The potentially disease-causing variants (PDVs) in POAG as compared with control.

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| **THE POTENTIALLY DISEASE-CAUSING VARIANTS (PDVS) IN POAG AS COMPARED WITH CONTROL.** | | | | | | |
| **Gene** | **PDV in POAG**  **(n=235)** | **No. with PDVs (%)** | **PDV in Control**  **(n=241)** | **No. with PDVs (%)** | ***p*-value** | **Odds Ratio Cases:Cont (95% Cl)** |
| *ABCA1* (NM\_005502) | p.Asn161Lys, p.Arg530Met, p.(Asp677fs), p.Met1037Thr, p.Glu1253Lys, p.Gly1321Ala, | 6 (2.6) | p.Ile1876Val, p.Asp1892Ala, p.Asp1894Efs, p.His2102Pro, p. Arg2189Trp (3 cases) | 7 (3.0) | 1.0000 | 0.88 (0.24-3.10) |
| *ABO* (NM\_020469) | p.Arg337Gly, p.Met142Ile | 2 (0.9) | - | 0 (0) | 0.4989 | - |
| *AFAP1* (NM\_001134647) | p.Val151Ile, p.Ser442Trp, p.Pro494Leu | 3 (1.3) | - | 0 (0) | 0.1203 | - |
| *APOE* (NM\_000041) | p.Thr85Asn, p.Leu100Met, p.Leu111Met, p.(Ser241fs) | 4 (1.7) | p.Ala18Thr | 1 (0.4) | 0.2110 | 4.14 (0.41-205.29) |
| *ASB10* (NM\_080871) | p.Arg195Trp, p.Ala270Thr, p.Leu327Met | 3 (1.3) | p.Arg363Trp (2 cases) | 2 (0.9) | 1.5439 | 0.58 (0.18-18.63) |
| ***ATXN2* (NM\_002973)** | **p.Pro514Leu, p.Arg614Cys, p.Thr672Met, p.Arg939Gln (3 cases), p.S1186I, p.Phe1297Val** | **8 (3.4)** | **-** | **0 (0)** | **0.0033** | **-** |
| ***CDKN2B* (NM\_004936,**  **NM\_078487\*)** | **p.S10I, p.Pro72Ser, p.Ser58Ile, p.Ala70Ser; p.(Gly77fs)\*** | **5 (2.1)** | **-** | **0 (0)** | **0.0287** | **-** |
| *CYP1B1* (NM\_000104) | p.Asp218Tyr | 1 (0.4) | p. Arg368His | 1 (0.4) | 1.0000 | 1.03 (0.01-80.79) |
| *EFEMP1* (NM\_001039349) | p.Gly204Val, p.Arg477Cys, p.Leu451Pro (2 cases), p.Ter494Glu | 5 (2.1) | p. Arg141Gln | 1 (0.4) | 0.1184 | 5.20 (0.58-247.49) |
| *FNDC3B* (NM\_001135095) | p.His80Asn, p.Gly640Cys, p.Pro695Thr, p.Tyr848Ter | 4 (1.7) | - | 0 (0.4) | 0.0586 | - |
| ***FOXC1* (NM\_001453)** | **p.Tyr115His, p.Asp225Tyr, p.Ser305Ile, p.(Gly453fs), p.Ala478Glu, p.Arg541His** | **6 (2.6)** | **-** | **0 (0.4)** | **0.0140** | **-** |
| *GAS7* (NM\_201433) | p.Trp39Cys, p.Gly50Val, p.Val57Leu, p.Thr98Met, p.Arg415Ser | 5 (2.1) | p.Gly160Arg | 1 (0.4) | 0.1184 | 5.20 (0.58-247.49) |
| *LOXL1* (NM\_005576) | p.Ser69Tyr, p.Ala115Glu, p.Tyr188His, p.Cys448Phe, p.Gln519His, p.Asn530Lys | 6 (2.6) | p.Arg562His | 1 (0.4) | 0.0648 | - |
| ***MYOC* (NM\_000261)** | **p.Arg272Ter, p.Gln337Arg, p.Gln337His, p.Gln368Ter, p.Pro370Leu, p.Asp384Asn** | **6 (2.6)** | **-** | **0 (0)** | **0.0140** | **-** |
| *OPTN* (NM\_021980) | p.Glu230Gly, p.Val498Asp | 2 (0.9) | p.Leu32Arg, p.Lys557Glu | 2 (0.9) | 0.6195 | 1.03 (0.11-121.95) |
| *PAK7* (NM\_177990) | p.Gly291Glu, p.Gly310Glu, p.Ser707Phe | 3 (1.3) | p.Ser132Cys, p.Asn541Lys | 2 (0.9) | 0.6235 | 0.68 (0.18-18.63) |
| *PAX6* (NM\_001258465) | p.Thr63Ser, p.Arg266Ile | 2 (0.9) | p. Arg92Gln | 1 (0.4) | 0.6195 | 2.06 (0.11-121.95) |
| *PITX2* (NM\_000325) | p.Asp64Tyr, p.Arg115Cys, p.Arg130Trp, p.Ala265Thr | 4 (1.7) | - | 0 (0.4) | 0.0586 | - |
| *TMCO1* (NM\_001256165) | p.Gly12Ser | 1 (0.4) | **-** | 0 (0) | 0.4937 | - |
| ***TXNRD2* (NM\_006440)** | **p.Val67Met, p.Tyr228Asp, p.Gly290Val (3 cases), p.Ala429Thr, p.Arg492Trp, p.Lys511Met** | **8(3.4)** | **p.Gly83Ser** | **1 (0.4)** | **0.0190** | **7.34 (0.1-376.19)** |
| *WDR36* (NM\_139281) | p.Arg95Gly, p.Ala147Thr, p.Pro780Leu | 3 (1.3) | p.Ile276Met | 1 (0.4) | 0.3672 | 3.10 (0.25-163.45) |

\* indicates the transcripts ID and the position when the variants occur only in the corresponding transcript. The odds ratio is calculated from the ratio of cases with and without PDVs in each gene in cases divided by the corresponding ratio in controls. P-values were calculated using a two-sided Fisher's Exact Test.