

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.

<i>Class</i>	<i>MHC gene</i>	<i>Clone</i>	<i>Locus</i>	<i>Start</i>	<i>End</i>	<i>BLAST Match</i>	<i>P-value</i>
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	RXR	AL160058.8.1.155369	1q23.3	163005239	163049202	RXR	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	RXR	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	CYP11B1	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	RXR8	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	RXR8	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	RXR8	AC090937.1.1.160696	3p25.1	15002136	15024392	NR2C2	6.60E-09
xI	HMG4	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	HMGNA4	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/I	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	RXR8	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	RXR	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	Q8NKN2	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	RXR	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	Q9Y210	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	RXR8	AC090589.8.1.190017	11p11.2	48157255	48168103	NR1H3	1.40E-06
xII	RXR8	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	RXR8	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	MIR68	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	AP000713.2.1.113116	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	RXR	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	RXR	AL359457.12.1.129779	13q12.11	14106712	14124427	ESRRAP	3.40E-27
xII	RXR	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	RXR	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	RXR	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	RXR	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	RXR	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	RXR	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	ABC6	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	AC010311.9.1.191172	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	RXR8	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	RXR8	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	VAR52	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