



Report: Solution sol_2

Generated: 2025-12-10 01:04:56

Type: solution | Origin: Pareto Plot | Timestamp: 2025-12-09 23:12:00

Comment: Individual solution sol_2 (Front: front_from_csv_filtered9) with 1-Auc = 0.0208333333333334.

Summary

Genes: 188

Front: front_from_csv_filtered9

Solution ID: sol_2

Analysis settings

gprofiler | Organism: hsapiens | Namespace: HGNC | Validation: on | Sources: GO:BP, GO:MF, GO:CC, KEGG, REAC

Validated gene sets

| Source | Namespace | Genes (count) |
|-----------|-----------|---------------|
| gprofiler | HGNC | 201 |

g:Profiler Results

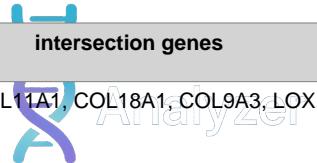


| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|----------------------------|---|--------------------------------|-----------|-------------------|-------------------------|--------------------------|--------|---|
| 1 | protein binding | "Binding to a protein." [GOC:go_curators] | 2.3836927 20237096 e-05 | 15123 | 165 | 0.906593406 5934066 | 0.010910533 624280896 | GO:MF | ACAA1, ADCY2, ADNP, ADRA2B, AFF4, AFTPH, AKAP7, ANP32E, AP1B1, APOBEC3A, ARMH3, ARMT1, ARPC2, ARPP19, ASXL1, ATG9A, ATP5F1A, B3GALT5, BARX2, BAZ1B, BCAN, BCL2A1, BLOC1S1, BMAL2, BNIP3, BRWD1, C1QL1, CACNA1I, CAMK2N1, CCDC102B, CCL5, CD200, CEP76, CHMP1A, CLDN7, CNR1, COL18A1, COL9A3, COQ4, CPT2, CREB3L1, DDIR4, DNAH9, ECI2, EGLN3, EIF2B3, ENTPD4, EP300, EXD3, EXOSC5, EXOSC7, FAF1, FAM53B, FILIP1L, FNTA, FUT3, GAREM1, GNA11, GNAI3, GORASP1, GPA33, GPN2, GPRC5D, GUCY1B1, HINFP, HNRNPA0, HNRNPH2, HPX, HSD17B12, HSD17B3, IKZF5, IL22RA1, INAVA, IP6K2, ITM2A, KBTBD2, KIF1C, KIF3A, KLRC1, KLRC2, KRT20, LAT, LOX, LRP8, MAGOH, MAL, MAPK9, MARCHF8, MASP2, MEF2D, METTL17, METTL22, MT1G, MXI1, NAA10, NDOR1, NEUROD1, NKX2-5, NLRX1, NOS3, PALB2, PALMD, PARP8, PCGF3, PCMTD2, PLA2G6, POLA1, POLR2B, POMP, POP1, PPCDC, PRKAR1A, PRKG2, PRR16, PSMG1, PTPN4, QTRT2, RAD52, REC8, REG1B, RFC5, RPL36A, RPS18, RUNX3, S100A2, SACS, SCG3, SEPHS1, SERPINE2, SKP2, SLC11A2, SLC27A5, SLC9A1, SMC4, SNTA1, SPINK5, STK3, SULT1A2, SULT1A3, TBCA, TBL1Y, TERT, TEX28, THOC7, TLE4, TMUB2, TNFRSF11A, TNXB, TRIM27, TRIM5, TRMT61B, TRRAP, TTLL4, UNC93A, UTP18, VPS37B, VWA5A, WAPL, WDR43, WDR5B, WNT5B, WWOX, ZFC3H1, ZNF32, ZNF337 |
| 2 | nucleoplasm | "That part of the nuclear content other than the chromosomes or the nucleolus." [GOC:ma, ISBN:0124325653] | 0.0001422 51510266 15217 | 4255 | 64 | 0.347826086 95652173 | 0.015041128 084606345 | GO:CC | AFF4, AFTPH, ANP32E, APOBEC3A, ARPC2, ARPP19, ASXL1, BARX2, BAZ1B, BMAL2, BNIP3, BRWD1, CHMP1A, CPT2, CREB3L1, EGLN3, EP300, EXOSC5, EXOSC7, FAF1, GNAI3, HINFP, HNRNPA0, HNRNPH2, INAVA, IP6K2, MAGOH, MAPK9, MEF2D, METTL17, METTL22, MXI1, NDOR1, NEUROD1, NKX2-5, PALB2, PCGF3, PLA2G6, POLA1, POLR2B, POMP, POP1, PSMG1, PTPN4, RAD52, RFC5, RPS18, RUNX3, SKP2, SLC9A1, SMC4, SMOX, TBL1Y, TERT, THOC7, TLE4, TRIM27, TRIM5, TRRAP, UTP18, VWA5A, WAPL, WDR43, WDR5B |
| 3 | cGMP-PKG signaling pathway | cGMP-PKG signaling pathway | 0.0040293 12682932 962 | 164 | 10 | 0.091743119 26605505 | 0.060975609 75609756 | KEGG | ADCY2, ADORA3, ADRA2B, CREB3L1, GNA11, GNAI3, GUCY1B1, MEF2D, NOS3, PRKG2 |

| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|--|--|-------------------------------|-----------|-------------------|------------------------|--------------------------|--------|--|
| 4 | cytoplasm | "The contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures." [ISBN:0198547684] | 0.0046851 82672180 4385 | 12527 | 132 | 0.717391304 347826 | 0.010537239 562544903 | GO:CC | ACAA1, ADCY2, ADPRM, ADRA2B, AFTPH, AKAP7, ANP32E, AP1B1, APOBEC3A, ARMH3, ARPC2, ARPP19, ATG9A, ATP5F1A, B3GALT5, BARX2, BCAN, BCL2A1, BLOC1S1, BMAL2, BNIP3, BRWD1, C1QL1, C2CD2, CCDC102B, CCL5, CEP76, CFD, CHMP1A, CNR1, COL11A1, COL18A1, COL9A3, COQ4, CPT2, CREB3L1, DDI4, DNAH9, DSE, ECI2, EGLN3, EIF2B3, ENTPD4, EP300, EXOSC5, EXOSC7, FAF1, FILIP1L, FNTA, FRMD4B, FUT3, GLT8D1, GNA11, GNAI3, GORASP1, GUCY1B1, HNRNPH2, HPX, HSD17B12, HSD17B3, INAVA, IP6K2, ITM2A, KBTBD2, KIF1C, KIF3A, KRT20, LAT, MAGOH, MAL, MAPK9, MARCHF8, MEF2D, METTL17, MT1G, MXI1, NAA10, NDOR1, NEUROD1, NIPSNAP3B, NKX2-5, NLRX1, NOS3, PALMD, PARP8, PCMTD2, PLA2G6, POLA1, POMP, PPCDC, PRKAR1A, PRKG2, PSMG1, PTPN4, QTRT2, RETSAT, RPL36A, RPL36A-HNRNPH2, RPS18, RUNX3, SACS, SCG3, SEPHS1, SERPINE2, SKP2, SLC11A2, SLC25A15, SLC27A5, SLC9A1, SMC4, SMOX, SNTA1, SPINK5, ST3GAL4, STK3, SULT1A2, SULT1A3, SULT1A4, TBCA, TERT, THOC7, TNFRSF11A, TRIM27, TRIM5, TRMT61B, TRRAP, TTLL4, TUBAL3, VPS37B, WAPL, WNT5B, WWOX |
| 5 | response to oxygen-containing compound | "Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of an oxygen-containing compound stimulus." [GOC:pr, GOC:TermGenie] | 0.0069901 36890650 769 | 1669 | 33 | 0.185393258 4269663 | 0.019772318 753744758 | GO:BP | ADCY2, ADNP, AKAP7, ASXL1, ATP5F1A, BNIP3, CHRNA1, CLDN7, CNR1, COL18A1, DDI4, EIF2B3, EP300, GNA11, GNAI3, GUCY1B1, HNRNPA0, INAVA, IP6K2, KBTBD2, KIF3A, LRP8, MAPK9, NEUROD1, NOS3, PLA2G6, PRKAR1A, REG1B, SLC9A1, SULT1A3, TNFRSF11A, TRIM5, WNT5B |
| 6 | response to stress | "Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a disturbance in organismal or cellular homeostasis, usually, but not necessarily, exogenous (e.g. temperature, humidity, ionizing radiation)." [GOC:mah] | 0.0284211 93438827 763 | 3948 | 57 | 0.320224719 1011236 | 0.014437689 969604863 | GO:BP | ADORA3, ADRA2B, AFF4, APOBEC3A, ARMT1, BAZ1B, BCL2A1, BNIP3, CAMK2N1, CCL5, CD200, CFD, CHMP1A, CNR1, COL18A1, CREB3L1, DDI4, EGLN3, EIF2B3, EP300, EXOSC5, FAF1, HINFP, HNRNPA0, HPX, IL22RA1, INAVA, KLRC1, KLRC2, KRT20, LAT, LRP8, MAPK9, MASP2, MT1G, NLRX1, NOS3, PALB2, PARP8, PLA2G6, POLA1, RAD52, REC8, REG1B, RFC5, SERPINE2, SKP2, SLC11A2, SLC9A1, SPINK5, ST3GAL4, TERT, TMUB2, TNFRSF11A, TRIM27, TRIM5, TRRAP |

| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|--------------------------------|--|------------------------------|-----------|-------------------|--------------------------|-------------------------|--------|--|
| 7 | intracellular organelle lumen | "An organelle lumen that is part of an intracellular organelle." [GOC:mah] | 0.0301102 36803565 886 | 6695 | 80 | 0.434782608 69565216 | 0.011949215 83271098 | GO:CC | ACAA1, AFF4, AFTPH, ANP32E, APOBEC3A, ARPC2, ARPP19, ASXL1, ATP5F1A, BARX2, BAZ1B, BCAN, BLOC1S1, BMAL2, BNIP3, BRWD1, CFD, CHMP1A, COL11A1, COL18A1, COL9A3, CPT2, CREB3L1, ECI2, EGLN3, EP300, EXOSC5, EXOSC7, FAF1, GNAI3, HINFP, HNRNPA0, HNRNPH2, HPX, INAVA, IP6K2, MAGOH, MAPK9, MEF2D, METTL17, METTL22, MXI1, NAA10, NDOR1, NEUROD1, NKX2-5, PALB2, PCGF3, PLA2G6, POLA1, POLR2B, POMP, POP1, PSMG1, PTPN4, RAD52, REC8, RFC5, RPS18, RUNX3, SCG3, SKP2, SLC9A1, SMC4, SMOX, TBCA, TBL1Y, TERT, THOC7, TLE4, TRIM27, TRIM5, TRMT61B, TRRAP, UTP18, VWA5A, WAPL, WDR43, WDR5B, WNT5B |
| 8 | membrane-enclosed lumen | "The enclosed volume within a sealed membrane or between two sealed membranes. Encompasses the volume enclosed by the membranes of a particular organelle, e.g. endoplasmic reticulum lumen, or the space between the two lipid bilayers of a double membrane surrounding an organelle, e.g. nuclear envelope lumen." [GOC:add, GOC:mah] | 0.0301102 36803565 886 | 6695 | 80 | 0.434782608 69565216 | 0.011949215 83271098 | GO:CC | ACAA1, AFF4, AFTPH, ANP32E, APOBEC3A, ARPC2, ARPP19, ASXL1, ATP5F1A, BARX2, BAZ1B, BCAN, BLOC1S1, BMAL2, BNIP3, BRWD1, CFD, CHMP1A, COL11A1, COL18A1, COL9A3, CPT2, CREB3L1, ECI2, EGLN3, EP300, EXOSC5, EXOSC7, FAF1, GNAI3, HINFP, HNRNPA0, HNRNPH2, HPX, INAVA, IP6K2, MAGOH, MAPK9, MEF2D, METTL17, METTL22, MXI1, NAA10, NDOR1, NEUROD1, NKX2-5, PALB2, PCGF3, PLA2G6, POLA1, POLR2B, POMP, POP1, PSMG1, PTPN4, RAD52, REC8, RFC5, RPS18, RUNX3, SCG3, SKP2, SLC9A1, SMC4, SMOX, TBCA, TBL1Y, TERT, THOC7, TLE4, TRIM27, TRIM5, TRMT61B, TRRAP, UTP18, VWA5A, WAPL, WDR43, WDR5B, WNT5B |
| 9 | organelle lumen | "The internal volume enclosed by the membranes of a particular organelle; includes the volume enclosed by a single organelle membrane, e.g. endoplasmic reticulum lumen, or the volume enclosed by the innermost of the two lipid bilayers of an organelle envelope, e.g. nuclear lumen." [GOC:jl, GOC:mah] | 0.0301102 36803565 886 | 6695 | 80 | 0.434782608 69565216 | 0.011949215 83271098 | GO:CC | ACAA1, AFF4, AFTPH, ANP32E, APOBEC3A, ARPC2, ARPP19, ASXL1, ATP5F1A, BARX2, BAZ1B, BCAN, BLOC1S1, BMAL2, BNIP3, BRWD1, CFD, CHMP1A, COL11A1, COL18A1, COL9A3, CPT2, CREB3L1, ECI2, EGLN3, EP300, EXOSC5, EXOSC7, FAF1, GNAI3, HINFP, HNRNPA0, HNRNPH2, HPX, INAVA, IP6K2, MAGOH, MAPK9, MEF2D, METTL17, METTL22, MXI1, NAA10, NDOR1, NEUROD1, NKX2-5, PALB2, PCGF3, PLA2G6, POLA1, POLR2B, POMP, POP1, PSMG1, PTPN4, RAD52, REC8, RFC5, RPS18, RUNX3, SCG3, SKP2, SLC9A1, SMC4, SMOX, TBCA, TBL1Y, TERT, THOC7, TLE4, TRIM27, TRIM5, TRMT61B, TRRAP, UTP18, VWA5A, WAPL, WDR43, WDR5B, WNT5B |
| 10 | aryl sulfotransferase activity | "Catalysis of the reaction: 3'-phosphoadenosine 5'-phosphosulfate + a phenol = adenosine 3',5'-bisphosphate + an aryl sulfate." [EC:2.8.2.1] | 0.0356051 05805924 554 | 9 | 3 | 0.016483516 483516484 | 0.333333333 3333333 | GO:MF | SULT1A2, SULT1A3, SULT1A4 |

| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|--------------------------------------|---|------------------------------|-----------|-------------------|-------------------------|--------------------------|--------|---|
| 11 | collagen trimer | "A protein complex consisting of three collagen chains assembled into a left-handed triple helix. These trimers typically assemble into higher order structures." [GOC:dos, GOC:mah, ISBN:0721639976, PMID:19693541, PMID:21421911] | 0.0365228 95442025 194 | 91 | 6 | 0.032608695 65217391 | 0.065934065 93406594 | GO:CC | C1QL1, COL11A1, COL18A1, COL9A3, LOX, RPS18 |
| 12 | RNA-directed RNA polymerase activity | "Catalysis of the reaction: nucleoside triphosphate + RNA(n) = diphosphate + RNA(n+1); uses an RNA template, i.e. the catalysis of RNA-template-directed extension of the 3'-end of an RNA strand by one nucleotide at a time." [EC:2.7.7.48, GOC:mah, GOC:pf] | 0.0496109 94696657 564 | 2 | 2 | 0.010989010 98901099 | 1 | GO:MF | POLR2B, TERT |
| 13 | catalytic complex | "A protein complex which is capable of catalytic activity." [GOC:bhm, GOC:TermGenie, PMID:8077207] | 0.0499726 96679453 47 | 1779 | 30 | 0.163043478 26086957 | 0.016863406 408094434 | GO:CC | ANP32E, ATP5F1A, BAZ1B, COQ4, DNAH9, EP300, EXOSC5, EXOSC7, FNTA, GNA11, GNAI3, GUCY1B1, HSD17B12, MAGOH, NAA10, PALB2, PCGF3, POLA1, POLR2B, POP1, PPCDC, PRKAR1A, QTRT2, SKP2, TBL1Y, TERT, TRMT61B, TRRAP, WDR5B, ZFC3H1 |
| 14 | membrane raft | "Any of the small (10-200 nm), heterogeneous, highly dynamic, sterol- and sphingolipid-enriched membrane domains that compartmentalize cellular processes. Small rafts can sometimes be stabilized to form larger platforms through protein-protein and protein-lipid interactions." [PMID:16645198, PMID:20044567] | 0.0611098 87505464 15 | 295 | 10 | 0.054347826 08695652 | 0.033898305 08474576 | GO:CC | ADCY2, ATP5F1A, CNR1, LAT, LRP8, MAL, NOS3, PRKAR1A, SLC9A1, TNFRSF11A |
| 15 | membrane microdomain | "A membrane region with a lipid composition that is distinct from that of the membrane regions that surround it." [PMID:20044567, PMID:26253820] | 0.0645263 38643140 8 | 297 | 10 | 0.054347826 08695652 | 0.033670033 67003367 | GO:CC | ADCY2, ATP5F1A, CNR1, LAT, LRP8, MAL, NOS3, PRKAR1A, SLC9A1, TNFRSF11A |
| 16 | Gap junction | Gap junction | 0.0799811 02700401 55 | 88 | 6 | 0.055045871 55963303 | 0.068181818 18181818 | KEGG | ADCY2, GNA11, GNAI3, GUCY1B1, PRKG2, TUBAL3 |



| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|---|--|-----------------------------|-----------|-------------------|-------------------------|--------------------------|--------|---|
| 17 | RNA polymerase II transcription regulator complex | "A transcription factor complex that acts at a regulatory region of a gene transcribed by RNA polymerase II." [GOC:tb] | 0.0980718 36819821 53 | 256 | 9 | 0.048913043 47826087 | 0.03515625 | GO:CC | ADNP, BMAL2, MXI1, NEUROD1, NKX2-5, RUNX3, TLE4, TRRAP, WWOX |
| 18 | catalytic activity | "Catalysis of a biochemical reaction at physiological temperatures. In biologically catalyzed reactions, the reactants are known as substrates, and the catalysts are naturally occurring macromolecular substances known as enzymes. Enzymes possess specific binding sites for substrates, and are usually composed wholly or largely of protein, but RNA that has catalytic activity (ribozyme) is often also regarded as enzymatic." [GOC:vw, ISBN:0198506732] | 0.1064040 07362831 38 | 6817 | 85 | 0.467032967 03296704 | 0.012468827 930174564 | GO:MF | ACAA1, ADCY2, ADPRM, AKAP7, ANP32E, APOBEC3A, ARMT1, ARPP19, ATP5F1A, B3GALT5, BAZ1B, CAMK2N1, CCL5, CFD, CHMP1A, CPT2, DNAH9, DSE, ECI2, EGLN3, EIF2B3, ENTPD4, EP300, EXD3, EXOSC5, EXOSC7, FAF1, FNTA, FUT3, GLT8D1, GNA11, GNAI3, GPN2, GPRC5D, GUCY1B1, HSD17B12, HSD17B3, IP6K2, KIF1C, KIF3A, LOX, MAL, MAPK9, MARCHF8, MASP2, METTL17, METTL22, NAA10, NDOR1, NOS3, PARP8, PCGF3, PCMTD2, PLA2G6, POLA1, POLR2B, POP1, PPCDC, PRKAR1A, PRKG2, PTPN4, QTRT2, RETSAT, RFC5, SEPHS1, SERPINE2, SKP2, SLC27A5, SMC4, SMOX, SPINK5, ST3GAL4, STK3, SULT1A2, SULT1A3, SULT1A4, TERT, TRIM27, TRIM5, TRMT61B, TRRAP, TTLL4, TUBAL3, WAPL, WWOX |
| 19 | protein-containing complex | "A stable assembly of two or more macromolecules, i.e. proteins, nucleic acids, carbohydrates or lipids, in which at least one component is a protein and the constituent parts function together." [GOC:dos, GOC:mah] | 0.1098314 25757806 65 | 7956 | 89 | 0.483695652 173913 | 0.011186525 892408246 | GO:CC | ADNP, AFF4, AFTPH, AKAP7, ANP32E, AP1B1, ARPC2, ASXL1, ATP5F1A, BARX2, BAZ1B, BLOC1S1, BMAL2, C1QL1, CACNA1I, CEP76, CHMP1A, CHRNA1, COL11A1, COL18A1, COL9A3, COQ4, DNAH9, EIF2B3, EP300, EXOSC5, EXOSC7, FAF1, FNTA, GFRA2, GNA11, GNAI3, GPRC5D, GUCY1B1, HNRNPA0, HNRNPH2, HSD17B12, IKZF5, KIF1C, KIF3A, KLRC1, KLRC2, LAT, LOX, LRP8, MAGOH, METTL17, METTL22, MXI1, NAA10, NEUROD1, NKX2-5, PALB2, PCGF3, POLA1, POLR2B, POP1, PPCDC, PRKAR1A, PSMG1, QTRT2, RAD52, REC8, RFC5, RPL36A, RPL36A-HNRNPH2, RPS18, RUNX3, SKP2, SLC11A2, SLC27A5, SLC9A1, SMC4, SNTA1, STK3, TBL1Y, TERT, THOC7, TLE4, TNXB, TRIM27, TRMT61B, TRRAP, UTP18, VPS37B, WDR43, WDR5B, WWOX, ZFC3H1 |

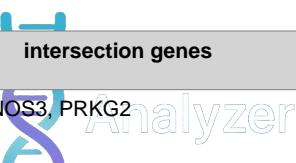
| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|-----------------------------|--|-----------------------------|-----------|-------------------|--------------------------|--------------------------|--------|--|
| 20 | nuclear lumen | "The volume enclosed by the nuclear inner membrane." [GOC:mah, GOC:pz] | 0.1203432 38134971 39 | 5540 | 67 | 0.364130434 7826087 | 0.012093862 815884477 | GO:CC | AFF4, AFTPH, ANP32E, APOBEC3A, ARPC2, ARPP19, ASXL1, BARX2, BAZ1B, BMAL2, BNIP3, BRWD1, CHMP1A, CPT2, CREB3L1, EGLN3, EP300, EXOSC5, EXOSC7, FAF1, GNAI3, HINFP, HNRNPA0, HNRNPH2, INAVA, IP6K2, MAGOH, MAPK9, MEF2D, METTL17, METTL22, MXI1, NAA10, NDOR1, NEUROD1, NKX2-5, PALB2, PCGF3, PLA2G6, POLA1, POLR2B, POMP, POP1, PSMG1, PTPN4, RAD52, REC8, RFC5, RPS18, RUNX3, SKP2, SLC9A1, SMC4, SMOX, TBCA, TBL1Y, TERT, THOC7, TLE4, TRIM27, TRIM5, TRRAP, UTP18, VWA5A, WAPL, WDR43, WDR5B |
| 21 | chromatin binding | "Binding to chromatin, the network of fibers of DNA, protein, and sometimes RNA, that make up the chromosomes of the eukaryotic nucleus during interphase." [GOC:jl, ISBN:0198506732, PMID:20404130] | 0.1299151 68975459 9 | 636 | 16 | 0.087912087 91208792 | 0.025157232 704402517 | GO:MF | ADNP, ASXL1, BARX2, CREB3L1, EP300, HINFP, IKZF5, NEUROD1, NKX2-5, POLA1, POLR2B, REC8, SMC4, TBL1Y, TLE4, TRRAP |
| 22 | RNA-templated transcription | "The synthesis of an RNA transcript from an RNA template." [GOC:txnOH] | 0.1319796 11097984 78 | 2 | 2 | 0.011235955 056179775 | 1 | GO:BP | POLR2B, TERT |
| 23 | FMN binding | "Binding to flavin mono nucleotide. Flavin mono nucleotide (FMN) is the coenzyme or the prosthetic group of various flavoprotein oxidoreductase enzymes." [GOC:tb] | 0.1853386 53419312 47 | 15 | 3 | 0.016483516 483516484 | 0.2 | GO:MF | NDOR1, NOS3, PPCDC |
| 24 | cytosol | "The part of the cytoplasm that does not contain organelles but which does contain other particulate matter, such as protein complexes." [GOC:hjd, GOC:jl] | 0.2053361 19638941 33 | 5534 | 66 | 0.358695652 173913 | 0.011926273 942898446 | GO:CC | ACAA1, ADPRM, ADRA2B, AFTPH, AKAP7, AP1B1, ARMH3, ARPC2, BARX2, BCL2A1, BLOC1S1, BRWD1, C2CD2, CEP76, CHMP1A, CREB3L1, DDIT4, ECI2, EGLN3, EIF2B3, EP300, EXOSC5, EXOSC7, FAF1, FNTA, GUCY1B1, HNRNPH2, KIF3A, KRT20, MAGOH, MAPK9, MXI1, NAA10, NDOR1, NLRX1, NOS3, PLA2G6, POLA1, POMP, PPCDC, PRKAR1A, PRKG2, PSMG1, PTPN4, RPL36A, RPL36A-HNRNPH2, RPS18, RUNX3, SERPINE2, SKP2, SMC4, SMOX, SPINK5, STK3, SULT1A2, SULT1A3, SULT1A4, TBCA, TERT, THOC7, TNFRSF11A, TRIM27, TRIM5, TTLL4, WAPL, WWOX |

| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|---|---|-----------------------------|-----------|-------------------|--------------------------|--------------------------|--------|--|
| 25 | positive regulation of extrinsic apoptotic signaling pathway via death domain receptors | "Any process that activates or increases the frequency, rate or extent of extrinsic apoptotic signaling pathway via death domain receptors." [GOC:TermGenie, PMID:17245429] | 0.2297658 99356868 72 | 12 | 3 | 0.016853932 584269662 | 0.25 | GO:BP | FAF1, MAL, STK3  |
| 26 | transferase activity | "Catalysis of the transfer of a group, e.g. a methyl group, glycosyl group, acyl group, phosphorus-containing, or other groups, from one compound (generally regarded as the donor) to another compound (generally regarded as the acceptor). Transferase is the systematic name for any enzyme of EC class 2." [EC:2.-.-.] | 0.2445542 13398972 18 | 2594 | 40 | 0.219780219 78021978 | 0.015420200 462606014 | GO:MF | ACAA1, AKAP7, ARMT1, B3GALT5, BAZ1B, CAMK2N1, CCL5, CPT2, EP300, FAF1, FNTA, FUT3, GLT8D1, GPRC5D, IP6K2, MAPK9, MARCHF8, METTL17, METTL22, NAA10, PARP8, PCGF3, PCMTD2, POLA1, POLR2B, PRKAR1A, PRKG2, QTRT2, SEPHS1, SKP2, ST3GAL4, STK3, SULT1A2, SULT1A3, SULT1A4, TERT, TRIM27, TRIM5, TRMT61B, TRRAP |
| 27 | exosome (RNase complex) | "A ribonuclease complex that has 3-prime to 5-prime exoribonuclease activity and possibly endoribonuclease activity, producing 5-prime-phosphomonoesters. Participates in a multitude of cellular RNA processing and degradation events preventing nuclear export and/or translation of aberrant RNAs. Restricted to processing linear and circular single-stranded RNAs (ssRNA) only. RNAs with complex secondary structures may have to be unwound or pre-processed by co-factors prior to entering the complex, esp if the 3-prime end is structured." [PMID:17174896, PMID:20531386, PMID:26726035] | 0.2510407 01392889 3 | 22 | 3 | 0.016304347 826086956 | 0.136363636 36363635 | GO:CC | EXOSC5, EXOSC7, ZFC3H1 |
| 28 | Cushing syndrome | Cushing syndrome | 0.3071360 29308437 9 | 153 | 7 | 0.064220183 48623854 | 0.045751633 9869281 | KEGG | ADCY2, CACNA1I, CREB3L1, GNA11, GNAI3, WDR5B, WNT5B |

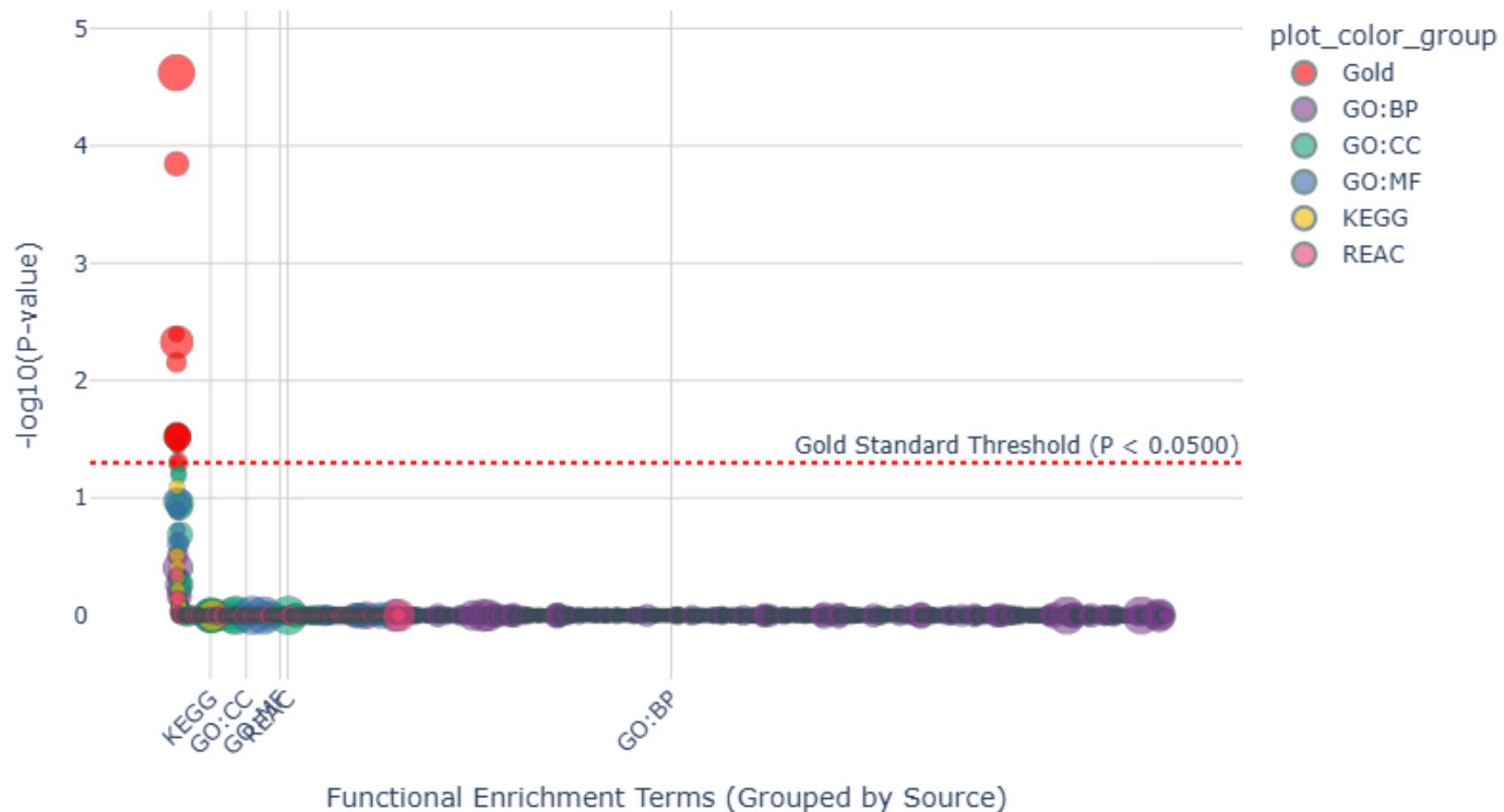
| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|--|---|-----------------------------|-----------|-------------------|--------------------------|--------------------------|--------|---|
| 29 | cellular response to chemical stimulus | "Any process that results in a change in state or activity of a cell (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a chemical stimulus." [GOC:mah] | 0.3075105 72498745 | 2192 | 35 | 0.196629213 48314608 | 0.015967153 284671534 | GO:BP | ACAA1, ADCY2, AKAP7, ASXL1, ATP5F1A, BNIP3, CCL5, CHRNA1, DDIT4, EGLN3, EP300, GNA11, GNAI3, GUCY1B1, IP6K2, KBTBD2, LOX, LRP8, MAPK9, MT1G, NEUROD1, NOS3, PLA2G6, PRKAR1A, RAD52, SKP2, SLC11A2, SLC9A1, SMOX, SULT1A2, SULT1A3, TERT, TNFRSF11A, TRIM5, WNT5B |
| 30 | Growth hormone synthesis, secretion and action | Growth hormone synthesis, secretion and action | 0.3874668 58549587 35 | 120 | 6 | 0.055045871 55963303 | 0.05 | KEGG | ADCY2, CREB3L1, EP300, GNA11, GNAI3, MAPK9 |
| 31 | response to stimulus | "Any process that results in a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a stimulus. The process begins with detection of the stimulus and ends with a change in state or activity of the cell or organism." [GOC:ai, GOC:bf] | 0.3922698 53056130 44 | 8999 | 100 | 0.561797752 8089888 | 0.011112345 8162018 | GO:BP | ACAA1, ADCY2, ADNP, ADORA3, ADRA2B, AFF4, AKAP7, APOBEC3A, ARMT1, ASXL1, ATP5F1A, B3GALT5, BAZ1B, BCL2A1, BMAL2, BNIP3, CACNA1I, CAMK2N1, CCL5, CD200, CFD, CHMP1A, CHRNA1, CLDN7, CNR1, COL11A1, COL18A1, CREB3L1, DDIT4, EGLN3, EIF2B3, EP300, EXOSC5, FAF1, FAM53B, FNTA, GAREM1, GFRA2, GNA11, GNAI3, GPRC5D, GUCY1B1, HINFP, HNRNPA0, HPX, IL22RA1, INAVA, IP6K2, ITM2A, KBTBD2, KIF3A, KLRC1, KLRC2, KRT20, LAT, LOX, LRP8, MAL, MAPK9, MARCHF8, MASP2, MT1G, NEUROD1, NKX2-5, NLRX1, NOS3, PALB2, PARP8, PLA2G6, POLA1, PRKAR1A, PRKG2, PTGDR2, RAD52, REC8, REG1B, RFC5, RUNX3, SERPINE2, SKP2, SLC11A2, SLC9A1, SMOX, SPINK5, ST3GAL4, STK3, SULT1A2, SULT1A3, TBL1Y, TERT, TLE4, TMEM204, TMUB2, TNFRSF11A, TNXB, TRIM27, TRIM5, TRRAP, WNT5B, WWOX |
| 32 | Lewis blood group biosynthesis | Lewis blood group biosynthesis | 0.4469726 52338604 34 | 18 | 3 | 0.023809523 809523808 | 0.166666666 66666666 | REAC | B3GALT5, FUT3, ST3GAL4 |
| 33 | calcium-dependent protein binding | "Binding to a protein or protein complex in the presence of calcium." [GOC:jid, PMID:10485905] | 0.4515120 33873356 64 | 79 | 5 | 0.027472527 472527472 | 0.063291139 24050633 | GO:MF | LRP8, MASP2, S100A2, SLC9A1, VPS37B |
| 34 | exoribonuclease complex | "A protein complex which is capable of exoribonuclease activity." [GO_REF:0000088, GOC:bhm, GOC:TermGenie, PMID:17174896] | 0.4624928 05582478 96 | 27 | 3 | 0.016304347 826086956 | 0.111111111 1111111 | GO:CC | EXOSC5, EXOSC7, ZFC3H1 |

| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|--|---|-----------------------------|-----------|-------------------|--------------------------|--------------------------|--------|--|
| 35 | positive regulation of response to stimulus | "Any process that activates, maintains or increases the rate of a response to a stimulus. Response to stimulus is a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a stimulus." [GOC:jid] | 0.4694701 65325283 96 | 2331 | 36 | 0.202247191 01123595 | 0.015444015 444015444 | GO:BP | ADNP, ADRA2B, ASXL1, CAMK2N1, CCL5, CFD, CNR1, EIF2B3, EP300, FAF1, FAM53B, FNTA, GAREM1, HPX, INAVA, KLRC1, KLRC2, LAT, MAL, MAPK9, MASP2, NLRX1, NOS3, PLA2G6, PTGDR2, SKP2, SLC9A1, ST3GAL4, STK3, TERT, TNFRSF11A, TNXB, TRIM5, TRRAP, WNT5B, WWOX |
| 36 | Glycosphingolipid biosynthesis - lacto and neolacto series | Glycosphingolipid biosynthesis - lacto and neolacto series | 0.4734479 65390606 1 | 28 | 3 | 0.027522935 779816515 | 0.107142857 14285714 | KEGG | B3GALT5, FUT3, ST3GAL4 |
| 37 | transcription regulator complex | "A protein complex that is capable of associating with DNA by direct binding, or via other DNA-binding proteins or complexes, and regulating transcription." [GOC:jl] | 0.4790622 66681156 | 523 | 12 | 0.065217391 30434782 | 0.022944550 669216062 | GO:CC | ADNP, BARX2, BMAL2, EP300, MXI1, NEUROD1, NKX2-5, RUNX3, TBL1Y, TLE4, TRRAP, WWOX |
| 38 | cadmium ion binding | "Binding to a cadmium ion (Cd)." [GOC:ai] | 0.4873459 72460592 | 5 | 2 | 0.010989010 98901099 | 0.4 | GO:MF | NOS3, SLC11A2 |
| 39 | organelle envelope | "A double membrane structure enclosing an organelle, including two lipid bilayers and the region between them. In some cases, an organelle envelope may have more than two membranes." [GOC:mah, GOC:pz] | 0.5156280 02568919 7 | 1329 | 22 | 0.119565217 39130435 | 0.016553799 84951091 | GO:CC | ATG9A, ATP5F1A, BCL2A1, BLOC1S1, BNIP3, CHMP1A, CNR1, COQ4, CPT2, FAF1, NLRX1, PARP8, POLA1, PRKG2, QTRT2, RETSAT, SEPHS1, SLC11A2, SLC25A15, SMOX, TRIM27, UTP18 |
| 40 | endomembrane system | "A collection of membranous structures involved in transport within the cell. The main components of the endomembrane system are endoplasmic reticulum, Golgi bodies, vesicles, cell membrane and nuclear envelope. Members of the endomembrane system pass materials through each other or though the use of vesicles." [GOC:lh] | 0.5473830 83339220 6 | 4872 | 58 | 0.315217391 30434784 | 0.011904761 904761904 | GO:CC | ACAA1, AFTPH, ANP32E, AP1B1, ARMH3, ARPC2, ATG9A, B3GALT5, BARX2, BCAN, BLOC1S1, BNIP3, CFD, CHMP1A, COL11A1, COL18A1, COL9A3, CREB3L1, DSE, ENTPD4, FAF1, FUT3, GLT8D1, GNAI3, GORASP1, HSD17B12, HSD17B3, ITM2A, KIF1C, LAT, MAL, MARCHF8, NOS3, PARP8, POLA1, POMP, PRKAR1A, PRKG2, PSMG1, RETSAT, RPL36A, RPL36A-HNRNPH2, SCG3, SEPHS1, SERPINE2, SLC11A2, SLC27A5, SMOX, SPINK5, ST3GAL4, TEX28, TRIM27, TRIM5, TRRAP, UTP18, VPS37B, WNT5B, WWOX |

| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|---|---|----------------------------|-----------|-------------------|--------------------------|--------------------------|--------|---|
| 41 | positive regulation of biological process | "Any process that activates or increases the frequency, rate or extent of a biological process. Biological processes are regulated by many means; examples include the control of gene expression, protein modification or interaction with a protein or substrate molecule." [GOC:jid] | 0.5483949 37304075 4 | 6264 | 75 | 0.421348314 60674155 | 0.011973180 076628353 | GO:BP | ADNP, ADRA2B, AKAP7, APOBEC3A, ARPC2, ARPP19, ASXL1, ATP5F1A, BARX2, BAZ1B, BCAN, BMAL2, BNIP3, CAMK2N1, CCL5, CD200, CFD, CLDN7, CNR1, CPT2, CREB3L1, EIF2B3, EP300, EXOSC7, FAF1, FAM53B, FNTA, FUT3, GAREM1, GNA11, GNAI3, HINFP, HNRNPA0, HPX, HSD17B12, INAVA, IP6K2, KIF3A, KLRC1, KLRC2, LAT, LRP8, MAL, MAPK9, MASP2, MEF2D, NEUROD1, NKX2-5, NLRX1, NOS3, PLA2G6, PRKAR1A, PRKG2, PRR16, PTGDR2, REG1B, RFC5, RUNX3, SERPINE2, SKP2, SLC9A1, SMC4, ST3GAL4, STK3, TBL1Y, TERT, TNFRSF11A, TNXB, TRIM27, TRIM5, TRRAP, VPS37B, WDR43, WNT5B, WWOX |
| 42 | regulation of sodium ion transport | "Any process that modulates the frequency, rate or extent of the directed movement of sodium ions (Na+) into, out of or within a cell, or between cells, by means of some agent such as a transporter or pore." [GOC:dph] | 0.5519987 14623654 4 | 69 | 5 | 0.028089887 640449437 | 0.072463768 11594203 | GO:BP | NKX2-5, NOS3, SERPINE2, SLC9A1, SNTA1 |
| 43 | Long-term depression | Long-term depression | 0.6037995 24114487 2 | 59 | 4 | 0.036697247 70642202 | 0.067796610 16949153 | KEGG | GNA11, GNAI3, GUCY1B1, PRKG2 |
| 44 | regulation of response to stimulus | "Any process that modulates the frequency, rate or extent of a response to a stimulus. Response to stimulus is a change in state or activity of a cell or an organism (in terms of movement, secretion, enzyme production, gene expression, etc.) as a result of a stimulus." [GOC:jid] | 0.6127169 68043934 4 | 3993 | 53 | 0.297752808 98876405 | 0.013273228 149261207 | GO:BP | ADNP, ADRA2B, AKAP7, ASXL1, CAMK2N1, CCL5, CD200, CFD, CNR1, CREB3L1, DDIT4, EIF2B3, EP300, FAF1, FAM53B, FNTA, GAREM1, HPX, IL22RA1, INAVA, KBTBD2, KLRC1, KLRC2, LAT, LOX, LRP8, MAL, MAPK9, MASP2, NEUROD1, NKX2-5, NLRX1, NOS3, PLA2G6, PRKAR1A, PTGDR2, RAD52, SERPINE2, SKP2, SLC9A1, SPINK5, ST3GAL4, STK3, TERT, TLE4, TMEM204, TNFRSF11A, TNXB, TRIM27, TRIM5, TRRAP, WNT5B, WWOX |
| 45 | protein metabolic process | "The chemical reactions and pathways involving a protein. Includes protein modification." [GOC:ma] | 0.6830177 86563718 6 | 4721 | 60 | 0.337078651 68539325 | 0.012709171 785638636 | GO:BP | ADNP, ADRA2B, ANP32E, B3GALT5, BAZ1B, BLOC1S1, BNIP3, CCL5, CFD, CHMP1A, COL11A1, DSE, EGLN3, EIF2B3, EP300, FAF1, FNTA, FUT3, GORASP1, HPX, INAVA, IP6K2, ITM2A, KBTBD2, LAT, LOX, LRP8, MAGOH, MAPK9, MARCHF8, MASP2, METTL17, METTL22, NAA10, PARP8, PCMTD2, PRKAR1A, PRKG2, PRR16, PTPN4, RPL36A, RPL36A-HNRNPH2, RPS18, RUNX3, SACS, SEPHS1, SERPINE2, SKP2, SNTA1, SPINK5, ST3GAL4, STK3, TBCA, TBL1Y, TMUB2, TNFRSF11A, TRIM27, TRIM5, TTLL4, VPS37B |

| No. | term name | description | p value | term size | intersection size | precision | recall | source | intersection genes |
|-----|---|--|----------------------------|-----------|-------------------|--------------------------|-------------------------|--------|--|
| 46 | Nitric oxide stimulates guanylate cyclase | Nitric oxide stimulates guanylate cyclase | 0.7104919 54833153 6 | 21 | 3 | 0.023809523 809523808 | 0.142857142 85714285 | REAC | GUCY1B1, NOS3, PRKG2  |
| 47 | Blood group systems biosynthesis | Blood group systems biosynthesis | 0.7104919 54833153 6 | 21 | 3 | 0.023809523 809523808 | 0.142857142 85714285 | REAC | B3GALT5, FUT3, ST3GAL4 |
| 48 | Circadian entrainment | Circadian entrainment | 0.7144062 18306585 8 | 97 | 5 | 0.045871559 633027525 | 0.051546391 75257732 | KEGG | ADCY2, CACNA1I, GNAI3, GUCY1B1, PRKG2 |
| 49 | Viral life cycle - HIV-1 | Viral life cycle - HIV-1 | 0.7187196 89959795 3 | 62 | 4 | 0.036697247 70642202 | 0.064516129 03225806 | KEGG | AFF4, APOBEC3A, EP300, TRIM5 |
| 50 | MHC class Ib receptor activity | "Combining with an MHC class Ib protein complex and transmitting the signal from one side of the membrane to the other to initiate a change in cell activity. Class Ib here refers to non-classical class I molecules, such as those of the CD1 or HLA-E gene families." [GOC:add, GOC:signaling, ISBN:0781735149] | 0.7266949 33246235 9 | 6 | 2 | 0.010989010 98901099 | 0.333333333 3333333 | GO:MF | KLRC1, KLRC2 |

Manhattan Plot



Gene-Term Heatmap



Functional Clustergram (Term vs. Gene Membership) - Clustered Successfully

