

**Appendix 1:** Significant SNP p values with odds ratio (OR) from the combined GLAUGEN-NEIGHBOR dataset for genes in the estrogen metabolic pathway that were significantly associated with POAG overall or with its subtypes among women.

Gene, Chromosome (Chr), # of SNPs assessed <sup>1</sup>	SNP <sup>2</sup>	POAG Overall			High Pressure Glaucoma			Normal Pressure Glaucoma		
		Gene p-value, % SNPs with SNP p<0.05 <sup>3</sup>	SNP OR	SNP p-value	Gene p-value, % SNPs with SNP p<0.05 <sup>3</sup>	SNP OR	SNP p-value	Gene p-value, % SNPs with SNP p<0.05 <sup>3</sup>	SNP OR	SNP p value
ESR1 Chr 6 # SNPs: 127	rs11155813	p<0.001, 19%	1.15	0.10	p<0.001, 18%	1.35	0.01	p=0.39, 8%	1.08	0.60
	rs12154178		0.84	0.002		0.84	0.02		0.85	0.10
	rs13203975		1.17	0.06		1.12	0.30		1.45	0.01
	rs1884051		0.89	0.04		0.89	0.12		0.90	0.26
	rs1884054		0.84	0.001		0.82	0.01		0.85	0.08
	rs2295193		0.90	0.05		0.83	0.01		0.92	0.38
	rs2347869		0.84	0.001		0.82	0.01		0.85	0.07
	rs2347871		0.84	0.001		0.83	0.01		0.83	0.05
	rs2485209		0.88	0.02		0.89	0.11		0.90	0.24
	rs2813487		1.09	0.12		1.21	0.01		1.04	0.70
	rs2813550		0.90	0.11		0.85	0.049		0.95	0.61
	rs2881766		1.09	0.22		1.23	0.02		0.96	0.75
	rs2982683		0.84	0.003		0.85	0.04		0.80	0.03
	rs3003925		0.87	0.04		0.93	0.41		0.85	0.15
	rs3020314		0.88	0.03		0.87	0.06		0.86	0.12
	rs3020318		1.19	0.002		1.22	0.01		1.17	0.10
	rs3020343		0.90	0.046		0.89	0.11		0.94	0.50
	rs3020348		0.89	0.04		0.88	0.08		0.93	0.46
	rs3020410		1.19	0.02		1.15	0.18		1.50	0.002
	rs3778082		1.11	0.23		1.04	0.73		1.37	0.03
	rs3778084		0.90	0.23		0.97	0.79		0.72	0.02
	rs3778089		1.11	0.23		1.03	0.77		1.38	0.02
	rs3798577		1.10	0.07		1.20	0.01		1.11	0.27
	rs3818109		1.14	0.02		1.23	0.01		1.08	0.41
	rs6557171		1.13	0.03		1.13	0.11		1.12	0.25
	rs6927072		1.16	0.01		1.18	0.03		1.21	0.049

	rs6932864		1.11	0.22		1.04	0.71		1.34	0.04
	rs718527		1.10	0.08		1.22	0.01		1.11	0.27
	rs722208		0.89	0.04		0.90	0.19		0.80	0.03
	rs726281		0.84	0.004		0.84	0.03		0.88	0.19
	rs7743290		0.87	0.03		0.94	0.44		0.77	0.01
	rs7753153		0.88	0.13		0.79	0.03		0.97	0.83
	rs7761846		0.76	0.005		0.75	0.02		0.76	0.09
	rs866457		1.12	0.04		1.17	0.02		1.07	0.48
	rs926777		1.21	0.002		1.22	0.02		1.12	0.29
	rs9322361		0.93	0.32		0.81	0.04		0.95	0.67
	rs9397463		1.27	0.002		1.32	0.01		1.25	0.09
	rs985695		1.31	1.72E-04		1.40	2.65E-04		1.25	0.06
AKR1D1 Chr 7 # SNPs: 37	rs10954596		1.09	0.14		1.11	0.15		1.26	0.02
	rs11982192		0.90	0.09		0.89	0.17		0.79	0.03
	rs11984112	p=0.05, 8%	1.19	0.02	p>0.999, 0%	1.20	0.07	p=0.046, 8%	1.12	0.38
	rs12666806		1.22	0.02		1.20	0.11		1.17	0.26
	rs1872929		1.10	0.15		1.13	0.17		1.30	0.02
	rs2120846		1.14	0.03		1.14	0.11		1.22	0.05
CYP3A4 Chr 7 # SNPs: 22	rs585071		0.81	0.045		0.73	0.02		0.86	0.41
	rs667660	p=0.01, 14%	0.83	0.08	p<0.001, 18%	0.75	0.04	p>0.999, 0%	0.91	0.58
	rs678040		0.79	0.03		0.72	0.01		0.82	0.26
	rs800667		0.79	0.03		0.72	0.01		0.82	0.26
AKR1C4 Chr 10 # SNPs: 47	rs10904442		0.91	0.22		0.80	0.02		1.00	0.99
	rs2398152		1.08	0.23		1.21	0.04		1.07	0.53
	rs11253059		0.86	0.10		0.71	0.01		1.02	0.92
	rs1931676	p>0.999, 0%	0.83	0.09	p=0.002, 17%	0.67	0.01	p>0.999, 0%	1.05	0.79
	rs1931677		1.20	0.09		1.49	0.01		0.95	0.79
	rs2895056		1.15	0.11		1.40	0.01		0.98	0.90
	rs12260226		1.15	0.13		1.39	0.01		1.00	0.99
	rs1889457		0.87	0.12		0.72	0.01		1.02	0.91
CYP17A1 Chr 10 # SNPs: 49	rs10786706		1.07	0.20		1.02	0.74		1.29	0.01
	rs4290163	p>0.999, 0%	1.03	0.56	p>0.999, 0%	0.98	0.75	p=0.04, 6%	1.21	0.048
	rs6163		1.05	0.43		0.99	0.91		1.22	0.04

ESR2 Chr 14 # SNPs: 38	rs10137185		1.18	0.07		1.15	0.23		1.44	0.02
	rs1152592		0.99	0.91		1.16	0.04		0.94	0.50
	rs1256044		1.05	0.42		0.93	0.32		1.21	0.04
	rs1256063		1.00	0.97		1.14	0.34		0.60	0.01
	rs1256114	p=0.11, 5%	1.16	0.06	p=0.10, 5%	1.13	0.25	p<0.001, 21%	1.52	0.002
	rs1268656		0.84	0.046		0.83	0.10		0.66	0.004
	rs1952586		0.87	0.12		0.88	0.30		0.70	0.02
	rs7159462		1.22	0.049		1.32	0.03		1.52	0.01
	rs7161192		1.11	0.07		1.01	0.88		1.23	0.04
CYP1A1/CYP1A2 <sup>4</sup> Chr 15 # SNPs: 54	rs2470893		1.07	0.28	CYP1A1: p>0.999, 0%	1.04	0.60	CYP1A1: p<0.001, 8%	1.24	0.03
	rs2472297		1.08	0.25		0.96	0.63		1.37	0.004
	rs3743484		1.31	0.08		1.05	0.84		1.97	0.01
	rs8025170	CYP1A2: p>0.999, 0%	0.94	0.45	CYP1A2: p=0.21, 2%	0.81	0.03	CYP1A2: p=0.004, 6%	0.93	0.58
HSD17B1 Chr 17 # SNPs: 18	rs2134808	p=0.06, 6%	0.88	0.03	p<0.001, 11%	0.83	0.02	p>0.999, 0%	0.95	0.60
	rs7208107		1.12	0.25		1.32	0.048		0.94	0.69
COMT Chr 22 # SNPs: 58	rs1005873		0.87	0.11		0.76	0.01		0.81	0.13
	rs11541479		0.85	0.04		0.82	0.06		0.85	0.22
	rs165722		0.98	0.76		0.84	0.02		0.97	0.75
	rs165728		0.70	0.003		0.61	0.001		0.92	0.70
	rs165815		0.85	0.04		0.79	0.02		0.95	0.68
	rs17210001		0.86	0.16		0.87	0.34		0.69	0.04
	rs174699		0.67	0.001		0.56	8.36E-05		0.87	0.51
	rs1978058	p<0.001, 19%	0.89	0.049	p<0.001, 19%	0.86	0.048	p=0.01, 12%	0.81	0.03
	rs2531697		1.55	1.89E-04		1.83	4.10E-05		1.10	0.65
	rs3788322		0.88	0.03		0.84	0.02		0.92	0.38
	rs3804047		0.87	0.02		0.85	0.04		0.75	0.003
	rs4680		0.91	0.09		0.85	0.02		0.98	0.81
	rs4819850		0.91	0.07		0.90	0.16		0.77	0.01
	rs7410379		1.15	0.02		1.11	0.17		1.33	0.005
rs756661		1.10	0.08		1.10	0.20		1.29	0.01	

	rs887199		1.18	0.03		1.26	0.02		1.07	0.63
	rs9605030		1.17	0.047		1.12	0.28		1.40	0.01
STS Chr X # SNPs: 25	rs1465067		1.11	0.10		1.21	0.02		1.08	0.44
	rs2694751		0.89	0.03		0.81	0.003		0.90	0.29
	rs4131206		0.88	0.04		0.79	0.004		0.91	0.40
	rs4830608		0.89	0.03		0.80	0.002		0.92	0.39
	rs5933846		1.14	0.04		1.28	0.004		1.08	0.47
	rs5933912		1.13	0.03		1.25	0.002		1.04	0.67
	rs5934907	p<0.001, 36%	0.89	0.04	p<0.001, 52%	0.81	0.003	p<0.001, 4%	0.91	0.33
	rs5978904		1.11	0.05		1.23	0.005		1.08	0.42
	rs5979364		0.91	0.15		0.82	0.02		0.96	0.72
	rs5979467		0.99	0.86		1.01	0.93		0.79	0.03
	rs5979866		0.88	0.02		0.81	0.003		0.93	0.44
	rs7058445		1.12	0.07		1.27	0.004		1.07	0.51
	rs802898		1.13	0.03		1.25	0.002		1.10	0.33
	rs809104		0.88	0.02		0.80	0.002		0.90	0.27

1. The number of single nucleotide polymorphisms (SNPs) within the gene represents the number of SNPs within  $\pm 50$ kb of the gene that were available after quality control filters.
2. All SNPs have reference alleles of A except for rs3743484 and rs3743484, which have C reference alleles.
3. Gene p-values are permuted p-values calculated from pathway analysis. SNP p-values are meta-analyzed values adjusted for covariates generated with PLINK and METAL (see methods for details).
4. CYP1A1 and CYP1A2 are adjacent and hence share 38 SNPs in common within their  $\pm 50$  kb windows. The genes were treated separately in PARIS and no features overlap between the two, but since the focus of this table is to highlight potentially interesting SNPs, the genes were included together.

