

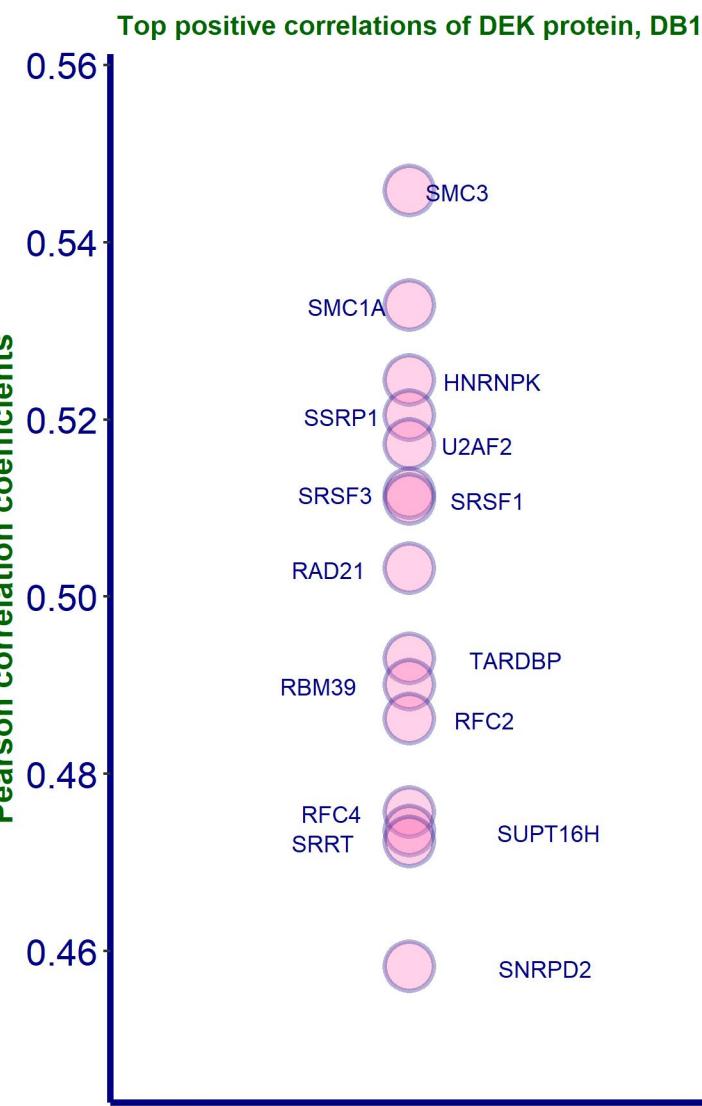
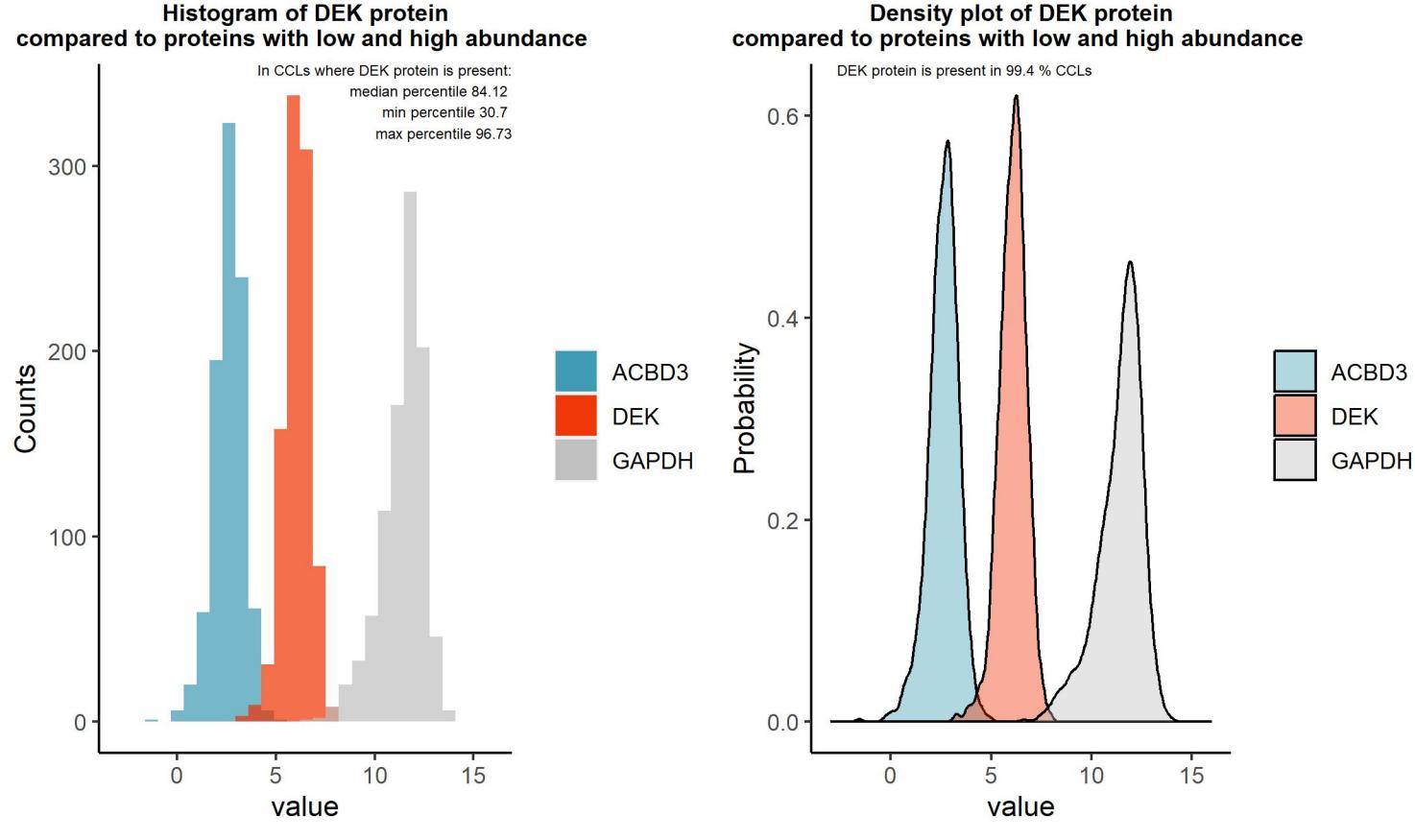
DEK

Protein name: DEK ; UNIPROT: P35659 ; Gene name: DEK proto-oncogene

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

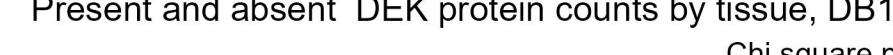
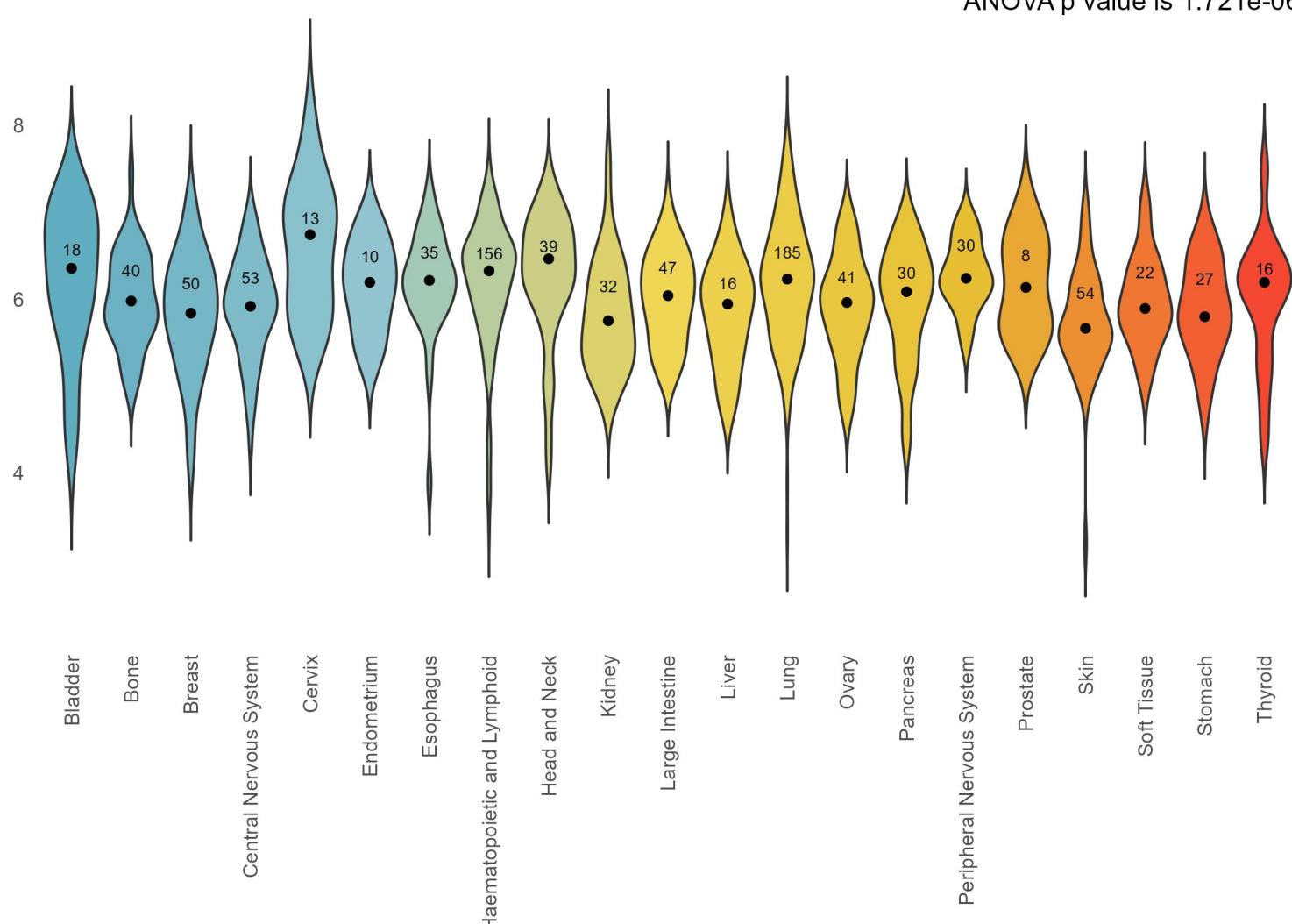
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

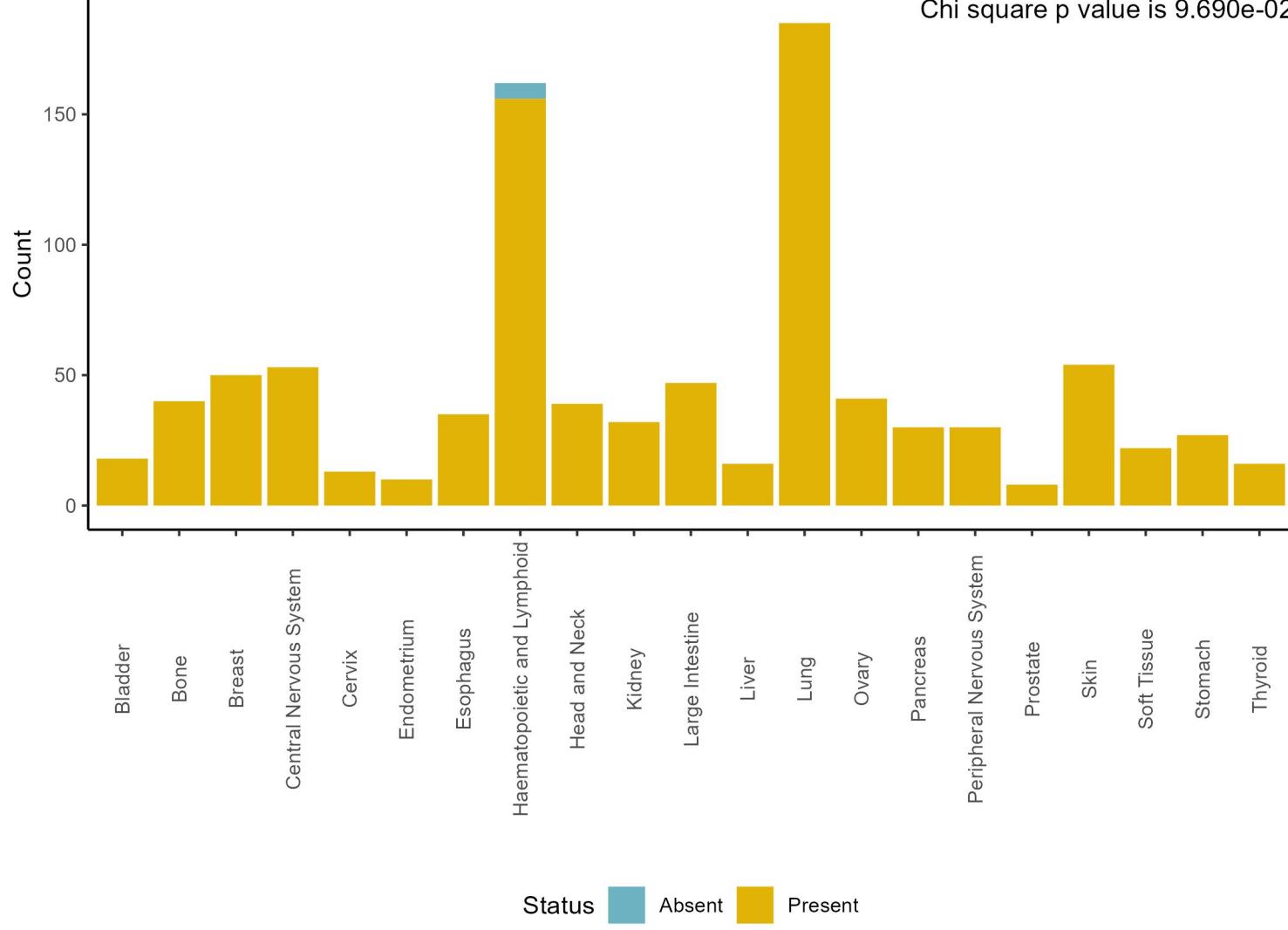


Amount of DEK protein, number of CCLs where it is present by tissue, DB1
ANOVA p value is 1.7

ANOVA p value is 1.721e-06



Chi square p value is 9.890e-02

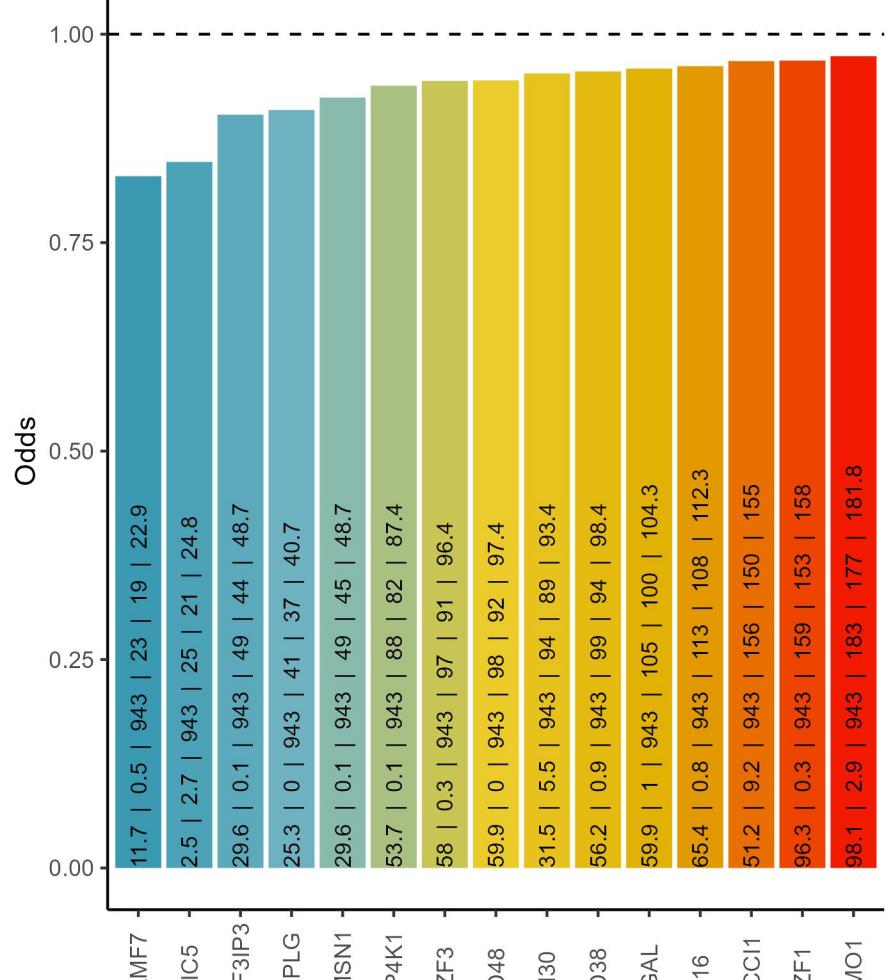


Cooccurrence with DEK protein, DB1

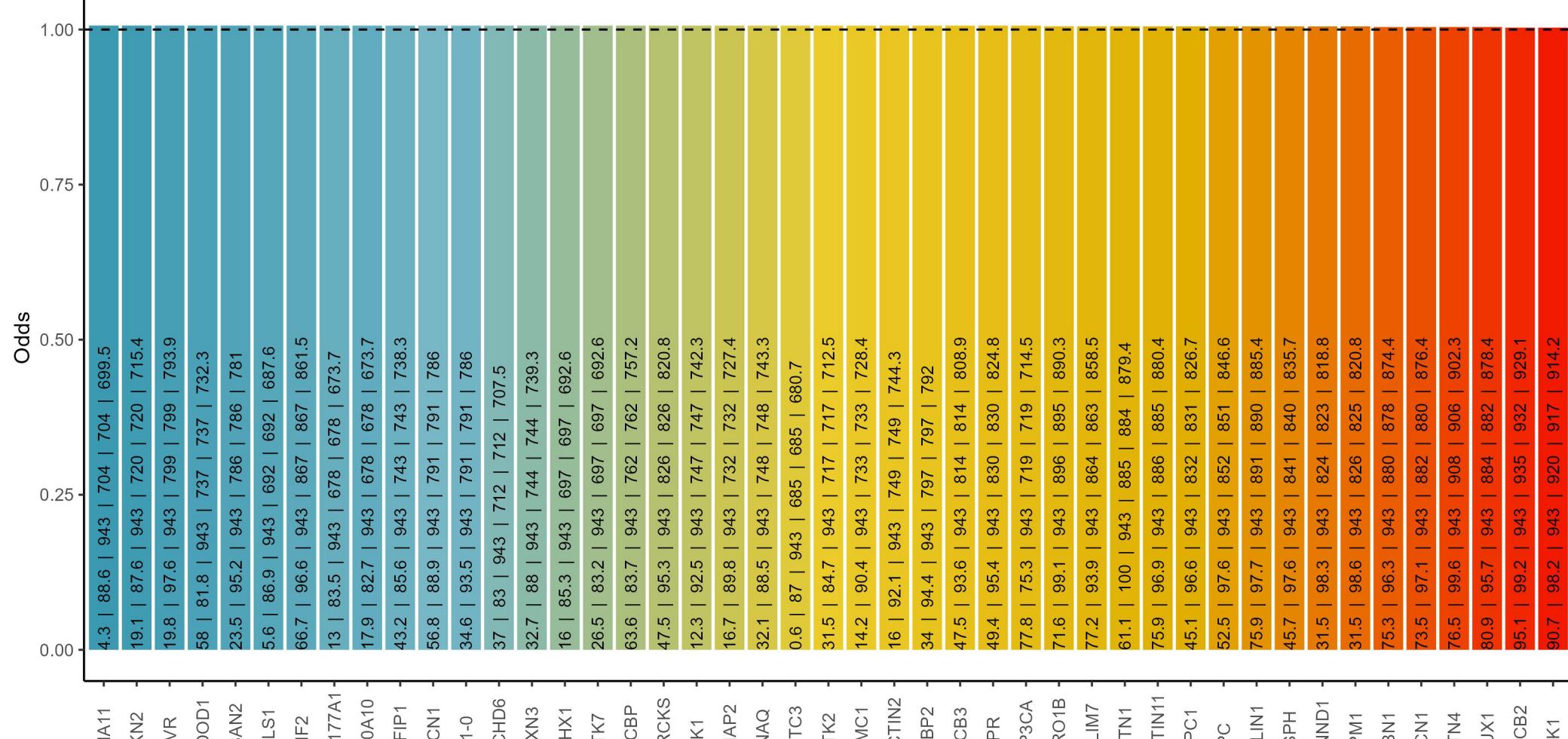
% of DEK in blood cancers: 96.3 ; % of DEK in solid cancers: 100
 of Protein 3 in solid cancers | Incidence of DEK | Incidence of Protein

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

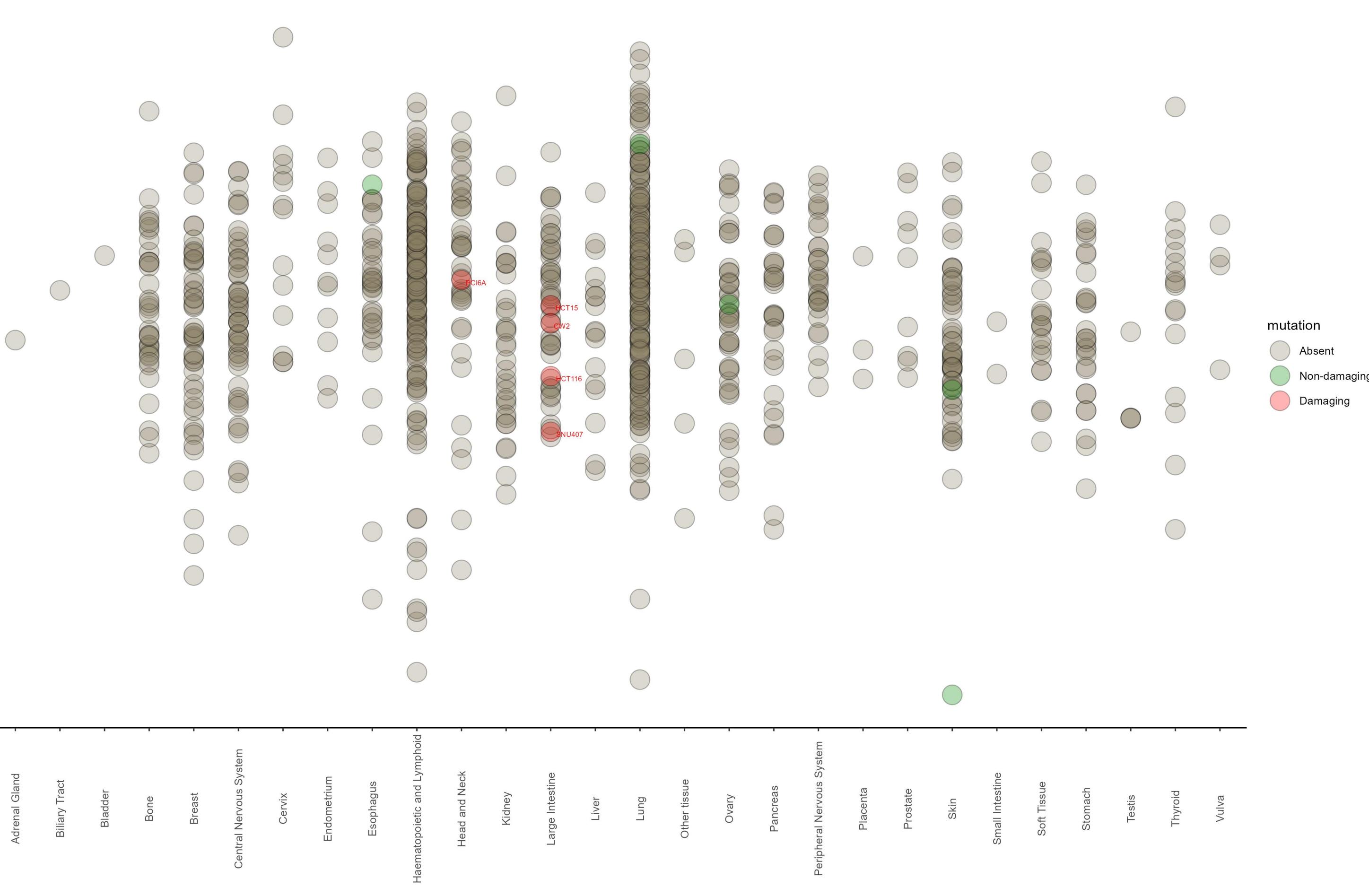
Negative cooccurrence



Positive cooccurrence



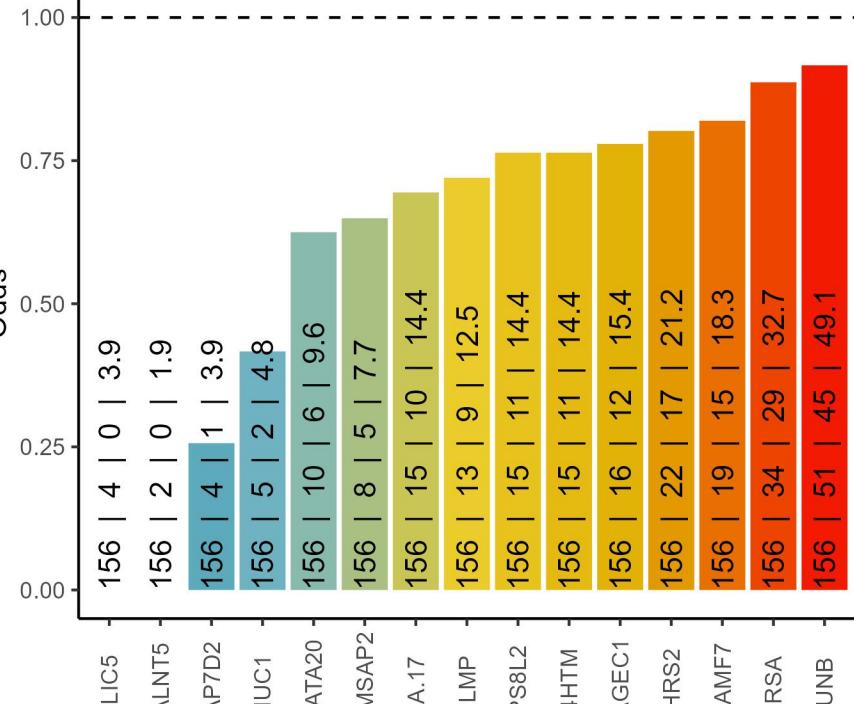
Amount of DEK protein and mutation status by tissue, DB1



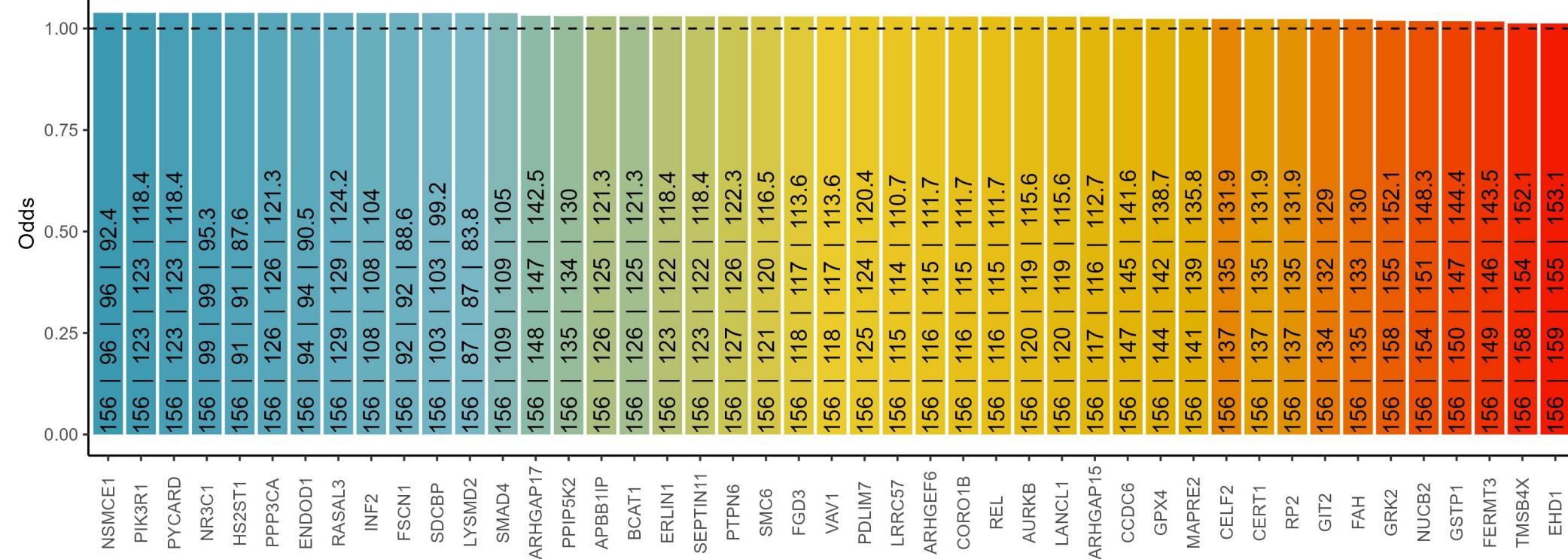
Cooccurrence with DEK protein in blood cancers, DB1

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

Negative cooccurrence



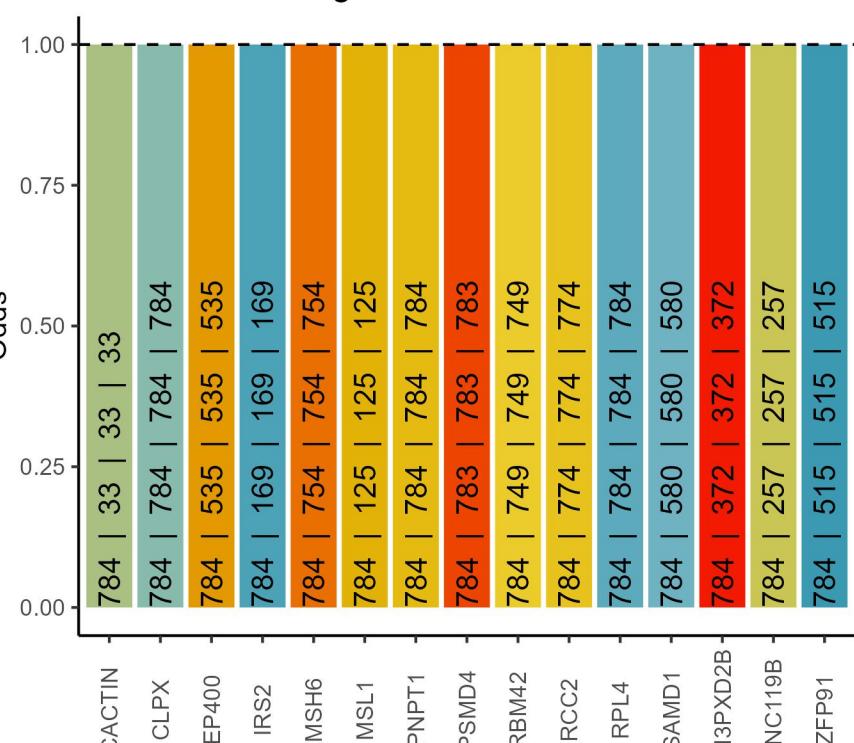
Positive cooccurrence



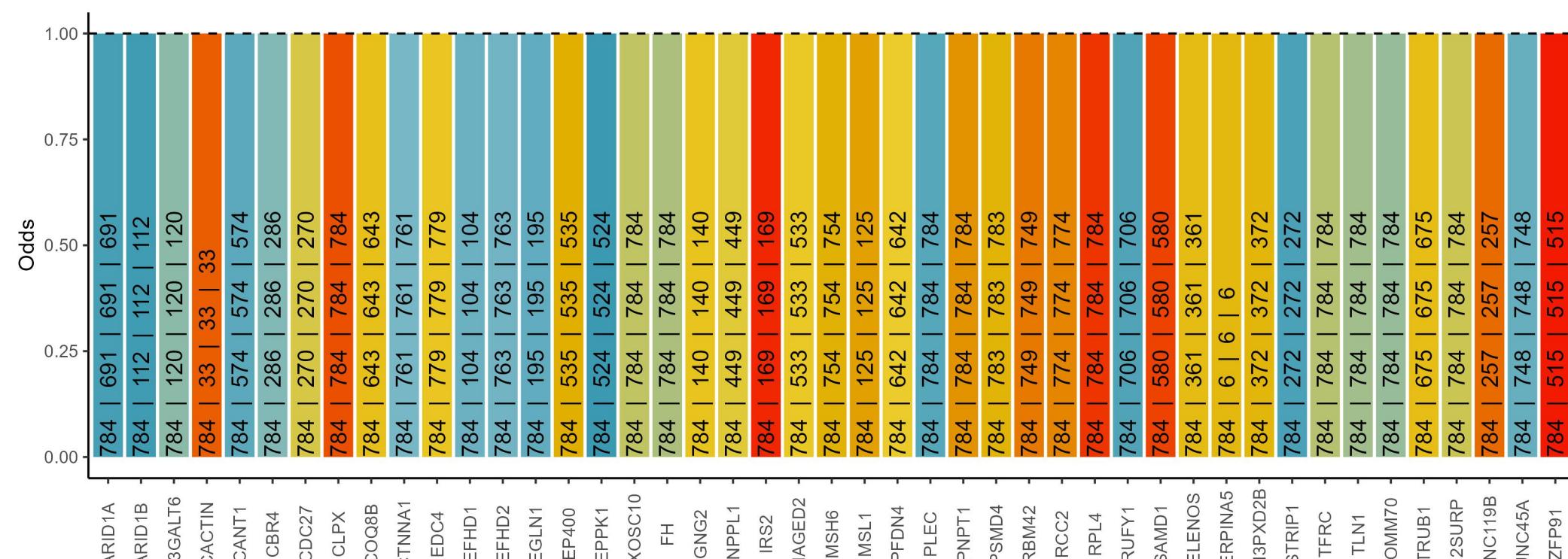
Cooccurrence with DEK protein in solid cancers, DB1

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

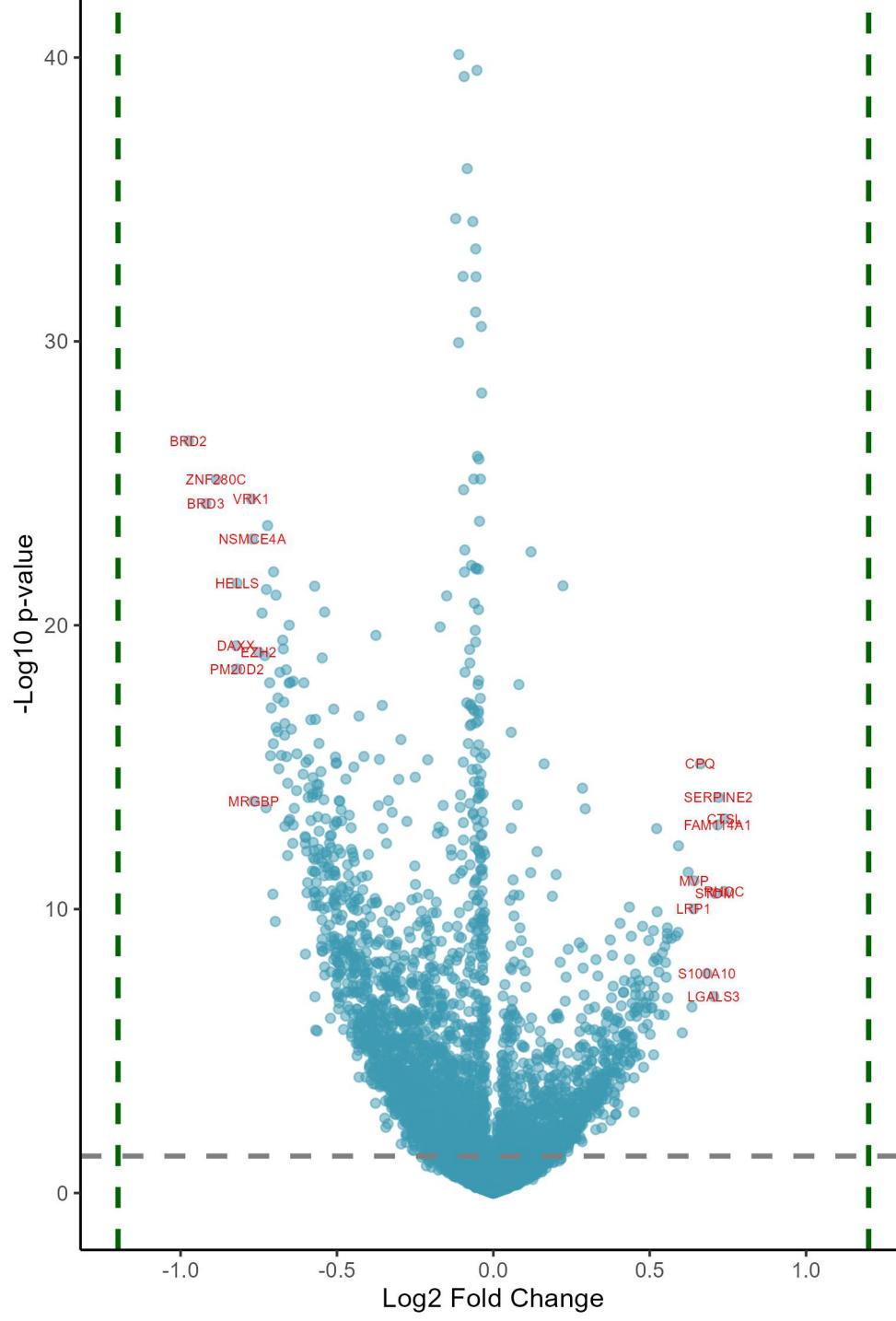
Negative cooccurrence



Positive cooccurrence

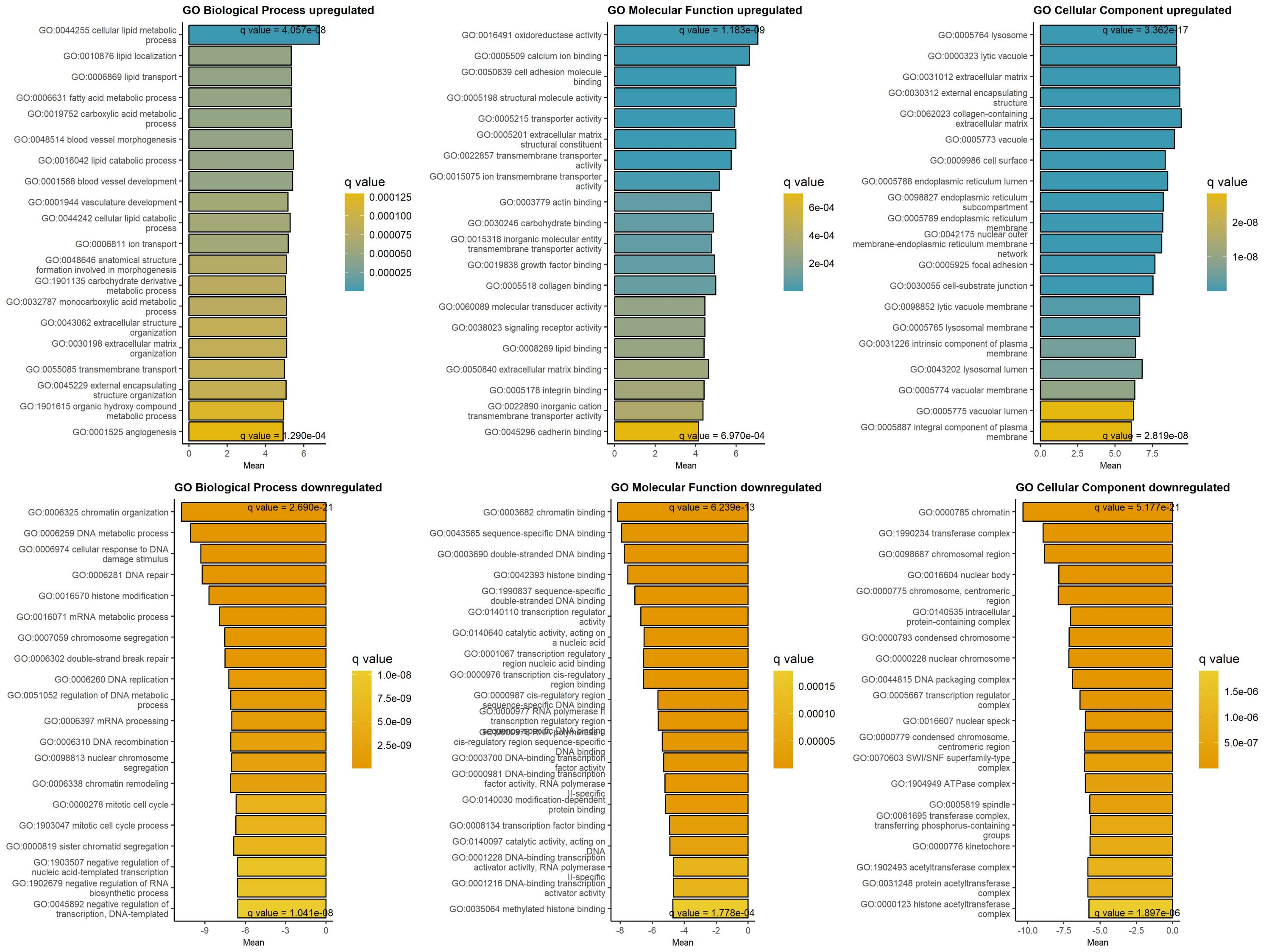


Downregulated at low/absent DEK Upregulated at low/absent DEK



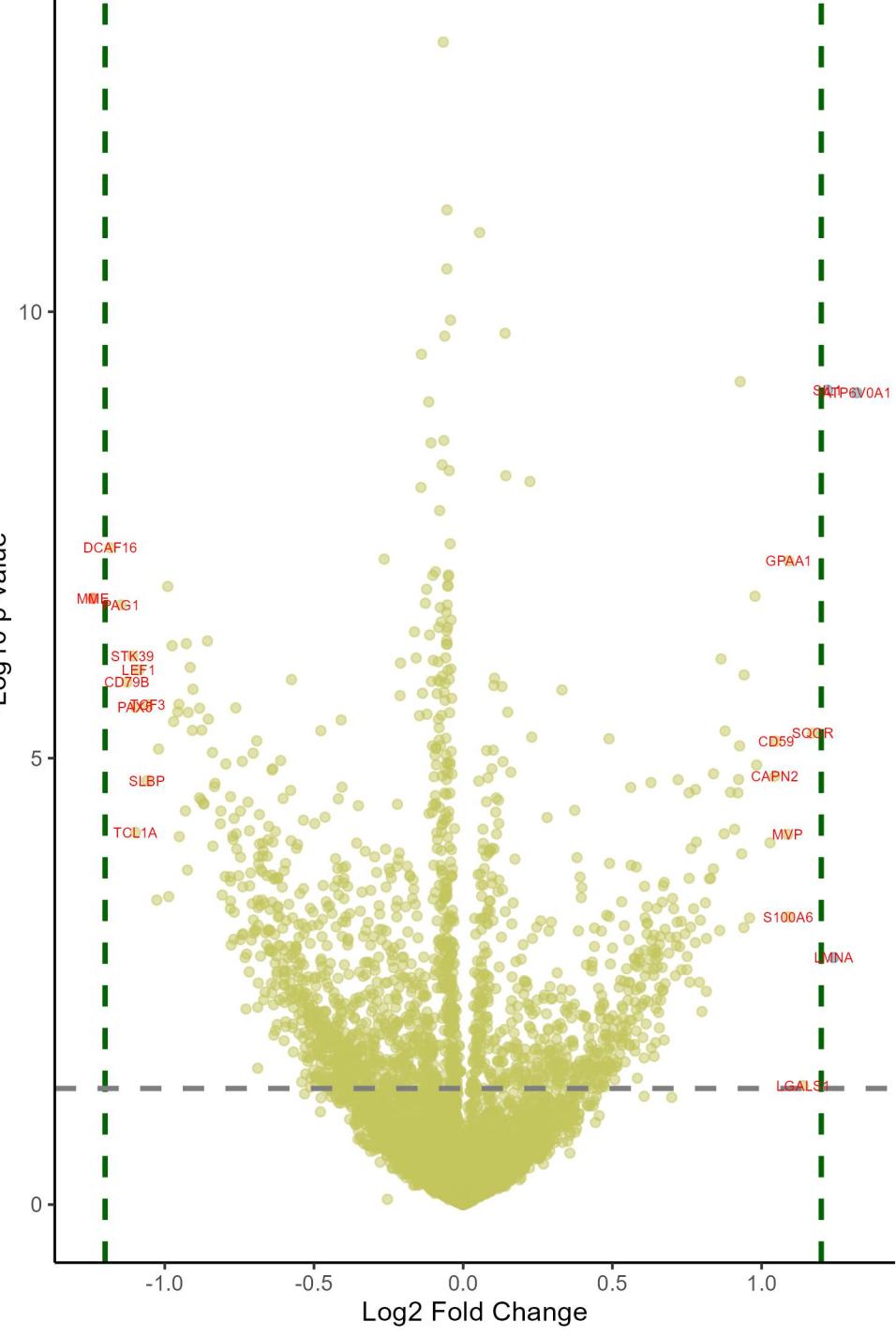
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.97	1.42e-24	BRD2	bromodomain containing 2	0.74	2.57e-12	CTSL	cathepsin L
-0.92	1.50e-22	BRD3	bromodomain containing 3	0.74	5.57e-10	RHOC	ras homolog family member C
-0.89	2.41e-23	ZNF280C	zinc finger protein 280C	0.72	5.22e-13	SERPINE2	serpin family E member 2
-0.82	6.90e-18	DAXX	death domain associated protein	0.72	3.92e-12	FAM114A1	family with sequence similarity 114
-0.82	3.99e-17	PM20D2	peptidase M20 domain containing 2	0.71	6.37e-10	STOM	stomatin
-0.82	6.28e-20	HELLS	helicase, lymphoid specific	0.7	1.18e-06	LGALS3	galectin 3
-0.77	1.08e-22	VRK1	VRK serine/threonine kinase 1	0.68	2.18e-07	S100A10	S100 calcium binding protein A10
-0.77	2.36e-21	NSMCE4A	NSE4 homolog A, SMC5-SMC6 complex c	0.66	4.32e-14	CPQ	carboxypeptidase Q
-0.77	6.79e-13	MRGBP	MRG domain binding protein	0.64	2.46e-10	MVP	major vault protein
-0.75	1.10e-17	EZH2	enhancer of zeste 2 polycomb repres	0.64	1.95e-09	LRP1	LDL receptor related protein 1
-0.74	5.64e-19	AURKB	aurora kinase B	0.64	2.57e-06	LGALS1	galectin 1
-0.73	1.41e-17	CDCA5	cell division cycle associated 5	0.62	1.30e-10	WFS1	wolframin ER transmembrane glycopro
-0.73	1.11e-12	PMF1	polyamine modulated factor 1	0.6	1.64e-05	NQO1	NAD(P)H quinone dehydrogenase 1
-0.73	9.61e-20	KAT7	lysine acetyltransferase 7	0.59	1.87e-11	DAB2	DAB adaptor protein 2
-0.72	8.18e-22	PHF3	PHD finger protein 3	0.59	1.12e-08	EPDR1	ependymin related 1
-0.72	1.08e-16	UPF3B	UPF3B regulator of nonsense mediate	0.58	1.47e-08	LACTB	lactamase beta
-0.71	2.50e-14	SREK1	splicing regulatory glutamic acid a	0.57	1.75e-08	NEU1	neuraminidase 1
-0.71	7.05e-16	CKAP2	cytoskeleton associated protein 2	0.56	1.31e-06	NES	nestin
-0.7	6.76e-10	CHRAC1	chromatin accessibility complex sub	0.56	7.96e-09	RETSAT	retinol saturase
-0.7	1.00e-14	KIF2C	kinesin family member 2C	0.56	1.22e-08	DEC2	2,4-dienoyl-CoA reductase 2
-0.7	2.61e-20	KIFC1	kinesin family member C1	0.56	1.81e-08	SLC4A2	solute carrier family 4 member 2
-0.7	5.02e-09	CORO1A	coronin 1A	0.55	2.87e-07	CPS1	carbamoyl-phosphate synthase 1
-0.7	1.48e-19	SUZ12	SUZ12 polycomb repressive complex 2	0.55	9.87e-08	COL6A1	collagen type VI alpha 1 chain
-0.69	2.89e-15	MEAF6	MYST/Esa1 associated factor 6	0.55	3.07e-08	APOL2	apolipoprotein L2
-0.69	4.01e-15	FRG1	FSHD region gene 1	0.55	4.60e-06	CD59	CD59 molecule (CD59 blood group)
-0.69	3.47e-16	CHAF1A	chromatin assembly factor 1 subunit	0.54	4.85e-08	BAG3	BAG cochaperone 3
-0.69	6.29e-14	SUDS3	SDS3 homolog, SIN3A corepressor com	0.53	4.40e-06	NNMT	nicotinamide N-methyltransferase
-0.68	4.95e-17	BUD13	BUD13 homolog	0.53	1.98e-07	HMOX1	heme oxygenase 1
-0.68	2.44e-14	HIRIP3	HIRA interacting protein 3	0.53	8.22e-08	LAMB2	laminin subunit beta 2

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



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

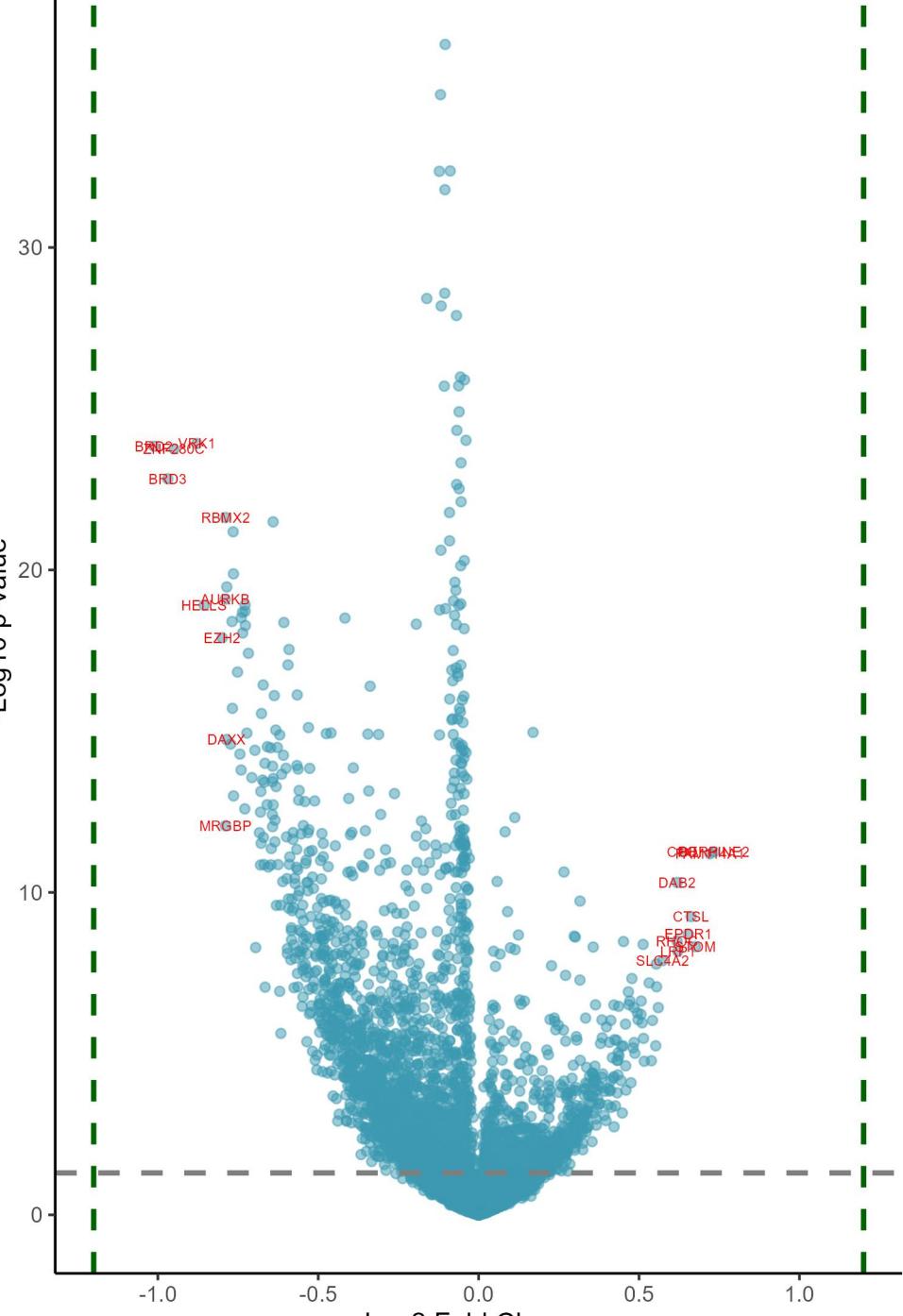
Downregulated in blood cancers at low/absent DEK Upregulated in blood cancers at low/absent DEK



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.24	3.09e-05	MME	membrane metalloendopeptidase	1.32	4.89e-07	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-1.18	1.27e-05	DCAF16	DDB1 and CUL4 associated factor 16	1.24	1.94e-02	LMNA	lamin A/C
-1.15	3.36e-05	PAG1	phosphoprotein membrane anchor with	1.22	4.89e-07	SIL1	SIL1 nucleotide exchange factor
-1.13	1.28e-04	CD79B	CD79b molecule	1.17	3.28e-04	SQOR	sulfide quinone oxidoreductase
-1.11	8.85e-05	STK39	serine/threonine kinase 39	1.14	1.35e-01	LGALS1	galectin 1
-1.1	2.06e-04	PAX5	paired box 5	1.09	1.64e-05	GPAA1	glycosylphosphatidylinositol anchor
-1.1	2.11e-03	TCL1A	TCL1 family AKT coactivator A	1.09	9.56e-03	S100A6	S100 calcium binding protein A6
-1.09	1.08e-04	LEF1	lymphoid enhancer binding factor 1	1.09	2.18e-03	MVP	major vault protein
-1.06	7.87e-04	SLBP	stem-loop binding protein	1.05	3.84e-04	CD59	CD59 molecule (CD59 blood group)
-1.06	1.94e-04	TCF3	transcription factor 3	1.04	7.30e-04	CAPN2	calpain 2
-1.03	7.10e-03	PTPRCAP	protein tyrosine phosphatase recept	1.03	2.58e-03	STOM	stomatin
-1.02	4.45e-04	ZHX2	zinc fingers and homeoboxes 2	0.98	5.87e-04	TYMP	thymidine phosphorylase
-0.99	2.48e-05	CYFIP2	cytoplasmic FMR1 interacting protei	0.98	3.00e-05	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.99	6.72e-03	SEPTIN1	septin 1	0.96	9.68e-03	LGALS3	galectin 3
-0.98	6.90e-05	ARID1B	AT-rich interaction domain 1B	0.94	1.20e-04	NME3	NME/NM23 nucleoside diphosphate kin
-0.97	2.58e-04	GTSE1	G2 and S-phase expressed 1	0.94	1.14e-02	ANXA1	annexin A1
-0.96	2.22e-04	IGLL1	immunoglobulin lambda like polypept	0.93	3.11e-03	RAB27A	RAB27A, member RAS oncogene family
-0.95	1.94e-04	GPALPP1	GPALPP motifs containing 1	0.93	4.49e-07	ALDH1L2	aldehyde dehydrogenase 1 family mem
-0.95	2.28e-03	CD22	CD22 molecule	0.93	4.22e-04	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.93	1.39e-03	CD19	CD19 molecule	0.92	7.73e-04	DNAJC1	DnaJ heat shock protein family (Hsp
-0.93	6.76e-05	KAT8	lysine acetyltransferase 8	0.92	9.99e-04	GNPDA1	glucosamine-6-phosphate deaminase 1
-0.92	4.24e-03	SASH3	SAM and SH3 domain containing 3	0.91	1.99e-03	ACP2	acid phosphatase 2, lysosomal
-0.92	2.22e-04	SDCBP	syndecan binding protein	0.9	9.99e-04	NEU1	neuraminidase 1
-0.91	1.05e-04	PIK3R1	phosphoinositide-3-kinase regulator	0.88	3.14e-04	CYB5R1	cytochrome b5 reductase 1
-0.91	3.14e-04	ASMTL	acetylserotonin O-methyltransferase	0.87	2.16e-03	NPTN	neuroplastin
-0.91	1.46e-04	PHC2	polyhomeotic homolog 2	0.86	9.03e-05	EDEM3	ER degradation enhancing alpha-mann
-0.88	2.07e-04	CARMIL2	capping protein regulator and myosi	0.86	1.19e-02	CTTN	cortactin
-0.88	1.10e-03	HS2ST1	heparan sulfate 2-O-sulfotransferas	0.84	6.98e-04	ERMP1	endoplasmic reticulum metallopeptid
-0.88	1.14e-03	SMYD3	SET and MYND domain containing 3	0.84	4.14e-03	ARID3B	AT-rich interaction domain 3B

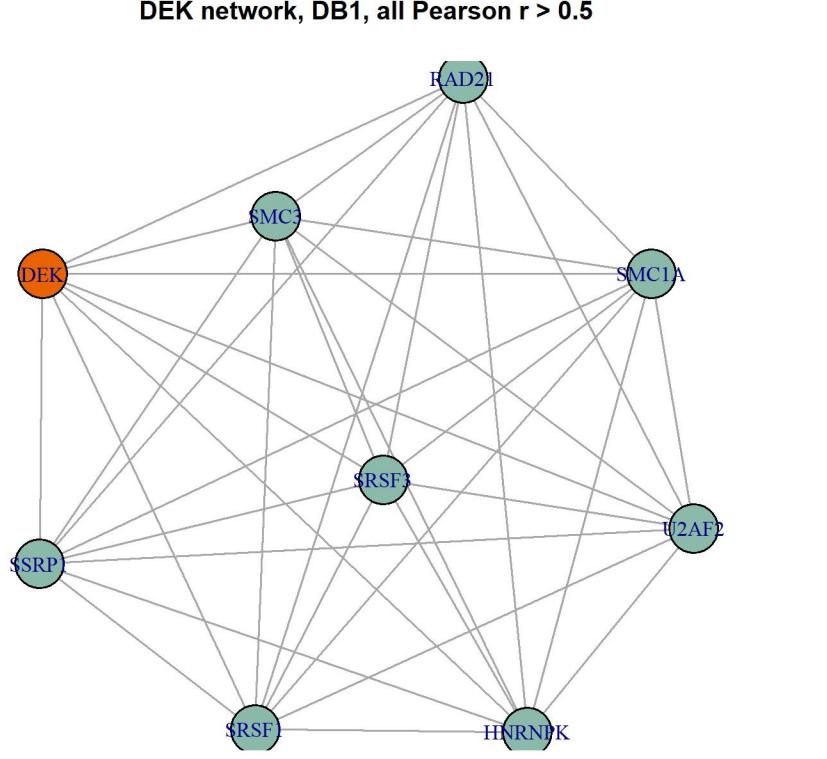
Differentially expressed proteins in solid cancers at absence/low amount of DEK , DB1
p-value < 0.05 & logFC > 1.2

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

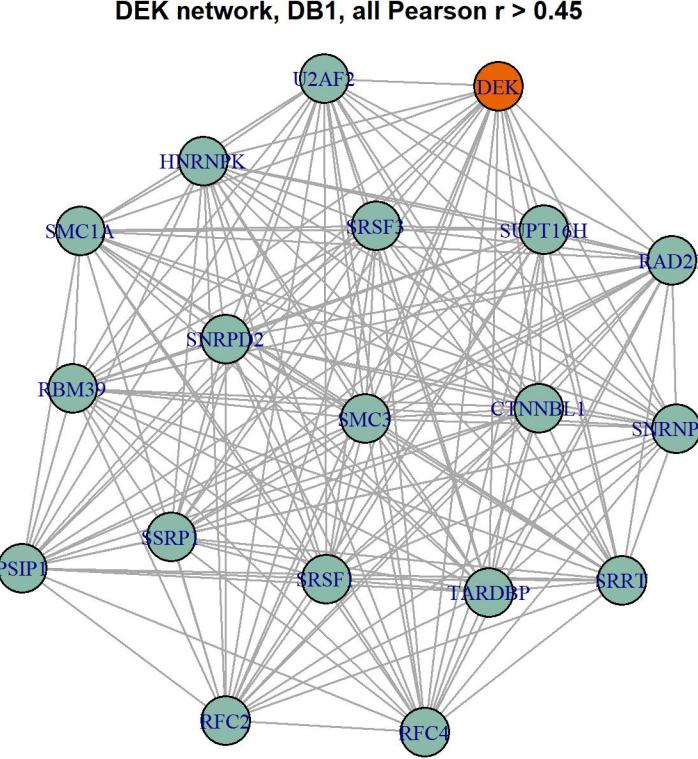


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.01	5.13e-22	BRD2	bromodomain containing 2	0.73	1.77e-10	SERPINE2	serpin family E member 2
-0.97	4.50e-21	BRD3	bromodomain containing 3	0.72	2.01e-10	FAM114A1	family with sequence similarity 114
-0.95	5.85e-22	ZNF280C	zinc finger protein 280C	0.68	8.23e-08	STOM	stomatin
-0.88	4.45e-22	VRK1	VRK serine/threonine kinase 1	0.66	1.20e-08	CTSL	cathepsin L
-0.86	1.95e-17	HELLS	helicase, lymphoid specific	0.65	3.73e-08	EPDR1	ependymin related 1
-0.8	1.46e-16	EZH2	enhancer of zeste 2 polycomb repres	0.64	1.77e-10	CPQ	carboxypeptidase Q
-0.79	1.41e-17	AURKB	aurora kinase B	0.62	1.10e-07	LRP1	LDL receptor related protein 1
-0.79	3.52e-11	MRGBP	MRG domain binding protein	0.62	1.24e-09	DAB2	DAB adaptor protein 2
-0.79	5.82e-20	RBMX2	RNA binding motif protein X-linked	0.62	5.84e-08	RHOC	ras homolog family member C
-0.79	1.26e-13	DAXX	death domain associated protein	0.57	1.96e-07	SLC4A2	solute carrier family 4 member 2
-0.79	6.20e-18	NSMCE4A	NSE4 homolog A, SMC5-SMC6 complex c	0.56	4.03e-06	RAB8B	RAB8B, member RAS oncogene family
-0.77	1.68e-13	PM20D2	peptidase M20 domain containing 2	0.55	1.10e-06	FAH	fumarylacetoacetate hydrolase
-0.77	5.17e-17	BUD13	BUD13 homolog	0.55	2.46e-07	TLN2	talin 2
-0.77	1.69e-14	FRG1	FSHD region gene 1	0.55	4.46e-05	NNMT	nicotinamide N-methyltransferase
-0.77	1.50e-19	PHF3	PHD finger protein 3	0.54	9.02e-06	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa
-0.76	2.58e-18	KIFC1	kinesin family member C1	0.54	1.16e-04	LGALS1	galectin 1
-0.76	4.72e-12	PMF1	polyamine modulated factor 1	0.53	8.53e-07	RPS27L	ribosomal protein S27 like
-0.75	1.48e-15	CHAF1A	chromatin assembly factor 1 subunit	0.52	1.20e-04	NES	nestin
-0.74	3.14e-13	KIF2C	kinesin family member 2C	0.51	2.82e-05	S100A10	S100 calcium binding protein A10
-0.74	8.73e-13	PHF2	PHD finger protein 2	0.51	7.11e-08	BLVRB	biliverdin reductase B
-0.74	4.11e-17	ATAD2	ATPase family AAA domain containing	0.51	1.06e-05	LACTB	lactamase beta
-0.74	2.91e-17	VIRMA	vir like m6A methyltransferase asso	0.51	2.70e-06	GYS1	glycogen synthase 1
-0.74	1.05e-16	KAT7	lysine acetyltransferase 7	0.51	6.12e-06	RBPMS	RNA binding protein, mRNA processin
-0.73	1.13e-11	ZNF148	zinc finger protein 148	0.5	8.63e-06	LAMB2	laminin subunit beta 2
-0.73	1.95e-17	KMT2A	lysine methyltransferase 2A	0.49	5.58e-06	APOL2	apolipoprotein L2
-0.73	2.77e-17	INCENP	inner centromere protein	0.49	7.21e-05	CPS1	carbamoyl-phosphate synthase 1
-0.73	6.40e-17	SUZ12	SUZ12 polycomb repressive complex 2	0.48	3.63e-05	HMOX1	heme oxygenase 1
-0.72	8.57e-14	CDCA5	cell division cycle associated 5	0.48	4.03e-06	RETSAT	retinol saturase
-0.72	4.19e-16	NSMCE3	NSE3 homolog, SMC5-SMC6 complex com	0.48	5.09e-05	COL6A1	collagen type VI alpha 1 chain

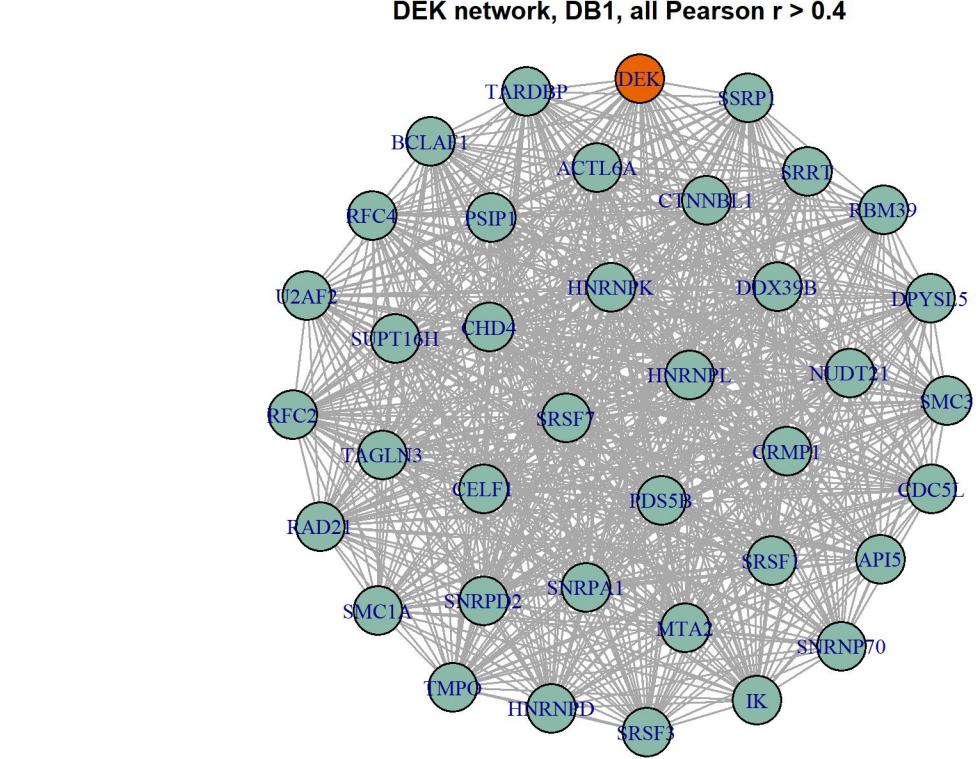
DEK network, DB1, all Pearson r > 0.5



DEK network, DB1, all Pearson r > 0.45

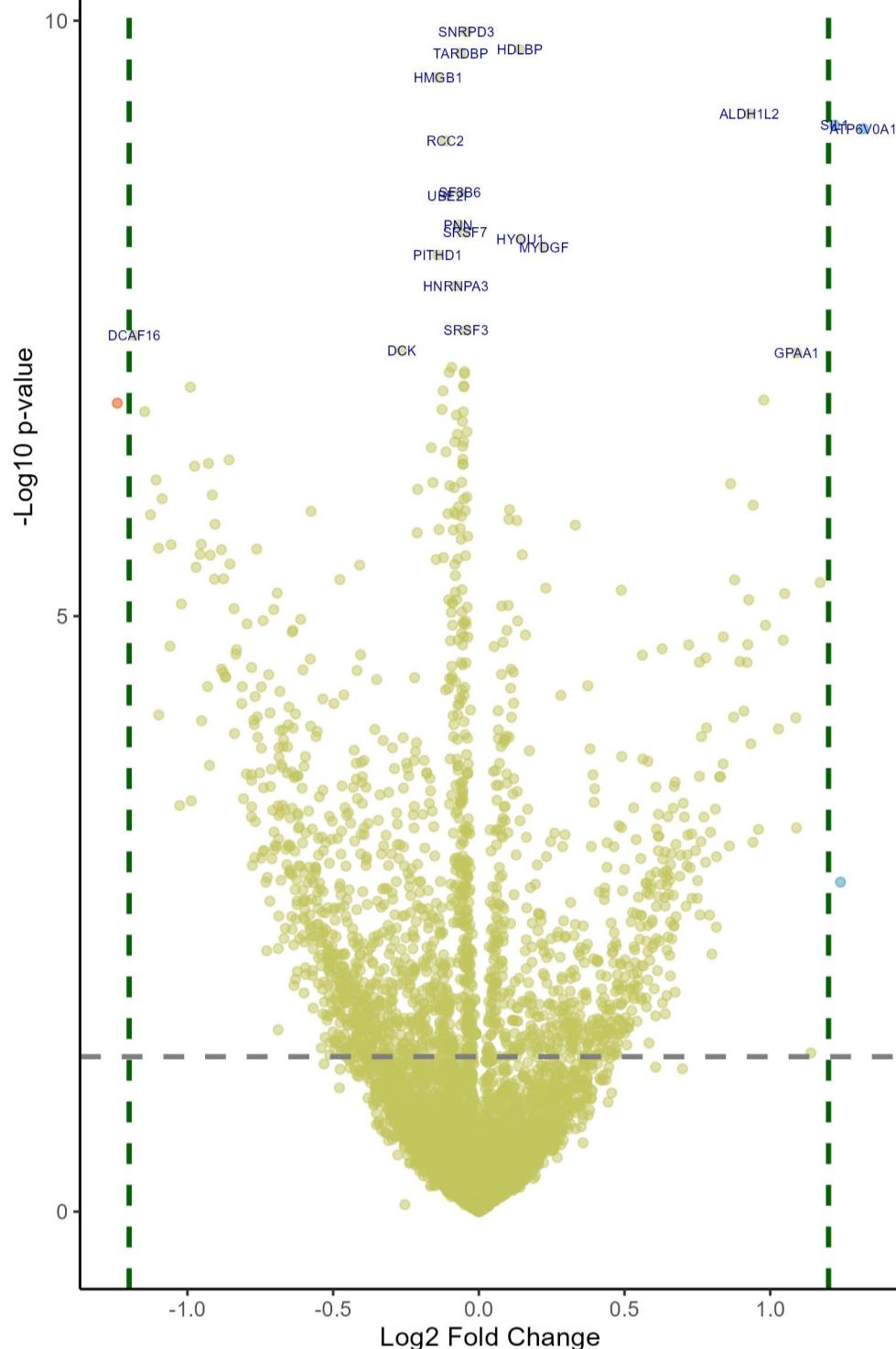


DEK network, DB1, all Pearson r > 0.4



Sorted by p values!

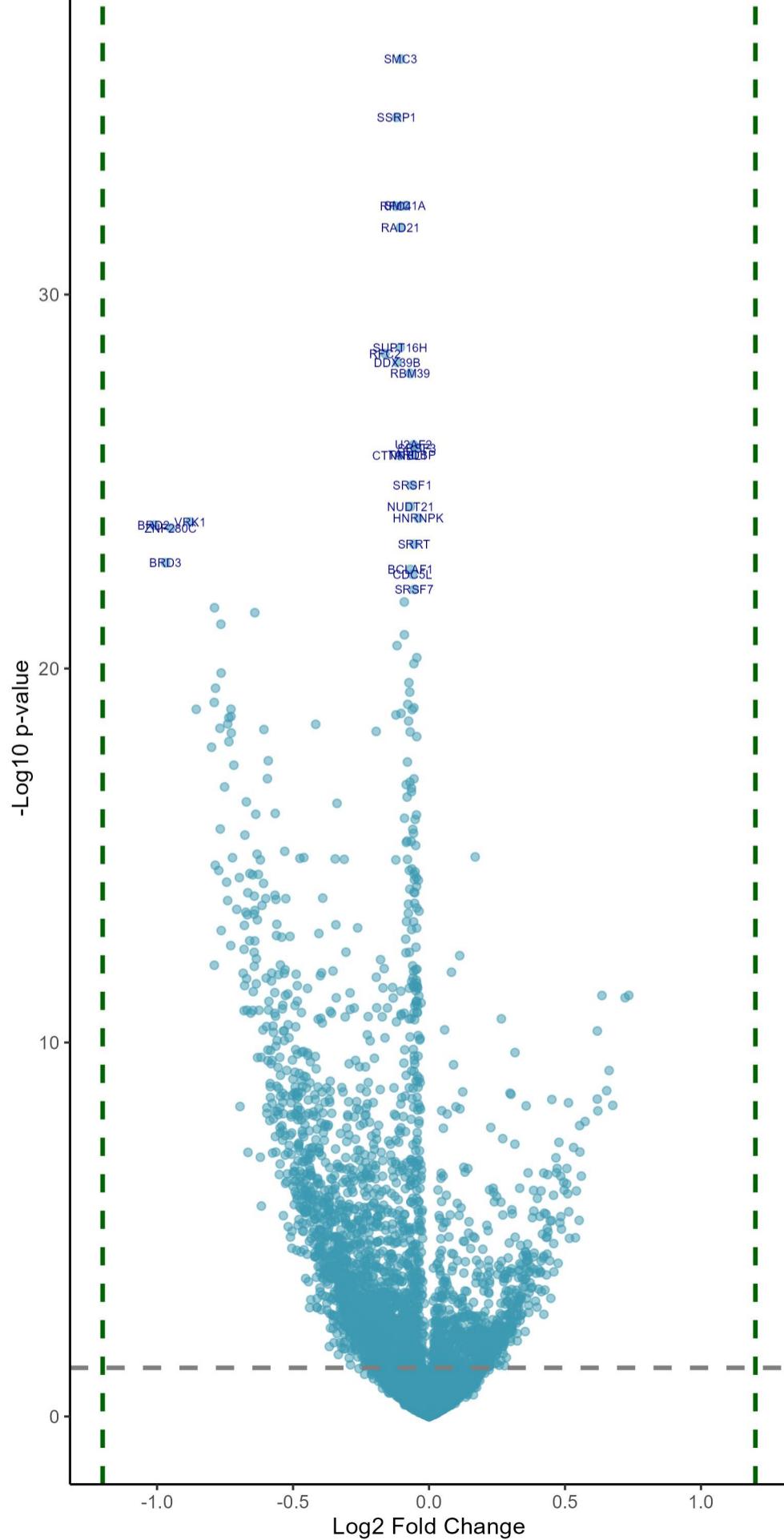
Downregulated in blood cancers at low/absent DEK Upregulated in blood cancers at low/absent DEK



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.07	6.36e-10	SRSF1	serine and arginine rich splicing f	0.06	2.88e-08	GAPDH	glyceraldehyde-3-phosphate dehydrog
-0.05	2.41e-08	SNRNP70	small nuclear ribonucleoprotein U1	0.14	1.78e-07	HDLBP	high density lipoprotein binding pr
-0.05	5.51e-08	HNRNPL	heterogeneous nuclear ribonucleopro	0.93	4.49e-07	ALDH1L2	aldehyde dehydrogenase 1 family mem
-0.04	1.65e-07	SNRPD3	small nuclear ribonucleoprotein D3	1.22	4.89e-07	SIL1	SIL1 nucleotide exchange factor
-0.06	1.78e-07	TARDBP	TAR DNA binding protein	1.32	4.89e-07	ATP6VOA1	ATPase H ⁺ transporting V0 subunit a
-0.14	2.49e-07	HMGB1	high mobility group box 1	0.14	2.54e-06	HYOU1	hypoxia up-regulated 1
-0.12	5.66e-07	RCC2	regulator of chromosome condensatio	0.22	2.79e-06	MYDGF	myeloid derived growth factor
-0.06	1.31e-06	SF3B6	splicing factor 3b subunit 6	1.09	1.64e-05	GPAA1	glycosylphosphatidylinositol anchor
-0.11	1.31e-06	UBE2I	ubiquitin conjugating enzyme E2 I	0.98	3.00e-05	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-0.07	2.16e-06	PNN	pinin, desmosome associated protein	0.86	9.03e-05	EDEM3	ER degradation enhancing alpha-mann
-0.05	2.35e-06	SRSF7	serine and arginine rich splicing f	0.94	1.20e-04	NME3	NME/NM23 nucleoside diphosphate kin
-0.14	3.09e-06	PITHD1	PITH domain containing 1	0.11	1.26e-04	HSPA5	heat shock protein family A (Hsp70)
-0.08	5.34e-06	HNRNPA3	heterogeneous nuclear ribonucleopro	0.1	1.36e-04	COPG1	COPI coat complex subunit gamma 1
-0.04	1.20e-05	SRSF3	serine and arginine rich splicing f	0.13	1.38e-04	UGGT1	UDP-glucose glycoprotein glucosyltr
-1.18	1.27e-05	DCAF16	DDB1 and CUL4 associated factor 16	0.33	1.47e-04	RRBP1	ribosome binding protein 1
-0.26	1.63e-05	DCK	deoxyribonuclease kinase	0.15	2.22e-04	P4HB	prolyl 4-hydroxylase subunit beta
-0.09	2.09e-05	DNAJC8	DnaJ heat shock protein family (Hsp	0.88	3.14e-04	CYB5R1	cytochrome b5 reductase 1
-0.05	2.12e-05	SAP18	Sin3A associated protein 18	1.17	3.28e-04	SQOR	sulfide quinone oxidoreductase
-0.1	2.12e-05	CBFB	core-binding factor subunit beta	0.23	3.62e-04	SPCS2	signal peptidase complex subunit 2
-0.05	2.12e-05	SF3B1	splicing factor 3b subunit 1	0.49	3.70e-04	FNDC3B	fibronectin type III domain contain
-0.05	2.48e-05	SNRPD2	small nuclear ribonucleoprotein D2	1.05	3.84e-04	CD59	CD59 molecule (CD59 blood group)
-0.05	2.48e-05	U2AF2	U2 small nuclear RNA auxiliary fact	0.93	4.22e-04	PLOD3	procollagen-lysine,2-oxoglutarate 5
-0.99	2.48e-05	CYFIP2	cytoplasmic FMR1 interacting protei	0.1	4.54e-04	PPIB	peptidylprolyl isomerase B
-0.12	2.59e-05	DDX39B	DExD-box helicase 39B	0.08	4.56e-04	CALR	calreticulin
-1.24	3.09e-05	MME	membrane metalloendopeptidase	0.13	5.68e-04	SSR4	signal sequence receptor subunit 4
-0.13	3.36e-05	TCEA1	transcription elongation factor A1	0.98	5.87e-04	TYMP	thymidine phosphorylase
-1.15	3.36e-05	PAG1	phosphoprotein membrane anchor with	0.1	6.40e-04	CLPP	caseinolytic mitochondrial matrix p
-0.05	3.36e-05	THRAP3	thyroid hormone receptor associated	0.16	6.83e-04	TOR1AIP1	torsin 1A interacting protein 1
-0.08	3.50e-05	LUC7L3	LUC7 like 3 pre-mRNA splicing facto	0.84	6.98e-04	ERMP1	endoplasmic reticulum metallopeptid
-0.06	3.85e-05	SNRPA1	small nuclear ribonucleoprotein pol	1.04	7.30e-04	CAPN2	calpain 2
-0.04	4.59e-05	HNRNPK	heterogeneous nuclear ribonucleopro	0.08	7.49e-04	PRKCSH	protein kinase C substrate 80K-H
-0.07	4.71e-05	SSRP1	structure specific recognition prot	0.92	7.73e-04	DNAJC1	DnaJ heat shock protein family (Hsp
-0.05	5.19e-05	MATR3	matrin 3	0.72	7.73e-04	PAGE5	PAGE family member 5
-0.08	5.19e-05	RFC4	replication factor C subunit 4	0.05	7.89e-04	ARCN1	archain 1
-0.06	5.53e-05	RBM39	RNA binding motif protein 39	0.63	8.17e-04	SDC1	syndecan 1
-0.16	5.56e-05	CBX5	chromobox 5	0.56	9.00e-04	MAGEC1	MAGE family member C1
-0.11	5.90e-05	TAF15	TATA-box binding protein associated	0.78	9.43e-04	LRPAP1	LDL receptor related protein associ
-0.06	6.61e-05	SF3B3	splicing factor 3b subunit 3	0.9	9.99e-04	NEU1	neuraminidase 1
0.86	6.61e-05	BRCA1	breast cancer 1	0.76	9.99e-04	GOLIIM4	golgi integral membrane protein 4

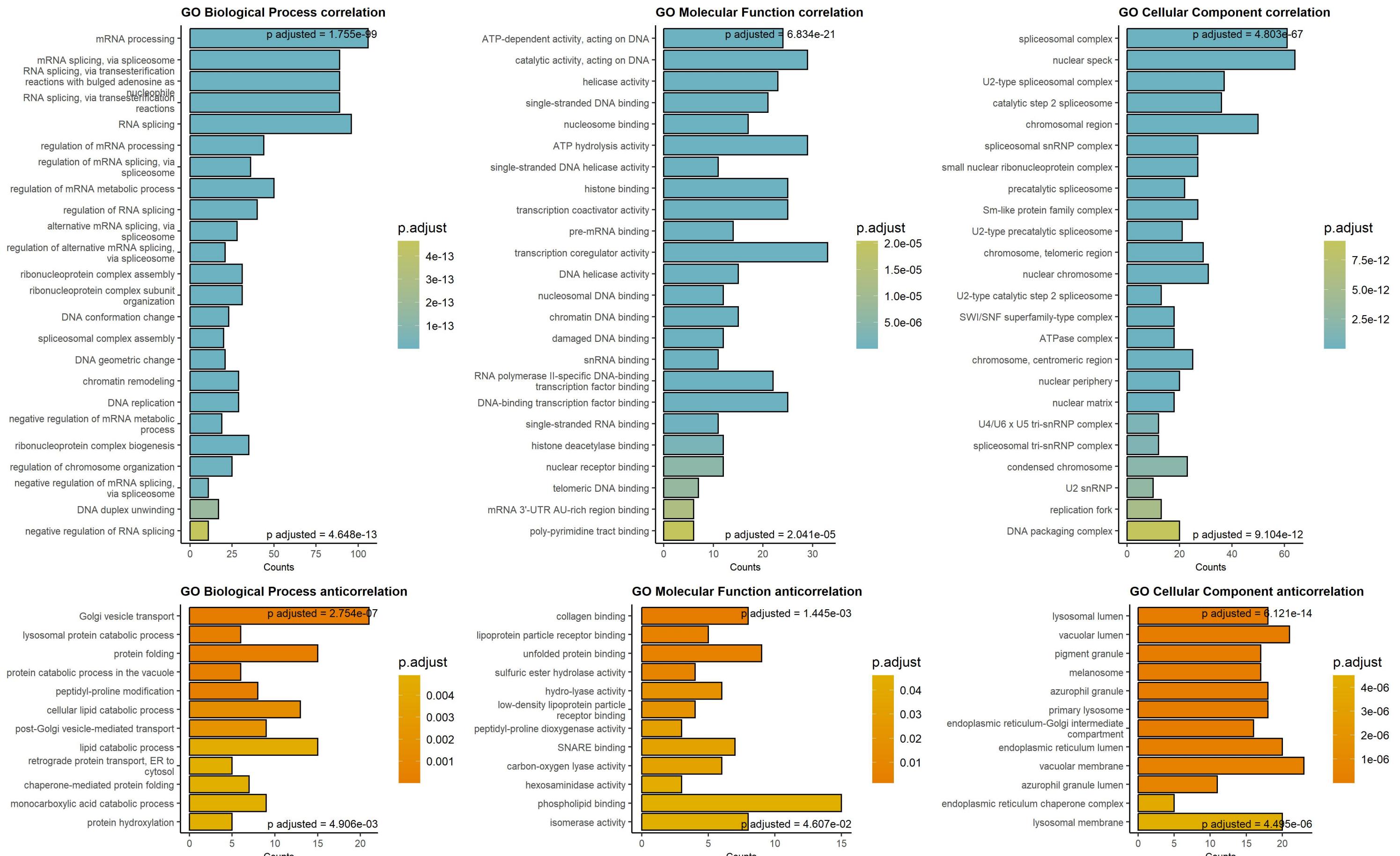
Sorted by p values!

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

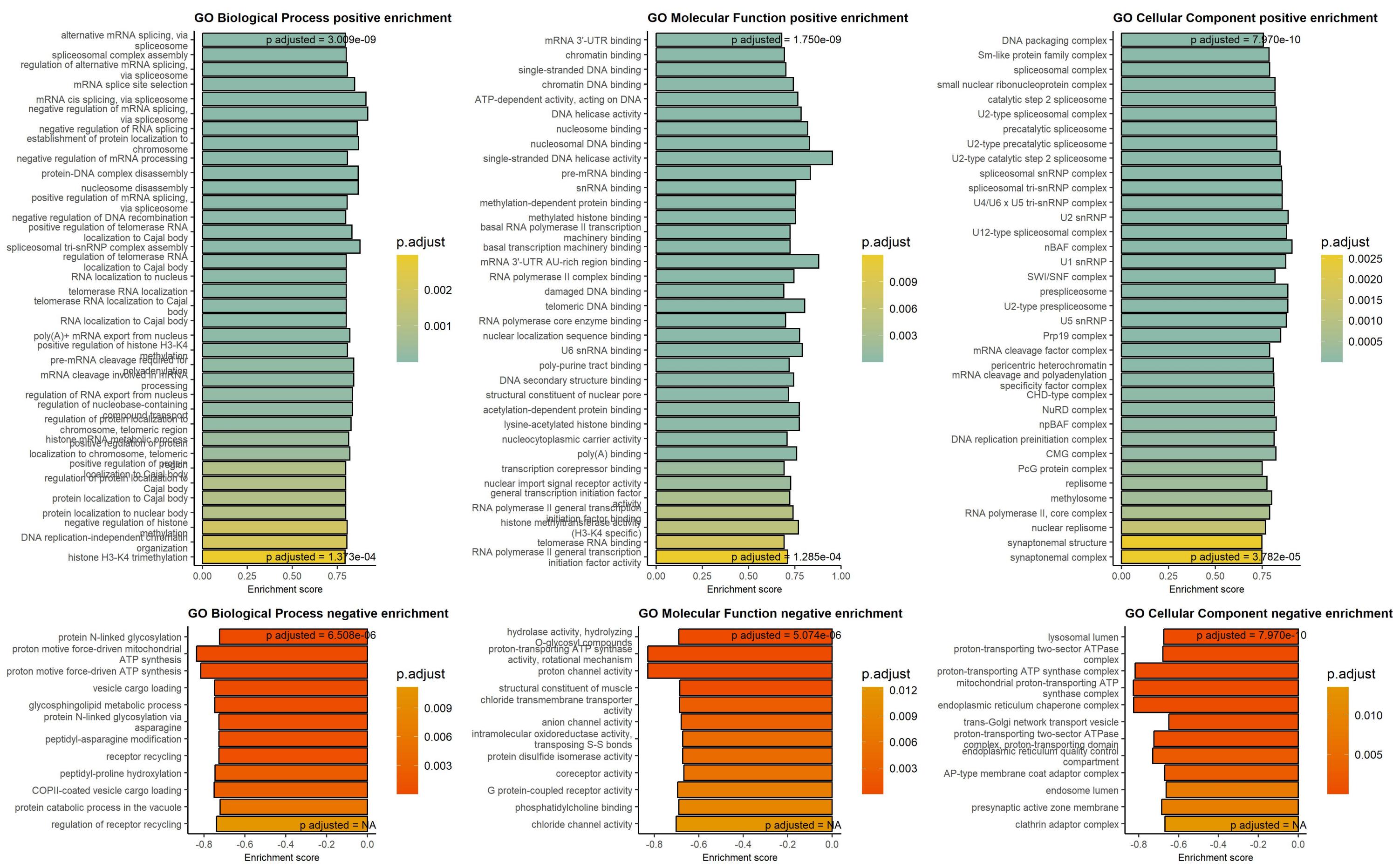


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.1	1.68e-33	SMC3	structural maintenance of chromosom	0.17	8.34e-14	RRBP1	ribosome binding protein 1
-0.12	4.04e-32	SSRP1	structure specific recognition prot	0.11	2.00e-11	GNS	glucosamine (N-acetyl)-6-sulfatase
-0.09	5.77e-30	SMC1A	structural maintenance of chromosom	0.08	5.13e-11	MYDGF	myeloid derived growth factor
-0.12	5.77e-30	RFC4	replication factor C subunit 4	0.73	1.77e-10	SERPINE2	serpin family E member 2
-0.11	1.79e-29	RAD21	RAD21 cohesin complex component	0.64	1.77e-10	CPQ	carboxypeptidase Q
-0.11	2.49e-26	SUPT16H	SPT16 homolog, facilitates chromati	0.72	2.01e-10	FAM114A1	family with sequence similarity 114
-0.16	3.17e-26	RFC2	replication factor C subunit 2	0.27	6.19e-10	SUCLG2	succinate-CoA ligase GDP-forming su
-0.12	4.80e-26	DDX39B	DExD-box helicase 39B	0.06	1.17e-09	P4HB	prolyl 4-hydroxylase subunit beta
-0.07	8.56e-26	RBM39	RNA binding motif protein 39	0.62	1.24e-09	DAB2	DAB adaptor protein 2
-0.06	6.29e-24	U2AF2	U2 small nuclear RNA auxiliary fact	0.32	4.35e-09	PLIN3	perilipin 3
-0.04	7.04e-24	SRSF3	serine and arginine rich splicing f	0.09	8.59e-09	CALU	calumenin
-0.06	9.45e-24	TARDBP	TAR DNA binding protein	0.66	1.20e-08	CTSL	cathepsin L
-0.11	9.45e-24	CTNNBL1	catenin beta like 1	0.65	3.73e-08	EPDR1	ependymin related 1
-0.06	5.52e-23	SRSF1	serine and arginine rich splicing f	0.12	3.98e-08	LRPAP1	LDL receptor related protein associ
-0.07	1.95e-22	NUDT21	nudix hydrolase 21	0.3	4.23e-08	GSTK1	glutathione S-transferase kappa 1
-0.04	3.73e-22	HNRNPK	heterogeneous nuclear ribonucleopro	0.3	4.53e-08	SQSTM1	sequestosome 1
-0.88	4.45e-22	VRK1	VRK serine/threonine kinase 1	0.62	5.84e-08	RHOC	ras homolog family member C
-1.01	5.13e-22	BRD2	bromodomain containing 2	0.45	5.97e-08	SIAE	sialic acid acetyltransferase
-0.95	5.85e-22	ZNF280C	zinc finger protein 280C	0.51	7.11e-08	BLVRB	biliverdin reductase B
-0.05	1.51e-21	SRRT	serrate, RNA effector molecule	0.68	8.23e-08	STOM	stomatin
-0.97	4.50e-21	BRD3	bromodomain containing 3	0.36	8.46e-08	CTSA	cathepsin A
-0.07	6.44e-21	BCLAF1	BCL2 associated transcription facto	0.1	8.92e-08	CTSD	cathepsin D
-0.06	8.43e-21	CDC5L	cell division cycle 5 like	0.11	9.90e-08	LMNA	lamin A/C
-0.05	2.04e-20	SRSF7	serine and arginine rich splicing f	0.05	1.09e-07	EEF1D	eukaryotic translation elongation f
-0.09	4.25e-20	MTA2	metastasis associated 1 family memb	0.62</			

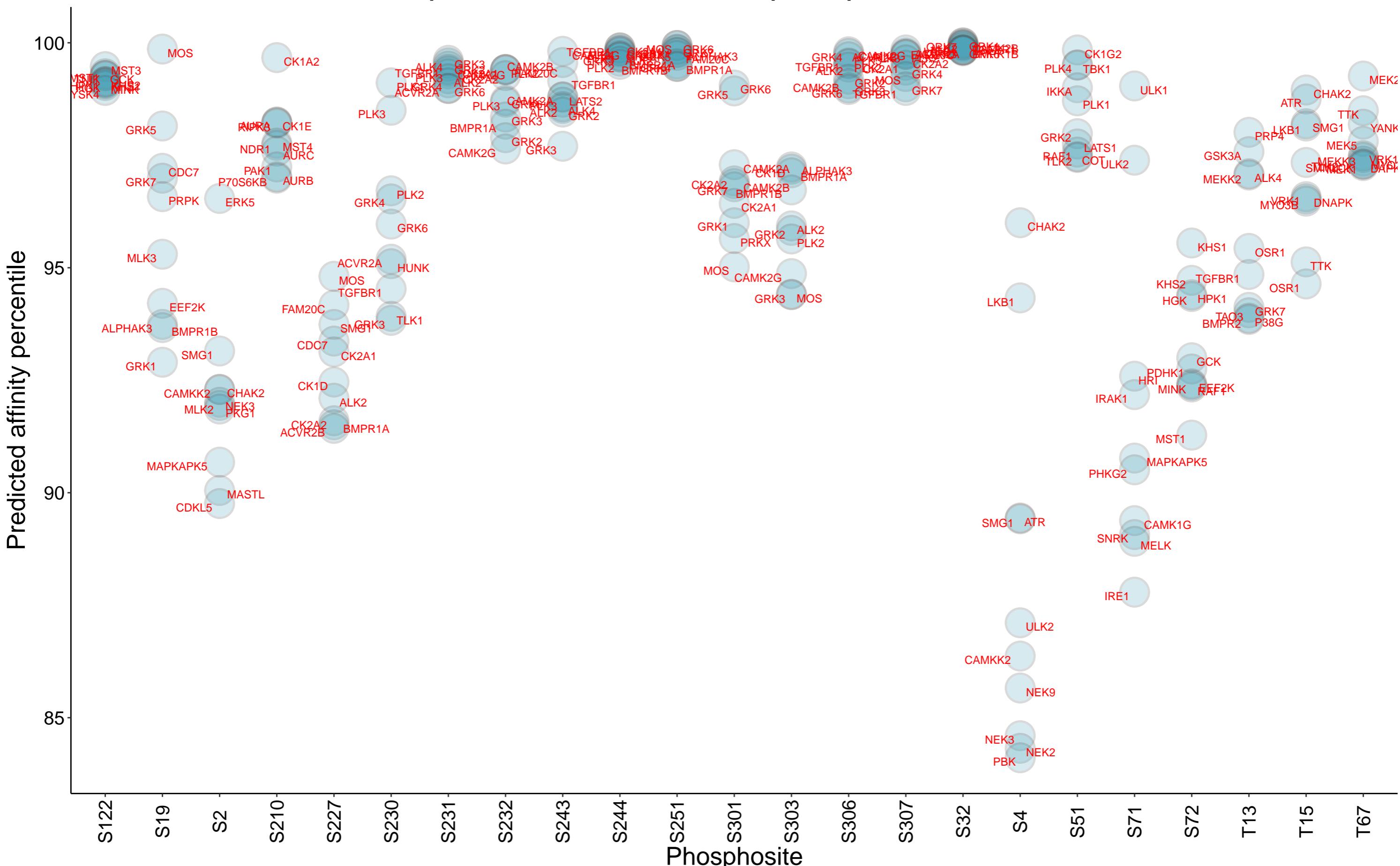
Top 250 correlation coefficients overrepresentation, DEK protein, DB1



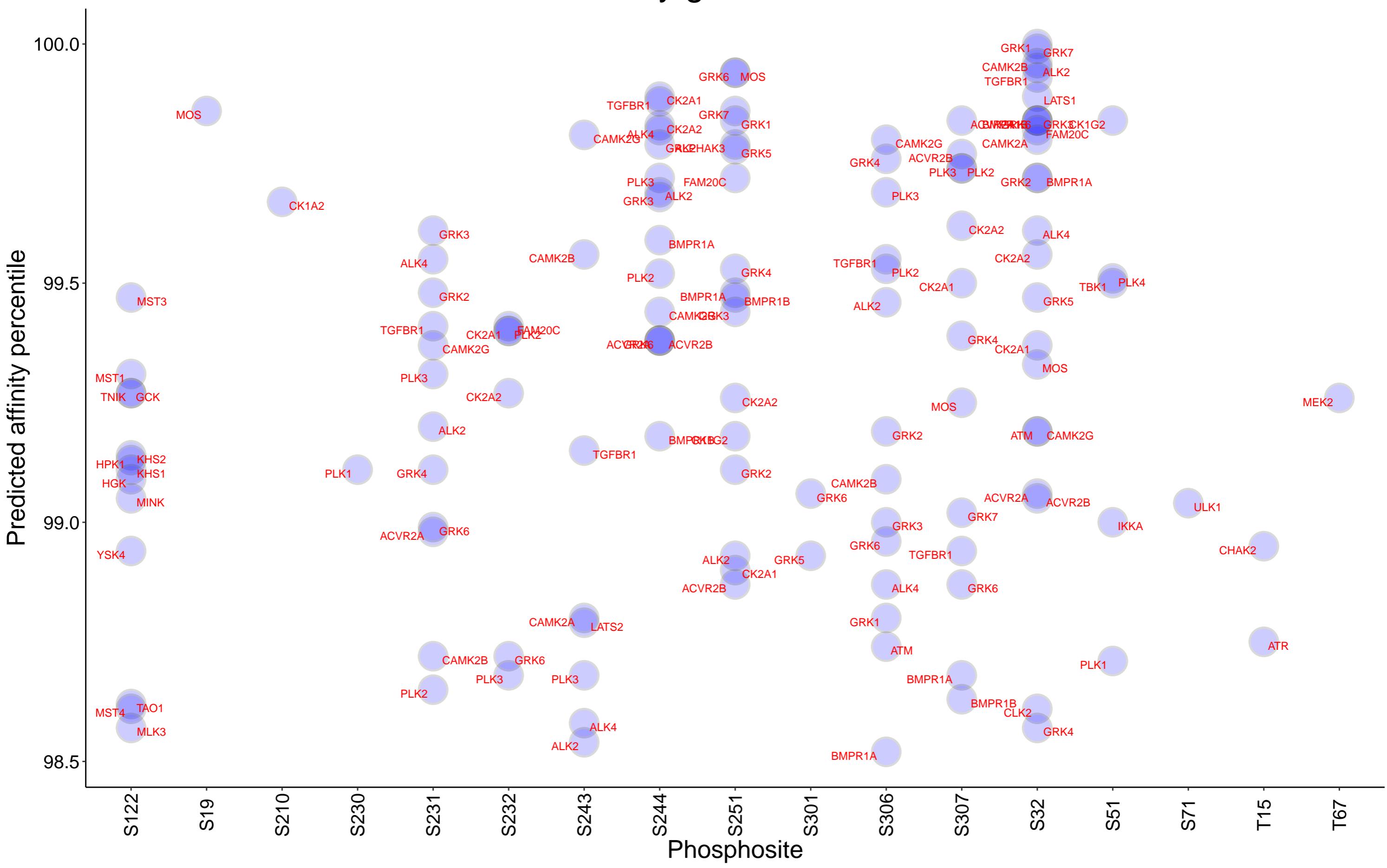
Gene Set Enrichment analysis on protein correlation coefficients, DEK protein, DB1



Top 10 kinases for each phosphosite in DEK



Kinases with affinity greater than 98.5% to DEK



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

Beware of false positives in tissues with small number of samples

