

DONSON

Protein name: DONS ; UNIPROT: Q9NYP3 ; Gene name: DNA replication fork stabilization factor DONSON

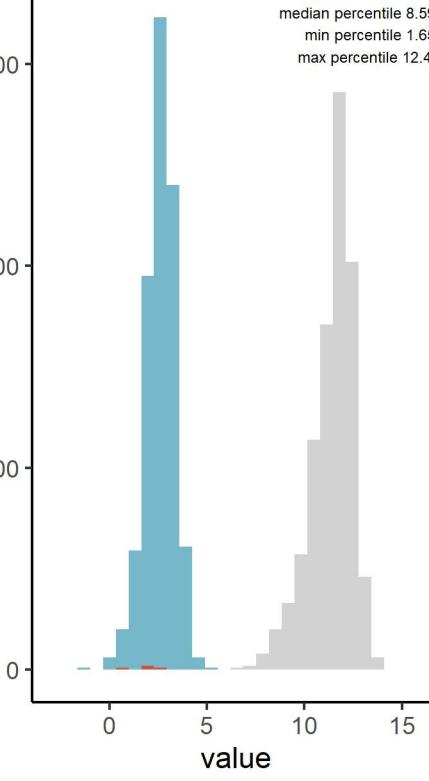
Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

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

6692 proteins in 949 CCLs

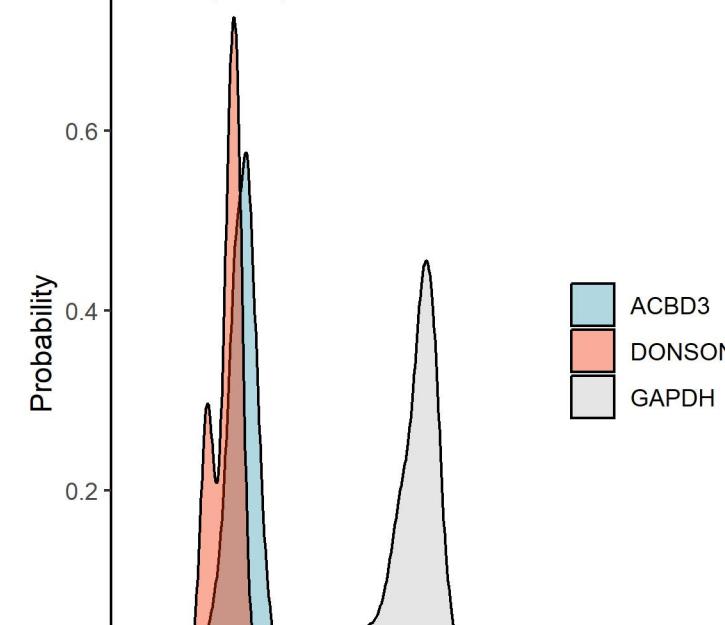
Histogram of DONSON protein compared to proteins with low and high abundance

In CCLs where DONSON protein is present:
median percentile 8.59
min percentile 1.65
max percentile 12.48



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

DONSON protein is present in 0.4 % CCLs



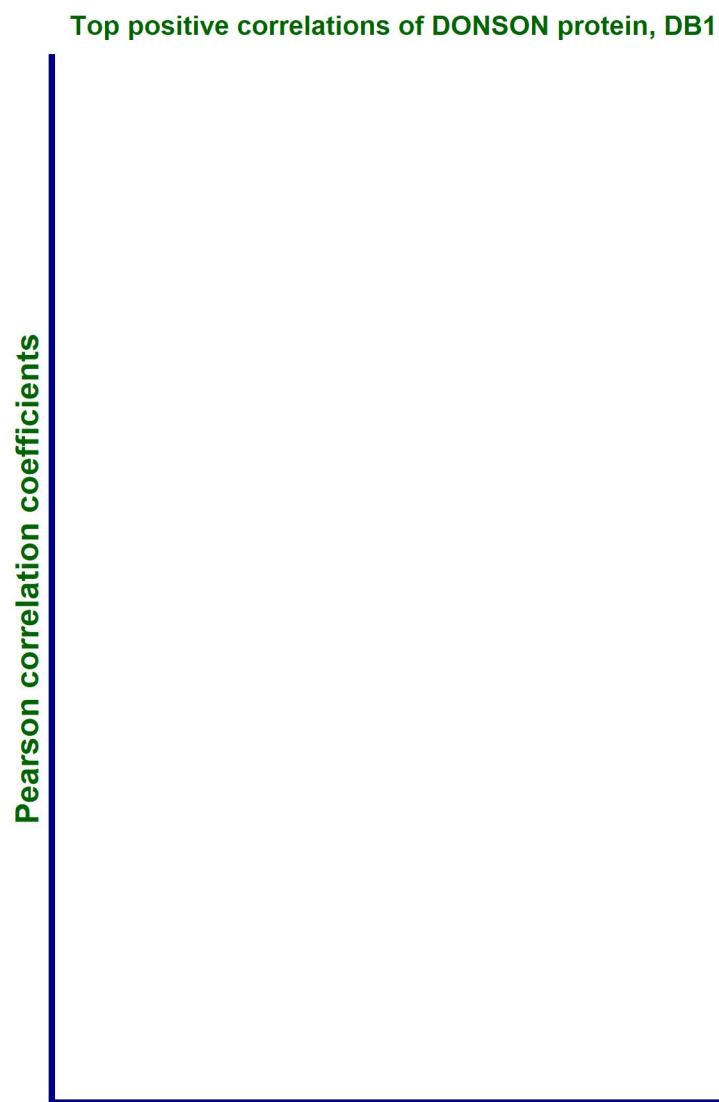
Top negative correlations of DONSON protein, DB1

Pearson correlation coefficients



Top positive correlations of DONSON protein, DB1

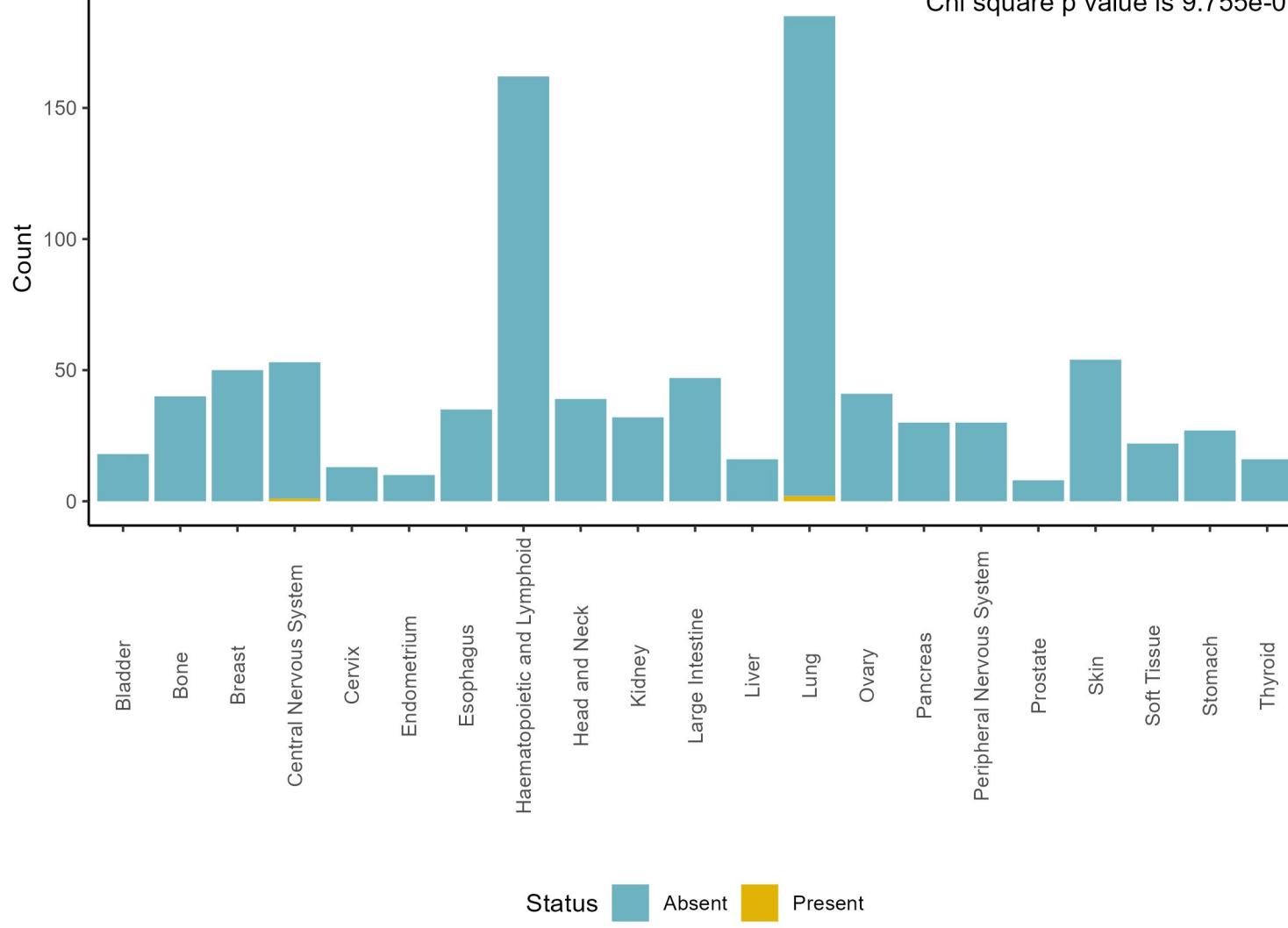
Pearson correlation coefficients



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

Present and absent DONSON protein counts by tissue, DB1

Chi square p value is 9.755e-01

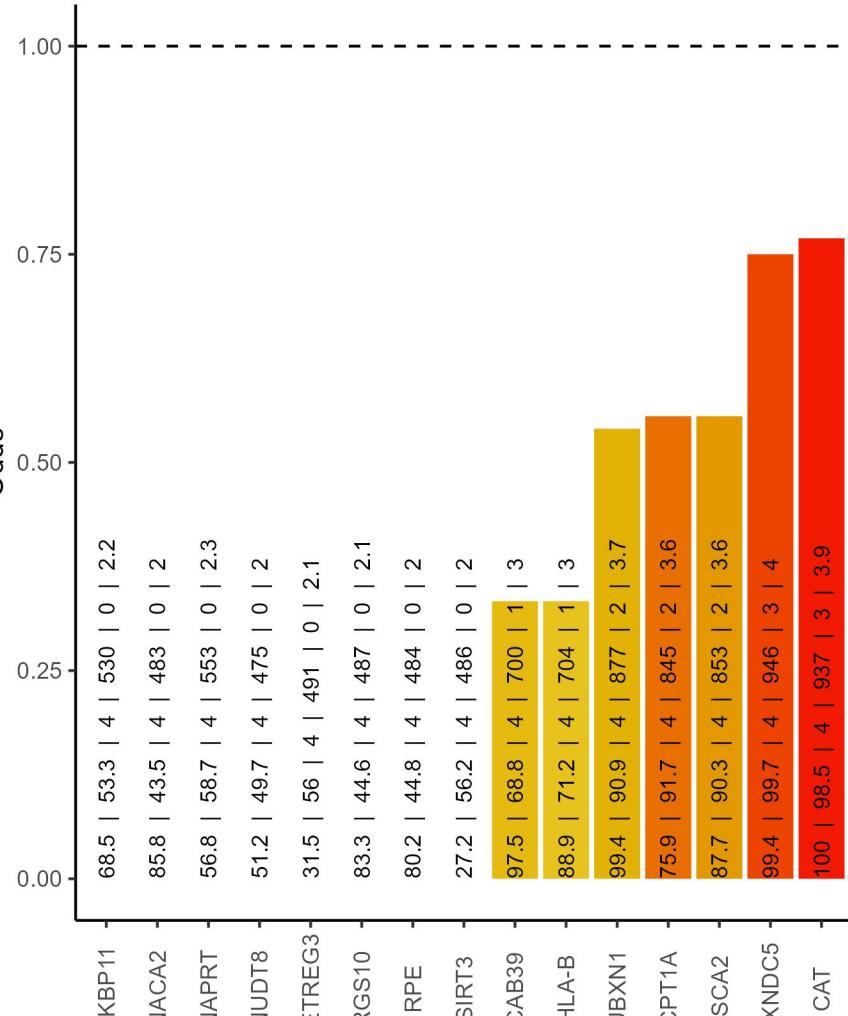


Cooccurrence with DONSON protein, DB1

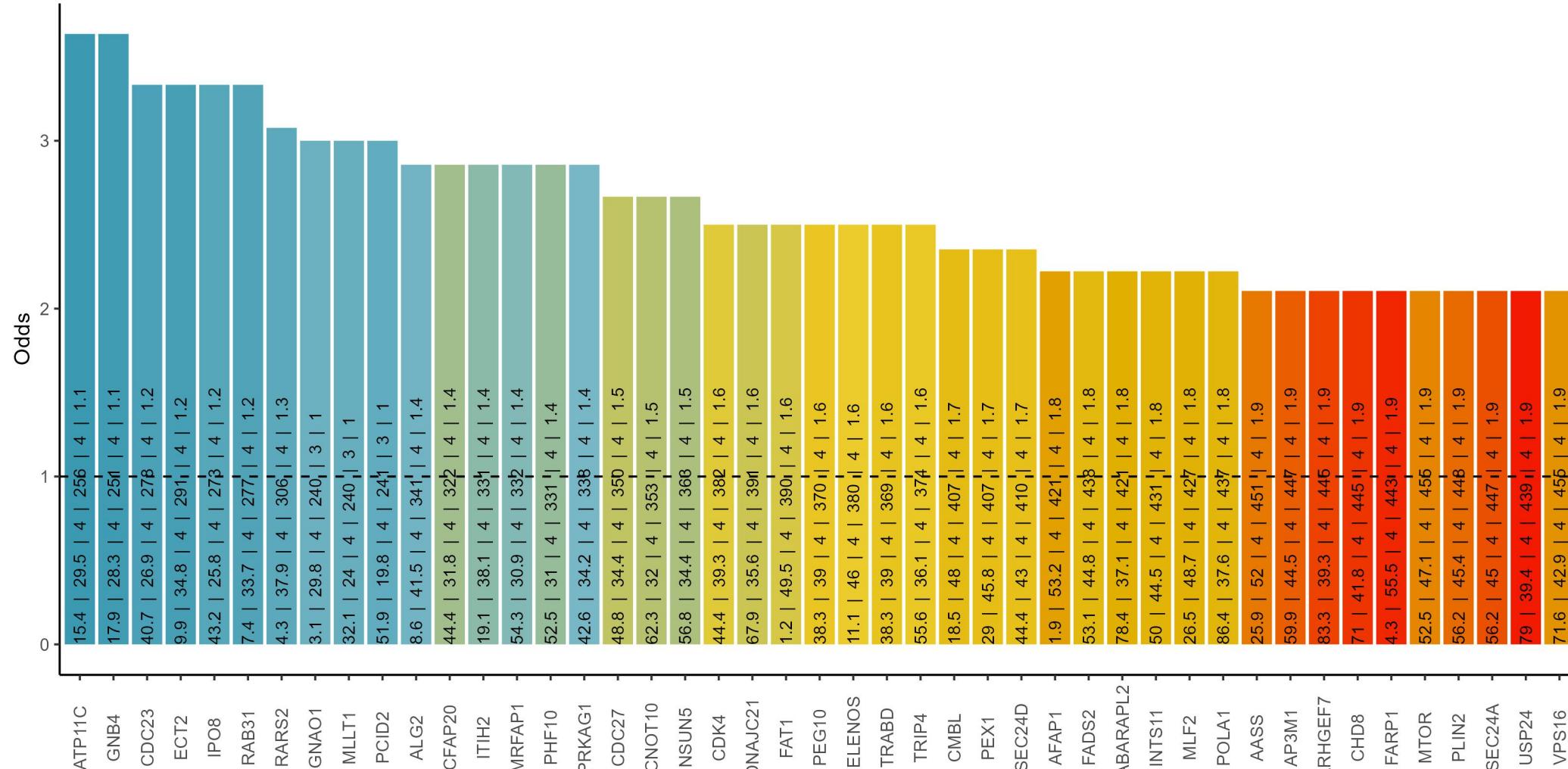
% of DONSON in blood cancers: 0 ; % of DONSON in solid cancers: 0.5

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

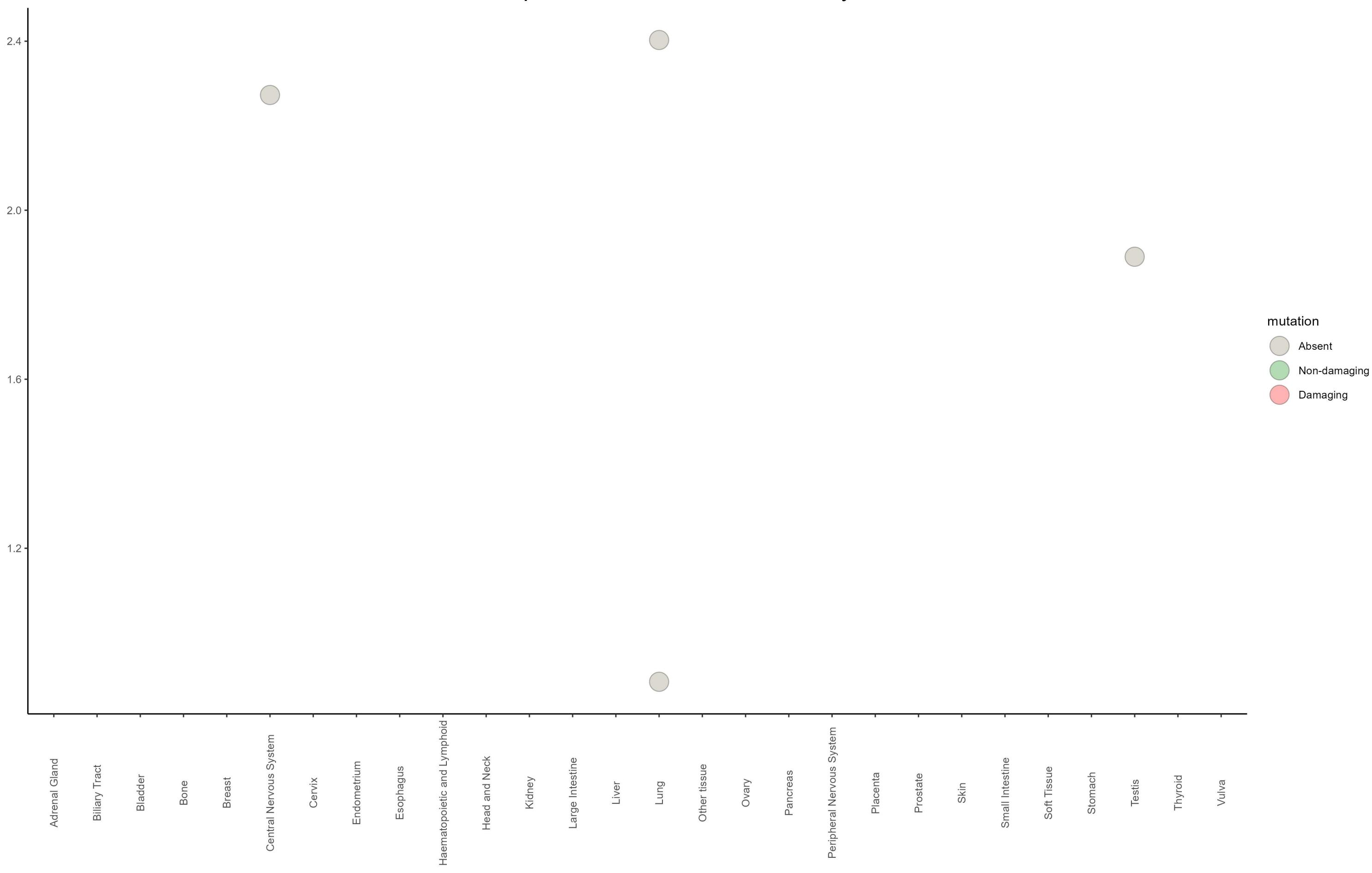
Negative cooccurrence



Positive cooccurrence

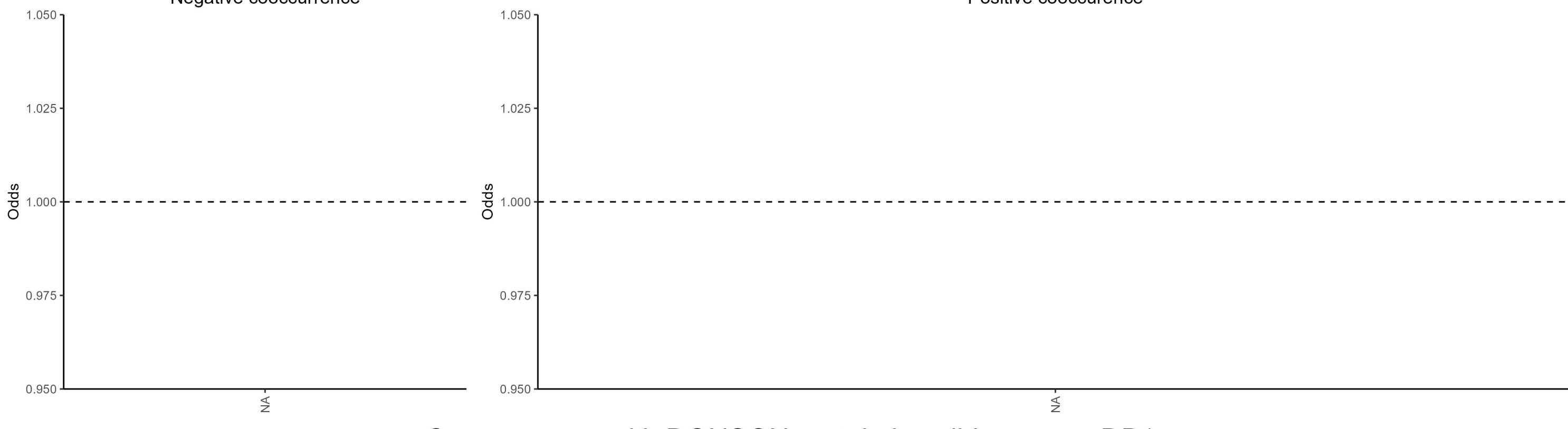


Amount of DONSON protein and mutation status by tissue, DB1



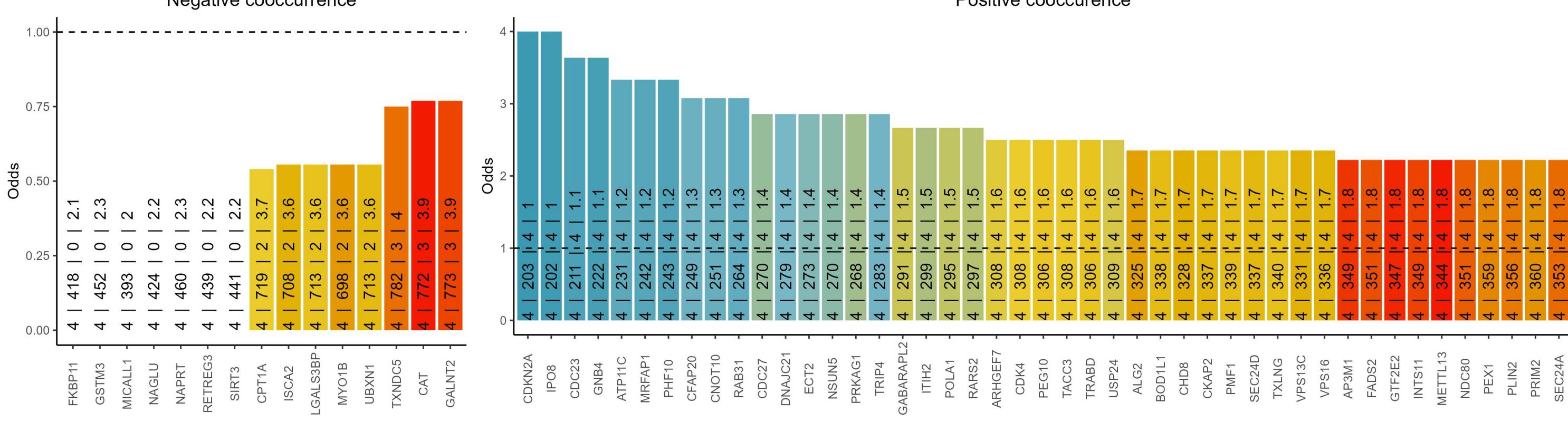
Cooccurrence with DONSON protein in blood cancers, DB1

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

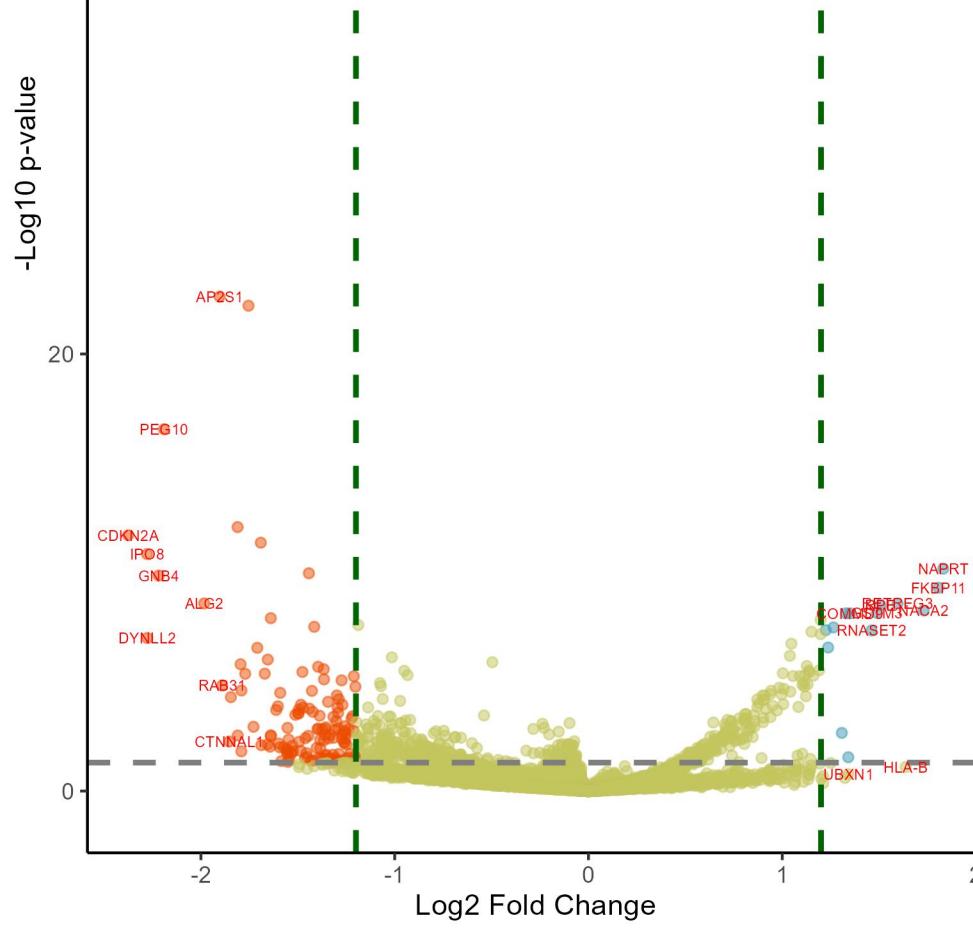


Cooccurrence with DONSON protein in solid cancers, DB1

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

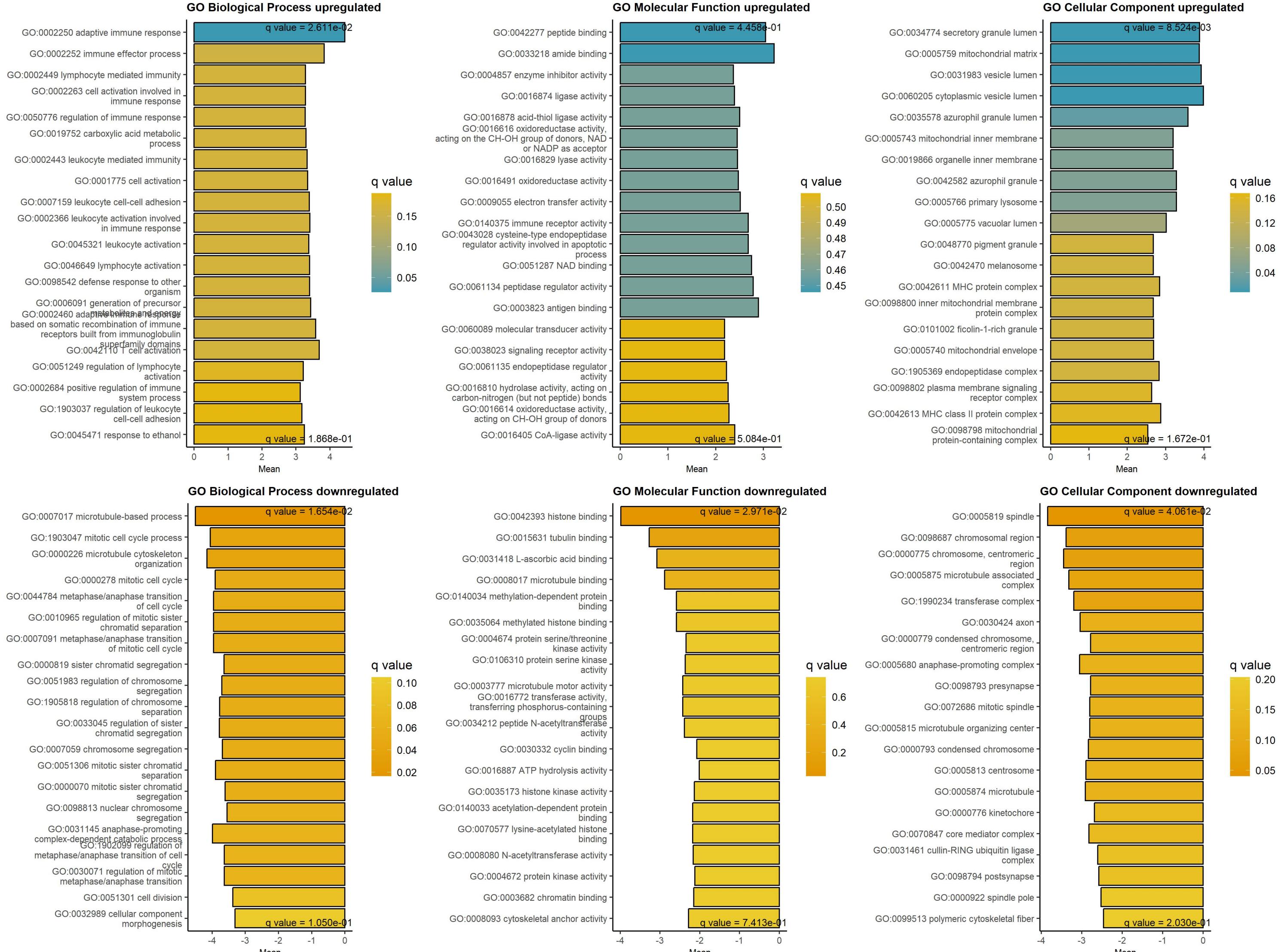


Downregulated at low/absent DONSON Upregulated at low/absent DONSON



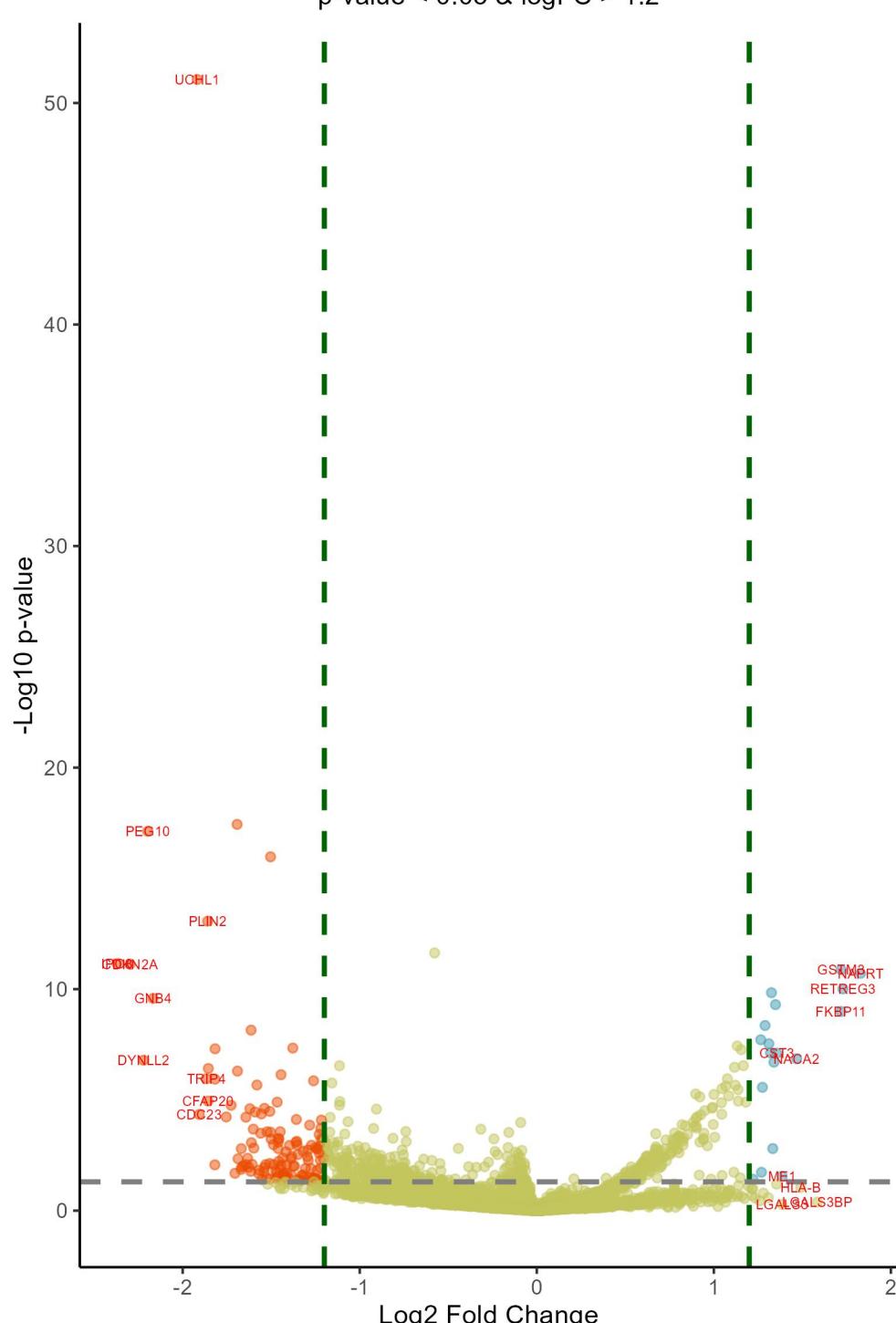
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.38	1.87e-09	CDKN2A	cyclin dependent kinase inhibitor 2	1.83	4.46e-08	NAPRT	nicotinate phosphoribosyltransferas
-2.28	1.06e-08	IPO8	importin 8	1.81	2.55e-07	FKBP11	FKBP prolyl isomerase 11
-2.28	2.21e-05	DYNLL2	dynein light chain LC8-type 2	1.73	2.13e-06	NACA2	nascent polypeptide associated comp
-2.22	7.63e-08	GNB4	G protein subunit beta 4	1.64	6.51e-01	HLA-B	major histocompatibility complex, c
-2.19	3.72e-14	PEG10	paternally expressed 10	1.6	1.15e-06	RETREG3	reticulophagy regulator family memb
-2	9.35e-54	UCHL1	ubiquitin C-terminal hydrolase L1	1.51	1.29e-06	RPE	ribulose-5-phosphate-3-epimerase
-1.98	1.15e-06	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer	1.49	2.46e-06	GSTM3	glutathione S-transferase mu 3
-1.9	5.23e-20	AP2S1	adaptor related protein complex 2 s	1.46	1.11e-05	RNASET2	ribonuclease T2
-1.89	1.59e-03	RAB31	RAB31, member RAS oncogene family	1.35	2.46e-06	COMMD9	COMM domain containing 9
-1.85	1.45e-01	CTNNAL1	catenin alpha like 1	1.34	8.64e-01	UBXN1	UBX domain protein 1
-1.85	4.25e-03	CDC23	cell division cycle 23	1.34	4.03e-01	OGFR	opioid growth factor receptor
-1.81	9.24e-10	PLIN2	perilipin 2	1.33	2.46e-06	RGS10	regulator of G protein signaling 10
-1.81	9.65e-02	RAB3B	RAB3B, member RAS oncogene family	1.32	9.59e-01	B2M	beta-2-microglobulin
-1.8	2.76e-04	CDK4	cyclin dependent kinase 4	1.31	7.96e-02	HEXIM1	HEXIM P-TEFb complex subunit 1
-1.79	2.84e-01	CDH6	cadherin 6	1.26	8.67e-06	NUDT8	nudix hydrolase 8
-1.79	2.45e-03	CFAP20	cilia and flagella associated prote	1.25	5.45e-01	MIEN1	migration and invasion enhancer 1
-1.77	5.86e-04	TRIP4	thyroid hormone receptor interactor	1.24	5.62e-05	GALE	UDP-galactose-4-epimerase
-1.75	1.03e-19	MAP1B	microtubule associated protein 1B	1.22	1.11e-05	MICALL1	MICAL like 1
-1.73	5.12e-02	ATP11C	ATPase phospholipid transporting 11	1.21	1.00e+00	LGALS3BP	galectin 3 binding protein
-1.71	5.63e-05	MLF2	myeloid leukemia factor 2	1.21	9.01e-01	VAMP8	vesicle associated membrane protein
-1.69	3.59e-09	DPYSL3	dihydropyrimidinase like 3	1.2	9.70e-01	CPT1A	carnitine palmitoyltransferase 1A
-1.69	1.88e-01	COL1A1	collagen type I alpha 1 chain	1.2	1.52e-05	NAGLU	N-acetyl-alpha-glucosaminidase
-1.67	5.86e-04	CMBL	carboxymethylenebutenolidase homolo	1.2	4.49e-06	SIRT3	sirtuin 3
-1.66	1.78e-01	NAV1	neuron navigator 1	1.19	5.55e-01	CAB39	calcium binding protein 39
-1.65	1.78e-04	FADS2	fatty acid desaturase 2	1.19	4.71e-04	CST3	cystatin C
-1.64	2.06e-01	INTS5	integrator complex subunit 5	1.16	6.72e-04	PYCARD	PYD and CARD domain containing
-1.64	9.95e-02	INA	internexin neuronal intermediate fi	1.15	1.23e-05	ABRAXAS2	abraxas 2, BRISC complex subunit
-1.64	3.91e-06	UQCR10	ubiquinol-cytochrome c reductase, c	1.15	6.14e-01	ME1	malic enzyme 1
-1.64	9.49e-02	CRYBG3	crystallin beta-gamma domain contai	1.15	7.15e-01	GPHN	gephyrin

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



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

p-value < 0.05 & logFC > 1.2

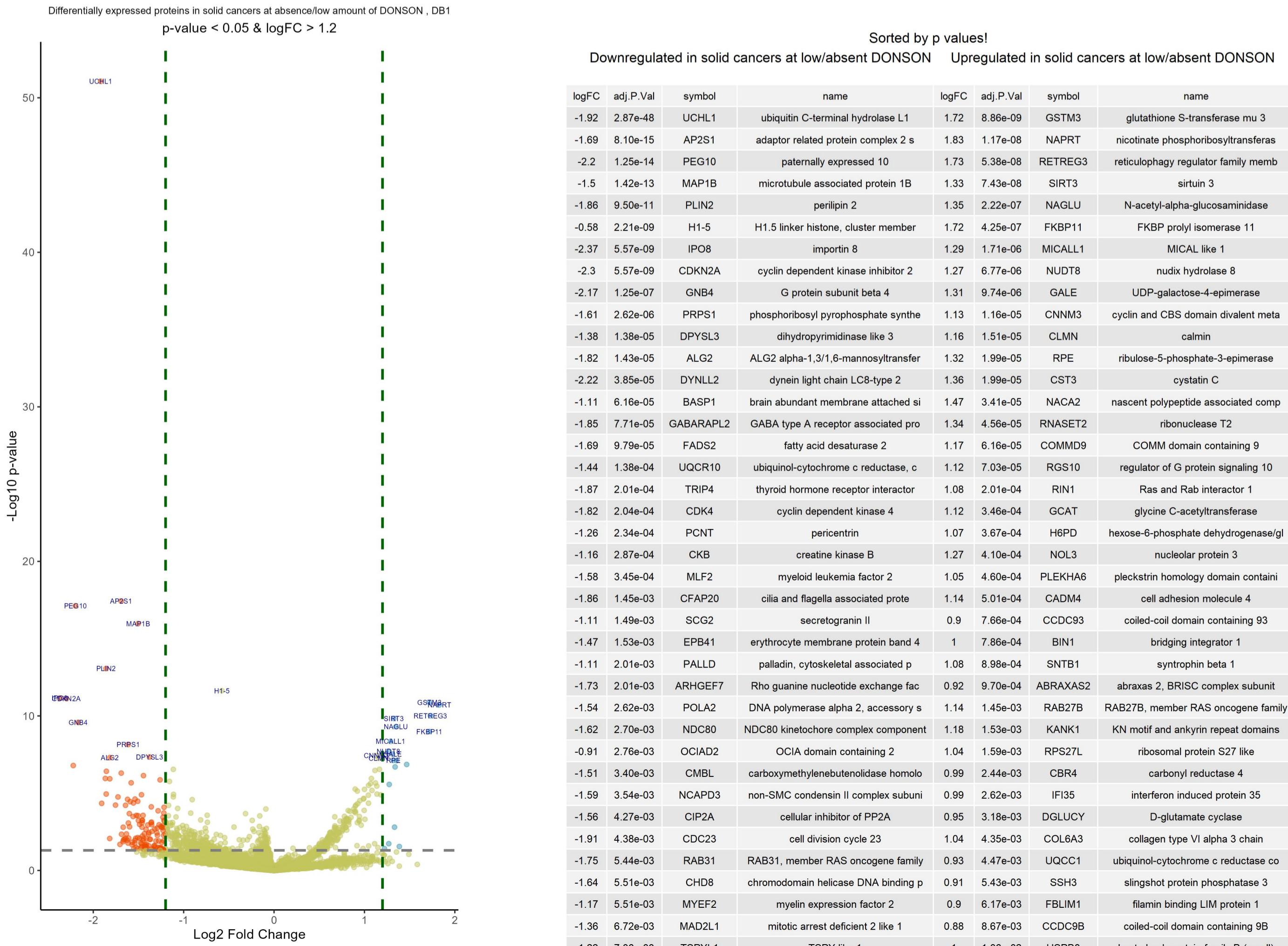


Downregulated in solid cancers at low/absent DONSON Upregulated in solid cancers at low/absent DONSON

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.37	5.57e-09	IPO8	importin 8	1.83	1.17e-08	NAPRT	nicotinate phosphoribosyltransferase
-2.3	5.57e-09	CDKN2A	cyclin dependent kinase inhibitor 2	1.73	5.38e-08	RETREG3	reticulophagy regulator family memb
-2.22	3.85e-05	DYNLL2	dynein light chain LC8-type 2	1.72	8.86e-09	GSTM3	glutathione S-transferase mu 3
-2.2	1.25e-14	PEG10	paternally expressed 10	1.72	4.25e-07	FKBP11	FKBP prolyl isomerase 11
-2.17	1.25e-07	GNB4	G protein subunit beta 4	1.58	1.00e+00	LGALS3BP	galectin 3 binding protein
-1.92	2.87e-48	UCHL1	ubiquitin C-terminal hydrolase L1	1.49	6.90e-01	HLA-B	major histocompatibility complex, c
-1.91	4.38e-03	CDC23	cell division cycle 23	1.47	3.41e-05	NACA2	nascent polypeptide associated comp
-1.87	2.01e-04	TRIP4	thyroid hormone receptor interactor	1.39	4.07e-01	ME1	malic enzyme 1
-1.86	9.50e-11	PLIN2	perilipin 2	1.39	1.00e+00	LGALS3	galectin 3
-1.86	1.45e-03	CFAP20	cilia and flagella associated prote	1.36	1.99e-05	CST3	cystatin C
-1.85	7.71e-05	GABARPL2	GABA type A receptor associated pro	1.35	5.92e-01	CEPB	CCAAT enhancer binding protein beta
-1.82	1.97e-01	CTNNAL1	catenin alpha like 1	1.35	2.22e-07	NAGLU	N-acetyl-alpha-glucosaminidase
-1.82	2.04e-04	CDK4	cyclin dependent kinase 4	1.34	4.56e-05	RNASET2	ribonuclease T2
-1.82	1.43e-05	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer	1.33	6.60e-02	HEXIM1	HEXIM P-TEFb complex subunit 1
-1.75	5.44e-03	RAB31	RAB31, member RAS oncogene family	1.33	7.43e-08	SIRT3	sirtuin 3
-1.73	2.01e-03	ARHGEF7	Rho guanine nucleotide exchange fac	1.32	1.99e-05	RPE	ribulose-5-phosphate-3-epimerase
-1.7	3.37e-01	CDH6	cadherin 6	1.31	9.74e-06	GALE	UDP-galactose-4-epimerase
-1.69	8.10e-15	AP2S1	adaptor related protein complex 2 s	1.31	9.68e-01	CPT1A	carnitine palmitoyltransferase 1A
-1.69	9.79e-05	FADS2	fatty acid desaturase 2	1.29	1.71e-06	MICALL1	MICAL like 1
-1.69	1.32e-01	RAB3B	RAB3B, member RAS oncogene family	1.28	8.58e-01	UBXN1	UBX domain protein 1
-1.67	2.66e-01	HAUS8	HAUS augmin like complex subunit 8	1.27	4.10e-04	NOL3	nucleolar protein 3
-1.67	6.60e-02	ATP11C	ATPase phospholipid transporting 11	1.27	3.17e-01	ECSIT	ECSIT signaling integrator
-1.67	2.25e-01	INTS5	integrator complex subunit 5	1.27	6.77e-06	NUDT8	nudix hydrolase 8
-1.66	2.10e-01	COL1A1	collagen type I alpha 1 chain	1.26	1.00e+00	MVP	major vault protein
-1.64	5.51e-03	CHD8	chromodomain helicase DNA binding p	1.23	9.79e-01	B2M	beta-2-microglobulin
-1.64	1.94e-01	SINHCAF	SIN3-HDAC complex associated factor	1.22	4.77e-01	OGFR	opioid growth factor receptor
-1.63	1.29e-01	CRYBG3	crystallin beta-gamma domain contai	1.22	7.21e-01	NDRG1	N-myc downstream regulated 1
-1.63	2.30e-01	PNISR	PNN interacting serine and arginine	1.21	9.18e-01	MYO1B	myosin IB
-1.62	2.70e-03	NDC80	NDC80 kinetochore complex component	1.21	7.20e-01	PIGT	phosphatidylinositol glycan anchor

fficient data for blood cancers differential expression of DONSON

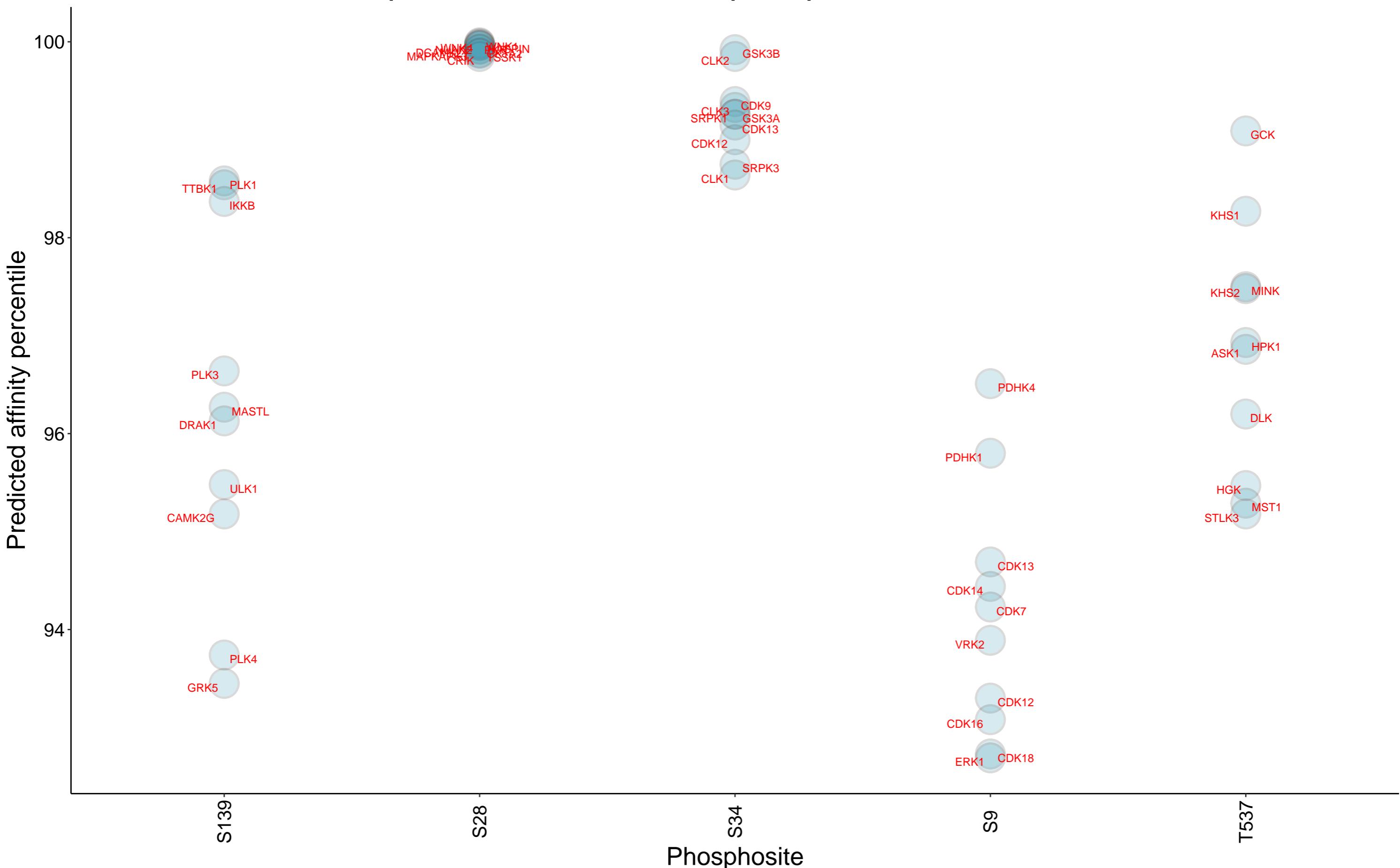
Insufficient data for blood cancers differential expression of DONSON



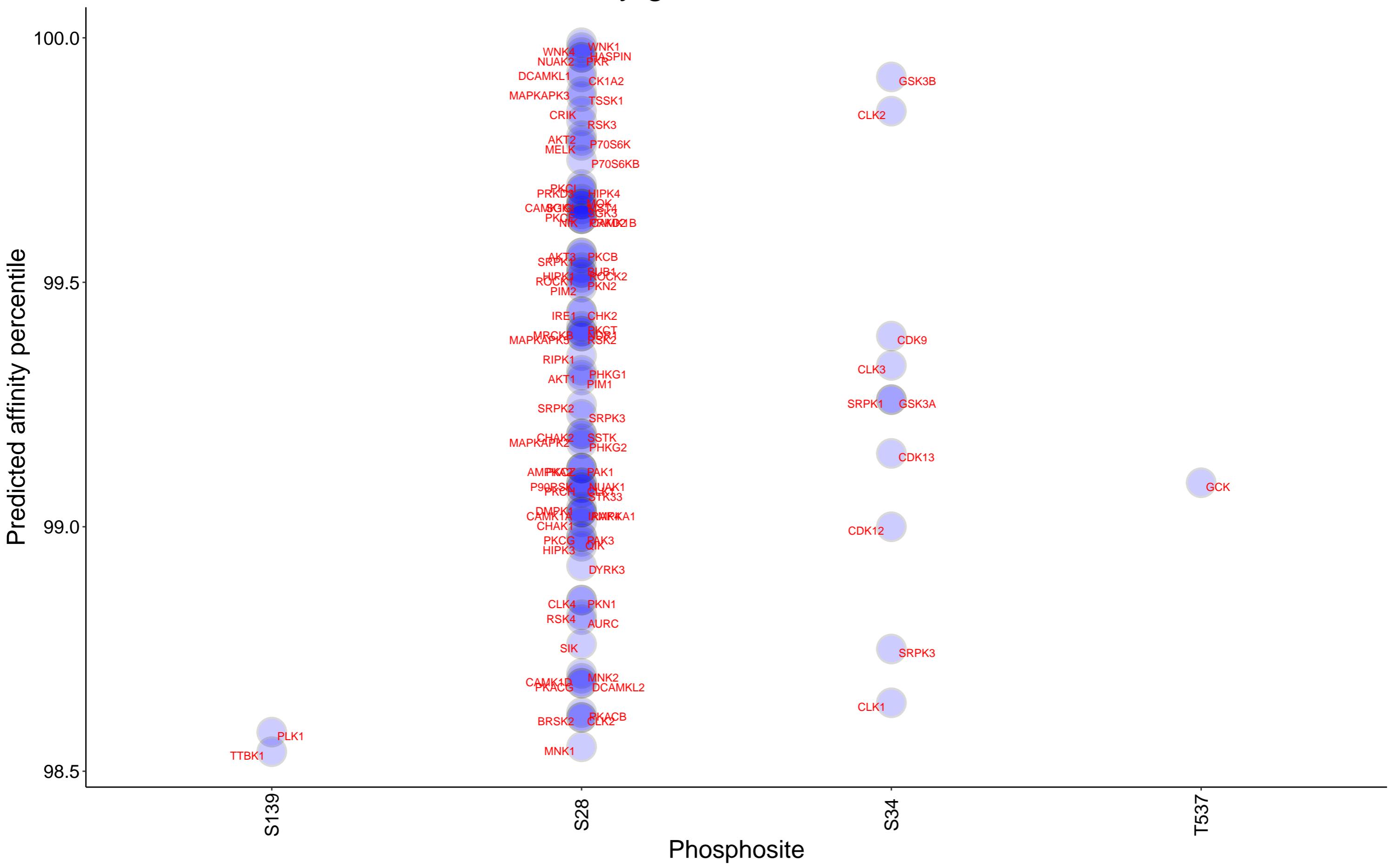
Insufficient number of paired observations in DB1 for DONSON

Insufficient number of paired observations in DB1 for DONSON

Top 10 kinases for each phosphosite in DONSON



Kinases with affinity greater than 98.5% to DONSON



No sufficient paired observations in DB1 for DONSON