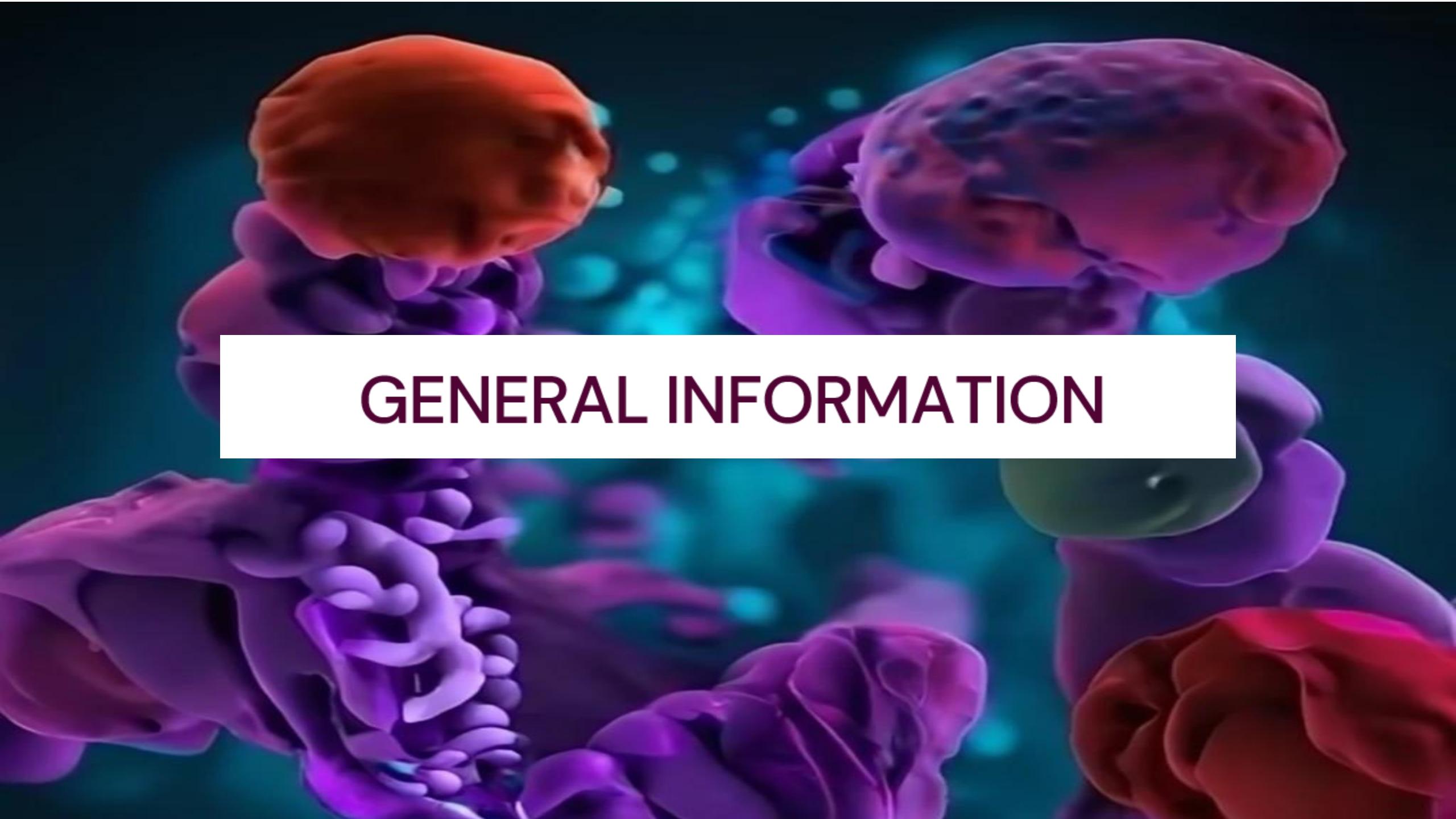


A landscape of protein profiles in a DepMap database

Viktoriia Tsuber, PhD



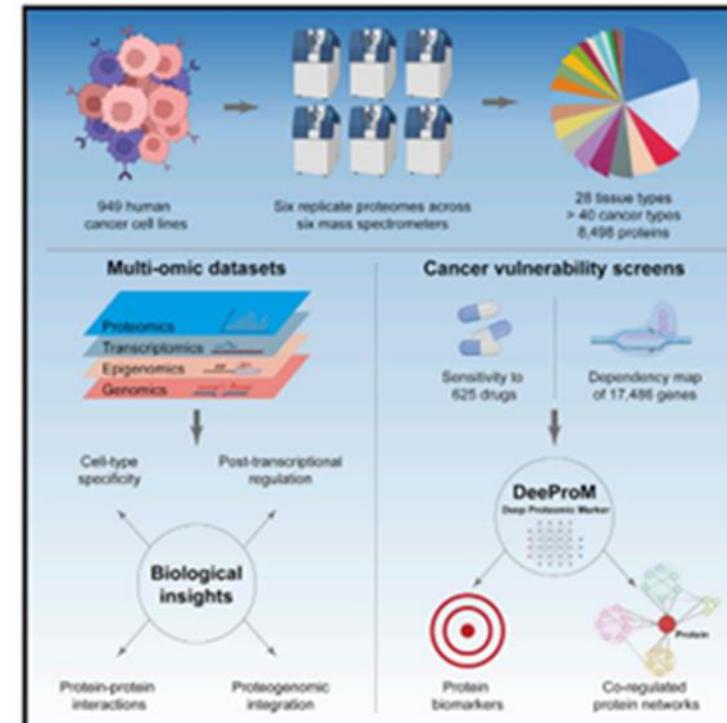
GENERAL INFORMATION

- 949 cancer cell lines
- 8498 proteins
- of these, 6692 proteins with more than one supporting peptide
- 28 tissue types
- 40 cancer types
- DIA-MS (data-independent acquisition mass spectrometry)
- high throughput
- DIA-NN data processing
- Origin: Wellcome Sanger Institute

Cancer Cell

Pan-cancer proteomic map of 949 human cell lines

Graphical abstract



Authors

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Rebecca C. Poulos, Zhaoxiang Cai, ...,
Qing Zhong, Mathew J. Garnett,
Roger R. Reddel

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qzhong@cmri.org.au (Q.Z.),
mg12@sanger.ac.uk (M.J.G.),
rreddel@cmri.org.au (R.R.R.)

In brief

Gonçalves et al. generate a comprehensive proteomic map of 949 human cancer cell lines across more than 40 cancer types. Proteomic data are integrated with multi-omic, drug response, and CRISPR-Cas9 gene essentiality datasets. Deep learning is used to identify biomarkers of cancer vulnerabilities, providing evidence for highly connected protein networks.

Highlights

- Pan-cancer proteomic map of 949 human cancer cell lines across over 40 cancer types
- There are 8,498 proteins with evidence of cell types and broad post-transcriptional regulation

BLM

Protein name: BLM ; UNIPROT: P54132 ; Gene name: BLM RecQ like helicase
Ligandable: Yes ; Ligandable_by_Chem: Yes ; Is_enzyme: Yes (<https://cansar.ai/>)

BABAM1

Protein name: BABA1 ; UNIPROT: Q9NWV8 ; Gene name: BRISC and BRCA1 A complex member 1
Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

BRCA2

Protein name: BRCA2 ; UNIPROT: P51587 ; Gene name: BRCA2 DNA repair associated
Ligandable: NA ; Ligandable_by_Chem: Yes ; Is_enzyme: NA (<https://cansar.ai/>)

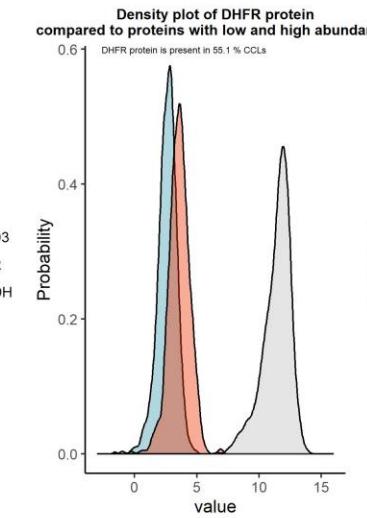
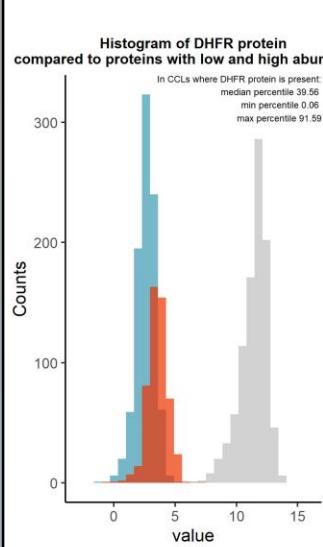
ANLN

Protein name: ANLN ; UNIPROT: Q9NQW6 ; Gene name: anillin actin binding protein
Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

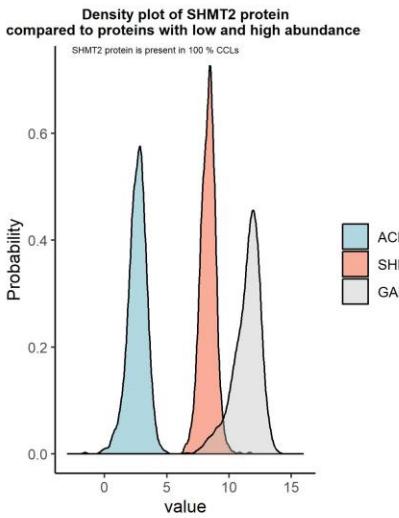
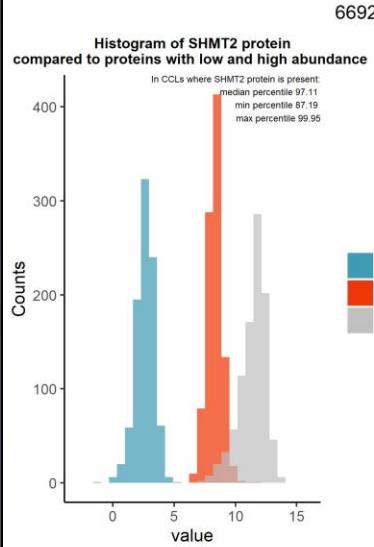
AURKAIP1

Protein name: AKIP ; UNIPROT: Q9NWT8 ; Gene name: aurora kinase A interacting protein 1
Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

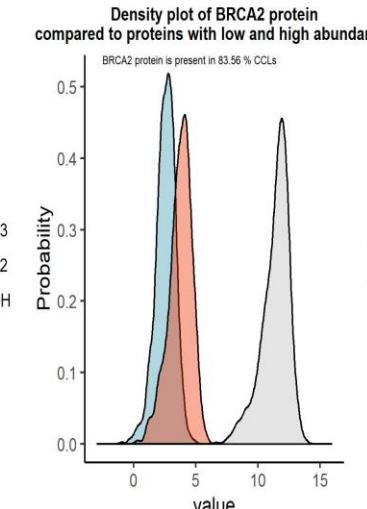
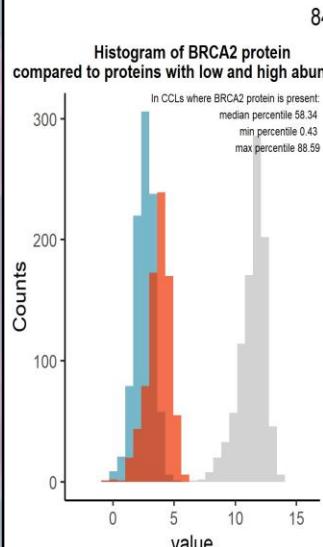
Sanger Institute Protein Database 1 (DB1), protein presence is certain



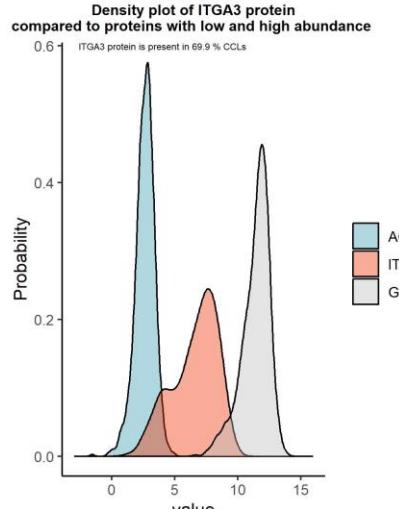
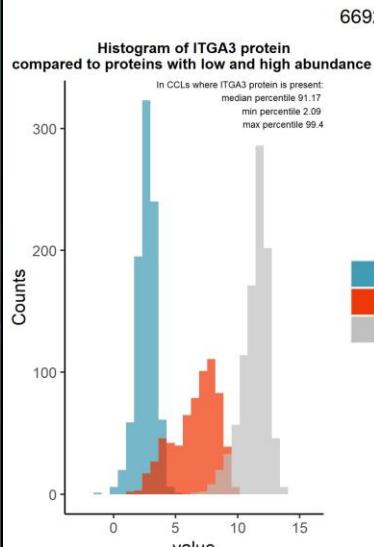
Sanger Institute Protein Database 1 (DB1), protein presence is certain

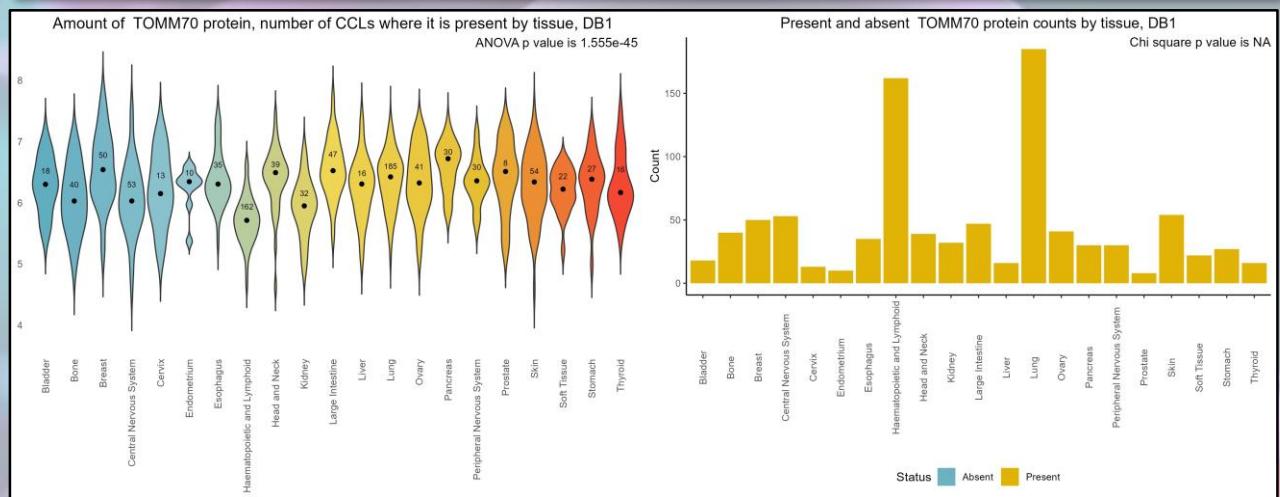
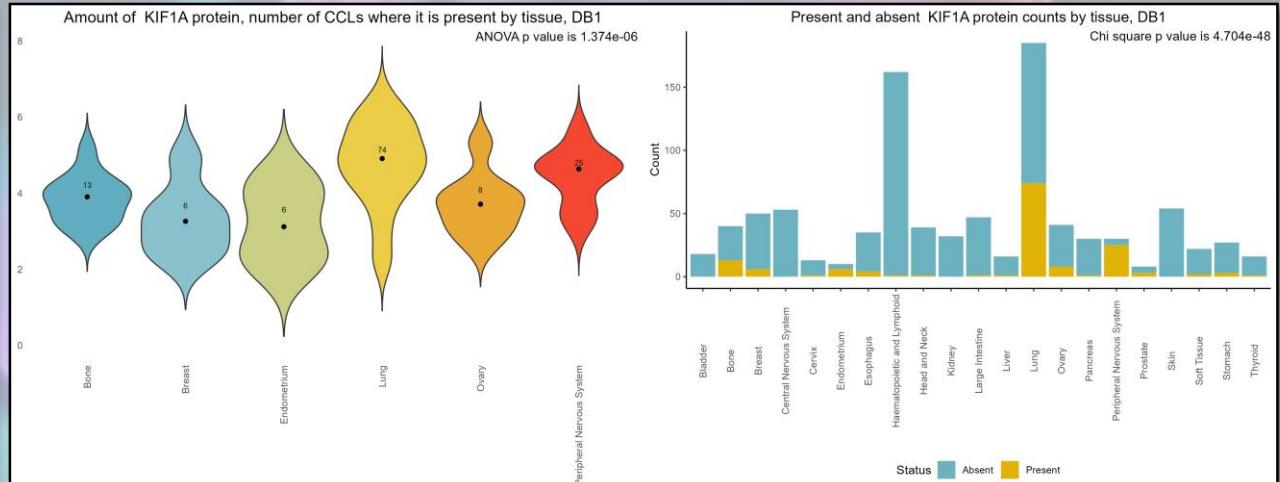
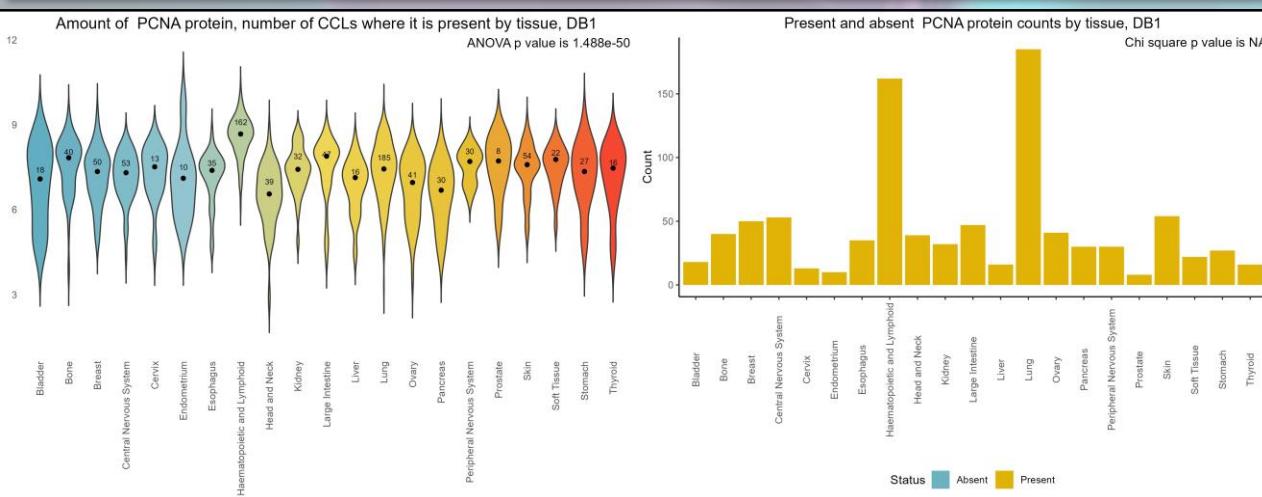
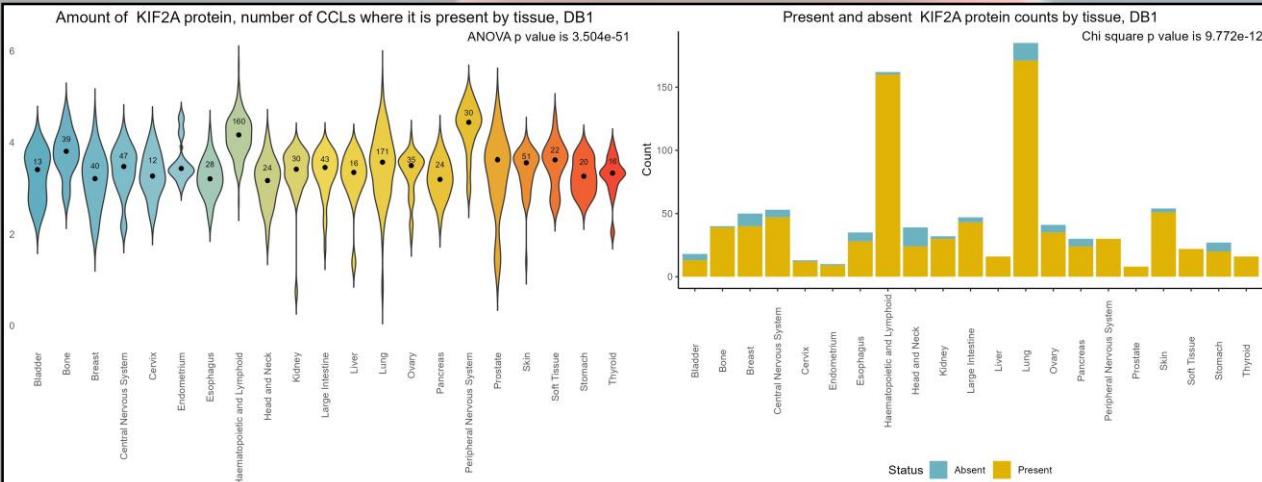


Sanger Institute Protein Database 2 (DB2), protein presence is less certain



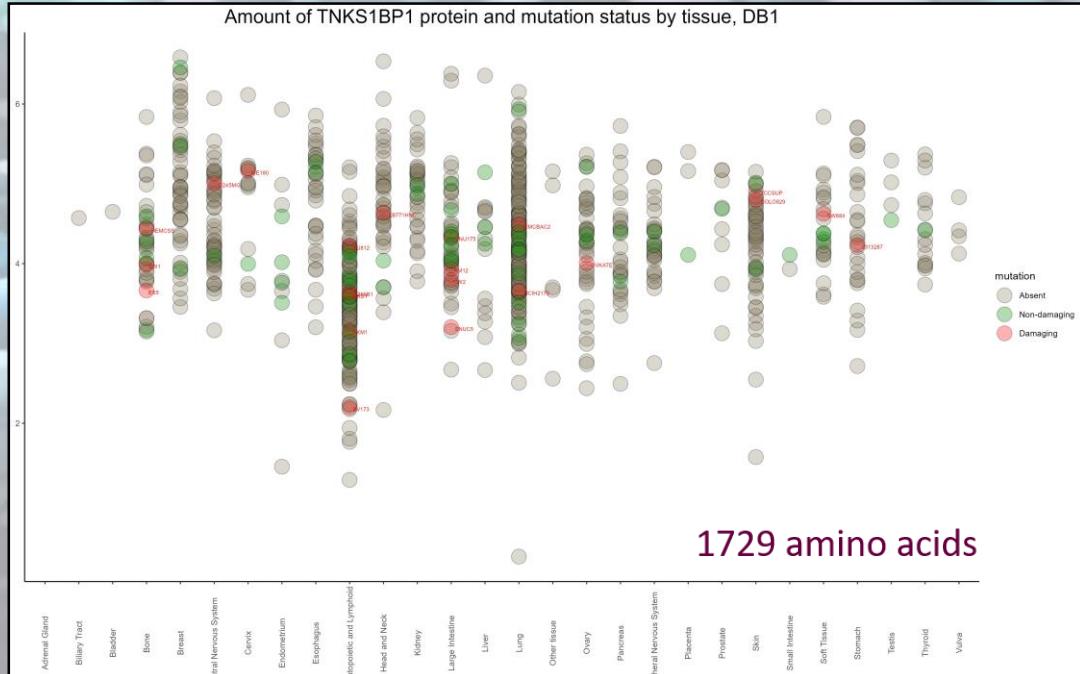
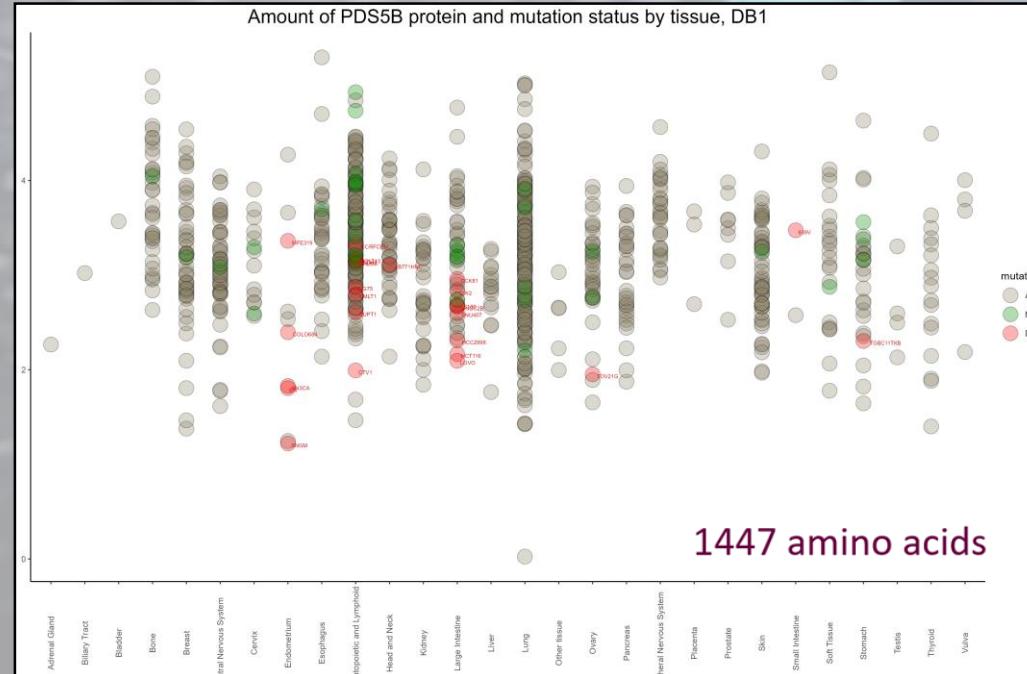
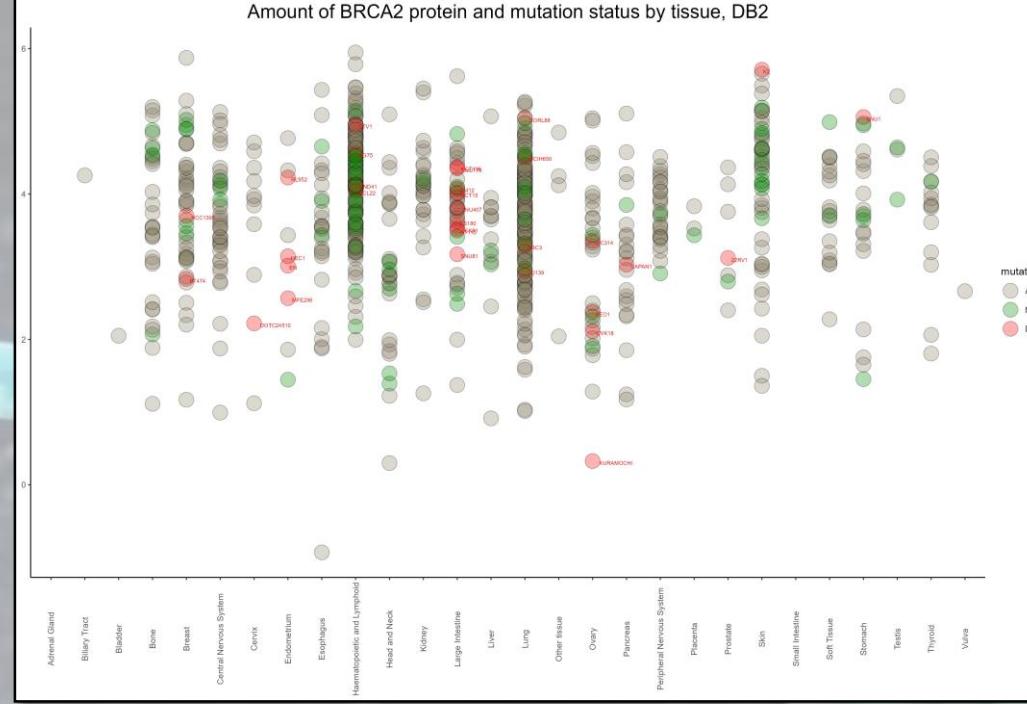
Sanger Institute Protein Database 1 (DB1), protein presence is certain

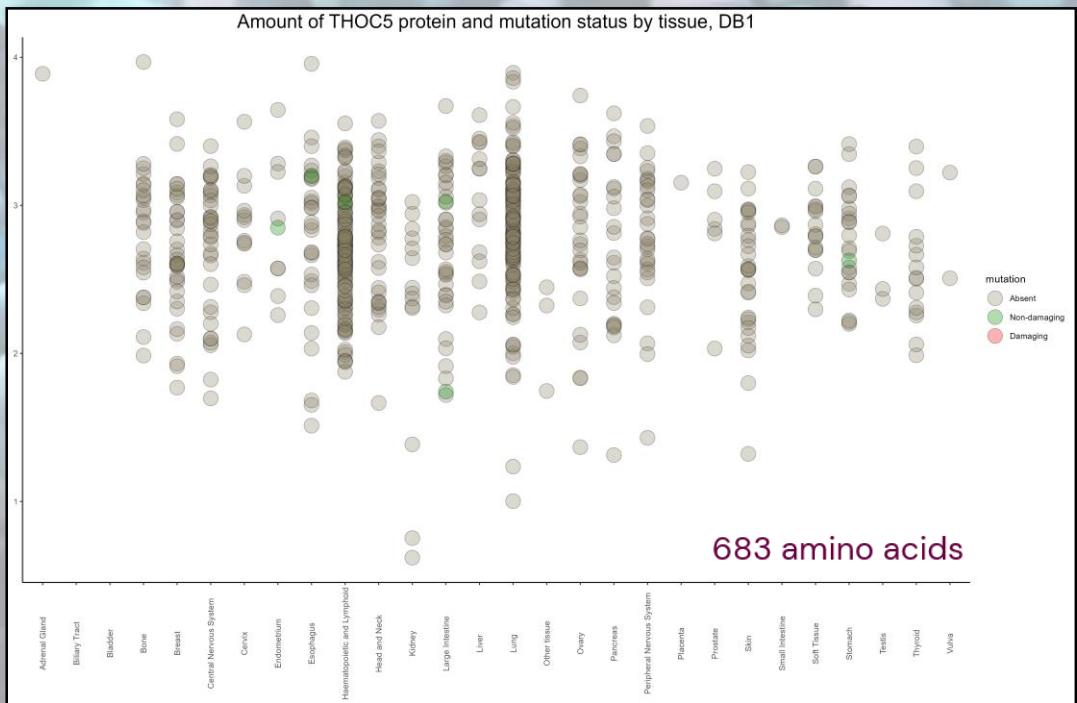
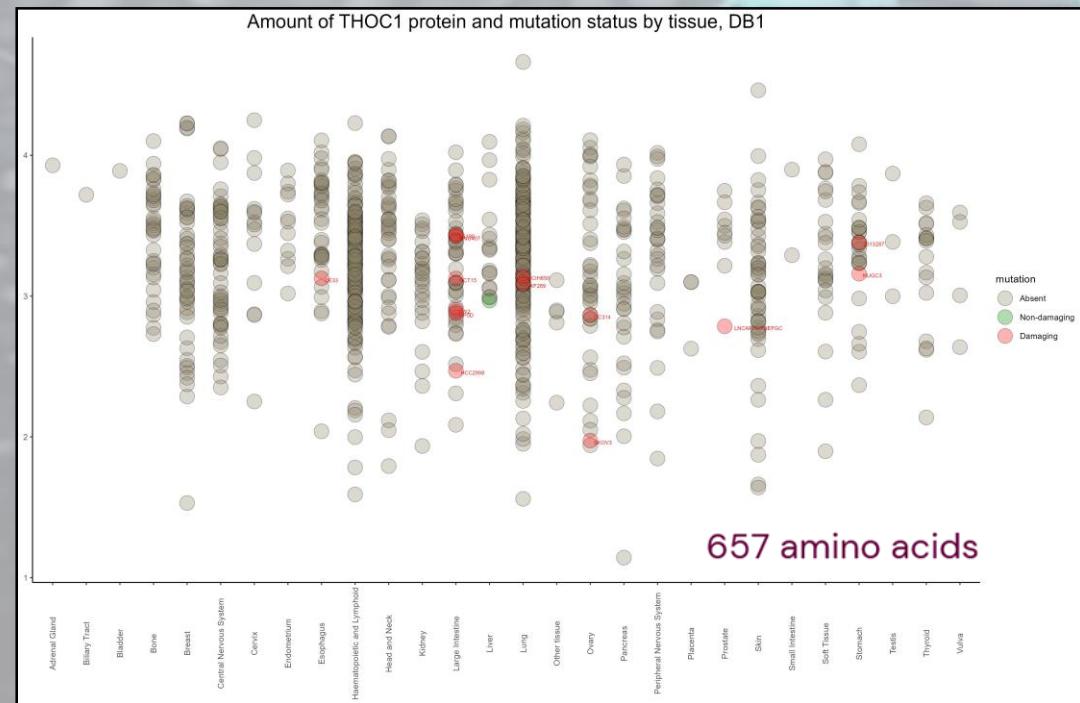
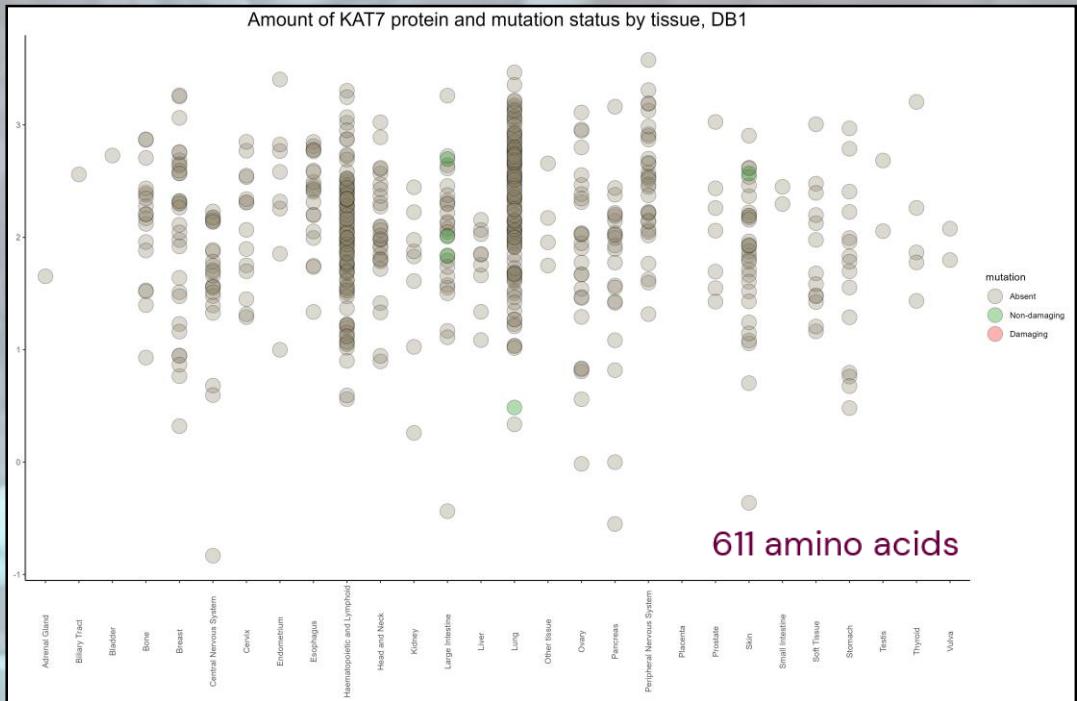
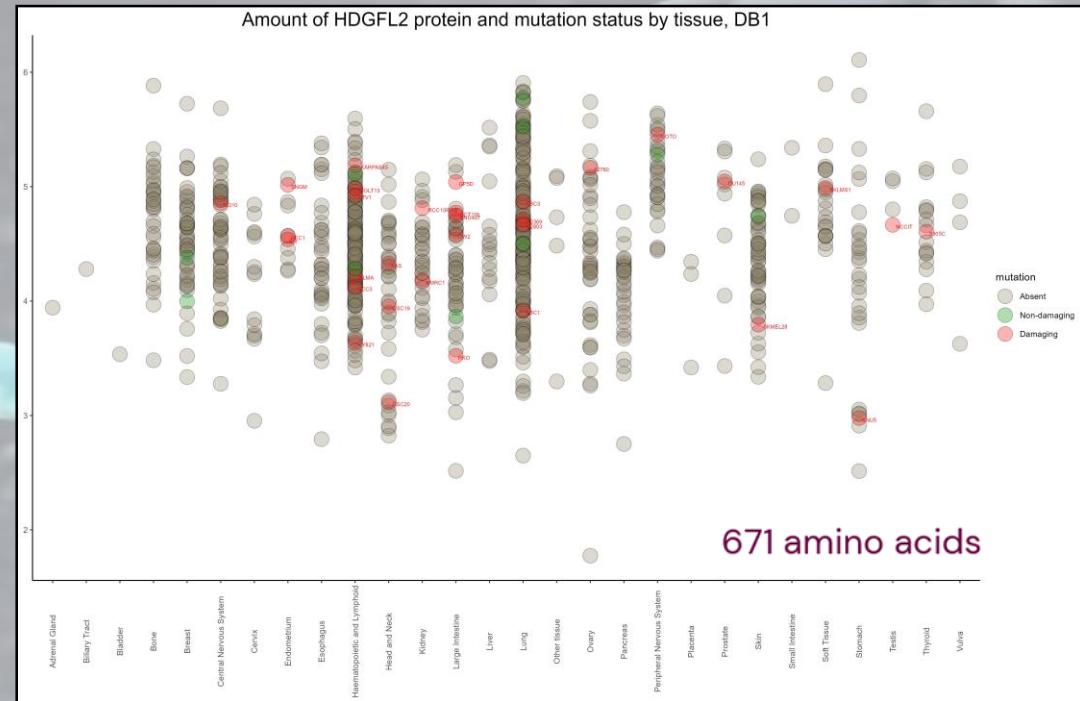






MUTATIONS







KINASES

- 303 Ser/Thr kinases
- 90000 phosphosites
- large MS phosphoproteomic datasets
- combinatorial peptide library that systematically substitutes each amino acid at nine positions surrounding a central phosphoacceptor

Article

An atlas of substrate specificities for the human serine/threonine kinase

<https://doi.org/10.1038/s41586-022-05575-3>

Received: 1 May 2022

Accepted: 17 November 2022

Published online: 11 January 2023

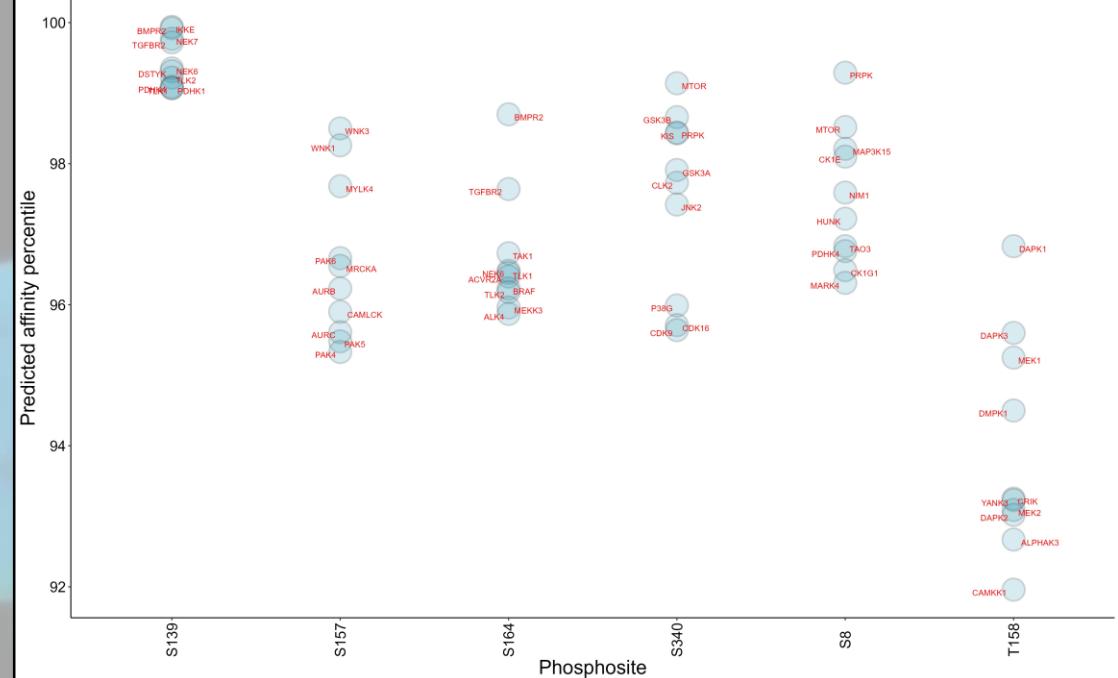
Open access

 Check for updates

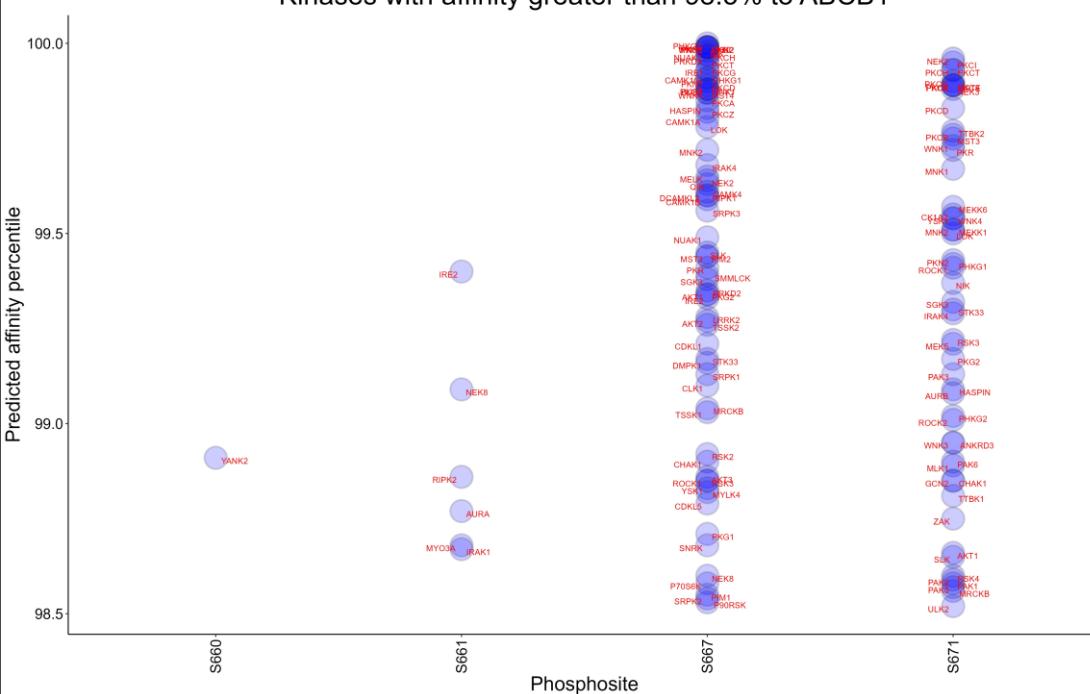
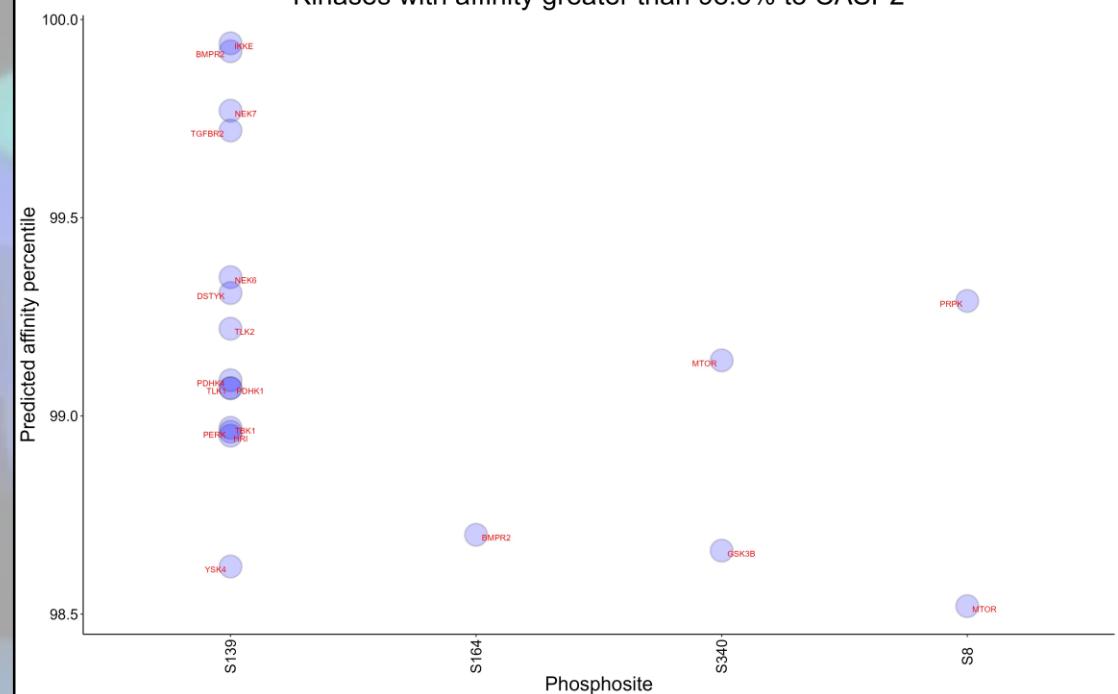
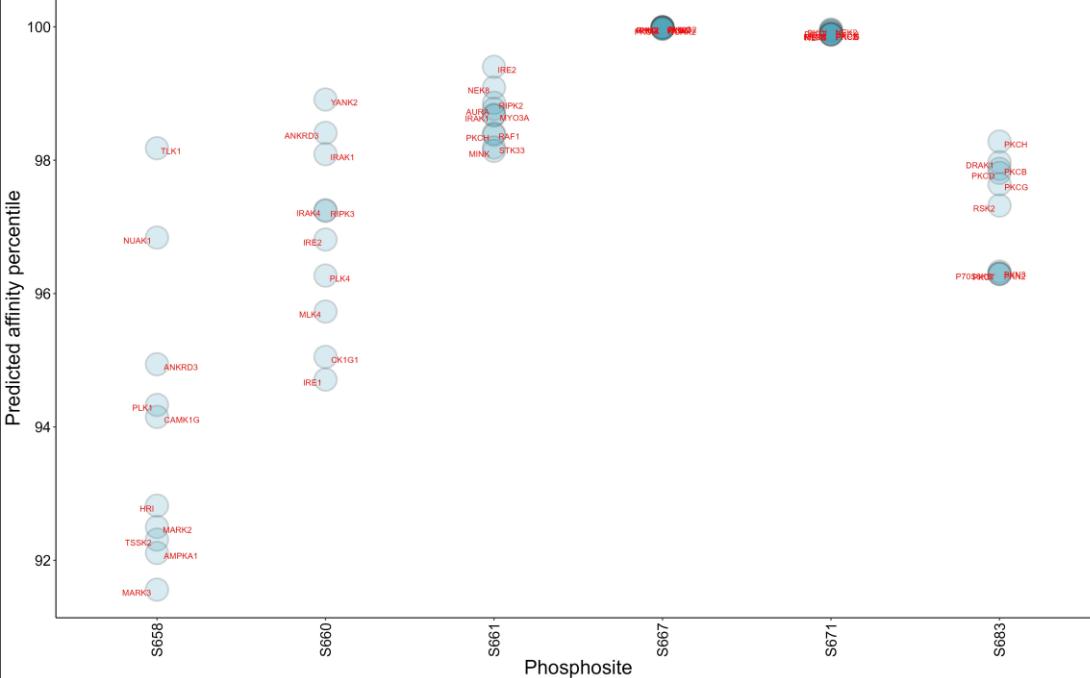
Jared L. Johnson^{1,2,28}, Tomer M. Yaron^{1,2,3,4,5,28}, Emily M. Huntsman^{1,2}, Alexander Kerelsky^{1,2,3}, Junho Song^{1,2}, Amit Regev^{1,2}, Ting-Yu Lin^{1,2,6}, Katarina Liberatore^{1,2}, Daniel M. Cizin^{1,2}, Benjamin M. Cohen^{1,2}, Neil Vasan^{7,8}, Yilun Ma^{1,2}, Konstantin Krismer^{9,10}, Jaylissa Torres Robles^{1,12}, Bert van de Kooij¹⁰, Anne E. van Vlimmeren¹⁰, Nicole Andréa-Busch¹³, Norbert F. Käufer¹³, Maxim V. Dorovkov¹⁴, Alexey G. Ryazanov¹⁴, Yuichiro Takagi¹⁵, Edward R. Kastenhuber¹², Marcus D. Goncalves^{1,16}, Benjamin D. Hopkins¹⁷, Olivier Elemento^{3,4}, Dylan J. Taatjes¹⁸, Alexandre Maucuer¹⁹, Akio Yamashita²⁰, Alexei Degterev²¹, Mohamed Uduman²², Jingyi Lu²², Sean D. Landry²², Bin Zhang²², Ian Cossentino²², Rune Linding²³, John Blenis^{1,24,25}, Peter V. Hornbeck²², Benjamin E. Turk^{11,22}, Michael B. Yaffe^{10,26,27,28} & Lewis C. Cantley^{1,2,22}

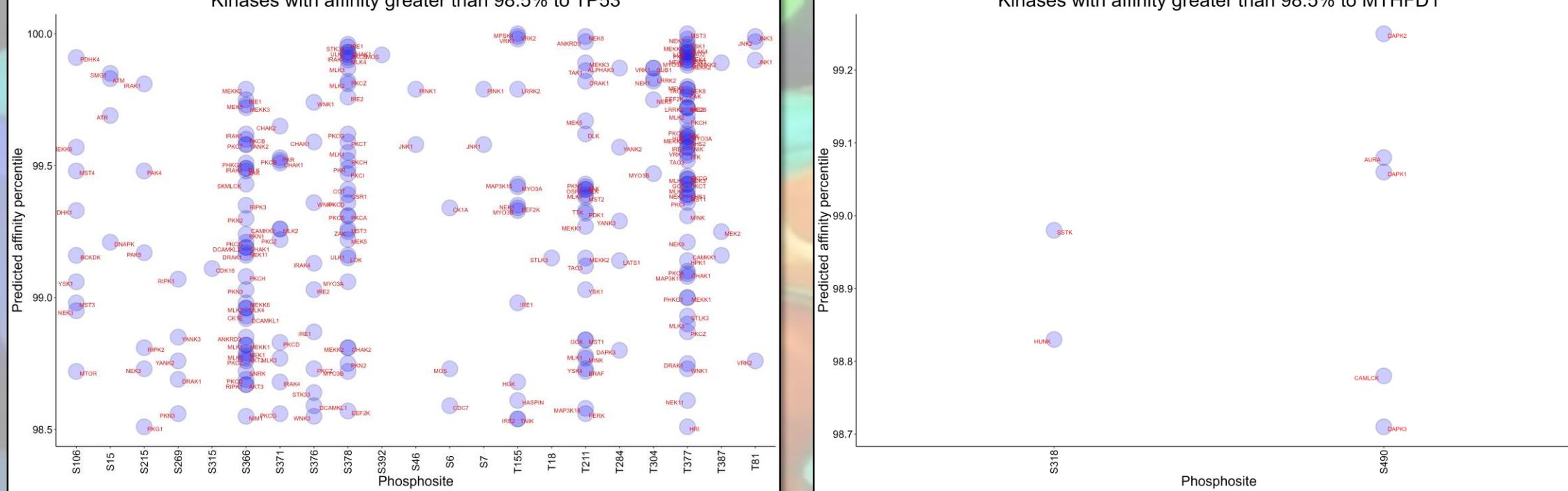
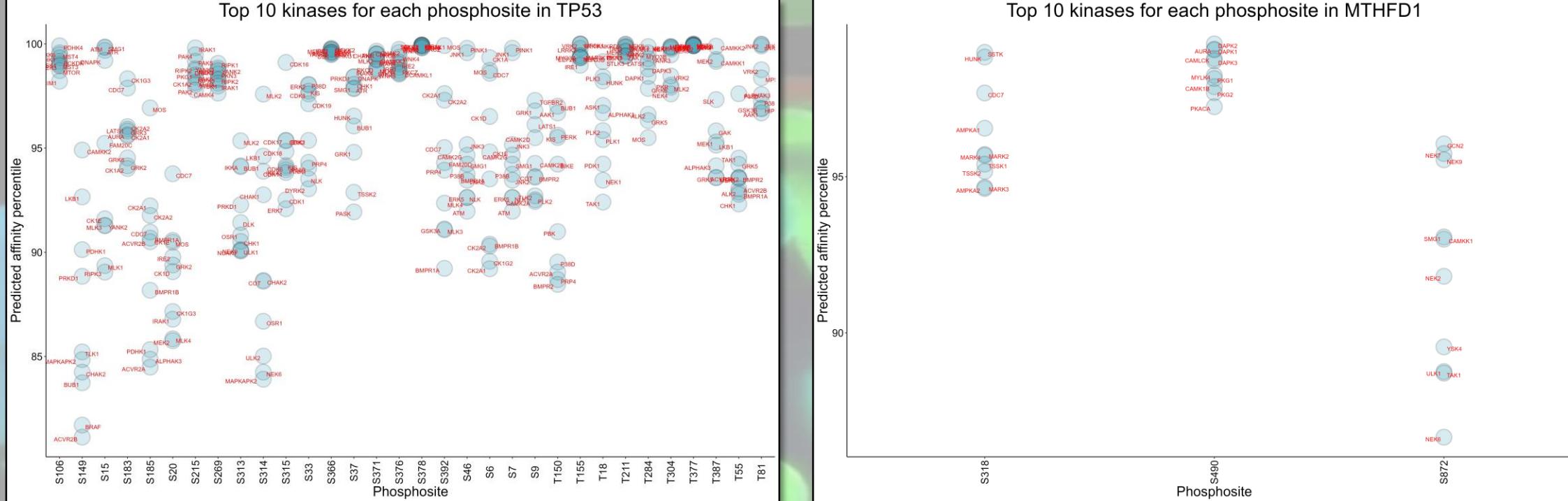
Protein phosphorylation is one of the most widespread post-translational modifications in biology^{1,2}. With advances in mass-spectrometry-based phosphoproteomics, 90,000 sites of serine and threonine phosphorylation have so far been identified, and several thousand have been associated with human diseases and biological processes^{3–4}. For the vast majority of phosphorylation events, it is not yet known which of the more than 300 protein serine/threonine (Ser/Thr) kinases encoded in the human genome are responsible⁵. Here we used synthetic peptide

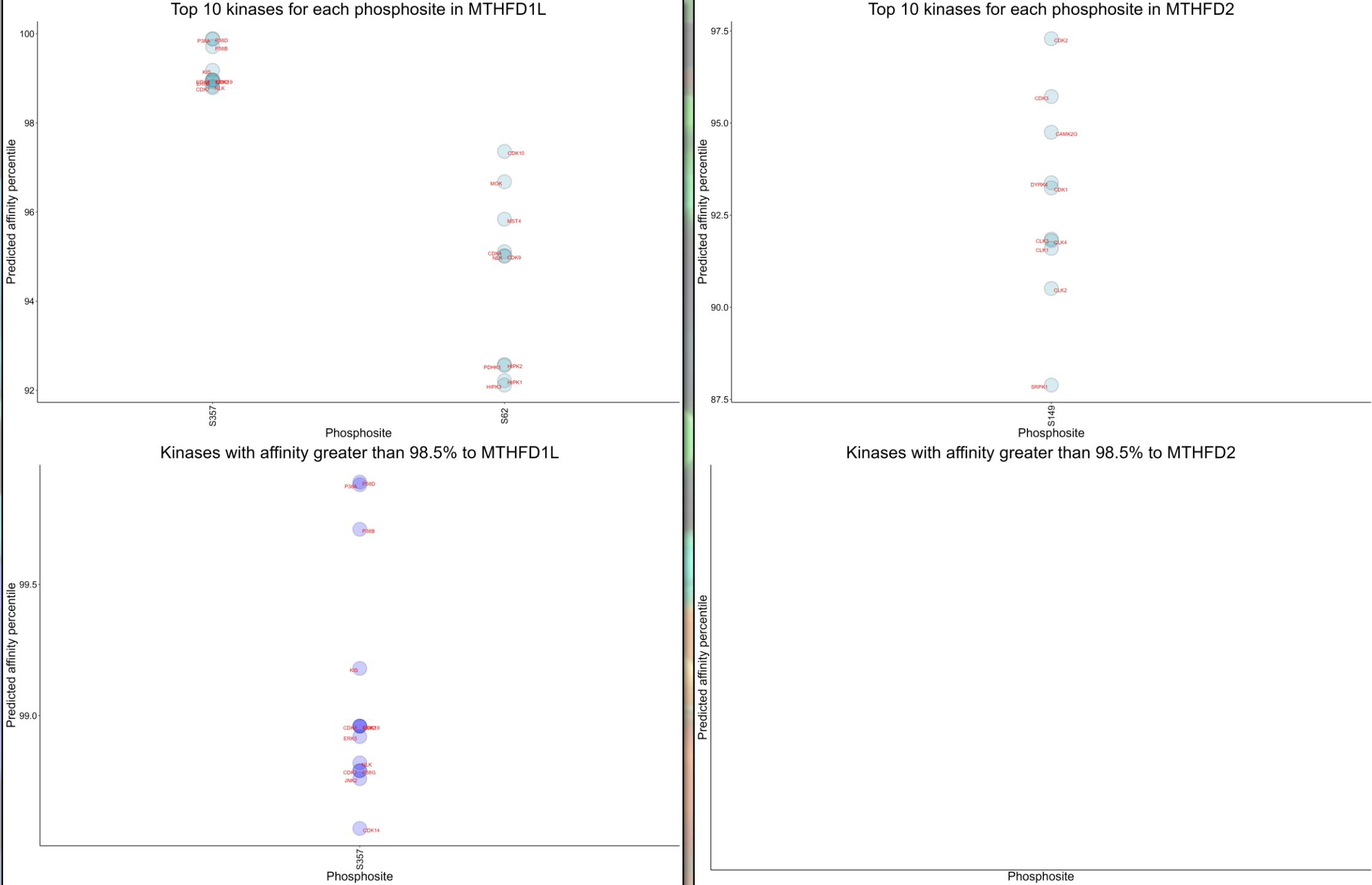
Top 10 kinases for each phosphosite in CASP2

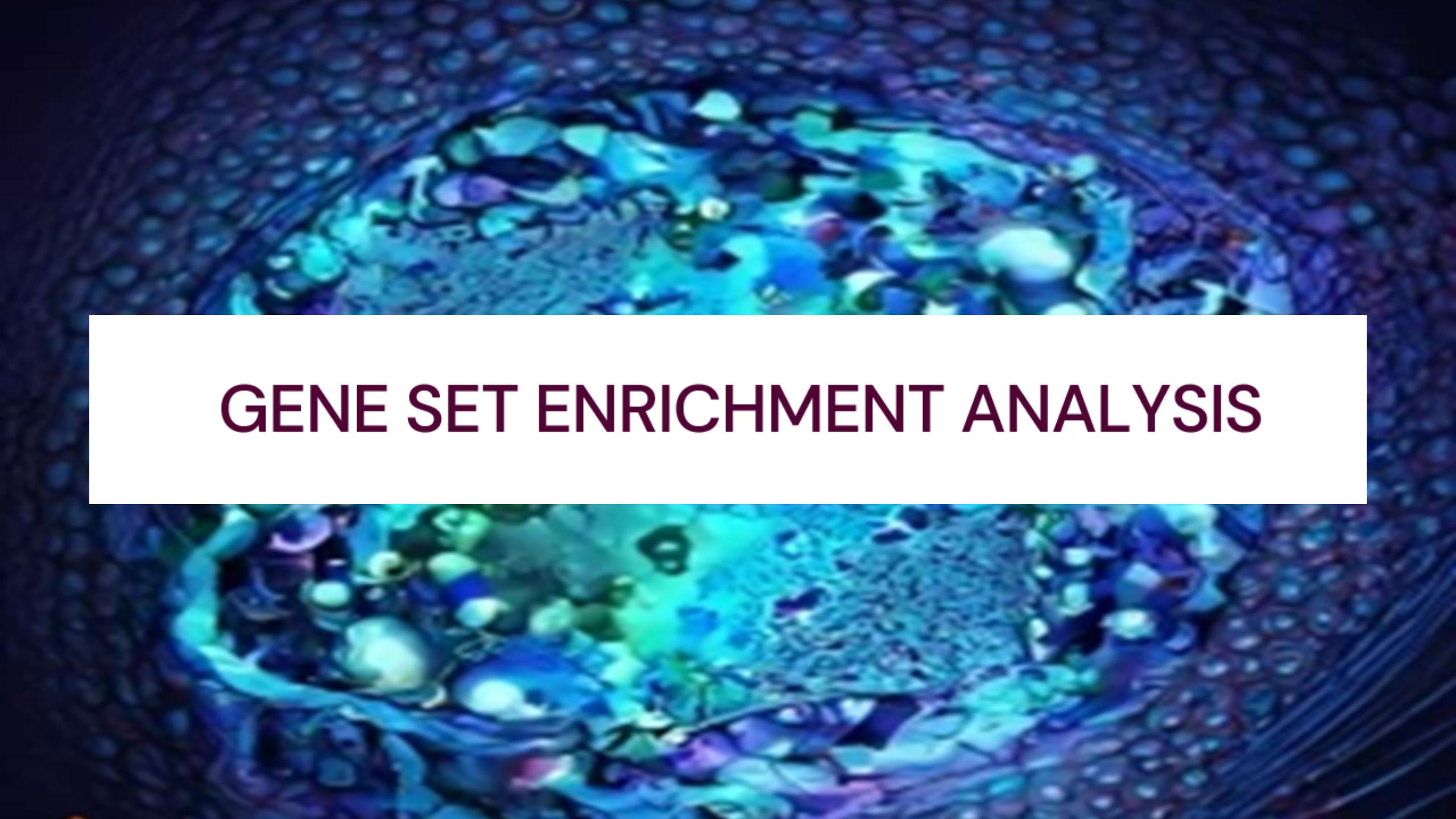


Top 10 kinases for each phosphosite in ABCB1



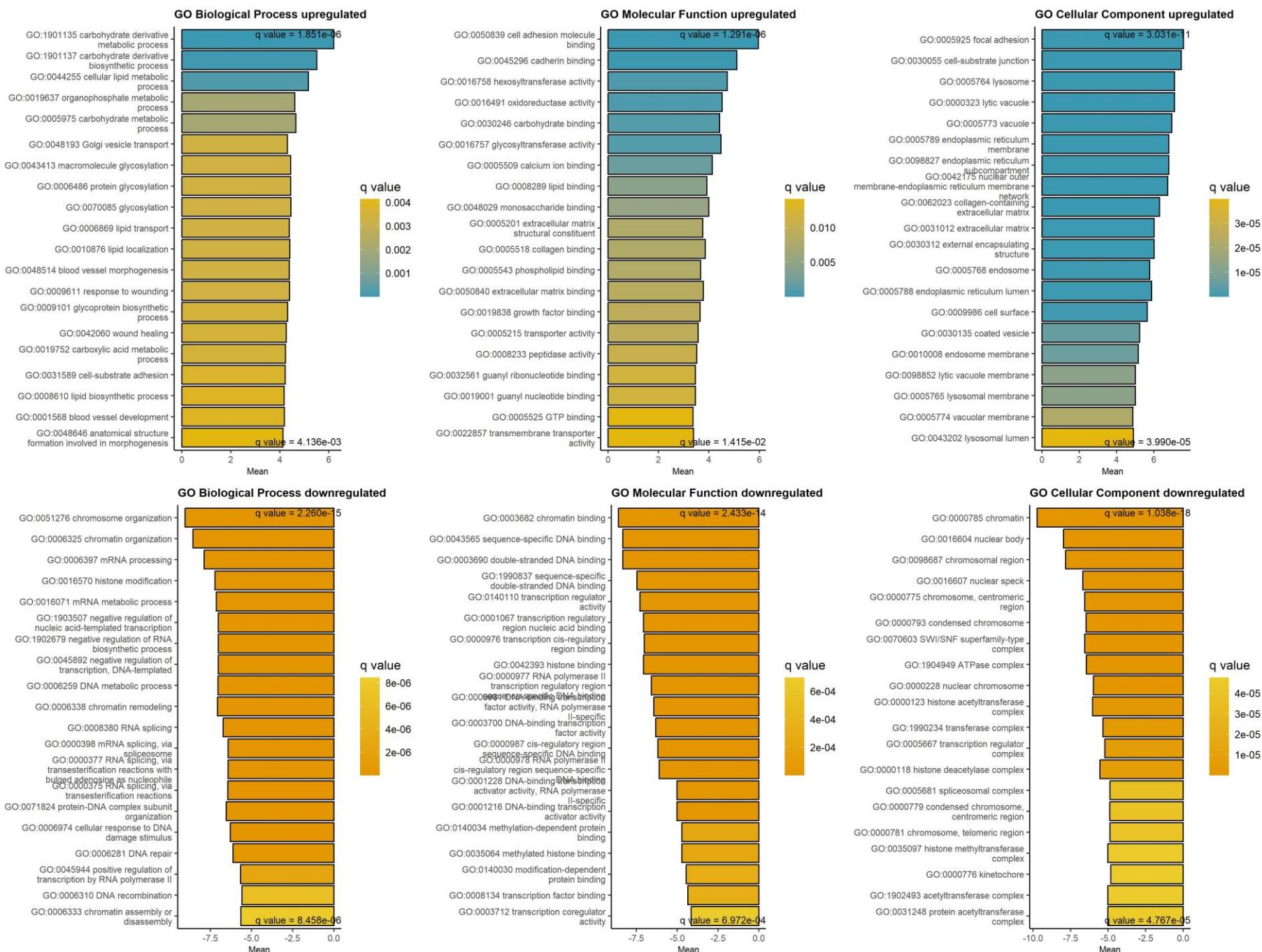




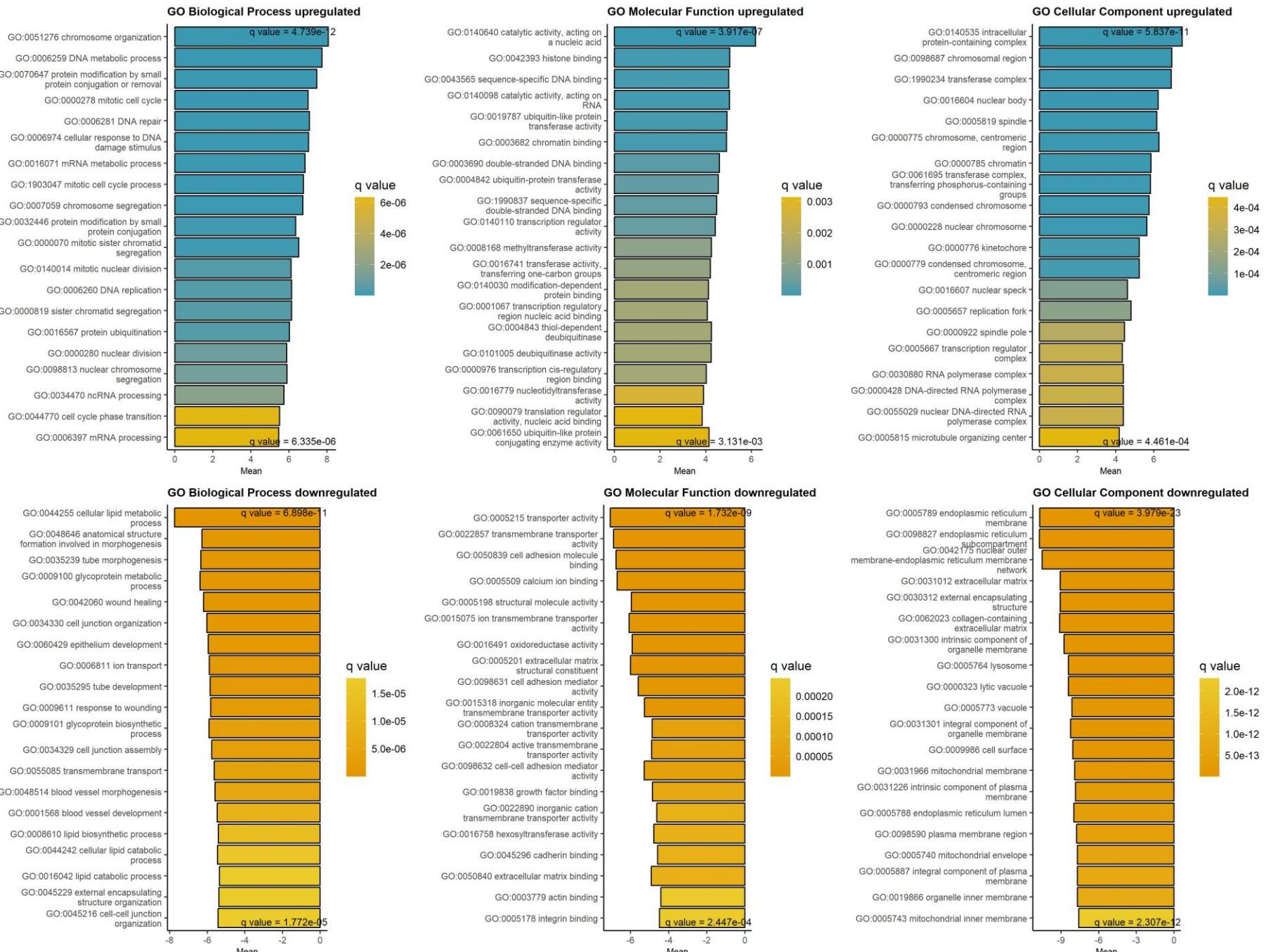


GENE SET ENRICHMENT ANALYSIS

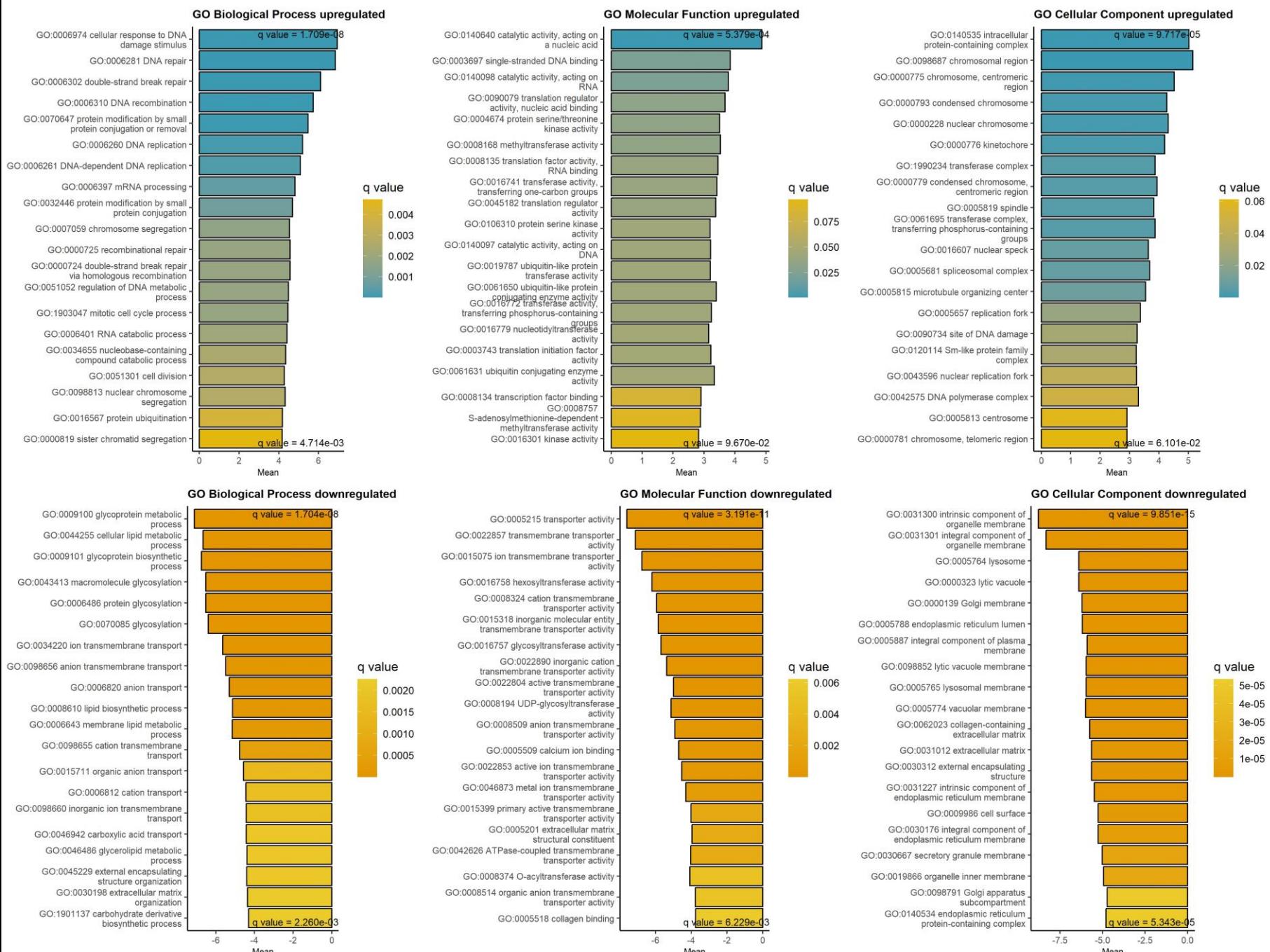
GAGE analysis on upregulated and downregulated proteins at low/absent CENPC protein, DB1



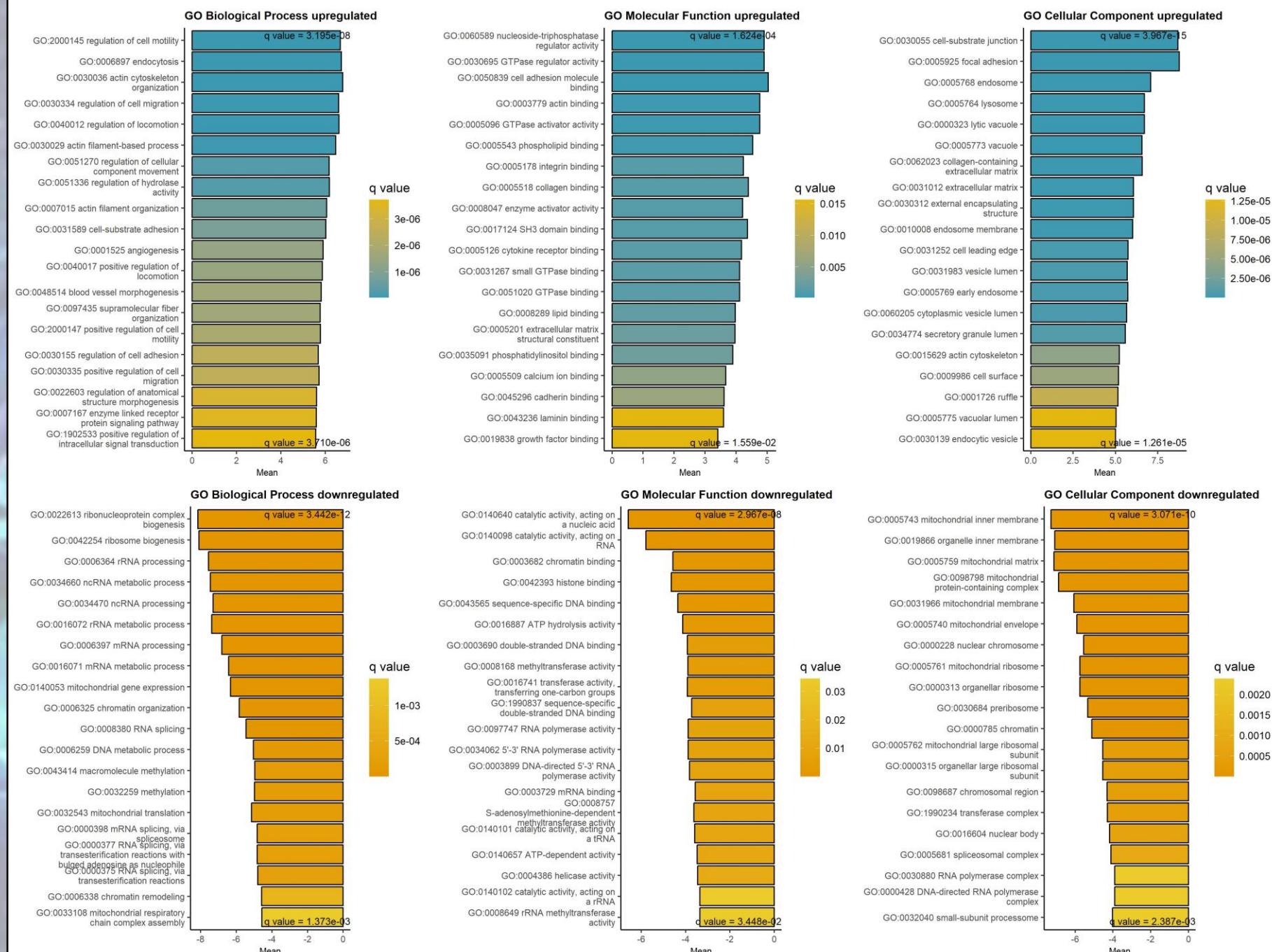
GAGE analysis on upregulated and downregulated proteins at low/absent RAB5B protein, DB1



GAGE analysis on upregulated and downregulated proteins at low/absent GPR180 protein, DB2



GAGE analysis on upregulated and downregulated proteins at low/absent MTHFD2 protein, DB1



OPEN

The folate-coupled enzyme MTHFD2 is a nuclear protein and promotes cell proliferation

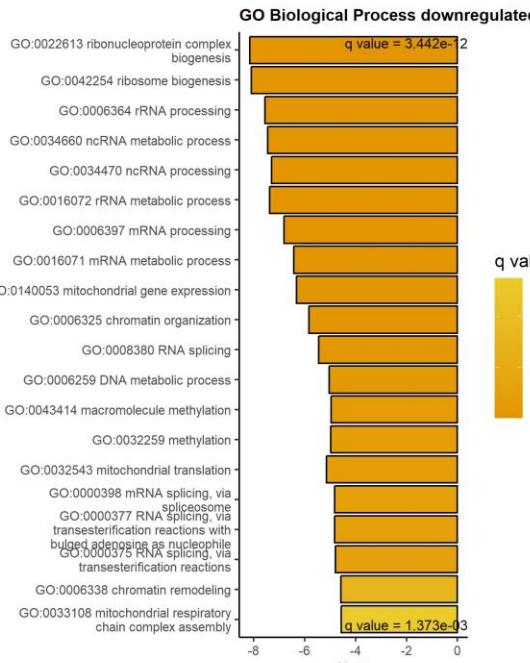
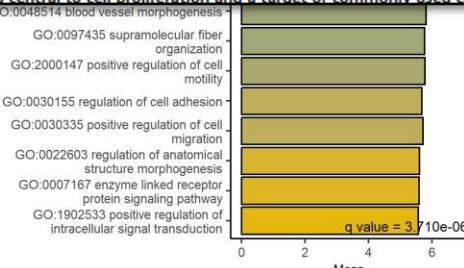
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Accepted: 11 September 2015

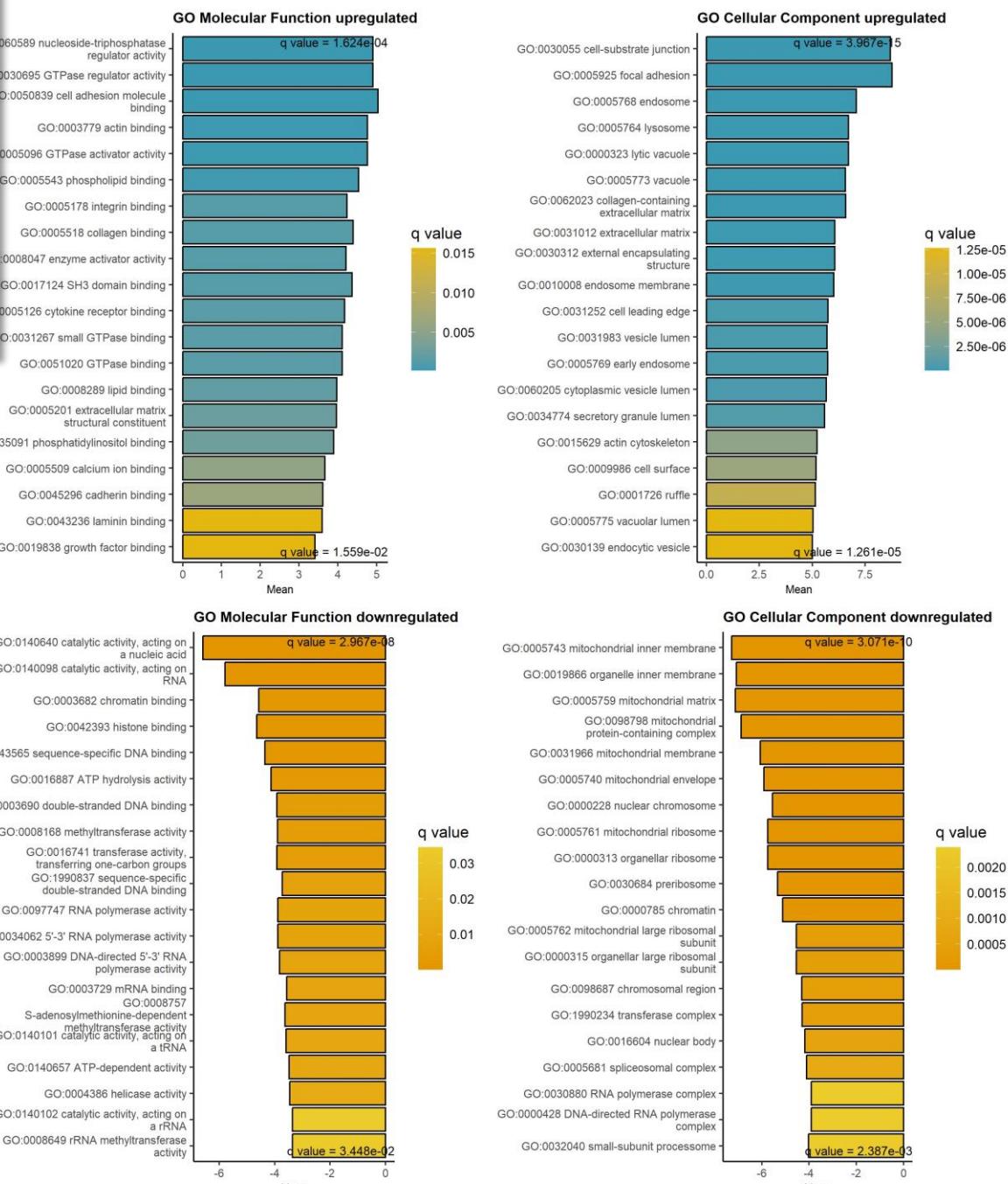
Published: 13 October 2015

Nina Gustafsson Sheppard^{1,2,3}, Lisa Jarl^{1,2}, Diana Mahadevan⁴, Laura Strittmatter⁵, Angelika Schmidt^{4,2}, Nikhil Madhusudan⁵, Jesper Tegnér^{1,2}, Emma K. Lundberg⁴, Anna Asplund⁶, Mohit Jain⁷ & Roland Nilsson^{1,2}

Folate metabolism is central to cell proliferation and a target of commonly used cancer



Upregulated and downregulated proteins at low/absent MTHFD2 protein, DB1



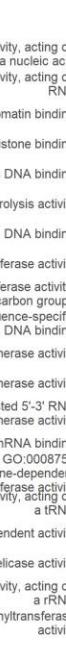
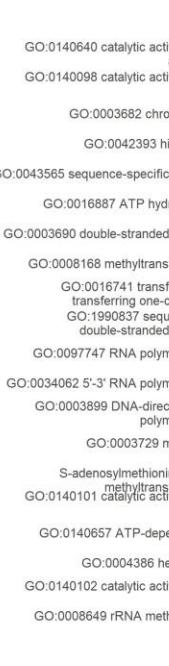
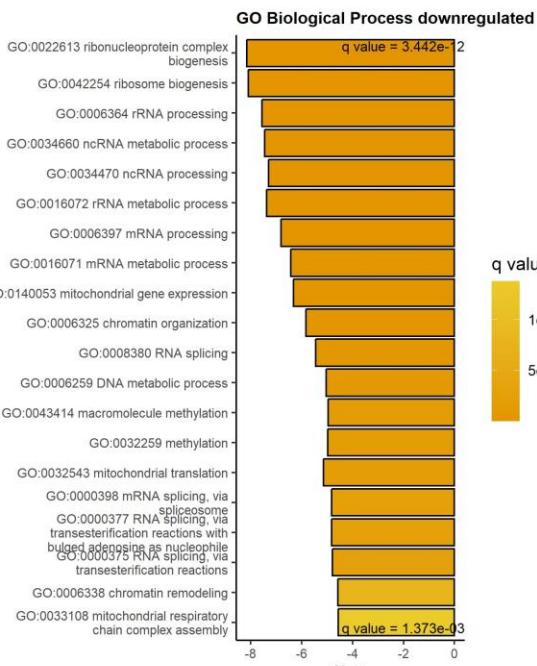
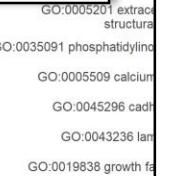
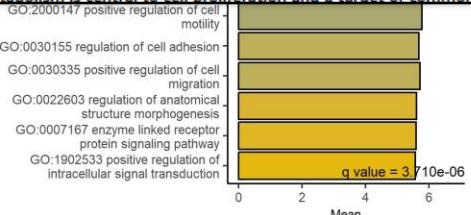
OPEN

The folate-coupled enzyme MTHFD2 is a nuclear protein and promotes cell proliferation

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Nina Gustafsson Sheppard^{1,2,3}, Lisa Jarl^{1,2}, Diana Mahadevan⁴, Laura Strittmatter⁵, Angelika Schmidt^{1,2}, Nikhil Madhusudan⁵, Jesper Tegnér^{1,2}, Emma K. Lundberg⁴, Anna Asplund⁶, Mohit Jain⁷ & Roland Nilsson^{1,2}

Folate metabolism is central to cell proliferation and a target of commonly used cancer



Koufaris and Nilsson *Cancer & Metabolism* (2018) 6:12
<https://doi.org/10.1186/s40170-018-0185-4>

Cancer & Metabolism

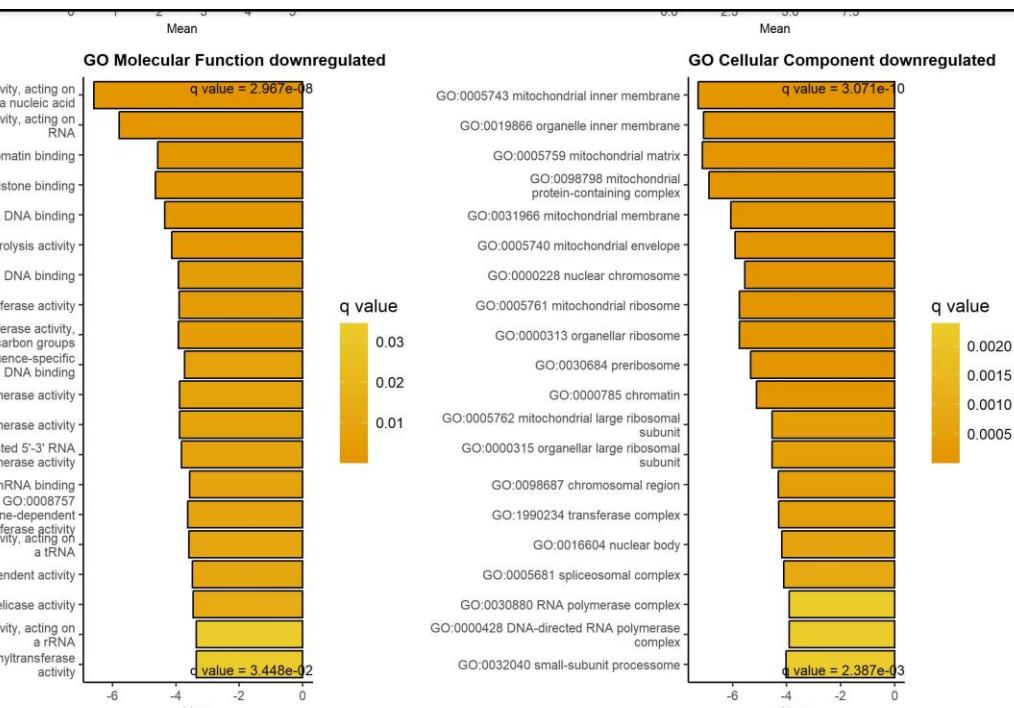
RESEARCH

Open Access



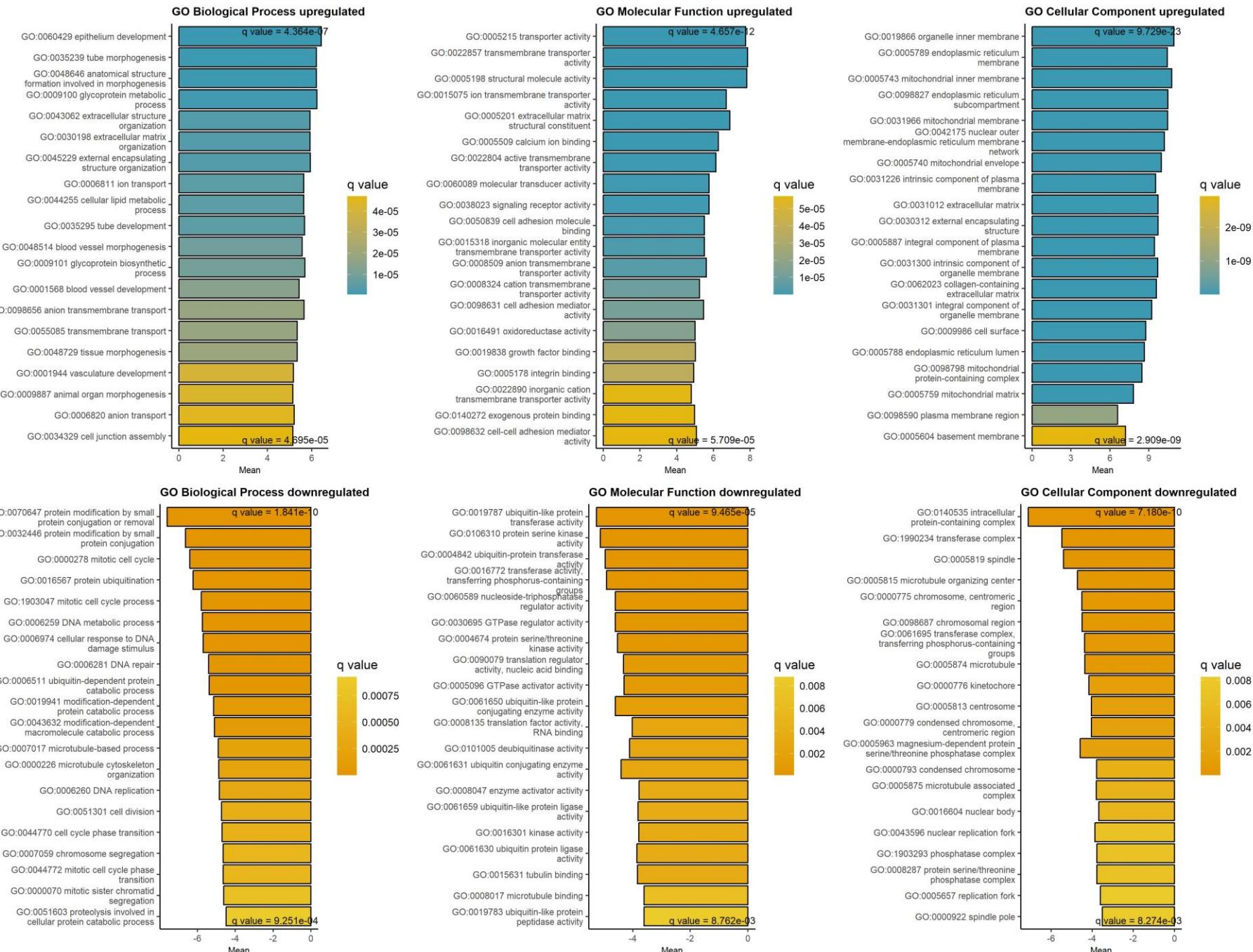
Protein interaction and functional data indicate MTHFD2 involvement in RNA processing and translation

Costas Koufaris^{1,2,3} and Roland Nilsson^{1,2,3*}

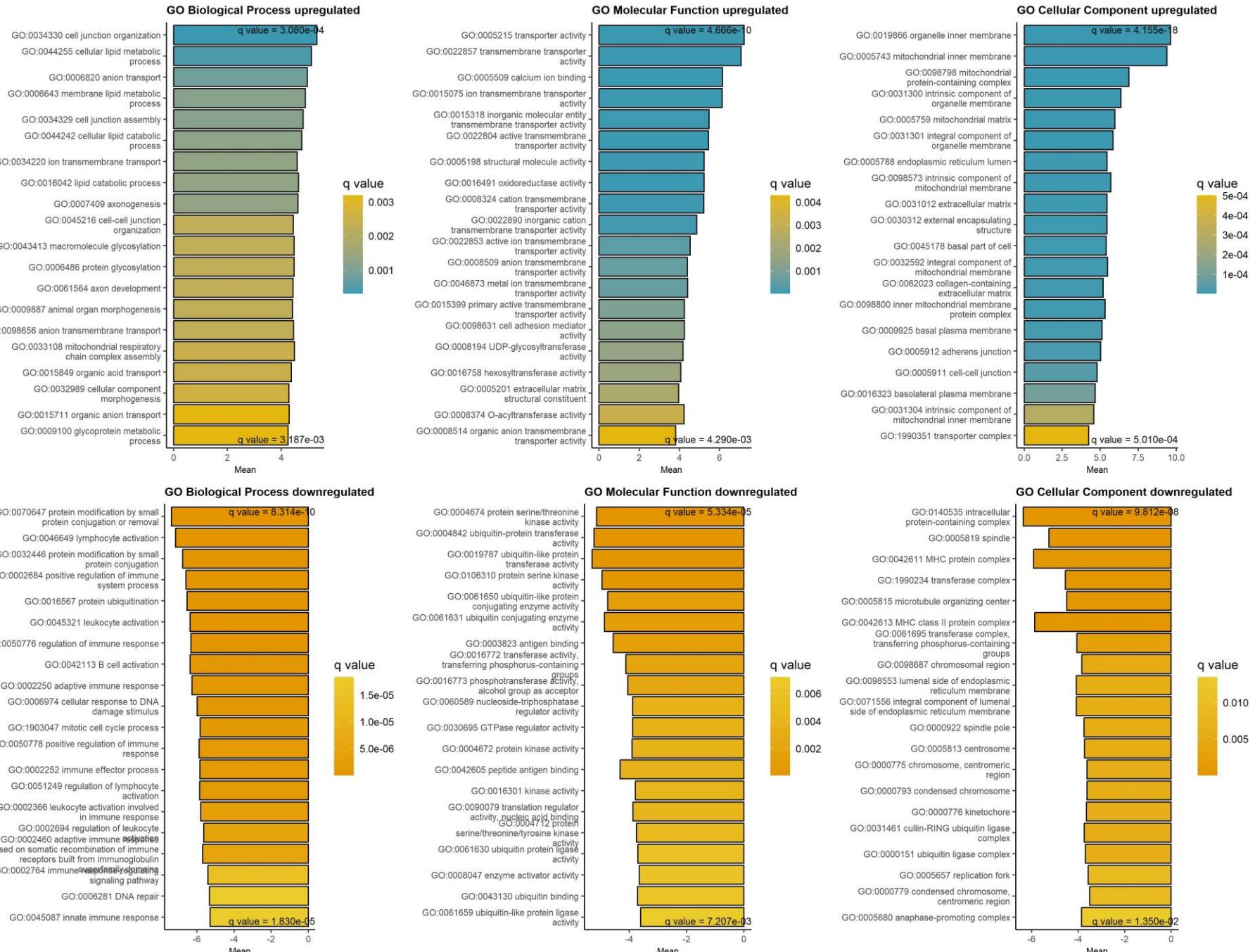


*Correspondence: roland.nilsson@kth.se

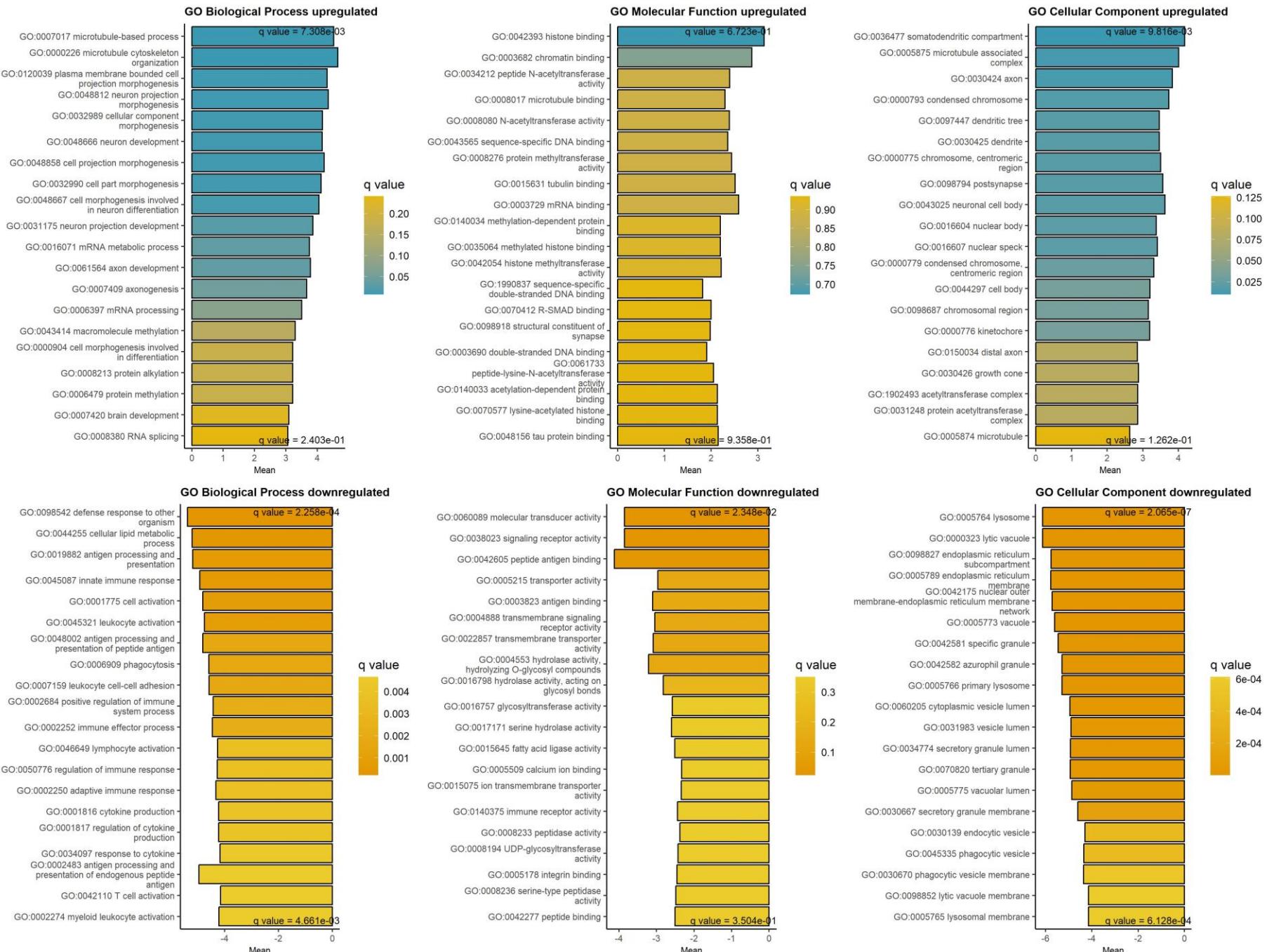
GAGE analysis on upregulated and downregulated proteins at low/absent MTHFD1 protein, DB1



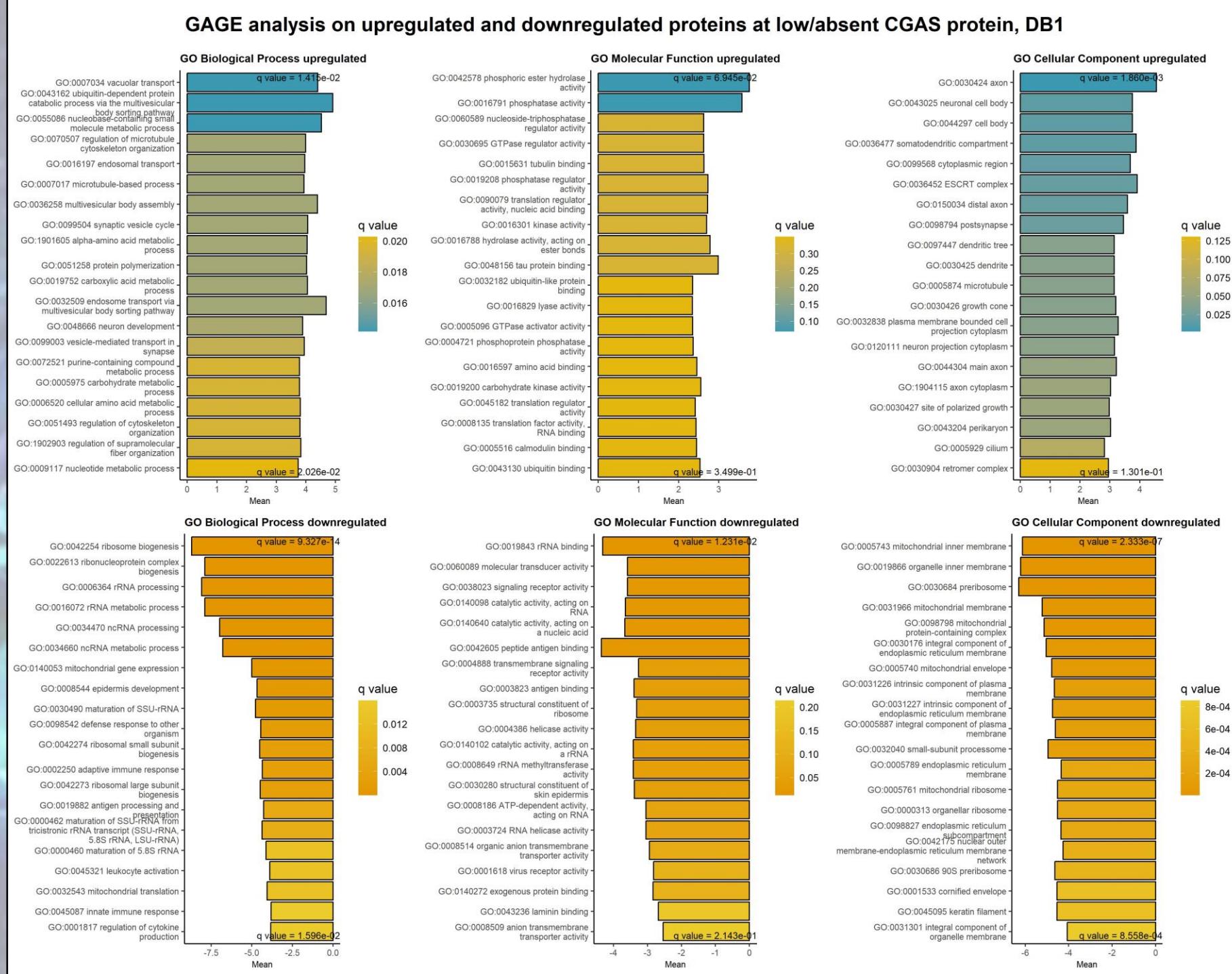
GAGE analysis on upregulated and downregulated proteins at low/absent TNIP1 protein, DB2



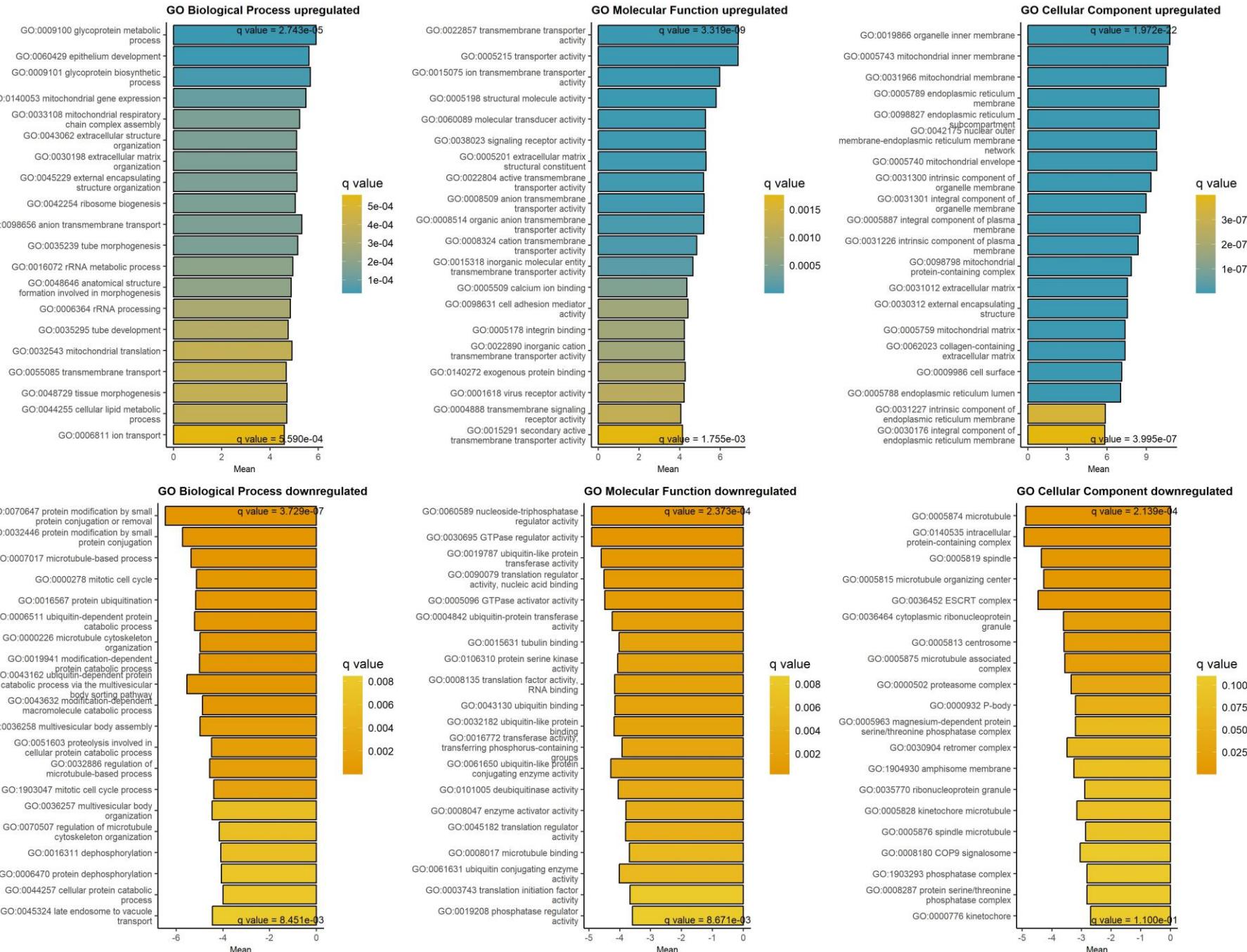
GAGE analysis on upregulated and downregulated proteins at low/absent STING1 protein, DB1

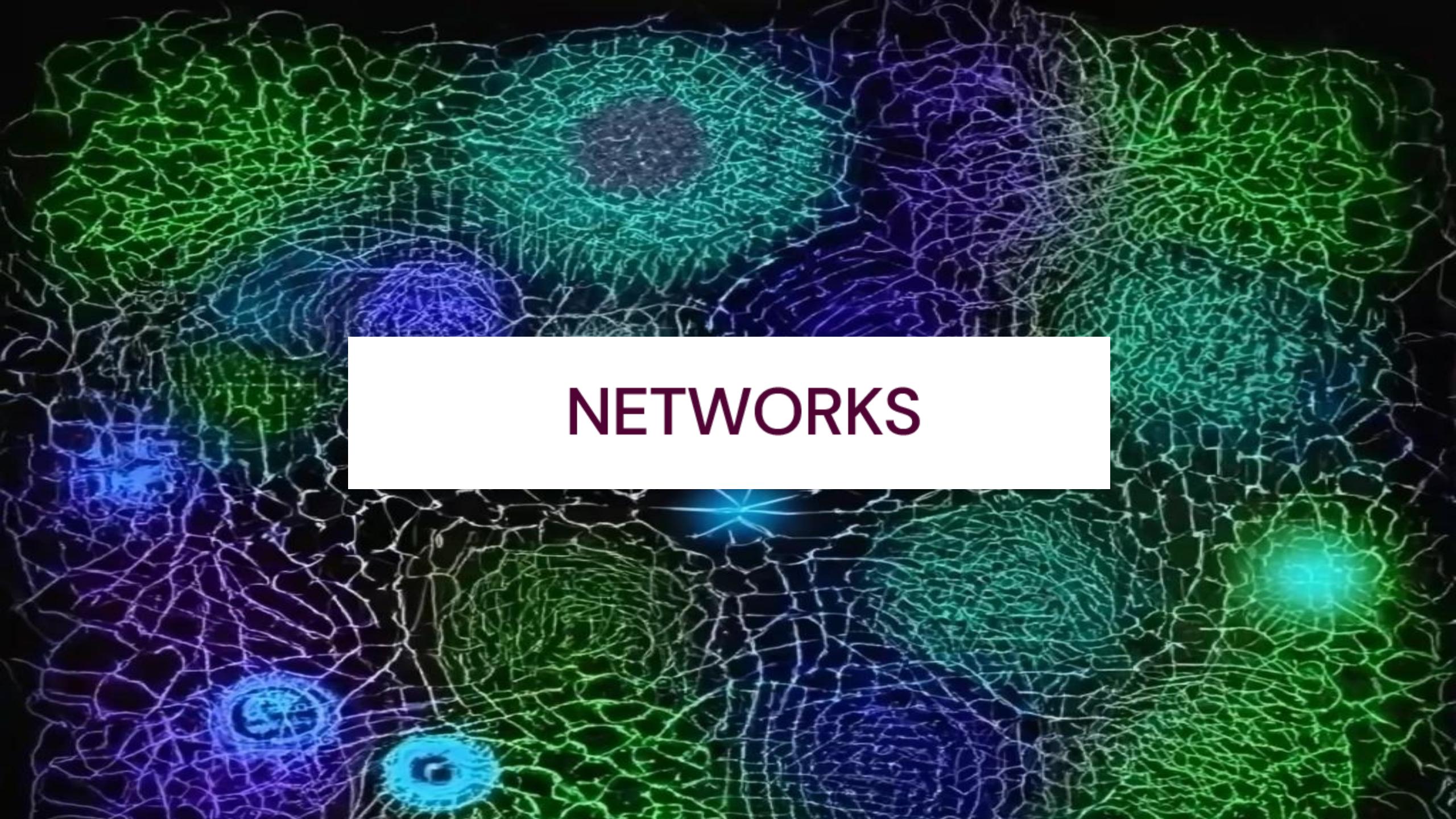


GAGE analysis on upregulated and downregulated proteins at low/absent CGAS protein, DB1



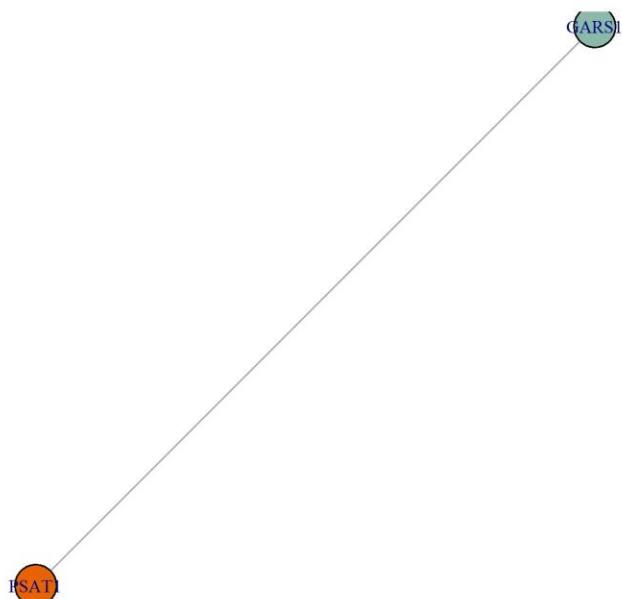
GAGE analysis on upregulated and downregulated proteins at low/absent SOD1 protein, DB1



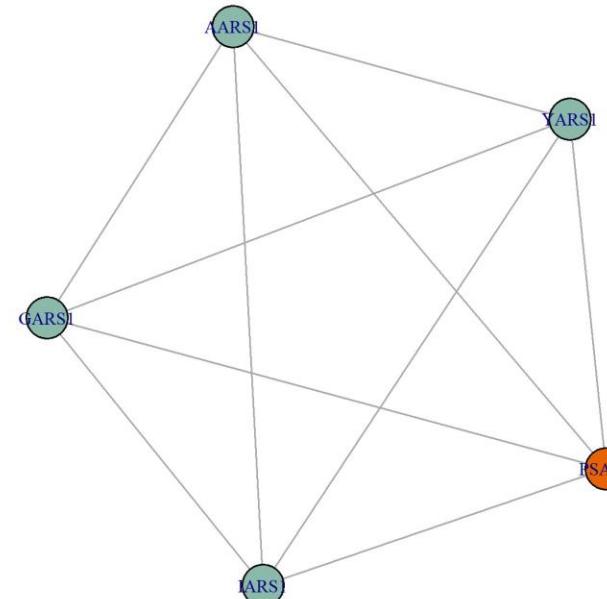
The background of the image is a complex, abstract network graph. It consists of numerous small, glowing nodes connected by thin, white lines forming a mesh-like structure. The nodes are primarily colored in shades of green, blue, and purple, with some brighter highlights. A prominent feature is a large, bright blue circular node in the bottom left corner, which has several white lines radiating outwards towards other nodes. The overall effect is one of a dense, interconnected system.

NETWORKS

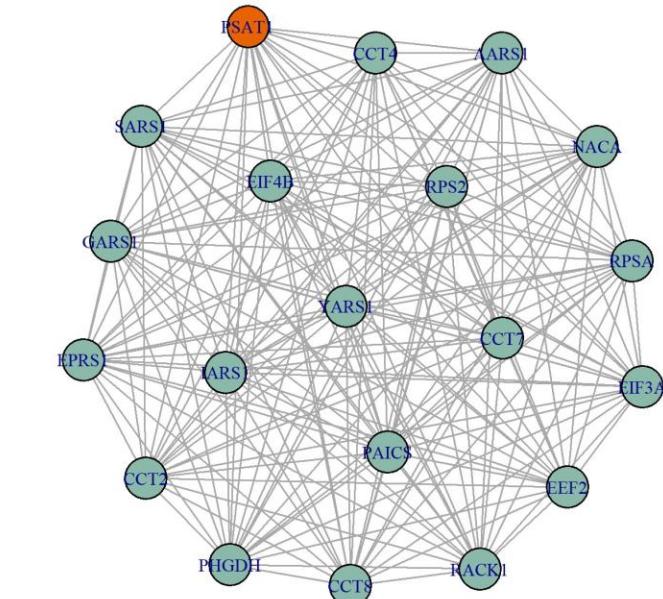
PSAT1 network, DB1, all Pearson r > 0.6



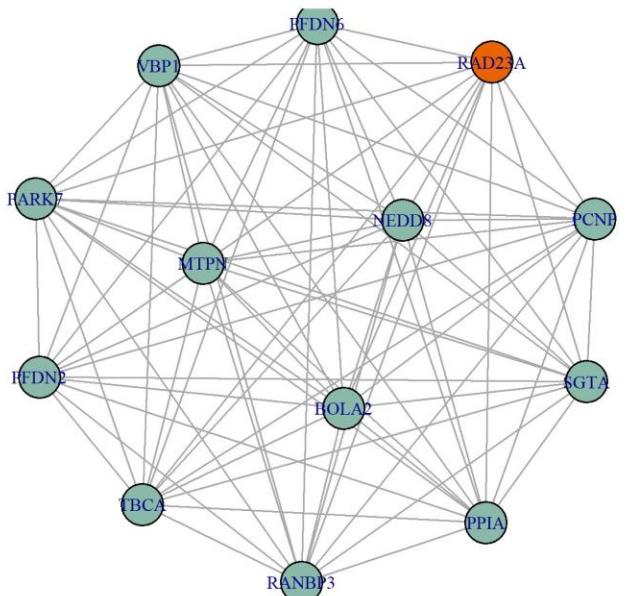
PSAT1 network, DB1, all Pearson r > 0.55



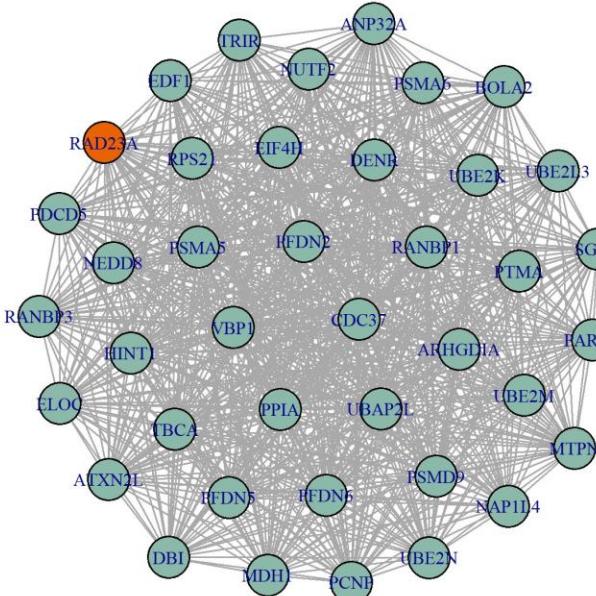
PSAT1 network, DB1, all Pearson r > 0.5



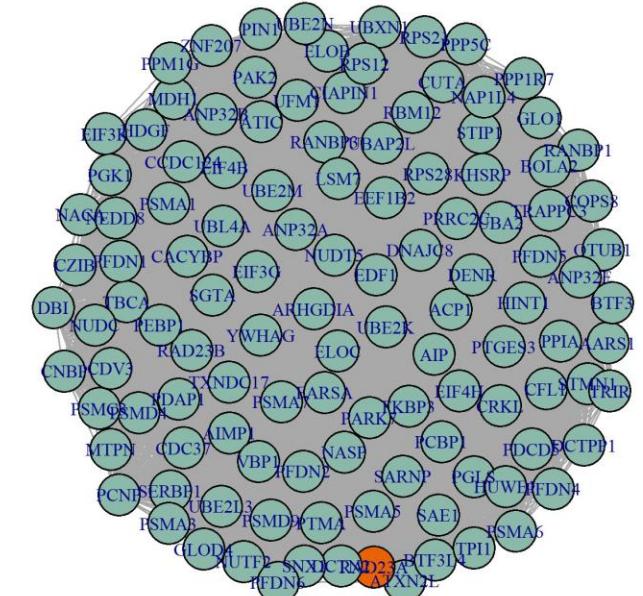
RAD23A network, DB1, all Pearson r > 0.6



RAD23A network, DB1, all Pearson r > 0.55



RAD23A network, DB1, all Pearson r > 0.5



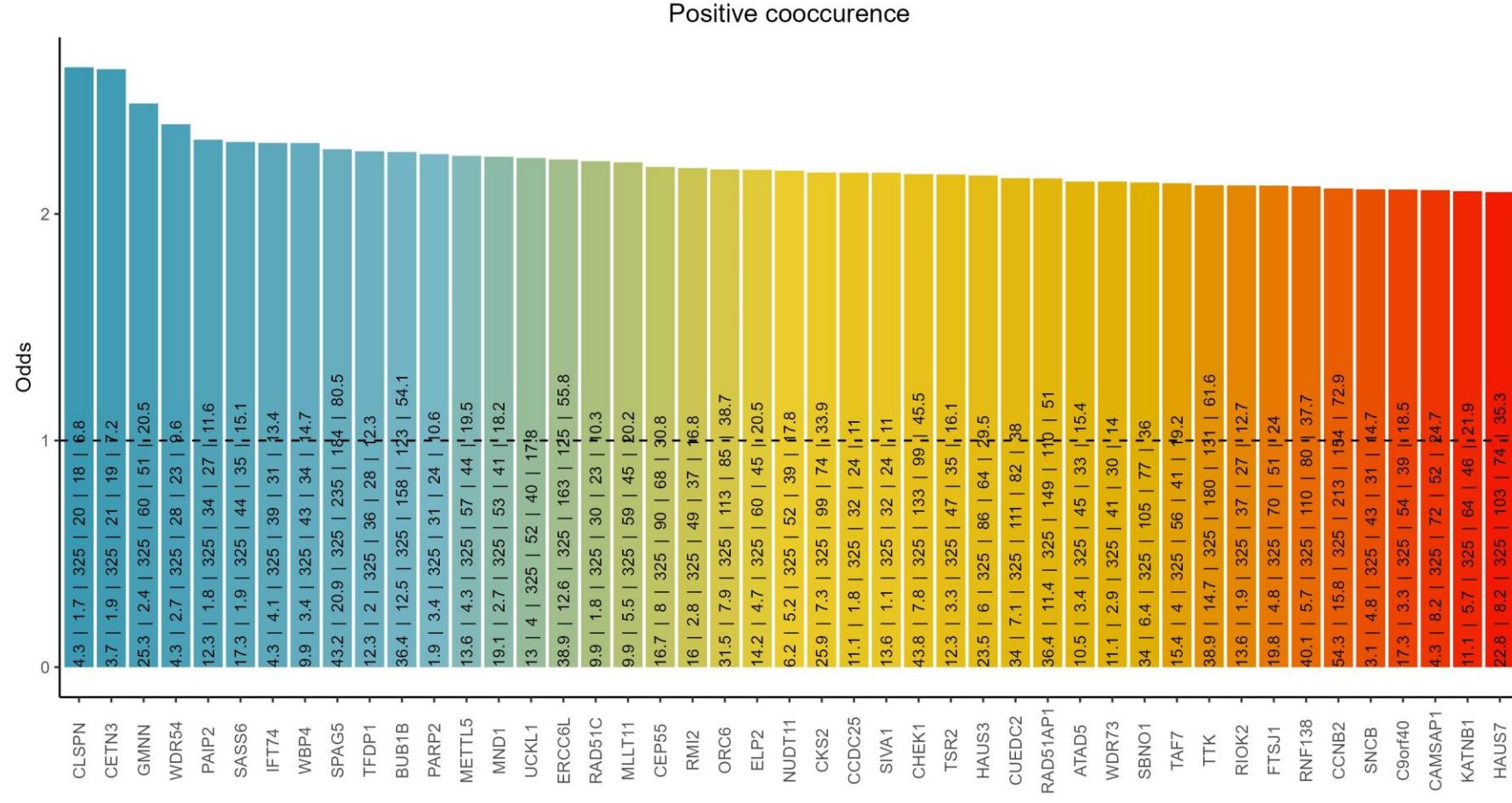
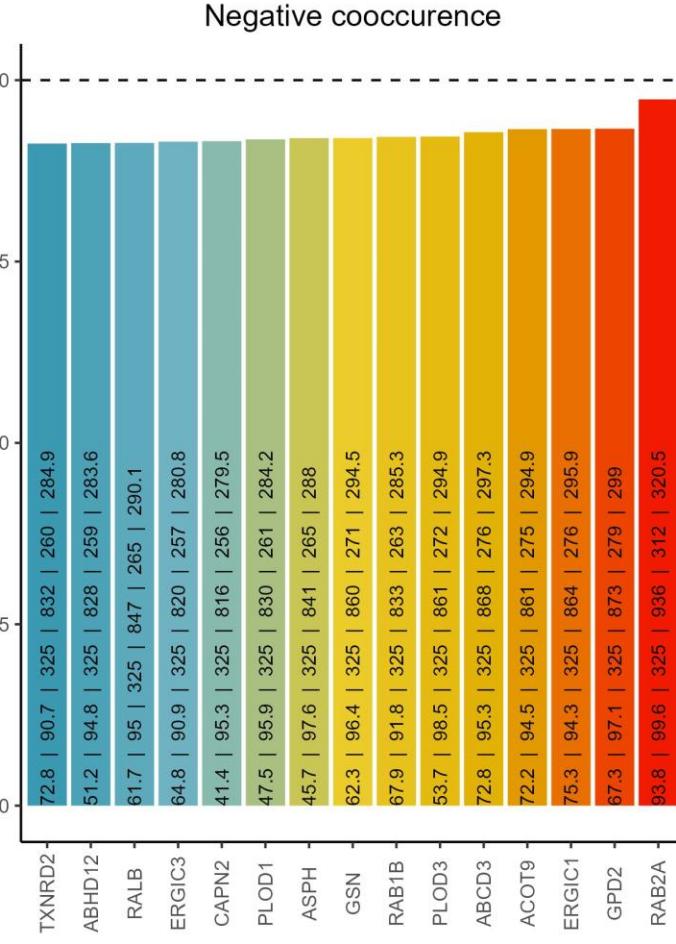


COOCCURRENCE

Cooccurrence with KNSTRN protein, DB1

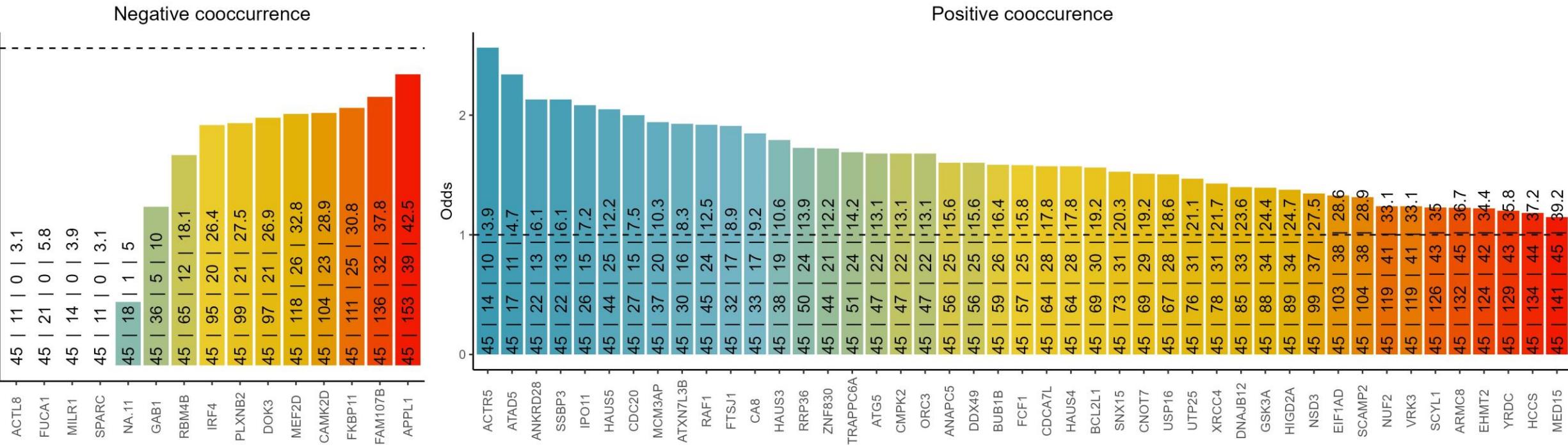
% of KNSTRN in blood cancers: 51.9 ; % of KNSTRN in solid cancers: 30.6

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



Cooccurrence with ORC1 protein in blood cancers, DB1

The text in the bars: incidence of ORC1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Nat Commun. 2021; 12: 2681.

Published online 2021 May 11. doi: [10.1038/s41467-021-23003-4](https://doi.org/10.1038/s41467-021-23003-4)

PMCID: PMC8113569

PMID: [33976210](https://pubmed.ncbi.nlm.nih.gov/33976210/)

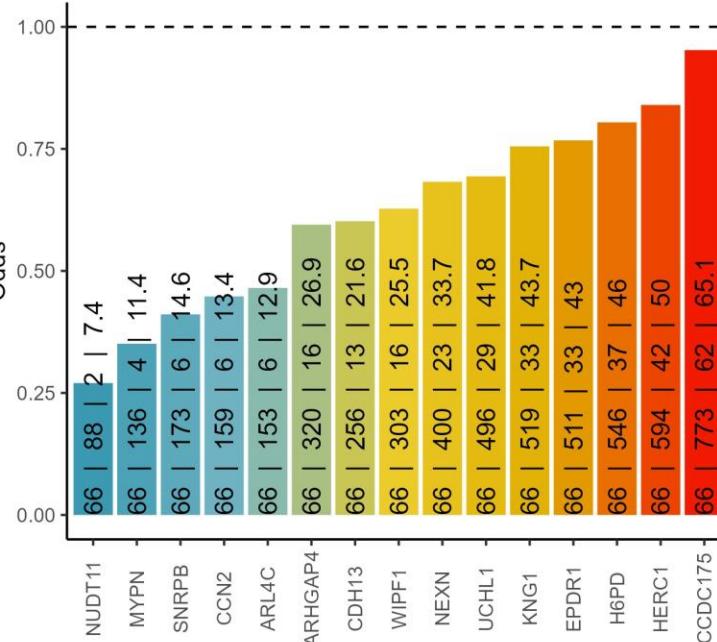
Identification of poly(ADP-ribose) polymerase 9 (PARP9) as a noncanonical sensor for RNA virus in dendritic cells

Junji Xing,¹ Ao Zhang,^{1,2} Yong Du,¹ Mingli Fang,^{1,3} Laurie J. Minze,¹ Yong-Jun Liu,⁴ Xian Chang Li,^{1,5} and Zhiqiang Zhang^{*1,5}

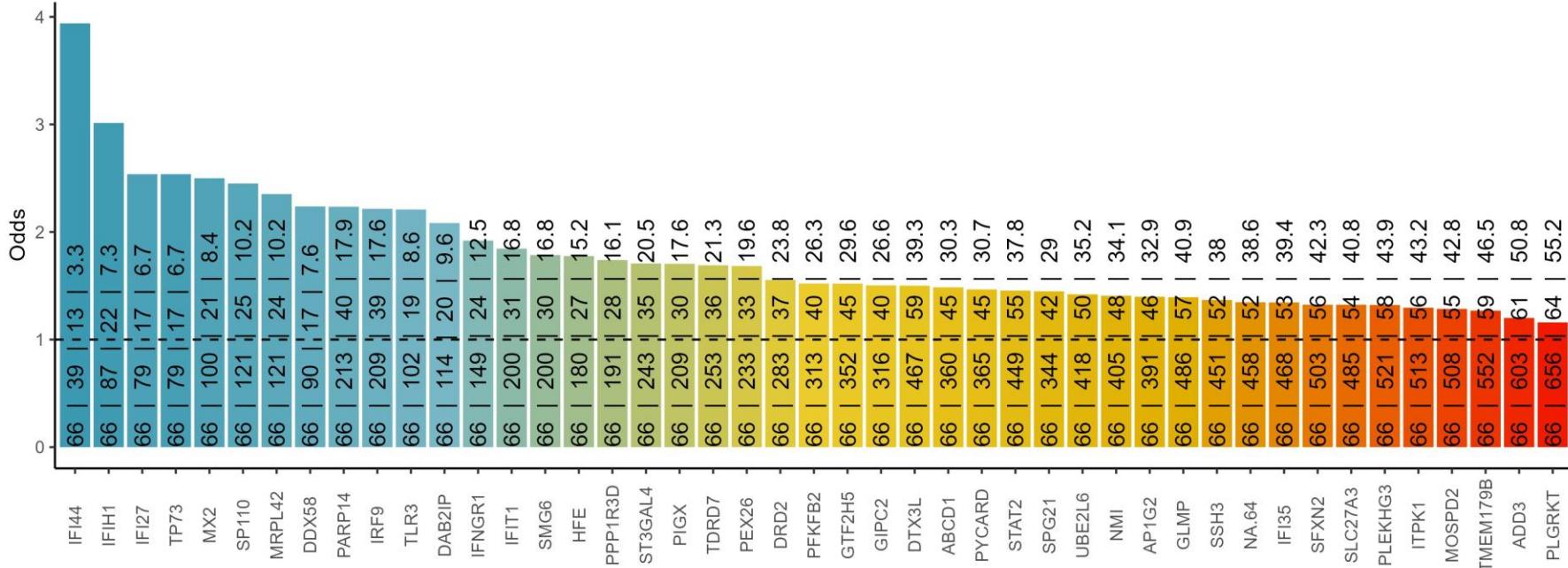
Cooccurrence with PARP9 protein in solid cancers, DB2

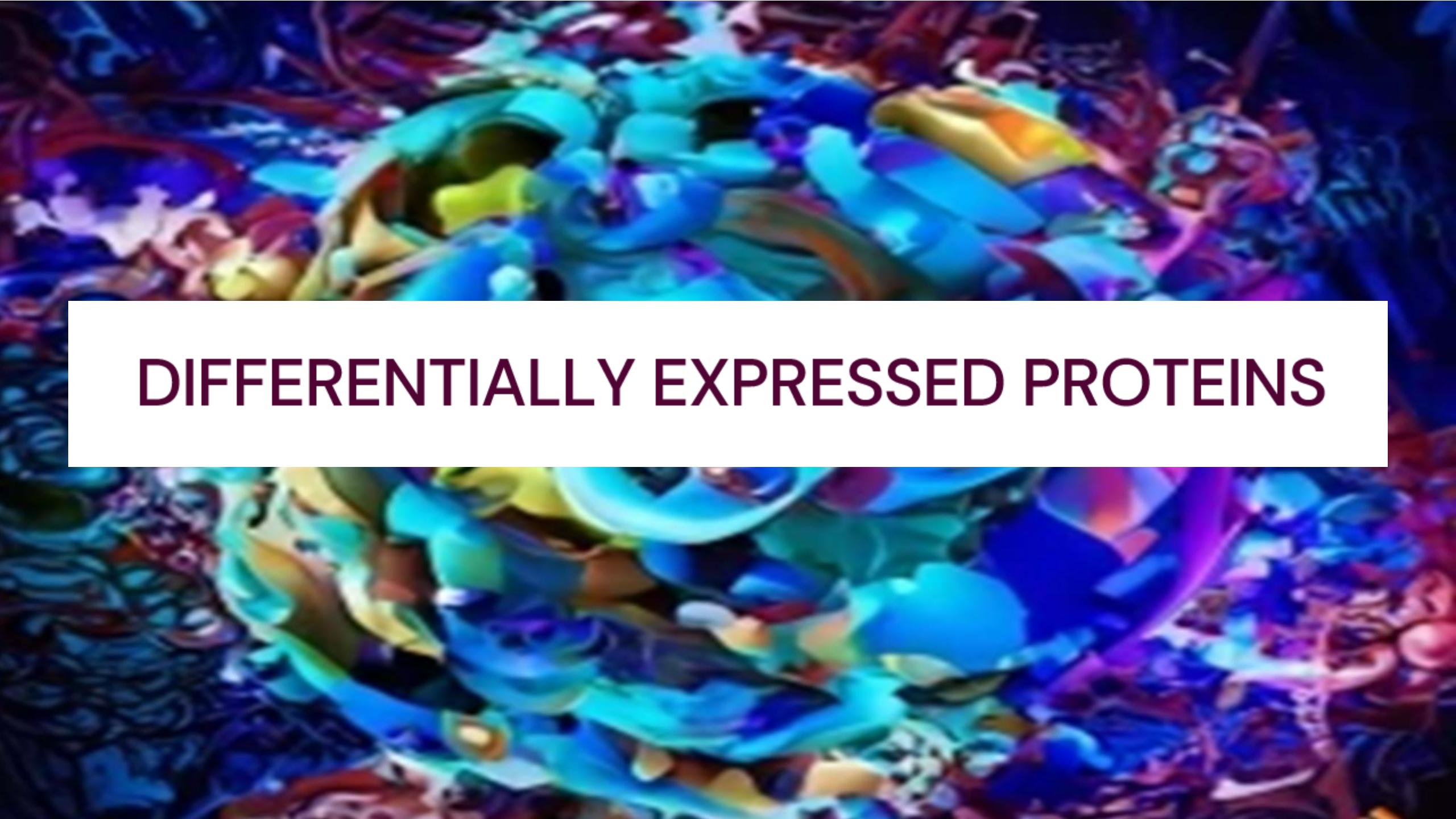
The text in the bars: incidence of PARP9 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

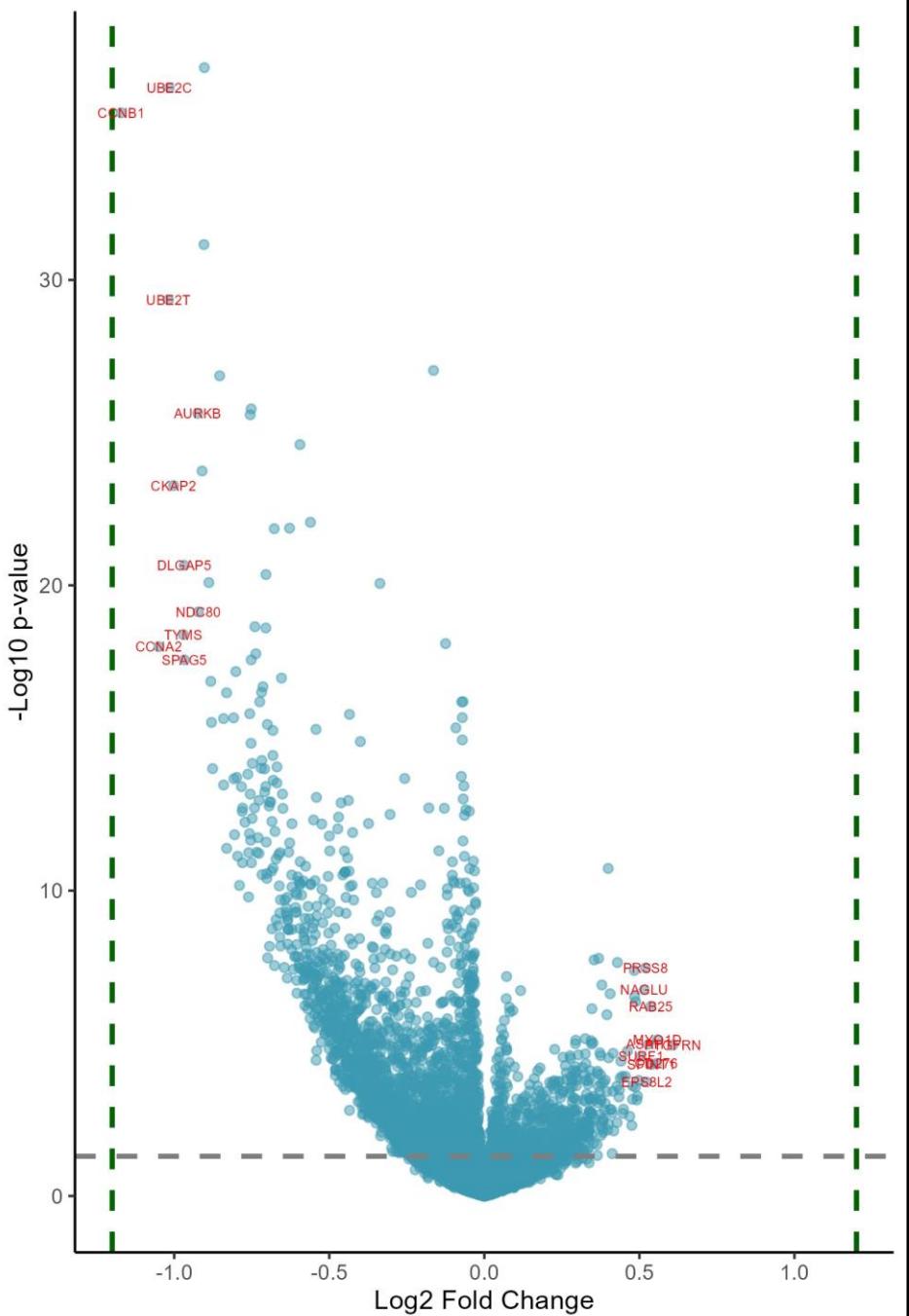




DIFFERENTIALLY EXPRESSED PROTEINS

Differentially expressed proteins at absence/low amount of AURKA , DB1

p-value < 0.05 & logFC > 1.2

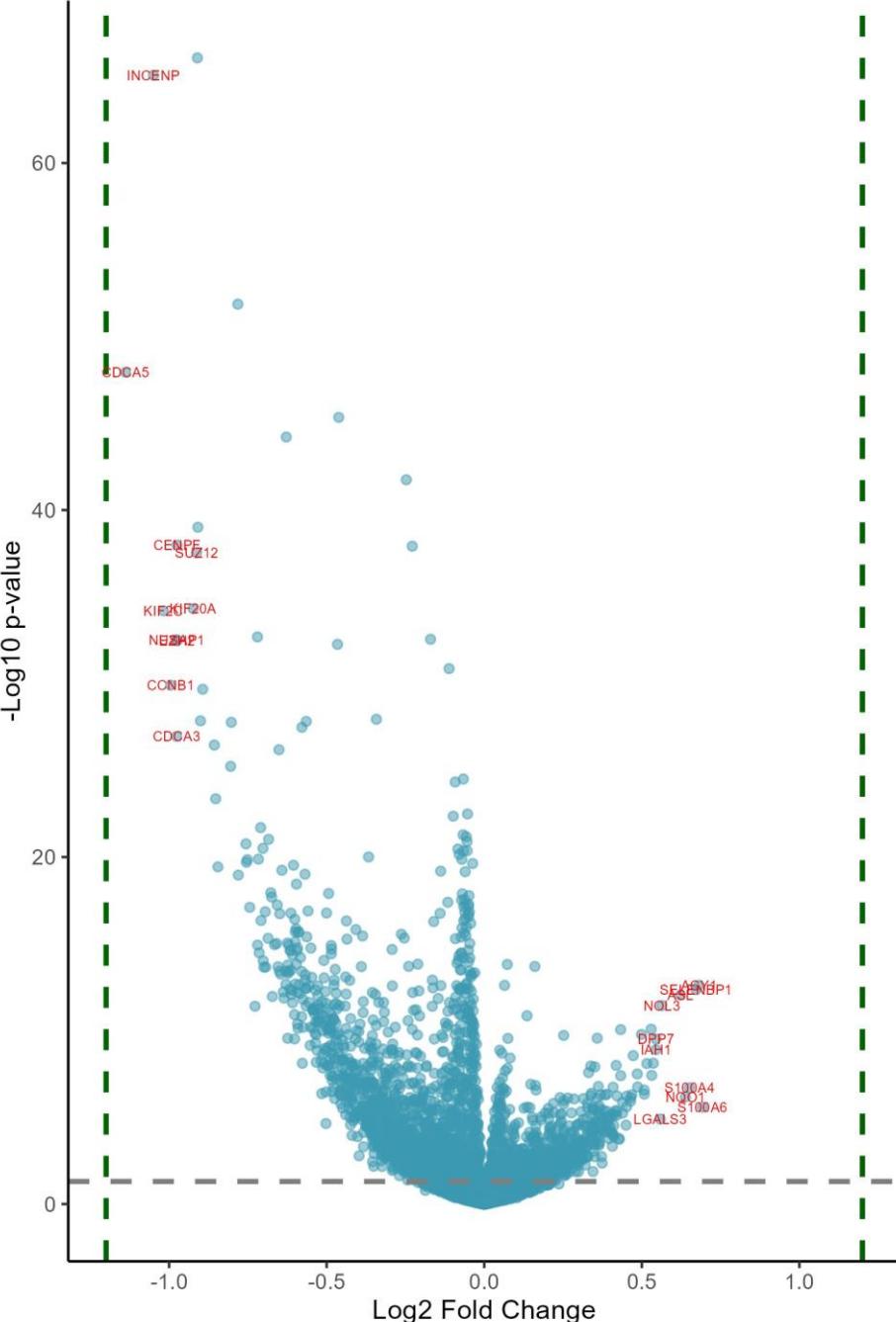


Downregulated at low/absent AURKA Upregulated at low/absent AURKA

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|---------|--------------------------------------|-------|-----------|---------|-------------------------------------|
| -1.17 | 5.57e-33 | CCNB1 | cyclin B1 | 0.61 | 1.01e-04 | PTGFRN | prostaglandin F2 receptor inhibitor |
| -1.05 | 2.50e-16 | CCNA2 | cyclin A2 | 0.56 | 7.32e-05 | MYO1D | myosin ID |
| -1.02 | 4.92e-27 | UBE2T | ubiquitin conjugating enzyme E2 T | 0.55 | 3.28e-04 | CD276 | CD276 molecule |
| -1.02 | 1.11e-33 | UBE2C | ubiquitin conjugating enzyme E2 C | 0.54 | 3.51e-04 | SPINT1 | serine peptidase inhibitor, Kunitz |
| -1 | 2.56e-21 | CKAP2 | cytoskeleton associated protein 2 | 0.54 | 8.46e-06 | RAB25 | RAB25, member RAS oncogene family |
| -0.97 | 1.09e-16 | TYMS | thymidylate synthetase | 0.53 | 9.55e-05 | ASAHI | N-acylsphingosine amidohydrolase 1 |
| -0.97 | 8.16e-19 | DLGAP5 | DLG associated protein 5 | 0.52 | 1.07e-03 | EPS8L2 | EPS8 like 2 |
| -0.97 | 6.13e-16 | SPAG5 | sperm associated antigen 5 | 0.52 | 7.07e-07 | PRSS8 | serine protease 8 |
| -0.92 | 1.54e-23 | AURKB | aurora kinase B | 0.52 | 2.95e-06 | NAGLU | N-acetyl-alpha-glucosaminidase |
| -0.92 | 2.23e-17 | NDC80 | NDC80 kinetochore complex component | 0.51 | 2.11e-04 | SURF1 | SURF1 cytochrome c oxidase assembly |
| -0.91 | 9.20e-22 | MRGBP | MRG domain binding protein | 0.5 | 9.63e-04 | S100A14 | S100 calcium binding protein A14 |
| -0.9 | 9.20e-29 | KIF2C | kinesin family member 2C | 0.49 | 2.62e-03 | AGR2 | anterior gradient 2, protein disulf |
| -0.9 | 3.70e-34 | UBE2S | ubiquitin conjugating enzyme E2 S | 0.49 | 3.35e-03 | SFXN3 | sideroflexin 3 |
| -0.89 | 2.70e-18 | NUF2 | NUF2 component of NDC80 kinetochore | 0.49 | 6.32e-06 | ERBB2 | erb-b2 receptor tyrosine kinase 2 |
| -0.88 | 2.82e-15 | TACC3 | transforming acidic coiled-coil con | 0.49 | 1.47e-03 | LAD1 | ladinin 1 |
| -0.88 | 4.57e-14 | CDCA3 | cell division cycle associated 3 | 0.48 | 4.57e-06 | SYTL1 | synaptotagmin like 1 |
| -0.88 | 1.16e-12 | PCLAF | PCNA clamp associated factor | 0.48 | 8.41e-07 | TRPM4 | transient receptor potential cation |
| -0.85 | 1.14e-24 | NUSAP1 | nucleolar and spindle associated pr | 0.48 | 1.36e-03 | FAM83H | family with sequence similarity 83 |
| -0.84 | 3.50e-14 | KNSTRN | kinetochore localized astrin (SPAG5) | 0.48 | 3.22e-03 | CDH1 | cadherin 1 |
| -0.84 | 3.45e-12 | GTSE1 | G2 and S-phase expressed 1 | 0.48 | 1.64e-02 | KRT7 | keratin 7 |
| -0.83 | 6.11e-15 | POLA2 | DNA polymerase alpha 2, accessory s | 0.47 | 9.29e-03 | ITGA2 | integrin subunit alpha 2 |
| -0.83 | 2.46e-10 | BLM | BLM RecQ like helicase | 0.46 | 1.48e-04 | OCLN | occludin |
| -0.81 | 3.39e-14 | PRMT3 | protein arginine methyltransferase | 0.46 | 7.54e-04 | ACSF2 | acyl-CoA synthetase family member 2 |
| -0.81 | 2.26e-12 | ZWINT | ZW10 interacting kinetochore protei | 0.45 | 6.02e-03 | EPHX1 | epoxide hydrolase 1 |
| -0.81 | 9.44e-11 | C9orf78 | chromosome 9 open reading frame 78 | 0.45 | 7.75e-03 | PPL | periplakin |
| -0.8 | 1.43e-15 | SAAL1 | serum amyloid A like 1 | 0.44 | 7.45e-04 | NME3 | NME/NM23 nucleoside diphosphate kin |
| -0.8 | 2.09e-12 | ZNF593 | zinc finger protein 593 | 0.44 | 2.81e-04 | GGCX | gamma-glutamyl carboxylase |
| -0.8 | 4.08e-10 | YTHDF1 | YTH N6-methyladenosine RNA binding | 0.44 | 8.37e-04 | CIB1 | calcium and integrin binding 1 |
| -0.79 | 2.75e-09 | NACA2 | nascent polypeptide associated comp | 0.44 | 1.75e-03 | ABLIM1 | actin binding LIM protein 1 |

Differentially expressed proteins at absence/low amount of AURKB , DB1

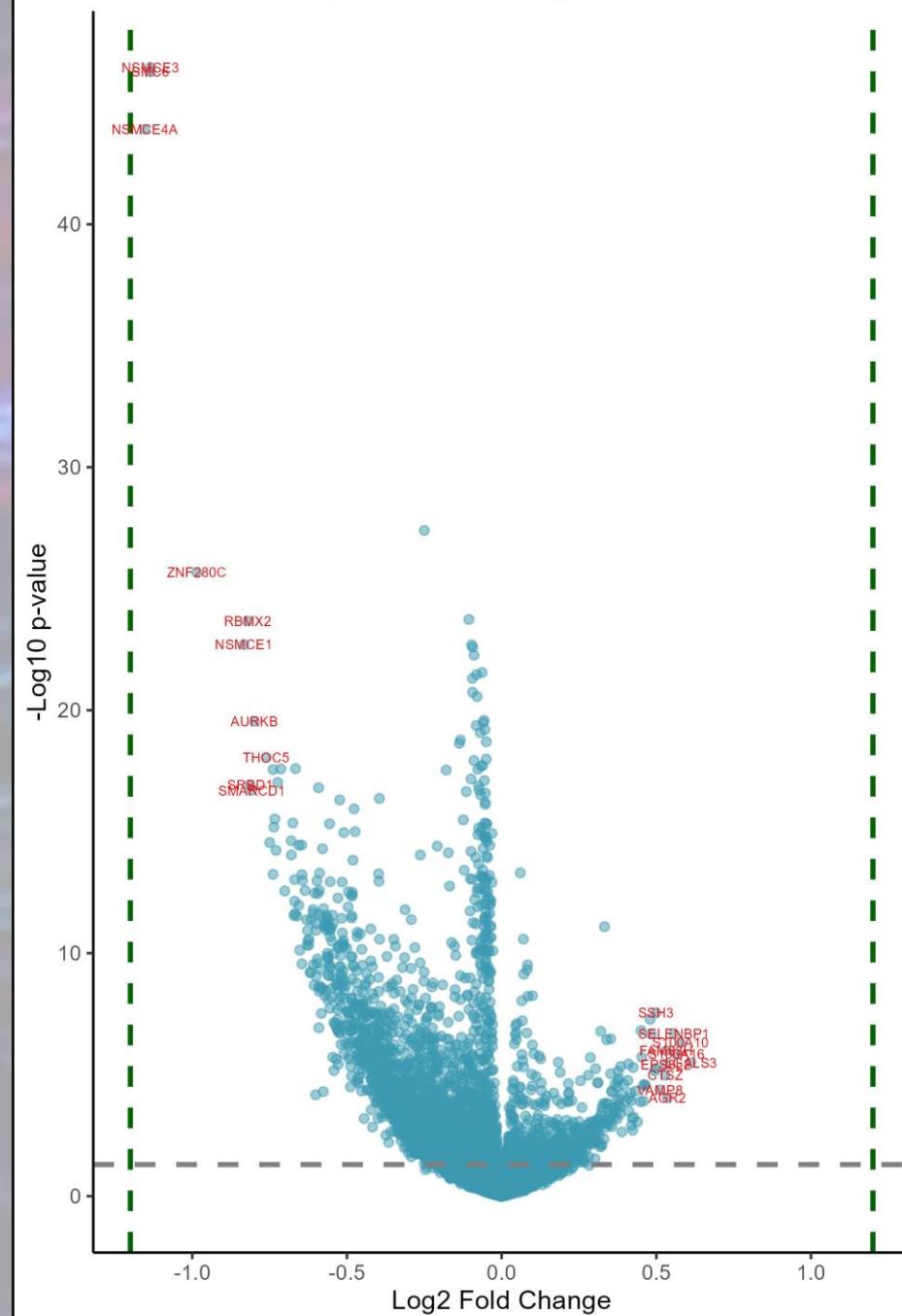
p-value < 0.05 & logFC > 1.2



Downregulated at low/absent AURKB Upregulated at low/absent AURKB

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|--------|-------------------------------------|-------|-----------|----------|-------------------------------------|
| -1.14 | 1.52e-45 | CDCA5 | cell division cycle associated 5 | 0.69 | 2.25e-05 | S100A6 | S100 calcium binding protein A6 |
| -1.05 | 1.94e-62 | INCENP | inner centromere protein | 0.68 | 9.17e-12 | ACY1 | aminoacylase 1 |
| -1.02 | 3.05e-32 | KIF2C | kinesin family member 2C | 0.67 | 1.50e-11 | SELENBP1 | selenium binding protein 1 |
| -1 | 3.90e-28 | CCNB1 | cyclin B1 | 0.65 | 2.21e-06 | S100A4 | S100 calcium binding protein A4 |
| -0.98 | 2.64e-25 | CDCA3 | cell division cycle associated 3 | 0.64 | 6.60e-06 | NQO1 | NAD(P)H quinone dehydrogenase 1 |
| -0.98 | 1.17e-30 | NUSAP1 | nucleolar and spindle associated pr | 0.62 | 2.84e-11 | ASL | argininosuccinate lyase |
| -0.97 | 1.27e-30 | EZH2 | enhancer of zeste 2 polycomb repres | 0.56 | 1.02e-10 | NOL3 | nucleolar protein 3 |
| -0.97 | 6.97e-36 | CENPF | centromere protein F | 0.56 | 9.25e-05 | LGALS3 | galectin 3 |
| -0.92 | 2.45e-32 | KIF20A | kinesin family member 20A | 0.55 | 2.15e-08 | IAH1 | isoamyl acetate hydrolyzing esteras |
| -0.91 | 1.62e-35 | SUZ12 | SUZ12 polycomb repressive complex 2 | 0.54 | 5.78e-09 | DPP7 | dipeptidyl peptidase 7 |
| -0.91 | 2.88e-63 | CDCA8 | cell division cycle associated 8 | 0.54 | 1.13e-07 | DUSP23 | dual specificity phosphatase 23 |
| -0.91 | 7.25e-37 | KIFC1 | kinesin family member C1 | 0.53 | 4.99e-07 | FAM114A1 | family with sequence similarity 114 |
| -0.9 | 3.90e-26 | CKAP2 | cytoskeleton associated protein 2 | 0.53 | 1.74e-09 | CPQ | carboxypeptidase Q |
| -0.89 | 6.47e-28 | CHAF1A | chromatin assembly factor 1 subunit | 0.52 | 1.18e-07 | GALE | UDP-galactose-4-epimerase |
| -0.86 | 8.04e-25 | PRC1 | protein regulator of cytokinesis 1 | 0.51 | 4.74e-06 | RNASET2 | ribonuclease T2 |
| -0.85 | 8.53e-22 | HELLS | helicase, lymphoid specific | 0.51 | 2.91e-06 | ME1 | malic enzyme 1 |
| -0.85 | 4.47e-18 | BLM | BLM RecQ like helicase | 0.5 | 3.32e-09 | SSH3 | slingshot protein phosphatase 3 |
| -0.8 | 1.27e-23 | KIF11 | kinesin family member 11 | 0.49 | 2.01e-06 | FAH | fumarylacetoacetate hydrolase |
| -0.8 | 4.37e-26 | ATAD2 | ATPase family AAA domain containing | 0.49 | 4.18e-07 | RBPMS | RNA binding protein, mRNA processin |
| -0.78 | 2.26e-49 | KIF22 | kinesin family member 22 | 0.47 | 4.48e-08 | APPL2 | adaptor protein, phosphotyrosine in |
| -0.78 | 1.22e-17 | NDC80 | NDC80 kinetochore complex component | 0.47 | 5.12e-06 | MVP | major vault protein |
| -0.76 | 2.75e-19 | CCNA2 | cyclin A2 | 0.46 | 7.15e-06 | ARSA | arylsulfatase A |
| -0.75 | 2.56e-18 | UBE2S | ubiquitin conjugating enzyme E2 S | 0.46 | 1.11e-05 | WASL | WASP like actin nucleation promotin |
| -0.75 | 1.86e-18 | NSD2 | nuclear receptor binding SET domain | 0.45 | 6.01e-06 | TRIOBP | TRIO and F-actin binding protein |
| -0.74 | 7.06e-16 | DLGAP5 | DLG associated protein 5 | 0.45 | 2.13e-05 | S100P | S100 calcium binding protein P |
| -0.73 | 1.10e-10 | CHRAC1 | chromatin accessibility complex sub | 0.45 | 1.88e-04 | EPS8L2 | EPS8 like 2 |
| -0.72 | 9.14e-31 | BIRC5 | baculoviral IAP repeat containing 5 | 0.44 | 4.52e-05 | PAPSS2 | 3'-phosphoadenosine 5'-phosphosulfa |
| -0.72 | 6.85e-14 | KIF23 | kinesin family member 23 | 0.44 | 1.25e-05 | RPS27L | ribosomal protein S27 like |
| -0.72 | 1.80e-18 | NUF2 | NUF2 component of NDC80 kinetochore | 0.43 | 5.20e-07 | BLVRB | biliverdin reductase B |

p-value < 0.05 & logFC > 1.2

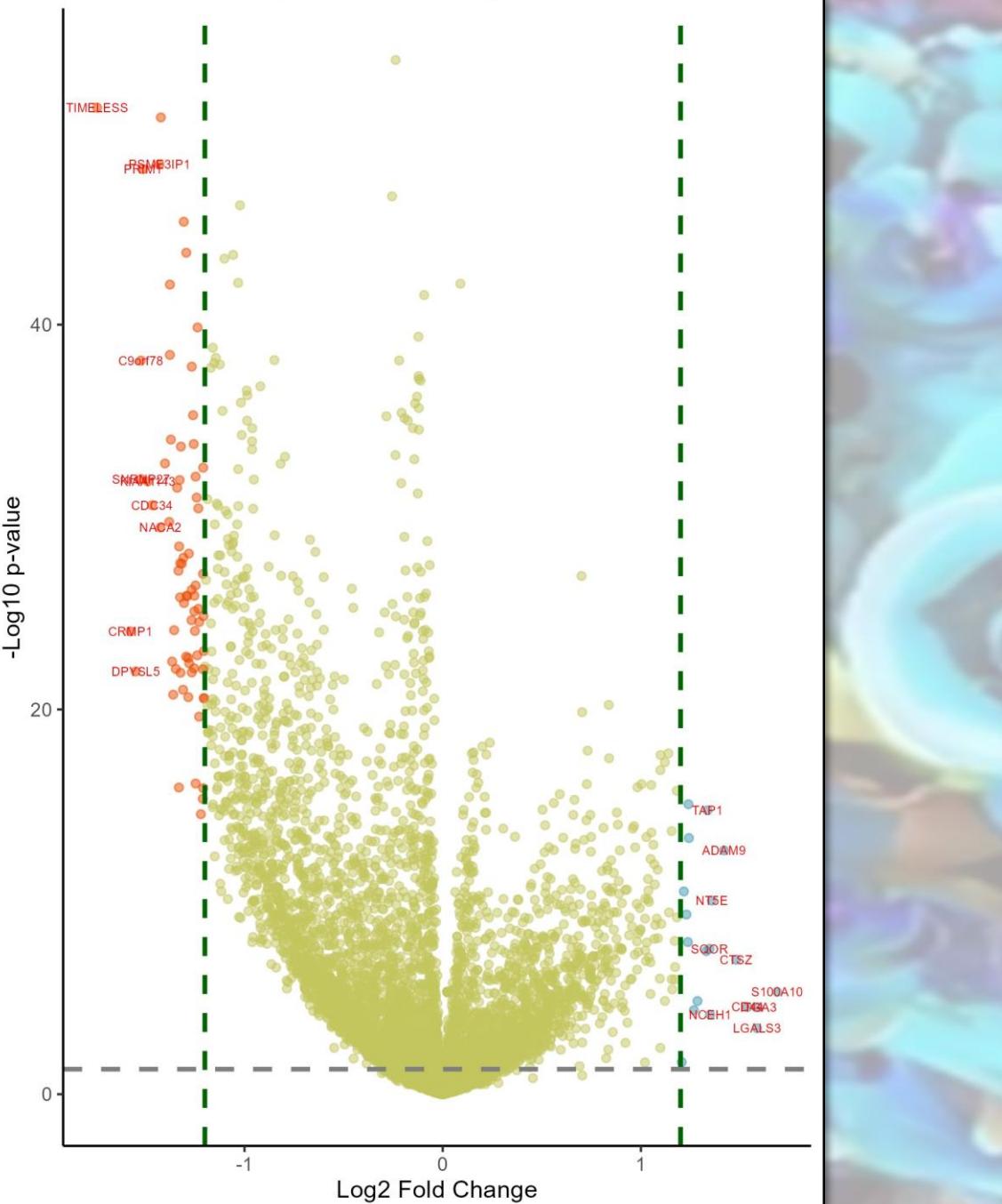


Downregulated in solid cancers at low/absent SMC5 Upregulated in solid cancers at low/absent SMC5

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|---------|-------------------------------------|-------|-----------|----------|-------------------------------------|
| -1.15 | 2.04e-41 | NSMCE4A | NSE4 homolog A, SMC5-SMC6 complex c | 0.61 | 2.97e-05 | LGALS3 | galectin 3 |
| -1.14 | 1.17e-43 | NSMCE3 | NSE3 homolog, SMC5-SMC6 complex com | 0.58 | 5.63e-06 | S100A10 | S100 calcium binding protein A10 |
| -1.14 | 1.17e-43 | SMC6 | structural maintenance of chromosom | 0.57 | 1.49e-05 | S100A16 | S100 calcium binding protein A16 |
| -0.99 | 2.36e-23 | ZNF280C | zinc finger protein 280C | 0.56 | 2.65e-06 | SELENBP1 | selenium binding protein 1 |
| -0.83 | 1.37e-20 | NSMCE1 | NSE1 homolog, SMC5-SMC6 complex com | 0.54 | 5.57e-04 | AGR2 | anterior gradient 2, protein disulp |
| -0.82 | 1.77e-21 | RBMX2 | RNA binding motif protein X-linked | 0.53 | 1.09e-05 | FAM83H | family with sequence similarity 83 |
| -0.81 | 2.01e-15 | SRBD1 | S1 RNA binding domain 1 | 0.53 | 3.47e-05 | EPS8L2 | EPS8 like 2 |
| -0.81 | 3.03e-15 | SMARCD1 | SWI/SNF related, matrix associated, | 0.53 | 8.70e-05 | CTSZ | cathepsin Z |
| -0.8 | 9.94e-18 | AURKB | aurora kinase B | 0.51 | 2.93e-04 | VAMP8 | vesicle associated membrane protein |
| -0.76 | 2.20e-16 | THOC5 | THO complex 5 | 0.5 | 4.60e-07 | SSH3 | slingshot protein phosphatase 3 |
| -0.75 | 2.53e-13 | HELLS | helicase, lymphoid specific | 0.5 | 4.90e-05 | SQOR | sulfide quinone oxidoreductase |
| -0.74 | 5.25e-16 | NSMCE2 | NSE2 (MMS21) homolog, SMC5-SMC6 com | 0.49 | 6.07e-05 | S100P | S100 calcium binding protein P |
| -0.74 | 3.95e-12 | BRD3 | bromodomain containing 3 | 0.48 | 2.72e-06 | KIAA1217 | KIAA1217 |
| -0.74 | 7.16e-14 | EZH2 | enhancer of zeste 2 polycomb repres | 0.48 | 7.99e-07 | BLVRB | biliverdin reductase B |
| -0.73 | 3.77e-14 | NOL9 | nucleolar protein 9 | 0.46 | 1.98e-04 | PAPSS2 | 3'-phosphoadenosine 5'-phosphosulfa |
| -0.73 | 4.82e-13 | SENP3 | SUMO specific peptidase 3 | 0.46 | 2.09e-04 | NDRG1 | N-myc downstream regulated 1 |
| -0.72 | 1.60e-15 | MDN1 | midasin AAA ATPase 1 | 0.46 | 1.87e-04 | RNASET2 | ribonuclease T2 |
| -0.71 | 5.24e-16 | VIRMA | vir like m6A methyltransferase asso | 0.46 | 7.18e-04 | CAPG | capping actin protein, gelsolin lik |
| -0.7 | 1.51e-11 | TMEM209 | transmembrane protein 209 | 0.45 | 1.91e-05 | S100A11 | S100 calcium binding protein A11 |
| -0.68 | 2.17e-13 | RRP7A | ribosomal RNA processing 7 homolog | 0.45 | 2.07e-06 | LPP | LIM domain containing preferred tra |
| -0.68 | 7.14e-13 | RBM45 | RNA binding motif protein 45 | 0.45 | 7.63e-04 | DDT | D-dopachrome tautomerase |
| -0.68 | 5.24e-14 | TRRAP | transformation/transcription domain | 0.44 | 3.95e-03 | S100A4 | S100 calcium binding protein A4 |
| -0.67 | 1.19e-10 | PHF2 | PHD finger protein 2 | 0.43 | 3.22e-04 | HSPB8 | heat shock protein family B (small) |
| -0.67 | 5.89e-12 | CWC22 | CWC22 spliceosome associated protei | 0.43 | 2.70e-03 | ANXA3 | annexin A3 |
| -0.67 | 3.55e-11 | MEAF6 | MYST/Esa1 associated factor 6 | 0.43 | 4.47e-05 | NQO2 | N-ribosyldihydronicotinamide:quinon |
| -0.67 | 1.02e-10 | SUDS3 | SDS3 homolog, SIN3A corepressor com | 0.42 | 7.66e-03 | NQO1 | NAD(P)H quinone dehydrogenase 1 |
| -0.67 | 5.23e-16 | EED | embryonic ectoderm development | 0.42 | 3.00e-03 | ITGB4 | integrin subunit beta 4 |
| -0.66 | 1.25e-10 | ABT1 | activator of basal transcription 1 | 0.42 | 5.23e-03 | S100A14 | S100 calcium binding protein A14 |
| -0.66 | 3.13e-13 | FCF1 | FCF1 rRNA-processing protein | 0.42 | 6.96e-04 | SERF2 | small EDRK-rich factor 2 |

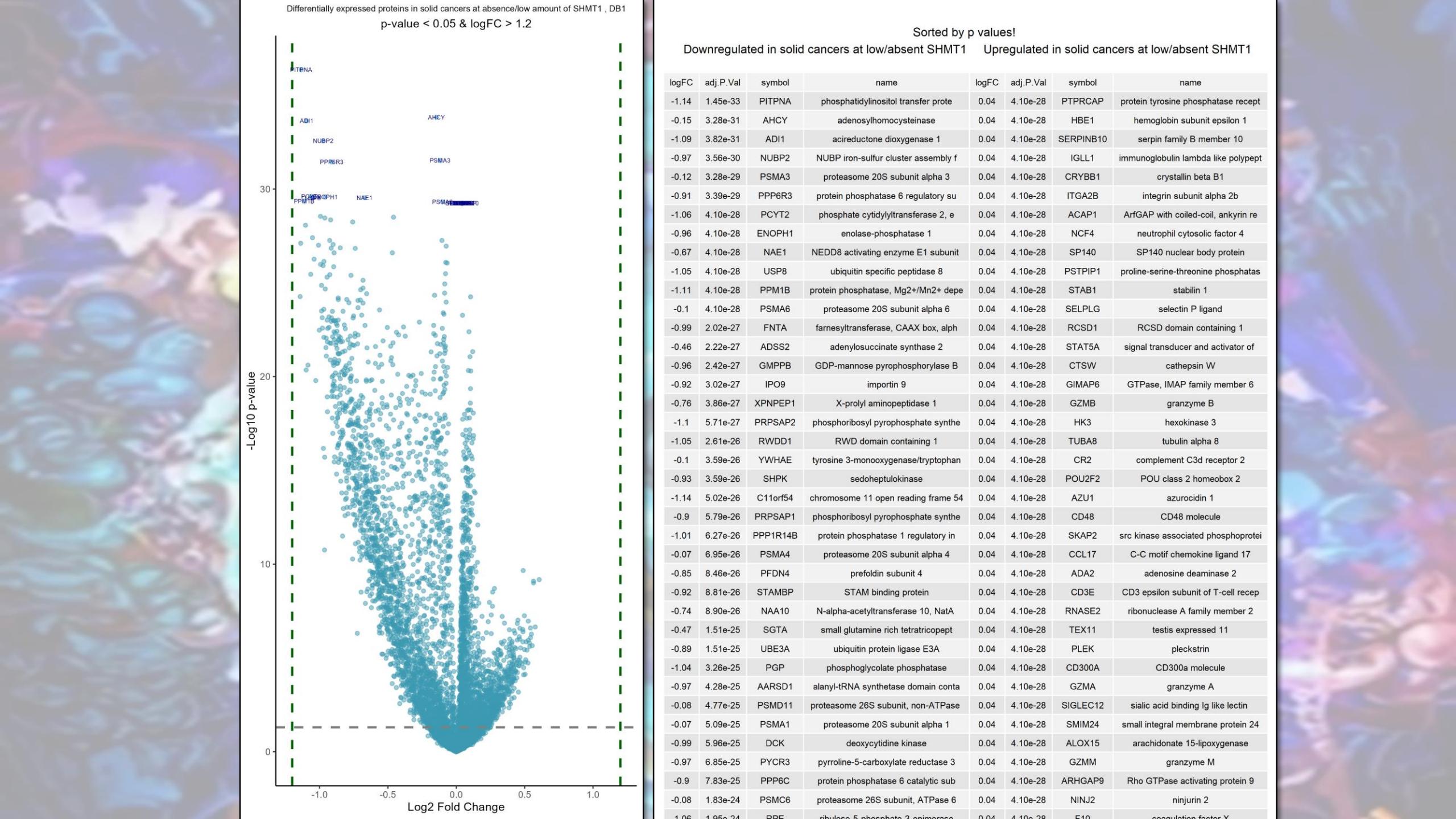
Differentially expressed proteins in solid cancers at absence/low amount of TIPIN , DB1

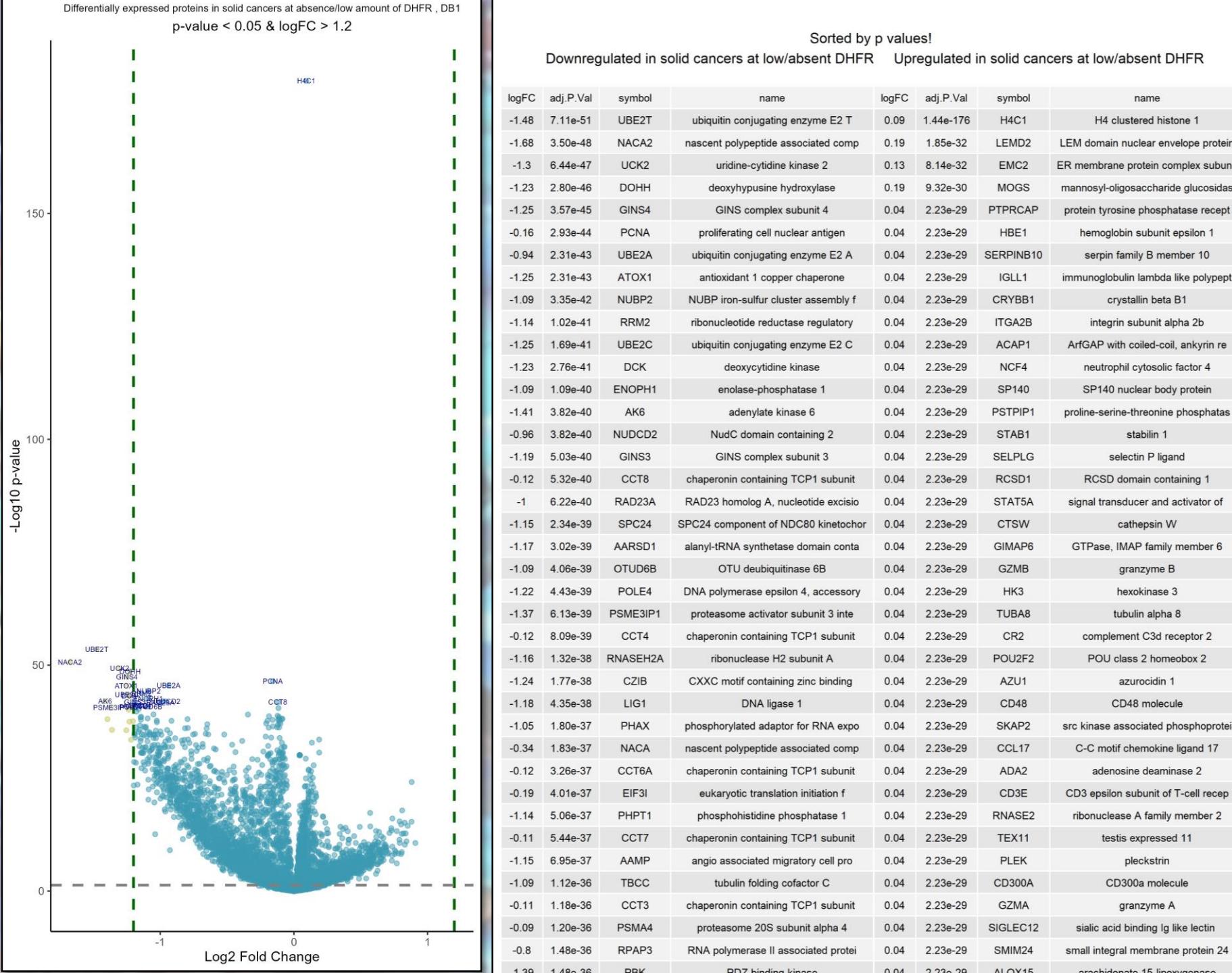
p-value < 0.05 & logFC > 1.2



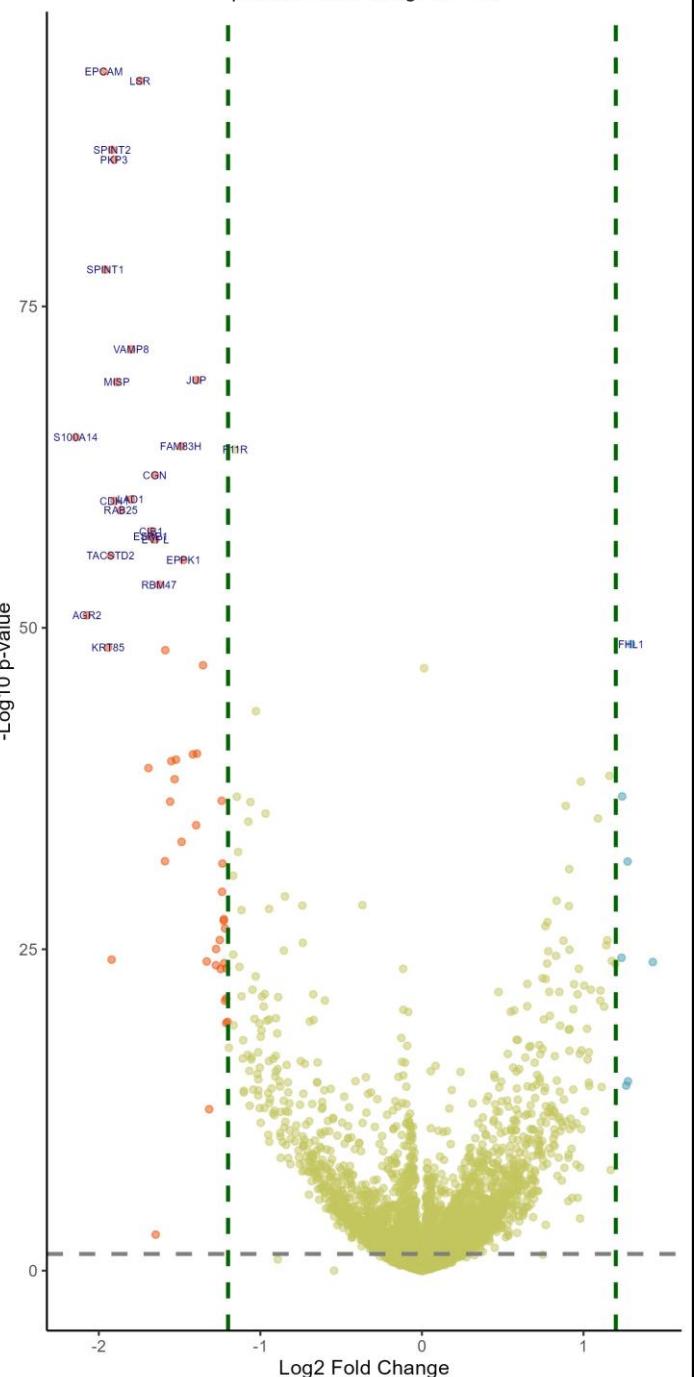
Downregulated in solid cancers at low/absent TIPIN Upregulated in solid cancers at low/absent TIPIN

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|--|-------|-----------|---------|---|
| -1.74 | 1.16e-48 | TIMELESS | timeless circadian regulator | 1.69 | 1.42e-05 | S100A10 | S100 calcium binding protein A10 |
| -1.58 | 3.22e-23 | CRMP1 | collapsin response mediator protein | 1.59 | 7.90e-05 | ITGA3 | integrin subunit alpha 3 |
| -1.55 | 3.00e-21 | DPYSL5 | dihydropyrimidinase like 5 | 1.59 | 8.08e-04 | LGALS3 | galectin 3 |
| -1.52 | 2.04e-36 | C9orf78 | chromosome 9 open reading frame 78 | 1.54 | 7.59e-05 | CD44 | CD44 molecule (Indian blood group) |
| -1.52 | 1.12e-30 | SNRNP27 | small nuclear ribonucleoprotein U4/6 | 1.48 | 4.12e-07 | CTSZ | cathepsin Z |
| -1.51 | 9.04e-46 | PRIM1 | DNA primase subunit 1 | 1.42 | 1.88e-12 | ADAM9 | ADAM metallopeptidase domain 9 |
| -1.49 | 1.42e-30 | KIAA1143 | KIAA1143 | 1.36 | 5.37e-10 | NT5E | 5'-nucleotidase ecto |
| -1.47 | 2.21e-29 | CDC34 | cell division cycle 34, ubiquitin c | 1.35 | 1.80e-04 | NCEH1 | neutral cholesterol ester hydrolase |
| -1.43 | 6.26e-46 | PSME3IP1 | proteasome activator subunit 3 inte | 1.35 | 1.20e-07 | SQOR | sulfide quinone oxidoreductase |
| -1.42 | 2.75e-28 | NACA2 | nascent polypeptide associated comp | 1.34 | 2.06e-14 | TAP1 | transporter 1, ATP binding cassette |
| -1.42 | 2.81e-48 | UBE2T | ubiquitin conjugating enzyme E2 T | 1.33 | 1.56e-07 | S100A16 | S100 calcium binding protein A16 |
| -1.4 | 1.88e-31 | YRDC | yrdC N6-threonylcarbamoyltransferas | 1.29 | 3.94e-05 | MYOF | myoferlin |
| -1.38 | 1.49e-28 | SMAD4 | SMAD family member 4 | 1.27 | 1.09e-04 | CAVIN1 | caveolae associated protein 1 |
| -1.38 | 1.24e-36 | POLA2 | DNA polymerase alpha 2, accessory s | 1.24 | 4.77e-13 | CD109 | CD109 molecule |
| -1.38 | 3.64e-40 | CCDC43 | coiled-coil domain containing 43 | 1.24 | 1.02e-14 | TAP2 | transporter 2, ATP binding cassette |
| -1.37 | 1.25e-32 | PRRC2B | proline rich coiled-coil 2B | 1.24 | 5.66e-08 | PPIC | peptidylprolyl isomerase C |
| -1.37 | 9.91e-22 | GINS2 | GINS complex subunit 2 | 1.23 | 2.57e-09 | HLA-B | major histocompatibility complex, class I |
| -1.36 | 4.22e-20 | CRIP1 | CXXC repeat containing interactor o | 1.22 | 1.94e-10 | ENDOD1 | endonuclease domain containing 1 |
| -1.36 | 2.84e-23 | TUBB2B | tubulin beta 2B class IIb | 1.21 | 3.39e-02 | S100A6 | S100 calcium binding protein A6 |
| -1.35 | 2.27e-21 | HIRIP3 | HIRA interacting protein 3 | 1.18 | 3.55e-09 | RRAS | RAS related |
| -1.34 | 2.94e-30 | TXLNG | taxilin gamma | 1.18 | 2.27e-15 | FNDC3B | fibronectin type III domain contain |
| -1.33 | 3.76e-26 | TLE5 | TLE family member 5, transcriptional | 1.17 | 9.38e-07 | EGFR | epidermal growth factor receptor |
| -1.33 | 1.56e-15 | KIF1A | kinesin family member 1A | 1.17 | 3.76e-06 | MVP | major vault protein |
| -1.33 | 2.42e-27 | ACYP1 | acylphosphatase 1 | 1.17 | 5.00e-08 | CD59 | CD59 molecule (CD59 blood group) |
| -1.33 | 1.22e-30 | PIN4 | peptidylprolyl cis/trans isomerase, endoplasmic reticulum-associated | 1.16 | 1.12e-05 | TAPBP | TAP binding protein |
| -1.32 | 7.08e-25 | HDHD2 | haloacid dehalogenase like hydrolase | 1.16 | 2.19e-13 | SP100 | SP100 nuclear antigen |
| -1.32 | 1.64e-26 | POLA1 | DNA polymerase alpha 1, catalytic subunit | 1.15 | 3.65e-06 | ITGA2 | integrin subunit alpha 2 |
| -1.32 | 3.43e-21 | TCF12 | transcription factor 12 | 1.14 | 2.02e-09 | MMP14 | matrix metallopeptidase 14 |
| -1.32 | 2.72e-32 | PM20D2 | peptidase M20 domain containing 2 | 1.14 | 3.32e-17 | RETSAT | retinol saturase |





Differentially expressed proteins in solid cancers at absence/low amount of MUC1 , DB1
p-value < 0.05 & logFC > 1.2



Sorted by p values!
Downregulated in solid cancers at low/absent MUC1 Upregulated in solid cancers at low/absent MUC1

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|-----------|-------------------------------------|-------|-----------|---------|--|
| -1.97 | 1.81e-90 | EPCAM | epithelial cell adhesion molecule | 1.29 | 5.12e-47 | FHL1 | four and a half LIM domains 1 |
| -1.74 | 6.28e-90 | LSR | lipolysis stimulated lipoprotein re | 0.01 | 3.25e-45 | H4C1 | H4 clustered histone 1 |
| -1.92 | 1.07e-84 | SPINT2 | serine peptidase inhibitor, Kunitz | 1.16 | 6.12e-37 | NCS1 | neuronal calcium sensor 1 |
| -1.91 | 5.17e-84 | PKP3 | plakophilin 3 | 0.98 | 1.64e-36 | PLCG1 | phospholipase C gamma 1 |
| -1.96 | 1.51e-75 | SPINT1 | serine peptidase inhibitor, Kunitz | 1.24 | 2.25e-35 | SYNM | synemin |
| -1.8 | 2.09e-69 | VAMP8 | vesicle associated membrane protein | 0.89 | 1.09e-34 | ELMO2 | engulfment and cell motility 2 |
| -1.39 | 4.54e-67 | JUP | junction plakoglobin | 1.09 | 9.96e-34 | THY1 | Thy-1 cell surface antigen |
| -1.89 | 5.54e-67 | MISP | mitotic spindle positioning | 1.27 | 1.96e-30 | SPARC | secreted protein acidic and cystein |
| -2.14 | 9.97e-63 | S100A14 | S100 calcium binding protein A14 | 0.91 | 7.36e-30 | GSDME | gasdermin E |
| -1.49 | 4.48e-62 | FAM83H | family with sequence similarity 83 | 0.83 | 1.98e-27 | TBC1D13 | TBC1 domain family member 13 |
| -1.16 | 7.25e-62 | F11R | F11 receptor | 0.91 | 4.86e-27 | DAB2 | DAB adaptor protein 2 |
| -1.65 | 6.92e-60 | CGN | cingulin | 0.78 | 7.81e-26 | TGFBI1 | transforming growth factor beta 1 i |
| -1.8 | 4.89e-58 | LAD1 | ladinin 1 | 0.76 | 1.63e-25 | DPYSL4 | dihydropyrimidinase like 4 |
| -1.9 | 5.88e-58 | CDH1 | cadherin 1 | 1.15 | 1.91e-24 | TUBB2A | tubulin beta 2A class Ila |
| -1.86 | 2.96e-57 | RAB25 | RAB25, member RAS oncogene family | 0.88 | 2.05e-24 | USP13 | ubiquitin specific peptidase 13 |
| -1.68 | 1.21e-55 | CIB1 | calcium and integrin binding 1 | 1.14 | 4.56e-24 | P3H3 | prolyl 3-hydroxylase 3 |
| -1.68 | 2.95e-55 | ESRP1 | epithelial splicing regulatory prot | 0.91 | 9.60e-24 | RFTN1 | raftlin, lipid raft linker 1 |
| -1.65 | 4.69e-55 | EVPL | envoplakin | 0.78 | 1.27e-23 | CNTNAP1 | contactin associated protein 1 |
| -1.93 | 8.02e-54 | TACSTD2 | tumor associated calcium signal tra | 0.83 | 2.78e-23 | CDH13 | cadherin 13 |
| -1.48 | 1.68e-53 | EPPK1 | epiplakin 1 | 1.24 | 3.89e-23 | CEP170 | centrosomal protein 170 |
| -1.63 | 1.33e-51 | RBM47 | RNA binding motif protein 47 | 1.18 | 6.60e-23 | CSRP2 | cysteine and glycine rich protein 2 |
| -2.07 | 3.07e-49 | AGR2 | anterior gradient 2, protein disulp | 1.43 | 7.93e-23 | CDH2 | cadherin 2 |
| -1.94 | 9.06e-47 | KRT85 | keratin 85 | 0.77 | 1.01e-22 | MICAL1 | microtubule associated monooxygenases |
| -1.59 | 1.40e-46 | ST14 | ST14 transmembrane serine protease | 1.2 | 1.06e-22 | CCDC50 | coiled-coil domain containing 50 |
| -1.36 | 2.01e-45 | EPS8L2 | EPS8 like 2 | 0.97 | 2.42e-22 | CAP2 | cyclase associated actin cytoskelet |
| -1.03 | 6.91e-42 | DSP | desmoplakin | 0.75 | 1.26e-21 | SARM1 | sterile alpha and TIR motif contain |
| -1.39 | 1.34e-38 | OCLN | occludin | 0.77 | 1.43e-21 | MAP7D3 | MAP7 domain containing 3 |
| -1.42 | 1.48e-38 | MAP7 | microtubule associated protein 7 | 0.65 | 3.44e-21 | ARMCX4 | armadillo repeat containing X-link |
| -1.52 | 3.73e-38 | LLGL2 | LLGL scribble cell polarity complex | 0.94 | 3.60e-21 | PHLDB1 | pleckstrin homology like domain fam |
| -1.55 | 4.72e-38 | AP1M2 | adaptor related protein complex 1 s | 1 | 4.57e-21 | FKBP7 | FKBP prolyl isomerase 7 |
| -1.69 | 1.58e-37 | PRSS8 | serine protease 8 | 1.05 | 9.42e-21 | MRC2 | mannose receptor C type 2 |
| -1.53 | 1.10e-36 | TJP3 | tight junction protein 3 | 1.11 | 1.07e-20 | SPART | spartin |
| -1.15 | 2.36e-35 | PPL | periplakin | 0.79 | 1.33e-20 | SRGAP2 | SLIT-ROBO Rho GTPase activating pro |
| -1.24 | 4.70e-35 | KIAA1522 | KIAA1522 | 0.85 | 1.34e-20 | SIRPA | signal regulatory protein alpha |
| -1.56 | 5.31e-35 | TSTD1 | thiosulfate sulfurtransferase like | 0.47 | 1.36e-20 | ZEB2 | zinc finger E-box binding homeobox |
| -1.06 | 5.60e-35 | DSG2 | desmoglein 2 | 0.96 | 1.99e-20 | ERC1 | ELKS/RAB6-interacting/CAST family m |
| -0.97 | 4.19e-34 | HTATIP2 | HIV-1 Tat interactive protein 2 | 1.1 | 5.77e-20 | PPM1F | protein phosphatase, Mg ²⁺ /Mn ²⁺ depe |
| -1.07 | 1.71e-33 | RAB11FIP1 | RAB11 family interacting protein 1 | 0.65 | 1.57e-19 | GNG2 | G protein subunit gamma 2 |
| -1.4 | 3.17e-33 | PAT1 | PAT1 crumbs cell polarity complex c | 1.13 | 1.66e-19 | MAD2L1 | mitotic arrest deficient 2 like 1 |