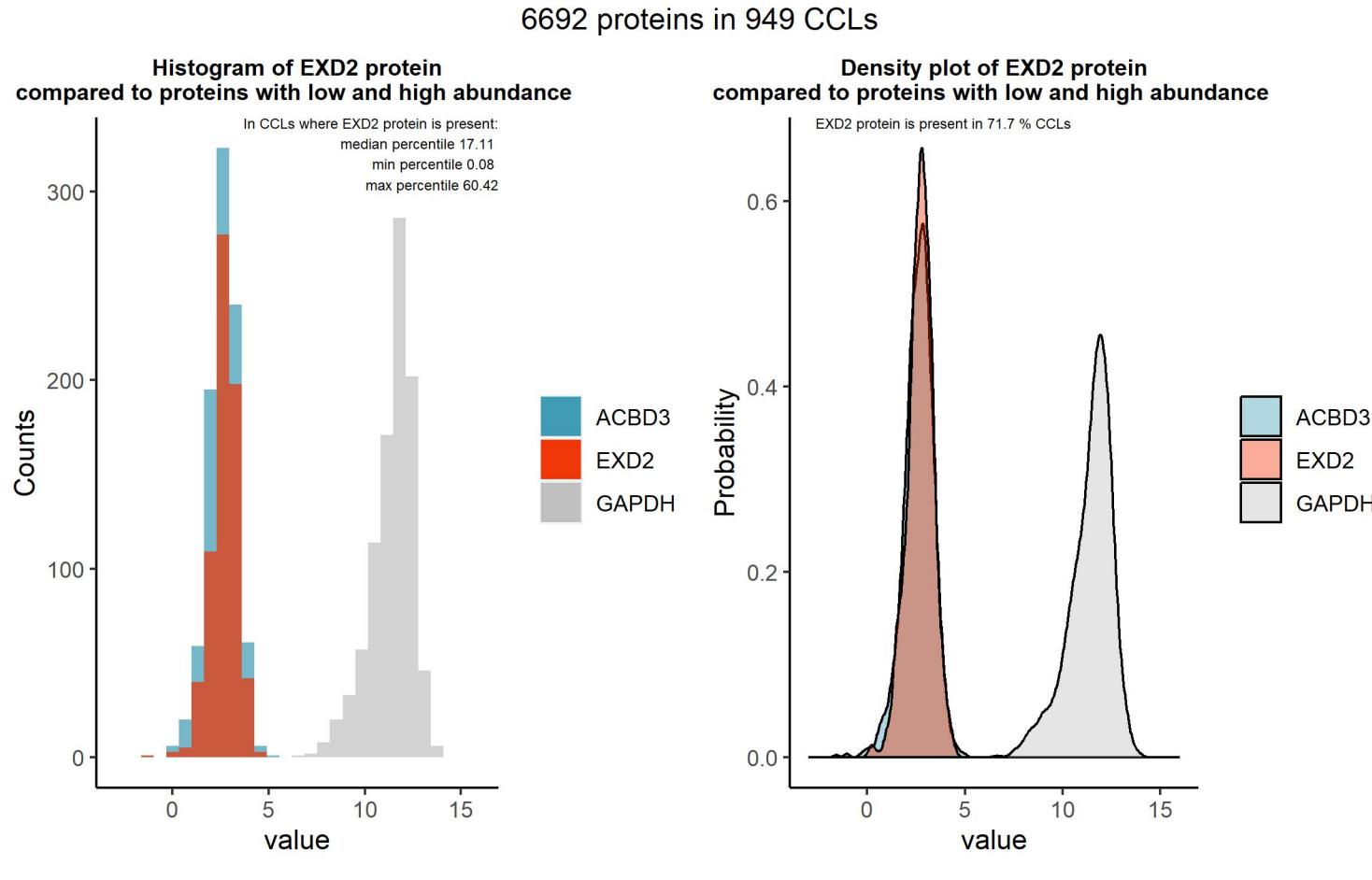


EXD2

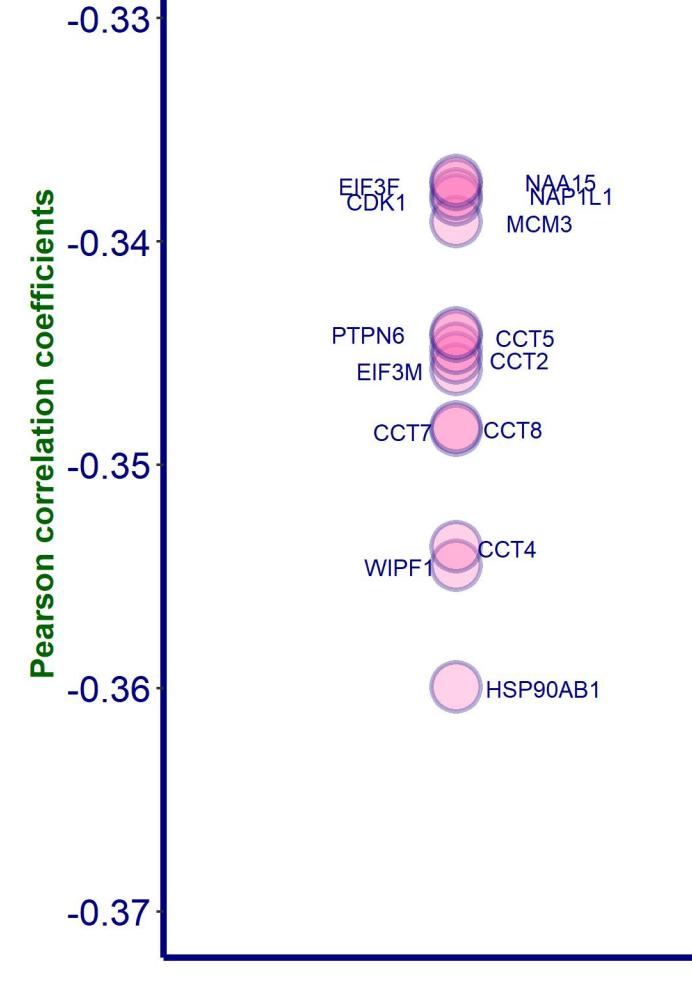
Protein name: EXD2 ; UNIPROT: Q9NVH0 ; Gene name: exonuclease 3'-5' domain containing 2

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

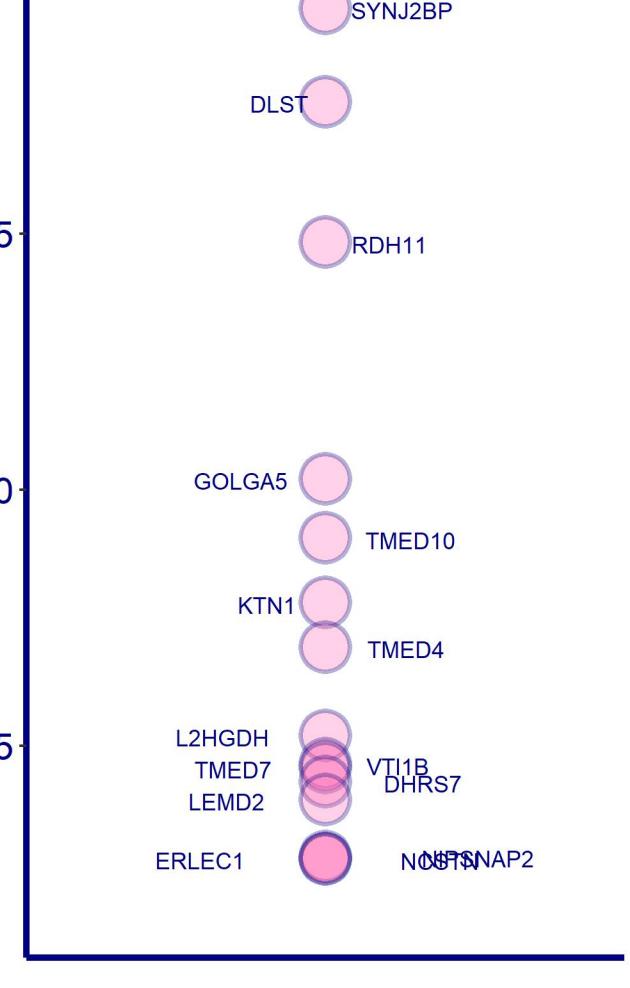
Sanger Institute Protein Database 1 (DB1), protein presence is certain



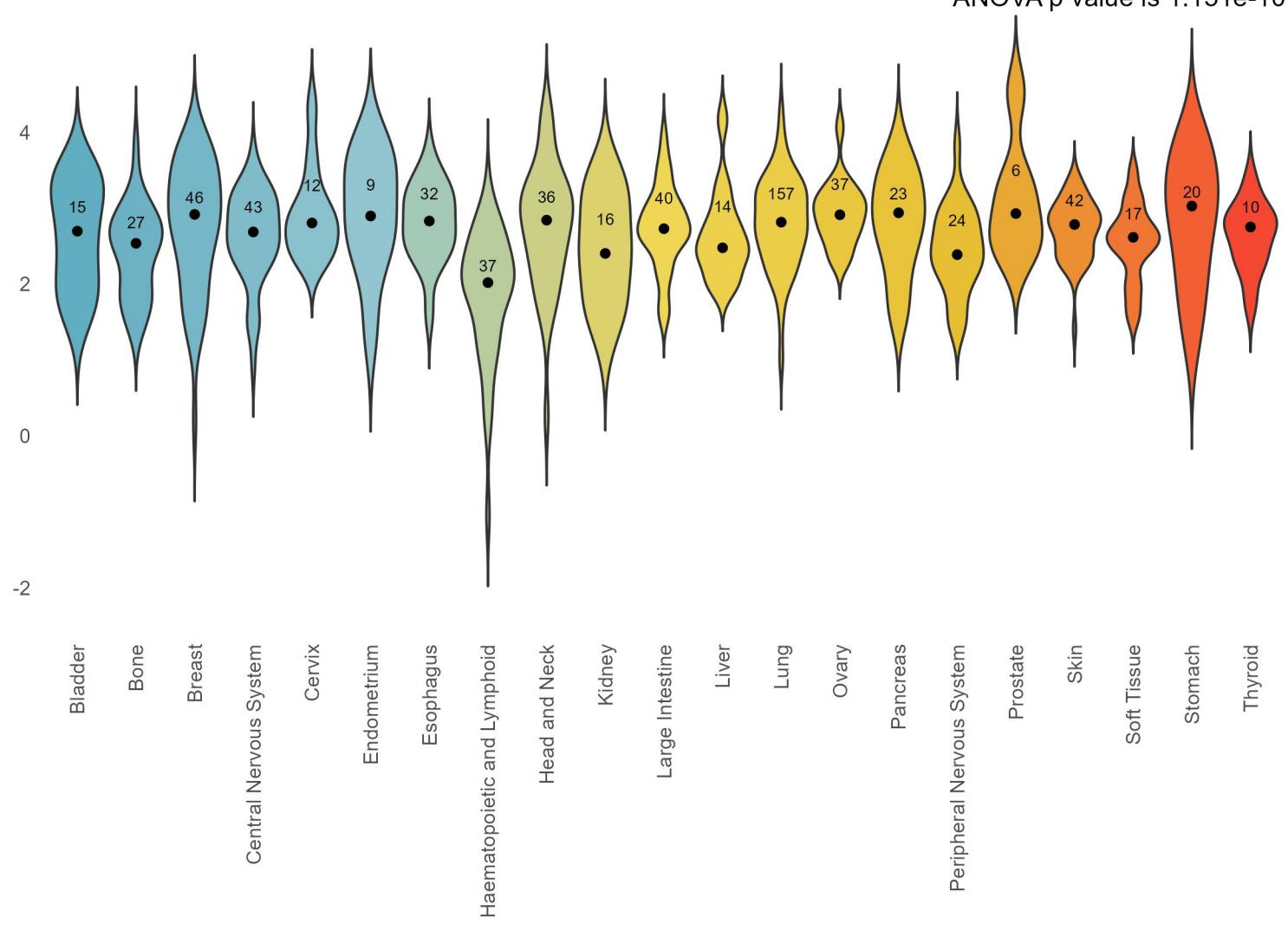
Top negative correlations of EXD2 protein, DB1



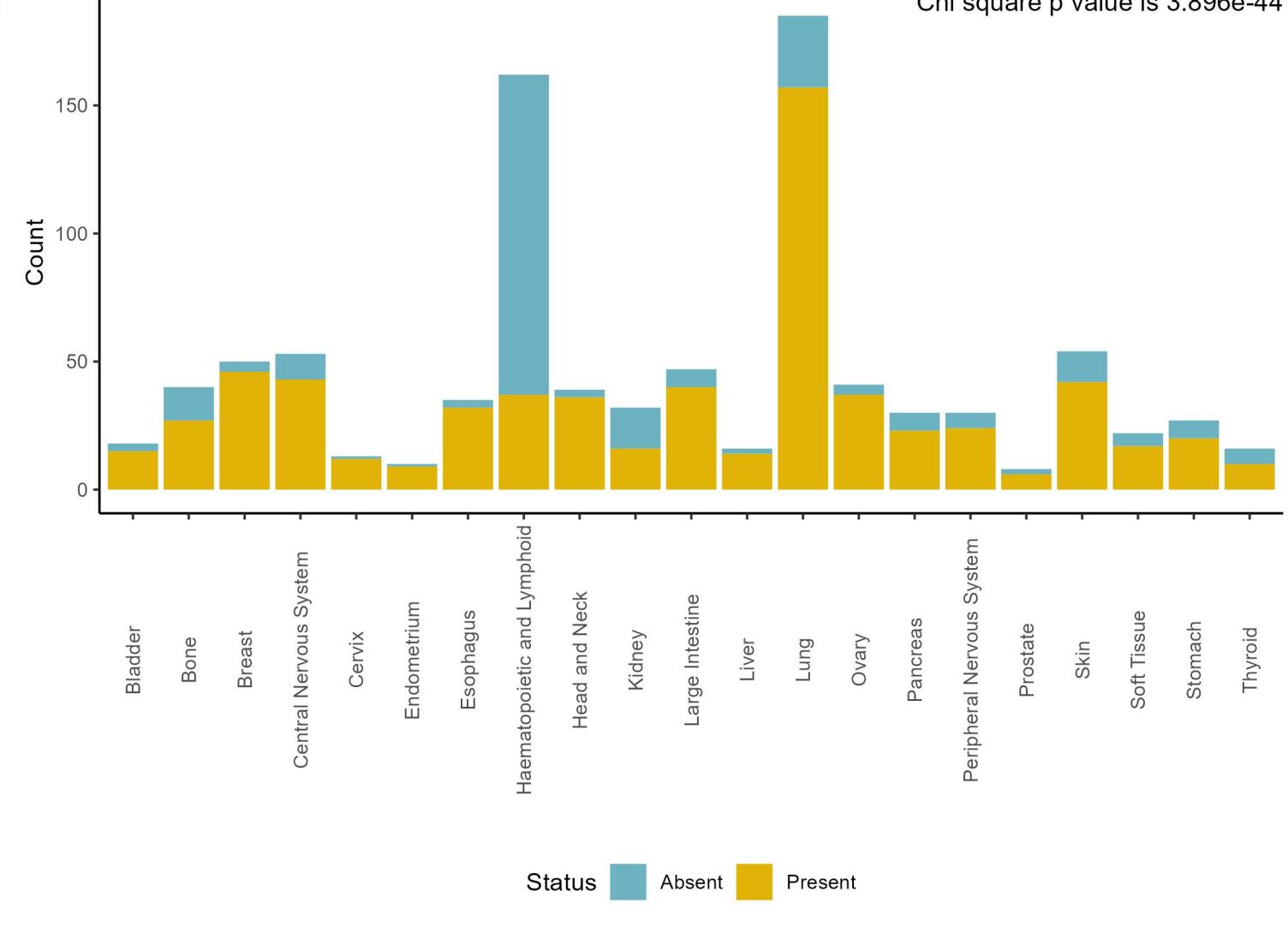
Top positive correlations of EXD2 protein, DB1



Amount of EXD2 protein, number of CCLs where it is present by tissue, DB1



Present and absent EXD2 protein counts by tissue, DB1

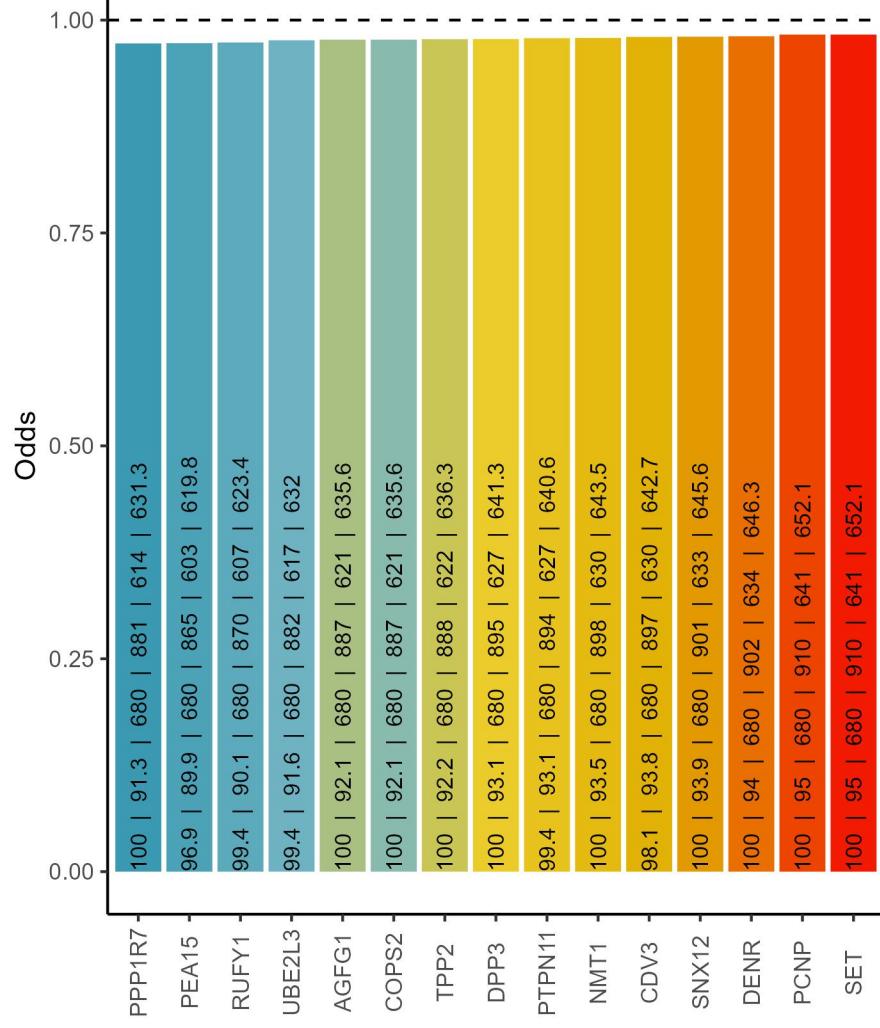


Cooccurrence with EXD2 protein, DB1

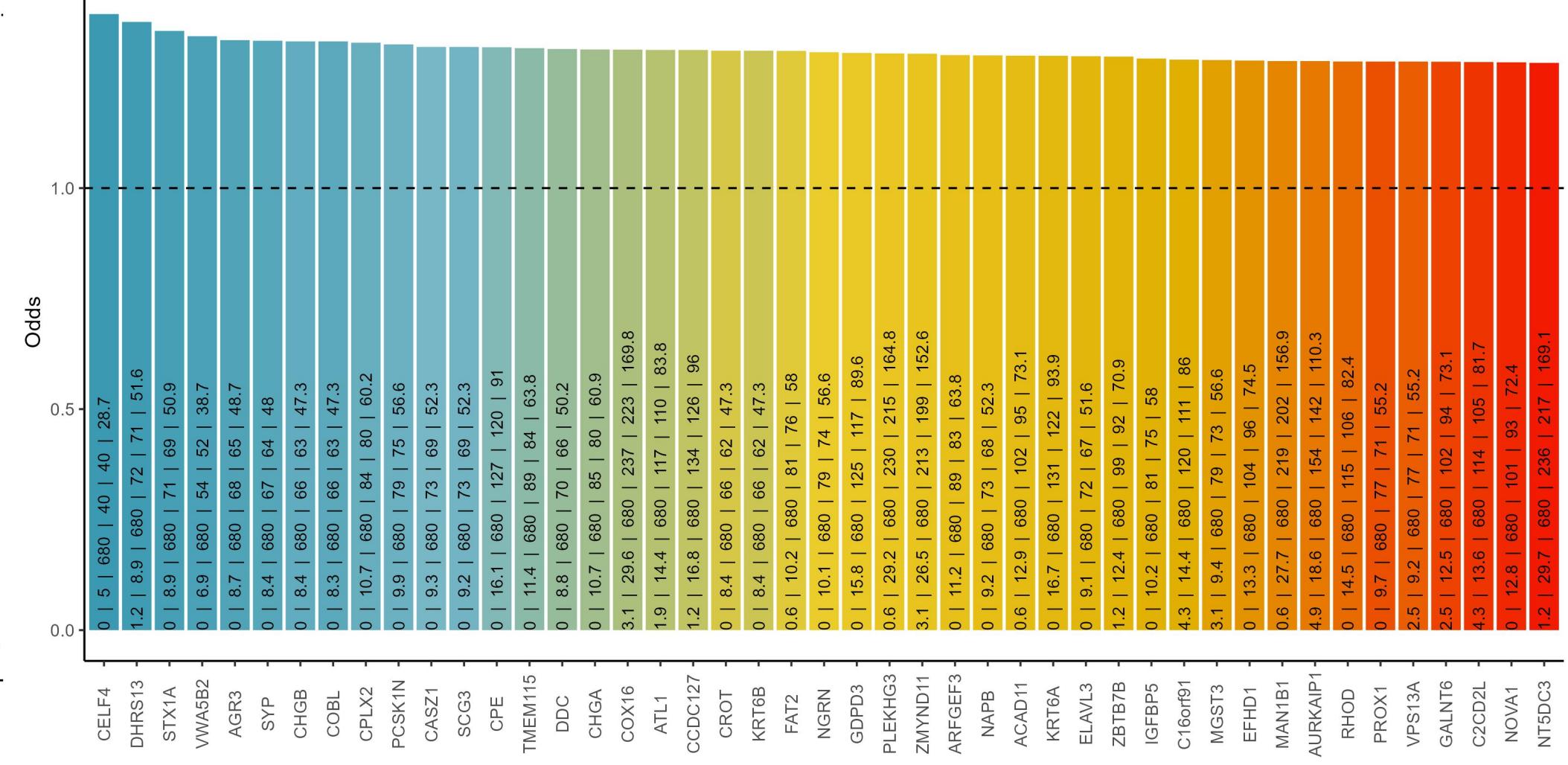
% of EXD2 in blood cancers: 22.8 ; % of EXD2 in solid cancers: 81.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EXD2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

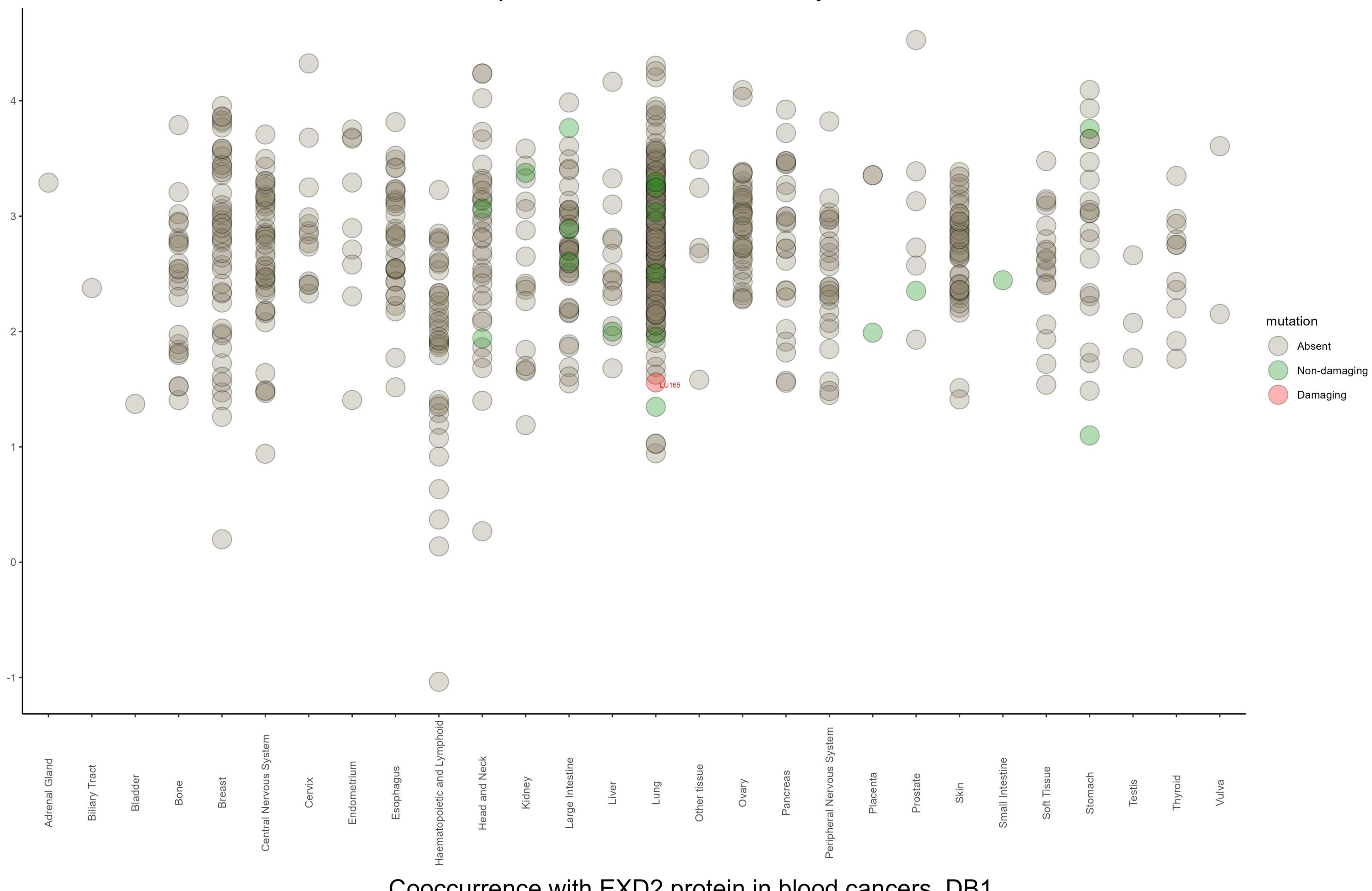
Negative cooccurrence



Positive cooccurrence

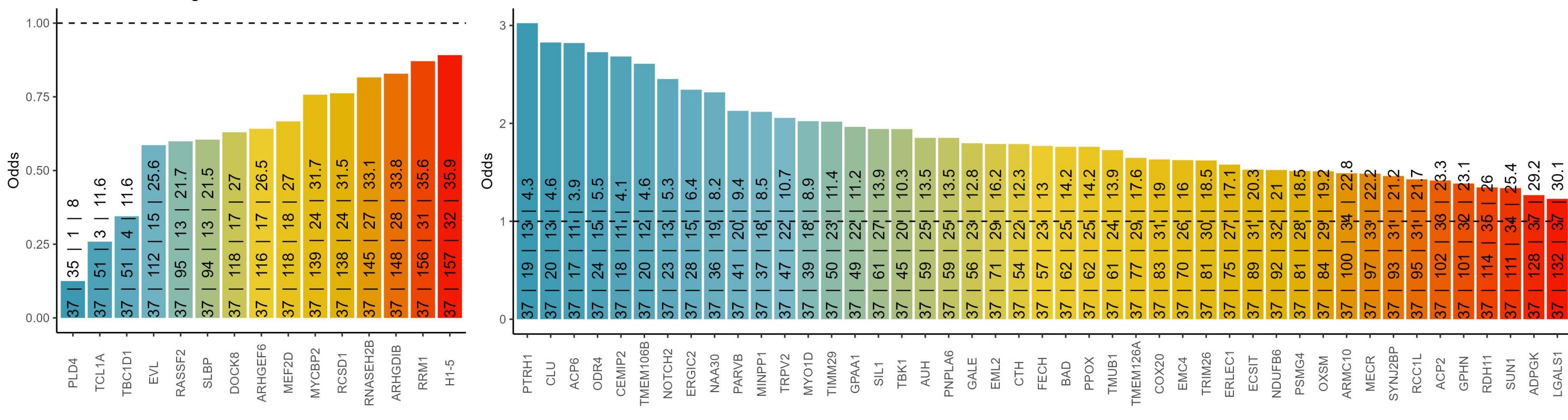


Amount of EXD2 protein and mutation status by tissue, DB1



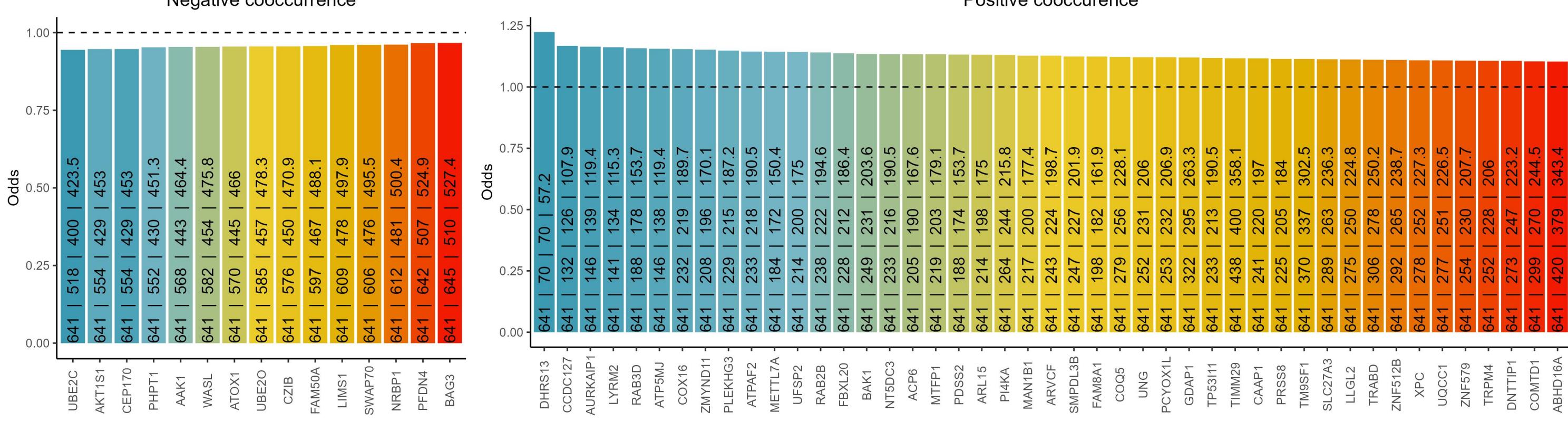
Cooccurrence with EXD2 protein in blood cancers, DB1

The text in the bars: incidence of EXD2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

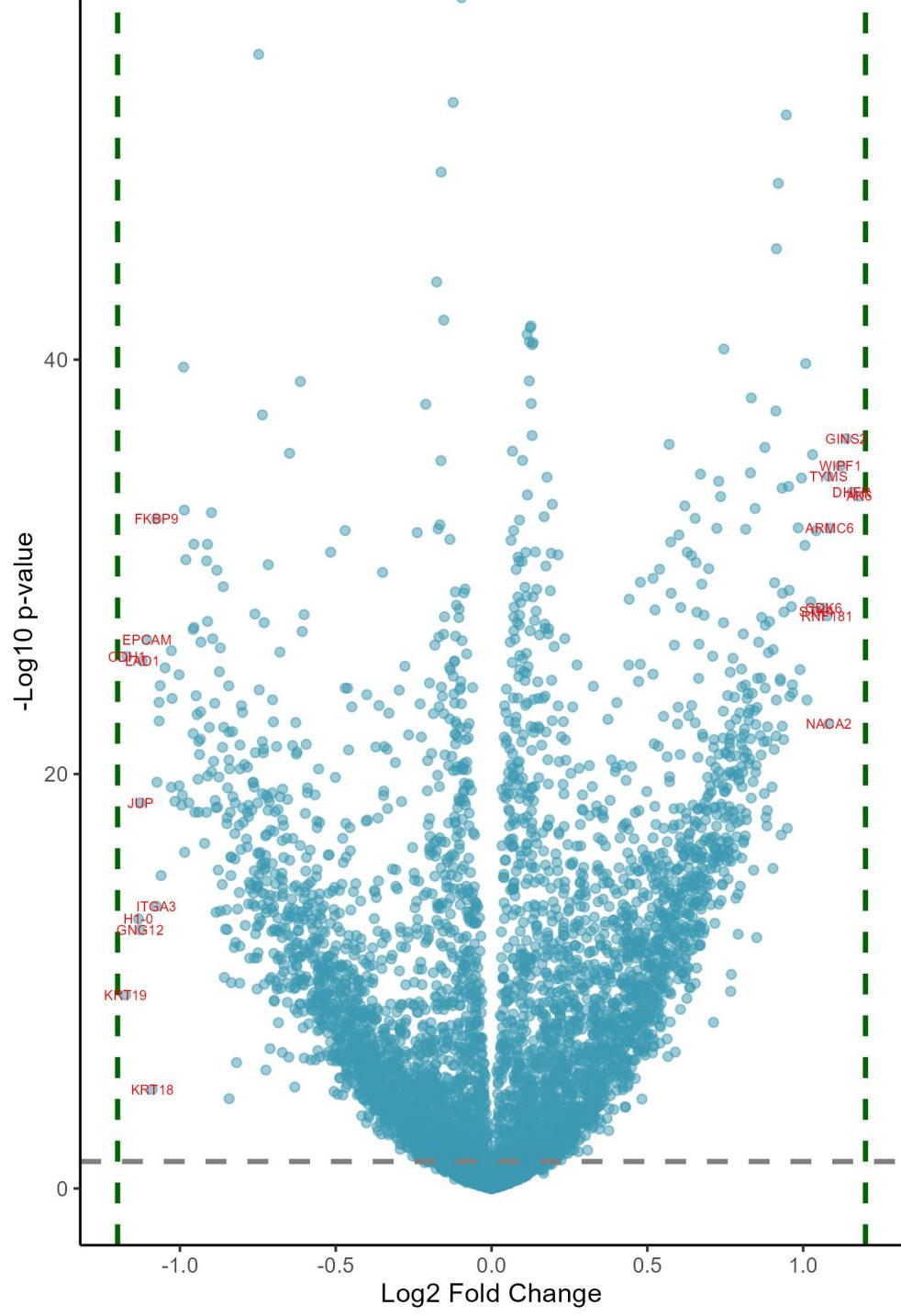


Cooccurrence with EXD2 protein in solid cancers, DB1

The text in the bars: incidence of EXD2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

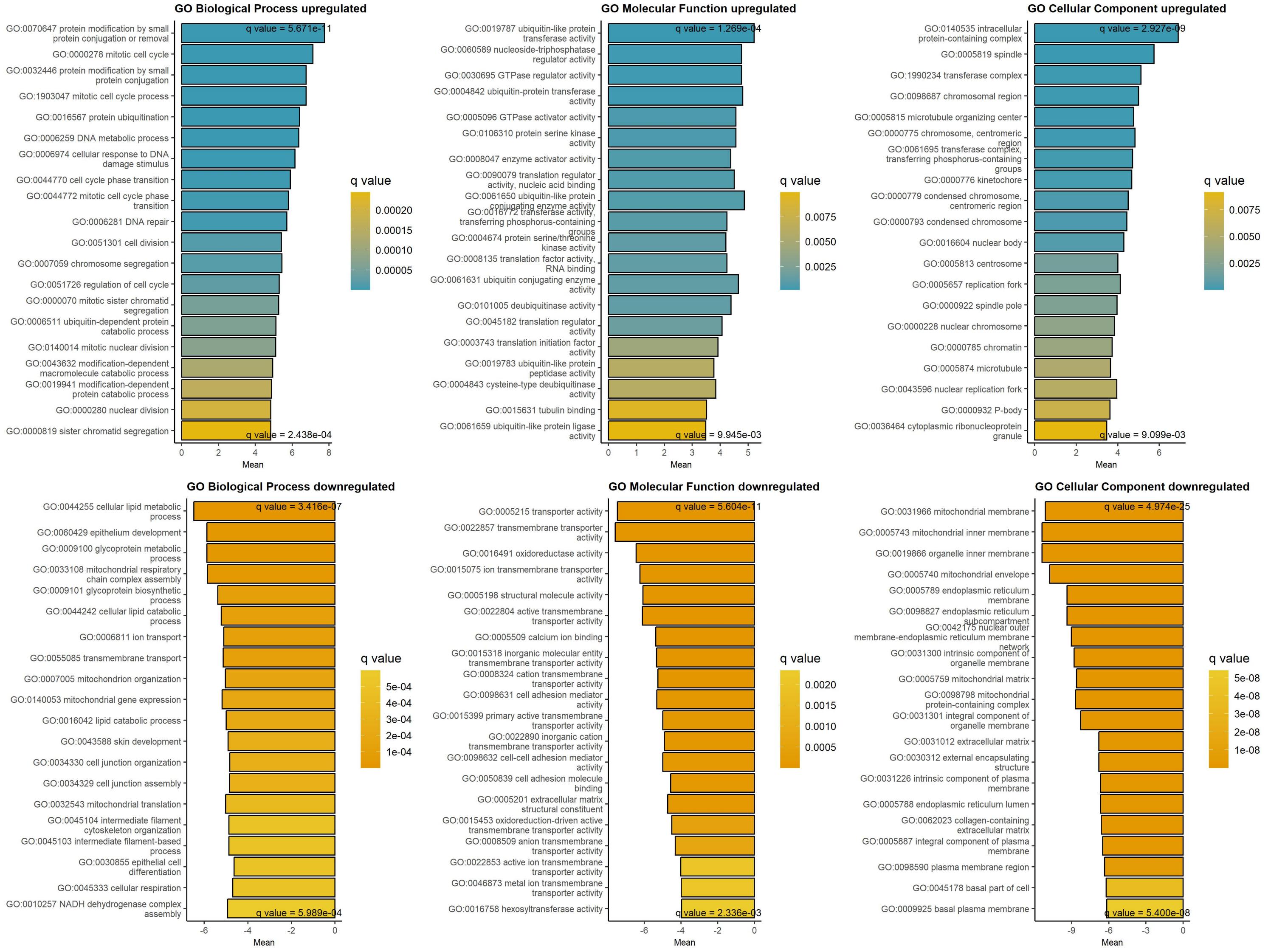


Downregulated at low/absent EXD2 Upregulated at low/absent EXD2



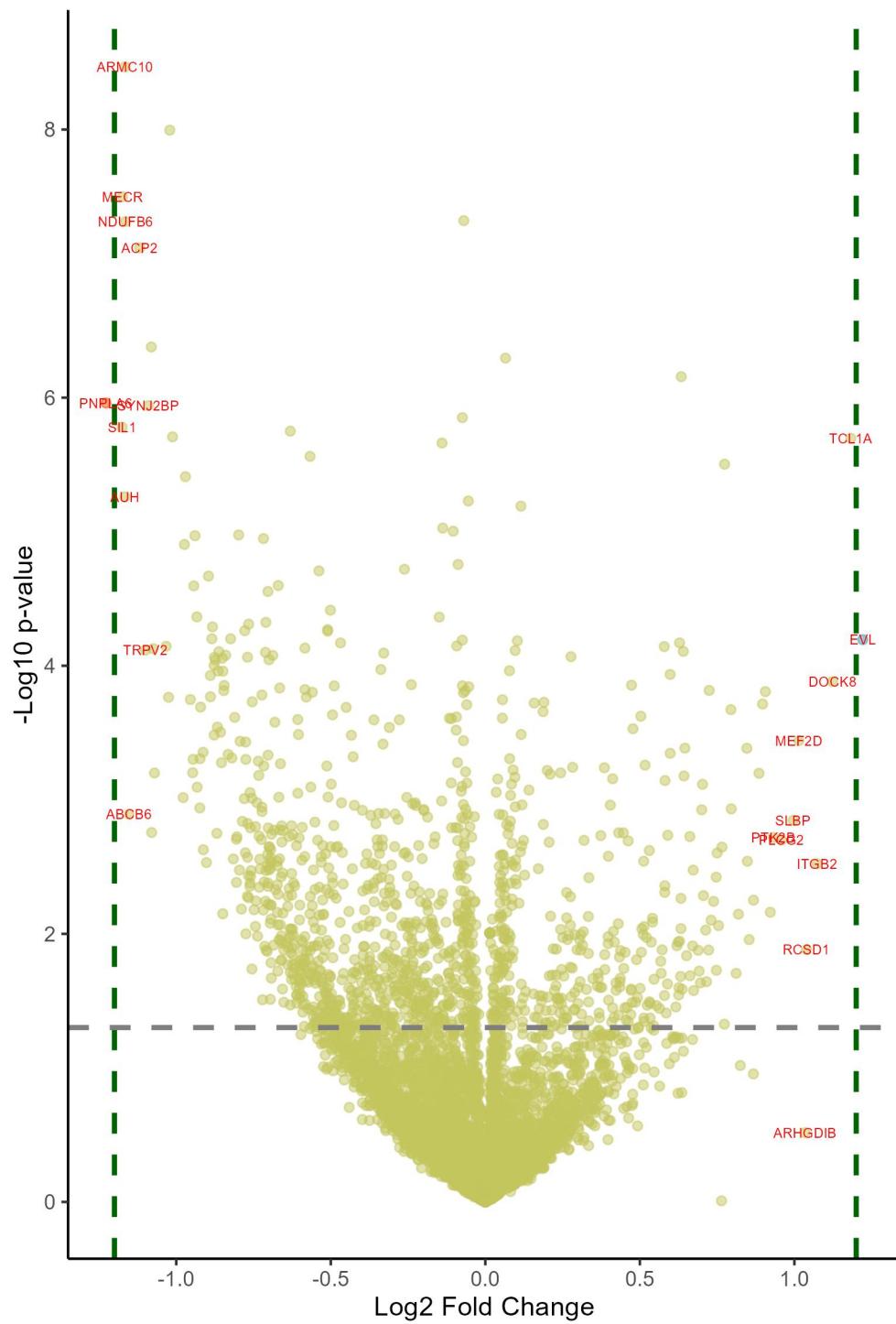
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.17	1.60e-09	KRT19	keratin 19	1.18	5.42e-32	AK6	adenylate kinase 6
-1.17	7.96e-25	CDH1	cadherin 1	1.16	3.71e-32	DHFR	dihydrofolate reductase
-1.13	5.34e-13	H1-0	H1.0 linker histone	1.14	1.54e-34	GINS2	GINS complex subunit 2
-1.13	1.72e-12	GNG12	G protein subunit gamma 12	1.12	2.47e-33	WIPF1	WAS/WASL interacting protein family
-1.13	3.00e-18	JUP	junction plakoglobin	1.08	1.51e-30	ARMC6	armadillo repeat containing 6
-1.12	1.27e-24	LAD1	ladinin 1	1.08	8.28e-22	NACA2	nascent polypeptide associated comp
-1.11	1.36e-25	EPCAM	epithelial cell adhesion molecule	1.08	7.26e-33	TYMS	thymidylate synthetase
-1.09	3.50e-05	KRT18	keratin 18	1.08	1.20e-26	RNF181	ring finger protein 181
-1.08	1.44e-13	ITGA3	integrin subunit alpha 3	1.07	5.56e-27	CDK6	cyclin dependent kinase 6
-1.08	5.56e-31	FKBP9	FKBP prolyl isomerase 9	1.04	7.61e-27	STK4	serine/threonine kinase 4
-1.07	3.54e-19	ITGA2	integrin subunit alpha 2	1.04	1.83e-30	HCLS1	hematopoietic cell-specific Lyn sub
-1.07	9.18e-23	SPINT1	serine peptidase inhibitor, Kunitz	1.03	7.74e-34	GMFG	glia maturation factor gamma
-1.07	6.32e-22	MISP	mitotic spindle positioning	1.02	2.86e-27	CORO7	coronin 7
-1.06	1.67e-23	CD276	CD276 molecule	1.01	7.11e-23	SEPTIN6	septin 6
-1.06	5.87e-15	KRT7	keratin 7	1.01	5.77e-38	ARHGAP45	Rho GTPase activating protein 45
-1.05	2.59e-24	CTNNB1	catenin beta 1	1.01	8.26e-30	TXNDC9	thioredoxin domain containing 9
-1.03	5.89e-19	PKP3	plakophilin 3	0.99	8.40e-33	GINS4	GINS complex subunit 4
-1.03	4.32e-25	GNA11	G protein subunit alpha 11	0.99	3.14e-24	PPP6R1	protein phosphatase 6 regulatory su
-1.03	6.11e-23	EPHX1	epoxide hydrolase 1	0.98	1.49e-30	TACC3	transforming acidic coiled-coil con
-1.02	2.58e-18	DSG2	desmoglein 2	0.97	3.50e-23	PCLAF	PCNA clamp associated factor
-1	5.32e-24	MYO1D	myosin ID	0.97	1.52e-23	COPS7B	COP9 signalosome subunit 7B
-1	5.16e-19	SPINT2	serine peptidase inhibitor, Kunitz	0.96	4.82e-27	RNASEH2B	ribonuclease H2 subunit B
-0.99	3.85e-18	PPIC	peptidylprolyl isomerase C	0.96	5.03e-23	UBE2L6	ubiquitin conjugating enzyme E2 L6
-0.99	1.37e-18	S100A14	S100 calcium binding protein A14	0.96	8.72e-28	FERMT3	FERM domain containing kindlin 3
-0.99	8.01e-38	FAM177A1	family with sequence similarity 177	0.95	2.04e-32	DOHH	deoxyhypusine hydroxylase
-0.99	2.34e-31	TM9SF1	transmembrane 9 superfamily member	0.95	4.19e-17	CORO1A	coronin 1A
-0.98	5.20e-16	CKMT1A	creatine kinase, mitochondrial 1A	0.95	2.06e-49	RCSD1	RCSD domain containing 1
-0.98	3.62e-29	CASK	calcium/calmodulin dependent serine	0.94	8.13e-27	FNBPI	formin binding protein 1
-0.97	3.00e-18	PPL	periplakin	0.94	4.23e-21	PSME3IP1	proteasome activator subunit 3 inte

GAGE analysis on upregulated and downregulated proteins at low/absent EXD2 protein, DB1



Differentially expressed proteins in blood cancers at absence/low amount of EXD2 , DB1

p-value < 0.05 & logFC > 1.2

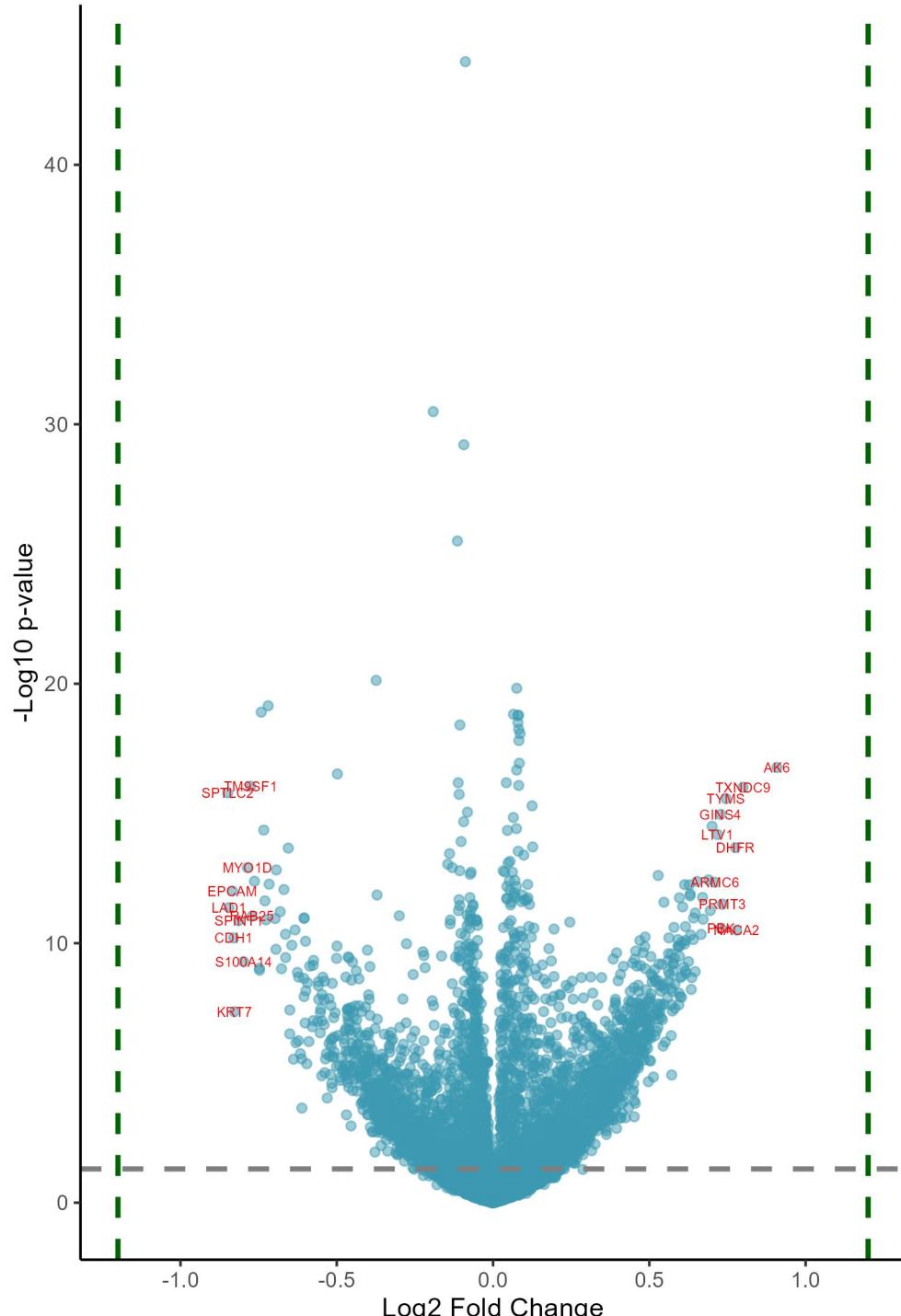


Downregulated in blood cancers at low/absent EXD2 Upregulated in blood cancers at low/absent EXD2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.23	6.36e-04	PNPLA6	patatin like phospholipase domain c	1.22	8.34e-03	EVL	Enah/Vasp-like
-1.18	7.86e-04	SIL1	SIL1 nucleotide exchange factor	1.18	7.86e-04	TCL1A	TCL1 family AKT coactivator A
-1.17	5.27e-05	MECR	mitochondrial trans-2-enoyl-CoA red	1.12	1.09e-02	DOCK8	dedicator of cytokinesis 8
-1.17	1.66e-03	AUH	AU RNA binding methylglutaconyl-CoA	1.07	5.97e-02	ITGB2	integrin subunit beta 2
-1.17	1.13e-05	ARMC10	armadillo repeat containing 10	1.04	7.37e-02	RCSD1	RCSD domain containing 1
-1.16	5.39e-05	NDUFB6	NADH:ubiquinone oxidoreductase subu	1.03	5.34e-01	ARHGDI	Rho GDP dissociation inhibitor beta
-1.15	3.97e-02	ABC6	ATP binding cassette subfamily B me	1.01	1.84e-02	MEF2D	myocyte enhancer factor 2D
-1.12	7.24e-05	ACP2	acid phosphatase 2, lysosomal	1	4.25e-02	SLBP	stem-loop binding protein
-1.1	8.34e-03	TRPV2	transient receptor potential cation	0.96	4.93e-02	PLCG2	phospholipase C gamma 2
-1.09	6.36e-04	SYNJ2BP	synaptjanin 2 binding protein	0.93	4.85e-02	PTK2B	protein tyrosine kinase 2 beta
-1.08	3.48e-04	TRIM26	tripartite motif containing 26	0.92	5.97e-02	SASH3	SAM and SH3 domain containing 3
-1.08	4.73e-02	SFN	stratifin	0.91	1.13e-02	PAX5	paired box 5
-1.07	8.34e-03	GPA1	glycosylphosphatidylinositol anchor	0.9	1.23e-02	IGHM	immunoglobulin heavy constant mu
-1.07	2.60e-02	LGALS3	galectin 3	0.89	2.60e-02	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan
-1.03	8.34e-03	TMUB1	transmembrane and ubiquitin like do	0.87	5.97e-02	LAT2	linker for activation of T cells fa
-1.02	1.17e-02	OPTN	optineurin	0.87	3.06e-01	SPN	sialophorin
-1.02	2.24e-05	RDH11	retinol dehydrogenase 11	0.85	6.49e-02	ITGAL	integrin subunit alpha L
-1.01	7.86e-04	COX20	cytochrome c oxidase assembly facto	0.85	5.86e-02	PIK3AP1	phosphoinositide-3-kinase adaptor p
-0.98	3.42e-02	MINPP1	multiple inositol-polyphosphate pho	0.85	2.02e-02	MME	membrane metalloendopeptidase
-0.97	2.76e-03	TMEM126A	transmembrane protein 126A	0.82	2.80e-01	COTL1	coactosin like F-actin binding prot
-0.97	1.23e-03	LGALS1	galectin 1	0.82	5.97e-02	FAM107B	family with sequence similarity 107
-0.95	1.19e-02	GALE	UDP-galactose-4-epimerase	0.81	9.93e-02	TUBB6	tubulin beta 6 class V
-0.95	2.60e-02	MBOAT7	membrane bound O-acyltransferase do	0.8	3.83e-02	RASSF2	Ras association domain family membe
-0.95	2.27e-02	PARVB	parvin beta	0.79	1.31e-02	MYCBP2	MYC binding protein 2
-0.94	4.68e-03	PSMG4	proteasome assembly chaperone 4	0.77	1.04e-03	PLD4	phospholipase D family member 4
-0.94	2.54e-03	OXSM	3-oxoacyl-ACP synthase, mitochondri	0.77	1.79e-01	PTPN6	protein tyrosine phosphatase non-re
-0.93	7.21e-03	SCAMP2	secretory carrier membrane protein	0.77	5.15e-02	RNASEH2B	ribonuclease H2 subunit B
-0.93	3.02e-02	CTTN	cortactin	0.76	9.91e-01	H1-5	H1.5 linker histone, cluster member
-0.92	3.79e-02	FTL	ferritin light chain	0.75	5.97e-02	TRIM22	tripartite motif containing 22

Differentially expressed proteins in solid cancers at absence/low amount of EXD2 , DB1

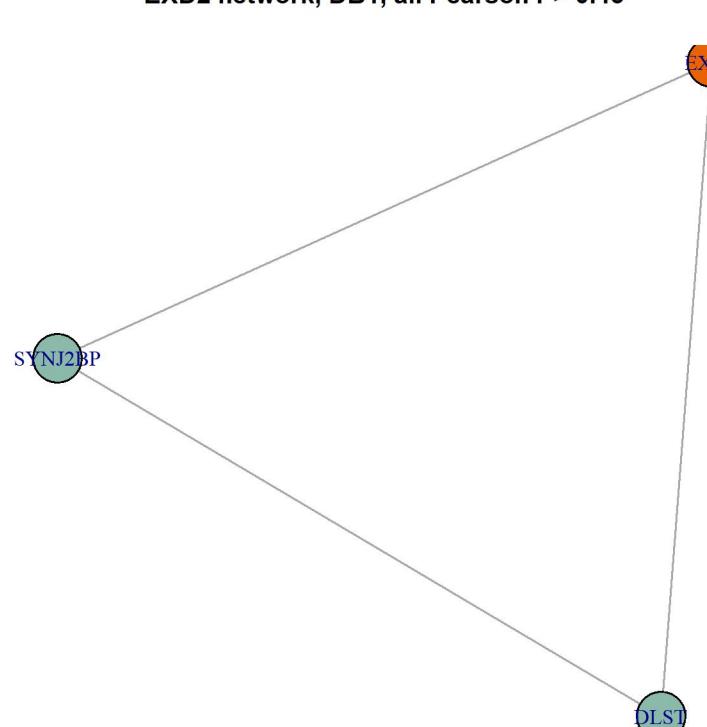
p-value < 0.05 & logFC > 1.2



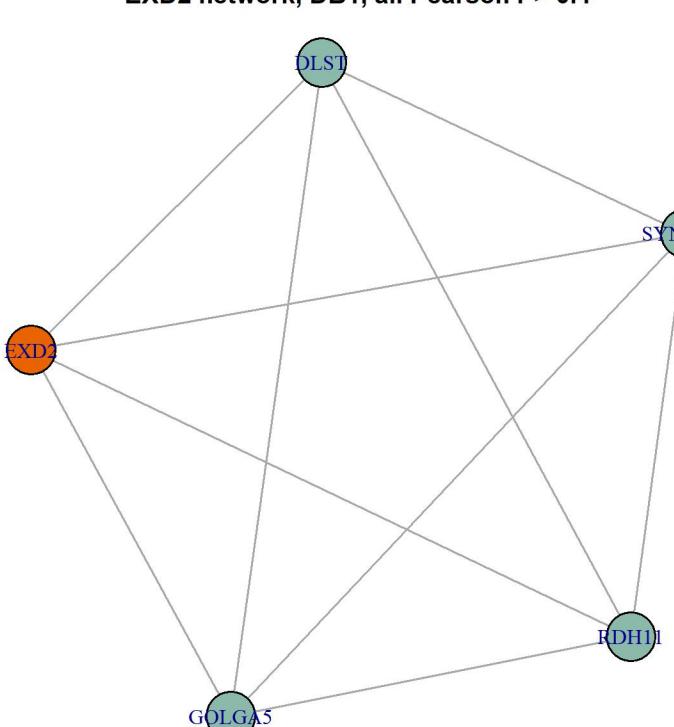
Downregulated in solid cancers at low/absent EXD2 Upregulated in solid cancers at low/absent EXD2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.85	3.92e-14	SPTLC2	serine palmitoyltransferase long ch	0.91	5.90e-15	AK6	adenylate kinase 6
-0.85	2.79e-10	LAD1	ladinin 1	0.8	2.51e-14	TXND9	thioredoxin domain containing 9
-0.83	8.72e-11	EPCAM	epithelial cell adhesion molecule	0.78	1.49e-09	NACA2	nascent polypeptide associated comp
-0.83	2.69e-09	CDH1	cadherin 1	0.78	3.29e-12	DHFR	dihydrofolate reductase
-0.83	6.30e-07	KRT7	keratin 7	0.75	6.11e-14	TYMS	thymidylate synthetase
-0.81	7.29e-10	SPINT1	serine peptidase inhibitor, Kunitz	0.73	2.19e-10	PRMT3	protein arginine methyltransferase
-0.8	1.51e-08	S100A14	S100 calcium binding protein A14	0.73	1.28e-09	PKB	PDZ binding kinase
-0.79	1.60e-11	MYO1D	myosin ID	0.73	2.26e-13	GINS4	GINS complex subunit 4
-0.78	2.37e-14	TM9SF1	transmembrane 9 superfamily member	0.72	1.10e-12	LTV1	LTV1 ribosome biogenesis factor
-0.77	5.45e-10	RAB25	RAB25, member RAS oncogene family	0.71	4.58e-11	ARMC6	armadillo repeat containing 6
-0.76	4.31e-11	FUT8	fucosyltransferase 8	0.7	5.91e-13	DOHH	deoxyhypusine hydroxylase
-0.75	2.43e-08	SPINT2	serine peptidase inhibitor, Kunitz	0.69	3.51e-10	CDK6	cyclin dependent kinase 6
-0.75	2.84e-08	MISP	mitotic spindle positioning	0.69	4.03e-11	UBE2S	ubiquitin conjugating enzyme E2 S
-0.74	9.16e-17	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.67	6.76e-10	PPM1F	protein phosphatase, Mg2+/Mn2+ depe
-0.73	7.82e-13	TIMM29	translocase of inner mitochondrial	0.67	1.39e-10	UBE2C	ubiquitin conjugating enzyme E2 C
-0.73	1.71e-10	ST14	ST14 transmembrane serine protease	0.67	2.09e-09	UBE2T	ubiquitin conjugating enzyme E2 T
-0.73	7.00e-10	ESRP1	epithelial splicing regulatory prot	0.65	4.32e-11	SPC24	SPC24 component of NDC80 kinetochor
-0.72	5.88e-17	SDR39U1	short chain dehydrogenase/reductase	0.65	4.27e-10	PDCL	phosducin like
-0.72	5.34e-11	SMPDL3B	sphingomyelin phosphodiesterase aci	0.65	3.15e-08	FKBP1A	FKBP prolyl isomerase 1A
-0.7	6.49e-10	ABHD16A	abhydrolase domain containing 16A,	0.64	6.29e-10	UBE2R2	ubiquitin conjugating enzyme E2 R2
-0.69	6.25e-09	PRSS8	serine protease 8	0.64	3.04e-09	RWDD1	RWD domain containing 1
-0.69	1.92e-11	PLEKHG3	pleckstrin homology and RhoGEF doma	0.64	4.86e-08	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran
-0.68	3.81e-10	LLGL2	LLGL scribble cell polarity complex	0.63	1.19e-07	UBE2V2	ubiquitin conjugating enzyme E2 V2
-0.68	2.54e-08	CGN	cingulin	0.63	2.18e-09	GTPBP1	GTP binding protein 1
-0.67	7.88e-11	PIP4P1	phosphatidylinositol-4,5-bisphospa	0.63	1.10e-10	KIF11	kinesin family member 11
-0.66	2.08e-09	PATJ	PATJ crumbs cell polarity complex c	0.63	1.25e-10	BCAR1	BCAR1 scaffold protein, Cas family
-0.66	1.14e-08	PEX11B	peroxisomal biogenesis factor 11 be	0.63	5.44e-11	RRM2	ribonucleotide reductase regulatory
-0.66	3.34e-12	NUBPL	NUBP iron-sulfur cluster assembly f	0.63	1.51e-08	PDCL3	phosducin like 3
-0.65	3.36e-06	TACSTD2	tumor associated calcium signal tra	0.62	3.65e-08	PPP2CA	protein phosphatase 2 catalytic sub

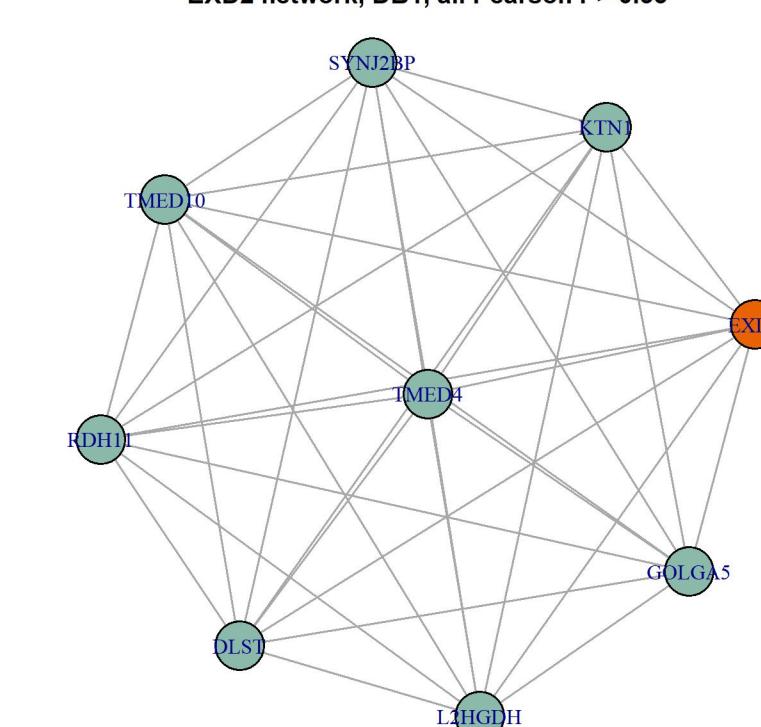
EXD2 network, DB1, all Pearson r > 0.45

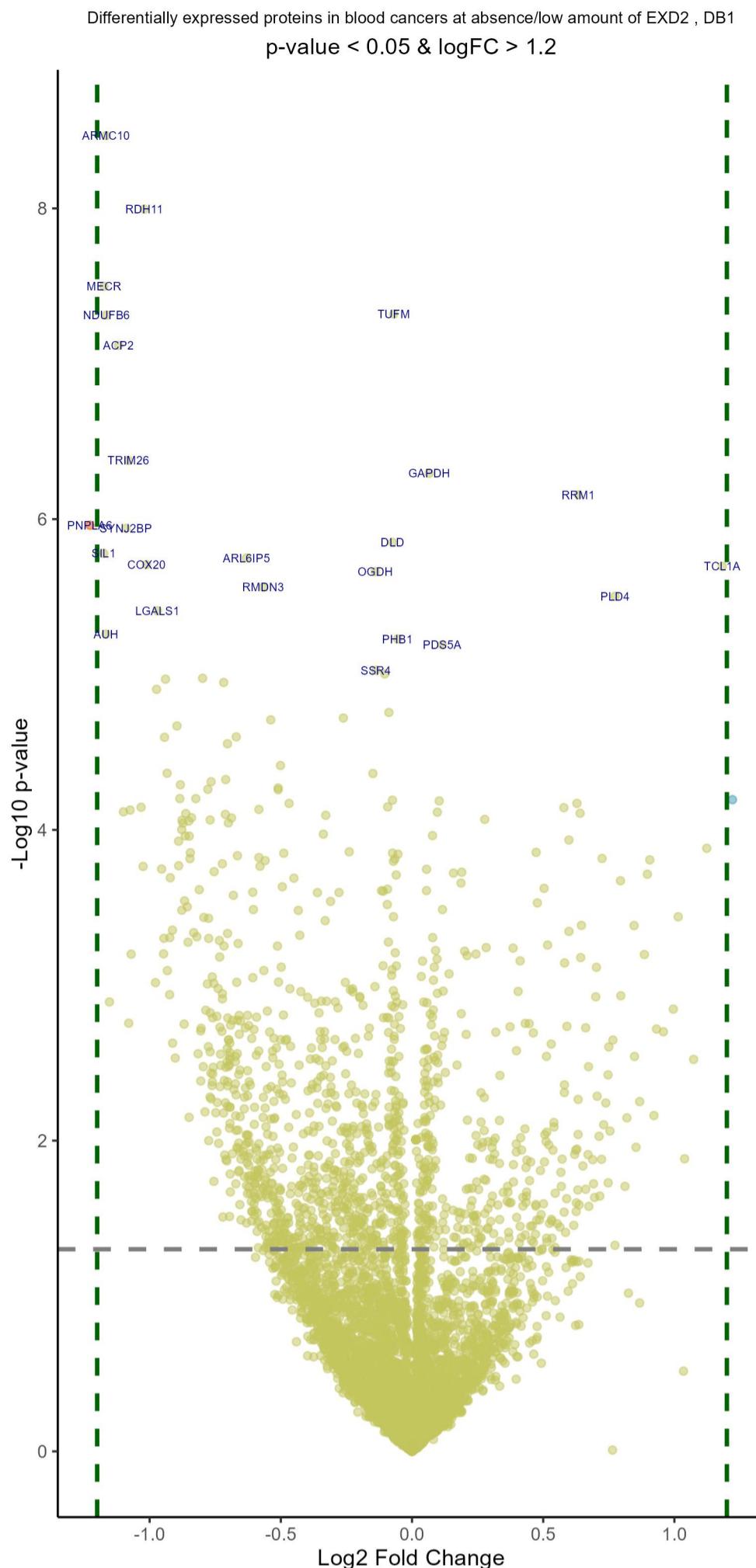


EXD2 network, DB1, all Pearson r > 0.4

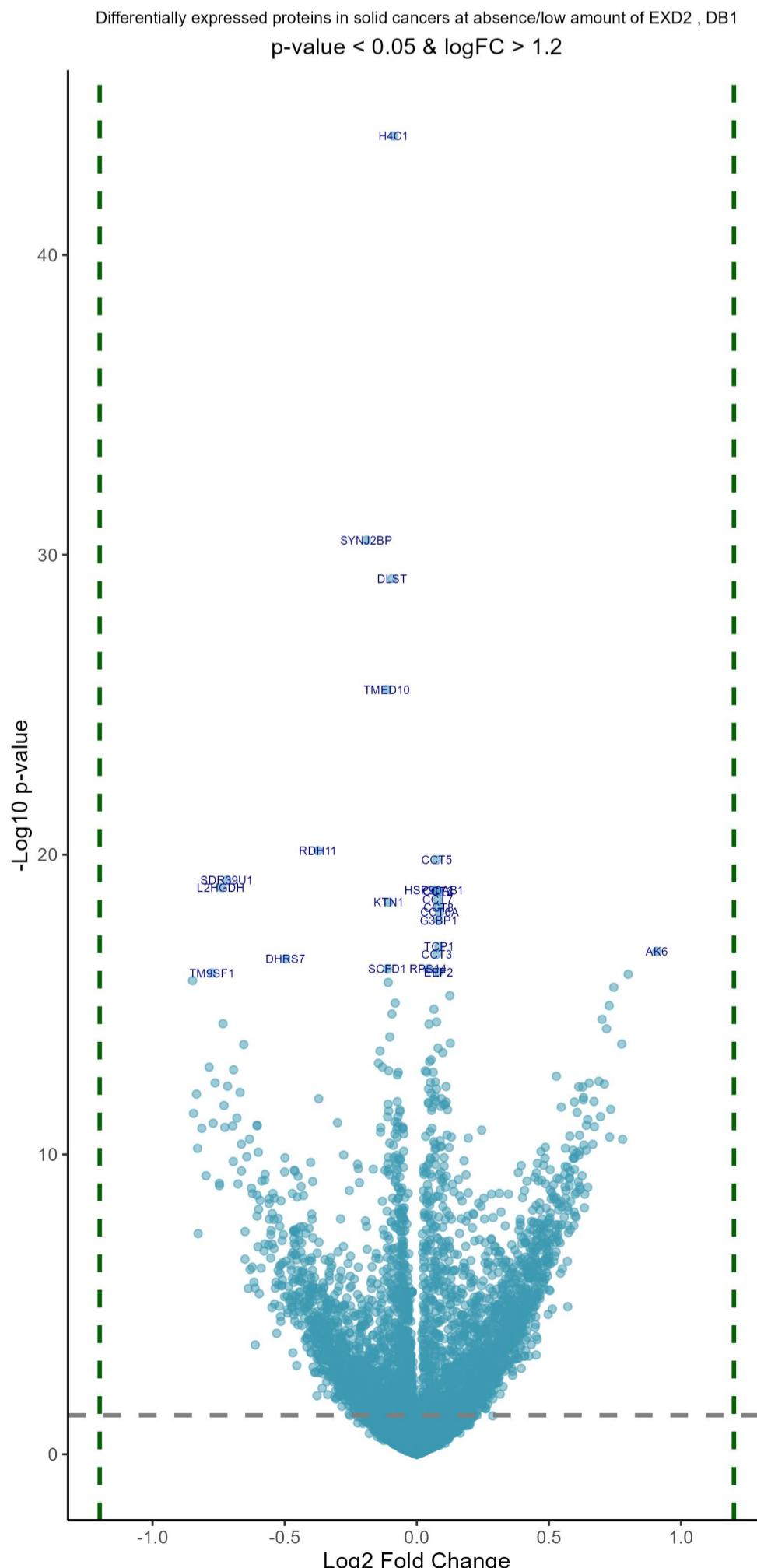


EXD2 network, DB1, all Pearson r > 0.35



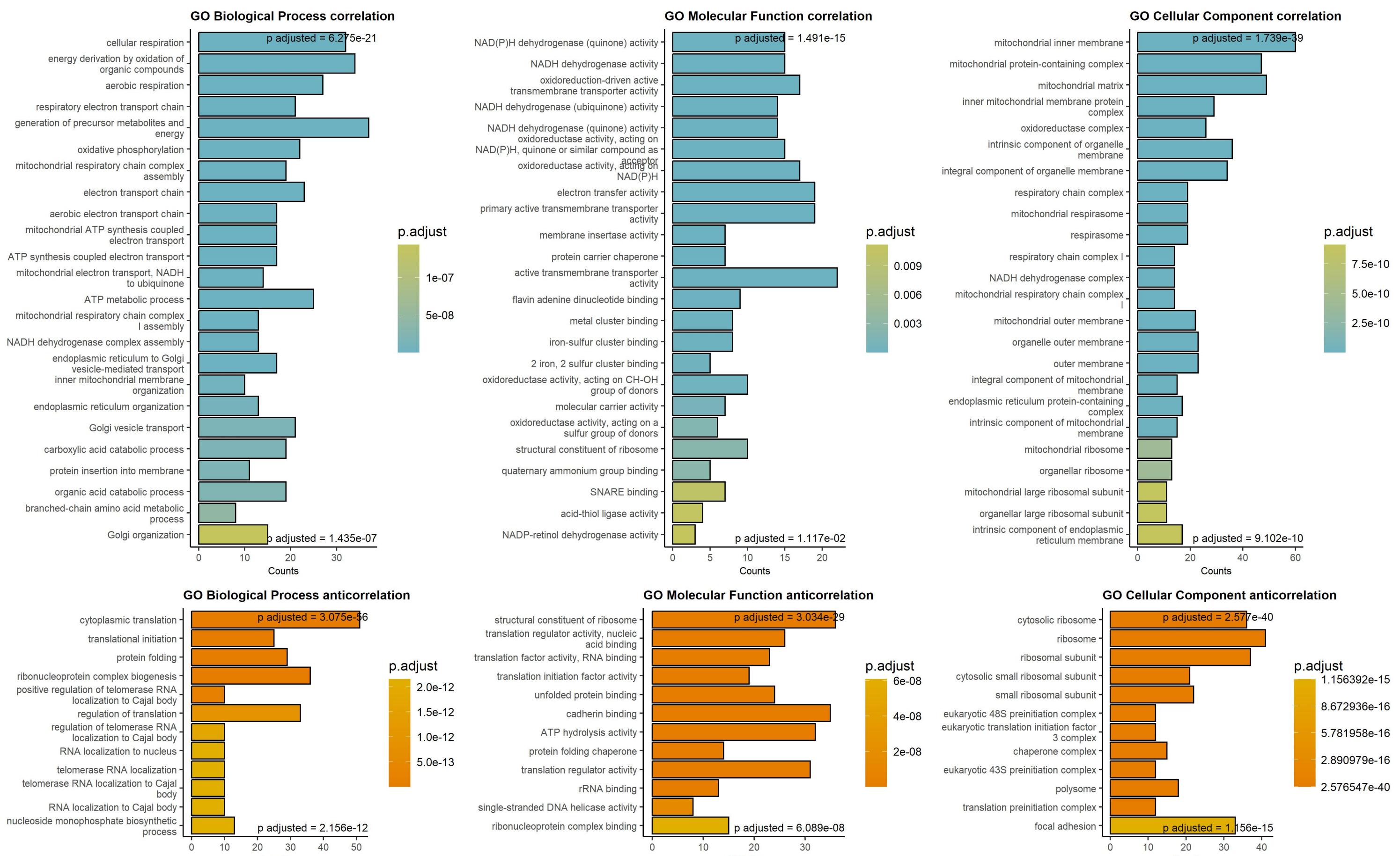


Sorted by p values!							
Downregulated in blood cancers at low/absent EXD2				Upregulated in blood cancers at low/absent EXD2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.17	1.13e-05	ARMC10	armadillo repeat containing 10	0.07	3.75e-04	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-1.02	2.24e-05	RDH11	retinol dehydrogenase 11	0.63	4.64e-04	RRM1	ribonucleotide reductase catalytic subunit RRM1
-1.17	5.27e-05	MECR	mitochondrial trans-2-enoyl-CoA reductase	1.18	7.86e-04	TCL1A	TCL1 family AKT coactivator A
-0.07	5.39e-05	TUFM	Tu translation elongation factor, m	0.77	1.04e-03	PLD4	phospholipase D family member 4
-1.16	5.39e-05	NDUFB6	NADH:ubiquinone oxidoreductase subunit 6	0.12	1.78e-03	PDS5A	PDS5 cohesin associated factor A
-1.12	7.24e-05	ACP2	acid phosphatase 2, lysosomal	1.22	8.34e-03	EVL	Enah/Vasp-like
-1.08	3.48e-04	TRIM26	tripartite motif containing 26	0.1	8.34e-03	LASP1	LIM and SH3 protein 1
-1.23	6.36e-04	PNPLA6	patatin like phospholipase domain containing 6	0.63	8.34e-03	MNDA	myeloid cell nuclear differentiation antigen
-1.09	6.36e-04	SYNJ2BP	synaptjanin 2 binding protein	0.58	8.34e-03	TBC1D1	TBC1 domain family member 1
-0.07	7.22e-04	DLD	dihydrolipoamide dehydrogenase	0.1	8.34e-03	PCNP	PEST proteolytic signal containing protein
-1.18	7.86e-04	SIL1	SIL1 nucleotide exchange factor	0.64	8.34e-03	CPNE2	copine 2
-0.63	7.86e-04	ARL6IP5	ADP ribosylation factor like GTPase	0.28	8.34e-03	DCK	deoxycytidine kinase
-1.01	7.86e-04	COX20	cytochrome c oxidase assembly factor 20	0.08	9.47e-03	PFDN1	prefoldin subunit 1
-0.14	8.05e-04	OGDH	oxoglutarate dehydrogenase	0.6	9.90e-03	PRTN3	proteinase 3
-0.57	9.60e-04	RMDN3	regulator of microtubule dynamics 3	1.12	1.09e-02	DOCK8	dedicator of cytokinesis 8
-0.97	1.23e-03	LGALS1	galectin 1	0.47	1.11e-02	SERPINB8	serpin family B member 8
-1.17	1.66e-03	AUH	AU RNA binding methylglutaconyl-CoA	0.72	1.12e-02	CYBB	cytochrome b-245 beta chain
-0.06	1.71e-03	PHB1	prohibitin 1	0.91	1.13e-02	PAX5	paired box 5
-0.14	2.50e-03	SSR4	signal sequence receptor subunit 4	0.06	1.19e-02	SERBP1	SERPINE1 mRNA binding protein 1
-0.1	2.54e-03	STOML2	stomatin like 2	0.19	1.22e-02	IWS1	interacts with SUPT6H, CTD assembly factor IWS1
-0.8	2.54e-03	SUN1	Sad1 and UNC84 domain containing 1	0.16	1.22e-02	PAC SIN2	protein kinase C and casein kinase
-0.94	2.54e-03	OXSM	3-oxoacyl-ACP synthase, mitochondrial	0.9	1.23e-02	IGHM	immunoglobulin heavy constant mu
-0.72	2.58e-03	ADPGK	ADP dependent glucokinase	0.79	1.31e-02	MYCBP2	MYC binding protein 2
-0.97	2.76e-03	TMEM126A	transmembrane protein 126A	0.19	1.34e-02	DBI	diazepam binding inhibitor, acyl-CoA binding protein DBI
-0.09	3.77e-03	NDUFS3	NADH:ubiquinone oxidoreductase core	0.5	1.42e-02	AZU1	azurocidin 1
-0.26	3.95e-03	ZFYVE1	zinc finger FYVE-type containing 1	0.06	1.42e-02	ZNF207	zinc finger protein 207
-0.54	3.95e-03	HEXA	hexosaminidase subunit alpha	0.48	1.60e-02	CES1	carboxylesterase 1
-0.9	4.19e-03	ZMPSTE24	zinc metallopeptidase STE24	0.12	1.70e-02	HMGB1	high mobility group box 1
-0.67	4.68e-03	NDUFB3	NADH:ubiquinone oxidoreductase subunit 3	1.01	1.84e-02	MEF2D	myocyte enhancer factor 2D
-0.94	4.68e-03	PSMG4	proteasome assembly chaperone 4	0.65	2.02e-02	ELF1	E74 like ETS transcription factor 1
-0.7	5.02e-03	SCYL1	SCY1 like pseudokinase 1	0.85	2.02e-02	MME	membrane metalloendopeptidase
-0.5	6.74e-03	RPLP1	ribosomal protein lateral stalk subunit 5	0.6	2.17e-02	CEP97	centrosomal protein 97
-0.93	7.21e-03	SCAMP2	secretory carrier membrane protein	0.08	2.27e-02	DNAJC8	DnaJ heat shock protein family (Hsp 70) member 8
-0.15	7.21e-03	CISD2	CDGSH iron sulfur domain 2	0.52	2.43e-02	ZMYM2	zinc finger MYM-type containing 2
-0.71	7.70e-03	TOR1AIP2	torsin 1A interacting protein 2	0.28	2.47e-02	OGFR	opioid growth factor receptor
-0.77	7.75e-03	GHDC	GH3 domain containing	0.39	2.47e-02	CEBPA	CCAAT enhancer binding protein alpha
-0.88	7.93e-03	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.09	2.55e-02	PTMA	prothymosin alpha
-0.51	7.98e-03	MTIF2	mitochondrial translational initiation factor 2	0.2	2.56e-02	NCAPD2	non-SMC condensin I complex subunit D
-0.78	7.98e-03	DCAF6	DDI1 and CUL4 associated factor 6	0.24	2.60e-02	CYBIR	CYBIR related Pco1 interactor B

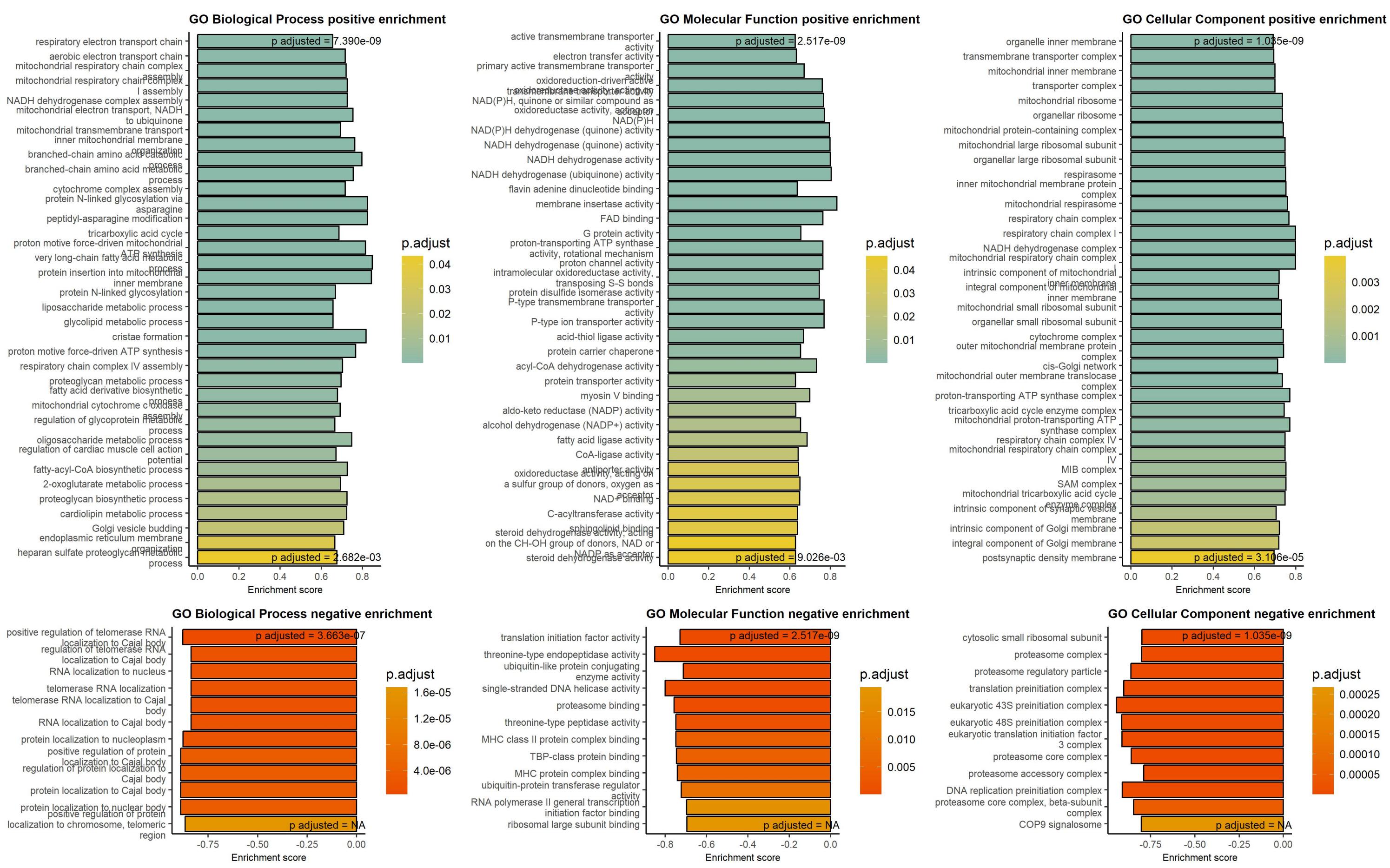


Sorted by p values!							
Downregulated in solid cancers at low/absent EXD2				Upregulated in solid cancers at low/absent EXD2			
C	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
9	3.54e-41	H4C1	H4 clustered histone 1	0.08	1.42e-17	CCT5	chaperonin containing TCP1 subunit
9	7.21e-28	SYNJ2BP	synaptojanin 2 binding protein	0.07	9.16e-17	HSP90AB1	heat shock protein 90 alpha family
9	1.02e-26	DLST	dihydrolipoamide S-succinyltransfer	0.08	9.16e-17	CCT4	chaperonin containing TCP1 subunit
11	4.19e-23	TMED10	transmembrane p24 trafficking prote	0.08	9.16e-17	CCT2	chaperonin containing TCP1 subunit
7	8.20e-18	RDH11	retinol dehydrogenase 11	0.08	1.61e-16	CCT7	chaperonin containing TCP1 subunit
2	5.88e-17	SDR39U1	short chain dehydrogenase/reductase	0.08	2.54e-16	CCT8	chaperonin containing TCP1 subunit
4	9.16e-17	L2HGDH	L-2-hydroxyglutarate dehydrogenase	0.09	3.46e-16	CCT6A	chaperonin containing TCP1 subunit
11	1.84e-16	KTN1	kinectin 1	0.08	6.06e-16	G3BP1	G3BP stress granule assembly factor
5	9.49e-15	DHRS7	dehydrogenase/reductase 7	0.08	4.27e-15	TCP1	t-complex 1
11	1.89e-14	SCFD1	sec1 family domain containing 1	0.91	5.90e-15	AK6	adenylate kinase 6
3	2.37e-14	TM9SF1	transmembrane 9 superfamily member	0.08	7.04e-15	CCT3	chaperonin containing TCP1 subunit
5	3.92e-14	SPTLC2	serine palmitoyltransferase long ch	0.04	1.89e-14	RPS14	ribosomal protein S14
11	4.34e-14	OGDH	oxoglutarate dehydrogenase	0.08	2.31e-14	EEF2	eukaryotic translation elongation f
3	1.91e-13	ATP2A2	ATPase sarcoplasmic/endoplasmic ret	0.8	2.51e-14	TXNDC9	thioredoxin domain containing 9
9	4.04e-13	OPA1	OPA1 mitochondrial dynamin like GTP	0.75	6.11e-14	TYMS	thymidylate synthetase
3	7.82e-13	TIMM29	translocase of inner mitochondrial	0.12	1.12e-13	EIF3I	eukaryotic translation initiation f
	2.00e-12	CISD2	CDGSH iron sulfur domain 2	0.73	2.26e-13	GINS4	GINS complex subunit 4
6	3.34e-12	NUBPL	NUBP iron-sulfur cluster assembly f	0.06	2.88e-13	EEF1B2	eukaryotic translation elongation f
4	5.22e-12	GLRX5	glutaredoxin 5	0.7	5.91e-13	DOHH	deoxyhypusine hydroxylase
5	1.23e-11	TMED4	transmembrane p24 trafficking prote	0.07	7.03e-13	STIP1	stress induced phosphoprotein 1
3	1.60e-11	MTX1	metaxin 1	0.05	7.87e-13	RPS19	ribosomal protein S19
9	1.60e-11	MYO1D	myosin ID	0.72	1.10e-12	LTV1	LTV1 ribosome biogenesis factor
9	1.92e-11	PLEKHG3	pleckstrin homology and RhoGEF doma	0.13	3.16e-12	NUDC	nuclear distribution C, dynein comp
11	2.00e-11	TMX1	thioredoxin related transmembrane p	0.78	3.29e-12	DHFR	dihydrofolate reductase
7	2.15e-11	ATP5PB	ATP synthase peripheral stalk-membr	0.08	4.29e-12	PFN1	profilin 1
7	2.53e-11	TMED9	transmembrane p24 trafficking prote	0.1	5.80e-12	SERBP1	SERPINE1 mRNA binding protein 1
6	4.31e-11	FUT8	fucosyltransferase 8	0.05	9.87e-12	RPSA	ribosomal protein SA
2	5.34e-11	SMPDL3B	sphingomyelin phosphodiesterase aci	0.05	1.11e-11	RPL24	ribosomal protein L24
7	7.88e-11	PIP4P1	phosphatidylinositol-4,5-bisphosphha	0.03	2.00e-11	RPS25	ribosomal protein S25
3	8.72e-11	EPCAM	epithelial cell adhesion molecule	0.04	2.15e-11	RPS3A	ribosomal protein S3A
7	1.18e-10	VTI1B	vesicle transport through interacti	0.06	2.15e-11	RPS28	ribosomal protein S28
7	1.40e-10	SDHB	succinate dehydrogenase complex iro	0.53	2.76e-11	MCMBP	minichromosome maintenance complex
11	1.59e-10	LEMD2	LEM domain nuclear envelope protein	0.69	4.03e-11	UBE2S	ubiquitin conjugating enzyme E2 S
3	1.71e-10	ST14	ST14 transmembrane serine protease	0.07	4.14e-11	YWHAE	tyrosine 3-monooxygenase/tryptophan
6	2.23e-10	ATP5F1C	ATP synthase F1 subunit gamma	0.05	4.25e-11	RPS2	ribosomal protein S2
11	2.38e-10	MLEC	malectin	0.65	4.32e-11	SPC24	SPC24 component of NDC80 kinetochro
6	2.49e-10	PDHA1	pyruvate dehydrogenase E1 subunit a	0.71	4.58e-11	ARMC6	armadillo repeat containing 6
5	2.79e-10	LAD1	Iadinin 1	0.11	5.38e-11	EIF4A1	eukaryotic translation initiation f

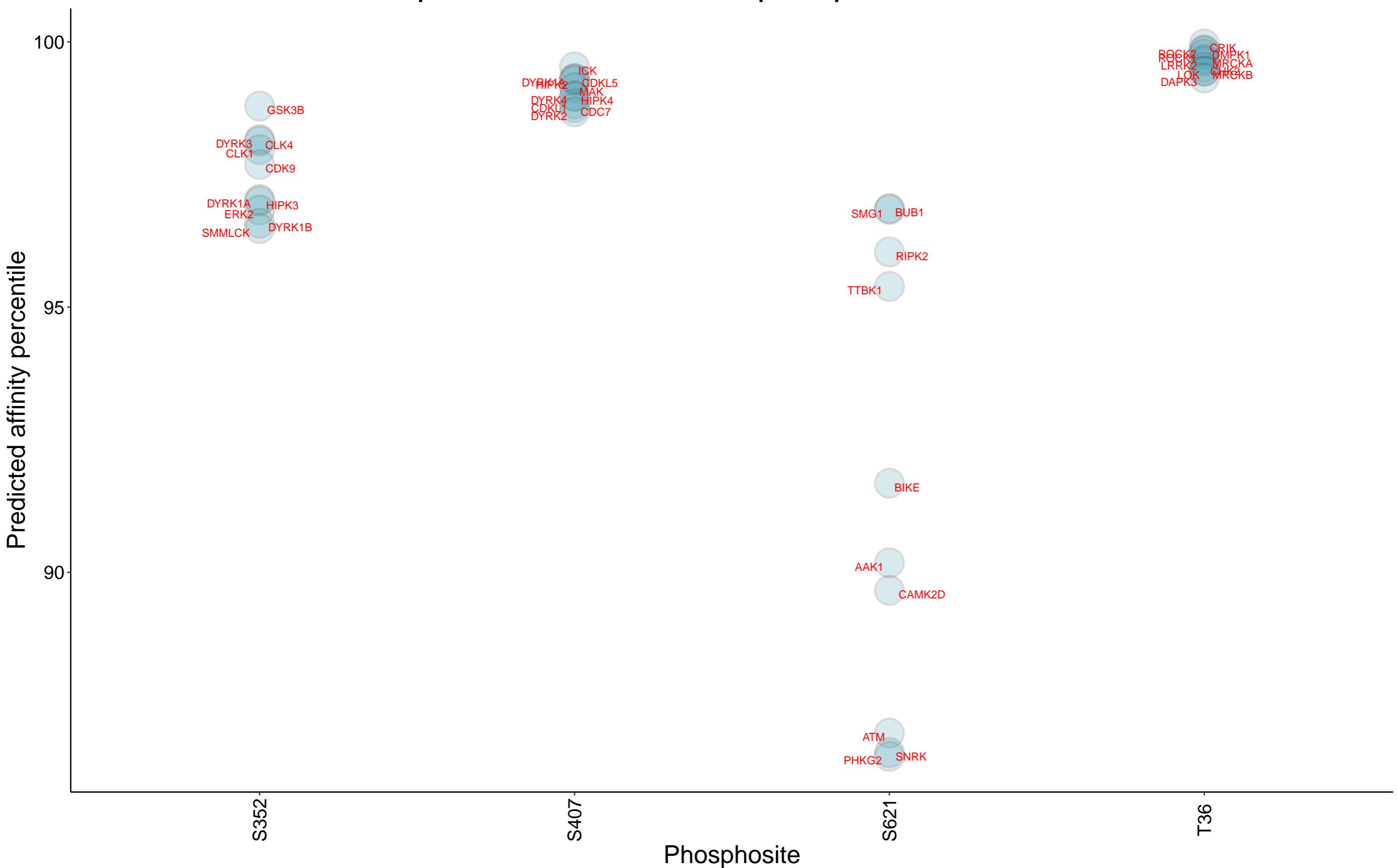
Top 250 correlation coefficients overrepresentation, EXD2 protein, DB1



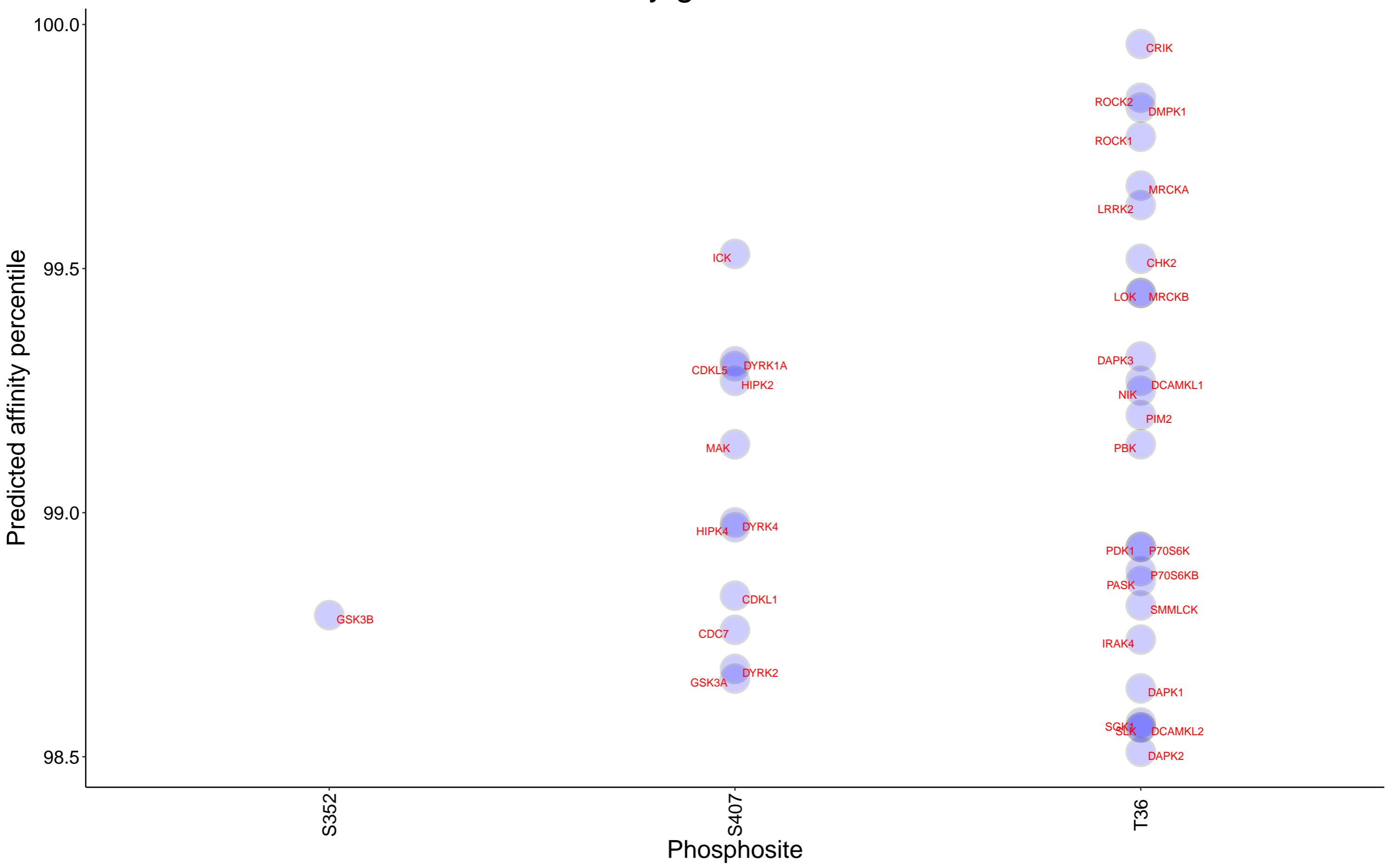
Gene Set Enrichment analysis on protein correlation coefficients, EXD2 protein, DB1



Top 10 kinases for each phosphosite in EXD2



Kinases with affinity greater than 98.5% to EXD2



Top 15 positive correlation coefficients for EXD2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

