

Appendix 1. Oligonucleotide primer sequences. PCR primers with their product size range and annealing temperature (T_a) for the amplification of markers flanking the canine cataract candidate genes are presented.

Gene	Position on canine chromosome (Mb)	Name of microsatellite/SNP	Position on canine chromosome	Sequence (5' – 3') of primers	T _a (°C)	Size range (bp)
<i>CHX10</i>	CFA8_50.50	<i>REN288F11</i>	CFA8_51.36	ATTAGCAGAAGGACGGGGAT GAGGGTTTTAGGGGTCAAGG	55	270
<i>CRYBA4</i>	CFA26_23.30	<i>REN01O23</i>	CFA26_23.32	TTCCCTGCAGCCCTTCCTCA TGTGCCTCATTCTTTTAT	55	192-202
<i>CRYBB1</i>	CFA26_23.29	<i>REN01O23</i>				
<i>CRYBB3</i>	CFA26_22.32	<i>REN131L06</i>	CFA26_23.08	GGCTTTTATTTTCCCATCAT ACTTGCTAAAAATCCACTAAA	55	114-130
<i>CRYGB</i>	CFA37_19.45	<i>REN105M20</i>	CFA37_19.63	ACCCCTGATAACAACCTTAGT TAAAACAACAATTCATCTGTC	55	137-151
<i>CRYGC</i>	CFA37_19.44	<i>REN105M20</i>				
<i>CRYGD</i>	CFA37_19.43	<i>REN105M20</i>				
<i>CRYGS</i>	CFA34_22.17	<i>REN266K05</i>	CFA34_21.98	CCACACTCCAAGCTGCTACA TTTGTGGCCACCTCTATTC	55	329-337
<i>SPARC</i>	CFA4_60.87	<i>REN195B08</i>	CFA4_60.34	GCTTTCCTATTGTGTCCTCA TGATTGATGCCCTTTCAACA	58	132-140
<i>SIX5</i>	CFA1_112.73	<i>FH2598</i>	CFA1_112.01	CCTTGACTCAGCAGCCCTAC CGACCTATCCATACATGCCC	58	309-405
<i>SOX1</i>	CFA22_62.86	<i>REN202B14</i>	CFA22_63.77	GGCCTGCTTACCAAATGTGT AGAAGCCGTGAAGAACAGGA	55	139-149
Additional markers on CFA1						
Microsatellites		<i>FH3322</i>	110.55	AACAGGCGGATTCTGTAGC CTGAACTGGTCCCTCAAGC	58	344-358
		<i>FH3505</i>	110.81	ACTGGCCAAAGAGTACAAGG AGTCATGCTGATTTCTGTGC	56	190-244
		<i>FH3922</i>	35.33	TTTTGTCAAGCAGCCCTATATC TGGCCTTTAATTTATCATGGAG	60	462-554
		<i>C01.424</i>	58.80	AGCTTAGCTTACTGCCCTGG TCCTTTGGTTTTTAGCAGGG	58	187-193
		<i>FH3894</i>	80.18	TTGCCACAAATCACTTAAAGG GCAAAGGTGTATTTACATGATGG	58	228-264
		<i>FH2309</i>	85.77	GACTGAGTTCTTTCAGCACAGTG GGCAGCCTTATTATTCATGGA	60	361-413
		<i>REN06N11</i>	105.96	AAAATAACACAGCATCAGG ACACAGGCACAGGAGCATC	52	347-350
		<i>FH2294</i>	115.87	GGGTCCTGGGATCAAGCC TTAGTAAAGAGACAGCTGATTGCC	58	208-220
		<i>FH3652</i>	82.738	TGATTGAACACAAAATGAGAGC GACACCAAATGTCTGTTTCTGC	60	221-233
		<i>REN192P12</i>	83.769	TGCTGTATGTCAACAATACTTCAAT GCACTTTAGAAGAAAGCCTGG	60	150-158
		<i>FH3883</i>	96.397	GGTGAATCAAGAAAGCATGG TTCCAGGCTAAGGAAAATAGC	58	256-276
		<i>REN123E09</i>	104.696	CTGCGCCAGAAGTGTCAT TGTTTTGGGAAGAACTCAGTC	58	92-104

<i>FH2774</i>	104.893	AGCACATCAGAGCTTGCTTC GCATTTTCAGCACCTTCTGTC	58	157-165
<i>REN47D17</i>	85.993	GGCACTTGAGCTCTAATCCTA TGCTAATGAATCCACAGAATG	58	328-350
<i>FH3120</i>	87.172	GATGAATAAACGAAGCACAGG GGTTAGTCTTTAAACCCACACG	58	281-283
<i>FH5120</i>	91.983	CAGAGCCATAGCCCAAGAAG TTCAGGTGAGGTTGATGGAC	58	460-480
<i>FH2793</i>	97.844	CTATGTGCACGCTGAGAGAG TACCATAAAAGTTGGGCTTG	58	192-208
<i>REN211B17</i>	100.644	CTTACTCAATCCCTCCGTGC GGTTGCATGTTGCAAAGAAG	58	218-228
<i>C01.643</i>	102.041	AAGTCTCCTGACGATGAACACA CCTAGAGTCTGCTGGAGATTGC	58	155-159
<i>ABGc002</i>	93.109	TCCACATCTGGCTAAACTCC GGAAAAATGAGGGACTCTCC	58	175-185
<i>ABGc003</i>	93.693	ACAGCCGTCTCCTTTAAACC AATTCTTCAACAGGCAGCAC	58	196-206
<i>ABGc004</i>	94.387	CAAAGAAAGCAGCAACTTGAG CAATGGGACTGACGAGTTTC	58	199-219
<i>ABGc005</i>	95.105	TGAACGGAGAAAGTTTCAGG GTGGGGAGAATGCCATTTAG	58	198-197
<i>ABGc006</i>	96.070	GCCTAATAGAAAGCCGTGTG AAGGGGAATGTCAGAAGAGG	58	262-278
<i>ABGc007</i>	99.282	TGTGTTCAATCTCTCATTCCTTC AAAAGAGAAAGACTTTTTGTGATTATG	58	292-308
<i>ABGc008</i>	101.969	ACCTCCCCTCCTTTCTTTG CTCTTGCTGGCTGAATTTATG	58	216-238
<i>ABGc009</i>	69.940	CATAACTGGCAGGTGGTAGC TCTTTTGCACGGTCACAG	58	198-204
<i>REN172C02</i>	76.364	CCCTTAGGAGGAGGCAAGAC CGTGCTTTGTTATGGCTTGA	58	340-348
<i>REN04H08</i>	78.098	GGGTGGGAAATGTGACTCTG ACTAACTCGCCAGACTATTC	55	100-102
<i>ABGc010</i>	79.969	AGTGAGGAGCAAATGGAATG GGACTCTACCTAAATGCAGCAG	58	220-248

LIM2
CFA1_108.472-108.480
SNPs

LOC611737g.4367G>A	Intron2	CACCCATTAGCAAACCAAAC	58	599
LOC611737g.4396A>G	Intron2	GAGAAGAAACACCCCAGAAAG		
LOC611737g.6430T>G	3'UTR	TGAGCCAGAAGACAGACTCC AGAATTTGACCTATACATCTGTTTCC	58	667