

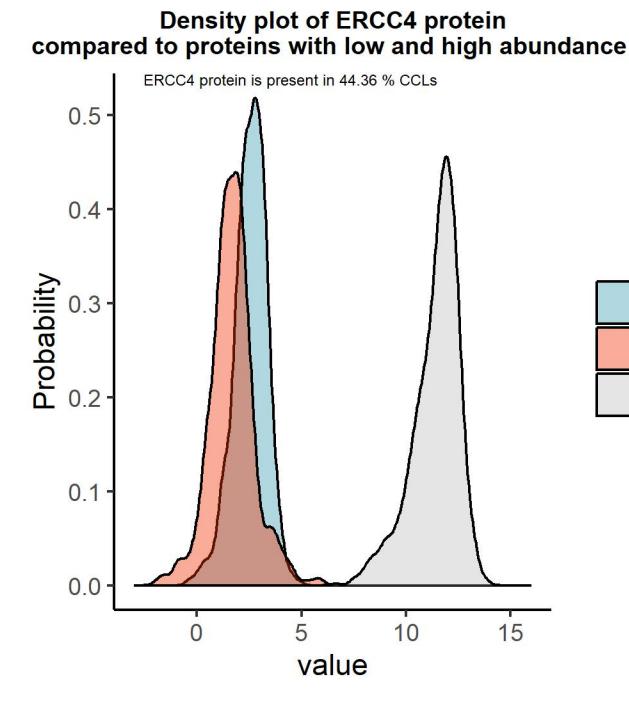
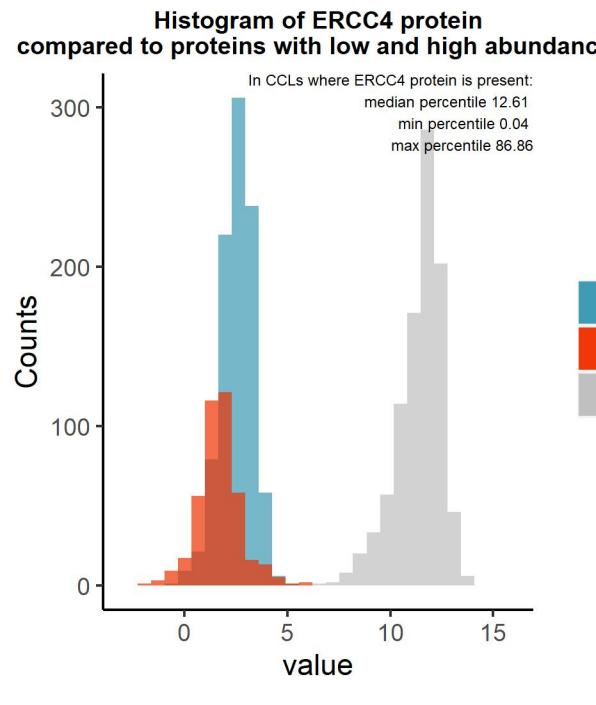
ERCC4

Protein name: XPF ; UNIPROT: Q92889 ; Gene name: ERCC excision repair 4, endonuclease catalytic subunit

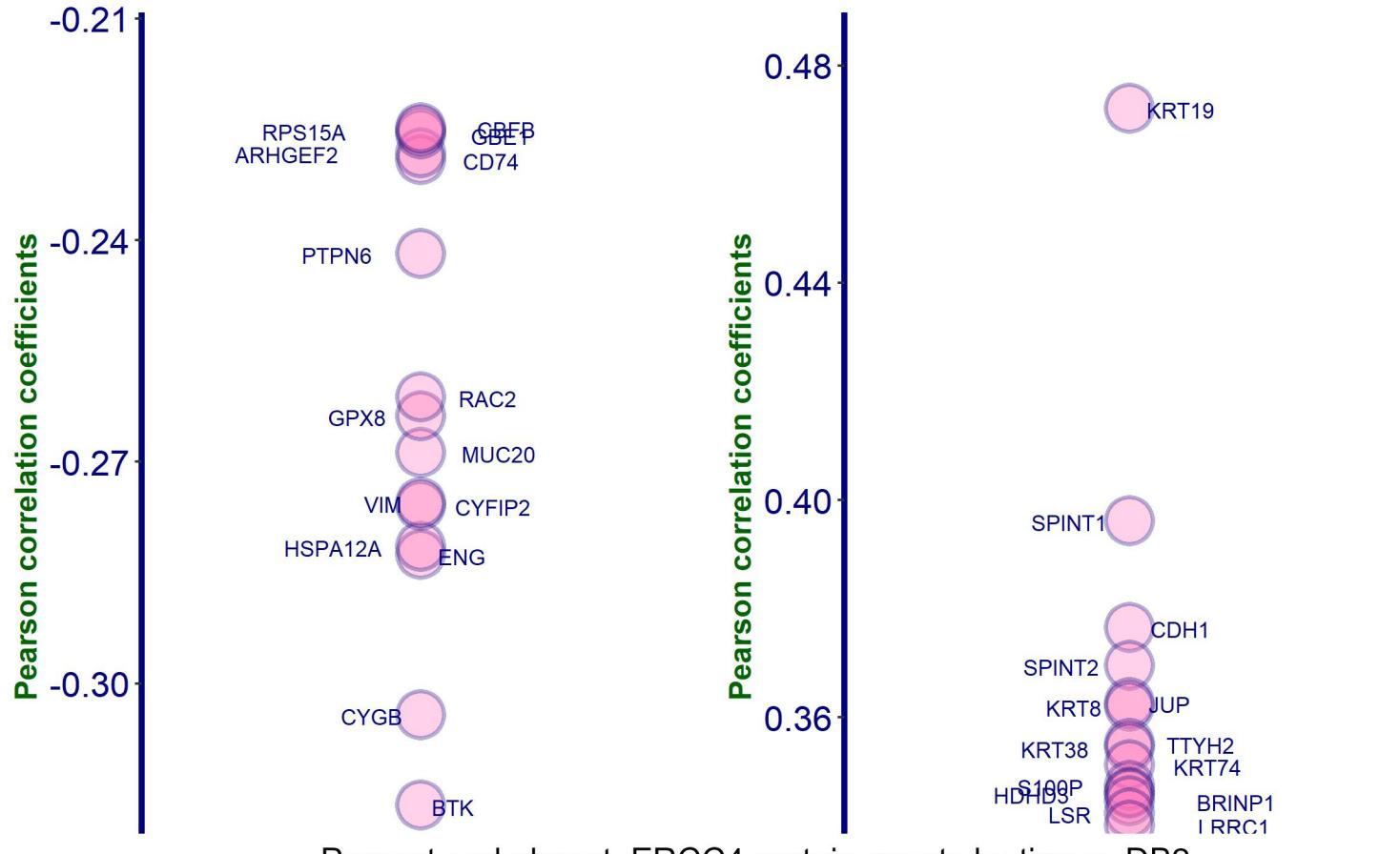
Ligandable: Yes ; Ligandable_by_Chem: Yes ; Is_enzyme: Yes (<https://cansar.ai/>)

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

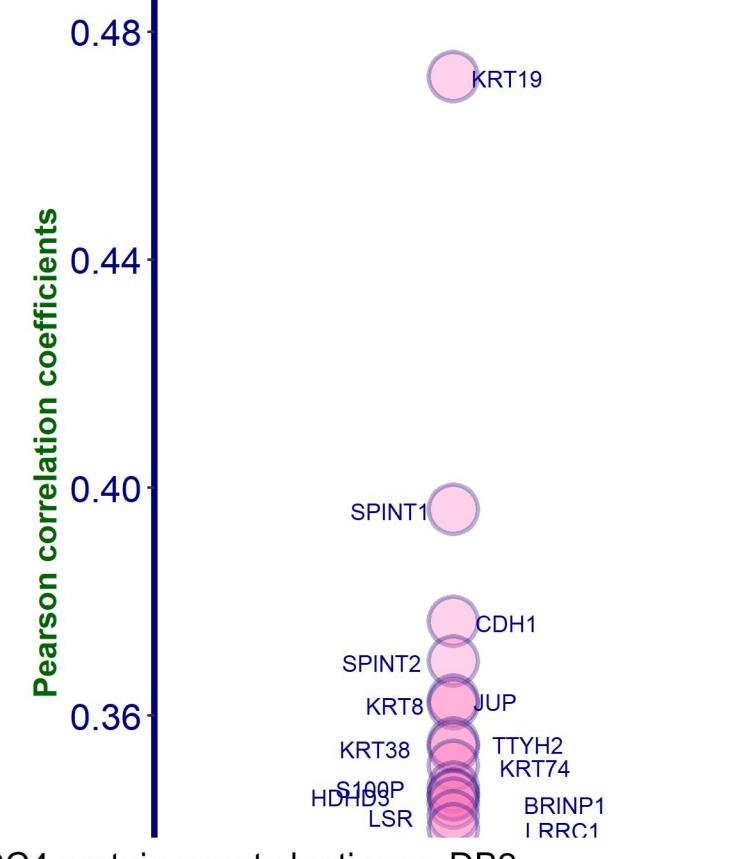
8498 proteins in same 949 CCLs



Negative correlations of ERCC4 protein, DB2

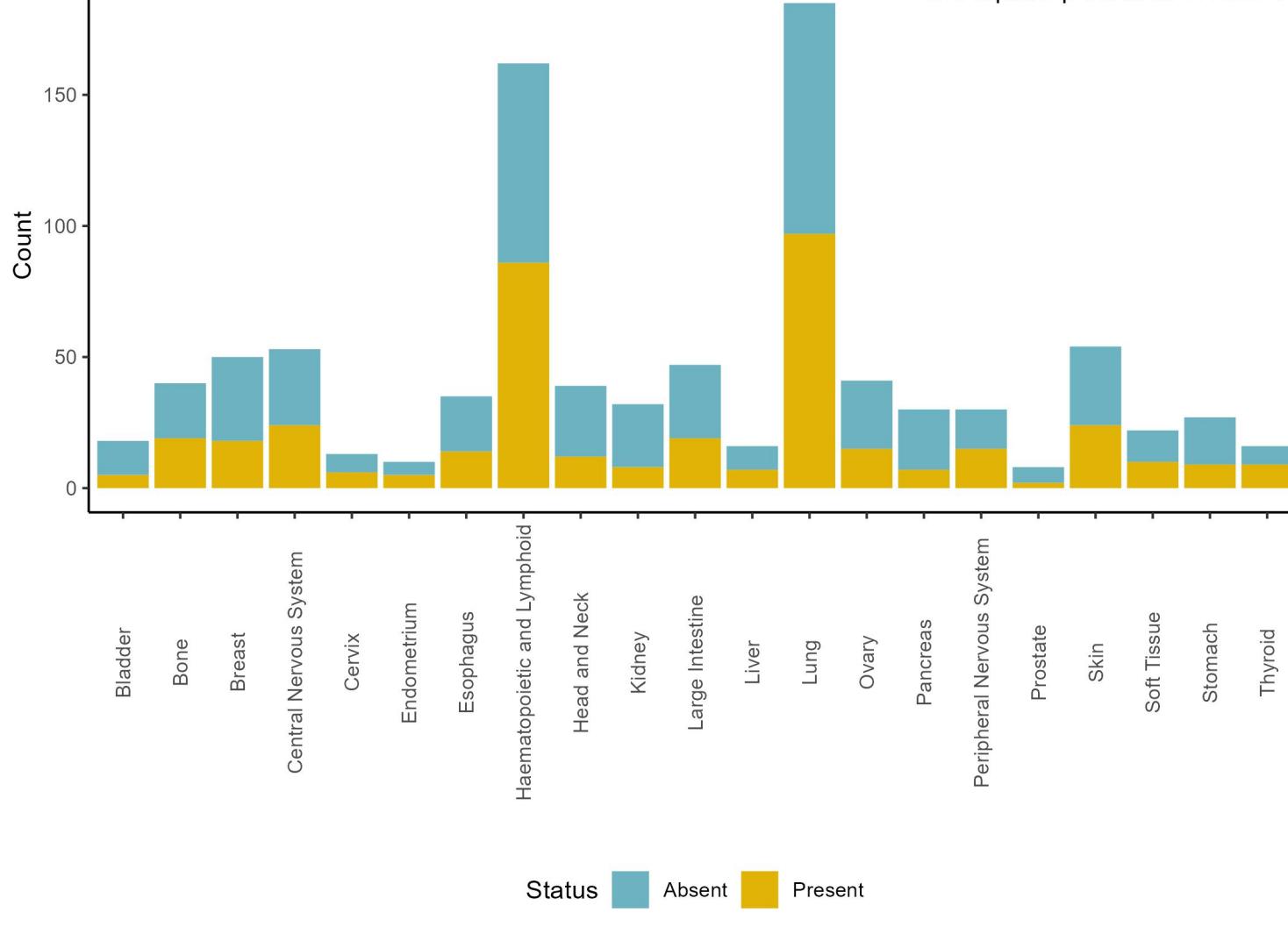
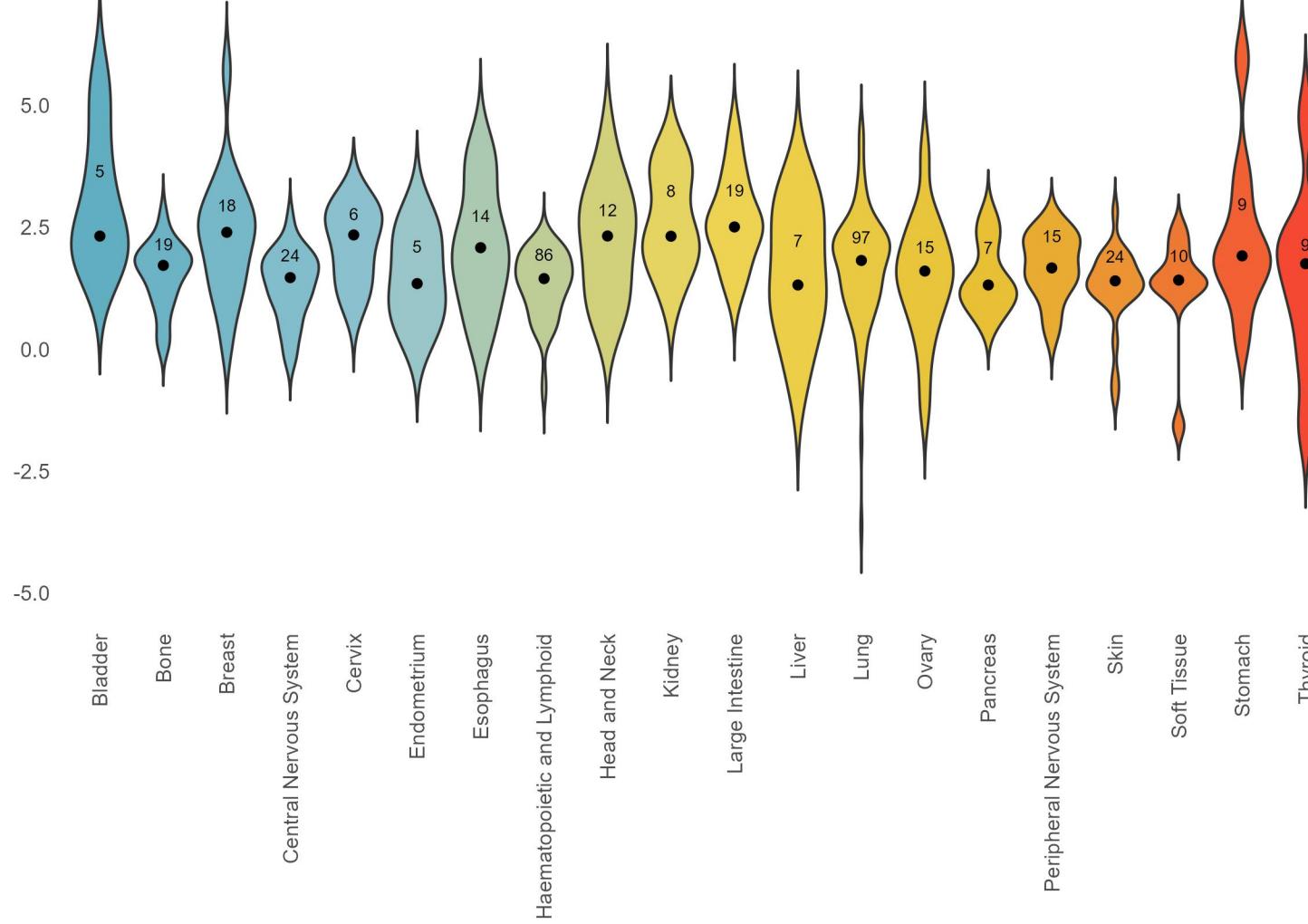


Positive correlations of ERCC4 protein, DB2



Amount of ERCC4 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 3.530e-07

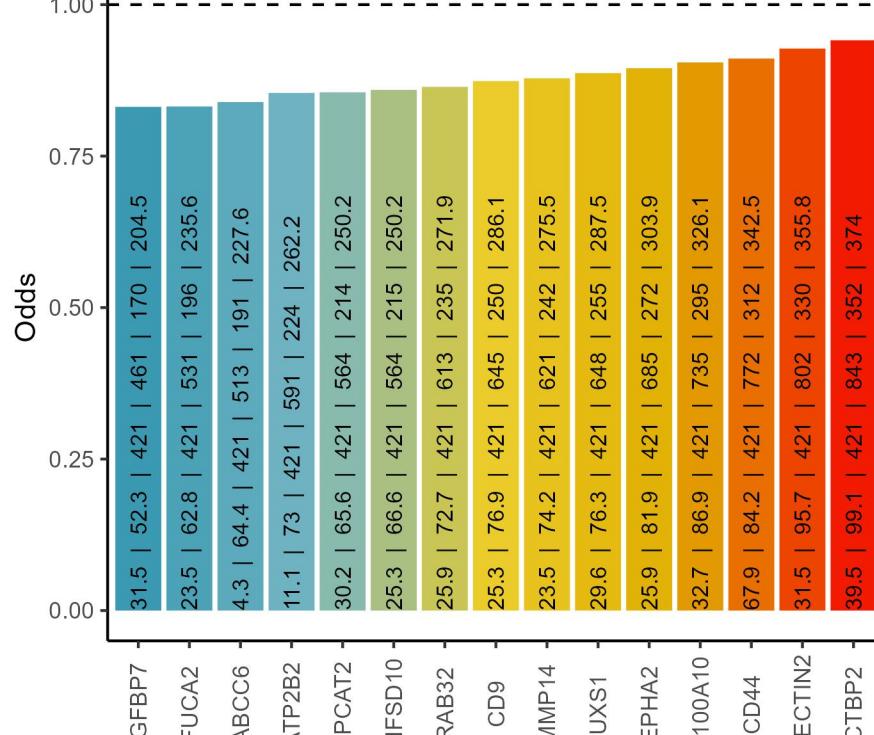


Cooccurrence with ERCC4 protein, DB2

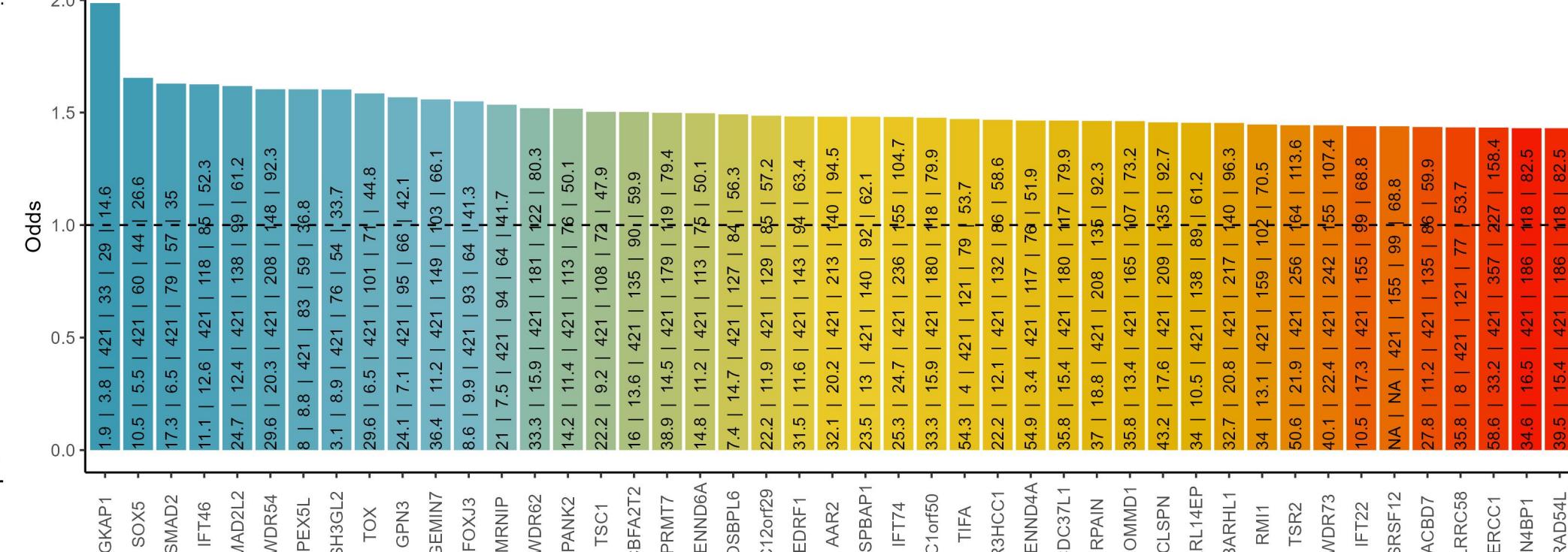
% of ERCC4 in blood cancers: 53.1 ; % of ERCC4 in solid cancers: 42.5

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ERCC4 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



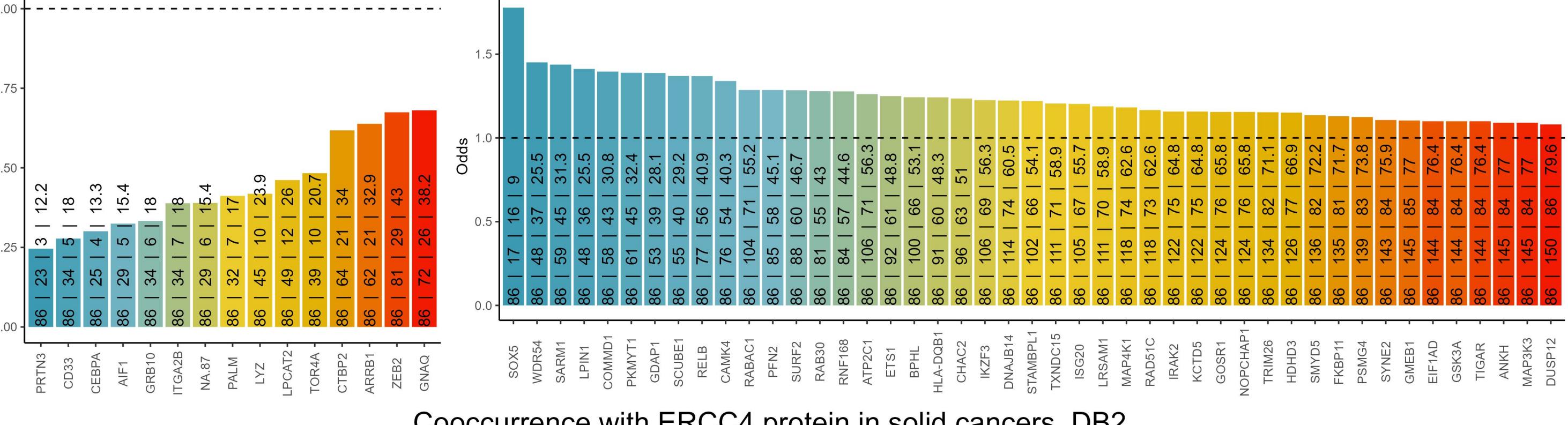
Positive cooccurrence





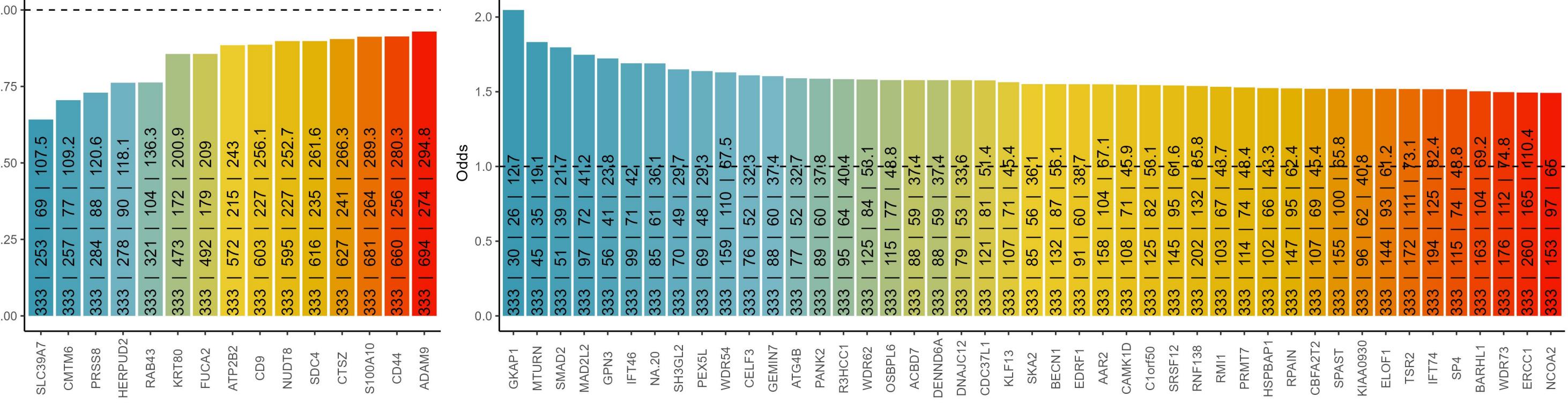
ncidence of ERCC4 | incidence of Protein 2 | observed cooccurrence | e

negative cooccurrence Positive cooccurrence

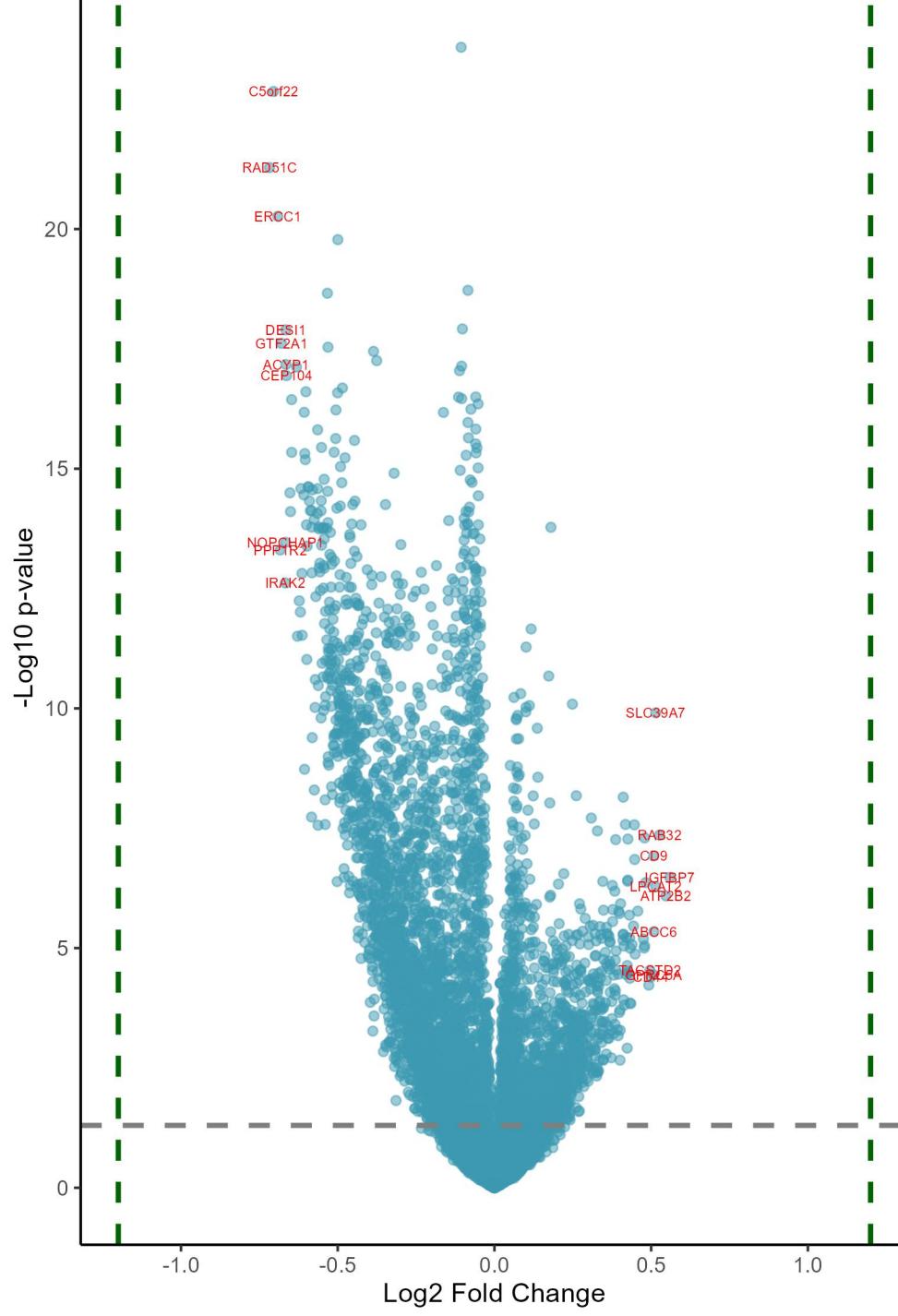


Incidence of ERCC4 | incidence of Protein 2 | observed cooccurrence | e

negative cooccurrence Positive cooccurrence

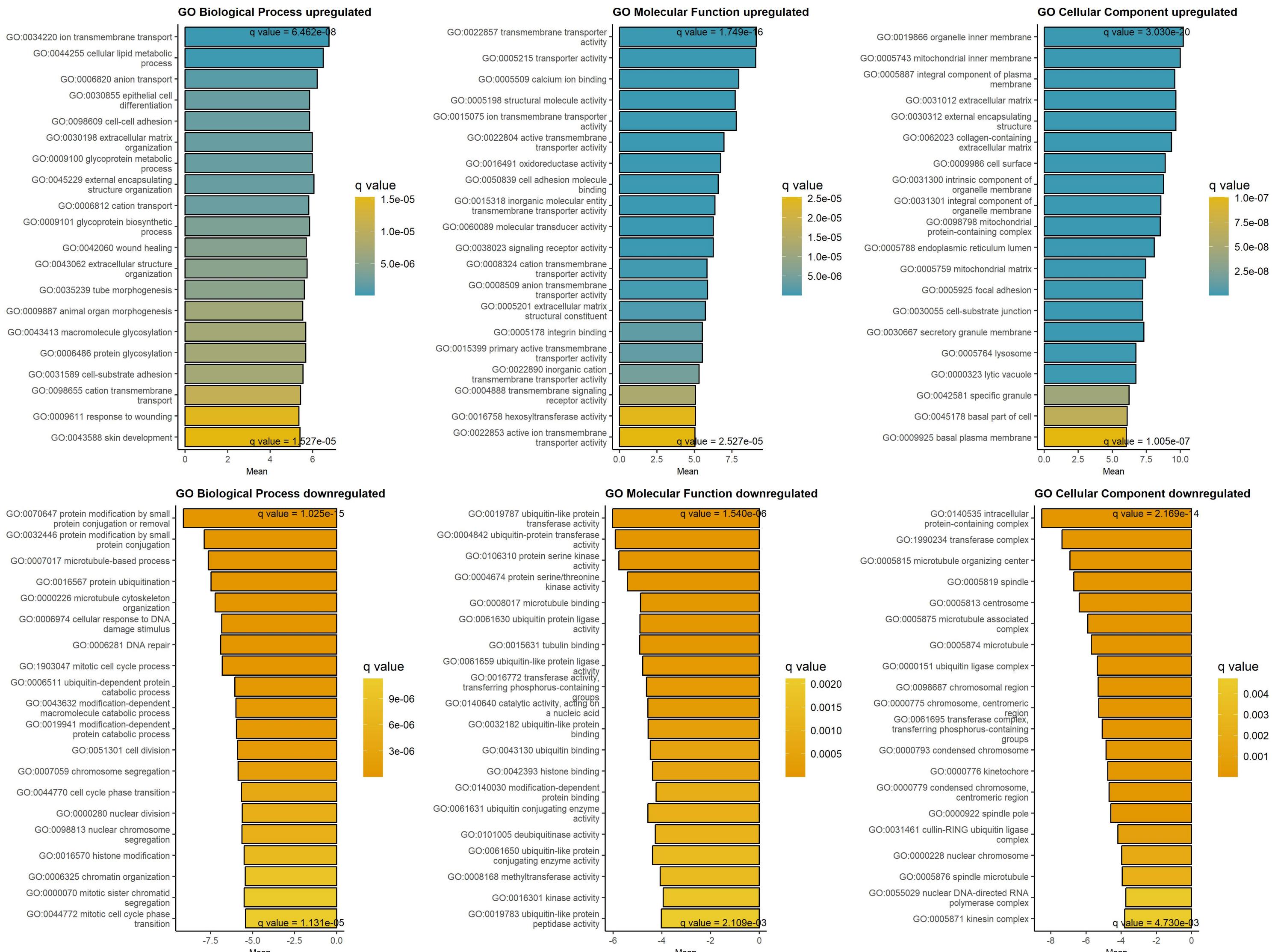


Downregulated at low/absent ERCC4 Upregulated at low/absent ERCC4



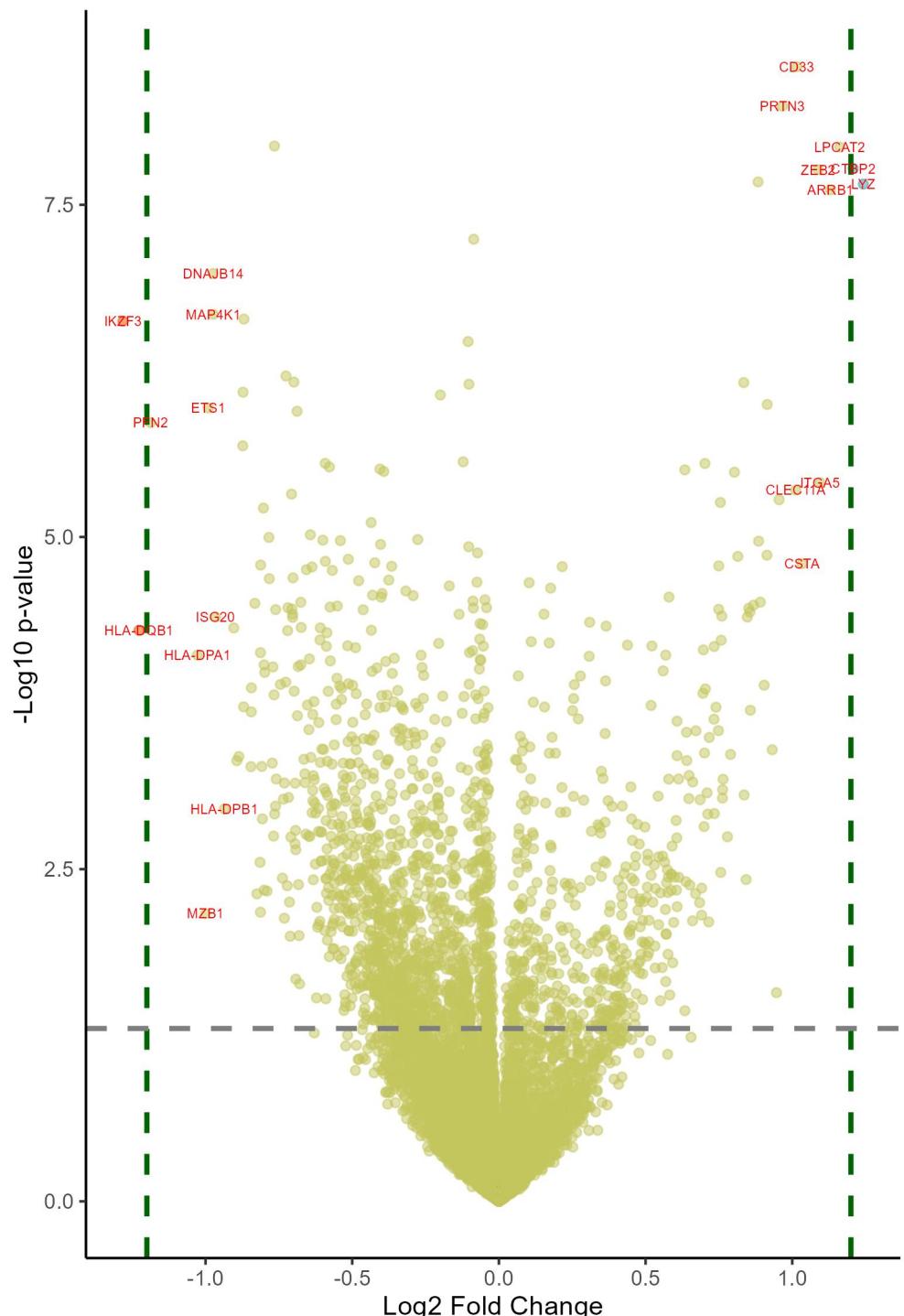
| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|--------------------------------------|-------|-----------|----------|---|
| -0.72 | 1.09e-18 | RAD51C | RAD51 paralog C | 0.56 | 2.55e-06 | IGFBP7 | insulin like growth factor binding |
| -0.7 | 3.76e-20 | C5orf22 | chromosome 5 open reading frame 22 | 0.55 | 5.62e-06 | ATP2B2 | ATPase plasma membrane Ca ²⁺ transpo |
| -0.69 | 9.10e-18 | ERCC1 | ERCC excision repair 1, endonucleas | 0.53 | 4.13e-07 | RAB32 | RAB32, member RAS oncogene family |
| -0.68 | 3.71e-12 | PPP1R2 | protein phosphatase 1 regulatory in | 0.51 | 3.74e-06 | LPCAT2 | lysophosphatidylcholine acyltransfe |
| -0.68 | 1.85e-15 | GTF2A1 | general transcription factor II A su | 0.51 | 2.44e-09 | SLC39A7 | solute carrier family 39 member 7 |
| -0.67 | 1.34e-11 | IRAK2 | interleukin 1 receptor associated k | 0.51 | 2.62e-05 | ABCC6 | ATP binding cassette subfamily C me |
| -0.67 | 2.67e-12 | NOPCHAP1 | NOP protein chaperone 1 | 0.51 | 1.62e-04 | GPRC5A | G protein-coupled receptor class C |
| -0.67 | 1.06e-15 | DESI1 | desumoylating isopeptidase 1 | 0.51 | 1.02e-06 | CD9 | CD9 molecule |
| -0.67 | 3.72e-15 | ACYP1 | acylphosphatase 1 | 0.5 | 1.79e-04 | CD44 | CD44 molecule (Indian blood group) |
| -0.66 | 5.05e-15 | CEP104 | centrosomal protein 104 | 0.5 | 1.34e-04 | TACSTD2 | tumor associated calcium signal tra |
| -0.65 | 4.30e-13 | CCDC73 | coiled-coil domain containing 73 | 0.49 | 2.50e-04 | S100A10 | S100 calcium binding protein A10 |
| -0.65 | 8.52e-13 | CEP97 | centrosomal protein 97 | 0.48 | 3.15e-06 | FUCA2 | alpha-L-fucosidase 2 |
| -0.65 | 1.16e-14 | HAUST | HAUS augmin like complex subunit 7 | 0.48 | 4.78e-05 | KRT80 | keratin 80 |
| -0.65 | 9.07e-14 | CRLF3 | cytokine receptor like factor 3 | 0.48 | 4.66e-07 | MGST2 | microsomal glutathione S-transferas |
| -0.63 | 3.72e-15 | KNSTRN | kinetochore localized astrin (SPAG5 | 0.48 | 5.27e-05 | MMP14 | matrix metallopeptidase 14 |
| -0.63 | 1.08e-10 | UBE2B | ubiquitin conjugating enzyme E2 B | 0.48 | 3.57e-05 | EPHA2 | EPH receptor A2 |
| -0.62 | 2.70e-11 | COMM8 | COMM domain containing 8 | 0.46 | 1.09e-05 | UXS1 | UDP-glucuronate decarboxylase 1 |
| -0.62 | 4.13e-11 | CNOT6L | CCR4-NOT transcription complex subu | 0.45 | 6.84e-05 | EHD2 | EH domain containing 2 |
| -0.62 | 3.68e-13 | SMYD3 | SET and MYND domain containing 3 | 0.45 | 1.18e-06 | ALDH3B1 | aldehyde dehydrogenase 3 family mem |
| -0.61 | 9.15e-12 | HDHD2 | haloacid dehalogenase like hydrolas | 0.45 | 2.68e-07 | TOR4A | torsin family 4 member A |
| -0.61 | 1.04e-10 | C18orf63 | chromosome 18 open reading frame 63 | 0.44 | 2.06e-05 | SDC4 | syndecan 4 |
| -0.61 | 4.66e-13 | RMI2 | RecQ mediated genome instability 2 | 0.44 | 4.55e-05 | PRSS8 | serine protease 8 |
| -0.61 | 1.81e-14 | ARIH2 | ariadne RBR E3 ubiquitin protein li | 0.44 | 5.51e-04 | MAL2 | mal, T cell differentiation protein |
| -0.61 | 2.56e-08 | ZSWIM8 | zinc finger SWIM-type containing 8 | 0.43 | 5.30e-05 | ADAM9 | ADAM metallopeptidase domain 9 |
| -0.61 | 9.20e-14 | PDE6D | phosphodiesterase 6D | 0.43 | 5.37e-04 | S100A16 | S100 calcium binding protein A16 |
| -0.6 | 1.15e-13 | GPATCH11 | G-patch domain containing 11 | 0.43 | 1.89e-04 | F3 | coagulation factor III, tissue fact |
| -0.6 | 9.88e-15 | POLR3D | RNA polymerase III subunit D | 0.43 | 3.41e-05 | FAM83H | family with sequence similarity 83 |
| -0.6 | 1.39e-12 | CFAP298 | cilia and flagella associated prote | 0.43 | 1.29e-05 | NECTIN2 | nectin cell adhesion molecule 2 |
| -0.6 | 2.78e-10 | SSNA1 | SS nuclear autoantigen 1 | 0.43 | 1.51e-04 | C15orf48 | chromosome 15 open reading frame 48 |

GAGE analysis on upregulated and downregulated proteins at low/absent ERCC4 protein, DB2



Differentially expressed proteins in blood cancers at absence/low amount of ERCC4 , DB2

p-value < 0.05 & logFC > 1.2

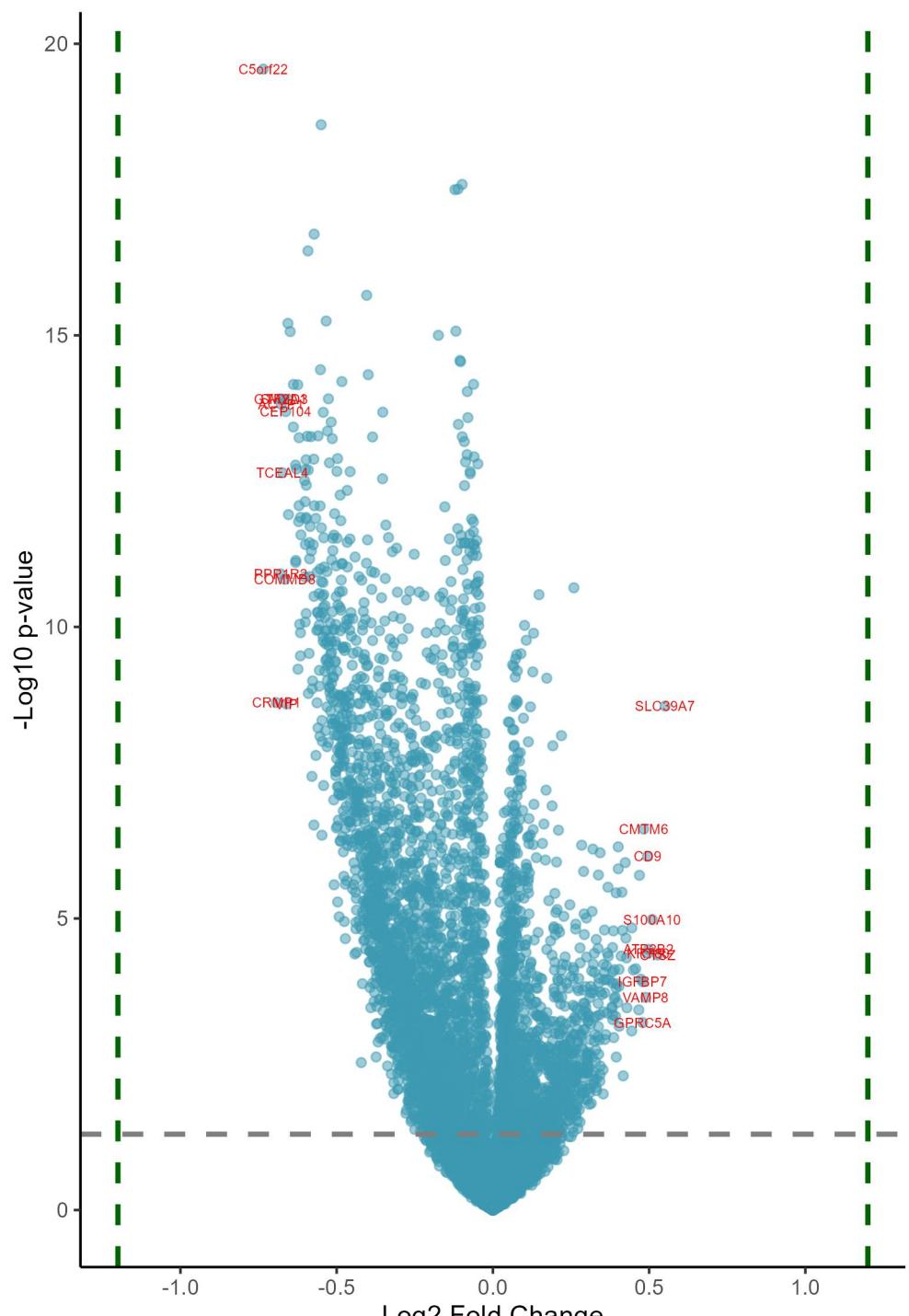


Downregulated in blood cancers at low/absent ERCC4 Upregulated in blood cancers at low/absent ERCC4

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|---|-------|-----------|----------|-------------------------------------|
| -1.28 | 1.32e-04 | IKZF3 | IKAROS family zinc finger 3 | 1.24 | 2.04e-05 | LYZ | lysozyme |
| -1.23 | 3.78e-03 | HLA-DQB1 | major histocompatibility complex, c | 1.21 | 2.04e-05 | CTBP2 | C-terminal binding protein 2 |
| -1.19 | 4.44e-04 | PFN2 | profilin 2 | 1.16 | 1.94e-05 | LPCAT2 | lysophosphatidylcholine acyltransfe |
| -1.03 | 4.88e-03 | HLA-DPA1 | major histocompatibility complex, c | 1.13 | 2.04e-05 | ARRB1 | arrestin beta 1 |
| -1 | 6.70e-02 | MZB1 | marginal zone B and B1 cell specifi | 1.09 | 9.07e-04 | ITGA5 | integrin subunit alpha 5 |
| -0.99 | 3.73e-04 | ETS1 | ETS proto-oncogene 1, transcription | 1.09 | 2.04e-05 | ZEB2 | zinc finger E-box binding homeobox |
| -0.97 | 7.26e-05 | DNAJB14 | DnaJ heat shock protein family (Hsp | 1.03 | 2.27e-03 | CSTA | cystatin A |
| -0.97 | 1.32e-04 | MAP4K1 | mitogen-activated protein kinase ki | 1.02 | 1.21e-05 | CD33 | CD33 molecule |
| -0.97 | 3.31e-03 | ISG20 | interferon stimulated exonuclease g | 1.01 | 1.00e-03 | CLEC11A | C-type lectin domain containing 11A |
| -0.94 | 2.36e-02 | HLA-DPB1 | major histocompatibility complex, c | 0.97 | 1.60e-05 | PRTN3 | proteinase 3 |
| -0.9 | 3.71e-03 | CAMK4 | calcium/calmodulin dependent protei | 0.96 | 1.12e-03 | NECTIN2 | nectin cell adhesion molecule 2 |
| -0.89 | 1.46e-02 | MS4A1 | membrane spanning 4-domains A1 | 0.95 | 1.53e-01 | S100A4 | S100 calcium binding protein A4 |
| -0.89 | 1.41e-02 | CDH26 | cadherin 26 | 0.93 | 1.30e-02 | CTSG | cathepsin G |
| -0.87 | 6.39e-04 | NOPCHAP1 | NOP protein chaperone 1 | 0.91 | 3.66e-04 | PSTPIP2 | proline-serine-threonine phosphatas |
| -0.87 | 3.24e-04 | RABAC1 | Rab acceptor 1 | 0.91 | 2.20e-03 | DUSP23 | dual specificity phosphatase 23 |
| -0.87 | 8.06e-03 | TRO | trophinin | 0.9 | 6.72e-03 | LCP2 | lymphocyte cytosolic protein 2 |
| -0.87 | 1.32e-04 | ATP2C1 | ATPase secretory pathway Ca2+ trans | 0.89 | 3.14e-03 | CST7 | cystatin F |
| -0.85 | 1.53e-02 | CD40 | CD40 molecule | 0.89 | 1.87e-03 | MRC2 | mannose receptor C type 2 |
| -0.84 | 8.49e-03 | SIT1 | signaling threshold regulating tran | 0.88 | 2.04e-05 | GRB10 | growth factor receptor bound protei |
| -0.84 | 6.92e-03 | CD86 | CD86 molecule | 0.87 | 3.14e-03 | HEBP1 | heme binding protein 1 |
| -0.83 | 3.14e-03 | GLTP | glycolipid transfer protein | 0.86 | 8.34e-03 | HSD17B11 | hydroxysteroid 17-beta dehydrogenas |
| -0.83 | 5.47e-02 | TSTD1 | thiosulfate sulfurtransferase like | 0.86 | 3.23e-03 | SIRPA | signal regulatory protein alpha |
| -0.81 | 4.10e-02 | HLA-DRB5 | major histocompatibility complex, c | 0.85 | 3.14e-03 | PECAM1 | platelet and endothelial cell adhes |
| -0.81 | 6.63e-02 | PTPRCAP | protein tyrosine phosphatase recept | 0.85 | 3.31e-03 | GNAQ | G protein subunit alpha q |
| -0.81 | 4.78e-03 | IFI30 | IFI30 lysosomal thiol reductase | 0.84 | 4.80e-02 | SPN | sialophorin |
| -0.81 | 2.27e-03 | APOL2 | apolipoprotein L2 | 0.84 | 2.08e-02 | NAPRT | nicotinate phosphoribosyltransfers |
| -0.81 | 1.53e-02 | SLAMF6 | SLAM family member 6 | 0.83 | 2.96e-04 | PALM | paralemmin |
| -0.81 | 2.63e-02 | ZBTB42 | zinc finger and BTB domain containi | 0.81 | 2.21e-03 | ARR3 | arrestin 3 |
| -0.8 | 1.24e-03 | RELB | RELB proto-oncogene, NF- κ b subunit | 0.8 | 7.78e-04 | ITGA2B | integrin subunit alpha 2b |

Differentially expressed proteins in solid cancers at absence/low amount of ERCC4 , DB2

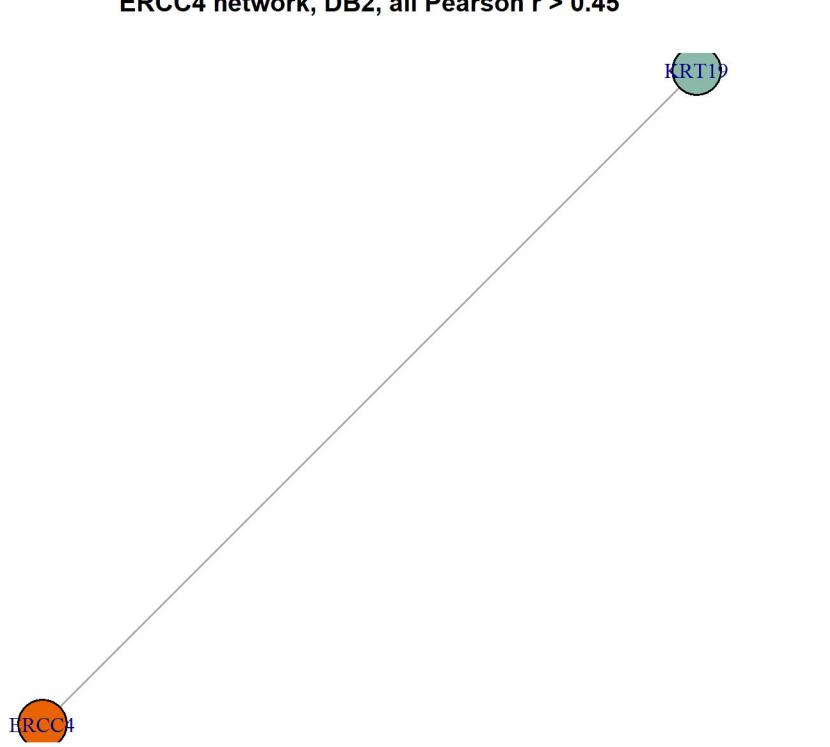
p-value < 0.05 & logFC > 1.2



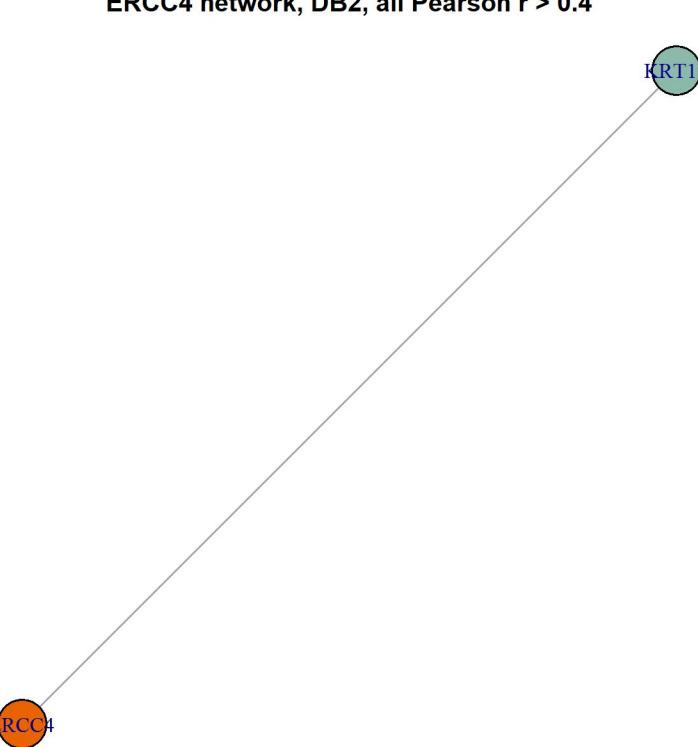
Downregulated in solid cancers at low/absent ERCC4 Upregulated in solid cancers at low/absent ERCC4

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|-------------------------------------|-------|-----------|----------|-------------------------------------|
| -0.73 | 1.14e-16 | C5orf22 | chromosome 5 open reading frame 22 | 0.55 | 4.52e-08 | SLC39A7 | solute carrier family 39 member 7 |
| -0.69 | 4.08e-08 | CRMP1 | collapsin response mediator protein | 0.53 | 2.09e-04 | CTSZ | cathepsin Z |
| -0.68 | 3.87e-12 | GTF2A1 | general transcription factor IIA su | 0.51 | 6.24e-05 | S100A10 | S100 calcium binding protein A10 |
| -0.68 | 7.42e-10 | PPP1R2 | protein phosphatase 1 regulatory in | 0.5 | 1.73e-04 | ATP2B2 | ATPase plasma membrane Ca2+ transpo |
| -0.68 | 4.55e-12 | ACYP1 | acylphosphatase 1 | 0.5 | 1.97e-04 | KRT80 | keratin 80 |
| -0.67 | 3.18e-11 | TCEAL4 | transcription elongation factor A I | 0.49 | 7.21e-06 | CD9 | CD9 molecule |
| -0.67 | 3.87e-12 | SMYD3 | SET and MYND domain containing 3 | 0.49 | 8.91e-04 | VAMP8 | vesicle associated membrane protein |
| -0.67 | 8.80e-10 | COMM8 | COMM domain containing 8 | 0.48 | 2.85e-06 | CMTM6 | CKLF like MARVEL transmembrane doma |
| -0.66 | 5.63e-12 | CEP104 | centrosomal protein 104 | 0.48 | 5.22e-04 | IGFBP7 | insulin like growth factor binding |
| -0.66 | 4.22e-08 | VIP | vasoactive intestinal peptide | 0.48 | 2.10e-03 | GPRC5A | G protein-coupled receptor class C |
| -0.66 | 4.74e-13 | ERCC1 | ERCC excision repair 1, endonucleas | 0.47 | 4.77e-04 | ABCC6 | ATP binding cassette subfamily C me |
| -0.66 | 3.87e-12 | DESI1 | desumoylating isopeptidase 1 | 0.47 | 1.37e-05 | SDC4 | syndecan 4 |
| -0.65 | 1.34e-10 | HDHD2 | haloacid dehalogenase like hydrolas | 0.47 | 1.36e-03 | CD44 | CD44 molecule (Indian blood group) |
| -0.65 | 5.54e-13 | RAD51C | RAD51 paralog C | 0.46 | 3.35e-04 | PRSS8 | serine protease 8 |
| -0.64 | 8.92e-12 | PDE6D | phosphodiesterase 6D | 0.45 | 3.49e-04 | NEXN | nexilin F-actin binding protein |
| -0.64 | 2.68e-12 | KNSTRN | kinetochore localized astrin (SPAG5 | 0.44 | 8.31e-05 | RAB32 | RAB32, member RAS oncogene family |
| -0.63 | 2.65e-11 | RMI2 | RecQ mediated genome instability 2 | 0.44 | 2.81e-03 | TACSTD2 | tumor associated calcium signal tra |
| -0.63 | 5.20e-10 | CCDC73 | coiled-coil domain containing 73 | 0.43 | 1.27e-03 | F3 | coagulation factor III, tissue fact |
| -0.63 | 4.86e-10 | IVNS1ABP | influenza virus NS1A binding protei | 0.43 | 2.31e-04 | FUCA2 | alpha-L-fucosidase 2 |
| -0.63 | 3.04e-11 | CRLF3 | cytokine receptor like factor 3 | 0.43 | 1.18e-04 | FAM83H | family with sequence similarity 83 |
| -0.62 | 2.68e-12 | POLR3D | RNA polymerase III subunit D | 0.42 | 8.79e-06 | RAB43 | RAB43, member RAS oncogene family |
| -0.62 | 1.39e-08 | IRAK2 | interleukin 1 receptor associated k | 0.42 | 1.28e-02 | AGR2 | anterior gradient 2, protein disulp |
| -0.62 | 1.60e-10 | CKS1B | CDC28 protein kinase regulatory sub | 0.41 | 9.03e-05 | SLC16A3 | solute carrier family 16 member 3 |
| -0.62 | 9.94e-11 | CRIP7 | CXXC repeat containing interactor o | 0.41 | 2.43e-05 | B4GALT5 | beta-1,4-galactosyltransferase 5 |
| -0.62 | 1.13e-11 | GPATCH11 | G-patch domain containing 11 | 0.41 | 2.18e-04 | UXS1 | UDP-glucuronate decarboxylase 1 |
| -0.62 | 3.49e-09 | SSNA1 | SS nuclear autoantigen 1 | 0.4 | 2.39e-03 | C15orf48 | chromosome 15 open reading frame 48 |
| -0.62 | 8.95e-09 | UBE2B | ubiquitin conjugating enzyme E2 B | 0.4 | 3.43e-04 | CAV2 | caveolin 2 |
| -0.62 | 4.36e-09 | CNOT6L | CCR4-NOT transcription complex subu | 0.4 | 6.09e-04 | EPHA2 | EPH receptor A2 |
| -0.62 | 1.46e-10 | PCSK6 | proprotein convertase subtilisin/ke | 0.4 | 1.09e-05 | MFSD10 | major facilitator superfamily domai |

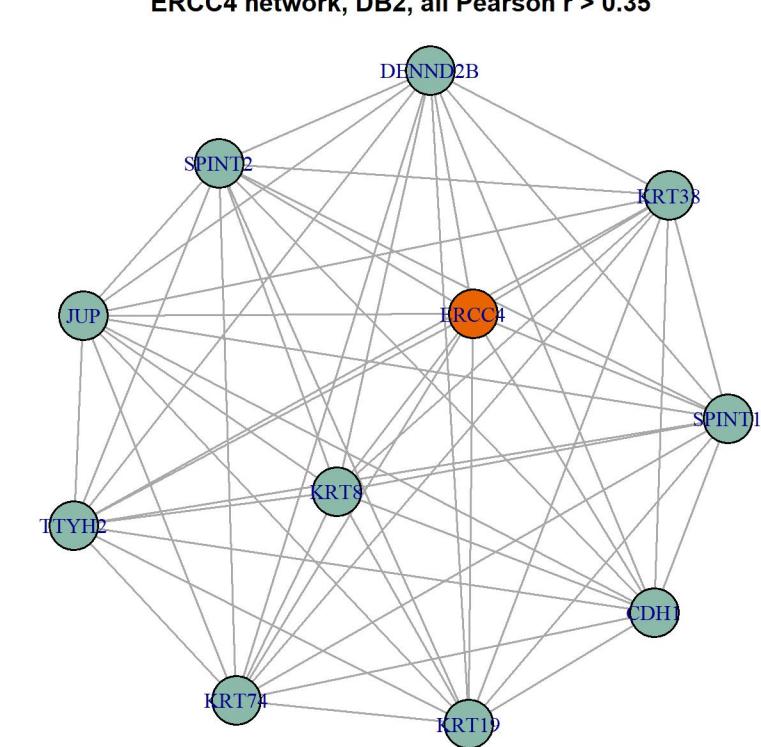
ERCC4 network, DB2, all Pearson r > 0.45

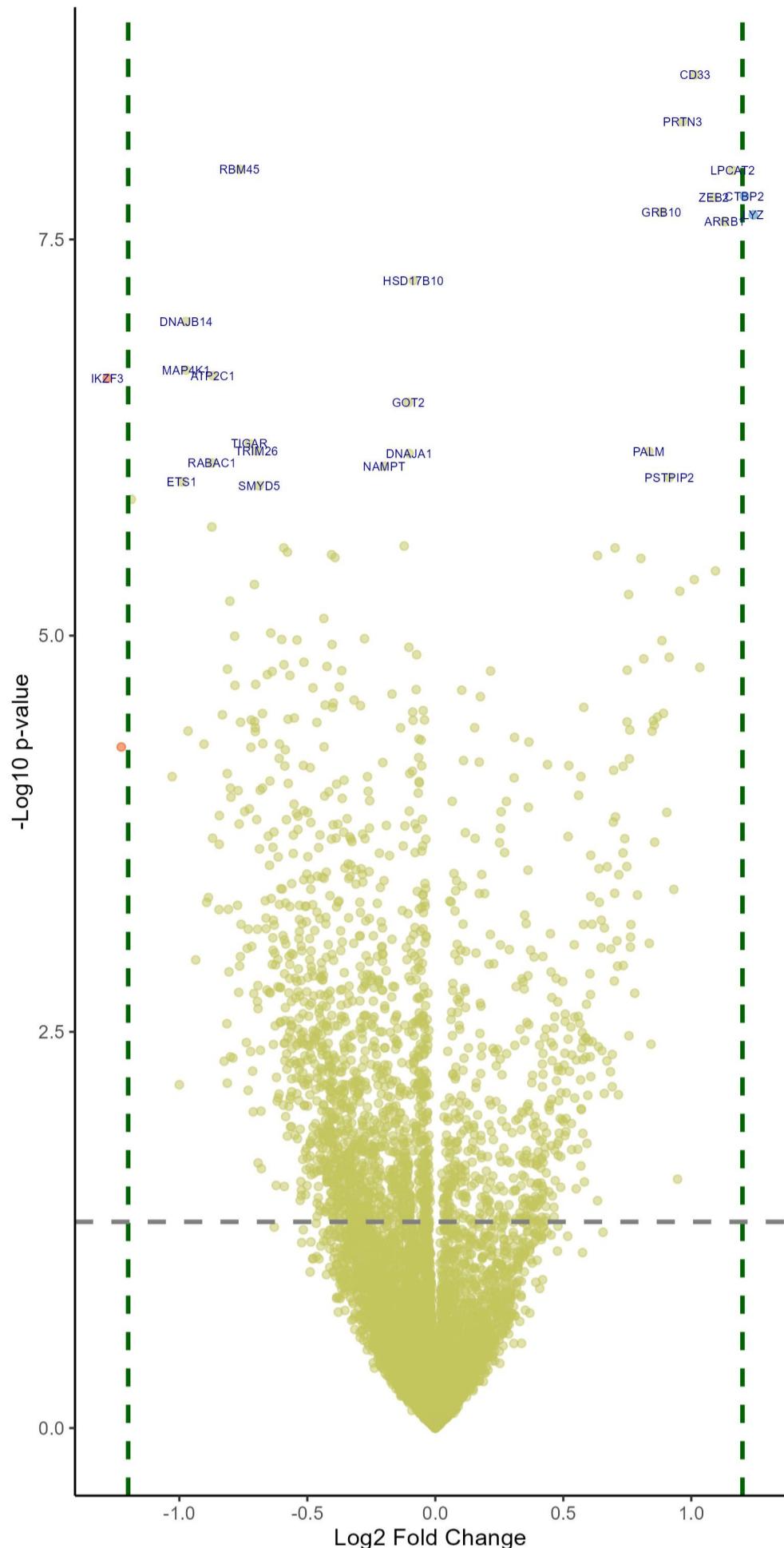


ERCC4 network, DB2, all Pearson r > 0.4

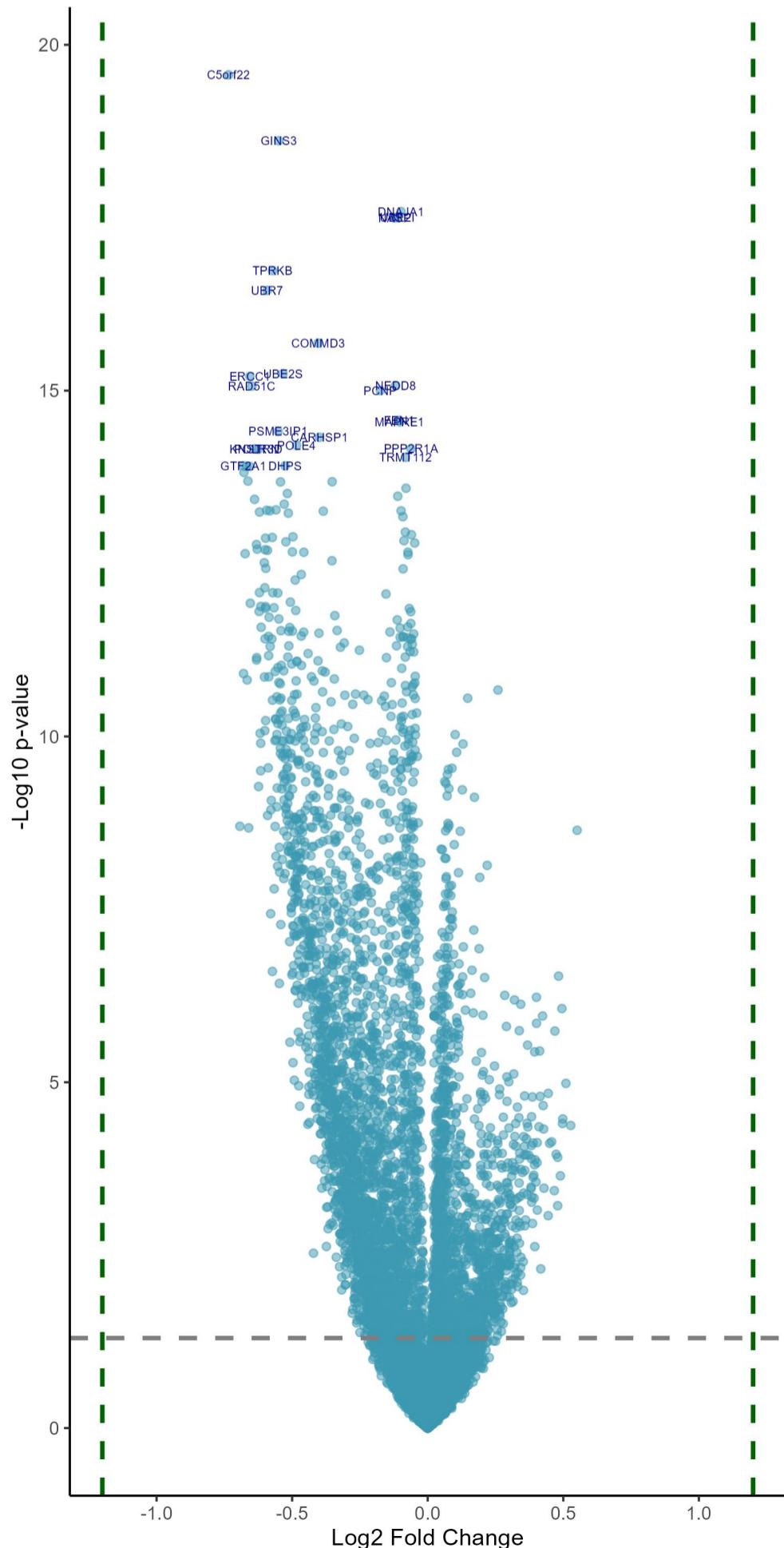


ERCC4 network, DB2, all Pearson r > 0.35



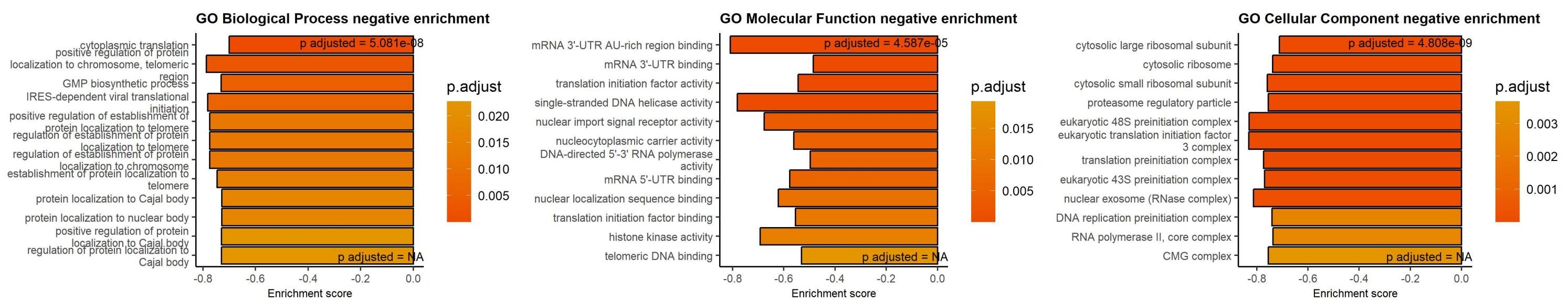
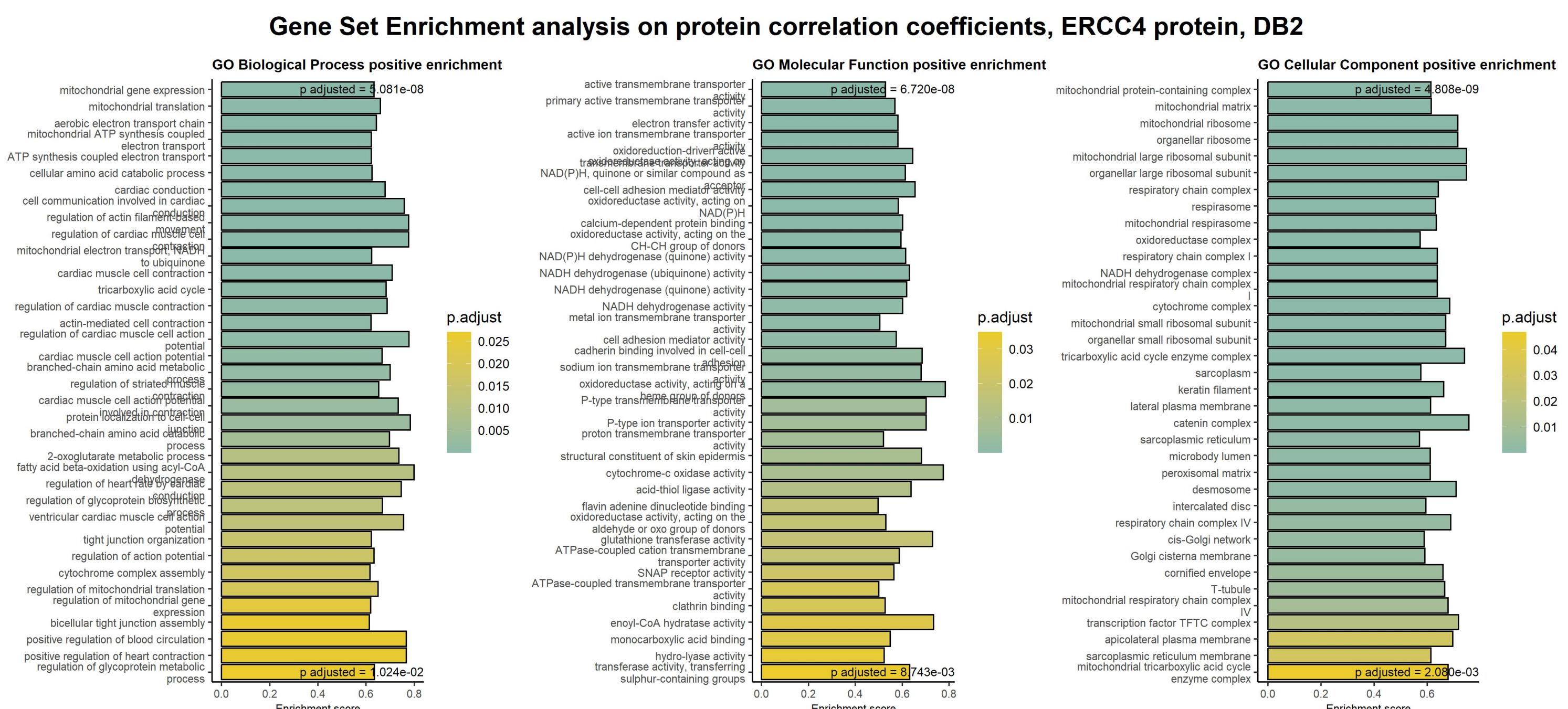
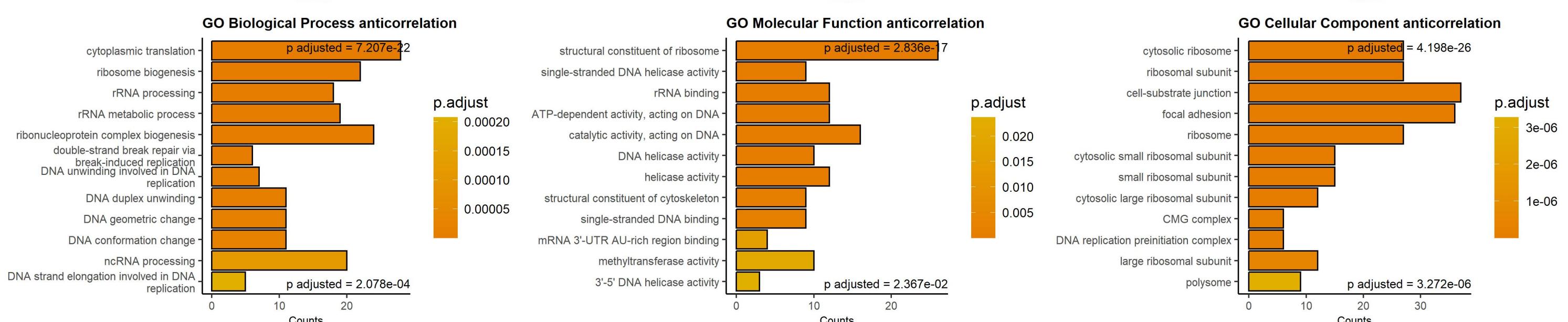
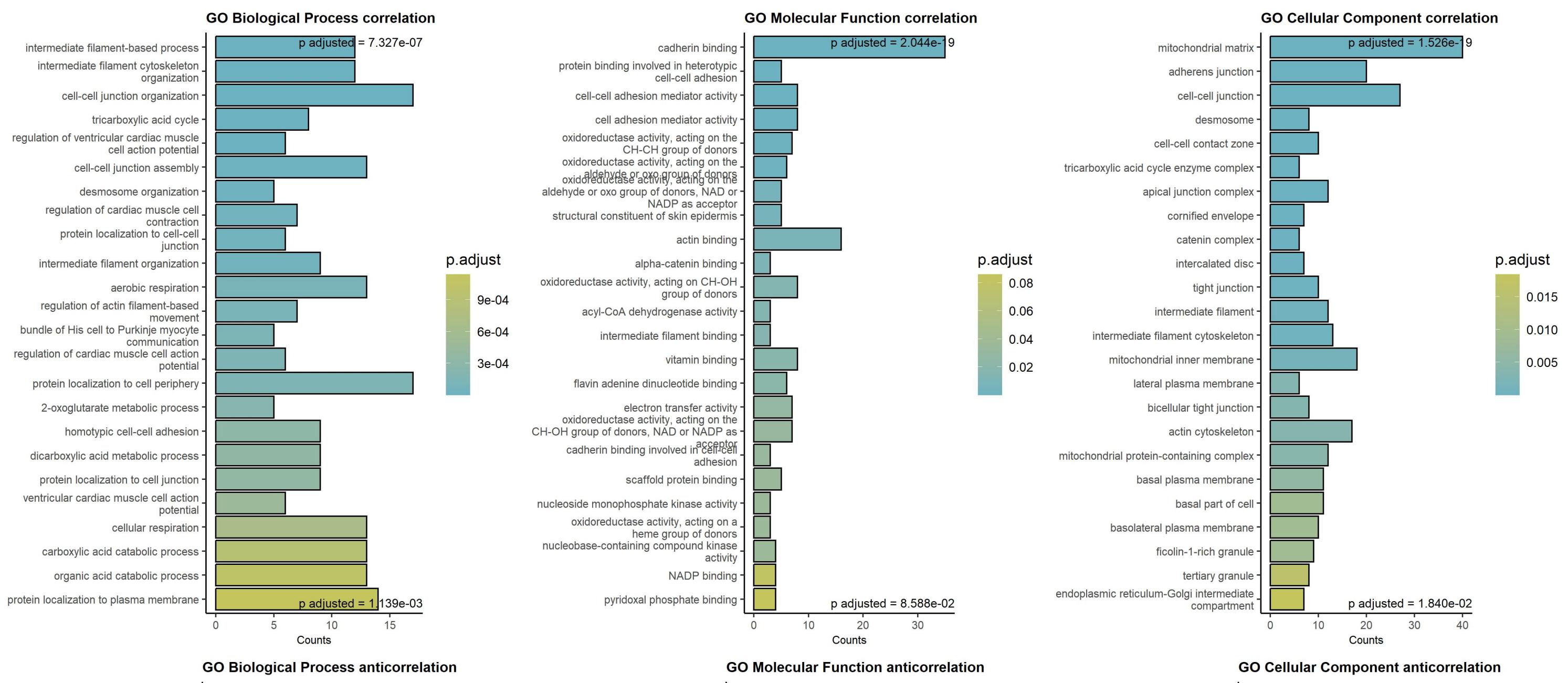


| Downregulated in blood cancers at low/absent ERCC4 | | | | Upregulated in blood cancers at low/absent ERCC4 | | | |
|--|-----------|----------|---|--|-----------|----------|---|
| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
| -0.77 | 1.94e-05 | RBM45 | RNA binding motif protein 45 | 1.02 | 1.21e-05 | CD33 | CD33 molecule |
| -0.09 | 4.37e-05 | HSD17B10 | hydroxysteroid 17-beta dehydrogenase | 0.97 | 1.60e-05 | PRTN3 | proteinase 3 |
| -0.97 | 7.26e-05 | DNAJB14 | DnaJ heat shock protein family (Hsp) | 1.16 | 1.94e-05 | LPCAT2 | lysophosphatidylcholine acyltransferase |
| -0.97 | 1.32e-04 | MAP4K1 | mitogen-activated protein kinase kinase | 1.21 | 2.04e-05 | CTBP2 | C-terminal binding protein 2 |
| -0.87 | 1.32e-04 | ATP2C1 | ATPase secretory pathway Ca ²⁺ trans | 1.09 | 2.04e-05 | ZEB2 | zinc finger E-box binding homeobox |
| -1.28 | 1.32e-04 | IKZF3 | IKAROS family zinc finger 3 | 0.88 | 2.04e-05 | GRB10 | growth factor receptor bound protein |
| -0.1 | 1.77e-04 | GOT2 | glutamic-oxaloacetic transaminase 2 | 1.24 | 2.04e-05 | LYZ | lysozyme |
| -0.73 | 2.96e-04 | TIGAR | TP53 induced glycolysis regulatory | 1.13 | 2.04e-05 | ARRB1 | arrestin beta 1 |
| -0.7 | 2.96e-04 | TRIM26 | tripartite motif containing 26 | 0.83 | 2.96e-04 | PALM | paralemmin |
| -0.1 | 2.96e-04 | DNAJA1 | DnaJ heat shock protein family (Hsp) | 0.91 | 3.66e-04 | PSTPIP2 | proline-serine-threonine phosphatases |
| -0.87 | 3.24e-04 | RABAC1 | Rab acceptor 1 | 0.7 | 7.78e-04 | TOR4A | torsin family 4 member A |
| -0.2 | 3.25e-04 | NAMPT | nicotinamide phosphoribosyltransferase | 0.63 | 7.78e-04 | CEBPA | CCAAT enhancer binding protein alpha |
| -0.99 | 3.73e-04 | ETS1 | ETS proto-oncogene 1, transcription | 0.8 | 7.78e-04 | ITGA2B | integrin subunit alpha 2b |
| -0.69 | 3.79e-04 | SMYD5 | SMYD family member 5 | 1.09 | 9.07e-04 | ITGA5 | integrin subunit alpha 5 |
| -1.19 | 4.44e-04 | PFN2 | profilin 2 | 1.01 | 1.00e-03 | CLEC11A | C-type lectin domain containing 11A |
| -0.87 | 6.39e-04 | NOPCHAP1 | NOP protein chaperone 1 | 0.96 | 1.12e-03 | NECTIN2 | nectin cell adhesion molecule 2 |
| -0.12 | 7.78e-04 | IDH3B | isocitrate dehydrogenase (NAD(+)) 3 | 0.76 | 1.15e-03 | AIF1 | allograft inflammatory factor 1 |
| -0.59 | 7.78e-04 | C1orf122 | chromosome 1 open reading frame 122 | 0.89 | 1.87e-03 | MRC2 | mannose receptor C type 2 |
| -0.58 | 7.78e-04 | SPTY2D1 | SPT2 chromatin protein domain conta | 0.91 | 2.20e-03 | DUSP23 | dual specificity phosphatase 23 |
| -0.41 | 7.78e-04 | SH3GLB2 | SH3 domain containing GRB2 like, en | 0.81 | 2.21e-03 | ARR3 | arrestin 3 |
| -0.39 | 7.78e-04 | FAHD2A | fumarylacetoacetate hydrolase domai | 1.03 | 2.27e-03 | CSTA | cystatin A |
| -0.71 | 1.05e-03 | CLSPN | claspin | 0.75 | 2.27e-03 | ENG | endoglin |
| -0.8 | 1.24e-03 | RELB | RELB proto-oncogene, NF- κ B subunit | 0.22 | 2.27e-03 | CAT | catalase |
| -0.44 | 1.55e-03 | GABARPL2 | GABA type A receptor associated pro | 0.1 | 2.64e-03 | LAMP1 | lysosomal associated membrane prote |
| -0.64 | 1.87e-03 | IFT122 | intraflagellar transport 122 | 0.18 | 2.82e-03 | NUDT3 | nudix hydrolase 3 |
| -0.78 | 1.87e-03 | CARMIL2 | capping protein regulator and myosi | 0.58 | 3.04e-03 | OSBPL1A | oxysterol binding protein like 1A |
| -0.28 | 1.87e-03 | SNAPIN | SNAP associated protein | 0.89 | 3.14e-03 | CST7 | cystatin F |
| -0.6 | 1.87e-03 | KNOP1 | lysine rich nucleolar protein 1 | 0.87 | 3.14e-03 | HEBP1 | heme binding protein 1 |
| -0.54 | 1.87e-03 | EIF1AD | eukaryotic translation initiation f | 0.85 | 3.14e-03 | PECAM1 | platelet and endothelial cell adhes |
| -0.4 | 1.94e-03 | CEP85 | centrosomal protein 85 | 0.75 | 3.14e-03 | AZU1 | azurocidin 1 |
| -0.1 | 1.98e-03 | CD2BP2 | CD2 cytoplasmic tail binding protei | 0.86 | 3.23e-03 | SIRPA | signal regulatory protein alpha |
| -0.07 | 2.16e-03 | ATIC | 5-aminoimidazole-4-carboxamide ribo | 0.15 | 3.26e-03 | DIAPH1 | diaphanous related formin 1 |
| -0.51 | 2.27e-03 | RFX5 | regulatory factor X5 | 0.76 | 3.31e-03 | EIF4EBP1 | eukaryotic translation initiation f |
| -0.59 | 2.27e-03 | GOLM2 | golgi membrane protein 2 | 0.85 | 3.31e-03 | GNAQ | G protein subunit alpha q |
| -0.42 | 2.27e-03 | TXLNG | taxilin gamma | 0.31 | 3.56e-03 | TBXAS1 | thromboxane A synthase 1 |
| -0.81 | 2.27e-03 | APOL2 | apolipoprotein L2 | 0.37 | 3.70e-03 | NELFB | negative elongation factor complex |
| -0.37 | 2.27e-03 | ACYP1 | acylphosphatase 1 | 0.76 | 4.32e-03 | CYBRD1 | cytochrome b reductase 1 |
| -0.64 | 2.27e-03 | IGSF8 | immunoglobulin superfamily member 8 | 0.11 | 4.39e-03 | SNX3 | sorting nexin 3 |
| 0.66 | 2.32e-03 | RGCM | ribonucleic acid nucleic mutase | 0.17 | 4.44e-03 | DNIDED | arginyl aminopeptidase |

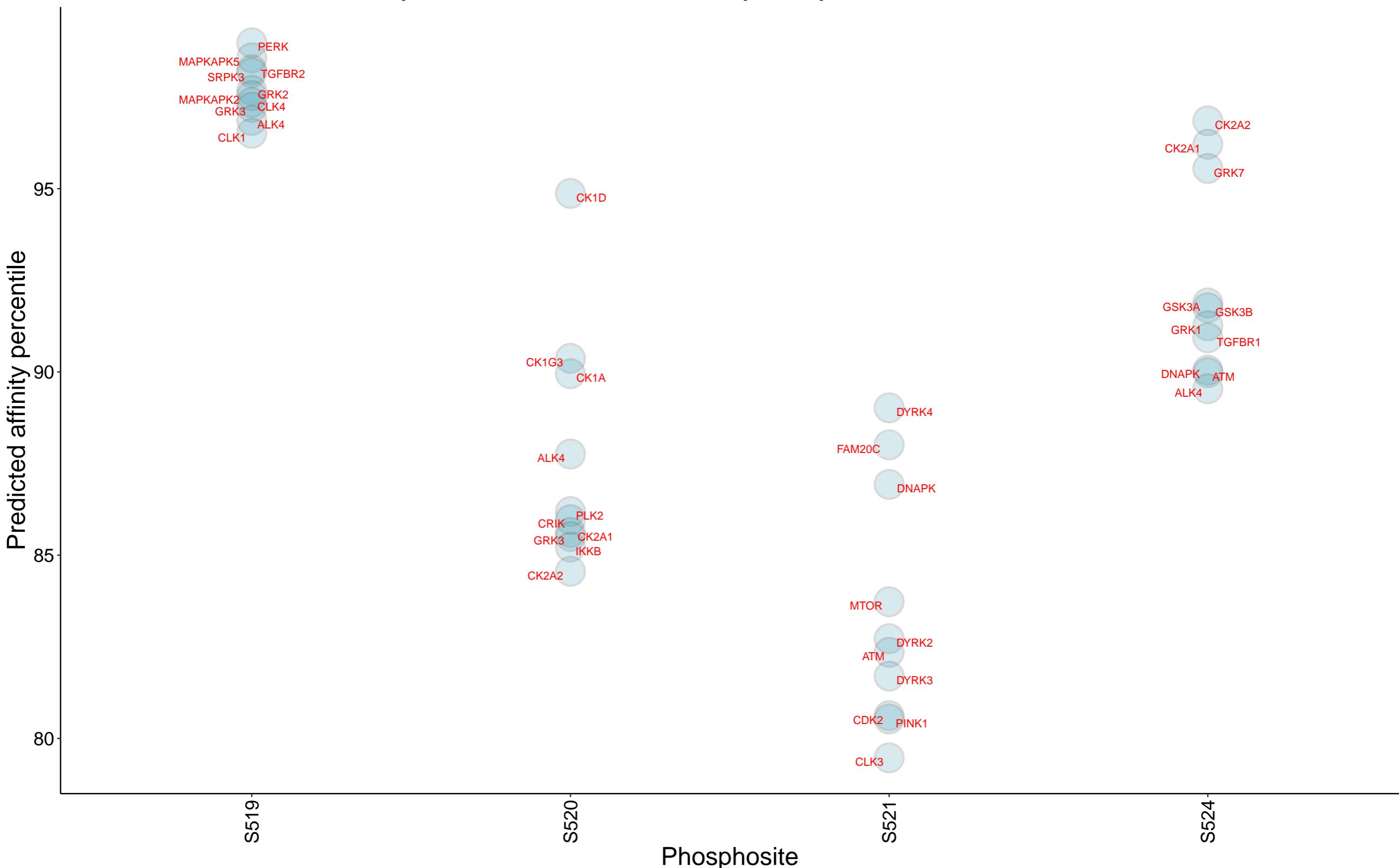


| Downregulated in solid cancers at low/absent ERCC4 | | | | Upregulated in solid cancers at low/absent ERCC4 | | | |
|--|-----------|----------|--------------------------------------|--|-----------|----------|-------------------------------------|
| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
| -0.73 | 1.14e-16 | C5orf22 | chromosome 5 open reading frame 22 | 0.26 | 1.15e-09 | MYO1C | myosin IC |
| -0.55 | 6.81e-16 | GINS3 | GINS complex subunit 3 | 0.15 | 1.40e-09 | ESYT2 | extended synaptotagmin 2 |
| -0.1 | 4.42e-15 | DNAJA1 | DnaJ heat shock protein family (Hsp) | 0.1 | 3.56e-09 | TM9SF3 | transmembrane 9 superfamily member |
| -0.11 | 4.42e-15 | UBE2I | ubiquitin conjugating enzyme E2 I | 0.13 | 4.42e-09 | ABCD3 | ATP binding cassette subfamily D me |
| -0.12 | 4.42e-15 | NASP | nuclear autoantigenic sperm protein | 0.11 | 5.63e-09 | MLEC | malectin |
| -0.57 | 2.20e-14 | TPRKB | TP53RK binding protein | 0.09 | 8.42e-09 | RPN2 | ribophorin II |
| -0.59 | 3.72e-14 | UBR7 | ubiquitin protein ligase E3 compone | 0.08 | 8.62e-09 | TOR1AIP1 | torsin 1A interacting protein 1 |
| -0.4 | 1.91e-13 | COMM3 | COMM domain containing 3 | 0.07 | 9.85e-09 | PGRMC2 | progesterone receptor membrane comp |
| -0.53 | 4.74e-13 | UBE2S | ubiquitin conjugating enzyme E2 S | 0.06 | 1.21e-08 | CCDC47 | coiled-coil domain containing 47 |
| -0.66 | 4.74e-13 | ERCC1 | ERCC excision repair 1, endonucleas | 0.07 | 1.26e-08 | NCLN | nicalin |
| -0.12 | 5.54e-13 | NEDD8 | NEDD8 ubiquitin like modifier | 0.08 | 1.47e-08 | ECHS1 | enoyl-CoA hydratase, short chain 1 |
| -0.65 | 5.54e-13 | RAD51C | RAD51 paralog C | 0.13 | 1.51e-08 | TBL2 | transducin beta like 2 |
| -0.17 | 5.96e-13 | PCNP | PEST proteolytic signal containing | 0.07 | 1.81e-08 | MTX2 | metaxin 2 |
| -0.11 | 1.48e-12 | FEN1 | flap structure-specific endonucleas | 0.17 | 1.88e-08 | PLEC | plectin |
| -0.1 | 1.48e-12 | MAPRE1 | microtubule associated protein RP/E | 0.07 | 3.78e-08 | RAB15 | RAB15, member RAS oncogene family |
| -0.55 | 1.91e-12 | PSME3IP1 | proteasome activator subunit 3 inte | 0.08 | 3.98e-08 | SEC61B | SEC61 translocon subunit beta |
| -0.4 | 2.20e-12 | CARHSP1 | calcium regulated heat stable prote | 0.07 | 4.22e-08 | SPTLC1 | serine palmitoyltransferase long ch |
| -0.48 | 2.68e-12 | POLE4 | DNA polymerase epsilon 4, accessory | 0.55 | 4.52e-08 | SLC39A7 | solute carrier family 39 member 7 |
| -0.06 | 2.68e-12 | PPP2R1A | protein phosphatase 2 scaffold subu | 0.07 | 4.59e-08 | MRPL13 | mitochondrial ribosomal protein L13 |
| -0.64 | 2.68e-12 | KNSTRN | kinetochore localized astrin (SPAG5 | 0.12 | 4.63e-08 | REEP5 | receptor accessory protein 5 |
| -0.62 | 2.68e-12 | POLR3D | RNA polymerase III subunit D | 0.1 | 6.82e-08 | MOGS | mannosyl-oligosaccharide glucosidas |
| -0.08 | 3.35e-12 | TRMT112 | tRNA methyltransferase activator su | 0.05 | 7.77e-08 | RPN1 | ribophorin I |
| -0.53 | 3.87e-12 | DHPS | deoxyhypusine synthase | 0.05 | 7.87e-08 | RAB1A | RAB1A, member RAS oncogene family |
| -0.68 | 3.87e-12 | GTF2A1 | general transcription factor IIA su | 0.06 | 9.90e-08 | DDOST | dolichyl-diphosphooligosaccharide-- |
| -0.67 | 3.87e-12 | SMYD3 | SET and MYND domain containing 3 | 0.07 | 9.93e-08 | MRPL19 | mitochondrial ribosomal protein L19 |
| -0.66 | 3.87e-12 | DESI1 | desumoylating isopeptidase 1 | 0.22 | 1.21e-07 | DPM1 | dolichyl-phosphate mannosyltransfer |
| -0.68 | 4.55e-12 | ACYP1 | acylphosphatase 1 | 0.11 | 1.49e-07 | TM9SF4 | transmembrane 9 superfamily member |
| -0.66 | 5.63e-12 | CEP104 | centrosomal protein 104 | 0.07 | 1.66e-07 | EMC2 | ER membrane protein complex subunit |
| -0.35 | 5.63e-12 | COMM3 | COMM domain containing 2 | 0.19 | 1.69e-07 | | |

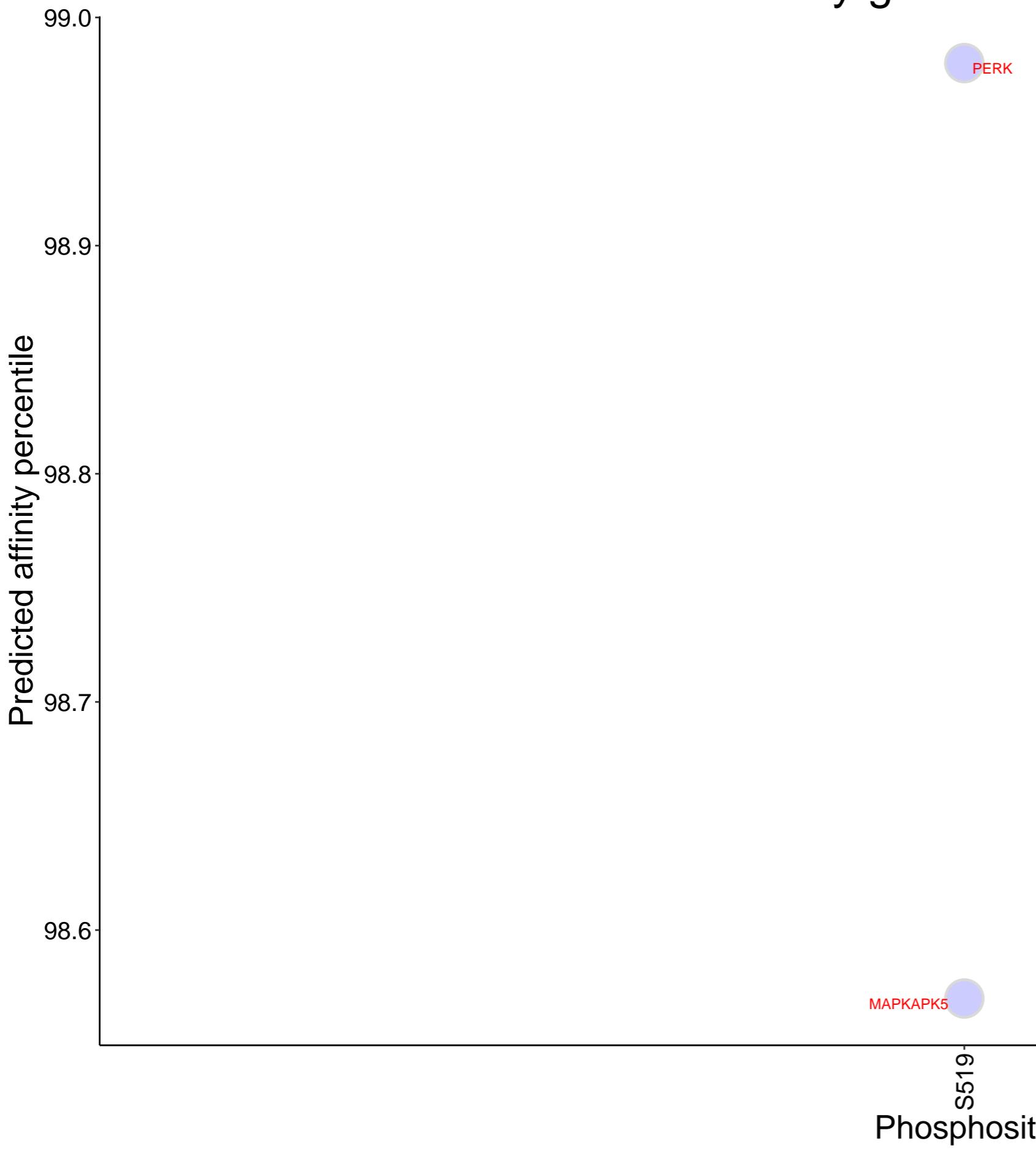
Top 250 correlation coefficients overrepresentation, ERCC4 protein, DB2



Top 10 kinases for each phosphosite in ERCC4



Kinases with affinity greater than 98.5% to ERCC4



Top 15 positive correlation coefficients for ERCC4 protein by tissue, DB2

Beware of false positives in tissues with small number of samples

