

**Evaluation of Genetic Association of the INK4 Locus with Primary Open Angle
Glaucoma in East Indian Population**

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Supplementary Table S1: Studies done on the association of 9p21 region SNPs with POAG and its subtypes

Population ancestry	Top associated SNP from 9p21 region (minor allele)	p- value/OR	Type of study	POAG subtype	Reference
African	rs10120688 (A), rs10965245 (A)	0.002/1.21, 0.0005/0.73	Case-control	POAG, NTG	Liu et al, IOVS 2013 [1]
European	rs2157719 (G)	1.86E ⁻¹⁸ /0.69	Meta-analysis	POAG	Wiggs et al, PLoS One 2013 [2]
European	rs1063192 (G)	2.2*10 ⁻⁵ /0.74	Case-control	POAG	Dimasi et al, Am J Ophthalmol 2012 [3]
Japanese	rs523096 (A)	1.59*10 ⁻⁵ /1.99	GWAS	NTG	Takamato et al, PLoS One 2012 [4]
African	rs1063192 (C)	0.0008/0.39	Case-control	POAG	Cao D et al, PLoS One 2012 [5]
European	rs10120688	1.2×10 ⁻⁵ /NA	GWAS	POAG	Gibson et al, MolVis 2012 [6]
Japanese	rs1063192 (C)	0.0023/NA	Case-control	NTG	Mabuchi et al, Ophthalmology 2012 [7]
European	rs10120688 (A)	0.005/1.25	Case-control	Advanced POAG, HTG, NTG	Burdon et al, Ophthalmology 2012 [8]
Japanese	rs523096 (A)	3.8*10 ⁻⁹ /1.86	GWAS	POAG, NPG, HPG	Nakano et al, PLoS One 2012 [9]
Japanese	rs1063192 (C)	5.68*10 ⁻⁵ /0.79	GWAS	POAG	Osman et al, Hum Mol Genet 2012 [10]
European	rs1063192 (G)	1.41*10 ⁻⁸ /0.76	Meta-analysis	POAG	Ramdas et al, Hum Mol Genet 2011 [11]
European	rs1063192 (G)	0.0045/0.73	Case-control	VCDR, POAG	Fan et al, IOVS 2011 [12]
European	rs4977756 (A)	4.7*10 ⁻⁹ /1.5	GWAS	POAG	Burdon et al, Nat Genet 2011 [13]
European	rs1063192 (G)	6.15*10 ⁻¹¹ /NA	GWAS	VCDR	Ramdas et al, PLoS Genet 2010 [14]

Abbreviations: POAG- Primary Open Angle Glaucoma, NTG- Normal Tension Glaucoma, HTG- High Tension Glaucoma, HPG- High Pressure Glaucoma, NPG- Normal Pressure Glaucoma, VCDR- Vertical Cup-disc ratio, NA-Not available.

Note: Abbreviations used under 'POAG subtype' column are same as described in the original study. Numbers in parenthesis used in the last column denote the reference numbers.

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Supplementary Table S2: Haplotype association using 20 tag SNPs in 9p21 region

Haplotype	Frequency in cases (n=700)	Frequency in controls (n=708)	p-value
AAAGAGCAGAAGGAAAAACG*	0.005	0.017	0.0381
CAGGAAAAGAAGAAAAAGCA	0.024	0.043	0.0597
CAGGAAAAGAGGCACAAACG	0.335	0.288	0.0614
AAAGAGCAGAAGGAAAAGCA	0.008	0.0200	0.0633
AAAGAGCAGAAGACAAACG	0.016	0.006	0.0783
CAGGAAAAGAGGCACAAACA	0.016	0.023	0.3866
CAGAAAAAGAAGAAAAAGCA	0.078	0.067	0.4198
CAGGAAAGGAAGGCAGAGCA	0.011	0.016	0.4555
AAGGCGAAGAAGGCGAAAAA	0.06	0.070	0.4694
AAGGCAAAGGGACAACACG	0.013	0.010	0.5949
CGGGAAAGGAAGGCAGAGCA	0.171	0.161	0.6284
CGGGAAAGGAAGGCAGAGCG	0.011	0.010	0.8504
CAGAAAAAGAAGAAAAACG	0.085	0.085	0.9707

* Haplotype with significant p-value

Supplementary Figure 1: Linkage Disequilibrium (LD) plot of 34 SNPs at 9p21 in East Indian population

The plot represents the LD structure of 9p21 region in the East Indian population. Arrows show relative location of 20 tag SNPs selected to study the haplotype association. Overall the data indicates low level of LD in this region, which is consistent with high recombination rates as shown in Figure 1 (right vertical axis).

