

ACTR5

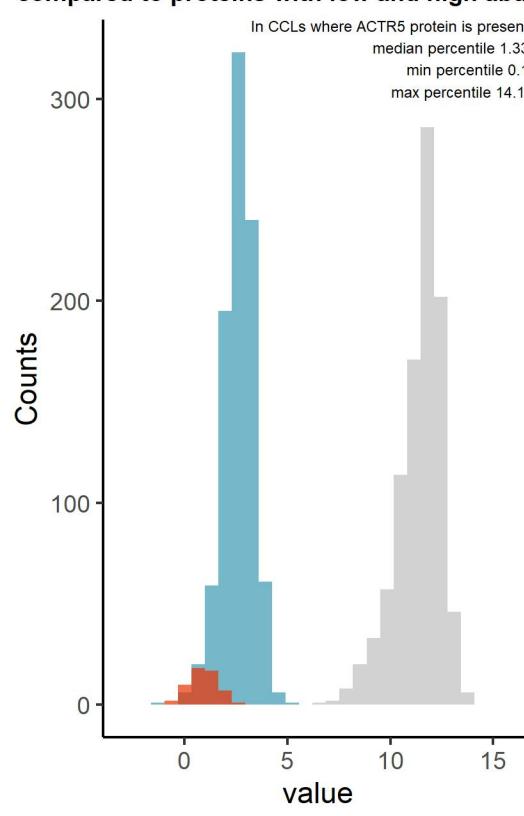
Protein name: ARP5 ; UNIPROT: Q9H9F9 ; Gene name: actin related protein 5

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

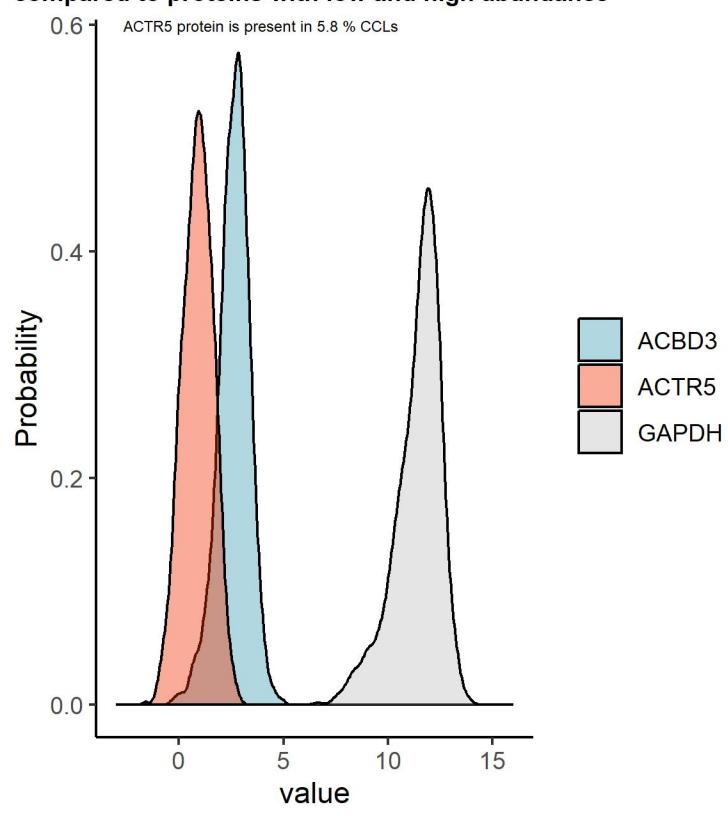
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of ACTR5 protein compared to proteins with low and high abundance



Density plot of ACTR5 protein compared to proteins with low and high abundance



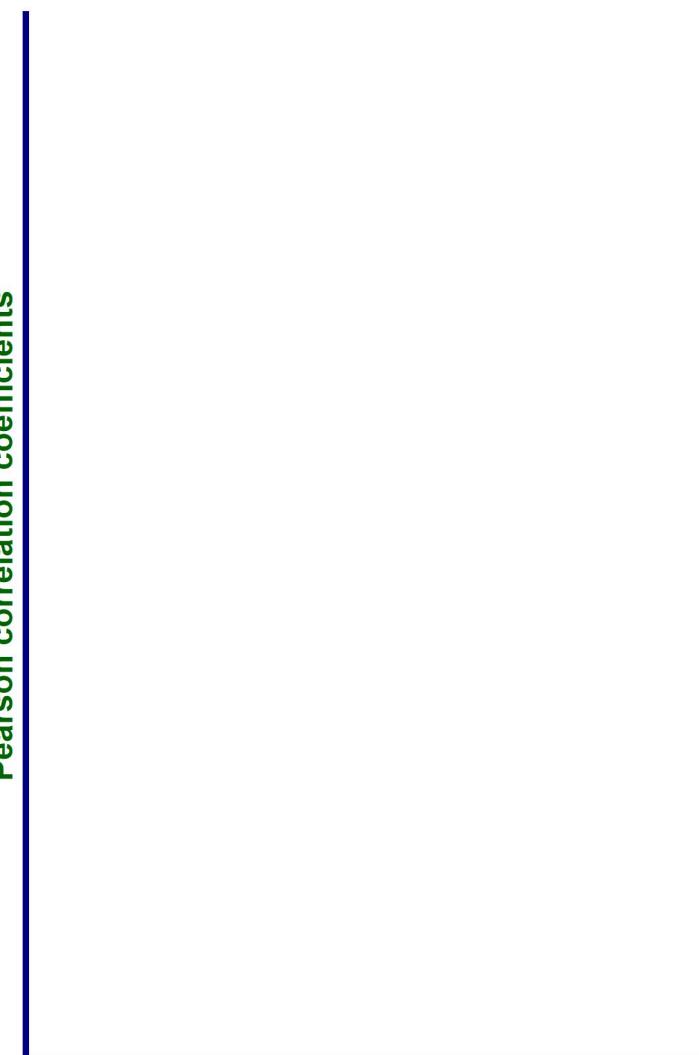
Top negative correlations of ACTR5 protein, DB1

Pearson correlation coefficients



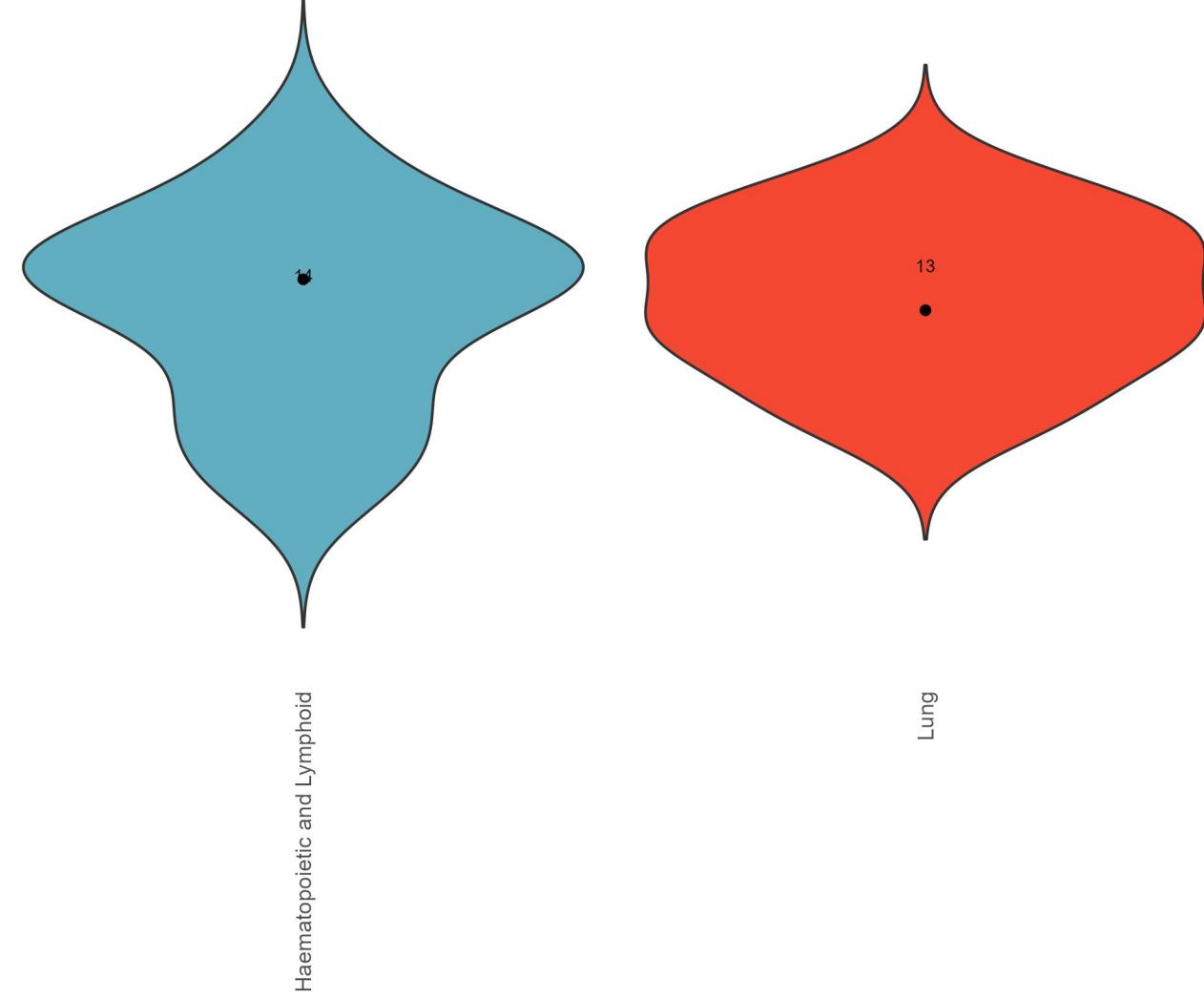
Top positive correlations of ACTR5 protein, DB1

Pearson correlation coefficients



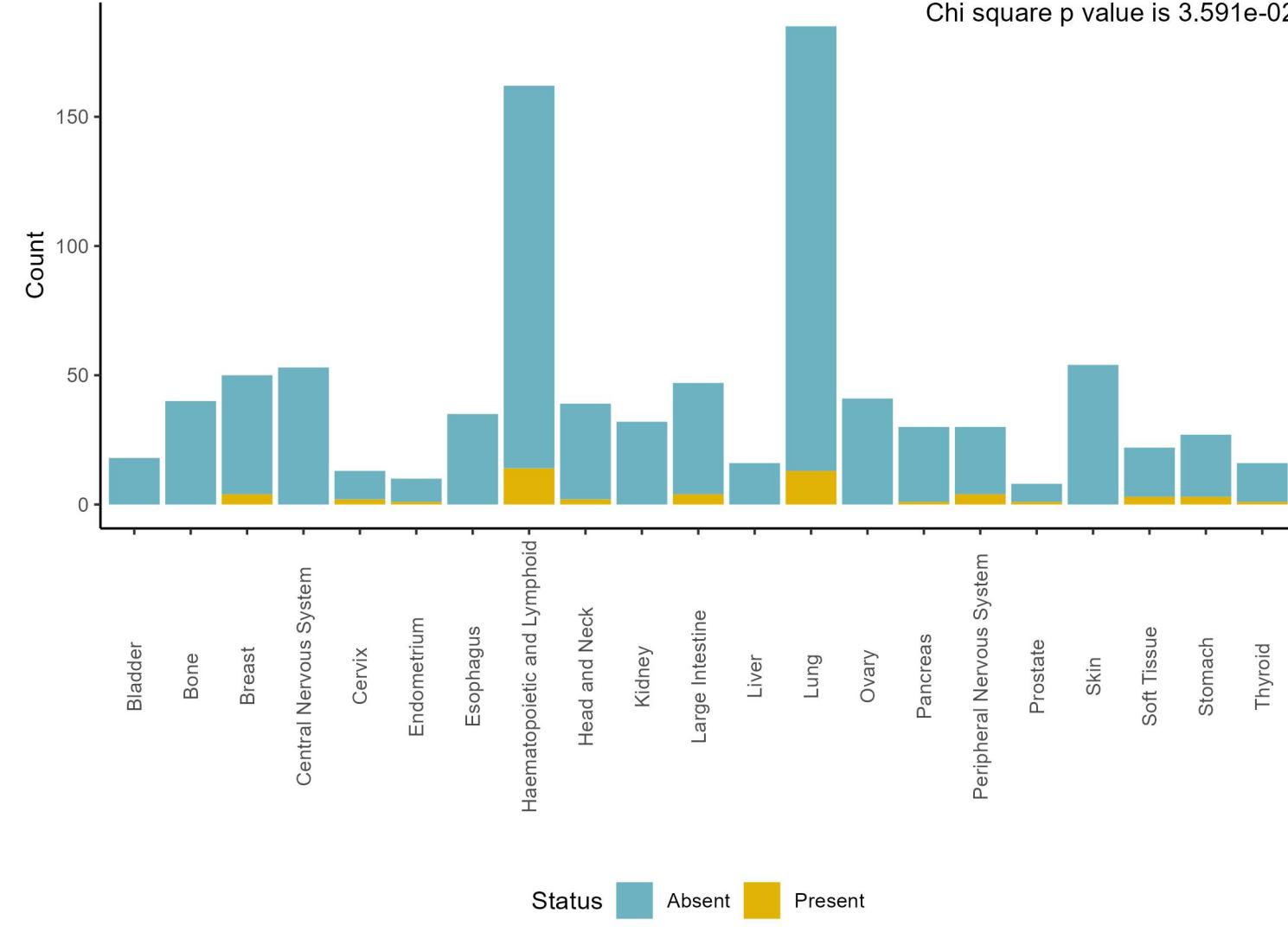
Amount of ACTR5 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 9.804e-01



Present and absent ACTR5 protein counts by tissue, DB1

Chi square p value is 3.591e-02

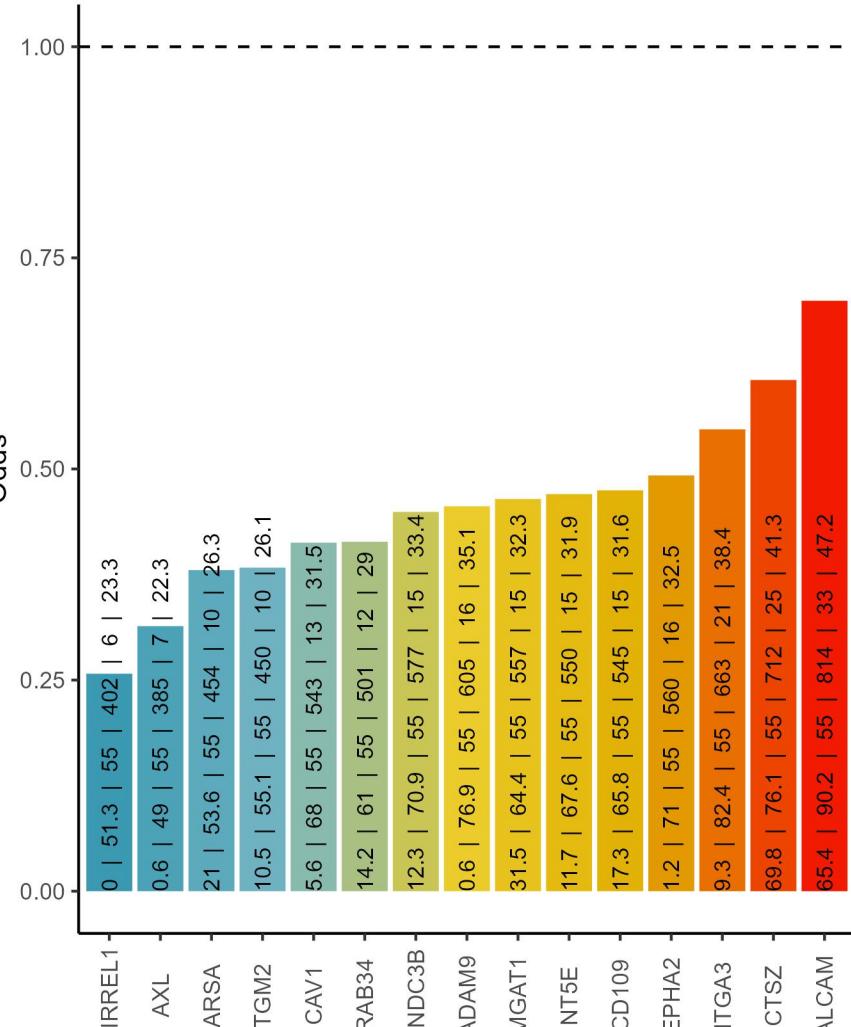


Cooccurrence with ACTR5 protein, DB1

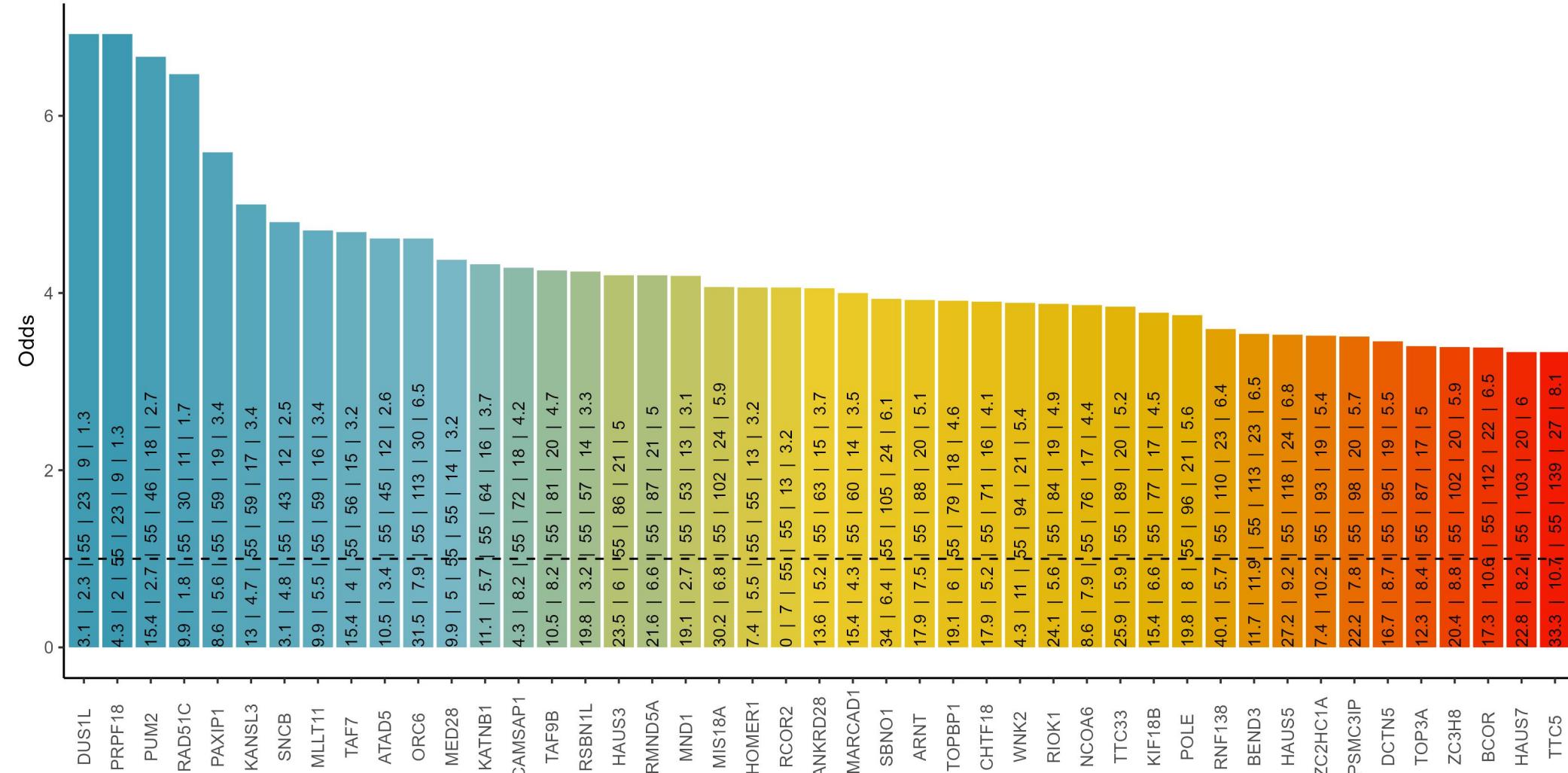
% of ACTR5 in blood cancers: 8.6 ; % of ACTR5 in solid cancers: 5.2

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ACTR5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

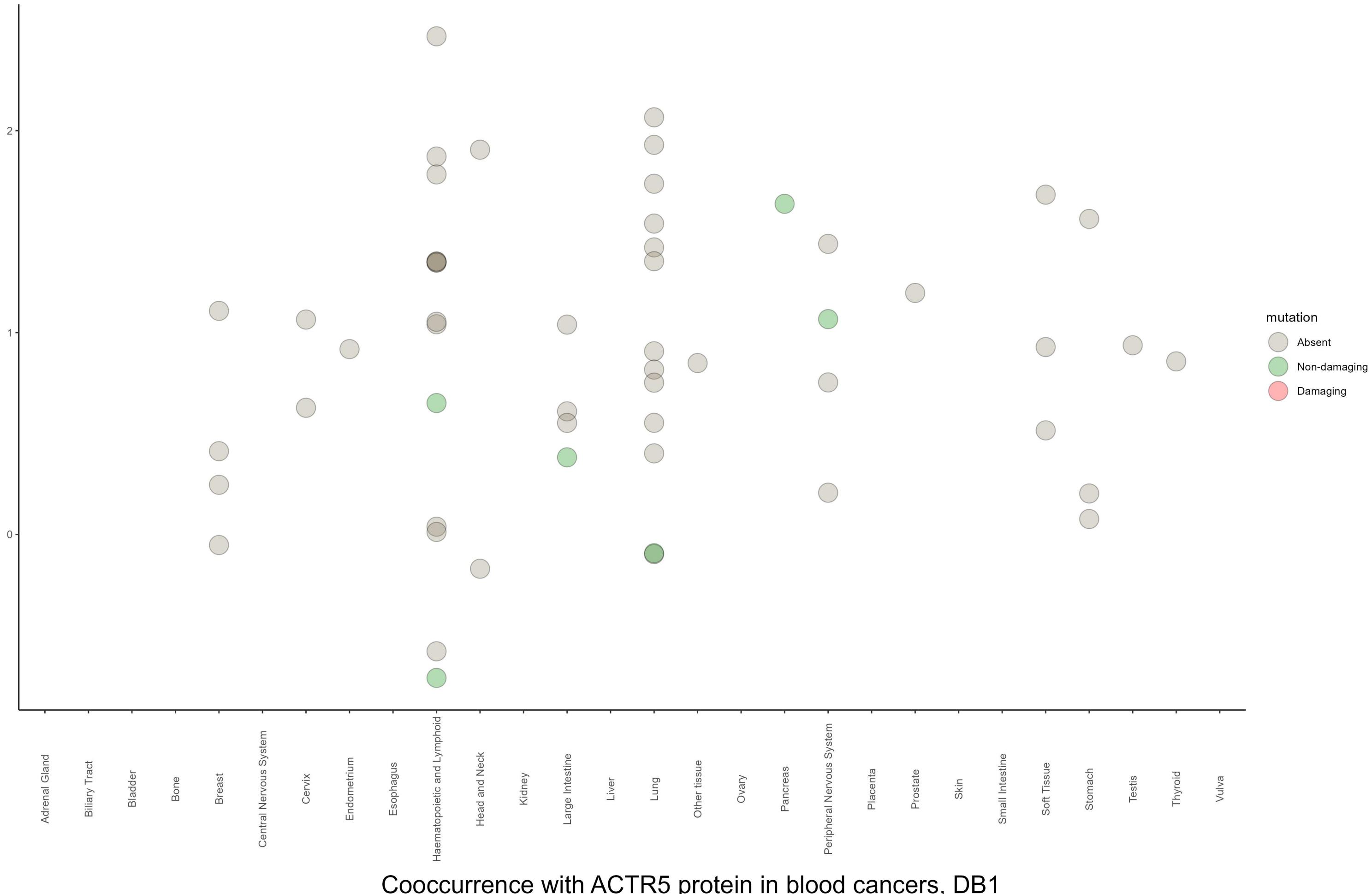
Negative cooccurrence



Positive cooccurrence

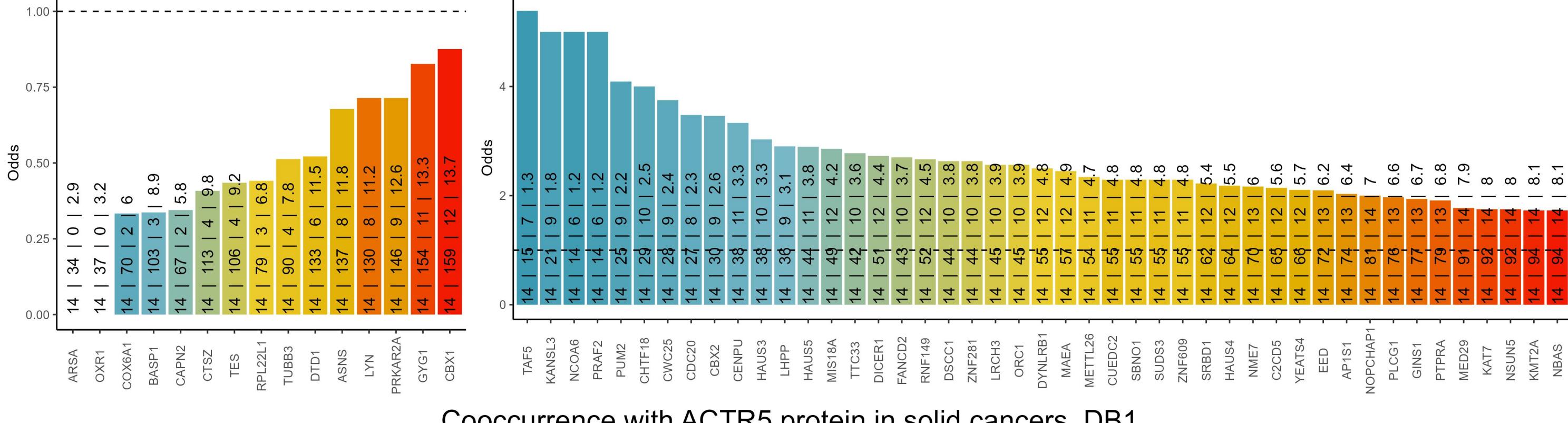


Amount of ACTR5 protein and mutation status by tissue, DB1



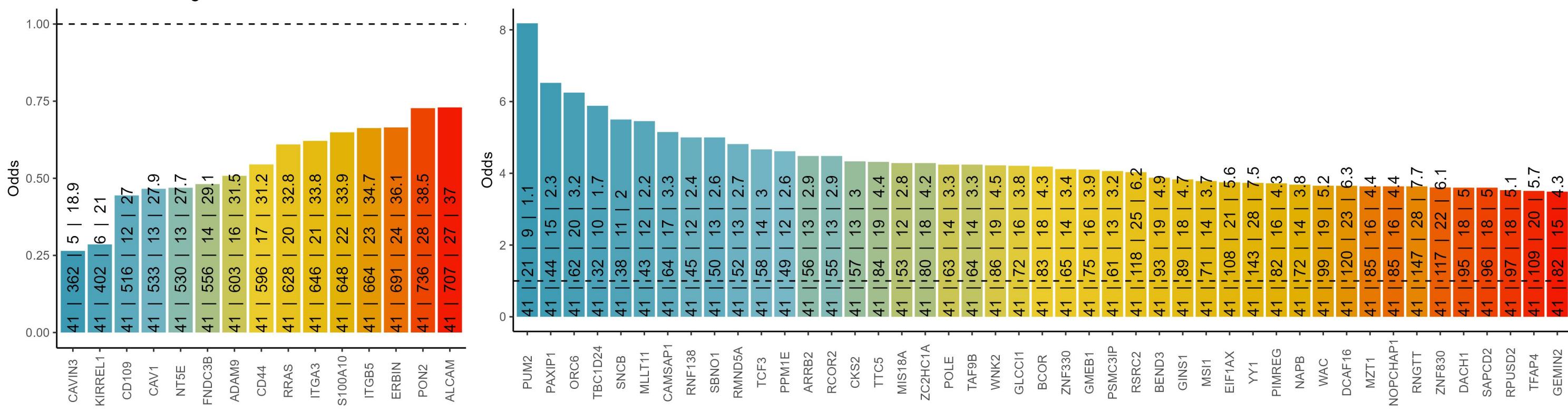
Cooccurrence with ACTR5 protein in blood cancers, DB1

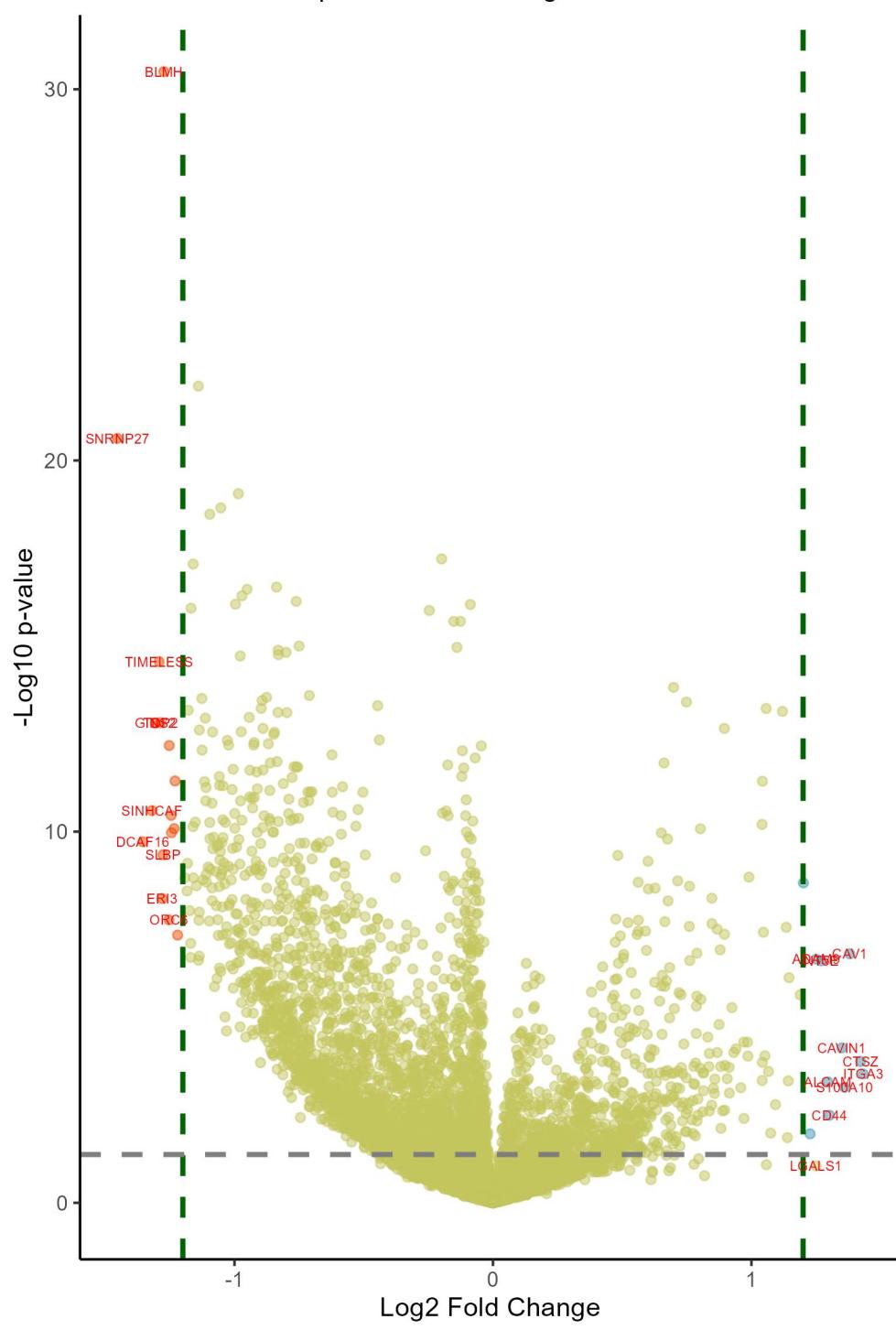
The text in the bars: incidence of ACTR5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with ACTR5 protein in solid cancers, DB1

The text in the bars: incidence of ACTR5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

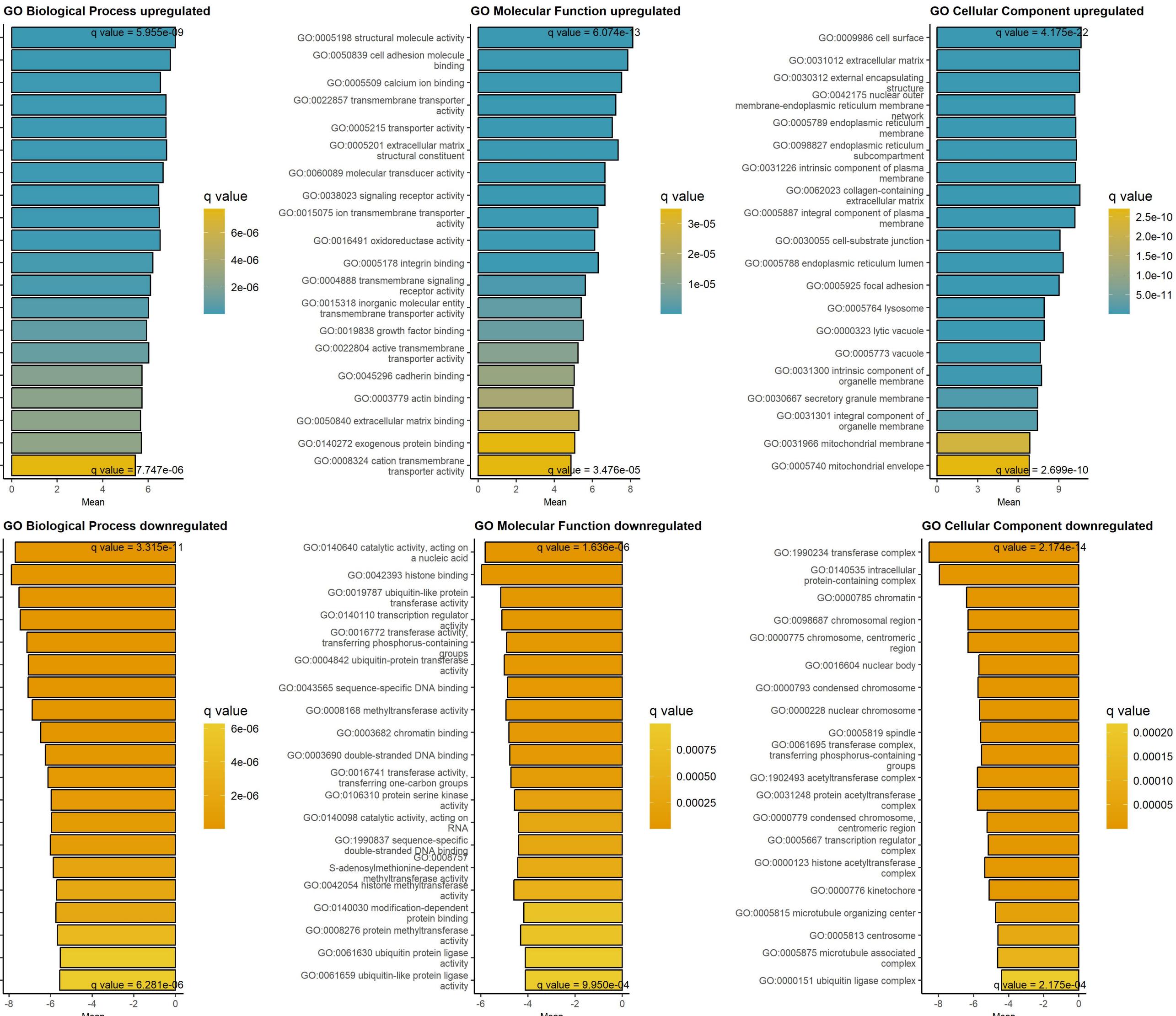


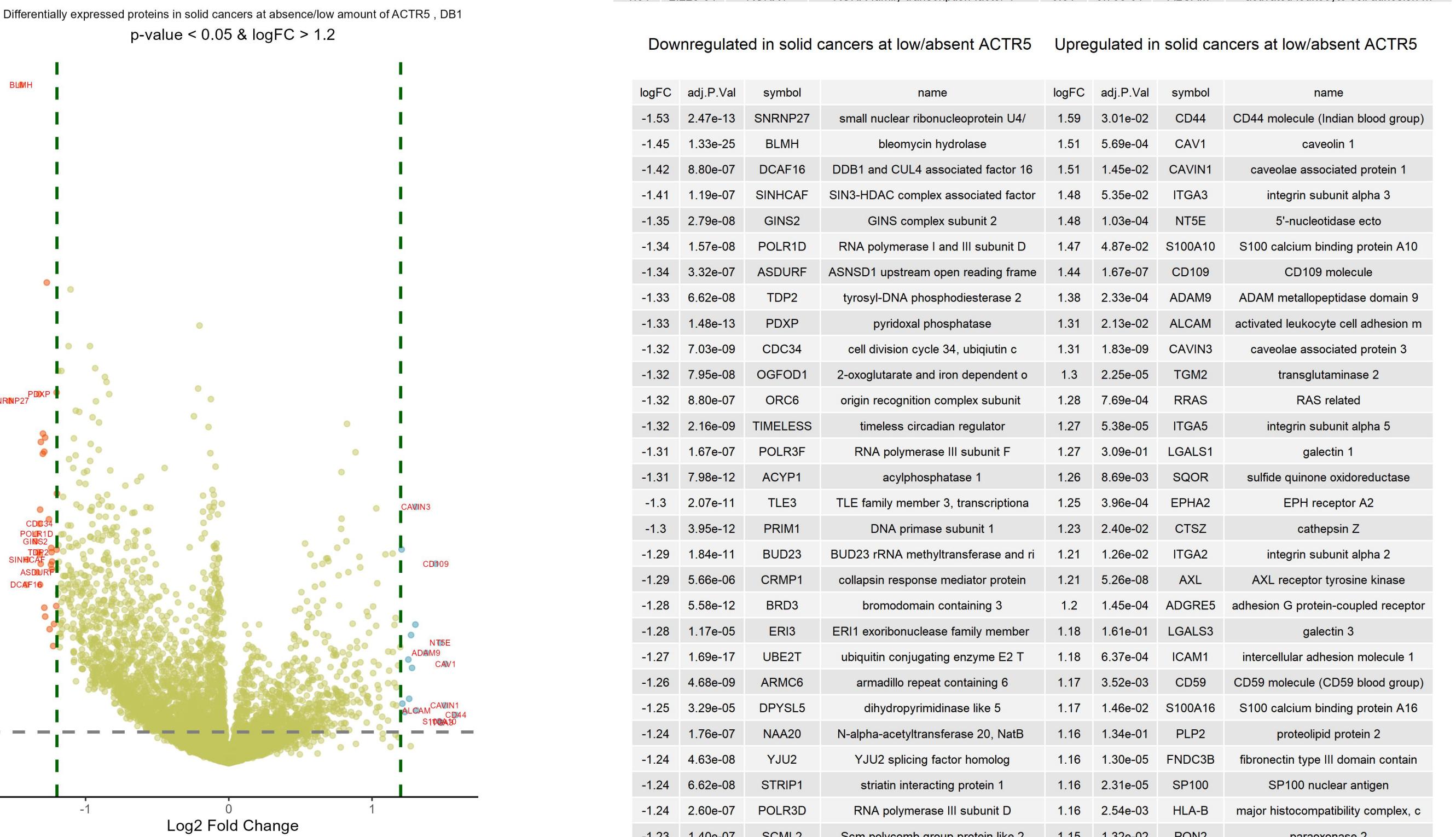
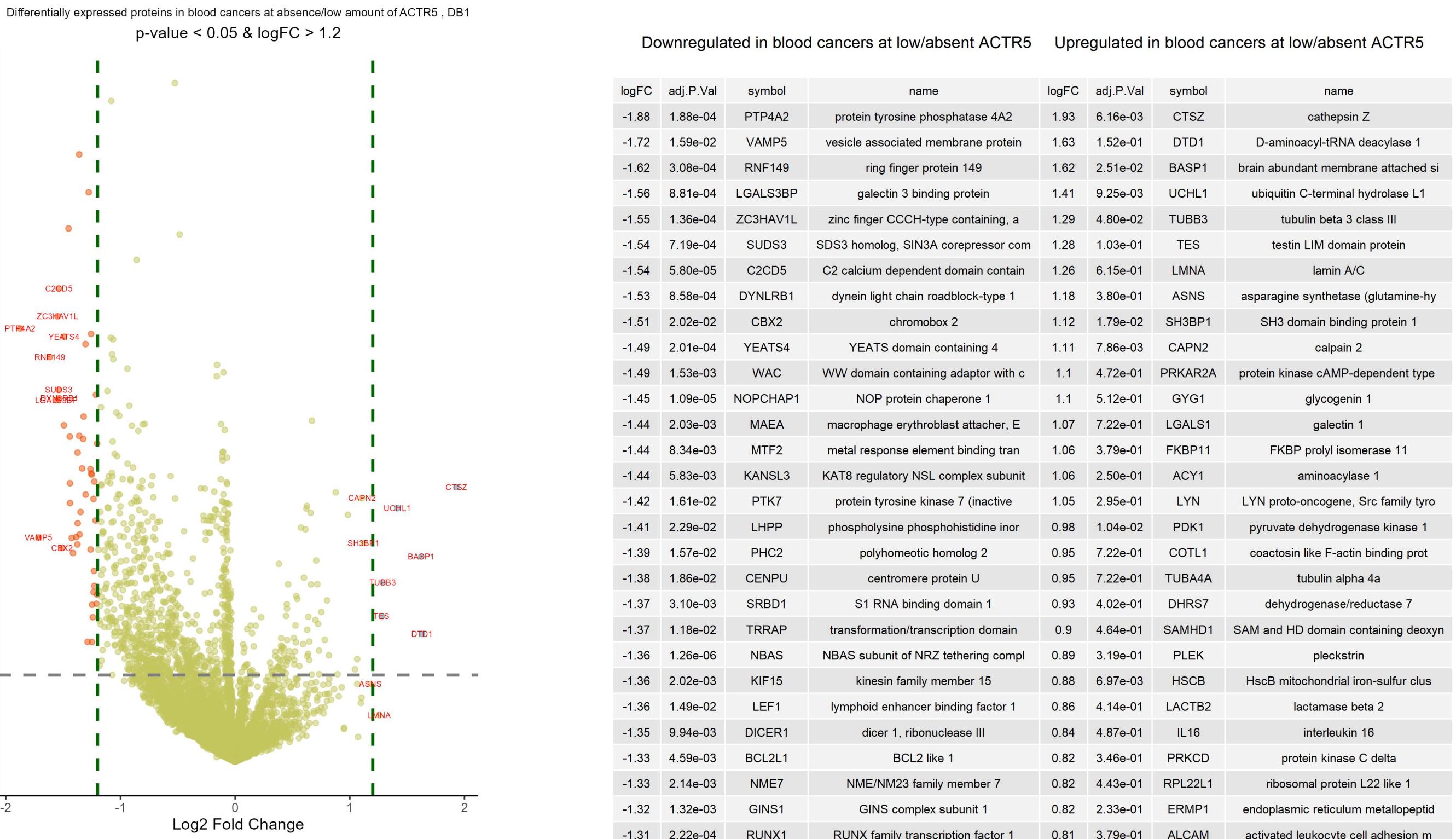


Downregulated at low/absent ACTR5 Upregulated at low/absent ACTR5

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|---|-------|-----------|---------|--|
| -1.45 | 4.23e-18 | SNRNP27 | small nuclear ribonucleoprotein U4/6 | 1.43 | 1.73e-03 | ITGA3 | integrin subunit alpha 3 |
| -1.36 | 8.25e-09 | DCAF16 | DDB1 and CUL4 associated factor 16 | 1.42 | 9.07e-04 | CTSZ | cathepsin Z |
| -1.32 | 1.70e-09 | SINHCAF | SIN3-HDAC complex associated factor | 1.38 | 2.93e-06 | CAV1 | caveolin 1 |
| -1.31 | 1.84e-11 | GINS2 | GINS complex subunit 2 | 1.36 | 3.45e-03 | S100A10 | S100 calcium binding protein A10 |
| -1.29 | 6.75e-13 | TIMELESS | timeless circadian regulator | 1.35 | 4.38e-04 | CAVIN1 | caveolae associated protein 1 |
| -1.29 | 1.83e-11 | TDP2 | tyrosyl-DNA phosphodiesterase 2 | 1.3 | 1.44e-02 | CD44 | CD44 molecule (Indian blood group) |
| -1.28 | 1.62e-07 | ERI3 | ERI1 exoribonuclease family member | 1.3 | 2.60e-03 | ALCAM | activated leukocyte cell adhesion molecule |
| -1.28 | 1.64e-08 | SLBP | stem-loop binding protein | 1.27 | 4.24e-06 | NT5E | 5'-nucleotidase ecto |
| -1.27 | 1.11e-27 | BLMH | bleomycin hydrolase | 1.25 | 3.88e-06 | ADAM9 | ADAM metallopeptidase domain 9 |
| -1.25 | 4.92e-07 | ORC6 | origin recognition complex subunit | 1.25 | 1.84e-01 | LGALS1 | galectin 1 |
| -1.25 | 5.59e-11 | STRIP1 | striatin interacting protein 1 | 1.23 | 3.70e-02 | LGALS3 | galectin 3 |
| -1.25 | 2.14e-09 | POLR1D | RNA polymerase I and III subunit D | 1.2 | 6.99e-08 | CD109 | CD109 molecule |
| -1.24 | 5.08e-09 | ASDURF | ASNSD1 upstream open reading frame | 1.19 | 2.66e-05 | RRAS | RAS related |
| -1.23 | 4.11e-09 | POLR3F | RNA polymerase III subunit F | 1.15 | 1.06e-05 | EPHA2 | EPH receptor A2 |
| -1.23 | 3.68e-10 | OGFOD1 | 2-oxoglutarate and iron dependent oxygenase | 1.14 | 2.47e-03 | SQOR | sulfide quinone oxidoreductase |
| -1.22 | 1.08e-06 | WAC | WW domain containing adaptor with cyclophilin domains and coiled-coil | 1.14 | 4.45e-02 | PLP2 | proteolipid protein 2 |
| -1.19 | 5.36e-08 | MAZ | MYC associated zinc finger protein | 1.13 | 7.18e-07 | TGM2 | transglutaminase 2 |
| -1.18 | 1.07e-07 | RSRC2 | arginine and serine rich coiled-coil | 1.12 | 1.03e-11 | CAVIN3 | caveolae associated protein 3 |
| -1.18 | 2.55e-08 | YY1 | YY1 transcription factor | 1.09 | 8.45e-03 | PON2 | paraoxonase 2 |
| -1.18 | 9.87e-12 | BRD3 | bromodomain containing 3 | 1.07 | 3.55e-02 | NCEH1 | neutral cholesterol ester hydrolase |
| -1.17 | 3.04e-07 | CCNA2 | cyclin A2 | 1.07 | 1.52e-03 | S100A16 | S100 calcium binding protein A16 |
| -1.17 | 3.54e-06 | GINS1 | GINS complex subunit 1 | 1.06 | 1.73e-01 | S100A6 | S100 calcium binding protein A6 |
| -1.17 | 1.71e-06 | RABIF | RAB interacting factor | 1.06 | 9.14e-12 | ARSA | arylsulfatase A |
| -1.17 | 3.97e-14 | PRIM1 | DNA primase subunit 1 | 1.05 | 6.68e-04 | ICAM1 | intercellular adhesion molecule 1 |
| -1.16 | 3.71e-09 | CDC34 | cell division cycle 34, ubiquitin c | 1.05 | 9.26e-07 | FNDC3B | fibronectin type III domain containing 3 |
| -1.16 | 4.57e-15 | PDXP | pyridoxal phosphatase | 1.04 | 3.69e-10 | AXL | AXL receptor tyrosine kinase |
| -1.16 | 5.36e-08 | CFAP20 | cilia and flagella associated protein | 1.04 | 9.53e-04 | CD59 | CD59 molecule (CD59 blood group) |
| -1.15 | 2.92e-09 | CCDC12 | coiled-coil domain containing 12 | 1.04 | 2.43e-03 | ITGA2 | integrin subunit alpha 2 |
| -1.15 | 8.19e-08 | RNGTT | RNA guanylyltransferase and 5'-phosphoryl transferase | 1.04 | 3.30e-09 | MGAT1 | alpha-1,3-mannosyl-glycoprotein 2-beta |

GAGE analysis on upregulated and downregulated proteins at low/absent ACTR5 protein, DB1

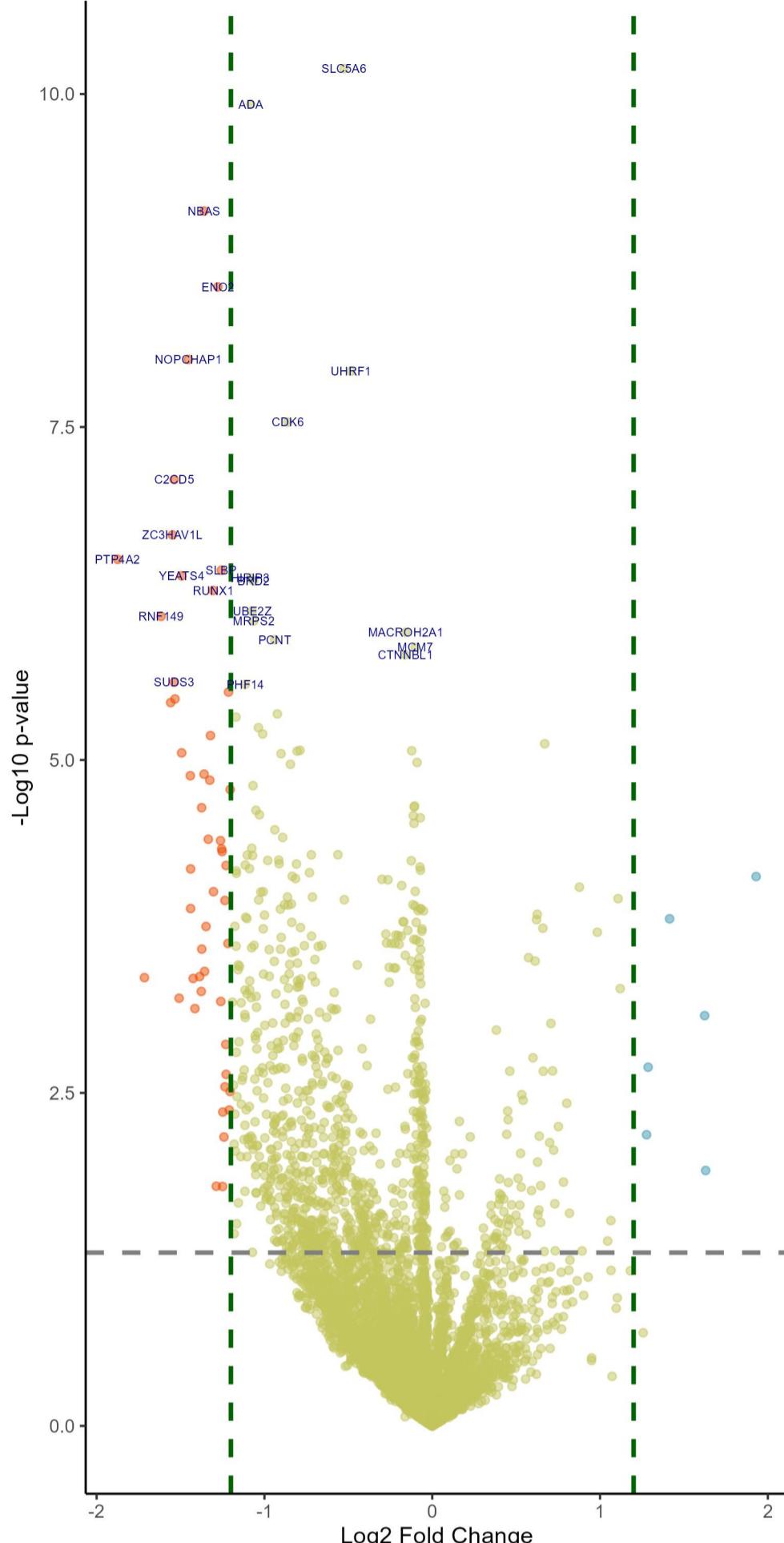




ACTR5 network, DB1, no Pearson r > 0.3

Differentially expressed proteins in blood cancers at absence/low amount of ACTR5 , DB1

p-value < 0.05 & logFC > 1.2



Sorted by p values!

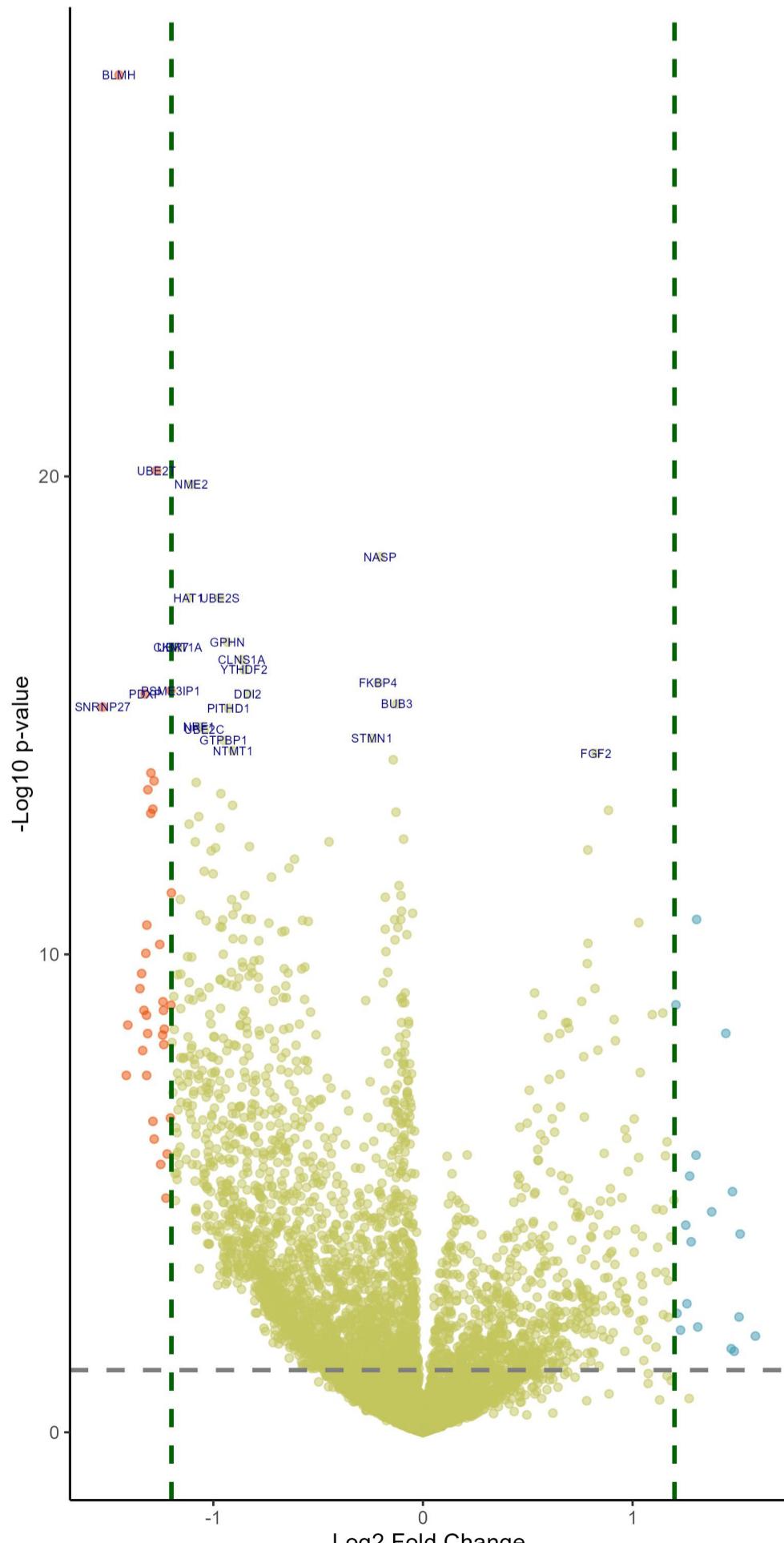
Downregulated in blood cancers at low/absent ACTR5

Upregulated in blood cancers at low/absent ACTR5

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|-----------|-------------------------------------|-------|-----------|-----------|---|
| -0.53 | 2.14e-07 | SLC5A6 | solute carrier family 5 member 6 | 0.67 | 1.48e-03 | SDF2 | stromal cell derived factor 2 |
| -1.08 | 2.64e-07 | ADA | adenosine deaminase | 1.93 | 6.16e-03 | CTSZ | cathepsin Z |
| -1.36 | 1.26e-06 | NBAS | NBAS subunit of NRZ tethering compl | 0.88 | 6.97e-03 | HSCB | HscB mitochondrial iron-sulfur clus |
| -1.28 | 3.73e-06 | ENO2 | enolase 2 | 1.11 | 7.86e-03 | CAPN2 | calpain 2 |
| -1.45 | 1.09e-05 | NOPCHAP1 | NOP protein chaperone 1 | 0.63 | 8.88e-03 | OXR1 | oxidation resistance 1 |
| -0.48 | 1.14e-05 | UHRF1 | ubiquitin like with PHD and ring fi | 1.41 | 9.25e-03 | UCHL1 | ubiquitin C-terminal hydrolase L1 |
| -0.86 | 2.41e-05 | CDK6 | cyclin dependent kinase 6 | 0.62 | 9.31e-03 | WDFY1 | WD repeat and FYVE domain containin |
| -1.54 | 5.80e-05 | C2CD5 | C2 calcium dependent domain contain | 0.66 | 1.00e-02 | ST14 | ST14 transmembrane serine protease |
| -1.55 | 1.36e-04 | ZC3HAV1L | zinc finger CCCH-type containing, a | 0.98 | 1.04e-02 | PDK1 | pyruvate dehydrogenase kinase 1 |
| -1.88 | 1.88e-04 | PTP4A2 | protein tyrosine phosphatase 4A2 | 0.57 | 1.32e-02 | OSBP3 | oxysterol binding protein like 3 |
| -1.26 | 2.01e-04 | SLBP | stem-loop binding protein | 0.61 | 1.36e-02 | ARSA | arylsulfatase A |
| -1.49 | 2.01e-04 | YEATS4 | YEATS domain containing 4 | 1.12 | 1.79e-02 | SH3BP1 | SH3 domain binding protein 1 |
| -1.08 | 2.01e-04 | HIRIP3 | HIRA interacting protein 3 | 1.62 | 2.51e-02 | BASP1 | brain abundant membrane attached si |
| -1.06 | 2.01e-04 | BRD2 | bromodomain containing 2 | 0.71 | 2.73e-02 | COL6A3 | collagen type VI alpha 3 chain |
| -1.31 | 2.22e-04 | RUNX1 | RUNX family transcription factor 1 | 0.38 | 3.03e-02 | MCCC2 | methylcrotonyl-CoA carboxylase subu |
| -1.07 | 2.99e-04 | UBE2Z | ubiquitin conjugating enzyme E2 Z | 0.6 | 4.27e-02 | MNDA | myeloid cell nuclear differentiatio |
| -1.62 | 3.08e-04 | RNF149 | ring finger protein 149 | 1.29 | 4.80e-02 | TUBB3 | tubulin beta 3 class III |
| -1.06 | 3.16e-04 | MRPS2 | mitochondrial ribosomal protein S2 | 0.72 | 4.97e-02 | COX6A1 | cytochrome c oxidase subunit 6A1 |
| -0.16 | 3.65e-04 | MACROH2A1 | macroH2A.1 histone | 0.46 | 4.97e-02 | KDM4B | lysine demethylase 4B |
| -0.94 | 3.95e-04 | PCNT | pericentrin | 0.66 | 4.97e-02 | KIDINS220 | kinase D interacting substrate 220 |
| -0.1 | 4.31e-04 | MCM7 | minichromosome maintenance complex | 0.53 | 6.45e-02 | ALDH1L2 | aldehyde dehydrogenase 1 family mem |
| -0.16 | 4.69e-04 | CTNNBL1 | catenin beta like 1 | 0.54 | 6.91e-02 | NECTIN2 | nectin cell adhesion molecule 2 |
| -1.54 | 7.19e-04 | SUDS3 | SDS3 homolog, SIN3A corepressor com | 0.8 | 7.15e-02 | MCEE | methylmalonyl-CoA epimerase |
| -1.11 | 7.19e-04 | PHF14 | PHD finger protein 14 | 0.45 | 7.92e-02 | CARMIL1 | capping protein regulator and myosi |
| -1.21 | 7.91e-04 | KAT7 | lysine acetyltransferase 7 | 0.45 | 8.72e-02 | ERGIC2 | ERGIC and golgi 2 |
| -1.53 | 8.58e-04 | DYNLRB1 | dynein light chain roadblock-type 1 | 0.16 | 8.92e-02 | MRPL45 | mitochondrial ribosomal protein L45 |
| -1.56 | 8.81e-04 | LGALS3BP | galectin 3 binding protein | 0.75 | 9.43e-02 | GOLGA5 | golgin A5 |
| -0.92 | 1.03e-03 | TMEM263 | transmembrane protein 263 | 0.44 | 1.03e-01 | GLT8D1 | glycosyltransferase 8 domain contai |
| -1.17 | 1.06e-03 | THUMPD3 | THUMP domain containing 3 | 1.28 | 1.03e-01 | TES | testin LIM domain protein |
| -1.04 | 1.23e-03 | HSPA2 | heat shock protein family A (Hsp70) | 0.64 | 1.04e-01 | SLC25A4 | solute carrier family 25 member 4 |
| -1.01 | 1.32e-03 | MYH10 | myosin heavy chain 10 | 0.23 | 1.05e-01 | PPIF | peptidylprolyl isomerase F |
| -1.32 | 1.32e-03 | GINS1 | GINS complex subunit 1 | 0.7 | 1.12e-01 | TUBB2B | tubulin beta 2B class IIb |
| -0.79 | 1.53e-03 | ATAD2 | ATPase family AAA domain containing | 0.72 | 1.21e-01 | RAB11FIP1 | RAB11 family interacting protein 1 |
| -0.12 | 1.53e-03 | VPS35 | VPS35 retromer complex component | 0.53 | 1.26e-01 | RELB | RELB proto-oncogene, NF- κ B subunit |
| -0.81 | 1.53e-03 | ADGRG1 | adhesion G protein-coupled receptor | 0.13 | 1.26e-01 | CLPP | caseinolytic mitochondrial matrix p |
| -1.49 | 1.53e-03 | WAC | WW domain containing adaptor with c | 0.18 | 1.26e-01 | FKBP2 | FKBP prolyl isomerase 2 |
| -0.9 | 1.53e-03 | FOXK2 | forkhead box K2 | 0.11 | 1.34e-01 | ATP6V1B2 | ATPase H ⁺ transporting V1 subunit B |
| -0.09 | 1.73e-03 | BUB3 | BUB3 mitotic checkpoint protein | 0.63 | 1.37e-01 | CYBB | cytochrome b-245 beta chain |
| 0.85 | 1.75e-03 | SHMT1 | serine hydroxymethyltransferase 1 | 0.15 | 1.49e-01 | EPR11 | endothelial reticulum protein 11 |

Differentially expressed proteins in solid cancers at absence/low amount of ACTR5 , DB1

p-value < 0.05 & logFC > 1.2



Sorted by p values!

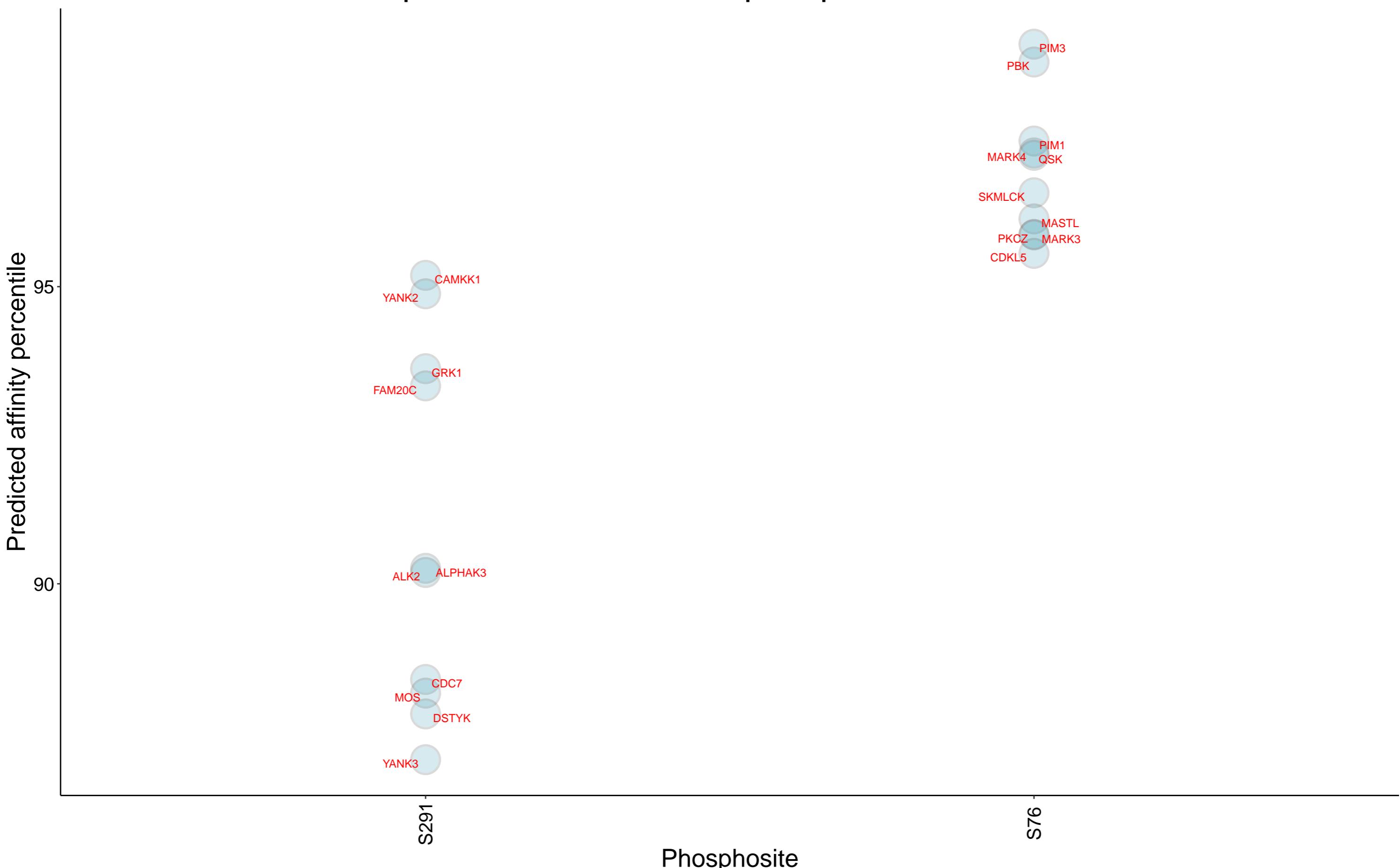
Downregulated in solid cancers at low/absent ACTR5 Upregulated in solid cancers at low/absent ACTR5

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|-------------------------------------|-------|-----------|----------|-------------------------------------|
| -1.45 | 1.33e-25 | BLMH | bleomycin hydrolase | 0.83 | 1.66e-12 | FGF2 | fibroblast growth factor 2 |
| -1.27 | 1.69e-17 | UBE2T | ubiquitin conjugating enzyme E2 T | 0.89 | 1.89e-11 | CCN1 | cellular communication network fact |
| -1.1 | 2.45e-17 | NME2 | NME/NM23 nucleoside diphosphate kin | 0.79 | 9.68e-11 | SERPINE1 | serpin family E member 1 |
| -0.2 | 6.40e-16 | NASP | nuclear autoantigenic sperm protein | 1.31 | 1.83e-09 | CAVIN3 | caveolae associated protein 3 |
| -0.97 | 3.32e-15 | UBE2S | ubiquitin conjugating enzyme E2 S | 1.03 | 1.98e-09 | KIRREL1 | kirre like nephrin family adhesion |
| -1.12 | 3.32e-15 | HAT1 | histone acetyltransferase 1 | 0.79 | 4.50e-09 | DAB2 | DAB adaptor protein 2 |
| -0.93 | 2.45e-14 | GPHN | gephyrin | 0.78 | 1.07e-08 | QSOX1 | quiescin sulfhydryl oxidase 1 |
| -1.19 | 2.53e-14 | UBR7 | ubiquitin protein ligase E3 compone | 0.82 | 2.79e-08 | CAVIN2 | caveolae associated protein 2 |
| -1.17 | 2.53e-14 | CKMT1A | creatine kinase, mitochondrial 1A | 0.53 | 3.34e-08 | CD99L2 | CD99 molecule like 2 |
| -0.87 | 4.13e-14 | CLNS1A | chloride nucleotide-sensitive chann | 0.76 | 4.59e-08 | SLC12A4 | solute carrier family 12 member 4 |
| -0.85 | 6.11e-14 | YTHDF2 | YTH N6-methyladenosine RNA binding | 1.21 | 5.26e-08 | AXL | AXL receptor tyrosine kinase |
| -0.21 | 1.06e-13 | FKBP4 | FKBP prolyl isomerase 4 | 1.14 | 7.40e-08 | MGAT1 | alpha-1,3-mannosyl-glycoprotein 2-b |
| -1.2 | 1.44e-13 | PSME3IP1 | proteasome activator subunit 3 inte | 1.09 | 7.89e-08 | ARSA | arylsulfatase A |
| -1.33 | 1.48e-13 | PDXP | pyridoxal phosphatase | 0.57 | 7.89e-08 | AKR1C2 | aldo-keto reductase family 1 member |
| -0.84 | 1.48e-13 | DDI2 | DNA damage inducible 1 homolog 2 | 0.91 | 9.73e-08 | NEXN | nexilin F-actin binding protein |
| -0.13 | 2.26e-13 | BUB3 | BUB3 mitotic checkpoint protein | 0.69 | 1.10e-07 | CPQ | carboxypeptidase Q |
| -1.53 | 2.47e-13 | SNRNP27 | small nuclear ribonucleoprotein U4/ | 0.68 | 1.10e-07 | KRT14 | keratin 14 |
| -0.93 | 2.49e-13 | PITHD1 | PITH domain containing 1 | 0.7 | 1.36e-07 | CCDC9B | coiled-coil domain containing 9B |
| -1.07 | 5.84e-13 | NRF1 | nuclear respiratory factor 1 | 1.44 | 1.67e-07 | CD109 | CD109 molecule |
| -1.04 | 6.24e-13 | UBE2C | ubiquitin conjugating enzyme E2 C | 0.65 | 1.67e-07 | CAV2 | caveolin 2 |
| -0.24 | 9.08e-13 | STMN1 | stathmin 1 | 0.6 | 1.94e-07 | IGFBP3 | insulin like growth factor binding |
| -0.95 | 9.61e-13 | GTPBP1 | GTP binding protein 1 | 0.92 | 2.23e-07 | PHLDB2 | pleckstrin homology like domain fam |
| -0.91 | 1.52e-12 | NTMT1 | N-terminal Xaa-Pro-Lys N-methyltran | 0.83 | 3.29e-07 | GPNMB | glycoprotein nmb |
| -0.14 | 2.17e-12 | PCNA | proliferating cell nuclear antigen | 0.77 | 4.22e-07 | RFTN1 | raftlin, lipid raft linker 1 |
| -1.3 | 3.95e-12 | PRIM1 | DNA primase subunit 1 | 1. | | | |

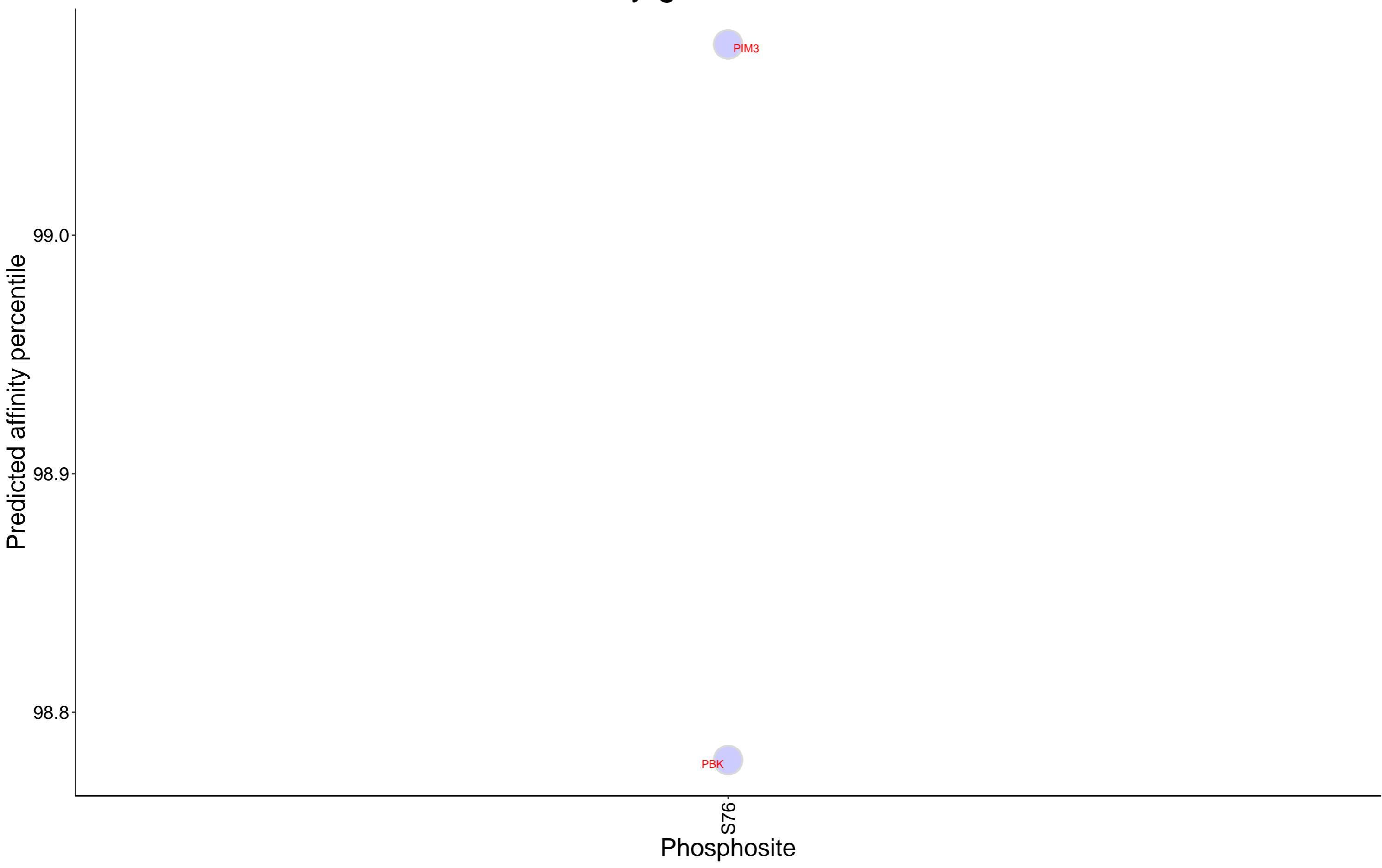
Insufficient number of paired observations in DB1 for ACTR5

Insufficient number of paired observations in DB1 for ACTR5

Top 10 kinases for each phosphosite in ACTR5



Kinases with affinity greater than 98.5% to ACTR5



No sufficient paired observations in DB1 for ACTR5