

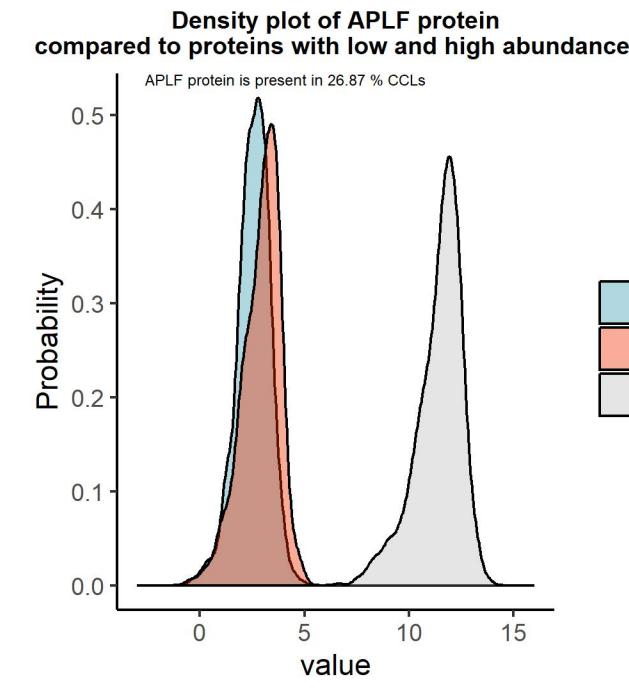
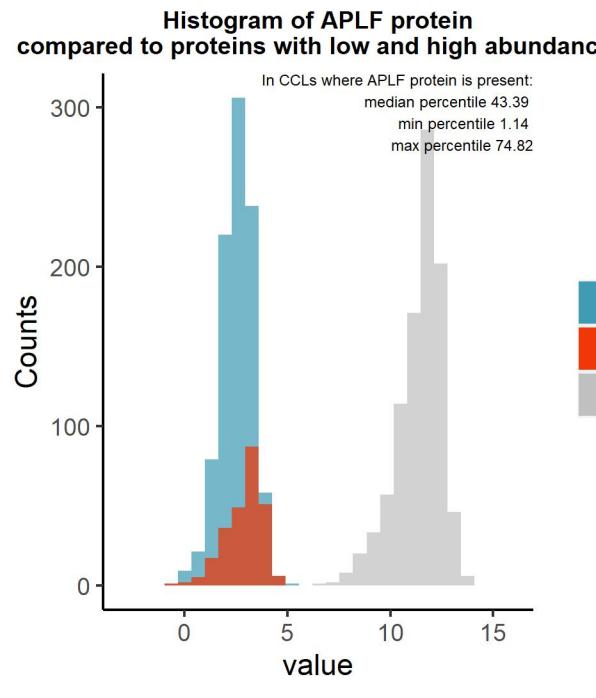
# APLF

Protein name: APLF ; UNIPROT: Q8IW19 ; Gene name: aprataxin and PNKP like factor

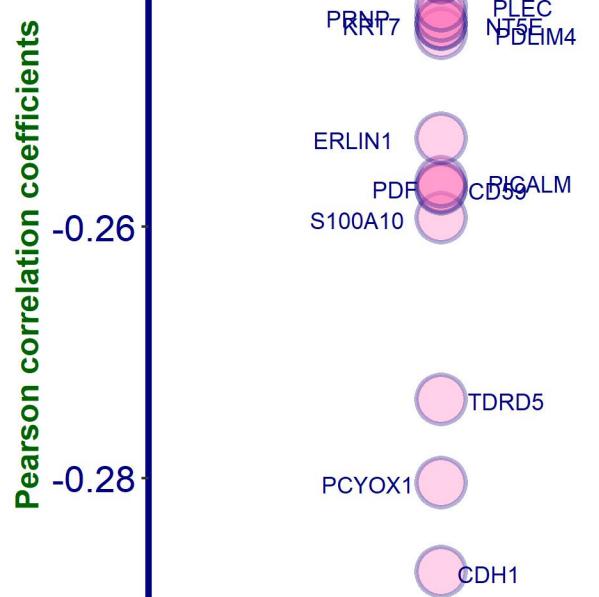
Ligandable: Yes ; Ligandable\_by\_Chem: NA ; Is\_enzyme: Yes (<https://cansar.ai/>)

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

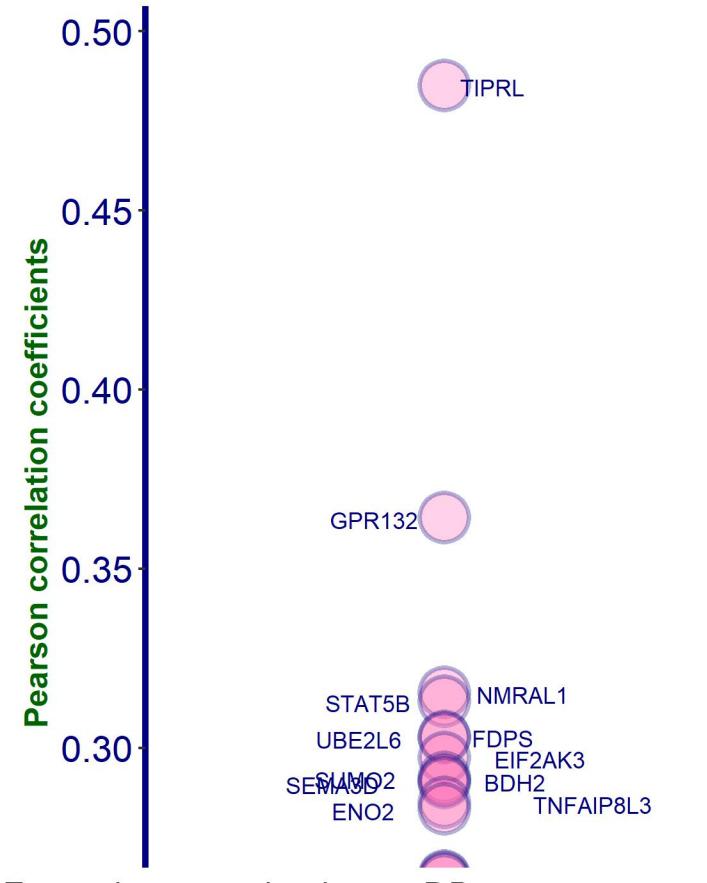
8498 proteins in same 949 CCLs



## Negative correlations of APLF protein, DB2

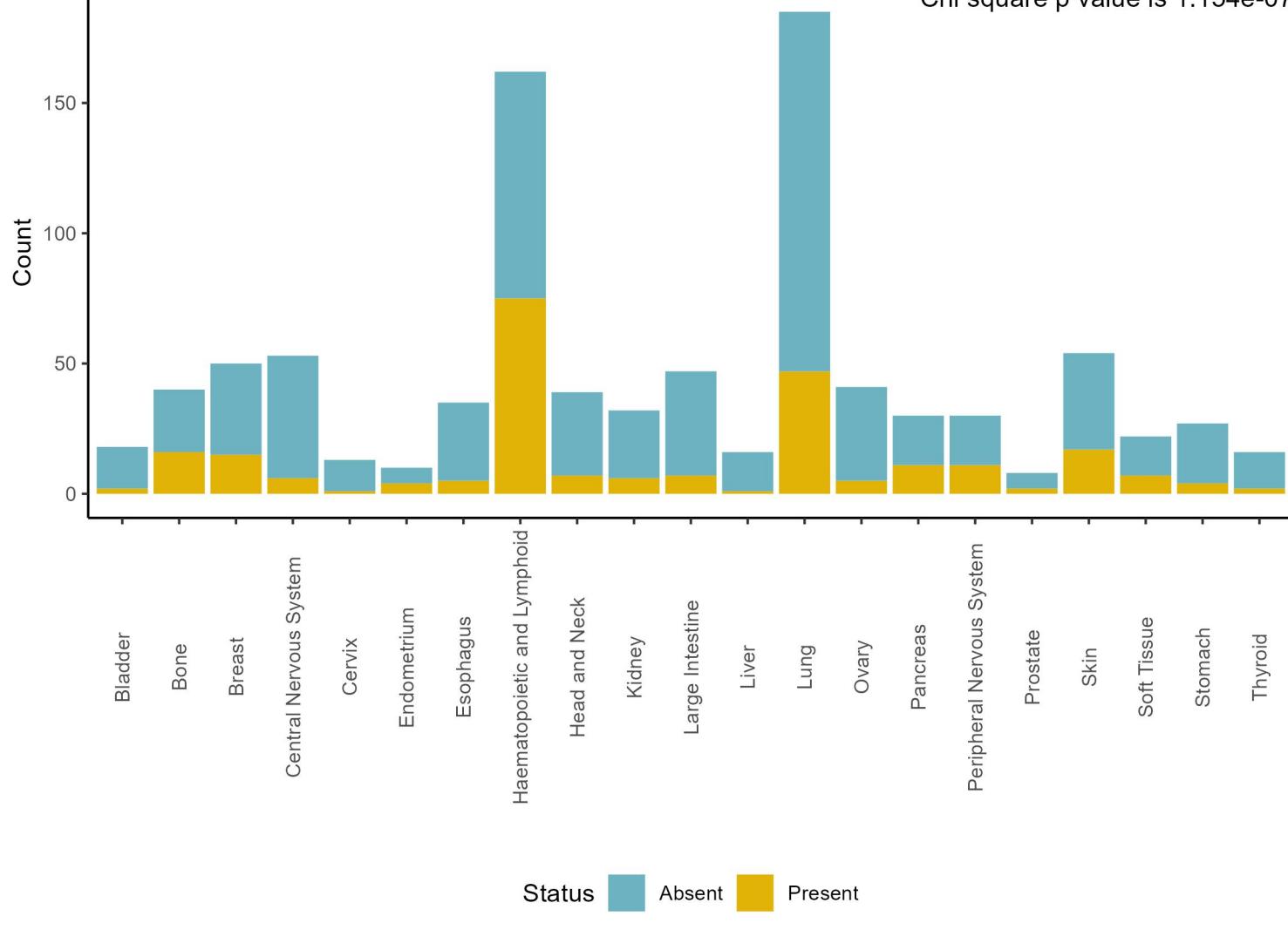
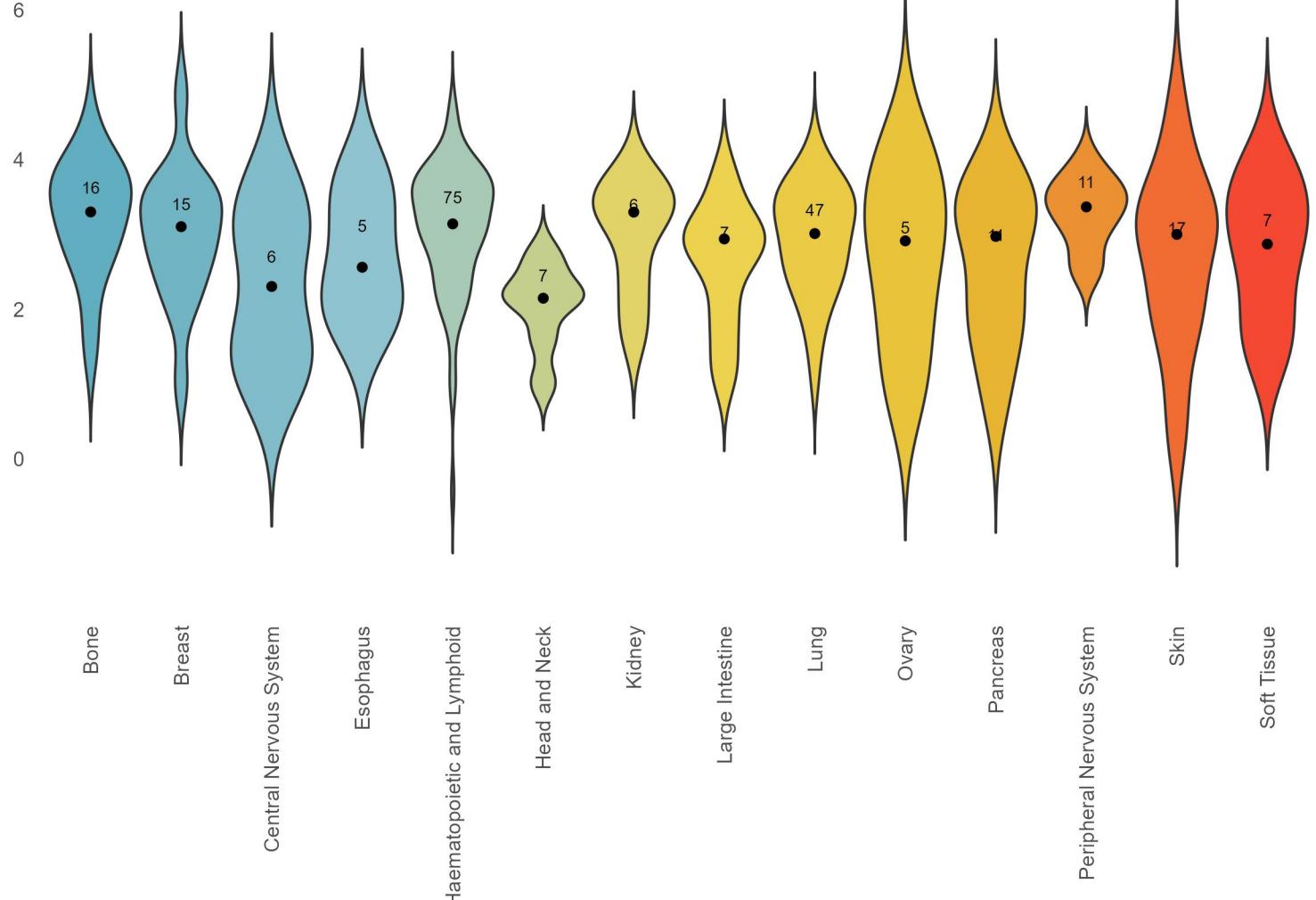


## Positive correlations of APLF protein, DB2



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

ANOVA p value is 1.422e-01

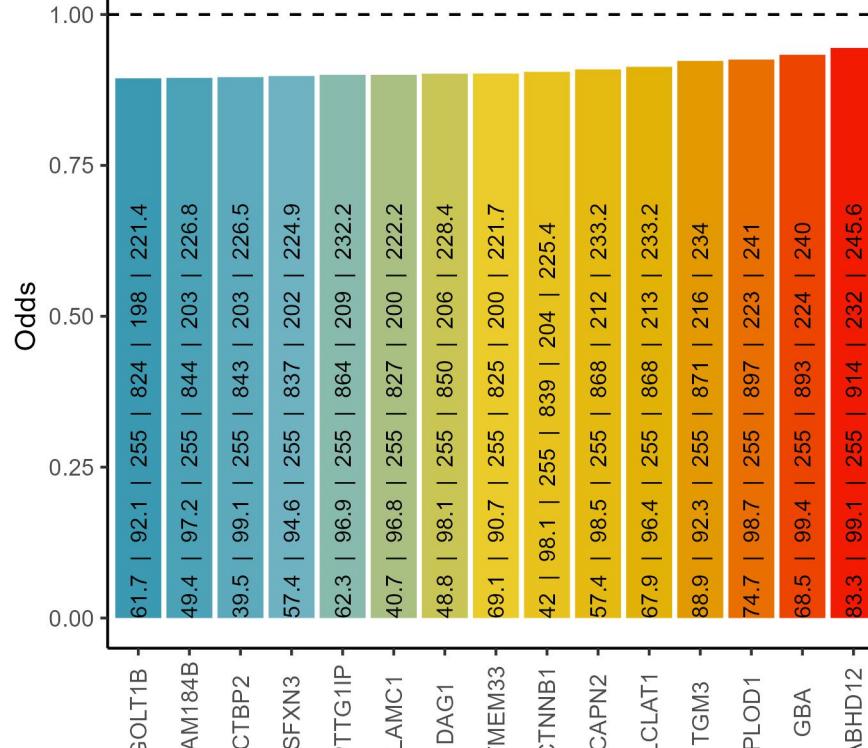


## Cooccurrence with APLF protein, DB2

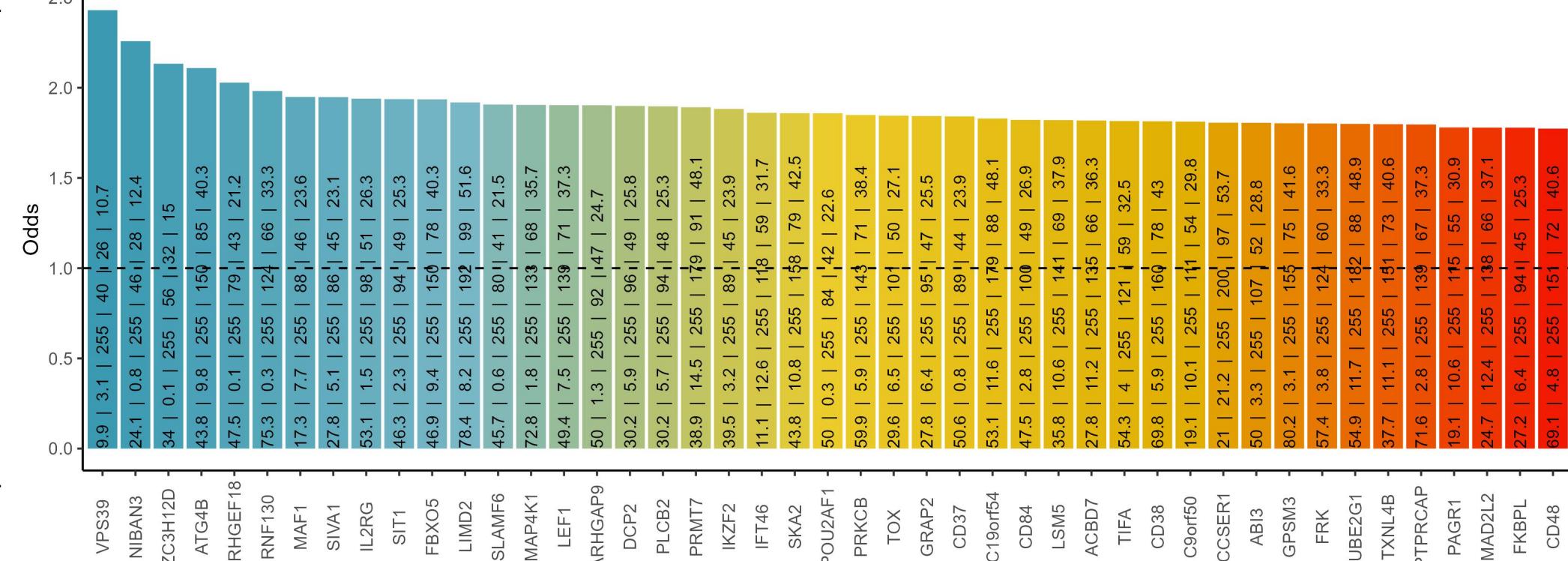
% of APLF in blood cancers: 46.3 ; % of APLF in solid cancers: 22.8

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

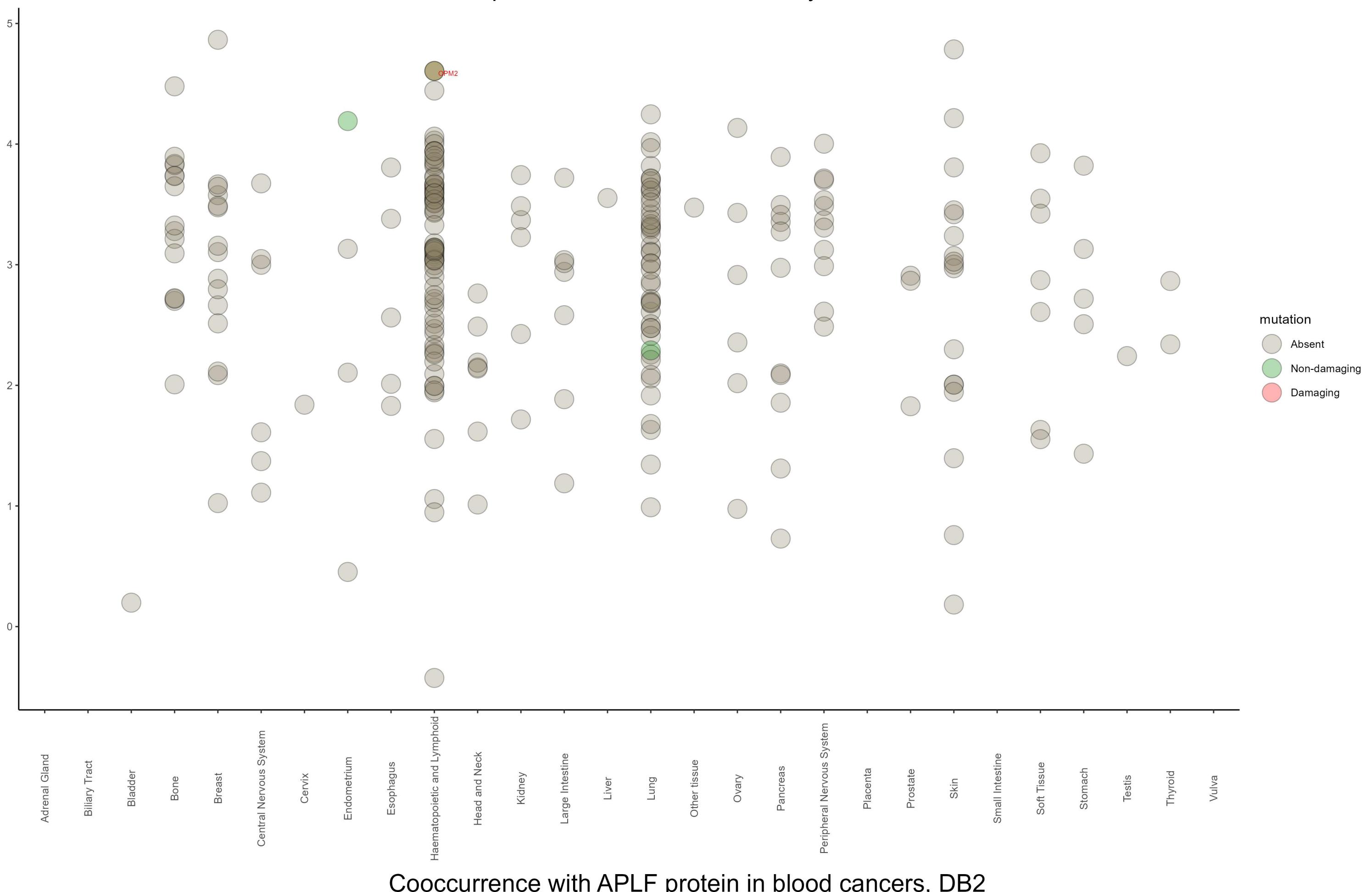
### Negative cooccurrence



### Positive cooccurrence

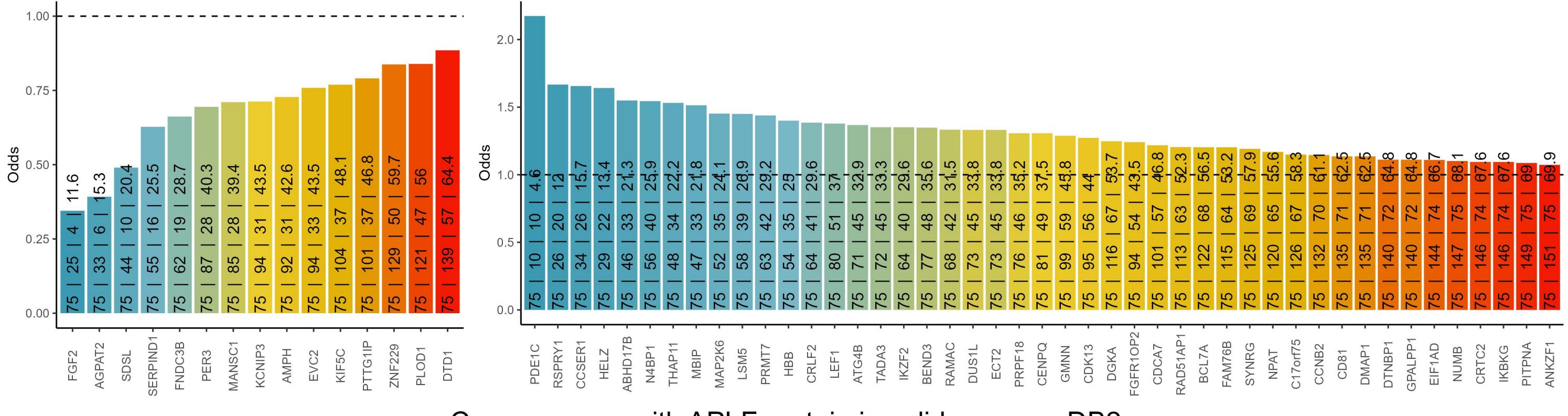


# Amount of APLF protein and mutation status by tissue, DB2



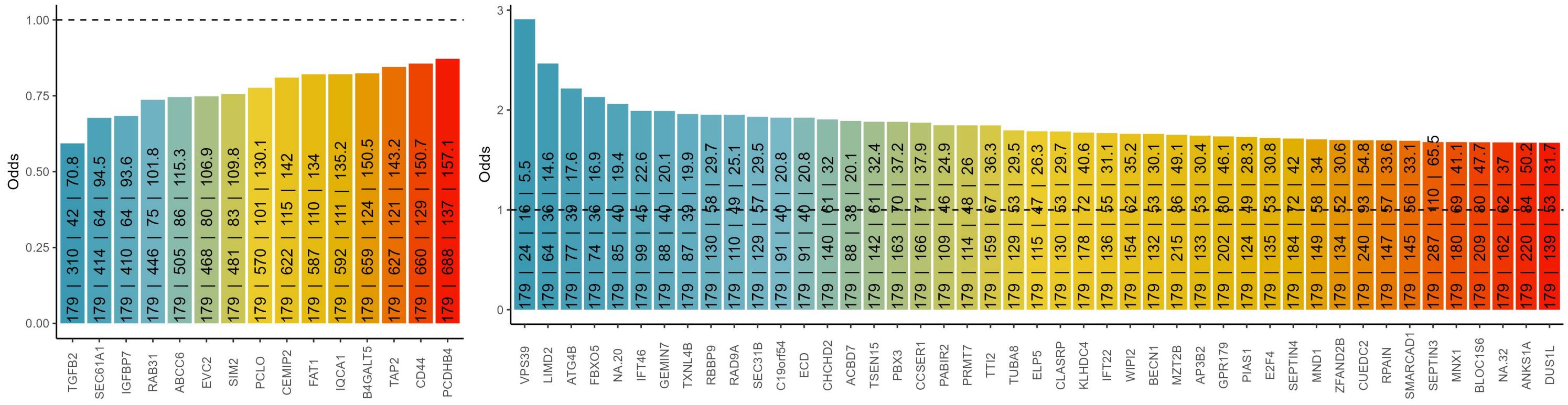
## Cooccurrence with APLF protein in blood cancers, DB2

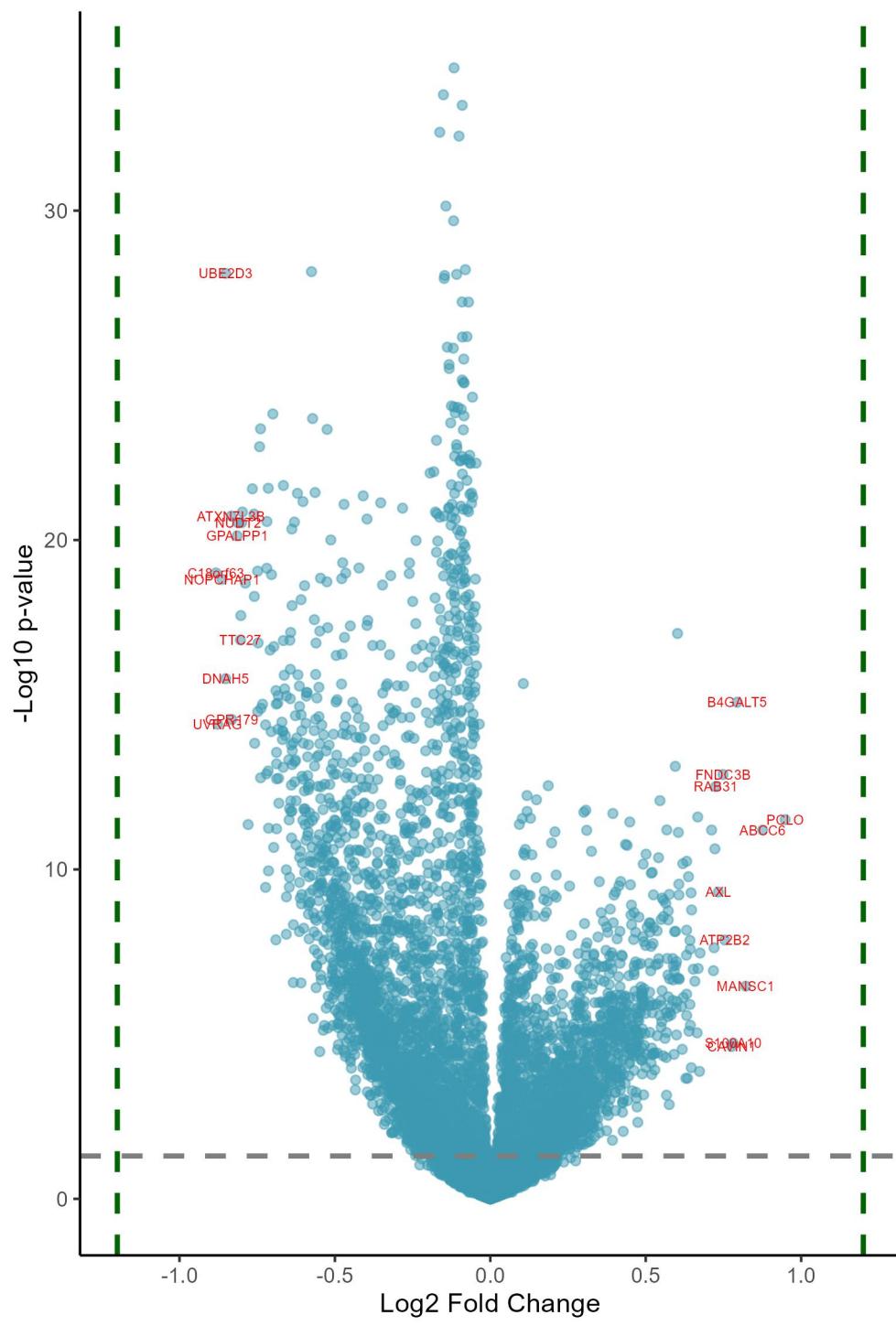
The text in the bars: incidence of APLF | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with APLF protein in solid cancers, DB2

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

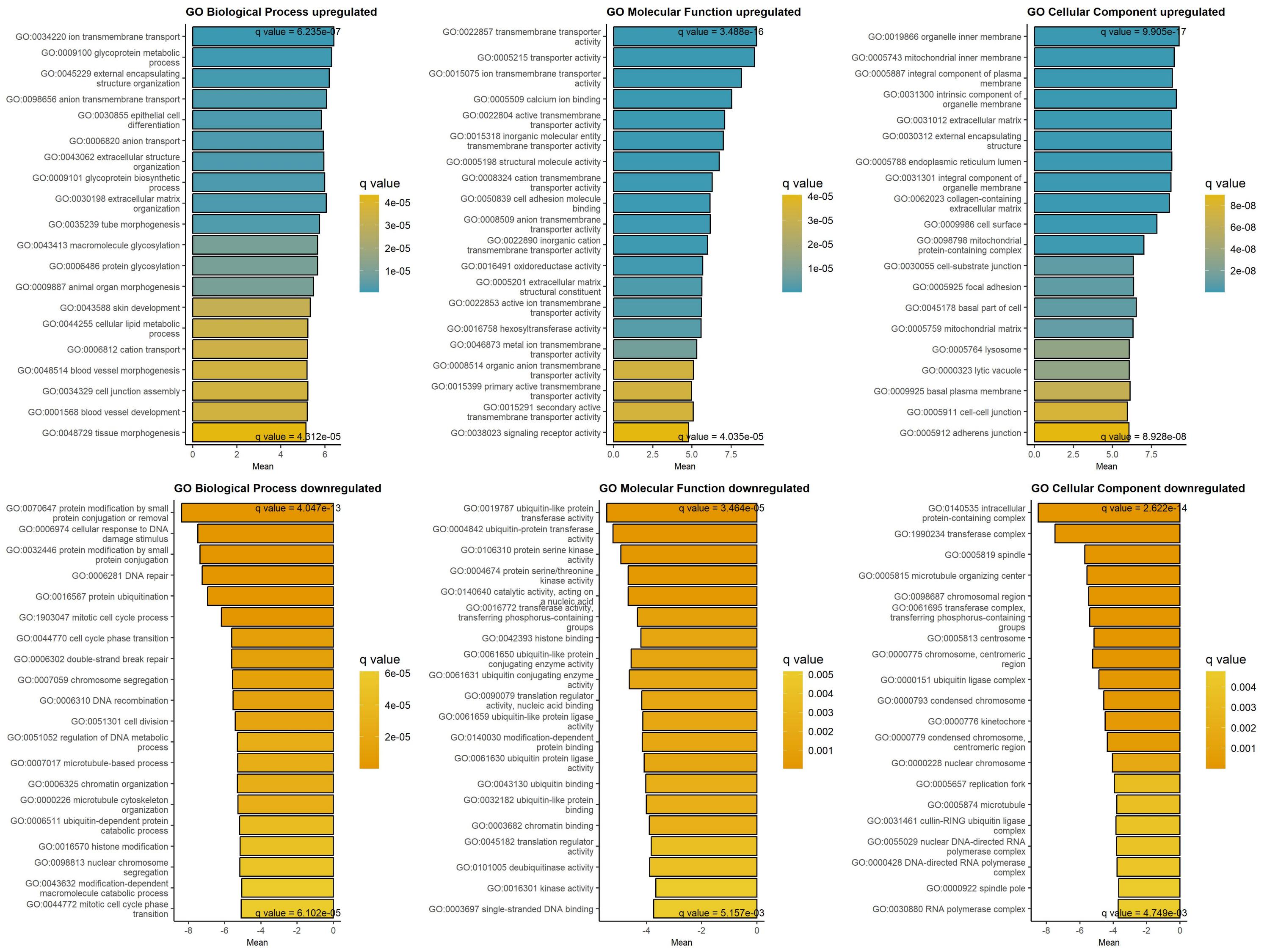


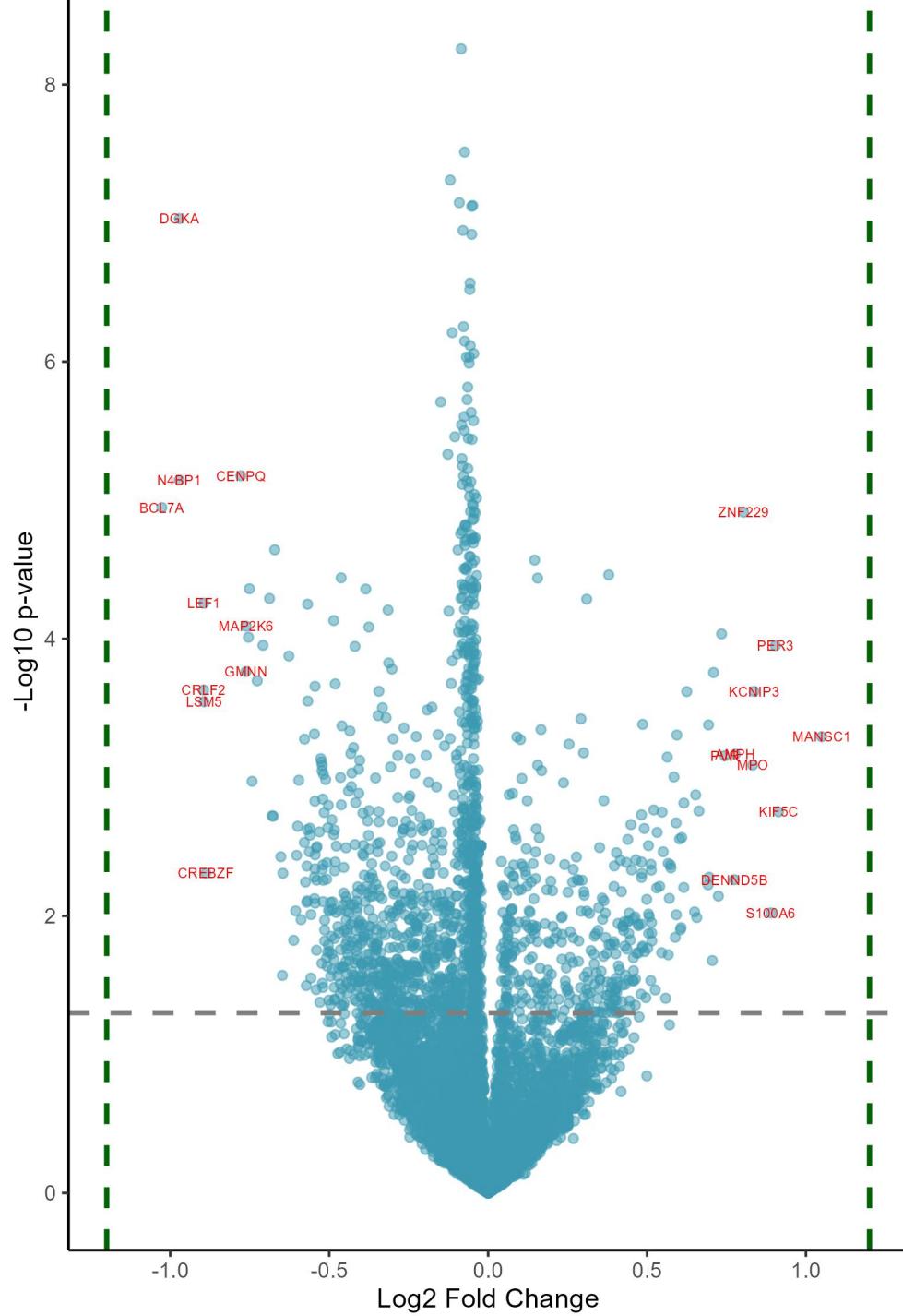


## Downregulated at low/absent APLF Upregulated at low/absent APLF

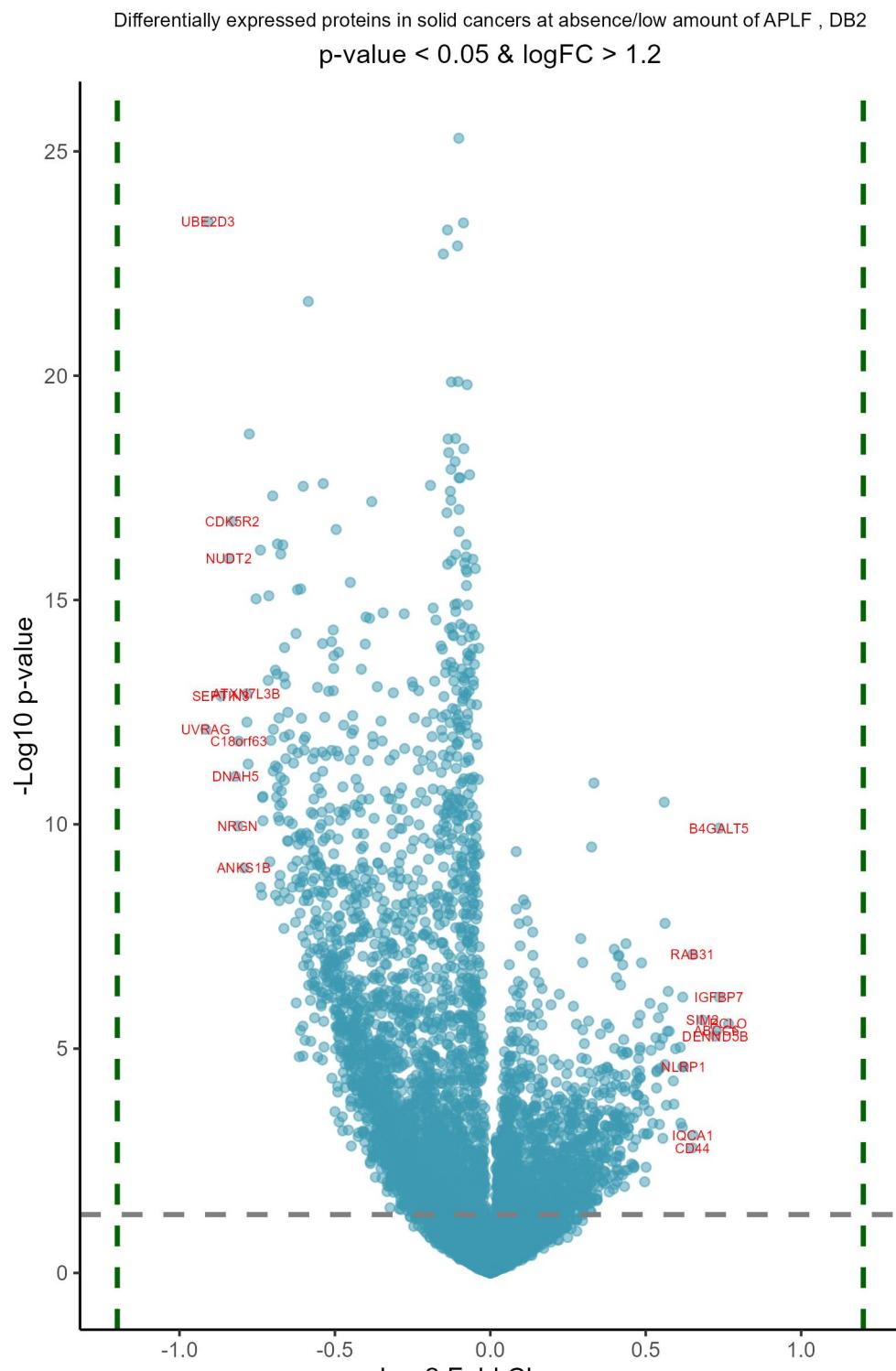
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.88	6.55e-18	C18orf63	chromosome 18 open reading frame 63	0.95	4.60e-11	PCLO	piccolo presynaptic cytomatrix prot
-0.88	9.97e-14	UVRAG	UV radiation resistance associated	0.88	8.91e-11	ABCC6	ATP binding cassette subfamily C me
-0.86	9.33e-18	NOPCHAP1	NOP protein chaperone 1	0.82	1.96e-06	MANSC1	MANSC domain containing 1
-0.85	5.53e-15	DNAH5	dynein axonemal heavy chain 5	0.79	2.51e-14	B4GALT5	beta-1,4-galactosyltransferase 5
-0.85	5.99e-26	UBE2D3	ubiquitin conjugating enzyme E2 D3	0.78	6.84e-05	S100A10	S100 calcium binding protein A10
-0.83	1.79e-19	ATXN7L3B	ataxin 7 like 3B	0.78	8.48e-05	CAVIN1	caveolae associated protein 1
-0.83	7.41e-14	GPR179	G protein-coupled receptor 179	0.75	1.04e-07	ATP2B2	ATPase plasma membrane Ca <sup>2+</sup> transpo
-0.81	6.13e-19	GPALPP1	GPALPP motifs containing 1	0.75	2.55e-12	FNDC3B	fibronectin type III domain contain
-0.81	2.60e-19	NUDT2	nudix hydrolase 2	0.73	4.87e-09	AXL	AXL receptor tyrosine kinase
-0.8	4.68e-16	TTC27	tetratricopeptide repeat domain 27	0.72	5.61e-12	RAB31	RAB31, member RAS oncogene family
-0.8	9.91e-17	DCAF16	DDB1 and CUL4 associated factor 16	0.72	3.04e-10	KRT74	keratin 74
-0.8	2.60e-19	CRLF3	cytokine receptor like factor 3	0.72	1.71e-07	BEX4	brain expressed X-linked 4
-0.8	1.41e-19	CDK5R2	cyclin dependent kinase 5 regulator	0.72	7.35e-07	DENN5B	DENN domain containing 5B
-0.79	1.18e-17	ASF1B	anti-silencing function 1B histone	0.71	8.91e-11	CACUL1	CDK2 associated cullin domain 1
-0.78	6.30e-11	CREBZF	CREB/ATF bZIP transcription factor	0.67	2.42e-07	IGFBP7	insulin like growth factor binding
-0.77	3.76e-20	RANBP6	RAN binding protein 6	0.67	4.05e-04	GNG12	G protein subunit gamma 12
-0.76	1.59e-19	CRYZL1	crystallin zeta like 1	0.67	6.41e-07	TDRD5	tudor domain containing 5
-0.76	2.83e-17	TLK2	tousled like kinase 2	0.67	3.88e-11	SLC35B2	solute carrier family 35 member B2
-0.76	3.36e-13	STK36	serine/threonine kinase 36	0.67	3.62e-05	S100A16	S100 calcium binding protein A16
-0.75	5.88e-18	OARD1	O-acetyl-ADP-ribose deacylase 1	0.66	1.43e-06	ADAM9	ADAM metallopeptidase domain 9
-0.75	4.56e-14	CUEDC2	CUE domain containing 2	0.65	6.70e-07	SIM2	SIM bHLH transcription factor 2
-0.75	5.61e-16	BLOC1S5	biogenesis of lysosomal organelles	0.65	1.53e-08	KCNIP3	potassium voltage-gated channel int
-0.74	2.92e-21	PDE6D	phosphodiesterase 6D	0.65	3.22e-04	NQO1	NAD(P)H quinone dehydrogenase 1
-0.74	9.50e-22	ACBD6	acyl-CoA binding domain containing	0.65	5.14e-09	P3H2	prolyl 3-hydroxylase 2
-0.74	3.16e-12	UBE2B	ubiquitin conjugating enzyme E2 B	0.64	2.26e-05	GPRC5A	G protein-coupled receptor class C
-0.74	3.67e-14	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	0.64	1.88e-07	COL4A2	collagen type IV alpha 2 chain
-0.73	2.83e-14	SYNRG	synergin gamma	0.64	1.06e-07	SDC4	syndecan 4
-0.72	1.04e-13	CHEK1	checkpoint kinase 1	0.64	6.19e-06	MISP	mitotic spindle positioning
-0.72	3.62e-09	ANKS1B	ankyrin repeat and sterile alpha mo	0.64	3.26e-05	EGFR	epidermal growth factor receptor

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



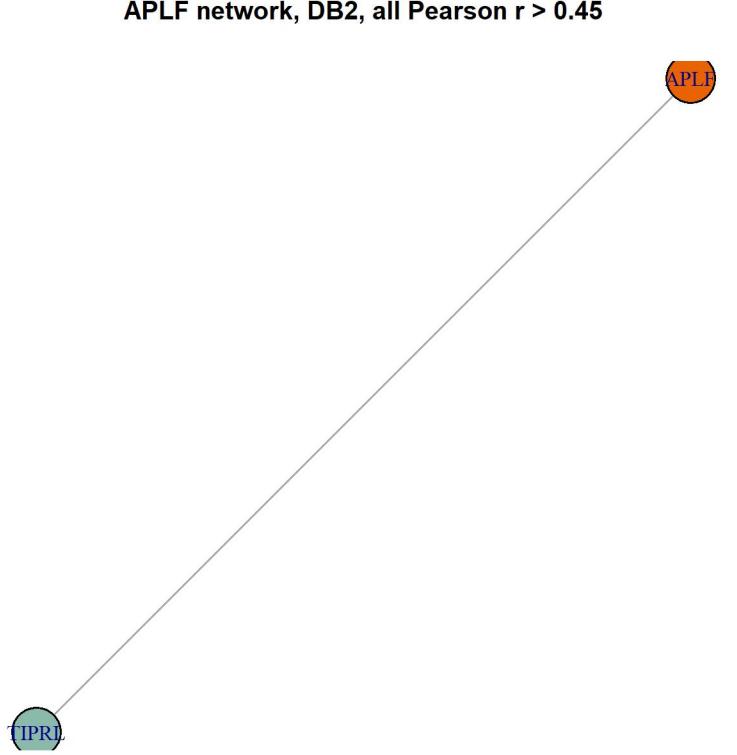


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.03	1.97e-03	BCL7A	BAF chromatin remodeling complex su	1.05	1.88e-02	MANSC1	MANSC domain containing 1
-0.97	1.54e-03	N4BP1	NEED4 binding protein 1	0.91	3.91e-02	KIF5C	kinesin family member 5C
-0.97	9.69e-05	DGKA	diacylglycerol kinase alpha	0.9	7.12e-03	PER3	period circadian regulator 3
-0.89	1.11e-02	CRLF2	cytokine receptor like factor 2	0.89	8.18e-02	S100A6	S100 calcium binding protein A6
-0.89	4.49e-03	LEF1	lymphoid enhancer binding factor 1	0.84	1.12e-02	KCNIP3	potassium voltage-gated channel int
-0.89	1.28e-02	LSM5	LSM5 homolog, U6 small nuclear RNA	0.83	2.69e-02	MPO	myeloperoxidase
-0.89	5.39e-02	CREBZF	CREB/ATF bZIP transcription factor	0.8	1.98e-03	ZNF229	zinc finger protein 229
-0.78	1.51e-03	CENPQ	centromere protein Q	0.78	2.38e-02	AMPH	amphiphysin
-0.76	9.19e-03	GMNN	geminin DNA replication inhibitor	0.77	5.80e-02	DENND5B	DENN domain containing 5B
-0.76	5.90e-03	MAP2K6	mitogen-activated protein kinase ki	0.74	2.40e-02	PVR	PVR cell adhesion molecule
-0.75	6.52e-03	ATG4B	autophagy related 4B cysteine pepti	0.73	6.27e-03	PLOD1	procollagen-lysine,2-oxoglutarate 5
-0.75	3.89e-03	RAD51AP1	RAD51 associated protein 1	0.72	6.88e-02	MYH1	myosin heavy chain 1
-0.74	3.21e-02	LCK	LCK proto-oncogene, Src family tyro	0.71	9.28e-03	SLC35B2	solute carrier family 35 member B2
-0.73	1.02e-02	CCSER1	coiled-coil serine rich protein 1	0.71	1.33e-01	TMEM70	transmembrane protein 70
-0.71	7.12e-03	ABHD17B	abhydrolase domain containing 17B,	0.7	5.66e-02	SIM2	SIM bHLH transcription factor 2
-0.69	4.28e-03	CD81	CD81 molecule	0.69	1.66e-02	FNDC3B	fibronectin type III domain contain
-0.68	3.91e-02	CNTLN	centlein	0.69	6.14e-02	STOM	stomatin
-0.68	3.91e-02	HDGFL3	HDGF like 3	0.66	3.91e-02	EVC2	EvC ciliary complex subunit 2
-0.67	2.73e-03	SYNRG	synergin gamma	0.66	8.56e-02	NLRP1	NLR family pyrin domain containing
-0.65	4.44e-02	CD38	CD38 molecule	0.65	3.77e-02	CYP51A1	cytochrome P450 family 51 subfamily
-0.65	1.55e-01	KIAA0100	KIAA0100	0.65	8.11e-02	WDPCP	WD repeat containing planar cell po
-0.65	5.39e-02	FAM117B	family with sequence similarity 117	0.62	1.12e-02	AGPAT2	1-acylglycerol-3-phosphate O-acyltr
-0.63	7.63e-03	CENPV	centromere protein V	0.62	3.91e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.61	1.08e-01	SEPTIN1	septin 1	0.62	6.30e-02	GBA	glucosylceramidase beta
-0.61	8.06e-02	ZSWIM8	zinc finger SWIM-type containing 8	0.61	3.91e-02	PTTG1IP	PTTG1 interacting protein
-0.6	4.37e-02	DBN1	drebrin 1	0.61	9.43e-02	DNHD1	dynein heavy chain domain 1
-0.6	3.91e-02	WASF1	WASP family member 1	0.6	9.64e-02	LCLAT1	lysocardiolipin acyltransferase 1
-0.6	3.17e-02	KIF16B	kinesin family member 16B	0.6	3.91e-02	C15orf62	chromosome 15 open reading frame 62
-0.59	8.76e-02	FREM3	FRAS1 related extracellular matrix	0.59	1.86e-02	SDSL	serine dehydratase like

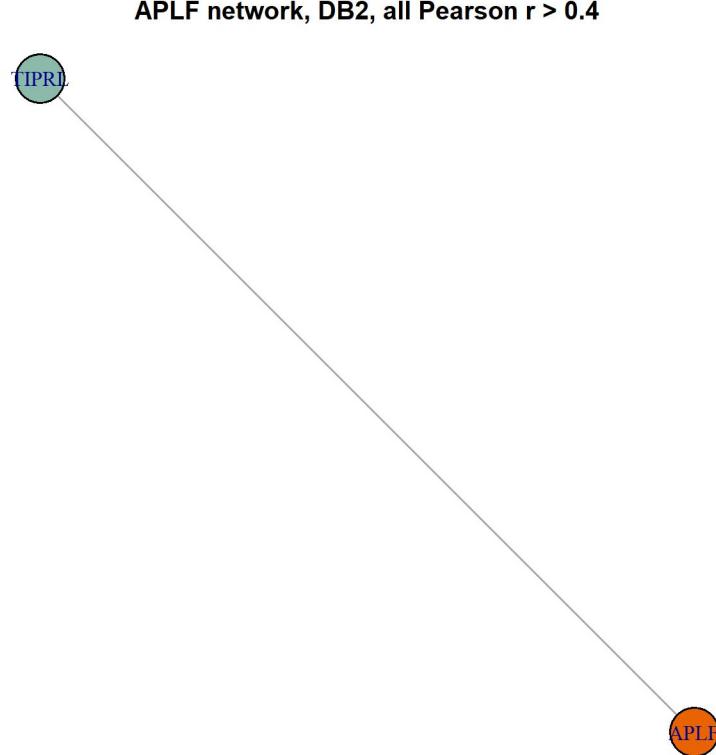


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.92	4.02e-11	UVRAG	UV radiation resistance associated	0.77	2.31e-05	PCLO	piccolo presynaptic cytomatrix prot
-0.91	8.23e-21	UBE2D3	ubiquitin conjugating enzyme E2 D3	0.74	3.20e-09	B4GALT5	beta-1,4-galactosyltransferase 5
-0.87	9.00e-12	SEPTIN3	septin 3	0.74	7.04e-06	IGFBP7	insulin like growth factor binding
-0.84	2.44e-14	NUDT2	nudix hydrolase 2	0.73	3.11e-05	ABCC6	ATP binding cassette subfamily C me
-0.83	4.76e-15	CDK5R2	cyclin dependent kinase 5 regulator	0.72	4.06e-05	DENND5B	DENN domain containing 5B
-0.82	3.25e-10	DNAH5	dynein axonemal heavy chain 5	0.68	1.96e-05	SIM2	SIM bHLH transcription factor 2
-0.81	2.90e-09	NRGN	neurogranin	0.65	3.30e-03	IQCA1	IQ motif containing with AAA domain
-0.81	6.66e-11	C18orf63	chromosome 18 open reading frame 63	0.65	9.94e-07	RAB31	RAB31, member RAS oncogene family
-0.79	1.93e-08	ANKS1B	ankyrin repeat and sterile alpha mo	0.65	5.71e-03	CD44	CD44 molecule (Indian blood group)
-0.78	8.15e-12	ATXN7L3B	ataxin 7 like 3B	0.62	1.62e-04	NLRP1	NLR family pyrin domain containing
-0.78	2.92e-11	DCAF16	DBB1 and CUL4 associated factor 16	0.62	1.62e-04	MYH1	myosin heavy chain 1
-0.78	1.81e-10	NOPCHAP1	NOP protein chaperone 1	0.62	7.03e-06	KCNIP3	potassium voltage-gated channel int
-0.78	1.39e-16	ACBD6	acyl-CoA binding domain containing	0.62	2.35e-03	MANSC1	MANSC domain containing 1
-0.75	1.46e-13	RANBP6	RAN binding protein 6	0.61	1.97e-03	TMEM70	transmembrane protein 70
-0.74	1.75e-14	PDE6D	phosphodiesterase 6D	0.61	6.77e-05	KRT74	keratin 74
-0.74	4.59e-08	GPR179	G protein-coupled receptor 179	0.6	7.23e-05	TGFBI	transforming growth factor beta ind
-0.74	6.49e-08	CREBZF	CREB/ATF bZIP transcription factor	0.59	8.67e-04	BORCS8-MEF2B	BORCS8-MEF2B readthrough
-0.73	8.40e-10	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	0.59	3.07e-04	AXL	AXL receptor tyrosine kinase
-0.73	8.01e-10	TTC27	tetratricopeptide repeat domain 27	0.58	3.22e-05	P3H2	prolyl 3-hydroxylase 2
-0.73	2.27e-09	ASPA	aspartoacylase	0.57	5.41e-06	FAT1	FAT atypical cadherin 1
-0.71	4.84e-12	CRYZL1	crystallin zeta like 1	0.57	3.23e-05	PER3	period circadian regulator 3
-0.71	1.27e-13	ACYP1	acylphosphatase 1	0.57	9.07e-04	CCDC170	coiled-coil domain containing 170
-0.71	1.48e-08	STK36	serine/threonine kinase 36	0.56	2.37e-07	TGFB2	transforming growth factor beta 2
-0.71	6.47e-11	PCSK6	proprotein convertase subtilisin/ke	0.56	1.47e-04	RYR1	ryanodine receptor 1
-0.7	1.54e-15	RPE	ribulose-5-phosphate-3-epimerase	0.56	1.02e-09	SEC61A1	SEC61 translocon subunit alpha 1
-0.7	2.51e-10	KIF3A	kinesin family member 3A	0.56	1.13e-05	CEMIP2	cell migration inducing hyaluronida
-0.7	4.02e-11	EIF4EBP1	eukaryotic translation initiation f	0.56	3.78e-03	VAMP8	vesicle associated membrane protein
-0.69	3.13e-12	VPS26B	VPS26, retromer complex component B	0.55	4.50e-05	TAP1	transporter 1, ATP binding cassette
-0.69	1.97e-10	EIF1AX	eukaryotic translation initiation f	0.55	6.11e-05	EVC2	EvC ciliary complex subunit 2

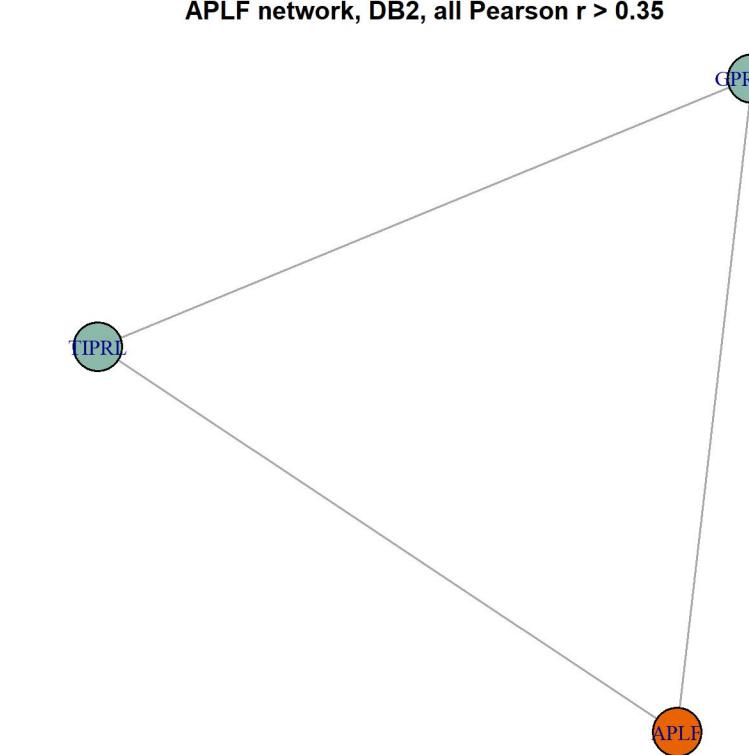
APLF network, DB2, all Pearson r &gt; 0.45



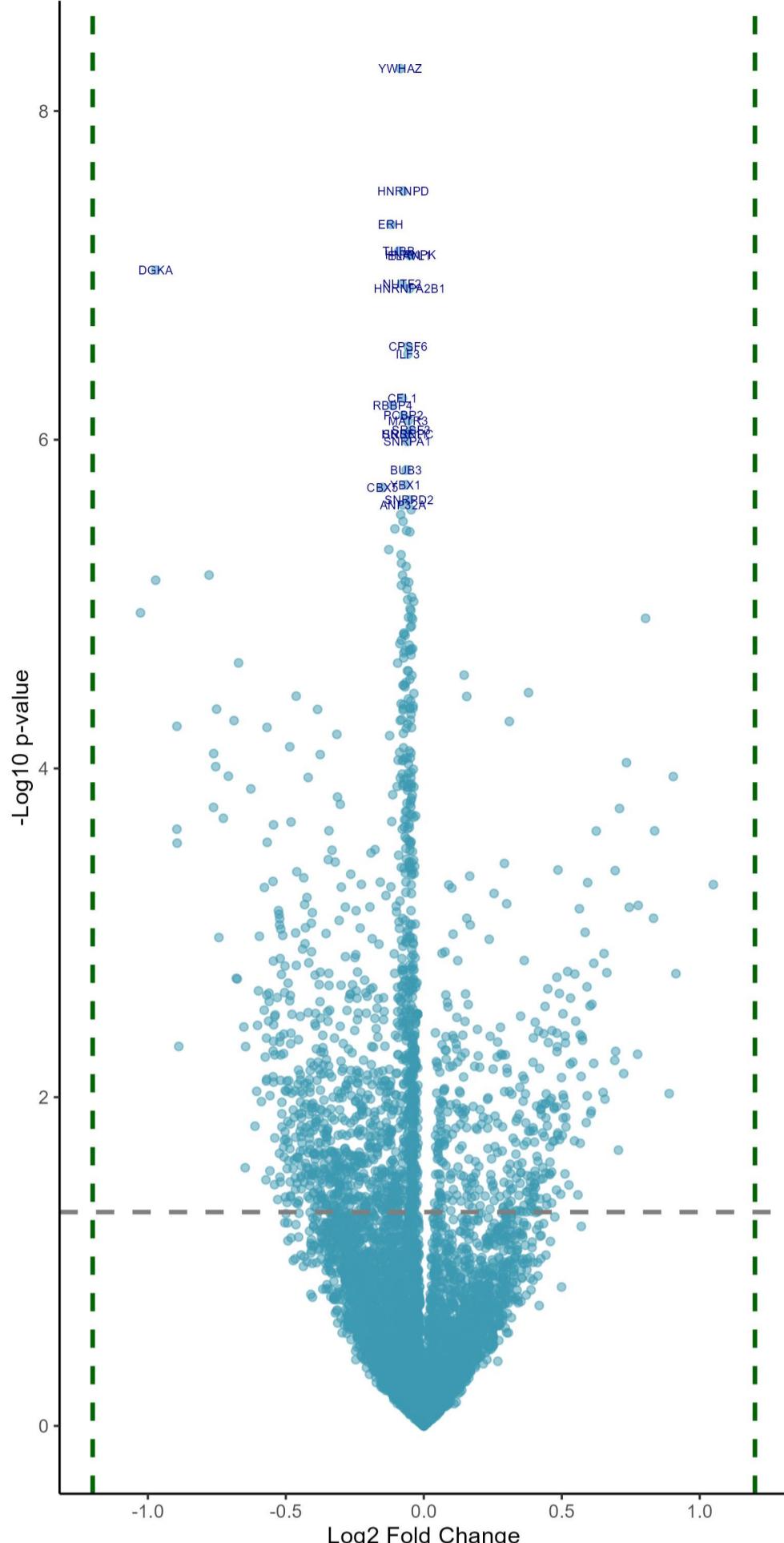
APLF network, DB2, all Pearson r &gt; 0.4



APLF network, DB2, all Pearson r &gt; 0.35

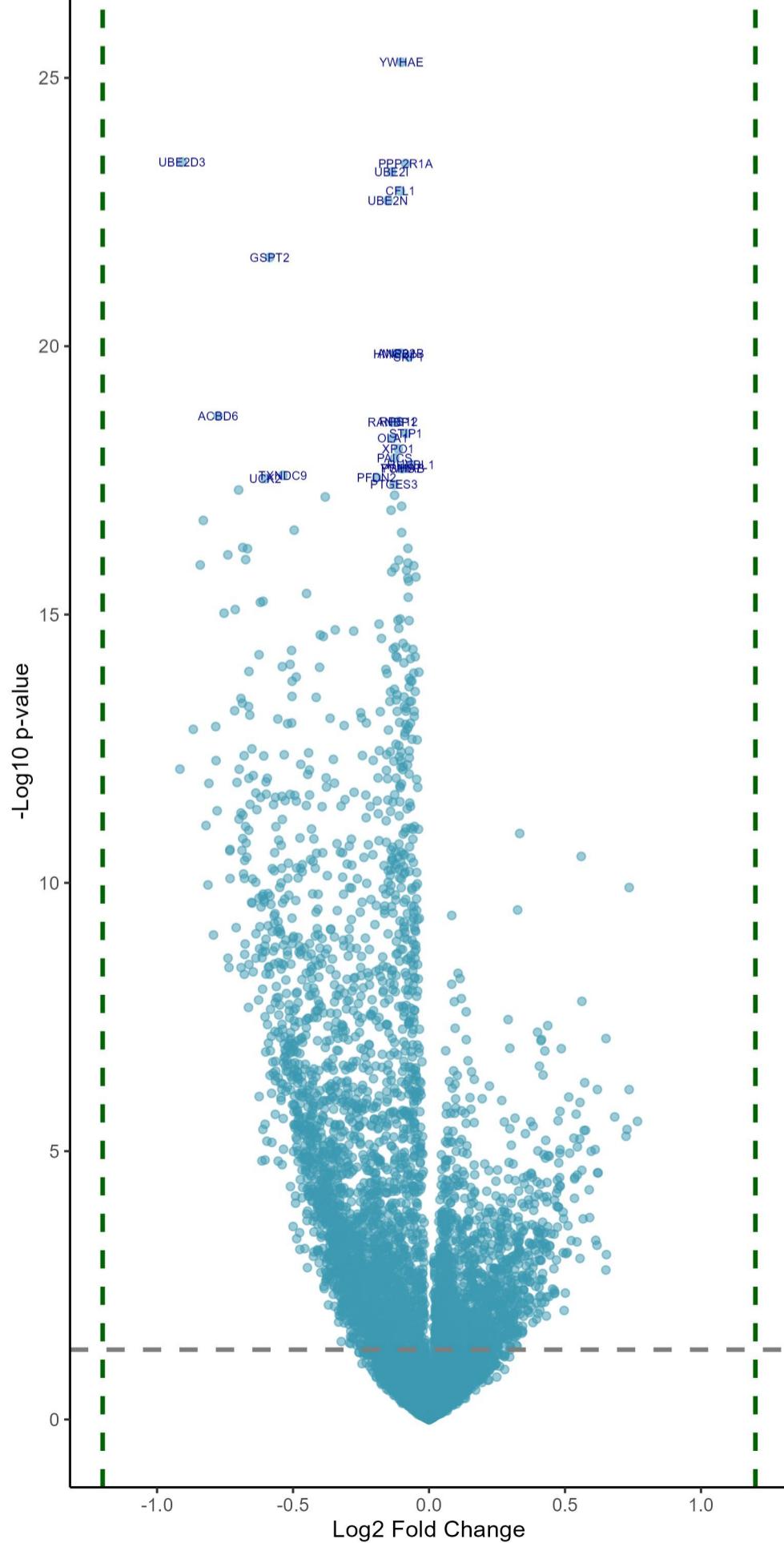


Sorted by p values!  
 Downregulated in blood cancers at low/absent APLF      Upregulated in blood cancers at low/absent APLF



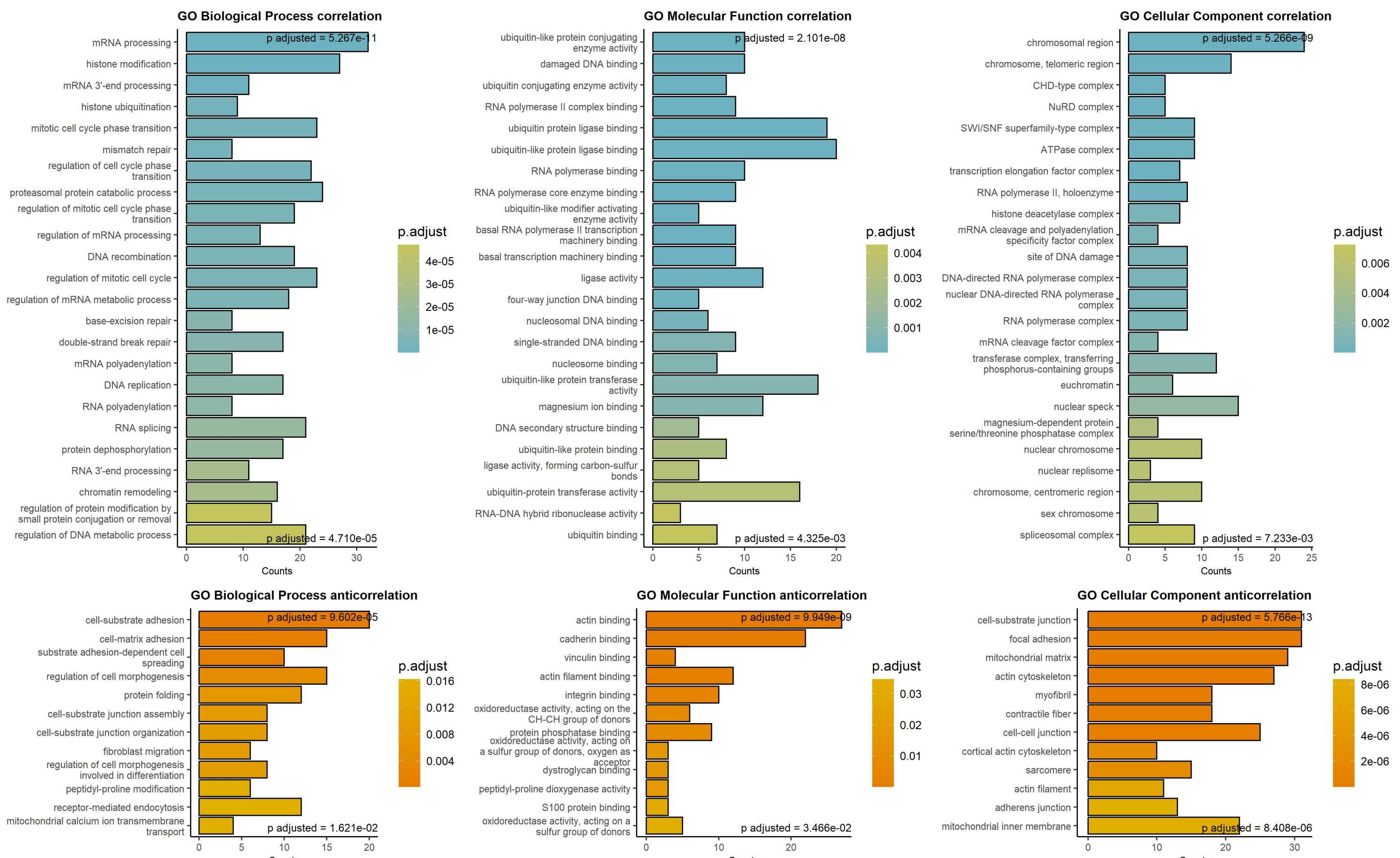
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.08	2.31e-05	YWHAZ	tyrosine 3-monoxygenase/trypophan	0.8	1.98e-03	ZNF229	zinc finger protein 229
-0.07	8.56e-05	HNRNPD	heterogeneous nuclear ribonucleoprotein D	0.15	3.07e-03	MOGS	mannosyl-oligosaccharide glucosidase
-0.12	9.03e-05	ERH	ERH mRNA splicing and mitosis factor	0.38	3.61e-03	WDR27	WD repeat domain 27
-0.09	9.03e-05	TUBB	tubulin beta class I	0.16	3.67e-03	CEP290	centrosomal protein 290
-0.05	9.03e-05	HNRNPK	heterogeneous nuclear ribonucleoprotein K	0.31	4.29e-03	AIFM2	apoptosis inducing factor mitochondria
-0.05	9.03e-05	ELAVL1	ELAV like RNA binding protein 1	0.73	6.27e-03	PLOD1	procollagen-lysine,2-oxoglutarate 5
-0.97	9.69e-05	DGKA	diacylglycerol kinase alpha	0.9	7.12e-03	PER3	period circadian regulator 3
-0.08	1.01e-04	NUTF2	nuclear transport factor 2	0.71	9.28e-03	SLC35B2	solute carrier family 35 member B2
-0.05	1.01e-04	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2B1	0.84	1.12e-02	KCNIP3	potassium voltage-gated channel int
-0.06	2.06e-04	CPSF6	cleavage and polyadenylation specific	0.62	1.12e-02	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase
-0.06	2.10e-04	ILF3	interleukin enhancer binding factor	0.29	1.57e-02	UBE2G2	ubiquitin conjugating enzyme E2 G2
-0.08	3.60e-04	CFL1	cofilin 1	0.49	1.65e-02	PIGS	phosphatidylinositol glycan anchor
-0.11	3.69e-04	RBBP4	RB binding protein 4, chromatin rem	0.69	1.66e-02	FNDC3B	fibronectin type III domain contain
-0.07	3.96e-04	PCBP2	poly(rC) binding protein 2	0.17	1.73e-02	ATP6AP1	ATPase H <sup>+</sup> transporting accessory protein
-0.06	4.00e-04	MATR3	matrin 3	0.59	1.86e-02	SDSL	serine dehydratase like
-0.05	4.08e-04	SRSF3	serine and arginine rich splicing factor 3	1.05	1.88e-02	MANSC1	MANSC domain containing 1
-0.06	4.08e-04	HNRNPC	heterogeneous nuclear ribonucleoprotein C	0.09	1.88e-02	NCLN	nicalin
-0.07	4.08e-04	SRSF11	serine and arginine rich splicing factor 11	0.1	1.93e-02	PRDX4	peroxiredoxin 4
-0.06	4.29e-04	SNRPA1	small nuclear ribonucleoprotein pol	0.25	2.06e-02	FURIN	furin, paired basic amino acid clea
-0.06	6.08e-04	BUB3	BUB3 mitotic checkpoint protein	0.3	2.34e-02	ALG5	ALG5 dolichyl-phosphate beta-glucosidase
-0.07	7.10e-04	YBX1	Y-box binding protein 1	0.78	2.38e-02	AMPH	amphiphysin
-0.15	7.10e-04	CBX5	chromobox 5	0.74	2.40e-02	PVR	PVR cell adhesion molecule
-0.05	8.11e-04	SNRPD2	small nuclear ribonucleoprotein D2	0.56	2.44e-02	SUMF1	sulfatase modifying factor 1
-0.08	8.33e-04	ANP32A	acidic nuclear phosphoprotein 32 fa	0.83	2.69e-02	MPO	myeloperoxidase
-0.05	8.58e-04	HNRNPL	heterogeneous nuclear ribonucleoprotein L	0.16	2.69e-02	ARF4	ADP ribosylation factor 4
-0.08	8.84e-04	YWHAB	tyrosine 3-monoxygenase/trypophan	0.17	2.84e-02	MIA3	MIA SH3 domain ER export factor 3
-0.08	9.37e-04	SKP1	S-phase kinase associated protein 1	0.58	3.07e-02	FGF2	fibroblast growth factor 2
-0.1	9.81e-04	SRP9	signal recognition particle 9	0.11	3.11e-02	MRPL47	mitochondrial ribosomal protein L47
-0.06	9.81e-04	DDX42	DEAD-box helicase 42	0.24	3.24e-02	TMEM43	transmembrane protein 43
-0.05	9.81e-04	CCAR1	cell division cycle and apoptosis r	0.08	3.70e-02	ATP2A2	ATPase sarcoplasmic/endoplasmic reticulum Ca <sup>2+</sup> /Mg <sup>2+</sup> -ATPase 2
-0.13	1.22e-03	GLOD4	glyoxalase domain containing 4	0.07	3.77e-02	MRPS9	mitochondrial ribosomal protein S9
-0.08	1.27e-03	SRRM1	serine and arginine repetitive matr	0.65	3.77e-02	CYP51A1	cytochrome P450 family 51 subfamily A
-0.08	1.39e-03	HNRNPA0	heterogeneous nuclear ribonucleoprotein A	0.36	3.91e-02	PRKAR2A	protein kinase cAMP-dependent type II
-0.06	1.41e-03	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1	0.12	3.91e-02	SPCS2	signal peptidase complex subunit 2
-0.78	1.51e-03	CENPQ	centromere protein Q	0.62	3.91e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.08	1.51e-03	YWHAH	tyrosine 3-monoxygenase/trypophan	0.52	3.91e-02	JAGN1	jagunal homolog 1
-0.97	1.54e-03	N4BP1	NEDD4 binding protein 1	0.66	3.91e-02	EVC2	EvC ciliary complex subunit 2
-0.07	1.54e-03	RTRAF	RNA transcription, translation and	0.91	3.91e-02	KIF5C	kinesin family member 5C
0.05	1.54e-03	SE1	splicing factor 1	0.55	3.91e-02	PIGT	phosphatidylinositol glycan anchor

Sorted by p values!  
 Downregulated in solid cancers at low/absent APLF      Upregulated in solid cancers at low/absent APLF

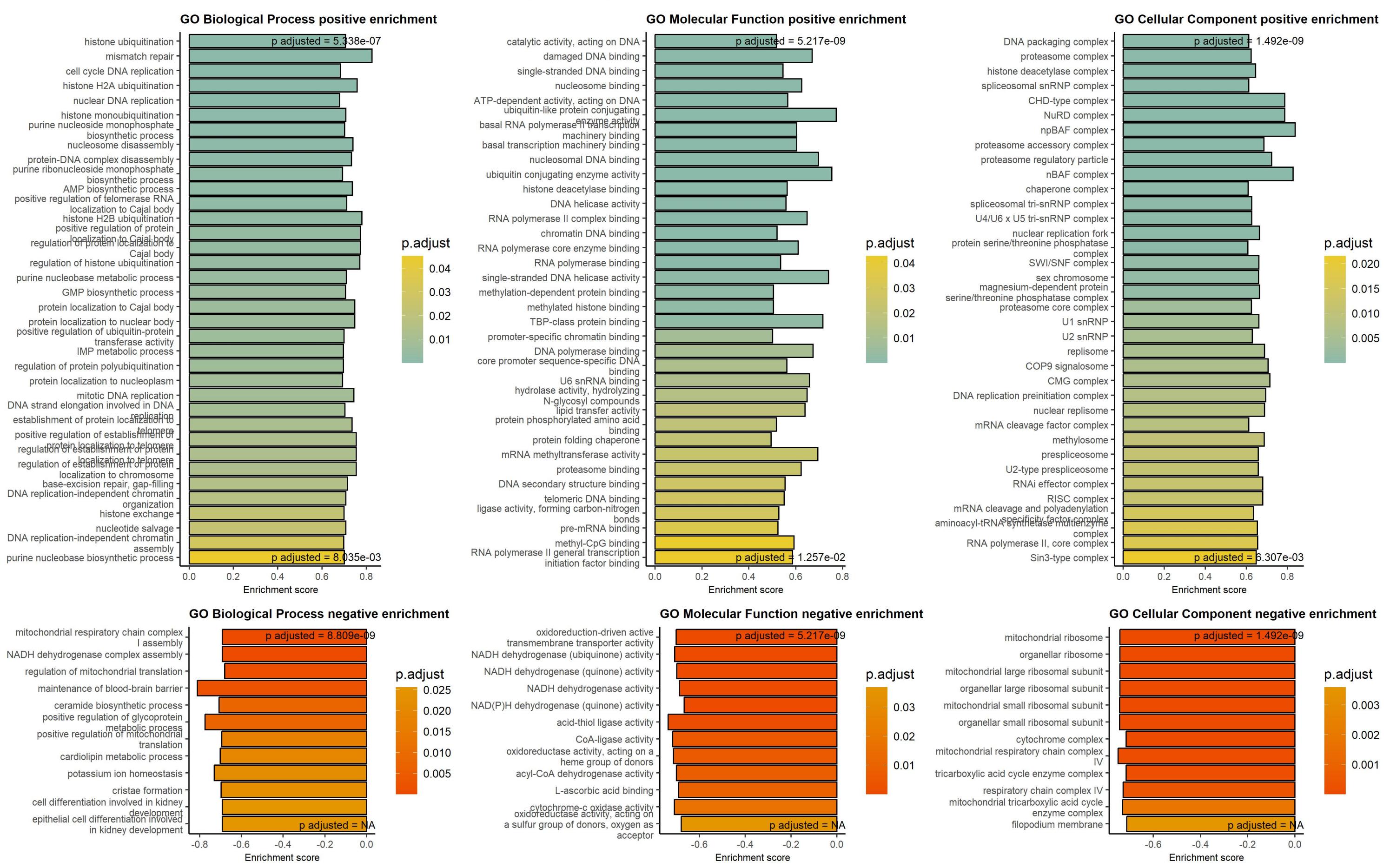


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.1	2.13e-22	YWHAE	tyrosine 3-monoxygenase/trypophan	0.33	4.35e-10	ATP4A	ATPase H <sup>+</sup> /K <sup>+</sup> transporting subunit a
-0.91	8.23e-21	UBE2D3	ubiquitin conjugating enzyme E2 D3	0.56	1.02e-09	SEC61A1	SEC61 translocon subunit alpha 1
-0.09	8.23e-21	PPP2R1A	protein phosphatase 2 scaffold subunit 1A	0.74	3.20e-09	B4GALT5	beta-1,4-galactosyltransferase 5
-0.14	9.46e-21	UBE2I	ubiquitin conjugating enzyme E2 I	0.33	7.46e-09	B4GALT7	beta-1,4-galactosyltransferase 7
-0.11	1.78e-20	CFL1	cofilin 1	0.08	9.16e-09	NCLN	nicalin
-0.15	2.32e-20	UBE2N	ubiquitin conjugating enzyme E2 N	0.11	8.07e-08	POLDIP2	DNA polymerase delta interacting protein
-0.59	2.32e-19	GSPT2	G1 to S phase transition 2	0.11	9.78e-08	TTC22	tetratricopeptide repeat domain 22
-0.1	1.16e-17	ANP32B	acidic nuclear phosphoprotein 32 fa	0.08	1.23e-07	PGRMC2	progesterone receptor membrane component
-0.13	1.16e-17	HMGBl	high mobility group box 1	0.12	2.13e-07	COLGALT1	collagen beta(1-O)galactosyltransferase
-0.07	1.21e-17	SKP1	S-phase kinase associated protein 1	0.56	2.37e-07	TGFB2	transforming growth factor beta 2
-0.78	1.39e-16	ACBD6	acyl-CoA binding domain containing	0.09	2.40e-07	TBRG4	transforming growth factor beta regulator
-0.11	1.54e-16	RPS12	ribosomal protein S12	0.14	3.54e-07	ALB	albumin
-0.14	1.54e-16	RANBP1	RAN binding protein 1	0.29	4.78e-07	WDR27	WD repeat domain 27
-0.09	2.36e-16	STIP1	stress induced phosphoprotein 1	0.44	6.01e-07	TINAGL1	tubulointerstitial nephritis antigen
-0.13	2.71e-16	OLA1	Obg like ATPase 1	0.1	6.64e-07	OGDH	oxoglutarate dehydrogenase
-0.11	4.04e-16	XPO1	exportin 1	0.4	7.78e-07	ALPK3	alpha kinase 3
-0.13	5.67e-16	PAICS	phosphoribosylaminoimidazole carboxamide	0.65	9.94e-07	RAB31	RAB31, member RAS oncogene family
-0.07	7.12e-16	RUVBL1	RuvB like AAA ATPase 1	0.41	1.03e-06	LRP10	LDL receptor related protein 10
-0.1	7.56e-16	PSMB7	proteasome 20S subunit beta 7	0.14	1.04e-06	TBL2	transducin beta like 2
-0.1	7.56e-16	YWHAB	tyrosine 3-monoxygenase/trypophan	0.41	1.08e-06	FOSL2	FOS like 2, AP-1 transcription factor
-0.54	9.69e-16	TXND9	thioredoxin domain containing 9	0.3	1.45e-06	ITGAV	integrin subunit alpha V
-0.19	1.02e-15	PFDN2	prefoldin subunit 2	0.49	1.46e-06	PIEZO1	piezo type mechanosensitive ion channel
-0.6	1.02e-15	UCK2	uridine-cytidine kinase 2	0.06	1.59e-06	EMC8	ER membrane protein complex subunit
-0.13	1.26e-15	PTGES3	prostaglandin E synthase 3	0.43	1.60e-06	CLDN7	claudin 7
-0.7	1.54e-15	RPE	ribulose-5-phosphate-3-epimerase	0.14	2.37e-06	ESYT2	extended synaptotagmin 2
-0.13	1.85e-15	ELOB	elongin B	0.41	2.90e-06	EFCAB14	EF-hand calcium binding domain 14
-0.38	1.92e-15	DYNLRB1	dynein light chain roadblock-type 1	0.09	3.45e-06	HTRA2	HtrA serine peptidase 2
-0.1	2.77e-15	ELOC	elongin C	0.16	3.55e-06	SSR3	signal sequence receptor subunit 3
-0.14	3.18e-15	FKBP4	FKBP prolyl isomerase 4	0.42	4.05e-06	KDM4E	lysine demethylase 4E
-0.83	4.76e-15	CDK5R2	cyclin dependent kinase 5 regulator	0.1	4.11e-06	AP2M1	adaptor related protein complex 2 subunit
-0.5	7.00e-15	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.17	4.79e-06	P4HA1	prolyl 4-hydroxylase subunit alpha</td

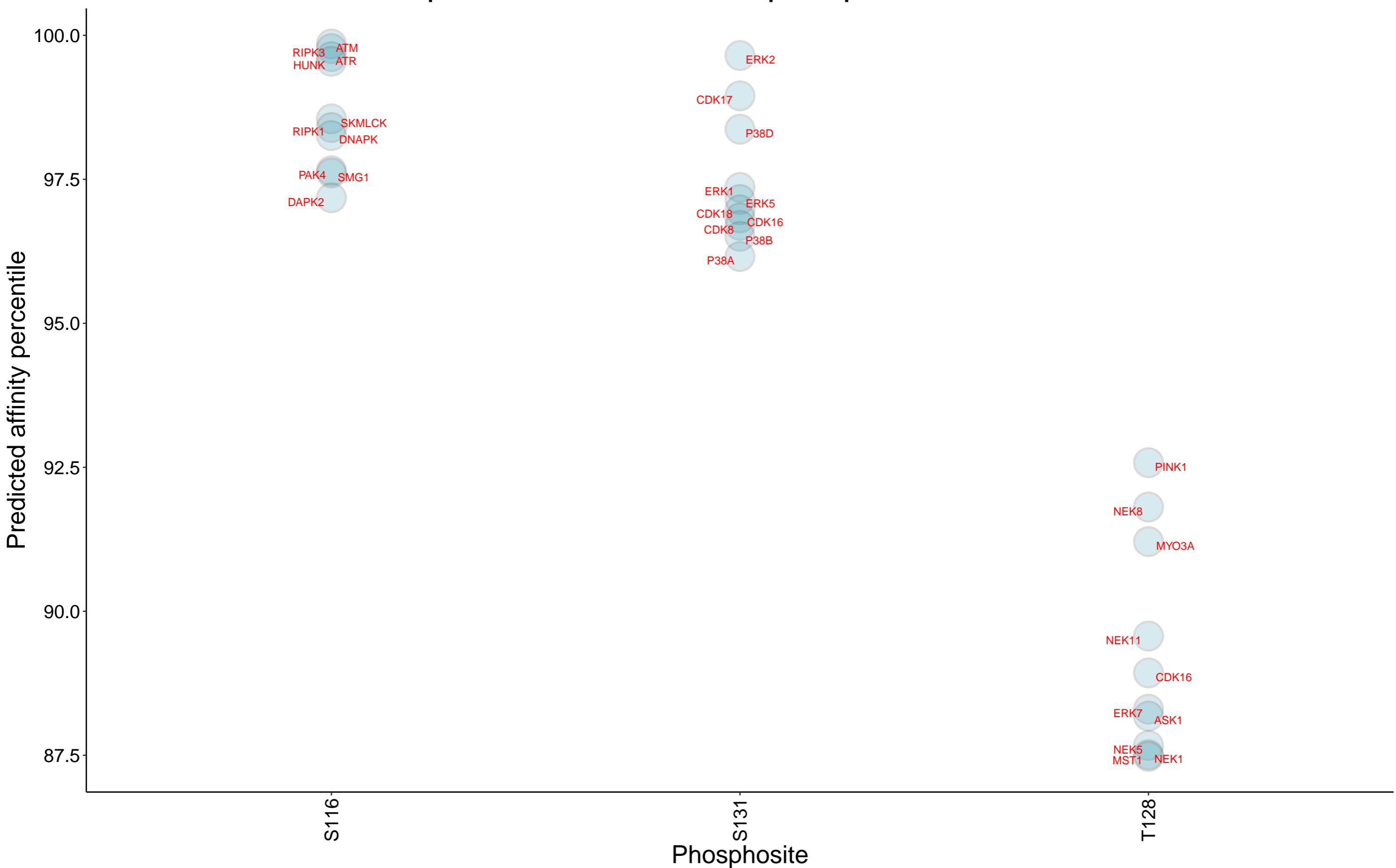
# Top 250 correlation coefficients overrepresentation, APLF protein, DB2



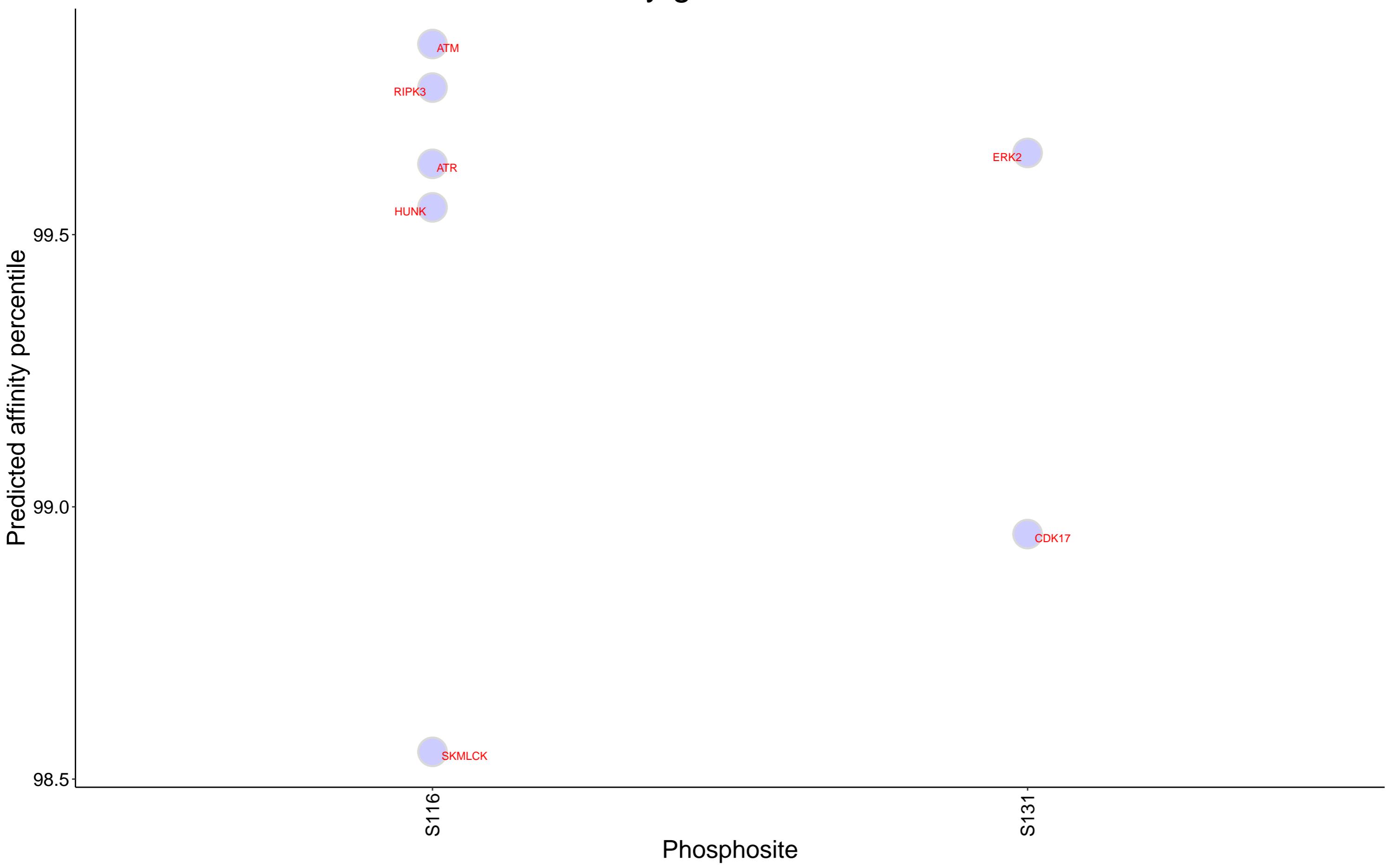
## Gene Set Enrichment analysis on protein correlation coefficients, APLF protein, DB2



# Top 10 kinases for each phosphosite in APLF



Kinases with affinity greater than 98.5% to APLF



No sufficient number of paired observations in DB2 for APLF