

# FIGNL1

Protein name: FIGL1 ;

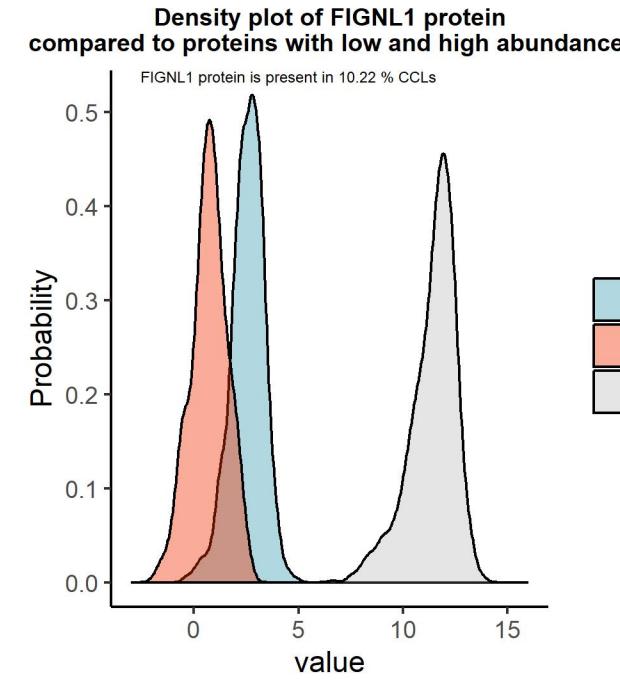
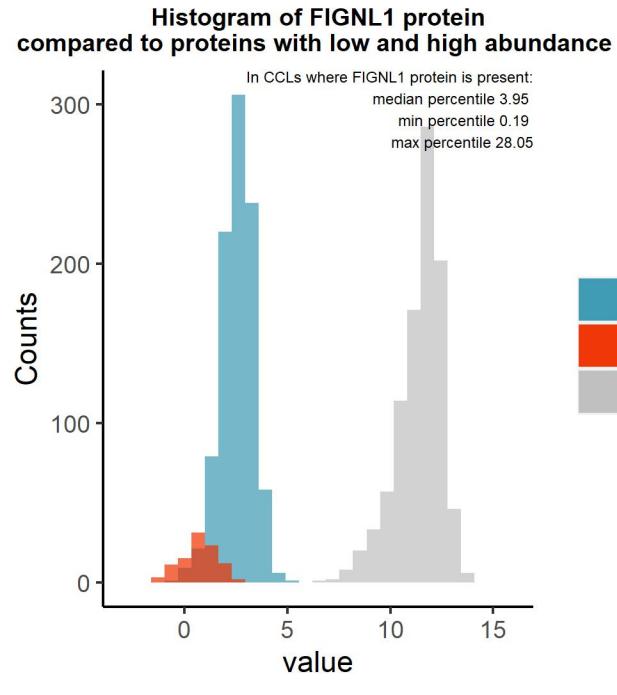
UNIPROT: Q6PIW4 ;

Gene name: fidgetin like 1

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 FIGNL1 protein, DB2

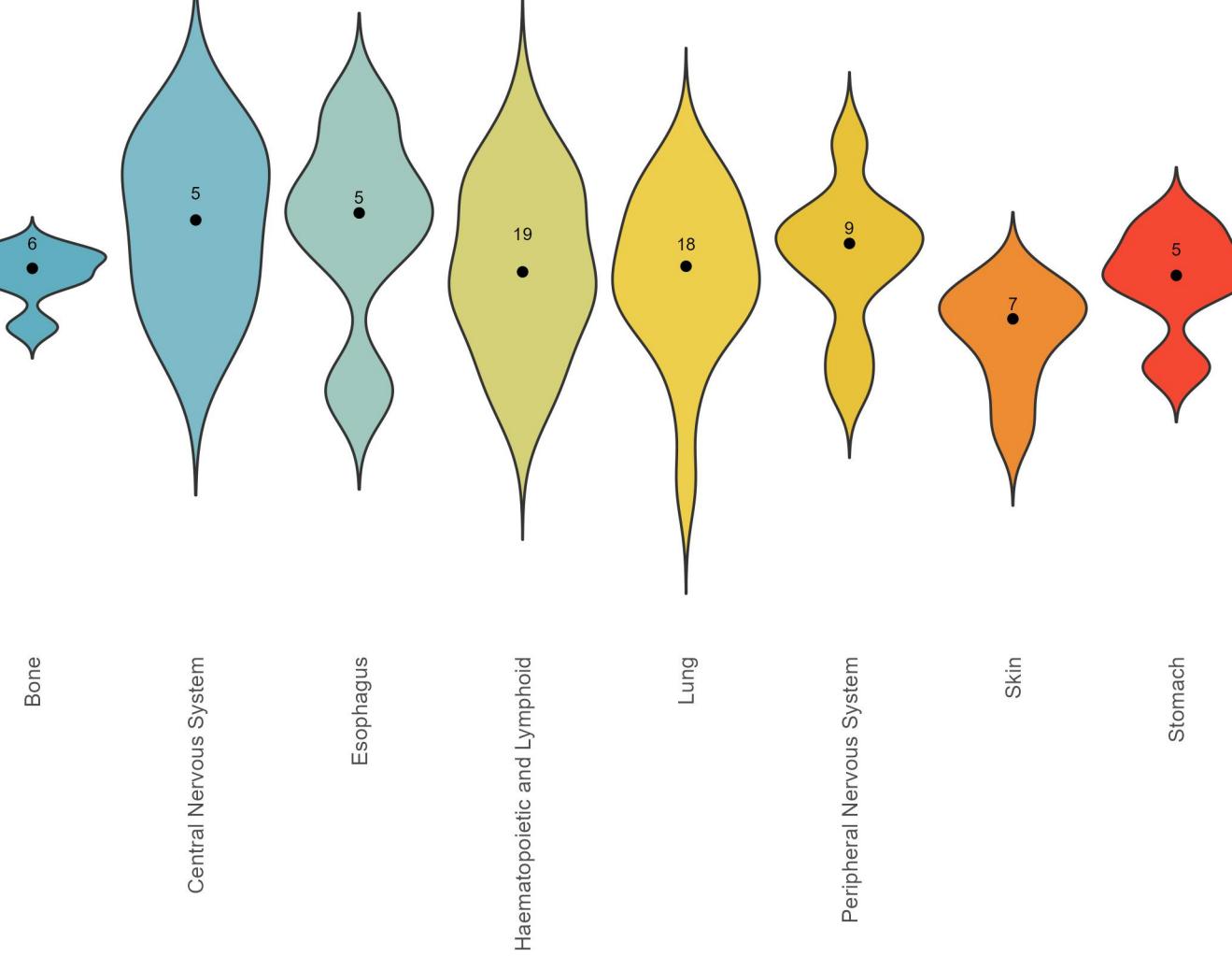
#### Pearson correlation coefficients

### Positive correlations of FIGNL1 protein, DB2

#### Pearson correlation coefficients

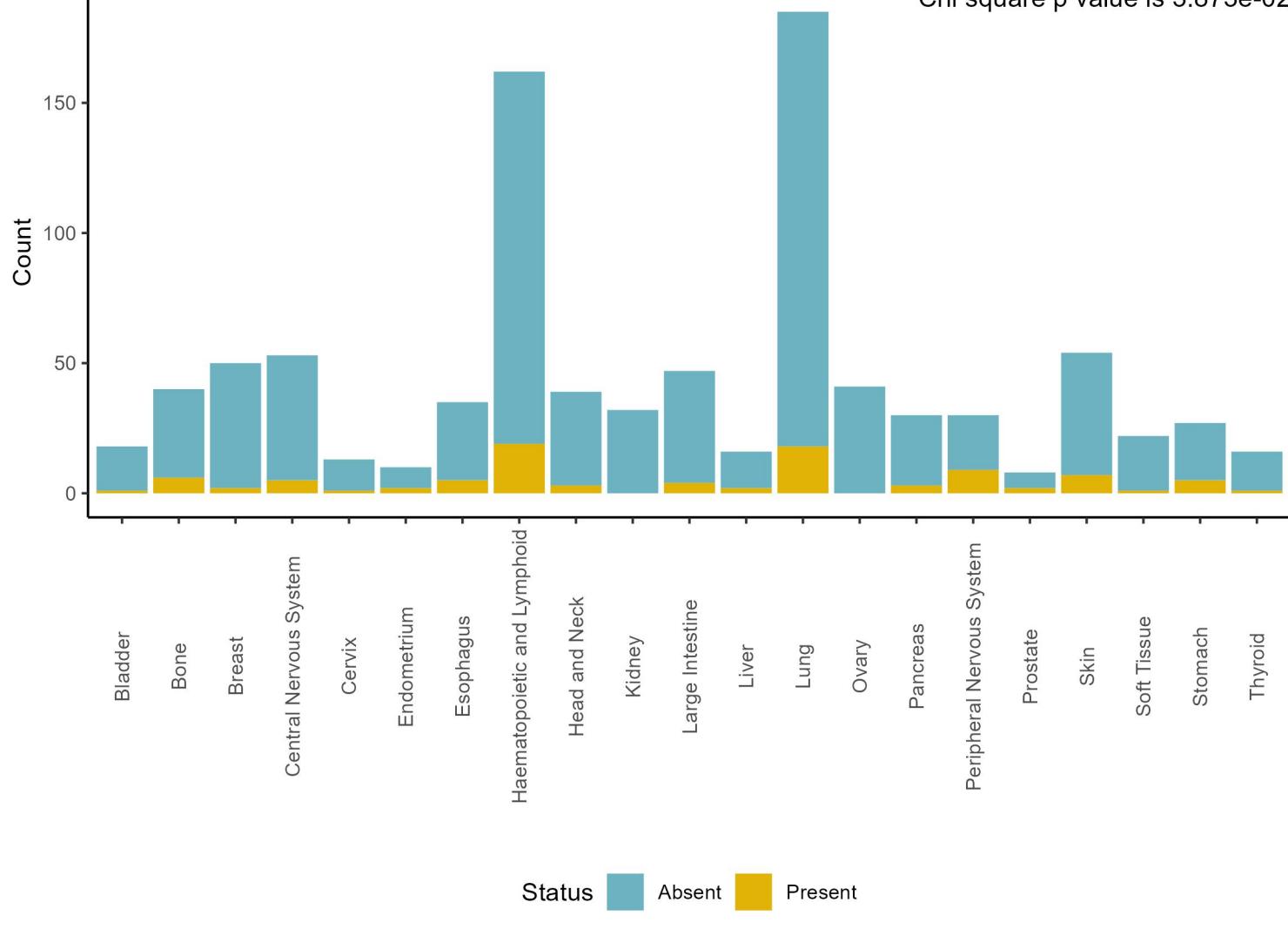
## Amount of FIGNL1 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 2.301e-01



## Present and absent FIGNL1 protein counts by tissue, DB2

Chi square p value is 3.873e-02

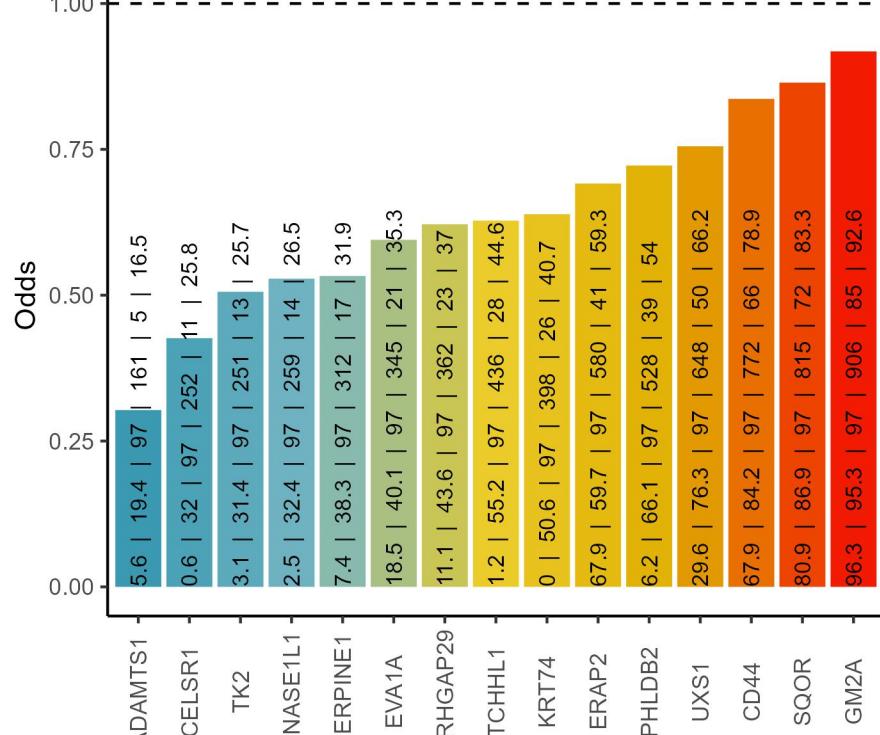


## Cooccurrence with FIGNL1 protein, DB2

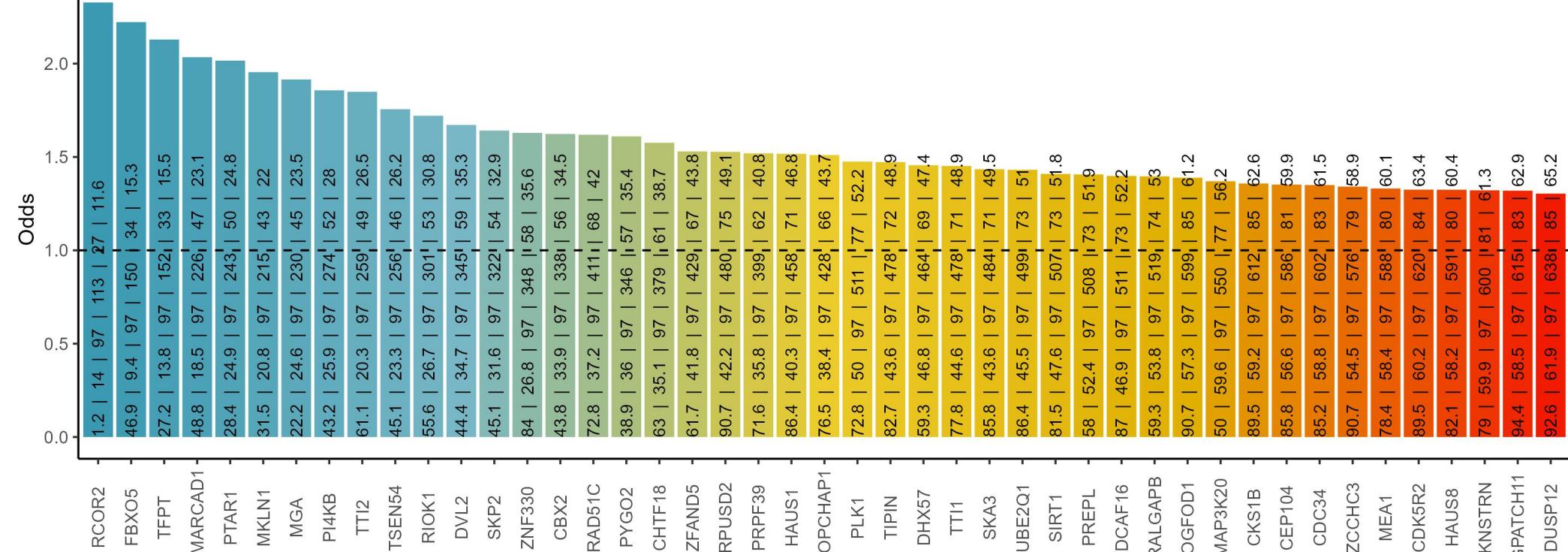
% of FIGNL1 in blood cancers: 11.7 ; % of FIGNL1 in solid cancers: 9.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of FIGNL1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

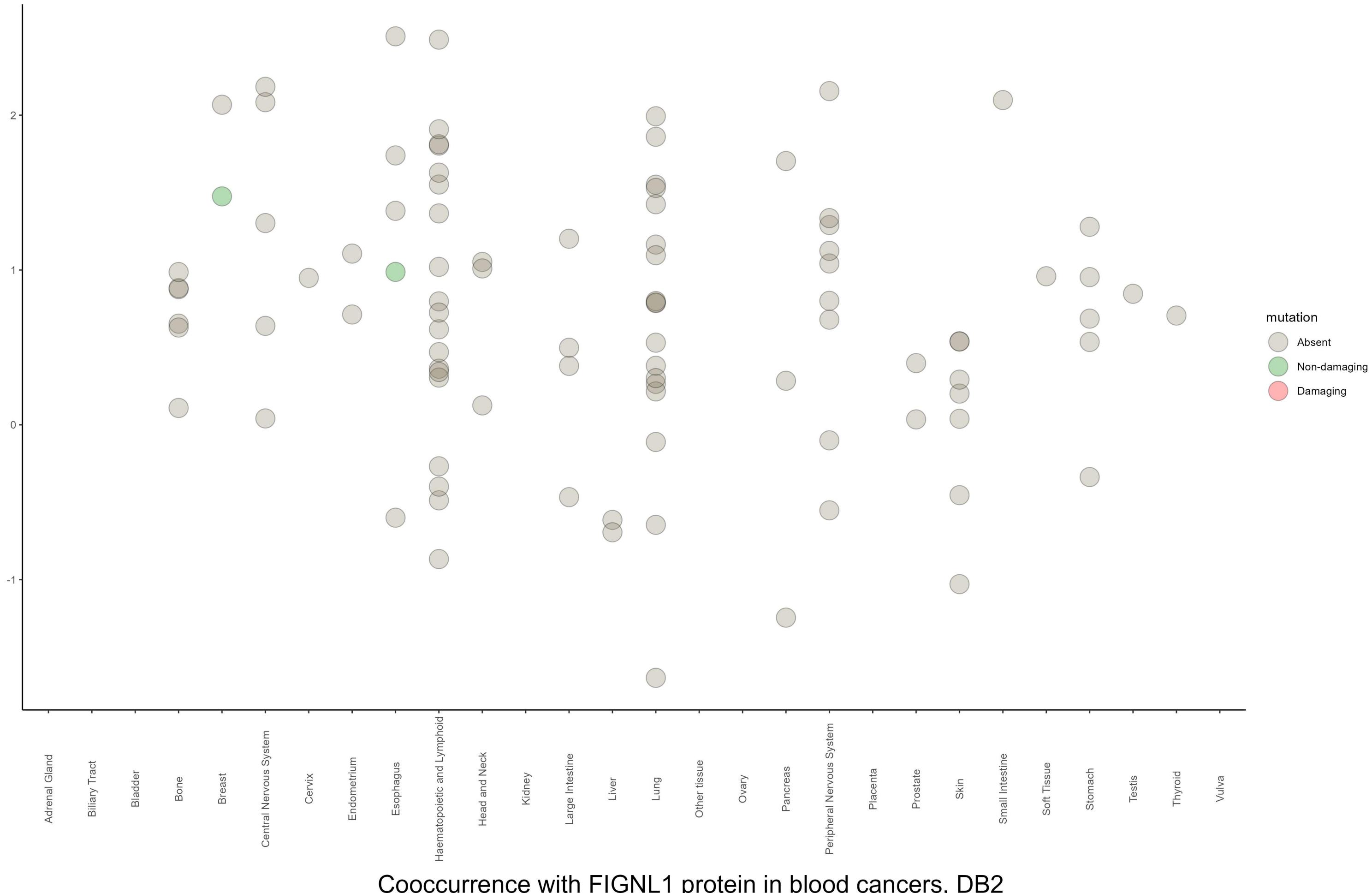
### Negative cooccurrence



### Positive cooccurrence

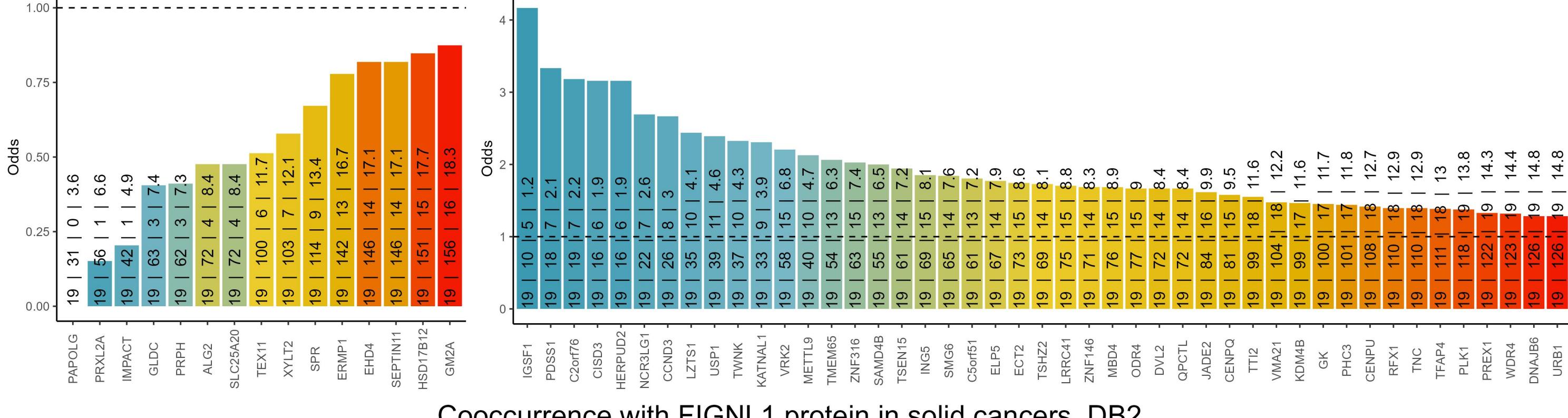


# Amount of FIGNL1 protein and mutation status by tissue, DB2



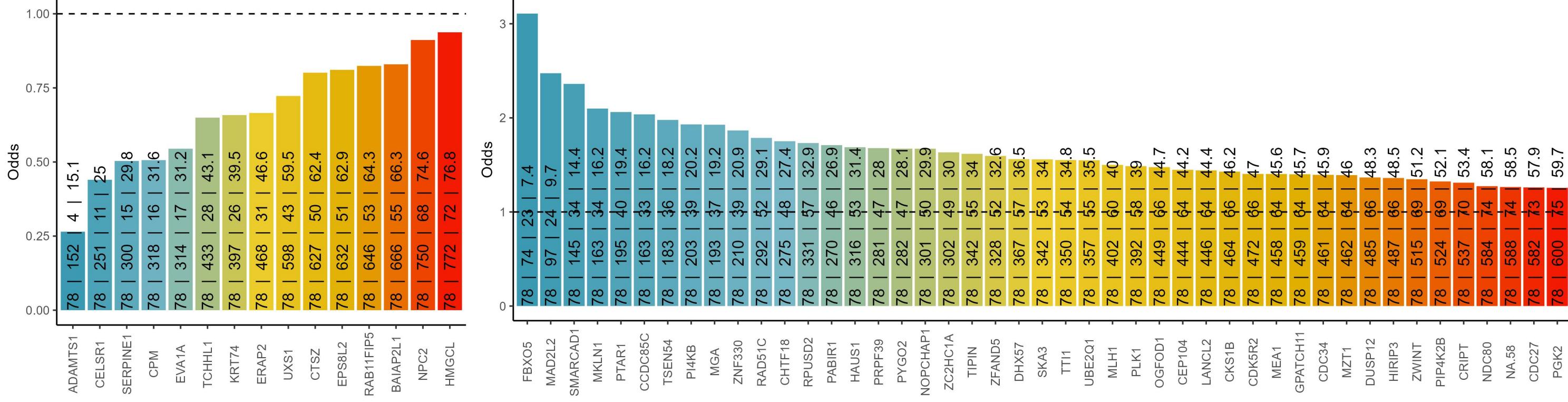
## Cooccurrence with FIGNL1 protein in blood cancers, DB2

The text in the bars: incidence of FIGNL1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

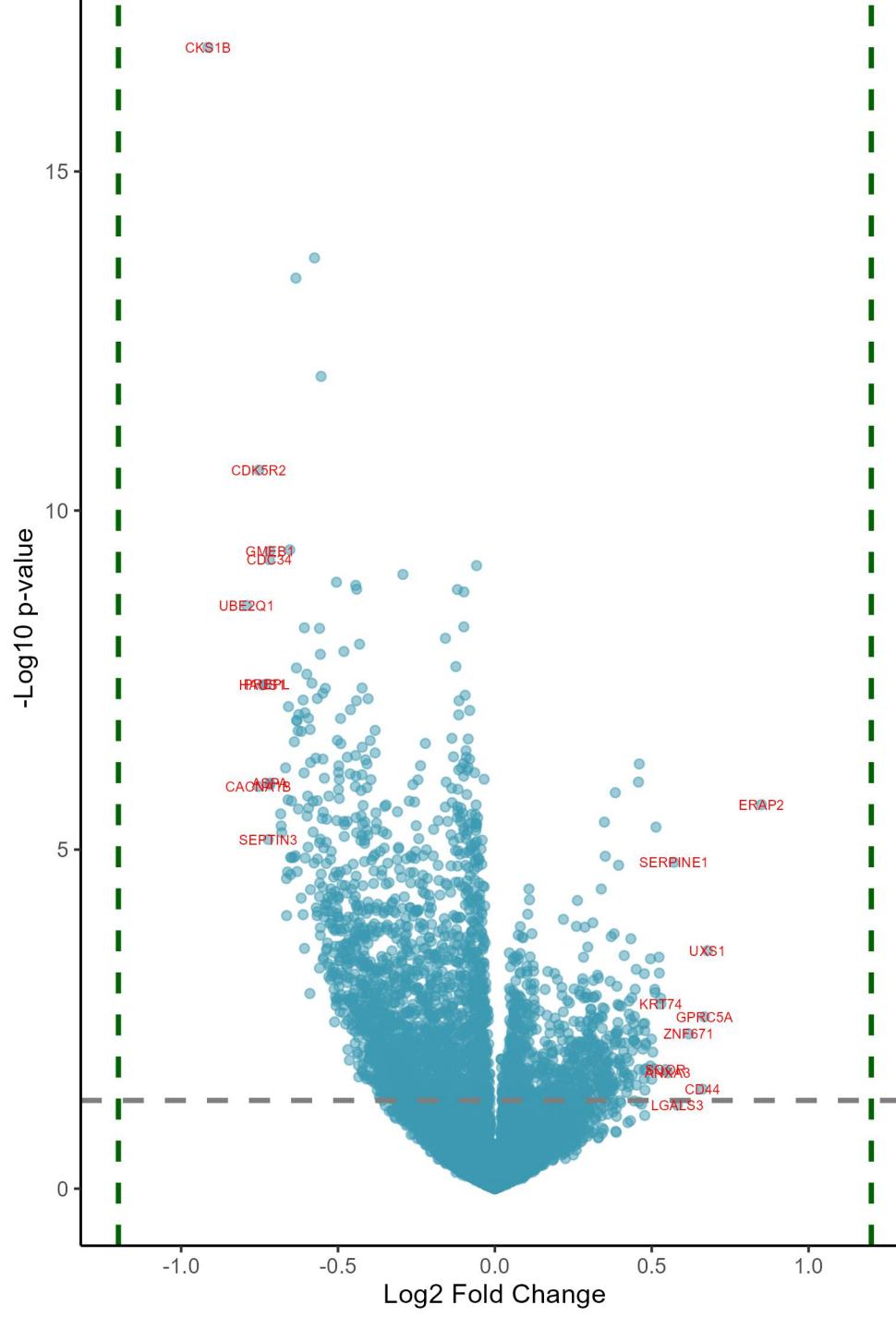


## Cooccurrence with FIGNL1 protein in solid cancers, DB2

The text in the bars: incidence of FIGNL1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

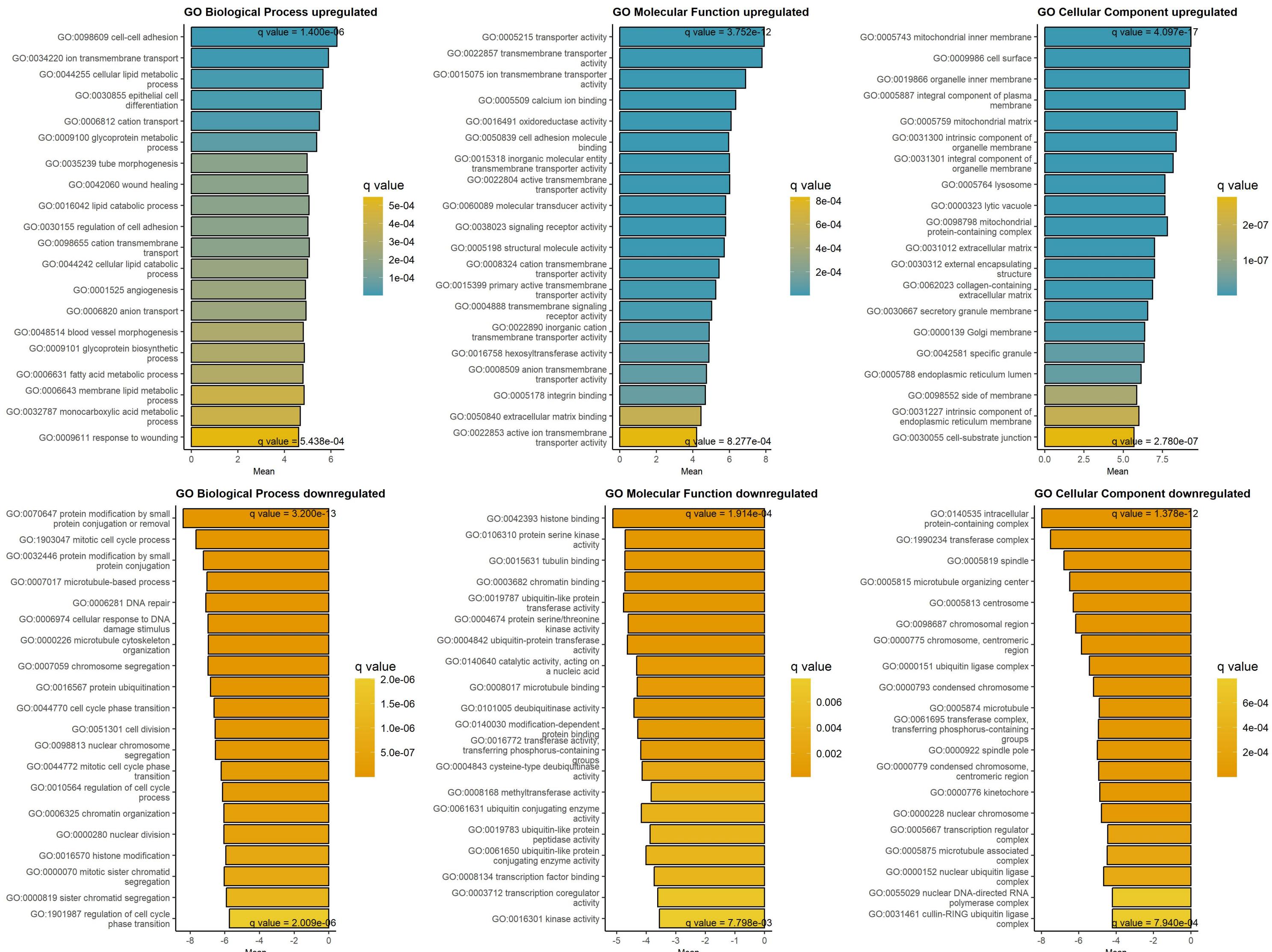


## Downregulated at low/absent FIGNL1 Upregulated at low/absent FIGNL1

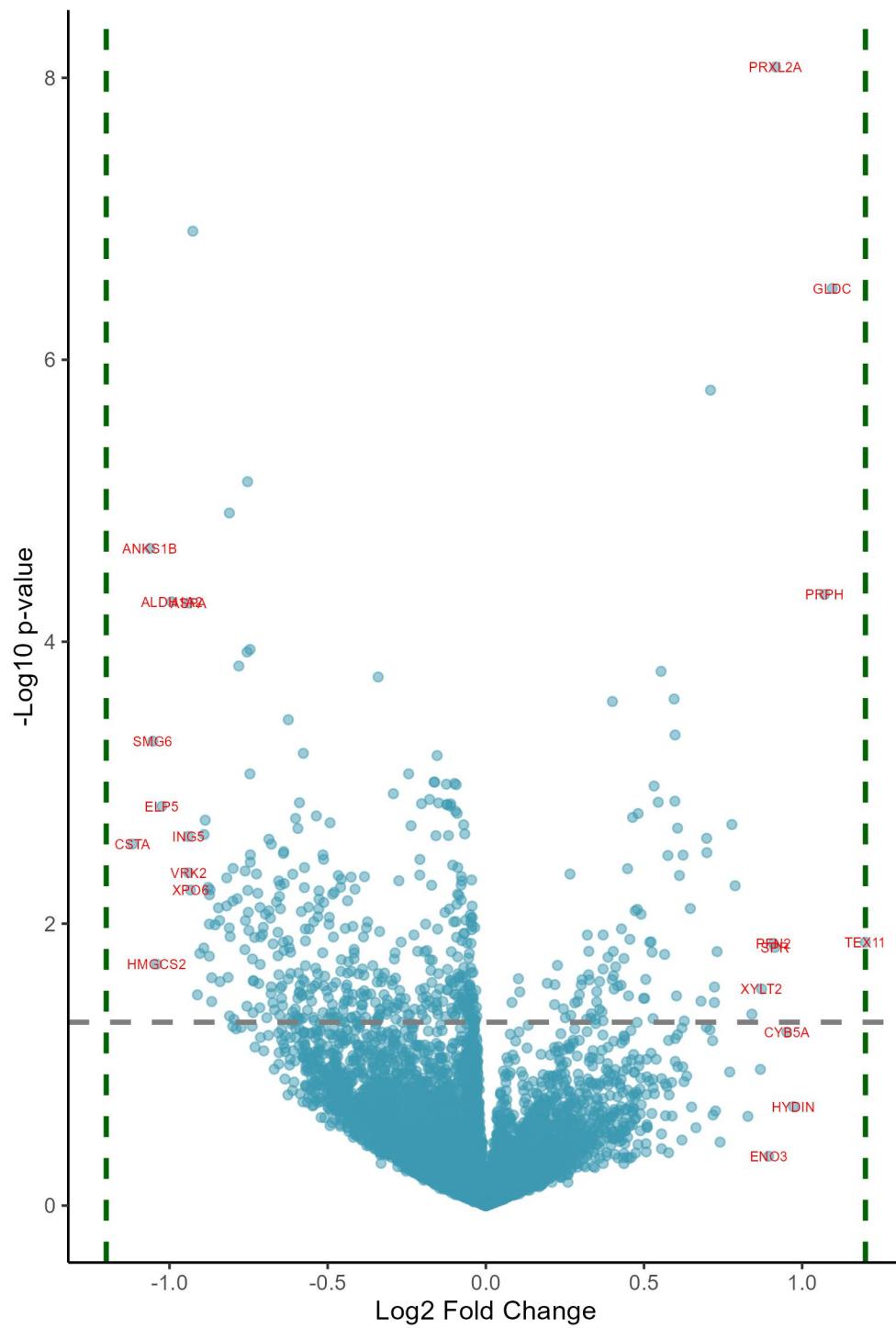


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.91	6.17e-14	CKS1B	CDC28 protein kinase regulatory sub	0.85	1.52e-04	ERAP2	endoplasmic reticulum aminopeptidase
-0.79	1.24e-06	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	0.68	4.74e-03	UXS1	UDP-glucuronate decarboxylase 1
-0.75	9.74e-05	CACNA1B	calcium voltage-gated channel subun	0.67	2.25e-02	GPRC5A	G protein-coupled receptor class C
-0.75	3.53e-08	CDK5R2	cyclin dependent kinase 5 regulator	0.66	1.20e-01	CD44	CD44 molecule (Indian blood group)
-0.74	1.04e-05	HAUS1	HAUS augmin like complex subunit 1	0.62	3.38e-02	ZNF671	zinc finger protein 671
-0.73	1.04e-05	PREPL	prolyl endopeptidase like	0.58	1.72e-01	LGALS3	galectin 3
-0.72	3.20e-04	SEPTIN3	septin 3	0.57	5.39e-04	SERPINE1	serpin family E member 1
-0.72	4.92e-07	CDC34	cell division cycle 34, ubiquitin c	0.55	8.33e-02	ANXA3	annexin A3
-0.72	9.02e-05	ASPA	aspartoacylase	0.54	7.69e-02	SQOR	sulfide quinone oxidoreductase
-0.72	4.17e-07	GMEB1	glucocorticoid modulatory element b	0.53	1.68e-02	KRT74	keratin 74
-0.72	9.37e-05	NOPCHAP1	NOP protein chaperone 1	0.53	1.45e-02	IGFBP3	insulin like growth factor binding
-0.68	1.86e-04	PYGO2	pygopus family PHD finger 2	0.52	8.03e-03	LAMTOR4	late endosomal/lysosomal adaptor, M
-0.68	2.31e-04	PTAR1	protein prenyltransferase alpha sub	0.52	5.54e-03	TCHHL1	trichohyalin like 1
-0.68	2.69e-04	PABIR1	PP2A Aalpha (PPP2R1A) and B55A (PPP	0.51	2.38e-04	PIEZO1	piezo type mechanosensitive ion cha
-0.67	6.53e-05	ZFAND5	zinc finger AN1-type containing 5	0.51	1.29e-02	CARD19	caspase recruitment domain family m
-0.66	8.17e-04	FAM168A	family with sequence similarity 168	0.51	1.18e-02	OR8B8	olfactory receptor family 8 subfami
-0.66	2.01e-03	ASRGL1	asparaginase and isoaspartyl peptid	0.51	7.57e-02	PCLLO	piccolo presynaptic cytomatrix prot
-0.66	6.87e-04	STK36	serine/threonine kinase 36	0.5	5.18e-02	KRT80	keratin 80
-0.66	1.38e-04	DCAF16	DDB1 and CUL4 associated factor 16	0.5	9.58e-02	DSG2	desmoglein 2
-0.66	1.63e-05	MEA1	male-enhanced antigen 1	0.5	3.86e-02	SDC4	syndecan 4
-0.65	4.17e-07	CCDC73	coiled-coil domain containing 73	0.5	5.74e-03	EVA1A	eva-1 homolog A, regulator of progr
-0.65	7.37e-04	C18orf63	chromosome 18 open reading frame 63	0.5	7.04e-02	EPS8L2	EPS8 like 2
-0.65	4.85e-04	SKP2	S-phase kinase associated protein 2	0.48	4.38e-02	CYBRD1	cytochrome b reductase 1
-0.65	4.85e-04	CUEDC2	CUE domain containing 2	0.48	7.54e-02	CAVIN3	caveolae associated protein 3
-0.65	1.40e-04	IVNS1ABP	influenza virus NS1A binding protei	0.48	4.22e-02	MET	MET proto-oncogene, receptor tyrosi
-0.64	4.85e-04	DVL2	dishevelled segment polarity protei	0.48	1.23e-01	F11R	F11 receptor
-0.64	3.71e-05	MLH1	mutL homolog 1	0.48	3.16e-02	EHHADH	enoyl-CoA hydratase and 3-hydroxyac
-0.64	4.70e-04	PRUNE1	prune exopolyphosphatase 1	0.48	2.14e-01	CAVIN1	caveolae associated protein 1
-0.63	7.82e-11	UBE2T	ubiquitin conjugating enzyme E2 T	0.48	2.66e-02	LAMB2	laminin subunit beta 2

## GAGE analysis on upregulated and downregulated proteins at low/absent FIGNL1 protein, DB2

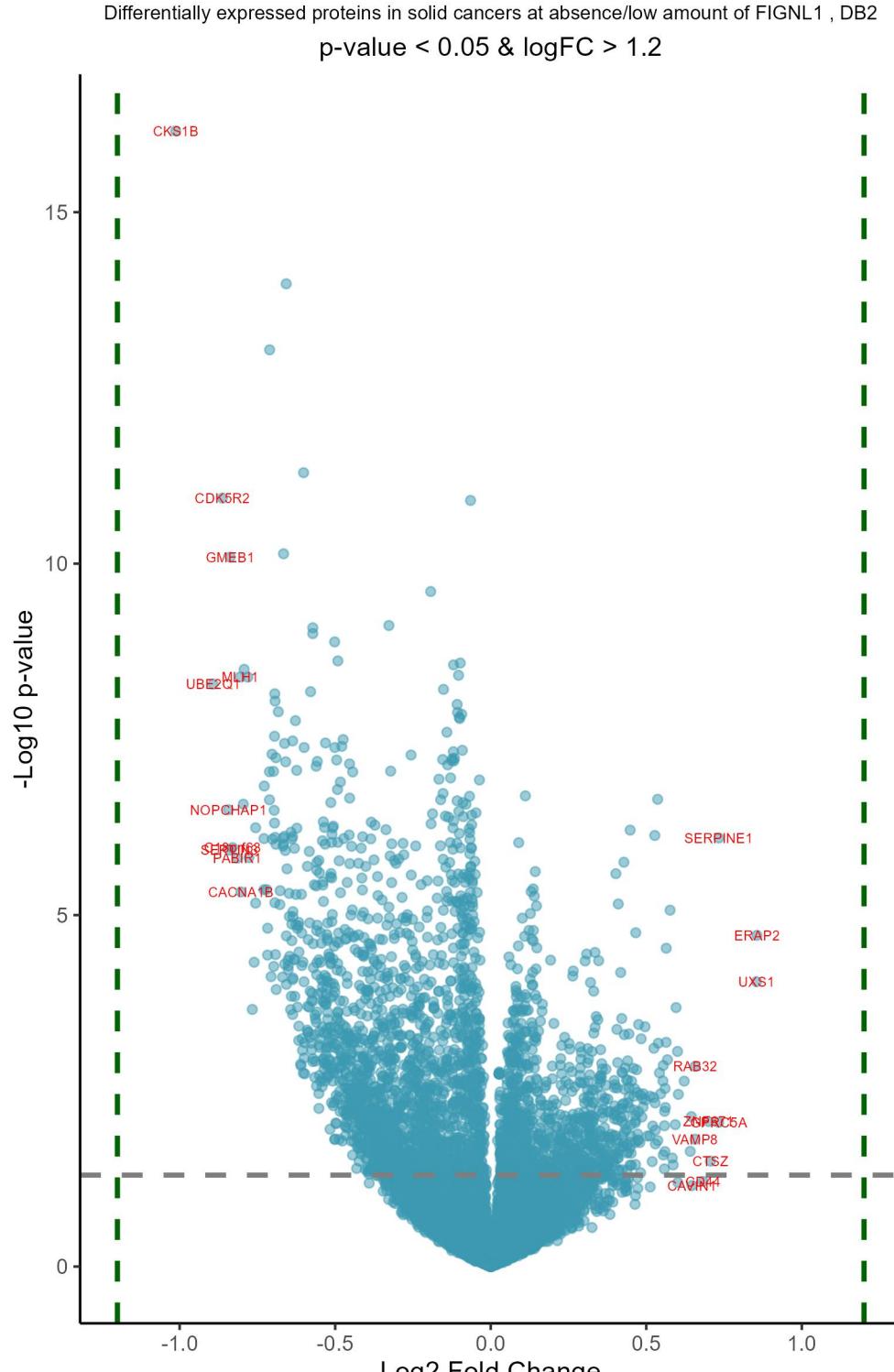


p-value &lt; 0.05 &amp; logFC &gt; 1.2



Downregulated in blood cancers at low/absent FIGNL1 Upregulated in blood cancers at low/absent FIGNL1

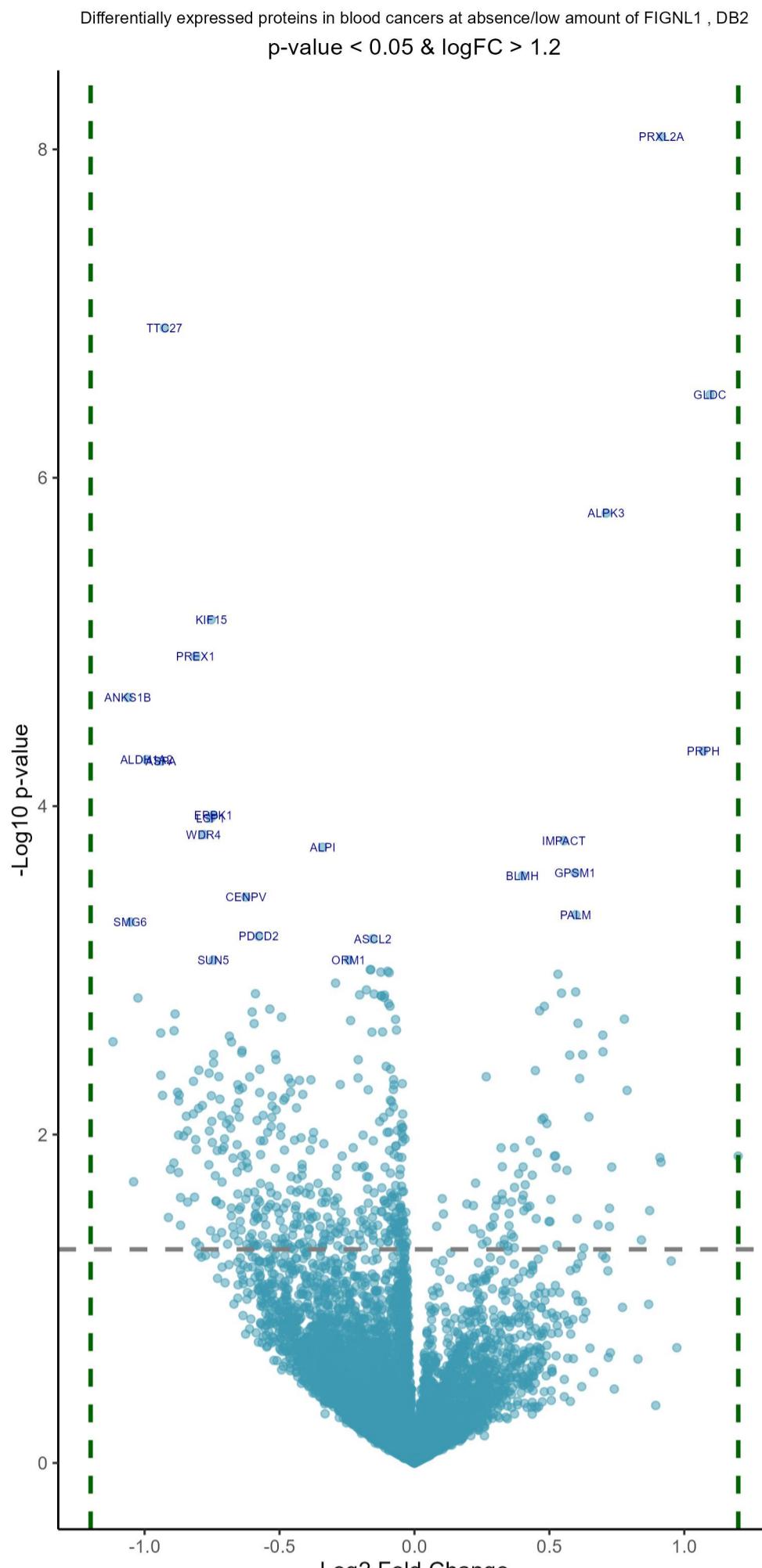
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.12	3.51e-01	CSTA	cystatin A	1.2	5.78e-01	TEX11	testis expressed 11
-1.06	2.27e-02	ANKS1B	ankyrin repeat and sterile alpha mo	1.1	6.52e-04	GLDC	glycine decarboxylase
-1.05	2.02e-01	SMG6	SMG6 nonsense mediated mRNA decay f	1.07	4.04e-02	PRPH	peripherin
-1.04	6.90e-01	HMGCS2	3-hydroxy-3-methylglutaryl-CoA synt	0.97	9.63e-01	HYDIN	HYDIN axonemal central pair apparat
-1.02	2.87e-01	ELP5	elongator acetyltransferase complex	0.95	8.73e-01	CYB5A	cytochrome b5 type A
-0.99	4.04e-02	ALDH1A2	aldehyde dehydrogenase 1 family mem	0.92	3.50e-05	PRXL2A	peroxiredoxin like 2A
-0.94	3.30e-01	ING5	inhibitor of growth family member 5	0.91	6.13e-01	SPR	sepiapterin reductase
-0.94	4.30e-01	VRK2	VRK serine/threonine kinase 2	0.91	5.81e-01	PFN2	profilin 2
-0.94	4.04e-02	ASPA	aspartoacylase	0.89	9.86e-01	ENO3	enolase 3
-0.93	4.45e-01	XPO6	exportin 6	0.87	7.54e-01	XYLT2	xylosyltransferase 2
-0.93	3.41e-04	TTC27	tetratricopeptide repeat domain 27	0.87	9.63e-01	SEPTIN11	septin 11
-0.91	7.60e-01	CYGB	cytoglobin	0.84	8.09e-01	ERAP2	endoplasmic reticulum aminopeptidas
-0.9	6.19e-01	FRRS1	ferric chelate reductase 1	0.83	9.63e-01	FSCN1	fascin actin-bundling protein 1
-0.89	6.14e-01	DNAH6	dynein axonemal heavy chain 6	0.79	4.41e-01	HOXB1	homeobox B1
-0.89	3.30e-01	MTHFR	methylenetetrahydrofolate reductase	0.78	3.13e-01	DDAH1	dimethylarginine dimethylaminohydro
-0.89	3.09e-01	KRT33B	keratin 33B	0.77	9.63e-01	WFIKKN2	WAP, follistatin/kazal, immunoglobu
-0.88	4.42e-01	FAM184B	family with sequence similarity 184	0.74	9.63e-01	ENTPD1	ectonucleoside triphosphate diphosp
-0.87	6.38e-01	IVL	involucrin	0.73	6.18e-01	ATF7IP	activating transcription factor 7 i
-0.87	5.31e-01	PLS3	plastin 3	0.73	9.63e-01	MAPK15	mitogen-activated protein kinase 15
-0.87	4.54e-01	TSHZ2	teashirt zinc finger homeobox 2	0.72	7.47e-01	DSG2	desmoglein 2
-0.87	4.45e-01	ZNF316	zinc finger protein 316	0.72	7.73e-01	TMOD1	tropomodulin 1
-0.87	7.73e-01	CPE	carboxypeptidase E	0.72	9.63e-01	CSPG4	chondroitin sulfate proteoglycan 4
-0.87	7.43e-01	COLGALT2	collagen beta(1-O)galactosyltransfe	0.72	9.01e-01	PCCB	propionyl-CoA carboxylase subunit b
-0.86	5.33e-01	TIMM17B	translocase of inner mitochondrial	0.71	2.75e-03	ALPK3	alpha kinase 3
-0.85	4.91e-01	PRKAR2B	protein kinase cAMP-dependent type	0.71	8.67e-01	HAO2	hydroxyacid oxidase 2
-0.84	5.24e-01	STMN2	stathmin 2	0.7	3.82e-01	ERC1	ELKS/RAB6-interacting/CAST family m
-0.84	7.45e-01	NPHS1	NPHS1 adhesion molecule, nephrin	0.7	3.34e-01	SNX18	sorting nexin 18
-0.82	4.91e-01	ODR4	odr-4 GPCR localization factor homo	0.7	8.57e-01	FAM83H	family with sequence similarity 83
-0.82	4.30e-01	CDS1	CDP-diacylglycerol synthase 1	0.68	7.73e-01	ZNF101	zinc finger protein 101



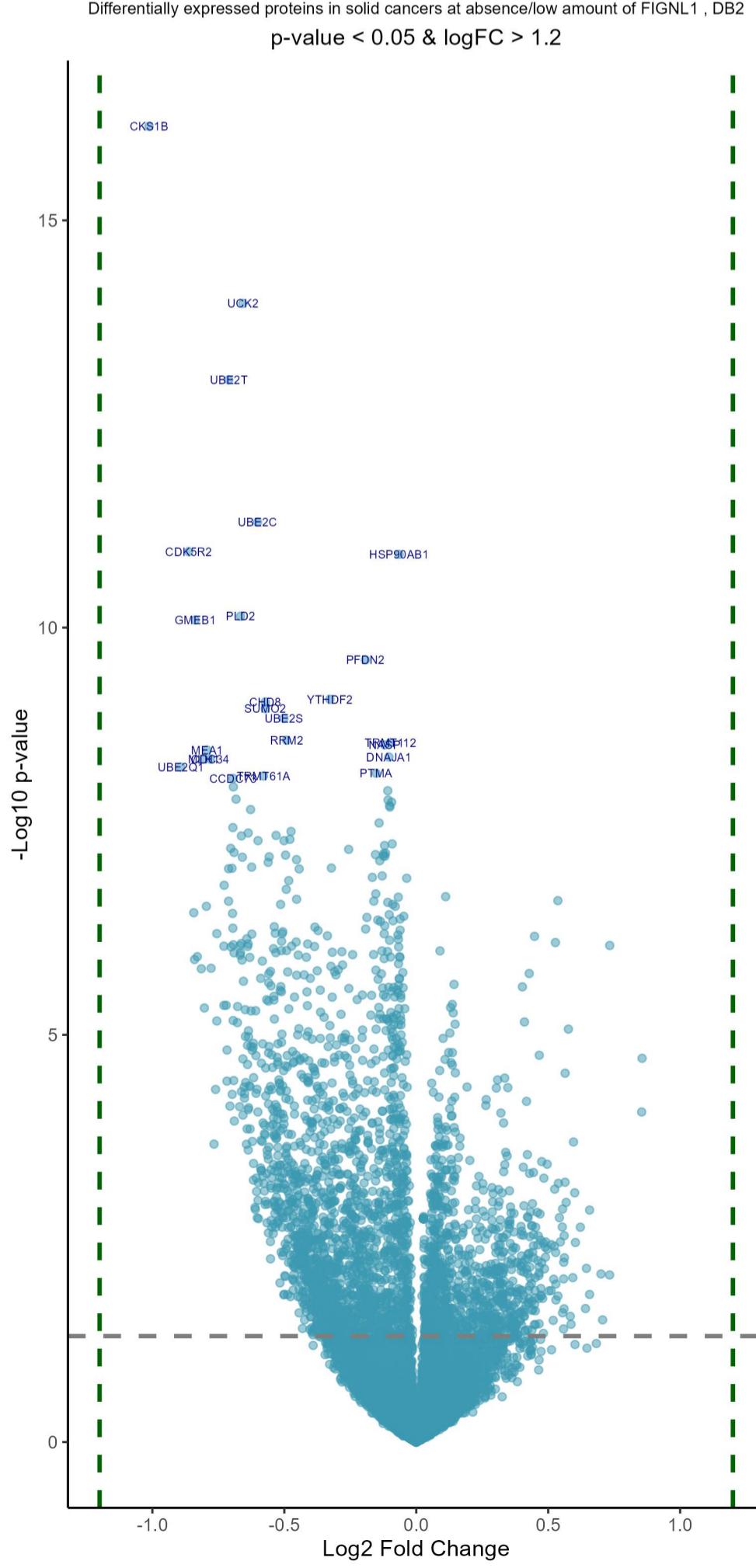
Downregulated in solid cancers at low/absent FIGNL1 Upregulated in solid cancers at low/absent FIGNL1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.01	2.93e-13	CKS1B	CDC28 protein kinase regulatory sub	0.86	5.11e-04	ERAP2	endoplasmic reticulum aminopeptidas
-0.89	1.96e-06	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	0.85	1.58e-03	UXS1	UDP-glucuronate decarboxylase 1
-0.86	1.51e-08	CDK5R2	cyclin dependent kinase 5 regulator	0.73	5.62e-05	SERPINE1	serpin family E member 1
-0.84	3.23e-05	NOPCHAP1	NOP protein chaperone 1	0.73	4.23e-02	GPRC5A	G protein-coupled receptor class C
-0.84	6.77e-05	SEPTIN3	septin 3	0.71	1.03e-01	CTSZ	cathepsin Z
-0.84	7.50e-08	GMEB1	glucocorticoid modulatory element b	0.7	4.15e-02	ZNF671	zinc finger protein 671
-0.83	6.47e-05	C18orf63	chromosome 18 open reading frame 63	0.68	1.60e-01	CD44	CD44 molecule (Indian blood group)
-0.81	8.39e-05	PABIR1	PP2A Aalpha (PPP2R1A) and B55A (PPP	0.66	1.17e-02	RAB32	RAB32, member RAS oncogene family
-0.81	1.64e-06	MLH1	mutL homolog 1	0.66	6.31e-02	VAMP8	vesicle associated membrane protein
-0.8	1.84e-04	CACNA1B	calcium voltage-gated channel subun	0.65	1.76e-01	CAVIN1	caveolae associated protein 1
-0.8	2.73e-05	HAUS1	HAUS augmin like complex subunit 1	0.64	3.73e-02	EPS8L2	EPS8 like 2
-0.79	1.48e-06	MEA1	male-enhanced antigen 1	0.64	8.25e-02	ANXA3	annexin A3
-0.78	1.64e-06	CDC34	cell division cycle 34, ubiquitin c	0.62	1.63e-02	MET	MET proto-oncogene, receptor tyrosi
-0.78	8.32e-05	PYGO2	pygopus family PHD finger 2	0.6	2.21e-02	KRT74	keratin 74
-0.77	3.15e-03	TEX11	testis expressed 11	0.6	1.63e-01	LGALS3	galectin 3
-0.76	9.85e-04	ASRGL1	asparaginase and isoaspartyl peptid	0.6	8.41e-03	TCHHL1	trichohyalin like 1
-0.76	2.38e-04	PTAR1	protein prenyltransferase alpha sub	0.6	3.01e-03	MGAT4B	alpha-1,3-mannosyl-glycoprotein 4-b
-0.76	4.71e-05	ZFAND5	zinc finger AN1-type containing 5	0.59	4.48e-02	KRT80	keratin 80
-0.73	1.75e-04	DCAF16	DDB1 and CUL4 associated factor 16	0.59	1.12e-01	F11R	F11 receptor
-0.73	5.62e-05	PREPL	prolyl endopeptidase like	0.58	9.62e-02	SQOR	sulfide quinone oxidoreductase
-0.73	1.79e-05	MSTO1	misato mitochondrial distribution a	0.58	2.85e-04	PIEZO1	piezo type mechanosensitive ion cha
-0.72	1.75e-04	SSNA1	SS nuclear autoantigen 1	0.57	1.02e-02	CARD19	caspase recruitment domain family m
-0.72	8.34e-04	CUEDC2	CUE domain containing 2	0.56	6.97e-04	CPM	carboxypeptidase M
-0.72	4.38e-04	KCTD15	potassium channel tetramerization d	0.56	6.79e-03	EVA1A	eva-1 homolog A, regulator of progr
-0.71	2.52e-05	CCDC97	coiled-coil domain containing 97	0.56	3.04e-02	SDC4	syndecan 4
-0.71	1.22e-05	KNSTRN	kinetochore localized astrin (SPAG5	0.56	1.92e-02	EHHADH	enoyl-CoA hydratase and 3-hydroxyac
-0.71	1.90e-10	UBE2T	ubiquitin conjugating enzyme E2 T	0.56	8.30e-02	PCLO	piccolo presynaptic cytomatrix prot
-0.71	1.41e-03	FAM168A	family with sequence similarity 168	0.56	3.31e-02	IGFBP3	insulin like growth factor binding
-0.7	9.54e-06	NSRP1	nuclear speckle splicing regulatory	0.56	4.58e-02	CDCP1	CUB domain containing protein 1

FIGNL1 network, DB2, no Pearson r &gt; 0.3



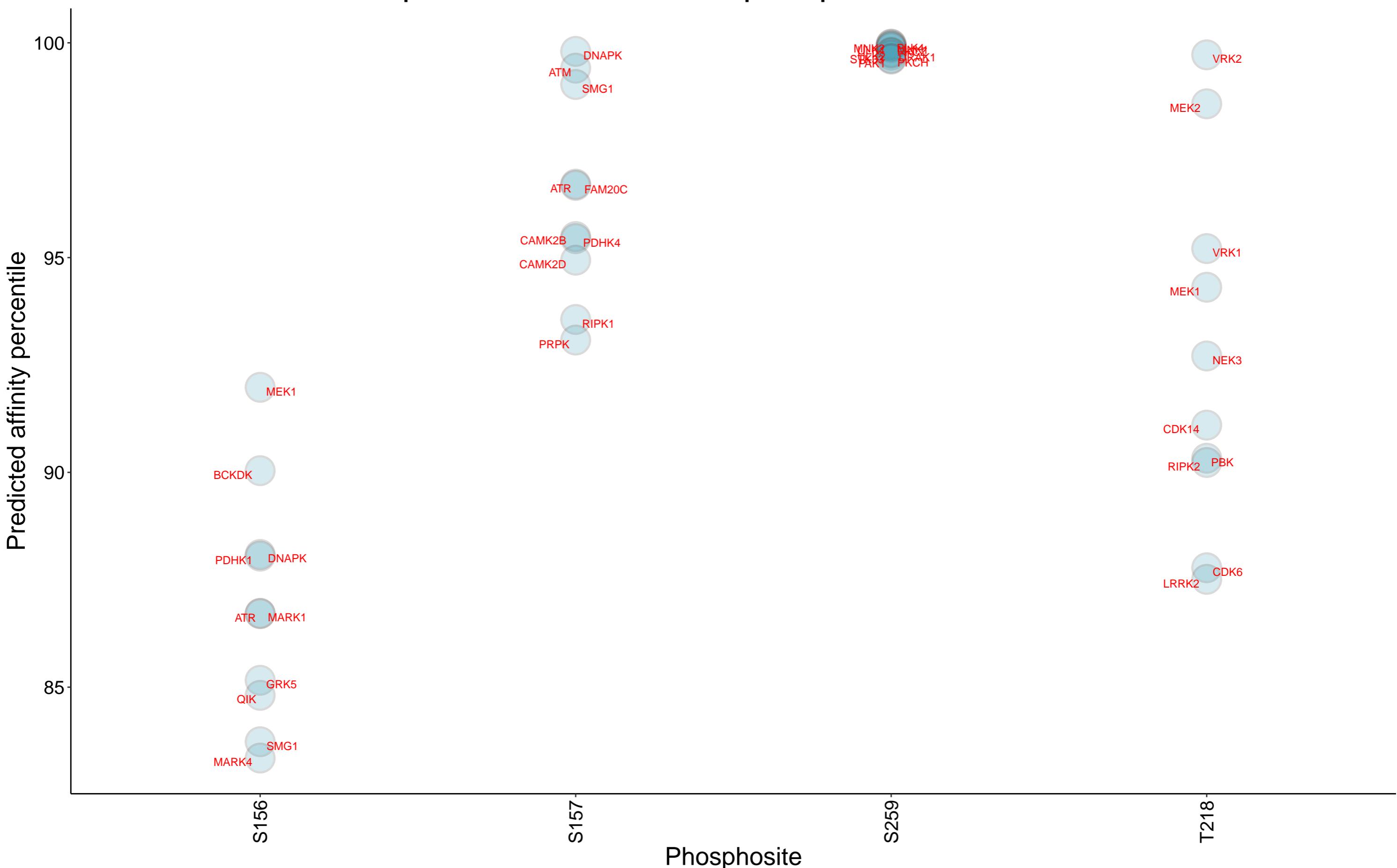
Sorted by p values!							
Downregulated in blood cancers at low/absent FIGNL1				Upregulated in blood cancers at low/absent FIGNL1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.93	3.41e-04	TTC27	tetratricopeptide repeat domain 27	0.92	3.50e-05	PRXL2A	peroxiredoxin like 2A
-0.75	1.02e-02	KIF15	kinesin family member 15	1.1	6.52e-04	GLDC	glycine decarboxylase
-0.81	1.46e-02	PREX1	phosphatidylinositol-3,4,5-trisphos	0.71	2.75e-03	ALPK3	alpha kinase 3
-1.06	2.27e-02	ANKS1B	ankyrin repeat and sterile alpha mo	1.07	4.04e-02	PRPH	peripherin
-0.99	4.04e-02	ALDH1A2	aldehyde dehydrogenase 1 family mem	0.55	9.04e-02	IMPACT	impact RWD domain protein
-0.94	4.04e-02	ASPA	aspartoacylase	0.6	1.23e-01	GPSM1	G protein signaling modulator 1
-0.75	7.61e-02	EPPK1	epiplakin 1	0.4	1.23e-01	BLMH	bleomycin hydrolase
-0.75	7.61e-02	LSP1	lymphocyte specific protein 1	0.6	1.92e-01	PALM	paralemmmin
-0.78	8.89e-02	WDR4	WD repeat domain 4	0.53	2.85e-01	RBBP9	RB binding protein 9, serine hydrol
-0.34	9.30e-02	ALPI	alkaline phosphatase, intestinal	0.6	2.87e-01	TAGLN3	transgelin 3
-0.62	1.57e-01	CENPV	centromere protein V	0.54	2.87e-01	BTN2A1	butyrophilin subfamily 2 member A1
-1.05	2.02e-01	SMG6	SMG6 nonsense mediated mRNA decay f	0.48	3.01e-01	MLST8	MTOR associated protein, LST8 homol
-0.58	2.34e-01	PDCD2	programmed cell death 2	0.46	3.06e-01	CENPM	centromere protein M
-0.15	2.34e-01	ASCL2	achaete-scute family bHLH transcrip	0.78	3.13e-01	DDAH1	dimethylarginine dimethylaminohydro
-0.24	2.85e-01	ORM1	orosomucoid 1	0.61	3.15e-01	ECHDC2	enoyl-CoA hydratase domain containi
-0.75	2.85e-01	SUN5	Sad1 and UNC84 domain containing 5	0.7	3.34e-01	SNX18	sorting nexin 18
-0.16	2.85e-01	MAGEB3	MAGE family member B3	0.7	3.82e-01	ERC1	ELKS/RAB6-interacting/CAST family m
-0.16	2.85e-01	FAT4	FAT atypical cadherin 4	0.62	3.82e-01	SDC1	syndecan 1
-0.1	2.85e-01	EIF5B	eukaryotic translation initiation f	0.58	3.82e-01	DLG3	discs large MAGUK scaffold protein
-0.12	2.85e-01	PPFIA2	PTPRF interacting protein alpha 2	0.45	4.26e-01	PKIG	cAMP-dependent protein kinase inhib
-0.09	2.85e-01	POU3F2	POU class 3 homeobox 2	0.27	4.30e-01	SPOUT1	SPOUT domain containing methyltrans
-0.29	2.87e-01	AMOTL2	angiotonin like 2	0.61	4.30e-01	CNN3	calponin 3
-0.18	2.87e-01	LRRC8E	leucine rich repeat containing 8 VR	0.79	4.41e-01	HOXB1	homeobox B1
-0.59	2.87e-01	PRKAG1	protein kinase AMP-activated non-ca	0.65	4.91e-01	ALG2	ALG2 alpha-1,3/1,6-mannosyltransfer
-0.15	2.87e-01	PCSK9	proprotein convertase subtilisin/ke	0.48	4.91e-01	ACY3	aminoacylase 3
-0.2	2.87e-01	ARSL	arylsulfatase L	0.47	4.95e-01	CASP14	caspase 14
-0.11	2.87e-01	CES2	carboxylesterase 2	0.49	5.05e-01	GRP	gastrin releasing peptide
-0.12	2.87e-01	NEBL	nebulette	0.43	5.34e-01	CAMSAP3	calmodulin regulated spectrin assoc
-0.12	2.87e-01	PALMD	palmdelphin	0.37	5.57e-01	ALG11	ALG11 alpha-1,2-mannosyltransferase
-0.11	2.87e-01	UGT1A10	UDP glucuronosyltransferase family	0.32	5.57e-01	FXN	frataxin
-1.02	2.87e-01	ELP5	elongator acetyltransferase complex	0.46	5.74e-01	TSPAN13	tetraspanin 13
-0.1	3.01e-01	DEFA5	defensin alpha 5	0.52	5.78e-01	DSC2	desmocollin 2
-0.09	3.01e-01	EIF3H	eukaryotic translation initiation f	1.2	5.78e-01	TEX11	testis expressed 11
-0.54	3.06e-01	PTPN7	protein tyrosine phosphatase non-re	0.52	5.78e-01	CNN1	calponin 1
-0.6	3.06e-01	SRFBP1	serum response factor binding prote	0.91	5.81e-01	PFN2	profilin 2
-0.89	3.09e-01	KRT33B	keratin 33B	0.91	6.13e-01	SPR	sepiapterin reductase
-0.49	3.13e-01	PTP4A2	protein tyrosine phosphatase 4A2	0.33	6.18e-01	STRIP2	striatin interacting protein 2
-0.07	3.13e-01	H3-5	H3.5 histone	0.4	6.18e-01	CD276	CD276 molecule
-0.24	3.13e-01	NUDT12	nudix hydrolase 12	0.73	6.18e-01	ATET7ID	activating transcription factor 7 i



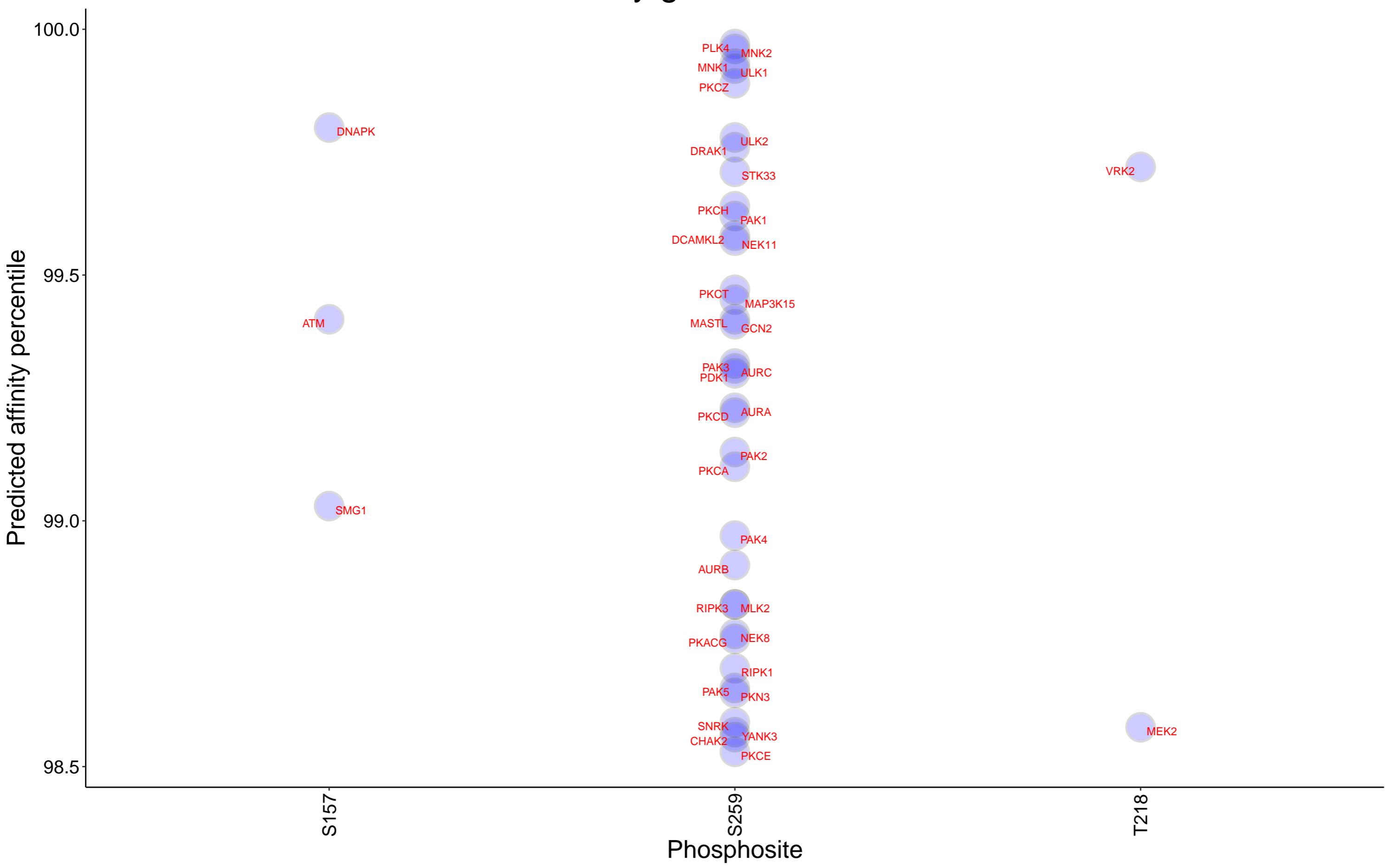
Insufficient number of paired observations in DB2 for FIGNL1

Insufficient number of paired observations in DB2 for FIGNL1

# Top 10 kinases for each phosphosite in FIGNL1



## Kinases with affinity greater than 98.5% to FIGNL1



No sufficient number of paired observations in DB2 for FIGNL1