

CRIP1

Protein name: CRIP1 ;

UNIPROT: P50238 ;

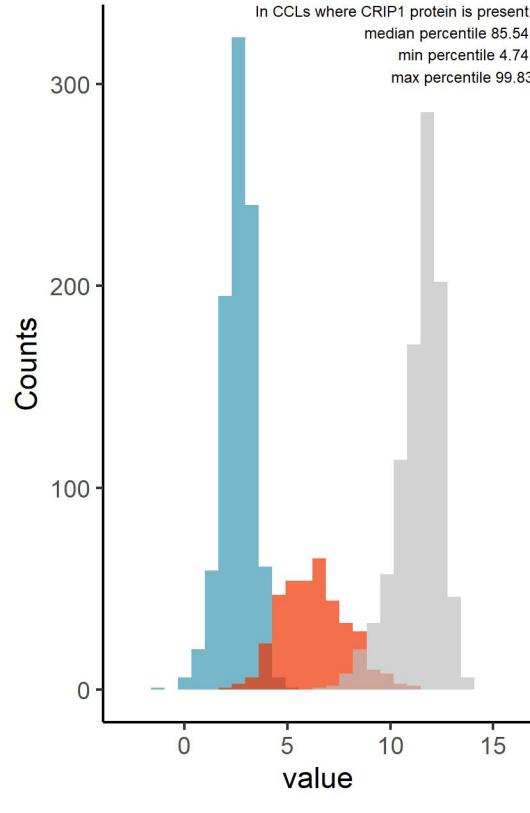
Gene name: cysteine rich protein 1

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

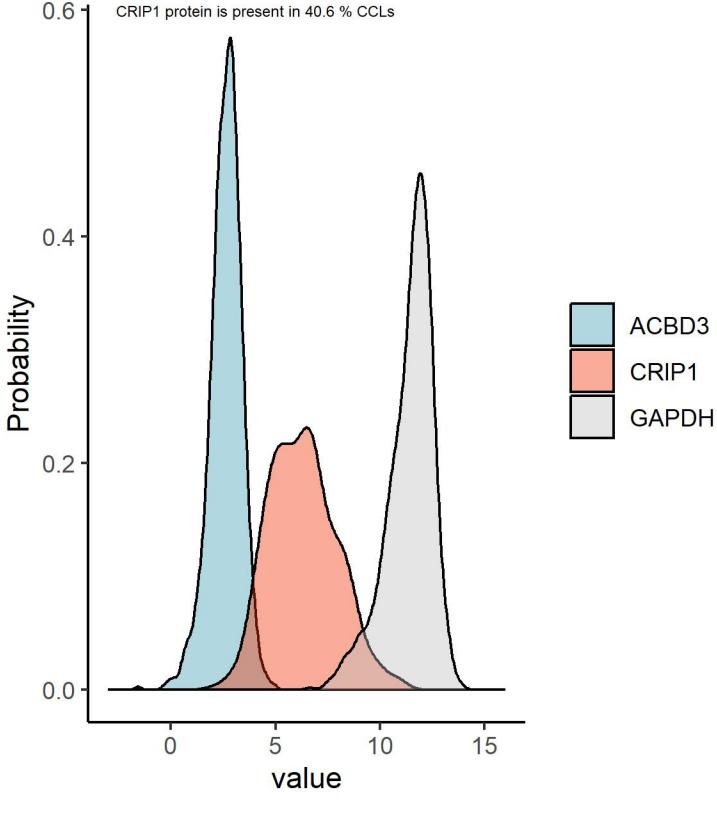
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of CRIP1 protein compared to proteins with low and high abundance



Density plot of CRIP1 protein compared to proteins with low and high abundance



Top negative correlations of CRIP1 protein, DB1

EFTUD2
RCL1
RRP9
DDX18
LAMB3
NUP93

HEATR1
CAV1
NAT10
WDR43
NOP56
NUP107

LAMC2

Top positive correlations of CRIP1 protein, DB1

NOL3

CRIP2

AP1M2
S100P

STARD10

BAG1

ITPK1

PPIA

PYM1

CMPK1
ADIRF

CRABP2

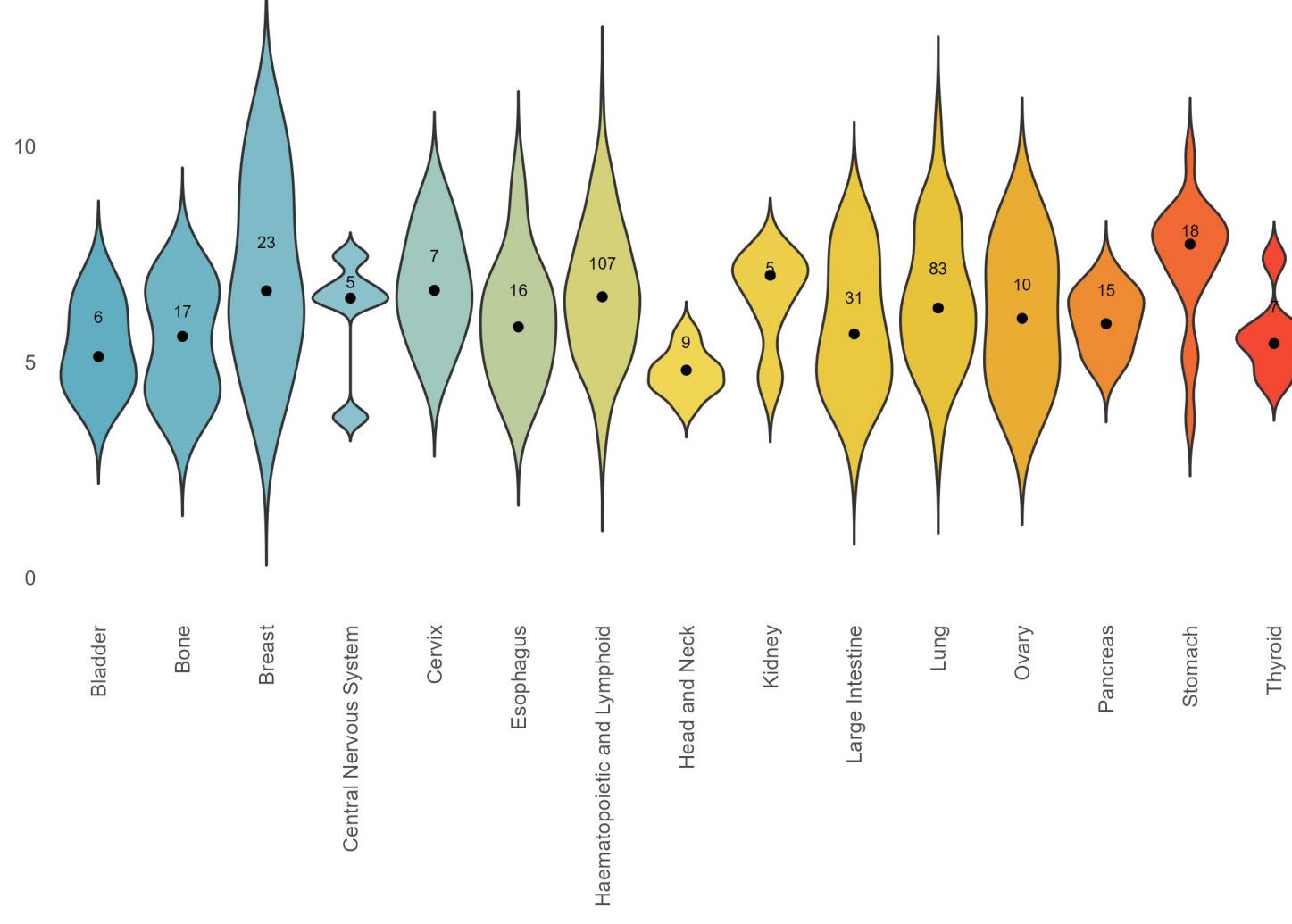
SPAG7

AP1G2

SOD1

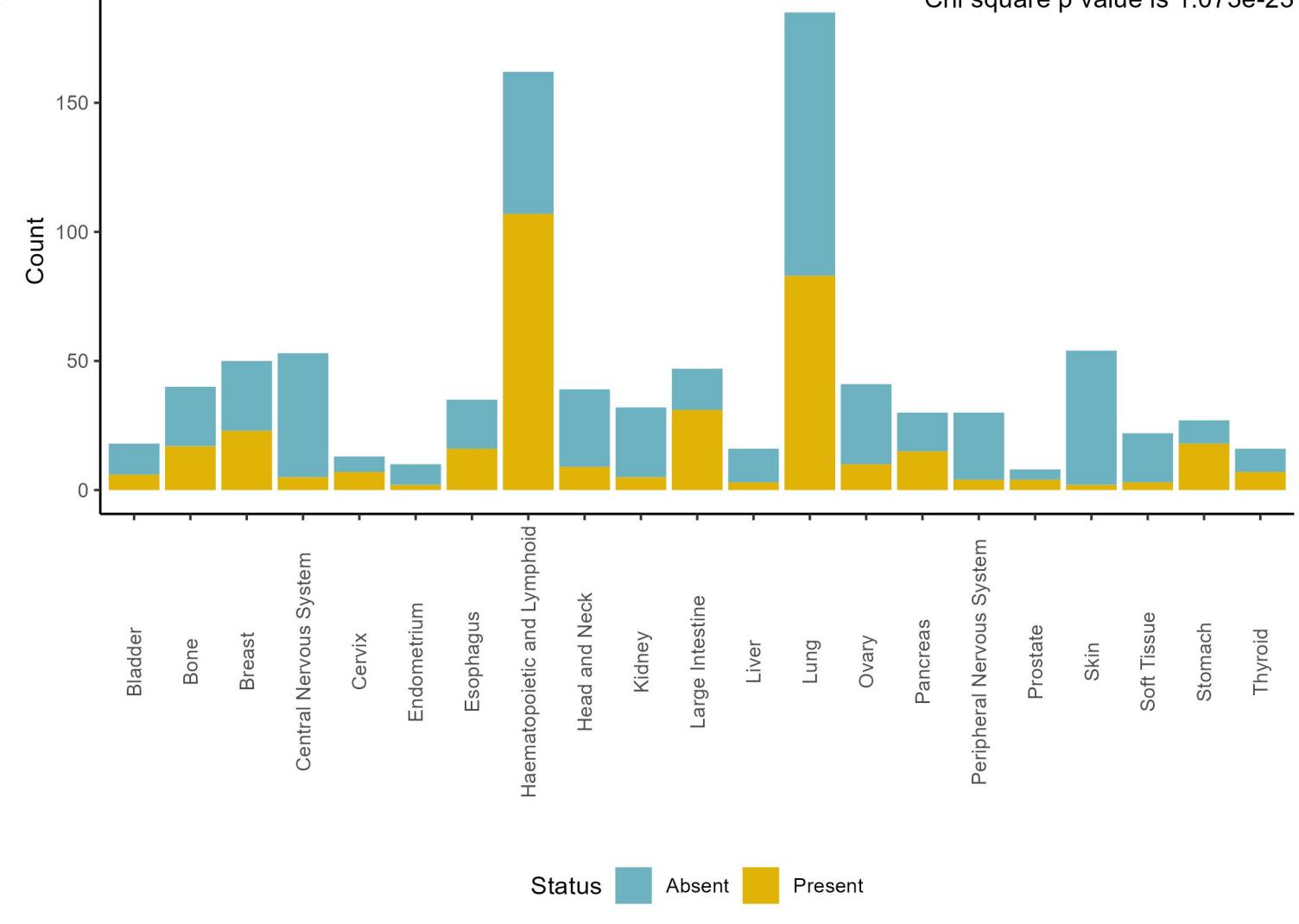
Amount of CRIP1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 3.217e-04



Present and absent CRIP1 protein counts by tissue, DB1

Chi square p value is 1.073e-23

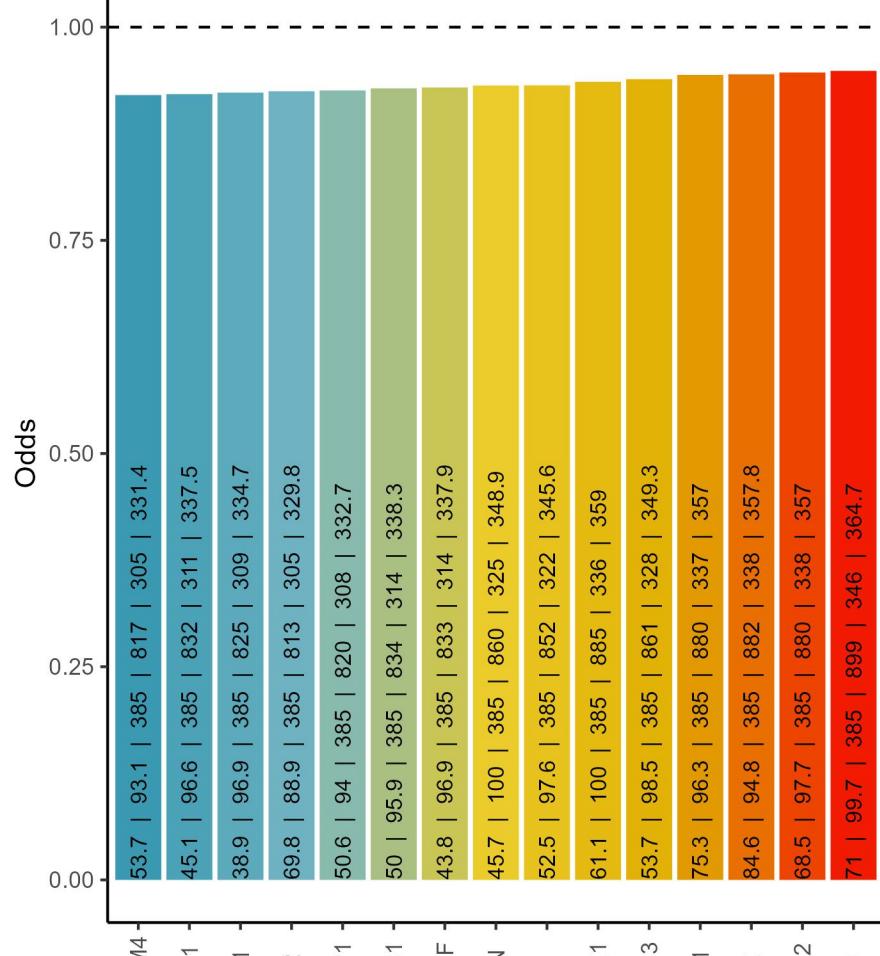


Cooccurrence with CRIP1 protein, DB1

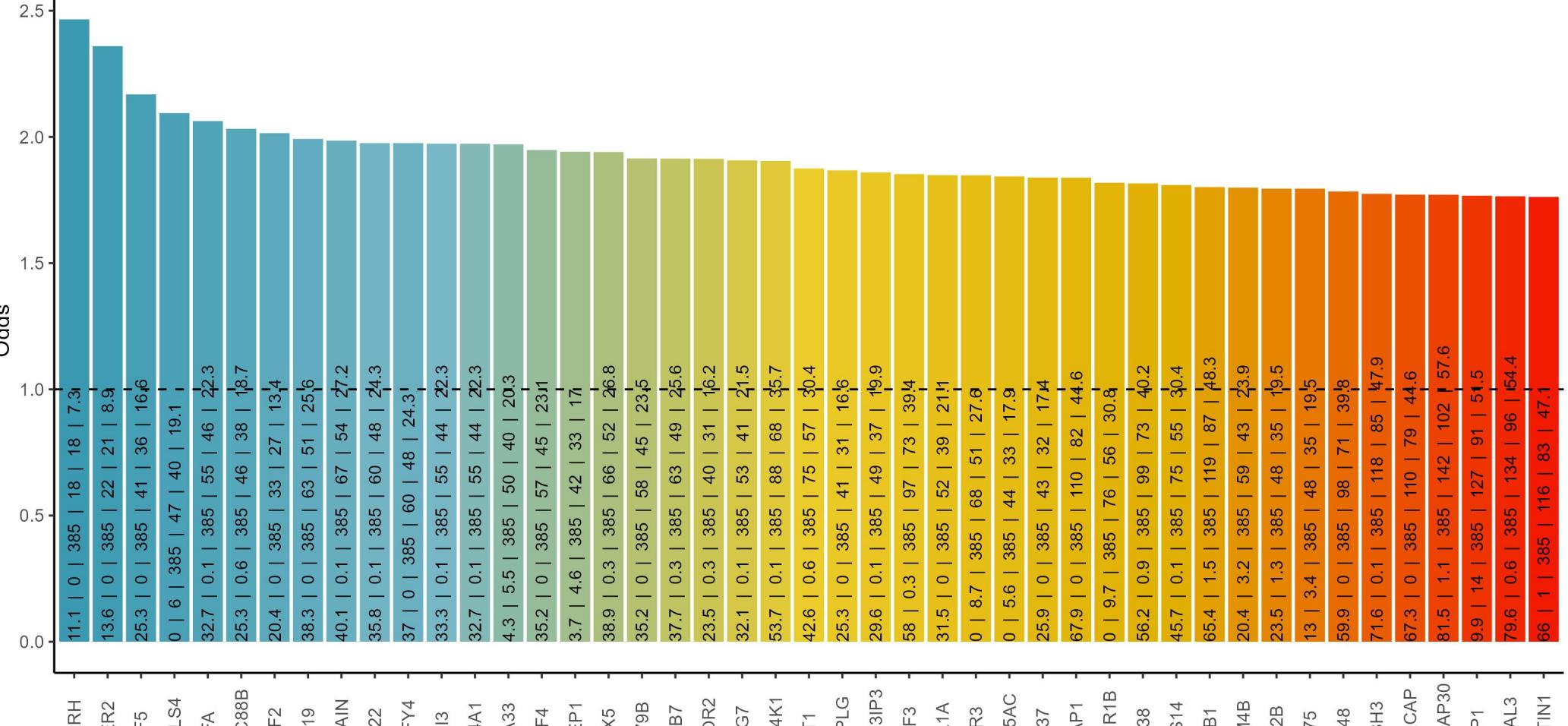
% of CRIP1 in blood cancers: 66 ; % of CRIP1 in solid cancers: 35.1

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CRIP1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

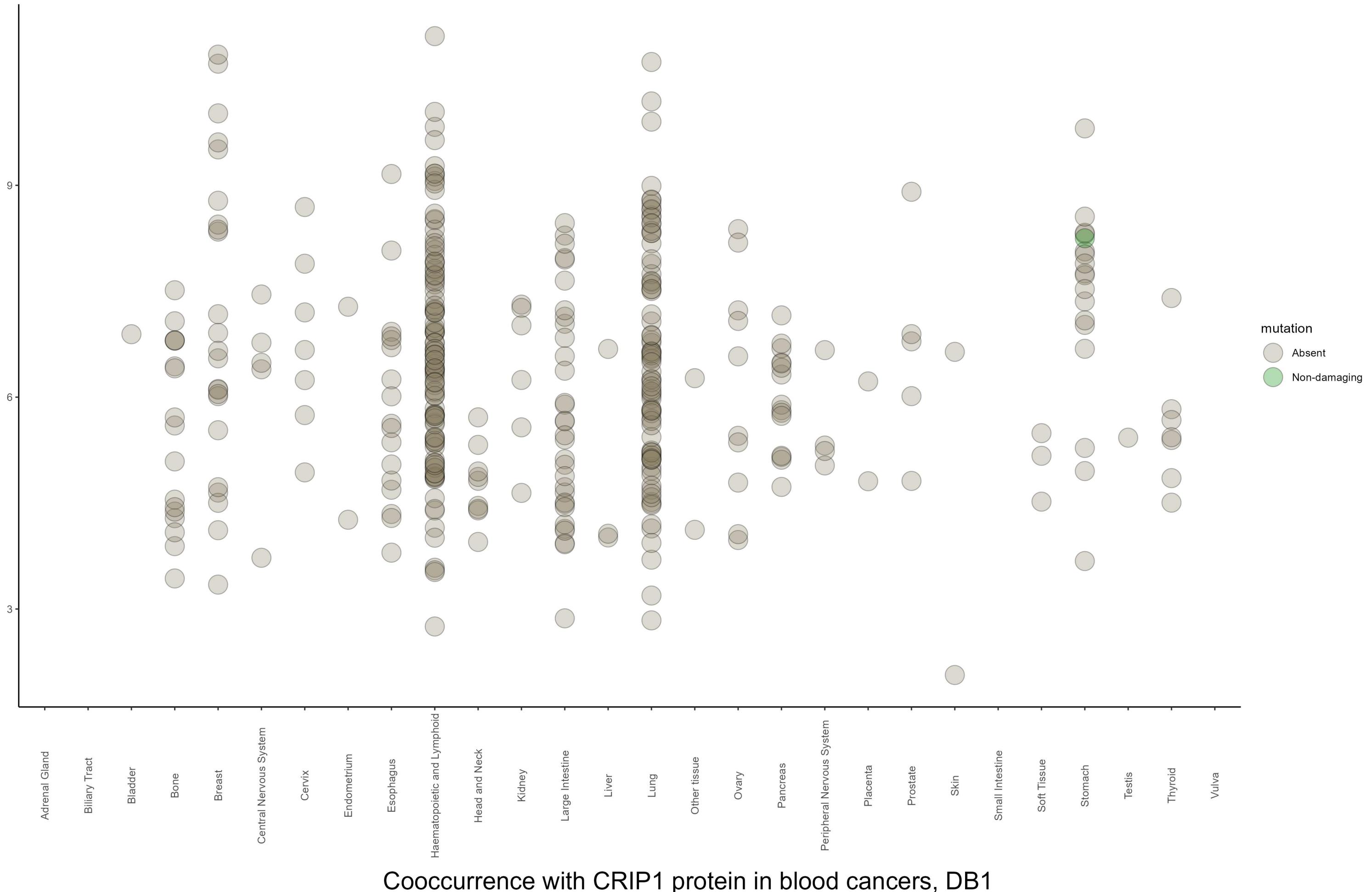
Negative cooccurrence



Positive cooccurrence

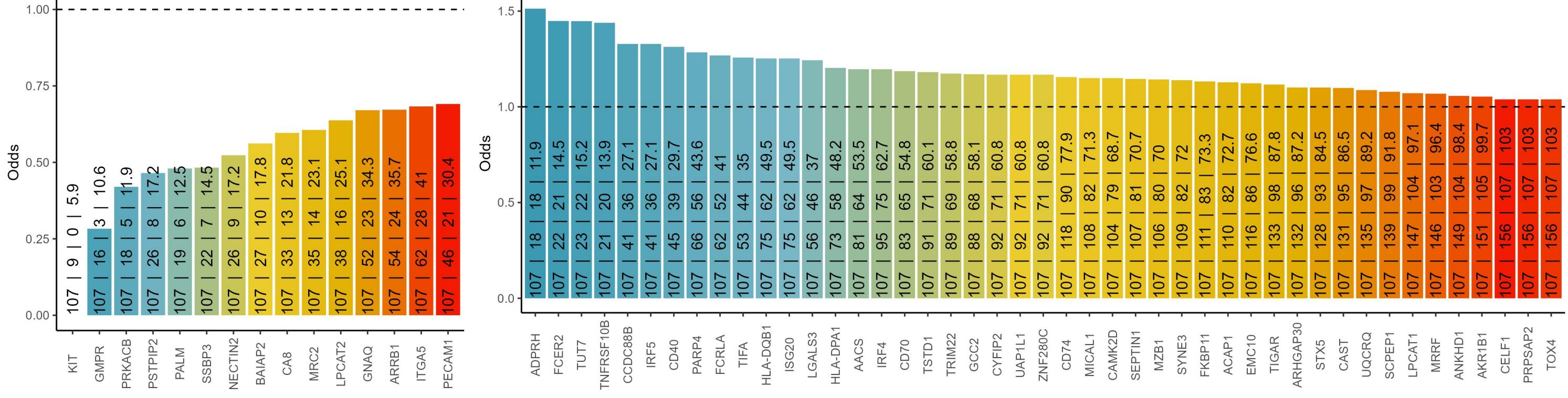


Amount of CRIP1 protein and mutation status by tissue, DB1



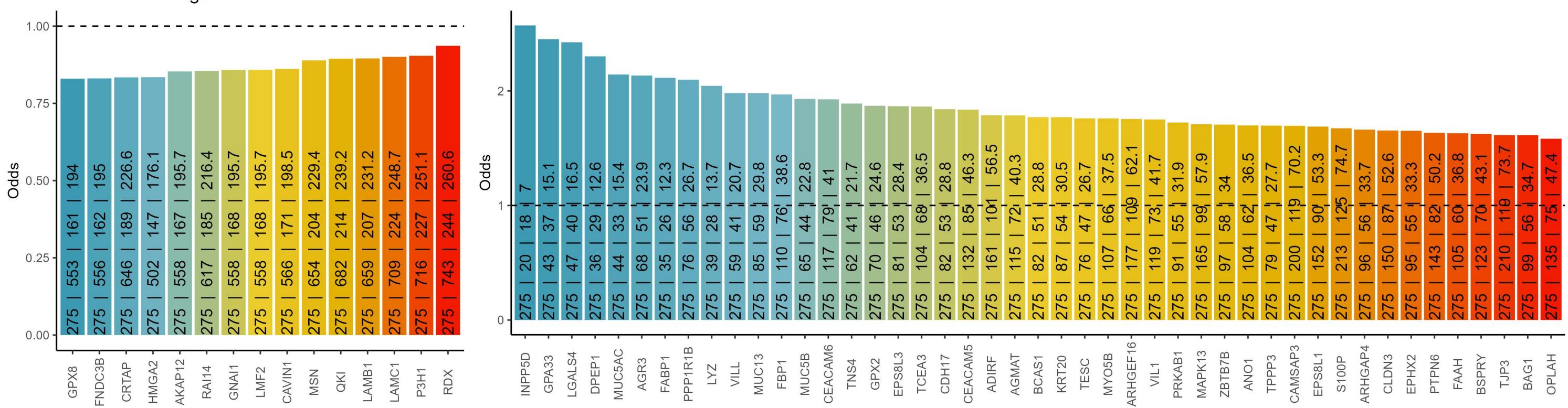
Cooccurrence with CRIP1 protein in blood cancers, DB1

The text in the bars: incidence of CRIP1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

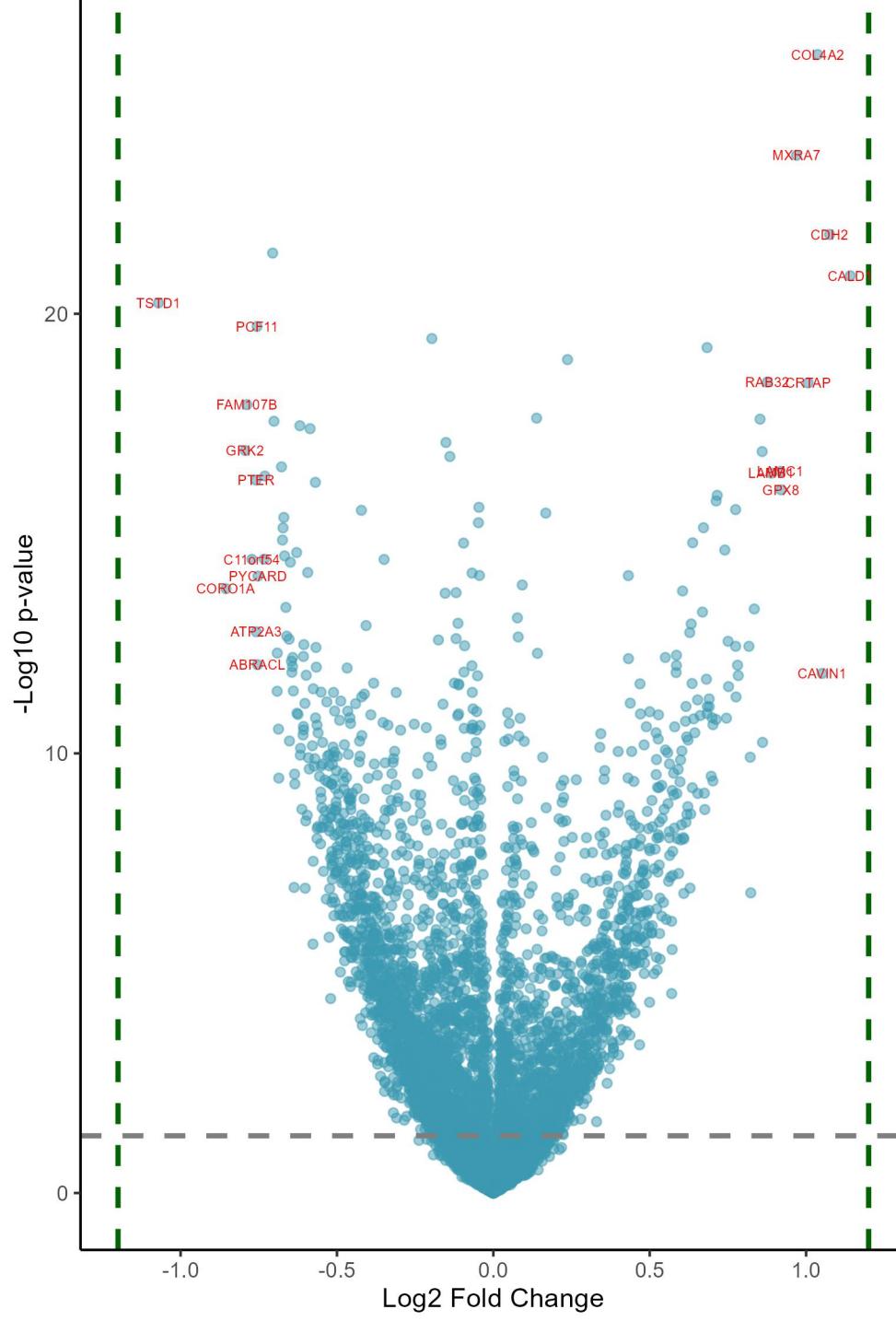


Cooccurrence with CRIP1 protein in solid cancers, DB1

The text in the bars: incidence of CRIP1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

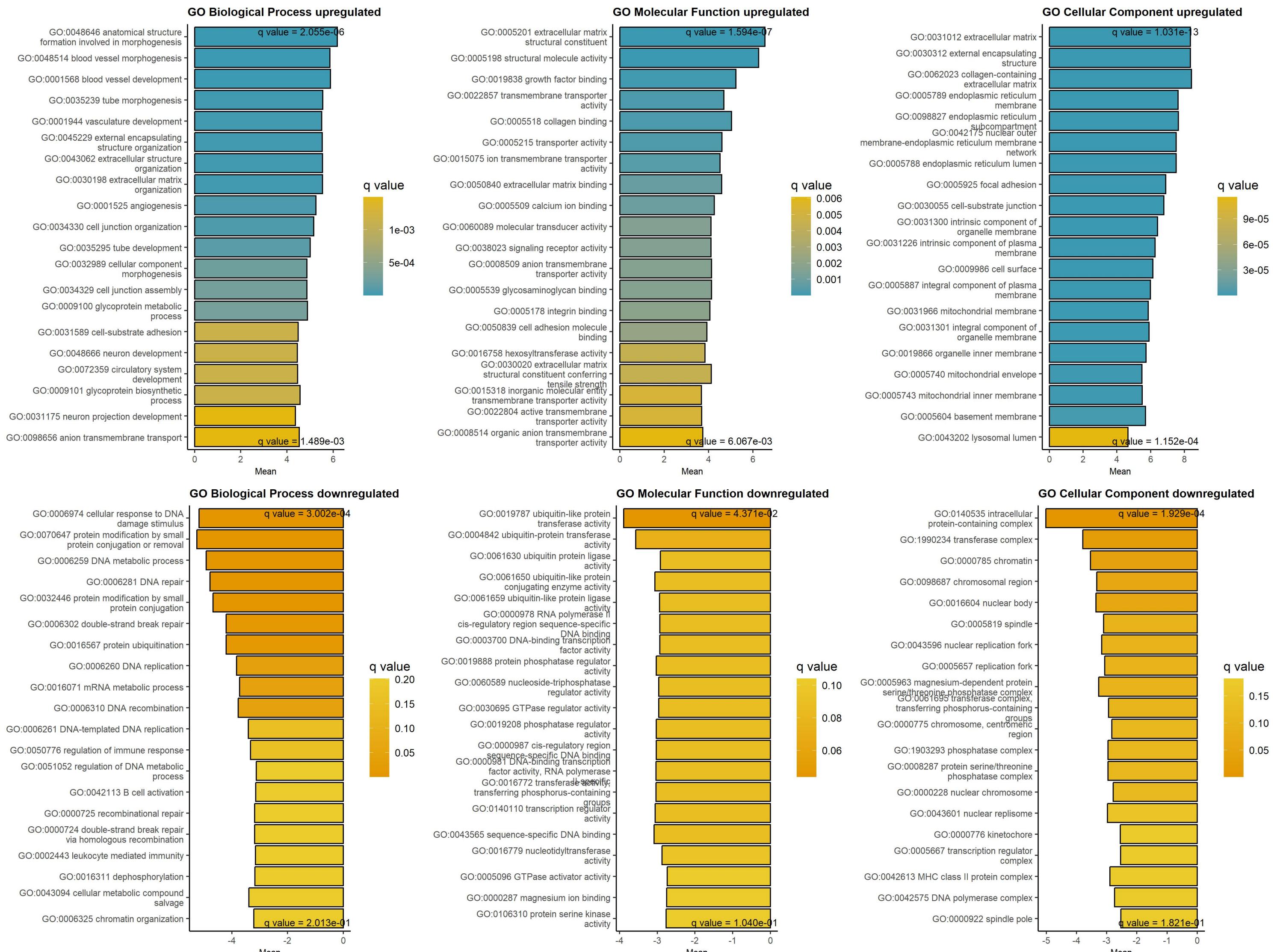


Downregulated at low/absent CRIP1 Upregulated at low/absent CRIP1



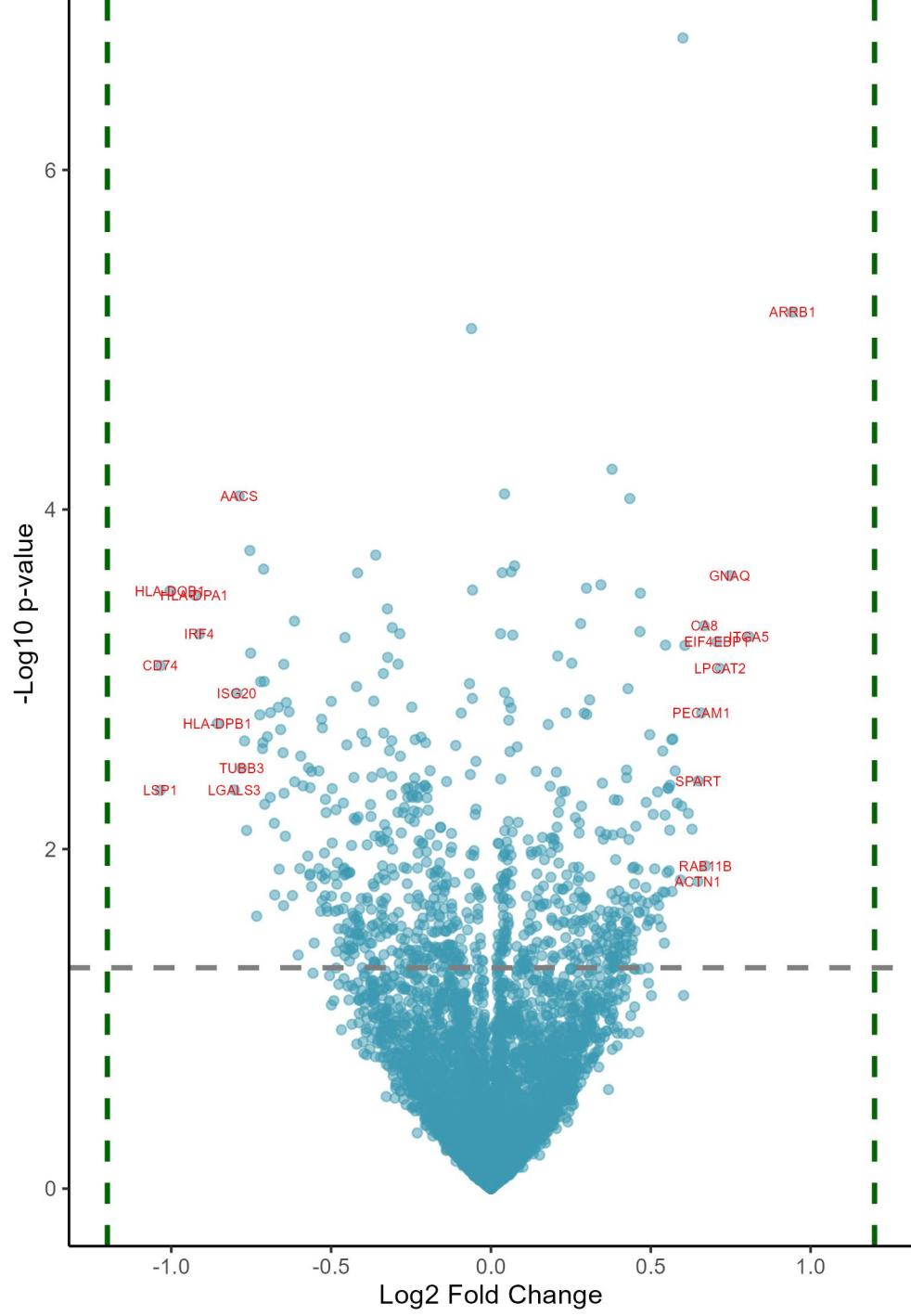
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.07	5.39e-18	TSTD1	thiosulfate sulfurtransferase like	1.14	1.51e-18	CALD1	caldesmon 1
-0.86	2.09e-12	CORO1A	coronin 1A	1.08	2.61e-19	CDH2	cadherin 2
-0.79	4.08e-15	GRK2	G protein-coupled receptor kinase 2	1.05	1.02e-10	CAVIN1	caveolae associated protein 1
-0.79	5.55e-16	FAM107B	family with sequence similarity 107	1.04	4.22e-23	COL4A2	collagen type IV alpha 2 chain
-0.77	5.26e-13	C11orf54	chromosome 11 open reading frame 54	1.01	1.91e-16	CRTAP	cartilage associated protein
-0.76	1.44e-14	PTER	phosphotriesterase related	0.97	5.51e-21	MXRAT7	matrix remodeling associated 7
-0.76	1.68e-11	ATP2A3	ATPase sarcoplasmic/endoplasmic reticulum Ca ²⁺ /Mg ²⁺ transporting 2A	0.92	2.24e-14	GPX8	glutathione peroxidase 8 (putative)
-0.76	1.61e-17	PCF11	PCF11 cleavage and polyadenylation specific factor 1	0.92	1.02e-14	LAMC1	laminin subunit gamma 1
-0.75	7.16e-11	ABRACL	ABRA C-terminal like	0.89	1.08e-14	LAMB1	laminin subunit beta 1
-0.75	1.12e-12	PYCARD	PYD and CARD domain containing	0.88	1.91e-16	RAB32	RAB32, member RAS oncogene family
-0.73	5.26e-13	PTPN6	protein tyrosine phosphatase non-receptor type 6	0.86	1.93e-09	FKBP10	FKBP prolyl isomerase 10
-0.73	1.21e-14	ARHGAP4	Rho GTPase activating protein 4	0.86	4.12e-15	SPARC	secreted protein acidic and cysteine rich
-0.71	5.53e-19	PLS1	plastin 1	0.85	1.04e-15	RAI14	retinoic acid induced 14
-0.7	1.09e-15	CHMP4A	charged multivesicular body protein A	0.83	5.56e-12	IKBIP	IKBKB interacting protein
-0.69	2.27e-10	SERF2	small EDRK-rich factor 2	0.82	1.56e-06	GNG12	G protein subunit gamma 12
-0.69	4.29e-11	GCA	grancalcin	0.82	3.73e-09	CAV1	caveolin 1
-0.69	1.09e-09	HPDL	4-hydroxyphenylpyruvate dioxygenase	0.82	3.09e-11	THBS1	thrombospondin 1
-0.69	9.52e-09	VAMP8	vesicle associated membrane protein 8	0.78	1.12e-10	P4HA2	prolyl 4-hydroxylase subunit alpha
-0.68	8.41e-15	OSGEF	O-sialoglycoprotein endopeptidase	0.78	7.30e-11	ITGA5	integrin subunit alpha 5
-0.67	2.28e-13	TKFC	triokinase and FMN cyclase	0.78	2.88e-10	MMP14	matrix metallopeptidase 14
-0.67	1.23e-13	STXBP2	syntaxin binding protein 2	0.77	3.09e-11	HMGA2	high mobility group AT-hook 2
-0.67	7.72e-14	LRBA	LPS responsive beige-like anchor protein	0.77	5.57e-14	FNDC3B	fibronectin type III domain containing protein 3
-0.67	4.66e-13	GMPR2	guanosine monophosphate reductase 2	0.75	1.83e-10	CD276	CD276 molecule
-0.66	5.21e-12	RNF113A	ring finger protein 113A	0.75	2.50e-11	GNAI1	G protein subunit alpha i1
-0.66	2.04e-11	SEPHS2	seleophosphate synthetase 2	0.75	6.98e-10	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.65	2.30e-11	NFATC2IP	nuclear factor of activated T cells 2	0.74	3.58e-13	SYNM	synemin
-0.65	1.85e-09	GMDS	GDP-mannose 4,6-dehydratase	0.72	2.90e-14	COL18A1	collagen type XVIII alpha 1 chain
-0.65	5.97e-13	TPRKB	TP53RK binding protein	0.71	3.76e-14	KIRREL1	kirre like nephrin family adhesion molecule
-0.65	6.05e-11	TP53RK	TP53 regulating kinase	0.71	7.35e-10	AXL	AXL receptor tyrosine kinase

GAGE analysis on upregulated and downregulated proteins at low/absent CRIP1 protein, DB1

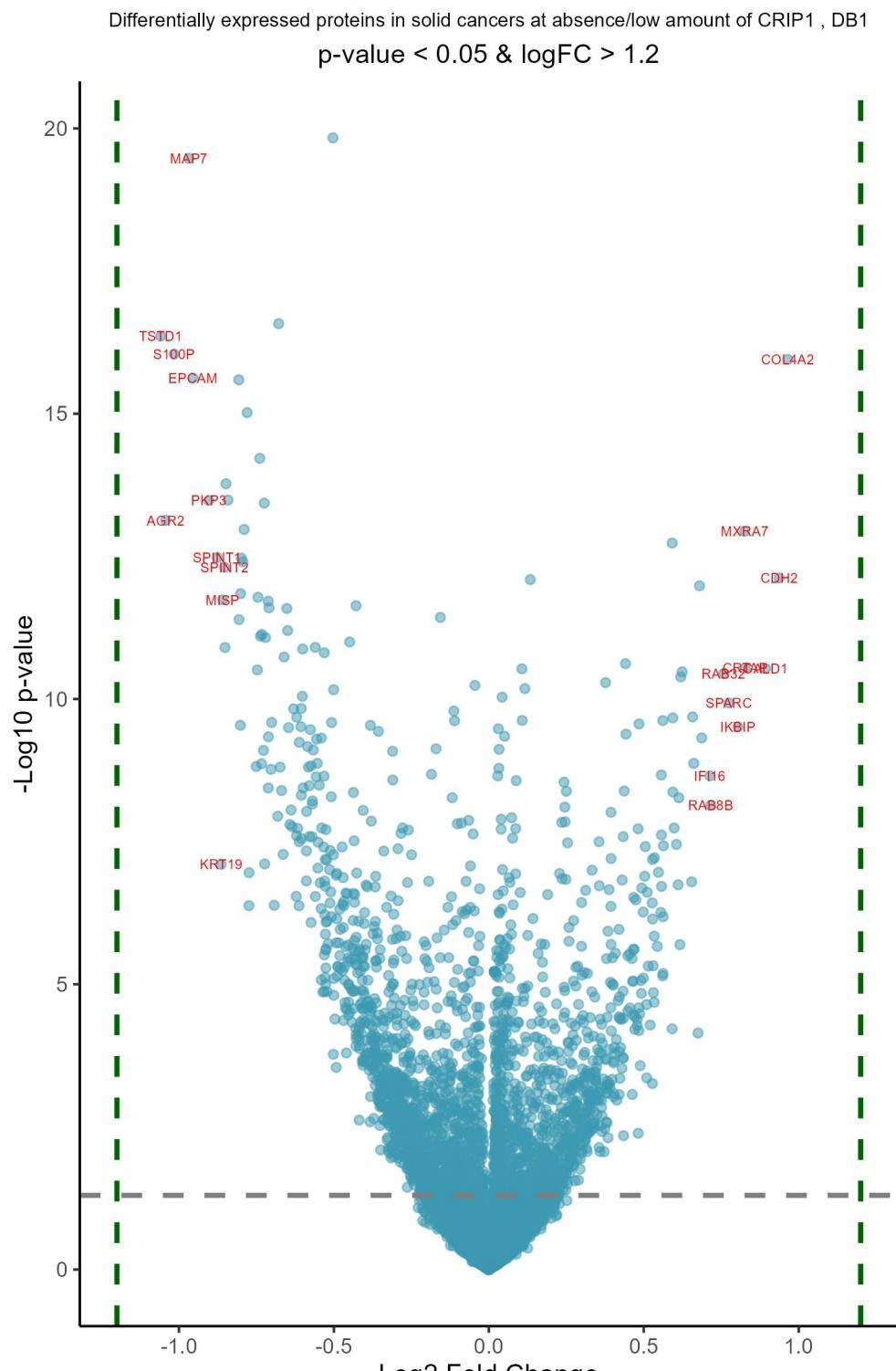


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent CRIP1 Upregulated in blood cancers at low/absent CRIP1

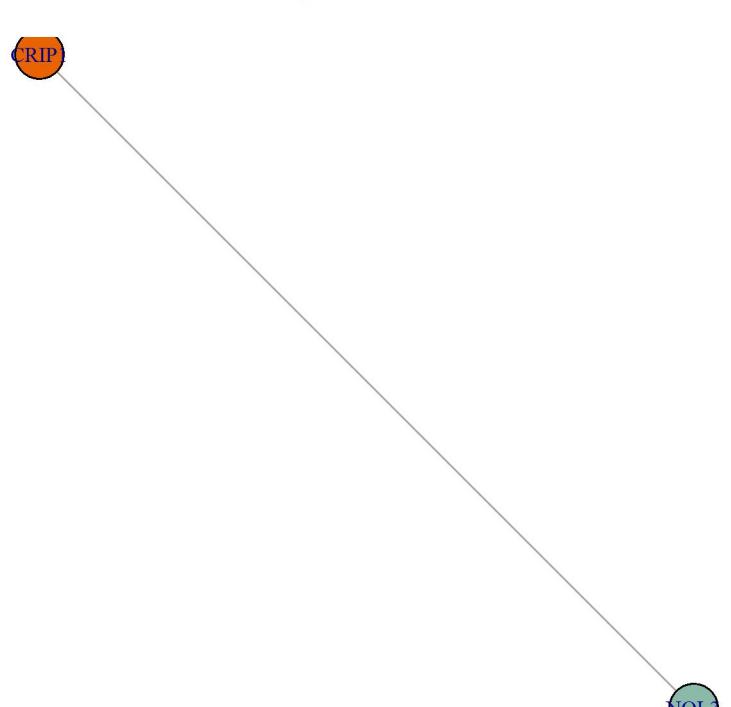


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.03	2.19e-01	LSP1	lymphocyte specific protein 1	0.94	1.43e-02	ARRB1	arrestin beta 1
-1.03	1.26e-01	CD74	CD74 molecule	0.81	1.11e-01	ITGA5	integrin subunit alpha 5
-1	9.64e-02	HLA-DQB1	major histocompatibility complex, c	0.75	9.64e-02	GNAQ	G protein subunit alpha q
-0.93	9.64e-02	HLA-DPA1	major histocompatibility complex, c	0.72	1.28e-01	LPCAT2	lysophosphatidylcholine acyltransfe
-0.91	1.11e-01	IRF4	interferon regulatory factor 4	0.71	1.13e-01	EIF4EBP1	eukaryotic translation initiation f
-0.86	1.66e-01	HLA-DPB1	major histocompatibility complex, c	0.67	3.21e-01	RAB11B	RAB11B, member RAS oncogene family
-0.8	2.19e-01	LGALS3	galectin 3	0.67	1.11e-01	CA8	carbonic anhydrase 8
-0.79	1.52e-01	ISG20	interferon stimulated exonuclease g	0.66	1.54e-01	PECAM1	platelet and endothelial cell adhes
-0.79	7.16e-02	AACS	acetoacetyl-CoA synthetase	0.65	2.18e-01	SPART	spartin
-0.78	2.15e-01	TUBB3	tubulin beta 3 class III	0.65	3.30e-01	ACTN1	actinin alpha 1
-0.77	1.77e-01	FKBP11	FKBP prolyl isomerase 11	0.63	2.66e-01	SAMSN1	SAM domain, SH3 domain and nuclear
-0.76	2.67e-01	CD70	CD70 molecule	0.62	2.40e-01	CFAP20	cilia and flagella associated prote
-0.75	9.64e-02	SYNE3	spectrin repeat containing nuclear	0.61	1.13e-01	PSTPIP2	proline-serine-threonine phosphatas
-0.75	1.23e-01	ACAP1	ArfGAP with coiled-coil, ankyrin re	0.6	5.09e-01	SPN	sialophorin
-0.73	3.77e-01	MZB1	marginal zone B and B1 cell specifi	0.6	5.55e-04	ALDH1A1	aldehyde dehydrogenase 1 family mem
-0.72	1.54e-01	MYOF	myoferlin	0.6	2.32e-01	IREB2	iron responsive element binding pro
-0.72	1.43e-01	SAMHD1	SAM and HD domain containing deoxyn	0.59	3.28e-01	LCP2	lymphocyte cytosolic protein 2
-0.71	1.83e-01	ISG15	ISG15 ubiquitin like modifier	0.58	2.29e-01	MCU	mitochondrial calcium uniporter
-0.71	1.77e-01	TES	testin LIM domain protein	0.58	2.15e-01	MTF2	metal response element binding tran
-0.71	9.64e-02	FAM107B	family with sequence similarity 107	0.57	1.77e-01	STAT3	signal transducer and activator of
-0.71	1.43e-01	UAP1L1	UDP-N-acetylgalcosamine pyrophospho	0.57	3.47e-01	MPP1	MAGUK p55 scaffold protein 1
-0.71	2.30e-01	VPS37C	VPS37C subunit of ESCRT-I	0.57	1.77e-01	NECTIN2	nectin cell adhesion molecule 2
-0.7	1.77e-01	TYMP	thymidine phosphorylase	0.56	2.18e-01	KATNA1	katanin catalytic subunit A1
-0.69	2.23e-01	IKZF3	IKAROS family zinc finger 3	0.56	2.67e-01	HNRNPLL	heterogeneous nuclear ribonucleopro
-0.69	1.54e-01	NFKB2	nuclear factor kappa B subunit 2	0.56	3.21e-01	HEBP1	heme binding protein 1
-0.68	2.53e-01	CAMK2D	calcium/calmodulin dependent protei	0.55	2.18e-01	NDUFC2	NADH:ubiquinone oxidoreductase subu
-0.68	3.50e-01	JCHAIN	joining chain of multimeric IgA and	0.55	2.18e-01	CAMK2G	calcium/calmodulin dependent protei
-0.67	1.54e-01	SLC4A2	solute carrier family 4 member 2	0.55	3.21e-01	SCML2	Scm polycomb group protein like 2
-0.66	3.21e-01	SEPTIN1	septin 1	0.55	1.13e-01	RAB32	RAB32, member RAS oncogene family



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.06	5.82e-14	TSTD1	thiosulfate sulfurtransferase like	0.96	1.06e-13	COL4A2	collagen type IV alpha 2 chain
-1.04	3.08e-11	AGR2	anterior gradient 2, protein disulp	0.94	2.09e-10	CDH2	cadherin 2
-1.02	1.00e-13	S100P	S100 calcium binding protein P	0.89	4.01e-09	CALD1	caldesmon 1
-0.97	7.40e-17	MAP7	microtubule associated protein 7	0.83	4.01e-09	CRTAP	cartilage associated protein
-0.95	1.88e-13	EPCAM	epithelial cell adhesion molecule	0.83	4.23e-11	MXRA7	matrix remodeling associated 7
-0.9	1.57e-11	PKP3	plakophilin 3	0.8	2.69e-08	IKBIP	IKBKB interacting protein
-0.88	1.08e-10	SPINT1	serine peptidase inhibitor, Kunitz	0.77	1.30e-08	SPARC	secreted protein acidic and cystein
-0.86	2.84e-06	KRT19	keratin 19	0.76	4.56e-09	RAB32	RAB32, member RAS oncogene family
-0.86	4.20e-10	MISP	mitotic spindle positioning	0.72	3.82e-07	RAB8B	RAB8B, member RAS oncogene family
-0.85	1.42e-10	SPINT2	serine peptidase inhibitor, Kunitz	0.71	1.40e-07	IFI16	interferon gamma inducible protein
-0.85	1.98e-09	CKMT1A	creatine kinase, mitochondrial 1A	0.69	3.77e-08	SYNM	synemin
-0.85	9.35e-12	EVPL	envoplakin	0.68	2.65e-10	RFTN1	raftlin, lipid raft linker 1
-0.84	1.57e-11	CGN	cingulin	0.68	6.74e-04	CAVIN1	caveolae associated protein 1
-0.81	1.88e-13	RPP25	ribonuclease P and MRP subunit p25	0.66	9.42e-08	AASS	aminoacidate-semialdehyde synthase
-0.81	7.72e-10	HPDL	4-hydroxyphenylpyruvate dioxygenase	0.66	2.13e-08	COL18A1	collagen type XVIII alpha 1 chain
-0.8	2.61e-08	CDH1	cadherin 1	0.65	5.09e-06	GPX8	glutathione peroxidase 8 (putative)
-0.8	3.51e-10	LSR	lipolysis stimulated lipoprotein re	0.62	4.37e-09	SERpine1	serpin family E member 1
-0.8	1.08e-10	NAPRT	nicotinate phosphoribosyltransferas	0.62	5.14e-09	LAMC1	laminin subunit gamma 1
-0.79	1.20e-10	EPPK1	epiplakin 1	0.62	4.17e-05	THBS1	thrombospondin 1
-0.79	4.17e-11	JUP	junction plakoglobin	0.61	2.89e-07	FNDC3B	fibronectin type III domain contain
-0.78	6.36e-13	DLG3	discs large MAGUK scaffold protein	0.61	5.62e-06	GPNMB	glycoprotein nmb
-0.77	1.11e-05	SFN	stratifin	0.61	1.41e-06	QKI	QKI, KH domain containing RNA bindi
-0.77	3.83e-06	KRT7	keratin 7	0.6	8.30e-07	P3H2	prolyl 3-hydroxylase 2
-0.75	1.03e-07	LAD1	ladinin 1	0.59	2.38e-07	KIRREL1	kirre like nephrin family adhesion
-0.75	4.11e-09	ESRP1	epithelial splicing regulatory prot	0.59	2.16e-08	POGLUT2	protein O-glucosyltransferase 2
-0.75	3.91e-10	GCA	grancalcin	0.59	6.46e-11	P3H1	prolyl 3-hydroxylase 1
-0.74	3.65e-12	ARHGEF16	Rho guanine nucleotide exchange fac	0.59	5.76e-04	MSN	moesin
-0.74	1.38e-09	LLGL2	LLGL scribble cell polarity complex	0.56	1.48e-06	RAI14	retinoic acid induced 14
-0.73	9.46e-08	SERPINB5	serpin family B member 5	0.56	1.61e-05	FN1	fibronectin 1

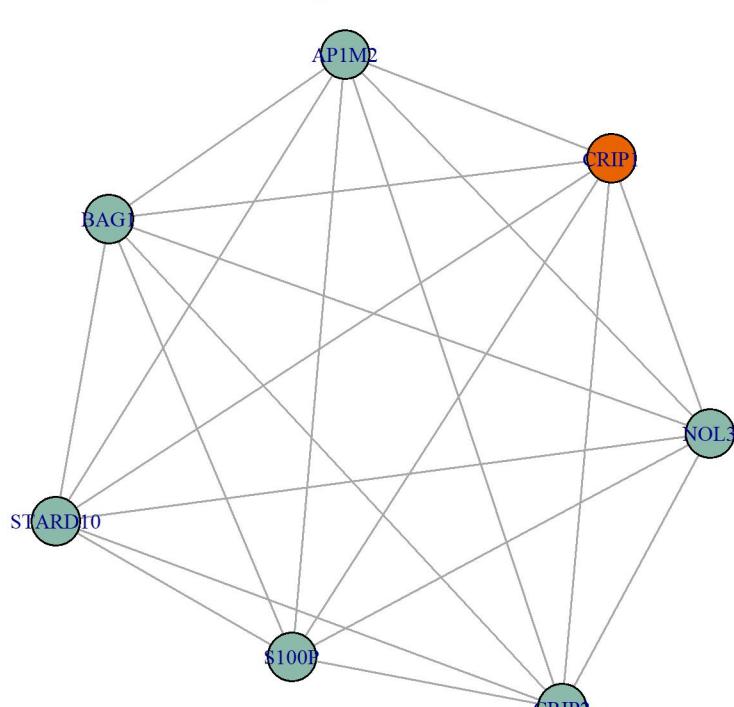
CRIP1 network, DB1, all Pearson r > 0.45

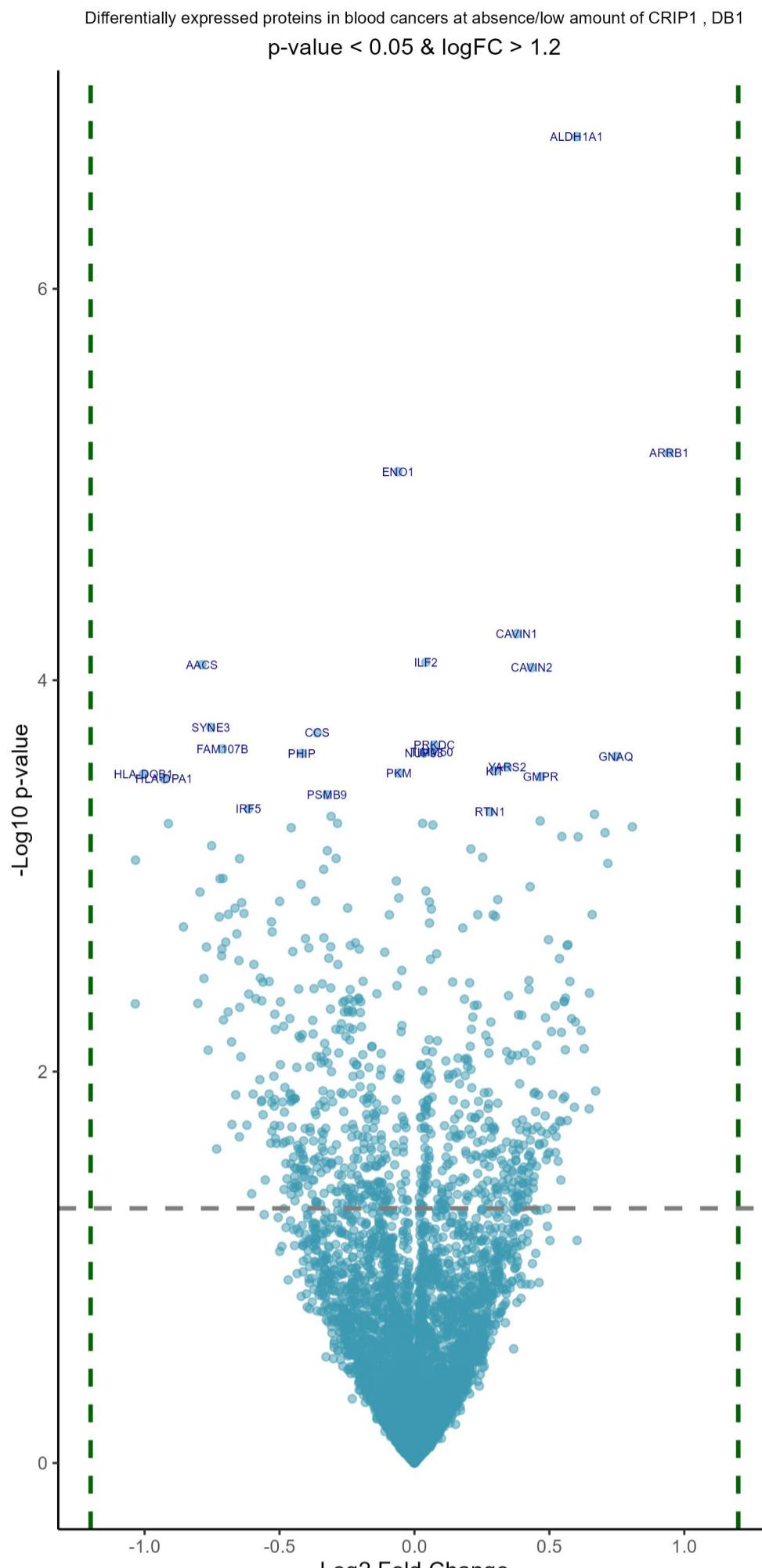


CRIP1 network, DB1, all Pearson r > 0.4

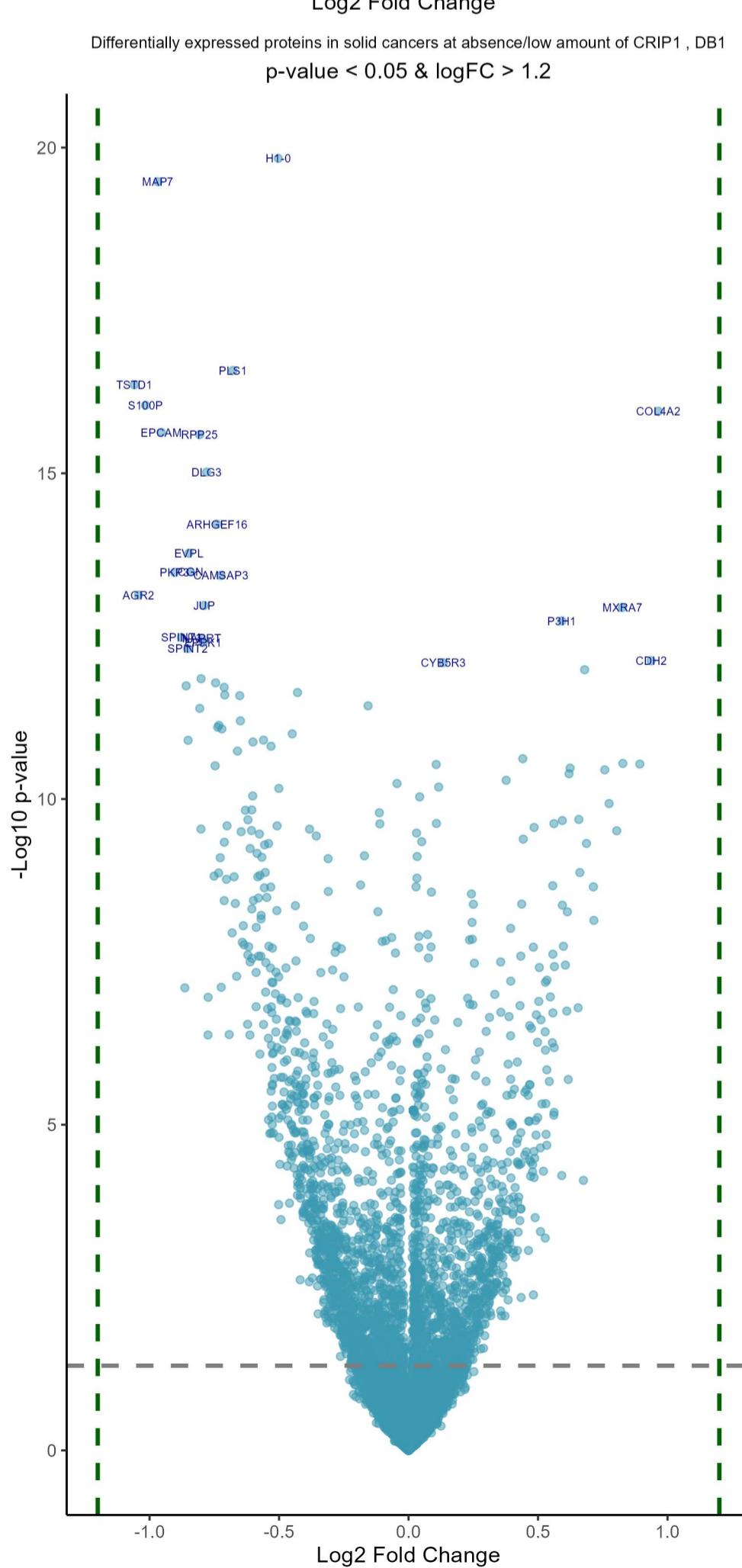


CRIP1 network, DB1, all Pearson r > 0.35



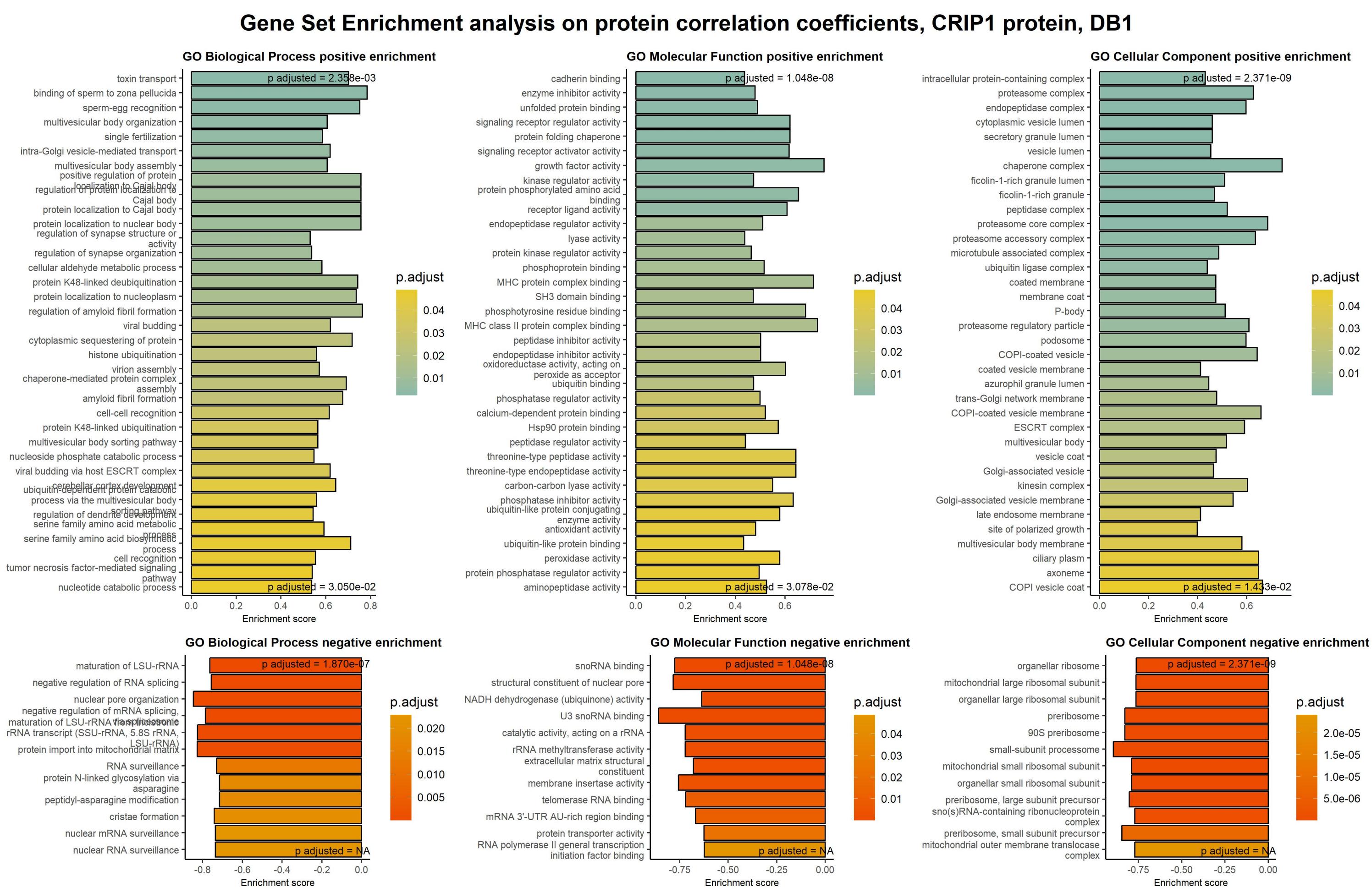
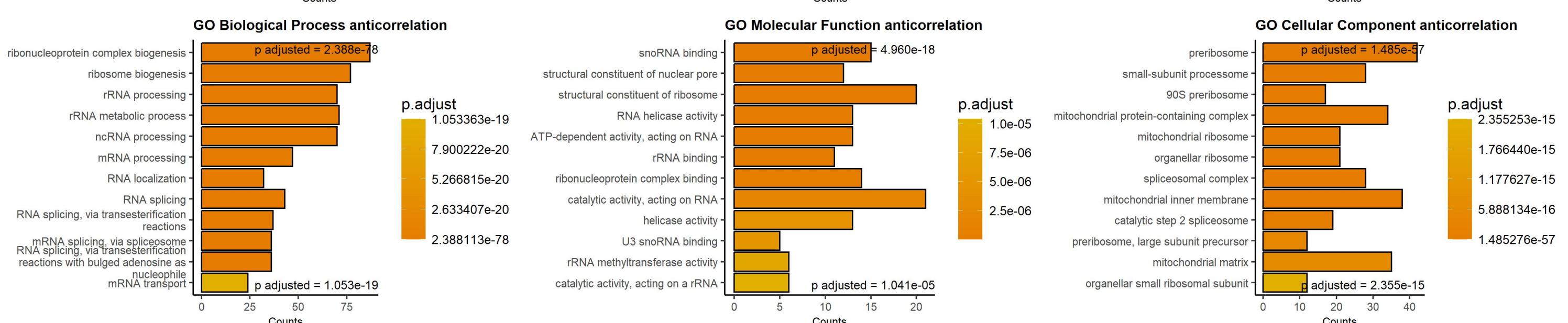
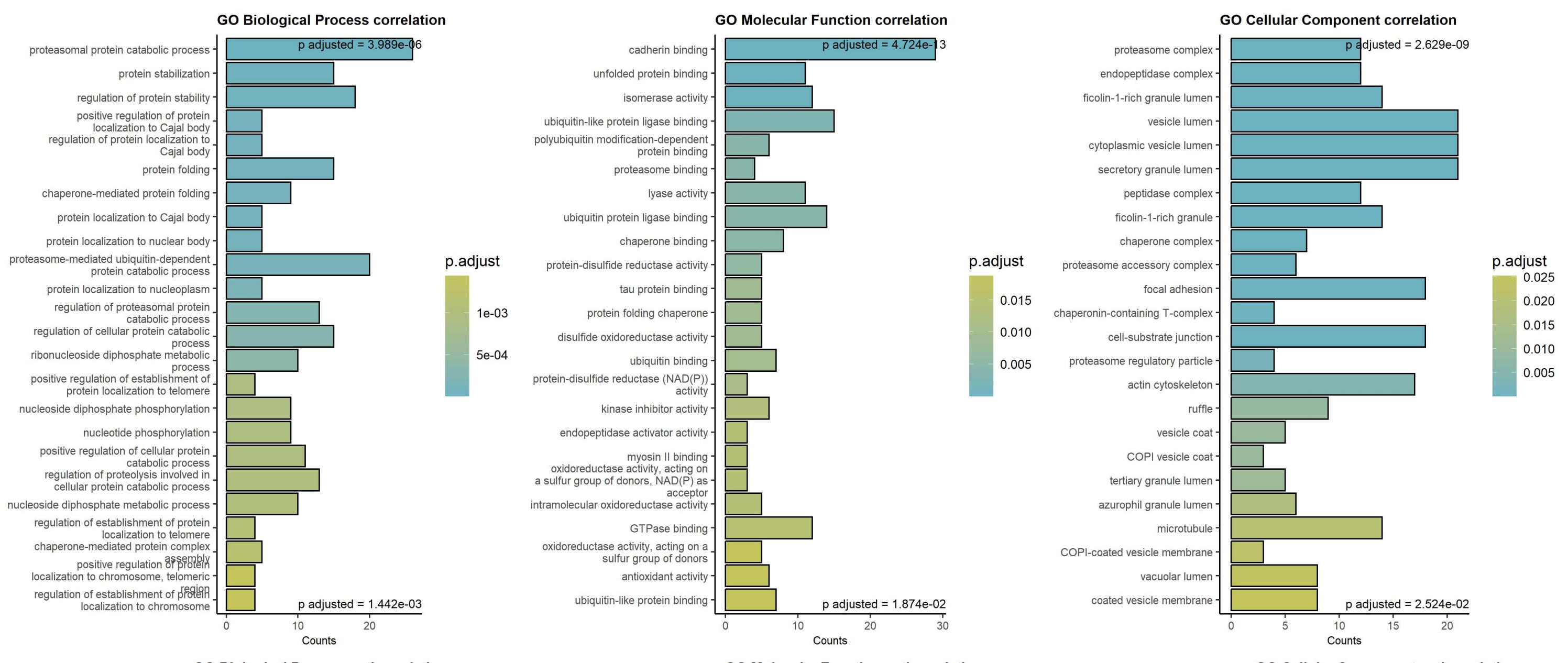


Sorted by p values!							
Downregulated in blood cancers at low/absent CRIP1				Upregulated in blood cancers at low/absent CRIP1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.06	1.43e-02	ENO1	enolase 1	0.6	5.55e-04	ALDH1A1	aldehyde dehydrogenase 1 family mem
-0.79	7.16e-02	AACS	acetoacetyl-CoA synthetase	0.94	1.43e-02	ARRB1	arrestin beta 1
-0.75	9.64e-02	SYNE3	spectrin repeat containing nuclear	0.38	7.16e-02	CAVIN1	caveolae associated protein 1
-0.36	9.64e-02	CCS	copper chaperone for superoxide dis	0.04	7.16e-02	ILF2	interleukin enhancer binding factor
-0.71	9.64e-02	FAM107B	family with sequence similarity 107	0.43	7.16e-02	CAVIN2	caveolae associated protein 2
-0.42	9.64e-02	PHIP	pleckstrin homology domain interact	0.07	9.64e-02	PRKDC	protein kinase, DNA-activated, cata
-0.06	9.64e-02	PKM	pyruvate kinase M1/2	0.06	9.64e-02	TIMM50	translocase of inner mitochondrial
-1	9.64e-02	HLA-DQB1	major histocompatibility complex, c	0.04	9.64e-02	NUP93	nucleoporin 93
-0.93	9.64e-02	HLA-DPA1	major histocompatibility complex, c	0.75	9.64e-02	GNAQ	G protein subunit alpha q
-0.32	1.11e-01	PSMB9	proteasome 20S subunit beta 9	0.34	9.64e-02	YARS2	tyrosyl-tRNA synthetase 2
-0.61	1.11e-01	IRF5	interferon regulatory factor 5	0.3	9.64e-02	KIT	KIT proto-oncogene, receptor tyrosi
-0.31	1.11e-01	STUB1	STIP1 homology and U-box containing	0.47	9.64e-02	GMPR	guanosine monophosphate reductase
-0.29	1.11e-01	DNPEP	aspartyl aminopeptidase	0.28	1.11e-01	RTN1	reticulon 1
-0.91	1.11e-01	IRF4	interferon regulatory factor 4	0.67	1.11e-01	CA8	carbonic anhydrase 8
-0.46	1.11e-01	LPCAT1	lysophosphatidylcholine acyltransfe	0.47	1.11e-01	ITGA2B	integrin subunit alpha 2b
-0.75	1.23e-01	ACAP1	ArfGAP with coiled-coil, ankyrin re	0.03	1.11e-01	PRPF19	pre-mRNA processing factor 19
-0.32	1.24e-01	SNRPE	small nuclear ribonucleoprotein pol	0.07	1.11e-01	ABCE1	ATP binding cassette subfamily E me
-0.29	1.26e-01	PRPSAP2	phosphoribosyl pyrophosphate synthe	0.81	1.11e-01	ITGA5	integrin subunit alpha 5
-0.65	1.26e-01	S100A10	S100 calcium binding protein A10	0.71	1.13e-01	EIF4EBP1	eukaryotic translation initiation f
-1.03	1.26e-01	CD74	CD74 molecule	0.55	1.13e-01	RAB32	RAB32, member RAS oncogene family
-0.34	1.34e-01	TAPBP	TAP binding protein	0.61	1.13e-01	PSTPIP2	proline-serine-threonine phosphatas
-0.71	1.43e-01	UAP1L1	UDP-N-acetylglucosamine pyrophospho	0.21	1.24e-01	CRTC1	CREB regulated transcription coacti
-0.72	1.43e-01	SAMHD1	SAM and HD domain containing deoxyn	0.25	1.26e-01	ACSM3	acyl-CoA synthetase medium chain fa
-0.07	1.44e-01	PSME2	proteasome activator subunit 2	0.72	1.28e-01	LPCAT2	lysophosphatidylcholine acyltransfe
-0.42	1.47e-01	EPS8L2	EPS8 like 2	0.43	1.48e-01	IPO11	importin 11
-0.79	1.52e-01	ISG20	interferon stimulated exonuclease g	0.04	1.52e-01	CNOT1	CCR4-NOT transcription complex sub
-0.06	1.54e-01	MYL6	myosin light chain 6	0.31	1.54e-01	CA1	carbonic anhydrase 1
-0.37	1.54e-01	NFKB1	nuclear factor kappa B subunit 1	0.06	1.54e-01	TRIM28	tripartite motif containing 28
-0.5	1.54e-01	NOM1	nucleolar protein with MIF4G domain	0.06	1.54e-01	PGD	phosphogluconate dehydrogenase
-0.64	1.54e-01	CAST	calpastatin	0.66	1.54e-01	PECAM1	platelet and endothelial cell adhes
-0.25	1.54e-01	HSDL2	hydroxysteroid dehydrogenase like 2	0.23	1.54e-01	FN3K	fructosamine 3 kinase
-0.67	1.54e-01	SLC4A2	solute carrier family 4 member 2	0.29	1.54e-01	PDZD8	PDZ domain containing 8
-0.63	1.54e-01	ADGRE5	adhesion G protein-coupled receptor	0.3	1.54e-01	PTGS1	prostaglandin-endoperoxide synthase
-0.69	1.54e-01	NFKB2	nuclear factor kappa B subunit 2	0.06	1.61e-01	YARS1	tyrosyl-tRNA synthetase 1
-0.09	1.54e-01	DBNL	drebrin like	0.18	1.66e-01	CLSPN	claspin
-0.72	1.54e-01	MYOF	myoferlin	0.5	1.77e-01	EXOC7	exocyst complex component 7
-0.53	1.61e-01	KIF21A	kinesin family member 21A	0.57	1.77e-01	STAT3	signal transducer and activator of
-0.86	1.66e-01	HLA-DPB1	major histocompatibility complex, c	0.57	1.77e-01	NECTIN2	nectin cell adhesion molecule 2
-0.53	1.71e-01	SCPRP1	cerine carboxypeptidase 1	0.08	1.81e-01	PAB5C	PAB5C, member PABP oncogene family

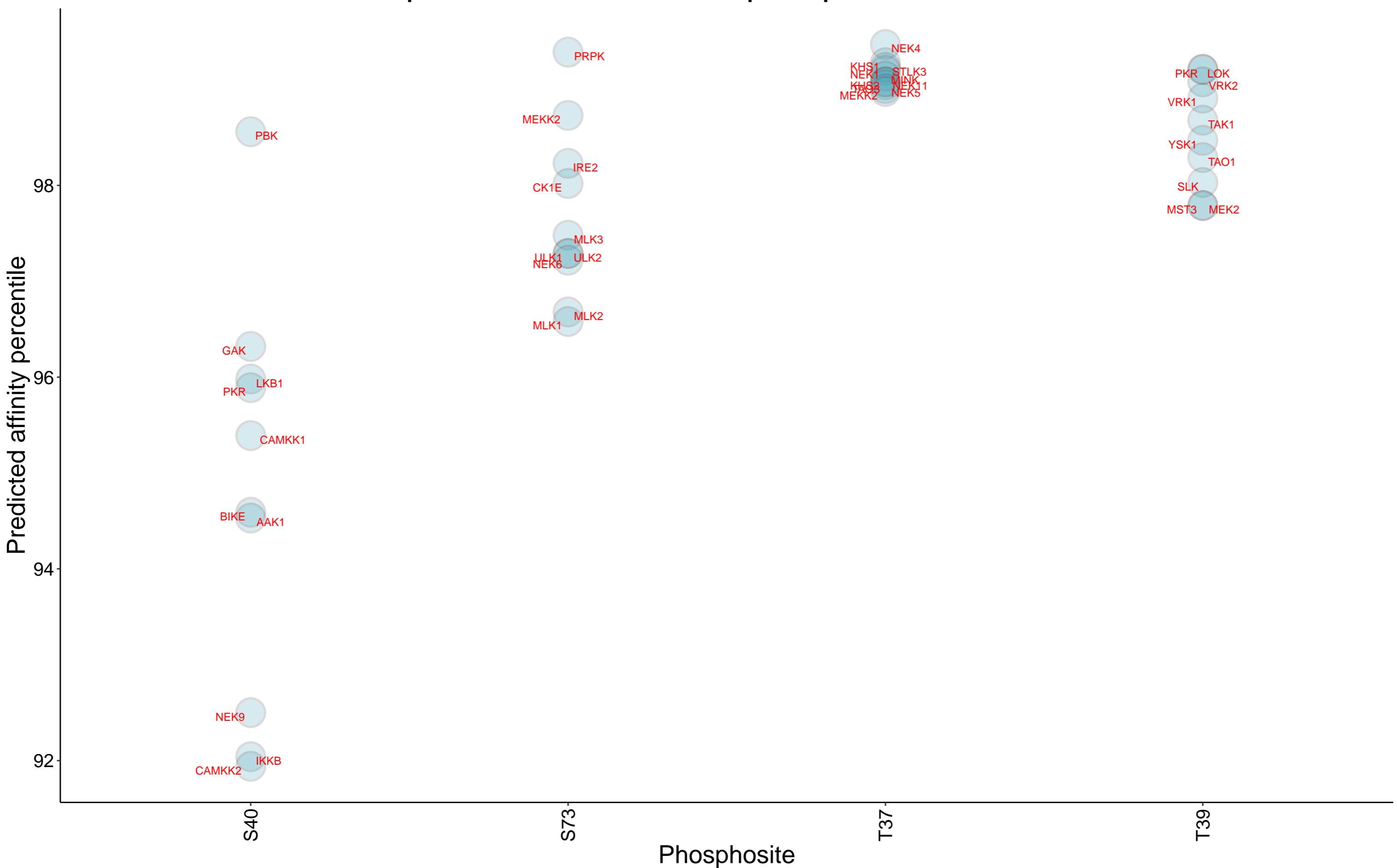


Sorted by p values!							
Downregulated in solid cancers at low/absent CRIP1				Upregulated in solid cancers at low/absent CRIP1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.5	4.87e-17	H1-0	H1.0 linker histone	0.96	1.06e-13	COL4A2	collagen type IV alpha 2 chain
-0.97	7.40e-17	MAP7	microtubule associated protein 7	0.83	4.23e-11	MXRA7	matrix remodeling associated 7
-0.68	4.39e-14	PLS1	plastin 1	0.59	6.46e-11	P3H1	prolyl 3-hydroxylase 1
-1.06	5.82e-14	TSTD1	thiosulfate sulfurtransferase like	0.94	2.09e-10	CDH2	cadherin 2
-1.02	1.00e-13	S100P	S100 calcium binding protein P	0.13	2.15e-10	CYB5R3	cytochrome b5 reductase 3
-0.95	1.88e-13	EPCAM	epithelial cell adhesion molecule	0.68	2.65e-10	RFTN1	raftlin, lipid raft linker 1
-0.81	1.88e-13	RPP25	ribonuclease P and MRP subunit p25	0.44	3.47e-09	COL4A1	collagen type IV alpha 1 chain
-0.78	6.36e-13	DLG3	discs large MAGUK scaffold protein	0.83	4.01e-09	CRTAP	cartilage associated protein
-0.74	3.65e-12	ARHGEF16	Rho guanine nucleotide exchange fac	0.89	4.01e-09	CALD1	caldesmon 1
-0.85	9.35e-12	EVPL	envoplakin	0.11	4.01e-09	CALU	calumenin
-0.84	1.57e-11	CGN	cingulin	0.62	4.37e-09	SERPINE1	serpin family E member 1
-0.9	1.57e-11	PKP3	plakophilin 3	0.76	4.56e-09	RAB32	RAB32, member RAS oncogene famil
-0.72	1.64e-11	CAMSAP3	calmodulin regulated spectrin assoc	0.62	5.14e-09	LAMC1	laminin subunit gamma 1
-1.04	3.08e-11	AGR2	anterior gradient 2, protein disulp	0.38	6.35e-09	LZTS1	leucine zipper tumor suppressor 1
-0.79	4.17e-11	JUP	junction plakoglobin	0.12	7.79e-09	COLGALT1	collagen beta(1-O)galactosyltransfe
-0.88	1.08e-10	SPINT1	serine peptidase inhibitor, Kunitz	0.04	1.05e-08	RPL35A	ribosomal protein L35a
-0.8	1.08e-10	NAPRT	nicotinate phosphoribosyltransferas	0.77	1.30e-08	SPARC	secreted protein acidic and cystein
-0.79	1.20e-10	EPPK1	epiplakin 1	0.66	2.13e-08	COL18A1	collagen type XVIII alpha 1 chain
-0.85	1.42e-10	SPINT2	serine peptidase inhibitor, Kunitz	0.59	2.16e-08	POGLUT2	protein O-glucosyltransferase 2
-0.8	3.51e-10	LSR	lipolysis stimulated lipoprotein re	0.11	2.32e-08	RAB5C	RAB5C, member RAS oncogene famil
-0.75	3.91e-10	GCA	grancalcin	0.56	2.32e-08	GSDME	gasdermin E
-0.86	4.20e-10	MISP	mitotic spindle positioning	0.48	2.52e-08	ITGB3	integrin subunit beta 3
-0.71	4.28e-10	ALDH2	aldehyde dehydrogenase 2 family mem	0.8	2.69e-08	IKBIP	IKBKB interacting protein
-0.43	4.98e-10	GPA33	glycoprotein A33	0.03	2.84e-08	RPL10A	ribosomal protein L10a
-0.71	5.22e-10	HOOK1	hook microtubule tethering protein	0.44	3.39e-08	LOXL2	lysyl oxidase like 2
-0.65	5.22e-10	PCF11	PCF11 cleavage and polyadenylation	0.05	3.66e-08	RPL27	ribosomal protein L27
-0.16	7.25e-10	PTMA	prothymosin alpha	0.69	3.77e-08	SYNM	synemin
-0.81	7.72e-10	HPDL	4-hydroxyphenylpyruvate dioxygenase	0.03	5.64e-08	RPL30	ribosomal protein L30
-0.65	1.17e-09	LRBA	LPS responsive beige-like anchor pr	0.66	9.42e-08	AASS	aminoacidate-semialdehyde synthase
-0.73	1.33e-09	STARD10	StAR related lipid transfer domain	0.03	1.08e-07	RPL7A	ribosomal protein L7a
-0.74	1.38e-09	LLGL2	LLGL scribble cell polarity complex	0.56	1.37e-07	DAB2	DAB adaptor protein 2
-0.72	1.43e-09	ADIRF	adipogenesis regulatory factor	0.03	1.40e-07	RPL6	ribosomal protein L6
-0.45	1.66e-09	LGALS4	galectin 4	0.71	1.40e-07	IFI16	interferon gamma inducible protein
-0.56	1.98e-09	PPP4R3A	protein phosphatase 4 regulatory su	0.09	1.62e-07	MYBBP1A	MYB binding protein 1a
-0.85	1.98e-09	CKMT1A	creatine kinase, mitochondrial 1A	0.24	1.72e-07	DCT	dopachrome tautomerase
-0.6	2.06e-09	DDAH1	dimethylarginine dimethylaminohydro	0.44	2.33e-07	SLC4A7	solute carrier family 4 member 7
-0.53	2.34e-09	THUMPD1	THUMP domain containing 1	0.25	2.33e-07	ACP5	acid phosphatase 5, tartrate resist
-0.66	2.71e-09	TJP3	tight junction protein 3	0.59	2.38e-07	KIRREL1	kirre like nephrin family adhesion
-0.75	4.11e-09	FCBP1	fibulin binding protein 1	0.21	2.39e-07	ENOCBP	filamentous virus C-terminal binding protein

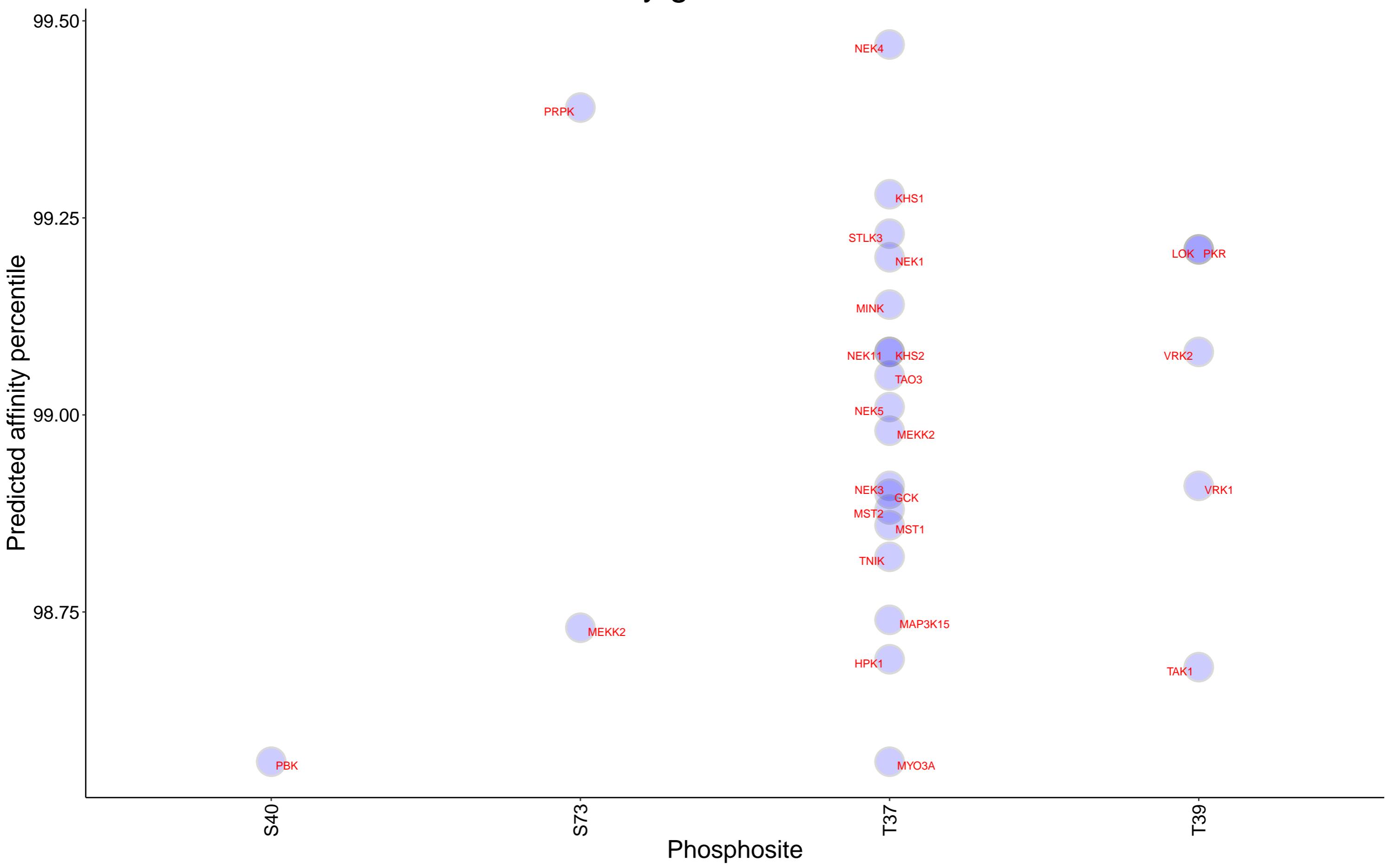
Top 250 correlation coefficients overrepresentation, CRIP1 protein, DB1



Top 10 kinases for each phosphosite in CRIP1



Kinases with affinity greater than 98.5% to CRIP1



Top 15 positive correlation coefficients for CRIP1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

