

Supplementary Table S1: *Rdy* Candidate Genes/Genomic Regions

Candidate Gene	Former Name*	Disease Category*	Candidate region Human (Chr:position, Mb)[†]	Candidate region Cat (Chr:position, Mb)[‡]	Function	Exons
<i>CA4</i>	RP17	adRP	Chr17:55.58	ChrE1:51.62	carbonic anhydrase IV	8
<i>CRX</i>	CORD2, LCA7	adLCA, arLCA, adRP, adCoRD	Chr19:53.02	ChrE2:9.88	transcription factor for rod/cone photoreceptor development	4
<i>FSCN2</i>	RP30	adRP, adMD	Chr17:77.11	ChrE1:132.82	photoreceptor-specific paralog of the actin-binding protein fascin	5
<i>GUCA1B</i>		adRP, adMD	Chr6:42.26	ChrB2:43.33	guanylate cyclase activating protein 1B	4
<i>IMPDH1</i>	LCA11, RP10	adLCA, arLCA,	Chr7:12.78	ChrA2:211.18	inosine monophosphate dehydrogenase 1	16
<i>NRL</i>	RP27	adRP, arRP	Chr14:23.62	ChrB3:81.25	retinal transcription factor	3
<i>PRPF3</i>	RP18	adRP	Chr1:14.86	ChrC1:110.54	homolog of yeast pre-mRNA splicing factor 3	16
<i>PRPF31</i>	RP11	adRP	Chr19:59.31	ChrE2:3.84	homolog of yeast pre-mRNA splicing factor 31	14
<i>PRPF8</i>		adRP	Chr17:15.01	ChrE1:40.46	homolog of yeast pre-mRNA splicing factor C8	43
<i>PRPH2</i>	RP7, RDS	adRP, adMD	Chr6:42.77	ChrB2:43.93	peripherin 2	3
<i>RHO</i>	RP4	adRP, arRP, adCSNB	Chr3:13.07	ChrA2:61.17	rhodopsin	5
<i>ROM1</i>		adRP	Chr11:62.14	ChrD1:134.78	retinal outer segment membrane protein 1	3
<i>RP1</i>		adRP, arRP	Chr8:55.69	ChrF2:2.39	retinitis pigmentosa 1 protein	4
<i>TOPORS</i>	RP31	adRP	Chr9:32.53	ChrD4:46.22	topoisomerase I-binding arginine/serine-rich protein	3
<i>RP33</i>		adRP	Chr2:cen-q12.1 [§]	ChrA3:81.954 [§]	unknown gene [§]	---
<i>RP9</i>		adRP	Chr7:33.10	ChrA2:181.69	RP9 protein or PIM1-kinase associated protein 1	6
<i>NR2E3</i>	RP37	arESC, arRP, adRP, adR, arR	Chr15:69.89	ChrB3:42.13	nuclear receptor subfamily 2 group E3	8
<i>RDH12</i>		arLCA, adRP	Chr14:67.24	ChrB3:116.96	retinol dehydrogenase 12	7
<i>SEMA4A</i>	RP35	adRP	Chr1:15.44	ChrF1:87.61	semaphorin 4A	15

*<http://www.sph.uth.tmc.edu/Retnet/disease.htm#14.207d>; [†]UCSC Genome Browser was used to identify human gene locations;

[‡]GARField: Genome Annotation Resource Field *Felis catus* v12.2 was used to identify feline gene locations (17); [§]Linkage region not gene.

NT not tested; ad: autosomal dominant; ar: autosomal recessive; MD: macular dystrophy; RP: retinitis pigmentosa; CoRD: cone rod dystrophy; ESC: enhanced S-cone syndrome; R: retinopathy; CSNB: congenital stationary night blindness.