Table 1. List of genes printed in the HC5 microarray employed in the screening phase of the second study in this research

CloneID	Plate	Position	Well	Length	GeneSymbol	GeneID	Accession	Description	Vector
692672	HsxXG013989	2	B01		STK32A	202374	null	serine/threonine kinase 32A	pANT7_cGST
692675	HsxXG013989	3	C01		RPS10-NUDT3	100529239	null	RPS10-NUDT3 readthrough	pANT7_cGST
692678	HsxXG013989	4	D01		SPATA6L	55064	null	spermatogenesis associated 6-like	pANT7_cGST
692679	HsxXG013989	5	E01		ATP1A4	480	null	ATPase, Na+/K+ transporting, alpha 4 polypeptide	pANT7_cGST
692689	HsxXG013989	6	F01		ZNF816-ZNF321P	100529240	null	ZNF816-ZNF321P readthrough	pANT7_cGST
692691	HsxXG013989	7	G01		NKAIN1	79570	null	Na+/K+ transporting ATPase interacting 1	pANT7_cGST
693155	HsxXG013989	8	H01		TNFSF12-TNFSF13	407977	NM_172089	TNFSF12-TNFSF13 readthrough	pANT7_cGST
693161	HsxXG013989	9	A02		RAB12	201475	NM_001025300	RAB12, member RAS oncogene family	pANT7_cGST
693169	HsxXG013989	10	B02		SYN1	6853	NM_133499	synapsin I	pANT7_cGST
693176	HsxXG013989	11	C02		GJD3	125111	NM_152219	gap junction protein, delta 3, 31.9kDa	pANT7_cGST
693181	HsxXG013989	12	D02		CHCHD10	400916	null	coiled-coil-helix-coiled-coil-helix domain containing 10	pANT7_cGST
693184	HsxXG013989	13	E02		IDNK	414328	null	idnK, gluconokinase homolog (E. coli)	pANT7_cGST
693187	HsxXG013989	14	F02		LYPD6B	130576	null	LY6/PLAUR domain containing 6B	pANT7_cGST
693189	HsxXG013989	15	G02		C8orf86	389649	null	chromosome 8 open reading frame 86	pANT7_cGST
693194	HsxXG013989	16	H02		CENPQ	55166	null	centromere protein Q	pANT7_cGST
693197	HsxXG013989	17	A03		SHISA5	51246	null	shisa family member 5	pANT7_cGST

693200	HsxXG013989	18	B03		TSR3	115939	null	TSR3, 20S rRNA accumulation, homolog (S. cerevisiae)	pANT7_cGST
693202	HsxXG013989	19	C03		KRTAP9-9	81870	null	keratin associated protein 9-9	pANT7_cGST
693203	HsxXG013989	20	D03		TPO	7173	null	thyroid peroxidase	pANT7_cGST
693204	HsxXG013989	21	E03		RIPK3	11035	null	receptor-interacting serine-threonine kinase 3	pANT7_cGST
693207	HsxXG013989	22	F03		FGFR1OP2	26127	null	FGFR1 oncogene partner 2	pANT7_cGST
693216	HsxXG013989	23	G03		BRD4	23476	null	bromodomain containing 4	pANT7_cGST
693222	HsxXG013989	24	H03		SREK1	140890	null	splicing regulatory glutamine/lysine-rich protein 1	pANT7_cGST
695080	HsxXG013989	25	A04		CPEB2	132864	null	cytoplasmic polyadenylation element binding protein 2	pANT7_cGST
695083	HsxXG013989	26	B04		ZNF85	7639	null	zinc finger protein 85	pANT7_cGST
695102	HsxXG013989	27	C04		SCARA5	286133	null	scavenger receptor class A, member 5 (putative)	pANT7_cGST
695116	HsxXG013989	28	D04		LONRF1	91694	null	LON peptidase N-terminal domain and ring finger 1	pANT7_cGST
695122	HsxXG013989	29	E04		HJURP	55355	null	Holliday junction recognition protein	pANT7_cGST
695126	HsxXG013989	30	F04		RBM42	79171	null	RNA binding motif protein 42	pANT7_cGST
695137	HsxXG013989	31	G04		SLC26A5	375611	null	solute carrier family 26 (anion exchanger), member 5	pANT7_cGST
695148	HsxXG013989	32	H04		L3HYPDH	112849	null	L-3-hydroxyproline dehydratase (trans-)	pANT7_cGST

695152	HsxXG013989	33	A05		ATP6V0D2	245972	null	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2	pANT7_cGST
695154	HsxXG013989	34	B05		AIRE	326	null	autoimmune regulator	pANT7_cGST
695155	HsxXG013989	35	C05		CYLC2	1539	null	cylicin, basic protein of sperm head cytoskeleton 2	pANT7_cGST
695183	HsxXG013989	36	D05		ZC3H14	79882	BC027607	zinc finger CCCH-type containing 14	pANT7_cGST
695186	HsxXG013989	37	E05		CDC25C	995	BC019089	cell division cycle 25C	pANT7_cGST
695194	HsxXG013989	38	F05		C16orf59	80178	EU832694	chromosome 16 open reading frame 59	pANT7_cGST
695197	HsxXG013989	39	G05		SF1	7536	BC020217	splicing factor 1	pANT7_cGST
695212	HsxXG013989	40	H05		CRLF1	9244	BC044634	cytokine receptor-like factor 1	pANT7_cGST
695224	HsxXG013989	41	A06		ALDH3A1	218	null	aldehyde dehydrogenase 3 family, member A1	pANT7_cGST
695226	HsxXG013989	42	B06		KLHL33	123103	null	kelch-like family member 33	pANT7_cGST
695227	HsxXG013989	43	C06		CDC73	79577	null	cell division cycle 73	pANT7_cGST
695234	HsxXG013989	44	D06		C7orf26	79034	null	chromosome 7 open reading frame 26	pANT7_cGST
695235	HsxXG013989	45	E06		GPATCH2L	55668	null	G patch domain containing 2-like	pANT7_cGST
695243	HsxXG013989	46	F06		HEATR1	55127	null	HEAT repeat containing 1	pANT7_cGST
695245	HsxXG013989	47	G06		P2RX2	22953	null	purinergic receptor P2X, ligand-gated ion channel, 2	pANT7_cGST
695247	HsxXG013989	48	H06		CYLC2	1539	null	cylicin, basic protein of sperm head cytoskeleton 2	pANT7_cGST
695248	HsxXG013989	49	A07		ARMCX4	100131755	null	armadillo repeat containing, X-linked 4	pANT7_cGST

695253	HsxXG013989	50	B07		CARKD	55739	null	carbohydrate kinase domain containing	pANT7_cGST
696700	HsxXG013989	51	C07		A1BG	1	null	alpha-1-B glycoprotein	pANT7_cGST
696704	HsxXG013989	52	D07		NUP214	8021	null	nucleoporin 214kDa	pANT7_cGST
696711	HsxXG013989	53	E07		GYS1	2997	null	glycogen synthase 1 (muscle)	pANT7_cGST
696720	HsxXG013989	54	F07		LOC100132705	100132705	null	immunoglobulin superfamily member 3-like	pANT7_cGST
696721	HsxXG013989	55	G07		MEF2BNB	729991	null	MEF2B neighbor	pANT7_cGST
696754	HsxXG013989	56	H07		GIGYF2	26058	EU831674	GRB10 interacting GYF protein 2	pANT7_cGST
696831	HsxXG013989	57	A08		E4F1	1877	null	E4F transcription factor 1	pANT7_cGST
696832	HsxXG013989	58	B08		BAZ2B	29994	null	bromodomain adjacent to zinc finger domain, 2B	pANT7_cGST
696843	HsxXG013989	59	C08		D2HGDH	728294	null	D-2-hydroxyglutarate dehydrogenase	pANT7_cGST
696845	HsxXG013989	60	D08		PON2	5445	null	paraoxonase 2	pANT7_cGST
696848	HsxXG013989	61	E08		ZNF658	26149	null	zinc finger protein 658	pANT7_cGST
696858	HsxXG013989	62	F08		ULK4	54986	null	unc-51 like kinase 4	pANT7_cGST
696870	HsxXG013989	63	G08		PCOLCE2	26577	null	procollagen C-endopeptidase enhancer 2	pANT7_cGST
696880	HsxXG013989	64	H08		TTC26	79989	null	tetratricopeptide repeat domain 26	pANT7_cGST
696881	HsxXG013989	65	A09		PFKFB1	5207	null	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	pANT7_cGST
696883	HsxXG013989	66	B09		C6orf58	352999	null	chromosome 6 open reading frame 58	pANT7_cGST
696884	HsxXG013989	67	C09		COL2A1	1280	null	collagen, type II, alpha 1	pANT7_cGST

696886	HsxXG013989	68	D09		RBM33	155435	null	RNA binding motif protein 33	pANT7_cGST
696914	HsxXG013989	69	E09		CCDC11	220136	null	coiled-coil domain containing 11	pANT7_cGST
696917	HsxXG013989	70	F09		RBMX2	51634	null	RNA binding motif protein, X-linked 2	pANT7_cGST
696922	HsxXG013989	71	G09		OR2M2	391194	null	olfactory receptor, family 2, subfamily M, member 2	pANT7_cGST
696923	HsxXG013989	72	H09		FAM175B	23172	null	family with sequence similarity 175, member B	pANT7_cGST
696932	HsxXG013989	73	A10		UBQLN4	56893	null	ubiquilin 4	pANT7_cGST
696933	HsxXG013989	74	B10		MXD4	10608	null	MAX dimerization protein 4	pANT7_cGST
696935	HsxXG013989	75	C10		FDX1L	112812	null	ferredoxin 1-like	pANT7_cGST
696936	HsxXG013989	76	D10		POLD4	57804	null	polymerase (DNA-directed), delta 4, accessory subunit	pANT7_cGST
696938	HsxXG013989	77	E10		FAM19A5	25817	null	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	pANT7_cGST
696939	HsxXG013989	78	F10		HEATR5A	25938	null	HEAT repeat containing 5A	pANT7_cGST
696942	HsxXG013989	79	G10		MFAP3L	9848	null	microfibrillar-associated protein 3-like	pANT7_cGST
696960	HsxXG013989	80	H10		EHMT2	10919	null	euchromatic histone-lysine N-methyltransferase 2	pANT7_cGST
696964	HsxXG013989	81	A11		OXLD1	339229	null	oxidoreductase-like domain containing 1	pANT7_cGST

696965	HsxXG013989	82	B11		POLE3	54107	null	polymerase (DNA directed), epsilon 3, accessory subunit	pANT7_cGST
696970	HsxXG013989	83	C11		NAT8B	51471	null	N-acetyltransferase 8B (GCN5-related, putative, gene/pseudogene)	pANT7_cGST
696971	HsxXG013989	84	D11		PRPF38B	55119	null	pre-mRNA processing factor 38B	pANT7_cGST
696979	HsxXG013989	85	E11		ZNF451	26036	null	zinc finger protein 451	pANT7_cGST
696981	HsxXG013989	86	F11		PLEKHG5	57449	null	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	pANT7_cGST
696987	HsxXG013989	87	G11		CCDC180	100499483	null	coiled-coil domain containing 180	pANT7_cGST
697004	HsxXG013989	88	H11		ACAT1	38	null	acetyl-CoA acetyltransferase 1	pANT7_cGST
697069	HsxXG013989	89	A12		PARPBP	55010	null	PARP1 binding protein	pANT7_cGST
697072	HsxXG013989	90	B12		TRIM51	84767	null	tripartite motif-containing 51	pANT7_cGST
697075	HsxXG013989	91	C12		SYNE4	163183	null	spectrin repeat containing, nuclear envelope family member 4	pANT7_cGST
697079	HsxXG013989	92	D12		LOC100506688	100506688	null	uncharacterized LOC100506688	pANT7_cGST
701773	HsxXG013989	93	E12		NRAS	4893	BC005219	neuroblastoma RAS viral (v-ras) oncogene homolog	pANT7_cGST
701776	HsxXG013989	94	F12		MNDA	4332	BC032319	myeloid cell nuclear differentiation antigen	pANT7_cGST

701779	HsxXG013989	95	G12		RELA	5970	BC110830	v-rel avian reticuloendotheliosis viral oncogene homolog A	pANT7_cGST
	HsxXG014242	1	A01						pANT7_cGST
677058	HsxXG014242	2	B01	2900	NUP210			nucleoporin 210kDa	pANT7_cGST
677105	HsxXG014242	3	C01	2777	KIAA1324			KIAA1324	pANT7_cGST
677109	HsxXG014242	4	D01	641	SETD3			SET domain containing 3	pANT7_cGST
677224	HsxXG014242	5	E01	680	MRPS35			mitochondrial ribosomal protein S35	pANT7_cGST
677286	HsxXG014242	6	F01	1931	SULF1			sulfatase 1	pANT7_cGST
677345	HsxXG014242	7	G01	671	DDX54			DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	pANT7_cGST
677372	HsxXG014242	8	H01	659	MEPCE			methylphosphate capping enzyme	pANT7_cGST
677396	HsxXG014242	9	A02	653	PDGFRA			platelet-derived growth factor receptor, alpha polypeptide	pANT7_cGST
677018	HsxXG014242	10	B02	569	C11orf57			chromosome 11 open reading frame 57	pANT7_cGST
677020	HsxXG014242	11	C02	569	UBTD2			ubiquitin domain containing 2	pANT7_cGST
677043	HsxXG014242	12	D02	2936	SEL1L3			sel-1 suppressor of lin-12-like 3 (C. elegans)	pANT7_cGST
677055	HsxXG014242	13	E02	2906	NID2			nidogen 2 (osteonidogen)	pANT7_cGST
677075	HsxXG014242	14	F02	2858	ZNF518A			zinc finger protein 518A	pANT7_cGST
677076	HsxXG014242	15	G02	2858	CKAP5			cytoskeleton associated protein 5	pANT7_cGST
677102	HsxXG014242	16	H02	2786	DGKZ			diacylglycerol kinase, zeta	pANT7_cGST

677106	HsxXG014242	17	A03	2771	SETD5			SET domain containing 5	pANT7_cGST
677112	HsxXG014242	18	B03	641	HDHD1			haloacid dehalogenase-like hydrolase domain containing 1	pANT7_cGST
677216	HsxXG014242	19	C03	683	EXOG			endo/exonuclease (5'-3'), endonuclease G-like	pANT7_cGST
677221	HsxXG014242	20	D03	683	IDI1			isopentenyl-diphosphate delta isomerase 1	pANT7_cGST
677226	HsxXG014242	21	E03	680	SULT1C4			sulfotransferase family, cytosolic, 1C, member 4	pANT7_cGST
677233	HsxXG014242	22	F03	677	TEFM			transcription elongation factor, mitochondrial	pANT7_cGST
677243	HsxXG014242	23	G03	674	CCDC158			coiled-coil domain containing 158	pANT7_cGST
677258	HsxXG014242	24	H03	1967	MAP3K13			mitogen-activated protein kinase kinase kinase 13	pANT7_cGST
677274	HsxXG014242	25	A04	1952	CDHR5			cadherin-related family member 5	pANT7_cGST
677285	HsxXG014242	26	B04	1931	NRP1			neuropilin 1	pANT7_cGST
677299	HsxXG014242	27	C04	1919	RNF214			ring finger protein 214	pANT7_cGST
677300	HsxXG014242	28	D04	1919	AP1G2			adaptor-related protein complex 1, gamma 2 subunit	pANT7_cGST
677307	HsxXG014242	29	E04	1913	SCNN1D			sodium channel, non-voltage-gated 1, delta subunit	pANT7_cGST
677310	HsxXG014242	30	F04	1910	PHTF1			putative homeodomain transcription factor 1	pANT7_cGST
677312	HsxXG014242	31	G04	1910	COL20A1			collagen, type XX, alpha 1	pANT7_cGST
677326	HsxXG014242	32	H04	1895	ITGA9			integrin, alpha 9	pANT7_cGST

677329	HsxXG014242	33	A05	1892	IKBKE			inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	pANT7_cGST
677334	HsxXG014242	34	B05	1889	CDH7			cadherin 7, type 2	pANT7_cGST
677351	HsxXG014242	35	C05	668	TMEM26			transmembrane protein 26	pANT7_cGST
677352	HsxXG014242	36	D05	668	AP5B1			adaptor-related protein complex 5, beta 1 subunit	pANT7_cGST
677353	HsxXG014242	37	E05	668	C17orf59			chromosome 17 open reading frame 59	pANT7_cGST
677354	HsxXG014242	38	F05	668	RAB37			RAB37, member RAS oncogene family	pANT7_cGST
677355	HsxXG014242	39	G05	668	RHBDD2			rhomboid domain containing 2	pANT7_cGST
677361	HsxXG014242	40	H05	668	PLBD1			phospholipase B domain containing 1	pANT7_cGST
677362	HsxXG014242	41	A06	665	CADPS			Ca++-dependent secretion activator	pANT7_cGST
677364	HsxXG014242	42	B06	665	THNSL1			threonine synthase-like 1 (S. cerevisiae)	pANT7_cGST
677368	HsxXG014242	43	C06	662	LSM14B			LSM14B, SCD6 homolog B (S. cerevisiae)	pANT7_cGST
677369	HsxXG014242	44	D06	662	TSPY8			testis specific protein, Y-linked 8	pANT7_cGST
677382	HsxXG014242	45	E06	656	COG8			component of oligomeric golgi complex 8	pANT7_cGST
677392	HsxXG014242	46	F06	653	SDS			serine dehydratase	pANT7_cGST
677393	HsxXG014242	47	G06	653	MAU2			MAU2 chromatid cohesion factor homolog (C. elegans)	pANT7_cGST
677399	HsxXG014242	48	H06	650	HOXD12			homeobox D12	pANT7_cGST

677401	HsxXG014242	49	A07	650	GH1			growth hormone 1	pANT7_cGST
701783	HsxXG014242	50	B07	2027	CD22	933	BC109306	Homo sapiens CD22 molecule	pANT7_cGST
701789	HsxXG014242	51	C07	773	NROB2	8431	NM_021969	nuclear receptor subfamily 0, group B, member 2	pANT7_cGST
701794	HsxXG014242	52	D07	1736			BC044640	phosphatidylinositol glycan anchor biosynthesis, class Z	pANT7_cGST
701796	HsxXG014242	53	E07	1733			BC001371	ER degradation enhancer, mannosidase alpha-like 2	pANT7_cGST
676797	HsxXG014242	54	F07	848	ELMOD1			ELMO/CED-12 domain containing 1	pANT7_cGST
676799	HsxXG014242	55	G07	848	STEAP4			STEAP family member 4	pANT7_cGST
676802	HsxXG014242	56	H07	845	ZDHHC19			zinc finger, DHHC-type containing 19	pANT7_cGST
676803	HsxXG014242	57	A08	845	PLEKHS1			pleckstrin homology domain containing, family S member 1	pANT7_cGST
676813	HsxXG014242	58	B08	842	PIP4K2B			phosphatidylinositol-5-phosphate 4-kinase, type II, beta	pANT7_cGST
676815	HsxXG014242	59	C08	842	ZNF783			zinc finger family member 783	pANT7_cGST
676819	HsxXG014242	60	D08	839	GFOD2			glucose-fructose oxidoreductase domain containing 2	pANT7_cGST
676821	HsxXG014242	61	E08	839	PPP1R7			protein phosphatase 1, regulatory subunit 7	pANT7_cGST
676823	HsxXG014242	62	F08	839	UGGT2			UDP-glucose glycoprotein glucosyltransferase 2	pANT7_cGST

713216	HsxXG014242	63	G08	1448	GSK3A		BC027984	glycogen synthase kinase 3 alpha	pANT7_cGST
713218	HsxXG014242	64	H08	533	TMEM65		BC032396	transmembrane protein 65	pANT7_cGST
713219	HsxXG014242	65	A09	1952	TDRD3		BC030514	tudor domain containing 3	pANT7_cGST
713220	HsxXG014242	66	B09	653	CLDN5		BC032363	claudin 5	pANT7_cGST
713221	HsxXG014242	67	C09	425	CHCHD4		BC033775	coiled-coil-helix-coiled-coil-helix domain containing 4	pANT7_cGST
713224	HsxXG014242	68	D09	347	VAMP2		BC033870	vesicle-associated membrane protein 2 (synaptobrevin 2)	pANT7_cGST
713226	HsxXG014242	69	E09	575	RNF185		BC035684	ring finger protein 185	pANT7_cGST
713227	HsxXG014242	70	F09	545	CMTM3		BC036042	CKLF-like MARVEL transmembrane domain containing 3	pANT7_cGST
713228	HsxXG014242	71	G09	1469	ZNF512		BC043221	zinc finger protein 512	pANT7_cGST
713229	HsxXG014242	72	H09	1406	ETS2		BC042954	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	pANT7_cGST
713232	HsxXG014242	73	A10	1628	TTLL7		BC048970	tubulin tyrosine ligase-like family, member 7	pANT7_cGST
713233	HsxXG014242	74	B10	1397	SCARA3		BC060811	scavenger receptor class A, member 3	pANT7_cGST
713235	HsxXG014242	75	C10	644	HMGB1		BC003378	high mobility group box 1	pANT7_cGST
713237	HsxXG014242	76	D10	386	C7orf49		BC000168	chromosome 7 open reading frame 49	pANT7_cGST
713238	HsxXG014242	77	E10	614	ADPRM		BC001294	ADP-ribose/CDP-alcohol diphosphatase, manganese-dependent	pANT7_cGST
713239	HsxXG014242	78	F10	659	CREG1		BC006786	cellular repressor of E1A-stimulated genes 1	pANT7_cGST

713240	HsxXG014242	79	G10	521	FAM156A		BC000867	family with sequence similarity 156, member A	pANT7_cGST
713243	HsxXG014242	80	H10	728	ECI1		BC009631	enoyl-CoA delta isomerase 1	pANT7_cGST
713244	HsxXG014242	81	A11	1154	ARMC8		BC013424	armadillo repeat containing 8	pANT7_cGST
713245	HsxXG014242	82	B11	758	TMCO6		BC009618	transmembrane and coiled-coil domains 6	pANT7_cGST
713246	HsxXG014242	83	C11	821	UBR7		BC015046	ubiquitin protein ligase E3 component n-recognin 7 (putative)	pANT7_cGST
713247	HsxXG014242	84	D11	878	RPS2		BC016178	ribosomal protein S2	pANT7_cGST
713249	HsxXG014242	85	E11	752	C11orf68		BC010512	chromosome 11 open reading frame 68	pANT7_cGST
713250	HsxXG014242	86	F11	437	CST3		BC013083	cystatin C	pANT7_cGST
713251	HsxXG014242	87	G11	725	HTATIP2		BC015358	HIV-1 Tat interactive protein 2, 30kDa	pANT7_cGST
713252	HsxXG014242	88	H11	1133	FIP1L1		BC017724	FIP1 like 1 (S. cerevisiae)	pANT7_cGST
713254	HsxXG014242	89	A12	752	RAB34		BC016841	RAB34, member RAS oncogene family	pANT7_cGST
713256	HsxXG014242	90	B12	1043	ACTR3B		BC015207	ARP3 actin-related protein 3 homolog B (yeast)	pANT7_cGST
713257	HsxXG014242	91	C12	713	EFNA3		BC017722	ephrin-A3	pANT7_cGST
713259	HsxXG014242	92	D12	893	FAM105B		BC015392	family with sequence similarity 105, member B	pANT7_cGST
713261	HsxXG014242	93	E12	1187	DENND1B		BC022561	DENN/MADD domain containing 1B	pANT7_cGST
713264	HsxXG014242	94	F12	686	HS2ST1		BC025990	heparan sulfate 2-O-sulfotransferase 1	pANT7_cGST
713269	HsxXG014242	95	G12	785	EMC10		BC032948	ER membrane protein complex subunit 10	pANT7_cGST

	HsxXG014242	96	H12						pANT7_cGST
	HsxXG014243	1	A01						pANT7_cGST
713274	HsxXG014243	2	B01	935	SLC1A6		BC028721	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	pANT7_cGST
713279	HsxXG014243	3	C01	338	FAM27E3		BC032035	family with sequence similarity 27, member E3	pANT7_cGST
713281	HsxXG014243	4	D01	167	RPS29		BC035313	ribosomal protein S29	pANT7_cGST
713282	HsxXG014243	5	E01	884	AEBP2		BC022220	AE binding protein 2	pANT7_cGST
713283	HsxXG014243	6	F01	356	RPS20		BC087850	ribosomal protein S20	pANT7_cGST
713284	HsxXG014243	7	G01	248	TIMM8B		BC105986	translocase of inner mitochondrial membrane 8 homolog B (yeast)	pANT7_cGST
713286	HsxXG014243	8	H01	626	HMGB2		BC100019	high mobility group box 2	pANT7_cGST
713287	HsxXG014243	9	A02	227	NDUFC1		BC107682	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa	pANT7_cGST
713293	HsxXG014243	10	B02	818	ZNF80		BC069606	zinc finger protein 80	pANT7_cGST
713294	HsxXG014243	11	C02	341	XCL2		BC069360	chemokine (C motif) ligand 2	pANT7_cGST
713295	HsxXG014243	12	D02	281	DEFA1		BC069423	defensin, alpha 1	pANT7_cGST
713301	HsxXG014243	13	E02	260	SEPW1		BC047893	selenoprotein W, 1	pANT7_cGST
713306	HsxXG014243	14	F02	266	CCL18		BC069700	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	pANT7_cGST
713311	HsxXG014243	15	G02	770	PSMD8		BC065006	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	pANT7_cGST

713312	HsxXG014243	16	H02	524	PPAPDC1B		BC106014	phosphatidic acid phosphatase type 2 domain containing 1B	pANT7_cGST
713313	HsxXG014243	17	A03	1175	TMEM201		BC121187	transmembrane protein 201	pANT7_cGST
713314	HsxXG014243	18	B03	488	C19orf66		BC010847	chromosome 19 open reading frame 66	pANT7_cGST
713316	HsxXG014243	19	C03	1082	UBR7		BC017013	ubiquitin protein ligase E3 component n-recognin 7 (putative)	pANT7_cGST
713317	HsxXG014243	20	D03	557	SPATC1L		BC065570	spermatogenesis and centriole associated 1-like	pANT7_cGST
713318	HsxXG014243	21	E03	1079	SEC14L4		BC139912	SEC14-like 4 (S. cerevisiae)	pANT7_cGST
713319	HsxXG014243	22	F03	359	TMEM230		BC110408	transmembrane protein 230	pANT7_cGST
713323	HsxXG014243	23	G03	551	GPIHBP1		BC035810	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	pANT7_cGST
713329	HsxXG014243	24	H03	383	RPL22		BC066314	ribosomal protein L22	pANT7_cGST
713330	HsxXG014243	25	A04	638	AMN1		BC067906	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	pANT7_cGST
713332	HsxXG014243	26	B04	662	SRSF2		BC070086	serine/arginine-rich splicing factor 2	pANT7_cGST
713335	HsxXG014243	27	C04	434	SELM		BC068004	selenoprotein M	pANT7_cGST
713337	HsxXG014243	28	D04	602	SRSF1		BC033785	serine/arginine-rich splicing factor 1	pANT7_cGST
713338	HsxXG014243	29	E04	959	HNRNPA1		BC074502	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST
713341	HsxXG014243	30	F04	1091	OAS1		BC061587	2'-5'-oligoadenylate synthetase 1, 40/46kDa	pANT7_cGST

713345	HsxXG014243	31	G04	407	SRP14		BC071716	signal recognition particle 14kDa (homologous Alu RNA binding protein)	pANT7_cGST
713347	HsxXG014243	32	H04	584	SELT		BC071699	selenoprotein T	pANT7_cGST
713349	HsxXG014243	33	A05	455	IL3		BC066273	interleukin 3 (colony-stimulating factor, multiple)	pANT7_cGST
713351	HsxXG014243	34	B05	1112	SMYD2		BC049367	SET and MYND domain containing 2	pANT7_cGST
713352	HsxXG014243	35	C05	470	RFESD		BC048979	Rieske (Fe-S) domain containing	pANT7_cGST
713353	HsxXG014243	36	D05	1097	PKM		BC094767	pyruvate kinase, muscle	pANT7_cGST
713355	HsxXG014243	37	E05	1271	MIPOL1		BC036124	mirror-image polydactyly 1	pANT7_cGST
713357	HsxXG014243	38	F05	719	SNRPN		BC024777	small nuclear ribonucleoprotein polypeptide N	pANT7_cGST
713359	HsxXG014243	39	G05	944	RAB3IP		BC059358	RAB3A interacting protein	pANT7_cGST
713360	HsxXG014243	40	H05	794	CLEC17A		BC144665	C-type lectin domain family 17, member A	pANT7_cGST
713361	HsxXG014243	41	A06	347	LRRD1		BC144674	leucine-rich repeats and death domain containing 1	pANT7_cGST
713362	HsxXG014243	42	B06	236	SMR3B		BC144529	submaxillary gland androgen regulated protein 3B	pANT7_cGST
713364	HsxXG014243	43	C06	566	CT45A5		BC144527	cancer/testis antigen family 45, member A5	pANT7_cGST
713366	HsxXG014243	44	D06	566	CT45A5		BC144528	cancer/testis antigen family 45, member A5	pANT7_cGST
713367	HsxXG014243	45	E06	893	C2orf54		BC125154	chromosome 2 open reading frame 54	pANT7_cGST

713369	HsxXG014243	46	F06	1109	MIER1		BC125217	mesoderm induction early response 1, transcriptional regulator	pANT7_cGST
713371	HsxXG014243	47	G06	1109	MIER1		BC125218	mesoderm induction early response 1, transcriptional regulator	pANT7_cGST
713373	HsxXG014243	48	H06	275	LCE3D		BC120935	late cornified envelope 3D	pANT7_cGST
713377	HsxXG014243	49	A07	371	TAF13		BC121181	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	pANT7_cGST
713378	HsxXG014243	50	B07	350	GAGE12F		BC121182	G antigen 12F	pANT7_cGST
713379	HsxXG014243	51	C07	671	PLSCR2		BC120969	phospholipid scramblase 2	pANT7_cGST
713380	HsxXG014243	52	D07	350	GAGE12F		BC121183	G antigen 12F	pANT7_cGST
713381	HsxXG014243	53	E07	650	HOXD12		BC121104	homeobox D12	pANT7_cGST
713382	HsxXG014243	54	F07	257	SNRPF		BC128452	small nuclear ribonucleoprotein polypeptide F	pANT7_cGST
713387	HsxXG014243	55	G07	530	TMEM190		BC128190	transmembrane protein 190	pANT7_cGST
713389	HsxXG014243	56	H07	995	C4orf29		BC128143	chromosome 4 open reading frame 29	pANT7_cGST
713392	HsxXG014243	57	A08	671	LRP5L		BC139736	low density lipoprotein receptor-related protein 5-like	pANT7_cGST
713394	HsxXG014243	58	B08	1769	TMEM132B		BC131621	transmembrane protein 132B	pANT7_cGST
713396	HsxXG014243	59	C08	374	RUSC1-AS1		BC131614	RUSC1 antisense RNA 1	pANT7_cGST
713399	HsxXG014243	60	D08	1163	PDHA2		BC127637	pyruvate dehydrogenase (lipoamide) alpha 2	pANT7_cGST

713401	HsxXG014243	61	E08	671	CHIC1		BC127728	cysteine-rich hydrophobic domain 1	pANT7_cGST
713407	HsxXG014243	62	F08	911	KIR2DS4		BC171788	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	pANT7_cGST
713414	HsxXG014243	63	G08	416	CCDC169		BC171882	coiled-coil domain containing 169	pANT7_cGST
713416	HsxXG014243	64	H08	266	FAM25A		BC171878	family with sequence similarity 25, member A	pANT7_cGST
713417	HsxXG014243	65	A09	416	CCDC169		BC171880	coiled-coil domain containing 169	pANT7_cGST
713419	HsxXG014243	66	B09	266	FAM25C		BC171871	family with sequence similarity 25, member C	pANT7_cGST
713422	HsxXG014243	67	C09	266	FAM25C		BC146972	family with sequence similarity 25, member C	pANT7_cGST
713423	HsxXG014243	68	D09	284	DEFB132		BC137292	defensin, beta 132	pANT7_cGST
713426	HsxXG014243	69	E09	257	SPINK9		BC137531	serine peptidase inhibitor, Kazal type 9	pANT7_cGST
713429	HsxXG014243	70	F09	1376	XKR3		BC137522	XK, Kell blood group complex subunit-related family, member 3	pANT7_cGST
713430	HsxXG014243	71	G09	1400	ZMAT1		BC140920	zinc finger, matrin-type 1	pANT7_cGST
713432	HsxXG014243	72	H09	266	FAM25BP		BC146968	family with sequence similarity 25, member B	pANT7_cGST
713435	HsxXG014243	73	A10	455	BOLA2B		BC137534	bolA family member 2B	pANT7_cGST
713436	HsxXG014243	74	B10	446	FAM72A		BC146992	family with sequence similarity 72, member A	pANT7_cGST
713437	HsxXG014243	75	C10	266	FAM25C		BC146991	family with sequence similarity 25, member C	pANT7_cGST
713440	HsxXG014243	76	D10	266	FAM25C		BC146955	family with sequence similarity 25, member C	pANT7_cGST
713444	HsxXG014243	77	E10	374	NPB		BC146890	neuropeptide B	pANT7_cGST

713449	HsxXG014243	78	F10	902	GPR108		BC150657	G protein-coupled receptor 108	pANT7_cGST
713453	HsxXG014243	79	G10	413	03-Mar		BC146964	membrane-associated ring finger (C3HC4) 3, E3 ubiquitin protein ligase	pANT7_cGST
713456	HsxXG014243	80	H10	266	FAM25C		BC147022	family with sequence similarity 25, member C	pANT7_cGST
713457	HsxXG014243	81	A11	986	GATSL2		BC147030	GATS protein-like 2	pANT7_cGST
713459	HsxXG014243	82	B11	266	FAM25C		BC147026	family with sequence similarity 25, member C	pANT7_cGST
713463	HsxXG014243	83	C11	350	GAGE12F		BC144193	G antigen 12F	pANT7_cGST
713464	HsxXG014243	84	D11	389	TEX38		BC144027	testis expressed 38	pANT7_cGST
713467	HsxXG014243	85	E11	677	HYKK		BC144383	hydroxylysine kinase	pANT7_cGST
713469	HsxXG014243	86	F11	377	HIST1H2BH		BC096118	histone cluster 1, H2bh	pANT7_cGST
713470	HsxXG014243	87	G11	1916	KRT2		BC096294	keratin 2	pANT7_cGST
713471	HsxXG014243	88	H11	461	CDX1		BC096252	caudal type homeobox 1	pANT7_cGST
713472	HsxXG014243	89	A12	929	SOAT2		BC099626	sterol O-acyltransferase 2	pANT7_cGST
713479	HsxXG014243	90	B12	2132	ALOXE3		BC101938	arachidonate lipoxygenase 3	pANT7_cGST
713480	HsxXG014243	91	C12	488	NKAIN1		BC098249	Na+/K+ transporting ATPase interacting 1	pANT7_cGST
713483	HsxXG014243	92	D12	554	APOA1BP		BC100932	apolipoprotein A-I binding protein	pANT7_cGST
713484	HsxXG014243	93	E12	500	KRTAP1-3		BC101151	keratin associated protein 1-3	pANT7_cGST
713485	HsxXG014243	94	F12	842	PTCRA		BC100771	pre T-cell antigen receptor alpha	pANT7_cGST
713492	HsxXG014243	95	G12	263	COX6B2		BC100899	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	pANT7_cGST
	HsxXG014243	96	H12						pANT7_cGST

	HsxXG014244	1	A01						pANT7_cGST
713493	HsxXG014244	2	B01	263	COX6B2		BC100900	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	pANT7_cGST
713494	HsxXG014244	3	C01	383	KRTAP2-4		BC101147	keratin associated protein 2-4	pANT7_cGST
713495	HsxXG014244	4	D01	188	KRTAP19-7		BC103837	keratin associated protein 19-7	pANT7_cGST
713496	HsxXG014244	5	E01	194	DEFB106B		BC100845	defensin, beta 106B	pANT7_cGST
713501	HsxXG014244	6	F01	2741	SAFB		BC143938	scaffold attachment factor B	pANT7_cGST
713504	HsxXG014244	7	G01	2588	AAK1		BC143710	AP2 associated kinase 1	pANT7_cGST
713506	HsxXG014244	8	H01	344	TMEM218		BC144270	transmembrane protein 218	pANT7_cGST
713507	HsxXG014244	9	A02	1250	SERINC5		BC101281	serine incorporator 5	pANT7_cGST
713509	HsxXG014244	10	B02	1310	PNPLA1		BC103907	patatin-like phospholipase domain containing 1	pANT7_cGST
713512	HsxXG014244	11	C02	1334	PLD5		BC101374	phospholipase D family, member 5	pANT7_cGST
713513	HsxXG014244	12	D02	1763	CWF19L2		BC110439	CWF19-like 2, cell cycle control (S. pombe)	pANT7_cGST
713516	HsxXG014244	13	E02	1808	CWF19L2		BC110440	CWF19-like 2, cell cycle control (S. pombe)	pANT7_cGST
713517	HsxXG014244	14	F02	503	RASSF3		BC100952	Ras association (RalGDS/AF-6) domain family member 3	pANT7_cGST
713519	HsxXG014244	15	G02	494	NRN1L		BC100864	neuritin 1-like	pANT7_cGST
713520	HsxXG014244	16	H02	785	FBXW12		BC101303	F-box and WD repeat domain containing 12	pANT7_cGST
713522	HsxXG014244	17	A03	1295	ZIK1		BC103959	zinc finger protein interacting with K protein 1	pANT7_cGST

713524	HsxXG014244	18	B03	1766	CPEB2		BC103940	cytoplasmic polyadenylation element binding protein 2	pANT7_cGST
713526	HsxXG014244	19	C03	1196	ANKDD1A		BC101273	ankyrin repeat and death domain containing 1A	pANT7_cGST
713527	HsxXG014244	20	D03	1268	ANKDD1A		BC101275	ankyrin repeat and death domain containing 1A	pANT7_cGST
713528	HsxXG014244	21	E03	1643	ARHGAP27		BC101388	Rho GTPase activating protein 27	pANT7_cGST
713529	HsxXG014244	22	F03	2216	ZNF624		BC103944	zinc finger protein 624	pANT7_cGST
713531	HsxXG014244	23	G03	1643	ARHGAP27		BC101389	Rho GTPase activating protein 27	pANT7_cGST
713532	HsxXG014244	24	H03	248	COX7A2		BC100852	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	pANT7_cGST
713533	HsxXG014244	25	A04	413	NANOS2		BC117484	nanos homolog 2 (Drosophila)	pANT7_cGST
713536	HsxXG014244	26	B04	1616	SLC17A8		BC117229	solute carrier family 17 (vesicular glutamate transporter), member 8	pANT7_cGST
713538	HsxXG014244	27	C04	1052	RRM2B		BC117496	ribonucleotide reductase M2 B (TP53 inducible)	pANT7_cGST
713540	HsxXG014244	28	D04	1868	FOXP2		BC126104	forkhead box P2	pANT7_cGST
713541	HsxXG014244	29	E04	1211	TTLL10		BC126152	tubulin tyrosine ligase-like family, member 10	pANT7_cGST
713543	HsxXG014244	30	F04	584	KRTAP4-11		BC126131	keratin associated protein 4-11	pANT7_cGST
713544	HsxXG014244	31	G04	1943	C1orf127		BC126349	chromosome 1 open reading frame 127	pANT7_cGST
713546	HsxXG014244	32	H04	890	CCDC102B		BC126450	coiled-coil domain containing 102B	pANT7_cGST

713547	HsxXG014244	33	A05	620	AANAT		BC126332	aralkylamine N-acetyltransferase	pANT7_cGST
713552	HsxXG014244	34	B05	242	NEDD8		BC104201	neural precursor cell expressed, developmentally down-regulated 8	pANT7_cGST
713553	HsxXG014244	35	C05	1382	BTBD3		BC109315	BTB (POZ) domain containing 3	pANT7_cGST
713554	HsxXG014244	36	D05	275	CCL4		BC104226	chemokine (C-C motif) ligand 4	pANT7_cGST
713557	HsxXG014244	37	E05	1034	FAM117B		BC106906	family with sequence similarity 117, member B	pANT7_cGST
713558	HsxXG014244	38	F05	1199	ZNF514		BC110525	zinc finger protein 514	pANT7_cGST
713559	HsxXG014244	39	G05	746	DIO1		BC107170	deiodinase, iodothyronine, type I	pANT7_cGST
713561	HsxXG014244	40	H05	683	EXOG		BC104212	endo/exonuclease (5'-3'), endonuclease G-like	pANT7_cGST
713563	HsxXG014244	41	A06	1160	GALR2		BC109052	galanin receptor 2	pANT7_cGST
713564	HsxXG014244	42	B06	1319	GABRP		BC109106	gamma-aminobutyric acid (GABA) A receptor, pi	pANT7_cGST
713569	HsxXG014244	43	C06	506	SUDS3		BC093990	suppressor of defective silencing 3 homolog (S. cerevisiae)	pANT7_cGST
713570	HsxXG014244	44	D06	530	TNFSF18		BC093986	tumor necrosis factor (ligand) superfamily, member 18	pANT7_cGST
705688	HsxXG014244	45	E06	344	TMEM218		BC144277	transmembrane protein 218	pANT7_cGST
705689	HsxXG014244	46	F06	911	KIR2DS4		BC144566	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	pANT7_cGST

705690	HsxXG014244	47	G06	959	FRMPD2		BC144636	FERM and PDZ domain containing 2	pANT7_cGST
705691	HsxXG014244	48	H06	959	FRMPD2		BC144639	FERM and PDZ domain containing 2	pANT7_cGST
705692	HsxXG014244	49	A07	1553	LRRTM4		BC110058	leucine rich repeat transmembrane neuronal 4	pANT7_cGST
705694	HsxXG014244	50	B07	1748	SPIRE1		BC125207	spire-type actin nucleation factor 1	pANT7_cGST
705695	HsxXG014244	51	C07	257	SNRPF		BC063397	small nuclear ribonucleoprotein polypeptide F	pANT7_cGST
705696	HsxXG014244	52	D07	1628	TTLL7		BC048970	tubulin tyrosine ligase-like family, member 7	pANT7_cGST
705697	HsxXG014244	53	E07	3071	ITGA10		BC144637	integrin, alpha 10	pANT7_cGST
705698	HsxXG014244	54	F07	2510	TBC1D2B		BC144482	TBC1 domain family, member 2B	pANT7_cGST
705702	HsxXG014244	55	G07	2429	PCDHGB1		BC103926	protocadherin gamma subfamily B, 1	pANT7_cGST
705705	HsxXG014244	56	H07	2402	CDH20		BC101048	cadherin 20, type 2	pANT7_cGST
705707	HsxXG014244	57	A08	2375	ZNF541		BC101050	zinc finger protein 541	pANT7_cGST
705708	HsxXG014244	58	B08	2375	ZNF541		BC101051	zinc finger protein 541	pANT7_cGST
705709	HsxXG014244	59	C08	2375	ZNF541		BC101051	zinc finger protein 541	pANT7_cGST
705710	HsxXG014244	60	D08	2375	ZNF541		BC101053	zinc finger protein 541	pANT7_cGST
705712	HsxXG014244	61	E08	3407	CENPJ		BC113111	centromere protein J	pANT7_cGST
705725	HsxXG014244	62	F08	1280	GLDN		BC113397	gliomedin	pANT7_cGST
705729	HsxXG014244	63	G08	2093	WDR65		BC117306	WD repeat domain 65	pANT7_cGST
705730	HsxXG014244	64	H08	1319	NFIX		BC117115	nuclear factor I/X (CCAAT-binding transcription factor)	pANT7_cGST
705733	HsxXG014244	65	A09	1094	GABRE		BC047108	gamma-aminobutyric acid (GABA) A receptor, epsilon	pANT7_cGST

705735	HsxXG014244	66	B09	1121	FANCF		BC047028	Fanconi anemia, complementation group F	pANT7_cGST
705738	HsxXG014244	67	C09	881	PKDCC		BC094697	protein kinase domain containing, cytoplasmic	pANT7_cGST
705739	HsxXG014244	68	D09	959	HNRNPA1L2		BC108266	heterogeneous nuclear ribonucleoprotein A1-like 2	pANT7_cGST
705740	HsxXG014244	69	E09	776	RAB34		BC091510	RAB34, member RAS oncogene family	pANT7_cGST
705745	HsxXG014244	70	F09	1655	AP5B1		BC126905	adaptor-related protein complex 5, beta 1 subunit	pANT7_cGST
705746	HsxXG014244	71	G09	557	VCX3A		BC126902	variable charge, X-linked 3A	pANT7_cGST
705749	HsxXG014244	72	H09	416	VCX2		BC134350	variable charge, X-linked 2	pANT7_cGST
705750	HsxXG014244	73	A10	344	H2AFB2		BC134365	H2A histone family, member B2	pANT7_cGST
705751	HsxXG014244	74	B10	476	C9orf135		BC150564	chromosome 9 open reading frame 135	pANT7_cGST
705754	HsxXG014244	75	C10	926	ASB12		BC104946	ankyrin repeat and SOCS box containing 12	pANT7_cGST
705755	HsxXG014244	76	D10	971	TMEM165		BC104980	transmembrane protein 165	pANT7_cGST
705756	HsxXG014244	77	E10	971	TMEM165		BC104978	transmembrane protein 165	pANT7_cGST
705758	HsxXG014244	78	F10	1040	C15orf27		BC104955	chromosome 15 open reading frame 27	pANT7_cGST
705759	HsxXG014244	79	G10	377	NPPC		BC105065	natriuretic peptide C	pANT7_cGST
705761	HsxXG014244	80	H10	236	KRTAP21-1		BC105029	keratin associated protein 21-1	pANT7_cGST

705763	HsxXG014244	81	A11	935	MAMSTR		BC105056	MEF2 activating motif and SAP domain containing transcriptional regulator	pANT7_cGST
705765	HsxXG014244	82	B11	662	HIST1H1D		BC111971	histone cluster 1, H1d	pANT7_cGST
705766	HsxXG014244	83	C11	929	AK9		BC111948	adenylate kinase 9	pANT7_cGST
705769	HsxXG014244	84	D11	1235	PTPRR		BC122866	protein tyrosine phosphatase, receptor type, R	pANT7_cGST
705772	HsxXG014244	85	E11	593	CXXC4		BC119752	CXXC finger protein 4	pANT7_cGST
705773	HsxXG014244	86	F11	491	ZNF321P		BC119627	zinc finger protein 321, pseudogene	pANT7_cGST
705775	HsxXG014244	87	G11	1553	ANKRD13D		BC121024	ankyrin repeat domain 13 family, member D	pANT7_cGST
705776	HsxXG014244	88	H11	926	CDYL		BC119682	chromodomain protein, Y-like	pANT7_cGST
705778	HsxXG014244	89	A12	1565	TTC39C		BC121035	tetratricopeptide repeat domain 39C	pANT7_cGST
705780	HsxXG014244	90	B12	959	HNRNPA1		BC121133	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST
705781	HsxXG014244	91	C12	476	SNRPC		BC121082	small nuclear ribonucleoprotein polypeptide C	pANT7_cGST
705782	HsxXG014244	92	D12	908	FBXL17		BC126144	F-box and leucine-rich repeat protein 17	pANT7_cGST
705784	HsxXG014244	93	E12	497	C2orf73		BC126246	chromosome 2 open reading frame 73	pANT7_cGST
705785	HsxXG014244	94	F12	1301	WNK1		BC130467	WNK lysine deficient protein kinase 1	pANT7_cGST
705787	HsxXG014244	95	G12	1730	HECTD3		BC130470	HECT domain containing E3 ubiquitin protein ligase 3	pANT7_cGST
	HsxXG014244	96	H12						pANT7_cGST
	HsxXG014245	1	A01						pANT7_cGST

705790	HsxXG014245	2	B01	374	BLOC1S1		BC130640	biogenesis of lysosomal organelles complex-1, subunit 1	pANT7_cGST
705791	HsxXG014245	3	C01	371	BOLA2		BC130401	bolA family member 2	pANT7_cGST
705793	HsxXG014245	4	D01	371	BOLA2		BC130403	bolA family member 2	pANT7_cGST
705796	HsxXG014245	5	E01	2039	COL10A1		BC130623	collagen, type X, alpha 1	pANT7_cGST
705798	HsxXG014245	6	F01	539	CTAG1A		BC130364	cancer/testis antigen 1A	pANT7_cGST
705799	HsxXG014245	7	G01	1052	RRM2B		BC130628	ribonucleotide reductase M2 B (TP53 inducible)	pANT7_cGST
705801	HsxXG014245	8	H01	311	PF4V1		BC130657	platelet factor 4 variant 1	pANT7_cGST
705806	HsxXG014245	9	A02	1637	PRPF38B		BC132963	pre-mRNA processing factor 38B	pANT7_cGST
705807	HsxXG014245	10	B02	1865	C17orf104		BC132822	chromosome 17 open reading frame 104	pANT7_cGST
705808	HsxXG014245	11	C02	710	SLC25A29		BC132966	solute carrier family 25 (mitochondrial carnitine/acylcarnitine carrier), member 29	pANT7_cGST
705809	HsxXG014245	12	D02	494	PLA2G10		BC106731	phospholipase A2, group X	pANT7_cGST
705811	HsxXG014245	13	E02	452	RIPPLY1		BC105692	ripply transcriptional repressor 1	pANT7_cGST
705812	HsxXG014245	14	F02	344	H2AFB2		BC101415	H2A histone family, member B2	pANT7_cGST
705813	HsxXG014245	15	G02	371	CCDC153		BC101443	coiled-coil domain containing 153	pANT7_cGST
705814	HsxXG014245	16	H02	377	PPP1R11		BC102010	protein phosphatase 1, regulatory (inhibitor) subunit 11	pANT7_cGST
705815	HsxXG014245	17	A03	524	DLX6		BC103688	distal-less homeobox 6	pANT7_cGST
705816	HsxXG014245	18	B03	524	DLX6		BC103690	distal-less homeobox 6	pANT7_cGST
705817	HsxXG014245	19	C03	524	DLX6		BC109381	distal-less homeobox 6	pANT7_cGST

705818	HsxXG014245	20	D03	416	VCX2		BC104153	variable charge, X-linked 2	pANT7_cGST
705821	HsxXG014245	21	E03	494	PLA2G10		BC111804	phospholipase A2, group X	pANT7_cGST
705825	HsxXG014245	22	F03	566	IFNA7		BC114000	interferon, alpha 7	pANT7_cGST
705827	HsxXG014245	23	G03	1406	PRR5-ARHGAP8		BC132755	PRR5-ARHGAP8 readthrough	pANT7_cGST
705831	HsxXG014245	24	H03	1859	SLC6A6		BC137128	solute carrier family 6 (neurotransmitter transporter), member 6	pANT7_cGST
705840	HsxXG014245	25	A04	734	KRTAP10-12		BC137339	keratin associated protein 10-12	pANT7_cGST
705854	HsxXG014245	26	B04	278	CCL3L1		BC146914	chemokine (C-C motif) ligand 3-like 1	pANT7_cGST
705859	HsxXG014245	27	C04	824	FAM166B		BC146933	family with sequence similarity 166, member B	pANT7_cGST
705864	HsxXG014245	28	D04	278	CCL3L3		BC147013	chemokine (C-C motif) ligand 3-like 3	pANT7_cGST
705866	HsxXG014245	29	E04	278	CCL3L3		BC147008	chemokine (C-C motif) ligand 3-like 3	pANT7_cGST
705869	HsxXG014245	30	F04	266	FAM25C		BC146989	family with sequence similarity 25, member C	pANT7_cGST
705870	HsxXG014245	31	G04	878	RPS2		BC068051	ribosomal protein S2	pANT7_cGST
705873	HsxXG014245	32	H04	878	RPS2		BC075830	ribosomal protein S2	pANT7_cGST
705874	HsxXG014245	33	A05	878	RPS2		BC071923	ribosomal protein S2	pANT7_cGST
705875	HsxXG014245	34	B05	959	HNRNPA1		BC071945	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST
705876	HsxXG014245	35	C05	878	RPS2		BC071922	ribosomal protein S2	pANT7_cGST
705877	HsxXG014245	36	D05	878	RPS2		BC071924	ribosomal protein S2	pANT7_cGST
705882	HsxXG014245	37	E05	692	SNRPB		BC080516	small nuclear ribonucleoprotein polypeptides B and B1	pANT7_cGST

705888	HsxXG014245	38	F05	1196	MBOAT7		BC015857	membrane bound O-acyltransferase domain containing 7	pANT7_cGST
705889	HsxXG014245	39	G05	647	DCAF16		BC068025	DDB1 and CUL4 associated factor 16	pANT7_cGST
705890	HsxXG014245	40	H05	746	TPI1		BC017917	triosephosphate isomerase 1	pANT7_cGST
705894	HsxXG014245	41	A06	677	LAPTM4B		BC031021	lysosomal protein transmembrane 4 beta	pANT7_cGST
705895	HsxXG014245	42	B06	851	GPN3		BC031024	GPN-loop GTPase 3	pANT7_cGST
705899	HsxXG014245	43	C06	584	SELT		BC006012	selenoprotein T	pANT7_cGST
705901	HsxXG014245	44	D06	560	VTCN1		BC065717	V-set domain containing T cell activation inhibitor 1	pANT7_cGST
705903	HsxXG014245	45	E06	1754	MCMDC2		BC063108	minichromosome maintenance domain containing 2	pANT7_cGST
705904	HsxXG014245	46	F06	293	RNASEK		BC062705	ribonuclease, RNase K	pANT7_cGST
705905	HsxXG014245	47	G06	374	RPL31		BC070373	ribosomal protein L31	pANT7_cGST
705908	HsxXG014245	48	H06	278	HIGD1A		BC070277	HIG1 hypoxia inducible domain family, member 1A	pANT7_cGST
705910	HsxXG014245	49	A07	959	HNRNPA1		BC070315	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST
705912	HsxXG014245	50	B07	419	MED22		BC024225	mediator complex subunit 22	pANT7_cGST
705914	HsxXG014245	51	C07	656	NGRN		BC017192	neugrin, neurite outgrowth associated	pANT7_cGST
705916	HsxXG014245	52	D07	1247	TLE6		BC013986	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)	pANT7_cGST
705917	HsxXG014245	53	E07	650	HYI		BC006140	hydroxypyruvate isomerase (putative)	pANT7_cGST

705918	HsxXG014245	54	F07	719	EFHD2		BC023611	EF-hand domain family, member D2	pANT7_cGST
705919	HsxXG014245	55	G07	1529	INTS4		BC015664	integrator complex subunit 4	pANT7_cGST
705920	HsxXG014245	56	H07	569	GPX2		BC022820	glutathione peroxidase 2 (gastrointestinal)	pANT7_cGST
705923	HsxXG014245	57	A08	419	LYPD6B		BC018203	LY6/PLAUR domain containing 6B	pANT7_cGST
705925	HsxXG014245	58	B08	491	ZNF321P		BC046449	zinc finger protein 321, pseudogene	pANT7_cGST
705929	HsxXG014245	59	C08	1484	FERMT1		BC035882	fermitin family member 1	pANT7_cGST
705930	HsxXG014245	60	D08	260	SEPW1		BC032546	selenoprotein W, 1	pANT7_cGST
705931	HsxXG014245	61	E08	434	SELM		BC030236	selenoprotein M	pANT7_cGST
705932	HsxXG014245	62	F08	1214	TBC1D16		BC036947	TBC1 domain family, member 16	pANT7_cGST
705934	HsxXG014245	63	G08	623	ADORA3		BC041707	adenosine A3 receptor	pANT7_cGST
705936	HsxXG014245	64	H08	1151	SUCLG2		BC047024	succinate-CoA ligase, GDP-forming, beta subunit	pANT7_cGST
705937	HsxXG014245	65	A09	353	ZNF767		BC047675	zinc finger family member 767	pANT7_cGST
705938	HsxXG014245	66	B09	1067	RBMY1A1		BC047768	RNA binding motif protein, Y-linked, family 1, member A1	pANT7_cGST
705940	HsxXG014245	67	C09	860	STPG1		BC047705	sperm-tail PG-rich repeat containing 1	pANT7_cGST
705942	HsxXG014245	68	D09	1256	IKBKG		BC000299	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	pANT7_cGST
705943	HsxXG014245	69	E09	455	NME1		BC000293	NME/NM23 nucleoside diphosphate kinase 1	pANT7_cGST
705945	HsxXG014245	70	F09	959	HNRNPA1		BC002355	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST

705948	HsxXG014245	71	G09	443	RNF24		BC000213	ring finger protein 24	pANT7_cGST
705949	HsxXG014245	72	H09	485	CCDC28A		BC004464	coiled-coil domain containing 28A	pANT7_cGST
705950	HsxXG014245	73	A10	656	NGRN		BC001682	neugrin, neurite outgrowth associated	pANT7_cGST
705952	HsxXG014245	74	B10	257	SNRPF		BC002505	small nuclear ribonucleoprotein polypeptide F	pANT7_cGST
705953	HsxXG014245	75	C10	1469	CLK3		BC002555	CDC-like kinase 3	pANT7_cGST
705954	HsxXG014245	76	D10	272	UQCRH		BC001426	ubiquinol-cytochrome c reductase hinge protein	pANT7_cGST
705956	HsxXG014245	77	E10	293	S100A13		BC000632	S100 calcium binding protein A13	pANT7_cGST
705961	HsxXG014245	78	F10	611	DLK2		BC000230	delta-like 2 homolog (Drosophila)	pANT7_cGST
705963	HsxXG014245	79	G10	728	MACROD1		BC003188	MACRO domain containing 1	pANT7_cGST
705964	HsxXG014245	80	H10	548	SRSF10		BC001107	serine/arginine-rich splicing factor 10	pANT7_cGST
705965	HsxXG014245	81	A11	701	KCTD15		BC001185	potassium channel tetramerisation domain containing 15	pANT7_cGST
705969	HsxXG014245	82	B11	719	U2AF1		BC001923	U2 small nuclear RNA auxiliary factor 1	pANT7_cGST
705970	HsxXG014245	83	C11	1652	EPS8L1		BC004907	EPS8-like 1	pANT7_cGST
705971	HsxXG014245	84	D11	665	CHAC1		BC001683	ChaC, cation transport regulator homolog 1 (E. coli)	pANT7_cGST
705973	HsxXG014245	85	E11	314	RPL36		BC004971	ribosomal protein L36	pANT7_cGST
705974	HsxXG014245	86	F11	1544	MTA3		BC004227	metastasis associated 1 family, member 3	pANT7_cGST
711607	HsxXG014245	87	G11	923	HAGH		BC002627	hydroxyacylglutathione hydrolase	pANT7_cGST
711608	HsxXG014245	88	H11	947	PRMT6		BC002729	protein arginine methyltransferase 6	pANT7_cGST

711609	HsxXG014245	89	A12	851	PEF1		BC002773	penta-EF-hand domain containing 1	pANT7_cGST
711610	HsxXG014245	90	B12	347	VAMP2		BC002737	vesicle-associated membrane protein 2 (synaptobrevin 2)	pANT7_cGST
711613	HsxXG014245	91	C12	1040	JUNB		BC004250	jun B proto-oncogene	pANT7_cGST
711615	HsxXG014245	92	D12	344	RPLP2		BC005354	ribosomal protein, large, P2	pANT7_cGST
711616	HsxXG014245	93	E12	830	IMPA1		BC008381	inositol(myo)-1(or 4)-monophosphatase 1	pANT7_cGST
711617	HsxXG014245	94	F12	299	VAMP3		BC007050	vesicle-associated membrane protein 3	pANT7_cGST
711621	HsxXG014245	95	G12	626	ZSCAN31		BC008490	zinc finger and SCAN domain containing 31	pANT7_cGST
	HsxXG014245	96	H12						pANT7_cGST
	HsxXG014246	1	A01						pANT7_cGST
711625	HsxXG014246	2	B01	746	TPI1		BC007086	triosephosphate isomerase 1	pANT7_cGST
711629	HsxXG014246	3	C01	878	RPS2		BC006559	ribosomal protein S2	pANT7_cGST
711632	HsxXG014246	4	D01	440	PPP1R14B		BC014522	protein phosphatase 1, regulatory (inhibitor) subunit 14B	pANT7_cGST
711633	HsxXG014246	5	E01	884	STARD7		BC014274	StAR-related lipid transfer (START) domain containing 7	pANT7_cGST
711634	HsxXG014246	6	F01	668	C17orf59		BC018880	chromosome 17 open reading frame 59	pANT7_cGST
711635	HsxXG014246	7	G01	746	TPI1		BC011611	triosephosphate isomerase 1	pANT7_cGST
711637	HsxXG014246	8	H01	1271	SF3B4		BC013886	splicing factor 3b, subunit 4, 49kDa	pANT7_cGST
711639	HsxXG014246	9	A02	476	UBE2W		BC010900	ubiquitin-conjugating enzyme E2W (putative)	pANT7_cGST
711640	HsxXG014246	10	B02	359	TMEM230		BC009768	transmembrane protein 230	pANT7_cGST

711643	HsxXG014246	11	C02	278	HIGD1A		BC009583	HIG1 hypoxia inducible domain family, member 1A	pANT7_cGST
711644	HsxXG014246	12	D02	959	HNRNPA1		BC009600	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST
711645	HsxXG014246	13	E02	1754	UBE3A		BC009271	ubiquitin protein ligase E3A	pANT7_cGST
711648	HsxXG014246	14	F02	878	RPS2		BC021545	ribosomal protein S2	pANT7_cGST
711649	HsxXG014246	15	G02	884	STARD7		BC012774	StAR-related lipid transfer (START) domain containing 7	pANT7_cGST
711650	HsxXG014246	16	H02	557	SPATC1L		BC009497	spermatogenesis and centriole associated 1-like	pANT7_cGST
711653	HsxXG014246	17	A03	884	STARD7		BC012793	StAR-related lipid transfer (START) domain containing 7	pANT7_cGST
711654	HsxXG014246	18	B03	746	TPI1		BC009329	triosephosphate isomerase 1	pANT7_cGST
711656	HsxXG014246	19	C03	1154	SLC18A1		BC009387	solute carrier family 18 (vesicular monoamine), member 1	pANT7_cGST
711659	HsxXG014246	20	D03	428	H2AFX		BC011694	H2A histone family, member X	pANT7_cGST
711663	HsxXG014246	21	E03	878	RPS2		BC010165	ribosomal protein S2	pANT7_cGST
711664	HsxXG014246	22	F03	884	STARD7		BC014076	StAR-related lipid transfer (START) domain containing 7	pANT7_cGST
711666	HsxXG014246	23	G03	959	HNRNPA1		BC012158	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST
711669	HsxXG014246	24	H03	1691	KRT6A		BC014152	keratin 6A	pANT7_cGST
711671	HsxXG014246	25	A04	443	PRR13		BC014257	proline rich 13	pANT7_cGST
711675	HsxXG014246	26	B04	410	ITGB3BP		BC014385	integrin beta 3 binding protein (beta3-endonexin)	pANT7_cGST

711676	HsxXG014246	27	C04	329	TMEM126B		BC017574	transmembrane protein 126B	pANT7_cGST
711678	HsxXG014246	28	D04	725	NDFIP2		BC021988	Nedd4 family interacting protein 2	pANT7_cGST
711681	HsxXG014246	29	E04	644	ARL6IP4		BC015569	ADP-ribosylation-like factor 6 interacting protein 4	pANT7_cGST
711684	HsxXG014246	30	F04	791	ZNF524		BC014666	zinc finger protein 524	pANT7_cGST
711686	HsxXG014246	31	G04	374	RPL31		BC017343	ribosomal protein L31	pANT7_cGST
711688	HsxXG014246	32	H04	1346	TLE6		BC020206	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)	pANT7_cGST
711690	HsxXG014246	33	A05	575	RNF185		BC009504	ring finger protein 185	pANT7_cGST
711691	HsxXG014246	34	B05	1031	TRIM44		BC024031	tripartite motif containing 44	pANT7_cGST
711692	HsxXG014246	35	C05	1094	FBXL18		BC024256	F-box and leucine-rich repeat protein 18	pANT7_cGST
711693	HsxXG014246	36	D05	878	RPS2		BC023541	ribosomal protein S2	pANT7_cGST
711694	HsxXG014246	37	E05	1577	FUS		BC026062	fused in sarcoma	pANT7_cGST
711695	HsxXG014246	38	F05	374	GFER		BC028348	growth factor, augmenter of liver regeneration	pANT7_cGST
711697	HsxXG014246	39	G05	1505	WDR48		BC037168	WD repeat domain 48	pANT7_cGST
711698	HsxXG014246	40	H05	884	STARD7		BC032106	StAR-related lipid transfer (START) domain containing 7	pANT7_cGST
711699	HsxXG014246	41	A06	878	RPS2		BC032129	ribosomal protein S2	pANT7_cGST
711702	HsxXG014246	42	B06	1139	RBFOX2		BC025281	RNA binding protein, fox-1 homolog (C. elegans) 2	pANT7_cGST
705976	HsxXG014246	43	C06	881	TRIM4		BC025949	tripartite motif containing 4	pANT7_cGST

705978	HsxXG014246	44	D06	356	OSTCP1		BC024224	oligosaccharyltransferase complex subunit pseudogene 1	pANT7_cGST
705979	HsxXG014246	45	E06	398	SZRD1		BC023988	SUZ RNA binding domain containing 1	pANT7_cGST
705982	HsxXG014246	46	F06	1769	KRT5		BC042132	keratin 5	pANT7_cGST
705985	HsxXG014246	47	G06	428	LAGE3		BC062330	L antigen family, member 3	pANT7_cGST
705986	HsxXG014246	48	H06	1079	BLOC1S5-TXNDC5		BC052310	BLOC1S5-TXNDC5 readthrough (non-protein coding)	pANT7_cGST
705987	HsxXG014246	49	A07	569	GPX2		BC005277	glutathione peroxidase 2 (gastrointestinal)	pANT7_cGST
705989	HsxXG014246	50	B07	293	S100A13		BC070291	S100 calcium binding protein A13	pANT7_cGST
705990	HsxXG014246	51	C07	1331	TUBB		BC070326	tubulin, beta class I	pANT7_cGST
705994	HsxXG014246	52	D07	272	UQCRH		BC107703	ubiquinol-cytochrome c reductase hinge protein	pANT7_cGST
705995	HsxXG014246	53	E07	242	NEDD8		BC104664	neural precursor cell expressed, developmentally down-regulated 8	pANT7_cGST
705996	HsxXG014246	54	F07	296	CCL7		BC092436	chemokine (C-C motif) ligand 7	pANT7_cGST
705997	HsxXG014246	55	G07	467	CUTA		BC107751	cutA divalent cation tolerance homolog (E. coli)	pANT7_cGST
705998	HsxXG014246	56	H07	497	PRH2		BC095488	proline-rich protein HaeIII subfamily 2	pANT7_cGST
705999	HsxXG014246	57	A08	386	LLPH		BC107780	LLP homolog, long-term synaptic facilitation (Aplysia)	pANT7_cGST
706000	HsxXG014246	58	B08	875	NME1-NME2		BC107894	NME1-NME2 readthrough	pANT7_cGST

706004	HsxXG014246	59	C08	959	HNRNPA1		BC052296	heterogeneous nuclear ribonucleoprotein A1	pANT7_cGST
706009	HsxXG014246	60	D08	680	PCMT1		BC008748	protein-L-isoaspartate (D-aspartate) O-methyltransferase	pANT7_cGST
706014	HsxXG014246	61	E08	1082	ZBTB37		BC006315	zinc finger and BTB domain containing 37	pANT7_cGST
706016	HsxXG014246	62	F08	1592	PKM		BC007952	pyruvate kinase, muscle	pANT7_cGST
706017	HsxXG014246	63	G08	584	MARCKSL1		BC007904	MARCKS-like 1	pANT7_cGST
706018	HsxXG014246	64	H08	803	PITPNC1		BC007905	phosphatidylinositol transfer protein, cytoplasmic 1	pANT7_cGST
706019	HsxXG014246	65	A09	917	ZNF625		BC007868	zinc finger protein 625	pANT7_cGST
706021	HsxXG014246	66	B09	344	RPLP2		BC007573	ribosomal protein, large, P2	pANT7_cGST
706023	HsxXG014246	67	C09	1325	IFRD2		BC007265	interferon-related developmental regulator 2	pANT7_cGST
706025	HsxXG014246	68	D09	1424	TRIM62		BC007999	tripartite motif containing 62	pANT7_cGST
706026	HsxXG014246	69	E09	878	RPS2		BC008862	ribosomal protein S2	pANT7_cGST
706028	HsxXG014246	70	F09	947	NSMCE4A		BC005212	non-SMC element 4 homolog A (S. cerevisiae)	pANT7_cGST
706033	HsxXG014246	71	G09	512	MBP		BC143350	myelin basic protein	pANT7_cGST
706037	HsxXG014246	72	H09	1217	TPRN		BC143385	taperin	pANT7_cGST
706038	HsxXG014246	73	A10	350	GAGE12B		BC143615	G antigen 12B	pANT7_cGST
706040	HsxXG014246	74	B10	1199	ZNF514		BC074901	zinc finger protein 514	pANT7_cGST
706045	HsxXG014246	75	C10	1160	GALR2		BC074914	galanin receptor 2	pANT7_cGST
706047	HsxXG014246	76	D10	1190	P2RX3		BC074793	purinergic receptor P2X, ligand-gated ion channel, 3	pANT7_cGST
706051	HsxXG014246	77	E10	422	CST4		BC074953	cystatin S	pANT7_cGST

706056	HsxXG014246	78	F10	1634	TCERG1L		BC093639	transcription elongation regulator 1-like	pANT7_cGST
706061	HsxXG014246	79	G10	578	CBLN1		BC093718	cerebellin 1 precursor	pANT7_cGST
706062	HsxXG014246	80	H10	248	PDE6H		BC093740	phosphodiesterase 6H, cGMP-specific, cone, gamma	pANT7_cGST
706064	HsxXG014246	81	A11	605	LIF		BC093735	leukemia inhibitory factor	pANT7_cGST
706068	HsxXG014246	82	B11	1526	SCARB1		BC093732	scavenger receptor class B, member 1	pANT7_cGST
706071	HsxXG014246	83	C11	281	DEFA1		BC093791	defensin, alpha 1	pANT7_cGST
706072	HsxXG014246	84	D11	1598	TBC1D10B		BC093814	TBC1 domain family, member 10B	pANT7_cGST
706073	HsxXG014246	85	E11	293	KRTAP3-3		BC093845	keratin associated protein 3-3	pANT7_cGST
706076	HsxXG014246	86	F11	356	CXCL17		BC093946	chemokine (C-X-C motif) ligand 17	pANT7_cGST
706081	HsxXG014246	87	G11	1184	TRIM10		BC093926	tripartite motif containing 10	pANT7_cGST
706082	HsxXG014246	88	H11	203	OAZ1		BC093652	ornithine decarboxylase antizyme 1	pANT7_cGST
706085	HsxXG014246	89	A12	1910	R3HDM2		BC104995	R3H domain containing 2	pANT7_cGST
706086	HsxXG014246	90	B12	1910	R3HDM2		BC112226	R3H domain containing 2	pANT7_cGST
706088	HsxXG014246	91	C12	296	CCL7		BC112260	chemokine (C-C motif) ligand 7	pANT7_cGST
706092	HsxXG014246	92	D12	1151	TYW1		BC051888	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	pANT7_cGST
706093	HsxXG014246	93	E12	1217	RING1		BC051866	ring finger protein 1	pANT7_cGST
706096	HsxXG014246	94	F12	1172	PLEKHA8P1		BC063575	pleckstrin homology domain containing, family A member 8 pseudogene 1	pANT7_cGST

706097	HsxXG014246	95	G12	1127	GPATCH2		BC063474	G patch domain containing 2	pANT7_cGST
	HsxXG014246	96	H12						pANT7_cGST
	HsxXG014273	1	A01						pANT7_cGST
677091	HsxXG014273	2	B01	2822	ERAP1			endoplasmic reticulum aminopeptidase 1	pANT7_cGST
677093	HsxXG014273	3	C01	2819	XPC			xeroderma pigmentosum, complementation group C	pANT7_cGST
677262	HsxXG014273	4	D01	1964	SRPK1			SRSF protein kinase 1	pANT7_cGST
677280	HsxXG014273	5	E01	1940	CEP72			centrosomal protein 72kDa	pANT7_cGST
677288	HsxXG014273	6	F01	1931	INPP5E			inositol polyphosphate-5-phosphatase, 72 kDa	pANT7_cGST
677348	HsxXG014273	7	G01	671	CRP			C-reactive protein, pentraxin-related	pANT7_cGST
637219	HsxXG014273	8	H01	323	GRO-beta		M36820		pANT7_cGST
637220	HsxXG014273	9	A02	341			D15057		pANT7_cGST
637221	HsxXG014273	10	B02	428			BC034148		pANT7_cGST
637226	HsxXG014273	11	C02	596	NKEFB		L19185		pANT7_cGST
637230	HsxXG014273	12	D02	665			L06895		pANT7_cGST
637236	HsxXG014273	13	E02	938	Ich-1		U13022		pANT7_cGST
637238	HsxXG014273	14	F02	953	IBSP		J05213		pANT7_cGST
637239	HsxXG014273	15	G02	1040			X05908		pANT7_cGST
637246	HsxXG014273	16	H02	1562	OXCT		U62961		pANT7_cGST
637251	HsxXG014273	17	A03	347	MIF		NM_002415		pANT7_cGST
637252	HsxXG014273	18	B03	404	ID2		NM_002166		pANT7_cGST
637254	HsxXG014273	19	C03	575	ARHG		NM_001665		pANT7_cGST
637258	HsxXG014273	20	D03	782	GDB		M36532		pANT7_cGST
637259	HsxXG014273	21	E03	782	DCK		NM_000788		pANT7_cGST
637263	HsxXG014273	22	F03	482	TNNC2		NM_003279		pANT7_cGST

637267	HsxXG014273	23	G03	485	TNNC1		BC030244		pANT7_cGST
637269	HsxXG014273	24	H03	509	EREG		NM_001432		pANT7_cGST
637270	HsxXG014273	25	A04	545	CD160		BC014465		pANT7_cGST
637271	HsxXG014273	26	B04	443	HBB		NM_000518		pANT7_cGST
637276	HsxXG014273	27	C04	1256	BAAT		NM_001701		pANT7_cGST
637280	HsxXG014273	28	D04	635	GDNF		NM_000514		pANT7_cGST
637281	HsxXG014273	29	E04	743	YWHAG		BC020963		pANT7_cGST
637285	HsxXG014273	30	F04	992	GRAP2		BC025692		pANT7_cGST
637288	HsxXG014273	31	G04	857	STAR		BC010550		pANT7_cGST
637293	HsxXG014273	32	H04	803	POMC		NM_000939		pANT7_cGST
637295	HsxXG014273	33	A05	812	VDRIP		NM_014166		pANT7_cGST
637298	HsxXG014273	34	B05	821	HLA-DOB		BC006097		pANT7_cGST
637301	HsxXG014273	35	C05	827	TPSB1		NM_003294		pANT7_cGST
637304	HsxXG014273	36	D05	950	HMOX2		BC002396		pANT7_cGST
637305	HsxXG014273	37	E05	833	RSU1		BC008691		pANT7_cGST
637308	HsxXG014273	38	F05	842	HRY		NM_005524		pANT7_cGST
637312	HsxXG014273	39	G05	596	PRDX2		BC039428		pANT7_cGST
637315	HsxXG014273	40	H05	1133	ACTA1		BC012597		pANT7_cGST
637316	HsxXG014273	41	A06	596	DUSP14		BC004448		pANT7_cGST
637319	HsxXG014273	42	B06	1007	POLB		NM_002690		pANT7_cGST
637324	HsxXG014273	43	C06	389	KCNE1		NM_000219		pANT7_cGST
637327	HsxXG014273	44	D06	1049	CTGF		AY395801		pANT7_cGST
637339	HsxXG014273	45	E06	1148	PRELP		BC032498		pANT7_cGST
637340	HsxXG014273	46	F06	959	GPR55		BC032694		pANT7_cGST
637341	HsxXG014273	47	G06	665	RAB27A		NM_183234		pANT7_cGST
637342	HsxXG014273	48	H06	677			BC060858		pANT7_cGST
637345	HsxXG014273	49	A07	1022	DNAJB1		BC002352		pANT7_cGST
637349	HsxXG014273	50	B07	647			AY113186		pANT7_cGST
637350	HsxXG014273	51	C07	1034	TOB2		BC038957		pANT7_cGST
637351	HsxXG014273	52	D07	608	PTTG1		NM_004219		pANT7_cGST
637352	HsxXG014273	53	E07	611	RAB13		NM_002870		pANT7_cGST

637363	HsxXG014273	54	F07	656	RAB11B		AF498947		pANT7_cGST
637364	HsxXG014273	55	G07	851	MTAP		NM_002451		pANT7_cGST
637372	HsxXG014273	56	H07	395	MIA		NM_006533		pANT7_cGST
637374	HsxXG014273	57	A08	1088	GPR4		NM_005282		pANT7_cGST
637376	HsxXG014273	58	B08	719	PSME2		NM_002818		pANT7_cGST
637383	HsxXG014273	59	C08	617	LTA		BC034729		pANT7_cGST
637384	HsxXG014273	60	D08	812	HOXA5		NM_019102		pANT7_cGST
637385	HsxXG014273	61	E08	815	FOSL1		BC016648		pANT7_cGST
637386	HsxXG014273	62	F08	1355	FARS1		NM_006567		pANT7_cGST
637408	HsxXG014273	63	G08	1016	FOSB		NM_006732		pANT7_cGST
637409	HsxXG014273	64	H08	1058	SH3GL2		NM_003026		pANT7_cGST
637411	HsxXG014273	65	A09	383	FABP1		BC032801		pANT7_cGST
637423	HsxXG014273	66	B09	761	CD151		BC013302		pANT7_cGST
637428	HsxXG014273	67	C09	386	SH2D1A		BC020732		pANT7_cGST
637430	HsxXG014273	68	D09	743	PEX11A		BC009697		pANT7_cGST
637440	HsxXG014273	69	E09	752	TNFSF13		NM_003808		pANT7_cGST
637441	HsxXG014273	70	F09	1052	PLEK		BC018549		pANT7_cGST
637442	HsxXG014273	71	G09	1103	UROD		BC001778		pANT7_cGST
637445	HsxXG014273	72	H09	1112	OPRL1		BC038433		pANT7_cGST
637446	HsxXG014273	73	A10	1121	PEX3		BC015506		pANT7_cGST
637447	HsxXG014273	74	B10	404	NPPB		BC025785		pANT7_cGST
637448	HsxXG014273	75	C10	584	AK1		NM_000476		pANT7_cGST
637453	HsxXG014273	76	D10	632	TNNI3		M64247		pANT7_cGST
637454	HsxXG014273	77	E10	638	DTYMK		BC001827		pANT7_cGST
637461	HsxXG014273	78	F10	797	AQP5		BC032946		pANT7_cGST
637462	HsxXG014273	79	G10	815	AQP2		BC042496		pANT7_cGST
637469	HsxXG014273	80	H10	563	GDB		J04760		pANT7_cGST
637472	HsxXG014273	81	A11	497	DSTN		BC009477		pANT7_cGST
637473	HsxXG014273	82	B11	500	MYL2		BC031006		pANT7_cGST
637477	HsxXG014273	83	C11	1127	hsp-D		X65018		pANT7_cGST
637479	HsxXG014273	84	D11	464	ID1		NM_002165		pANT7_cGST

637480	HsxXG014273	85	E11	1406	IL6R		NM_000565		pANT7_cGST
637481	HsxXG014273	86	F11	1409	ETS2		NM_005239		pANT7_cGST
637483	HsxXG014273	87	G11	1703	TGFBR2		NM_003242		pANT7_cGST
637484	HsxXG014273	88	H11	953	NFKBIA		NM_020529		pANT7_cGST
637488	HsxXG014273	89	A12	680	GJB2		NM_004004		pANT7_cGST
637490	HsxXG014273	90	B12	1367	TNFRSF1A		NM_001065		pANT7_cGST
637493	HsxXG014273	91	C12	446	GRP		NM_002091		pANT7_cGST
637496	HsxXG014273	92	D12	887	SULT1A1		NM_001055		pANT7_cGST
637497	HsxXG014273	93	E12	1820	ARAF1		NM_001654		pANT7_cGST
637498	HsxXG014273	94	F12	866	IFI35		BC001356		pANT7_cGST
637507	HsxXG014273	95	G12	971	CCNH		NM_001239		pANT7_cGST
	HsxXG014273	96	H12						pANT7_cGST
	HsxXG014274	1	A01						pANT7_cGST
637509	HsxXG014274	2	B01	293	COX6A2		NM_005205		pANT7_cGST
637512	HsxXG014274	3	C01	392	PEA15		NM_003768		pANT7_cGST
637514	HsxXG014274	4	D01	1295	SGK		NM_005627		pANT7_cGST
637520	HsxXG014274	5	E01	1364	BMP5		NM_021073		pANT7_cGST
637525	HsxXG014274	6	F01	1064	WNT11		NM_004626		pANT7_cGST
637531	HsxXG014274	7	G01	323	GRO1		NM_001511		pANT7_cGST
637532	HsxXG014274	8	H01	344	SCYB6		NM_002993		pANT7_cGST
637541	HsxXG014274	9	A02	569	IFNA21		NM_002175		pANT7_cGST
634027	HsxXG014274	10	B02	1043	MAP2K		BC032478.1		pANT7_cGST
634033	HsxXG014274	11	C02	2663			BC033004.1		pANT7_cGST
634035	HsxXG014274	12	D02	2843	MAP3K1		BC035576.1		pANT7_cGST
634037	HsxXG014274	13	E02	1247	CSNK1G2		BC020972.1		pANT7_cGST
634038	HsxXG014274	14	F02	2696	JIK		BC002756.1		pANT7_cGST
634046	HsxXG014274	15	G02	1574	G		BC037549.1		pANT7_cGST
634050	HsxXG014274	16	H02	1409	PFKFB		BC010269.1		pANT7_cGST
634052	HsxXG014274	17	A03	1775	PAK4		BC011368.1		pANT7_cGST
634053	HsxXG014274	18	B03	1811			BC011392.1		pANT7_cGST
634054	HsxXG014274	19	C03	1811	PLK		BC014846.1		pANT7_cGST

634055	HsxXG014274	20	D03	1631	CHEK2		BC004207.1		pANT7_cGST
634056	HsxXG014274	21	E03	911	CDK4		BC003644.1		pANT7_cGST
634059	HsxXG014274	22	F03	2201	RPS6KA2		BC002363.1		pANT7_cGST
634060	HsxXG014274	23	G03	1202	MAP2K2		BC000471.1		pANT7_cGST
634061	HsxXG014274	24	H03	1619	LCK		BC013200.1		pANT7_cGST
634064	HsxXG014274	25	A04	1256	ALS2CR2		BC008302.1		pANT7_cGST
634066	HsxXG014274	26	B04	1301	STK11		BC007981.1		pANT7_cGST
634067	HsxXG014274	27	C04	1421			BC016695.1		pANT7_cGST
634068	HsxXG014274	28	D04	3020	PTK		BC035404.2		pANT7_cGST
634069	HsxXG014274	29	E04	1985			BC035782.1		pANT7_cGST
634074	HsxXG014274	30	F04	1280			BC038295.1		pANT7_cGST
634080	HsxXG014274	31	G04	584	AK1		BC001116.1		pANT7_cGST
634082	HsxXG014274	32	H04	956	PRPS1		BC001605.1		pANT7_cGST
634086	HsxXG014274	33	A05	2066	SRPK		BC035214.1		pANT7_cGST
634088	HsxXG014274	34	B05	1436	CAMK2		BC032784.1		pANT7_cGST
634091	HsxXG014274	35	C05	2159	PAK		BC024179.1		pANT7_cGST
634095	HsxXG014274	36	D05	896	CDK2		BC003065.1		pANT7_cGST
634096	HsxXG014274	37	E05	1037	ADK		BC003568.1		pANT7_cGST
634097	HsxXG014274	38	F05	1778			BC014270.1		pANT7_cGST
634098	HsxXG014274	39	G05	1055	PRKAC		BC039888.1		pANT7_cGST
634099	HsxXG014274	40	H05	1253	CKMT1		BC001926.1		pANT7_cGST
634101	HsxXG014274	41	A06	1964	SPHK2		BC006161.1		pANT7_cGST
634102	HsxXG014274	42	B06	1250	CSNK1E		BC006490.1		pANT7_cGST
634104	HsxXG014274	43	C06	1139			BC013992.1		pANT7_cGST
634105	HsxXG014274	44	D06	686			BC014961.1		pANT7_cGST
634106	HsxXG014274	45	E06	3563			BC014243.1		pANT7_cGST
634114	HsxXG014274	46	F06	584	NM23-H6		BC001808.1		pANT7_cGST
634119	HsxXG014274	47	G06	1235	PDK		BC040239.1		pANT7_cGST
634124	HsxXG014274	48	H06	1103			BC015741.1		pANT7_cGST
634134	HsxXG014274	49	A07	1190	MVK		BC016140.1		pANT7_cGST
634136	HsxXG014274	50	B07	1220	PHKG2		BC002541.1		pANT7_cGST

634139	HsxXG014274	51	C07	2270	MLH1		BC006850.1		pANT7_cGST
634144	HsxXG014274	52	D07	1583			BC034044.1		pANT7_cGST
634155	HsxXG014274	53	E07	1562	CAMKK		BC031647.1		pANT7_cGST
634161	HsxXG014274	54	F07	1598			BC028383.1		pANT7_cGST
634165	HsxXG014274	55	G07	1607	NRBP		BC001221.1		pANT7_cGST
634167	HsxXG014274	56	H07	3707			BC014036.1		pANT7_cGST
634172	HsxXG014274	57	A08	2930	EPHA		BC037166.2		pANT7_cGST
634173	HsxXG014274	58	B08	1724	PKL		BC025737.1		pANT7_cGST
634175	HsxXG014274	59	C08	2684	AX		BC032229.1		pANT7_cGST
634176	HsxXG014274	60	D08	1310	PDK		BC039158.1		pANT7_cGST
634177	HsxXG014274	61	E08	2462	FGFR		BC018128.1		pANT7_cGST
634178	HsxXG014274	62	F08	1661	GK		BC029820.1		pANT7_cGST
634183	HsxXG014274	63	G08	2045	PAK		BC035596.1		pANT7_cGST
634184	HsxXG014274	64	H08	1649			BC030587.1		pANT7_cGST
634185	HsxXG014274	65	A09	2051			BC037268.1		pANT7_cGST
634188	HsxXG014274	66	B09	1295	PLAU		BC013575.1		pANT7_cGST
634189	HsxXG014274	67	C09	1397	GCK		BC001890.1		pANT7_cGST
634190	HsxXG014274	68	D09	1145	CKM		BC007462.1		pANT7_cGST
645505	HsxXG014274	69	E09	815	PITPNB		CR456541		pANT7_cGST
645523	HsxXG014274	70	F09	923	SLC25A17		CR456577		pANT7_cGST
645538	HsxXG014274	71	G09	635	TIMP3		CR456593		pANT7_cGST
645553	HsxXG014274	72	H09	380	SNRPD3		CR456583		pANT7_cGST
645573	HsxXG014274	73	A10	725	PDGFB		CR456538		pANT7_cGST
645579	HsxXG014274	74	B10	1118	Em		CT841507		pANT7_cGST
645602	HsxXG014274	75	C10	2204	MCM5		CR456517		pANT7_cGST
645610	HsxXG014274	76	D10	965	MFNG		CR456518		pANT7_cGST
645617	HsxXG014274	77	E10	1337	KCNJ4		CR456507		pANT7_cGST
645618	HsxXG014274	78	F10	1601	MGAT3		CR456519		pANT7_cGST
645631	HsxXG014274	79	G10	992	GRAP2		CR456498		pANT7_cGST
645636	HsxXG014274	80	H10	1271	Em		CR456350		pANT7_cGST
645647	HsxXG014274	81	A11	734	GSTT2		CR456500		pANT7_cGST

645663	HsxXG014274	82	B11	2162	GTSE1		CT841519		pANT7_cGST
645672	HsxXG014274	83	C11	5882	MYH9		CR456526		pANT7_cGST
645702	HsxXG014274	84	D11	614	dJ347H13.5		CR456459		pANT7_cGST
656754	HsxXG014274	85	E11	1358			BC009395.1		pANT7_cGST
656756	HsxXG014274	86	F11	1568			BC014020.1		pANT7_cGST
656757	HsxXG014274	87	G11	1787			BC011913.1		pANT7_cGST
656758	HsxXG014274	88	H11	2408			BC011847.1		pANT7_cGST
656760	HsxXG014274	89	A12	413			BC010173.1		pANT7_cGST
656762	HsxXG014274	90	B12	764			BC011678.1		pANT7_cGST
656763	HsxXG014274	91	C12	803	APOA1		BC005380.1		pANT7_cGST
656767	HsxXG014274	92	D12	1220			BC009585.1		pANT7_cGST
656771	HsxXG014274	93	E12	1598	ZBRK1		BC009921.1		pANT7_cGST
656772	HsxXG014274	94	F12	2426			BC014081.1		pANT7_cGST
656773	HsxXG014274	95	G12	287			BC008450.1		pANT7_cGST
	HsxXG014274	96	H12						pANT7_cGST
	HsxXG014275	1	A01						pANT7_cGST
656774	HsxXG014275	2	B01	428			BC009363.1		pANT7_cGST
656775	HsxXG014275	3	C01	545	ARL1		BC007000.1		pANT7_cGST
656777	HsxXG014275	4	D01	767			BC014460.1		pANT7_cGST
656781	HsxXG014275	5	E01	1232	SIGIRR		BC003591.1		pANT7_cGST
656782	HsxXG014275	6	F01	1283			BC009960.1		pANT7_cGST
656788	HsxXG014275	7	G01	317	HCS		BC005299.1		pANT7_cGST
656791	HsxXG014275	8	H01	776			BC014006.1		pANT7_cGST
656792	HsxXG014275	9	A02	812	HSPC126		BC005189.1		pANT7_cGST
656793	HsxXG014275	10	B02	1016	MDH2		BC001917.1		pANT7_cGST
656797	HsxXG014275	11	C02	1289			BC011899.1		pANT7_cGST
656798	HsxXG014275	12	D02	1418	SLC38A5		BC019246.1		pANT7_cGST
656799	HsxXG014275	13	E02	1502			BC015628.1		pANT7_cGST
656801	HsxXG014275	14	F02	1961	TRIM32		BC003154.1		pANT7_cGST
656802	HsxXG014275	15	G02	2804	PCDHGC3		BC019299.1		pANT7_cGST
656803	HsxXG014275	16	H02	326			BC011932.1		pANT7_cGST

656804	HsxXG014275	17	A03	479	SDHD		BC005263.1		pANT7_cGST
656806	HsxXG014275	18	B03	719			BC011909.1		pANT7_cGST
656807	HsxXG014275	19	C03	782			BC009956.1		pANT7_cGST
656808	HsxXG014275	20	D03	839	FHL2		BC014397.1		pANT7_cGST
656814	HsxXG014275	21	E03	1517	GRP58		BC014433.1		pANT7_cGST
656820	HsxXG014275	22	F03	722	GSTT1		BC007065.1		pANT7_cGST
656821	HsxXG014275	23	G03	788			BC015739.1		pANT7_cGST
656822	HsxXG014275	24	H03	845			BC017502.1		pANT7_cGST
656824	HsxXG014275	25	A04	1091	RFC4		BC017452.1		pANT7_cGST
656826	HsxXG014275	26	B04	1259	FDP		BC010004.1		pANT7_cGST
656827	HsxXG014275	27	C04	1355			BC015752.1		pANT7_cGST
656828	HsxXG014275	28	D04	1433			BC015625.1		pANT7_cGST
656832	HsxXG014275	29	E04	4331			BC017232.1		pANT7_cGST
656835	HsxXG014275	30	F04	650	RAB11A		BC013348.1		pANT7_cGST
656837	HsxXG014275	31	G04	788	KLK1		BC005313.1		pANT7_cGST
656838	HsxXG014275	32	H04	845	DC8		BC007067.1		pANT7_cGST
656841	HsxXG014275	33	A05	1436	VTN		BC005046.1		pANT7_cGST
656842	HsxXG014275	34	B05	1550	DHCR24		BC004375.1		pANT7_cGST
656843	HsxXG014275	35	C05	1709	GGT		BC025927.1		pANT7_cGST
656846	HsxXG014275	36	D05	458			BC010175.1		pANT7_cGST
635812	HsxXG014275	37	E05	722			BC018991.1		pANT7_cGST
635838	HsxXG014275	38	F05	341	SUI1		BC005118.1		pANT7_cGST
635842	HsxXG014275	39	G05	926	COPE		BC003155.1		pANT7_cGST
635843	HsxXG014275	40	H05	944	APG		BC024221.2		pANT7_cGST
635846	HsxXG014275	41	A06	1220	PYGO		BC032099.2		pANT7_cGST
635853	HsxXG014275	42	B06	407			BC009407.1		pANT7_cGST
635854	HsxXG014275	43	C06	533			BC018970.1		pANT7_cGST
635855	HsxXG014275	44	D06	713	TGIF		BC012816.2		pANT7_cGST
635860	HsxXG014275	45	E06	1142	FOS		BC004490.1		pANT7_cGST
635864	HsxXG014275	46	F06	1757			BC011885.1		pANT7_cGST
635865	HsxXG014275	47	G06	2123	MMP9		BC006093.1		pANT7_cGST

635883	HsxXG014275	48	H06	554	DUSP2		BC022847.2		pANT7_cGST
635906	HsxXG014275	49	A07	2405	PRDM		BC035581.1		pANT7_cGST
635907	HsxXG014275	50	B07	2876			BC039245.1		pANT7_cGST
635910	HsxXG014275	51	C07	575	CDC42		BC003682.1		pANT7_cGST
635913	HsxXG014275	52	D07	896			BC037273.1		pANT7_cGST
635915	HsxXG014275	53	E07	1133	GNA1		BC036756.1		pANT7_cGST
635916	HsxXG014275	54	F07	1211	STK15		BC001280.1		pANT7_cGST
635938	HsxXG014275	55	G07	581	AP3S1		BC000804.1		pANT7_cGST
635940	HsxXG014275	56	H07	1013			BC028723.1		pANT7_cGST
635943	HsxXG014275	57	A08	1268	GFI		BC032751.1		pANT7_cGST
635947	HsxXG014275	58	B08	2009			BC036518.1		pANT7_cGST
635951	HsxXG014275	59	C08	584			BC000802.1		pANT7_cGST
635953	HsxXG014275	60	D08	797			BC032946.1		pANT7_cGST
635954	HsxXG014275	61	E08	1028	HAN11		BC001264.1		pANT7_cGST
635956	HsxXG014275	62	F08	1154			BC036657.1		pANT7_cGST
635961	HsxXG014275	63	G08	1868	GALNT		BC035822.1		pANT7_cGST
635962	HsxXG014275	64	H08	2198	LS		BC035638.1		pANT7_cGST
635965	HsxXG014275	65	A09	494	DU		BC033645.1		pANT7_cGST
635970	HsxXG014275	66	B09	1106	SH3GL1		BC001270.1		pANT7_cGST
635973	HsxXG014275	67	C09	1226	ACY1		BC000545.1		pANT7_cGST
635974	HsxXG014275	68	D09	1322			BC011655.1		pANT7_cGST
635975	HsxXG014275	69	E09	1370	DDOST		BC002594.1		pANT7_cGST
635976	HsxXG014275	70	F09	155	RPL39		BC001019.1		pANT7_cGST
635980	HsxXG014275	71	G09	755			BC009566.1		pANT7_cGST
635982	HsxXG014275	72	H09	926	GPSN2		BC002425.1		pANT7_cGST
635983	HsxXG014275	73	A10	1076			BC013313.1		pANT7_cGST
635984	HsxXG014275	74	B10	1106	BGN		BC002416.1		pANT7_cGST
635985	HsxXG014275	75	C10	1256			BC009567.1		pANT7_cGST
635986	HsxXG014275	76	D10	1331			BC021195.1		pANT7_cGST
635991	HsxXG014275	77	E10	227			BC015563.1		pANT7_cGST
635992	HsxXG014275	78	F10	413	NDUFB7		BC002595.1		pANT7_cGST

635994	HsxXG014275	79	G10	764	PSME3		BC001423.1		pANT7_cGST
635996	HsxXG014275	80	H10	926			BC011645.1		pANT7_cGST
635997	HsxXG014275	81	A11	986	P2RY6		BC000571.1		pANT7_cGST
635998	HsxXG014275	82	B11	1076	TKT		BC002578.1		pANT7_cGST
636001	HsxXG014275	83	C11	1343			BC018905.1		pANT7_cGST
636002	HsxXG014275	84	D11	1430	MMP10		BC002591.1		pANT7_cGST
636004	HsxXG014275	85	E11	1982	MMP2		BC002576.1		pANT7_cGST
636006	HsxXG014275	86	F11	260	COX6B		BC001015.1		pANT7_cGST
636009	HsxXG014275	87	G11	767			BC009944.1		pANT7_cGST
636010	HsxXG014275	88	H11	878			BC011616.1		pANT7_cGST
636013	HsxXG014275	89	A12	1094	OAS1		BC000562.1		pANT7_cGST
636014	HsxXG014275	90	B12	1127			BC011634.1		pANT7_cGST
636016	HsxXG014275	91	C12	1349	PCOLCE		BC000574.1		pANT7_cGST
636017	HsxXG014275	92	D12	1433			BC009748.1		pANT7_cGST
636018	HsxXG014275	93	E12	2078	SLC21A11		BC000585.1		pANT7_cGST
636024	HsxXG014275	94	F12	941	MGLL		BC000551.1		pANT7_cGST
636025	HsxXG014275	95	G12	1022	GNB3		BC002454.1		pANT7_cGST
	HsxXG014275	96	H12						pANT7_cGST
	HsxXG014276	1	A01						pANT7_cGST
636028	HsxXG014276	2	B01	1277	F2R		BC002464.1		pANT7_cGST
636029	HsxXG014276	3	C01	1355	TUBG1		BC000619.1		pANT7_cGST
636032	HsxXG014276	4	D01	2573	TTK		BC000633.1		pANT7_cGST
636034	HsxXG014276	5	E01	446	RAMP1		BC000548.1		pANT7_cGST
636036	HsxXG014276	6	F01	686			BC021214.1		pANT7_cGST
636037	HsxXG014276	7	G01	797	UROS		BC002573.1		pANT7_cGST
636043	HsxXG014276	8	H01	1286	HDAC3		BC000614.1		pANT7_cGST
636051	HsxXG014276	9	A02	734	QDPR		BC000576.1		pANT7_cGST
636052	HsxXG014276	10	B02	827	RRP40		BC002437.1		pANT7_cGST
636054	HsxXG014276	11	C02	956			BC013973.1		pANT7_cGST
636056	HsxXG014276	12	D02	1337	EIF3S6		BC000734.1		pANT7_cGST
636060	HsxXG014276	13	E02	2294	BF		BC004143.1		pANT7_cGST

636065	HsxXG014276	14	F02	650	PPIB		BC001125.1		pANT7_cGST
636066	HsxXG014276	15	G02	785			BC012106.1		pANT7_cGST
636072	HsxXG014276	16	H02	1352	PAX8		BC001060.1		pANT7_cGST
636078	HsxXG014276	17	A03	440	PPIL		BC030142.2		pANT7_cGST
636082	HsxXG014276	18	B03	866	HMOX1		BC001491.1		pANT7_cGST
636087	HsxXG014276	19	C03	1505			BC001692.1		pANT7_cGST
636133	HsxXG014276	20	D03	986	MSI2		BC001526.1		pANT7_cGST
636149	HsxXG014276	21	E03	1307	ORC5		BC023652.2		pANT7_cGST
636152	HsxXG014276	22	F03	1871	ABCF2		BC001661.1		pANT7_cGST
636155	HsxXG014276	23	G03	2807	MTHFD1		BC009806.1		pANT7_cGST
636156	HsxXG014276	24	H03	407	LGALS1		BC001693.1		pANT7_cGST
636163	HsxXG014276	25	A04	1205	TNFRSF11		BC030155.2		pANT7_cGST
636166	HsxXG014276	26	B04	1907			BC012355.1		pANT7_cGST
636169	HsxXG014276	27	C04	416	CRABP2		BC001109.1		pANT7_cGST
636172	HsxXG014276	28	D04	959	OR2C		BC030717.1		pANT7_cGST
636176	HsxXG014276	29	E04	1688	PLAT		BC007231.1		pANT7_cGST
636178	HsxXG014276	30	F04	2159			BC013375.1		pANT7_cGST
636179	HsxXG014276	31	G04	203	POLR2L		BC005903.1		pANT7_cGST
636180	HsxXG014276	32	H04	431	ETV		BC022868.1		pANT7_cGST
636181	HsxXG014276	33	A05	509	COX4I1		BC008704.1		pANT7_cGST
636182	HsxXG014276	34	B05	581	ARHC		BC007245.1		pANT7_cGST
636183	HsxXG014276	35	C05	659	HSPC177		BC006974.1		pANT7_cGST
636186	HsxXG014276	36	D05	1028	P2RY1		BC017898.1		pANT7_cGST
636095	HsxXG014276	37	E05	1343	TEAD2		BC007556.1		pANT7_cGST
636098	HsxXG014276	38	F05	1691			BC007581.1		pANT7_cGST
636099	HsxXG014276	39	G05	1910			BC015958.1		pANT7_cGST
636102	HsxXG014276	40	H05	434	PLA2G2A		BC005919.1		pANT7_cGST
636103	HsxXG014276	41	A06	509			BC012731.1		pANT7_cGST
636104	HsxXG014276	42	B06	599	PRDX1		BC007063.1		pANT7_cGST
636108	HsxXG014276	43	C06	1280	INHBA		BC007858.1		pANT7_cGST
636111	HsxXG014276	44	D06	1532			BC010423.1		pANT7_cGST

636112	HsxXG014276	45	E06	1763	MGC15548		BC007263.1		pANT7_cGST
636114	HsxXG014276	46	F06	2567	HCNP		BC007208.1		pANT7_cGST
636116	HsxXG014276	47	G06	443	HBB		BC007075.1		pANT7_cGST
636118	HsxXG014276	48	H06	734	CKAP1		BC005969.1		pANT7_cGST
636119	HsxXG014276	49	A07	851	VDAC1		BC008482.1		pANT7_cGST
636120	HsxXG014276	50	B07	911	STUB1		BC007545.1		pANT7_cGST
636124	HsxXG014276	51	C07	1388	GTF2H4		BC004935.1		pANT7_cGST
636126	HsxXG014276	52	D07	1535	AMY2A		BC007060.1		pANT7_cGST
636128	HsxXG014276	53	E07	2018	CAPN10		BC004260.1		pANT7_cGST
636190	HsxXG014276	54	F07	605			BC009200.1		pANT7_cGST
636192	HsxXG014276	55	G07	851	GJB2		BC002805.1		pANT7_cGST
636193	HsxXG014276	56	H07	923	HSPC228		BC006989.1		pANT7_cGST
636194	HsxXG014276	57	A08	1064	CA1		BC023981.1		pANT7_cGST
636195	HsxXG014276	58	B08	1262	KREMEN2		BC003533.1		pANT7_cGST
636196	HsxXG014276	59	C08	1391	UBE1		BC022853.1		pANT7_cGST
636202	HsxXG014276	60	D08	377			BC018634.1		pANT7_cGST
636205	HsxXG014276	61	E08	623	NFYB		BC005317.1		pANT7_cGST
636206	HsxXG014276	62	F08	854	HOXB13		BC007092.1		pANT7_cGST
636207	HsxXG014276	63	G08	935			BC009196.1		pANT7_cGST
636210	HsxXG014276	64	H08	1316	NOT56L		BC002839.1		pANT7_cGST
636211	HsxXG014276	65	A09	1466			BC007294.1		pANT7_cGST
636212	HsxXG014276	66	B09	1616			BC007580.1		pANT7_cGST
636214	HsxXG014276	67	C09	2102	MYBL2		BC007585.1		pANT7_cGST
636215	HsxXG014276	68	D09	3797	PLCG2		BC007565.1		pANT7_cGST
636221	HsxXG014276	69	E09	1184			BC009828.1		pANT7_cGST
636222	HsxXG014276	70	F09	1229	ARRB2		BC007427.1		pANT7_cGST
636223	HsxXG014276	71	G09	1394			BC015645.1		pANT7_cGST
636225	HsxXG014276	72	H09	1682	KNS2		BC008881.1		pANT7_cGST
636231	HsxXG014276	73	A10	728	MYF		BC017834.1		pANT7_cGST
636233	HsxXG014276	74	B10	953	MC1R		BC007856.1		pANT7_cGST
636234	HsxXG014276	75	C10	1121			BC009861.1		pANT7_cGST

636237	HsxXG014276	76	D10	1424	GSS		BC007927.1		pANT7_cGST
636241	HsxXG014276	77	E10	230	PKI		BC022265.2		pANT7_cGST
636245	HsxXG014276	78	F10	749			BC007812.1		pANT7_cGST
636247	HsxXG014276	79	G10	977			BC009483.1		pANT7_cGST
636250	HsxXG014276	80	H10	1199	CASQ		BC022288.1		pANT7_cGST
636255	HsxXG014276	81	A11	2144			BC008751.1		pANT7_cGST
636257	HsxXG014276	82	B11	287			BC009192.1		pANT7_cGST
636260	HsxXG014276	83	C11	638	BOK		BC006203.1		pANT7_cGST
636268	HsxXG014276	84	D11	1778	ATIC		BC008879.1		pANT7_cGST
636274	HsxXG014276	85	E11	863	SLC25A10		BC007355.1		pANT7_cGST
636275	HsxXG014276	86	F11	1055	ATP6V0D1		BC008861.1		pANT7_cGST
636277	HsxXG014276	87	G11	1175	RBMX		BC007435.1		pANT7_cGST
636278	HsxXG014276	88	H11	1220	SERPINA5		BC008915.1		pANT7_cGST
657961	HsxXG014276	89	A12	1184			BC021161.1		pANT7_cGST
657967	HsxXG014276	90	B12	377			BC017112.1		pANT7_cGST
657973	HsxXG014276	91	C12	1055	ATF4		BC008090.1		pANT7_cGST
657974	HsxXG014276	92	D12	1145	PRKAR1		BC036285.1		pANT7_cGST
657978	HsxXG014276	93	E12	1562	OXCT		BC009001.1		pANT7_cGST
657984	HsxXG014276	94	F12	644	KDELR3		BC001277.1		pANT7_cGST
657986	HsxXG014276	95	G12	956	APEX		BC008145.1		pANT7_cGST
	HsxXG014276	96	H12						pANT7_cGST
	HsxXG014277	1	A01						pANT7_cGST
657987	HsxXG014277	2	B01	1040	SAE1		BC018271.1		pANT7_cGST
657988	HsxXG014277	3	C01	1148	PPM1		BC026691.1		pANT7_cGST
657989	HsxXG014277	4	D01	1250	PSTPIP1		BC008602.1		pANT7_cGST
658000	HsxXG014277	5	E01	983	CACNG		BC034532.1		pANT7_cGST
657947	HsxXG014277	6	F01	1172	ESAM		BC016868.1		pANT7_cGST
657908	HsxXG014277	7	G01	1280	IHPK		BC019694.1		pANT7_cGST
657909	HsxXG014277	8	H01	1406	TNFRSF10A		BC012866.1		pANT7_cGST
657911	HsxXG014277	9	A02	1670	GPC		BC017166.1		pANT7_cGST
657913	HsxXG014277	10	B02	428	HBA2		BC008572.1		pANT7_cGST

657929	HsxXG014277	11	C02	671	DNAJB		BC028912.1		pANT7_cGST
657936	HsxXG014277	12	D02	1418	EIF2S		BC019906.1		pANT7_cGST
636381	HsxXG014277	13	E02	587	PGRMC		BC034238.1		pANT7_cGST
636383	HsxXG014277	14	F02	680	GJB2		BC017048.1		pANT7_cGST
636384	HsxXG014277	15	G02	833	TNFRSF5		BC012419.1		pANT7_cGST
636390	HsxXG014277	16	H02	1808	SLC13A		BC035966.1		pANT7_cGST
636391	HsxXG014277	17	A03	1973	EDE		BC019088.1		pANT7_cGST
636392	HsxXG014277	18	B03	2381	SF3A1		BC007684.1		pANT7_cGST
636394	HsxXG014277	19	C03	497	PPIA		BC000689.1		pANT7_cGST
636399	HsxXG014277	20	D03	1124	TRAM		BC000687.1		pANT7_cGST
636400	HsxXG014277	21	E03	1202			BC017305.1		pANT7_cGST
636401	HsxXG014277	22	F03	1253			BC021288.1		pANT7_cGST
636402	HsxXG014277	23	G03	1313			BC019094.1		pANT7_cGST
636403	HsxXG014277	24	H03	1451	KRT8		BC000654.1		pANT7_cGST
636405	HsxXG014277	25	A04	1820	ARAF1		BC002466.1		pANT7_cGST
636407	HsxXG014277	26	B04	2582			BC017282.1		pANT7_cGST
636408	HsxXG014277	27	C04	410	H3F3		BC029405.1		pANT7_cGST
636409	HsxXG014277	28	D04	659	PIG		BC029408.1		pANT7_cGST
636410	HsxXG014277	29	E04	998	DYT1		BC000674.1		pANT7_cGST
636411	HsxXG014277	30	F04	1091	ADA		BC007678.1		pANT7_cGST
636412	HsxXG014277	31	G04	1130	ACTR1A		BC000693.1		pANT7_cGST
636413	HsxXG014277	32	H04	1274	AMSH		BC007682.1		pANT7_cGST
636419	HsxXG014277	33	A05	437			BC017360.1		pANT7_cGST
636420	HsxXG014277	34	B05	575			BC014261.1		pANT7_cGST
636422	HsxXG014277	35	C05	815	ICAM		BC029364.1		pANT7_cGST
636424	HsxXG014277	36	D05	1094	GDF		BC030959.1		pANT7_cGST
636425	HsxXG014277	37	E05	1139			BC017292.1		pANT7_cGST
636431	HsxXG014277	38	F05	3323	POLD1		BC008800.1		pANT7_cGST
636438	HsxXG014277	39	G05	1160			BC019035.1		pANT7_cGST

Table 2. Mean and SD (expressed in arbitrary units (a.u.)) of the immunoreactivity levels against all the proteins expressed in the array for the incident and not-incident group

	Incident group		**Not-Inciden group**	
Protein	**Mean**	**SD**	**Mean**	**SD**
NUP210	0.21	0.08	0.23	0.07
SETD3	0.28	0.07	0.32	0.08
SULF1	1.66	0.76	1.88	0.71
MEPCE	0.49	0.22	0.72	0.26
CD22	1.69	0.44	1.58	0.71
PIGZ	0.59	0.18	0.55	0.25
ELMOD1	0.08	0.05	0.12	0.08
STK32A	1.11	0.22	0.99	0.12
SPATA6L	1.45	0.28	1.46	0.22
ZNF816-ZNF321P	2.06	0.43	2.07	0.33
TNFSF12-TNFSF13	1.90	0.51	1.89	0.40
CARKD	1.92	0.55	1.81	0.41
NUP214	0.37	0.29	0.24	0.12
LOC100132705	0.46	0.11	0.38	0.13
KIAA1324	0.14	0.05	0.16	0.12
MRPS35	2.19	0.53	1.88	0.83
DDX54	0.90	0.31	0.82	0.38
GH1	0.77	0.30	0.72	0.41
NR0B2	2.03	0.58	1.85	0.81
EDEM2	0.53	0.20	0.45	0.28
RPS10-NUDT3	1.92	0.38	1.75	0.33

ATP1A4	1.53	0.25	1.47	0.36
ARMCX4	2.29	0.63	1.99	0.40
A1BG	1.66	0.32	1.39	0.49
GYS1	0.47	0.11	0.36	0.13
ZDHHC19	0.46	0.20	0.68	0.27
PPP1R14B	1.46	0.34	1.88	0.80
SF3B4	2.33	0.78	2.27	0.91
GIGYF2	1.13	0.27	1.03	0.36
BLOC1S1	0.30	0.15	0.35	0.20
CTAG1A	1.60	0.91	2.12	0.82
PF4V1	1.80	0.57	2.05	0.88
MED22	0.17	0.10	0.36	0.28
STEAP4	1.71	0.43	1.63	0.89
TUBB	0.11	0.08	0.08	0.07
MEF2BNB	0.72	0.26	0.58	0.18
BOLA2	0.21	0.19	0.20	0.17
COL10A1	0.78	0.42	0.63	0.38
PRH2	2.30	0.74	2.38	0.88
TTK	1.03	0.34	0.97	0.36
EIF4H	1.32	0.33	1.39	0.23
HDAC3	1.76	0.50	1.66	0.24
STUB1	1.63	0.34	1.56	0.15
EFHD2	0.21	0.09	0.14	0.09
GPX2	0.14	0.11	0.15	0.11
TOMM22	1.27	0.29	1.18	0.35
CTSG	0.20	0.09	0.20	0.11
IL13RA1	1.06	0.25	0.98	0.36
PGLS	1.68	0.49	1.44	0.29

DSE	0.94	0.16	0.84	0.40
CUTA	0.09	0.05	0.14	0.11
TUBG1	2.19	0.43	2.08	0.61
RAMP1	1.47	0.31	1.46	0.34
UROS	1.69	0.40	1.59	0.22
VDAC1	1.63	0.35	1.62	0.24
HYI	0.20	0.09	0.09	0.09
INTS4	0.20	0.10	0.10	0.13
ARL1	1.98	0.45	1.81	0.24
SIGIRR	2.44	0.63	2.22	0.44
CYCS	1.54	0.38	1.42	0.35
PRDM4	2.84	0.90	2.64	0.63
AMY2A	2.83	1.18	3.44	1.61
ARHGDIB	3.63	0.68	3.53	1.11
VTA1	1.99	0.32	1.95	0.23
PSMC3	1.24	0.31	1.27	0.41
RPS16	1.77	0.35	1.82	0.22
HSP90AB1	1.92	0.40	1.96	0.49
OGN	2.14	0.43	2.18	0.31
AURKA	0.16	0.05	0.16	0.10
CSNK1A1L	0.49	0.16	0.49	0.31
ALB	1.21	0.26	1.12	0.36
PCNA	1.64	0.30	1.63	0.37
GNB2L1	1.10	0.23	0.98	0.23
ATP5G3	1.49	0.30	1.39	0.31
GTF2H4	2.10	0.26	2.06	1.11
CAPN10	4.44	0.63	3.78	1.33
RASSF5	2.22	0.62	2.15	0.18

MKNK1	1.83	0.46	1.81	0.38
WNT7A	0.99	0.20	0.94	0.33
CDC42	2.58	0.46	2.53	0.41
GNA13	5.22	1.11	4.71	1.75
AP3S1	5.11	1.18	4.79	1.51
CD63	1.16	0.30	0.98	0.41
PDHB	1.65	0.40	1.42	0.41
MPG	2.74	0.37	3.09	0.49
CDC6	1.60	0.24	1.48	0.32
NNMT	4.17	0.70	3.63	1.30
TBPL1	1.90	0.39	1.87	0.28
IRF9	2.04	0.42	2.07	0.26
ARNTL	1.19	0.15	1.10	0.37
FGD2	2.11	0.53	2.32	0.54
ARG1	1.09	0.18	1.00	0.34
RAG2	1.60	0.30	1.56	0.20
CCL11	2.67	0.54	2.44	0.70
SNAPC2	1.65	0.30	1.54	0.31
SNRPA1	2.43	0.68	2.37	0.51
CXCL10	1.59	0.23	1.47	0.29
OGG1	2.66	0.52	2.76	0.62
TFRC	5.34	1.10	4.54	1.27
ZNF668	1.45	0.25	1.41	0.46
MED20	1.77	0.22	1.66	0.55
CYP4B1	1.98	0.42	1.94	0.31
CCL20	0.86	0.17	0.74	0.30
ALG2	0.82	0.15	0.69	0.23
NF2	2.97	0.56	2.61	0.46

NKX3-2	2.55	0.65	2.29	0.52
RXRA	0.92	0.16	0.90	0.28
SCRIB	1.89	0.33	1.80	0.28
UGT1A7	2.19	0.32	1.86	0.24
SLC6A19	3.37	0.42	3.05	1.10
DEFB106A	0.96	0.15	1.00	0.46
PHB2	2.13	0.50	1.75	0.20
GSTM3	4.01	2.06	2.80	0.64
ZNF550	0.79	0.22	0.58	0.17
TFDP2	1.21	0.17	1.15	0.20
ZNF597	1.63	0.20	1.59	0.29
PSMC2	2.69	0.35	2.44	0.39
DEPDC7	1.48	0.26	1.38	0.22
CXCL14	1.70	0.29	1.80	0.13
SEC61G	0.93	0.10	0.87	0.31
KLHL13	1.28	0.17	1.25	0.48
TBC1D4	2.91	0.42	2.78	0.55
SLC27A5	0.68	0.22	0.78	0.31
RGS11	1.56	0.47	1.44	0.31
RPS19	1.93	0.31	1.89	0.27
TBX5	1.07	0.21	1.00	0.35
KLF8	2.08	0.51	1.95	0.24
LHX2	2.55	0.51	2.25	0.42
TRIP13	1.79	0.30	1.50	0.38
CBX5	3.63	0.65	3.14	0.71
PPP3CA	2.67	0.59	2.13	0.48
ATP1A1	3.25	0.51	3.89	1.11
ZNF480	1.89	0.20	1.72	0.30

SUMF2	1.92	0.25	1.69	0.27
YIF1B	1.90	0.41	1.69	0.27
CTSK	3.05	0.97	2.77	0.82
CYP19A1	4.37	0.83	3.50	0.98
NT5C3A	1.24	0.15	1.06	0.27
TRPV1	2.39	0.40	2.18	0.33
SPRY2	2.35	0.39	1.98	0.35
RAB1B	2.00	0.34	1.99	0.25
DAB2	1.43	0.18	1.31	0.45
TBCD	2.23	0.31	2.33	0.47
EIF3K	0.79	0.19	0.67	0.21
HLA-DRB3	1.81	0.32	1.75	0.35
GLYATL2	2.17	0.36	1.92	0.37
RFFL	2.19	0.48	2.00	0.30
USP6NL	0.67	0.13	0.54	0.15
PLD2	2.49	0.40	2.16	0.44
NAT9	2.33	0.40	1.95	0.27
MAT2B	2.82	0.47	2.24	0.35
TMEM126A	2.83	0.52	1.99	0.63
SLC36A1	2.08	0.56	1.63	0.50
L1	0.07	0.04	0.02	0.02
KRTAP19-7	1.51	0.40	1.45	0.52
SAFB	1.66	0.39	1.60	0.66
SPIRE1	0.77	0.13	0.67	0.21
TBC1D2B	2.69	0.65	2.60	1.24
SLC1A6	2.95	0.56	2.79	1.37
RPS20	0.44	0.10	0.49	0.20
HMGB2	2.57	0.66	2.51	0.93

KRTAP2-4	1.82	0.53	1.82	0.63
DEFB106B	1.92	0.55	1.80	0.70
AAK1	1.40	0.37	1.54	0.52
LRRTM4	2.26	0.55	2.24	0.76
ITGA10	0.91	0.29	0.81	0.27
FAM27E3	0.35	0.14	0.33	0.17
AEBP2	0.30	0.15	0.28	0.15
TIMM8B	0.67	0.25	0.53	0.24
TAF13	0.15	0.10	0.15	0.15
PLSCR2	0.13	0.09	0.06	0.08
CDH20	0.09	0.07	0.09	0.07
COX6A2	1.92	0.34	1.96	0.20
SGK1	1.95	0.29	1.98	0.27
WNT11	1.09	0.20	1.08	0.26
CXCL6	1.41	0.26	1.47	0.19
PHKG2	0.27	0.11	0.25	0.11
CAMK2D	0.37	0.11	0.25	0.11
C4orf29	0.15	0.08	0.22	0.14
ERAP1	0.75	0.15	0.63	0.18
SRPK1	1.10	0.16	1.14	0.23
INPP5E	1.01	0.18	1.02	0.29
CXCL2	0.96	0.16	0.98	0.28
CSNK2B	2.07	0.41	1.94	0.41
PTTG1	2.91	0.80	3.42	0.84
PCDHGB1	0.12	0.06	0.15	0.10
PEA15	2.12	0.38	2.22	0.25
BMP5	3.33	0.77	3.42	0.84
CXCL1	1.50	0.23	1.53	0.18

MVK	2.07	0.53	1.96	0.55
MLH1	0.15	0.07	0.10	0.07
TMEM190	0.22	0.15	0.21	0.16
XPC	0.83	0.18	0.65	0.22
CEP72	1.20	0.24	1.11	0.32
CRP	1.23	0.35	1.04	0.39
DNAJB1	1.56	0.42	1.36	0.36
TOB2	5.57	1.41	4.46	1.07
BMPR1A	0.21	0.07	0.17	0.07
PHKA2	0.15	0.11	0.16	0.10
SLC22A5	1.82	0.41	1.66	0.21
RIN1	1.90	0.55	2.06	0.52
LAMP2	2.26	0.45	2.17	0.22
RPS4Y1	2.41	0.36	2.29	0.44
RAB11B	1.19	0.44	1.36	0.54
MIA	0.78	0.32	0.79	0.30
SAE1	1.50	0.30	1.46	0.15
PSTPIP1	1.48	0.30	1.45	0.12
ESAM	1.87	0.40	1.80	0.27
TNFRSF10A	1.79	0.42	1.73	0.19
GSTP1	1.69	0.33	1.60	0.13
CAMKK1	0.15	0.06	0.14	0.07
NRBP1	0.30	0.19	0.34	0.20
ENG	1.36	0.36	1.33	0.55
SLC25A20	1.45	0.27	1.44	0.20
MGAT1	1.56	0.32	1.56	0.25
ALDH1A2	0.93	0.12	0.82	0.30
RAB13	0.45	0.23	0.59	0.28

MTAP	1.07	0.31	0.83	0.31
PPM1A	2.69	0.86	2.29	0.48
CACNG4	1.66	0.41	1.49	0.10
IP6K2	2.09	0.64	1.77	0.19
RPL9	1.83	0.54	1.50	0.37
PROK1	1.76	0.22	1.62	0.31
TRAF2	1.82	0.32	1.64	0.26
PARP1	0.30	0.14	0.28	0.14
GFPT2	1.10	0.20	0.87	0.21
GSTA4	1.77	0.28	1.85	0.24
CTSD	1.86	0.39	1.99	0.27
B4GAT1	1.48	0.28	1.40	0.16
TUBGCP4	0.47	0.07	0.40	0.11
CSTF1	1.20	0.15	1.14	0.24
PSMC1	1.29	0.32	1.10	0.29
09/02/2015	1.46	0.23	1.41	0.16
ITGB7	2.14	0.48	2.06	0.26
SURF1	1.54	0.25	1.54	0.13
ILK	1.76	0.26	1.58	0.31
SNAI1	0.61	0.23	0.68	0.26
RAD17	0.48	0.20	0.60	0.33
IGFBP3	0.97	0.18	1.02	0.24
COX7A1	0.74	0.10	0.74	0.30
KLK2	2.17	0.41	2.13	0.27
SORD	2.06	0.48	2.00	0.19
ALG9	0.20	0.08	0.18	0.10
HADHA	0.20	0.11	0.15	0.08
SLC39A8	1.58	0.40	1.48	0.19

PISD	1.61	0.44	1.37	0.24
ANAPC2	2.38	0.80	2.31	0.46
TNFRSF21	2.28	0.41	2.08	0.50
C1QBP	2.23	0.44	2.15	0.34
RPS29	0.80	0.43	0.72	0.37
IL13	1.42	0.22	1.40	0.15
CSH1	1.71	0.31	1.64	0.27
CTSZ	1.42	0.18	1.39	0.15
CDKN2D	1.52	0.22	1.40	0.17
PDGFRL	1.78	0.25	1.70	0.26
PMPCB	0.36	0.08	0.34	0.10
GABRA4	0.15	0.04	0.17	0.12
OR7C2	1.44	0.21	1.31	0.18
CYP26A1	1.75	0.34	1.69	0.21
E2F5	1.09	0.21	1.01	0.17
AP1S2	1.79	0.38	1.96	0.33
NEU1	1.78	0.33	1.57	0.42
AKR1C1	2.97	0.58	2.86	0.80
GABRB1	1.73	0.41	1.55	0.23
IL10	1.00	0.16	0.96	0.29
CTSC	1.44	0.19	1.48	0.14
AP2M1	2.00	0.40	1.96	0.24
RPS3	1.71	0.21	1.63	0.17
GMPPA	1.65	0.30	1.49	0.26
AREG	1.69	0.37	1.50	0.26
OPLAH	1.77	0.44	1.29	0.30
P3H3	2.47	0.84	2.30	0.48
WNT2	1.40	0.24	1.33	0.23

GPR84	1.25	0.25	1.13	0.33
CCKBR	1.27	0.22	1.12	0.31
OPN3	1.47	0.22	1.32	0.17
LPAR6	1.45	0.24	1.32	0.29
KLHDC3	1.37	0.22	1.31	0.39
GNAS	1.07	0.13	0.94	0.16
NPHS1	0.50	0.10	0.41	0.12
PTGIR	0.95	0.06	0.86	0.26
TAAR5	0.69	0.10	0.64	0.17
CNR2	1.56	0.16	1.42	0.22
SMO	3.31	0.61	3.14	0.85
NCEH1	0.99	0.15	0.92	0.30
MYL6	1.24	0.13	1.13	0.23
CXCL8	1.21	0.22	1.17	0.26
F2R	0.91	0.46	0.86	0.42
GPR75	0.68	0.11	0.65	0.29
GPR27	0.87	0.14	0.86	0.36
ADGRL4	2.26	0.51	1.93	0.41
GNA15	1.18	0.15	1.06	0.30
PDE8B	0.74	0.15	0.62	0.16
CCR9	1.56	0.18	1.44	0.24
GPR25	0.58	0.08	0.49	0.24
GHRHR	0.45	0.08	0.39	0.12
NTSR2	3.53	0.58	3.42	1.21
BCL2L11	1.64	0.40	1.28	0.33
RBM17	1.94	0.20	1.78	0.30
RBMS1	1.88	0.24	1.69	0.32
NTF3	1.56	0.17	1.24	0.29

KCNAB1	2.74	0.39	2.41	0.51
ZNF19	2.17	0.40	1.63	0.45
CDC26	1.55	0.33	1.49	0.37
CENPP	1.09	0.10	1.00	0.26
AGPAT3	1.51	0.14	1.31	0.27
NDEL1	1.17	0.09	0.91	0.17
SULT2B1	1.08	0.11	0.83	0.21
AADAT	1.90	0.23	1.55	0.24
CORO1C	1.23	0.18	1.23	0.22
GALT	0.89	0.14	0.75	0.20
MTERF3	1.37	0.14	1.33	0.31
EFNB2	0.86	0.13	0.71	0.23
IL1R2	1.17	0.18	0.99	0.30
PELI1	0.84	0.20	0.65	0.29
ZNF529	1.01	0.19	1.10	0.22
L2	0.05	0.03	0.03	0.02
RAD9B	1.65	0.16	1.44	0.26
SPRY1	1.90	0.20	1.60	0.31
QKI	1.58	0.19	1.29	0.38
BDH1	1.52	0.21	1.22	0.31
MAPKAPK3	1.82	0.27	1.79	0.27
TUBB2B	2.33	0.60	2.06	0.39
C11orf57	1.24	0.38	1.28	0.54
SEL1L3	0.56	0.17	0.47	0.19
ZNF518A	0.76	0.16	0.63	0.22
DGKZ	0.44	0.11	0.49	0.22
PIP4K2B	0.30	0.17	0.29	0.16
GFOD2	0.41	0.17	0.40	0.28

UGGT2	0.05	0.05	0.06	0.07
SYN1	1.94	0.36	1.80	0.30
CHCHD10	1.28	0.18	1.35	0.17
CENPQ	1.36	0.19	1.45	0.07
BAZ2B	2.06	0.28	1.99	0.15
PON2	1.86	0.28	1.78	0.20
ULK4	2.37	0.25	2.34	0.20
PDGFRA	0.16	0.05	0.19	0.10
UBTD2	1.29	0.25	1.39	0.57
NID2	1.62	0.44	1.47	0.60
CKAP5	0.16	0.06	0.22	0.10
PLEKHS1	0.41	0.17	0.48	0.20
ZNF783	0.36	0.15	0.41	0.16
PPP1R7	2.15	0.53	2.09	0.81
RAB12	1.40	0.23	1.27	0.11
GJD3	1.97	0.36	1.85	0.27
IDNK	1.97	0.19	1.85	0.21
C8orf86	1.66	0.19	1.71	0.13
E4F1	2.22	0.53	2.07	0.39
D2HGDH	2.30	0.46	1.98	0.14
ZNF658	3.49	0.74	3.17	0.38
TMEM65	0.47	0.18	0.47	0.20
NME1-NME2	0.45	0.26	0.41	0.26
PCMT1	1.57	0.34	1.49	0.56
TTC26	1.13	0.09	1.12	0.29
C17orf104	0.06	0.04	0.08	0.07
PPP1R11	0.05	0.04	0.06	0.05
GSK3A	0.50	0.22	0.55	0.24

UBE2W	0.21	0.10	0.31	0.16
UBE3A	0.66	0.22	0.78	0.29
LLPH	0.15	0.24	0.14	0.10
PCOLCE2	1.60	0.21	1.52	0.17
SLC25A29	0.08	0.06	0.04	0.05
RIPPLY1	0.06	0.09	0.02	0.04
CCDC153	0.10	0.07	0.11	0.08
LYPD6B	1.12	0.62	1.14	0.68
FERMT1	0.31	0.23	0.17	0.21
PITPNC1	0.62	0.15	0.70	0.33
EXOSC3	1.54	0.22	1.38	0.21
EIF3E	3.62	0.57	3.21	0.85
PPIB	2.99	0.63	2.47	0.64
PAX8	1.77	0.33	1.59	0.34
KREMEN2	1.86	0.32	1.65	0.24
TBC1D16	0.17	0.05	0.13	0.10
SUCLG2	0.20	0.08	0.16	0.14
MDH2	1.69	0.20	1.67	0.20
SLC38A5	1.16	0.15	1.16	0.25
TRIM32	1.56	0.27	1.56	0.22
POLR3K	1.31	0.20	1.36	0.11
GALC	0.78	0.44	0.56	0.18
ZBTB37	0.14	0.19	0.15	0.10
MARCKSL1	0.24	0.14	0.33	0.20
QDPR	1.41	0.20	1.30	0.15
UBE2J1	3.20	0.54	3.42	0.80
CFB	1.75	0.40	1.68	0.43
HLA-DQB1	3.37	0.61	3.45	0.89

CA12	1.24	0.18	1.31	0.31
TMIGD3	0.10	0.06	0.11	0.09
IFT57	1.57	0.13	1.49	0.23
ABAT	1.21	0.20	1.11	0.26
PCDHGC3	2.28	0.43	2.09	0.43
GFI1	2.38	0.74	2.07	0.26
MAP1LC3B	2.83	0.50	2.51	0.69
HOXB13	2.15	0.34	1.92	0.35
ALG3	1.61	0.34	1.49	0.20
ERCC1	2.13	0.46	1.58	0.33
LPAR5	1.18	0.45	0.93	0.26
CNOT10	1.37	0.52	1.21	0.19
RPS7	1.88	0.25	1.86	0.33
NPY1R	1.17	0.29	1.10	0.42
LSS	1.69	0.30	1.72	0.26
GSTA3	1.29	0.15	1.33	0.12
AKR1C4	1.50	0.17	1.65	0.17
BLZF1	1.19	0.18	1.19	0.16
NDUFA3	1.43	0.23	1.56	0.08
UBA3	2.04	0.27	1.96	0.35
NFYB	1.39	0.16	1.32	0.15
PPAP2B	1.35	0.18	1.25	0.14
IGFBP6	1.74	0.25	1.84	0.19
CSNK2A2	0.72	0.12	0.69	0.25
NKX2-1	1.73	0.37	1.77	0.32
RPS9	2.42	0.32	2.25	0.40
DCAF7	1.46	0.19	1.43	0.12
GALNT6	2.38	0.37	2.16	0.35

HNMT	1.68	0.28	1.57	0.25
GPR183	0.91	0.16	0.72	0.16
KPNA1	1.32	0.40	1.02	0.24
TCAP	2.53	0.43	2.72	0.54
IL10RA	2.55	0.41	2.52	0.30
TUBGCP3	2.29	0.40	2.20	0.39
MAT1A	2.37	0.38	2.04	0.35
ZKSCAN5	1.36	0.46	1.08	0.33
ZNF473	2.53	0.77	2.13	0.25
LUZP1	0.39	0.07	0.37	0.10
LYVE1	1.16	0.13	1.13	0.18
C4BPA	1.70	0.16	1.80	0.19
NPM1	1.15	0.18	1.05	0.14
NEUROG3	1.40	0.21	1.46	0.23
ZBTB16	1.84	0.32	1.88	0.28
ZNF558	5.39	1.38	5.35	1.44
GNAT2	2.02	0.20	2.01	0.21
ANXA4	3.12	0.25	3.30	0.79
CX3CR1	2.01	0.25	1.98	0.35
CHST10	1.86	0.30	1.90	0.20
ZHX2	1.15	0.16	1.01	0.33
CLOCK	0.64	0.11	0.57	0.26
NFKB1	2.87	0.55	2.67	0.69
PSMB4	1.84	0.27	1.78	0.31
TFB1M	1.85	0.21	1.86	0.15
SLC3A1	1.21	0.14	1.11	0.18
DNM1L	1.59	0.20	1.50	0.24
TCEB2	1.01	0.16	0.91	0.20

ZNF432	1.55	0.18	1.42	0.22
PRMT1	1.54	0.31	1.28	0.29
TRIM11	2.81	0.47	2.51	0.47
UGT1A5	1.14	0.13	1.02	0.21
LIFR	2.50	0.43	2.28	0.34
DEFB112	2.03	0.31	1.93	0.32
B3GNT7	2.60	0.48	2.25	0.82
PSMB1	1.09	0.15	1.01	0.24
SKIV2L	2.15	0.37	2.00	0.33
ZNF577	0.69	0.09	0.64	0.13
CBFA2T3	2.11	0.28	2.11	0.34
SOX2	1.93	0.34	1.79	0.30
TCF12	2.38	0.29	2.14	0.28
YEATS4	1.90	0.21	1.83	0.16
PTP4A2	1.37	0.20	1.28	0.19
C1QC	1.43	0.17	1.28	0.23
NR5A1	1.41	0.19	1.44	0.25
SULT1A3	1.74	0.32	1.48	0.27
SLC5A1	2.46	0.41	2.35	0.38
OR4E2	1.87	0.49	2.04	0.63
EPHA8	2.12	0.30	1.99	0.32
CLDN3	1.55	0.19	1.56	0.29
PRPF4	1.67	0.11	1.53	0.17
CFAP20	1.50	0.12	1.38	0.13
ATF1	1.14	0.14	1.10	0.22
GTF2H3	1.90	0.26	1.89	0.26
ZNF510	1.89	0.27	1.82	0.36
LEF1	1.54	0.23	1.33	0.28

FARP1	0.97	0.14	0.74	0.22
SPOP	2.43	0.56	2.05	0.25
SQSTM1	2.31	0.38	2.06	0.32
CLDN8	2.10	0.29	1.84	0.22
ANTXR1	1.69	0.22	1.45	0.20
DCTN2	1.73	0.22	1.59	0.26
POGLUT1	1.97	0.23	1.75	0.32
DPAGT1	2.40	0.40	1.95	0.29
JAM2	1.87	0.16	1.74	0.20
PRLR	2.12	0.19	1.91	0.22
MAP3K7CL	1.46	0.14	1.22	0.26
MIS12	1.64	0.13	1.54	0.27
TMEM43	1.67	0.19	1.36	0.28
HDAC11	2.19	0.31	1.88	0.23
L3	0.06	0.02	0.04	0.03
GSN	1.82	0.23	1.60	0.23
MAPKAP1	1.97	0.17	1.84	0.22
CHST11	1.34	0.14	1.22	0.16
DCPS	1.51	0.21	1.34	0.19
ATP6V1C1	1.90	0.30	1.61	0.22
ZNF302	1.13	0.24	0.82	0.26
ORC6	1.93	0.18	1.84	0.17
PRKAR2B	1.27	0.13	1.03	0.32
KIF20A	2.10	0.25	1.88	0.22
MED23	1.36	0.32	1.02	0.39
DEPTOR	2.83	0.45	2.37	0.39
USP1	2.85	0.49	2.30	0.49
PNPLA1	1.21	0.24	1.19	0.46

RASSF3	0.92	0.20	0.82	0.27
FBXW12	1.61	0.35	1.43	0.63
GLDN	0.43	0.16	0.46	0.21
ZNF80	0.12	0.05	0.11	0.08
PPAPDC1B	0.43	0.14	0.41	0.15
TMEM132B	0.33	0.11	0.40	0.17
PDHA2	1.06	0.28	1.00	0.29
SERINC5	1.13	0.19	0.99	0.36
PLD5	0.81	0.15	0.76	0.20
CWF19L2	0.79	0.17	0.75	0.25
NRN1L	1.74	0.48	1.89	0.69
ZNF541	0.60	0.35	0.62	0.37
CENPJ	2.03	0.48	2.16	0.83
NDUFC1	0.23	0.07	0.24	0.11
XCL2	0.21	0.07	0.18	0.10
SEPW1	0.32	0.28	0.39	0.39
PSMD8	0.10	0.07	0.14	0.12
LRP5L	0.06	0.06	0.06	0.08
RUSC1-AS1	0.69	0.25	0.65	0.30
CHIC1	3.84	0.82	2.85	1.15
NFIX	0.19	0.09	0.14	0.09
MAP3K14	3.15	0.58	2.79	0.56
TAOK3	3.27	0.54	3.03	0.91
PFKFB4	3.09	0.48	2.81	0.55
PKLR	0.14	0.05	0.12	0.07
PDK1	0.13	0.05	0.08	0.06
FAM25A	0.18	0.11	0.20	0.11
MXD1	1.25	0.14	1.21	0.19

IBSP	0.79	0.10	0.76	0.24
PSME2	2.12	0.39	2.02	0.54
HOXA5	3.84	0.61	3.94	1.43
CFAP57	0.29	0.10	0.41	0.19
IFNA21	1.67	0.17	1.71	0.18
PIK3C3	2.92	0.54	2.85	0.70
CSNK1G2	0.82	0.31	0.74	0.35
EPHA2	0.35	0.27	0.15	0.08
AXL	0.09	0.05	0.07	0.07
DAD1	1.50	0.21	1.34	0.24
CASP2	1.58	0.36	1.54	0.25
ANXA1	0.83	0.13	0.76	0.20
GPR4	1.65	0.38	1.50	0.11
LTA	3.06	1.09	3.01	1.03
GK	0.39	0.23	0.39	0.26
PIP5K1B	0.22	0.13	0.28	0.17
GLRX	1.49	0.36	1.36	0.25
RAB8A	1.42	0.23	1.38	0.12
SPP1	1.20	0.17	1.13	0.26
PDE6B	2.86	0.55	2.58	0.36
PAX6	3.28	0.68	2.91	0.89
FARS2	1.51	0.48	1.79	0.89
SH3GL2	2.23	0.44	2.22	0.52
HBA2	1.04	0.15	1.04	0.11
EIF2S3	0.15	0.05	0.17	0.10
SLC13A3	1.12	0.20	1.16	0.15
FGFR1	0.16	0.05	0.11	0.10
PAK6	0.19	0.16	0.27	0.23

NSDHL	1.10	0.12	1.06	0.27
SAA1	1.02	0.18	1.05	0.14
FGF12	0.63	0.12	0.63	0.18
ZNF426	2.23	0.21	2.25	0.31
MSX2	2.08	0.35	1.89	0.56
FOSL1	3.67	0.68	3.85	1.50
FOSB	1.40	0.39	1.41	0.49
GPC4	1.39	0.21	1.43	0.16
DNAJB9	1.55	0.29	1.36	0.47
PGRMC1	1.32	0.22	1.34	0.13
CD40	1.69	0.40	1.61	0.17
NDUFV3	0.72	0.17	0.49	0.20
FRK	2.81	0.48	2.54	0.44
GNG11	2.42	0.48	2.21	0.56
DNTT	1.89	0.29	1.77	0.26
KLK6	1.97	0.31	1.90	0.43
MAOA	0.41	0.09	0.41	0.14
RND3	1.47	0.23	1.54	0.10
KRAS	1.58	0.19	1.72	0.18
ITGB5	0.28	0.06	0.27	0.09
IGF2	1.18	0.14	1.15	0.09
CCNG2	1.54	0.19	1.53	0.21
ACADL	1.48	0.18	1.52	0.14
ATP4B	2.07	0.39	2.09	0.25
DOK2	2.02	0.37	2.04	0.23
CLU	2.04	0.40	1.71	0.59
CSGALNACT2	1.58	0.37	1.70	0.52
CYC1	3.08	0.51	3.24	1.11

ETV5	0.53	0.10	0.52	0.17
AKR1A1	1.22	0.13	1.29	0.18
CAV1	1.48	0.17	1.78	0.33
NAE1	1.54	0.25	1.54	0.16
CHRM1	0.29	0.04	0.26	0.10
CDC27	0.95	0.09	0.94	0.21
ACSL4	0.71	0.08	0.68	0.20
GAPDHS	1.63	0.32	1.57	0.24
SLC22A4	0.26	0.06	0.21	0.09
TOB1	2.34	0.59	2.20	0.22
GPR135	1.38	0.28	1.36	0.28
NPY	1.72	0.23	1.86	0.34
TESK1	1.44	0.32	1.47	0.36
IL4	1.26	0.19	1.30	0.14
GRB2	0.79	0.12	0.75	0.24
IGFBP4	1.63	0.27	1.54	0.12
TNF	1.51	0.21	1.49	0.15
DGKA	1.77	0.29	1.80	0.21
PDCD4	0.28	0.06	0.29	0.13
COX5A	1.36	0.20	1.31	0.11
GTF2E1	1.75	0.36	1.85	0.35
EHD3	1.10	0.21	1.06	0.13
SLC16A8	1.08	0.23	0.96	0.26
F8A3	0.49	0.32	0.67	0.48
CYP2S1	1.04	0.19	1.02	0.10
RAMP2	1.70	0.33	1.74	0.41
IL9	1.34	0.21	1.49	0.20
IL7	1.18	0.12	1.25	0.13

SST	1.46	0.18	1.43	0.21
SLC25A16	1.63	0.19	1.66	0.12
CRABP1	1.56	0.14	1.51	0.10
DLX1	1.62	0.20	1.66	0.13
CYP4X1	1.52	0.18	1.45	0.41
LAMC3	2.36	0.46	2.55	0.72
TUBB8	1.88	0.42	1.73	0.16
HCN3	1.95	0.54	1.60	0.21
AKR1B1	1.13	0.22	1.04	0.33
PROKR2	1.01	0.15	0.93	0.21
ADGRE5	1.39	0.28	1.33	0.19
ACKR2	1.15	0.19	1.13	0.12
C5AR2	1.46	0.23	1.36	0.15
SLC37A4	1.44	0.22	1.31	0.16
EIF5	1.58	0.14	1.43	0.19
OR51A2	0.85	0.11	0.79	0.14
MAS1L	1.64	0.19	1.58	0.21
SCTR	1.68	0.20	1.59	0.18
P2RY10	0.68	0.08	0.62	0.11
FPR2	0.81	0.17	0.87	0.17
GORASP1	1.73	0.28	1.66	0.12
KCNG3	1.54	0.25	1.57	0.11
KRT19	0.86	0.14	0.86	0.21
CRHR1	0.59	0.09	0.57	0.13
GPR20	0.60	0.11	0.58	0.11
CCR7	0.97	0.15	0.96	0.11
PTGDR2	1.39	0.16	1.44	0.21
SERPINA3	0.66	0.07	0.56	0.13

DLST	1.06	0.09	0.97	0.19
KCNC3	0.46	0.07	0.42	0.10
GHSR	1.77	0.18	1.69	0.27
P2RY13	1.53	0.50	1.58	0.64
S1PR4	0.55	0.10	0.48	0.09
ACER3	1.01	0.19	0.83	0.15
PRKAG2	2.23	0.53	1.75	0.25
GCNT3	1.81	0.24	1.73	0.32
PARS2	1.88	0.26	1.81	0.36
ST6GALNAC3	1.43	0.19	1.26	0.21
PARD6B	2.20	0.31	1.90	0.36
HS3ST1	2.29	0.30	1.91	0.38
VPS4B	1.78	0.30	1.42	0.15
RPL18A	1.56	0.14	1.38	0.16
FBXL3	2.21	0.33	1.99	0.40
SNAP25	1.81	0.17	1.62	0.27
OR2L13	1.67	0.22	1.31	0.36
RCHY1	2.07	0.32	2.05	0.46
FXN	1.63	0.45	1.75	0.37
CALCOCO2	1.41	0.15	1.35	0.19
ERO1A	1.25	0.16	1.19	0.15
UBE2S	1.71	0.19	1.59	0.20
MAGT1	1.49	0.20	1.39	0.22
PSMB5	2.40	0.39	2.32	0.41
ZCCHC12	2.16	0.33	1.78	0.37
L4	0.06	0.03	0.04	0.03
IL21	1.42	0.16	1.23	0.23
GRPEL2	1.62	0.22	1.29	0.16

PAM16	1.50	0.31	1.20	0.24
ATG5	1.28	0.26	1.07	0.29
DHFRL1	1.76	0.28	1.41	0.30
RNF144B	1.24	0.19	1.16	0.19
HDHD1	1.22	0.27	1.28	0.51
IDI1	0.70	0.18	0.69	0.28
TEFM	0.42	0.12	0.42	0.16
MAP3K13	0.32	0.09	0.41	0.18
CLDN5	0.27	0.10	0.26	0.11
CMTM3	0.09	0.06	0.09	0.08
TSR3	1.13	0.16	1.18	0.10
TPO	1.40	0.13	1.26	0.17
FGFR1OP2	1.48	0.14	1.48	0.18
SREK1	1.00	0.16	0.96	0.19
C6orf58	1.32	0.18	1.39	0.11
RBM33	1.50	0.27	1.48	0.21
RBMX2	1.01	0.25	1.07	0.10
SETD5	1.15	0.22	1.25	0.48
SULT1C4	0.32	0.07	0.38	0.17
CCDC158	0.31	0.06	0.41	0.20
TDRD3	0.43	0.09	0.52	0.18
CHCHD4	1.17	0.20	1.23	0.53
SHISA5	0.98	0.14	1.02	0.13
KRTAP9-9	1.38	0.24	1.24	0.28
RIPK3	1.54	0.24	1.64	0.29
BRD4	1.57	0.23	1.58	0.22
PFKFB1	1.25	0.19	1.29	0.11
COL2A1	2.03	0.25	1.75	0.22

CCDC11	1.77	1.10	1.50	0.49
H2AFX	0.08	0.07	0.10	0.07
KRT6A	0.08	0.05	0.07	0.06
TRIM62	0.84	0.31	0.75	0.27
FAM175B	1.36	0.22	1.31	0.15
IFNA7	0.09	0.03	0.08	0.07
SLC6A6	0.08	0.05	0.06	0.06
RBMY1A1	0.56	0.18	0.70	0.30
IKBKG	0.25	0.14	0.36	0.18
ZNF512	0.19	0.10	0.24	0.11
SLC18A1	0.82	0.80	0.84	0.78
ZNF625	0.36	0.15	0.44	0.24
IFRD2	0.23	0.15	0.32	0.17
OR2M2	1.69	0.22	1.64	0.24
DLX6	0.12	0.08	0.16	0.14
PLA2G10	0.08	0.08	0.04	0.07
PRR5-ARHGAP8	0.11	0.09	0.04	0.08
ZNF767P	0.83	0.35	0.85	0.47
STPG1	0.20	0.12	0.11	0.10
NSMCE4A	0.29	0.12	0.37	0.19
TPRN	0.43	0.18	0.48	0.27
HMOX1	1.27	0.19	1.15	0.22
MSI2	1.82	0.49	1.43	0.53
ABCF2	3.11	0.41	2.85	0.88
LGALS1	1.60	0.23	1.35	0.23
AJUBA	1.27	0.19	1.15	0.14
CCDC28A	0.10	0.06	0.18	0.12
DIABLO	1.41	0.15	1.36	0.09

FHL2	2.30	0.43	2.16	0.69
GSTT1	1.20	0.18	1.15	0.15
FASLG	0.72	0.13	0.72	0.15
SH3GL1	1.25	0.23	1.23	0.10
MBP	0.20	0.06	0.26	0.14
LRR1	1.05	0.47	1.00	0.45
SLC2A5	2.96	0.73	2.99	0.93
ORC5	1.76	0.48	1.83	0.62
MTHFD1	2.96	0.30	2.52	0.59
HLX	1.18	0.27	1.24	0.31
NME1	0.14	0.06	0.07	0.07
RNF24	0.15	0.08	0.13	0.11
SDHD	1.12	0.13	1.17	0.16
HLA-DPA1	1.22	0.14	1.29	0.16
PDIA3	4.43	0.77	4.33	1.31
GZMA	1.03	0.21	0.94	0.25
DUT	1.90	0.45	1.67	0.16
PLCG2	1.99	0.33	1.61	0.42
ARRB2	1.74	0.36	1.56	0.21
KLC1	0.25	0.07	0.25	0.08
SKAP2	2.08	0.27	2.00	0.27
SNTA1	1.92	0.34	1.76	0.39
TIMP1	1.76	0.33	1.39	0.28
KRT17	2.01	0.31	1.99	0.49
CTBP1	1.57	0.37	1.51	0.21
RPL39	0.93	0.12	1.01	0.10
TECR	1.47	0.19	1.43	0.21
CASP6	1.19	0.15	1.21	0.13

GTF2H1	1.12	0.22	1.17	0.07
GTF2A2	0.85	0.15	0.85	0.07
PEX19	0.82	0.19	0.85	0.10
MYBL2	2.27	0.33	2.14	0.35
CERS4	1.36	0.17	1.34	0.27
NDUFV1	1.37	0.17	1.36	0.13
SLC25A15	0.86	0.15	0.90	0.21
TFAP2E	2.24	0.26	2.30	0.55
PFN1	1.74	0.19	1.83	0.60
FKBP3	2.05	0.21	2.07	0.63
ACY1	1.13	0.18	1.04	0.29
DDOST	1.89	0.27	1.73	0.32
TAF9B	1.32	0.22	1.42	0.12
RBP4	1.26	0.16	1.36	0.22
EIF3I	1.58	0.27	1.57	0.23
CTNNA1	2.79	0.49	2.46	0.48
OLR1	2.06	0.49	1.85	0.15
GGT5	1.79	0.41	1.52	0.20
GABRA5	1.76	0.34	1.52	0.14
MAD2L2	1.53	0.30	1.35	0.19
SLC20A1	0.91	0.17	0.76	0.14
OR5V1	0.72	0.09	0.58	0.15
SLC26A4	1.28	0.20	1.00	0.38
RGS21	2.12	0.31	2.08	0.70
STAM2	0.77	0.10	0.74	0.12
UBE2C	0.42	0.07	0.42	0.08
ADORA3	0.22	0.05	0.24	0.11
PTGS1	1.37	0.18	1.33	0.13

CNOT2	0.56	0.12	0.56	0.15
SIRT2	0.80	0.16	0.80	0.13
PHF5A	1.51	0.30	1.63	0.17
CHN1	1.85	0.31	1.75	0.26
HLA-DOA	1.39	0.19	1.47	0.15
AGT	1.75	0.16	1.79	0.22
MSMO1	0.58	0.09	0.67	0.13
TCF7	1.09	0.14	1.07	0.13
NPS	1.96	0.18	1.94	0.38
MLNR	2.06	0.40	1.80	0.59
GIF	0.46	0.06	0.42	0.08
PDE4A	0.56	0.05	0.48	0.13
RRAS	1.33	0.20	1.36	0.17
FMO3	1.01	0.12	0.96	0.22
HAND1	0.67	0.10	0.56	0.15
HNF1A	1.88	0.45	1.69	0.18
BRF2	2.50	0.55	2.25	0.34
DEFB110	1.40	0.21	1.31	0.28
OR52M1	1.88	0.24	1.53	0.39
FOLR3	1.94	0.39	1.54	0.40
ZNF713	2.45	0.37	2.01	0.54
PAX2	2.55	0.44	2.16	0.71
ZNF567	1.23	0.15	1.08	0.19
PROS1	0.60	0.07	0.51	0.15
PLAG1	0.60	0.12	0.58	0.07
ZNF691	1.71	0.22	1.72	0.35
ZNF184	2.03	0.19	2.00	0.38
ZNF566	1.90	0.23	1.99	0.31

KLF9	1.72	0.30	1.76	0.31
MIB2	1.88	0.27	1.82	0.22
SOX6	0.42	0.13	0.46	0.11
12/01/2015	1.67	0.33	1.73	0.49
UGT2B15	0.82	0.11	0.85	0.16
CAPN12	1.83	0.46	2.01	0.60
TAS1R2	2.13	0.42	1.77	0.49
OR2M4	1.62	0.23	1.57	0.12
HSD3B1	1.16	0.09	1.04	0.14
NMU	1.50	0.14	1.41	0.21
UBE2K	1.00	0.12	0.90	0.24
SNAI2	1.67	0.26	1.66	0.54
PHF21A	0.89	0.20	0.84	0.22
ZNF493	0.81	0.15	0.80	0.17
ETV6	1.28	0.25	1.10	0.23
PPA2	1.48	0.26	1.26	0.15
ARHGAP4	2.31	0.64	2.01	0.28
CYBB	1.39	0.19	1.17	0.28
B3GALT4	1.58	0.29	1.31	0.23
IDO1	1.07	0.16	0.89	0.17
POLR3D	1.44	0.20	1.20	0.22
ARRB1	1.71	0.23	1.34	0.21
VAT1L	1.63	0.20	1.31	0.27
UBA6	1.01	0.11	0.87	0.16
SLC30A7	1.62	0.19	1.50	0.22
ZMYM2	1.35	0.12	1.28	0.23
TKT	1.78	0.19	1.58	0.19
SHMT1	1.88	0.22	1.67	0.19

SNCA	1.85	0.26	1.61	0.19
USP16	1.12	0.17	1.07	0.35
COX7B	1.19	0.12	1.08	0.16
NDUFA9	1.26	0.18	1.22	0.13
TDO2	1.37	0.20	1.35	0.19
SNIP1	1.65	0.21	1.46	0.21
CASP9	1.93	0.23	1.63	0.24
YIPF6	3.16	0.51	2.64	0.69
ELMO2	1.35	0.21	1.07	0.31
ITGB6	1.49	0.27	1.43	0.23
TAF12	1.84	0.31	1.57	0.26
TGOLN2	2.23	0.32	1.77	0.31
OTX2	3.42	0.71	2.77	0.56
L5	0.05	0.04	0.01	0.02
ZNF624	0.64	0.20	0.56	0.19
COX7A2	0.34	0.14	0.35	0.17
FANCF	0.16	0.11	0.13	0.09
HNRNPA1L2	0.33	0.16	0.40	0.19
C19orf66	0.20	0.10	0.17	0.11
SPATC1L	0.25	0.19	0.19	0.12
TMEM230	0.10	0.05	0.08	0.07
RPL22	0.25	0.06	0.28	0.12
DEFB132	0.34	0.09	0.41	0.15
XKR3	0.36	0.09	0.52	0.18
ZIK1	0.96	0.15	0.99	0.30
ANKDD1A	1.21	0.52	1.17	0.55
ARHGAP27	0.19	0.13	0.28	0.18
GABRE	0.78	0.16	0.99	0.33

PKDCC	0.65	0.14	0.79	0.28
TMEM201	1.04	0.24	0.85	0.40
SEC14L4	0.12	0.11	0.12	0.11
GPIHBP1	0.11	0.06	0.09	0.09
CCDC169	0.24	0.12	0.25	0.13
SPINK9	0.29	0.18	0.20	0.19
VCX2	0.46	0.39	0.46	0.34
PAPSS1	0.08	0.05	0.06	0.05
CHEK2	0.14	0.10	0.10	0.07
RPS6KA2	0.10	0.07	0.09	0.06
LCK	0.34	0.15	0.28	0.09
PLAU	0.17	0.07	0.12	0.04
CKM	0.09	0.04	0.05	0.05
FAM25BP	0.25	0.11	0.26	0.13
TNNC2	1.44	0.32	1.62	0.67
EREG	1.28	0.26	1.31	0.22
CD151	1.20	0.24	1.20	0.24
PEX11A	1.67	0.49	1.87	0.69
VCX3A	0.04	0.03	0.08	0.07
PAK4	1.13	0.17	1.12	0.23
PLK1	0.34	0.12	0.46	0.19
CDK4	0.06	0.05	0.08	0.07
MAP2K2	0.05	0.05	0.07	0.07
PRKCH	0.81	0.24	0.84	0.31
GCK	0.15	0.07	0.06	0.09
ZMAT1	0.04	0.04	0.03	0.07
MIF	0.97	0.13	1.00	0.10
RHOG	1.76	0.52	1.81	0.32

DCK	2.81	0.74	3.04	1.15
TNNC1	2.93	0.80	2.80	0.72
FABP1	1.27	0.26	1.13	0.15
SNRPD3	0.01	0.05	0.01	0.05
FKBP14	1.88	0.34	1.77	0.21
IL11RA	2.22	0.50	2.05	0.35
CXCL11	1.65	0.32	1.57	0.17
BAK1	1.66	0.27	1.51	0.21
LMO4	3.29	0.58	3.26	1.25
PLEK	0.81	0.33	0.91	0.43
OPRL1	0.80	0.23	0.65	0.23
SF3A1	1.18	0.20	1.23	0.21
TRAM1	0.73	0.12	0.76	0.11
LAMP1	1.17	0.14	1.19	0.16
EHD4	1.32	0.30	1.34	0.13
PITPNB	-0.02	0.03	-0.01	0.04
CXCL5	0.81	0.15	0.76	0.16
PSMA6	1.35	0.19	1.41	0.06
EPHX1	3.27	0.56	3.22	1.28
UBE2V2	2.25	0.18	1.97	0.56
IFITM2	1.56	0.12	1.43	0.15
TNFSF13	0.65	0.30	0.95	0.50
UROD	2.00	0.49	2.29	1.00
EDEM1	1.39	0.25	1.43	0.21
PPIA	1.33	0.17	1.36	0.18
SIRT7	1.54	0.29	1.52	0.20
ERAL1	1.56	0.39	1.47	0.18
DUSP13	2.05	0.58	1.84	0.20

DAPP1	4.16	0.77	3.60	0.66
CES1	2.04	0.40	1.92	0.29
SLC25A6	1.78	0.41	1.56	0.38
ENO2	0.11	0.06	0.15	0.09
RGS1	1.53	0.27	1.42	0.16
AKR1C3	1.46	0.20	1.40	0.25
CA7	2.10	0.42	1.99	0.37
GARS	0.38	0.07	0.36	0.06
ATF3	1.14	0.18	1.16	0.11
MGAT2	0.54	0.05	0.57	0.10
ABCG1	1.19	0.16	1.21	0.08
HOMER1	1.17	0.16	1.30	0.10
S1PR5	1.51	0.21	1.71	0.24
UBE2L6	0.91	0.20	1.00	0.08
RPL13	2.97	0.34	3.35	0.98
RUVBL1	2.34	0.48	2.41	0.70
PYGB	2.98	0.54	3.18	1.09
ELF3	1.14	0.13	1.26	0.19
FMO4	0.24	0.06	0.27	0.08
GSTM4	3.19	0.33	3.21	1.23
HMGCL	1.57	0.16	1.44	0.26
PPP2R1A	1.83	0.31	1.66	0.48
GLYAT	1.18	0.11	1.25	0.09
RHAG	0.42	0.08	0.38	0.08
LNX1	1.41	0.25	1.49	0.18
S100A7	1.08	0.16	0.94	0.09
FBXO17	1.64	0.39	1.57	0.23
ACAA1	2.37	0.64	2.22	0.31

SSTR1	1.70	0.39	1.62	0.28
CD8A	0.40	0.07	0.42	0.11
NKX2-5	2.08	0.43	1.93	0.40
IL24	1.85	0.32	1.65	0.28
CCR10	0.40	0.11	0.34	0.09
CXCR1	0.88	0.13	0.79	0.12
ACKR3	1.00	0.14	1.02	0.09
MTERF1	0.89	0.14	0.87	0.09
SIAH1	1.10	0.15	1.11	0.12
PTS	1.58	0.24	1.55	0.20
ABCD1	0.50	0.10	0.43	0.08
SRMS	1.26	0.20	1.29	0.11
DEFB115	0.93	0.16	0.93	0.12
LEFTY1	1.53	0.33	1.46	0.30
HNRNPU	0.20	0.09	0.25	0.09
COMP	1.95	0.23	1.91	0.36
NDUFB8	0.72	0.10	0.74	0.18
BRS3	0.66	0.07	0.63	0.12
CCR4	0.44	0.05	0.44	0.10
GPR65	0.89	0.09	0.77	0.18
IL13RA2	1.49	0.17	1.40	0.45
FKBP2	1.06	0.09	1.03	0.10
MAP4K5	0.25	0.05	0.26	0.12
ANXA2	1.32	0.15	1.17	0.25
SLC12A1	0.22	0.06	0.18	0.09
ATP2A1	1.62	0.37	1.43	0.16
NMS	1.96	0.47	1.77	0.22
ADGRE1	0.73	0.12	0.64	0.19

HRAS	1.41	0.30	1.35	0.15
EIF4E	1.16	0.22	1.11	0.19
BAG1	1.22	0.24	1.08	0.12
RAD51	1.42	0.30	1.30	0.16
KLF10	1.13	0.18	1.02	0.12
VPS25	1.39	0.20	1.36	0.21
ZNF383	1.73	0.25	1.81	0.29
FZD7	0.66	0.09	0.66	0.06
ADRA2B	0.21	0.03	0.27	0.10
ADRA1D	1.13	0.17	1.13	0.14
FFAR2	0.31	0.08	0.36	0.09
CHORDC1	0.98	0.17	1.00	0.13
GJA4	1.20	0.22	1.20	0.13
GPR35	0.46	0.11	0.48	0.10
NCOA4	0.75	0.10	0.74	0.15
CDKN1B	1.28	0.15	1.26	0.14
BCL2L1	0.96	0.12	0.95	0.10
CCND2	1.37	0.09	1.39	0.18
SHC1	1.54	0.17	1.41	0.26
RPRM	1.78	0.20	1.52	0.34
OR6C2	0.22	0.04	0.22	0.12
GABBR1	1.25	0.10	1.18	0.13
OR14C36	0.71	0.10	0.69	0.12

Table 3. Median intensity absolute deviation rule for each protein through all the pooled serum

PROTEIN	Median (a.u.)
ZNF558	5.37
TOB2	5.02
GNA13	4.97
AP3S1	4.95
TFRC	4.94
PDIA3	4.38
EBNA	4.24
CAPN10	4.11
L10	4.10
CYP19A1	3.93
NNMT	3.90
HOXA5	3.89
DAPP1	3.88
FOSL1	3.76
ARHGDIB	3.58
ATP1A1	3.57
NTSR2	3.47
L11	3.45
EIF3E	3.41
HLA-DQB1	3.41
GSTM3	3.40
CBX5	3.39
BMP5	3.38
CHIC1	3.35

ZNF658	3.33
UBE2J1	3.31
SFTPD	3.28
LMO4	3.28
L9	3.25
EPHX1	3.25
SMO	3.22
GPR83	3.22
ANXA4	3.21
SLC6A19	3.21
GSTM4	3.20
PTTG1	3.17
RPL13	3.16
CYC1	3.16
TAOK3	3.15
CXADR	3.15
AMY2A	3.13
PAX6	3.10
OTX2	3.09
PYGB	3.08
NRIP1	3.04
LTA	3.03
ABCF2	2.98
TCL1A	2.98
SLC2A5	2.97
MAP3K14	2.97
PFKFB4	2.95
DCK	2.93

MPG	2.92
AKR1C1	2.92
CTSK	2.91
YIPF6	2.90
PIK3C3	2.88
RPL18	2.88
SLC1A6	2.87
TNNC1	2.87
TBC1D4	2.85
L12	2.84
CH25H	2.80
NF2	2.79
NUP133	2.79
SLC6A8	2.78
GDNF	2.78
NFKB1	2.77
MTHFD1	2.74
PRDM4	2.74
PPIB	2.73
FOS	2.72
PDE6B	2.72
OGG1	2.71
FRK	2.68
MAP1LC3B	2.67
TRIM11	2.66
CDC25C	2.66
TBC1D2B	2.64
TNNI3	2.63

CTNNA1	2.62
TCAP	2.62
DEPTOR	2.60
MMP9	2.59
USP1	2.58
KCNAB1	2.57
ARPC5	2.57
PSMC2	2.57
DEFB130	2.57
CDC42	2.56
CCL11	2.55
PABPC1	2.55
DLK1	2.55
HMGB2	2.54
MAT2B	2.53
CCNH	2.53
IL10RA	2.53
NSL1	2.52
SH2D1A	2.52
STRADB	2.51
ETV3	2.51
PPM1A	2.49
CA2	2.48
TNNI1	2.47
APOA2	2.46
LAMC3	2.45
NPBWR2	2.45
RHOD	2.44

B3GNT7	2.42
GSTT2	2.42
NKX3-2	2.42
TMEM126A	2.41
SLC5A1	2.41
LHX2	2.40
SNRPA1	2.40
PPP3CA	2.40
LIFR	2.39
P3H3	2.39
BRF2	2.38
RUVBL1	2.37
IL6R	2.37
PSMB5	2.36
ULK4	2.36
PAX2	2.36
RPS4Y1	2.35
ANAPC2	2.34
PRH2	2.34
RPS9	2.33
PLD2	2.33
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