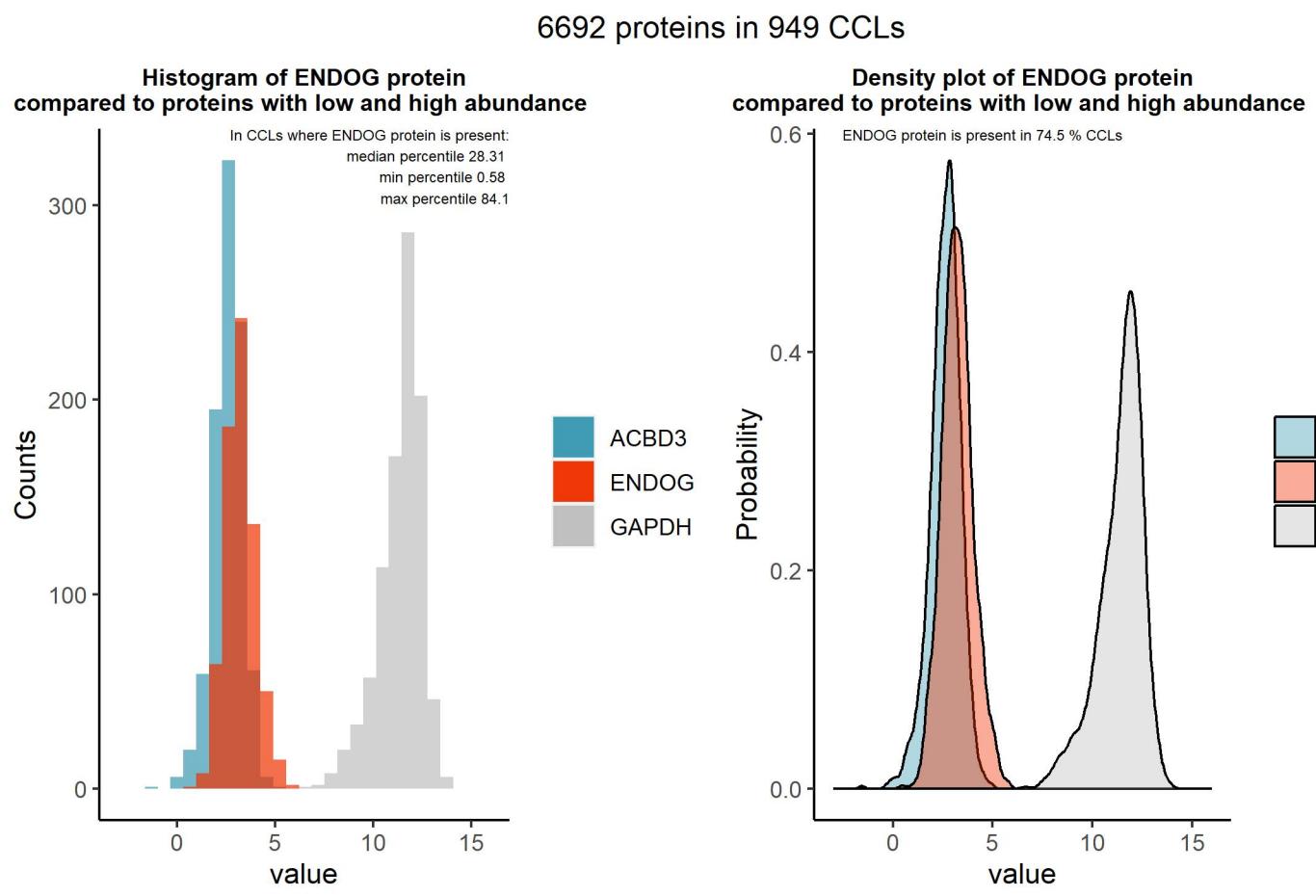


# ENDOG

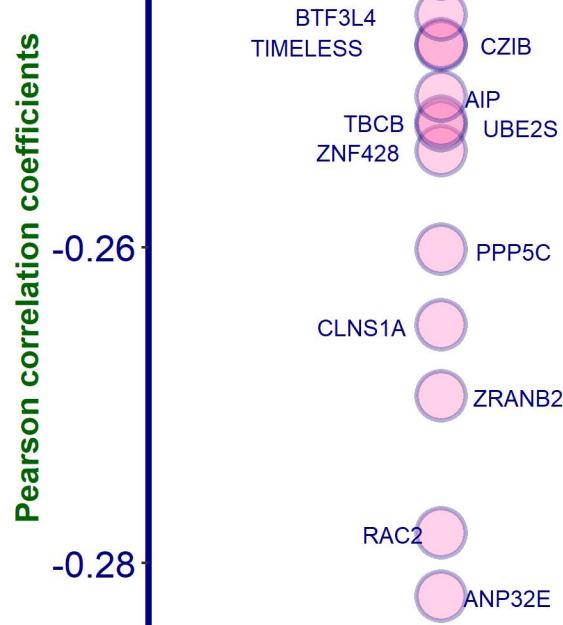
Protein name: NUCG ; UNIPROT: Q14249 ; Gene name: endonuclease G

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

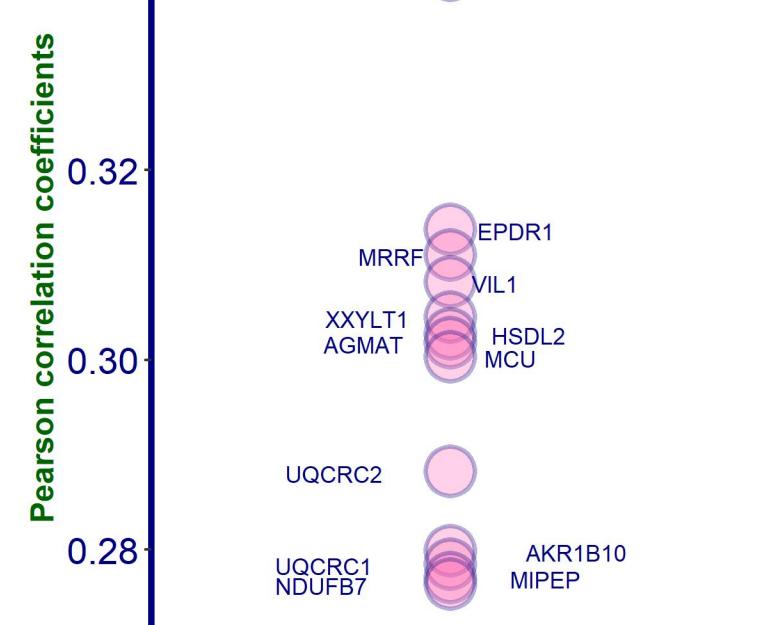
## Sanger Institute Protein Database 1 (DB1), protein presence is certain



## Top negative correlations of ENDOG protein, DB1

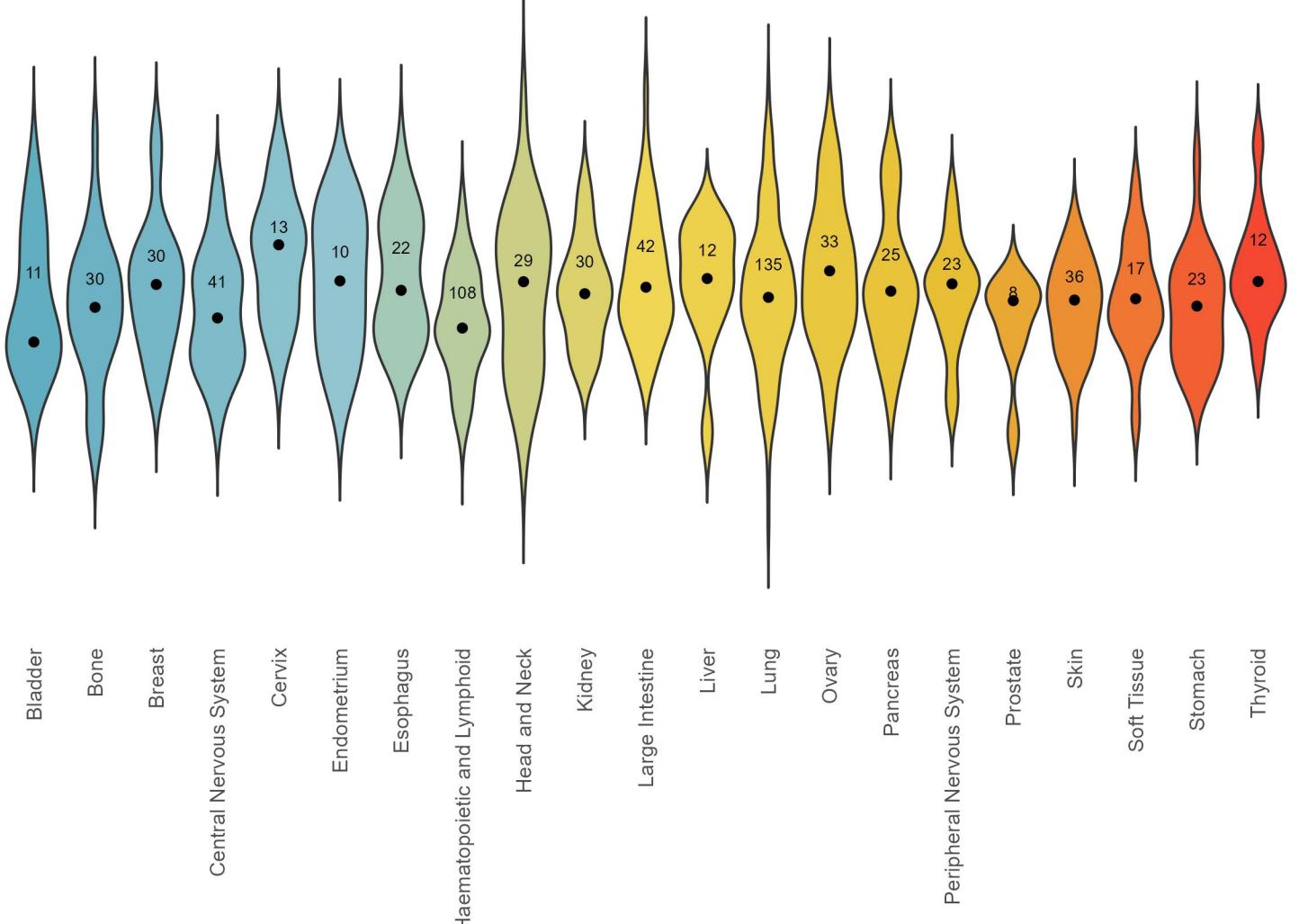


## Top positive correlations of ENDOG protein, DB1



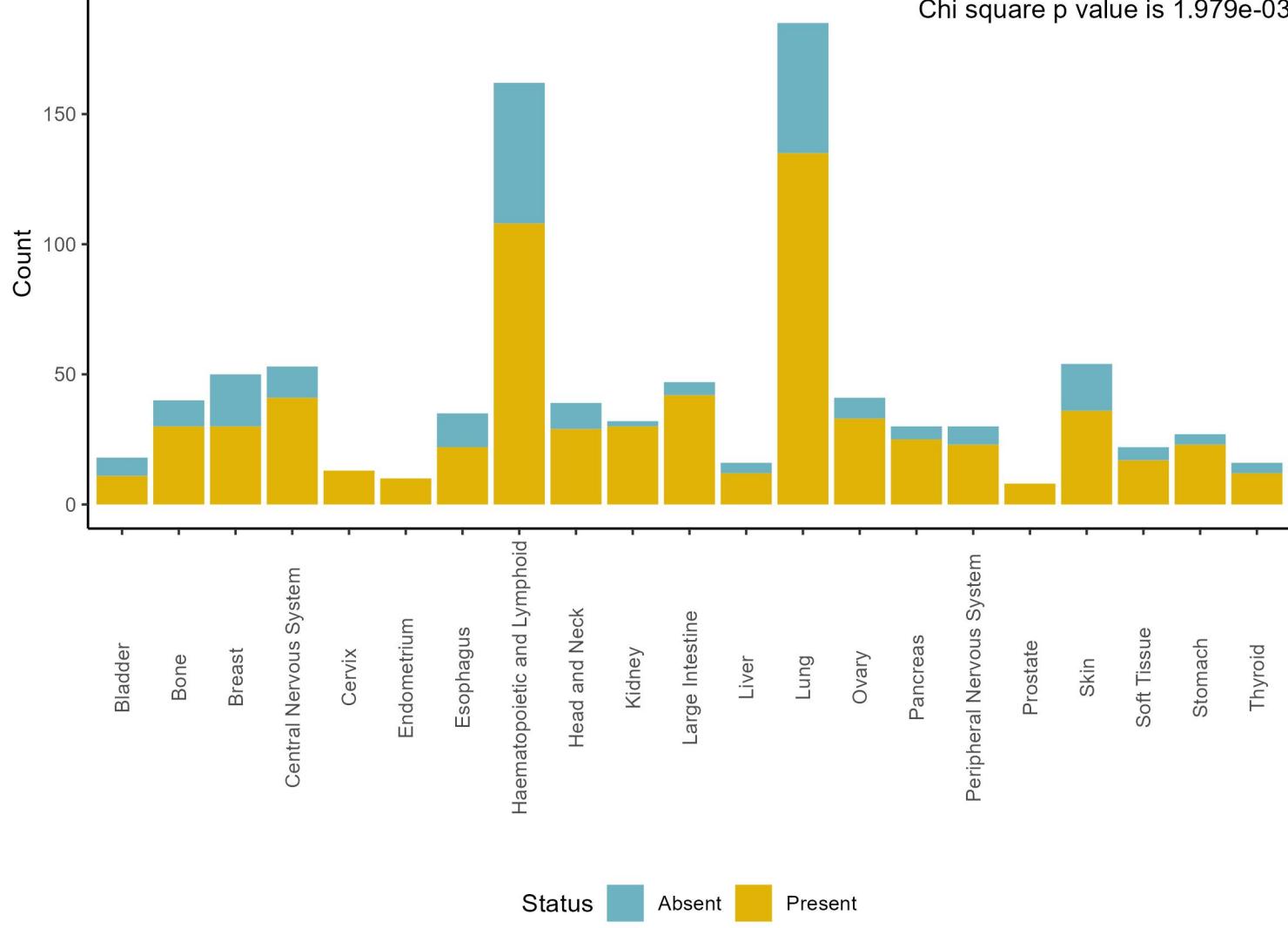
## Amount of ENDOG protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 6.698e-04



## Present and absent ENDOG protein counts by tissue, DB1

Chi square p value is 1.979e-03

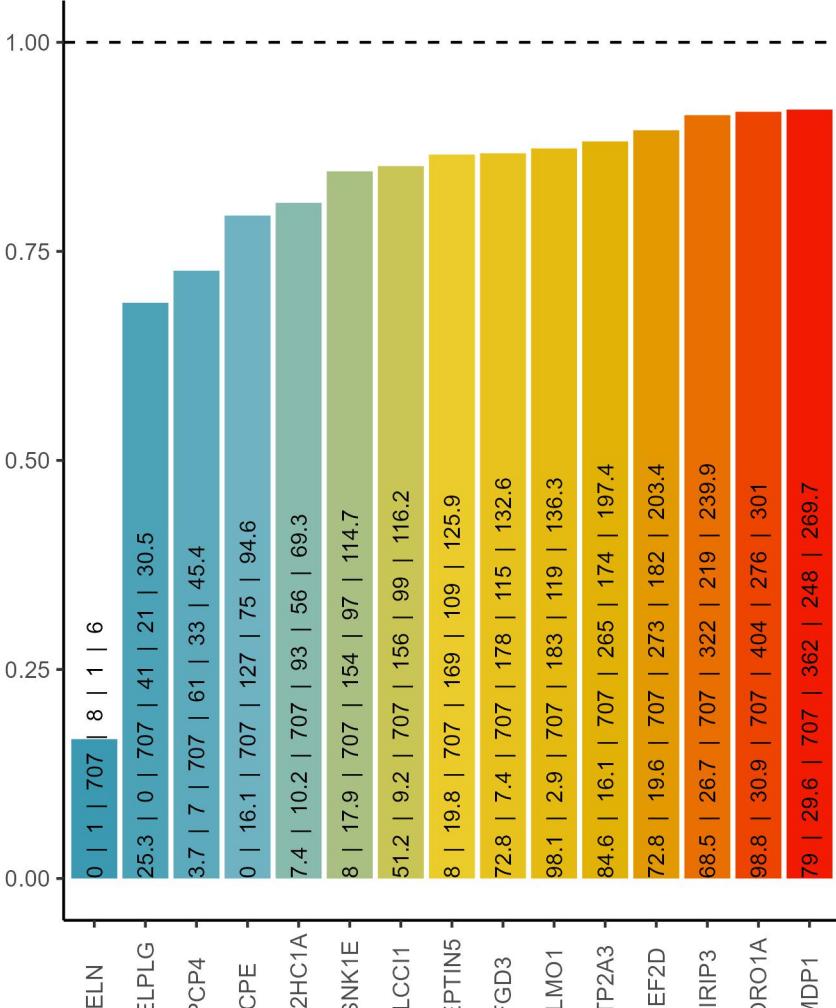


## Cooccurrence with ENDOG protein, DB1

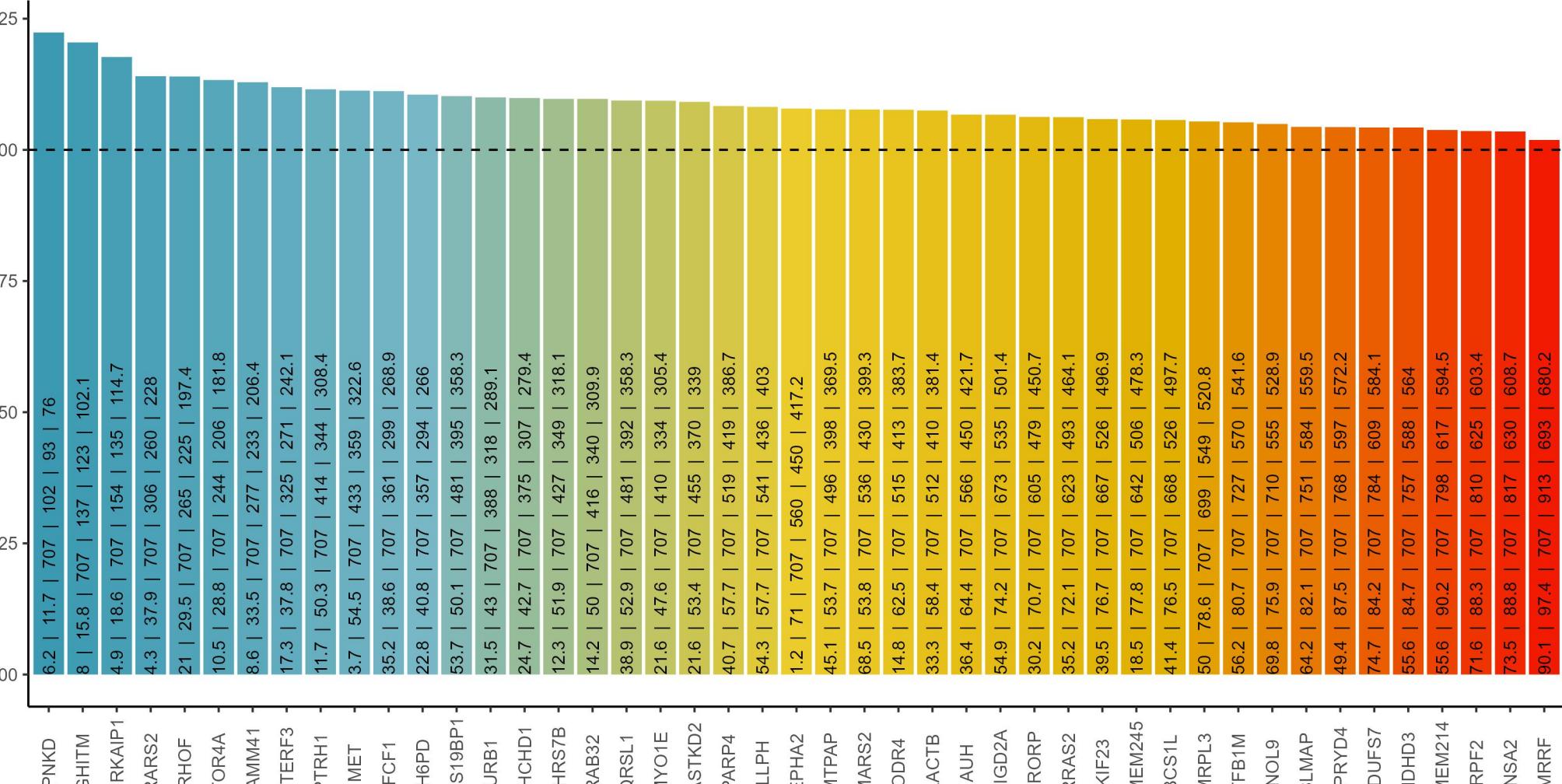
% of ENDOG in blood cancers: 66.7 ; % of ENDOG in solid cancers: 76

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

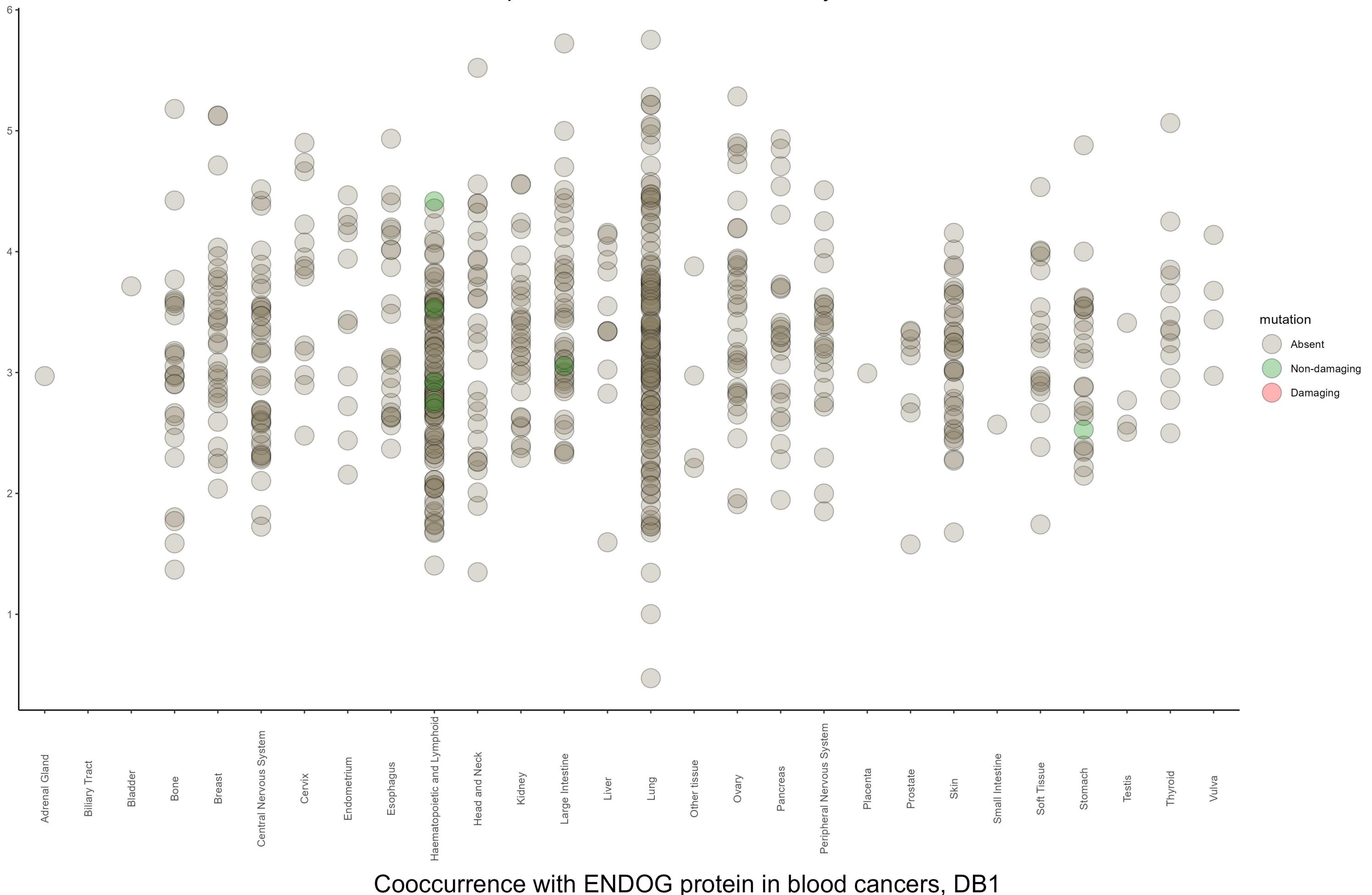
### Negative cooccurrence



### Positive cooccurrence



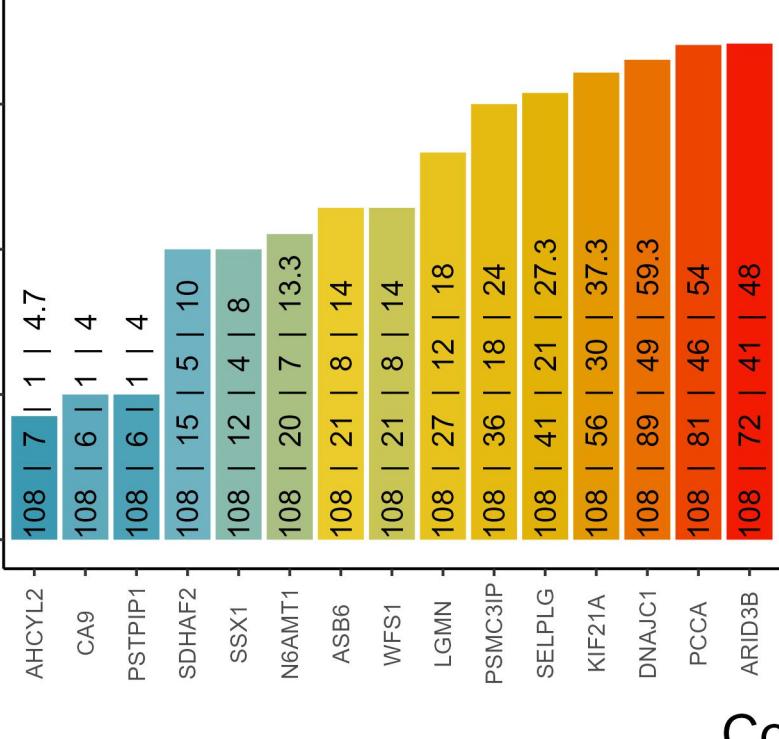
# Amount of ENDOG protein and mutation status by tissue, DB1



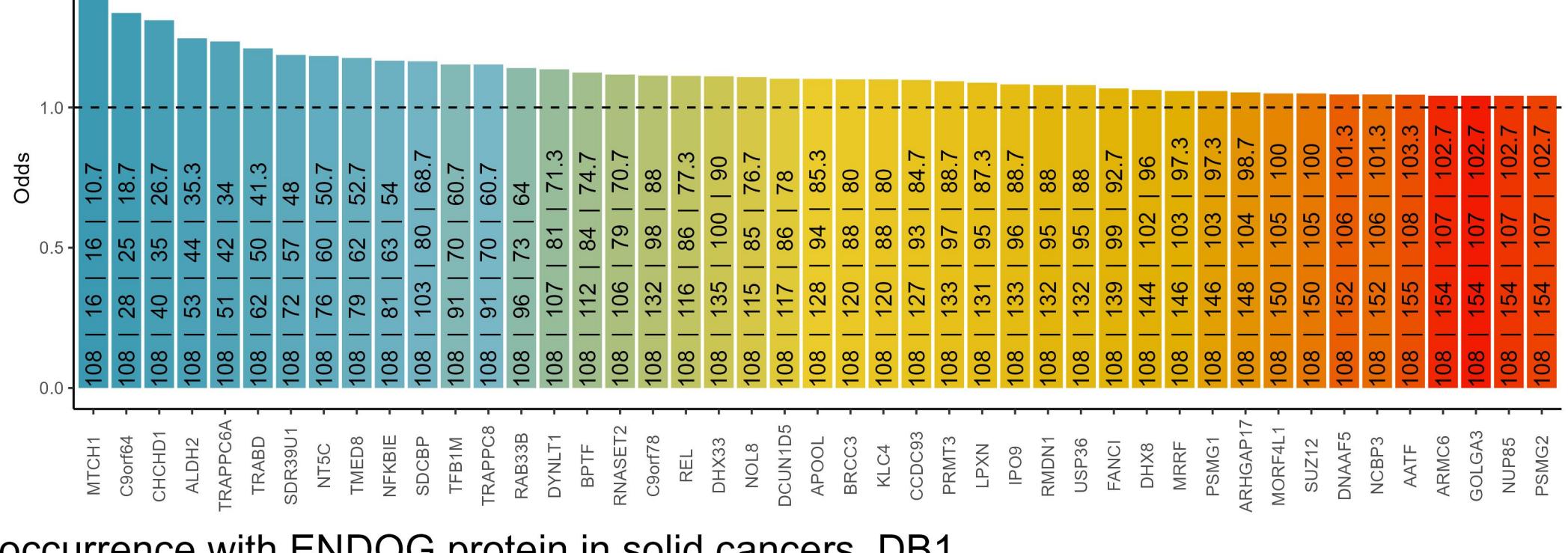
## Cooccurrence with ENDOG protein in blood cancers, DB1

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

Negative cooccurrence



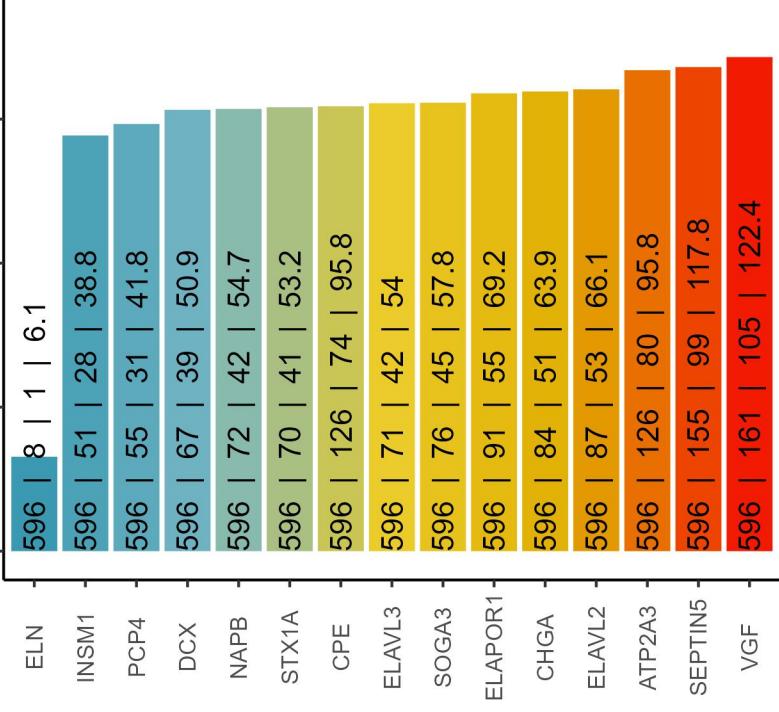
Positive cooccurrence



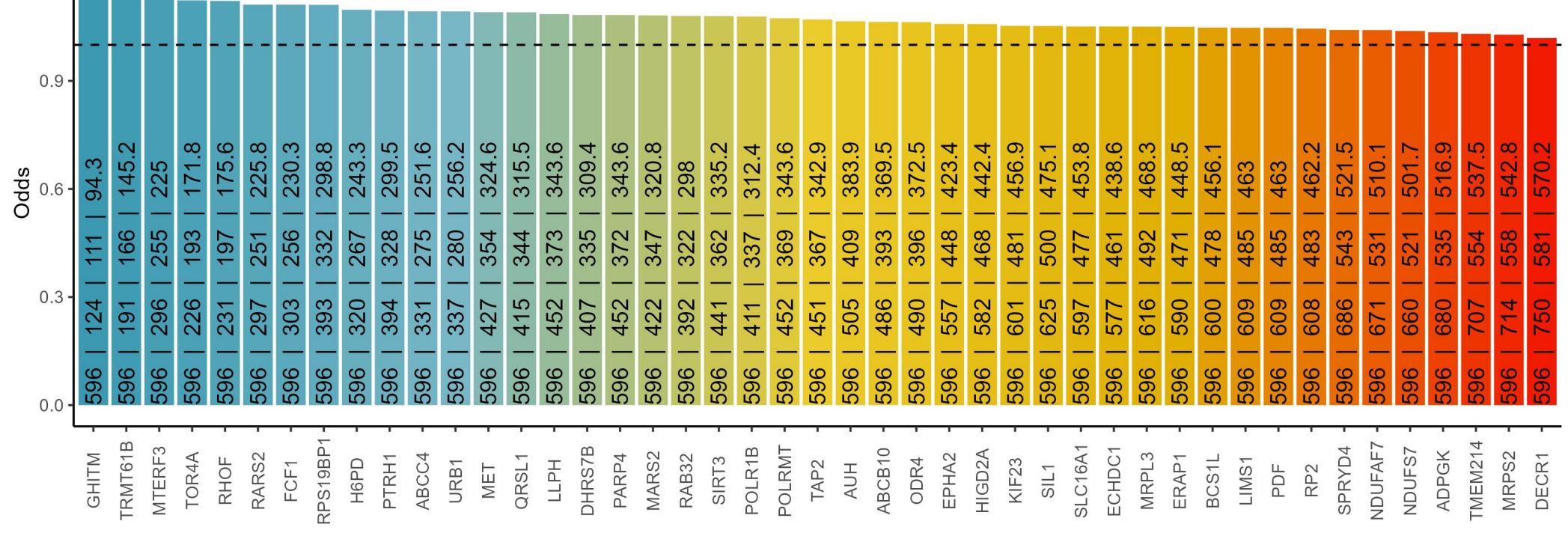
## Cooccurrence with ENDOG protein in solid cancers, DB1

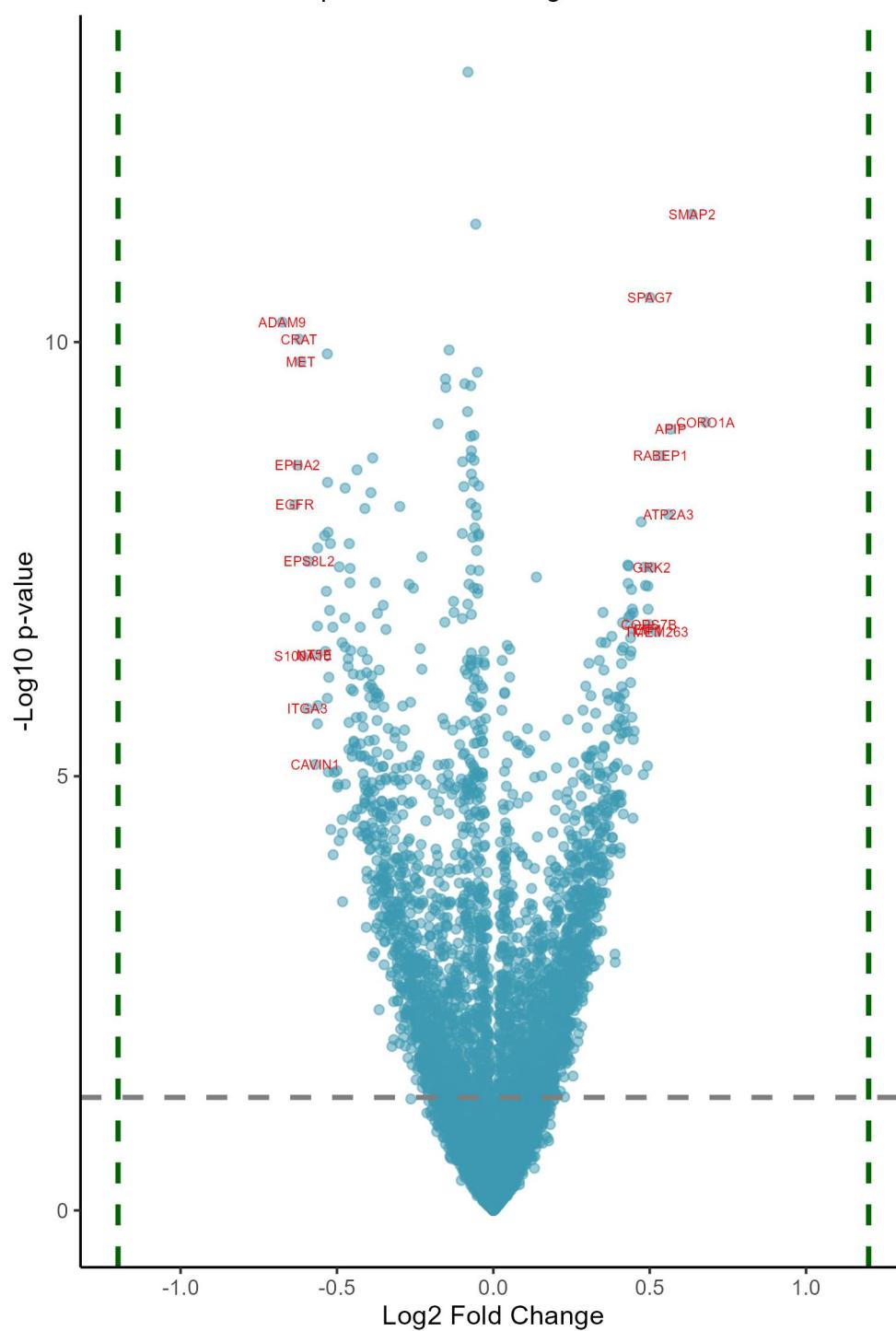
The text in the bars: incidence of ENDOG | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

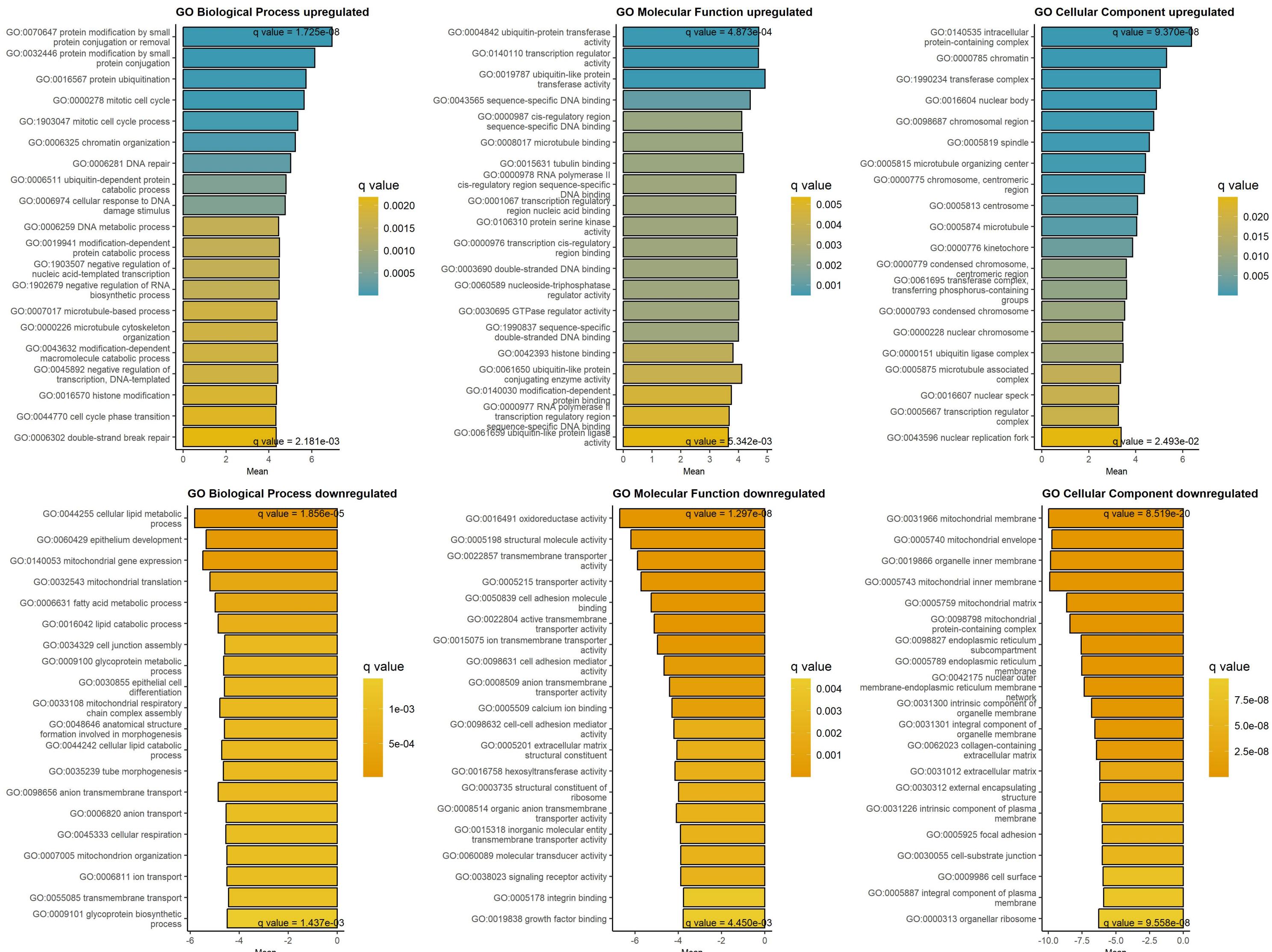


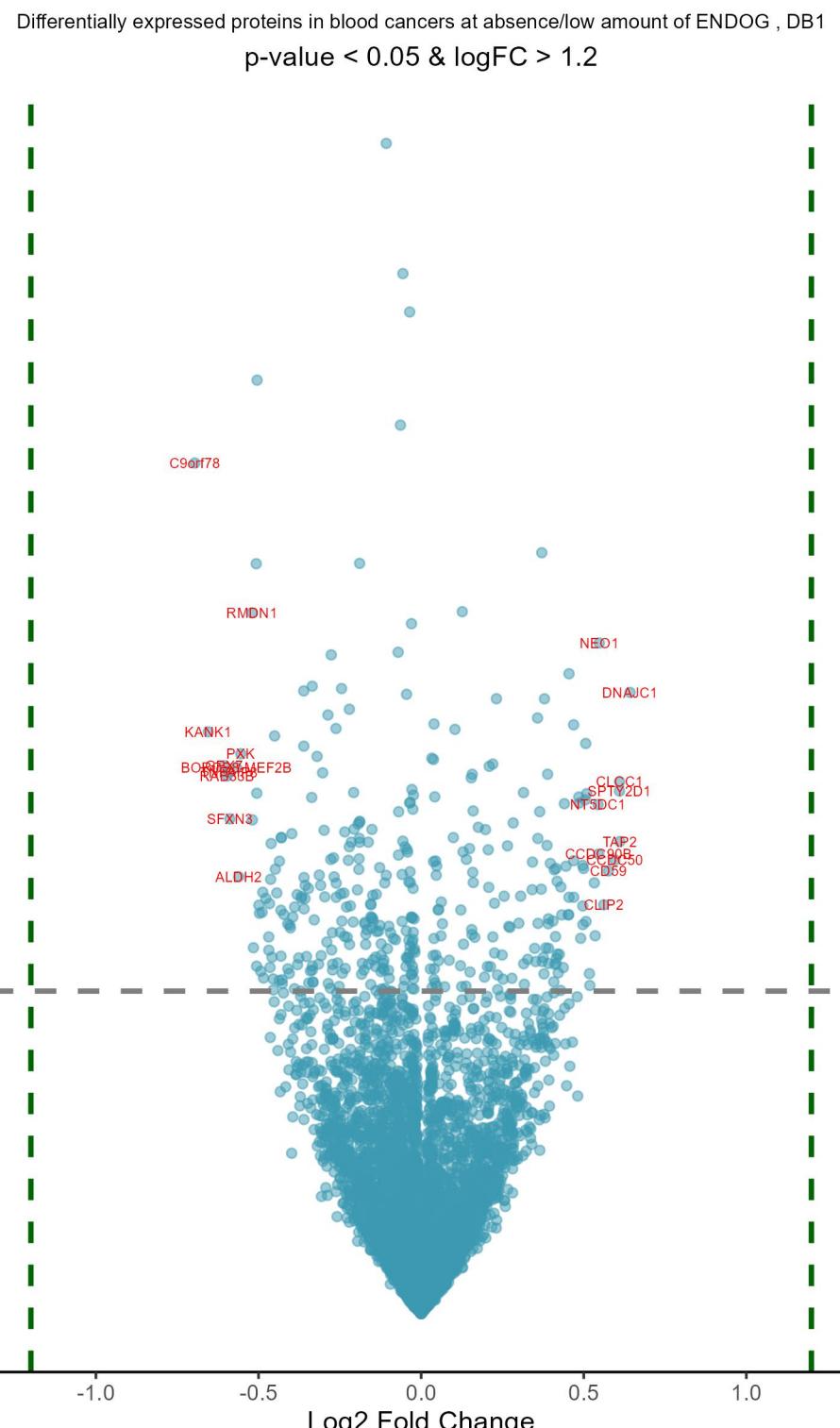


## Downregulated at low/absent ENDOG Upregulated at low/absent ENDOG

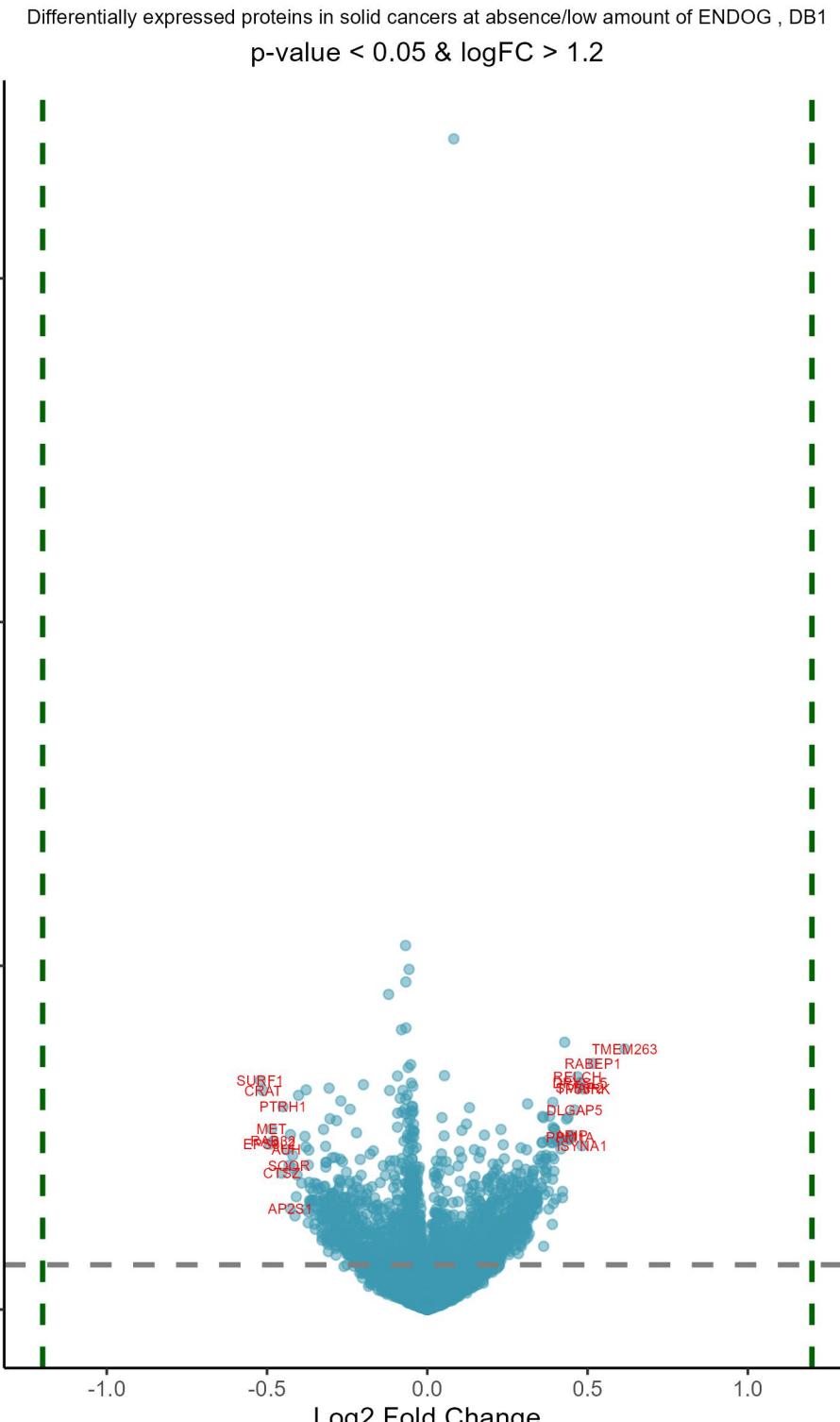
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.67	6.53e-08	ADAM9	ADAM metallopeptidase domain 9	0.68	3.22e-07	CORO1A	coronin 1A
-0.64	1.31e-06	EGFR	epidermal growth factor receptor	0.64	7.28e-09	SMAP2	small ArfGAP2
-0.63	6.22e-07	EPHA2	EPH receptor A2	0.57	3.52e-07	APIP	APAF1 interacting protein
-0.62	8.78e-08	CRAT	carnitine O-acetyltransferase	0.56	1.53e-06	ATP2A3	ATPase sarcoplasmic/endoplasmic ret
-0.62	1.12e-07	MET	MET proto-oncogene, receptor tyrosi	0.53	5.75e-07	RABEP1	rabaptin, RAB GTPase binding effect
-0.61	2.21e-05	S100A10	S100 calcium binding protein A10	0.52	1.38e-05	TMEM263	transmembrane protein 263
-0.59	5.79e-05	ITGA3	integrin subunit alpha 3	0.51	4.21e-06	GRK2	G protein-coupled receptor kinase 2
-0.59	3.91e-06	EPS8L2	EPS8 like 2	0.5	4.07e-08	SPAG7	sperm associated antigen 7
-0.57	2.18e-05	NT5E	5'-nucleotidase ecto	0.5	1.23e-05	COPS7B	COP9 signalosome subunit 7B
-0.57	1.72e-04	CAVIN1	caveolae associated protein 1	0.5	1.32e-05	EIF1	eukaryotic translation initiation f
-0.56	7.95e-05	GNG12	G protein subunit gamma 12	0.49	9.45e-06	HDHD2	haloacid dehalogenase like hydrolas
-0.56	1.27e-05	PPIC	peptidylprolyl isomerase C	0.49	5.89e-06	PPM1A	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> depe
-0.56	2.89e-06	CDCP1	CUB domain containing protein 1	0.49	1.75e-04	NACA2	nascent polypeptide associated comp
-0.56	5.51e-05	GPRC5A	G protein-coupled receptor class C	0.49	5.86e-06	TP53RK	TP53 regulating kinase
-0.54	2.28e-06	SFXN3	sideroflexin 3	0.48	4.21e-06	CDKN2C	cyclin dependent kinase inhibitor 2
-0.54	2.04e-05	GPX8	glutathione peroxidase 8 (putative)	0.48	2.03e-04	ABRACL	ABRA C-terminal like
-0.53	6.32e-06	RRAS	RAS related	0.47	1.78e-06	SZRD1	SUZ RNA binding domain containing 1
-0.53	1.01e-07	PTRH1	peptidyl-tRNA hydrolase 1 homolog	0.45	8.96e-05	PMF1	polyamine modulated factor 1
-0.53	4.72e-05	ITGA2	integrin subunit alpha 2	0.45	1.07e-04	STK4	serine/threonine kinase 4
-0.53	8.57e-07	ITGAV	integrin subunit alpha V	0.45	9.92e-06	RABEP2	rabaptin, RAB GTPase binding effect
-0.53	2.24e-06	SURF1	SURF1 cytochrome c oxidase assembly	0.45	4.33e-04	BLMH	bleomycin hydrolase
-0.53	1.94e-04	AP2S1	adaptor related protein complex 2 s	0.45	1.29e-05	MDP1	magnesium dependent phosphatase 1
-0.53	3.19e-05	MYOF	myoferlin	0.44	9.45e-06	INPPL1	inositol polyphosphate phosphatase
-0.52	9.62e-06	RAB32	RAB32, member RAS oncogene family	0.44	7.05e-05	HCLS1	hematopoietic cell-specific Lyn sub
-0.52	2.63e-06	NECTIN2	nectin cell adhesion molecule 2	0.44	6.10e-06	RBMM33	RNA binding motif protein 33
-0.52	5.54e-04	NQO1	NAD(P)H quinone dehydrogenase 1	0.44	2.04e-05	TAB1	TGF-beta activated kinase 1 (MAP3K7)
-0.51	1.28e-05	P4HA2	prolyl 4-hydroxylase subunit alpha	0.44	3.61e-05	KIAA1143	KIAA1143
-0.51	9.24e-04	S100A6	S100 calcium binding protein A6	0.44	1.60e-05	MYL6B	myosin light chain 6B
-0.51	1.96e-04	TGM2	transglutaminase 2	0.44	1.01e-05	RWDD4	RWD domain containing 4

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



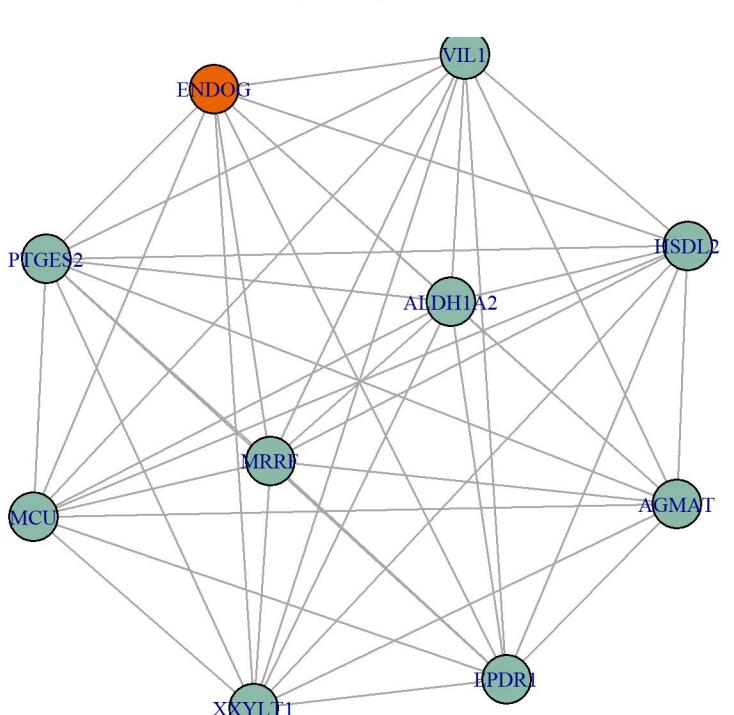


Downregulated in blood cancers at low/absent LENDG				Upregulated in blood cancers at low/absent LENDG			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.7	3.51e-01	C9orf78	chromosome 9 open reading frame 78	0.64	8.27e-01	DNAJC1	DnaJ heat shock protein family (Hsp
-0.65	8.27e-01	KANK1	KN motif and ankyrin repeat domains	0.61	8.27e-01	TAP2	transporter 2, ATP binding cassette
-0.61	8.27e-01	GPX7	glutathione peroxidase 7	0.61	8.27e-01	CLCC1	chloride channel CLIC like 1
-0.6	8.27e-01	RAB33B	RAB33B, member RAS oncogene family	0.61	8.27e-01	SPTY2D1	SPT2 chromatin protein domain conta
-0.59	8.27e-01	TNFAIP8	TNF alpha induced protein 8	0.6	8.27e-01	CCDC50	coiled-coil domain containing 50
-0.59	8.27e-01	SFXN3	sideroflexin 3	0.58	8.27e-01	CD59	CD59 molecule (CD59 blood group)
-0.57	8.27e-01	BORCS8-MEF2B	BORCS8-MEF2B readthrough	0.56	8.28e-01	CLIP2	CAP-Gly domain containing linker pr
-0.56	8.27e-01	ALDH2	aldehyde dehydrogenase 2 family mem	0.55	8.27e-01	NEO1	neogenin 1
-0.55	8.27e-01	PXK	PX domain containing serine/threoni	0.55	8.27e-01	CCDC90B	coiled-coil domain containing 90B
-0.52	8.24e-01	RMDN1	regulator of microtubule dynamics 1	0.54	8.27e-01	NT5DC1	5'-nucleotidase domain containing 1
-0.52	8.27e-01	SDCBP	syndecan binding protein	0.54	8.32e-01	PLCH1	phospholipase C eta 1
-0.52	8.48e-01	RNASET2	ribonuclease T2	0.53	8.27e-01	NUDT2	nudix hydrolase 2
-0.51	6.27e-01	C9orf64	chromosome 9 open reading frame 64	0.52	8.78e-01	IRF4	interferon regulatory factor 4
-0.51	8.48e-01	ICAM3	intercellular adhesion molecule 3	0.52	8.48e-01	PABPC1L	poly(A) binding protein cytoplasmic
-0.51	8.27e-01	PRMT3	protein arginine methyltransferase	0.51	8.27e-01	GMEB2	glucocorticoid modulatory element b
-0.5	2.28e-01	PSMG1	proteasome assembly chaperone 1	0.51	8.28e-01	ENTPD1	ectonucleoside triphosphate diphosp
-0.5	8.28e-01	TRAPPC4	trafficking protein particle comple	0.51	8.27e-01	HEXIM1	HEXIM P-TEFb complex subunit 1
-0.5	8.28e-01	NCF4	neutrophil cytosolic factor 4	0.5	8.27e-01	ENPP4	ectonucleotide pyrophosphatase/phos
-0.49	8.48e-01	MRPL30	mitochondrial ribosomal protein L30	0.5	8.27e-01	HLA-E	major histocompatibility complex, c
-0.49	8.28e-01	IAH1	isoamyl acetate hydrolyzing esteras	0.5	8.28e-01	SCARB2	scavenger receptor class B member 2
-0.49	8.27e-01	RAB11FIP1	RAB11 family interacting protein 1	0.5	8.27e-01	HDAC7	histone deacetylase 7
-0.48	8.63e-01	TRAPPC8	trafficking protein particle comple	0.5	8.28e-01	MSI2	musashi RNA binding protein 2
-0.48	8.27e-01	RASSF2	Ras association domain family membe	0.49	8.32e-01	ARID3B	AT-rich interaction domain 3B
-0.47	8.32e-01	TMED8	transmembrane p24 trafficking prote	0.49	8.27e-01	SNX18	sorting nexin 18
-0.47	8.48e-01	CTPS2	CTP synthase 2	0.48	8.27e-01	MPST	mercaptopyruvate sulfurtransferase
-0.47	8.28e-01	EXOSC3	exosome component 3	0.48	8.96e-01	SFN	stratin
-0.46	8.48e-01	LCK	LCK proto-oncogene, Src family tyro	0.48	8.88e-01	ISG20	interferon stimulated exonuclease g
-0.46	8.96e-01	ITGB2	integrin subunit beta 2	0.47	8.27e-01	SEL1L	SEL1L adaptor subunit of ERAD E3 ub
-0.46	8.27e-01	GCHFR	GTP cyclohydrolase I feedback regul	0.47	8.27e-01	ZGPAT	zinc finger CCCH-type and G-patch d

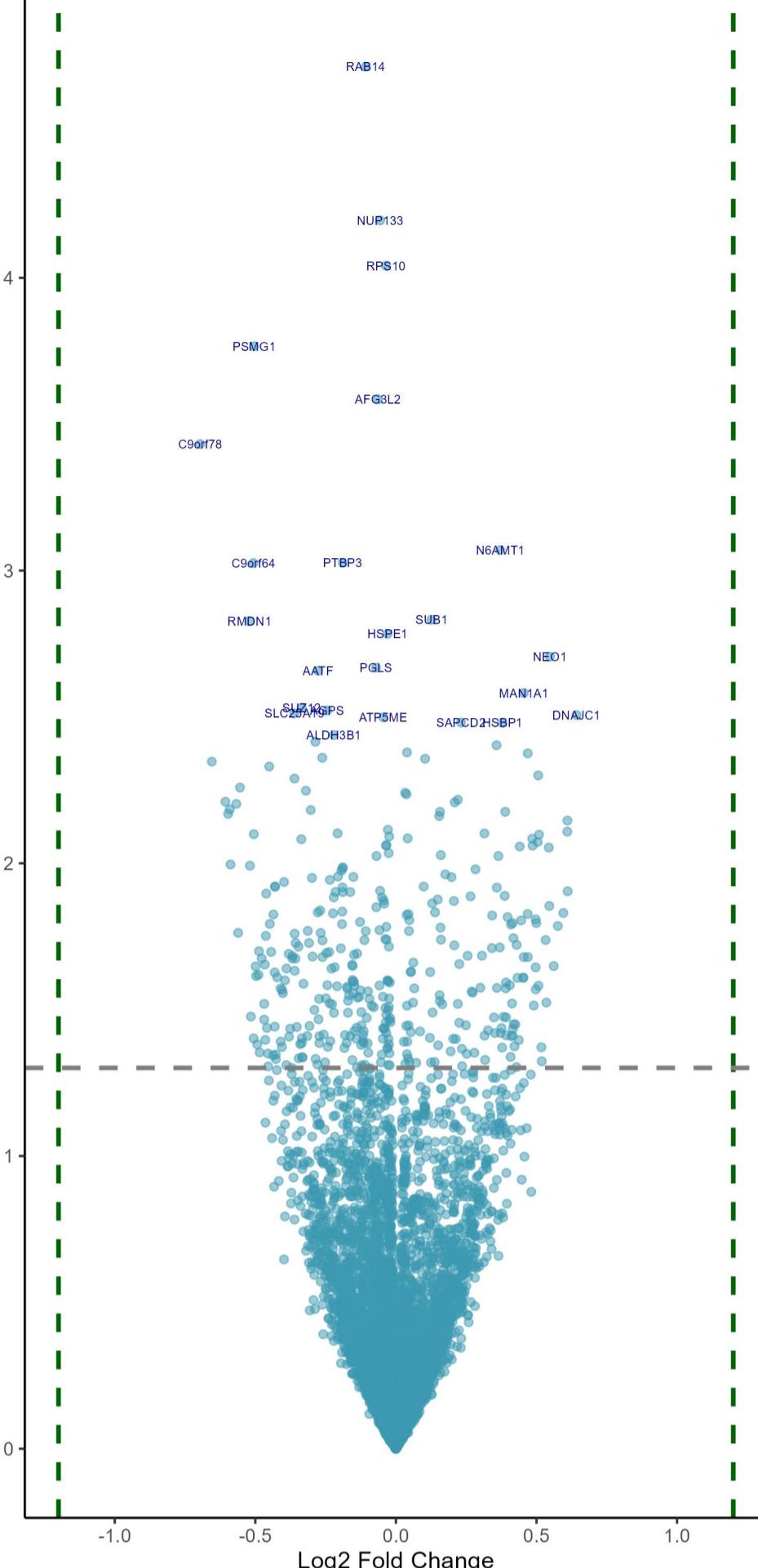


Downregulated in solid cancers at low/absent ENDOG				Upregulated in solid cancers at low/absent ENDOG			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.52	8.59e-05	SURF1	SURF1 cytochrome c oxidase assembly	0.62	1.75e-05	TMEM263	transmembrane protein 263
-0.51	1.02e-04	CRAT	carnitine O-acetyltransferase	0.52	4.16e-05	RABEP1	rabaptin, RAB GTPase binding effect
-0.49	1.05e-03	EPS8L2	EPS8 like 2	0.49	1.02e-04	TP53RK	TP53 regulating kinase
-0.49	5.65e-04	MET	MET proto-oncogene, receptor tyrosi	0.48	1.14e-03	ISYNA1	inositol-3-phosphate synthase 1
-0.48	9.20e-04	RAB32	RAB32, member RAS oncogene family	0.48	9.06e-05	DPYSL5	dihydropyrimidinase like 5
-0.45	3.91e-03	CTSZ	cathepsin Z	0.48	1.02e-04	SMAP2	small ArfGAP2
-0.45	2.21e-04	PTRH1	peptidyl-tRNA hydrolase 1 homolog	0.47	7.07e-05	RELCH	RAB11 binding and LisH domain, coil
-0.44	1.37e-03	AUH	AU RNA binding methylglutaconyl-CoA	0.46	2.47e-04	DLGAP5	DLG associated protein 5
-0.43	2.82e-03	SQOR	sulfide quinone oxidoreductase	0.45	7.36e-04	APIP	APAF1 interacting protein
-0.43	1.65e-02	AP2S1	adaptor related protein complex 2 s	0.45	7.95e-04	PPM1A	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> depe
-0.43	7.31e-04	HKDC1	hexokinase domain containing 1	0.44	8.56e-04	COPS7B	COP9 signalosome subunit 7B
-0.42	1.84e-03	ADAM9	ADAM metallopeptidase domain 9	0.44	8.66e-04	WDHD1	WD repeat and HMG-box DNA binding p
-0.42	3.18e-03	SCO2	synthesis of cytochrome C oxidase 2	0.44	3.29e-04	INPPL1	inositol polyphosphate phosphatase
-0.41	2.23e-02	GPRC5A	G protein-coupled receptor class C	0.43	3.50e-04	MYL6B	myosin light chain 6B
-0.41	1.03e-02	ATP5MF	ATP synthase membrane subunit f	0.43	1.24e-05	SPAG7	sperm associated antigen 7
-0.41	4.23e-03	AKR1C3	aldo-keto reductase family 1 member	0.42	8.19e-03	NACA2	nascent polypeptide associated comp
-0.4	1.31e-04	TST	thiosulfate sulfurtransferase	0.42	1.07e-02	DPYSL3	dihydropyrimidinase like 3
-0.39	5.75e-03	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer	0.42	8.66e-04	MAP1A	microtubule associated protein 1A
-0.38	7.72e-04	DNAJC1	DnaJ heat shock protein family (Hsp	0.42	1.34e-03	EIF1	eukaryotic translation initiation f
-0.38	1.21e-03	MARS2	methionyl-tRNA synthetase 2, mitoch	0.41	8.66e-04	RBM33	RNA binding motif protein 33
-0.38	1.69e-02	KRT73	keratin 73	0.4	9.24e-04	PRCC	proline rich mitotic checkpoint con
-0.38	1.02e-04	TEX264	testis expressed 264, ER-phagy rece	0.4	1.13e-02	CPVL	carboxypeptidase vitellogenin like
-0.37	3.02e-02	CD44	CD44 molecule (Indian blood group)	0.4	5.65e-04	SZRD1	SUZ RNA binding domain containing 1
-0.37	2.76e-03	RHOF	ras homolog family member F, filopo	0.4	5.65e-04	MDP1	magnesium dependent phosphatase 1
-0.37	1.38e-03	SIRT3	sirtuin 3	0.4	3.60e-03	CRMP1	collapsin response mediator protein
-0.37	1.94e-02	LGALS3	galectin 3	0.39	2.11e-03	TAB1	TGF-beta activated kinase 1 (MAP3K7
-0.37	5.69e-03	ITGB5	integrin subunit beta 5	0.39	1.31e-02	TUBB2B	tubulin beta 2B class IIb
-0.37	1.21e-02	MRPS18C	mitochondrial ribosomal protein S18	0.39	9.80e-04	AAMDC	adipogenesis associated Mth938 doma
-0.37	1.21e-02	ERH2	ERH receptor A2	0.39	5.36e-04	KLC2	kinasin light chain 2

ENDOG network DB1 all Pearson r > 0.3

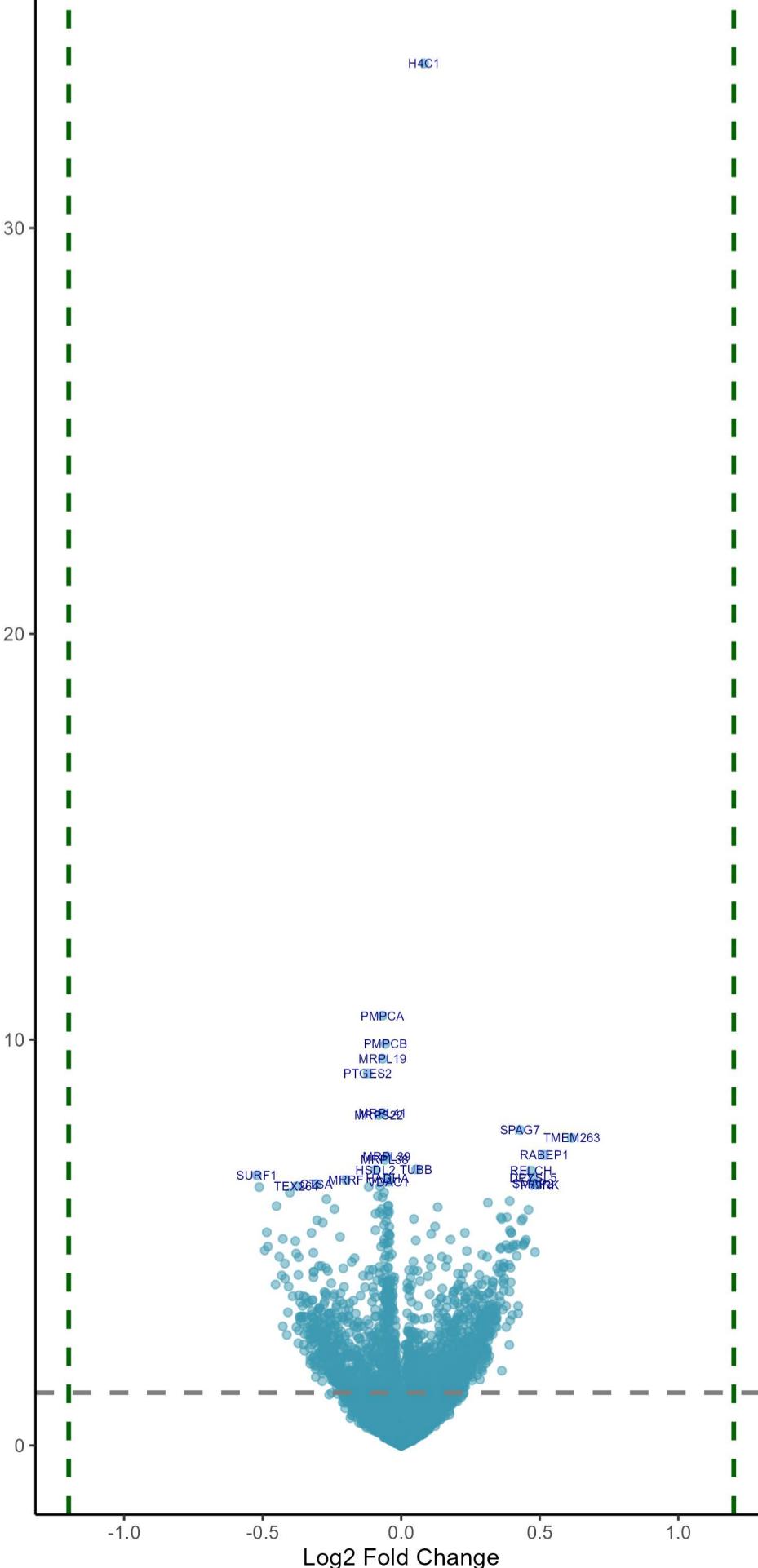


Sorted by p values!  
 Downregulated in blood cancers at low/absent ENDOG      Upregulated in blood cancers at low/absent ENDOG



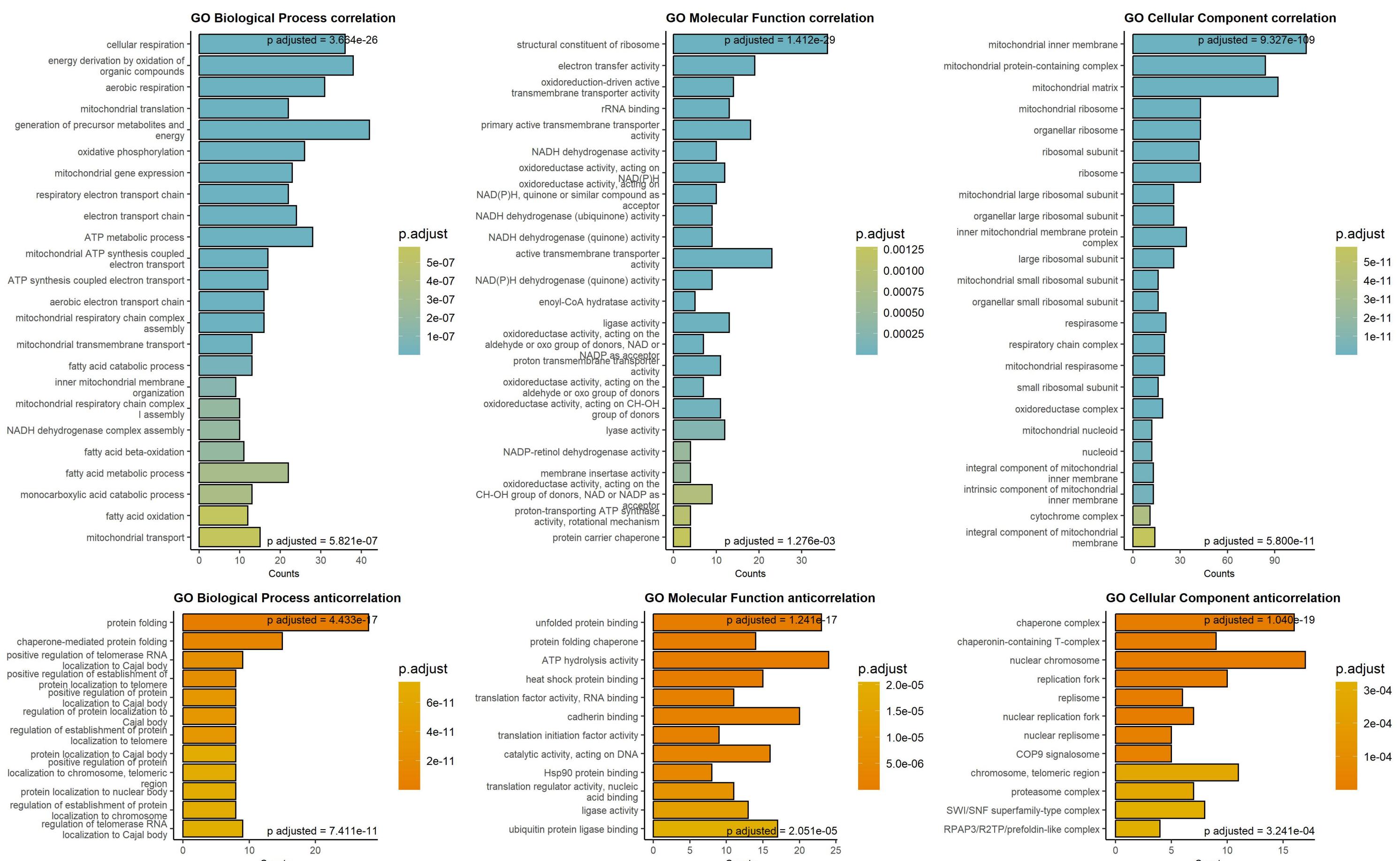
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.11	6.31e-02	RAB14	RAB14, member RAS oncogene family	0.37	6.27e-01	N6AMT1	N-6 adenine-specific DNA methyltran
-0.06	1.41e-01	NUP133	nucleoporin 133	0.13	8.24e-01	SUB1	SUB1 regulator of transcription
-0.04	1.51e-01	RPS10	ribosomal protein S10	0.55	8.27e-01	NEO1	neogenin 1
-0.5	2.28e-01	PSMG1	proteasome assembly chaperone 1	0.45	8.27e-01	MAN1A1	mannosidase alpha class 1A member 1
-0.06	2.88e-01	AFG3L2	AFG3 like matrix AAA peptidase subu	0.64	8.27e-01	DNAJC1	DnaJ heat shock protein family (Hsp
-0.7	3.51e-01	C9orf78	chromosome 9 open reading frame 78	0.23	8.27e-01	SAPCD2	suppressor APC domain containing 2
-0.19	6.27e-01	PTBP3	polypyrimidine tract binding protei	0.38	8.27e-01	HSBP1	heat shock factor binding protein 1
-0.51	6.27e-01	C9orf64	chromosome 9 open reading frame 64	0.36	8.27e-01	MVB12A	multivesicular body subunit 12A
-0.52	8.24e-01	RMDN1	regulator of microtubule dynamics 1	0.04	8.27e-01	VBP1	VHL binding protein 1
-0.03	8.27e-01	HSPE1	heat shock protein family E (Hsp10)	0.47	8.27e-01	ZGPAT	zinc finger CCCH-type and G-patch d
-0.07	8.27e-01	PGLS	6-phosphogluconolactonase	0.1	8.27e-01	DOHH	deoxyhypusine hydroxylase
-0.28	8.27e-01	AATF	apoptosis antagonizing transcriptio	0.51	8.27e-01	HEXIM1	HEXIM P-TEFb complex subunit 1
-0.34	8.27e-01	SUZ12	SUZ12 polycomb repressive complex 2	0.03	8.27e-01	ENO1	enolase 1
-0.24	8.27e-01	AGPS	alkylglycerone phosphate synthase	0.04	8.27e-01	PFDN6	prefoldin subunit 6
-0.36	8.27e-01	SLC25A19	solute carrier family 25 member 19	0.22	8.27e-01	JMY	junction mediating and regulatory p
-0.04	8.27e-01	ATP5ME	ATP synthase membrane subunit e	0.21	8.27e-01	APMAP	adipocyte plasma membrane associate
-0.22	8.27e-01	ALDH3B1	aldehyde dehydrogenase 3 family mem	0.39	8.27e-01	SLAMF7	SLAM family member 7
-0.29	8.27e-01	PSMG2	proteasome assembly chaperone 2	0.16	8.27e-01	PLXNA1	plexin A1
-0.26	8.27e-01	NUP85	nucleoporin 85	0.15	8.27e-01	MCC	MCC regulator of WNT signaling path
-0.65	8.27e-01	KANK1	KN motif and ankyrin repeat domains	0.61	8.27e-01	CLCC1	chloride channel CLIC like 1
-0.45	8.27e-01	DHX33	DEAH-box helicase 33	0.61	8.27e-01	SPTY2D1	SPT2 chromatin protein domain conta
-0.36	8.27e-01	VAT1	vesicle amine transport 1	0.31	8.27e-01	TIMM9	translocase of inner mitochondrial
-0.55	8.27e-01	PXK	PX domain containing serine/threoni	0.51	8.27e-01	GMEB2	glucocorticoid modulatory element b
-0.32	8.27e-01	CTR9	CTR9 homolog, Paf1/RNA polymerase I	0.04	8.27e-01	PFDN5	prefoldin subunit 5
-0.61	8.27e-01	GPX7	glutathione peroxidase 7	0.48	8.27e-01	MPST	mercaptopyruvate sulfurtransferase
-0.57	8.27e-01	BORCS8-MEF2B	BORCS8-MEF2B readthrough	0.5	8.27e-01	ENPP4	ectonucleotide pyrophosphatase/phos
-0.59	8.27e-01	TNFAIP8	TNF alpha induced protein 8	0.49	8.27e-01	SNX18	sorting nexin 18
-0.3	8.27e-01	GHITM	growth hormone inducible transmembr	0.44	8.27e-01	ITM2C	integral membrane protein 2C
-0.6	8.27e-01	RAB33B	RAB33B, member RAS oncogene family	0.54	8.27e-01	NT5DC1	5'-nucleotidase domain containing 1
-0.03	8.27e-01	RPS23	ribosomal protein S23	0.16	8.27e-01	RHOB	ras homolog family member B
-0.21	8.27e-01	IGHG4	immunoglobulin heavy constant gamma	0.36	8.27e-01	FLOT1	flotillin 1
-0.51	8.27e-01	PRMT3	protein arginine methyltransferase	0.28	8.27e-01	FKBP5	FKBP prolyl isomerase 5
-0.02	8.27e-01	RPS13	ribosomal protein S13	0.18	8.27e-01	CA9	carbonic anhydrase 9
-0.34	8.27e-01	P4HA2	prolyl 4-hydroxylase subunit alpha	0.2	8.27e-01	PTPRK	protein tyrosine phosphatase recept
-0.03	8.27e-01	RPL21	ribosomal protein L21	0.1	8.27e-01	SAMD4B	sterile alpha motif domain containi
-0.04	8.27e-01	COX4I1	cytochrome c oxidase subunit 4I1	0.36	8.27e-01	PXN	paxillin
-0.03	8.27e-01	RPL10A	ribosomal protein L10a	0.61	8.27e-01	TAP2	transporter 2, ATP binding cassette
-0.07	8.27e-01	MTHFD1L	methylenetetrahydrofolate dehydroge	0.39	8.27e-01	TJAP1	tight junction associated protein 1
0.50	8.27e-01	SEYNN3	ciderolexin 3	0.27	8.27e-01	SSY1	SSY family member 1

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

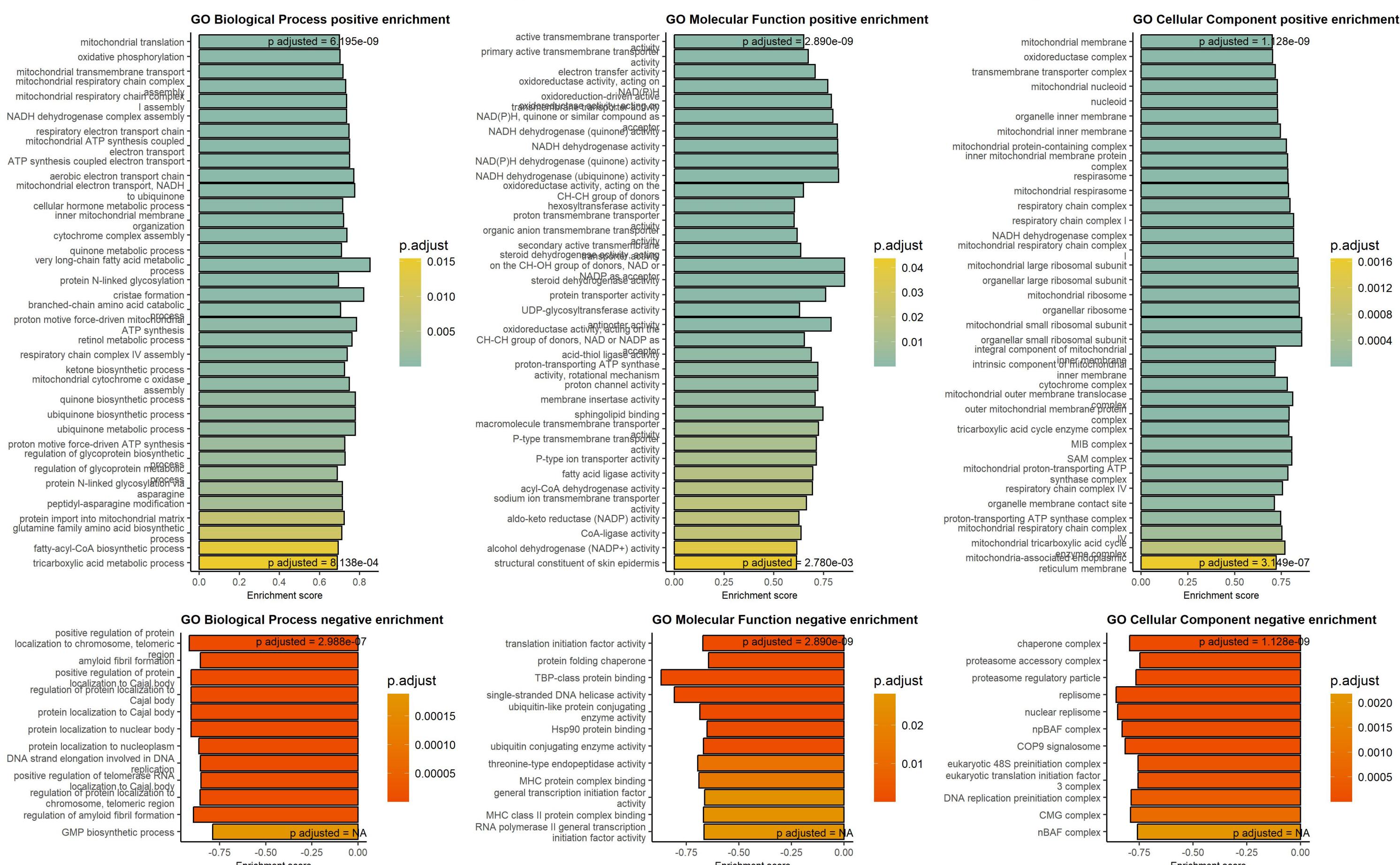


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.07	5.70e-08	PMPCA	peptidase, mitochondrial processing	0.08	2.91e-31	H4C1	H4 clustered histone 1
-0.06	2.11e-07	PMPCB	peptidase, mitochondrial processing	0.43	1.24e-05	SPAG7	sperm associated antigen 7
-0.07	3.93e-07	MRPL19	mitochondrial ribosomal protein L19	0.62	1.75e-05	TMEM263	transmembrane protein 263
-0.12	7.52e-07	PTGES2	prostaglandin E synthase 2	0.52	4.16e-05	RABEP1	rabaptin, RAB GTPase binding effect
-0.07	6.03e-06	MRPL41	mitochondrial ribosomal protein L41	0.05	7.07e-05	TUBB	tubulin beta class I
-0.08	6.03e-06	MRPS22	mitochondrial ribosomal protein S22	0.47	7.07e-05	RELCH	RAB11 binding and LisH domain, coil
-0.05	4.16e-05	MRPL39	mitochondrial ribosomal protein L39	0.48	9.06e-05	DPYSL5	dihydropyrimidinase like 5
-0.06	4.67e-05	MRPL38	mitochondrial ribosomal protein L38	0.48	1.02e-04	SMAP2	small ArfGAP2
-0.09	7.07e-05	HSDL2	hydroxysteroid dehydrogenase like 2	0.49	1.02e-04	TP53RK	TP53 regulating kinase
-0.52	8.59e-05	SURF1	SURF1 cytochrome c oxidase assembly	0.39	1.85e-04	SEPTIN5	septin 5
-0.05	9.06e-05	HADHA	hydroxyacyl-CoA dehydrogenase triflu	0.31	1.98e-04	FSD1	fibronectin type III and SPRY domai
-0.2	9.56e-05	MRRF	mitochondrial ribosome recycling fa	0.13	2.29e-04	AIP	aryl hydrocarbon receptor interacti
-0.05	1.00e-04	VDAC1	voltage dependent anion channel 1	0.46	2.47e-04	DLGAP5	DLG associated protein 5
-0.31	1.02e-04	CTSA	cathepsin A	0.38	3.21e-04	C1orf198	chromosome 1 open reading frame 198
-0.38	1.02e-04	TEX264	testis expressed 264, ER-phagy rece	0.36	3.21e-04	BPGM	bisphosphoglycerate mutase
-0.08	1.02e-04	MRPS23	mitochondrial ribosomal protein S23	0.44	3.29e-04	INPPL1	inositol polyphosphate phosphatase
-0.12	1.02e-04	SURF6	surfeit 6	0.05	3.29e-04	YWHAE	tyrosine 3-monooxygenase/trypophan
-0.51	1.02e-04	CRAT	carnitine O-acetyltransferase	0.36	3.29e-04	HMG20B	high mobility group 20B
-0.06	1.31e-04	ALDH18A1	aldehyde dehydrogenase 18 family me	0.43	3.50e-04	MYL6B	myosin light chain 6B
-0.4	1.31e-04	TST	thiosulfate sulfurtransferase	0.12	4.49e-04	TBC1D24	TBC1 domain family member 24
-0.08	1.53e-04	POLDIP2	DNA polymerase delta interacting pr	0.39	5.36e-04	KLC2	kinesin light chain 2
-0.07	1.57e-04	SLC25A3	solute carrier family 25 member 3	0.4	5.65e-04	MDP1	magnesium dependent phosphatase 1
-0.27	1.72e-04	DECRI	2,4-dienoyl-CoA reductase 1	0.4	5.65e-04	SZRD1	SUZ RNA binding domain containing 1
-0.05	2.21e-04	MRPL17	mitochondrial ribosomal protein L17	0.23	5.65e-04	TTC5	tetratricopeptide repeat domain 5
-0.45	2.21e-04	PTRH1	peptidyl-tRNA hydrolase 1 homolog	0.11	5.83e-04	PRRC2A	proline rich coiled-coil 2A
-0.05	2.21e-04	HADHB	hydroxyacyl-CoA dehydrogenase triflu	0.18	7.36e-04	CBFA2T2	CBFA2/RUNX1 partner transcriptional
-0.07	2.43e-04	MRPL15	mitochondrial ribosomal protein L15	0.45	7.36e-04	APIP	APAF1 interacting protein
-0.24	2.43e-04	ITGAV	integrin subunit alpha V	0.05	7.56e-04	NUMA1	nuclear mitotic apparatus protein 1
-0.05	2.57e-04	MRPL13	mitochondrial ribosomal protein L13	0.45	7.95e-04	PPM1A	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> depe
-0.04	2.65e-04	MRPS28	mitochondrial ribosomal protein S28	0.44			

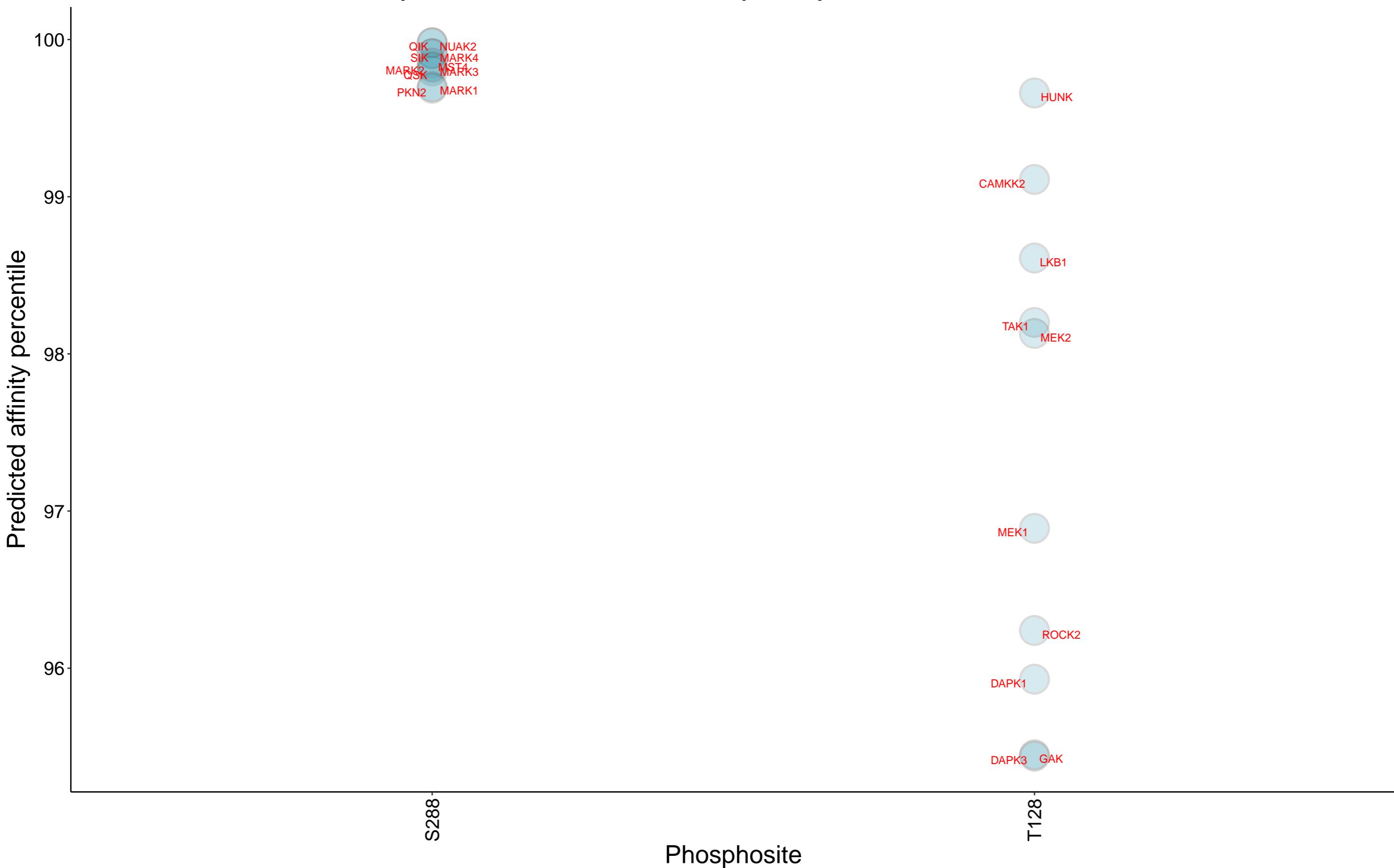
# Top 250 correlation coefficients overrepresentation, ENDOG protein, DB1



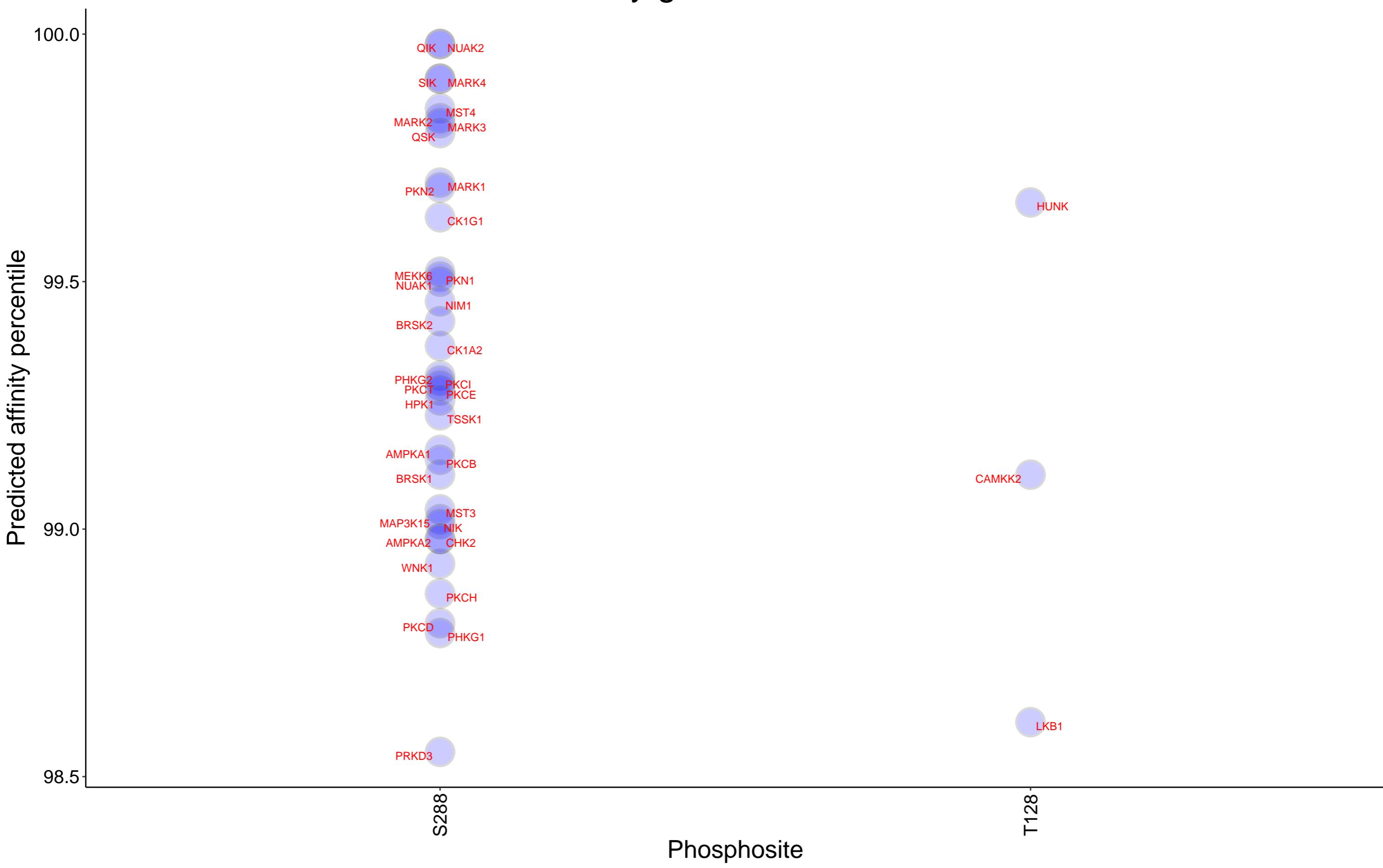
## Gene Set Enrichment analysis on protein correlation coefficients, ENDOG protein, DB1



# Top 10 kinases for each phosphosite in ENDOG



## Kinases with affinity greater than 98.5% to ENDOG



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

Beware of false positives in tissues with small number of samples

