

# BID

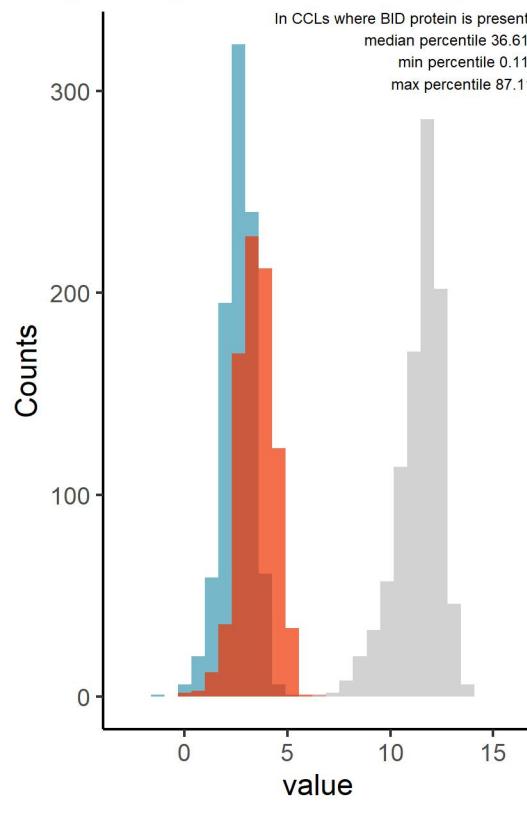
Protein name: BID ; UNIPROT: P55957 ; Gene name: BH3 interacting domain death agonist

Ligandable: NA ; Ligandable\_by\_Chem: NA ; Is\_enzyme: NA (<https://cansar.ai/>)

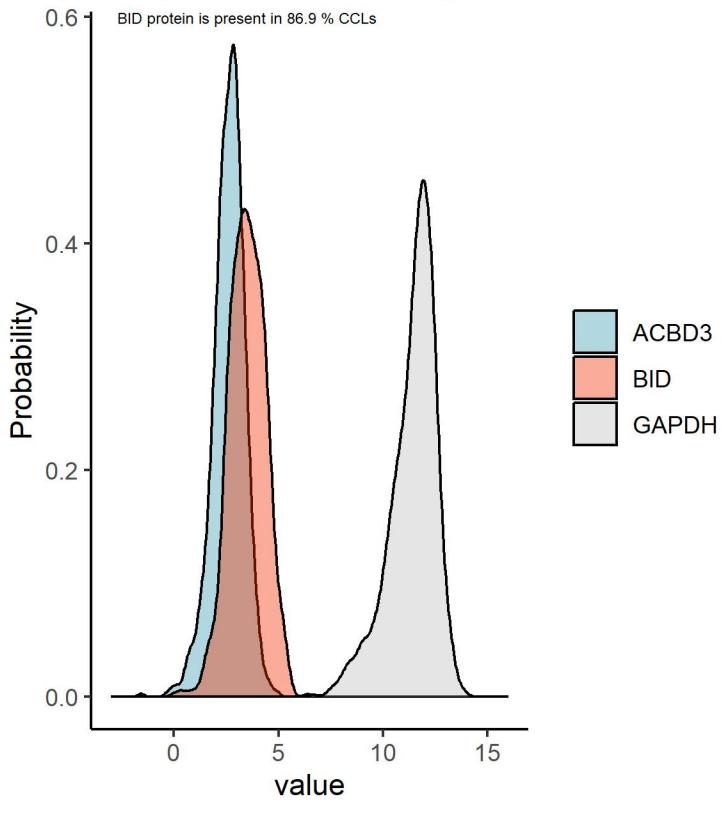
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

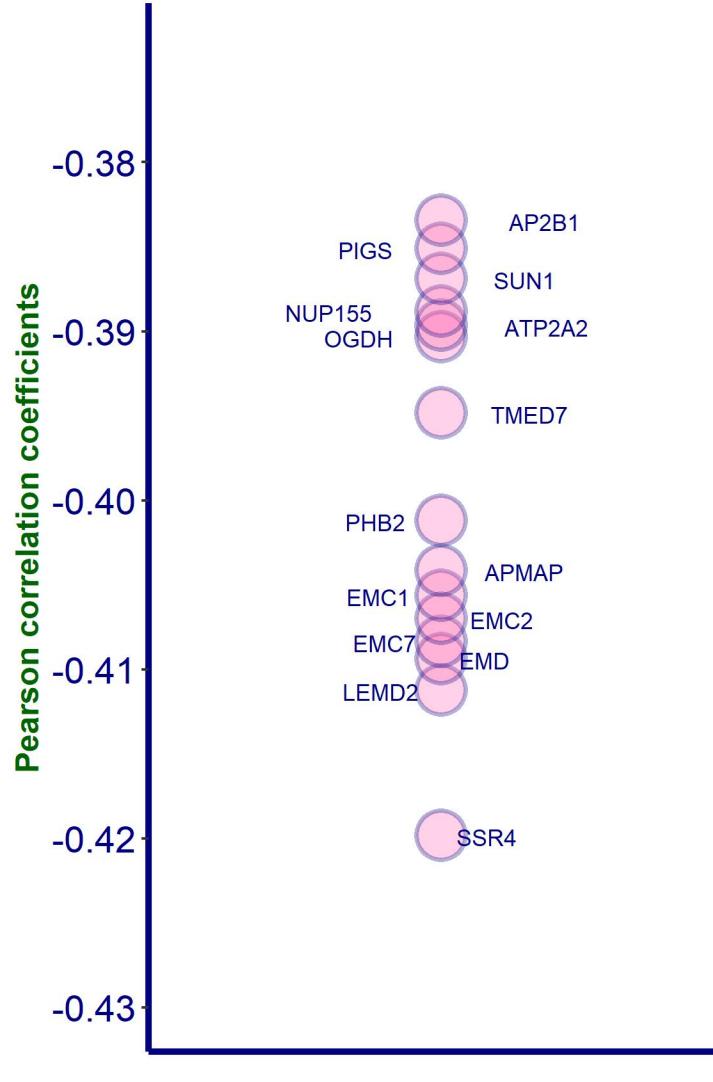
Histogram of BID protein compared to proteins with low and high abundance



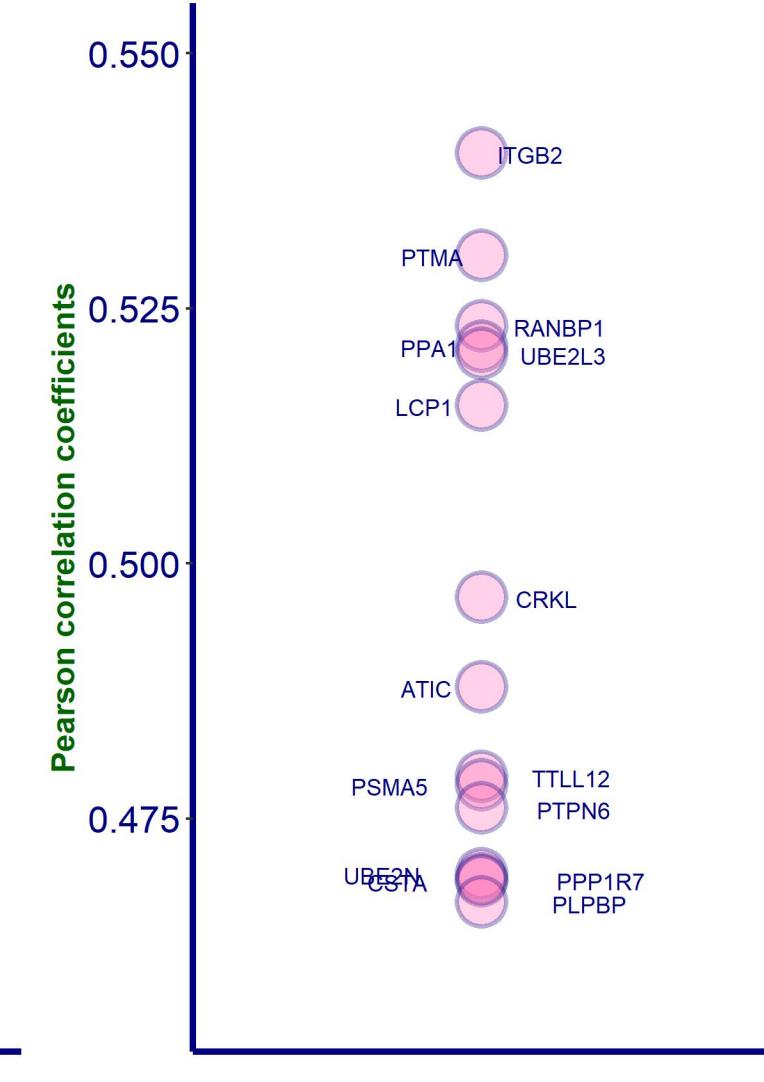
Density plot of BID protein compared to proteins with low and high abundance



Top negative correlations of BID protein, DB1

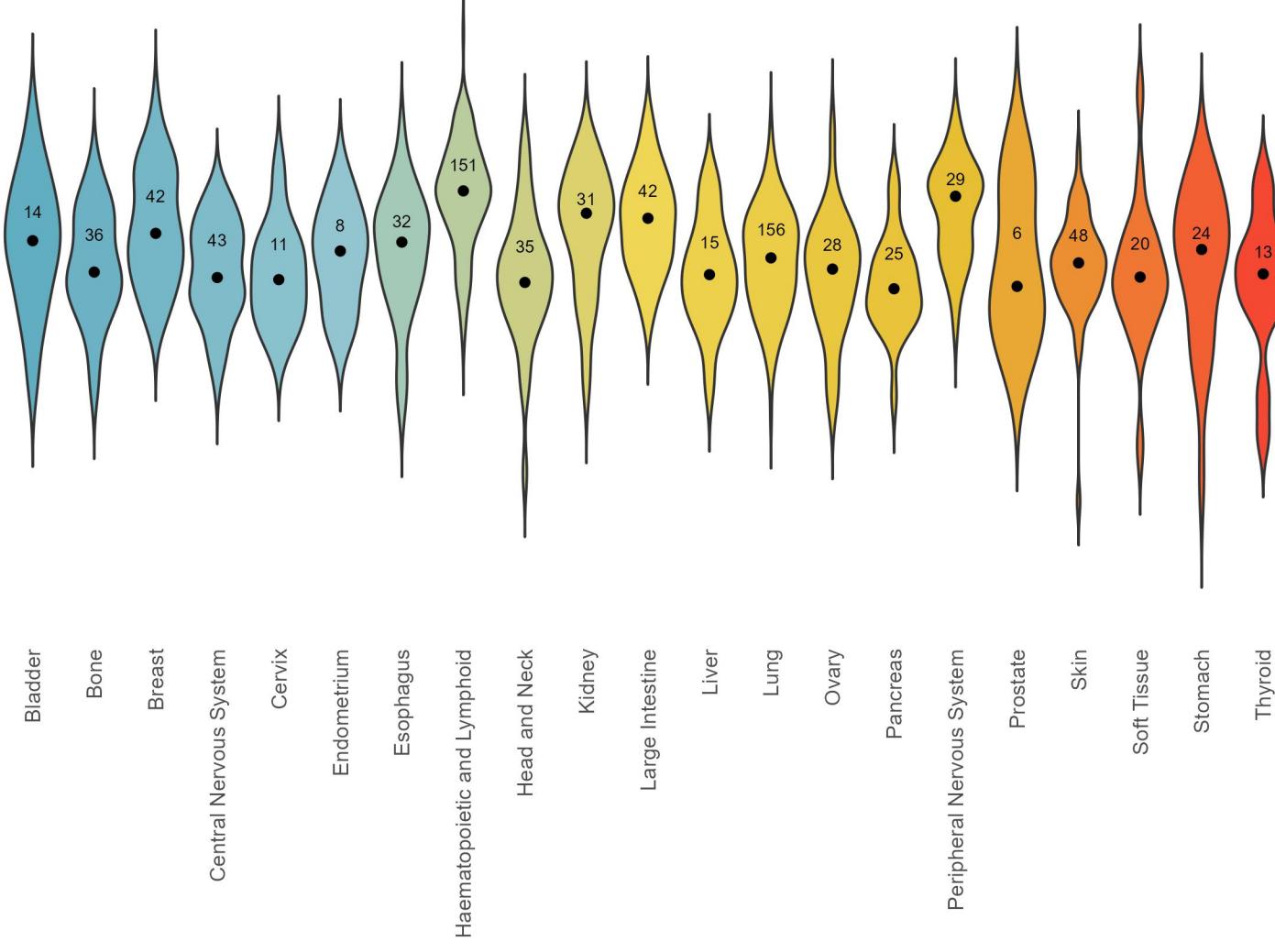


Top positive correlations of BID protein, DB1



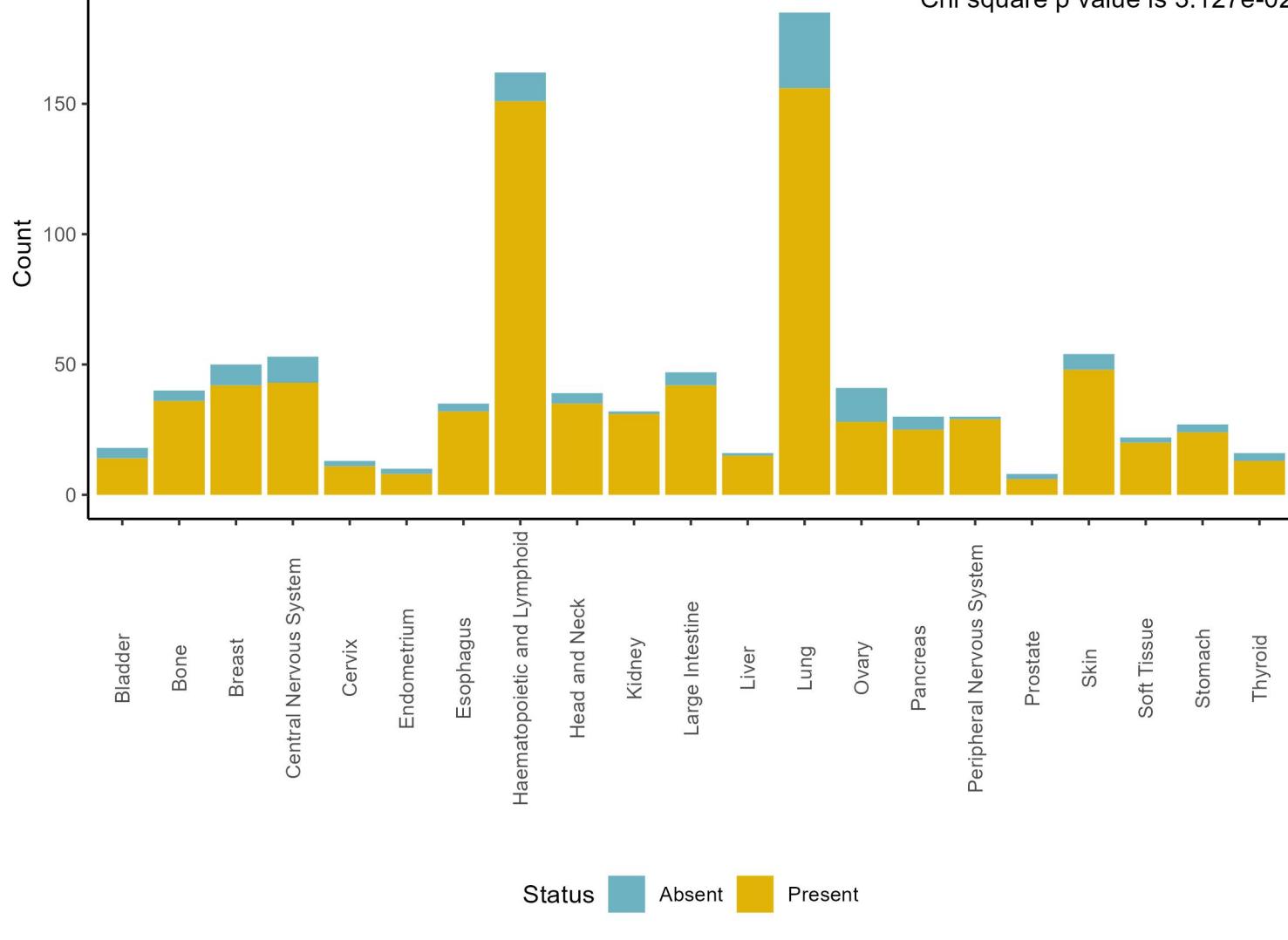
Amount of BID protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.752e-32



Present and absent BID protein counts by tissue, DB1

Chi square p value is 3.127e-02

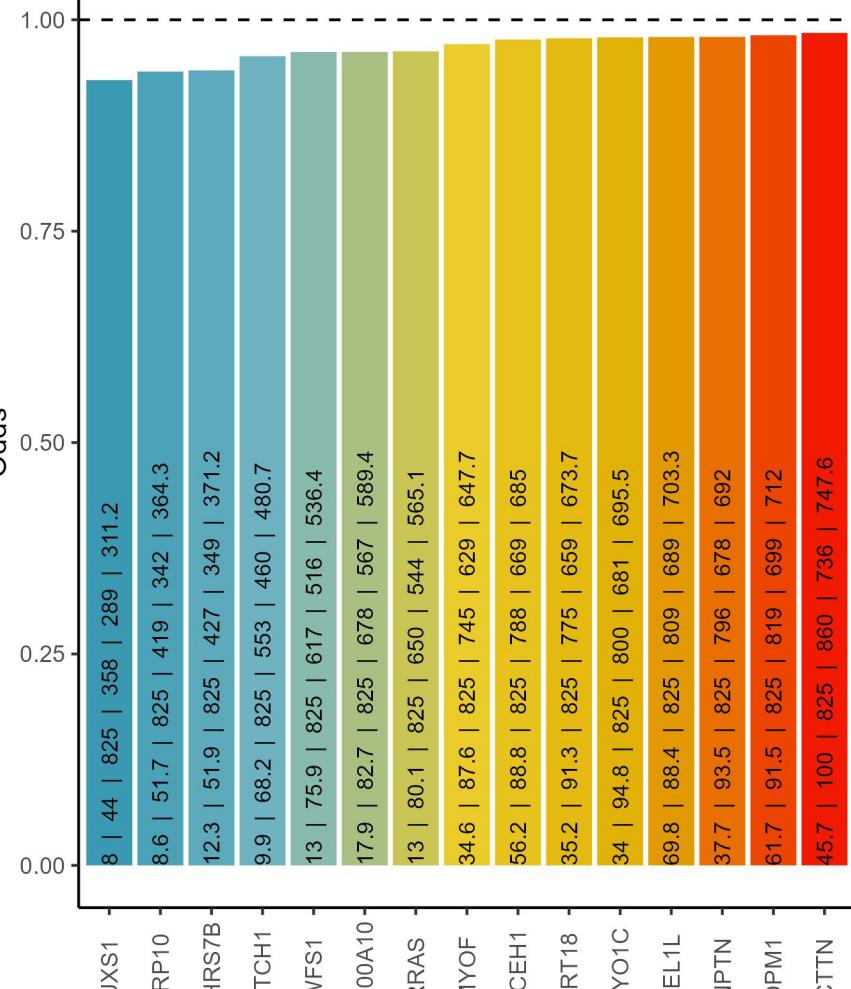


## Cooccurrence with BID protein, DB1

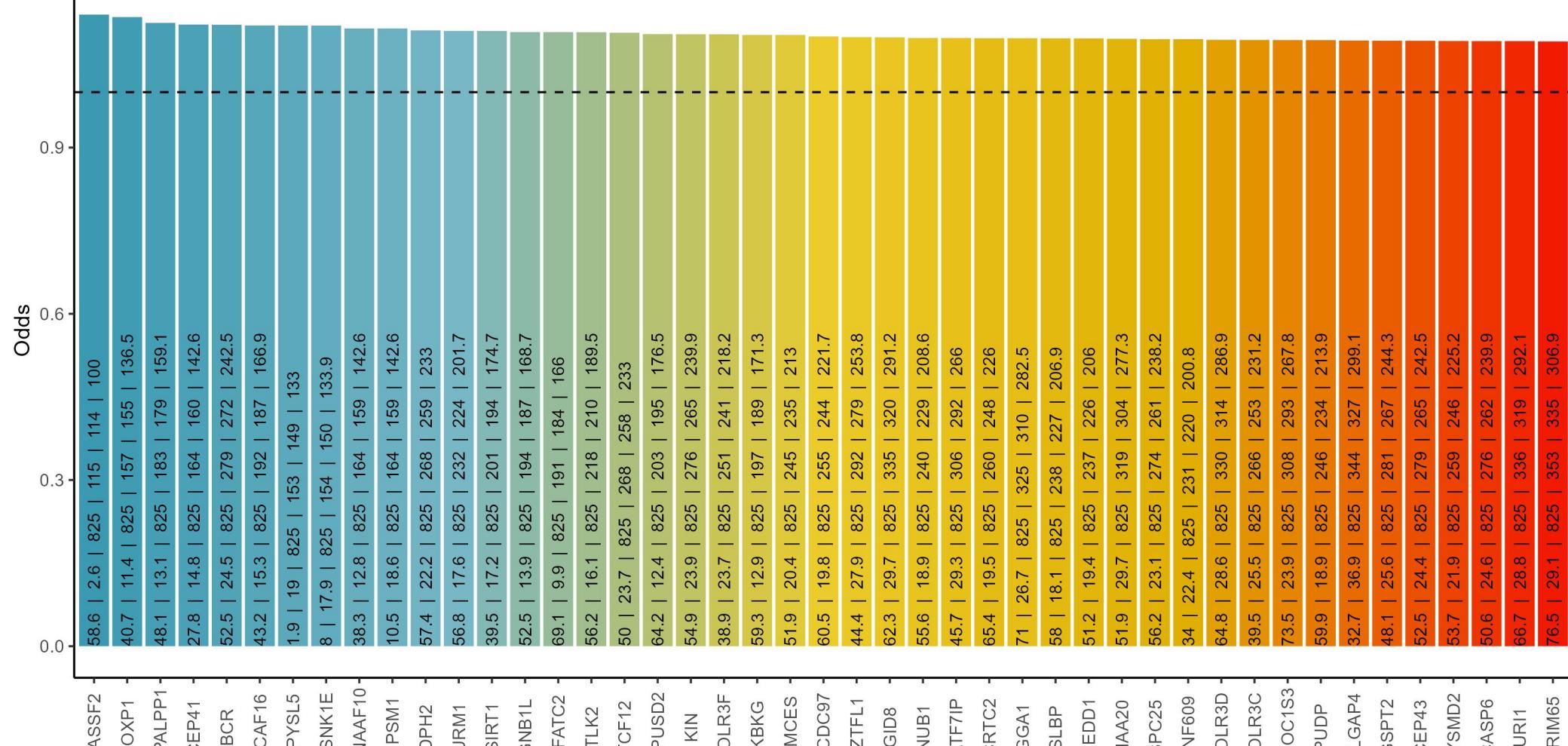
% of BID in blood cancers: 93.2 ; % of BID in solid cancers: 85.6

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

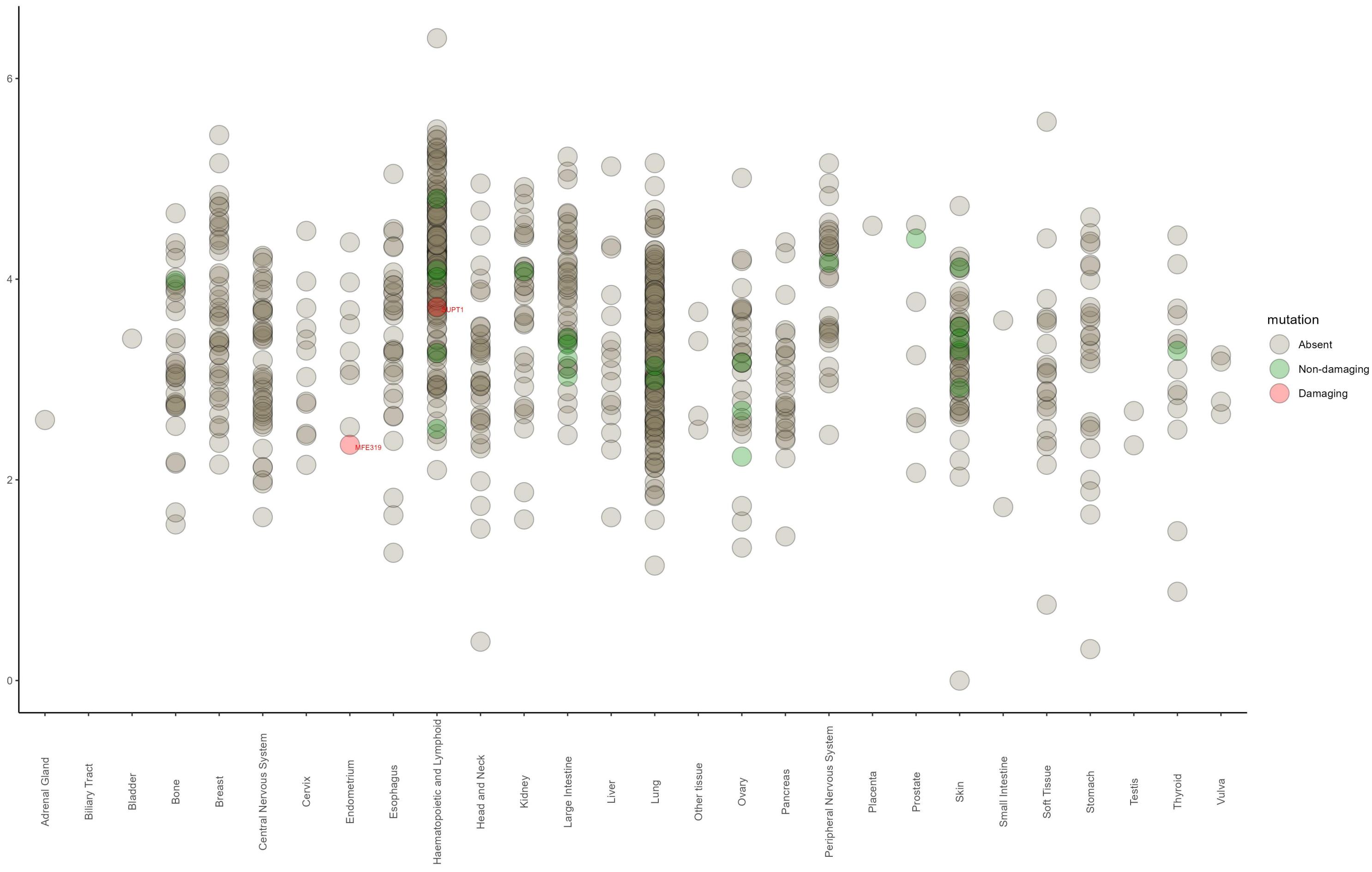
### Negative cooccurrence



### Positive cooccurrence

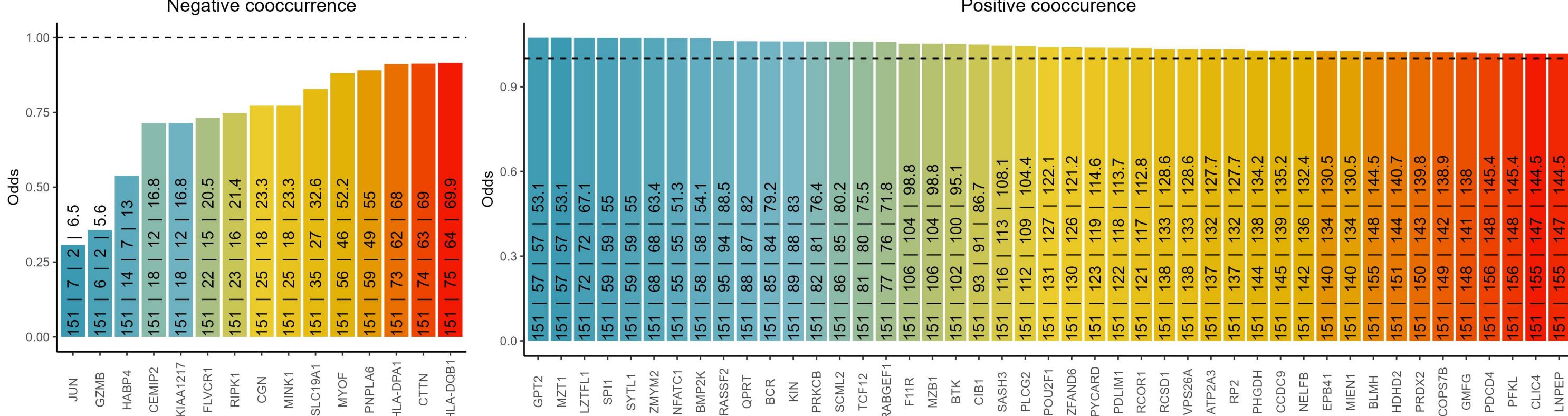


# Amount of BID protein and mutation status by tissue, DB1



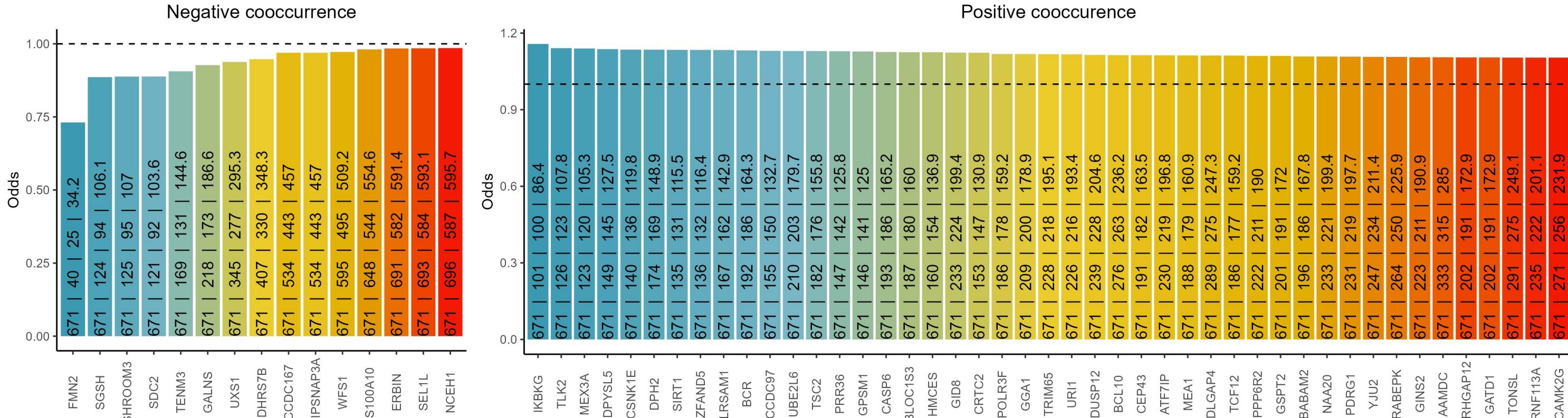
## Cooccurrence with BID protein in blood cancers, DB1

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

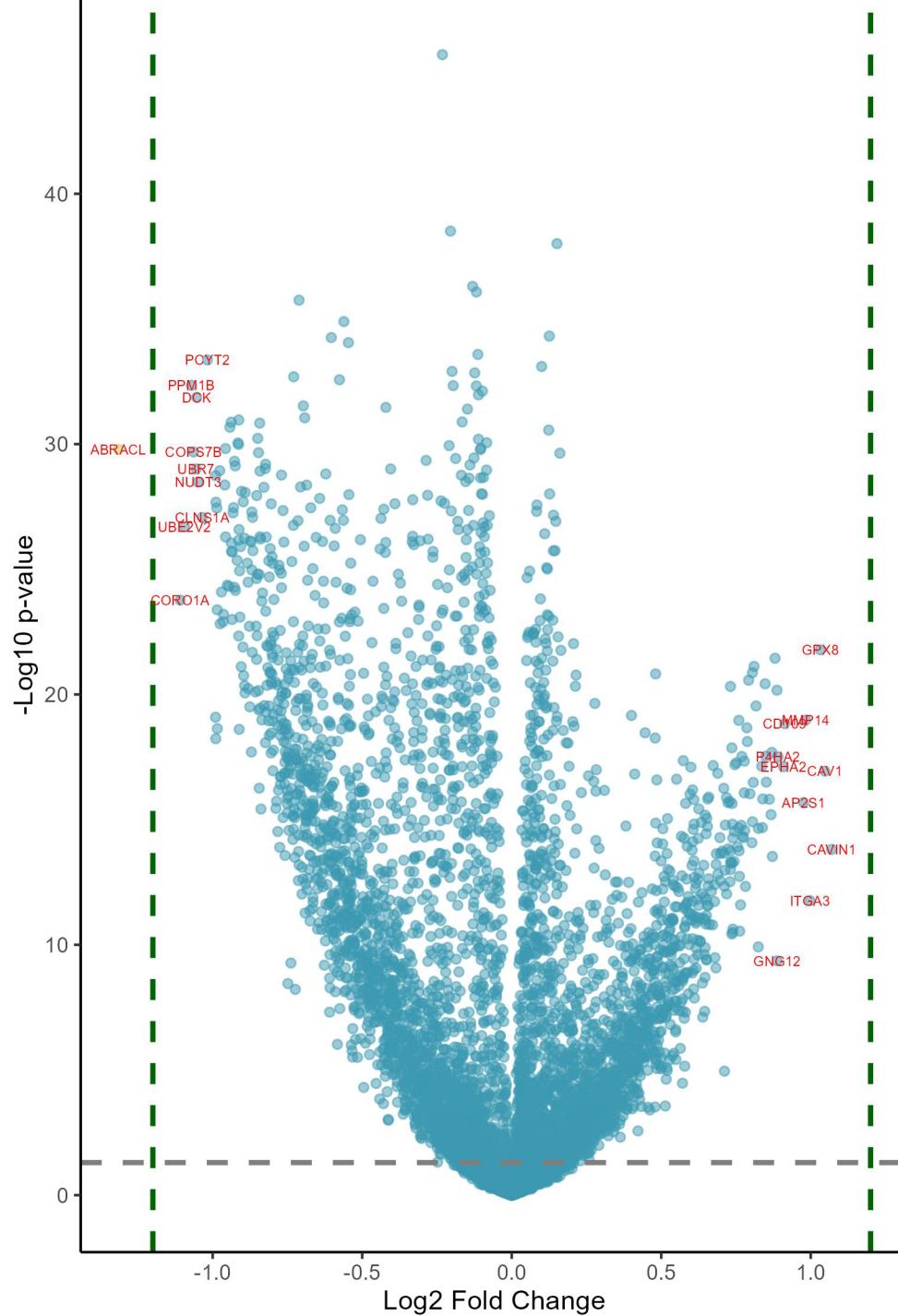


## Cooccurrence with BID protein in solid cancers, DB1

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

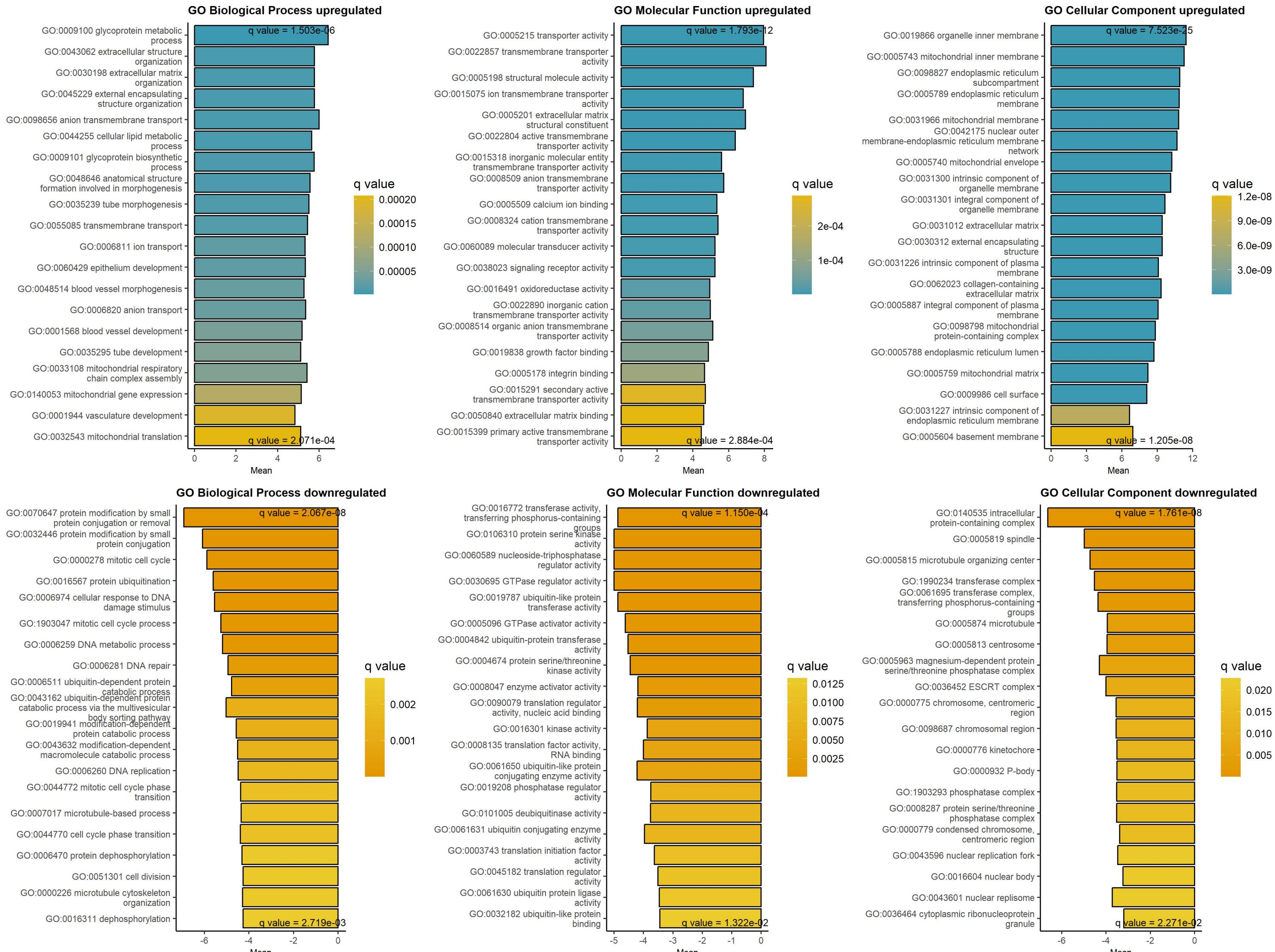


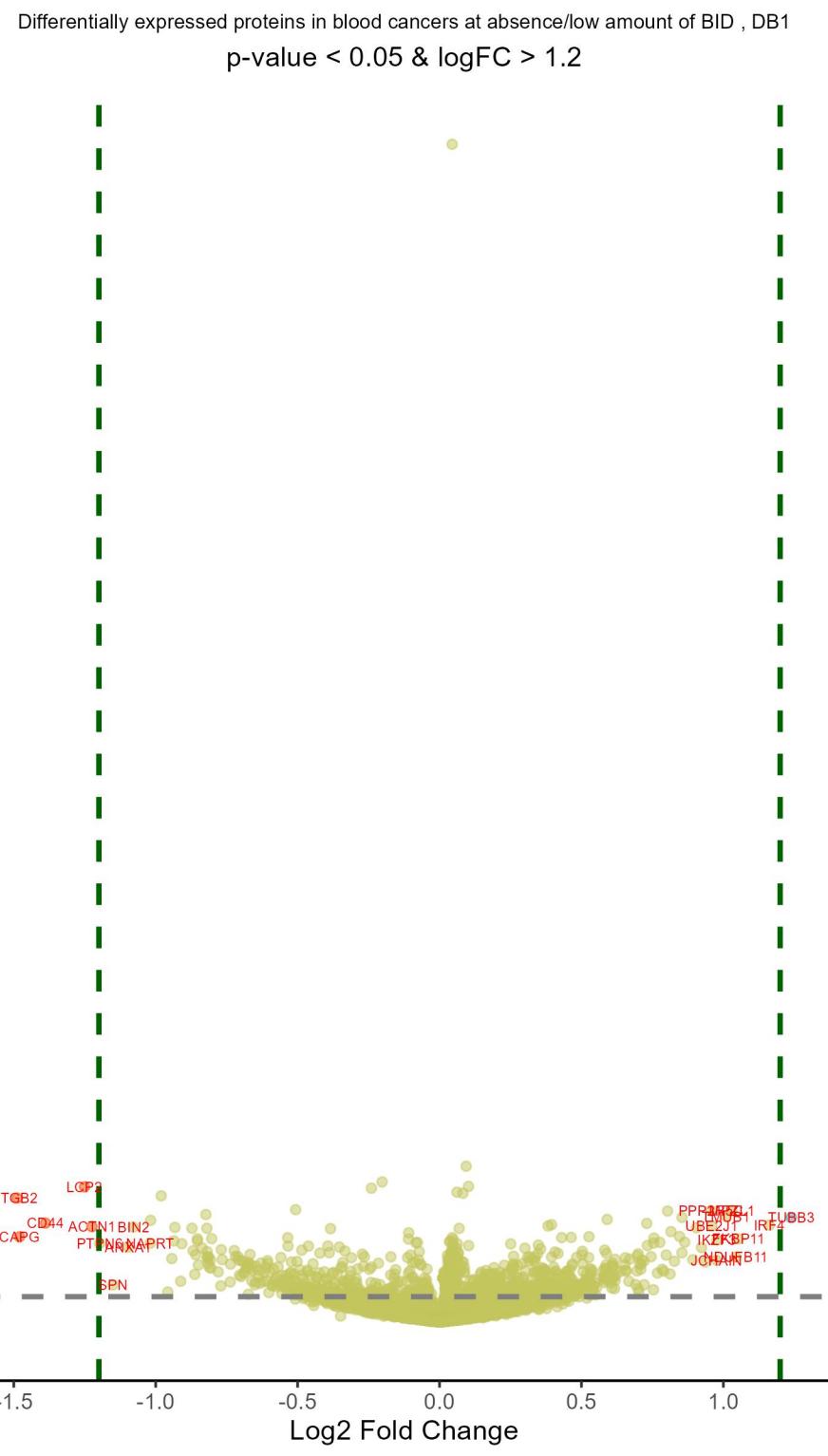
## Downregulated at low/absent BID Upregulated at low/absent BID



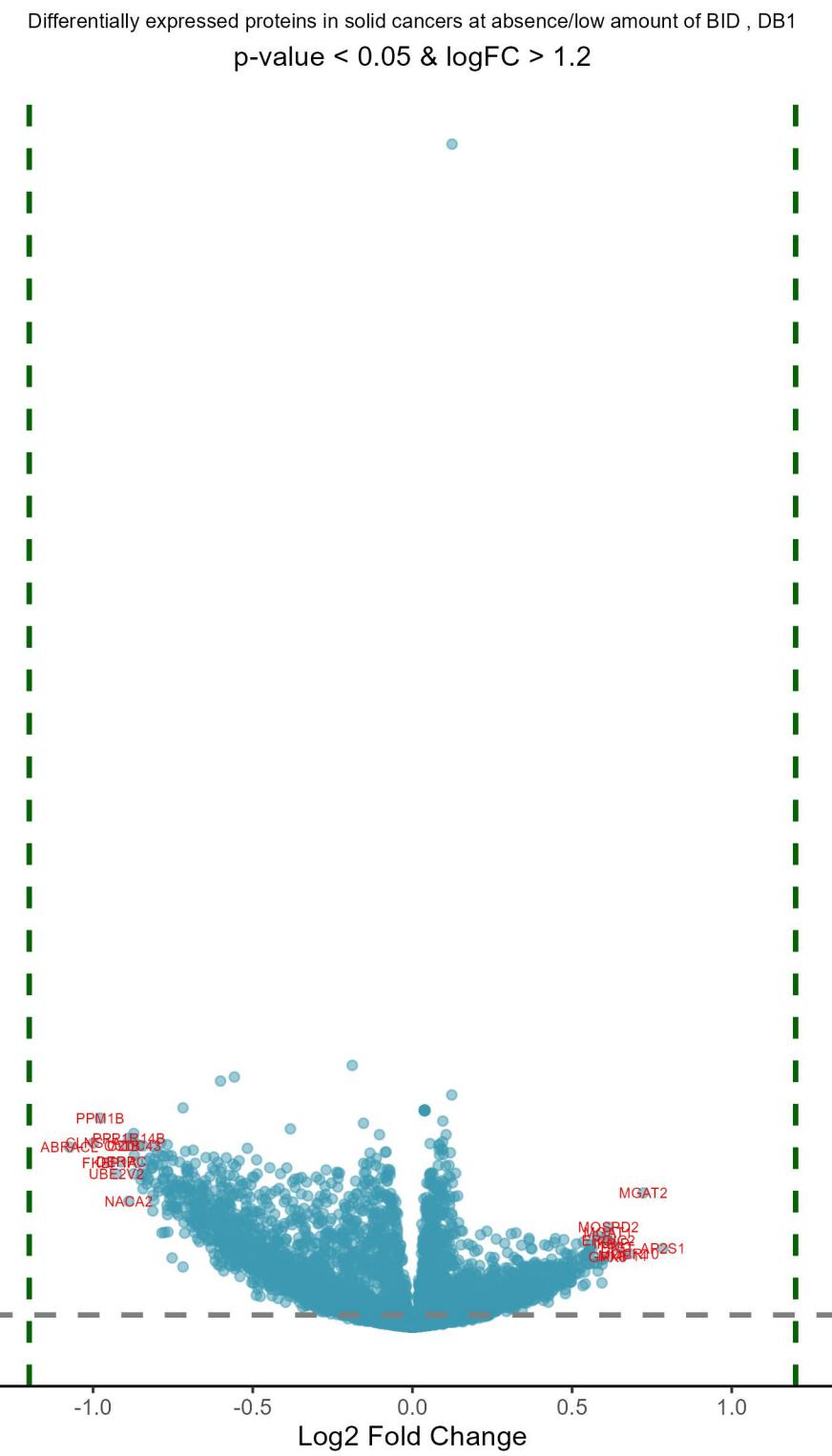
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.32	2.52e-28	ABRACL	ABRA C-terminal like	1.07	9.85e-14	CAVIN1	caveolae associated protein 1
-1.11	5.18e-23	CORO1A	coronin 1A	1.05	1.11e-16	CAV1	caveolin 1
-1.09	1.15e-25	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.03	3.55e-21	GPX8	glutathione peroxidase 8 (putative)
-1.07	1.51e-30	PPM1B	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> depe	1	8.77e-12	ITGA3	integrin subunit alpha 3
-1.06	3.02e-28	COPS7B	COP9 signalosome subunit 7B	0.98	1.41e-18	MMP14	matrix metallopeptidase 14
-1.06	1.15e-27	UBR7	ubiquitin protein ligase E3 compone	0.98	1.67e-15	AP2S1	adaptor related protein complex 2 s
-1.05	3.77e-30	DCK	deoxycytidine kinase	0.91	1.89e-18	CD109	CD109 molecule
-1.05	3.16e-27	NUDT3	nudix hydrolase 3	0.91	7.60e-17	EPHA2	EPH receptor A2
-1.04	5.39e-26	CLNS1A	chloride nucleotide-sensitive chann	0.89	3.24e-17	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.02	2.22e-31	PCYT2	phosphate cytidylyltransferase 2, e	0.89	1.67e-09	GNG12	G protein subunit gamma 12
-0.99	1.88e-27	PITHD1	PITH domain containing 1	0.89	1.09e-19	ITGAV	integrin subunit alpha V
-0.99	1.09e-18	BLMH	bleomycin hydrolase	0.88	7.36e-21	FNDC3B	fibronectin type III domain contain
-0.99	6.82e-18	ZNF706	zinc finger protein 706	0.87	1.82e-13	NT5E	5'-nucleotidase ecto
-0.99	1.62e-26	UBA5	ubiquitin like modifier activating	0.87	2.23e-17	PIGT	phosphatidylinositol glycan anchor
-0.99	2.55e-26	PPM1A	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> depe	0.87	4.80e-15	UQCR10	ubiquinol-cytochrome c reductase, c
-0.98	1.21e-22	C11orf54	chromosome 11 open reading frame 54	0.86	1.26e-15	AXL	AXL receptor tyrosine kinase
-0.98	2.85e-18	NACA2	nascent polypeptide associated comp	0.85	2.89e-16	RRAS	RAS related
-0.98	1.30e-27	KIAA1143	KIAA1143	0.85	3.09e-17	RAB13	RAB13, member RAS oncogene family
-0.97	3.88e-22	FKBP1A	FKBP prolyl isomerase 1A	0.85	6.40e-20	ERGIC2	ERGIC and golgi 2
-0.97	2.55e-23	PPP6R1	protein phosphatase 6 regulatory su	0.84	1.23e-15	MTCH1	mitochondrial carrier 1
-0.97	3.26e-22	PSME3IP1	proteasome activator subunit 3 inte	0.84	1.48e-14	BCAM	basal cell adhesion molecule (Luthe
-0.96	1.79e-22	DHFR	dihydrofolate reductase	0.84	7.35e-17	LAMC1	laminin subunit gamma 1
-0.96	4.07e-27	CCDC43	coiled-coil domain containing 43	0.82	1.57e-14	PLOD2	procollagen-lysine,2-oxoglutarate 5
-0.96	2.39e-28	EIPR1	EARP complex and GARP complex inter	0.82	4.96e-10	S100A10	S100 calcium binding protein A10
-0.96	2.67e-25	BABAM1	BRISC and BRCA1 A complex member 1	0.82	4.14e-19	TMT3	transmembrane O-mannosyltransferase
-0.95	1.42e-23	CORO7	coronin 7	0.81	1.47e-20	LMAN2L	lectin, mannose binding 2 like
-0.95	1.58e-23	HDHD2	haloacid dehalogenase like hydrolas	0.81	2.95e-16	LMF2	lipase maturation factor 2
-0.94	4.28e-29	ADI1	acireductone dioxygenase 1	0.81	8.87e-15	IKBIP	IKBKB interacting protein
-0.94	4.14e-25	HDDC2	HD domain containing 2	0.8	2.49e-20	MYO1C	myosin IC

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



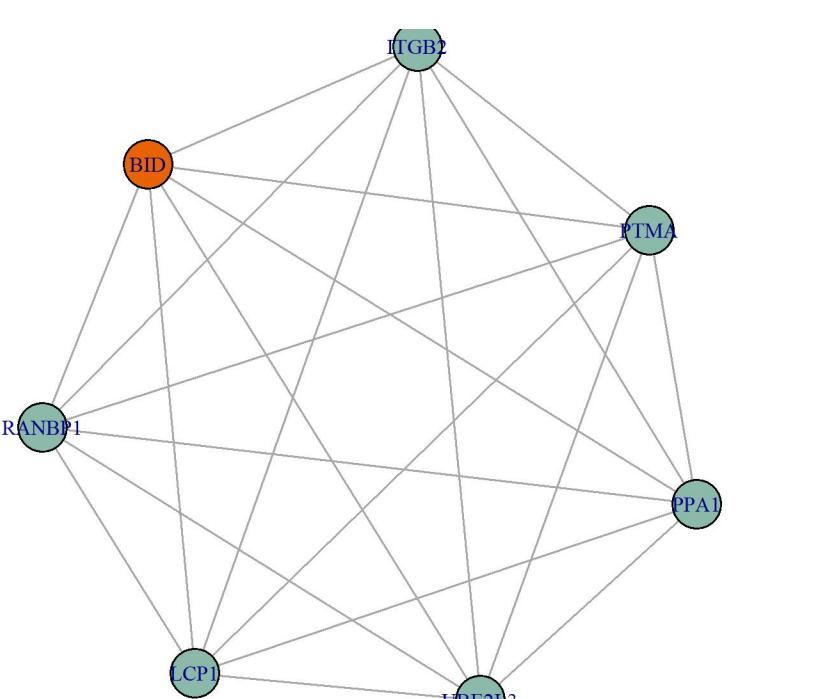


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.49	2.39e-04	ITGB2	integrin subunit beta 2	1.24	1.42e-03	TUBB3	tubulin beta 3 class III
-1.48	6.65e-03	CAPG	capping actin protein, gelsolin lik	1.16	2.61e-03	IRF4	interferon regulatory factor 4
-1.39	2.35e-03	CD44	CD44 molecule (Indian blood group)	1.05	7.07e-03	FKBP11	FKBP prolyl isomerase 11
-1.25	1.15e-04	LCP2	lymphocyte cytosolic protein 2	1.04	2.41e-02	NDUFB11	NADH:ubiquinone oxidoreductase subu
-1.22	2.84e-03	ACTN1	actinin alpha 1	1.03	8.21e-04	MPZL1	myelin protein zero like 1
-1.2	9.33e-03	PTPN6	protein tyrosine phosphatase non-re	1.01	1.42e-03	TMUB1	transmembrane and ubiquitin like do
-1.15	7.70e-02	SPN	sialophorin	0.98	7.70e-03	IKZF3	IKAROS family zinc finger 3
-1.1	1.23e-02	ANXA1	annexin A1	0.98	2.95e-02	JCHAIN	joining chain of multimeric IgA and
-1.08	2.86e-03	BIN2	bridging integrator 2	0.96	2.70e-03	UBE2J1	ubiquitin conjugating enzyme E2 J1
-1.02	9.33e-03	NAPRT	nicotinate phosphoribosyltransferas	0.96	8.21e-04	PPP2R5C	protein phosphatase 2 regulatory su
-1.02	1.77e-03	LGALS9	galectin 9	0.93	3.32e-02	TCL1A	TCL1 family AKT coactivator A
-0.98	2.00e-04	APOBR	apolipoprotein B receptor	0.92	1.27e-02	MME	membrane metalloendopeptidase
-0.96	1.42e-01	S100A4	S100 calcium binding protein A4	0.91	2.86e-03	GTPBP3	GTP binding protein 3, mitochondria
-0.94	2.61e-02	BLVRA	biliverdin reductase A	0.89	2.87e-02	IGHM	immunoglobulin heavy constant mu
-0.94	8.15e-03	LYSMD2	LysM domain containing 2	0.86	9.00e-03	PFKM	phosphofructokinase, muscle
-0.93	2.86e-03	PARVG	parvin gamma	0.85	1.42e-03	BAZ2A	bromodomain adjacent to zinc finger
-0.91	5.48e-02	ITGB5	integrin subunit beta 5	0.85	1.85e-02	CD79B	CD79b molecule
-0.91	9.45e-03	FADS2	fatty acid desaturase 2	0.85	6.65e-03	PAWR	pro-apoptotic WT1 regulator
-0.87	2.86e-03	SYTL1	synaptotagmin like 1	0.83	3.17e-02	ISG20	interferon stimulated exonuclease g
-0.87	1.65e-02	ITGA5	integrin subunit alpha 5	0.82	3.96e-03	CEP97	centrosomal protein 97
-0.86	4.01e-02	FSCN1	fascin actin-bundling protein 1	0.81	4.01e-02	HLA-DQB1	major histocompatibility complex, c
-0.86	2.10e-02	MPP1	MAGUK p55 scaffold protein 1	0.8	8.21e-04	LIN7C	lin-7 homolog C, crumbs cell polari
-0.85	8.15e-03	ARRB1	arrestin beta 1	0.8	2.14e-02	LDAH	lipid droplet associated hydrolase
-0.85	7.07e-03	MYO1F	myosin IF	0.79	4.01e-02	APOE	apolipoprotein E
-0.85	4.01e-02	ITGAL	integrin subunit alpha L	0.78	4.01e-02	CAMK2D	calcium/calmodulin dependent protei
-0.84	1.31e-02	LYZ	lysozyme	0.78	9.00e-03	BPGM	bisphosphoglycerate mutase
-0.82	1.17e-03	RREB1	ras responsive element binding prot	0.77	4.01e-02	HLA-DPA1	major histocompatibility complex, c
-0.82	2.86e-03	FNBP1	formin binding protein 1	0.76	6.84e-03	ST14	ST14 transmembrane serine protease
-0.82	2.55e-02	MYO1G	myosin IG	0.75	9.33e-03	KNOP1	lysine rich nucleolar protein 1

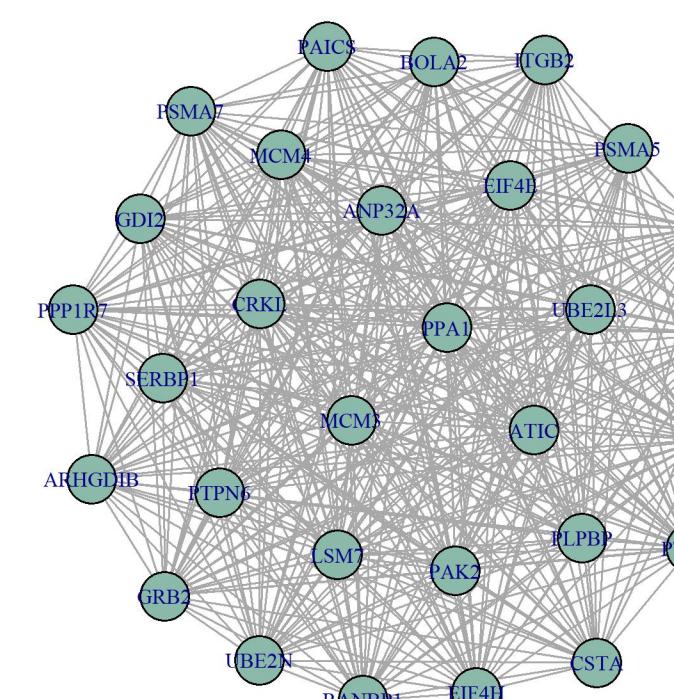


Downregulated in solid cancers at low/absent BID				Upregulated in solid cancers at low/absent BID			
adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name	
2.67e-18	ABRACL	ABRA C-terminal like	0.78	2.19e-08	AP2S1	adaptor related protein complex 2 s	
1.06e-18	CLNS1A	chloride nucleotide-sensitive chann	0.72	7.90e-14	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b	
2.54e-21	PPM1B	protein phosphatase, Mg2+/Mn2+ depe	0.68	7.37e-08	UQCR10	ubiquinol-cytochrome c reductase, c	
9.65e-17	FKBP1A	FKBP prolyl isomerase 1A	0.66	1.11e-07	MMP14	matrix metallopeptidase 14	
1.16e-15	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.64	1.60e-08	PIGT	phosphatidylinositol glycan anchor	
7.93e-17	DERPC	DERPC proline and glycine rich nucl	0.62	7.44e-09	IKBIP	IKBKB interacting protein	
1.85e-18	CZIB	CXXC motif containing zinc binding	0.61	1.77e-10	MOSPD2	motile sperm domain containing 2	
4.84e-13	NACA2	nascent polypeptide associated comp	0.61	3.67e-09	ERGIC2	ERGIC and golgi 2	
3.40e-19	PPP1R14B	protein phosphatase 1 regulatory in	0.61	6.14e-10	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b	
1.91e-18	CCDC43	coiled-coil domain containing 43	0.61	1.56e-07	GPX8	glutathione peroxidase 8 (putative)	
4.18e-19	DCK	deoxycytidine kinase	0.6	3.11e-09	FNDC3B	fibronectin type III domain contain	
1.12e-15	ZNRD2	zinc ribbon domain containing 2	0.59	2.88e-07	UXS1	UDP-glucuronate decarboxylase 1	
1.08e-19	PHPT1	phosphohistidine phosphatase 1	0.59	8.70e-07	ITGA5	integrin subunit alpha 5	
1.81e-17	STK39	serine/threonine kinase 39	0.59	5.91e-05	CAVIN1	caveolae associated protein 1	
8.73e-17	FN3KRP	fructosamine 3 kinase related prote	0.59	2.91e-07	CD109	CD109 molecule	
1.67e-18	EIPR1	EARP complex and GARP complex inter	0.58	1.17e-09	SLC12A4	solute carrier family 12 member 4	
4.00e-15	UBR7	ubiquitin protein ligase E3 compone	0.58	3.98e-06	AXL	AXL receptor tyrosine kinase	
1.50e-15	MIEN1	migration and invasion enhancer 1	0.58	1.82e-07	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer	
3.14e-14	PSME3IP1	proteasome activator subunit 3 inte	0.58	7.06e-07	RAB32	RAB32, member RAS oncogene family	
1.96e-18	ADI1	acireductone dioxygenase 1	0.57	6.58e-07	MFGE8	milk fat globule EGF and factor V/V	
3.44e-16	PMM2	phosphomannomutase 2	0.57	1.90e-09	LMAN2L	lectin, mannose binding 2 like	
1.26e-15	PITHD1	PITH domain containing 1	0.56	2.18e-08	BAK1	BCL2 antagonist/killer 1	
6.63e-17	TAB1	TGF-beta activated kinase 1 (MAP3K7	0.56	1.02e-08	KIAA2013	KIAA2013	
1.10e-14	RPE	ribulose-5-phosphate-3-epimerase	0.56	7.59e-07	FUT8	fucosyltransferase 8	
4.26e-15	SORD	sorbitol dehydrogenase	0.55	2.53e-08	TIMM29	translocase of inner mitochondrial	
2.92e-15	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.55	2.50e-08	ATP6AP2	ATPase H+ transporting accessory pr	
3.35e-17	AVL9	AVL9 cell migration associated	0.55	7.22e-07	COL12A1	collagen type XII alpha 1 chain	
3.56e-16	TKFC	trioleinase and FMN cyclase	0.55	5.51e-08	PTDSS2	phosphatidylserine synthase 2	
3.10e-16	PCYT2	phosphate cytidylyltransferase 2, e	0.55	7.86e-07	TOR1B	torsin family 1 member B	

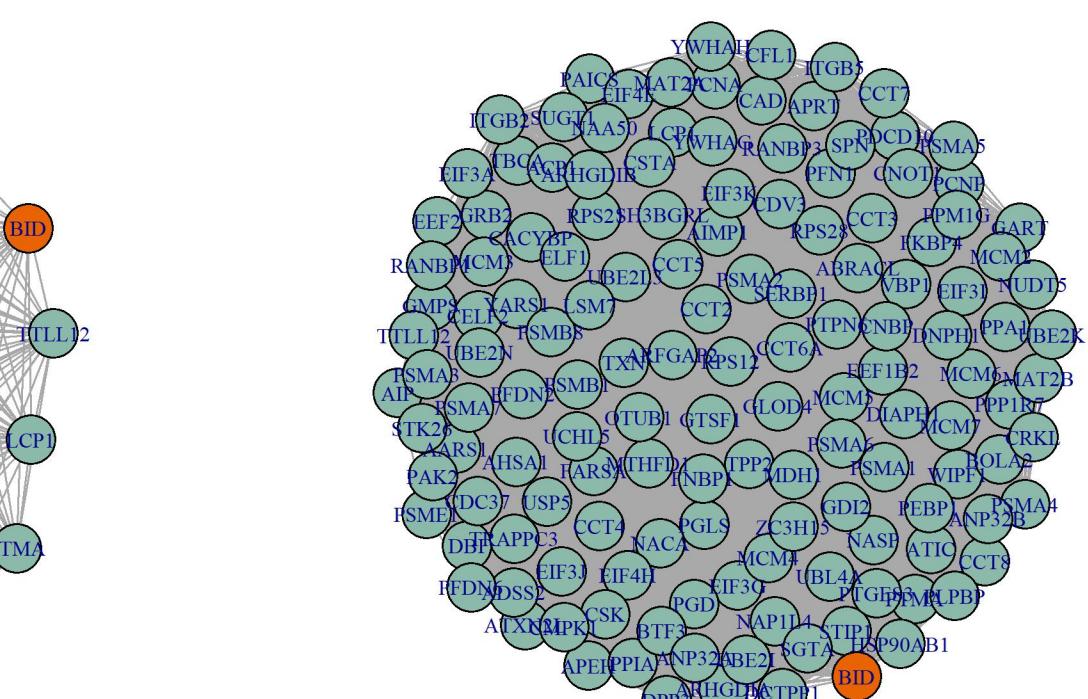
### BID network, DB1, all Pearson $r > 0.5$



BID network, DB1, all Pearson r > 0.4

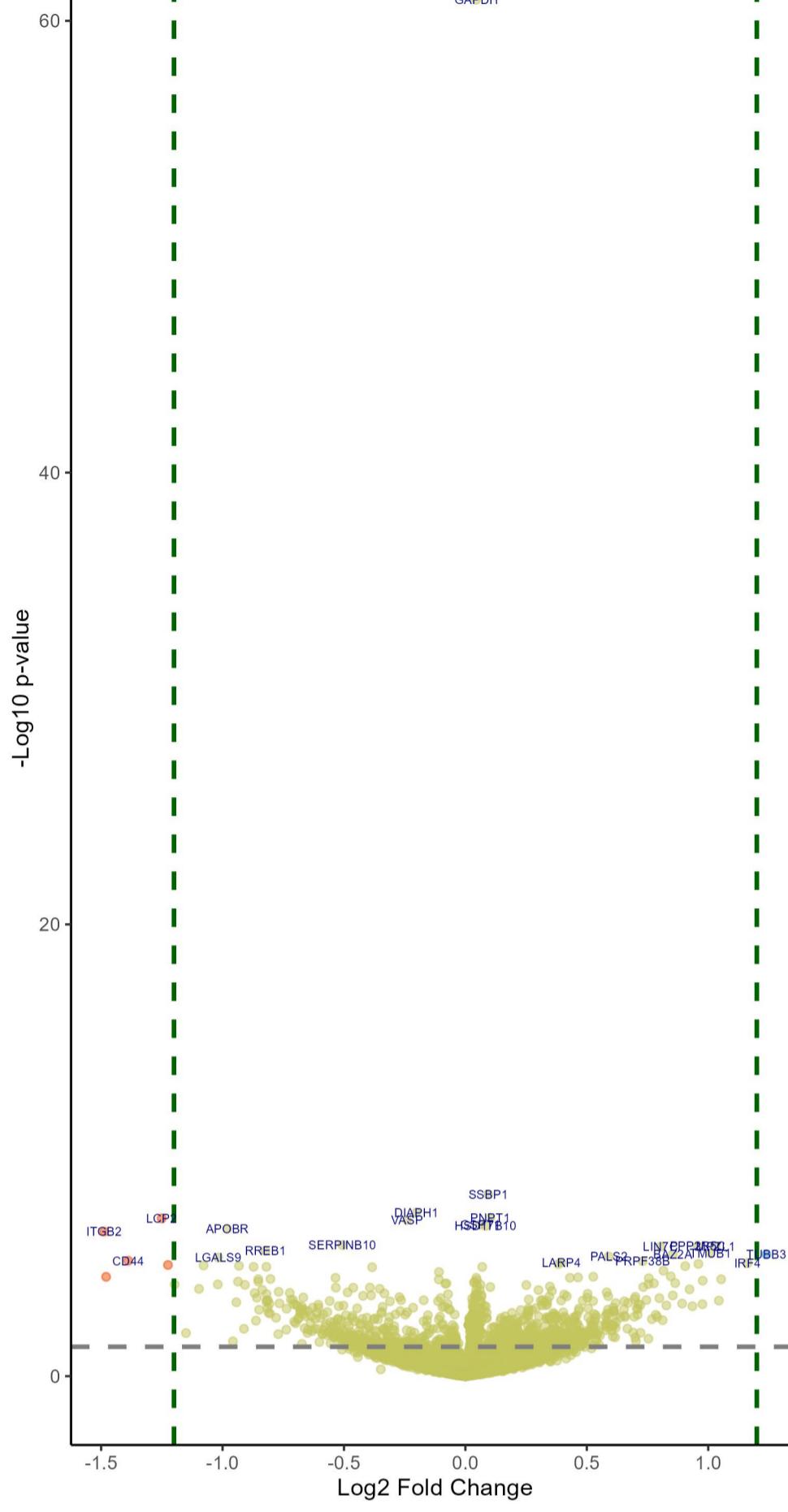


BID network, DB1, all Pearson r > 0.4



Sorted by p values!

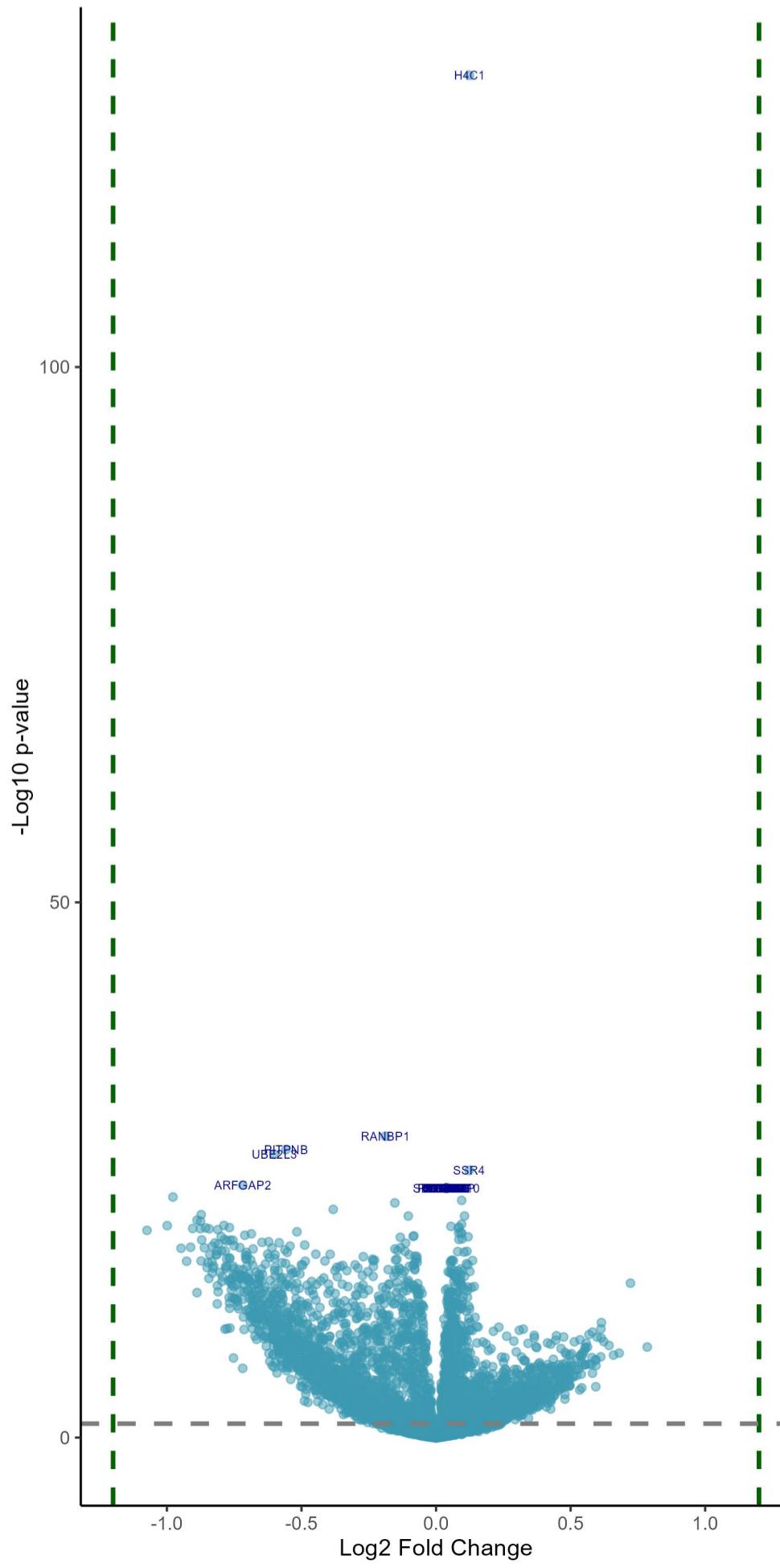
Downregulated in blood cancers at low/absent BID Upregulated in blood cancers at low/absent BID



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.2	9.62e-05	DIAPH1	diaphanous related formin 1	0.04	7.72e-58	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-1.25	1.15e-04	LCP2	lymphocyte cytosolic protein 2	0.09	1.97e-05	SSBP1	single stranded DNA binding protein
-0.24	1.16e-04	VASP	vasodilator stimulated phosphoprotein	0.1	1.15e-04	PNPT1	polyribonucleotide nucleotidyltransferase
-0.98	2.00e-04	APOBR	apolipoprotein B receptor	0.06	1.62e-04	GSPT1	G1 to S phase transition 1
-1.49	2.39e-04	ITGB2	integrin subunit beta 2	0.08	1.64e-04	HSD17B10	hydroxysteroid 17-beta dehydrogenase
-0.51	8.21e-04	SERPINB10	serpin family B member 10	0.96	8.21e-04	PPP2R5C	protein phosphatase 2 regulatory subunit 5C
-0.82	1.17e-03	RREB1	ras responsive element binding protein 1	1.03	8.21e-04	MPZL1	myelin protein zero like 1
-1.02	1.77e-03	LGALS9	galectin 9	0.8	8.21e-04	LIN7C	lin-7 homolog C, crumbs cell polarity gene
-1.39	2.35e-03	CD44	CD44 molecule (Indian blood group)	1.01	1.42e-03	TMUB1	transmembrane and ubiquitin like domain containing 1
-1.22	2.84e-03	ACTN1	actinin alpha 1	0.85	1.42e-03	BAZ2A	bromodomain adjacent to zinc finger 2A
-1.08	2.86e-03	BIN2	bridging integrator 2	1.24	1.42e-03	TUBB3	tubulin beta 3 class III
-0.93	2.86e-03	PARVG	parvin gamma	0.59	1.67e-03	PALS2	protein associated with LIN7 2, MAG
-0.87	2.86e-03	SYTL1	synaptotagmin like 1	0.73	2.35e-03	PRPF38B	pre-mRNA processing factor 38B
-0.82	2.86e-03	FNBP1	formin binding protein 1	0.39	2.59e-03	LARP4	La ribonucleoprotein 4
-0.38	2.86e-03	PFKL	phosphofructokinase, liver type	1.16	2.61e-03	IRF4	interferon regulatory factor 4
-0.11	4.43e-03	PLPBP	pyridoxal phosphate binding protein	0.96	2.70e-03	UBE2J1	ubiquitin conjugating enzyme E2 J1
-1.48	6.65e-03	CAPG	capping actin protein, gelsolin like	0.38	2.70e-03	CELF1	CUGBP Elav-like family member 1
-0.53	6.71e-03	S100P	S100 calcium binding protein P	0.91	2.86e-03	GTPBP3	GTP binding protein 3, mitochondria
-0.8	7.07e-03	CMPK2	cytidine/uridine monophosphate kinase	0.07	2.86e-03	VDAC1	voltage dependent anion channel 1
-0.85	7.07e-03	MYO1F	myosin IF	0.82	3.96e-03	CEP97	centrosomal protein 97
-0.11	7.07e-03	SNX3	sorting nexin 3	0.85	6.65e-03	PAWR	pro-apoptotic WT1 regulator
-0.85	8.15e-03	ARRB1	arrestin beta 1	0.53	6.65e-03	RBM6	RNA binding motif protein 6
-0.94	8.15e-03	LYSMD2	LysM domain containing 2	0.46	6.71e-03	C11orf98	chromosome 11 open reading frame 98
-0.08	9.00e-03	DPP3	dipeptidyl peptidase 3	0.43	6.71e-03	ARL3	ADP ribosylation factor like GTPase
-0.08	9.07e-03	COX7C	cytochrome c oxidase subunit 7C	0.04	6.71e-03	EPRS1	glutamyl-prolyl-tRNA synthetase 1
-1.02	9.33e-03	NAPRT	nicotinate phosphoribosyltransferase	0.76	6.84e-03	ST14	ST14 transmembrane serine protease
-1.2	9.33e-03	PTPN6	protein tyrosine phosphatase non-receptor type 6	1.05	7.07e-03	FKBP11	FKBP prolyl isomerase 11
-0.91	9.45e-03	FADS2	fatty acid desaturase 2	0.05	7.55e-03	MDH2	malate dehydrogenase 2
-0.53	1.12e-02	IGFBP2	insulin like growth factor binding protein 2	0.98	7.70e-03	IKZF3	IKAROS family zinc finger 3
-0.39	1.12e-02	GRK6	G protein-coupled receptor kinase 6	0.04	8.32e-03	EIF2S1	eukaryotic translation initiation factor 2S1
-0.46	1.12e-02	CEBPA	CCAAT enhancer binding protein alpha	0.03	8.68e-03	RPSA	ribosomal protein SA
-0.35	1.23e-02	TMSB4X	thymosin beta 4 X-linked	0.86	9.00e-03	PFKM	phosphofructokinase, muscle
-1.1	1.23e-02	ANXA1	annexin A1	0.78	9.00e-03	BPGM	bisphosphoglycerate mutase
-0.84	1.31e-02	LYZ	lysozyme	0.75	9.33e-03	KNOP1	lysine rich nucleolar protein 1
-0.77	1.51e-02	GNAQ	G protein subunit alpha q	0.06	9.42e-03	SHMT2	serine hydroxymethyltransferase 2
-0.49	1.57e-02	DEF6	DEF6 guanine nucleotide exchange factor	0.25	9.50e-03	FAM98A	family with sequence similarity 98
-0.72	1.64e-02	NUDT4	nudix hydrolase 4	0.05	1.01e-02	TUFM	Tu translation elongation factor, m
-0.87	1.65e-02	ITGA5	integrin subunit alpha 5	0.35	1.07e-02	CAV1	caveolin 1
0.33	1.67e-02	DNPDCD	granular amine oxidase	0.73	1.09e-02	PPBP30	ribonuclease D/MRP subunit p30

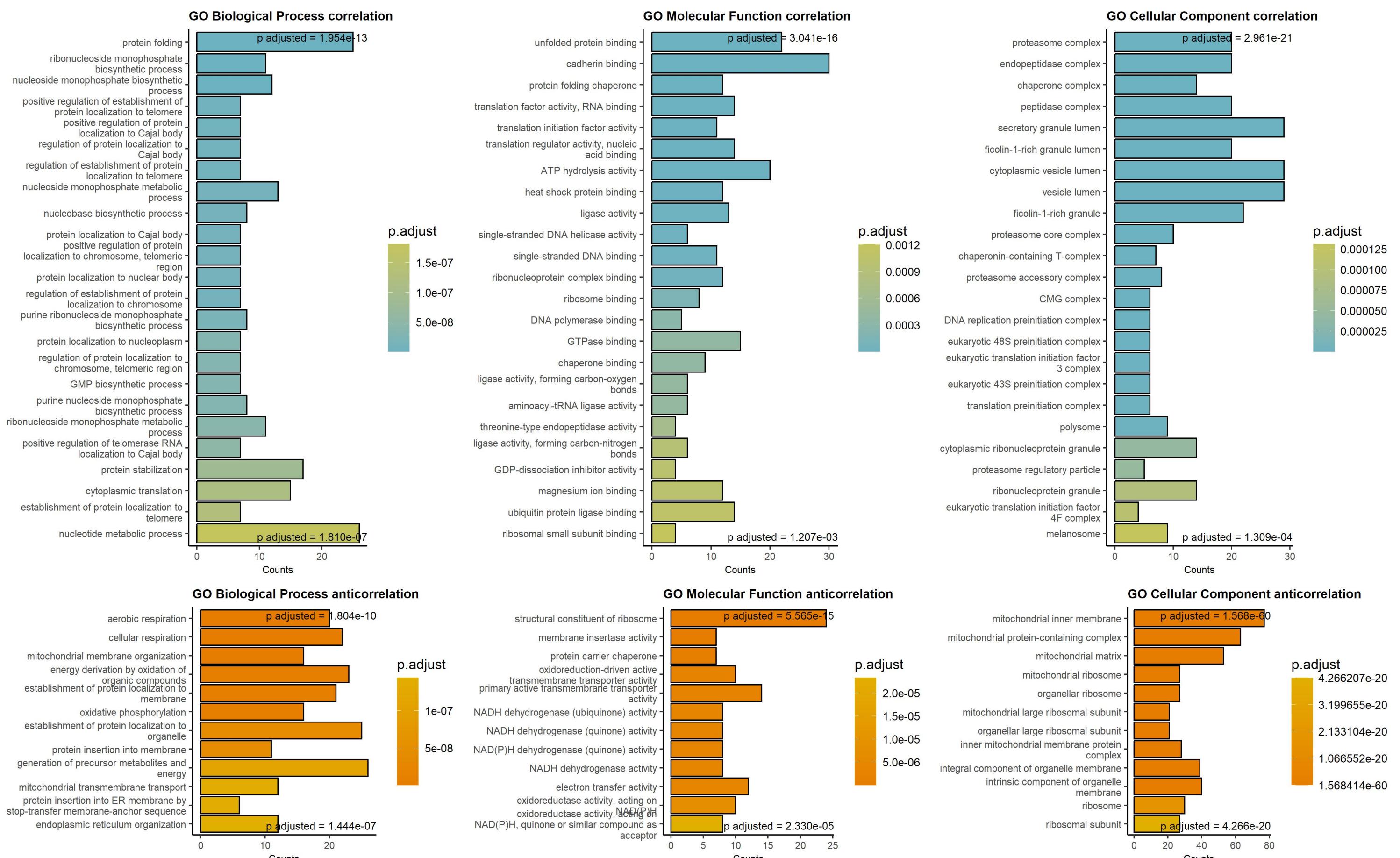
Sorted by p values!

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

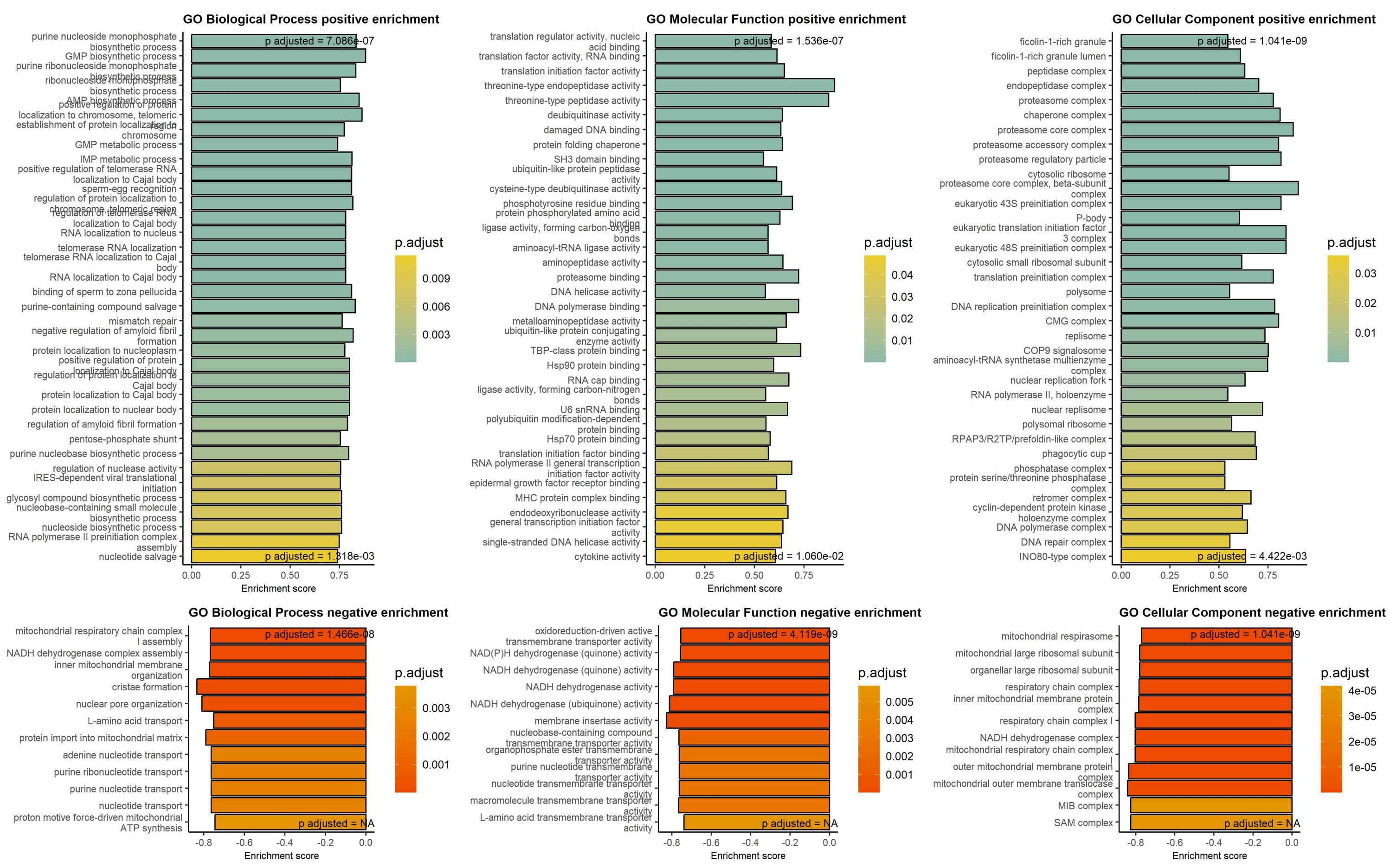


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.19	1.57e-25	RANBP1	RAN binding protein 1	0.12	3.74e-124	H4C1	H4 clustered histone 1
-0.56	2.08e-24	PITPNB	phosphatidylinositol transfer protein	0.12	1.19e-22	SSR4	signal sequence receptor subunit 4
-0.6	4.55e-24	UBE2L3	ubiquitin conjugating enzyme E2 L3	0.04	3.74e-22	PTPRCAP	protein tyrosine phosphatase receptor type C
-0.72	3.74e-22	ARFGAP2	ADP ribosylation factor GTPase activating factor 2	0.04	3.74e-22	HBE1	hemoglobin subunit epsilon 1
-0.98	2.54e-21	PPM1B	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> dependent	0.04	3.74e-22	SERPINB10	serpin family B member 10
-0.15	8.85e-21	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide	0.04	3.74e-22	IGLL1	immunoglobulin lambda like polypeptide 1
-0.38	3.52e-20	CRKL	CRK like proto-oncogene, adaptor protein	0.04	3.74e-22	CRYBB1	crystallin beta B1
-0.87	1.08e-19	PHPT1	phosphohistidine phosphatase 1	0.04	3.74e-22	ITGA2B	integrin subunit alpha 2b
-0.1	1.42e-19	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-hydroxylase	0.04	3.74e-22	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains
-0.89	3.40e-19	PPP1R14B	protein phosphatase 1 regulatory subunit 14B	0.04	3.74e-22	NCF4	neutrophil cytosolic factor 4
-0.88	4.18e-19	DCK	deoxyribonucleoside kinase	0.04	3.74e-22	SP140	SP140 nuclear body protein
-0.79	1.03e-18	DCUN1D1	defective in cullin neddylation 1 domain	0.04	3.74e-22	PSTPIP1	proline-serine-threonine phosphatases with an invariant threonine
-1	1.06e-18	CLNS1A	chloride nucleotide-sensitive channel	0.04	3.74e-22	STAB1	stabilin 1
-0.77	1.58e-18	NUBP2	NUBP iron-sulfur cluster assembly factor	0.04	3.74e-22	SEPL1G	selectin P ligand
-0.86	1.67e-18	EIPR1	EARP complex and GARP complex interacting protein	0.04	3.74e-22	RCSD1	RCSD domain containing 1
-0.9	1.85e-18	CZIB	CXXC motif containing zinc binding protein	0.04	3.74e-22	STAT5A	signal transducer and activator of transcription 5A
-0.88	1.91e-18	CCDC43	coiled-coil domain containing 43	0.04	3.74e-22	CTSW	cathepsin W
-0.84	1.96e-18	ADI1	acireductone dioxygenase 1	0.04	3.74e-22	GIMAP6	GTPase, IMAP family member 6
-0.81	2.31e-18	CASP3	caspase 3	0.04	3.74e-22	GZMB	granzyme B
-1.07	2.67e-18	ABRACL	ABRA C-terminal like	0.04	3.74e-22	HK3	hexokinase 3
-0.52	3.62e-18	PPP1R7	protein phosphatase 1 regulatory subunit 7	0.04	3.74e-22	TUBA8	tubulin alpha 8
-0.69	5.41e-18	ILKAP	ILK associated serine/threonine kinase	0.04	3.74e-22	CR2	complement C3d receptor 2
-0.71	7.30e-18	THUMPD1	THUMP domain containing 1	0.04	3.74e-22	POU2F2	POU class 2 homeobox 2
-0.08	8.17e-18	PSMA5	proteasome 20S subunit alpha 5	0.04	3.74e-22	AZU1	azurocidin 1
-0.09	9.12e-18	STIP1	stress induced phosphoprotein 1	0.04	3.74e-22	CD48	CD48 molecule
-0.8	9.32e-18	DOHH	deoxyhypusine hydroxylyase	0.04	3.74e-22	SKAP2	src kinase associated phosphoprotein
-0.13	1.08e-17	TXN	thioredoxin	0.04	3.74e-22	CCL17	C-C motif chemokine ligand 17
-0.79	1.68e-17	POLD3	DNA polymerase delta 3, accessory subunit	0.04	3.74e-22	ADA2	adenosine deaminase 2
-0.87	1.81e-17	STK39	serine/threonine kinase 39	0.04	3.74e-22	CD3E</td	

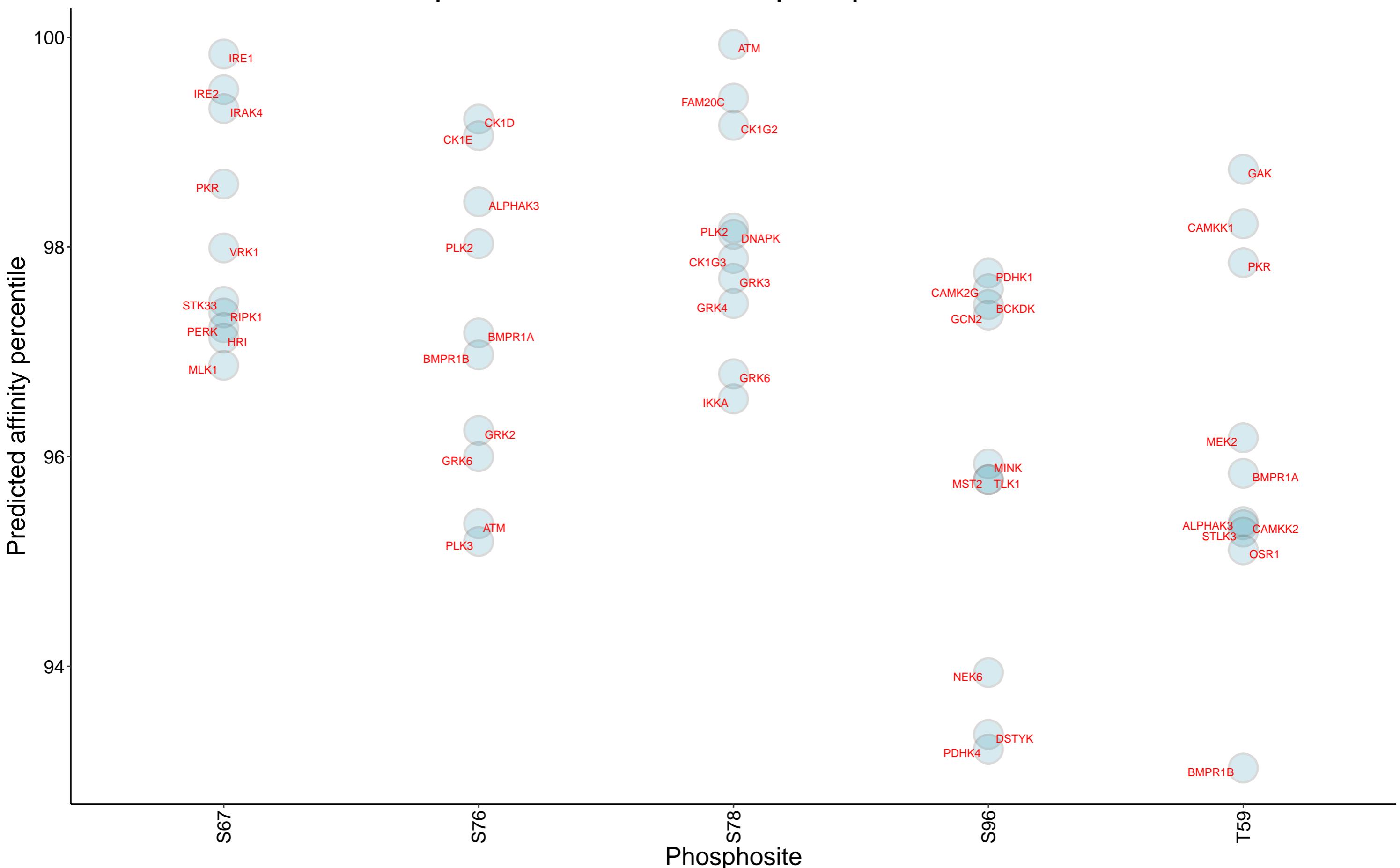
# Top 250 correlation coefficients overrepresentation, BID protein, DB1



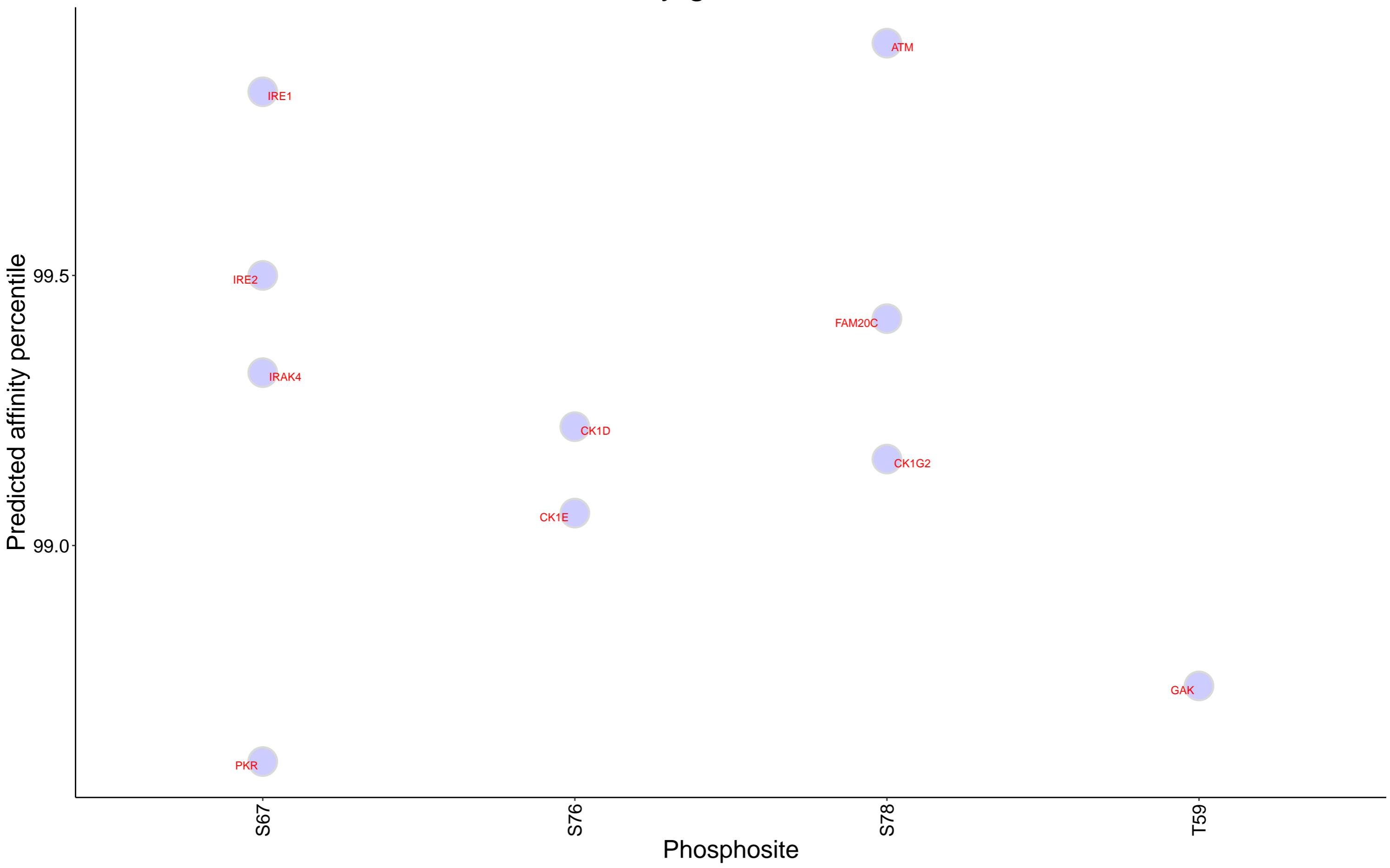
## Gene Set Enrichment analysis on protein correlation coefficients, BID protein, DB1



# Top 10 kinases for each phosphosite in BID



Kinases with affinity greater than 98.5% to BID



# Top 15 positive correlation coefficients for BID protein by tissue, DB1

Beware of false positives in tissues with small number of samples

