Table 4: Enriched Pathways for WGCNA modules

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| Module | Library | Enriched Categories |
| Black\* | Brain | Ribosome |
| *Ribosome/Translation* | GO BP | viral transcription, translational initiation, translational termination, cellular protein com- |
|  |  | plex disassembly, translational elongation, SRP-dependent cotranslational protein targeting |
|  |  | to membrane, cotranslational protein targeting to membrane, protein complex disassem- |
|  |  | bly, viral life cycle, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, |
|  |  | protein targeting to ER, macromolecular complex disassembly, establishment of protein lo- |
|  |  | calization to endoplasmic reticulum, protein localization to endoplasmic reticulum, protein |
|  |  | targeting to membrane, translation, nuclear-transcribed mRNA catabolic process |
|  | GO MF | structural constituent of ribosome |
| Blue\*2 | KEGG  Blood | Ribosome Homo sapiens  RedBloodCell, Neutrophils genesCorrelatedAcrossIndividuals |
| *Immune System* | GO BP | response to lipopolysaccharide, response to molecule of bacterial origin, extracellular matrix |
|  |  | organization, extracellular structure organization, leukocyte migration, blood coagulation, |
|  |  | coagulation, hemostasis, phagosome maturation, inflammatory response |
|  | GO MF | cell adhesion molecule binding, integrin binding, phospholipid binding |
|  | Immune | General chemokine pathways |
|  | KEGG | Fc gamma R-mediated phagocytosis, Osteoclast differentiation, Epithelial cell signaling in |
| Brown\*2 | Brain | Helicobacter pylori infection, Chemokine signaling pathway  GlutatmatergicSynapse, GlutamatergicSynapticFunction |
| *Glutamate Association* |  |  |
| Green\* | Blood | RedBloodCell |
| *Neuronal Association* | Brain | Nucleus, turquoise Cerebellum, Astrocyte probable, Nucleus, Oligodendrocyte, Oligoden- |
|  |  | drocytes, Neuron, brown pyramidalNeurons Layer5/basolateralAmygdala, AitGhezala, |
|  |  | turquoise CingulateNeurons(allTypes)/Layer5, GlutamatergicSynapticFunction, Neu- |
|  |  | ron probable, Astrocytes |
|  | GO BP | multicellular organismal reproductive process, regulation of protein complex assembly |
|  | GO MF | zinc ion binding, ubiquitin-protein transferase activity |
| Greenyellow | Blood | NKcell, Lymphcytes genesCorrelatedAcrossIndividuals |
| *Immune Association* |  |  |
| Pink | Blood | Reticulocytes genesCorrelatedAcrossIndividuals, RedBloodCell, BloodPlatelets |
| *Cell Cycle Association* | Brain | Oligodendrocyte probable |
|  | GO BP | posttranscriptional regulation of gene expression, negative regulation of cell cycle |
| Purple | Immune | IFN alpha/beta |
| *Cytokine Signalling* | GO BP | cellular response to type I interferon, type I interferon signaling pathway, response to type I |
|  |  | interferon, response to virus, defense response to virus, cytokine-mediated signaling pathway, |
|  |  | cellular response to cytokine stimulus, response to other organism, defense response to other |
|  |  | organism, response to interferon-gamma, regulation of multi-organism process, regulation of |
|  |  | cytokine production |
| Turquoise\*2 | KEGG  Blood | Herpes simplex infection, Measles, Influenza A, Hepatitis C  BloodPlatelets |
| *Glucose Metabolism* | GO BP | gluconeogenesis, monocarboxylic acid metabolic process, hexose biosynthetic process, pyru- |
|  |  | vate metabolic process, glycolytic process, monosaccharide biosynthetic process, blood co- |
|  |  | agulation, coagulation, platelet activation, positive regulation of immune effector process, |
|  |  | hemostasis, lipid catabolic process, single-organism carbohydrate catabolic process, regu- |
|  |  | lation of production of molecular mediator of immune response, carbohydrate catabolic |
|  |  | process |
|  | GO MF | phosphatase binding, protein phosphatase binding, isomerase activity |
|  | KEGG | Glycolysis / Gluconeogenesis |
| Yellow\* | GO MF | transferase activity, transferring one-carbon groups |
| *Metabolism/CellCycle* | GO BP | ncRNA metabolic process, ncRNA processing, regulation of proteasomal ubiquitin- |
|  |  | dependent protein catabolic process, cellular amino acid metabolic process, regulation of |
|  |  | proteasomal protein catabolic process, mitotic cell cycle, rRNA processing, regulation of |
|  |  | translation, establishment of RNA localization, nucleic acid transport, regulation of prote- |
|  |  | olysis involved in cellular protein catabolic process, RNA transport |
|  | KEGG | RNA transport |
|  | Brain | Autism associated module M12, AitGhezala, Mitochondria, Neuron probable, |
|  |  | Autism differential splicing events |

Table of WGCNA modules and corresponding gene enrichment results. Criteria for inclusion of Enrichment Category were a p-value below 0.05 and a minimum of 5 probes overlapping with the pathway. The grey and magenta modules are not included as they did not contain any Pathways that passed the inclusion criteria. For complete results see Supplementary Table 4. Only probes with above average module membership were used for enrichment analysis. \*Modules with an association to Psychosis status (p-value < 0.05) \*2 Modules with high association to Psychosis status (p-value < 0.001). For these modules probes were further subset to only include those with above average correlation with psychosis.