

# CHEK2

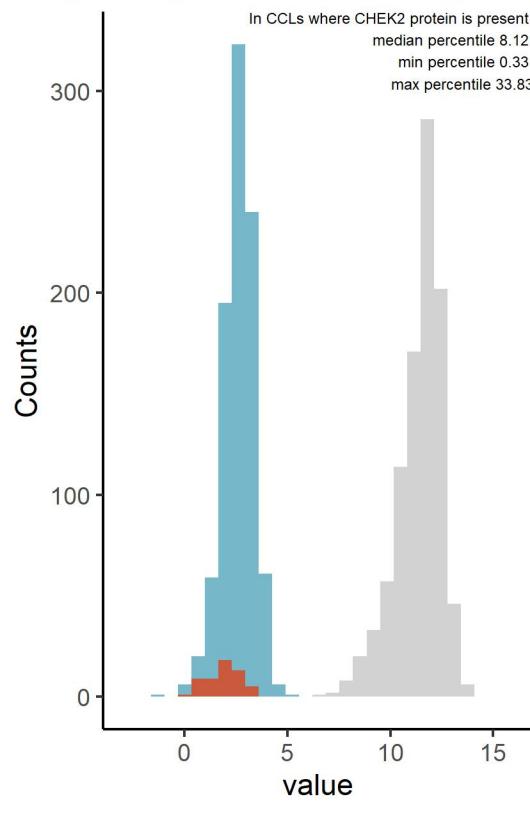
Protein name: CHK2 ; UNIPROT: O96017 ; Gene name: checkpoint kinase 2

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

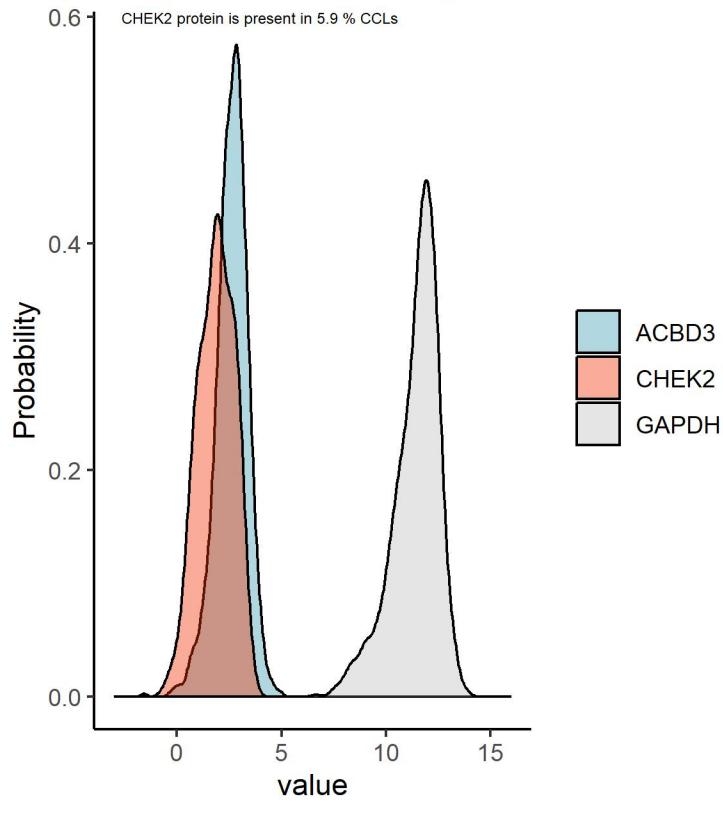
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of CHEK2 protein compared to proteins with low and high abundance



Density plot of CHEK2 protein compared to proteins with low and high abundance



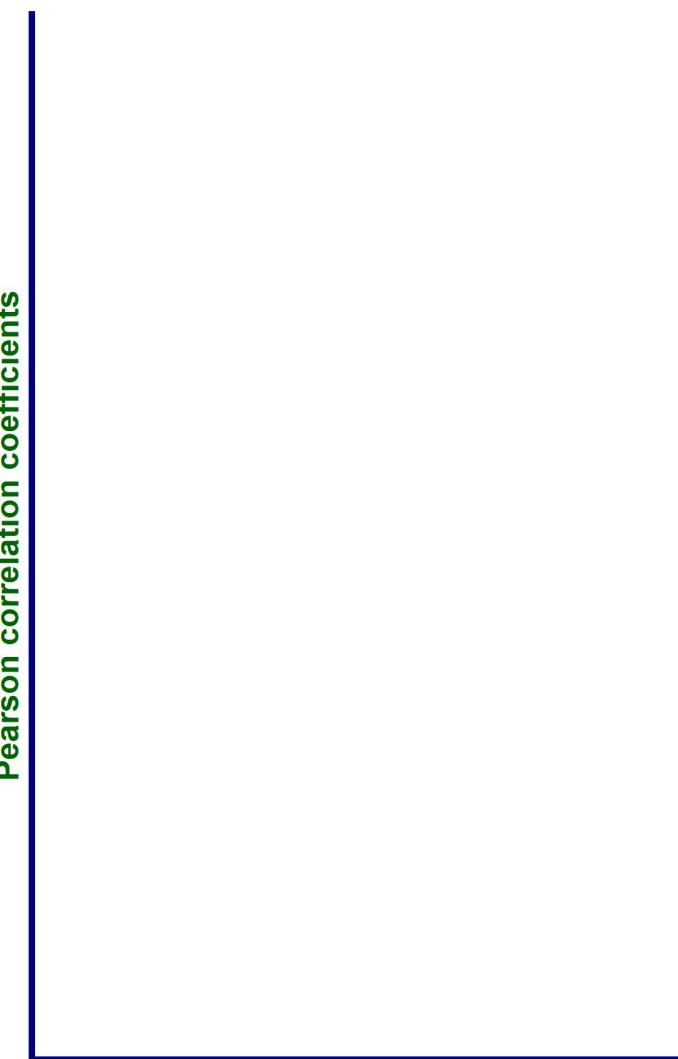
### Top negative correlations of CHEK2 protein, DB1

Pearson correlation coefficients



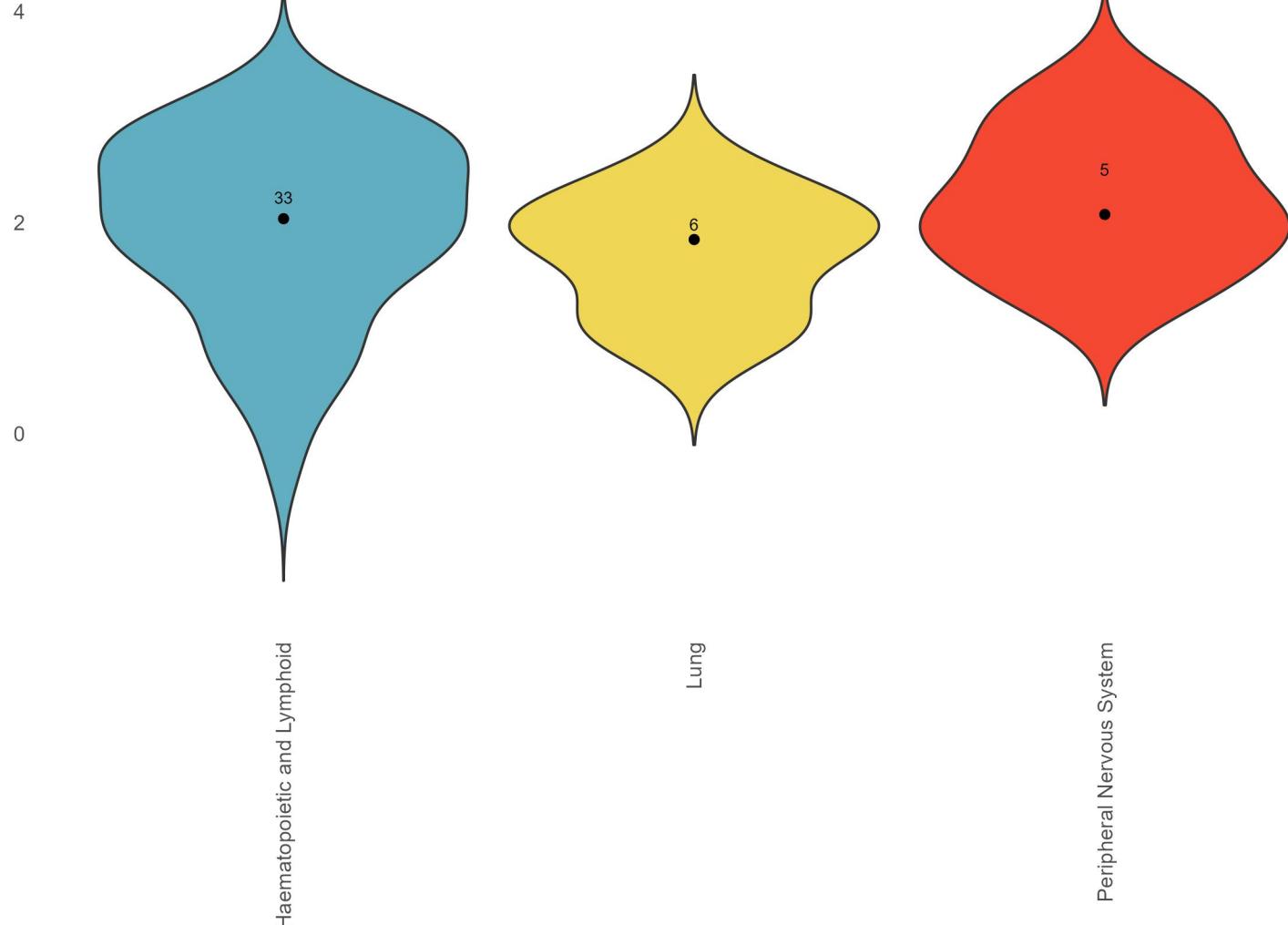
### Top positive correlations of CHEK2 protein, DB1

Pearson correlation coefficients



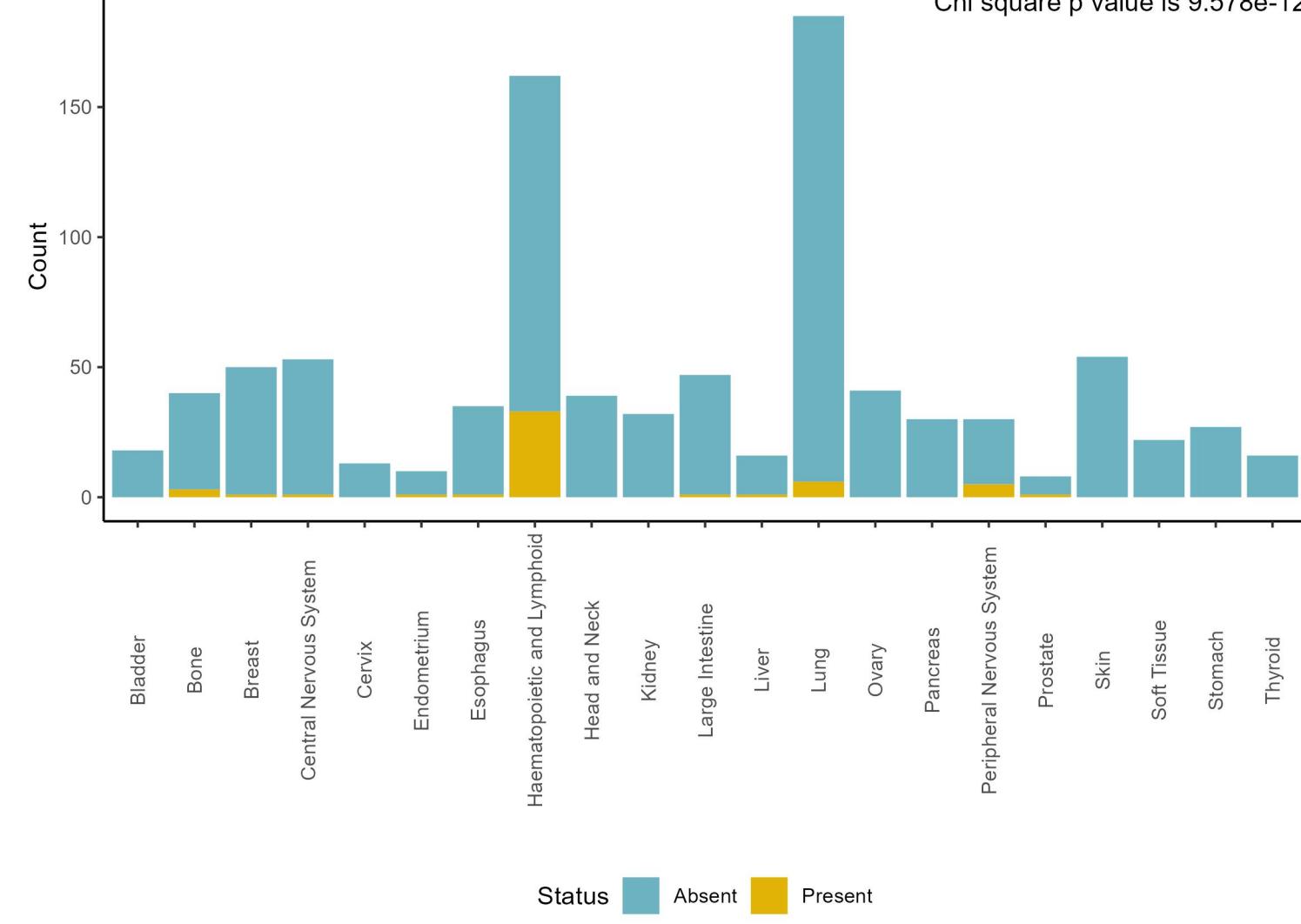
## Amount of CHEK2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.688e-01



## Present and absent CHEK2 protein counts by tissue, DB1

Chi square p value is 9.578e-12

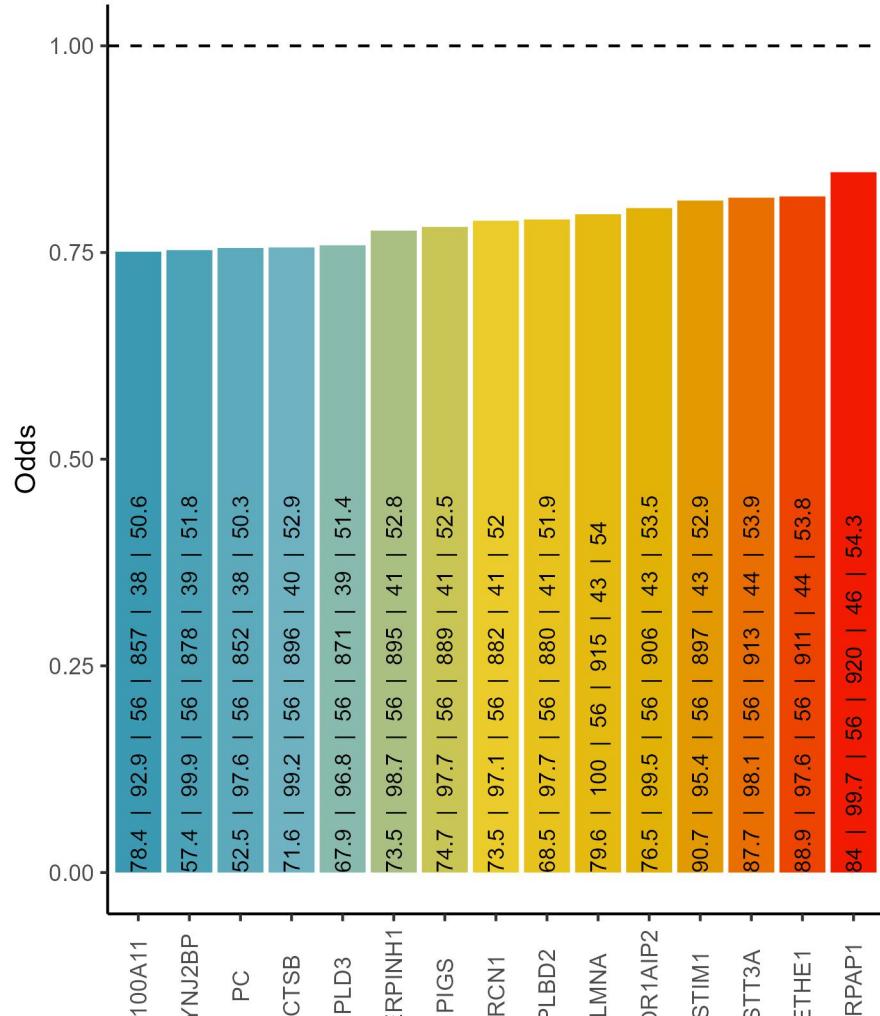


## Cooccurrence with CHEK2 protein, DB1

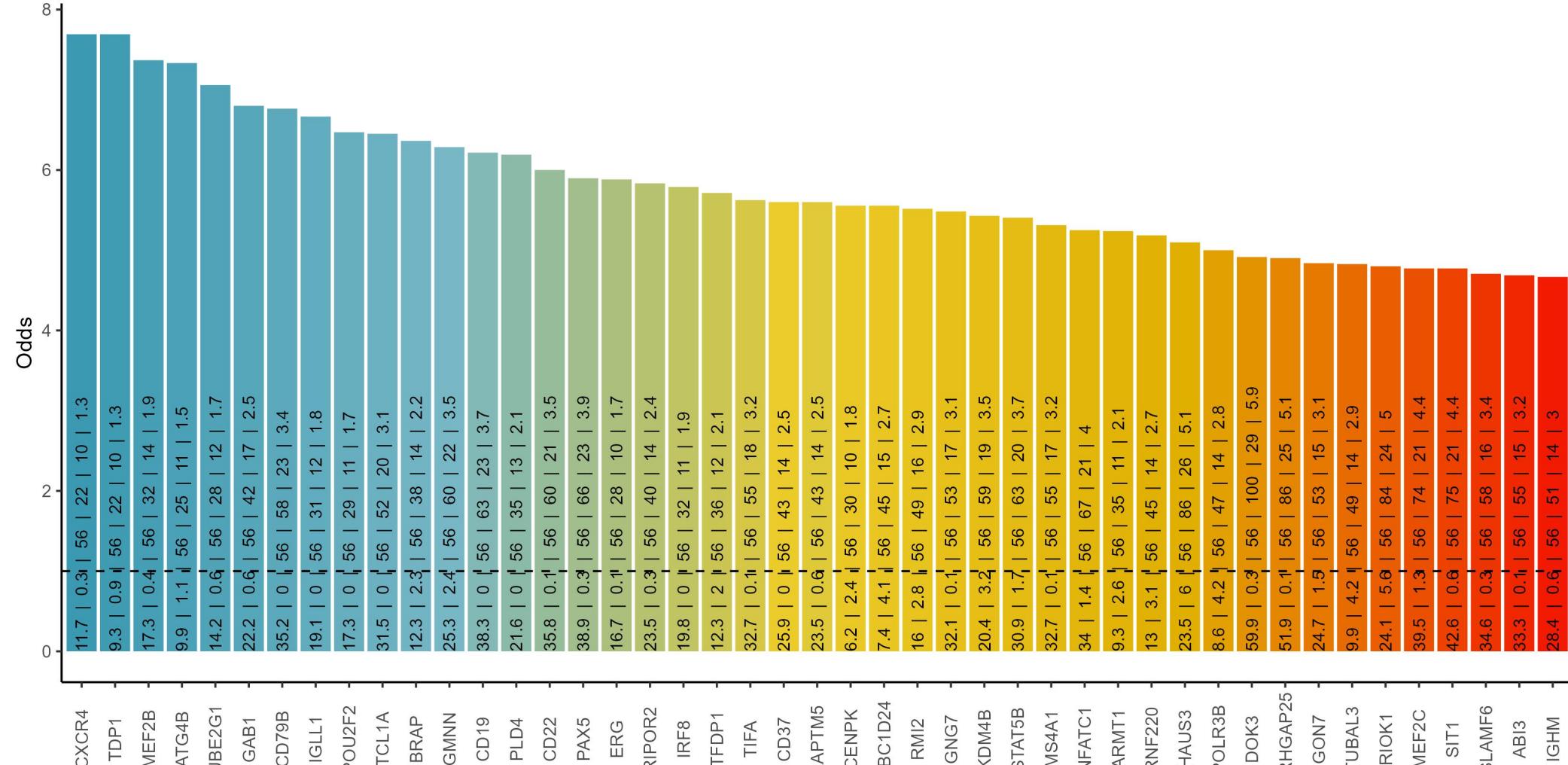
% of CHEK2 in blood cancers: 20.4 ; % of CHEK2 in solid cancers: 2.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CHEK2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

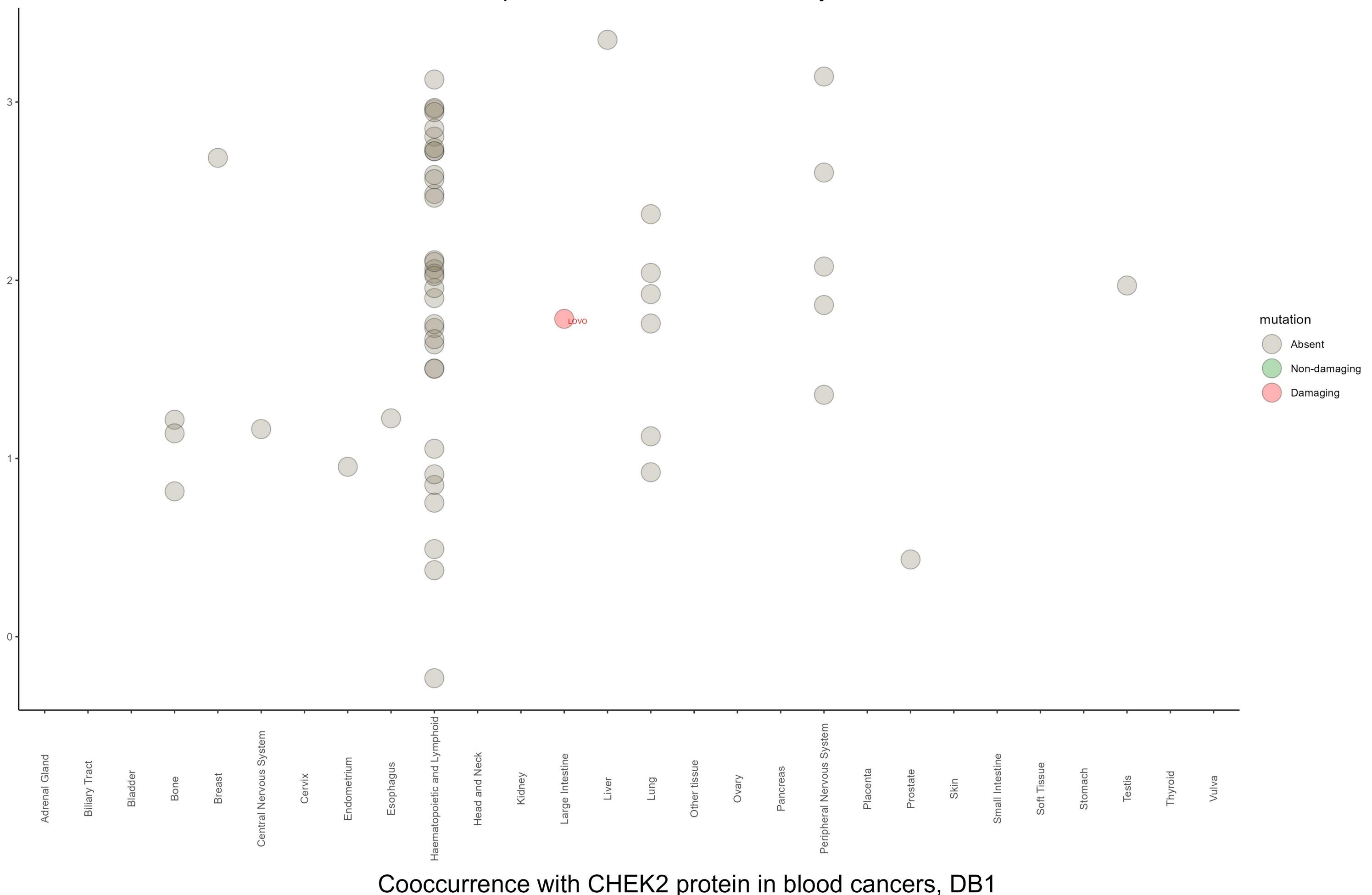
### Negative cooccurrence



### Positive cooccurrence



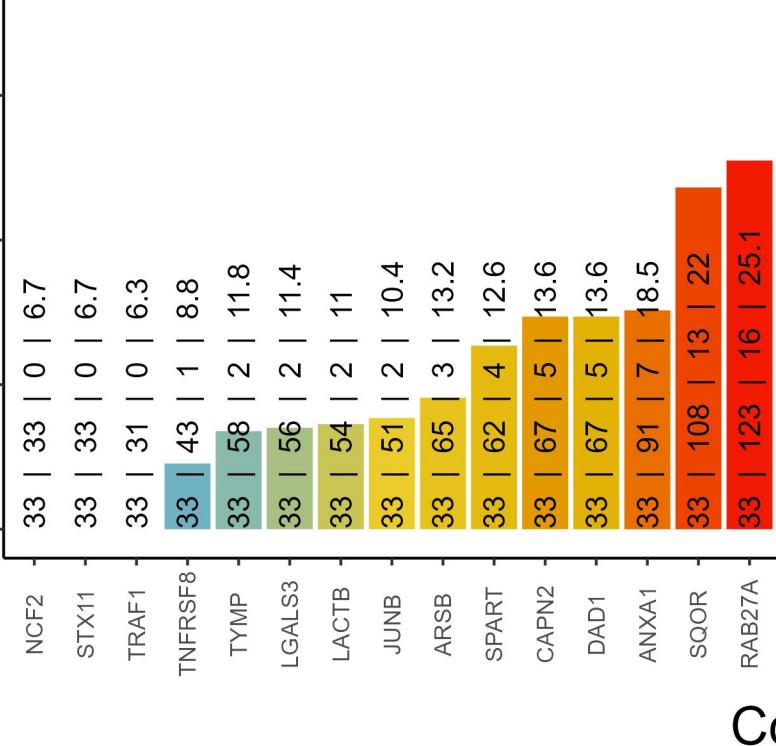
# Amount of CHEK2 protein and mutation status by tissue, DB1



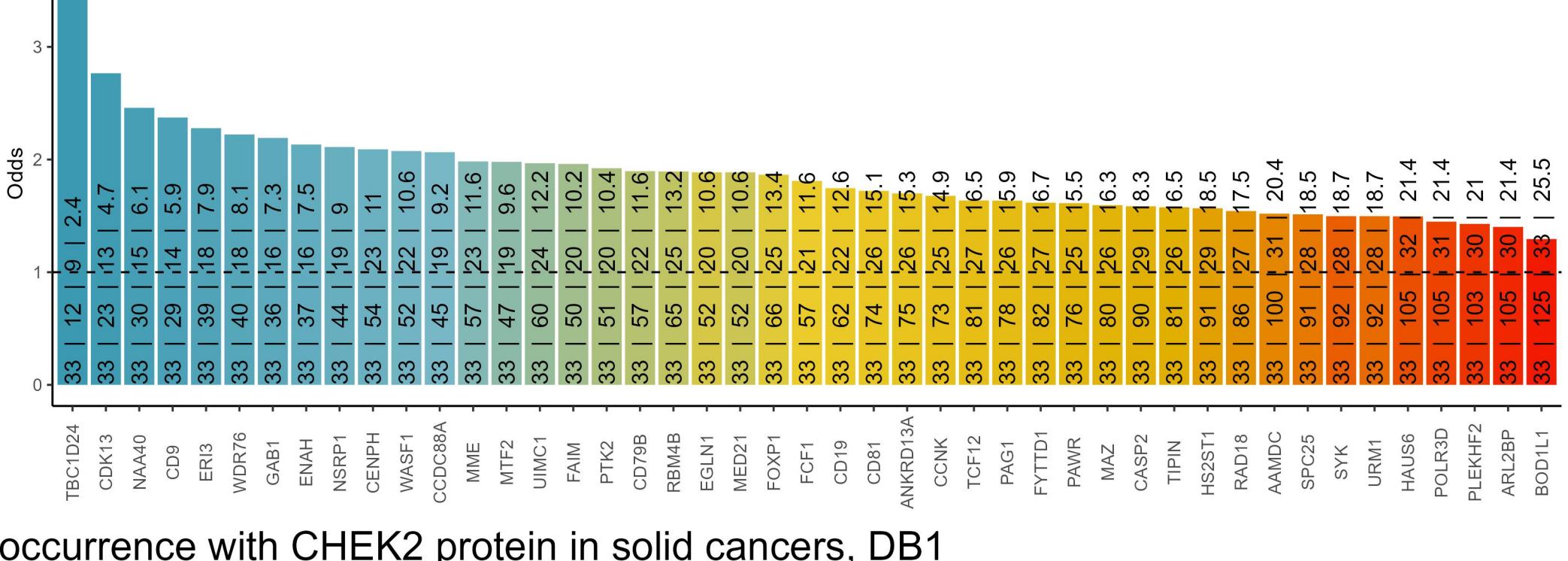
## Cooccurrence with CHEK2 protein in blood cancers, DB1

The text in the bars: incidence of CHEK2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

### Negative cooccurrence



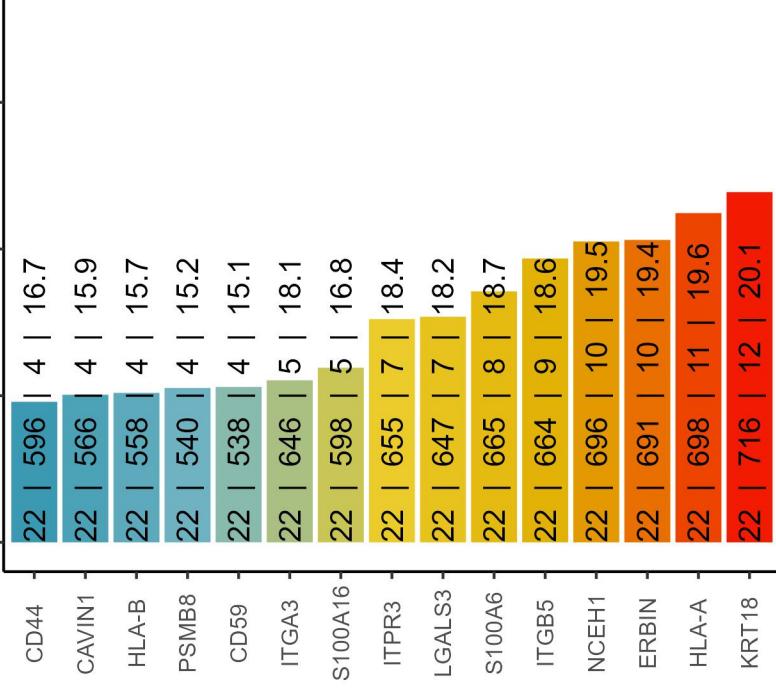
### Positive cooccurrence



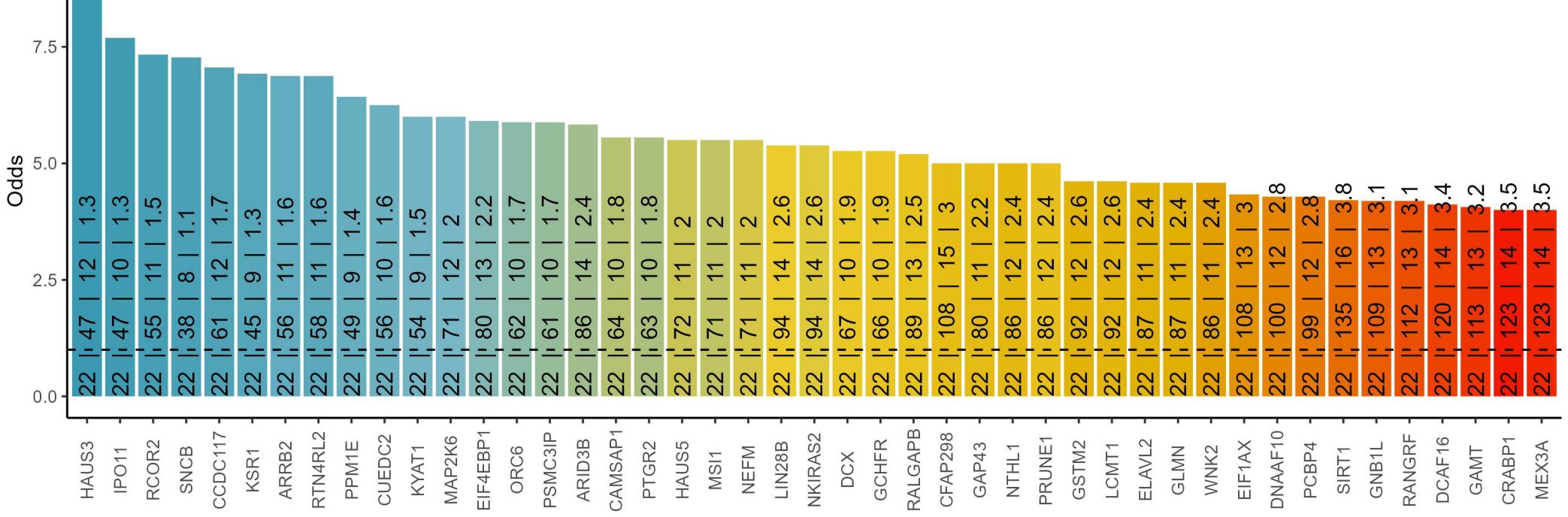
## Cooccurrence with CHEK2 protein in solid cancers, DB1

The text in the bars: incidence of CHEK2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

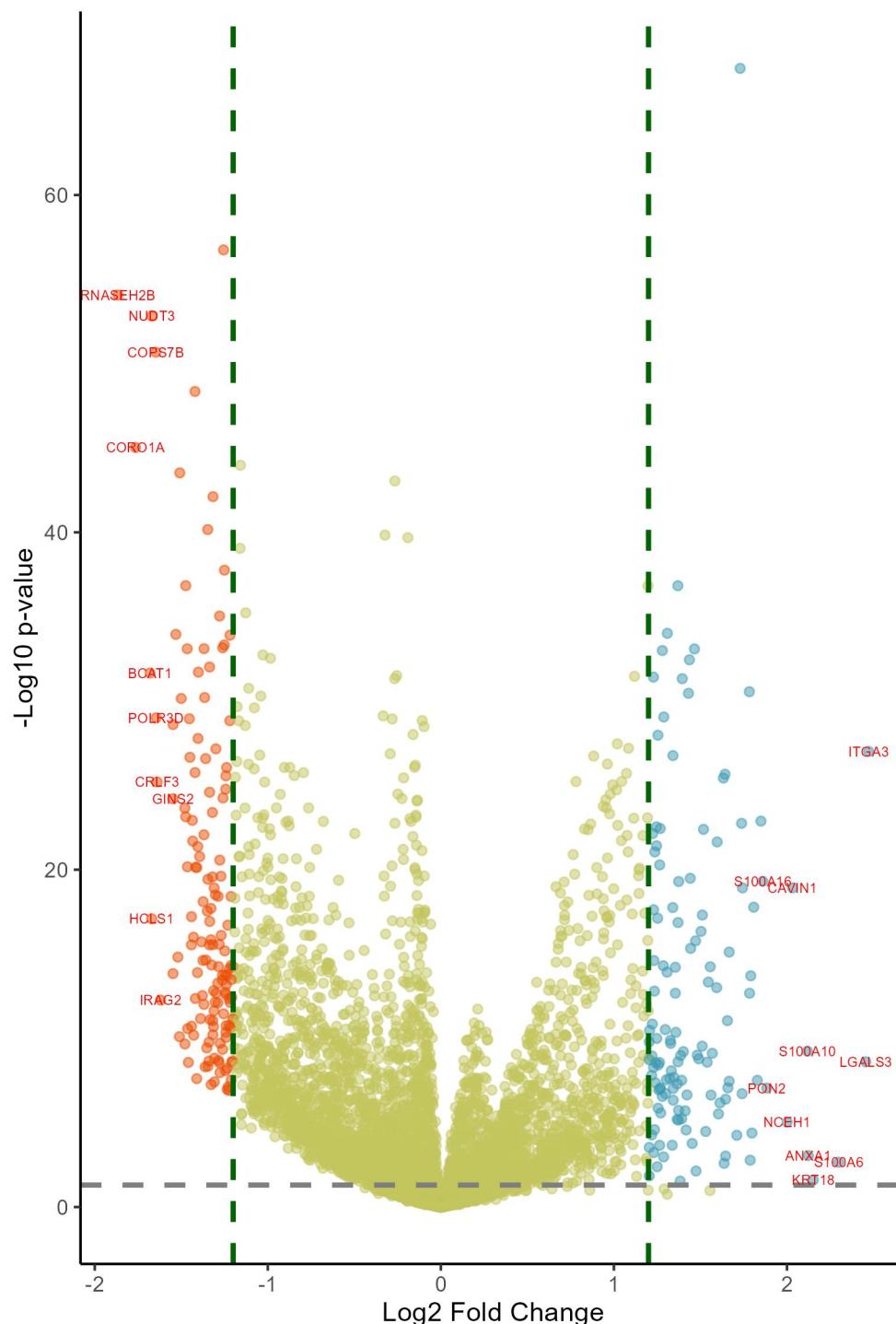
### Negative cooccurrence



### Positive cooccurrence



p-value &lt; 0.05 &amp; logFC &gt; 1.2

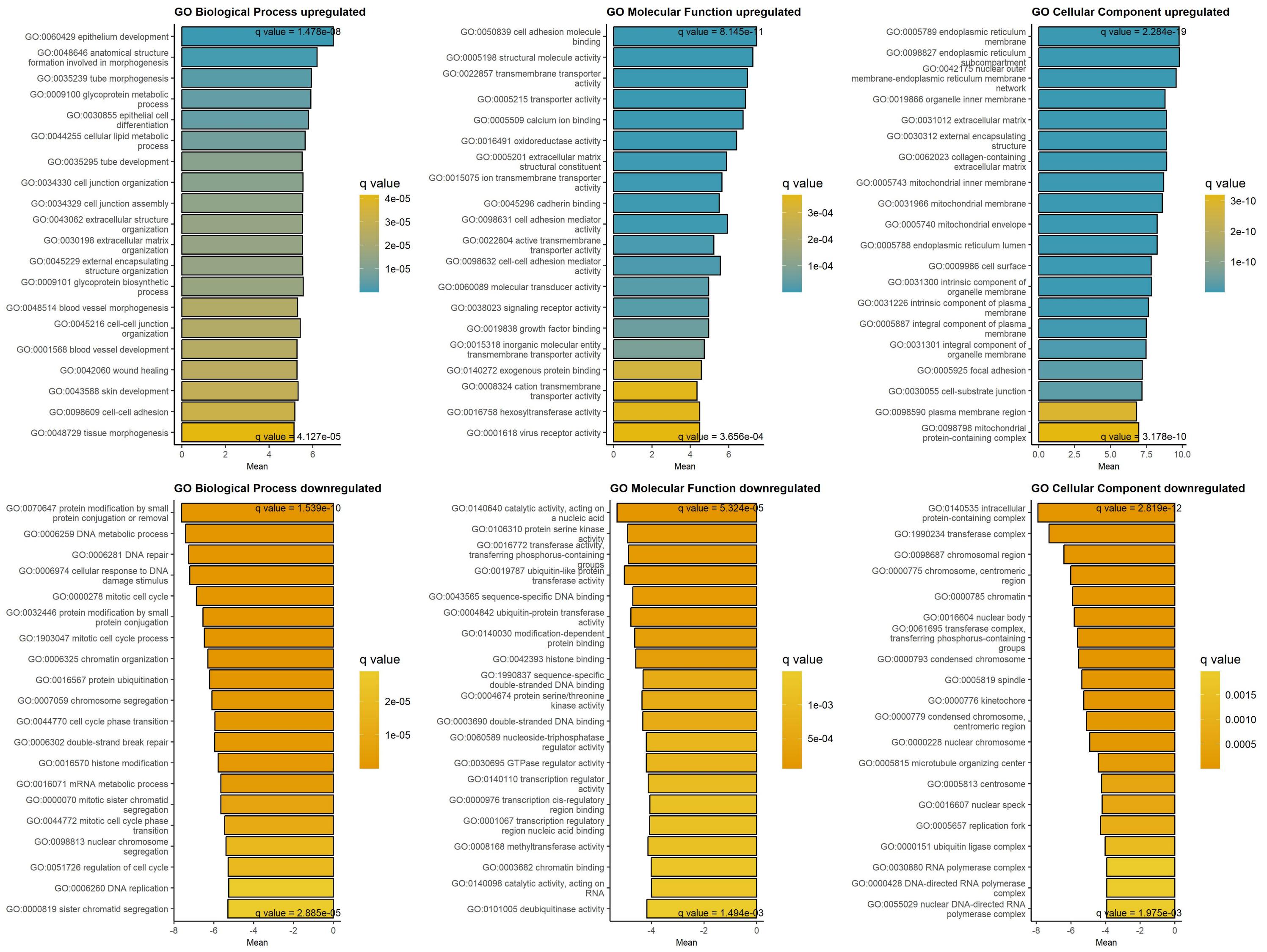


## Downregulated at low/absent CHEK2

## Upregulated at low/absent CHEK2

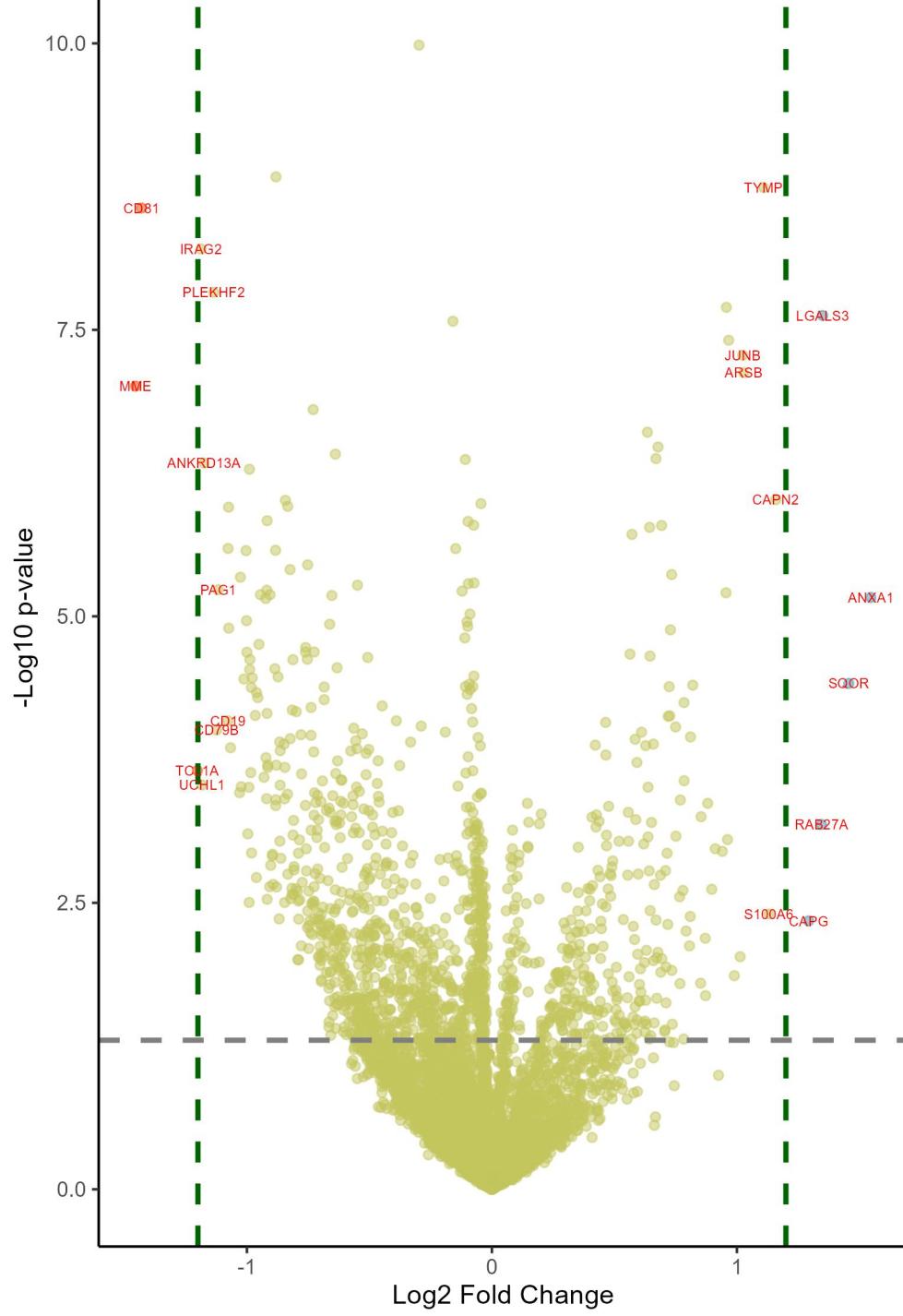
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.87	1.42e-51	RNASEH2B	ribonuclease H2 subunit B	2.47	9.57e-26	ITGA3	integrin subunit alpha 3
-1.76	7.75e-43	CORO1A	coronin 1A	2.46	1.74e-08	LGALS3	galectin 3
-1.68	3.91e-30	BCAT1	branched chain amino acid transamin	2.3	5.03e-03	S100A6	S100 calcium binding protein A6
-1.67	1.93e-16	HCLS1	hematopoietic cell-specific Lyn sub	2.15	4.31e-02	KRT18	keratin 18
-1.67	1.99e-50	NUDT3	nudix hydrolase 3	2.12	2.18e-03	ANXA1	annexin A1
-1.65	2.31e-48	COPS7B	COP9 signalosome subunit 7B	2.12	4.54e-09	S100A10	S100 calcium binding protein A10
-1.65	1.24e-27	POLR3D	RNA polymerase III subunit D	2.03	3.67e-18	CAVIN1	caveolae associated protein 1
-1.64	4.37e-24	CRLF3	cytokine receptor like factor 3	2	3.36e-05	NCEH1	neutral cholesterol ester hydrolase
-1.62	6.77e-12	IRAG2	inositol 1,4,5-triphosphate recepto	1.88	4.78e-07	PON2	paraoxonase 2
-1.55	3.91e-23	GINS2	GINS complex subunit 2	1.86	1.55e-18	S100A16	S100 calcium binding protein A16
-1.55	2.32e-13	FERMT3	FERM domain containing kindlin 3	1.85	6.74e-22	PPIC	peptidylprolyl isomerase C
-1.55	2.81e-27	POU2F1	POU class 2 homeobox 1	1.83	1.79e-07	ITGAV	integrin subunit alpha V
-1.53	3.10e-32	SEPTIN6	septin 6	1.81	4.49e-17	EGFR	epidermal growth factor receptor
-1.52	2.78e-14	RANGRF	RAN guanine nucleotide release fact	1.8	1.33e-04	CD44	CD44 molecule (Indian blood group)
-1.51	7.27e-10	RCSD1	RCSD domain containing 1	1.79	3.03e-13	NQO1	NAD(P)H quinone dehydrogenase 1
-1.51	1.98e-41	ACYP1	acylphosphatase 1	1.79	3.87e-03	GNG12	G protein subunit gamma 12
-1.5	9.79e-29	ARPP19	cAMP regulated phosphoprotein 19	1.78	2.81e-12	ITGA2	integrin subunit alpha 2
-1.48	1.28e-22	PPIPK2	diphosphoinositol pentakisphosphate	1.78	4.26e-29	NT5E	5'-nucleotidase ecto
-1.48	1.83e-09	GMFG	glia maturation factor gamma	1.74	3.68e-18	CAV1	caveolin 1
-1.47	4.01e-22	RNF113A	ring finger protein 113A	1.74	9.65e-07	RHOC	ras homolog family member C
-1.47	4.91e-35	USP11	ubiquitin specific peptidase 11	1.74	8.81e-22	ADAM9	ADAM metallopeptidase domain 9
-1.47	1.82e-31	ARMC6	armadillo repeat containing 6	1.73	1.03e-64	FNDC3B	fibronectin type III domain contain
-1.46	2.49e-19	SCML2	Scm polycomb group protein like 2	1.71	1.76e-04	FKBP9	FKBP prolyl isomerase 9
-1.46	2.66e-10	IKZF1	IKAROS family zinc finger 1	1.67	1.44e-14	RRAS	RAS related
-1.46	1.87e-08	PTPRCAP	protein tyrosine phosphatase recept	1.67	2.01e-07	MYO1C	myosin IC
-1.45	1.38e-27	HDHD2	haloacid dehalogenase like hydrolas	1.66	4.58e-07	SQOR	sulfide quinone oxidoreductase
-1.45	1.98e-25	STK4	serine/threonine kinase 4	1.66	9.56e-11	DSG2	desmoglein 2
-1.44	5.60e-15	ASF1B	anti-silencing function 1B histone	1.65	1.92e-06	ITGA6	integrin subunit alpha 6
-1.44	1.49e-16	OARD1	O-acetyl-ADP-ribose deacetylase 1	1.65	2.32e-03	PLP2	proteolipid protein 2

## GAGE analysis on upregulated and downregulated proteins at low/absent CHEK2 protein, DB1



Differentially expressed proteins in blood cancers at absence/low amount of CHEK2 , DB1

p-value &lt; 0.05 &amp; logFC &gt; 1.2

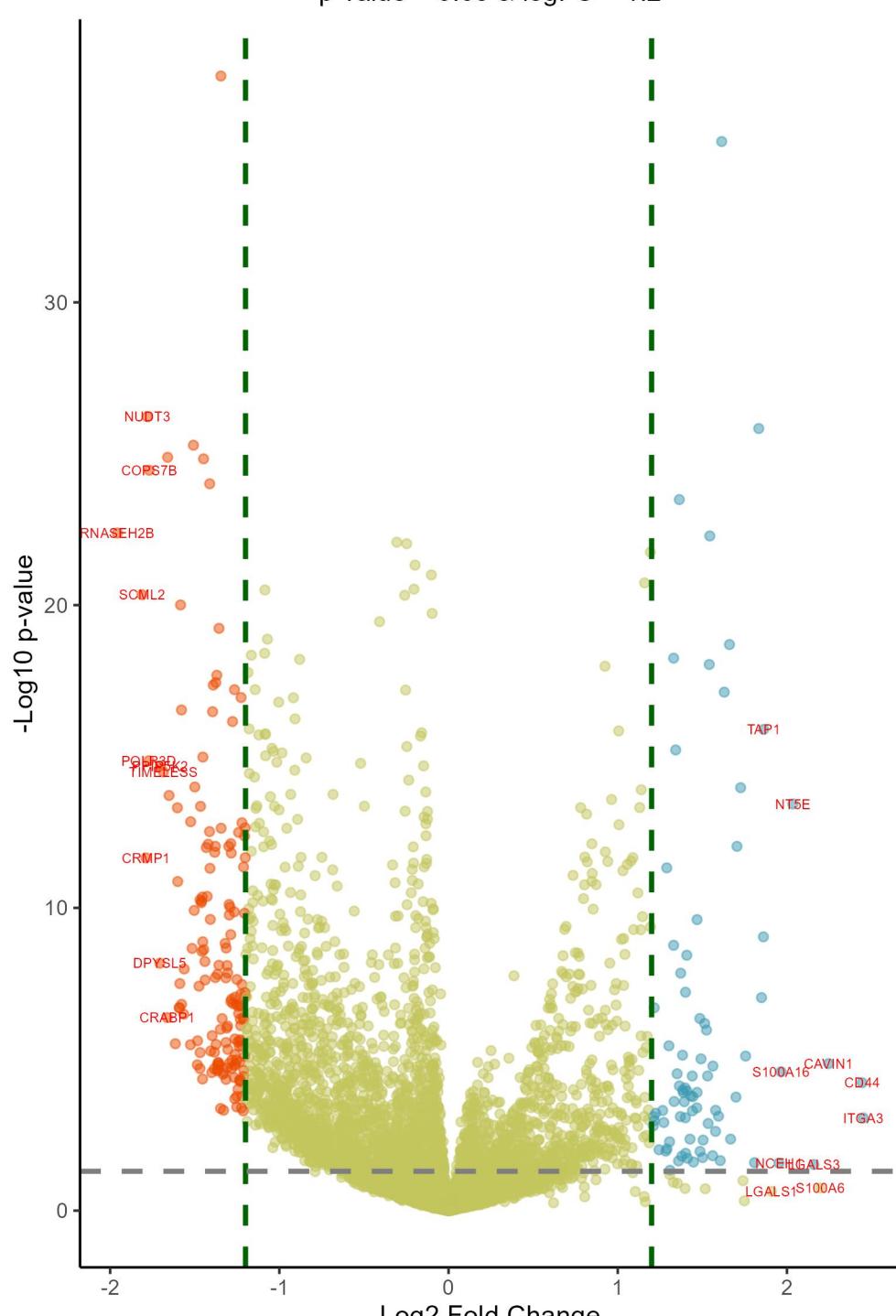


Downregulated in blood cancers at low/absent CHEK2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.45	4.66e-05	MME	membrane metalloendopeptidase	1.55	8.75e-04	ANXA1	annexin A1
-1.43	3.63e-06	CD81	CD81 molecule	1.46	3.19e-03	SQOR	sulfide quinone oxidoreductase
-1.2	1.01e-02	TCL1A	TCL1 family AKT coactivator A	1.35	1.75e-05	LGALS3	galectin 3
-1.19	6.91e-06	IRAG2	inositol 1,4,5-triphosphate receptor	1.34	1.94e-02	RAB27A	RAB27A, member RAS oncogene family
-1.18	1.24e-02	UCHL1	ubiquitin C-terminal hydrolase L1	1.29	6.25e-02	CAPG	capping actin protein, gelsolin like
-1.17	1.46e-04	ANKRD13A	ankyrin repeat domain 13A	1.16	2.69e-04	CAPN2	calpain 2
-1.14	1.41e-05	PLEKHG2	pleckstrin homology and FYVE domain	1.13	5.75e-02	S100A6	S100 calcium binding protein A6
-1.12	5.92e-03	CD79B	CD79b molecule	1.11	3.01e-06	TYMP	thymidine phosphorylase
-1.12	8.52e-04	PAG1	phosphoprotein membrane anchor with	1.03	3.82e-05	ARSB	arylsulfatase B
-1.08	5.22e-03	CD19	CD19 molecule	1.02	2.92e-05	JUNB	JunB proto-oncogene, AP-1 transcript
-1.08	4.79e-04	DOK3	docking protein 3	1.01	9.38e-02	BLVRA	biliverdin reductase A
-1.07	2.75e-04	MGMT	O-6-methylguanine-DNA methyltransferase	0.99	1.19e-01	ANXA4	annexin A4
-1.07	1.43e-03	ZHX2	zinc fingers and homeoboxes 2	0.97	2.35e-05	TNFRSF8	TNF receptor superfamily member 8
-1.07	7.29e-03	PAX5	paired box 5	0.96	2.33e-02	BIN2	bridging integrator 2
-1.03	1.37e-02	PTK2	protein tyrosine kinase 2	0.96	1.67e-05	LACTB	lactamase beta
-1.03	7.39e-04	HS2ST1	heparan sulfate 2-O-sulfotransferase	0.96	8.57e-04	SPART	spartin
-1.02	1.25e-02	FAIM	Fas apoptotic inhibitory molecule	0.94	2.72e-02	HTATIP2	HIV-1 Tat interactive protein 2
-1.01	2.97e-03	FOXP1	forkhead box P1	0.92	2.78e-01	LMNA	lamin A/C
-1	4.79e-04	CASP2	caspase 2	0.91	2.60e-02	NDRG1	N-myc downstream regulated 1
-1	1.32e-03	HMCES	5-hydroxymethylcytosine binding, ES	0.9	4.27e-02	NCEH1	neutral cholesterol ester hydrolase
-1	2.07e-03	TCF12	transcription factor 12	0.88	1.52e-02	CA2	carbonic anhydrase 2
-1	2.17e-02	ALDH2	aldehyde dehydrogenase 2 family member	0.87	1.48e-01	ACTN1	actinin alpha 1
-0.99	1.25e-02	WASF1	WASP family member 1	0.87	7.57e-02	GPHN	gephyrin
-0.99	4.98e-02	BORCS8-MEF2B	BORCS8-MEF2B readthrough	0.85	1.78e-02	MFF	mitochondrial fission factor
-0.99	1.57e-04	ARL2BP	ADP ribosylation factor like GTPase	0.85	1.28e-01	ETHE1	ETHE1 persulfide dioxygenase
-0.99	2.58e-03	CCNK	cyclin K	0.82	3.19e-03	TMEM205	transmembrane protein 205
-0.99	2.21e-03	ATXN3	ataxin 3	0.81	6.46e-03	DAD1	defender against cell death 1
-0.98	1.04e-02	TUBB3	tubulin beta 3 class III	0.81	5.92e-02	TRIM21	tripartite motif containing 21
-0.98	3.19e-03	GPALPP1	GPALPP motifs containing 1	0.81	8.39e-02	NIBAN1	niban apoptosis regulator 1

Differentially expressed proteins in solid cancers at absence/low amount of CHEK2 , DB1

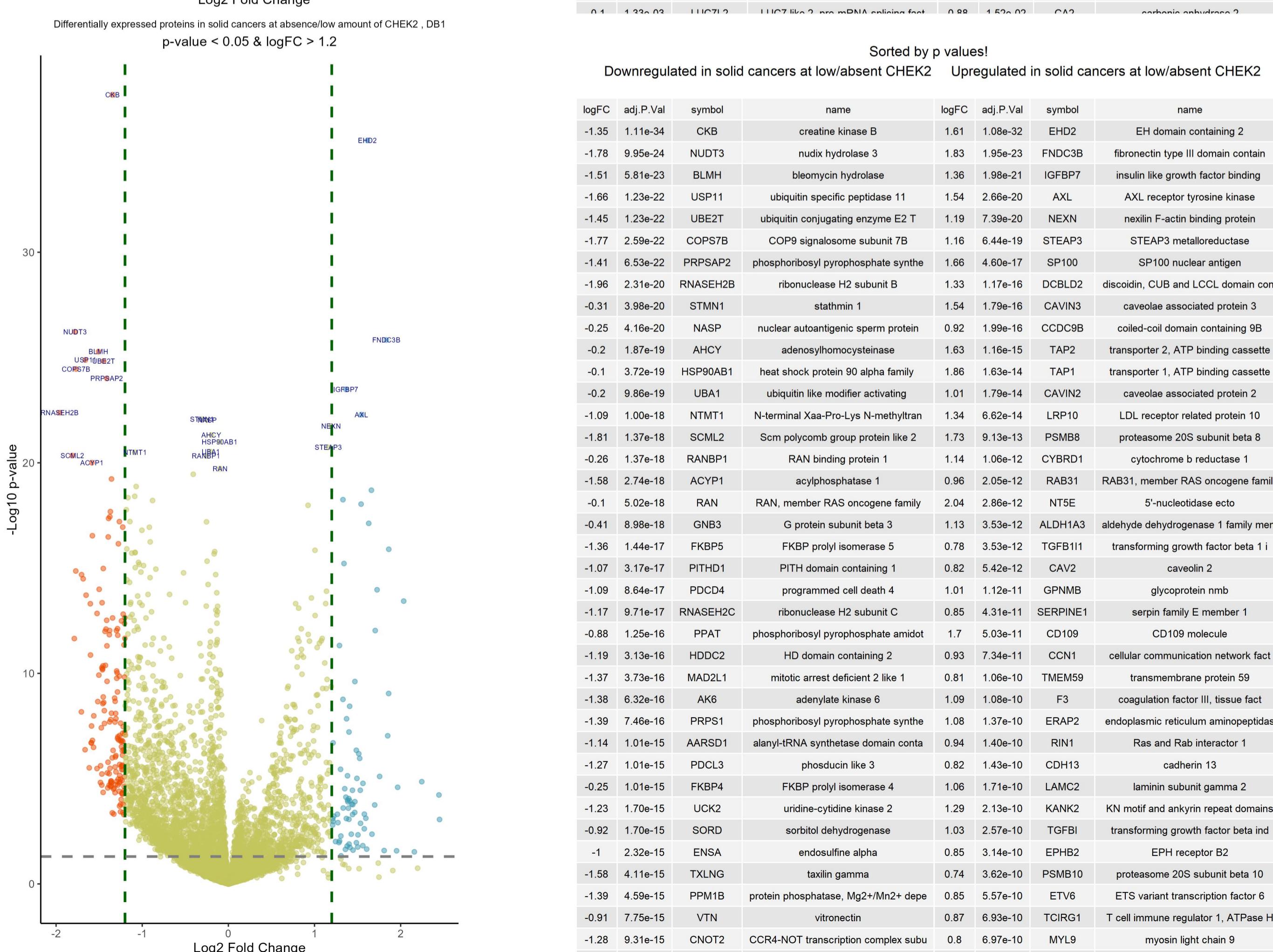
p-value &lt; 0.05 &amp; logFC &gt; 1.2



Downregulated in solid cancers at low/absent CHEK2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.96	2.31e-20	RNASEH2B	ribonuclease H2 subunit B	2.45	4.25e-03	ITGA3	integrin subunit alpha 3
-1.81	1.37e-18	SCML2	Scm polycomb group protein like 2	2.44	4.43e-04	CD44	CD44 molecule (Indian blood group)
-1.79	1.09e-10	CRMP1	collapsin response mediator protein	2.24	1.30e-04	CAVIN1	caveolae associated protein 1
-1.78	9.95e-24	NUDT3	nudix hydrolase 3	2.2	3.00e-01	S100A6	S100 calcium binding protein A6
-1.77	1.36e-13	POLR3D	RNA polymerase III subunit D	2.16	7.48e-02	LGALS3	galectin 3
-1.77	2.59e-22	COPS7B	COP9 signalosome subunit 7B	2.04	2.86e-12	NT5E	5'-nucleotidase ecto
-1.71	1.56e-07	DPYSL5	dihydropyrimidinase like 5	1.97	2.16e-04	S100A16	S100 calcium binding protein A16
-1.7	1.92e-13	PPIP5K2	diphosphoinositol pentakisphosphate	1.95	6.83e-02	NCEH1	neutral cholesterol ester hydrolase
-1.69	2.94e-13	TIMELESS	timeless circadian regulator	1.91	3.65e-01	LGALS1	galectin 1
-1.66	6.20e-06	CRABP1	cellular retinoic acid binding protein	1.86	1.63e-14	TAP1	transporter 1, ATP binding cassette
-1.66	1.23e-22	USP11	ubiquitin specific peptidase 11	1.86	2.54e-08	HLA-B	major histocompatibility complex, c
-1.65	1.55e-12	HPF1	histone PARylation factor 1	1.85	1.61e-06	CD59	CD59 molecule (CD59 blood group)
-1.61	3.48e-05	ARID3B	AT-rich interaction domain 3B	1.83	1.95e-23	FNDC3B	fibronectin type III domain containing
-1.6	3.53e-12	VPS36	vacuolar protein sorting 36 homolog	1.81	6.70e-02	S100A10	S100 calcium binding protein A10
-1.6	5.63e-10	NAA20	N-alpha-acetyltransferase 20, NatB	1.76	7.81e-05	ITPR3	inositol 1,4,5-trisphosphate receptor
-1.59	3.14e-06	CSNK1E	casein kinase 1 epsilon	1.75	6.00e-01	KRT18	keratin 18
-1.59	3.25e-06	ERI3	ERI1 exoribonuclease family member	1.74	1.95e-01	HLA-A	major histocompatibility complex, c
-1.59	6.25e-07	C20orf27	chromosome 20 open reading frame 27	1.73	9.13e-13	PSMB8	proteasome 20S subunit beta 8
-1.58	2.74e-18	ACYP1	acylphosphatase 1	1.7	5.03e-11	CD109	CD109 molecule
-1.58	4.11e-15	TXNLNG	taxilin gamma	1.7	1.13e-03	PPIC	peptidylprolyl isomerase C
-1.58	2.57e-06	GPSM1	G protein signaling modulator 1	1.67	1.62e-02	CTS2	cathepsin Z
-1.57	4.91e-06	KIF1A	kinesin family member 1A	1.66	4.60e-17	SP100	SP100 nuclear antigen
-1.56	2.31e-07	SMYD3	SET and MYND domain containing 3	1.63	1.16e-15	TAP2	transporter 2, ATP binding cassette
-1.53	3.71e-05	LIN7A	lin-7 homolog A, crumbs cell polar	1.61	1.08e-32	EHD2	EH domain containing 2
-1.52	9.29e-12	SMAD4	SMAD family member 4	1.61	5.91e-02	ITGB5	integрин subunit beta 5
-1.52	5.67e-08	NECAP1	NECAP endocytosis associated 1	1.6	3.80e-03	CAV1	caveolin 1
-1.51	5.81e-23	BLMH	bleomycin hydrolase	1.58	2.60e-03	CAPG	capping actin protein, gelsolin like
-1.5	4.15e-09	CNOT10	CCR4-NOT transcription complex subunit	1.58	9.95e-03	SQOR	sulfide quinone oxidoreductase
-1.5	8.77e-13	EIF2B1	eukaryotic translation initiation factor	1.56	1.50e-04	GPX8	glutathione peroxidase 8 (putative)

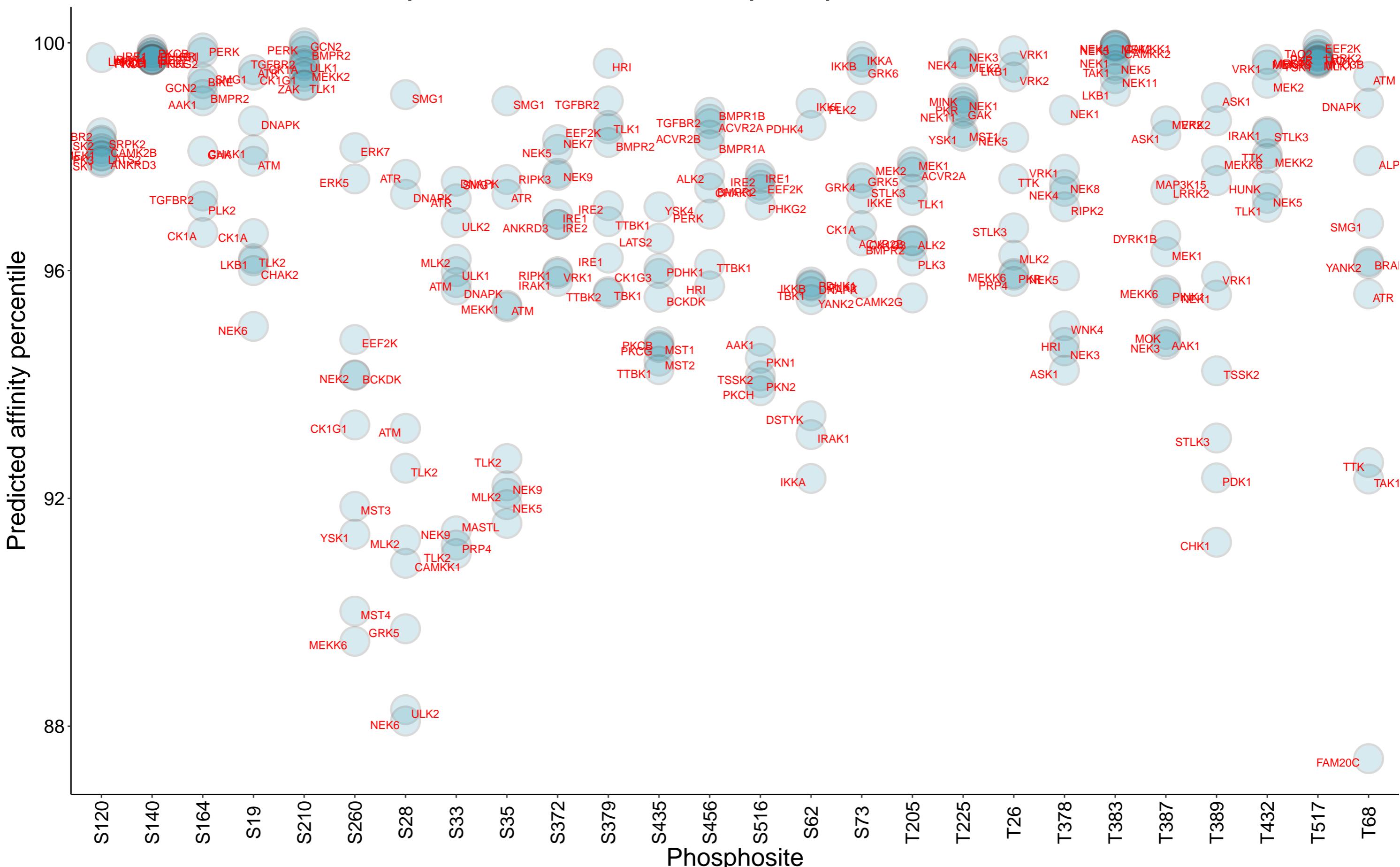
CHEK2 network, DB1, no Pearson r &gt; 0.3



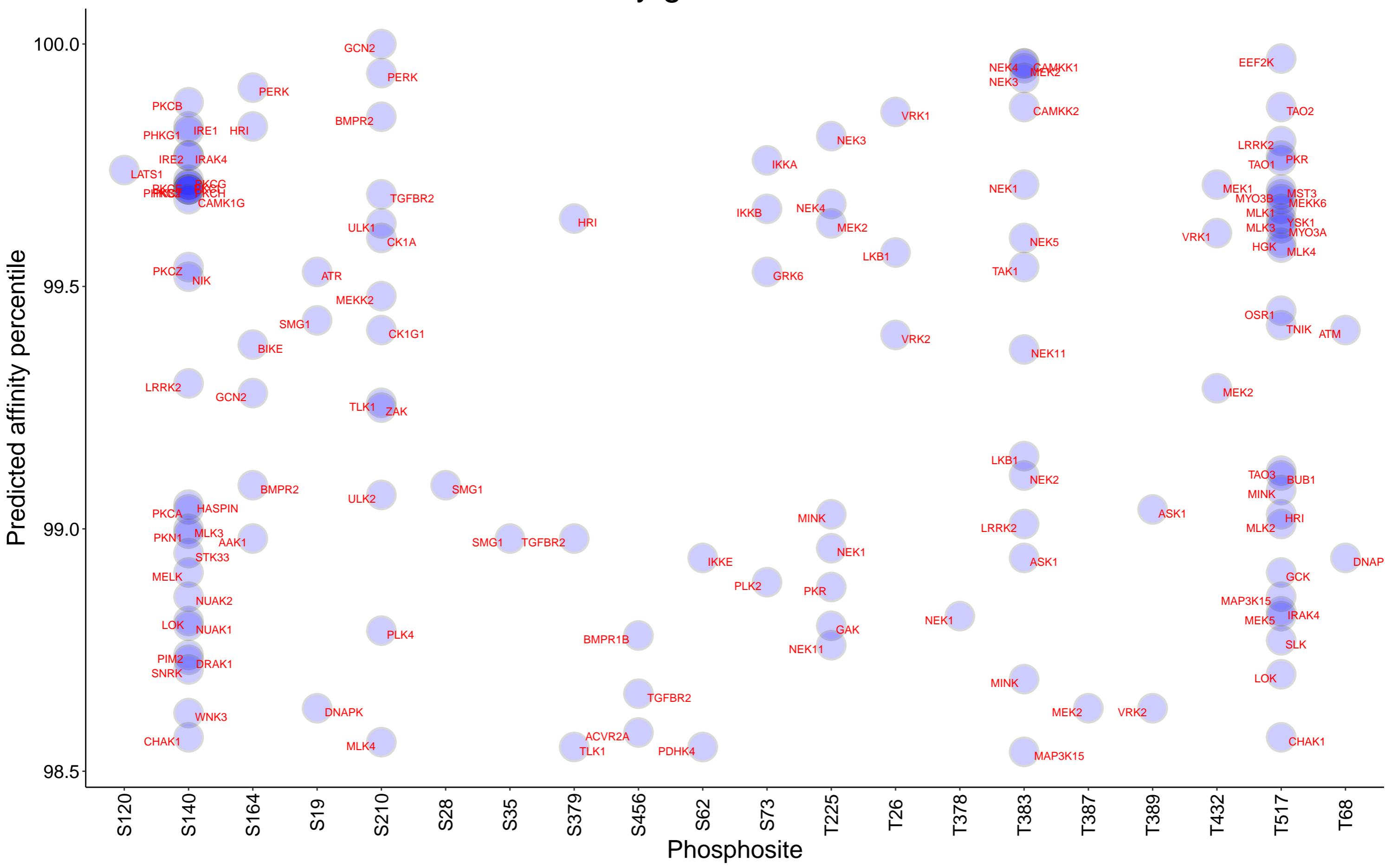
Insufficient number of paired observations in DB1 for CHEK2

Insufficient number of paired observations in DB1 for CHEK2

# Top 10 kinases for each phosphosite in CHEK2



Kinases with affinity greater than 98.5% to CHEK2



No sufficient paired observations in DB1 for CHEK2