Appendix 1

Summary of the annotation of the chromosomal region 9q32 to 9q34.3. Putative paralogues are in bold text.

Clone		***Ensembl Symbol***	***SPTR, Refseq or Ensembl entry***	***Transcript Start***	***Transcript end***	***Protein length (aa)***	***Description***
AL160275	**q32**	**ATP6V1G1**	**O75348**	**109082196**	**109092823**	**118**	**Vacuolar ATP synthase subunit**
	q32	NM_153045	Q8ND43	109118880	109140873	281	Unknown
AL390240	**q32**	**TNFSF15**	**O95150**	**109283763**	**109300582**	**251**	**Tumor necrosis factor ligand**
AL133412	**q32**	**TNFSF8**	**P32971**	**109398384**	**109424753**	**234**	**Tumor necrosis factor ligand**
AL162425	**q33.1**	**TNC**	**P24821**	**109514975**	**109612609**	**2201**	**Tenascin precursor**
AL355601	q33.1	NM_017418	O17418	109636267	109897093	95	Deleted in esophageal cancer 1
AL731824	q33.1	No genes					
AL714001	q33.1	No genes					
AL691420	q33.1	No genes					
AL731897	q33.1	No genes					
AL731813	q33.1	No genes					
AL732367	q33.1	EST-YD1	Q9P2X8	110398837	110399090	84	EST-YD1 protein
AL691426	q33.1	No genes					
AL353141	q33.1	No genes					
AL137024	q33.1	PAPPA	Q13219	110677328	110808083	716	Pregnancy associated plasma protein A
AL669963	q33.1	No genes					
AL133282	q33.1	ASTN2	O75129	110836698	111823883	1321	Astrotactin 1
	q33.1	Novel	ENSG00000179990	110963536	110981401	73	Unknown
AL133284	q33.1	TRIM32	Q13049	111098800	111112220	653	Zing finger protein HT2A
AL157829	q33.1	Novel	ENSG00000136913	111196159	111196227	23	Unknown
	q33.1	FLJ20958	Q9BQ00	111205755	111205826	24	Unknown
AL392085	q33.1	No genes					
AL354981	q33.1	No genes					
AL355608	q33.1	No genes					
AL358792	q33.1	No genes					
AL445644	q33.1	No genes					
AL161630	q33.1	Novel	ENSG00000179956	112057445	112065871	72	Unknown
AL160272	q33.1	TLR4	O00206	112113140	112124614	839	TOLL-like receptor 4 precursor
AL354754	q33.1	No genes					
AL445663	q33.1	No genes					
AL158831	q33.1	No genes					
AL365195	q33.1	No genes					
AL445440	q33.1	No genes					
AL355592	q33.1	No genes					
AL589703	q33.1	No genes					

AL157780	q33.1	No genes					
AL512602	q33.1	No genes					
AL445310	q33.1	No genes					
AL353773	q33.1	DCBBR1	O14618	113575169	113778264	761	Deleted in bladder cancer chromosome region
AL138894	q33.1	No genes					
AL353630	q33.1	No genes					
AC006288	q33.1	No genes					
AL445683	q33.1	No genes					
AL354931	q33.1	No genes					
AL441989	q33.1	No genes					
AL355589	q33.1	No genes					
AL592549	q33.1	No genes					
AL353736	q33.1	No genes					
AL391870	q33.2	CDK5RAP2	Q9NV90	114797706	114988994	943	CDK5 regulatory subunit associated protein 2
AL590642	q33.2	No genes					
AL138836	q33.2	EGFL5	Q9H1U4	115009649	115068409	401	EGF like domain multiple 5 protein
	q33.2	Novel	ENSG00000176341	115098762	115122988	236	Unknown
AL161911	q33.2	FBXW2	Q9UKT8	115160814	115202253	454	F-BOX/WD-repeat protein 2
	q33.2	PSMD5	Q16401	115224889	115251748	504	26S proteasome non-ATPase regulatory subunit 5
	q33.2	Novel	ENSG00000180095	115251902	115263209	105	Unknown
AL354792	q33.2	Q9UFS9	Q9UFS9	115264535	115286029	473	Transcription factor
AC006430	q33.2	PRO1995	Q9P1F7	115299108	115300075	105	Unknown
	q33.2	TRAF1	EBI6	115311227	115337603	350	TNF receptor associated factor 1
	q33.2	**C5**	**P01031**	**115361172**	**11549110**	**1676**	**Complement C5 precursor**
AL137068	q33.2	Novel	ENSG00000171635	115499108	115516745	219	Testis specfic
	q33.2	CEP1	O07018	115521379	115586444	1800	Centrosomal protein 1
	q33.2	RAB14	P35287	115586971	115610724	215	Ras-related protein
AL513122	q33.2	Novel	ENSG00000180552	115647510	115648753	409	Unknown
	q33.2	MOST2	Q9NRJ2	115689602	115694364	209	MOST2 protein
	q33.2	GSN	O06396	115708681	115741676	782	Gelosin precursor, plasma
AL161784	q33.2	EPB72	P27105	115747913	115779060	288	Erythrocyte band 7 integral membrane protein
AL359644	q33.2	Novel	ENSG00000165196	115868813	115888025	174	Unknown
AL357936	q33.2	No genes					
AL365274	q33.2	DAP2IP	Q8TDL2	115974718	116194365	964	DOC-2/DAB2 interactive protein
AL450285	q33.2	Novel					
AL596244	q33.2	Novel					
AL445587	q33.2	Novel	ENSG00000171539	116362696	116383814	140	Unknown
AL442634	q33.2	Q8NHH0	Q8NHH0	116397745	116502441	538	Unknown
AL162423	q33.2	NDUFA8	P51970	116552893	116568579	172	NADH-Ubiquinone oxidoreductase subunit
AL162424	q33.2	LHX6	Q9UPM6	116611414	11667540	363	LIM/Homeobox protein
	q33.2	NM_033117	Q96H35	116648845	11667367	190	Unknown
	q33.2	NM_138777	Q9BU92	116679683	116732299	262	RIKEN cDNA D02
	q33.2	PTGS1	P23219	116779785	116804538	596	Prostaglandin G/H synthase 1 precursor
AL359636	**q33.2**	**OR**	**Q8NGS3**	**116885796**	**116886761**	**322**	**Olfactory receptor**
		OR	**OR1J5**	**116919637**	**116920575**	**313**	**Olfactory receptor**
		OR	**Q8NGS1**	**116927976**	**116928914**	**313**	**Olfactory receptor**
		OR	**OR1N1**	**116935199**	**116936125**	**309**	**Olfactory receptor**
		OR	**Q8NGR9**	**116960247**	**116962994**	**316**	**Olfactory receptor**
		OR	**Q8NGR8**	**116976386**	**116977312**	**309**	**Olfactory receptor**
Al162254	**q33.2**	**OR**	**Q9UDD7**	**117016871**	**117017632**	**254**	**Olfactory receptor**
		OR	**OR1Q1**	**117023573**	**117024514**	**314**	**Olfactory receptor**
AC006313	**q33.2**	**OR**	**Q8NGR6**	**117037417**	**117038367**	**295**	**Olfactory receptor**
		OR	**Q8NH94**	**117070551**	**117071480**	**317**	**Olfactory receptor**
		OR	**Q8NH93**	**117083965**	**117084936**	**324**	**Olfactory receptor**
		OR	**Q8NGR5**	**117132825**	**117133757**	**311**	**Olfactory receptor**

		OR	**Q96R80**	**117158887**	**117159534**	**216**	**Olfactory receptor**
		OR	**Q8WVK7**	**117170703**	**117171065**	**121**	**Olfactory receptor**
AL359512	**q33.2**	**OR**	**Q8NGR3**	**117208958**	**117209905**	**316**	**Olfactory receptor**
	q33.2	PDCL	Q13371	117226985	117237466	301	Phosdusin-like protein
	q33.2	MNAB	O18835	117253391	117314050	1191	Membrane associated binding protein
AL731645	q33.2	ZID	Q15916	117317457	117320910	424	Zinc finger protein
	q33.2	**BIOR**	**Q9HCK0**	**117326928**	**117340094**	**441**	**Zinc finger protein**
	q33.2	GAPCenA	Q9Y3P9	117349852	117513707	997	RAB6 GTPase activating protein
AL358946	q33.3	No genes					
AL365338	q33.2	NM_030814	Q9H2N8	117518337	117522309	167	Unknown
	q33.2	STRBP	Q96S19	117533552	117593141	658	RNA binding protein
AL365504	q33.3	PRO226	Q9P180	117674928	117675167	80	Unknown
AL445489	q33.3	FLJ38464	Q8N930	117782642	117787587	215	Unknown
	q33.3	FLJ00224	Q8TEH3	117788495	118338969	896	Unknown
AL161790	q33.3	No genes					
AL390774	q33.3	No genes					
AL158208	q33.3	No genes					
AC006450	q33.3	LHX2	P50458	118420439	118441992	406	LIM/Homeobox protein
AL158052	q33.3	No genes					
Al445284	q33.3	No genes					
AL162724	q33.3	NEK6	Q9HC98	118666435	118761271	338	Serine-threonine protein kinase
AL137846	**q33.3**	**PSMB7**	**Q99436**	**118762294**	**118824271**	**277**	**Proteasome subunit beta type 7**
	q33.3	Q8NH12	Q8NH12	118874053	118892161	984	Seven transmembrane helix receptor
AL354979	q33.3	NR5A1	Q13285	118890062	118916249	461	Steroidogenic factor 1
	q33.3	NR6A1	Q15406	118928956	119180139	476	Orphan nuclear receptor
AL669818	q33.3	No genes					
AL158075	q33.3	No genes					
AL354928	q33.3	FLJ90228	Q8NCI9	119186100	119223707	318	Unknown
	q33.3	Novel	ENSG00000136918	119263034	119266399	233	Unknown
	q33.3	RPL35	P42766	119266713	119270796	141	60S ribosomal protein L35
	q33.3	NM_030978	Q9BPX5	119278120	119286561	159	Actin related protein
	q33.3	GOLGA1	Q92805	119287196	119349928	767	Golgin 97,gap junction protein
AL451125	q33.3	FLJ40705	Q8N1I4	119360938	119552351	629	Unknown
AL445930	q33.3	PPP6C	O00743	119557957	119598620	305	Serine/threonine protein phospatase 6
	q33.3	Novel	ENSG00000173602	119603477	119604650	282	40S ribosomal protein
AL354710	q33.3	P40	O00568	119609374	119642831	372	RAB9 effector P40
	q33.3	**HSPA5**	**P11021**	**119643682**	**119650159**	**654**	**78 KDA Glucose regulated protein**
	q33.3	Novel	ENSG00000176094	119672414	119672919	158	40S ribosomal protein
AL627223	q33.3	FLJ20119	Q9NXQ1	119670661	119773833	833	Unknown
AL359632	q33.3	MAPKAP1	Q9BPZ7	119846225	120116031	486	MAP kinase interacting protein 1
AL162584	q33.3	Novel	ENSG00000178022	120004502	120005454	316	Unknown
AL358074	q33.3	SIN1		119846225	120116031	522	SAPK interacting protein 1
	q33.3	NM_016158	Q9UN39	120153187	120155380	129	Erythrocyte transmembrane protein
AL627303	q33.3	No genes					
AL445186	**q33.3**	**PBX3**	**P40426**	**120156161**	**120376205**	**434**	**Pre-B-cell leukaemia transcription factor 3**
AL589923	q33.3	No genes					
AL445664	q33.3	No genes					
AL162391	q33.3	No genes					
AC006443	q33.3	FLJ00022	Q9H7P6	120735668	120915859	344	Unknown
AL356309	q33.3	No genes					
AL161908	q33.3	No genes					
AL161731	q33.3	LMX1B	O60663	121023337	121105270	379	LIM/Homeobox protein
	q33.3	Q8N243	Q8N243	121212014	121214492	115	Unknown
	q33.3	**ZNF297B**	**O43298**	**121213845**	**121244041**	**467**	**Zinc finger 297B**
AL354944	q33.3	KIAA1993	Q8NCN2	121269484	121289729	532	Unknown

AL160169	q33.3	No genes					
AL356862	q33.3	RalGPS1A	Q8WUV7	121323592	121631982	590	Ral guanine nuceotide factor
	q33.3	ANGPTL2	Q9UKU9	121496150	121531456	493	Angiopoietin-related protein 2
AL357623	q33.3	No genes					
AL450263	q33.3	Novel	ENSG00000176889	121633429	121650133	78	Unknown
	q33.3	NM_032293	Q9BQH6	121673400	121802357	802	Unknown
AL445222	q33.3	SLC2A8	Q9NY64	121806004	121816716	477	Solute carrier family 2
	q33.3	**RPL12**	**P30050**	**128564940**	**121860226**	**164**	**60S ribosomal protein L12**
	q33.3	FLJ31641	Q96MZ7	121860323	121912317	696	Unknown
	q33.3	Novel	ENSG00000176217	121901370	121904622	109	Unknown
	q33.3	NBL_HUMAN	Q96TA1	121914157	121987798	733	Niban-like protein.
AL390116	q33.3	No genes					
AL162426	q34.11	STXBP1	Q64320	122021098	122101525	594	Syntaxin binding protein 1
	q34.11	Novel	ENSG00000160401	122108029	122124506	785	Unknown
	q34.11	FLJ00176	Q8TEL7	122124875	122140409	867	Unknown
	q34.11	TOR2A	Q96LSL7	122140333	122144087	253	Torsin family 2, member A
	q34.11	SH2D3C	Q9Y2X5	122147126	122187504	703	SH2 Domain containing protein 3
AL162586	q34.11	CDK9	P50750	122194861	122198896	372	Cell division protein kinase 9
	q34.11	Novel	ENSG00000177953	122199888	122201861	85	Unknown
	q34.11	FPGS	Q05932	122211733	122222873	587	Folypolyglutamate synthase
	q34.11	FLJ33157	Q96LW6	122225388	122225972	195	Unknown
	q34.11	ENG	P17813	122224494	122263514	658	Endoglin procursor
AL157935	q34.11	AK1	P00568	122275199	122286472	194	Adenylate kinase isoenzyme 1
	q34.11	FLJ13838	Q9H8A2	122294130	122308407	352	Beta-N-Acetylgalactosaminide
	q34.11	SIAT7D	Q9H4F1	122316695	122325831	298	Sialyltransferase
	q34.11	Novel	ENSG00000167103	122330677	122339810	471	Kinase
	q34.11	Novel	ENSG00000136908	122343908	122347297	162	Unknown
	q34.11	FLJ00179	Q8TEL4	122349392	122356974	194	Unknown
	q34.11	NM_018033	Q9NW83	122374689	122375144	152	Unknown
AL360268	q34.11	Q8WU12	Q8WU12	122472894	122475975	172	Unknown
AL590708	q34.11	KIAA1896	Q96PZ1	122500273	122518054	568	Mitochondrial solute carrier
	q34.11	PTGES2	Q9H7Z7	122529502	122537271	379	Prostaglandin E synthase 2
	q34.11	Q9N1Y9	Q9N1Y9	122537454	122538008	185	Unknown
	q34.11	LCN2	P80188	122558275	122562260	192	Lipocalin
	q34.11	C9orf16	Q9BUW7	122569160	122572735	83	Unknown
	q34.11	CIZ1	Q9ULV3	122574874	122613197	967	Zinc finger protein
	q34.11	DNM1	Q05193	122612217	122664055	864	Dynamin-1
	q34.11	GOLGA2	Q08379	122665504	122684750	1008	Golgin-95
AL590722	q34.11	Q8N2W6	Q8N2W6	122685026	122697798	209	Unknown
	q34.11	FLJ21673	Q9H6Y8	122709723	122710145	423	Unknown
AL359091	q34.11	FLJ11094	O95900	122717908	122731245	331	Unknown
	q34.11	C0Q4	Q9Y3A0	122731344	122742880	265	Coenzyme Q biosynthesis protein 4
	q34.11	SLC27A4	O95186	122749454	122770025	640	Fatty acid transport protein 4
	q34.11	NM_030914	Q9BTM9	122780169	122799542	101	Unknown
	q34.11	KIAA1502	Q9P226	122820574	122846159	560	Cerebral cell adhesion molecule
	q34.11	ODF2	O14721	122864961	122909768	638	Outer dense fibre of sperm tails 2
AL445287	q34.11	GLE1L	O75458	122913513	122951096	698	Gle-1 like RNA export mediator
AL356481	q34.11	SPTAN1	Q13813	122961411	123042401	2474	Spectrin alpha chain
	q34.11	NM_052844	Q9BV46	123042469	123065595	522	Unknown
	q34.11	SET	Q01105	123092703	123105196	290	SET (HLA-DR associated protein II)
AL359678	q34.11	No genes					
AL441992	q34.11	PKNbeta	O13355	123111331	123129414	889	Protein kinase
	q34.11	ZDHHC12	O32799	123129677	123132930	267	Zinc finger protein
	q34.11	ZYG	O00156	123138594	123180701	766	ZYG homologue
	q34.11	FLJ10743	Q9NVG8	123196140	123219240	275	Unknown

	q34.11	ENDOG	Q14249	123227276	123231484	297	Endonuclease G
	q34.11	HSPC109	Q9P041	123228459	123238629	384	Unknown
	q34.11	CCBL1	Q16773	123241750	123290846	422	Cyoplasmic cysteine
AL672142	q34.11	KIAA1437	Q9P2B1	123294854	12336844	811	Unknown
	q34.11	Q96GM4	Q96GM4	123329703	123351210	206	Unknown
	q34.11	KIAA1094	Q9UPQ8	123354339	123356427	538	Unknown
AL592211	q34.11	KIAA0169	Q14675	123357991	123415903	1739	Unknown
	q34.11	SH3GLB2	Q9BRZ5	123416600	123437108	130	SH3-containing protein
	q34.11	FLJ00199	Q9TEJ6	123445452	123480880	383	Unknown
	q34.11	Q96GF8	Q96GF8	123489937	123499243	237	Unknown
AL158151	q34.11	CRAT	P43155	123503602	123519612	626	Cartinine o-acetyltransferase
	q34.11	PPP2R4	Q15257	123519773	123557754	358	Protein phosphatase 2A
	q34.11	Novel	ENSG00000167133	123585649	123586860	290	Unknown
AL161785	q34.11	FLJ35269	Q8NAJ2	123729824	123733713	232	Unknown
AL353803	q34.11	FLJ34873	Q8NAS2	123745332	123747103	144	Unknown
AL391056	q34.11	Novel	ENSG00000179068	123897948	123913240	98	Unknown
	q34.11	FLJ35803	Q8NA65	124021035	124029584	377	Unknown
AL590369	q34.11	AD003	Q9UI28	124034981	124044744	223	Adrenal gland protein
	q34.11	ASB6	Q9NWX5	124043412	124050973	421	Ankyrin repeat containing protein
	q34.11	PMX2	Q99811	12074444	124131482	253	Paired mesoderm protein
	q34.11	PTGES	O14684	124147139	124161855	152	Prostaglandin E synthase
AL592219	q34.11	No genes					
AL158207	q34.11	TOR1B	O14657	124211961	124220092	336	Torsin B precursor
	q34.11	DYT1	Q96CA0	124221751	124232942	336	Torsin A precursor
	q34.11	HSPC220	Q9NZ63	124236100	124244083	289	Unknown
	q34.11	USP20	Q9Y2K6	124244254	12490636	914	Ubiquitin carboxyl-terminal hydrolase
	q34.11	FNBP1	Q96RU3	124295995	124451976	672	Thyroid receptor interacting protein
AL136141	q34.11	GPR107	Q96T26	124462729	124548972	416	G Protein-coupled receptor
AL392105	q34.11	No genes					
AL360004	q34.11	FREQ	P36610	124581381	124645435	190	Neuronal calcium sensor 1
	q34.11	Novel	ENSG00000178890	124674690	124718869	822	Unknown
50 kb Gap							
AL354898	q34.11	Q8NDA2	Q8NDA2	124808356	124841498	1187	Unknown
	q34.11	FLJ23816	Q8TCI8	124852198	124856039	220	Unknown
	q34.11	ASS	P00966	124866845	124923190	412	Argininosuccinate synthase
AL353695	q34.11	No genes					
AL359092	q34.11	FUBP3	Q92946	125001544	125060268	542	Fuse binding protein 3
	q34.12	PRDM12	Q9H4Q4	125086510	125104913	367	PR domain containing protein 12
	q34.12	RRP4	Q13868	125115687	125126785	293	Exosome complex exonuclease RRP4
AL161733	q34.12	ABL1	P00519	125136236	125309589	1130	Abelson murine leukaemia viral oncogene
	q34.12	FLJ14810	Q96SJ7	125324358	125360767	198	Unknown
AL583807	q34.12	LAMC3	Q9Y6N6	125431028	125516389	1575	Laminin gamma-3 chain precursor
AL355872	q34.12	No genes					
AL157938	**q34.12**	**AIF1L**	**Q9BQI0**	**125518441**	**125545061**	**150**	**Ionised cacium binding adaptor molecule 2**
	q34.13	NUP214	P35658	125547506	125656586	2140	Nuclear pore complex protein
	q34.13	Q8N2W3	Q8N2W3	125679994	125698463	191	Unknown
AL354855	q34.13	FLJ90726	Q8NBV4	125711653	12731177	271	Unknown
	q34.13	Novel	ENSG00000130710	125729227	125729298	24	Unknown
AL358781	**q34.13**	**BAT2L**	**Q9BU62**	**125852061**	**125869120**	**325**	**HLA-B associated transcript**
	q34.13	LQFBS-1	O95209	125921328	125922066	245	Unknown
	q34.13	POMT1	Q9UNT2	125924841	125945722	747	Protein-o-mannosyltransferase 1
	q34.13	UCK1_HUMAN	Q9HA47	125945717	125953181	201	Uridine cytidine kinase 1
AL160276	q34.13	GRF2	Q13905	126000707	126159454	1077	Guanine nucleotide releasing factor 2
AL160271	q34.13	CRSP8	O95401	126282028	126512112	273	Cofactor required transcriptional activation
AL603649	q34.13	No genes					

AL713892	q34.13	No genes					
AL691506	q34.13	No genes					
AL513102	q34.13	No genes					
AL353631	q34.13	No genes					
AL159997	q34.13	KIAA1857	Q96JH0	126594193	126675069	541	Netrin G2
	q34.13	KIAA0625	Q8WX33	126693686	126761056	915	Unknown
AL353701	q34.13	TTF1	Q15361	126808230	126835074	882	Transcription termination factor
AL354735	q34.13	Novel	ENSG00000178595	126930940	126975292	179	Unknown
	q34.13	BARHL1	Q9BZE3	127014851	127022519	327	BARH (Drosophila)-like 1
AL160165	q34.13	DDX31	Q96NY2	127026534	127102646	851	DEAD/H Box Helicase
	q34.13	GTF3C4	Q9UKN8	127102586	127122695	822	General transcription factor
AL445645	q34.13	FLJ32704	Q96MA6	127157823	127310564	479	Unknown
	q34.13	C9orf9	Q96E40	127310608	127322275	222	Unknown
	q34.13	TSC1	Q92574	127323595	127376866	1164	Tuberous sclerosis 1 gene
	q34.13	Novel	ENSG00000176140	127379314	127383801	47	Unknown
AL593851	q34.13	GFI1B	O95270	127418923	127426295	330	Growth factor independent 1B
AL162417	q34.2	GTF3C5	Q9H4P2	127462958	12790748	528	General transcription factor
	q34.2	CEL	P19835	127494229	127504006	756	Carboxyl ester lipase
	q34.2	NM_173692		127513557	127514144	196	Unknown
	q34.2	CELL	Q14018	127514780	127519600	59	Carboxyl ester lipase-like
	q34.2	**RALGDS**	**Q12967**	**127529965**	**127553410**	**914**	**Ral Guanine nucleotide**
	q34.2	FRS	Q9UKI5	127585198	127596144	347	Forssman synthetase
AL732364	q34.2	OBPIIB	Q9NPH6	127637537	127641486	170	Odorant binding protein 2B
AL158826	q34.2	ABO	P16442	127687850	127694413	287	ABO blood group system
	q34.2	SURF6	O75683	127754393	127759885	361	SURFEIT locus protein 6
	q34.2	SURF5	Q15528	127764596	127771813	200	SURFEIT locus protein 5
	q34.2	SURF3	P11518	127771906	127775122	265	SURFEIT locus protein 3
	q34.2	Q9H3B2	Q9H3B2	127774377	127775089	101	Unknown
	q34.2	SURF1	Q15526	127775504	127780202	300	SURFEIT locus protein 1
	q34.2	SURF2	Q15527	127780269	127784875	256	SURFEIT locus protein 2
	q34.2	SURF4	O15260	127785181	127799817	269	SURFEIT locus protein 4
	q34.2	Q8NE28	Q8NE28	127800125	127828061	651	Unknown
	q34.2	Novel	ENSG00000175977	127821374	127824619	97	Unknown
	q34.2	XPMC2H	Q9GZR2	127828027	127840010	422	Prevents mitotic catastrophe 2
	q34.2	ADAMTS13	Q96L37	127843961	127881349	1427	Von Willebrand factor-cleaving protease
AL593848	q34.2	C9orf7	Q9UGQ2	127881962	127892726	172	Unknown
	q34.2	SLC2A6	Q8NCC2	127893058	127901068	515	Solute carrier family 2
BX324209	q34.2	No genes					
AC002321	q34.2	No genes					
<5 kb Gap							
AC002101	q34.2	No genes					
AL365494	q34.2	DBH	P09172	128007020	128030001	603	Dopamine beta-monooxygenase precursor
	q34.2	SARDH	Q9UL10	128056341	128124046	832	Sarcosine dehydrogenase
	q34.2	PP3781	Q8WY83	123131956	128132329	124	Unknown
AL590710	q34.2	Novel	ENSG00000176983	128211430	128251481	432	Unknown
	q34.2	SARDH	Q9UL10	128252348	128272381	396	Unknown
AL357934	q34.2	VAV2	P52735	128297977	12826304	878	Oncogene VAV-2 protein
AL445931	q34.2	Novel	ENSG00000179483	128559910	128562122	119	Unknown
	q34.2	**BRD3**	**Q15059**	**128566862**	**128602533**	**726**	**Bromodomain containing protein3**
	q34.2	Novel	ENSG00000179457	128588311	128592826	216	Unknown
AL591386	q34.2	No genes					
200kb Gap							
AL354796	q34.2	No genes					
AL683798	q34.2	No genes					
13 kb Gap							

AL669970	**q34.2**	**RXRA**	**P19793**	**129062693**	**129101647**	**453**	**Retinoid X receptor, alpha**
AL591890	**q34.3**	**COL5A1**	**Q96HC0**	**129302868**	**129503955**	**590**	**Collagen alpha 1 (V) chain precursor**
AL603650	q34.3	FCN2	Q15485	129541874	129548582	313	Ficolin 2 precursor
AL353611	q34.3	FCN1	O00602	129570647	129579025	326	Ficolin 1 precursor
AL159992	q34.3	No genes					
AL390778	q34.3	OLFM1	Q9BWJ9	129736484	129782241	467	Olfactomedin related ER localised protein
AL353615	q34.3	NM_173520	Q8N4C0	130006614	130009927	152	Unknown
AL161452	q34.3	Novel	ENSG00000178197	130131516	130144083	96	Unknown
	q34.3	NM_014811	Q9Y4D3	130146060	130152258	1209	Unknown
	q34.3	NM_144654	Q8WU44	130158546	130165104	92	Unknown
	q34.3	MRPS2	Q9Y399	130164060	130168038	296	Mitochondrial ribosomal protein S2
	q34.3	LCN1	P31025	130184820	130189897	176	Lipocalin 1
	q34.3	OBPIIA	Q9NY56	130209504	130213321	170	Odorant-binding protein 2A
AL354761	q34.3	PAEP	P09466	130225123	130230141	157	Progestagen associated endometrial
	q34.3	Novel	ENSG00000176541	130238316	130250477	104	Unknown
AL158822	q34.3	MUPL	Q8WX39	130326687	130329116	172	Putative MUP-like lipocalin
	q34.3	Q8NEE3	Q8NEE3	130356772	130362893	348	Unknown
	q34.3	KCNT1	Q9WX41	130365551	130455523	1151	Unknown
AL353636	q34.3	NM_018627	Q9WX42	130472946	130570503	1298	Unknown
AL355574	q34.3	GPDR1	Q9BSL1	130596334	130624745	405	Glialblastoma related protein
	q34.3	NM_144653	Q96BF6	130674721	130713948	587	Unknown
AL591038	q34.3	Novel	ENSG00000180858	130715097	130738981	273	Unknown
AL138781	q34.3	Q96GU2	Q96GU2	130777953	130782228	29	Unknown
	q34.3	Q8N3G2	Q8N3G2	130869698	130887479	541	Unknown
	q34.3	LHX3	Q9UBR4	130859621	130868480	397	LIM Homeobox gene 3
30 kb Gap							
AL603784	q34.3	AGS3	Q9UFS8	130939617	130943166	530	Unknown
AL592301	q34.3	CARD9	Q9H257	130947895	130957602	536	Caspase recruitment protein
	q34.3	SNAPC4	Q9Y6P7	130959516	130982736	1469	Small nuclear RNA activating complex
	q34.3	SDCCAG3	O60525	130985862	130994412	192	Serologically defined colon cancer antigen
	q34.3	INPP5E	Q10713	130994603	131007700	525	Mitochondrial processing peptidase subunit
	q34.3	PPI5PIV	Q9NRR6	131012558	131023761	644	Phosphatidylinositol (4,5) bisphosphate 5-phophatase
	q34.3	KIAA0310	Q96HP1	131024036	131059908	1433	Unknown
	q34.3	NM_152571	Q8N9P6	131067482	131070005	203	Unknown
	q34.3	**NOTCH1**	**P46531**	**131078383**	**131129726**	**2559**	**Neurogenic locus NOTCH homologue protein**
AL590226	q34.3	Novel	ENSG00000180360	131211094	131230721	251	Unknown
	q34.3	Q9P058	Q9P058	131232664	131244366	146	Unknown
	q34.3	ZNEU1	Q9UHF1	131242795	131256617	273	ZNEU1/NEU1 protein
	q34.3	**AGPAT2**	**O15120**	**131257082**	**131271362**	**278**	**Acylglycerol-phophate-acyltransferase 2**
	q34.3	NM_152421	Q8WYU5	131296511	131307989	431	Unknown
AL355987	q34.3	NM_032887	Q96IC0	131309173	131312123	37	Unknown
	q34.3	Novel	ENSG00000169672	131313093	131332422	726	Unknown
	q34.3	FLJ33328	Q8NBE9	131338327	131341477	333	Unknown, has IG_MHC domain
	q34.3	FLJ10101	Q96BU21	131383198	131425126	307	Unknown
	q34.3	FLJ30985	Q96NE7	131387866	131392787	197	Unknown
	q34.3	Nov-01	ENSG00000054148	131433033	131434977	186	Unknown
	q34.3	Novel	ENSG00000148406	131436356	131438789	350	Unknown
	q34.3	Novel	ENSG00000179285	131439193	131440765	264	Unknown
	q34.3	Q8NCX7	Q8NCX7	131440944	131444739	236	Unknown
	q34.3	EDF1	O60869	131446058	131450225	148	Endothelial differentiation-related factor 1
AL449425	q34.3	TRAF2	TRA2_HUMAN	131482651	131510546	501	TNF receptor associated factor 2
AL807752	q34.3	NM_018998	Q969U6	131524374	131528545	566	Unknown
	q34.3	C8G	P07360	131529200	131530906	198	Complement component 8, gamma subunit
	q34.3	PTGDS	P41222	131561509	131565680	190	Prostaglandin D2 synthase
	q34.3	Novel	ENSG00000176785	131567941	131570349	137	Unknown

	q34.3	**CLIC3**	**O95833**	**131578574**	**131580807**	**207**	**Chloride intracellular channel protein 3**
	q34.3	**ABCA2**	**Q9BZC7**	**131591173**	**131612250**	**2440**	**ATP-binding cassette, subfamily A, member 2**
	q34.3	Q9BUH6	Q9BUH6	131576357	131577915	212	Unknown
	q34.3	FUT7	Q11130	131614669	131615685	339	Fucosyltransferase 7
AL929554	q34.3	Q8N224	Q8N224	131618602	131619006	135	Unknown
	q34.3	NPDC1	Q9NQX5	131623413	131630157	325	Neuronal proliferation protein 1
	q34.3	ENTPD2	Q9Y5L3	131632616	131638290	494	Ectonucleoside triphosphate diphosphydrolase 2
	q34.3	Q8TEI1	Q8TEI1	131662043	131670905	270	Unknown
	q34.3	Q8WUC7	Q8WUC7	131669250	131671114	104	Unknown
	q34.3	MAN1B1	Q9UKM7	131671245	131695076	699	Endoplasmic reticulum mannosidase
	q34.3	Novel	ENSG00000179395	131687948	131691411	989	Unknown
	q34.3	**DPP7**	**Q9UHL4**	**131696546**	**131699393**	**331**	**Dipeptidyl-peptidase**
	q34.3	GRIN1	Q05586	131724505	131753424	928	Glutamate receptor subunit zeta 1
	q34.3	NM_013366	Q9UJX6	131759296	131773049	822	Anaphase-promoting complex subunit 2
	q34.3	SSNA1	O43805	131773159	131774882	119	Sjorgen's syndrome nuclear autoantigen 1
	q34.3	FLJ90254	Q8NCH2	131776627	131784420	433	Unknown
	q34.3	NM_053045	Q969S6	131788473	131790029	136	Unknown
BX255925	q34.3	Unfinished					
BX322799	q34.3	Unfinished					
AL365502	q34.3	AD038	Q96F01	132035782	132039264	205	AD038 protein, function unknown
	q34.3	NM_152285	Q8N5I2	132039236	132048941	433	Unknown
	q34.3	MZIP	Q96E35	132064147	132072376	227	Melanin-concentrating hormone receptor 1
	q34.3	NM_138778	Q9BTV6	132075663	132096389	484	Unknown
	q34.3	MRPL41	NM_032477	132098739	132099406	137	Mitochondrial ribosomal protein L41
	q34.3	NTE-L	Q8TAY5	132153193	132190541	702	Neuropathy Target Esterase
	q34.3	FLJ14568		132192950	132200987	327	Unknown
	q34.3	Q9NTU2		13295160	132200984	130	Unknown
AL590627	q34.3	Novel	ENSG00000181090	132289873	132374235	436	Unknown
AL611925	**q34.3**	**HMT1**	**Q9H9B1**	**132395728**	**132553855**	**1247**	**Histone methyltransferase**
AL772363	q34.3	CACNA1B	Q00975	132562084	132806329	2357	Calcium channel voltage-dependent
AL591424	q34.3	IL9R	ENSG00000165830	132821281	132832099	216	Interleukin 9 receptor IL 9R
	q34.3	**Novel**	**ENSG00000159247**	**132859209**	**132861370**	**425**	**Tubulin pseudogene**
	q34.3	Novel	ENSG00000179338	132868297	132868767	157	LINE 1 Reverse Transcriptase Homologue
AL954642	q34.3	No genes					

Appendix 2

Table of results the whole-genome survey. The P-values are coloured according to the level of confidence; black are L0-paralogues, green L1-paralogues, blue L2-paralogues and red are L3-paralogues.

Class	*MHC gene*	*Clone*	*Locus*	*Start*	*End*	*BLAST Match*	*P-value*
III	NOTCH4	AL390719.31.31331.88824	1p36.33	708136	744003	AGRN	1.50E-23
xII	B3GALT4	AL162741.35.1.111409	1p26.33	919626	921479	B3GALT6	1.40E-08
III	NOTCH4	AL391244.11.1.67923	1p36.33	1073552	1087162	NM_030937	9.10E-09
III	BAT8	AL391244.11.1.67923	1p36.33	1089751	1108843	Novel	7.60E-12
III	NOTCH4	AL512413.21.1.101803	1p36.32	2844459	2886399	EGFL3	2.20E-42
xI	BTN1A1	AL662907.11.1.64693	1p35.1	3343046	33466609	Q9BVG3	1.10E-18
III	NOTCH4	AL513320.27.1.132592	1p36.32	3364015	3405344	EGFL3	2.00E-25
III	C2	AL109811.40.1.112769	1p36.22	10930224	10950939	MASP2	1.30E-05
xI	BTN1A1	AC074003.3.23107.35032	1p36.13	14652770	14656331	Novel	4.20E-14
III	C6orf46/ZNF297	AL034555.2.1.86897	1p36.13	15447174	15481304	ZNF151	2.40E-14
I	DDR1	AL451042.10.1.88098	1p36.13	15564788	15596501	EPHA2	1.10E-17
xII	KIFC1	AL663074.13.1.8581	1p36.12	20071643	20079710	Novel	2.60E-24
III	NOTCH4	AL590103.12.1.175162	1p36.12	21183949	21258020	HSPG2	1.10E-16
I	DDR1	AL035703.21.1.160705	1p36.12	21925207	21965283	EPHA8	1.40E-15
I	DDR1	AL035704.9.1.113956	1p36.12	22143606	22277501	EPHB2	3.10E-20
xII	LYPLA2L	AL031295.1.1.124001	1p36.11	23188619	23193014	LYPLA2	9.00E-75
III	CLIC1	AL662924.15.1.121762	1p35.3	24141534	24239539	CLIC4	3.80E-27
I	DDR1	AL031729.16.1.125287	1p36.11	26912974	26924738	FGR	3.20E-15
xII	COL11A2	AC114488.1.90406.184673	1p35.2	31102432	31154233	COL16A1	2.10E-11
xII	ZNF297	AL033529.25.1.147167	1p35.1	31870816	32006551	NM_144621	1.00E-13
xI	RFP	AL662907.11.1.64693	1p35.1	32565928	32602196	NM_018207	7.60E-46
III	C2	AC115285.1.63883.124348	1p35.1	33035623	33094251	Q96Q03	9.80E-08
III	BF	AC115285.1.63883.124348	1p35.1	33799053	33862505	Q9H4W4	9.50E-08
I	POU5F1	AL139158.11.1.115614	1p34.3	37518563	37519168	no gene	4.50E-44
III	HSPA1L	AL354702.7.1.107422	1p34.3	38182110	38184069	Novel	4.30E-158
xII	ZNF297	AL356379.10.1.64960	1p34.2	40000812	40017418	NM_152373	7.80E-09
xI	RFP/MOG/BTNL2	AL512353.16.1.81704	1p34.2	42286363	42314156	ERMAP	6.60E-49
I	DDR1	AC093420.1.127596.194462	1p34.2	42767145	42789215	TIE	4.80E-05
II	BTNL2	AL109659.20.1.181678	1p33	47521181	181364180	genscan	1.10E-24
xI	BTN1A1	AL109659.20.1.181678	1p33	48243776	48288207	no gene	3.40E-29
xI	MOG	AL109659.20.1.181678	1p33	48253780	48253842	genscan	4.00E-22
xI	GPX5	AL356976.30.1.64323	1p32.3	51957064	51963742	NM_015696	8.30E-09
I	TUBB	AL445183.19.1.193774	1p32.3	53049002	53152605	SCP2	8.90E-12
I	DDR1	AL445205.14.1.115936	1p31.3	63525514	63564266	EST gene	3.10E-45
I	DDR1	AC093427.2.1.131877	1p31.3	64219769	64351748	JAK1	2.50E-09
III	C6orf29	AC107627.2.1.90513	1p31.1	74605198	75011843	NM_152697	8.70E-49
III	MSH5	AL445464.9.1.103097	1p31.1	75197713	75313965	MSH4	4.30E-05
III	DDAH2	AL078459.8.1.83946	1p22.3	84926028	85072691	DDAH1	3.50E-15
xII	COL11A2	AL356059.27.1.76418	1p22.3	85351949	85791154	NM_152890	1.90E-05
II	BRD2	AC004798.1.1.42497	1p22.1	91625907	91677611	BRDT	6.50E-101
III	C9orf29	AC093429.2.1.182165	1p21.3	94491811	94566684	NM_152369	1.30E-08

xII	COL11A2	AC093150.2.1.189945	1p21.1	104172486	104410718	COL11A1	4.10E-42
III	NOTCH4	AL390252.9.1.169241	1p13.3	108785784	108869934	SORT1	6.40E-22
III	BAT1	AL445483.13.1.164008	1p13.2	112714422	112726367	DDX20	3.00E-14
xI	MOG/BTN1A1	AL391476.20.1.171595	1p13.1	118145476	118212809	NM_024626	9.30E-05
III	NOTCH4	AL359752.11.1.137955	1p11.2	119292037	119450143	NOTCH2	2.30E-61
III	NOTCH4	AL592307.24.14836.157830	1q21.1	141809266	141890630	Novel	3.20E-27
III	NOTCH4	AC018381.3.23653.71017	1q21.1	141956297	141968135	Novel	3.70E-28
xI	HIST1H2AC	AL591493.13.1.113370	1q21.2	145553544	145555199	Histones	3.30E-48
III	BAT8	AL590133.32.1.192096	1q21.3	146646159	146684482	SETDB1	1.90E-12
xII	ZNF297	AL451085.20.1.182166	1q22	150706074	150720422	ZFP67	5.40E-14
I	POU5F1	AL139410.20.1.166288	1q22	151143602	151144684	Q9BZW0	4.10E-105
III	NOTCH4	AL158169.17.1.99802	1q23.1	152575891	152593889	INSRR	6.10E-12
I	DDR1	AL158169.17.1.99802	1q23.1	152595949	152616657	NTRK1	1.70E-30
xI	HFE	AL138899.23.1.134137	1q23.1	153882029	153886978	CD1D	2.50E-05
III	NOTCH4	AL356104.6.1.96693	1q23.1	154745243	154755113	Q8TEK2	4.20E-22
III	HSPA1L	AL590385.22.1.110781	1q23.3	157226591	157228843	HSPA6	6.20E-263
III	CREBL1	AL391825.15.1.211662	1q23.3	157386942	157579736	ATF6	4.30E-25
I	DDR1	AL445197.4.1.117040	1q23.3	158253102	158401084	DDR2	1.50E-131
III	PBX2	AL357568.14.1.71359	1q23.3	160179905	160302546	PBX1	3.40E-88
I	POU5F1	AL136984.20.1.169627	1q24.2	162840972	163036179	POU2F1	5.70E-19
xII	RXRB	AL160058.8.1.155369	1q23.3	163005239	163049202	RXRG	3.00E-63
xII	RPS18	AL031733.3.1.215861	1q24.2	163211499	163211834	no gene	7.20E-14
III	BAT2	AL021579.1.1.99886	1q24.3	167083736	167191695	BAT2-ISO	1.60E-63
III	TNF	Z96050.1.1.85811	1q24.3	168257203	168265061	TNFSF6	5.90E-06
III	TNXB	Z94055.1.1.134539	1q25.1	170720587	170804587	TNR	6.00E-07
III	C6orf46	AL136170.12.1.127541	1q25.1	171377563	171488882	NM_032522	2.10E-33
I	DDR1	AL139132.16.1.157866	1q25.2	174505391	174627374	ABL2	7.90E-12
I	HLA-A/HLA-E	AL162431.17.1.139006	1q25.3	176341488	176402911	STX6	1.60E-20
xI	HLA Class I and II	AL356267.27.1.181808	1q25.3	176431452	176452972	HLALS	3.50E-31
III	BAT1	AL049557.19.1.128379	1q25.2	176601093	176723077	ABL2	3.40E-10
III	BAT8	AL138776.10.1.100549	1q25.3	177972880	177984295	RNASEL	3.30E-05
xII	RAB2L	AL590422.14.1.198210	1q25.3	179033557	179326003	RGL1	8.30E-17
xII	RING1	AL109865.36.1.201823	1q25.3	180442880	180499976	RNF2	4.20E-50
I	DHX16	AL355999.9.1.76504	1q31.1	185516454	185517347	genscan	1.10E-07
xII	B3GALT4	AL390863.9.1.122864	1q31.2	188662474	188670039	B3GALT2	2.20E-21
III	NOTCH4	AL513325.13.1.212888	1q31.3	192695849	192906025	CRB1	4.20E-52
III	ATP6V1G2	AL157402.19.1.210331	1q31.3	193950307	193968515	ATP6V1G3	2.40E-09
xII	RXRB	AC096633.2.1.178152	1q32.1	195455200	195604973	NR5A2	1.50E-15
xII	KIFC1	AL445483.13.1.164008	1q32.1	195979729	196048406	KIF14	7.50E-10
III	BAT1	AL512326.24.1.189269	1q32.1	198323462	198369154	NM_031306	4.00E-06
xII	RPS18	AL606462.5.1.112401	1q42.13	223356887	223357135	genscan	1.20E-40
xI	RFP	AL139288.15.1.151563	1q42.13	224319970	224333114	TRIM11	2.10E-64
xI	HIST1H2AC	AL139288.15.1.151563	1q42.13	224383273	224384153	H2AFL	4.80E-49
xI	BTN1A1	AL139288.15.1.151563	1q42.13	224436665	224436976	genscan	4.50E-64
II	BTNL2	AL139288.15.1.151563	1q42.13	224436716	224436991	genscan	3.70E-19
II	TAP2/1	AL121990.33.1.147913	1q42.13	225346509	225388622	ABCB10	5.10E-24
III	PBX2	AL359255.12.1.20809	1q42.13	226893037	227045628	OBSCN	5.40E-11
xI	BTN1A1	AC026657.4.97959.109520	1q42.13	227053394	227055850	TRIM11	1.20E-16
xI	MOG	AL139288.15.1.151563	1q42.13	227195475	227197055	Novel	9.50E-16
xI	RFP	AL591686.9.1.150680	1q43	237498626	237934567	NM_152666	2.40E-11
III	C6orf46/ZNF297	AL590483.25.118180.187060	1q44	239460483	239466676	ZNF238	9.20E-16
III	HSPA1L	AL390728.34.1.206255	1q44	242630342	242630950	no gene	5.80E-218
xI	RFP	AC099571.1.86529.165648	1q44	243256848	243277448	NM_015431	1.50E-65
xI	BTN1A1	AC099571.1.86529.165648	1q44	245957656	245974557	Q9Y4N9	3.50E-37
III	NOTCH4	AC105450.1.1.163782	2p25.3	1491150	1620306	TP0	2.10E-07
xII	KIFC1	AC013449.8.1.120997	2q23.3	26242053	26297524	KIF3C	3.30E-37

III	BAT1	AL121658.4.1.162692	2p22.3	32334563	32390404	Q96NC3	6.30E-05
xI	HIST1H2AC/NOTCH4	AL133244.1.1.200368	2p22.3	33311500	33772726	LTBP1	6.50E-18
III	CYP21A2	AC009229.5.1.209156	2p22.2	38259590	38268136	CYP1B1	9.30E-15
I	DHX16	AC092833.4.1.143506	2p22.1	39171874	39237365	NM_145646	5.30E-10
I	DHX16	AC018693.8.1.164125	2p22.1	39282730	39282825	no gene	1.00E-09
xI	NEFAL	AC016722.9.1.149995	2p21	47297756	47311689	NM_139279	3.80E-32
III	MSH5	AC009600.19.1.215260	2p21	47798999	47879105	MSH2	5.00E-09
xI	UBD	AC079807.5.1.156175	2p16.3	48126446	48126718	genscan	5.80E-05
III	MSH5	AC006509.15.1.124015	2p16.3	48179027	48202837	MSH6	7.80E-08
xII	B3GALT4	AC093401.4.1.99088	2p15	62609435	62638037	B3GNT1	2.30E-13
I	DHX16	AC005041.2.1.191356	2p13.1	74958046	74966106	NM_133637	1.30E-10
III	BAT2	AC068279.6.1.135351	2p11.2	87959386	87959877	no gene	3.10E-05
III	BAT2	AC026106.12.36729.68570	2p11.2	90750748	90751398	no gene	6.50E-05
xII	ZNF297	AC092835.4.1.158404	2q-tel	94264885	94283773	ZNF2	3.70E-10
xI	RFP	AC018892.8.1.191055	2q11.2	96145683	96151491	Novel	1.60E-21
I	DDR1	AC016699.10.1.54480	2q11.2	96793061	96808883	ZAP70	3.30E-15
I	POU5F1	AC018730.7.1.154728	2q12.1	103925142	103926146	POU3F3	2.60E-44
xI	BTN1A1	AC005040.2.1.189949	2q12.3	106059831	106060295	genscan	3.40E-08
xII	ZNF297	AC013268.5.1.206457	2q13	109008786	109017957	NM_152518	4.40E-13
I	C6ORF18	AC018737.9.1.206454	2q14.3	120015449	120327116	CLASP1	9.70E-06
xII	RPS18	AC018737.9.1.206454	2q14.3	120421203	120421337	no gene	9.80E-10
I	TUBB	AC018804.9.1.195514	2q21.1	128250367	128259530	genscan	3.00E-08
I	TUBB	AC073869.5.1.195280	2q21.2	129791442	129796126	TUBA2	1.80E-10
I	MRPS18B	AC012497.8.1.212104	2q22.1	138733844	138734416	genscan	1.20E-75
xII	RXRB	AC074099.6.1.143653	2q24.1	155709873	155718141	NR4A2	1.00E-06
xII	B3GALT4	AC016723.11.1.202001	2q24.3	167216857	167269041	B3GALT1	8.10E-30
II	TAP2/1	AC069137.6.1.108836	2q24.3	168321109	168292498	ABCB11	6.90E-21
xII	COL11A2	AC066694.7.1.120381	2q32.2	187975163	188013419	COL3A1	5.40E-32
III	HSPA1L	AC013409.8.1.195478	2q34	208662170	208666396	Novel	1.00E-116
I	TUBB	AC068946.4.1.172260	2q35	218133730	218152718	TUBA4	2.00E-10
I	DDR1	AC010899.8.1.210232	2q36.1	221011996	221158367	EPHA4	9.20E-15
III	HSPA1L	AC009302.2.1.180970	2q36.1	221548101	221549027	genscan	7.00E-113
xI	BTN1A1	AC104772.3.1.106526	2q36.1	221566190	222241888	SYFB	1.40E-19
xI	RFP	AC104772.3.1.106526	2q36.1	222156619	222241888	SYFB	4.40E-44
xI	PRSS16	AC008072.3.1.206177	2q36.1	223964489	223987825	NM_024785	4.20E-10
xII	COL11A2	AC073869.5.1.195280	2q36.3	226590998	226750349	COL4A4	3.50E-07
xII	COL11A2	AC097662.4.37779.206758	2q36.3	226750355	226900581	COL4A3	8.90E-12
III	NOTCH4	AC008273.2.1.151297	2q36.3	228954450	229310970	NM_139072	3.30E-23
xII	B3GALT4	AC017104.8.1.168880	2q37.1	230992101	230995454	B3GNT7	3.50E-15
III	NOTCH4	AC005237.2.1.175179	2q37.3	240214701	240251678	PASK	2.30E-53
xII	KIFC1	AC011298.6.31675.58437	2q37.3	240584194	240668241	ATSV	3.00E-06
III	BAT8	AC034191.5.1.172215	3p26.1	4284929	4298795	SETMAR	2.00E-25
xII	RXRB	AC090947.1.1.166043	3p25.2	12270465	12415723	PPARG	5.30E-09
III	NOTCH4	AC090509.1.1.165994	3p25.1	13551690	13619799	FBLN2	2.40E-09
xII	RXRB	AC090937.1.1.160696	3p25.1	15002136	15024392	NR2C2	6.60E-09
xI	HMGN4	AC027125.4.1.173836	3p25.1	15346179	15346391	no gene	1.90E-06
III	BAT8	AC090950.1.1.199282	3p25.1	15648627	15776696	Y379	3.60E-05
III	HSPA1L	AC097635.2.1.162887	3p24.3	19380503	19387078	Novel	2.90E-102
xII	ZNF297	AC006059.3.1.185161	3p22.1	41880829	41889031	NM_145166	1.10E-11
III	C6orf46	AC099669.2.1.217035	3p21.32	43776685	43804920	Novel	4.10E-13
III	C6orf46	AC124045.1.109944.135528	3p21.32	43934102	43945288	NM_033210	5.10E-12
I	DDR1	AC104439.2.1.197279	3p21.32	45363297	45363752	genscan	7.20E-14
I	DHX16	AC026318.7.1.19068	3p21.31	47135873	47174627	DDX30	5.00E-25
xII	COL11A2	AC005903.3.1.60660	3p21.31	47884518	47915700	COL7A1	5.00E-11
III	NOTCH4	AC005923.2.1.88326	3p21.31	47956918	47983375	CELSR3	3.60E-22
xI	GPX5	AC121247.1.77964.92674	3p21.31	48542852	48544273	GPX1	2.40E-34

III	NOTCH4	AC112215.1.181144.198956	3p21.31	51781935	51811071	STAB1	1.20E-16
I	ABCF1	AC021123.4.149752.161126	3q-tel	91147420	91149286	Novel	1.50E-63
I	DDR1	AC107028.4.1.185539	3q11.2	92010160	92148744	EPHA3	1.20E-15
xII	RPS18	AC108715.2.1.176462	3q11.2	94194400	94194576	no gene	2.40E-15
xII	RPS18	AC108695.2.1.190845	3q11.2	94194185	94194358	Novel	4.30E-24
xII	COL11A2	AC069222.23.1.117000	3q12.1	96016863	96137341	COL8A1	3.50E-23
I	POU5F1	AC117460.7.1.183595	3q12.1	97141764	97141988	EST gene	2.20E-18
I	TUBB	AC046144.15.1.188840	3q13.11	100051837	100051959	genscan	2.00E-11
xII	RPS18	AC073861.18.98940.165924	3q12.3	100725089	100725481	EST gene	4.20E-62
xII	ZNF297	AC084198.24.86116.155268	3q12.3	100797978	100825652	NM_014415	3.60E-12
I	POU5F1	AC079945.13.52386.74222	3q21.3	128590475	128590648	genscan	4.70E-55
III	NOTCH4	AC080007.26.1.168551	3q21.3	129795525	129875755	WDR10	8.50E-10
III	HSPA1L	AC020632.16.1.162029	3q22.1	133021872	133186190	NM_153240	1.90E-22
I	DDR1	AC092969.6.71736.203901	3q22.2	135625566	135694383	Novel	5.10E-21
III	HSPA1L	AC117478.3.1.77155	3q22.3	138390731	138391456	genscan	4.20E-215
III	PBX2	AC018450.26.1.191474	3q24	139874190	139875716	PBXP1	4.50E-161
III	C6orf46/ZNF297	AC010184.18.1.190580	3q23	141935447	141992349	Q8NAP3	6.00E-07
III	BAT1	AC112907.4.101183.186560	3q25.2	151048380	151140293	Novel	2.00E-24
xII	B3GALT4	AC021649.18.1.209521	3q25.33	161749105	161770594	B3GALT3	9.40E-19
III	BAT1	AC092946.7.1.115500	3q27.3	183276473	183282793	EIF4A2	8.70E-15
xII	B3GALT4	AC069417.16.47453.72677	3q27.1	183826771	183845940	B3GNT5	8.40E-28
I	ABCF1	AC048331.32.147427.232441	3q27.1	184898582	184906494	NM_018358	1.60E-37
I	GNL1	AC046143.20.1.180365	3q29	197722675	197769579	NM_018385	3.90E-07
III	NOTCH4	AC021118.6.1.194612	4p15.31	20338712	20704631	SLIT2	1.00E-25
I	DHX16	AC115110.2.23128.113396	4p15.2	24612486	24669565	DDX15	4.30E-58
III	C6orf46/ZNF297	AC105287.4.52544.192873	4p14	39946115	39947420	Novel	1.40E-163
II	HLA Class II	AC097451.2.1.146808	4p13	43676798	43677424	EST gene	1.10E-22
III	LSM2	AC108054.2.101121.147995	4p12	48652844	48737332	Q9P270	1.40E-20
I	DDR1	AC098587.1.9710.175365	4q12	55065587	55126000	PDGFRA	3.00E-05
xI	RFP	AC107058.4.1.126135	4q13.1	65884515	65884994	genscan	1.00E-24
III	BAT8	AC053527.8.1.233250	4q13.3	74230262	74364018	Q9H288	8.00E-05
xI	HIST1H2AC	AC097460.3.1.164370	4q23	101179583	101181853	H2AFZ	2.70E-15
III	BAT1	AC105460.4.1.185755	4q24	104893633	104894151	Genscan	4.00E-10
III	CYP21A2	AC096564.3.1.163317	4q25	109292353	109297744	Novel	2.10E-15
xII	LYPLA2L	AC004062.1.1.154252	4q25	112148688	112149080	no gene	7.40E-66
I	TUBB	AC093663.4.1.171745	4q25	113404522	113404635	genscan	1.20E-09
I	TUBB/RNF5	AC093816.3.1.170227	4q27	123297626	123297751	genscan	4.50E-36
III	BAT8/NOTCH4	AC105421.2.1.162793	4q28.1	125865162	125873003	YB23	2.50E-16
III	NOTCH4	AC092629.2.1.148673	4q28.1	126653380	126692458	NM_024582	2.20E-30
III	HSPA1L	AC093591.3.1.158758	4q28.1	128982992	129034039	OS94	2.00E-16
I	POU5F1	AC093887.3.1.192886	4q31.22	147935518	147939053	POU4F2	5.90E-28
II	TAP1	AC017037.10.1.186106	4q32.1	159166512	159166844	no gene	8.50E-05
III	HSPA1L	AC105250.3.1.70449	4q32.3	165537822	165539805	Novel	3.40E-147
I	IER3	AC106872.5.1.174535	4q32.3	166282549	166282689	no gene	1.10E-07
xI	RFP	AC106872.5.1.174535	4q32.3	166359709	166359709	Novel	8.10E-63
xI	BTN1A1/RFP	AC106872.5.1.174535	4q32.3	166381434	166391179	NM_152620	3.00E-31
xI	BTN1A1	AC108465.3.1.48677	4q32.3	166812464	166832879	Butyrophilin	5.20E-34
xI	RFP	AC080079.5.1.112516	4q32.3	167014840	167015103	genscan	7.60E-22
xII	HSD17B8	AC021151.8.1.175081	4q32.3	170330785	170353453	NM_032783	7.10E-06
III	NOTCH4	AC079226.7.1.184032	4q35.1	184330635	184402306	NM_018104	1.30E-11
III	NOTCH4	AC110761.3.1.153458	4q35.2	188188876	188324915	FAT	2.50E-13
xI	BTN1A1/RFP	AC108073.2.107221.165848	4q35.2	189692345	189706326	NM_173553	8.20E-19
xI	POM121L2	AC093308.2.104996.134015	5p14.3	21925895	21928486	Novel	1.10E-09
xI	SMA3L	AL157879.7.1.161460	5p13.3	34638648	34642503	Novel	2.00E-45
xI	SMA3L	AC114970.1.37696.100300	5p13.3	34737381	34778708	Novel	1.40E-46

xI	POM121L2	AC114970.1.37696.100300	5p13.3	34761244	34778854	Q9H1S5	1.30E-10
I	TUBB	AC106800.1.2657.73135	5p12	43538759	43538860	genscan	8.00E-05
III	BAT1	AC016632.6.1.176784	5q11.2	55195823	55274550	DDX4	6.10E-09
xI	GPX5	AC091977.3.1.183494	5q11.2	55884790	55889596	Q8TED1	2.50E-05
I	DHX16	AC020728.4.1.201404	5q11.2	55980727	56032245	NM_019030	9.30E-13
III	SKIV2L	AC020728.4.1.201404	5q11.2	56032666	56149658	KIAA0052	9.80E-50
xI	SMA3L	AC108108.1.77200.116688	5q13.2	70698028	70703834	Novel (SMA3)	2.00E-48
III	MSH5	AC022493.12.1.153078	5q14.1	80189323	80411166	MSH3	3.90E-15
xII	RPS18	AC008799.6.1.123098	5q14.3	90941311	90941703	genscan	4.70E-49
xII	RXRB	AC106818.1.6855.31297	5q15	93388022	933399296	NRF1	6.60E-19
I	POU5F1	AC108102.2.1.161056	5q15	93545276	93545938	genscan	4.20E-48
III	BAT1	AC016567.8.1.159734	5q15	97361820	97362176	Genscan	1.30E-11
xI	POM121L2	AC114324.1.39743.91827	5q21.1	99294853	99295455	no gene	6.90E-07
xI	SMA3L	AC114324.1.39743.91827	5q21.1	99303064	99303249	genscan	8.30E-27
xI	SMA3L	AC092278.3.1.123469	5q21.1	99829117	99834848	Novel (SMA3)	1.30E-42
III	LSM2/DDR1	AC109481.3.1.20673	5q21.3	108524961	108964792	FER	9.90E-36
I	DHX16	AC093208.2.1.112115	5q22.2	113296938	113337241	Novel	7.10E-07
III	BAT8	AC010226.5.1.147140	5q22.3	115264395	115288381	FEM1C	7.20E-06
xI	HMGN4	AC109456.3.1.121848	5q23.1	115322895	115323107	no gene	5.80E-05
III	NOTCH4	AC008682.6.1.217221	5q23.2	127062260	127232628	NM_032446	1.30E-18
III	NOTCH4	AC010424.9.1.192282	5q23.2	127289102	127326544	NM_130809	9.10E-10
III	NOTCH4	AC025169.5.1.161920	5q23.2	128029494	128309063	FBN2	4.50E-35
III	HSPA1L	AC005373.1.1.112220	5q23.3	129911964	129912584	genscan	6.20E-159
xII	KIFC1	AC004237.1.1.38715	5q23.3	132479552	132517394	KIF3A	4.20E-18
III	HSPA1L	AC113410.2.1.123851	5q31.1	132834893	132887389	HSPA4	3.00E-19
III	BAT1	AC010301.7.1.155067	5q31.1	133745073	133815582	NM_014829	1.40E-09
xI	HIST1H2AC	AC026691.5.1.135062	5q31.1	135237074	135302580	H2AFY	2.10E-21
III	HSPA1L	AC011385.6.1.134599	5q31.2	138566125	138586223	HSPA9B	2.50E-72
I	POU5F1	AC011396.4.1.87692	5q32	146300493	146301825	POU4F3	5.50E-28
III	ATP6V1G2	AC008385.7.1.151712	5q33.1	150765251	150795891	Novel	1.50E-06
xI	GPX5	AC008666.5.1.99108	5q33.1	151002039	151004829	GPX3	4.20E-64
xII	KIFC1	AC008410.5.53020.91332	5q33.2	154988937	154992638	Novel	1.80E-38
III	NOTCH4	AC011369.4.1.141529	5q34	167774142	168258463	Novel	8.20E-10
III	NOTCH4	AC011365.4.1.81930	5q34	168684275	168685047	Novel	7.40E-29
xII	ZNF297	AC104117.1.114225.124230	5q35.3	179277145	179302355	Q8N9F8	5.60E-10
xI	BTN1A1/MOG	AC016572.6.1.143687	5q35.3	180455914	180507663	Butyrophilin	3.30E-54
xI	BTN1A1/MOG	AC091874.2.1.13312	5q35.3	180545631	180563128	BTNL3	4.10E-32
xI	BTN1A1	AC091874.2.13413.147570	5q35.3	180597001	180613745	Butyrophilin	9.10E-53
xI	BTN1A1	AC008443.9.1.120524	5q35.3	180699946	180712464	Q8WV44	4.00E-31
xI	BTN1A1/MOG/BTNL2	AC022413.4.1.166525	5q35.3	181312424	181364180	NM_024850	5.60E-26
II	BTNL2	AC091874.2.13413.147570	5q35.3	181402141	181419638	Butyrophilin	7.20E-23
II	BTNL2	AC091874.2.1.13312	5q35.3	181453511	151470537	NM_152547	2.70E-27
xI	RFP	AC008443.9.1.120524	5q35.3	181733455	181735630	TRIM7	3.80E-58
I	TUBB	AL031963.40.1.149546	6p25.2	3138899	3142759	TUBBL	2.40E-208
I	TUBB	AL445309.13.1.136587	6p25.2	3209729	3212968	TUBBL	2.40E-208
xII	RPS18	AL359643.27.1.166863	6p25.1	4964305	4964649	genscan	7.50E-35
III	C6orf46	AL161903.19.1.47104	6p21.32	33384295	33421772	SYNGAP1	3.30E-17
xII	ZNF297	AL161903.19.1.47104	6p21.32	33407966	33421769	NM_152735	2.90E-50
xII	RXRB	AL022721.1.1.170245	6p21.31	35306800	35392369	PPARD	5.50E-09
xII	KIFC1	AL590387.7.1.76075	6p21.2	39560349	39603922	Novel	1.20E-12
I	TUBB	AL136089.15.1.99479	6p21.2	39962644	39962751	genscan	1.00E-10
I	DDR1	AL355385.15.1.129884	6p21.1	43040485	43125871	PTK7	2.20E-17
xI	BTN1A1	AL512353.16.1.81704	6p34.2	43256510	43284362	ERMAP	2.60E-68
II	TAP2/1	AL359813.23.1.102892	6p21.1	43391706	43414579	ABCB10	2.00E-15
III	NOTCH4	AL359813.23.1.102892	6p21.1	43414506	43420784	NM_023932	5.70E-28
III	CLIC1	AL357057.19.1.58133	6p21.1	45865819	46044480	CLIC5	8.00E-53

xI	SMA3L	AL021368.1.1.188642	6p11.2	58109978	58115773	Novel(SMA3)	7.30E-41
III	NOTCH4	AL137007.9.1.105779	6q12	65571522	65587322	Q9H557	2.30E-24
xII	COL11A2	AL080275.20.1.113983	6q13	70892928	70979474	COL9A1	8.90E-08
xII	LYPLA2L	AL365267.11.1.49616	6q13	71841661	71842056	no gene	7.60E-71
III	C4B	AL590428.7.1.163577	6q13	74364147	74493108	NM_133493	4.10E-08
xII	RPS18	AL355796.11.1.152086	6q14.1	79954508	79954717	no gene	1.60E-22
I	DDR1	AL354857.13.1.199223	6q16.1	93918505	94095966	EPHA7	1.20E-14
I	POU5F1	AL022395.2.1.126882	6q16.2	99299451	99300710	POU3F2	8.00E-43
xII	HSD17B8	AL591803.10.1.90325	6q16.2	99639262	99640282	Novel	1.90E-20
xII	RXRB	AL078596.8.1.64183	6q21	108510126	108532877	NR2E1	2.00E-21
xII	ZNF297	AL109947.19.1.128960	6q21	109806583	109827304	Y441	3.50E-12
I	DDR1	Z97989.1.1.155937	6q21	112005349	112217491	FYN	2.00E-11
I	DDR1	AL357141.8.1.125184	6q22.1	116285557	115404785	FRK	9.00E-20
xII	COL11A2	AL121963.10.1.107553	6q22.1	116462985	116470164	COL10A1	4.00E-23
I	DDR1	Z98880.1.1.108260	6q22.1	117632394	117769882	ROS1	2.60E-14
xII	RPS18	AL357084.12.1.76042	6q24.1	141090774	141091166	genscan	1.60E-48
I	TUBB	AL031320.6.1.133574	6q24.2	143380844	143380963	genscan	1.10E-51
xII	RPS18	AL078581.11.1.102019	6q25.1	149763293	149791539	KATNA1	8.40E-51
III	HSPA1L	AL590413.18.1.104939	6q25.1	151621254	151668524	NM_017909	1.70E-16
xI	MAS1L	AL035691.17.1.129968	6q25.3	160201536	160202670	MAS1	3.10E-36
xII	KIFC1	AL589733.20.1.201088	6q27	168140261	168167477	KIF25	4.00E-07
III	NOTCH4	AL078605.30.1.119563	6q27	170231439	170329846	NM_032448	3.70E-41
III	CYP21A2	AC073957.7.1.196204	7p22.3	667370	673509	NM_017781	2.60E-09
III	BAT8	AC005995.3.1.80010	7p22.1	5716846	5720381	Novel	3.80E-07
III	C6orf46	AC073343.6.1.173967	7p22.1	6374466	6390938	Z325	3.10E-14
III	C4B	AC060834.8.1.113686	7p21.3	9410581	9410991	genscan	4.50E-06
III	HSPA1L	AC009945.2.1.75517	7p21.3	10135315	10136415	genscan	2.30E-231
III	NOTCH4	AC013470.10.1.170723	7p21.3	12014883	12054396	Q96SQ3	1.00E-08
II	TAP2/1	AC002486.1.1.79611	7p21.1	20327136	20342642	O14573	6.30E-24
II	TAP2/1	AC005060.3.1.120169	7p21.1	20365471	20439590	Novel	1.80E-20
I	POU5F1	AC005483.1.1.161667	7p14.1	39025428	39150485	NM_007252	1.80E-11
xI	HIST1H2AC	AC004854.3.1.98697	7p13	44512586	44533943	H2-like	7.00E-15
xI	POM121L2	AC074397.7.1.114576	7p12.1	52567227	52568144	Q8N7R1	8.00E-26
III	C6orf26	AC073057.6.1.178105	7p11.2	56890588	56890821	genscan	5.90E-05
xII	ZNF297	AC115220.1.1.115916	7q11.21	62137099	62202401	Novel	7.80E-08
xI	SMA3L	AC115220.1.1.115916	7q11.21	62213350	62213517	genscan	6.70E-11
xII	ZNF297	AC092685.2.1.183263	7q11.21	63492669	63505908	NM_152626	1.30E-10
xI	SMA3L	AC073261.8.1.93403	7q11.21	64065461	64086982	GUSB	1.00E-24
III	BAT2	AC073089.5.1.171788	7q11.21	65101611	65344287	NM_018264	3.10E-24
III	BAT2	AC091738.4.1.131928	7q11.23	70715527	70834138	Novel	2.00E-22
xI	POM121L2	AC005488.2.1.185737	7q11.23	70990215	71062258	POM121	5.30E-92
xI	POM121L2	AC073841.9.1.55588	7q11.23	71351007	71352683	EST gene	2.90E-72
xI	RFP	AC073841.9.1.55588	7q11.23	71357485	71363082	WBSCR20A	8.90E-39
xI	POM121L2	AC006014.3.1.127761	7q11.23	73578273	73650919	POM121	7.40E-71
II	TAP2/1	AC005045.2.1.123947	7q21.12	85566663	85640217	ABCB4	8.00E-22
II	TAP2/1	AC005068.2.1.98472	7q21.12	85668428	85877856	ABCB1	4.90E-25
xII	COL11A2	AC002528.1.1.141120	7q21.3	92559772	92595972	COL1A2	8.10E-24
III	HSPA1L	AC004957.1.1.160687	7q21.3	95968910	95969113	no gene	3.30E-93
xI	BTN1A1/RFP	AC011904.3.1.113879	7q22.1	98022613	98051761	TRIM4	2.30E-19
xI	HLA Class I	AC004522.2.1.100096	7q22.1	98099206	98108247	AZGP1	1.10E-24
I	DDR1	AC011895.4.1.172358	7q22.1	98934759	98959566	EPHB4	8.80E-21
I	HLA-E	AC006329.5.1.145253	7q22.1	99414126	99414392	genscan	1.10E-05
I	DDR1	AC004416.1.1.32173	7q31.2	114790113	114916094	MET	1.20E-13
xII	LYPLA2L	AC073054.2.1.154419	7q21.32	121348077	121348109	genscan	1.20E-37
III	VARS2	AC008038.1.1.202945	7q33	131061808	131063239	Novel	1.00E-11
I	TUBB	AC083874.2.1.186281	7q33	132762314	132762403	genscan	4.00E-09

I	DDR1	AC104597.3.1.161425	7q34	140878465	140894489	EPHB6	2.70E-09
I	DDR1	AC092214.3.1.72045	7q34	141413870	141431627	EPHA1	1.40E-16
III	C6orf46/ZNF297	AC073422.8.1.80743	7q36.1	147046333	147070069	Novel	2.00E-05
III	C6orf46/ZNF297	AC073314.4.1.73888	7q36.1	147374895	147404413	NM_015694	7.40E-05
II	TAP2/1	AC010973.6.1.222605	7q36.1	148971967	148989086	ABCB8	8.10E-24
III	BAT8	AC010973.6.1.222605	7q36.1	149119222	149130915	ABS10	3.60E-06
I	ABCF1	AC021097.5.1.35899	7q36.1	149151360	149170753	ABCF2	1.20E-36
III	NOTCH4	AC110288.6.1.84664	8p23.3	1266863	1277550	Novel	6.60E-11
III	BF	AC023296.6.1.189532	8p23.2	2642344	3292997	CSMD1	3.00E-06
III	C2	AC023296.6.1.189532	8p23.2	2953246	3468313	CSMD1	3.60E-05
III	BAT1	AC012119.7.1.154898	8p21.2	23396081	23396278	Genscan	3.10E-06
III	HSPA1L	AC090820.6.1.138021	8p12	30546063	30546623	genscan	7.10E-170
III	RNF5	AC069120.4.60762.91265	8p11.23	38073473	38073760	genscan	6.20E-73
III	ATP6V1G2	AC120036.3.58309.177413	8q-tel	46087951	46088247	genscan	5.50E-08
xII	RING1	AC016113.9.1.185419	8q11.23	53945099	53945155	no gene	2.20E-19
xII	LYPLA2L	AC060764.10.163950.183771	8q11.23	54898165	54953804	LYPLA1	2.10E-27
I	DDR1	AC046176.11.1.132489	8q12.1	56731370	56862134	LYN	2.10E-12
xI	HIST1H2AC	AC084251.13.1.181400	8q13.3	70956550	70956840	no gene	3.70E-18
xII	RPS18	AC022730.7.1.155468	8q13.3	71276927	71277244	genscan	1.30E-31
xII	RXRB	AC040917.6.1.158031	8q21.11	76308140	76464431	HNF4G	5.80E-28
xII	ZNF297	AC009812.17.1.155405	8q21.13	81446105	81481018	NM_023929	2.30E-10
I	TUBB	AC007992.12.1.146921	8q22.1	96147896	96147985	genscan	1.40E-09
I	POU5F1	AP002851.2.1.200610	8q22.3	103702017	103702310	no gene	1.70E-17
III	BF	AC007719.7.1.150831	8q23.3	112280606	112310596	Novel	3.10E-05
xI	HIST1H2AC	AC022360.23.1.171991	8q23.3	112695588	112695632	no gene	3.60E-05
III	C2	AC007719.7.1.150831	8q23.3	113296979	113550957	Q96PZ3	9.60E-05
I	DDR1	AC022239.14.1.171829	8q23.1	113344396	11414823	BLK	6.00E-10
xII	ZNF297	AC105210.4.125110.131923	8q24.3	145036223	145040537	Q96C28	1.20E-07
xII	HKE4	AC022505.17.153698.191078	8q24.3	145675676	145680153	SLC39A4	7.40E-08
xII	KIFC1	AC084125.8.1.197314	8q24.3	145729611	145737380	NM_145754	2.40E-17
III	NOTCH4	AC084125.4.1.26696	8q24.3	145753310	145765393	PPP1R16A	2.60E-12
III	C6orf46	AF235103.3.1.344150	8q24.3	146143706	146164020	ZNF64	1.10E-14
I	DDR1	AL161450.14.1.171146	9p24.1	5003251	5108156	JAK2	1.60E-06
xII	RING1	AL162411.23.1.59964	9p24.1	6650955	6651159	no gene	7.00E-39
III	CLIC1	AC017067.4.1.191373	9p21.3	23075247	23075813	genscan	1.30E-48
xI	NOL5B	AL445623.2.1.198637	9p21.3	23903514	23903843	genscan	1.10E-15
III	HSPA1L	AL353745.7.1.174850	9p21.1	31159147	31159635	genscan	5.50E-17
II	BRD2	AL589642.6.1.92982	9p21.1	32799398	32805026	TAF1L	2.80E-08
xII	ZNF297	AL158155.24.1.192336	9p13.2	37607553	37634838	NM_014872	2.30E-10
III	C6orf46	AL353770.18.1.130898	9p13.1	39619983	39630670	Q96M55	1.10E-14
III	CYP21A2	AL359997.8.1.169102	9q21.13	66702026	66702607	genscan	1.20E-14
xII	LYPLA2L	AL353637.16.1.133212	9q21.2	71442203	71442490	no gene	3.50E-59
III	BAT1	AL158047.9.1.201629	9q21.32	75746587	75747222	Genscan	2.30E-19
xII	KIFC1	AL354733.15.1.189579	9q21.32	78368024	78383954	Novel	5.50E-27
I	DDR1	AL445532.8.1.171629	9q21.33	79138134	79490850	NTRK2	1.80E-35
xII	ZNF297	AL136981.22.1.182280	9q22.31	87336127	87368066	Q9H559	2.80E-10
xI	GABBR1	AL445495.5.1.155837	9q22.33	92793899	93215009	GPR51	1.60E-09
xII	COL11A2	AL354923.12.1.134965	9q22.33	93449719	93576588	COL15A1	3.10E-12
III	C6orf29	AL450265.11.1.68871	9q31.1	99804995	99897178	CTL1	1.40E-12
III	C9orf29	AL450265.11.1.68871	9q31.1	99804995	99897178	NM_022109	1.40E-12
III	BF	AL158158.14.1.194835	9q31.3	103971543	103990925	Novel	1.70E-11
III	C2	AL158158.14.1.194835	9q31.3	104860730	104923764	NM_153366	2.50E-15
III	NOTCH4	AL354982.12.1.119077	9q31.3	104936930	105074331	Novel	1.20E-33
I	DDR1	AL157881.14.1.162726	9q31.3	105163309	105295448	MUSK	1.80E-41
III	C6orf46	AL159168.15.1.129010	9q31.3	106019666	106038882	Q8TF39	1.80E-14

III	BAT2	AL354877.25.1.116236	9q31.3	106181071	106289393	NM_173521	3.30E-17
xII	ZNF297	AL162588.22.1.76606	9q31.3	107536344	107551166	ZFP37	7.80E-09
III	NOTCH4	AL162425.15.1.177728	9q31.3	108581009	108678635	Novel	6.30E-28
xII	COL11A2	AL445543.20.1.140327	9q31.3	108662161	108805998	Q96JF7	2.60E-13
III	ATP6V1G2	AL160275.14.1.189709	9q32	109082196	109092823	ATP6V1G1	1.50E-12
III	TNF	AL390240.18.1.93876	9q32	109283763	109300763	TNFSF15	3.80E-10
III	TNXB	AL162425.15.1.177728	9q33.1	109514975	109612609	TNC	7.80E-25
I	TUBB	AL589703.6.1.48697	9q33.1	112631091	112631204	genscan	1.60E-10
xII	B3GALT4	AL161911.17.1.109176	9q33.2	115207621	115207998	genscan	6.40E-31
III	C4B	AC006430.22.1.194799	9q33.2	115361172	115459110	C5	5.70E-20
III	C6orf46	AC007066.4.1.190815	9q33.2	117340094	117340094	BIOR	9.80E-65
III	NOTCH4	AL445489.10.1.175869	9q33.3	117788495	118338969	NM_024820	2.20E-76
xII	RXRB	AL354979.17.1.85997	9q33.3	118928956	119180139	NR6A1	9.70E-13
III	HSPA1L	AL354710.17.1.131708	9q33.3	119643682	119650159	HSPA5	8.1E-161
III	PBX2	AL445186.4.1.156124	9q33.3	120156161	120376205	PBX3	9.10E-85
III	C6orf46/ZNF297	AL161731.20.1.182452	9q33.3	121213845	121244041	ZNF297B	7.30E-33
xII	C6orf46/ZNF297	AL354944.22.1.49144	9q33.3	121269484	121289729	Q8NCN2	9.50E-39
I	DDR1	AL161733.20.1.176466	9q34.12	125136236	125309589	ABL1	8.50E-12
III	AIF1	AL157938.22.1.197019	9q34.12	125518441	125545061	NM_031426	1.20E-56
III	BAT2	AL358781.19.1.147492	9q34.13	125852061	125869120	NM_032640	2.20E-65
xII	RAB2L	AL162417.23.1.152863	9q34.2	127529965	127553410	RALGDS	3.70E-29
II	BRD2	AL445931.29.1.175033	9q34.2	128566862	128602533	BRD3	1.90E-133
xII	RXRB	AL669970.6.1.58552	9q34.2	129062693	129101647	RXRA	6.30E-88
xII	COL11A2	AL603650.10.1.131466	9q34.3	129302868	129503955	COL5A1	2.10E-43
III	NOTCH4	AL390778.30.1.221373	9q34.3	129736484	129782241	OLFM1	4.60E-11
III	NOTCH4	AL353615.27.1.37093	9q34.3	130006614	130009927	NM_173520	6.00E-10
xII	ZNF297	AL591038.9.1.51295	9q34.3	130674721	130713948	NM_144653	7.90E-15
III	NOTCH4	AL592301.14.1.188462	9q34.3	131078383	131129726	NOTCH1	2.40E-224
III	EGFL8	AL590226.23.1.149567	9q34.3	131242795	131256617	ZNEU1	9.70E-12
III	AGPAT1	AL590226.23.1.149567	9q34.3	131257082	131271362	AGPAT2	2.50E-29
III	CLIC1	AC068451.2.53215.58850	9q34.3	131578574	131580507	CLIC3	3.30E-35
III	BAT8	AL611925.20.31668.168509	9q34.3	132395728	132553855	HMT1	7.30E-142
I	TUBB	AL713922.8.1.121218	10p15.3	33000	35178	TUBBL	2.70E-190
III	NOTCH4	AL513304.27.1.163243	10p15.3	1427949	1428792	no gene	3.20E-06
xII	KIFC1	AL161932.15.1.143423	10p11.22	3016668	32061904	KIF5B	1.00E-06
III	HSPA1L	AC069544.9.1.214866	10p13	14843884	14877306	NM_016299	1.00E-15
III	BAT8	AC069544.9.1.214866	10p13	14884428	14909880	SU92	1.40E-17
III	NOTCH4	AL133415.12.1.179912	10p13	17152297	17207242	DNMT2	1.10E-15
xII	HKE4	AL590111.14.1.41069	10p12.33	17957452	18048843	NM_152725	7.10E-08
xII	RPS18	AL513128.11.1.184685	10p12.2	22534350	22534484	no gene	1.20E-05
xII	ZNF297	AL117337.25.1.161452	10q11.21	37982417	38009185	ZNF25	1.00E-07
xII	ZNF297	AL161931.13.1.19853	10q11.21	38043229	38099906	ZNF33A	1.30E-10
xII	ZNF297	AL022345.2.1.146328	10q11.21	42553027	42602464	ZNF11B	1.30E-10
III	C6orf46	AL353801.13.1.222490	10q11.21	44964852	44969243	ZNF22	4.10E-14
III	BAT8	AL359377.18.1.172177	10q21.2	60813515	61174843	ANK3	6.70E-05
I	POU5F1	AL356741.11.1.87244	10q21.3	68768389	68953381	Q9HCH9	1.40E-75
III	BAT1	AL359844.15.1.171364	10q22.1	69527140	69554693	DDX21	1.20E-05
III	BAT1	AC016394.13.1.149726	10q22.2	73713068	73782589	Q9Y2I0	1.90E-10
xI	HIST1H2AC	AL391421.27.1.168239	10q22.3	78922958	78923248	no gene	1.00E-14
III	BAT1	AL365434.12.1.158357	10q23.31	91694792	91695643	Genscan	7.30E-17
III	BAT1	AL731553.9.1.161141	10q23.31	91759982	91760050	Genscan	7.40E-17
III	BAT1	AL158040.13.1.213648	10q23.32	92777959	92779325	Novel	1.50E-24
xII	KIFC1	AL356128.27.1.191935	10q23.33	93574641	93636806	KIF11	1.50E-11
III	CYP21A2	AL359672.19.1.143181	10q23.33	95689793	95722511	CYP2C8	3.20E-05
III	NOTCH4	AL442123.12.1.96660	10q24.1	97651046	97838934	SLIT1	6.90E-33
xII	ZNF297	AL135791.12.1.66975	10q24.1	97820294	3785029	Q9NQN2	7.80E-09

II	TAP2	AL392107.16.1.94970	10q24.2	100776166	100845227	ABCC2	7.70E-05
III	CYP21A2	AL358790.22.1.131753	10q24.32	103483494	103490378	CYP17	4.20E-12
xI	RFP	AL391121.29.1.166600	10q24.32	103638012	103651712	TRIM8	1.90E-07
I	DHX16	AL360176.22.1.155699	10q26.2	126728551	126773529	DDX32	1.10E-21
III	CYP21A2	AL161645.14.1.161644	10q26.3	134255131	134266884	CYP2E	2.00E-07
xI	MAS1L	AC108448.5.135208.198047	11p15.4	3499638	3500522	Novel	5.70E-29
xI	RFP/RING1	AC009758.8.1.141485	11p15.4	4708183	4716972	SSA1	9.40E-71
xI	RFP	AC090719.8.1.179177	11p15.4	4921932	4931481	NM_018073	6.50E-72
xI	BTN1A1	AC009758.8.1.141485	11p15.4	4972222	4981011	SSA1	6.10E-38
xI	BTN1A1	AC090719.8.1.179177	11p15.4	5185974	5195520	Novel	1.40E-35
xI	RFP	AC015691.6.1.203036	11p15.4	5919434	5967728	TRIM6	1.30E-45
xI	RFP	AC109341.7.1.202761	11p15.4	5986894	6008393	TRIM5	9.10E-44
xI	BTN1A1	AC015691.6.1.203036	11p15.4	6372568	6413722	TRIM34	1.70E-16
xI	BTN1A1	AC109341.7.1.202761	11p15.4	6459104	6478807	TRIM22	1.70E-16
III	CYP21A2	AC018795.10.1.187836	11p15.2	15932556	15932621	no gene	2.90E-18
III	CYP21A2	AC090835.6.82428.167443	11p15.2	16080713	16094757	Novel	3.10E-19
xI	MAS1L	AC090099.10.28570.173306	11p15.1	19101039	19102007	MRGX3	1.70E-39
xI	MAS1L	AC107948.7.1.156839	11p15.1	19137100	19138068	MRGX4	3.30E-38
xI	MAS1L	AC023078.9.1.163718	11p15.1	19899153	19900121	MRGX1	2.00E-40
xI	MAS1L	AC023078.9.1.163718	11p15.1	19926836	19991360	Novel	2.40E-17
xI	MAS1L	AC027026.9.1.155376	11p15.1	20020747	20021739	MRGX2	1.10E-35
xII	KIFC1	AC023206.6.1.208561	11p14.1	28817128	28904683	NM_031217	5.40E-07
III	BF	AL354921.12.1.106657	11p13	37005965	37099743	Q96JW2	2.60E-06
III	NOTCH4	AC061999.6.1.182549	11p12	37290819	37297112	RAG2	3.90E-26
xII	RXRB	AC090589.8.1.190017	11p11.2	48157255	48168103	NR1H3	1.40E-06
xII	RXRB	AC018410.19.7721.155276	11p11.2	48168666	48229300	MADD	1.10E-06
xII	HKE4	AC090559.5.26090.106816	11p11.2	48306544	48315768	NM_152264	8.60E-14
xII	RXRB	AP001453.4.1.166300	11q13.1	65754594	65765769	ESRRA	9.70E-18
III	NOTCH4	AP000769.4.1.114794	11q13.1	66974259	66987851	SCYL1	1.20E-19
III	NOTCH4	AP001362.5.1.211382	11q13.1	67025483	67041797	Novel	1.70E-22
xI	MAS1L	AP000808.4.1.176380	11q13.3	70444307	70445269	Q8TDS7	7.50E-35
xI	MAS1L	AP003071.2.1.192759	11q13.3	70468658	70477508	MRGF	4.00E-27
xI	HIST1H2AC	AP002336.3.1.112484	11q13.3	71639671	71753357	PPFIA1	4.50E-14
III	NOTCH4	AP000867.4.1.199996	11q13.4	72870983	72871905	Q8NH65	3.20E-07
I	C6ORF18	AP000719.4.1.196424	11q13.4	73253747	73331398	NUMA1	1.90E-06
xII	B3GALT4	AP000752.4.1.194140	11q13.5	78289628	78290785	NM_138706	5.70E-25
III	NOTCH4	AP002768.3.1.186084	11q14.1	79903349	79952134	Q9P2P4	1.50E-09
xI	PRSS16	AP001646.4.1.182328	11q14.1	84074231	84150294	PRCP	4.10E-06
III	BAT1	AP003390.1.1.221091	11q23.3	91694792	91695643	Genscan	2.10E-106
I	TUBB	AP002364.3.1.165702	11q14.3	92344989	92345090	genscan	1.50E-11
I	TUBB	AP002799.3.1.177564	11q14.3	94012104	94012214	genscan	2.30E-14
III	NOTCH4	AP003171.2.1.137000	11q14.3	94081540	94134035	Q8TDW7	2.90E-10
III	BAT8	AP000786.4.1.75440	11q21	95734866	95740452	NM_017704	7.20E-06
III	BAT8	AP002840.2.1.177034	11q23.2	114770675	114783056	Q98NFD2	3.30E-15
III	NOTCH4	AP002840.2.1.177034	11q23.1	114792387	114857963	DRD2	2.10E-10
III	BAT8	AP001267.4.1.194310	11q23.3	119819041	119907224	MLL	2.50E-05
xI	HIST1H2AC	AP003391.1.1.46239	11q23.3	120476378	120477968	H2AFX	2.80E-42
III	BAT1	AP000713.2.1.11316	11q23.3	120964857	120979716	DDX6	1.20E-06
I	POU5F1	AP001150.4.1.157282	11q23.3	121622699	121702405	POU2F3	6.50E-21
III	BAT1	AP001994.4.1.167376	11q23.3	121762568	121762732	No gene	1.50E-105
III	HSPA1L	AP000926.5.1.196973	11q24.1	124441468	124446116	HSPA8	9.10E-243
III	BAT1	AP000842.4.1.179369	11q24.2	127774844	147793446	DDX25	1.80E-10
III	C6orf46/ZNF297	AP001183.4.1.174526	11q24.3	131612944	131697119	NM_014155	7.80E-15
III	BAT1	AC019227.4.1.190314	11q24.3	132166105	132166485	Genscan	1.50E-13
I	PPP1R10	AP000824.4.1.186920	11q24.3	132172516	132173124	genscan	7.20E-17
I	PPP1R10	AP003486.2.1.217488	11q24.3	132258421	132299008	SNXJ	9.60E-17

III	BAT1	AP000435.5.1.124067	11q12.1	60403473	60403808	Genscan	3.00E-12
III	HSPA1L	AC007207.22.1.191877	12p13.32	4100374	4101084	genscan	1.80E-215
xII	TAPBP	AC005840.2.1.140026	12p13.31	6535709	6550143	TAPBP-R	3.30E-05
III	BF	AC006512.12.1.157115	12p13.31	7087044	7087106	no gene	3.10E-06
III	C2	AC006512.12.1.157115	12p13.31	7243215	7245179	C10	6.10E-09
III	C4B	AC006581.16.1.172931	12p13.31	8712438	8724661	Novel	2.80E-05
III	C4B	AC007436.1.1.163881	12p13.31	8928367	8976544	A2M	3.20E-09
III	C4B	AC010175.4.1.127277	12p13.31	9009493	9069023	PZP	6.20E-09
III	BAT1	AC007215.43.2235.65215	12p13.2	12695938	12712573	NM_016355	1.60E-11
xI	HIST1H2AC	AC010168.6.1.104926	12p12.3	15072102	15073039	H2AFJ	1.10E-44
xII	COL11A2	AC004801.1.1.193561	12q13.11	48379436	48410949	COL2A1	2.80E-38
III	BAT1	AC025557.4.146238.171945	12q13.13	49116936	49138712	NM_004818	1.10E-14
I	TUBB	AC011603.33.10243.45426	12q13.12	49484144	49487748	TUBA1	9.00E-11
I	TUBB	AC010173.22.67252.90665	12q13.12	49586964	49595224	TUBA6	2.20E-12
I	TUBB	AC010173.22.160578.20759	12q13.12	49655804	49660085	TUBA1	1.00E-11
xII	RXRB	AC025259.48.1.210158	12q13.13	52474503	52482549	NR4A1	1.10E-07
III	BAT1	AC055716.24.1.110819	12q13.13	53260460	53260801	Genscan	5.40E-27
III	BAT1	AC068988.19.27848.161382	12q13.13	53292388	53292489	Genscan	7.70E-27
III	BAT1	AC073573.27.1.157807	12q13.13	53706088	53706432	Genscan	4.30E-35
III	BAT8	AC073896.29.107190.140910	12q13.2	56645899	56649310	NM_173594	2.30E-05
xII	ZNF297	AC026120.33.1.171998	12q13.3	57617302	57624914	Y352	1.10E-11
III	BAT1	AC117498.1.134066.149599	12q14.1	61110934	61180767	Novel	1.50E-15
xI	NOL5B	AC027288.26.1.177080	12q12.2	80316560	80316925	genscan	6.20E-24
xI	BTN1A1	AC009771.13.122068.178104	12q23.3	107466485	107466640	no gene	2.10E-30
xI	MAS1L	AC063957.22.1.71430	12q23.3	108566149	108613888	CMKLR1	8.80E-05
III	HSPA1L	AC005805.9.96579.142875	12q24.11	111438197	111439237	Novel	1.20E-134
III	CLIC1	AC078875.25.5011.18452	12q24.31	120214564	120215259	Novel	1.60E-14
xII	B3GALT4	AC048338.22.82693.113969	12q24.31	122667939	122671768	B3GNT4	2.10E-23
II	TAP2/1	AC026362.34.74237.162900	12q24.31	123114813	123152304	ABCB9	5.50E-45
I	DHX16	AC093719.6.127047.199959	12q24.31	125177591	125220663	DDX37	8.20E-17
xII	ZNF297	AC026786.5.1.160615	12q24.33	133310141	133338979	ZNF10	6.10E-10
xII	RXRB	AL359457.12.1.129779	13q12.11	14106712	14124427	ESRRAP	3.40E-27
xII	RXRB	AL158032.32.1.172004	13q12.11	15813801	15815722	Novel	4.50E-27
I	TUBB	AL139327.18.1.149559	13q12.11	17727916	17735936	TUBA2	1.10E-09
III	BAT1	AL354828.12.1.168114	13q12.12	21259290	21260180	Genscan	1.10E-111
I	DDR1	AL591024.14.1.76721	13q12.2	22557753	22654705	FLT3	9.00E-05
xI	POM121L2	AL359741.9.1.139877	13q12.3	23332361	23332804	genscan	1.20E-19
xI	POM121L2	AL596092.8.1.153841	13q12.3	23579447	24059956	O94872	2.70E-15
III	HSPA1L	AL137142.20.1.113850	13q12.3	25697387	25722697	H105	8.20E-22
III	BAT1	AL138822.13.1.126502	13q12.3	27152990	27154150	Genscan	1.50E-50
xI	HIST1H2AC	AL159980.14.1.162044	13q13.3	31050674	31050910	genscan	5.60E-20
III	BAT1	AL138706.9.1.195032	13q13.3	35499252	35499851	Genscan	1.40E-45
III	BAT8	AL136218.26.1.159863	13q14.2	44005950	44053746	C13ORF4	3.20E-06
xII	RXRB	AL138997.18.1.172342	13q21.1	50568900	50569076	genscan	5.20E-14
III	BAT1	AL161901.18.1.150054	13q21.2	59178906	59179631	Genscan	1.90E-31
xI	RFP	AL136145.23.1.83809	13q21.32	60838247	60838498	genscan	9.90E-09
I	DHX16	AC001226.1.1.106988	13q22.3	71554239	71557564	Novel	4.40E-10
I	POU5F1	AL445209.4.1.157302	13q31.1	73168139	73172615	POU4F1	7.40E-28
II	TAP2/1	AL157818.12.1.182485	13q32.1	90059271	90340865	ABCC4	7.60E-05
xI	HIST1H2AC	AL160155.19.1.149478	13q32.3	94254802	94255185	H2A-like	1.60E-11
xII	COL11A2	AL390755.5.1.186120	13q34	105188574	105346678	COL4A1	3.30E-17
xII	COL11A2	AL159153.17.1.102319	13q34	105346805	105553028	COL4A2	2.40E-16
III	NOTCH4	AL137002.19.1.132933	13q34	108397279	108411519	F7	2.60E-18
III	NOTCH4	AL161774.49.1.162296	13q34	110946220	111086222	RASA3	9.60E-09

II	PSMB8	AL132780.5.1.191946	14q11.2	17282361	17291410	PSMB5	2.40E-67
xI	HMGN4	AL163052.4.1.181905	14q12	23108107	23108319	no gene	8.20E-06
I	TUBB	AL445383.5.1.172914	14q21.2	41065751	41065876	genscan	7.00E-10
xII	RXRB	AL161756.6.1.176257	14q23.2	58487079	58598473	ESR2	8.90E-05
III	HSPA1L	AL049869.6.1.195840	14q23.3	58801222	58803614	HSPA2	4.80E-266
xI	GPX5	AL139022.4.1.190517	14q23.3	59199531	59203136	GPX2	1.50E-27
III	BAT1	AL391262.3.1.171296	14q24.1	67056068	67056841	Genscan	1.00E-18
III	NOTCH4	AC005479.2.1.140425	14q24.3	68764077	68777511	NPC2	3.70E-22
xII	RXRB	AC008050.6.1.176975	14q24.3	70654841	70785295	ESRRB	5.10E-09
xII	RPS18	AL122020.5.1.149904	14q32.11	85048919	85049456	Novel	4.40E-53
III	NOTCH4	AL132711.4.1.184924	14q32.2	95016286	95017418	no gene	6.90E-22
III	C6orf46/ZNF297	AL590327.3.1.59297	14q32.33	99258499	99259764	Novel	3.20E-14
III	NOTCH4	AL512356.5.1.158468	14q32.33	99443586	99452823	C14orf79	1.60E-59
III	NOTCH4	AL512355.5.1.196132	14q32.33	99772045	99852517	O60342	1.90E-54
III	ATP6V1G2	AL122127.6.1.169802	14q32.33	103287219	103287536	no gene	1.00E-07
II	TAP1	AC116165.3.1.90200	15q11.2	16305068	16351483	Novel	1.70E-35
II	TAP2	AC116165.3.1.90200	15q11.2	16305068	16351483	Novel	7.20E-22
II	TAP1	AC016033.7.99902.141149	15q11.2	16392186	16403533	Novel	7.70E-36
II	TAP2	AC016033.7.99902.141149	15q11.2	16392186	16403533	Novel	7.50E-23
xI	POM121L2	AC090983.10.101166.203171	15q11.2	17724332	17724397	no gene	2.20E-11
II	TAP2	AC091304.12.1.179219	15q13.1	21513802	21524551	Novel	1.50E-44
II	TAP1	AC091304.12.1.179219	15q13.1	21513802	21524551	Novel	2.30E-40
xI	HMGN4	AC022613.13.1.188117	15q13.1	25526308	25530507	HMG17	6.40E-06
III	NOTCH4	AC020661.8.1.191655	15q15.1	34166830	34304183	Q9ULG1	1.70E-42
II	HLA Class II	AC025270.6.1.128484	15q21.1	37899544	37906166	B2M	7.10E-05
xI	BTN1A1/RFP	AC018901.8.1.199503	15q21.1	37924579	37955869	RNF36	1.20E-29
II	HLA-DPB1	AC018901.8.1.199503	15q21.1	38056731	38056793	no gene	6.90E-06
III	CYP21A2	AC020705.4.136565.149466	15q21.1	38739399	68813334	CYP1A2	1.10E-12
III	NOTCH4	AC022467.7.1.193703	15q21.1	41748164	41983082	FBN1	8.10E-27
III	BAT1	AC091700.4.1.97653	15q22.2	55722396	55722959	Genscan	4.20E-08
III	NOTCH4	AC009433.11.1.169638	15q22.31	59286605	59645098	NM_032445	4.90E-28
III	BAT8	AC067837.6.1.173919	15q23	61668952	61687004	FEM1B	1.70E-09
III	BAT8	AC021553.14.1.185596	15q23	61692853	61823052	ITGA11	2.50E-07
xII	RXRB	AC104938.2.66191.114293	15q23	65200660	65208271	NR2E3	3.40E-22
III	RNF5	AC048383.8.169960.172969	15q23	66533763	66534050	genscan	2.30E-74
II	BTNL2	AC022188.7.15746.68046	15q24.1	67107924	67122957	NM_025240	5.80E-18
III	CYP21A2	AC020705.4.92855.102206	15q24.1	68848252	68854305	CYP1A1	4.90E-15
I	DDR1	AC027243.13.89123.218680	15q24.2	69598117	69693731	ETFA	1.90E-13
xI	MOG	AC022188.7.15746.68046	15q24.1	70012753	70027796	NM_025240	9.70E-10
III	CYP21A2	AC091230.8.108454.128536	15q24.1	70970184	70976444	Novel	9.00E-12
I	DDR1	AC011966.7.1.167862	15q25.3	81649264	82028917	NTRK3	7.20E-24
xII	KIFC1	AC079075.5.54114.209978	15q26.1	83693866	83715674	ANPEP	1.10E-15
xI	HIST1H2AC	AC091544.9.1.126968	15q26.1	87091764	87110331	H2 -like	9.40E-17
xII	RXRB	AC016251.9.1.182943	15q26.2	90630767	90631006	no gene	4.20E-43
I	DDR1	AC069029.9.1.191018	15q26.3	93033248	93342019	IGF1R	3.10E-07
xI	BTN1A1/RFP	AJ003147.1.1.239566	16p13.3	3325667	3340266	MEFV	2.70E-35
II	BRD2	AC004651.1.1.42016	16p13.3	3810213	3964357	CREBBP	1.80E-05
xII	B3GALT4	AC040160.4.1.209574	16q22.1	6761048	67659124	FHOD1	3.70E-19
II	TAP2	AC025778.7.1.207614	16p13.12	15526117	15599260	ABCB6	1.30E-06
III	NOTCH4	AC106796.1.45233.67716	16p12.3	19774406	19794065	UMOD	2.00E-11
xI	HMGN4	AC093509.2.1.120576	16p12.1	25470563	25470814	Q96C64	3.90E-06
xII	KIFC1	AC023831.8.22510.115251	16p11.2	30014062	30032892	QPRT	2.00E-09
III	C6orf46	AC002310.1.1.120955	16p11.2	31053573	31058082	NM_033410	5.30E-09
III	C6orf46	AC093249.3.1.185664	16p11.2	31102367	31110170	Q96CS4	5.30E-08
xII	ZNF297	AC106886.2.20127.148471	16p11.2	31281559	31287006	Q9UEG4	6.00E-10

xI	RFP	AC009088.7.1.233305	16p11.2	31722146	31734564	Q8N4X6	1.40E-33
II	PSMB8	AC007494.7.1.206113	16q12.1	47130249	47435934	PSMB10	3.80E-43
II	TAP1	AC096996.1.1.194627	16q12.1	48249418	48329904	ABCC11	2.80E-05
xI	UBD	AC026473.7.1.170393	16q21	51486489	51486719	genscan	6.60E-05
xII	KIFC1	AC092118.2.1.148401	16q13	57876138	57920423	KIFC3	1.20E-25
III	BAT1	AC004531.1.1.191565	16q22.1	58750455	58752074	DDX28	2.00E-18
xII	B3GALT4	AC074143.4.1.152953	16q22.1	67560936	67562065	NM_033309	2.70E-19
I	DHX16	AC009087.4.1.174933	16q22.2	72851029	72870003	DDX38	2.90E-50
xII	ZNF297	AC009078.6.1.176926	16q23.1	76142879	76166439	NM_153688	7.80E-09
III	BAT1	AC093491.2.1.162178	16q24.1	76485011	76485421	Genscan	5.20E-16
III	CLIC1	AC092327.3.1.189757	16q24.1	77844902	77845267	Genscan	7.10E-08
xII	ZNF297	AC009113.5.61390.188481	16q24.3	90272052	90283297	Q96MU6	3.70E-10
I	TUBB	AC092143.3.1.183047	16q24.3	90971498	90989716	TUBBL	9.20E-195
xII	ZNF297	AC090617.7.1.169947	17p13.3	2300029	2302554	HIC1	4.70E-10
III	BAT1	AC015799.7.1.66824	17p13.3	2858331	2858387	genscan	1.70E-20
I	DDR1	AC087742.7.63895.97713	17p13.2	4468643	4469263	EST gene	4.80E-11
II	PSMB9	AC027820.9.1.56340	17p13.2	5044936	5047269	PSMB6	3.50E-26
xII	KIFC1	AC004771.1.1.91927	17q13.2	5239168	5273857	KIF1C	8.70E-05
xII	ZNF297	AC087500.12.1.136618	17p13.2	5420893	5425754	Q96JF6	6.10E-10
I	DHX16	AC004148.1.1.118276	17p13.2	5683637	5710243	DDX33	2.10E-45
I	DDR1	AC113189.3.50089.71700	17p13.1	8014004	8022650	TNK1	1.10E-16
III	BAT1	AC016876.5.1.48645	17p13.1	8215901	8221709	EIF4A1	3.20E-18
III	BAT1	AC007421.12.1.95240	17p13.1	8215901	8221709	EIF4A1	1.30E-05
xII	RPS18	AC013248.5.1.66571	17p12	15723309	15723764	Novel	5.60E-60
xII	ZNF297	AC005324.1.1.176643	17p12	16717966	16767419	ZNF386	2.20E-10
III	C6orf46	AJ009612.5.1.148978	17p11.2	17565367	17583130	ZNF287	4.10E-13
III	C6orf46	AC005822.1.1.169931	17p11.2	17634716	17638760	YD49	4.10E-14
xII	ZNF297	AC026271.6.1.171978	17p11.2	20226123	20246008	Novel	1.70E-10
III	PBX2	AC087499.8.20079.65528	17p11.2	20668666	20668839	genscan	2.80E-05
xI	UBD	AC087575.3.156902.181085	17q	24638783	24639010	UBB	1.30E-12
I	FLOT1	AC024267.9.50190.98519	17q11.2	29105687	29123905	FLOT2	1.70E-31
xII	RXRB	AC068669.4.36251.62842	17q21.1	40302169	40309811	NR1D1	6.20E-10
xII	RXRB	AC080112.4.61535.75578	17q21.2	40640652	40689179	RARA	7.90E-13
III	NOTCH4	AC006070.1.1.161987	17q21.2	41487285	41488289	KRTAP9-9	4.80E-18
III	NOTCH4	AC003958.1.1.127834	17q21.2	41624135	41630437	KRTHA3B	6.70E-10
I	DHX16	AC068675.9.124153.141665	17q21.31	43738377	43778728	DDX8	4.80E-52
xII	KIFC1	AC015936.7.29291.133312	17q21.31	45189863	45189988	no gene	1.50E-05
xII	COL11A2	AC015909.8.44136.121814	17q21.33	47864916	47882452	COL1A1	4.00E-32
xII	KIFC1	AC019315.9.1.152057	17q22	54381662	54383970	NM_032559	6.40E-24
xI	RFP	AC004584.1.1.104871	17q23.2	57450065	57472912	ZNF147	3.60E-19
I	DHX16	AC004167.1.1.124876	17q23.2	60092562	60135284	NM_024612	4.60E-25
I	DHX16	AC005702.1.1.147686	17q23.2	60503679	60528304	Novel	7.50E-15
III	BAT1	AC015651.18.1.191583	17q23.3	64290823	64323079	NM_007372	1.20E-08
III	CLIC1	AC004805.1.1.184263	17q24.1	64773117	64773701	Novel	5.70E-08
III	BAT1	AC009994.6.166827.180372	17q24.2	68976215	68982889	DDX5	2.00E-07
III	BAT1	AC087741.2.60294.77121	17q25.3	81412654	81424538	IF4N	6.80E-06
I	TUBB	AP001005.5.1.137000	18p11.32	35028	37159	TUBBL	2.80E-184
III	BAT1	AP002449.2.169334.172757	18p11.21	12998814	12998903	genscan	7.60E-17
II	C6orf10	AC006238.1.1.211945	18q11.2	23904177	23904497	genscan	2.10E-06
xII	ZNF297	AC105101.6.1.172381	18q12.1	45351393	45363238	O75453	5.40E-18
xII	ZNF297	AC006130.1.1.84984	19p13.3	2936627	2947795	NM_024967	4.90E-11
I	DDR1	AC005777.1.1.43190	19p13.3	3847245	3871088	MATX	9.30E-07
xII	ZNF297	AC016586.7.116093.145761	19p13.3	4117018	4136099	O00456	5.40E-16
III	BAT8	AC005523.1.1.41468	19p13.3	4860388	4864189	FEM1A	2.70E-09

I	TUBB	AC010503.8.1.141295	19p13.3	6562943	6570948	TUBBL	1.30E-202
III	TNF	AC008760.7.1.200167	19p13.3	6733175	673234	TNFSF14	6.20E-10
III	C4B	AC008760.7.1.200167	19p13.3	6746489	6789295	C3	3.50E-27
III	NOTCH4	AC020895.8.1.139846	19p13.3	6959105	7022006	EMR1	1.00E-08
I	DDR1	AC010311.9.1.91172	19p13.2	7254547	7432507	INSR	3.10E-12
xII	LYPLA2L	AC010336.7.1.160769	19p13.2	8042351	8049685	Novel	3.30E-96
III	NOTCH4	AC022146.6.66353.150193	19p13.2	8235200	8317297	FBN3	5.30E-34
III	EGFL8	AC022146.6.66353.150193	19p13.2	8275726	8322330	NM_032447	2.60E-08
xII	COL11A2	AC008742.8.1.194623	19p13.2	10191743	10242653	COL5A3	3.10E-67
I	DDR1	AC011557.6.1.30505	19p13.2	10684031	10714039	TYK2	2.20E-07
III	LSM2	AC011475.6.1.179953	19p13.2	10932292	10932453	no gene	5.70E-23
III	C6orf29	AC011475.6.1.179953	19p13.2	10959135	10978061	CTL2	5.20E-59
xII	RAB2L	AC024575.6.1.119638	19p13.2	11718017	11752815	Q8TEP0	1.30E-24
xII	ZNF297	AC011446.6.1.115932	19p13.2	13622357	13628643	STX10	2.20E-14
III	BAT1	AC008569.7.1.227245	19p13.13	14887089	14897635	DDX39	4.10E-98
III	NOTCH4	AC005327.1.1.37988	19p13.12	15236788	15282936	EMR2	5.70E-05
III	EGFL8	AC004663.1.1.41150	19p13.12	15649643	15690991	NOTCH3	6.00E-05
III	NOTCH4	AC004663.1.1.41150	19p13.12	15664050	15705404	NOTCH3	7.70E-227
II	BRD2	AC114486.2.1.179070	19p13.12	15741907	15784868	BRD4	2.30E-90
xII	RXRB	AC010646.5.1.41461	19p13.12	17734984	17748449	NR2F6	7.00E-41
xII	B3GALT4	AC008761.7.1.226170	19p13.12	18106912	18149110	Q9UPW8	1.10E-12
xII	B3GALT4	AC005952.1.1.39976	19p13.11	18298235	18315904	B3GNT3	2.50E-14
xII	RPS18	AC020904.7.1.148824	19p13.11	18551604	18551837	EST gene	5.30E-46
III	BAT1	AC002985.1.1.38041	19p13.11	19422473	19431417	NM_019070	1.50E-05
III	PBX2	AC011448.4.1.165122	19p13.11	20063771	20120711	PBX4	2.10E-68
xII	ZNF297	AC008751.6.1.169089	19p13.11	21436099	21452779	ZNF85	2.20E-10
III	C6orf46	AC016628.6.1.41153	19p13.11	23871643	23887148	Novel	6.70E-16
xII	ZNF297	AC020910.7.1.203201	19q13.12	35697932	35713073	Q96NL3	2.30E-11
III	BAT8	AD000671.1.1.46251	19q13.12	36657876	36678735	TRX2	1.70E-05
xII	ZNF297	AC092295.2.1.165566	19q13.12	37465837	37479151	EST gene	1.00E-10
III	C6orf46	AC008806.4.1.135173	19q13.13	38293492	38349772	NM_152484	5.30E-10
xII	ZNF297	AC022148.5.1.198751	19q13.13	38430631	38431506	Q8N3U1	1.00E-10
III	NOTCH4	AC011500.7.1.200430	19q13.2	40327364	40358466	SUPT5H	1.10E-27
III	NOTCH4	AC010412.8.1.155085	19q13.2	41494937	41527447	LTBP4	1.50E-33
III	CYP21A2	AC008537.5.1.169089	19q13.2	41988964	41996369	CYP2A6	1.60E-09
I	DDR1	AC011510.7.1.129402	19q13.2	42116547	42159395	AXL	5.40E-09
III	CYP21A2	AC008962.9.1.154169	19q13.2	42259850	42273778	CYP2F1	2.90E-08
xII	B3GALT4	AC011526.7.1.40887	19q13.2	42323217	42324407	Novel	6.40E-20
III	CYP21A2	AC011510.7.1.129402	19p13.2	42338667	42352612	CYP2S1	9.30E-06
I	POU5F1	AC024076.4.1.39443	19q13.2	42986837	43028331	POU2F2	4.30E-23
III	NOTCH4	AC011497.6.1.168586	19q13.2	43248294	43273290	EGFL4	4.00E-09
I	DHX16	AC008754.8.1.66792	19p13.32	48246893	48270700	DDX34	7.80E-27
I	DHX16	AC073548.4.1.66051	19q13.32	48322806	48366009	SLC8A2	2.20E-17
xI	HLA Class I	AC010619.7.1.179394	19q13.33	50384629	50397727	FCGRT	8.50E-10
xII	RXRB	AC008655.7.1.123149	19p13.33	51241040	51247541	NR1H2	1.10E-06
xI	MAS1L	AC005946.1.1.37392	19q13.33	52688362	52689423	FPRL2	9.40E-06
III	C6orf46	AC010320.9.1.220458	19q13.41	53262462	53283017	Q96JK0	3.60E-15
III	C6orf46	AC022150.6.1.228156	19q13.41	53461403	53462023	ZNF137	9.00E-16
xII	ZNF297	AC013256.1.1.36095	19q13.43	57406251	57442939	NM_022103	1.40E-10
xII	ZNF297	AC005498.1.1.37321	19q13.43	57504539	57522397	ZFP28	2.80E-10
xII	ZNF297	AC003682.1.1.153875	19q13.43	58536894	58544255	Q9BWM5	1.10E-11
III	C6orf46	AC003682.1.1.153875	19q13.43	58579587	58587258	ZNF134	1.60E-15
III	C6orf46	AC003006.1.1.84114	19q13.43	58734983	58745942	NM_017652	5.20E-12
III	C6orf46	AC012313.7.1.185417	19q13.43	59398153	59405560	ZNF132	1.70E-25
xII	ZNF297	AC012313.7.1.185417	19q13.43	59478868	59485159	NM_032792	5.20E-29
xI	NOL5B	AL049712.12.1.159272	20p13	2580791	2587039	NOL5A	4.00E-29

III	NOTCH4	AL035456.26.1.125952	20p12.2	10566334	10602636	JAG1	1.30E-49
xII	KIFC1	AL049794.16.1.119696	20p12.1	16200749	16502021	C20ORF23	1.30E-09
III	NOTCH4	AL049651.2.1.97912	20p11.21	22964121	22965287	SSTR4	4.00E-10
III	EGFL8	AL118508.27.1.123832	20p11.21	23048052	23055034	C1QR1	1.90E-05
III	NOTCH4	AL118508.27.1.123832	20p11.21	23054616	23054911	Q8WY72	1.90E-16
xI	BTN1A1	AL080312.14.1.94664	20p11.21	25027858	25028403	genscan	1.60E-08
I	DDR1	AL049539.21.1.111694	20q11.21	30388101	30437940	HCK	6.80E-11
xII	KIFC1	AL121897.32.1.145414	20q11.21	30613467	30669435	KIF3B	3.10E-46
I	DDR1	AL133293.28.1.68662	20q11.23	35700500	35722250	SRC	3.00E-15
I	DHX16	AL023803.3.1.155379	20q11.23	37279429	37356793	DDX35	2.10E-19
xII	RXRB	AL132772.14.1.83798	20q13.12	42718338	42747410	HNFA4	4.50E-26
xII	ZNF297	AL354745.11.1.13535	20q13.12	44818128	44830619	ZNF334	1.60E-05
III	BAT1	AL049766.14.1.110293	20q13.13	47524305	47549031	DDX27	1.70E-10
I	TUBB	AL109840.24.1.142094	20q13.32	57282669	57290069	TUBBL	3.02E-165
III	NOTCH4	AL354836.13.1.141056	20q13.33	60601582	60607445	ADRM1	2.50E-09
III	NOTCH4	AL121673.41.1.151163	20q13.33	61421476	61437370	C20orf59	2.90E-07
I	DDR1	AL121829.30.1.113196	20q13.33	61996950	62006900	PTK6	3.20E-14
xII	ZNF297	AL121845.20.1.120917	20q13.33	62212439	62299987	Novel	3.90E-12
III	BAT5	AL118506.27.1.139505	20q13.33	62330271	62331761	C20ORF135	1.50E-117
III	HSPA1L	AF130358.2.1.197778	21q11.2	12307991	12372209	ABCC13	1.80E-44
III	HSPA1L	AF130249.1.1.97083	21q11.2	12405307	12417341	STCH	3.30E-46
III	CLIC1	AP000330.2.1.170377	21q22.12	32702115	32750955	CLIC6	2.60E-38
xII	B3GALT4	AF064860.2.1.170121	21q22.2	37690022	37690381	genscan	9.90E-32
III	BAT8	AP001615.1.1.124516	21q22.3	39783391	39784221	genscan	4.60E-17
xII	ZNF297	AP001620.1.1.95449	21q22.3	40039452	40061155	ZNF295	5.40E-10
xI	HIST1H2AC	AB001523.1.1.122638	21q22.3	42024993	42118907	TMEM1	7.20E-08
III	NOTCH4	AP001067.1.1.148845	21q22.3	42510546	42724266	C21orf29	2.10E-24
III	NOTCH4	AL163301.2.1.340000	21q22.3	43278171	43300571	C21orf80	5.40E-06
xII	COL11A2	AL163302.2.1.340000	21q22.3	43527445	43550695	SLC19A1	9.70E-12
III	BAT1	AP001604.1.1.186930	21q21.3	25401349	25401540	genscan	4.90E-09
I	TUBB	AC008079.23.1.170102	22q11.21	15544495	15554618	TUBA8	4.00E-10
xI	POM121L2	AC008103.27.1.98557	22q11.21	15773964	15776531	C22.2	5.60E-08
xI	POM121L2	AC000095.3.1.43728	22q11.21	15945799	15947779	C22.3	3.00E-10
III	NOTCH4	AC005500.2.1.192592	22q11.21	17480798	17552052	SRC2	1.00E-09
III	NOTCH4	AC007731.14.1.182617	22q11.21	17480798	17552052	SRC2	2.60E-09
xI	POM121L2	AC007050.25.1.163908	22q11.21	17742343	17744900	C22.3	1.50E-09
III	C6orf46/ZNF297	AP000557.2.1.150036	22q11.21	18470386	18504441	H1C2	6.00E-19
II	HLA-DRB3/1	D87023.1.1.40392	22q11.22	19936243	19936975	IGLC1	2.80E-06
xI	POM121L2	AP000354.1.1.164756	22q11.23	21343934	21357627	NM_014549	9.60E-10
xI	POM121L2	AP000356.1.1.163795	22q11.23	21749568	21750854	POM121L1	1.70E-10
I	DDR1	AL022329.9.1.221507	22q12.1	22656954	22816015	ADRBK2	6.00E-21
xI	BTN1A1/RNF	AC002059.3.1.173029	22q12.2	26530668	26534540	RFPL1	2.40E-26
III	RNF5	AC002073.1.1.128978	22q12.2	28252236	28299047	Q96GF1	8.10E-20
xI	HIST1H2AC	AL096701.14.1.168110	22q12.2	28613161	28613624	novel	2.50E-07
xI	BTN1A1/RFP	AL008723.8.1.154414	22q12.3	29282473	29295511	RFPL2	5.70E-26
xI	BTN1A1/RFP	AL021937.1.1.173354	22q12.3	29447342	29453195	RFPL3	5.70E-26
III	BAT1	Z97056.1.1.124990	22q13.1	35496212	35516829	DDX17	2.00E-05
II	BRD2	AL096765.12.1.13053	22q13.2	38102320	38190075	EP300	1.20E-05
III	CYP21A2	AL021878.1.1.114847	22q13.2	39138588	39142847	CYP2D6	3.30E-09
III	NOTCH4	Z98047.1.1.47542	22q13.31	42534087	42532337	FBLN1	5.30E-12
III	NOTCH4	AL031588.1.1.127168	22q13.31	43322995	43499263	CELSR1	1.20E-09
III	BAT1	AC117517.7.1.121628	Xp22.11	21589340	21590458	genscan	4.40E-37
xI	HIST1H2AC	AL121577.1.1.175531	Xq21.1	35832664	35878934	XK	2.40E-08
xI	HIST1H2AC	AL121578.1.1.337101	Xp11.4	36141216	36141440	genscan	2.80E-08

III	CLIC1	AL391259.15.1.163520	Xp11.4	38963014	38963730	Genscan	2.90E-07
III	BAT1	AL391647.16.1.60310	Xp11.4	39441330	39472404	DDX39	6.20E-07
xII	ZNF297	AL590223.12.1.40331	Xp11.3	45567068	45603010	ZNF41	4.60E-10
xII	ZNF297	Z98304.1.1.209618	Xp11.23	46096233	46103478	Q96QH7	4.70E-10
III	BAT8	AC115618.1.1.158455	Xp11.23	46756067	46756093	no gene	3.40E-15
III	BAT8	AF196970.1.1.112595	Xp11.23	46815791	46828063	SUV39H1	1.30E-15
III	BAT1	AL445236.22.1.149749	Xp11.22	50567899	50607906	Novel	9.90E-39
xII	HSD17B8	Z97054.1.1.132805	Xp11.22	51162495	51165605	HADH2	3.60E-06
xII	KIFC1	AL357752.19.1.178868	Xq13.1	66987254	67117990	KIF4A	2.70E-08
III	BAT1	AL359740.24.1.98104	Xq13.2	70525227	70526105	genscan	1.00E-13
II	TAP2/1	AL359545.12.1.127243	Xq13.3	71447688	71550705	ABCB7	2.90E-08
xII	KIFC1	AL021786.2.1.70665	Xq21.1	75540478	75573738	Novel	1.40E-15
I	POU5F1	Z82170.1.1.127247	Xq21.1	79839811	79841286	POU3F4	6.20E-39
III	BAT1	AL136362.10.1.135240	Xq21.31	88337615	88338796	EST gene	1.30E-57
I	TUBB	AL390840.17.1.197611	Xq21.32	88819807	88819917	genscan	1.50E-09
xII	COL11A2	AL136080.6.1.116106	Xq23	104474931	104758796	COL4A6	2.50E-15
xII	COL11A2	AL031622.1.1.104674	Xq23	104759239	105016860	COL4A5	1.80E-17
III	HSPA1L	AC004822.1.1.127824	Xq23	111134972	111136228	genscan	1.30E-208
III	VARS2	AC005000.2.1.107314	Xq23	112024040	112063337	Novel	3.30E-05
I	TUBB	AC003012.1.1.104810	Xq24	112252763	112252876	genscan	4.60E-12
xII	ZNF297	AC002086.1.1.112686	Xq24	116370267	116377851	NM_006777	6.50E-09
III	HSPA1L	AC002377.1.1.141779	Xq24	117230333	117231259	genscan	1.50E-221
III	HSPA1L	AL391241.21.1.157860	Xq25	120232224	120232373	genscan	9.40E-65
III	NOTCH4	AL627231.9.1.146366	Xq25	121306552	121307673	Novel	6.10E-12
xII	ZNF297	AL590282.6.1.139296	Xq26.3	131228672	131323794	ZNF75	3.70E-10
III	C6orf46	U82670.3.1.279526	Xq28	149081175	149084483	ZNF275	5.30E-12
III	CLIC1	AL356738.14.1.174693	Xq28	150871755	150929271	CLIC2	8.80E-52
xI	HIST1H2AC	AC019175.4.37111.45694	Xq28	151078382	151078898	H2AFB	1.80E-13
xI	HIST1H2AC	AL592156.4.1.134995	Xq21.1	35423125	35423349	genscan	2.00E-11
III	BAT1	AC010129.3.1.44145	Yp11.2	5171386	5172558	Novel	6.30E-59
III	BAT1	AC004474.1.1.148280	Yq11.21	14326902	14356562	DBY	4.00E-05

Appendix 3

Primers used to amplify a paralogue specific probe for use in Northern blot, Dot blot and Southern blot analyses. ‘T’ stands for the annealing temperature.

Gene	*Primer*	*Sequence*	*T (°C)*	*Size (bp)*
AIF1	F	TGACCATGCTGATGTATGAGGAAAAAGCGA	62	200
	R	GATCTGGAGGAGGGGGTAAT		
AIF1-L	F	TGACCATGTTAAGGGAGGAGAGCAAGCA	62	251
	R	CTGAGCCCTTAGCCAGAGAA		
BRD2	F	TGACCATGGAGGGATGCAGGGACATTT	62	411
	R	AACAAAGACAGTCCAGGGGA		
BRDT	F	TGACCATGGGGTACCATTGATATGACCCTT	62	199
	R	CTGTTTAATCATTTTAGAGCAGTCA		
BRD3	F	TGACCATGGACAGATGGATGTCGCACAC	62	425
	R	CAAATGACAAGGACAATGCG		
BRD4	F	TGACCATGGTGAAAGGGACAGGACTCCA	65	508
	R	CAGTGAGAAGCATGCTGTGG		
C4	F	TGACCATGAGAGATGACTCCGCGTCTGT	65	395
	R	ATTCTCCTTCTGCCCCAGAT		
C3	F	TGACCATGCATTCCCCCACTCCAGATAA	65	214
	R	ACATGAAGGTGAGGCAGGTC		
C5	F	TGACCATGTTGCACTTATGGACTCCTGTTG	65	352
	R	GATCAGTTTCCTGTTCCTTGGT		
CLIC1	F	TGACCATGAAGTACCGGGGATTCACCAT	65	310
	R	CTTTCCCTCATCCCCTCTTC		
CLIC4	F	TGACCATGGGAGATTGGAGTCTGAATGGA	65	384
	R	AATGGGTTTAAGGGCACAGA		
CLIC3	F	TGACCATGGTACGCCGCTACCTGGAC	65	153
	R	CCCGACAAAGATGCCTTTATT		
CLIC5	F	TGACCATGTGTTGATGCCAAAATACCCA	65	427
	R	GACCACCTCCTAAATGTGGC		
CLIC6	F	TGACCATGTGTGGCCAAGAAGTACAGAGAT	65	146
	R	TTGCAACATCTGAATATGCG		
CLIC2	F	TGACCATGGAATTCTCAGGAGTCTGGCG	65	350
	R	GCAGTGGTTTGCCATACAGA		
GPX5	F	TGACCATGTAGCAATGGGGTCACAGTCA	65	277
	R	TCCTCTCCAGGTGCCATAAC		
GPX4	F	TGACCATGTCCACAAGTGTGTGGCCC	65	186
	R	CACAAGGTAGCCAGGGGTG		
GPX3	F	TGACCATGAACCCAAAGGAAAAACCAGC	62	451
	R	GAGTCTCAAGCCAGTGGACC		
GPX1	F	TGACCATGCTCTTCGAGAAGTGCGAGGT	65	439
	R	ACTGGGATCAACAGGACCAG		
GPX2	F	TGACCATGTCCTACTCCATCCAGTCCTGA	62	256
	R	CTTCACGCCTCTCAGACACC		
NOTCH4	F	TGACCATGCATTAAAAGGCAGGCTGGAA	65	475
	R	CATCCCCACAGTGGAGTTCT		
NOTCH2	F	TGACCATGATGAGGAGGACAACACTGCC	65	395
	R	GCATCACAGCCAATTGCTTA		
NOTCH1	F	TGACCATGCAATACTGCATCCATGGCCT	65	244

	R	GTCCCTGAGCAACCATCTGT		
NOTCH3	F	TGACCATGATGTTCCATAGCCTTGCTGG	65	294
	R	GGGAATTCAGCTACACAGGG		
PBX2	F	TGACCATGGCAGGGCTGGACTCAGTAAT	62	409
	R	CACTTCCAACCTGTCCCAGT		
PBX1	F	TGACCATGCAGGAGGGAGGGTTTCTCTC	62	267
	R	TCAGTGATATGAGAGAGGGCG		
PBX3	F	TGACCATGCGAGTGTGGAAACATTGGGT	62	325
	R	TCAATCCAGGGTGTAATCCA		
PBX4	F	TGACCATGGTTTGGGGGATAAGCAGGAA	62	286
	R	GAAAATCTGTGCCCAGTCCT		
RXRB	F	TGACCATGAAGAAATGCCAGTGGTGGAG	62	263
	R	AAAGGAGCCCCAAAGAGAAG		
RXRG	F	TGACCATGTCCTGACTAATCCCAGAGGG	62	215
	R	CATAGCCTGCGGGAAACTT		
RXRA	F	TGACCATGTATACTTGGATATGGCGGGG	65	299
	R	CGGAGAAGCCACTTCACAGT		
TUBB_6p21.3	F	TGACCATGAGAGCAACATGAACGACCTG	65	200
	R	TGGAGGGAGATTGAAAGTGG		
TUBB2_18p11.3	F	TGACCATG TTCCTTCTTGAACCCTGGTG	65	225
	R	TTTATTTTGTGGCCCCTCAG		
TUBB5_19p13.3	F	TGACCATGCTGAATCCCCTCTGACTCCA	65	293
	R	CCTCTCTTCCTCACAGGCAC		
TUBB4QL_10p15.3	F	TGACCATGACAGCATCTGGTTTTGCCTC	65	130
	R	CCACTGGAATGCTTGTTCCT		
TUBB4_16q24.3	F	TGACCATGCAGCTGGAGTGAGAGGCAG	65	201
	R	GCCTGGAGCTGCAATAAGAC		
TUBB1_20q13.3	F	TGACCATGTGCACTCACCATTAGCTTCG	65	396
	R	TAGTCAGGCACCTGGCTCTT		

Appendix 4

Primers used to generate paralogue specific PCR products for each paralogue. The products were used to spot on to the microarrays and were also labelled and used to hybridise to the ‘Paralogue Microarray’. ‘T’ stands for the annealing temperature. They were also used in the RT-PCR experiments.

Gene	*Primer*	*Sequence*	*T (°C)*	*Size (bp)*
AIF1	F	TGACCATGCTGATGTATGAGGAAAAAGCGA	62.5	200
	R	GATCTGGAGGAGGGGGTAAT		
AIF1-L	F	TGACCATGTTAAGGGAGGAGAGCAAGCA	62.5	251
	R	CTGAGCCCTTAGCCAGAGAA		
BRD2	F	TGACCATGGAGGGATGCAGGGACATTT	62.5	411
	R	AACAAAGACAGTCCAGGGGA		
BRDT	F	TGACCATGGGGTACCATTGATATGACCCTT	62.5	199
	R	CTGTTTAATCATTTTAGAGCAGTCA		
BRD3	F	TGACCATGGACAGATGGATGTCGCACAC	62.5	425
	R	CAAATGACAAGGACAATGCG		
BRD4	F	TGACCATGGTGAAAGGGACAGGACTCCA	65	508
	R	CAGTGAGAAGCATGCTGTGG		
C4	F	TGACCATGAGAGATGACTCCGCGTCTGT	65	395
	R	ATTCTCCTTCTGCCCCAGAT		
C3	F	TGACCATGCATTCCCCCACTCCAGATAA	65	214
	R	ACATGAAGGTGAGGCAGGTC		
C5	F	TGACCATGTTGCACTTATGGACTCCTGTTG	65	352
	R	GATCAGTTTCCTGTTCCTTGGT		
CLIC1	F	TGACCATGAAGTACCGGGGATTCACCAT	62.5	310
	R	CTTTCCCTCATCCCCTCTTC		
CLIC4	F	TGACCATGGGAGATTGGAGTCTGAATGGA	65	384
	R	AATGGGTTTAAGGGCACAGA		
CLIC3	F	TGACCATGGTACGCCGCTACCTGGAC	65	153
	R	CCCGACAAAGATGCCTTTATT		
CLIC5	F	TGACCATGTGTTGATGCCAAAATACCCA	65	427
	R	GACCACCTCCTAAATGTGGC		
CLIC6	F	TGACCATGTGTGGCCAAGAAGTACAGAGAT	65	146
	R	TTGCAACATCTGAATATGCG		
CLIC2	F	TGACCATGGAATTCTCAGGAGTCTGGCG	65	350
	R	GCAGTGGTTTGCCATACAGA		
GPX5	F	TGACCATGTAGCAATGGGGTCACAGTCA	62.5	277
	R	TCCTCTCCAGGTGCCATAAC		
GPX4	F	TGACCATGTCCACAAGTGTGTGGCCC	62.5	186
	R	CACAAGGTAGCCAGGGGTG		
GPX3	F	TGACCATGTCTGGGTCTACCACACTCCC	62.5	329
	R	GAGTCTCAAGCCAGTGGACC		
GPX1	F	TGACCATGCTCTTCGAGAAGTGCGAGGT	62.5	439
	R	ACTGGGATCAACAGGACCAG		
GPX2	F	TGACCATGTCCTACTCCATCCAGTCCTGA	62.5	256
	R	CTTCACGCCTCTCAGACACC		
NOTCH4	F	TGACCATGCATTAAAAGGCAGGCTGGAA	62.5	475
	R	CATCCCCACAGTGGAGTTCT		
NOTCH2	F	TGACCATGATGAGGAGGACAACACTGCC	65	395
	R	GCATCACAGCCAATTGCTTA		

NOTCH1	F	TGACCATGCAATACTGCATCCATGGCCT	65	244
	R	GTCCCTGAGCAACCATCTGT		
NOTCH3	F	TGACCATGATGTTCCATAGCCTTGCTGG	65	294
	R	GGGAATTCAGCTACACAGGG		
PBX2	F	TGACCATGGCAGGGCTGGACTCAGTAAT	62.5	409
	R	CACTTCCAACCTGTCCCAGT		
PBX1	F	TGACCATGCAGGAGGGAGGGTTTCTCTC	62.5	267
	R	TCAGTGATATGAGAGAGGGCG		
PBX3	F	TGACCATGACCGAGTGTGGAAACATTGG	62.5	328
	R	TTCAATCCAGGGTGTAATCCA		
PBX4	F	TGACCATGAAGTTTGGGGGATAAGCAGG	62.5	288
	R	GAAAATCTGTGCCCAGTCCTA		
RXRB	F	TGACCATGGCCTTCCTCCTCTCAAACCT	62.5	263
	R	CTCCACCACTGGCATTTCTT		
RXRG	F	TGACCATGCGATCTAGAGGCAGATTCCTGA	62.5	231
	R	CATAGCCTGCGGGAAACTT		
RXRA	F	TGACCATGTATACTTGGATATGGCGGGG	65	299
	R	CGGAGAAGCCACTTCACAGT		
TUBB_6p21.3	F	TGACCATGACCAACCAGGTGCTGAAAAC	65	242
	R	TGGAGGGAGATTGAAAGTGG		
TUBB2_18p11.3	F	TGACCATG TTCCTTCTTGAACCCTGGTG	65	225
	R	TTTATTTTGTGGCCCCTCAG		
TUBB5_19p13.3	F	TGACCATGCTGAATCCCCTCTGACTCCA	62.5	293
	R	CCTCTCTTCCTCACAGGCAC		
TUBB4QL_10p15.3	F	TGACCATGACAGCATCTGGTTTTGCCTC	65	130
	R	CCACTGGAATGCTTGTTCCT		
TUBB4_16q24.3	F	TGACCATGCAGCTGGAGTGAGAGGCAG	65	201
	R	GCCTGGAGCTGCAATAAGAC		
TUBB1_20q13.3	F	TGACCATGTGCACTCACCATTAGCTTCG	65	396
	R	TAGTCAGGCACCTGGCTCTT		

Appendix 5

Summary of *in-silico* results.

Gene	***Brain(whole)***	***Ear***	***Eye***	***Nervous_normal***	***Heart***	***Aorta***	***Pharynx***	***Oesophagus***	***Stomach***	***Liver***	***Pancreas***	***Intestine***	***Colon***	***Gallbladder***	***Kidney***	***Bladder***	***Prostate***	***Genitourinary***	***Endometrium***	***Uterus***	***Cervix***	***Cervical carcinoma cell-line, Hela S3***	***Ovary***	***Breast***
AIF1_6p21.33	0	0	1	1	1	1	0	0	1	1	0	0	1	0	1	0	1	0	0	1	0	0	1	1
AIF1-L_9q34.12	1	0	1	1	1	0	0	0	1	1	1	0	1	0	1	0	1	0	0	1	1	0	1	1
BRD2_6p21.32	1	0	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1
BRDT_1p22.1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRD3_9q34.2	1	0	1	1	0	1	0	0	1	0	1	1	1	0	1	0	0	0	0	1	1	0	1	1
BRD4_19p13.12	1	0	1	1	1	1	0	1	1	1	1	0	1	0	1	1	1	0	0	1	1	0	1	1
C4_6p21.33	1	0	1	1	1	0	0	1	1	1	0	0	1	1	1	1	1	0	1	0	0	0	1	1
C5_9q33.2	1	0	1	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	1	0	0	0
C3_19p13.3	1	0	1	1	1	0	0	0	1	1	1	0	1	1	1	0	1	0	1	1	1	1	1	1
CLIC1_6p21.33	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1
CLIC4_1p35.3	1	1	1	1	1	1	0	0	1	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1
CLIC3_9q34.3	1	1	0	0	1	0	0	0	0	1	1	0	1	0	1	1	1	0	0	1	1	0	0	0
CLIC5_6p21.1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	1	1
CLIC6_21q22.12	0	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
CLIC2_Xq28	1	0	0	0	0	0	0	0	0	1	1	0	0	0	1	1	1	0	0	1	0	0	1	1
GPX5_6p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	1	0	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1
GPX1_3p21.31	1	0	1	1	1	1	0	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1
GPX3_5q33.1	1	0	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1	1
GPX2_14q23.3	1	0	0	0	0	0	0	1	1	1	1	0	1	1	1	1	1	0	0	1	0	0	1	1
NOTCH4_6p21.33	1	0	0	1	1	0	0	0	0	1	1	0	1	0	1	0	1	0	0	1	0	0	1	1
NOTCH2_1p11.2	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1
NOTCH1_9q34.3	1	0	0	1	1	0	0	1	1	0	1	1	1	0	1	0	0	0	0	1	0	0	0	1
NOTCH3_19p13.12	1	1	1	1	1	0	0	1	1	1	1	1	1	0	1	0	1	1	0	1	0	0	1	1
PBX2_6p21.33	0	0	1	1	0	0	0	0	1	1	1	1	1	0	1	0	1	0	0	1	0	1	1	0
PBX1_1q23.3	1	0	1	0	1	0	0	0	1	1	0	0	1	0	1	0	1	1	0	1	0	0	1	1
PBX3_9q33.3	1	1	1	1	1	0	0	0	1	1	1	1	1	0	1	1	1	0	0	0	0	1	1	1
PBX4_19p13.11	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
RXRB_6p21.32	1	0	1	1	1	0	0	0	1	1	1	1	1	0	1	1	1	0	1	1	1	0	1	1
RXRG_1q23.3	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
RXRA_9q34.2	1	0	1	1	1	0	0	0	1	1	1	0	1	0	1	1	1	0	0	1	1	0	1	1
TUBB_6p21.3	1	1	1	1	1	1	0	0	1	1	1	1	1	0	1	1	1	0	1	1	1	0	1	1
TUBB4_16q24.3	1	0	1	1	1	0	0	0	1	1	1	0	1	0	1	0	0	0	0	1	0	0	1	1
TUBBL_18p11.3	1	1	1	0	1	1	0	0	1	1	1	0	0	0	1	0	1	0	1	1	1	0	0	1
TUBB5_19p13.3	1	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1
TUBB1_20q13.3	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0

In-silico results continued (part 2 of 3).

Gene	***Testis***	***Epididymis***	***Placenta***	***Germ cell***	***Amnion_normal***	***Spleen***	***Thymus***	***Leukocyte***	***Lymph node***	***Lymphatic***	***Bone marrow***	***B cell***	***T cell***	***Macrophage***	***Monocyte***	***Blood***	***Nose***	***Trachea***	***Lung***	***Adrenal gland***	***Parathyroid***	***Thyroid gland***	***Pineal***	***Pituitary***
AIF1_6p21.33	1	0	1	0	0	1	1	0	0	0	1	0	0	0	0	1	0	0	1	1	1	0	0	0
AIF1-L_9q34.12	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0
BRD2_6p21.32	1	0	1	0	0	1	0	0	0	1	1	1	1	1	0	1	0	0	1	1	1	1	1	1
BRDT_1p22.1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRD3_9q34.2	1	0	0	0	1	0	0	0	0	1	1	1	1	0	0	0	0	0	1	1	0	0	0	0
BRD4_19p13.12	1	1	1	1	0	1	1	1	0	1	1	1	1	0	0	1	1	0	1	1	1	1	0	0
C4_6p21.33	0	1	1	1	0	1	0	0	1	0	1	1	1	0	0	1	1	0	1	1	1	0	0	1
C5_9q33.2	0	0	1	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0
C3_19p13.3	1	1	1	1	0	1	0	0	1	0	1	0	1	1	0	0	1	0	1	1	1	1	0	0
CLIC1_6p21.33	1	1	1	1	1	1	1	0	1	0	1	1	1	0	0	1	0	0	1	1	1	1	0	1
CLIC4_1p35.3	1	0	1	1	1	0	0	0	1	0	1	1	1	0	0	1	0	0	1	1	1	1	1	0
CLIC3_9q34.3	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
CLIC5_6p21.1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
CLIC6_21q22.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
CLIC2_Xq28	0	0	1	1	0	1	0	0	1	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0
GPX5_6p22.1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	1	1	1	1	0	0	0	1	1	0	1	1	1	0	0	1	0	0	1	1	1	0	1	0
GPX1_3p21.31	1	1	1	1	0	1	1	1	1	0	1	1	1	0	0	1	1	0	1	1	1	1	1	1
GPX3_5q33.1	1	0	1	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1
GPX2_14q23.3	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
NOTCH4_6p21.33	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
NOTCH2_1p11.2	1	1	1	1	1	0	0	0	1	0	1	1	1	1	1	1	1	0	1	1	1	0	1	0
NOTCH1_9q34.3	1	0	1	1	0	0	0	1	1	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0
NOTCH3_19p13.12	1	1	1	1	0	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0
PBX2_6p21.33	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0
PBX1_1q23.3	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
PBX3_9q33.3	1	0	0	1	0	0	0	1	1	0	0	1	0	0	0	0	0	0	1	1	1	1	0	1
PBX4_19p13.11	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
RXRB_6p21.32	1	1	1	1	0	1	0	1	1	0	0	1	0	0	0	1	0	0	1	0	1	1	0	0
RXRG_1q23.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
RXRA_9q34.2	1	0	1	0	0	0	0	1	1	0	1	1	0	0	0	0	0	0	1	0	1	0	0	0
TUBB_6p21.3	1	0	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	0	1	1	0	1	1	1
TUBB4_16q24.3	1	0	1	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	1	0	0	0	1
TUBBL_18p11.3	0	0	1	1	0	1	0	0	1	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0
TUBB5_19p13.3	1	1	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0
TUBB1_20q13.3	1	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0

In-silico results continued (part 3 of 3).

Gene	***Salivary gland***	***Mammary gland***	***Skin***	***Bone***	***Adipose***	***Connective***	***Fibroblast***	***Cartilage***	***Muscle***	***Tongue***	***Synovial membrane***	***Mixed***	***Unknown***
AIF1_6p21.33	0	0	1	1	0	0	0	0	1	0	0	1	1
AIF1-L_9q34.12	0	0	1	1	0	0	0	0	1	0	0	1	1
BRD2_6p21.32	0	0	1	1	1	1	1	0	1	1	1	1	1
BRDT_1p22.1	0	0	0	0	0	0	0	0	0	0	0	1	1
BRD3_9q34.2	0	0	1	1	0	0	0	1	1	0	0	1	1
BRD4_19p13.12	1	0	0	1	1	0	1	1	1	1	0	1	1
C4_6p21.33	0	0	1	0	1	0	0	1	0	1	0	1	1
C5_9q33.2	0	0	1	0	0	0	0	1	0	1	0	1	1
C3_19p13.3	0	0	1	1	1	0	1	1	1	1	0	1	1
CLIC1_6p21.33	0	0	1	1	1	0	1	1	1	0	0	1	1
CLIC4_1p35.3	0	0	1	1	1	0	1	1	1	0	0	1	1
CLIC3_9q34.3	0	0	0	0	0	0	1	0	0	0	0	1	0
CLIC5_6p21.1	0	0	0	0	0	0	0	0	0	0	0	1	1
CLIC6_21q22.12	0	0	0	1	0	0	0	0	0	0	0	1	1
CLIC2_Xq28	0	0	0	1	0	0	0	0	1	0	0	1	0
GPX5_6p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	0	0	1	1	1	0	1	1	1	0	0	1	1
GPX1_3p21.31	1	0	1	1	0	0	1	1	1	1	1	1	1
GPX3_5q33.1	1	0	1	0	1	0	0	1	1	1	1	1	1
GPX2_14q23.3	0	0	1	0	0	0	0	0	0	0	0	1	1
NOTCH4_6p21.33	0	0	1	0	0	0	0	0	0	0	0	1	1
NOTCH2_1p11.2	0	0	1	1	0	1	1	1	1	0	1	1	1
NOTCH1_9q34.3	0	0	0	0	0	0	0	0	0	0	0	1	1
NOTCH3_19p13.12	0	0	1	0	0	0	1	0	0	1	0	1	1
PBX2_6p21.33	0	0	1	0	0	0	0	0	1	0	0	1	1
PBX1_1q23.3	0	0	0	0	0	0	0	1	0	0	0	1	0
PBX3_9q33.3	0	0	0	1	0	0	1	1	0	0	0	1	1
PBX4_19p13.11	0	0	1	0	0	0	0	0	0	0	0	1	0
RXRB_6p21.32	0	0	1	0	0	0	1	1	0	0	0	1	1
RXRG_1q23.3	0	0	1	0	0	0	0	0	1	0	0	1	1
RXRA_9q34.2	0	0	1	1	0	0	1	1	1	0	0	1	1
TUBB_6p21.3	0	1	1	1	1	0	1	1	1	0	1	1	1
TUBB4_16q24.3	0	0	1	1	0	0	1	1	0	0	0	1	1
TUBBL_18p11.3	0	1	1	1	1	0	1	0	1	0	0	1	1
TUBB5_19p13.3	0	1	0	0	0	0	0	0	0	0	0	1	1
TUBB1_20q13.3	0	0	0	0	0	0	0	0	0	0	0	1	1

Appendix 6

Summary of dot blot results

Gene	***Brain***	***Cerebral cortex***	***Frontal lobe***	***Parietal lobe***	***Occipital lobe***	***Temporal lobe***	***Paracentral gyrus of cerebral cortex***	***Pons***	***Cerebellum, left***	***Cerebellum, right***	***Corpus callosum***	***Amygdala***	***Caudate nucleus***	***Hippocampus***	***Medulla oblongata***	***Putamen***	***Accumbens nucleus***	***Thalamus***	***Heart***	***Aorta***	***Atrium, left***	***Atrium, right***	***Ventricle, left***	***Ventrcle, right***
AIF1_6p21.33	0	0	0	0	1	0	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
AIF1-L_9q34.12	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BRD2_6p21.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BRDT_1p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRD3_9q34.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BRD4_19p13.12	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
C4_6p21.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C5_9q33.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1
C3_19p13.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CLIC1_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CLIC4_1p35.3	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1
CLIC3_9q34.3	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CLIC5_6p21.1	0	1	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0
CLIC6_21q22.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CLIC2_Xq28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX5_6p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX1_3p21.31	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX3_5q33.1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX2_14q23.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
NOTCH4_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1
NOTCH2_1p11.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
NOTCH1_9q34.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0
NOTCH3_19p13.12	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX2_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX1_1q23.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX3_9q33.3	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX4_19p13.11	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RXRB_6p21.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RXRG_1q23.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RXRA_9q34.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB_6p21.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB4QL_10p15.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0
TUBB4_16q24.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0
TUBBL_18p11.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB5_19p13.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1
TUBB1_20q13.3	0	1	1	1	1	1	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0

Dot blot results continued (2 of 3).

Gene	***Interventricular septum***	***Apex of heart***	***Oesophagus***	***Stomach***	***Duodenum***	***Jejunum***	***Ileum***	***Ileocecum***	***Appendix***	***Colon, ascending***	***Colon, transverse***	***Colon, descending***	***Rectum***	***Kidney***	***Skeletalmuscle***	***Spleen***	***Thymus***	***Pripheral blood leukocyte***	***Lymph node***	***Bone marrow***	***Trachea***	***Lung***	***Placenta***	***Bladder***
AIF1_6p21.33	1	1	0	1	1	1	1	1	1	1	0	0	0	1	1	1	1	1	1	1	1	1	1	1
AIF1-L_9q34.12	1	1	1	0	0	1	0	1	1	1	0	0	1	1	0	1	0	1	1	0	1	0	1	0
BRD2_6p21.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BRDT_1p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRD3_9q34.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BRD4_19p13.12	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	1
C4_6p21.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
C5_9q33.2	1	0	0	1	1	1	1	1	1	0	0	0	0	1	1	1	0	0	1	1	0	0	1	1
C3_19p13.3	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1
CLIC1_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CLIC4_1p35.3	1	0	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	1	1	0
CLIC3_9q34.3	1	1	1	1	0	1	0	0	0	0	1	0	0	0	1	0	0	1	1	0	0	1	1	1
CLIC5_6p21.1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
CLIC6_21q22.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
CLIC2_Xq28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX5_6p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX1_3p21.31	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX3_5q33.1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX2_14q23.3	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
NOTCH4_6p21.33	1	1	0	1	1	1	1	1	1	0	0	1	1	0	0	0	1	0	1	0	0	1	1	1
NOTCH2_1p11.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
NOTCH1_9q34.3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
NOTCH3_19p13.12	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX2_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX1_1q23.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	1	1	1	1	1	1
PBX3_9q33.3	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX4_19p13.11	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	1	1	1	1	1	0
RXRB_6p21.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RXRG_1q23.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
RXRA_9q34.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB_6p21.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB4QL_10p15.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TUBB4_16q24.3	1	1	1	1	1	1	1	1	1	0	0	0	0	1	0	0	0	1	1	1	1	1	1	1
TUBBL_18p11.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB5_19p13.3	1	1	0	1	1	1	1	1	1	0	1	1	1	0	0	0	1	1	1	1	1	0	0	1
TUBB1_20q13.3	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	1	1	0	1	0	0	1	0

Dot blot results continued (3 of 3).

Gene	***Uterus***	***Prostate***	***Testis***	***Ovary***	***Liver***	***Pancreas***	***Adrenalgland***	***Thyroid gland***	***Salivary gland***	***Leukemia, HL-60***	***HeLa S3***	***Leukemia, HK-562***	***Molt4 (T cell)***	***Raji (B cell)***	***Burkitt's lymphoma, Daudi***	***Colorectal adenocarcinoma***	***Lung carcinoma, A549***	***Foetal brain***	***Foetal heart***	***Foetal kidney***	***Foetal liver***	***Foetal spleen***	***Foetal thymus***	***Foetal lung***
AIF1_6p21.33	1	1	0	0	1	1	1	1	1	0	0	0	1	0	0	0	0	0	1	1	1	1	1	1
AIF1-L_9q34.12	1	1	1	1	0	0	0	1	1	0	0	0	0	0	0	1	0	1	0	1	0	1	0	0
BRD2_6p21.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BRDT_1p22.1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BRD3_9q34.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1
BRD4_19p13.12	1	1	1	1	1	1	1	1	1	0	0	0	0	1	0	0	0	1	0	1	1	1	1	1
C4_6p21.33	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C5_9q33.2	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1
C3_19p13.3	1	1	1	0	1	1	1	1	1	0	1	1	1	0	0	0	0	1	1	1	1	1	1	1
CLIC1_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CLIC4_1p35.3	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CLIC3_9q34.3	1	1	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	1
CLIC5_6p21.1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
CLIC6_21q22.12	0	0	0	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
CLIC2_Xq28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX5_6p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX1_3p21.31	1	1	1	1	1	1	1	1	1	0	1	0	1	1	0	1	0	1	1	1	1	1	1	1
GPX3_5q33.1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	1	1	1	1	1	1	1	1	1
GPX2_14q23.3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0
NOTCH4_6p21.33	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NOTCH2_1p11.2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
NOTCH1_9q34.3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NOTCH3_19p13.12	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
PBX2_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1
PBX1_1q23.3	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	0	1	1	1	1	1	1	1	1
PBX3_9q33.3	1	1	1	1	1	1	1	1	1	0	1	1	0	1	0	0	0	1	1	1	1	1	1	1
PBX4_19p13.11	1	1	1	1	1	1	0	1	1	1	1	1	0	0	0	0	0	1	1	1	1	1	1	1
RXRB_6p21.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
RXRG_1q23.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RXRA_9q34.2	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1
TUBB_6p21.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB4QL_10p15.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
TUBB4_16q24.3	1	1	1	1	1	1	0	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1
TUBBL_18p11.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB5_19p13.3	1	1	1	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1	0	1	1	1	1	0
TUBB1_20q13.3	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	0	1	0	0	0	0	0	0	0

Appendix 7

Northern blot results and transcript sizes (kb). The most dominant transcripts are in bold.

Gene	***heart***	***brain***	***placenta***	***lung***	***liver***	***skeletal muscle***	***kidney***	***pancreas***
AIF1_6p21.33	- 3.0 1.25 0.6	- 3.0 - -	- 3.0 1.25 -	- 3.0 - -	- - 1.25 0.6	5.0 3.0 - 0.6	- 3.0 - 0.6	- 3.0 - 0.6
AIF1-L_9q34.12	3.4	3.4	3.4	0	0	0	**3.4**	0
BRD2_6p21.32	**4.6** **3.8**	4.6 3.8	4.6 3.8	4.6 3.8	4.6 3.8	4.6 3.8	4.6 3.8	**4.6** **3.8**
BRDT_1p22.1	7.0 - -	7.0 - -	7.0 - -	0	7.0 - -	7.0 - -	7.0 - -	7.0 4.0 3.5
BRD3_9q34.2	6.5	6.5	6.5	6.5	6.5	**6.5**	6.5	6.5
BRD4_19p13.12	6.0 4.4	6.0 4.4	6.0 4.4	6.0 4.4	6.0 4.4	**6.0** **4.4**	6.0 4.4	6.0 4.4
C4_6p21.33	0	0	0	0	5.4	0	5.4	0
C5_9q33.2	0	0	0	0	6.0 **5.0** 4.2 1.6 1.0	0	- 5.0 - - -	- 5.0 4.2 - -
C3_19p13.3	0	0	0	0	5.0	0	0	0
CLIC1_6p21.33	1.25 1.1	0	**1.25** **1.1**	1.251.1	1.25 1.1	1.25 1.1	1.25 1.1	1.25 1.1
CLIC4_1p35.3	4.0	0	4.0	4.0	4.0	4.0	4.0	0
CLIC3_9q34.3	- 4.4 - -	0	5.5 - 2.6 **0.7**	- - - 0.7	- - - 0.7	- 4.4 - -	- 4.4 - -	- 4.4 - -
CLIC5_6p21.1	0	**2.7** **2.4**	0	2.7 -	2.7 -	0	**2.7** **2.4**	2.7 -
CLIC6_21q22.12	6.0 **3.8** 3.0 2.3	0	0	- 3.8 3.0 -	- - - 0	6.0 **3.8** - -	- - - 0	- - 3.0 -
CLIC2_Xq28	1.7 1.25	0	1.7 1.25	1.7 1.25	1.7 1.25	1.7 1.25	1.7 1.25	1.7 1.25
GPX5_6p22.1	- 0.8 0.6	- 0.8 -	- - 0.6	0	- 0.8 0.6	3.8 0.8 0.6	0	- 0.8 0.6
GPX4_19p13.3	4.4 2.6 2.0 **0.9**	- - - 0.9	- 2.6 2.0 **0.9**	- - - 0.9	4.4 2.6 2.0 **0.9**	4.4 - 2.0 **0.9**	- - 2.0 **0.9**	- - - 0.9
GPX1_3p21.31	**0.8**	**0.8**	**0.8**	**0.8**	**0.8**	**0.8**	**0.8**	**0.8**
GPX3_5q33.1	- 0.7	0	- 0.7	- 0.7	1.8 **0.7**	1.8 0.7	- 0.7	- 0.7
GPX2_14q23.3	0	0	0	0	0	0	**0.9**	0
NOTCH4_6p21.33	7.8 6.8 2.4	- - -	7.5 6.8 -	7.5 6.8 -	- - 2.4	- 6.8 2.4	- 6.8 -	- 6.8 2.4

	- 0.8	1.6 -	- 0.8	- -	- 0.8	- 0.8	- -	1.6 0.8
NOTCH2_1p11.2	**10** 1.9	10 -	**10** 1.9	10 1.9	10 1.9	**10** 1.9	**10** 1.9	10 1.9
NOTCH1_9q34.3	9.3	0	9.3	0	9.3	9.3	9.3	0
NOTCH3_19p13.12	8	8	8	0	8	8	8	8
PBX2_6p21.33	**3.2**	3.2	**3.2**	3.2	3.2	3.2	3.2	3.2
PBX1_1q23.3	7.5 - 2.9 -	7.5 - - -	7.5 - 2.9 -	7.5 - 2.9 -	7.5 - 2.9 -	**7.5** 4.4 2.9 2.6	**7.5** - 2.9 -	**7.5** 4.4 2.9 -
PBX3_9q33.3	**2.5** 2.2 1.4	2.5 - -	2.5 - -	2.5 - -	2.5 - -	2.5 2.2 -	0	**2.5** 2.2 -
PBX4_19p13.11	- 4.5 1.4 1.2	- 4.5 - -	- 4.5 1.4 1.2	0	- 4.5 1.4 1.2	6.0 4.5 1.4 -	- 4.5 - -	- 4.5 1.4 -
RXRB_6p21.32	7.7 2.8 1.7	- 2.8 -	- 2.8 -	0	- - 1.7	7.7 **2.8** 1.7	- 2.8 -	- 2.8 -
RXRG_1q23.3	1.7	0	2.8 0.9	0	1.7 1.5	**1.7**	0	1.7 1.5
RXRA_9q34.2	5.4	5.4	5.4	0	5.4	5.4	0	0
TUBB_6p21.3	- 4.8 4.0 2.5 1.7 -	- - - 2.5 **1.7** -	5.1 - - - 1.7 -	- - - - 1.7 -	- - - 1.7 -	- - 4.8 4.0 1.7 1.35	- - - - 1.7 -	- - - - 1.7 1.35
TUBB4QL_10p15.3	0	2.8	0	0	0	0	0	0
TUBB4_16q24.3	1.7 1.3	1.7 1.3	1.7 1.3	1.7 1.3	1.7 1.3	1.7 1.3	1.7 1.3	1.7 1.3
TUBBL_18p11.1	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3
TUBB5_19p13.3	0	2.3	0	0	0	0	0	2.3
TUBB1_20q13.32	0	0	0	0	0	0	0	0

Appendix 8

Summary of microarray results.

Gene	***Adrenal gland***	***Brain***	***Skeletal muscle***	***Spleen***	***Testis***	***293T (kidney)***	***Jurkat***	***Raji***	***THP1***	***U937 (lung)***
AIF1_6p21.33	0	0	0	1	0	0	1	0	0	1
AIF1-L_9q34.12	0	1	0	1	0	0	0	0	0	0
BRD2_6p21.32	1	1	1	1	1	1	1	1	1	1
BRDT_1p22.1	0	0	0	0	1	0	0	0	0	0
BRD3_9q34.2	1	1	0	0	1	0	1	1	0	0
BRD4_19p13.12	0	1	1	0	0	0	0	1	0	0
C4_6p21.33	0	0	0	0	0	0	0	0	0	0
C5_9q33.2	0	0	0	0	0	0	0	0	0	0
C3_19p13.3	0	0	0	0	0	0	0	0	0	0
CLIC1_6p21.33	1	1	1	1	1	1	1	1	1	1
CLIC4_1p35.3	0	1	1	1	1	0	1	1	0	1
CLIC3_9q34.3	0	0	1	0	0	0	0	0	0	0
CLIC5_6p21.1	0	0	1	1	0	0	0	0	0	0
CLIC6_21q22.12	0	0	0	0	0	0	0	0	0	0
CLIC2_Xq28	0	0	0	1	0	0	0	0	0	0
GPX5_6p22.1	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	1	1	1	1	1	1	1	1	1	1
GPX1_3p21.31	1	1	1	1	1	1	1	1	1	1
GPX3_5q33.1	1	1	1	1	1	0	0	0	0	0
GPX2_14q23.3	0	0	0	0	0	0	0	0	0	0
NOTCH4_6p21.33	0	0	0	0	0	0	0	0	0	0
NOTCH2_1p11.2	0	1	0	1	1	0	0	1	0	0
NOTCH1_9q34.3	0	0	0	0	0	0	0	0	0	0
NOTCH3_19p13.12	1	1	0	1	1	0	1	0	0	0
PBX2_6p21.33	0	0	0	0	0	0	0	0	0	0
PBX1_1q23.3	1	1	0	0	1	1	0	1	0	0
PBX3_9q33.3	0	0	0	0	1	0	0	1	0	0
PBX4_19p13.11	0	1	0	0	1	0	1	1	0	0
RXRB_6p21.32	1	1	1	1	1	0	1	1	1	1
RXRG_1q23.3	0	0	1	0	0	0	0	0	0	0
RXRA_9q34.2	1	1	0	1	1	0	0	0	1	1
TUBB_6p21.3	1	1	1	1	1	1	1	1	0	1
TUBB4QL_10p15.3	0	1	1	0	1	0	0	1	0	0
TUBB4_16q24.3	0	1	0	0	1	0	0	0	0	0
TUBBL_18p11.3	1	1	1	1	1	0	0	1	1	0
TUBB5_19p13.3	1	1	0	0	1	0	0	0	0	0
TUBB1_20q13.3	0	0	0	1	0	0	0	0	0	0

Appendix 9

Comparison of three methods used to generate the expression profiles for nine MHC paralogous gene families. The differences between the three methods are highlighted in yellow for the nine tissues common to each method.

Gene	*Adrenal gland*			*Brain*			*Skeletal muscle*			*Spleen*			*Testis*			*Kidney*			*T cell*			*B cell*			*Lung*		
	M	**D**	**S**	**M**	**D**	**S**	**M**	**D**	**S**	**M**	**D**	**S**	**M**	**D**	**S**	**M**	**D**	**S**	**M**	**D**	**S**	**M**	**D**	**S**	**M**	**D**	**S**
AIF1_6p21.33	0	1	0	0	0	1	0	1	1	1	1	1	0	0	1	0	1	1	1	1	0	0	0	0	1	1	1
AIF1-L_9q34.12	0	0	1	1	1	1	0	0	1	1	1	1	0	1	0	0	1	1	0	0	0	0	0	0	0	0	1
BRD2_6p21.32	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
BRDT_1p22.1	0	0	0	0	0	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
BRD3_9q34.2	1	1	1	1	1	1	0	1	1	0	1	0	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1
BRD4_19p13.12	0	1	1	1	1	1	1	1	1	0	1	1	0	1	1	0	1	1	0	0	1	1	1	1	0	1	1
C4_6p21.33	0	0	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	0	1	0	0	1
C5_9q33.2	0	1	0	0	1	1	0	1	0	0	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	1
C3_19p13.3	0	1	1	0	1	1	0	1	1	0	1	1	0	1	1	0	1	1	0	1	1	0	0	0	0	1	1
CLIC1_6p21.33	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
CLIC4_1p35.3	0	0	1	1	1	1	1	1	1	1	1	0	1	0	1	0	1	1	1	0	1	1	0	1	1	1	1
CLIC3_9q34.3	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
CLIC5_6p21.1	0	0	1	0	0	0	1	1	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0
CLIC6_21q22.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
CLIC2_Xq28	0	0	0	0	0	1	0	0	1	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
GPX5_6p22.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
GPX4_19p13.3	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX1_3p21.31	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
GPX3_5q33.1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	0	0	0	0	0	0	0	1	1
GPX2_14q23.3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1
NOTCH4_6p21.33	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
NOTCH2_1p11.2	0	1	1	1	1	1	0	1	1	1	1	0	1	1	1	0	1	1	0	1	1	1	1	1	0	1	1
NOTCH1_9q34.3	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	1	0	0	1
NOTCH3_19p13.12	1	1	0	1	1	1	0	1	0	1	1	0	1	1	1	0	1	1	1	1	0	0	1	1	0	1	1
PBX2_6p21.33	0	1	0	0	1	0	0	1	1	0	1	0	0	1	1	0	1	1	0	0	0	0	0	0	0	1	1
PBX1_1q23.3	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	1	1	0	0	1	1
PBX3_9q33.3	0	1	1	0	0	1	0	1	0	0	1	0	1	1	1	0	1	1	0	0	0	1	1	1	0	1	1
PBX4_19p13.11	0	0	0	1	1	1	0	1	0	0	0	0	1	1	1	0	1	0	1	0	0	1	0	0	0	1	1
RXRB_6p21.32	1	1	0	1	1	1	1	1	0	1	1	1	1	1	1	0	1	1	1	1	0	1	1	1	1	1	1
RXRG_1q23.3	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
RXRA_9q34.2	1	1	0	1	1	1	0	1	1	1	1	0	1	1	1	0	1	1	0	0	0	0	0	1	1	1	1
TUBB_6p21.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
TUBB5_19p13.3	0	0	1	1	1	1	1	0	0	0	0	0	1	0	1	0	0	1	0	0	0	1	0	1	0	0	1
TUBB4_16q24.3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1	0	1	1	0	0	1	1
TUBB2_18p11.1	1	1	0	1	1	1	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1
TUBB1_20q13.32	0	0	0	0	0	1	0	0	0	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
Total differences	**5**	**3**	**9**	**4**	**1**	**8**	**5**	**4**	**5**	**3**	**5**	**7**	**4**	**4**	**5**	**16**	**1**	**8**	**3**	**2**	**5**	**2**	**2**	**5**	**15**	**0**	**10**
% difference	**14**	**8**	**25**	**11**	**3**	**22**	**14**	**11**	**14**	**8**	**14**	**19**	**11**	**11**	**14**	**44**	**3**	**22**	**8**	**6**	**14**	**6**	**6**	**14**	**42**	**0**	**28**