

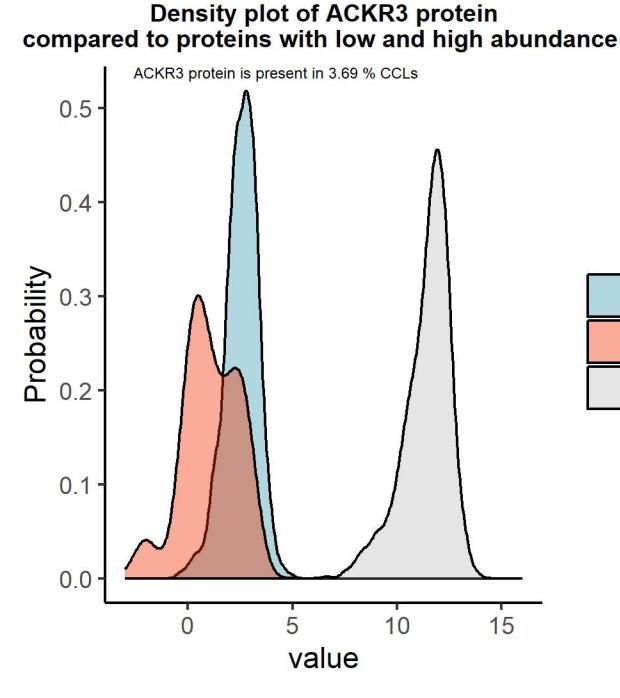
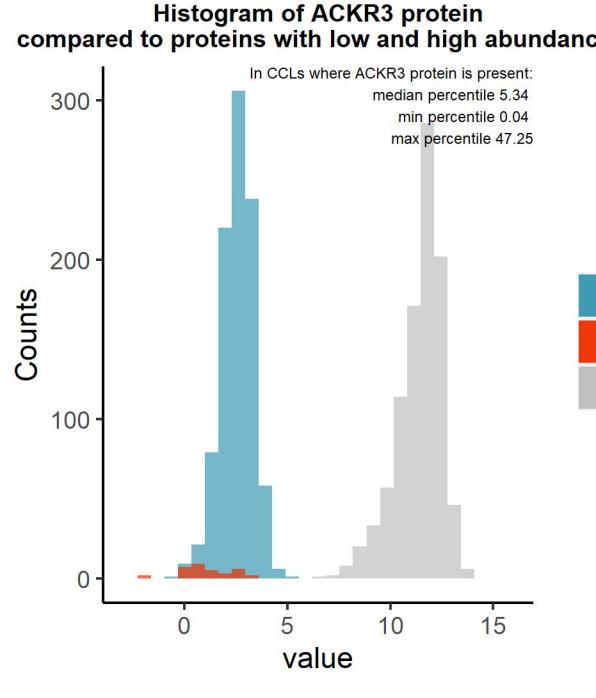
# ACKR3

Protein name: ACKR3 ; UNIPROT: P25106 ; Gene name: atypical chemokine receptor 3

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

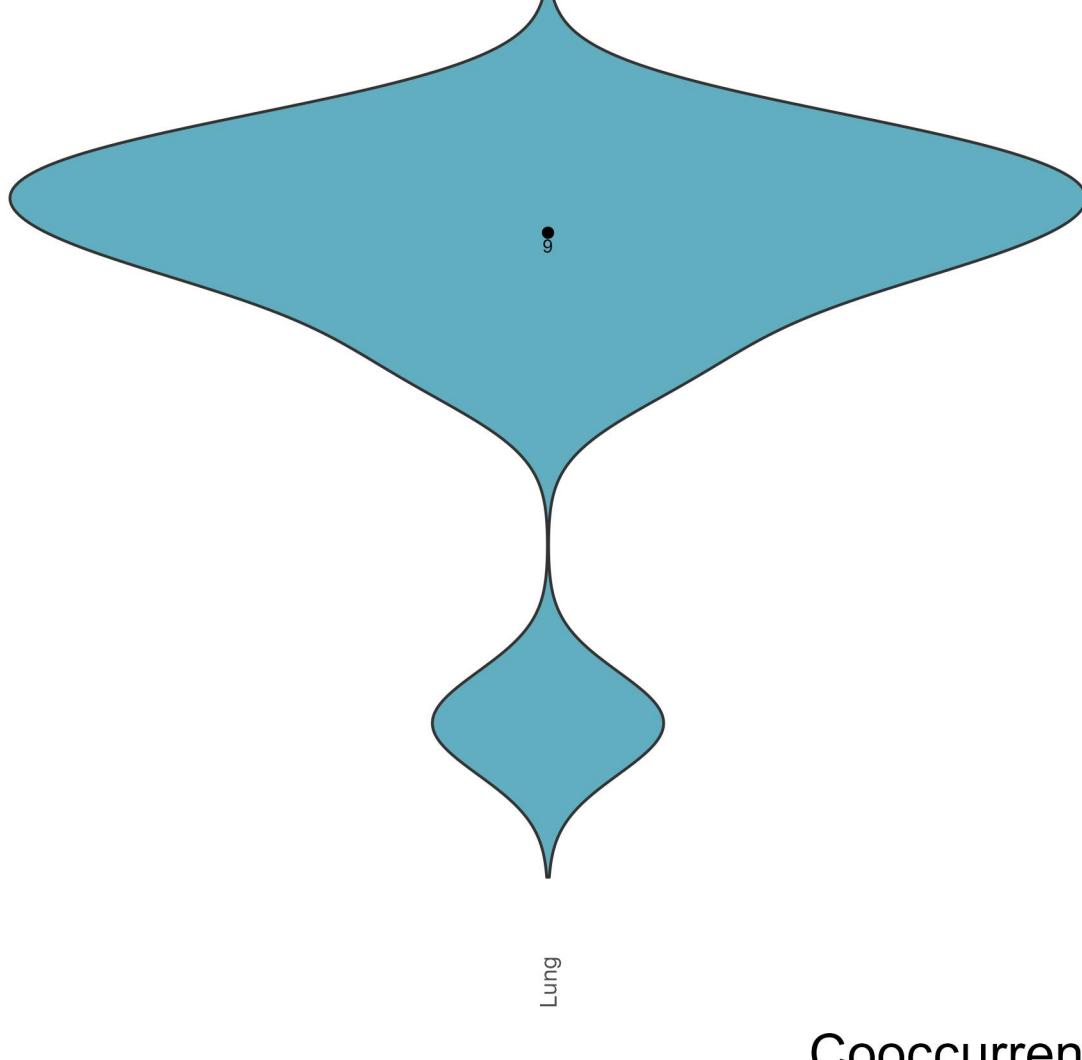
## Sanger Institute Protein Database 2 (DB2), protein presence is less certain

8498 proteins in same 949 CCLs



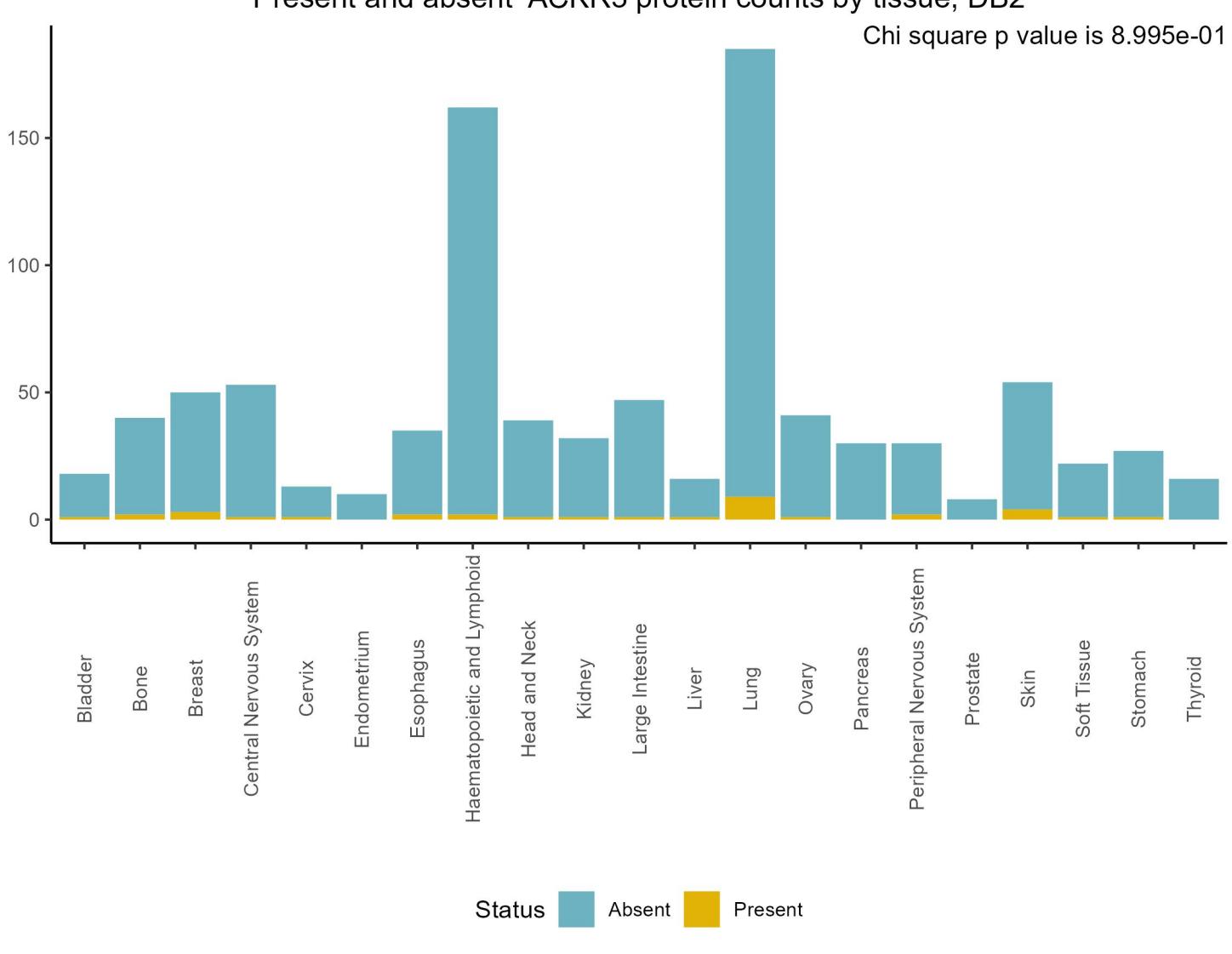
## Amount of ACKR3 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 7.149e-01



## Negative correlations of ACKR3 protein, DB2

### Pearson correlation coefficients

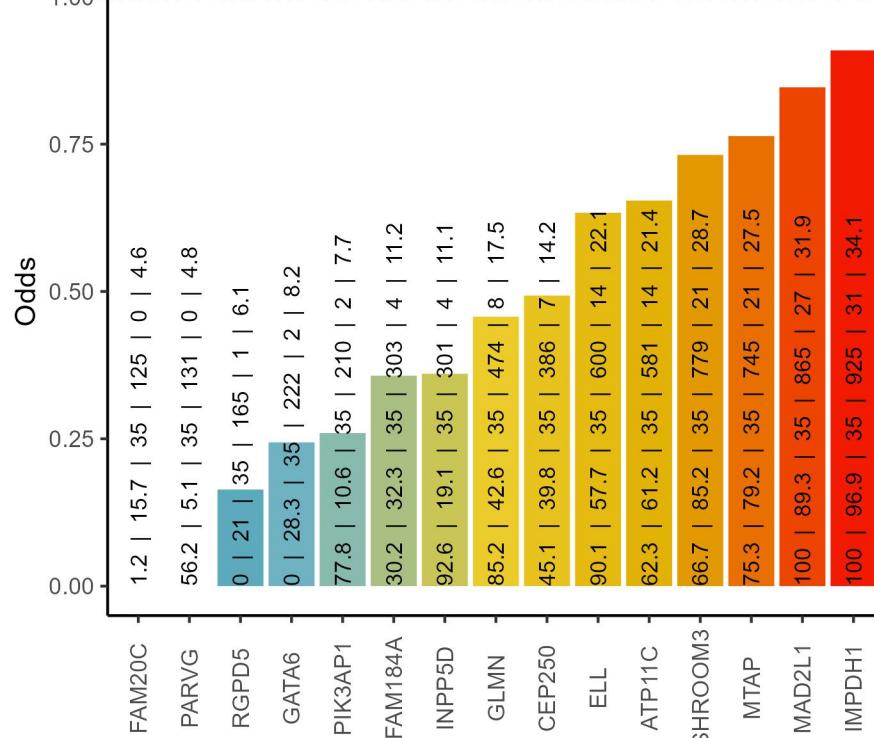


## Cooccurrence with ACKR3 protein, DB2

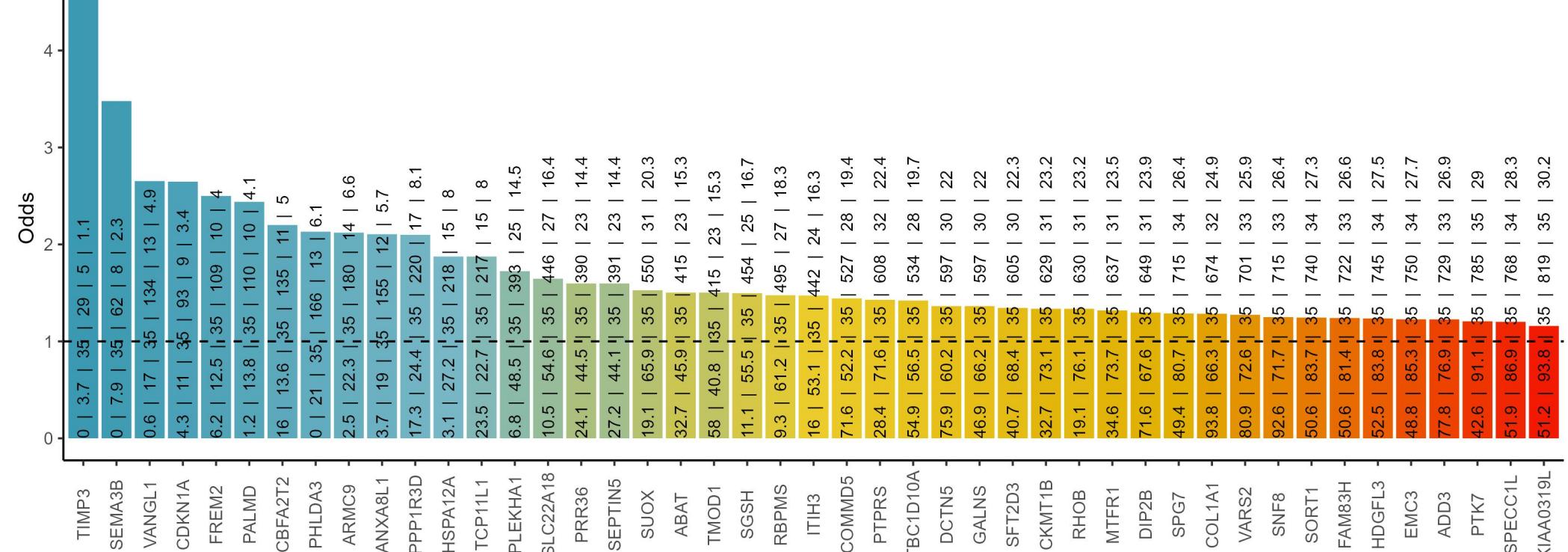
% of ACKR3 in blood cancers: 1.2 ; % of ACKR3 in solid cancers: 4.2

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ACKR3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

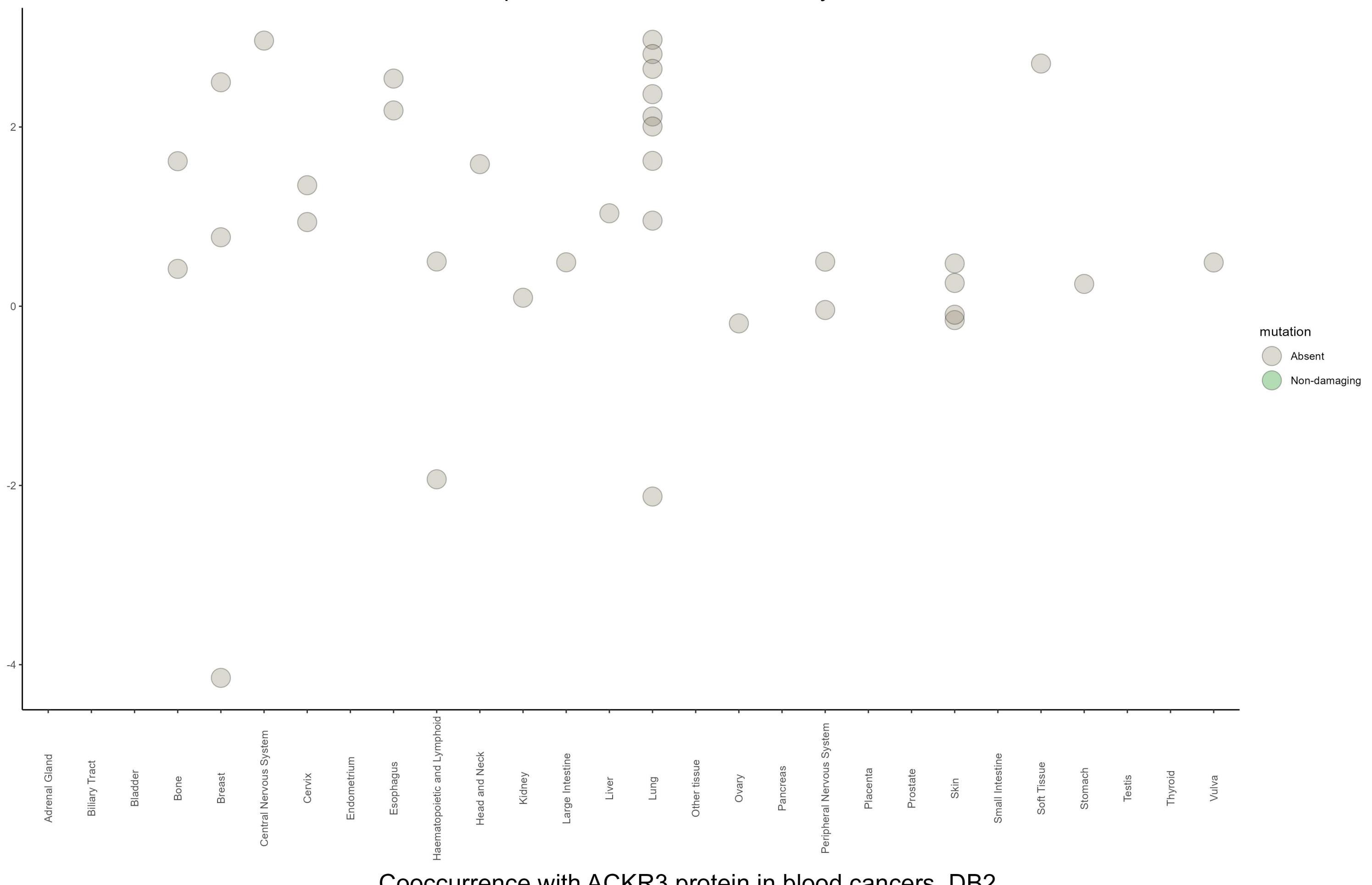
### Negative cooccurrence



### Positive cooccurrence



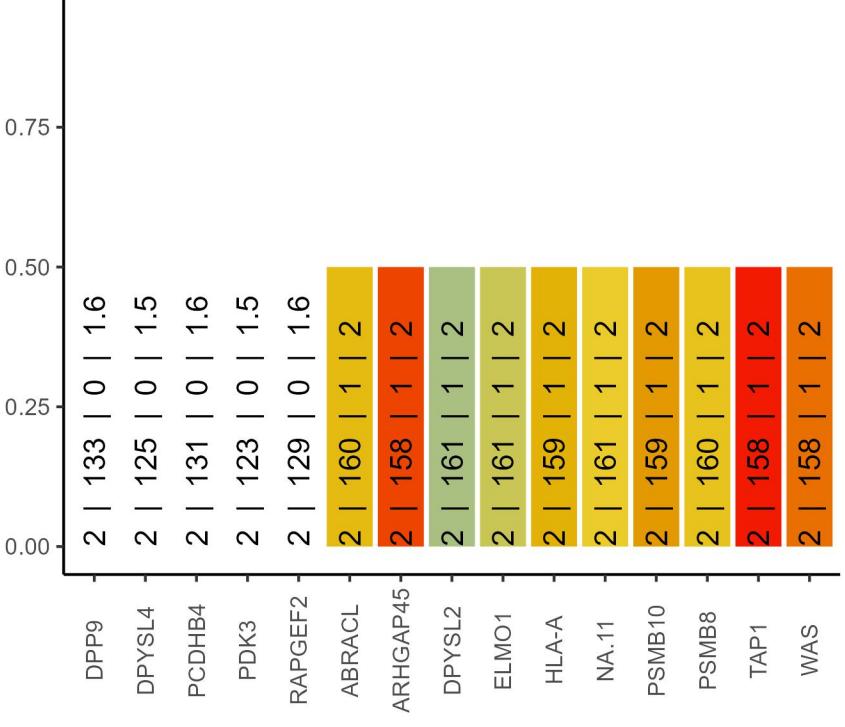
# Amount of ACKR3 protein and mutation status by tissue, DB2



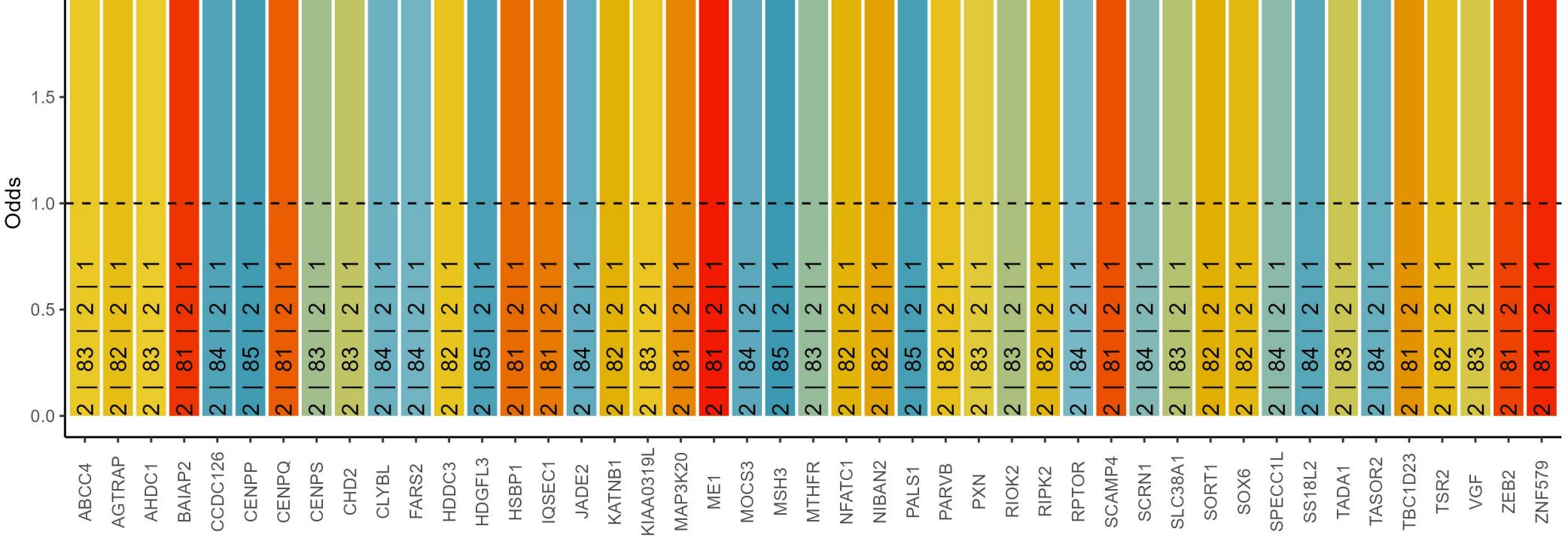
## Cooccurrence with ACKR3 protein in blood cancers, DB2

The text in the bars: incidence of ACKR3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



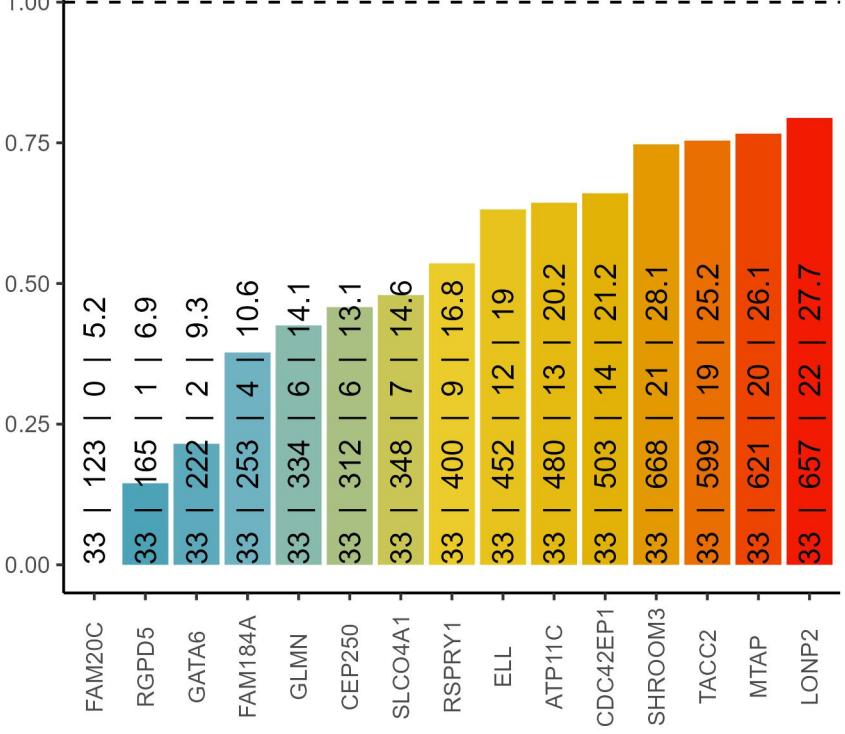
Positive cooccurrence



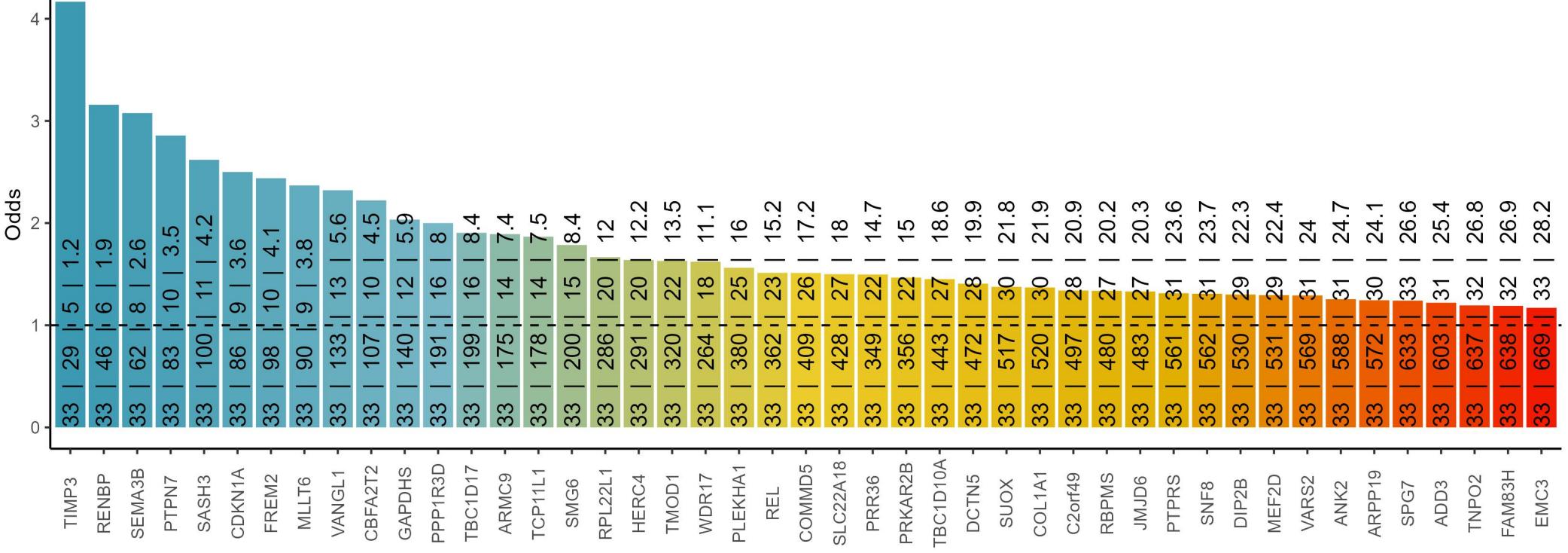
## Cooccurrence with ACKR3 protein in solid cancers, DB2

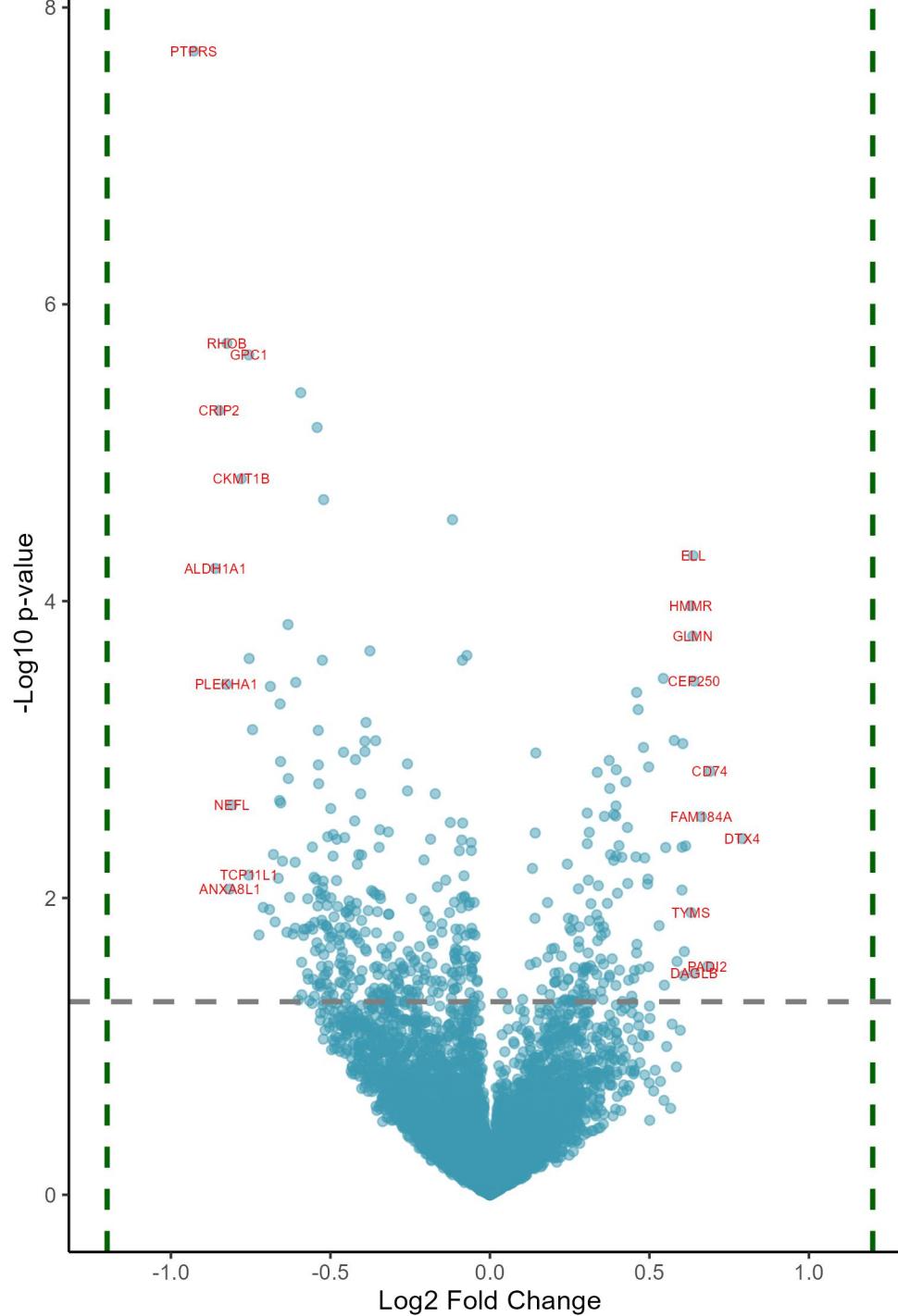
The text in the bars: incidence of ACKR3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

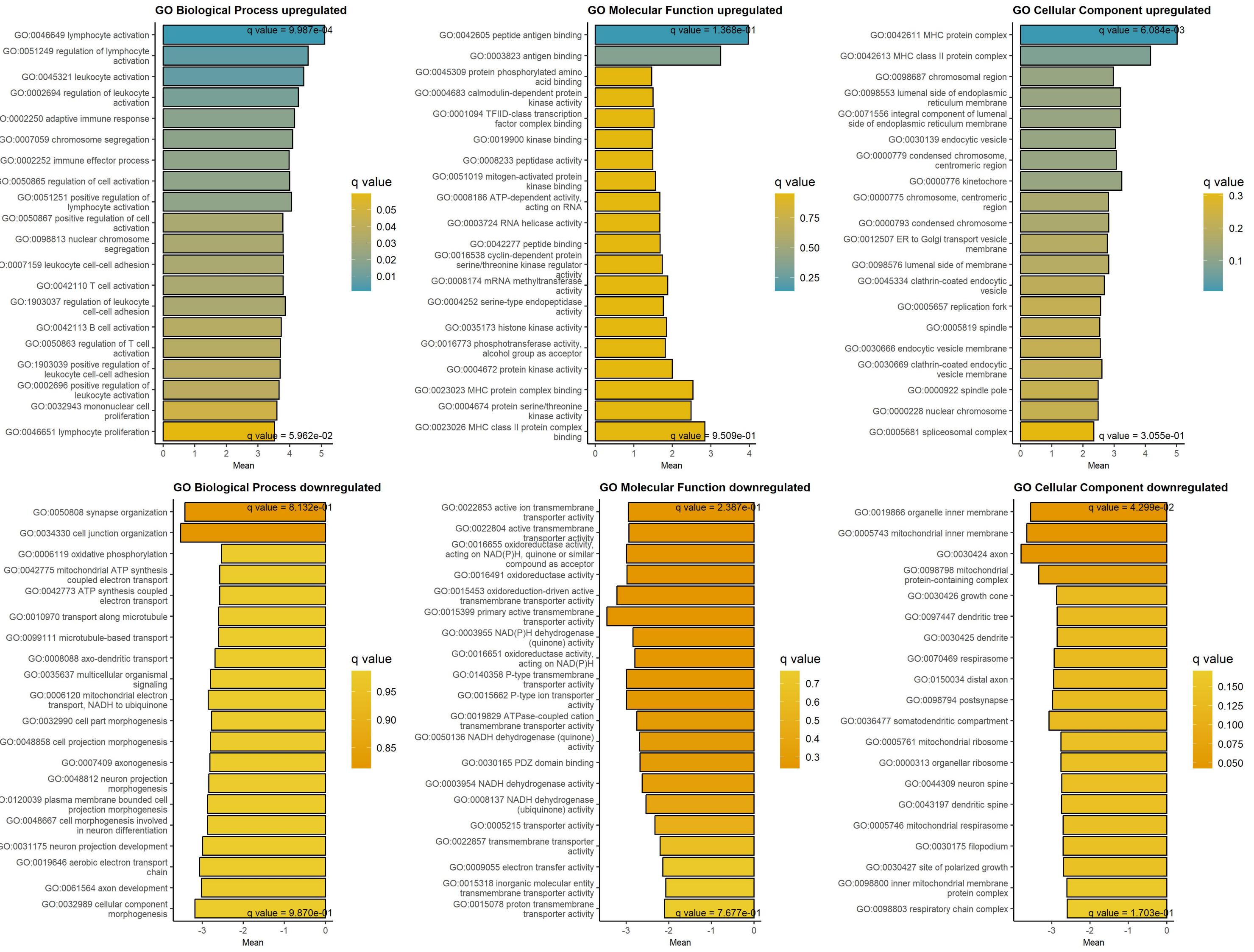




## Downregulated at low/absent ACKR3 Upregulated at low/absent ACKR3

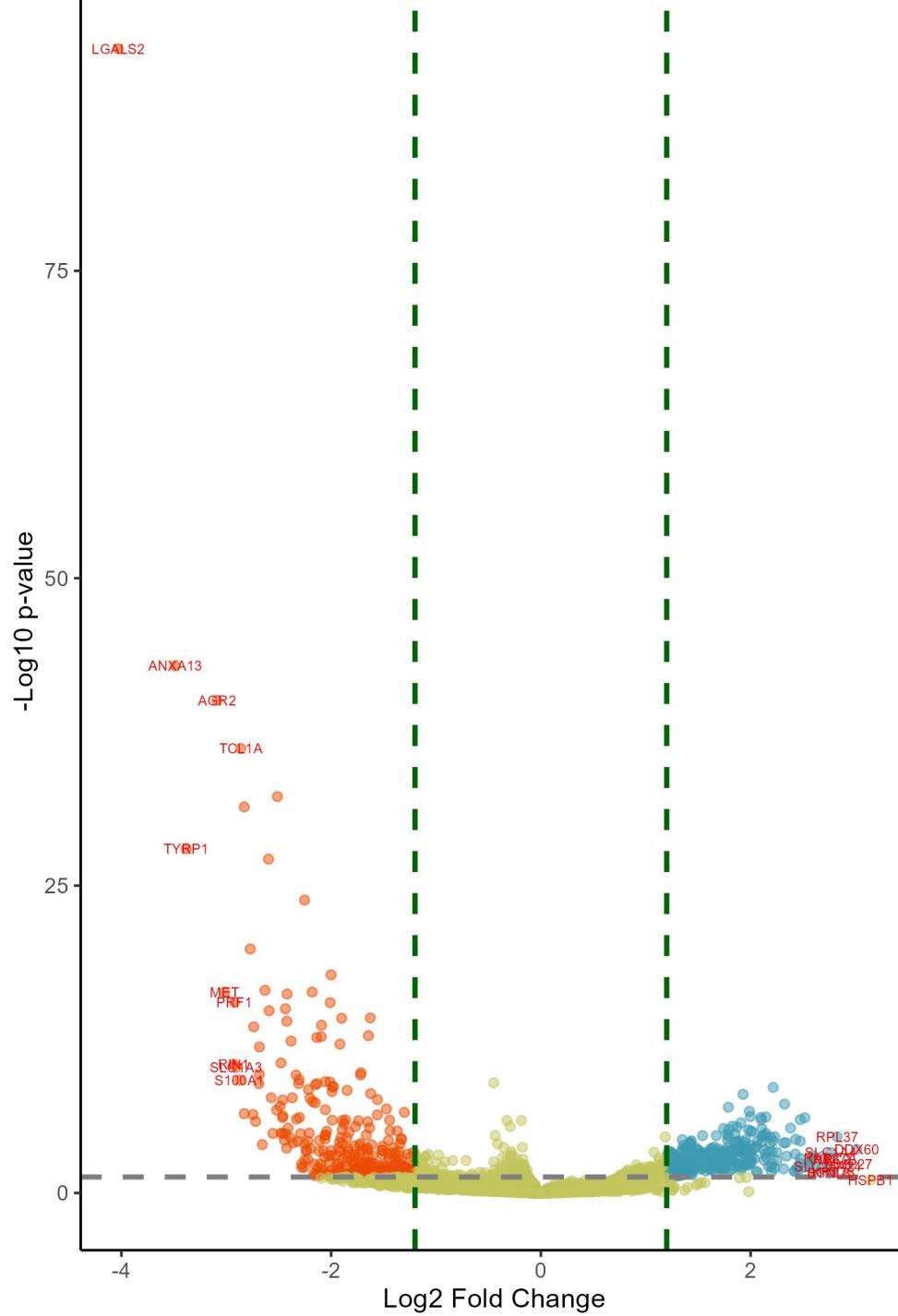
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.93	8.23e-05	PTPRS	protein tyrosine phosphatase recept	0.79	4.26e-01	DTX4	deltex E3 ubiquitin ligase 4
-0.86	4.20e-02	ALDH1A1	aldehyde dehydrogenase 1 family mem	0.69	2.48e-01	CD74	CD74 molecule
-0.85	7.24e-03	CRIP2	cysteine rich protein 2	0.68	8.13e-01	PADI2	peptidyl arginine deiminase 2
-0.83	1.26e-01	PLEKHA1	pleckstrin homology domain containi	0.66	3.65e-01	FAM184A	family with sequence similarity 184
-0.82	4.59e-03	RHOB	ras homolog family member B	0.64	8.15e-01	DAGLB	diacylglycerol lipase beta
-0.82	5.94e-01	ANXA8L1	annexin A8 like 1	0.64	1.26e-01	CEP250	centrosomal protein 250
-0.81	3.40e-01	NEFL	neurofilament light chain	0.64	3.76e-02	ELL	elongation factor for RNA polymeras
-0.78	1.57e-02	CKMT1B	creatine kinase, mitochondrial 1B	0.64	9.58e-02	GLMN	glomulin, FKBP associated protein
-0.76	5.48e-01	TCP11L1	t-complex 11 like 1	0.63	6.33e-01	TYMS	thymidylate synthetase
-0.76	4.59e-03	GPC1	glypican 1	0.63	6.90e-02	HMMR	hyaluronan mediated motility recept
-0.75	1.05e-01	SUOX	sulfite oxidase	0.61	4.35e-01	MAP3K20	mitogen-activated protein kinase ki
-0.74	2.01e-01	TRIM29	tripartite motif containing 29	0.61	7.65e-01	SHROOM3	shroom family member 3
-0.72	6.79e-01	ANXA8	annexin A8	0.61	8.18e-01	TRPC3	transient receptor potential cation
-0.71	6.24e-01	AKR1D1	aldo-keto reductase family 1 member	0.6	2.18e-01	CTSS	cathepsin S
-0.69	6.33e-01	RPL22L1	ribosomal protein L22 like 1	0.6	4.35e-01	CACNA1B	calcium voltage-gated channel subun
-0.69	1.26e-01	CLN5	CLN5 intracellular trafficking prot	0.6	5.97e-01	PDLIM2	PDZ and LIM domain 2
-0.68	4.54e-01	HERC4	HECT and RLD domain containing E3 u	0.6	9.37e-01	MTAP	methylthioadenosine phosphorylase
-0.67	6.73e-01	IGFBP3	insulin like growth factor binding	0.59	8.11e-01	GMIP	GEM interacting protein
-0.66	5.55e-01	ITIH3	inter-alpha-trypsin inhibitor heavy	0.58	9.97e-01	BST2	bone marrow stromal cell antigen 2
-0.66	3.29e-01	GDAP1	ganglioside induced differentiation	0.58	2.16e-01	DDX3Y	DEAD-box helicase 3 Y-linked
-0.66	1.53e-01	PPFIBP1	PPFIA binding protein 1	0.57	9.33e-01	COL5A2	collagen type V alpha 2 chain
-0.66	2.40e-01	FTL	ferritin light chain	0.57	9.97e-01	ENO3	enolase 3
-0.66	3.36e-01	UCHL1	ubiquitin C-terminal hydrolase L1	0.55	9.63e-01	ENTPD1	ectonucleoside triphosphate diphosp
-0.65	4.63e-01	PDE3A	phosphodiesterase 3A	0.55	4.35e-01	TRIP13	thyroid hormone receptor interactor
-0.64	6.79e-01	AKR1C3	aldo-keto reductase family 1 member	0.55	8.50e-01	CCNA2	cyclin A2
-0.63	8.59e-02	FECH	ferrochelatase	0.55	9.97e-01	MAN2C1	mannosidase alpha class 2C member 1
-0.63	2.68e-01	JMJD6	jumonji domain containing 6, argini	0.54	1.26e-01	PTK2B	protein tyrosine kinase 2 beta
-0.63	6.01e-01	PRR36	proline rich 36	0.53	9.97e-01	ARHGDIB	Rho GDP dissociation inhibitor beta
-0.62	6.79e-01	LAD1	ladinin 1	0.53	6.73e-01	CTH	cystathione gamma-lyase

## GAGE analysis on upregulated and downregulated proteins at low/absent ACKR3 protein, DB2

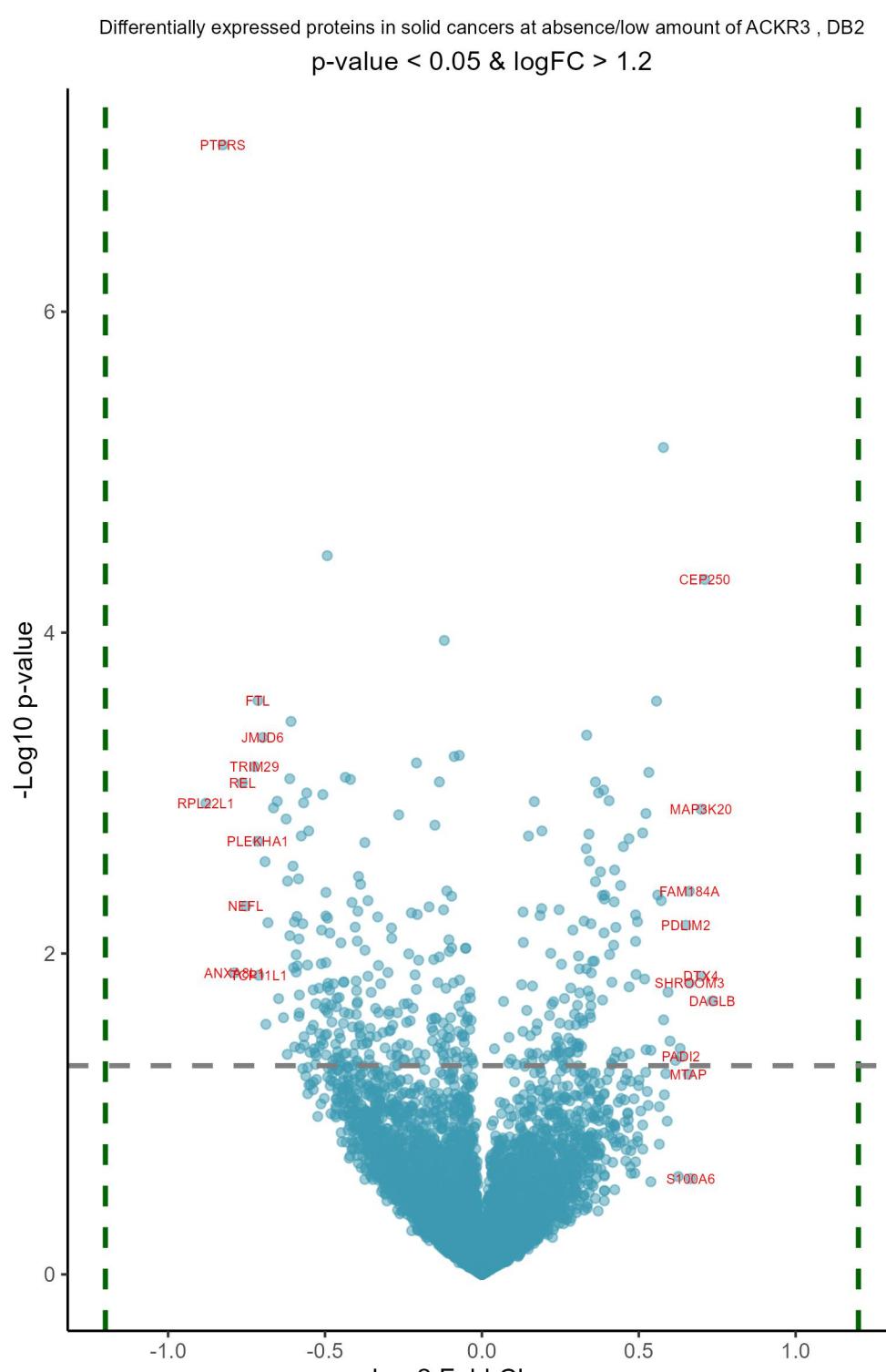


p-value &lt; 0.05 &amp; logFC &gt; 1.2

Downregulated in blood cancers at low/absent ACKR3 Upregulated in blood cancers at low/absent ACKR3

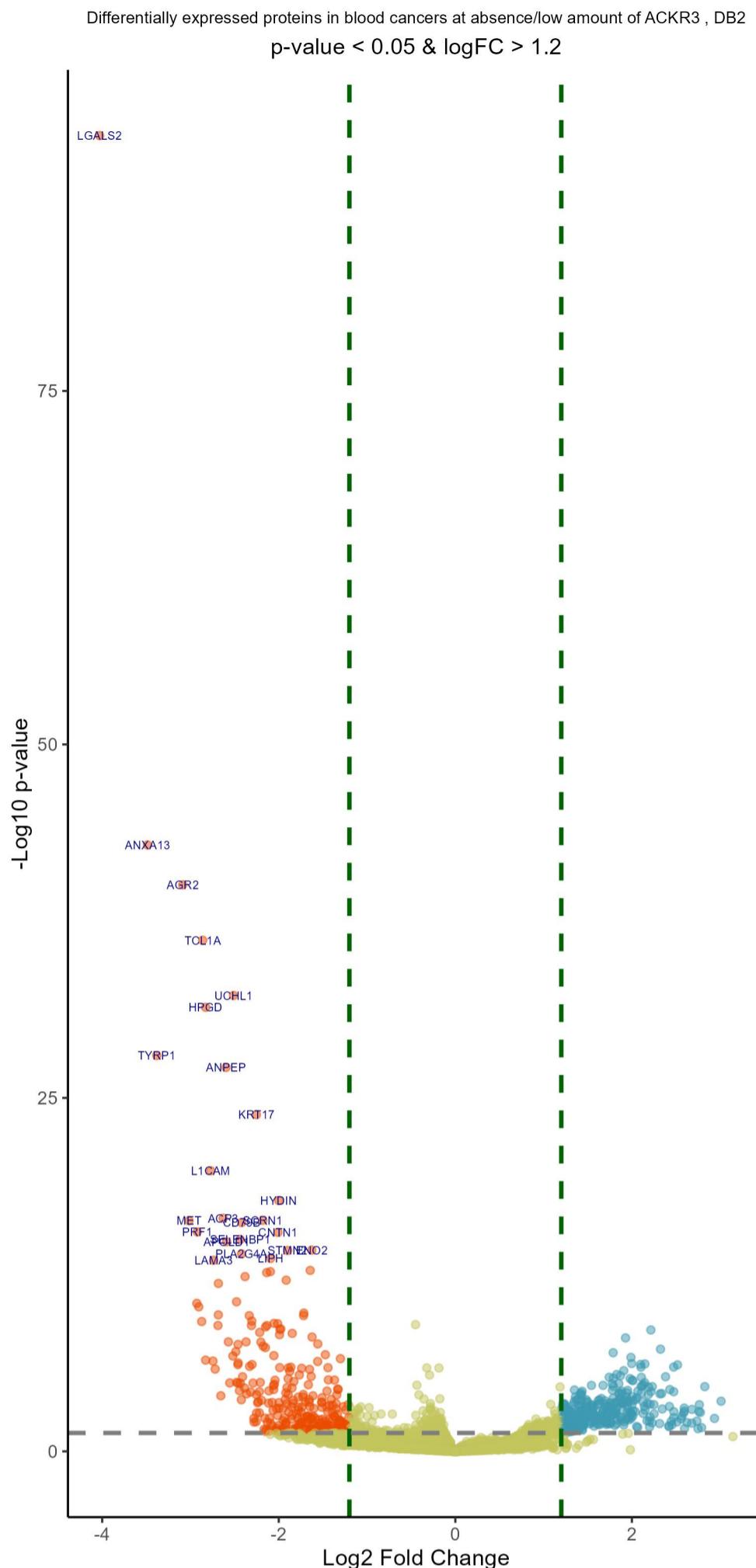


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-4.03	7.31e-90	LGALS2	galectin 2	3.14	5.75e-01	HSPB1	heat shock protein family B (small)
-3.49	5.40e-40	ANXA13	annexin A13	3.01	1.16e-02	DDX60	DExD/H-box helicase 60
-3.38	1.21e-25	TYRP1	tyrosinase related protein 1	2.94	9.02e-02	MMP27	matrix metallopeptidase 27
-3.09	2.40e-37	AGR2	anterior gradient 2, protein dislup	2.83	1.66e-03	RPL37	ribosomal protein L37
-3.02	2.89e-14	MET	MET proto-oncogene, receptor tyrosi	2.79	2.43e-01	KRT73	keratin 73
-2.93	8.59e-09	RIN1	Ras and Rab interactor 1	2.78	4.43e-02	NPC2	NPC intracellular cholesterol trans
-2.92	1.57e-13	PRF1	perforin 1	2.76	1.72e-02	SLC1A4	solute carrier family 1 member 4
-2.91	1.49e-08	SLC1A3	solute carrier family 1 member 3	2.76	3.97e-02	RAB27A	RAB27A, member RAS oncogene family
-2.87	1.37e-07	S100A1	S100 calcium binding protein A1	2.75	2.75e-01	BTNL8	butyrophilin like 8
-2.86	1.48e-33	TCL1A	TCL1 family AKT coactivator A	2.74	1.22e-01	SLC25A24	solute carrier family 25 member 24
-2.83	5.50e-29	HPGD	15-hydroxyprostaglandin dehydrogena	2.68	3.09e-02	TGM3	transglutaminase 3
-2.83	4.15e-05	FBLN2	fibulin 2	2.68	1.52e-01	RCN1	reticulocalbin 1
-2.77	1.19e-17	L1CAM	L1 cell adhesion molecule	2.62	1.42e-01	EFCAB5	EF-hand calcium binding domain 5
-2.75	4.81e-05	RNF141	ring finger protein 141	2.6	2.71e-01	HERC1	HECT and RLD domain containing E3 u
-2.74	1.07e-11	LAMA3	laminin subunit alpha 3	2.59	3.74e-02	HESX1	HESX homeobox 1
-2.72	1.39e-04	PTGES	prostaglandin E synthase	2.59	2.63e-02	DOCK9	dedicator of cytokinesis 9
-2.69	2.29e-07	ADH7	alcohol dehydrogenase 7 (class IV),	2.59	4.68e-02	ASB7	ankyrin repeat and SOCS box contain
-2.68	5.16e-08	MYT1L	myelin transcription factor 1 like	2.57	6.82e-02	PCDHB4	protocadherin beta 4
-2.68	3.59e-10	CYGB	cytoglobin	2.56	9.52e-02	ZYX	zyxin
-2.66	5.62e-03	S100A14	S100 calcium binding protein A14	2.52	7.93e-05	VTI1B	vesicle transport through interacti
-2.63	2.29e-14	ACP3	acid phosphatase 3	2.51	1.35e-01	ACTN1	actinin alpha 1
-2.6	7.29e-25	ANPEP	alanyl aminopeptidase, membrane	2.47	4.04e-02	CPT1A	carnitine palmitoyltransferase 1A
-2.59	6.57e-13	APOLD1	apolipoprotein L domain containing	2.47	3.29e-03	DYNC2H1	dynein cytoplasmic 2 heavy chain 1
-2.57	2.65e-06	WSCD1	WSC domain containing 1	2.47	1.11e-04	KRT9	keratin 9
-2.55	1.04e-03	NELL1	neural EGFL like 1	2.47	8.28e-02	SERPINB1	serpin family B member 1
-2.52	2.22e-05	MAP7D2	MAP7 domain containing 2	2.45	1.82e-01	TMEM70	transmembrane protein 70
-2.51	9.54e-30	UCHL1	ubiquitin C-terminal hydrolase L1	2.45	1.25e-01	BLVRA	biliverdin reductase A
-2.49	1.15e-05	IGSF3	immunoglobulin superfamily member 3	2.43	2.51e-03	DHRS4	dehydrogenase/reductase 4
-2.48	6.92e-09	MAPT	microtubule associated protein tau	2.42	2.18e-02	ARL8A	ADP ribosylation factor like GTPase

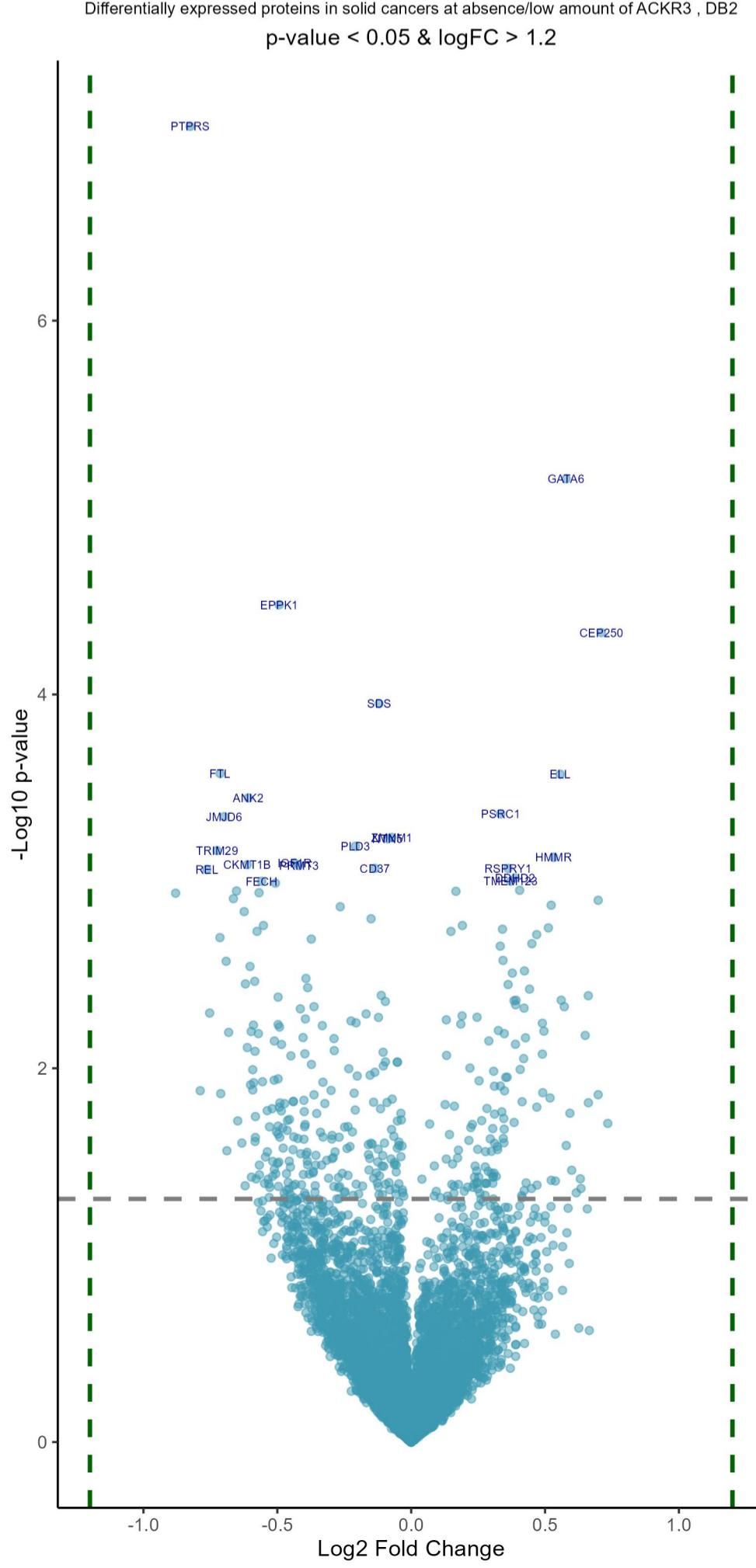


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.88	3.12e-01	RPL22L1	ribosomal protein L22 like 1	0.73	9.14e-01	DAGLB	diacylglycerol lipase beta
-0.83	3.82e-04	PTPRS	protein tyrosine phosphatase recept	0.71	7.81e-02	CEP250	centrosomal protein 250
-0.79	8.06e-01	ANXA8L1	annexin A8 like 1	0.7	3.20e-01	MAP3K20	mitogen-activated protein kinase ki
-0.76	3.12e-01	REL	REL proto-oncogene, NF- $\kappa$ B subunit	0.7	8.17e-01	DTX4	deltex E3 ubiquitin ligase 4
-0.75	5.82e-01	NEFL	neurofilament light chain	0.67	1.00e+00	S100A6	S100 calcium binding protein A6
-0.72	3.12e-01	TRIM29	tripartite motif containing 29	0.66	8.39e-01	SHROOM3	shroom family member 3
-0.71	3.70e-01	PLEKHA1	pleckstrin homology domain containi	0.66	5.56e-01	FAM184A	family with sequence similarity 184
-0.71	2.79e-01	FTL	ferritin light chain	0.66	1.00e+00	MTAP	methylthioadenosine phosphorylase
-0.71	8.17e-01	TCP11L1	t-complex 11 like 1	0.65	6.00e-01	PDLIM2	PDZ and LIM domain 2
-0.7	3.12e-01	JMJD6	jumonji domain containing 6, argini	0.63	1.00e+00	PADI2	peptidyl arginine deiminase 2
-0.69	4.48e-01	ALDH1A1	aldehyde dehydrogenase 1 family mem	0.63	1.00e+00	CDC42EP1	CDC42 effector protein 1
-0.69	9.80e-01	ANXA8	annexin A8	0.63	1.00e+00	ENO3	enolase 3
-0.68	5.93e-01	HERC4	HECT and RLD domain containing E3 u	0.62	1.00e+00	ANPEP	alanyl aminopeptidase, membrane
-0.66	3.20e-01	COL1A1	collagen type I alpha 1 chain	0.6	1.00e+00	TRPC3	transient receptor potential cation
-0.65	3.12e-01	C2orf49	chromosome 2 open reading frame 49	0.59	8.64e-01	TP53	tumor protein p53
-0.65	8.99e-01	SMG6	SMG6 nonsense mediated mRNA decay f	0.59	1.00e+00	ALDH1A2	aldehyde dehydrogenase 1 family mem
-0.63	9.62e-01	TMOD1	tropomodulin 1	0.59	1.00e+00	RGS22	regulator of G protein signaling 22
-0.62	3.37e-01	CLN5	CLN5 intracellular trafficking prot	0.58	1.00e+00	COL5A2	collagen type V alpha 2 chain
-0.62	1.00e+00	SNRPB	small nuclear ribonucleoprotein pol	0.58	9.71e-01	CPNE2	copine 2
-0.62	5.23e-01	MAZ	MYC associated zinc finger protein	0.58	1.96e-02	GATA6	GATA binding protein 6
-0.61	3.12e-01	CKMT1B	creatine kinase, mitochondrial 1B	0.57	5.67e-01	TRIP13	thyroid hormone receptor interactor
-0.61	6.42e-01	POLE	DNA polymerase epsilon, catalytic s	0.57	1.00e+00	C2CD2	C2 calcium dependent domain contain
-0.61	3.12e-01	ANK2	ankyrin 2	0.57	1.00e+00	EGFR	epidermal growth factor receptor
-0.6	4.68e-01	SUOX	sulfite oxidase	0.56	5.56e-01	LONP2	ion peptidase 2, peroxisomal
-0.6	7.83e-01	DDB2	damage specific DNA binding protein	0.56	2.79e-01	ELL	elongation factor for RNA polymeras
-0.6	5.93e-01	TSC22D4	TSC22 domain family member 4	0.54	1.00e+00	MAN2C1	mannosidase alpha class 2C member 1
-0.6	1.00e+00	AKR1D1	aldo-keto reductase family 1 member	0.54	1.00e+00	TMEM63A	transmembrane protein 63A
-0.59	7.21e-01	PNMA8B	PNMA family member 8B	0.53	3.12e-01	HMMR	hyaluronan mediated motility recept
-0.59	8.06e-01	PDE3A	phosphodiesterase 3A	0.53	1.00e+00	DCBLD2	discoidin, CUB and LCCL domain cont

ACKR3 network, DB2, no Pearson r &gt; 0.3



Sorted by p values!							
Downregulated in blood cancers at low/absent ACKR3				Upregulated in blood cancers at low/absent ACKR3			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-4.03	7.31e-90	LGALS2	galectin 2	2.21	4.34e-07	MRPL34	mitochondrial ribosomal protein L34
-3.49	5.40e-40	ANXA13	annexin A13	1.93	1.44e-06	SRP19	signal recognition particle 19
-3.09	2.40e-37	AGR2	anterior gradient 2, protein disulf	2.32	7.83e-06	ARF6	ADP ribosylation factor 6
-2.86	1.48e-33	TCL1A	TCL1 family AKT coactivator A	1.79	1.36e-05	DDA1	DET1 and DDB1 associated 1
-2.51	9.54e-30	UCHL1	ubiquitin C-terminal hydrolase L1	1.99	2.75e-05	DNAJB12	DnaJ heat shock protein family (Hsp)
-2.83	5.50e-29	HPGD	15-hydroxyprostaglandin dehydrogena	2	6.86e-05	L2HGDH	L-2-hydroxyglutarate dehydrogenase
-3.38	1.21e-25	TYRP1	tyrosinase related protein 1	2.15	7.24e-05	DAD1	defender against cell death 1
-2.6	7.29e-25	ANPEP	alanyl aminopeptidase, membrane	2.1	7.71e-05	TOR1A	torsin family 1 member A
-2.25	1.41e-21	KRT17	keratin 17	2.52	7.93e-05	VTI1B	vesicle transport through interacti
-2.77	1.19e-17	L1CAM	L1 cell adhesion molecule	2.47	1.11e-04	KRT9	keratin 9
-2	1.37e-15	HYDIN	HYDIN axonemal central pair apparat	2.1	1.11e-04	TMEM41B	transmembrane protein 41B
-2.63	2.29e-14	ACP3	acid phosphatase 3	1.91	1.77e-04	ECSIT	ECSIT signaling integrator
-2.18	2.89e-14	SCRN1	secernin 1	1.83	3.19e-04	XRN1	5'-3' exoribonuclease 1
-3.02	2.89e-14	MET	MET proto-oncogene, receptor tyrosi	1.87	3.82e-04	COX6A1	cytochrome c oxidase subunit 6A1
-2.42	3.64e-14	CD79B	CD79b molecule	2.38	4.38e-04	DERL1	derlin 1
-2.92	1.57e-13	PRF1	perforin 1	1.74	4.69e-04	CNOT7	CCR4-NOT transcription complex sub
-2.01	1.61e-13	CNTN1	contactin 1	2.11	4.71e-04	OPA3	outer mitochondrial membrane lipid
-2.44	4.80e-13	SELENBP1	selenium binding protein 1	1.79	5.32e-04	INTS5	integrator complex subunit 5
-2.59	6.57e-13	APOLD1	apolipoprotein L domain containing	1.98	5.67e-04	PRKAG1	protein kinase AMP-activated non-ca
-1.63	2.44e-12	ENO2	enolase 2	2	7.10e-04	ERMP1	endoplasmic reticulum metallopeptid
-1.9	2.48e-12	STMN2	stathmin 2	2.01	7.49e-04	MAP7D3	MAP7 domain containing 3
-2.42	4.08e-12	PLA2G4A	phospholipase A2 group IVA	2.14	1.01e-03	TLN2	talin 2
-2.09	8.27e-12	LIPH	lipase H	1.85	1.13e-03	MIDEAS	mitotic deacetylase associated SANT
-2.74	1.07e-11	LAMA3	laminin subunit alpha 3	1.78	1.18e-03	SPATA16	spermatogenesis associated 16
-1.64	5.31e-11	CTNNA1	catenin alpha 1	2.13	1.31e-03	RBM15B	RNA binding motif protein 15B
-2.1	6.23e-11	JCHAIN	joining chain of multimeric IgA and	1.67	1.42e-03	DAP	death associated protein
-2.14	7.03e-11	MAP1A	microtubule associated protein 1A	1.54	1.42e-03	ARFGEF1	ADP ribosylation factor guanine nuc
-2.38	1.26e-10	PHYH	phytanoyl-CoA 2-hydroxylase	2.12	1.52e-03	COX7A2L	cytochrome c oxidase subunit 7A2 li
-1.92	2.17e-10	ITGB4	integrin subunit beta 4	2.1	1.60e-03	ABCB10	ATP binding cassette subfamily B me
-2.68	3.59e-10	CYGB	cytoglobin	1.79	1.62e-03	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-2.48	6.92e-09	MAPT	microtubule associated protein tau	2.83	1.66e-03	RPL37	ribosomal protein L37
-2.93	8.59e-09	RIN1	Ras and Rab interactor 1	2.23	1.66e-03	ENDOG	endonuclease G
-2.91	1.49e-08	SLC1A3	solute carrier family 1 member 3	1.19	1.73e-03	NFRKB	nuclear factor related to kappaB bi
-1.72	3.96e-08	IGF2BP1	insulin like growth factor 2 mRNA b	2.19	1.76e-03	NUDT19	nudix hydrolase 19
-2.68	5.16e-08	MYT1L	myelin transcription factor 1 like	2.43	2.51e-03	DHRS4	dehydrogenase/reductase 4
-1.72	5.55e-08	KRT19	keratin 19	1.35	2.67e-03	YIPF5	Yip1 domain family member 5
-2.33	5.55e-08	HLA-DRB5	major histocompatibility complex, c	1.78	2.72e-03	NEK7	NIMA related kinase 7
-2.31	1.31e-07	CPQ	carboxypeptidase Q	1.95	2.81e-03	YIPF1	Yip1 domain family member 1
-2.27	1.27e-07	S100A11	S100 calcium binding protein A11	2.07	2.97e-03	S100A11	solute carrier family 25 member 11

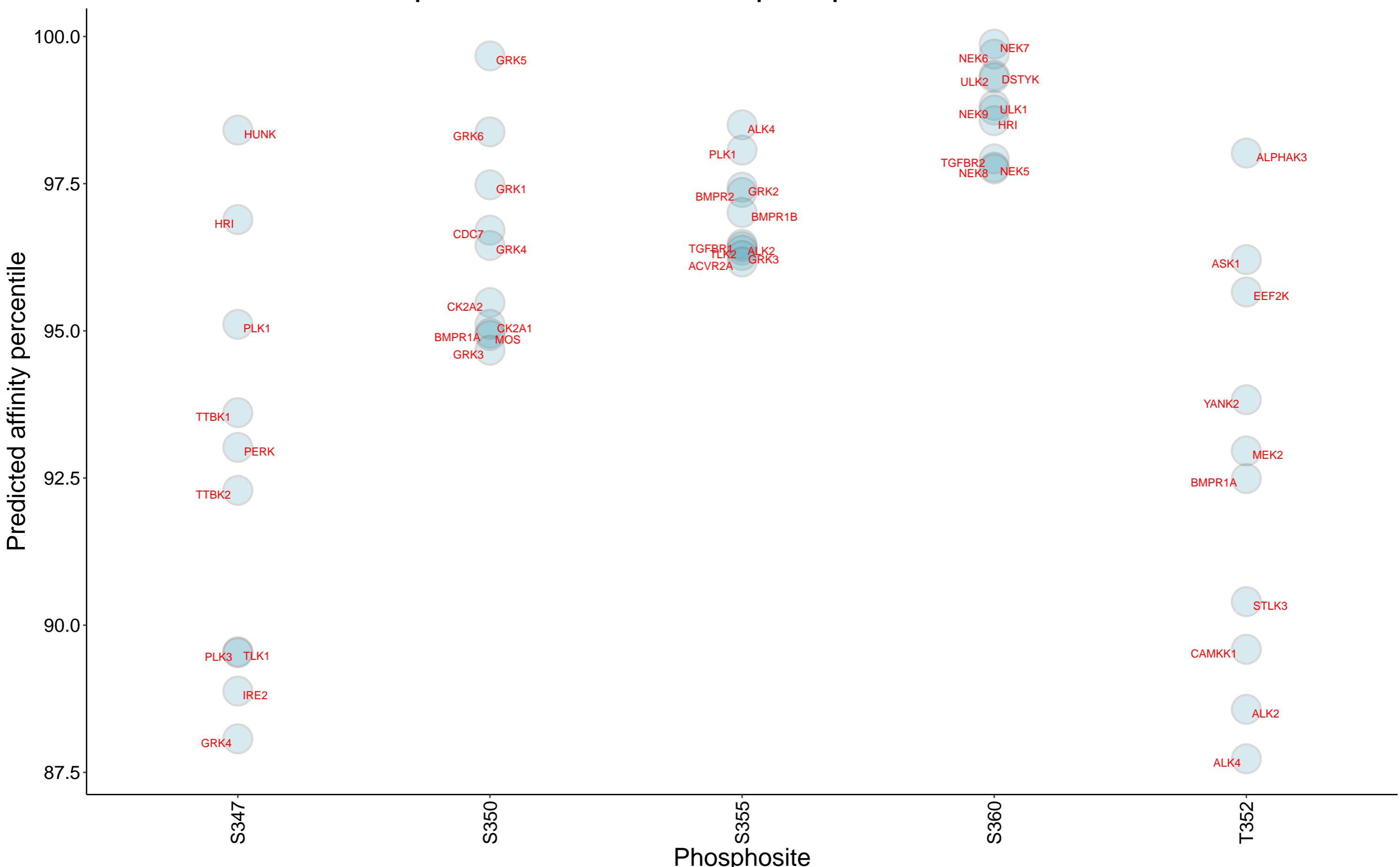


Sorted by p values!							
Downregulated in solid cancers at low/absent ACKR3				Upregulated in solid cancers at low/absent ACKR3			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.83	3.82e-04	PTPRS	protein tyrosine phosphatase recept	0.58	1.96e-02	GATA6	GATA binding protein 6
-0.49	6.93e-02	EPPK1	epiplakin 1	0.71	7.81e-02	CEP250	centrosomal protein 250
-0.12	1.56e-01	SDS	serine dehydratase	0.56	2.79e-01	ELL	elongation factor for RNA polymeras
-0.71	2.79e-01	FTL	ferritin light chain	0.33	3.12e-01	PSRC1	proline and serine rich coiled-coil
-0.61	3.12e-01	ANK2	ankyrin 2	0.53	3.12e-01	HMMR	hyaluronan mediated motility recept
-0.7	3.12e-01	JMJD6	jumonji domain containing 6, argini	0.36	3.12e-01	RSPRY1	ring finger and SPRY domain contain
-0.07	3.12e-01	ZMYM1	zinc finger MYM-type containing 1	0.39	3.12e-01	DDHD2	DDHD domain containing 2
-0.09	3.12e-01	NTN5	netrin 5	0.37	3.12e-01	TMEM123	transmembrane protein 123
-0.21	3.12e-01	PLD3	phospholipase D family member 3	0.41	3.12e-01	BST1	bone marrow stromal cell antigen 1
-0.72	3.12e-01	TRIM29	tripartite motif containing 29	0.17	3.12e-01	PDHX	pyruvate dehydrogenase complex comp
-0.44	3.12e-01	IGF1R	insulin like growth factor 1 recept	0.7	3.20e-01	MAP3K20	mitogen-activated protein kinase ki
-0.61	3.12e-01	CKMT1B	creatine kinase, mitochondrial 1B	0.52	3.27e-01	IMMP2L	inner mitochondrial membrane peptid
-0.42	3.12e-01	PRMT3	protein arginine methyltransferase	0.19	3.60e-01	STX16	syntaxis 16
-0.14	3.12e-01	CD37	CD37 molecule	0.51	3.60e-01	GLMN	glomulin, FKBP associated protein
-0.76	3.12e-01	REL	REL proto-oncogene, NF- $\kappa$ B subunit	0.34	3.60e-01	TRIM44	tripartite motif containing 44
-0.56	3.12e-01	FECH	ferrochelatase	0.15	3.60e-01	IWS1	interacts with SUPT6H, CTD assembly
-0.51	3.12e-01	GPC1	glypican 1	0.47	3.66e-01	YTHDC2	YTH domain containing 2
-0.65	3.12e-01	C2orf49	chromosome 2 open reading frame 49	0.45	3.84e-01	ACAD11	acyl-CoA dehydrogenase family memb
-0.57	3.12e-01	RHOB	ras homolog family member B	0.33	3.87e-01	FAM20C	FAM20C golgi associated secretory p
-0.88	3.12e-01	RPL22L1	ribosomal protein L22 like 1	0.34	4.48e-01	ATG7	autophagy related 7
-0.66	3.20e-01	COL1A1	collagen type I alpha 1 chain	0.42	4.85e-01	SIPA1L1	signal induced proliferation associ
-0.27	3.27e-01	GAA	alpha glucosidase	0.38	4.89e-01	STBD1	starch binding domain 1
-0.62	3.37e-01	CLN5	CLN5 intracellular trafficking prot	0.36	5.23e-01	GOLM1	golgi membrane protein 1
-0.15	3.58e-01	GBP5	guanylate binding protein 5	0.44	5.35e-01	KLHL7	kelch like family member 7
-0.55	3.60e-01	SHOC2	SHOC2 leucine rich repeat scaffold	0.66	5.56e-01	FAM184A	family with sequence similarity 184
-0.58	3.60e-01	CRIP2	cysteine rich protein 2	0.56	5.56e-01	LONP2	ion peptidase 2, peroxisomal
-0.71	3.70e-01	PLEKHA1	pleckstrin homology domain containi	0.39	5.56e-01	PAX8	paired box 8
-0.37	3.70e-01	DYNLL1	dynein light chain LC8-type 1	0.38	5.56e-01	ITM2A	integral membrane protein 2A
-0.69	4.48e-01	ALDH1A1	aldehyde dehydrogenase 1 family mem	0.39	5.67e-01	OBI1	ORC ubiquitin ligase 1
-0.6	4.68e-01	SUOX	sulfite oxidase	0.57	5.67e-01	TRIP13	thyroid hormone receptor interactor
-0.39	5.12e-01	RABIF	RAB interacting factor	0.42	5.67e-01	JPH2	junctophilin 2
-0.58	5.21e-01	UNC119B	unc-119 lipid binding chaperone B	0.19	5.82e-01	TJP1	tight junction protein 1
-0.62	5.23e-01	MAZ	MYC associated zinc finger protein	0.25	5.82e-01	MVB12B	multivesicular body subunit 12B
-0.39	5.34e-01	TIMP3	TIMP metallopeptidase inhibitor 3	0.13	5.82e-01	NCSTN	nicastrin
-0.11	5.56e-01	CD34	CD34 molecule	0.49	5.82e-01	DDX3Y	DEAD-box helicase 3 Y-linked
-0.5	5.56e-01	COQ3	coenzyme Q3, methyltransferase	0.19	5.82e-01	SETX	senataxin
-0.1	5.56e-01	FCGR2B	Fc gamma receptor IIb	0.33	5.93e-01	SLC39A4	solute carrier family 39 member 4
-0.36	5.67e-01	ZAP70	zeta chain of T cell receptor assoc	0.5	5.93e-01	STX2	syntaxin 2
-0.11	5.67e-01	CCAPP1	CCAPP1	0.25	5.93e-01	TYRPB1	tyrosinase related protein 1

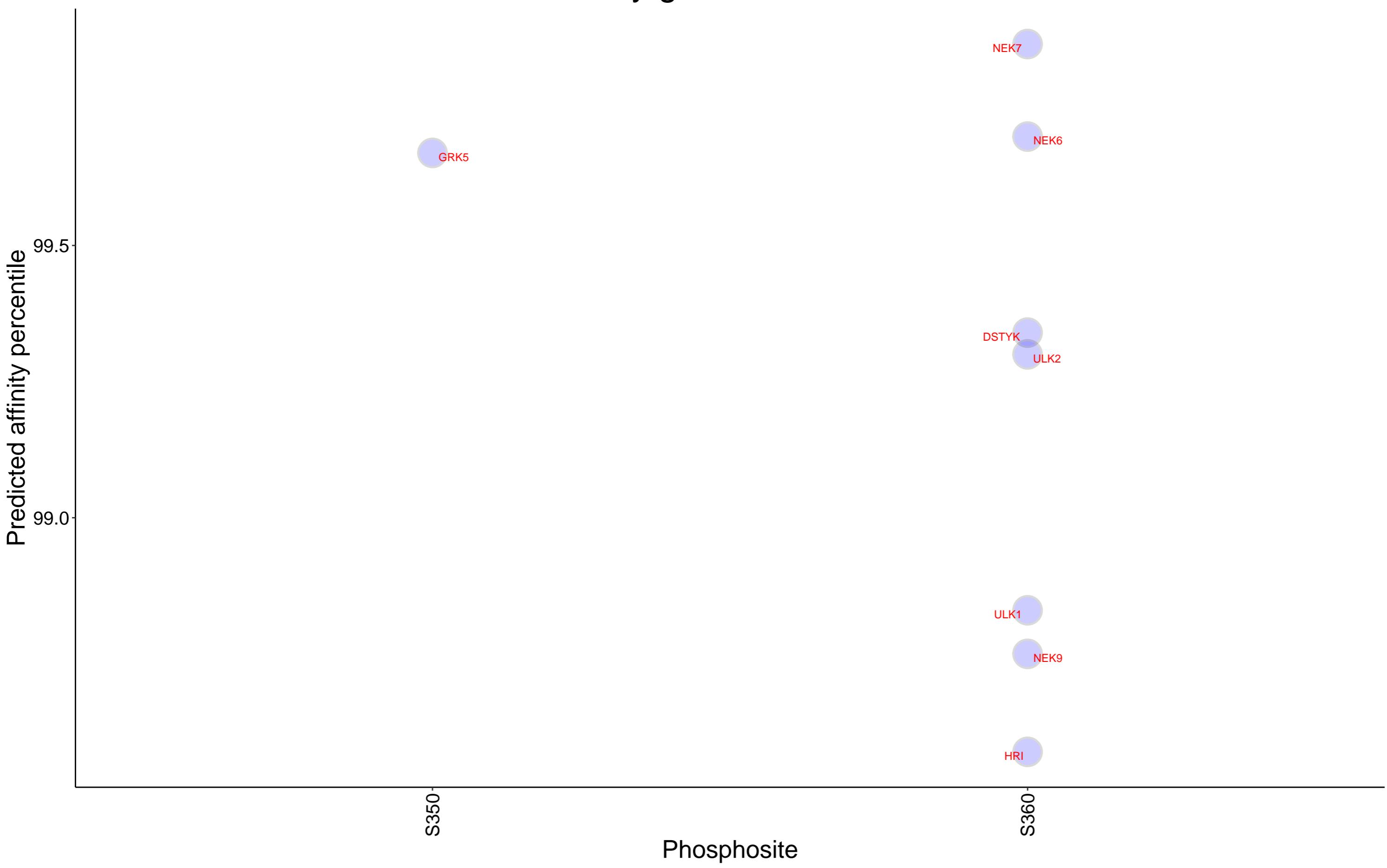
Insufficient number of paired observations in DB2 for ACKR3

Insufficient number of paired observations in DB2 for ACKR3

# Top 10 kinases for each phosphosite in ACKR3



**Kinases with affinity greater than 98.5% to ACKR3**



No sufficient number of paired observations in DB2 for ACKR3