

Supplementary Materials:

Genes	Retina/RPE		Choroid		Sclera	
	Fold Change	p-value	Fold Change	p-value	Fold Change	p-value
<i>PPFIA2</i>	NS	NS	2.35	1.3X10 ⁻³	1.5	1.6X10 ⁻³
<i>PTPRF</i>	1.24	2.65X10 ⁻⁵	6.42	7X10 ⁻⁴	1.11	1X10 ⁻⁴
	1.19	2.65X10 ⁻⁵	NS	NS	1.11	3.3X10 ⁻³
<i>PTPRR</i>	1.44	2.65X10 ⁻⁵	3.04	4.7X10 ⁻³	NS	NS

Supplementary Table S1. Genes Differentially Expressed Related to Candidate Genes from Association. Genes selected for follow up validation by real time quantitative PCR. Multiple values for each gene indicate multiple probes within the same gene. NS indicates the fold change was not statistically significant.

Gene/SNP	Assay ID
<i>rs4764971</i>	C_30866249_10
<i>rs7134216</i>	C_30023434_10
<i>rs17306116</i>	C_33218892_10
<i>rs3803036</i>	C_25749934_20
<i>rs824311</i>	C_8342112_10
<i>PPFIA2</i>	Hs00170308_m1
<i>PTPRF</i>	Hs00160858_m1
<i>PTPRR</i>	Hs00373136_m1
<i>18S</i>	Hs03003631_g1
<i>GAPDH</i>	Hs02758991_g1

Supplementary Table S2. Taqman® Genotyping and Gene Expression Assay Identification Numbers.

SNP	Chimp	Orangutan	Rhesus	Marmoset	Mouse	Rat	Cow	Pig	Guinea Pig	Dog	Elephant	Opossum	Chicken
<i>rs3803036</i>	X	X	X	X	X	X	X	X	X	X	X	X	X
<i>rs1520562</i>	X	X	X	X					X		X		
<i>rs1358228</i>	X	X	X	X	X	X	X	X	X	X	X		
<i>rs17306116</i>	X	X	X	X						X	X		
<i>rs790436</i>	X	X	X	X					X	X	X		
<i>rs1558726</i>	X	X	X	X	X	X			X		X		
<i>rs741525</i>	X	X		X			X	X	X	X	X		
<i>rs7134216</i>	X	X	X	X			X		X				
<i>rs4764971</i>	X	X	X			X	X			X	X		

Supplementary Table S3. Conservation of Top SNPs from Association. X indicates SNP is conserved.

Locus	OMIM	Location	Reference study	Myopia severity	Genes	Nearby Genes
				Age of onset		
MYP1	310460	Xq28	Schwartz et al. 1990	High: -6.75 D to -11.25 D	<i>MTM1 DUSP9</i> <i>MTMR1</i>	
			Young et al. 2004	Early: 1.5 to 5 years		
MYP2	160700	18p11.31	Young et al. 1998	High: -6 D to -21 D/	<i>PTPRM PTPN2</i>	

				Early: 6.8 years (average)		
MYP3	603221	12q21 – q23	Young et al. 1998	High: -6.25 D to -15 D	<i>PTPRR PTPRB PTPRQ DUSP6</i>	<i>PTPN11 SSH1</i>
				Early: 5.9 years (average)		
MYP4	608367	7q36	Naiglin et al. 2002	High: -13.05 D (average)	<i>PTPRN2</i>	
MYP5	608474	17q21 – q22	Paluru et al. 2003	High: -5.5 D to -50 D	<i>MTMR4</i>	
				Early: 8.9 years (average)		
MYP6	608908	22q12	Stambolian et al. 2004	Mild-moderate: -1.00 D or lower	<i>MTMR3 DUSP18</i>	
MYP7	609256	11p13	Hammond et al. 2004	-12.12 D to +7.25 D		
MYP8	609257	3q26	Hammond et al. 2004	-12.12 D to +7.25 D		
MYP9	609258	4q12	Hammond et al. 2004	-12.12 D to +7.25 D		
MYP10	609259	8p23	Hammond et al. 2004	-12.12 D to +7.25 D	<i>MTMR9</i>	
MYP11	609994	4q22 – q27	Zhang, Guo et al. 2005	High: -5 D to -20 D		<i>PTPN13</i>
				Early: before school age		
MYP12	609995	2q37.1	Paluru et al. 2005	High: -7.25 D to -27 D	<i>DUSP28</i>	
				Early: before 12 years		
MYP13	300613	Xq23 – q25	Zhang, Guo et al. 2006	High: -6 D to -20 D		
				Early: before school age		
MYP14	610320	1p36	Wojciechowski R, Moy C et al. 2006	Moderate to high: -3.46 D (average)	<i>EYA3</i>	
MYP15	612717	10q21.1	Nallasamy et al 2007			
MYP16	612554	5p15.33-15.2	Lam et al 2008	High grade myopia	<i>MTMR12</i>	
HMYO21		21q22.3	Nishizaki 2009			
MYOX		DXS6800 and DXS6789	Stambolian et al. 2005			
HMYOX		Xq25-q27.2	Zhang et al 2007			
		7p15	Ciner et al 2008	Quantitative trait locus in AA		
		20 (47-62 cM)	Ciner et al 2009			
		14q22.1-24.2	Yang et al 2009		<i>STYX</i>	
		15q12-13	Yu et al 2007		<i>MTMR10</i>	
		5q (98 cM)	Zhu et al 2008		<i>DUSP1</i>	

Supplementary Table S4. PTP Related Genes in Known Myopia Loci. Myopia Loci were taken from NEIBank: Candidate Disease Loci – Myopia and Hornbeak et al 2009.

A)

Qualitative (APL)											
Notes	Marker	SE	Marker	SPH	Notes	Marker	Cauc SPH	Notes	Marker	Cauc SE	Notes
	RS741525	0.001547	RS741525	0.000628	55 kb from <i>SLC9A7P1</i>	RS741525	0.000509		RS790436	0.000998	
	RS3803036	0.002173	RS7134216	0.00008	intronic <i>UHRF1BP1L</i>	RS790436	0.00078		RS1358228	0.001603	
	RS2698746	0.002434	RS3803036	0.001224	nonsyn. In <i>PTPRR</i>	RS1358228	0.001293		RS741525	0.00212	
	RS7134216	0.003104	RS1370780	0.001899	5' UTR <i>LOC253724</i>	RS7134216	0.00274		RS2698746	0.004536	
	RS790436	0.003335	RS1358228	0.002341	76 kb upstream <i>NAV3</i>	RS1493418	0.004395		RS7134216	0.004708	
	RS1358228	0.003589	RS12300992	0.004937	27 kb upstream of <i>MYBPC1</i>	RS3803036	0.005651		RS7297574	0.005339	intronic <i>MGAT4C</i>
30 kb from <i>LOC552889</i>	RS1389496	0.004111	RS4842643	0.005714	36 kb upstream of <i>LOC728084</i>	RS953832	0.005668		RS3803036	0.005679	
intronic <i>TMTC2</i>	RS17779858	0.008538	RS824311	0.005908	3 kb upstream of <i>UTP20</i>	RS4573768	0.005923		RS1163038	0.007154	intronic <i>PTPRQ</i>

Quantitative (QTL)											
Notes	Marker	SE	Marker	SPH	Notes	Marker	Cauc SPH	Notes	Marker	Cauc SE	Notes
	RS7134216	2.84E-06	RS4764971	5.462E-07	3' UTR of <i>DEPDC4</i> , intronic <i>ACTR6</i>	RS4764971	2.25E-07		RS7134216	4.64E-06	
	RS4764971	3.94E-05	RS7134216	3.098E-06	intronic <i>UHRF1BP1L</i>	RS17306116	0.0000265		RS4764971	2.01E-05	
	RS12297646	4.24E-05	RS17306116	9.01E-06	intronic <i>PPFIA2</i>	RS1520562	0.0000351		RS12814689	6.93E-05	
	RS12814689	8.24E-05	RS1520562	0.0000495		RS7134216	0.0000449		RS3817552	6.95E-05	nonsyn. in <i>MYBPC1</i>
nonsyn. in <i>MYBPC1</i>	RS3817552	9.58E-05	RS11104117	0.0001566	intronic <i>MGAT4C</i>	RS1558726	0.0000636		RS1971036	0.000147	66 kb from <i>MIR4303</i>
	RS7304135	0.000136	RS1558726	0.000194		RS1045741	0.0000938	3' UTR of <i>PRDM4</i>	RS1163038	0.000187	intronic <i>PTPRQ</i>
66 kb from <i>MIR4303</i>	RS1971036	0.000143	RS7315130	0.0002194		RS12814689	0.0002117		RS17805748	0.000199	intronic <i>HCFC2</i>
intronic <i>PTPRQ</i>	RS1163038	0.000207	RS10506977	0.0002209		RS17805748	0.0002591		RS7304135	0.000295	

B)

Qualitative (APL) SPH

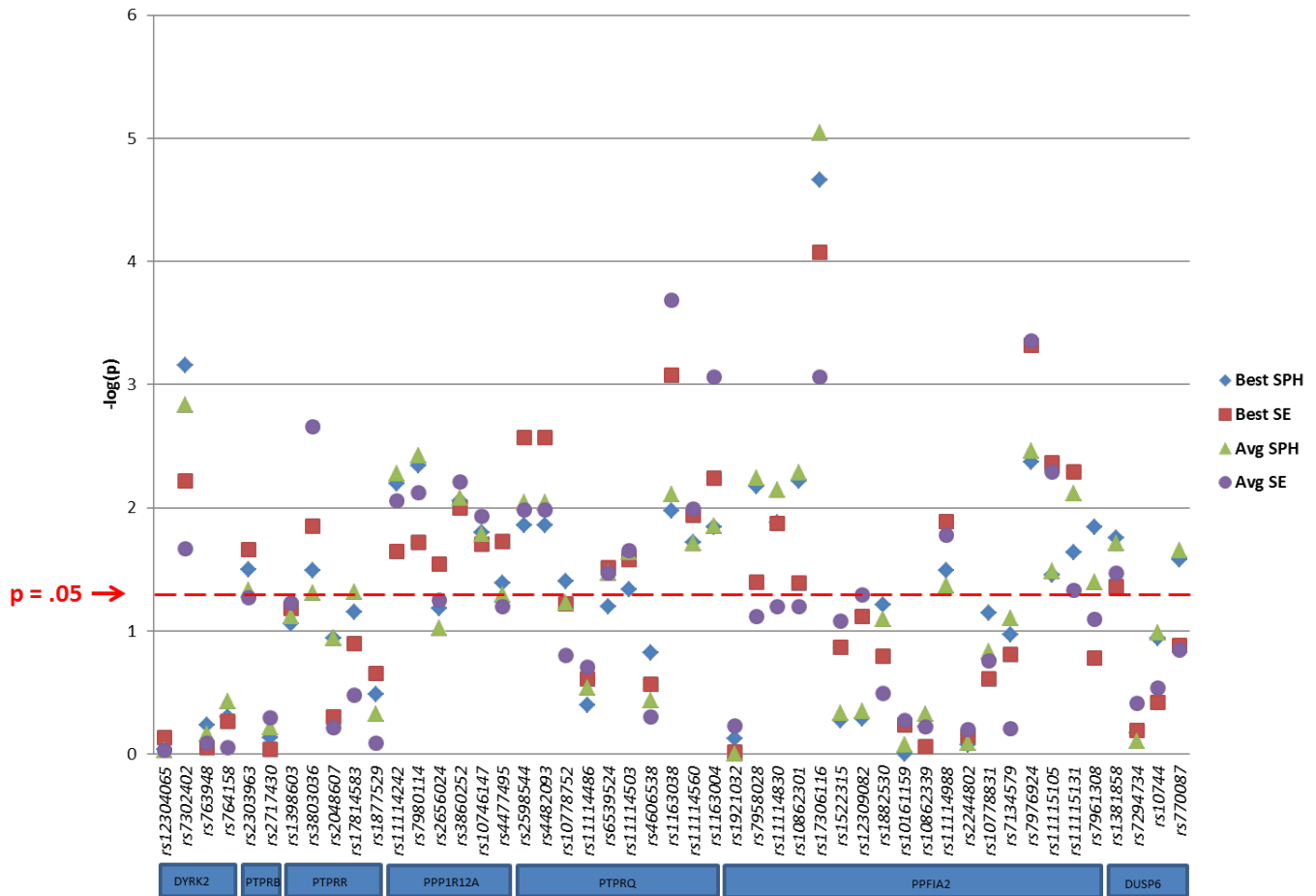
Notes	Marker	≤-5D SPH	Marker	≤-6D SPH	Notes
	RS741525	0.000509	RS790436	0.000547	
	RS790436	0.00078	RS1522315	0.001231	intronic <i>PPFIA2</i>
76 kb upstream <i>NAV3</i>	RS1358228	0.001293	RS2730523	0.001656	
intronic <i>UHRF1BP1L</i>	RS7134216	0.00274	RS7134216	0.002071	intronic <i>UHRF1BP1L</i>
intronic <i>MGAT4C</i>	RS1493418	0.004395	RS4482093	0.002881	21 kb upstream <i>PTPRQ</i>
nonsyn. In <i>PTPRR</i>	RS3803036	0.005651	RS2598544	0.003437	32 kb upstream <i>PTPRQ</i>
	RS953832	0.005668	RS4842643	0.003755	
	RS4573768	0.005923	RS741525	0.004515	
3 kb upstream of <i>UTP20</i>	RS824311	0.006785	RS3803036	0.006703	nonsyn. In <i>PTPRR</i>
	RS2698746	0.00779	RS17782889	0.00698	9 kb from <i>LOC338758</i>

Qualitative (APL) SE

Notes	Marker	≤-5D SE	Marker	≤-6D SE	Notes
	RS790436	0.000998	RS790436	0.000123	
76 kb upstream <i>NAV3</i>	RS1358228	0.001603	RS809285	0.000358	intronic <i>RIC8B</i>
	RS741525	0.00212	RS4842643	0.000527	
	RS2698746	0.004536	RS4762535	0.00322	intronic <i>ANKS1B</i>
intronic <i>UHRF1BP1L</i>	RS7134216	0.004708	RS3803036	0.003619	nonsyn. In <i>PTPRR</i>
intronic <i>MGAT4C</i>	RS7297574	0.005339	RS741525	0.005731	
nonsyn. In <i>PTPRR</i>	RS3803036	0.005679	RS2698746	0.005962	
intronic <i>PTPRQ</i>	RS1163038	0.007154	RS7297574	0.006125	intronic <i>MGAT4C</i>
intronic <i>TMTC2</i>	RS17779858	0.007614	RS2730523	0.007474	
	RS4842643	0.008589	RS1370938	0.012457	intronic <i>MSRB3</i>

Supplementary Figure S1. Concordance of Tests. A.) Top eight Qualitative and Quantitative SNPs (listed in order if statistical significance) comparing complete and Caucasian-only data for SE and SPH. B.) Top ten Qualitative SPH and SE SNPs (listed in order of statistical significance) comparing data by -5D and -6D affection criteria. Both) P-values are

color coded as blue, green and yellow for p-values $< 10^{-4}$, 10^{-3} and 10^{-2} respectively. Red lines indicate the same SNP while dashed orange lines indicate SNPs in or near the same gene. SNPs lacking descriptions of location relative to genes are $> 150\text{kb}$ from any gene. Concordance of the data can be seen at both the SNP (red lines) and gene (orange lines) level.



Supplementary Figure S2. Quantitative Association by $-\log(p)$ for All SNPs in PTP Related Genes. SNPs are placed adjacent to one another for the purposes of this graph, but they are not representative of the chromosomal distance between genes. SPH is sphere; SE is spherical equivalence; avg is average of both eyes; best is the least myopic eye.