

# APEX1

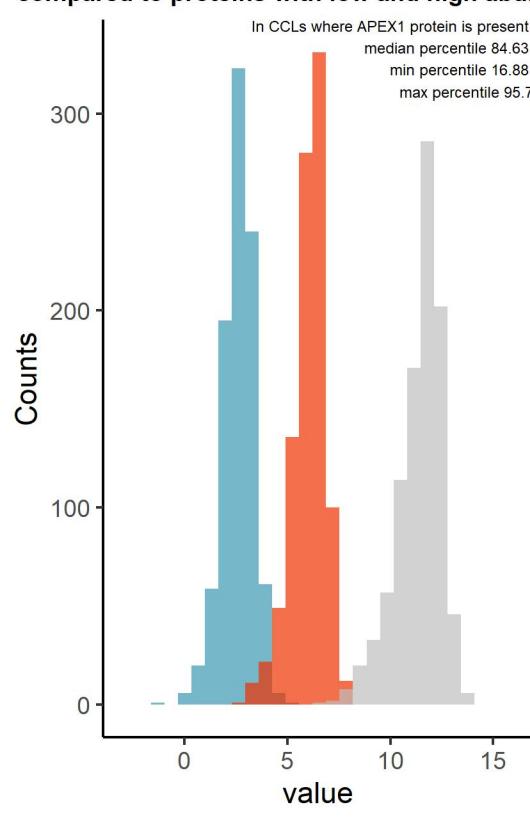
Protein name: APEX1 ; UNIPROT: P27695 ; Gene name: apurinic/apyrimidinic endodeoxyribonuclease 1

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

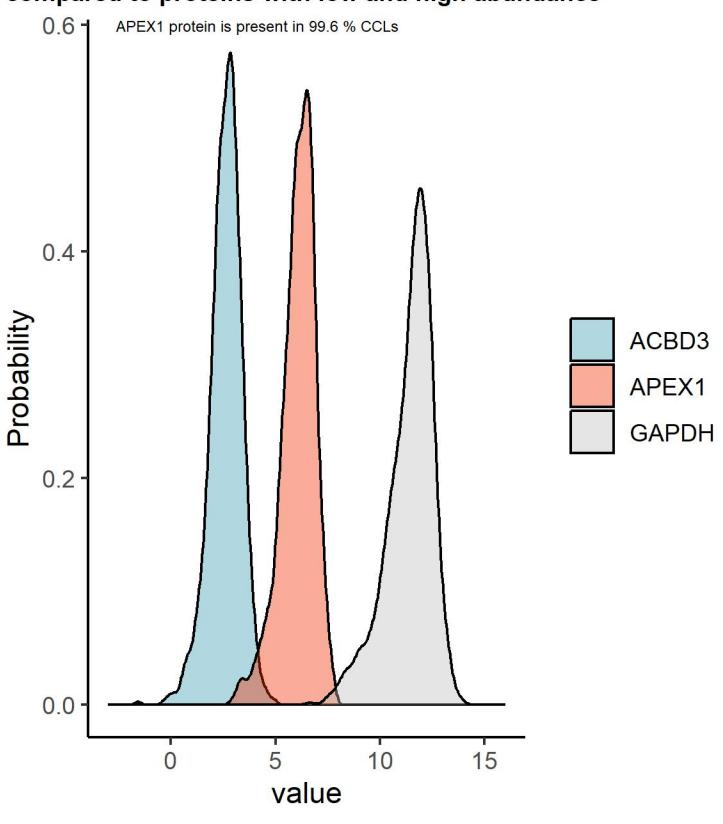
## Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

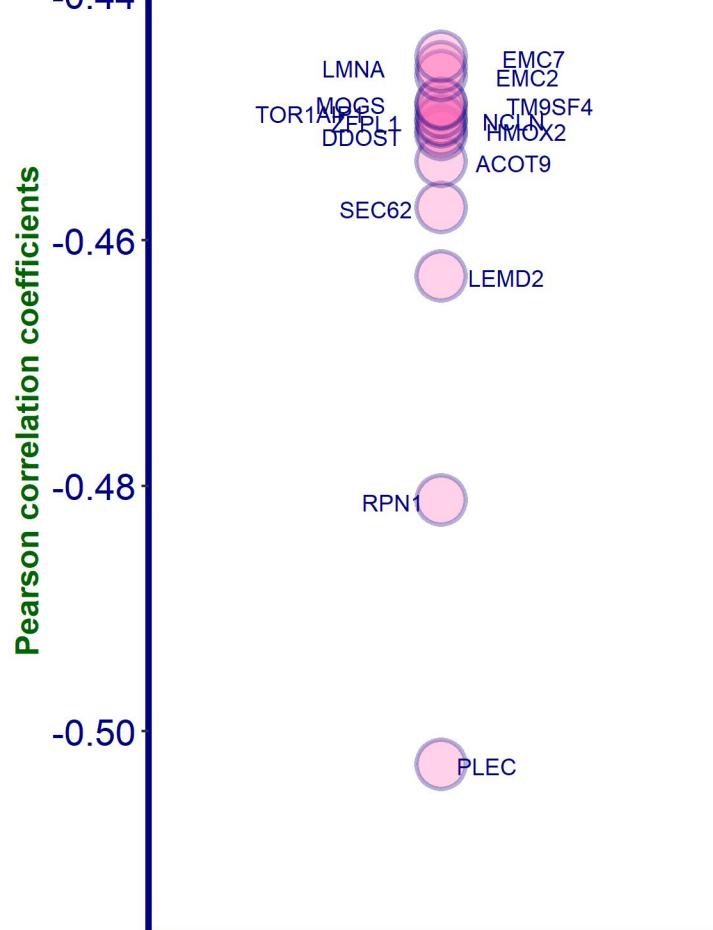
Histogram of APEX1 protein compared to proteins with low and high abundance



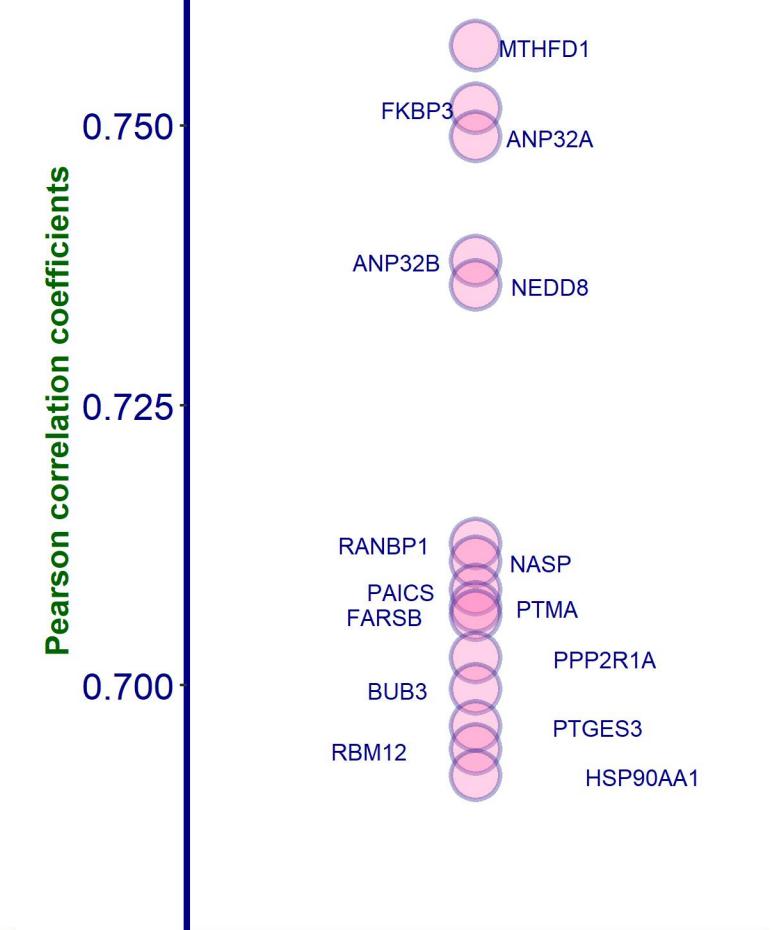
Density plot of APEX1 protein compared to proteins with low and high abundance



### Top negative correlations of APEX1 protein, DB1

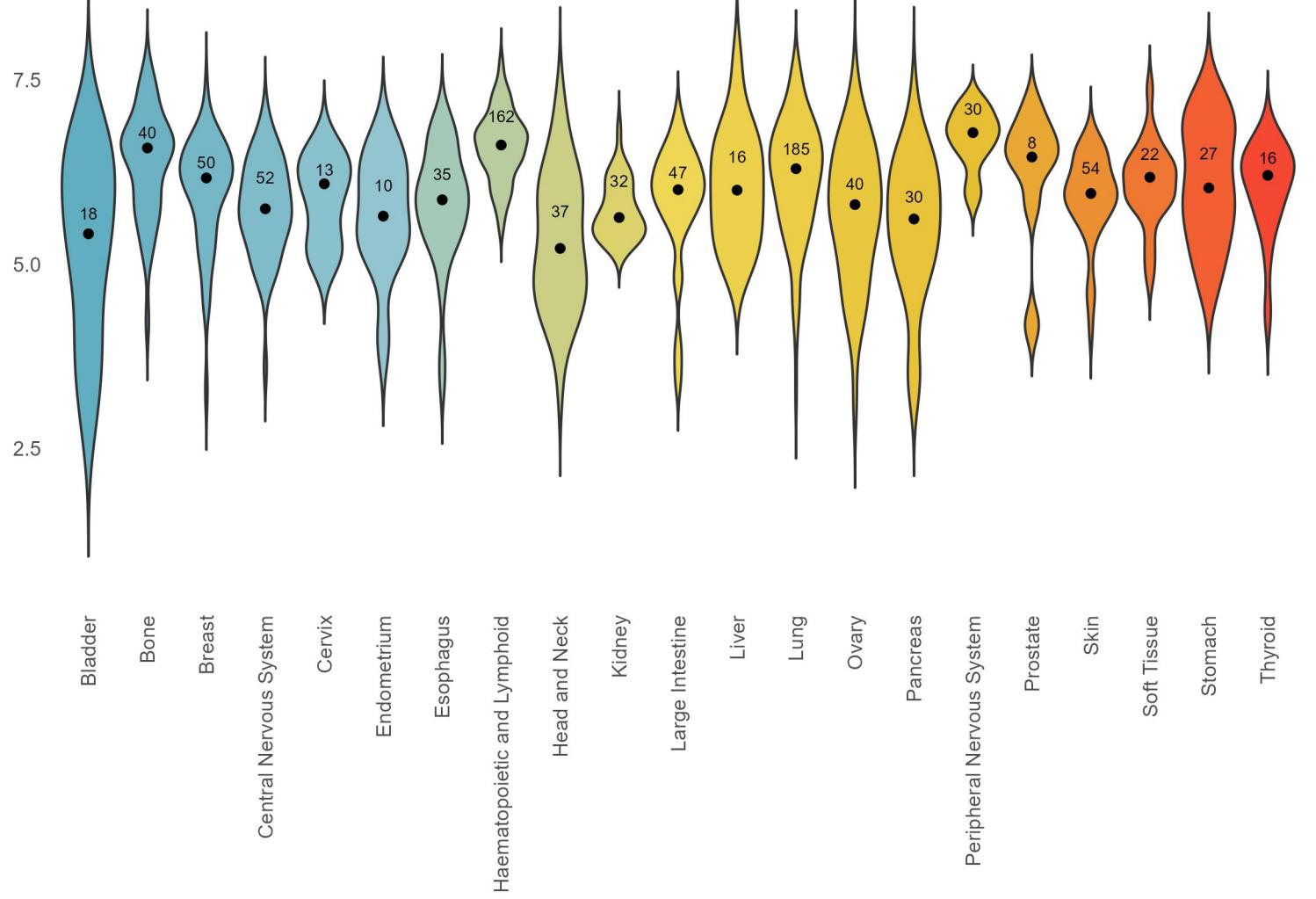


### Top positive correlations of APEX1 protein, DB1



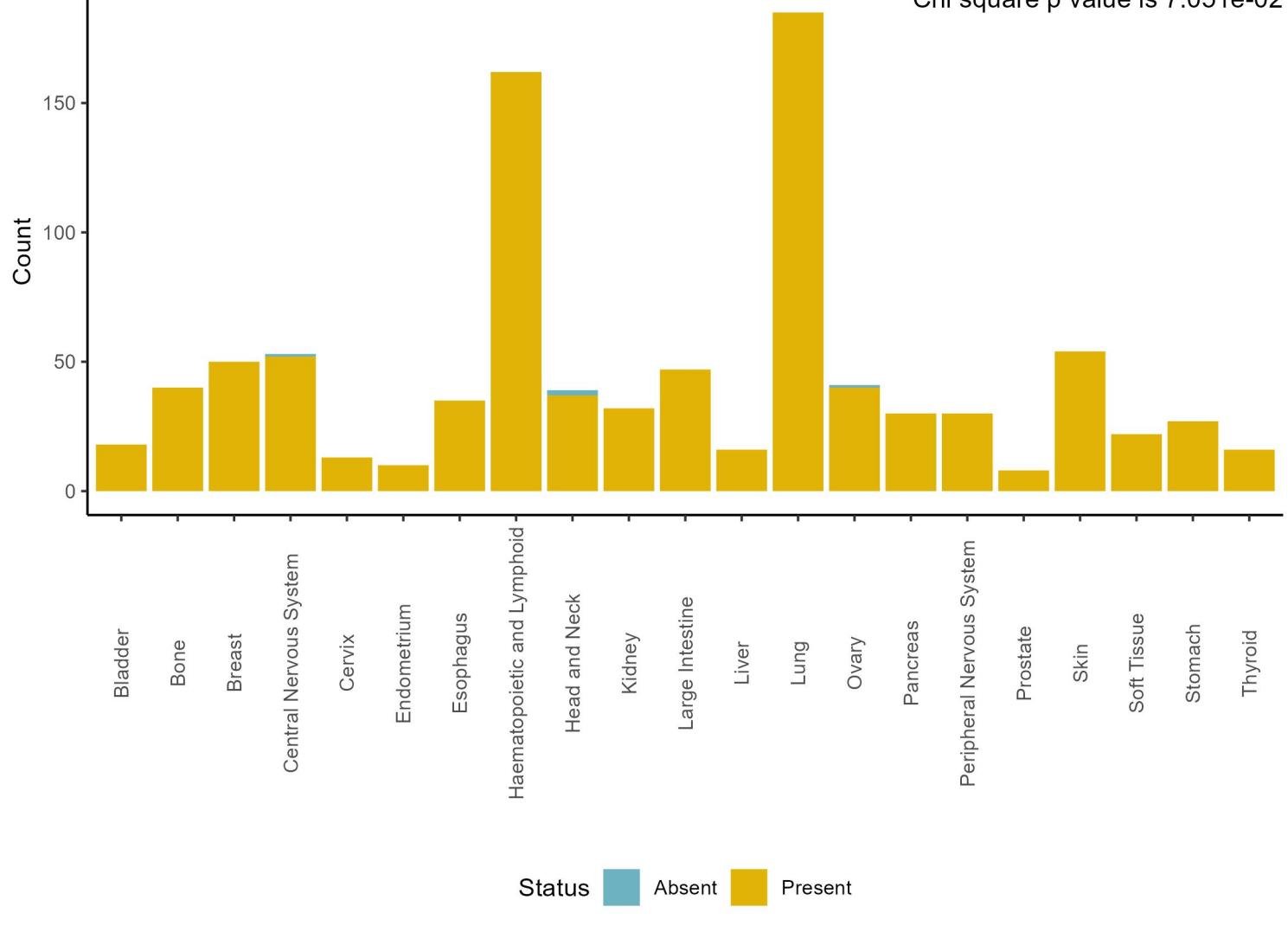
## Amount of APEX1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 3.730e-35



## Present and absent APEX1 protein counts by tissue, DB1

Chi square p value is 7.051e-02

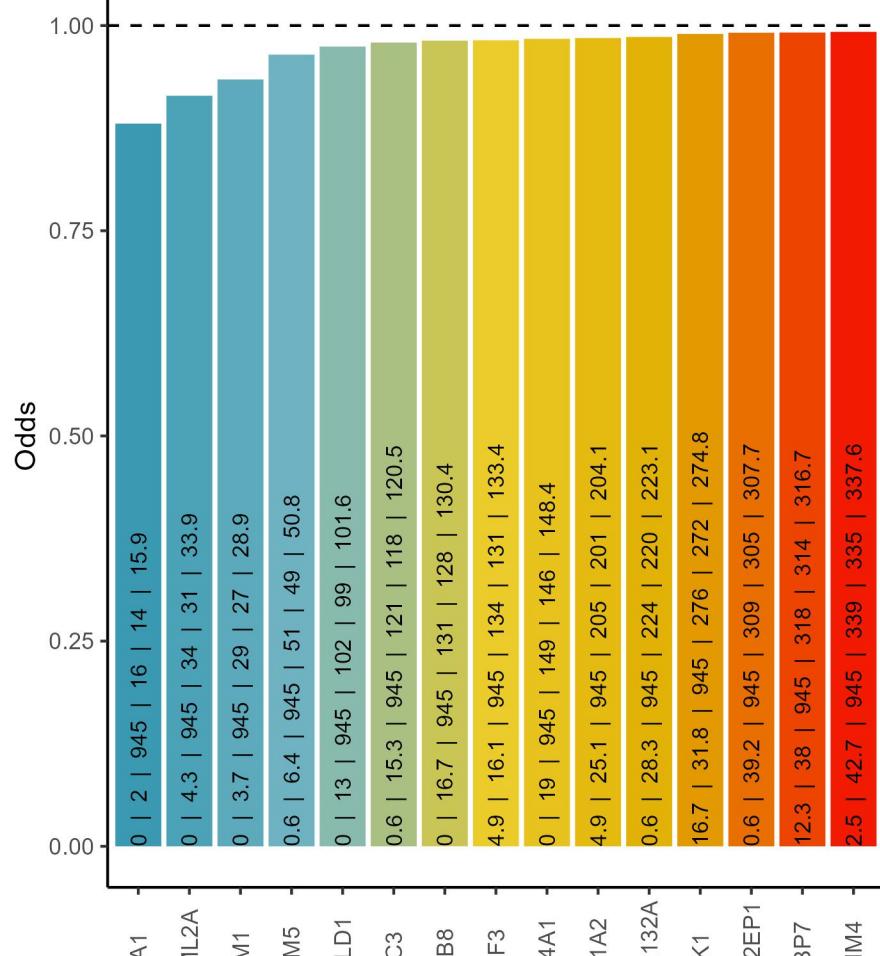


## Cooccurrence with APEX1 protein, DB1

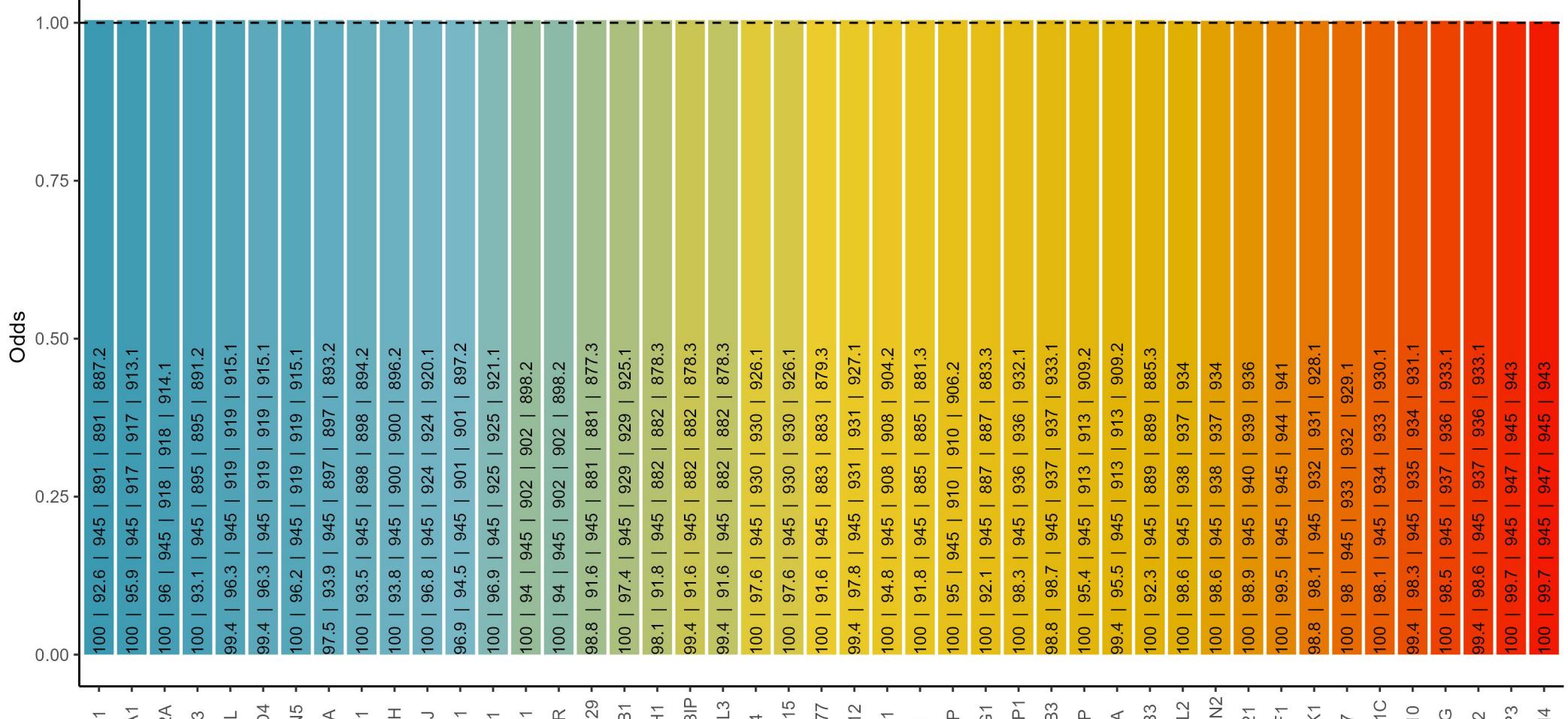
% of APEX1 in blood cancers: 100 ; % of APEX1 in solid cancers: 99.5

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of APEX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

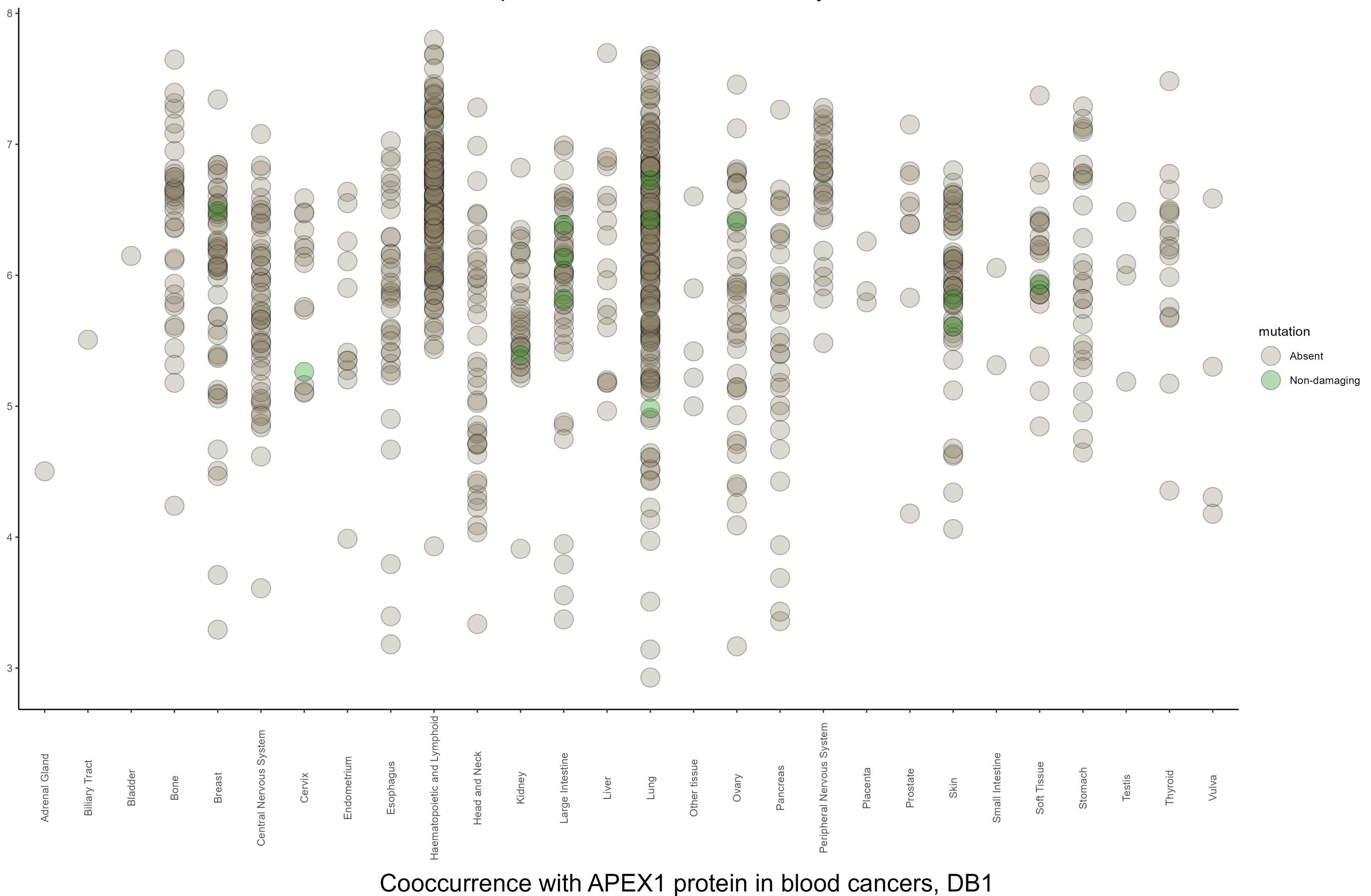
### Negative cooccurrence



### Positive cooccurrence

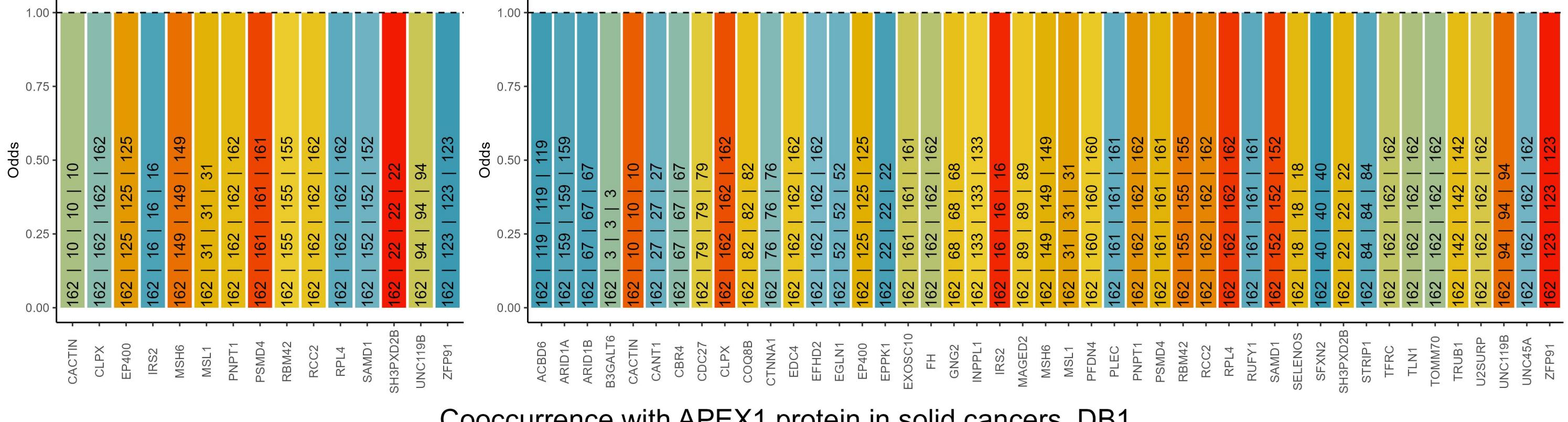


# Amount of APEX1 protein and mutation status by tissue, DB1



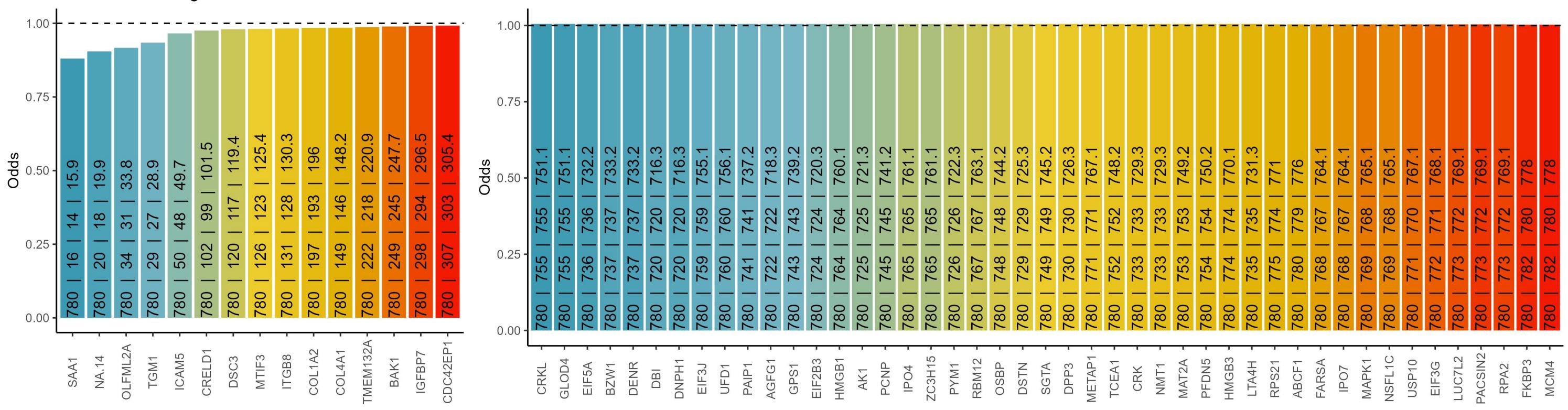
## Cooccurrence with APEX1 protein in blood cancers, DB1

The text in the bars: incidence of APEX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

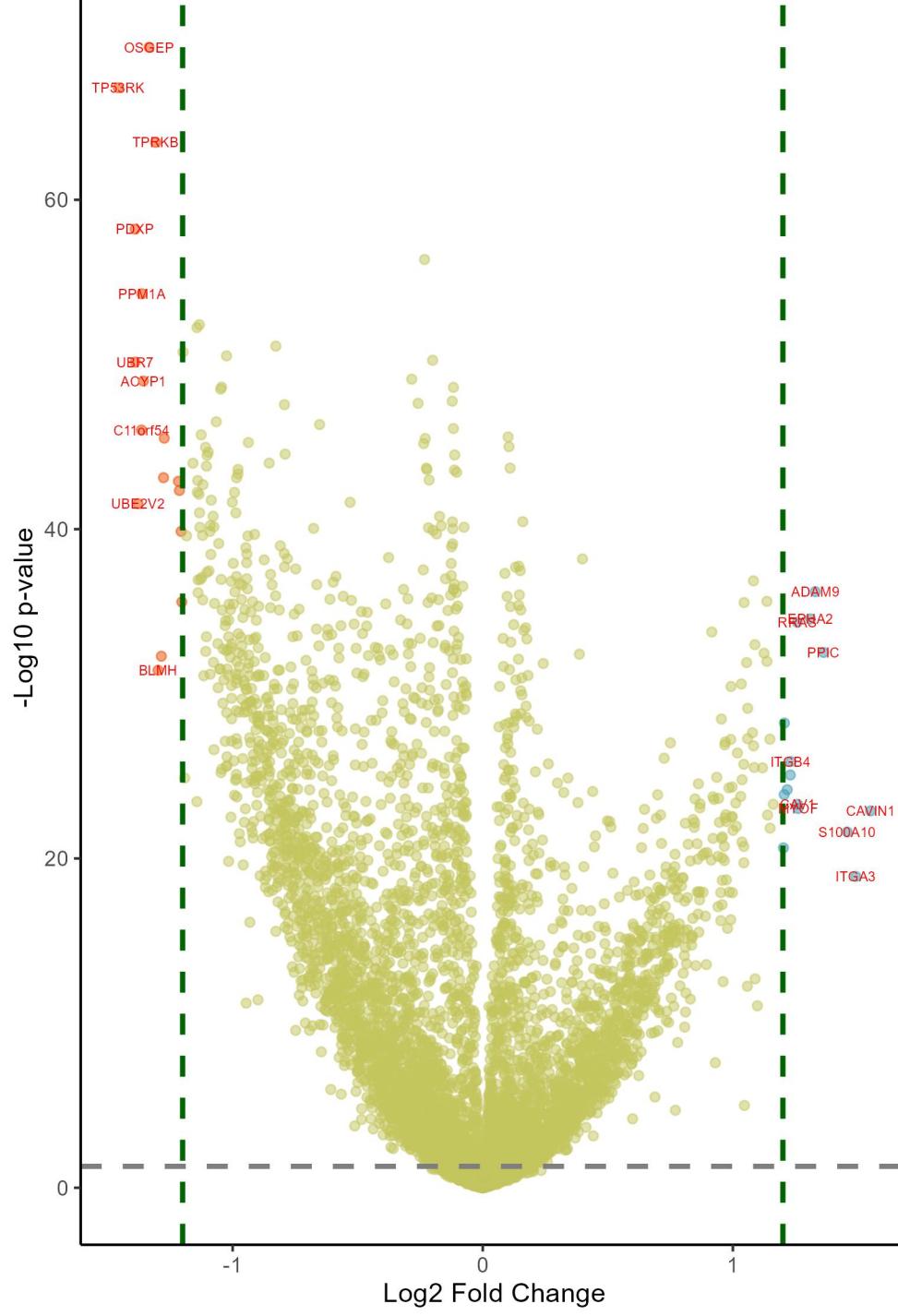


## Cooccurrence with APEX1 protein in solid cancers, DB1

The text in the bars: incidence of APEX1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



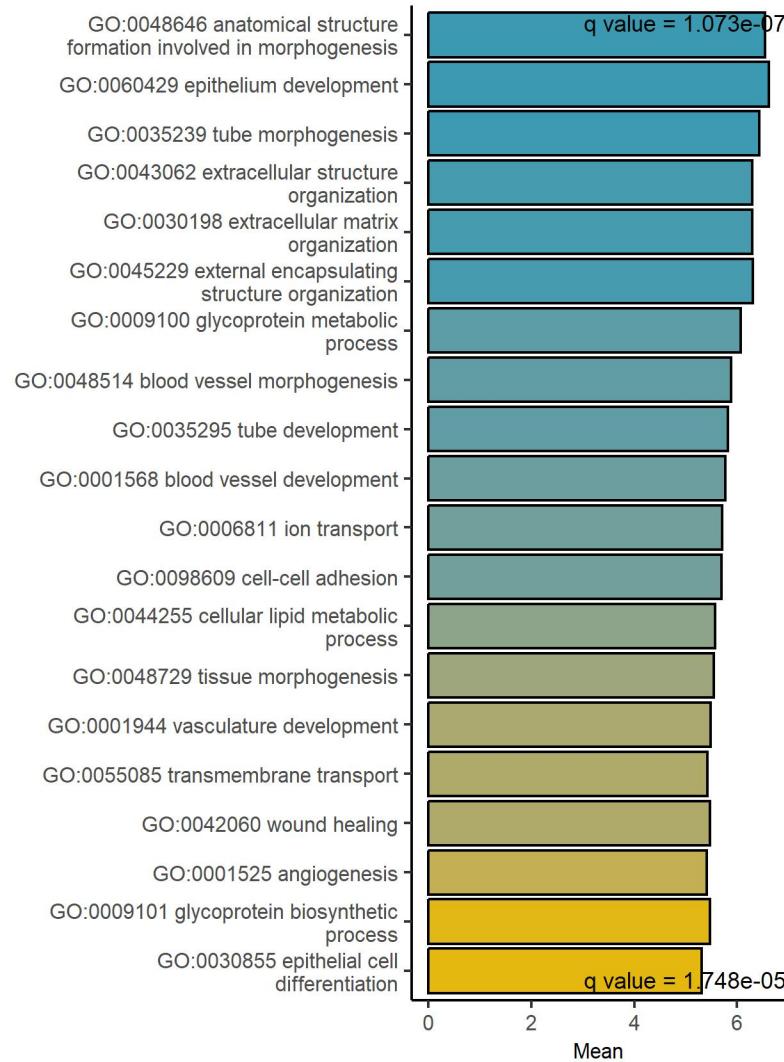
### Downregulated at low/absent APEX1      Upregulated at low/absent APEX1



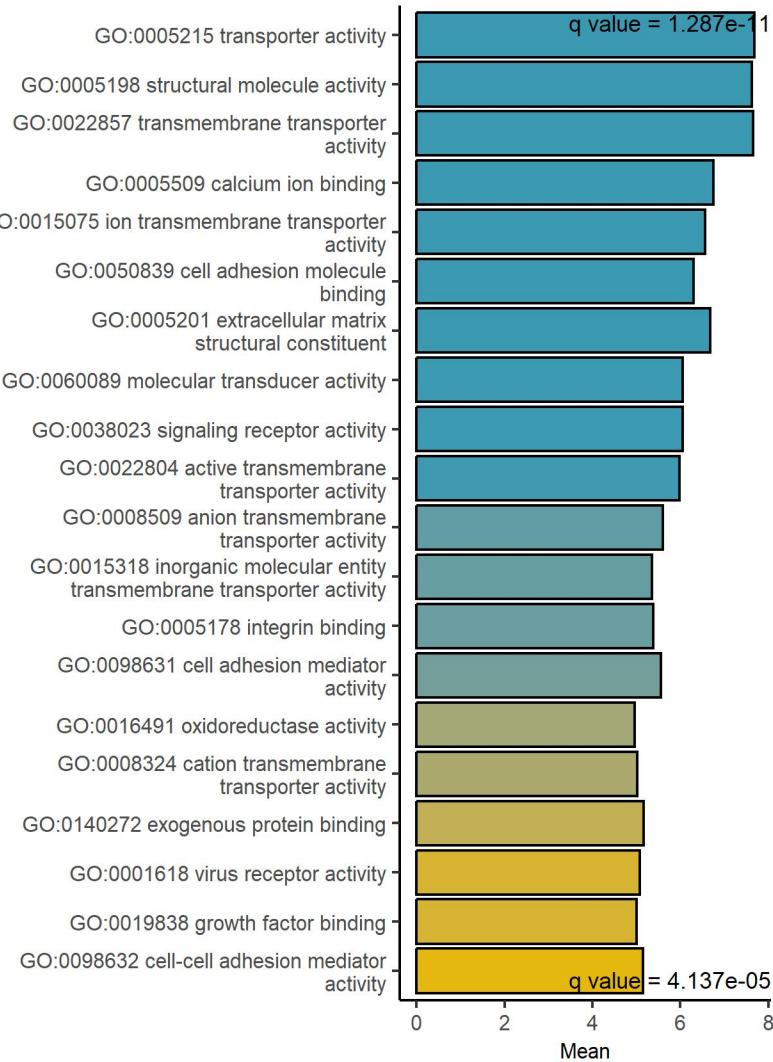
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.46	2.61e-64	TP53RK	TP53 regulating kinase	1.55	1.28e-22	CAVIN1	caveolae associated protein 1
-1.39	6.69e-56	PDXP	pyridoxal phosphatase	1.49	8.03e-19	ITGA3	integrin subunit alpha 3
-1.39	3.19e-48	UBR7	ubiquitin protein ligase E3 compone	1.46	2.12e-21	S100A10	S100 calcium binding protein A10
-1.38	3.01e-40	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.36	8.66e-32	PPIC	peptidylprolyl isomerase C
-1.36	2.37e-44	C11orf54	chromosome 11 open reading frame 54	1.33	3.13e-35	ADAM9	ADAM metallopeptidase domain 9
-1.36	4.23e-52	PPM1A	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> depe	1.31	1.07e-33	EPHA2	EPH receptor A2
-1.36	4.00e-47	ACYP1	acylphosphatase 1	1.26	9.23e-23	MYOF	myoferlin
-1.33	1.20e-66	OSGEP	O-sialoglycoprotein endopeptidase	1.26	5.32e-23	CAV1	caveolin 1
-1.31	4.26e-61	TPRKB	TP53RK binding protein	1.26	1.65e-33	RRAS	RAS related
-1.3	8.99e-31	BLMH	bleomycin hydrolase	1.23	1.71e-25	ITGB4	integrin subunit beta 4
-1.29	1.40e-31	CORO1A	coronin 1A	1.23	1.03e-24	EGFR	epidermal growth factor receptor
-1.28	9.90e-42	NUDT3	nudix hydrolase 3	1.22	7.38e-24	ITGA2	integrin subunit alpha 2
-1.27	6.61e-44	HDHD2	haloacid dehalogenase like hydrolas	1.21	9.67e-28	THBS1	thrombospondin 1
-1.22	1.54e-41	SMAP2	small ArfGAP2	1.21	1.43e-23	RHOC	ras homolog family member C
-1.21	5.33e-41	DCK	deoxycytidine kinase	1.2	1.77e-20	NCEH1	neutral cholesterol ester hydrolase
-1.21	1.15e-38	ARMC6	armadillo repeat containing 6	1.16	5.24e-23	NT5E	5'-nucleotidase ecto
-1.2	1.17e-34	PSME3IP1	proteasome activator subunit 3 inte	1.15	1.26e-21	S100A16	S100 calcium binding protein A16
-1.2	9.74e-49	GMPR2	guanosine monophosphate reductase 2	1.15	8.55e-27	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.19	1.52e-24	ZNF706	zinc finger protein 706	1.14	2.21e-22	GPRC5A	G protein-coupled receptor class C
-1.18	2.01e-38	USP11	ubiquitin specific peptidase 11	1.14	2.77e-31	SDC4	syndecan 4
-1.16	1.61e-42	CHD8	chromodomain helicase DNA binding p	1.14	1.08e-34	AGRN	agrin
-1.14	3.69e-23	ABRACL	ABRA C-terminal like	1.12	9.53e-32	UXS1	UDP-glucuronate decarboxylase 1
-1.14	3.82e-50	PAPOLA	poly(A) polymerase alpha	1.12	3.94e-25	GPX8	glutathione peroxidase 8 (putative)
-1.14	6.65e-41	LIG1	DNA ligase 1	1.1	2.95e-11	GNG12	G protein subunit gamma 12
-1.14	1.39e-41	MDP1	magnesium dependent phosphatase 1	1.09	7.93e-13	LGALS3	galectin 3
-1.14	3.57e-35	PRPSAP2	phosphoribosyl pyrophosphate synthetase	1.09	3.14e-32	FNDC3B	fibronectin type III domain contain
-1.14	6.73e-36	GRK2	G protein-coupled receptor kinase 2	1.09	3.77e-25	KRT80	keratin 80
-1.13	8.55e-41	GABPA	GA binding protein transcription fa	1.08	2.06e-26	GPC1	glypican 1
-1.13	2.82e-50	METTL3	methyltransferase 3, N6-adenosine-m	1.08	7.67e-36	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b

### GAGE analysis on upregulated and downregulated proteins at low/absent APEX1 protein, DB1

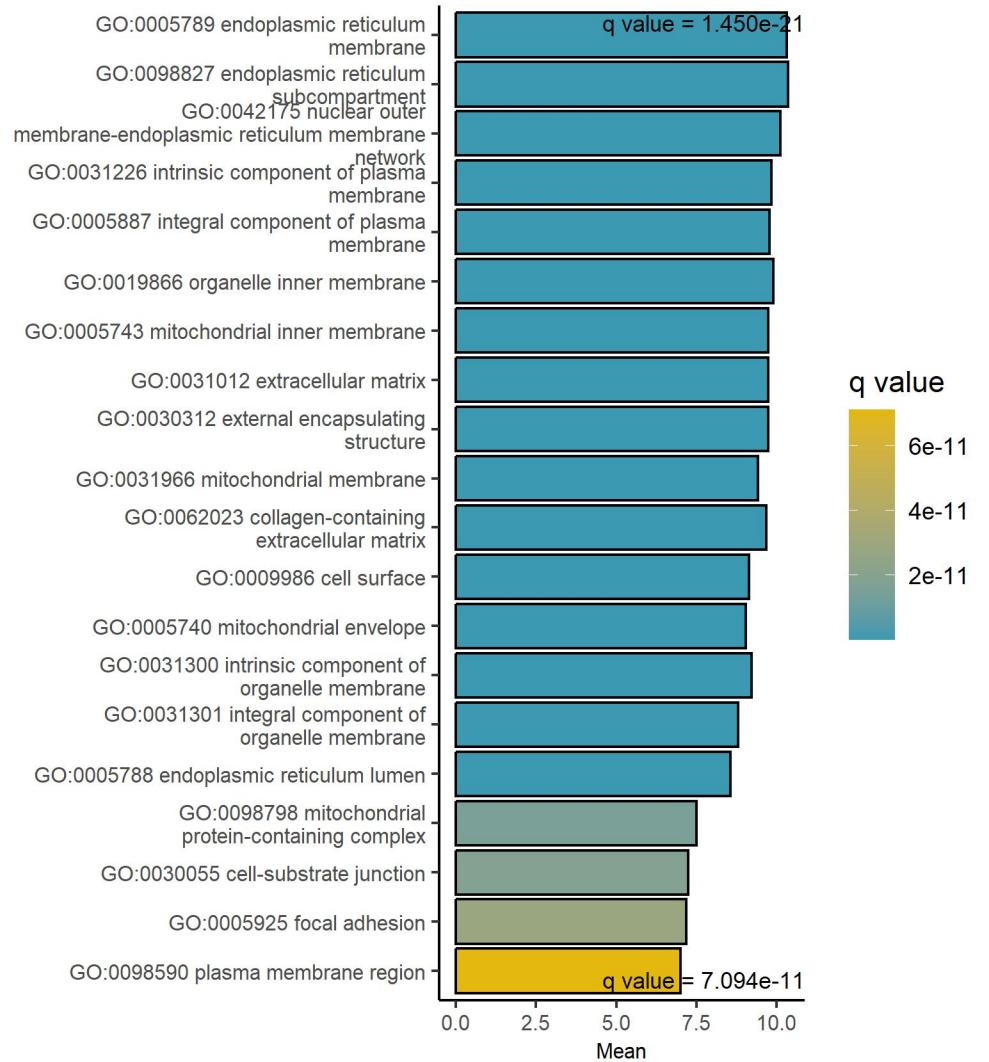
#### GO Biological Process upregulated



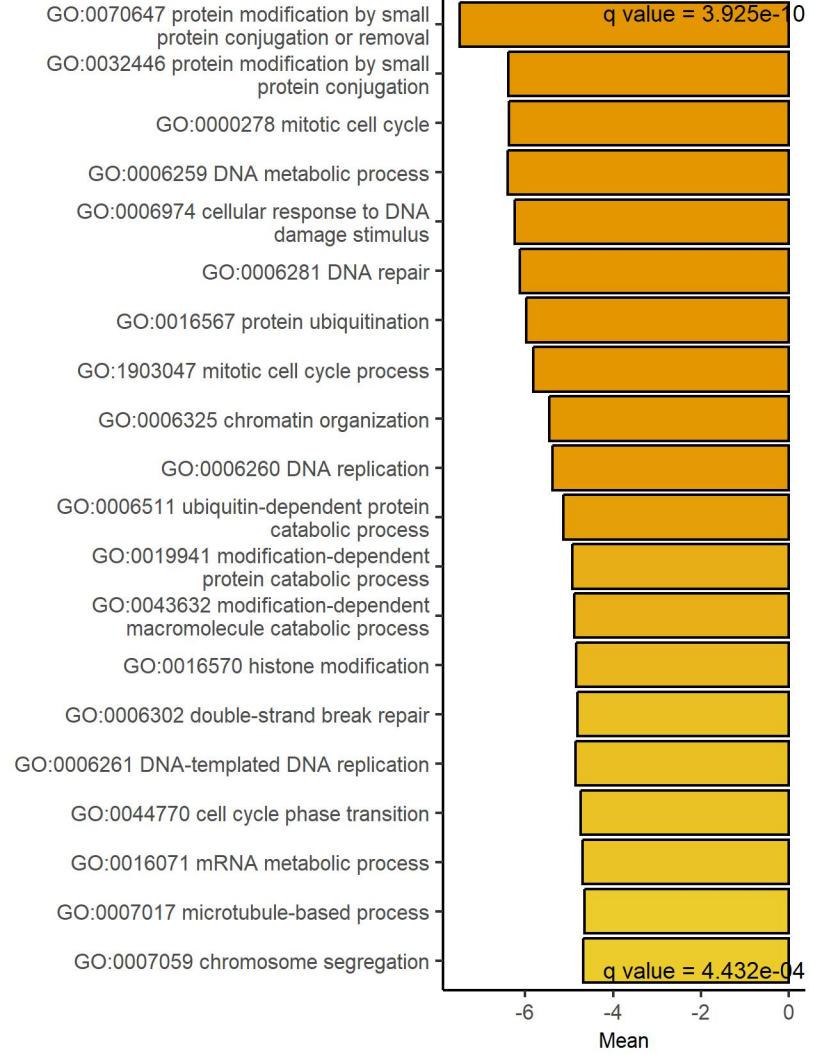
#### GO Molecular Function upregulated



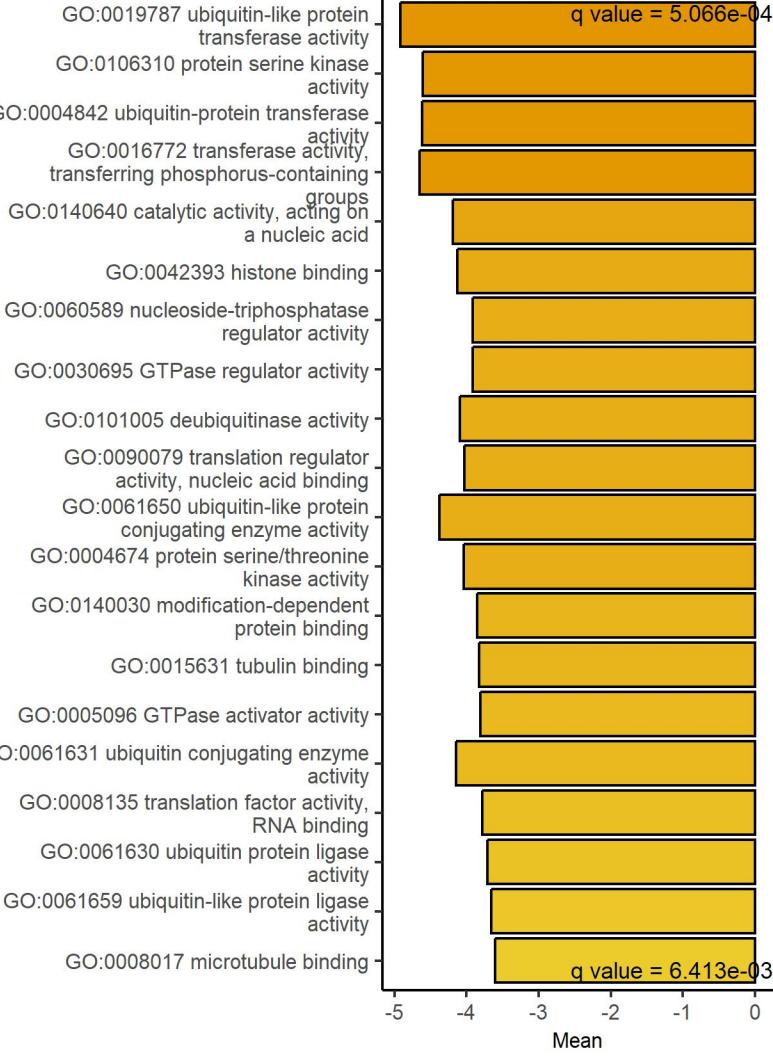
#### GO Cellular Component upregulated



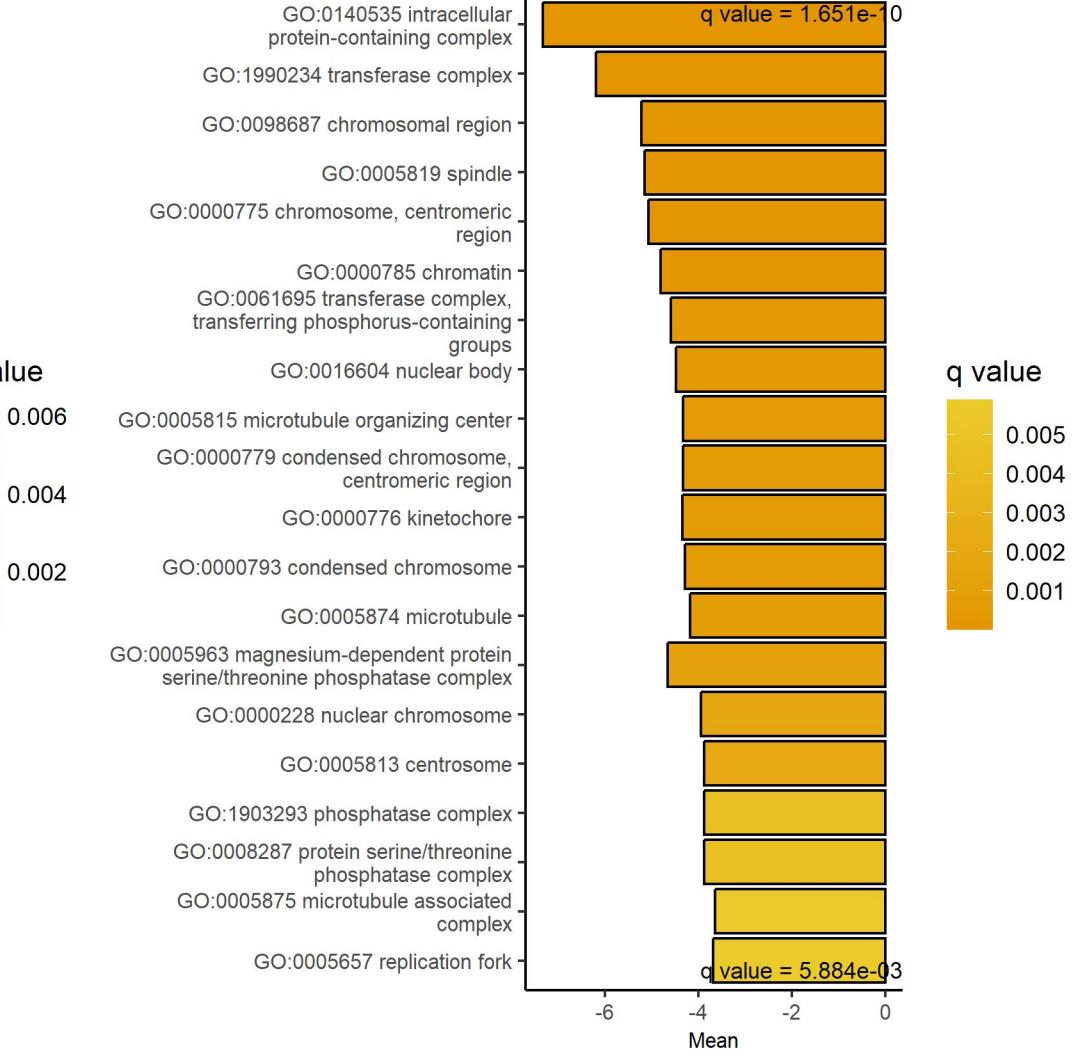
#### GO Biological Process downregulated

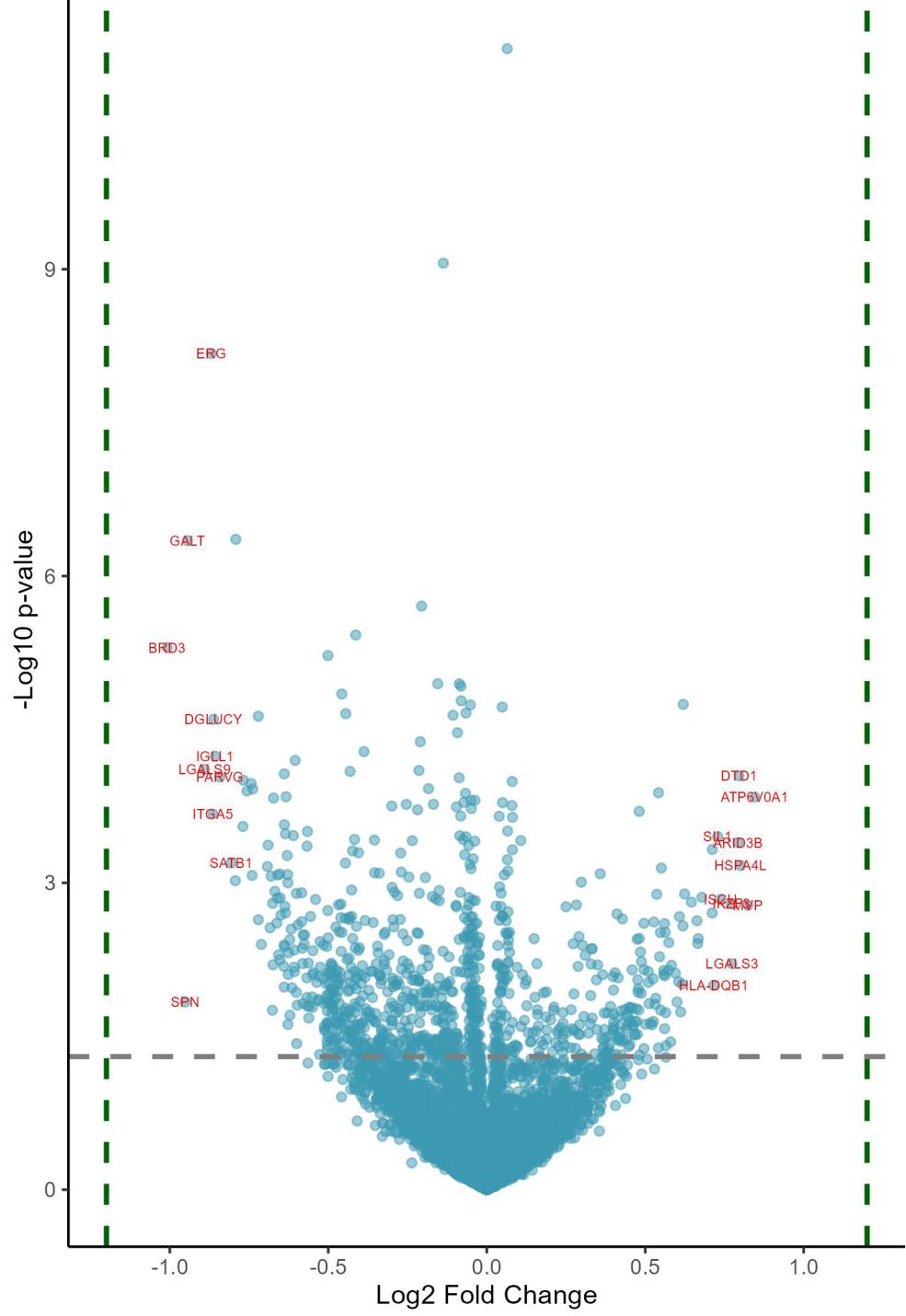


#### GO Molecular Function downregulated

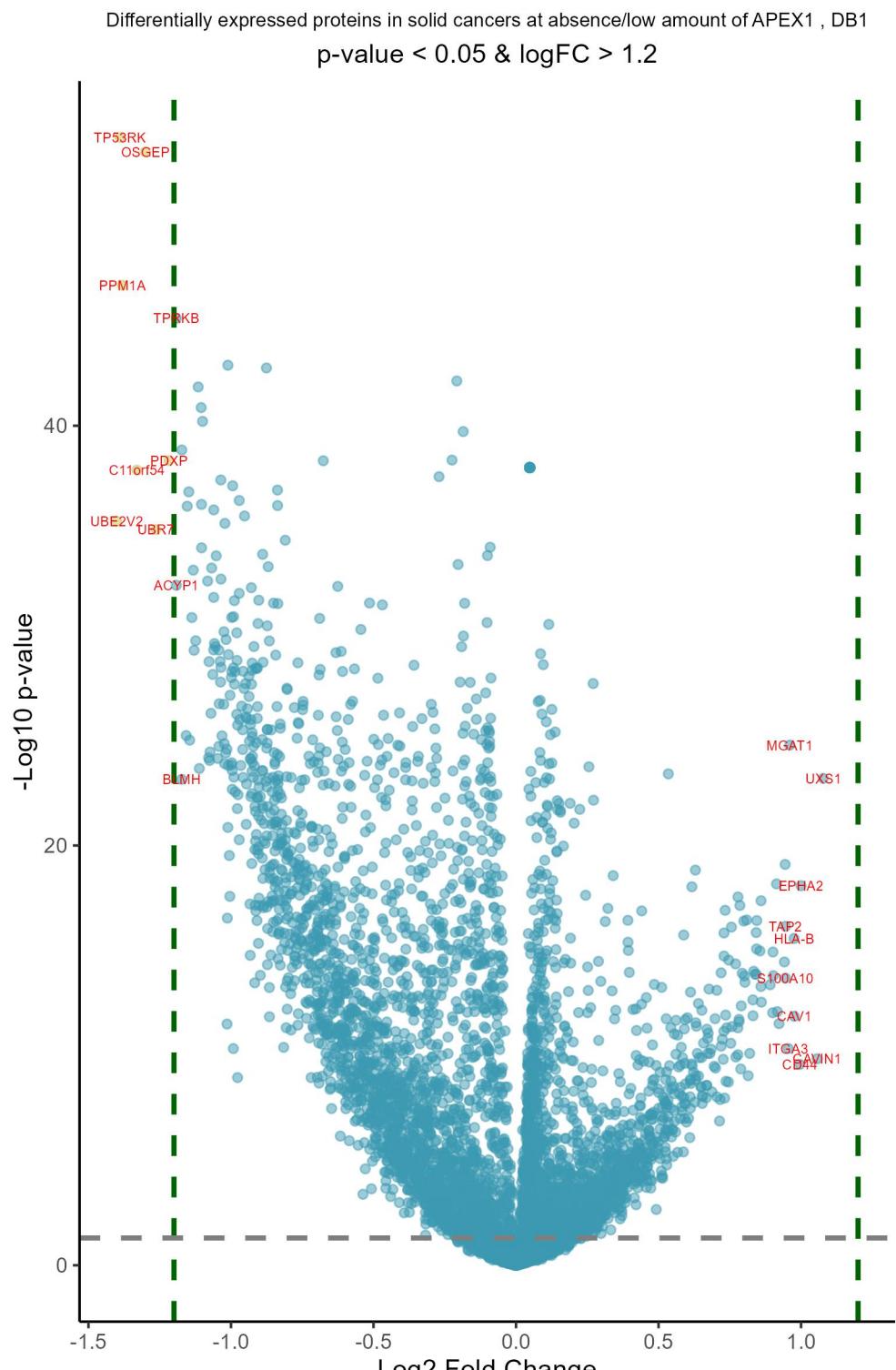


#### GO Cellular Component downregulated



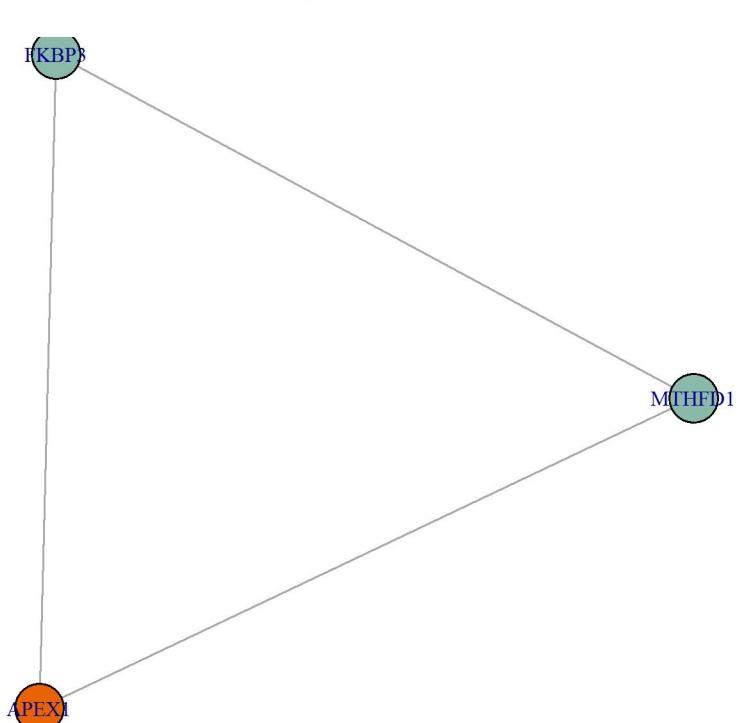


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.01	3.71e-03	BRD3	bromodomain containing 3	0.85	2.14e-02	ATP6V0A1	ATPase H <sup>+</sup> transporting V0 subunit a
-0.95	1.96e-01	SPN	sialophorin	0.82	7.50e-02	MVP	major vault protein
-0.94	4.99e-04	GALT	galactose-1-phosphate uridylyltrans	0.8	4.78e-02	HSPA4L	heat shock protein family A (Hsp70)
-0.89	1.74e-02	LGALS9	galectin 9	0.8	1.79e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.87	1.11e-05	ERG	ETS transcription factor ERG	0.79	3.44e-02	ARID3B	AT-rich interaction domain 3B
-0.86	2.39e-02	ITGA5	integrin subunit alpha 5	0.77	1.38e-01	LGALS3	galectin 3
-0.86	7.29e-03	DGLUCY	D-glutamate cyclase	0.77	7.50e-02	IKZF3	IKAROS family zinc finger 3
-0.86	1.42e-02	IGLL1	immunoglobulin lambda like polypept	0.74	7.16e-02	ISCU	iron-sulfur cluster assembly enzyme
-0.84	1.79e-02	PARVG	parvin gamma	0.73	3.31e-02	SIL1	SIL1 nucleotide exchange factor
-0.81	4.63e-02	SATB1	SATB homeobox 1	0.72	1.60e-01	HLA-DQB1	major histocompatibility complex, c
-0.79	5.70e-02	DOK3	docking protein 3	0.71	3.80e-02	IFI30	IFI30 lysosomal thiol reductase
-0.79	4.99e-04	SDR39U1	short chain dehydrogenase/reductase	0.71	8.34e-02	TNFRSF8	TNF receptor superfamily member 8
-0.77	2.92e-02	ARRB1	arrestin beta 1	0.68	7.10e-02	MAP4K1	mitogen-activated protein kinase ki
-0.77	1.83e-02	CREB1	cAMP responsive element binding pro	0.67	1.03e-01	SPTY2D1	SPT2 chromatin protein domain conta
-0.76	2.05e-02	ZNF22	zinc finger protein 22	0.67	1.09e-01	SYNGR2	synaptogyrin 2
-0.74	1.87e-02	SLFN11	schlafen family member 11	0.66	8.64e-02	NT5C3A	5'-nucleotidase, cytosolic IIIA
-0.74	5.26e-02	FLI1	Fli-1 proto-oncogene, ETS transcrip	0.65	7.38e-02	MYO1C	myosin IC
-0.74	2.01e-02	PIK3R1	phosphoinositide-3-kinase regulator	0.62	6.83e-02	QSOX2	quiescin sulfhydryl oxidase 2
-0.72	7.10e-03	UBASH3B	ubiquitin associated and SH3 domain	0.62	7.06e-03	ITGAV	integrin subunit alpha V
-0.72	8.64e-02	SASH3	SAM and SH3 domain containing 3	0.62	9.17e-02	SVIP	small VCP interacting protein
-0.71	1.09e-01	ARPC1A	actin related protein 2/3 complex s	0.62	1.59e-01	BST2	bone marrow stromal cell antigen 2
-0.69	4.85e-02	AHCYL1	adenosylhomocysteinase like 1	0.61	2.15e-01	CTTN	cortactin
-0.69	3.58e-02	SPIN1	spindlin 1	0.61	8.56e-02	ASNS	asparagine synthetase (glutamine-hy
-0.68	9.33e-02	SFXN3	sideroflexin 3	0.61	1.55e-01	FTL	ferritin light chain
-0.68	5.31e-02	APBB1IP	amyloid beta precursor protein bind	0.6	1.96e-01	SQOR	sulfide quinone oxidoreductase
-0.68	2.10e-01	CAPG	capping actin protein, gelsolin lik	0.6	1.46e-01	TRIP10	thyroid hormone receptor interactor
-0.68	7.50e-02	PTK7	protein tyrosine kinase 7 (inactive)	0.58	1.39e-01	AKT1S1	AKT1 substrate 1
-0.67	1.38e-01	RGS19	regulator of G protein signaling 19	0.58	2.94e-01	LMNA	lamin A/C
-0.67	2.14e-02	POLR2G	RNA polymerase II subunit G	0.57	1.08e-01	PIP4K2C	phosphatidylinositol-5-phosphate 4-

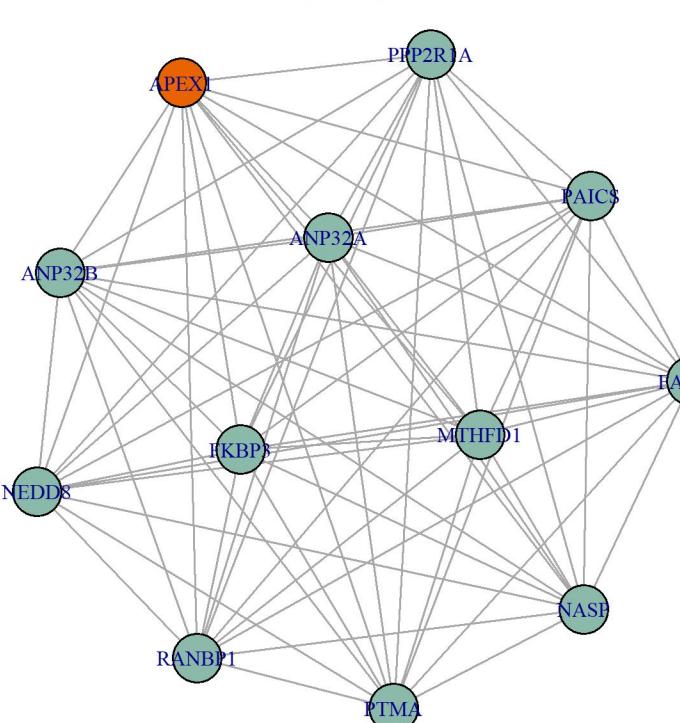


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.4	2.15e-34	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.08	1.15e-22	UXS1	UDP-glucuronate decarboxylase 1
-1.39	6.11e-51	TP53RK	TP53 regulating kinase	1.06	6.08e-10	CAVIN1	caveolae associated protein 1
-1.38	3.38e-44	PPM1A	protein phosphatase, Mg <sup>2+</sup> /Mn <sup>2+</sup> depe	1	8.48e-18	EPHA2	EPH receptor A2
-1.33	8.99e-37	C11orf54	chromosome 11 open reading frame 54	1	1.09e-09	CD44	CD44 molecule (Indian blood group)
-1.3	2.00e-50	OSGEP	O-sialoglycoprotein endopeptidase	0.98	6.96e-12	CAV1	caveolin 1
-1.26	5.32e-34	UBR7	ubiquitin protein ligase E3 compone	0.98	2.04e-15	HLA-B	major histocompatibility complex, c
-1.22	6.86e-37	PDXP	pyridoxal phosphatase	0.96	3.93e-24	MGAT1	alpha-1,3-mannosyl-glycoprotein 2-b
-1.19	2.14e-31	ACYP1	acylphosphatase 1	0.96	2.06e-10	ITGA3	integrin subunit alpha 3
-1.19	1.01e-42	TPRKB	TP53RK binding protein	0.95	5.78e-16	TAP2	transporter 2, ATP binding cassette
-1.17	1.27e-22	BLMH	bleomycin hydrolase	0.95	1.28e-13	S100A10	S100 calcium binding protein A10
-1.17	6.86e-37	ADI1	acireductone dioxygenase 1	0.94	9.17e-19	ADAM9	ADAM metallopeptidase domain 9
-1.16	1.47e-24	CLNS1A	chloride nucleotide-sensitive chann	0.94	2.37e-14	THBS1	thrombospondin 1
-1.15	4.30e-35	LZIC	leucine zipper and CTNNB1P1 domain	0.92	1.52e-11	GPRC5A	G protein-coupled receptor class C
-1.15	9.20e-36	PHPT1	phosphohistidine phosphatase 1	0.92	4.27e-12	ITGB4	integrin subunit beta 4
-1.15	2.36e-24	NTMT1	N-terminal Xaa-Pro-Lys N-methyltran	0.91	7.01e-18	NCEH1	neutral cholesterol ester hydrolase
-1.14	6.65e-30	NUDT3	nudix hydrolase 3	0.9	9.90e-14	KRT80	keratin 80
-1.13	4.16e-32	TKFC	trioleinase and FMN cyclase	0.9	8.37e-15	PPIC	peptidylprolyl isomerase C
-1.13	2.11e-28	PITHD1	PITH domain containing 1	0.9	4.80e-12	NT5E	5'-nucleotidase ecto
-1.12	7.81e-29	CZIB	CXXC motif containing zinc binding	0.89	2.56e-13	SQOR	sulfide quinone oxidoreductase
-1.12	1.05e-39	PAPOLA	poly(A) polymerase alpha	0.86	1.60e-12	AXL	AXL receptor tyrosine kinase
-1.11	4.21e-23	PBK	PDZ binding kinase	0.86	4.03e-17	RRAS	RAS related
-1.1	9.11e-39	ENOPH1	enolase-phosphatase 1	0.86	3.08e-13	F3	coagulation factor III, tissue fact
-1.1	3.58e-35	TBCC	tubulin folding cofactor C	0.86	7.51e-15	SP100	SP100 nuclear antigen
-1.1	3.83e-33	CHD8	chromodomain helicase DNA binding p	0.84	3.15e-16	MYOF	myoferlin
-1.1	3.74e-38	METTL3	methyltransferase 3, N6-adenosine-m	0.84	6.09e-15	NPC1	NPC intracellular cholesterol trans
-1.08	1.35e-31	AARSD1	alanyl-tRNA synthetase domain conta	0.84	8.64e-14	LAMC2	laminin subunit gamma 2
-1.08	1.45e-23	PSME3IP1	proteasome activator subunit 3 inte	0.84	1.11e-15	RAP2B	RAP2B, member of RAS oncogene famil
-1.08	6.98e-28	USP11	ubiquitin specific peptidase 11	0.84	8.57e-14	RAB32	RAB32, member RAS oncogene family
-1.08	1.89e-23	PIN1	peptidylprolyl cis/trans isomerase,	0.83	6.28e-14	TAP1	transporter 1, ATP binding cassette

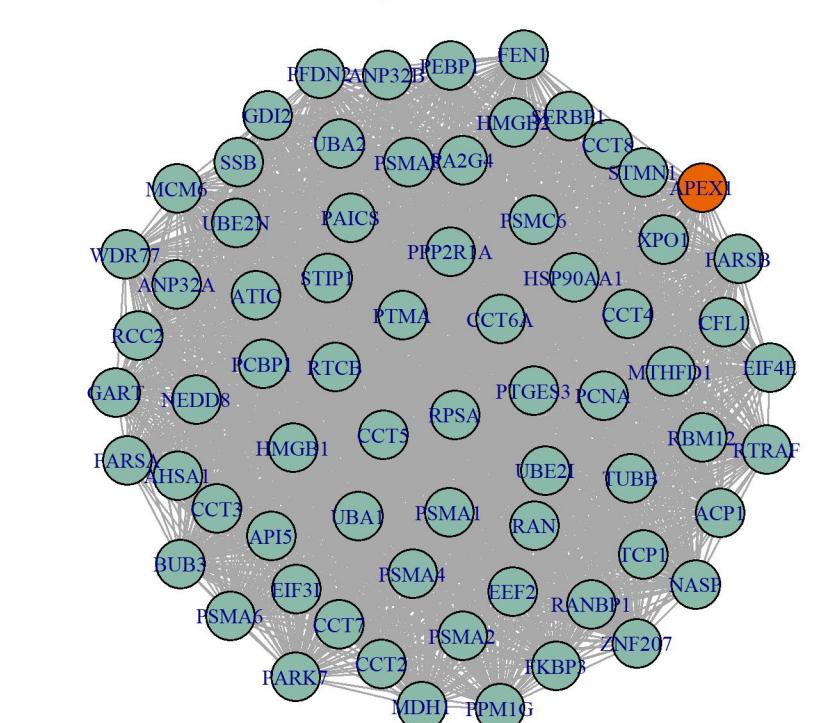
APEX1 network, DB1, all Pearson r &gt; 0.75

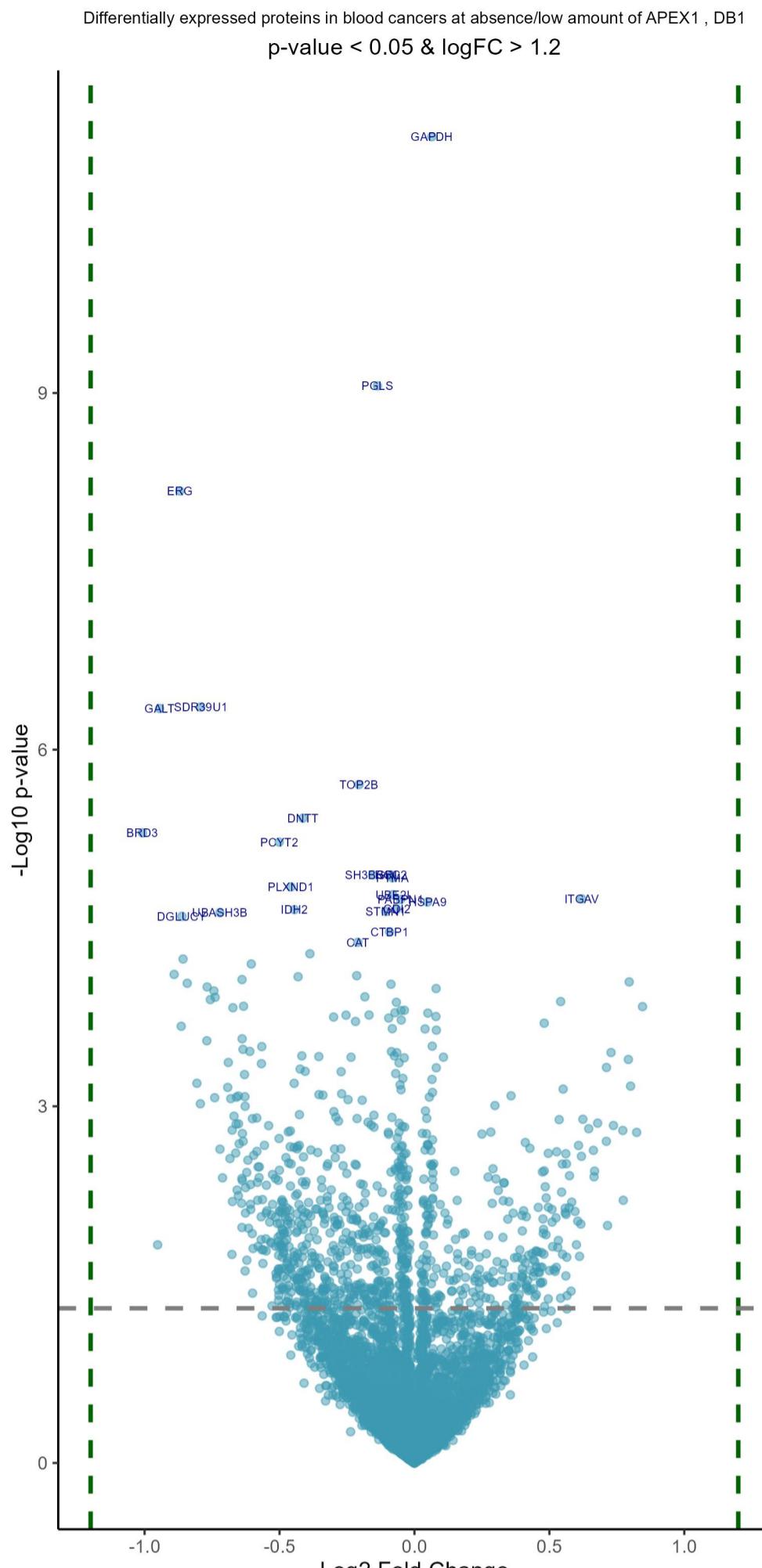


APEX1 network, DB1, all Pearson r &gt; 0.7

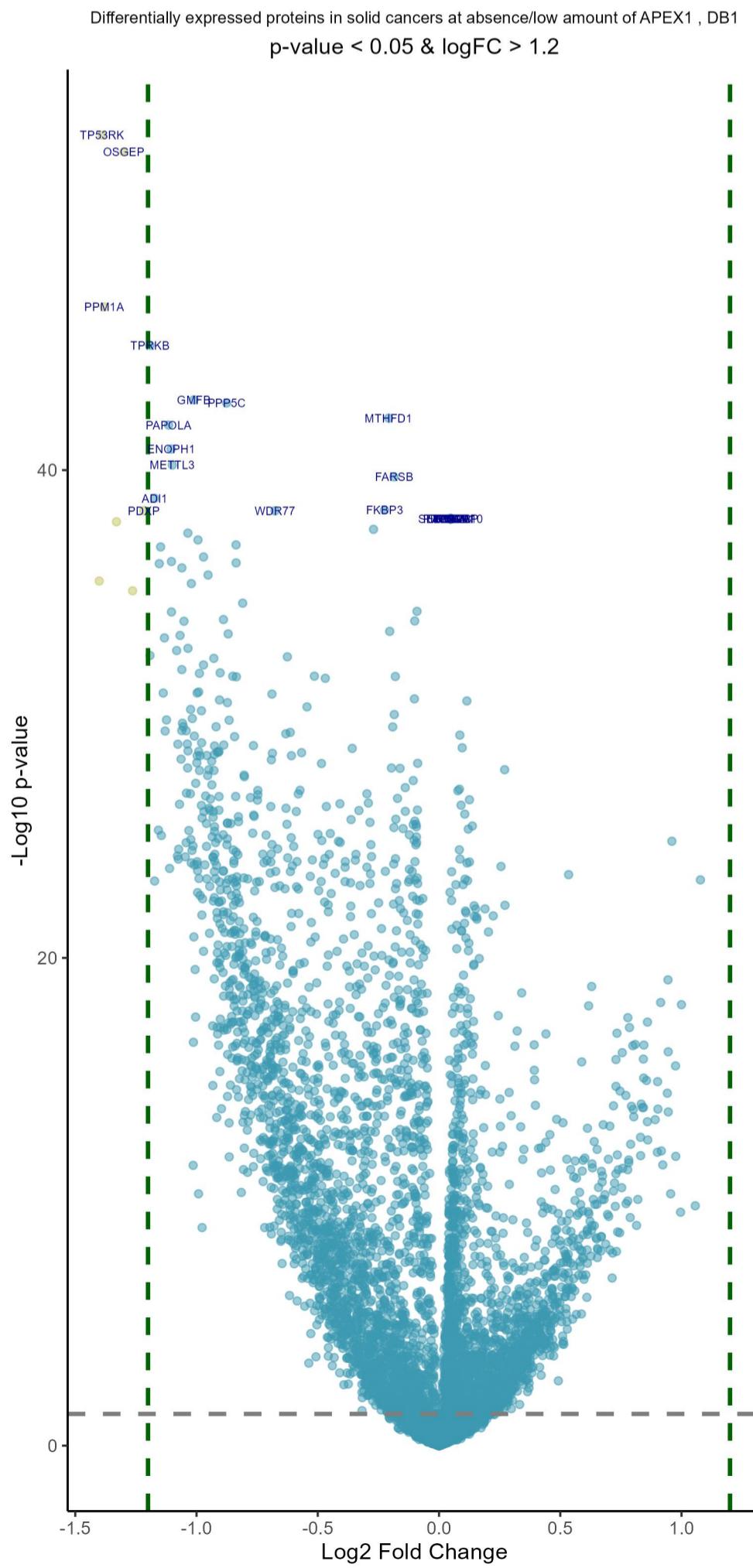


APEX1 network, DB1, all Pearson r &gt; 0.65



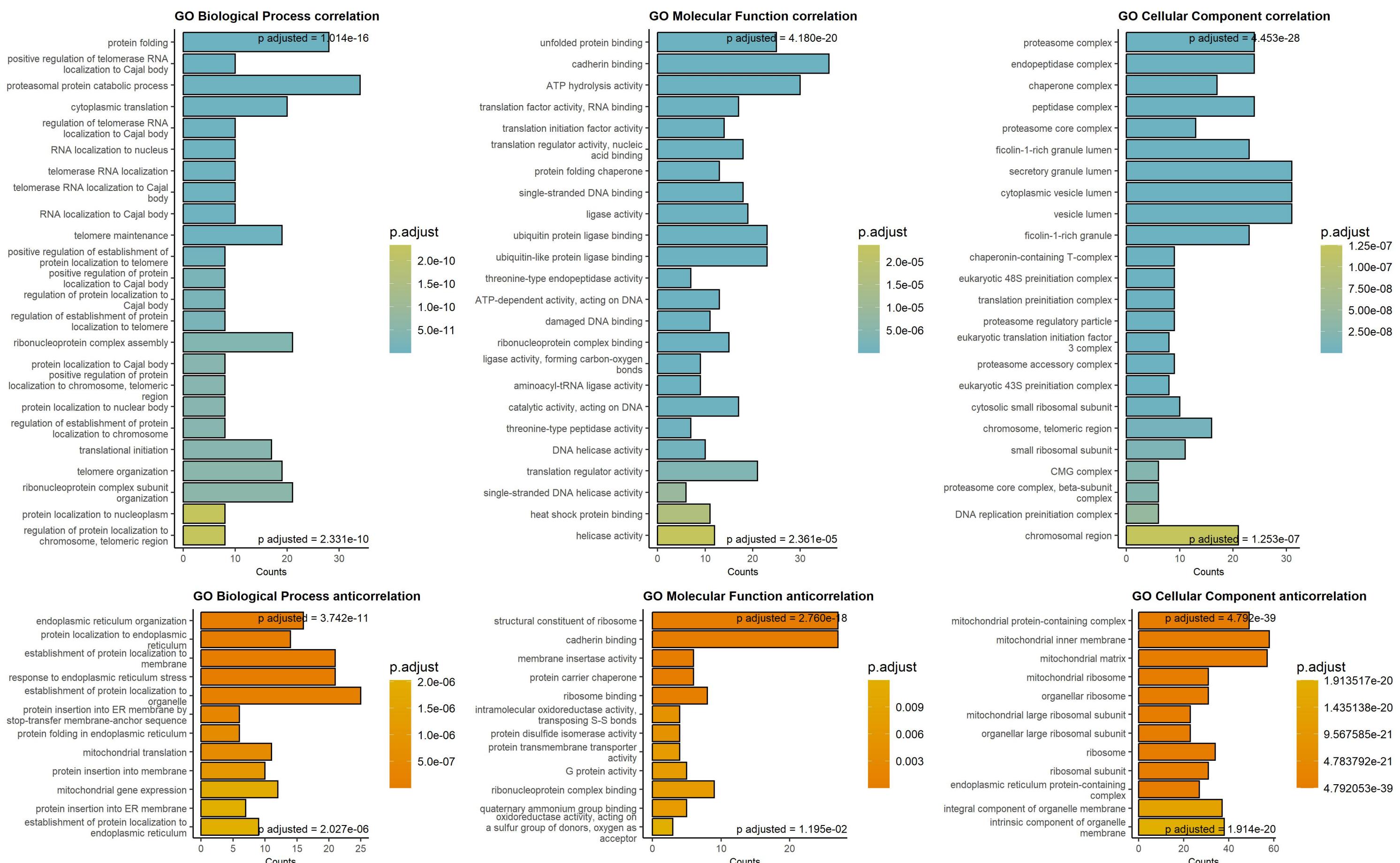


Sorted by p values!							
Downregulated in blood cancers at low/absent APEX1				Upregulated in blood cancers at low/absent APEX1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.14	1.93e-06	PGLS	6-phosphogluconolactonase	0.06	2.32e-08	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.87	1.11e-05	ERG	ETS transcription factor ERG	0.62	7.06e-03	ITGAV	integrin subunit alpha V
-0.79	4.99e-04	SDR39U1	short chain dehydrogenase/reductase	0.05	7.06e-03	HSPA9	heat shock protein family A (Hsp70)
-0.94	4.99e-04	GALT	galactose-1-phosphate uridylyltransferase	0.8	1.79e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.21	1.87e-03	TOP2B	DNA topoisomerase II beta	0.08	1.84e-02	HSPA5	heat shock protein family A (Hsp70)
-0.41	3.14e-03	DNTT	DNA nucleotidyltransferase	0.54	2.06e-02	JSRP1	junctional sarcoplasmic reticulum p
-1.01	3.71e-03	BRD3	bromodomain containing 3	0.85	2.14e-02	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.5	3.98e-03	PCYT2	phosphate cytidylyltransferase 2, e	0.05	2.18e-02	EIF4G1	eukaryotic translation initiation f
-0.15	6.12e-03	SH3BGRL	SH3 domain binding glutamate rich p	0.08	2.18e-02	EBNA1BP2	EBNA1 binding protein 2
-0.09	6.12e-03	RCC2	regulator of chromosome condensatio	0.48	2.29e-02	WFS1	wolframin ER transmembrane glycopro
-0.08	6.12e-03	PTMA	prothymosin alpha	0.04	2.44e-02	PSMC2	proteasome 26S subunit, ATPase 2
-0.46	6.77e-03	PLXND1	plexin D1	0.08	2.45e-02	CLPP	caseinolytic mitochondrial matrix p
-0.08	7.06e-03	UBE2I	ubiquitin conjugating enzyme E2 I	0.07	3.17e-02	TRAP1	TNF receptor associated protein 1
-0.05	7.06e-03	PABPN1	poly(A) binding protein nuclear 1	0.73	3.31e-02	SIL1	SIL1 nucleotide exchange factor
-0.07	7.10e-03	GDI2	GDP dissociation inhibitor 2	0.11	3.38e-02	SLC1A5	solute carrier family 1 member 5
-0.44	7.10e-03	IDH2	isocitrate dehydrogenase (NADP(+))	0.79	3.44e-02	ARID3B	AT-rich interaction domain 3B
-0.11	7.10e-03	STMN1	stathmin 1	0.71	3.80e-02	IFI30	IFI30 lysosomal thiol reductase
-0.72	7.10e-03	UBASH3B	ubiquitin associated and SH3 domain	0.08	3.80e-02	DNAJA3	DnaJ heat shock protein family (Hsp
-0.86	7.29e-03	DGLUCY	D-glutamate cyclase	0.07	4.39e-02	RRP1	ribosomal RNA processing 1
-0.09	9.43e-03	CTBP1	C-terminal binding protein 1	0.8	4.78e-02	HSPA4L	heat shock protein family A (Hsp70)
-0.21	1.11e-02	CAT	catalase	0.55	4.96e-02	NQO1	NAD(P)H quinone dehydrogenase 1
-0.39	1.33e-02	FPGS	folylpolyglutamate synthase	0.07	5.18e-02	POLR2H	RNA polymerase II, I and III subuni
-0.86	1.42e-02	IGLL1	immunoglobulin lambda like polypept	0.36	5.26e-02	SLC20A1	solute carrier family 20 member 1
-0.6	1.51e-02	GNAI1	G protein subunit alpha i1	0.06	5.26e-02	MRPS28	mitochondrial ribosomal protein S28
-0.89	1.74e-02	LGALS9	galectin 9	0.3	5.85e-02	ZFC3H1	zinc finger C3H1-type containing
-0.21	1.74e-02	RNASEH2A	ribonuclease H2 subunit A	0.04	6.38e-02	PSMC5	proteasome 26S subunit, ATPase 5
-0.43	1.74e-02	GSTO1	glutathione S-transferase omega 1	0.05	6.81e-02	PSMC4	proteasome 26S subunit, ATPase 4
-0.64	1.78e-02	NT5C2	5'-nucleotidase, cytosolic II	0.62	6.83e-02	QSOX2	quiescin sulfhydryl oxidase 2
-0.84	1.79e-02	PARVG	parvin gamma	0.54	6.83e-02	DHX29	DExH-box helicase 29
-0.09	1.79e-02	SIN3A	SIN3 transcription regulator family	0.68	7.10e-02	MAP4K1	mitogen-activated protein kinase ki
-0.77	1.83e-02	CREB1	cAMP responsive element binding pro	0.74	7.16e-02	ISCU	iron-sulfur cluster assembly enzyme
-0.74	1.87e-02	SLFN11	schlafin family member 11	0.65	7.38e-02	MYO1C	myosin IC
-0.18	2.01e-02	DCK	deoxycytidine kinase	0.77	7.50e-02	IKZF3	IKAROS family zinc finger 3
-0.74	2.01e-02	PIK3R1	phosphoinositide-3-kinase regulator	0.28	7.50e-02	ADAM15	ADAM metallopeptidase domain 15
-0.76	2.05e-02	ZNF22	zinc finger protein 22	0.82	7.50e-02	MVP	major vault protein
-0.07	2.06e-02	VPS35	VPS35 retromer complex component	0.03	7.51e-02	PSMD11	proteasome 26S subunit, non-ATPase
-0.63	2.14e-02	CUTC	cutC copper transporter	0.04	7.51e-02	PSMD2	proteasome 26S subunit ubiquitin re
-0.67	2.14e-02	POLR2G	RNA polymerase II subunit G	0.25	7.51e-02	GGT1	gamma-glutamyltransferase 1
0.04	2.17e-02	DTRD1	polyuridylic tract binding prot	0.07	8.22e-02	RVS1	hystin-like

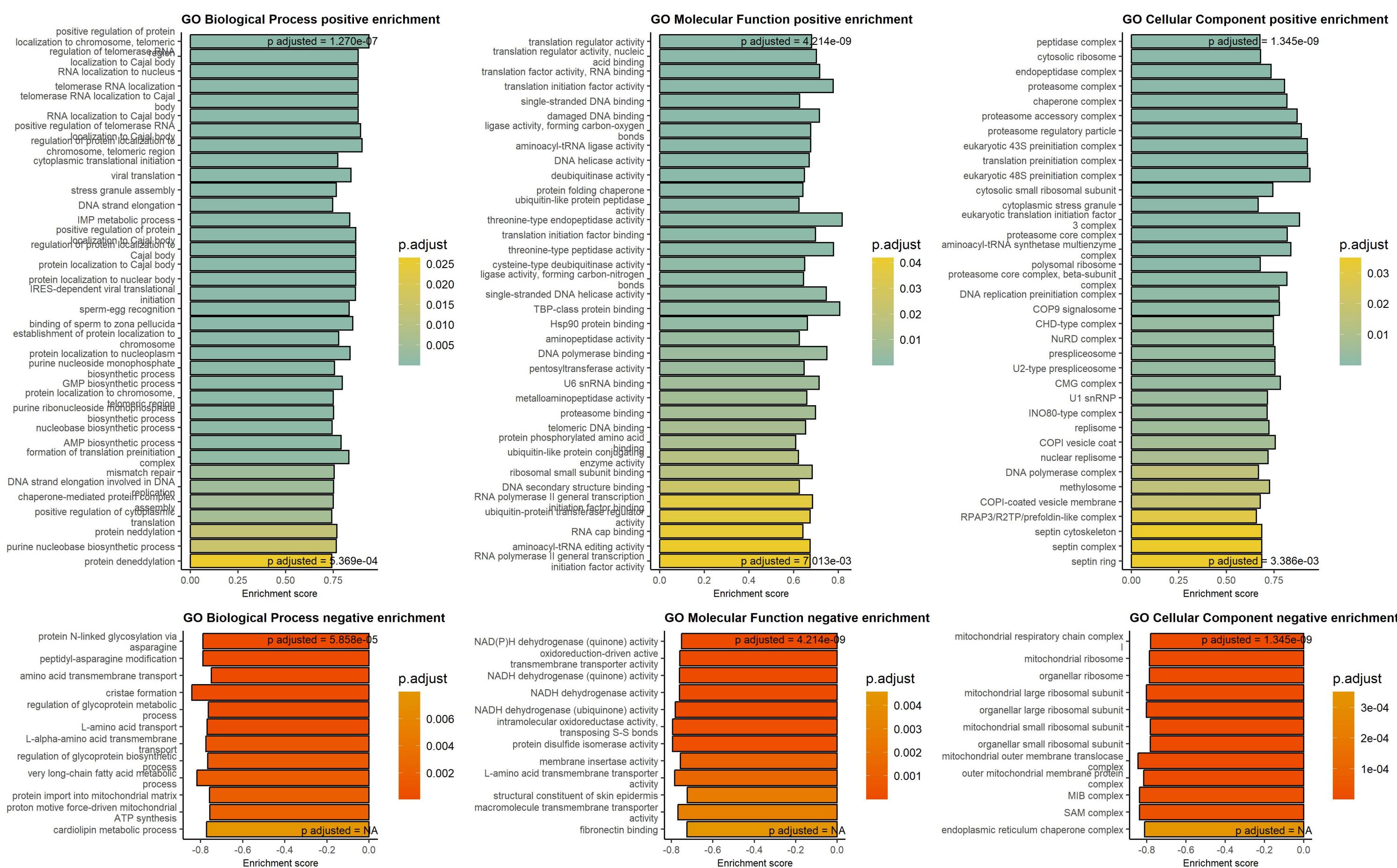


Sorted by p values!							
Downregulated in solid cancers at low/absent APEX1				Upregulated in solid cancers at low/absent APEX1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
1.39	6.11e-51	TP53RK	TP53 regulating kinase	0.05	6.86e-37	PTPRCAP	protein tyrosine phosphatase receptor
1.3	2.00e-50	OSGEP	O-sialoglycoprotein endopeptidase	0.05	6.86e-37	HBE1	hemoglobin subunit epsilon 1
1.38	3.38e-44	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	0.05	6.86e-37	SERPINB10	serpin family B member 10
1.19	1.01e-42	TPRKB	TP53RK binding protein	0.05	6.86e-37	IGLL1	immunoglobulin lambda like polypept
1.01	1.45e-40	GMFB	glia maturation factor beta	0.05	6.86e-37	CRYBB1	crystallin beta B1
0.88	1.68e-40	PPP5C	protein phosphatase 5 catalytic sub	0.05	6.86e-37	ITGA2B	integrin subunit alpha 2b
0.21	6.13e-40	MTHFD1	methylenetetrahydrofolate dehydroge	0.05	6.86e-37	ACAP1	ArfGAP with coiled-coil, ankyrin re
1.12	1.05e-39	PAPOLA	poly(A) polymerase alpha	0.05	6.86e-37	NCF4	neutrophil cytosolic factor 4
1.1	9.11e-39	ENOPH1	enolase-phosphatase 1	0.05	6.86e-37	SP140	SP140 nuclear body protein
1.1	3.74e-38	METTL3	methyltransferase 3, N6-adenosine-m	0.05	6.86e-37	PSTPIP1	proline-serine-threonine phosphatas
0.19	1.05e-37	FARSB	phenylalanyl-tRNA synthetase subuni	0.05	6.86e-37	STAB1	stabilin 1
1.17	6.86e-37	ADI1	acireductone dioxygenase 1	0.05	6.86e-37	SELPLG	selectin P ligand
0.22	6.86e-37	FKBP3	FKBP prolyl isomerase 3	0.05	6.86e-37	RCSD1	RCSD domain containing 1
1.22	6.86e-37	PDXP	pyridoxal phosphatase	0.05	6.86e-37	STAT5A	signal transducer and activator of
0.68	6.86e-37	WDR77	WD repeat domain 77	0.05	6.86e-37	CTSW	cathepsin W
1.33	8.99e-37	C11orf54	chromosome 11 open reading frame 54	0.05	6.86e-37	GIMAP6	GTPase, IMAP family member 6
0.27	1.82e-36	NEDD8	NEDD8 ubiquitin like modifier	0.05	6.86e-37	GZMB	granzyme B
1.04	2.57e-36	NUBP2	NUBP iron-sulfur cluster assembly f	0.05	6.86e-37	HK3	hexokinase 3
0.99	4.84e-36	PPP4R3A	protein phosphatase 4 regulatory su	0.05	6.86e-37	TUBA8	tubulin alpha 8
0.84	7.65e-36	PRMT5	protein arginine methyltransferase	0.05	6.86e-37	CR2	complement C3d receptor 2
1.15	9.20e-36	PHPT1	phosphohistidine phosphatase 1	0.05	6.86e-37	POU2F2	POU class 2 homeobox 2
0.97	2.35e-35	PPP2R5E	protein phosphatase 2 regulatory su	0.05	6.86e-37	AZU1	azurocidin 1
1.1	3.58e-35	TBCC	tubulin folding cofactor C	0.05	6.86e-37	CD48	CD48 molecule
0.84	4.03e-35	NAA10	N-alpha-acetyltransferase 10, NatA	0.05	6.86e-37	SKAP2	src kinase associated phosphoprotei
1.15	4.30e-35	LZIC	leucine zipper and CTNNBIP1 domain	0.05	6.86e-37	CCL17	C-C motif chemokine ligand 17
1.06	6.35e-35	GMPPB	GDP-mannose pyrophosphorylase B	0.05	6.86e-37	ADA2	adenosine deaminase 2
0.95	1.23e-34	THUMPD1	THUMP domain containing 1	0.05	6.86e-37	CD3E	CD3 epsilon subunit of T-cell recep
1.4	2.15e-34	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.05	6.86e-37	RNASE2	ribonuclease A family member 2
1.02	2.71e-34	UBE3A	ubiquitin protein ligase E3A	0.05	6.86e-37	TEX11	testis expressed 11
1.26	5.32e-34	UBR7	ubiquitin protein ligase E3 compone	0.05	6.86e-37	PLEK	pleckstrin
0.81	1.69e-33	SEPHS1	selenophosphate synthetase 1	0.05	6.86e-37	CD300A	CD300a molecule
0.09	3.62e-33	PSMC6	proteasome 26S subunit, ATPase 6	0.05	6.86e-37	GZMA	granzyme A
1.1	3.83e-33	CHD8	chromodomain helicase DNA binding p	0.05	6.86e-37	SIGLEC12	sialic acid binding Ig like lectin
0.89	7.76e-33	ADSL	adenylosuccinate lyase	0.05	6.86e-37	SMIM24	small integral membrane protein 24
0.1	8.78e-33	PPP2R1A	protein phosphatase 2 scaffold subu	0.05	6.86e-37	ALOX15	arachidonate 15-lipoxygenase
1.05	8.93e-33	CHMP4A	charged multivesicular body protein	0.05	6.86e-37	GZMM	granzyme M
0.2	2.30e-32	RANBP1	RAN binding protein 1	0.05	6.86e-37	ARHGAP9	Rho GTPase activating protein 9
0.87	2.90e-32	ILKAP	ILK associated serine/threonine pho	0.05	6.86e-37	NINJ2	ninjurin 2

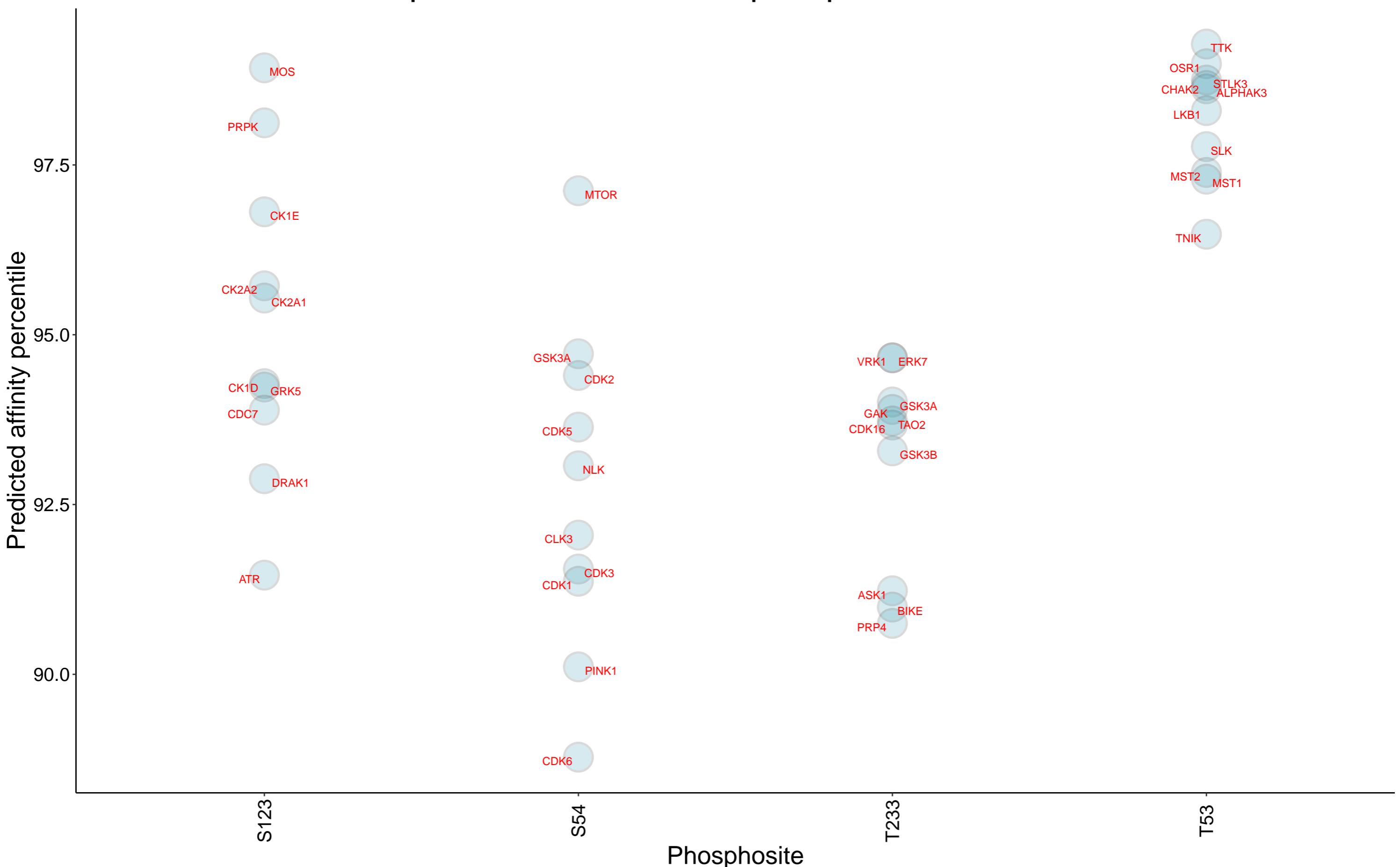
# Top 250 correlation coefficients overrepresentation, APEX1 protein, DB1



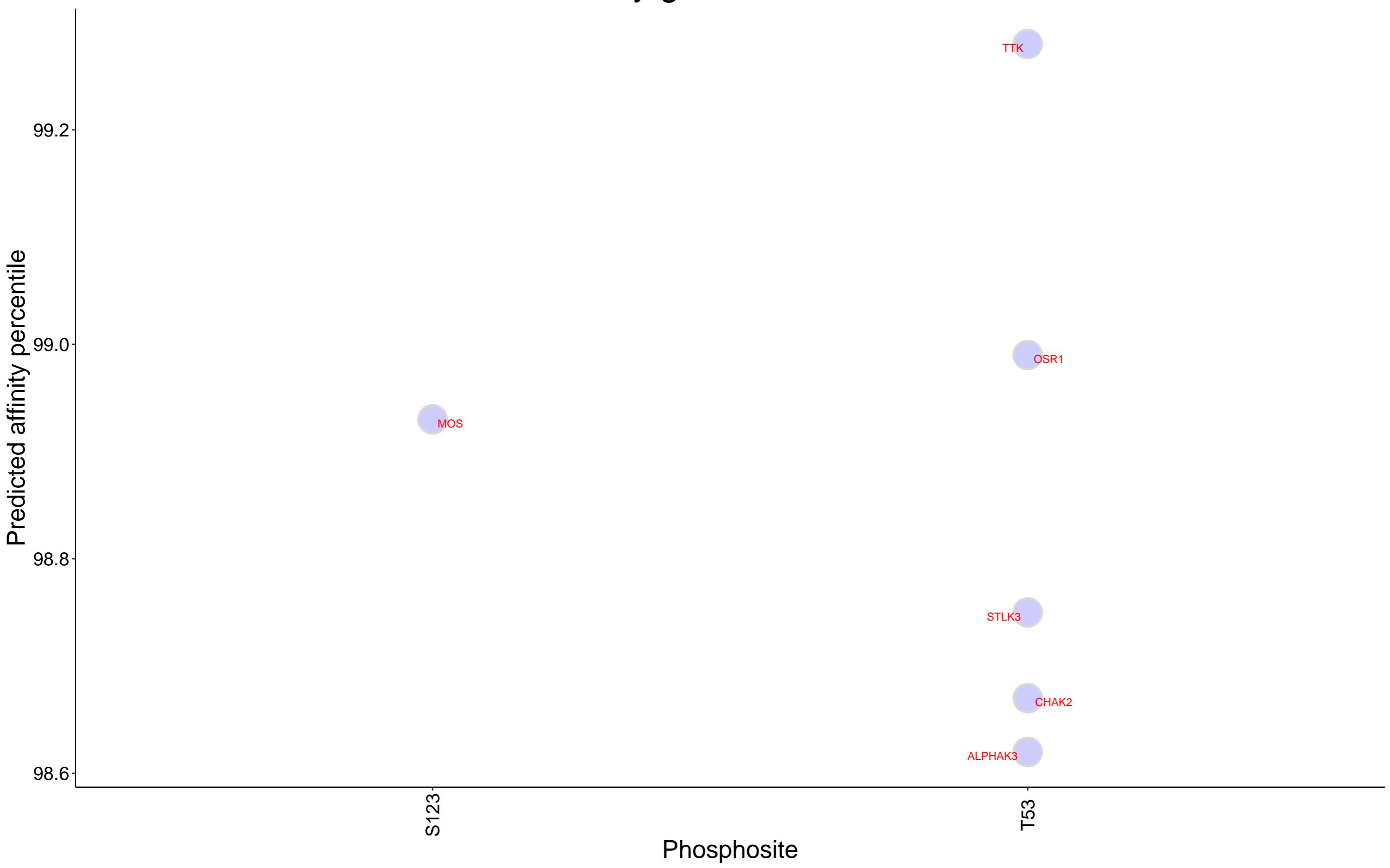
## Gene Set Enrichment analysis on protein correlation coefficients, APEX1 protein, DB1



# Top 10 kinases for each phosphosite in APEX1



Kinases with affinity greater than 98.5% to APEX1



## Top 15 positive correlation coefficients for APEX1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

