

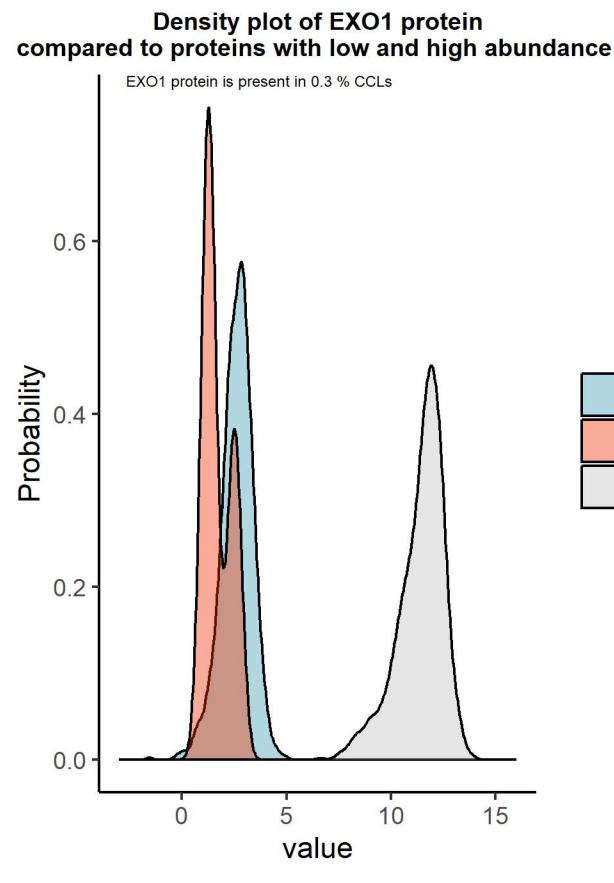
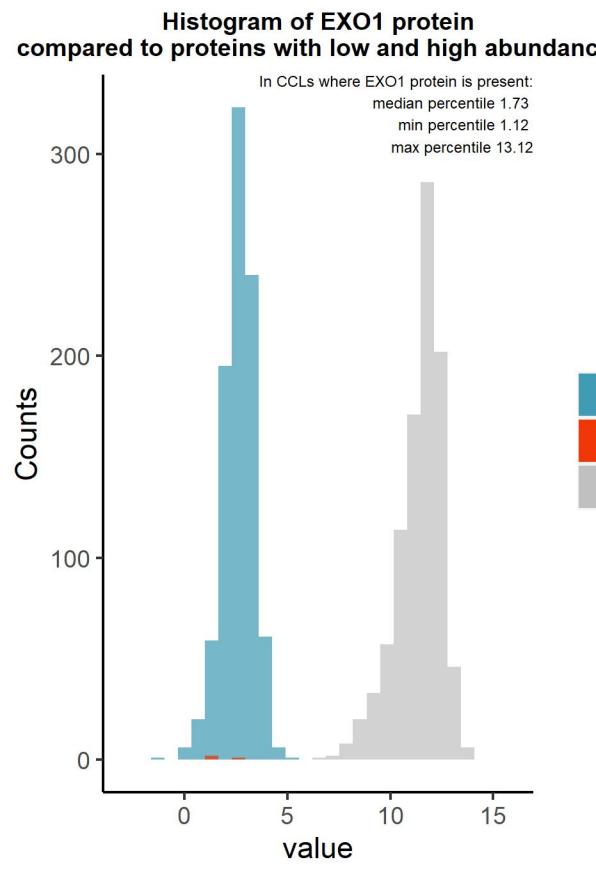
# EXO1

Protein name: EXO1 ; UNIPROT: Q9UQ84 ; Gene name: exonuclease 1

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

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

6692 proteins in 949 CCLs



### Top negative correlations of EXO1 protein, DB1

Pearson correlation coefficients

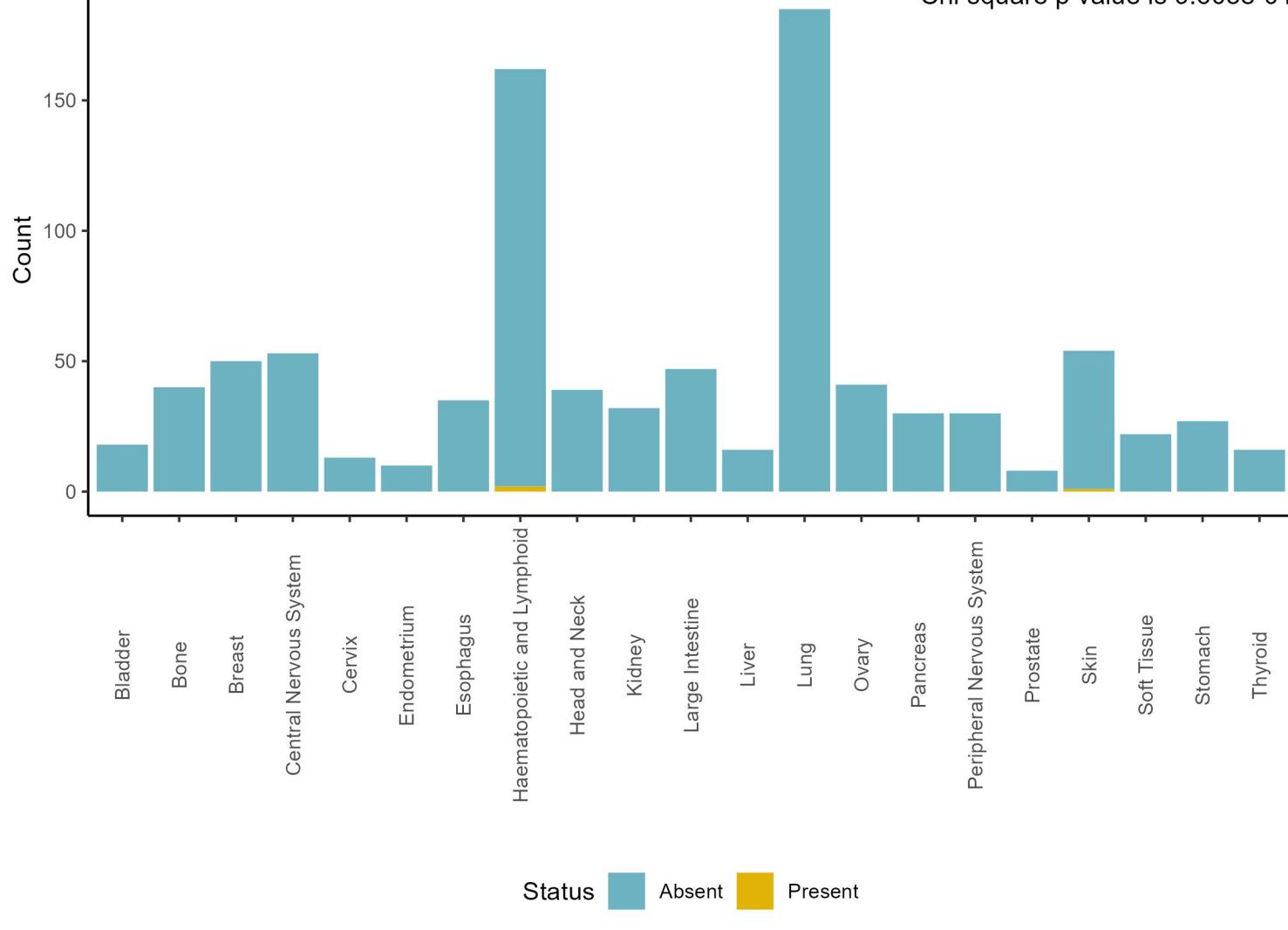
### Top positive correlations of EXO1 protein, DB1

Pearson correlation coefficients

## Amount of EXO1 protein, number of CCLs where it is present by tissue, DB1

## Present and absent EXO1 protein counts by tissue, DB1

Chi square p value is 9.603e-01

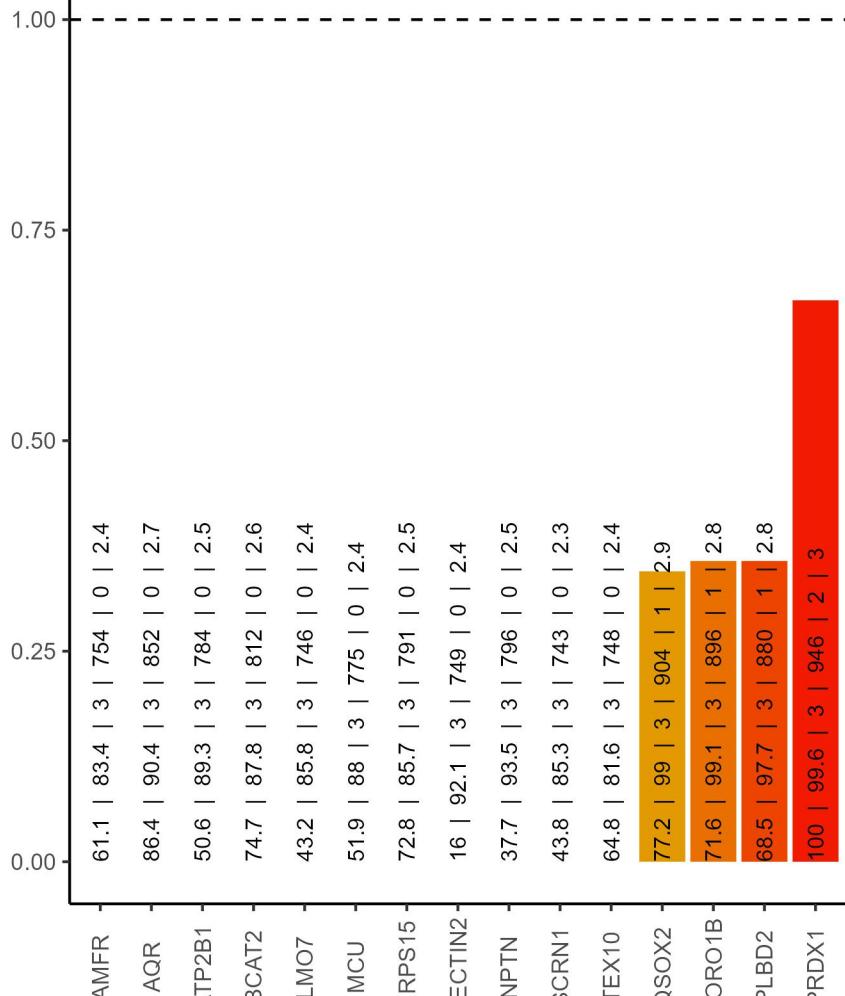


## Cooccurrence with EXO1 protein, DB1

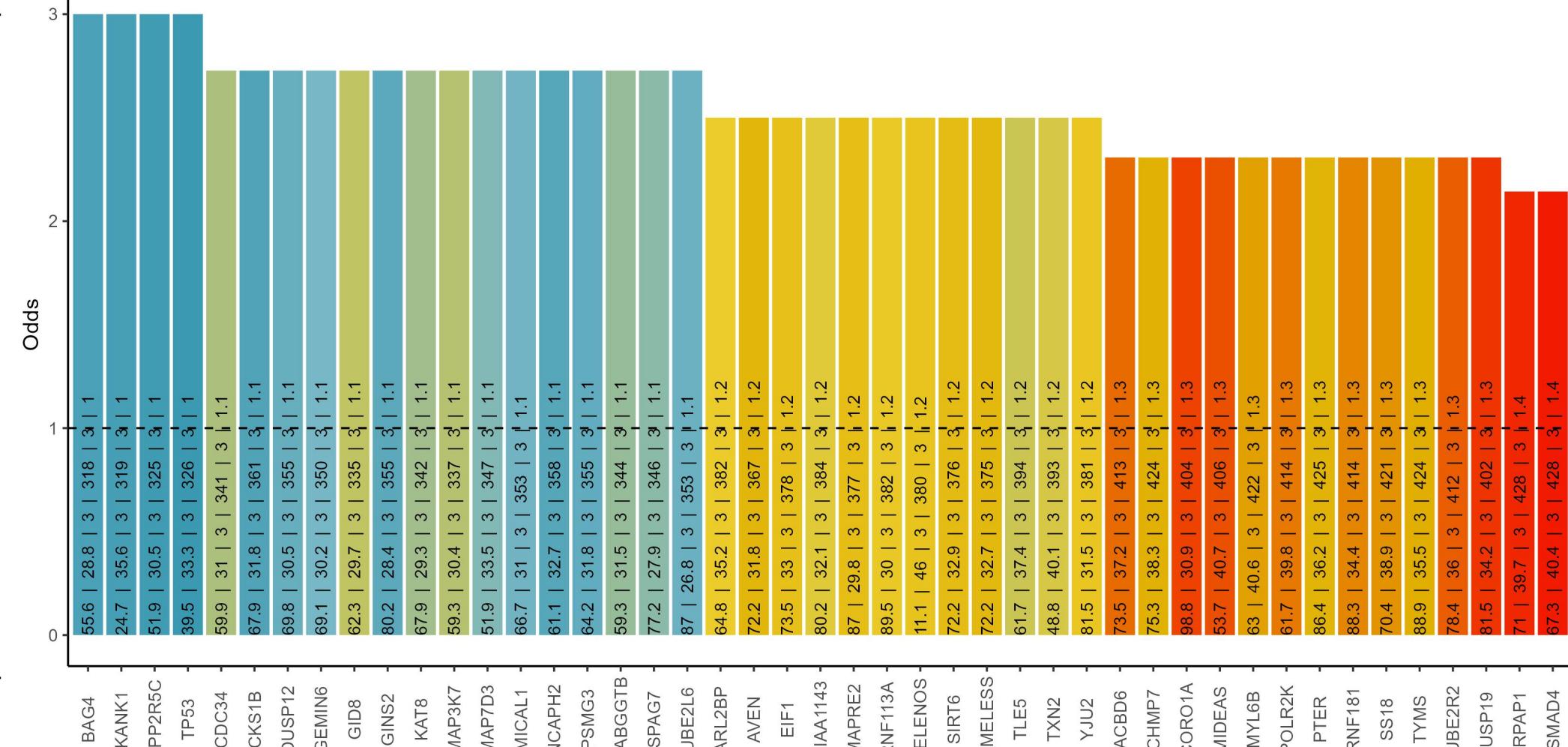
% of EXO1 in blood cancers: 1.2 ; % of EXO1 in solid cancers: 0.1

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EXO1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

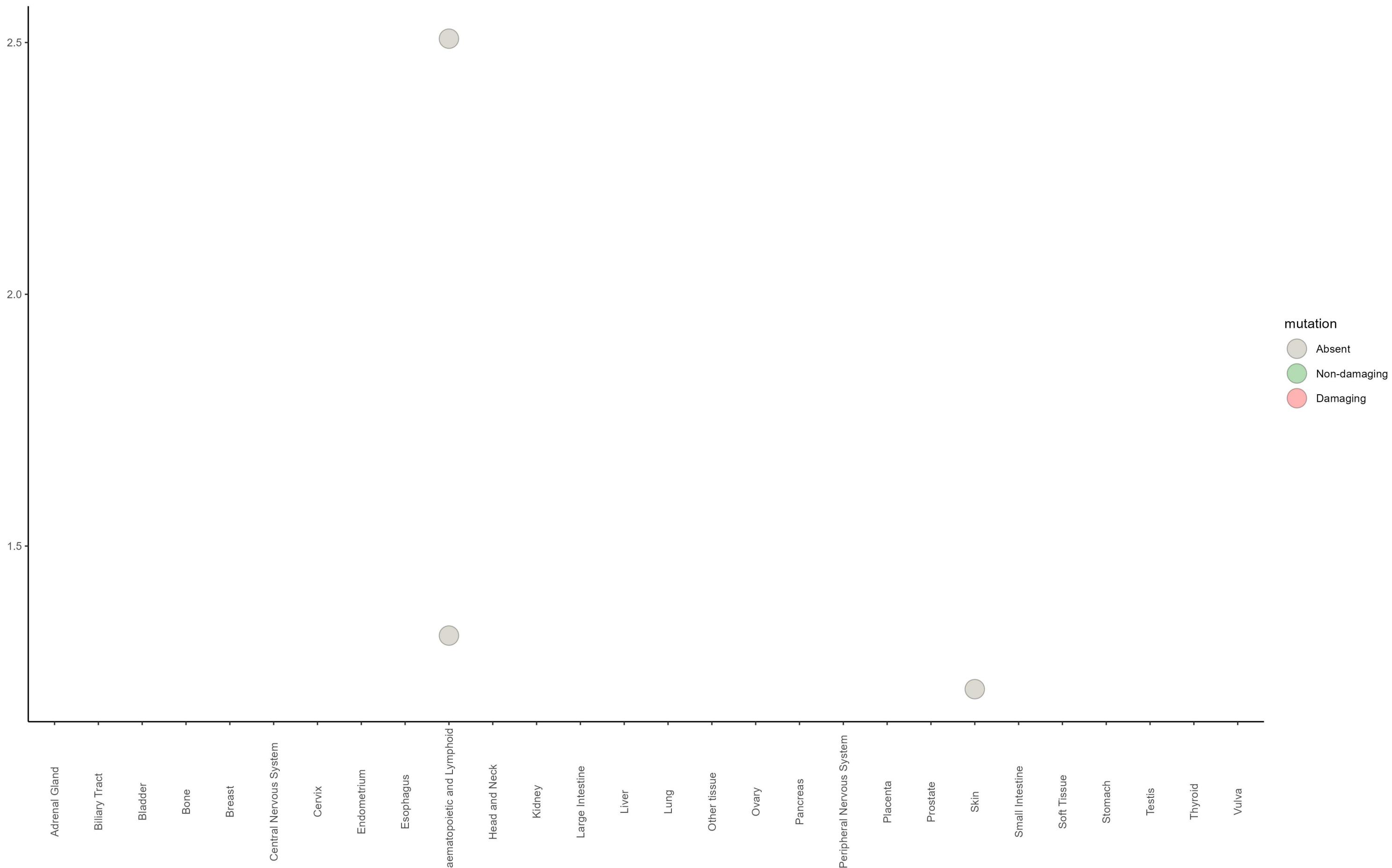
### Negative cooccurrence



### Positive cooccurrence



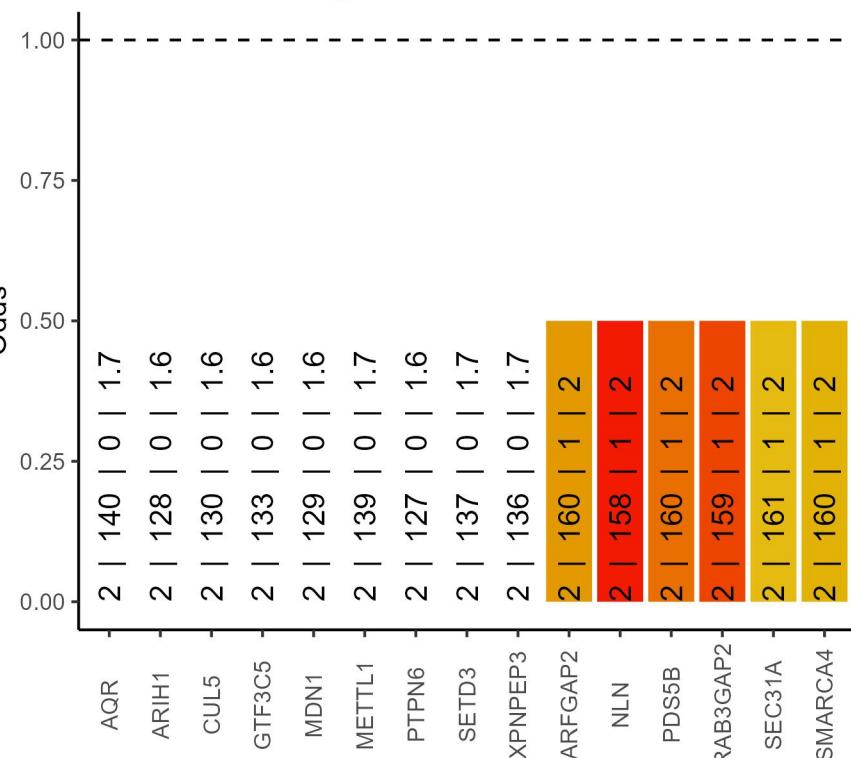
# Amount of EXO1 protein and mutation status by tissue, DB1



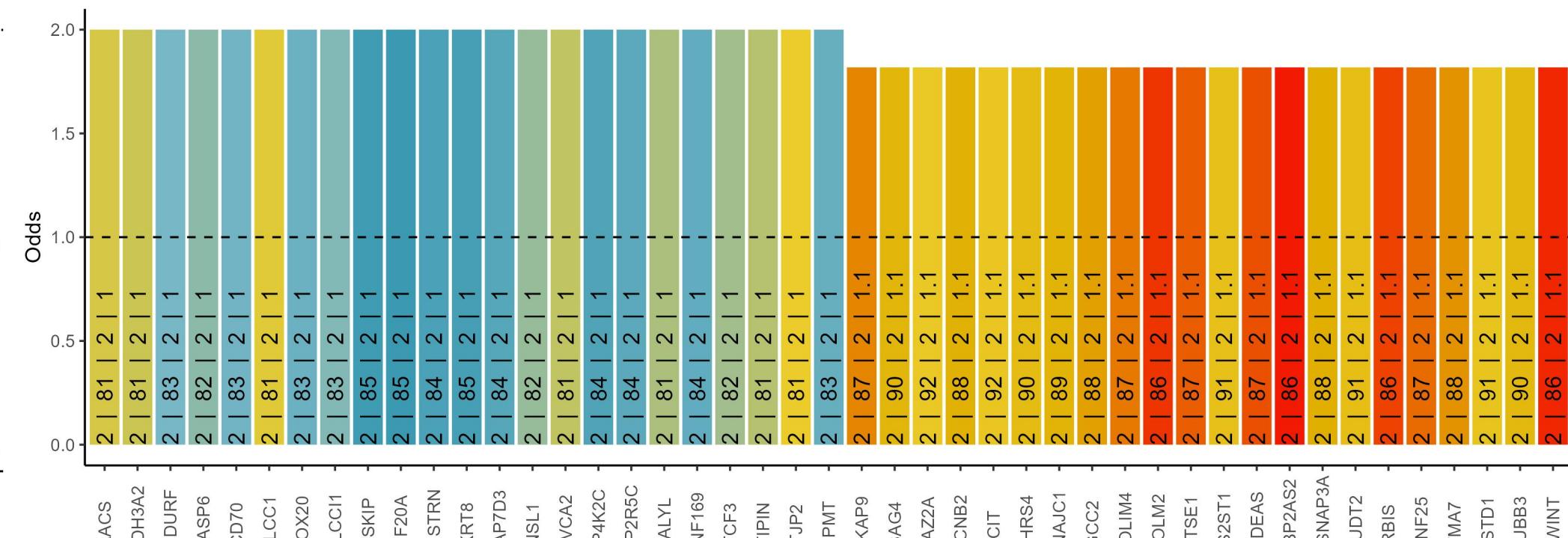
## Cooccurrence with EXO1 protein in blood cancers, DB1

The text in the bars: incidence of EXO1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



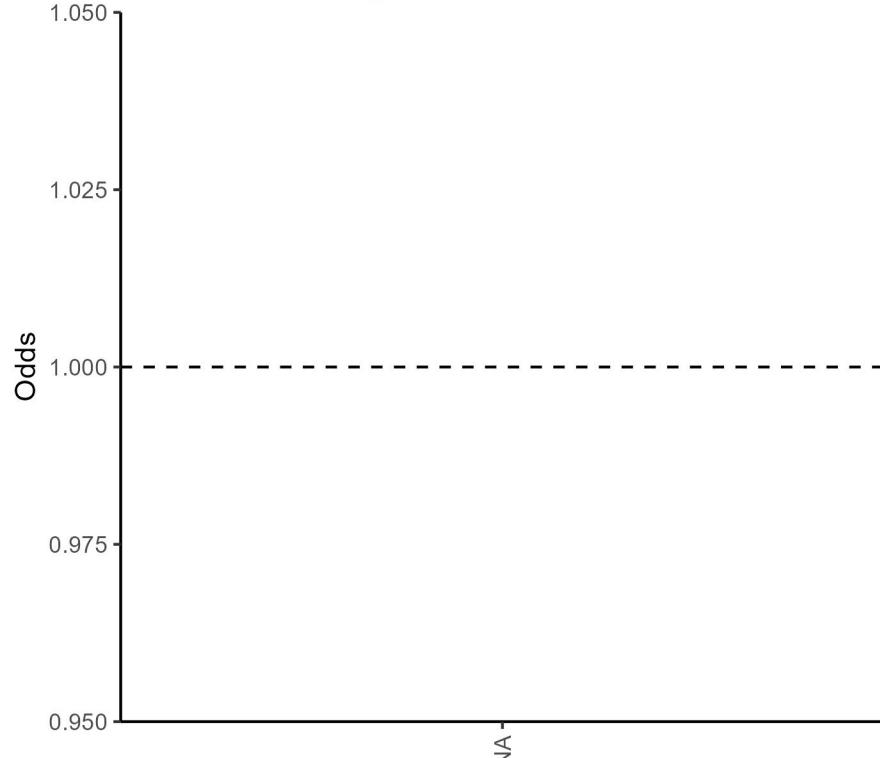
Positive cooccurrence



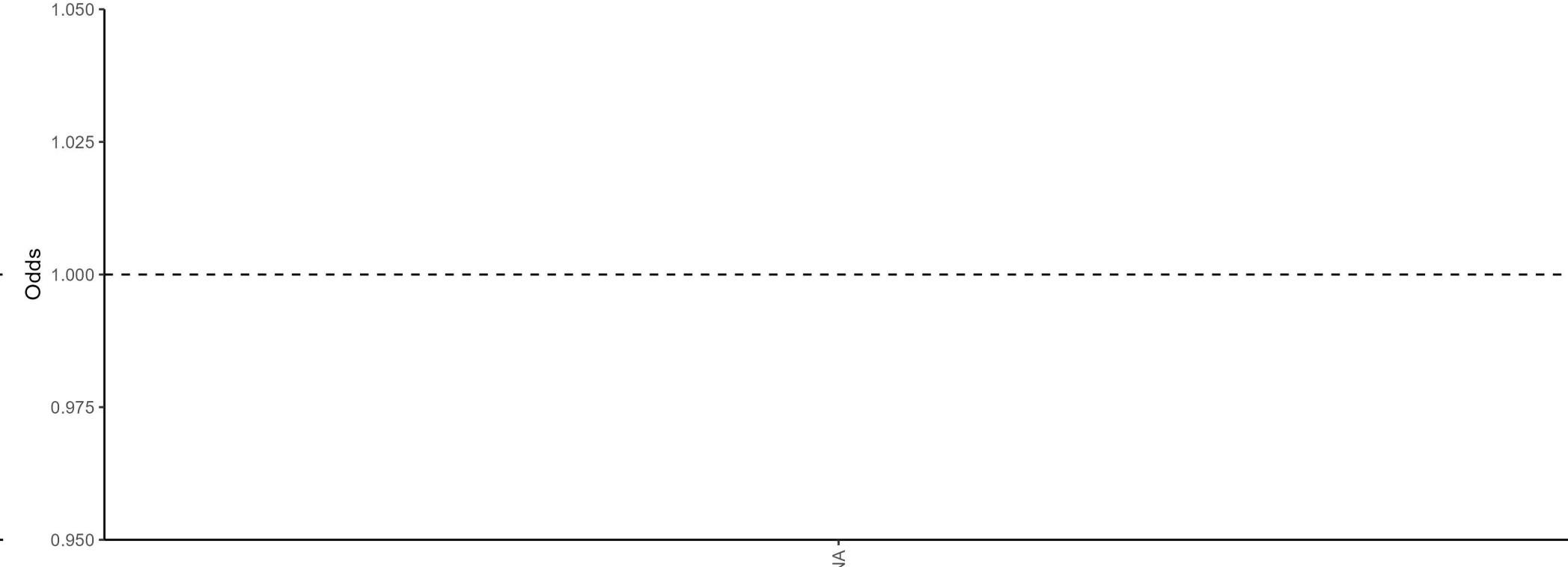
## Cooccurrence with EXO1 protein in solid cancers, DB1

The text in the bars: incidence of EXO1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

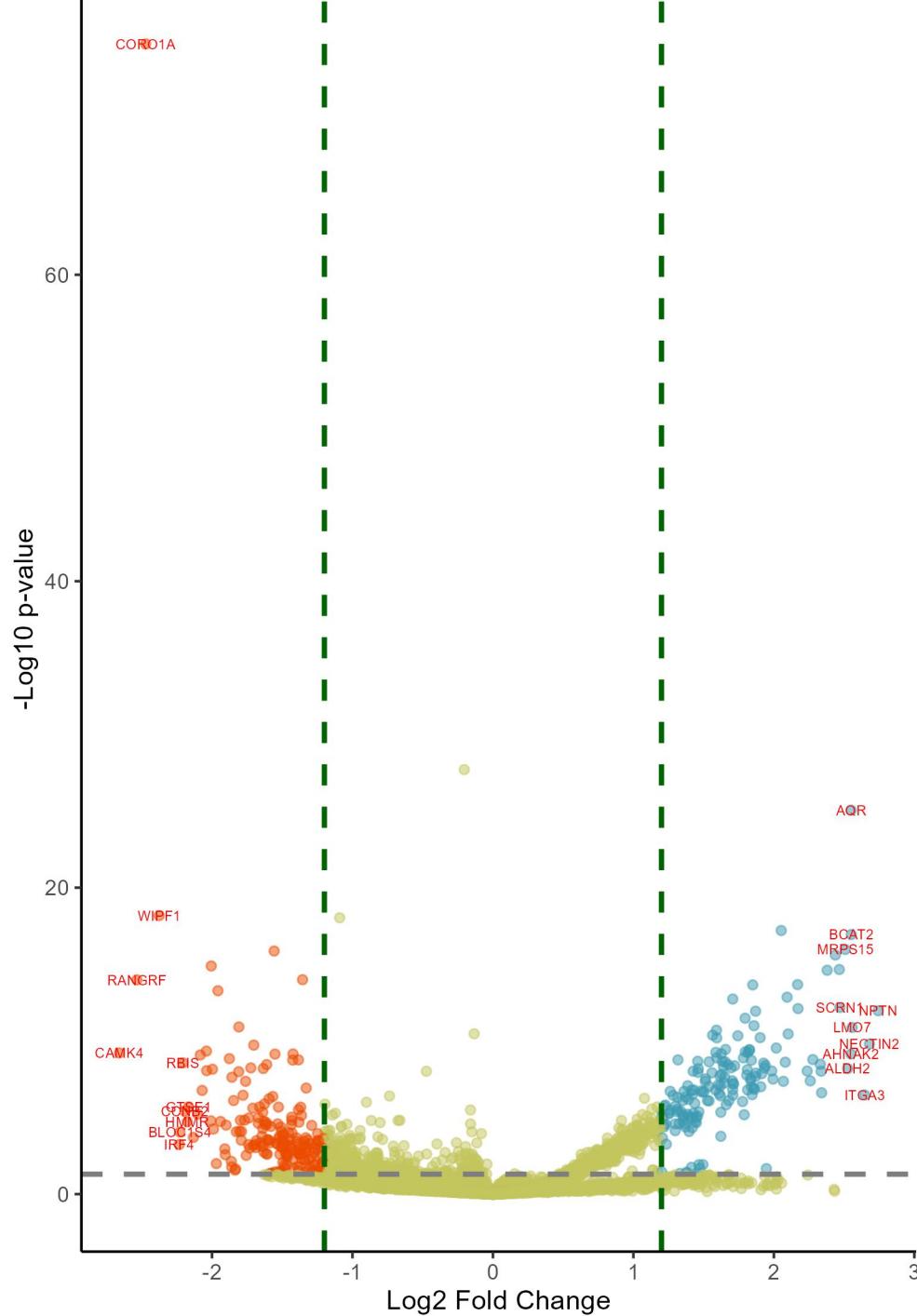
Negative cooccurrence



Positive cooccurrence



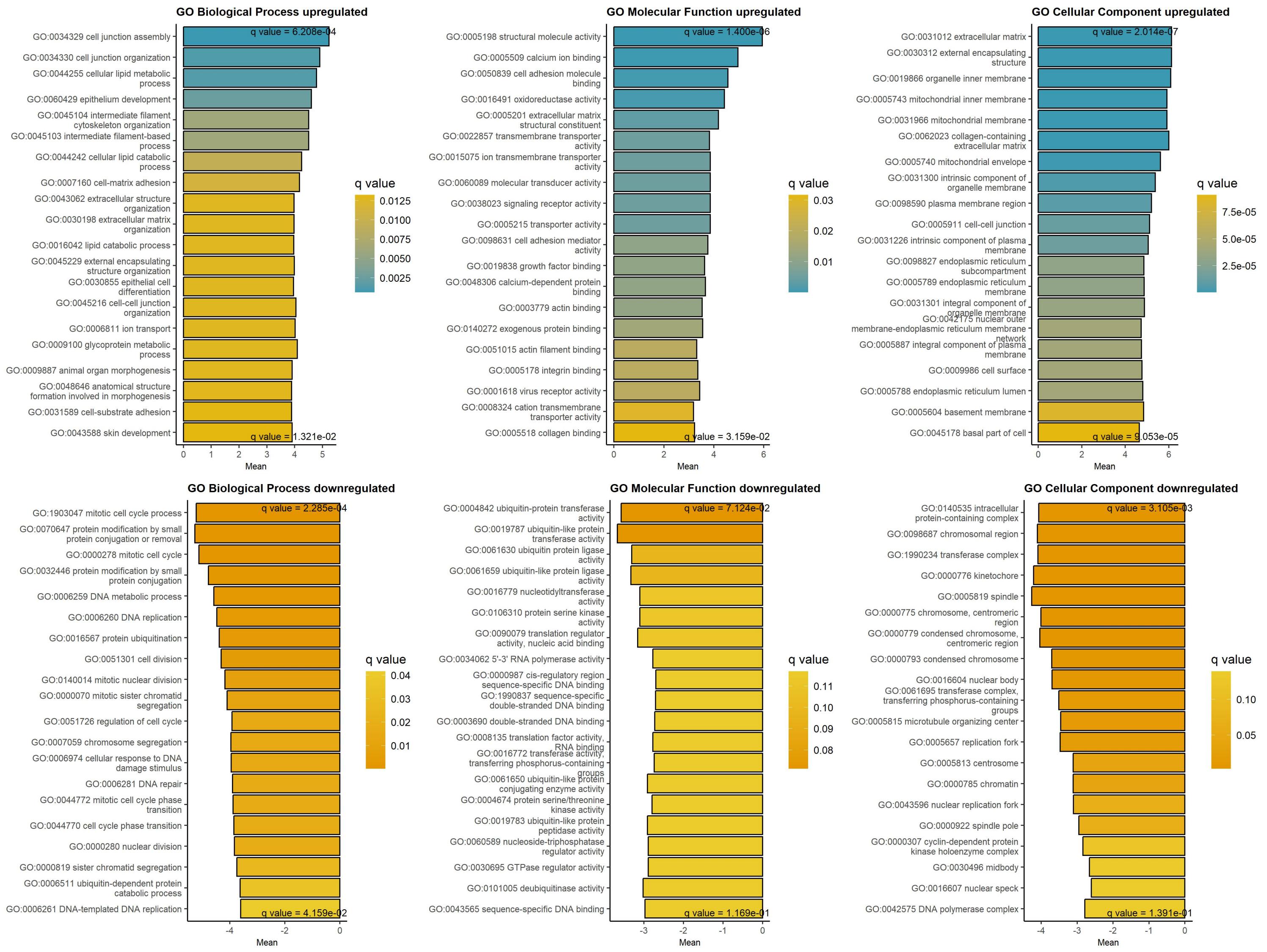
p-value &lt; 0.05 &amp; logFC &gt; 1.2



## Downregulated at low/absent EXO1 Upregulated at low/absent EXO1

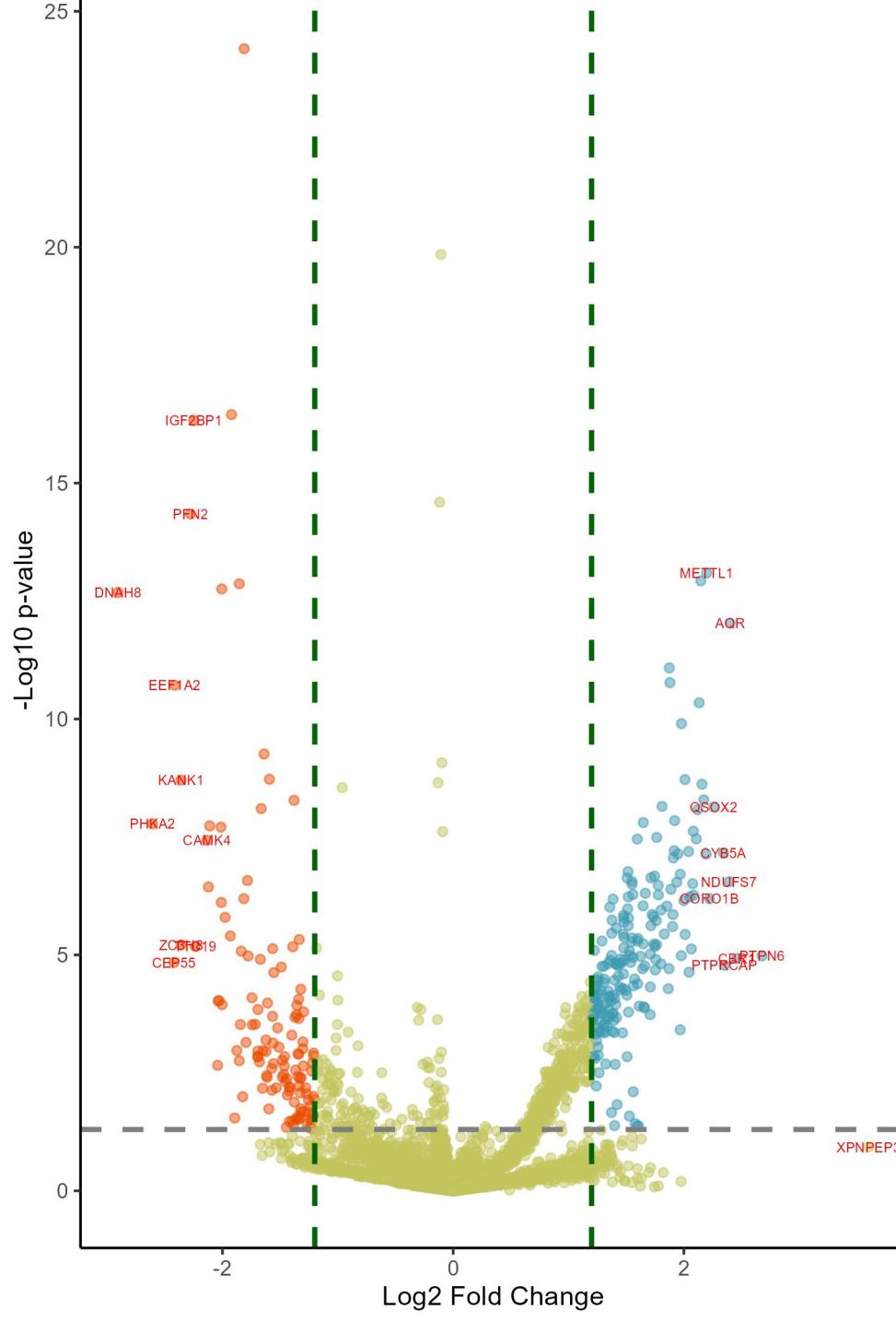
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.66	8.70e-08	CAMK4	calcium/calmodulin dependent protein kinase IV	2.74	2.99e-10	NPTN	neuroplastin
-2.54	4.35e-12	RANGRF	RAN guanine nucleotide release fact	2.68	2.84e-08	NECTIN2	nectin cell adhesion molecule 2
-2.47	2.86e-72	CORO1A	coronin 1A	2.65	1.67e-05	ITGA3	integrin subunit alpha 3
-2.38	8.80e-16	WIPF1	WAS/WASL interacting protein family member 1	2.56	3.05e-09	LMO7	LIM domain 7
-2.23	9.58e-03	IRF4	interferon regulatory factor 4	2.55	9.55e-15	BCAT2	branched chain amino acid transaminase
-2.23	2.10e-03	BLOC1S4	biogenesis of lysosomal organelles complex 1 subunit 4	2.55	1.46e-22	AQR	aquarius intron-binding spliceosoma
-2.21	2.76e-07	RBIS	ribosomal biogenesis factor	2.55	9.47e-08	AHNAK2	AHNAK nucleoprotein 2
-2.19	1.50e-04	CCNB2	cyclin B2	2.53	5.48e-07	ALDH2	aldehyde dehydrogenase 2 family member 2
-2.18	5.79e-04	HMMR	hyaluronan mediated motility receptor	2.51	7.94e-14	MRPS15	mitochondrial ribosomal protein S15
-2.17	8.27e-05	GTSE1	G2 and S-phase expressed 1	2.47	1.98e-10	SCRN1	secernin 1
-2.13	4.16e-03	TMA7	translation machinery associated 7	2.47	1.13e-12	MCU	mitochondrial calcium uniporter
-2.1	2.23e-04	MEA1	male-enhanced antigen 1	2.44	1.50e-13	ATP2B1	ATPase plasma membrane Ca <sup>2+</sup> transporter
-2.08	1.06e-07	KANK1	KN motif and ankyrin repeat domains	2.43	8.85e-01	XPNPEP3	X-prolyl aminopeptidase 3
-2.07	9.10e-06	TSC22D4	TSC22 domain family member 4	2.43	8.68e-01	KRT18	keratin 18
-2.04	7.19e-08	UBE2L6	ubiquitin conjugating enzyme E2 L6	2.38	1.17e-12	AMFR	autocrine motility factor receptor
-2.04	7.12e-07	CKS1B	CDC28 protein kinase regulatory subunit 1B	2.34	1.24e-05	CAVIN1	caveolae associated protein 1
-2.01	5.23e-04	BPGM	bisphosphoglycerate mutase	2.34	7.35e-07	JUP	junction plakoglobin
-2.01	7.15e-13	POLR2K	RNA polymerase II, I and III subunit K	2.33	3.27e-07	ITGA2	integrin subunit alpha 2
-2	5.87e-07	GINS2	GINS complex subunit 2	2.28	1.96e-07	DSG2	desmoglein 2
-1.99	1.45e-03	ASDURF	ASNSD1 upstream open reading frame	2.26	2.61e-06	CKB	creatine kinase B
-1.97	9.53e-02	DNAH8	dynein axonemal heavy chain 8	2.24	3.30e-01	CYB5A	cytochrome b5 type A
-1.96	1.86e-11	PCLAF	PCNA clamp associated factor	2.24	7.33e-07	S100A16	S100 calcium binding protein A16
-1.94	5.56e-04	PDCD2	programmed cell death 2	2.17	2.25e-10	TMTC3	transmembrane O-mannosyltransferase
-1.91	1.61e-02	ZWINT	ZW10 interacting kinetochore protein	2.17	8.20e-12	NOL9	nucleolar protein 9
-1.91	3.19e-02	NFATC2	nuclear factor of activated T cells	2.1	7.38e-09	DDAH1	dimethylarginine dimethylaminohydroxide
-1.9	8.70e-04	CC2D1B	coiled-coil and C2 domain containing 1B	2.09	4.68e-11	MYO6	myosin VI
-1.88	1.74e-07	RNF181	ring finger protein 181	2.08	2.51e-07	PPL	periplakin
-1.86	7.14e-02	TTC33	tetratricopeptide repeat domain 33	2.07	2.71e-06	PROCR	protein C receptor
-1.86	1.39e-01	GTSF1	gameteocyte specific factor 1	2.06	6.41e-01	ASPH	aspartate beta-hydroxylase

## GAGE analysis on upregulated and downregulated proteins at low/absent EXO1 protein, DB1

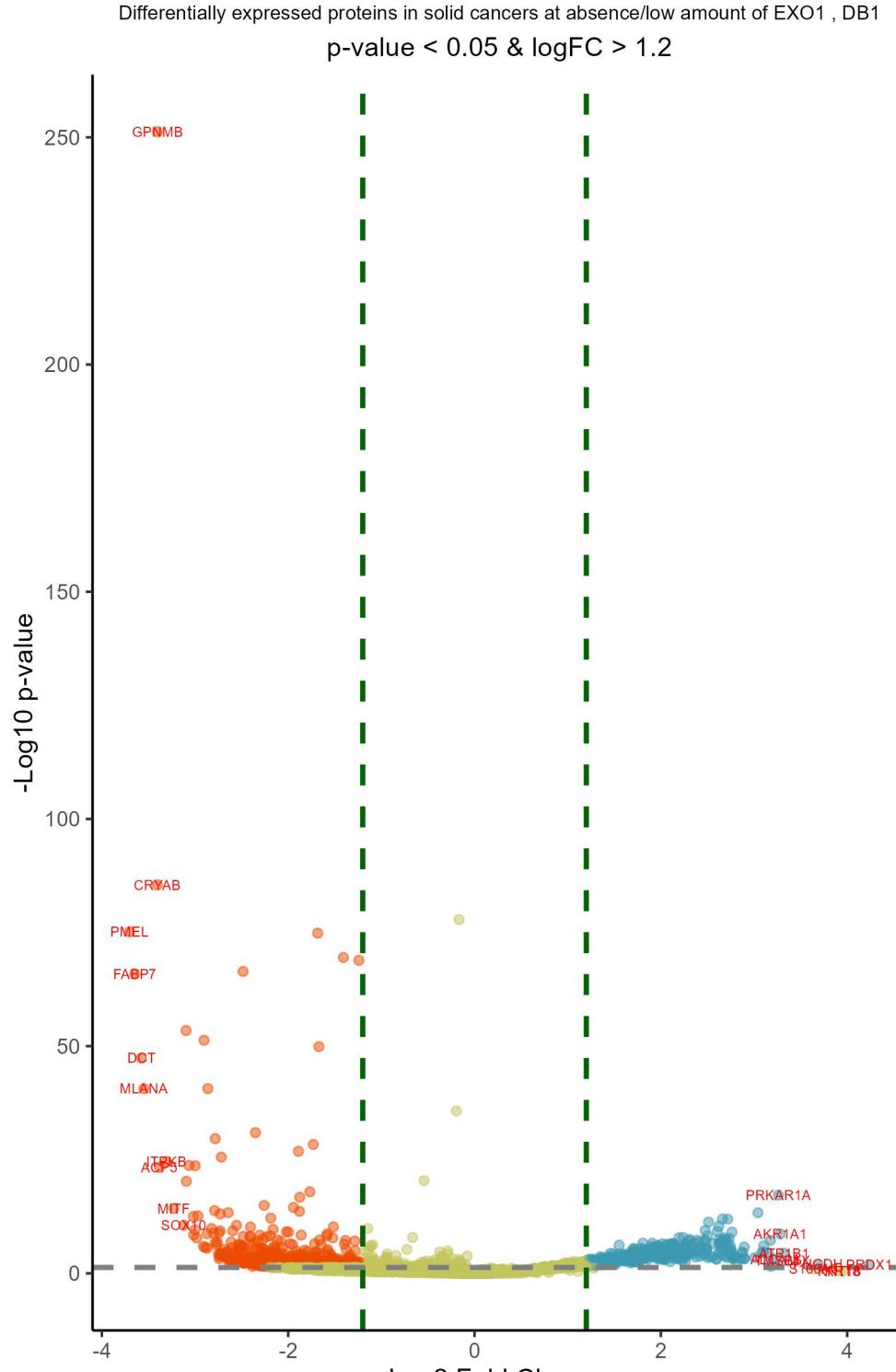


p-value &lt; 0.05 &amp; logFC &gt; 1.2

Downregulated in blood cancers at low/absent EXO1 Upregulated in blood cancers at low/absent EXO1



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.91	1.15e-10	DNAH8	dynein axonemal heavy chain 8	3.6	7.43e-01	XPNPEP3	X-prolyl aminopeptidase 3
-2.61	3.15e-06	PHKA2	phosphorylase kinase regulatory sub	2.68	5.60e-04	PTPN6	protein tyrosine phosphatase non-re
-2.42	7.15e-04	CEP55	centrosomal protein 55	2.46	6.20e-04	CBR1	carbonyl reductase 1
-2.41	8.00e-09	EEF1A2	eukaryotic translation elongation f	2.4	4.74e-10	AQR	aquarius intron-binding spliceosoma
-2.36	5.69e-07	KANK1	KN motif and ankyrin repeat domains	2.39	3.27e-05	NDUFS7	NADH:ubiquinone oxidoreductase core
-2.36	3.72e-04	ZC3H8	zinc finger CCCH-type containing 8	2.35	7.76e-04	PTPRCAP	protein tyrosine phosphatase recept
-2.28	4.28e-12	PFN2	profilin 2	2.34	9.93e-06	CYB5A	cytochrome b5 type A
-2.25	6.26e-14	IGF2BP1	insulin like growth factor 2 mRNA b	2.26	1.63e-06	QSOX2	quiescin sulfhydryl oxidase 2
-2.24	3.97e-04	TTC19	tetratricopeptide repeat domain 19	2.22	6.00e-05	CORO1B	coronin 1B
-2.13	5.74e-06	CAMK4	calcium/calmodulin dependent protei	2.2	6.66e-11	METTL1	methyltransferase 1, tRNA methylgu
-2.12	3.89e-05	ITPK1	inositol-tetrakisphosphate 1-kinase	2.19	1.01e-05	DOCK8	dedicator of cytokinesis 8
-2.11	3.40e-06	PODXL	podocalyxin like	2.17	1.26e-06	NAGA	alpha-N-acetylgalactosaminidase
-2.04	3.84e-02	PAK4	p21 (RAC1) activated kinase 4	2.16	6.42e-07	RB1	RB transcriptional corepressor 1
-2.04	3.21e-03	SRXN1	sulfiredoxin 1	2.15	8.70e-11	SETD3	SET domain containing 3, actin hist
-2.03	3.19e-03	DHCR24	24-dehydrocholesterol reductase	2.13	1.77e-08	CUL5	cullin 5
-2.01	3.51e-06	BAG3	BAG cochaperone 3	2.12	1.74e-06	BCAT2	branched chain amino acid transamin
-2.01	6.95e-05	RHOC	ras homolog family member C	2.11	5.55e-06	VAV1	vav guanine nucleotide exchange fac
-2.01	1.06e-10	GTSF1	gametocyte specific factor 1	2.08	5.37e-05	EVL	Enah/Vasp-like
-2	3.71e-03	SLC25A4	solute carrier family 25 member 4	2.08	4.14e-06	MRPS15	mitochondrial ribosomal protein S15
-1.98	1.27e-04	ATP1A3	ATPase Na+/K+ transporting subunit	2.08	3.48e-05	PLBD2	phospholipase B domain containing 2
-1.93	2.68e-04	COMMD4	COMM domain containing 4	2.06	4.28e-04	GSN	gelsolin
-1.92	5.87e-14	RALYL	RALY RNA binding protein like	2.05	5.68e-05	GPD2	glycerol-3-phosphate dehydrogenase
-1.89	2.80e-01	SELENOS	selenoprotein S	2.04	1.02e-03	CD48	CD48 molecule
-1.88	2.18e-02	SRR	serine racemase	2.04	9.50e-06	DAXX	death domain associated protein
-1.85	3.17e-02	DOCK7	dedicator of cytokinesis 7	2.01	2.52e-04	TAP2	transporter 2, ATP binding cassette
-1.85	9.03e-11	CD70	CD70 molecule	2.01	5.69e-07	TRIM65	tripartite motif containing 65
-1.84	7.66e-03	RAD51AP1	RAD51 associated protein 1	2	6.44e-05	SCARB1	scavenger receptor class B member 1
-1.84	4.64e-04	BCL2L1	BCL2 like 1	1.98	4.63e-08	MDN1	midasin AAA ATPase 1
-1.82	1.24e-01	UBAC1	UBA domain containing 1	1.98	5.60e-04	ITGAL	integrin subunit alpha L



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-3.7	1.13e-72	PMEL	premelanosome protein	4.24	8.93e-02	PRDX1	peroxiredoxin 1
-3.65	8.60e-64	FABP7	fatty acid binding protein 7	3.95	7.42e-01	KRT8	keratin 8
-3.58	2.04e-45	DCT	dopachrome tautomerase	3.92	7.09e-01	KRT18	keratin 18
-3.55	9.82e-39	MLANA	melan-A	3.69	7.02e-02	PHGDH	phosphoglycerate dehydrogenase
-3.41	1.05e-82	CRYAB	crystallin alpha B	3.64	3.97e-01	S100A6	S100 calcium binding protein A6
-3.4	3.87e-248	GPNMB	glycoprotein nmb	3.32	8.89e-04	ATP1B1	ATPase Na+/K+ transporting subunit
-3.38	1.31e-21	ACP5	acid phosphatase 5, tartrate resist	3.3	1.91e-02	TMSB4X	thymosin beta 4 X-linked
-3.3	7.19e-23	ITPKB	inositol-trisphosphate 3-kinase B	3.28	2.15e-07	AKR1A1	aldo-keto reductase family 1 member
-3.23	1.00e-12	MITF	melanocyte inducing transcription f	3.26	1.31e-15	PRKAR1A	protein kinase cAMP-dependent type
-3.12	3.72e-09	SOX10	SRY-box transcription factor 10	3.22	1.01e-02	ALCAM	activated leukocyte cell adhesion m
-3.1	2.41e-51	SNCA	synuclein alpha	3.18	1.60e-01	KRT19	keratin 19
-3.09	1.29e-18	RUNX3	RUNX family transcription factor 3	3.18	3.84e-06	ALDH3A2	aldehyde dehydrogenase 3 family mem
-3.06	5.07e-22	FAM184B	family with sequence similarity 184	3.16	6.14e-02	ITGA3	integrin subunit alpha 3
-3.02	4.73e-11	RAB38	RAB38, member RAS oncogene family	3.15	7.33e-04	NECTIN2	nectin cell adhesion molecule 2
-3.02	3.50e-07	SGCD	sarcoglycan delta	3.1	4.17e-05	NPTN	neuroplastin
-3	3.12e-08	LZTS1	leucine zipper tumor suppressor 1	3.1	5.49e-04	SERPINB6	serpin family B member 6
-3	5.91e-22	ZFYVE16	zinc finger FYVE-type containing 16	3.08	7.33e-04	CPT1A	carnitine palmitoyltransferase 1A
-2.98	1.30e-06	GMPR	guanosine monophosphate reductase	3.04	8.11e-12	GLG1	golgi glycoprotein 1
-2.97	3.77e-11	UBE2D3	ubiquitin conjugating enzyme E2 D3	3.01	5.71e-03	HLA-C	major histocompatibility complex, c
-2.91	5.42e-05	MTF2	metal response element binding tran	2.9	8.49e-03	F11R	F11 receptor
-2.9	3.06e-49	CORO1A	coronin 1A	2.9	6.75e-05	MACROD1	mono-ADP ribosylhydrolase 1
-2.89	8.70e-05	GRB10	growth factor receptor bound protei	2.89	7.51e-03	FBLL1	fibrillarin like 1
-2.87	2.01e-07	ZEB2	zinc finger E-box binding homeobox	2.88	6.78e-04	S100A13	S100 calcium binding protein A13
-2.87	1.16e-04	PLD2	phospholipase D2	2.87	6.80e-04	LMO7	LIM domain 7
-2.86	9.82e-39	EPDR1	ependymin related 1	2.87	8.49e-03	ALDH2	aldehyde dehydrogenase 2 family mem
-2.82	1.71e-08	NEFL	neurofilament light chain	2.85	6.80e-03	VTN	vitronectin
-2.8	1.30e-07	WIPF1	WAS/WASL interacting protein family	2.81	3.02e-02	CAVIN1	caveolae associated protein 1
-2.79	2.91e-12	MLPH	melanophilin	2.8	4.50e-03	ITGA2	integrin subunit alpha 2
-2.78	8.54e-28	DDT	D-dopachrome tautomerase	2.78	2.61e-03	AHNAK2	AHNAK nucleoprotein 2

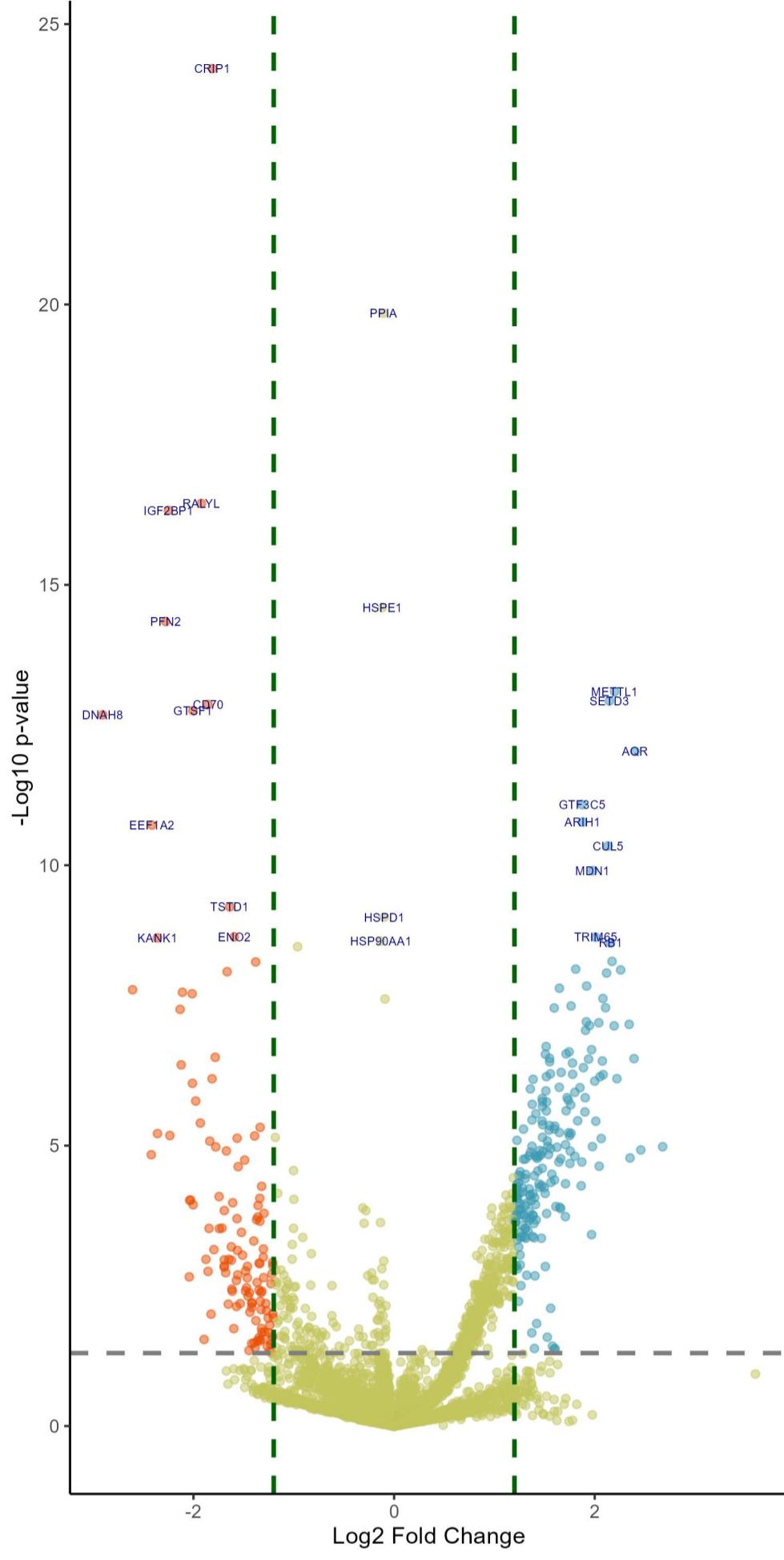
EXO1 network, DB1, no Pearson r &gt; 0.3

Differentially expressed proteins in blood cancers at absence/low amount of EXO1 , DB1

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

Sorted by p values!

Downregulated in blood cancers at low/absent EXO1 Upregulated in blood cancers at low/absent EXO1



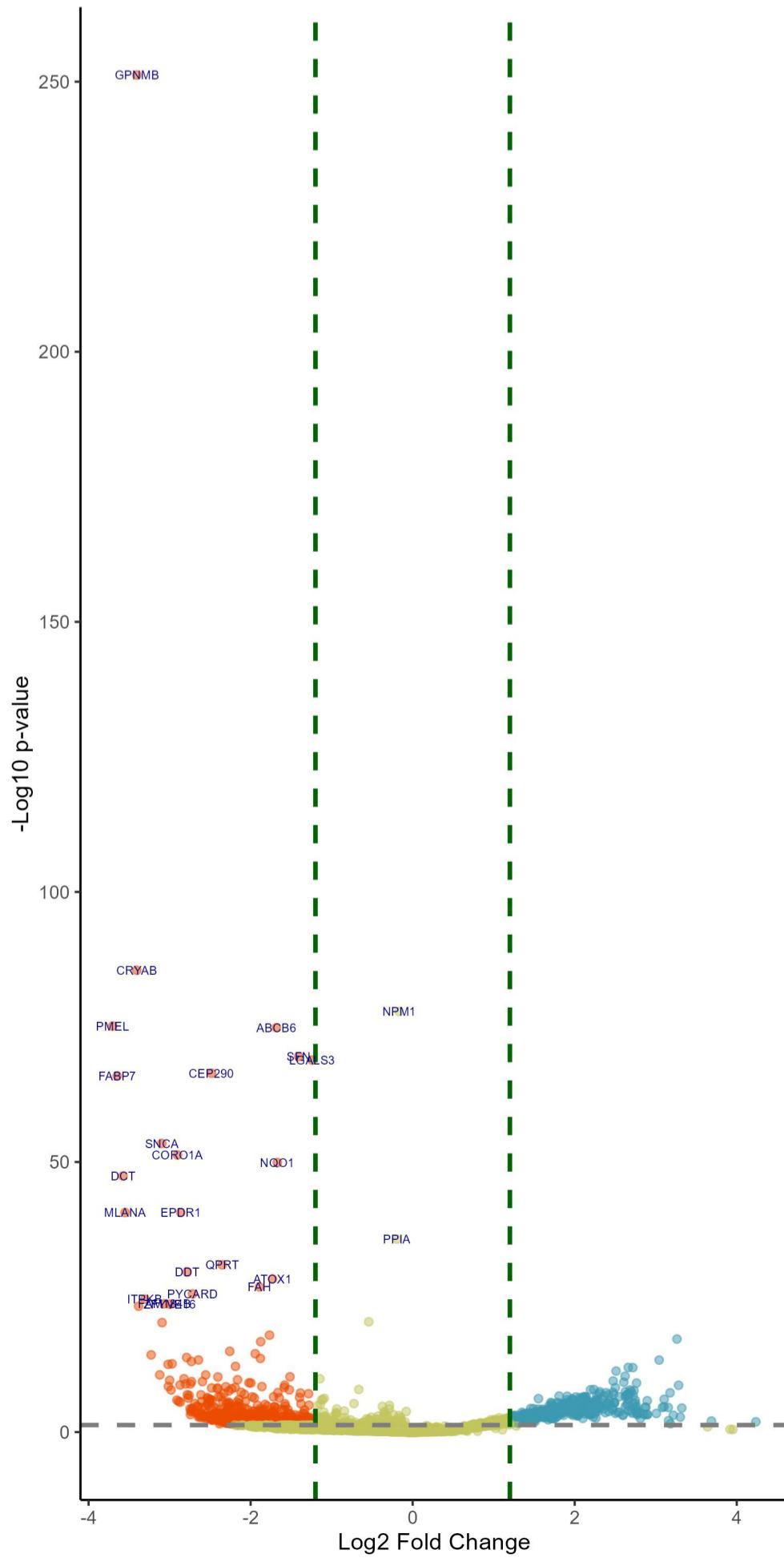
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.81	2.07e-21	CRIP1	cysteine rich protein 1	2.2	6.66e-11	METTL1	methyltransferase 1, tRNA methylguan
-0.11	3.16e-17	PP1A	peptidylprolyl isomerase A	2.15	8.70e-11	SETD3	SET domain containing 3, actin hist
-1.92	5.87e-14	RALYL	RALY RNA binding protein like	2.4	4.74e-10	AQR	aquarius intron-binding spliceosoma
-2.25	6.26e-14	IGF2BP1	insulin like growth factor 2 mRNA b	1.87	3.93e-09	GTF3C5	general transcription factor IIIC s
-0.12	2.82e-12	HSPE1	heat shock protein family E (Hsp10)	1.88	7.50e-09	ARIH1	ariadne RBR E3 ubiquitin protein li
-2.28	4.28e-12	PFN2	profilin 2	2.13	1.77e-08	CUL5	cullin 5
-1.85	9.03e-11	CD70	CD70 molecule	1.98	4.63e-08	MDN1	midasin AAA ATPase 1
-2.01	1.06e-10	GTSF1	gameteocyte specific factor 1	2.01	5.69e-07	TRIM65	tripartite motif containing 65
-2.91	1.15e-10	DNAH8	dynein axonemal heavy chain 8	2.16	6.42e-07	RB1	RB transcriptional corepressor 1
-2.41	8.00e-09	EEF1A2	eukaryotic translation elongation f	2.17	1.26e-06	NAGA	alpha-N-acetylgalactosaminidase
-1.64	1.93e-07	TSTD1	thiosulfate sulfurtransferase like	1.81	1.63e-06	POLR3A	RNA polymerase III subunit A
-0.1	2.81e-07	HSPD1	heat shock protein family D (Hsp60)	2.26	1.63e-06	QSOX2	quiescin sulfhydryl oxidase 2
-1.59	5.69e-07	ENO2	enolase 2	2.12	1.74e-06	BCAT2	branched chain amino acid transamin
-2.36	5.69e-07	KANK1	KN motif and ankyrin repeat domains	1.92	2.87e-06	ALAD	aminolevulinate dehydratase
-0.13	6.24e-07	HSP90AA1	heat shock protein 90 alpha family	1.65	3.05e-06	INTS1	integrator complex subunit 1
-0.96	7.26e-07	LGALS1	galectin 1	2.08	4.14e-06	MRPS15	mitochondrial ribosomal protein S15
-1.38	1.26e-06	PCBD1	pterin-4 alpha-carbinolamine dehydr	1.76	5.37e-06	MPI	mannose phosphate isomerase
-1.66	1.70e-06	RANGRF	RAN guanine nucleotide release fact	2.11	5.55e-06	VAV1	vav guanine nucleotide exchange fac
-2.61	3.15e-06	PHKA2	phosphorylase kinase regulatory sub	1.6	5.55e-06	DNAJC13	DnaJ heat shock protein family (Hsp
-2.11	3.40e-06	PODXL	podocalyxin like	1.92	9.34e-06	NOL9	nucleolar protein 9
-2.01	3.51e-06	BAG3	BAG cochaperone 3	2.04	9.50e-06	DAXX	death domain associated protein
-0.09	4.14e-06	NPM1	nucleophosmin 1	2.34	9.93e-06	CYB5A	cytochrome b5 type A
-2.13	5.74e-06	CAMK4	calcium/calmodulin dependent protei	1.95	1.01e-05	ECI2	enoyl-CoA delta isomerase 2
-1.78	3.21e-05	TJP2	tight junction protein 2	2.19	1.01e-05	DOCK8	dedicator of cytokinesis 8
-2.12	3.89e-05	ITPK1	inositol-tetrakisphosphate 1-kinase	1.91	1.19e-05	EARS2	glutamyl-tRNA synthetase 2, mito
-1.81	6.00e-05	SEPTIN8	septin 8	1.52	2.28e-05	CREC2	CREB regulated transcription coacti
-2.01	6.95e-05	RHOC	ras homolog family member C	1.97	2.53e-05	CHID1	chitinase domain containing 1
-1.98	1.27e-04	ATP1A3	ATPase Na+/K+ transporting subunit	1.75	2.72e-05	C1orf131	chromosome 1 open reading frame 131
-1.93	2.68e-04	COMM4	COMM domain containing 4	1.71	2.88e-05	COQ9	coenzyme Q9
-1.34	3.08e-04	BRI3BP	BRI3 binding protein	1.51	2.88e-05	HAUS6	HAUS augmin like complex subunit 6
-2.36	3.72e-04	ZC3H8	zinc finger CCCH-type containing 8	1.55	3.27e-05	NAA25	N-alpha-acetyltransferase 25, NatB
-2.24	3.97e-04	TTC19	tetratricopeptide repeat domain 19	2.39	3.27e-05	NDUFS7	NADH:ubiquinone oxidoreductase core
-1.39	3.99e-04	POLR2K	RNA polymerase II, I and III subuni	1.94	3.28e-05	URI1	URI1 prefoldin like chaperone
-1.18	4.16e-04	PTMS	parathymosin	2.08	3.48e-05	PLBD2	phospholipase B domain containing 2
-1.56	4.26e-04	DHRS4	dehydrogenase/reductase 4	1.55	3.53e-05	TEX10	testis expressed 10
-1.84	4.64e-04	BCL2L1	BCL2 like 1	1.78	3.66e-05	HDAC7	histone deacetylase 7
-1.78	5.60e-04	CTPS2	CTP synthase 2	1.89	4.29e-05	EXOC2	exocyst complex component 2
-1.67	6.35e-04	TPMT	thiopurine S-methyltransferase	1.67	5.13e-05	PDRG1	p53 and DNA damage regulated 1
-2.42	7.15e-04	CEP55	centrosomal protein 55	1.56	5.26e-05	EEESSC	eukaryotic elongation factor, elong

Differentially expressed proteins in solid cancers at absence/low amount of EXO1 , DB1

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

Sorted by p values!

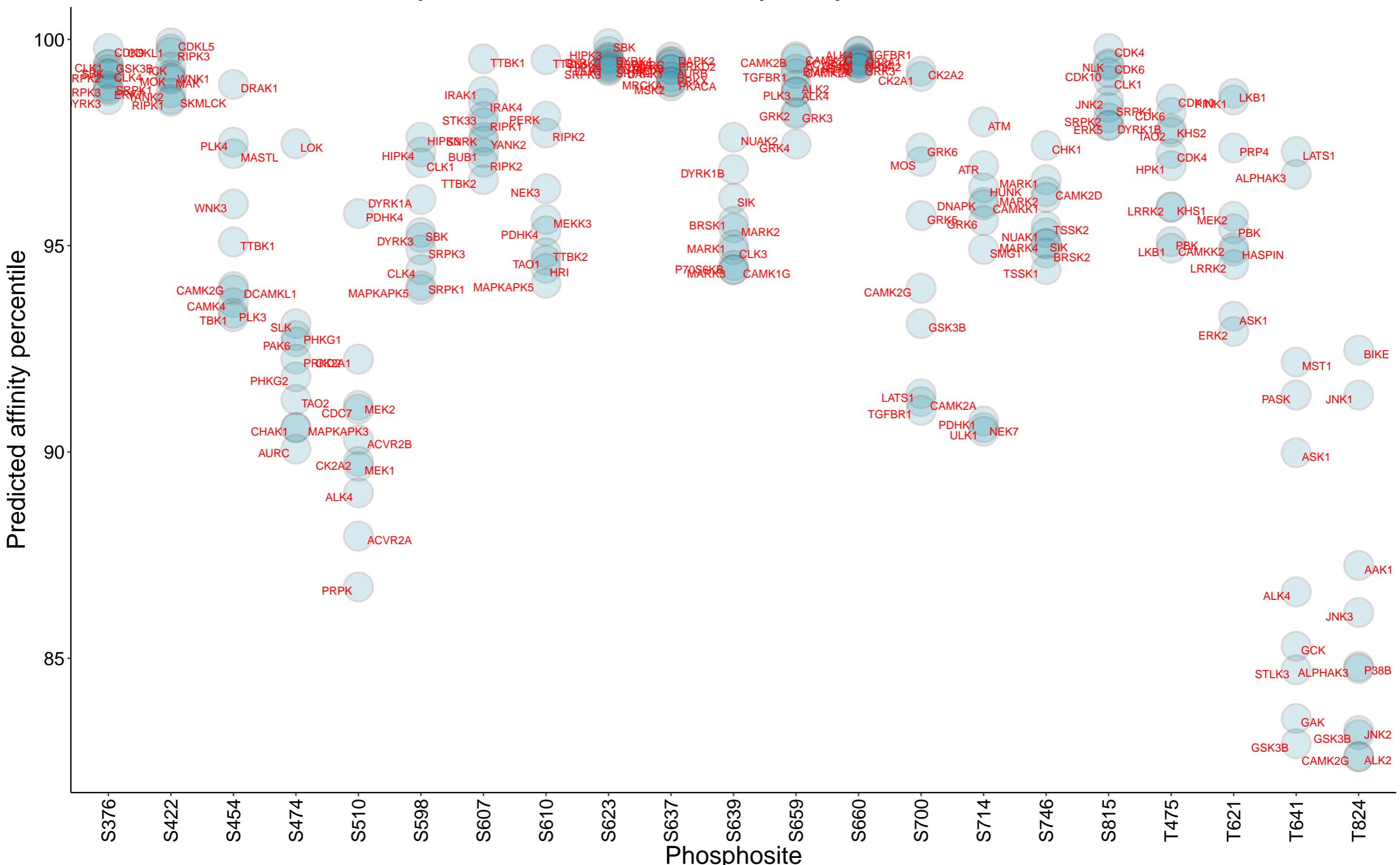
Downregulated in solid cancers at low/absent EXO1 Upregulated in solid cancers at low/absent EXO1



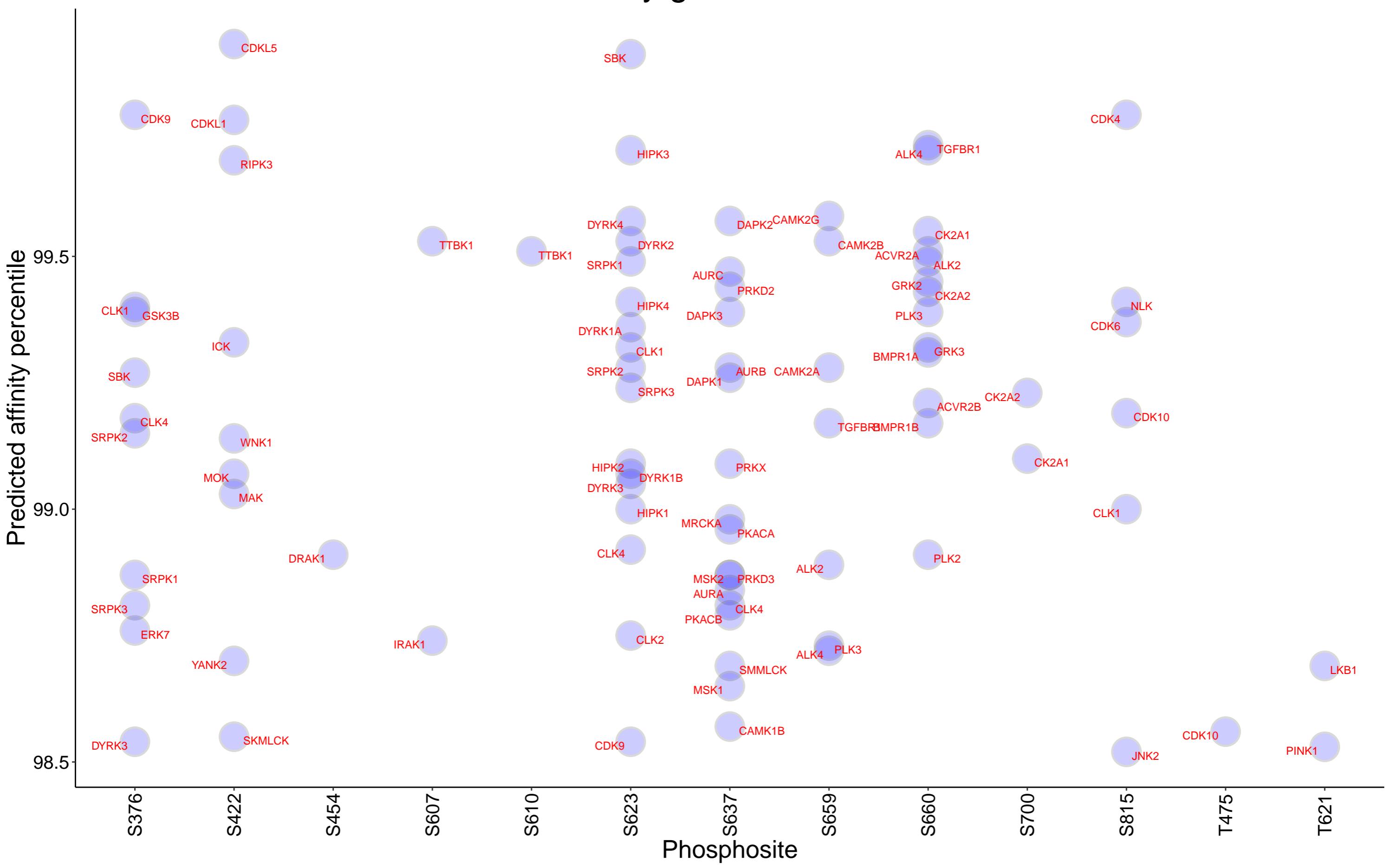
Insufficient number of paired observations in DB1 for EXO1

Insufficient number of paired observations in DB1 for EXO1

# Top 10 kinases for each phosphosite in EXO1



Kinases with affinity greater than 98.5% to EXO1



No sufficient paired observations in DB1 for EXO1