Supporting information for Katsanis *et al.* (2002) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.222409099

Table 2. Retinal EST sequences predicted to be enriched in the retina by *in silico* subtraction that match known or predicted genes

EST accession no.	GenBank accession no.	Gene	Map position, Mb	Disease interval(s)
AA019831	NM_014638	KIAA0450	Chr 1 (08–1.8)	
AA219094	XM_031283	KIAA1710	Chr 1 (16–24.4)	
H82118	AF458851	SMP1	Chr 1 (16–24.4)	
AA058857	XM_00182	GRIK3	Chr 1 (27.8–38.1)	
AA663078	XM_099435	LOC163744	Chr 1 (47.1–72.9)	
AA167221	XM_042708	FLJ14743	Chr 1 (108.5–112.8)	CORD8 and RP18
H86446	XM_001667	BY55	Chr 1 (121.9–122)	CORD8 and RP18
AA780848	NG_000833	IGK–distal		
AA169173	AF186782	RalGDS–like	Chr 1 (149.3–174.6)	ARMD1
R85656	NM_003626	PTPRF	Chr 1 (175.7–181)	ARMD1
AA457366	NM_014359	OPTC	Chr 1 (175.7–181)	ARMD1
AA668471	NM_032122	DTNBP1	Chr 1 (175.7–181)	ARMD1
AA015982	XM_001962	**USH2A**	Chr 1 (183.8–200.5)	
AA013474	AF246631	SM–20	Chr 1 (205.5–210.3)	
AA668282	AF230315	TRAX/DISC1	Chr 1 (205.5–210.3)	
AA663244	AF324889S2	MYPT2	Chr1 (212)	
AA169152	NM_021186	ZP4	Chr 1 (212.2–219.4)	
AA019197	NM_006794	GPR75	Chr 2 (0.5–5.8)	
H38931	XM_052615	NXPH2	Chr 2 (129.7–179.1)	
H92143	NM_012476	VAX2	Chr 2 (70.6–90)	RP28
AA054133	NM_033066	MPP4	Chr 2 (178.5–192.2)	RP26
AA169176	U58767	G3–PDH	Chr 2 (129.7–179.1)	RP26
AA663353	XM_092459	KIAA1946	Chr 2 (178.5–192.2)	RP26
AA174136	XM_087044	FLJ10785	Chr 2 (225.8–240.5)	
H92234	NM_004321	ATSV	Chr 2 (225.8–240.5)	
AA001706	AB047965	Macaca brain cDNA	Chr 3 (5–11)	
AA668377	AJ289880	KIAA0851	Chr 3 (36.5–50.7)	USH2B
AA019845	NM_000539	**RHO**	Chr 3 (129–133)	
AA017196	NM_000539	**RHO**	Chr 3 (129–133)	
AA001079	S42457	**CNGA1**	Chr 4 (50–50.5)	
H41063	AL079280	cDNA clone EUROIMAGE 413639	Chr 4 (68.4–82.4)	
AA663155	XM_059601	LOC132806	Chr 4 (68.4–82.4)	
H84403	AJ238093	AF–4	Chr 4 (83.2–102.8)	
AA018223	XM_042301	KIAA1546 protein	Chr 4 (103.1–118.5)	
AA167280	AK023115	FLJ13053	Chr 4 (133.8–144)	
H82639	XM_106227	LOC166773	Chr 4 (174.6–190)	
AA489781	similar to XM_094206	KIAA1399	Chr 5 (15.4–18.7)	
AA180157	AF247457	MYO10	Chr 5 (15.4–18.7)	

EST accession no.	GenBank accession no.	Gene	Map position, Mb	Disease interval(s)
AA489784	XM_094580	LOC167598	Chr 5 (130.9–138.9)	
AA137094	similar to XM_116372	Similar to KIAA0825	Chr 5 (139–178.3)	
AA058851	NM_005906	MAK	Chr 6 (03–16.8)	
AA019704	Y09912	AP–2 beta	Chr 6 (34.2–57.6)	
H87285	AB075843	KIAA1963	Chr 6 (67.7–86.1)	
AA013196	XM_050424	KIAA1244	Chr 6 (124.7–149.3)	
AA218915	XM_087834	SYNE–1	Chr 6 (150.5–161.1)	
AA489853	XM_068951	LOC134657	Chr 6 (150.5–161.1)	
AA668336	AB011399	AF–6	Chr 6 (161.2–170)	
AA179164	XM_040262	KIAA0415	Chr 7 (1.6–5.6)	
AA010974	AF440395	C7orf9	Chr 7 (25.7)	CYMD
AA047767	XM_004926	KIAA0087	Chr 7 (8–30.6)	CYMD
AA780455	XM_167243	ERO1–like	Chr 7 (95–97.9)	
H83407	XM_168551	HDCMC04P	Chr 7 (101.1–126.2)	
AA058772	XM_011554	DGKI	Chr 7 (126.8–140.2)	
AA169345	XM_054682	LOC113763	Chr 7 (148–149.8)	
AA169370	XM_064055	Similar to FGFR–3	Chr 16 (20.9)	
AA001426	XM_088347	LOC157627	Chr 8 (8.4–12.1)	
AA219106	XM_108741	LOC169427	Chr 8 (12.7–43.7)	
AA018812	NM_006269	**RP1**	Chr 8 (44.5–75.8)	
AA663527	XM_108274	LOC168954	Chr 8 (76.2–84.50	
AA167599	XM_059909	LOC137485	Chr 8 (121.6–136.8)	
AA010843	NM_030895	FLJ14129	Chr 8 (121.6–136.8)	
H86059	NM_004519	KCNQ3	Chr 8 (121.6–136.8)	
AA179949	XM_117522	LOC203274	Chr 9 (35.3–40.1)	
H83981	NM_032536	netrin G2 (KIAA1857)	Chr 9 (89.1–109.3)	
AA015747	NM_016335	PRODH	Chr 9 (63.8–65)	
AA490022	XM_089151	similar to Kilon (LOC163789)	Chr 1 (47.1–72.9)	
AA218895	AK023957	FLJ13895	Chr 10 (17.6–33.9)	
AA167219	AJ246004	RET	Chr 10 (43.1–44.1)	
AA434482	AK022219	FLJ12157	Chr 10 (89.3–126.9)	
AA663077	XM_089803	LOC143393	Chr 10 (89.3–126.9)	
AA662968	AJ006345	KVLQT1	Chr 11 (0.04–2.9)	
AA015755	XM_166226	LOC220001	Chr 11 (54–58.1)	BBS1
AA010976	NM_033036	GAL3ST2	Chr 11 (58.3–62.9)	BBS1
H41098	NM_133266	SHANK2	Chr 11 (63.8–67.3)	
AA021504	similar to BC014937	similar to DKFZp566M1046)	Chr 4 (149.3–153.2)	
AA491468	similar to XM_061871	similar to fat3 (LOC120114)	Chr 11 (86–92.4)	EVR1
AA136893	XM_061943	LOC120260	?	
AA018120	XM_006987	KCNA1	Chr 12 (0.2–8.3)	
H84977	AJ272204	C12orf3	Chr 12 (0.2–8.3)	
AA457412	AF329081	PRKAG1	Chr 12 (36.4–49)	
AA047806	AB027567	SCN8A	Chr 12 (49.2–51.2)	
H38140	AK001482	FLJ10620	Chr 12 (90.1–123.5)	

EST accession no.	GenBank accession no.	Gene	Map position, Mb	Disease interval(s)
AA179159	XM_101207	LOC160765	Chr 12 (90.1–123.5)	
AA017137	XM_083890	CDV–1	Chr 12 (90.1–123.5)	
AA218854	XM_038784	FLJ12750	Chr 12 (90.1–123.5)	
R85833	AF284094	BRI3BP	Chr 12 (124.9–133.8)	
AA679237	AF203901	Neurod4	Chr 12 (51.3–62.5)	
AA456921	XM_052767	PIWIL1	Chr 12 (124.9–133.8)	
AA663137	XM_062607	LOC121376	Chr 12 (90.1–123.5)	
AA218906	NM_018451	CENPJ	Chr 13 (6.9–13.4)	
AA679158	NM_006439	MAB21L2	Chr 13 (149.3–153.2) Or 4?	
AA169144	L11910	retinoblastoma susceptibility gene	Chr 13 (13.7–35)	
AA057387	XM_007132	CHM–I	Chr 13 (35.1–46.2)	
AA059474	similar to XM_093929	similar to BC013764	Chr 4 (45–50.5)	
AA017727	NM_017693	FLJ20159	Chr 13 (69.3–96.7)	
AA504859	XM_007129	SLC10A2	Chr 13 (69.3–96.7)	
AA021554	NM_006177	**NRL**	Chr 14 (0.3–15.1)	
AA046477	XM_046651	INSM2	Chr 14 (15.4–85.5)	LCA3
AA018455	similar to XM_115235	similar to NTF–2	Chr 14 (15.4–85.5)	LCA3
R85569	similar to XM_085133	similar to RIKEN	Chr 14 (15.4–85.5)	LCA3
AA012899	NM_058240	SLC8A3	Chr 14 (15.4–85.5)	LCA3
AA057442	AB032978	KIAA1152	Chr 14 (15.4–85.5)	LCA3
H83986	AK056249	FLJ31687	Chr 14 (15.4–85.5)	LCA3
AA169252	XM_102130	LOC145963	Chr 15 (7.6–8.8)	
AA020814	XM_007543	SPTBN5	Chr 15 (13.3–23.3)	
AA663033	similar to XM_113821	similar to PADI–H	Chr 15 (13.3–23.3)	
W96166	XM_102130	SPTBN5	Chr 15 (13.3–23.3)	
H87737	XM_102130	SPTBN5	Chr 15 (13.3–23.3)	
H91666	XM_167000	FLJ13993	Chr 18 (43.2–63.7)	
AA001457	XM_050910	SLC24A1	Chr 15 (23.3–53.6)	
H82641	AJ276674	PNR	Chr 15 (23.3–53.6)	
AA780734	AK025037	FLJ21384	Chr 15 (56.3–63.5)	
AA173695	XM_101965	LOC161519	Chr 15 (65.7–82.9)	
AA458577	similar to XM_063611	similar to polyhomeotic 2 protein	Chr 15 (65.7–82.9)	
AA780546	XM_102167	LOC146001	Chr 15 (65.7–82.9)	
AA058999	NM_001374	DNASE1L2	Chr 16 (3.2–5.7)	
W96167	AJ303140	NOD2	Chr 16 (33.5–42.8)	
AA679178	AB075868	KIAA1988	Chr 16 (53.7–58.5)	
AA015957	XM_049311	MLYCD	Chr 16 (71.5–77.6)	
AA019599	XM_102732	LOC147043	Chr 17 (0.8–15.9)	
AA457377	NM_014336	**AIPL1**	Chr 17 (0.8–15.9)	LCA
AA179177	XM_118978	LOC204553	Chr 17 (0.8–15.9)	CACD, CORD5
AA021562	X05196	HSALDC	Chr 17 (24.4–28.1)	

EST accession no.	GenBank accession no.	Gene	Map position, Mb	Disease interval(s)
AA457638	XM_012658	ACCN1	Chr 17 (30.2–34.3)	
AA668255	similar to AK027210	similar to MKP–1	Chr 17 (35.1–36.5)	
AA780746	XM_119091	LOC204673	Chr 17 (34.8)	
AA018445	similar to XM_091460	similar to Stac protein	Chr 17 (36.6–41.5)	
AA013425	similar to NM_006455	similar to rat	Chr 17 (36.6–41.5)	
AA017693	XM_050159	GFAP	Chr 17 (43.1–45.2)	
H92155	XM_091469	LOC162287	Chr 17 (46.5–58.9)	
H85425	XM_057257	ABCA5	Chr 17 (68.9–76.3)	
AA018407	XM_119056	LOC204634	Chr 17 (76.5–82)	
AA219325	NM_023879	**Rpgrip1**	Chr 18 (0.4–14.5)	
AA487286	XM_102990	LOC162800	Chr 18 (16.7–42)	OPA4
AA001080	similar to XM_084525	similar to Dihydrofolate reductase	Chr 18 (16.7–42)	OPA4
AA019834	similar to XM_064632	similar to Zinc finger protein 24	Chr 18 (16.7–42)	OPA4
AA490176	AB024742	beta4GalT–VI	Chr 18 (16.7–42)	OPA4
H85883	NM_015847	D1	Chr 18 (43.2–63.7)	
H85866	similar to XM_114827	LOC205024	Chr 1 (200.9–205.4)	
H84237	NM_138966	NETO1	Chr 18 (63.8–71)	
AA013001	NM_138999	NETO1	Chr 18 (63.8–71)	
AA663289	Y16271	PALM	Chr 19 (0.01–0.4)	
AA780552	XM_064973	LOC126178	Chr 19 (25.7–34.3)	
AA001040	NM_025213	SPTBN4	Chr 19 (35.6–41)	
AA457494	similar to XM_103254	LOC163104	Chr 19 (25.7–34.3)	OPA3
AA679225	XM_084016	SPTBN4	Chr 19 (35.6–41)	
H85545	XM_009125	GLTSCR1	Chr 19 (41.3–45.9)	
R93872	NM_000554	**CRX**	Chr 19 (41.3–45.9)	
AA020775	U62631	B–cell receptor CD22–B isoform	Chr 19 (51)	
H87216	AF228339	GILZ	Chr X (96.6–97.7)	
AA169188	XM_066154	LOC128775	Chr 20 (0.06–23.7)	
AA668128	XM_029763	KIAA1335	Chr 20 (28.1–59.4)	
AA015730	similar to BC025147	Mouse, Similar to par–6 homolog	Chr 20 (28.1–59.4)	
AA451924	NM_006526	ZNF217	Chr 20 (28.1–59.4)	
AA219245	XM_071315	LOC140273	Chr 21 (16.3–18.1)	USH1E
AA663051	XM_092811	LOC164506	Chr 21 (20.6–28.7)	
AA668320	AB063285	HLCS	Chr 21 (20.6–28.7)	
W96421	NM_014758	KIAA0254	Chr 21?	
W96421	XM_165577	SNX19 (LOC219798)	Chr 21?	
AA663110	XM_032955	CECR2	Chr 22 (0.8–23.6)	
AA015620	XM_009846	Armadillo	Chr 22 (3.3–4.7)	
R93807	NG_000002	IGL2	Chr 22 (6.4–22.5)	

EST accession no.	GenBank accession no.	Gene	Map position, Mb	Disease interval(s)
AA663017	AF169558	BUP1	Chr 22 (6.4–22.5)	
AA679504	similar to XM_066306	similar to HP–20	Chr 22 (6.4–22.5)	
H87280	Y18000	NF2	Chr 22 (6.4–22.5)	
AA176617	XM_093107	LOC170110	Chr X (6.3–9.7)	RP23, OPA2, PRD
H30729	similar to NM_008778	CDKN1A–activated kinase 3	Chr X (97.7–98.6)	
H92506	XM_010096	FACL4	Chr X (98.6–100.1)	AIED
AA058579	XM_104940	LOC170194	Chr X (98.6–100.1)	AIED
AA489808	similar to XM_090831	similar to bB128O4.1.1	Chr X (104.2–107.2)	AIED, RP24
AA018572	NM_012418	FSCN2	?	
AA015746	AJ010395	DKC1	Chr X (150.2)	
XM_072511	XM_072511	LOC137861	Chr 8 (12.7–43.7)	
AA056098	Similar to X81561	Similar to *Escherichia coli* pqi5 gene	?	
AA457392	AF056719	SLC21A2	Chr 3 (138.2–198.4) ?	USH3A
AA481798	XM_113410	CRTAP	Chr 3 (36.5–50.7) ?	USH2B
AA668129	NM_003803	MYOM1	Chr 18 (0.4–14.5) ?	
AA668397	XM_119693	LOC200682	Chr 2 (0.5–57.7) ?	
H85579	similar to XM_116752	similar to LOC206839	Chr 8 (8.4–12.1)	

Genes in boldface indicate retinopathy loci. Chr, chromosome.