

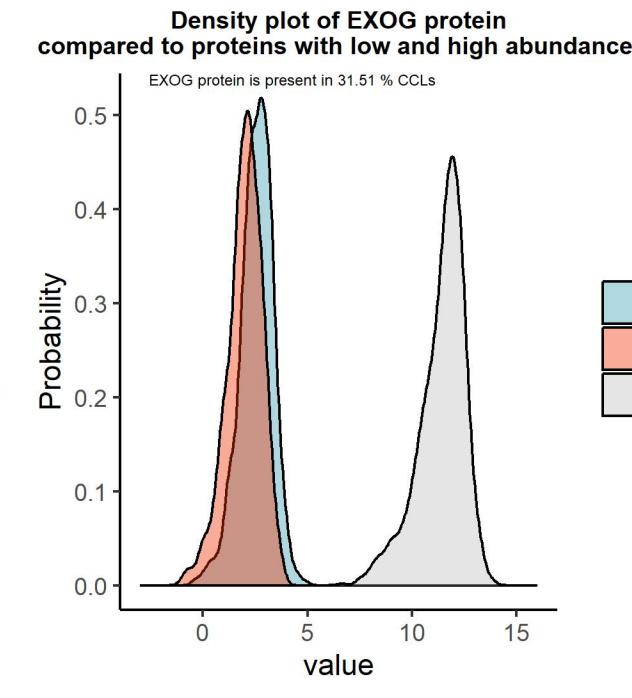
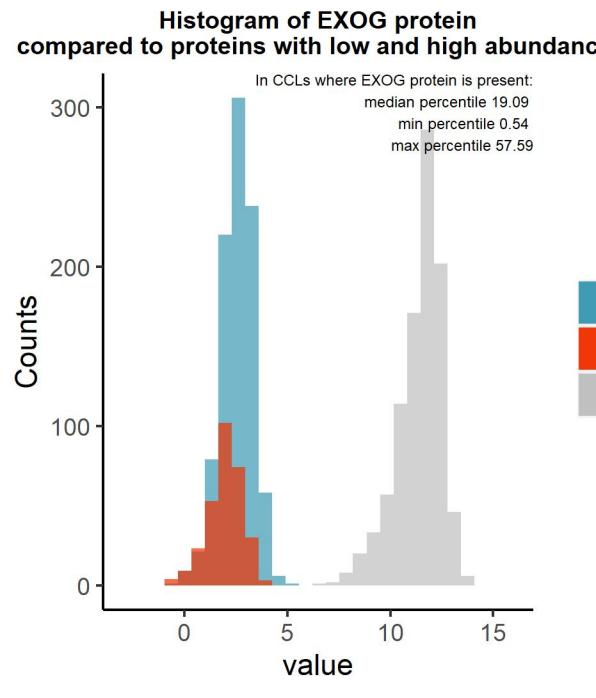
EXOG

Protein name: EXOG ; UNIPROT: Q9Y2C4 ; Gene name: exo/endonuclease G

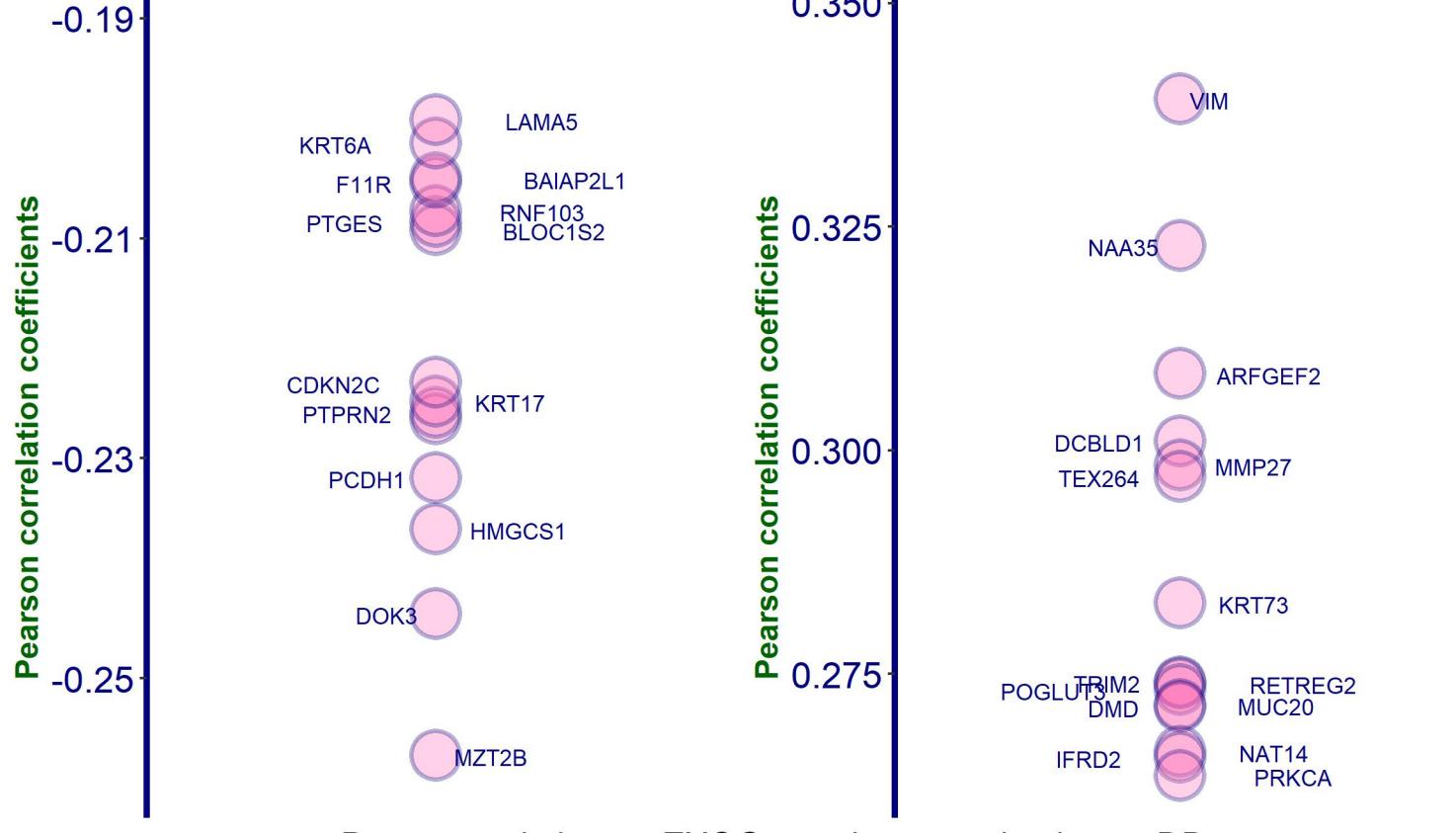
Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: Yes (<https://cansar.ai/>)

Sanger Institute Protein Database 2 (DB2), protein presence is less certain

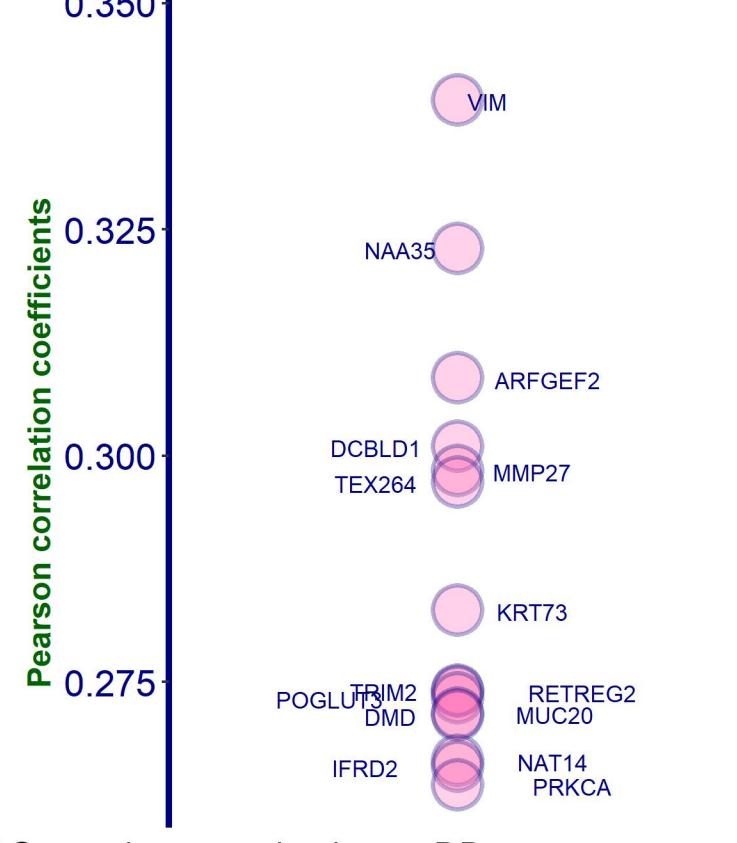
8498 proteins in same 949 CCLs



Negative correlations of EXOG protein, DB2

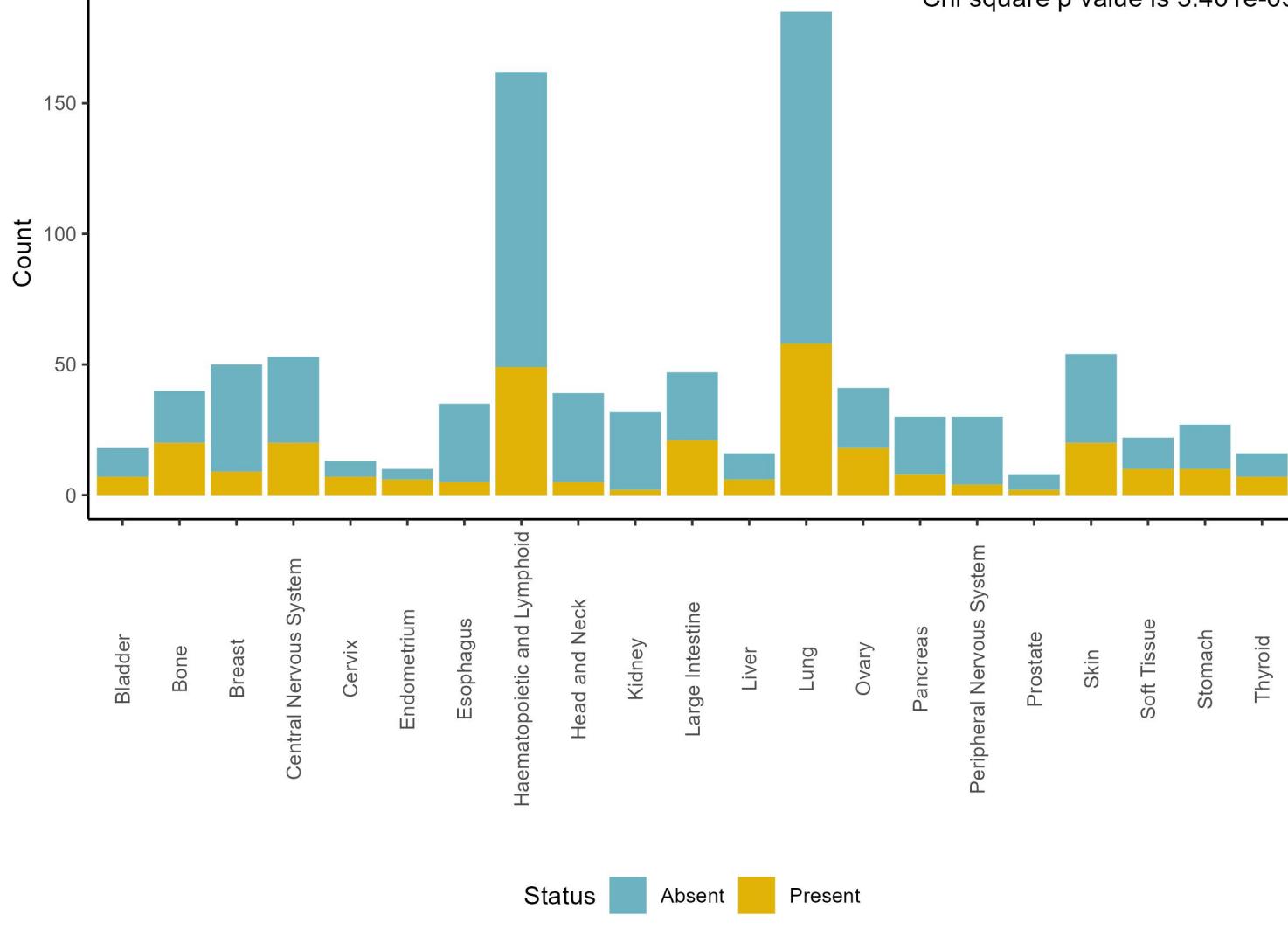
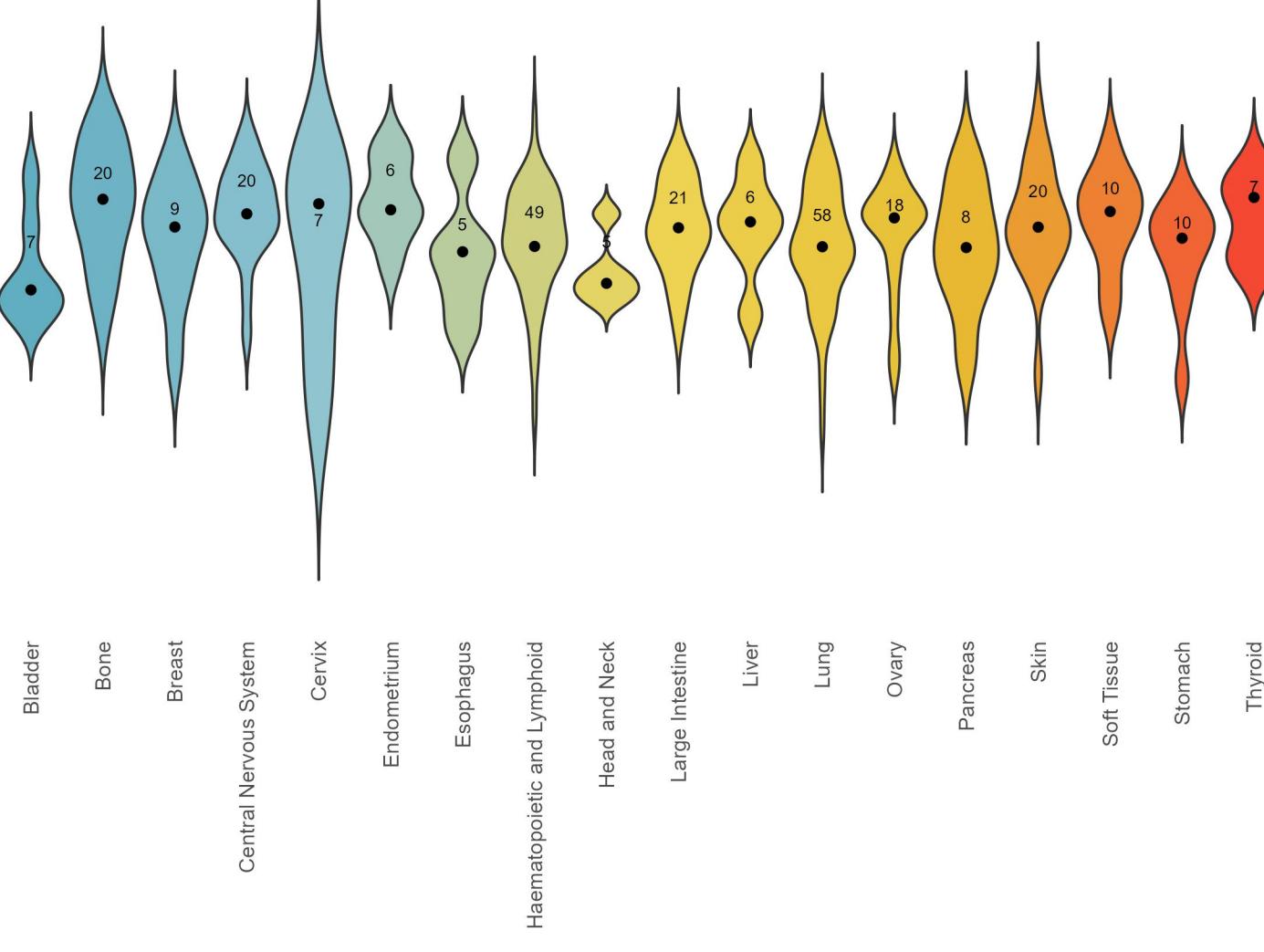


Positive correlations of EXOG protein, DB2



Amount of EXOG protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 1.577e-01

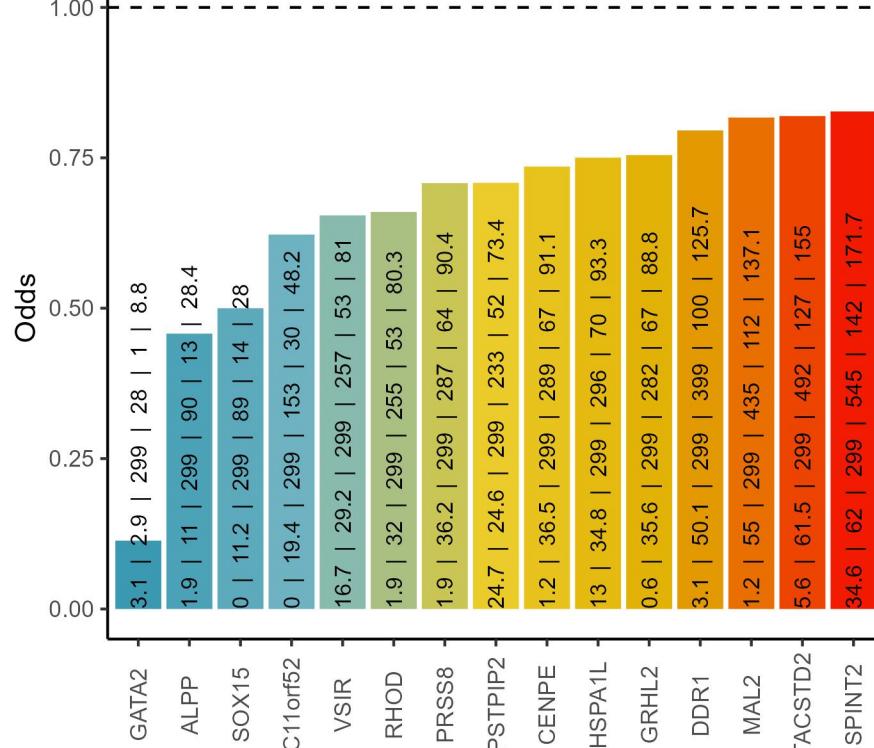


Cooccurrence with EXOG protein, DB2

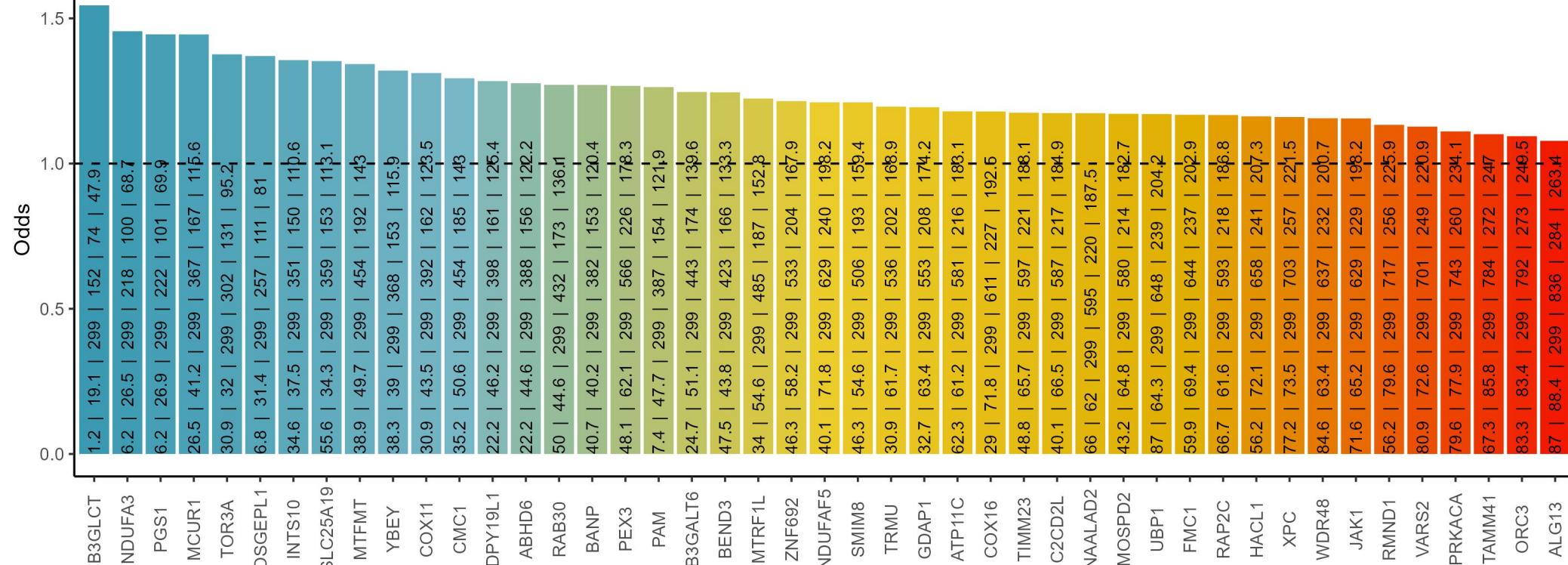
% of EXOG in blood cancers: 30.2 ; % of EXOG in solid cancers: 31.8

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

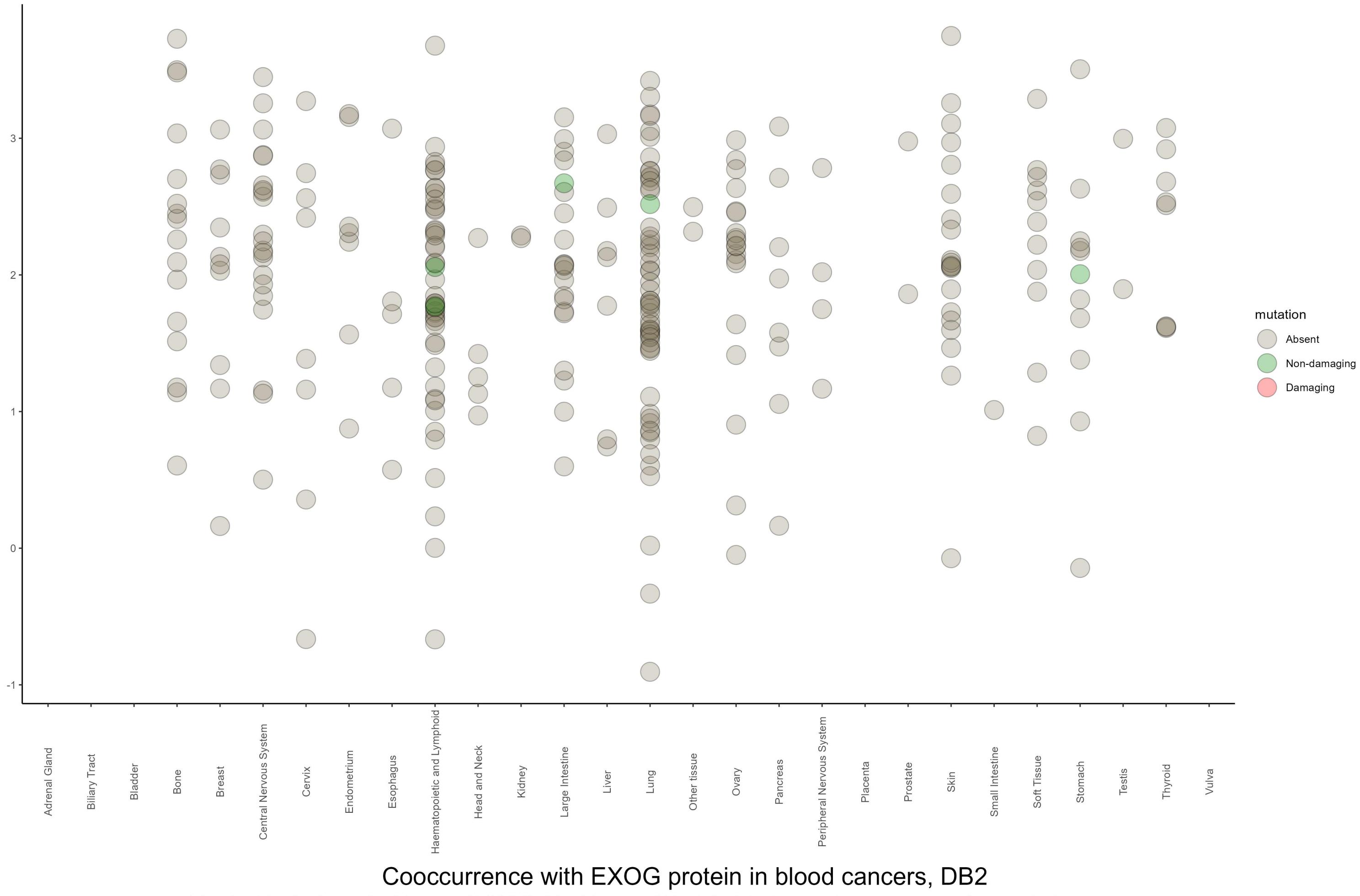
Negative cooccurrence



Positive cooccurrence



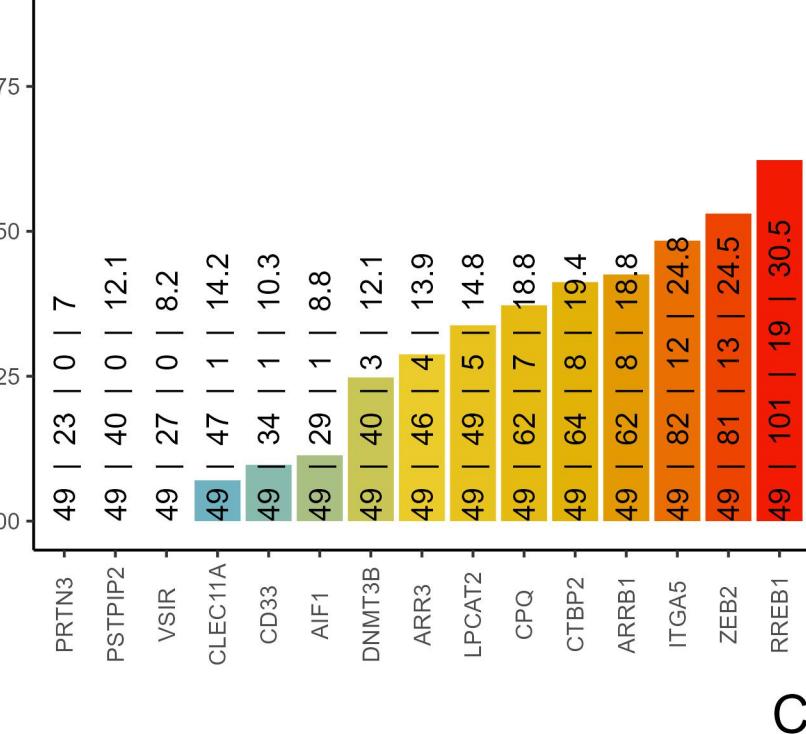
Amount of EXOG protein and mutation status by tissue, DB2



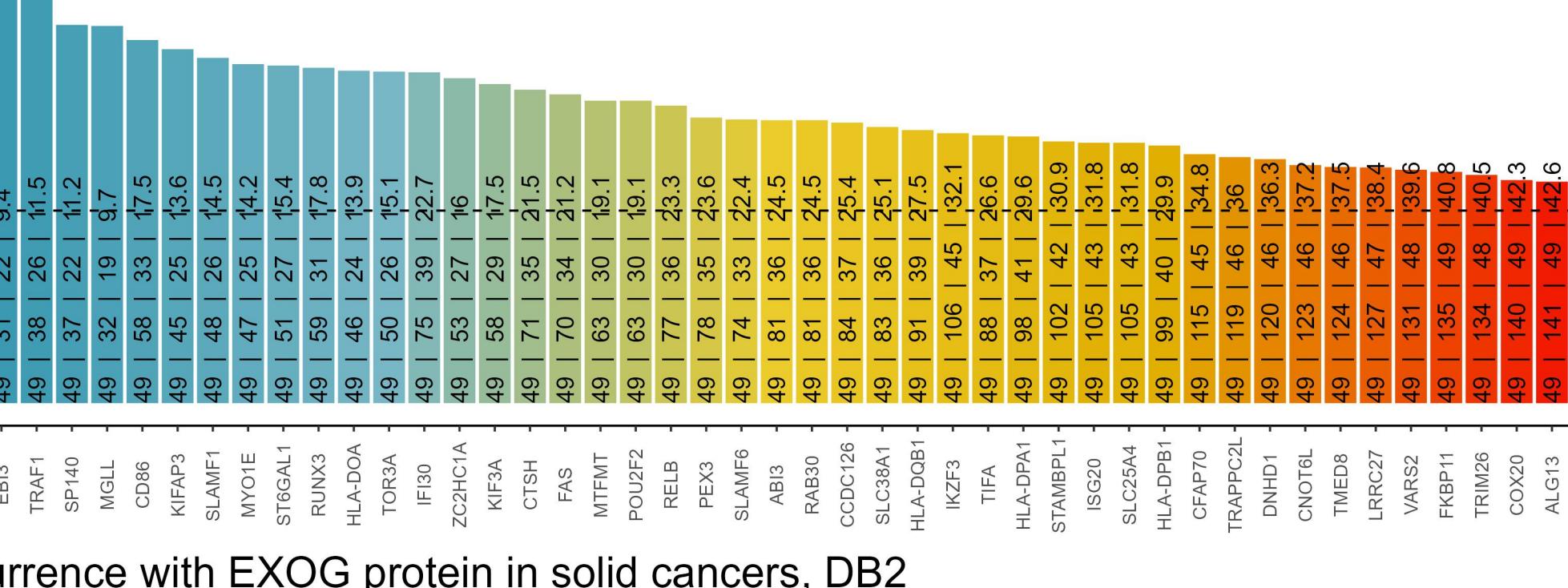
Cooccurrence with EXOG protein in blood cancers, DB2

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

Negative cooccurrence



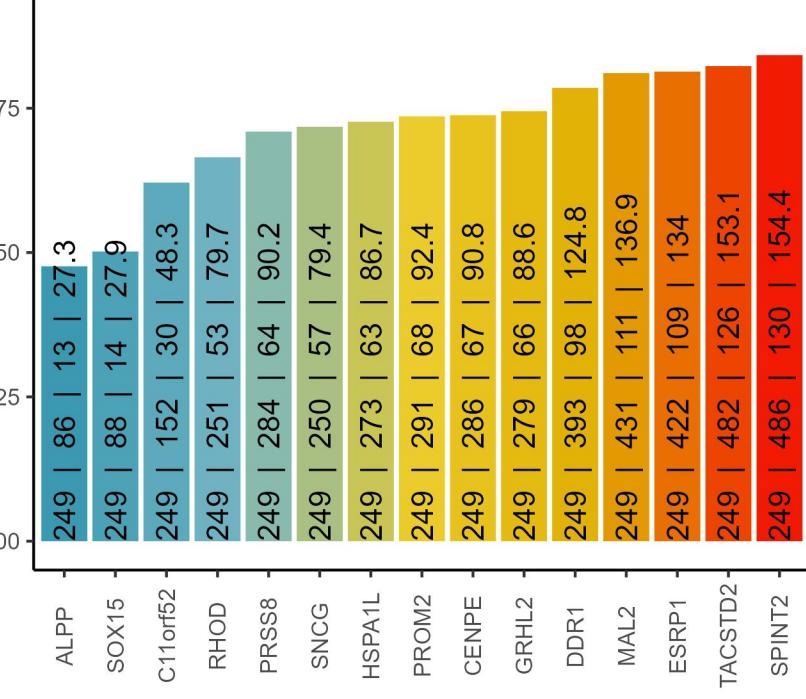
Positive cooccurrence



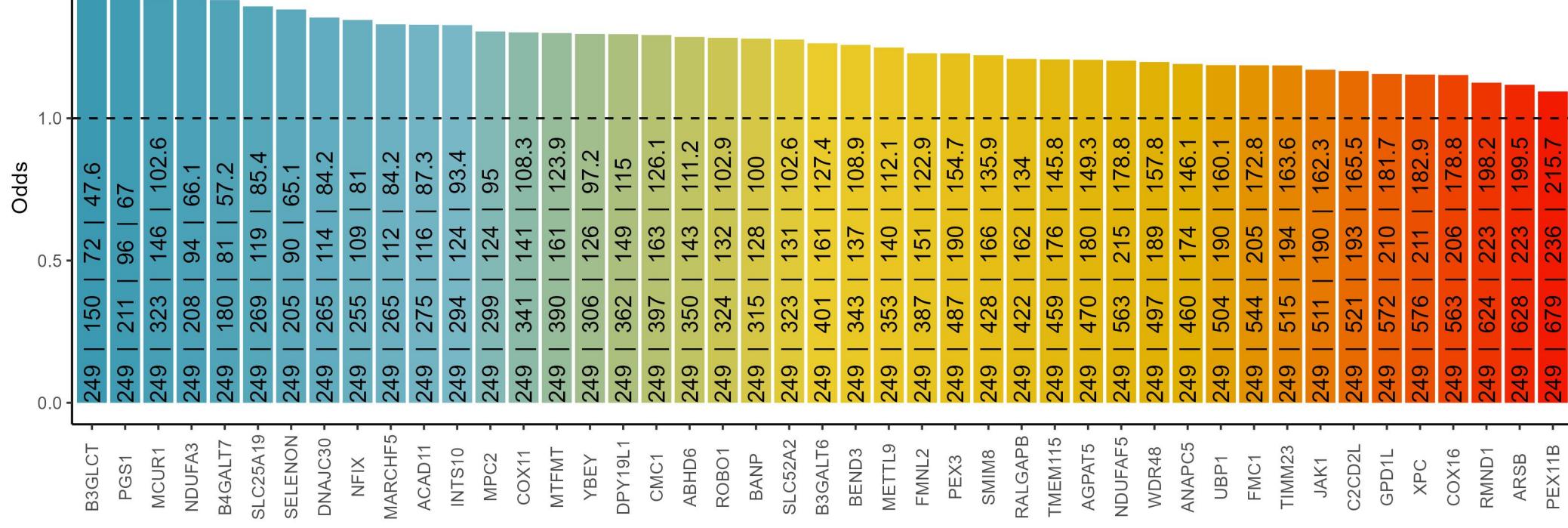
Cooccurrence with EXOG protein in solid cancers, DB2

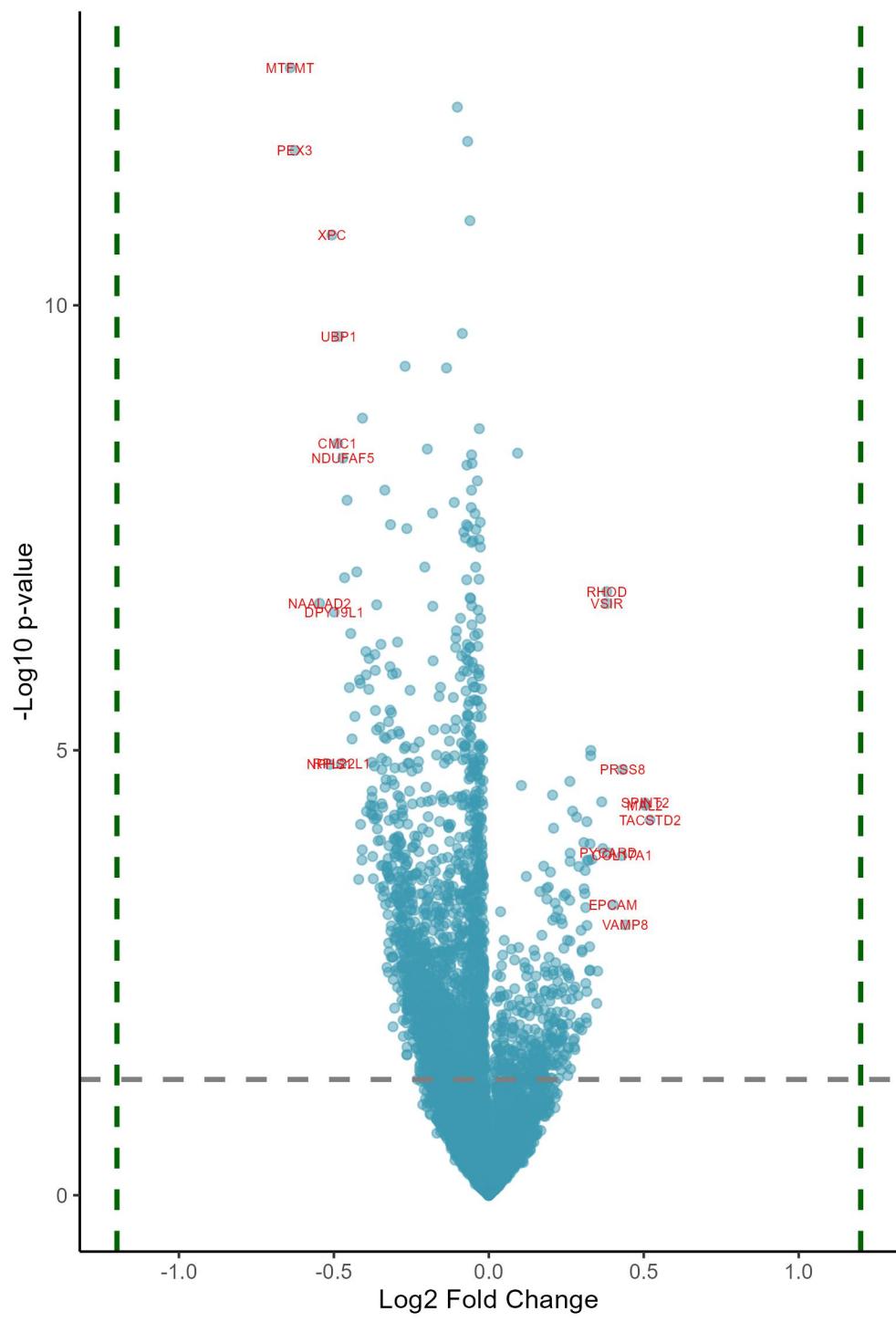
The text in the bars: incidence of EXOG | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

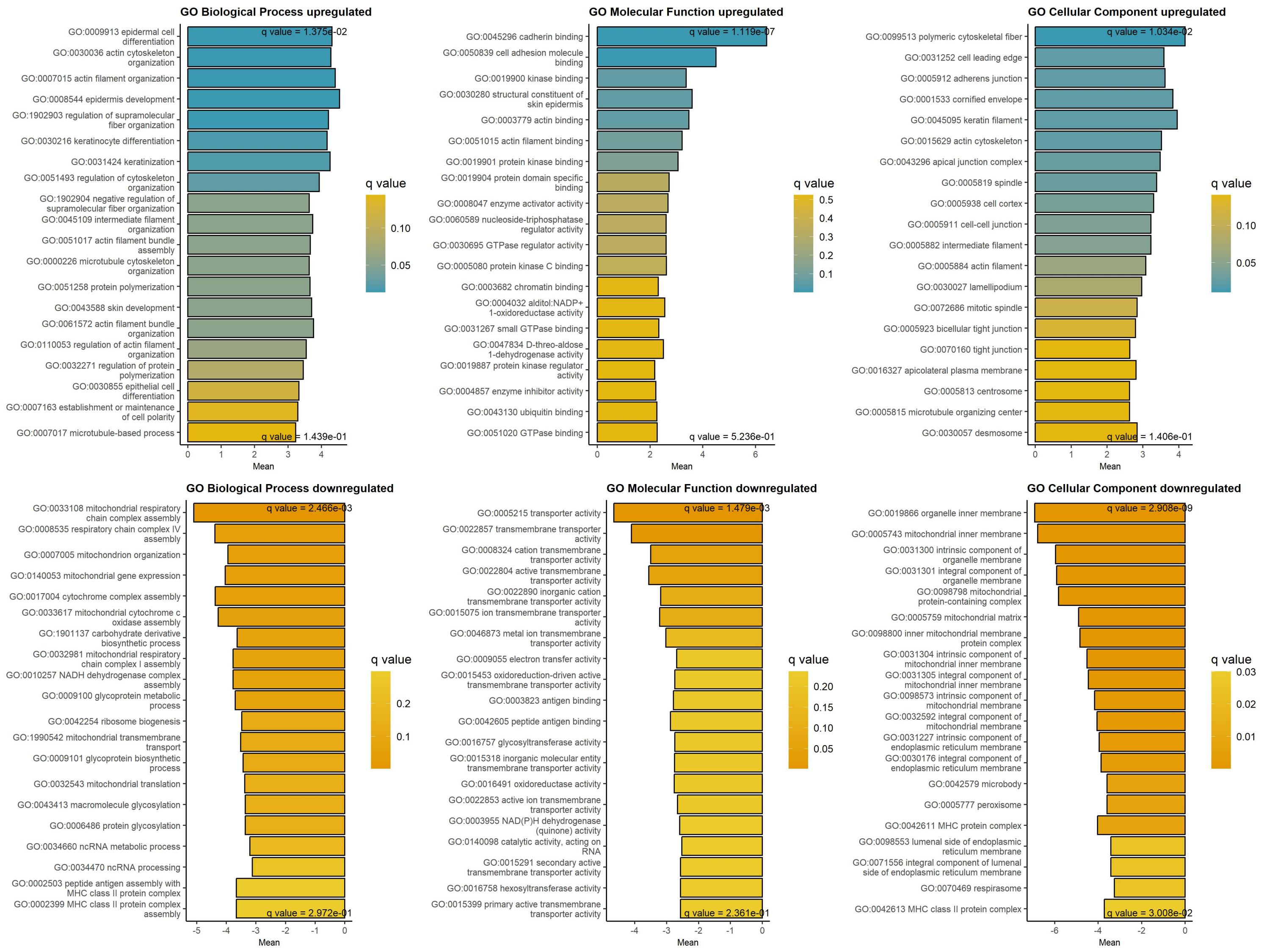




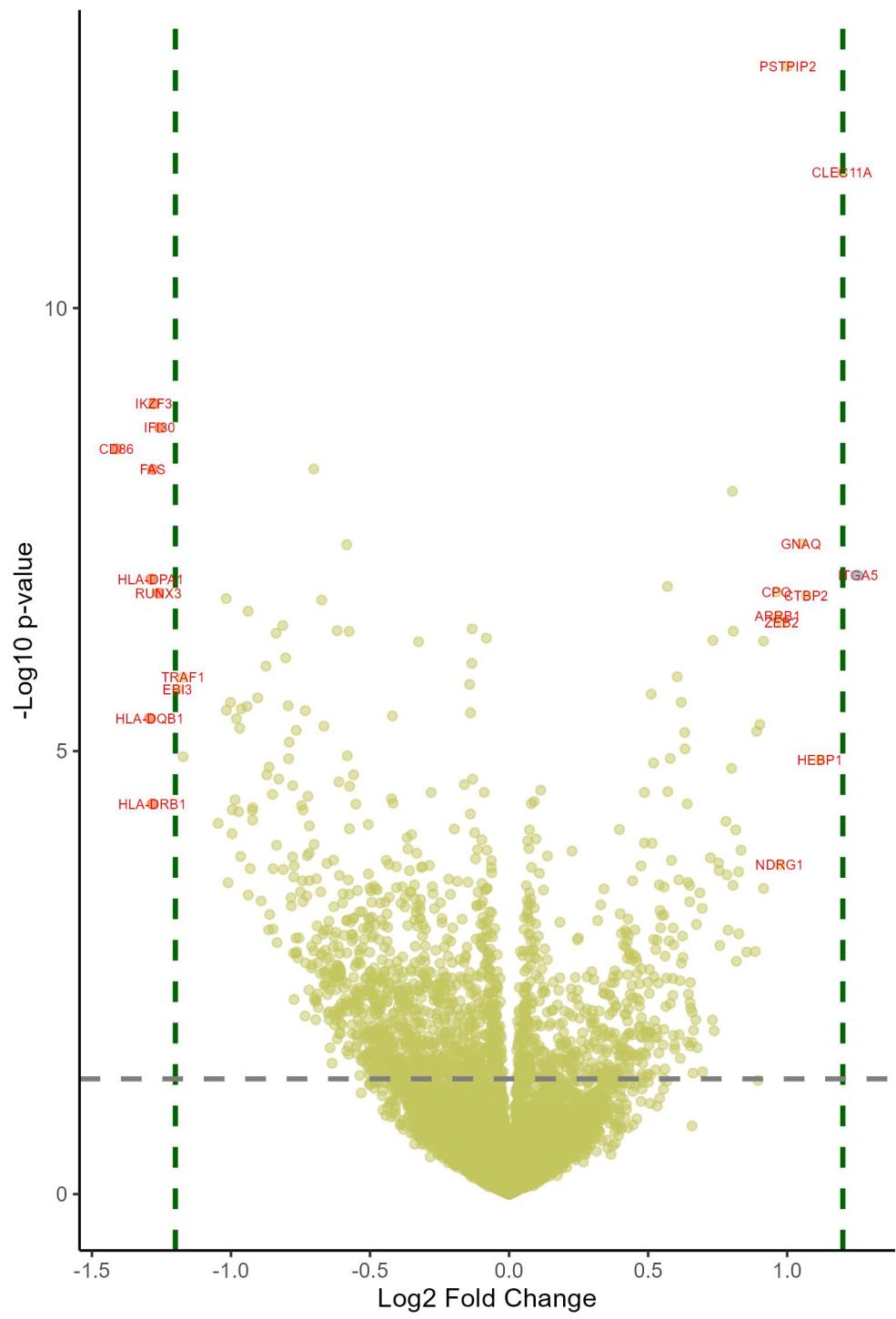
Downregulated at low/absent EXOG Upregulated at low/absent EXOG

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.64	8.94e-10	MTFMT	mitochondrial methionyl-tRNA formyl	0.52	1.83e-03	TACSTD2	tumor associated calcium signal tra
-0.63	3.05e-09	PEX3	peroxisomal biogenesis factor 3	0.5	1.35e-03	SPINT2	serine peptidase inhibitor, Kunitz
-0.55	3.67e-05	NAALAD2	N-acetylated alpha-linked acidic di	0.5	1.39e-03	MAL2	mal, T cell differentiation protein
-0.51	6.74e-04	NPHS1	NPHS1 adhesion molecule, nephrin	0.44	1.24e-02	VAMP8	vesicle associated membrane protein
-0.5	4.18e-05	XPC	XPC complex subunit, DNA damage rec	0.43	7.29e-04	PRSS8	serine protease 8
-0.49	2.13e-06	DPY19L1	dpy-19 like C-mannosyltransferase 1	0.43	3.58e-03	COL17A1	collagen type XVII alpha 1 chain
-0.48	2.08e-07	UBP1	upstream binding protein 1	0.39	3.44e-03	PYCARD	PYD and CARD domain containing
-0.48	6.60e-04	RPL22L1	ribosomal protein L22 like 1	0.38	3.67e-05	VSIR	V-set immunoregulatory receptor
-0.47	2.43e-06	NDUFAF5	NADH:ubiquinone oxidoreductase comp	0.38	2.94e-05	RHOD	ras homolog family member D
-0.47	2.19e-05	SLC25A19	solute carrier family 25 member 19	0.37	3.16e-03	DDR1	discoidin domain receptor tyrosine
-0.46	5.40e-06	MCUR1	mitochondrial calcium uniporter reg	0.36	1.34e-03	SSH3	slingshot protein phosphatase 3
-0.45	1.67e-04	SMIM8	small integral membrane protein 8	0.35	2.79e-02	ASS1	argininosuccinate synthase 1
-0.45	6.60e-05	TIMM23	translocase of inner mitochondrial	0.35	5.05e-02	S100A14	S100 calcium binding protein A14
-0.44	4.49e-04	P3H3	prolyl 3-hydroxylase 3	0.33	3.83e-03	ZNRF2	zinc and ring finger 2
-0.43	2.94e-04	SARM1	sterile alpha and TIR motif contain	0.33	5.42e-04	HSPA1L	heat shock protein family A (Hsp70)
-0.43	1.93e-05	HAACL	2-hydroxyacyl-CoA lyase 1	0.33	6.07e-04	CORO2A	coronin 2A
-0.42	5.39e-03	BRCA1	BRCA1 DNA repair associated	0.33	2.89e-03	ELF1	E74 like ETS transcription factor 1
-0.42	1.45e-04	RAB30	RAB30, member RAS oncogene family	0.33	2.74e-02	KRT74	keratin 74
-0.41	1.56e-04	ZNF692	zinc finger protein 692	0.33	2.78e-02	F11R	F11 receptor
-0.41	1.98e-03	GNG2	G protein subunit gamma 2	0.33	1.84e-02	CTSG	cathepsin G
-0.41	3.89e-03	DES	desmin	0.32	3.92e-03	ARRB1	arrestin beta 1
-0.41	3.21e-03	ITK	IL2 inducible T cell kinase	0.32	3.89e-03	AP1M2	adaptor related protein complex 1 s
-0.41	1.29e-06	TAMM41	TAMM41 mitochondrial translocator as	0.32	1.25e-02	UNC13D	unc-13 homolog D
-0.4	9.04e-05	COX16	cytochrome c oxidase assembly facto	0.32	1.87e-03	GRHL2	grainyhead like transcription facto
-0.4	1.32e-04	ROBO1	roundabout guidance receptor 1	0.32	4.06e-02	CAPG	capping actin protein, gelsolin lik
-0.39	1.57e-03	ARMCX2	armadillo repeat containing X-link	0.32	6.91e-02	CDH1	cadherin 1
-0.39	1.71e-04	CD320	CD320 molecule	0.31	6.40e-02	LAD1	ladinin 1
-0.39	1.02e-04	FMC1	formation of mitochondrial complex	0.31	3.50e-02	KRT15	keratin 15

GAGE analysis on upregulated and downregulated proteins at low/absent EXOG protein, DB2



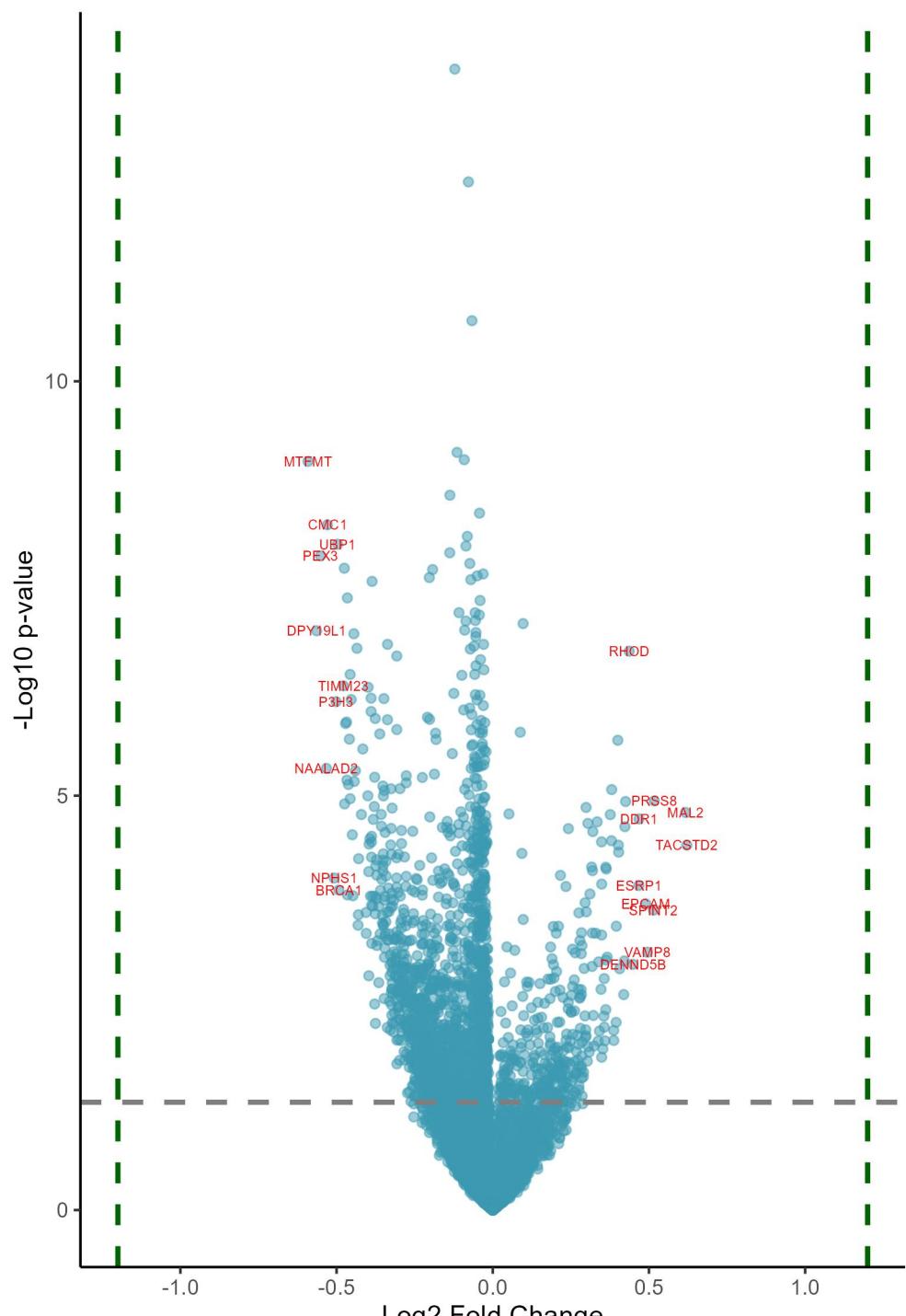
Differentially expressed proteins in blood cancers at absence/low amount of EXOG , DB2
p-value < 0.05 & logFC > 1.2



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

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.41	5.41e-06	CD86	CD86 molecule	1.25	7.25e-05	ITGA5	integrin subunit alpha 5
-1.29	6.91e-04	HLA-DQB1	major histocompatibility complex, c	1.2	8.22e-09	CLEC11A	C-type lectin domain containing 11A
-1.29	7.39e-05	HLA-DPA1	major histocompatibility complex, c	1.12	1.62e-03	HEBP1	heme binding protein 1
-1.28	3.65e-03	HLA-DRB1	major histocompatibility complex, c	1.07	8.69e-05	CTBP2	C-terminal binding protein 2
-1.28	6.90e-06	FAS	Fas cell surface death receptor	1.05	3.56e-05	GNAQ	G protein subunit alpha q
-1.28	2.50e-06	IKZF3	IKAROS family zinc finger 3	1	7.82e-10	PSTPIP2	proline-serine-threonine phosphatases
-1.26	8.61e-05	RUNX3	RUNX family transcription factor 3	0.98	1.35e-04	ZEB2	zinc finger E-box binding homeobox
-1.26	3.74e-06	IFI30	IFI30 lysosomal thiol reductase	0.97	1.14e-02	NDRG1	N-myc downstream regulated 1
-1.19	4.32e-04	EBI3	Epstein-Barr virus induced 3	0.97	1.20e-04	ARRB1	arrestin beta 1
-1.17	3.32e-04	TRAF1	TNF receptor associated factor 1	0.96	8.61e-05	CPQ	carboxypeptidase Q
-1.17	1.56e-03	HLA-DPB1	major histocompatibility complex, c	0.92	1.59e-02	GLUL	glutamate-ammonia ligase
-1.05	5.41e-03	IL4I1	interleukin 4 induced 1	0.92	1.53e-04	LPCAT2	lysophosphatidylcholine acyltransfe
-1.02	8.69e-05	SLC25A4	solute carrier family 25 member 4	0.9	7.93e-04	RREB1	ras responsive element binding prot
-1.02	6.10e-04	ISG20	interferon stimulated exonuclease g	0.89	2.63e-01	SPN	sialophorin
-1.01	1.49e-02	SERPINB9	serpin family B member 9	0.89	8.78e-04	AGTRAP	angiotensin II receptor associated
-1	5.48e-04	IRF4	interferon regulatory factor 4	0.89	4.05e-02	MACROD1	mono-ADP ribosylhydrolase 1
-1	6.51e-03	SLAMF1	signaling lymphocytic activation mo	0.85	4.09e-02	LCP2	lymphocyte cytosolic protein 2
-1	4.06e-03	PFN2	profilin 2	0.83	8.86e-03	KATNA1	katanin catalytic subunit A1
-0.99	3.50e-03	CD37	CD37 molecule	0.83	3.10e-02	CTSG	cathepsin G
-0.98	6.91e-04	PEX3	peroxisomal biogenesis factor 3	0.83	1.24e-02	CPNE2	copine 2
-0.97	4.16e-03	SLAMF6	SLAM family member 6	0.82	4.69e-02	HSD17B11	hydroxysteroid 17-beta dehydrogenas
-0.97	8.38e-04	ABI3	ABI family member 3	0.82	6.00e-03	LYZ	lysozyme
-0.97	9.93e-03	CD40	CD40 molecule	0.81	1.38e-04	ARR3	arrestin 3
-0.96	6.04e-04	RAB30	RAB30, member RAS oncogene family	0.81	1.55e-02	EIF4EBP1	eukaryotic translation initiation f
-0.94	5.82e-04	CD74	CD74 molecule	0.8	1.09e-05	CD33	CD33 molecule
-0.94	1.10e-04	MAP4K1	mitogen-activated protein kinase ki	0.8	1.92e-03	IGLL1	immunoglobulin lambda like polypept
-0.94	1.71e-02	MS4A1	membrane spanning 4-domains A1	0.79	2.89e-02	LGALS9	galectin 9
-0.93	1.18e-02	CD22	CD22 molecule	0.78	1.31e-02	EHD2	EH domain containing 2
-0.92	4.09e-03	PEG10	paternally expressed 10	0.78	5.20e-03	NECTIN2	nectin cell adhesion molecule 2

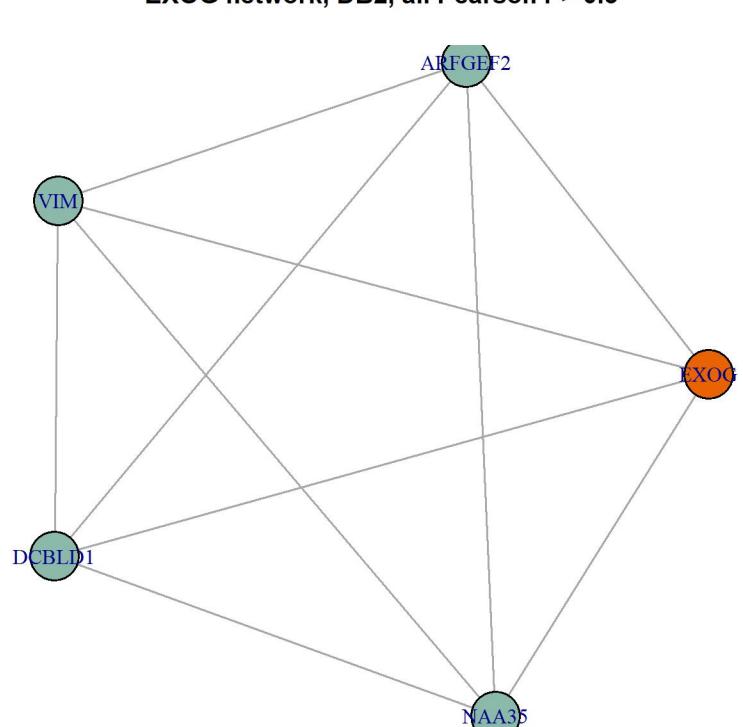
Differentially expressed proteins in solid cancers at absence/low amount of EXOG , DB2
p-value < 0.05 & logFC > 1.2



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

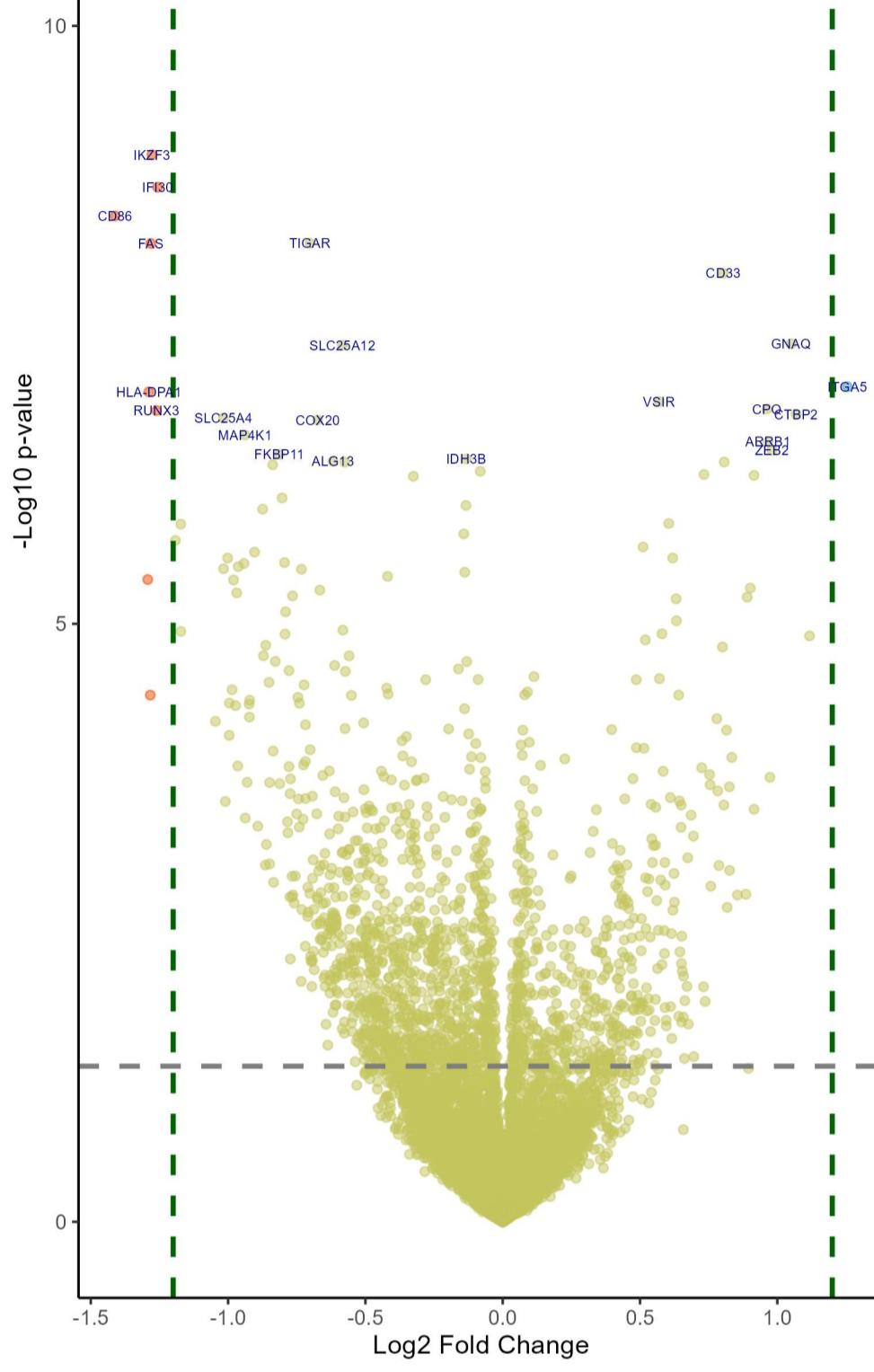
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.59	1.11e-06	MTFMT	mitochondrial methionyl-tRNA formyl	0.62	1.55e-03	TACSTD2	tumor associated calcium signal tra
-0.56	2.60e-05	DPY19L1	dpy-19 like C-mannosyltransferase 1	0.62	9.14e-04	MAL2	mal, T cell differentiation protein
-0.55	7.13e-06	PEX3	peroxisomal biogenesis factor 3	0.52	7.33e-04	PRSS8	serine protease 8
-0.53	3.77e-04	NAALAD2	N-acetylated alpha-linked acidic di	0.51	5.46e-03	SPINT2	serine peptidase inhibitor, Kunitz
-0.53	4.51e-06	CMC1	C-X9-C motif containing 1	0.5	1.22e-02	VAMP8	vesicle associated membrane protein
-0.51	2.95e-03	NPHS1	NPHS1 adhesion molecule, nephrin	0.49	4.77e-03	EPCAM	epithelial cell adhesion molecule
-0.5	1.04e-04	P3H3	prolyl 3-hydroxylase 3	0.47	1.02e-03	DDR1	discoidin domain receptor tyrosine
-0.5	6.26e-06	UBP1	upstream binding protein 1	0.47	3.36e-03	ESRP1	epithelial splicing regulatory prot
-0.49	3.66e-03	BRCA1	BRCA1 DNA repair associated	0.45	1.55e-02	DENND5B	DENN domain containing 5B
-0.48	7.90e-05	TIMM23	translocase of inner mitochondrial	0.44	3.60e-05	RHOD	ras homolog family member D
-0.48	8.69e-06	NDUFAF5	NADH:ubiquinone oxidoreductase comp	0.43	7.40e-04	PROM2	prominin 2
-0.47	7.79e-04	ARMCX2	armadillo repeat containing X-linker	0.42	1.17e-03	ZNRF2	zinc and ring finger 2
-0.47	1.57e-04	AGPAT5	1-acylglycerol-3-phosphate O-acyltr	0.42	1.45e-02	COL17A1	collagen type XVII alpha 1 chain
-0.47	1.55e-04	SLC25A19	solute carrier family 25 member 19	0.42	2.71e-02	ANXA3	annexin A3
-0.47	4.85e-04	SMIM8	small integral membrane protein 8	0.41	1.67e-02	KRT74	keratin 74
-0.47	1.43e-05	FMC1	formation of mitochondrial complex	0.4	1.78e-03	SSH3	slingshot protein phosphatase 3
-0.47	4.05e-03	DES	desmin	0.4	1.55e-03	AP1M2	adaptor related protein complex 1 s
-0.46	5.28e-04	DNAJC30	DnaJ heat shock protein family (Hsp	0.4	2.14e-04	HSPA1L	heat shock protein family A (Hsp70)
-0.46	2.11e-04	SUOX	sulfite oxidase	0.4	7.34e-03	TFAP2A	transcription factor AP-2 alpha
-0.46	6.01e-05	MCUR1	mitochondrial calcium uniporter reg	0.39	4.58e-02	CDH1	cadherin 1
-0.46	6.99e-04	SLC52A2	solute carrier family 52 member 2	0.39	6.30e-02	S100A14	S100 calcium binding protein A14
-0.45	1.01e-04	ROBO1	roundabout guidance receptor 1	0.39	5.33e-02	TSTD1	thiosulfate sulfurtransferase like
-0.45	1.31e-03	P3H4	prolyl 3-hydroxylase family member	0.38	5.74e-04	CORO2A	coronin 2A
-0.45	4.07e-03	ITK	IL2 inducible T cell kinase	0.38	1.48e-03	GRHL2	grainyhead like transcription facto
-0.44	2.66e-05	XPC	XPC complex subunit, DNA damage rec	0.38	9.39e-04	ELF1	E74 like ETS transcription factor 1
-0.44	4.99e-04	TIMP1	TIMP metallopeptidase inhibitor 1	0.37	1.36e-02	GALNT3	polypeptide N-acetylgalactosaminylt
-0.44	3.98e-04	NT5DC3	5'-nucleotidase domain containing 3	0.36	2.46e-03	FAM107B	family with sequence similarity 107
-0.43	3.48e-05	WDR48	WD repeat domain 48	0.36	1.43e-02	SNCG	synuclein gamma
-0.43	7.26e-03	RCN3	reticulocalbin 3	0.36	3.54e-02	SIM2	SIM bHLH transcription factor 2

EXOG network, DB2, all Pearson r > 0.3



Sorted by p values!

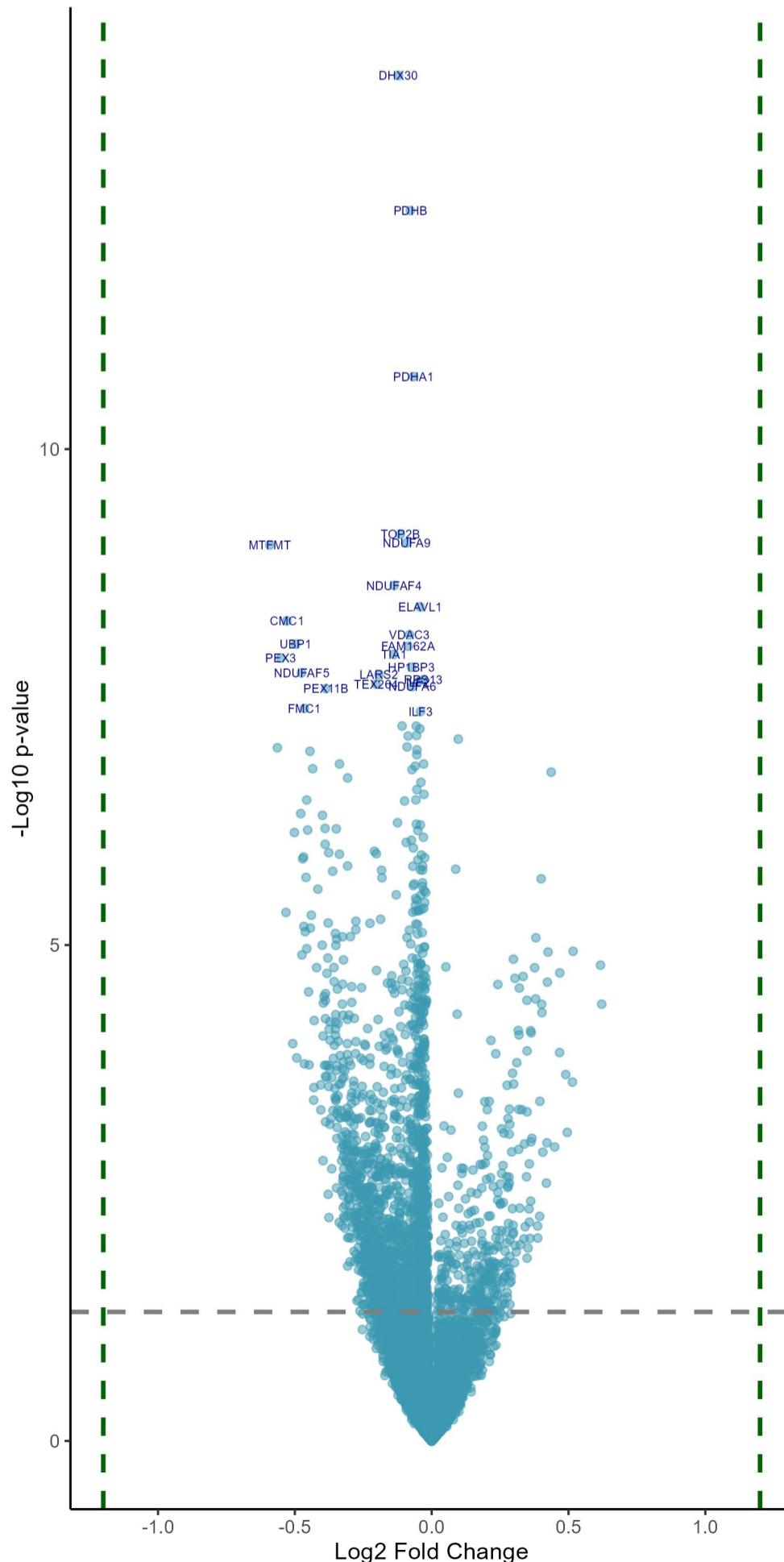
Downregulated in blood cancers at low/absent EXOG Upregulated in blood cancers at low/absent EXOG



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.28	2.50e-06	IKZF3	IKAROS family zinc finger 3	1	7.82e-10	PSTPIP2	proline-serine-threonine phosphatase
-1.26	3.74e-06	IFI30	IFI30 lysosomal thiol reductase	1.2	8.22e-09	CLEC11A	C-type lectin domain containing 11A
-1.41	5.41e-06	CD86	CD86 molecule	0.8	1.09e-05	CD33	CD33 molecule
-0.7	6.90e-06	TIGAR	TP53 induced glycolysis regulatory	1.05	3.56e-05	GNAQ	G protein subunit alpha q
-1.28	6.90e-06	FAS	Fas cell surface death receptor	1.25	7.25e-05	ITGA5	integrin subunit alpha 5
-0.58	3.56e-05	SLC25A12	solute carrier family 25 member 12	0.57	8.29e-05	VSIIR	V-set immunoregulatory receptor
-1.29	7.39e-05	HLA-DPA1	major histocompatibility complex, c	0.96	8.61e-05	CPQ	carboxypeptidase Q
-1.26	8.61e-05	RUNX3	RUNX family transcription factor 3	1.07	8.69e-05	CTBP2	C-terminal binding protein 2
-1.02	8.69e-05	SLC25A4	solute carrier family 25 member 4	0.97	1.20e-04	ARRB1	arrestin beta 1
-0.67	8.69e-05	COX20	cytochrome c oxidase assembly facto	0.98	1.35e-04	ZEB2	zinc finger E-box binding homeobox
-0.94	1.10e-04	MAP4K1	mitogen-activated protein kinase ki	0.81	1.38e-04	ARR3	arrestin 3
-0.81	1.38e-04	FKBP11	FKBP prolyl isomerase 11	0.73	1.53e-04	PRTN3	proteinase 3
-0.13	1.38e-04	IDH3B	isocitrate dehydrogenase (NAD(+)) 3	0.92	1.53e-04	LPCAT2	lysophosphatidylcholine acyltransfe
-0.62	1.38e-04	ALG13	ALG13 UDP-N-acetylglucosaminyltrans	0.6	3.32e-04	MORC3	MORC family CW-type zinc finger 3
-0.58	1.38e-04	RFX5	regulatory factor X5	0.51	4.76e-04	SKAP2	src kinase associated phosphoprotei
-0.84	1.39e-04	CNOT6L	CCR4-NOT transcription complex subu	0.62	5.48e-04	DNMT3B	DNA methyltransferase 3 beta
-0.08	1.53e-04	HSD17B10	hydroxysteroid 17-beta dehydrogenas	0.9	7.93e-04	RREB1	ras responsive element binding prot
-0.33	1.53e-04	MBD2	methyl-CpG binding domain protein 2	0.89	8.78e-04	AGTRAP	angiotensin II receptor associated
-0.8	2.25e-04	XPC	XPC complex subunit, DNA damage rec	0.63	8.90e-04	AIF1	allograft inflammatory factor 1
-0.13	2.52e-04	OGDH	oxoglutarate dehydrogenase	0.63	1.32e-03	GRB10	growth factor receptor bound protei
-0.87	2.63e-04	CFAP70	cilia and flagella associated prote	0.58	1.59e-03	GMPR	guanosine monophosphate reductase
-1.17	3.32e-04	TRAF1	TNF receptor associated factor 1	1.12	1.62e-03	HEBP1	heme binding protein 1
-0.14	3.90e-04	NIP7	nucleolar pre-rRNA processing prote	0.52	1.73e-03	BST1	bone marrow stromal cell antigen 1
-1.19	4.32e-04	EBI3	Epstein-Barr virus induced 3	0.8	1.92e-03	IGLL1	immunoglobulin lambda like polypept
-0.9	5.13e-04	DNHD1	dynein heavy chain domain 1	0.11	3.00e-03	TXND12	thioredoxin domain containing 12
-1	5.48e-04	IRF4	interferon regulatory factor 4	0.57	3.03e-03	ZMIZ1	zinc finger MIZ-type containing 1
-0.79	5.82e-04	LRRC27	leucine rich repeat containing 27	0.49	3.03e-03	FCER1G	Fc epsilon receptor Ig
-0.94	5.82e-04	CD74	CD74 molecule	0.09	3.61e-03	MYCBP	MYC binding protein
-0.96	6.04e-04	RAB30	RAB30, member RAS oncogene family	0.08	3.65e-03	CUTA	cutA divalent cation tolerance homo
-1.02	6.10e-04	ISG20	interferon stimulated exonuclease g	0.64	3.65e-03	IGFBP2	insulin like growth factor binding
-0.73	6.10e-04	LPXN	leupaxin	0.78	5.20e-03	NECTIN2	nectin cell adhesion molecule 2
-0.14	6.32e-04	ACADM	acyl-CoA dehydrogenase medium chain	0.4	6.00e-03	PRAM1	PML-RARA regulated adaptor molecule
-0.42	6.71e-04	SQSTM1	sequestosome 1	0.82	6.00e-03	LYZ	lysozyme
-1.29	6.91e-04	HLA-DQB1	major histocompatibility complex, c	0.07	6.00e-03	PFDN2	prefoldin subunit 2
-0.98	6.91e-04	PEX3	peroxisomal biogenesis factor 3	0.1	7.25e-03	HDGF	heparin binding growth factor
-0.67	8.09e-04	VARS2	valyl-tRNA synthetase 2, mitochondr	0.07	7.49e-03	TKT	transketolase
-0.97	8.38e-04	ABI3	ABI family member 3	0.49	7.84e-03	RAP1GAP2	RAP1 GTPase activating protein 2
-0.77	8.73e-04	TMED8	transmembrane p24 trafficking prote	0.51	7.85e-03	TOR4A	torsin family 4 member A
0.79	1.13e-02	COMMD1	cysteine C methyletransferase domain	0.07	8.76e-03	TALDO1	transaldolase 1

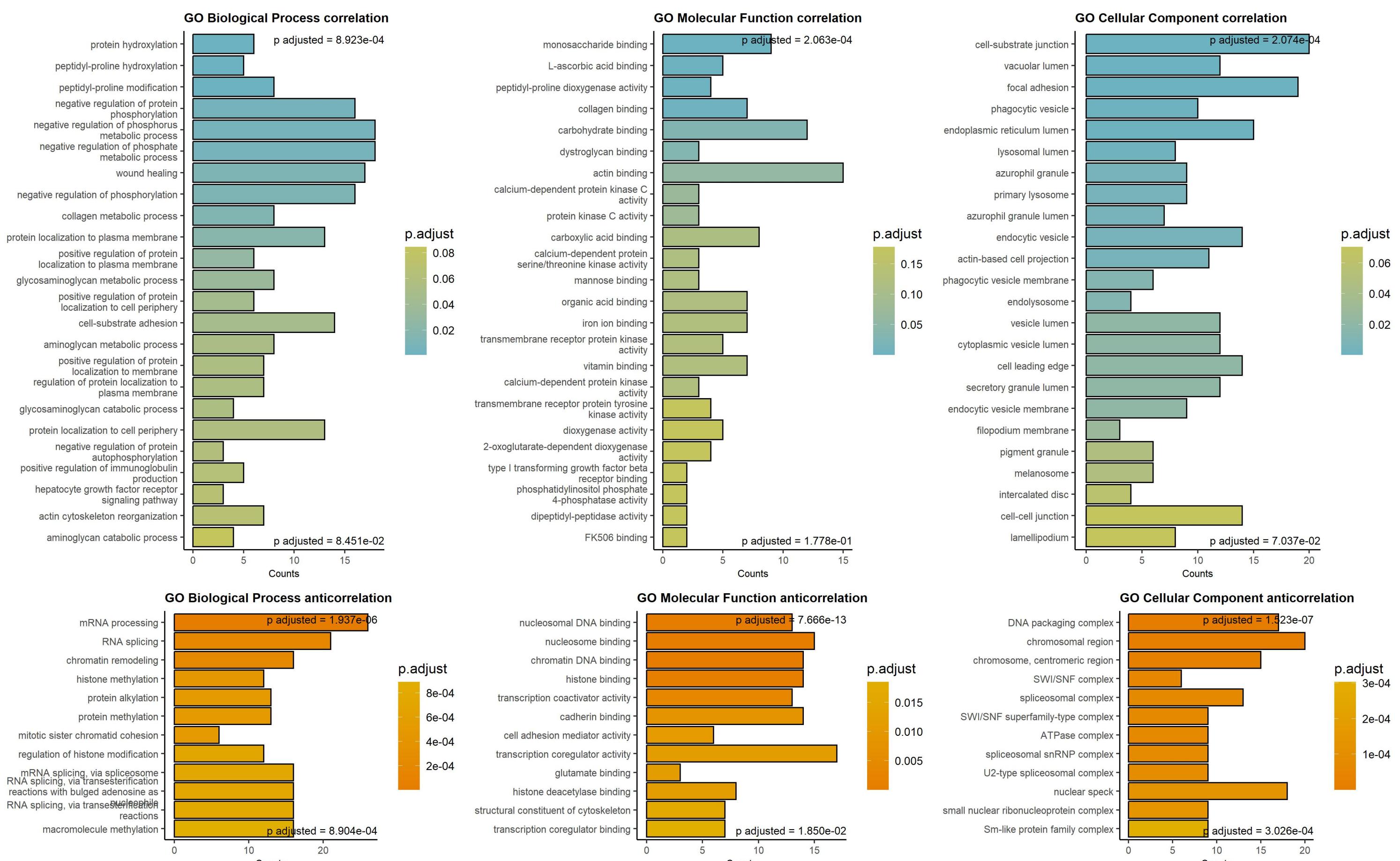
Sorted by p values!

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

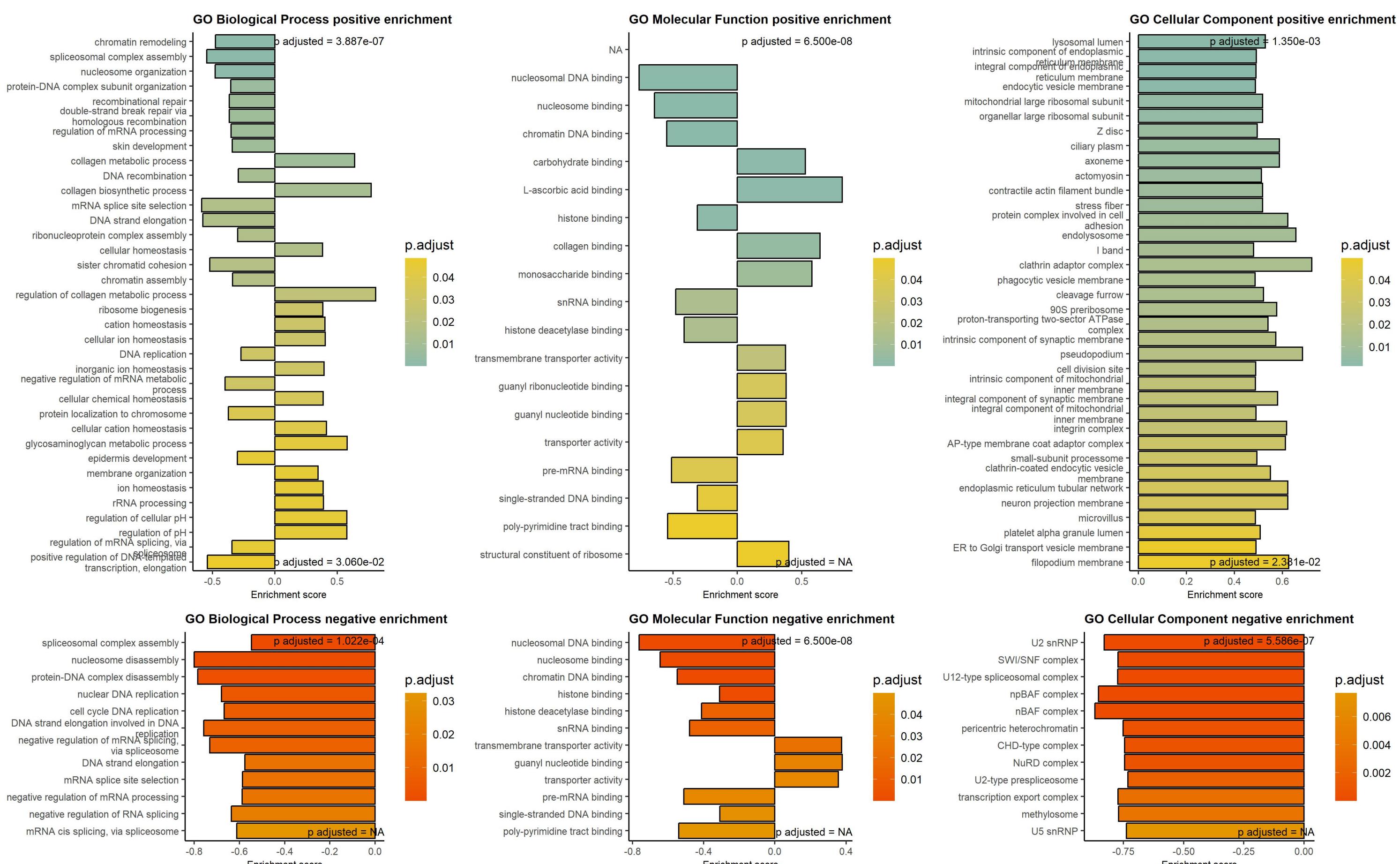


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.12	7.15e-11	DHX30	DExH-box helicase 30	0.1	2.26e-05	SEC16A	SEC16 homolog A, endoplasmic reticu
-0.08	1.10e-09	PDHB	pyruvate dehydrogenase E1 subunit b	0.44	3.60e-05	RHOD	ras homolog family member D
-0.07	3.88e-08	PDHA1	pyruvate dehydrogenase E1 subunit a	0.09	1.84e-04	TNKS1BP1	tankyrase 1 binding protein 1
-0.11	1.11e-06	TOP2B	DNA topoisomerase II beta	0.4	2.14e-04	HSPA1L	heat shock protein family A (Hsp70)
-0.09	1.11e-06	NDUFA9	NADH:ubiquinone oxidoreductase subu	0.38	5.74e-04	CORO2A	coronin 2A
-0.59	1.11e-06	MTFMT	mitochondrial methionyl-tRNA formyl	0.52	7.33e-04	PRSS8	serine protease 8
-0.14	2.48e-06	NDUFA4	NADH:ubiquinone oxidoreductase comp	0.43	7.40e-04	PROM2	prominin 2
-0.04	3.62e-06	ELAVL1	ELAV like RNA binding protein 1	0.3	8.35e-04	CSNK1D	casein kinase 1 delta
-0.53	4.51e-06	CMC1	C-X9-C motif containing 1	0.62	9.14e-04	MAL2	mal, T cell differentiation protein
-0.08	5.66e-06	VDAC3	voltage dependent anion channel 3	0.05	9.39e-04	CTTN	cortactin
-0.5	6.26e-06	UBP1	upstream binding protein 1	0.38	9.39e-04	ELF1	E74 like ETS transcription factor 1
-0.09	6.26e-06	FAM162A	family with sequence similarity 162	0.47	1.02e-03	DDR1	discoidin domain receptor tyrosine
-0.14	7.00e-06	TIA1	TIA1 cytotoxic granule associated R	0.33	1.08e-03	TSC22D2	TSC22 domain family member 2
-0.55	7.13e-06	PEX3	peroxisomal biogenesis factor 3	0.3	1.11e-03	KRT76	keratin 76
-0.07	8.26e-06	HP1BP3	heterochromatin protein 1 binding p	0.42	1.17e-03	ZNRF2	zinc and ring finger 2
-0.48	8.69e-06	NDUFA5	NADH:ubiquinone oxidoreductase comp	0.24	1.20e-03	SOX15	SRY-box transcription factor 15
-0.19	8.69e-06	LARS2	leucyl-tRNA synthetase 2, mitochond	0.32	1.25e-03	IRF6	interferon regulatory factor 6
-0.03	9.30e-06	RPS13	ribosomal protein S13	0.38	1.48e-03	GRHL2	grainyhead like transcription facto
-0.05	9.30e-06	ILF2	interleukin enhancer binding factor	0.35	1.49e-03	VSIIR	V-set immunoregulatory receptor
-0.2	9.30e-06	TEX264	testis expressed 264, ER-phagy rece	0.62	1.55e-03	TACSTD2	tumor associated calcium signal tra
-0.07	9.41e-06	NDUFA6	NADH:ubiquinone oxidoreductase subu	0.4	1.55e-03	AP1M2	adaptor related protein complex 1 s
-0.39	9.45e-06	PEX11B	peroxisomal biogenesis factor 11 be	0.4	1.78e-03	SSH3	slingshot protein phosphatase 3
-0.47	1.43e-05	FMC1	formation of mitochondrial complex	0.09	1.83e-03	DYNC1LI2	dynein cytoplasmic 1 light intermed
-0.04	1.48e-05	ILF3	interleukin enhancer binding factor	0.32	2.36e-03	ANXA8	annexin A8
-0.11	1.92e-05	APOO	apolipoprotein O	0.36	2.37e-03	FAM83B	family with sequence similarity 83
-0.06	1.92e-05	ATP5PB	ATP synthase peripheral stalk-membr	0.36	2.46e-03	FAM107B	family with sequence similarity 107
-0.04	1.97e-05	HNRNPR	heterogeneous nuclear ribonucleopro	0.32	2.56e-03	NECTIN4	nectin cell adhesion molecule 4
-0.06	2.18e-05	NSF	N-ethylmaleimide sensitive factor,	0.22	2.80e-03	C11orf52	chromosome 11 open reading frame 52
-0.09	2.18e-05	RNPS1	RNA binding protein with serine ric	0.35	3.31e-03	CENPE	centromere protein E
-0.09	2.60e-05	TIMM13	translocase of inner mitochondrial	0.47	3.36e-03	ESRP1	epithelial splicing regulatory prot
-0.56	2.60e-05	DPY19L1	dpy-19 like C-mannosyltransfer				

Top 250 correlation coefficients overrepresentation, EXOG protein, DB2



Gene Set Enrichment analysis on protein correlation coefficients, EXOG protein, DB2



No information on Ser/Thr kinase phosphorylation sites for EXOG

No information on Ser/Thr kinase phosphorylation sites for EXOG

Top 15 positive correlation coefficients for EXOG protein by tissue, DB2

Beware of false positives in tissues with small number of samples



Cervix