

**Supplemental Table 2.** Summary of *CYP1B1* polymorphisms in PMRP POAG cases and non-POAG controls.

<b><i>CYP1B1</i> polymorphisms<sup>a</sup></b>	<b>dbSNP#</b>	<b>Allele frequency in POAG cases</b>	<b>Allele frequency in non-POAG controls</b>	<b>Allele frequency in ExAC (Eu)</b>	<b>Homozygote frequency in POAG cases</b>	<b>Homozygote frequency in non-POAG controls</b>	<b>Homozygote frequency in ExAC (Eu)</b>
c.-1-12C>T	rs2617266	31.66%	28.14%	29.03%	8.88%	6.51%	8.16%
c.142C>G,p.Arg48Gly	rs10012	31.95%	28.84%	34.63%	8.88%	6.98%	9.65%
c.355G>T,p.Ala119Ser	rs1056827	33.43%	28.60%	39.15%	10.65%	6.98%	11.6%
c.685G>A, p.Glu229Lys	rs57865060	1.57%	0.96%	0.98%	0	0	0
c.1294G>C,p.Val432Leu	rs1056836	62.72%	58.24%	56.75%	39.05%	35.63%	32.40%
c.1347T>C,p.Asp449Asp	rs1056837	61.83%	58.05%	56.81%	37.87%	35.63%	32.50%
c.1358A>G,p.Asn453Ser	rs1800440	20.41%	19.54%	18.13%	2.37%	3.45%	3.33%

Eu=European (non-Finnish) population frequency provided since the PMRP cohort is primarily Caucasian

<sup>a</sup> Nucleotide numbering is relative to reference sequence NM\_000104.3 where +1 is the A of the ATG initiation codon