

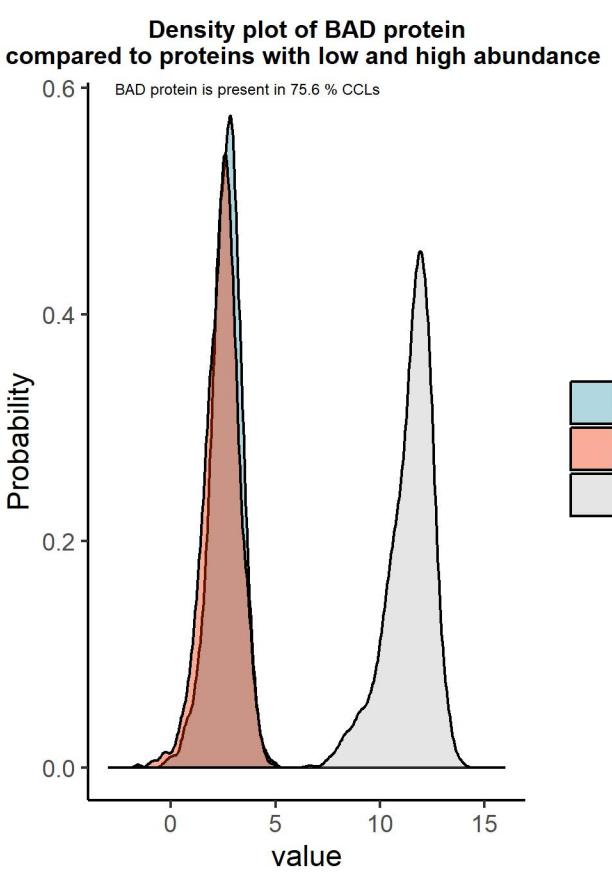
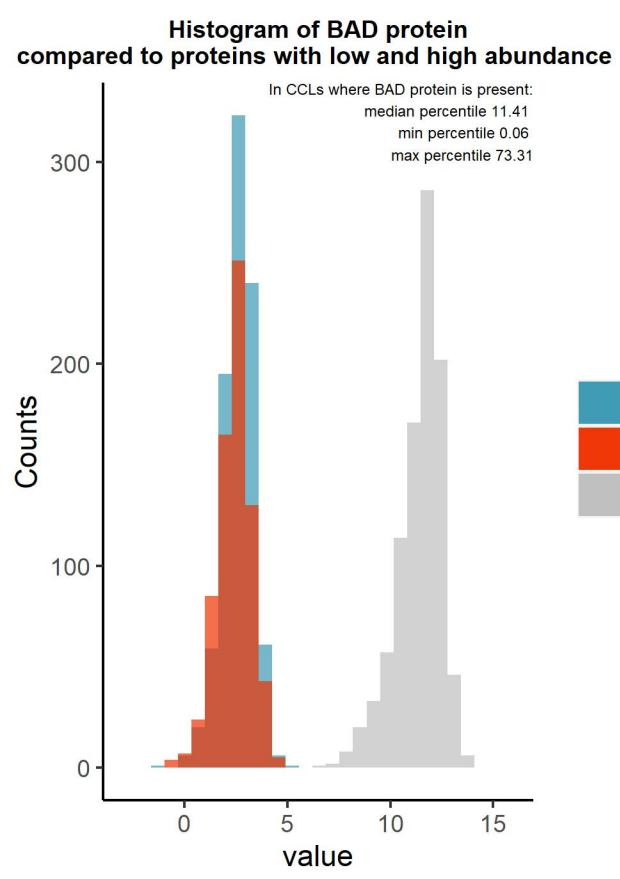
BAD

Protein name: BAD ; UNIPROT: Q92934 ; Gene name: BCL2 associated agonist of cell death

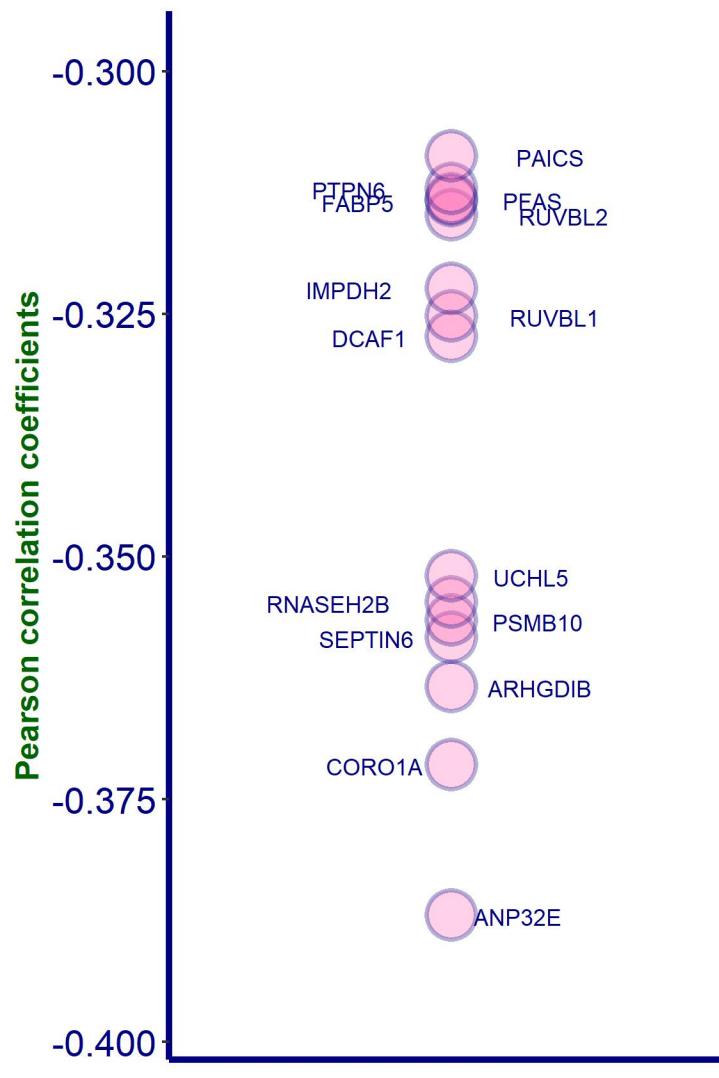
Ligandable: NA ; Ligandable_by_Chem: Yes ; Is_enzyme: NA (<https://cansar.ai/>)

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

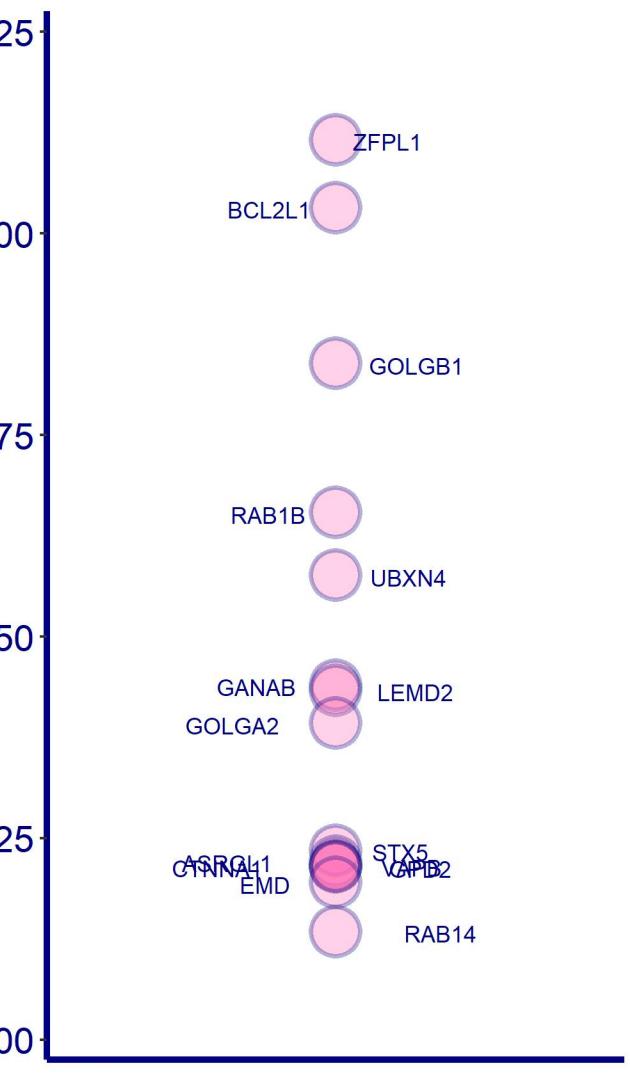
6692 proteins in 949 CCLs



Top negative correlations of BAD protein, DB1

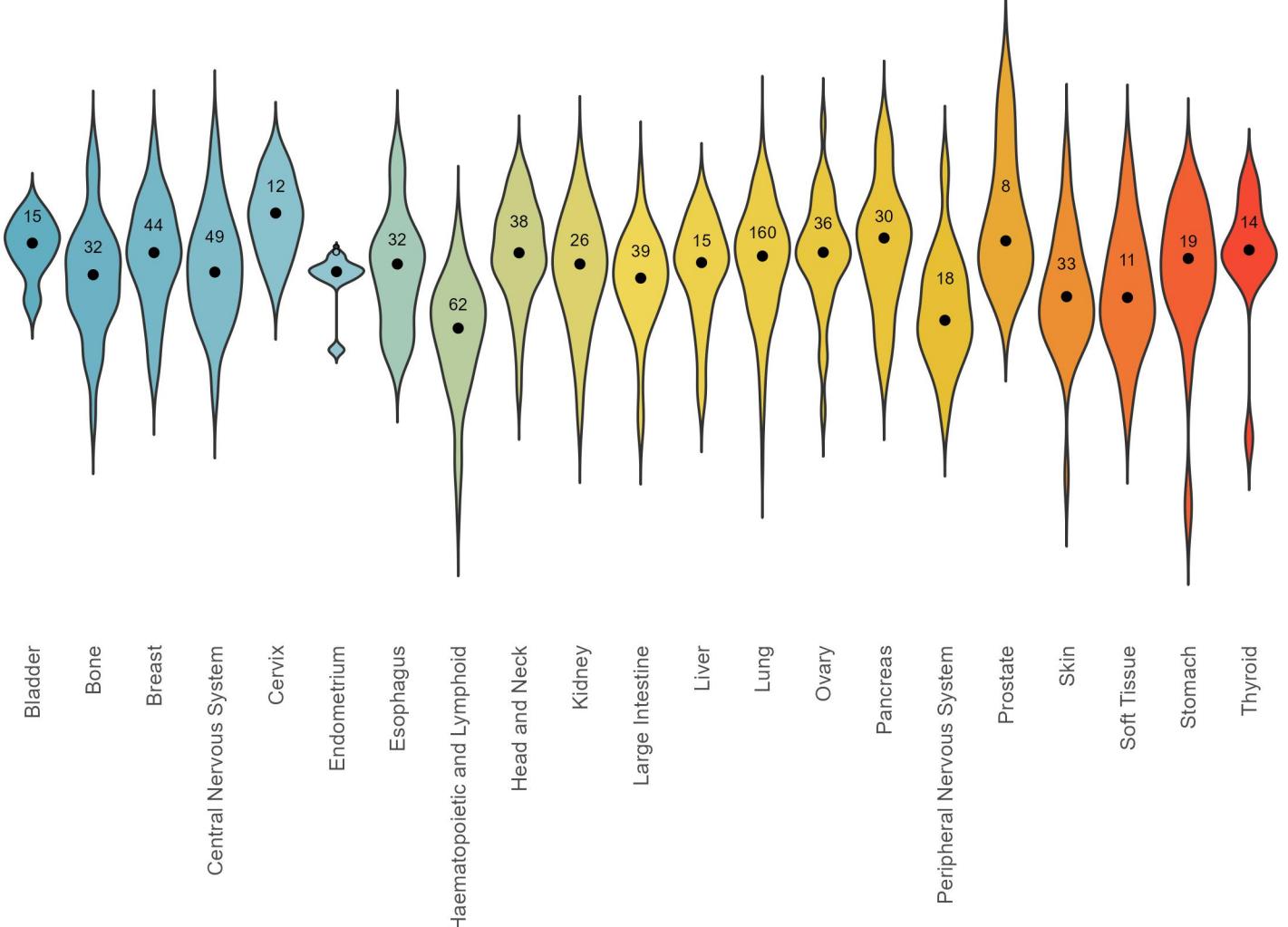


Top positive correlations of BAD protein, DB1



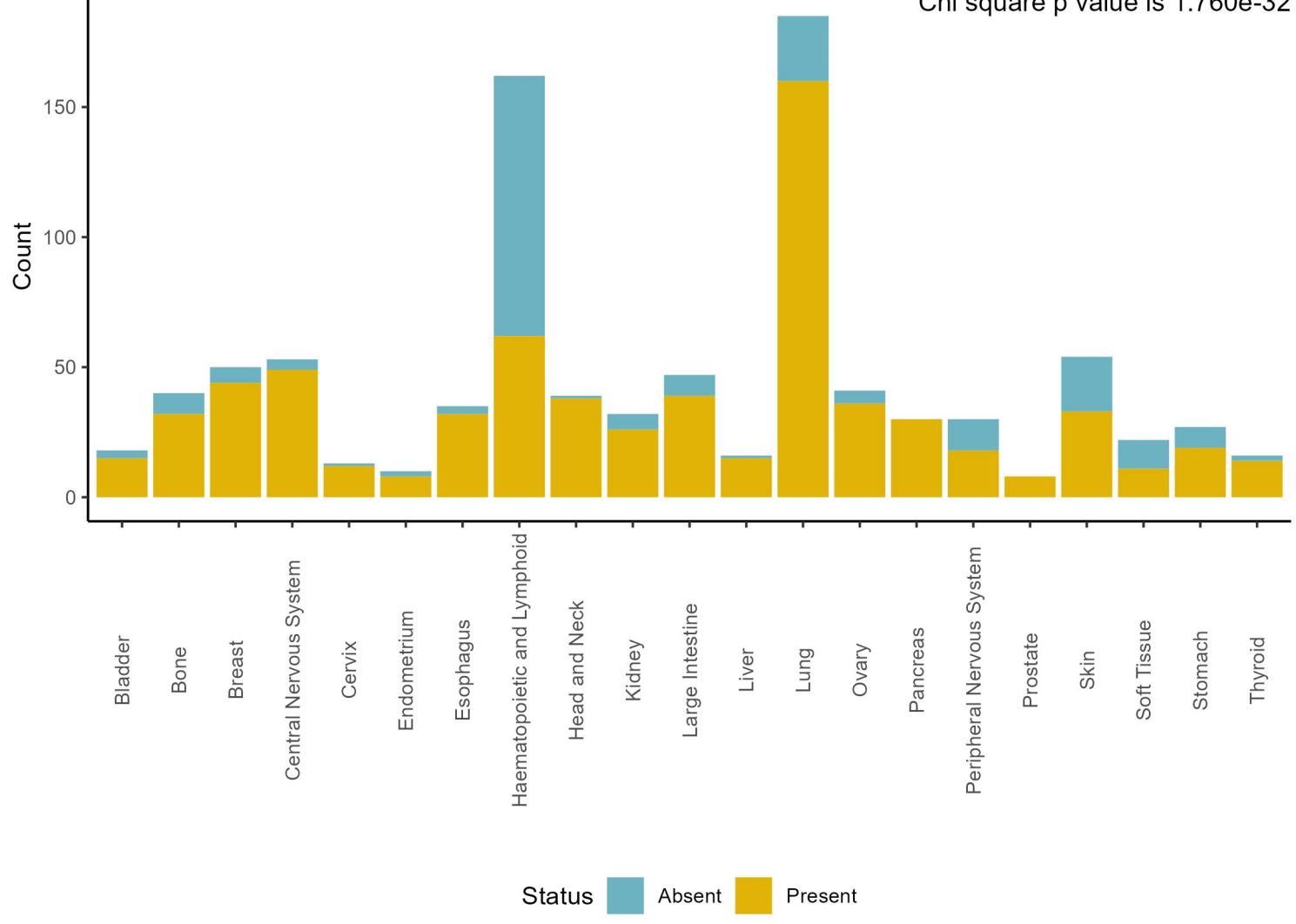
Amount of BAD protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 2.546e-18



Present and absent BAD protein counts by tissue, DB1

Chi square p value is 1.760e-32

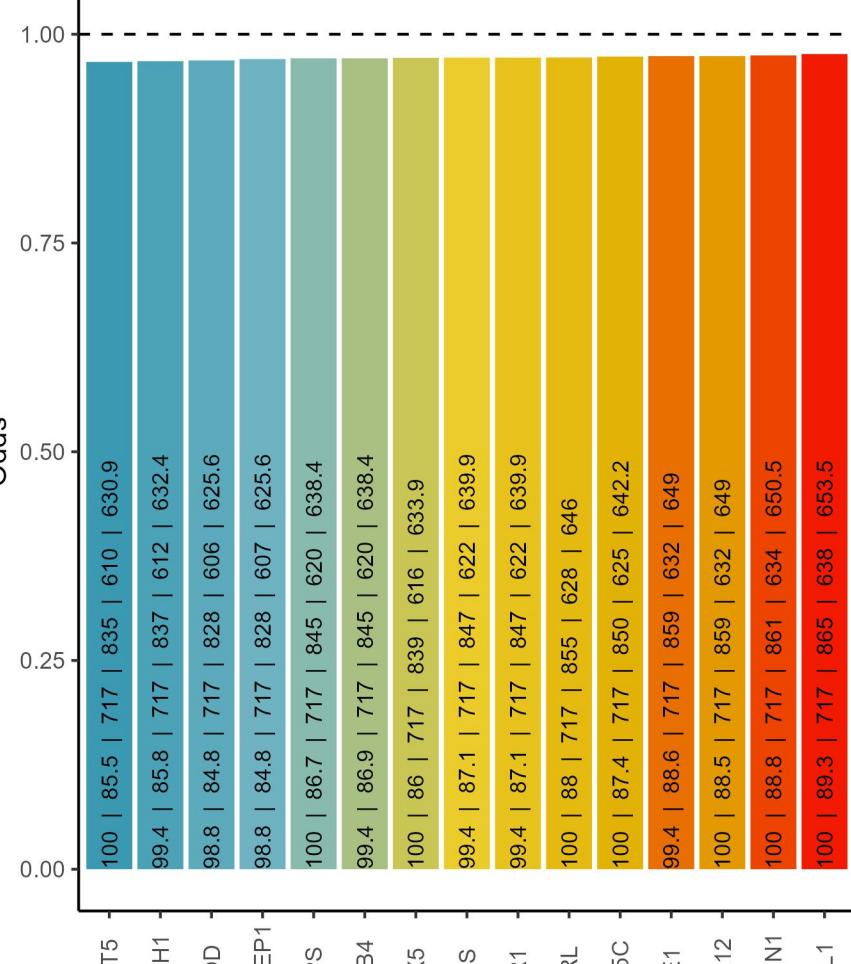


Cooccurrence with BAD protein, DB1

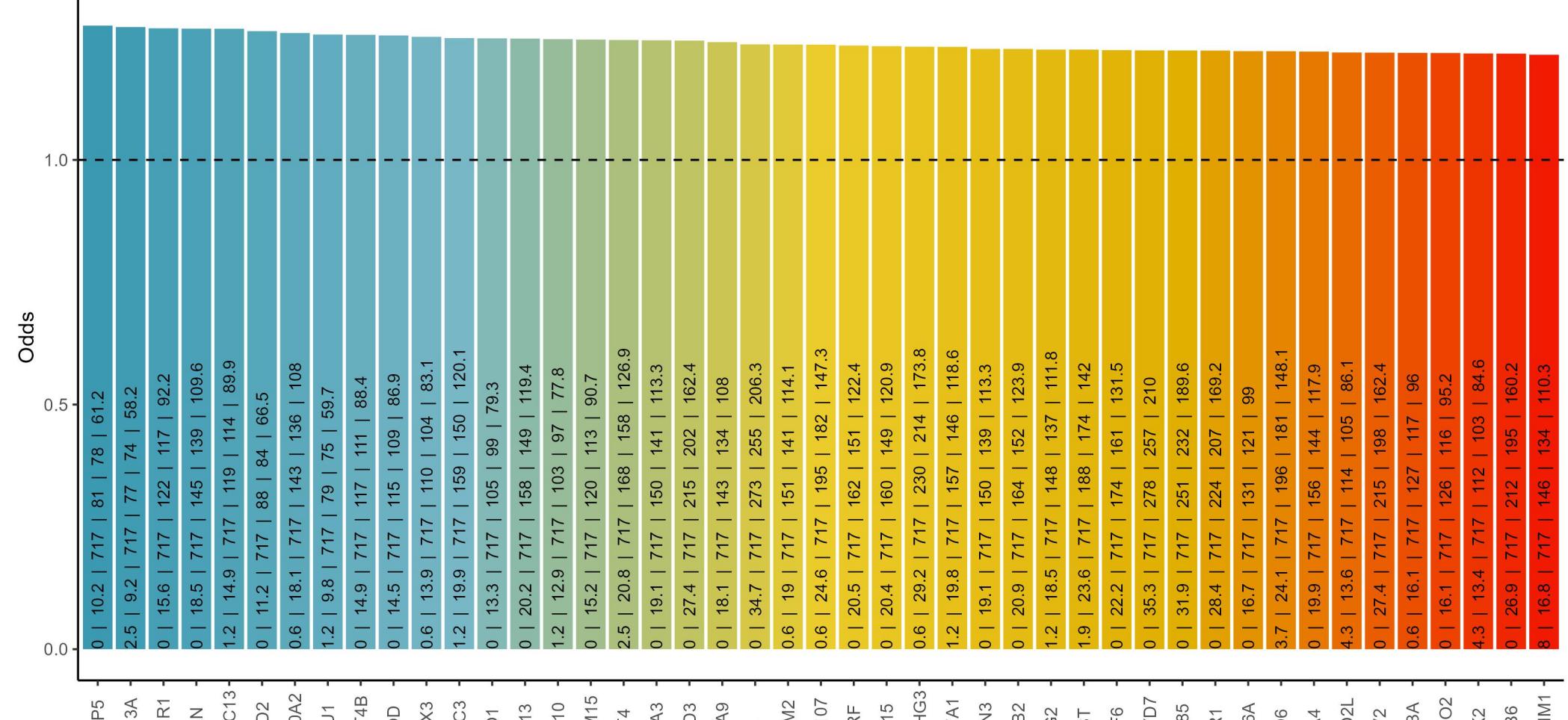
% of BAD in blood cancers: 38.3 ; % of BAD in solid cancers: 83.2

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

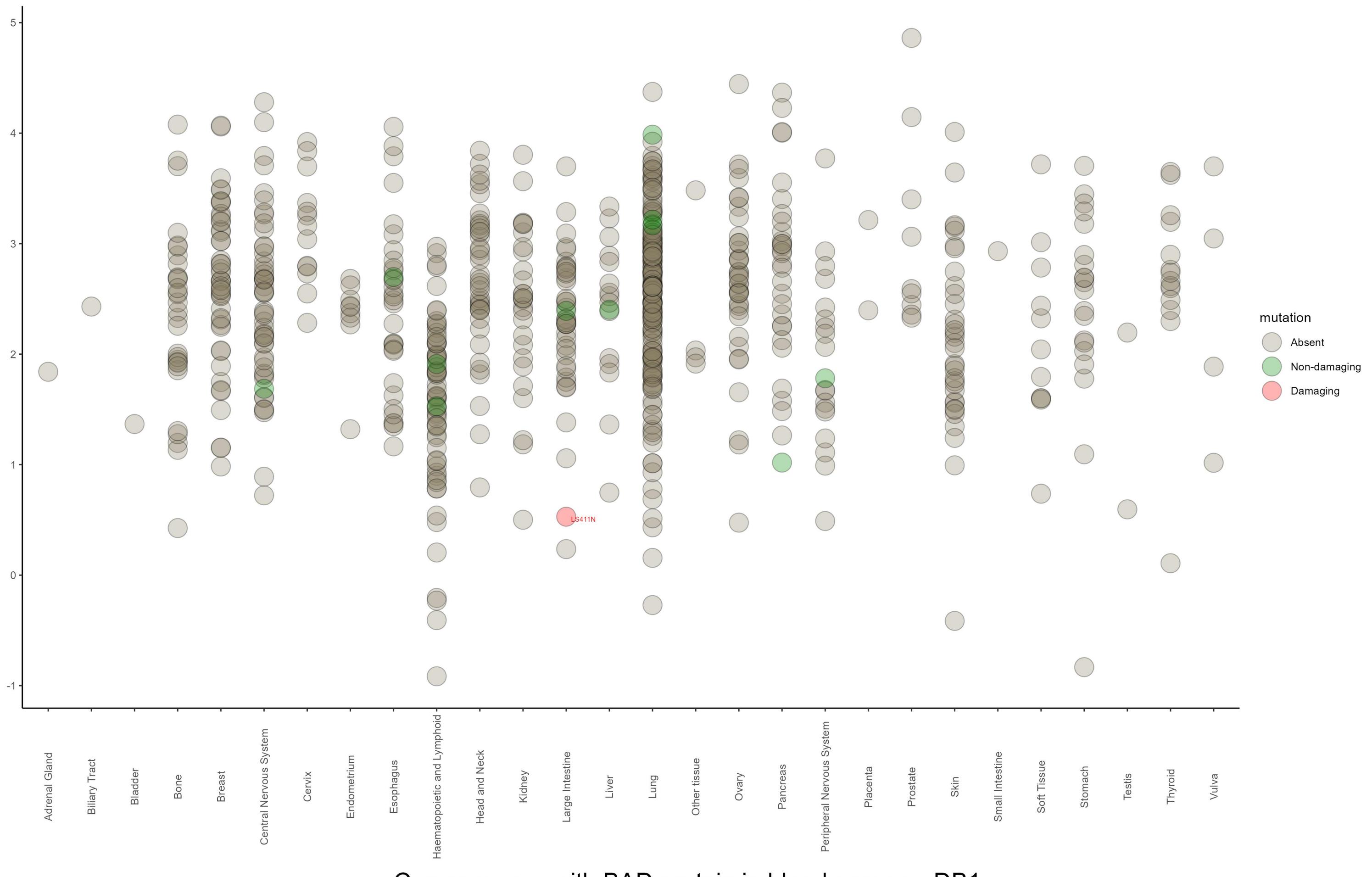
Negative cooccurrence



Positive cooccurrence

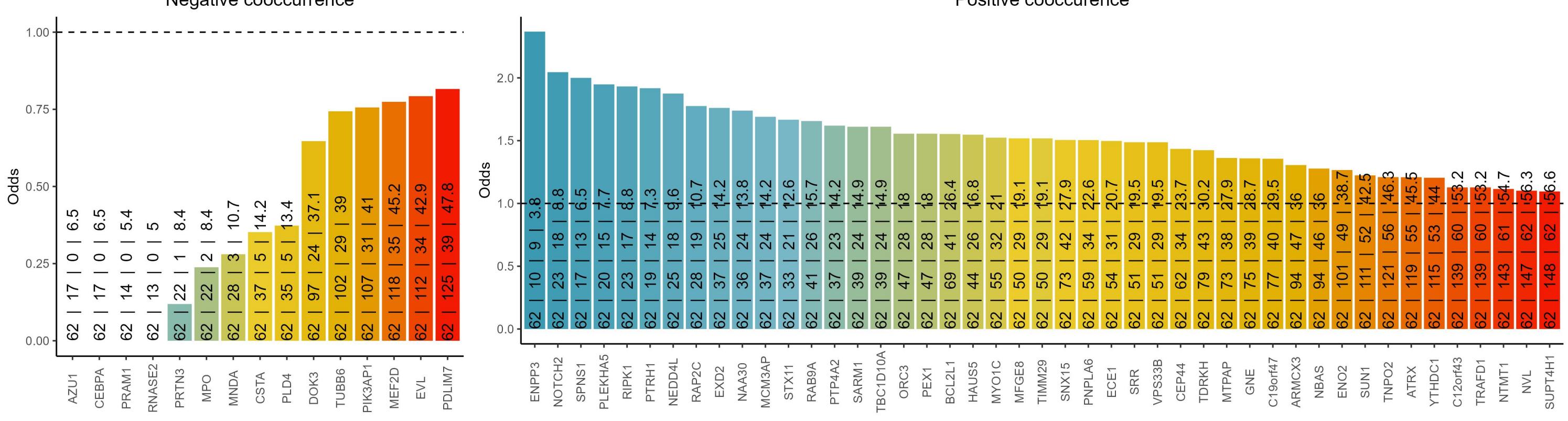


Amount of BAD protein and mutation status by tissue, DB1



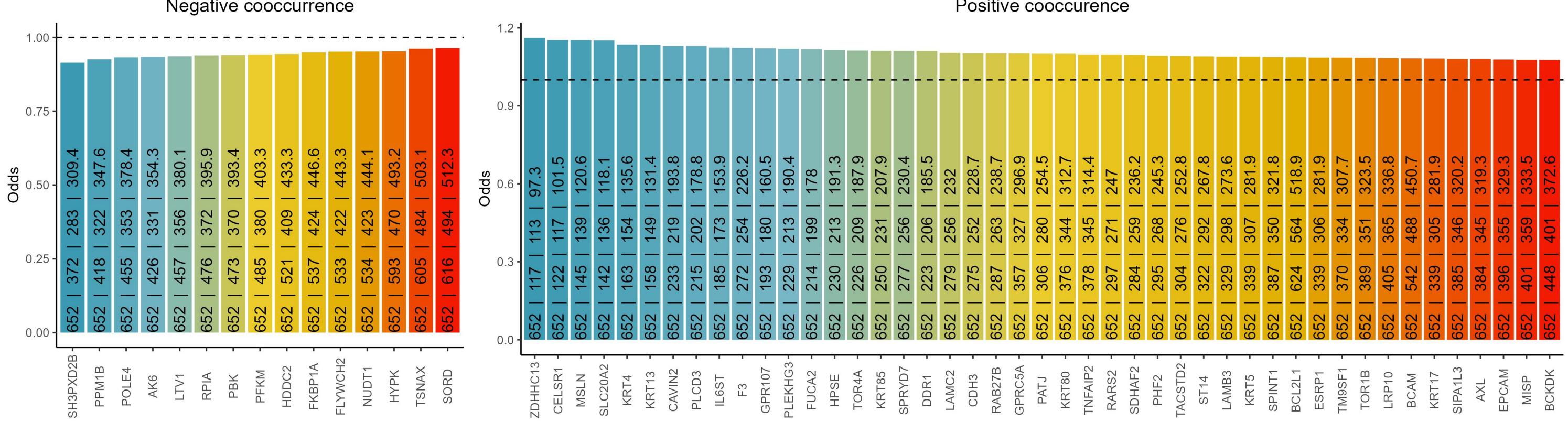
Cooccurrence with BAD protein in blood cancers, DB1

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

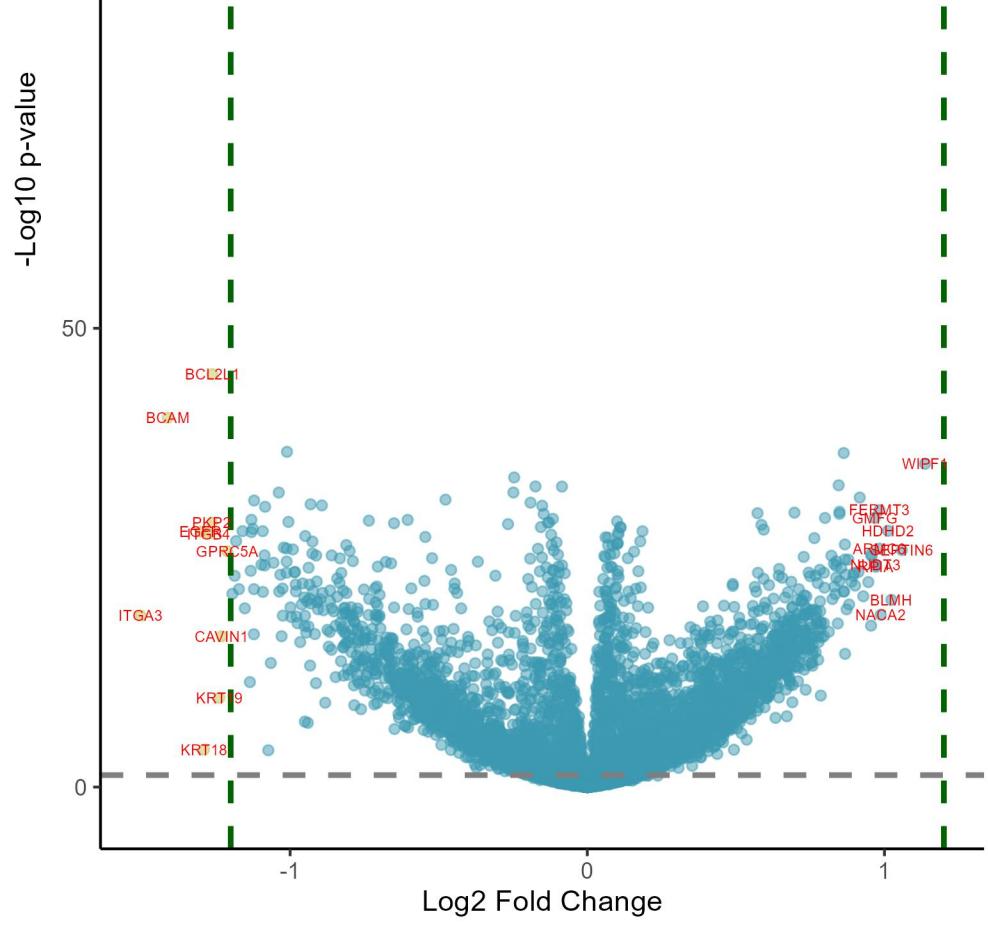


Cooccurrence with BAD protein in solid cancers, DB1

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

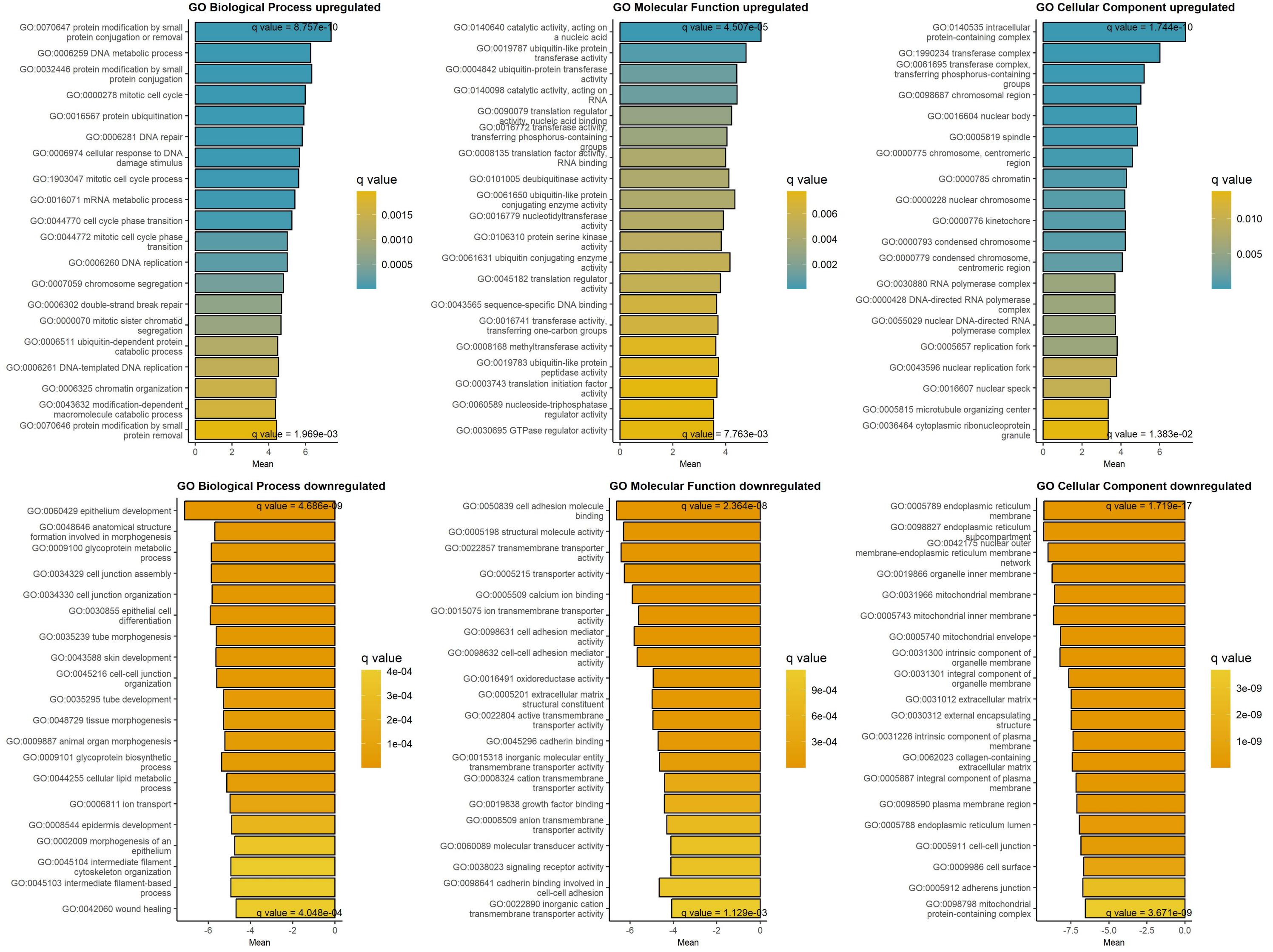


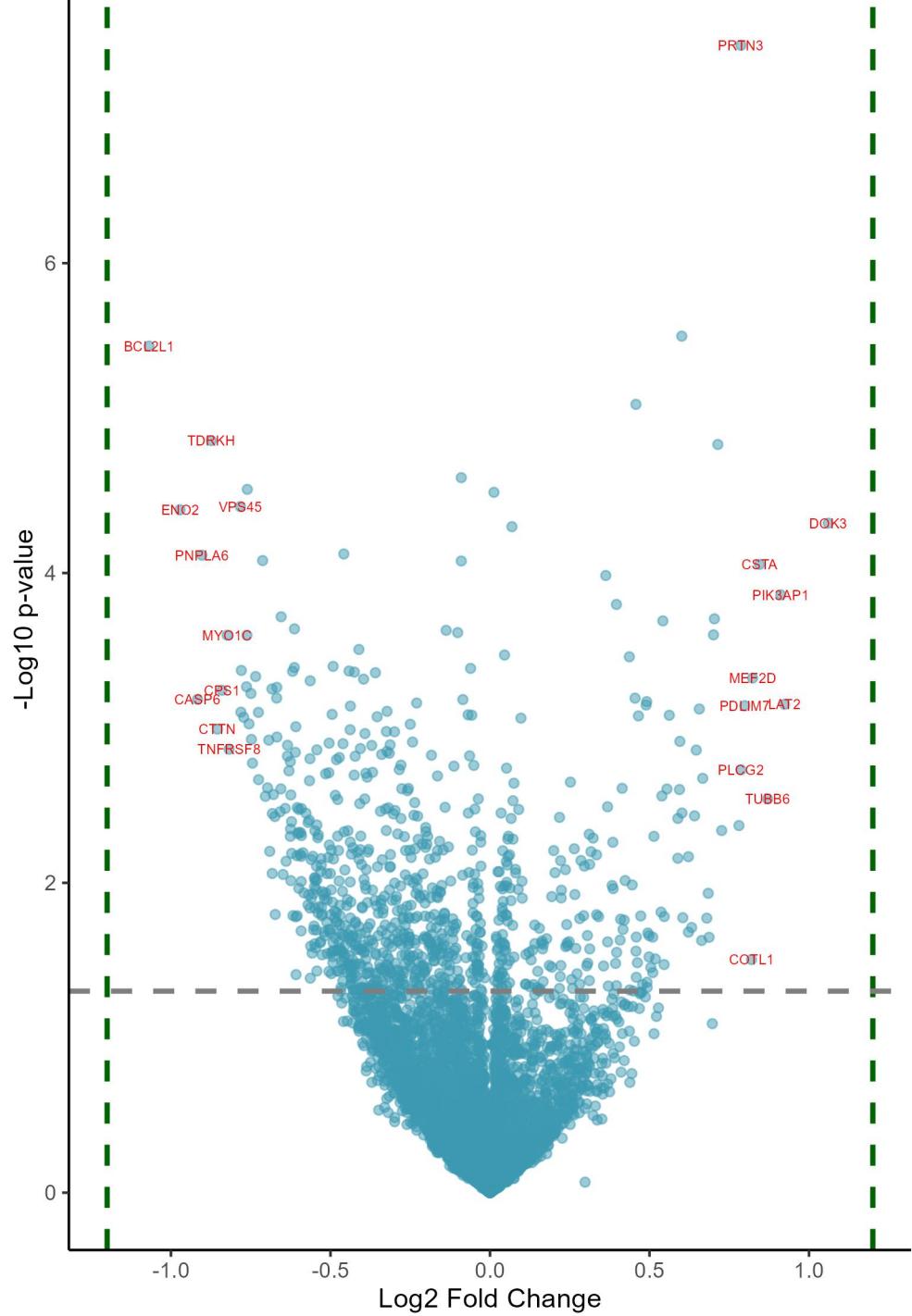
Downregulated at low/absent BAD Upregulated at low/absent BAD



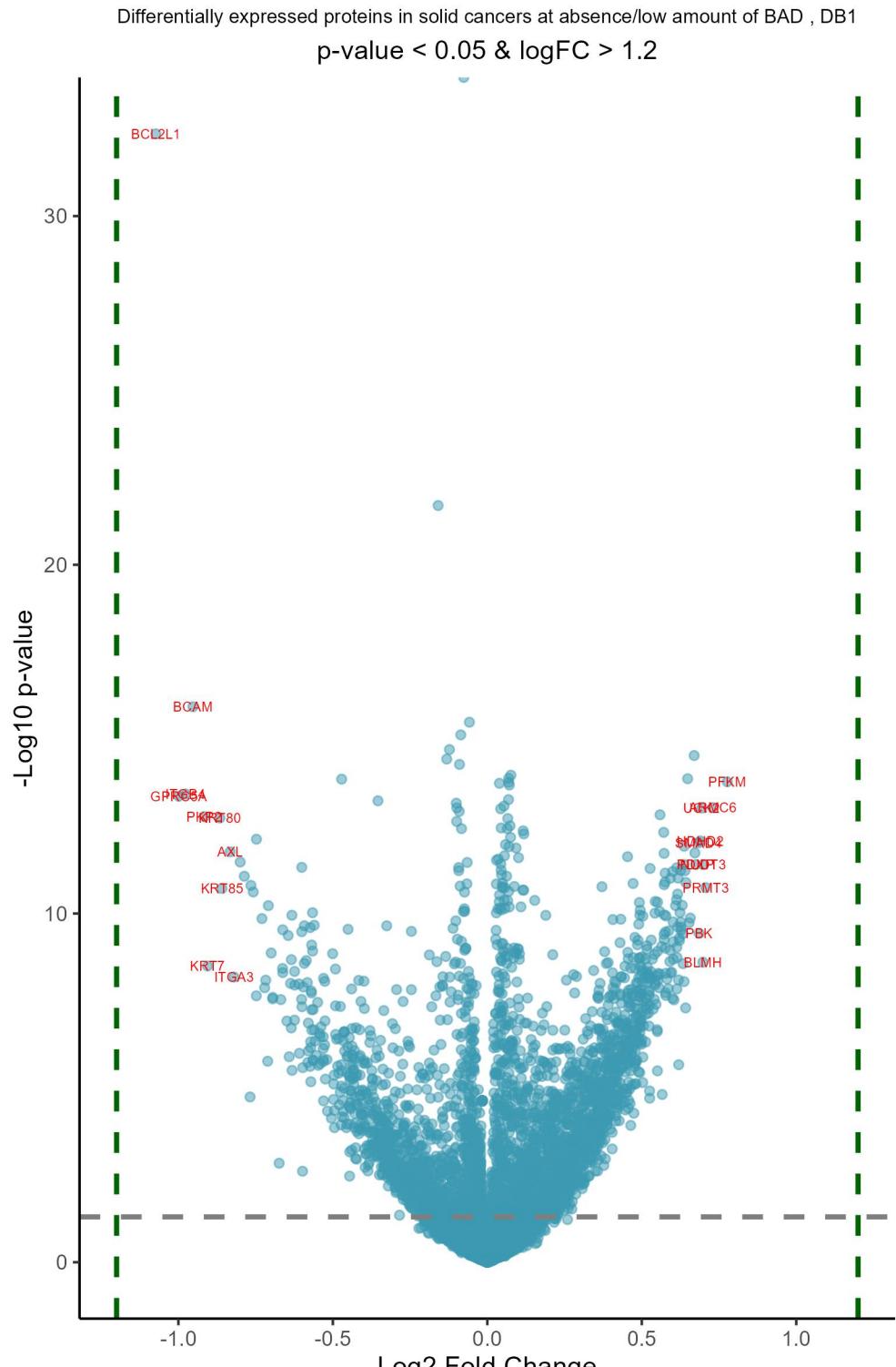
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.5	4.17e-18	ITGA3	integrin subunit alpha 3	1.14	5.54e-33	WIPF1	WAS/WASL interacting protein family
-1.41	9.53e-38	BCAM	basal cell adhesion molecule (Luthe)	1.06	1.25e-24	SEPTIN6	septin 6
-1.3	1.97e-26	EGFR	epidermal growth factor receptor	1.02	1.09e-19	BLMH	bleomycin hydrolase
-1.29	1.85e-04	KRT18	keratin 18	1.01	1.68e-26	HDHD2	haloacid dehalogenase like hydrolase
-1.27	3.07e-26	ITGB4	integrin subunit beta 4	0.99	3.40e-18	NACA2	nascent polypeptide associated comp
-1.26	2.73e-27	PKP2	plakophilin 2	0.98	1.96e-28	FERMT3	FERM domain containing kindlin 3
-1.24	8.60e-10	KRT19	keratin 19	0.97	5.50e-23	RPIA	ribose 5-phosphate isomerase A
-1.23	4.92e-16	CAVIN1	caveolae associated protein 1	0.97	3.43e-23	NUDT3	nudix hydrolase 3
-1.21	1.62e-24	GPRC5A	G protein-coupled receptor class C	0.97	1.08e-27	GMFG	glia maturation factor gamma
-1.19	2.65e-20	CAV1	caveolin 1	0.96	4.85e-24	GINS2	GINS complex subunit 2
-1.19	4.14e-22	ITGA2	integrin subunit alpha 2	0.95	4.29e-17	CORO1A	coronin 1A
-1.18	1.68e-25	PP1	periplakin	0.95	3.23e-24	HCLS1	hematopoietic cell-specific Lyn sub
-1.17	9.06e-21	S100A16	S100 calcium binding protein A16	0.95	1.81e-21	DHFR	dihydrofolate reductase
-1.16	1.74e-26	ADAM9	ADAM metallopeptidase domain 9	0.93	4.77e-20	AK6	adenylate kinase 6
-1.15	7.69e-19	JUP	junction plakoglobin	0.92	1.33e-29	ELMO1	engulfment and cell motility 1
-1.14	2.16e-11	GNG12	G protein subunit gamma 12	0.91	1.73e-22	SMAP2	small ArfGAP2
-1.13	1.38e-22	PKP3	plakophilin 3	0.9	4.06e-21	CORO7	coronin 7
-1.13	2.10e-26	KRT80	keratin 80	0.9	2.16e-22	TYMS	thymidylate synthetase
-1.13	1.59e-27	TPBG	trophoblast glycoprotein	0.9	4.01e-22	PDXP	pyridoxal phosphatase
-1.13	1.05e-26	ZNF185	zinc finger protein 185 with LIM do	0.89	1.68e-21	UBA5	ubiquitin like modifier activating
-1.12	3.10e-16	KRT7	keratin 7	0.88	3.20e-19	PPP6R1	protein phosphatase 6 regulatory su
-1.12	9.06e-21	NT5E	5'-nucleotidase ecto	0.88	1.05e-23	TTC4	tetratricopeptide repeat domain 4
-1.12	2.46e-29	SDC4	syndecan 4	0.87	9.68e-19	STK4	serine/threonine kinase 4
-1.1	3.45e-23	EPS8L2	EPS8 like 2	0.87	3.14e-22	CCDC43	coiled-coil domain containing 43
-1.09	1.74e-26	CDCP1	CUB domain containing protein 1	0.87	2.93e-14	ZNF706	zinc finger protein 706
-1.09	1.68e-20	DSG2	desmoglein 2	0.87	1.03e-23	UCK2	uridine-cytidine kinase 2
-1.09	4.17e-24	AXL	AXL receptor tyrosine kinase	0.87	3.52e-25	PPIP5K2	diphosphoinositol pentakisphosphate
-1.09	4.07e-23	EPHA2	EPH receptor A2	0.86	1.56e-20	SAAL1	serum amyloid A like 1

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



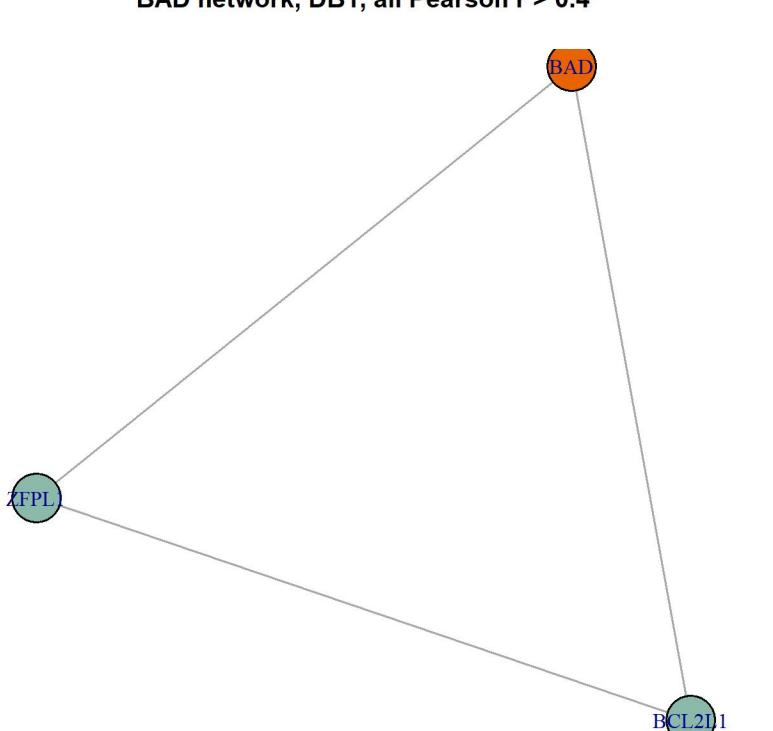


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.07	5.70e-03	BCL2L1	BCL2 like 1	1.06	2.39e-02	DOK3	docking protein 3
-0.97	2.17e-02	ENO2	enolase 2	0.92	7.87e-02	LAT2	linker for activation of T cells fa
-0.92	7.87e-02	CASP6	caspase 6	0.91	4.38e-02	PIK3AP1	phosphoinositide-3-kinase adaptor p
-0.9	3.08e-02	PNPLA6	patatin like phospholipase domain c	0.87	1.34e-01	TUBB6	tubulin beta 6 class V
-0.87	1.41e-02	TDRKH	tudor and KH domain containing	0.84	3.08e-02	CSTA	cystatin A
-0.85	8.75e-02	CTTN	cortactin	0.82	7.15e-02	MEF2D	myocyte enhancer factor 2D
-0.84	7.60e-02	CPS1	carbamoyl-phosphate synthase 1	0.82	3.18e-01	COTL1	coactosin like F-actin binding prot
-0.82	5.41e-02	MYO1C	myosin IC	0.8	7.87e-02	PDLIM7	PDZ and LIM domain 7
-0.82	9.73e-02	TNFRSF8	TNF receptor superfamily member 8	0.79	1.09e-01	PLCG2	phospholipase C gamma 2
-0.78	2.17e-02	VPS45	vacuolar protein sorting 45 homolog	0.79	1.30e-04	PRTN3	proteinase 3
-0.78	7.87e-02	MFF	mitochondrial fission factor	0.78	1.59e-01	PLEK	pleckstrin
-0.78	6.97e-02	RAB9A	RAB9A, member RAS oncogene family	0.73	1.65e-01	BTK	Bruton tyrosine kinase
-0.77	7.87e-02	AUH	AU RNA binding methylglutaconyl-CoA	0.71	1.41e-02	MNDA	myeloid cell nuclear differentiatio
-0.76	7.58e-02	ACP2	acid phosphatase 2, lysosomal	0.7	5.41e-02	PLD4	phospholipase D family member 4
-0.76	5.41e-02	SNX15	sorting nexin 15	0.7	5.41e-02	LPCAT2	lysophosphatidylcholine acyltransfe
-0.76	2.00e-02	ETFDH	electron transfer flavoprotein dehy	0.7	3.70e-01	SPN	sialophorin
-0.76	8.39e-02	NBAS	NBAS subunit of NRZ tethering compl	0.69	2.92e-01	JCHAIN	joining chain of multimeric IgA and
-0.75	7.81e-02	MPRIP	myosin phosphatase Rho interacting	0.68	2.28e-01	RNASET2	ribonuclease T2
-0.75	9.48e-02	MFGE8	milk fat globule EGF and factor V/V	0.68	2.62e-01	QPRT	quinolinate phosphoribosyltransfера
-0.74	1.04e-01	TAP2	transporter 2, ATP binding cassette	0.67	1.14e-01	PYGL	glycogen phosphorylase L
-0.73	7.15e-02	GNE	glucosamine (UDP-N-acetyl)-2-epimer	0.66	2.94e-01	ITGB2	integrin subunit beta 2
-0.73	7.87e-02	SRBD1	S1 RNA binding domain 1	0.66	7.87e-02	MYO1F	myosin IF
-0.73	1.16e-01	OPTN	optineurin	0.65	9.73e-02	CTSG	cathepsin G
-0.71	3.08e-02	EXD2	exonuclease 3'-5' domain containing	0.64	1.46e-01	SNTB1	syntrophin beta 1
-0.7	1.31e-01	ECE1	endothelin converting enzyme 1	0.63	2.78e-01	IL16	interleukin 16
-0.7	1.24e-01	MTPAP	mitochondrial poly(A) polymerase	0.62	2.87e-01	PYCARD	PYD and CARD domain containing
-0.69	9.48e-02	STAT5B	signal transducer and activator of	0.62	1.82e-01	GPD1L	glycerol-3-phosphate dehydrogenase
-0.69	1.79e-01	BLVRA	biliverdin reductase A	0.6	2.62e-01	PTK2B	protein tyrosine kinase 2 beta
-0.68	7.60e-02	PACS1	phosphofuran acid cluster sorting	0.6	1.44e-01	RB1	RB transcriptional corepressor 1

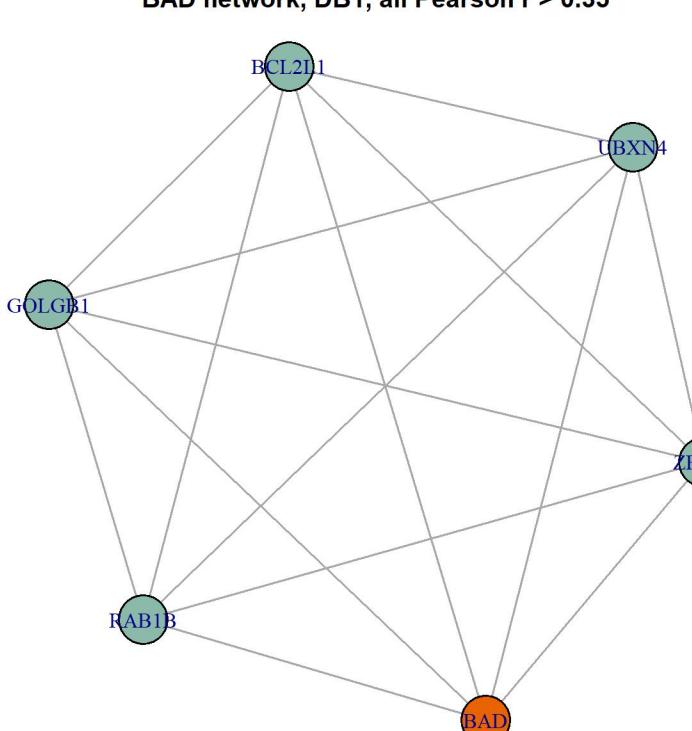


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.07	9.74e-30	BCL2L1	BCL2 like 1	0.78	6.74e-12	PFKM	phosphofructokinase, muscle
-1	1.37e-11	GPRC5A	G protein-coupled receptor class C	0.73	2.24e-11	ARMC6	armadillo repeat containing 6
-0.98	1.25e-11	ITGB4	integrin subunit beta 4	0.71	1.29e-09	PRMT3	protein arginine methyltransferase
-0.95	1.56e-13	BCAM	basal cell adhesion molecule (Luthe	0.7	4.11e-10	NUDT3	nudix hydrolase 3
-0.92	3.46e-11	PKP2	plakophilin 2	0.7	7.23e-08	BLMH	bleomycin hydrolase
-0.91	8.98e-08	KRT77	keratin 7	0.69	2.24e-11	UCK2	uridine-cytidine kinase 2
-0.87	3.67e-11	KRT80	keratin 80	0.69	1.22e-10	HDHD2	haloacid dehalogenase like hydrolas
-0.86	1.33e-09	KRT85	keratin 85	0.69	1.55e-08	PBK	PDZ binding kinase
-0.83	2.22e-10	AXL	AXL receptor tyrosine kinase	0.68	1.35e-10	SMAD4	SMAD family member 4
-0.82	1.61e-07	ITGA3	integrin subunit alpha 3	0.67	4.11e-10	PDXP	pyridoxal phosphatase
-0.8	3.77e-10	F3	coagulation factor III, tissue fact	0.67	2.34e-10	GABPA	GA binding protein transcription fa
-0.79	7.37e-10	EPS8L2	EPS8 like 2	0.67	2.18e-12	PAPOLA	poly(A) polymerase alpha
-0.77	1.15e-04	KRT19	keratin 19	0.66	6.64e-09	RPIA	ribose 5-phosphate isomerase A
-0.77	1.20e-09	EHD2	EH domain containing 2	0.65	8.69e-09	SH3PXD2B	SH3 and PX domains 2B
-0.76	1.62e-09	PPL	periplakin	0.65	6.21e-12	DUSP12	dual specificity phosphatase 12
-0.75	4.22e-07	CAV1	caveolin 1	0.64	1.06e-09	TTC4	tetratricopeptide repeat domain 4
-0.75	1.12e-10	SDC4	syndecan 4	0.64	8.26e-07	NACA2	nascent polypeptide associated comp
-0.73	6.84e-09	ZNF185	zinc finger protein 185 with LIM do	0.64	5.46e-10	DHPS	deoxyhypusine synthase
-0.72	2.80e-07	TACSTD2	tumor associated calcium signal tra	0.64	1.63e-10	DDI2	DNA damage inducible 1 homolog 2
-0.72	1.87e-07	PKP3	plakophilin 3	0.64	2.02e-07	TUBB4A	tubulin beta 4A class IVa
-0.71	1.59e-05	CAVIN1	caveolae associated protein 1	0.64	4.11e-10	DUS3L	dihydrouridine synthase 3 like
-0.71	3.50e-09	CDCP1	CUB domain containing protein 1	0.63	7.82e-08	FKBP1A	FKBP prolyl isomerase 1A
-0.7	4.55e-08	EGFR	epidermal growth factor receptor	0.63	1.57e-08	PRPSAP2	phosphoribosyl pyrophosphate synth
-0.69	4.96e-07	ANXA3	annexin A3	0.63	3.48e-09	CCDC43	coiled-coil domain containing 43
-0.69	4.61e-07	NT5E	5'-nucleotidase ecto	0.63	1.10e-08	ENSA	endosulfine alpha
-0.67	4.63e-03	KRT18	keratin 18	0.63	1.30e-08	UBA5	ubiquitin like modifier activating
-0.67	5.16e-07	SPINT1	serine peptidase inhibitor, Kunitz	0.63	5.46e-10	METTL13	methyltransferase 13, eEF1A lysine
-0.66	1.03e-07	LAMB3	laminin subunit beta 3	0.63	8.33e-09	PITHD1	PITH domain containing 1
-0.66	1.28e-08	COL12A1	collagen type XII alpha 1 chain	0.62	5.00e-09	GTPBP1	GTP binding protein 1

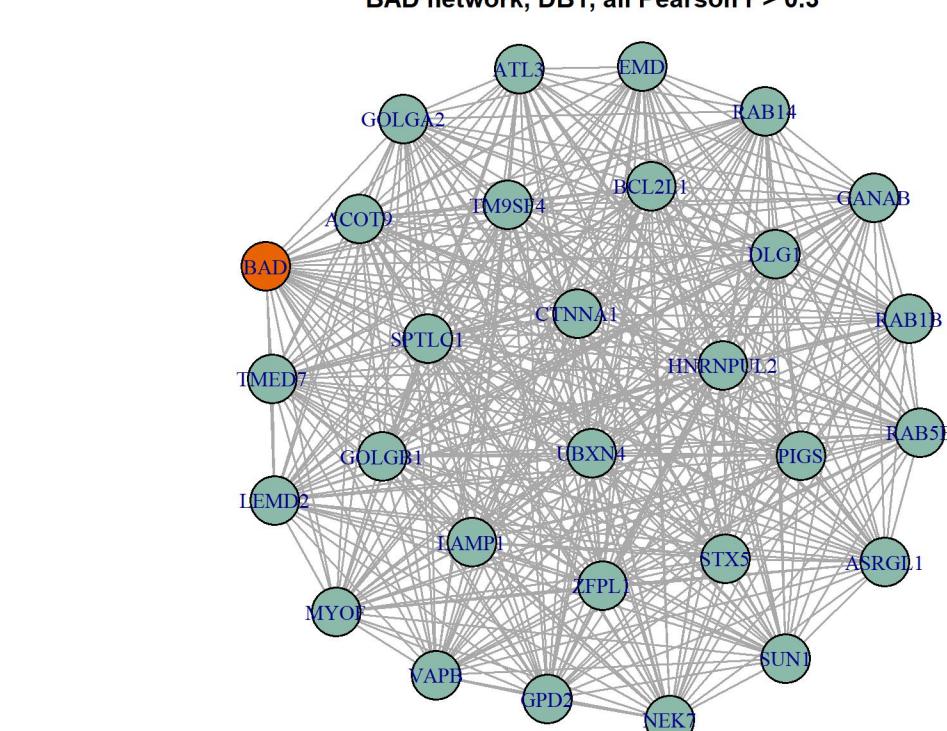
BAD network, DB1, all Pearson r > 0.4



BAD network, DB1, all Pearson r > 0.35



BAD network, DB1, all Pearson r > 0.3



Differentially expressed proteins in blood cancers at absence/low amount of BAD , DB1
p-value < 0.05 & logFC > 1.2

Sorted by p values!

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

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.07	5.70e-03	BCL2L1	BCL2 like 1	0.79	1.30e-04	PRTN3	proteinase 3
-0.87	1.41e-02	TDRKH	tudor and KH domain containing	0.6	5.70e-03	AZU1	azurocidin 1
-0.09	2.00e-02	ANXA7	annexin A7	0.46	1.08e-02	CEBPA	CCAAT enhancer binding protein alph
-0.76	2.00e-02	ETFDH	electron transfer flavoprotein dehy	0.71	1.41e-02	MNDA	myeloid cell nuclear differentiatio
-0.78	2.17e-02	VPS45	vacuolar protein sorting 45 homolog	0.01	2.00e-02	GAPDH	glyceraldehyde-3-phosphate dehydrog
-0.97	2.17e-02	ENO2	enolase 2	1.06	2.39e-02	DOK3	docking protein 3
-0.46	3.08e-02	SUPT4H1	SPT4 homolog, DSIF elongation facto	0.07	2.39e-02	PFDN1	prefoldin subunit 1
-0.9	3.08e-02	PNPLA6	patatin like phospholipase domain c	0.84	3.08e-02	CSTA	cystatin A
-0.71	3.08e-02	EXD2	exonuclease 3'-5' domain containing	0.36	3.45e-02	PRAM1	PML-RARA regulated adaptor molecule
-0.09	3.08e-02	CARS1	cysteinyl-tRNA synthetase 1	0.91	4.38e-02	PIK3AP1	phosphoinositide-3-kinase adaptor p
-0.65	5.41e-02	NAA30	N-alpha-acetyltransferase 30, NatC	0.4	4.82e-02	RNASE2	ribonuclease A family member 2
-0.61	5.41e-02	STX5	syntaxin 5	0.7	5.41e-02	PLD4	phospholipase D family member 4
-0.14	5.41e-02	PRKAR1A	protein kinase cAMP-dependent type	0.54	5.41e-02	BID	BH3 interacting domain death agonis
-0.1	5.41e-02	HINT2	histidine triad nucleotide binding	0.7	5.41e-02	LPCAT2	lysophosphatidylcholine acyltransfe
-0.82	5.41e-02	MYO1C	myosin IC	0.05	6.80e-02	SERBP1	SERPINE1 mRNA binding protein 1
-0.76	5.41e-02	SNX15	sorting nexin 15	0.44	6.80e-02	BST1	bone marrow stromal cell antigen 1
-0.41	6.47e-02	GUK1	guanylate kinase 1	0.82	7.15e-02	MEF2D	myocyte enhancer factor 2D
-0.49	6.97e-02	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.45	7.87e-02	IGFBP7	insulin like growth factor binding
-0.61	6.97e-02	ATRX	ATRX chromatin remodeler	0.49	7.87e-02	NUCB2	nucleobindin 2
-0.06	6.97e-02	GET3	guided entry of tail-anchored prote	0.92	7.87e-02	LAT2	linker for activation of T cells fa
-0.78	6.97e-02	RAB9A	RAB9A, member RAS oncogene family	0.49	7.87e-02	MPO	myeloperoxidase
-0.44	6.97e-02	RBM6	RNA binding motif protein 6	0.8	7.87e-02	PDLM7	PDZ and LIM domain 7
-0.62	6.97e-02	SHMT1	serine hydroxymethyltransferase 1	0.66	7.87e-02	MYO1F	myosin IF
-0.42	6.97e-02	LRWD1	leucine rich repeats and WD repeat	0.56	7.87e-02	DNMBP	dynamin binding protein
-0.36	6.97e-02	SAMD1	sterile alpha motif domain containi	0.47	7.87e-02	CES1	carboxylesterase 1
-0.73	7.15e-02	GNE	glucosamine (UDP-N-acetyl)-2-epimer	0.1	7.87e-02	PNP	purine nucleoside phosphorylase
-0.4	7.15e-02	ZC2HC1A	zinc finger C2HC-type containing 1A	0.6	9.48e-02	NRGN	neurogranin
-0.56	7.17e-02	MAVS	mitochondrial antiviral signaling p	0.65	9.73e-02	CTSG	cathepsin G
-0.76	7.58e-02	ACP2	acid phosphatase 2, lysosomal	0.05	1.08e-01	PFDN2	prefoldin subunit 2
-0.67	7.58e-02	YTHDC1	YTH domain containing 1	0.79	1.09e-01	PLCG2	phospholipase C gamma 2
-0.68	7.60e-02	PACS1	phosphofuran acidic cluster sorting	0.67	1.14e-01	PYGL	glycogen phosphorylase L
-0.84	7.60e-02	CPS1	carbamoyl-phosphate synthase 1	0.25	1.18e-01	ABCD1	ATP binding cassette subfamily D me
-0.75	7.81e-02	MPRIP	myosin phosphatase Rho interacting	0.08	1.19e-01	PSMB6	proteasome 20S subunit beta 6
-0.67	7.87e-02	TAP1	transporter 1, ATP binding cassette	0.41	1.24e-01	AIF1	allograft inflammatory factor 1
-0.92	7.87e-02	CASP6	caspase 6	0.55	1.24e-01	APOBR	apolipoprotein B receptor
-0.09	7.87e-02	RELA	RELA proto-oncogene, NF- κ b subunit	0.59	1.24e-01	LYZ	lysozyme
-0.23	7.87e-02	HELZ2	helicase with zinc finger 2	0.54	1.31e-01	PXK	PX domain containing serine/threonine
-0.44	7.87e-02	GLE1	GLE1 RNA export mediator	0.87	1.34e-01	TUBB6	tubulin beta 6 class V
0.32	7.87e-02	TAPBD	TAP binding protein	0.07	1.35e-01	HMGR1	high mobility group box 1

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

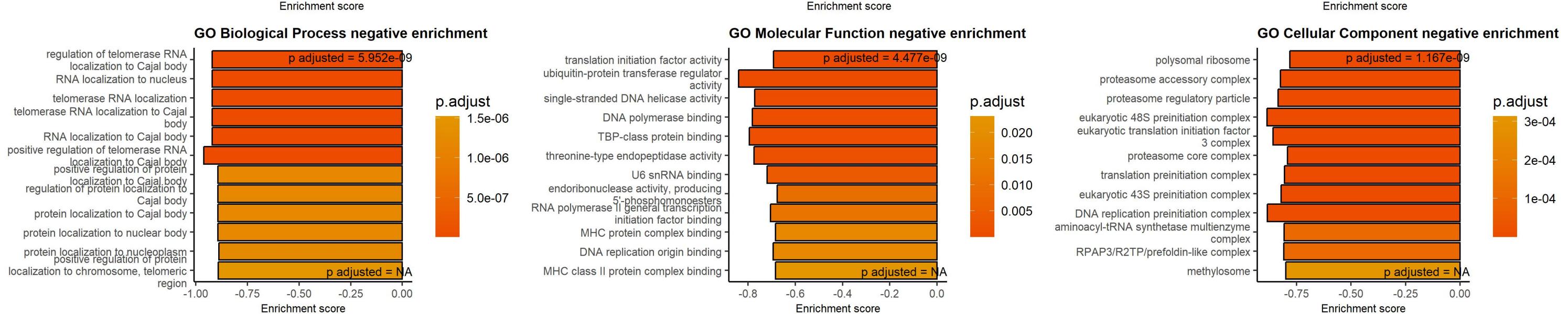
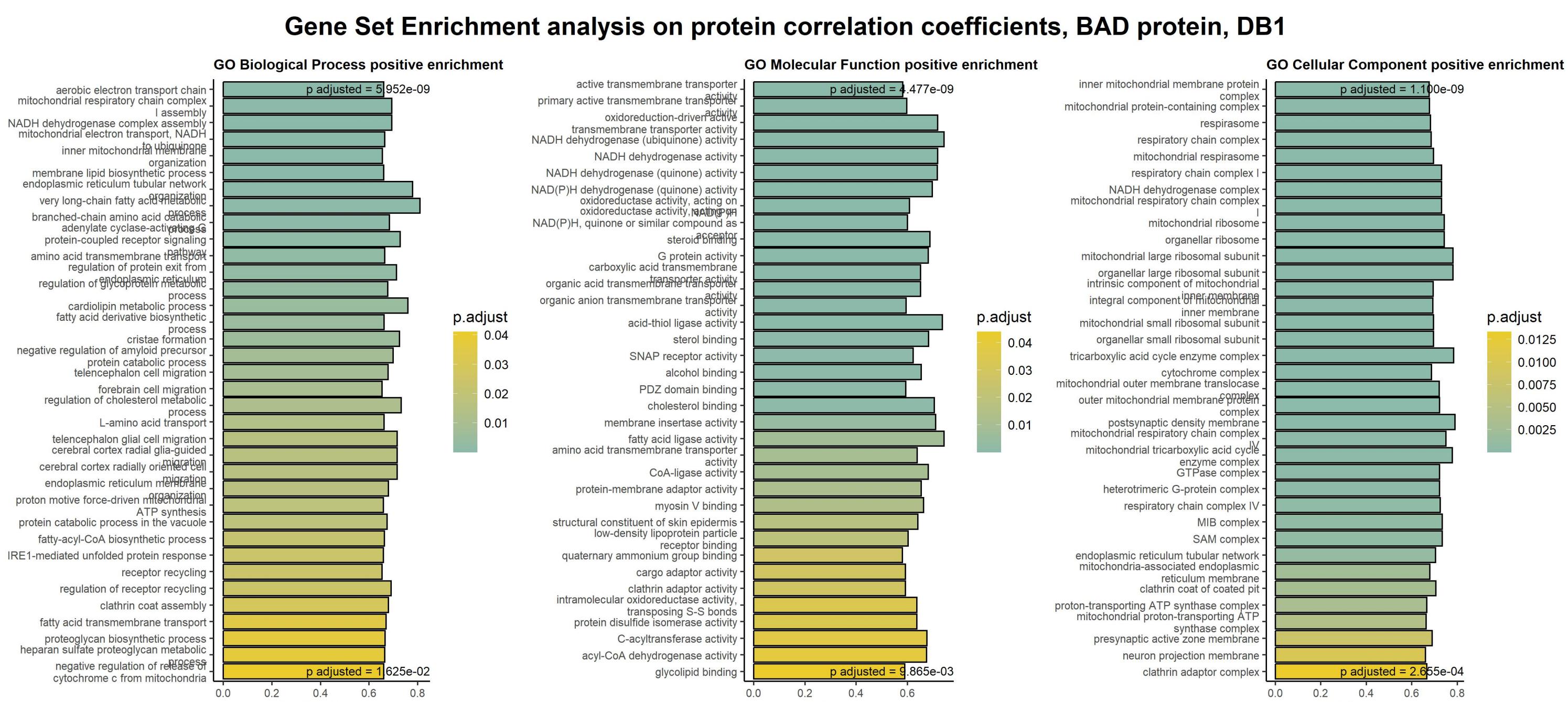
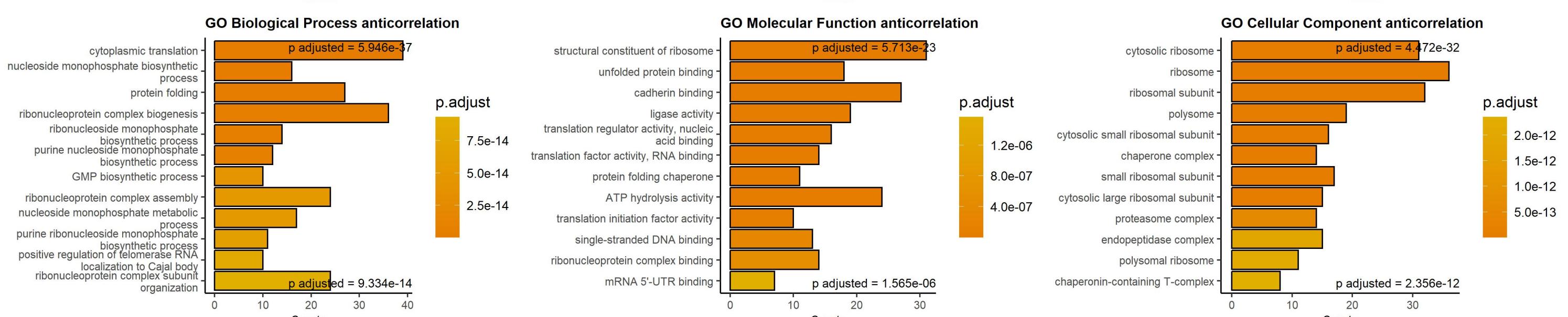
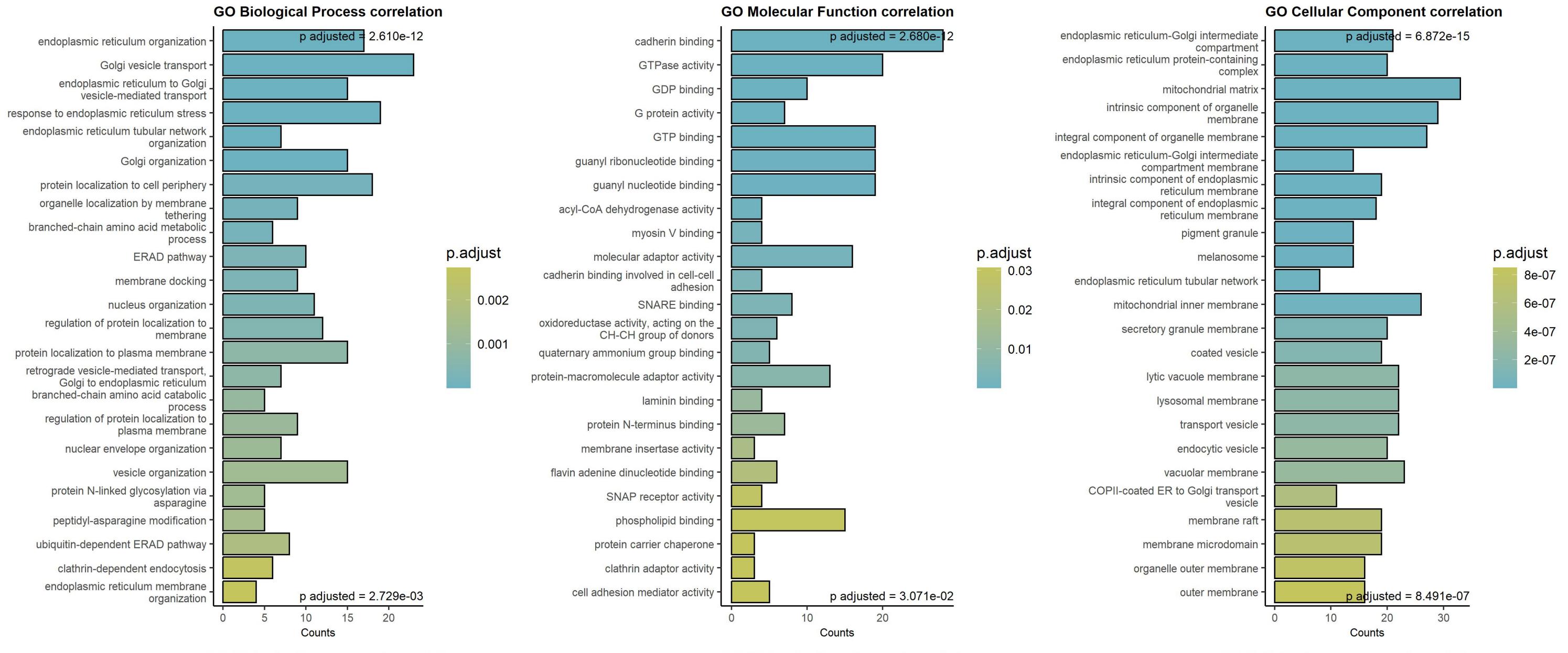
p-value < 0.05 & logFC > 1.2

Sorted by p values!

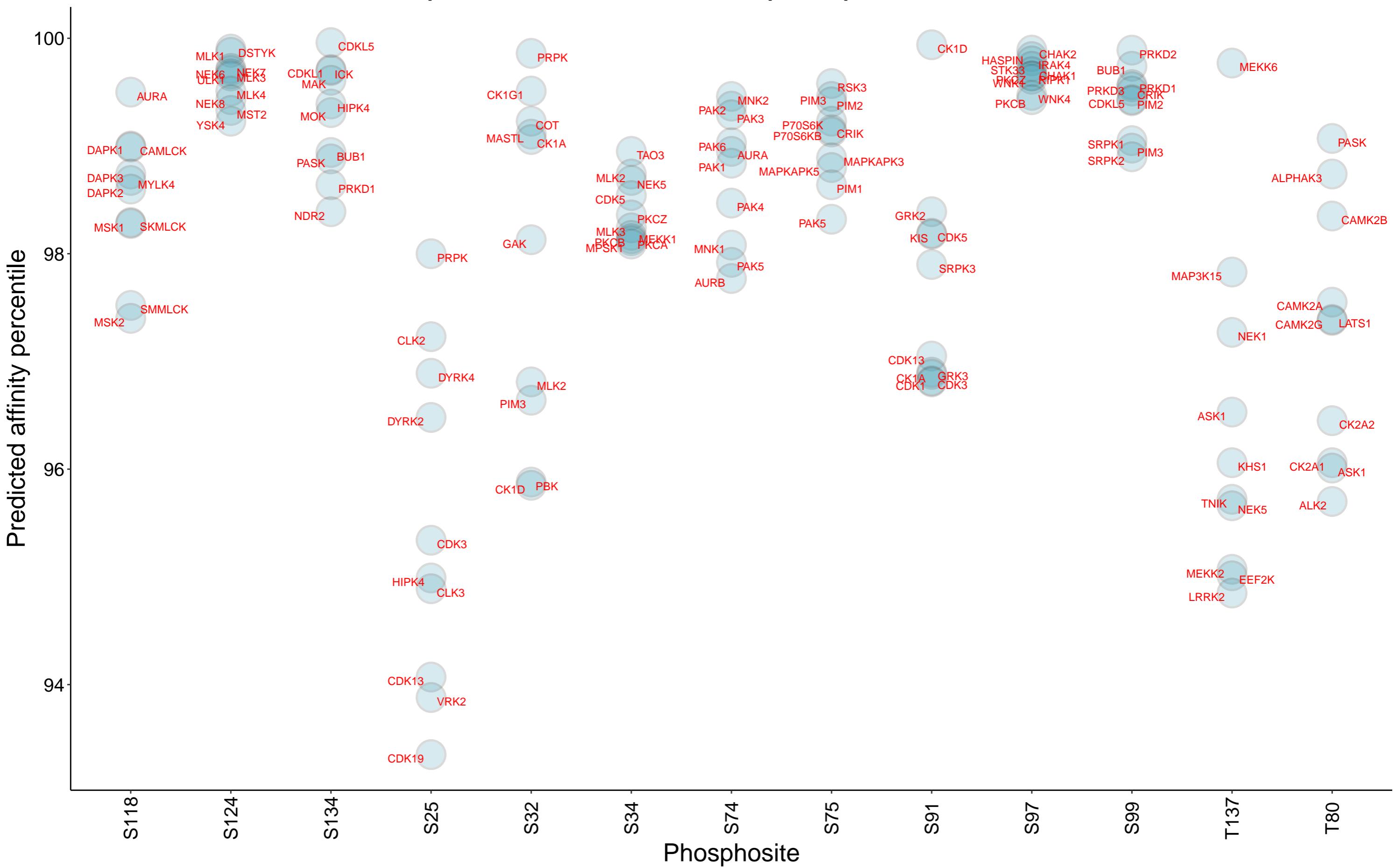
Downregulated in solid cancers at low/absent BAD Upregulated in solid cancers at low/absent BAD

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.08	0.00e+00	H4C1	H4 clustered histone 1	0.67	2.18e-12	PAPOLA	poly(A) polymerase alpha
-1.07	9.74e-30	BCL2L1	BCL2 like 1	0.08	5.99e-12	CCT6A	chaperonin containing TCP1 subunit
-0.16	3.32e-19	ZFPFL1	zinc finger protein like 1	0.07	6.21e-12	CCT3	chaperonin containing TCP1 subunit
-0.95	1.56e-13	BCAM	basal cell adhesion molecule (Luthe	0.65	6.21e-12	DUSP12	dual specificity phosphatase 12
-0.06	3.62e-13	GANAB	glucosidase II alpha subunit	0.78	6.74e-12	PFKM	phosphofructokinase, muscle
-0.09	7.15e-13	HNRNPUL2	heterogeneous nuclear ribonucleoprotein	0.07	6.74e-12	SSB	small RNA binding exonuclease prote
-0.12	1.65e-12	LEMD2	LEM domain nuclear envelope protein	0.04	6.81e-12	RPS14	ribosomal protein S14
-0.13	2.47e-12	GOLGB1	golgin B1	0.07	7.22e-12	CCT8	chaperonin containing TCP1 subunit
-0.09	3.21e-12	SPTLC1	serine palmitoyltransferase long ch	0.07	1.64e-11	CCT4	chaperonin containing TCP1 subunit
-0.47	6.21e-12	RAB1B	RAB1B, member RAS oncogene family	0.05	2.20e-11	HSP90AB1	heat shock protein 90 alpha family
-0.98	1.25e-11	ITGB4	integrin subunit beta 4	0.73	2.24e-11	ARMC6	armadillo repeat containing 6
-1	1.37e-11	GPRC5A	G protein-coupled receptor class C	0.69	2.24e-11	UCK2	uridine-cytidine kinase 2
-0.35	1.69e-11	STX5	syntaxin 5	0.04	2.28e-11	PCBP1	poly(rC) binding protein 1
-0.1	1.90e-11	SCFD1	sec1 family domain containing 1	0.56	3.16e-11	HAUS6	HAUS augmin like complex subunit 6
-0.1	2.24e-11	OGDH	oxoglutarate dehydrogenase	0.07	3.69e-11	CCT7	chaperonin containing TCP1 subunit
-0.09	2.62e-11	RAB14	RAB14, member RAS oncogene family	0.07	5.63e-11	RTCB	RNA 2',3'-cyclic phosphate and 5'-O
-0.92	3.46e-11	PKP2	plakophilin 2	0.04	6.31e-11	RPS17	ribosomal protein S17
-0.87	3.67e-11	KRT80	keratin 80	0.06	6.31e-11	CCT2	chaperonin containing TCP1 subunit
-0.1	4.36e-11	ACAD9	acyl-CoA dehydrogenase family membe	0.12	7.07e-11	ATIC	5-aminoimidazole-4-carboxamide ribo
-0.08	6.31e-11	GOLGA2	golgin A2	0.57	7.63e-11	GGA1	golgi associated, gamma adaptin ear
-0.75	1.12e-10	SDC4	syndecan 4	0.12	8.26e-11	NASP	nuclear autoantigenic sperm protein
-0.83	2.22e-10	AXL	AXL receptor tyrosine kinase	0.08	1.01e-10	HSPA4	heat shock protein family A (Hsp70)
-0.8	3.77e-10	F3	coagulation factor III, tissue fact	0.69	1.22e-10	HDHD2	haloacid dehalogenase like hydrolas
-0.07	3.81e-10	FKBP2	FKBP prolyl isomerase 2	0.68	1.35e-10	SMAD4	SMAD family member 4
-0.6	4.84e-10	ITPR3	inositol 1,4,5-trisphosphate recept	0.06	1.49e-10	CCT5	chaperonin containing TCP1 subunit
-0.09	4.84e-10	TMOD3	tropomodulin 3	0.64	1.63e-10	DDI2	DNA damage inducible 1 homolog 2
-0.79	7.37e-10	EPS8L2	EPS8 like 2	0.09	1.76e-10	SERBP1	SERPINE1 mRNA binding protein 1
-0.07	1.11e-09	AP2B1	adaptor related protein complex 2 s	0.67	2.34e-10	GABPA	GA binding protein transcription fa
-0.77	1.20e-09	EHD2	EH domain containing 2	0.57	2.37e-10	GEMIN6	gem nuclear organelle associated pr
-0.09	1.24e-09	AP2A1	adaptor related protein complex 2 s	0.06	2.72e-10	PSMC4	proteasome 26S subunit, ATPase 4
-0.86	1.33e-09	KRT85	keratin 85	0.45	2.84e-10	ARIH2	ariadne RBR E3 ubiquitin protein li
-0.76	1.62e-09	PPL	periplakin	0.1	2.98e-10	IMPDH2	inosine monophosphate dehydrogenase
-0.07	1.62e-09	PGRMC2	progesterone receptor membrane comp	0.04	3.20e-10	RPS3A	ribosomal protein S3A
-0.71	3.50e-09	CDCP1	CUB domain containing protein 1	0.03	3.38e-10	RPL11	ribosomal protein L11
-0.07	4.09e-09	LAMP1	lysosomal associated membrane prote	0.04	4.11e-10	RPS20	ribosomal protein S20
-0.07	4.66e-09	EMC2	ER membrane protein complex subunit	0.64	4.11e-10	DUS3L	dihydrouridine synthase 3 like
-0.08	4.66e-09	KTN1	kinectin 1	0.7	4.1		

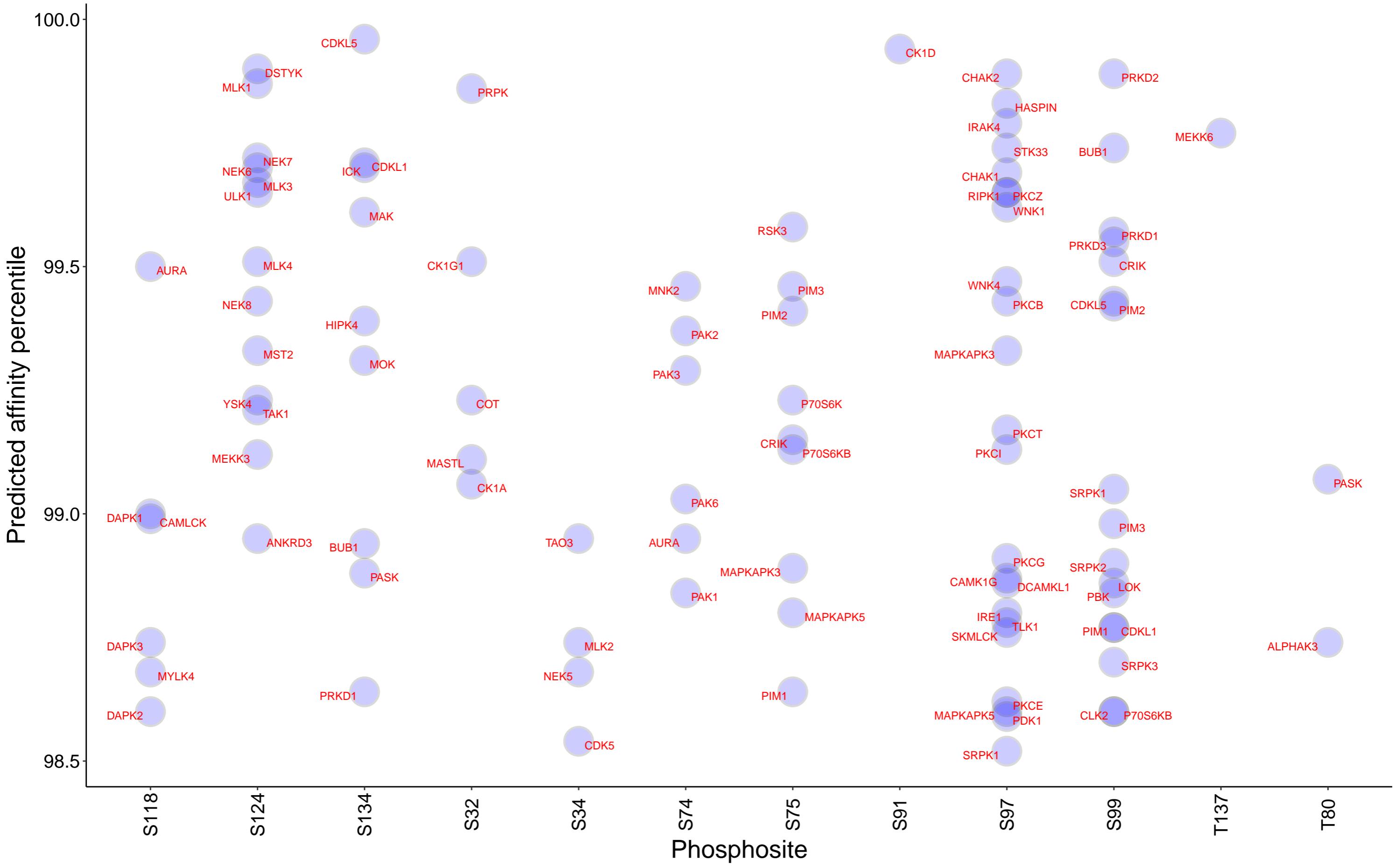
Top 250 correlation coefficients overrepresentation, BAD protein, DB1



Top 10 kinases for each phosphosite in BAD



Kinases with affinity greater than 98.5% to BAD



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

Beware of false positives in tissues with small number of samples

