# Table S1

| Study | Bonferroni correciton threshold[a] | SNP: risk allele | Chromosome | Position | Frequency[b] | *P* | OR (95% CI) |
|---|---|---|---|---|---|---|---|
| POAG vs Control | $7.65 \times 10^{-8}$ (0.05/653,519) | | | | | | |
| | | rs6689160:A | 1q25.2 | 178,158,188 | 0.9988/0.9782 | $5.8 \times 10^{-8}$ | 17.88 (4.91-65.17) |
| | | rs41524744:T | 5p15.32 | 5,360,913 | 0.9981/0.9762 | $4.7 \times 10^{-8}$ | 12.98 (4.29-39.27) |
| | | rs523096:A | 9p21.3 | 22,009,129 | 0.8944/0.8200 | $3.8 \times 10^{-9}$ | 1.86 (1.51-2.29) |
| | | rs518394:C | 9p21.3 | 22,009,673 | 0.8944/0.8207 | $5.2 \times 10^{-9}$ | 1.85 (1.50-2.28) |
| | | rs564398:A | 9p21.3 | 22,019,547 | 0.8956/0.8219 | $4.6 \times 10^{-9}$ | 1.86 (1.51-2.29) |
| | | rs7865618:A | 9p21.3 | 22,021,005 | 0.8956/0.8200 | $2.0 \times 10^{-9}$ | 1.88 (1.53-2.32) |
| | | rs8181047:G | 9p21.3 | 22,054,465 | 0.8637/0.7837 | $6.5 \times 10^{-9}$ | 1.75 (1.45-2.12) |
| | | rs1239904:A | 12q15 | 68,726,913 | 0.9976/0.9747 | $3.0 \times 10^{-8}$ | 10.63 (3.97-28.45) |
| NPG vs Control | $7.64 \times 10^{-8}$ (0.05/654,200) | | | | | | |
| | | rs523096:A | 9p21.3 | 22,009,129 | 0.9036/0.8200 | $1.0 \times 10^{-8}$ | 2.06 (1.60-2.64) |
| | | rs518394:C | 9p21.3 | 22,009,673 | 0.9036/0.8207 | $1.3 \times 10^{-8}$ | 2.05 (1.59-2.63) |
| | | rs564398:A | 9p21.3 | 22,019,547 | 0.9056/0.8219 | $8.3 \times 10^{-9}$ | 2.08 (1.61-2.67) |
| | | rs7865618:A | 9p21.3 | 22,021,005 | 0.9056/0.8200 | $4.2 \times 10^{-9}$ | 2.11 (1.64-2.71) |
| HPG vs Control | $7.65 \times 10^{-8}$ (0.05/653,317) | *not applicable* | | | | | |

[a] Bonferroni correction threshold is set as (significance level 0.05) / (the number of filtered SNPs in each study).

[b] Risk allele frequency in POAG or NPG/controls.