

ABL1

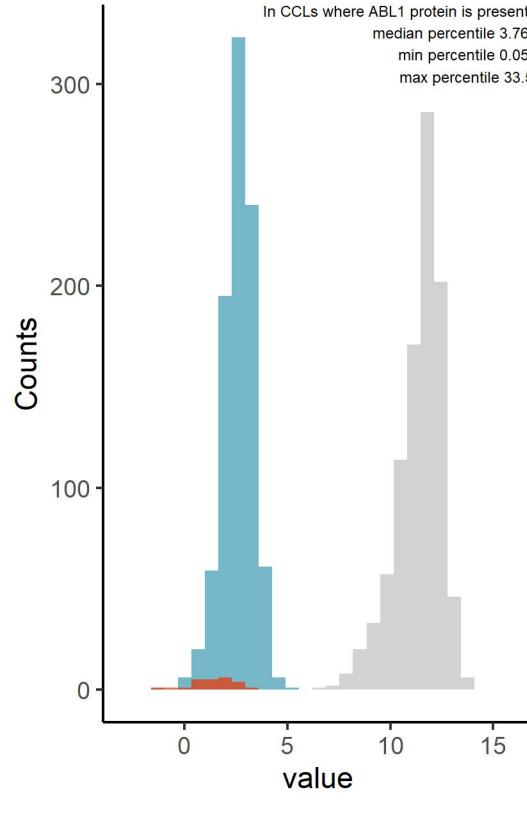
Protein name: ABL1 ; UNIPROT: P00519 ; Gene name: ABL proto-oncogene 1, non-receptor tyrosine kinase

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

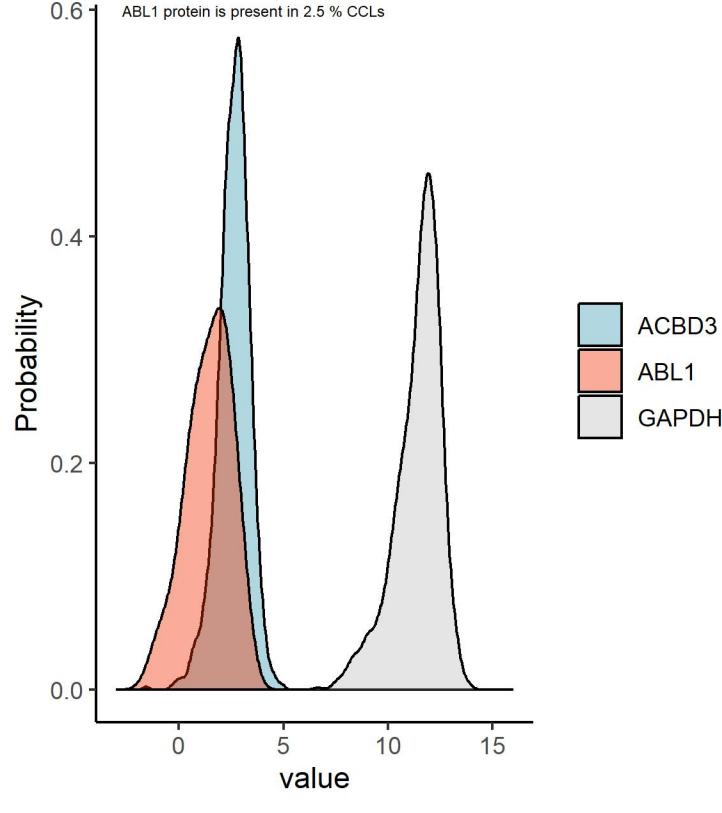
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of ABL1 protein compared to proteins with low and high abundance



Density plot of ABL1 protein compared to proteins with low and high abundance



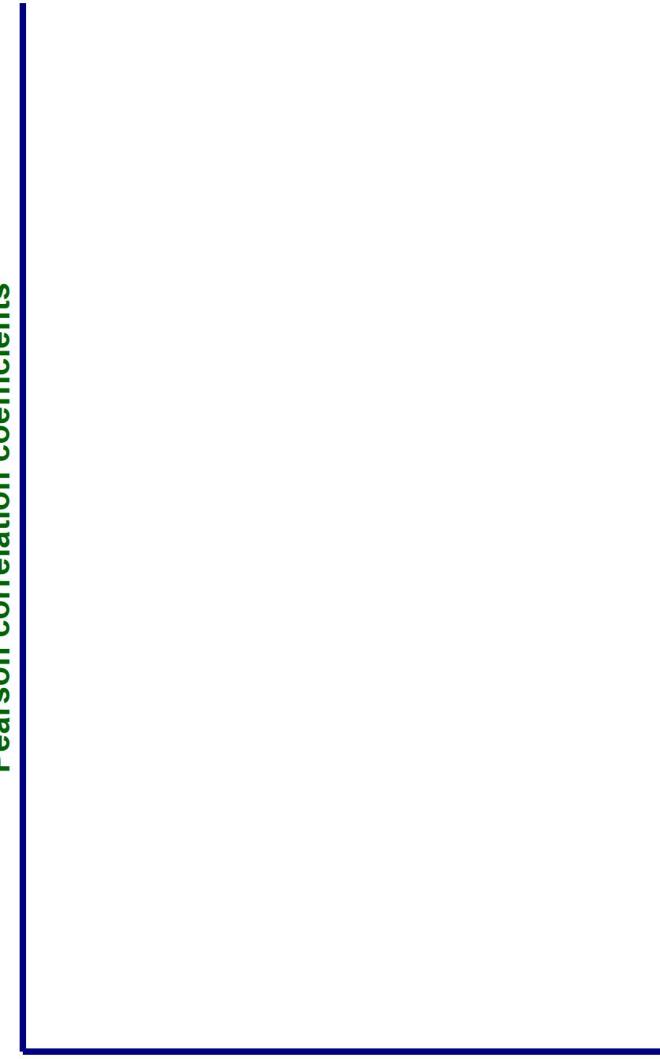
Top negative correlations of ABL1 protein, DB1

Pearson correlation coefficients



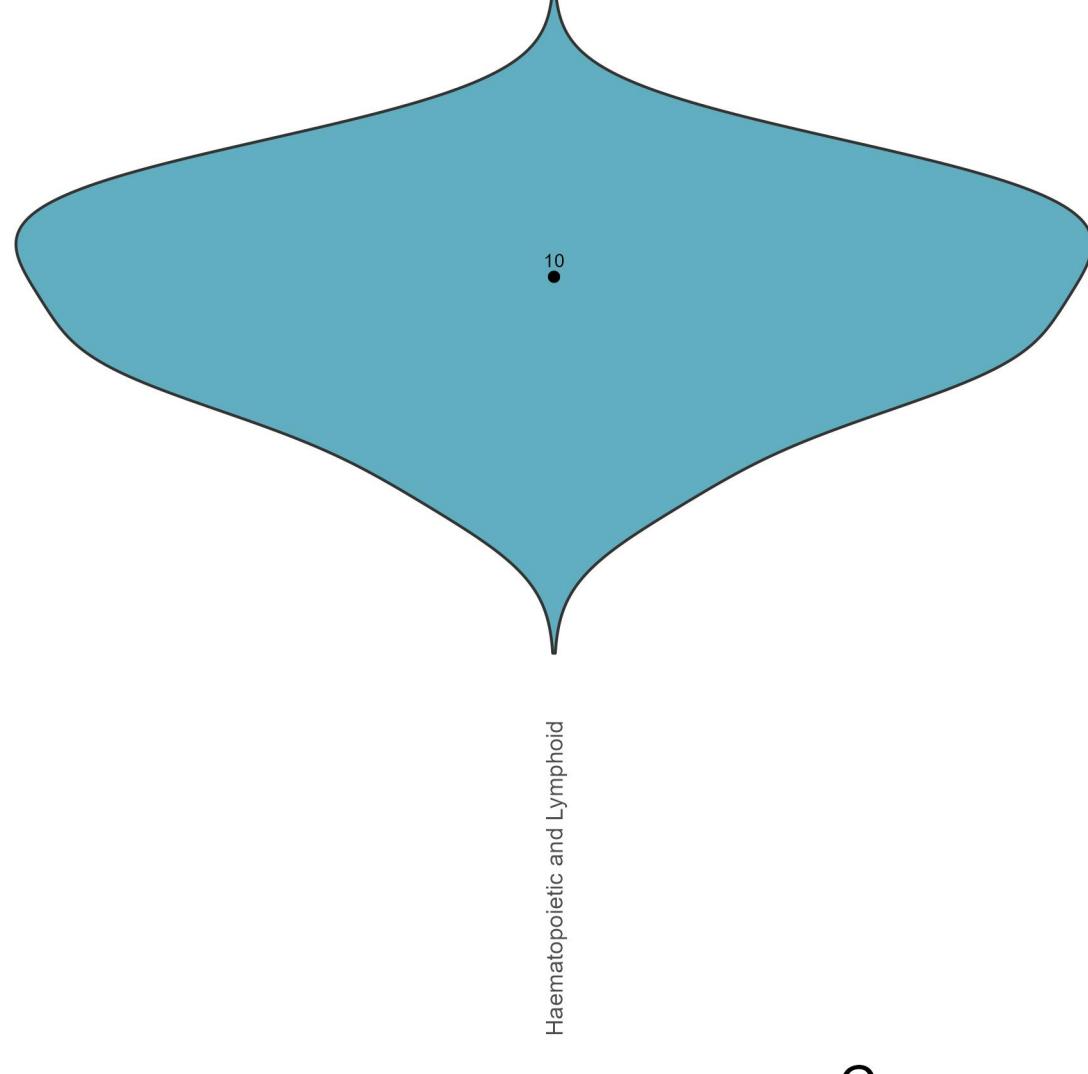
Top positive correlations of ABL1 protein, DB1

Pearson correlation coefficients



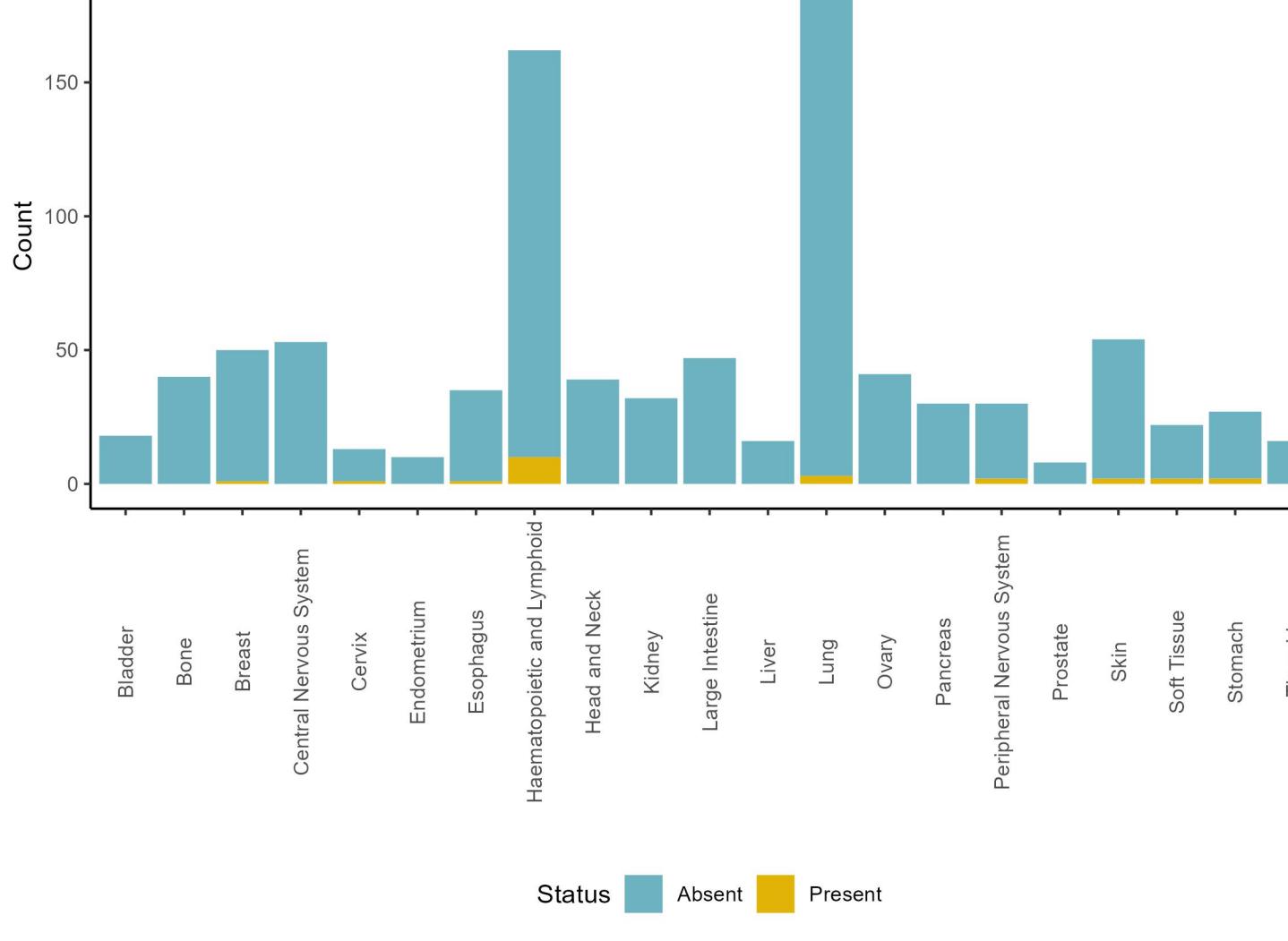
Amount of ABL1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 2.138e-02



Present and absent ABL1 protein counts by tissue, DB1

Chi square p value is 1.069e-01

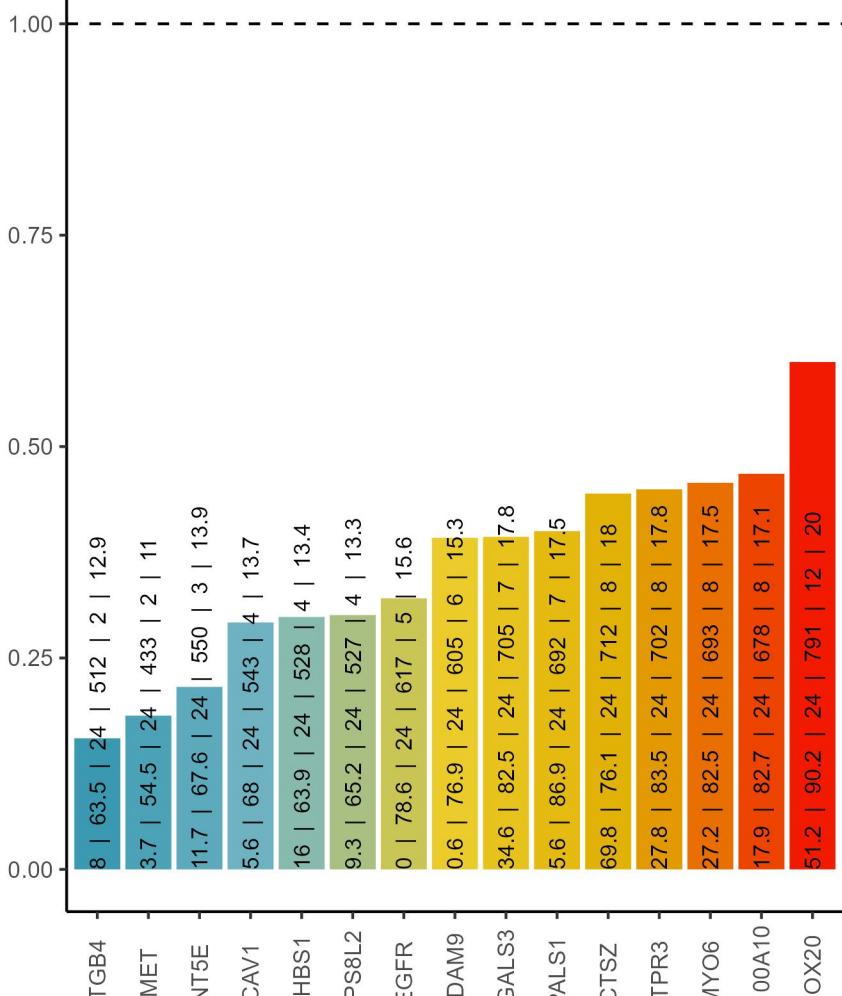


Cooccurrence with ABL1 protein, DB1

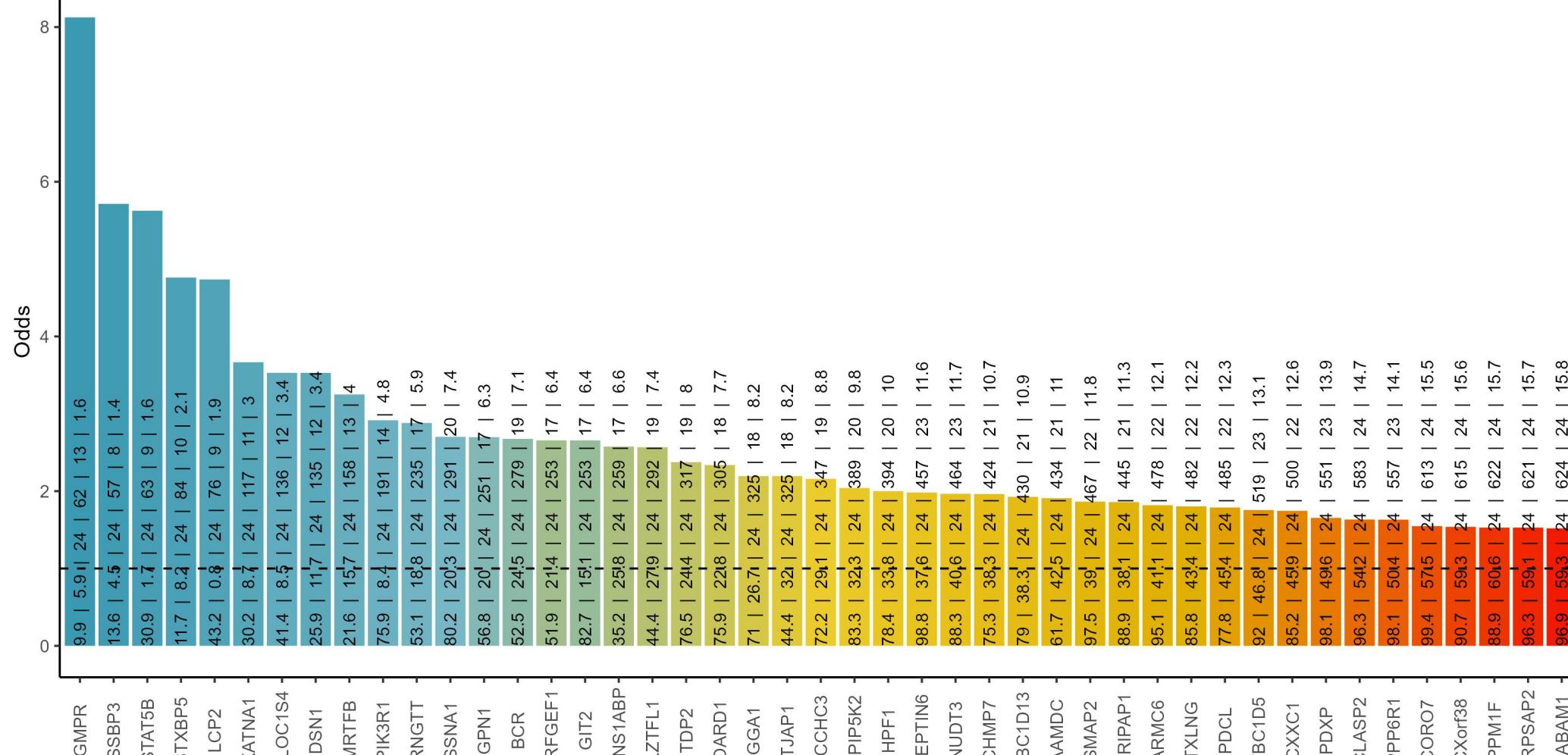
% of ABL1 in blood cancers: 6.2 ; % of ABL1 in solid cancers: 1.8

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ABL1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

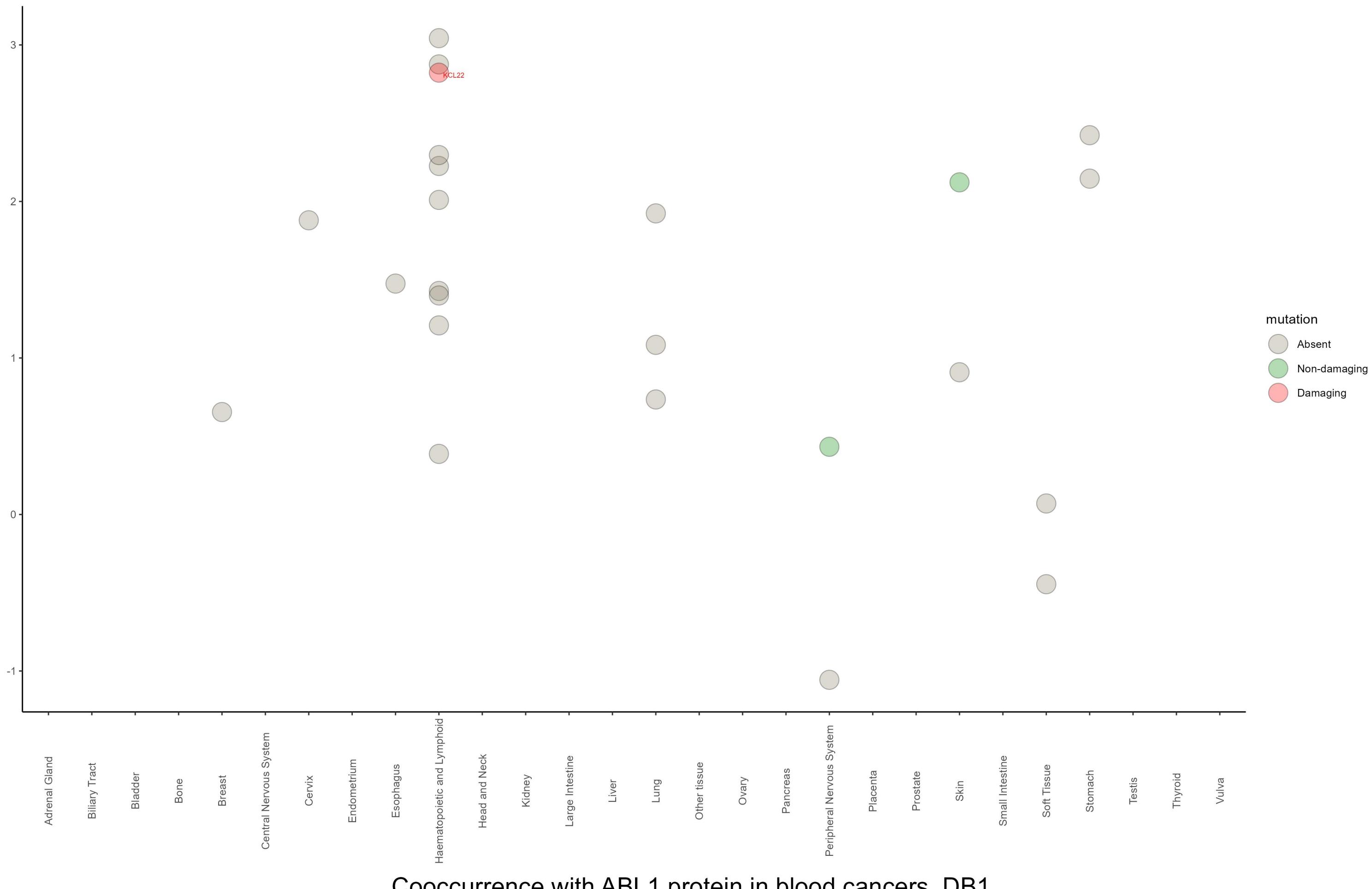
Negative cooccurrence



Positive cooccurrence

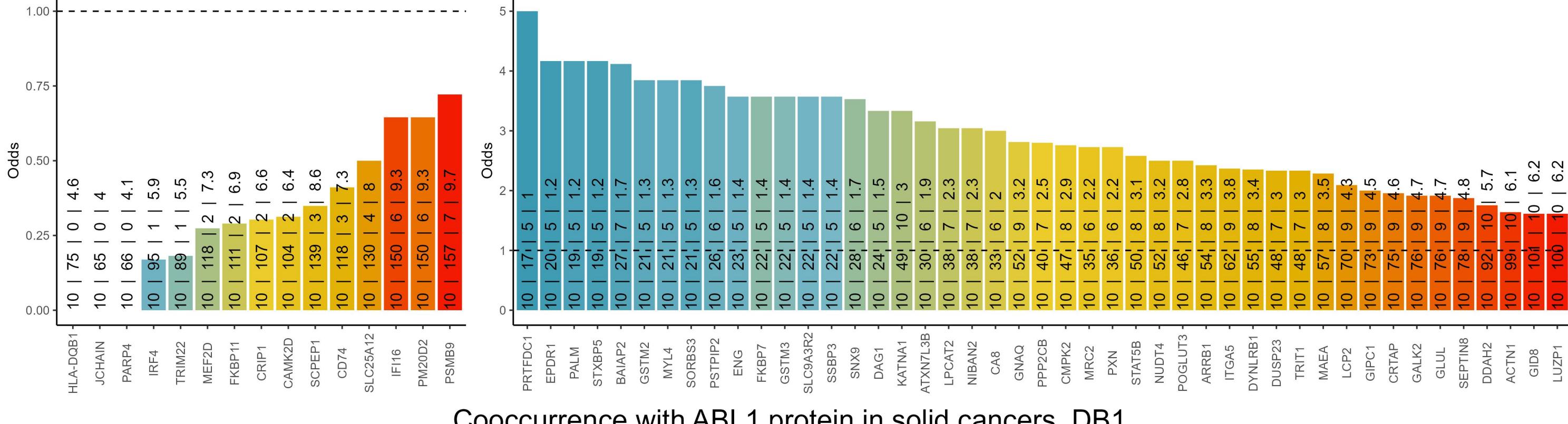


Amount of ABL1 protein and mutation status by tissue, DB1



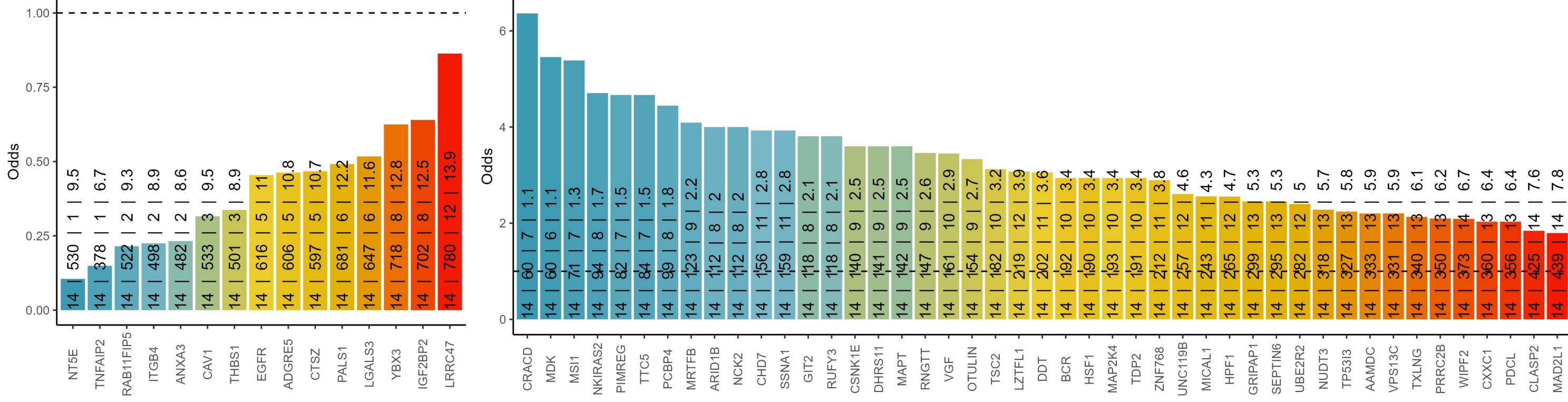
Cooccurrence with ABL1 protein in blood cancers, DB1

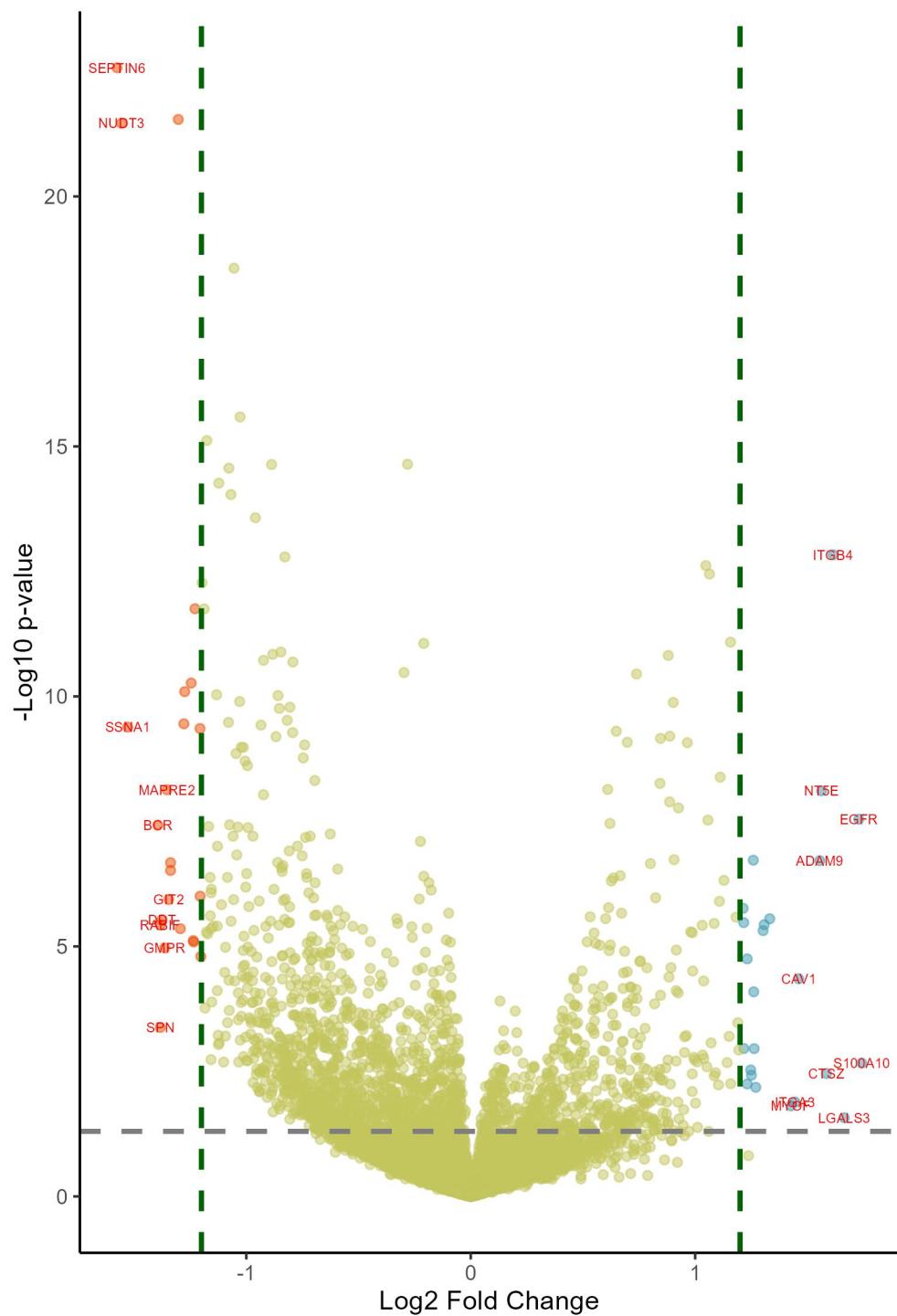
The text in the bars: incidence of ABL1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with ABL1 protein in solid cancers, DB1

The text in the bars: incidence of ABL1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

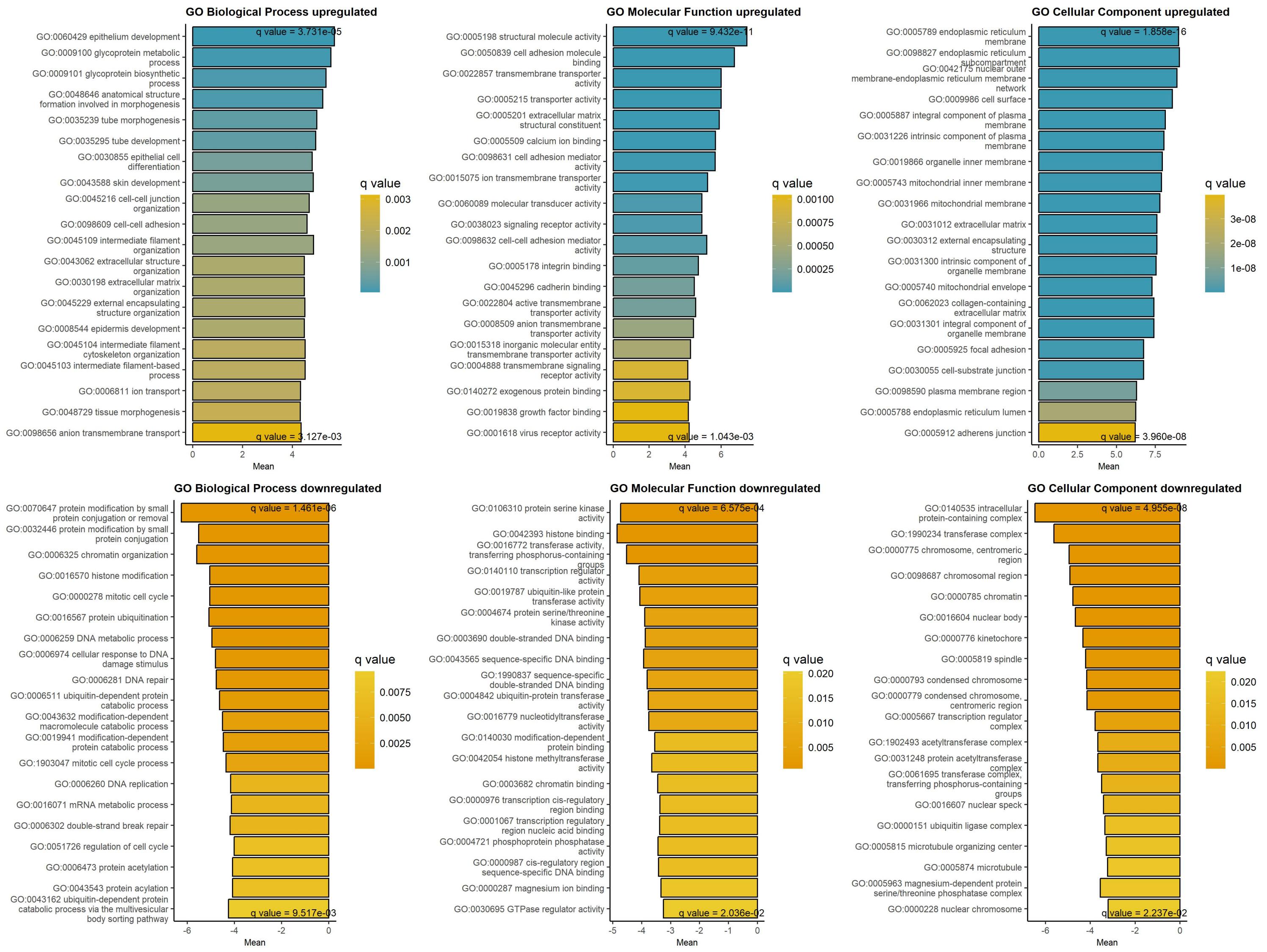


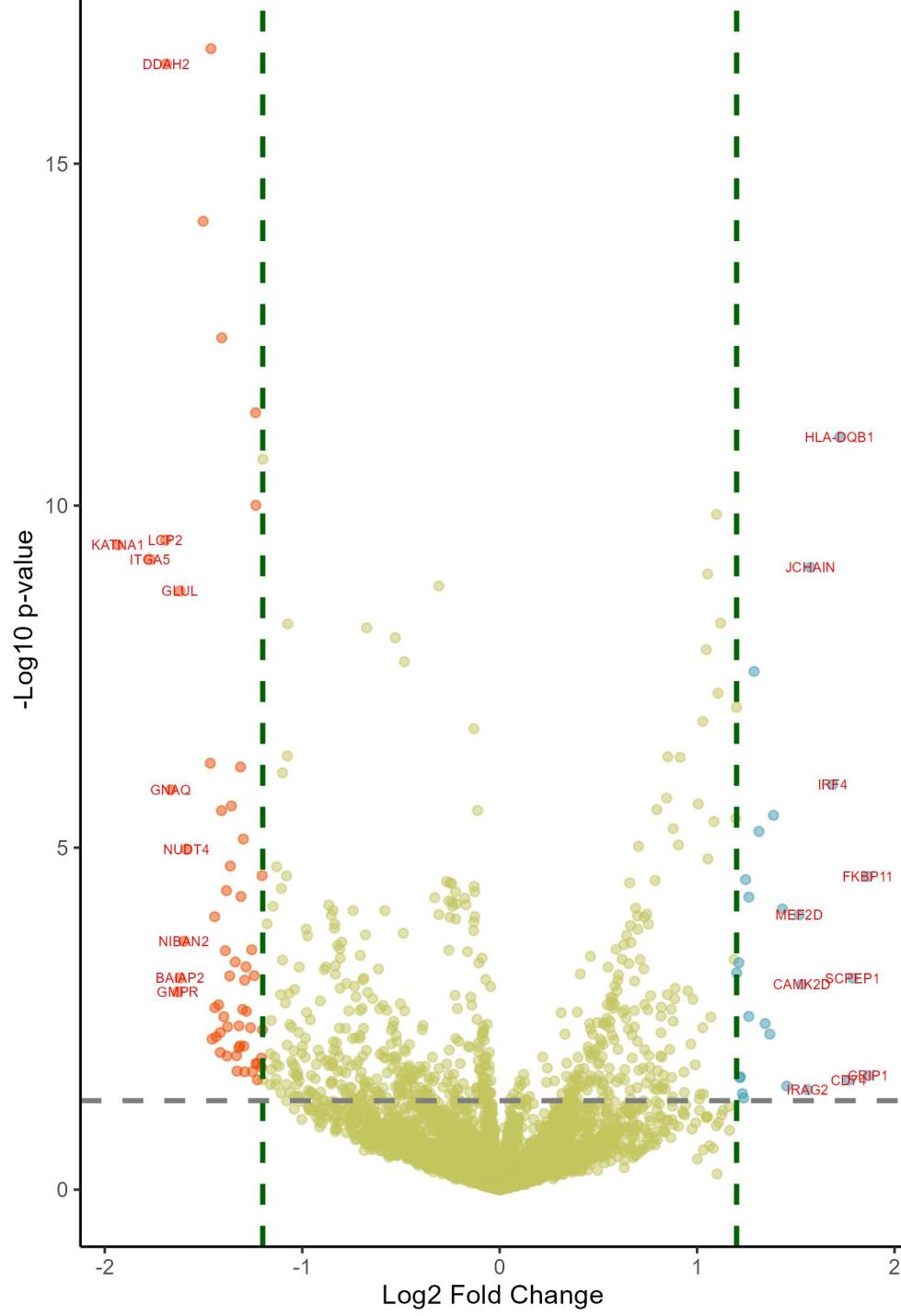


Downregulated at low/absent ABL1 Upregulated at low/absent ABL1

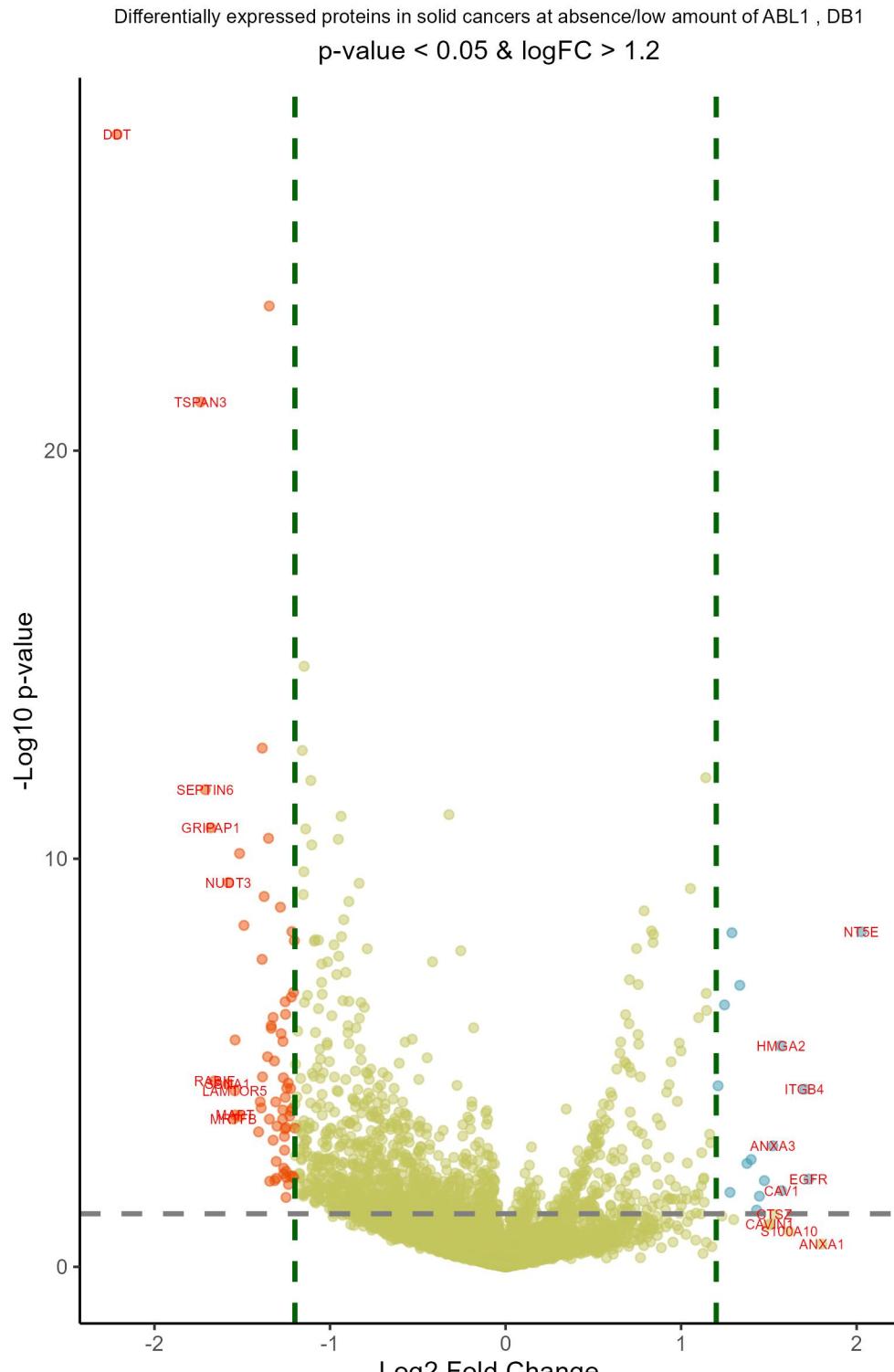
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.58	8.88e-20	SEPTIN6	septin 6	1.74	2.00e-02	S100A10	S100 calcium binding protein A10
-1.56	5.71e-19	NUDT3	nudix hydrolase 3	1.73	2.83e-06	EGFR	epidermal growth factor receptor
-1.53	6.50e-08	SSNA1	SS nuclear autoantigen 1	1.66	1.13e-01	LGALS3	galectin 3
-1.39	3.53e-06	BCR	BCR activator of RhoGEF and GTPase	1.61	6.97e-11	ITGB4	integrin subunit beta 4
-1.38	1.60e-04	RABIF	RAB interacting factor	1.58	2.82e-02	CTSZ	cathepsin Z
-1.38	6.11e-03	SPN	sialophorin	1.56	8.15e-07	NT5E	5'-nucleotidase ecto
-1.38	1.35e-04	DDT	D-dopachrome tautomerase	1.55	1.46e-05	ADAM9	ADAM metallopeptidase domain 9
-1.36	3.65e-04	GMPR	guanosine monophosphate reductase	1.46	1.13e-03	CAV1	caveolin 1
-1.35	7.91e-07	MAPRE2	microtubule associated protein RP/E	1.44	6.99e-02	ITGA3	integrin subunit alpha 3
-1.35	6.37e-05	GIT2	GIT ArfGAP 2	1.43	7.93e-02	MYOF	myoferlin
-1.34	2.11e-05	LZTFL1	leucine zipper transcription factor	1.33	1.30e-04	MYO6	myosin VI
-1.34	1.56e-05	OARD1	O-acyl-ADP-ribose deacetylase 1	1.31	1.59e-04	THBS1	thrombospondin 1
-1.3	5.71e-19	BLMH	bleomycin hydrolase	1.3	1.90e-04	EPS8L2	EPS8 like 2
-1.29	1.77e-04	ASF1A	anti-silencing function 1A histone	1.27	4.38e-02	MYO1C	myosin IC
-1.28	5.87e-08	SMAP2	small ArfGAP2	1.26	1.26e-02	PROCR	protein C receptor
-1.27	1.72e-08	ARMC6	armadillo repeat containing 6	1.26	1.79e-03	EPHA2	EPH receptor A2
-1.25	1.20e-08	NACA2	nascent polypeptide associated comp	1.26	1.44e-05	HMGA2	high mobility group AT-hook 2
-1.24	2.80e-04	IVNS1ABP	influenza virus NS1A binding protei	1.25	2.98e-02	ITGA2	integrin subunit alpha 2
-1.23	2.90e-04	GPN1	GPN-loop GTPase 1	1.25	2.51e-02	S100A16	S100 calcium binding protein A16
-1.23	5.90e-10	PDXP	pyridoxal phosphatase	1.24	3.37e-01	ANXA1	annexin A1
-1.21	6.78e-08	ACYP1	acylphosphatase 1	1.23	5.34e-04	LDLR	low density lipoprotein receptor
-1.21	5.72e-05	CORO1A	coronin 1A	1.23	3.93e-02	PLS3	plastin 3
-1.2	4.84e-04	RNGTT	RNA guanylyltransferase and 5'-phos	1.22	1.26e-02	ITPR3	inositol 1,4,5-trisphosphate recept
-1.2	1.97e-10	APIP	APAF1 interacting protein	1.22	1.48e-04	PALS1	protein associated with LIN71, MAG
-1.19	5.90e-10	PPP6R1	protein phosphatase 6 regulatory su	1.21	8.92e-05	GPC1	glycan 1
-1.18	3.14e-03	PIK3R1	phosphoinositide-3-kinase regulator	1.19	1.31e-02	RRAS	RAS related
-1.18	2.01e-04	TDP2	tyrosyl-DNA phosphodiesterase 2	1.19	5.18e-03	GPX8	glutathione peroxidase 8 (putative)
-1.18	7.25e-13	CORO7	coronin 7	1.18	1.24e-04	FNDC3B	fibronectin type III domain contain
-1.17	2.13e-04	ZCHC3	zinc finger CCHC-type containing 3	1.16	3.90e-02	PODXL	podocalyxin like

GAGE analysis on upregulated and downregulated proteins at low/absent ABL1 protein, DB1





logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.93	2.08e-07	KATNA1	katanin catalytic subunit A1	1.87	3.43e-01	CRIP1	cysteine rich protein 1
-1.77	3.10e-07	ITGA5	integrin subunit alpha 5	1.86	3.09e-03	FKBP11	FKBP prolyl isomerase 11
-1.69	1.93e-07	LCP2	lymphocyte cytosolic protein 2	1.79	3.68e-02	SCPEP1	serine carboxypeptidase 1
-1.69	7.71e-14	DDAH2	dimethylarginine dimethylaminohydro	1.77	3.67e-01	CD74	CD74 molecule
-1.67	2.64e-04	GNAQ	G protein subunit alpha q	1.72	9.48e-09	HLA-DQB1	major histocompatibility complex, c
-1.63	5.22e-02	GMPR	guanosine monophosphate reductase	1.69	2.27e-04	IRF4	interferon regulatory factor 4
-1.62	6.91e-07	GLUL	glutamate-ammonia ligase	1.57	3.79e-07	JCHAIN	joining chain of multimeric IgA and
-1.62	3.68e-02	BAIAP2	BAR/IMD domain containing adaptor p	1.56	4.38e-01	IRAG2	inositol 1,4,5-triphosphate recepto
-1.6	1.44e-02	NIBAN2	niban apoptosis regulator 2	1.53	4.29e-02	CAMK2D	calcium/calmodulin dependent protei
-1.59	1.37e-03	NUDT4	nudix hydrolase 4	1.52	7.29e-03	MEF2D	myocyte enhancer factor 2D
-1.5	1.15e-11	ACTN1	actinin alpha 1	1.45	4.13e-01	CTSZ	cathepsin Z
-1.47	1.21e-04	GALK2	galactokinase 2	1.43	6.47e-03	HLA-DPB1	major histocompatibility complex, c
-1.46	6.93e-14	SPN	sialophorin	1.39	5.19e-04	TRIM22	tripartite motif containing 22
-1.46	1.57e-01	S100P	S100 calcium binding protein P	1.37	1.39e-01	PLCG2	phospholipase C gamma 2
-1.44	7.44e-03	ARRB1	arrestin beta 1	1.34	1.11e-01	SLC25A12	solute carrier family 25 member 12
-1.44	7.70e-02	PTP4A2	protein tyrosine phosphatase 4A2	1.31	8.19e-04	SH3BP1	SH3 domain binding protein 1
-1.44	1.49e-01	PSTPIP2	proline-serine-threonine phosphatas	1.29	7.35e-06	HLA-DRB3	major histocompatibility complex, c
-1.42	7.18e-02	CAVIN1	caveolae associated protein 1	1.26	5.01e-03	RABGAP1L	RAB GTPase activating protein 1 lik
-1.42	1.35e-01	CAVIN2	caveolae associated protein 2	1.26	9.34e-02	DOK3	docking protein 3
-1.42	2.14e-01	CRABP1	cellular retinoic acid binding prot	1.25	3.36e-03	ISG20	interferon stimulated exonuclease g
-1.41	4.55e-04	SEPTIN8	septin 8	1.24	5.04e-01	TIGAR	TP53 induced glycolysis regulatory
-1.41	4.68e-10	MPP1	MAGUK p55 scaffold protein 1	1.23	4.66e-01	CD48	CD48 molecule
-1.4	9.38e-02	LPCAT2	lysophosphatidylcholine acyltransfe	1.22	3.52e-01	CD70	CD70 molecule
-1.39	1.83e-02	LGALS3BP	galectin 3 binding protein	1.22	3.55e-01	SLC25A13	solute carrier family 25 member 13
-1.38	4.28e-03	UNC13D	unc-13 homolog D	1.21	2.50e-02	BUD23	BUD23 rRNA methyltransferase and ri
-1.38	2.32e-01	MLLT11	MLLT11 transcription factor 7 cofac	1.2	3.24e-02	SYK	spleen associated tyrosine kinase
-1.38	1.19e-01	SNX9	sorting nexin 9	1.2	2.27e-05	MS4A1	membrane spanning 4-domains A1
-1.37	3.47e-02	STAT5B	signal transducer and activator of	1.2	5.62e-04	ALDH3A2	aldehyde dehydrogenase 3 family mem
-1.36	2.33e-03	GIPC1	GIPC PDZ domain containing family m	1.19	2.31e-02	HLA-DPA1	major histocompatibility complex, c

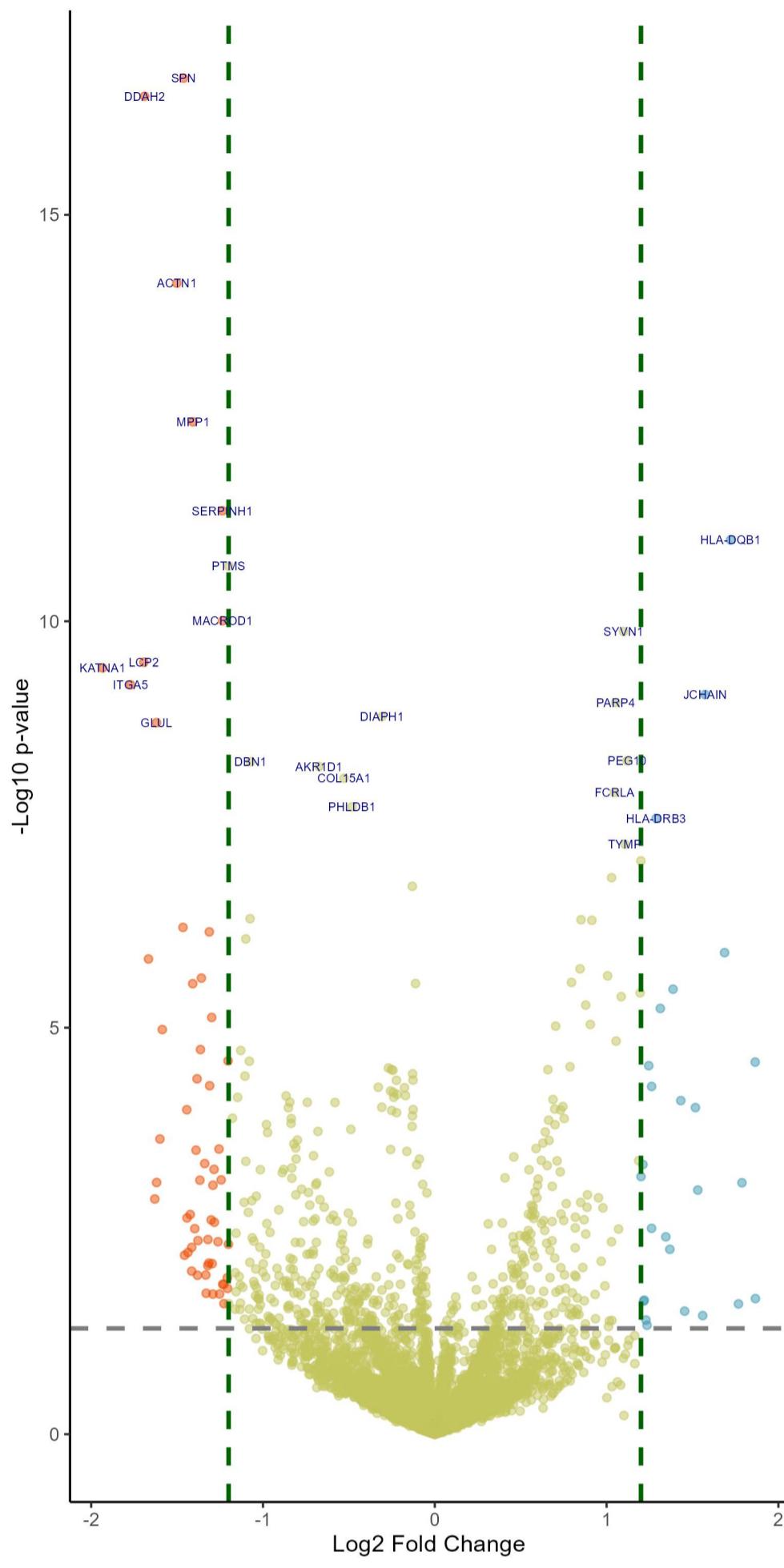


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.21	5.89e-25	DDT	D-dopachrome tautomerase	2.03	1.28e-06	NT5E	5'-nucleotidase ecto
-1.74	1.07e-18	TSPAN3	tetraspanin 3	1.8	5.79e-01	ANXA1	annexin A1
-1.71	1.35e-09	SEPTIN6	septin 6	1.73	8.49e-02	EGFR	epidermal growth factor receptor
-1.68	8.84e-09	GRIPAP1	GRIP1 associated protein 1	1.7	2.01e-03	ITGB4	integrin subunit beta 4
-1.66	1.37e-03	RABIF	RAB interacting factor	1.62	4.16e-01	S100A10	S100 calcium binding protein A10
-1.58	1.62e-03	SSNA1	SS nuclear autoantigen 1	1.57	1.26e-01	CAV1	caveolin 1
-1.58	1.27e-07	NUDT3	nudix hydrolase 3	1.57	2.63e-04	HMGA2	high mobility group AT-hook 2
-1.55	7.39e-03	MRTFB	myocardin related transcription fac	1.53	2.67e-01	CTSZ	cathepsin Z
-1.54	2.16e-03	LAMTOR5	late endosomal/lysosomal adaptor, M	1.52	2.18e-02	ANXA3	annexin A3
-1.54	6.29e-03	MAPT	microtubule associated protein tau	1.5	3.39e-01	CAVIN1	caveolae associated protein 1
-1.54	2.08e-04	LZTFL1	leucine zipper transcription factor	1.5	3.49e-01	IGF2BP2	insulin like growth factor 2 mRNA b
-1.52	2.74e-08	ACYP1	acylphosphatase 1	1.47	8.85e-02	ADAM9	ADAM metallopeptidase domain 9
-1.51	6.62e-03	VGF	VGF nerve growth factor inducible	1.45	1.49e-01	YBX3	Y-box binding protein 3
-1.49	9.84e-07	TUBB2B	tubulin beta 2B class IIb	1.43	2.33e-01	S100A16	S100 calcium binding protein A16
-1.41	1.19e-02	CHD7	chromodomain helicase DNA binding p	1.4	3.85e-02	THBS1	thrombospondin 1
-1.4	3.56e-03	CNPY4	canopy FGF signaling regulator 4	1.38	4.51e-02	ADGRE5	adhesion G protein-coupled receptor
-1.39	4.63e-03	IVNS1ABP	influenza virus NS1A binding protei	1.33	1.53e-05	RAB11FIP5	RAB11 family interacting protein 5
-1.39	4.22e-06	C11orf54	chromosome 11 open reading frame 54	1.3	2.95e-01	ITGA2	integrin subunit alpha 2
-1.39	2.11e-10	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	1.29	1.31e-06	RAC2	Rac family small GTPase 2
-1.38	1.16e-03	UNC119B	unc-119 lipid binding chaperone B	1.28	1.33e-01	EPHA2	EPH receptor A2
-1.38	2.33e-07	COMM2	COMM domain containing 2	1.25	3.84e-05	KRT5	keratin 5
-1.36	4.63e-04	EXOC5	exocyst complex component 5	1.23	2.80e-01	PROCR	protein C receptor
-1.35	1.39e-08	BLMH	bleomycin hydrolase	1.21	1.73e-03	MET	MET proto-oncogene, receptor tyrosi
-1.35	6.33e-21	CHMP1B	charged multivesicular body protein	1.18	6.11e-01	LGALS3	galectin 3
-1.35	7.40e-03	AMACR	alpha-methylacyl-CoA racemase	1.17	1.93e-02	ADAM17	ADAM metallopeptidase domain 17
-1.34	8.96e-02	SCGN	secretogogin, EF-hand calcium bindi	1.16	1.33e-02	AXL	AXL receptor tyrosine kinase
-1.34	1.05e-04	NACA2	nascent polypeptide associated comp	1.15	5.01e-05	UXS1	UDP-glucuronate decarboxylase 1
-1.33	1.17e-04	PDCL	phosducin like	1.14	2.33e-05	TNC	tenascin C
-1.32	7.03e-05	WIPF2	WAS/WASL interacting protein family	1.14	5.57e-01	CD44	CD44 molecule (Indian blood group)

ABL1 network, DB1, no Pearson r > 0.3

Differentially expressed proteins in blood cancers at absence/low amount of ABL1 , DB1

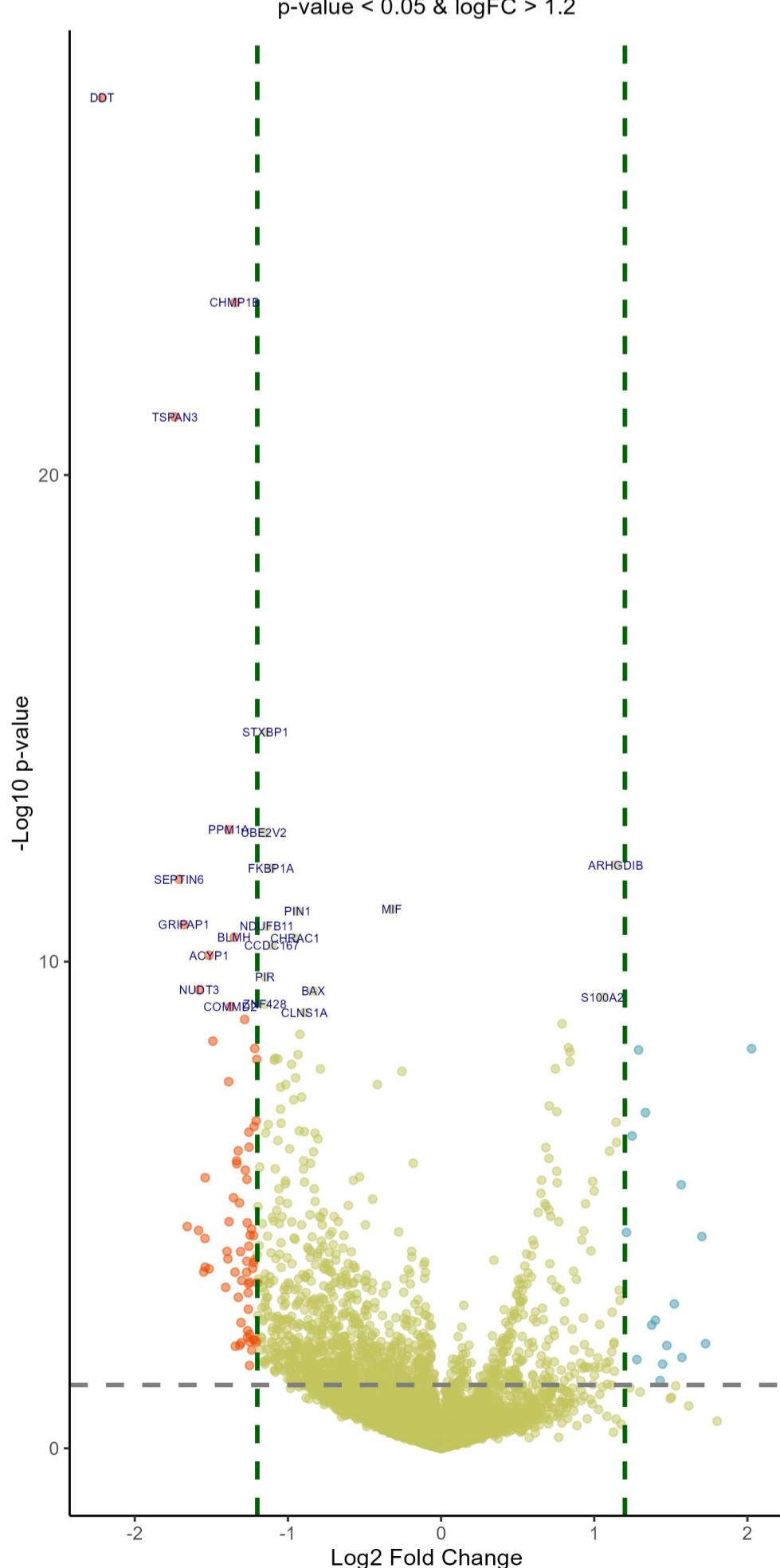
p-value < 0.05 & logFC > 1.2

Sorted by p values!
Downregulated in blood cancers at low/absent ABL1 Upregulated in blood cancers at low/absent ABL1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.46	6.93e-14	SPN	sialophorin	1.72	9.48e-09	HLA-DQB1	major histocompatibility complex, c
-1.69	7.71e-14	DDAH2	dimethylarginine dimethylaminohydro	1.1	8.90e-08	SYVN1	synoviolin 1
-1.5	1.15e-11	ACTN1	actinin alpha 1	1.57	3.79e-07	JCHAIN	joining chain of multimeric IgA and
-1.41	4.68e-10	MPP1	MAGUK p55 scaffold protein 1	1.05	4.42e-07	PARP4	poly(ADP-ribose) polymerase family
-1.24	4.85e-09	SERPINH1	serpin family H member 1	1.12	1.87e-06	PEG10	paternally expressed 10
-1.2	1.74e-08	PTMS	parathymosin	1.05	3.85e-06	FCRLA	Fc receptor like A
-1.24	7.29e-08	MACROD1	mono-ADP ribosylhydrolase 1	1.29	7.35e-06	HLA-DRB3	major histocompatibility complex, c
-1.69	1.93e-07	LCP2	lymphocyte cytosolic protein 2	1.11	1.47e-05	TYMP	thymidine phosphorylase
-1.93	2.08e-07	KATNA1	katatin catalytic subunit A1	1.2	2.27e-05	MS4A1	membrane spanning 4-domains A1
-1.77	3.10e-07	ITGA5	integrin subunit alpha 5	1.03	3.51e-05	TMEM205	transmembrane protein 205
-0.31	6.19e-07	DIAPH1	diaphanous related formin 1	0.85	1.02e-04	TIFA	TRAF interacting protein with forkh
-1.62	6.91e-07	GLUL	glutamate-ammonia ligase	0.91	1.02e-04	IFI30	IFI30 lysosomal thiol reductase
-1.07	1.87e-06	DBN1	drebrin 1	1.69	2.27e-04	IRF4	interferon regulatory factor 4
-0.67	2.03e-06	AKR1D1	aldo-keto reductase family 1 member	0.85	3.39e-04	DHRS1	dehydrogenase/reductase 1
-0.53	2.70e-06	COL15A1	collagen type XV alpha 1 chain	1.01	4.02e-04	CD40	CD40 molecule
-0.48	5.53e-06	PHLDB1	pleckstrin homology like domain fam	0.8	4.55e-04	MYO5A	myosin VA
-0.13	4.32e-05	CLIC1	chloride intracellular channel 1	1.39	5.19e-04	TRIM22	tripartite motif containing 22
-1.08	1.02e-04	CORO1B	coronin 1B	1.2	5.62e-04	ALDH3A2	aldehyde dehydrogenase 3 family mem
-1.47	1.21e-04	GALK2	galactokinase 2	1.09	6.13e-04	PAWR	pro-apoptotic WT1 regulator
-1.31	1.33e-04	FSCN1	fascin actin-bundling protein 1	0.88	7.62e-04	CYBB	cytochrome b-245 beta chain
-1.1	1.58e-04	ASF1A	anti-silencing function 1A histone	1.31	8.19e-04	SH3BP1	SH3 domain binding protein 1
-1.67	2.64e-04	GNAQ	G protein subunit alpha q	0.91	1.24e-03	CD37	CD37 molecule
-1.36	4.18e-04	BCR	BCR activator of RhoGEF and GTPase	0.7	1.27e-03	SNX4	sorting nexin 4
-0.11	4.55e-04	GART	phosphoribosylglycinamide formyltra	1.06	1.87e-03	AACS	acetoacetyl-CoA synthetase
-1.41	4.55e-04	SEPTIN8	septin 8	1.86	3.09e-03	FKBP11	FKBP prolyl isomerase 11
-1.3	1.04e-03	PC	pyruvate carboxylase	1.25	3.36e-03	ISG20	interferon stimulated exonuclease g
-1.59	1.37e-03	NUDT4	nudix hydrolase 4	0.79	3.40e-03	FAS	Fas cell surface death receptor
-1.36	2.33e-03	GIPC1	GIPC PDZ domain containing family m	0.66	3.51e-03	AHSG	alpha 2-HS glycoprotein
-1.13	2.34e-03	GID8	GID complex subunit 8 homolog	1.26	5.01e-03	RABGAP1L	RAB GTPase activating protein 1 lik
-1.2	3.07e-03	IGF2BP2	insulin like growth factor 2 mRNA b	0.69	6.35e-03	CCDC88B	coiled-coil domain containing 88B
-1.08	3.07e-03	BLVRA	biliverdin reductase A	1.43	6.47e-03	HLA-DPB1	major histocompatibility complex, c
-0.27	3.47e-03	SDK2	sidekick cell adhesion molecule 2	0.75	7.29e-03	COX19	cytochrome c oxidase assembly facto
-0.25	3.51e-03	JCAD	junctional cadherin 5 associated	1.52	7.29e-03	MEF2D	myocyte enhancer factor 2D
-0.24	3.52e-03	RASIP1	Ras interacting protein 1	0.7	7.44e-03	RAB30	RAB30, member RAS oncogene family
-0.13	3.84e-03	GLO1	glyoxalase I	0.73	7.44e-03	EVI2B	ecotropic viral integration site 2B
-1.11	4.02e-03	LUZP1	leucine zipper protein 1	0.75	8.90e-03	DNTTIP1	deoxynucleotidyltransferase termina
-1.38	4.28e-03	UNC13D	unc-13 homolog D	0.66	9.21e-03	IRF5	interferon regulatory factor 5
-0.13	4.33e-03	PGD	phosphogluconate dehydrogenase	0.7	1.02e-02	KCTD12	potassium channel tetramerization d
0.22	4.33e-03	ANTYRP1	ANTYRP cell adhesion molecule 1	0.64	1.20e-02	PRCNC	phosphopantetheoyltransferase desorbo

Differentially expressed proteins in solid cancers at absence/low amount of ABL1 , DB1

p-value < 0.05 & logFC > 1.2

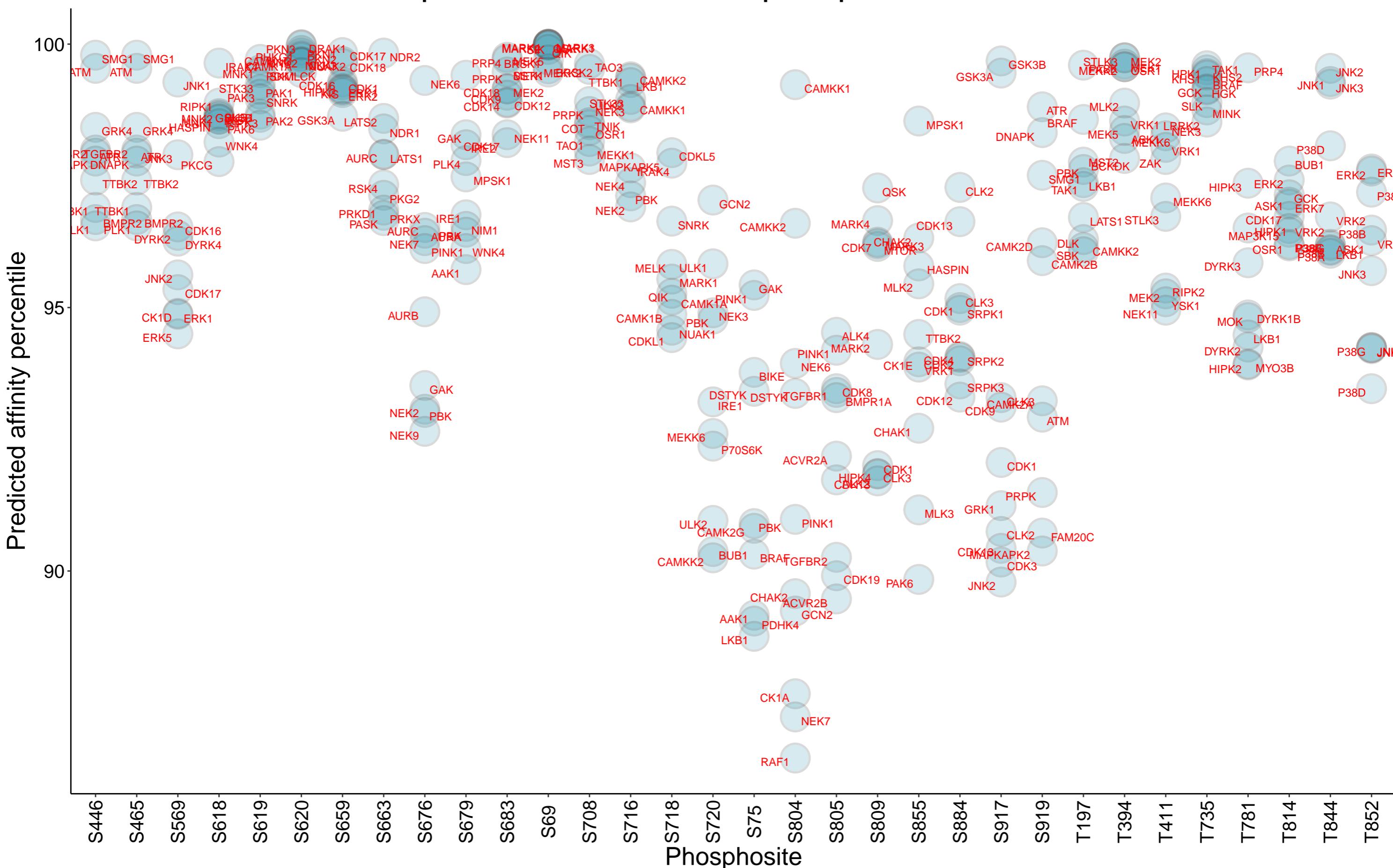
Sorted by p values!
Downregulated in solid cancers at low/absent ABL1 Upregulated in solid cancers at low/absent ABL1

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.21	5.89e-25	DDT	D-dopachrome tautomerase	1.14	8.59e-10	ARHGDI	Rho GDP dissociation inhibitor beta
-1.35	6.33e-21	CHMP1B	charged multivesicular body protein	1.05	1.62e-07	S100A2	S100 calcium binding protein A2
-1.74	1.07e-18	TSPAN3	tetraspanin 3	0.79	4.65e-07	MICAL2	microtubule associated monooxygenas
-1.15	2.55e-12	STXBP1	syntaxin binding protein 1	0.83	1.28e-06	SCEL	scillin
-1.39	2.11e-10	PPM1A	protein phosphatase, Mg2+/Mn2+ depe	2.03	1.28e-06	NT5E	5'-nucleotidase ecto
-1.16	2.11e-10	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.29	1.31e-06	RAC2	Rac family small GTPase 2
-1.11	8.93e-10	FKBP1A	FKBP prolyl isomerase 1A	0.84	1.40e-06	COL6A2	collagen type VI alpha 2 chain
-1.71	1.35e-09	SEPTIN6	septin 6	0.84	1.88e-06	CA2	carbonic anhydrase 2
-0.32	5.01e-09	MIF	macrophage migration inhibitory fac	0.75	2.48e-06	PLCD3	phospholipase C delta 3
-0.94	5.04e-09	PIN1	peptidylprolyl cis/trans isomerase,	0.71	1.18e-05	PROSER2	proline and serine rich 2
-1.68	8.84e-09	GRIPAP1	GRIP1 associated protein 1	0.76	1.49e-05	CYP2S1	cytochrome P450 family 2 subfamily
-1.14	8.84e-09	NDUFB11	NADH:ubiquinone oxidoreductase subu	1.33	1.53e-05	RAB11FIP5	RAB11 family interacting protein 5
-1.35	1.39e-08	BLMH	bleomycin hydrolase	1.14	2.33e-05	TNC	tenascin C
-0.95	1.39e-08	CHRAC1	chromatin accessibility complex sub	1.25	3.84e-05	KRT5	keratin 5
-1.1	1.79e-08	CCDC167	coiled-coil domain containing 167	1.15	5.01e-05	UXS1	UDP-glucuronate decarboxylase 1
-1.52	2.74e-08	ACYP1	acylphosphatase 1	0.68	6.19e-05	SLFN5	schlafen family member 5
-1.15	2.78e-08	PIR	pirin	1.1	7.03e-05	TNFAIP2	TNF alpha induced protein 2
-1.58	1.27e-07	NUDT3	nudix hydrolase 3	0.7	9.66e-05	DYSF	dysferlin
-0.83	1.27e-07	BAX	BCL2 associated X, apoptosis regula	0.75	1.57e-04	KRT4	keratin 4
-1.15	2.18e-07	ZNF428	zinc finger protein 428	0.66	2.26e-04	SLC39A11	solute carrier family 39 member 11
-1.38	2.33e-07	COMM2	COMM domain containing 2	0.99	2.35e-04	NEXN	nexilin F-actin binding protein
-0.89	2.97e-07	CLNS1A	chloride nucleotide-sensitive chann	0.76	2.45e-04	KRT13	keratin 13
-1.28	3.94e-07	CORO7	coronin 7	1.57	2.63e-04	HMGA2	high mobility group AT-hook 2
-0.92	7.38e-07	ITPA	inosine triphosphatase	1	3.42e-04	LAMC2	laminin subunit gamma 2
-1.49	9.84e-07	TUBB2B	tubulin beta 2B class IIb	0.65	3.78e-04	GPAT3	glycerol-3-phosphate acyltransf
-1.22	1.28e-06	PRPSAP2	phosphoribosyl pyrophosphate synthe	0.68	5.77e-04	CPA4	carboxypeptidase A4
-0.93	1.54e-06	CZIB	CXXC motif containing zinc binding	0.94	5.77e-04	PATJ	PATJ crumbs cell polarity complex c
-1.08	1.78e-06	ZFP91	ZFP91 zinc finger protein, atypical	0.69	6.28e-04	RGS19	regulator of G protein signaling 19
-1.07	1.78e-06	MTFR1L	mitochondrial fission regulator 1 I	0.71	7.46e-04	LAMA3	laminin subunit alpha 3
-1.2	1.78e-06	BABAM1	BRISC and BRCA1 A complex member 1	0.63	8.17e-04	ADIRF	adipogenesis regulatory factor
-1.09	1.80e-06	FLYWCH2	FLYWCH family member 2	0.72	9.58e-04	COL17A1	collagen type XVII alpha 1 chain
-0.98	2.08e-06	LZIC	leucine zipper and CTNNBIP1 domain	0.77	1.16e-03	KRT6A	keratin 6A
-0.79	2.48e-06	ARPC5	actin related protein 2/3 complex s				

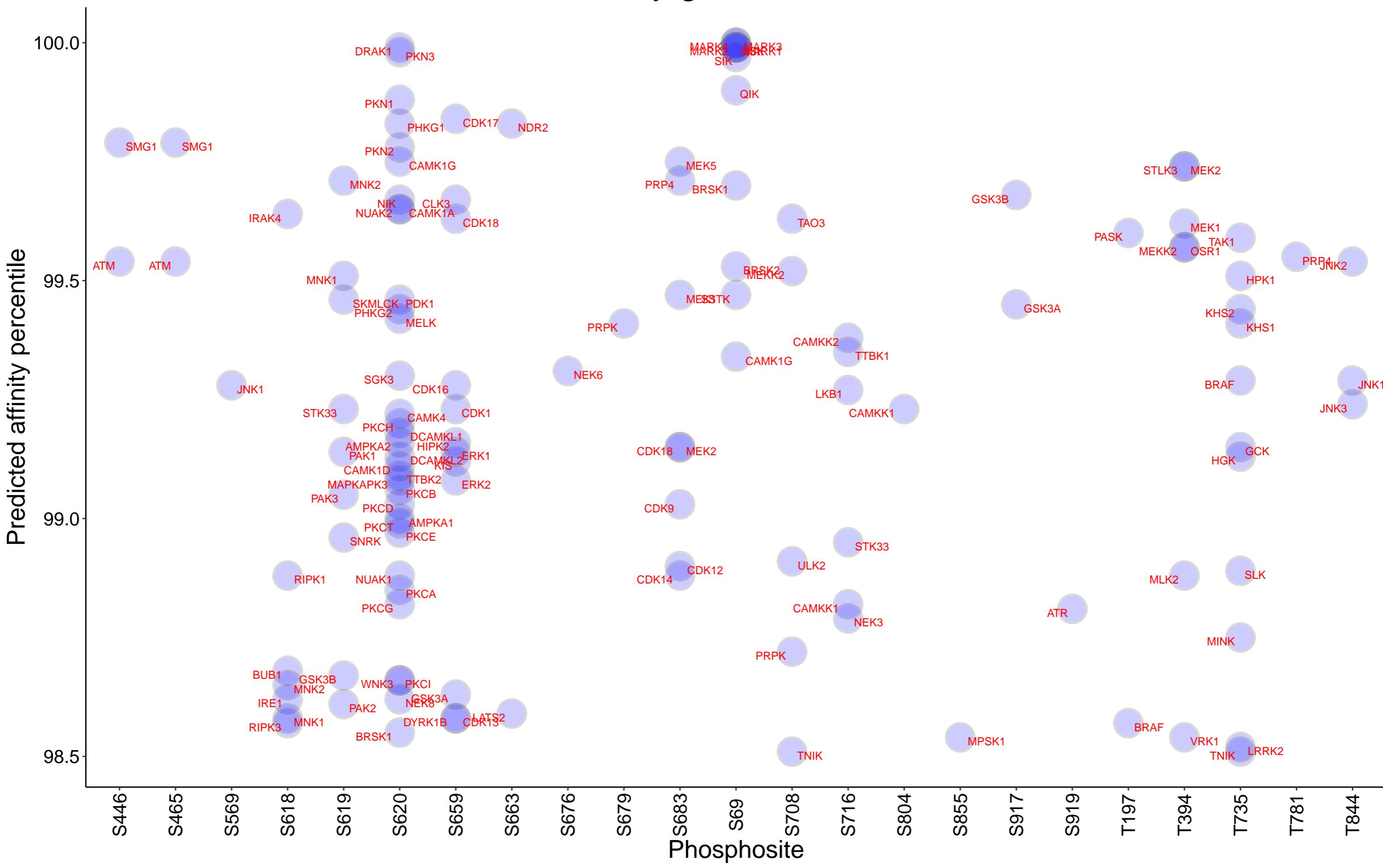
Insufficient number of paired observations in DB1 for ABL1

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Top 10 kinases for each phosphosite in ABL1



Kinases with affinity greater than 98.5% to ABL1



No sufficient paired observations in DB1 for ABL1