9	DKFZp761K1	NM_017597.1				
GI_8922178-S	100.9	101.8	92.2	DKFZp761P1	NM_018423.1	STYK1	protein-		protein
GI_8922193-I	73.1	90.8	96.1	APG16L	NM_017974.1	WDR30;FLJ00045;FLJ10035;FLJ10828;FLJ2			
GI_8922197-S	841.9	1119.1	1222.3	FLJ10038	NM_017976.1		DNA	nucleus	regulation
GI_8922199-S	298.2	363.1	308	AIM1L	NM_017977.1	FLJ10040	DNA	nucleus	regulation

GI_8922201-A	117.9	137.3	137.5	SMAP-1	NM_017979.1	FLJ10043;IRO039700			
GI_8922201-I	3601.8	3914.5	3815.3	SMAP-1	NM_017979.1	FLJ10043;IRO039700			
GI_8922205-S	125.7	420	127.6	FLJ10052	NM_017982.1				
GI_8922211-S	99.7	92.7	97.7	C9orf68	NM_017985.1	FLJ10058			
GI_8922226-S	199.4	162	147	FLJ10094	NM_017993.1		nucleic		
GI_8922232-S	627.8	521.7	506.8	C9orf40	NM_017998.1	FLJ10110	actin		
GI_8922236-S	225	201.2	232.8	FLJ10116	NM_018000.1				
GI_8922238-S	80.6	89.2	81.8	FLJ10120	NM_018001.1				
GI_8922242-S	308.1	712.4	329	FLJ10134	NM_018004.1	DERP7		integral to	
GI_8922258-S	1118.2	1574.3	1208.2	FLJ10154	NM_018011.1				
GI_8922262-S	379.7	396.7	187.1	FLJ10159	NM_018013.1				
GI_8922276-S	2166.3	2168.5	1655.6	FLJ10199	NM_018022.1				
GI_8922280-S	842.1	747.6	449.8	FLJ10204	NM_018024.1				
GI_8922306-A	97.3	112.4	113.7	RALGPS2	NM_018037.1	FLJ10244;FLJ25604	guanyl-		intracellula
GI_8922306-I	75.6	79.7	80.8	RALGPS2	NM_018037.1	FLJ10244;FLJ25604	guanyl-		intracellula
GI_8922308-S	157.4	181.5	158.6	FLJ10246	NM_018038.1				
GI_8922312-S	190.9	211.8	194.5	FLJ10252	NM_018040.1		nucleic	intracellula	
GI_8922327-S	2834.1	2080	2465.6	FLJ10290	NM_018047.1		nucleic		
GI_8922332-S	544.1	454	628	PLEKHJ1	NM_018049.1	GNRPX;FLJ10297			
GI_8922347-S	1097.3	917.3	715.4	FLJ10315	NM_018056.1				
GI_8922357-S	301.4	339.5	245.6	FLJ10330	NM_018061.1		DNA	nucleus	regulation
GI_8922359-S	324.8	245.5	287	FANCL	NM_018062.1	POG;PHF9;FLJ10335	ligase	nucleus	DNA
GI_8922387-S	454	452.1	407.4	FLJ10377	NM_018077.1		nucleic		
GI_8922395-S	228.8	255.3	312	FLJ10385	NM_018081.1				
GI_8922406-S	145.3	151.7	148.3	FIGN	NM_018086.1	FLJ10405;FLJ22094			
GI_8922410-S	78.6	87.2	90.3	FLJ10408	NM_018088.1		nucleic	nucleus	regulation
GI_8922412-S	1953.8	2193.9	1657.4	FLJ10415	NM_018089.1				
GI_8922421-S	981.9	695.4	631.6	FLJ10439	NM_018093.1				
GI_8922423-S	307.2	642.3	478.8	GSPT2	NM_018094.1	GST2;ERF3B;FLJ10441	GTP		translation
GI_8922429-S	250.5	302.2	273.7	FLJ10460	NM_018097.1				
GI_8922435-S	467.5	609.6	540.1	EFHC1	NM_018100.1	FLJ10466	calcium		
GI_8922437-S	1023.2	923	1275.6	CDCA8	NM_018101.1	FLJ10468;FLJ12042			
GI_8922458-S	291.1	324.8	343.3	FLJ10490	NM_018111.1				
GI_8922460-S	345.2	262.8	469.9	C9orf87	NM_018112.1	FLJ10493;bA219P18.1			
GI_8922462-S	525.5	723.5	320	LIMR	NM_018113.1	FLJ10494;KIAA1174			
GI_8922466-S	778.6	721.4	648.8	FLJ10498	NM_018115.1				
GI_8922473-S	191.6	199.2	167.6	MCM3APAS	NM_018118.1	C21orf85;FLJ10508		integral to	
GI_8922490-S	179.6	198.4	169.2	FLJ10525	NM_018126.1		molecular	integral to	
GI_8922497-S	154.3	156.8	140.6	PNPO	NM_018129.1	FLJ10535	pyridoxam		pyridoxine
GI_8922499-S	1424.1	1469.1	1234.1	FLJ10539	NM_018130.1				
GI_8922508-S	322.6	285.8	316.7	FLJ10547	NM_018134.1				
GI_8922514-S	486.5	591.2	679.1	PRMT6	NM_018137.1	FLJ10559	S-	nucleus	
GI_8922516-S	171	186.3	173.3	FLJ10560	NM_018138.1		sugar		phosphoe
GI_8922518-S	432.8	434.8	345.7	C14orf104	NM_018139.1	FLJ10563			

GI_8922520-S	164.4	174.5	164.6	FLJ10565	NM_018140.1			
GI_8922524-S	755.8	1031.5	1113.6	FLJ10569	NM_018142.1			
GI_8922527-S	105.5	108.2	105.5	KLHL11	NM_018143.1	FLJ10572	protein		
GI_8922531-S	839.8	1068.2	1022.7	FLJ10579	NM_018145.1		DNA		DNA
GI_8922535-S	132.8	212.7	232.7	FAIM	NM_018147.1	FAIM1;FLJ10582			
GI_8922541-I	344.6	303.4	299.8	FLJ10597	NM_018150.1				
GI_8922548-S	197.3	233.2	315.5	ASF1B	NM_018154.1	CIA-II;FLJ10604			
GI_8922550-S	346.4	362.2	276.8	FLJ10618	NM_018155.1		binding	mitochond	mitochond
GI_8922554-S	489.2	536	501.5	hSyn	NM_018157.1	RIC-8;FLJ10620			
GI_8922556-S	395.3	441.4	431	SLC4A1AP	NM_018158.1	HLC3;FLJ10624	double-	intracellula	
GI_8922562-S	389.4	523.5	498.7	FLJ10634	NM_018163.1		nucleic		protein
GI_8922566-S	1918.4	1841.3	1797.9	FLJ10647	NM_018166.1				
GI_8922570-S	97.9	89.5	90.8	C14orf105	NM_018168.1	FLJ10650			
GI_8922572-S	435.8	542.3	491.1	FLJ10652	NM_018169.1				
GI_8922580-S	111	124.7	111.9	FLJ10665	NM_018173.1				
GI_8922595-S	575.5	704.1	685.5	FLJ10700	NM_018182.1				
GI_8922600-S	2554.3	2517.6	2603.1	ARL10C	NM_018184.1	FLJ10702	small		small
GI_8922602-S	143.8	124.1	134.1	C13orf17	NM_018185.1	FLJ10704;FLJ20092			
GI_8922611-S	118.9	140.1	117.4	DPPA4	NM_018189.1	FLJ10713			
GI_8922620-S	494.1	470.4	688	MART2	NM_018194.1	SKI1;MART-2;FLJ10724			
GI_8922624-S	116.3	137.1	130	TMLHE	NM_018196.1	TMLH;FLJ10727	oxidoredu	mitochond	carnitine
GI_8922628-S	1459.9	1619.2	1527.8	FLJ10737	NM_018198.1				
GI_8922630-S	554.9	550.5	479.8	C14orf114	NM_018199.1	FLJ10738	nucleic	intracellula	electron
GI_8922639-S	126.8	153.1	136.2	FLJ10748	NM_018203.1				
GI_8922643-A	367	330.1	368.1	FLJ10751	NM_018205.1	FLJ10844			
GI_8922643-I	180	224.6	201.5	FLJ10751	NM_018205.1	FLJ10844			
GI_8922647-S	146.2	217.7	146.5	FLJ10759	NM_018207.1		zinc ion	intracellula	
GI_8922649-S	202.5	263.6	329.8	FLJ10761	NM_018208.1		choline	cellular_co	biological_
GI_8922653-S	806.9	889.7	774	FLJ10769	NM_018210.1				
GI_8922664-S	720.2	810.4	801.5	PANK4	NM_018216.1	FLJ10782;DKFZp547M242	ATP		coenzyme
GI_8922666-S	1195.8	1424.4	2033.1	C20orf31	NM_018217.1	C20orf49;FLJ10783;bA4204.1	mannosyl-	membran	N-linked
GI_8922668-S	257.5	328.2	281.5	FLJ10786	NM_018219.1				
GI_8922670-S	91.5	85.7	89.8	C2orf6	NM_018221.1	MOB1;Mob4B;MOBK1B;FLJ10788;FLJ11595			
GI_8922674-S	856.2	1141.1	1368.2	CHFR	NM_018223.1	RNF116;FLJ10796			
GI_8922676-S	186.5	172.2	146.7	FLJ10803	NM_018224.1				
GI_8922678-S	214.1	336.4	238.7	SMU-1	NM_018225.1	BWD;FLJ10805			
GI_8922685-S	116.5	113.7	108.5	C14orf115	NM_018228.1	FLJ10811			
GI_8922691-S	205.7	328.7	378.4	FLJ10815	NM_018231.1		amino	membran	amino
GI_8922698-S	1000.2	979.7	1207.8	CN2	NM_018235.1	FLJ10830			
GI_8922702-I	143.3	145	131.3	FLJ10751	NM_018239.1	FLJ10844			
GI_8922706-S	587.2	514.7	519.9	FLJ10846	NM_018241.1				
GI_8922715-S	260.2	303.6	248.2	FLJ10851	NM_018245.1		oxidoredu		metabolis
GI_8922717-S	4099	3395.6	2562.6	FLJ10853	NM_018246.1				
GI_8922719-S	398	599.5	567.5	C6orf67	NM_018247.1	FLJ10856			

GI_8922721-S	96.2	98.7	99.9	FLJ10858	NM_018248.1	hFPG2			DNA
GI_8922725-S	797.1	791.8	687	FLJ10871	NM_018250.1				
GI_8922727-S	136.7	146.3	131.3	FLJ10874	NM_018252.1				
GI_8922734-S	1634.9	1807.9	1482.6	STATIP1	NM_018255.1	ELP2;FLJ10879			
GI_8922738-S	601.1	512.2	574.8	C20orf36	NM_018257.1	FLJ10883	protein-L-		protein
GI_8922743-S	105.5	117.9	105.3	FLJ10891	NM_018260.1		nucleic	nucleus	regulation
GI_8922751-S	818.3	735.4	733.4	FLJ10900	NM_018264.1		flavodoxin		electron
GI_8922753-S	155.2	180	146.1	FLJ10901	NM_018265.1				
GI_8922755-S	231.6	237.5	197.1	FLJ10902	NM_018266.1				
GI_8922761-S	2234.5	2151	2800	SIPL	NM_018269.1	FLJ10913			
GI_8922778-S	214.6	222.4	206	C21orf77	NM_018277.1	FLJ10932			
GI_8922780-S	206.6	254.3	232.4	KIF24	NM_018278.1				
GI_8922784-S	156	192.1	170.5	FLJ10945	NM_018280.1				
GI_8922786-S	432.8	1176.7	396.3	FLJ10948	NM_018281.1		catalytic		metabolis
GI_8922788-S	688.4	668	671.3	PSPC1	NM_018282.1	PSP1;FLJ10955	nucleic		
GI_8922791-S	356.6	422.6	385.3	NUDT15	NM_018283.1	MTH2;FLJ10956			
GI_8922793-S	3475.1	3388	4043.8	C15orf12	NM_018285.1	BRMS2;MRPS4;FLJ10968;DKFZp586L0118	structural		
GI_8922795-S	89	107.5	104	FLJ10970	NM_018286.1				
GI_8922803-S	722.9	613.5	422.6	PGM2	NM_018290.1	FLJ10983	transporte		transport
GI_8922809-S	108.9	115.8	103.8	FLJ10997	NM_018293.1	FLJ21142			
GI_8922813-S	120.2	117.5	108	FLJ11000	NM_018295.1				
GI_8922821-S	888.2	1077	740.7	FLJ11011	NM_018299.1				
GI_8922827-S	113	109.7	93.2	FLJ11017	NM_018302.1				
GI_8922831-S	1023.4	1071.4	938.6	FLJ11029	NM_018304.1				
GI_8922839-S	89.4	98.3	96.2	ACOXL	NM_018308.1	FLJ11042			
GI_8922841-S	156.8	153.3	136.5	FLJ11046	NM_018309.1				
GI_8922853-S	495.3	571.9	523	FLJ11078	NM_018316.1		protein		
GI_8922855-S	191.5	305.3	270.7	FLJ11082	NM_018317.1				
GI_8922866-S	208	209.6	206.6	C6orf64	NM_018322.1	FLJ11101			
GI_8922870-S	426.8	575.5	531.8	FLJ11106	NM_018324.1				
GI_8922874-S	122.2	116.6	109.1	C20orf38	NM_018327.1	FLJ11112			
GI_8922878-S	149.6	172.5	155	FLJ11117	NM_018329.1				
GI_8922889-S	505	438.2	402.9	C14orf131	NM_018335.1	FLJ11132	ATP	membran	transport
GI_8922891-S	258.2	358.6	294.6	FLJ11136	NM_018336.1				
GI_8922900-S	125.9	171.1	127.2	FLJ11151	NM_018340.1		hydrolase		
GI_8922904-S	665.4	593.9	623.2	RIOK2	NM_018343.1	FLJ11159	molecular		
GI_8922910-S	668.7	499.3	418.5	FLJ11164	NM_018346.1		coproporp	cytoplasm	porphyrin
GI_8922912-S	477	560	489.8	C20orf29	NM_018347.1	FLJ11168			
GI_8922916-S	160.3	593.8	529.4	FLJ11175	NM_018349.1				
GI_8922918-S	114.8	126.4	120.5	FLJ11181	NM_018350.1				
GI_8922922-S	125.7	126.6	109.6	FLJ11184	NM_018352.1				
GI_8922926-S	447.3	436.8	161.7	C20orf46	NM_018354.1	FLJ11190		integral to	
GI_8922930-S	485.3	511.5	500.7	FLJ11193	NM_018356.1				
GI_8922935-S	227.3	282.5	311.3	ABCF3	NM_018358.1	FLJ11198;EST201864	nucleotide	membran	transport

GI_8922937-S	1306.2	1015	931.4	FLJ11200	NM_018359.1				
GI_8922939-S	136.8	131.4	126.8	CXorf15	NM_018360.1	LSR5;FLJ11209			
GI_8922941-S	974.6	881.4	690.5	LPAAT-e	NM_018361.1	FLJ11210	acyltransf	integral to	metabolis
GI_8922945-S	94.9	99.9	90.9	FLJ11218	NM_018363.1				
GI_8922949-S	122.5	139.3	162.6	MNS1	NM_018365.1	FLJ11222			
GI_8922957-S	1544.8	1213.1	1340.4	FLJ11259	NM_018370.1		nucleic		
GI_8922963-S	355.3	528.5	383.4	SYNJ2BP	NM_018373.1	Arip2;FLJ11271	protein	mitochond	intracellula
GI_8922978-S	606.8	708.1	590.7	FLJ11286	NM_018381.1				
GI_8922980-S	108.8	113	97.5	FLJ11292	NM_018382.1				
GI_8922986-S	1829.2	1496.4	1215.5	FLJ11305	NM_018386.1				
GI_8922994-S	353.6	276.9	252.3	FLJ11323	NM_018390.1		phospholi		intracellula
GI_8923000-S	739.3	744	779.9	FLJ11342	NM_018394.1		catalytic		
GI_8923004-S	336.9	295.5	267.4	METTL2	NM_018396.1	METL;PSENIP1;FLJ11350			
GI_8923008-S	2092.8	1683.3	2107.9	C10orf86	NM_017615.1	FLJ20003;bA500G22.3	DNA	nucleus	regulation
GI_8923014-S	564	803.4	653.2	FLJ20006	NM_017618.1				
GI_8923020-S	849.4	1106.7	1526.9	FLJ20014	NM_017622.1	PRO2472			
GI_8923025-S	115.6	117.7	114.9	FLJ20019	NM_017624.1				
GI_8923035-S	187.5	233	203.3	C14orf113	NM_017630.1				
GI_8923039-S	322.2	381.5	345.7	CARF	NM_017632.1	FLJ20036	double-	intracellula	
GI_8923041-S	708.7	1073.1	873.7	C6orf37	NM_017633.1	FLJ20037			
GI_8923052-S	146.5	152.5	154	FLJ20045	NM_017638.1				
GI_8923054-S	240	312.7	271	FLJ20047	NM_017639.1		calcium	membran	homophili
GI_8923058-S	249.3	293.2	261.1	MBTD1	NM_017643.1	SA49P01;FLJ20055			
GI_8923076-S	813.7	651.1	678.8	ZNF586	NM_017652.1	FLJ20070	nucleic	intracellula	regulation
GI_8923085-S	197.4	186.6	196.2	ZNF562	NM_017656.1	FLJ20079		nucleus	
GI_8923089-S	267.3	296.5	257.6	BTBD5	NM_017658.1	FLJ20081	protein		
GI_8923091-S	144.4	166.2	163.5	FLJ20084	NM_017659.1				
GI_8923103-S	428.9	447.2	278.7	ANKRD10	NM_017664.1	FLJ20093			
GI_8923105-S	311.9	318.2	295.2	ZCCHC10	NM_017665.1	FLJ20094	nucleic		
GI_8923109-S	772.4	724.9	804.3	NDE1	NM_017668.1	NUDE;NUDE1;FLJ20101			
GI_8923113-S	1982.5	2277.4	2564.3	OTUB1	NM_017670.1	OTB1;OTU1;FLJ20113			
GI_8923119-S	138.9	133.2	132.3	FLJ20123	NM_017674.1				
GI_8923123-S	251.2	265.8	239.1	FLJ20125	NM_017676.1		DNA		DNA
GI_8923128-S	123.4	139	127.6	C11orf33	NM_017678.1	FLJ20127			
GI_8923134-S	199.5	238.2	217.9	FLJ20130	NM_017681.1				
GI_8923136-S	191	248.2	213.9	VMD2L1	NM_017682.1	FLJ20132	molecular	integral to	biological_
GI_8923140-S	89.7	89.2	102.1	FLJ20139	NM_017685.1				
GI_8923142-S	193.9	218.4	181	GDAP2	NM_017686.1	FLJ20142			
GI_8923144-S	70.5	78.4	76.3	FLJ20147	NM_017687.1				
GI_8923147-S	95.3	99.3	85.7	BSPRY	NM_017688.1	FLJ20150	zinc ion	intracellula	
GI_8923149-S	185.2	205.7	188.3	FLJ20151	NM_017689.1				
GI_8923153-S	391.3	341.2	274.4	FLJ20156	NM_017691.1				
GI_8923164-S	136.9	133	132.4	C6orf61	NM_017696.1				
GI_8923166-S	148.3	162.6	156.4	FLJ20171	NM_017697.1		nucleic		

GI_8923170-S	136.7	157	152.5	FLJ20174	NM_017699.1	SID1			
GI_8923172-S	111.9	122.1	114.6	FLJ20184	NM_017700.1				
GI_8923176-S	550.9	653.9	807.1	FLJ20186	NM_017702.1				
GI_8923178-S	1029.3	878.7	842.6	FBXL12	NM_017703.1	FLJ20188			
GI_8923189-S	120.6	112.3	119.9	FLJ20200	NM_017708.1				
GI_8923197-S	128.5	148	153.7	PGPEP1	NM_017712.1	PGP;Pcp;PGPI;PGP-I;FLJ20208	pyrogluta		proteolysis
GI_8923199-S	104.9	105.6	102.1	FLJ20211	NM_017713.1				
GI_8923201-S	256.7	344.4	204.9	C20orf13	NM_017714.1	FLJ20212;dJ585I14.2	asparagin		glycoprote
GI_8923203-A	297.7	358.6	293.5	ZNF3	NM_017715.1	A8-			
GI_8923203-I	122.5	139.5	114.3	ZNF3	NM_017715.1	A8-			
GI_8923205-S	233.3	297.8	257.5	MS4A12	NM_017716.1	Ms4a10;FLJ20217	receptor	integral to	
GI_8923213-S	369.5	230.9	174.9	STAP2	NM_017720.1	BKS;STAP-2;FLJ20234			
GI_8923220-S	414.3	418.8	561.1	FLJ20245	NM_017723.1		nucleotide		
GI_8923223-A	423.7	421	347	LRRFIP2	NM_017724.1	HUFI-2;FLJ20248			
GI_8923223-I	671.3	741.9	550.6	LRRFIP2	NM_017724.1	HUFI-2;FLJ20248			
GI_8923229-S	151.6	165.3	187.9	FLJ20255	NM_017728.1		amino	membran	amino
GI_8923248-S	199.3	204.7	163.6	TOCA1	NM_017737.1	FLJ20275		intracellula	signal
GI_8923250-S	390.9	457.3	452.8	C9orf39	NM_017738.1	FLJ20276	two-	membran	signal
GI_8923252-S	3580.5	4310.4	4680.8	FLJ20277	NM_017739.1	MEB;GnTI.2;MGAT1.2;POMGNT1;UDP-	alpha-1,3-	Golgi	N-linked
GI_8923254-S	1877.9	1958.5	1372.9	ZDHHC7	NM_017740.1	ZNF370;FLJ10792;FLJ20279	zinc ion	integral to	regulation
GI_8923256-S	231.4	226.3	220.3	FLJ20280	NM_017741.1				
GI_8923268-S	2546.7	2091.3	1729.3	TEX10	NM_017746.1	FLJ20287;bA208F1.2			
GI_8923276-I	131.4	149.4	144.9	FLJ20297	NM_017751.1	FLJ20756			
GI_8923280-S	101	112.7	111.2	PRG-3	NM_017753.1	FLJ20300			
GI_8923286-S	79.3	89.6	92.6	FLJ20306	NM_017756.1				
GI_8923288-S	98.5	95.8	91.4	ZNF407	NM_017757.1	FLJ13839;FLJ20307;KIAA1703			
GI_8923296-S	103	128.1	122.7	FLJ20313	NM_017762.1				
GI_8923298-S	122.5	320.2	164.2	FLJ20315	NM_017763.1	RNF124	DNA	nucleus	regulation
GI_8923300-S	158.1	153.9	149.9	PQLC2	NM_017765.1	FLJ20320			
GI_8923304-I	100.9	92.5	90.9	SLC39A4	NM_017767.1	AEZ;ZIP4;FLJ20327	metal ion	membran	metal ion
GI_8923315-S	115	116.1	116.7	LAX	NM_017773.1	FLJ20340			
GI_8923317-S	274.6	324.5	290.3	CDKAL1	NM_017774.1	FLJ20342	molecular		
GI_8923321-S	289.6	234	197.9	FLJ20344	NM_017776.1		nucleic	intracellula	regulation
GI_8923323-S	500.3	534.2	505.2	FLJ20345	NM_017777.1				
GI_8923331-S	107.1	111	91.7	FLJ20359	NM_017781.1	CYP2W1	monooxyg		electron
GI_8923340-S	344.6	286.1	278.9	FLJ20366	NM_017786.1			kinesin	
GI_8923349-S	314.7	306.7	581.9	C14orf58	NM_017791.1	FLJ20371			
GI_8923351-S	2045.3	1804.5	1103.6	FLJ20373	NM_017792.1				
GI_8923354-S	140.3	149.7	147.5	RPP25	NM_017793.1	FLJ20374	DNA	nucleus	regulation
GI_8923377-S	601	678.5	662.4	FLJ20406	NM_017806.1	dJ583P15.4			
GI_8923379-S	512.5	452.6	356.5	OSGEP	NM_017807.1	GCPL1;OSGEP1;PRSMG1;FLJ20411	peptidase		proteolysis
GI_8923381-S	111.8	98.7	101.5	FLJ20413	NM_017808.1				
GI_8923389-S	3823.6	4111.7	4073.6	CHCHD3	NM_017812.1	FLJ20420			
GI_8923391-S	765	1545	1345.5	FLJ20421	NM_017813.1		inositol/ph		

GI_8923393-S	3666.2	3823.3	2985.3	FLJ20422	NM_017814.1				
GI_8923395-S	1938	1247.9	1288.5	C14orf94	NM_017815.1	FLJ20424			
GI_8923397-S	1703.5	1161.1	773.8	LYAR	NM_017816.1	FLJ20425			
GI_8923400-S	307.4	628	311.1	RAB20	NM_017817.1	FLJ20429	small		small
GI_8923404-S	546	582.7	500.3	RG9MTD1	NM_017819.1	FLJ20432			
GI_8923410-S	1646.3	1595.5	1255.1	FLJ20436	NM_017822.1	FLJ12670			
GI_8923416-S	2572.9	2085.4	1507.3	ADPRHL2	NM_017825.1	ARH3;FLJ20446	hydrolase		
GI_8923418-S	129.4	144.4	126.6	FLJ20449	NM_017826.1				
GI_8923426-S	435.3	387.1	352.6	OCIA	NM_017830.1	FLJ20455			
GI_8923434-S	184.3	244.6	230.4	FLJ20464	NM_017834.1				
GI_8923436-I	265.9	315.5	294.1	C21orf59	NM_017835.1	C21orf48;FLJ20467			
GI_8923445-S	348.2	439.9	369.5	FLJ20481	NM_017839.1		acyltransf		metabolis
GI_8923449-S	1200.1	974.4	1300.6	FLJ20487	NM_017841.1		peroxidas		electron
GI_8923451-S	282.6	251	230	FLJ20489	NM_017842.1				
GI_8923455-A	141.4	147.6	142.3	ANKMY1	NM_017844.1	ZMYND13;FLJ20499			
GI_8923455-I	173.5	180.9	177.4	ANKMY1	NM_017844.1	ZMYND13;FLJ20499			
GI_8923465-S	236.6	258	280.8	FLJ20507	NM_017849.1	FLJ22257			
GI_8923468-S	597.9	429.7	362	FLJ20508	NM_017850.1				
GI_8923472-S	128.8	151	139.4	NALP2	NM_017852.1	PYPAF2;FLJ20510			
GI_8923474-S	371	329.7	229.9	FLJ20511	NM_017853.1		electron	spliceoso	electron
GI_8923476-S	902	785.4	974.4	FLJ20512	NM_017854.1				
GI_8923480-S	144.4	145.4	121.8	FLJ20514	NM_017856.1				
GI_8923484-S	216.5	215.2	201.8	FLJ20516	NM_017858.1				
GI_8923486-S	591.2	758.9	1051.5	URKL1	NM_017859.1	FLJ20517	uridine		carbohydr
GI_8923495-S	581.7	599.3	452.4	FLJ20530	NM_017864.1				
GI_8923502-S	1032.9	810.5	822.8	FLJ20534	NM_017867.1				
GI_8923519-S	757.9	661.8	632.9	FLJ20551	NM_017875.1		binding	mitochond	transport
GI_8923525-S	113.7	147.1	120	HRASLS2	NM_017878.1	FLJ20556			
GI_8923527-S	845.8	727.3	670.9	FLJ20558	NM_017880.1		cysteine-		proteolysis
GI_8923529-S	397	480.8	379	C9orf95	NM_017881.1	FLJ20559	uridine		
GI_8923531-S	1116.4	1147.4	1303.9	CLN6	NM_017882.1	FLJ20561		integral to	
GI_8923535-S	7082.6	5171.6	6495.8	HCFC1R1	NM_017885.1	HPIP;FLJ20568			
GI_8923538-S	187.7	202.4	195.8	FLJ20574	NM_017886.1				
GI_8923540-S	1012.1	944.4	873	FLJ20580	NM_017887.1				
GI_8923558-S	385.9	394.6	336.6	FLJ20604	NM_017897.1		structural	ribosome	protein
GI_8923562-S	174	160.5	134.3	TSC	NM_017899.1	FLJ20607	calcium		
GI_8923564-S	1863.7	2052.4	1948.2	AKIP	NM_017900.1	AIP;FLJ20608			
GI_8923568-S	632	789.2	821	HIF1AN	NM_017902.1	FIH1;FLJ20615;FLJ22027;DKFZp762F1811			
GI_8923572-S	226.7	270.8	251.6	FLJ20619	NM_017904.1				
GI_8923576-S	1031	765.4	591.1	PAK1IP1	NM_017906.1	PIP1;hPIP1;FLJ20624;bA421M1.5			
GI_8923578-S	2564.8	3383.5	3589.1	FLJ20625	NM_017907.1				
GI_8923581-S	753.7	823.4	811.3	FLJ20626	NM_017908.1				
GI_8923583-S	399.8	356.7	268.7	C6orf96	NM_017909.1	FLJ20627;bA351K16.3			
GI_8923587-S	185.8	201.6	180.7	FLJ20635	NM_017911.1				

GI_8923591-S	600.5	807.5	645	HARC	NM_017913.1	FLJ20639			cytokinesi
GI_8923595-S	397.7	339.3	398.5	FLJ20641	NM_017915.1				
GI_8923597-S	7054	8312.6	7628.3	FLJ20643	NM_017916.1				
GI_8923603-S	132.3	146.7	142.9	STX17	NM_017919.1	FLJ20651		kinesin	transport
GI_8923608-S	581	757.9	806.3	NPL4	NM_017921.1	FLJ20657;KIAA1499			
GI_8923612-S	105	101.2	95.9	FLJ20668	NM_017923.1				
GI_8923622-S	105	111.8	115.8	FLJ20694	NM_017928.1				
GI_8923627-S	351.6	372.9	391.9	FLJ20699	NM_017931.1				
GI_8923629-S	646.2	894.3	726.7	FLJ20700	NM_017932.1				
GI_8923640-S	124.1	115.9	113.4	FLJ20712	NM_017937.1				
GI_8923658-S	290.6	386	338.5	FKBP14	NM_017946.1	FKBP22;FLJ20731	cyclophilin	endoplas	protein
GI_8923660-S	1626.2	1609.6	714.8	MOCOS	NM_017947.1	MOS;HMCS;FLJ20733			
GI_8923664-S	936.6	723	990.5	CUEDC1	NM_017949.1	FLJ20739			
GI_8923675-S	825.5	657.7	671.7	FLJ20772	NM_017956.1				
GI_8923677-S	259.3	302.4	293.6	EPN3	NM_017957.1	FLJ20778			
GI_8923679-S	311.2	338.1	371	PLEKHB2	NM_017958.1	EVT2;FLJ20783			
GI_8923681-S	189.8	214.9	199.3	FLJ20802	NM_017959.1				
GI_8923683-S	127.6	155.9	142.2	FLJ20808	NM_017960.1				
GI_8923687-S	93.6	97.5	91.1	FLJ20825	NM_017962.1				
GI_8923696-S	3271.6	2907.9	3057.4	FLJ20850	NM_017967.1				
GI_8923700-S	158.6	408.7	383.8	GPR48	NM_018490.1	LGR4	G-protein	integral to	G-protein
GI_8923704-S	108.5	123.1	107.3	GPRC5D	NM_018654.1		metabotro	membran	vision
GI_8923711-S	1484.7	1426	1483.7	ACTR10	NM_018477.1	HARP11	structural	actin	
GI_8923719-S	126	164.6	123.4	HCA127	NM_018684.1				
GI_8923721-S	2561.5	2406.6	2066.1	HCA66	NM_018428.1			intracellula	RNA
GI_8923736-S	617.3	630.9	782.9	NAGK	NM_017567.1	GNK;HSA242910	ATP		N-
GI_8923741-S	205	283	222	CHRNA9	NM_017581.1	NACHRA9;HSA243342	extracellul	integral to	ion
GI_8923753-S	258	326.8	272.8	HSA250839	NM_018401.1		protein		protein
GI_8923755-S	102.2	121.2	125.2	IL26	NM_018402.1	AK155;IL-26	cytokine	soluble	cell-cell
GI_8923762-S	108.3	129.5	107.2	CENTA2	NM_018404.1	HSA272195	GTPase	nucleus	biological_
GI_8923764-S	93.8	123.9	100.2	CACNA2D3	NM_018398.1	HSA272268		membran	
GI_8923766-S	422.8	293.8	184.6	HSA275986	NM_018403.1	SMIF;DCP1A			
GI_8923768-S	426.3	535.3	439.5	HDAC8	NM_018486.1	RPD3;HDACL1	histone	nuclear	chromatin
GI_8923770-S	747.6	835.6	711.2	HSA277841	NM_018553.1				
GI_8923788-S	235.6	280.9	244.1	HSRNAFEV	NM_017521.1	FEV;PET-1	transcripti	nucleus	transcripti
GI_8923792-S	102	108.1	91.8	PLXN3	NM_017514.1	HSSEXGENE			
GI_8923805-S	104.5	99.7	84.2	HT009	NM_018470.1				
GI_8923807-S	2235.1	2159	1881.9	LEREPO4	NM_018471.1	HT010	nucleic		
GI_8923809-S	1434.1	1538.9	1552.7	HT011	NM_018472.1				
GI_8923818-S	180.5	173.6	143.7	IMPACT	NM_018439.1		molecular	cellular_co	biological_
GI_8923829-S	356.8	454.1	382	LENEP	NM_018655.1	LEP503	DNA		developm
GI_8923837-S	105.9	112.5	105.2	LOC55580	NM_017571.1				
GI_8923845-S	126.5	138.4	123.3	TSNAXIP1	NM_018430.1	TXI1			
GI_8923850-A	100.4	95.6	102	ZNF302	NM_018443.1	ZNF327;ZNF135L;ZNF140L	DNA	nucleus	regulation

GI_8923850-I	165.8	193.9	146.2	ZNF302	NM_018443.1	ZNF327;ZNF135L;ZNF140L	DNA	nucleus	regulation
GI_8923854-A	1202.8	1564.3	1203.9	AD-017	NM_018446.1	FLJ14611			
GI_8923854-I	269.1	353.8	267.4	AD-017	NM_018446.1	FLJ14611			
GI_8923856-S	1285.7	1511.4	1457.5	LOC55831	NM_018447.1				
GI_8923863-S	773.2	834.9	694	ECHDC1	NM_018479.1	dJ351K20.2	catalytic		metabolis
GI_8923872-S	140.6	169.4	163	GPR77	NM_018485.1	C5L2	C5a	integral to	G-protein
GI_8923886-S	348.3	365.9	299.7	PBF	NM_018660.1	PRF1;HDBP2			
GI_8923891-S	594.3	682	819.1	PXMP2	NM_018663.1	PMP22		peroxisom	
GI_8923906-A	5820.3	5680.7	4882.3	ARL6IP4	NM_018694.1	SR-25;SRp25		nucleus	RNA
GI_8923906-I	98.1	113.2	109.2	ARL6IP4	NM_018694.1	SR-25;SRp25		nucleus	RNA
GI_8923908-S	1660.9	1424.2	897.4	ERBB2IP	NM_018695.1	ERBIN		basement	oncogene
GI_8923919-S	209.2	504.6	122.1	H2AFY2	NM_018649.1	MACROH2A2			
GI_8923929-S	809.2	868.4	705.8	C10orf70	NM_018464.1	MDS029			
GI_8923931-S	1072.6	1061.8	1157.9	C9orf46	NM_018465.1	AD025;MDS030;FLJ14688			
GI_8923935-S	751.3	847.7	706.8	MDS032	NM_018467.1				
GI_8923943-S	413.8	394.2	397.9	NRF	NM_017544.1	ITBA4	double-	nucleus	regulation
GI_8923945-S	89.5	97.6	90.9	SMPD3	NM_018667.1	NSMASE2	sphingom	membran	sphingom
GI_8923955-S	2536.7	2712.5	2259.5	PC326	NM_018442.1				
GI_8923959-S	107.5	130.9	117.2	PPM2C	NM_018444.1	PDH;PDP;PDP1	protein	mitochond	protein
GI_8923971-S	93.8	84.3	88.6	PRO0386	NM_018562.1				
GI_8923994-S	205.8	233.8	211.5	PRO0943	NM_018568.1				
GI_8924004-S	154.9	161	157.1	PRO1051	NM_018572.1				
GI_8924025-S	96.6	100.4	94.4	PRO1257	NM_018578.1				
GI_8924053-S	110	101.5	108.7	PRO1496	NM_018603.1				
GI_8924082-S	2121.3	1949.2	1587.3	PRO1843	NM_018507.1				
GI_8924091-S	92.9	93.5	96.9	PRO1866	NM_018510.1				
GI_8924095-S	119.3	113	110.3	PRO1905	NM_018608.1				
GI_8924099-S	93.8	93.5	91.1	PRO1942	NM_018610.1				
GI_8924109-S	101.1	103.9	101	PRO2015	NM_018512.1				
GI_8924175-S	178	271.7	173.3	GSDML	NM_018530.1	PRO2521			
GI_8924224-S	107	115.8	109.6	PRO2964	NM_018547.1				
GI_8924241-S	192.5	229.5	170.3	SAGE	NM_018666.1		tumor		
GI_8924245-S	455.5	217.4	153.8	SNFT	NM_018664.1	JUNDM1	transcripti	nucleus	response
GI_8924257-S	197.8	236.6	210.7	GABRQ	NM_018558.1	THETA	neurotran	integral to	signal
GI_8924263-S	114.9	117.7	118.3	ZNF167	NM_018651.1	ZFP;FLJ12738			
GI_9055269-S	106.1	107.6	106.8	LRP1B	NM_018557.1	LRPDIT;LRP-DIT	internaliza	membran	protein
GI_9055283-S	122.5	146.5	132.3	MYO5C	NM_018728.1		actin	kinesin	
GI_9256536-S	219.8	312.9	291.1	MNAB	NM_018835.1	FLJ20301;FLJ20713	nucleic		
GI_9257187-A	115.2	115.2	127.4	ADD2	NM_017487.1	ADDB	actin	membran	
GI_9257189-I	156.1	177.3	181.2	ADD2	NM_017488.1	ADDB	actin	membran	
GI_9257194-S	150.7	186.6	168.4	BAIAP1	NM_004742.1	AIP3;BAP1;WWP3;MAGI-	protein C-	intercellula	cell
GI_9257196-I	260.5	339.6	315.6	BAIAP2	NM_017450.1	BAP2;IRSP53	protein C-	cytoplasm	insulin
GI_9257198-I	181.6	217.6	210.8	BAIAP2	NM_017451.1	BAP2;IRSP53	protein C-	cytoplasm	insulin
GI_9257200-S	237.2	283.8	241.5	CALCYON	NM_015722.2			integral to	dopamine

GI_9257201-I	207.4	160.1	145.9	CLTCL1	NM_007098.1	CLTD;CLH22;CLTCL	signal	coated pit	receptor
GI_9257203-S	929.5	1033.3	883	MAEA	NM_005882.2	EMP	cell	membran	cell
GI_9257206-I	403.5	469.6	447.6	FOLR1	NM_016725.1	FBP;FOLR;MOv18;FR-alpha	folic acid	peripheral	receptor
GI_9257214-I	117.9	106	128.7	FOLR1	NM_016730.1	FBP;FOLR;MOv18;FR-alpha	folic acid	peripheral	receptor
GI_9257218-S	180.7	211.7	178.7	FOLR2	NM_000803.2	FR-P3;FR-beta;FBP/PL-1;beta-hFR	folic acid	membran	folate
GI_9257219-S	120.8	135.2	120.1	FOLR3	NM_000804.2	FR-G;FR-gamma;gamma-hFR	folic acid	membran	folate
GI_9257221-S	772.9	636.5	724	FOXO1A	NM_002015.2	FKH1;FKHR;FOXO1	transcripti	nucleus	anti-
GI_9257223-S	132.9	146.7	143.5	INHA	NM_002191.2		hormone	extracellul	cell
GI_9257224-S	125.4	152.6	123.9	INHBB	NM_002193.1		hormone	extracellul	cell-cell
GI_9257226-S	129.5	139.2	115.4	KLKB1	NM_000892.2	KLK3	plasma	extracellul	proteolysis
GI_9257227-A	148.1	160.6	151.6	LDHC	NM_017448.1	LDH3;LDHX	L-lactate		glycolysis
GI_9257229-I	109.7	124.4	103.2	LDHC	NM_002301.2	LDH3;LDHX	L-lactate		glycolysis
GI_9257230-S	140.1	133.6	108.6	OCLN	NM_002538.2		cell	tight	protein
GI_9257231-S	94.2	91.1	99.2	ORM1	NM_000607.1	ORM;AGP1;AGP-A	acute-	extracellul	acute-
GI_9257235-S	198.2	270.2	229.2	QPCT	NM_012413.2	QC;GCT	acyltransf		protein
GI_9257237-S	238.4	221.8	126	RABL4	NM_006860.2	RAYL	small		small
GI_9257238-S	156.2	204.2	154.7	SC4MOL	NM_006745.2	DESP4;ERG25	C-4	integral to	steroid
GI_9257239-A	4862.2	6230.4	4850.7	SDFR1	NM_017455.1	GP55;GP65			
GI_9257241-S	1222.4	1478.1	1232.9	SDHB	NM_003000.1	IP;SDH;SDH1;SDHIP	electron	mitochond	aerobic
GI_9257243-S	2647.9	3218.9	3074	SDHC	NM_003001.2	PGL3;SDH3	cytochrom	mitochond	tricarboxyli
GI_9257244-A	386.4	407.8	391.7	TERF1	NM_003218.2	TRF;PIN2;TRF1;TRBF1;hTRF1-AS	protein	telomere	telomere
GI_9257245-I	165.9	199.3	158.1	TERF1	NM_017489.1	TRF;PIN2;TRF1;TRBF1;hTRF1-AS	protein	telomere	telomere
GI_9257247-S	1056.3	1276.6	1029.6	TIMP2	NM_003255.2		metalloen		
GI_9257255-S	145.5	185.3	137.2	VWF	NM_000552.2	VWD;F8VWF	binding	secretory	hemostasi
GI_9257259-S	126	128.5	124	XDH	NM_000379.2	XO;XOR	xanthine		purine
GI_9506400-S	1141.4	1556.5	1408.7	ARHGEF3	NM_019555.1	GEF3;STA3;XPLN;DKFZP434F2429	Rho		Rho
GI_9506430-S	90.4	91.3	93.5	C15orf2	NM_018958.1		molecular	cellular_co	spermatog
GI_9506436-S	417.1	374.6	385.8	C21orf45	NM_018944.1	B28;FASP1;C21orf46	molecular	cellular_co	biological_
GI_9506542-S	612.4	835.9	815.4	MOSPD1	NM_019556.1	DJ473B4	structural		cell
GI_9506556-S	100.9	97	100.5	DSCR6	NM_018962.1		molecular	cellular_co	biological_
GI_9506596-S	123.7	149	144.3	FGF21	NM_019113.1		fibroblast	soluble	signal
GI_9506602-S	103.9	99.7	108.1	SPATA6	NM_019073.1	SRF1;SRF-1;FLJ10007			
GI_9506604-S	202.4	307.2	369.5	FLJ10156	NM_019013.1	FLJ10491			
GI_9506614-S	960	775.2	812.6	FLJ10640	NM_019023.1	KIAA1933	S-		
GI_9506622-S	322	333.7	422.5	HIP14L	NM_019028.1	HIP3RP;ZDHHC13;FLJ10852;FLJ10941			
GI_9506640-S	141.7	138.7	123.4	FLJ11127	NM_019018.1				
GI_9506642-S	128.4	127.7	109.4	FLJ11235	NM_019033.1		DNA	nucleus	regulation
GI_9506646-S	320.6	512.9	378.1	FLJ20010	NM_019021.1				
GI_9506650-S	245.4	268.5	245	KCTD5	NM_018992.1	FLJ20040	voltage-	membran	potassium
GI_9506652-S	118.7	142.5	117	ARFRP2	NM_019087.1	FLJ20051			
GI_9506654-S	209.6	186.8	183.5	FLJ20054	NM_019049.1				
GI_9506662-S	84.6	94.9	84.7	FLJ20225	NM_019062.1		electron		electron
GI_9506668-S	76.3	86.7	98.4	KRT24	NM_019016.1	FLJ20261		kinesin	
GI_9506670-S	119.6	157	165.7	FLJ20273	NM_019027.1				

GI_9506672-S	622	474	535.5	FLJ20323	NM_019005.1				
GI_9506674-S	313.9	256.8	317.5	GFOD1	NM_018988.1	FLJ20330	oxidoredu		electron
GI_9506686-S	2518.3	2498.1	971.2	DDIT4	NM_019058.1	Dig2;REDD1;REDD-1;RTP801;FLJ20500			
GI_9506688-S	1958.8	2954.3	2595	RRP41	NM_019037.1	p12A;FLJ20591	exonuclea	nucleolus	rRNA
GI_9506696-S	1209.8	1057.5	991.3	NS3TP1	NM_019048.1	FLJ20752	protein		protein
GI_9506716-S	100	112.3	114.9	GDAP1	NM_018972.1	CMT2G;CMT2H;CMT2K;CMT4A			signal
GI_9506744-S	168.9	224.7	207	GPR14	NM_018949.1	UTR;UTR2	G-protein	membran	circulation
GI_9506746-S	248.2	287.8	277	GPR27	NM_018971.1	SREB1	G-protein	integral to	signal
GI_9506770-S	89.2	93.4	89.6	HCG4	NM_018985.1	HCGIV.9			
GI_9506784-S	139.5	129.6	126	HMX1	NM_018942.1	H6	transcripti		
GI_9506786-S	114.1	119.3	97.2	NLGN3	NM_018977.1	HNL3;KIAA1480			
GI_9506798-S	120.7	124.6	126.3	OR7A5	NM_017506.1	HTPCR2	G-protein		physiologi
GI_9506850-S	97.4	87.8	86.8	SPIN2	NM_019003.1		molecular	cellular_co	gametoge
GI_9506858-S	4031.7	3958	2700.3	TOMM7	NM_019059.1	TOM7	protein	mitochond	intracellula
GI_9506862-S	258	235.4	221.3	LOC55954	NM_019103.1		nucleic	nucleus	
GI_9506922-S	104.6	110.6	101.1	NICE-1	NM_019060.1				
GI_9506930-S	3636.8	3317.5	2941	DDX56	NM_019082.1	NOH61	ATP	nucleolus	ribosome
GI_9507032-S	3059.1	3985.9	3815.5	TERF2IP	NM_018975.1	RAP1	telomeric	nuclear	telomere
GI_9507162-S	92.7	88.2	94.1	SNTG1	NM_018967.1	SYN4;G1SYN	actin	peripheral	cell
GI_9507164-S	147.6	162.4	156	SNTG2	NM_018968.1	SYN5;G2SYN	actin	peripheral	central
GI_9507172-S	117.2	120.6	115.8	TAS2R5	NM_018980.1	T2R5	taste	integral to	taste [goid
GI_9507202-S	280.1	335.3	244.6	TREM2	NM_018965.1	Trem2a	receptor		humoral
GI_9507214-S	116.3	121.8	122.5	TUBA8	NM_018943.1	TUBAL2	GTP	cytoskelet	microtubul
GI_9507220-S	222.6	247.9	217	UBASH3A	NM_018961.1		catalytic	nucleus	metabolis
GI_9507222-S	439.6	509.9	432.5	UBPH	NM_019116.1		DNA	nucleus	regulation
GI_9507236-A	125.7	141	128	DDX4	NM_019039.1	VASA	nucleic		developm
GI_9558724-S	1036.8	943.8	970.4	CPSF1	NM_013291.1	CPSF160;HSU37012	mRNA 3'	nucleus	mRNA
GI_9558730-S	91.8	109.1	97.7	HSU24186	NM_013347.1		single-	DNA	DNA
GI_9558738-S	709.8	578.2	814.8	HSU79266	NM_013299.1		DNA	nucleus	regulation
GI_9558740-S	2741.5	2369.5	1733.2	HSU79274	NM_013300.1				
GI_9558742-S	1355.3	1690.8	2220.4	HSU79303	NM_013301.1				
GI_9558744-I	113.4	132.4	101.4	HSU84971	NM_013303.1	VG5Q;FLJ10283;HUS84971			
GI_9558754-S	800.7	805.6	744.4	DNAJB9	NM_012328.1	MDG1;ERdj4;DKFZP564F1862	chaperone	nucleus	protein
GI_9558760-S	351.6	438.2	207.5	GAGEB1	NM_003785.2	PAGE1;GAGE-9;PAGE-1	tumor		cellular
GI_9558763-I	103.7	114.9	107.2	STAU	NM_017453.1		double-	microtubul	
GI_9558765-A	3529.1	3998.1	4583.6	STAU	NM_017454.1		double-	microtubul	
GI_9624968-S	107	116.9	121	BTNL2	NM_019602.1	BTL-II;HSBLMHC1			
GI_9624970-S	266.6	295.3	258.9	C21orf62	NM_019596.1	B37	molecular	cellular_co	biological_
GI_9624976-S	130.3	141.6	110	CRTAM	NM_019604.1				
GI_9624987-S	126.1	135	123	FLJ11267	NM_019607.1				
GI_9625042-S	158.8	166.5	173.7	TAS2R1	NM_019599.1	T2R1;TRB7	taste	integral to	chemosen
GI_9625245-S	106.5	265.8	316.3	ANXA10	NM_007193.2	ANX14	calcium		
GI_9665231-S	137.6	166	119.2	HLA-F	NM_018950.1	HLAF;HLA-5.4;HLA-CDA12	class I	integral to	antigen
GI_9665246-S	174.1	199.3	148.8	SERPINA3	NM_001085.2	ACT;AACT	serine		acute-

GI_9665251-S	100.2	106.6	88.6	AMBN	NM_016519.2		structural	extracellul	bone
GI_9665252-A	3041.4	6014	2618.9	EFEMP1	NM_018894.1	DHRD;DRAD;FBNL;MLVT;S1-5;FBLN3	calcium	extracellul	vision
GI_9665252-I	98.1	90.8	87.2	EFEMP1	NM_018894.1	DHRD;DRAD;FBNL;MLVT;S1-5;FBLN3	calcium	extracellul	vision
GI_9665258-I	109.9	122.3	99.4	MFAP2	NM_017459.1	MAGP;MAGP1	extracellul	extracellul	
GI_9665260-A	134.2	138.5	114.5	MFAP2	NM_002403.2	MAGP;MAGP1	extracellul	extracellul	
GI_9665261-I	490.5	1359.6	394.4	EFEMP1	NM_004105.2	DHRD;DRAD;FBNL;MLVT;S1-5;FBLN3	calcium	extracellul	vision
GI_9789896-S	115.1	129.7	124.1	LTB4R2	NM_019839.1	BLT2;BLTR2;JULF2	leukotrien	integral to	negative
GI_9789946-S	85.4	94.2	86.5	FGF20	NM_019851.1		fibroblast	soluble	signal
GI_9790006-S	101.9	89.2	105.6	ANKRD7	NM_019644.1	TSA806			male
GI_9790192-S	128.1	166.9	127.9	REPRIMO	NM_019845.1			cytoplasm	cell cycle
GI_9790232-S	339.7	267.3	223.7	SLCO1B3	NM_019844.1	OATP8;OATP1B3;SLC21A8	organic	integral to	organic
GI_9790234-S	112.3	114	105.2	SLC7A10	NM_019849.1	asc-1;HASC-1;FLJ20839	L-serine	membran	amino
GI_9790902-S	5512.2	2247.1	2935.4	PPP1R15A	NM_014330.2	GADD34			cell cycle
GI_9790904-S	3782.3	2367.7	1059.2	GADD45A	NM_001924.2	DDIT1;GADD45	structural	ribosome	cell cycle
GI_9790905-S	93	84.3	84.5	GADD45G	NM_006705.2	CR6;DDIT2;GRP17;GADD45gamma;GADD4	structural	ribosome	activation
GI_9845266-S	148.2	157.9	134.4	ASAH2	NM_019893.1	HNAC1		mitochond	ceramide
GI_9845286-S	106.4	120.1	97.4	PAX1	NM_006192.1	HUP48	transcripti		skeletal
GI_9845292-S	208.7	259.6	219.9	REC8L1	NM_005132.1	REC8;Rec8p		nucleus	sister
GI_9845486-A	2534	1858.8	2106.8	MARK2	NM_017490.1	EMK1	protein	microtubul	protein
GI_9845486-I	162.7	183.7	161.2	MARK2	NM_017490.1	EMK1	protein	microtubul	protein
GI_9845488-A	2043.5	1546.7	1661.2	MARK2	NM_004954.2	EMK1	protein	microtubul	protein
GI_9845492-I	127	140.5	128.5	GGT1	NM_013430.1	GGT;GTG;CD224;D22S672;D22S732	gamma-	membran	amino
GI_9845494-S	799.9	866.3	257.1	LAMA4	NM_002290.2	LAMA3	extracellul	basal	
GI_9845495-S	501.7	537.8	418.6	LAMB2	NM_002292.2	LAMS	structural	basal	synaptic
GI_9845497-S	6526.9	7698.5	4964.6	LAMC1	NM_002293.2	LAMB2	structural	basement	endoderm
GI_9845499-A	441.9	510	443.9	LAMC2	NM_018891.1	EBR2;BM600;EBR2A;LAMB2T;LAMNB2;KAL	heparin	laminin-5	epidermal
GI_9845499-I	129.5	149.1	140.8	LAMC2	NM_018891.1	EBR2;BM600;EBR2A;LAMB2T;LAMNB2;KAL	heparin	laminin-5	epidermal
GI_9845501-S	42004.8	39694	31564	LAMR1	NM_002295.2	LRP;p40;67LR;RPSA;37LRP;LAMBR	laminin	laminin	regulation
GI_9845506-S	1707.4	2387.3	2191.3	OAZ2	NM_002537.1		ornithine		polyamine
GI_9845514-I	352.3	438.2	387.6	S100A4	NM_002961.2	42A;18A2;CAPL;MTS1;P9KA;PEL98	calcium		invasive
GI_9845515-A	291	269.3	221.1	S100A4	NM_019554.1	42A;18A2;CAPL;MTS1;P9KA;PEL98	calcium		invasive
GI_9845517-S	16154.8	14071	17943	S100A6	NM_014624.2	2A9;PRA;5B10;CABP;CACY	calcium	nuclear	cell cycle
GI_9845518-S	98.7	91.5	94.4	S100A7	NM_002963.2	PSOR1	calcium		epidermal
GI_9845520-S	113.8	123.6	108.2	S100A9	NM_002965.2	MIF;NIF;P14;CAGB;CFAG;CGLB;L1AG;LIAG	calcium	extracellul	cell-cell
GI_9845521-S	3601.1	4561.8	4485.5	UROD	NM_000374.2	PCT	uroporphy		heme
GI_9845523-S	136.6	164.7	164.5	EGR2	NM_000399.2	CMT1D;CMT4E;KROX20	DNA	nucleus	brain
GI_9910116-S	123.2	150.5	176.3	ABCC8	NM_000352.2	HI;SUR;MRP8;PHHI;SUR1;ABC36;HRINS	sulfonylur	integral to	potassium
GI_9910143-S	94.1	95.9	90	C1GALT1	NM_020156.1		transferas		
GI_9910155-S	81.2	92.2	96.8	ZA20D1	NM_020205.1	CEZANNE			
GI_9910179-S	341.8	271.2	232.6	ACN9	NM_020186.1	DC11			
GI_9910181-S	1749.2	2427.8	2508.5	DC12	NM_020187.1				
GI_9910195-S	91.9	95.1	84.8	DKFZp547H0	NM_020161.1		folic acid	membran	transport
GI_9910199-S	218.4	256.3	240.6	DKFZp547I01	NM_020217.1				
GI_9910203-S	293.6	322	345	DKFZp547O1	NM_020224.1				

GI_9910205-S	1379.3	1980.9	1284.8	C14orf132	NM_020215.1	DKFZp761F2014			
GI_9910225-S	369.1	448.3	438.9	FN5	NM_020179.1		molecular	cellular_co	biological_
GI_9910241-S	456.1	477.6	365.4	GK001	NM_020198.1				
GI_9910257-S	573.3	723.8	682.1	C14orf124	NM_020195.1	HCDI			
GI_9910259-S	1112.1	946.1	990.2	XAB2	NM_020196.1	HCNP;HCRN	protein	nucleus	RNA
GI_9910265-S	199.4	233.4	275.5	KNSL7	NM_020242.1	HKLP2	adenosine	plus-end	mitosis
GI_9910269-S	454.3	550.3	447.4	HNOEL-iso	NM_020190.1				
GI_9910273-S	381.3	459.3	402.8	SMYD2	NM_020197.1	HSKM-B;ZMYND14			
GI_9910277-S	2248.9	3015.7	3209.9	HTGN29	NM_020199.1	KCT2			
GI_9910279-S	484.3	572.2	485.7	UGCGL1	NM_020120.1	HUGT1	UDP-	soluble	protein
GI_9910341-S	165.5	207.2	166.9	SLAMF8	NM_020125.1	BLAME;SBBI42			
GI_9910345-S	1521.1	1885.4	1541.3	LOC56851	NM_020154.1	HT022;ORF1-FL1	purine	cytoplasm	biological_
GI_9910361-S	170.9	185.1	147.4	LOC56920	NM_020163.1	FLJ00014			developm
GI_9910373-I	92.7	93.5	93.9	LOC56965	NM_020213.1				
GI_9910375-S	324	425.6	401.9	INCENP	NM_020238.1			kinesin	cell cycle
GI_9910377-S	147.4	142.5	144.1	SPEC2	NM_020240.1		protein	plasma	signal
GI_9910383-S	1219.7	856.5	1065.5	CHPT1	NM_020244.1	CPT1	diacylglyc	membran	lipid
GI_9910389-S	1324.6	909.8	860.8	CTNNBIP1	NM_020248.1	ICAT	protein	nucleus	regulation
GI_9910391-S	174.3	209.7	184.2	AGPAT4	NM_020133.1	dJ473J16.2;LPAAT-delta	acyltransf	integral to	metabolis
GI_9910417-A	112	126.4	133.4	MDM1	NM_020128.1				
GI_9910417-I	144.7	139.4	142.6	MDM1	NM_020128.1				
GI_9910429-S	84.8	93.4	85.2	MEPE	NM_020203.1	OF45	extracellul	extracellul	skeletal
GI_9910447-S	134.4	154.3	168.9	C8orf17	NM_020237.1	MOST-1			
GI_9910449-S	157.2	176.6	160.1	MOST2	NM_020250.1				
GI_9910495-S	112.8	119.9	107.1	C14orf162	NM_020181.1	PLPL			
GI_9910507-S	112	106.9	94.4	PRDM8	NM_020226.1	PFM5			
GI_9910509-S	113.7	126	117.9	PRDM9	NM_020227.1	PFM6	DNA	nucleus	regulation
GI_9910525-S	112.7	128.5	115.7	OPN1LW	NM_020061.1	CBP;RCP;CBBM	red-	integral to	vision
GI_9910553-S	227.4	259.4	220.4	SLC2A9	NM_020041.1	GLUTX;Glut9			
GI_9910595-S	854.8	687.5	422.1	TUFT1	NM_020127.1		structural	kinesin	bone
GI_9938031-S	210	270.5	203.7	SLC2A6	NM_017585.2	GLUT6;GLUT9;HSA011372			
GI_9943840-S	1902.4	2295.5	928.9	TAF12	NM_005644.2	TAF2J;TAFII20	protein	transcripti	transcripti
GI_9943841-S	219.9	241.2	201.4	PDCL	NM_005388.2	PhLP;DKFZp564M1863	receptor	cellular_co	regulation
GI_9945309-S	105.9	107.9	101.8	PRH1	NM_006250.1	Pa		extracellul	
GI_9945313-S	8717.8	9330.6	5958.1	EIF4A2	NM_001967.2	DDX2B;EIF4A;EIF4F;BM-010	helicase	eukaryotic	regulation
GI_9945317-S	546.5	604.7	789	MNT	NM_020310.1	ROX;MAD6;MXD6	transcripti	nucleus	negative
GI_9945319-S	1108.6	1204.7	957	CCNL1	NM_020307.1	BM-001;ania-6a			
GI_9945321-S	210.7	249.8	222.5	SLC17A7	NM_020309.1	BNPI;VGLUT1	sodium-	integral to	phosphate
GI_9945331-S	504.6	337	337.7	GADD45B	NM_015675.1	MYD118;GADD45BETA;DKFZP566B133			activation
GI_9945333-S	1830	1673.5	1712.5	GALE	NM_000403.2		UDP-		nucleotide-
GI_9945384-S	252.9	327.9	319.9	GALNS	NM_000512.2	GAS;MPS4A;GALNAC6S	N-	lysosome	metabolis
GI_9945385-S	3299	5774.1	5051.5	GALNT2	NM_004481.2	GalNAc-T2	polypeptid		O-linked
GI_9945386-S	126.9	148.5	140.8	GALNT3	NM_004482.2	GalNAc-T3	polypeptid	integral to	carbohydr
GI_9945387-S	591.4	778.5	501.1	GP1BB	NM_000407.3	CD42c	thrombin	integral to	blood

GI_9945438-S	297.8	354.3	311.5	PNUTL1	NM_002688.2	H5;SEPT5;CDCREL;CDCREL1;CDCREL-	GTPase		cytokinesi
GI_9951912-I	98.6	133.1	107.9	GRCA	NM_019858.1				
GI_9951914-S	4577.4	4727.1	7207.1	AHCY	NM_000687.1	SAHH	adenosylh	cytoplasm	one-
GI_9951918-S	1334.7	764.8	688.5	KATNA1	NM_007044.2		nucleotide	cytoskelet	mitosis
GI_9951919-S	91.8	92.9	88.6	PAX5	NM_016734.1	BSAP	transcripti	nucleus	humoral
GI_9951921-S	3630.9	4000	4995.8	CIB1	NM_006384.2	CIB;KIP;SIP2-28;CALMYRIN	protein		double-
GI_9951922-S	239.3	330.3	271.2	CA11	NM_001217.2	CARP2;CA-RP XI	carbonate		one-
GI_9951924-S	1156.2	1823.4	574.2	CA12	NM_001218.2	FLJ20151;HsT18816	carbonate	integral to	one-
GI_9951925-S	196	232.9	192	CA4	NM_000717.2	CAIV	carbonate	membran	one-
GI_9955947-S	809.6	1048.1	577.8	CA9	NM_001216.1	MN	carbonate	nucleus	one-
GI_9955953-A	340.3	391.4	290.8	ABCC1	NM_019899.1	MRP;ABCC;GS-X;MRP1;ABC29	ATP	membran	drug
GI_9955962-S	216.8	235.1	223.9	ABCB6	NM_005689.1	umat;ABC14;MTABC3;EST45597	ATP-		oncogene
GI_9955964-S	124.8	129.4	150.2	ABCB8	NM_007188.2	MABC1;M-ABC1;EST328128	ATP	mitochond	small
GI_9955969-A	470	714.2	400.3	ABCC3	NM_003786.2	MLP2;MRP3;ABC31;CMOAT2;MOAT-	organic	membran	small
GI_9955973-I	164.1	194.9	153.4	ABCC3	NM_020038.1	MLP2;MRP3;ABC31;CMOAT2;MOAT-	organic	membran	small
GI_9961243-S	403.5	500	500.3	ABCB10	NM_012089.1	M-ABC2;MTABC2;EST20237	nucleotide	mitochond	transport
GI_9961245-I	306.3	323.7	328.1	TAP2	NM_000544.2	APT2;PSF2;ABC18;ABCB3;RING11;D6S217	peptide	membran	peptide
GI_9961247-A	98	112.4	113.1	TAP2	NM_018833.1	APT2;PSF2;ABC18;ABCB3;RING11;D6S217	peptide	membran	peptide
GI_9961247-I	117.3	127.8	114.5	TAP2	NM_018833.1	APT2;PSF2;ABC18;ABCB3;RING11;D6S217	peptide	membran	peptide
GI_9961251-A	159.3	145.4	109.5	ABCB4	NM_018850.1	MDR3;PGY3;ABC21;MDR2/3;PFIC-3	ATP-	membran	drug
GI_9961350-S	142.6	156	144.2	F10	NM_000504.2	FX;FXA	blood	extracellul	blood
GI_9961351-I	96.5	104.3	99.9	F11	NM_000128.2	FXI	molecular	membran	blood
GI_9961352-A	121.9	117.1	115.5	F11	NM_019559.1	FXI	molecular	membran	blood
GI_9961354-S	481.3	526.1	356.2	F12	NM_000505.2	HAF	serine-	extracellul	blood
GI_9961355-S	124	124.7	124.9	F13A1	NM_000129.2	F13A	blood	extracellul	blood
GI_9961356-S	131.9	155.8	130.9	F13B	NM_001994.1	FXIIIB	blood		blood
GI_9966760-S	125.5	116.7	121.2	CHM	NM_000390.1	TCD;GGTA;REP-1;DXS540	RAB-	Rab-	C-terminal
GI_9966762-S	345.2	405	340.9	ARIH1	NM_005744.2	ARI;HARI;HHARI;UBCH7BP	enzyme	kinesin	ubiquitin-
GI_9966771-S	110.9	118.3	115.8	ITGB6	NM_000888.3		cell	integrin	cell
GI_9966778-S	446.5	524	361.7	EIF2B3	NM_020365.1	EIF-2B;EIF2Bgamma	translation	cytoplasm	response
GI_9966786-S	126.8	155.1	139.7	SLC24A2	NM_020344.1	NCKX2	symporter	integral to	sodium
GI_9966788-S	158.7	177.1	148.9	CNNM1	NM_020348.1	ACDP1			
GI_9966790-S	142.1	166.3	163	FSCN3	NM_020369.1		actin	cytoskelet	cell shape
GI_9966792-S	937.8	1187.4	642.7	LZTFL1	NM_020347.1				
GI_9966794-S	89.6	90.6	84.2	PLSCR2	NM_020359.1		calcium	integral to	phospholi
GI_9966798-S	675.3	771.5	768.1	SAS10	NM_020368.1				
GI_9966810-S	102.2	98	98	SLC17A6	NM_020346.1	DNPI;VGLUT2	transporte	integral to	transport
GI_9966818-S	478.7	324.3	435.4	PLSCR4	NM_020353.1		calcium	integral to	blood
GI_9966820-S	110.7	127.3	144.3	ENTPD7	NM_020354.1	LALP1;FLJ30978	hydrolase		
GI_9966824-S	98.3	94.9	81.3	C20orf32	NM_020356.1	HEFL			
GI_9966826-S	2715	2668.2	2376.9	PCNP	NM_020357.1			nucleus	
GI_9966838-S	169.2	187	168.7	GPR84	NM_020370.1	EX33;GPCR4	receptor	integral to	G-protein
GI_9966840-S	615.4	995.4	962.3	AVEN	NM_020371.1	PDCD12	apoptosis	intracellula	apoptosis
GI_9966844-S	135.4	137.8	126.9	TMEM16B	NM_020373.1	C12orf3			

GI_9966848-S	338.2	427.4	454.6	C12orf5	NM_020375.1		catalytic		metabolis
GI_9966856-S	794.5	603.1	504.2	XPMC2H	NM_020385.1	XPMC2	exonuclea	nucleus	regulation
GI_9966860-S	86.7	100	93.2	RAB25	NM_020387.1	CATX-8	GTP		small
GI_9966864-S	100.1	91.8	97.4	TRPC7	NM_020389.1	TRP7	calcium	integral to	cation
GI_9966868-S	102.8	107.7	100.3	PGLYRP4	NM_020393.1	PGRPIB;SBBI67;PGRP-Ibeta;PGLYRPIbeta	protein	membran	metabolis
GI_9966874-A	144.6	225.1	245.6	CAMK1D	NM_020397.1	CKLiK	ATP		protein
GI_9966874-I	117.3	131.3	118.4	CAMK1D	NM_020397.1	CKLiK	ATP		protein
GI_9966876-S	198.1	211.7	225.1	GOPC	NM_020399.1	CAL;FIG;PIST;GOPC1	protein		intracellula
GI_9966880-S	1411.1	1254	1180.2	NUP107	NM_020401.1	NUP84	nucleocyto	nucleus	transport
GI_9966888-S	114.5	132.8	127.4	PRV1	NM_020406.1	NB1;CD177;HNA2A	receptor		
GI_9966890-S	113.8	142.3	108.4	RHBG	NM_020407.1		ammoniu	membran	transport
GI_9966896-S	1121.9	937.9	830.9	ATP13A	NM_020410.1	CGI-152;FLJ31858;KIAA1825			
GI_9966898-I	102.7	111.8	101.8	GAGED2	NM_020411.1	XAGE1;XAGE-1			
GI_9966902-S	101.6	113.8	98.8	MAN1C1	NM_020379.1	HMIC	mannosyl-	Golgi	N-linked
GI_9966904-S	82.4	91.3	87.3	LOC57151	NM_020426.1		lysozyme	extracellul	cell wall
GI_9966912-S	146.4	154.1	160.5	ARP3BETA	NM_020445.1	ARP11	actin	cytoskelet	cell shape
GI_9994164-S	96	103.1	101.1	ABO	NM_020469.1				
GI_9994168-S	701.9	870.4	905.1	YIF1	NM_020470.1	54TM;YIF1P			
GI_9994186-S	1049	700.4	729.8	PDGFC	NM_016205.1	SCDGF			
GI_9994198-S	281.1	301.4	266.1	BCAP29	NM_018844.1	BAP29	protein	endoplas	intracellula
GI_9998947-A	111.6	135.9	117.1	ACCN3	NM_020322.1	ASIC3;TNaC1;SLNAC1	sodium	integral to	sensory
lysA	113.8	122.6	112.9						
pheA	90.3	97.5	95.6						
thrB	89.8	96.8	91.8						
trpF	102	113.8	102.4						