

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
A1	0.0	FCA214	SSR	AF130569				AGAATCCAACTTGGCCAGG	GGGAAGCAAGAGCACAGTC
A1	bin:LOD 1.92	FCA1053	SSR	AY435033	13	21693700	21696100	TTTCACTGGCAGCTTCTGCG	AACACAGGAGATGGACAGGC
A1	35.3	FCA752	SSR	AY434736	13	25436651	25438681	GCTTCGATGCTATGAACAAGC	TTACCGTGGGAGTCTTGTG
A1	bin:LOD 0.18	FCA753	SSR	AY434737				TTGGAAACTTAAACCCCTGCA	ATGGCTTTTCAGAGCTTGG
A1	84.7	RD114-6J	STS					ACCCACCTAGCTCATAAGAGC	TTGGGACACAGAAACCTTACA
A1	100.0	FCA754	SSR	AY434738	13	31488486	31488736	AGGCTCTACAGGAGGTTCAAGC	TCGTGTACTCCATTTAAGCAG
A1	111.0	FCA755	SSR	AY434739	13	28996700	28997000	AAAGAAACGAGCGAGGGGAAG	AGTACTGTGCGCGGAGAATC
A1	136.3	UBL3	STS	AW646755	13	29268546	29354715	CTTTGGAAACAGAGAGAGCAA	TGGGGCAATTAAGCCATTTA
A1	165.7	FCA721	SSR	AY434740	13	37065044	37067254	CAATTTTTAATTGGTGGTGT	CACCTCCGATAGGAATGAAAAGA
A1	195.5	FCA274	SSR	AF130592	13			TTGGATTCTCTCTTTCC	TGCCATCCAAATAGGTTATTT
A1	226.0	CHDC1	STS	X79682	13	46063972	46262332	CACGTTTTCTGGTGTGTTGTA	GGGTGCTCTGATTTTCAG
A1	248.8	FCA176	SSR	AF130555	13	44051536	44052586	GGAACCTGGAAAGCAAACC	TCCACAGTTGGAGTCTTAAAG
A1	274.3	F141	SSR					GCAATGAGACTAGATGGAAGGA	GGCTCCAGATCTCTGTAGCA
A1	299.1	FCA280	SSR	AF130596	13	58094086	58095636	ACCTCAAACGGTATGAATACCA	GTCCCCAGAAAGATTTGCA
A1	343.0	FCA756	SSR	AY434740				AACCAGTTGAGCCATTGAG	AACTGGTGCAGCCACTCTG
A1	378.7	F42	SSR					CCCACGTGGACTAATCAAT	CACCTGCACAAATTAAGAGGC
A1	388.0	FCA499	SSR	AF130637				TGTTTATACAGGCTGATAGC	AGGTGCTGAGGAGTTGA
A1	414.1	KLF12	STS	AW646754	13	73196786	73644679	GAAATAAAGGGGCGCTCAG	AGGCTCCACTGAAATGTCG
A1	419.4	FCA757	SSR	AY434741				AGGCTGGGATAGGCTTCT	CAGCATCCACTCAGGTTCAA
A1	446.8	FBXL3A	STS	AW646753	13	76516034	76537968	GCCTGTCAAAATCCATTTTC	TTGTAATTTTCCCTTGGTAAA
A1	464.2	EDNRB	STS		13	77406254	77430541	ACGTTACCTGCGAATCTGCT	CGGTCCAGAGGCTTACACTG
A1	495.0	FCA229	SSR	AF130576				CAAACCTGACAAGCTTAGAGGGC	GCAGAGTCCAATCTCAAAGTC
A1	501.7	FCA758	SSR	AY434742	13	86552943	86554988	GCTTAGCCTTGTGACATGCA	AGCAAATGCCTAAGGCCTT
A1	507.2	FCA759	SSR	AY434743				TTACCACCGGTGTTGAACT	TCTCTTTGTGTTGCCAAGGA
A1	531.7	FCA760	SSR	AY434744				TGCCATTTTTGTGAAATTTCC	CCTAGGACAGGGCTCAAGT
A1	bin:LOD 0.02	FCA761	SSR	AY434745	13	95133586	95134386	ATGAAAGTAGAAAGGCCATTGC	TGAAATGTTGCCATGCTTA
A1	601.9	FCA024	SSR					CCCAGCTTTGTCTTACTGTG	CATCTCCCTTAATGCC
A1	635.3	FCA762	SSR	AY434746				ACACGCACACAGCTGAGG	AGGGCCAGTTACGAAGCC
A1	722.9	FCA218	SSR	AF130570				CCACCCATGTGCTCCATGTT	GGGCTCATGCTGACAGCTC
A1	750.6	F10	STS		13	112863783	112890479	CTGTCTGCCCCAGAAAGGAC	GACAGCTTGACAGTGTCTC
A1	754.4	LAMP1	STS		13	113038160	113064379	AGGAGGAGTGTCTCCCTAC	TCAAACCTCAGTCAGGAACGA
A1	804.2	FLJ20531	STS	AW646766	1	245115007	245124084	TTGGGTCACAGCCAGAACTC	AATTCCTTGGGGCAATCT
A1	892.0	FCA763	SSR	AY434747				AGCAACAGCCATTCCAGG	ATCCCTGGAGGACAGAA
A1	906.2	FCA566	SSR	AF130660				TCAAACAGATAAGGCTGAACCA	TCTGTGATGACGGCTCAAAG
A1	917.7	GUK1	STS	AZ081286	1	224713326	224722192	GACAGAGTGGGAGGACAGA	CCCAGCACAGTGTACTCT
A1	942.3	GNB2L1	STS	AW646765	5	180725965	180732931	AGTACACTGGGGTGGCTCTG	GCCCTGTGCTTCAGCTCAA
A1	1031.7	FCA090	SSR	AF130516				ATCAAAGCTTGAAGAGCATGG	TGTTAGCTCATGTTACGTGTC
A1	1053.3	FCA722	SSR		5	124098797	124101063	GCTTTTTGTGATGGTGCCTA	ACAATGGTGTGCCCTACA
A1	1061.3	FCA1054	SSR	AY435034	5	124099797	124100047	GCTTTTTGTGATGGTGCCTA	ACAATGGTGTGCCCTACA
A1	1077.8	FCA723	SSR		5	125527497	125529637	TGAAGGCTAAGCCACATAGA	CGGAAGATACAGGAAGGTA
A1	1102.7	IL4	STS	X87408	5	132040541	132049233	CCTGTCTGTGAATGAAGTCAA	ATTCAGCTCAGTCTTGTAG
A1	1104.8	IL5	STS	AF068770	5	131907999	131910077	CTTTCTCCAGTGTGCTCC	GGAACTAGCCCAACCTGAA
A1	1114.9	UBE2B	STS	AW646764	5	133737733	133758546	TTCAAAAATAAGGCATTCAA	TGCATGGTGAAGTAAATTTG
A1	1134.6	FCA083	SSR	AF130511				CTGCCCTACACACACAAA	CCAGAGCAGAGATTCAAACATG
A1	1163.0	FCA764	SSR	AY434748	5	136116647	136116847	TGAGGGTGAGATGGAAGGAG	ACTAACCAATCCTGGTGCCTC
A1	1200.0	GNPI	STS	AW646763	5	141363385	141375767	CTCCCTCTGGCACTGTTCTC	CTCAAGAGGGGCTTTAGAG
A1	1235.8	FCA765	SSR	AY434749				GGGTATTTGTGCATGCAGG	ATAGGCTGTGTGAGAATGTA
A1	1240.4	LOC345651	STS	AZ081285	5	56747660	56749802	TGGGCACCACTTCTACTCA	TTGAAGGCCTAAAACATGA
A1	1262.4	DKFZp761C169	STS	AW646762	5	56440181	56527173	AGTCTCCCTATCCATTTTC	CCCCATCACTACCTCTCAG
A1	1284.4	FCA766	SSR	AY434750				GGGTGCCCTGGGCTGATT	CTGACTCAATCCAGGGGTTT
A1	1297.9	FLJ23654	STS	AW646761	5	145426012	145426012	CAATTCACCTTTTGGGCTCT	CCATTCAGGACAGCAGACAG
A1	1305.2	PPAP2A	STS	AW646760	5	54801002	54801002	TGTACAGGTGGGCTGTTT	CCTTTAAGGGACTGCTGCTG
A1	1311.8	CKN1	STS	AW646759	5	60140179	60211403	CCACAAAACAGCTGCATTT	TTTGAAGTGCATGGAGCAG
A1	1323.0	HTR1A	STS		5	63226802	63228070	CTTACCTGTGCCCTGGT	TGTTGAAGTAGGGTAAATGACC
A1	1348.4	FCA084	SSR	AF130512				TAGGTGAATGTTGGGATTTATGG	AACTGAAGACAAATGATGAG
A1	1364.7	SMN1	STS	AF503618	5	70377637	70405708	agacgctgactgattgacc	tctctgccctcccactta
A1	1388.7	FCA767	SSR	AY434751				CCTTCGCTACCTTACACCATCC	CCGAAGGCTAGATACTCTCGG
A1	1428.5	FCA768	SSR	AY434752	5	81873132	81875503	CCTTTAAGAGGTGAGGGGC	ATAGGCACTGGGGCAGAG
A1	1445.8	FCA071	SSR	AF130502	5	88102583	88105156	AGAAGCAGGACAGCAAAAT	TTCCCTAAGTAATCTGTCTAGA
A1	1471.8	CRTL1	STS		5	82975450	83055609	GGCGCTACAACCTCAATTTTC	TTGGATGTAAACAGAAAACATCAT
A1	1493.2	FCA689	SSR	AF130698				GGGGTAACATGCTGACTTGG	ACAGTCCAGGATTTCCCTACC
A1	1498.5	ARSB	STS	S48472	5	78114307	78320498	CTCATTTCAAACCCAGTGC	CCAGCCTTAGGACTCAAGC
A1	1523.6	HEXB	STS	AF014805	5	74019724	74055826	TGCCAGATTACGAGGATTC	AGGTCCAAAGTCCAGACT
A1	1587.1	FCA769	SSR	AY434753				CAGCTTGGCTAGAAAATGGC	CATGATGTGCATATGTGTGCA
A1	1620.6	FCA770	SSR	AY434754	5	111487736	111490607	TCAAAGAGTCTTTGCTCAAGGG	TTTACTTAGGACTGACAGGGCA
A1	1632.2	CAMK4	STS	AZ081284	5	110590510	110592688	ACCACCTCAAATCGGTGAGG	CCTCTAGGCACTGATTCCA
A1	1665.5	FCA771	SSR	AY434755	5	171060048	171063848	GGTGGGTGCTCAGGTAACAT	TTGTAACGTGATGAAAACCCAGC
A1	1695.5	GFBR4	STS	AZ081283	5	176449458	176449698	TGCTTCTCCGCAACAATGTT	TTAGTGTCCCGAGGATGACC
A1	1727.1	FCA772	SSR	AY434756	5	176007148	176008708	TCATCAGCACTGAGCCAGC	CATGCAGACACTGCCACC
A1	1759.7	IL12b	STS	AF054607	5	158677334	158693024	CTCCTCCGTGGCAAGACCTC	CAGTTGTCTCAGGATGAGC
A1	1779.4	FCA146	SSR	AF130544	5	162033366	162035708	TATTTAGAAAGCTTGACAGAGC	GACAGTGAACCTCCCTATGG
A1	1799.1	IL7R	STS	AW646758	5	35857133	35876984	TGAGGAGGTCTGTGCCCTAT	TTTGACCATGTTCTCCCTCAA
A1	1807.6	UCMFC01	SSR	AF121909				CAGTTATCCATTTGGACCCTAA	GTCTCCAAATCTGCTCCTGTT
A1	1828.9	nF-AGTT	STS					Roca et al. in prep.	Roca et al. in prep.
A1	1840.2	SEPP1	STS	AW646757	5	42800132	42812303	TTTGCCAACTGTGTGTACC	TGTTGTCTGTCTTGTATTGCTT
A1	1849.5	FCA178	SSR	AF130556				GTGCCCATGAATCTCACTT	TACAACCTAGGGGTCGTATGG
A1	1852.0	FCA008	SSR	AF130476	5	52506019	52508337	ACTGTAATTTCTGAGCTGGCC	TGACAGACTGTCTGGGTATGG
A1	1854.0	FCA724	SSR		5	45595513	45598192	GGTGTATAAACGTCAAAGGATC	GGTGCTGTGCCAGATTTGA
A1	1874.5	ADRB2	STS	AY011306	5	148190997	148191259	ATCGTCTGGCCATCGTGT	CTCCTGGAAGGCAATCTGTA
A1	1884.0	CSF1R	STS	J03149	5	149416016	149476093	AGGTGCTCAGAGAGCTGCTT	GCCTTCCAGCTAGAACAC
A1	1886.2	SPARC	STS	AW646735	5	151025155	151050039	AAAAAGTGGGAGGAGGGAGA	CCAAGGCTAGAGCGAGGTTG
A1	1888.5	FCA453	SSR	AF130627				AATTCCTGAGAACAGCTGAGGG	ATCCTTATGGCAGGACTTTG
A1	1902.1	FCA773	SSR	AY434757				ATCATCAATATCCATTTGGGC	CTGGCTTGTGGACCATCC
A1	1904.7	FCA678	SSR	AF130693				AGCAATCTCCAGAATGTGGG	TCAAAAGATTAAGCCTTCCAA
A1	1931.2	FCA129	SSR	AF130534				ACATAGAGCCGACACGGG	CGCCTATGTTTACTGCAGCA
A1	1940.9	FCA357	SSR					TCTGGAGGGAATTTAGCTCG	ATATGCCCAAGAACACTG
A1	1972.4	BASP1	STS	AW646756	5	17250430	17309480	CATTACTCGGATTTGAAACGA	CATTACTCGGATTTGAAACGA
A1	1998.6	FCA725	SSR					TGAATCACTATGTTGTACACCTGAAA	GAGGCTCAATCTGATACCAAG
A1	2000.1	FCA774	SSR	AY434758				CCGGGGCTGAATGACTCTA	TGTCAAATGTTCTCTGTACTGC
A1	2029.6	FCA775	SSR	AY434759				TTCCACAGATTCATCTCATGG	AGGGTGTGAACTGACCGGC
A1	2043.1	FCA776	SSR	AY434760				AGTCTGACTCTGGGGTCT	AGTGGGGATTTCAAGGTTCT
A1	2066.0	Hs.17138	STS		5	6632091	6666142	GGAGCTTCTGACCACAAAC	GCCCAATGAGGCGGTGACT
A1	2096.9	TEB4	STS	AW646734	5	10386526	10468229	TATCCCGTGTCTCAGCAG	ACGATCGACAGTGAAGCACA

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
A2	0.0	GPX4	STS	AW646768	19	1043934	1046786	CTCAGTCCATGCACGAGTTC	GAGGCCACGTTGGTACTAT
A2	7.9	ADTD	STS	AW646769	19	2040995	2091346	TTCTGGAACTCACTGCACAGG	CCGTGAGAGATGATGGTCTCT
A2	15.8	NFIC	STS	AW646736	19	3306573	3403635	TTGCTTTGTTTCTCCTCGTGG	CTGGCCACGTTTTTCAGT
A2	34.4	RANBP3	STS	AW646770	19	5856154	5918113	GCCAAGAAATCAATCAGTTTATTC	CGCCTGGTGTCTAACAGTGA
A2	62.3	RAD23A	STS	AW646771	19	12901865	12909994	AGCTGAGAAGGGTCTGTGATG	GATGCGATAGTCCCTGATGG
A2	75.4	FCA777	SSR	AY434761	19	9718113	9720753	GGCAGAGCTGTTGACACAA	CGGTGACTGAATGACGAGA
A2	91.6	MAN2B1	STS	AF010191	19	12602534	12623037	GGACTGGGAAAAGCATGAAA	TGCTGAGTTGGGAGGTATC
A2	99.8	PTD008	STS	AW646772	19	12624120	12624220	CAACAACAACAAAACGAGTGG	AGAACCCTCAGCCCATGAC
A2	123.5	FCA778	SSR	AY434762	19	15753194	15755511	GAGATTGAGTTGCTGTCTCCTG	TTTATCCCTGTCATAGGCC
A2	142.9	INSL3	STS	AW646773	19	17772636	17772799	GGAGAGTGTGGGAGGTGAT	AGCACCTGTTGACCTGTGT
A2	154.0	KIAA0892	STS	AW646774	19	19276832	19314097	TCCAAAAACGGGAAGCTATG	CAGCCTGTAACTTCAGCTGGT
A2	176.8	MGC39725	STS	AW646775	3	51752207	51753995	GTGACCCCAAGAAAATCTCG	GATACTGCCGTTTGTCTCAT
A2	190.2	FCA581	SSR	AF130667	3	50272111	50274566	TCTTGTCCCAACACTTGCAC	GGACCCACACACTGACTGCT
A2	198.4	APEH	STS	AW646776	3	49565850	49575349	TCCAGGAGAAACACTTTGATG	GGCCACACTGAGGTCTG
A2	205.9	MPDH2	STS	AW646776	3	48916172	48921232	AGTGACAGGAGCTGCCCTTA	CTTGTGGCAGAAAGACAAA
A2	209.3	COL7A1	STS	AW646777	3	48420739	48451921	TGAGCGTGTCCGTATTCTCA	GCAGTCACATCCCGTCACT
A2	214.0	FCA056	SSR	AF130495				TTTATAGTAATGCGCATGTTGG	TTGTTGAAATGACATGCTCC
A2	220.0	FCA726	SSR					GCACAGAGGATCCCCATAA	GCCCTGTTTGTCTGTACT
A2	220.0	MYL3	STS	AW646737	3	46718599	46724163	CTGGGGTGAAGCAGAGAGGG	CTCATCCCCACTTCTCAGC
A2	226.2	CCR3	STS	AF226006	3	46125852	46127052	GTACCTGGCCATCTGCCAC	TTCAGGAGAGGGCCGCTAT
A2	227.9	CCR5	STS	U82796	3	46230871	46236924	GAGATAGGAGGCACAGGTG	TTCCCAAGCCCTTAGAGT
A2	237.1	FCA052	SSR	AF130493	3	45755641	45762141	TGTATCCTCTGCTCTGAAACA	ACCTGTCAGTGTCTGTG
A2	248.7	FCA355	SSR	AF130618	3			GGAGCCCTCTTATGAATT	ACCACCTGTTGACCAGAGCC
A2	263.3	PRKCD	STS		3	53050080	53081586	CCTCTTGAGAGTGGGGTCTG	TTGTTGAGACCCCTGAAAGG
A2	294.0	FCA304	SSR	AF130601				TCATTGGTACCACAAAGTAGG	CTGCATGCCATTGGGTAAC
A2	314.3	FCA779	SSR	AY434763	3	1451745	1452345	GATCATAGAATCTTTACTCT	CATGTAAGTCCACCTTCT
A2	362.8	FCA687	SSR	AF130696				CCTTCCCACTCATGCTCTC	CCATTACTTGGTCTCAGGAAAC
A2	390.0	LOC55831	STS	AW646778	3	9997024	10020649	CTCCACTTCAAGGCATGTT	TTTTATTCCGAGAGCCTCA
A2	431.4	MDS027	STS	AW646779	3	10160284	10160434	CTGTGGGTACCAACAACA	AGCTCTATTGCCTTGTGAT
A2	500.7	ITPR1	STS		3	4526981	4880924	AGTTCTGATCCACCAACAAGA	GAATTTTATCTGCCAACAA
A2	564.4	PPARG	STS		3	12321215	12467696	GGGTGTCAGTCCGCTCA	CACCAAGGGTTTTTCTCAGG
A2	575.6	RHO	STS	AZ081287	3	130529093	130535798	TGCTGGGCACACATACATTG	GTAGGACACCAACAGATCA
A2	638.8	FCA780	SSR	AY434764	3	13164676	13166476	TTAACTCAGGGAAGACTCCAGG	TTCCCTGGGAAGAGGTCATG
A2	729.4	KIAA1886	STS		7	44504390	44515072	CAGACAGGGGACACGACTG	TCCGTGAACGTGAGAATTG
A2	781.9	DDC	STS	AW646783	7	50233891	50340856	TCCTAGAATGCCCTGGAAA	GTGTGGCCTGATGTTTCCT
A2	821.3	FeLV-016	STS					Roca et al. in prep.	
A2	870.5	FCA781	SSR	AY434765	7			AAAAAGCCTGTTAGTGCAGG	TTTAAACCCTGAGGCATCC
A2	903.2	FCA782	SSR	AY434766				TATATGCATACACTCGCCG	GCGTCTCACTGAGAAGACC
A2	925.9	INHBA	STS		7	41435576	41449455	CAGTGCACAGACCTTCTCAT	GCACCTCTCCACGATCATGTTCT
A2	943.4	TCRG	STS	D89023	7	37986196	37986521	ACCTCCATAAGCTGGAACA	TCCAGAATGTTTTCGCCATT
A2	986.3	FCA783	SSR	AY434767	7	103882428	103884909	TGAGCCCATACTCTCAACACC	ATGTCACTAAGCCGAGTGGG
A2	1019.8	HGF	STS	AB046610	7	80926574	80997693	TCTGATGCTATTACAGTAGCA	GACACAATATTTCCGCACCT
A2	1030.2	FCA784	SSR	AY434768				CAGATACTGGTGTCTTAGGGTAAACA	TTGAGTAATGCACACCCAAA
A2	1043.1	ABCB1	STS	AB029153	7	86731407	86940797	AATGGCAACATTTTCATCG	ATAGCAGCCGACAGCTCAAG
A2	1053.6	FCA124	SSR	AF130531				CCATTCCCTCCTGTCTGTA	GCCTCAAGCCTATTGCTACT
A2	1072.8	CALCR	STS		7	92652026	92802263	TCAACTCTCTTTTGTCTCAACAT	TGGAAGTGGATCAGAGATGTC
A2	1097.9	FCA656	SSR	AF130686				TTGTAGGGACAGATTTCCACA	CTGGTGTCTCCACATGAAA
A2	1122.2	FCA105	SSR	AF130523	7	128456457	128458535	TTGACCCCTCATCTCTTTGG	TGGGAGAATAAATTTGCAAAAGC
A2	1143.7	FCA340	SSR	AF130611				GACTGAGCCACCCAGGTG	CCCTTCTCCCAATTATC
A2	1167.4	Fc.100234	STS	AW646738	7			TGATGGAGAAAGGAGGAGA	GCTGAAGTCGGACGTTAAC
A2	bin:LOD 2.04	FCA785	SSR	AY434769	7			TTGGTGGATAGAGACCTGTGG	TGGGTCTCTGGCTCTGTTCT
A2	1243.1	TAX1BP1	STS	AC098703	7	27488013	27578570	GAAAACGGGCATTGAGTAT	ACTTTAGGAAACGCCCACT
A2	bin:LOD 0.86	FCA786	SSR	AY434770	7	30977984	30980430	CTTCACTCAACTTTTCAGATG	TCAGCTGTCTAGGACCTCTCA
A2	1261.8	IL6	STS	AF054603	7	22475068	22479888	CTGGGCATCTAAGATTGCTG	CGCTCATACTTTCTGTTCTCA
A2	1282.4	FCA621	SSR	AF130675				CACATGCACTTTTATGCACA	CTCAACTGGGAAACTGGGT
A2	1324.9	FCA727	SSR					GCCATTTCTCAGCCATTGTT	TAGGAACACCCGCTGAGTGC
A2	1341.9	LEP	STS	AB041360	7	127421491	127437841	TCCTGAGCAGGTGGGAAA	TGGTCTCAGGCATGTTCTCA
A2	1352.5	FCA787	SSR	AY434771	7	128533849	128536028	GAGTTGAAGGAGGAAAGTTCA	AGCAAAGTCCAGGATAGGAA
A2	bin:LOD 4.41	FCA788	SSR	AY434772				ACCTCTCCCCCAACTCAGT	ATCATGTGCTGGGCACAGT
A2	bin:LOD 0.37	FCA728	SSR					TTCACTTTTCTCCTGACAA	CCTGCCTGATTCTCACA
A2	bin:LOD 1.37	FCA532	SSR	AF130649	7	121632398	121632498	TTCCATTGCATTATTCCAG	CATGAGCTGAGCTGAAACCA
A2	1383.6	DKFZP434G154	STS	AW646784	7	127970971	128002342	ATGGAGGCCAATACCAAGTGA	GGGCTATGTCAACTCTGCT
A2	1402.6	FCA789	SSR	AY434773	7	131599004	131601627	GGCCTCTCTGAGCAAGAGG	CTGCATTAGTCAAGGTTCTTCA
A2	bin:LOD 1.48	FCA790	SSR	AY434774	7	120783291	120785464	AAGCCACAGATGTAACCATGG	CCCAACTTGGCATGCGAG
A2	1445.1	EN2	STS	AZ081249	7	154552051	154560138	ACCCAACAAGAGGACAAGA	ACCTGTTGTCTGGAACTCG
A2	1477.8	FCA791	SSR	AY434775				GGGAACAGAACAGATGTAAGC	AGAATGCCCTGCGAAGTG
A2	1495.0	FCA327	SSR	AF130608				GAGATTGGAAACACAGGCCAT	CTGAATGGATACCAGGCAT
A2	1511.0	FCA792	SSR	AY434776	7	143530823	143534308	GTTGGGAAAACACTTTTCCA	ATATAAATGACGAGCCTCGGC
A2	1526.5	CHRM2	STS		7	136101824	136103224	ATGAATCTGCTCATCATGCTT	TGGAACCTGTGTTTCTCCTG
A2	1545.1	TRB@	STS	AZ081250	7	141801815	141885016	AGTCACTCTCCCTCTTCT	CTGCTGATGAGACGCTGTG
A2	1567.9	MKRN1	STS	AW646785	7	139486493	139486574	CGGGAAACAGAGGAAACAAAC	GTGCCCGTGTTCCTGCTCA
A2	1605.6	FCA793	SSR	AY434777	7			AGTGTCTCATCTCATGTTTG	TTGTTGCCCTCTTTGTTCC

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
A3	0.0	TCFL5	STS	AW646787	20	62151817	62172325	GGAGGGAGAAACAAAAGAGTGA	TGCTTTTACTCTTTATCTGCAT
A3	29.6	SANG	STS	AW646739	20	58032384	58064368	GTAGGCCCGCTTAAGCTTTC	TAAGTCAAGCCTTGAGCACAA
A3	50.6	STK15	STS	AW646786	20	55828267	55605718	GAAAGCGAGATGCACACGTAG	AGGGCACTGCAGACAAGG
A3	63.4	FCA102	SSR	AF130522				GAAATCGTATGTCAAAATTCTG	GAAAGCACAGGTTTCTGGTT
A3	92.2	YWHAB	STS	AW646788	20	44152772	44175589	TCCATGCTGCAGGAATATG	CTGTGTTTGGGCTTTGATG
A3	129.4	UBE2C	STS	AW646789	20	45079685	45084012	TAGAACCACGTCGCATTCTG	ACACTGGCAGCCCTCT
A3	141.6	FCA794	SSR	AY434778				CGACCTAAGCCGAAATCAAA	GGGTAGAGCTTAAAGTGTCCCA
A3	157.1	FCA729	SSR		20	44346300	44347000	AGCTCTCCAGTGGCTTCAGA	TTGTCCTTCCCAAGTAC
A3	175.5	FCA688	SSR	AF130697				GTCAGGCTTTGTCTGACAA	TACAGATCTGCACAAGAAATCC
A3	179.8	FCA795	SSR	AY434779				ACCTAAGGATGTCCCCAGC	TACGTAAGTCAAGGCCATTGG
A3	200.4	ASIP	STS	AY237394	20	33516847	33525824	GGGCTGACATTGAACATCT	CACCTGGGTTTGAATCTGG
A3	202.8	AHCY	STS	AZ081251	20	33536752	33559867	CACCTGGATGACCTATGGA	GGCACAACCCAGGTTGAC
A3	215.5	BLCAP	STS	AW646790	20	36784249	36794735	GAGAGTAGGGGTTGAAGAAA	AGGGCTTCCCAAGGCCCA
A3	222.7	SRC	STS		20	36650500	36672254	ACTTCGACAACGCCAAGG	CTCACTGGATAGTAGGCCACC
A3	256.6	CSNK2A	STS	AW646740	20	411734	472434	AAATCCACAAGCAACGGTTC	AAATCCACAAGCAACGGTTC
A3	301.3	PRNP	STS	AF003087	20	4615105	4630233	AGGCCACTTATCATTTTGG	CGCTGCTTGACAGTGATGT
A3	330.7	CHGB	STS		20	5840106	5854003	TGGAGCAAAGGCCAGTTTTA	GGCAAATAAAGCATTTCCA
A3	350.1	FCA796	SSR	AY434780	20	6413043	6415682	AACCATAAACTGCCAATTGG	TGTCATTAAGSACTTGTTCAGC
A3	383.3	FCA797	SSR	AY434781	20	6765977	6768438	TGCTGAGGTCGAGAGC	CCACACAGTGTCTCTAAACA
A3	405.5	FCA514	SSR	AF130641				AAAAGGTAATCCCAATGATGG	TACAAGGGGCTATCTCCGG
A3	426.6	PLCB4	STS	AY011802	20	9299581	9409460	GTGAAATGTGAAGCCGAGAT	CACCAAGCTTACTTACTGTGA
A3	461.1	FCA080	SSR	AF130508	20	14153062	14155629	AAGCTCTCTGCATTTTCTGC	TGTAAGGCCCAAAAATCTGC
A3	492.0	FCA798	SSR	AY434782				AGGTGGTCTCCTTGACCAG	GGTGGAGGTGTACAAATGG
A3	581.0	FCA498	SSR	AF130636	2	99934431	99936679	GATAGATGGGTTTTGGGG	TGATTGCTATGGCCAAAAT
A3	627.7	ZFP36L2	STS	AW646791	2	43408416	43411455	AGTGAAGTATTTCCCAAAA	CAGCGGATGAAGGACAGTA
A3	670.6	LHCGR	STS		2	48871622	48940556	TGATTTGGCTGATTAATTTCTAGC	GAAGGCTTATTGATCCAGTGAAG
A3	692.8	FCA799	SSR	AY434783				CACCTGGTCAAGCAAGCTTCA	GTGGAAGACCTTTGGTTCCA
A3	711.8	FCA208	SSR	AF130665	2	51860375	51860525	TCAGGGTCAAAAAGAAAAA	CAAAGCACCAGCTTAGAAGTCA
A3	749.1	CCT4	STS	AW646792	2	62052963	62073737	CCATCCGTCTCCCAAG	GTTCCTCCGGATGGCAAG
A3	764.9	FCA536	SSR	AF130651				CACAGCACCTGGTCTTTGA	CGCGTACTCTCTCTCGCT
A3	786.6	FCA800	SSR	AY434784				CTTTTTGGTGAGAACTACT	GACCTGAGCCAAAATGGTG
A3	829.3	PCBP1	STS	AW646793	2	70272410	70274041	CATTCCACTTACATTTCTATCG	GCTGTTAATGCTGGGATCCAT
A3	859.1	FLJ13057	STS	AW646794	2	70014447	70065093	GGCATTATCAGAATATGAGGAGAAA	ACAATGCTGAAGGAGCGCAT
A3	872.8	HK2	STS		2	75018967	75078821	CTGCGACGTCGGTTCTCT	GGTATTCTGGCGGGCTCT
A3	903.0	FCA161	SSR	AF130549				TTACCGATACACCTGCCA	CACAGACGTGCTCTAGCCAA
A3	915.2	FCA801	SSR	AY434785				CTGTGGTCCATCAGACATG	ACCTTTTCCCATGGAATCC
A3	966.5	FCA493	SSR	AF130635	2	35871353	35873540	TTCTGCGTCTGCATTTTTTGG	GCAAGCAATGGCAATTCCT
A3	1010.6	PPP1CB	STS	AW646795	2	28932216	28982229	CGGGTGCATTTGAAAGAACT	TGTGCTACCATTGATGTGAAA
A3	1048.7	APOB	STS		2	21182012	21224656	TCCTTTAAATCAAGTGCATCACAC	CCAGCAAAAATTTTCTTACTCAA
A3	1076.2	XDH	STS	AF286379	2	31515982	31560554	GGGTGGCTCAGTTGGTTAAA	ATGGGAGAGGCAGAGACAGA
A3	1089.7	FCA802	SSR	AY434786				AGGAGGAAGTCCACCATGG	TATGAGTTTCTTGAAGCCACTG
A3	1119.8	AACT	STS						
A3	1143.2	CD8A	STS	D16536	2	86969573	86975746	GAGATACGTCTAACATGGAGATGG	TCCTCATAAAGAGAGTTTTATTTGGTC
A3	1154.3	IGKC	STS	AF198257	2	89042189	89042511	GTCCAGGACGGAGTACCAAA	CTGACACTCGCTCTGTTGA
A3	1165.3	SLC20A1	STS	AF074085	2	113310278	113328217	CCATTTCTGGCGTTATCAGTG	TCAAACAGCTTCCAGCTCAG
A3	1178.7	IL1A	STS	AF047012	2	113438310	11344884	AAGACCCCAAGCTTACCTT	TCCAGGTATCAGCAGTGAG
A3	1199.0	ADRA2B	STS	AJ251174	2	96246550	96249815	CCGTCCCTACTGGAACCTTCA	CAGGATCTTCCAGGGTCTCC
A3	1219.0	MOPT	STS	AW646796	2	39066275	39067575	CTGTGTGTTTATTAAGGAATCA	TGCCAATAAACCATCACTCA
A3	1258.5	FCA181	SSR	AF130558				AAGCTATGTTAAAAAAGCA	TCCACATTTGTCAAAATGGC
A3	1279.7	NSE1	STS	AW646797	2	14777725	14781362	TTGACAAATCCCCTGGAAAG	TGGCTTTTCCCTCTCTT
A3	1310.8	MYCN	STS	U82198	2	16125801	16125926	GACAGTATCTGTCTGGAGCG	AAAAGGATTAGGGCGGGTCT
A3	1320.8	YWHAB	STS	AW646798	2	9729021	9776045	GAGATGGTCCACACAATGTC	GCATCCTCATTTAAGGCACA
A3	1334.3	ODC1	STS	AZ081252	2	10585423	10593545	TGGGTCCTCCAGAGAG	TGCTTTGGAATCATCAGTTGG
A3	1359.8	FCA334	SSR	AF130609				TGTTACACCCAGTGGGAAGA	CAAAATTCAGGCAATGAATTG

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
B1	binLOD 0.00	FCA803	SSR	AY434787				GATACTGAAATGGCTCCGGA	TACAACCAGCATGCTTTCA
B1	0.0	FCA014	SSR	AF130478				AGCCAAGAGGGGAAACAAC	TGTCACAAATGGCAGGTTGT
B1	29.8	FCA804	SSR	AY434788	4	182527928	182530011	TCACTGTTTTCTCCTTCTTCC	CTTGAGGGCAGAATGAGAGC
B1	53.2	FCA805	SSR	AY434789				AAAAACAACCTGTGCACATGC	ACTGGTTGAGCACTGTGAGG
B1	73.8	Fc.es1TBD11	STS	AW646799				TGCCAGTCCATATTAAGAAATGTC	TGTTCAAGTATCATGGGCAACA
B1	106.8	FCA806	SSR	AY434790				GGACAGCATCACACATACATCA	TTGCCAGTCAAACGATATG
B1	120.7	Fc.32922	STS		4	184950239	184953796	TGTTCAAGTATCATGGGCAACA	ACCCCAAGCTGAATAAACCT
B1	129.8	SLC25A4	STS		4	186648872	186652876	TCTTCAAGTCTGATGGCCTG	TCACACTTGGGCATCATC
B1	156.7	FCA577	SSR	AF130666				AAGCAGCATGATTCACACA	GTGTCCACAGAGATTATCAGG
B1	163.6	F85	SSR					TCTGGTCTCACGTTTTCTCT	ATGTCTGTATGAGATCGGCT
B1	189.0	MGC8721	STS	AW646800	8	29776810	29796848	TGACTGGAAAGCTAAGGCAAGA	TCTTTCTAGCAGCCTTGACACA
B1	216.1	FCA522	SSR	AF130645	8	12616348	12618463	GGGGGGGGTAAATATCCAT	GAGAAACAAGGGAAAGTTGG
B1	248.7	FCA519	SSR	AF130643	8	32272962	32276183	ATGGGAGAGGAGGGTAATGG	GAACCTCTGCATTAAAGCGC
B1	277.0	FCA807	SSR	AY434791				ACATCGCTTTGTGAGGTATGG	AGTTGGTCTGGTACCCTTCC
B1	332.2	LPL	STS	U42725	8	19606082	19634073	CCAGCTGGACCTAAGTTTGG	CCTCCATTGGGGTAAATGTC
B1	359.8	NAT2	STS	AF030398	8	18058059	18067986	TGGTGTCTCCAGGCTAATCA	GTCCAAATCCAGACTCCACT
B1	388.4	FCA808	SSR	AY434792				TCCTGGCTCCTAGAAGCTGA	CAAAGTTGGCTCCTCTCC
B1	416.9	FCA559	SSR	AF130659	8	19310854	19313105	GCCAAATGTTCAGAGTGG	TTTTGGCTGTATGAGCATCA
B1	432.8	SLC20A2	STS	AF394194	8	42015917	42016234	CACCGGCTCAGTGTATTGG	TCCCAAGCCATTAGTGTTC
B1	469.6	POLB	STS	AZ081253	8	41970120	41970246	GAACACGGACATGCTCACAG	AAGGGACAGTGACCTACGC
B1	554.4	ADRB3	STS	AF192488	8	27275788	27292759	TCGGTGTCTCATGTGGTCAT	TCCTGGGTGAAGACAATC
B1	566.1	FCA339	SSR	AF130610				GTAAGGACACTGTACCAAGCC	TCTTTTCTGTTTCCAAAAG
B1	582.5	FGFR1	STS		8	38010941	38067280	CCAGCAAATGCTCCAGAT	TGCCATTATTCTGTATGCTG
B1	597.1	FCA023	STS	AF130481				CAGTTCCTTTTTCTCAAGATTGC	GCAACTCTTAATCAAGATTCCATT
B1	601.9	CLU	STS	AZ081254	8	37696942	37700610	CCCTTACTCTGTGGATGAATGG	CCTGTAGTTCCTCCCTTCA
B1	608.7	FCA809	SSR	AY434793	8	27392414	27394476	GATCAGGACACTGATGGGCT	CAGAATGGACCCTCTGGTGT
B1	618.1	FCA810	SSR	AY434794				CAGCAGCAAGGAAATGACAA	AATGCCATAGCCAGTGAGCT
B1	630.2	FCA811	SSR	AY434795				TTTTCTGCCAAGCTACGGAGT	TCACCGTAAACAGTCACTCC
B1	648.1	FCA812	SSR	AY434796				TCACACAACCTGTGTAATGTGC	AGCAGAGTGGGCAACAGG
B1	663.0	FCA700	SSR	AF130701	4	175314651	175316794	CCCTTAAATCGCAGCTCTG	AATCCAAGGAAACAGGCTC
B1	679.7	FCA254	SSR	AF130586				CAGATGCTCAACCGACTAAGC	GCTTTGGCAACCCCTCATC
B1	701.2	FCA813	SSR	AY434797				AGGAAGACCCCACTGATGTG	ATGTGCTAGGACATTGTGGTG
B1	731.8	FCA550	SSR	AF130657				GAGGTAATGTCTACAAGTGC	GAATTTGGCATTACTGCACTG
B1	774.0	FCA814	SSR	AY434798				GAGGACAGGATGAGAATTC	CACTCAGGTGCCCTTATGT
B1	783.6	FCA815	SSR	AY434799				AAACATCTACATATGTGCGCG	ATTATCAAGGGGCACAAAAGC
B1	793.6	FCA513	SSR	AF130640				TCCTTTTTATCAGCCCATGC	GCCTATGGGGAATTGGAATTT
B1	826.1	FCA816	SSR	AY434800	4	155273360	155274360	TGCATTTGGTGAATGAATCC	GTATACAAGCCAGGAAAGCC
B1	856.9	FCA817	SSR	AY434801				AATTGATGCTGCACCAAGG	CCAATAGCTGCATAGCTCC
B1	867.5	FCA818	SSR	AY434802				ACACACACTTGCATGCTCCTC	TCCTTTTGCATGTTCTCTGG
B1	874.6	KIAA1046	STS		4	146546476	146566935	GCCTTCAGAAATCTCCACT	AAGCAGAGCCGAGATGAAG
B1	883.9	NR3C2	STS		4	149466107	149829710	GCTCAGTTTCCAGCCCTTC	AGTCACACATTGAGATGGC
B1	895.8	FGG	STS	AF012097	4	155991476	15599995	TCAAGACATTCGCAATAAGGG	CCAGTAGGACAGATGTCCAAA
B1	921.5	FCA564	SSR					GAGGTGAGGTCCTTGATC	GGGACAGGATGTGTAAGATG
B1	936.3	IL15	STS	AF108148	4	14312104	143121275	GGATGCAGAAAGATGTGAGGAA	CAAAAATCTGCAGAAATCTTAAAT
B1	951.1	FCA819	SSR	AY434803				TGTCAACAATGAGGTCATAGC	CTCCAGTTAAACAGACGTTCC
B1	969.0	IL2	STS	L25408	4	123765831	123771086	AAACTCTCCAGATGCTCACA	GCACCTCTCCAGAGGTTTG
B1	990.2	FCA820	SSR	AY434804				TCGATCAATGACACAGA	GGCCTAGTTGATTTCCCTTGA
B1	1040.5	FCA126	SSR	AF130532				GCCCTGATACCCCTGAATG	CTATCCTTGTGGCTGAAGG
B1	1066.0	FCA821	SSR	AY434805				ATTTCTCCTGTGTCATGGC	AGTGACCATCAATGGATGAATG
B1	1074.7	FCA822	SSR	AY434806				TTAAGAACATGCTCTTTGGTGG	AGAAGCCTTCTGAGAACTTGC
B1	1086.1	FCA212	SSR	AF130568				TTTGATTCACGTAAGGTTGCC	GACATTTGATGCTTCTGTGGTG
B1	1100.2	EGF	STS	AB050947	4	111227255	111326624	TGTCATGAATGTGCTTTTGG	TCAGGAAGCAGAAATAATCTCACA
B1	1120.2	FCA074	SSR	AF130503				CTATCCTGGGCATGGCTTTA	GGCCTGAATGCCCTCATCA
B1	1148.0	SID6-306	STS	AW646801	4	106683439	106788395	AGAGGGAGTCTGAGGATCCT	GGTCTCTGCTCCCTGAATA
B1	1162.9	FCA612	SSR	AF130673				TTGGGGCCCTTTAAGGAG	TTCTTCTAGCTTCTTTTGGCC
B1	1201.0	PKD2	STS		4	89321600	89391705	AACCCAGCAACAATACTGACG	CCGTCTCAGCTTTGAGCTG
B1	1214.4	MLL2	STS	AW646802	4	88249006	88454970	CAATCAAGGGCTCAGAAAGTC	GAGGTGCTGATGCTGCTCA
B1	1220.0	ODF1	STS	AW646803	8	102569288	102578626	TCGGGGTCGAAAAGTACAG	GTCATCGCTTCTACGCTTT
B1	1243.7	ALB	STS		4	74670642	74687768	GCCCAAGGCAACAGAGGAA	CCTCCTGTCTTCCAGCTGC
B1	1252.0	CNS2	STS	U53906	4	71070905	71076956	CCAGCCACAGCCTCTAGTC	GGGGATTTCCATTATTTCAGG
B1	1284.0	FCA257	SSR	AF130587	4	61607411	61759288	ATTGCATTTTTTGGCTTTCA	TTAAACTGCACCTGACGAA
B1	1296.5	FCA823	SSR	AY434807				AGGGTGTCTGAGAACTAGCTGG	CATTTAGAGTTTCCAGGCTGG
B1	1296.5	FCA097	SSR	AF130520	4	66676848	66679446	TAATGTTCAACTTGAATTTGCTTC	GAACAGTATTTGCCATACAGG
B1	1322.0	IL8	STS	AF158598	4	75006911	75010067	GTGGGCTGTGGTGTAGGGTTG	CAAAACATATCCAGGATTTCCA
B1	1347.7	FCA824	SSR	AY434808				ACCGAATGATGTAGTCTGTGC	AAACTGACTGACCCACCCAG
B1	1371.6	FCA825	SSR	AY434809				TCAGCCTGACCCACAATACA	CAGGTTATGAGGTGCATATTG
B1	1418.3	KIT	STS	S76596	4	55374029	55456778	GATCGATGAGCGACGAAAGA	GAGCATTTTTCCATGCGCTA
B1	1437.0	FCA149	SSR	AF130546				CCTATCAAAGTTCTCACCAAATCA	GTCTCACCATGTGTGGGATG
B1	1458.8	FCA826	SSR	AY434810				ATTTCCAGGCTCTCCACTT	GAGCTTAAATCCTGACCCACC
B1	1486.1	FCA827	SSR	AY434811				CCTGAGAGGGATTCTAAACA	TGCTTACTTCTGTGGCTTT
B1	1511.4	FCA828	SSR	AY434812				CACCTGAGTACAGGACAGAAACA	CATTACATTTGGCGAGATTGA
B1	1552.8	FLJ20425	STS	AW646804	4	4262159	4284602	GCTTTGAAAAGCAATATTGGAG	AACTCAAAGCTTTGAAATGAAGC
B1	1590.5	FCA152	SSR	AF130547				TTTTGATCAGCTTAGGCTTTCA	CITCCCAGCTTCCAGAAATG
B1	1599.7	FCA731	SSR		4	5741915	5744421	GATCCGTCTATCCATCTGTCC	ATGCTCCCTGAAGCTGTAA
B1	1638.1	FCA829	SSR	AY434813				GAAACAATGTTGGAGAAATCG	GAGTGCCTTTGAAATGTGACTG
B1	1640.9	FCA830	SSR	AY434814				ACACGTATGCACACATATGC	GTTACTTGGAGTCGAGGAGG
B1	1659.7	FCA730	SSR		4	30151064	30153318	ATTGGGAATGTAGCCAAAGG	CTCCAAGTGGATGGAGCATT
B1	1681.5	Fc.25119	STS	AW646741	4	15852101	15866154	CTTCGGTGAACCCAGGAAGT	CCCCAAACTATTCCATTCA
B1	1692.1	FCA528	SSR	AF130647				CITTTGGGCTCCAAAATAGTTG	AATCAGTGTTCAGAGCCTGA
B1	1714.2	FCA831	SSR	AY434815				TCATTTGCTCTTTGCCATCC	ATCAAAAATAAATGAAAAGGGG
B1	1726.9	FCA832	SSR	AY434816				CATTCTGTACACAGGCAAGG	ACAGACTTACTGACCAAGTCC
B1	1759.4	MYL5	STS	S70434	4	657730	665817	CGCTTTTCCAACCTCGAGC	GGAGGCATAGGTGCTCTTCA

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
B2	0.0	FCA833	SSR	AY434817				GCATTACCCCTTGCCCTGTTA	GTGGACGTGACTGTGGACC
B2	22.6	GPX5	STS		6	28564328	28564483	TCCCTGGGAACCTTGAGAAG	TGTTGTGGCAGACTGAACCA
B2	36.7	BTN1A1	STS	AZ081256	6	26563110	26573189	GTTCTGGGCTGTGGAGTTGT	ATAGATATGGGCTCCGTTGG
B2	53.1	FCA275	SSR	AF130693				TTGGCTGCCAGTTTTAGTT	ACGAAGGGGCGAGACTATCT
B2	62.3	FCA834	SSR	AY434818				CACGTGCGCATGTAGACAC	TCCAGGTTGGTCAAATGTGA
B2	66.3	PRL	STS	U25974	6	22350018	22365571	GCAACTGCTAAGCCCGTATC	CGCCATGCATAAAAAGCTA
B2	74.2	FCA835	SSR	AY434819	6	19032416	19034119	TTAAATGCTTTCAACTCTTGCC	GACTGAATCGGTGACCTCTTG
B2	86.3	FCA305	SSR	AF130602				GGGTATTTACCCAAGAACATGG	TGTTACATACACATCCTGCGC
B2	103.8	EDN1	STS	AF320770	6	12353031	12359321	GAGAAGCCGGCTCCAGT	GACCCAGATGATGTCCAGGT
B2	140.3	FCA836	SSR	AY434820				CTGAGGCACATGCCACTG	CGCACATTAATAGATGGCTGG
B2	159.5	FCA837	SSR	AY434821	6	5979971	5982488	TTCTGAATGAATGCATACCCA	CAGAGGGAATAAGGTCAAGGC
B2	178.8	F13A	STS	AZ081257	6	6134317	6137588	GTCTCACAGCTGCAGAAAGG	GGGGTCCAGACGCAACATA
B2	201.3	PRP4	STS	AZ081258	6	4011595	4055215	GCCTGATTGATGCTAATTCGTT	CGCACTCTGAGAACCAAC
B2	255.6	MKPX	STS		6	282097	341353	AGGATGCAGAAAGGCCAAA	CTTCAGGTACATTACAGTCTTCTGAG
B2	298.6	FLAB2	STS	M26319	6	29926866	29957088	AGGAAAGGGACACGCTATT	ACCAAGTGGGAGTGGAAACAG
B2	304.2	FLAI	STS	U07670	6	31375574	31375688	ACACCGGATTTACTTGGAC	TCCAGCTCACAGCCATACAT
B2	312.6	TNFA	STS	M92061	6	31648849	31648895	GAGGCTGTAGCTGGAGGATG	GTTCTGAGTGTCCCCCTCAA
B2	317.9	CSN/K2B	STS	AW646806	6	31696412	31701228	GGGGCACAAAGGAATAGAG	CCAGGCTCTACGTTTCAAG
B2	320.5	CAA	STS	AW646807	6	32008576	32029200	CACAATGGAAAGCAATGAGG	GCACACGGGTACTGCACTC
B2	345.7	DRA	STS	U51578	6	32434178	32441266	ACCCCAACACCAATGTAA	GTGAGCACCTCAGGAAAGGA
B2	353.1	FCA838	SSR	AY434822	6			CTCAGGCTTTAAGTGCCAC	CTGAGTTTCTTAGGGCCG
B2	357.1	DOB	STS	AY152833	6	32782083	32786349	CGCTTCGACAGCGAAGTGG	AGACCTCACCTTCCACCTCA
B2	361.2	DPA	STS	AY152833	6	33034240	33042825	TCAAGAAAAGAAAGGCTGAAGG	ATTGCACAGCCATGTGACAT
B2	373.3	RPS18	STS	AW646808	6	33285954	33286954	AACACAGAAAGTCTACAGATTTATTC	AAAGATTCGGGCCACAG
B2	386.0	MLN	STS		6	33763864	33773208	CTACAGGGGAAAGTGGATGA	GGCTTGCTGGGAGAGATGA
B2	423.7	TCP11	STS	AW646809	6	35087264	35110597	CAGCTGGTGTTCATGCTGA	CCCAGGAGACTCCTTATCA
B2	426.0	FCA053	SSR	AF130494				TGCTTACACTCATGCACAGATG	GAGCCTTGACATTGCTCTCC
B2	466.0	CDKN1A	STS	D84650	6	36647902	36656523	TGCACTCTCATGCCTCACTC	GGCAGATAGAGGGCTCCTCT
B2	505.9	PIM1	STS	U82197	6	37139394	37144617	CTTCGGCTGGTCTACTCAG	CCCCAAGAGTCCCAATAG
B2	533.3	FCA839	SSR	AY434823	6	41016580	41020428	GATCACGGGTACAAGGCG	ATGCAACAAGTCTGCGAG
B2	555.1	RDS	STS	M94047	6	42665755	42691724	TCTGTCTCTTCAACATTG	TGAAATCTCAAAACAGTCTCGA
B2	574.0	CDCSL	STS	AW646810	6	44356666	44419576	TTTTGGCAAATATGACACTGC	GACAAATTTGCCACGATCT
B2	647.8	COL9A1	STS	AZ081259	6	70876385	70962931	ATCAGGATTGGCCAAAGATGA	GCATGCTTCTACAACCTACC
B2	680.0	EEF1A1	STS		6	74174583	74180913	ACCCTACTGGTCTATGATCTACA	TAAAGGAGCCCTTCCCATC
B2	731.4	FCA840	SSR	AY434824				TGTGTTTTCTGCTGAAAATCCA	TTTTCAACACTATCTGATACCA
B2	758.9	ME1	STS		6	83871513	84090936	GTGGTGACTGATGGAGAAGCTA	CATTTTCTGTCCCAAGTCC
B2	775.2	FCA841	SSR	AY434825				ATTAAGTGCCCAATCCACCA	GTCTTCTGAATTTCTGTGAGCC
B2	785.8	CGA	STS	AZ081260	6	87717503	87755280	ACCTTGCAGTACCACCCGCT	TCCCACCTGCATCTAAGTCC
B2	806.9	CNR1	STS	U94342	6	88799742	88825718	CTCCTTACGGGCTCAGTAG	AATGAGCGGGAAAAATGTCTG
B2	826.9	b5+b5R	STS	AW646815	6	84519461	84620300	GATCATTTCTGAGTTAACAAGTGC	TTTGTGATGAGTACAGACTCC
B2	858.1	RD114-6F	STS					TGCCATCTGTGCACTGAAT	TTGGAAGAATGACCATCTTTCA
B2	896.0	CLAPB1	STS					TCTACTTACAGTGCCTCATCC	CCATGTGCAAGGAAGACCT
B2	908.0	CD164	STS	AW646811	6	109687849	109703800	TGCTGCTGTGCAACAAAT	CAGAACTCATGGCCCTTTCC
B2	956.6	ESR1	STS	X98005	6	15203817	152379537	AGCGCCAGAGAGATGAGG	GGGCTGTTCTTCTAGTATGCTT
B2	994.8	TBP	STS	AW646814	6	170538995	170557420	AGCACAGCAGCAACACTTA	GTTGTGAGGGTCCCAAGTTT
B2	1024.6	TCP1	STS		6	160032959	160044151	GCAAATGATTTCTGTTGTGATG	AGCCTATTGTGAAAAGCTC
B2	1034.7	QKI	STS	AB061272	6	16369634	163825168	CAGGCTGCTCCAAGGATT	AAGGATTGATGAGTGGTG
B2	1048.6	FCA842	SSR	AY434826	6	163978346	163980433	ATGTGGCTTGTGTGTGCC	AGCAACGTGGACACTTGTCA
B2	1073.5	FCA843	SSR	AY434827				TGCACAAATGCACATCCC	CACGCGCACAGAAACATC
B2	1097.7	EPB41L2	STS	AW646812	6	131095620	131212770	GGGTCAAAAAGCAAAAGAAAA	TTTTGATGGTTGTGAGGAAGC
B2	bin: LOD 0.11	FCA844	SSR	AY434828				GGACAGTGATTGAGCAAGAGC	CACCTTGCCACACATTTGAC
B2	1128.2	RPS12	STS	AW646813	6	133070838	133079031	ATTCGGCTCCATCCGTAAC	CGGTCTTACAGACCTCTTGT
B2	1152.8	FCA133	SSR	AF130536	6	126450678	126452963	ATGAGGACCGGATGACTTTTT	GGAAATGTTGACAGAGGGACA
B2	1182.6	FCA845	SSR	AY434829	6	123905267	123907370	TCTTCATGCATGAGGAGAACA	ATCATCACCATCATATTTTGG
B2	1208.6	FCA680	SSR	AF130694	6	106553793	106558987	GTTTCCAGGGTTCCTAAG	TCCGGAAATGCCCTTCCAG
B2	1224.3	POU3F2	STS		6	99282756	99284693	ACTGGGCAATACCCAAGC	ATGGAGTCCGCTTTTCTCT
B2	1237.1	FCA733	SSR					GAAGATGTGGGATAGATACACCAA	TGTTACAGAGGGCAATTTCA
B2	1260.8	FCA732	SSR					CCTGTGGTGCCTTACTT	AGAATTGCAAGGAGGCCACT
B2	1286.1	FCA846	SSR	AY434830	6	92138810	92140060	CACAATACTCTGCTGCTGCC	CTTGACTCCCACTTGGGAAA
B2	1310.5	FCA847	SSR	AY434831	6	94055260	94055660	ATGCATAGCAAATGAAGCCC	TGTAATAATGCATCCAGTGT

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
B3	0.0	DNAJ4	STS	AW646817	15	76132408	76148964	ATCCAGGCATATGAAGTGC	CCGAGCCTCCTCCTTAATC
B3	18.9	IL16	STS	AF003701	15	79163394	79178043	AACAGAGCGAAGACGATCCAG	CAGGCAACGCTTGTATAACG
B3	43.4	BTBD1	STS	AW646818	15	81263552	81314475	AAACTGGGGAAAGACCATGA	CATGTTTAAAAGGACAGATTTTCC
B3	52.7	FES	STS	L77675	15	89014953	89026239	GGTGGCCGTGAAATCTTGTA	CGGAATTATGGGATCGTTCT
B3	70.1	CIB1	STS	AW646819	15	88361059	88396864	TTAGTAGAACACAAATAGAGCGCAGCA	TGTGCAGTCTGCTCCAG
B3	97.8	ANPEP	STS	U59920	15	87915360	87945327	AGATGCCTATTCTGTGTGTCTGTC	GCCAGGACTGAGAAGTGT
B3	128.5	FCA848	SSR	AY434832				GCTTCTCTCTGTCAGCATGG	CGGAGCCTCCATCAGTAAG
B3	143.2	FCA849	SSR	AY434833	15	84268789	84270935	TGTAGCATAATGCCCTCAAGG	GGAAAGCAGCAAAATGTCCAT
B3	bin: LOD 0.00	FCA349	SSR	AF130616	15			CGGAATTTGAAATTTCTCTCC	TGCCCTAGCTCAGAGCACC
B3	261.4	IGF1R	STS		15	96785448	97094240	CGAGTACTTGTCTGTCTGTC	GTCGCTTCTCCGACAA
B3	bin: LOD 4.60	TJP1	STS		15	27572440	27694790	TGCATTTAAAAGATACAGTTACTCAGA	CACAGCATGGTATCAGAAATTAACA
B3	375.4	CYP1A1	STS	U82184	15	72587809	72593868	GTCCCAAAGGCCGTGAAG	AAGGCATGCTTTGGCCCTC
B3	405.2	TSPAN-3	STS	AW646820	15	74914249	74939446	CTTTGGCCAAAGATTTCTCCA	TCAGAACCATTTGCGAGGTTG
B3	451.0	FCA205	SSR	AF130564	15	27067283	27070326	CCTGCTCTCAAGGAGCTCC	CCCATTTCTCTACCAGTTCC
B3	464.9	FCA660	SSR					ATCTTGGCTTACCAATTTTTCC	TCCCTTTTTGCTTTGGG
B3	481.4	RPLP1	STS		15	67324075	67326784	CACCTTCCACCCGGCAGTA	AGGATGAGGGCCGAGATAGAT
B3	517.0	TPM1	STS	AW646742	15	60913786	60937190	GCTGGTTGAGGAAGAGTTGG	CTCATTTGCTGCCCTCTCG
B3	526.0	PSFL	STS	AW646821	15	61148705	61176970	AACGCAAGGCTGACATTAC	AACGCAAGGCTGACATTAC
B3	554.2	FCA201	SSR	AF130563				TCTGCAGGACGATCAGATG	AGCATACACAAATGATGCTGG
B3	566.9	FCA850	SSR	AY434834				AAACAGCTCACGGGCTTG	GGGGACACACAGCACTG
B3	600.3	CYP19	STS	AZ081261	15	49080809	49209932	CCCAAGCCCAATGAATTTAC	TAGGGGAAACGCTGTGCTGT
B3	632.2	KIAA0256	STS	AW646822	15	46859975	46917796	GAGGGTCCCAATCAGAAGC	TAGGCAGATTTGGCGACTGT
B3	660.2	TYRO3	STS		15	39430370	39450673	AGGATTTGGGGGAGGGTAG	CAAACTGGGCAATTAAGCC
B3	694.8	THBS1	STS		15	37452423	37468803	TCCCAATAAGGAAATAGCATTTA	TTCCAAAGGCAATGAGAAAG
B3	704.5	FCA391	SSR	AF130617				GCCTTCTACTTCTCTGCAGA	TTTAGTAGGCCAATTTTCATCA
B3	707.6	CHP	STS	AW646829	15	39102493	39153223	TGCAGTCTCGCTGCTAATG	GAGACGAGAGGGCAGTGTC
B3	726.2	FCA013	SSR	AF130477				GGCAGGGAGCCTAATTAAGA	AAGAGTTGGATGCTTAAACCA
B3	738.6	NRL	STS	AW646823	14	22539472	22543947	TACTTTTTGGGTCCCACTG	AAACAAGCTCAGGCAAGCTG
B3	740.9	MYH6	STS		14	21841325	21867612	CGTCTTTTCCAACCTTCGAGC	GGAGGCAATAGGTCCTTCA
B3	743.3	MYH7	STS	U51472	14	21894978	21894978	CATCCAAAGGGGCTGCTAT	CTTCTGATCTGCCAGTCC
B3	750.7	APEX	STS		14	18913418	18916053	TGCTGGCTTCACTCCACA	TCATGTAGGTCCAAAGGTATATG
B3	754.1	TRA @	STS	D89022	14	20455926	20456546	CTGCCTGTTCACTGATTTTGA	GCCAGTTGCTCTTGGAAAT
B3	bin: LOD 2.82	TRD @	STS	D89018	14	20554984	20909237	CCGTAAACCAAAACCAACG	ACTCTTGGCAACACCATCC
B3	762.9	NDRG2	STS	AW646827	14	19475061	19483987	GCACCCTCCACACATAACAC	GCCATTTGGCTGACTAATCT
B3	772.6	DAD1	STS	AW646828	14	21023934	21048257	AGGAGCGGCATGGAGTTTAT	TGTAGTTGGAGAGCCCAAAG
B3	782.3	OXA1L	STS	AW646826	14	21225858	21230895	GCATAAATCCAGTAAGTTCTGAAT	CCACCCACAGCCATAAGG
B3	789.4	PABPN	STS	AW646825	14	21780802	21784700	CCCTCGGAAGAAAGAGGAG	TTTCTGGGTAATGGGGTCA
B3	798.9	PNN	STS	AW646824	14	37634492	37641462	TTGGATTTCAAGGTCAAAA	CCCTTACACAACCCAGTGAG
B3	bin: LOD 0.00	ACTC	STS		15	32762771	32762771	CTTCCAGCAGATGTGGATT	AGATAAGGGAGGGTGGTTGG
B3	816.3	CMA1	STS		14	22964692	22967569	GGCTGGCTGGGGAAGAAC	TGTAGTGTCTGCGAGGCTGA
B3	845.5	HNF3A	STS		14	36049228	36054278	TCAGAGCCATTTGTTATTCAGC	TTGGTCAGGCAACTTTGAA
B3	878.5	FCA851	SSR	AY434835	14	40586176	40588213	TCAAATCAGAGCCTGCTGTG	GTTTCTCACTGCCAAAAGC
B3	905.2	FCA852	SSR	AY434836	14	53063050	53063300	AGCCCCACCTTTTAGGAGAT	TAAGCAGCACAAGCAAGAT
B3	918.0	FCA230	SSR	AF130577	14	53718578	53721401	AAGAATGGACTTGGGAAATGG	AAACCACAACAGGCAAAAAG
B3	941.4	PYGL	STS		14	49362098	49401210	CCAGCTGTAACACACCATGT	TGGGTCTTGTCTTAAACCTTCC
B3	956.3	ESR2	STS		14	62689895	62751119	CCAGTAACTCCGAAGGTGGA	ACTGGCAATGGATCGCTAAG
B3	958.6	MPP5	STS	AW646830	14	65749363	65790720	GTGTAGGGGGATGCTGTGT	GCACAGGCCATGTCAAAGTA
B3	971.5	ATP6V1D	STS	AW646743	14	65794630	65816632	ATTGGCAGAACTCCCATGAC	GCACCCCTTGTCTCCTACTG
B3	983.6	KIAA0759	STS	AW646832	14	75243626	75269222	CCCCACTTCAATCCAAAAC	GTGCCATTTGGTTGTCCAGG
B3	1016.6	FCA853	SSR	AY434837				TGGTTTACATACATGTTTGCA	ATCAGCAATCTCTTCAGAGC
B3	1072.4	FCA854	SSR	AY434838	14	72074046	72076158	GTGACCCAGGGAATGATCC	AGATCACAAGGGATAGG
B3	1108.8	FCA734	SSR					TGCTAGCTTCTCTCTTGACA	ACTGGAGGGGTGAGGACTTT
B3	1121.8	FCA855	SSR	AY434839				TTATTTCACTTAGCATGTGTGCC	AAACAACCTTACGTGCCACC
B3	1134.9	MAX	STS	D37796	14	63531888	63559213	AAGTCCGTGCACTGGAGAAG	CGGAGCTTCTTCTGCTTT
B3	1141.9	RD114-8D	STS					ATCCTGGCTTTGTCCCTCTT	CAGAAGAAAACACACAAAACG
B3	1151.5	FCA592	SSR	AF130669				TCCTCGACAAGCGGAGATT	TCACCAGAAGGGATATGTGG
B3	1166.7	FCA856	SSR	AY434840	14	76760827	76764208	AATGCCACCACTTCTCAAG	TACTGTACCCGTACCAATGCC
B3	1186.8	TSHR	STS	AF218264	14	79411966	79600813	GCAGCTGGCGTTACTTCTCT	GTAGGCTGGGATACGGTGA
B3	bin: LOD 0.00	FCA088	SSR	AF130515	14	81560915	81563309	AGGAAAATGAAGTCAAGAAAATGG	TTTTTCTTTTCCCATAATACACA
B3	1201.8	RD114-8A	STS					TATCTGTGCTGCTCAGAAAG	GGCACTTCAAGTATCTCAGG
B3	1204.1	RD114-5B	STS					GTGCTGCTCAGAAAGTTTACC	CCTATTCTTGAAGATTCCC
B3	1204.1	RD114-6E	STS					GGGATTAAGGGTTCAACAT	TTGGCTGTCATGTAATTGAGG
B3	1233.4	EIF5	STS	AW646744	14	101790587	101799549	CAGGAAAATTTAAAACCGTTGAA	ACCCATTCGGGCTCTTAAAC
B3	1240.8	FLJ22558	STS	AW646833	14	97967633	97968714	TCATGCTGTAAACCAAGATGGAA	GGCTTTTTCTTTTCTCCCA
B3	1255.9	WARS	STS	AW646834	14	98790167	98831698	GTGCTCCCTCTGGAACCT	TTTCACTGTGGTGCCTTT
B3	1285.9	IGHM	STS	AB01672	14	104289715	105142078	GCAGAAGCCACGACATA	GGTGACTTGGCAAGTGTAGG

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
B4	0.0	FCA857	SSR	AY434841				TAAAAAGCCCTCGCGACTG	CAGGCACATGCACAAAGC
B4	21.7	IL2RA	STS	AW646835	10	6203745	6254511	GTGAGATCTCTGGGCTTTG	CTCCCTGTCCCTCAATGAC
B4	30.7	Fc.26434	STS	AW646835	10	5940612	5955942	CTCAGGAGGAGAGTTCTGG	CAGAAAAGCCATCCATCTCCA
B4	42.3	FCA858	SSR	AY434842				TCCCTCAACTTTGCAACAAA	CACAGTCGTTAATTGGGAAGG
B4	64.2	GATA3	STS		10	8246906	8267092	CTTGTTCACAAAGCGTGTGG	CATTGTTCACAAAGCGTGTGG
B4	114.2	VIM	STS	AZ081262	10	17421516	17429831	ATTGAGATTGCCACCTACAGG	CTGACCSAAGTTCCTGTATC
B4	136.1	NMT2	STS	AW646836	10	15298636	15360931	TGCAGCAGCAGCAAGTCTA	AGGAGCAGGTCGCCAAATA
B4	157.9	Fc.112998	STS		10	13414005	13426567	GCCTTAAGCGAACACGCTAT	CTCCTGGCACAACACCTC
B4	191.1	CACNB2	STS		10	18579845	18980277	CCAGAATTTGGCCACAGATAA	TCAGCCAGAGGTACAACGAA
B4	bin: LOD 1.08	BM11	STS	AZ081263	10	22770301	22770461	AGCCATGCTCACTGTGAATAACG	TTTACTTCTTGTATCGGTTTTG
B4	229.0	FCA859	SSR	AY434843				CTGTTATGAGCAATGTTTCCCTAGTAT	CCCTGATTTCCCATCTTTTC
B4	bin: LOD 0.52	CREM	STS	AY011679	10	35666144	35651317	AGGCAGGAGATGCAGCAAT	TGGCTGCATTTCCAAATCTT
B4	333.8	FCA860	SSR	AY434844				AGGTGAATTTTACCAAAAATGTG	CAGCCCAATGGATTTAAAAAG
B4	341.1	ITGB1	STS	UZ7351	10	33339559	33397437	CCATGCAAAATTCACAGCAC	CTGCACATGAGAAAAACCA
B4	353.0	FCA861	SSR	AY434845	10	31706539	31709212	ATATAGAGGCGGAGCTGGGT	TCTTGAGGTCAGCTAGTATGCA
B4	405.4	FCA356	SSR	AF130612				CTTAAACAGGACATGGAAGGC	TCAATTTTCAATGCACATCCA
B4	417.2	VWF	STS	U31613	12	6188760	6226688	TACAGGCGCTGAGAAGAAGA	TGGACCCACAGTACGGTGA
B4	bin: LOD 0.02	NTF3	STS	AF192538	12	5420747	5483481	GCCAAGTCGGAGTCCAG	TCTTGTGCTCTGCCTACCTC
B4	bin: LOD 1.32	FCA862	SSR	AY434846				GCATGGTTGGACTGCAATC	TCTGTACACCTGCTCTTCT
B4	429.0	TNFRSF1A	STS	U72344	12	6317185	6330514	TACTGACTGTCCCTCACC	TTCACATTTCTGCAGTCCG
B4	433.5	CD9	STS	D30786	12	6188760	6226688	TCATTCGCATTGCTAAACAAA	AGCAAACTCAATCCCAAT
B4	435.8	TP11	STS	U82194	12	6855619	6859528	GGGGAAGAGCTAGATGAAAGG	TACCAATGGCCCAACACAG
B4	440.4	Fc.estTDE7	STS		12			TGCTTCTCGGCACCTTCTT	CAGCCTAGCCCACTGACTT
B4	449.7	GAPD	STS	U82186	12	6522945	6526797	CAAAGTCTCCATGACAAAC	GCTTCACCACCTTCTTGATG
B4	461.6	CD4	STS	AB000483	12	6777980	6809234	AGTAACCTCTCGGTGCAATG	AGTGTCTTCTGGCTCTGGGA
B4	517.6	FCA677	SSR	AF130692				GGATATTTGGCATATAATGTG	AGTCTCAACTGACGGAGCTACC
B4	527.8	CSDA	STS	AW646750	12	10751956	10776218	TGAGAACTCCATACTGCACA	GCTAAACTTCCAAAGTGTGTGA
B4	539.3	CDKN1B	STS	D84649	12	12770575	12775569	GCACTGAAAGCAACACACA	GAAAAACCTAATGCAACAATGC
B4	569.1	JAPP	STS	M25388	12	21322094	21456864	CAGTGACAGCCTCATCAAGG	CAAAAACAGGGGAGAAACA
B4	589.2	FCA016	SSR	AF130479				TGCTTTGGGCTCTTTTGGG	GCTTGTGAAAAGAAATCACA
B4	612.1	FCA863	SSR	AY434847				GCCAGGAGGAACTCAGTGA	CCACCAAGCTCCTATTCCA
B4	626.2	PTHLH	STS	AF114698	12	28011291	28025905	TCCAAGACTACGACGACGA	GCGTTTTCCAGGTTTACC
B4	643.7	F98	SSR					TCAGAGCCTGTTGGGATTC	GTTTGTACTGCTATTGGTGG
B4	685.0	FCA683	SSR	AF130695				GAGCATAGAACCCTGTTGGG	TTGAACCTTGATTATGGCAGTG
B4	697.7	COL2A1	STS	U85406	12	48083496	48115008	TGGTGGAGCAGCAAGAGC	CCTTCTTGAGGTTGCCAGC
B4	714.6	TEGT	STS	AW646838	12	49852087	49875257	CCTGAGCTGAAACCAAGGA	TGAAGCCAACTCCACCTCT
B4	754.3	SLC11A2	STS	AW646839	12	51089950	51136913	CTCAGTTGTCACCACCTGGAA	AAATCCGCTCTTGTCTCCA
B4	791.2	HOX3A	STS	M62698	12	54095720	54100807	AGCAAGCAACCATAGTCTACC	CAGATTTGATCTGCCTCTCAG
B4	808.7	RPL41	STS	U22229	12	56227120	56228362	AGTCCCTTTTGGTCCGTTG	TTGAGCTAAGACAGCAGAAGAGAA
B4	813.3	NACA	STS	AW646805	12	56823032	56835830	AAGAGCAAGGCAAGTCCGAG	AAAAGGGTCCCTGTTTCCAGA
B4	841.6	RPS26	STS	AW646840	12	56152672	56154752	CATAGGCTTTGGTGGAGTCC	TGCCATTCACAGCAAGGTAG
B4	873.9	FCA864	SSR	AY434848				CATCCAGTGGGCACTAAGT	TTTGATTTGGCCCTCATCA
B4	880.9	FCA865	SSR	AY434849				CTGACAGCTCAGAGCCTGGA	AGCTGATCGTCCCACTCAAAA
B4	892.7	FCA866	SSR	AY434850	12	71493575	71496217	GAAAGCAACTTTCCACATTTCC	AGGTGCCTTTTGTGTTGTAACC
B4	904.6	JFNG	STS	AF012099	12	68265296	68270250	TCTGCCTCAACAATTTGAATTT	CATTGTATCATCAAGTGAATAA
B4	926.4	FCA867	SSR	AY434851	12	62139180	62139380	ACGTTGCTGTGATCTGCTCC	CTCCCTCTCCCTCAAT
B4	943.3	FCA051	SSR	AF130492				GCGCCCTGATATCAAAATA	CCTATGAGGAAAACCTCTGCC
B4	956.3	FCA044	SSR	AF130488				AGGGCCTGAACCAAGAGAAT	TATTTACAGAGTGCACAGAGGAGG
B4	981.5	FCA868	SSR	AY434852	12	67116191	67118282	GAGGAAACATTTCCCTTGCA	GTGCATTTAAGAGCTGTGGG
B4	1025.6	FCA652	SSR	AF130685	12	87890468	87893049	GAAAAATCAACTGAAGTGGCAT	CTGGGGGAGAAAACCATAT
B4	1032.8	MGF	STS	U82188	12	88823453	88907186	ATCCATTGATGCTTCAAGG	CTGTGATCCTAAGGAGGCTG
B4	1040.6	RD114-3B	STS					GGTATCACCAAATGCAAGAAGC	TCCATCACACTTTGCCAAA
B4	1045.9	FCA210	SSR	AF130566				TGAGCCACCTAGGCACCTTT	AGAAGCATCCAGTGACAATGG
B4	1056.5	FCA187	SSR	AF130559	12	95939474	95941634	CCAACCTGAACCCACAGG	TGGATGGTTGATTTCTCCTCA
B4	1064.2	FCA735	SSR					TCAAGGCCAATTGTAGAGCA	TTCCATTTCTATGGAATAGTCA
B4	1069.4	FCA869	SSR	AY434853				CAAGGAGCCATTTGTGACTG	GATCACCAGATAATTTCCAG
B4	1088.9	PAH	STS	AF114700	12	103165051	103277571	CTGTGGAGTTTGGGCTTTGC	AGTCCCTCACTTCTCCTTGGCA
B4	1104.6	Fc.40342	STS	AW646842	22	36385286	36413556	GTCAGAGTCCCAAGGTGTG	CCACCCTTCTACCCTACC
B4	1112.2	FCA870	SSR	AY434854				AAATGACTGCATAGGGTCCAG	TGTGGCTCCTCAAAAAGGC
B4	1112.2	PDGFB	STS	AF114699	22	37862403	37884099	ATGGTTCTGTCTCCAGGTG	CCTTCTGTATGCGTGTGCT
B4	1116.8	FCA871	SSR	AY434855	22	35505433	35507554	ACACCCCTTTCAGCTTG	AGTCCCTTCTCTTGGAGC
B4	1119.8	TST	STS	AW646841	22	35649946	35659265	ATCTGAACAACGAGGGAAGC	CCTGTTACTGAACTGGAGGT
B4	1129.0	FCA520	SSR	AF130644				TCTATGACCCATTTACATTTGC	GTGTATCACACGTAATCAGGGG
B4	1132.8	FCA232	SSR	AF130578	22	32688487	32691046	ATGACCATCTCAAACTCATGG	AGCTGAGTTTGCCTTATCATG
B4	bin: LOD 0.11	FCA460	SSR	AF130628				TCCCCCACTAGTGTCTGTCT	TTGTCTCTTTGGATTGTGAGA
B4	1171.7	FCA069	SSR	AF130500	22	42446347	42449570	AATCACTCATGCAGGAATGC	AATTTAACGTTAGGCTTTTGGC
B4	1190.7	FCA1056	SSR	AY435036				GGTGTGAGGGCCTTATCTGA	GGATGTCTCCTTGAAGTGTG
B4	1203.1	FCA736	SSR					ACCGAGCTCTGTTCTGGGTA	CAGACTGCACCACTGCCTAA
B4	1220.5	KIAA0685	STS	AW646844	22	49002007	49015920	CAGTCTCTGCACCCCTGT	TGCAAAATTTGACTGCCTTAA
B4	1243.1	NDUFA6	STS	AW646843	22	40724570	40729998	AGACATCACCTGAAACAGG	CCTAATGACCAGAGTCAACCAC
B4	1295.5	FCA872	SSR	AY434856				TGCTTTTACCCAGATTTCTGC	CTTCTCTCTGTTCTCCCTCTG

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
C1	0.0	GNB1	STS	CC596505	1	1585750	1691558	GGCTGATTCTGTGCTGACTG	GACTGTGCTGACTGGTCAA
C1	8.2	FCA873	SSR	AY434857				CCAGCCAGGCCCTCTATA	CCTGAGAGTCTGTGCCACCT
C1	44.5	VAMP3	STS	AW646847	1	7428061	7438223	CCAGCCAAATGCAGACATAC	GGCCGTGTCTGACTCTGAA
C1	68.4	UBE4B	STS	AW646846	1	9702456	9850709	AAAGCATATTATCATGGAAGCACA	CCTTTGATCAGCCCTCCCAA
C1	83.7	ENO1	STS	CC596510	1	8517795	8536080	ATGATCCTCCCGTGGT	GGCTCTTTGCCGATTCTCT
C1	86.8	Fc.esrTDA1	STS					GGGTGGGCTCACATCATAAC	GATTCCTCCGATGTACTG
C1	93.3	TNFRS1B	STS	U51429	1	11836475	11878691	CACGGGACCCAGGTCAC	ACGTCCCCCATCGTGTAG
C1	96.0	NPPA	STS	AZ081264	1	11526939	11528403	CGAAGATAACACGCCAGGAGG	CTTTCAAGTATGGGTGAGCG
C1	117.9	Fc.Z5129	STS	AW646845	1	15995102	16015493	TACGGGTCACTGTGATGAA	GTCTGGAGCATGACCCTCTC
C1	144.4	FCA874	SSR	AY434858	1	26074487	26076590	CCAGGCCCTGTCTAAGGTT	ATGGTGCCTCACATGTGGTA
C1	154.7	FCA875	SSR	AY434859	1	24503572	24506026	GTTGGGAGGATGACAGGAGA	TACAGAGGTGGGAGCCAGT
C1	163.3	FCA876	SSR	AY434860	1	26430838	26433209	CTATGGCTCTCCAGAAAGG	ACTGTGGGTCAAGTTGGCAA
C1	171.9	FGR	STS	AZ081265	1	27171854	27194712	GGCTGCTTCGGAACAGTGTG	GTGGCCGGCTTCTGTCAG
C1	174.3	CDW52	STS	AW646848	1	25877529	25880057	CTCCAGCTGGGTGACTTG	GGGGTTAGTCCAGAGATGA
C1	193.6	FCA877	SSR	AY434861	1	22280478	22282965	GGGGCTTTATTCTGTTCTTC	CTGTGGGACTGGAAAGATG
C1	245.8	FCA878	SSR	AY434862				CCCTCAACGTCAATGATGTG	TAGGCATAGCTTACAGAGGC
C1	271.0	LEPR	STS		1	65244166	65460889	GCTTGAGAGCAGCGTGGT	TCTCCATGAGCTGTTAGAGAA
C1	309.4	TESK2	STS	AW646854	1	45239387	45386664	TGTGGTGTCTGGCTCTTA	AGCCATAGCAGGAAGGGAAG
C1	324.9	KNSL6	STS	AW646853	1	44635323	44663247	GGCCGTTTCTGTTGCTTAT	GGCCGTTTCTGTTGCTTAT
C1	357.8	CAP	STS	AW646852	1	39969450	40001858	AGGAACTGCACCACTTCAA	AGGCCTCAGGAAATGGGTAG
C1	379.6	YARS	STS	AW646850	1	32667484	32710223	GCATACGTACAAATATACACACATACA	CCCCTTCCCTCTTGTITTA
C1	391.4	COL16A1	STS	AW646849	1	31544491	31596292	CACCCATCACAGAGTCCTG	CCCTCCAGGATGTGGTAA
C1	410.2	LOC127540	STS	AW646851	1	33756337	33757036	CCCAAGGCAAAATGCTCTTC	TTGGCTTTTTCATGTTTGA
C1	431.0	GJA4	STS	CC596506	1	35079924	35082670	GCGACGAGCAGTCAGATTTCT	GGTGGGTGCTGACACAAA
C1	449.2	FCA879	SSR	AY434863				CCAGAGAGTCCAGGTCACCC	TATCAGTGCATGACTCTGCATG
C1	463.2	FCA880	SSR	AY434864				TGGCAGCTTGAAGAGTTG	GTGATAGTCACCTTCCAGCA
C1	482.8	FCA247	SSR	AF130583				GGAAATAGGAGGCTGTCCA	AAGTATAGCCAGTTGCCCC
C1	506.1	PTGER3	STS	CC596507	1	70702760	70898221	AGACCTGGTCGGGCAACT	GGAGGCCCAAGACAGACTCA
C1	532.6	ACADM	STS		1	75606195	75645096	GTTACCAGAGGAGCCTGG	CTGATAGATCTTGGCCTGCC
C1	534.9	PTGFR	STS	AF272340	1	78347817	78395277	ACAGCCTTGCCATTGCTATT	GCAAGAGTCTCAACTGGT
C1	571.7	ABCD3	STS		1	94234530	94234641	AAAACCTGGTCATCATT	ACTTTAAAACCTCAACTGCTG
C1	598.5	FCA737	SSR		1	89751545	89753873	TCTCCACTTCCCTCACTCA	CCACACCTTTGGTCTCAGT
C1	601.4	FCA289	SSR					TATGTGGCTGCCAGTTTTCC	TCAACAGAAAAGAAATGCAACC
C1	624.1	FCA738	SSR		1	96325961	96329688	TCTTCACTGCTCTGCCTCA	GTGGCTGAGTCTGCTGAT
C1	637.3	EDG1	STS	AY001738	1	100993730	100998254	CGTCCGGATTACAACATACA	GAGCTTTCCAGAGACATAATGG
C1	662.3	FCA057	SSR	AF130496				AAAGTGTGGGATGGGTGAAA	CCATAAGAGCTCTTAAAAACTGA
C1	686.3	GNAT2	STS		1	109247822	109257813	CACAAGTCTTTCGGCCACTTC	GAGGCAAAACCAGTATACCAAG
C1	701.5	FCA881	SSR	AY434865				GTTTTGGGCTTGGAAAACC	AAGTCAGCATGTCTGAATGG
C1	713.9	F37	SSR					CGCCTTTCACATTACCAT	CAGTACAGATGATCTCGT
C1	bin: LOD 0.73	ADORA3	STS	AY011246	1	111144163	111148851	ACCCCATGTTTGGCTGAA	GATAGGCTTATCATGAGATT
C1	751.0	NRAS	STS	AW646856	1	114347190	114360086	CCCAACTTGGATCATATGGAT	GCAGCTCCAGCAGCTGATG
C1	bin: LOD 0.07	NGFB	STS	U82190	1	114828637	114980955	ACCCCAACATCACTGTG	TCCAAGTCCAGCCCTGAGT
C1	813.0	FCA882	SSR	AY434866				CACCCAGGTGTCCCATTA	GCAATCAAAGACATAGGGTGA
C1	849.4	HSD3B1	STS		1	119196864	119204730	CATCCAGAATGGCCATGAAGAA	CCTGAGGACCAATGGGATCATCC
C1	876.8	GJA8	STS	CC596511	1	144724142	144725443	TCTTCACTTCCGGATCCTC	CCTCGTGTAGCAGCAGTT
C1	883.7	FCA290	SSR	AF130597				GTAAGTCCCTGCCACACAT	GTATCTGCCATTTGAGAAAGG
C1	930.0	FCA883	SSR	AY434867				ATTTCAAGGGGCTCATCAATG	GCTACTGTGGAGTCAAGTATG
C1	962.6	PROC	STS	D43750	2	126080954	126091756	CAGCAGAAAGCCTCAGACA	GCCACTCACCAGTCTCTCT
C1	997.5	FCA739	SSR					GTGTCTGATTTGTATCTGTATCTGT	AAAGGGAAGTGACCACATGGA
C1	1019.9	FCA884	SSR	AY434868	2	120318716	120320886	ITCACAGTCTCTTCGGCT	AACACAGATCTTTGCATCC
C1	1080.7	FCA343	SSR	AF130612				TCTTTCACACATTTGTTCCACA	AGCCGGACACTCAACTGACT
C1	1137.1	FCA885	SSR	AY434869				TGCACTGAGAAGGACCCAG	TTTGGTCTGTTTCAAGTTTCC
C1	1161.8	FCA740	SSR		2	135763565	135820434	CACCTTCTGAAGGAGCAGCA	AACCAATGGGAGTTTGTGG
C1	1194.3	FCA480	SSR	AF130633				GATCTCACACTCATGGGACTG	ACTGCATCCCAAGGTTTGG
C1	1219.8	FCA293	SSR	AF130598				GATGGCCAAAAGCACAC	CCCACATCTTGTCAACATGG
C1	1248.5	CXCR4	STS	U63558	2	136894235	136898046	TCTGTGGCAGACCTCCTCTT	TTTACAGCAACAGCTTCCCT
C1	1311.9	FCA279	SSR	AF130595				AGCCAAGTAAATCTCTCTGTG	GTCCATCCGAGATGAAATG
C1	1367.6	CL2502	STS	AW646857	2	150424375	150442541	GAGGTTTTTCCATAAAGGGAAG	CATTGCCAAGTGGTTGTGA
C1	1389.3	FCA173	SSR	AF130554				GGCTAATGGCTACCGTGTGT	CCCAGGGAACCCATAGAAAT
C1	1426.5	FCA886	SSR	AY434870				GACCTGGCTGAAGTCAGAGG	CTTTTCAATTTTGGTTTCC
C1	1461.5	LOC253782	STS	AW646858	2	169511568	169593838	GCTTCCAGAGATCAGGAATGAA	ATTCAAGTCTTGGGCATCTC
C1	1472.4	FCA573	SSR	AF130664				TTGACAGAGACAGAGTCAAGC	TCTTGCATTTGGTGGTTTACG
C1	1485.5	GAD1	STS	M18629	2	171637096	171681673	GCTTCCAGAGATCAGGAATGAA	ATTAGCATCTTGGGCATCTC
C1	1489.7	FCA887	SSR	AY434871				TCCACAACATCACCTTCCA	ATGCTGCTCTGCCACC
C1	1502.2	CHRNA1	STS	AZ081266	2	175576352	175593205	TCTGTGACTTGAACCCACA	CCACTCAAAGCCCGTAACAT
C1	1518.0	PACT	STS	AW646859	2	179260174	179279982	ITGCGCAAAGAGAGGTTAAG	GCGAGAGTGTAGCACCATT
C1	1551.0	HSPD1	STS	AW646861	2	198315449	198315685	TGGTATGGCAAGCACTAAA	GAAGAAAAGGCTGGCTGATG
C1	1576.5	FCA888	SSR	AY434872				ATCCAAAAGAAAAGCAAAACA	GATCAATGTGCCACAT
C1	1588.1	FCA544	SSR	AF130654				AAAGCTTGGCTCTTAACCTCCA	AATACCCCAAAATTAGCATTTG
C1	1596.4	INPP1	STS	AW646860	2	191172219	191200330	GGAGAAGTGGACATCCAT	TCCTGAGCTCTTATCCAA
C1	1623.9	KIAA0005	STS		2	201640308	201652582	CATTTTGCCTGTGCATTAATA	AAAGTTATCTTGGGGAATATG
C1	1653.4	CD28	STS	U57754	2	204535223	204566581	GCAATGGGACCATATCCAC	AAGCAACCAAGGCCACTGTT
C1	1658.1	CTLA4	STS	AF154844	2	204696534	204702706	CAAAGGTTTGAAGGAGTCT	ACTTTCACTCCCCGTTCTG
C1	1676.0	FCA889	SSR	AY434873	2	208071218	208073663	CTTTGCTGGCTTTGGGTGT	TGAACGAAGGAAGGCTTGG
C1	1688.2	FCA243	SSR	AF130582				ACATGTGATTCACATGAATAT	CCAGAAAAGCAATTTGTGCA
C1	1707.5	FN1	STS	AW646863	2	216189609	216264815	GGGCTGTCTCCATCAGACT	GGTCTCCAGCTGCTGACAT
C1	1736.9	DNPEP	STS	AW646864	2	220202287	220217617	CAGCTGCAACTTCTCAAGTGC	CAAGGCTCTTTGAGCTGT
C1	1772.5	PAX3	STS		2	223029824	223127603	CACCCCAATCAGATGAAGGCTC	GGTTCTCTAAAAGCTCTT
C1	1790.8	FCA649	SSR	AF130682				ACTGCCTGCACACTGACTTG	TTAGTCTGGTGGAGACTTTTGTG
C1	1813.6	FCA364	SSR					GTGTGCCTCTGGCAGGAC	TGGAGGTGCTGTAAAGTGG
C1	1835.7	FCA664	SSR	AF130687	2	230057579	230059791	AGAAAAATGACTACCAGACTGG	AAATGCTTTGAGTGGGGCT
C1	1836.5	HRB	STS	AW646865	2	228301072	228385350	ITCAAAGTAAATAAACTTCCA	CCCCTTTAAGTGTCTGTCA
C1	1839.3	TRIP12	STS	AW646866	2	230595949	230750744	GACATTTATTGTTTCAAGCTGA	TGATCACAGCCGAAAGTGGC
C1	1842.1	Fc.98104	STS	AW646867	2	232423106	232438447	GCTCCCTGGCAGATATCCTCA	GGATGCCCTATAGCTCTC
C1	1856.4	NCL	STS		2	232283481	232293333	CACCTGTATGCACAAGTAT	GCATAGACTTAATTTCCAGTGTG
C1	1874.4	FCA890	SSR	AY434874				CATGACCTGAGCTGAAACCA	GGAAAGCCCAAGTATG
C1	1883.4	FCA891	SSR	AY434875				CCCCACATGTCCATTTGT	CTGCTGACTGAACAATGTTCG
C1	1954.7	AGXT	STS	X75923	2	241827972	241838347	ACTGAGGGGACATCGTCAAC	GATCACTGGTCCACGTTCA

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
C2	0.0	FCA568	SSR	AF130662				CCATAATCATGTGGGCAAT	CTGCTCCCTGACACTCTGC
C2	4.1	HRMT1L1	STS	AW646868	21	46912209	46941497	ATGCAGAGTCCCCTCAT	CAACCTTGTAGCCTGTGAA
C2	22.2	FCA892	SSR	AY434876				GACTGGCTTCTGCTACTTAGCA	AGAATGCCCTATCAAGCCA
C2	42.9	FCA346	SSR	AF130614	21	35222698	35225004	GAATGCCTAGGTAGCACTGTCC	AGAGATGAAGCCAGAACCA
C2	63.1	FCA893	SSR	AY434877				GGGGTACATCCATAACACGG	GCACAGACATTTGTGGATG
C2	93.3	FCA638	SSR	AF130679				CCCCAGCACTGAATTGATT	GTGGAGCTGCTTGAGATTC
C2	118.7	SON	STS	S79173	21	33835745	33870207	TCAGCTACACCTAGATAGACGTTAA	AACCTTTCAGTCAACAAAATAGTG
C2	142.9	C21orf59	STS	AW646869	21	32892883	32893049	GATGCTTTTTACCCCGTGG	AGAACCAGTATCAGCAGCTG
C2	161.0	APP	STS	AY011369	21	26174732	26465008	TCCAAGATGCAGCAGAACG	CTAATGTGTGCACATAAAACAGG
C2	184.2	FCA894	SSR	AY434878				CATGCCAGACTGCATTGT	TTGCATCAAGTGTAAATTGCC
C2	198.8	NCAM2	STS		21	21574767	21834285	TGACCAAACTATTCATTGACC	AAGCTGAGGGCAGAAATCAA
C2	211.1	FCA895	SSR	AY434879				GAGCTAGCAGGGGAAGGGG	CTAGCAGTCTCATTTCAGG
C2	213.5	FCA535	SSR	AF130650				TAGATTAGGGAGGGGATGTC	ACATGGCTGCTCCTTCC
C2	220.9	FCA543	SSR	AF130653				TTTCCAATGATGCTCTTCCA	AATTGGGTGTTAAAGCCCC
C2	238.4	NRIP1	STS		21	15255433	15359126	ATAATGCTTCTCGCCAC	CCTCATGACCTAATGTAAAGCAA
C2	262.8	FCA896	SSR	AY434880	21	22810238	22812275	CACGAAGAATCTTTAGAGGCA	ATTCCATCATCTGGCATTTCC
C2	277.0	FCA897	SSR	AY434881	3	76765804	76769288	CCGTCATTTCCCTGTGC	ACAATTTGGGGTCTTTGAC
C2	283.1	FCA898	SSR	AY434882				TAGTGCTGCAGAAATGGCC	GCCTGGACTGGACTCTCTG
C2	285.3	FCA899	SSR	AY434883				AGACATTAATTCAGCCTTTCC	AAGAACTGTGCTTCCCACT
C2	299.7	GBE1	STS		3	81345648	81616631	CAAGTGATTGACTTTCTGGTCTC	CAGATGCCGTAGGAACCAAGTC
C2	312.4	FCA900	SSR	AY434884	3	83008028	83010218	TCACTGTGTTTCATCTTGTCACTC	TGGAGTGAATGAATAAGAAATTGG
C2	322.6	FCA901	SSR	AY434885				CTTCACTCCAGCTACACTGGC	GTGCATGTGATGGTATAGCA
C2	338.1	F164	SSR		3	86443708	86445799	CTATATGACAAGTGAAGT	AGATGATACAGGTAGAGTGC
C2	bin LOD: 0.02	FCA576	SSR	AF130665	3	95130641	95134163	GTGCCATTTGGATTGACCTT	ATGGCCAGCTGCTTCAATT
C2	368.2	PROS1	STS		3	94884704	94974139	ATTAACCTCTGCTAGATGGATGTA	AATTGAGCAACTCCAGAACCAG
C2	402.1	FCA902	SSR	AY434886				ACCCAGAATGGAGAAAGTGC	TGCAGATATGTTGAGTTTTATTGA
C2	415.1	FCA903	SSR	AY434887				TGATTTCTTTCATGATGATCC	CTGGCAGAAAAAGACACAGA
C2	427.3	FCA048	SSR	AF130490				TCCATACATGTTATTGCAGATGG	GAAAAAACTTAAGTTGGTATGGC
C2	431.1	FCA904	SSR	AY434888	3	100261258	100261298	ACCAAAAAGACTGGCCAGG	ATTGGCAATTTGTCCAAGG
C2	438.3	FCA077	SSR	AF130506	3	100785200	100787237	GGCACATAACTACCAGTGTGA	ATCTCTGGGAAATAAATTTGG
C2	489.1	FCA905	SSR	AY434889				TGACGAAATGGAGAAATGATGC	CACCATGCCTCTCCATCC
C2	524.9	FLJ20730	STS	AW646870	3	113562124	113584232	AGAAGTGAATGCCCCAGAT	CTCCACCACTTTGCCTGT
C2	548.2	DRD3	STS		3	115128789	115178969	TTCACTGCTGCTCTTCTACCTG	TCCTCTGCTCAACACACA
C2	584.0	CD80	STS	U57755	3	120527540	120559690	TCTGCAGAACCACTGTATGC	AAGAGCTAAGAGGCTACCTCCA
C2	608.4	CD86	STS	AF157827	3	123055460	123119896	GTTCCCTTTCTGCTATTTGA	GTGACATTCAGGAGGAACAC
C2	617.6	FCA483	SSR	AF130634	3	123696913	123699021	CTAACACAAAATGAAGAGGGGC	ACTGAGACTTCTCAGGGTGG
C2	629.3	FCA906	SSR	AY434890				GAAGCAACCAAGTGCCTTTC	GTCCCTGTACTTCCATGACTCC
C2	661.8	TFR3	STS	AF276984	3	197182805	197215954	CTGGCTCTCACACTCTGTCA	CCCAATGTCCAGCAGAGG
C2	770.0	FCA907	SSR	AY434891				AGCCTCCATAATCATGTGAACC	GTTTTCCAGAGAAAACAAAACA
C2	828.1	DGKG	STS		3	187269039	187482030	GAGCTGAGGCTGTGAGTTT	CTGGAGAGCATGCACAGTA
C2	852.5	FLJ11198	STS	AW646871	3	185313653	185313796	ATGCAGAGGATGCTCCAGTT	AGGGCTTCTTTAGGGTCCAC
C2	875.7	FCA908	SSR	AY434892				TTGCATATGCTCACTATCACA	GCCACTACTGCTCAACAA
C2	886.3	FCA909	SSR	AY434893	3	179131214	179132214	GGGCCACAAAATAAATGTGC	CCAAATGTTTGGCCATAAAA
C2	919.9	SLC2A2	STS		3	172116164	172146795	GCATGATAGCCATCTTCTCTT	TTTTCTTTGGTTCTGGAACCT
C2	936.6	FCA424	SSR	AF130625				TGGAAAAATGTGGAATACTGAA	CCAATTTGTAGTGACATCCCC
C2	958.8	BCH1	STS	AF053483	3	166892720	166957277	GTGAGGCTTGGATGATGT	GCATCACTCCATCCATCT
C2	965.9	FCA910	SSR	AY434894	3	165734991	165737804	AACCAGGATTAGCTTTTGATGG	AATCAACAATTTGAAGCCACA
C2	977.8	FCA911	SSR	AY434895	3	165265580	165267849	CCAGAGAGAAGCATATAACAAGGAA	AAGATAGCTCCTGGTTTTGCAC
C2	997.5	IL12A	STS	AF054605	3	160888263	160995420	GCTGTTACAGGCCCTGAATG	ATTGATGGTCACTGACAGAA
C2	1010.4	FCA912	SSR	AY434896				TTCAATAAGCCAAAACATGG	AAGCTCATCTGTGTTCTCACA
C2	1045.0	FCA310	SSR	AF130604				TTAATTTGATCCCAAGTGGTCA	TAATGCTGCAATGTAGGGCA
C2	1052.3	FCA913	SSR	AY434897				TCTGCTCCCTGGAACAC	TGTGACTGCCATAGGCTCTG
C2	1059.5	CP	STS	U82183	3	150161827	150221396	CTAGTCTCTGCTATTTGGGC	GGACAGTTTTTCCCTGGTGA
C2	1091.4	RASA2	STS		3	142487537	142613464	GCAGGAGCTGGAAGTGAAG	GACAAGGAATCATGCCATT
C2	1095.0	FLJ23751	STS	AW646872	3	142232320	142235086	CGTATGATCCAAAGGCAACATT	TGGTGCTAGTTGCTTGTGAAGA
C2	1108.0	FCA914	SSR	AY434898				CCCGGAAATTCCTACTTTTT	AGCCAGAGGCAATGGAATAA
C2	1133.0	PCCB	STS	AW646873	3	137250759	137331051	AAGGCACAAATGAAATCTTCC	AAACCAAGGCCAGTTACCG
C2	1150.7	TF	STS	AW646874	3	134746710	134779460	TGGTGACTGTCTCAAATCA	GCTGAACTGGAGCCCTTAC
C2	1160.8	RD114-3D	STS					TTCTTCTGGTCAACAGCCTT	AGCCTGGAGCCTGTTTCC
C2	1173.6	DAZLA	STS	AF114697	3	16620157	16638860	CCAGTGATGATCTCCGATG	CCCATCTATCAGATCTGC
C2	1181.3	FCA915	SSR	AY434899				AAGAGATAGGCGAGATTTTGG	CCCATTCTGAGCATTACGCT
C2	1202.5	FCA117	SSR	AF130527	3	17803558	17806005	AGCTCTTTAACCATGGGAAATG	CCCTTTTTCAGCATTAGTCCC
C2	1234.8	TGFBR2	STS		3	30497808	30585375	ACACCTGGTGGGCAAG	GGTTGATGCTGAGAAAATGTCC
C2	1260.0	FCA148	SSR	AF130545				TGACTTCAGGAAGTTACTCAGC	GATGCTTAAGTCCGAGGCC
C2	1273.8	FCA916	SSR	AY434900				CCTGTACAATCTCCAGAAGG	ATAAGGGCTCCAAGCTAGGC
C2	1278.5	GORASP1	STS	AW646875	3	38951468	38951627	CCTCCTGGAGGACAGCTT	TGGAGGCTGAAGAGGAGTCT
C2	1290.5	GLB1	STS	AF029974	3	32884713	32985324	TTAGCACGGGTTTCTTCC	CCTTTGAAGCTTCCATTTCC
C2	1295.2	FCA917	SSR	AY434901	3	34484585	34484935	TTAATGTTAACGTGAGCGCG	GGCAGCGTATGAGATAAAT
C2	1327.4	FCA918	SSR	AY434902				CCCTAAATGCTCCTCAGTGG	TTTGTCTCTGTGCATGCTT
C2	1355.6	FCA919	SSR	AY434903	3	19362170	19363870	TACTTGGTTTCCCATCTG	AGATTCTTGGTGGATCGAG
C2	1375.8	FCA043	SSR	AF130487				GAGCCACCTAGCACATATACC	AGACGGGATTGCGTAAAAAG
C2	1397.0	RARB	STS	AZ081268	3	25309493	25489220	ATGCGAGCTTTGAGGACT	TGCAAAAAGCTTCCGAAT

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
D1		0.0 MMP7	STS	U04444	11	102425313	102435552	TCCAACCAAGAACTAATGCACA	TGAGACTCAGGCCACAAG
D1	46.2	ACAT1	STS	AW646746	11	108026269	108052286	TGGAGAGCATGTCCAACGCTC	ATGGATTTATTGTAAGACGTCACTCAG
D1	58.1	FC920	SSR	AY434904	11	107737661	107738361	CAGATGCTAGTTGTAAGGGCC	TGCTCTGGCCAGCCCATAG
D1	81.9	FC921	SSR	AY434905				AGGACCTAAATCCACACCCC	TCCTCTTGTGCAATGTTTGC
D1	87.1	IL18	STS	AB046211	11	112047886	112068716	TTTGGCAAGCTTGAACATAAAC	TCAGGCATATCCTAAACACA
D1	112.9	DRD2	STS		11	113314228	113379803	GAGTGGAAATTCAGCAGGATT	AGGAGATGCTGAAGCAGCAG
D1	140.1	FC922	SSR	AY434906				AGGGAAGCAGCTTATACTCAGG	GCTGAAGTCGGACGCTTAAAC
D1	160.6	MGC13125	STS	AW646880	11	116652809	116677606	TTATTCGCCAGAGCCCTAAA	TGTGTGGGCTTAAGAGATTGG
D1	180.6	KIAA0999	STS	AW646879	11	116748085	117003018	CGCACACTGATGAACCAAAG	CAGCTCGGGAAATGAAAGAC
D1	197.7	Fc.23690	STS	AW646881	11	119259821	119260671	AAGTGCACACCAGCCCTTT	CTTGGAGCCTGAAGCTTTCT
D1	215.1	FC9193	SSR	AF130561	11	118065342	118067419	TATCTGGTAAGCCCTGGG	CCCTGTTTTATGCCTCTGC
D1	227.2	MLL	STS		11	118341118	118426821	ATTTCCAGGAGCTCGGTGTTG	GGAACCGGAGAACTTAAAGATGG
D1	239.0	H2AFX	STS		11	118998748	118998901	AACAAGAAAGACGGGATCAT	GGTGGCCTGGTTTTCTT
D1	276.6	THY1	STS	U82192	11	119322800	119327831	CCCATCCAGCATGAGTTCAG	GGTGGTAGACTGCCACAGAGA
D1	335.2	FC9087	SSR	AF130514				AGTGAAGACACAGCTCACC	TGACCGGAGGAGGTAATTTG
D1	350.1	FC91057	SSR	AY435037	11	123312796	123315642	CAGGCTCTGTGCTAACAGTCC	TTATACAGCTTGCATGGGCTCC
D1	357.5	FC9144	SSR	AF130542	11	123094210	123096594	GGAAATCTCGGAAACTTCTGC	CCCGCAAAATTTAGAAGG
D1	365.7	FC9923	SSR	AY434907				CGTCAACCACTTCTCCAT	TCTGAGGACCCTGGGTAC
D1	367.2	FC91055	SSR	AY435035	11	125583532	125585783	GATCACCTGAATGCTAGCTGG	AACCAGTGTCAAACCTGTGGC
D1	371.7	PATE	STS	AW646884	11	125650106	125653634	ACTTGGCTTGGGACCTTCTG	ATCATGACCTGAGCCCAAGT
D1	391.9	FLJ21103	STS	AW646883	11	126115107	126166349	GCCATTGAGCTTAATGAAAAA	TGTGTCCACACAGCAGATCA
D1	405.7	SPA17	STS	AW646882	11	124577718	124598603	GCATGTGTTCAATGGCATGT	GCTCCCAAAAAATGTGAA
D1	462.5	FC924	SSR	AY434908				ACACACCGGACAATTCAT	TGGCTGTACACCATGAATAGC
D1	490.2	FC925	SSR	AY434909				CTTATCAAACTTCTGGTCCG	ATCTAGTAACTGGCCTGCTGC
D1	527.7	FC926	SSR	AY434910				CCTTGGGAATGAAGCGCTA	TTCTGAAGAGTTTCTTATGTTCAA
D1	584.1	FC927	SSR	AY434911				CCACGTAGTCGAGATGCTA	AAATCTGAGGGCAGCAATG
D1	618.7	Fc.estTCE6	STS					TGCAAAATAACGAAAGAACTATGGA	GGTGTGTGAGACATTTTTCACACTA
D1	698.2	PGR	STS		11	100943181	101035333	ATGAAAGCCAGCCCTAAGC	GGCAGTGAATTAAGCACTTGAC
D1	725.5	FC9341	SSR					CCCTTGCAAAATGAAAGAAA	GCCCAATATCCATCAATCG
D1	772.2	FC928	SSR	AY434912	11	96151674	96153774	GGAGCTGAAGAAGCCCTGA	CAGGTAAGTAAACCCCAA
D1	802.4	FC929	SSR	AY434913	11	95922528	95925247	TGCCAAGATAGACCTGCCTTA	TCTGTGAATAAATAGATTAGGGATG
D1	851.6	FC930	SSR	AY434914				TTTTCAAGAAATTCGCAATTTG	CATGACCTGAGCTAAAGTCGG
D1	892.5	FC931	SSR	AY434915	11	91891303	91893563	AAGTGAAGTCAGCAATGCAGC	GTGGCTTCCCTTTATCATCA
D1	914.0	TYR	STS	U40716	11	89095162	89213368	GCTTTATGTGATGGAAGCTCCA	CAGCTTATCCATGSAATCC
D1	933.9	FC932	SSR	AY434916	11	82459852	82462482	ATCATTTTGCCTCGCATG	AGTGTGAGCTTGGTATGCTGC
D1	955.3	FC933	SSR	AY434917				TCCACCATCTAATTTTATTCC	TATCAGCCAAATTTATCACCAGC
D1	973.7	FC9067	SSR	AF130499				GGCCTGAGCTGAAGTCAGAC	GGCTCCACCTGGGAAACTA
D1	993.9	FC9076	SSR	AF130505				TCCAAGTGTCCATCATAGATG	TTTTAATGGCAAGTAACTTCC
D1	1025.8	FC9347	SSR	AF130615				ACGTCCCACTCCCACTC	GGCTAGGTAGAAGACAAATGCG
D1	1035.5	HBB	STS	AF114701	11	5205733	5207338	ATGAAGTTGGTGGTAGGCCC	AGACCACCCAGCAGCTAAGGG
D1	1048.8	FC934	SSR	AY434918	11	72389623	72392448	CATGAGGAGCTCAGATGACC	ATCACCAATATCCCAATGACC
D1	1076.7	FC935	SSR	AY434919	11	11523231	11525834	GCTCTGCTATATGTGGTAGGCG	CACCTGGCTGATCTCCACATG
D1	1088.6	FC936	SSR	AY434920	11	15712152	15714328	CTCAGCAATGTGGCATGC	CACCTCGCCCATCATG
D1	1096.6	PTH	STS	AF309967	11	13552760	13556721	TCTACTTTTATTCATGTAAGGCCCTT	TGATCATTAATTTTATTTGCAATG
D1	1107.5	F49	SSR					GTCGAATGCTTAAGTACTG	GACATCTGTGCAATTTCTCTC
D1	1114.2	LDHA	STS	AZ081271	11	18455264	18468547	TTTGGCCAGCGTAATGTGA	TGCCATCAGTGTACTCAAGC
D1	1142.3	SAA	STS	AF136718	11	18326873	18330666	CTCCTCTATAGCGGGCACCT	ACCAAGTGTGTGGCCAAA
D1	1154.9	WT1	STS		11	32448475	32496231	CACCAAAAGGAGACACACAGG	GGGGAGGGAATTAATGGAAA
D1	1162.3	F5HB	STS	AZ081269	11	30292604	30294719	GCAATGGACATTTCAAGTGAC	AATTCCTGGACCTCCTCTGC
D1	1180.6	FC9741	SSR					GCATGAGAGGGTTTAGGCC	TTGCTCAAGTCCATGATAAATG
D1	1194.0	BDNF	STS	AF192537	11	27718016	27762310	CATCCCTTTTCTACTATGGTT	TTCCAGTGCCTTTTGTCTATG
D1	1196.5	FC937	SSR	AY434921	11	26740657	26742882	TTTCATACCACCATCTATTCC	ATATCCATTCTCTGCATCCC
D1	1204.5	FC938	SSR	AY434922				ACAGCATATCGCGCTCAGG	ATGTTTGCACAATGATGAATGG
D1	1208.7	FC939	SSR	AY434923				ATTTGAGCCATTTTCAAGC	TTTAGGTATACATGCAGGCAGC
D1	1215.4	FC938	SSR	AF130700				GGGAAATAACAGGCTAGCAGG	TGAGGTTTCACTCACAGTGC
D1	1229.4	FC940	SSR	AY434924	11	32890555	32892937	AGCTAGCTCATCCATTGCCTA	GCTGAGTGTATAACCTTCCA
D1	bin: LOD 0.40	FC941	SSR	AY434925	11	34590717	34592915	TGCAAGTCAATTAATCATGCT	TCCAAAAGAAAGAAAGTCCC
D1	1237.7	CAT	STS	U82180	11	34499647	34532761	AAAGACTGACCAAGGCATCA	GAAAATCAAAGAGGCCCA
D1	1240.5	FC942	SSR	AY434926	11	34679035	34681207	TAGCACCACCACCACTACA	CACCTACCCACCAGCTGCT
D1	1243.1	SLC1A2	STS	AF354649	11	35315122	35480178	TCAATGTTTGGGTGACTCC	TTTCAATATCTTATGCATCGAT
D1	1244.9	FC9180	SSR	AF130557				AAATTGGAGACATTTGATTTGC	CTAGGCTTGTGGAGCTGAGC
D1	1248.9	RAG2	STS	AY011977	11	36652649	36658940	TCAATGGAGGAAACACCCAAA	TGCACTGGAGACAGAGATTC
D1	1271.1	FC9239	SSR	AF130579				TGAAGGTGTGGAGATAAGTGT	AGCAAAAGAAAAGATGTCCC
D1	1314.7	ROM1	STS	AJ417433	11	62630160	62633471	CTCCTTATAGCGGGCACCT	ACCACTCTGTGCCAAA
D1	1322.3	SF3B2	STS	AW646877	11	66069779	66086334	CTGAAAGAGTTGGAGCTGGA	GCATCCAGACAAGAGCTGA
D1	1327.7	CTSW	STS		11	65897428	65901353	AGGGCTCCAGTTGGTTAAA	ATGGCGACCATCTGACTAA
D1	1346.2	Fc.132216	STS	AW646878	11	61528002	61529373	CTCCAGAACCTCTCCGACTG	ACTACACATGGGGCCACT
D1	1353.7	FC943	SSR	AY434927	11	61510980	61513097	GAGAGAGCGCTCATCAGTC	CCTCCAGCCACGGTTTC
D1	1357.5	PGA5	STS	AF036953	11	61259553	61269801	CCAGCTCCAGGAAGCAAC	CTCCACTGGGAGGAGGATT
D1	1361.2	FC944	SSR	AY434928				CCCAGTGTAGCTGCACCATT	CTGGCTGGGTGGATGAG
D1	1366.9	IGHMBP2	STS	AF503619	11	68921351	68958076	unpublished data	unpublished data
D1	1394.8	KCNQ1	STS	AF013961	11	2426367	2829324	GGAGCTCATCACCACTTGT	CGTAGCTGCCAACTCCACT
D1	1415.5	AP2A2	STS	AW646745	11	181724	272300	CGACTGGGCTGTTTATTGTC	AGTTTTAATCGCCGAGGATG
D1	1432.9	HRAS	STS	U62092	11	664646	667968	TGAACATCCCAATGCCAC	AGCCGAAAACCAAGTCAAG

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
D2	bin: LOD 0.0	FCA165	SSR	AF130551				TTGGCATCCCCTTGATCTC	AAACCGGATGCTACTGGGA
D2	0.0	FCA091	SSR	AF130517				TGAGAACAGCCATAATAGCA	CCCAACATAAGGCTGCATT
D2	25.3	CHRM3	STS		1	235946452	236369030	GGGTCAATTCGAATGAATCTGTTTA	ACAAGATATTGCCAGAAAGAATG
D2	58.8	LGALS8	STS	AW646886	1	232978157	233010879	CCTCCTAGGTGTCTGGGTCT	GCAGTCTGGCAGGAAATA
D2	86.0	FCA262	SSR	AF130589	1	231681438	231683188	ATCTCTCCATGGTGTGTGATG	TACAGAATACTCCCCCGC
D2	bin: LOD 4.64	NUMT	STS	U20754				TTAACACAAGCCACCCTA	GGTTAAGGCTTTTAAATGGTT
D2	159.8	FCA462	SSR	AF130629	1	225692983	225696283	TCATGAGATGGGAAAAGAGAGA	GCCATTACTGAAGGATCAGGC
D2	202.2	FCA945	SSR	AY434929	10	60165227	60167375	TGAGTTACACTCAGTTCATGAAAATCT	GAGAAACCAACCATCCCAT
D2	204.5	FCA946	SSR	AY434930				TGGTGGCTTACAGGTAGGC	TTCATGAAAATCTTCTGTACTATGG
D2	211.3	FCA477	SSR	AF130631				TTAGGAATGGATGGGCAGAG	AAGGGAAATATGAATAAGGGG
D2	257.9	FCA263	SSR	AF130590	10	65674198	65674798	CAGCTAAATTTCTGGCTCC	CAGGAGGTCCTATCAAGAGC
D2	292.4	EGR2	STS	AZ081272	10	64464158	64468528	CATGAGAGACCTATCCGTGC	GCAGATCCGACACTGGAAG
D2	316.0	FCA081	SSR	AF130509				TCATGGAGATAGAAAATGACAACA	TGTTTTATAGAACATTTCTCGGTGT
D2	357.8	FCA947	SSR	AY434931				TCITTAGGTGCCCATCTTG	CACCTAGTAGGAGCCCTTC
D2	371.7	FCA948	SSR	AY434932				TCCTGGCTTCTGTGAATGC	GGTGAAGATTTCTTGCCCAA
D2	401.5	RBP3	STS	Z11811	10	48317289	48326807	GAGGCCGTGCAGACCTACTA	CAGAAGAGCGCTCTTGG
D2	424.7	FCA949	SSR	AY434933				AGCAGAGAAATGCTGCAGAGC	CCCTCTCCACAGAAAGCATA
D2	bin: LOD 1.17	FCA950	SSR	AY434934	10	82412834	82414985	CTATCCTTTATCACCTCCACG	GGCTGGGCATACACTTGTG
D2	451.0	FCA951	SSR	AY434935				TTGAGTTGAGCATCTCCCC	GAACGAAACCCAGGTAGTCTGG
D2	453.7	VCL	STS		10	75650347	75772202	AATGACATCATTGCAGCAGC	CTGTAAAGGTTGGTTCTAATCCG
D2	465.2	FCA035	SSR	AF130486	10	85878364	85881167	CTTGCTCTGAAAATGTAAAATG	AAACGTAGTGGGGTTAGTGG
D2	488.3	GHITM	STS	AW646887	10	86030474	86044527	CCAACATCTGAACTGCTG	GCAACTGGAAGCAACAGAAA
D2	515.9	PLAU	STS	AF114703	10	75563339	75569684	CCAACAAGTACTTCCAAAGATTTC	AGTTCAGGACAGGAGCAG
D2	533.4	FCA952	SSR	AY434936	10	74510175	74512891	CACAGTCTCTCTGACATTTGC	CATCTCACCCAGCAATGCTT
D2	573.0	FCA107	SSR	AF130524	10	49819484	49821585	GGACTTCTGCAAAGCCACTC	TGTCCCCAAGAGACCTGC
D2	594.4	CHAT	STS	AF114702	10	50709549	50765558	GGAGACAGGATTTGGATGA	ATCCCATCTGTCCCTTTT
D2	610.0	RET	STS		10	43347708	43400989	GCAACATCGTTCTCTCTGC	TGCCTGAATGTAACCGGATG
D2	617.5	SDF1B	STS	AB011966	10	44640810	44655732	AGTGTGCATTGACCCGAAAT	CCAGGTATTCTGAAATCCACTTC
D2	636.4	FCA953	SSR	AY434937				TTTCTGAGTTTCCCGTGTCC	TGCCTCTCTCCACCTTGAAT
D2	661.7	CYP17	STS	AW646888	10	104718952	104728404	CTACCCTCATCTGGGCTTC	GCAGAGGTTGCACCTGGAG
D2	690.6	LOC119392	STS	AW646889	10	106013042	106017367	TGTGGCAAATAGATGGAAACA	TCTGGGCAATTTCTGGAAGTC
D2	713.7	BUB3	STS		10	124920853	124931845	AGGTCGAGTGGCAGTTGATG	AAACGGATCCCAATGTTGA
D2	728.8	OAT	STS		10	126126903	126148550	TGAGAAAGGAGCTCATGAAGC	AAAGGGCTCCATTTCCAAAG
D2	737.5	TRABID	STS	AW646747	10	126716900	126717000	AGGAGCAGCAGGAGAAGCTA	TGTAGCGTCAAGCCACTTC
D2	782.9	F41	SSR		10	122459159	122461532	GTCTGCATCTTCAAATAGGA	GTACCTGAGTTGGCTTGTGA
D2	813.2	FCA954	SSR	AY434938				ATGTTTTAAGTGCCAACGCC	CTTGACCGAGGTCAGAATTACC
D2	827.2	FCA668	SSR	AF130688	10	114513190	114515528	AATGGCTGAGACATCAAGTGG	AGAGCAGCCCAAAAAAGTCA
D2	840.7	ADRB1	STS	AF192344	10	115935041	115936754	GGGCATAGGCTGCTGAT	GCAGAAGAAGGAGCCGTAAT
D2	851.7	ADRA2A	STS	AZ081273	10	112968147	112971796	GGTCCATCAGGCAAGCCATC	CTTCTCGATGGAGATGAGCG
D2	876.3	FCA366	SSR					GAAGGCCATTCCACTTCAGG	TCCCATCTTGTACTCTCTTGC
D2	884.9	FCA955	SSR	AY434939	10	108657106	108659419	TCATCTTTAAGGCCAAGATTCC	GACAGTTGGGTTGGCACTT
D2	902.6	FCA956	SSR	AY434940				TTGGTAAATGGACTTGGATGTG	AACCCCTGAAGCAGTCC
D2	914.2	FCA957	SSR	AY434941	10	102400461	102403107	GATCATTCACCGACTCAAGG	GTTGCAATTTGCCCTGCATT
D2	917.1	FCA078	SSR	AF130507				TGAACTGAAGTCAGATGCTTAACC	CGGAATCAGTATTTTACGG
D2	922.9	FCA557	SSR	AF130658				TCTGGGGTGTCTTGAAT	ACATGCTACAGAGCGGGC
D2	931.1	GOT1	STS		10	101287854	101322450	GGTTTCTGTCCCTTCTTTG	GTAGAGCCCGAAGTCTTGG
D2	945.0	LOC159291	STS		10	99666091	99755279	GCATGGAGACCCACTACGAG	AGCTGACGACAGTGTG
D2	995.7	FCA958	SSR	AY434942				CGGTATGTGCTTAAGCTCTCA	TAGCAATGCGAAGGCTCTCC

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
D3	0.0	CHFR	STS	AW646891	12	133041910	133089157	TTCCAGATGACATGGCAAAC	CCCCATGGTCTTCTCTGTT
D3	32.6	FCA137	SSR	AF130539				AGTCCAGAGAACTTCAGATGCC	ACTGAGCCAGCCAGGTAC
D3	47.7	FCA959	SSR	AY434943	12	125463278	125465480	CTAATGCTGGGGAAACAATTAGC	CCGACTGACCCAGAAATCACT
D3	67.4	ATP2A2	STS	Z11500	12	110612631	110678314	CAGATGTTGGTGAATACGG	GTCTGTGCAATGCTTGTGTC
D3	81.6	MAPKAPK5	STS	AW646892	12	112090929	112114081	GGAACTGAGCTTTTCTACAACA	AAATCCATAAATTCATTCCACA
D3	108.7	ALDH2	STS	AF114704	12	111987198	112030635	TCCCGCTCTGATGCAAG	CCCCGAGACTGGCCCG
D3	127.6	FLJ14827	STS	AW646893	12	113406407	113412972	TCTTGCCACCAAGTGTGACT	GTCCACCCAGATCCTGTTTCC
D3	151.8	PBP	STS	AW646894	12	118356776	118366240	CCCTCAAGAGTCTTTGATGCT	GTACCAGGATGGGGTCATCA
D3	171.2	TCF1	STS	AF114705	12	121199401	121223165	CCCAGCAGATCCTGTCC	CTCCGTGACAAGGTTGGAG
D3	193.8	FCA200	SSR	AF130562				CTCCAGCCAGAAAGCTG	AGCATCTGGTTGGCTCAGTT
D3	205.8	FCA523	SSR	AF130646				GGTGTGTTTTTGACAAATTACC	GATCTCAAGTGTCTTACCACA
D3	208.8	JGLC6	STS	U85410	22	21580600	21580700	CCCGCCCTCCTGTAGG	GCCCGCTACTTGTGTGCT
D3	220.3	GNAZ	STS		22	21737228	21791772	CGCTCACGGGACATGAC	ACAGAAGATGATGGGCTTACG
D3	241.9	SLC5A1	STS	AF114706	22	30763813	30831199	TGAAGTGGGAGGTTATGATGC	CTGATCTGTCCACCACTACC
D3	258.8	FCA249	SSR	AF130584	22	30552848	30555021	CCAGAAAGCTATGATTGGAGA	ATCAATACCAATCTTTGCCCC
D3	292.3	FCA960	SSR	AY434944				TCAGGCTCTGTGTCAGACT	CCCTTCAATCAGGAACCA
D3	318.8	FCA961	SSR	AY434945				CTCGCAGCTGTGAGACTGAG	TGCTTAAATGATTGAGCCACC
D3	404.0	FCA962	SSR	AY434946				TGCCACAAAAGACTCACTCA	GCATCAGGCTCTGTGCT
D3	451.4	FCA963	SSR	AY434947	18	7741171	7743234	TTCCCTCCCTCAGTCCC	TTCAGCAGAAATCAACTGCG
D3	483.3	FCA964	SSR	AY434948	18	10110792	10113453	AAAGTTGTGCGAGATTGACG	TGCAACTTTATCAGCATGACC
D3	503.5	FCA965	SSR						
D3	537.8	FCA966	SSR	AY434949				TGCCCTCCCAATATTCTGAG	TCACTTCTGCCTCCCACT
D3	572.8	FCA967	SSR	AY434950				CCTCATACATGGATTGATGCC	AGGATGGAATAGTCAAGTTGCC
D3	583.8	FCA026	SSR	AF130482				GGAGCCCTTAGAGTCATGCA	TGTACACGCACCAAAAACAA
D3	615.4	SLC25A1	STS	AW646895	22	17537649	17540897	CGGAGGCAGCTTTGGTAG	CGGAGGCAGCTTTGGTAG
D3	692.4	LAMA1	STS	AW646896	18	6948557	7107815	CAGAAAAGCAAAACCCGCTTG	AGGCAGTTTGTCTTACGTCA
D3	709.0	FCA968	SSR	AY434951				TGTCATCCAGAAAGTGAAGTCC	ATCGGTGAGTAGATGCCAGG
D3	736.4	FCA132	SSR	AF130535				ATCAAGGCCAAGTGTCCG	GATGCCTCATTAGAAAAATGGC
D3	745.5	FCA369	SSR					TGAAGAGCAGAAATAGCTTCCA	TTTTTTGAGGTTTTTTGACGC
D3	761.8	FCA066	SSR	AF130498				GCCCCACATAGATATTTTACATC	GGCCTAGAACCTTGTCCAT
D3	780.7	TYMS	STS	AZ081274	18	970800	1000500	GGGTGTACCTTCAACATCG	AGCTGCAAGGTGAGCAAGTT
D3	805.5	FCA675	SSR	AF130691	18	21779040	21781104	CTATTGCTCCAGCCAGTCC	GCCATGGCAAGAGACTGGT
D3	833.2	CDH2	STS		18	25400834	25645400	ACTTACTCAGCTGGTTGC	CTGCACTTCCCATAGAC
D3	882.3	FCA603	SSR	AF130672				TAGCAGCATTATGTGGAAATGG	CAGCATTAAATGCTAGTCCCA
D3	1017.2	FCA969	SSR	AY434952				GATCGTAGATATGACCAGCAGC	CCTTAATAGGGCTGGATGCA
D3	1071.1	FCA623	SSR	AF130676				TTGGTTTTCTATTGAGAACGG	TCACACTCTCTCTCTCTCCC
D3	1109.3	MAN2A2	STS	AW646898	15	89033388	89051654	GTCATGCCACGGAAATATCC	CGTCACTCTGACACCTCACG
D3	1136.5	HSPC154	STS	AW646899	18	71600818	71611061	AGCAGAAACACTGTCCACGA	AGGAAAGAACACATGCGCTCA
D3	1155.8	FCA970	SSR	AY434953				TCATAATTATAGAAAGATGAAGAT	AATTAGGGTGGCAGCTAGGC
D3	1173.0	FCA971	SSR	AY434954				TACCTTTTCCCAAAAGCT	AAACGAGCCCTGAGCTCTTT
D3	1187.4	FCA277	SSR	AF130594				CTCCCTCTCTCTGCCCTT	GAAAACGGCAGAAAAGCAAA
D3	1204.1	RD114-8H	STS					TGCTGGGACAGCTGGATAG	TTAAGGTTTGCATCAATTTGA
D3	1216.2	MC4R	STS		18	57823558	57824556	TTGACTCTGTGATCTGAGCTCCT	AAATGAGACATGAAGCACACA
D3	1223.2	FCA221	SSR	AF130572	18	58779155	58782605	CTGGCCCAATTAAGCAAGAAG	TATGGCTATGCCAGCAGTTG
D3	1253.2	HNRPD	STS	AW646897	4	83736610	83736734	CCACATGGAGGACATGAAC	TCAATTTGCCATCAGATTTG

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
D4	0.0	FCA641	SSR	AF130680				AATGGGTTGTGAAGTAAAACGG	GAAATCAAGAGTCAGATGCCG
D4	67.7	FCA742	SSR					TCAATGTCTTGACAACGCATAA	AGGATTGCATGACCAGGAAC
D4	82.0	FCA743	SSR					CGACTCAGACTGGGTGTCTC	CATTTGGTGGAGGTTTTGGT
D4	103.8	FCA744	SSR					CATTGGCCCTACAGCCTACT	TCAACACCCTCACACCAATG
D4	163.2	FCA119	SSR	AF130528	9	11905550	11905600	AAAAAGGGAAATTTGACAGAAGC	GGATTGCTGGCAATCTTTGT
D4	227.5	CNTRF	STS	AZ081276	9	34863644	34902333	CCATCCCTGTTCTCTCAGT	TCACAGATGACCCTTCCAC
D4	244.7	FCA974	SSR	AY434955				GCAAGTGGAGTTGATGAGAAGC	AAAGCCCTGGAGTCATCCTT
D4	252.3	LOC259308	STS		9	34710300	34710360	AAACAGGAGGGGACTCCAAG	AGACCAACGTTCCCTCTGA
D4	271.1	FCA242	SSR	AF130581				ATAGCCAGGCACAGGCTG	CTCCCAGGACATTTGTCT
D4	298.1	KJAA0258	STS	AW646901	9	35739289	35747923	TGGTACCTTCAGGGTTCAGC	CCTGCCACTATGAAGGAAA
D4	312.8	VCP	STS	AW646900	9	35046066	35062689	GAGGTGACACAGTGTGCTG	CTGATGACATCCCCTAGATG
D4	357.1	FCA975	SSR	AY434956				GCAAAATTCACAAGCATGTACA	CTGAACTAAATTTGCCTGGG
D4	382.6	FCA030	SSR	AF130483	9	28797564	28804779	CTGTTGGAACGGGAGTAAAGG	ACACATTTCTCTGCCCC
D4	404.4	FCA618	SSR					GTCGTTCTCTTTTCGTTAGTGGG	AAAAATTCAGATTTGGAACA
D4	430.0	IFNB1	STS	U81267	9	21067106	21067933	CATCCTGTCTCTTGAGGCAAT	GCAGGCAAGACTTCTATTTTC
D4	445.6	IFN1	STS	AF114696	9	21155637	21431316	CCTCGTCTGCTGTTGGAAC	GGATCTCATGATTTCTGCTGAC
D4	493.7	FCA976	SSR	AY434957				TCCATTTACTGGGAAATTC	ACCCTCATGTCTGGCAATC
D4	560.8	FCA977	SSR	AY434958				GATCTCCAGTGGGACAGTCAG	CATCTCCAGAAAGCCGTA
D4	568.4	FCA978	SSR	AY434959				CCCCTGGTGACCTGACTG	GAGCAGGCCCTAAGGCTACT
D4	588.0	FCA979	SSR	AY434960				TCTCCAGTGGGACAGTCAGA	GTCTAGGCCAGCCTTACC
D4	599.6	FCA980	SSR	AY434961				GATCTCCAGTGGGACAGTCAG	GACAAGTGACGTGTCGC
D4	620.2	FCA981	SSR	AY434962				TCTCCAGTGGGACAGTCAGA	AGGACAAGTGACGTGTCAG
D4	628.8	PTGDS	STS	D62048	9	133313019	133317257	CCCTGCTGCTCTTTTCT	GGAGTTTATTCTCAGAGCCAGGT
D4	634.7	FCA982	SSR	AY434963				AACACCCTGAGGGCTAGGTT	TAAGGACCCACAAGAATGACG
D4	654.7	SURF4	STS	AW646905	9	129582010	129596640	CAATCGTAAAGGCATCACAA	CGCAACCTGACTTACCCT
D4	680.4	PAEP	STS	AF073785	9	131976702	131981897	GAGAGGATGACACCCTTCC	AGGGGCTCAGAGCAGGAG
D4	726.5	Fc.96704	STS	AW646904	9	124376305	124379872	AGTGGGGAGTGTCTGGAAT	GGCCACCCTTCTGTACTTCT
D4	761.4	CRAT	STS	AW646903	9	125310745	125326731	AAGCAGGACTCGGTCATCAG	TTCTCCAGTGCACGAAGAT
D4	780.0	Fc.178009	STS		9	123832028	123847549	CCCACACACACGCTCA	AATAAAGTTAGCATGGGACCAG
D4	782.5	FCA983	SSR	AY434964				ATTCCCTGCCCGAGCTAC	CCTGGGTGCTGACCTG
D4	796.1	HSPA5	STS		9	121452555	121457019	CTGAAGGGGAGCCTGTGAT	CCACCACCACCACTTTCTA
D4	806.5	FCA045	SSR	AF130489				TGAAGAAAAGAATCAGGCTGTG	GTATGAGCATCTCTGTGTTCTGTG
D4	813.4	FCA984	SSR	AY434965	9	117412966	117414016	ACAACCACAAAATTTCCAGG	AAGCAGCTATCTTGGCTCTGG
D4	842.4	DBCCR1	STS	AW646902	9	115382569	115585388	TCCTCCCAAGGAAAAATG	GGCCTCAGGTGCTGTATTGT
D4	878.9	TLR4	STS	AB060687	9	113920245	113931714	TGAATGGAAACTACCTCATGTTT	GGAGGTGCTCAATCAGGA
D4	895.1	FCA650	SSR	AF130683				GCACATTTGACAATACACACG	AGGTTTCTAGAAGTTCCACAGG
D4	913.2	FCA746	SSR					GCCTCCAGGATTATTCAA	TGCGGTAAGGTGTTCAAAG
D4	949.8	AMBP	STS		9	110276071	110294376	AGTGTCTGCAGACCTGCCG	AGTAGAACTTTGTCCTTGCC
D4	969.7	FCA985	SSR	AY434966				CTGTCCTCAGAGAAGGTGCC	GCCTTTCTTTGTTTTCTGGG
D4	996.6	FCA134	SSR	AF130537				CCTGGGAAAGTTGGGTTCC	CCCATAAATTCAGGCGATG
D4	1027.8	TXN	STS	AZ081277	9	106463545	106476345	GCTGGACAATAGGAAAACACG	CCCTGAAGCTGAGGTACAA

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
E1	0.0	FCA986	SSR	AY434967	17	14250490	14251890	CCAAATGTCCAACAAGCATG	ATGATGGTGTTCCTCTGG
E1	44.7	FCA987	SSR	AY434968	17	14427690	14430090	TGAGAAGGAGAGTGCACTTCTG	AGAGGCCCTGGAATCAACT
E1	76.3	UBB	STS		17	16227201	16235935	TAAACTGGGGCAAAATGGCTA	CCAGAAAGATCCACTCTCCA
E1	92.2	ULK2	STS	AW646906	17	19581985	19675749	GGTTTGAACCTGAGAGCCCAAG	CCTGGTGACTACCAAGACCA
E1	100.4	FCA140	SSR	AF130541	17	18934190	18934190	AACCTGTCCCTCCTGGTTCT	AAAGAAAGTTCCCGGAATAGG
E1	bin: LOD 2.70	PEMT	STS	AW646907	17	17351932	17428748	GCSAGATGGGAACAGAGAAC	GACGTTCCAGAGCAAAATGG
E1	187.6	RCV1	STS		17	9744083	9751740	TGGTACCAGTCCTTCTGTA	GCACITTCATTCTGCTGATGG
E1	241.7	TP53	STS	D26608	17	7514526	7533733	CGCCATAAAAGCCCAATGTT	CAAGGGTGAGGGGTGTCAGTT
E1	0.0	FCA988	SSR	AY434969				ACAGAGTGAAGCCTGCTTGG	CCACTGCTAGCTCCAGGATG
E1	18.5	HIC1	STS	AW646908	17	1910774	1912939	CAGGTCCTTGGTTACTGCT	GGCTGGAACGTGGTCTCT
E1	29.7	CRK	STS		17	1275985	1276187	TCATTCGCTGCTTTACTGGA	CAATCAGAGCCGATGACTGAGG
E1	31.6	PITPN	STS		17	1373378	1416911	CTTTTTGCAAGACAGTGGTC	CACCAGACGCTATTGTGTCA
E1	68.2	CRYBA1	STS	AF114707	17	27425744	27433370	AGGAGAGTACCCTCGCTGG	CTGTATACCCCTCTTACCG
E1	77.8	F124	SSR	AF130531				TGCTGGGTATGAAGCCTACT	ATTGCTCAACTCACTAGGC
E1	95.6	Fc.207471	STS		17	26882361	26890752	CCGATCAATAAGCCCAAGAG	TTCTGGGCACTGAAGACTC
E1	121.0	NF1	STS	U82189	17	29271863	29551562	TTGGCAGCTAAGACAAGCAA	TTTGTGACAATCCCAATAATGT
E1	141.3	Fc.8179	STS	AW646909	17	30028774	30036202	CCTCTGACACAGACACGAA	TGAGGACACATTCACAGTGA
E1	163.2	Fc.3447	STS	AW646910	17	31103744	31120785	CAAGCCTGTGTGAGAAACCA	ACCTCAAGSACTGGGTGGAT
E1	184.2	FCA005	SSR	AF130474	17	31826282	31829523	CCTAAGGAACAGTAATCCTGGC	TGGCAGGGATACCAAGGAT
E1	237.2	FCA989	SSR	AY434970	17	32310654	32312773	TGTCACTAATCTGCACCAAAC	CAAGGACTAGCCAGGAGGC
E1	366.8	FCA082	SSR	AF130510	17	59302455	59679495	TCCTTTGGACTAACCTGTG	AAGGTTGGAAGTTCCGAAA
E1	376.2	SUPT4H1	STS	AW646911	17	56764618	56771805	TGCTGTTTCATTGTGCGAAA	TTTTCCCCACCTTGATACC
E1	379.3	MTMR4	STS	AW646912	17	56908976	56937272	CATGTCGTGGTTGGGACAG	TTGACCTTTTATACCACTAGGA
E1	411.4	FCA567	SSR	AF130661				TCAGGGTTTTCCAGAGAAAACA	TAGACACATACAGATGGGGTGC
E1	460.1	FCA050	SSR	AF130491				CACCAGGCCCTATATAA	CCCTGCTTCTCTGTCTC
E1	502.8	FCA990	SSR	AY434971	17	40319759	40322059	AAAAATTTCTTTCTAGGAAGATCA	TGACCTACACCCCTGGAAC
E1	508.3	BRCA1	STS	AF284018	17	41105076	41186168	CTGGAGCCGAGGAGCGTAAC	TCAGACACGTGAATCTGTTCC
E1	508.3	STA75B	STS	AW646914	17	40261341	40261511	CTCTGGCAGGACGAGA	GACCTATGGAACAGTCAAGTGA
E1	508.3	FCA991	SSR	AY434972				AGGGCTCATAAACCATGCGAG	ACAACAATGCCGACACATA
E1	511.4	FCA298	SSR	AF130600				CCCCATATGCTTCACAAT	TCCCAGCTTATGCTCTCTC
E1	520.0	CSF3	STS	Y08558	17	38082011	38084403	GCTATCAACATCTGGCAGCA	GATTTTCAGGGCTTGGTGAA
E1	534.5	SGCA	STS	AW646913	17	48595174	48595350	GGCTCCTTTTATTCACACTGC	GGGCACAAGCAGTAAACA
E1	556.6	HOXB	STS		17	46948725	47034639	CCATTAATAACGAGTGCCT	CTCTGACTACCACCCCTTCC
E1	573.5	FCA992	SSR	AY434973	17			AAGCCTGGCTTAGACCCTA	TCTGACCTCCAGCAGCATG
E1	593.5	MYL4	STS		17	45619891	45647130	AAGGAGCAGGGCACCTATG	AGACAGGCCCTGAATCAGGA
E1	607.1	FCA993	SSR	AY434974				TCACTGTTCTGGCTTTCGG	CGGATGTCTCCATTCTCTAGG
E1	617.7	FLJ31795	STS	AW646915	17	42776590	42777895	CATTGCAGAGTGCTTTGTCC	TCTGATTACCACACACACATA
E1	631.9	HIS1	STS	AW646916	17	43236862	43240489	GGACAGTTTCAATTGCTGA	AGGCACTAAGCAGCACAAT
E1	634.2	Fc.182584	STS	AW646917	17	42293302	42293419	AAGACATTCCTCCACCTC	GGATGGTTGGAGTCAGAGGA
E1	675.6	GHI	STS	AZ081278	17	62335374	62336987	GCTCTGCCTGCCCTGG	CGAACACCAGGCTGTGG
E1	709.4	Fc.19235	STS	AW646918	17	62457341	62457741	GCCATCATGAATCAGCAGAA	TTAAAGGGCGAATGATTGG
E1	721.3	SCN4A	STS	AZ081279	17	62356699	62391090	CTCAAGGTGGACATCTGTACAA	GTGGGTGTAAGTGTCCGTGT
E1	733.0	DDX5	STS	AW646919	17	62913282	62919949	GCCTCCAGAGGGCTAGGTTA	TGCTTAGGCCCTGGCCAAA
E1	752.0	FCA312	SSR		17	65317276	65319447	GAAGCACCATCAGCCAC	TTGGCATTGGAGTGTATATGC
E1	785.4	SSTR2	STS		17	71625675	71632575	CCCTTCTACATATCAATGCTCC	AGACAAGAGGCATCAGGATA
E1	811.9	H3F3B	STS	AW646920	17	74237654	74239992	TGCATGCATCATGAGAAGCAAGAA	CCTCAGTATGTGAGCACTGTT
E1	876.6	TK1	STS		17	76631337	76631608	GCTGGATGGGACCTCCAGA	GGCTTCTCGAAGCACTCCA
E1	979.3	ACTG1	STS	AW646921	17	80049959	80050106	CTGGGGCCTAATGTTCTCAC	TTGGAACAGGTTTGCATTT
E1	1020.1	PDE6G	STS	AJ417434	17	80177485	80183558	ATCTGGTGGTGAGAAAAGC	GGAGTCAAGTTTCTGCTG
E1	1034.8	P4HB	STS	AZ081280	17	80336856	80354230	CCTGGAGGAGAGTAGACC	TGCTCCTGGCTCATCAGG
E1	1046.3	FCA113	SSR	AF130526				TGGGAGCTCATTGCTCCT	CCCACATTGGGCTAGAAAAT
E1	1066.5	FCA994	SSR	AY434975				ACTTGACTGAACCAACCCAGG	GTGCTTTACCATTTCAAAGGG
E1	bin: LOD 0.86	FCA995	SSR	AY434976				TTTCGATGTTCTGACTTACA	GAATGATGAACCTGGGGC

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
E2	0.0	FCA070	SSR	AF130501				TCCACCCTGAGTACTTCCTCC	GATCCCAGATATGTGAATGTGA
E2	24.4	PRKCG	STS	AW646748	19	59061575	59086387	CCGTAACCTAATTCCTATGGACC	ATTCCACACAGGGTTTAGCG
E2	42.0	TNN13	STS	AW646748	19	60339628	60354022	GGGCACTAGGGCTAAGGAGT	GCCCTCAAACCTTTTCTTCC
E2	62.6	FCA589	SSR	AF130668				TGGACCCCAAACTAAG	AATCATTACGGATATGGAAACA
E2	86.1	ZNF134	STS	AW646922	19	62808843	62808963	TCCCTGAATTGAATGGGGTTC	CACATGAGGCCAACAAATGTC
E2	161.4	FCA996	SSR	AY434977	19	51153946	51156008	CCAGGACACCCACAGTCAC	TGATGAAAACCTGTGATGT
E2	180.8	NUPE2	STS	AW646923	19	55056218	55108809	TTTCAGACAGTGCAGCGAAC	CTGAACCTGACCGACGTAA
E2	184.9	FCA997	SSR	AY434978				GTCCTCACCTTTGAAACTGC	GGGTGGCTTAGTGGATTAAAGC
E2	185.6	C3	STS	AW646924	19	6617715	6660660	GGGGTACATGCAGGTGTCT	GATCCTCCCACTCAAAGCTC
E2	190.6	LOC163223	STS	AW646925	19	22153700	22155800	GCCCGTCAACTGTGAGTTT	ATGTGGGAGACCTTCAATG
E2	194.3	FCA998	SSR	AY434979				AGCGACCCTAATTCAGAGG	TCGATCACGTGA
E2	201.3	LHB	STS	AF095716	19	54195258	54196388	TGTGTACCTTCACCACCAC	CACAGTCGGAGCTGCTGAG
E2	bin: LOD 0.02	FLJ22059	STS	AW646926	19	47265381	47261749	CTGTTCCATCTTGGGACCAC	CGTTGCTGAAGAACCTCCTC
E2	226.9	PFAH1B3	STS	AW646928	19	47477234	47483747	GGGGAAGAAGTACTGCTTAGG	ACGATTACCTGCATCTGAGC
E2	bin: LOD 1.71	LOC56269	STS	AW646927	19	48999809	48900109	TTGTCAAGGCTTGGTTTGTG	CGCGCTGCTCCTCAAGTAT
E2	270.0	PSMD8	STS	AW646929	19	43541027	43550512	TCCTCCCAAGGAAAAATG	AAACCTCCTCCCGACTTAC
E2	291.8	FCA999	SSR	AY434980	19	42016741	42018845	CCATACCCACAGTTCAGCAA	TGTAGCGTCTTTGACCCG
E2	300.4	FCA309	SSR	AF130603	19	42814620	42816666	AGAGATGGGCTCAGTTGCAT	CTGGTACCCTGAATCTCA
E2	303.6	FCA1000	SSR	AY434981				ACTGAGCCAGGAGATGC	TTCTGGCCAGAGATTTTAGTTG
E2	318.2	ETV2	STS	AF012094	19	40810594	40811805	AGCTGTGGCAGTTTCTCTG	CGGCTCAGCTTCTCGTAG
E2	327.7	FCA1001	SSR	AY434982				ACATTGATTTCCAACTGCA	GAAGGATTTCTCCTGAAACG
E2	337.0	ATP4A	STS	AW646930	19	40717148	40730610	GGAACAGAAGAGGGGTGCTC	GGAACAGAAGAGGGGTGCTC
E2	353.7	FCA531	SSR	AF130648				AAGTTGTGAGCAAACTCAACCA	TTGGCAATCTGCCCTTTATCA
E2	363.1	FCA1002	SSR	AY434983	19	37296253	37298467	CAGACGCTATTTGGCTCTCA	AGTCCAGTACACCTGCATGG
E2	389.3	UQCRRF5	STS	AW646931	19	34374288	34380093	TCAAAGACACTGTTCTTTAAGTC	TGTATTTGCAAAACATTATGTGAAG
E2	431.5	PHKB	STS	AW646749	16	47235351	47474568	GGTTAACAGTCCACTCTTGAAAAA	GTGCTGACTTAGGGGTTGG
E2	459.3	FCA665	SSR					AACCTGCTGAGCCAGTG	TCGGAGAAAATTCAGGGGCT
E2	481.3	FCA1003	SSR	AY434984				AGGACTCGGTAGTGAGGCAA	GGCACACAGTTTGCAATGG
E2	493.2	FCA1004	SSR	AY434985	16	55733181	55735276	ACCTTCTCTGACCTCTCCTGC	GAGCAAGCAAGACCTTCC
E2	510.3	Fc.4288	STS	AW646932	16	57333853	57335723	GCCAGGATCTTTGAGTTGC	CCAGCTGGACCTAAGGACT
E2	541.3	FCA096	SSR	AF130519				CACGCCAACTCTATGCTGA	CAATGTGCCGCTCAAGAAC
E2	563.7	FCA1005	SSR	AY434986				GACCTTGGTGTAGACCATGC	TGAAATCATTGCCAAGACCA
E2	bin: LOD 0.02	FCA1006	SSR	AY434987	16	64972778	64975928	CTACTCTGCCAGGCACTATGC	CTCCTTGTAGTTCTCGGATTGG
E2	573.3	FCA1007	SSR	AY434988	16	65165422	65167470	TTGACAGCAGCCAAAGAAATG	CTGAGTAACATTCATTGTGGG
E2	573.3	FCA1008	SSR						
E2	580.6	TRADD	STS	AW646934	16	66923569	66929254	GGACACAGCAAGTGCCTAATGA	ACAGAGTGCATGGGTGACCT
E2	580.6	FCA1009	SSR	AY434989	16	67019328	67020178	ATTGGATGCCCACTCCTTTG	GAAGGTATTCCAATCTCTCCCC
E2	583.6	FCA075	SSR	AF130504	16	65317228	65317428	ATGCTAATCAGTGGCATTGG	GAACAAAATTCAGACGTGC
E2	587.8	FCA1010	SSR	AY434990	16	66286578	66287708	AGCTGAACCTTGGAAAGCAAA	CTGCCGATTGGTGTATCT
E2	600.3		STS	AW646933				ACAACATGATGGGCAATGTT	GTGTTTTGGGGGAACCATC
E2	615.1	FCA085	SSR	AF130513	16	72491055	72493154	CTGTACATTTCTCTCCATTGC	CCCTACTGGGTGCACTG
E2	627.4	FCA032	SSR	AF130485				GGCAATTGATGTAGAGAAAAA	CAAGATGCATTGGCGAGTA
E2	636.9	FCA1011	SSR	AY434991				TCTCCTTTTTAAAGGCTGAA	TAGCCAAGATTTGAAAGCATC
E2	649.3	FCA1012	SSR	AY434992				GCACTCCGGCTCAAAGATAG	TAGTTCTGGTTGACCCAGG
E2	bin: LOD 0.02	FCA1013	SSR	AY434993				GCCGAAATCGAGAGTCAGAC	TGGAGAGATTCCACAGTCC
E2	698.3	FCA586	SSR					CATGACAAATGCTGAGAAATGG	TGTATCTGGAAAGACAGAGCCT
E2	726.2	MC1R	STS	AY237395	16	89685585	89688677	TTTCATCGCTACTACGATCACA	CCCCAGCAGAGAAAGAAATG

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
E3	0.0	FLJ12566	STS	AW646935	7	4840400	4840520	ATGCTACGAGGAGACCAGA	TGTGATTCTAATTGGATCAGACG
E3	40.0	GNB2	STS		7	99866756	99874386	AGTACACTGGGGTGGCTCTG	GCCCTGTGCTCAGTCTTAA
E3	bin: LOD 0.62	EPO	STS	L10606	7	99916018	99918916	CCGAGAGGAGACAGGTGAC	GACAGGGGTGAGGAGTGGT
E3	bin: LOD 0.78	FCA466	SSR					TGCAAAATGGCAGGGTTTC	GATCAAGAAAATGACACACG
E3	61.7	MCM7	STS	AW646936	7	99287685	99297030	CCTGCCAGACGTTTAACCTC	AGTGTCCGGTTTTCAGAAGC
E3	77.8	ACHE	STS	AF053485	7	100085213	100091187	GGTGGATGGAGACTTCCTCA	AGAAAATGCACCCACGTTTC
E3	97.1	CUTL1	STS	AC092732/30	7	101005619	101473628	AATGCCATTTGGAGCATTTC	TTCCCTGGAAATTCGTGTTGC
E3	106.1	PMS2L11	STS	AW646937	7	75079198	75080498	GGAGAAACTGCCGTGGTGT	TCCTTGTCCCATTCAGTAA
E3	109.3	MDH2	STS		7	75275656	75295091	ACGCCAGAAACCTGAGGTAA	AGAAATCCGTGTCTCGTTG
E3	118.8	ZP3	STS	D45068	7	75625155	75669671	CTCTGTGATGTTGGGCATAG	GAAGCAGACACAGGGCAGAT
E3	140.8	FCA628	SSR	AF130678				CCCCTGCTCATTTCTCTCA	GTGCCTGGCACAGCATAAG
E3	147.6	NPD007	STS	AW646938	7	75106553	75116526	ACGCTGGCATGAAAAGAAAG	CGTGGGCTCAGGTGTAGGTA
E3	159.3	BCL7B	STS	AC091696	7	72348981	72370619	CGTTTTCTCAATCTGGCCTA	TGCTCCTGTTTACCCTGTG
E3	166.3	BAZ1B	STS	AC091696	7	71886448	72026348	TGGCAATCTCTGCCATAGTG	TCACAAACAAACCCAAAGTGA
E3	180.6	FCA1014	SSR	AY434994	7	72666798	72666848	AAGTCCACTGGGCAAGACC	AATGTTAACCCGACGTTGGAC
E3	202.4	ELN	STS		7	72840742	72882302	TGAGTGCCAGTACCAAGCTG	GCTCTCTGAGGTCCTCATGC
E3	219.0	GTF2IRD1	STS	AC091543	7	73266415	73415206	TGTGGCCAGTTATGCAATTC	GAGGCTGACTGGATGGTGC
E3	247.1	FCA004	SSR	AF130473				TCTAAGTGCATTTGGGATGG	ACTTAACCGACTGAGCCACC
E3	321.7	GUSB	STS	AF012423	7	64823489	64845010	TGCTGACAGAGCAGATAGCA	GCACCTCTGACATTCCTCTC
E3	362.0	RNF6	STS	AW646939	13	25636253	25726513	TCCGCTTATATTTCCGACCA	TAACCCACGTCTGTGGAAGG
E3	374.0	MVP	STS	AW646940	16	29829714	29857874	GGAGCAGCGTCAAGTATTTT	GGAGCAGCGTCAAGTATTTT
E3	430.3	FCA031	SSR	AF130484				GCCAGGGACCTTTAGTTAGATT	GCCCTTGGAACTATTAACCA
E3	460.8	Fc.28607	STS	AW646941	16	20863055	20863135	CAGCAGCTGGCTGATTTCTT	GGCCAAGCCCTGAGAAGG
E3	470.6	ZP2	STS	D45067	16	21136211	21150306	TGGTGGACTCAAAAGGGTATG	CTGTTCTTGCAGGTTAGTGT
E3	512.7	FCA1015	SSR	AY434995				GAGAATCCCCAGAGTTTCTGG	CAACCTTGGTTGTGCATTTG
E3	528.5	PRM1	STS	AW646942	16	11341131	11341280	AGGTGGCATTGTTCTTATAGC	TGGGGAGGTGTAGGAGAAGA
E3	552.8	PM5	STS	AW646751	16	14854857	14893512	AGATACAGGCTGTGCGGTTT	CAGCGCTGTTTGTGAGAA
E3	587.3	FCA476	SSR	AF130630				GACCTTGAAGGAAAGGAGG	CCCTTTTCTCATGTTGTTACT
E3	611.5	PKD1	STS		16	2079409	2079658	GGTGTGATGTGGCTCCTCTC	ACATCCCACTCACCTTGAGC
E3	633.1	NY-CO-7	STS	AW646752	16	6727593	672746	GGGCTCACAGATTTTATTACAGG	ACCTGTCTGGGCCAAAAAC
E3	662.9	ZNF263	STS	AW646943	16	3333772	3341739	CACACTGAAAGAGATGCAACG	TTGCTGTGCAAAATGAGGTC

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
F1	0.0	FCA1016	SSR	AY434996				TGGTGACAGAGCATCTGCTC	AAACGTTTGAAGGTGTGCC
F1	55.5	CD3Z	STS	CC596509	1	164095901	164183913	GTCCCAACAACACAGAAGA	ATTGGTCACTCCATTTC
F1	89.4	Fc.97375	STS	AW646945	1	168911153	168911303	GGATCCAAATGTGATCTCAGC	GCACITGGCCTCAGAAAGAC
F1	106.8	KIAA1096	STS	AW646944	1	168035475	168143428	CCTTAGGAGGAAGCCTGGT	GTTCCAAAAGGAGACCACA
F1	127.1	FCA344	SSR	AF130613				CCAGAAATGCACATCCTACC	GATCAATGCACATGAGCAGGA
F1	171.2	FCA1017	SSR	AY434997				CATTAAGAATAATTCATCCATTAAGAA	CACAGAAACGGAGACGACAGC
F1	211.6	SERPINC1	STS	AZ081281	1	170453816	170467364	TGGAGACAAATCCCTTACCTTC	ATTGGCCTTCGGTCTTATT
F1	235.0	LAMC1	STS		1	179512811	179634985	ACGAACCCAAAGTTCTCAAGTC	TGTCCATGCTCCATGGTG
F1	245.4	Fc.112017	STS	AW646947	1	179389277	179392477	CCATTTCTGTGGGATATGAGA	GCAGAAAGCCTCAACAAGG
F1	272.3	FCA1018	SSR	AY434998				CATCACGGTCTCGGGAAC	CGTGTTTCTTGTGTCCGG
F1	299.3	KIAA0475	STS	AW646946	1	175575898	175604642	TGCATATCTGGCTTGTITGG	AGGAGGTGTGGGAACGAGTA
F1	320.9	PDC1	STS	L35314	1	182932583	182950099	CTAATCCACCGGACAAAAGA	CACAGCCTTAATGCCATCT
F1	342.2	FCA1019	SSR	AY434999				GATCCTGAAACTATACACAGAATTT	AGTGAGCATCCACGTTAGC
F1	357.2	FCA1020	SSR	AY435000				GAGCCCTGCTATCATTCAA	CCCTTCCCAGTTCGTGTG
F1	360.1	FCA1021	SSR	AY435001	1	210818617	210818867	TTAGAGGAATCATGTGCACACC	TACACAGCAGTCAATTTCTGG
F1	370.8	FCA1022	SSR	AY435002				CTAGTCCAGCTCCAGCAC	CTGCCCTTGGGAGTTCT
F1	373.4	FCA1023	SSR	AY435003				TGTACACAGGGCAACTTAGG	TCAGGGCTCTCACTCCCTA
F1	384.2	FCA1024	SSR	AY435004				GGCAGCTGCATGGGCTTC	GCACCCATCAAGGAACAA
F1	393.6	FCA223	SSR	AF130573				CTGGGCACTAGGTGTGAC	GGTCTTGGATTAGAACCAGGG
F1	395.6	FCA1025	SSR	AY435005				AAAGGACCTCAGCACCTTCA	TAGGCCCTCTCACTTTGTG
F1	404.0	JRF6	STS	AF459808	1	206600217	206600317	GGGTCTGTTGGACGTCACT	GCCACAGCTTATCTTATCC
F1	408.0	FCA1026	SSR	AY435006	1	204715917	204715967	CCCTTTTCTGGTTTGAAGTCC	CAAAACATGTTTGCATGC
F1	408.0	IL10	STS	U39569	1	203584364	203589226	ATCTGAAACATGGTGGGGAA	TCCAAGGAGCTGTTGGTTC
F1	429.7	FCA1027	SSR	AY435007				CAGAGACCTGTGCTCTGATG	ACAGGGAGAGGAAGACAGACTG
F1	440.5	TNNT2	STS	AF220219	1	197794598	197808915	AGGTCTTCTCTTTTACCC	GTCAGAAGGGGACACAGG
F1	461.7	LOC51706	STS	AW646948	1	199396998	199397048	TCCCAACGCTTTCTTTTG	TCCCAACGCTTTCTTTTG
F1	474.8	FCA1028	SSR	AY435008				ACACTCTTAGGCCTCATCTCG	CTTCTCTGATTACAGCACGTG
F1	495.0	FCA191	SSR	AF130560				TCCTGTTCTATTACCCTACA	GCATGGCACTTTTGTGAGA
F1	529.2	FCA120	SSR	AF130529				CCTCCTGCTCTTTTCCATCA	CTCCTCACTGAATTTTGTAGCA
F1	570.7	FCA1029	SSR	AY435009				TCCAGAGGTTGCTGAGAAAGT	GGTTCATAGTTCCTCAAGTGC
F1	604.7	RPS27	STS	AW646950	1	150738543	150739928	GGGGTGTACAAAATCACCA	CTCAGGGTGGTGTAGTGCT
F1	613.0	GBA	STS	U85409	1	151982117	151992323	AAAAGCTTCGGCTACAGCTC	CTGCTGGCAAGACTTAGCTC
F1	618.4	PKLR	STS	U82191	1	152037504	152049085	CTCTTCCAGCCTGCCTCT	TTTGAGCCAGAAAACCTTC
F1	621.1	CCT3	STS	AW646949	1	153056634	153085970	ATTACGTGTACGGCCTTTT	GAAGAAGGTTGACGACCAGA
F1	635.5	FCA1030	SSR	AY435010				CTGCAATTGATTTGAGTGTCT	CCCACAGCCAGAAGAACTT
F1	638.0	FCGR3A	STS	AB025315	1	158289045	158297247	CACAGTGGCTCCTACTTCTGC	TGATGTTACAGCCTCTGATG
F1	644.6	FCA1031	SSR	AY435011	1	161578555	161580755	GAGCTGGAATCGTCTCTG	TCGTGACCTGGCTGAAGTC
F1	656.6	FCA1032	SSR	AY435012				CTGGGCTCAGTTACTCA	CTCGCATGCAGTCAATTA
F1	664.9	FCA1033	SSR	AY435013	1	159857655	159859155	CCGCTTTTTGCCAAGTTGT	CTTCGTTGCCAATCCCC
F1	693.5	FCA1034	SSR	AY435014	1	186338948	186348198	CCCAGCAAACGGTAACCTTC	GATCCTTAATAGTCTCAATCTCA
F1	726.2	TGFB2	STS	AZ081282	1	215123128	215219029	TCGTGGCTCCAAGAAAACCTT	TCGAGAGTCAACGTCCAATG
F1	783.8	FCA1035	SSR	AY435015				TGGTGCATACAAATTTAGGA	TCAGACAATACACTCGGGA

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
F2	0.0	FCA136	SSR	AF130538				GAATGACATCGCCAATGAAA	CCCCCCCCAACTGATACTT
F2	63.4	KJAA0203	STS	AW646951	8	53258204	53350176	AAACCTGAAACAAGCCTCCTC	TCTGTACAATAGAATTGTGTAACCTCG
F2	bin: LOD 0.17	MOS	STS		8	56749866	56749726	CTGGGAGCAGGTGTGCTT	GTTGAGCTCAGCCCGAGAAAC
F2	105.6	PENK	STS	U24247	8	57076702	57082447	ATTCTCAAGATGGCACCCAG	ATGAAGCCCCGATCTCTT
F2	145.9	FCA1036	SSR	AY435016				CTCTGCATCAGTGCCGTG	TGTTTTGCTTCTAAATGCAGG
F2	182.0	FCA220	SSR	AF130571	8	65228774	65230824	CGATGGAAATTTGTATCCATGG	GAATGAAGGCAGTCAAACTAG
F2	199.5	FCA502	SSR	AF130638				TCTCTGAAGTGGTTACAAAGGA	ATGAGCAAAGTTATGTTTGACA
F2	214.0	CRH	STS		8	66811804	66814009	CAGAGGCCATCCGAGGAA	TGCTGCCCTAAGCTCTCA
F2	239.4	FCA294	SSR	AF130599	8	73434574	73436724	GGTGTTTTACTCAAGCCTTGG	ATGACACCATGTTCTGCCA
F2	244.7	FCA672	SSR	AF130689	8	73317624	73319824	AAGTTGCTGCACACACTGC	TCCAAGAGCCTTTTCAGTTAGG
F2	261.9	FCA1037	SSR	AY435017	8	80990282	80992470	GCTCTGCAACTACAAATTCATGC	GGGAAAAACCAAAACCAGT
F2	268.6	FCA602	SSR	AF130671				ATCATGGCCTGAGCTGAAGT	TGTATGTGAAGCCACCAACG
F2	289.2	FCA1038	SSR	AY435018	8	79746382	79748832	ATCCCTAAAATTTCTTCTGCACA	TGCCCTACAACAACCAACA
F2	317.3	FCA350	SSR	AF130617				TCAAAAATCTTTTGTATGGTTGA	CTATGAAAGGCCAAAGTGTCC
F2	363.8	FCA170	SSR	AF130552				CAAGGCGTTTGGTATTTTGG	TTTACAGTCTCCCTCCTGATGC
F2	388.7	FCA1039	SSR	AY435019	8	96696060	96698110	AACAGCCTTAGCTGGCAA	GATCAGCTCTGGCTCACATATT
F2	423.3	FCA1040	SSR	AY435020	8			GAGCATTCTCTGTGGAT	CCTGTTCTGCACCAAAGGTT
F2	433.0	FCA1041	SSR	AY435021				CTCATCTGAGCAGTGACCA	TCAGTTCTCCGAAGCACTT
F2	456.4	FCA1042	SSR	AY435022	8	104300210	104302310	TGTTCTTCACTGCCAGATG	GAGTCTTAAGCAGGTTCCATGC
F2	468.8	FCA506	SSR	AF130639	8	107513510	107515610	AATGACACCAAGCTGTTGTCC	AGAATGTTCTCCCGCTGT
F2	483.6	DC6	STS	AW646952	8	110015363	110026972	AACCAAGTGGGGCAAGATT	ACCAAAGCTGAGCCAGAAAA
F2	513.4	FCA094	SSR	AF130518				TCAAGCCCCATTTTACCTTC	CACCTGAGCCAAAGGCTATC
F2	bin: LOD 0.24	FCA1043	SSR	AY435023	8	121976010	121978110	GACTGAGAAATGCTTGTGGTG	CCATATTTGGCAATGATGACC
F2	550.3	FCA1044	SSR	AY435024				CCTCATTCCCTGATACGCAT	TGGGTAATTTTGGTAGTCTCCG
F2	562.7	FCA1045	SSR	AY435025	8	124802571	124804852	GCTGGATTCTGGCAGTAAA	GCATCAAAGCAAAGTTGATGA
F2	572.7	FCA1046	SSR	AY435026				TGGTTATCCTCTACTGTTGGGG	TGAGAGTTGCCATCTGTGTACA
F2	588.0	FCA748	SSR		8	118945920	118948977	CCCACAATACCATATGCTTCA	TTAGAGACTTTTCTTTGGTCTTTG
F2	609.3	MYC	STS	M15078	8	128418563	128424554	TACCCTCTCAACGACAGCAG	GGCTGTGAGGAGGTTTG
F2	613.2	FCA111	SSR	AF130525				CTTGAGAAAGAGAGAAAGAGAGGG	GCCTCTATCAGTATGGAGCC
F2	624.4	FCA750	SSR					TTGGCCATGAGTTCAAGGTT	TTCTGTTAAGCAGTGTTTGC
F2	628.0	FCA1047	SSR	AY435027	8	134537120	134539163	CTCCCATGACAGCAGTCATC	CTGCCATGACATCTTTCCAG
F2	630.3	FCA749	SSR					CTGGGGAGGAGCTTACTTA	GATTTGAAAGAGGCCAGCAG
F2	630.3	TG	STS	AF071756	8	133550088	133817997	CAGAGCCTCAACGAGATTCC	CTGAGCCAGCAGACTGAG
F2	637.8	FCA1048	SSR	AY435028				CAGCCAAACCCGAAAACC	CCCTCTGAAGCCTGCTC

Cat Map (supplemental data)

Cat Chromosome	RH positon	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
X	0.0	FCA1049	SSR	AY435029				CCAGAAGGATTAGGCAGCTG	CTGAGCTGGACTCTGCACTG
X	99.9	FCA478	SSR	AF130632				TATATGTATGTGGCCGTGTACC	GATCGTGGTTTTTGACACTTG
X	120.8	Fc.estTGF10	STS		X	16064738	16089692	TTGCATATCTGGGAACAGCA	TCCCGTTTTAAAATGCAAG
X	130.8	FCA240	SSR	AF130580				TCTTTAAGATGGCCGGACTG	TCCCTCAAATATGCAAAGG
X	140.1	AMELX	STS	AF114709	X	10607902	10615250	TTCCCAATTACCAGCTTCTCGT	CCCCAACTTTTACAGGCTGA
X	169.2	PHKA2	STS	AF197961	X	18112927	18204321	GTGGCAATCCAGGAAAGT	ACAAGCACAGGTGTGATCAG
X	189.7	ZFX	STS		X	23369816	23434575	TGGCCAGATGGACATCC	AATGCTTCCGGACTCATCG
X	201.4	EIF2S3	STS		X	29435728	29440260	unpublished data	unpublished data
X	211.2	MAGEB2	STS	AY052501	X	28733179	28737711	TTAGCGATGTGAAAGAATCTCA	TTGAGCAACTTGAAGTCTAAATCTC
X	220.9	FCA1050	SSR	AY435030				AAACCAGACATCAGCCATTT	ATGCTTACTCTTTGCCAGG
X	228.3	MAGEB3	STS	AF325359	X	29450607	29457683	CTGCAATTGCCATCTTTTTG	CAGAAGCAGAGTACATGGAA
X	261.5	DMD	STS	AF197958	X	30339399	32559780	AAGTGGAAATGTTGCCAAGG	CACACACACACACAGCATT
X	279.9	OTC	STS		X	37053547	37125257	GAGGTATGCCCTTATATGTAAGTT	TGTAATTAACACCTTGCTCCA
X	286.9	DFFR	STS	AF197970	X	39827422	39936785	CTGTTAATCTTAAAGCAAGAAAC	TTGCAGAGTCAATGGGTAG
X	290.7	Fc.estTEB11	STS		X			CAACCAGAACCCGGAGCAT	CTGGCTCGGGAGCTTCAC
X	bin: LOD 2.58	DBX	STS	AF197969	X	40037250	40068323	CAGATTTCTCAGATGTTTTGTC	ACATGTTGAGGATAGCAATGT
X	316.5	MAOA	STS	AF197960	X	42303086	42430386	GGCACTACTCGGATATTCTC	ACTTGACCAGATCCACCTAC
X	334.6	PCTK1	STS	AW646954	X	45914482	45914590	GCCTTCGGTCTCTGCAAT	CAGCATGAGTCAGGAGGTA
X	bin: LOD 0.05	UTX	STS	AF197965	X	43559086	43771798	GACGAATCTAGCAACCAGC	-CCTGAGTGTATGGGGAAAC
X	bin: LOD 2.12	UBE1X	STS	AF114711	X	45879624	45900855	GCACGGGATCTCAGAAGA	AATGCCAGGTAAGGAGA
X	374.9	ARAF1	STS	AF197956	X	46246836	46257634	GGACCTCAGCAAATCTCCA	GCCTAATGGGGAAGTACATC
X	394.5	FLJ10628	STS		X	49917720	49917856	GGCTGTCCGAGAGTGTTTC	ACCGAATCTCCAATCCTC
X	407.9	SMCX	STS	AF197964	X	51860958	51894109	CCCCACACTAGATGCAGAT	TCTCTCCAGACCTCTCCA
X	415.9	ALAS2	STS		X	53652922	53653050	CAGAAACAGGCCCTGTAA	CCTCCAGACTTCTCAGCA
X	458.9	FCA651	SSR	AF130684				CAGGGGCCCTGATTTCTAG	GGCCTACAAATGGCAAGA
X	548.2	IL2RG	STS		X	68559989	68564635	CAGCTCTGAGCCCATCC	CCCTCTCCCTCTCATACCA
X	564.4	RPS4X	STS	AF114710	X	69725120	69730364	TGATGGCAAGGTCCGAACTG	TGGTGTATAGATCAGGCGG
X	579.1	XIST	STS	AF197966	X	71260866	71261050	TGTTCCAGGCCAATGAGAAG	CACCTGTCCAGGACCAAT
X	591.1	ATP7	STS	AF197957	X	75207369	75347151	CTCTCAAGTCTCTGGAGAA	CATCAAATCCCATGCTTCTAT
X	603.3	FCA018	SSR	AF130480				CCCGGATATGGGTTTTTCAT	ATCCAAAAACACAGACAACA
X	660.2	BTK	STS	U82179	X	98640164	98676911	AACACAATCCTGTCTCCATCA	TTGAGTCAgcaagtggagctg
X	670.5	PLP	STS	AF197962	X	101064735	101080475	GCAGATTTACCTATGCCTCA	CATGTGGGCAAAAGCAAGT
X	684.0	FCA674	SSR	AF130690				TGTTGAAACAATGGCAGGA	GAAACAGCCTAAGTGCTGC
X	693.7	FCA145	SSR	AF130543	X	105840097	10597255	CCTACCTGCTGACTGTGTGC	AACTTTTGAGGAAGCCTGGG
X	714.7	TNFSF5	STS	AF079105	X	133675132	133687329	CAGTTCTCCAAACCCTGTG	TAAGCCAAAAGACGTGAAGC
X	738.5	FCA1051	SSR	AY435031				AGTCCCGTAGCCGTAATCT	CCCTGGAGCAAAGAATGTGT
X	776.3	F9	STS	AF459805	X	136557675	136590397	GGCCAAAGAGGTATAATTGAGG	CAACATACTGCTTCAAATTCAG
X	809.9	IDS	STS	AF197959	X	146459032	14650975	ACATTGACCACTGGCATCC	CACCGACATGGTCACTATG
X	821.4	BGN	STS	U82178	X	150346142	150360702	caggaaggctcagggagag	TTCAAAGCCACTGTTCTCCAG
X	836.1	FCA311	SSR	AF130605				CTCCCAACTGCTCCATCACT	GGTGTAAAGCCCTCCACAAA
X	846.8	MPP1	STS	AW646956	X	151592619	151592786	GATGCTTCCAAGACCAATGAA	CTGGCTGGGCTATGACTCTC
X	851.1	OPN1LW	STS	AF031532	X	150995461	151010210	CATCTTCTGGGAGAGGT	CAAATCCAGGAAAGGCAAT
X	864.2	TKTL1	STS	AW646955	X	151109853	151144403	TAAGAGATTTTCCGGCTGCT	GCTGCCGAGTTCGAGAGTT

Cat Map (supplemental data)

Cat Chromosome	RH position	Locus	Locus Type	Acc.Number	Human Chromosome	NCBI Human Build33 Start	NCBI Human Build33 End	Forward Primer	Reverse Primer
Y	0.0	FCA751	SSR					AAGAAAAGCTGGAGGCATCA	ACCATGTGCTTGTGGGGTAT
Y	82.8	FCA1052	SSR	AY435032				TCCAGAGCAAATGAGCTTCC	GTGGGACTGTTTGGAGCTG
Y	116.8	SRY	STS	AF114712	Y	2562646	2563491	GTTGAGAGTATTGAGCAGCG	ACTGTCTTGGAGGTTTGTGG
Y	138.8	ZFY	STS		Y	2729728	2756029	AAATGGTGCATAAAGAAAAAGC	TGGGGGTAGCTTTTCGTGT
Y	142.0	SMCY	STS	AF114714	Y	21063998	21103497	TCGCTCTAAAGCTCCCTTTT	GGGAGAGACAGTCCCATGA
Y	153.5	AMELY	STS	AF197967	Y	6699535	6707645	CCCAGCACACTCTATTGG	GGAATTCAGCTGCAAAAGGA
Y	160.6	UBE1Y	STS	AF114713	Y			ACCTTGGGGCAAATCATGTA	CCAAGCACTCCCTTGTGAT
Y	175.3	DFFRY	STS	AF197971	Y	14123306	14282242	GCAGAAATGCAGCAGACGTAA	CACCTGCAGGGGAAAGTGA
Y	182.5	DBY	STS	AF197972	Y	14326923	14342537	TGAAGAAACACTTCCAACATTG	ACTGAAAATGTTGCTGGATGAA
Y	189.7	UTY	STS	AF197968	Y	14670482	14902719	CCTCTACACTGCAGGAAGAA	GGGAAAAGTACTGACATGGA