

# CENPX

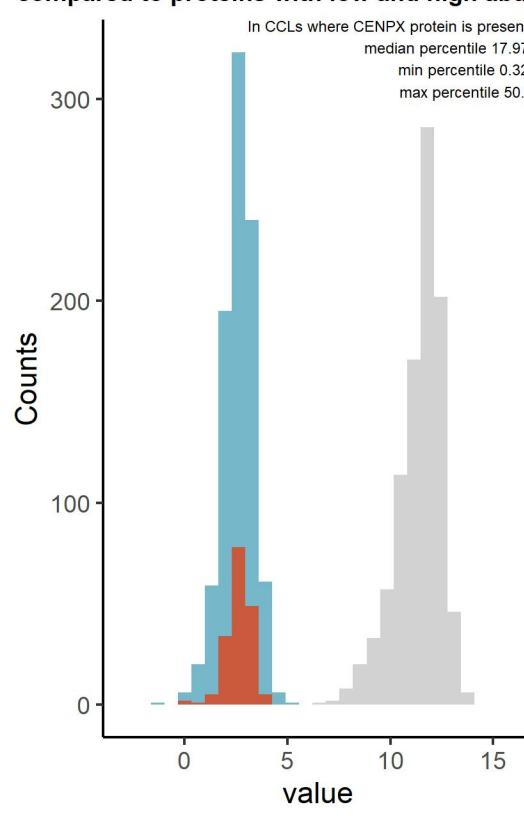
Protein name: CENPX ; UNIPROT: A8MT69 ; Gene name: centromere protein X

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

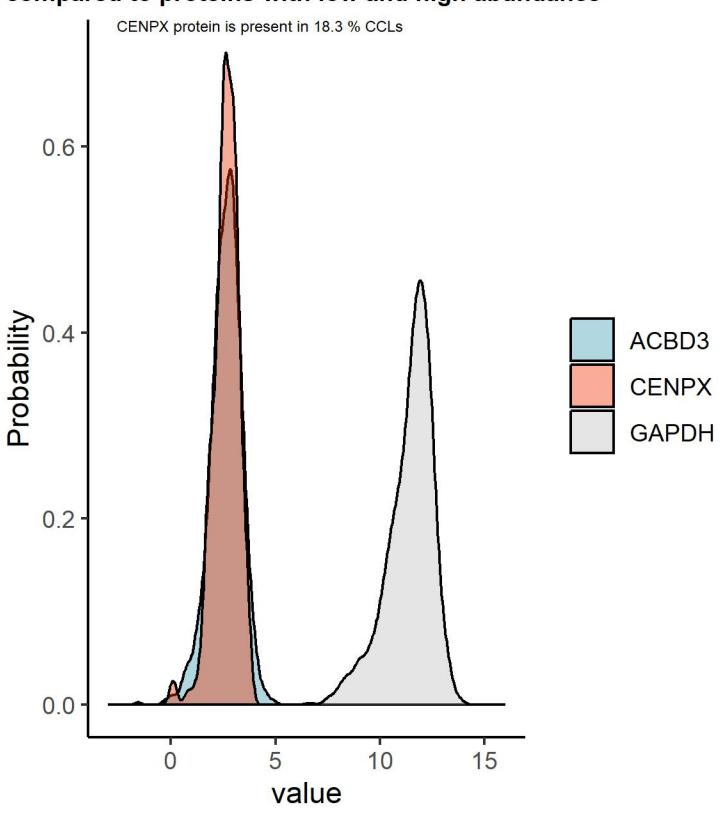
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

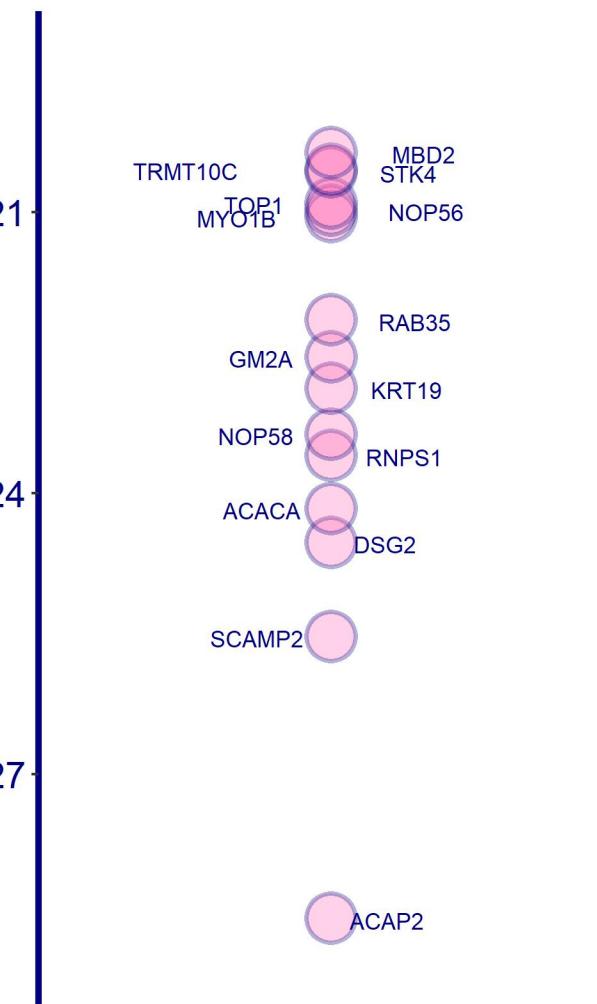
Histogram of CENPX protein compared to proteins with low and high abundance



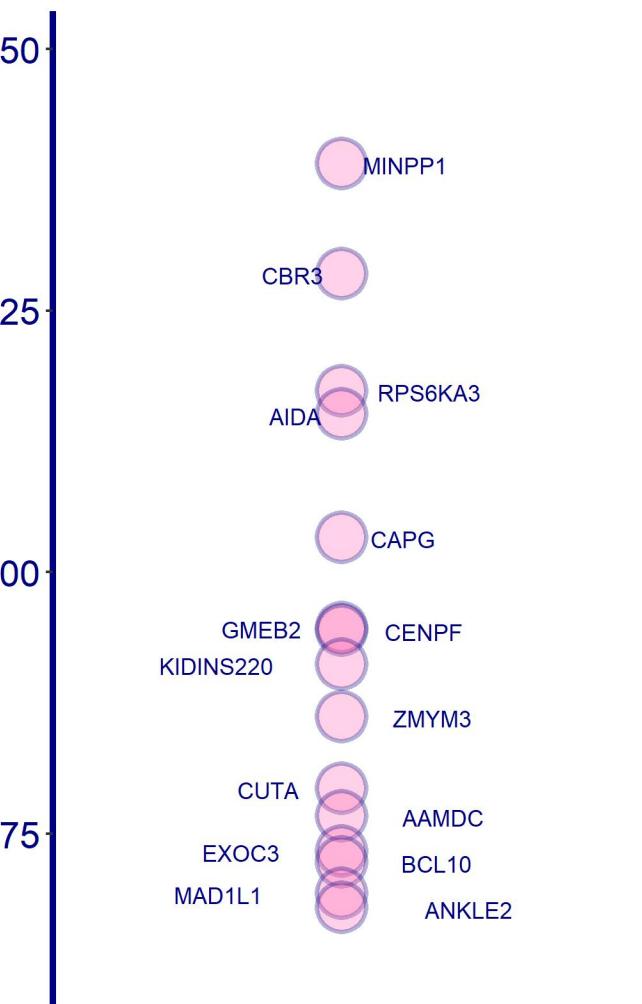
Density plot of CENPX protein compared to proteins with low and high abundance



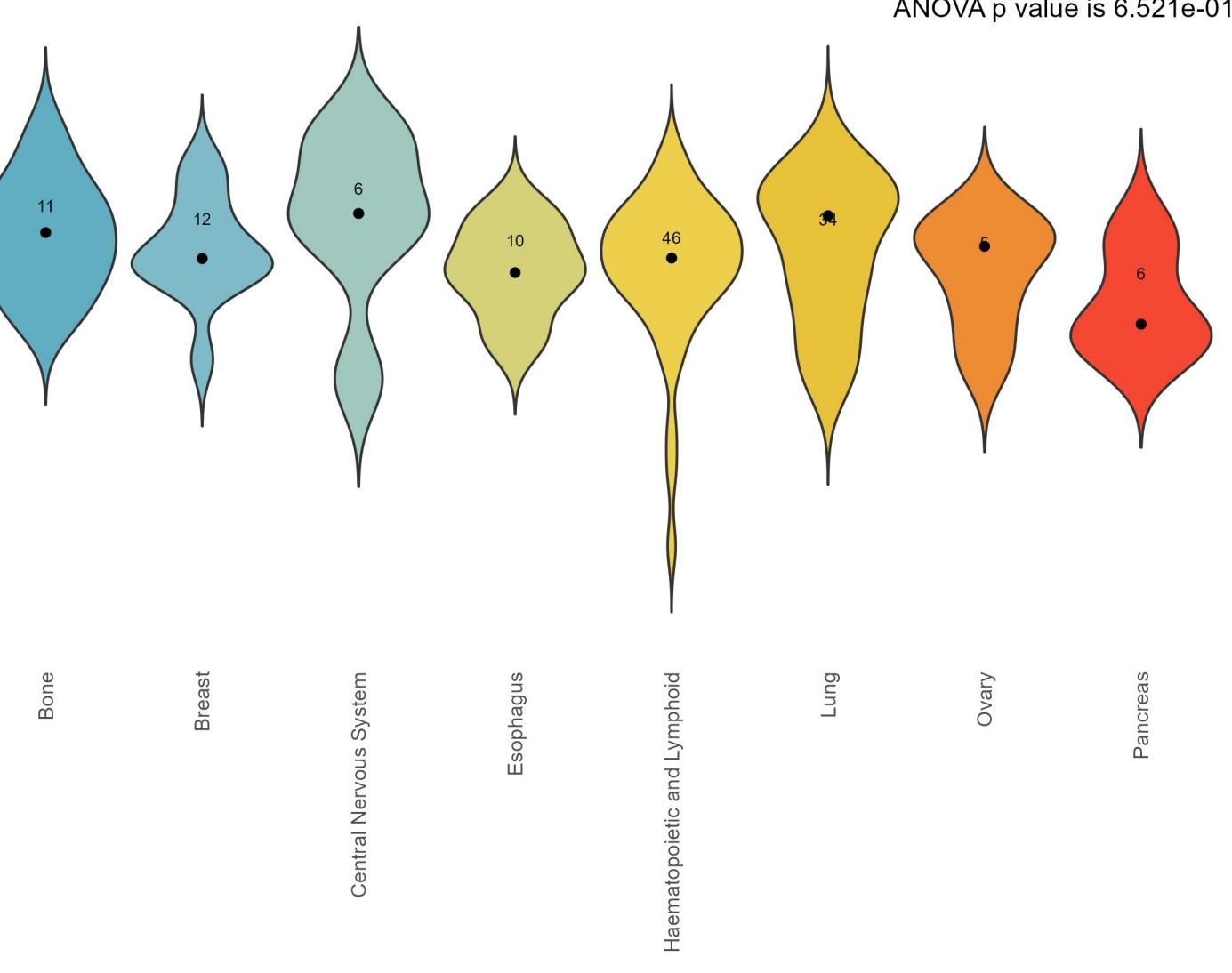
Top negative correlations of CENPX protein, DB1



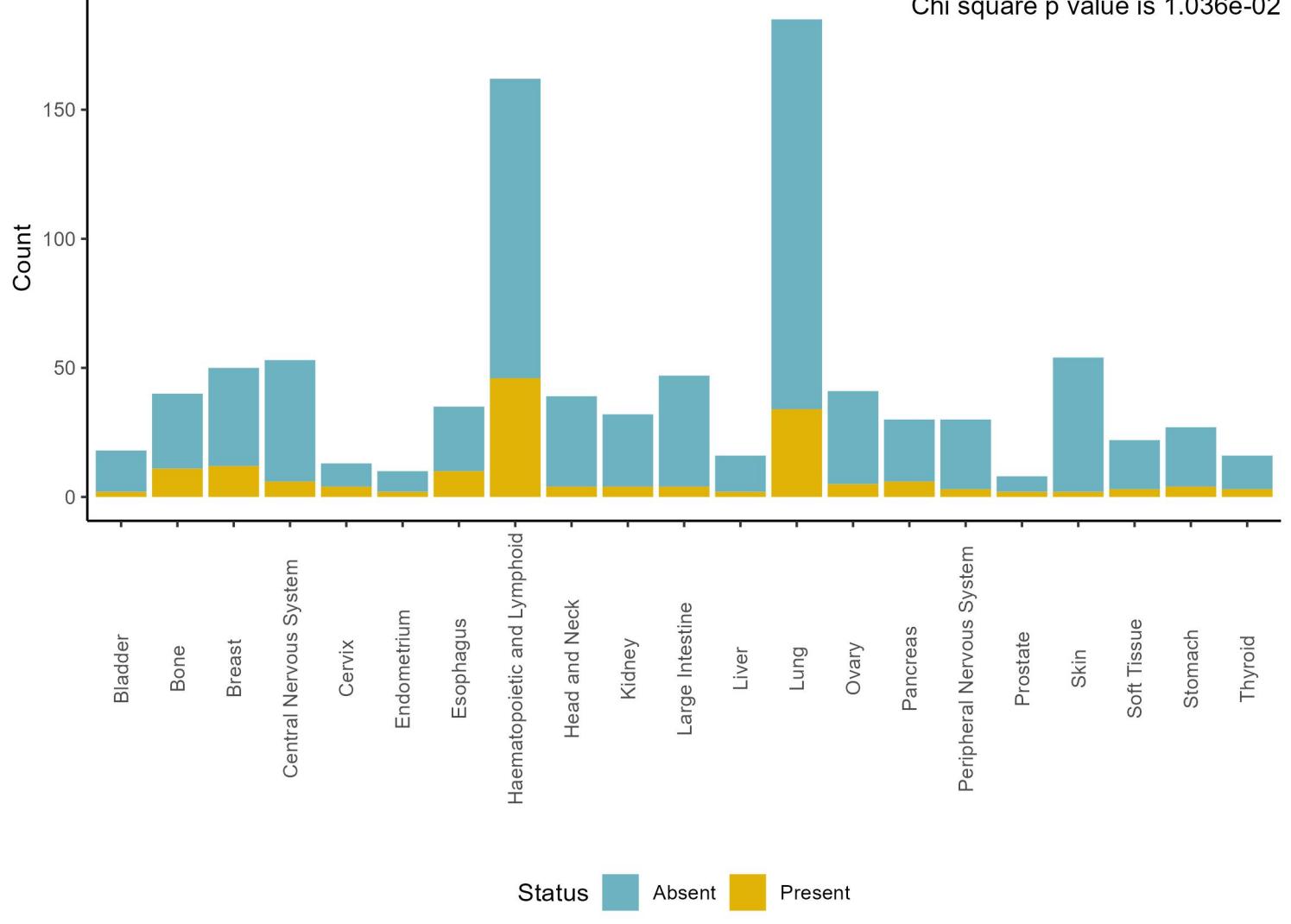
Top positive correlations of CENPX protein, DB1



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



Present and absent CENPX protein counts by tissue, DB1

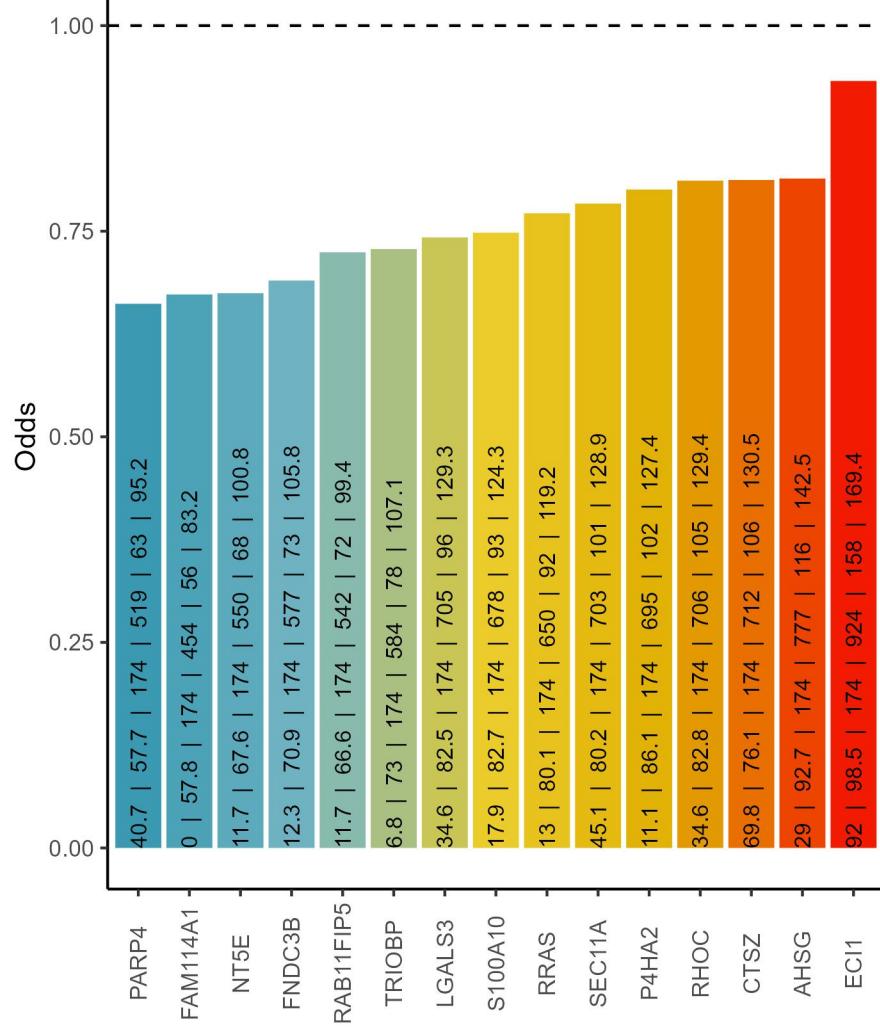


## Cooccurrence with CENPX protein, DB1

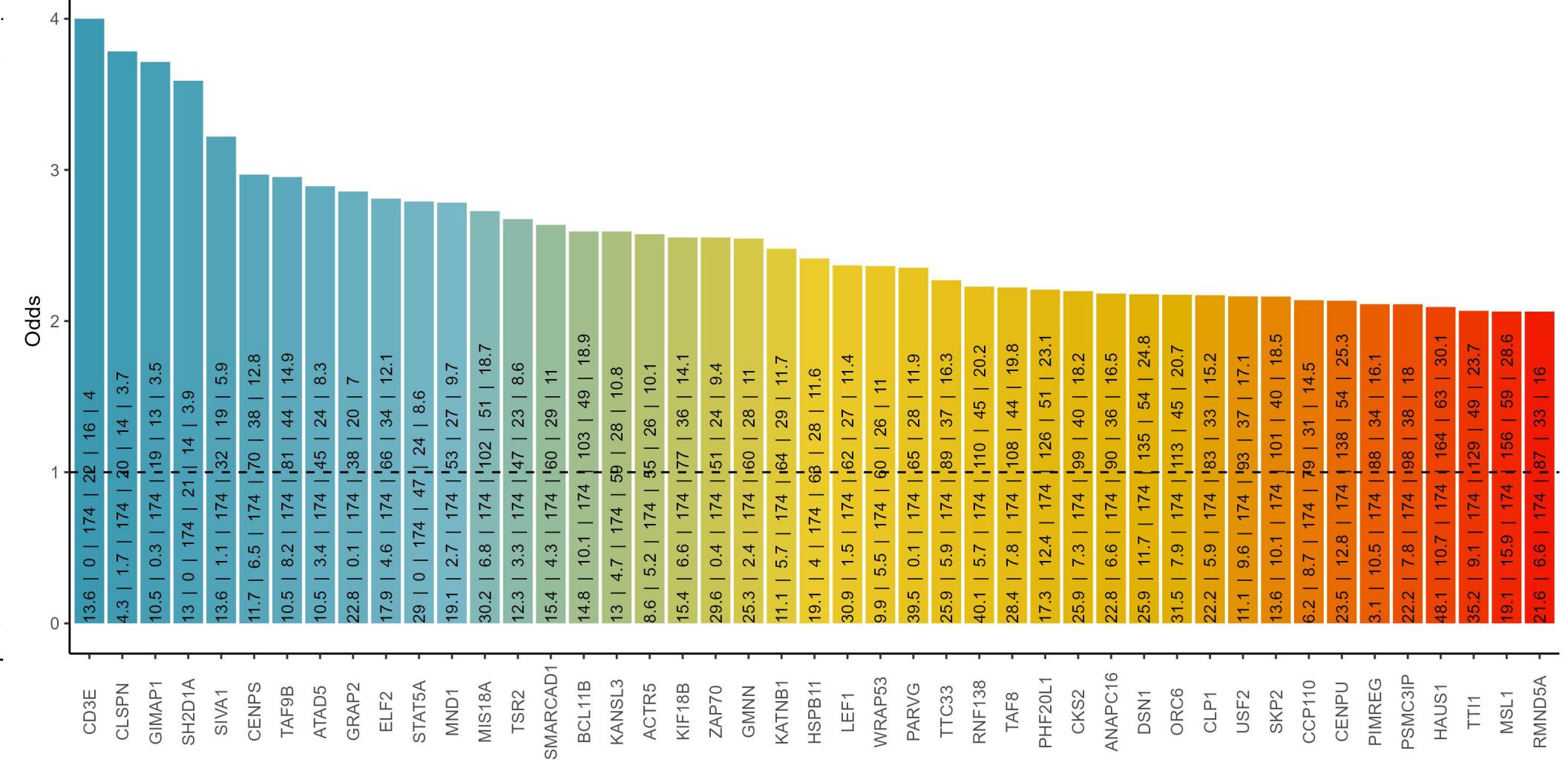
% of CENPX in blood cancers: 28.4 ; % of CENPX in solid cancers: 16.3

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

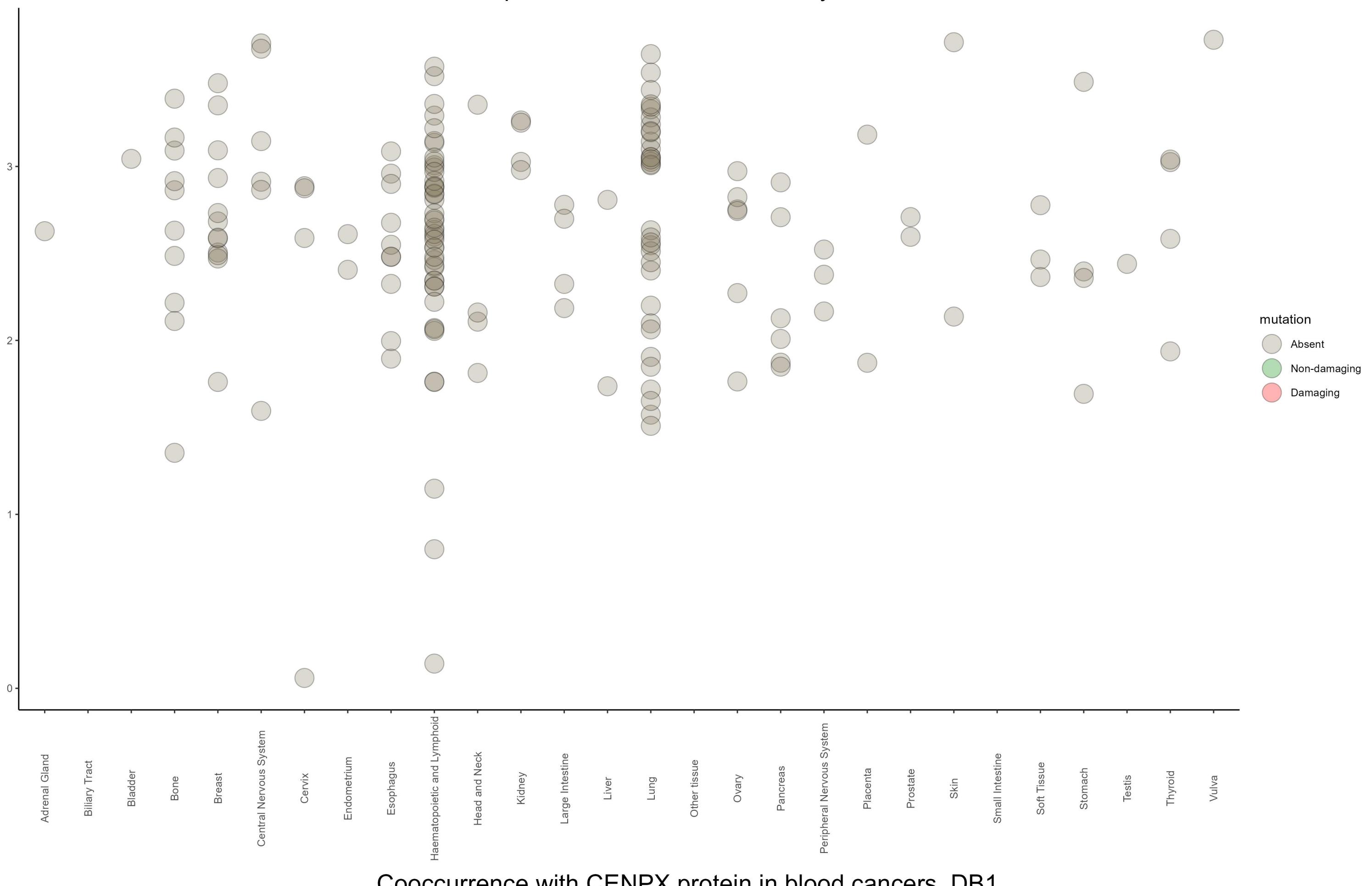
Negative cooccurrence



Positive cooccurrence

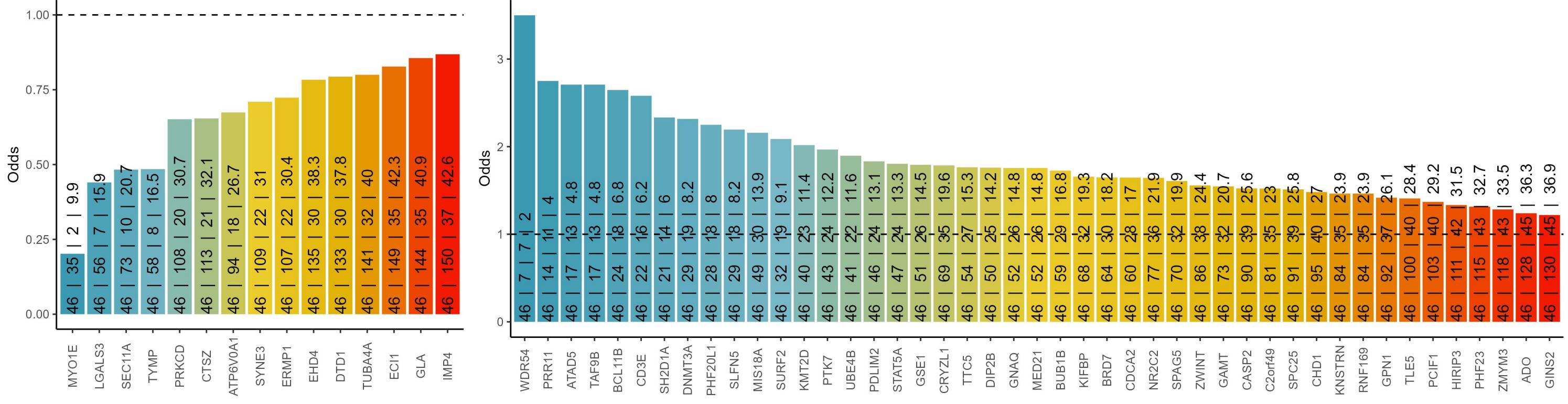


# Amount of CENPX protein and mutation status by tissue, DB1



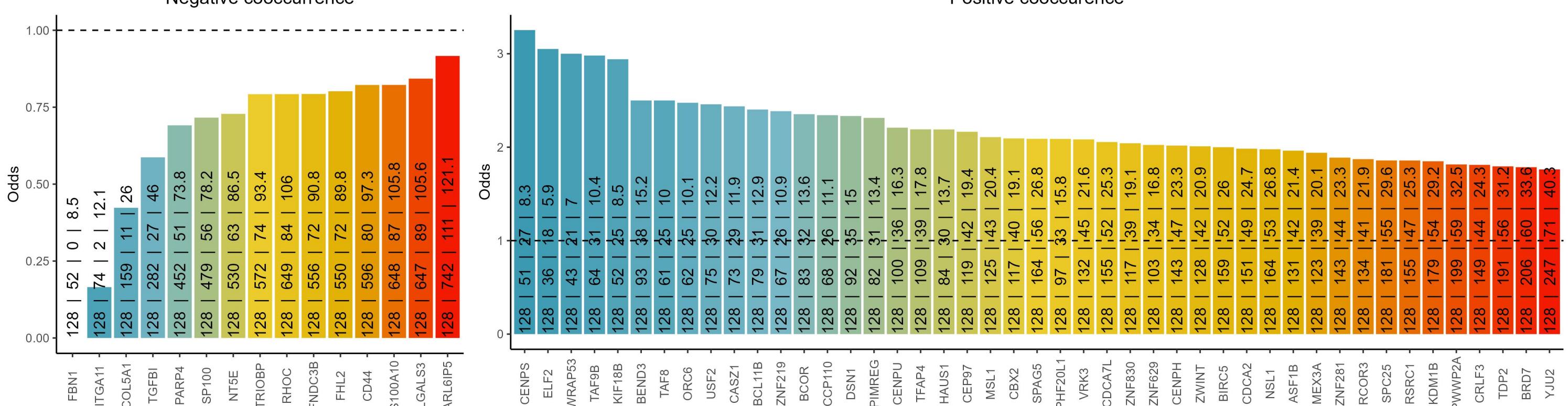
## Cooccurrence with CENPX protein in blood cancers, DB1

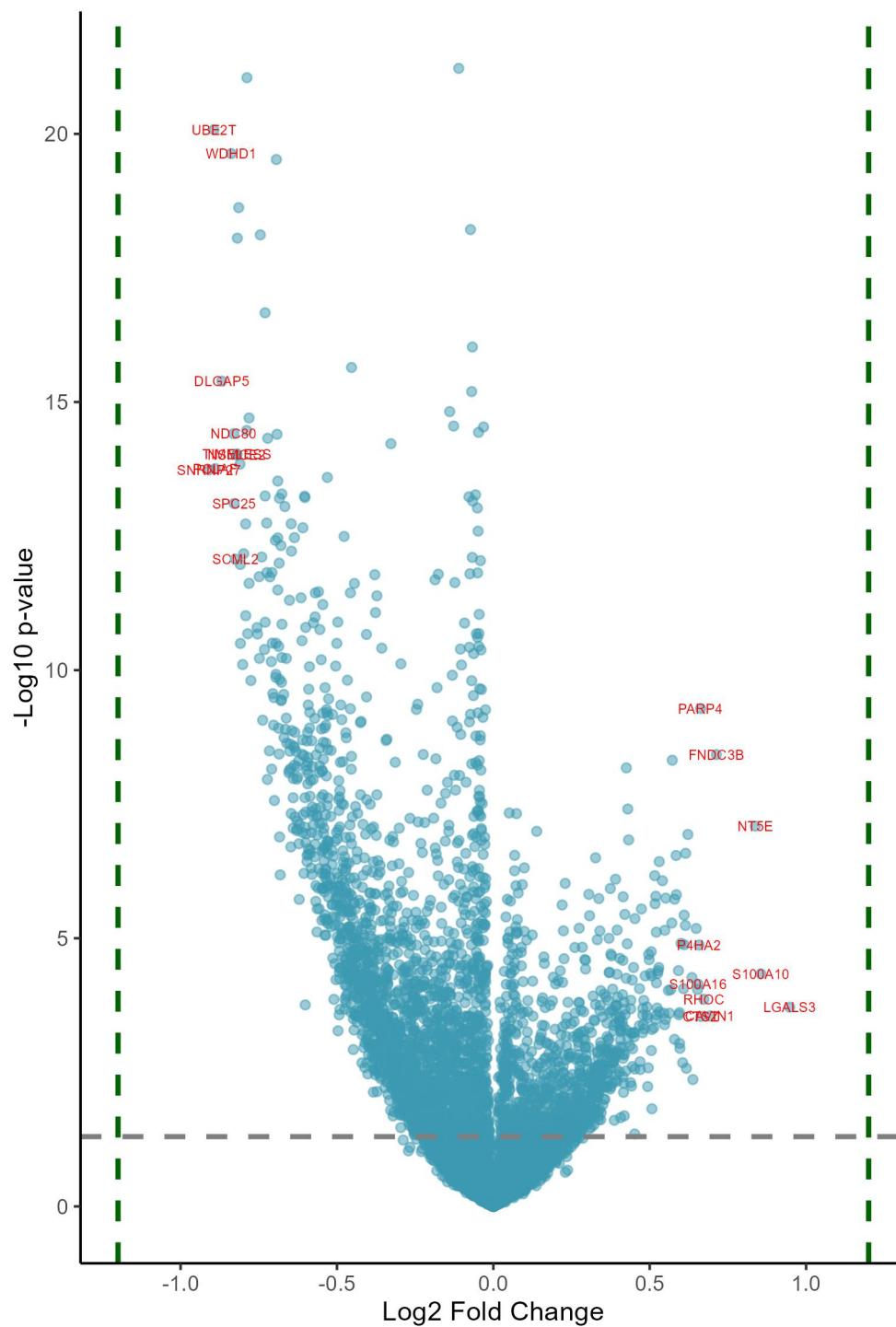
The text in the bars: incidence of CENPX | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with CENPX protein in solid cancers, DB1

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

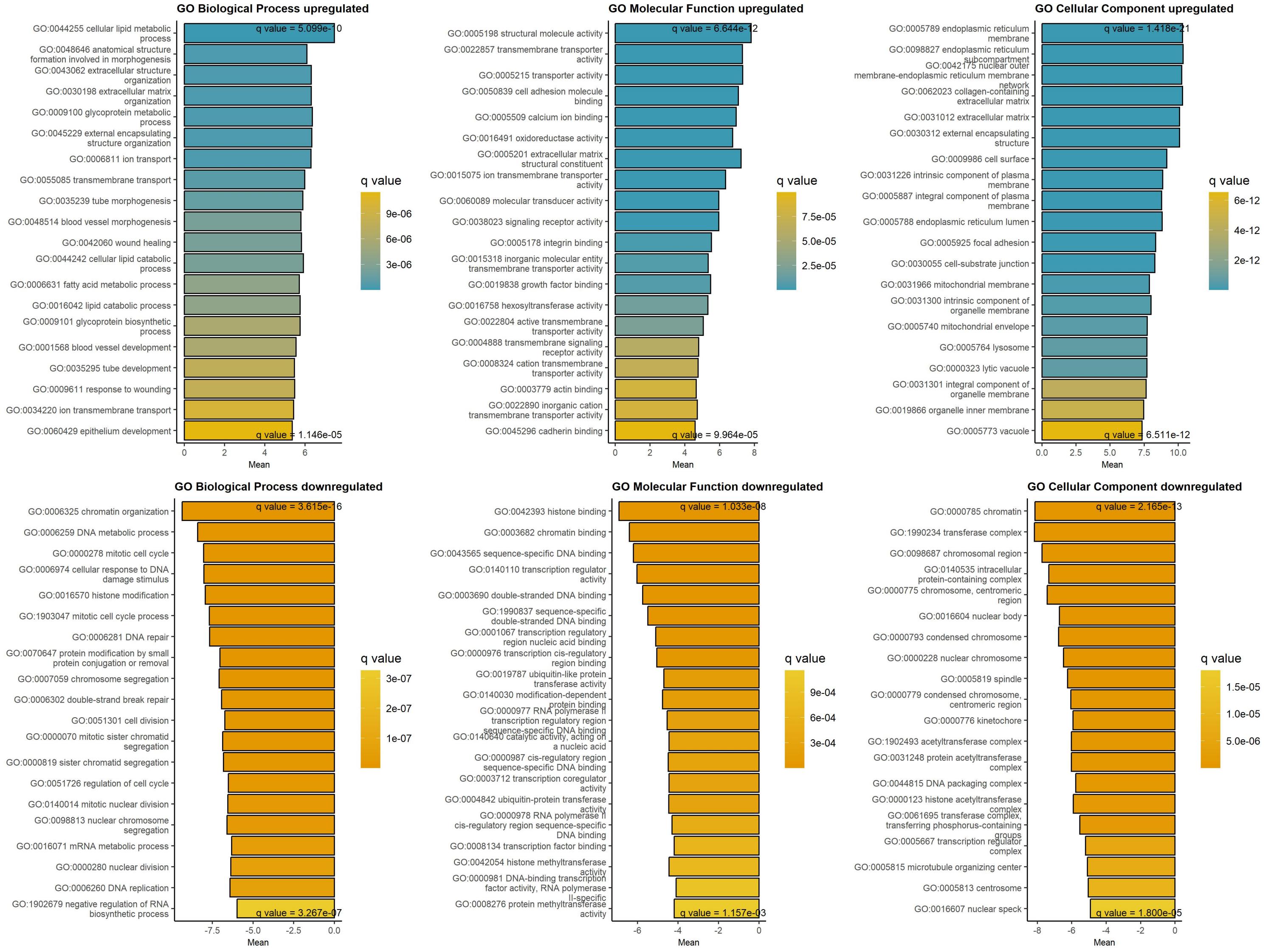




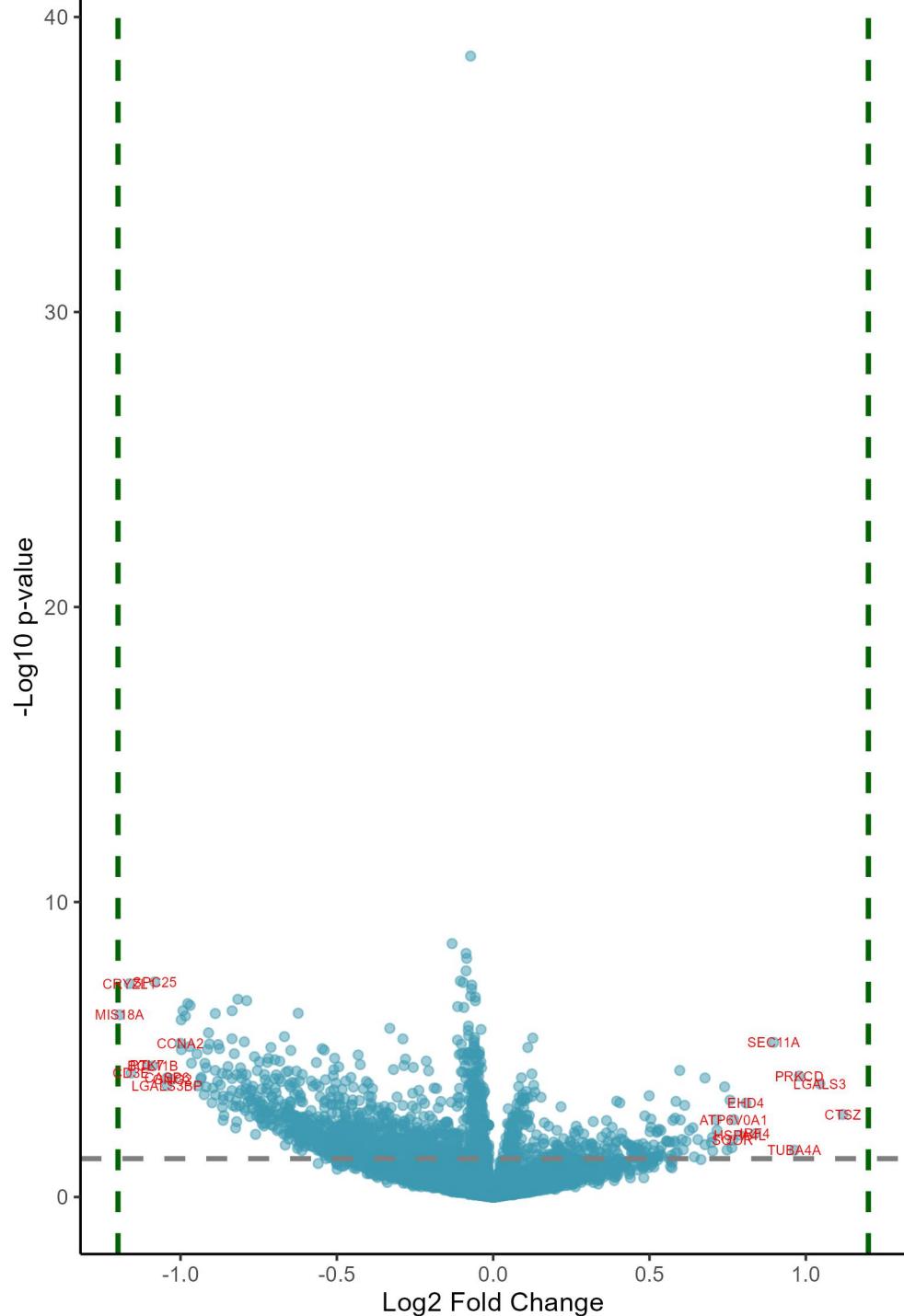
## Downregulated at low/absent CENPX Upregulated at low/absent CENPX

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.91	4.07e-12	SNRNP27	small nuclear ribonucleoprotein U4/	0.95	1.11e-03	LGALS3	galectin 3
-0.89	1.39e-17	UBE2T	ubiquitin conjugating enzyme E2 T	0.86	3.42e-04	S100A10	S100 calcium binding protein A10
-0.89	4.00e-12	PCLAF	PCNA clamp associated factor	0.84	1.69e-06	NT5E	5'-nucleotidase ecto
-0.87	1.94e-13	DLGAP5	DLG associated protein 5	0.71	1.21e-07	FNDC3B	fibronectin type III domain contain
-0.84	3.09e-17	WDHD1	WD repeat and HMG-box DNA binding p	0.69	1.50e-03	CAVIN1	caveolae associated protein 1
-0.83	1.16e-12	NDC80	NDC80 kinetochore complex component	0.67	8.34e-04	RHOC	ras homolog family member C
-0.83	1.27e-11	SPC25	SPC25 component of NDC80 kinetochor	0.66	1.51e-03	CTSZ	cathepsin Z
-0.82	9.75e-11	SCML2	Scm polycomb group protein like 2	0.66	2.35e-08	PARP4	poly(ADP-ribose) polymerase family
-0.82	2.39e-12	NSMCE2	NSE2 (MMS21) homolog, SMC5-SMC6 com	0.66	1.23e-04	P4HA2	prolyl 4-hydroxylase subunit alpha
-0.82	2.37e-12	TIMELESS	timeless circadian regulator	0.65	4.86e-04	S100A16	S100 calcium binding protein A16
-0.82	5.85e-16	NFYB	nuclear transcription factor Y subu	0.65	5.86e-04	MVP	major vault protein
-0.81	2.25e-16	CDCA5	cell division cycle associated 5	0.65	6.90e-05	RRAS	RAS related
-0.81	3.41e-12	YJU2	YJU2 splicing factor homolog	0.64	1.36e-02	GNG12	G protein subunit gamma 12
-0.81	1.16e-10	SPAG5	sperm associated antigen 5	0.64	3.88e-04	SFXN3	sideroflexin 3
-0.81	2.03e-09	GINS2	GINS complex subunit 2	0.62	2.27e-06	SEC11A	SEC11 homolog A, signal peptidase c
-0.8	4.40e-09	BLM	BLM RecQ like helicase	0.62	9.23e-03	CD44	CD44 molecule (Indian blood group)
-0.8	8.15e-11	ACYP1	acylphosphatase 1	0.61	4.53e-06	TRIOBP	TRIO and F-actin binding protein
-0.79	2.72e-11	SPINDOC	spindlin interactor and repressor o	0.61	6.20e-05	CD109	CD109 molecule
-0.79	7.64e-10	PMF1	polyamine modulated factor 1	0.61	1.22e-04	FHL2	four and a half LIM domains 2
-0.79	1.13e-12	ZMYM3	zinc finger MYM-type containing 3	0.61	4.27e-05	NPC1	NPC intracellular cholesterol trans
-0.79	1.98e-18	KIF2C	kinesin family member 2C	0.61	5.70e-04	PPIC	peptidylprolyl isomerase C
-0.79	1.45e-09	C9orf78	chromosome 9 open reading frame 78	0.61	7.55e-03	ITGA3	integrin subunit alpha 3
-0.78	7.75e-13	PRIM2	DNA primase subunit 2	0.6	4.60e-03	CAVIN3	caveolae associated protein 3
-0.78	2.20e-10	BRD2	bromodomain containing 2	0.6	4.60e-03	NCEH1	neutral cholesterol ester hydrolase
-0.78	8.11e-09	ASF1A	anti-silencing function 1A histone	0.6	3.88e-03	MYOF	myoferlin
-0.76	1.16e-09	NSL1	NSL1 component of MIS12 kinetochore	0.6	1.34e-03	ITGA2	integrin subunit alpha 2
-0.75	1.45e-09	BRD3	bromodomain containing 3	0.59	1.44e-03	SQOR	sulfide quinone oxidoreductase
-0.75	1.75e-10	ZNF280C	zinc finger protein 280C	0.59	3.07e-04	MMP14	matrix metallopeptidase 14
-0.75	3.50e-09	ASF1B	anti-silencing function 1B histone	0.59	2.04e-05	FAM114A1	family with sequence similarity 114

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

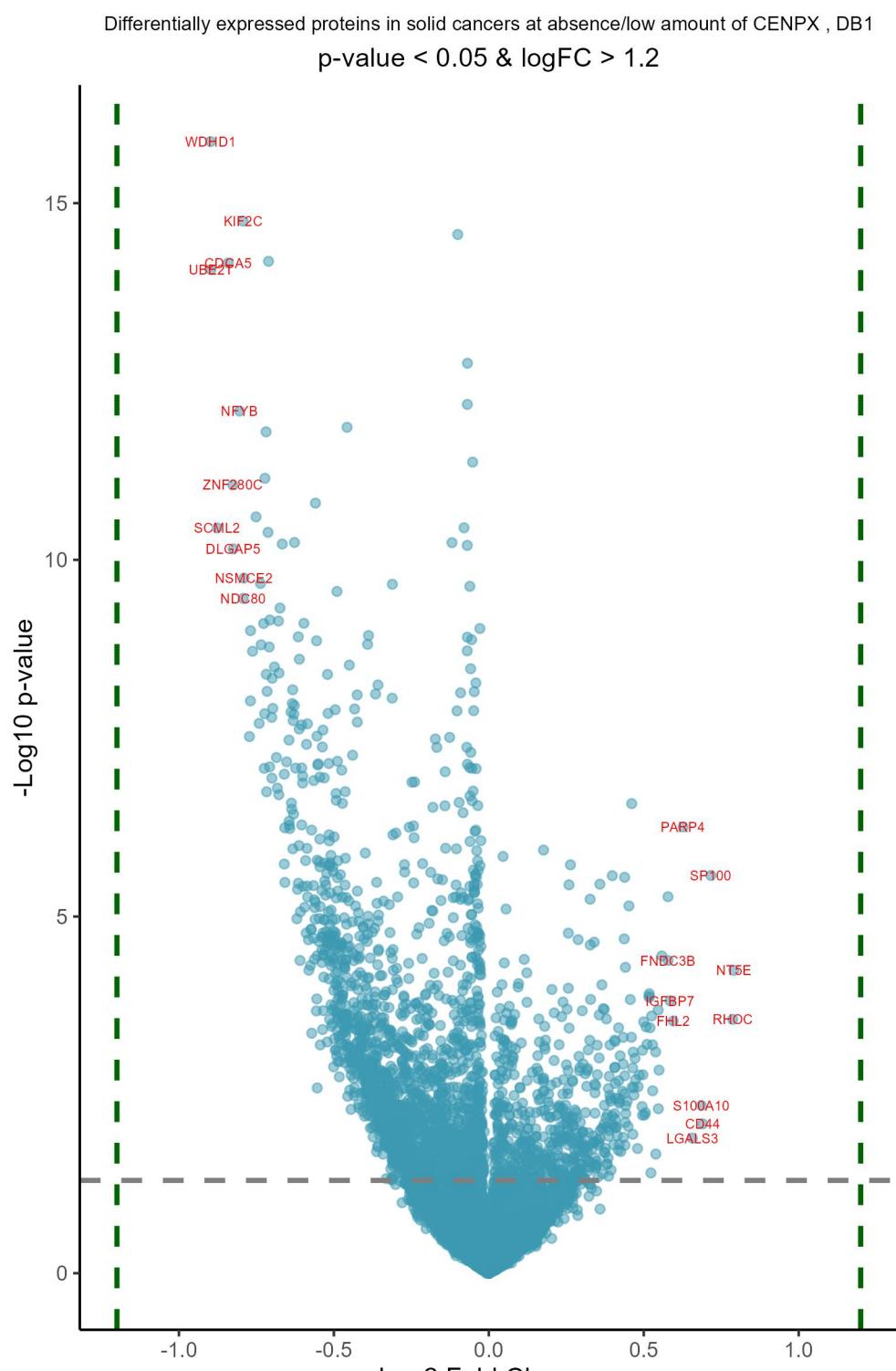


p-value &lt; 0.05 &amp; logFC &gt; 1.2



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

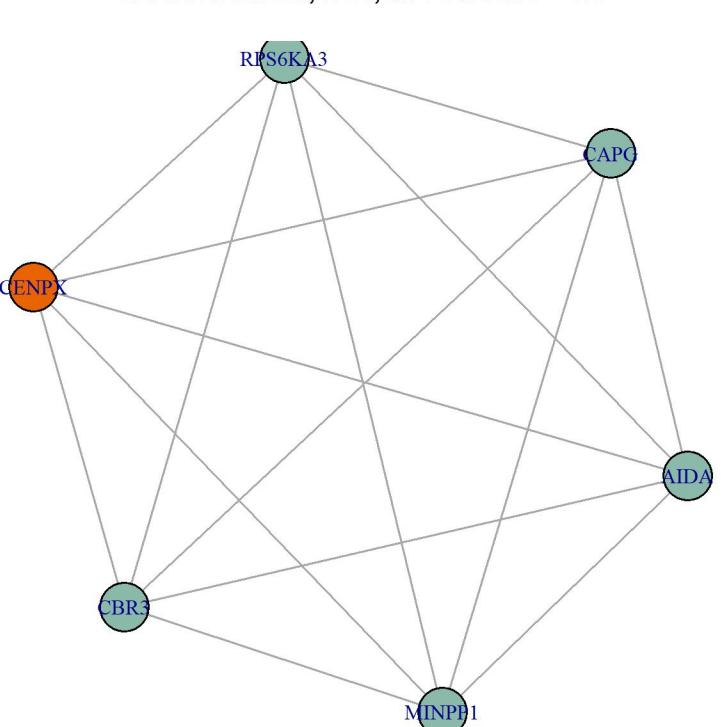
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.19	1.70e-04	MIS18A	MIS18 kinetochore protein A	1.12	2.21e-02	CTSZ	cathepsin Z
-1.16	3.91e-05	CRYZL1	crystallin zeta like 1	1.04	5.75e-03	LGALS3	galectin 3
-1.16	3.42e-03	CD3E	CD3 epsilon subunit of T-cell recep	0.98	3.80e-03	PRKCD	protein kinase C delta
-1.11	2.40e-03	PTK7	protein tyrosine kinase 7 (inactive	0.96	9.67e-02	TUBA4A	tubulin alpha 4a
-1.09	2.43e-03	BCL11B	BAF chromatin remodeling complex su	0.9	8.87e-04	SEC11A	SEC11 homolog A, signal peptidase c
-1.08	3.91e-05	SPC25	SPC25 component of NDC80 kinetochor	0.84	3.76e-02	IRF4	interferon regulatory factor 4
-1.04	6.21e-03	LGALS3BP	galectin 3 binding protein	0.81	1.40e-02	EHD4	EH domain containing 4
-1.04	4.20e-03	CASP6	caspase 6	0.79	4.07e-02	HSPA4L	heat shock protein family A (Hsp70)
-1.03	4.49e-03	GNG2	G protein subunit gamma 2	0.77	2.21e-02	ATP6VOA1	ATPase H <sup>+</sup> transporting V0 subunit a
-1	9.07e-04	CCNA2	cyclin A2	0.77	5.45e-02	SQOR	sulfide quinone oxidoreductase
-1	2.35e-03	ASF1A	anti-silencing function 1A histone	0.76	8.47e-02	BASP1	brain abundant membrane attached si
-1	1.17e-03	KIFBP	kinesin family binding protein	0.76	1.23e-02	TYMP	thymidine phosphorylase
-0.99	1.40e-04	CASP2	caspase 2	0.75	9.56e-02	CD70	CD70 molecule
-0.98	1.80e-04	NR2C2	nuclear receptor subfamily 2 group	0.74	6.57e-03	ECI1	enoyl-CoA delta isomerase 1
-0.98	1.02e-04	CKS1B	CDC28 protein kinase regulatory sub	0.72	3.04e-02	CA2	carbonic anhydrase 2
-0.97	1.06e-03	C2orf49	chromosome 2 open reading frame 49	0.71	2.21e-02	SYNE3	spectrin repeat containing nuclear
-0.97	1.12e-04	HIRIP3	HIRA interacting protein 3	0.7	1.01e-01	MVP	major vault protein
-0.97	2.10e-03	BRD3	bromodomain containing 3	0.7	4.59e-02	SCARB1	scavenger receptor class B member 1
-0.95	1.34e-03	RANGRF	RAN guanine nucleotide release fact	0.7	6.28e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.94	6.34e-03	ZAP70	zeta chain of T cell receptor assoc	0.68	4.26e-03	DERL1	derlin 1
-0.94	4.43e-03	GLUL	glutamate-ammonia ligase	0.68	7.12e-02	SAMHD1	SAM and HD domain containing deoxyn
-0.93	4.16e-03	SLBP	stem-loop binding protein	0.66	1.60e-01	CBR1	carbonyl reductase 1
-0.92	9.52e-03	LCP2	lymphocyte cytosolic protein 2	0.65	5.26e-02	CTSS	cathepsin S
-0.92	2.10e-03	SPAG5	sperm associated antigen 5	0.64	1.39e-01	JCHAIN	joining chain of multimeric IgA and
-0.92	6.57e-03	DDAH2	dimethylarginine dimethylaminohydro	0.64	2.58e-02	GHDC	GH3 domain containing
-0.92	2.60e-03	BRD7	bromodomain containing 7	0.63	3.06e-02	ADPGK	ADP dependent glucokinase
-0.91	1.17e-03	KNSTRN	kinetochore localized astrin (SPAG5)	0.62	5.82e-02	PRKAR2A	protein kinase cAMP-dependent type
-0.91	5.47e-04	TMEM263	transmembrane protein 263	0.61	1.56e-02	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.91	9.31e-04	TLE5	TLE family member 5, transcriptiona	0.61	9.41e-02	F5	coagulation factor V

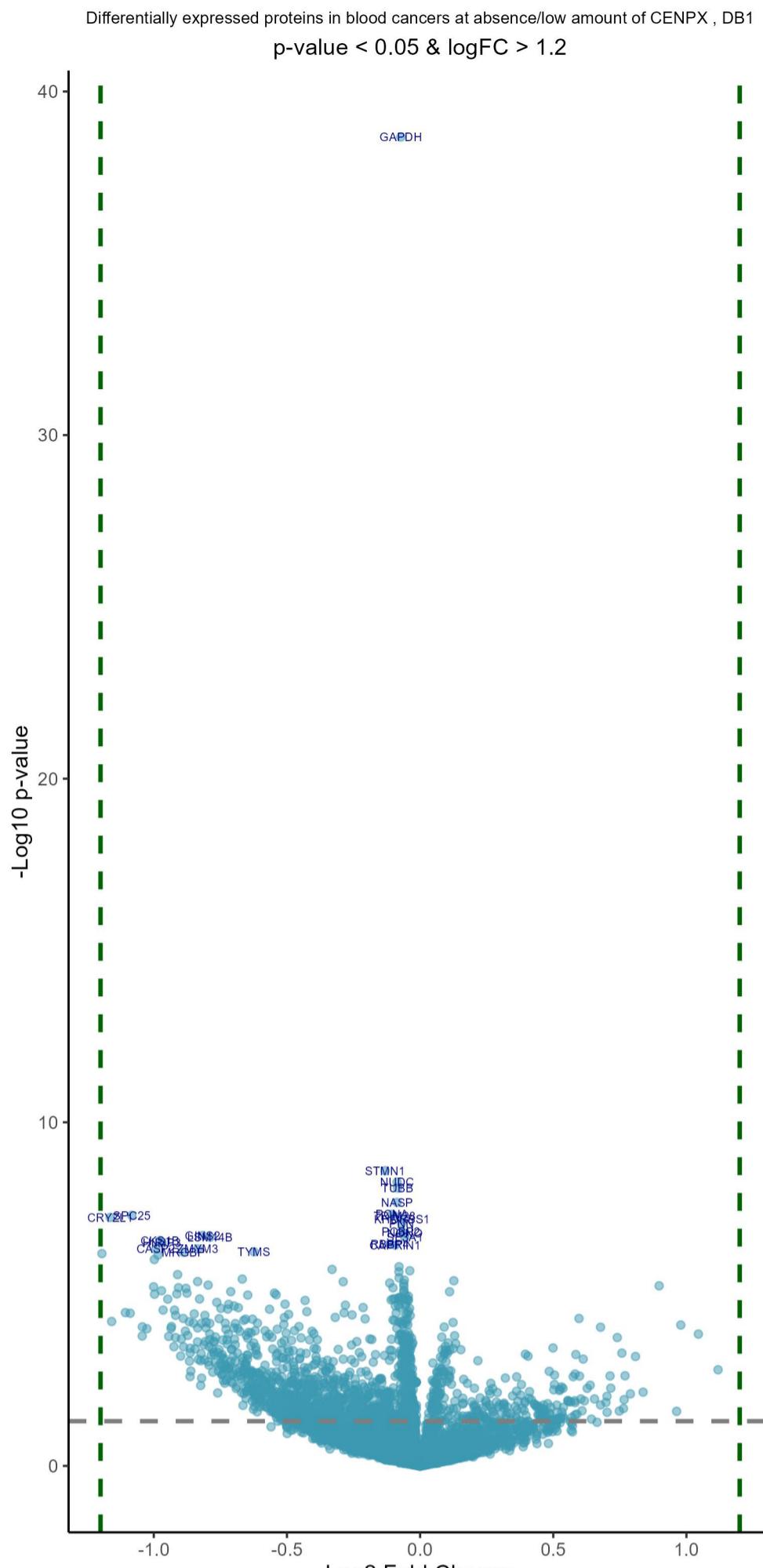


Downregulated in solid cancers at low/absent CENPX Upregulated in solid cancers at low/absent CENPX

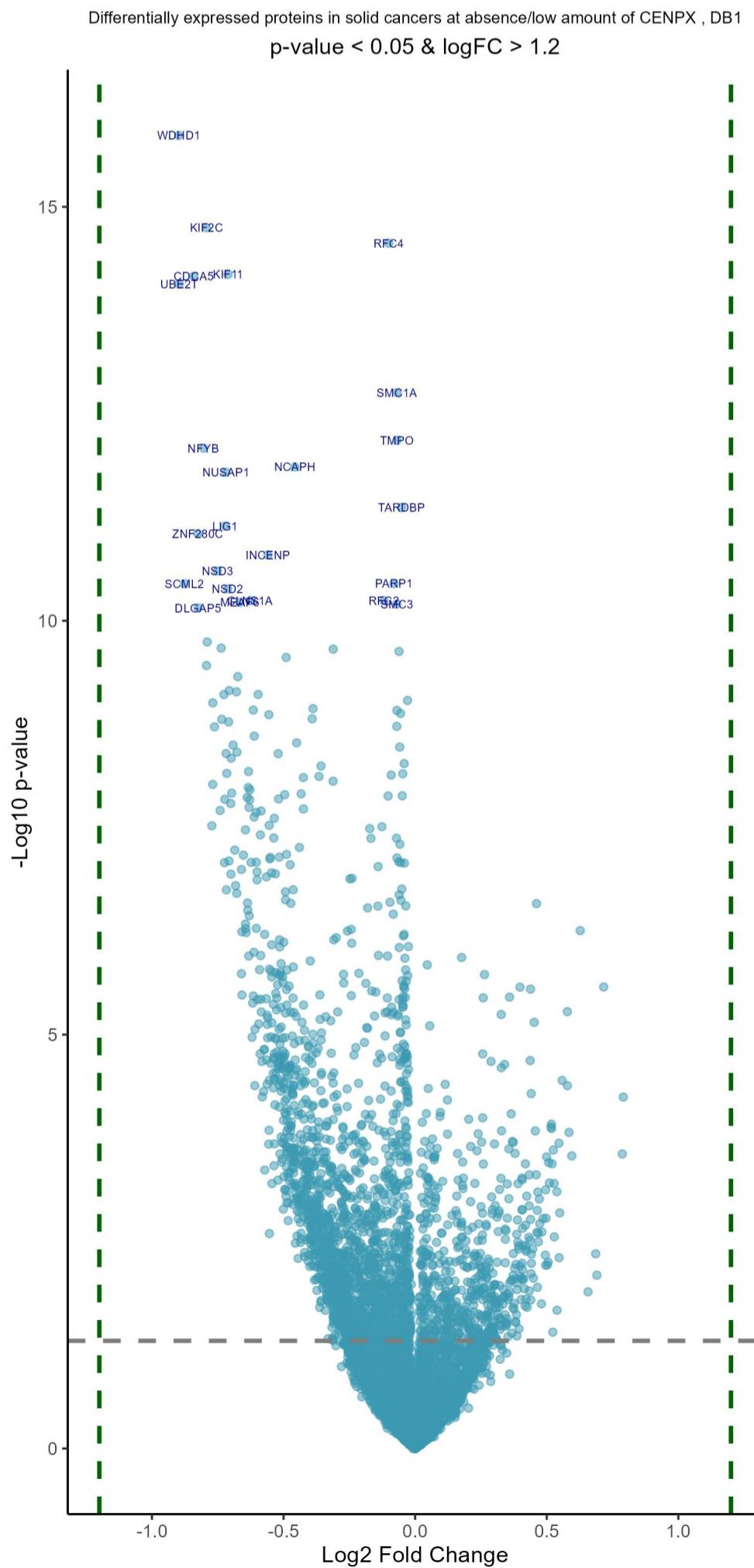
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.9	4.55e-13	WDHD1	WD repeat and HMG-box DNA binding p	0.79	9.04e-04	NTSE	5'-nucleotidase ecto
-0.9	8.09e-12	UBE2T	ubiquitin conjugating enzyme E2 T	0.79	3.14e-03	RHOC	ras homolog family member C
-0.88	1.25e-08	SCML2	Scm polycomb group protein like 2	0.72	8.99e-05	SP100	SP100 nuclear antigen
-0.84	7.64e-12	CDCA5	cell division cycle associated 5	0.69	3.67e-02	CD44	CD44 molecule (Indian blood group)
-0.83	3.94e-09	ZNF280C	zinc finger protein 280C	0.69	2.41e-02	S100A10	S100 calcium binding protein A10
-0.83	1.87e-08	DLGAP5	DLG associated protein 5	0.66	5.05e-02	LGALS3	galectin 3
-0.8	5.46e-10	NFYB	nuclear transcription factor Y subu	0.63	2.54e-05	PARP4	poly(ADP-ribose) polymerase family
-0.79	3.96e-12	KIF2C	kinesin family member 2C	0.6	3.25e-03	FHL2	four and a half LIM domains 2
-0.79	7.45e-08	NDC80	NDC80 kinetochore complex component	0.58	2.03e-03	IGFBP7	insulin like growth factor binding
-0.79	4.61e-08	NSMCE2	NSE2 (MMS21) homolog, SMC5-SMC6 com	0.58	7.02e-04	FNDC3B	fibronectin type III domain contain
-0.77	2.29e-06	SNRNP27	small nuclear ribonucleoprotein U4/	0.58	1.51e-04	TGFBI	transforming growth factor beta ind
-0.77	9.56e-07	ACYP1	acylphosphatase 1	0.56	6.36e-04	TRIOBP	TRIO and F-actin binding protein
-0.77	1.72e-07	SPINDOC	spindlin interactor and repressor o	0.55	1.05e-02	CAVIN3	caveolae associated protein 3
-0.76	2.65e-07	COMMD2	COMM domain containing 2	0.55	2.58e-02	S100A16	S100 calcium binding protein A16
-0.75	9.78e-09	NSD3	nuclear receptor binding SET domain	0.55	2.53e-03	RAB32	RAB32, member RAS oncogene family
-0.74	1.61e-06	BRD2	bromodomain containing 2	0.54	7.27e-02	CAVIN1	caveolae associated protein 1
-0.74	5.23e-08	PRIM2	DNA primase subunit 2	0.54	6.75e-03	CD109	CD109 molecule
-0.73	2.30e-07	PBK	PDZ binding kinase	0.53	1.70e-02	MVP	major vault protein
-0.73	1.44e-07	BPTF	bromodomain PHD finger transcriptio	0.53	5.73e-03	NPC1	NPC intracellular cholesterol trans
-0.72	5.11e-06	PCLAF	PCNA clamp associated factor	0.53	2.91e-03	PRNP	prion protein
-0.72	1.25e-06	ZNF148	zinc finger protein 148	0.52	1.12e-01	LGALS1	galectin 1
-0.72	3.42e-09	LIG1	DNA ligase 1	0.52	3.79e-03	FAM114A1	family with sequence similarity 114
-0.72	8.90e-10	NUSAP1	nucleolar and spindle associated pr	0.52	1.87e-03	EPS8	epidermal growth factor receptor pa
-0.72	4.88e-07	YJU2	YJU2 splicing factor homolog	0.52	1.70e-03	GPNMB	glycoprotein nmb
-0.72	9.48e-06	PMF1	polyamine modulated factor 1	0.52	1.81e-03	NEXN	nexilin F-actin binding protein
-0.72	7.69e-07	SDE2	SDE2 telomere maintenance homolog	0.51	5.69e-03	SPATS2L	spermatogenesis associated serine r
-0.71	1.37e-08	NSD2	nuclear receptor binding SET domain	0.51	3.70e-03	ACSF2	acyl-CoA synthetase family member 2
-0.71	7.64e-12	KIF11	kinesin family member 11	0.51	2.84e-02	CD59	CD59 molecule (CD59 blood group)
-0.71	2.41e-07	UPF3B	UPF3B regulator of nonsense mediate	0.5	3.00e-02	ICAM1	intercellular adhesion molecule 1

CENPX network, DB1, all Pearson r &gt; 0.3



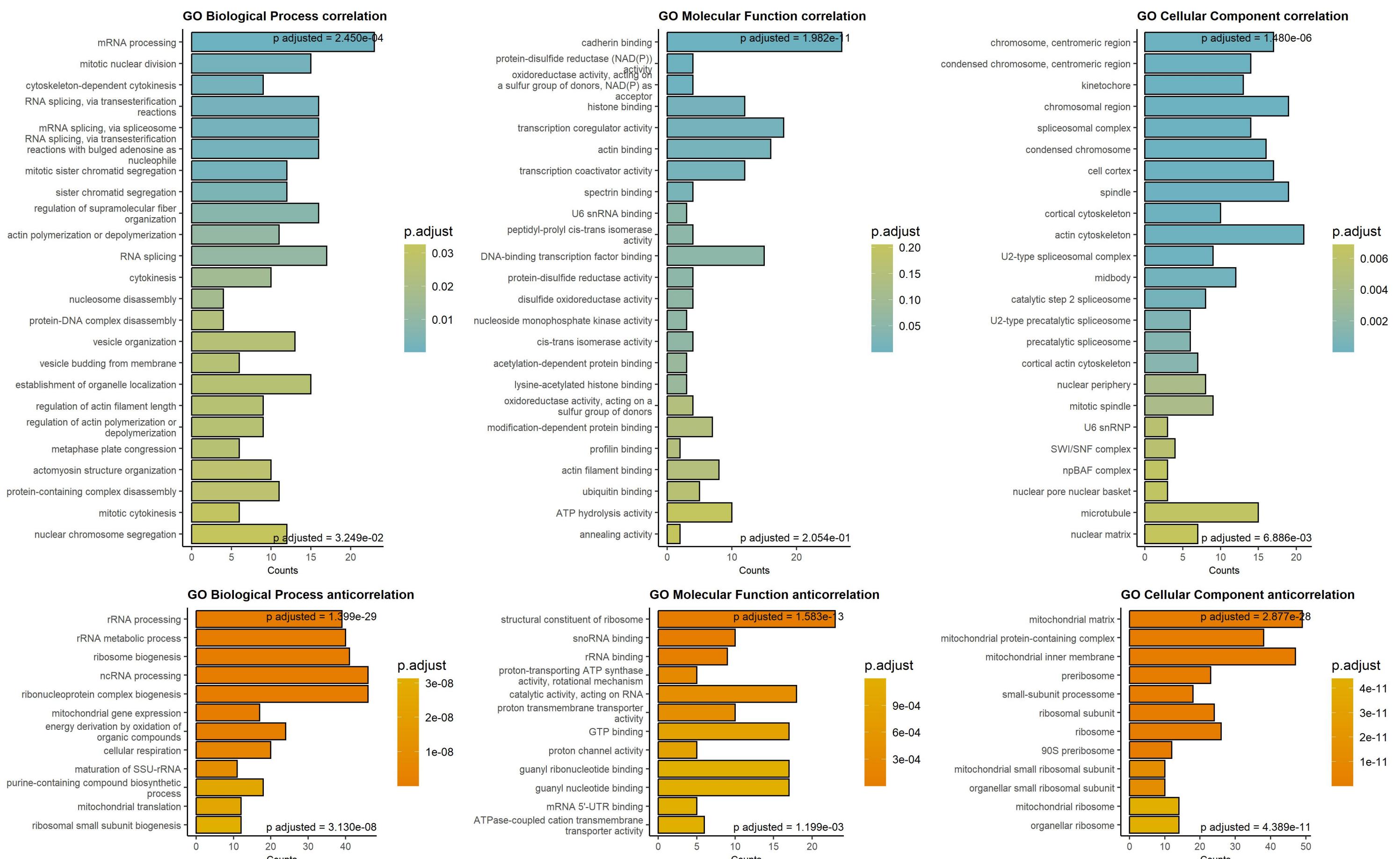


Sorted by p values!							
Downregulated in blood cancers at low/absent CENPX				Upregulated in blood cancers at low/absent CENPX			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.07	7.01e-36	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.13	7.35e-04	DNAJA3	DnaJ heat shock protein family (Hsp
-0.13	5.69e-06	STMN1	stathmin 1	0.9	8.87e-04	SEC11A	SEC11 homolog A, signal peptidase c
-0.09	9.16e-06	NUDC	nuclear distribution C, dynein comp	0.11	1.07e-03	SDHB	succinate dehydrogenase complex iro
-0.08	1.09e-05	TUBB	tubulin beta class I	0.6	3.07e-03	MYO1E	myosin IE
-0.09	2.39e-05	NASP	nuclear autoantigenic sperm protein	0.12	3.51e-03	UQCRB	ubiquinol-cytochrome c reductase bi
-0.11	3.91e-05	PCNA	proliferating cell nuclear antigen	0.98	3.80e-03	PRKCD	protein kinase C delta
-1.08	3.91e-05	SPC25	SPC25 component of NDC80 kinetochor	0.09	4.23e-03	TRAP1	TNF receptor associated protein 1
-0.1	3.91e-05	TRIM28	tripartite motif containing 28	0.68	4.26e-03	DERL1	derlin 1
-1.16	3.91e-05	CRYZL1	crystallin zeta like 1	1.04	5.75e-03	LGALS3	galectin 3
-0.07	3.94e-05	KHDRBS1	KH RNA binding domain containing, s	0.13	6.12e-03	HEATR1	HEAT repeat containing 1
-0.07	4.94e-05	PNN	pinin, desmosome associated protein	0.08	6.50e-03	TMED9	transmembrane p24 trafficking prote
-0.07	7.83e-05	PCBP2	poly(rC) binding protein 2	0.74	6.57e-03	ECI1	enoyl-CoA delta isomerase 1
-0.06	7.95e-05	NONO	non-POU domain containing octamer b	0.11	7.93e-03	UTP4	UTP4 small subunit processome comp
-0.82	8.73e-05	GINS2	GINS complex subunit 2	0.13	8.25e-03	CYC1	cytochrome c1
-0.79	8.73e-05	LSM14B	LSM family member 14B	0.09	9.40e-03	CLPP	caseinolytic mitochondrial matrix p
-0.06	8.73e-05	SF3A1	splicing factor 3a subunit 1	0.5	1.01e-02	ITIH2	inter-alpha-trypsin inhibitor heavy
-0.98	1.02e-04	CKS1B	CDC28 protein kinase regulatory sub	0.12	1.04e-02	OGDH	oxoglutarate dehydrogenase
-0.97	1.12e-04	HIRIP3	HIRA interacting protein 3	0.15	1.07e-02	CISD2	CDGSH iron sulfur domain 2
-0.11	1.17e-04	RBBP4	RB binding protein 4, chromatin rem	0.08	1.07e-02	MRPL17	mitochondrial ribosomal protein L17
-0.09	1.19e-04	CAPRIN1	cell cycle associated protein 1	0.09	1.07e-02	MRPL19	mitochondrial ribosomal protein L19
-0.99	1.40e-04	CASP2	caspase 2	0.11	1.09e-02	MRPL38	mitochondrial ribosomal protein L38
-0.84	1.40e-04	ZMYM3	zinc finger MYM-type containing 3	0.1	1.13e-02	ERP44	endoplasmic reticulum protein 44
-0.62	1.60e-04	TYMS	thymidylate synthetase	0.09	1.23e-02	HADHB	hydroxyacyl-CoA dehydrogenase trifu
-0.89	1.60e-04	MRGBP	MRG domain binding protein	0.76	1.23e-02	TYMP	thymidine phosphorylase
-1.19	1.70e-04	MIS18A	MIS18 kinetochore protein A	0.1	1.26e-02	TMED10	transmembrane p24 trafficking prote
-0.98	1.80e-04	NR2C2	nuclear receptor subfamily 2 group	0.4	1.29e-02	DPYSL3	dihydropyrimidinase like 3
-1	2.35e-04	ASF1A	anti-silencing function 1A histone	0.09	1.29e-02	MRPL13	mitochondrial ribosomal protein L13
-0.08	3.67e-04	ENY2	ENY2 transcription and export compl	0.58	1.29e-02	IMP4	IMP U3 small nucleolar ribonucleop
-0.33	4.24e-04	WDR54	WD repeat domain 54	0.41	1.39e-02	SPG21	SPG21 abhydrolase domain containing
-0.04	4.49e-04	HSPA8	heat shock protein family A (Hsp70)	0.81	1.40e-02	EHD4	EH domain containing 4
-0.08	4.68e-04	MAPRE1	microtubule associated protein RP/E	0.08	1.44e-02	PHB2	prohibitin 2
-0.91	5.47e-04	TMEM263	transmembrane protein 263	0.08	1.56e-02	MRPL58	mitochondrial ribosomal protein L58
-0.08	6.59e-04	RFC4	replication factor C subunit 4	0.61	1.56e-02	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.67	6.95e-04	PCLAF	PCNA clamp associated factor	0.22	1.68e-02	POP1	POP1 homolog, ribonuclease P/MRP su
-0.06	7.23e-04	SNRPF	small nuclear ribonucleoprotein pol	0.1	1.75e-02	NDUFS2	NADH:ubiquinone oxidoreductase core
-0.84	7.45e-04	BRD8	bromodomain containing 8	0.05	1.86e-02	RSL1D1	ribosomal L1 domain containing 1
-0.29	7.45e-04	JPH1	junctophilin 1	0.07	2.21e-02	SDHA	succinate dehydrogenase complex fla
-0.11	7.93e-04	SMC2	structural maintenance of chromosom	0.08	2.21e-02	SLC25A3	solute carrier family 25 member 3
-0.06	7.99e-04	ATYN21	atavin 2 like	0.08	2.21e-02	ATDFDR	ATP synthase peripheral stalk membr

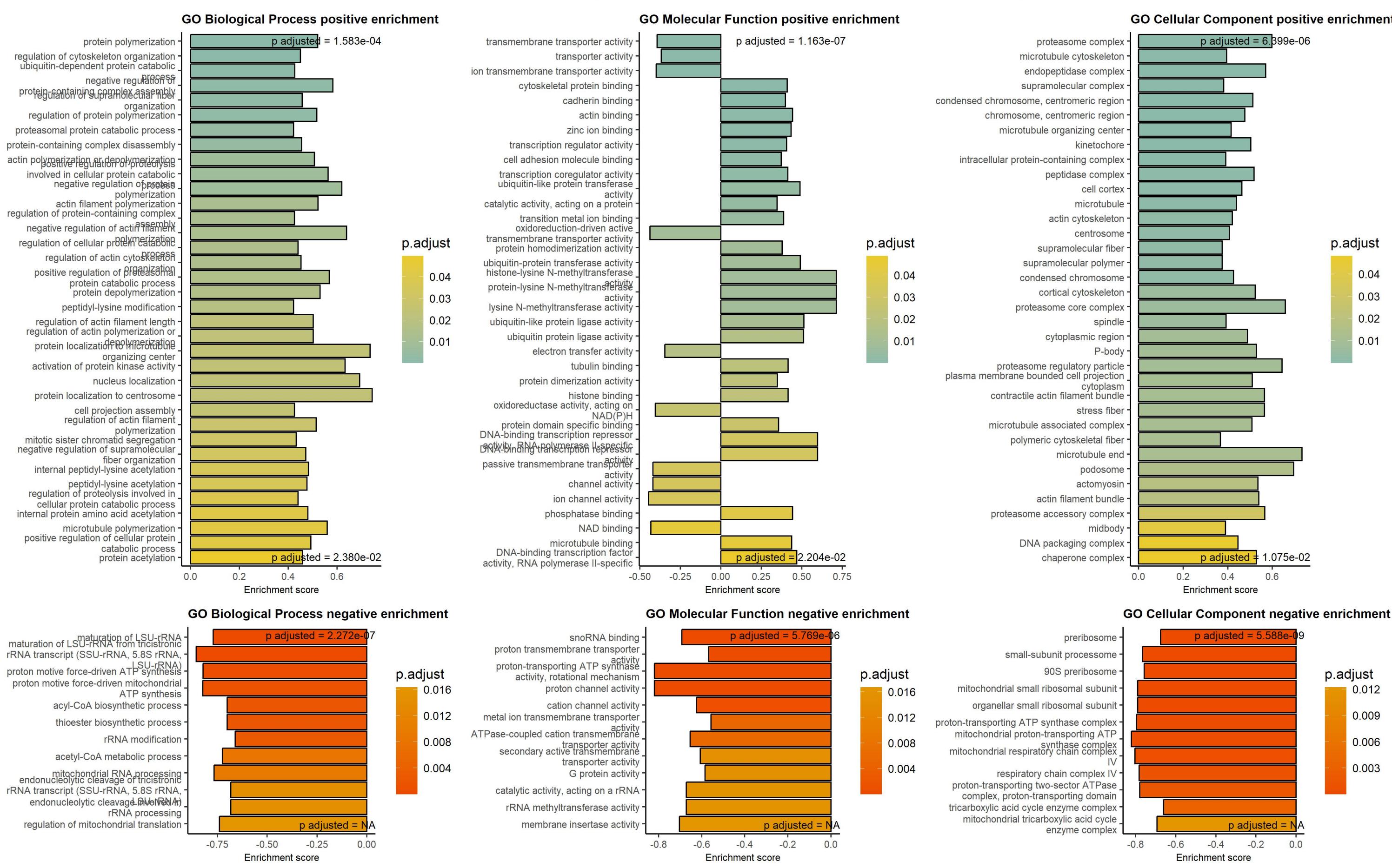


Sorted by p values!							
Downregulated in solid cancers at low/absent CENPX				Upregulated in solid cancers at low/absent CENPX			
C	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
4.55e-13	WDHD1	WD repeat and HMG-box DNA binding p	0.46	1.30e-05	COL5A1	collagen type V alpha 1 chain	
3.96e-12	KIF2C	kinesin family member 2C	0.63	2.54e-05	PARP4	Poly(ADP-ribose) polymerase family	
4.57e-12	RFC4	replication factor C subunit 4	0.18	4.69e-05	RRBP1	ribosome binding protein 1	
7.64e-12	KIF11	kinesin family member 11	0.05	5.62e-05	CLTC	clathrin heavy chain	
7.64e-12	CDCA5	cell division cycle associated 5	0.26	6.86e-05	FBN1	fibrillin 1	
8.09e-12	UBE2T	ubiquitin conjugating enzyme E2 T	0.72	8.99e-05	SP100	SP100 nuclear antigen	
1.46e-10	SMC1A	structural maintenance of chromosom	0.4	8.99e-05	SLFN5	schlafin family member 5	
4.89e-10	TMPO	thymopoietin	0.44	9.37e-05	CLCN7	chloride voltage-gated channel 7	
5.46e-10	NFYB	nuclear transcription factor Y subu	0.36	1.11e-04	LOXL2	lysyl oxidase like 2	
8.38e-10	NCAPH	non-SMC condensin I complex subunit	0.26	1.12e-04	ITGA11	integrin subunit alpha 11	
8.90e-10	NUSAP1	nucleolar and spindle associated pr	0.58	1.51e-04	TGFB1	transforming growth factor beta ind	
2.18e-09	TARDBP	TAR DNA binding protein	0.33	1.58e-04	WIPF1	WAS/WASL interacting protein family	
3.42e-09	LIG1	DNA ligase 1	0.45	1.87e-04	CPQ	carboxypeptidase Q	
3.94e-09	ZNF280C	zinc finger protein 280C	0.06	2.02e-04	RAB1A	RAB1A, member RAS oncogene family	
6.66e-09	INCENP	inner centromere protein	0.26	3.75e-04	SGCD	sarcoglycan delta	
9.78e-09	NSD3	nuclear receptor binding SET domain	0.44	4.17e-04	ALDH3B1	aldehyde dehydrogenase 3 family mem	
1.25e-08	PARP1	Poly(ADP-ribose) polymerase 1	0.29	4.25e-04	IFIT1	interferon induced protein with tet	
1.25e-08	SCML2	Scm polycomb group protein like 2	0.34	4.50e-04	TRPV2	transient receptor potential cation	
1.37e-08	NSD2	nuclear receptor binding SET domain	0.33	4.80e-04	ABCC3	ATP binding cassette subfamily C me	
1.73e-08	CLNS1A	chloride nucleotide-sensitive chann	0.56	6.36e-04	TRIOBP	TRIO and F-actin binding protein	
1.73e-08	RFC2	replication factor C subunit 2	0.11	6.87e-04	CTSD	cathepsin D	
1.74e-08	MEAF6	MYST/Esa1 associated factor 6	0.58	7.02e-04	FNDC3B	fibronectin type III domain contain	
1.74e-08	SMC3	structural maintenance of chromosom	0.05	7.46e-04	ARPC4	actin related protein 2/3 complex s	
1.87e-08	DLGAP5	DLG associated protein 5	0.44	8.34e-04	FGF2	fibroblast growth factor 2	
4.61e-08	NSMCE2	NSE2 (MMS21) homolog, SMC5-SMC6 com	0.79	9.04e-04	NT5E	5'-nucleotidase ecto	
5.23e-08	PRIM2	DNA primase subunit 2	0.12	9.70e-04	MYH9	myosin heavy chain 9	
5.23e-08	UHRF1	ubiquitin like with PHD and ring fi	0.1	1.30e-03	TXNDC5	thioredoxin domain containing 5	
5.39e-08	CBX3	chromobox 3	0.04	1.34e-03	RPL27	ribosomal protein L27	
6.15e-08	KIF4A	kinesin family member 4A	0.36	1.34e-03	IGFBP3	insulin like growth factor binding	
7.45e-08	NDC80	NDC80 kinetochore complex component	0.09	1.42e-03	COLGALT1	collagen beta(1-O)galactosyltransfe	
9.85e-08	GINS4	GINS complex subunit 4	0.26	1.47e-03	CHPF	chondroitin polymerizing factor	
1.40e-07	FANCI	FA complementation group I	0.2	1.52e-03	ACP5	acid phosphatase 5, tartrate resist	
1.41e-07	NRF1	nuclear respiratory factor 1	0.03	1.62e-03	RPL7A	ribosomal protein L7a	
1.44e-07	SUZ12	SUZ12 polycomb repressive complex 2	0.52	1.70e-03	GPNMB	glycoprotein nmb	
1.44e-07	BPTF	bromodomain PHD finger transcriptio	0.52	1.81e-03	NEXN	nexilin F-actin binding protein	
1.65e-07	HNRNPK	heterogeneous nuclear ribonucleoprotein	0.52	1.87e-03	EPS8	epidermal growth factor receptor pa	
1.72e-07	SPINDOC	spindlin interactor and repressor o	0.33	1.96e-03	ITGB3	integrin subunit beta 3	
1.96e-07	NCAPD2	non-SMC condensin I complex subunit	0.46	1.96e-03	ARL6IP5	ADP ribosylation factor like GTPase	

# Top 250 correlation coefficients overrepresentation, CENPX protein, DB1



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



No information on Ser/Thr kinase phosphorylation sites for CENPX

No information on Ser/Thr kinase phosphorylation sites for CENPX

No sufficient paired observations in DB1 for CENPX