Appendix 7. Functional enrichments for differentially abundant proteins also associated with human ocular pathologies (sub-clinical AMD, AMD, POAG, cataract, and choroidal neovascularization)**.** This analysis used the STRING database to identify gene ontologies and pathways that were overrepresented (FDR<0.05) in the protein list relative to the *Homo sapiens* genomic background. The results for each category are ordered from lowest-highest FDR. Abbreviations are as follows: AMD= Age-related macular degeneration, POAG= Primary open angle glaucoma.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Category** | **Pathway ID** | **Pathway description** | **Number of differentially abundant proteins** | **FDR** |
| Stress/ Oxidative Stress | GO.0006979 | Response to oxidative stress | 7 | 0.004 |
| GO.0000302 | Response to reactive oxygen species | 5 | 0.01 |
| GO.1901700 | Response to oxygen-containing compound | 10 | 0.03 |
| GO.0080134 | Regulation of response to stress | 10 | 0.045 |
| GO.0019430 | Removal of superoxide radicals | 2 | 0.046 |
| Cholesterol Homeostasis | GO.0034375 | High-density lipoprotein particle remodeling | 3 | 0.003 |
| GO.0043691 | Reverse cholesterol transport | 3 | 0.004 |
| KEGG\_4977 | Vitamin digestion and absorption | 3 | 0.005 |
| GO.0090208 | Positive regulation of triglyceride metabolic process | 3 | 0.005 |
| GO.0070508 | Cholesterol import | 2 | 0.006 |
| GO.0033344 | Cholesterol efflux | 3 | 0.01 |
| KEGG\_4975 | Fat digestion and absorption | 3 | 0.01 |
| GO.0070328 | Triglyceride homeostasis | 3 | 0.012 |
| GO.0034384 | High-density lipoprotein particle clearance | 2 | 0.019 |
| GO.0042627 | Chylomicron | 2 | 0.024 |
| GO.0030300 | Regulation of intestinal cholesterol absorption | 2 | 0.025 |
| GO.0034380 | High-density lipoprotein particle assembly | 2 | 0.025 |
| GO.0010873 | Positive regulation of cholesterol esterification | 2 | 0.028 |
| GO.0010898 | Positive regulation of triglyceride catabolic process | 2 | 0.028 |
| GO.0097006 | Regulation of plasma lipoprotein particle levels | 3 | 0.028 |
| GO.0050994 | Regulation of lipid catabolic process | 3 | 0.028 |
| GO.0034361 | Very-low-density lipoprotein particle | 2 | 0.033 |
| GO.0046889 | Positive regulation of lipid biosynthetic process | 3 | 0.037 |
| GO.0034372 | Very-low-density lipoprotein particle remodeling | 2 | 0.04 |
| GO.0034364 | High-density lipoprotein particle | 2 | 0.042 |
| GO.0051006 | Positive regulation of lipoprotein lipase activity | 2 | 0.045 |
| GO.0042632 | Cholesterol homeostasis | 3 | 0.046 |
| GO.0015914 | Phospholipid transport | 3 | 0.046 |
| Response to Stimulus | GO.0010035 | Response to inorganic substance | 9 | 0 |
| GO.0061045 | Negative regulation of wound healing | 4 | 0.004 |
| GO.0009628 | Response to abiotic stimulus | 11 | 0.004 |
| GO.0032102 | Negative regulation of response to external stimulus | 6 | 0.005 |
| GO.1903035 | Negative regulation of response to wounding | 5 | 0.006 |
| GO.0080184 | Response to phenylpropanoid | 2 | 0.045 |
| GO.0042060 | Wound healing | 7 | 0.049 |
| Protein Complex | GO.0071822 | Protein complex subunit organization | 15 | 0 |
| GO.0006461 | Protein complex assembly | 14 | 0 |
| GO.0070271 | Protein complex biogenesis | 14 | 0 |
| GO.0051258 | Protein polymerization | 5 | 0.001 |
| GO.0051260 | Protein homooligomerization | 6 | 0.005 |
| GO.0051259 | Protein oligomerization | 7 | 0.006 |
| GO.0031109 | Microtubule polymerization or depolymerization | 3 | 0.019 |
| Blood Coagulation | GO.0072562 | Blood microparticle | 9 | 0 |
| GO.0030195 | Negative regulation of blood coagulation | 3 | 0.028 |
| GO.0031639 | Plasminogen activation | 2 | 0.045 |
| Transport | GO.0051180 | Vitamin transport | 3 | 0.01 |
| GO.0015711 | Organic anion transport | 6 | 0.017 |
| GO.0071702 | Organic substance transport | 12 | 0.028 |
| GO.0005215 | Transporter activity | 10 | 0.043 |
| Binding | GO.0005515 | Protein binding | 23 | 0.006 |
| GO.0042802 | Identical protein binding | 10 | 0.023 |
| GO.0043178 | Alcohol binding | 4 | 0.043 |
| Catabolic Process | GO.0044712 | Single-organism catabolic process | 9 | 0.012 |
| GO.0009056 | Catabolic process | 11 | 0.049 |
| Biological Process Regulation (particularly regulation of cell structure/ adhesion) | GO.0034114 | Regulation of heterotypic cell-cell adhesion | 3 | 0.003 |
| GO.1900026 | Positive regulation of substrate adhesion-dependent cell spreading | 3 | 0.01 |
| GO.0065008 | Regulation of biological quality | 16 | 0.016 |
| GO.0034116 | Positive regulation of heterotypic cell-cell adhesion | 2 | 0.028 |
| GO.0010769 | Regulation of cell morphogenesis involved in differentiation | 5 | 0.046 |
| GO.0051492 | Regulation of stress fiber assembly | 3 | 0.046 |
| GO.0050878 | Regulation of body fluid levels | 7 | 0.047 |
| Cellular Component | GO.0044422 | Organelle part | 32 | 0 |
| GO.0031988 | Membrane-bounded vesicle | 23 | 0 |
| GO.0070062 | Extracellular exosome | 21 | 0 |
| GO.0044446 | Intracellular organelle part | 31 | 0 |
| GO.0005576 | Extracellular region | 22 | 0 |
| GO.0044421 | Extracellular region part | 21 | 0 |
| GO.0005615 | Extracellular space | 11 | 0.003 |
| GO.0060205 | Cytoplasmic membrane-bounded vesicle lumen | 4 | 0.003 |
| GO.0042470 | Melanosome | 4 | 0.005 |
| GO.0009986 | Cell surface | 8 | 0.005 |
| GO.0016023 | Cytoplasmic membrane-bounded vesicle | 9 | 0.01 |
| GO.0005577 | Fibrinogen complex | 2 | 0.01 |
| GO.0042995 | Cell projection | 11 | 0.016 |
| GO.0034774 | Secretory granule lumen | 3 | 0.021 |
| GO.0043209 | Myelin sheath | 4 | 0.021 |
| GO.0044444 | Cytoplasmic part | 25 | 0.022 |
| GO.0005901 | Caveola | 3 | 0.025 |
| GO.0043232 | Intracellular non-membrane-bounded organelle | 16 | 0.026 |
| GO.0043202 | Lysosomal lumen | 3 | 0.028 |
| GO.0098805 | Whole membrane | 11 | 0.028 |
| GO.0071682 | Endocytic vesicle lumen | 2 | 0.028 |
| GO.0044433 | Cytoplasmic vesicle part | 6 | 0.028 |
| GO.0005829 | Cytosol | 15 | 0.028 |
| GO.0005938 | Cell cortex | 4 | 0.033 |
| GO.0043233 | Organelle lumen | 17 | 0.037 |
| GO.0031902 | Late endosome membrane | 3 | 0.038 |
| GO.0030139 | Endocytic vesicle | 4 | 0.038 |
| GO.0009897 | External side of plasma membrane | 4 | 0.039 |
| GO.0044440 | Endosomal part | 5 | 0.04 |
| GO.0098552 | Side of membrane | 5 | 0.04 |
| GO.0005737 | Cytoplasm | 29 | 0.042 |
| GO.0098590 | Plasma membrane region | 7 | 0.046 |
| GO.0045121 | Membrane raft | 4 | 0.046 |
| GO.0012505 | Endomembrane system | 15 | 0.048 |
| Cellular Organization/ Localization | GO.0016043 | Cellular component organization | 27 | 0 |
| GO.0043933 | Macromolecular complex subunit organization | 19 | 0 |
| GO.0022607 | Cellular component assembly | 18 | 0 |
| GO.0044085 | Cellular component biogenesis | 18 | 0 |
| GO.0065003 | Macromolecular complex assembly | 17 | 0 |
| GO.0034622 | Cellular macromolecular complex assembly | 10 | 0 |
| GO.0043623 | Cellular protein complex assembly | 8 | 0 |
| GO.0048513 | Organ development | 14 | 0.044 |
| GO.0033036 | Macromolecule localization | 12 | 0.046 |