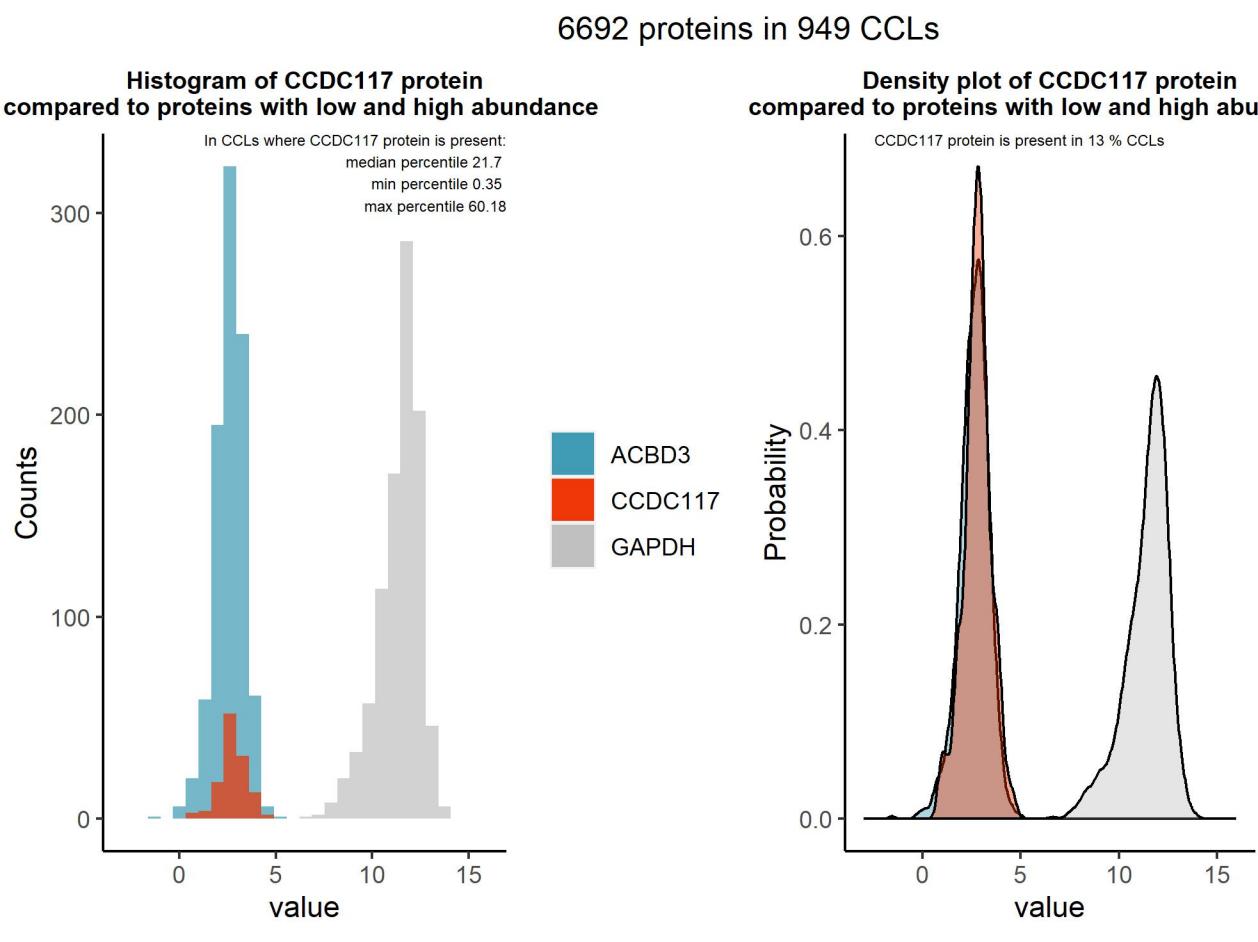


CCDC117

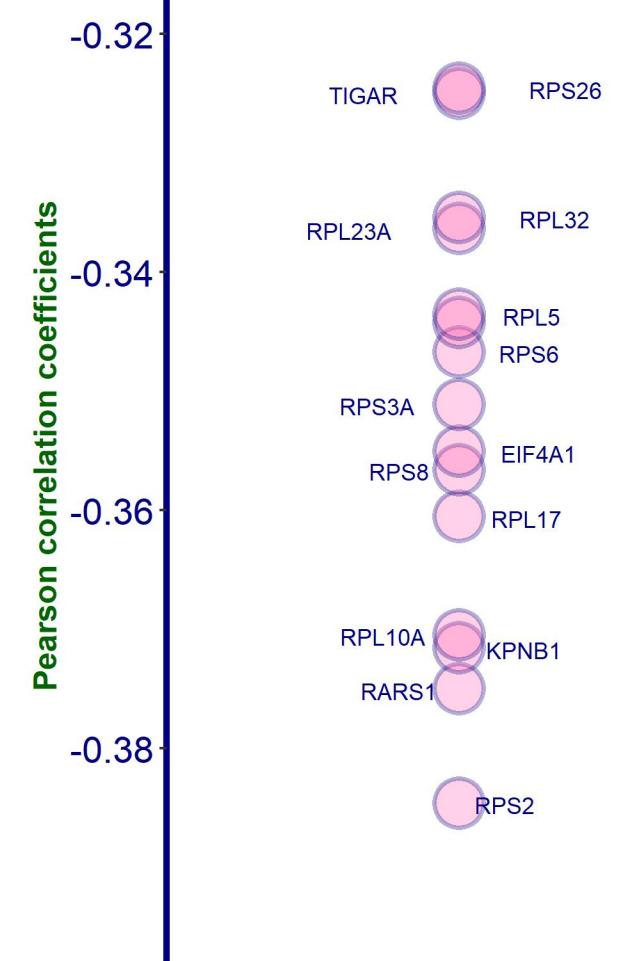
Protein name: CC117 ; UNIPROT: Q8IWD4 ; Gene name: coiled-coil domain containing 117

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

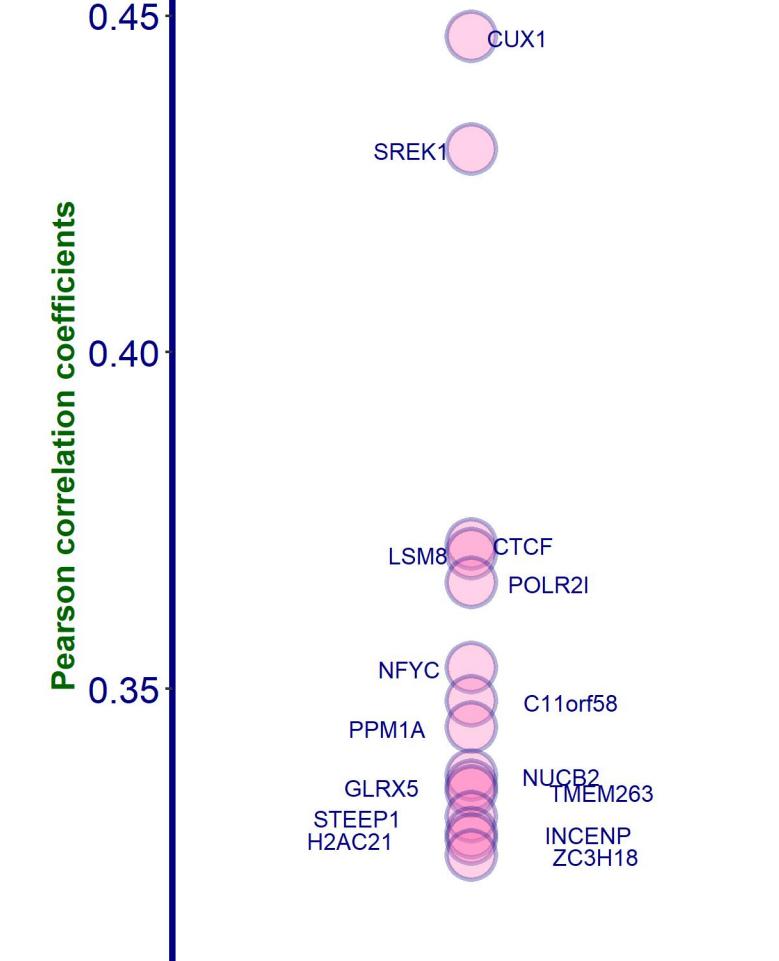
Sanger Institute Protein Database 1 (DB1), protein presence is certain



Top negative correlations of CCDC117 protein, DE

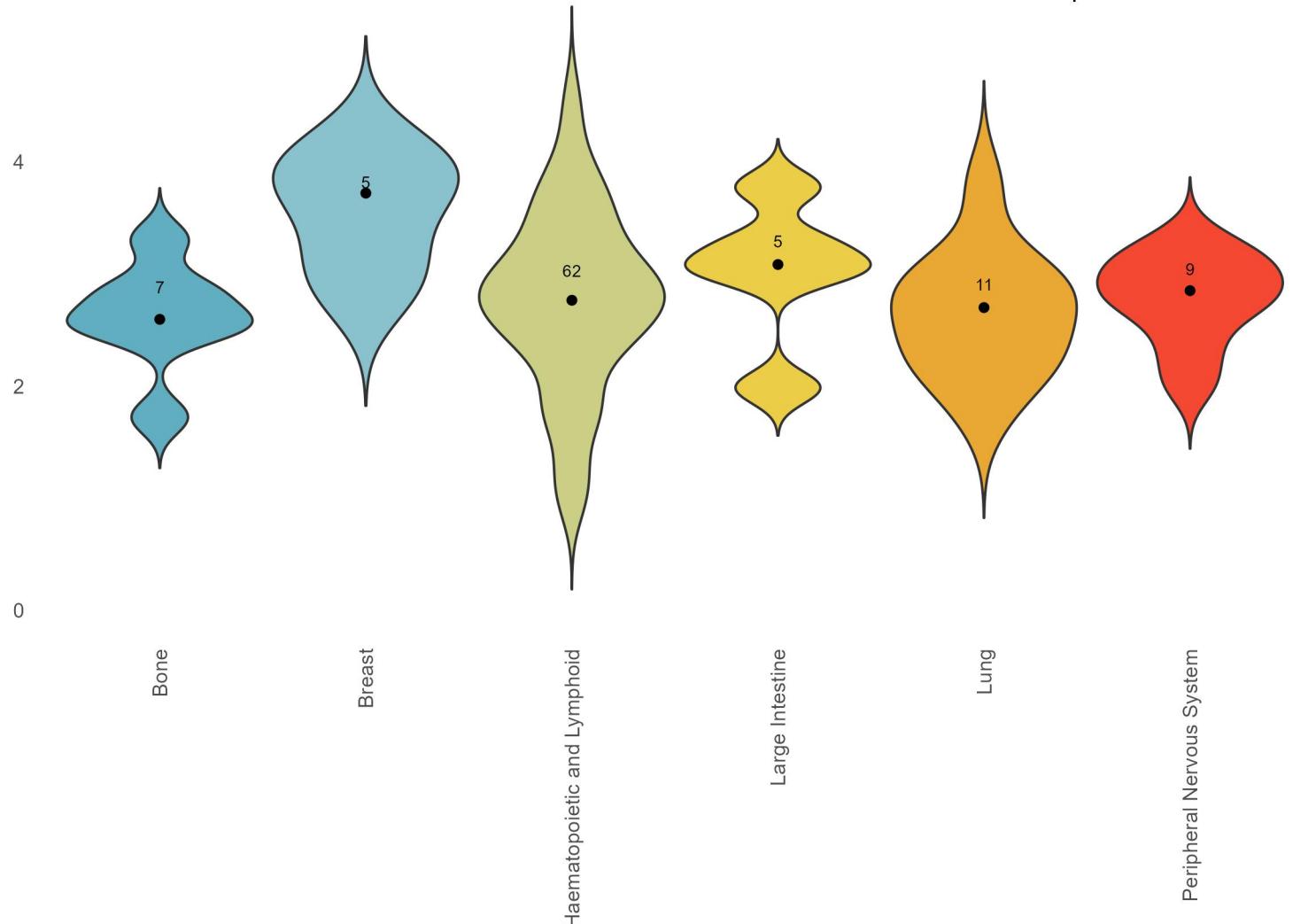


Top positive correlations of CCDC117 protein, DB



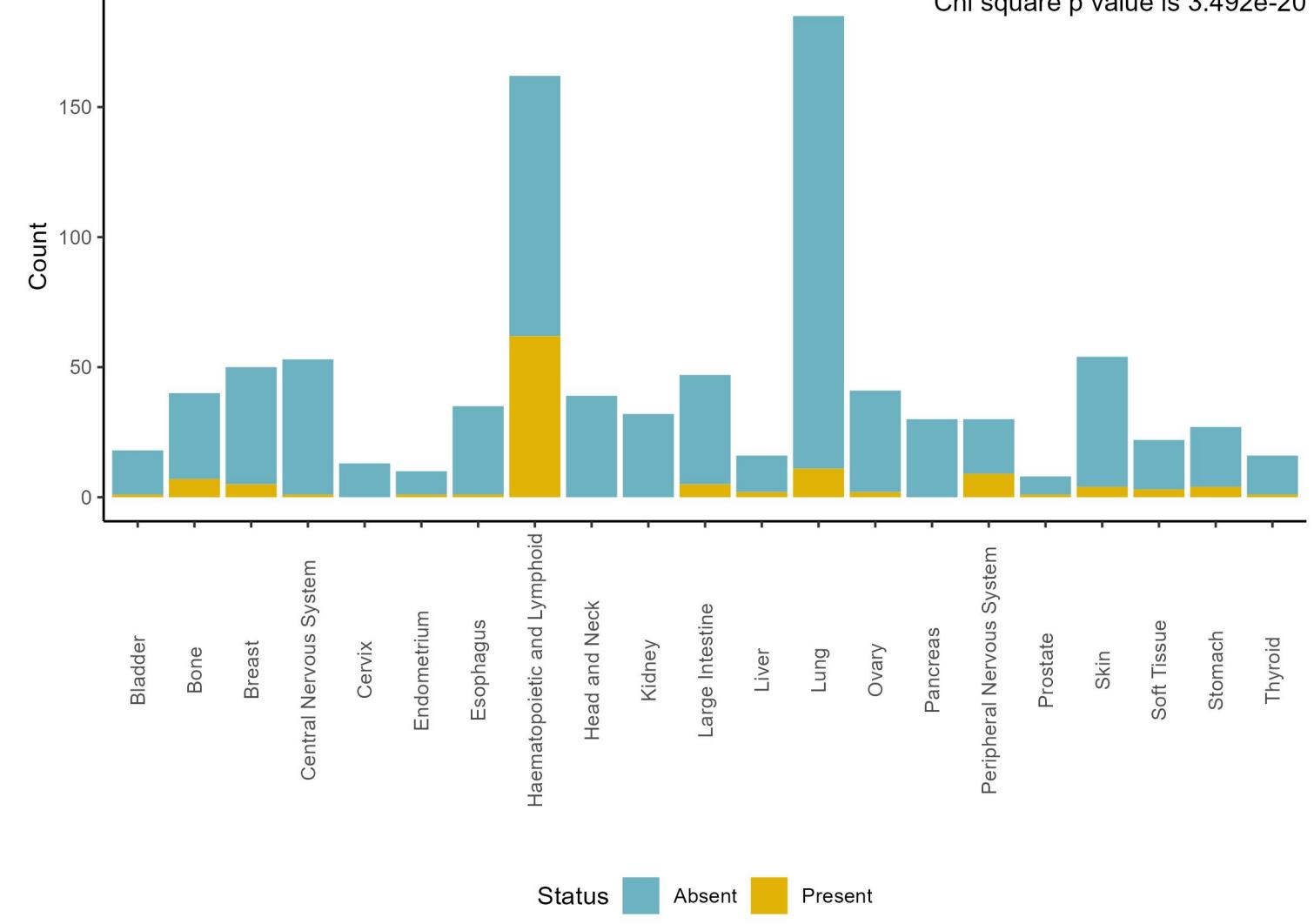
Amount of CCDC117 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 4.486e-01



Present and absent CCDC117 protein counts by tissue, DB1

Chi square p value is 3.492e-20

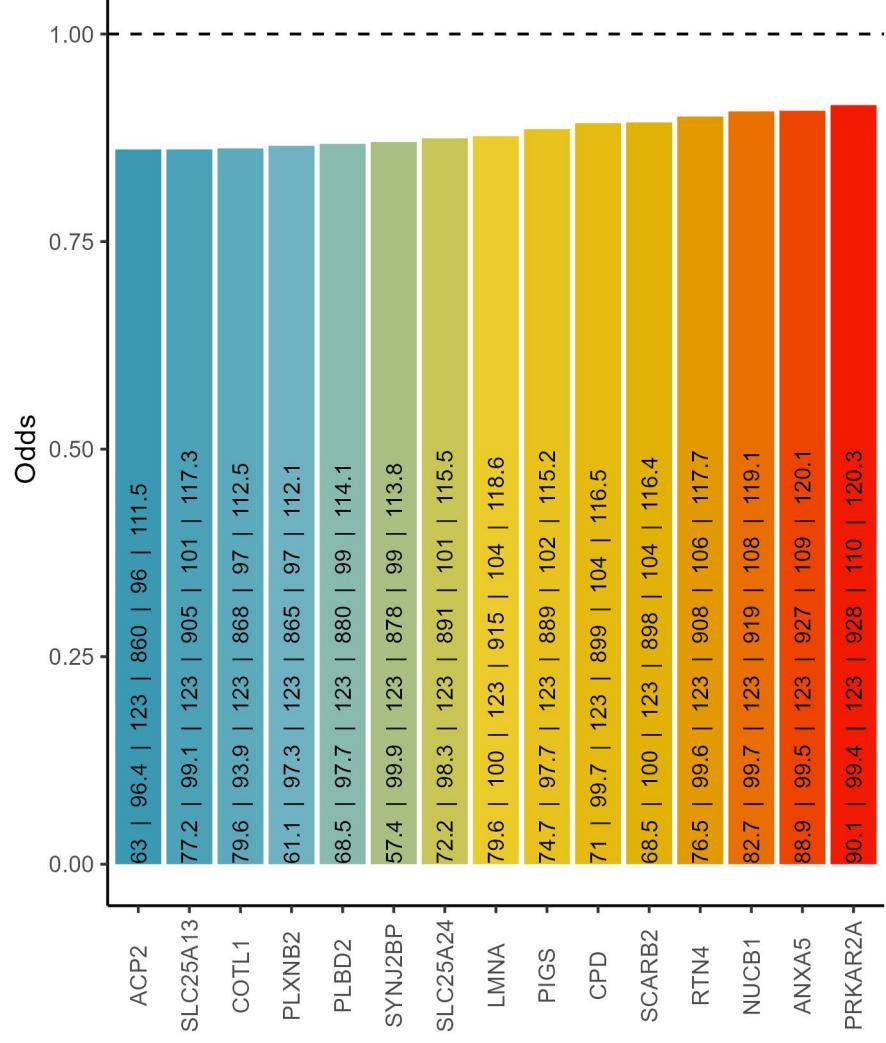


Cooccurrence with CCDC117 protein, DB1

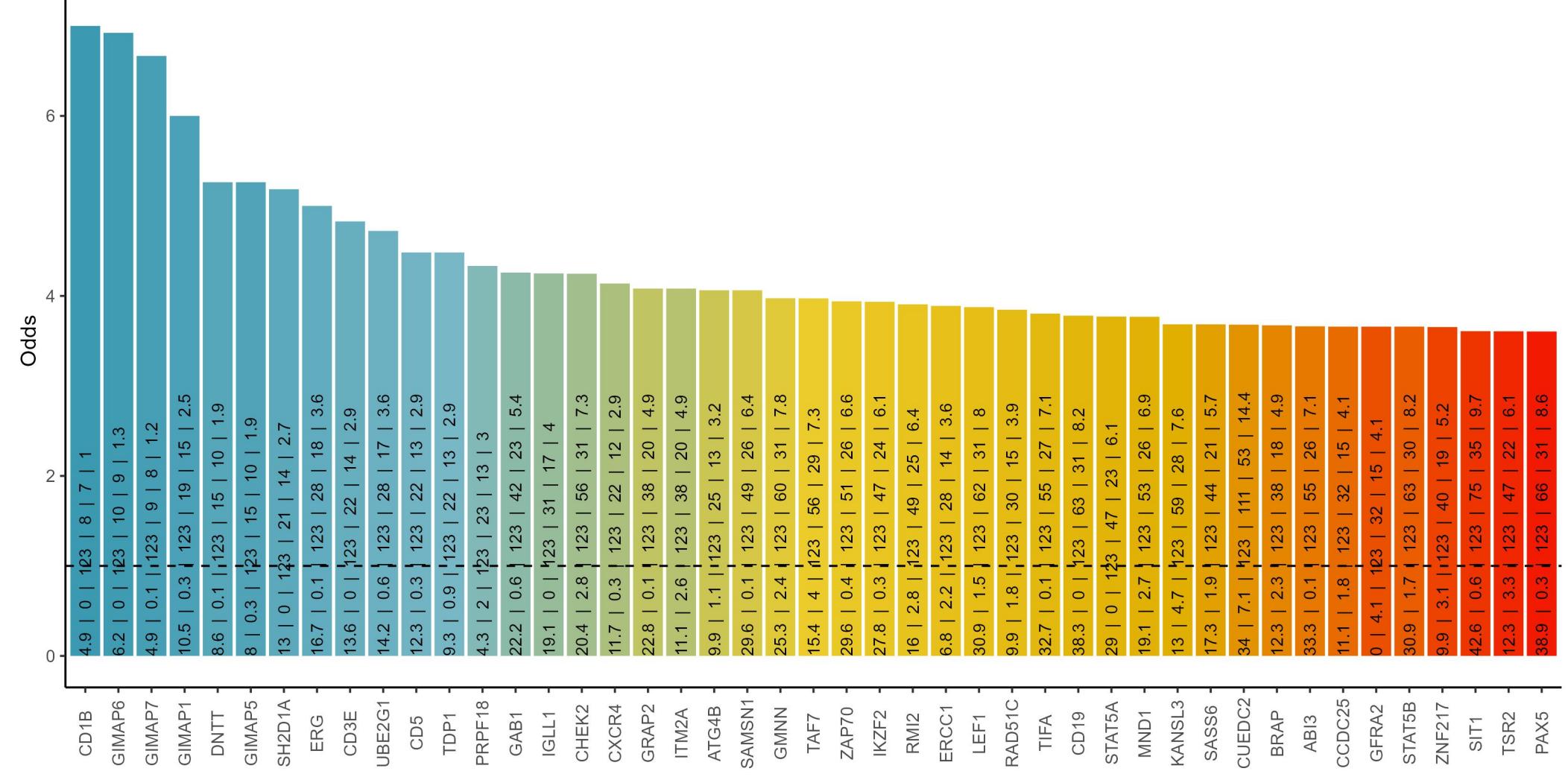
% of CCDC117 in blood cancers: 38.3 ; % of CCDC117 in solid cancers: 7.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CCDC117 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

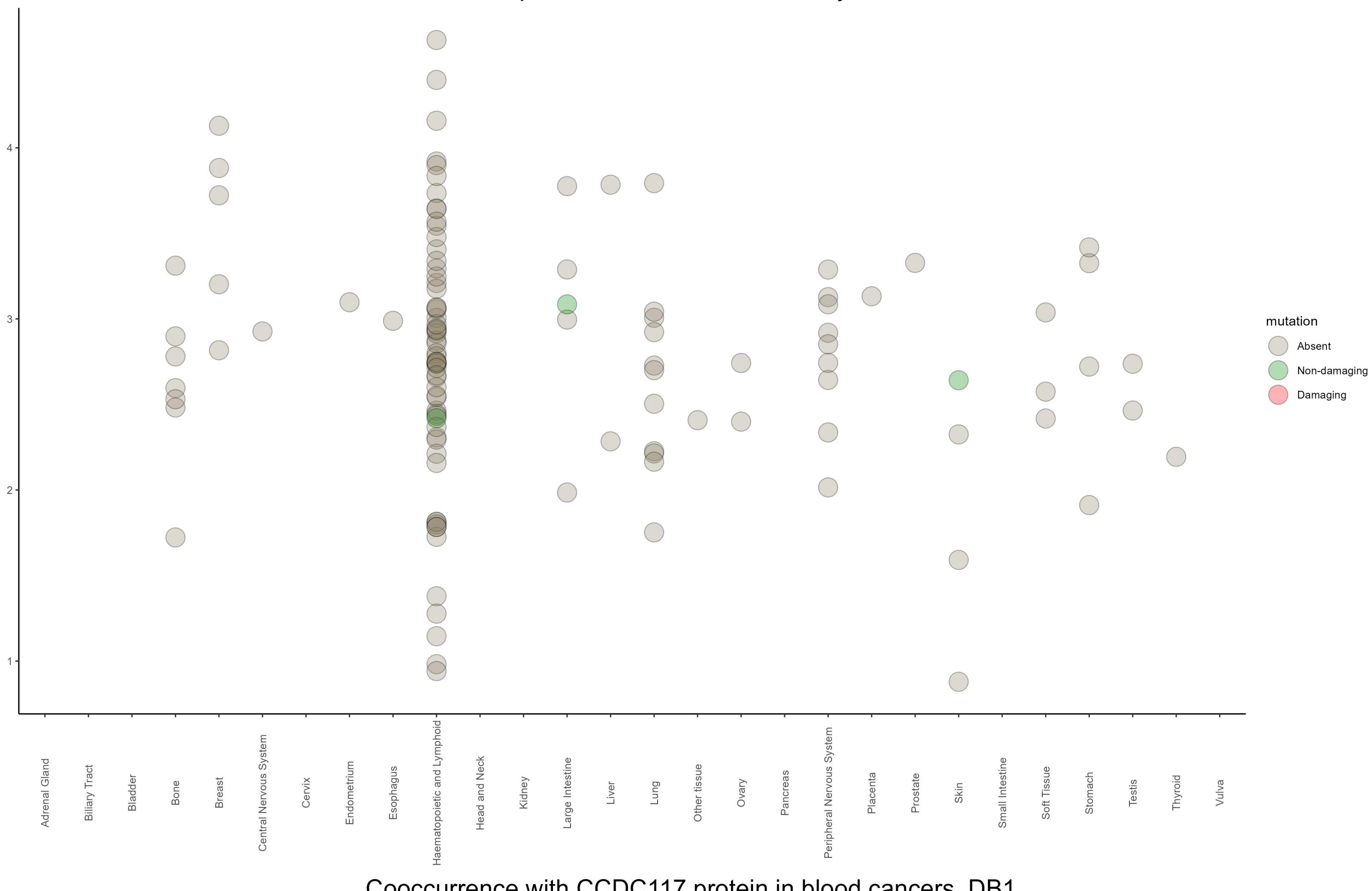
Negative cooccurrence



Positive cooccurrence



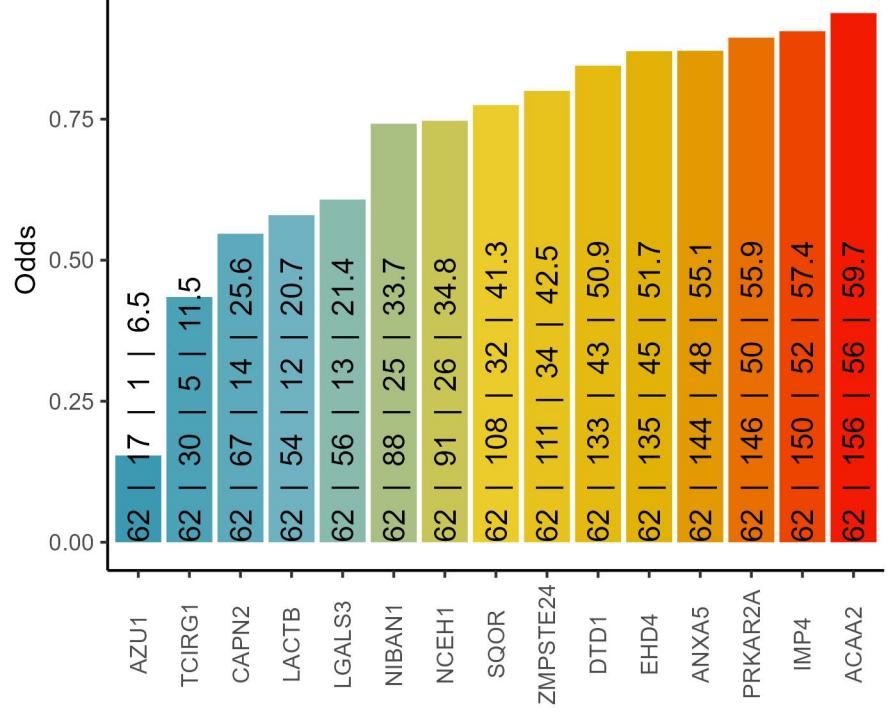
Amount of CCDC117 protein and mutation status by tissue, DB1



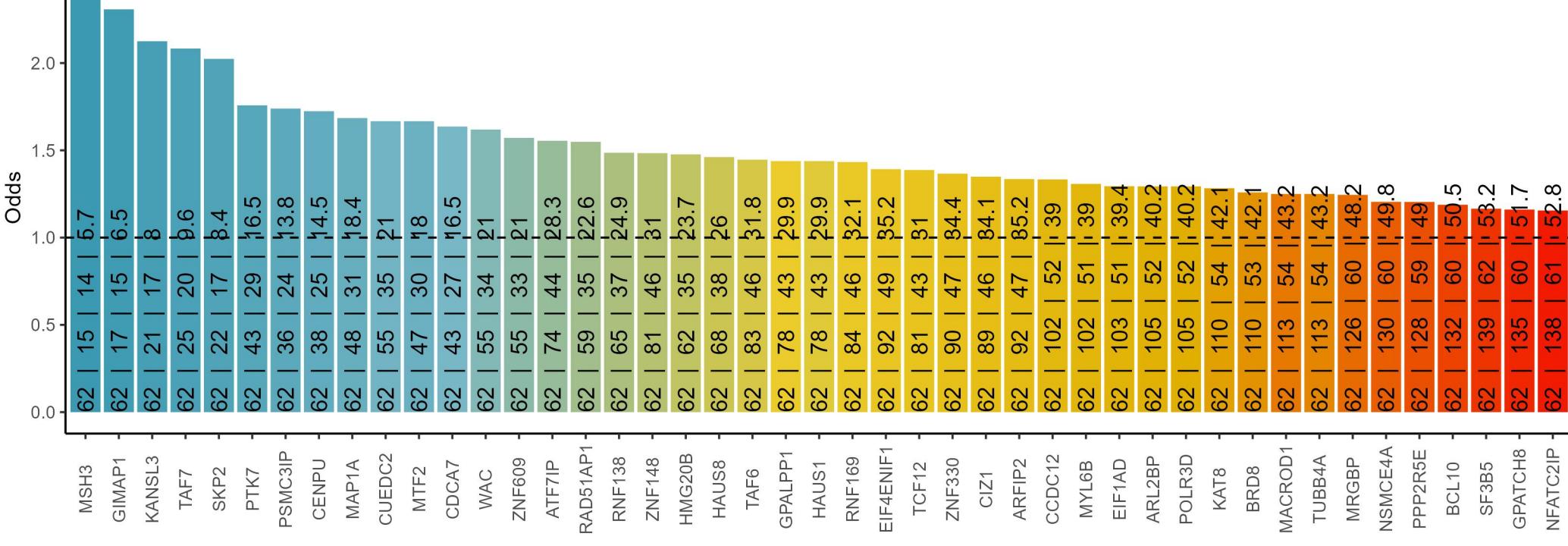
Cooccurrence with CCDC117 protein in blood cancers, DB1

The text in the bars: incidence of CCDC117 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



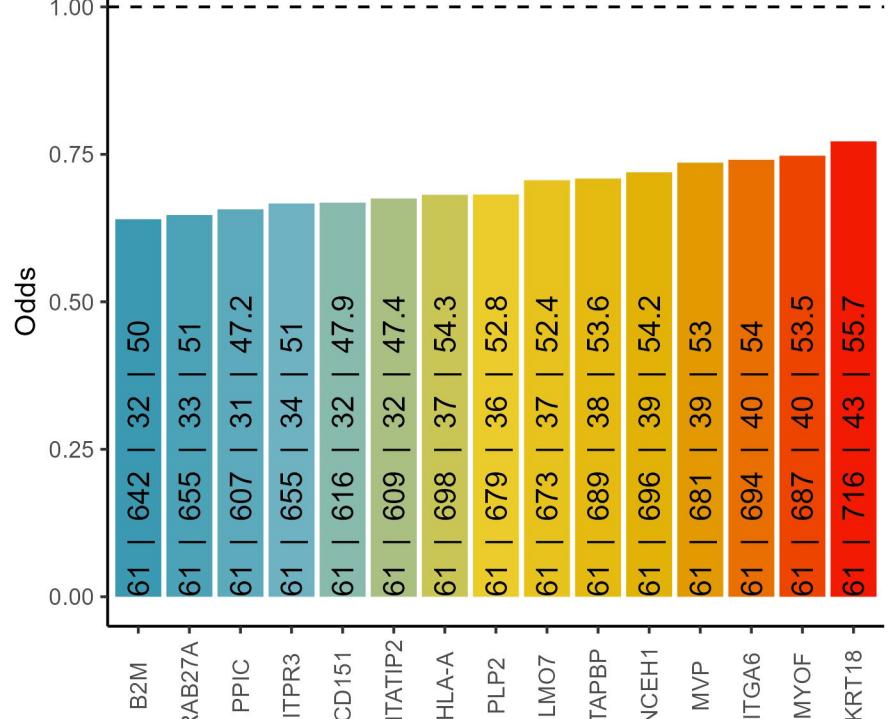
Positive cooccurrence



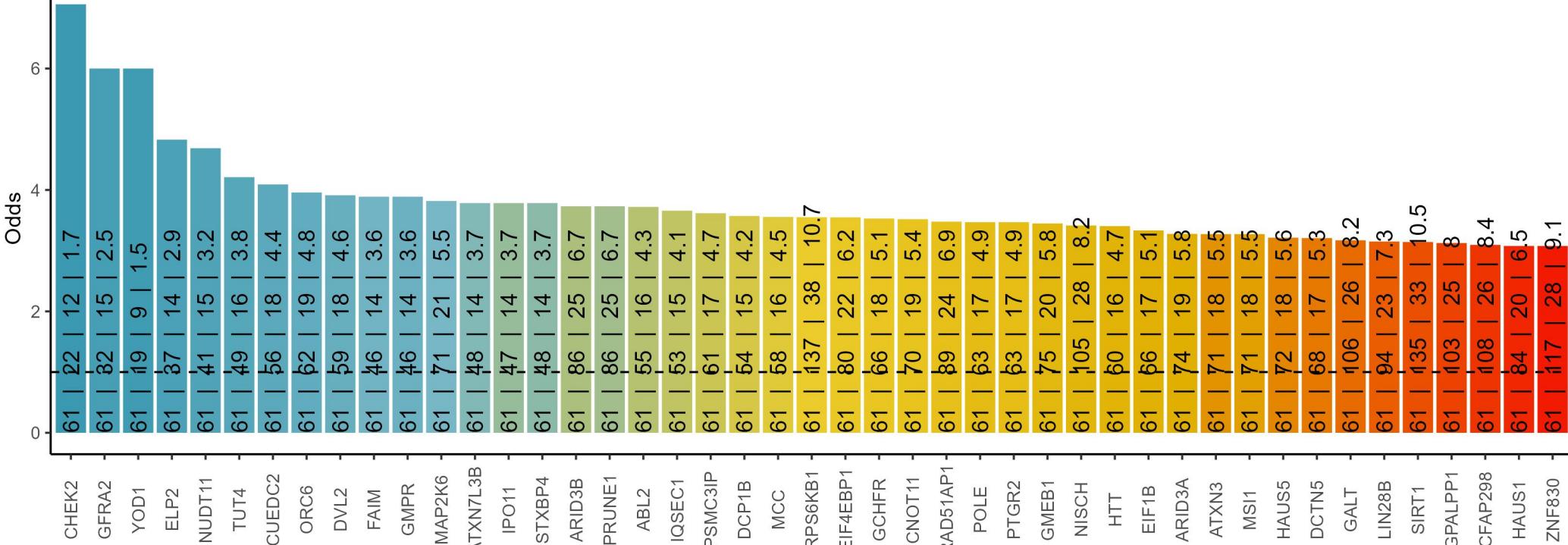
Cooccurrence with CCDC117 protein in solid cancers, DB1

The text in the bars: incidence of CCDC117 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

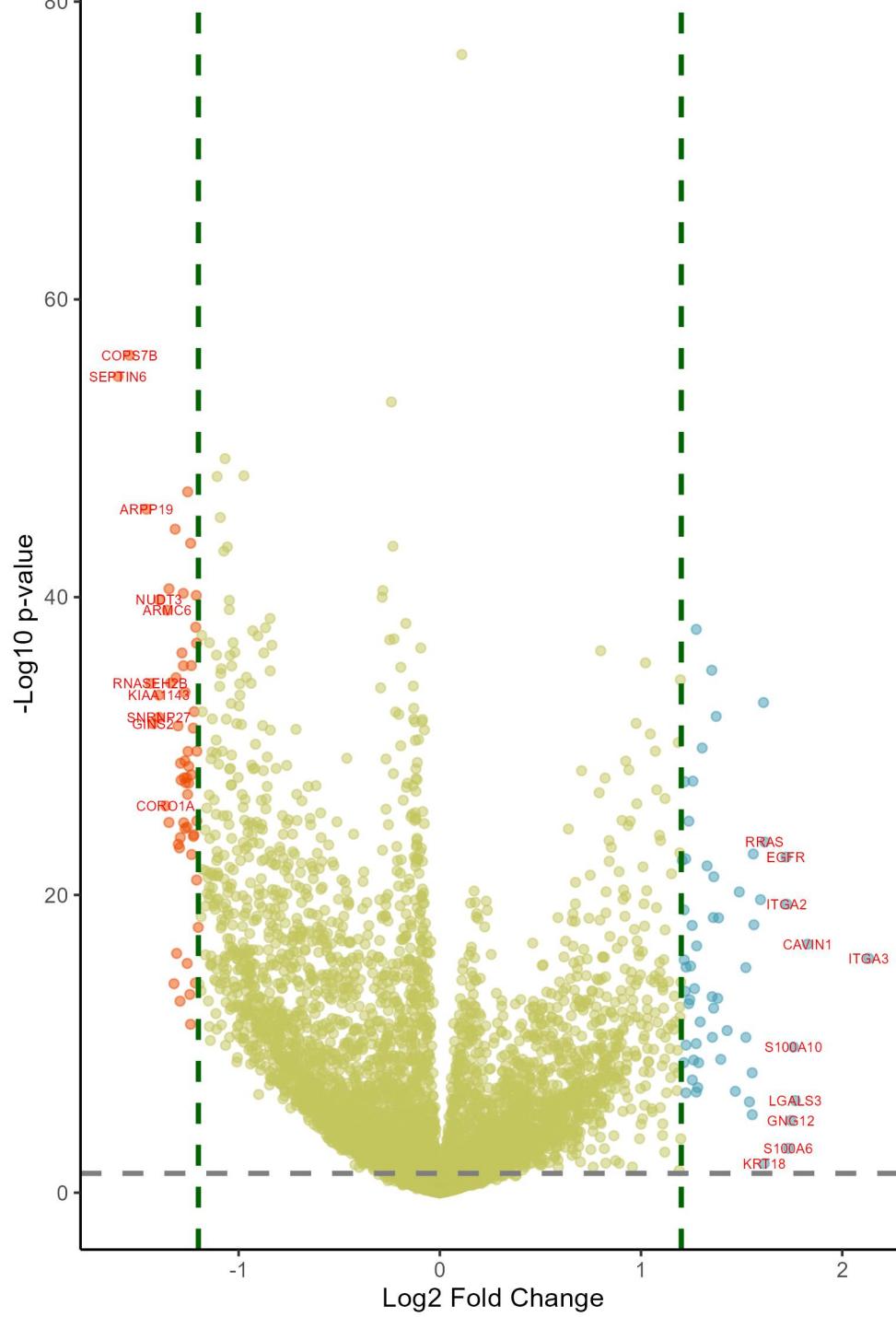
Negative cooccurrence



Positive cooccurrence

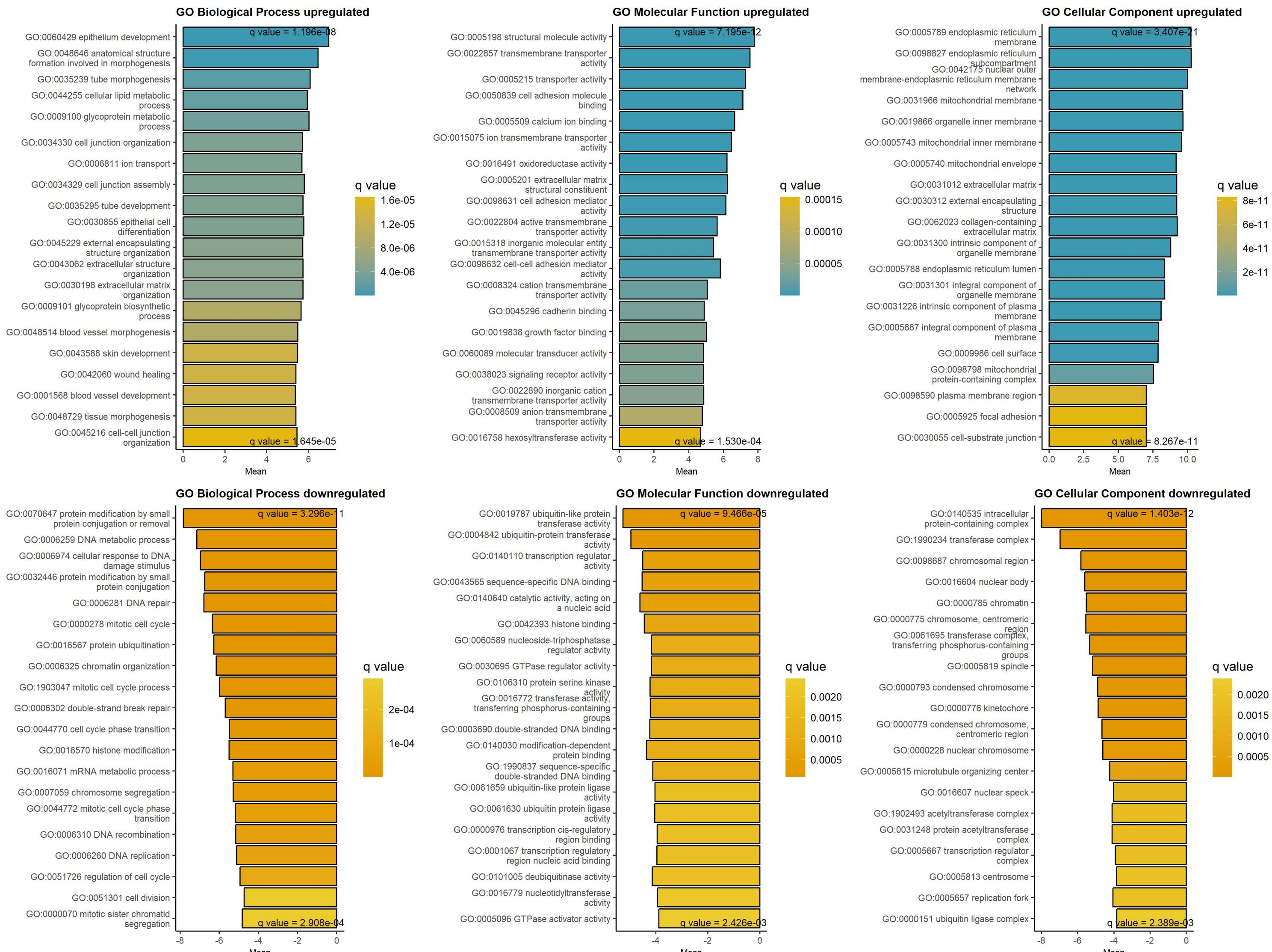


Downregulated at low/absent CCDC117 Upregulated at low/absent CCDC117

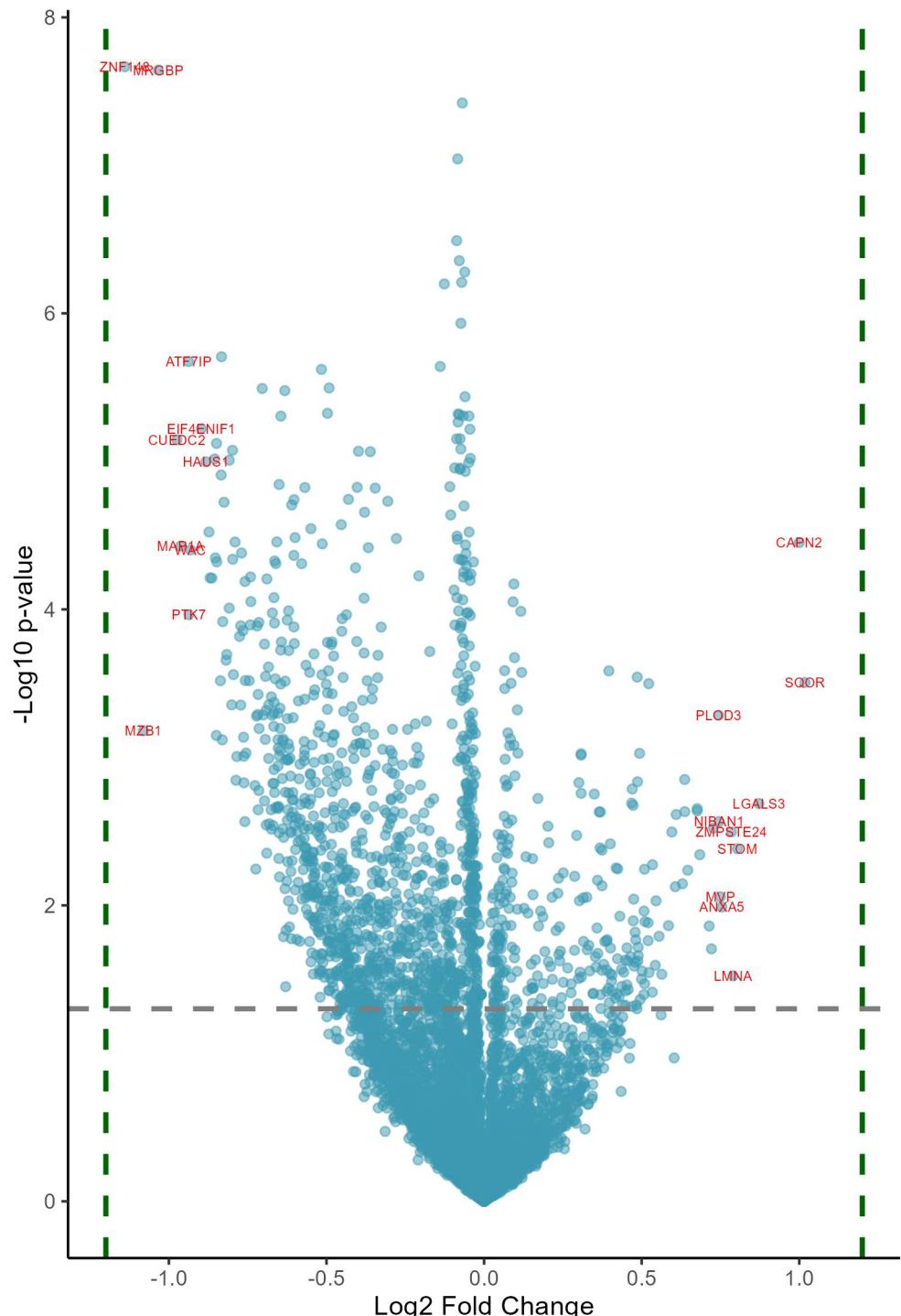


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.6	2.49e-52	SEPTIN6	septin 6	2.13	1.98e-15	ITGA3	integrin subunit alpha 3
-1.54	1.25e-53	COPS7B	COP9 signalosome subunit 7B	1.83	2.47e-16	CAVIN1	caveolae associated protein 1
-1.46	8.19e-44	ARPP19	cAMP regulated phosphoprotein 19	1.77	2.03e-06	LGALS3	galectin 3
-1.44	6.76e-33	RNASEH2B	ribonuclease H2 subunit B	1.76	8.16e-10	S100A10	S100 calcium binding protein A10
-1.43	2.40e-30	GINS2	GINS complex subunit 2	1.74	3.59e-05	GNG12	G protein subunit gamma 12
-1.4	3.74e-32	KIAA1143	KIAA1143	1.73	2.00e-03	S100A6	S100 calcium binding protein A6
-1.4	1.01e-30	SNRNP27	small nuclear ribonucleoprotein U4/U6/U11	1.72	7.06e-19	ITGA2	integrin subunit alpha 2
-1.39	4.52e-38	NUDT3	nudix hydrolase 3	1.72	7.27e-22	EGFR	epidermal growth factor receptor
-1.36	4.17e-25	CORO1A	coronin 1A	1.62	8.11e-23	RRAS	RAS related
-1.35	1.99e-37	ARMC6	armadillo repeat containing 6	1.61	1.75e-02	KRT18	keratin 18
-1.35	4.66e-24	SSNA1	SS nuclear autoantigen 1	1.61	1.15e-31	EPHA2	EPH receptor A2
-1.35	1.07e-38	RWDD1	RWD domain containing 1	1.59	3.67e-19	PPIC	peptidylprolyl isomerase C
-1.34	6.58e-33	NACA2	nascent polypeptide associated comp	1.56	1.46e-17	CAV1	caveolin 1
-1.32	7.75e-14	GMFG	glia maturation factor gamma	1.56	4.63e-22	NT5E	5'-nucleotidase ecto
-1.32	1.50e-42	BLMH	bleomycin hydrolase	1.55	1.55e-05	PLP2	proteolipid protein 2
-1.31	2.99e-33	UBFD1	ubiquitin family domain containing	1.55	3.51e-08	MYOF	myoferlin
-1.31	9.73e-16	HCLS1	hematopoietic cell-specific Lyn sub	1.54	2.42e-06	NCEH1	neutral cholesterol ester hydrolase
-1.3	3.27e-30	SUMO2	small ubiquitin like modifier 2	1.52	1.97e-10	ITGAV	integrin subunit alpha V
-1.3	1.13e-22	EIF4ENIF1	eukaryotic translation initiation f	1.52	7.56e-15	S100A16	S100 calcium binding protein A16
-1.29	1.91e-22	FNBP1	formin binding protein 1	1.49	1.21e-19	ADAM9	ADAM metallopeptidase domain 9
-1.29	1.02e-12	MZB1	marginal zone B and B1 cell specifi	1.47	5.25e-07	FKBP9	FKBP prolyl isomerase 9
-1.29	4.19e-23	CRLF3	cytokine receptor like factor 3	1.43	7.28e-11	SFXN3	sideroflexin 3
-1.29	8.08e-28	SPAG7	sperm associated antigen 7	1.4	4.95e-09	PVR	PVR cell adhesion molecule
-1.29	9.22e-27	UBE2R2	ubiquitin conjugating enzyme E2 R2	1.39	5.24e-18	ITGB4	integrin subunit beta 4
-1.28	8.46e-35	DHFR	dihydrofolate reductase	1.38	6.75e-13	EPHX1	epoxide hydrolase 1
-1.28	1.95e-38	PDXP	pyridoxal phosphatase	1.37	8.75e-31	FNDC3B	fibronectin type III domain contain
-1.27	5.52e-34	ACYP1	acylphosphatase 1	1.36	1.26e-20	MMP14	matrix metallopeptidase 14
-1.27	4.80e-24	TSC22D4	TSC22 domain family member 4	1.36	2.82e-12	DSG2	desmoglein 2
-1.27	6.66e-27	POU2F1	POU class 2 homeobox 1	1.36	5.04e-18	GPX8	glutathione peroxidase 8 (putative)

GAGE analysis on upregulated and downregulated proteins at low/absent CCDC117 protein, DB1



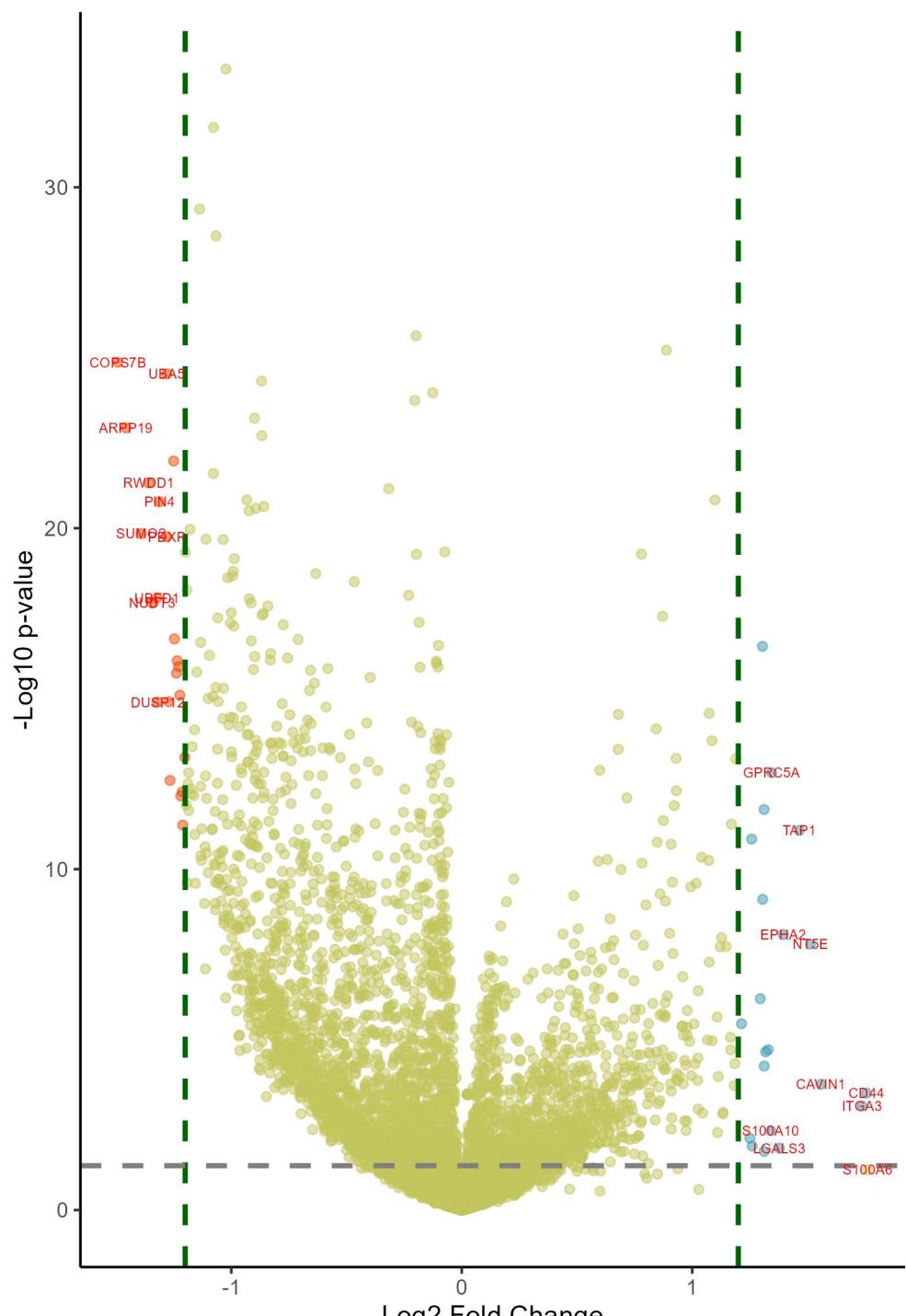
p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent CCDC117 Upregulated in blood cancers at low/absent CCDC117

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	5.04e-05	ZNF148	zinc finger protein 148	1.02	1.14e-02	SQOR	sulfide quinone oxidoreductase
-1.08	1.81e-02	MZB1	marginal zone B and B1 cell specific	1	3.36e-03	CAPN2	calpain 2
-1.03	5.04e-05	MRGBP	MRG domain binding protein	0.87	3.38e-02	LGALS3	galectin 3
-0.97	1.53e-03	CUEDC2	CUE domain containing 2	0.8	5.07e-02	STOM	stomatin
-0.96	3.41e-03	MAP1A	microtubule associated protein 1A	0.79	1.37e-01	LMNA	lamin A/C
-0.94	1.06e-03	ATF7IP	activating transcription factor 7 i	0.78	4.31e-02	ZMPSTE24	zinc metallopeptidase STE24
-0.94	6.13e-03	PTK7	protein tyrosine kinase 7 (inactive)	0.75	8.61e-02	ANXA5	annexin A5
-0.93	3.52e-03	WAC	WW domain containing adaptor with c	0.75	7.90e-02	MVP	major vault protein
-0.9	1.44e-03	EIF4ENIF1	eukaryotic translation initiation f	0.75	3.94e-02	NIBAN1	niban apoptosis regulator 1
-0.88	1.65e-03	HAUS1	HAUS augmin like complex subunit 1	0.74	1.56e-02	PLD3	procollagen-lysine,2-oxoglutarate 5
-0.87	3.17e-03	GPALPP1	GPALPP motifs containing 1	0.73	4.18e-02	NCEH1	neutral cholesterol ester hydrolase
-0.87	4.17e-03	MED10	mediator complex subunit 10	0.72	1.25e-01	CBR1	carbonyl reductase 1
-0.86	4.17e-03	MACROD1	mono-ADP ribosylhydrolase 1	0.71	1.02e-01	CTS2	cathepsin Z
-0.85	1.65e-03	RNF169	ring finger protein 169	0.68	5.35e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.85	3.70e-03	TUBB4A	tubulin beta 4A class IVa	0.68	3.60e-02	TYMP	thymidine phosphorylase
-0.85	1.88e-02	SEPTIN1	septin 1	0.68	3.53e-02	SFXN3	sideroflexin 3
-0.85	1.57e-03	CCDC12	coiled-coil domain containing 12	0.65	6.11e-02	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-0.85	3.70e-03	RNF138	ring finger protein 138	0.64	3.62e-02	ARSB	arylsulfatase B
-0.84	1.12e-02	GINS1	GINS complex subunit 1	0.64	2.74e-02	LACTB	lactamase beta
-0.83	1.79e-03	ARL2BP	ADP ribosylation factor like GTPase	0.63	6.96e-02	ALG1	ALG1 chitobiosyldiphosphodolichol b
-0.83	1.06e-03	BRD8	bromodomain containing 8	0.61	3.68e-02	EHD4	EH domain containing 4
-0.83	1.94e-02	CD38	CD38 molecule	0.61	7.14e-02	PRKCD	protein kinase C delta
-0.83	6.58e-03	MAZ	MYC associated zinc finger protein	0.6	2.64e-01	LGALS1	galectin 1
-0.83	2.28e-03	POLR3D	RNA polymerase III subunit D	0.6	4.31e-02	DUSP3	dual specificity phosphatase 3
-0.82	9.33e-03	MTF2	metal response element binding tran	0.58	1.02e-01	PIGK	phosphatidylinositol glycan anchor
-0.82	8.83e-03	RANGRF	RAN guanine nucleotide release fact	0.56	1.37e-01	CA2	carbonic anhydrase 2
-0.81	1.65e-03	KAT8	lysine acetyltransferase 8	0.56	1.70e-01	PLP2	proteolipid protein 2
-0.81	5.93e-03	TCF12	transcription factor 12	0.56	1.13e-01	CSTA	cystatin A
-0.8	1.41e-02	DCAF16	DDB1 and CUL4 associated factor 16	0.55	8.10e-02	LYPLAL1	lysophospholipase like 1

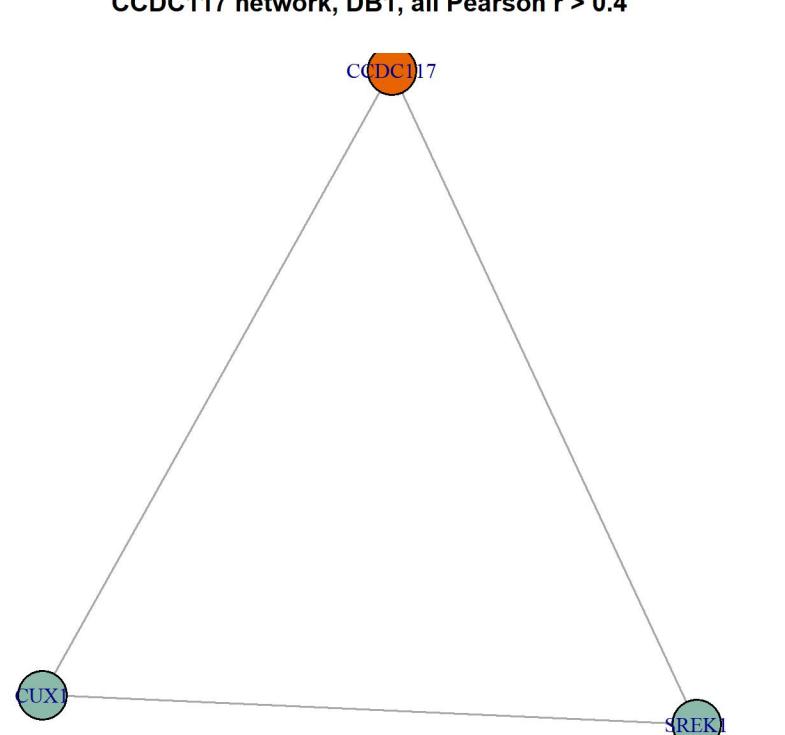
p-value < 0.05 & logFC > 1.2



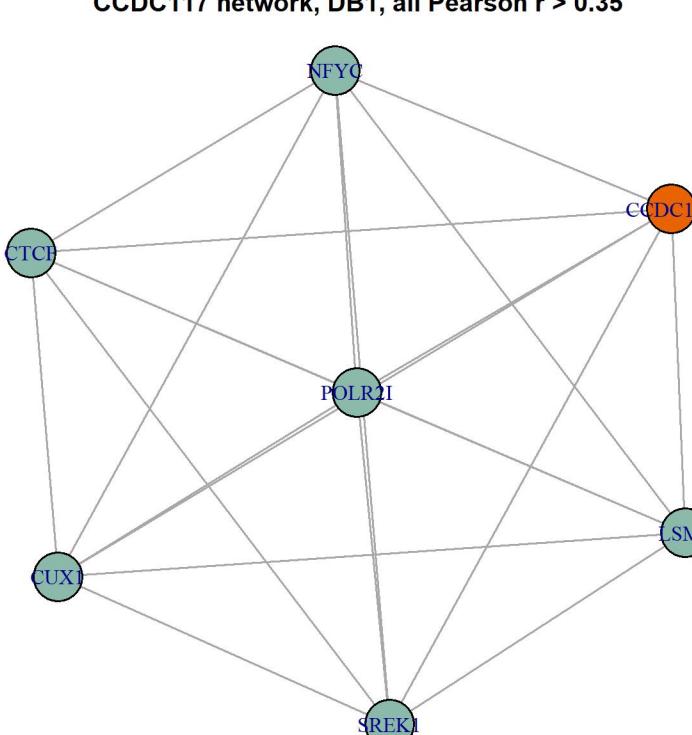
Downregulated in solid cancers at low/absent CCDC117 Upregulated in solid cancers at low/absent CCDC117

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.49	1.13e-22	COPS7B	COP9 signalosome subunit 7B	1.76	1.16e-01	S100A6	S100 calcium binding protein A6
-1.46	5.39e-21	ARPP19	cAMP regulated phosphoprotein 19	1.76	1.44e-03	CD44	CD44 molecule (Indian blood group)
-1.39	3.54e-18	SUMO2	small ubiquitin like modifier 2	1.74	2.97e-03	ITGA3	integrin subunit alpha 3
-1.36	1.74e-19	RWDD1	RWD domain containing 1	1.56	8.68e-04	CAVIN1	caveolae associated protein 1
-1.34	2.25e-16	NUDT3	nudix hydrolase 3	1.51	1.99e-07	NT5E	5'-nucleotidase ecto
-1.32	1.70e-16	UBFD1	ubiquitin family domain containing	1.46	1.96e-10	TAP1	transporter 1, ATP binding cassette
-1.32	9.42e-14	DUSP12	dual specificity phosphatase 12	1.39	1.11e-07	EPHA2	EPH receptor A2
-1.31	5.04e-19	PIN4	peptidylprolyl cis/trans isomerase,	1.38	3.42e-02	LGALS3	galectin 3
-1.28	2.19e-22	UBA5	ubiquitin like modifier activating	1.34	5.90e-12	GPRC5A	G protein-coupled receptor class C
-1.28	4.23e-18	PDXP	pyridoxal phosphatase	1.34	1.24e-02	S100A10	S100 calcium binding protein A10
-1.27	9.30e-14	QPRT	quinolinate phosphoribosyltransfera	1.33	1.13e-04	CAV1	caveolin 1
-1.27	9.35e-12	SNRNP27	small nuclear ribonucleoprotein U4/U6	1.32	1.28e-04	EGFR	epidermal growth factor receptor
-1.25	4.44e-20	CCDC43	coiled-coil domain containing 43	1.31	2.97e-04	ITGA2	integrin subunit alpha 2
-1.25	2.05e-15	MAP2K2	mitogen-activated protein kinase ki	1.31	4.10e-02	HLA-A	major histocompatibility complex, c
-1.24	1.51e-14	RPE	ribulose-5-phosphate-3-epimerase	1.31	5.60e-11	TAP2	transporter 2, ATP binding cassette
-1.23	7.52e-15	TXLNG	taxilin gamma	1.31	1.30e-08	CD109	CD109 molecule
-1.23	1.07e-14	C11orf54	chromosome 11 open reading frame 54	1.3	3.13e-15	AXL	AXL receptor tyrosine kinase
-1.22	6.23e-14	AAMDC	adipogenesis associated Mth938 doma	1.3	5.32e-06	RRAS	RAS related
-1.22	2.39e-11	KIAA1143	KIAA1143	1.26	3.04e-02	PLP2	proteolipid protein 2
-1.21	1.89e-11	CKS1B	CDC28 protein kinase regulatory sub	1.26	3.39e-10	FNDC3B	fibronectin type III domain contain
-1.21	1.46e-10	GGA1	golgi associated, gamma adaptin ear	1.25	1.94e-02	NCEH1	neutral cholesterol ester hydrolase
-1.2	2.32e-12	HPF1	histone PARylation factor 1	1.21	2.40e-05	HLA-B	major histocompatibility complex, c
-1.2	1.05e-17	PPM1B	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.19	2.51e-12	EHD2	EH domain containing 2
-1.2	4.18e-11	SEPTIN6	septin 6	1.19	2.58e-04	PPIC	peptidylprolyl isomerase C
-1.19	1.06e-16	BLMH	bleomycin hydrolase	1.18	9.35e-04	S100A16	S100 calcium binding protein A16
-1.19	4.78e-09	EIF4ENIF1	eukaryotic translation initiation f	1.17	1.40e-10	KRT80	keratin 80
-1.19	1.13e-11	HDHD2	haloacid dehalogenase like hydrolas	1.17	1.14e-04	CD59	CD59 molecule (CD59 blood group)
-1.18	5.91e-12	ARMC6	armadillo repeat containing 6	1.17	5.36e-05	ITGB4	integrin subunit beta 4
-1.18	5.95e-11	PPP6R2	protein phosphatase 6 regulatory su	1.15	2.31e-07	KRT17	keratin 17

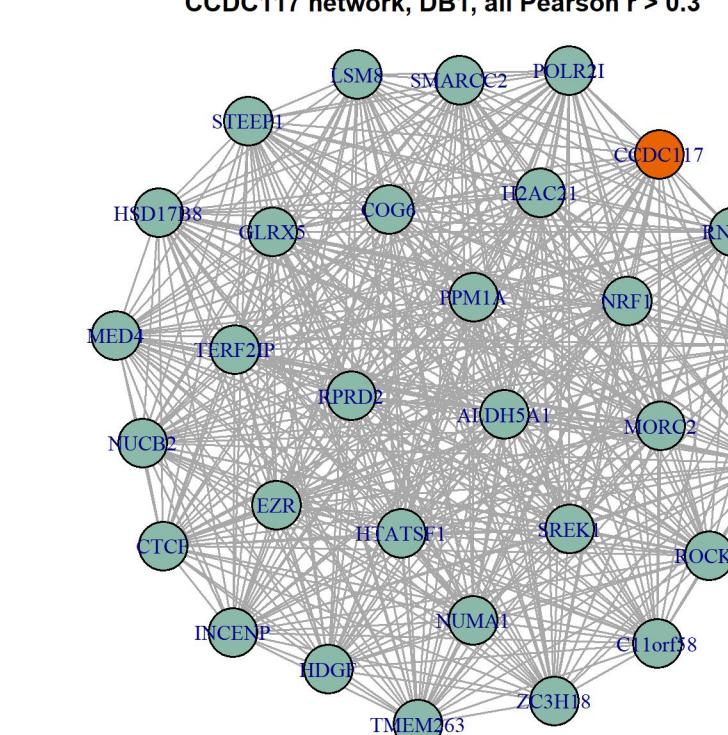
CCDC117 network, DB1, all Pearson r > 0.4



CCDC117 network, DB1, all Pearson r > 0.35

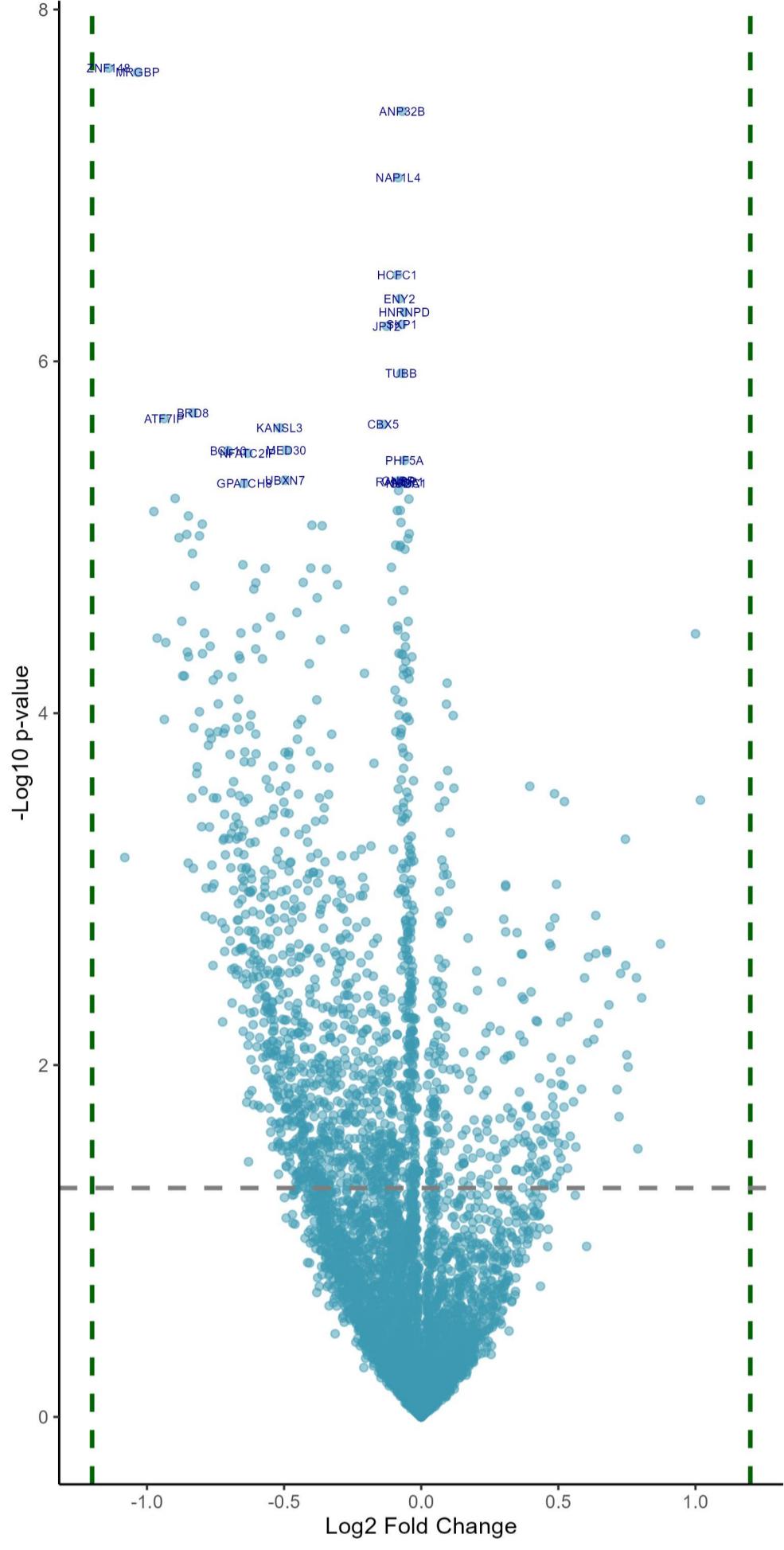


CCDC117 network, DB1, all Pearson r > 0.3

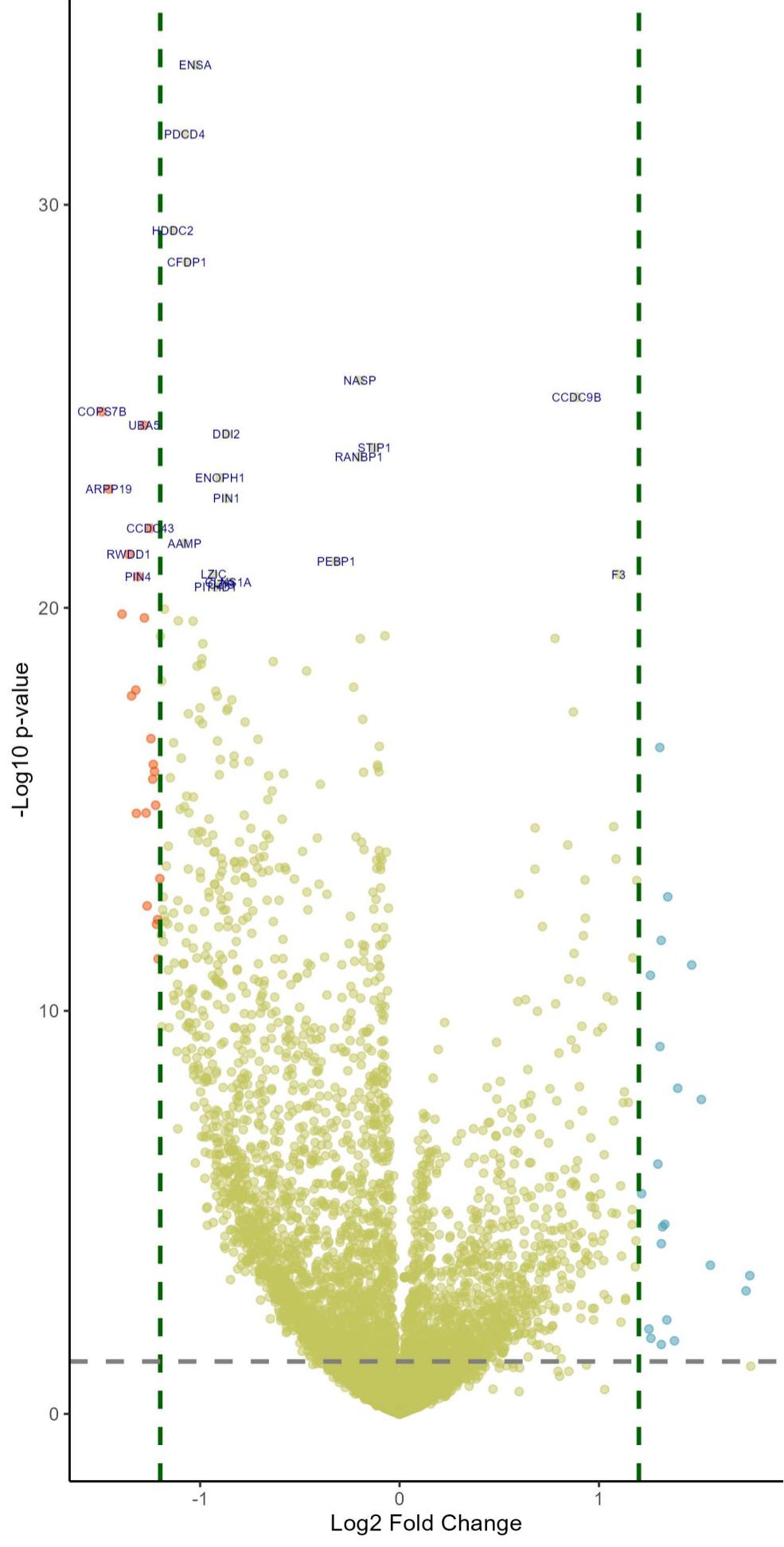


Differentially expressed proteins in blood cancers at absence/low amount of CCDC117 , DB1

p-value < 0.05 & logFC > 1.2

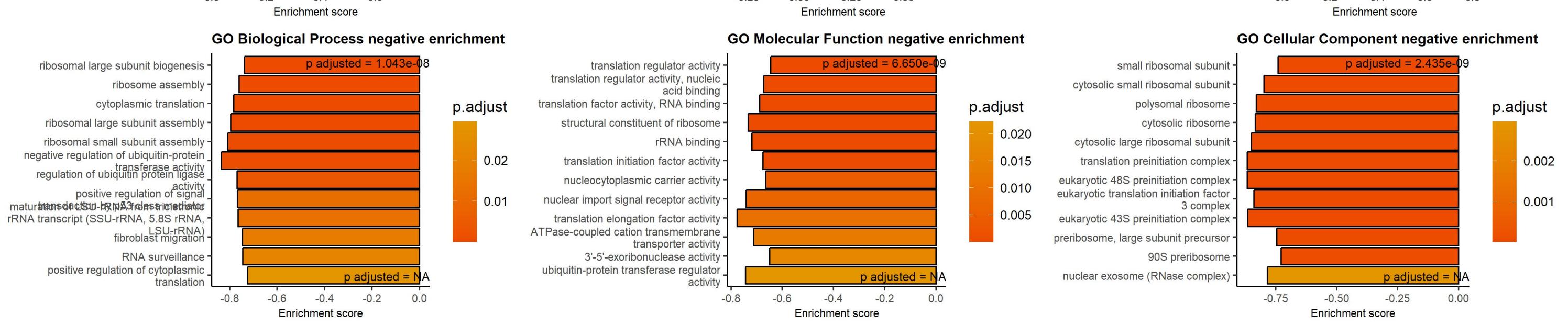
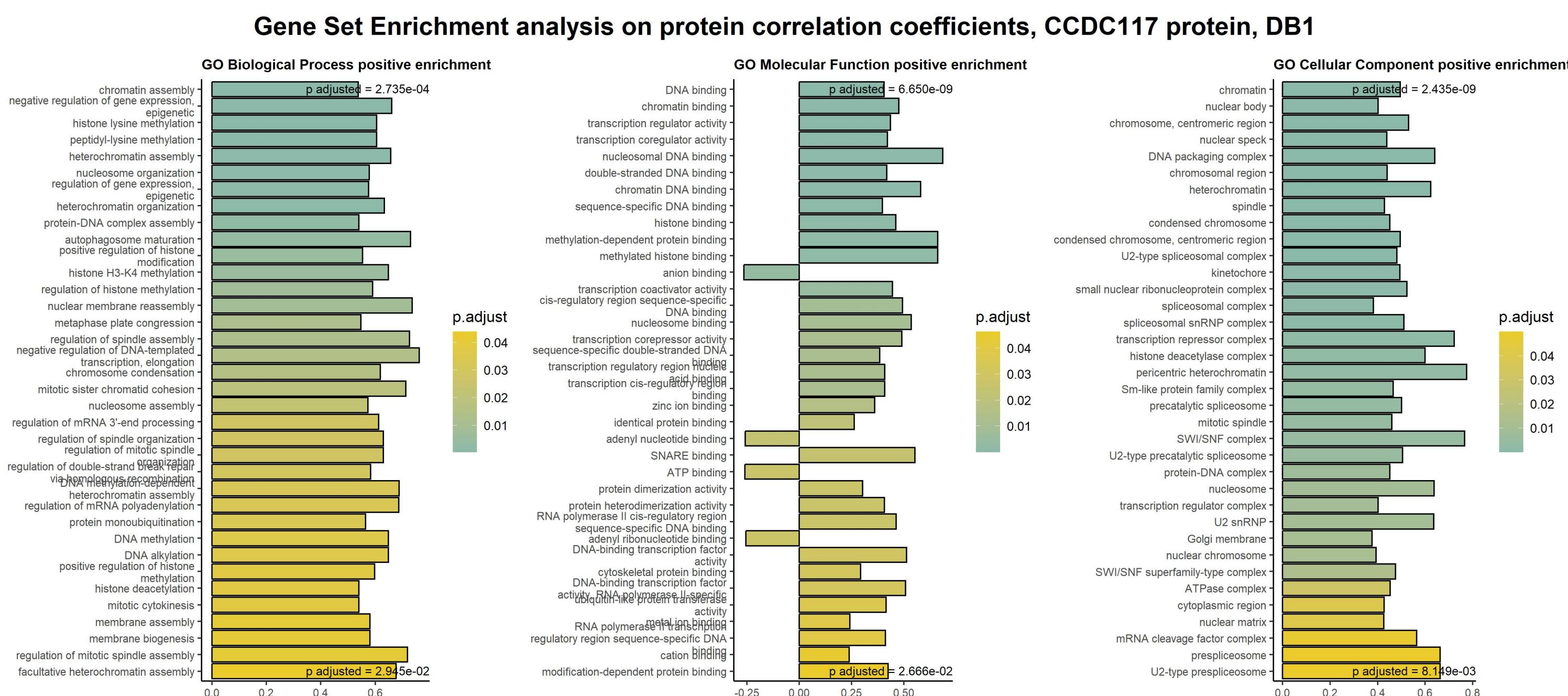
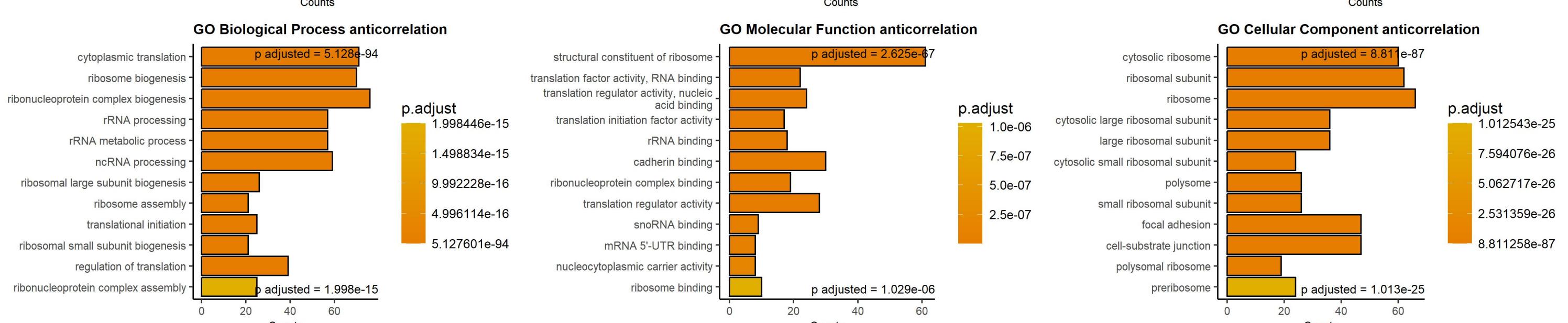
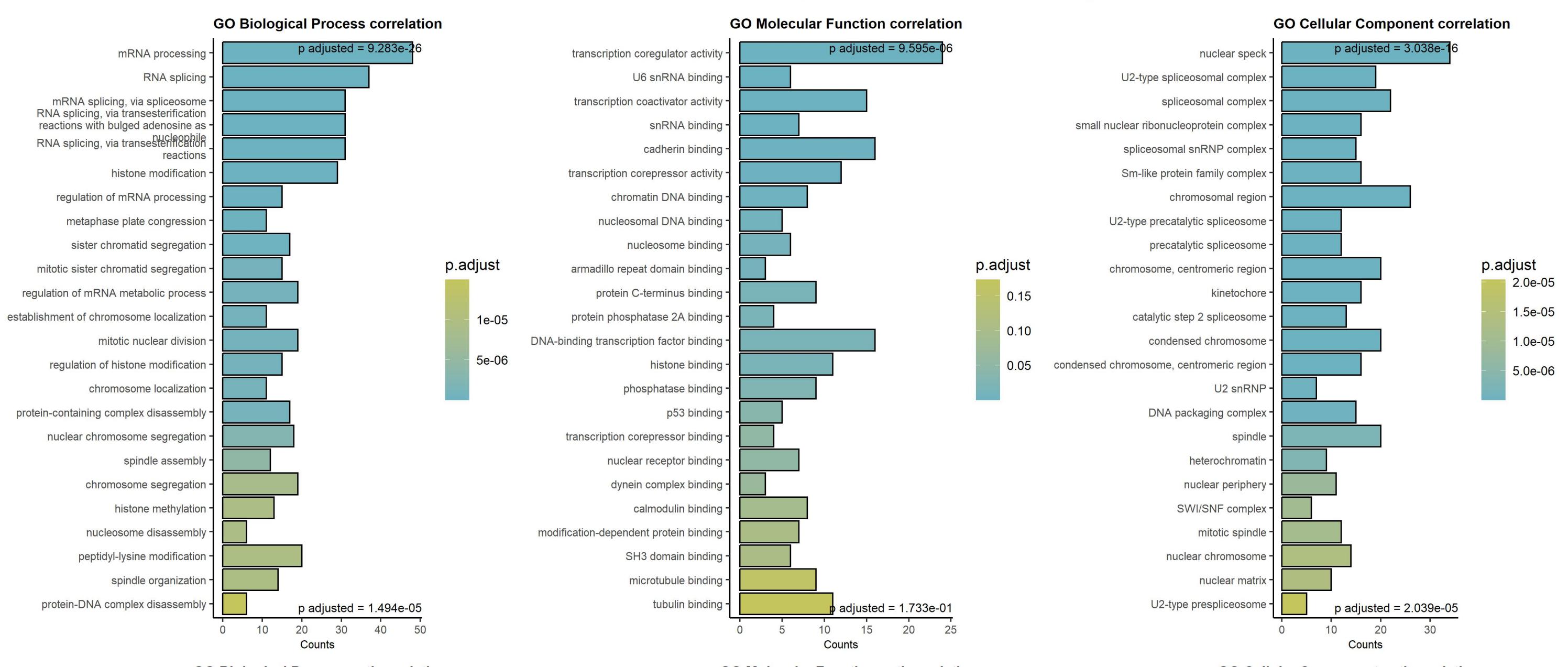
Sorted by p values!
Downregulated in blood cancers at low/absent CCDC117 Upregulated in blood cancers at low/absent CCDC117

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	5.04e-05	ZNF148	zinc finger protein 148	1	3.36e-03	CAPN2	calpain 2
-1.03	5.04e-05	MRGBP	MRG domain binding protein	0.09	4.40e-03	HADHA	hydroxyacyl-CoA dehydrogenase trifunctional
-0.07	6.30e-05	ANP32B	acidic nuclear phosphoprotein 32 kDa	0.09	5.43e-03	HADHB	hydroxyacyl-CoA dehydrogenase trifunctional
-0.08	1.20e-04	NAP1L4	nucleosome assembly protein 1 like	0.12	6.07e-03	LMAN2	lectin, mannose binding 2
-0.09	3.58e-04	HCFC1	host cell factor C1	0.1	9.03e-03	UQCRC2	ubiquinol-cytochrome c reductase complex II
-0.08	4.18e-04	ENY2	ENY2 transcription and export complex	0.07	1.06e-02	CS	citrate synthase
-0.06	4.21e-04	HNRNPD	heterogeneous nuclear ribonucleoprotein D	0.4	1.06e-02	ACAA2	acetyl-CoA acyltransferase 2
-0.07	4.21e-04	SKP1	S-phase kinase associated protein 1	0.12	1.07e-02	CYC1	cytochrome c1
-0.13	4.21e-04	JPT2	Jupiter microtubule associated homolog	0.49	1.11e-02	IMP4	IMP U3 small nucleolar ribonucleoprotein
-0.07	7.06e-04	TUBB	tubulin beta class I	1.02	1.14e-02	SQOR	sulfide quinone oxidoreductase
-0.83	1.06e-03	BRD8	bromodomain containing 8	0.09	1.15e-02	MRPL13	mitochondrial ribosomal protein L13
-0.94	1.06e-03	ATF7IP	activating transcription factor 7 i	0.52	1.15e-02	AZU1	azurocidin 1
-0.14	1.06e-03	CBX5	chromobox 5	0.07	1.21e-02	UQCRC1	ubiquinol-cytochrome c reductase complex II
-0.52	1.06e-03	KANSL3	KAT8 regulatory NSL complex subunit	0.11	1.49e-02	IARS2	isoleucyl-tRNA synthetase 2, mitochondrial
-0.49	1.23e-03	MED30	mediator complex subunit 30	0.74	1.56e-02	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.7	1.23e-03	BCL10	BCL10 immune signaling adaptor	0.08	1.85e-02	SLC25A3	solute carrier family 25 member 3
-0.63	1.23e-03	NFATC2IP	nuclear factor of activated T cells	0.08	1.94e-02	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ channel
-0.06	1.28e-03	PHF5A	PHD finger protein 5A	0.09	2.02e-02	MRPL38	mitochondrial ribosomal protein L38
-0.5	1.32e-03	UBXN7	UBX domain protein 7	0.08	2.03e-02	MRPL19	mitochondrial ribosomal protein L19
-0.08	1.32e-03	CNBP	CCHC-type zinc finger nucleic acid	0.11	2.16e-02	NDUFA13	NADH:ubiquinone oxidoreductase subunit 13
-0.08	1.32e-03	RANBP1	RAN binding protein 1	0.49	2.16e-02	EPHX1	epoxide hydrolase 1
-0.07	1.32e-03	NUDC	nuclear distribution C, dynein comp	0.31	2.16e-02	ABCF3	ATP binding cassette subfamily F member 3
-0.05	1.32e-03	SF3A1	splicing factor 3a subunit 1	0.31	2.20e-02	SIAE	sialic acid acetyltransferase
-0.64	1.32e-03	GPATCH8	G-patch domain containing 8	0.07	2.23e-02	GTPBP4	GTP binding protein 4
-0.08	1.39e-03	PTMA	prothymosin alpha	0.1	2.62e-02	OGDH	oxoglutarate dehydrogenase
-0.9	1.44e-03	EIF4ENIF1	eukaryotic translation initiation factor 4E nucleolar inhibitor 1	0.64	2.74e-02	LACTB	lactamase beta
-0.04	1.44e-03	SNRPD2	small nuclear ribonucleoprotein D2	0.07	2.75e-02	PSMD12	proteasome 26S subunit, non-ATPase
-0.08	1.53e-03	ZRANB2	zinc finger RANBP2-type containing	0.49	2.78e-02	SPECC1	sperm antigen with calponin homolog
-0.09	1.53e-03	NUP50	nucleoporin 50	0.3	2.81e-02	CPT2	carnitine palmitoyltransferase 2
-0.97	1.53e-03	CUEDC2	CUE domain containing 2	0.08	2.83e-02	CLPP	caseinolytic mitochondrial matrix peptidase
-0.85	1.57e-03	CCDC12	coiled-coil domain containing 12	0.07	2.86e-02	ATP5F1C	ATP synthase F1 subunit gamma
-0.07	1.59e-03	EIF4H	eukaryotic translation initiation factor 4H	0.47	2.96e-02	SRPRA	SRP receptor subunit alpha
-0.8	1.59e-03	SMARCD1	SWI/SNF related, matrix associated, chromatin-associating 1	0.31	3.06e-02	ECPAS	Ecm29 proteasome adaptor and scaffolding protein
-0.4	1.59e-03	GIMAP7	GTPase, IMAP family member 7	0.35	3.07e-02	ANKRD22	ankyrin repeat domain 22
-0.36	1.59e-03	MSH3	mutS homolog 3	0.17	3.24e-02	MOGS	mannosyl-oligosaccharide glucosidase
-0.04	1.65e-03	CPSF6	cleavage and polyadenylation specific	0.47	3.37e-02	MTIF2	mitochondrial translational initiator
-0.85	1.65e-03	RNF169	ring finger protein 169	0.87	3.38e-02	LGALS3	galectin 3
-0.81	1.65e-03	KAT8	lysine acetyltransferase 8	0.47	3.45e-02	TCIRG1	T cell immune regulator 1, ATPase H
0.98	1.65e-03	HALS1	HALS glutamin-like complex subunit 1	0.68	3.53e-02	SEVNL3	severoflin 3

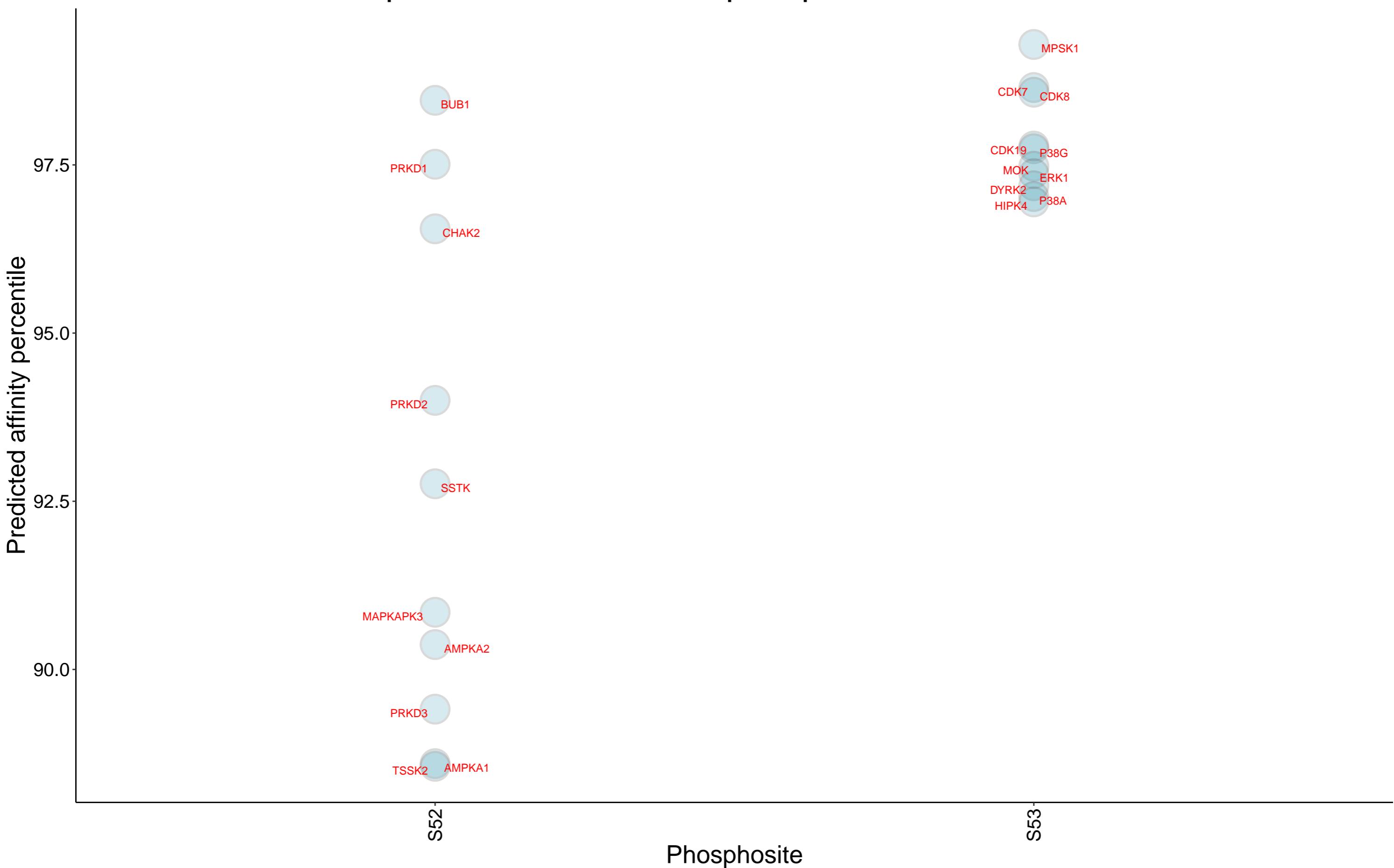
Differentially expressed proteins in solid cancers at absence/low amount of CCDC117 , DB1
p-value < 0.05 & logFC > 1.2Sorted by p values!
Downregulated in solid cancers at low/absent CCDC117 Upregulated in solid cancers at low/absent CCDC117

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.02	1.13e-30	ENSA	endosulfine alpha	0.89	5.67e-23	CCDC9B	coiled-coil domain containing 9B
-1.08	3.87e-29	PDCD4	programmed cell death 4	1.1	4.70e-19	F3	coagulation factor III, tissue factor
-1.14	7.24e-27	HDDC2	HD domain containing 2	0.78	1.14e-17	CAV2	caveolin 2
-1.07	3.54e-26	CFDP1	craniofacial development protein 1	0.87	4.99e-16	ITGB6	integrin subunit beta 6
-0.2	2.53e-23	NASP	nuclear autoantigenic sperm protein	1.3	3.13e-15	AXL	AXL receptor tyrosine kinase
-1.49	1.13e-22	COPS7B	COP9 signalosome subunit 7B	1.07	1.93e-13	LAMB3	laminin subunit beta 3
-1.28	2.19e-22	UBA5	ubiquitin like modifier activating	0.68	2.05e-13	MICAL2	microtubule associated monoxygenases
-0.87	3.23e-22	DDI2	DNA damage inducible 1 homolog 2	0.84	4.71e-13	CCN1	cellular communication network fact
-0.13	6.43e-22	STIP1	stress induced phosphoprotein 1	1.09	9.31e-13	IGFBP7	insulin like growth factor binding protein 7
-0.2	9.95e-22	RANBP1	RAN binding protein 1	0.68	1.46e-12	LAMA3	laminin subunit alpha 3
-0.9	3.04e-21	ENOPH1	enolase-phosphatase 1	0.93	2.47e-12	TGFBI	transforming growth factor beta induced
-1.46	5.39e-21	ARPP19	cAMP regulated phosphoprotein 19	1.19	2.51e-12	EHD2	EH domain containing 2
-0.87	8.54e-21	PIN1	peptidylprolyl cis/trans isomerase, endoplasmic reticulum	0.6	5.07e-12	ME3	malic enzyme 3
-1.25	4.44e-20	CCDC43	coiled-coil domain containing 43	1.34	5.90e-12	GPRC5A	G protein-coupled receptor class C
-1.08	9.80e-20	AAMP	angio associated migratory cell protein	0.93	1.75e-11	LAMC2	laminin subunit gamma 2
-1.36	1.74e-19	RWDD1	RWD domain containing 1	0.72	2.70e-11	CDH13	cadherin 13
-0.32	2.45e-19	PEBP1	phosphatidylethanolamine binding protein	0.92	4.34e-11	P3H2	prolyl 3-hydroxylase 2
-0.93	4.70e-19	LZIC	leucine zipper and CTNNB1IP1 domain	1.31	5.60e-11	TAP2	transporter 2, ATP binding cassette
-1.31	5.04e-19	PIN4	peptidylprolyl cis/trans isomerase, endoplasmic reticulum	0.87	1.11e-10	S100A2	S100 calcium binding protein A2
-0.86	6.67e-19	CLNS1A	chloride nucleotide-sensitive channel	1.17	1.40e-10	KRT80	keratin 80
-0.89	7.25e-19	CZIB	CXXC motif containing zinc binding	1.46	1.96e-10	TAP1	transporter 1, ATP binding cassette
-0.92	8.13e-19	PITH1	PITH domain containing 1	1.26	3.39e-10	FNDC3B	fibronectin type III domain containing 3
-1.18	2.77e-18	PSME3IP1	proteasome activator subunit 3 interacting protein 1	0.85	4.09e-10	NRP1	neuropilin 1
-1.39	3.54e-18	SUMO2	small ubiquitin like modifier 2	0.91	4.63e-10	PHLDB2	pleckstrin homology like domain family B
-1.28	4.23e-18	PDXP	pyridoxal phosphatase	1.04	1.02e-09	COL12A1	collagen type XII alpha 1 chain
-1.11	4.74e-18	CNOT2	CCR4-NOT transcription complex subunit 2	0.63	1.17e-09	CD70	CD70 molecule
-1.04	4.74e-18	GINS4	GINS complex subunit 4	1.07	1.21e-09	RAB32	RAB32, member RAS oncogene family
-0.07	1.05e-17	HSP90AB1	heat shock protein 90 alpha family	0.59	1.27e-09	DYSF	dysferlin
-1.2	1.05e-17	PPM1B	protein phosphatase, Mg2+/Mn2+ dependent	0.78	1.45e-09	CAVIN2	caveolae associated protein 2
-0.2	1.14e-17	FKBP4	FKBP prolyl isomerase 4	0.69	2.13e-09	SERPINE1	serpin family E member 1
-0.99	1.48e-17	RNASEH2C	ribonuclease H2 subunit C	0.23	3.84e-09	PICALM	phosphatidylinositol binding clathrin-associated protein
-0.99	3.40e-17						

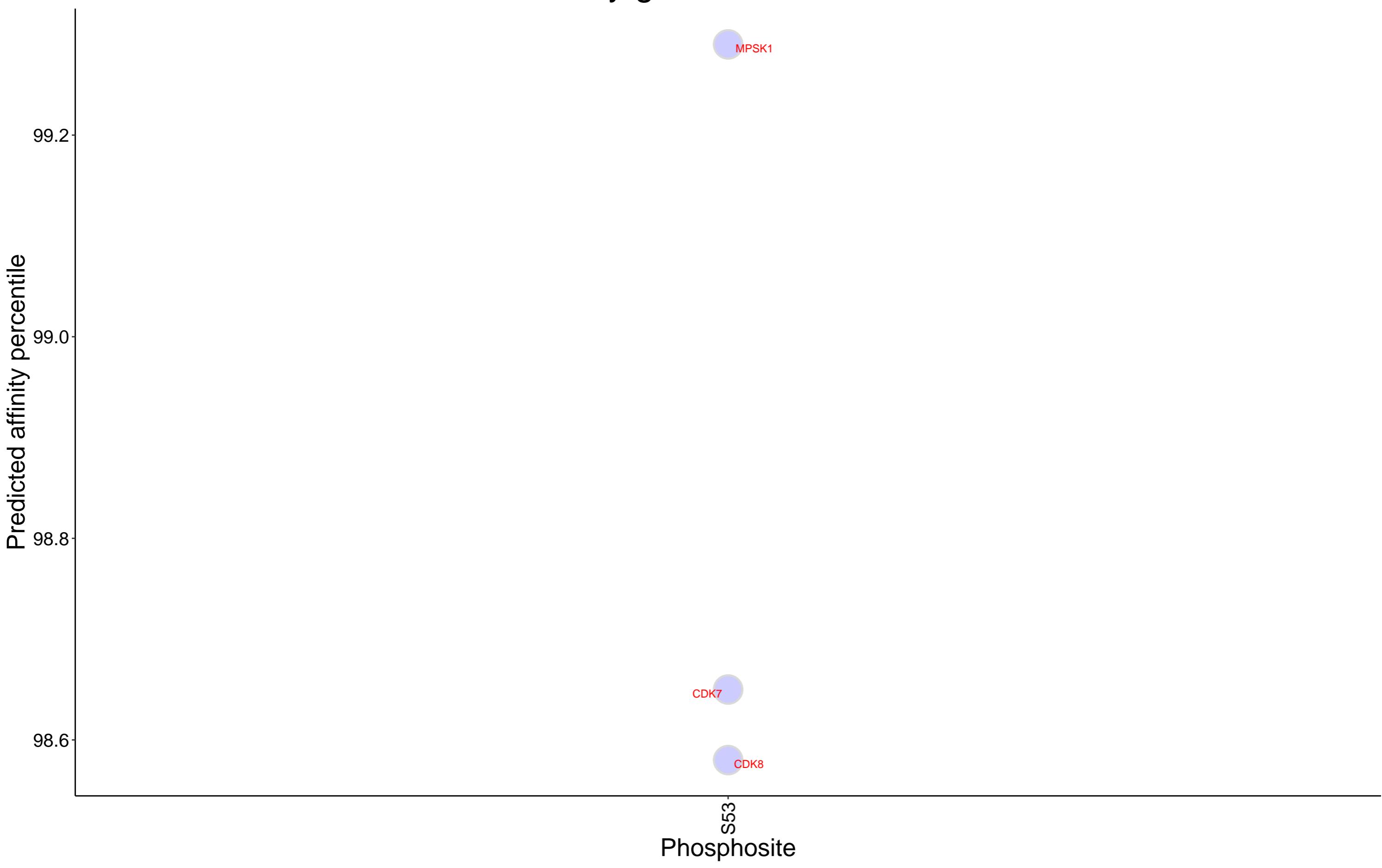
Top 250 correlation coefficients overrepresentation, CCDC117 protein, DB1



Top 10 kinases for each phosphosite in CCDC117



Kinases with affinity greater than 98.5% to CCDC117



No sufficient paired observations in DB1 for CCDC117