**S1 Table.** Summary of significant co-expression modules (FDR < 5%) associated with CVD or T2D

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Trait** | **Module** | **Tissue** | **Annotation** | **Size** | **CAR+C4D/DIAGRAM** | **JHS** | **FHS** | **WHI** | **WHI** | **WHI** | ***Pmeta*** | ***FDRmeta*** |
| **Mixed** | **AA** | **EA** | **EA** | **AA** | **HA** |
| CVD | 4406 | Oth | NA | 154 | 3.32E-10 | NS | - | 4.41E-03 | 2.83E-02 | NS | 5.73E-09 | 0.00% |
| CVD | 4522 | Adp, Lv, T | REACTOME\_SIGNALING\_BY\_FGFR\_MUTANTS | 2072 | 1.03E-04 | 1.62E-02 | - | 5.53E-03 | 3.80E-02 | 2.86E-02 | 3.39E-08 | 0.00% |
| CVD | 4540 | Oth | NA | 1233 | 9.72E-04 | NS | - | 1.50E-02 | NS | 5.52E-04 | 5.07E-07 | 0.06% |
| CVD | 5242 | Adr | REACTOME\_CHOLESTEROL\_BIOSYNTHESIS, REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, LIPID\_METABOLIC\_PROCESS, REACTOME\_FATTY\_ACID\_TRIACYLGLYCEROL\_AND\_KETONE\_BODY\_METABOLISM | 306 | 4.19E-06 | 4.71E-02 | - | 2.31E-02 | NS | NS | 2.64E-06 | 0.08% |
| CVD | 4087 | Adp, Dg | CARBOXYLIC\_ACID\_METABOLIC\_PROCESS, ORGANIC\_ACID\_METABOLIC\_PROCESS, REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES, KEGG\_PPAR\_SIGNALING\_PATHWAY | 158 | 2.34E-06 | NS | - | 8.63E-03 | NS | 2.17E-02 | 4.24E-06 | 0.09% |
| CVD | 4019 | Ly | REACTOME\_TRANSMEMBRANE\_TRANSPORT\_OF\_SMALL\_MOLECULES, KEGG\_GLYCINE\_SERINE\_AND\_THREONINE\_METABOLISM | 2876 | 1.89E-03 | 4.46E-02 | - | NS | NS | 6.85E-04 | 7.91E-06 | 0.20% |
| CVD | 4941 | Oth | ESTABLISHMENT\_OF\_LOCALIZATION, PHAGOCYTOSIS, TRANSPORT, REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT | 908 | 8.97E-06 | 1.52E-02 | - | NS | NS | 3.94E-02 | 2.72E-06 | 0.21% |
| CVD | 5023 | Ly | REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT, REACTOME\_STRIATED\_MUSCLE\_CONTRACTION, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_, KEGG\_ALZHEIMERS\_DISEASE | 2890 | NS | 6.37E-05 | - | NS | 1.53E-03 | 1.50E-02 | 1.15E-05 | 0.22% |
| CVD | blue | Oth | REACTOME\_CELL\_CYCLE, NEGATIVE\_REGULATION\_OF\_CELLULAR\_METABOLIC\_PROCESS, REACTOME\_CELL\_CYCLE\_MITOTIC, NEGATIVE\_REGULATION\_OF\_METABOLIC\_PROCESS | 657 | 1.08E-02 | NS | - | NS | NS | 1.77E-04 | 3.85E-06 | 0.30% |
| CVD | 5329 | Adr | REACTOME\_BIOLOGICAL\_OXIDATIONS, KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450, KEGG\_PEROXISOME, KEGG\_METABOLISM\_OF\_XENOBIOTICS\_BY\_CYTOCHROME\_P450 | 1028 | NS | 2.33E-02 | - | 3.26E-02 | 5.01E-03 | 2.26E-02 | 2.21E-05 | 0.35% |
| CVD | 124 | Oth | NA | 14 | NS | 1.48E-03 | - | 7.05E-07 | NS | NS | 4.86E-06 | 0.55% |
| CVD | 4656 | Oth | CELLULAR\_PROTEIN\_COMPLEX\_ASSEMBLY | 371 | NS | NS | - | 3.64E-03 | NS | 2.27E-04 | 8.85E-06 | 0.67% |
| CVD | 4147 | Oth | NA | 111 | 1.55E-02 | 2.06E-04 | - | 8.85E-03 | NS | NS | 5.72E-06 | 0.68% |
| CVD | 4989 | Adr | REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES, REACTOME\_BIOLOGICAL\_OXIDATIONS, ORGANIC\_ACID\_METABOLIC\_PROCESS, KEGG\_COMPLEMENT\_AND\_COAGULATION\_CASCADES | 453 | 1.86E-03 | 7.41E-03 | - | 3.71E-04 | NS | NS | 7.81E-05 | 0.82% |
| CVD | 5723 | Adp, Dg | NA | 656 | 9.30E-03 | NS | - | 8.98E-05 | NS | 3.06E-02 | 9.12E-06 | 1.07% |
| CVD | 4658 | Oth | REACTOME\_SHC\_MEDIATED\_CASCADE, REACTOME\_FGFR1\_LIGAND\_BINDING\_AND\_ACTIVATION, REACTOME\_SIGNALING\_BY\_ACTIVATED\_POINT\_MUTANTS\_OF\_FGFR1, REACTOME\_ACTIVATED\_POINT\_MUTANTS\_OF\_FGFR2 | 1293 | 3.38E-02 | 2.43E-03 | - | 2.39E-03 | NA | NS | 1.43E-05 | 1.12% |
| CVD | 4041 | Oth | REACTOME\_DNA\_REPLICATION, REACTOME\_MITOTIC\_M\_M\_G1\_PHASES, REACTOME\_ANTIGEN\_PROCESSING\_UBIQUITINATION\_PROTEASOME\_DEGRADATION, REACTOME\_CELL\_CYCLE\_MITOTIC | 717 | 6.24E-05 | NS | - | NS | NS | 1.86E-02 | 1.99E-05 | 1.17% |
| CVD | 4594 | Oth | REACTOME\_METABOLISM\_OF\_PROTEINS, REACTOME\_SRP\_DEPENDENT\_COTRANSLATIONAL\_PROTEIN\_TARGETING\_TO\_MEMBRANE, REACTOME\_TRANSLATION | 832 | 2.30E-03 | 5.17E-03 | - | NS | 1.71E-02 | NS | 2.07E-05 | 1.23% |
| CVD | 4335 | Aor | KEGG\_GLIOMA, KEGG\_PATHWAYS\_IN\_CANCER, REACTOME\_SMOOTH\_MUSCLE\_CONTRACTION, KEGG\_MAPK\_SIGNALING\_PATHWAY | 753 | 2.18E-03 | NS | - | NS | 8.37E-03 | NS | 6.07E-05 | 1.32% |
| CVD | 4387 | Adp, Aor | REACTOME\_COMMON\_PATHWAY, KEGG\_COMPLEMENT\_AND\_COAGULATION\_CASCADES, JAK\_STAT\_CASCADE, BIOCARTA\_FIBRINOLYSIS\_PATHWAY | 941 | NS | 4.46E-02 | - | NS | 6.66E-03 | 4.34E-02 | 4.67E-05 | 1.32% |
| CVD | 4561 | Aor, Dg | REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT, KEGG\_PARKINSONS\_DISEASE, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_, KEGG\_OXIDATIVE\_PHOSPHORYLATION | 148 | 1.82E-03 | 6.03E-03 | - | 4.79E-02 | NS | NS | 1.92E-05 | 1.32% |
| CVD | 4811 | Aor | REACTOME\_REGULATION\_OF\_WATER\_BALANCE\_BY\_RENAL\_AQUAPORINS, BIOCARTA\_CREB\_PATHWAY, REACTOME\_NGF\_SIGNALLING\_VIA\_TRKA\_FROM\_THE\_PLASMA\_MEMBRANE, REACTOME\_AQUAPORIN\_MEDIATED\_TRANSPORT | 998 | 1.89E-03 | NS | - | NS | 1.97E-04 | NS | 2.79E-05 | 1.32% |
| CVD | 4062 | Mn | REACTOME\_HOST\_INTERACTIONS\_OF\_HIV\_FACTORS, REACTOME\_HIV\_INFECTION | 107 | 2.93E-04 | 7.85E-03 | - | NS | 4.80E-05 | NS | 1.01E-05 | 1.45% |
| CVD | 4702 | Ve | NA | 1210 | NS | NA | - | 4.47E-03 | 4.26E-03 | NS | 3.93E-05 | 1.54% |
| CVD | 4037 | Oth | NA | 121 | 4.66E-04 | 7.46E-04 | - | NS | NS | NS | 3.39E-05 | 1.61% |
| CVD | 4281 | Aor | KEGG\_RIBOSOME, REACTOME\_SIGNALLING\_BY\_NGF, REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, POST\_TRANSLATIONAL\_PROTEIN\_MODIFICATION | 503 | 3.24E-02 | NS | - | 5.10E-05 | NS | 1.35E-02 | 1.11E-04 | 1.77% |
| CVD | 159 | Ly | REACTOME\_NONSENSE\_MEDIATED\_DECAY\_ENHANCED\_BY\_THE\_EXON\_JUNCTION\_COMPLEX, KEGG\_RIBOSOME, REACTOME\_3\_UTR\_MEDIATED\_TRANSLATIONAL\_REGULATION, REACTOME\_PEPTIDE\_CHAIN\_ELONGATION | 1218 | NS | 6.68E-06 | - | NS | 2.61E-02 | NS | 2.48E-04 | 1.88% |
| CVD | 4363 | Oth | REACTOME\_SRP\_DEPENDENT\_COTRANSLATIONAL\_PROTEIN\_TARGETING\_TO\_MEMBRANE, REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, REACTOME\_TRANSLATION, KEGG\_RIBOSOME | 796 | NS | 4.68E-06 | - | NS | NS | NS | 7.17E-05 | 1.89% |
| CVD | 5604 | Oth | RNA\_METABOLIC\_PROCESS | 387 | 3.69E-02 | 2.08E-03 | - | 2.95E-02 | NS | NS | 4.95E-05 | 1.89% |
| CVD | 4391 | Oth | KEGG\_PPAR\_SIGNALING\_PATHWAY, REACTOME\_GLUCOSE\_METABOLISM, REACTOME\_FATTY\_ACYL\_COA\_BIOSYNTHESIS, REACTOME\_TRIGLYCERIDE\_BIOSYNTHESIS | 175 | 9.15E-04 | NS | - | NS | 4.34E-02 | 4.87E-02 | 6.49E-05 | 2.16% |
| CVD | 6437 | Aor | NA | 121 | NS | 1.13E-02 | - | 3.50E-02 | 6.18E-03 | NS | 1.87E-04 | 2.36% |
| CVD | 4644 | Lv | REACTOME\_CELL\_CYCLE\_MITOTIC, REACTOME\_CELL\_CYCLE, REACTOME\_DNA\_REPLICATION, CELL\_CYCLE\_GO\_0007049 | 264 | 1.17E-02 | NS | - | 3.51E-02 | NS | NS | 5.13E-05 | 2.40% |
| CVD | 4461 | Adp | CHROMATIN\_ASSEMBLY\_OR\_DISASSEMBLY, CHROMATIN\_ASSEMBLY, NUCLEOBASENUCLEOSIDENUCLEOTIDE\_AND\_NUCLEIC\_ACID\_METABOLIC\_PROCESS, BIOPOLYMER\_METABOLIC\_PROCESS | 2296 | 3.80E-02 | NS | - | NS | 7.31E-03 | 1.68E-02 | 8.39E-05 | 2.47% |
| CVD | 4482 | Adp | REACTOME\_PACKAGING\_OF\_TELOMERE\_ENDS, REACTOME\_MEIOTIC\_SYNAPSIS, REACTOME\_RNA\_POL\_I\_PROMOTER\_OPENING, REACTOME\_DEPOSITION\_OF\_NEW\_CENPA\_CONTAINING\_NUCLEOSOMES\_AT\_THE\_CENTROMERE | 739 | 2.77E-03 | NS | - | NS | NS | 1.50E-02 | 5.44E-05 | 2.47% |
| CVD | 4904 | Adp | REACTOME\_HIV\_INFECTION, REACTOME\_HOST\_INTERACTIONS\_OF\_HIV\_FACTORS, REACTOME\_HIV\_LIFE\_CYCLE, KEGG\_UBIQUITIN\_MEDIATED\_PROTEOLYSIS | 1184 | 6.81E-03 | 1.63E-02 | - | NS | NS | 1.13E-04 | 5.75E-05 | 2.47% |
| CVD | 5005 | Adp | REACTOME\_HEMOSTASIS, REACTOME\_PLATELET\_ACTIVATION\_SIGNALING\_AND\_AGGREGATION, SIGNAL\_TRANSDUCTION, REACTOME\_RESPONSE\_TO\_ELEVATED\_PLATELET\_CYTOSOLIC\_CA2\_ | 1463 | NS | 6.81E-04 | - | NS | NS | 1.11E-02 | 4.24E-05 | 2.47% |
| CVD | 6664 | Adp | NA | 40 | 2.40E-04 | 1.95E-04 | - | NS | NS | NS | 8.24E-05 | 2.47% |
| CVD | 5201 | Oth | NA | 18 | 8.69E-05 | NS | - | NS | NS | 2.77E-04 | 4.23E-05 | 2.49% |
| CVD | 4309 | Oth | REACTOME\_COLLAGEN\_FORMATION, REACTOME\_EXTRACELLULAR\_MATRIX\_ORGANIZATION, KEGG\_ECM\_RECEPTOR\_INTERACTION, KEGG\_FOCAL\_ADHESION | 453 | 5.61E-03 | NS | - | 4.64E-04 | NS | NS | 4.36E-05 | 2.54% |
| CVD | 4226 | Oth | REACTOME\_TRANSPORT\_TO\_THE\_GOLGI\_AND\_SUBSEQUENT\_MODIFICATION | 568 | NS | NS | - | 3.24E-02 | 1.11E-02 | 6.40E-03 | 5.73E-05 | 2.64% |
| CVD | 4439 | Oth | NA | 90 | 1.64E-02 | NS | - | NS | 9.38E-03 | NS | 6.73E-05 | 2.64% |
| CVD | 4774 | Adr | REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_, REGULATION\_OF\_GROWTH, NEGATIVE\_REGULATION\_OF\_GROWTH, KEGG\_HUNTINGTONS\_DISEASE | 654 | NS | NS | - | NS | 1.20E-02 | 2.26E-04 | 3.86E-04 | 2.69% |
| CVD | 4820 | Mac | KEGG\_TYPE\_II\_DIABETES\_MELLITUS, KEGG\_OTHER\_GLYCAN\_DEGRADATION | 366 | NS | NS | - | 1.54E-02 | 2.23E-03 | 9.64E-03 | 1.99E-05 | 2.69% |
| CVD | 4530 | Oth | NA | 166 | 5.81E-03 | NS | - | NS | NS | 2.26E-02 | 1.38E-04 | 2.71% |
| CVD | 5426 | Lv | NA | 315 | NS | NS | - | NS | NS | 3.93E-06 | 1.08E-04 | 2.78% |
| CVD | 5671 | Lv | REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, KEGG\_RIBOSOME, REACTOME\_3\_UTR\_MEDIATED\_TRANSLATIONAL\_REGULATION, REACTOME\_INFLUENZA\_VIRAL\_RNA\_TRANSCRIPTION\_AND\_REPLICATION | 1558 | 7.31E-04 | NS | - | NS | NS | 5.65E-03 | 1.19E-04 | 2.78% |
| CVD | 6861 | Lv | KEGG\_OLFACTORY\_TRANSDUCTION, REACTOME\_OLFACTORY\_SIGNALING\_PATHWAY | 113 | NS | NS | - | 4.99E-04 | 1.90E-02 | 1.19E-02 | 8.24E-05 | 2.78% |
| CVD | 5422 | Oth | NA | 93 | NS | 1.28E-07 | - | NS | NS | NS | 1.47E-04 | 2.79% |
| CVD | 5473 | Oth | NA | 15 | NS | 4.14E-03 | - | 6.83E-04 | NS | 4.99E-03 | 1.31E-04 | 2.79% |
| CVD | 6392 | Oth | NA | 42 | NS | NS | - | 2.08E-04 | NS | 9.98E-04 | 1.21E-04 | 2.79% |
| CVD | 6627 | Oth | NA | 305 | 1.55E-02 | 1.69E-03 | - | NS | NS | 1.14E-02 | 1.85E-04 | 2.79% |
| CVD | 7231 | Oth | KEGG\_PPAR\_SIGNALING\_PATHWAY, REACTOME\_TRIGLYCERIDE\_BIOSYNTHESIS, REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, REACTOME\_FATTY\_ACID\_TRIACYLGLYCEROL\_AND\_KETONE\_BODY\_METABOLISM | 698 | 3.16E-03 | NS | - | NS | 8.79E-04 | 1.78E-03 | 1.79E-04 | 2.79% |
| CVD | 4590 | Ve | NA | 52 | 4.09E-03 | 1.52E-02 | - | NS | NA | 3.41E-03 | 1.93E-05 | 2.85% |
| CVD | 4184 | Mn | NA | 287 | NS | NS | - | 3.71E-02 | NS | 4.75E-04 | 1.45E-04 | 2.94% |
| CVD | 4295 | Mn | REACTOME\_HEMOSTASIS, SYSTEM\_DEVELOPMENT, REACTOME\_PLATELET\_ACTIVATION\_SIGNALING\_AND\_AGGREGATION, ANATOMICAL\_STRUCTURE\_DEVELOPMENT | 1166 | 1.04E-03 | 1.32E-02 | - | NS | NS | 1.74E-02 | 1.15E-04 | 2.94% |
| CVD | 5039 | Mn | REACTOME\_INFLUENZA\_VIRAL\_RNA\_TRANSCRIPTION\_AND\_REPLICATION, REACTOME\_SRP\_DEPENDENT\_COTRANSLATIONAL\_PROTEIN\_TARGETING\_TO\_MEMBRANE, REACTOME\_METABOLISM\_OF\_MRNA, REACTOME\_PEPTIDE\_CHAIN\_ELONGATION | 189 | 1.70E-02 | 1.16E-03 | - | NS | 3.42E-02 | NS | 1.44E-04 | 2.94% |
| CVD | 7236 | Oth | NA | 31 | NS | NS | - | NS | 9.38E-03 | 1.07E-04 | 1.04E-04 | 3.00% |
| CVD | 4141 | C | REACTOME\_GPCR\_LIGAND\_BINDING, REGULATION\_OF\_BIOLOGICAL\_QUALITY, REACTOME\_FORMATION\_OF\_FIBRIN\_CLOT\_CLOTTING\_CASCADE, KEGG\_COMPLEMENT\_AND\_COAGULATION\_CASCADES | 883 | 1.28E-02 | 3.64E-04 | - | NS | 4.05E-02 | NS | 1.12E-04 | 3.05% |
| CVD | 4524 | C | CARBOHYDRATE\_METABOLIC\_PROCESS, CELLULAR\_CARBOHYDRATE\_METABOLIC\_PROCESS, CARBOHYDRATE\_METABOLIC\_PROCESS, CELLULAR\_CARBOHYDRATE\_METABOLIC\_PROCESS | 748 | NS | 3.92E-03 | - | NS | 1.65E-02 | 3.58E-02 | 1.30E-04 | 3.05% |
| CVD | 4738 | Aor | REACTOME\_CHEMOKINE\_RECEPTORS\_BIND\_CHEMOKINES, DEFENSE\_RESPONSE, RESPONSE\_TO\_WOUNDING, KEGG\_CYTOKINE\_CYTOKINE\_RECEPTOR\_INTERACTION | 2036 | 1.06E-02 | NS | - | NS | 1.82E-02 | 3.07E-02 | 3.11E-04 | 3.31% |
| CVD | 6626 | Lv | REACTOME\_RNA\_POL\_I\_PROMOTER\_OPENING, REACTOME\_AMYLOIDS, REACTOME\_MEIOTIC\_SYNAPSIS, REACTOME\_MEIOSIS | 2780 | NS | 1.10E-02 | - | 3.14E-04 | NS | NS | 1.69E-04 | 3.40% |
| CVD | 5582 | Oth | BIOCARTA\_MET\_PATHWAY, INTRACELLULAR\_TRANSPORT, KEGG\_EPITHELIAL\_CELL\_SIGNALING\_IN\_HELICOBACTER\_PYLORI\_INFECTION, REACTOME\_CYTOKINE\_SIGNALING\_IN\_IMMUNE\_SYSTEM | 544 | 4.81E-02 | 1.50E-02 | - | 2.42E-04 | NS | NS | 1.47E-04 | 3.45% |
| CVD | 5570 | Oth | REACTOME\_DEVELOPMENTAL\_BIOLOGY | 24 | 3.15E-03 | NS | - | 1.31E-03 | NS | 1.56E-02 | 2.80E-04 | 3.49% |
| CVD | 4161 | Mn | KEGG\_FOCAL\_ADHESION, REACTOME\_TRANS\_GOLGI\_NETWORK\_VESICLE\_BUDDING, INTRACELLULAR\_TRANSPORT, ESTABLISHMENT\_OF\_CELLULAR\_LOCALIZATION | 1863 | NS | 1.33E-03 | - | 6.21E-04 | NS | NS | 2.51E-04 | 3.59% |
| CVD | 5270 | Oth | REACTOME\_NONSENSE\_MEDIATED\_DECAY\_ENHANCED\_BY\_THE\_EXON\_JUNCTION\_COMPLEX, REACTOME\_TRANSLATION, REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, KEGG\_RIBOSOME | 1100 | 3.41E-03 | 5.02E-03 | - | NS | 2.30E-02 | NS | 3.24E-04 | 3.66% |
| CVD | 6452 | Oth | NA | 28 | 2.20E-02 | NS | - | NS | NS | 2.57E-04 | 2.18E-04 | 3.72% |
| CVD | 4033 | Adp | REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, REACTOME\_TRANSLATION, KEGG\_RIBOSOME, REACTOME\_3\_UTR\_MEDIATED\_TRANSLATIONAL\_REGULATION | 105 | NS | NS | - | 1.04E-02 | NS | NS | 1.94E-04 | 3.81% |
| CVD | 5060 | Adp | REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, KEGG\_RIBOSOME, REACTOME\_INFLUENZA\_VIRAL\_RNA\_TRANSCRIPTION\_AND\_REPLICATION, REACTOME\_SRP\_DEPENDENT\_COTRANSLATIONAL\_PROTEIN\_TARGETING\_TO\_MEMBRANE | 1288 | 2.64E-02 | NS | - | NS | 9.33E-03 | 6.49E-03 | 1.86E-04 | 3.81% |
| CVD | 152 | Oth | NA | 17 | 3.74E-02 | NS | - | 1.64E-03 | 5.52E-03 | NS | 2.32E-04 | 3.82% |
| CVD | 4065 | Oth | NA | 38 | NS | NS | - | NS | 1.40E-02 | 1.51E-02 | 2.04E-04 | 3.82% |
| CVD | 4070 | Oth | REACTOME\_COLLAGEN\_FORMATION, REACTOME\_EXTRACELLULAR\_MATRIX\_ORGANIZATION, KEGG\_ECM\_RECEPTOR\_INTERACTION, REACTOME\_NCAM1\_INTERACTIONS | 861 | NS | 4.29E-02 | - | 9.44E-04 | NS | NS | 1.11E-04 | 3.82% |
| CVD | 4448 | Oth | REACTOME\_STRIATED\_MUSCLE\_CONTRACTION, REACTOME\_MUSCLE\_CONTRACTION, STRIATED\_MUSCLE\_CONTRACTION\_GO\_0006941 | 545 | 3.57E-03 | NS | - | 2.51E-02 | 2.20E-02 | NS | 1.64E-04 | 3.82% |
| CVD | 5194 | Oth | REACTOME\_RESPONSE\_TO\_ELEVATED\_PLATELET\_CYTOSOLIC\_CA2\_, EXCRETION, REGULATION\_OF\_BODY\_FLUID\_LEVELS | 339 | NS | NS | - | 1.20E-03 | 2.76E-02 | 1.07E-02 | 1.45E-04 | 3.82% |
| CVD | 6754 | Oth | NA | 54 | NS | 5.10E-03 | - | 3.28E-02 | NS | 2.44E-02 | 2.63E-04 | 3.82% |
| CVD | 4355 | Dg | REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, KEGG\_FATTY\_ACID\_METABOLISM, REACTOME\_AMYLOIDS, KEGG\_PPAR\_SIGNALING\_PATHWAY | 1549 | 1.00E-03 | 4.42E-03 | - | 1.11E-02 | NS | 3.57E-02 | 9.51E-05 | 3.85% |
| CVD | 4519 | Dg | REACTOME\_G\_ALPHA1213\_SIGNALLING\_EVENTS | 563 | 5.95E-03 | 1.96E-03 | - | NS | 3.51E-02 | NS | 9.33E-05 | 3.85% |
| CVD | 5515 | Is | NA | 501 | NS | 2.57E-02 | - | NS | 4.13E-02 | 1.48E-04 | 5.65E-05 | 4.54% |
| CVD | 5767 | Ve | REACTOME\_CELL\_CYCLE, REACTOME\_CELL\_CYCLE\_MITOTIC, REACTOME\_DNA\_REPLICATION, REACTOME\_MITOTIC\_M\_M\_G1\_PHASES | 226 | NS | 1.12E-02 | - | NS | 9.86E-04 | 2.01E-02 | 7.70E-05 | 4.58% |
| CVD | 4758 | Oth | REACTOME\_DEADENYLATION\_DEPENDENT\_MRNA\_DECAY, KEGG\_RNA\_DEGRADATION, CELL\_PROJECTION\_BIOGENESIS | 495 | NS | 5.10E-03 | - | 3.79E-02 | NS | NS | 2.71E-04 | 4.91% |
| T2D | 5323 | Mn | NA | 38 | 8.68E-04 | NS | NS | 1.05E-03 | 2.25E-04 | NS | 1.58E-07 | 0.02% |
| T2D | 5250 | Adp, Dg, Mn | NA | 37 | 4.78E-05 | NS | NS | 3.46E-07 | 3.01E-02 | NS | 4.32E-07 | 0.03% |
| T2D | 4880 | Mn | NA | 141 | 8.96E-03 | NS | 1.18E-02 | NS | 5.06E-04 | NS | 1.61E-06 | 0.06% |
| T2D | 6872 | Mn | NA | 119 | NS | 1.26E-03 | 7.44E-03 | NS | 7.79E-03 | NS | 1.26E-06 | 0.06% |
| T2D | 4879 | Ms | NA | 376 | 3.18E-02 | NS | 5.88E-04 | 2.66E-03 | NS | 2.20E-03 | 1.19E-06 | 0.14% |
| T2D | 6533 | Mn | REACTOME\_CHOLESTEROL\_BIOSYNTHESIS, KEGG\_STEROID\_BIOSYNTHESIS, REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, KEGG\_TERPENOID\_BACKBONE\_BIOSYNTHESIS | 48 | NS | 5.02E-03 | NS | NS | NA | 1.26E-06 | 1.06E-05 | 0.25% |
| T2D | 6977 | Bld | NA | 40 | 3.66E-02 | NS | 4.01E-05 | 1.81E-02 | NS | 4.05E-02 | 1.71E-06 | 0.39% |
| T2D | 6675 | Mn | REACTOME\_CHOLESTEROL\_BIOSYNTHESIS, REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, KEGG\_STEROID\_BIOSYNTHESIS, LIPID\_METABOLIC\_PROCESS | 152 | 3.72E-03 | 3.35E-02 | NS | NS | NS | 2.06E-05 | 2.56E-05 | 0.52% |
| T2D | 37 | Oth | NA | 34 | 1.94E-03 | 5.53E-03 | NS | 9.38E-04 | NS | NS | 4.95E-06 | 0.57% |
| T2D | 4302 | Adp | NA | 40 | 2.07E-03 | NS | NS | 4.05E-06 | 4.80E-03 | NS | 9.89E-06 | 0.71% |
| T2D | 6690 | Adr | KEGG\_COMPLEMENT\_AND\_COAGULATION\_CASCADES, REACTOME\_P130CAS\_LINKAGE\_TO\_MAPK\_SIGNALING\_FOR\_INTEGRINS, REACTOME\_GRB2\_SOS\_PROVIDES\_LINKAGE\_TO\_MAPK\_SIGNALING\_FOR\_INTERGRINS\_, BIOCARTA\_INTRINSIC\_PATHWAY | 641 | 1.93E-02 | 1.01E-04 | NS | NS | 2.24E-02 | NS | 1.36E-05 | 0.86% |
| T2D | 4059 | Dg | REACTOME\_SLC\_MEDIATED\_TRANSMEMBRANE\_TRANSPORT, REACTOME\_TRANSMEMBRANE\_TRANSPORT\_OF\_SMALL\_MOLECULES, CARBOXYLIC\_ACID\_METABOLIC\_PROCESS, ORGANIC\_ACID\_METABOLIC\_PROCESS | 51 | NS | 3.05E-02 | 5.80E-03 | 1.50E-02 | NS | NS | 1.29E-05 | 0.86% |
| T2D | 4937 | Dg | AMINO\_ACID\_METABOLIC\_PROCESS, REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES | 80 | 9.21E-03 | NS | 5.88E-03 | 1.37E-03 | NS | NS | 2.11E-05 | 0.89% |
| T2D | 5059 | Ve | REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT, KEGG\_OXIDATIVE\_PHOSPHORYLATION | 164 | 7.31E-04 | NS | 2.74E-02 | NS | 8.66E-04 | NS | 6.64E-06 | 0.95% |
| T2D | 133 | Mn | REACTOME\_CHOLESTEROL\_BIOSYNTHESIS, REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, KEGG\_STEROID\_BIOSYNTHESIS, KEGG\_TERPENOID\_BACKBONE\_BIOSYNTHESIS | 57 | 2.25E-02 | NS | 1.53E-02 | NS | NS | 4.95E-05 | 6.90E-05 | 1.03% |
| T2D | 5611 | Mn | NA | 91 | NS | 5.84E-03 | NS | NS | NS | NS | 7.19E-05 | 1.03% |
| T2D | 4155 | Mn | REACTOME\_CHOLESTEROL\_BIOSYNTHESIS, REACTOME\_GLYCOLYSIS | 197 | NS | 3.99E-02 | NS | NS | NS | 1.66E-05 | 8.49E-05 | 1.10% |
| T2D | 4820 | Ve | KEGG\_TYPE\_II\_DIABETES\_MELLITUS, KEGG\_OTHER\_GLYCAN\_DEGRADATION | 366 | 2.55E-03 | NS | NS | NS | 4.92E-05 | NS | 1.16E-04 | 1.10% |
| T2D | 6833 | Mn | REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, REACTOME\_FATTY\_ACID\_TRIACYLGLYCEROL\_AND\_KETONE\_BODY\_METABOLISM, KEGG\_FATTY\_ACID\_METABOLISM, KEGG\_PPAR\_SIGNALING\_PATHWAY | 93 | 9.32E-03 | NS | NS | 2.73E-02 | NS | 5.09E-04 | 1.02E-04 | 1.10% |
| T2D | 26 | Dg | REACTOME\_IMMUNE\_SYSTEM, IMMUNE\_SYSTEM\_PROCESS, REACTOME\_INTERFERON\_GAMMA\_SIGNALING, IMMUNE\_RESPONSE | 237 | 1.64E-04 | 1.06E-02 | NS | 4.01E-05 | NS | NA | 4.43E-05 | 1.24% |
| T2D | 5018 | Dg | KEGG\_PPAR\_SIGNALING\_PATHWAY, REACTOME\_GLUCOSE\_METABOLISM, REACTOME\_FATTY\_ACYL\_COA\_BIOSYNTHESIS, LIPID\_METABOLIC\_PROCESS | 416 | 1.98E-03 | NS | NS | 2.30E-05 | 5.69E-04 | NS | 2.77E-05 | 1.24% |
| T2D | 4238 | Ve | REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT, KEGG\_OXIDATIVE\_PHOSPHORYLATION | 265 | 4.72E-02 | 4.83E-02 | NS | 4.69E-02 | 1.06E-04 | NS | 2.00E-05 | 1.34% |
| T2D | 7038 | Ve | CELLULAR\_CATABOLIC\_PROCESS, CATABOLIC\_PROCESS | 55 | 4.96E-04 | NS | 2.72E-02 | NS | NS | 6.57E-04 | 2.79E-05 | 1.34% |
| T2D | 4956 | Oth | NA | 209 | 6.02E-07 | NS | 4.34E-03 | NS | NS | NS | 2.28E-05 | 1.35% |
| T2D | 4750 | Adp | NA | 51 | NS | 4.34E-02 | NS | 1.68E-02 | 1.58E-03 | NS | 1.87E-04 | 1.57% |
| T2D | 183 | Oth | NA | 19 | 3.62E-05 | NS | NS | 1.41E-03 | 4.31E-02 | NS | 2.12E-05 | 1.63% |
| T2D | 7249 | Mn | NA | 67 | 3.32E-02 | NS | 1.06E-03 | 2.02E-02 | NS | NS | 2.92E-04 | 2.08% |
| T2D | 5070 | Oth | NA | 20 | 7.34E-03 | NS | 4.48E-02 | NS | NS | 3.69E-03 | 1.84E-05 | 2.16% |
| T2D | 4862 | Bld | REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_, KEGG\_OXIDATIVE\_PHOSPHORYLATION, REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT, KEGG\_HUNTINGTONS\_DISEASE | 384 | 4.89E-04 | 2.60E-02 | NS | NS | 2.91E-02 | NS | 1.18E-05 | 2.16% |
| T2D | 7040 | Mn | KEGG\_TYPE\_I\_DIABETES\_MELLITUS, KEGG\_ANTIGEN\_PROCESSING\_AND\_PRESENTATION | 50 | 1.32E-02 | 3.88E-02 | NS | 1.89E-03 | 8.95E-04 | NS | 3.56E-04 | 2.42% |
| T2D | 4393 | Adp, Bld | REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, REACTOME\_INFLUENZA\_VIRAL\_RNA\_TRANSCRIPTION\_AND\_REPLICATION, KEGG\_RIBOSOME, REACTOME\_3\_UTR\_MEDIATED\_TRANSLATIONAL\_REGULATION | 160 | 4.46E-03 | NS | NS | 5.95E-03 | 8.48E-04 | NS | 1.03E-04 | 2.57% |
| T2D | 4844 | Ve | BIOPOLYMER\_METABOLIC\_PROCESS, CELLULAR\_MACROMOLECULE\_METABOLIC\_PROCESS, REACTOME\_GLUCOSE\_METABOLISM, CELLULAR\_PROTEIN\_METABOLIC\_PROCESS | 446 | NS | NS | NS | 1.70E-02 | 3.37E-03 | NS | 9.24E-05 | 2.76% |
| T2D | 4722 | Mn | REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, REACTOME\_CHOLESTEROL\_BIOSYNTHESIS, REACTOME\_FATTY\_ACYL\_COA\_BIOSYNTHESIS, REACTOME\_TRIGLYCERIDE\_BIOSYNTHESIS | 91 | 4.44E-02 | 1.50E-02 | 1.11E-02 | NS | NS | 5.22E-03 | 4.49E-04 | 2.79% |
| T2D | 5041 | Ve | NA | 52 | 1.34E-02 | 4.58E-02 | 2.03E-02 | 1.06E-02 | NS | NS | 1.18E-04 | 2.83% |
| T2D | 4721 | Mn | NA | 52 | 4.41E-03 | NS | 6.80E-03 | NS | 4.70E-02 | NS | 4.88E-04 | 2.90% |
| T2D | 6689 | Mn | KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450, BIOCARTA\_PAR1\_PATHWAY, REACTOME\_BIOLOGICAL\_OXIDATIONS, REACTOME\_GLYCOSPHINGOLIPID\_METABOLISM | 2151 | 7.75E-03 | 2.92E-03 | NS | NS | 1.16E-02 | NS | 5.20E-04 | 2.97% |
| T2D | 4524 | Bld | CARBOHYDRATE\_METABOLIC\_PROCESS, CELLULAR\_CARBOHYDRATE\_METABOLIC\_PROCESS, CARBOHYDRATE\_METABOLIC\_PROCESS, CELLULAR\_CARBOHYDRATE\_METABOLIC\_PROCESS | 748 | NS | NS | 1.46E-04 | NS | 7.32E-04 | NS | 6.37E-05 | 3.00% |
| T2D | 4428 | Mn | REACTOME\_METABOLISM\_OF\_RNA, REACTOME\_PEPTIDE\_CHAIN\_ELONGATION, KEGG\_RIBOSOME, REACTOME\_NONSENSE\_MEDIATED\_DECAY\_ENHANCED\_BY\_THE\_EXON\_JUNCTION\_COMPLEX | 713 | 3.51E-04 | NS | NS | 6.96E-03 | 2.71E-03 | NS | 4.15E-05 | 3.11% |
| T2D | 4566 | Adp, Mac | REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS, KEGG\_PPAR\_SIGNALING\_PATHWAY, REACTOME\_FATTY\_ACID\_TRIACYLGLYCEROL\_AND\_KETONE\_BODY\_METABOLISM, REACTOME\_TRIGLYCERIDE\_BIOSYNTHESIS | 569 | 1.35E-02 | 3.61E-03 | 3.47E-02 | NS | 1.53E-03 | NS | 2.33E-05 | 3.13% |
| T2D | 4998 | Adp | REACTOME\_IMMUNE\_SYSTEM, REACTOME\_INTERFERON\_GAMMA\_SIGNALING, REACTOME\_INTERFERON\_SIGNALING, REACTOME\_CYTOKINE\_SIGNALING\_IN\_IMMUNE\_SYSTEM | 107 | 9.96E-03 | NS | 5.18E-03 | 5.38E-06 | NS | NS | 1.58E-04 | 3.18% |
| T2D | 4669 | Mn | REACTOME\_GLUCOSE\_METABOLISM, KEGG\_PEROXISOME, REACTOME\_FATTY\_ACID\_TRIACYLGLYCEROL\_AND\_KETONE\_BODY\_METABOLISM, REACTOME\_METABOLISM\_OF\_LIPIDS\_AND\_LIPOPROTEINS | 401 | 3.65E-02 | NS | 5.04E-03 | NS | 2.71E-02 | 1.37E-03 | 5.90E-04 | 3.21% |
| T2D | 4651 | Mn | REACTOME\_TCA\_CYCLE\_AND\_RESPIRATORY\_ELECTRON\_TRANSPORT, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT\_ATP\_SYNTHESIS\_BY\_CHEMIOSMOTIC\_COUPLING\_AND\_HEAT\_PRODUCTION\_BY\_UNCOUPLING\_PROTEINS\_, REACTOME\_RESPIRATORY\_ELECTRON\_TRANSPORT, KEGG\_OXIDATIVE\_PHOSPHORYLATION | 319 | 4.95E-03 | NS | NS | 2.64E-04 | 7.33E-03 | NS | 6.81E-04 | 3.36% |
| T2D | 4822 | Bld | SYNAPTIC\_TRANSMISSION, TRANSMISSION\_OF\_NERVE\_IMPULSE, KEGG\_OXIDATIVE\_PHOSPHORYLATION, REACTOME\_TRANSMISSION\_ACROSS\_CHEMICAL\_SYNAPSES | 1426 | 9.71E-04 | NS | NS | NS | 1.18E-03 | 1.21E-02 | 9.66E-05 | 3.54% |
| T2D | 5539 | Dg | REACTOME\_BIOLOGICAL\_OXIDATIONS, KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450, KEGG\_METABOLISM\_OF\_XENOBIOTICS\_BY\_CYTOCHROME\_P450, REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES | 232 | 3.62E-02 | NS | 2.39E-02 | NS | NS | NS | 8.89E-05 | 3.54% |
| T2D | 5685 | Oth | NA | 13 | NS | NS | 1.63E-04 | NS | 5.47E-03 | NS | 1.08E-04 | 3.64% |
| T2D | brown | Mn | BIOCARTA\_AHSP\_PATHWAY, REACTOME\_METABOLISM\_OF\_PORPHYRINS, REACTOME\_MHC\_CLASS\_II\_ANTIGEN\_PRESENTATION, COFACTOR\_BIOSYNTHETIC\_PROCESS | 480 | 2.55E-02 | NS | NS | 2.81E-02 | NS | 1.91E-03 | 1.01E-04 | 3.64% |
| T2D | 4094 | Mn | KEGG\_ALZHEIMERS\_DISEASE, KEGG\_HUNTINGTONS\_DISEASE, KEGG\_PARKINSONS\_DISEASE, KEGG\_OXIDATIVE\_PHOSPHORYLATION | 65 | NS | NS | NS | NS | 3.11E-02 | NS | 9.31E-04 | 3.80% |
| T2D | 4127 | Mn | KEGG\_METABOLISM\_OF\_XENOBIOTICS\_BY\_CYTOCHROME\_P450, KEGG\_DRUG\_METABOLISM\_CYTOCHROME\_P450, REACTOME\_BIOLOGICAL\_OXIDATIONS, REACTOME\_METABOLISM\_OF\_AMINO\_ACIDS\_AND\_DERIVATIVES | 948 | NS | NS | NS | NS | 3.18E-02 | 5.97E-03 | 9.58E-04 | 3.80% |
| T2D | 4865 | Mn | NA | 122 | 4.43E-02 | NS | NS | 3.44E-02 | 5.33E-03 | NS | 9.42E-04 | 3.80% |
| T2D | 5055 | Mn | REACTOME\_STRIATED\_MUSCLE\_CONTRACTION, REACTOME\_MUSCLE\_CONTRACTION, REACTOME\_INTERFERON\_ALPHA\_BETA\_SIGNALING, TUBE\_DEVELOPMENT | 988 | NS | NS | NS | NS | 7.26E-05 | 1.43E-02 | 9.08E-04 | 3.80% |
| T2D | 6630 | Mn | REACTOME\_INTERFERON\_ALPHA\_BETA\_SIGNALING, REACTOME\_IMMUNE\_SYSTEM, REACTOME\_CYTOKINE\_SIGNALING\_IN\_IMMUNE\_SYSTEM, REACTOME\_INTERFERON\_SIGNALING | 73 | NS | NS | NS | 8.00E-04 | 1.33E-02 | NS | 9.36E-04 | 3.80% |
| T2D | 4555 | Oth | REACTOME\_ADP\_SIGNALLING\_THROUGH\_P2RY1, REACTOME\_SIGNAL\_AMPLIFICATION, REACTOME\_THROMBIN\_SIGNALLING\_THROUGH\_PROTEINASE\_ACTIVATED\_RECEPTORS\_PARS | 206 | 8.57E-04 | NS | NS | NS | 2.30E-02 | NS | 9.91E-05 | 3.92% |
| T2D | 4723 | Ve | INTRACELLULAR\_TRANSPORT, REACTOME\_HIV\_LIFE\_CYCLE, TRANSPORT, REACTOME\_HIV\_INFECTION | 2836 | NS | NS | 4.13E-02 | 1.32E-04 | 4.33E-02 | NS | 3.72E-04 | 4.11% |
| T2D | 5219 | Oth | NA | 13 | 7.64E-04 | 3.24E-02 | NS | 1.41E-02 | NS | NS | 1.59E-04 | 4.38% |

**\*** The annotation refers to the top 4 functional categories enriched in the co-expression modules (Bonferroni-corrected p< 0.05 based on Fisher’s exact test, number of direct overlapping genes > 5). Adp – adipose tissue; Adr – adrenal gland; Aor – Aorta; Art – artery; Bld – Blood; C – Coronary artery; Dg –digestive tract; Is – Islet; Hy – hypothalamus; Lv – liver; Ly – lymphocyte; Ms – muscle; Mac – Macrophage; Mn – Monocyte; Oth – Modules mapped by distance or ENCODE or all eQTLs combined; T – thyroid gland; Ve – vascular endothelium.