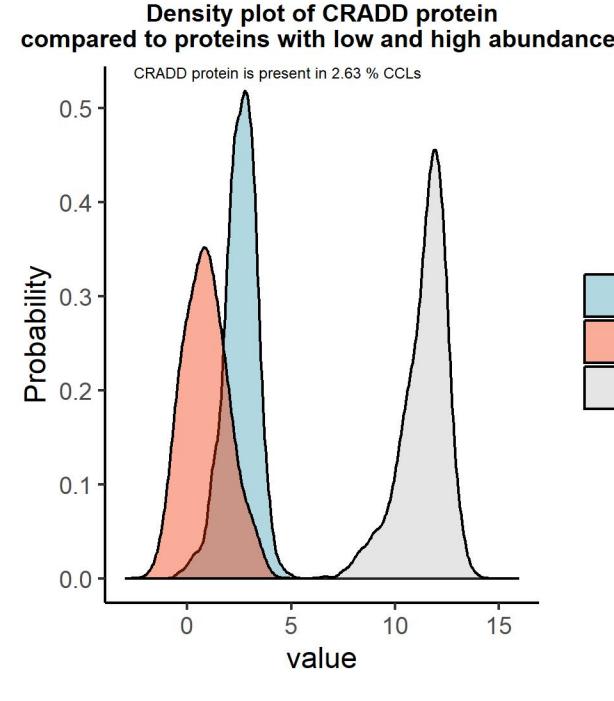
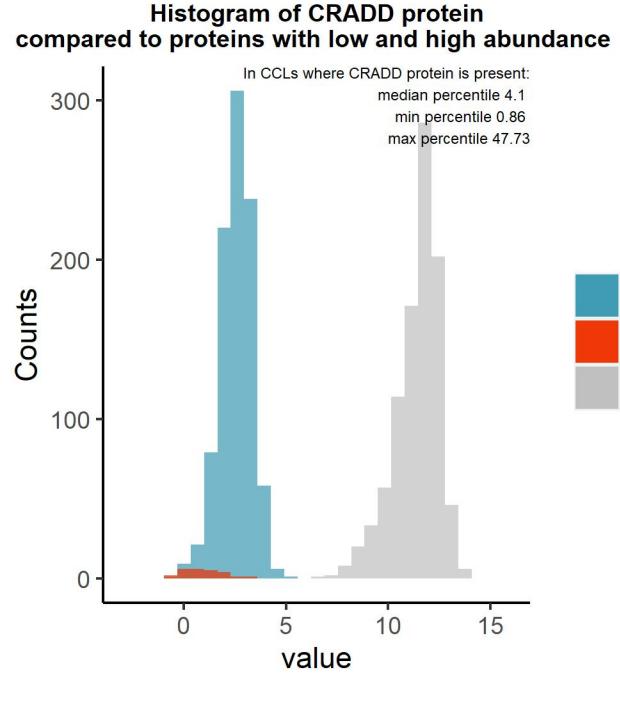


CRADD

Protein name: CRADD ; UNIPROT: P78560 ; Gene name: CASP2 and RIPK1 domain containing adaptor with death domain
 Ligandable: NA ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

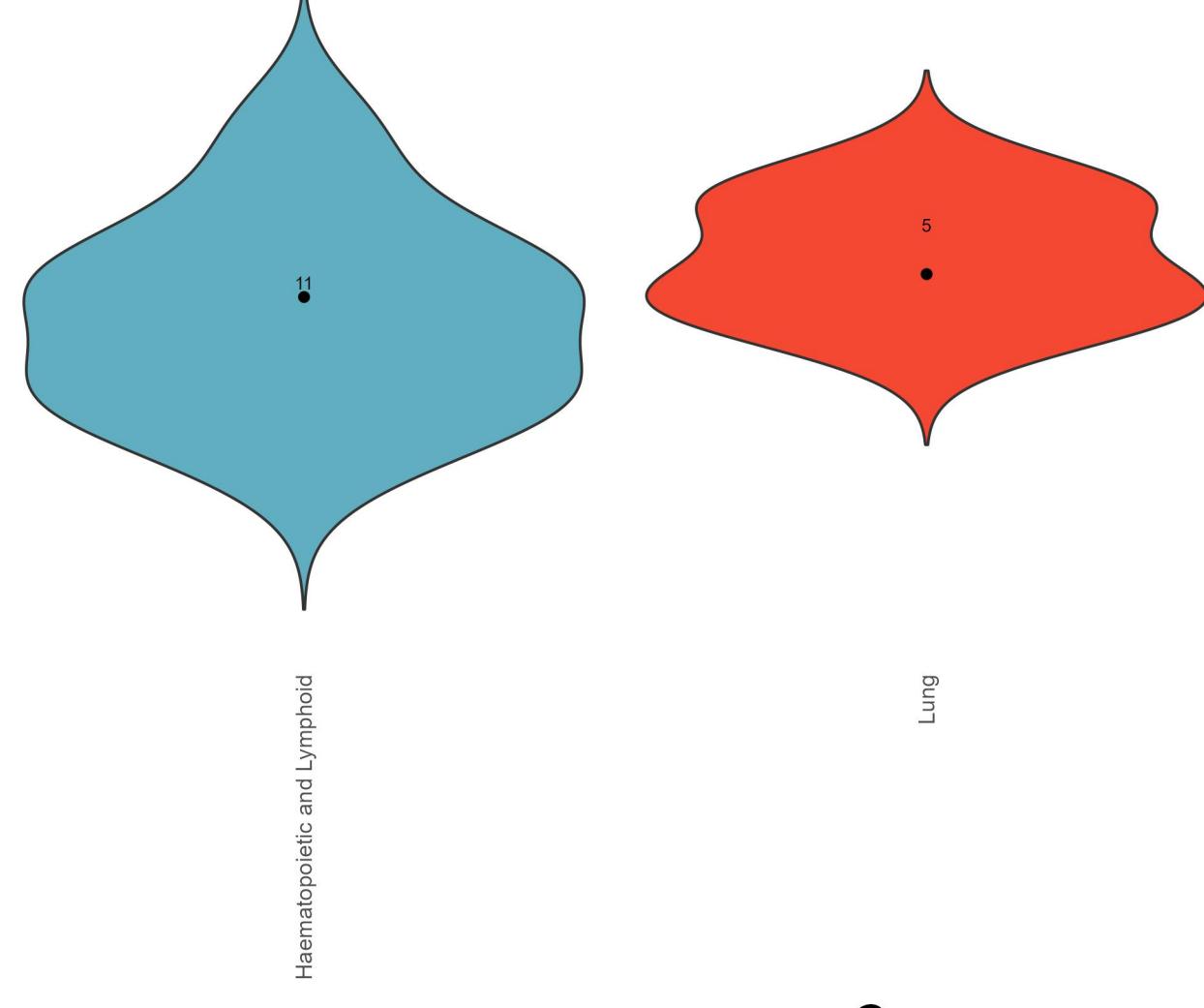
Sanger Institute Protein Database 2 (DB2), protein presence is less certain

8498 proteins in same 949 CCLs



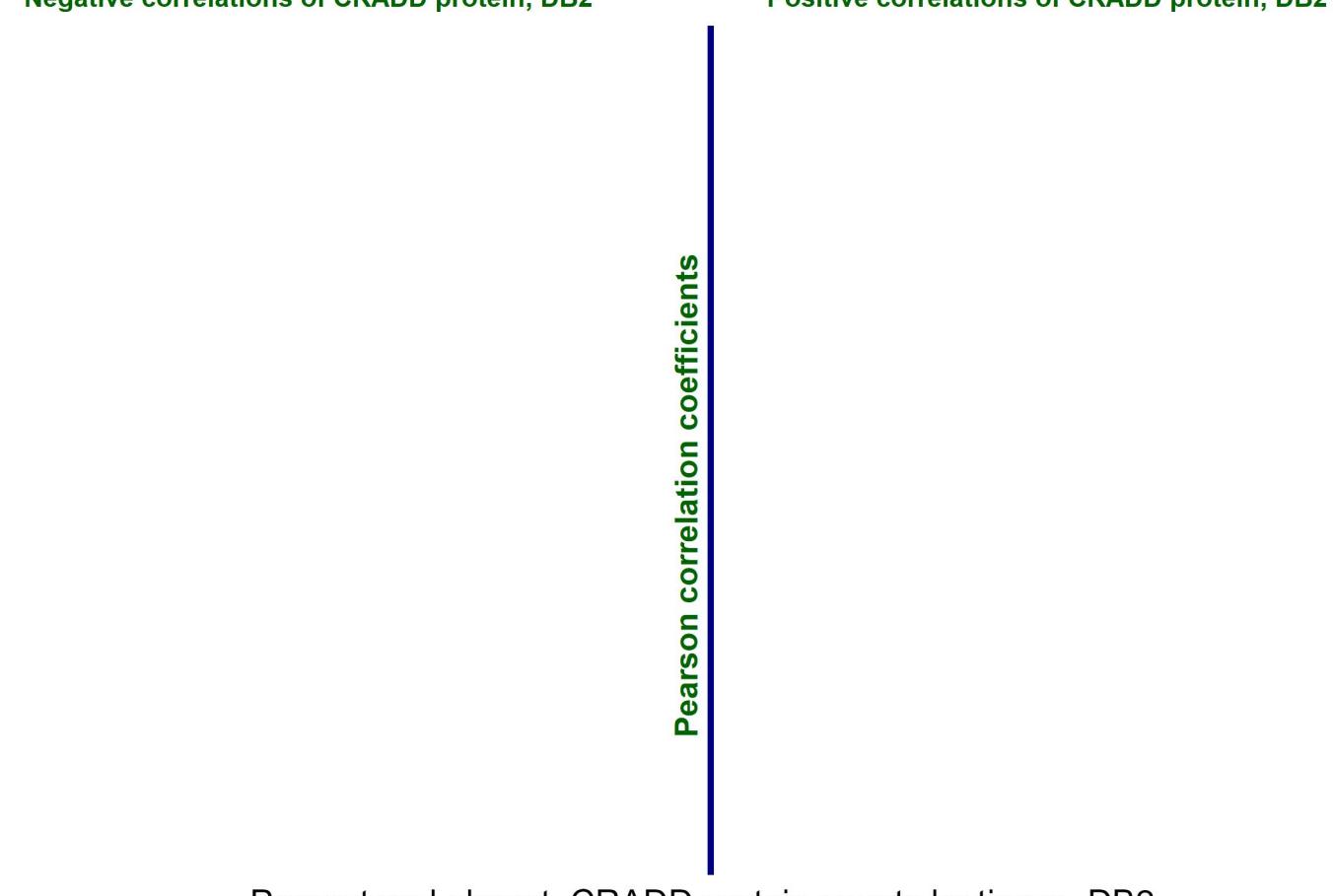
Amount of CRADD protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 1.546e-01



Negative correlations of CRADD protein, DB2

Pearson correlation coefficients

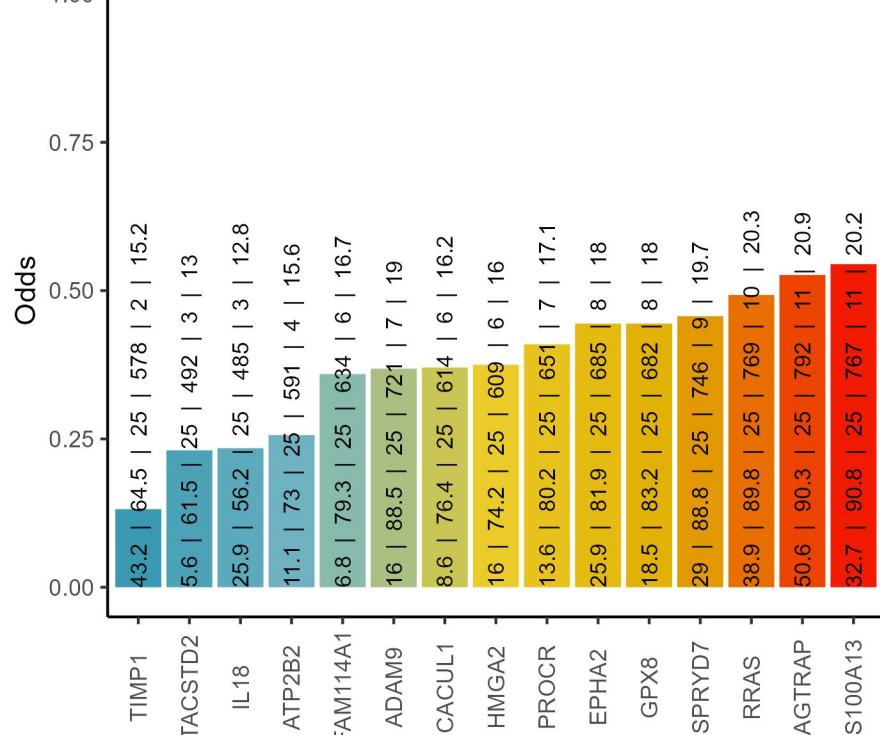


Cooccurrence with CRADD protein, DB2

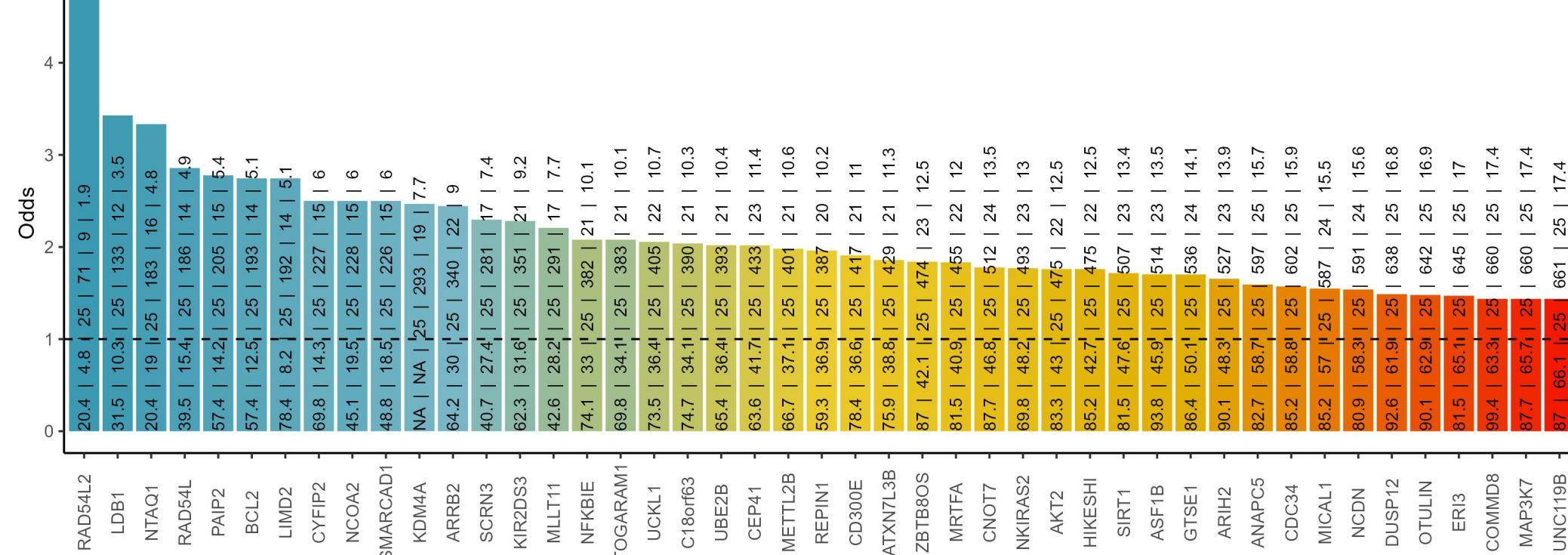
% of CRADD in blood cancers: 6.8 ; % of CRADD in solid cancers: 1.8

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

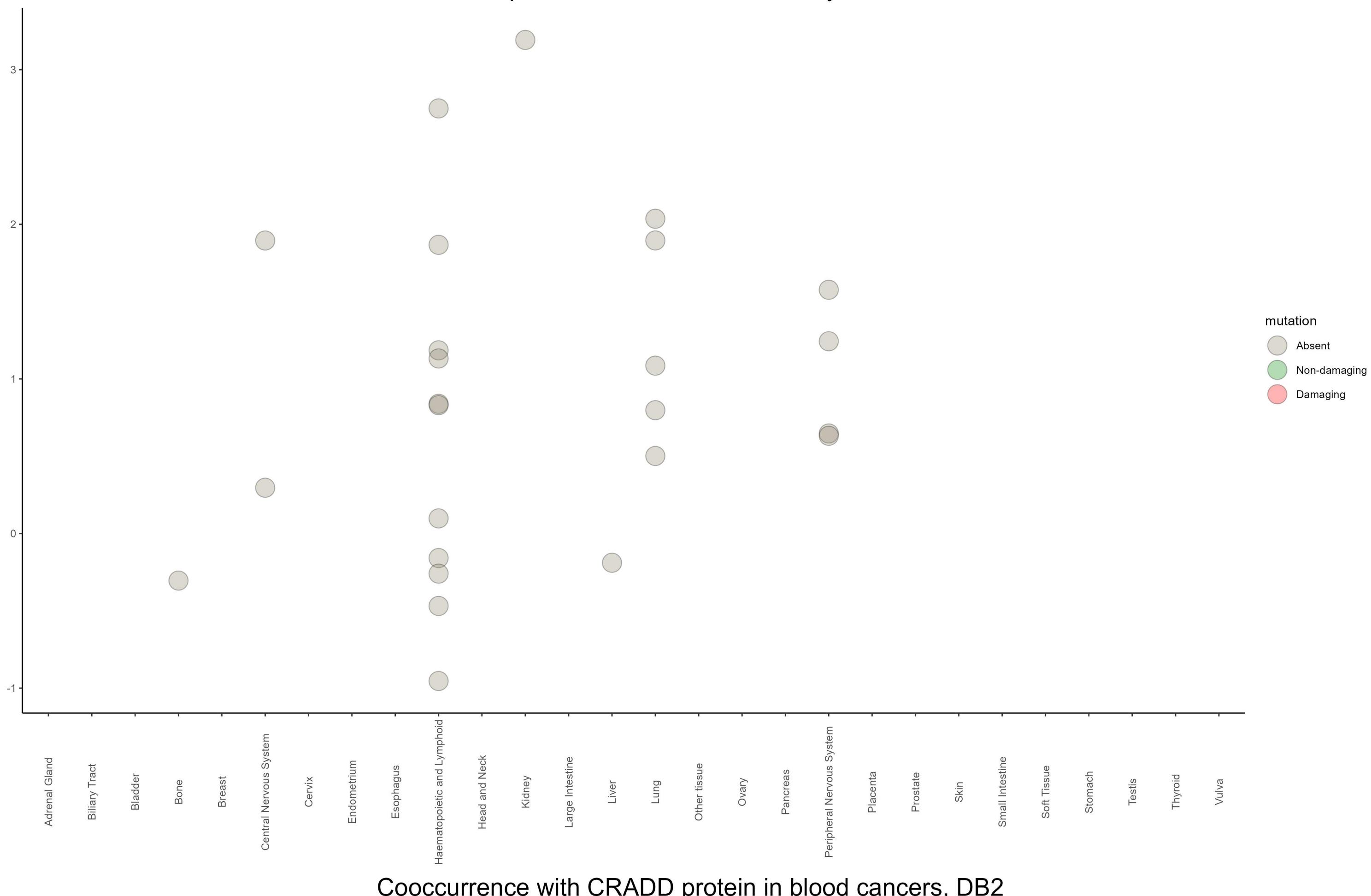
Negative cooccurrence



Positive cooccurrence



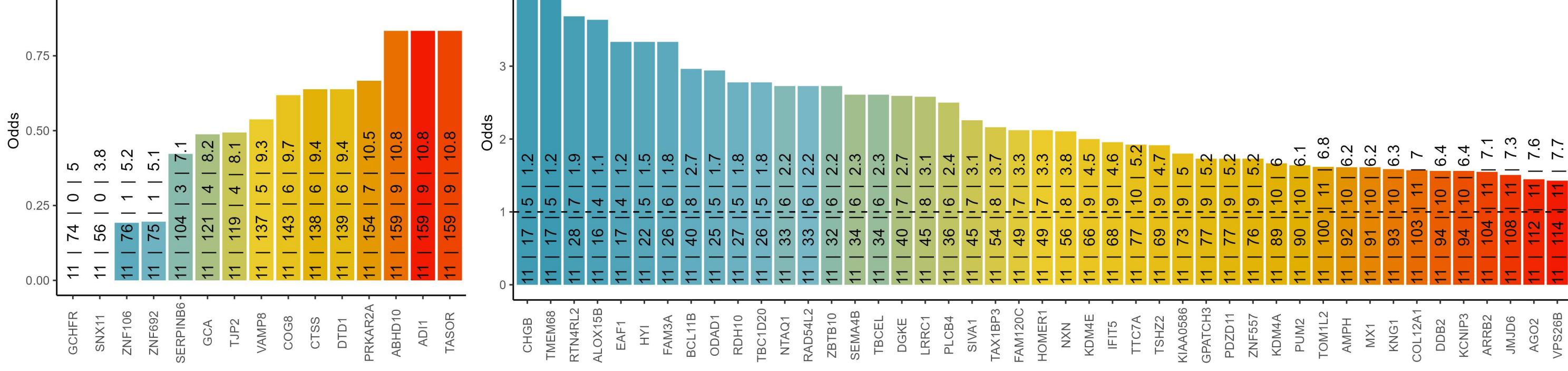
Amount of CRADD protein and mutation status by tissue, DB2



Cooccurrence with CRADD protein in blood cancers, DB2

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

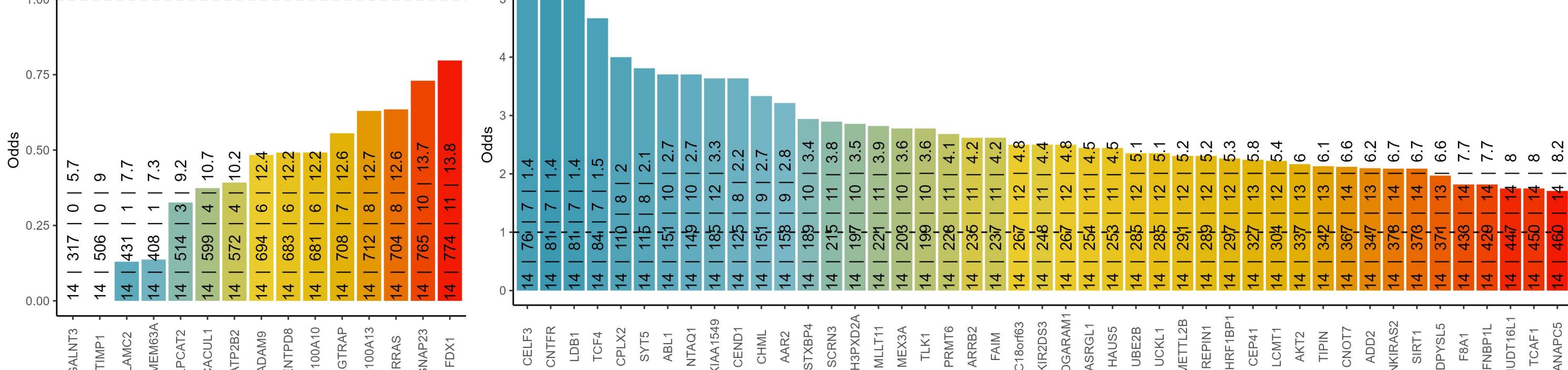
Negative cooccurrence



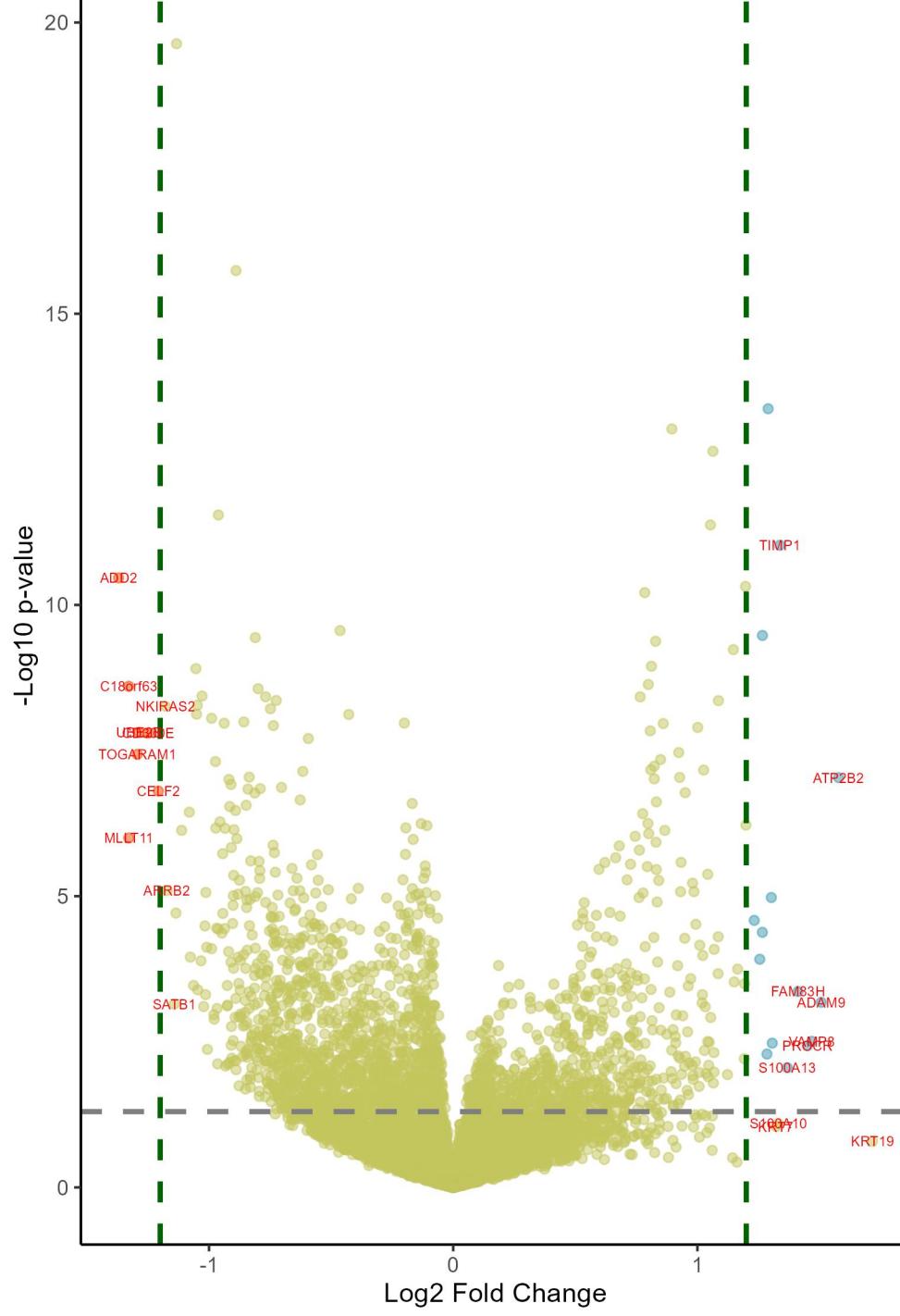
Cooccurrence with CRADD protein in solid cancers, DB2

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

Negative cooccurrence

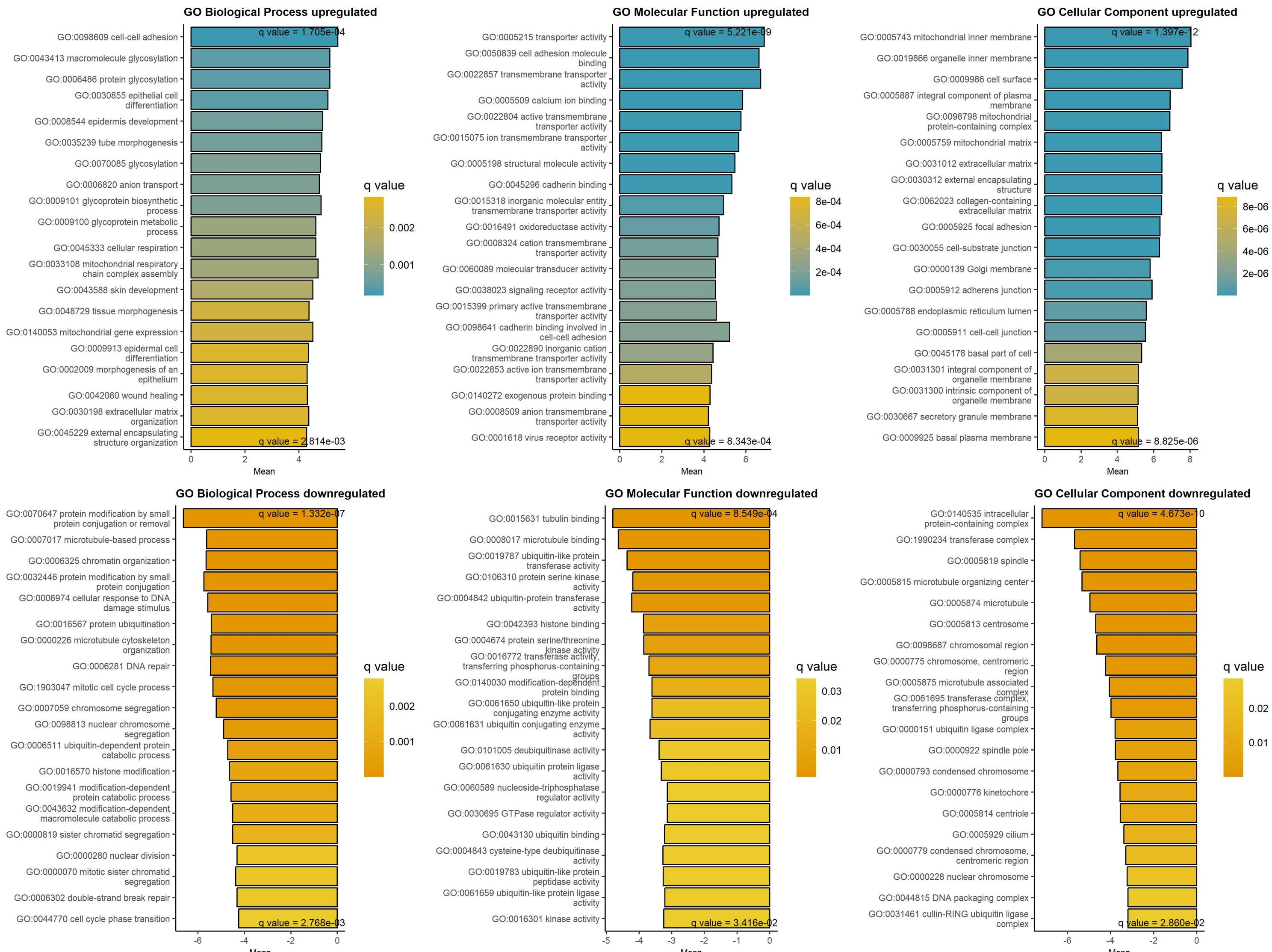


Downregulated at low/absent CRADD Upregulated at low/absent CRADD



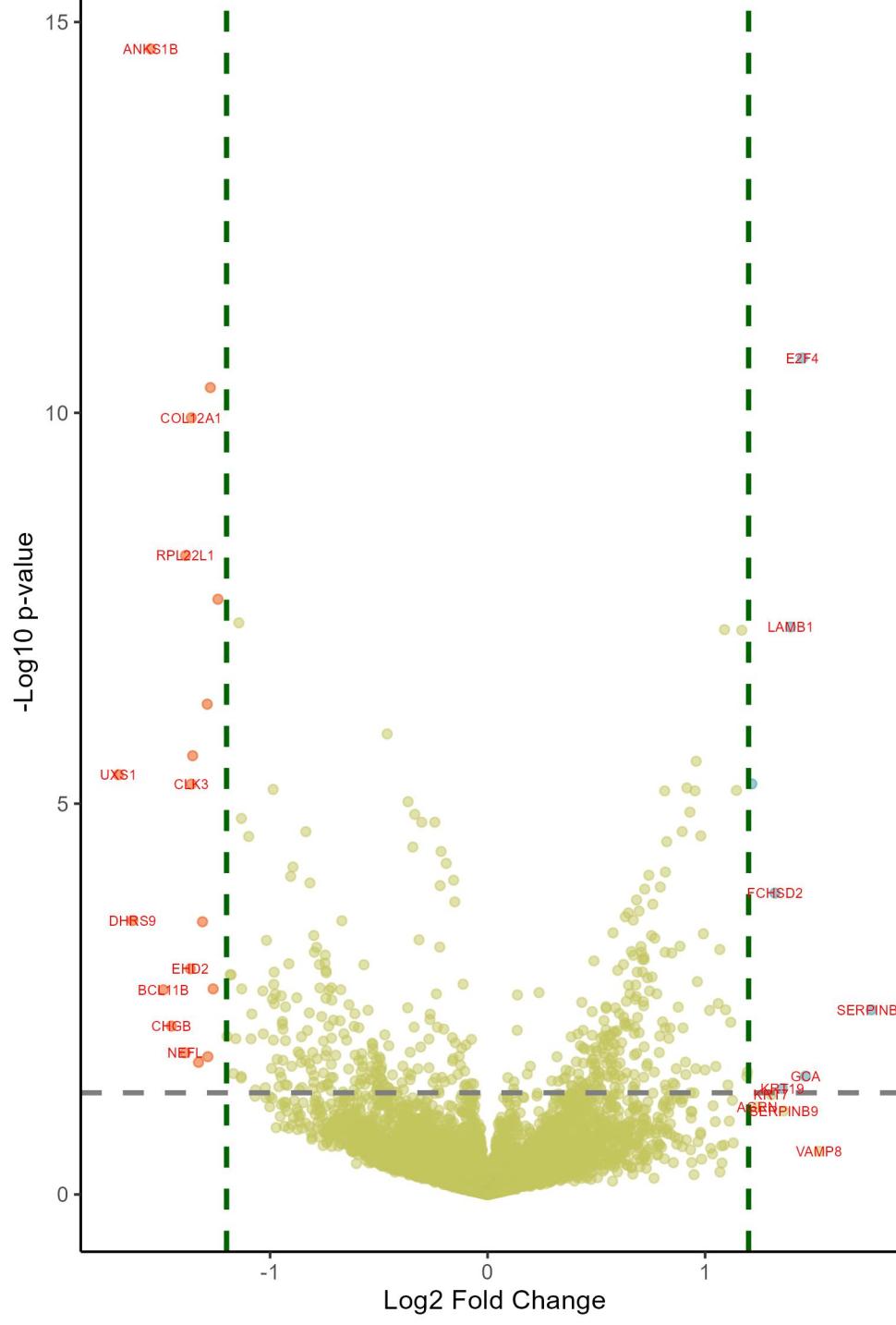
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.37	2.87e-08	ADD2	adducin 2	1.72	3.74e-01	KRT19	keratin 19
-1.33	9.88e-05	MLLT11	MLLT11 transcription factor 7 cofac	1.58	1.43e-05	ATP2B2	ATPase plasma membrane Ca ²⁺ transpo
-1.33	9.92e-07	C18orf63	chromosome 18 open reading frame 63	1.51	1.13e-02	ADAM9	ADAM metallopeptidase domain 9
-1.29	6.84e-06	TOGARAM1	TOG array regulator of axonemal mic	1.47	3.34e-02	VAMP8	vesicle associated membrane protein
-1.29	3.14e-06	UBE2B	ubiquitin conjugating enzyme E2 B	1.45	3.74e-02	PROCR	protein C receptor
-1.25	3.16e-06	CD300E	CD300e molecule	1.41	8.27e-03	FAM83H	family with sequence similarity 83
-1.21	2.15e-05	CELF2	CUGBP Elav-like family member 2	1.37	6.56e-02	S100A13	S100 calcium binding protein A13
-1.18	1.58e-06	NKIRAS2	NFKB inhibitor interacting Ras like	1.34	8.79e-09	TIMP1	TIMP metallopeptidase inhibitor 1
-1.17	5.28e-04	ARRB2	arrestin beta 2	1.33	2.53e-01	S100A10	S100 calcium binding protein A10
-1.14	1.18e-02	SATB1	SATB homeobox 1	1.32	2.69e-01	KRT7	keratin 7
-1.14	9.59e-04	SNX22	sorting nexin 22	1.31	3.50e-02	EPHA2	EPH receptor A2
-1.13	9.66e-17	VIP	vasoactive intestinal peptide	1.3	6.06e-04	HMGA2	high mobility group AT-hook 2
-1.11	7.57e-05	GPATCH3	G-patch domain containing 3	1.29	8.95e-11	TRPM4	transient receptor potential cation
-1.08	4.32e-05	CNOT7	CCR4-NOT transcription complex subu	1.28	4.63e-02	RRAS	RAS related
-1.08	3.23e-03	IGDCC4	immunoglobulin superfamily DCC subc	1.27	2.00e-07	UACA	uveal autoantigen with coiled-coil
-1.06	7.09e-03	LYSMD1	LysM domain containing 1	1.27	1.63e-03	SDC4	syndecan 4
-1.05	5.47e-07	CDC34	cell division cycle 34, ubiquitin c	1.26	3.46e-03	TACSTD2	tumor associated calcium signal tra
-1.05	1.99e-06	TYMS	thymidylate synthetase	1.23	1.18e-03	LPCAT2	lysophosphatidylcholine acyltransfe
-1.05	1.57e-06	MICAL1	microtubule associated monoxygenas	1.2	6.70e-05	RELL1	RELT like 1
-1.05	7.89e-03	ELMO1	engulfment and cell motility 1	1.2	3.65e-08	KRT74	keratin 74
-1.03	3.64e-03	TEX14	testis expressed 14, intercellular	1.19	6.79e-03	AGTRAP	angiotensin II receptor associated
-1.03	1.27e-06	DPYSL4	dihydropyrimidinase like 4	1.19	5.20e-02	GPX8	glutathione peroxidase 8 (putative)
-1.02	1.24e-02	ASRGL1	asparaginase and isoaspartyl peptid	1.16	4.48e-03	FAM114A1	family with sequence similarity 114
-1.02	1.38e-03	CEP41	centrosomal protein 41	1.16	5.67e-01	KRT18	keratin 18
-1.01	9.13e-03	KDM4A	lysine demethylase 4A	1.15	6.42e-03	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa
-1.01	5.43e-04	PPM1D	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	1.15	2.88e-07	OCLN	occludin
-1.01	2.40e-03	LCMT1	leucine carboxyl methyltransferase	1.14	5.19e-01	S100A6	S100 calcium binding protein A6
-1.01	4.16e-02	CHGB	chromogranin B	1.12	7.79e-02	FGFRL1	fibroblast growth factor receptor I
-0.99	2.50e-03	UCKL1	uridine-cytidine kinase 1 like 1	1.09	1.36e-06	PTGES	prostaglandin E synthase

GAGE analysis on upregulated and downregulated proteins at low/absent CRADD protein, DB2

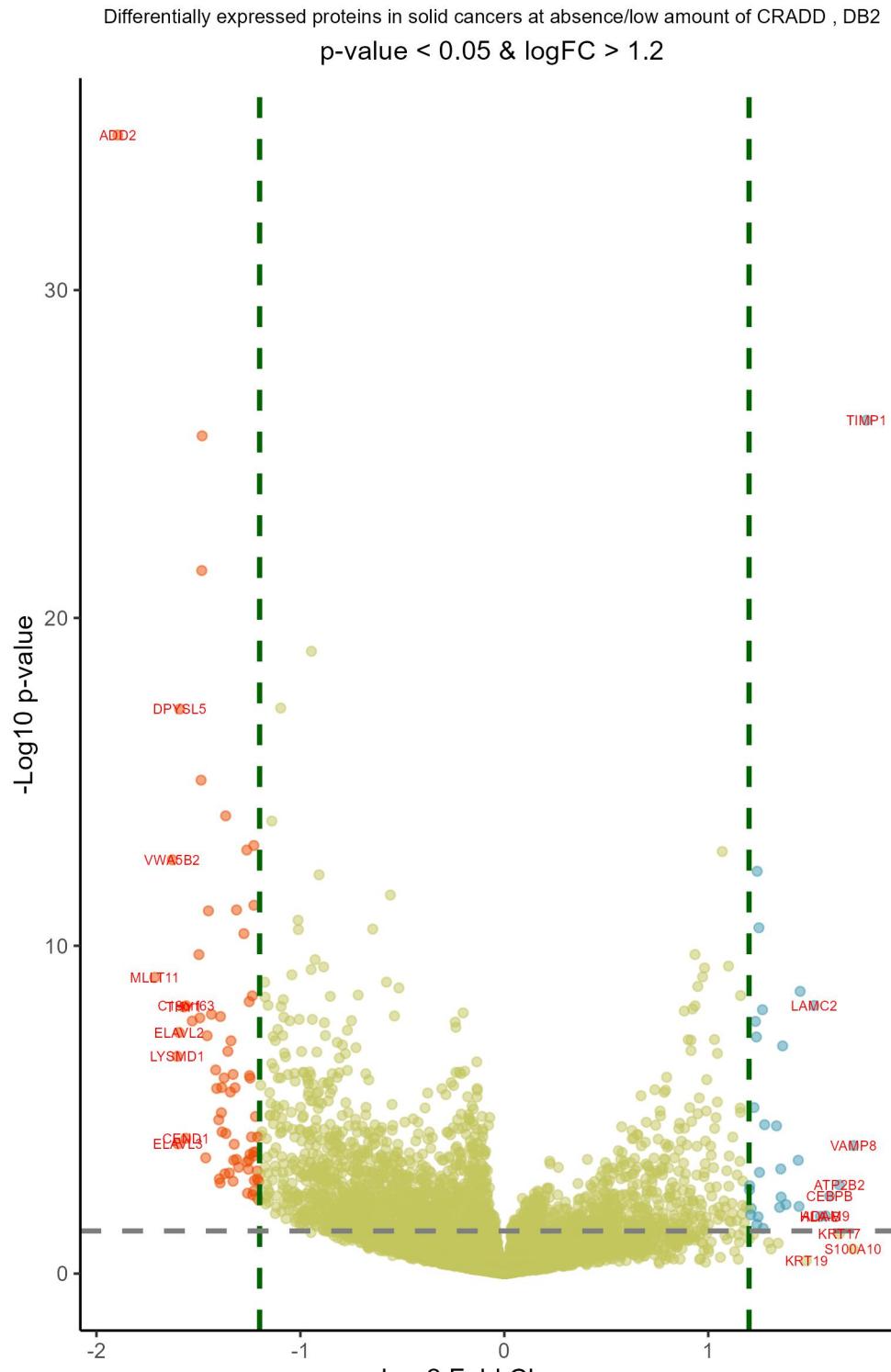


p-value < 0.05 & logFC > 1.2

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



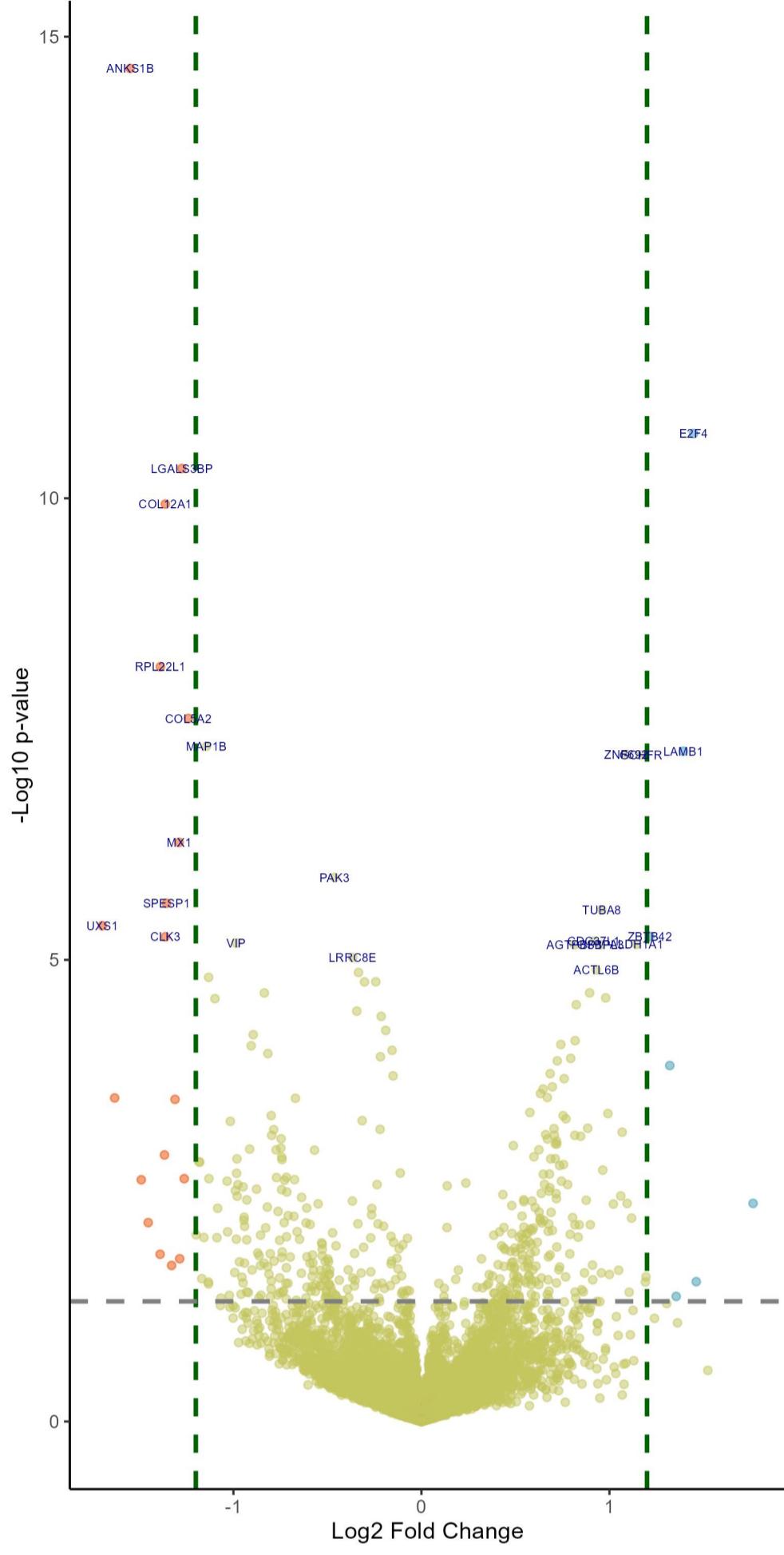
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.7	2.23e-03	UXS1	UDP-glucuronate decarboxylase 1	1.76	2.63e-01	SERPINB6	serpin family B member 6
-1.63	4.71e-02	DHRS9	dehydrogenase/reductase 9	1.52	9.76e-01	VAMP8	vesicle associated membrane protein
-1.55	9.22e-12	ANKS1B	ankyrin repeat and sterile alpha mo	1.46	7.73e-01	GCA	grancalcin
-1.49	1.88e-01	BCL11B	BAF chromatin remodeling complex su	1.45	5.55e-08	E2F4	E2F transcription factor 4
-1.45	3.61e-01	CHGB	chromogranin B	1.39	4.60e-05	LAMB1	laminin subunit beta 1
-1.39	5.47e-01	NEFL	neurofilament light chain	1.36	9.76e-01	SERPINB9	serpin family B member 9
-1.39	9.29e-06	RPL2L1	ribosomal protein L22 like 1	1.36	9.07e-01	KRT19	keratin 19
-1.37	1.26e-01	EHD2	EH domain containing 2	1.32	2.48e-02	FCHSD2	FCH and double SH3 domains 2
-1.36	2.49e-03	CLK3	CDC like kinase 3	1.3	9.76e-01	KRT7	keratin 7
-1.36	1.93e-07	COL12A1	collagen type XII alpha 1 chain	1.24	9.76e-01	AGRN	agrin
-1.36	1.46e-03	SPESP1	sperm equatorial segment protein 1	1.21	2.49e-03	ZBTB42	zinc finger and BTB domain containi
-1.33	6.37e-01	MUC1	mucin 1, cell surface associated	1.19	7.32e-01	TJP2	tight junction protein 2
-1.31	4.76e-02	LHPP	phospholysine phosphohistidine inor	1.19	7.75e-01	CD59	CD59 molecule (CD59 blood group)
-1.29	3.72e-04	MX1	MX dynamin like GTPase 1	1.17	4.60e-05	GCHFR	GTP cyclohydrolase I feedback regul
-1.29	5.84e-01	PIWIL1	piwi like RNA-mediated gene silenci	1.14	2.49e-03	ALDH1A1	aldehyde dehydrogenase 1 family mem
-1.27	9.94e-08	LGALS3BP	galectin 3 binding protein	1.13	9.76e-01	UCHL1	ubiquitin C-terminal hydrolase L1
-1.26	1.87e-01	RYR1	ryanodine receptor 1	1.13	9.76e-01	SH3BP1	SH3 domain binding protein 1
-1.24	2.90e-05	COL5A2	collagen type V alpha 2 chain	1.12	3.35e-01	MIDEAS	mitotic deacetylase associated SANT
-1.2	4.14e-01	KRT20	keratin 20	1.11	9.76e-01	TEX11	testis expressed 11
-1.18	1.38e-01	MTIF3	mitochondrial translational initiat	1.11	8.65e-01	TBC1D4	TBC1 domain family member 4
-1.18	1.38e-01	ZNF557	zinc finger protein 557	1.09	2.63e-01	BAIAP2	BAR/IMD domain containing adaptor p
-1.17	7.49e-01	NRP2	neuropilin 2	1.09	4.60e-05	ZNF692	zinc finger protein 692
-1.16	4.27e-01	PIGO	phosphatidylinositol glycan anchor	1.09	9.76e-01	CREBZF	CREB/ATF bZIP transcription factor
-1.14	4.60e-05	MAP1B	microtubule associated protein 1B	1.08	9.76e-01	ENTPD1	ectonucleoside triphosphate diphosp
-1.13	7.75e-01	KIAA0100	KIAA0100	1.08	9.76e-01	DTD1	D-aminoacyl-tRNA deacylase 1
-1.13	7.82e-01	DHRS3	dehydrogenase/reductase 3	1.07	9.76e-01	S100A4	S100 calcium binding protein A4
-1.13	4.79e-03	JMD6	jumonji domain containing 6, argini	1.07	8.91e-02	NECTIN1	nectin cell adhesion molecule 1
-1.13	1.87e-01	GPATCH3	G-patch domain containing 3	1.06	2.37e-01	EIF1AX	eukaryotic translation initiation f
-1.1	6.66e-03	NPR2	natriuretic peptide receptor 2	1.05	6.69e-01	RASSF2	Ras association domain membe



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.9	7.79e-32	ADD2	adducin 2	1.78	2.59e-23	TIMP1	TIMP metallopeptidase inhibitor 1
-1.71	2.15e-07	MLLT11	MLLT11 transcription factor 7 cofac	1.71	3.15e-03	VAMP8	vesicle associated membrane protein
-1.63	1.33e-10	VWA5B2	von Willebrand factor A domain cont	1.71	4.00e-01	S100A10	S100 calcium binding protein A10
-1.6	2.03e-05	LYSMD1	LysM domain containing 1	1.64	2.36e-02	ATP2B2	ATPase plasma membrane Ca2+ transpo
-1.6	2.88e-03	ELAVL3	ELAV like RNA binding protein 3	1.64	2.20e-01	KRT17	keratin 17
-1.59	4.91e-06	ELAVL2	ELAV like RNA binding protein 2	1.6	4.13e-02	CEBPB	CCAAT enhancer binding protein beta
-1.59	6.29e-15	DPYSL5	dihydropyrimidinase like 5	1.58	1.03e-01	ADAM9	ADAM metallopeptidase domain 9
-1.57	1.14e-06	THY1	Thy-1 cell surface antigen	1.55	1.05e-01	HLA-B	major histocompatibility complex, c
-1.56	2.13e-03	CEND1	cell cycle exit and neuronal differ	1.52	1.09e-06	LAMC2	laminin subunit gamma 2
-1.56	1.09e-06	C18orf63	chromosome 18 open reading frame 63	1.48	5.94e-01	KRT19	keratin 19
-1.53	2.42e-06	KIF1A	kinesin family member 1A	1.45	5.01e-07	TRPM4	transient receptor potential cation
-1.5	5.54e-08	CRMP1	collapsin response mediator protein	1.45	6.66e-02	FAM83H	family with sequence similarity 83
-1.49	2.11e-06	CD300E	CD300e molecule	1.44	6.78e-03	AGTRAP	angiotensin II receptor associated
-1.49	8.24e-13	TCAF1	TRPM8 channel associated factor 1	1.38	6.09e-02	ADGRE5	adhesion G protein-coupled receptor
-1.48	5.99e-19	KIF21A	kinesin family member 21A	1.36	1.08e-05	KRT74	keratin 74
-1.48	5.84e-23	DPYSL4	dihydropyrimidinase like 4	1.36	4.28e-02	HMGA2	high mobility group AT-hook 2
-1.46	6.07e-03	PCSK1N	proprotein convertase subtilisin/ke	1.36	1.06e-02	LPCAT2	lysophosphatidylcholine acyltransfe
-1.46	5.93e-06	LCMT1	leucine carboxyl methyltransferase	1.35	6.95e-02	FGFRL1	fibroblast growth factor receptor I
-1.45	3.43e-09	NKIRAS2	NFKB inhibitor interacting Ras like	1.34	3.18e-01	CD99	CD99 molecule (Xg blood group)
-1.44	1.74e-06	AKT2	AKT serine/threonine kinase 2	1.33	1.13e-03	RAC2	Rac family small GTPase 2
-1.42	4.99e-05	UBE2B	ubiquitin conjugating enzyme E2 B	1.31	4.00e-01	ENTPD8	ectonucleoside triphosphate diphosp
-1.41	1.33e-04	SNX22	sorting nexin 22	1.3	3.10e-01	PROCR	protein C receptor
-1.4	8.11e-04	FAIM	Fas apoptotic inhibitory molecule	1.28	1.09e-03	UACA	uveal autoantigen with coiled-coil
-1.4	1.72e-02	SYT5	synaptotagmin 5	1.27	1.77e-01	RRAS	RAS related
-1.39	2.12e-02	CPLX2	complexin 2	1.27	1.33e-06	LRRC1	leucine rich repeat containing 1
-1.39	1.98e-06	CNOT7	CCR4-NOT transcription complex subu	1.25	1.25e-02	SOAT1	sterol O-acyltransferase 1
-1.39	5.50e-04	ASRGL1	asparaginase and isoaspartyl peptid	1.25	1.03e-08	PRSS8	serine protease 8
-1.39	1.27e-04	TEX14	testis expressed 14, intercellular	1.24	1.07e-01	TAP1	transporter 1, ATP binding cassette
-1.38	1.53e-03	PRMT6	protein arginine methyltransferase	1.24	2.79e-10	GALNT3	polypeptide N-acetylgalactosaminylt

CRADD network, DB2, no Pearson r > 0.3

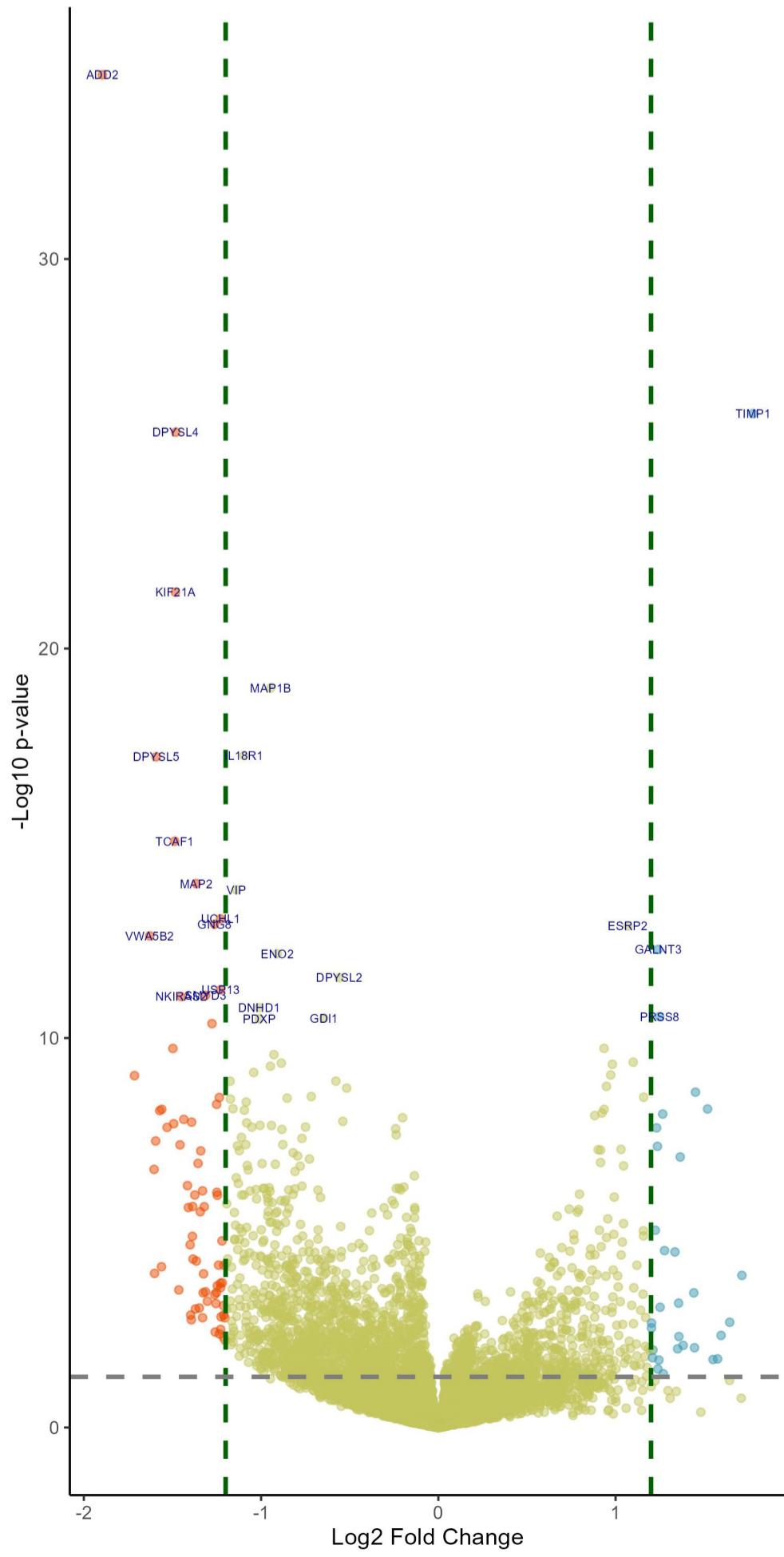
Differentially expressed proteins in blood cancers at absence/low amount of CRADD , DB2
p-value < 0.05 & logFC > 1.2



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

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.55	9.22e-12	ANKS1B	ankyrin repeat and sterile alpha mo	1.45	5.55e-08	E2F4	E2F transcription factor 4
-1.27	9.94e-08	LGALS3BP	galectin 3 binding protein	1.39	4.60e-05	LAMB1	laminin subunit beta 1
-1.36	1.93e-07	COL12A1	collagen type XII alpha 1 chain	1.09	4.60e-05	ZNF692	zinc finger protein 692
-1.39	9.29e-06	RPL22L1	ribosomal protein L22 like 1	1.17	4.60e-05	GCHFR	GTP cyclohydrolase I feedback regul
-1.24	2.90e-05	COL5A2	collagen type V alpha 2 chain	0.96	1.60e-03	TUBA8	tubulin alpha 8
-1.14	4.60e-05	MAP1B	microtubule associated protein 1B	1.21	2.49e-03	ZBTB42	zinc finger and BTB domain containi
-1.29	3.72e-04	MX1	MX dynamin like GTPase 1	0.92	2.49e-03	CDC37L1	cell division cycle 37 like 1
-0.46	8.24e-04	PAK3	p21 (RAC1) activated kinase 3	1.14	2.49e-03	ALDH1A1	aldehyde dehydrogenase 1 family mem
-1.36	1.46e-03	SPESP1	sperm equatorial segment protein 1	0.95	2.49e-03	OSBPL3	oxysterol binding protein like 3
-1.7	2.23e-03	UXS1	UDP-glucuronate decarboxylase 1	0.81	2.49e-03	AGTPBP1	ATP/GTP binding carboxypeptidase 1
-1.36	2.49e-03	CLK3	CDC like kinase 3	0.93	4.29e-03	ACTL6B	actin like 6B
-0.99	2.49e-03	VIP	vasoactive intestinal peptide	0.89	6.16e-03	NFYA	nuclear transcription factor Y subu
-0.37	3.29e-03	LRRC8E	leucine rich repeat containing 8 VR	0.98	6.66e-03	CHST9	carbohydrate sulfotransferase 9
-0.33	4.41e-03	TNS1	tensin 1	0.82	7.53e-03	SHKBP1	SH3KBP1 binding protein 1
-1.13	4.79e-03	JMD6	jumonji domain containing 6, argini	0.82	1.61e-02	CFAP36	cilia and flagella associated prote
-0.24	4.99e-03	PPFIA2	PTPRF interacting protein alpha 2	0.74	1.72e-02	HELZ2	helicase with zinc finger 2
-0.3	4.99e-03	NECTIN4	nectin cell adhesion molecule 4	0.79	2.17e-02	CBFA2T3	CBFA2/RUNX1 partner transcriptional
-0.84	6.16e-03	RCN1	reticulocalbin 1	0.72	2.26e-02	NAB2	NGFI-A binding protein 2
-1.1	6.66e-03	NPR2	natriuretic peptide receptor 2	1.32	2.48e-02	FCHSD2	FCH and double SH3 domains 2
-0.34	8.58e-03	ESPN	espin	0.68	2.98e-02	MED13	mediator complex subunit 13
-0.21	9.51e-03	CES2	carboxylesterase 2	0.76	3.24e-02	ZBTB32	zinc finger and BTB domain containi
-0.19	1.31e-02	TMCC2	transmembrane and coiled-coil domai	0.7	3.89e-02	MEF2A	myocyte enhancer factor 2A
-0.89	1.42e-02	PLOD3	procollagen-lysine,2-oxoglutarate 5	0.65	4.03e-02	PRMT7	protein arginine methyltransferase
-0.91	1.74e-02	WRAP73	WD repeat containing, antisense to	0.63	4.42e-02	MINK1	misshapen like kinase 1
-0.16	1.90e-02	PKIA	cAMP-dependent protein kinase inhib	0.67	4.71e-02	MGAT5	alpha-1,6-mannosylglycoprotein 6-be
-0.82	2.01e-02	CNTN5	contactin 5	0.58	6.49e-02	COX7A2	cytochrome c oxidase subunit 7A2
-0.22	2.13e-02	EIF2B4	eukaryotic translation initiation f	0.99	6.55e-02	VPS33A	VPS33A core subunit of CORVET and H
-0.15	3.08e-02	RBP4	retinol binding protein 4	0.75	6.68e-02	FZD6	frizzled class receptor 6
-1.63	4.71e-02	DHRS9	dehydrogenase/reductase 9	0.77	7.10e-02	POF1B	POF1B actin binding protein
-0.67	4.71e-02	THEM6	thioesterase superfamily member 6	0.88	8.48e-02	CIC	capicua transcriptional repressor
-1.31	4.76e-02	LHPP	phospholysine phosphohistidine inor	0.71	8.48e-02	SPRYD7	SPRY domain containing 7
-0.8	6.68e-02	AAK1	AP2 associated kinase 1	1.07	8.91e-02	NECTIN1	nectin cell adhesion molecule 1
-0.32	7.32e-02	EYA1	EYA transcriptional coactivator and	0.66	9.11e-02	SNX11	sorting nexin 11
-1.02	7.33e-02	TOM1L2	target of myb1 like 2 membrane traf	0.71	9.11e-02	NRM	nurim
-0.22	8.48e-02	LEMD2	LEM domain nuclear envelope protein	0.82	9.11e-02	EPHA2	EPH receptor A2
-0.79	8.48e-02	TICRR	TOPBP1 interacting checkpoint and r	0.85	9.20e-02	KIF21A	kinesin family member 21A
-0.8	9.11e-02	PREX1	phosphatidylinositol-3,4,5-trisphos	0.67	9.58e-02	CXXC5	CXXC finger protein 5
-0.75	9.58e-02	ARHGEF12	Rho guanine nucleotide exchange fac	0.72	9.98e-02	PAXIP1	PAX interacting protein 1
0.75	1.13e-01	TIP1	tight junction protein 1	0.71	1.05e-01	MAGI1	membrane associated guanylate kinase

Differentially expressed proteins in solid cancers at absence/low amount of CRADD , DB2
p-value < 0.05 & logFC > 1.2



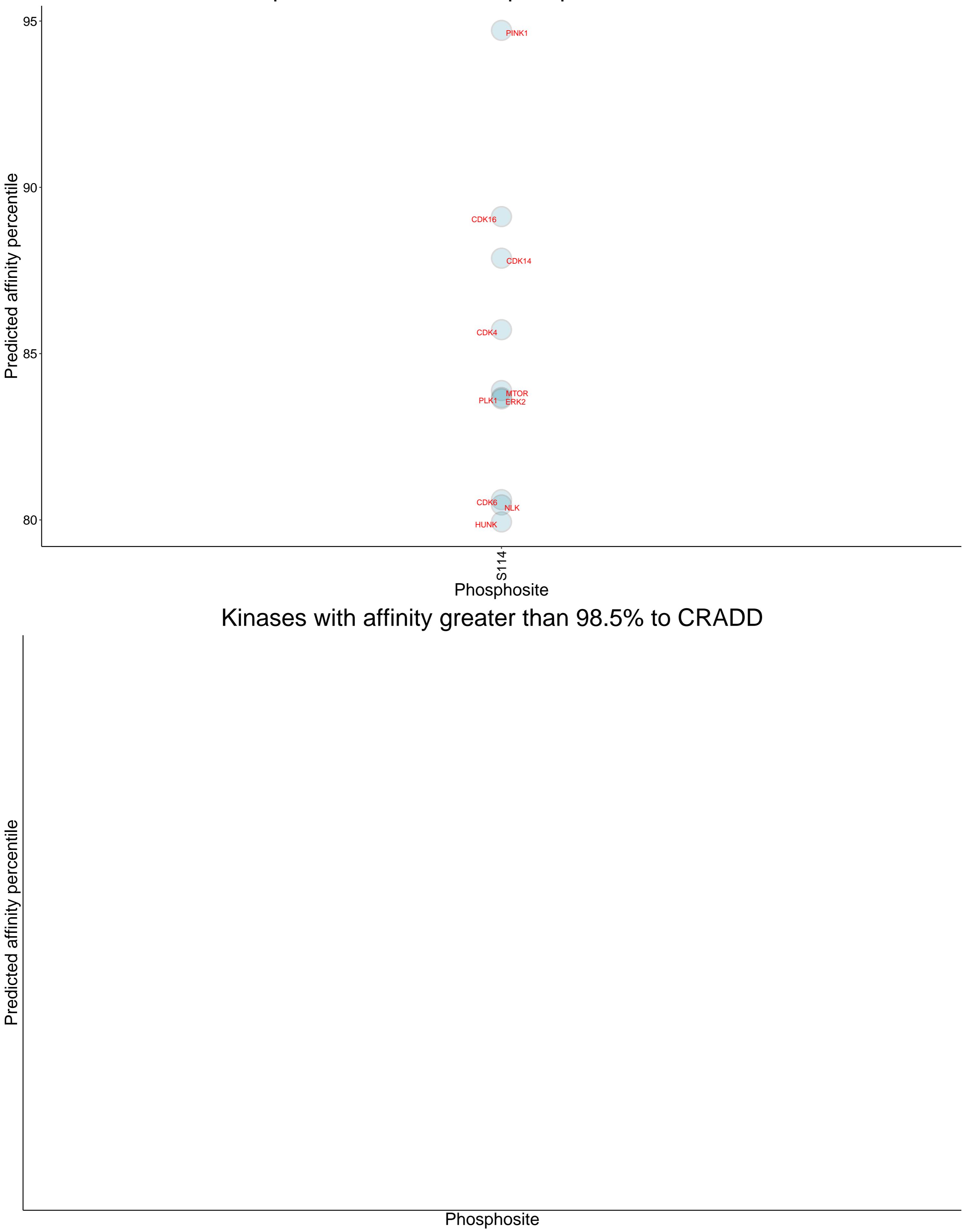
Sorted by p values!
Downregulated in solid cancers at low/absent CRADD Upregulated in solid cancers at low/absent CRADD

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.9	7.79e-32	ADD2	adducin 2	1.78	2.59e-23	TIMP1	TIMP metallopeptidase inhibitor 1
-1.48	5.84e-23	DPYSL4	dihydropyrimidinase like 4	1.07	7.96e-11	ESRP2	epithelial splicing regulatory prot
-1.48	5.99e-19	KIF21A	kinesin family member 21A	1.24	2.79e-10	GALNT3	polypeptide N-acetylgalactosaminylt
-0.95	1.45e-16	MAP1B	microtubule associated protein 1B	1.25	1.03e-08	PRSS8	serine protease 8
-1.1	6.29e-15	IL18R1	interleukin 18 receptor 1	0.94	5.54e-08	PHLDA1	pleckstrin homology like domain fam
-1.59	6.29e-15	DPYSL5	dihydropyrimidinase like 5	1.1	1.16e-07	SLC22A18	solute carrier family 22 member 18
-1.49	8.24e-13	TCAF1	TRPM8 channel associated factor 1	0.98	1.24e-07	GRHL2	grainyhead like transcription facto
-1.37	9.11e-12	MAP2	microtubule associated protein 2	0.97	2.12e-07	STING1	stimulator of interferon response c
-1.14	1.19e-11	VIP	vasoactive intestinal peptide	0.95	3.74e-07	CENPE	centromere protein E
-1.23	6.09e-11	UCHL1	ubiquitin C-terminal hydrolase L1	1.45	5.01e-07	TRPM4	transient receptor potential cation
-1.26	7.71e-11	GNG8	G protein subunit gamma 8	1.16	6.40e-07	CD46	CD46 molecule
-1.63	1.33e-10	VWA5B2	von Willebrand factor A domain cont	1.52	1.09e-06	LAMC2	laminin subunit gamma 2
-0.91	3.36e-10	ENO2	enolase 2	0.94	1.09e-06	FAM83B	family with sequence similarity 83
-0.56	1.31e-09	DPYSL2	dihydropyrimidinase like 2	0.92	1.28e-06	ECM1	extracellular matrix protein 1
-1.23	2.56e-09	USP13	ubiquitin specific peptidase 13	1.27	1.33e-06	LRRC1	leucine rich repeat containing 1
-1.31	3.37e-09	SMYD3	SET and MYND domain containing 3	0.88	1.44e-06	ITGB8	integrin subunit beta 8
-1.45	3.43e-09	NKIRAS2	NFKB inhibitor interacting Ras like	1.23	2.46e-06	HLA-F	major histocompatibility complex, c
-1.01	6.29e-09	DNHD1	dynein heavy chain domain 1	1.24	6.32e-06	TMEM63A	transmembrane protein 63A
-0.65	1.07e-08	GDI1	GDP dissociation inhibitor 1	1.03	7.47e-06	PHC3	polyhomeotic homolog 3
-1.01	1.07e-08	PDXP	pyridoxal phosphatase	0.9	7.52e-06	ANKRD22	ankyrin repeat domain 22
-1.28	1.37e-08	CDC34	cell division cycle 34, ubiquitin c	0.92	7.61e-06	MSLN	mesothelin
-1.5	5.54e-08	CRMP1	collapsin response mediator protein	1.36	1.08e-05	KRT74	keratin 74
-0.93	7.69e-08	NUDT3	nudix hydrolase 3	0.92	1.46e-05	OXLD1	oxidoreductase like domain containi
-0.89	1.19e-07	PBK	PDZ binding kinase	1.04	1.69e-05	GRN	granulin precursor
-0.95	1.35e-07	ZNF428	zinc finger protein 428	0.8	7.10e-05	MPP7	MAGUK p55 scaffold protein 7
-1.04	1.89e-07	CCDC73	coiled-coil domain containing 73	0.99	7.97e-05	GLMP	glycosylated lysosomal membrane pro
-1.71	2.15e-07	MLLT11	MLLT11 transcription factor 7 cofac	0.74	1.42e-04	MST1R	macrophage stimulating 1 receptor
-0.58	2.83e-07	TUBB2B	tubulin beta 2B class IIb	0.79	1.45e-04	GALNT5	polypeptide N-acetylgalactosaminylt
-1.18	2.83e-07	MROH2B	maestro heat like repeat family mem	0.78	1.64e-04	ADIRF	adipogenesis regulatory factor
-0.52	4.04e-07	AASDHPP1</					

Insufficient number of paired observations in DB2 for CRADD

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Top 10 kinases for each phosphosite in CRADD



No sufficient number of paired observations in DB2 for CRADD