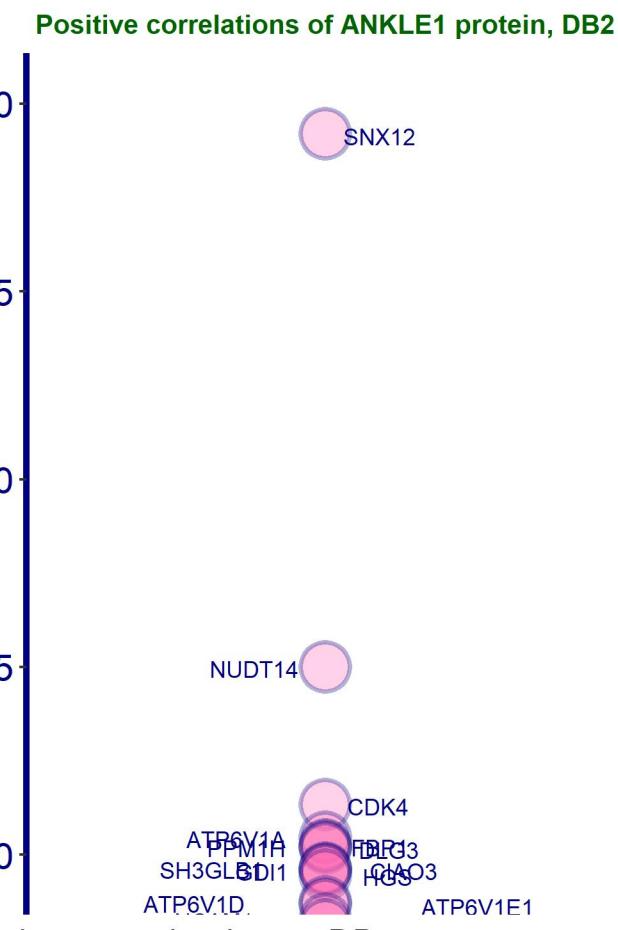
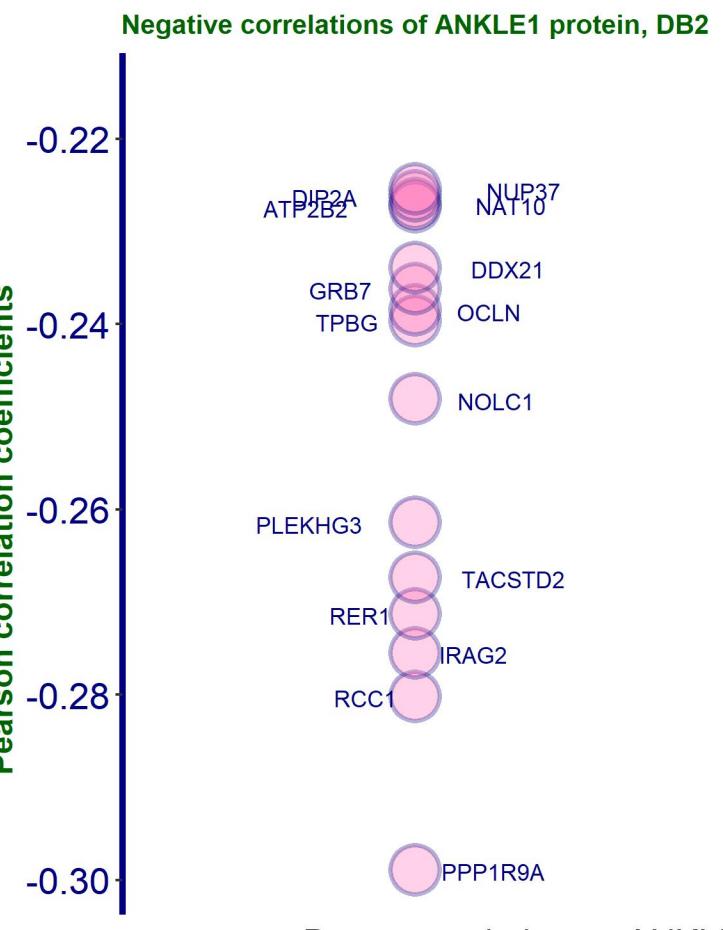
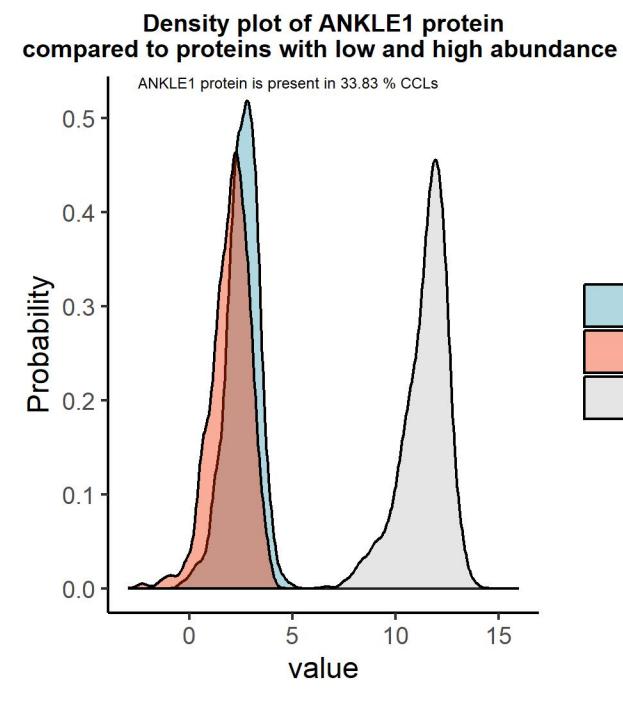
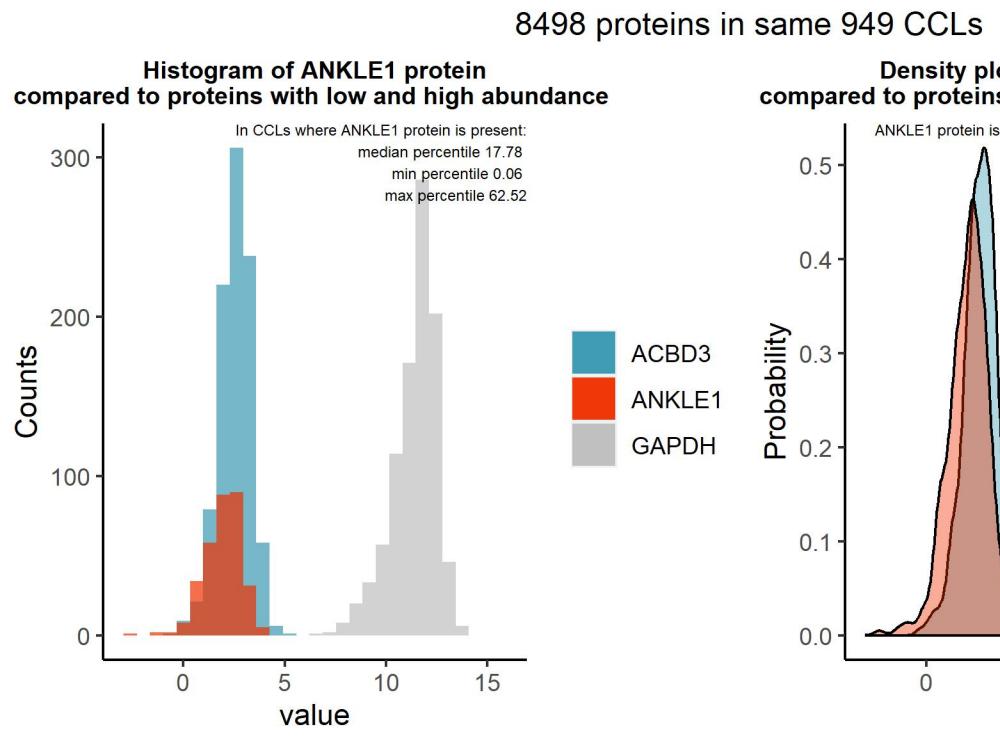


ANKLE1

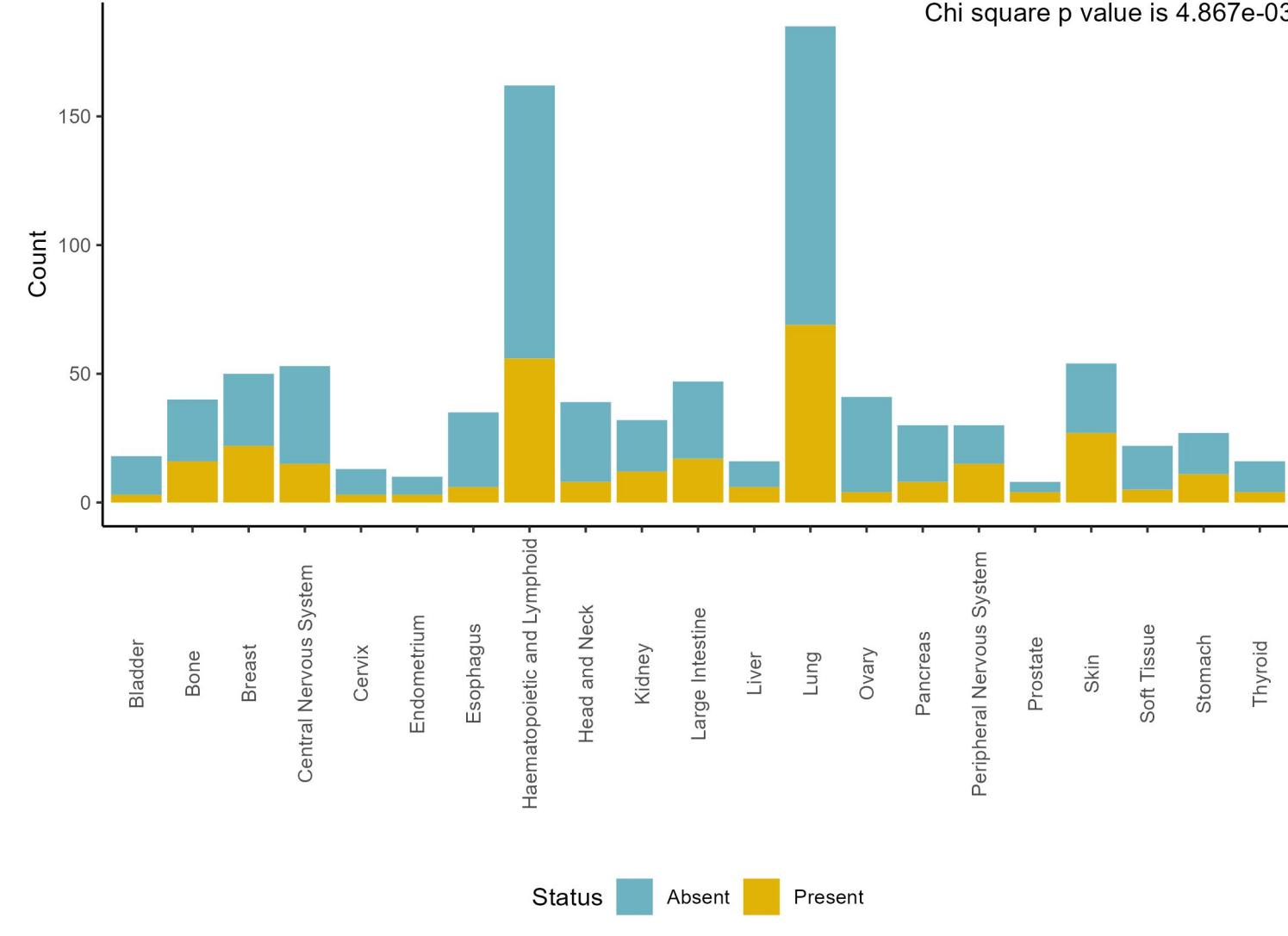
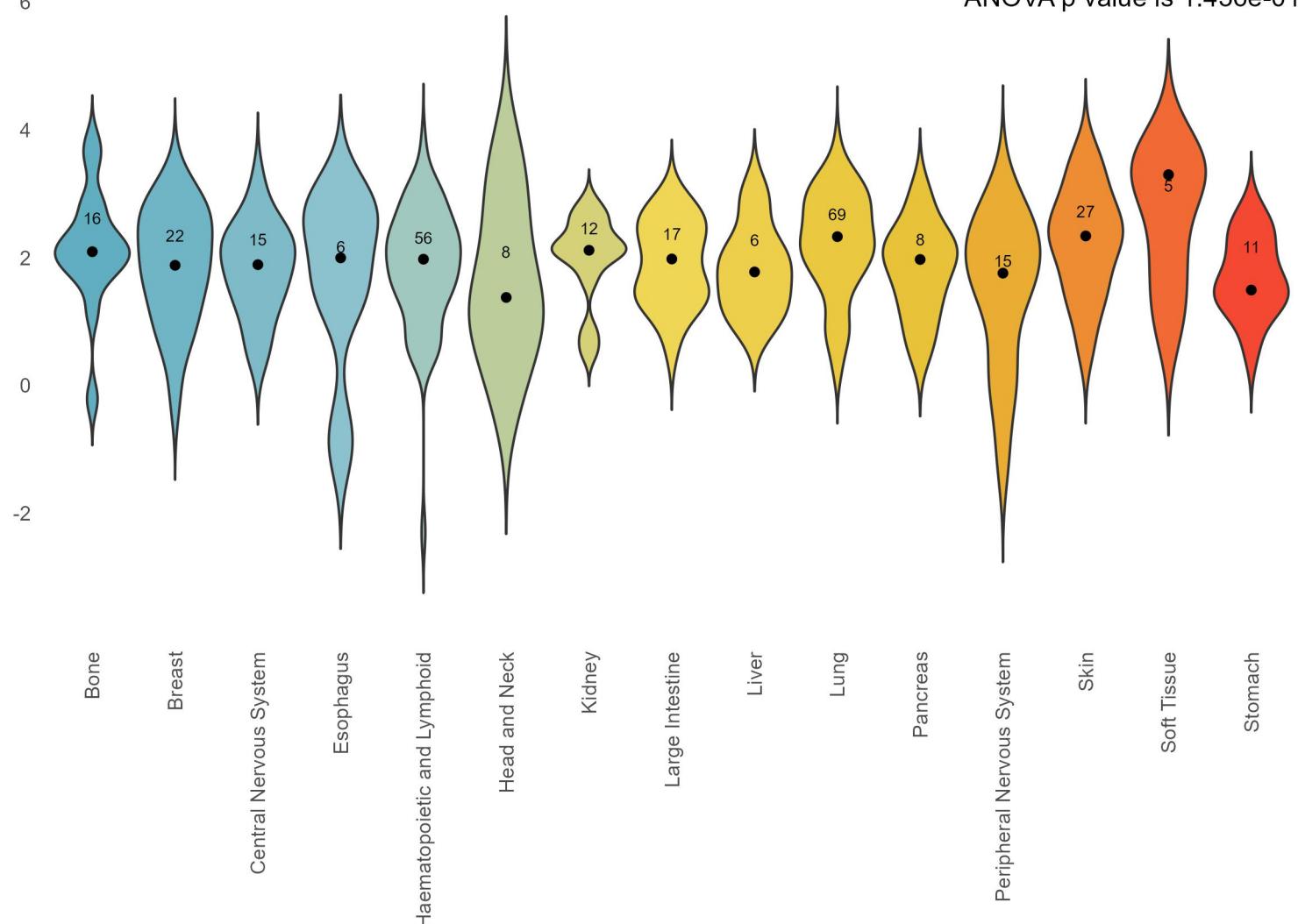
Protein name: ANKL1 ; UNIPROT: Q8NAG6 ; Gene name: ankyrin repeat and LEM domain containing 1

Ligandable: NA ; Ligandable_by_Chem: Yes ; Is_enzyme: Yes (<https://cansar.ai/>)

Sanger Institute Protein Database 2 (DB2), protein presence is less certain



Amount of ANKLE1 protein, number of CCLs where it is present by tissue, DB2

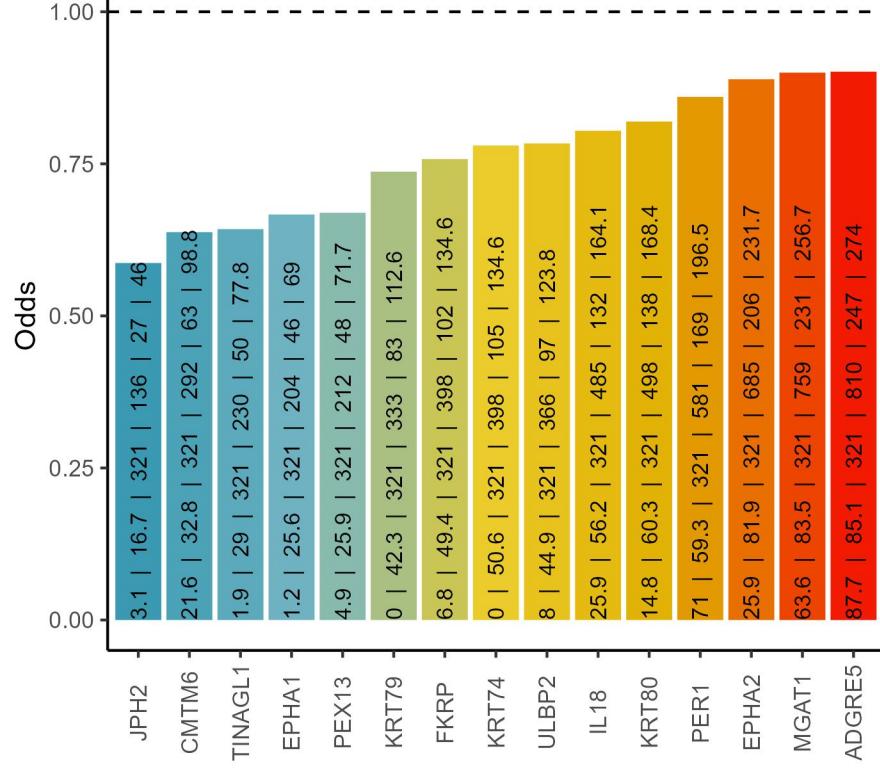


Cooccurrence with ANKLE1 protein, DB2

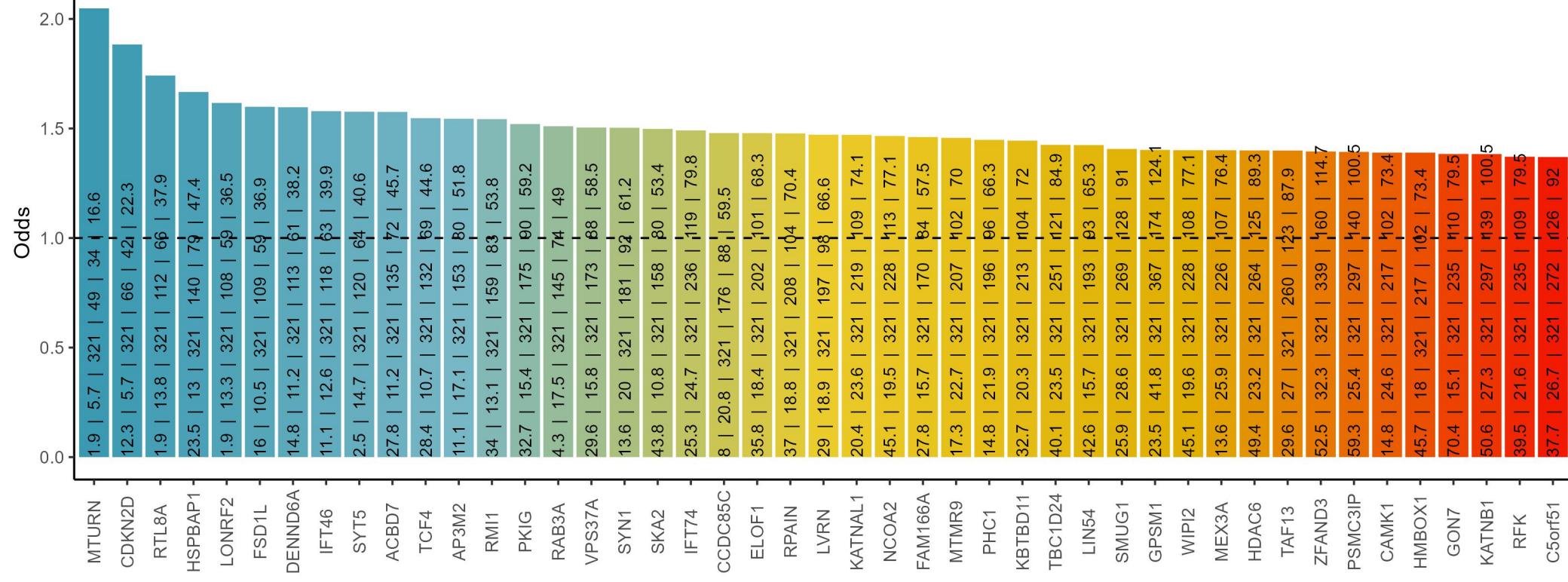
% of ANKLE1 in blood cancers: 34.6 ; % of ANKLE1 in solid cancers: 33.5

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ANKLE1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

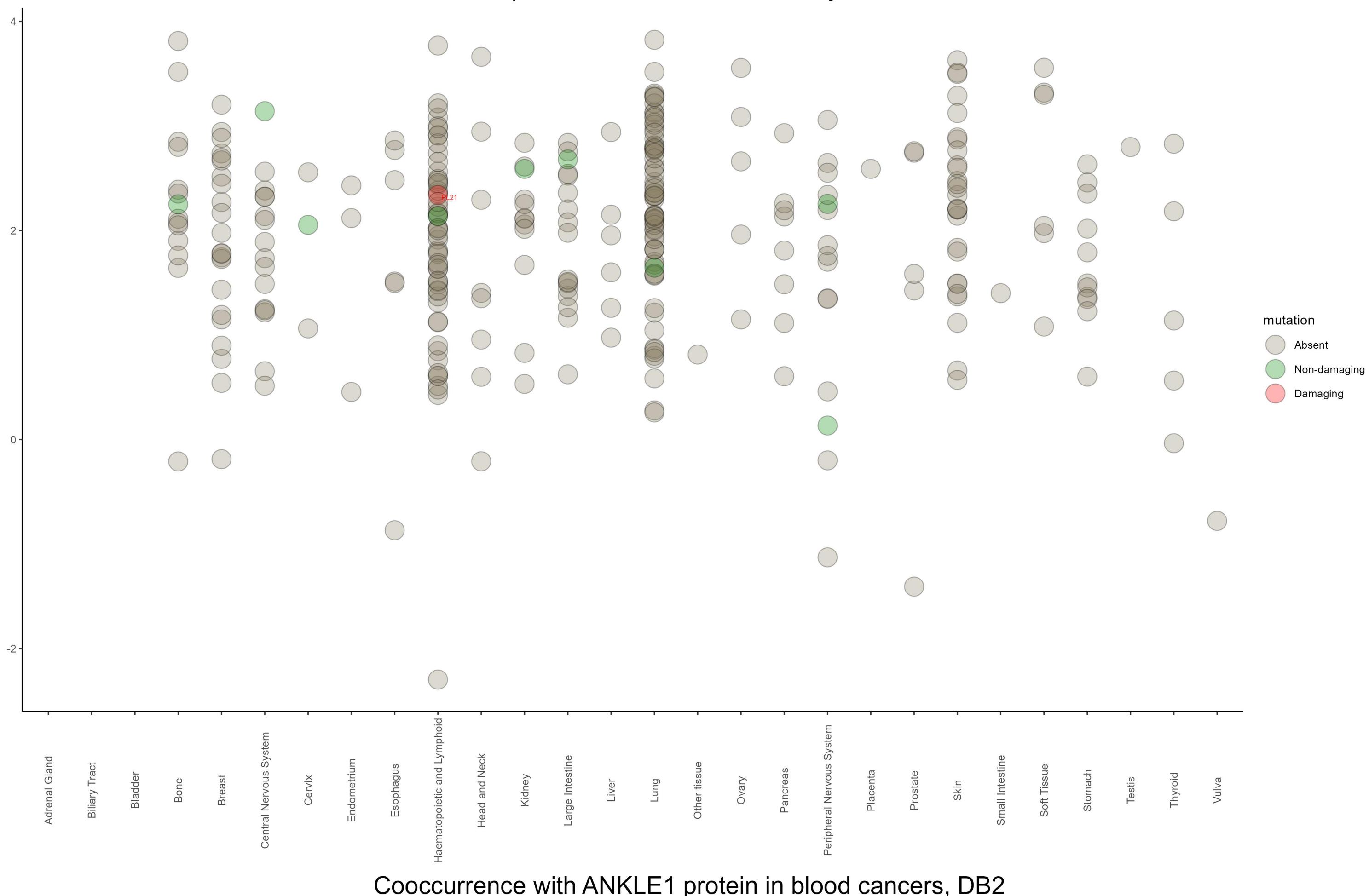
Negative cooccurrence



Positive cooccurrence



Amount of ANKLE1 protein and mutation status by tissue, DB2



Cooccurrence with ANKLE1 protein in blood cancers, DB2

The text in the bars: incidence of ANKLE1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Negative cooccurrence

Positive cooccurrence



Negative cooccurrence

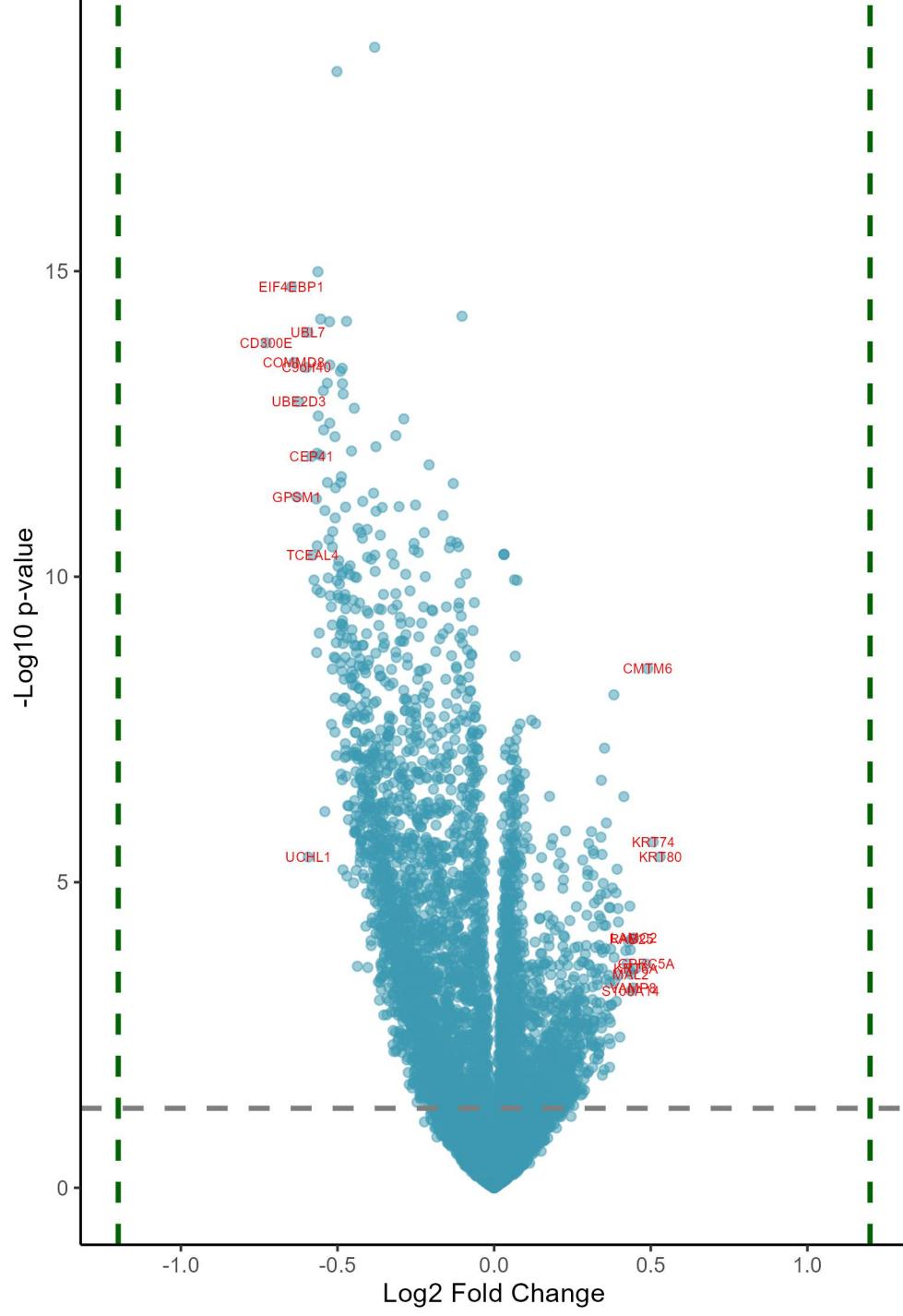
Positive cooccurrence



Negative cooccurrence

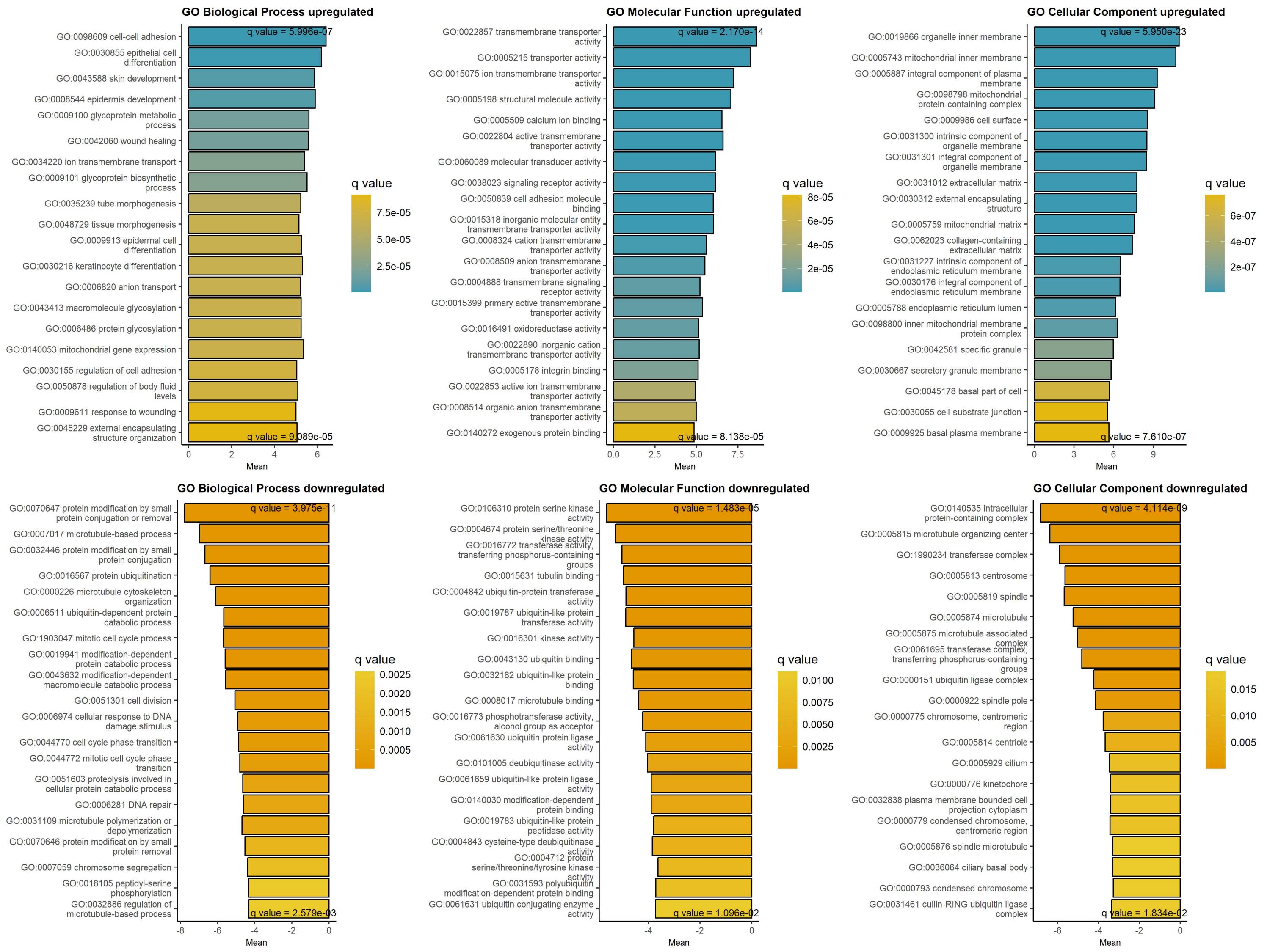
Positive cooccurrence

Downregulated at low/absent ANKLE1 Upregulated at low/absent ANKLE1

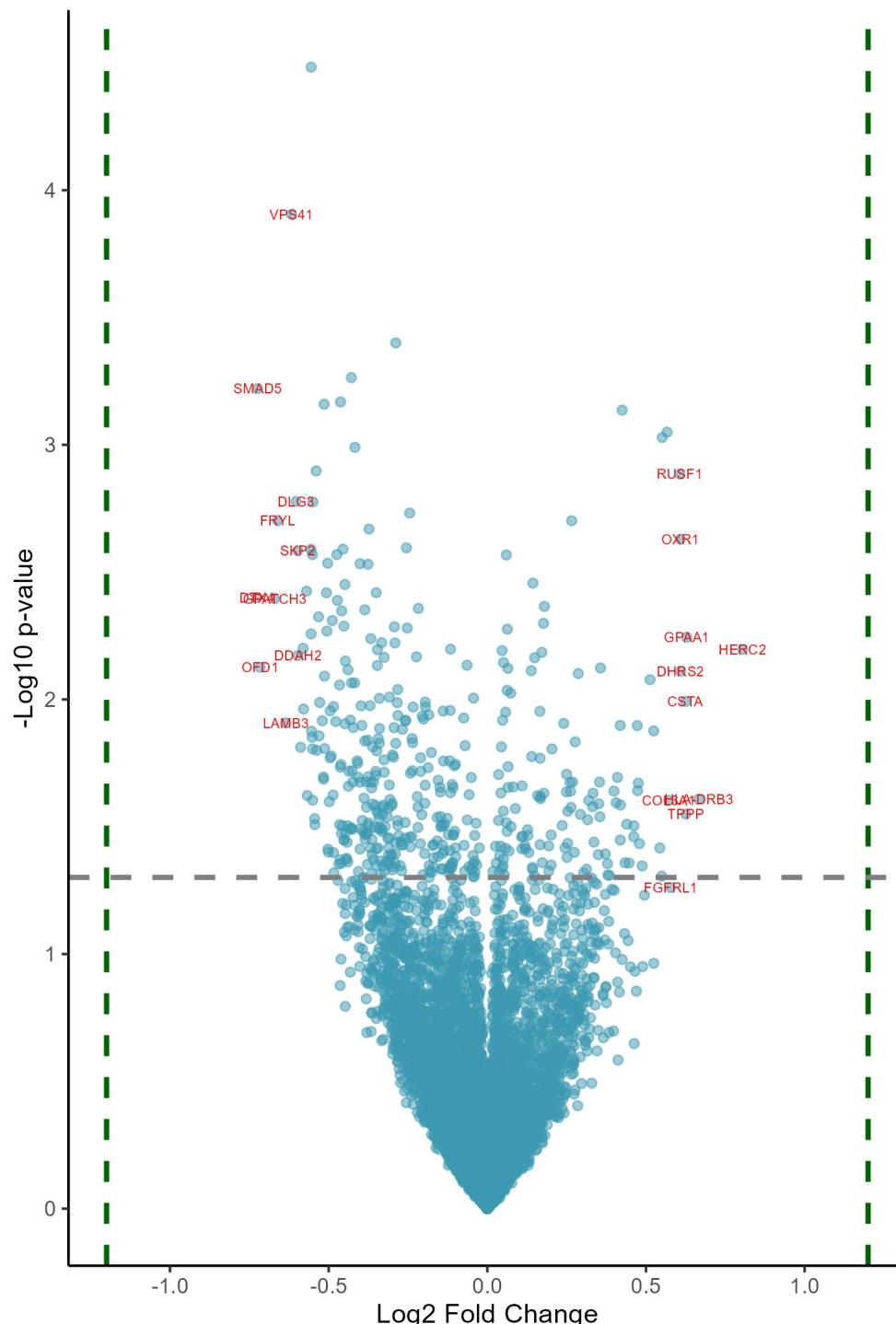


| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|-------------------------------------|-------|-----------|---------|-------------------------------------|
| -0.73 | 1.13e-11 | CD300E | CD300e molecule | 0.53 | 4.00e-05 | KRT80 | keratin 80 |
| -0.65 | 3.02e-12 | EIF4EBP1 | eukaryotic translation initiation f | 0.51 | 2.59e-05 | KRT74 | keratin 74 |
| -0.64 | 2.16e-11 | COMM8 | COMM domain containing 8 | 0.49 | 1.39e-07 | CMTM6 | CKLF like MARVEL transmembrane doma |
| -0.63 | 1.01e-09 | GPM1 | G protein signaling modulator 1 | 0.49 | 1.13e-03 | GPRC5A | G protein-coupled receptor class C |
| -0.62 | 5.44e-11 | UBE2D3 | ubiquitin conjugating enzyme E2 D3 | 0.45 | 1.30e-03 | KRT6A | keratin 6A |
| -0.6 | 2.16e-11 | C9orf40 | chromosome 9 open reading frame 40 | 0.45 | 5.01e-04 | LAMC2 | laminin subunit gamma 2 |
| -0.59 | 8.37e-12 | UBL7 | ubiquitin like 7 | 0.44 | 2.36e-03 | VAMP8 | vesicle associated membrane protein |
| -0.59 | 4.02e-05 | UCHL1 | ubiquitin C-terminal hydrolase L1 | 0.44 | 5.15e-04 | RAB25 | RAB25, member RAS oncogene family |
| -0.58 | 2.73e-10 | CEP41 | centrosomal protein 41 | 0.44 | 2.57e-03 | S100A14 | S100 calcium binding protein A14 |
| -0.58 | 5.03e-09 | TCEAL4 | transcription elongation factor A I | 0.44 | 1.55e-03 | MAL2 | mal, T cell differentiation protein |
| -0.57 | 1.02e-08 | MROH2B | maestro heat like repeat family mem | 0.43 | 7.29e-04 | EPHA2 | EPH receptor A2 |
| -0.57 | 1.06e-09 | PCSK6 | proprotein convertase subtilisin/ke | 0.43 | 1.40e-03 | KRT85 | keratin 85 |
| -0.57 | 8.57e-08 | PPP1R2 | protein phosphatase 1 regulatory in | 0.43 | 1.84e-04 | SDC4 | syndecan 4 |
| -0.57 | 2.58e-10 | SPC25 | SPC25 component of NDC80 kinetochor | 0.43 | 5.68e-04 | IL18 | interleukin 18 |
| -0.57 | 1.39e-08 | CEP97 | centrosomal protein 97 | 0.42 | 1.12e-03 | KRT14 | keratin 14 |
| -0.56 | 4.14e-09 | PNMA1 | PNMA family member 1 | 0.42 | 7.48e-04 | EPS8L2 | EPS8 like 2 |
| -0.56 | 2.13e-12 | RPE | ribulose-5-phosphate-3-epimerase | 0.41 | 6.54e-06 | MGAT1 | alpha-1,3-mannosyl-glycoprotein 2-b |
| -0.56 | 8.51e-11 | ACYP1 | acylphosphatase 1 | 0.4 | 1.10e-02 | KRT17 | keratin 17 |
| -0.56 | 4.93e-08 | SSNA1 | SS nuclear autoantigen 1 | 0.4 | 1.59e-03 | HMGA2 | high mobility group AT-hook 2 |
| -0.55 | 1.52e-08 | NUDT2 | nudix hydrolase 2 | 0.4 | 3.05e-04 | TCHHL1 | trichohyalin like 1 |
| -0.55 | 6.23e-12 | PGK2 | phosphoglycerate kinase 2 | 0.4 | 1.99e-04 | GALNT3 | polypeptide N-acetylgalactosaminylt |
| -0.55 | 2.71e-10 | AAMDC | adipogenesis associated Mth938 doma | 0.39 | 5.87e-05 | ADGRE5 | adhesion G protein-coupled receptor |
| -0.55 | 3.98e-11 | C5orf22 | chromosome 5 open reading frame 22 | 0.39 | 3.60e-03 | EGFR | epidermal growth factor receptor |
| -0.54 | 1.27e-10 | GINS2 | GINS complex subunit 2 | 0.39 | 1.21e-04 | B4GALT5 | beta-1,4-galactosyltransferase 5 |
| -0.54 | 1.02e-05 | CRMP1 | collapsin response mediator protein | 0.39 | 1.88e-03 | LPCAT2 | lysophosphatidylcholine acyltransfe |
| -0.54 | 1.44e-09 | ARL2BP | ADP ribosylation factor like GTPase | 0.38 | 9.28e-04 | SLC1A3 | solute carrier family 1 member 3 |
| -0.53 | 3.22e-11 | DUS3L | dihydrouridine synthase 3 like | 0.38 | 3.13e-07 | TINAGL1 | tubulointerstitial nephritis antige |
| -0.53 | 6.54e-10 | PDE6D | phosphodiesterase 6D | 0.38 | 1.04e-04 | KRT79 | keratin 79 |
| -0.53 | 9.65e-09 | HAUS7 | HAUS augmin like complex subunit 7 | 0.37 | 4.00e-03 | GTPBP8 | GTP binding protein 8 (putative) |

GAGE analysis on upregulated and downregulated proteins at low/absent ANKLE1 protein, DB2

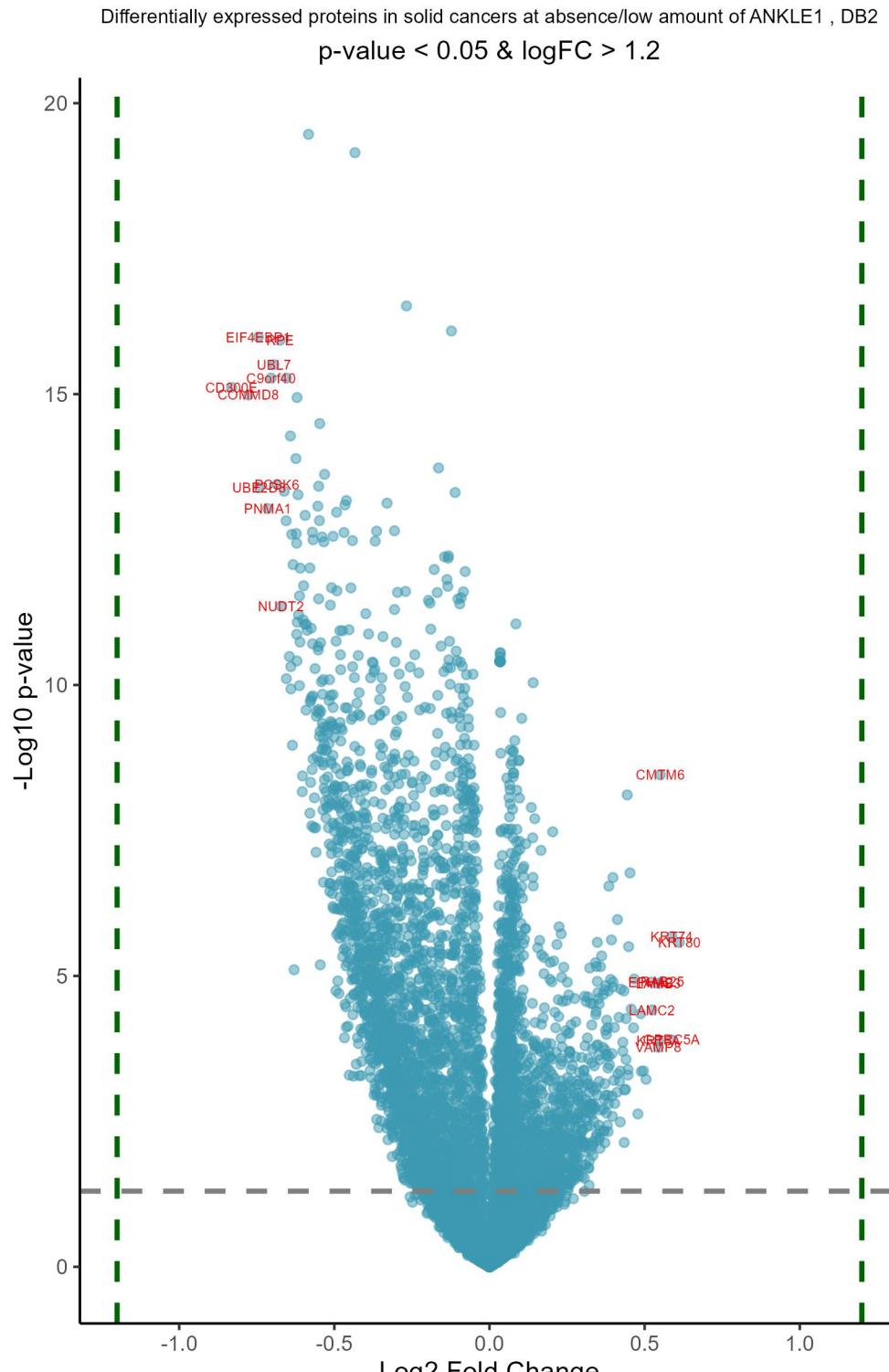


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent ANKLE1 Upregulated in blood cancers at low/absent ANKLE1

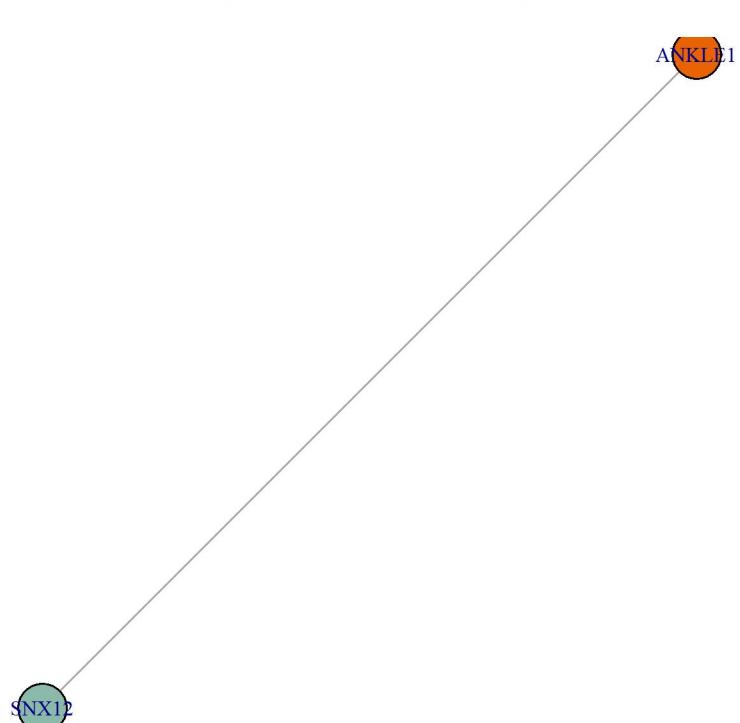
| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|---------|-------------------------------------|-------|-----------|-----------|-------------------------------------|
| -0.73 | 8.53e-01 | DTX4 | deltex E3 ubiquitin ligase 4 | 0.8 | 8.53e-01 | HERC2 | HECT and RLD domain containing E3 u |
| -0.72 | 6.79e-01 | SMAD5 | SMAD family member 5 | 0.67 | 9.18e-01 | HLA-DRB3 | major histocompatibility complex, c |
| -0.72 | 8.53e-01 | OFD1 | OFD1 centriole and centriolar satel | 0.63 | 8.53e-01 | GPAA1 | glycosylphosphatidylinositol anchor |
| -0.67 | 8.53e-01 | GPATCH3 | G-patch domain containing 3 | 0.63 | 9.18e-01 | TPPP | tubulin polymerization promoting pr |
| -0.66 | 7.95e-01 | FRYL | FRY like transcription coactivator | 0.62 | 8.84e-01 | CSTA | cystatin A |
| -0.64 | 8.84e-01 | LAMB3 | laminin subunit beta 3 | 0.61 | 8.53e-01 | DHRS2 | dehydrogenase/reductase 2 |
| -0.62 | 3.47e-01 | VPS41 | VPS41 subunit of HOPS complex | 0.61 | 7.95e-01 | OXR1 | oxidation resistance 1 |
| -0.6 | 7.95e-01 | DLG3 | discs large MAGUK scaffold protein | 0.61 | 7.78e-01 | RUSF1 | RUS family member 1 |
| -0.6 | 7.95e-01 | SKP2 | S-phase kinase associated protein 2 | 0.58 | 9.18e-01 | FGFRL1 | fibroblast growth factor receptor I |
| -0.6 | 8.53e-01 | DDAH2 | dimethylarginine dimethylaminohydro | 0.57 | 9.18e-01 | COL3A1 | collagen type III alpha 1 chain |
| -0.59 | 9.15e-01 | CCDC33 | coiled-coil domain containing 33 | 0.57 | 7.11e-01 | ITPR1 | inositol 1,4,5-trisphosphate recept |
| -0.58 | 8.53e-01 | PRXL2A | peroxiredoxin like 2A | 0.55 | 7.11e-01 | ANKRD27 | ankyrin repeat domain 27 |
| -0.58 | 8.84e-01 | GPR179 | G protein-coupled receptor 179 | 0.55 | 9.18e-01 | H2BC1 | H2B clustered histone 1 |
| -0.57 | 8.53e-01 | MIS18A | MIS18 kinetochore protein A | 0.54 | 9.18e-01 | LCLAT1 | lysocardiolipin acyltransferase 1 |
| -0.57 | 9.18e-01 | NRGN | neurogranin | 0.52 | 9.18e-01 | HLA-DRB1 | major histocompatibility complex, c |
| -0.56 | 7.95e-01 | QSER1 | glutamine and serine rich 1 | 0.52 | 8.85e-01 | DUSP23 | dual specificity phosphatase 23 |
| -0.56 | 8.53e-01 | TRIOBP | TRIO and F-actin binding protein | 0.51 | 8.84e-01 | RGS22 | regulator of G protein signaling 22 |
| -0.56 | 1.37e-01 | ZWINT | ZW10 interacting kinetochore protei | 0.49 | 9.18e-01 | ITGAL | integrin subunit alpha L |
| -0.55 | 8.85e-01 | LAPTM5 | lysosomal protein transmembrane 5 | 0.49 | 9.18e-01 | KIAA0100 | KIAA0100 |
| -0.55 | 9.15e-01 | DSG2 | desmoglein 2 | 0.49 | 9.18e-01 | SPART | spartin |
| -0.55 | 7.95e-01 | PLEKHM1 | pleckstrin homology and RUN domain | 0.48 | 9.18e-01 | PVR | PVR cell adhesion molecule |
| -0.55 | 9.15e-01 | ERBB2 | erb-b2 receptor tyrosine kinase 2 | 0.48 | 9.18e-01 | MFN1 | mitofusin 1 |
| -0.55 | 9.18e-01 | CRMP1 | collapsin response mediator protein | 0.47 | 9.18e-01 | P4HA2 | prolyl 4-hydroxylase subunit alpha |
| -0.55 | 7.95e-01 | MBD4 | methyl-CpG binding domain 4, DNA gl | 0.47 | 8.84e-01 | SCIN | scinderin |
| -0.54 | 9.18e-01 | ALDH2 | aldehyde dehydrogenase 2 family mem | 0.47 | 9.18e-01 | MORC4 | MORC family CW-type zinc finger 4 |
| -0.54 | 9.18e-01 | PFN2 | profilin 2 | 0.47 | 9.18e-01 | MACROH2A2 | macroH2A.2 histone |
| -0.54 | 7.78e-01 | PITPNM1 | phosphatidylinositol transfer prote | 0.46 | 9.18e-01 | CRACR2B | calcium release activated channel r |
| -0.54 | 9.18e-01 | TCEAL4 | transcription elongation factor A I | 0.46 | 9.18e-01 | DHX57 | DExH-box helicase 57 |
| -0.53 | 8.53e-01 | STAT2 | signal transducer and activator of | 0.46 | 9.18e-01 | YBX3 | Y-box binding protein 3 |



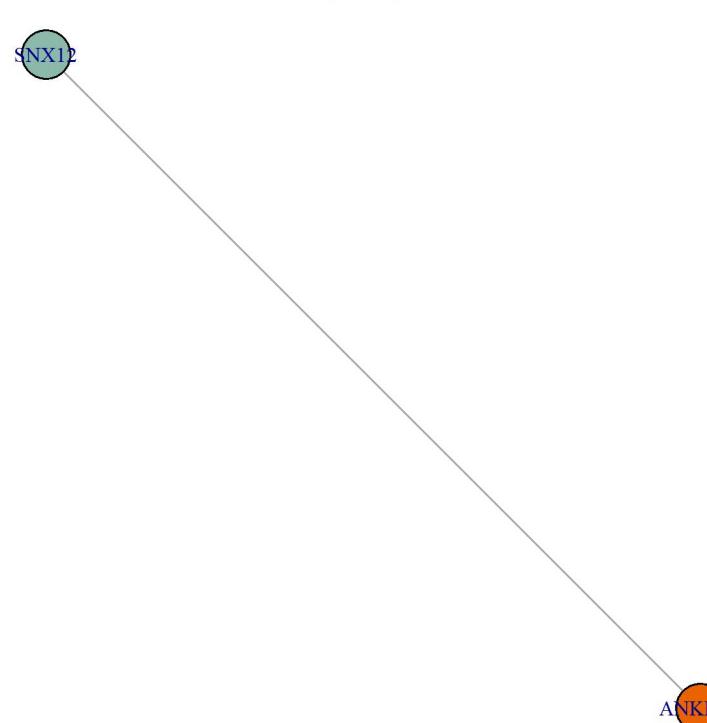
Downregulated in solid cancers at low/absent ANKLE1 Upregulated in solid cancers at low/absent ANKLE1

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|-------------------------------------|-------|-----------|---------|-------------------------------------|
| -0.83 | 5.83e-13 | CD300E | CD300e molecule | 0.61 | 2.27e-05 | KRT80 | keratin 80 |
| -0.78 | 7.19e-13 | COMMD8 | COMM domain containing 8 | 0.59 | 1.87e-05 | KRT74 | keratin 74 |
| -0.74 | 1.42e-13 | EIF4EBP1 | eukaryotic translation initiation f | 0.59 | 5.95e-04 | GPRC5A | G protein-coupled receptor class C |
| -0.74 | 1.63e-11 | UBE2D3 | ubiquitin conjugating enzyme E2 D3 | 0.56 | 8.33e-05 | RAB25 | RAB25, member RAS oncogene family |
| -0.71 | 2.67e-11 | PNMA1 | PNMA family member 1 | 0.55 | 9.54e-08 | CMTM6 | CKLF like MARVEL transmembrane doma |
| -0.7 | 4.42e-13 | C9orf40 | chromosome 9 open reading frame 40 | 0.55 | 6.16e-04 | KRT6A | keratin 6A |
| -0.69 | 3.26e-13 | UBL7 | ubiquitin like 7 | 0.54 | 7.67e-04 | VAMP8 | vesicle associated membrane protein |
| -0.69 | 1.57e-11 | PCSK6 | proprotein convertase subtilisin/ke | 0.54 | 8.91e-05 | LAMB3 | laminin subunit beta 3 |
| -0.67 | 1.42e-13 | RPE | ribulose-5-phosphate-3-epimerase | 0.52 | 2.17e-04 | LAMC2 | laminin subunit gamma 2 |
| -0.67 | 5.07e-10 | NUDT2 | nudix hydrolase 2 | 0.52 | 8.52e-05 | EPHA2 | EPH receptor A2 |
| -0.66 | 1.78e-11 | ACYP1 | acylphosphatase 1 | 0.5 | 2.22e-03 | S100A14 | S100 calcium binding protein A14 |
| -0.66 | 3.81e-11 | SPC25 | SPC25 component of NDC80 kinetochor | 0.5 | 1.67e-03 | KRT85 | keratin 85 |
| -0.65 | 4.23e-09 | GPSM1 | G protein signaling modulator 1 | 0.49 | 1.70e-03 | MAL2 | mal, T cell differentiation protein |
| -0.65 | 4.42e-13 | PGK2 | phosphoglycerate kinase 2 | 0.49 | 2.45e-04 | EGFR | epidermal growth factor receptor |
| -0.64 | 2.51e-09 | CEP97 | centrosomal protein 97 | 0.48 | 7.13e-03 | KRT17 | keratin 17 |
| -0.64 | 2.93e-12 | C5orf22 | chromosome 5 open reading frame 22 | 0.47 | 7.74e-05 | SDC4 | syndecan 4 |
| -0.64 | 2.93e-09 | MROH2B | maestro heat like repeat family mem | 0.46 | 3.97e-04 | EPS8L2 | EPS8 like 2 |
| -0.64 | 5.92e-09 | SSNA1 | SS nuclear autoantigen 1 | 0.46 | 2.10e-04 | TCHHL1 | trichohyalin like 1 |
| -0.64 | 5.51e-11 | HESX1 | HESX homeobox 1 | 0.45 | 2.30e-06 | MGAT1 | alpha-1,3-mannosyl-glycoprotein 2-b |
| -0.64 | 3.73e-08 | PPP1R2 | protein phosphatase 1 regulatory in | 0.45 | 2.64e-05 | B4GALT5 | beta-1,4-galactosyltransferase 5 |
| -0.63 | 1.43e-10 | ARL2BP | ADP ribosylation factor like GTPase | 0.45 | 1.93e-03 | KRT14 | keratin 14 |
| -0.63 | 5.66e-05 | UCHL1 | ubiquitin C-terminal hydrolase L1 | 0.45 | 1.60e-03 | F3 | coagulation factor III, tissue fact |
| -0.62 | 6.71e-12 | DUS3L | dihydrouridine synthase 3 like | 0.44 | 1.79e-07 | TINAGL1 | tubulointerstitial nephritis antig |
| -0.62 | 5.49e-11 | GINS2 | GINS complex subunit 2 | 0.44 | 2.89e-04 | GALNT3 | polypeptide N-acetylgalactosaminylt |
| -0.62 | 6.64e-11 | C18orf25 | chromosome 18 open reading frame 25 | 0.44 | 1.13e-03 | HMGA2 | high mobility group AT-hook 2 |
| -0.62 | 1.26e-09 | CCDC73 | coiled-coil domain containing 73 | 0.44 | 3.09e-03 | ITGB6 | integrin subunit beta 6 |
| -0.62 | 2.51e-09 | USP13 | ubiquitin specific peptidase 13 | 0.44 | 3.18e-03 | NT5E | 5'-nucleotidase ecto |
| -0.62 | 7.36e-13 | UBFD1 | ubiquitin family domain containing | 0.43 | 1.85e-02 | HYDIN | HYDIN axonemal central pair apparat |
| -0.62 | 8.91e-10 | CTDP1 | CTD phosphatase subunit 1 | 0.43 | 1.15e-04 | KRT79 | keratin 79 |

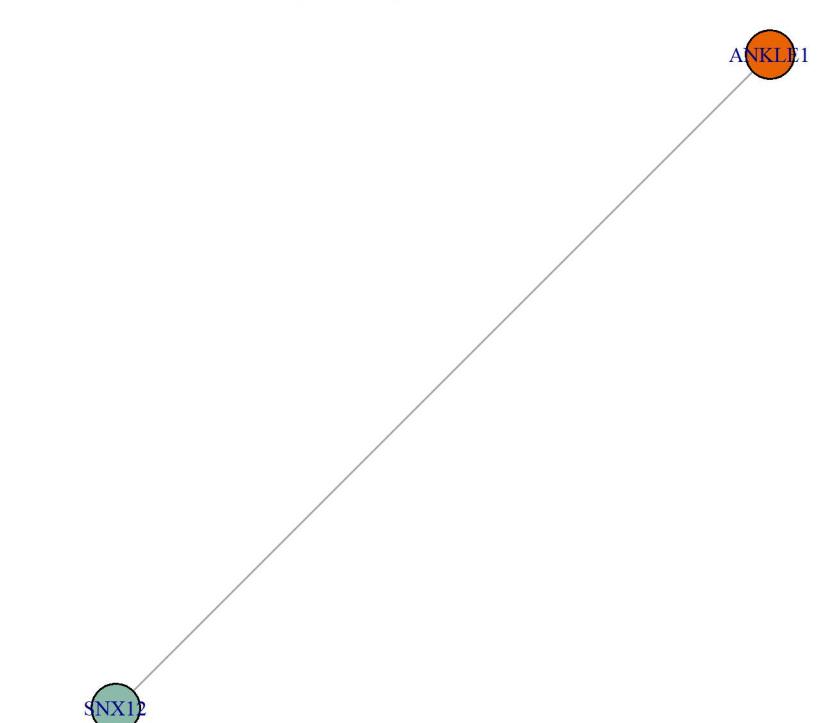
ANKLE1 network, DB2, all Pearson r > 0.45

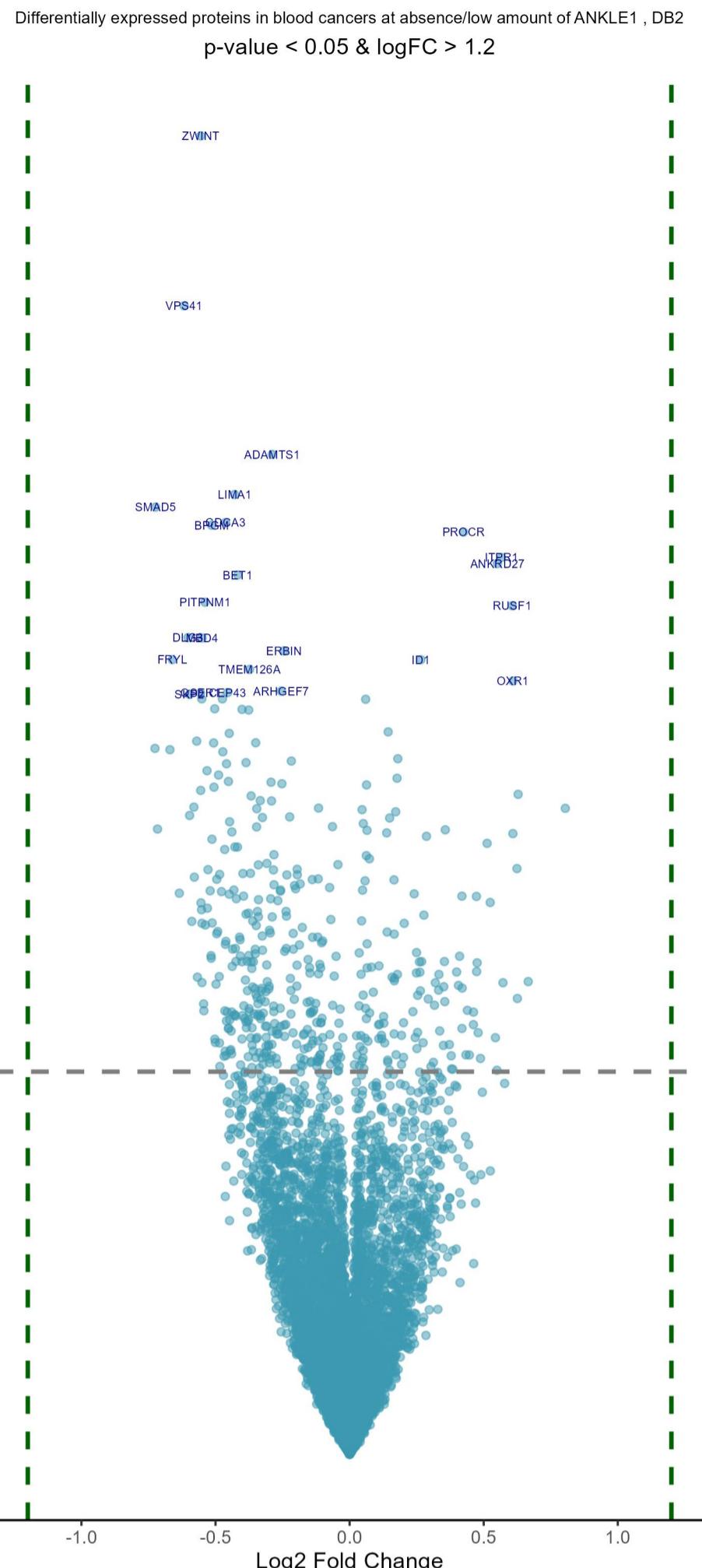


ANKLE1 network, DB2, all Pearson r > 0.4

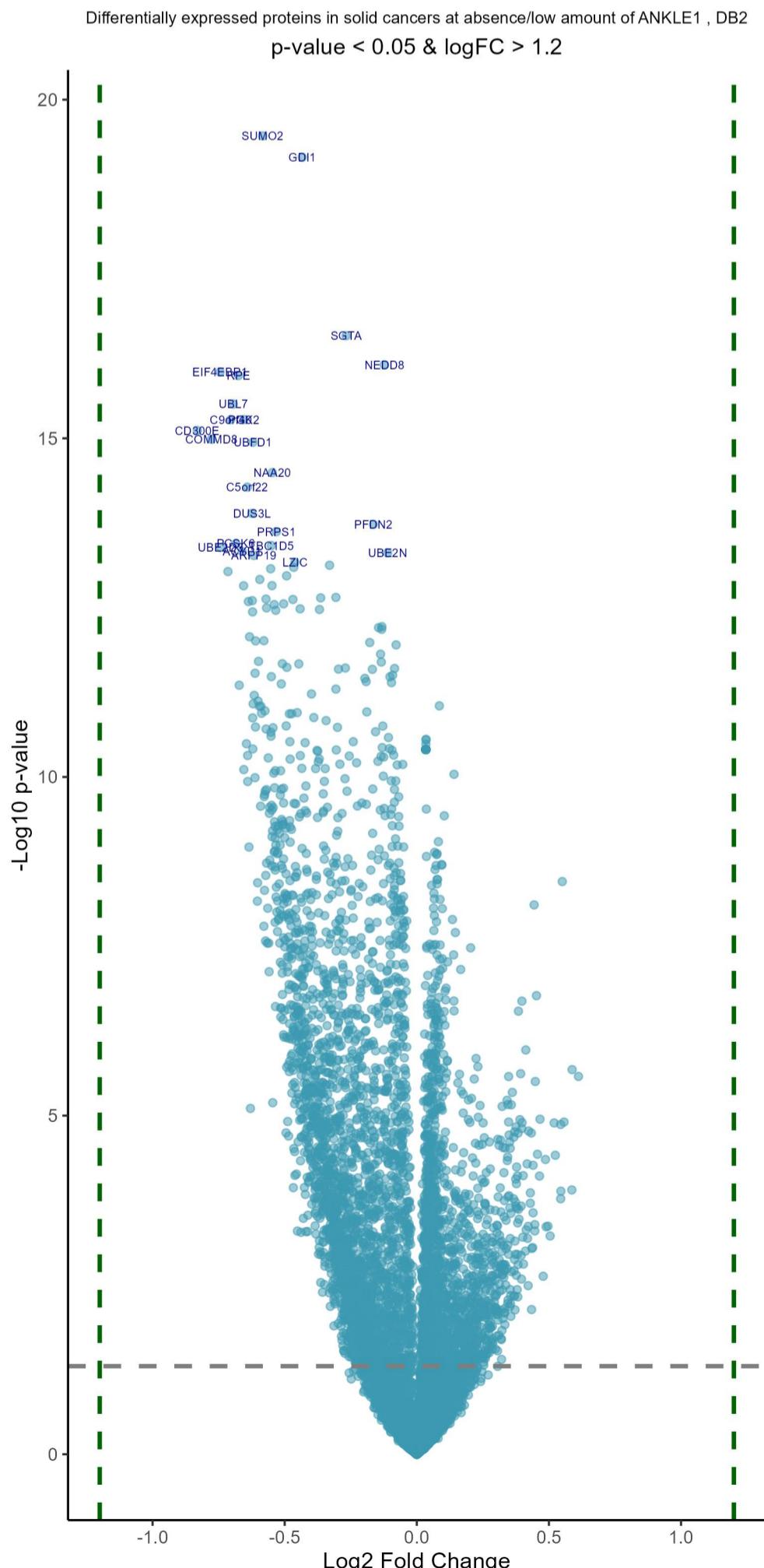


ANKLE1 network, DB2, all Pearson r > 0.35



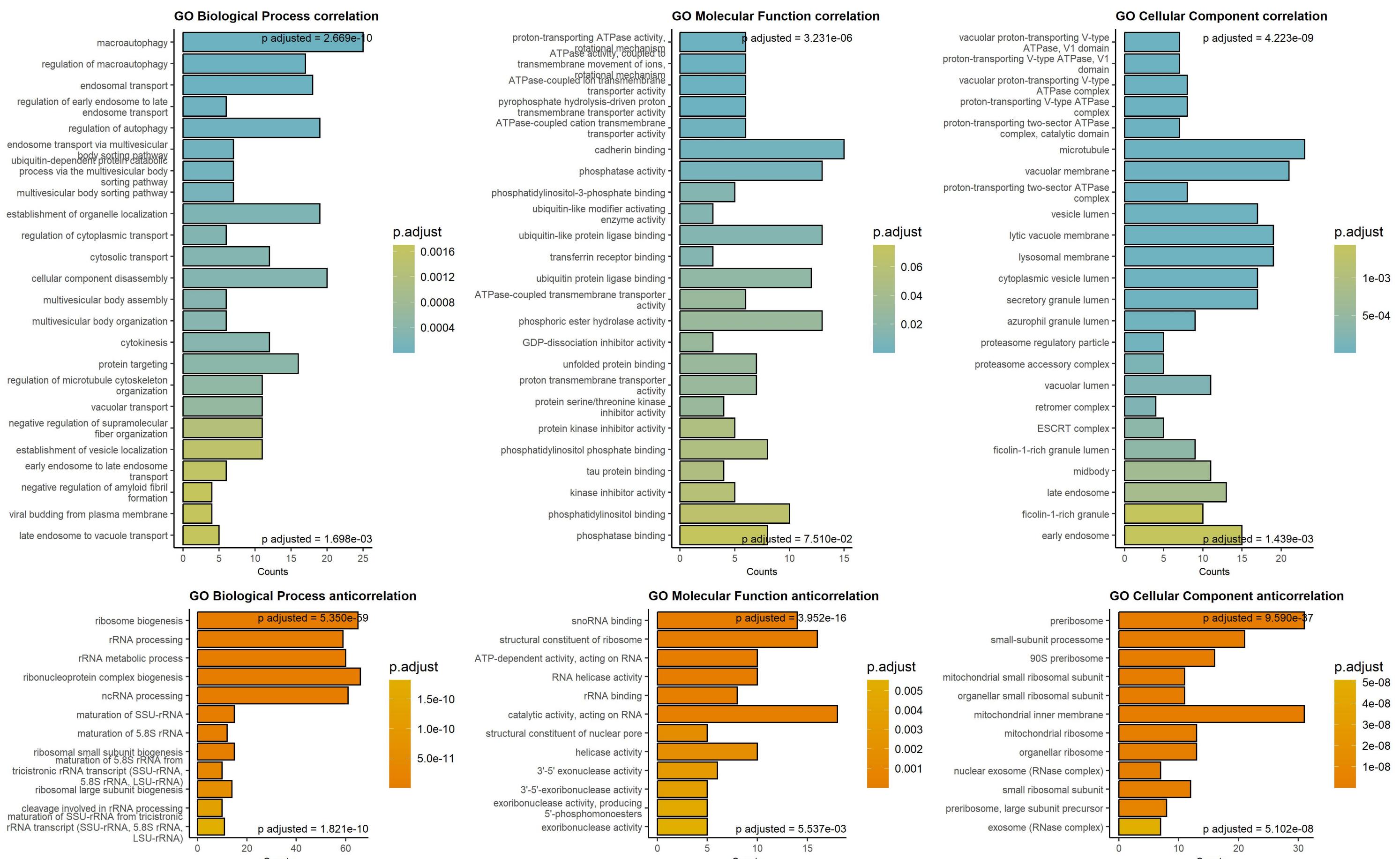


| Sorted by p values! | | | | | | | |
|---|-----------|----------|--------------------------------------|---|-----------|-----------|---------------------------------------|
| Downregulated in blood cancers at low/absent ANKLE1 | | | | Upregulated in blood cancers at low/absent ANKLE1 | | | |
| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
| -0.56 | 1.37e-01 | ZWINT | ZW10 interacting kinetochore protein | 0.42 | 6.79e-01 | PROCR | protein C receptor |
| -0.62 | 3.47e-01 | VPS41 | VPS41 subunit of HOPS complex | 0.57 | 7.11e-01 | ITPR1 | inositol 1,4,5-trisphosphate receptor |
| -0.29 | 6.79e-01 | ADAMTS1 | ADAM metallopeptidase with thrombos | 0.55 | 7.11e-01 | ANKRD27 | ankyrin repeat domain 27 |
| -0.43 | 6.79e-01 | LIMA1 | LIM domain and actin binding 1 | 0.61 | 7.78e-01 | RUSF1 | RUS family member 1 |
| -0.72 | 6.79e-01 | SMAD5 | SMAD family member 5 | 0.27 | 7.95e-01 | ID1 | inhibitor of DNA binding 1, HLH pro |
| -0.46 | 6.79e-01 | CDCA3 | cell division cycle associated 3 | 0.61 | 7.95e-01 | OXR1 | oxidation resistance 1 |
| -0.51 | 6.79e-01 | BPGM | bisphosphoglycerate mutase | 0.06 | 7.95e-01 | CIAO1 | cytosolic iron-sulfur assembly comp |
| -0.42 | 7.13e-01 | BET1 | Bet1 golgi vesicular membrane traff | 0.14 | 8.53e-01 | SPOUT1 | SPOUT domain containing methyltrans |
| -0.54 | 7.78e-01 | PITPNM1 | phosphatidylinositol transfer prote | 0.18 | 8.53e-01 | DERL2 | derlin 2 |
| -0.6 | 7.95e-01 | DLG3 | discs large MAGUK scaffold protein | 0.18 | 8.53e-01 | HSDL2 | hydroxysteroid dehydrogenase like 2 |
| -0.55 | 7.95e-01 | MBD4 | methyl-CpG binding domain 4, DNA gl | 0.06 | 8.53e-01 | EXOSC4 | exosome component 4 |
| -0.24 | 7.95e-01 | ERBIN | erbb2 interacting protein | 0.63 | 8.53e-01 | GPAA1 | glycosylphosphatidylinositol anchor |
| -0.66 | 7.95e-01 | FRYL | FRY like transcription coactivator | 0.8 | 8.53e-01 | HERC2 | HECT and RLD domain containing E3 u |
| -0.37 | 7.95e-01 | TMEM126A | transmembrane protein 126A | 0.05 | 8.53e-01 | MRPL11 | mitochondrial ribosomal protein L11 |
| -0.26 | 7.95e-01 | ARHGEF7 | Rho guanine nucleotide exchange fac | 0.17 | 8.53e-01 | MFSD6 | major facilitator superfamily domai |
| -0.45 | 7.95e-01 | CEP43 | centrosomal protein 43 | 0.15 | 8.53e-01 | TMEM115 | transmembrane protein 115 |
| -0.56 | 7.95e-01 | QSER1 | glutamine and serine rich 1 | 0.05 | 8.53e-01 | AFG3L2 | AFG3 like matrix AAA peptidase subu |
| -0.6 | 7.95e-01 | SKP2 | S-phase kinase associated protein 2 | 0.36 | 8.53e-01 | AHNAK2 | AHNAK nucleoprotein 2 |
| -0.55 | 7.95e-01 | PLEKHM1 | pleckstrin homology and RUN domain | 0.06 | 8.53e-01 | EXOSC7 | exosome component 7 |
| -0.47 | 7.95e-01 | UCKL1 | uridine-cytidine kinase 1 like 1 | 0.14 | 8.53e-01 | FDXR | ferredoxin reductase |
| -0.5 | 7.95e-01 | ICAM2 | intercellular adhesion molecule 2 | 0.61 | 8.53e-01 | DHRS2 | dehydrogenase/reductase 2 |
| -0.4 | 7.95e-01 | ANKH | ANKH inorganic pyrophosphate transp | 0.29 | 8.60e-01 | CEBPE | CCAAT enhancer binding protein epsi |
| -0.38 | 7.95e-01 | LIN28A | lin-28 homolog A | 0.51 | 8.84e-01 | RGS22 | regulator of G protein signaling 22 |
| -0.45 | 8.53e-01 | RAB2B | RAB2B, member RAS oncogene family | 0.06 | 8.84e-01 | EXOSC2 | exosome component 2 |
| -0.57 | 8.53e-01 | MIS18A | MIS18 kinetochore protein A | 0.07 | 8.84e-01 | BCAP31 | B cell receptor associated protein |
| -0.35 | 8.53e-01 | AMDHD2 | amidohydrolase domain containing 2 | 0.62 | 8.84e-01 | CSTA | cystatin A |
| -0.51 | 8.53e-01 | RAPGEF2 | Rap guanine nucleotide exchange fac | 0.17 | 8.84e-01 | SKI | SKI proto-oncogene |
| -0.73 | 8.53e-01 | DTX4 | deltex E3 ubiquitin ligase 4 | 0.06 | 8.84e-01 | ATP5MK | ATP synthase membrane subunit k |
| -0.67 | 8.53e-01 | GPATCH3 | G-patch domain containing 3 | 0.05 | 8.84e-01 | EXOSC6 | exosome component 6 |
| -0.47 | 8.53e-01 | IL18R1 | interleukin 18 receptor 1 | 0.24 | 8.84e-01 | SPON1 | spondin 1 |
| -0.22 | 8.53e-01 | MDK | midkine | 0.42 | 8.84e-01 | NDUFAF5 | NADH:ubiquinone oxidoreductase comp |
| -0.39 | 8.53e-01 | GOLGA7 | golgin A7 | 0.47 | 8.84e-01 | SCIN | scinderin |
| -0.46 | 8.53e-01 | TRAPPC12 | trafficking protein particle comple | 0.52 | 8.85e-01 | DUSP23 | dual specificity phosphatase 23 |
| -0.53 | 8.53e-01 | STAT2 | signal transducer and activator of | 0.28 | 9.15e-01 | MAGEB1 | MAGE family member B1 |
| -0.49 | 8.53e-01 | PUM2 | pumilio RNA binding family member 2 | 0.04 | 9.15e-01 | OCIAD1 | OCIA domain containing 1 |
| -0.45 | 8.53e-01 | CDCA2 | cell division cycle associated 2 | 0.2 | 9.15e-01 | CLPTM1 | CLPTM1 regulator of GABA type A rec |
| -0.29 | 8.53e-01 | ASF1A | anti-silencing function 1A histone | 0.14 | 9.18e-01 | CTTNBP2NL | CTTNBP2 N-terminal like |
| -0.25 | 8.53e-01 | NADK2 | NAD kinase 2, mitochondrial | 0.17 | 9.18e-01 | IDUA | alpha-L-iduronidase |
| -0.51 | 8.53e-01 | SPATS2 | spermatogenesis associated serine r | 0.07 | 9.18e-01 | EXOSC8 | exosome component 8 |

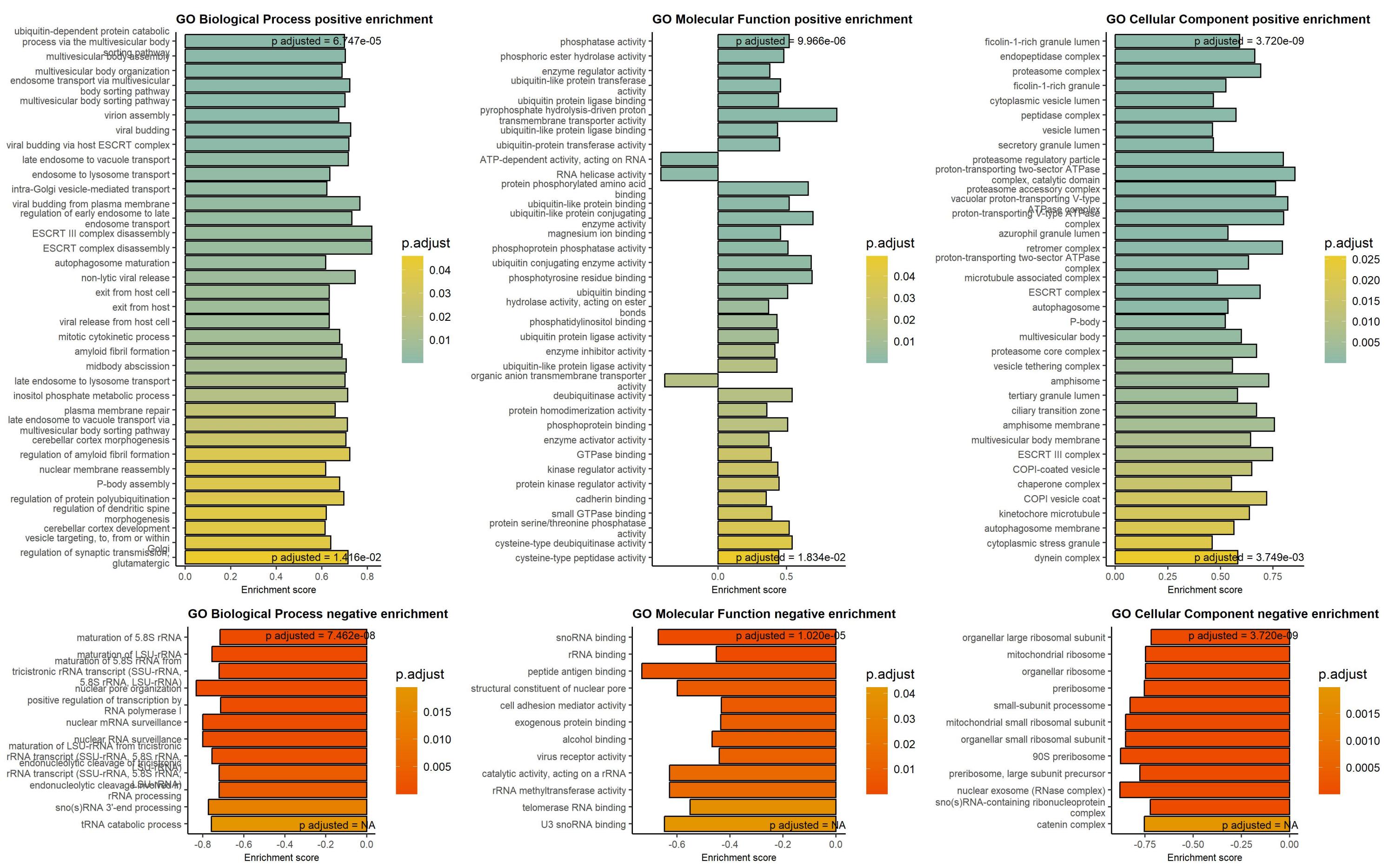


| Sorted by p values! | | | | | | | |
|---|-----------|----------|-------------------------------------|---|-----------|-----------|-------------------------------------|
| Downregulated in solid cancers at low/absent ANKLE1 | | | | Upregulated in solid cancers at low/absent ANKLE1 | | | |
| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
| -0.58 | 1.43e-16 | SUMO2 | small ubiquitin like modifier 2 | 0.09 | 9.33e-10 | KIF20B | kinesin family member 20B |
| -0.43 | 1.98e-16 | GDI1 | GDP dissociation inhibitor 1 | 0.03 | 2.31e-09 | HAUS2 | HAUS augmin like complex subunit 2 |
| -0.27 | 6.39e-14 | SGTA | small glutamine rich tetratricopept | 0.03 | 2.32e-09 | ARPP21 | cAMP regulated phosphoprotein 21 |
| -0.12 | 1.38e-13 | NEDD8 | NEDD8 ubiquitin like modifier | 0.03 | 2.51e-09 | ZC3H12D | zinc finger CCCH-type containing 12 |
| -0.74 | 1.42e-13 | EIF4EBP1 | eukaryotic translation initiation f | 0.03 | 2.51e-09 | NCR2 | natural cytotoxicity triggering rec |
| -0.67 | 1.42e-13 | RPE | ribulose-5-phosphate-3-epimerase | 0.03 | 2.51e-09 | TNFRSF13C | TNF receptor superfamily member 13C |
| -0.69 | 3.26e-13 | UBL7 | ubiquitin like 7 | 0.03 | 2.51e-09 | BPI | bactericidal permeability increasin |
| -0.7 | 4.42e-13 | C9orf40 | chromosome 9 open reading frame 40 | 0.03 | 2.51e-09 | TYROBP | transmembrane immune signaling adap |
| -0.65 | 4.42e-13 | PGK2 | phosphoglycerate kinase 2 | 0.03 | 2.51e-09 | ALKBH3 | alkB homolog 3, alpha-ketoglutarate |
| -0.83 | 5.83e-13 | CD300E | CD300e molecule | 0.03 | 2.51e-09 | S100A12 | S100 calcium binding protein A12 |
| -0.78 | 7.19e-13 | COMMD8 | COMM domain containing 8 | 0.03 | 2.51e-09 | CD3D | CD3 delta subunit of T-cell recepto |
| -0.62 | 7.36e-13 | UBFD1 | ubiquitin family domain containing | 0.03 | 2.51e-09 | SPIB | Spi-B transcription factor |
| -0.55 | 1.92e-12 | NAA20 | N-alpha-acetyltransferase 20, NatB | 0.03 | 2.51e-09 | BBS2 | Bardet-Biedl syndrome 2 |
| -0.64 | 2.93e-12 | C5orf22 | chromosome 5 open reading frame 22 | 0.03 | 2.51e-09 | GATA1 | GATA binding protein 1 |
| -0.62 | 6.71e-12 | DUS3L | dihydrouridine synthase 3 like | 0.03 | 2.51e-09 | LILRB4 | leukocyte immunoglobulin like recep |
| -0.16 | 9.16e-12 | PFDN2 | prefoldin subunit 2 | 0.03 | 2.51e-09 | TNFRSF4 | TNF receptor superfamily member 4 |
| -0.53 | 1.11e-11 | PRPS1 | phosphoribosyl pyrophosphate synthe | 0.03 | 2.51e-09 | ZBTB16 | zinc finger and BTB domain containi |
| -0.69 | 1.57e-11 | PCSK6 | proprotein convertase subtilisin/ke | 0.03 | 2.51e-09 | GNLY | granulysin |
| -0.55 | 1.60e-11 | TBC1D5 | TBC1 domain family member 5 | 0.03 | 2.51e-09 | ARHGEF18 | Rho/Rac guanine nucleotide exchange |
| -0.74 | 1.63e-11 | UBE2D3 | ubiquitin conjugating enzyme E2 D3 | 0.03 | 2.51e-09 | CD86 | CD86 molecule |
| -0.66 | 1.78e-11 | ACYP1 | acylphosphatase 1 | 0.03 | 2.51e-09 | ZZEF1 | zinc finger ZZ-type and EF-hand dom |
| -0.11 | 1.79e-11 | UBE2N | ubiquitin conjugating enzyme E2 N | 0.03 | 2.51e-09 | MAGEB3 | MAGE family member B3 |
| -0.62 | 1.87e-11 | ARPP19 | cAMP regulated phosphoprotein 19 | 0.03 | 2.51e-09 | CD6 | CD6 molecule |
| -0.46 | 2.26e-11 | LZIC | leucine zipper and CTNNBIP1 domain | 0.03 | 2.51e-09 | GZMK | granzyme K |
| -0.33 | 2.41e-11 | DYNLRB1 | dynein light chain roadblock-type 1 | 0.03 | 2.51e-09 | TBX21 | T-box transcription factor 21 |
| -0.47 | 2.49e-11 | DOHH | deoxyhypusine hydroxylase | 0.14 | 4.83e-09 | ABCD3 | ATP binding cassette subfamily D me |
| -0.55 | 2.52e-11 | USP47 | ubiquitin specific peptidase 47 | 0.04 | 1.28e-08 | SIRPG | signal regulatory protein gamma |
| -0.71 | 2.67e-11 | PNMA1 | PNMA family member 1 | 0.1 | 1.51e-08 | TM9SF3 | transmembrane 9 superfamily member |
| -0.49 | 2.99e-11 | TBCD | tubulin folding cofactor D | 0.08 | 3.21e-08 | RAB15 | RAB15, member RAS oncogene family |
| -0.59 | 3.27e-11 | KIAA1143 | KIAA1143 | 0.07 | 4.35e-08 | CLIP1 | CAP-Gly domain containing linker pr |
| -0.55 | 3.81e-11 | MAP2K2 | mitogen-activated protein kinase ki | 0.08 | 4.50e-08 | EMC2 | ER membrane protein complex subunit |
| -0.66 | 3.81e-11 | SPC25 | SPC25 component of NDC80 kinetochor | 0.07 | 4.61e-08 | UFL1 | UFM1 specific ligase 1 |
| -0.31 | 5.41e-11 | MTPN | myotrophin | 0.04 | 4.86e-08 | TMIGD2 | transmembrane and immunoglobulin do |
| -0.36 | 5.41e-11 | CARHSP1 | calcium regulated heat stable prote | 0.09 | 6.10e-08 | SCFD1 | sec1 family domain containing 1 |
| -0.57 | 5.41e-11 | EIF4E2 | eukaryotic translation initiation f | 0.09 | 6.19e-08 | POLDIP2 | DNA polymerase delta interacting pr |
| -0.47 | 5.41e-11 | PSMD10 | proteasome 26S subunit, non-ATPase | 0.07 | 6.19e-08 | MRPL19 | mitochondrial ribosomal protein L19 |
| -0.62 | 5.49e-11 | GINS2 | GINS complex subunit 2 | 0.07 | 6.88e-08 | DDOST | dolichyl-diphosphooligosaccharide-- |
| -0.64 | 5.51e-11 | HESX1 | HESX homeobox 1 | 0.08 | 9.10e-08 | SSR4 | signal sequence receptor subunit 4 |
| -0.5 | 5.51e-11 | TPRKP | TPRKP-like protein | 0.09 | 9.10e-08 | CBTRN1 | CBTRN1-like protein |

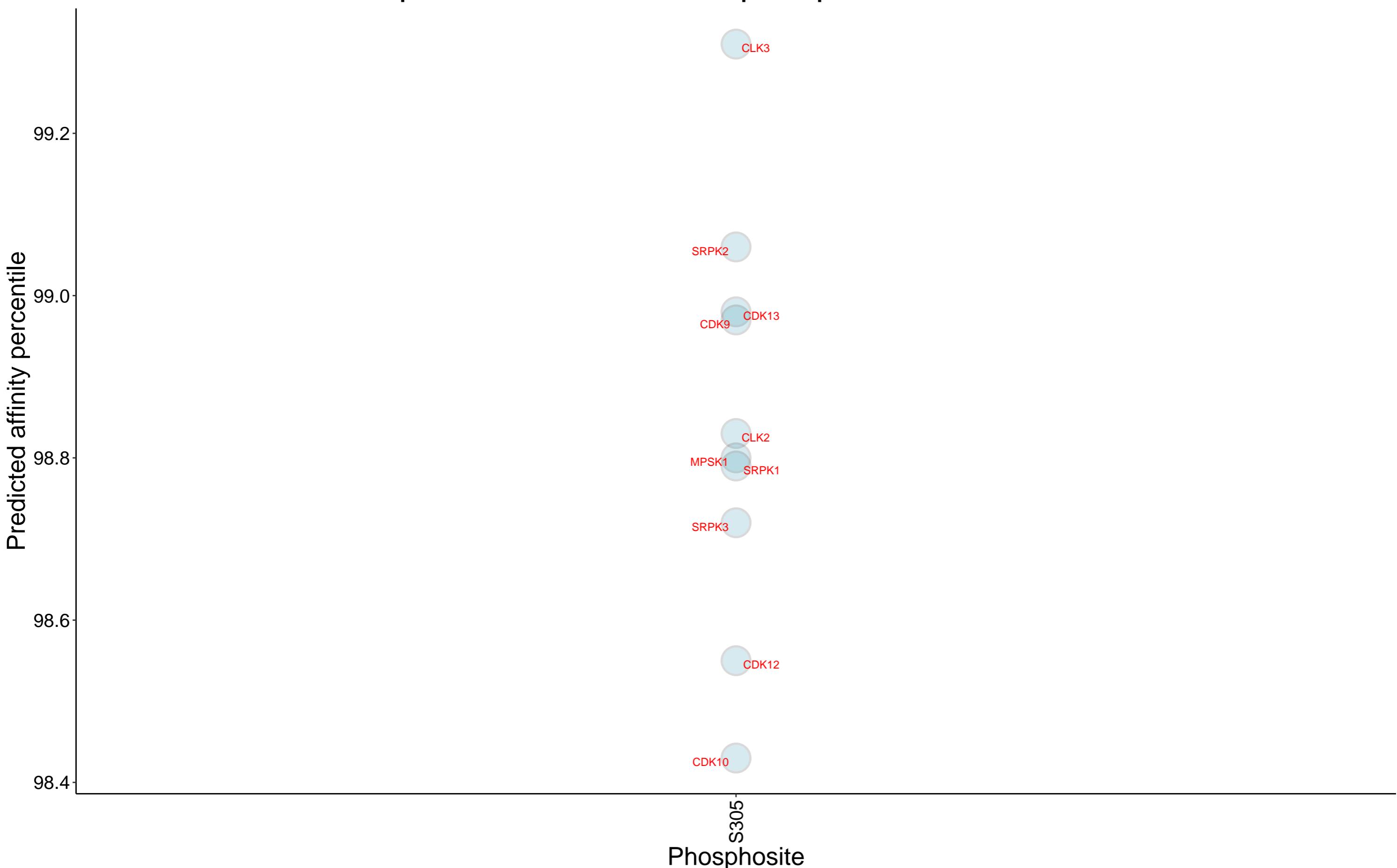
Top 250 correlation coefficients overrepresentation, ANKLE1 protein, DB2



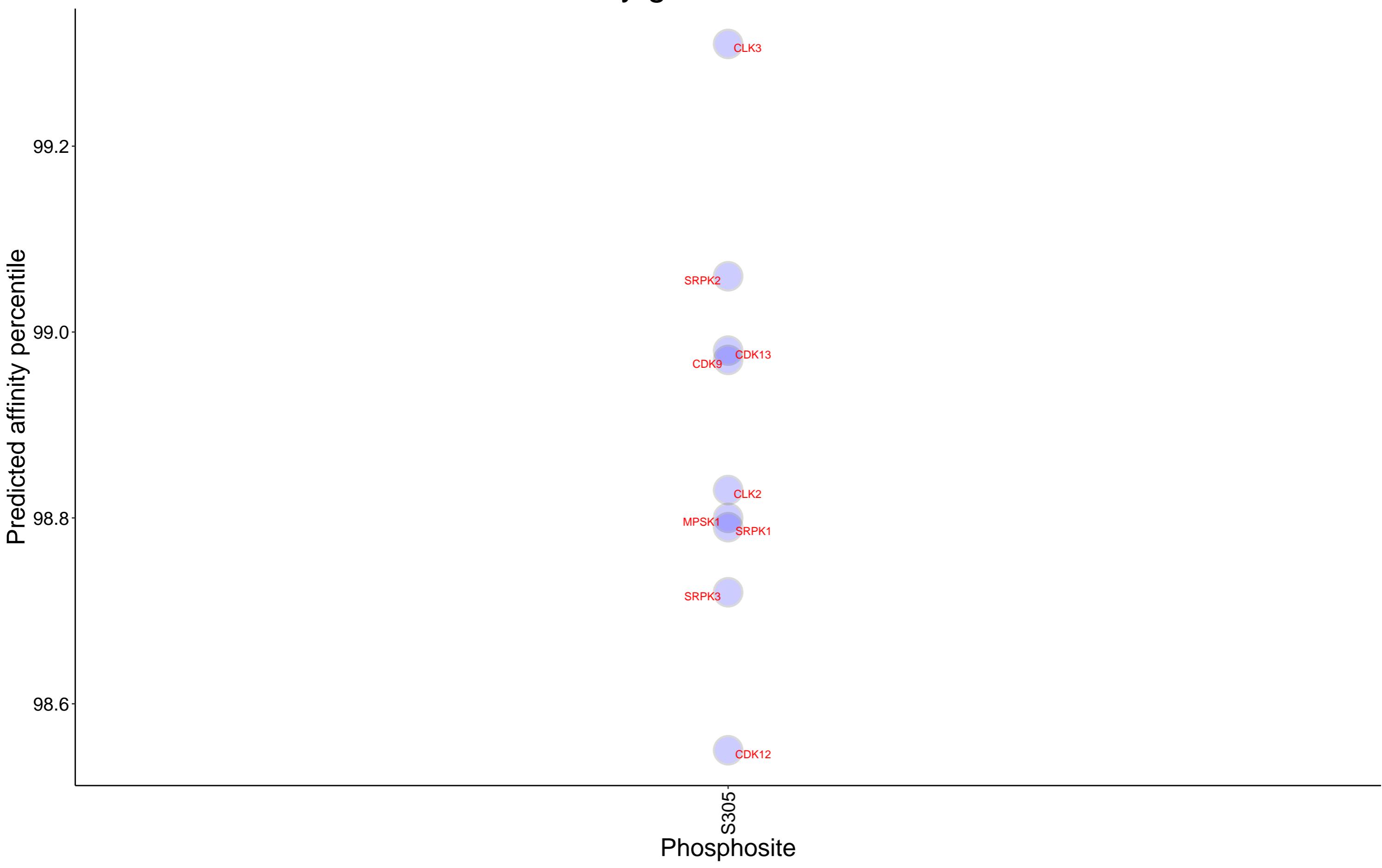
Gene Set Enrichment analysis on protein correlation coefficients, ANKLE1 protein, DB2



Top 10 kinases for each phosphosite in ANKLE1



Kinases with affinity greater than 98.5% to ANKLE1



No sufficient number of paired observations in DB2 for ANKLE1