

# CDC5L

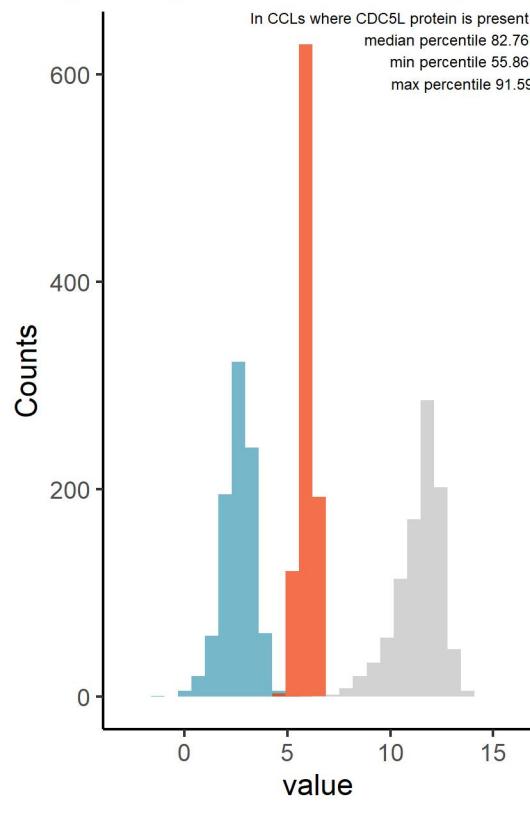
Protein name: CDC5L ; UNIPROT: Q99459 ; Gene name: cell division cycle 5 like

Ligandable: Yes ; Ligandable\_by\_Chem: NA ; Is\_enzyme: NA (<https://cansar.ai/>)

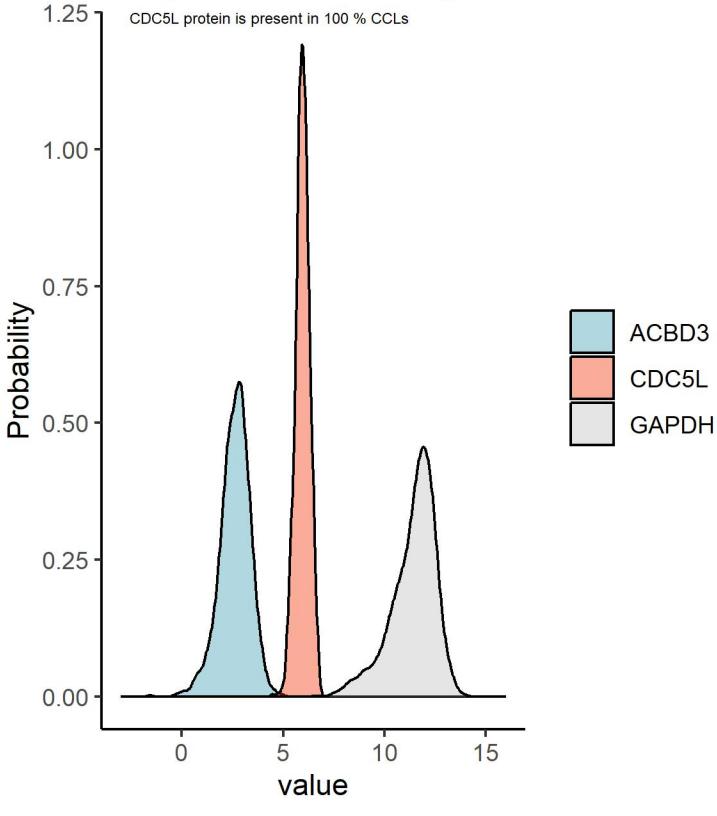
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

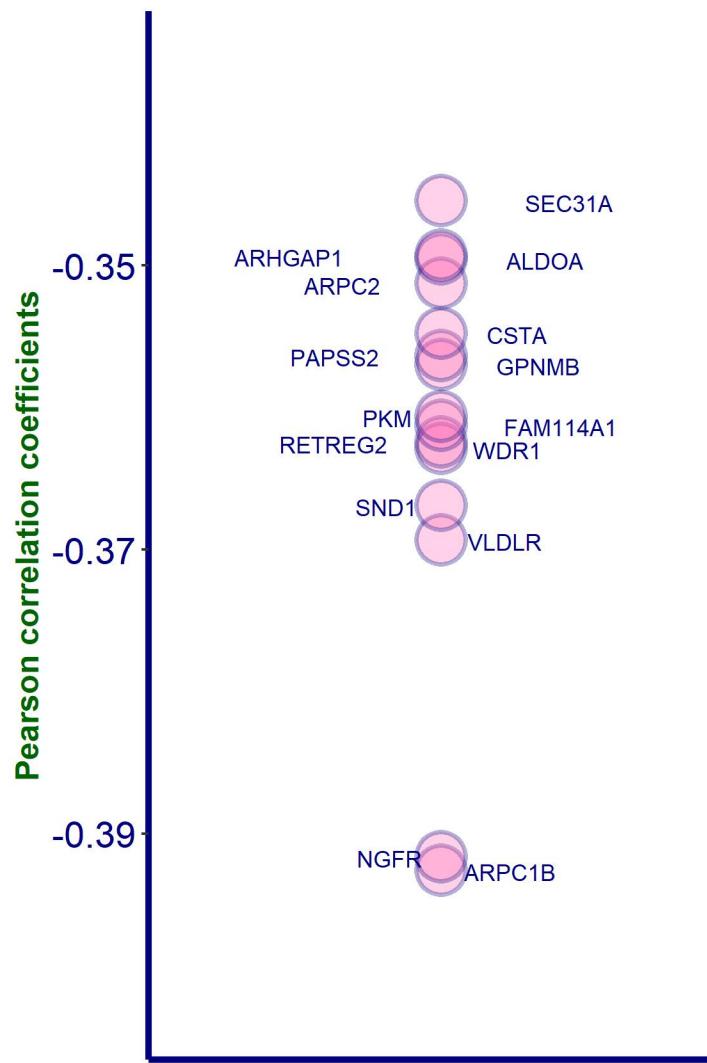
Histogram of CDC5L protein compared to proteins with low and high abundance



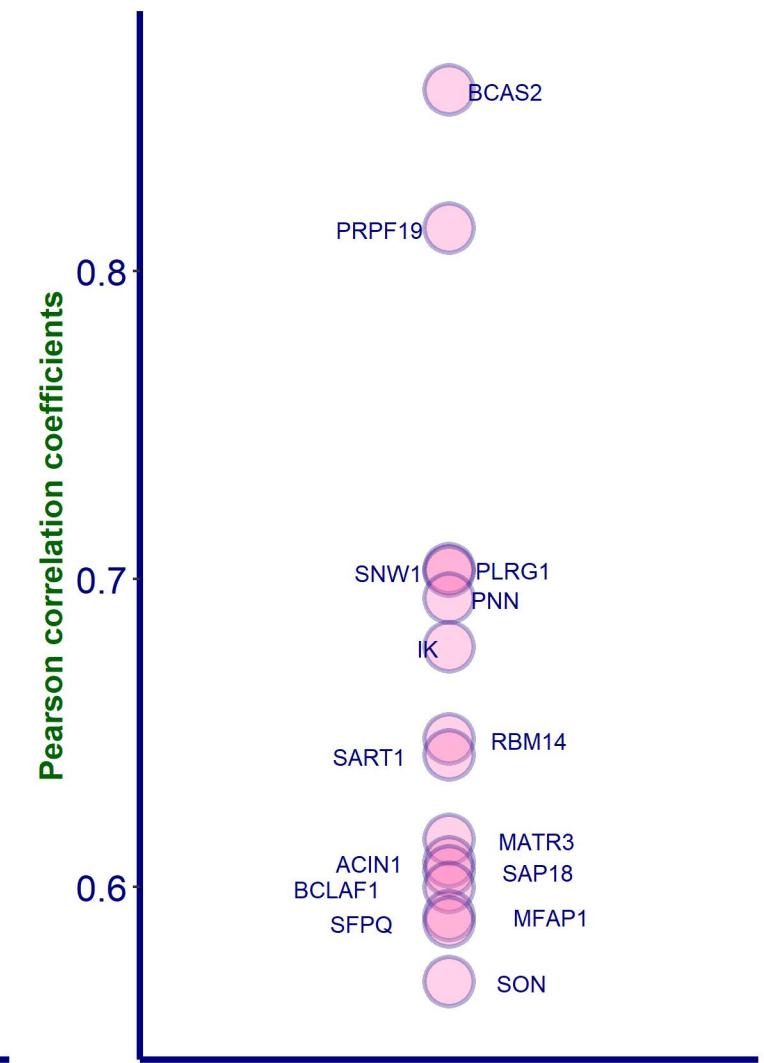
Density plot of CDC5L protein compared to proteins with low and high abundance



Top negative correlations of CDC5L protein, DB1

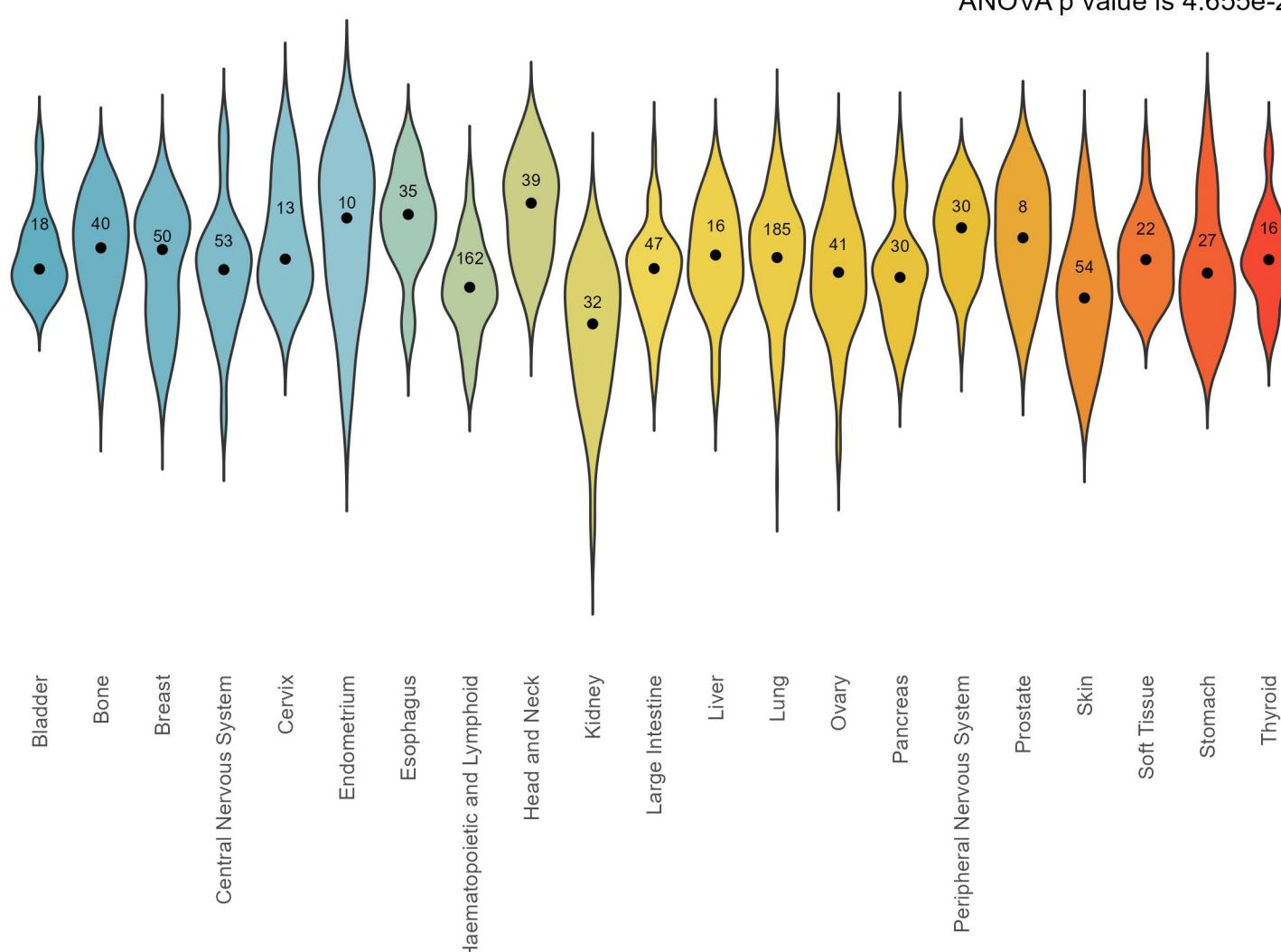


Top positive correlations of CDC5L protein, DB1



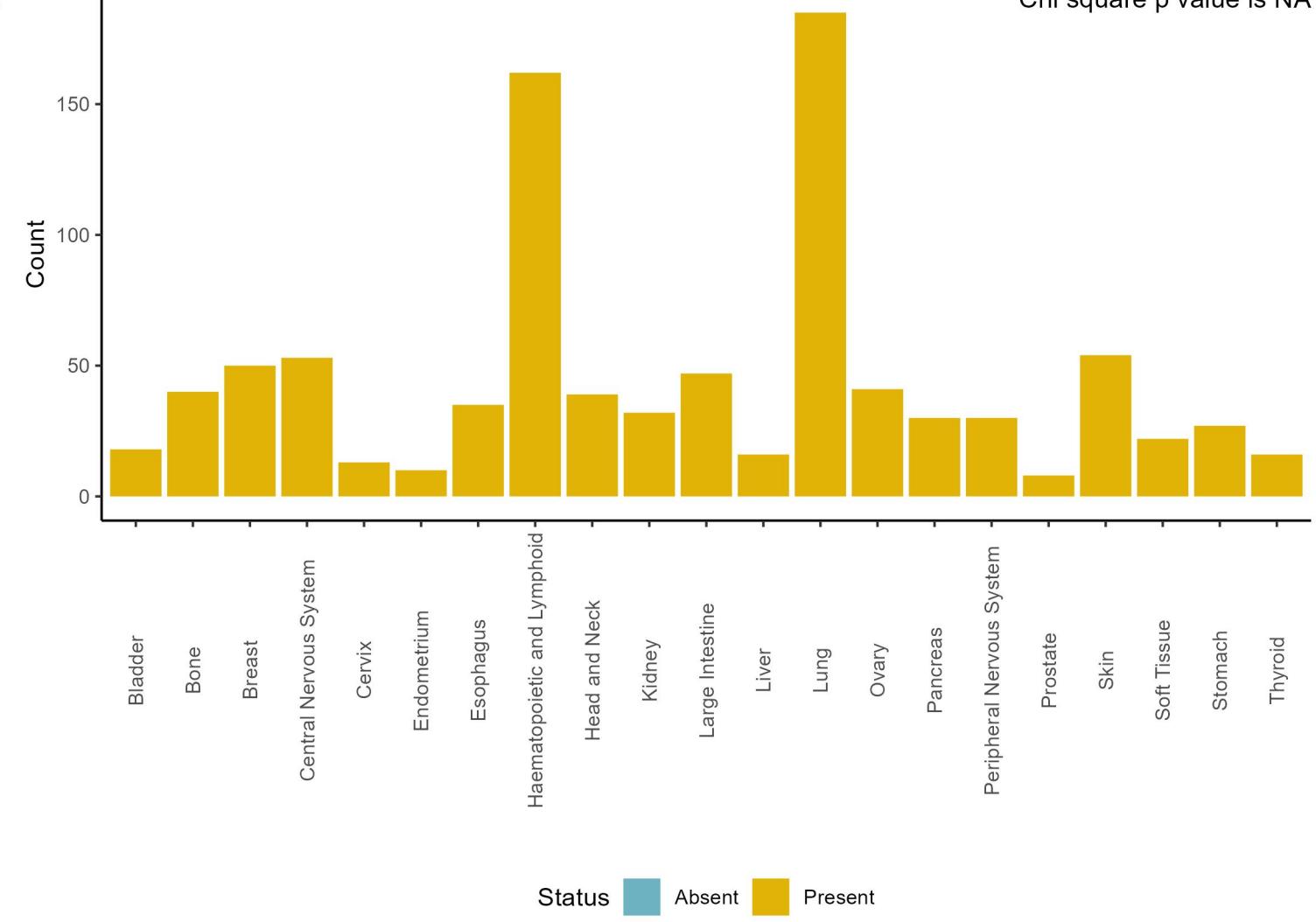
Amount of CDC5L protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 4.655e-26



Present and absent CDC5L protein counts by tissue, DB1

Chi square p value is NA

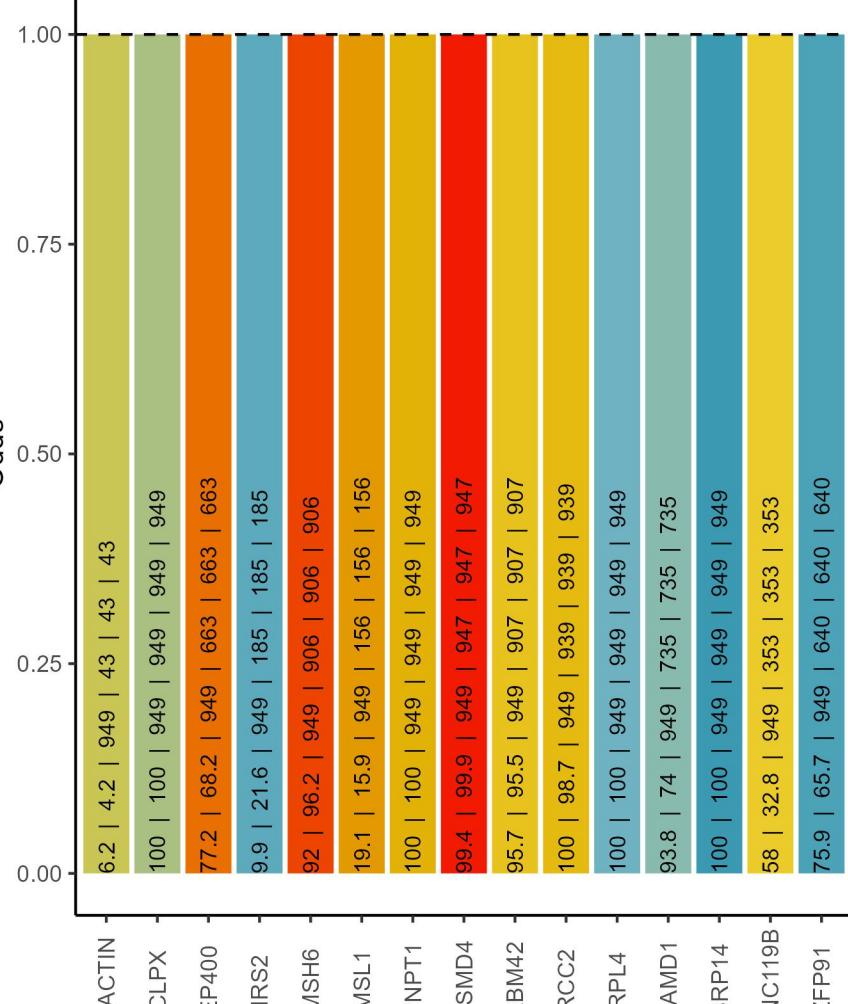


Cooccurrence with CDC5L protein, DB1

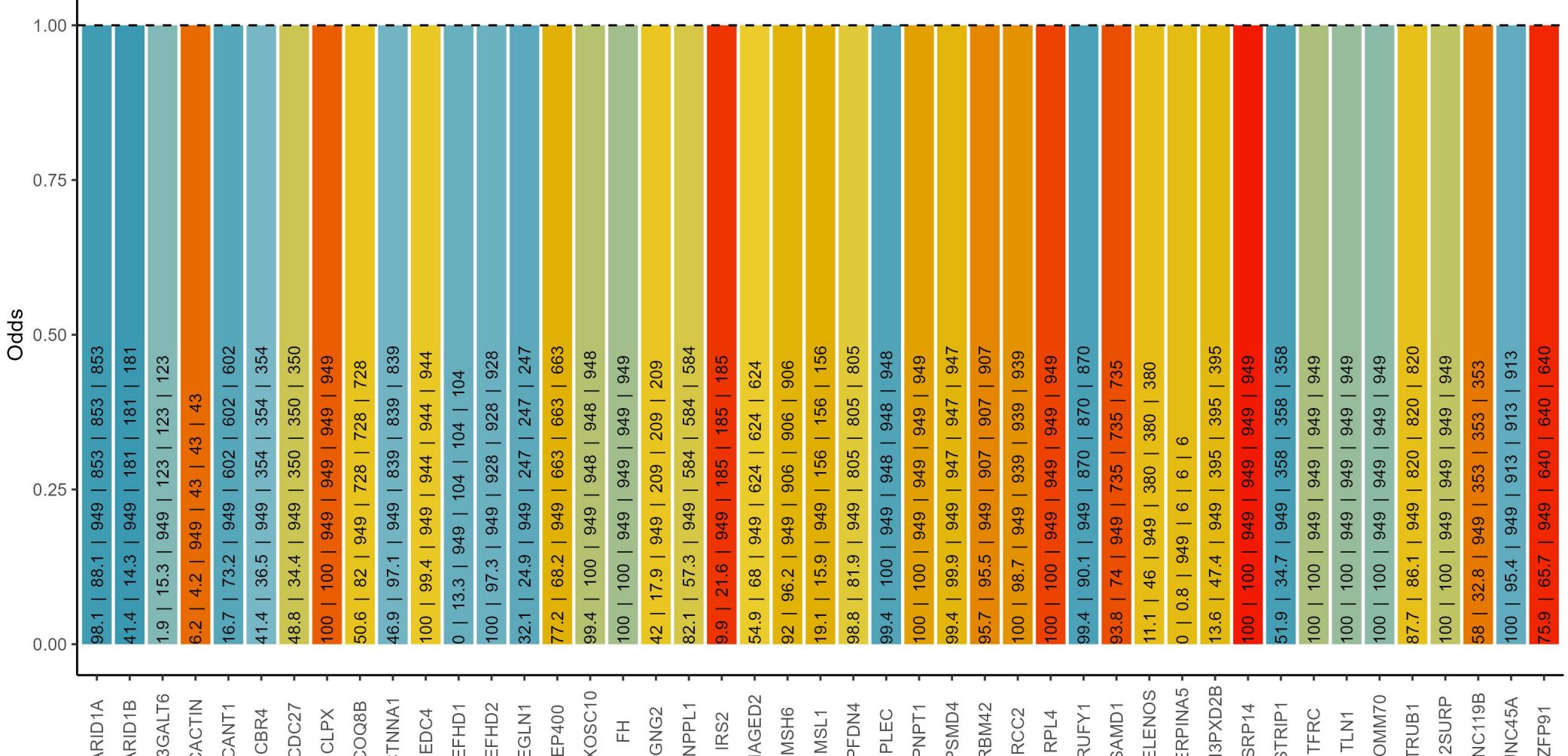
% of CDC5L in blood cancers: 100 ; % of CDC5L in solid cancers: 100

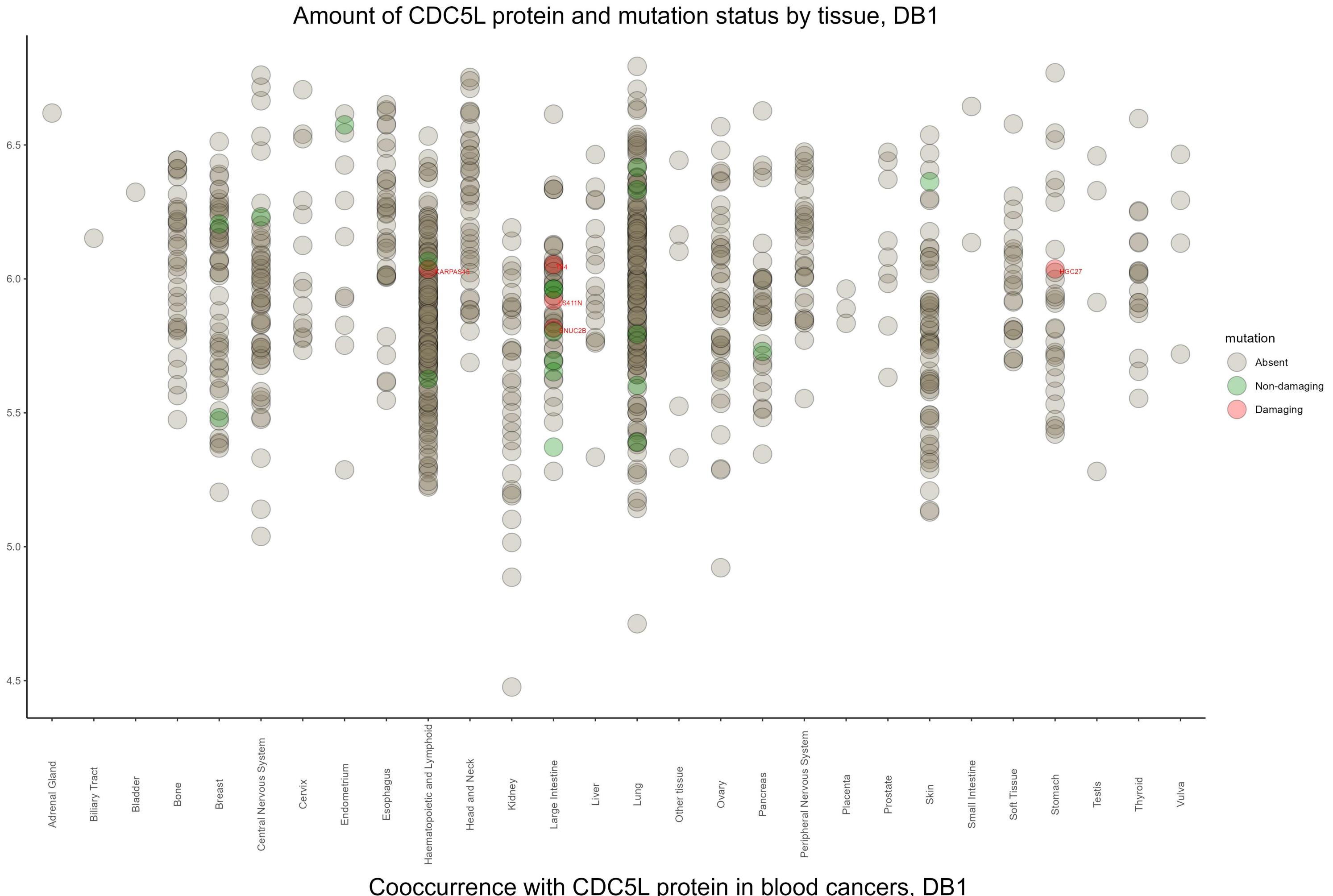
Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CDC5L | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



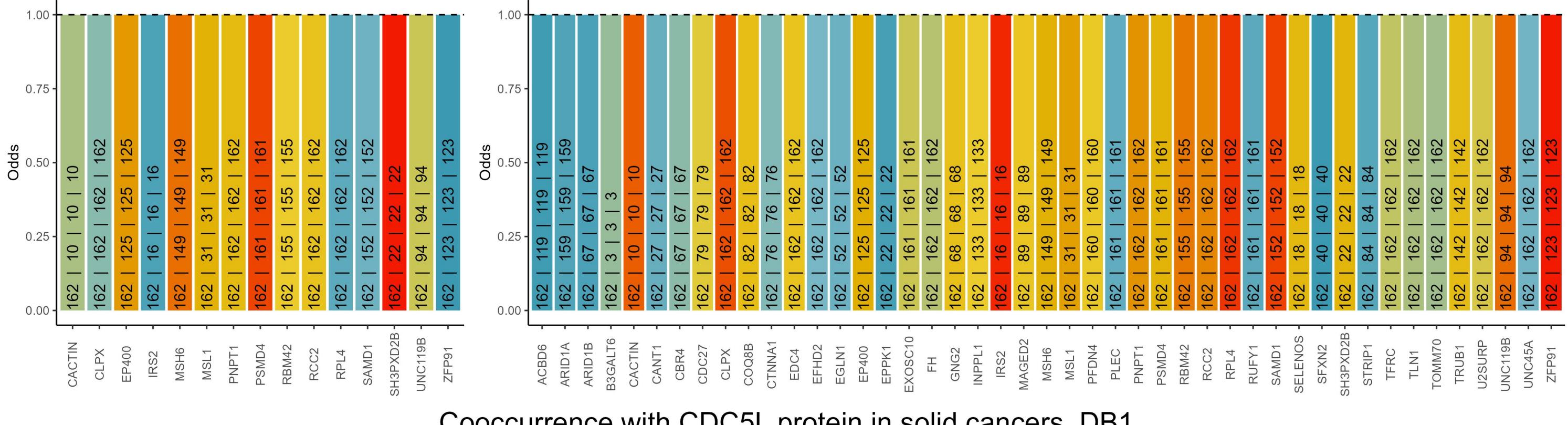
Positive cooccurrence





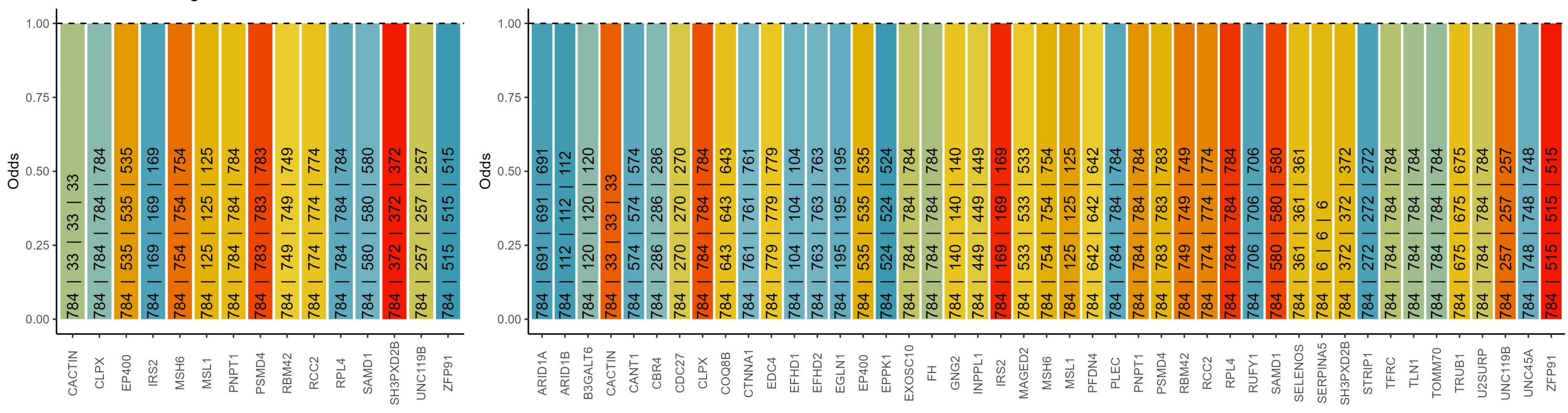
ncidence of CDC5L | incidence of Protein 2 | observed cooccurrence | ex

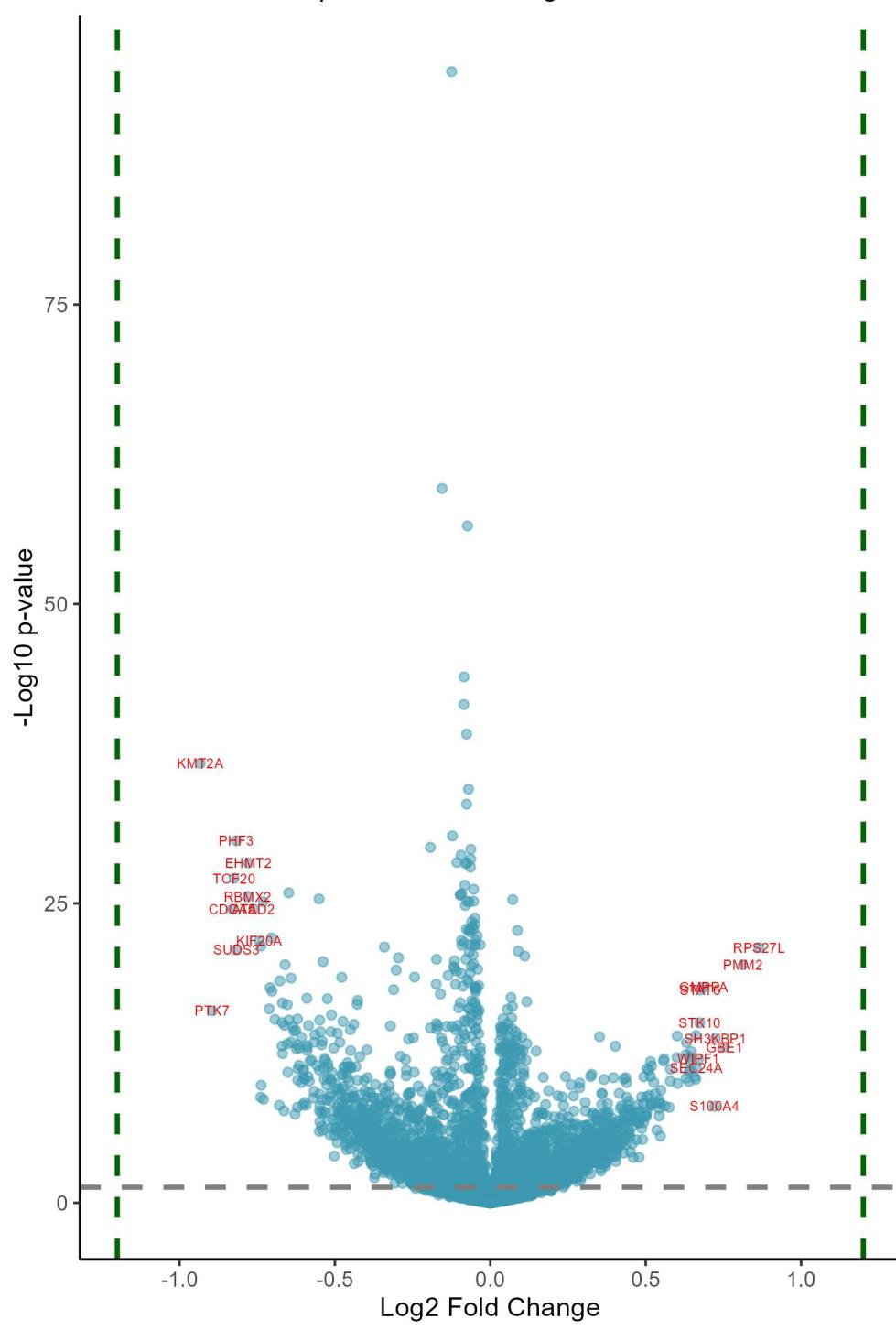
negative cooccurrence Positive cooccurrence



incidence of CDC5L | incidence of Protein 2 | observed cooccurrence | e

Positive cooccurrence

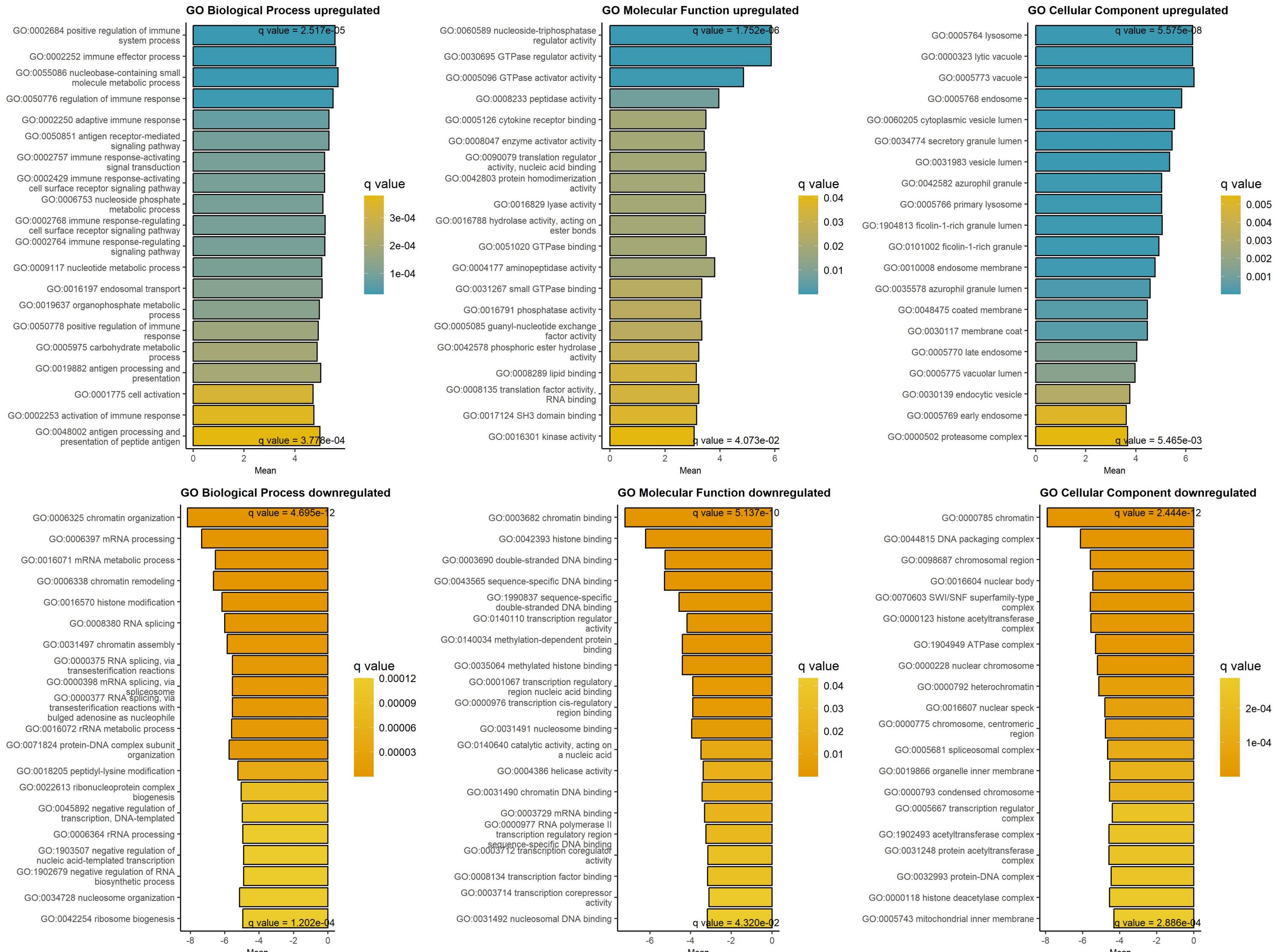


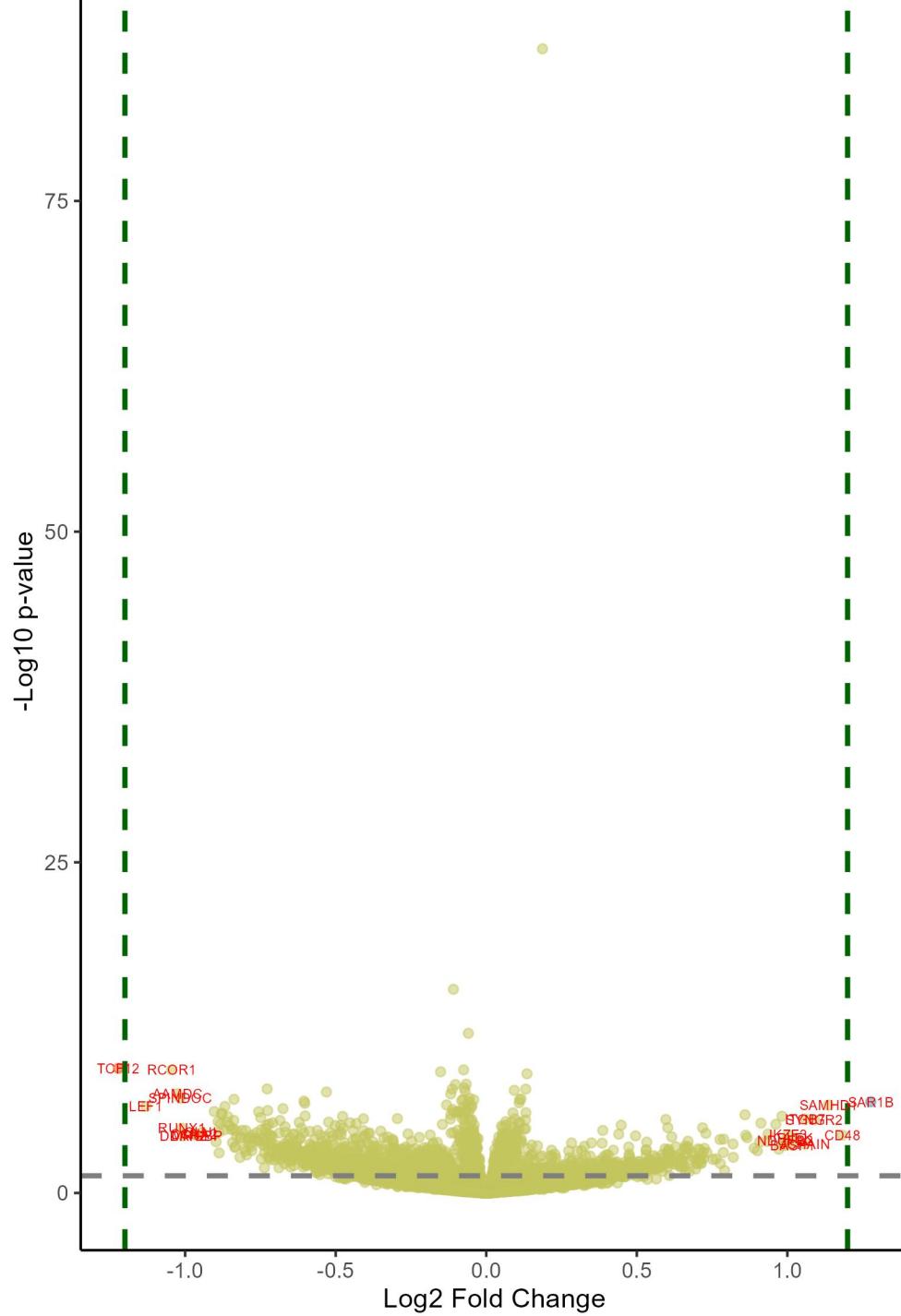


### Downregulated at low/absent CDC5L      Upregulated at low/absent CDC5L

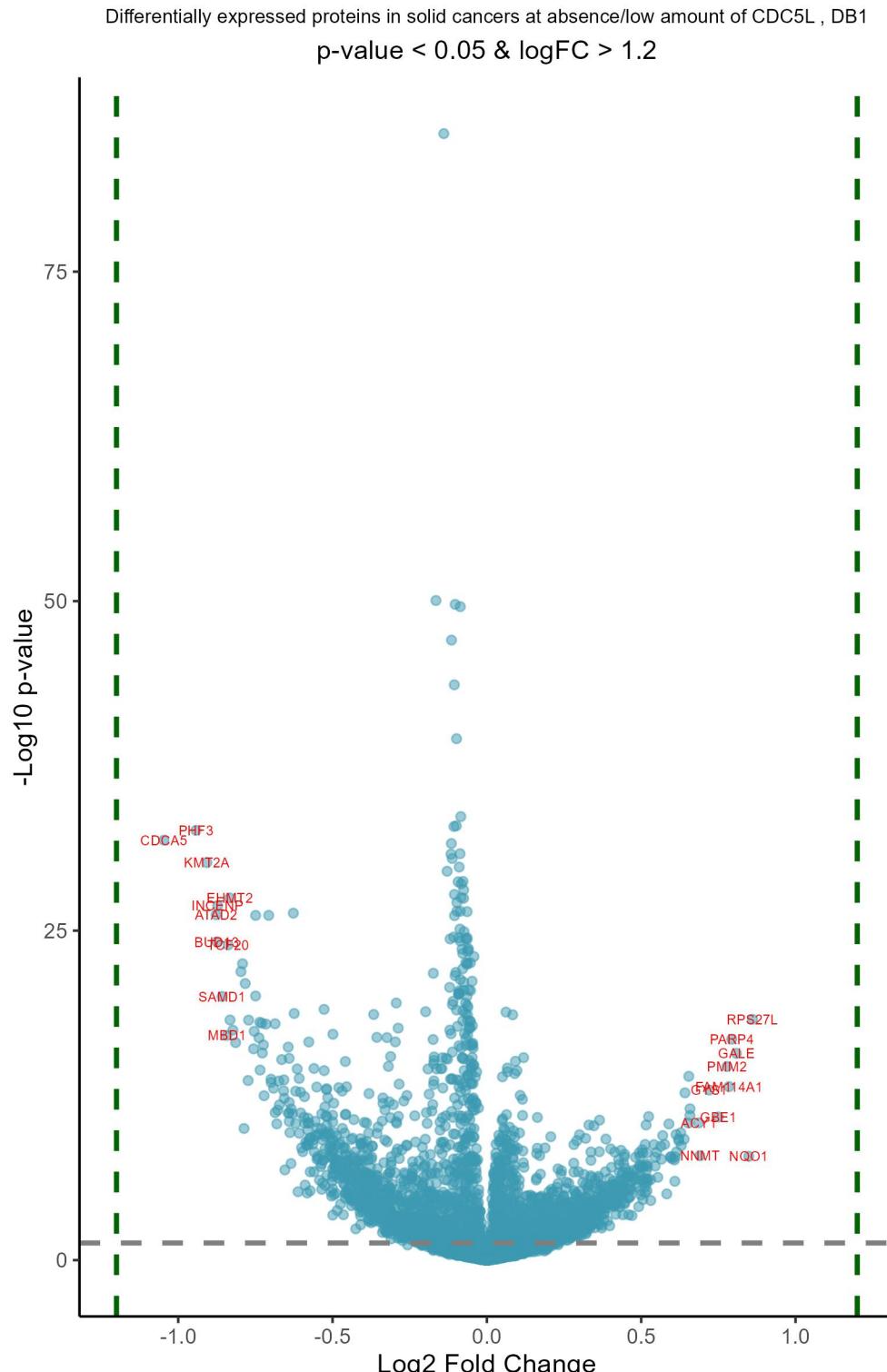
| logFC | adj.P.Val | symbol    | name                                 | logFC | adj.P.Val | symbol  | name                                |
|-------|-----------|-----------|--------------------------------------|-------|-----------|---------|-------------------------------------|
| -0.93 | 1.73e-34  | KMT2A     | lysine methyltransferase 2A          | 0.86  | 5.23e-20  | RPS27L  | ribosomal protein S27 like          |
| -0.9  | 4.85e-15  | PTK7      | protein tyrosine kinase 7 (inactive) | 0.81  | 1.18e-18  | PMM2    | phosphomannomutase 2                |
| -0.83 | 5.32e-23  | CDC45     | cell division cycle associated 5     | 0.75  | 3.12e-12  | GBE1    | 1,4-alpha-glucan branching enzyme 1 |
| -0.82 | 2.47e-25  | TCF20     | transcription factor 20              | 0.72  | 6.66e-13  | SH3KBP1 | SH3 domain containing kinase bindin |
| -0.82 | 3.28e-28  | PHF3      | PHD finger protein 3                 | 0.72  | 1.02e-07  | S100A4  | S100 calcium binding protein A4     |
| -0.82 | 7.85e-20  | SUDS3     | SDS3 homolog, SIN3A corepressor com  | 0.69  | 6.96e-17  | GMPPA   | GDP-mannose pyrophosphorylase A     |
| -0.78 | 6.20e-24  | RBMX2     | RNA binding motif protein X-linked   | 0.67  | 1.09e-16  | STAT6   | signal transducer and activator of  |
| -0.78 | 1.46e-26  | EHMT2     | euchromatic histone lysine methyltr  | 0.67  | 4.32e-14  | STK10   | serine/threonine kinase 10          |
| -0.76 | 5.14e-23  | ATAD2     | ATPase family AAA domain containing  | 0.67  | 2.35e-11  | WIPF1   | WAS/WASL interacting protein family |
| -0.74 | 1.66e-20  | KIF20A    | kinesin family member 20A            | 0.66  | 1.18e-10  | SEC24A  | SEC24 homolog A, COPII coat complex |
| -0.74 | 2.11e-08  | H1-0      | H1.0 linker histone                  | 0.66  | 3.95e-13  | PARP4   | poly(ADP-ribose) polymerase family  |
| -0.74 | 4.00e-20  | BUD13     | BUD13 homolog                        | 0.66  | 8.76e-10  | GLRX    | glutaredoxin                        |
| -0.74 | 2.53e-09  | MACROH2A2 | macroH2A.2 histone                   | 0.66  | 5.80e-10  | CD70    | CD70 molecule                       |
| -0.73 | 1.41e-23  | INCENP    | inner centromere protein             | 0.65  | 6.40e-12  | GYS1    | glycogen synthase 1                 |
| -0.73 | 3.00e-08  | CKB       | creatine kinase B                    | 0.64  | 2.64e-11  | ABHD14B | abhydrolase domain containing 14B   |
| -0.71 | 3.49e-15  | ZNF280C   | zinc finger protein 280C             | 0.64  | 1.43e-10  | ACY1    | aminoacylase 1                      |
| -0.71 | 7.45e-17  | BRD1      | bromodomain containing 1             | 0.64  | 1.73e-11  | GALE    | UDP-galactose-4-epimerase           |
| -0.7  | 9.98e-21  | EP400     | E1A binding protein p400             | 0.64  | 2.11e-10  | FAH     | fumarylacetoacetate hydrolase       |
| -0.7  | 1.38e-16  | SAMD1     | sterile alpha motif domain containi  | 0.64  | 1.33e-09  | SH3BGR  | SH3 domain binding glutamate rich p |
| -0.69 | 2.39e-14  | SRCAP     | Snf2 related CREBBP activator prote  | 0.63  | 1.36e-12  | LPXN    | leupaxin                            |
| -0.68 | 8.68e-08  | CKMT1A    | creatine kinase, mitochondrial 1A    | 0.63  | 7.10e-10  | PSMB10  | proteasome 20S subunit beta 10      |
| -0.68 | 2.22e-17  | KAT7      | lysine acetyltransferase 7           | 0.63  | 1.14e-11  | FAM107B | family with sequence similarity 107 |
| -0.67 | 2.55e-12  | CENPV     | centromere protein V                 | 0.6   | 1.84e-09  | ADA     | adenosine deaminase                 |
| -0.67 | 4.11e-14  | NSD3      | nuclear receptor binding SET domain  | 0.6   | 4.26e-13  | CASP8   | caspase 8                           |
| -0.67 | 1.18e-15  | AURKB     | aurora kinase B                      | 0.6   | 1.95e-11  | PRKCD   | protein kinase C delta              |
| -0.67 | 9.44e-12  | FADS1     | fatty acid desaturase 1              | 0.58  | 1.47e-10  | TCIRG1  | T cell immune regulator 1, ATPase H |
| -0.66 | 2.25e-07  | KRT17     | keratin 17                           | 0.58  | 1.24e-09  | PTER    | phosphotriesterase related          |
| -0.66 | 6.90e-14  | MEAF6     | MYST/Esa1 associated factor 6        | 0.58  | 1.25e-07  | RNASET2 | ribonuclease T2                     |
| -0.66 | 1.18e-18  | SNIP1     | Smad nuclear interacting protein 1   | 0.56  | 9.79e-08  | TIGAR   | TP53 induced glycolysis regulatory  |

### GAGE analysis on upregulated and downregulated proteins at low/absent CDC5L protein, DB1



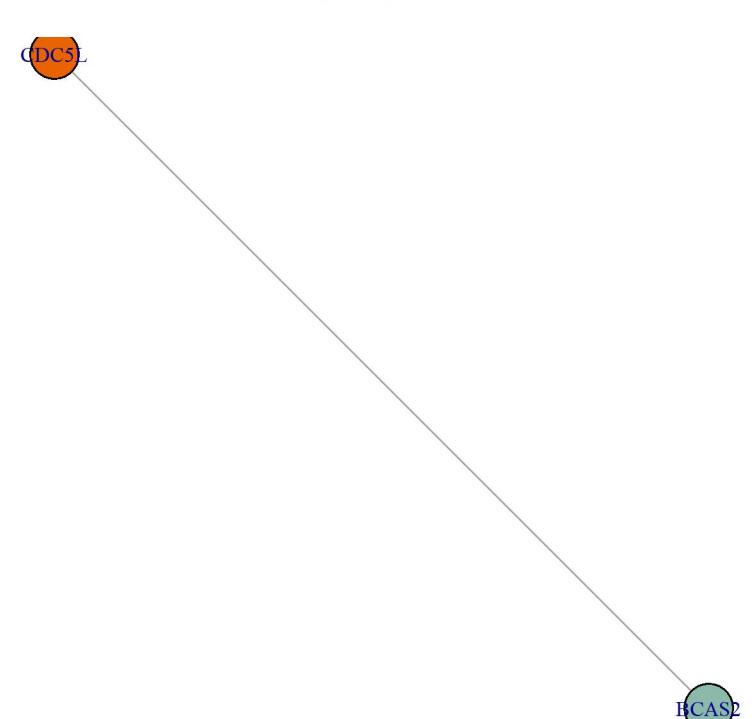


| logFC | adj.P.Val | symbol  | name                                | logFC | adj.P.Val | symbol   | name                                |
|-------|-----------|---------|-------------------------------------|-------|-----------|----------|-------------------------------------|
| -1.22 | 4.70e-07  | TCF12   | transcription factor 12             | 1.28  | 2.75e-05  | SAR1B    | secretion associated Ras related GT |
| -1.13 | 4.90e-05  | LEP1    | lymphoid enhancer binding factor 1  | 1.18  | 1.52e-03  | CD48     | CD48 molecule                       |
| -1.04 | 4.70e-07  | RCOR1   | REST corepressor 1                  | 1.14  | 4.26e-05  | SAMHD1   | SAM and HD domain containing deoxyn |
| -1.03 | 1.08e-05  | AAMDC   | adipogenesis associated Mth938 doma | 1.09  | 2.55e-04  | SYNGR2   | synaptogyrin 2                      |
| -1.02 | 2.06e-05  | SPINDOC | spindlin interactor and repressor o | 1.06  | 2.32e-04  | ITGB7    | integrin subunit beta 7             |
| -1.01 | 7.47e-04  | RUNX1   | RUNX family transcription factor 1  | 1.06  | 4.48e-03  | JCHAIN   | joining chain of multimeric IgA and |
| -1.01 | 1.64e-03  | DDAH2   | dimethylarginine dimethylaminohydro | 1.03  | 2.06e-03  | PLEK     | pleckstrin                          |
| -0.97 | 1.37e-03  | CCNA2   | cyclin A2                           | 1.02  | 5.18e-03  | BASP1    | brain abundant membrane attached si |
| -0.96 | 1.64e-03  | MRGBP   | MRG domain binding protein          | 1     | 1.45e-03  | IKZF3    | IKAROS family zinc finger 3         |
| -0.94 | 1.19e-03  | GLUL    | glutamate-ammonia ligase            | 0.99  | 2.76e-03  | NDUFB2   | NADH:ubiquinone oxidoreductase subu |
| -0.9  | 9.47e-05  | FOXP1   | forkhead box P1                     | 0.99  | 4.50e-03  | MVP      | major vault protein                 |
| -0.9  | 3.28e-03  | SATB1   | SATB homeobox 1                     | 0.99  | 5.34e-03  | CTSZ     | cathepsin Z                         |
| -0.89 | 3.25e-04  | NSD3    | nuclear receptor binding SET domain | 0.98  | 1.65e-04  | FAS      | Fas cell surface death receptor     |
| -0.89 | 1.20e-02  | DBN1    | drebrin 1                           | 0.97  | 7.69e-03  | HLA-DQB1 | major histocompatibility complex, c |
| -0.89 | 1.19e-03  | MAZ     | MYC associated zinc finger protein  | 0.96  | 4.43e-04  | ACSL1    | acyl-CoA synthetase long chain fami |
| -0.88 | 4.23e-04  | NSL1    | NSL1 component of MIS12 kinetochore | 0.94  | 1.40e-03  | TYMP     | thymidine phosphorylase             |
| -0.88 | 1.04e-04  | MAEA    | macrophage erythroblast attacher, E | 0.93  | 3.19e-03  | ISG20    | interferon stimulated exonuclease g |
| -0.88 | 1.29e-04  | MORC2   | MORC family CW-type zinc finger 2   | 0.91  | 3.77e-04  | IFI30    | IFI30 lysosomal thiol reductase     |
| -0.87 | 8.94e-04  | ZEB2    | zinc finger E-box binding homeobox  | 0.91  | 3.34e-03  | CD40     | CD40 molecule                       |
| -0.87 | 4.90e-05  | CKAP2   | cytoskeleton associated protein 2   | 0.9   | 9.26e-03  | RPL22L1  | ribosomal protein L22 like 1        |
| -0.86 | 3.50e-04  | PDCD2   | programmed cell death 2             | 0.89  | 7.13e-03  | SQOR     | sulfide quinone oxidoreductase      |
| -0.86 | 1.71e-04  | GSE1    | Gse1 coiled-coil protein            | 0.87  | 1.99e-03  | TMEM205  | transmembrane protein 205           |
| -0.85 | 5.25e-04  | CCDC12  | coiled-coil domain containing 12    | 0.86  | 1.52e-03  | MAP4K1   | mitogen-activated protein kinase ki |
| -0.85 | 8.78e-04  | SNX15   | sorting nexin 15                    | 0.86  | 1.35e-04  | EML2     | EMAP like 2                         |
| -0.84 | 3.65e-03  | BRD3    | bromodomain containing 3            | 0.82  | 2.01e-02  | IRF4     | interferon regulatory factor 4      |
| -0.84 | 8.24e-04  | CCNK    | cyclin K                            | 0.82  | 4.35e-03  | ALG1     | ALG1 chitobiosyldiphosphodolichol b |
| -0.84 | 2.73e-04  | SKA3    | spindle and kinetochore associated  | 0.79  | 9.33e-02  | LSP1     | lymphocyte specific protein 1       |
| -0.84 | 2.21e-05  | MEAF6   | MYST/Esa1 associated factor 6       | 0.79  | 2.33e-03  | MCEE     | methylmalonyl-CoA epimerase         |
| -0.84 | 6.43e-03  | MACROD1 | mono-ADP ribosylhydrolase 1         | 0.79  | 1.14e-02  | TES      | testin LIM domain protein           |

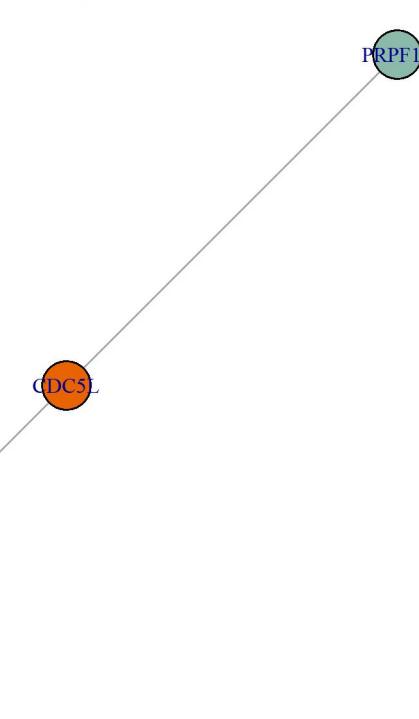


| logFC | adj.P.Val | symbol  | name                                | logFC | adj.P.Val | symbol   | name                                |
|-------|-----------|---------|-------------------------------------|-------|-----------|----------|-------------------------------------|
| -1.05 | 6.98e-30  | CDCA5   | cell division cycle associated 5    | 0.86  | 3.64e-17  | RPS27L   | ribosomal protein S27 like          |
| -0.94 | 1.36e-30  | PHF3    | PHD finger protein 3                | 0.85  | 1.74e-07  | NQO1     | NAD(P)H quinone dehydrogenase 1     |
| -0.91 | 2.53e-28  | KMT2A   | lysine methyltransferase 2A         | 0.81  | 9.45e-15  | GALE     | UDP-galactose-4-epimerase           |
| -0.88 | 1.17e-24  | ATAD2   | ATPase family AAA domain containing | 0.79  | 8.96e-16  | PARP4    | poly(ADP-ribose) polymerase family  |
| -0.88 | 9.84e-23  | BUD13   | BUD13 homolog                       | 0.78  | 2.17e-12  | FAM114A1 | family with sequence similarity 114 |
| -0.87 | 2.80e-25  | INCENP  | inner centromere protein            | 0.78  | 8.13e-14  | PMM2     | phosphomannomutase 2                |
| -0.86 | 8.15e-19  | SAMD1   | sterile alpha motif domain containi | 0.75  | 3.15e-10  | GBE1     | 1,4-alpha-glucan branching enzyme 1 |
| -0.84 | 4.84e-16  | MBD1    | methyl-CpG binding domain protein 1 | 0.72  | 3.77e-12  | GYS1     | glycogen synthase 1                 |
| -0.84 | 1.64e-22  | TCF20   | transcription factor 20             | 0.69  | 1.59e-07  | NNMT     | nicotinamide N-methyltransferase    |
| -0.83 | 8.21e-26  | EHMT2   | euchromatic histone lysine methyltr | 0.69  | 8.18e-10  | ACY1     | aminoacylase 1                      |
| -0.83 | 4.03e-17  | ZNF280C | zinc finger protein 280C            | 0.66  | 8.41e-11  | TCIRG1   | T cell immune regulator 1, ATPase H |
| -0.82 | 2.05e-16  | SUDS3   | SDS3 homolog, SIN3A corepressor com | 0.66  | 2.51e-10  | RPS6KA3  | ribosomal protein S6 kinase A3      |
| -0.81 | 1.58e-15  | POLR2D  | RNA polymerase II subunit D         | 0.65  | 4.01e-13  | GMPPA    | GDP-mannose pyrophosphorylase A     |
| -0.8  | 1.38e-20  | RBMX2   | RNA binding motif protein X-linked  | 0.65  | 8.42e-10  | IAH1     | isoamyl acetate hydrolyzing esteras |
| -0.79 | 3.66e-21  | EP400   | E1A binding protein p400            | 0.64  | 5.96e-12  | BLVRB    | biliverdin reductase B              |
| -0.79 | 2.04e-09  | CHRAC1  | chromatin accessibility complex sub | 0.64  | 1.15e-08  | FAH      | fumarylacetoacetate hydrolase       |
| -0.78 | 9.89e-20  | SUZ12   | SUZ12 polycomb repressive complex 2 | 0.63  | 3.16e-08  | SEC24A   | SEC24 homolog A, COPII coat complex |
| -0.77 | 7.85e-13  | CENPV   | centromere protein V                | 0.63  | 4.18e-09  | EPS8     | epidermal growth factor receptor pa |
| -0.77 | 4.07e-17  | ZNF384  | zinc finger protein 384             | 0.62  | 1.48e-08  | SH3KBP1  | SH3 domain containing kinase bindin |
| -0.76 | 4.34e-15  | NOL8    | nucleolar protein 8                 | 0.62  | 1.09e-08  | ABHD14B  | abhydrolase domain containing 14B   |
| -0.75 | 2.46e-16  | AURKB   | aurora kinase B                     | 0.61  | 8.57e-08  | HSPB8    | heat shock protein family B (small) |
| -0.75 | 7.65e-19  | SNIP1   | Smad nuclear interacting protein 1  | 0.61  | 5.47e-09  | ASL      | argininosuccinate lyase             |
| -0.75 | 1.26e-24  | CDCA8   | cell division cycle associated 8    | 0.61  | 1.89e-07  | GLRX     | glutaredoxin                        |
| -0.74 | 7.27e-16  | ZMYM3   | zinc finger MYM-type containing 3   | 0.61  | 8.65e-06  | PROCR    | protein C receptor                  |
| -0.74 | 5.64e-17  | KAT7    | lysine acetyltransferase 7          | 0.61  | 3.04e-07  | EPDR1    | ependymin related 1                 |
| -0.73 | 1.42e-13  | MEAF6   | MYST/Esa1 associated factor 6       | 0.6   | 2.54e-07  | SERPINE2 | serpin family E member 2            |
| -0.73 | 6.64e-17  | KIFC1   | kinesin family member C1            | 0.6   | 1.84e-07  | RHOC     | ras homolog family member C         |
| -0.73 | 8.94e-15  | CHAF1A  | chromatin assembly factor 1 subunit | 0.59  | 2.04e-07  | PTPRJ    | protein tyrosine phosphatase recept |
| -0.72 | 2.33e-15  | RBM6    | RNA binding motif protein 6         | 0.59  | 9.68e-10  | MYO1E    | myosin IE                           |

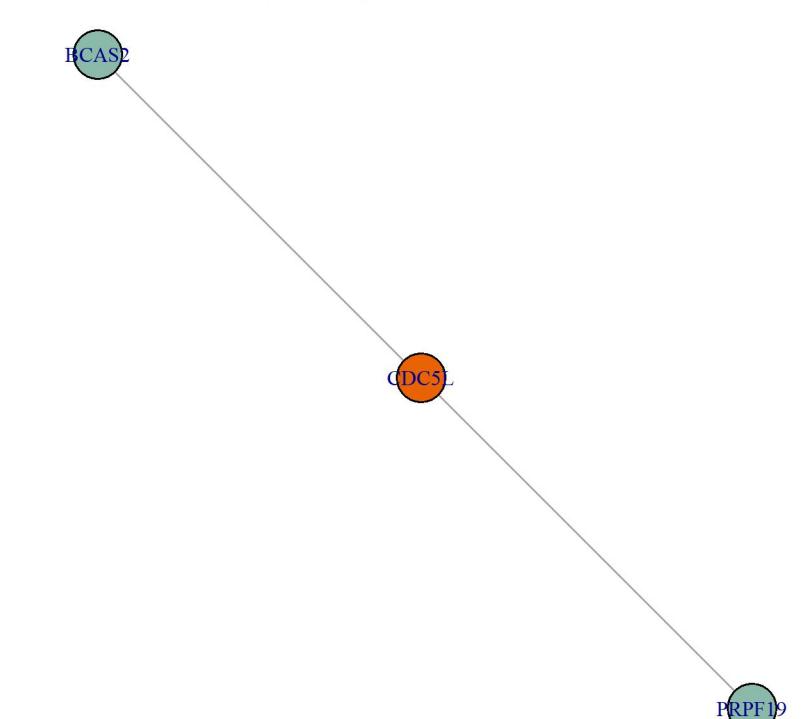
CDC5L network, DB1, all Pearson r &gt; 0.85



CDC5L network, DB1, all Pearson r &gt; 0.8

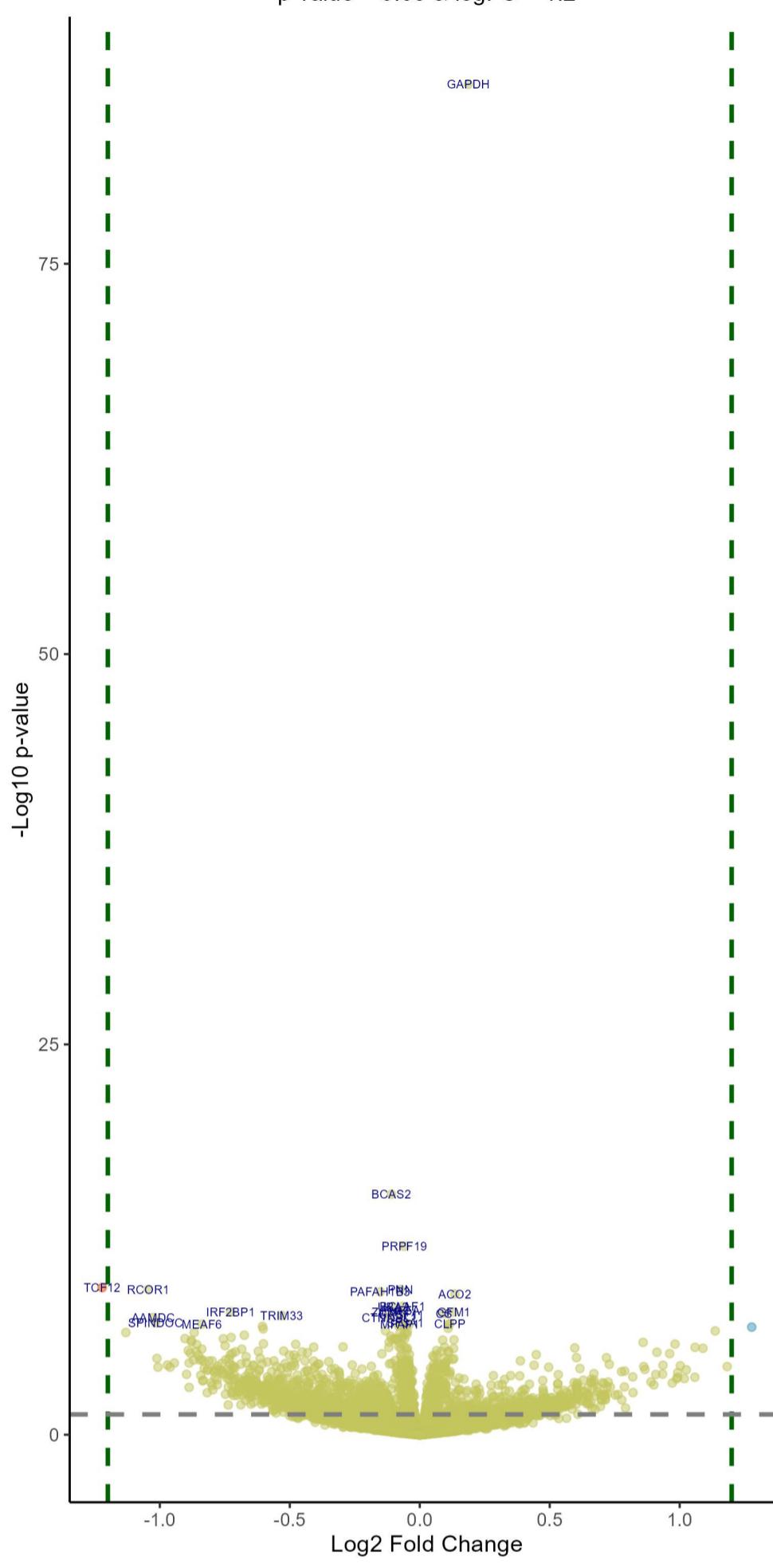


CDC5L network, DB1, all Pearson r &gt; 0.75



Sorted by p values!

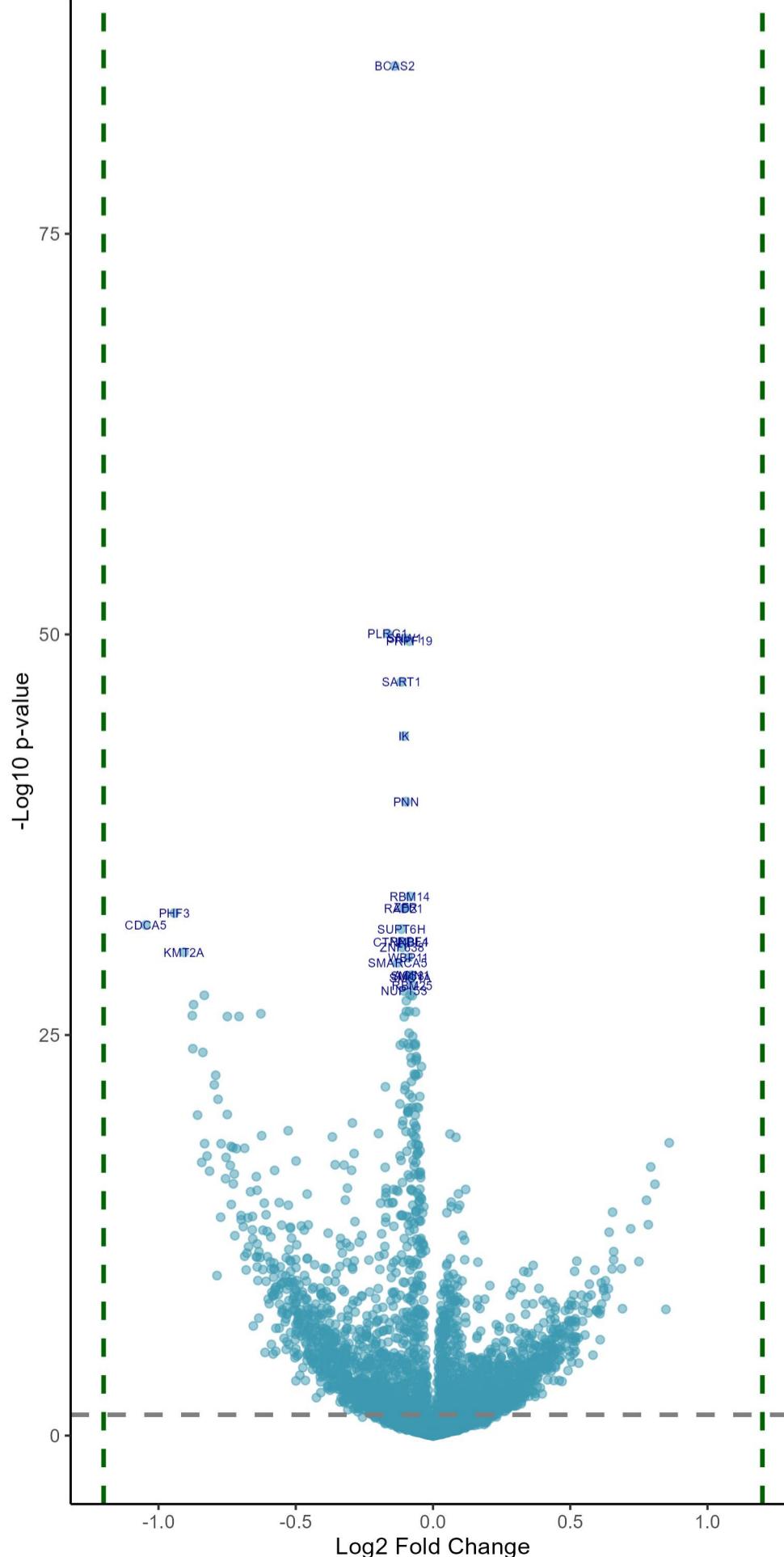
Downregulated in blood cancers at low/absent CDC5L Upregulated in blood cancers at low/absent CDC5L



| logFC | adj.P.Val | symbol   | name  | logFC | adj.P.Val | symbol  | name  |
|-------|-----------|----------|---|-------|-----------|---------|---|
| -0.11 | 8.83e-13  | BCAS2    | BCAS2 pre-mRNA processing factor  | 0.19  | 2.09e-83  | GAPDH   | glyceraldehyde-3-phosphate dehydrogenase              |
| -0.06 | 1.41e-09  | PRPF19   | pre-mRNA processing factor 19   | 0.14  | 7.22e-07  | ACO2    | aconitase 2   |
| -1.22 | 4.70e-07  | TCF12    | transcription factor 12   | 0.13  | 6.20e-06  | GFM1    | G elongation factor mitochondrial 1                   |
| -1.04 | 4.70e-07  | RCOR1    | REST corepressor 1  | 0.09  | 7.26e-06  | CS      | citrate synthase                                      |
| -0.07 | 4.70e-07  | PN       | pinin, desmosome associated protein                                     | 0.12  | 2.21e-05  | CLPP    | caseinolytic mitochondrial matrix protein p           |
| -0.15 | 5.75e-07  | PAFAH1B3 | platelet activating factor acetylhydrolase                              | 0.11  | 2.21e-05  | ATP5F1C | ATP synthase F1 subunit gamma                         |
| -0.07 | 3.83e-06  | BCLAF1   | BCL2 associated transcription factor 1                                  | 1.28  | 2.75e-05  | SAR1B   | secretion associated Ras related GTPase               |
| -0.1  | 3.83e-06  | UBA2     | ubiquitin like modifier activating enzyme                               | 0.11  | 3.16e-05  | ATP5PB  | ATP synthase peripheral stalk-membrane                |
| -0.07 | 6.20e-06  | PHF5A    | PHD finger protein 5A   | 1.14  | 4.26e-05  | SAMHD1  | SAM and HD domain containing deoxynucleoside kinase   |
| -0.73 | 6.20e-06  | IRF2BP1  | interferon regulatory factor 2 bind                                     | 0.13  | 1.02e-04  | UGGT1   | UDP-glucose glycoprotein glucosyltransferase          |
| -0.11 | 6.20e-06  | ZC3H4    | zinc finger CCCH-type containing 4                                      | 0.09  | 1.03e-04  | PHB2    | prohibitin 2  |
| -0.07 | 7.61e-06  | SRSF11   | serine and arginine rich splicing factor 11                             | 0.86  | 1.35e-04  | EML2    | EMAP like 2   |
| -0.53 | 8.59e-06  | TRIM33   | tripartite motif containing 33  | 0.98  | 1.65e-04  | FAS     | Fas cell surface death receptor                       |
| -1.03 | 1.08e-05  | AAMDC    | adipogenesis associated Mfh938 domain containing                        | 0.1   | 2.31e-04  | AIFM1   | apoptosis inducing factor mitochondria                |
| -0.12 | 1.08e-05  | CTNNBL1  | catenin beta like 1   | 1.06  | 2.32e-04  | ITGB7   | integrin subunit beta 7                               |
| -0.06 | 2.06e-05  | SF3A1    | splicing factor 3a subunit 1  | 0.6   | 2.48e-04  | SLAMF7  | SLAM family member 7                                  |
| -1.02 | 2.06e-05  | SPINDOC  | spindlin interactor and repressor o                                     | 1.09  | 2.55e-04  | SYNGR2  | synaptogyrin 2  |
| -0.84 | 2.21e-05  | MEAF6    | MYST/Esa1 associated factor 6   | 0.13  | 2.56e-04  | LMAN2   | lectin, mannose binding 2                             |
| -0.08 | 2.21e-05  | MFAP1    | microfibril associated protein 1  | 0.06  | 3.25e-04  | ATP5PO  | ATP synthase peripheral stalk subunit                 |
| -0.04 | 2.21e-05  | SRSF3    | serine and arginine rich splicing factor                                | 0.11  | 3.50e-04  | TMED10  | transmembrane p24 trafficking protein                 |
| -0.08 | 2.52e-05  | SAE1     | SUMO1 activating enzyme subunit 1                                       | 0.08  | 3.50e-04  | TMED9   | transmembrane p24 trafficking protein                 |
| -0.61 | 2.60e-05  | CHRAC1   | chromatin accessibility complex subunit                                 | 0.11  | 3.57e-04  | NDUFA6  | NADH:ubiquinone oxidoreductase subunit                |
| -0.06 | 2.68e-05  | SF3B6    | splicing factor 3b subunit 6  | 0.91  | 3.77e-04  | IFI30   | IFI30 lysosomal thiol reductase                       |
| -0.6  | 3.33e-05  | ITGA2B   | integrin subunit alpha 2b   | 0.96  | 4.43e-04  | ACSL1   | acyl-CoA synthetase long chain family member 1        |
| -0.13 | 4.26e-05  | NUMA1    | nuclear mitotic apparatus protein 1                                     | 0.07  | 4.82e-04  | COPB2   | COPI coat complex subunit beta 2                      |
| -0.05 | 4.56e-05  | SAP18    | Sin3A associated protein 18   | 0.45  | 4.94e-04  | SEC11C  | SEC11 homolog C, signal peptidase complex             |
| -1.13 | 4.90e-05  | LEF1     | lymphoid enhancer binding factor 1                                      | 0.05  | 5.51e-04  | RPS3    | ribosomal protein S3                                  |
| -0.87 | 4.90e-05  | CKAP2    | cytoskeleton associated protein 2                                       | 0.06  | 6.60e-04  | ATP5F1A | ATP synthase F1 subunit alpha                         |
| -0.06 | 4.90e-05  | ACIN1    | apoptotic chromatin condensation in                                     | 0.6   | 6.96e-04  | EBI3    | Epstein-Barr virus induced 3                          |
| -0.08 | 4.98e-05  | LUC7L3   | LUC7 like 3 pre-mRNA splicing factor                                    | 0.72  | 7.00e-04  | FCER2   | Fc epsilon receptor II                                |
| -0.05 | 5.90e-05  | SRRT     | serrate, RNA effector molecule  | 0.09  | 7.38e-04  | GPI     | glucose-6-phosphate isomerase                         |
| -0.68 | 6.64e-05  | RNF214   | ring finger protein 214   | 0.13  | 7.74e-04  | ME2     | malic enzyme 2  |
| -0.07 | 7.34e-05  | MCM3     | minichromosome maintenance complex subunit                              | 0.13  | 8.32e-04  | SRPRB   | SRP receptor subunit beta                             |
| -0.11 | 7.34e-05  | RBBP4    | RB binding protein 4, chromatin remodelling                             | 0.11  | 8.76e-04  | PDIA4   | protein disulfide isomerase family                    |
| -0.73 | 8.68e-05  | TAF4     | TATA-box binding protein associated                                     | 0.39  | 9.36e-04  | GSTK1   | glutathione S-transferase kappa 1                     |
| -0.07 | 9.47e-05  | CHERP    | calcium homeostasis endoplasmic reticulum                               | 0.1   | 1.09e-03  | ATP1A1  | ATPase Na+/K+ transporting subunit                    |
| -0.9  | 9.47e-05  | FOXP1    | forkhead box P1   | 0.1   | 1.25e-03  | ERP44   | endoplasmic reticulum protein 44                      |
| -0.1  | 9.47e-05  | SMARCE1  | SWI/SNF related, matrix associated, chromatin condensin complex subunit | 0.07  | 1.25e-03  | SND1    | staphylococcal nuclease and tudor domain containing 1 |
| 0.76  | 0.17e-05  | ARID2    | enhancer of zeste domain interacting protein 2                          | 0.08  | 1.25e-03  | TPRDP1  | TENR receptor associated protein 1                    |

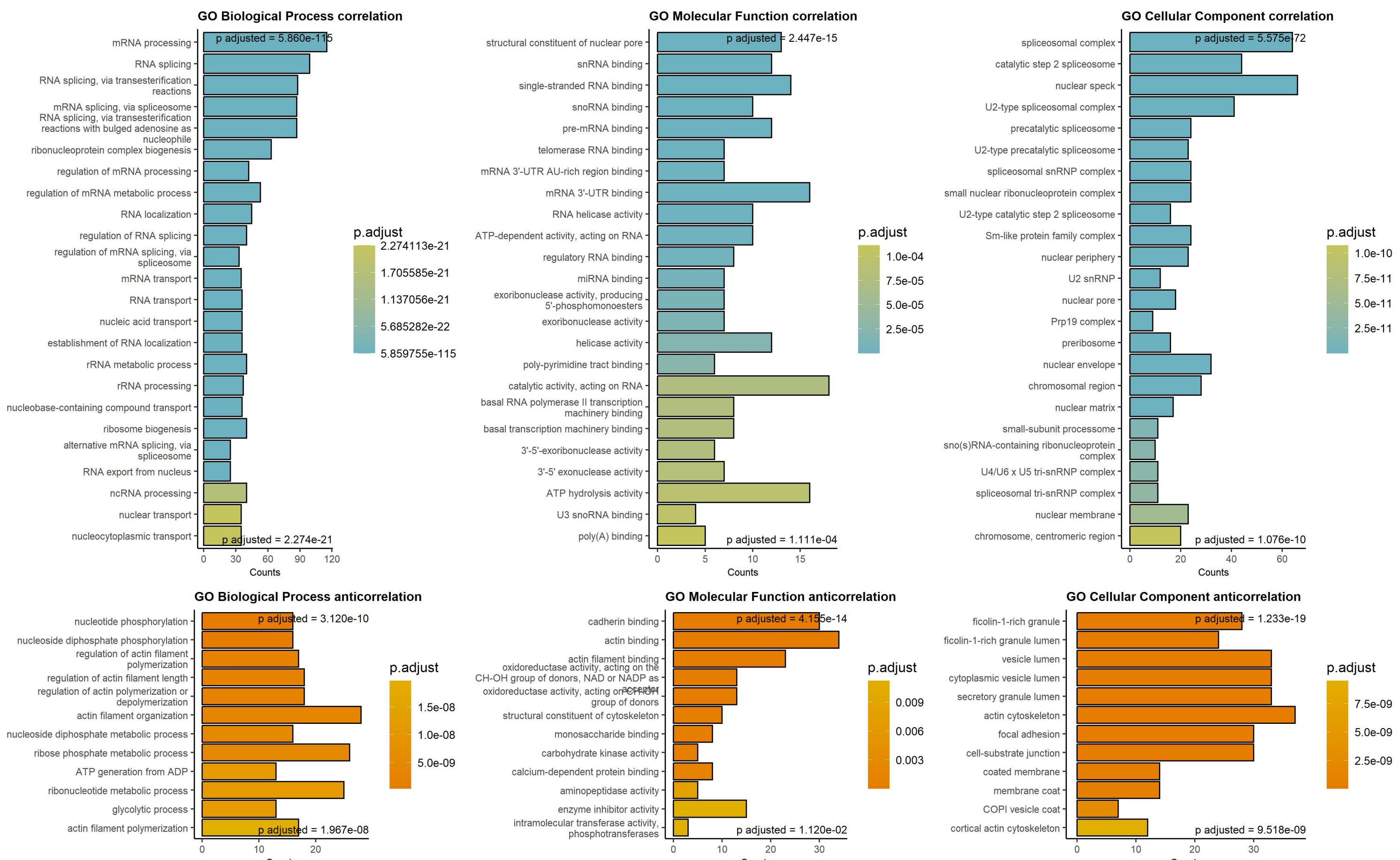
Sorted by p values!

Downregulated in solid cancers at low/absent CDC5L Upregulated in solid cancers at low/absent CDC5L

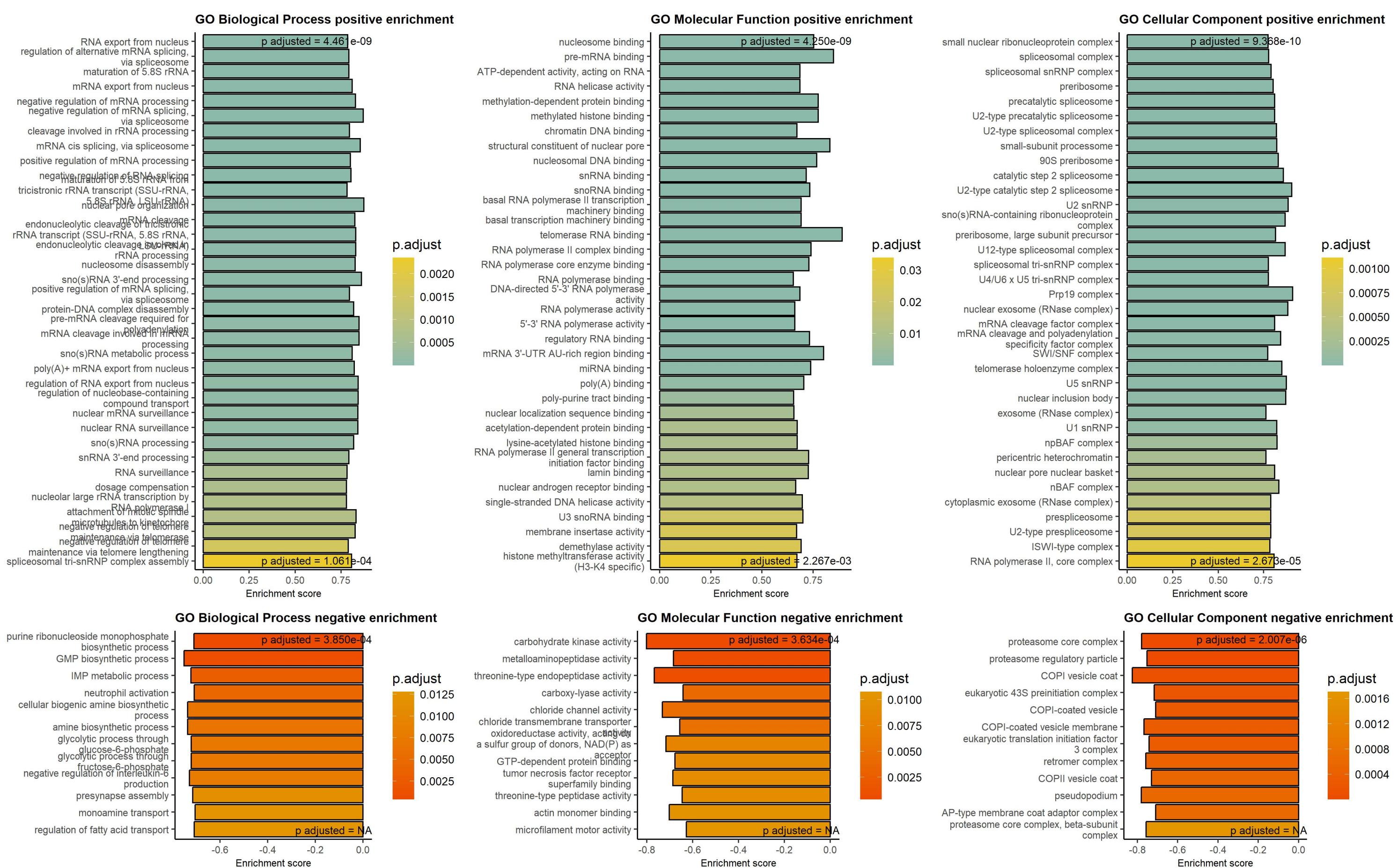


| logFC | adj.P.Val | symbol  | name  | logFC | adj.P.Val | symbol   | name  |
|-------|-----------|---------|---|-------|-----------|----------|---|
| -0.14 | 1.12e-82  | BCAS2   | BCAS2 pre-mRNA processing factor  | 0.06  | 1.09e-17  | SND1     | staphylococcal nuclease and tudor domain containing 1 |
| -0.17 | 1.99e-47  | PLRG1   | pleiotropic regulator 1   | 0.08  | 1.66e-17  | PKM2     | pyruvate kinase M1/2                                  |
| -0.1  | 2.92e-47  | SNW1    | SNW domain containing 1   | 0.86  | 3.64e-17  | RPS27L   | ribosomal protein S27 like                            |
| -0.09 | 3.48e-47  | PRPF19  | pre-mRNA processing factor 19   | 0.79  | 8.96e-16  | PARP4    | poly(ADP-ribose) polymerase family                    |
| -0.11 | 1.00e-44  | SART1   | spliceosome associated factor 1, repressor                              | 0.81  | 9.45e-15  | GALE     | UDP-galactose-4-epimerase                             |
| -0.11 | 2.11e-41  | IK      | IK cytokine   | 0.12  | 1.93e-14  | TKT      | transketolase   |
| -0.1  | 2.28e-37  | PNN     | pinin, desmosome associated protein                                     | 0.09  | 3.40e-14  | ALDOA    | aldolase, fructose-bisphosphate A                     |
| -0.08 | 1.65e-31  | RBM14   | RNA binding motif protein 14  | 0.78  | 8.13e-14  | PMM2     | phosphomannomutase 2                                  |
| -0.1  | 7.49e-31  | ZFR     | zinc finger RNA binding protein   | 0.07  | 1.04e-13  | ARPC4    | actin related protein 2/3 complex subunit             |
| -0.11 | 7.52e-31  | RAD21   | RAD21 cohesin complex component   | 0.1   | 1.55e-13  | IQGAP1   | IQ motif containing GTPase activating protein         |
| -0.94 | 1.36e-30  | PHF3    | PHD finger protein 3  | 0.07  | 1.88e-13  | COPA     | COPII coat complex subunit alpha                      |
| -1.05 | 6.98e-30  | CDCA5   | cell division cycle associated 5  | 0.09  | 2.55e-13  | MYL6     | myosin light chain 6                                  |
| -0.12 | 1.17e-29  | SUPT6H  | SPT6 homolog, histone chaperone and nucleophosmin                       | 0.65  | 4.01e-13  | GMPPA    | GDP-mannose pyrophosphorylase A                       |
| -0.09 | 6.44e-29  | PRPF4   | pre-mRNA processing factor 4  | 0.05  | 4.35e-13  | CLTC     | clathrin heavy chain                                  |
| -0.12 | 6.48e-29  | CTNNBL1 | catenin beta like 1   | 0.78  | 2.17e-12  | FAM114A1 | family with sequence similarity 114                   |
| -0.11 | 1.32e-28  | ZNF638  | zinc finger protein 638   | 0.72  | 3.77e-12  | GYS1     | glycogen synthase 1                                   |
| -0.91 | 2.53e-28  | KMT2A   | lysine methyltransferase 2A   | 0.64  | 5.96e-12  | BLVRB    | biliverdin reductase B                                |
| -0.09 | 5.27e-28  | WBP11   | WW domain binding protein 11  | 0.11  | 9.24e-12  | ACTN4    | actinin alpha 4                                       |
| -0.13 | 1.03e-27  | SMARCA5 | SWI/SNF related, matrix associated, chromatin condensin complex subunit | 0.12  | 1.74e-11  | WDR1     | WD repeat domain 1                                    |
| -0.08 | 5.86e-27  | ACIN1   | apoptotic chromatin condensation in                                     | 0.66  | 8.41e-11  | TCIRG1   | T cell immune regulator 1, ATPase H                   |
| -0.09 | 5.93e-27  | SMC3    | structural maintenance of chromosomes 3                                 | 0.06  | 2.21e-10  | TPM3     | tropomyosin 3   |
| -0.08 | 8.08e-27  | SMC1A   | structural maintenance of chromosomes 1A                                | 0.66  | 2.51e-10  | RPS6KA3  | ribosomal protein S6 kinase A3                        |
| -0.08 | 2.23e-26  | RBM25   | RNA binding motif protein 25  | 0.12  | 2.53e-10  | CTSD     | cathepsin D   |
| -0.11 | 4.76e-26  | NUP153  | nucleoporin 153   | 0.52  | 2.98e-10  | STAT6    | signal transducer and activator of transcription 6    |
| -0.08 | 8.04e-26  | SRSF10  | serine and arginine rich splicing factor                                | 0.75  | 3.15e-10  | GBE1     | 1,4-alpha-glucan branching enzyme 1                   |
| -0.83 | 8.21e-26  | EHMT2   | euchromatic histone lysine methyltransferase 2                          | 0.16  | 3.41e-10  | CSTB     | cystatin B  |
| -0.08 | 8.46e-26  | BCLAF1  | BCL2 associated transcription factor                                    | 0.05  | 4.16e-10  | GAPDH    | glyceraldehyde-3-phosphate dehydrogenase              |
| -0.1  | 1.66e-25  | CDC73   | cell division cycle 73  | 0.36  | 5.28e-10  | SEC23A   | SEC23 homolog A, COPII coat complex                   |
| -0.87 | 2.80e-25  | INCENP  | inner centromere protein  | 0.05  | 5.56e-10  | PSMB1    |   |

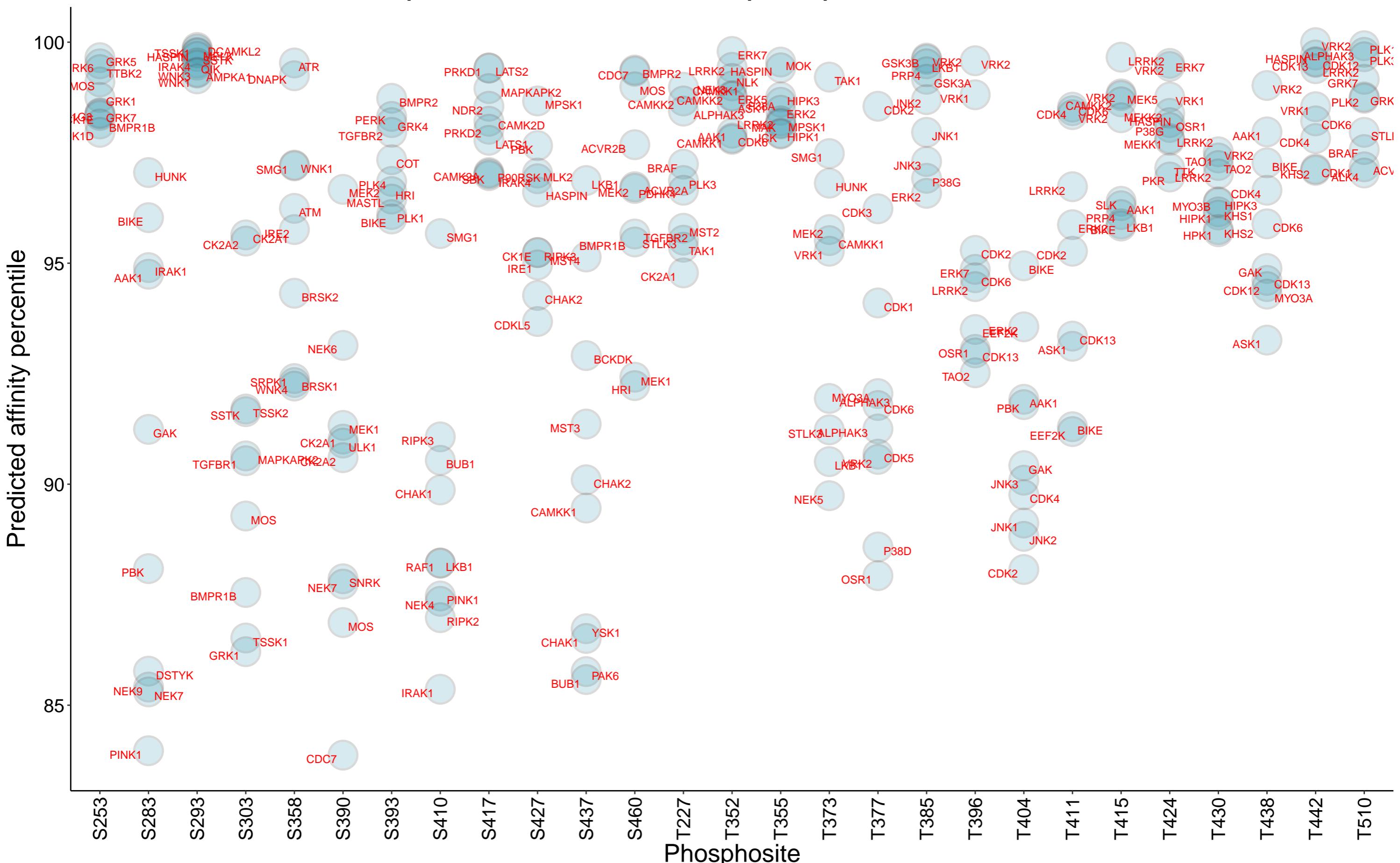
# Top 250 correlation coefficients overrepresentation, CDC5L protein, DB1



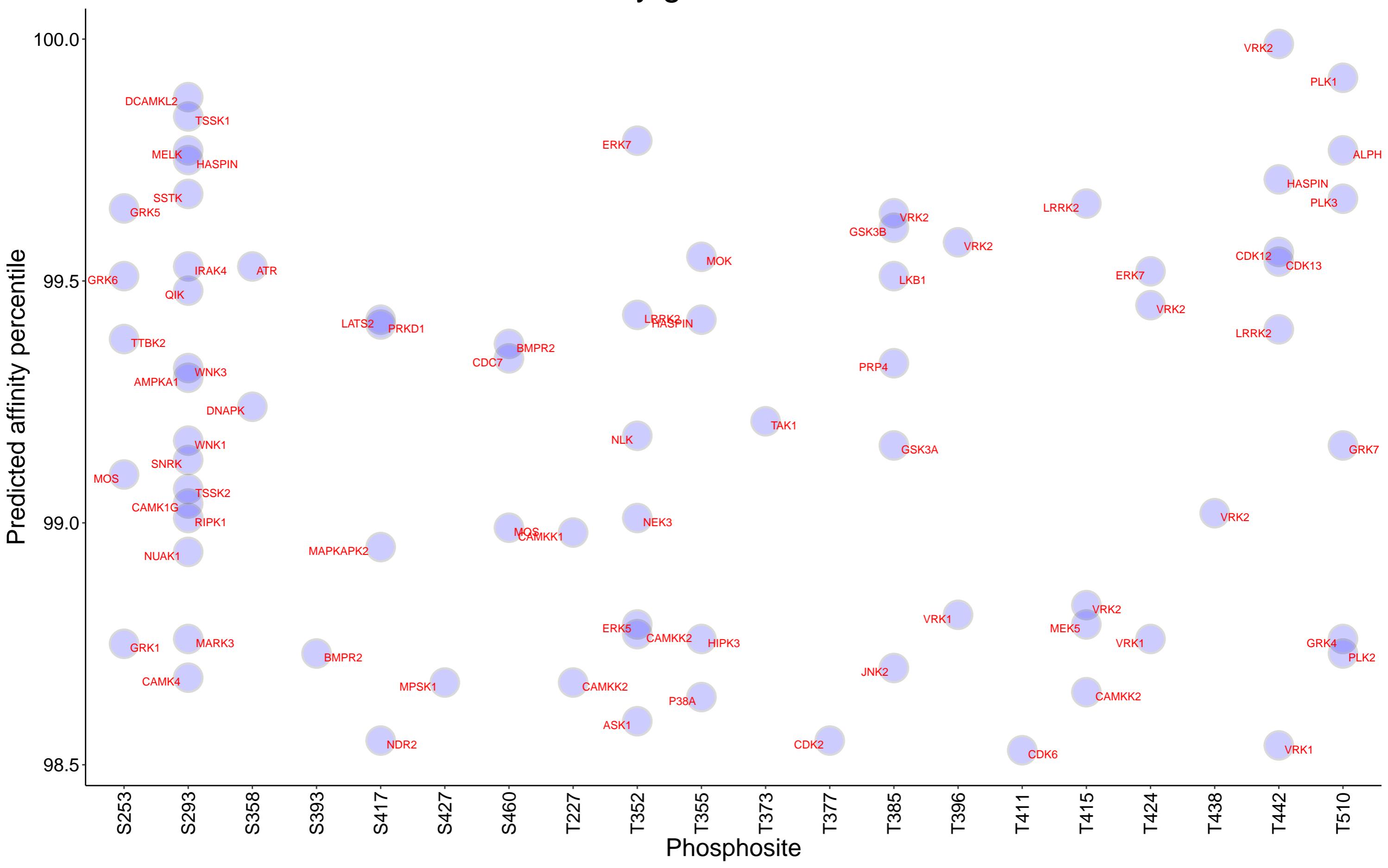
## Gene Set Enrichment analysis on protein correlation coefficients, CDC5L protein, DB1



# Top 10 kinases for each phosphosite in CDC5L



Kinases with affinity greater than 98.5% to CDC5L



# Top 15 positive correlation coefficients for CDC5L protein by tissue, DB1

Beware of false positives in tissues with small number of samples

