Supplementary Table S1. Dogs tested for the present of *PDE6B* mutation (*crd1* mutation) and *IQCB1* mutation (*crd2* mutation). All dogs were homozygous normal to both mutations.

#	Breed	Dogs tested for *crd1* mutation	Dogs tested for *crd2* mutation
1	American Cocker Spaniel	5	5
2	American Eskimo	7	6
3	Australian Cattle dog	5	5
4	Border Collie	5	5
5	Chesapeake Bay Retriever	6	5
6	Chinese Crested	-	5
7	Elkhound	8	3
8	English Cocker Spaniel	5	-
9	English Springer Spaniel	5	5
10	Entlebucher Mountain Dog	5	5
11	German Sheppard	9	-
12	Glen of Imaal Terrier	6	6
13	Golden retriever	5	5
14	Italian Greyhound	5	5
15	Labrador Retriever	6	5
16	Nova Scotia Duck Tolling retriever	6	6
17	Portuguese Water Dog	5	5
18	Siberian Husky	7	5
19	Tibetan Terrier	5	5
	Total	**105**	**86**

Supplementary Table S2. Primers used to screen candidate genes for *crd* diseases. A. Canine *PDE6B* primers sequences, locations and product sizes used to characterize the gene in retinal- cDNA- RT- PCR (**i**) and in genomic DNA (**ii**). Primers used for mutation screening are listed in A-**iii**. **B.** Canine *IQCB1* primers sequences, locations and product sizes used to characterize the gene in genomic PCR (**i**) and retinal- cDNA- RT- PCR (**ii**). Primers used for mutation screening are listed in B-**iii.**

Primer pair	**Forward Primer name**	**Forward primer sequence**	**Forward primer location**	**Reverse Primer name**	**Reverse primer sequence**	**Reverse primer location**	**Size**	
A. *PDE6B* screening.								
A-i. Primers used to amplify retinal cDNA.								
1	PDE6B_F1	`CTCCAGACAGACAGCCGGACAC`	5’UTR	PDE6B_R1	`CTTCAGGTTTAAGGTGCCGAAGTT`	Exon 3	686	
2	PDE6B_F2	`GCTACGAGACCAGGAACATCC`	Exon 2	PDE6B_R2	`TACCGACCAGCCCAGGAACTG`	Exon 10	782	
3	PDE6B_F3	`ACTCGGGCTGGGTCATCAAGA`	Exon 9	PDE6B_R3	`GGGTTCTGGGATTTCATCTGGTA`	Exons 14-15	721	
4	PDE6B_F4	`GGAGGATCACCTACCACAACTGG`	Exon 13	PDE6B_R4	`GAAGTCGATGAAGCCAACCTGTAG`	Exon 20	676	
5	PDE6B_F5	`TCGTGGATGAGTCTAAGAACTACGA`	Exon 17	PDE6B_R5	`TTAGTCATTTTCTGGGGCTTCCTC`	3’ UTR	602	
							Size observed in:	
A-ii. Primers used to validate deletion in exon 21 on genomic DNA							**Normal allele**	**Affected allele**
1	PD_intron20F	`cactgcctgggaactgtcgag`	Intron 20	PD_intron21R	`gaagccgcattcagttacttggtt`	Intron 21	417	414
A-iii. Primers used to genotype dogs for the mutation using allele-specific extension method.								
1	`crd1_AS_wt_F1`	GTTCGACCGACTGCAG**AAC**AAC	Exon 21	`crd1_R2`	`tgccccactgtccctttacac`	Intron 21	186	-
2	`crd1_F4`	`gcattctcggggtccttgctc`	Intron 20	`crd1_AS_mut_R6`	`AGGCCTTCCATTCCTTCCTGTaC`	Exon 21	-	362
B. *IQCB1* screening.								
B-i. Primers used to amplify genomic DNA.								
1	NPHP5_F1	atcttgactctccggctccag	5’ end	NPHP5_R1	ggcctcagtttccaccacagat	intron 1	470	
2	NPHP5_F2	gggaggaaggagaagggaaaaa	intron 1	NPHP5_R2	gtcaagtaagggagcagagcgtaa	intron 2	383	
3	NPHP5_F3	tcagagagagtgaatgtggagcac	intron 2	NPHP5_R3	gggagcagagagagagacagaaag	intron 3	558	
4	NPHP5_F4	cccctgccccaaataaataaataa	intron 3	NPHP5_R4	ctaccacacagaaagttgccagtg	intron 4	554	
5	NPHP5_F5	tggcaacaaaagcgataactaaaa	intron 4	NPHP5_R5	gatgggatgagcactgggtgt	intron 5	340	
6	NPHP5_F6	accatgttgtctcatttcacctct	intron 5	NPHP5_R6	aacacaggttttgatcccaggac	intron 6	462	
7	NPHP5_F7	gaaaggacaaatgaatcccaactg	intron 6	NPHP5_R7	agcttgcggtttgctaaataaaat	intron 7	500	
8	NPHP5_F8	ttcttgcatttcagcacagttagg	intron 7	NPHP5_R8	tccccatcactatttaaccactaaa	intron 8	466	

9	NPHP5_F9	tgttgtgcctttgttattccattt	intron 8	NPHP5_R9	atgctttaccgactttgcttgact	intron 9	449	
10	NPHP5_F10	gtcaagcaaagtcggtaaagcat	intron 9	NPHP5_R10	taggggaatggacaaaataggtga	intron 10	792	
11	NPHP5_F11	ttccctattgtgggatatacagtttg	intron 10	NPHP5_R11	caggtagcaggaaatctggttcat	intron 11	363	
12	NPHP5_F12	cctttttcattcctttgccacaa	intron 11	NPHP5_R12	atgtttttgcctcctaatccagta	intron 12	448	
13	NPHP5_F13	tttagtcacaatcccatccctctc	intron 12	NPHP5_R13	ccttttactccatcttgcctctca	intron 13	670	
14	NPHP5_F14	ccagaaagaaactacccccctgaat	intron 13	NPHP5_R14	ggaagagcagccaaaaaggag	intron 14	562	
15	NPHP5_F15	ttgctatcagccacacctacaact	intron 14	NPHP5_R15	aataaagtccaagagcacccttctt	3’ UTR	840	
B-ii. Primers used to amplify retinal cDNA.								
1	crd2_m_F1	cgagagaggctgagggatcttt	exon1+2	crd2_m_R1	ccagaagagagaatcggtcacaat	exon 6	560	
2	crd2_m_F2	attttctggttttggggagacgat	exon 5	crd2_m_R2	gggattcagtcatcagcagtagga	exon 8	381	
3	crd2_m_F3	gcttttatcaactcctaacccagtca	exon 8	crd2_m_R3	tttttcctttccctgtaccctctc	exon 12	567	
4	crd2_m_F5	gggaaatagaagagaaatcagccttg	exon 12	crd2_m_R5	tgagatagtcatccacttgttgcttt	exon 13	249	
5	crd2_m_F4	gcaaagtgccgtaagaaaaagaaa	exon 13	crd2_m_R4	tggtcgtgtggaaaaaggaaaata	3’ UTR	698	
							Size observed in:	
B-iii. Primers used to genotype dogs for the mutation.							**Normal allele**	**Affected allele**
1	CRD2_test2F	gcctcctgcccagcttatta	intron 9	CRD2_test2R	tttacctgaaactcctctgcaa	exon 10 +intron10	243	244
2	crd2_AST_F3	cctgcccagcttattagagttaga	intron 9	crd2_AST_RN1	ctctgcaaagtaatcacagcagatg**a**a	exon 10	225	-
3	crd2_AST_F3	cctgcccagcttattagagttaga	intron 9	crd2_AST_RA1	ctctgcaaagtaatcacagcagatg**a**g	exon 10	-	226

Supplementary Table S3. Heritability frequency analysis of dogs with either one parent genotyped (n=4) or both parents genotyped (n=30) in the *crd1* study. NA=not available.

Dog	Parent 1	Parent 2	# correct	# errors	Total	Heritability Freq
5	2	NA	169754	24	169778	0.9998
4	2	NA	170021	19	170040	0.9998
3	2	NA	169780	30	169810	0.9998
21	12	NA	169723	11	169734	0.9999
		Average:	**169819.5**	**21**	**169840.5**	**0.9998**
9	3	4	168728	30	168758	0.9998
6	3	4	167267	32	167299	0.9998
7	3	4	168912	21	168933	0.9999
12	5	4	168877	39	168916	0.9998
14	5	4	168793	43	168836	0.9997
15	5	4	168967	36	169003	0.9998
17	9	4	168993	21	169014	0.9999
19	9	4	169054	26	169080	0.9998
18	9	4	168888	22	168910	0.9999
28	17	21	165928	136	166064	0.9992
23	17	21	168991	27	169018	0.9998
22	17	21	169108	31	169139	0.9998
24	17	21	168813	29	168842	0.9998
26	17	21	169037	19	169056	0.9999
59	19	4	169353	16	169369	0.9999
41	19	4	169398	21	169419	0.9999
60	19	4	169329	18	169347	0.9999
43	19	4	169316	21	169337	0.9999
47	19	4	169100	21	169121	0.9999
58	19	4	169368	19	169387	0.9999
44	19	4	168868	36	168904	0.9998
54	19	4	169322	20	169342	0.9999
45	19	4	169393	16	169409	0.9999
55	19	4	169329	21	169350	0.9999
46	19	4	169283	16	169299	0.9999
56	19	4	169337	16	169353	0.9999
57	19	4	169437	22	169459	0.9999
32	19	21	168900	28	168928	0.9998
33	19	21	169064	28	169092	0.9998
31	19	21	169094	28	169122	0.9998
		Average:	**168941.5**	**28.6**	**168970.2**	**0.9998**

Supplementary Table S4. Genotype calls for disease- affected dogs (pink numbers) and obligated carriers (yellow numbers), or unaffected dogs (light green numbers) are shown. Number of dogs are corresponding to the numbers in the pedigrees. Columns = dogs, rows = SNPs genotypes. AA represents a homozygous genotype for allele 1, colored in green, BB represent homozygous genotype for allele 2, colored in orange, and AB represent heterozygous genotype, colored in yellow. White (--) = no call. The homozygous blocks are boxed and sizes are marked. Highlighted in purple are the boundaries of these blocks, and number of SNPs supporting each block is marked. Highlighted in brown are the SNPs with the highest $–\log_{10}(P)$ values.

A. Genotype calls from 17 *crd1*-affected cases 18 control dogs, in a 1.278 Mb interval on CFA3 are shown**. B.** Genotype calls from 14 *crd2*-affected cases and 13 obligated carrier control dogs, in a 7.76 Mb interval on CFA33 are shown.

Supplementary Table S5. Homozygous analysis results of the *crd1*- affected dogs (**A**) and *crd2*- affected dogs (**B**). In Bold is the mutation- bearing block.

Chromosome number	Position 1	Position 2	Size (Mb)	Number of SNPs within the homozygous block
A. ***crd1*- affected dogs**				
1	3,014,448	4,989,300	1.97	133
2	69,772,560	71,266,032	1.49	131
3	**93,388,160**	**94,693,816**	**1.30**	**114**
B. ***crd2*- affected dogs**				
33	**27,065,615**	**29,382,529**	**2.3**	**47**

Supplementary Table S6. Differences observed in *PDE6B* coding sequence of normal and *crd1*- affected dogs compared to the deposit gene NM00100293 and the boxer reference sequences.

Number	Location on CFA3 (CanFam2.0)	NM001002934	Boxer Database	Normal	*crd1*-affected	Position within the coding sequence
1	94,601,362	A	G	GG	GG	36
2	94,601,361	A	G	GG	GG	37
3	94,601,360	G	A	AA	AA	38
4	94,601,047	C	C	CT	CC	351
5	94,597,081	G	C	CC	CC	555
6	94,597,080	C	G	GG	GG	556
7	94,597,030	G	A	AA	AA	606
8	94,597,027	T	C	CC	CC	609
9	94,575,468	T	C	CC	CC	2,343
10	94,574,291	A	A	AA	del/del	2,404
11	94,574,290	A	A	AA	del/del	2,405
12	94,574,289	C	C	CC	del/del	2,406