

APTX

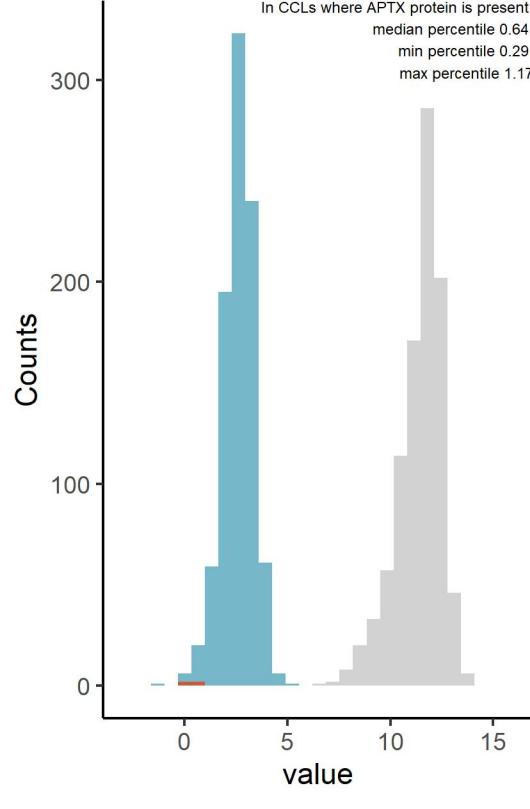
Protein name: APTX ; UNIPROT: Q7Z2E3 ; Gene name: aprataxin

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

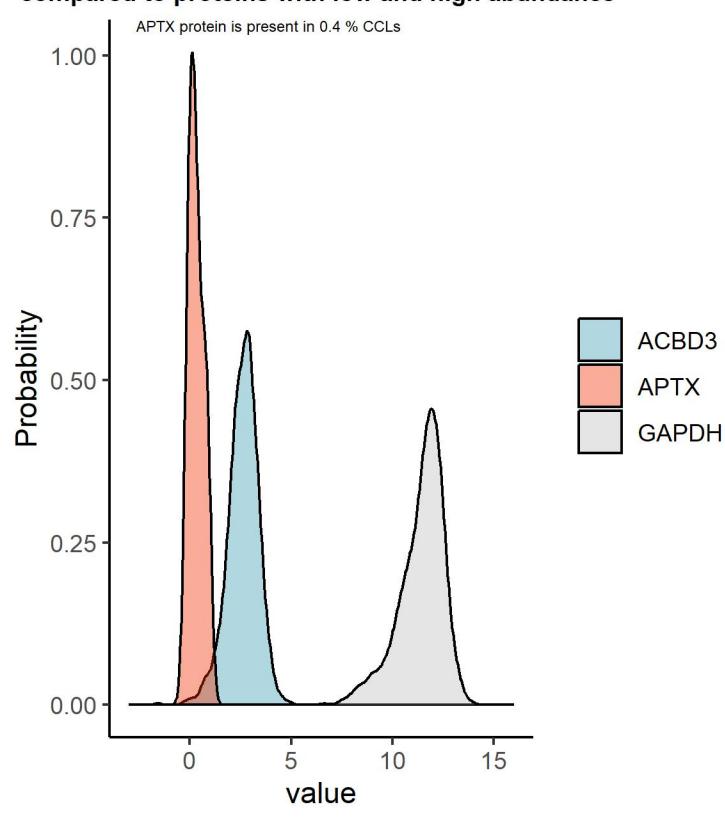
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

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



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



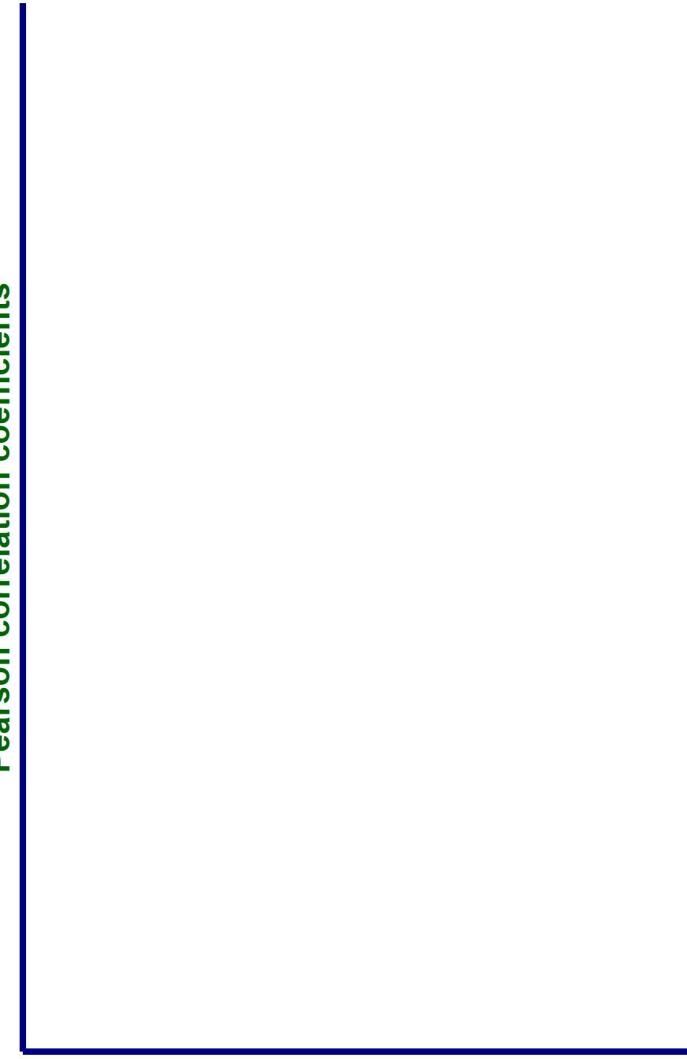
Top negative correlations of APTX protein, DB1

Pearson correlation coefficients



Top positive correlations of APTX protein, DB1

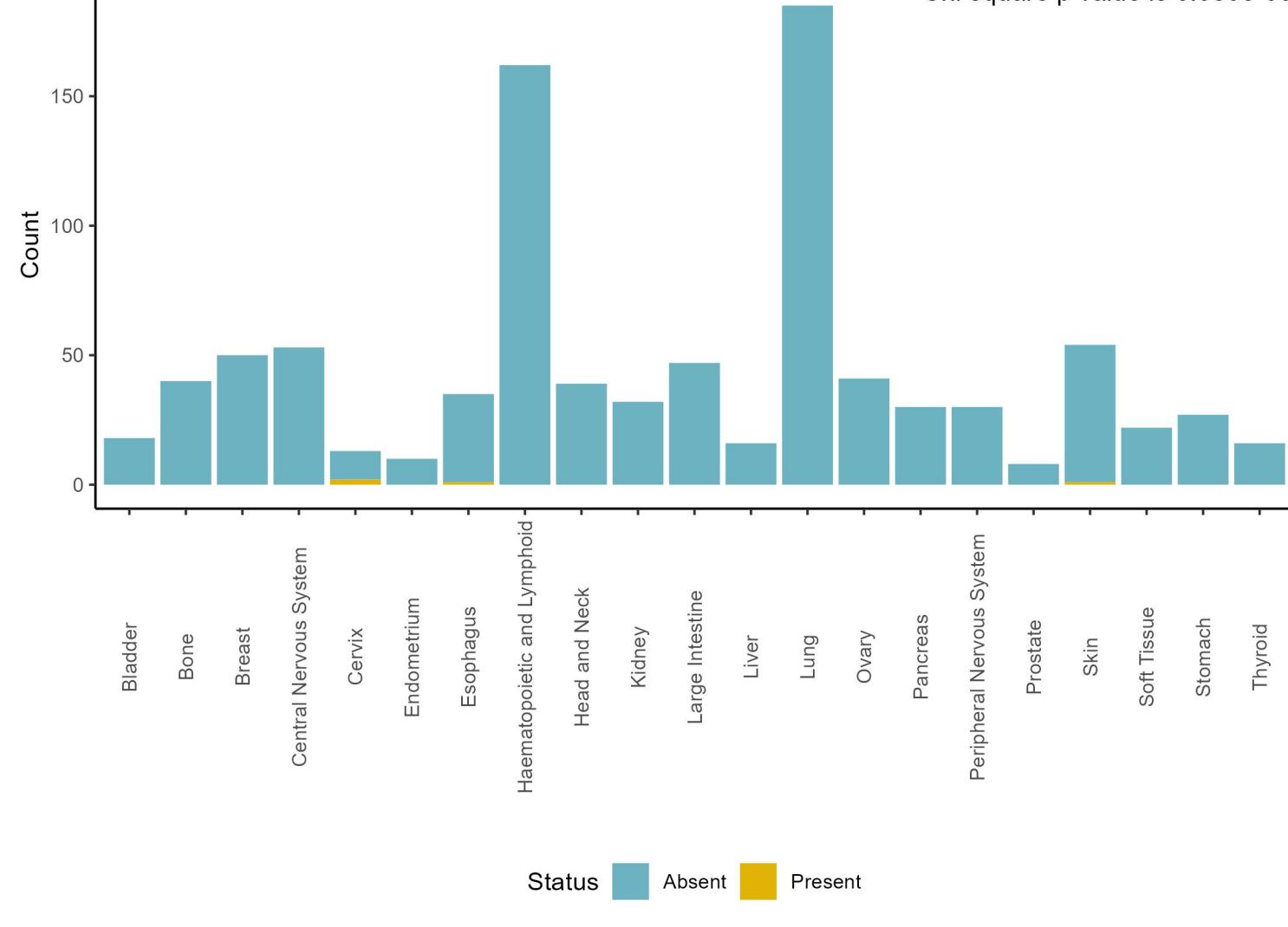
Pearson correlation coefficients



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

Present and absent APTX protein counts by tissue, DB1

Chi square p value is 6.650e-09

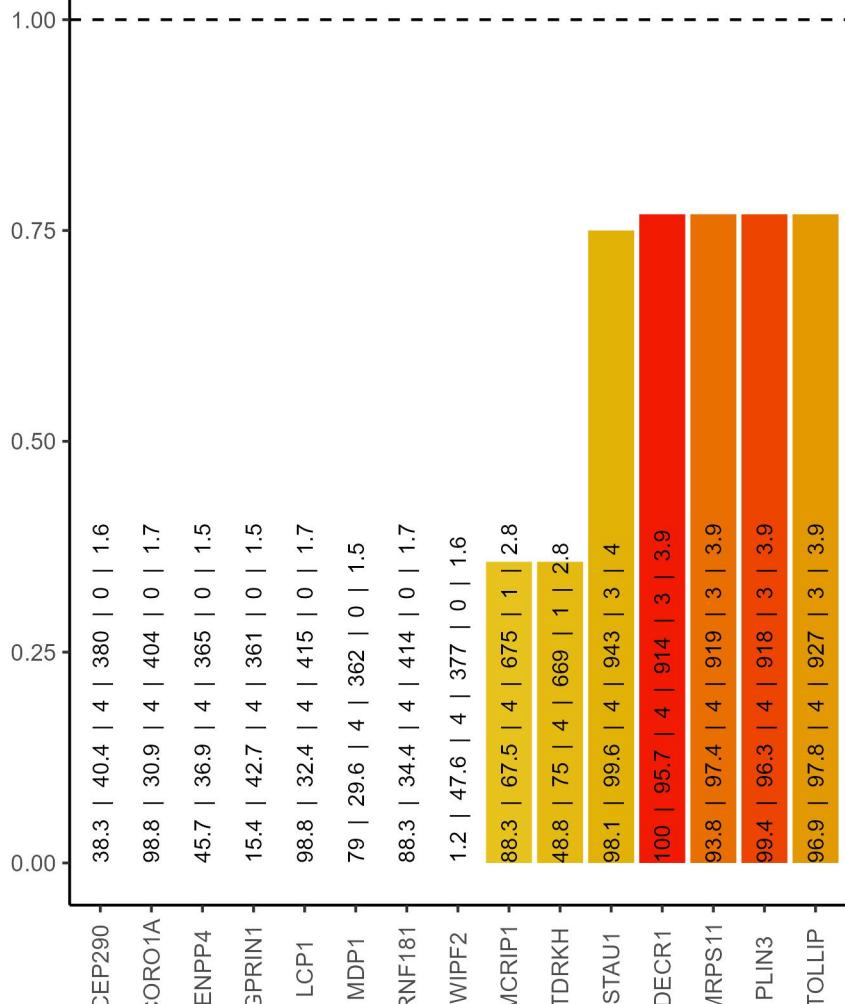


Cooccurrence with APTX protein, DB1

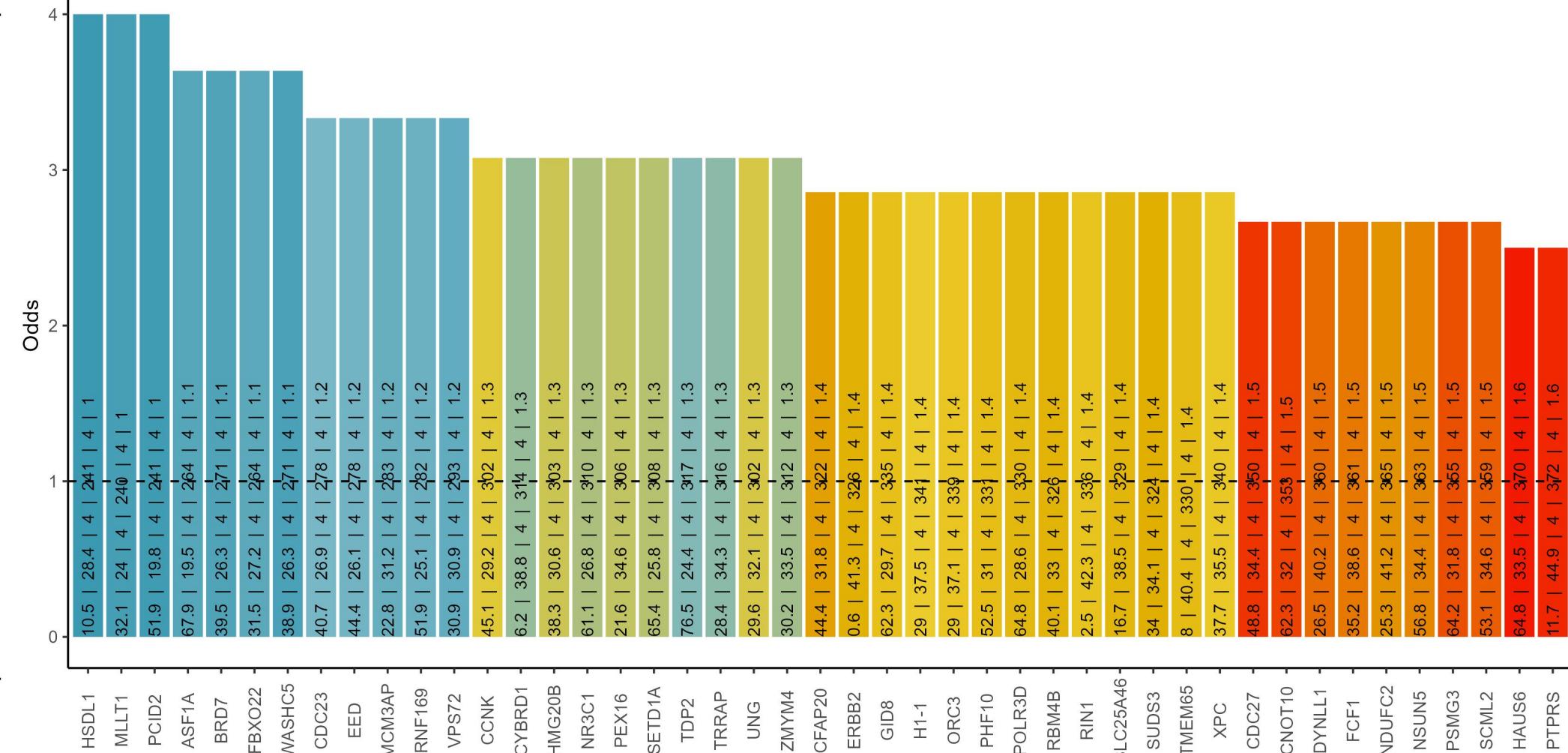
% of APTX in blood cancers: 0 ; % of APTX in solid cancers: 0.5

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

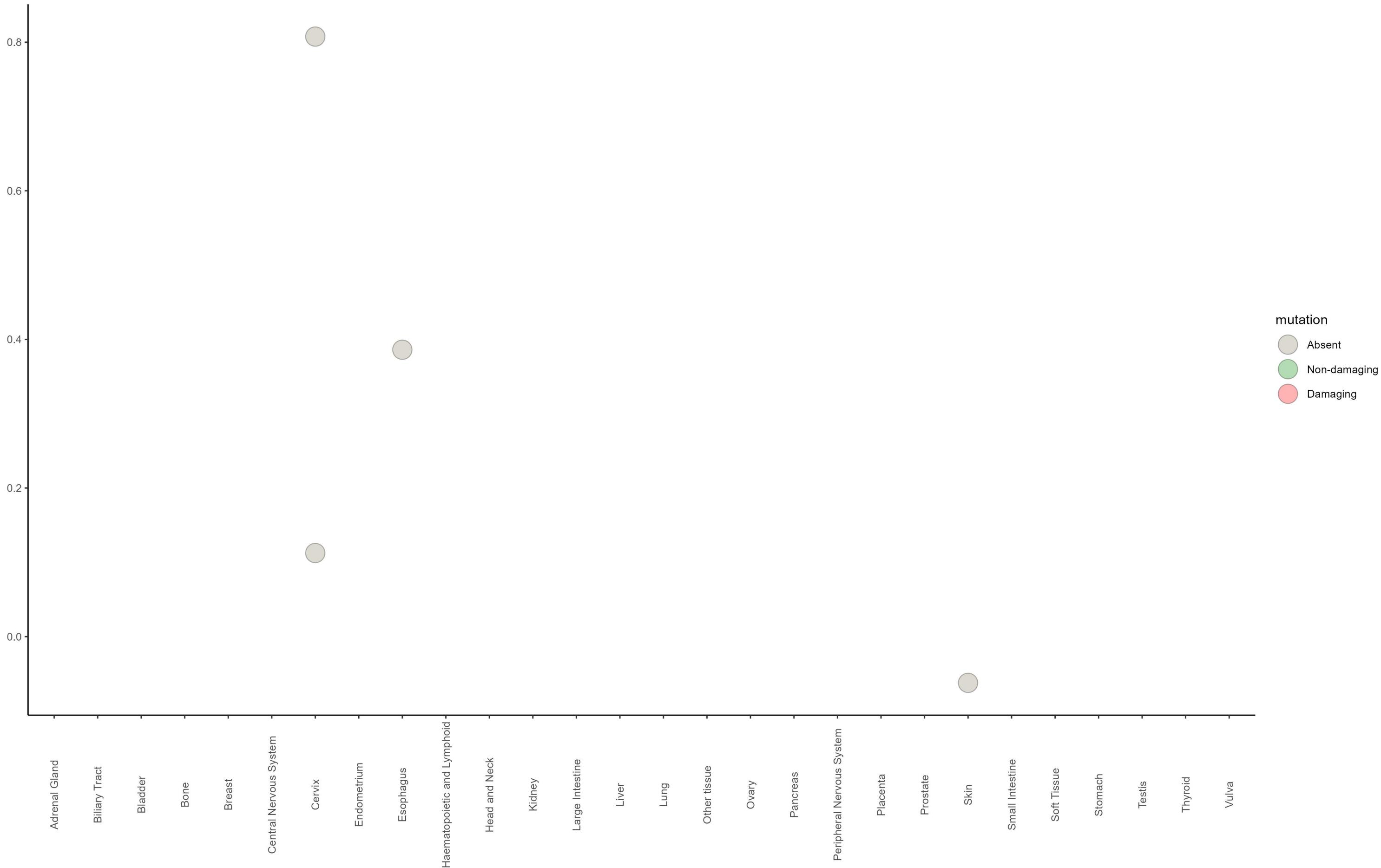
Negative cooccurrence



Positive cooccurrence



Amount of APTX protein and mutation status by tissue, DB1



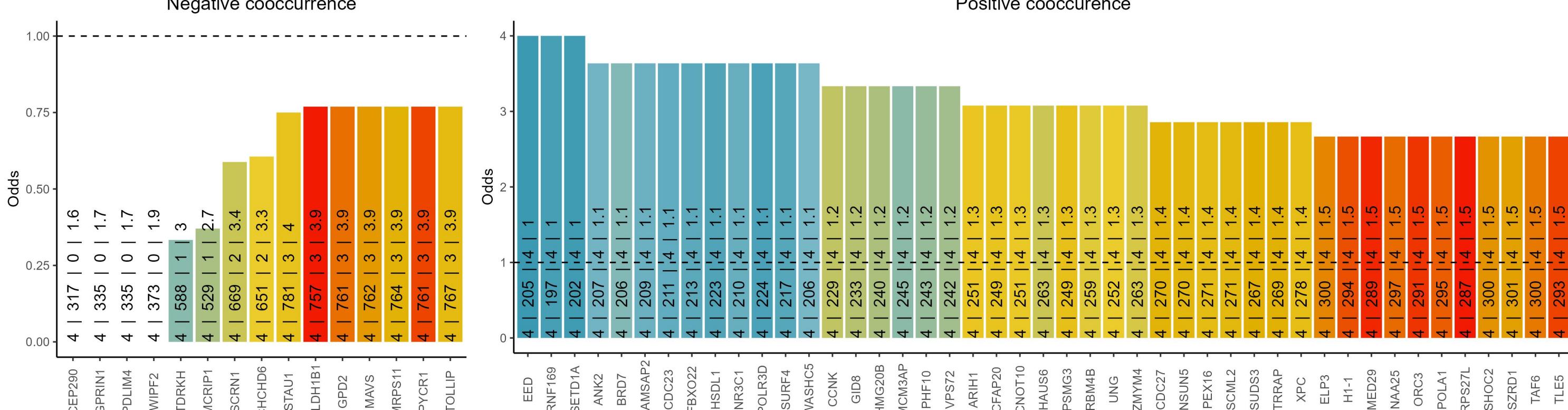
Cooccurrence with APTX protein in blood cancers, DB1

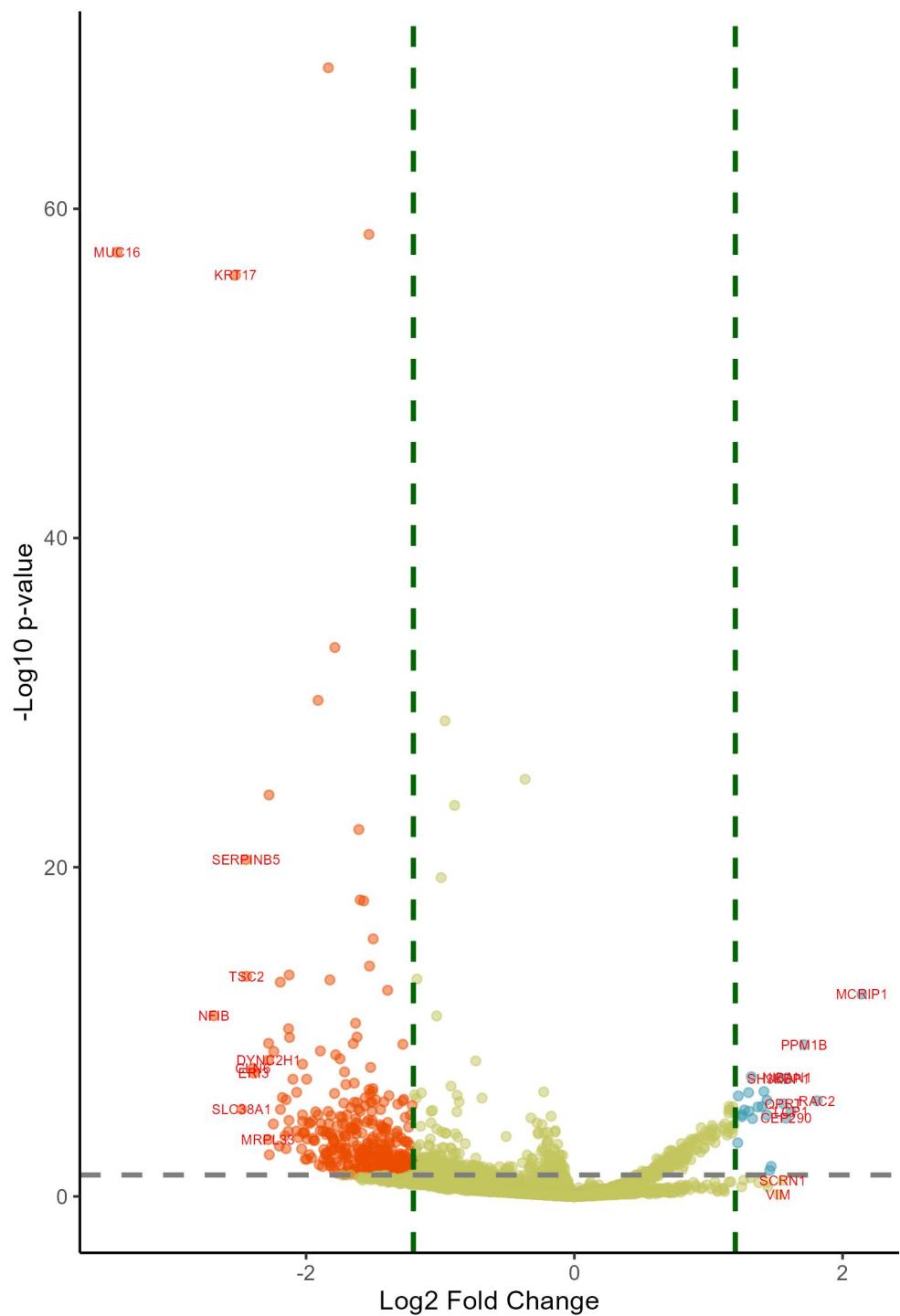
The text in the bars: incidence of APTX | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with APTX protein in solid cancers, DB1

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

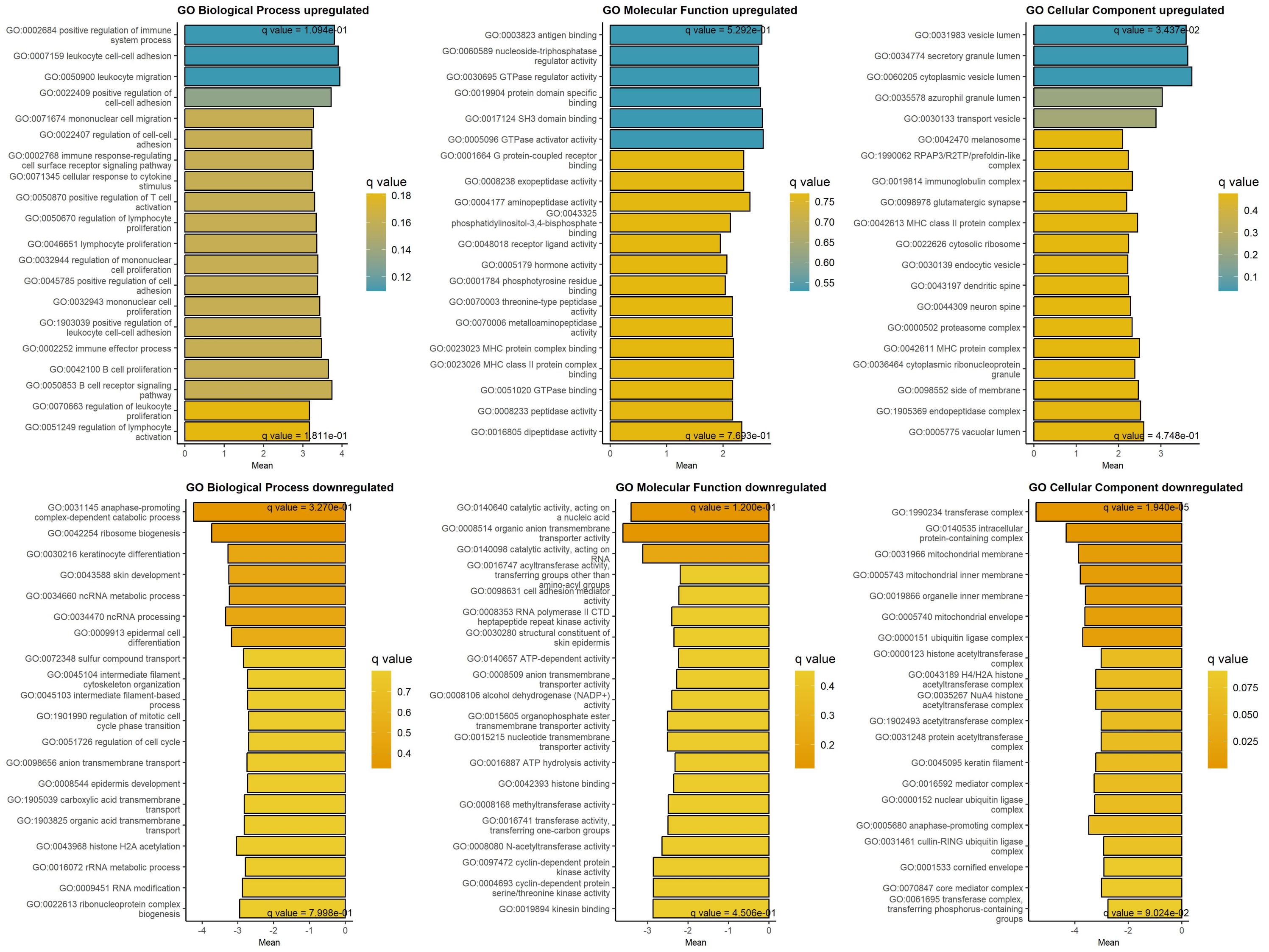


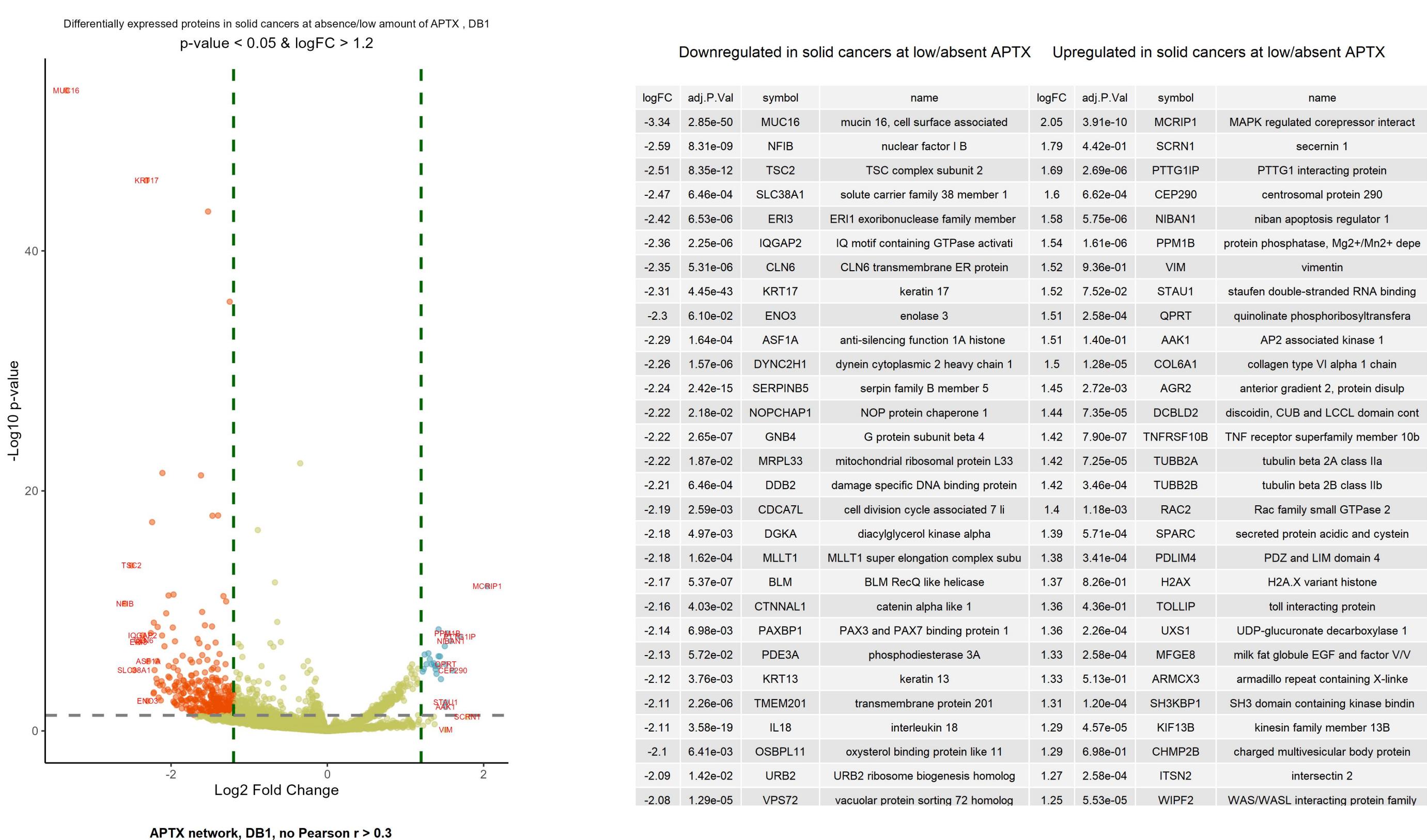


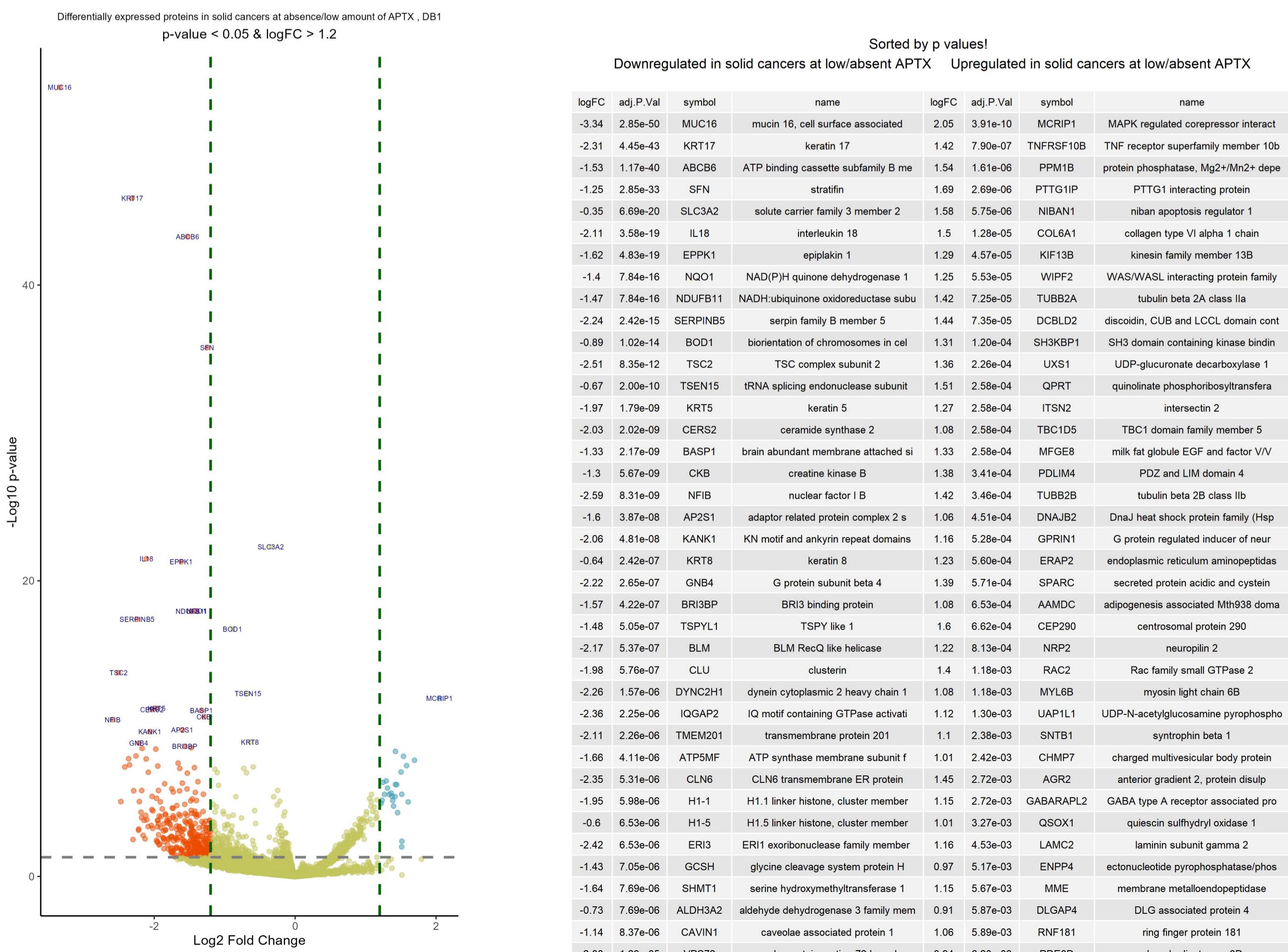
Downregulated at low/absent APTX Upregulated at low/absent APTX

| logFC | adj.P.Val | symbol | name | logFC | adj.P.Val | symbol | name |
|-------|-----------|----------|-------------------------------------|-------|-----------|-----------|--|
| -3.41 | 9.64e-55 | MUC16 | mucin 16, cell surface associated | 2.14 | 1.37e-10 | MCRIP1 | MAPK regulated corepressor interact |
| -2.69 | 2.68e-09 | NFIB | nuclear factor I B | 1.81 | 1.35e-04 | RAC2 | Rac family small GTPase 2 |
| -2.53 | 1.78e-53 | KRT17 | keratin 17 | 1.71 | 1.15e-07 | PPM1B | protein phosphatase, Mg ²⁺ /Mn ²⁺ depe |
| -2.48 | 3.48e-04 | SLC38A1 | solute carrier family 38 member 1 | 1.62 | 4.39e-04 | LCP1 | lymphocyte cytosolic protein 1 |
| -2.45 | 1.76e-18 | SERPINB5 | serpin family B member 5 | 1.59 | 8.56e-06 | NIBAN1 | niban apoptosis regulator 1 |
| -2.44 | 1.41e-11 | TSC2 | TSC complex subunit 2 | 1.58 | 9.41e-04 | CEP290 | centrosomal protein 290 |
| -2.4 | 2.52e-06 | CLN6 | CLN6 transmembrane ER protein | 1.56 | 1.81e-04 | QPRT | quinolinate phosphoribosyltransfера |
| -2.39 | 4.59e-06 | ERI3 | ERI1 exoribonuclease family member | 1.55 | 5.14e-01 | SCRN1 | secernin 1 |
| -2.28 | 1.00e-02 | MRPL33 | mitochondrial ribosomal protein L33 | 1.52 | 9.39e-06 | SH3KBP1 | SH3 domain containing kinase bindin |
| -2.28 | 8.98e-07 | DYNC2H1 | dynein cytoplasmic 2 heavy chain 1 | 1.52 | 9.60e-01 | VIM | vimentin |
| -2.28 | 1.05e-07 | GNB4 | G protein subunit beta 4 | 1.47 | 1.74e-01 | AAK1 | AP2 associated kinase 1 |
| -2.28 | 2.71e-22 | IL18 | interleukin 18 | 1.46 | 2.43e-01 | STAU1 | staufen double-stranded RNA binding |
| -2.27 | 5.62e-02 | ENO3 | enolase 3 | 1.44 | 7.60e-01 | H2AX | H2A.X variant histone |
| -2.24 | 1.80e-03 | KRT13 | keratin 13 | 1.44 | 5.79e-01 | SH3BGR1 | SH3 domain binding glutamate rich p |
| -2.24 | 2.78e-07 | TMEM201 | transmembrane protein 201 | 1.44 | 1.25e-04 | PTTG1IP | PTTG1 interacting protein |
| -2.2 | 2.14e-02 | CTNNAL1 | catenin alpha like 1 | 1.43 | 6.41e-04 | CORO1A | coronin 1A |
| -2.19 | 2.78e-11 | CERS2 | ceramide synthase 2 | 1.41 | 4.86e-05 | ITSN2 | intersectin 2 |
| -2.19 | 3.55e-04 | DDB2 | damage specific DNA binding protein | 1.4 | 2.55e-04 | GABARAPL2 | GABA type A receptor associated pro |
| -2.18 | 9.49e-05 | PLEKHG3 | pleckstrin homology and RhoGEF doma | 1.37 | 5.97e-01 | CHMP2B | charged multivesicular body protein |
| -2.16 | 6.67e-03 | URB2 | URB2 ribosome biogenesis homolog | 1.37 | 2.64e-04 | RNF181 | ring finger protein 181 |
| -2.15 | 2.88e-02 | PDE3A | phosphodiesterase 3A | 1.33 | 9.83e-04 | TUBB2B | tubulin beta 2B class IIb |
| -2.15 | 1.18e-04 | MLLT1 | MLLT1 super elongation complex subu | 1.32 | 7.68e-06 | TBC1D5 | TBC1 domain family member 5 |
| -2.13 | 4.08e-03 | PAXBP1 | PAX3 and PAX7 binding protein 1 | 1.31 | 4.29e-01 | TOLLIP | toll interacting protein |
| -2.13 | 1.49e-08 | KANK1 | KN motif and ankyrin repeat domains | 1.3 | 4.29e-04 | TUBB2A | tubulin beta 2A class IIa |
| -2.13 | 1.22e-03 | CDCA7L | cell division cycle associated 7 li | 1.3 | 5.37e-05 | KIF13B | kinesin family member 13B |
| -2.13 | 1.23e-11 | KRT5 | keratin 5 | 1.27 | 3.76e-04 | ERAP2 | endoplasmic reticulum aminopeptidas |
| -2.12 | 4.70e-08 | CLU | clusterin | 1.26 | 5.06e-01 | ECHDC1 | ethylmalonyl-CoA decarboxylase 1 |
| -2.1 | 9.85e-06 | VPS72 | vacuolar protein sorting 72 homolog | 1.25 | 6.36e-04 | COL6A1 | collagen type VI alpha 1 chain |
| -2.07 | 4.02e-03 | PLCD3 | phospholipase C delta 3 | 1.25 | 7.79e-04 | MFGE8 | milk fat globule EGF and factor V/V |

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



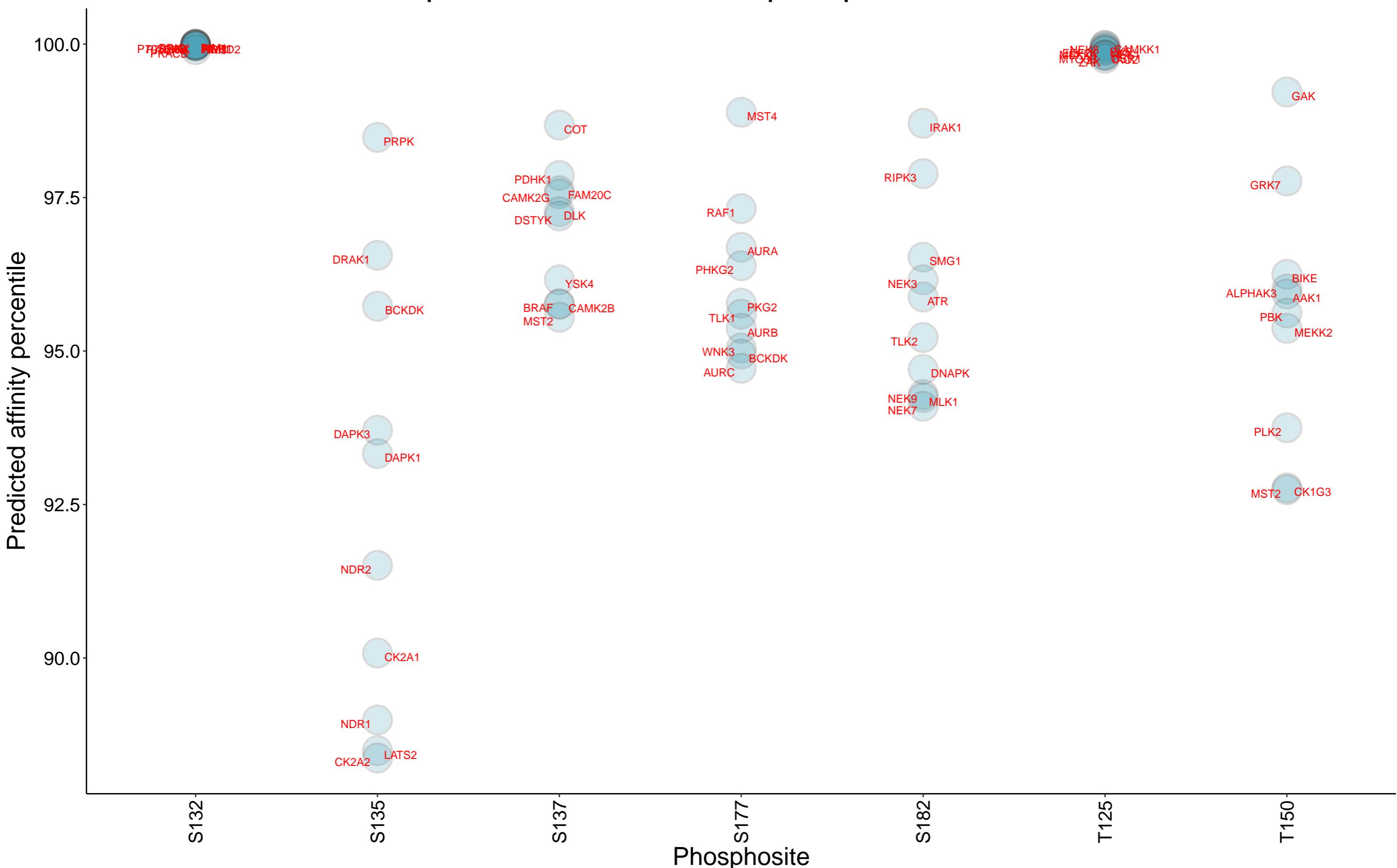




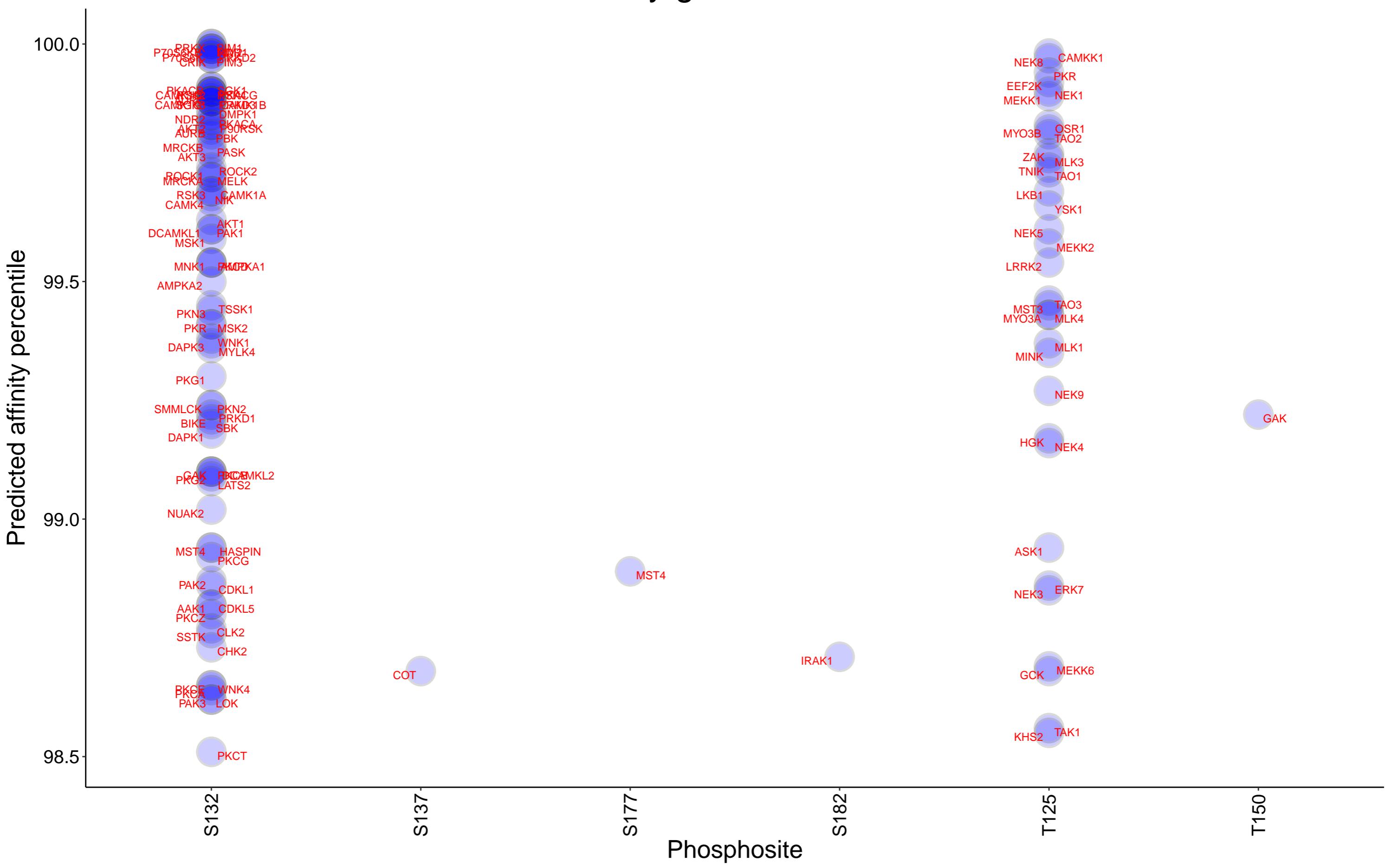
Insufficient number of paired observations in DB1 for APTX

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Top 10 kinases for each phosphosite in APTX



Kinases with affinity greater than 98.5% to APTX



No sufficient paired observations in DB1 for APTX