Supplementary Table S2: Primers Used for Linkage Analysis, RT-PCR and cDNA Amplification and Genomic Amplification

Locus	Cat Chromosome Position[*]	Repeat Motif	Cat Chromosome Position of Candidate Gene	Forward Primer	Reverse Primer	Expected PCR Product Size (bp)[†]
A. Candidate Genes for Linkage Analysis						
CRX-STR-1	chrE2_4411323	GT(17)	chrE2:9878631-9888696	AAATGGGAAATGATCACACCA	GGATTTGAACCTTGGTAGCC	180
CRX-STR-2	chrE2_8469995	GAAAA(11)	chrE2:9878631-9888696	AAGCCCACTTGGGATTCTCT	AACCCACAAACTGCAAGACC	212
CRX-STR-3	chrE2_9124338	TC(17)	chrE2:9878631-9888696	TTTGATTCCCCTTCCTTCCT	CCAGACCGAAAGAGCAAAAG	240
CRX-STR-4	chrE2_9844244	TGT (9)	chrE2:9878631-9888696	TCTCAGCCTACAGCCCTCAT	TACTCCAGGCCATGTTGGTT	195
CRX-STR-5	chrE2_9869856	TC(12)	chrE2:9878631-9888696	CCCTTTCTCCCTGTCCCTTC	TCAAACTCACACGGATGGAA	193
CRX-STR-6	chrE2_9930046	GATA(12)	chrE2:9878631-9888696	CATCAGTGGGTGGATACGTG	AGGCTGAGACCTCACCTCAA	187
CRX-STR-7	chrE2_10072470	AC(18)	chrE2:9878631-9888696	CAACTCTGAGCTGGGTCTCC	TGGAGCCTGCTTCATACACA	213
CA4-STR-1	chrE1_51619418	GT(14)	chrE1:51615939-51626834	ATTGTGTGGTGAGGGTGTCC	CTGCAAGATTCCCCTCATTC	153
CA4-STR-2	chrE1_51622966	AC(13)	chrE1:51615939-51626834	CTTTCTGTGTGGTGGGGACT	CAGGGACGATTCAGGTCACT	196
FSCN2-STR-1	chrE1_132791160	TG(16)	chrE1:132815471-132821820	AACACGTGGTCGCATATAGAAA	GTCCGTTTCCTGCTTCAGTC	238
FSCN2-STR-2	chrE1_132790694	TG(16)	chrE1:132815471-132821820	TAGGGGTGGAAACATCGGTA	GGATGTCCTTGCTTGTAGGC	166
GUCA1B-STR-1	chrB2_43336600	CA(12)	chrB2:43329491-43359312	GCTGTAGCAGTTCACCATGC	CCATCTGACTCCACACCTGA	151
GUCA1B-STR-2	chrB2_43349835	GA(23)	chrB2:43329491-43359312	AGGTCAGGGGTCAGTCTGTG	TCACAGCTCGTGAGTTCGAG	250
IMPDH1-STR-1	chrA2_211262168	GT(23)	chrA2:211178423-211195849	CCTGGTGACAGATTCCTTCC	GGGGGAAGTCACCAACTTAGA	176
IMPDH1-STR-2	chrA2_211280113	TG(18)	chrA2:211178423-211195849	TCTGCCCTTTGGCTCTTCTA	TGGGGCCTAATCCAATATGA	234
NRL-STR-1	chrB3_81136567	AC(13)	chrB3:81226799-81263900	CCAAGACAGGCAAGGGTAAA	AGCCCTTTTATCGGGTGAGT	209
NRL-STR-2	chrB3_81320847	AC(24)	chrB3:81226799-81263900	TGCCTCTCCTGAGATACTCCA	AGTTCAAAAAGCAGGGCAAA	246
PRPF3-STR-1	chrC1_110561470	AC(21)	chrC1:110537087-110565694	GGCGCCTCTTGAAAGAAGTT	AGGTCTGCAAAGGGGAGAAT	205
PRPF3-STR-2	chrC1_110445958	AC(18)	chrC1:110537087-110565694	CCCTTTGCCAATTTCAGAGA	ACGAGAGGTGGAACATGAGG	210
PRPF8-STR-1	chrE1_40285203	AC(15)	chrE1:40456491-40487323	TGTGCTAAGTGGGCTCACAG	TCACATCTGGTTGGTGTAGGA	163
PRPF8-STR-2	chrE1_40586866	GT(13)	chrE1:40456491-40487323	GTTTCTTGGAGGCTGTTCCA	GTAACAAAAGCGCCAAGTCC	150
PRPF31-STR-1	chrE2_3789762	CA(21)	chrE2:3841459-3861551	CCTTTTGCAAGTGGGATCAA	GATTACTTTGCTGCTGCTGCT	245
PRPF31-STR-2	chrE2_3748602	GT(20)	chrE2:3841459-3861551	CCTGTTCACCAAACCCAGTC	AGAGCTCTGGAAGGGGAGAG	188
RDS-STR-1	chrB2_43933483	CA(12)	chrB2:43925525-43956328	TGCATCCCTGTGTTCATTGT	AGATCCACCCACATTTTTGC	210
RDS-STR-2	chrB2_43919963	AG(25)	chrB2:43925525-43956328	GCTCTCGGTAGAGCATGGAA	AAGCAGCCAGAGGAGAAGTG	237
RHO-STR-1	chrA2_61216010	GT(18)	chrA2:61166303-61173482	GGGTAAAGGGTTAGGGAACG	TTTCTAAGTGTTTGACCCACTACC	156
RHO-STR-2	chrA2_61247220	AC(21)	chrA2:61166303-61173482	ATCAGTCCCCCTTGTCTTGA	CACCCTGGAGAAGCTCATGT	223
ROM1-STR-1	chrD1_134733919	TG(20)	chrD1:134776545-134778178	CCGCATAGTTCTTGCTGACA	GGAAGCTCAATTCCCAACTG	209
ROM1-STR-2	chrD1_134766392	GA(13)	chrD1:134776545-134778178	AGCACGCAGTAGTGAAGAAGG	GGTTGTGGGATGGAGACTTG	243
RP1-STR-1	chrF2_2382646	TG(16)	chrF2:2385740-2447214	ACCCCTTTGGGTTTCTTCAT	CCAGTTGCAGAAACACTGTCA	204
RP1-STR-2	chrF2_2458258	GT(14)	chrF2:2385740-2447214	CAAGGTGAGCCCATGATTCT	ACGGTAGTGCATGCCAGAAG	210
RP9-STR-1	chrA2_181685918	AC(20)	chrA2:181685950-181886624	CTGGGCTTTGTACTGGGTGT	TTCTGGAAATCCCTCCTTCC	235
RP9-STR-2	chrA2_181649004	AC(17)	chrA2:181685950-181886624	ACCTGAGCTGAAGTCGGATG	TTTGTGCTGACAGCTTGGAG	228
RP31-STR-1	chrD4_46253243	AC(20)	chrD4:46221928-46233690	GGGGTATATGCACCCTGATG	CACATGGTTGCAAATGGAAA	202
RP31-STR-2	chrD4_46126200	TG(21)	chrD4:46221928-46233690	TGGCATGTGGGCTTATATTTC	CCATATTATGTGCTGGCAAGT	187
RP33-STR-1	chrA3_82132784	GT(15)	chrA3:81.95	GGGAAGTTTGTGCAAAGGTG	AAAGCTTGTTGAGCTGAGATGA	206
RP33-STR-2	chrA3_82037512	GT(22)	chrA3:81.95	GTCACCTGGAACTGTCAGCA	GATGGGGAAGAAGCTCACTG	222
SEMA4A-STR-1	chrF1_87839498	AG(22)	chrF1:87605971-87632039	GAGGCTAGATCTGGGGCTCT	TCAGGCTCTGTGCTGACAGT	207
SEMA4A-STR-2	chrF1_87556640	GT(12)	chrF1:87605971-87632039	ACCTGACTCCTGGGATTGG	TGGGGATGGAATTAGTTGGA	159
NR2E3	NT[‡]		chrB3:42128408-42147338			
RDH12	NT		chrB3:116962316-116979737			

Primer Set Name	CRX Amplification Region	Cat Chromosome Position of Amplified Product[§]	Forward Primer	Reverse Primer	Expected PCR Product Size (bp)
B. RT PCR and cDNA Amplification					
CRX-PCR-1	Exon 1 to 4	9878864-9890005	GGCTTTGCCATCTGACAACT	CGGGACTCCAGATGGACA	600
CRX-PCR-2	Exon 1 to 3	9878770-9888437	CCAGGATTACCCTCCGAGAT	GGGCAGGTTGATCTTCAGAG	436
CRX-PCR-3	Exon 2 to 4	9887379-9890165	TGCACCAAGCTGTGTCCTAC	TCCAGGCCACTGAAATAGGA	583
CRX-PCR-4	Exon 3 to 4	9888410-9890096	GGAGGTGGCTCTGAAGATCA	GTGTAGGTCATGGCGTAGGG	378
CRX-PCR-5	Exon 1 to 4	9878770-9889778	CCAGGATTACCCTCCGAGAT	CGGTTCTTGAACCAAACCTG	468
CRX-PCR-6	Exon 3 to 4	9888410-9890451	GGAGGTGGCTCTGAAGATCA	GGTTCAGACGGTTCAGACGA	739
C. CRX Genomic Amplification					
CRX-PCR-7	Exon 1	9878770-9878960	CCAGGATTACCCTCCGAGAT	CTCTTCCCTCTGCCACTCCT	191
CRX-PCR-8	Exon 1	9878654-9879052	ATCAGCCCTAATTGCCAAGA	CTGTACCGGGTGCTGAGAA	399
CRX-PCR-9	Exon 2	9887144-9887518	ACGAACCACGAGATCCTGAC	CATTTGGTCTGTGGCTCTGA	375
CRX-PCR-10	Exon 2	9887176-9887425	CTGACGCTTCACCAACTGAG	GCCAGGAGAAGGACCGTA	250
CRX-PCR-11	Exon 3	9888377-9888625	CAAGACTCAGTACCCGGATG	CTGGGGGAAGAAGCAGCA	249
CRX-PCR-12	Exon 3	9888138-9888437	GACGGAGTGAGGGCTACAAG	GGGCAGGTTGATCTTCAGAG	300
CRX-PCR-13	Exon 4	9889916-9890165	TGGGCATCTCAGACTCCTACA	TCCAGGCCACTGAAATAGGA	250
CRX-PCR-14	Exon 4	9889914-9890296	CCTGGGCATCTCAGACTCCT	GGCTGTAGGGACCGTAGCTC	383
CRX-PCR-15	Exon 4	9889983-9890422	CACGGTGTCCATCTGGAGT	ACAGAGCTGGCTTCTACA	444
CRX-PCR-16	Exon 4	9889762-9890005	GTTTGGTTCAAGAACCGCAG	CGGGACTCCAGATGGACA	244
CRX-PCR-17	Exon 4	9890355-9890631	CACGGACCCCTTGGACTAC	GGGCTGGGTTGAGGGTTAC	277
CRX-PCR-18	Exon 4	9890264-9890661	CCCTGTCAGGCCAGAGCTA	CAAAAGGCAGCTAAGAATCCA	398

[*] Position based on 2x cat sequence assembly from GARField of STR used in linkage analysis. [†] Expected PCR product size is the size expected based on amplification of the locus described in column 2 characterized from the 2X whole genome cat sequence assembly. The expected product size does not include adaptors to primers. [‡] NT not tested.

[§] Location of all Exon 4 primers are estimated based on new sequence generated in this study and subsequently aligned with GARField 2X assembly.