

# CASP2

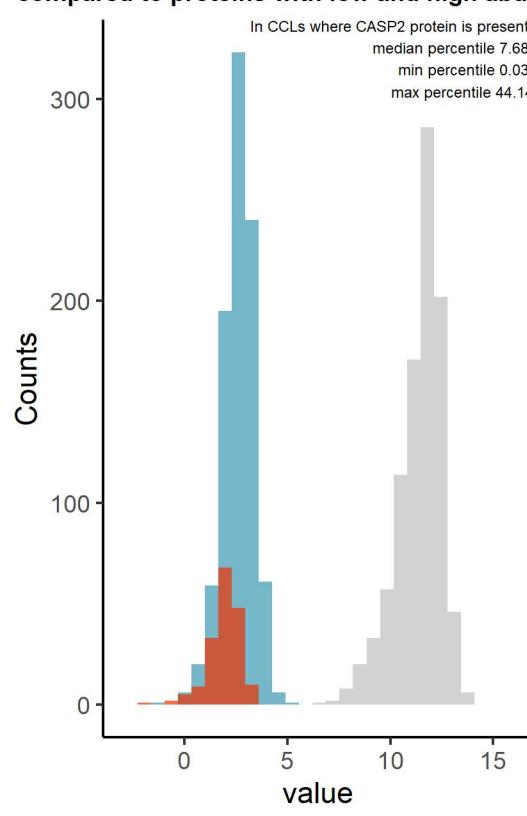
Protein name: CASP2 ; UNIPROT: P42575 ; Gene name: caspase 2

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

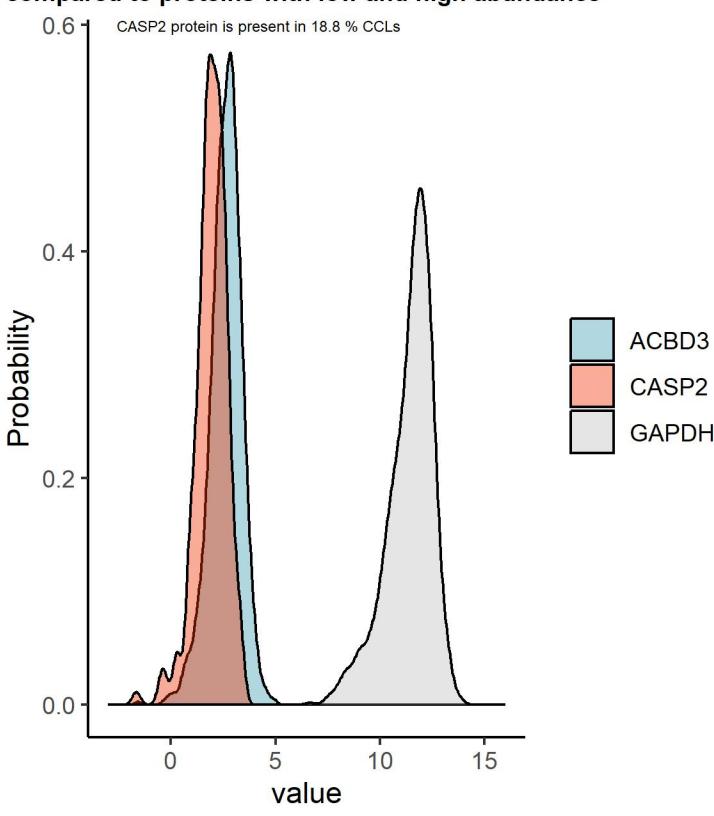
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

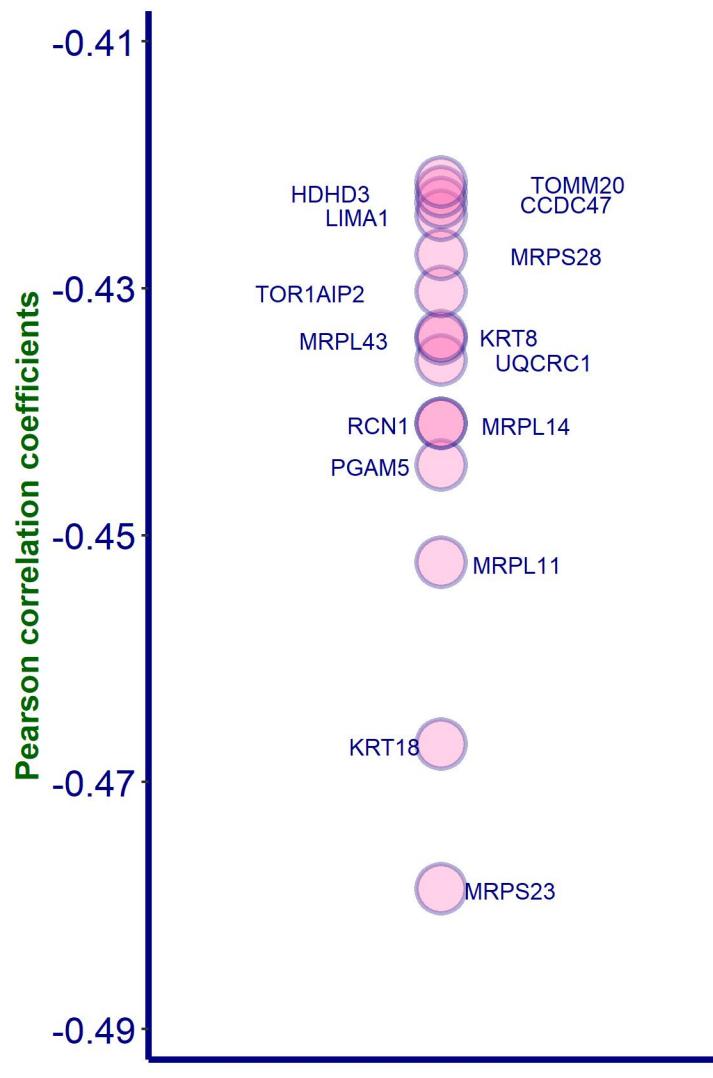
Histogram of CASP2 protein compared to proteins with low and high abundance



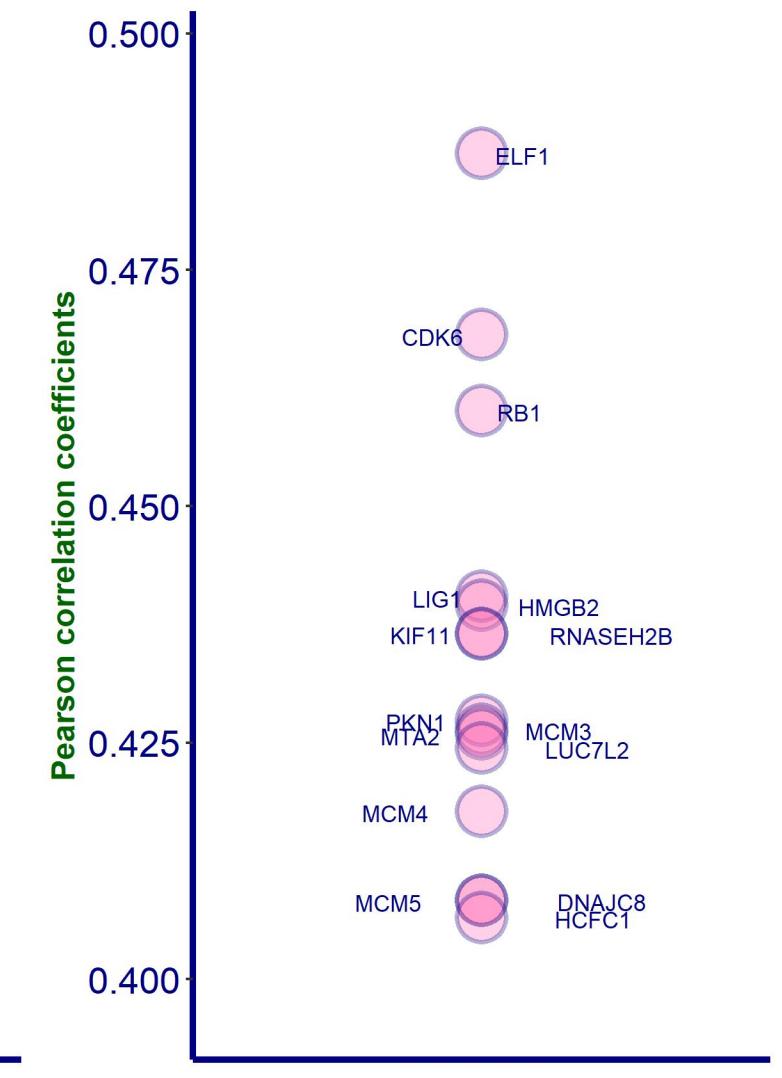
Density plot of CASP2 protein compared to proteins with low and high abundance



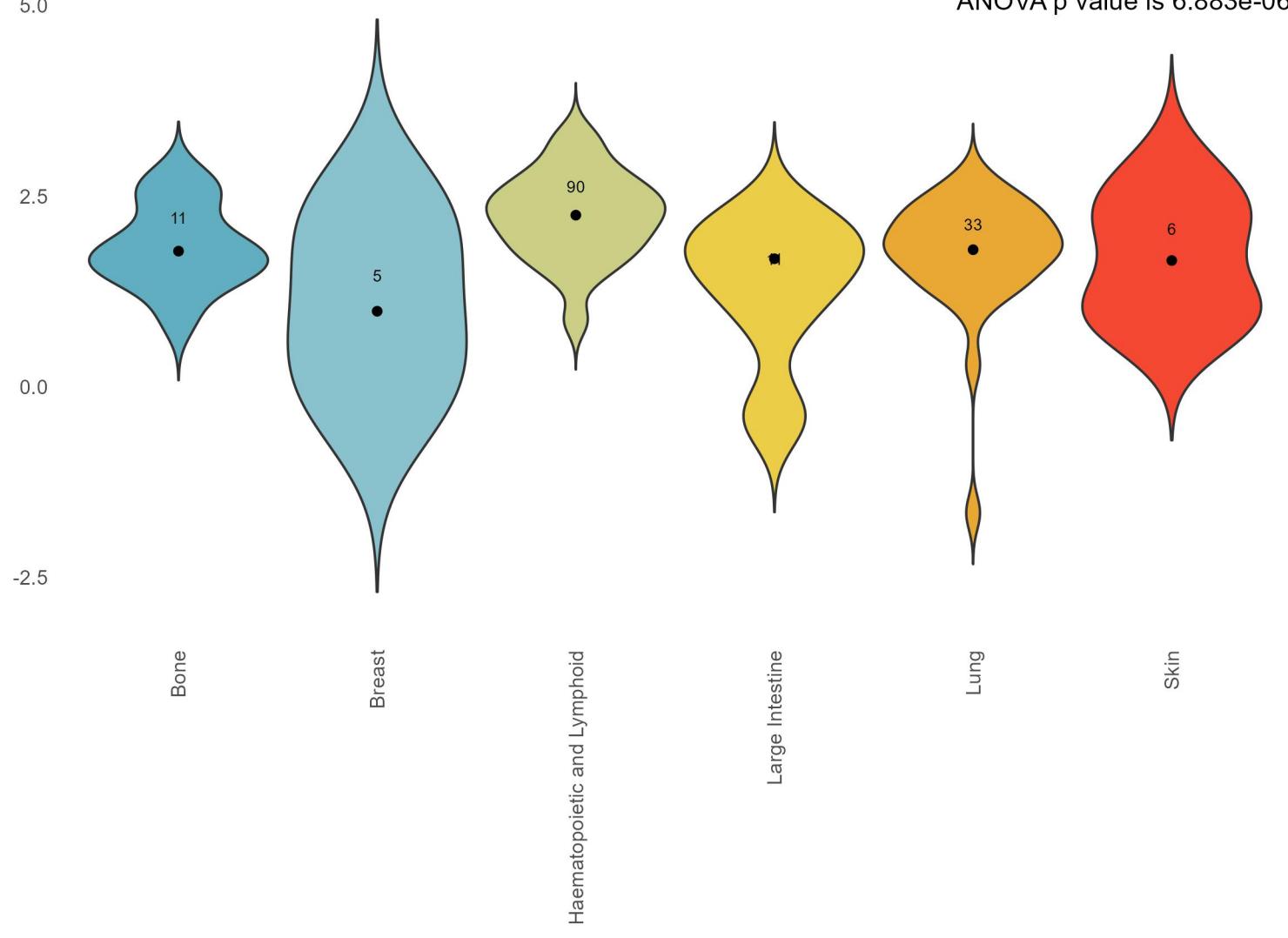
Top negative correlations of CASP2 protein, DB1



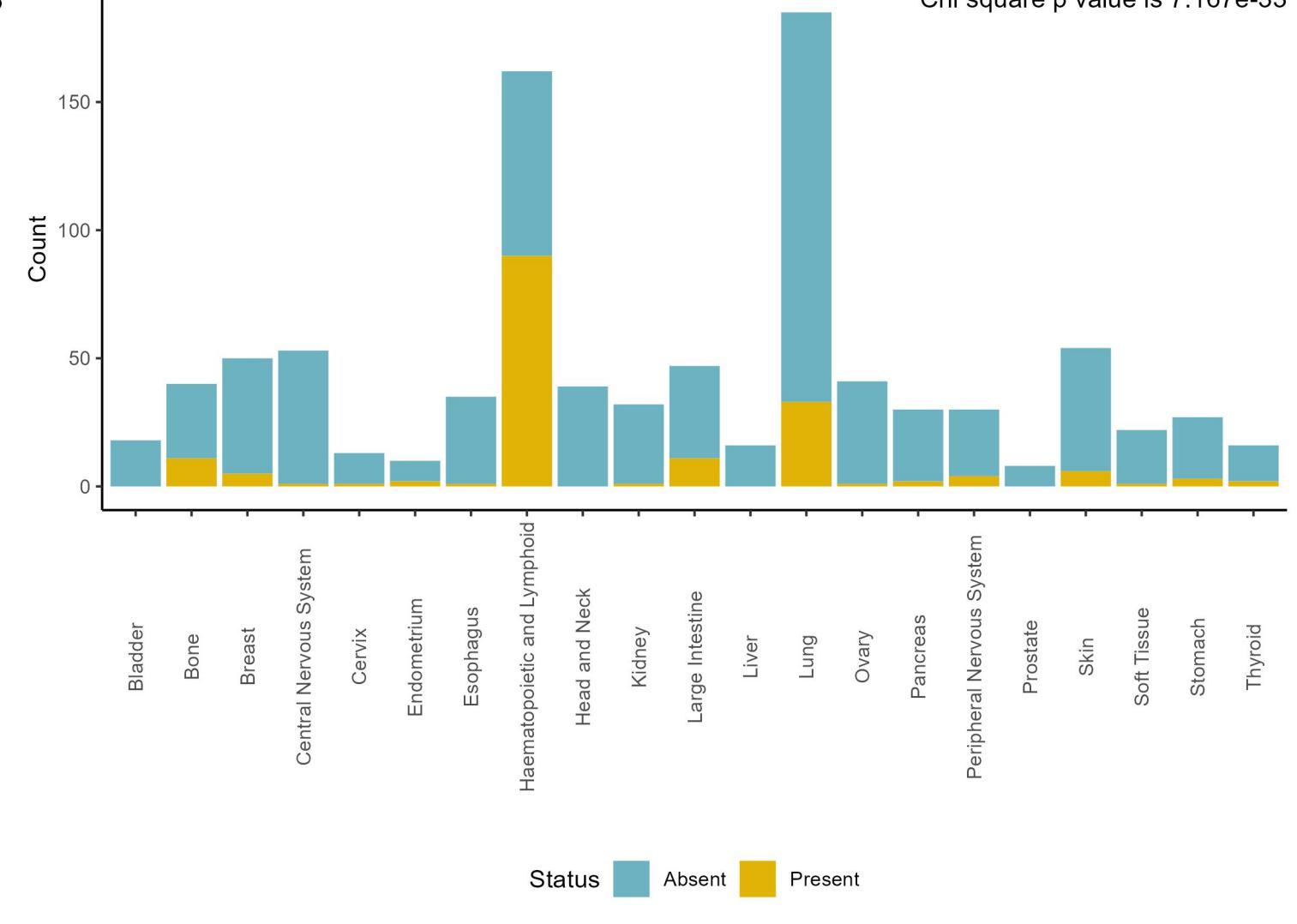
Top positive correlations of CASP2 protein, DB1



Amount of CASP2 protein, number of CCLs where it is present by tissue, DB1



Present and absent CASP2 protein counts by tissue, DB1

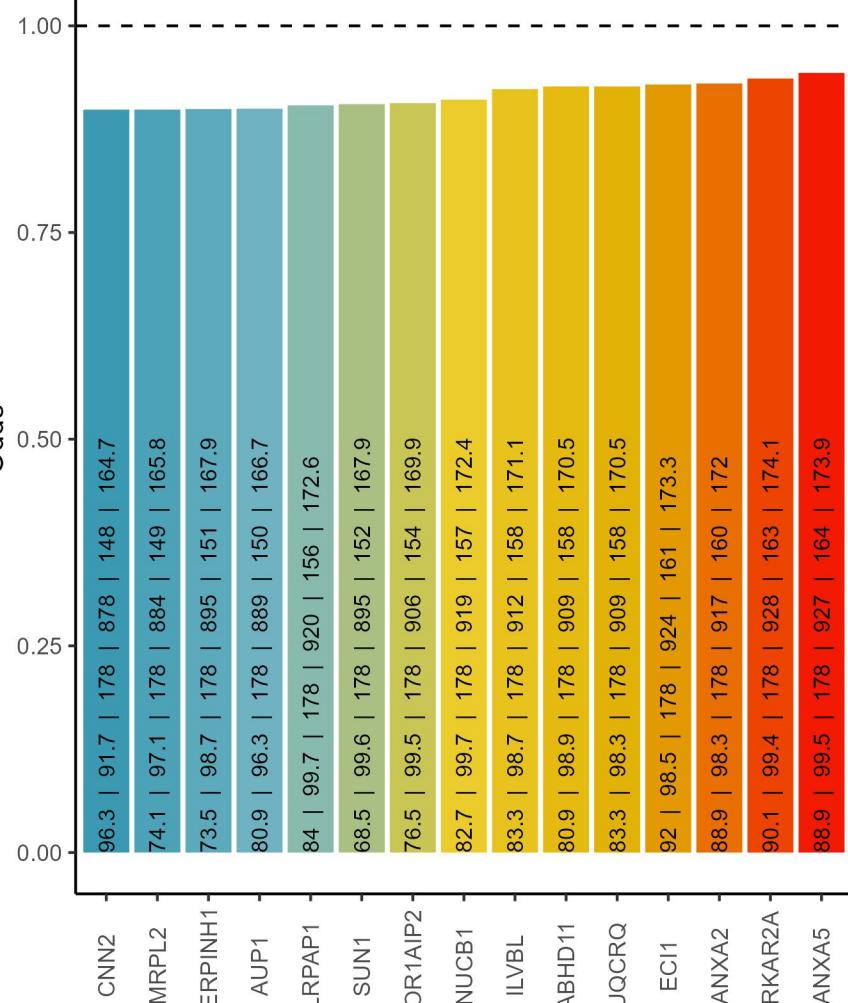


## Cooccurrence with CASP2 protein, DB1

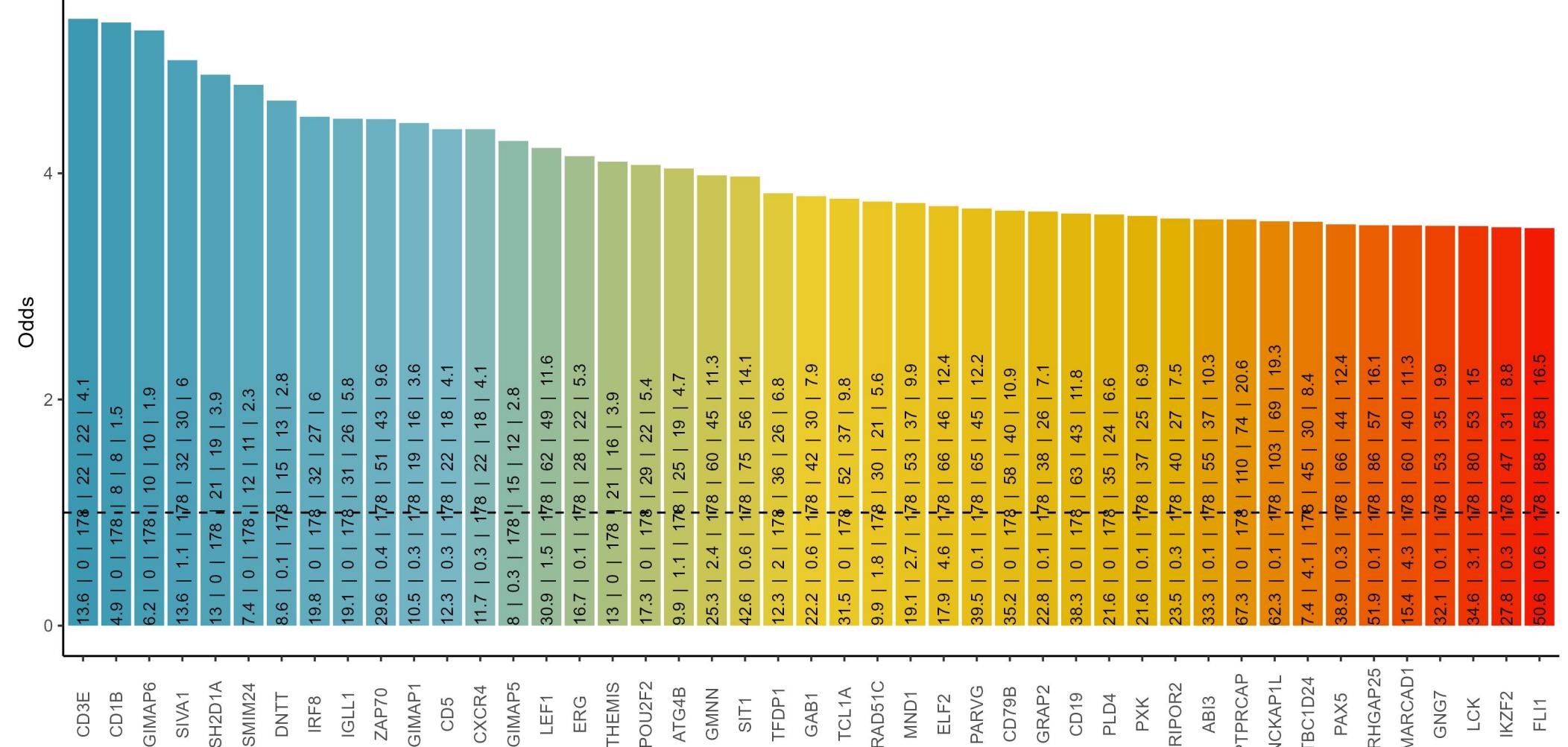
% of CASP2 in blood cancers: 55.6 ; % of CASP2 in solid cancers: 11

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CASP2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

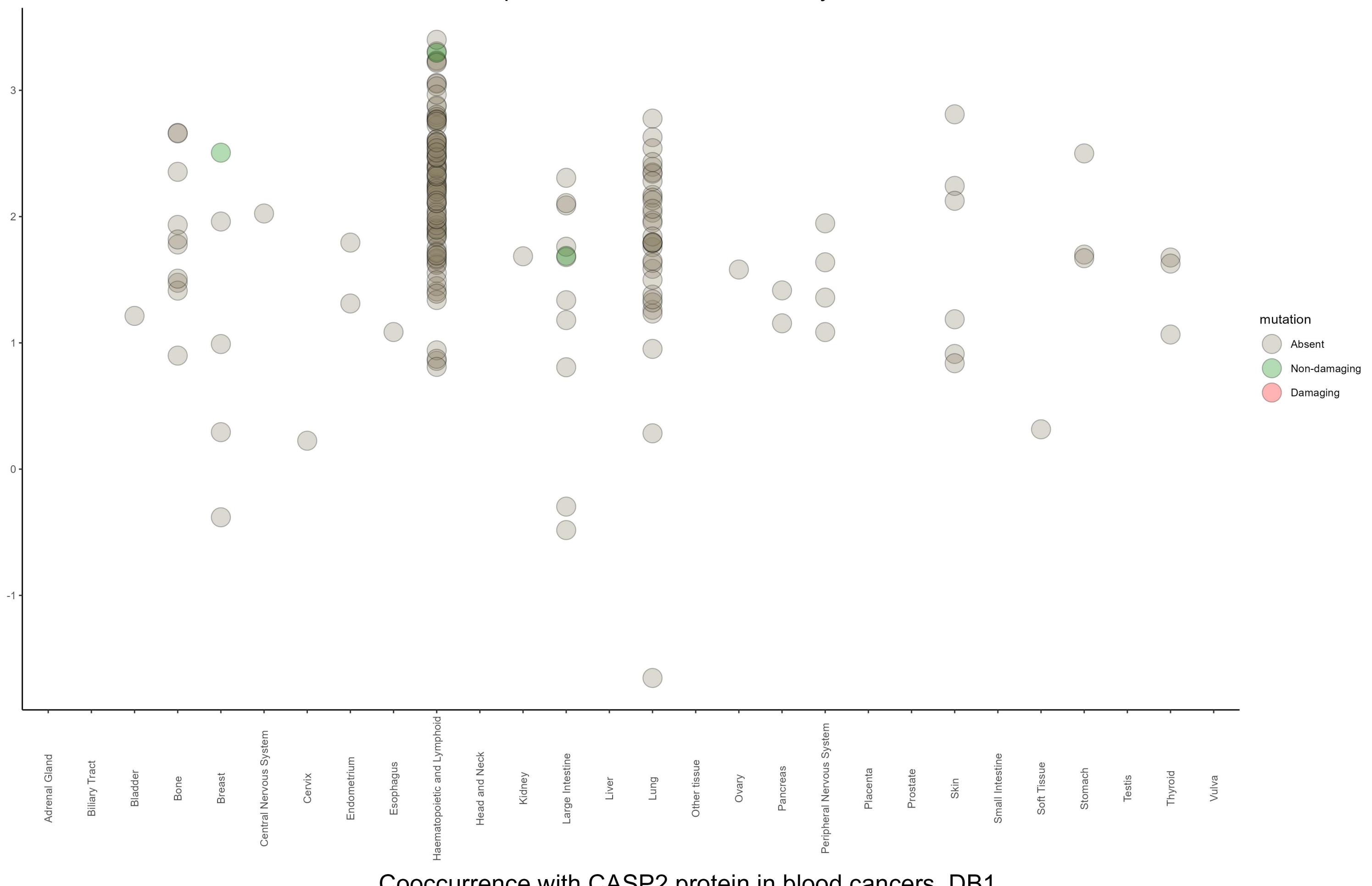
### Negative cooccurrence



### Positive cooccurrence

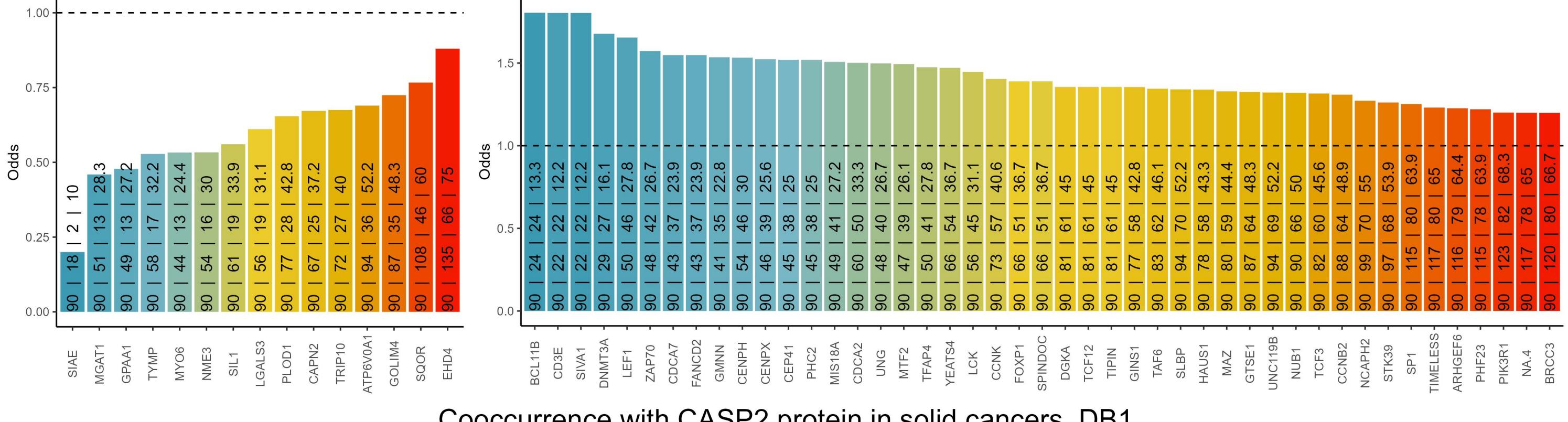


# Amount of CASP2 protein and mutation status by tissue, DB1



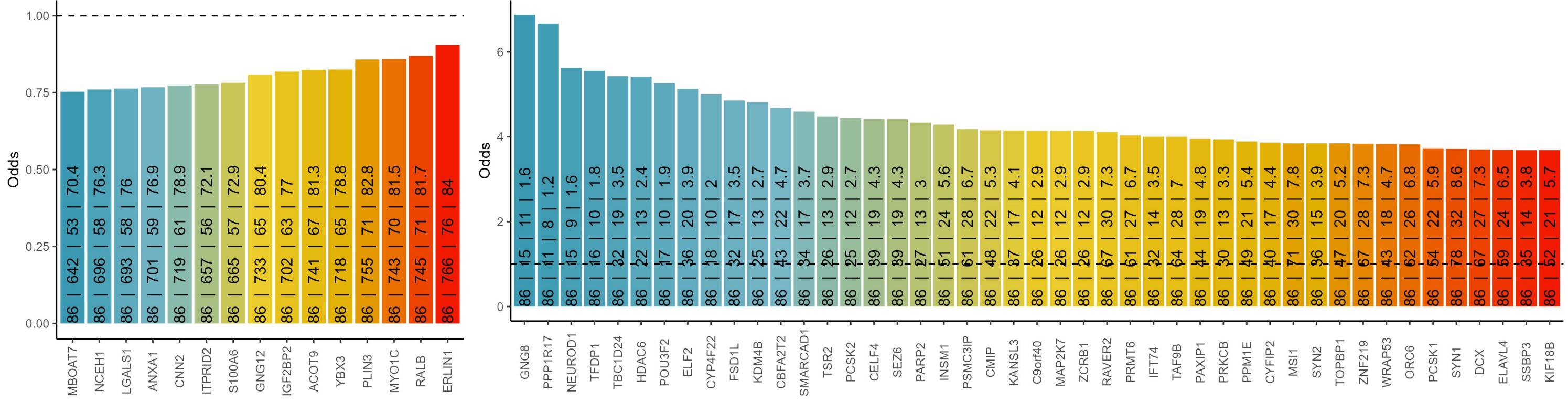
## Cooccurrence with CASP2 protein in blood cancers, DB1

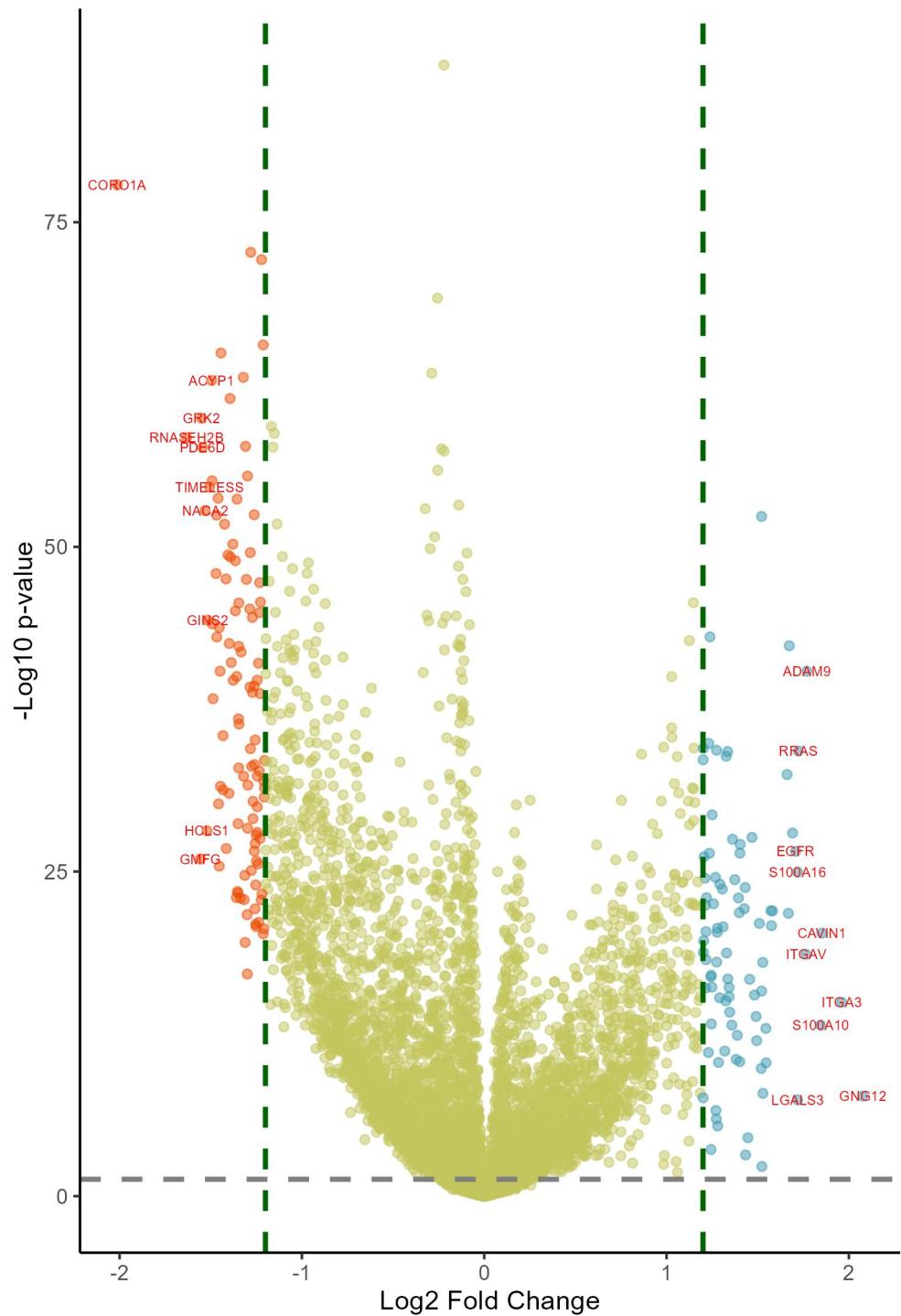
The text in the bars: incidence of CASP2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with CASP2 protein in solid cancers, DB1

The text in the bars: incidence of CASP2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

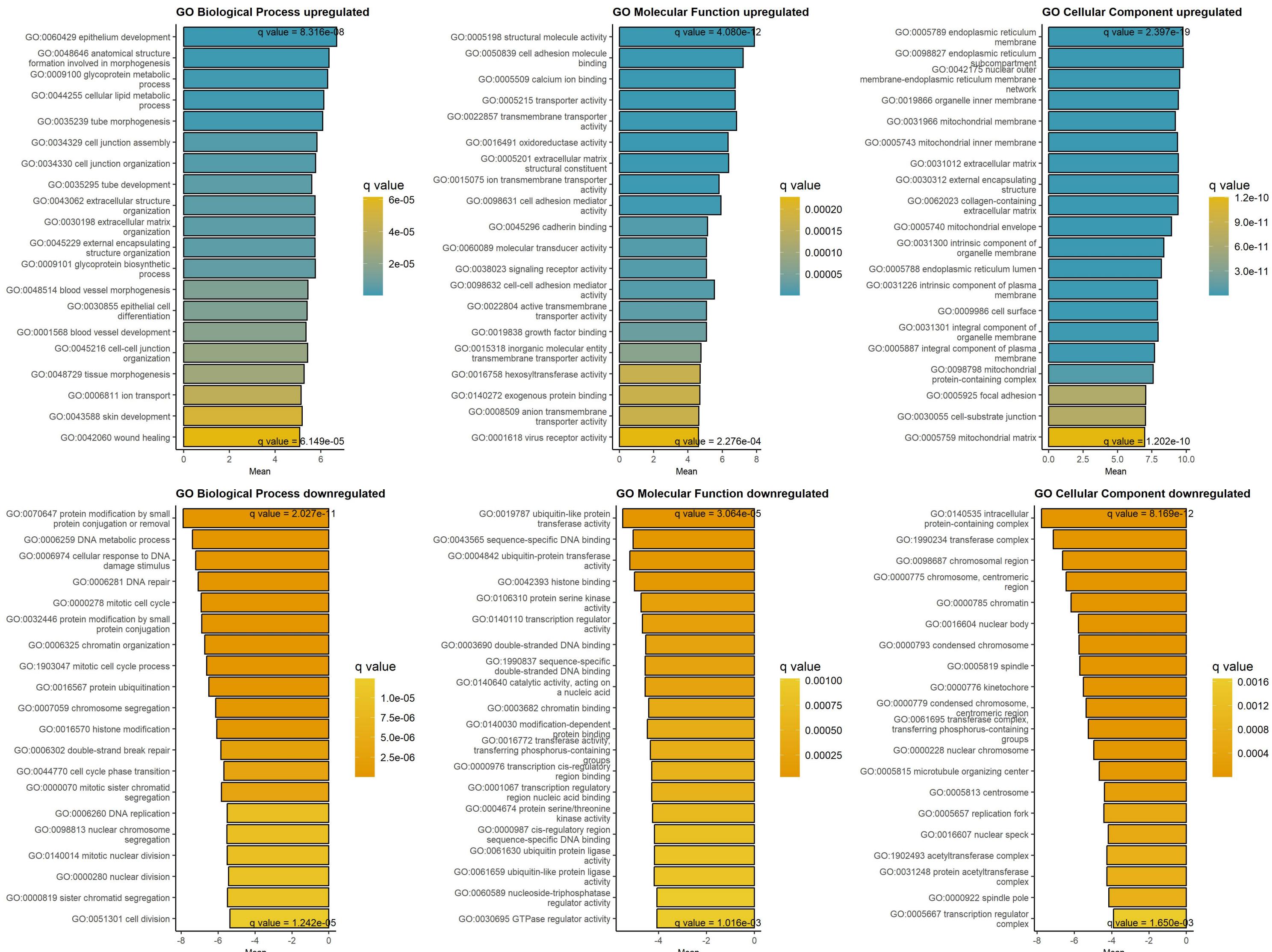




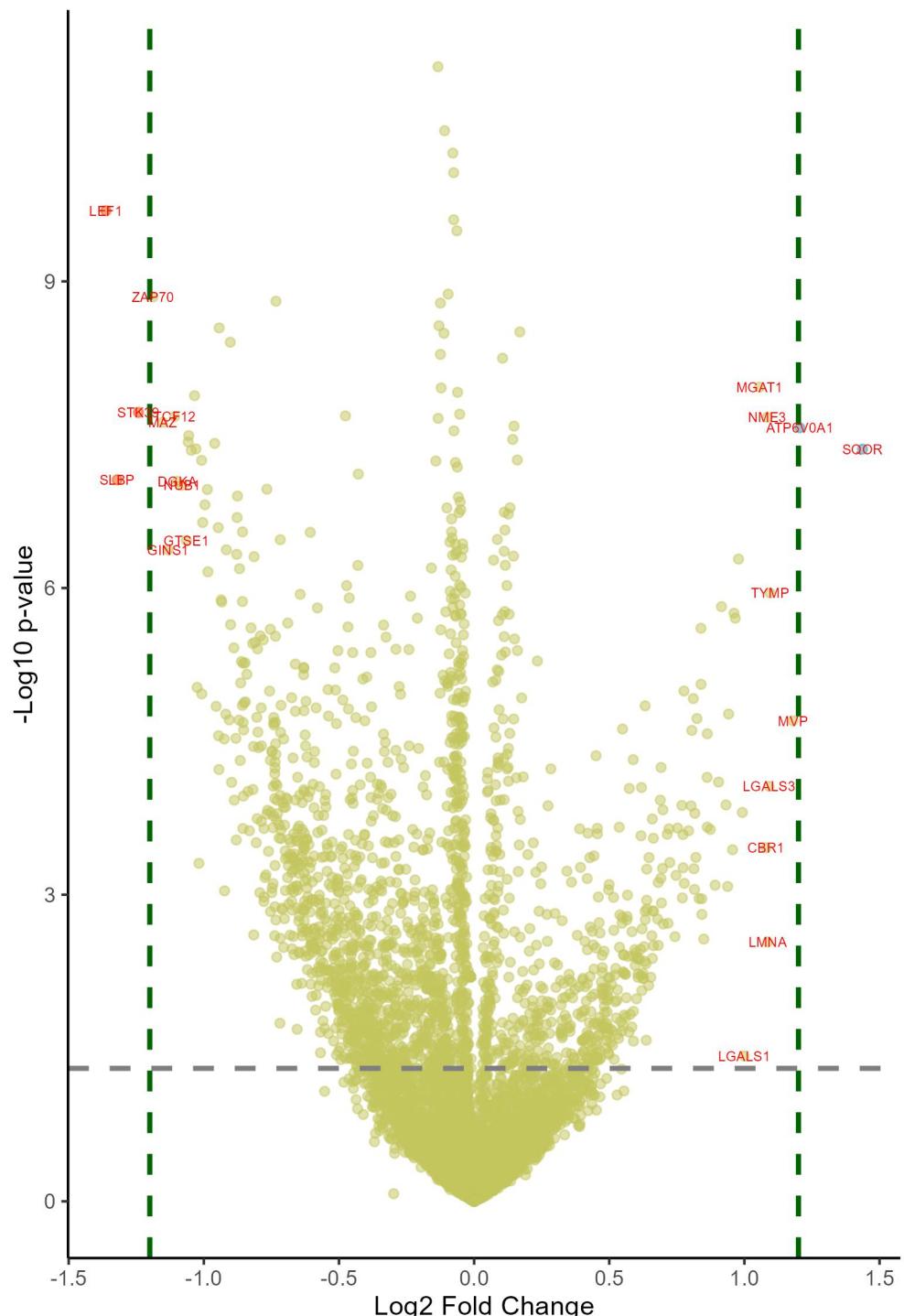
## Downregulated at low/absent CASP2   Upregulated at low/absent CASP2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.01	2.92e-75	CORO1A	coronin 1A	2.08	5.30e-08	GNG12	G protein subunit gamma 12
-1.63	1.57e-56	RNASEH2B	ribonuclease H2 subunit B	1.96	6.54e-15	ITGA3	integrin subunit alpha 3
-1.56	1.73e-25	GMFG	glia maturation factor gamma	1.85	4.90e-20	CAVIN1	caveolae associated protein 1
-1.55	6.14e-58	GRK2	G protein-coupled receptor kinase 2	1.85	3.15e-13	S100A10	S100 calcium binding protein A10
-1.54	7.67e-56	PDE6D	phosphodiesterase 6D	1.77	2.27e-39	ADAM9	ADAM metallopeptidase domain 9
-1.53	3.55e-51	NACA2	nascent polypeptide associated comp	1.77	1.84e-18	ITGAV	integrin subunit alpha V
-1.52	1.43e-27	HCLS1	hematopoietic cell-specific Lyn sub	1.72	1.87e-33	RRAS	RAS related
-1.52	4.09e-43	GINS2	GINS complex subunit 2	1.72	1.02e-07	LGALS3	galectin 3
-1.51	6.56e-53	TIMELESS	timeless circadian regulator	1.72	1.63e-24	S100A16	S100 calcium binding protein A16
-1.5	9.22e-61	ACYP1	acylphosphatase 1	1.71	4.69e-26	EGFR	epidermal growth factor receptor
-1.49	2.21e-53	HDHD2	haloacid dehalogenase like hydrolas	1.69	2.06e-27	PPIC	peptidylprolyl isomerase C
-1.49	7.47e-43	GABARPL2	GABA type A receptor associated pro	1.67	3.06e-41	EPHA2	EPH receptor A2
-1.49	2.48e-37	ASF1B	anti-silencing function 1B histone	1.67	1.65e-21	ITGA2	integrin subunit alpha 2
-1.47	1.53e-46	PCLAF	PCNA clamp associated factor	1.66	1.02e-31	NT5E	5'-nucleotidase ecto
-1.47	7.39e-51	NUDT3	nudix hydrolase 3	1.58	1.11e-21	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.47	7.26e-42	SNRNP27	small nuclear ribonucleoprotein U4/U6	1.58	1.37e-20	LAMC1	laminin subunit gamma 1
-1.46	4.56e-52	SMAP2	small ArfGAP2	1.57	1.07e-21	CAV1	caveolin 1
-1.46	1.45e-29	ATP2A3	ATPase sarcoplasmic/endoplasmic ret	1.55	1.89e-10	MYOF	myoferlin
-1.45	5.93e-25	RCSD1	RCSD domain containing 1	1.54	5.32e-13	PON2	paraoxonase 2
-1.45	1.43e-42	SEPTIN6	septin 6	1.53	3.35e-08	NCEH1	neutral cholesterol ester hydrolase
-1.45	2.27e-39	HIRIP3	HIRA interacting protein 3	1.53	7.07e-18	MYO1C	myosin IC
-1.45	7.52e-31	SLBP	stem-loop binding protein	1.52	7.98e-03	KRT18	keratin 18
-1.44	9.69e-63	PDXP	pyridoxal phosphatase	1.52	9.45e-16	FKBP10	FKBP prolyl isomerase 10
-1.43	1.39e-34	SSNA1	SS nuclear autoantigen 1	1.52	9.16e-51	FNDC3B	fibronectin type III domain contain
-1.43	1.37e-30	CELF2	CUGBP Elav-like family member 2	1.52	4.89e-10	FKBP9	FKBP prolyl isomerase 9
-1.42	3.36e-50	TACC3	transforming acidic coiled-coil con	1.51	9.33e-21	PROCR	protein C receptor
-1.42	3.90e-46	COPS7B	COP9 signalosome subunit 7B	1.49	4.26e-12	RHOC	ras homolog family member C
-1.41	2.91e-26	IKZF1	IKAROS family zinc finger 1	1.49	7.17e-14	PVR	PVR cell adhesion molecule
-1.41	6.78e-48	ARMC6	armadillo repeat containing 6	1.48	1.88e-15	NECTIN2	nectin cell adhesion molecule 2

## GAGE analysis on upregulated and downregulated proteins at low/absent CASP2 protein, DB1



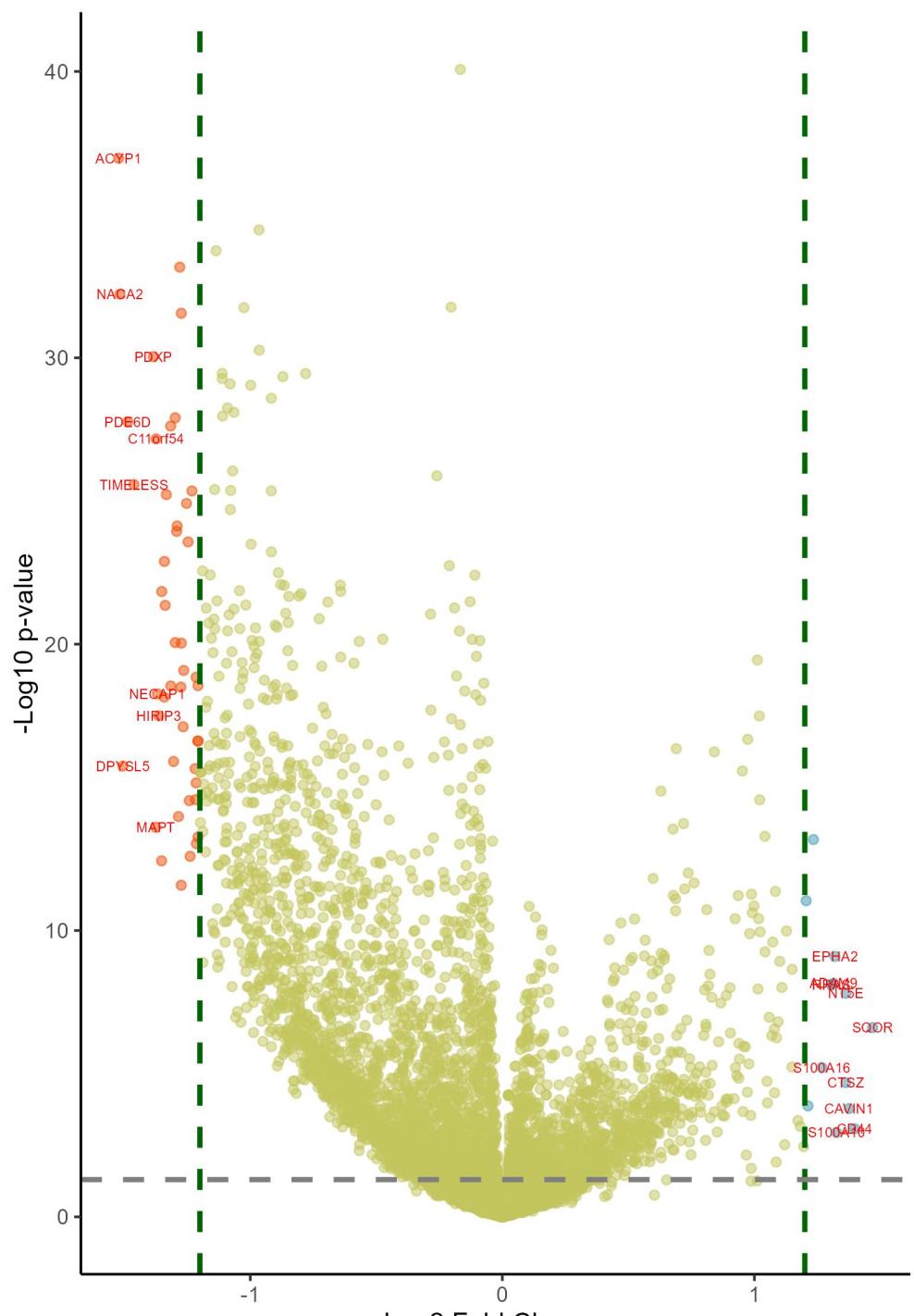
p-value &lt; 0.05 &amp; logFC &gt; 1.2



Downregulated in blood cancers at low/absent CASP2   Upregulated in blood cancers at low/absent CASP2

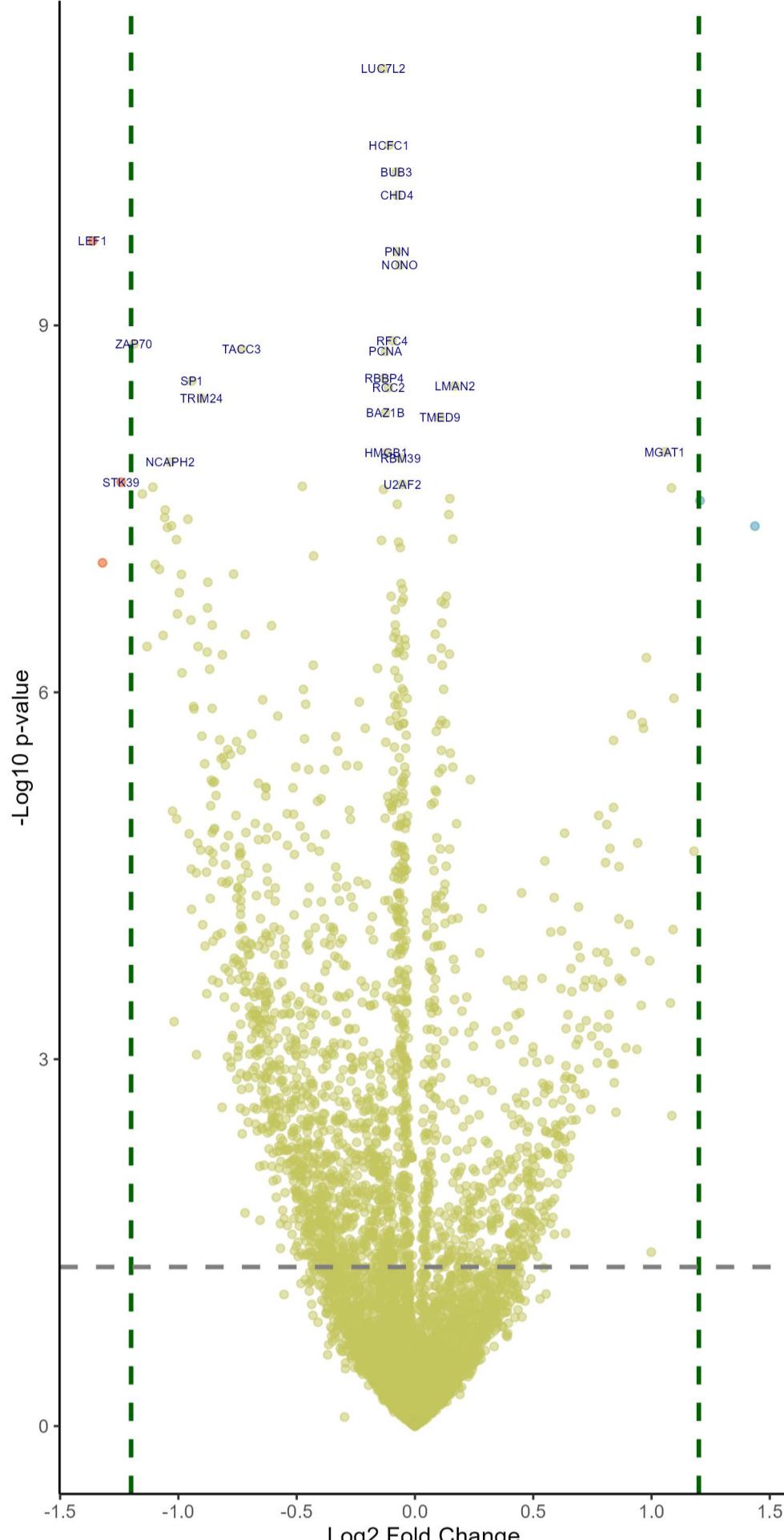
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.36	2.26e-07	LEF1	lymphoid enhancer binding factor 1	1.44	7.46e-06	SQOR	sulfide quinone oxidoreductase
-1.32	1.24e-05	SLBP	stem-loop binding protein	1.21	5.62e-06	ATP6V0A1	ATPase H <sup>+</sup> transporting V0 subunit a
-1.24	5.02e-06	STK39	serine/threonine kinase 39	1.18	5.32e-04	MVP	major vault protein
-1.19	9.03e-07	ZAP70	zeta chain of T cell receptor assoc	1.09	7.21e-05	TYMP	thymidine phosphorylase
-1.15	5.29e-06	MAZ	MYC associated zinc finger protein	1.09	1.57e-03	LGALS3	galectin 3
-1.13	3.56e-05	GINS1	GINS complex subunit 1	1.09	2.04e-02	LMNA	lamin A/C
-1.11	5.02e-06	TCF12	transcription factor 12	1.08	5.02e-06	NME3	NME/NM23 nucleoside diphosphate kin
-1.1	1.25e-05	DGKA	diacylglycerol kinase alpha	1.08	4.22e-03	CBR1	carbonyl reductase 1
-1.08	1.34e-05	NUB1	negative regulator of ubiquitin lik	1.06	3.49e-06	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-1.06	3.12e-05	GTSE1	G2 and S-phase expressed 1	1	1.03e-01	LGALS1	galectin 1
-1.06	6.88e-06	CCNK	cyclin K	0.99	2.37e-03	STOM	stomatin
-1.06	6.31e-06	UNC119B	unc-119 lipid binding chaperone B	0.98	3.93e-05	PLOD1	procollagen-lysine,2-oxoglutarate 5
-1.05	7.47e-06	YEATS4	YEATS domain containing 4	0.97	1.03e-04	GPAA1	glycosylphosphatidylinositol anchor
-1.03	3.79e-06	NCAPH2	non-SMC condensin II complex subuni	0.96	9.84e-05	SIL1	SIL1 nucleotide exchange factor
-1.03	7.46e-06	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan	0.96	4.36e-03	IGF2BP2	insulin like growth factor 2 mRNA b
-1.02	3.16e-04	RUNX1	RUNX family transcription factor 1	0.94	4.91e-04	TRIP10	thyroid hormone receptor interactor
-1.02	5.43e-03	PTPRCAP	protein tyrosine phosphatase recept	0.94	8.11e-03	PLP2	proteolipid protein 2
-1.01	8.85e-06	SPINDOC	spindlin interactor and repressor o	0.93	2.09e-03	HSPA4L	heat shock protein family A (Hsp70)
-1.01	3.52e-04	ZC3HAV1L	zinc finger CCCH-type containing, a	0.92	8.87e-05	MYO6	myosin VI
-1	2.37e-05	MTF2	metal response element binding tran	0.9	1.46e-03	JUNB	JunB proto-oncogene, AP-1 transcrip
-1	1.85e-05	SPIN1	spindlin 1	0.89	7.96e-03	CTSZ	cathepsin Z
-0.99	1.42e-05	PHC2	polyhomeotic homolog 2	0.87	3.17e-03	CKB	creatine kinase B
-0.98	4.86e-05	TLE5	TLE family member 5, transcriptiona	0.86	6.62e-04	LACTB	lactamase beta
-0.96	6.91e-06	TIMELESS	timeless circadian regulator	0.86	3.10e-03	NCEH1	neutral cholesterol ester hydrolase
-0.95	4.28e-04	SCML2	Scm polycomb group protein like 2	0.86	1.35e-03	TMEM205	transmembrane protein 205
-0.95	2.63e-05	CD3E	CD3 epsilon subunit of T-cell recep	0.85	1.93e-02	ANXA1	annexin A1
-0.95	6.82e-04	TCF3	transcription factor 3	0.84	1.28e-02	IRF4	interferon regulatory factor 4
-0.94	1.17e-03	BLM	BLM RecQ like helicase	0.84	9.83e-03	CTTN	cortactin
-0.94	1.34e-06	SP1	Sp1 transcription factor	0.84	3.00e-04	ACBD5	acyl-CoA binding domain containing

p-value &lt; 0.05 &amp; logFC &gt; 1.2

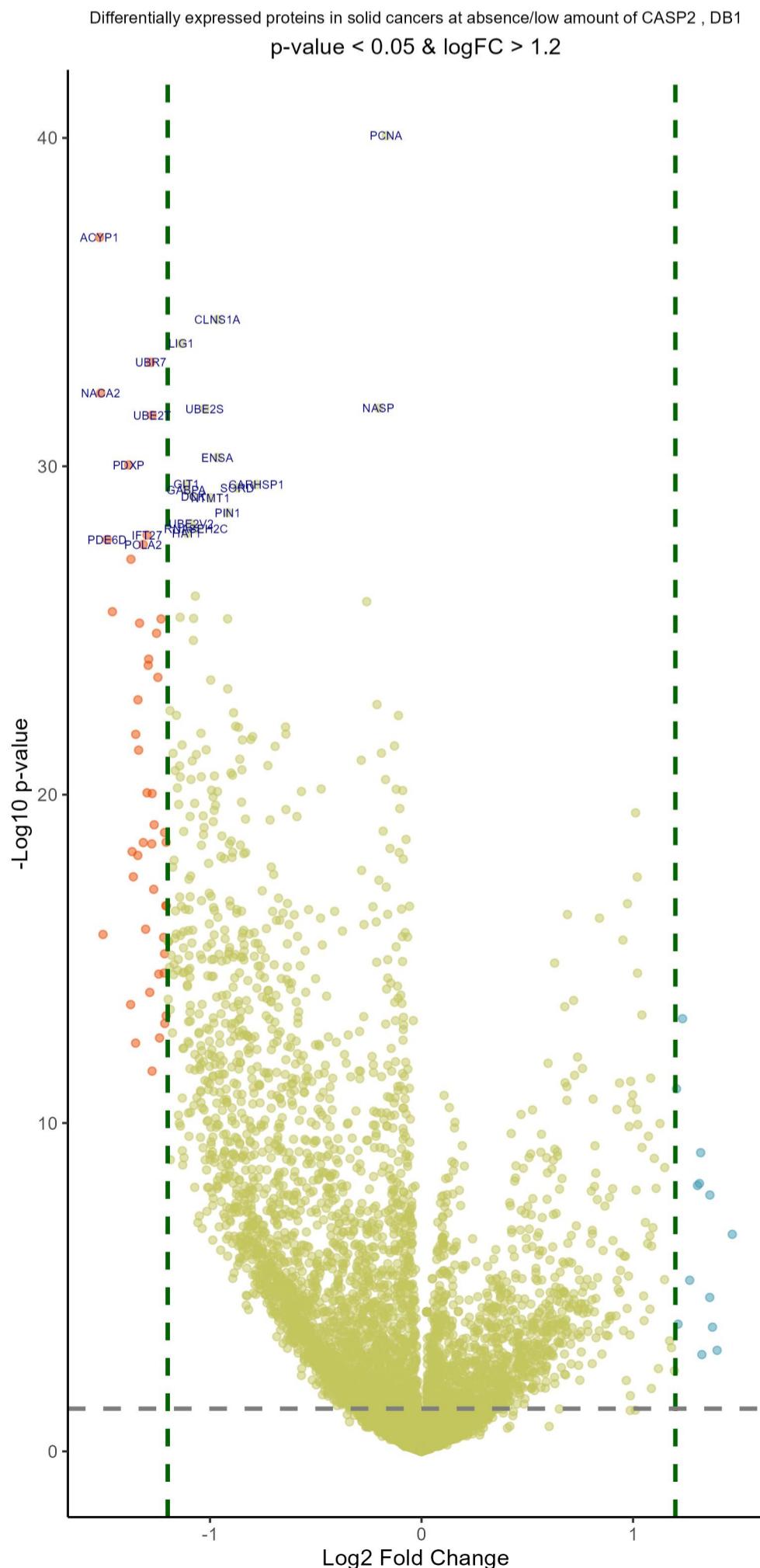


Sorted by p values!

Downregulated in blood cancers at low/absent CASP2 Upregulated in blood cancers at low/absent CASP2

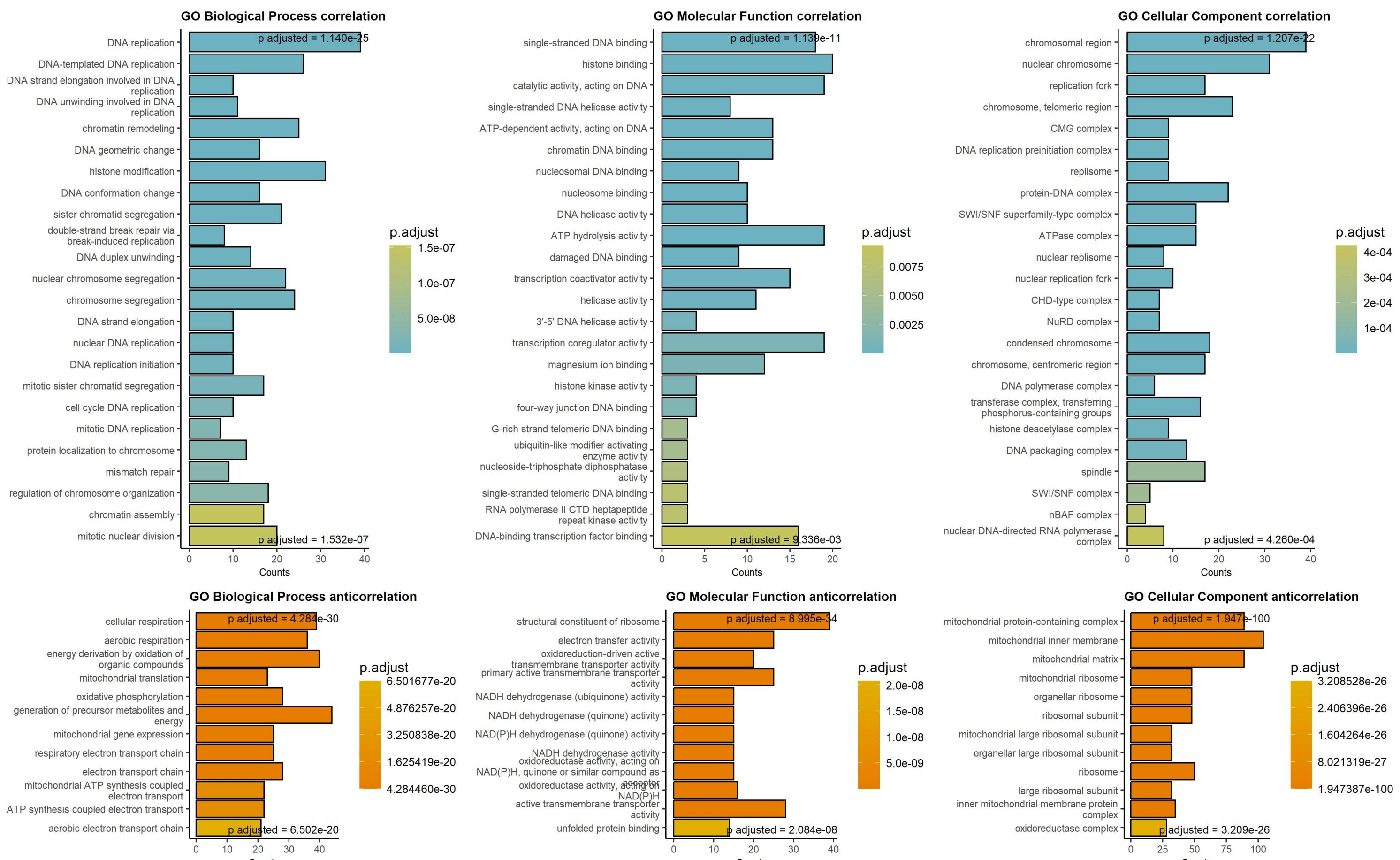


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.13	2.64e-08	LUC7L2	LUC7 like 2, pre-mRNA splicing fact	0.17	1.34e-06	LMAN2	lectin, mannose binding 2
-0.11	7.44e-08	HCFC1	host cell factor C1	0.11	1.98e-06	TMED9	transmembrane p24 trafficking prote
-0.08	9.23e-08	BUB3	BUB3 mitotic checkpoint protein	1.06	3.49e-06	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.08	1.15e-07	CHD4	chromodomain helicase DNA binding p	1.08	5.02e-06	NME3	NME/NM23 nucleoside diphosphate kin
-1.36	2.26e-07	LEF1	lymphoid enhancer binding factor 1	0.15	5.59e-06	FKBP2	FKBP prolyl isomerase 2
-0.08	2.37e-07	PNN	pinin, desmosome associated protein	1.21	5.62e-06	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.06	2.66e-07	NONO	non-POU domain containing octamer b	0.14	6.69e-06	UQCRCB	ubiquinol-cytochrome c reductase bi
-0.1	9.03e-07	RFC4	replication factor C subunit 4	1.44	7.46e-06	SQOR	sulfide quinone oxidoreductase
-1.19	9.03e-07	ZAP70	zeta chain of T cell receptor assoc	0.16	8.85e-06	CYC1	cytochrome c1
-0.73	9.03e-07	TACC3	transforming acidic coiled-coil con	0.13	1.92e-05	MTDH	metadherin
-0.12	9.03e-07	PCNA	proliferating cell nuclear antigen	0.11	2.03e-05	COPG1	COPI coat complex subunit gamma 1
-0.13	1.34e-06	RBBP4	RB binding protein 4, chromatin rem	0.13	2.06e-05	ERP44	endoplasmic reticulum protein 44
-0.94	1.34e-06	SP1	Sp1 transcription factor	0.11	2.73e-05	HDLBP	high density lipoprotein binding pr
-0.11	1.34e-06	RCC2	regulator of chromosome condensatio	0.09	3.11e-05	UQCRC1	ubiquinol-cytochrome c reductase co
-0.9	1.54e-06	TRIM24	tripartite motif containing 24	0.11	3.60e-05	CLPP	caseinolytic mitochondrial matrix p
-0.12	1.91e-06	BAZ1B	bromodomain adjacent to zinc finger	0.15	3.81e-05	SRPRB	SRP receptor subunit beta
-0.12	3.49e-06	HMGB1	high mobility group box 1	0.98	3.93e-05	PLOD1	procollagen-lysine,2-oxoglutarate 5
-0.06	3.68e-06	RBM39	RNA binding motif protein 39	0.07	3.99e-05	CANX	calnexin
-1.03	3.79e-06	NCAPH2	non-SMC condensin II complex subuni	0.12	4.39e-05	NDUFS1	NADH:ubiquinone oxidoreductase core
-1.24	5.02e-06	STK39	serine/threonine kinase 39	0.12	6.36e-05	TMED10	transmembrane p24 trafficking prote
-0.05	5.02e-06	U2AF2	U2 small nuclear RNA auxiliary fact	1.09	7.21e-05	TYMP	thymidine phosphorylase
-0.48	5.02e-06	PATZ1	POZ/BTB and AT hook containing zinc	0.92	8.87e-05	MYO6	myosin VI
-1.11	5.02e-06	TCF12	transcription factor 12	0.11	9.62e-05	UQCRC2	ubiquinol-cytochrome c reductase co
-0.13	5.02e-06	PAK2	p21 (RAC1) activated kinase 2	0.96	9.84e-05	SIL1	SIL1 nucleotide exchange factor
-1.15	5.29e-06	MAZ	MYC associated zinc finger protein	0.13	9.84e-05	UGGT1	UDP-glucose glycoprotein glucosyltr
-0.07	5.84e-06	CBX3	chromobox 3	0.1	9.88e-05	HSPA5	heat shock protein family A (Hsp70)
-1.06	6.31e-06	UNC119B	unc-119 lipid binding chaperone B	0.97	1.03e-04	GPAA1	glycosylphosphatidylinositol anchor
-1.06	6.88e-06	CCNK	cyclin K	0.09	1.08e-04	RPN1	ribophorin I
-0.96	6.91e-06	TIMELESS	timeless circadian regulator	0.84	1.22e-04	GOLIM4	golgi integral membrane protein 4
-1.03	7.46e-06	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan	0.11	1.40e-04	PPIB	peptidylprolyl isomerase B
-1.05	7.47e-06	YEATS4	YEATS domain containing 4	0.15	1.45e-04	P4HB	prolyl 4-hydroxylase subunit beta
-1.01	8.85e-06	SPINDOC	spindlin interactor and repressor o	0.16	1.76e-04	CISD2	CDGSH iron sulfur domain 2
-0.14	8.85e-06	STMN1	stathmin 1	0.12	1.80e-04	HYOU1	hypoxia up-regulated 1
-0.07	8.95e-06	PHF5A	PHD finger protein 5A	0.1	1.88e-04	MRPL13	mitochondrial ribosomal protein L13
-0.06	9.69e-06	ZNF207	zinc finger protein 207	0.23	2.11e-04	SPCS2	signal peptidase complex subunit 2
-0.43	1.11e-05	UHRF1	ubiquitin like with PHD and ring fi	0.09	2.41e-04	NDUFS3	NADH:ubiquinone oxidoreductase core
-1.32	1.24e-05	SLBP	stem-loop binding protein	0.09	2.48e-04	SSR1	signal sequence receptor subunit 1
-1.1	1.25e-05	DGKA	diacylglycerol kinase alpha	0.08	2.83e-04	TRAP1	TNF receptor associated protein 1
1.09	1.34e-05	NLRP1	negative regulator of ubiquitin lik	0.07	2.99e-04	ATP6V1A	ATPase H+ transporting V1 subunit A

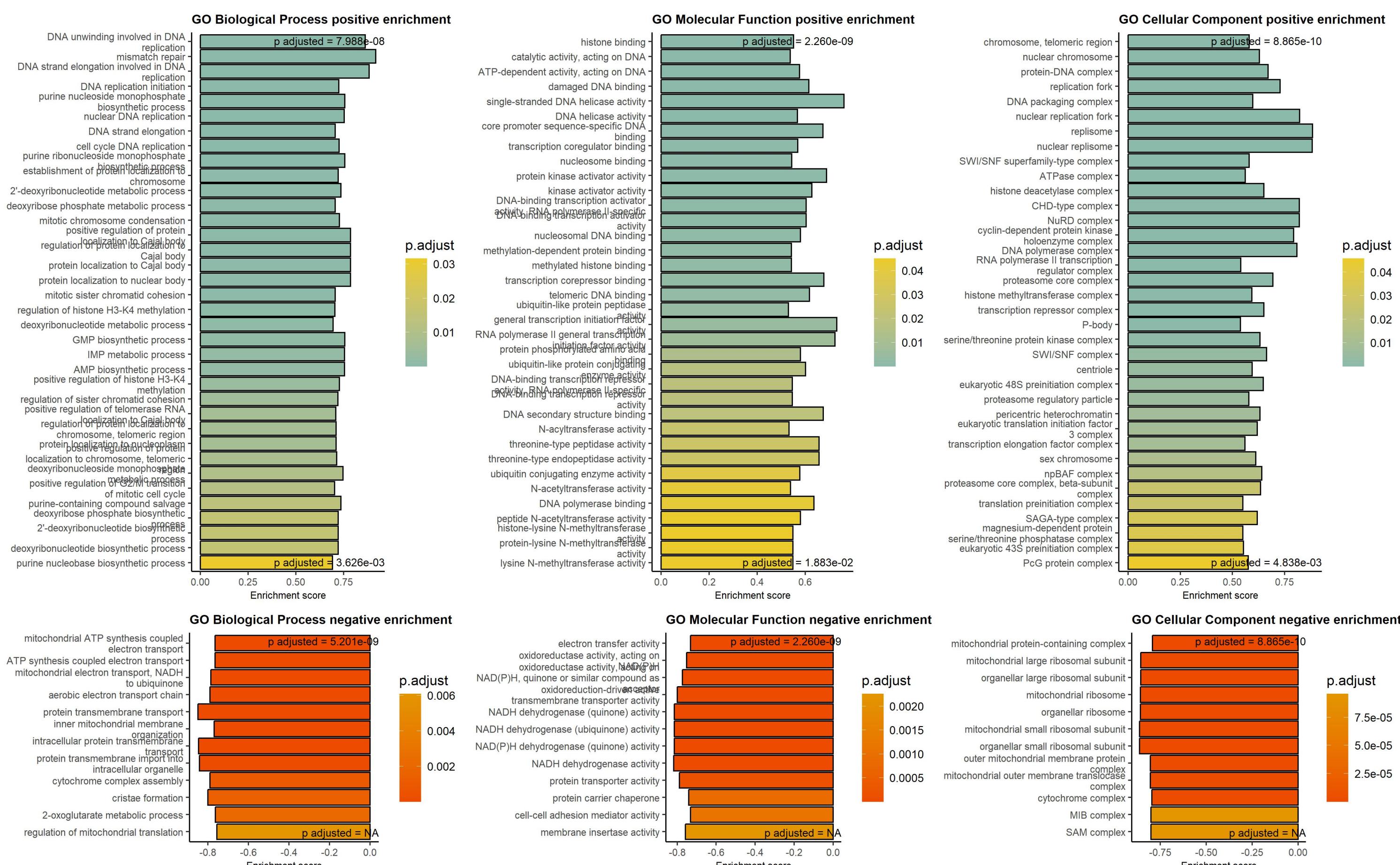


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.17	2.83e-37	PCNA	proliferating cell nuclear antigen	1.01	2.47e-18	NEXN	nexilin F-actin binding protein
-1.52	2.37e-34	ACYP1	acylphosphatase 1	1.02	1.57e-16	F3	coagulation factor III, tissue fact
-0.97	5.66e-32	CLNS1A	chloride nucleotide-sensitive chann	0.97	9.24e-16	LAMC2	laminin subunit gamma 2
-1.14	2.42e-31	LIG1	DNA ligase 1	0.69	1.73e-15	LAMA3	laminin subunit alpha 3
-1.28	7.56e-31	UBR7	ubiquitin protein ligase E3 compone	0.84	2.18e-15	CCN1	cellular communication network fact
-1.52	5.62e-30	NACA2	nascent polypeptide associated comp	0.95	8.67e-15	P3H2	prolyl 3-hydroxylase 2
-0.2	1.31e-29	NASP	nuclear autoantigenic sperm protein	0.63	3.62e-14	CD46	CD46 molecule
-1.03	1.31e-29	UBE2S	ubiquitin conjugating enzyme E2 S	1.02	6.94e-14	LAMB2	laminin subunit beta 2
-1.27	1.85e-29	UBE2T	ubiquitin conjugating enzyme E2 T	0.72	4.10e-13	CCDC9B	coiled-coil domain containing 9B
-0.96	3.27e-28	ENSA	endosulfine alpha	0.68	6.07e-13	COL17A1	collagen type XVII alpha 1 chain
-1.38	5.04e-28	PDXP	pyridoxal phosphatase	1.04	1.05e-12	IGFBP7	insulin like growth factor binding
-1.11	1.69e-27	GIT1	GIT ArfGAP 1	1.23	1.33e-12	FNDC3B	fibronectin type III domain contain
-0.78	1.69e-27	CARHSP1	calcium regulated heat stable prote	0.74	1.60e-11	QSOX1	quiescin sulphydryl oxidase 1
-0.87	2.01e-27	SORD	sorbitol dehydrogenase	0.6	2.38e-11	TGFB2	transforming growth factor beta 2
-1.11	2.20e-27	GABPA	GA binding protein transcription fa	0.76	3.32e-11	RAB31	RAB31, member RAS oncogene family
-1.08	3.20e-27	DCK	deoxyctydine kinase	0.72	5.10e-11	TCIRG1	T cell immune regulator 1, ATPase H
-1	3.35e-27	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	1.08	6.12e-11	EHD2	EH domain containing 2
-0.92	9.07e-27	PIN1	peptidylprolyl cis/trans isomerase,	0.99	7.51e-11	RAB11FIP5	RAB11 family interacting protein 5
-1.09	1.87e-26	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.68	8.24e-11	SYVN1	synoviolin 1
-1.06	2.55e-26	RNASEH2C	ribonuclease H2 subunit C	0.94	8.36e-11	GGCX	gamma-glutamyl carboxylase
-1.11	3.30e-26	HAT1	histone acetyltransferase 1	0.69	1.05e-10	CD58	CD58 molecule
-1.3	3.59e-26	IFT27	intraflagellar transport 27	1.21	1.21e-10	TAP2	transporter 2, ATP binding cassette
-1.49	4.72e-26	PDE6D	phosphodiesterase 6D	1	1.78e-10	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-1.32	6.40e-26	POLA2	DNA polymerase alpha 2, accessory s	0.11	1.85e-10	RAB1A	RAB1A, member RAS oncogene family
-1.37	1.73e-25	C11orf54	chromosome 11 open reading frame 54	0.81	2.34e-10	NRP1	neuropilin 1
-1.07	2.21e-24	UBE2C	ubiquitin conjugating enzyme E2 C	0.69	2.56e-10	FGF2	fibroblast growth factor 2
-0.26	3.14e-24	STMN1	stathmin 1	0.99	2.98e-10	COL12A1	collagen type XII alpha 1 chain
-1.46	6.15e-24	TIMELESS	timeless circadian regulator	0.13	4.10e-10	TMED9	transmembrane p24 trafficking prote
-1.14	8.81e-24	CNOT2	CCR4-NOT transcription complex subu	1.02	4.61e-10	RAB32	RAB32, member RAS oncogene family
-1.08	8.98e-24	UCK2	uridine-cytidine kinase 2	0.92	4.65e-10	LAMB3	laminin subunit beta 3
-0.92	8.98e-24	RPRD1A	regulation of nuclear pre-mRNA doma	0.52	4.76e-10	COL7A1	collagen type VII alpha 1 chain
-1.23	8.98e-24	ABRACL	ABRA C-terminal like	0.47	6.38e-10	MAN1B1	mannosidase alpha class 1B member 1
-1.33	1.17e-23	BRD2	bromodomain containing 2	0.16	1.07e-09	SSR4	signal sequence receptor subunit 4
-1.25	2.31e-23	POLR2F	RNA polymerase				

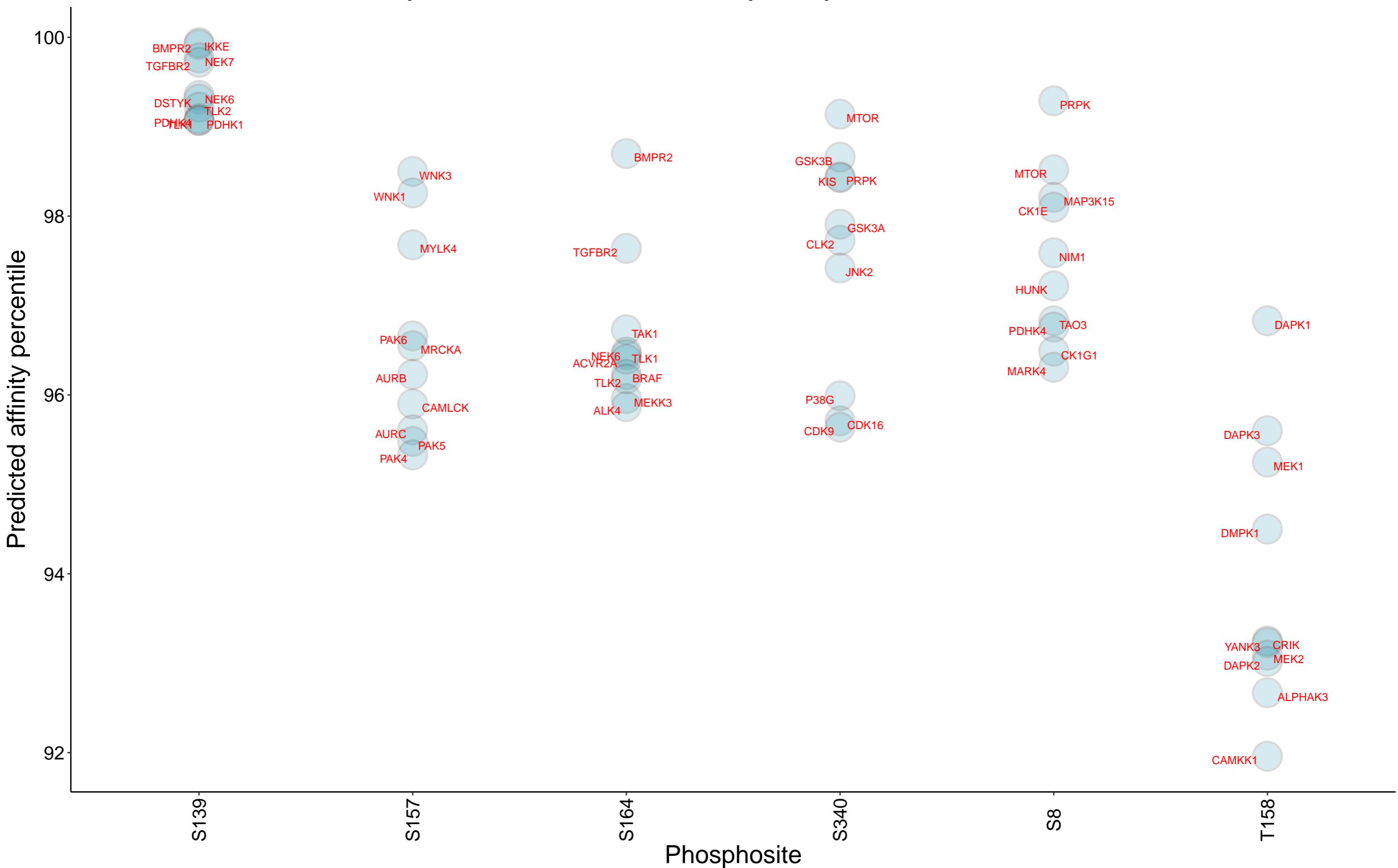
# Top 250 correlation coefficients overrepresentation, CASP2 protein, DB1



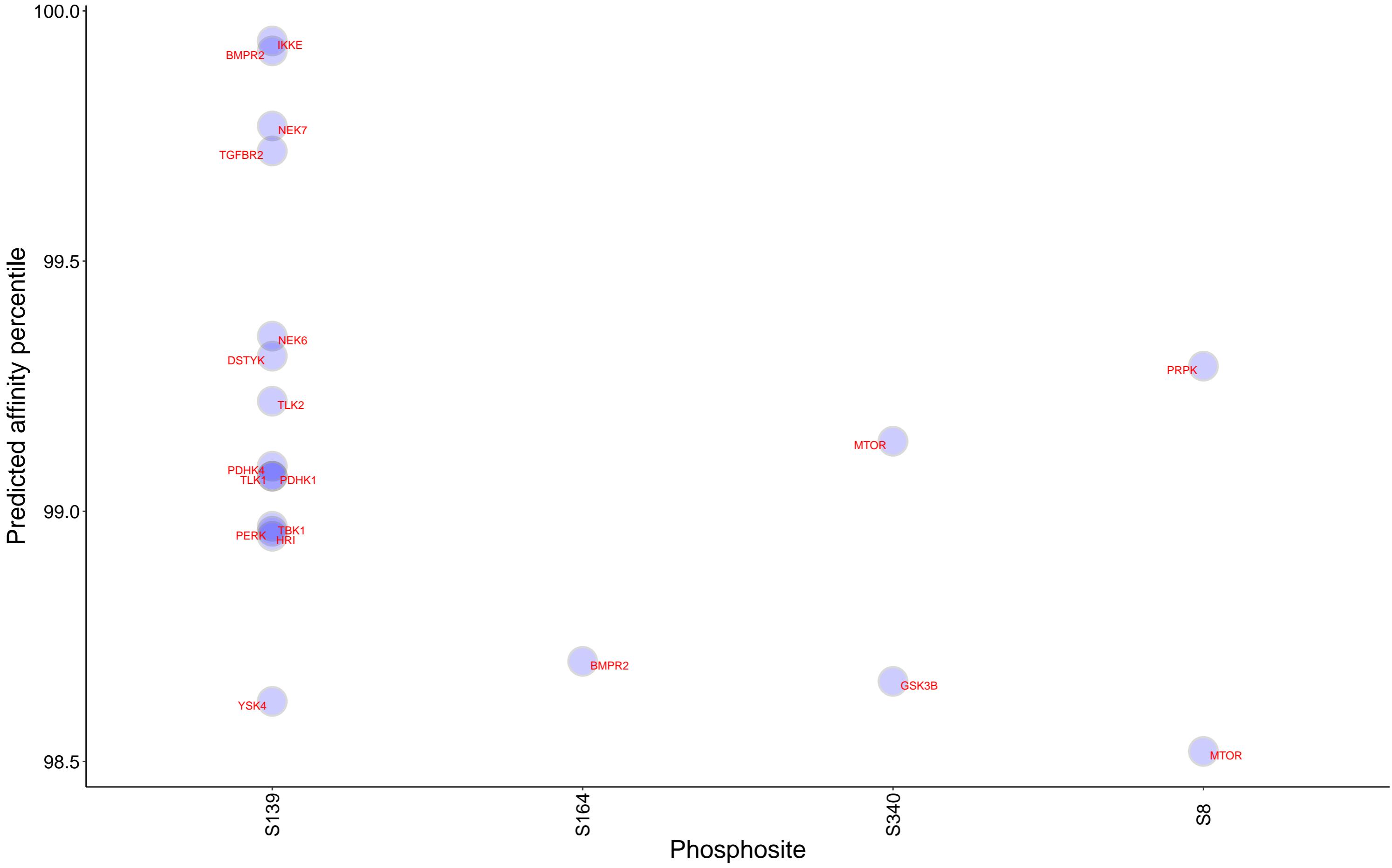
## Gene Set Enrichment analysis on protein correlation coefficients, CASP2 protein, DB1



# Top 10 kinases for each phosphosite in CASP2

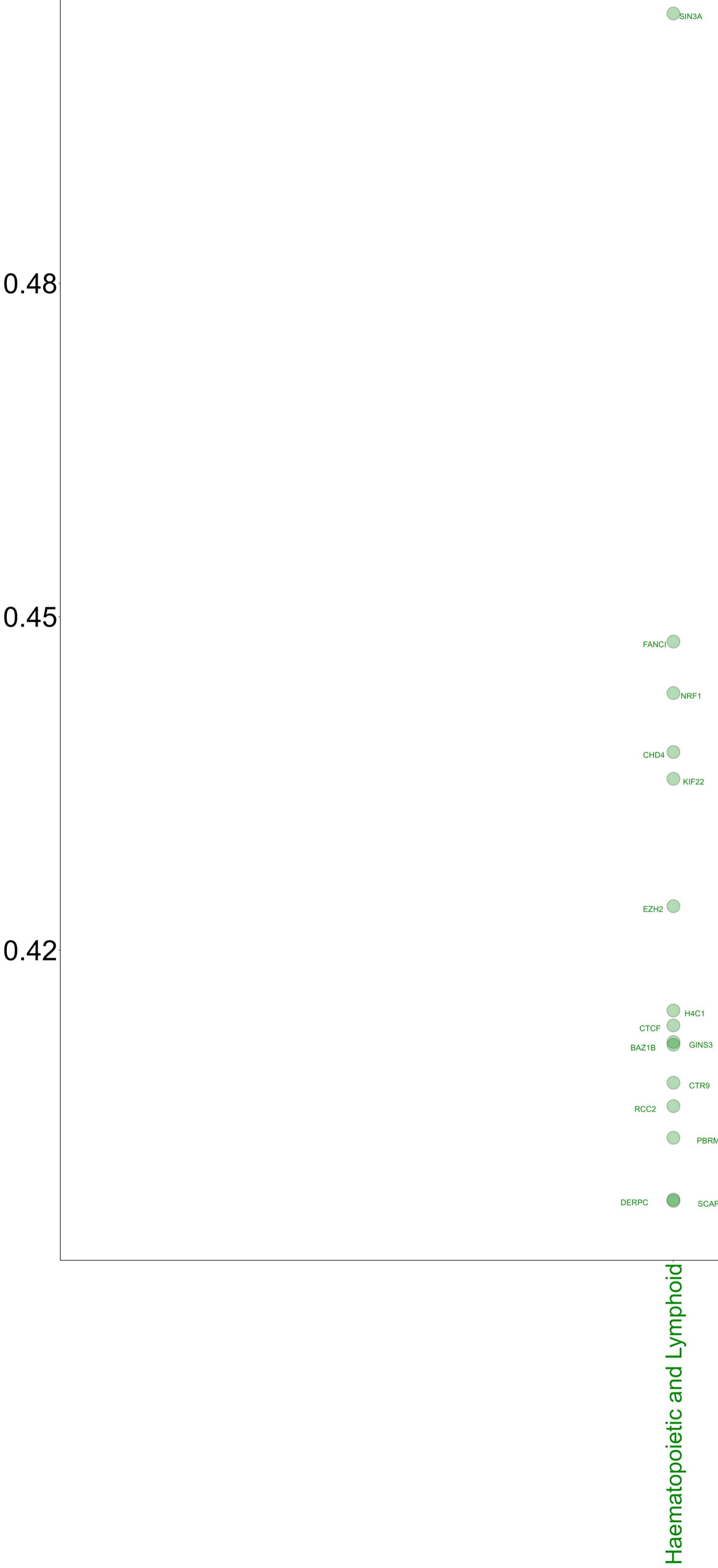


Kinases with affinity greater than 98.5% to CASP2



# Top 15 positive correlation coefficients for CASP2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples



Haematopoietic and Lymphoid