

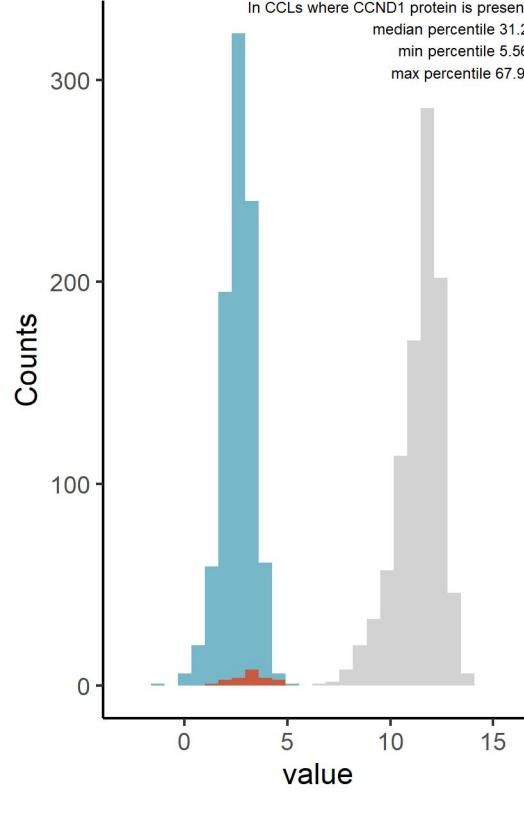
# CCND1

Protein name: CCND1 ; UNIPROT: P24385 ; Gene name: cyclin D1  
 Ligandable: Yes ; Ligandable\_by\_Chem: Yes ; Is\_enzyme: NA (<https://cansar.ai/>)

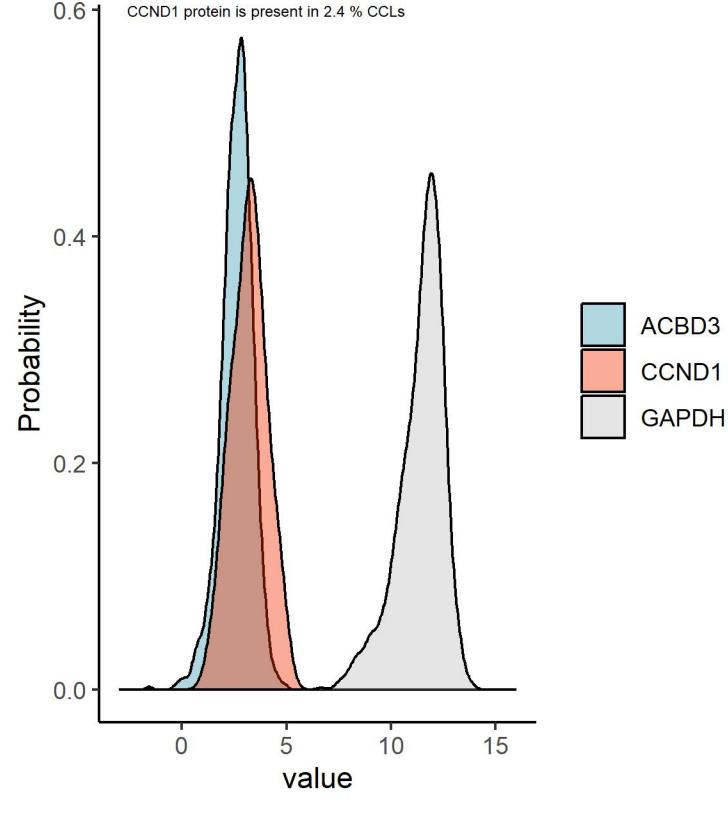
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of CCND1 protein compared to proteins with low and high abundance



Density plot of CCND1 protein compared to proteins with low and high abundance



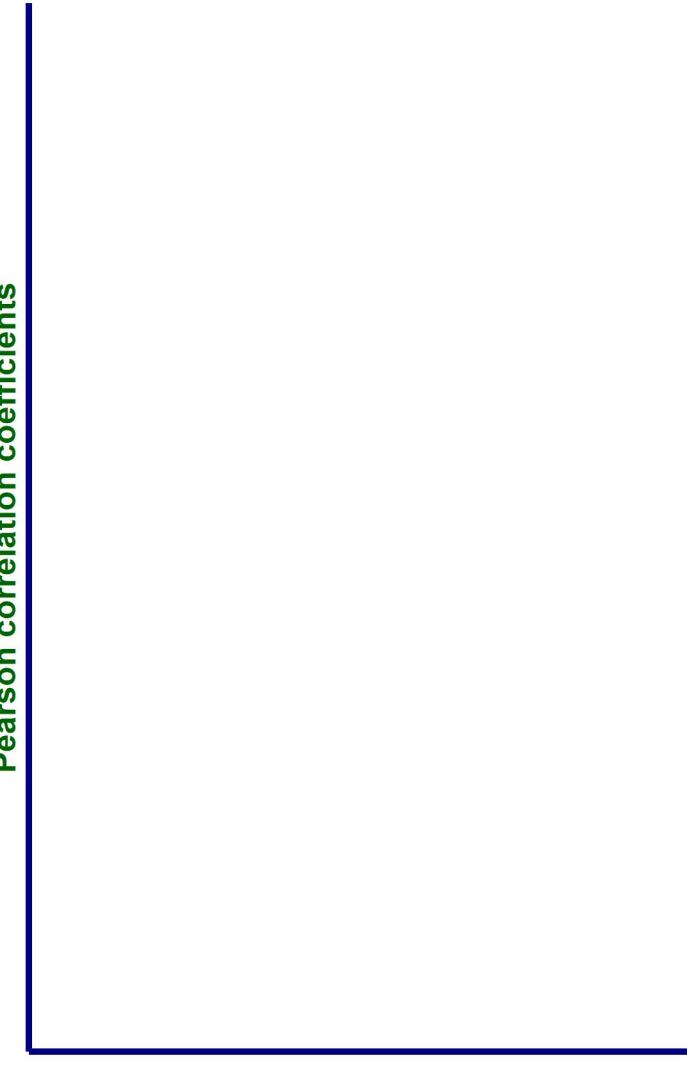
### Top negative correlations of CCND1 protein, DB1

Pearson correlation coefficients



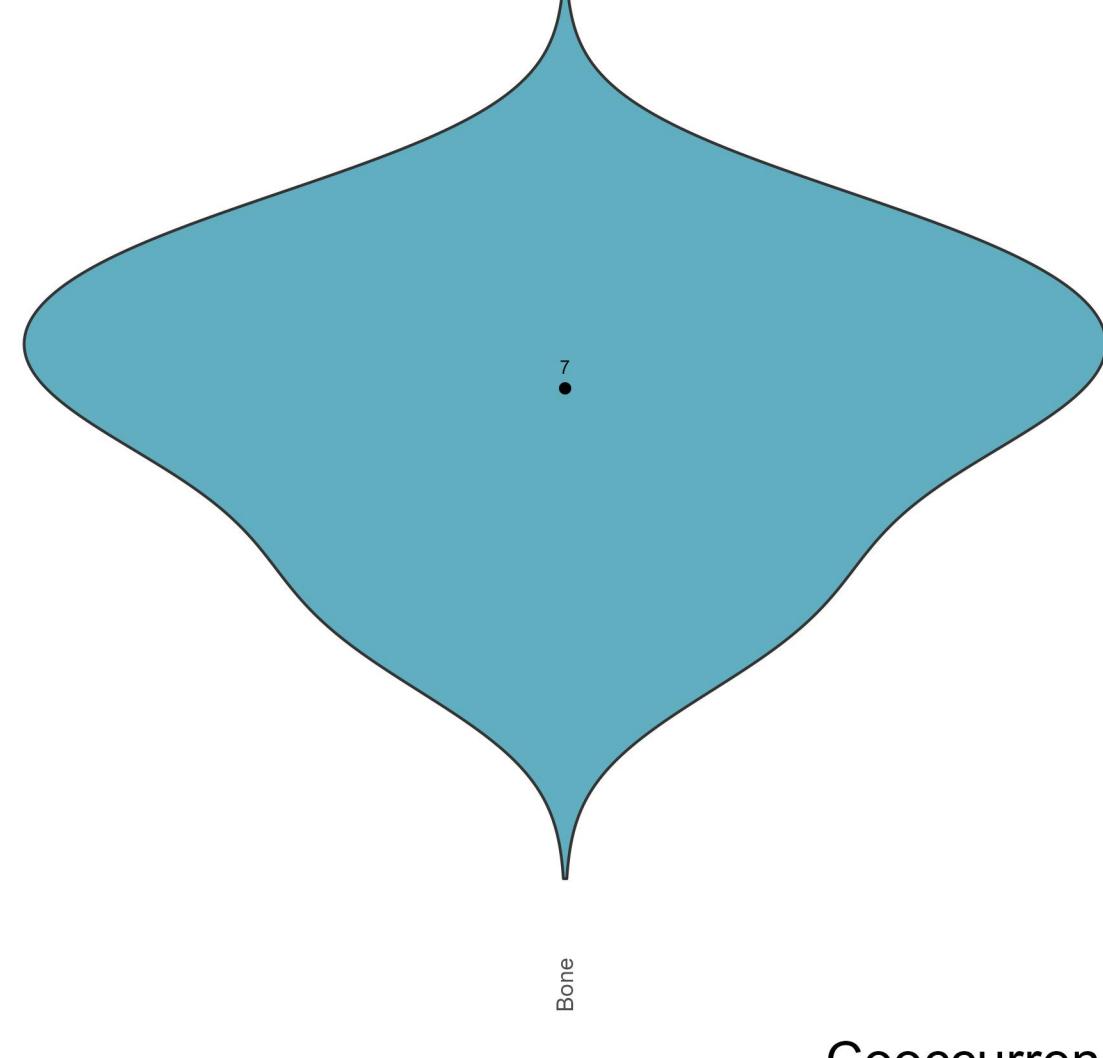
### Top positive correlations of CCND1 protein, DB1

Pearson correlation coefficients



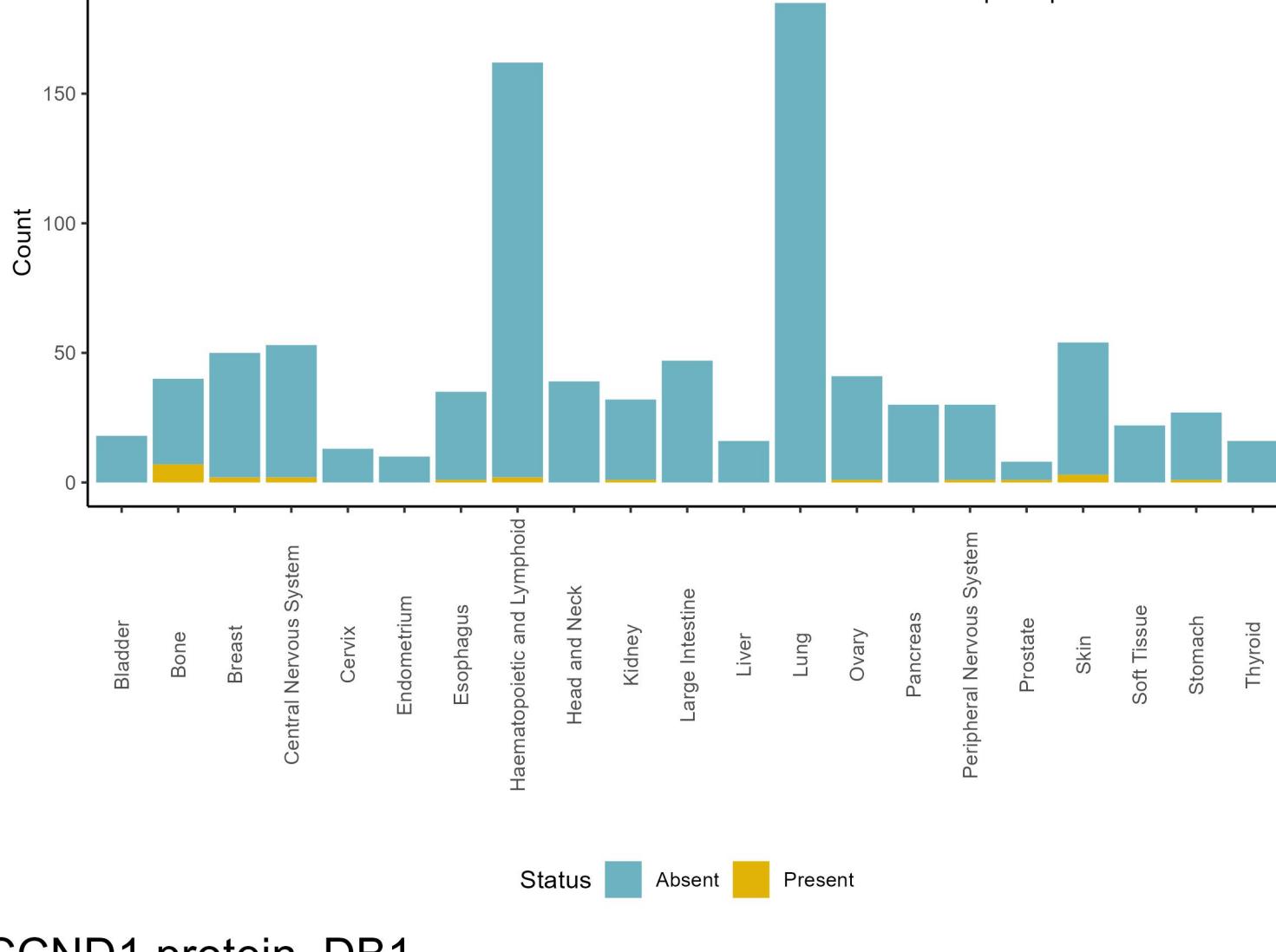
## Amount of CCND1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 7.156e-01



## Present and absent CCND1 protein counts by tissue, DB1

Chi square p value is 1.749e-05

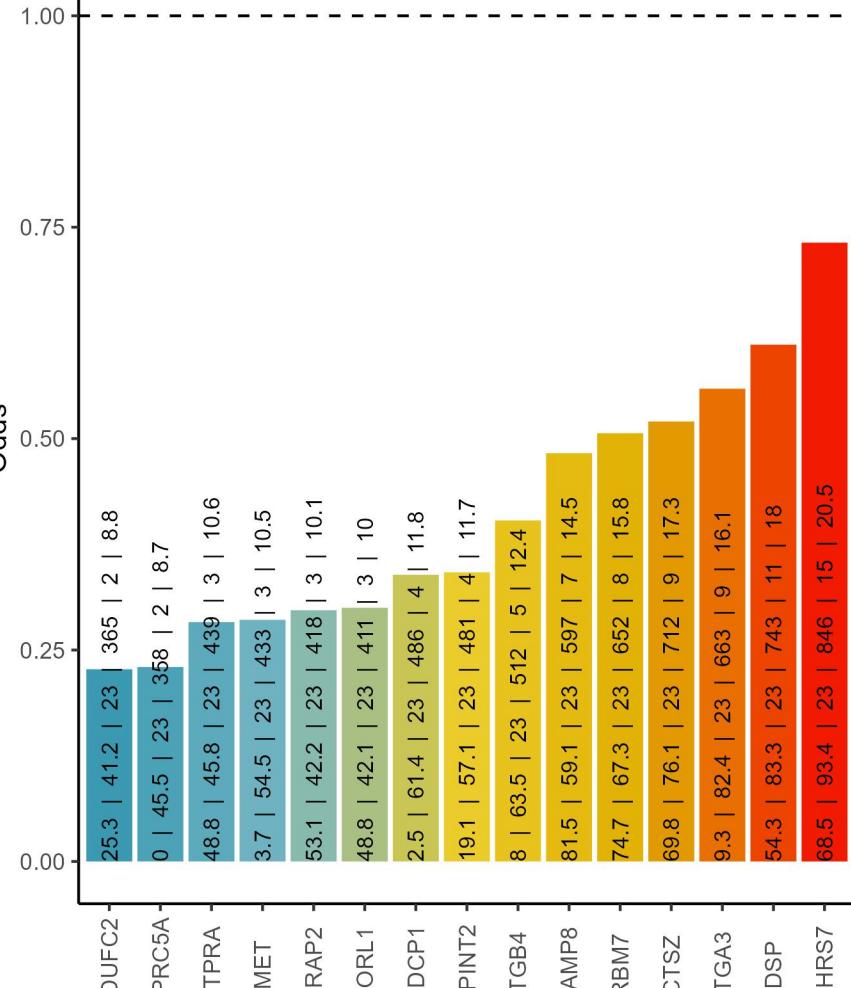


## Cooccurrence with CCND1 protein, DB1

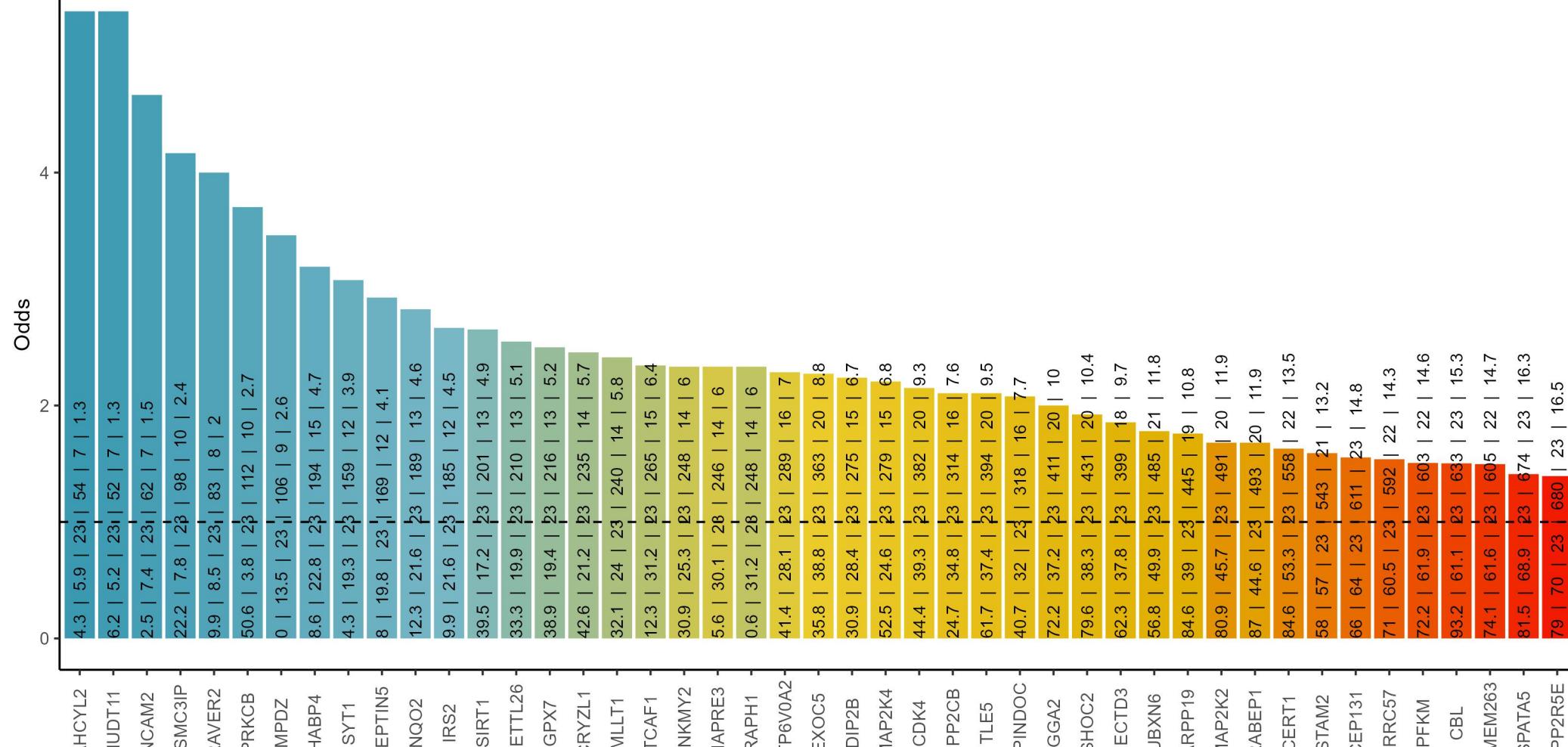
% of CCND1 in blood cancers: 1.2 ; % of CCND1 in solid cancers: 2.7

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CCND1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

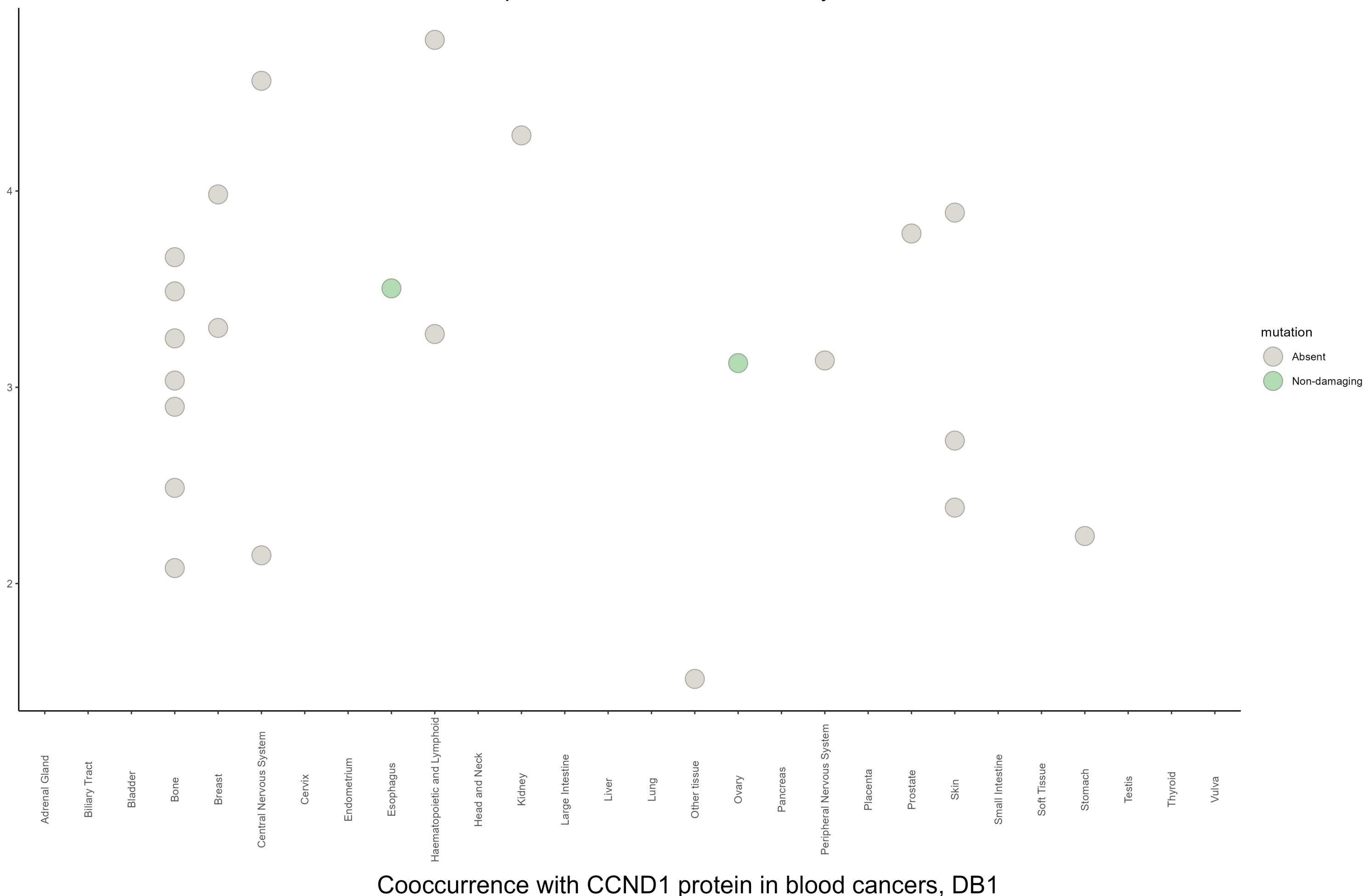
### Negative cooccurrence



### Positive cooccurrence



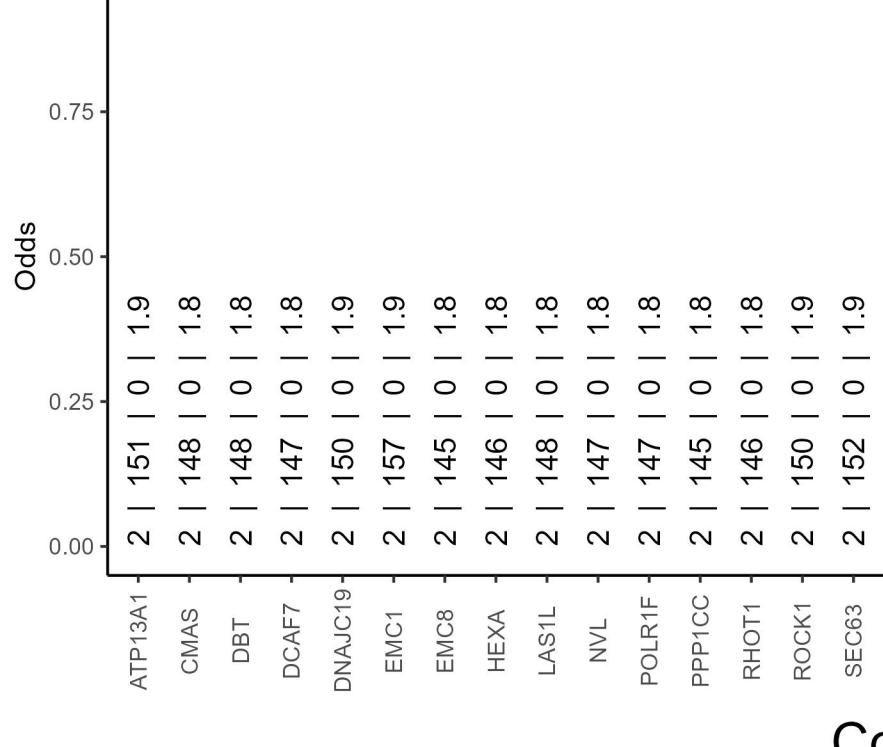
# Amount of CCND1 protein and mutation status by tissue, DB1



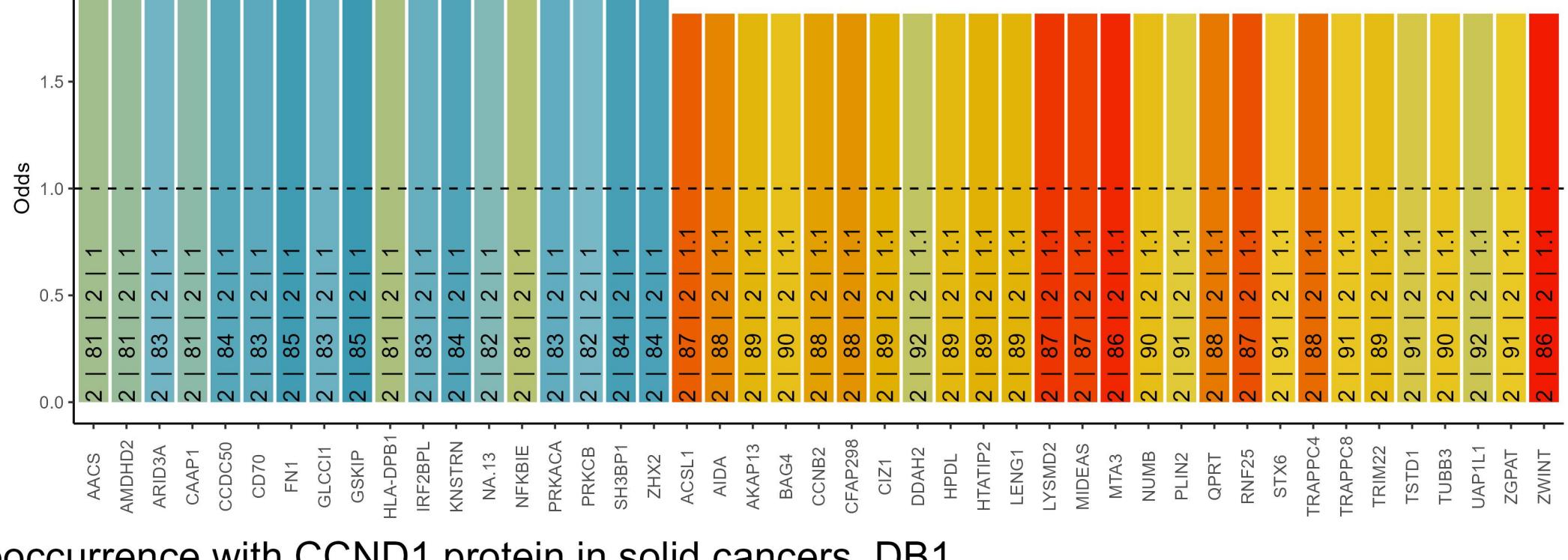
## Cooccurrence with CCND1 protein in blood cancers, DB1

The text in the bars: incidence of CCND1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

### Negative cooccurrence



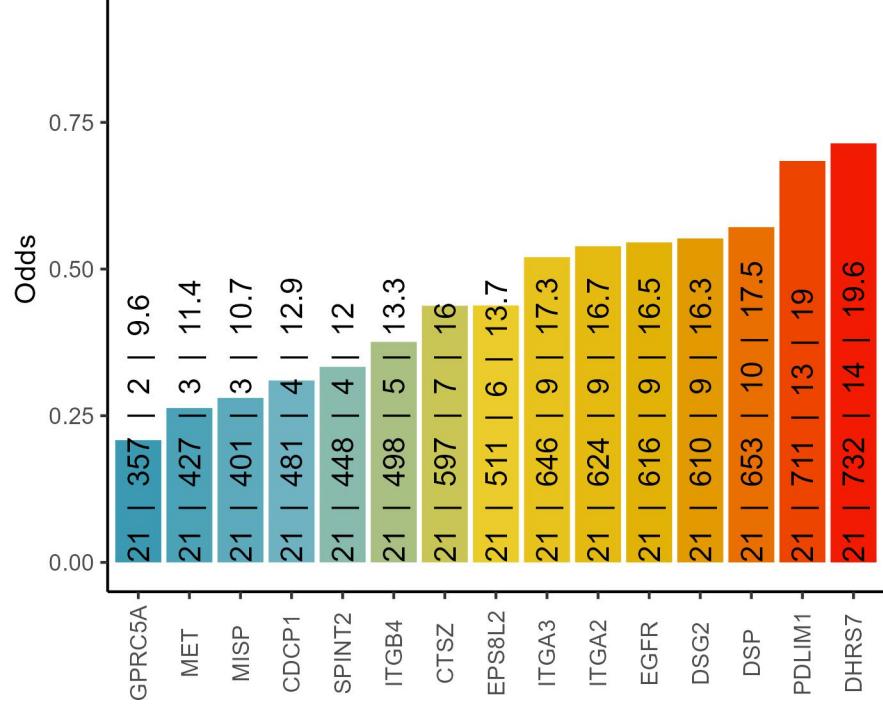
### Positive cooccurrence



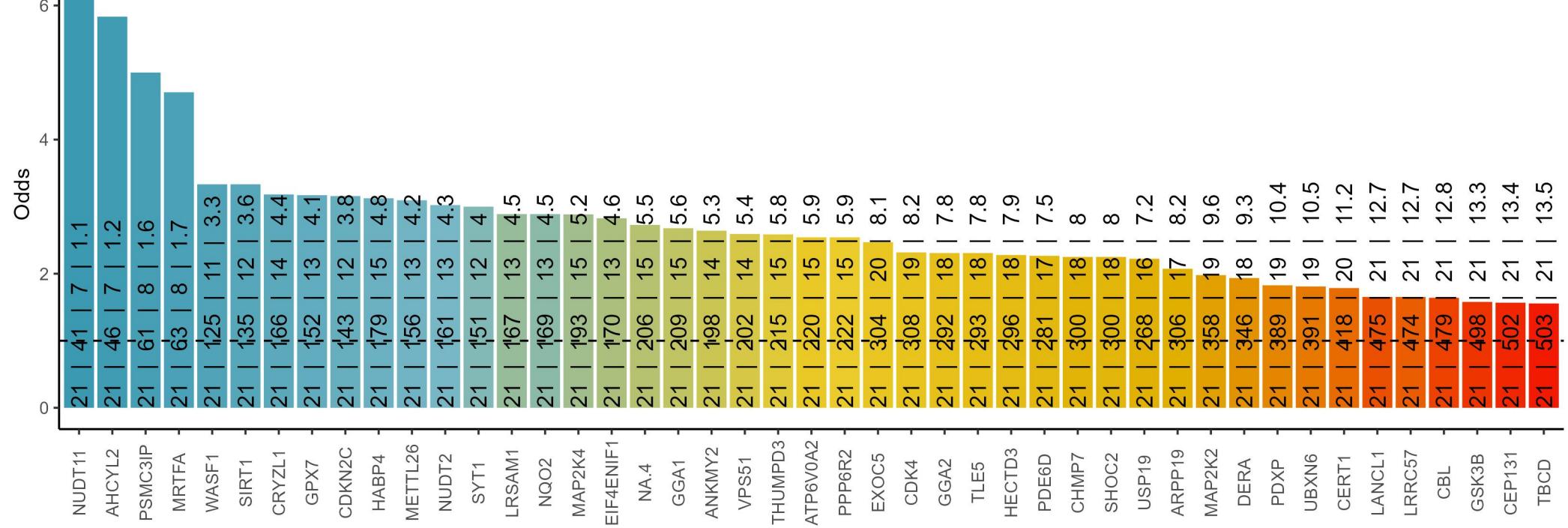
## Cooccurrence with CCND1 protein in solid cancers, DB1

The text in the bars: incidence of CCND1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

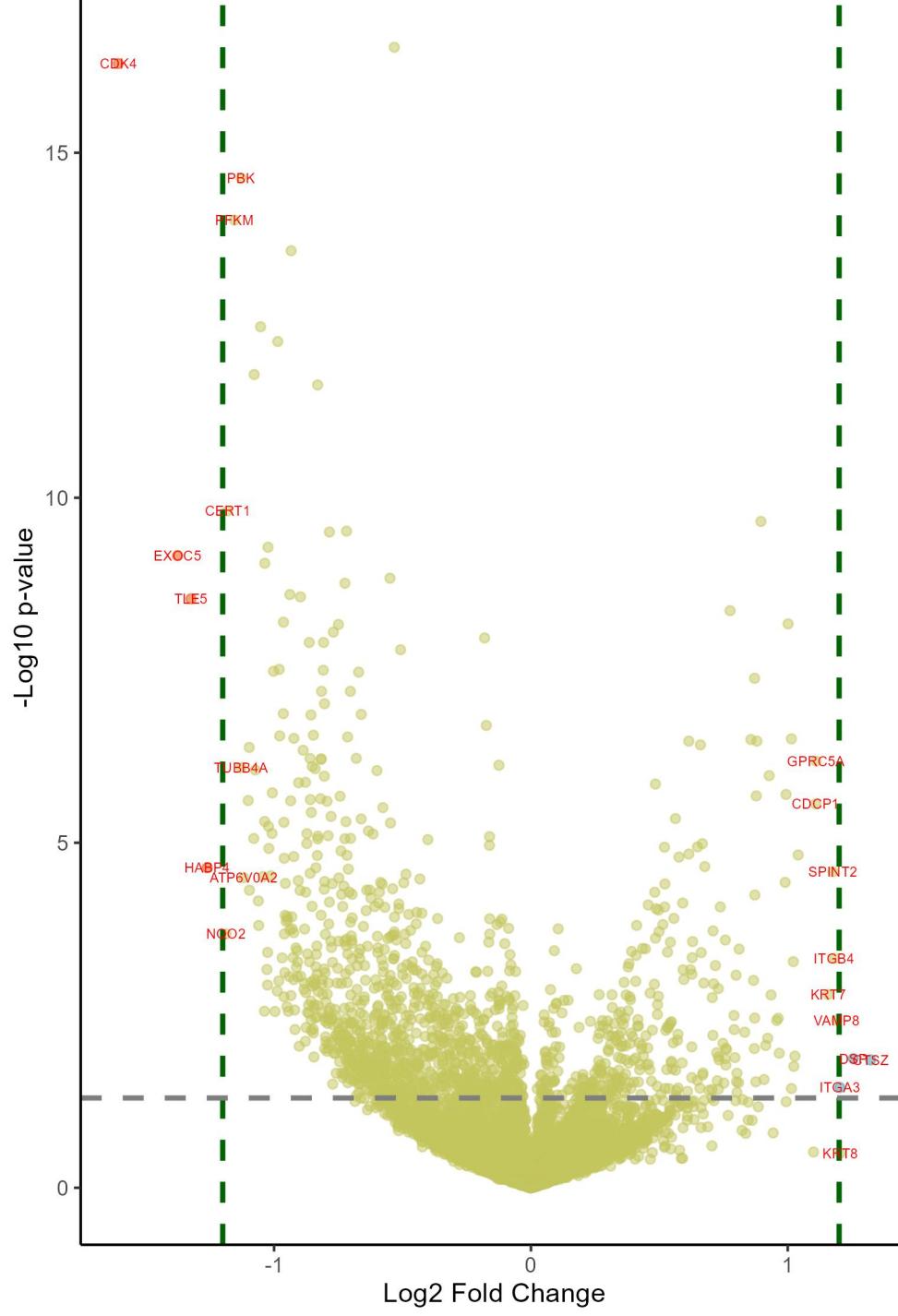
### Negative cooccurrence



### Positive cooccurrence

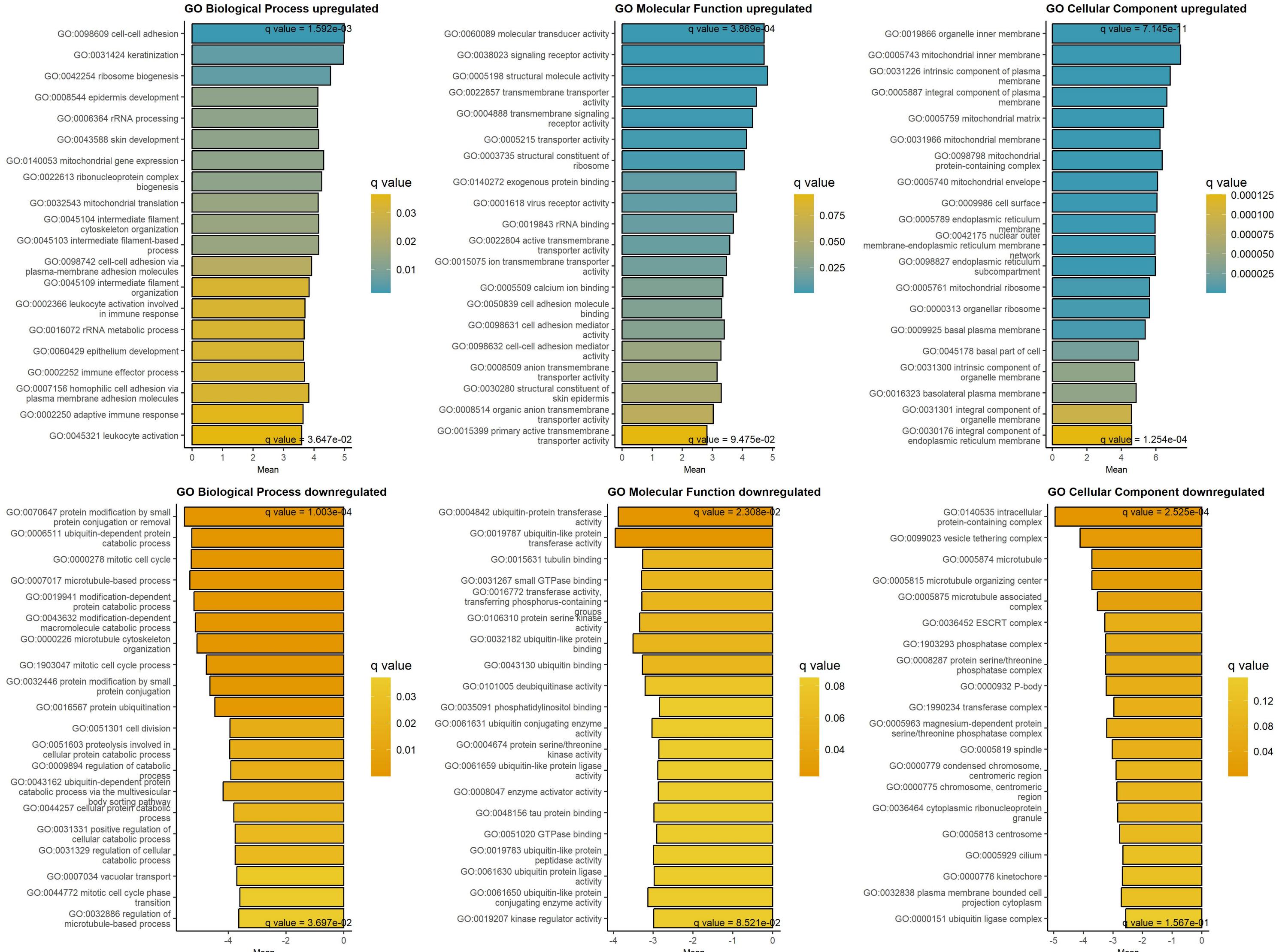


## Downregulated at low/absent CCND1 Upregulated at low/absent CCND1



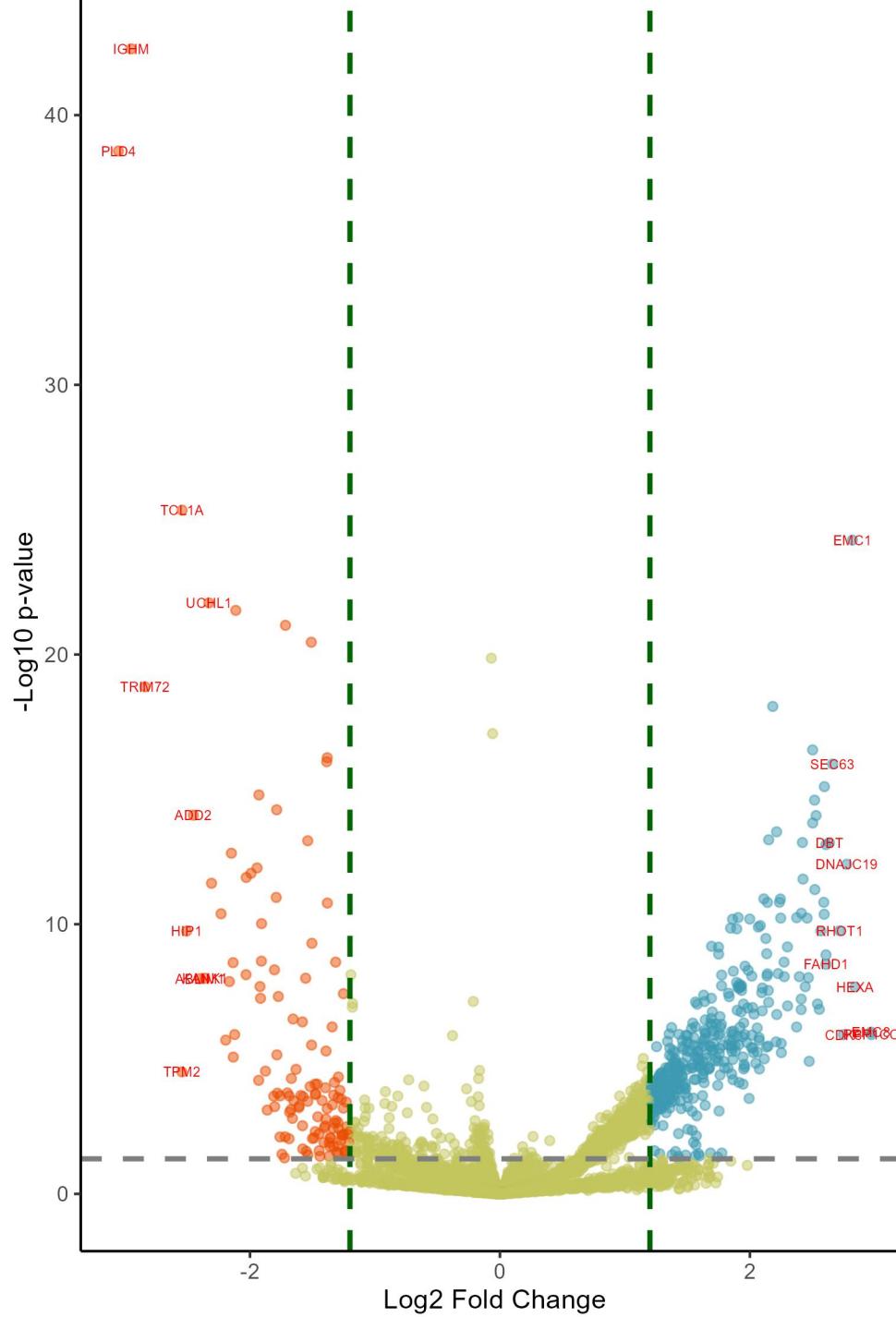
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.61	1.13e-13	CDK4	cyclin dependent kinase 4	1.32	1.10e-01	CTSZ	cathepsin Z
-1.38	2.87e-07	EXOC5	exocyst complex component 5	1.26	1.06e-01	DSP	desmoplakin
-1.32	8.82e-07	TLE5	TLE family member 5, transcriptional	1.2	6.06e-01	KRT8	keratin 8
-1.26	1.29e-03	HABP4	hyaluronan binding protein 4	1.2	1.91e-01	ITGA3	integrin subunit alpha 3
-1.19	6.81e-03	NQO2	N-ribosyldihydronicotamide:quinon	1.19	4.88e-02	VAMP8	vesicle associated membrane protein
-1.18	9.34e-08	CERT1	ceramide transporter 1	1.18	1.21e-02	ITGB4	integrin subunit beta 4
-1.15	1.26e-11	PFKM	phosphofructokinase, muscle	1.18	1.44e-03	SPINT2	serine peptidase inhibitor, Kunitz
-1.13	3.87e-12	PBK	PDZ binding kinase	1.16	2.86e-02	KRT7	keratin 7
-1.13	8.75e-05	TUBB4A	tubulin beta 4A class IVa	1.11	7.37e-05	GPRC5A	G protein-coupled receptor class C
-1.12	1.69e-03	ATP6V0A2	ATPase H+ transporting V0 subunit a	1.11	2.28e-04	CDCP1	CUB domain containing protein 1
-1.1	2.10e-04	IGF2BP1	insulin like growth factor 2 mRNA b	1.1	5.95e-01	KRT18	keratin 18
-1.1	5.21e-05	UBXN6	UBX domain protein 6	1.04	8.99e-04	MISP	mitotic spindle positioning
-1.1	2.26e-03	MON2	MON2 homolog, regulator of endosome	1.03	1.02e-01	DSG2	desmoglein 2
-1.08	5.80e-04	GGA2	golgi associated, gamma adaptin ear	1.02	1.23e-01	ITGA2	integrin subunit alpha 2
-1.08	1.21e-09	TMEM263	transmembrane protein 263	1.02	1.32e-02	RBMT7	RNA binding motif protein 7
-1.07	9.17e-05	ABI2	abl interactor 2	1.01	1.94e-01	ITGA6	integrin subunit alpha 6
-1.06	3.02e-03	PPP2CB	protein phosphatase 2 catalytic sub	1.01	4.32e-05	MET	MET proto-oncogene, receptor tyrosine kinase
-1.06	5.50e-03	CRYZL1	crystallin zeta like 1	1	1.76e-06	PTPRA	protein tyrosine phosphatase receptor type A
-1.05	3.16e-10	CBL	Cbl proto-oncogene	0.99	2.46e-01	NUP210	nucleoporin 210
-1.04	1.64e-03	PDE6D	phosphodiesterase 6D	0.99	1.84e-04	KRT80	keratin 80
-1.04	4.08e-02	PRKCB	protein kinase C beta	0.99	1.89e-03	SPINT1	serine peptidase inhibitor, Kunitz
-1.04	3.78e-04	CRIP2	cysteine rich protein 2	0.97	9.52e-02	NT5E	5'-nucleotidase ecto
-1.04	3.49e-07	CEP131	centrosomal protein 131	0.96	4.69e-02	TAP2	transporter 2, ATP binding cassette
-1.03	1.58e-02	MAPRE3	microtubule associated protein RP/E	0.96	4.89e-02	PKP3	plakophilin 3
-1.03	2.24e-02	SEPTIN5	septin 5	0.94	4.37e-01	KRT19	keratin 19
-1.02	1.05e-02	MLLT1	MLLT1 super elongation complex subunit	0.93	2.86e-02	EPB41L1	erythrocyte membrane protein band 4
-1.02	2.31e-07	GSK3B	glycogen synthase kinase 3 beta	0.93	1.07e-04	ERAP2	endoplasmic reticulum aminopeptidases
-1.02	4.28e-04	MAP2K2	mitogen-activated protein kinase kinase 2	0.92	7.10e-02	EPS8L2	EPS8 like 2
-1.02	7.45e-04	SHOC2	SHOC2 leucine rich repeat scaffold	0.91	8.24e-02	LSR	lipolysis stimulated lipoprotein receptor

## GAGE analysis on upregulated and downregulated proteins at low/absent CCND1 protein, DB1

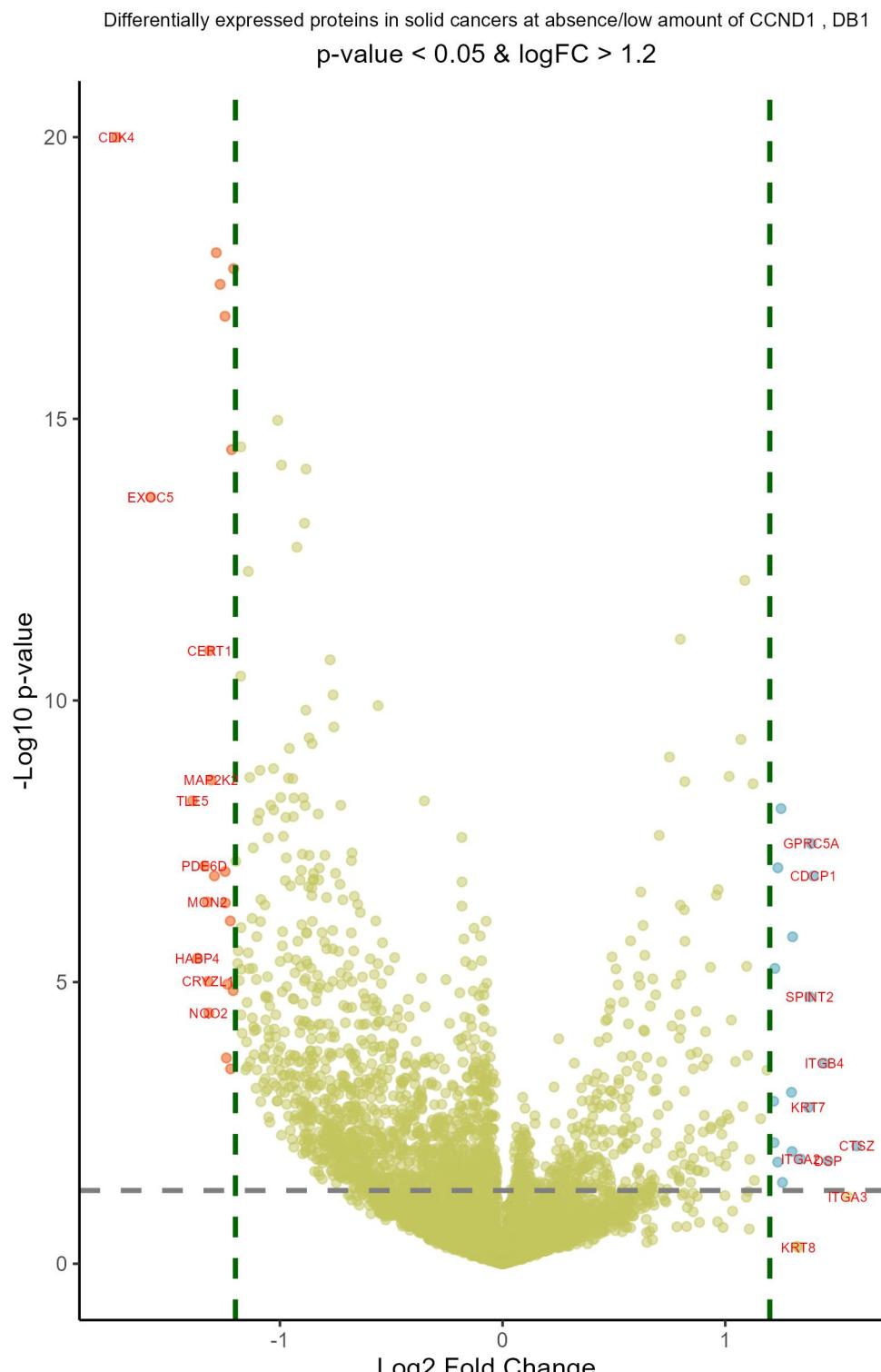


p-value &lt; 0.05 &amp; logFC &gt; 1.2

Downregulated in blood cancers at low/absent CCND1 Upregulated in blood cancers at low/absent CCND1



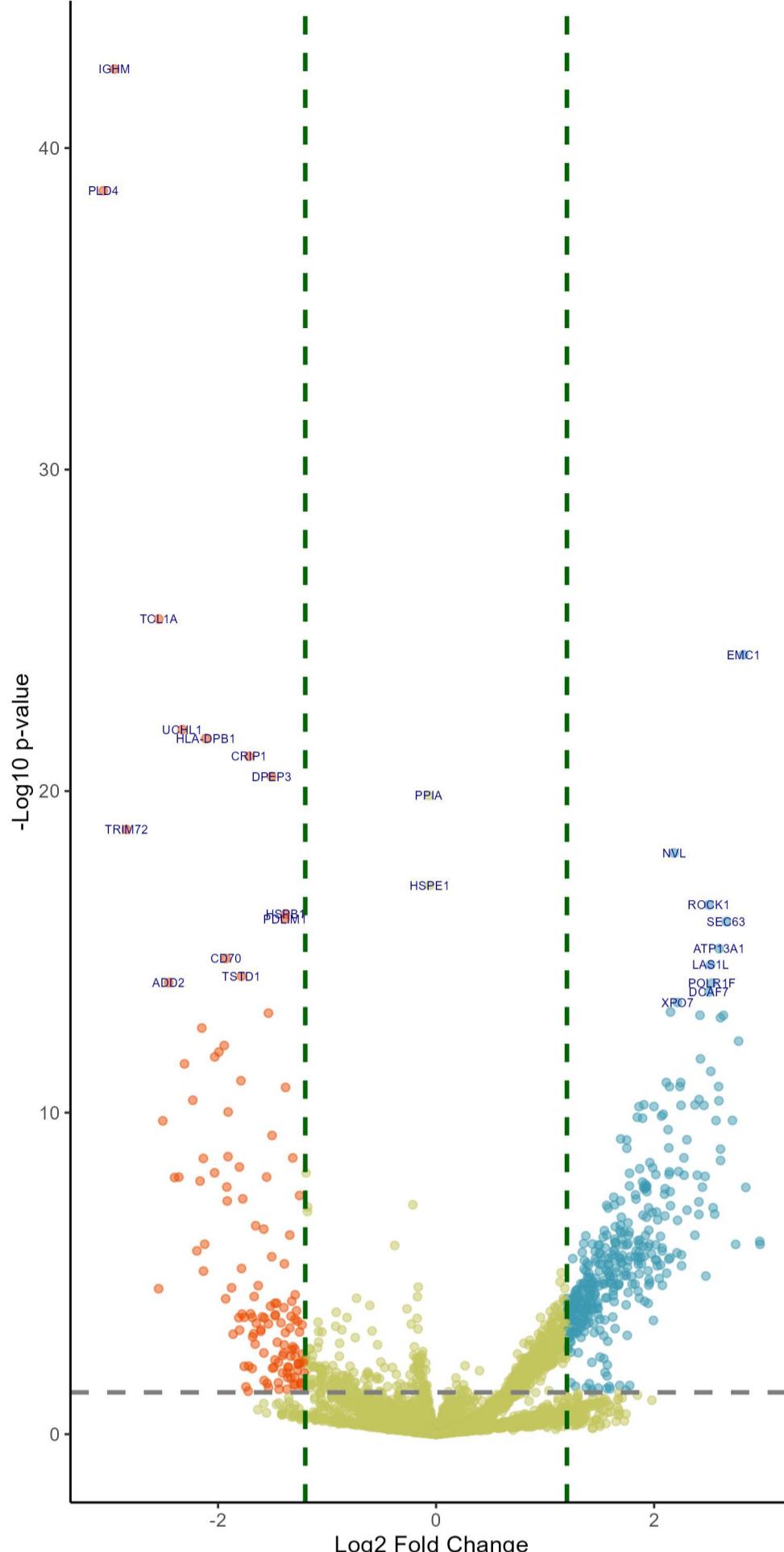
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-3.05	4.73e-36	PLD4	phospholipase D family member 4	2.97	4.89e-05	PPP1CC	protein phosphatase 1 catalytic sub
-2.95	1.16e-39	IGHM	immunoglobulin heavy constant mu	2.97	4.18e-05	EMC8	ER membrane protein complex subunit
-2.84	9.43e-17	TRIM72	tripartite motif containing 72	2.84	1.38e-06	HEXA	hexosaminidase subunit alpha
-2.55	6.81e-04	TPM2	tropomyosin 2	2.82	7.60e-22	EMC1	ER membrane protein complex subunit
-2.54	7.39e-23	TCL1A	TCL1 family AKT coactivator A	2.77	1.24e-10	DNAJC19	DnaJ heat shock protein family (Hsp
-2.51	1.93e-08	HIP1	huntingtin interacting protein 1	2.75	4.89e-05	CDK6	cyclin dependent kinase 6
-2.45	2.70e-12	ADD2	adducin 2	2.72	1.92e-08	RHOT1	ras homolog family member T1
-2.4	7.52e-07	ABLIM1	actin binding LIM protein 1	2.66	4.49e-14	SEC63	SEC63 homolog, protein translocatio
-2.36	7.39e-07	KANK1	KN motif and ankyrin repeat domains	2.64	2.17e-11	DBT	dihydrolipoamide branched chain tra
-2.33	1.35e-19	UCHL1	ubiquitin C-terminal hydrolase L1	2.61	2.72e-07	FAHD1	fumarylacetoacetate hydrolase domai
-2.31	5.45e-10	ALDH2	aldehyde dehydrogenase 2 family mem	2.61	1.30e-07	AGK	acylglycerol kinase
-2.23	5.81e-09	MS4A1	membrane spanning 4-domains A1	2.61	2.47e-11	CMAS	cytidine monophosphate N-acetyneur
-2.19	7.20e-05	GATM	glycine amidinotransferase	2.6	2.93e-13	ATP13A1	ATPase 13A1
-2.16	9.58e-07	PSME4	proteasome activator subunit 4	2.59	5.93e-09	NLE1	notchless homolog 1
-2.15	5.00e-11	SIT1	signaling threshold regulating tran	2.59	2.35e-09	KPNA6	karyopherin subunit alpha 6
-2.13	2.39e-07	CD79B	CD79b molecule	2.57	1.92e-08	ALKB5	alkB homolog 5, RNA demethylase
-2.13	2.36e-04	DNMBP	dynamin binding protein	2.56	7.40e-06	ZNF622	zinc finger protein 622
-2.12	4.89e-05	ORC6	origin recognition complex subunit	2.54	4.93e-06	STT3B	STT3 oligosaccharyltransferase comp
-2.11	2.19e-19	HLA-DPB1	major histocompatibility complex, c	2.53	2.70e-12	POLR1F	RNA polymerase I subunit F
-2.03	6.00e-07	CLIP2	CAP-Gly domain containing linker pr	2.52	9.10e-10	HMGCL	3-hydroxy-3-methylglutaryl-CoA lyas
-2.03	3.50e-10	MARCKS	myristoylated alanine rich protein	2.52	8.34e-13	LAS1L	LAS1 like ribosome biogenesis facto
-1.99	2.53e-10	HLA-DQB1	major histocompatibility complex, c	2.5	4.88e-12	DCAF7	DDB1 and CUL4 associated factor 7
-1.94	1.65e-10	CCDC50	coiled-coil domain containing 50	2.5	1.64e-14	ROCK1	Rho associated coiled-coil containi
-1.93	1.26e-03	HDGFL3	HDGF like 3	2.47	3.20e-04	APOE	apolipoprotein E
-1.93	5.61e-13	CD70	CD70 molecule	2.47	7.17e-07	CASP7	caspase 7
-1.92	1.38e-06	CASP1	caspase 1	2.46	7.58e-09	ERAL1	Era like 12S mitochondrial rRNA cha
-1.92	3.22e-06	VPS37C	VPS37C subunit of ESCRT-I	2.44	1.38e-06	ARMC8	armadillo repeat containing 8
-1.91	2.19e-07	HLA-DPA1	major histocompatibility complex, c	2.42	3.92e-10	SDF2L1	stromal cell derived factor 2 like
-1.91	1.15e-08	SERPINB9	serpin family B member 9	2.42	2.17e-11	TASOR	transcription activation suppressor



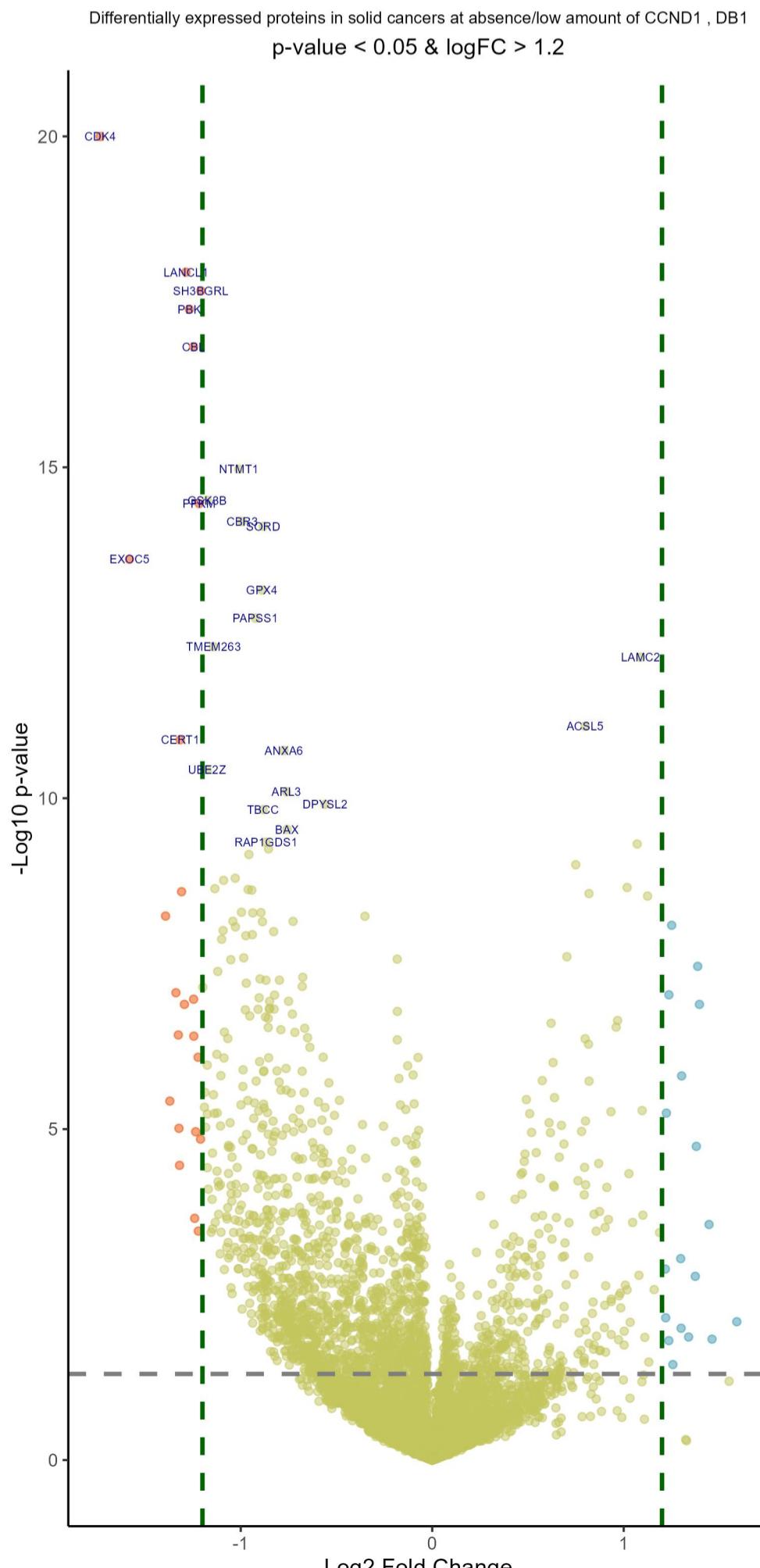
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.73	3.33e-17	CDK4	cyclin dependent kinase 4	1.59	5.61e-02	CTSZ	cathepsin Z
-1.58	1.36e-11	EXOC5	exocyst complex component 5	1.55	2.19e-01	ITGA3	integrin subunit alpha 3
-1.39	9.39e-07	TLE5	TLE family member 5, transcriptiona	1.46	8.32e-02	DSP	desmoplakin
-1.37	1.81e-04	HABP4	hyaluronan binding protein 4	1.45	4.92e-03	ITGB4	integrin subunit beta 4
-1.34	8.62e-06	PDE6D	phosphodiesterase 6D	1.4	1.16e-05	CDCP1	CUB domain containing protein 1
-1.33	2.67e-05	MON2	MON2 homolog, regulator of endosome	1.39	3.98e-06	GPRC5A	G protein-coupled receptor class C
-1.32	3.64e-04	CRYZL1	crystallin zeta like 1	1.38	5.99e-04	SPINT2	serine peptidase inhibitor, Kunitz
-1.32	1.01e-03	NQO2	N-ribosyldihydroneuroquinone	1.37	1.82e-02	KRT7	keratin 7
-1.32	4.83e-09	CERT1	ceramide transporter 1	1.34	7.91e-02	ITGA2	integrin subunit alpha 2
-1.31	4.77e-07	MAP2K2	mitogen-activated protein kinase ki	1.33	6.86e-01	KRT8	keratin 8
-1.29	1.16e-05	CHMP7	charged multivesicular body protein	1.32	6.67e-01	KRT18	keratin 18
-1.29	2.49e-15	LANCL1	LanC like 1	1.3	8.69e-05	MISP	mitotic spindle positioning
-1.27	5.44e-15	PBK	PDZ binding kinase	1.3	6.55e-02	DSG2	desmoglein 2
-1.25	1.67e-14	CBL	Cbl proto-oncogene	1.3	1.13e-02	VAMP8	vesicle associated membrane protein
-1.25	1.02e-05	CASP7	caspase 7	1.26	1.50e-01	ITGA6	integrin subunit alpha 6
-1.25	2.75e-05	HECTD3	HECT domain E3 ubiquitin protein li	1.25	1.18e-06	MET	MET proto-oncogene, receptor tyrosi
-1.24	4.28e-03	GPX7	glutathione peroxidase 7	1.24	9.09e-06	KRT80	keratin 80
-1.24	3.96e-04	ATP6V0A2	ATPase H+ transporting V0 subunit a	1.24	8.62e-02	EGFR	epidermal growth factor receptor
-1.22	5.22e-05	TUBB4A	tubulin beta 4A class IVa	1.22	2.46e-04	SPINT1	serine peptidase inhibitor, Kunitz
-1.22	5.86e-03	CDKN2C	cyclin dependent kinase inhibitor 2	1.22	5.09e-02	NTSE	5'-nucleotidase ecto
-1.22	2.61e-12	PFKM	phosphofructokinase, muscle	1.22	1.50e-02	PKP3	plakophilin 3
-1.21	4.90e-04	THUMPD3	THUMP domain containing 3	1.19	6.05e-03	EPB41L1	erythrocyte membrane protein band 4
-1.21	3.59e-15	SH3BGRL	SH3 domain binding glutamate rich p	1.16	2.56e-02	EPS8L2	EPS8 like 2
-1.2	7.22e-06	PDXP	pyridoxal phosphatase	1.13	1.42e-01	S100A16	S100 calcium binding protein A16
-1.19	2.14e-04	COPS7B	COP9 signalosome subunit 7B	1.12	5.26e-07	LAMB3	laminin subunit beta 3
-1.19	1.42e-04	GGA2	golgi associated, gamma adaptin ear	1.11	7.98e-02	CD59	CD59 molecule (CD59 blood group)
-1.18	3.59e-04	PPP2CB	protein phosphatase 2 catalytic sub	1.11	4.77e-01	KRT19	keratin 19
-1.18	1.23e-08	UBE2Z	ubiquitin conjugating enzyme E2 Z	1.1	1.92e-01	JUP	junction plakoglobin
-1.18	2.61e-12	GSK3B	glycogen synthase kinase 3 beta	1.1	4.00e-03	EPCAM	epithelial cell adhesion molecule

CCND1 network, DB1, no Pearson r &gt; 0.3

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

Sorted by p values!  
Downregulated in blood cancers at low/absent CCND1 Upregulated in blood cancers at low/absent CCND1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.95	1.16e-39	IGHM	immunoglobulin heavy constant mu	2.82	7.60e-22	EMC1	ER membrane protein complex subunit
-3.05	4.73e-36	PLD4	phospholipase D family member 4	2.18	4.65e-16	NVL	nuclear VCP like
-2.54	7.39e-23	TCL1A	TCL1 family AKT coactivator A	2.5	1.64e-14	ROCK1	Rho associated coiled-coil containi
-2.33	1.35e-19	UCHL1	ubiquitin C-terminal hydrolase L1	2.66	4.49e-14	SEC63	SEC63 homolog, protein translocatio
-2.11	2.19e-19	HLA-DPB1	major histocompatibility complex, c	2.6	2.93e-13	ATP13A1	ATPase 13A1
-1.72	6.85e-19	CRIP1	cysteine rich protein 1	2.52	8.34e-13	LAS1L	LAS1 like ribosome biogenesis facto
-1.51	2.59e-18	DPEP3	dipeptidase 3	2.53	2.70e-12	POLR1F	RNA polymerase I subunit F
-0.07	9.10e-18	PPIA	peptidylprolyl isomerase A	2.5	4.88e-12	DCAF7	DDB1 and CUL4 associated factor 7
-2.84	9.43e-17	TRIM72	tripartite motif containing 72	2.21	9.97e-12	XPO7	exportin 7
-0.06	4.37e-15	HSPE1	heat shock protein family E (Hsp10)	2.15	1.89e-11	VCPIP1	valosin containing protein interact
-1.38	2.98e-14	HSPB1	heat shock protein family B (small)	2.42	2.17e-11	TASOR	transcription activation suppressor
-1.39	3.92e-14	PDLM1	PDZ and LIM domain 1	2.64	2.17e-11	DBT	dihydrolipoamide branched chain tra
-1.93	5.61e-13	CD70	CD70 molecule	2.61	2.47e-11	CMAS	cytidine monophosphate N-acetylneur
-1.79	1.81e-12	TSTD1	thiosulfate sulfurtransferase like	2.77	1.24e-10	DNAJC19	DnaJ heat shock protein family (Hsp
-2.45	2.70e-12	ADD2	adducin 2	2.42	3.92e-10	SDF2L1	stromal cell derived factor 2 like
-1.54	1.98e-11	MZB1	marginal zone B and B1 cell specifi	2.52	9.10e-10	HMGCL	3-hydroxy-3-methylglutaryl-CoA lyas
-2.15	5.00e-11	SIT1	signaling threshold regulating tran	2.11	1.88e-09	STAU2	staufen double-stranded RNA binding
-1.94	1.65e-10	CCDC50	coiled-coil domain containing 50	2.24	1.88e-09	TEX264	testis expressed 264, ER-phagy rece
-1.99	2.53e-10	HLA-DQB1	major histocompatibility complex, c	2.24	2.35e-09	GMPR2	guanosine monophosphate reductase 2
-2.03	3.50e-10	MARCKS	myristoylated alanine rich protein	2.59	2.35e-09	KPNA6	karyopherin subunit alpha 6
-2.31	5.45e-10	ALDH2	aldehyde dehydrogenase 2 family mem	2.14	2.35e-09	MRPS25	mitochondrial ribosomal protein S25
-1.79	1.73e-09	QPRT	quinolinate phosphoribosyltransfера	2.41	5.66e-09	LARS2	leucyl-tRNA synthetase 2, mitochond
-1.38	2.42e-09	LSP1	lymphocyte specific protein 1	2.59	5.93e-09	NLE1	notchless homolog 1
-2.23	5.81e-09	MS4A1	membrane spanning 4-domains A1	1.91	7.58e-09	ANKFY1	ankyrin repeat and FYVE domain cont
-1.91	1.15e-08	SERPINB9	serpin family B member 9	2.37	7.58e-09	CHD1L	chromodomain helicase DNA binding p
-2.51	1.93e-08	HIP1	huntingtin interacting protein 1	2.25	7.58e-09	BUD13	BUD13 homolog
-1.5	5.31e-08	TMEM123	transmembrane protein 123	2.46	7.58e-09	ERAL1	Era like 12S mitochondrial rRNA cha
-1.91	2.19e-07	HLA-DPA1	major histocompatibility complex, c	2	8.04e-09	TGOLN2	trans-golgi network protein 2
-1.31	2.32e-07	IRAG2	inositol 1,4,5-triphosphate recepto	1.86	8.04e-09	ARIH1	ariadne RBR E3 ubiquitin protein li
-2.13	2.39e-07	CD79B	CD79b molecule	2.08	1.33e-08	RABGGTA	Rab geranylgeranyltransferase subun
-1.8	4.25e-07	UBE2D3	ubiquitin conjugating enzyme E2 D3	2.07	1.49e-08	UBE4A	ubiquitination factor E4A
-2.03	6.00e-07	CLIP2	CAP-Gly domain containing linker pr	1.85	1.60e-08	PHF3	PHD finger protein 3
-1.19	6.00e-07	PNMT	phenylethanolamine N-methyltransfer	1.89	1.67e-08	KPNA1	karyopherin subunit alpha 1
-1.55	7.39e-07	CKAP4	cytoskeleton associated protein 4	2.72	1.92e-08	RHOT1	ras homolog family member T1
-2.36	7.39e-07	KANK1	KN motif and ankyrin repeat domains	2.57	1.92e-08	ALKB5	alkB homolog 5, RNA demethylase
-2.4	7.52e-07	ABLM1	actin binding LIM protein 1	2.13	3.57e-08	NDUFB5	NADH:ubiquinone oxidoreductase subu
-2.16	9.58e-07	PSME4	proteasome activator subunit 4	1.69	6.72e-08	KTI12	KTI12 chromatin associated homolog
-1.92	1.38e-06	CASP1	caspase 1	2.3	7.00e-08	ERBIN	erbB2 interacting protein
-1.25	2.28e-06	S100A14	S100 calcium binding protein A14	1.75	7.02e-08	MED1	mediator complex subunit 1

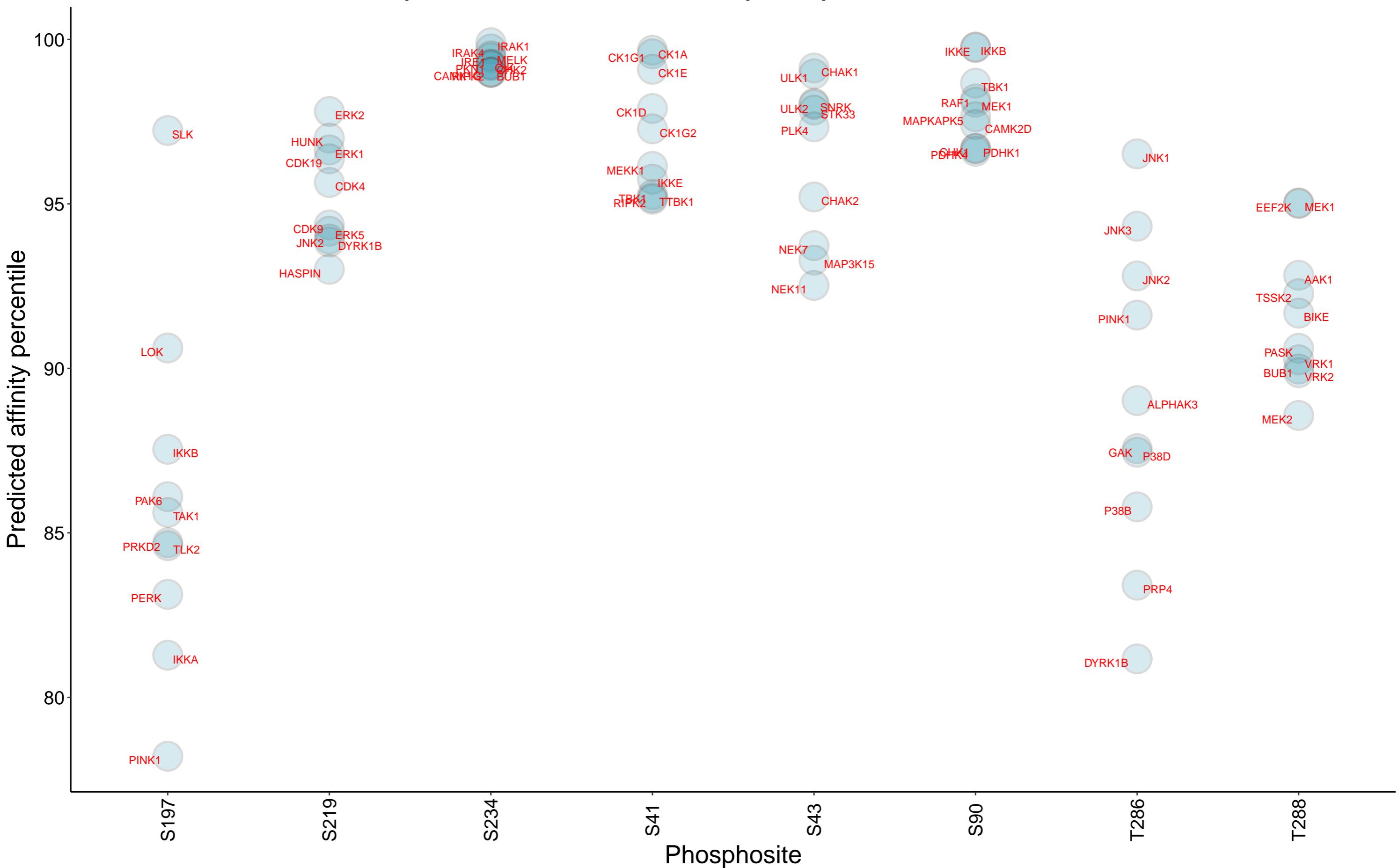
Sorted by p values!  
Downregulated in solid cancers at low/absent CCND1 Upregulated in solid cancers at low/absent CCND1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.73	3.33e-17	CDK4	cyclin dependent kinase 4	1.09	3.07e-10	LAMC2	laminin subunit gamma 2
-1.29	2.49e-15	LANC1	LanC like 1	0.8	3.20e-09	ACSL5	acyl-CoA synthetase long chain fami
-1.21	3.59e-15	SH3BGRL	SH3 domain binding glutamate rich p	1.07	1.26e-07	SERPINB5	serpin family B member 5
-1.27	5.44e-15	PBK	PDZ binding kinase	0.75	2.32e-07	LCN2	lipocalin 2
-1.25	1.67e-14	CBL	Cbl proto-oncogene	1.02	4.64e-07	ERAP2	endoplasmic reticulum aminopeptidas
-1.01	1.01e-12	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.82	4.96e-07	PCDH1	protocadherin 1
-1.18	2.61e-12	GSK3B	glycogen synthase kinase 3 beta	1.12	5.26e-07	LAMB3	laminin subunit beta 3
-1.22	2.61e-12	PFKM	phosphofructokinase, muscle	1.25	1.18e-06	MET	MET proto-oncogene, receptor tyrosi
-0.99	4.40e-12	CBR3	carbonyl reductase 3	0.7	3.06e-06	LAMA3	laminin subunit alpha 3
-0.88	4.73e-12	SORD	sorbitol dehydrogenase	1.39	3.98e-06	GPRC5A	G protein-coupled receptor class C
-1.58	1.36e-11	EXOC5	exocyst complex component 5	1.24	9.09e-06	KRT80	keratin 80
-0.89	3.66e-11	GPX4	glutathione peroxidase 4	1.4	1.16e-05	CDCP1	CUB domain containing protein 1
-0.92	9.03e-11	PAPSS1	3'-phosphoadenosine 5'-phosphosulfa	0.97	1.76e-05	PTPRA	protein tyrosine phosphatase recept
-1.14	2.27e-10	TMEM263	transmembrane protein 263	0.62	1.92e-05	PLSCR3	phospholipid scramblase 3
-1.32	4.83e-09	CERT1	ceramide transporter 1	0.96	2.17e-05	NDUFC2	NADH:ubiquinone oxidoreductase subu
-0.77	6.66e-09	ANXA6	annexin A6	0.8	2.92e-05	ITGB6	integrin subunit beta 6
-1.18	1.23e-08	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.82	3.46e-05	KRT16	keratin 16
-0.76	2.52e-08	ARL3	ADP ribosylation factor like GTPase	0.63	6.03e-05	CEACAM5	CEA cell adhesion molecule 5
-0.56	3.73e-08	DPYSL2	dihydropyrimidinase like 2	1.3	8.69e-05	MISP	mitotic spindle positioning
-0.88	4.30e-08	TBCC	tubulin folding cofactor C	0.57	1.01e-04	LOX	lysyl oxidase
-0.76	8.20e-08	BAX	BCL2 associated X, apoptosis regula	0.82	1.01e-04	TRIM29	tripartite motif containing 29
-0.87	1.23e-07	RAP1GDS1	Rap1 GTPase-GDP dissociation stimul	0.64	1.66e-04	CYP2S1	cytochrome P450 family 2 subfamily
-0.86	1.44e-07	WASL	WASP like actin nucleation promotin	0.49	1.76e-04	UTP23	UTP23 small subunit processome comp
-0.96	1.68e-07	NME2	NME/NM23 nucleoside diphosphate kin	1.1	2.32e-04	TACSTD2	tumor associated calcium signal tra
-1.03	3.58e-07	YTHDF3	YTH N6-methyladenosine RNA binding	0.93	2.39e-04	RAB25	RAB25, member RAS oncogene family
-1.09	3.73e-07	CNOT2	CCR4-NOT transcription complex subu	1.22	2.46e-04	SPINT1	serine peptidase inhibitor, Kunitz
-1.14	4.65e-07	TIGAR	TP53 induced glycolysis regulatory	0.51	2.47e-04	MST1R	macrophage stimulating 1 receptor
-0.96	4.65e-07	IAH1	isoamyl acetate hydrolyzing esteras	0.8	3.07e-04	SORL1	sortilin related receptor 1
-0.94	4.65e-07	ABCB6	ATP binding cassette subfamily B me	0.61	3.20e-04	FAM83B	

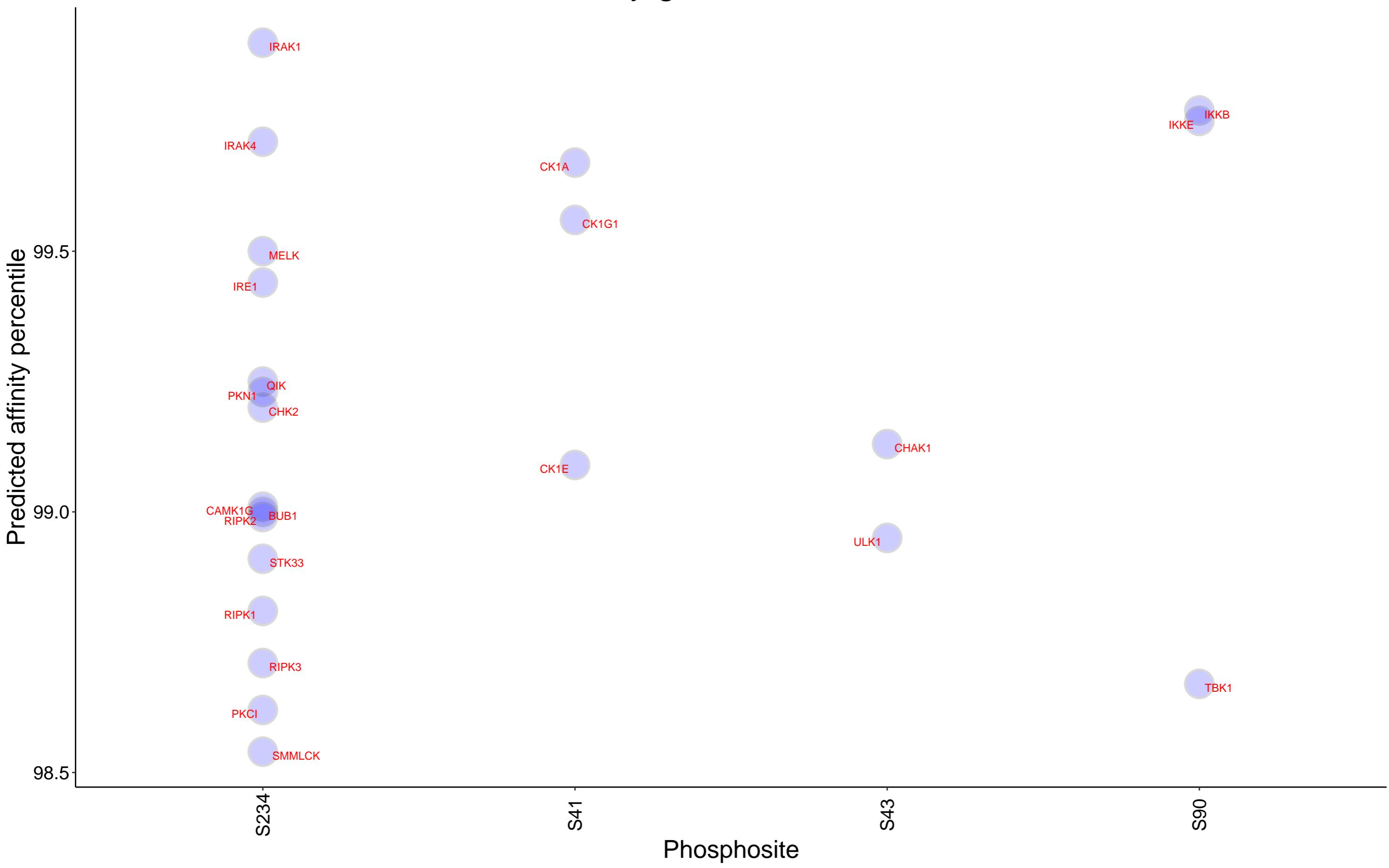
Insufficient number of paired observations in DB1 for CCND1

Insufficient number of paired observations in DB1 for CCND1

# Top 10 kinases for each phosphosite in CCND1



Kinases with affinity greater than 98.5% to CCND1



No sufficient paired observations in DB1 for CCND1