

# CHEK1

Protein name: CHK1 ;

UNIPROT: O14757 ;

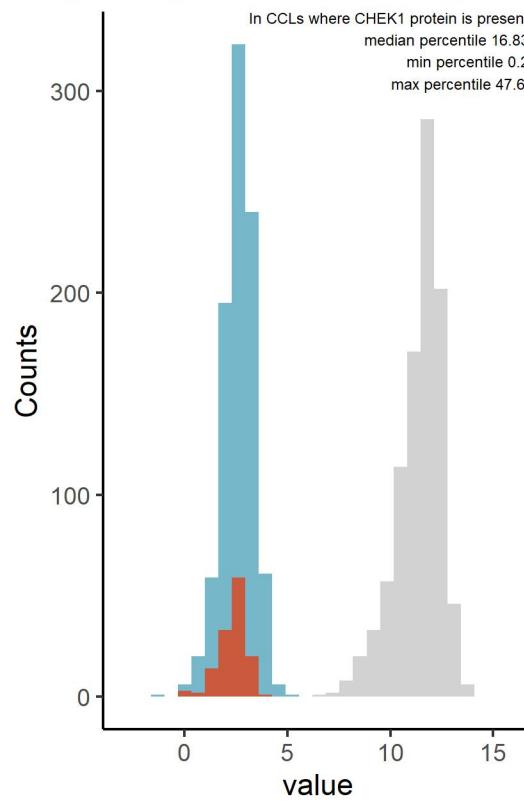
Gene name: checkpoint kinase 1

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

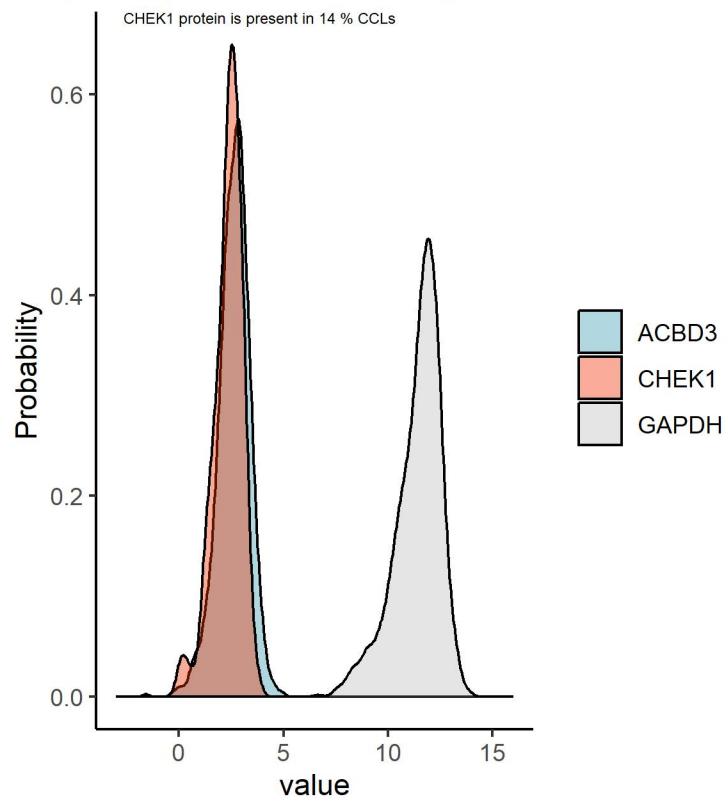
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

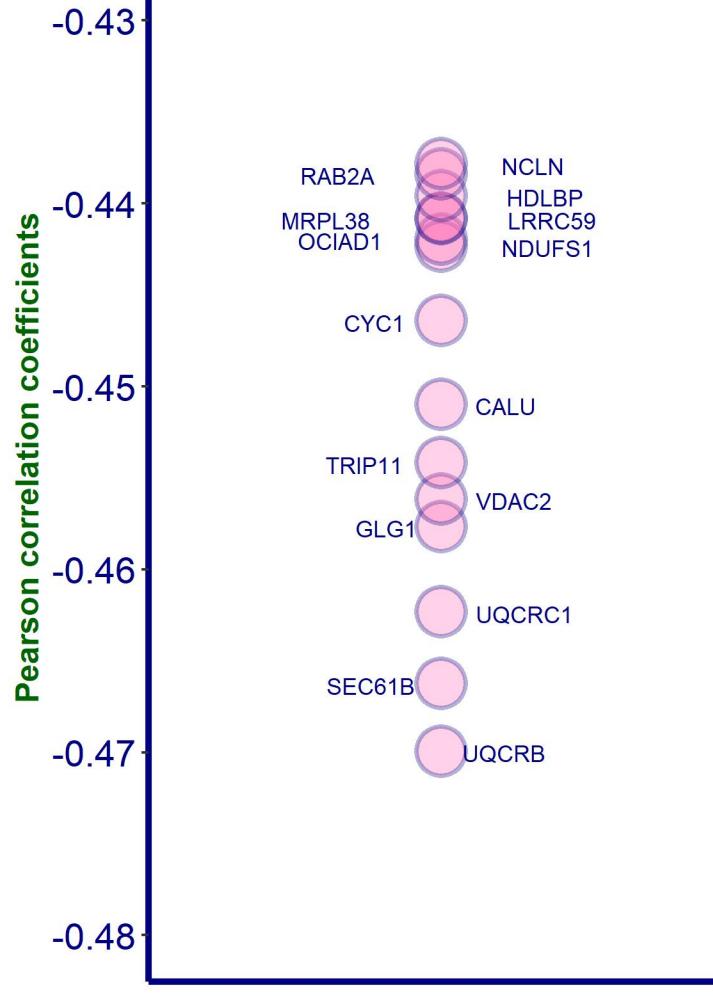
Histogram of CHEK1 protein compared to proteins with low and high abundance



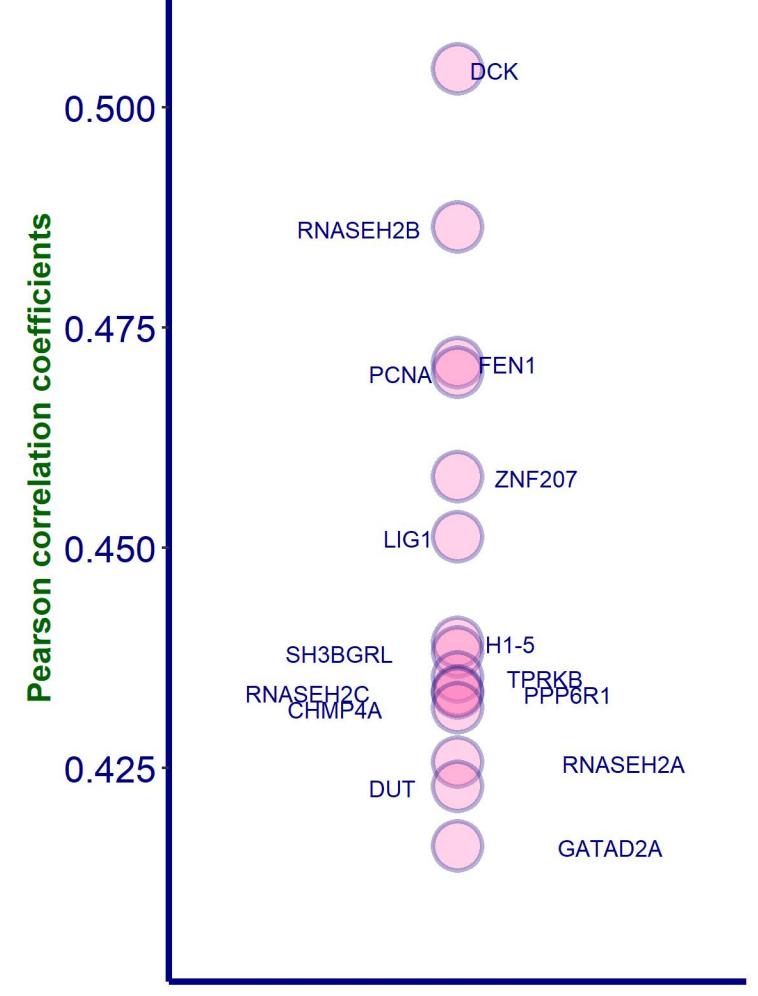
Density plot of CHEK1 protein compared to proteins with low and high abundance



Top negative correlations of CHEK1 protein, DB1

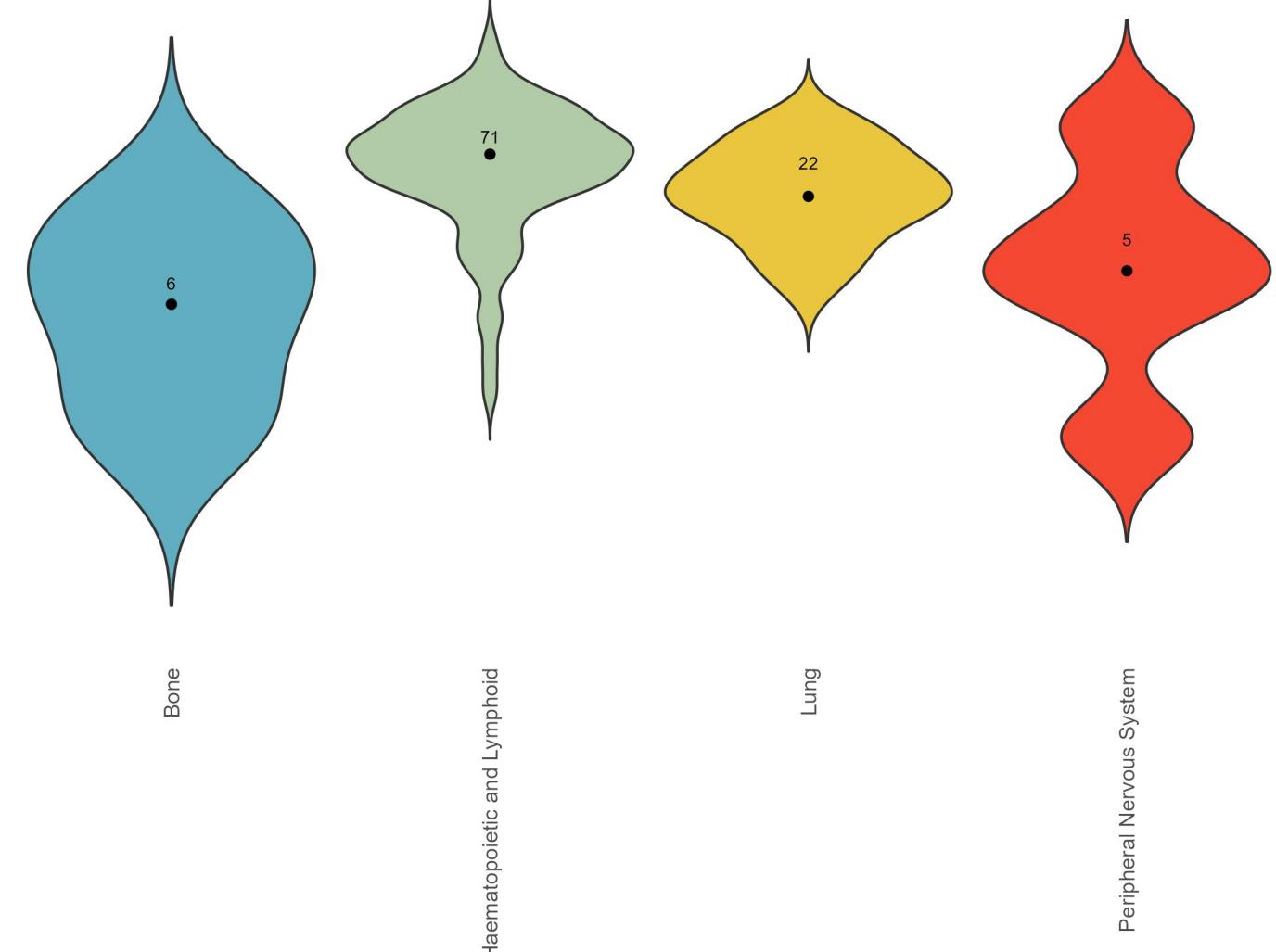


Top positive correlations of CHEK1 protein, DB1



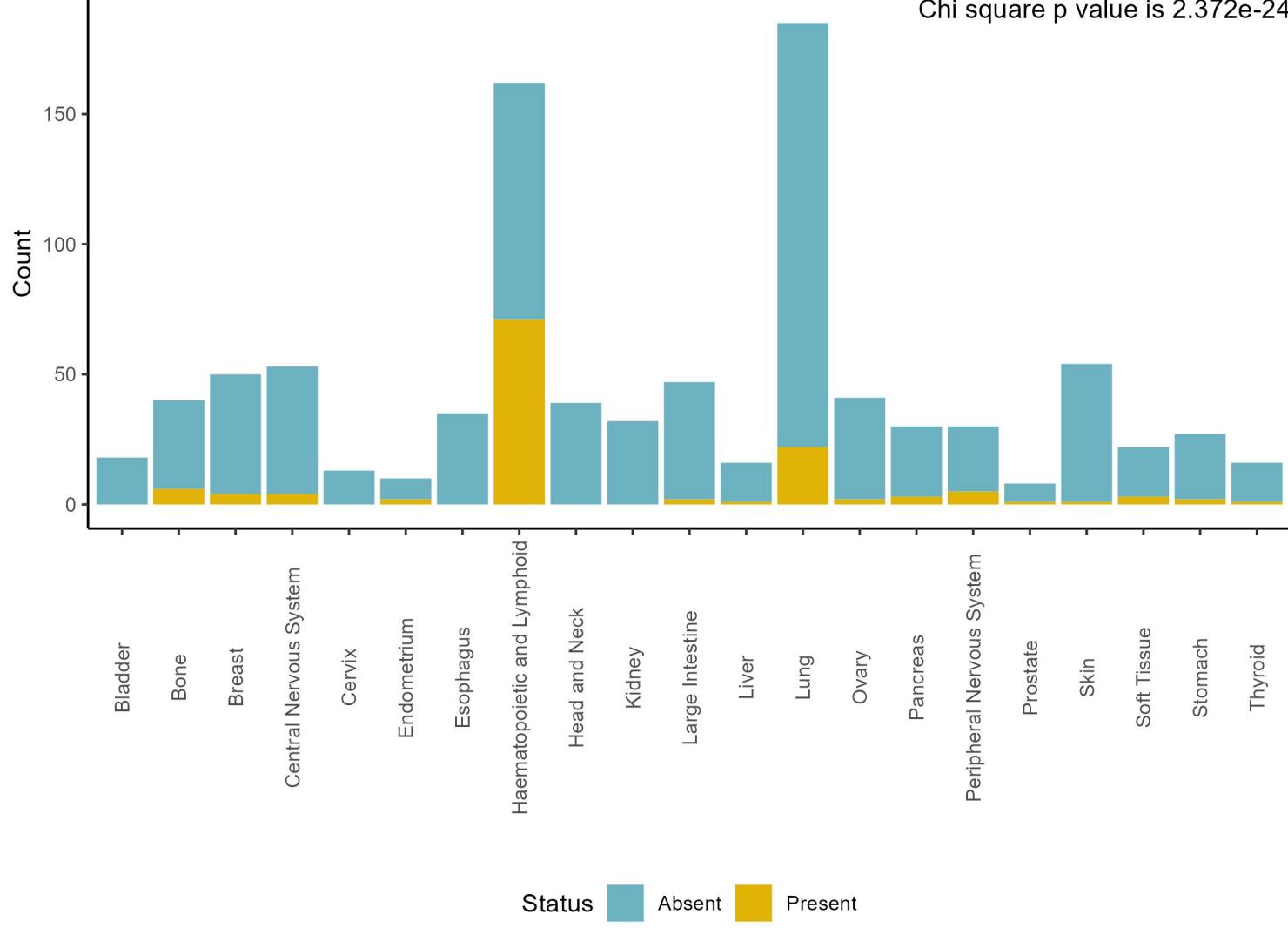
## Amount of CHEK1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 3.292e-05



## Present and absent CHEK1 protein counts by tissue, DB1

Chi square p value is 2.372e-24

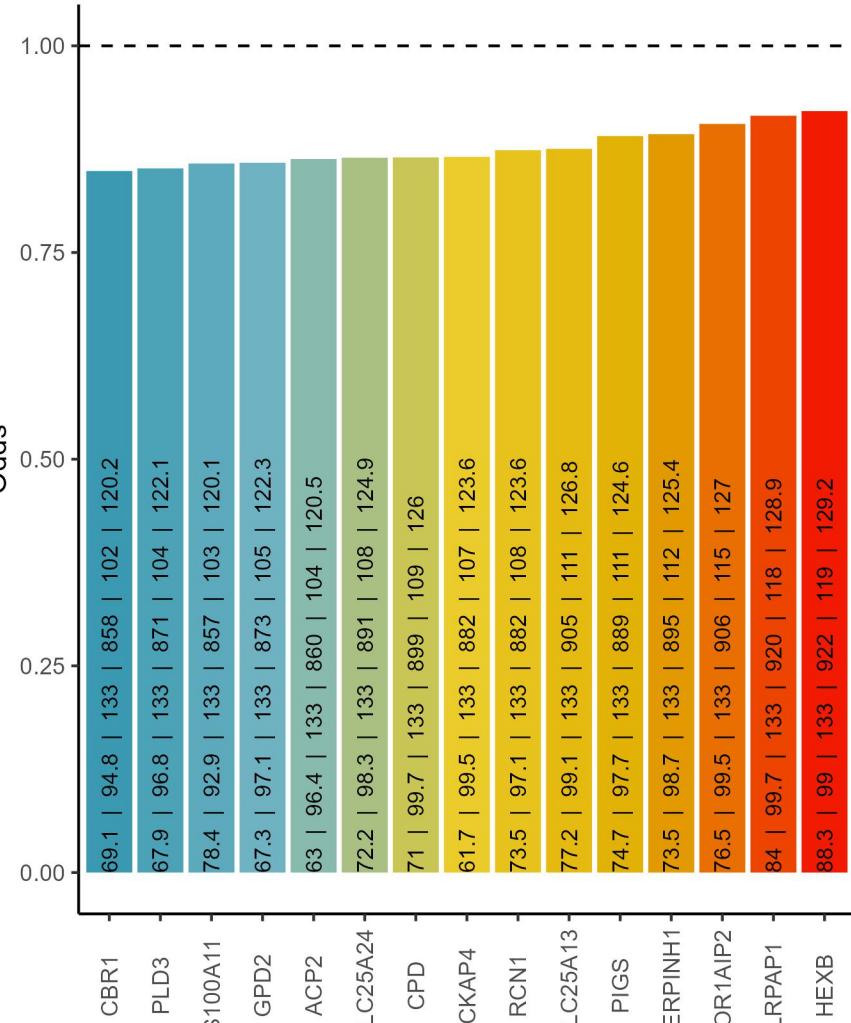


## Cooccurrence with CHEK1 protein, DB1

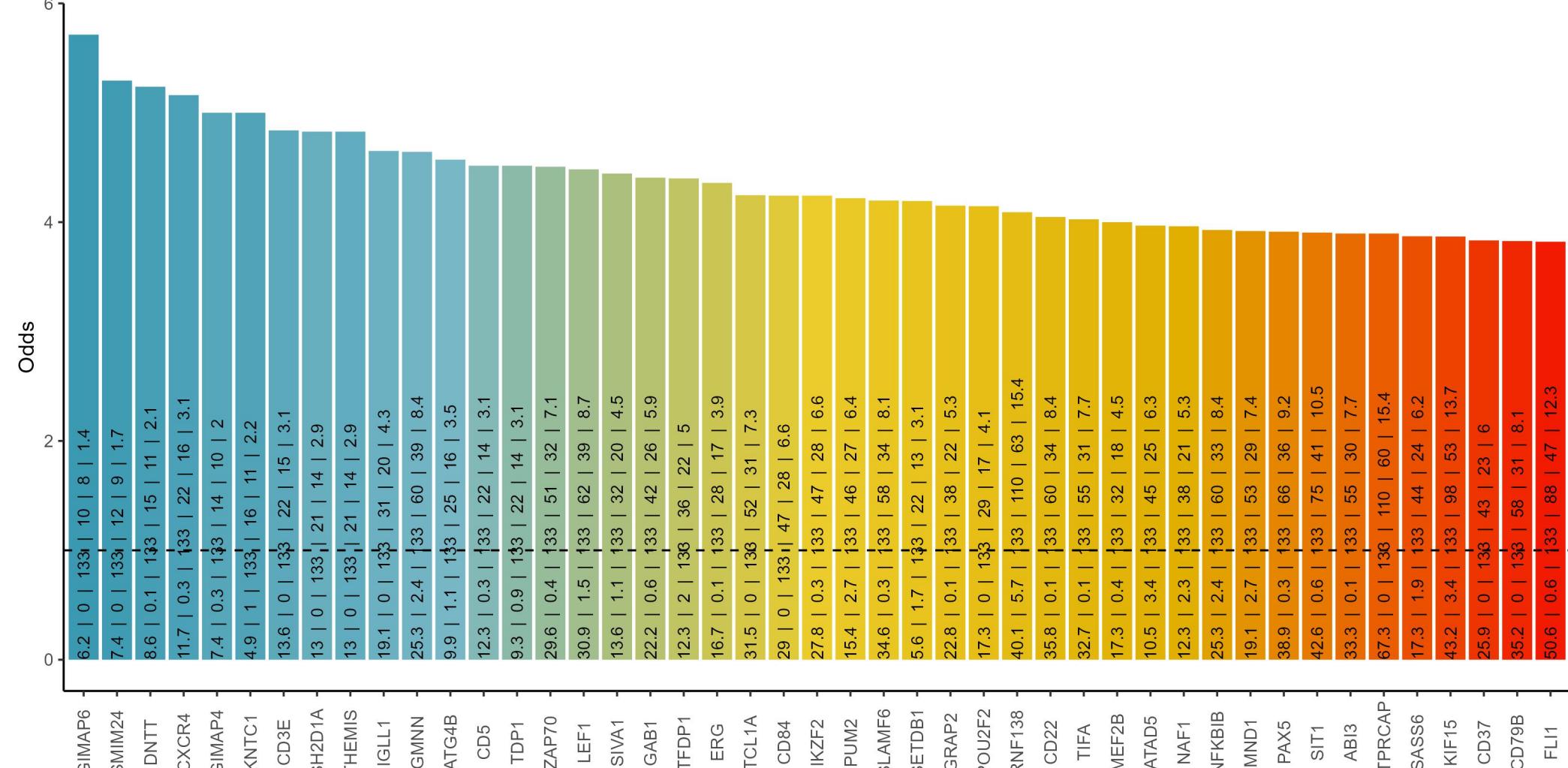
% of CHEK1 in blood cancers: 43.8 ; % of CHEK1 in solid cancers: 7.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CHEK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

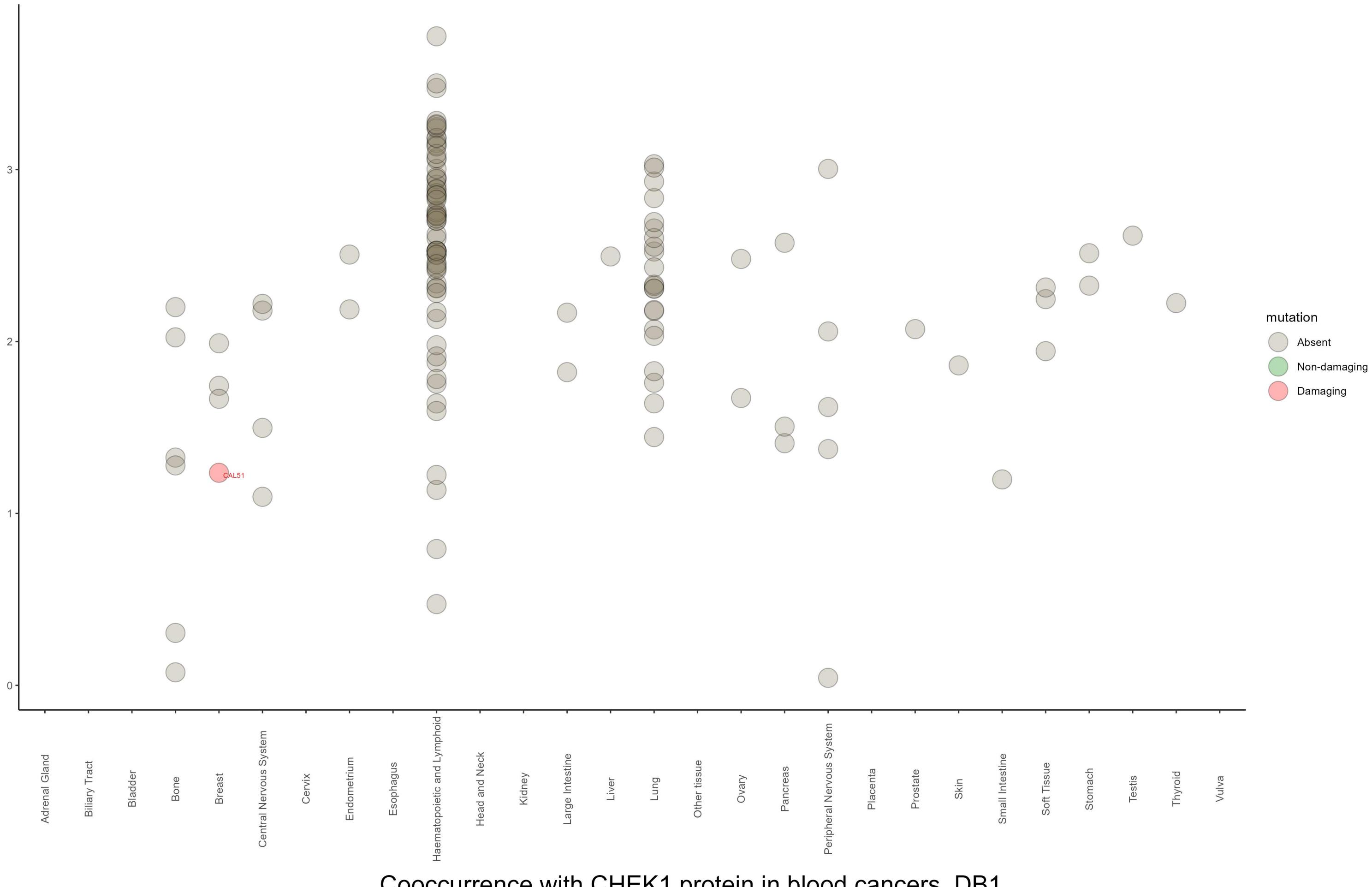
### Negative cooccurrence



### Positive cooccurrence

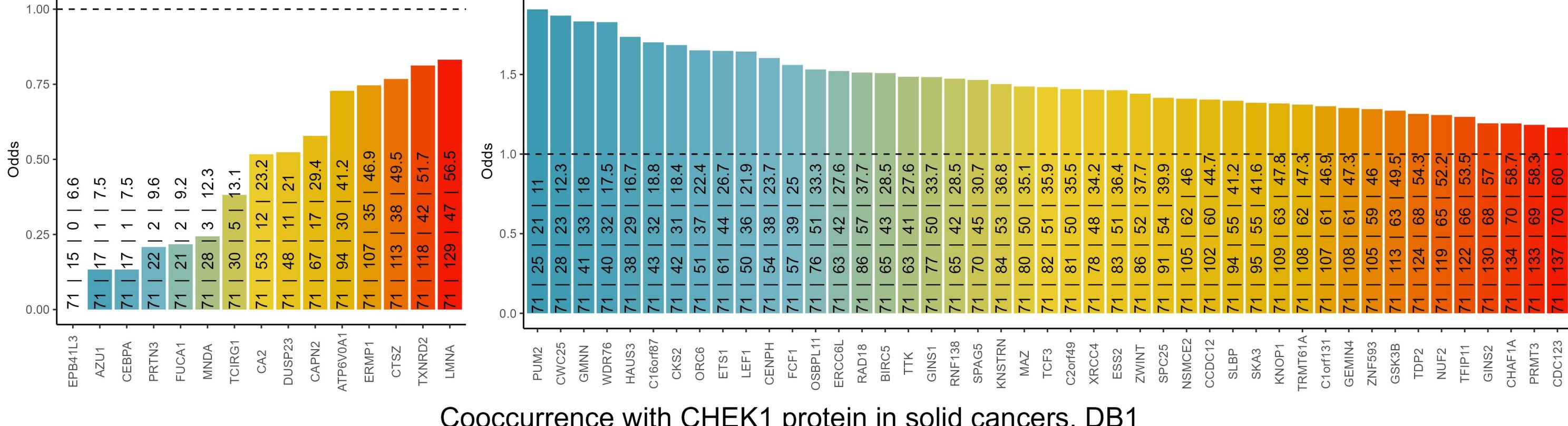


# Amount of CHEK1 protein and mutation status by tissue, DB1



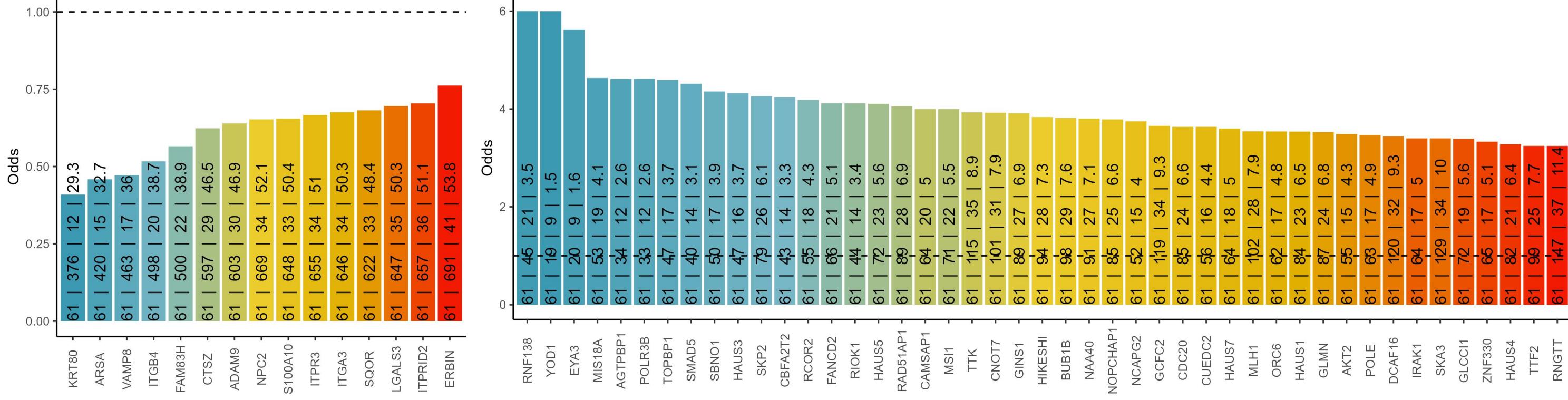
## Cooccurrence with CHEK1 protein in blood cancers, DB1

The text in the bars: incidence of CHEK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

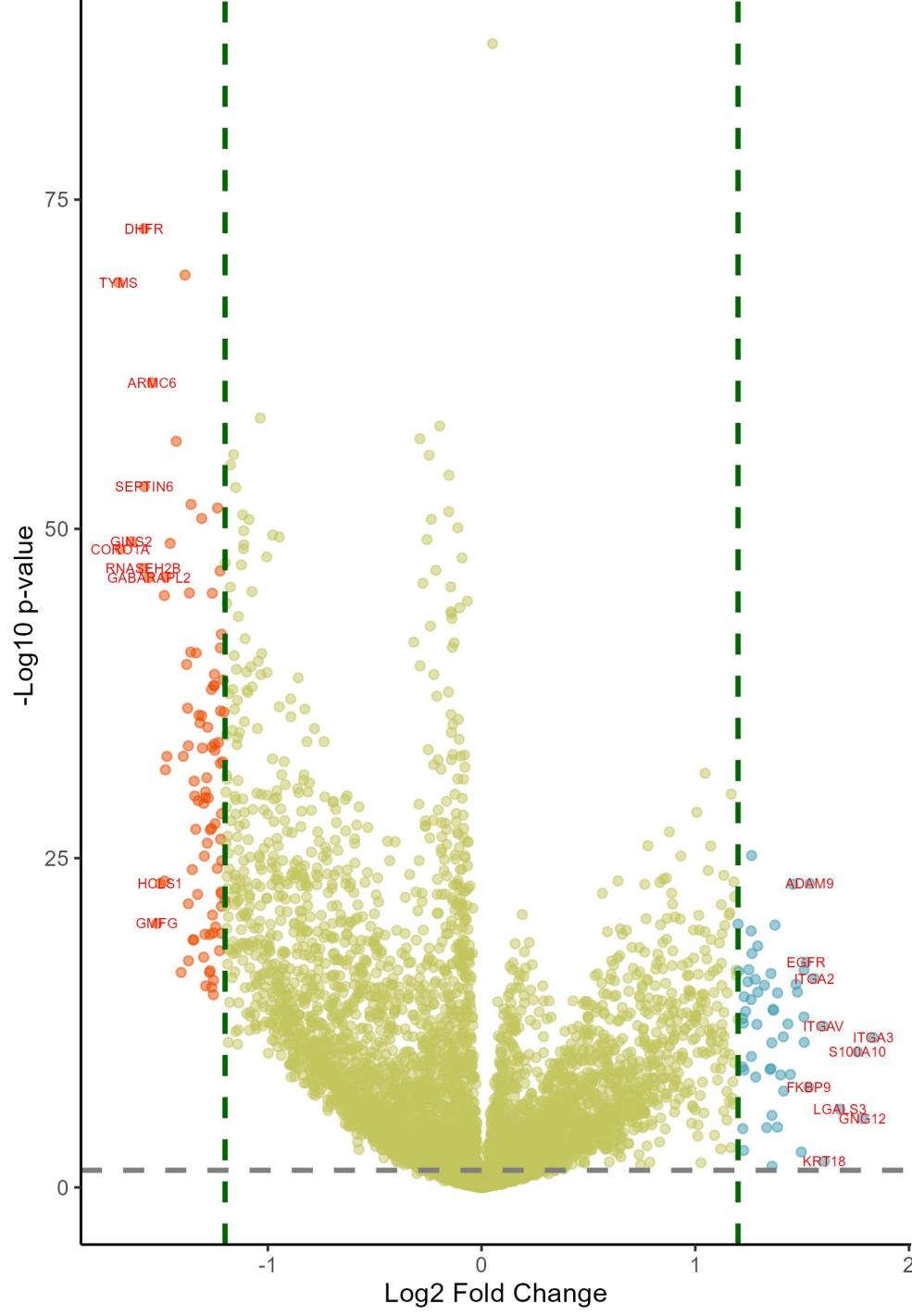


## Cooccurrence with CHEK1 protein in solid cancers, DB1

The text in the bars: incidence of CHEK1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

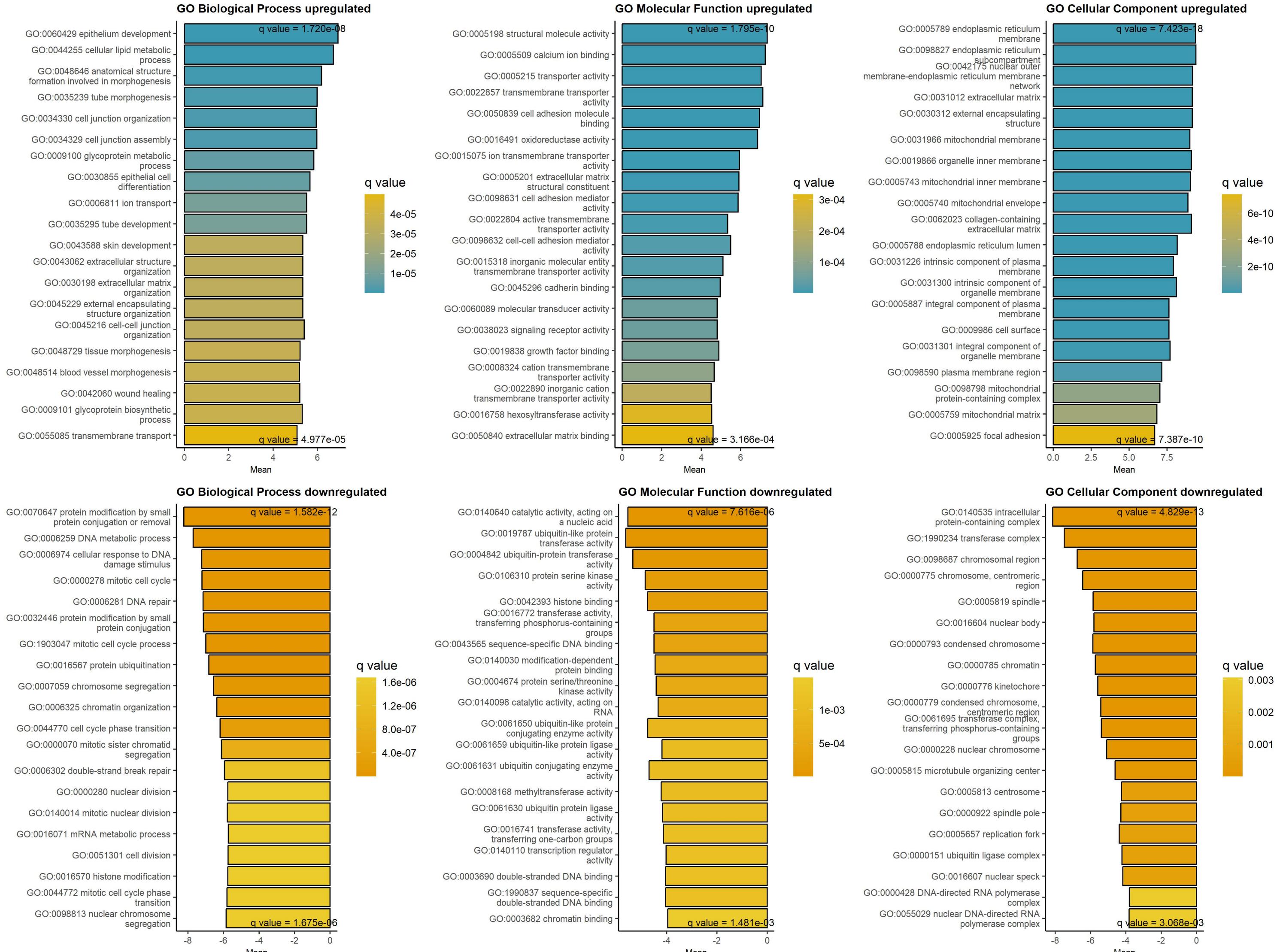


### Downregulated at low/absent CHEK1      Upregulated at low/absent CHEK1

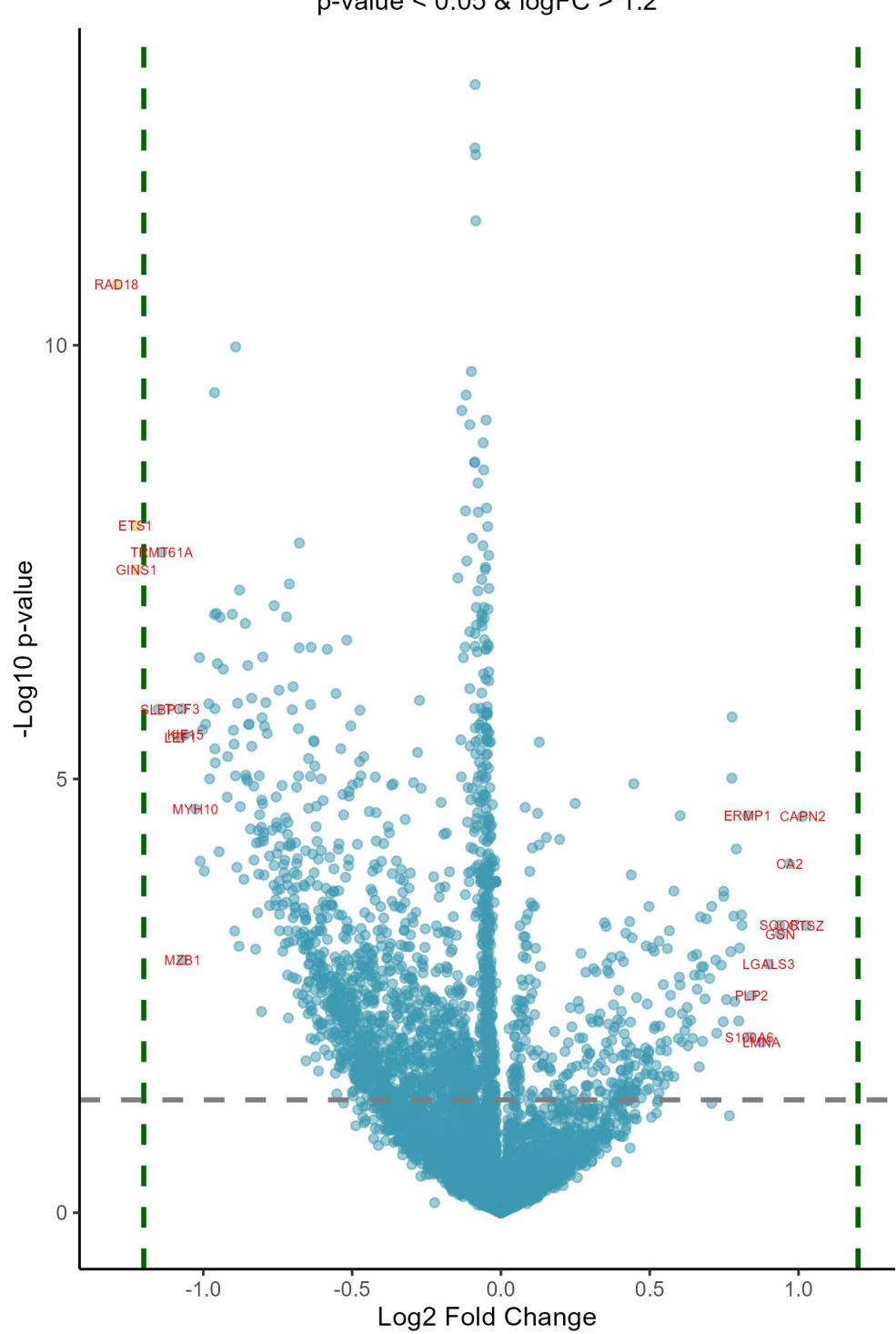


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.7	2.59e-66	TYMS	thymidylate synthetase	1.83	2.16e-11	ITGA3	integrin subunit alpha 3
-1.69	7.10e-47	CORO1A	coronin 1A	1.78	1.43e-05	GNG12	G protein subunit gamma 12
-1.64	2.18e-47	GINS2	GINS complex subunit 2	1.76	2.35e-10	S100A10	S100 calcium binding protein A10
-1.58	1.74e-45	RNASEH2B	ribonuclease H2 subunit B	1.68	3.16e-06	LGALS3	galectin 3
-1.58	3.50e-70	DHFR	dihydrofolate reductase	1.6	1.62e-02	KRT18	keratin 18
-1.58	2.75e-51	SEPTIN6	septin 6	1.6	3.23e-12	ITGAV	integrin subunit alpha V
-1.56	8.04e-45	GABARPL2	GABA type A receptor associated protein	1.56	1.21e-15	ITGA2	integrin subunit alpha 2
-1.54	8.68e-59	ARMC6	armadillo repeat containing 6	1.54	1.68e-22	ADAM9	ADAM metallopeptidase domain 9
-1.52	1.27e-19	GMFG	glia maturation factor gamma	1.53	8.00e-08	FKBP9	FKBP prolyl isomerase 9
-1.5	1.68e-22	HCLSL1	hematopoietic cell-specific Lyn sub	1.52	8.08e-17	EGFR	epidermal growth factor receptor
-1.48	1.57e-43	PCLAF	PCNA clamp associated factor	1.51	4.80e-11	CAVIN1	caveolae associated protein 1
-1.48	1.09e-22	FERMT3	FERM domain containing kindlin 3	1.51	2.92e-16	EPHX1	epoxide hydrolase 1
-1.48	9.43e-31	ASF1B	anti-silencing function 1B histone	1.51	7.06e-13	NQO1	NAD(P)H quinone dehydrogenase 1
-1.48	7.38e-45	NACA2	nascent polypeptide associated comp	1.5	3.58e-03	S100A6	S100 calcium binding protein A6
-1.47	9.72e-32	BCAT1	branched chain amino acid transamin	1.48	1.15e-14	S100A16	S100 calcium binding protein A16
-1.46	2.80e-47	TACC3	transforming acidic coiled-coil con	1.47	3.11e-15	DSG2	desmoglein 2
-1.43	1.49e-54	PRIM1	DNA primase subunit 1	1.46	1.85e-22	ITGB4	integrin subunit beta 4
-1.41	4.37e-16	MZB1	marginal zone B and B1 cell specifi	1.44	9.91e-09	CTNNB1	catenin beta 1
-1.4	9.62e-32	OGFOD1	2-oxoglutarate and iron dependent o	1.43	2.24e-12	MYO1C	myosin IC
-1.39	8.88e-67	UBE2T	ubiquitin conjugating enzyme E2 T	1.41	1.53e-07	MYOF	myoferlin
-1.38	1.90e-38	COPS7B	COP9 signalosome subunit 7B	1.41	1.93e-11	NECTIN2	nectin cell adhesion molecule 2
-1.38	2.98e-35	TIMELESS	timeless circadian regulator	1.4	1.08e-08	PON2	paraoxonase 2
-1.37	1.63e-32	TRMT61A	tRNA methyltransferase 61A	1.38	1.32e-14	PPIC	peptidylprolyl isomerase C
-1.37	4.78e-21	GINS1	GINS complex subunit 1	1.38	5.99e-05	KRT19	keratin 19
-1.37	6.37e-17	RCSD1	RCSD domain containing 1	1.37	1.71e-19	ITPRID2	ITPR interacting domain containing
-1.37	1.04e-43	NDC80	NDC80 kinetochore complex component	1.37	2.35e-13	CAV1	caveolin 1
-1.36	2.34e-39	NCK1	NCK adaptor protein 1	1.36	2.01e-13	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.36	5.40e-50	POLA2	DNA polymerase alpha 2, accessory s	1.36	3.62e-02	KRT8	keratin 8
-1.35	1.67e-23	WIPF1	WAS/WASL interacting protein family	1.36	8.63e-06	NCEH1	neutral cholesterol ester hydrolase

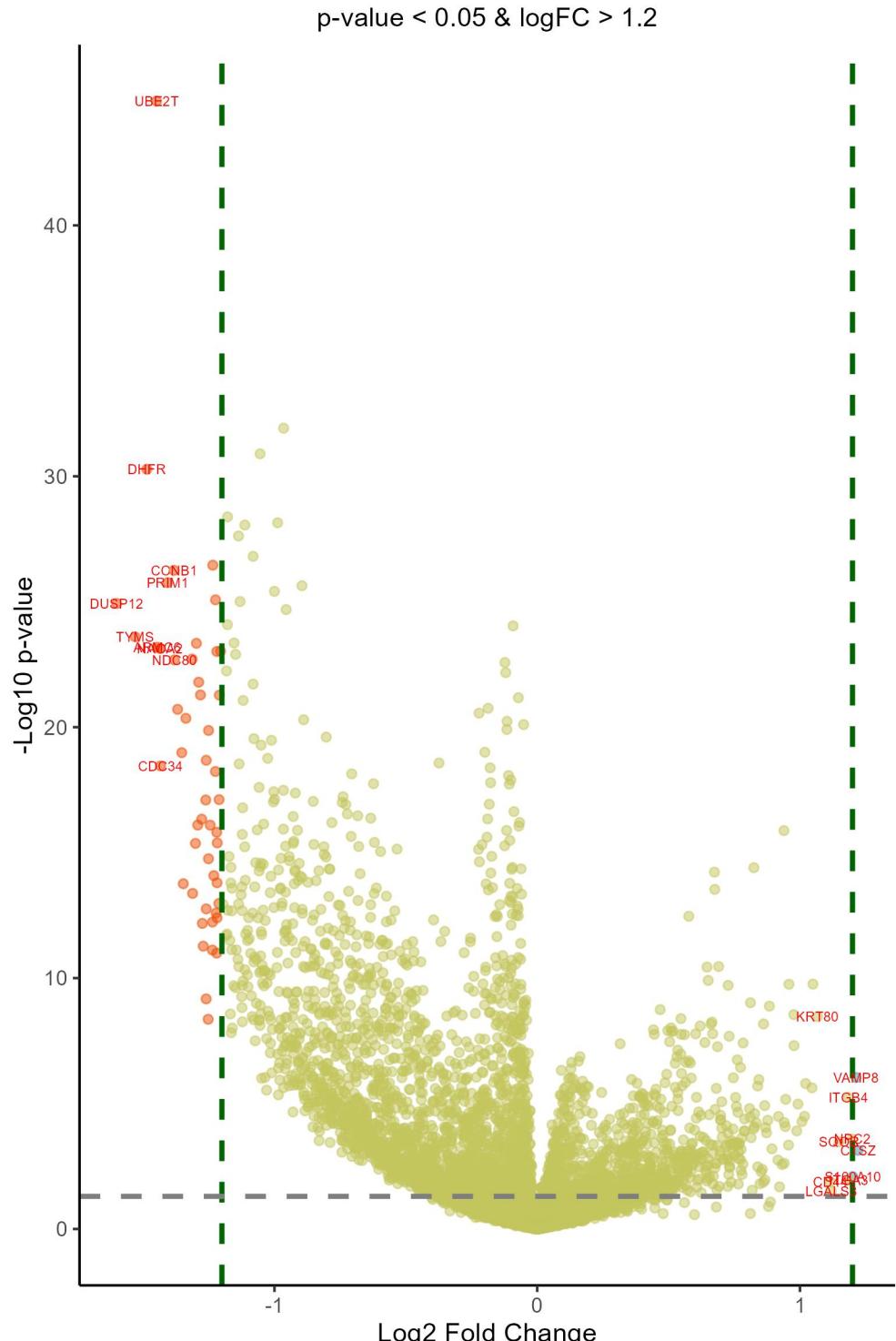
### GAGE analysis on upregulated and downregulated proteins at low/absent CHEK1 protein, DB1



## Differentially expressed proteins in blood cancers at absence/low amount of CHEK1, DB1 L = 1.0-0.5-0.1 - EG > 1.0



Differentially expressed proteins in solid cancers at absence/low amount of CHEK1 , DB1



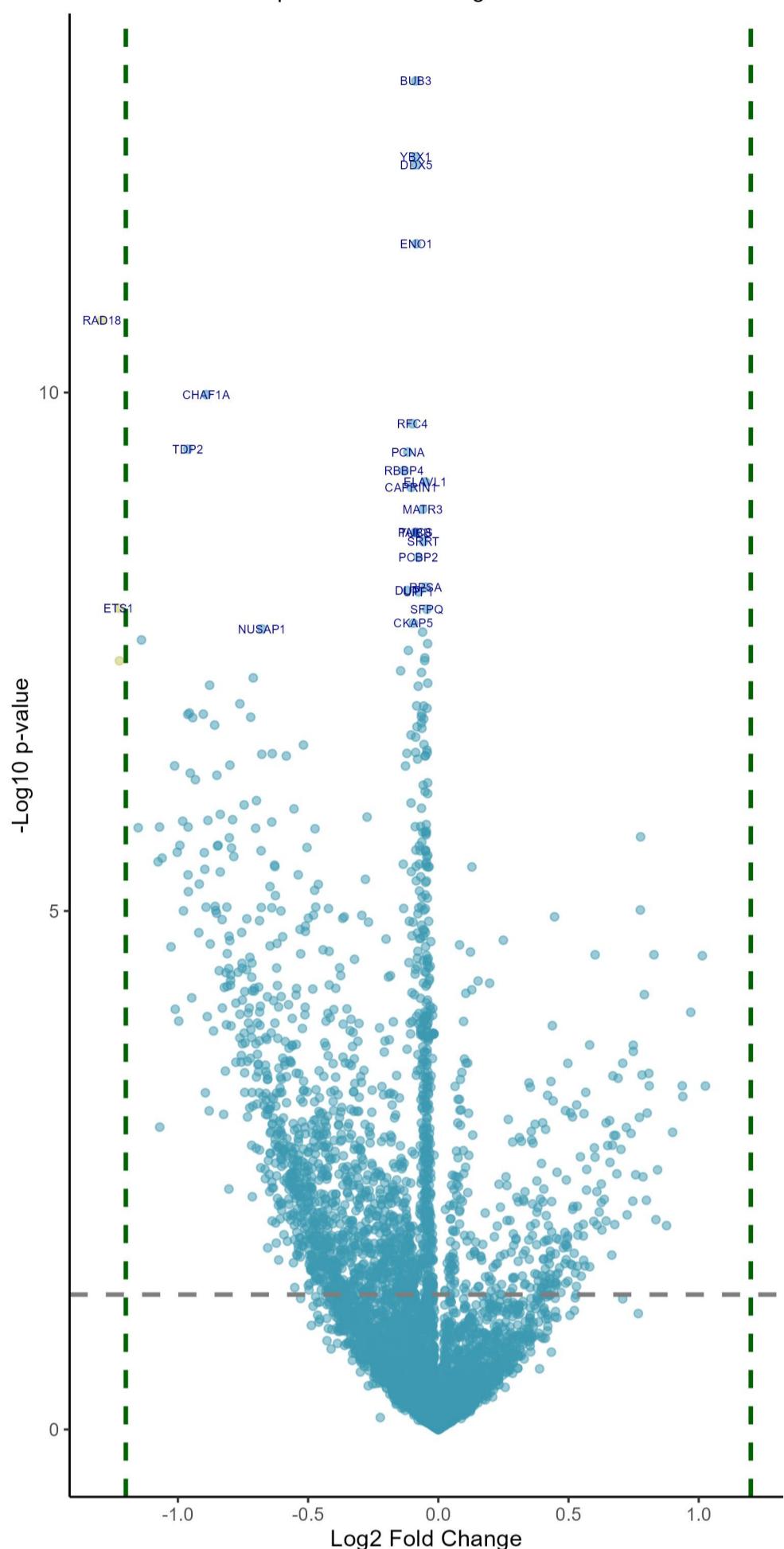
CHEK1 network, DB1, all Pearson r > 0.5

Downregulated in blood cancers at low/absent CHEK1      Upregulated in blood cancers at low/absent CHEK1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.29	2.22e-08	RAD18	RAD18 E3 ubiquitin protein ligase	1.03	3.17e-03	CTSZ	cathepsin Z
-1.23	3.56e-06	ETS1	ETS proto-oncogene 1, transcription	1.01	8.09e-04	CAPN2	calpain 2
-1.22	8.03e-06	GINS1	GINS complex subunit 1	0.97	1.13e-03	CA2	carbonic anhydrase 2
-1.15	1.10e-04	SLBP	stem-loop binding protein	0.94	3.86e-03	GSN	gelsolin
-1.14	5.99e-06	TRMT61A	tRNA methyltransferase 61A	0.94	3.16e-03	SQOR	sulfide quinone oxidoreductase
-1.08	1.80e-04	LEF1	lymphoid enhancer binding factor 1	0.9	7.68e-03	LGALS3	galectin 3
-1.07	1.10e-04	TCF3	transcription factor 3	0.88	4.11e-02	LMNA	lamin A/C
-1.07	6.97e-03	MZB1	marginal zone B and B1 cell specific	0.84	1.52e-02	PLP2	proteolipid protein 2
-1.06	1.67e-04	KIF15	kinesin family member 15	0.84	3.72e-02	S100A6	S100 calcium binding protein A6
-1.03	6.95e-04	MYH10	myosin heavy chain 10	0.83	7.99e-04	ERMP1	endoplasmic reticulum metallopeptid
-1.01	3.74e-05	GSK3B	glycogen synthase kinase 3 beta	0.81	3.16e-03	PLBD2	phospholipase B domain containing 2
-1.01	1.13e-03	C20orf27	chromosome 20 open reading frame 27	0.81	2.48e-03	ATP6V0A1	ATPase H+ transporting V0 subunit a
-1	1.53e-04	XRCC4	X-ray repair cross complementing 4	0.8	5.30e-03	NIBAN1	niban apoptosis regulator 1
-1	1.13e-03	SEPTIN1	septin 1	0.8	2.62e-02	ANXA1	annexin A1
-0.99	1.44e-04	MAZ	MYC associated zinc finger protein	0.79	1.13e-03	TXNRD2	thioredoxin reductase 2
-0.98	1.03e-04	GMNN	geminin DNA replication inhibitor	0.79	1.73e-02	STOM	stomatin
-0.98	3.88e-04	DCAF16	DDB1 and CUL4 associated factor 16	0.78	2.57e-03	SPART	spartin
-0.96	1.84e-05	KNOP1	lysine rich nucleolar protein 1	0.78	1.24e-04	PRTN3	proteinase 3
-0.96	2.50e-07	TDP2	tyrosyl-DNA phosphodiesterase 2	0.78	3.88e-04	MNDA	myeloid cell nuclear differentiatio
-0.96	2.13e-04	ZNF593	zinc finger protein 593	0.77	5.78e-03	PPCS	phosphopantethenoylcysteine synthet
-0.96	1.10e-04	SPAG5	sperm associated antigen 5	0.77	1.79e-01	LGALS1	galectin 1
-0.96	2.87e-04	ORC6	origin recognition complex subunit	0.76	1.66e-02	RNASET2	ribonuclease T2
-0.96	1.84e-05	GINS2	GINS complex subunit 2	0.75	1.61e-03	DUSP23	dual specificity phosphatase 23
-0.95	4.32e-05	ZWINT	ZW10 interacting kinetochore protei	0.75	1.42e-03	LYZ	lysozyme
-0.95	1.13e-03	GTF2E1	general transcription factor IIIE su	0.75	2.66e-02	MVP	major vault protein
-0.94	1.85e-05	NSMCE2	NSE2 (MMS21) homolog, SMC5-SMC6 com	0.74	7.85e-03	PIGK	phosphatidylinositol glycan anchor
-0.93	4.86e-05	CCDC12	coiled-coil domain containing 12	0.73	3.41e-02	IGF2BP2	insulin like growth factor 2 mRNA b
-0.92	5.52e-04	NOPCHAP1	NOP protein chaperone 1	0.72	7.00e-03	TYMP	thymidine phosphorylase
-0.92	2.50e-04	PPP2R5C	protein phosphatase 2 regulatory su	0.71	2.03e-03	HSD17B11	hydroxysteroid 17-beta dehydrogenas

Downregulated in solid cancers at low/absent CHEK1      Upregulated in solid cancers at low/absent CHEK1

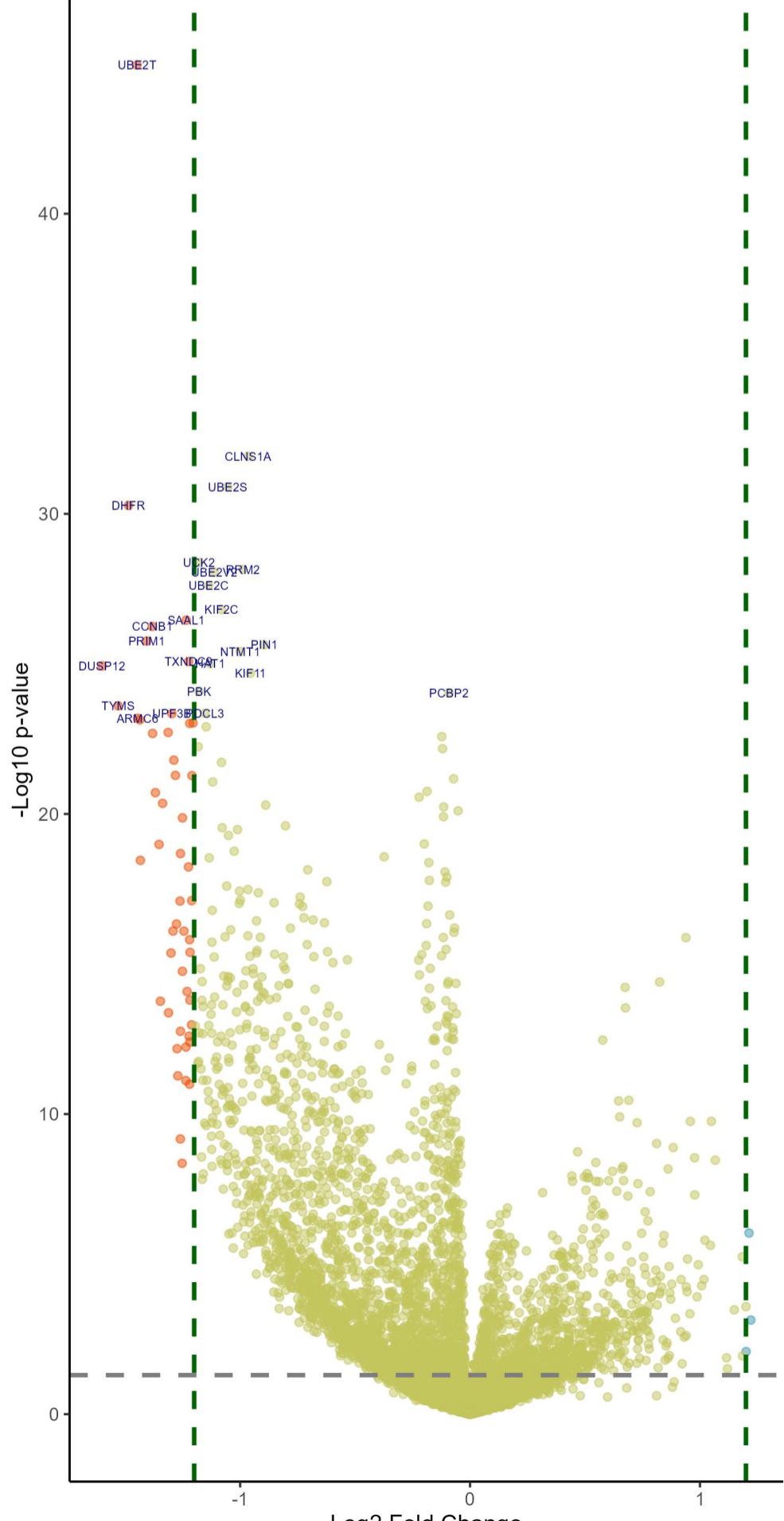
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.6	4.32e-23	DUSP12	dual specificity phosphatase 12	1.22	2.64e-03	CTSZ	cathepsin Z
-1.53	7.56e-22	TYMS	thymidylate synthetase	1.21	7.13e-06	VAMP8	vesicle associated membrane protein
-1.49	7.01e-28	DHFR	dihydrofolate reductase	1.2	2.10e-02	S100A10	S100 calcium binding protein A10
-1.45	3.69e-42	UBE2T	ubiquitin conjugating enzyme E2 T	1.2	1.08e-03	NPC2	NPC intracellular cholesterol trans
-1.45	1.73e-21	ARMC6	armadillo repeat containing 6	1.19	2.77e-02	ITGA3	integrin subunit alpha 3
-1.44	1.86e-21	NACA2	nascent polypeptide associated comp	1.18	3.65e-05	ITGB4	integrin subunit beta 4
-1.43	3.89e-17	CDC34	cell division cycle 34, ubiquitin c	1.15	1.35e-03	SQOR	sulfide quinone oxidoreductase
-1.41	8.83e-24	PRIM1	DNA primase subunit 1	1.12	6.25e-02	LGALS3	galectin 3
-1.38	3.12e-24	CCNB1	cyclin B1	1.12	3.12e-02	CD44	CD44 molecule (Indian blood group)
-1.38	4.46e-21	NDC80	NDC80 kinetochore complex component	1.07	4.50e-08	KRT80	keratin 80
-1.37	3.09e-19	NCK1	NCK adaptor protein 1	1.05	3.04e-09	S100A14	S100 calcium binding protein A14
-1.35	1.25e-17	TACC3	transforming acidic coiled-coil con	1.05	1.68e-05	CD109	CD109 molecule
-1.35	7.15e-13	OGFOD1	2-oxoglutarate and iron dependent o	1.02	1.17e-05	FAM83H	family with sequence similarity 83
-1.34	6.69e-19	DLGAP5	DLG associated protein 5	1.02	1.71e-04	ITPR3	inositol 1,4,5-trisphosphate recept
-1.31	4.26e-21	POLA2	DNA polymerase alpha 2, accessory s	1.01	2.64e-04	ICAM1	intercellular adhesion molecule 1
-1.31	1.58e-12	RNASEH2B	ribonuclease H2 subunit B	0.99	6.33e-05	KRT17	keratin 17
-1.3	2.60e-14	TIMELESS	timeless circadian regulator	0.99	5.59e-04	ADAM9	ADAM metallopeptidase domain 9
-1.3	1.26e-21	UPF3B	UPF3B regulator of nonsense mediate	0.98	4.93e-07	TACSTD2	tumor associated calcium signal tra
-1.29	5.67e-15	POLA1	DNA polymerase alpha 1, catalytic s	0.98	3.88e-08	ARSA	arylsulfatase A
-1.29	3.05e-20	RNF214	ring finger protein 214	0.96	3.06e-09	LAMB3	laminin subunit beta 3
-1.28	9.25e-20	NCAPD3	non-SMC condensin II complex subuni	0.96	1.74e-03	CD59	CD59 molecule (CD59 blood group)
-1.28	3.47e-15	YRDC	yrdC N6-threonylcarbamoyltransferas	0.95	4.29e-05	SPINT1	serine peptidase inhibitor, Kunitz
-1.27	1.89e-11	ZWILCH	zwilch kinetochore protein	0.94	3.95e-04	EPS8L2	EPS8 like 2
-1.27	1.26e-10	SPC25	SPC25 component of NDC80 kinetochor	0.94	2.86e-04	GPRC5A	G protein-coupled receptor class C
-1.26	6.99e-16	BRAT1	BRCA1 associated ATM activator 1	0.94	7.43e-03	ITGA2	integrin subunit alpha 2
-1.26	1.04e-08	C20orf27	chromosome 20 open reading frame 27	0.94	8.82e-15	GPNMB	glycoprotein nmb
-1.26	5.80e-12	GABARAPL2	GABA type A receptor associated pro	0.93	8.20e-03	S100A16	S100 calcium binding protein A16
-1.26	2.43e-17	PRIM2	DNA primase subunit 2	0.92	4.61e-02	NCEH1	neutral cholesterol ester hydrolase



Sorted by p values!

Downregulated in blood cancers at low/absent CHEK1    Upregulated in blood cancers at low/absent CHEK1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.09	3.28e-10	BUB3	BUB3 mitotic checkpoint protein	0.78	1.24e-04	PRTN3	proteinase 3
-0.09	1.06e-09	YBX1	Y-box binding protein 1	0.13	1.86e-04	UGGT1	UDP-glucose glycoprotein glucosyltransferase
-0.08	1.06e-09	DDX5	DEAD-box helicase 5	0.78	3.88e-04	MNDA	myeloid cell nuclear differentiation antigen
-0.08	4.89e-09	ENO1	enolase 1	0.45	4.28e-04	EPB41L3	erythrocyte membrane protein band 4
-1.29	2.22e-08	RAD18	RAD18 E3 ubiquitin protein ligase	0.25	6.24e-04	MAN2B1	mannosidase alpha class 2B member 1
-0.89	9.94e-08	CHAF1A	chromatin assembly factor 1 subunit	0.08	6.76e-04	LAMTOR1	late endosomal/lysosomal adaptor, M
-0.1	1.66e-07	RFC4	replication factor C subunit 4	0.12	7.65e-04	CNPY2	canopy FGF signaling regulator 2
-0.96	2.50e-07	TDP2	tyrosyl-DNA phosphodiesterase 2	0.83	7.99e-04	ERMP1	endoplasmic reticulum metallopeptidase
-0.12	2.50e-07	PCNA	proliferating cell nuclear antigen	0.6	7.99e-04	AZU1	azurocidin 1
-0.13	3.42e-07	RBBP4	RB binding protein 4, chromatin rem	1.01	8.09e-04	CAPN2	calpain 2
-0.05	4.04e-07	ELAVL1	ELAV like RNA binding protein 1	0.15	1.13e-03	TOR1AIP1	torsin 1A interacting protein 1
-0.1	4.21e-07	CAPRIN1	cell cycle associated protein 1	0.2	1.13e-03	ATP6AP1	ATPase H <sup>+</sup> transporting accessory protein
-0.06	6.33e-07	MATR3	matrin 3	0.13	1.13e-03	NDUFA13	NADH:ubiquinone oxidoreductase subunit
-0.09	9.40e-07	PAICS	phosphoribosylaminoimidazole carbox	0.11	1.13e-03	UQCRB	ubiquinol-cytochrome c reductase bi
-0.09	9.40e-07	TUBB	tubulin beta class I	0.79	1.13e-03	TXNRD2	thioredoxin reductase 2
-0.06	1.07e-06	SRRT	serrate, RNA effector molecule	0.97	1.13e-03	CA2	carbonic anhydrase 2
-0.08	1.43e-06	PCBP2	poly(rC) binding protein 2	0.1	1.13e-03	TMED10	transmembrane p24 trafficking protein
-0.05	2.64e-06	RPSA	ribosomal protein SA	0.44	1.13e-03	CEBPA	CCAAT enhancer binding protein alpha
-0.12	2.66e-06	DUT	deoxyuridine triphosphatase	0.58	1.41e-03	TCIRG1	T cell immune regulator 1, ATPase H
-0.08	2.66e-06	UPF1	UPF1 RNA helicase and ATPase	0.75	1.42e-03	LYZ	lysozyme
-1.23	3.56e-06	ETS1	ETS proto-oncogene 1, transcription	0.75	1.61e-03	DUSP23	dual specificity phosphatase 23
-0.04	3.56e-06	SFPQ	splicing factor proline and glutami	0.1	1.88e-03	BCAP31	B cell receptor associated protein
-0.1	4.64e-06	CKAP5	cytoskeleton associated protein 5	0.11	2.02e-03	CYC1	cytochrome c1
-0.68	5.06e-06	NUSAP1	nucleolar and spindle associated pr	0.11	2.02e-03	LMAN2	lectin, mannose binding 2
-0.06	5.22e-06	SNRPA1	small nuclear ribonucleoprotein pol	0.71	2.03e-03	HSD17B11	hydroxysteroid 17-beta dehydrogenase
-1.14	5.99e-06	TRMT61A	tRNA methyltransferase 61A	0.5	2.03e-03	AIF1	allograft inflammatory factor 1
-0.04	6.28e-06	HNRNPK	heterogeneous nuclear ribonucleoprotein	0.09	2.44e-03	NDUFS2	NADH:ubiquinone oxidoreductase core
-0.11	7.05e-06	WDR77	WD repeat domain 77	0.81	2.48e-03	ATP6V0A1	ATPase H <sup>+</sup> transporting V0 subunit a
-0.05	8.03e-06	U2AF2	U2 small nuclear RNA auxiliary fact	0.78	2.57e-03	SPART	spartin
-0.05	8.03e-06	SNRPD2	small nuclear ribonucleoprotein D2	0.67	2.60e-03	COQ7	coenzyme Q7, hydroxylase
-1.22	8.03e-06	GINS1	GINS complex subunit 1	0.69	2.71e-03	HOMER3	homer scaffold protein 3
-0.14	9.72e-06	KPNA2	karyopherin subunit alpha 2	0.08	2.78e-03	NDUFS1	NADH:ubiquinone oxidoreductase core
-0.06	9.79e-06	HNRNPD	heterogeneous nuclear ribonucleoprotein	0.43	2.89e-03	FUCA1	alpha-L-fucosidase 1
-0.71	1.07e-05	TYMS	thymidylate synthetase	0.35	2.98e-03	PRAM1	PML-RARA regulated adaptor molecule
-0.04	1.17e-05	SRSF3	serine and arginine rich splicing f	0.81	3.16e-03	PLBD2	phospholipase B domain containing 2
-0.88	1.19e-05	PRMT3	protein arginine methyltransferase	0.94	3.16e-03	SQOR	sulfide quinone oxidoreductase
-0.08	1.19e-05	PSME3	proteasome activator subunit 3	1.03	3.17e-03	CTSZ	cathepsin Z
-0.76	1.71e-05	MGME1	mitochondrial genome maintenance ex	0.06	3.19e-03	TMED9	transmembrane p24 trafficking protein
0.09	1.71e-05	MCM2	minichromosome maintenance complex	0.35	3.24e-03	IRSC2	insulin receptor substrate 2

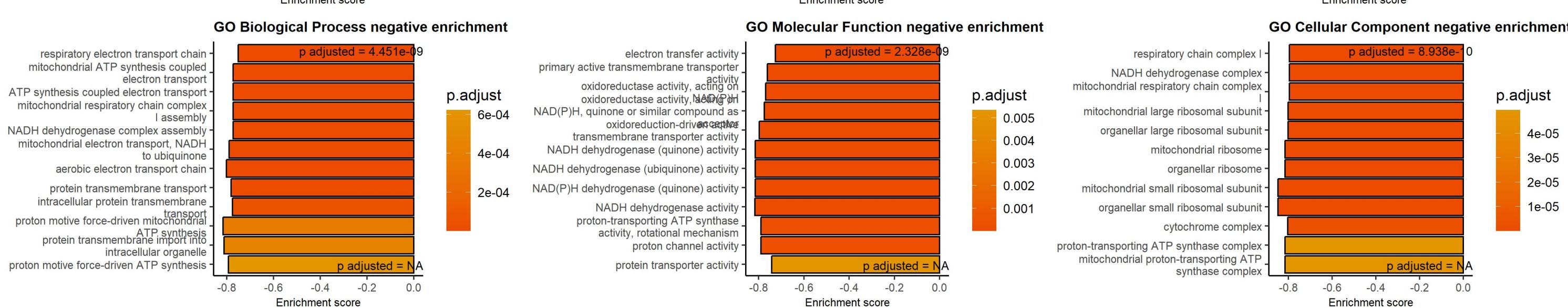
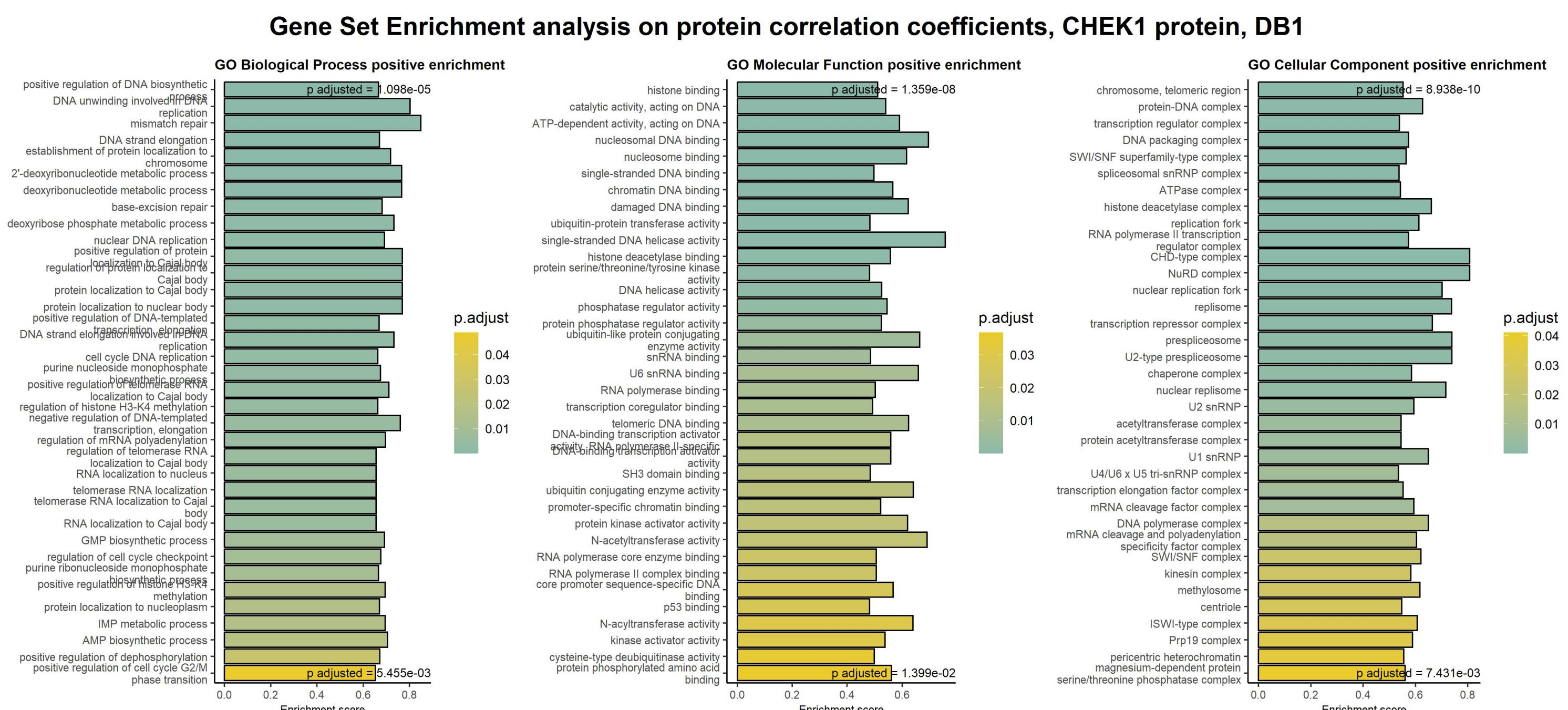
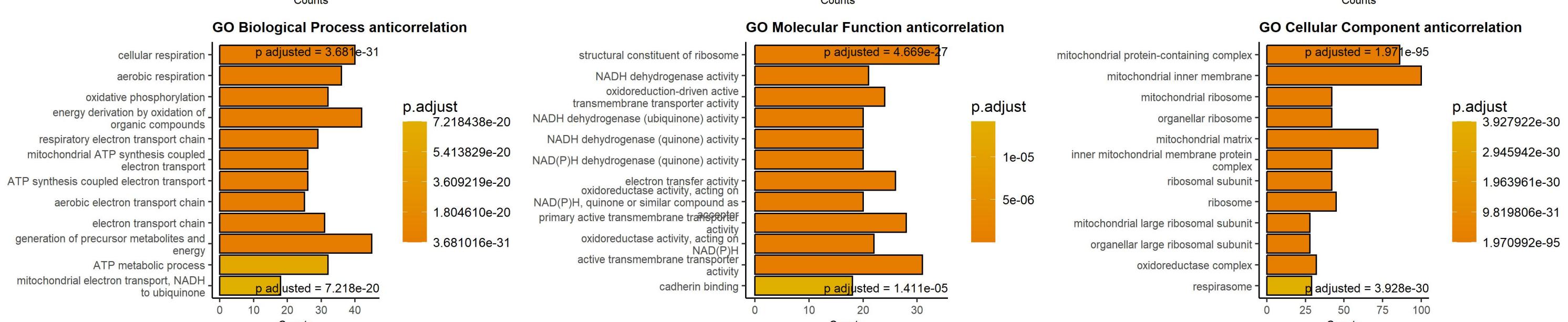
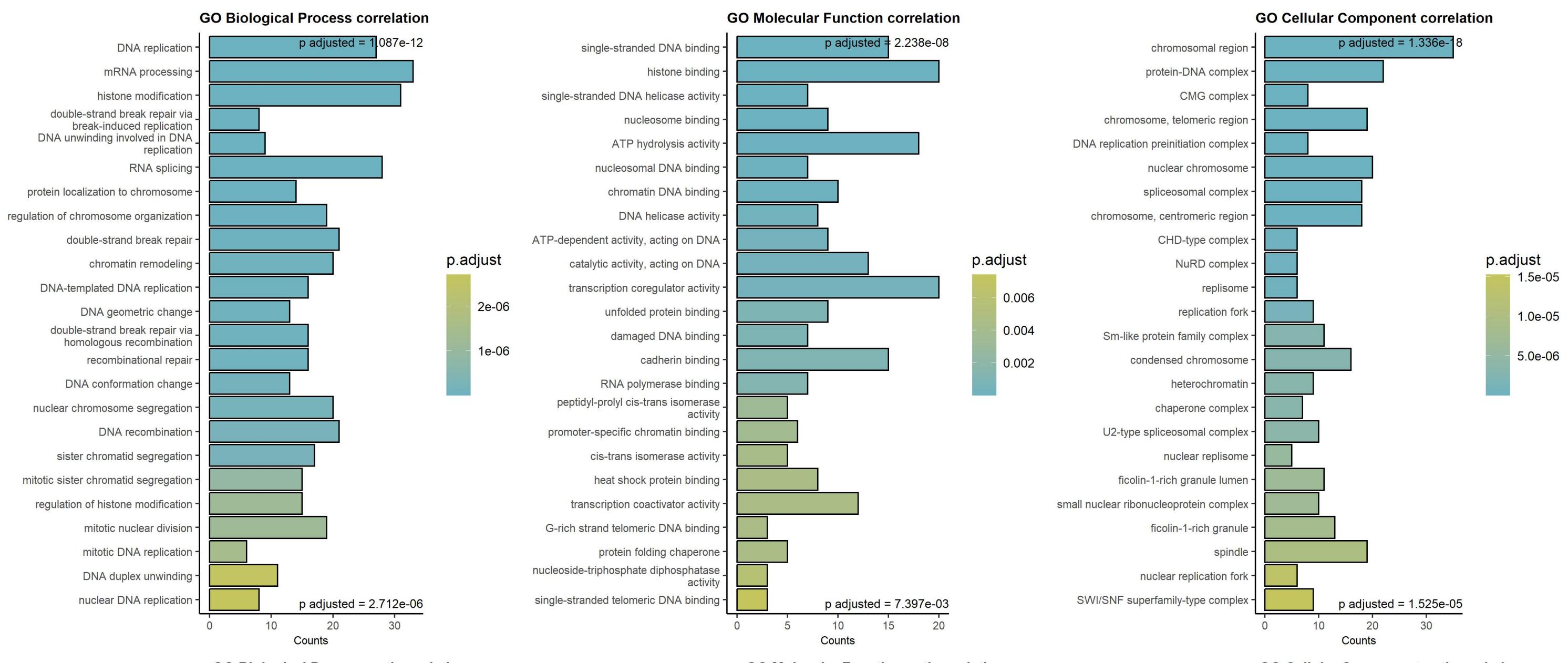


Sorted by p values!

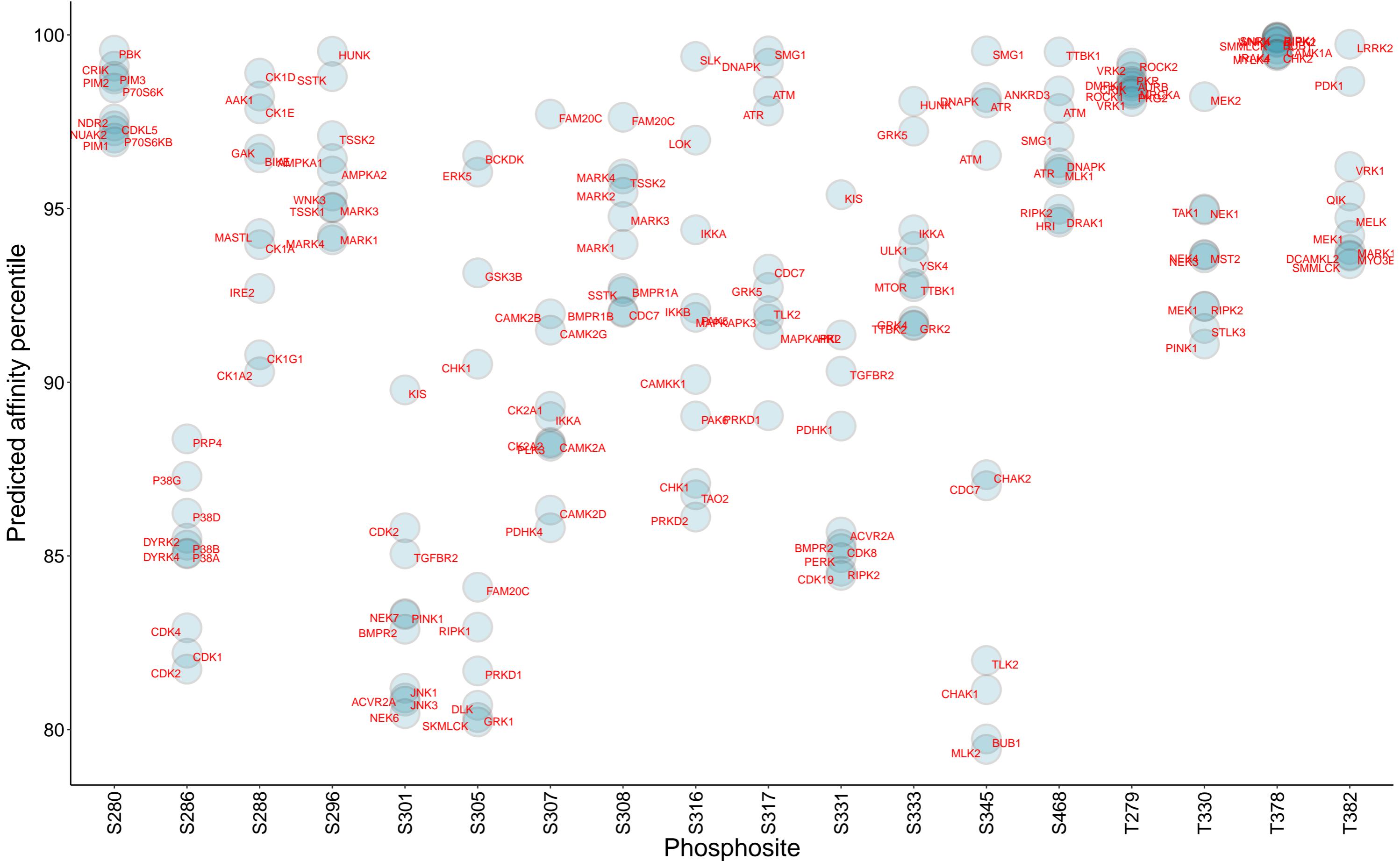
Downregulated in solid cancers at low/absent CHEK1    Upregulated in solid cancers at low/absent CHEK1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.45	3.69e-42	UBE2T	ubiquitin conjugating enzyme E2 T	0.94	8.82e-15	GPNMB	glycoprotein nmb
-0.97	2.69e-29	CLNS1A	chloride nucleotide-sensitive chann	0.82	1.93e-13	ITGB6	integrin subunit beta 6
-1.05	2.11e-28	UBE2S	ubiquitin conjugating enzyme E2 S	0.67	2.72e-13	GLMP	glycosylated lysosomal membrane pro
-1.49	7.01e-28	DHFR	dihydrofolate reductase	0.68	1.13e-12	LAMA3	laminin subunit alpha 3
-1.18	4.62e-26	UCK2	uridine-cytidine kinase 2	0.58	1.05e-11	ABCD1	ATP binding cassette subfamily D me
-0.99	6.79e-26	RRM2	ribonucleotide reductase regulatory	0.69	6.93e-10	SYVN1	synoviolin 1
-1.11	7.30e-26	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.65	7.22e-10	CLCN7	chloride voltage-gated channel 7
-1.14	1.78e-25	UBE2C	ubiquitin conjugating enzyme E2 C	0.65	2.23e-09	KRT4	keratin 4
-1.08	1.03e-24	KIF2C	kinesin family member 2C	1.05	3.04e-09	S100A14	S100 calcium binding protein A14
-1.23	2.11e-24	SAAL1	serum amyloid A like 1	0.96	3.06e-09	LAMB3	laminin subunit beta 3
-1.38	3.12e-24	CCNB1	cyclin B1	0.73	3.34e-09	QSOX1	quiescin sulfhydryl oxidase 1
-1.41	8.83e-24	PRIM1	DNA primase subunit 1	0.81	1.44e-08	C15orf48	chromosome 15 open reading frame 48
-0.9	1.09e-23	PIN1	peptidylprolyl cis/trans isomerase,	0.88	1.91e-08	MELTF	melanotransferrin
-1	1.72e-23	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.47	2.57e-08	RAB38	RAB38, member RAS oncogene family
-1.22	3.49e-23	TXND9C	thioredoxin domain containing 9	0.98	3.88e-08	ARSA	arylsulfatase A
-1.13	3.85e-23	HAT1	histone acetyltransferase 1	1.07	4.50e-08	KRT80	keratin 80
-1.6	4.32e-23	DUSP12	dual specificity phosphatase 12	0.55	5.30e-08	PIEZO1	piezo type mechanosensitive ion cha
-0.96	7.17e-23	KIF11	kinesin family member 11	0.67	7.07e-08	ACSS1	acyl-CoA synthetase short chain fam
-1.18	2.73e-22	PBK	PDZ binding kinase	0.86	8.30e-08	RAB25	RAB25, member RAS oncogene family
-0.09	2.90e-22	PCBP2	poly(rC) binding protein 2	0.66	8.34e-08	KRT6A	keratin 6A
-1.53	7.56e-22	TYMS	thymidylate synthetase	0.62	9.79e-08	KRT13	keratin 13
-1.15	1.26e-21	PDCL3	phosducin like 3	0.51	1.14e-07	ANXA9	annexin A9
-1.3	1.26e-21	UPF3B	UPF3B regulator of nonsense mediate	0.44	1.33e-07	GALNT6	polypeptide N-acetylgalactosaminylt
-1.45	1.73e-21	ARMC6	armadillo repeat containing 6	0.5	1.41e-07	FUCA1	alpha-L-fucosidase 1
-1.44	1.86e-21	NACA2	nascent polypeptide associated comp	0.52	1.48e-07	SLC27A1	solute carrier family 27 member 1
-1.2	2.28e-21	LTV1	LTV1 ribosome biogenesis factor	0.51	1.50e-07	DSG3	desmoglein 3
-1.22	2.28e-21	ELP1	elongator acetyltransferase complex	0.67	1.83e-07	SYTL1	synaptotagmin like 1
-1.15	2.86e-21	HELLS	helicase, lymphoid specific	0.6	1.84e-07	GDF15	growth differentiation factor 15
-1.31	4.26e-21	POLA2	DNA polymerase alpha 2, accessory s	0.45	1.92e-07	CELSR1	cadherin EGF LAG seven-pass G-type
-1.38	4.46e-21	NDC80	NDC80 kinetochore complex component	0.55	1.93e-07	AGA	aspartylglucosaminidase
-0.12	5.49e-21	BUB3	BUB3 mitotic checkpoint protein	0.56	1.97e-07	RGS19	regulator of G protein signaling 19
-1.18	1.15e-20	PSMG2	proteasome assembly chaperone 2	0.73	2.27e-07	PRSS8	serine protease 8
-0.12	1.31e-20	C					

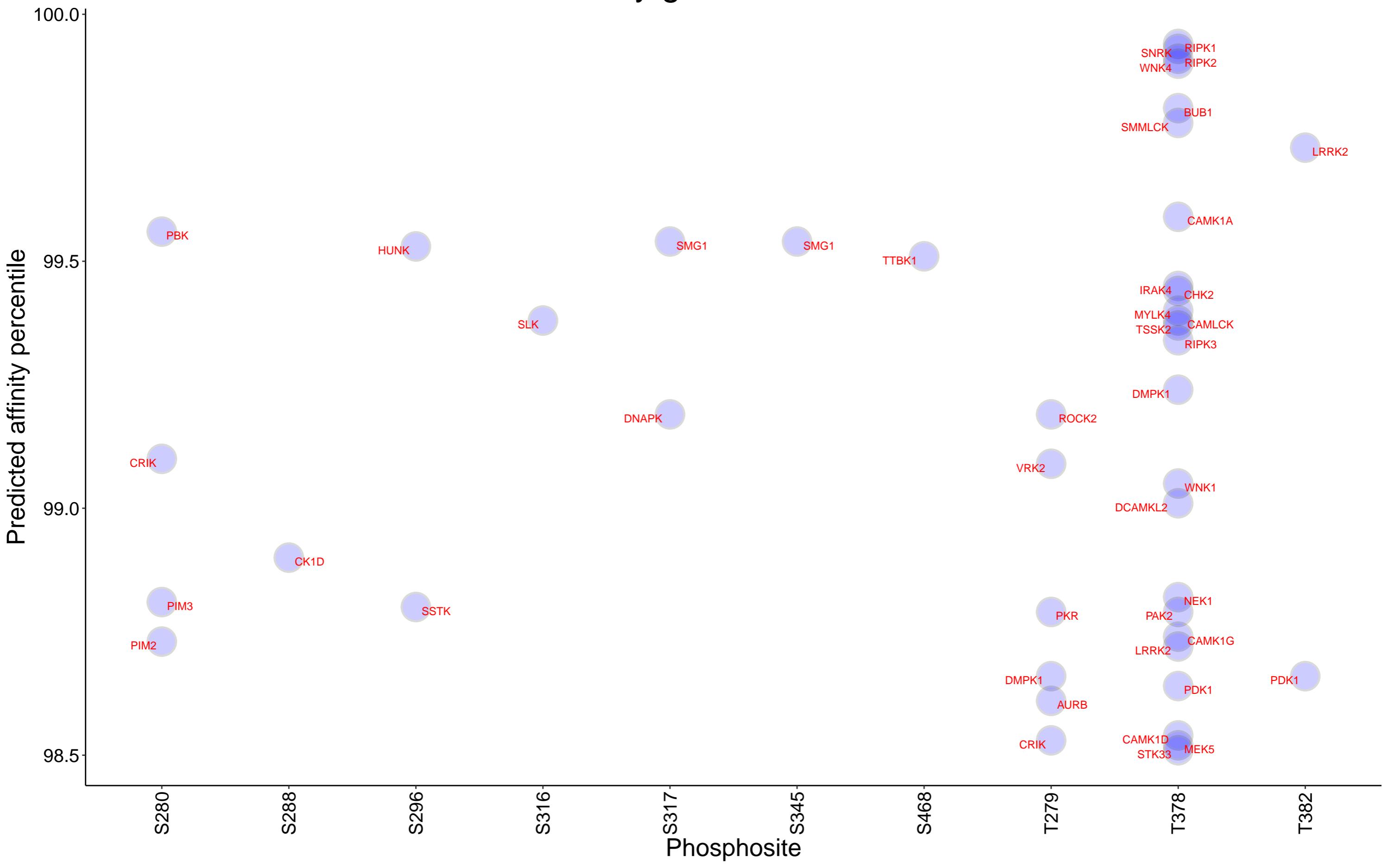
# Top 250 correlation coefficients overrepresentation, CHEK1 protein, DB1



## Top 10 kinases for each phosphosite in CHEK1



## Kinases with affinity greater than 98.5% to CHEK1



No sufficient paired observations in DB1 for CHEK1