

Supplementary Table 3. Uncommon genetic variants identified in RE+/FECD- exomes

Genes expressed in corneal endothelium										
Chromosome	Position	Reference Allele	Sample Allele	Gene Symbol	Protein Variant	SIFT Function Prediction	PolyPhen-2 Function Prediction	dbSNP ID	NHLBI ESP Frequency	ExAC Frequency
1	1597403	C	T	SLC35E2B	p.G346S	Tolerated	Possibly Damaging	114859950		0.264
1	1606926	G	A	SLC35E2B	p.R188W	Tolerated	Benign	776774099		0.014
1	117633170	G	A	TTF2	p.R838H	Damaging	Probably Damaging	148036415	0.5	0.424
1	150525418	G	C	ADAMTSL4	p.Q41H	Tolerated	Possibly Damaging			
1	150528789	C	T	ADAMTSL4	p.A508V; p.A531V	Tolerated	Possibly Damaging	768692911		0.002
1	150530958	C	T	ADAMTSL4	p.R759W; p.R821W; p.R798W	Tolerated	Benign	763279620		0.006
1	153747981	C	T	SLC27A3	p.A131V	Tolerated		145619769	0.177	0.17
1	153750665	G	A	SLC27A3	p.R525Q	Damaging		141932545	0.008	0.058
1	161736197	G	T	ATF6	p.S16I	Tolerated	Benign	112863172	0.392	0.291
2	58386928		TAAT	FANCL; VRK2	p.T372fs; p.T367fs			759217526	0.248	0.288
2	152320877	A	G	RIF1	p.K1615E	Tolerated	Benign			
2	152321091	G	A	RIF1	p.R1686Q	Tolerated	Benign	61748233	0.123	0.121
2	159519581	G	A	PKP4	p.R795K; p.R452K; p.R794K	Tolerated	Benign	139221917	0.038	0.108
2	190670540		A	PMS1	p.L164fs*4			3214425		
3	40503529		CTGCTGCTG	RPL14	p.A157_A159dup					
3	40503529		CTGCTGCTG CTGCTG	RPL14	p.A155_A159dup					
3	40503552		GCTGCTGCT GCTGCTGCT	RPL14	p.A154_A159dup					
3	42251580		GGAGGA	TRAK1	p.E639_E640dup; p.E623_E624dup; p.E697_E698dup					
3	42251609		AGGAGG	TRAK1	p.E639_E640dup;					

					p.E623_E624dup; p.E697_E698dup					
3	51251601	G	A	DOCK3	p.R392Q	Tolerated	Probably Damaging	199600118	0.075	0.058
3	51251618	A	G	DOCK3	p.I398V	Tolerated	Benign	373753412	0.008	0.001
3	69987114	G	A	MITF	p.D149N; p.D59N; p.D150N; p.D165N; p.D166N; p.D114N	Tolerated	Benign	145387068	0.008	0.002
3	70014091	G	A	MITF	p.E402K; p.E424K; p.E367K; p.E256K; p.E312K; p.E318K; p.E403K; p.E425K; p.E418K; p.E419K	Tolerated	Possibly Damaging	149617956	0.223	0.133
3	100523692	C	G	ABI3BP	p.R1170P; p.R744P; p.R564P; p.R1100P	Tolerated	Benign	146922324	0.083	0.159
3	100553585	G	A	ABI3BP	p.R678C; p.R628C; p.R654C			547246874		
3	100583718	G	A	ABI3BP	p.P348L	Damaging	Probably Damaging			
3	113376117	TGC		USF3	p.Q1478del					
3	113376119		TGCTGC	USF3	p.Q1477_Q1478dup					
3	113376159	T	A	USF3	p.H1457L	Tolerated	Benign	202124437	0.039	0.06
4	3076603		CAGCAGCAG CAGCAGCAG CAGCAGCAG CAGCAGCAG	HTT-AS; HTT	p.Q29_Q40dup					
4	3076609		CAGCAG	HTT-AS; HTT	p.Q39_Q40dup					
4	87638213	G	A	PTPN13	p.S443N	Tolerated	Benign	201331872	0.118	0.102

4	87684148	G	T	PTPN13	p.W1255C; p.W1274C; p.W1083C	Tolerated	Possibly Damaging	201633051	0.306	0.383
4	190876268	A	G	FRG1	p.I132V	Tolerated	Benign	528665769		0.009
4	190876272	G	A	FRG1	p.G133E	Damaging	Possibly Damaging	202104107		0.01
4	190876287	G	A	FRG1	p.W138*			113079586		0.006
4	190876307	G	A	FRG1				200854715		0.005
4	190878569	T	C	FRG1	p.L150S	Damaging	Benign	575384276		0.077
4	190878571	G	A	FRG1	p.A151T	Tolerated	Possibly Damaging	763602694		0.073
4	190878596	G	A	FRG1	p.C159Y	Tolerated	Possibly Damaging	777841400		0.099
4	190878599	A	G	FRG1	p.N160S	Tolerated	Benign	771525586		0.085
4	190878608	G	A	FRG1	p.G163E	Tolerated	Possibly Damaging	772516149		0.087
4	190883051	G	A	FRG1	p.R235Q	Tolerated	Benign	1803593		0.003
5	39153562	G	A	FYB1	p.P427L; p.P437L	Damaging	Benign	199876614	0.211	0.154
5	56177852	CAA		MAP3K1	p.T949del					
5	140594467	G	A	PCDHB13	p.V258I	Tolerated	Benign	17844609		0.284
5	140594470	G	A	PCDHB13	p.G259S	Damaging	Benign	17844610		0.144
6	12123785	G	A	HIVEP1	p.D1253N	Damaging	Possibly Damaging	148091729	0.091	0.061
6	12163868	C	T	HIVEP1	p.T2444M	Tolerated	Benign	2228214	0.202	0.205
6	26156953	C	T	HIST1H1E; HIST1H2BD	p.A112V	Tolerated	Benign	201133864	0.015	0.048
6	26157258	G	T	HIST1H1E; HIST1H2BD	p.A214S	Tolerated	Benign	776968459		
6	46593166	A	G	CYP39A1	p.F287S; p.F307S; p.F135S	Damaging	Probably Damaging	137900158	0.031	0.013
6	46604145	G	C	CYP39A1	p.S238C; p.S218C; p.S66C	Tolerated	Possibly Damaging	147866724	0.416	0.319
6	52317597	T	C	EFHC1	p.F210L; p.F229L	Tolerated	Benign	137852776	0.331	0.358
6	52343926	G	T	EFHC1	p.R457L; p.R438L	Damaging	Probably Damaging	369468811	0.015	0.007
6	106547325	A	G	PRDM1	p.K54E; p.K188E	Damaging	Probably Damaging	151324489	0.062	0.048

6	106553383	C	T	PRDM1	p.L450F; p.L316F	Tolerated	Benign	141465160	0.208	0.421
6	161519354	CTG		MAP3K4	p.A1195del; p.A1199del; p.A652del			752044838		
7	2296618	A	T	SNX8	p.F392Y	Tolerated	Possibly Damaging	150480674	0.208	0.154
7	2296622	A	T	SNX8	p.Y391N	Tolerated	Benign	138169290	0.208	0.154
7	117188750	C	T	CFTR	p.S422F		Benign	201880593		0.249
7	117188797	A	G	CFTR	p.T438A		Benign	201434579		0.235
7	117188841	GTT		CFTR	p.L454del					0.017
7	121985635	A	G	CADPS2	p.L1202S; p.L1161S; p.L1206S	Damaging	Benign			
7	122114500	A	C	CADPS2	p.F642V; p.F645V	Tolerated	Benign	201536376	0.075	0.053
8	67341451	G	A	RRS1; RRS1-AS1	p.E29K	Tolerated	Benign	375178198	0.008	0.023
8	67342031	T	C	RRS1; RRS1-AS1	p.M222T	Tolerated	Benign	137894990	0.371	0.334
8	67342165	A	T	RRS1; RRS1-AS1	p.N267Y	Damaging	Benign	144551617	0.454	0.401
8	135602591	C	T	ZFAT	p.R816K; p.R766K; p.R828K	Activating	Benign	138033806	0.375	0.32
8	135614553	G	C	ZFAT	p.S470C; p.S458C; p.S408C	Damaging	Probably Damaging	112892337	0.238	0.212
8	145738802	G	A	RECQL4	p.R755W		Probably Damaging			
8	145742480	G	A	RECQL4; LRRC14	p.P103L		Benign	199543866	0.048	0.063
8	145748143	G	C	LRRC14; LRRC24	p.L420V	Damaging	Probably Damaging	376131634	0.008	0.028
9	139835740	A	T	FBXW5	p.F474I	Tolerated	Benign	143554180	0.062	0.087
9	139839860		CATCCCC	FBXW5; C8G	p.S34fs*12			758635843	0.048	0.009
10	105178221	A	G	PDCD11	p.K646E	Damaging	Probably Damaging	141961630	0.008	0.008
10	105202091	G	T	PDCD11	p.R1610L	Damaging	Probably Damaging	146747336	0.085	0.176
10	105890027	C	T	CFAP43	p.R1623Q	Damaging	Probably	752348444		0.002

							Damaging			
10	105906085	C	T	CFAP43	p.R1264Q	Tolerated	Benign	754109266		0.002
11	5624917	C	G	TRIM6; TRIM6- TRIM34	p.H125Q; p.H153Q	Damaging	Probably Damaging			
11	5626614	G	C	TRIM6; TRIM6- TRIM34	p.Q189H; p.Q14H; p.Q217H	Tolerated	Benign	61758096	0.277	0.248
11	34988219	C	T	PDHX	p.T210M; p.T225M	Tolerated	Benign	148645836	0.054	0.068
11	34988294	C	T	PDHX	p.T250I; p.T235I	Tolerated	Benign	146876119	0.031	0.067
11	66454564	G	A	SPTBN2	p.A2266V		Benign	145891813	0.092	0.102
11	66475184	C	T	SPTBN2	p.A486T		Possibly Damaging	143155918	0.062	0.066
11	66512290		GGCGGCGGC GGC	C11orf80	p.A31_A34dup					0.158
11	95825378	TGCTGCTGC		MAML2	p.Q619_Q621del					
11	110007898	C	G	ZC3H12C	p.Q178E	Tolerated	Benign			
11	110035132	G	A	ZC3H12C	p.R441Q	Damaging	Probably Damaging	147027799		0.002
12	6777073	TGC		ZNF384	p.Q516del; p.Q455del; p.Q400del			747471532		
12	108686292	G	T	CMKLR1	p.H148N; p.H150N	Damaging	Possibly Damaging			
12	108686555	A	C	CMKLR1	p.I62S; p.I60S	Damaging	Probably Damaging	141421422	0.475	0.361
12	121678328		TTT	CAMKK2	p.K538dup			869098373		
12	121678329		TTT	CAMKK2	p.K538dup					
12	133219531	C	T	POLE	p.G1535S	Tolerated	Benign	138564205	0.008	0.007
12	133263886	C	G	POLE; PXMP2	p.G6R	Tolerated	Benign	202220778	0.161	0.195
13	78146303	C	T	SCEL	p.S175L	Tolerated	Benign	141416270	0.284	0.231
14	23517386	G	A	CDH24	p.P717S; p.P755S	Tolerated	Possibly Damaging	199930802		0.442
14	23522921	C	T	CDH24	p.R337H	Tolerated	Probably Damaging	370840001		0.006
14	68215328	A	T	ZFYVE26	p.L2482Q	Damaging	Probably			

							Damaging			
14	68274558	C	T	ZFYVE26	p.R148H		Benign	144919978	0.008	0.011
15	50154563	C	T	ATP8B4	p.R1059Q	Tolerated	Benign	146911077	0.239	0.229
15	50254207	A	C	ATP8B4	p.H418Q	Tolerated	Benign	143688108	0.008	0.001
15	74637567	T	C	CYP11A1	p.K148R	Tolerated	Benign			
15	74659692	C	T	CYP11A1	p.V79I	Tolerated	Benign	143655263	0.454	0.255
15	100252713	CAGCAG		MEF2A	p.Q419_Q420del; p.Q427_Q428del; p.Q351_Q352del; p.Q421_Q422del; p.Q425_Q426del; p.Q359_Q360del					
15	100252716	CAGCAG		MEF2A	p.Q419_Q420del; p.Q427_Q428del; p.Q351_Q352del; p.Q421_Q422del; p.Q425_Q426del; p.Q359_Q360del					
15	100252719	CAG		MEF2A	p.Q426del; p.Q428del; p.Q352del; p.Q360del; p.Q422del; p.Q420del					
17	17718592	C	T	SREBF1	p.R788Q; p.R842Q; p.R812Q	Damaging	Benign	141489278	0.2	0.315
17	17723595	G	A	SREBF1	p.P111L; p.P141L; p.P87L	Damaging	Benign	115855236	0.069	0.072
17	43315961	C	G	FMNL1	p.L309V		Probably Damaging	929854823		
17	43319458	GCC		FMNL1	p.P612del					
17	71228379	G	C	FAM104A; C17orf80	p.P23A	Tolerated	Benign	180917408	0.436	0.395
17	71228442	C	T	FAM104A; C17orf80	p.G2R	Damaging	Probably Damaging	544578624		0.019
18	65178507	T	C	DSEL	p.I1123M	Tolerated		72954698	0.1	0.08
18	65180987	C	T	DSEL	p.V297I	Activating		150905757	0.123	0.084

19	2114127	CTTCTC		AP3D1	p.E865_K866del			756601658	0.236	0.186
19	2115584	T	C	AP3D1	p.H701R	Tolerated	Possibly Damaging	774521539		0.003
19	11552120	G	A	PRKCSH	p.R139H	Tolerated	Benign	139991238	0.161	0.163
19	11558344	GAG		PRKCSH	p.E325del					
19	42827940	C	T	MEGF8; TMEM145	p.S467F		Benign	141686253	0.161	0.27
19	42880167	G	A	MEGF8	p.R2593Q; p.R2526Q	Damaging	Probably Damaging	371459258	0.008	0.003
19	58578228	G	T	ZNF135	p.G150C; p.G138C; p.G84C; p.G126C	Tolerated	Benign	150171641	0.092	0.065
21	40795408	C	T	WRB- SH3BGR; LCA5L	p.E111K	Tolerated	Possibly Damaging	147171239	0.188	0.127
22	23653975		CCGG	BCR	p.V1050fs*17; p.V1094fs*17			372013175		
22	25753349	C	T	LRP5L	p.R104H	Tolerated	Probably Damaging	139077409	0.085	0.105
22	25755942	C	G	LRP5L	p.A40P	Damaging	Probably Damaging	116871327	0.162	0.095
X	2833605	C	T	ARSD	p.W331*			111939179		0.014
X	2835989	A	C	ARSD	p.F240C	Tolerated	Benign	143238998		0.105
X	2835995	C	A	ARSD	p.C238F	Activating	Benign	150899882		0.118

Genes not Expressed in corneal endothelium

Chromosome	Position	Reference Allele	Sample Allele	Gene Symbol	Protein Variant	SIFT Function Prediction	PolyPhen-2 Function Prediction	dbSNP ID	NHLBI ESP Frequency	ExAC Frequency
1	17085590	GCGCTG		MST1L; LOC102724 562	p.Q376_R377del			371449598		0.278
1	17085592	G	A	MST1L; LOC102724 562	p.R377C			756977732		0.072
1	47904075	GCGGCGGC CGCAGCGG GGAGCCCCG		FOXD2	p.A93_A104del					

		GGGCCAGG CGCC								
1	47905161	T	A	FOXD2	p.L452M	Damaging	Possibly Damaging	61751017	0.174	0.118
1	152080352	G	T	TCHH	p.Q1781K	Tolerated	Benign	770476948		0.002
1	152083372	T	C	TCHH	p.E774G	Damaging	Possibly Damaging	201873363		
1	152083375	G	C	TCHH	p.A773G	Tolerated	Benign	200287676		0.009
1	160846458	C	G	ITLN1	p.R313P	Damaging	Probably Damaging	8144	0.408	0.39
1	168683471	G	A	DPT	p.P140L	Damaging	Possibly Damaging	78032017	0.108	0.143
1	168698208	A	T	DPT	p.S69T	Damaging	Possibly Damaging	143980534	0.223	0.195
2	28752614	C	G	PLB1	p.Q146E	Tolerated	Benign	141605399	0.062	0.017
2	28761981	G	A	PLB1	p.V212I; p.V223I	Damaging	Probably Damaging	6753929		0.048
2	241696844	TCC		KIF1A	p.E917del					
2	241696871	TCC		KIF1A	p.E917del					
3	39225650	C	T	XIRP1	p.G1763R; p.G446R	Tolerated	Benign	200656152	0.008	0.008
3	39227089	G	T	XIRP1	p.A1283D	Tolerated	Benign	773527256		0.002
3	121341019	A	T	FBXO40	p.K248I	Tolerated	Benign	142436040	0.292	0.476
3	121341882	T	C	FBXO40	p.Y536H	Tolerated	Probably Damaging	781782231		0.001
4	265024	C	T	ZNF732	p.R541H	Tolerated	Benign	200663767	0.131	0.14
4	265955	T	C	ZNF732	p.I231V	Tolerated	Benign	144919218	0.153	0.162
4	100515934	T	C	MTTP	p.M295T; p.M268T	Tolerated	Benign	146513720	0.008	0.006
4	100542308	G	C	MTTP	p.L838F; p.L811F	Tolerated	Benign	144590904	0.115	0.13
5	121515248	A	G	LOC100505 841	p.T13A			184376878		0.323
5	121515251	A	G	LOC100505 841	p.M14V					
5	145317769	C	A	SH3RF2	p.T93K		Benign	760499672		0.002
5	145379844	G	A	SH3RF2	p.R201Q		Possibly Damaging	35453884	0.323	0.231
6	1390276		CCGCCG	FOXF2	p.A40_A41dup					0.072

6	1390277	CCGCCG		FOXF2	p.A40_A41del			777365162		0.09
7	15725801	TGG		MEOX2	p.H80del			750338773		
8	144511957	TGG		MAFA	p.H208del			765697134		
8	144511957	TGGTGG		MAFA	p.H207_H208del					
8	144511960	TGG		MAFA	p.H208del					
9	33797828	C	T	PRSS3	p.R68C; p.R82C; p.R125C; p.R61C		Possibly Damaging	143209949		0.071
9	33797891	A	T	PRSS3	p.N89Y; p.N82Y; p.N146Y; p.N103Y		Benign	567341610		0.009
9	33797898	C	T	PRSS3	p.A105V; p.A84V; p.A91V; p.A148V		Benign	751456445		0.009
9	33798504	A	C	PRSS3	p.K152Q; p.K159Q; p.K173Q; p.K216Q		Benign	763882223		0.037
11	48387918	T	A	OR4C5	p.I34F	Tolerated				
11	48387919	G		OR4C5	p.F33fs*6					
11	48387947		TA	OR4C5	p.F24fs*5					
12	1902879	G	A	CACNA2D4	p.P1119L	Tolerated	Benign	145150489	0.191	0.18
12	11183720	T	A	PRH1- TAS2R31; PRH1- TAS2R14	p.N72I	Tolerated	Benign			
12	11214025	A	T	PRH1- TAS2R46; PRH1- TAS2R14	p.F290Y	Tolerated	Benign	372278369		0.009
12	11243936	C	G	PRH1- TAS2R43; PRH1- TAS2R14	p.R298T	Tolerated	Possibly Damaging	11537119		0.223
12	96377687	A	G	HAL				141634423	0.046	0.023
12	96388605	T	C	HAL				140799551	0.008	0.015
12	96389455	CTCGTTGTT		HAL	p.N76_E78del			745343950	0.104	0.001
13	25671700	T	C	PABPC3	p.V455A	Tolerated	Benign	201952806		0.016
16	89017420	CCTGGACCG GCACCGGCA		CBFA2T3; LOC100129	p.P323_G389del					0.012

		CAGAGGGTC AGAGTGTG GCACCTGTC TTCCGGATC TGTTACCC CTCCCCTGG ACCGGCACC GCCACAGAG GGTCAGAGT GTTGGCACC TGTCTTCCG GATCTGTTC ACCCCTCCC CTGGATCGG CACCGGCAC AGAGGGTCA GAGTGTGG CACCTGTCT TCCGGATCT GTTACCCG TCC		697						
16	89017620	C	G	CBFA2T3; LOC100129 697	p.P365R			71395352		0.027
18	29046607	T	G	DSG3	p.V509G	Tolerated	Possibly Damaging	149262687	0.377	0.268
20	42969950	G		R3HDML	p.G126fs*6			567545745	0.216	0.195
20	42973972	A	G	R3HDML	p.N195D	Tolerated	Benign	144380945	0.431	0.379
X	37028209	G	A	FAM47C	p.D576N	Tolerated	Benign	782543670		0.044
X	37028623	C	A	FAM47C	p.L714I	Tolerated	Probably Damaging	201919807	0.028	0.014
X	151869833	G	T	MAGEA3; MAGEA6	p.V175L	Tolerated	Benign	146486229	0.18	0.164
X	151935240	C	A	MAGEA3; MAGEA6	p.L309F	Damaging	Benign	61750034		0.441
X	151935244	A	G	MAGEA3 MAGEA6;	p.V308A	Activating	Benign	35780974	0.038	0.457
M	5460	G	A	MT-ND2	p.A331T			3021088		