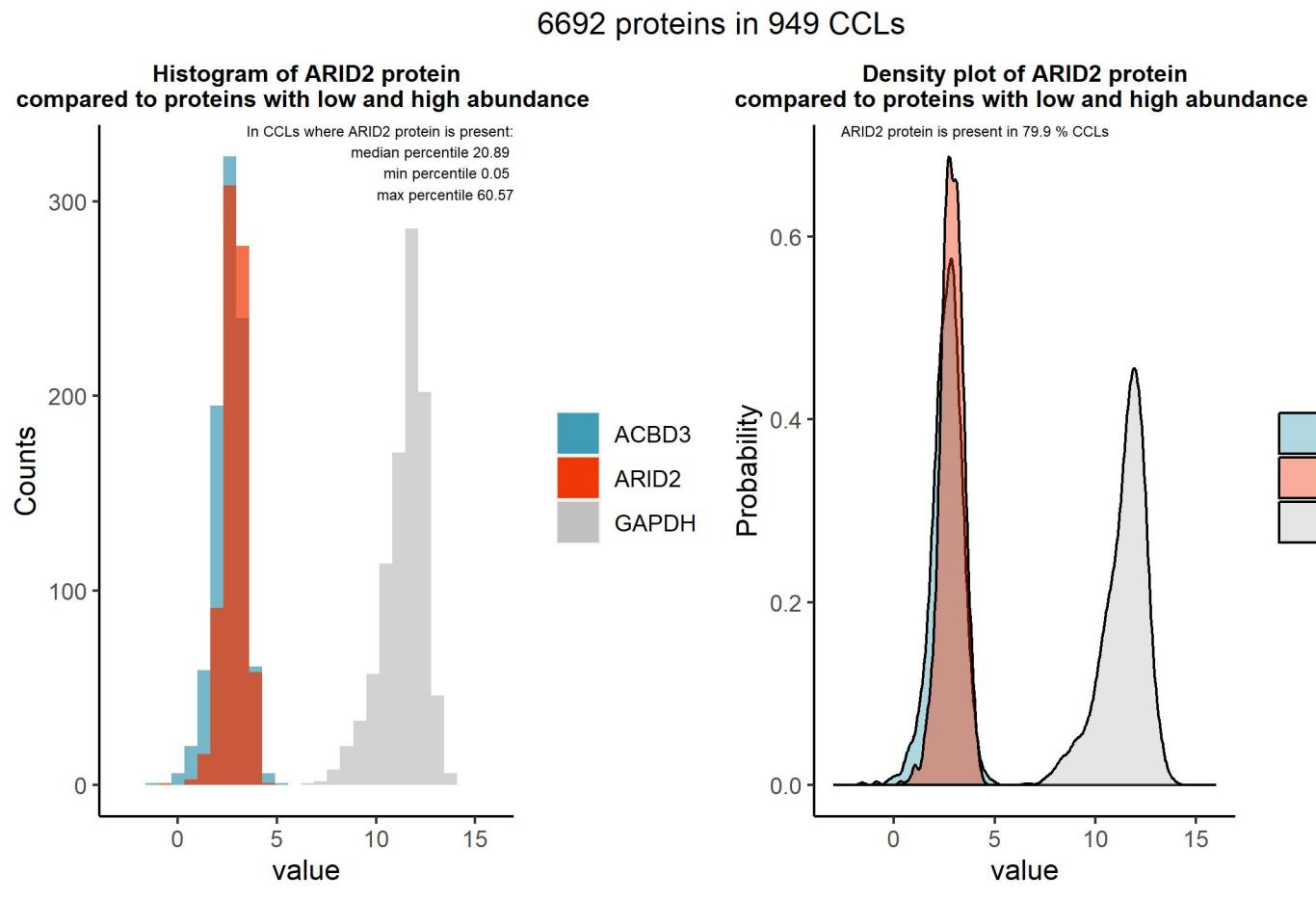


ARID2

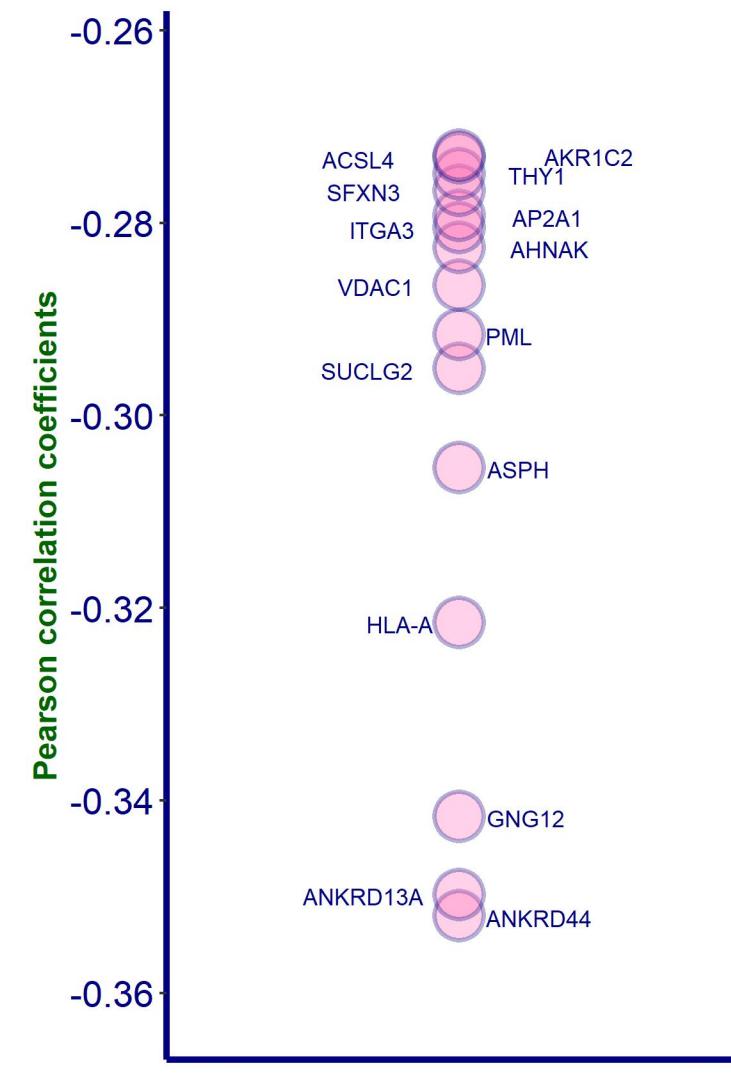
Protein name: ARID2 ; UNIPROT: Q68CP9 ; Gene name: AT-rich interaction domain 2

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

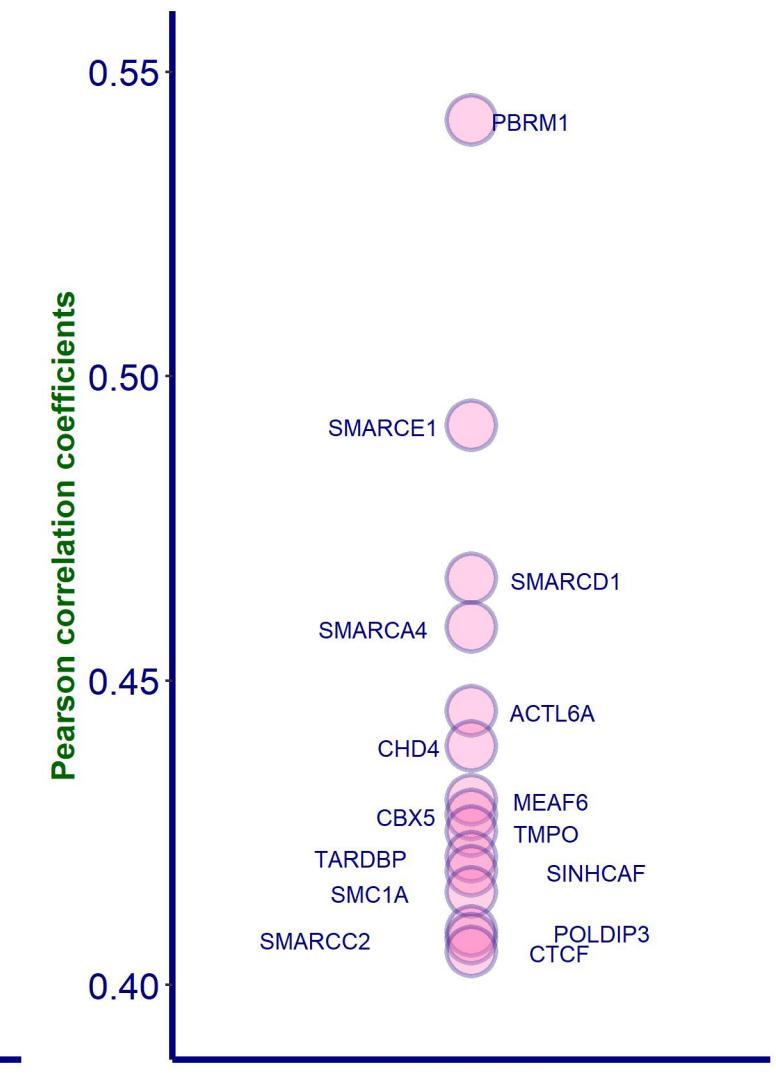
Sanger Institute Protein Database 1 (DB1), protein presence is certain



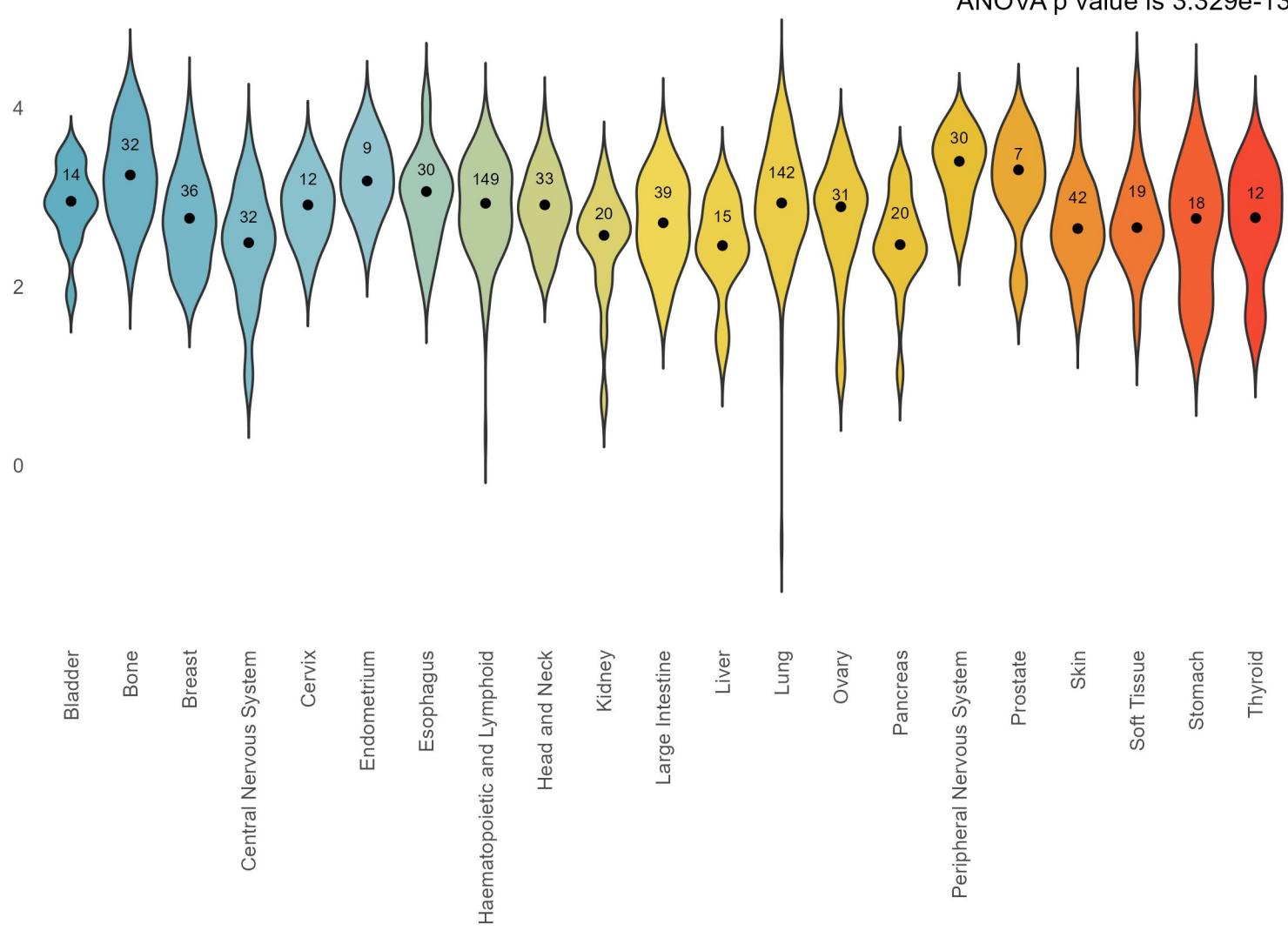
Top negative correlations of ARID2 protein, DB1



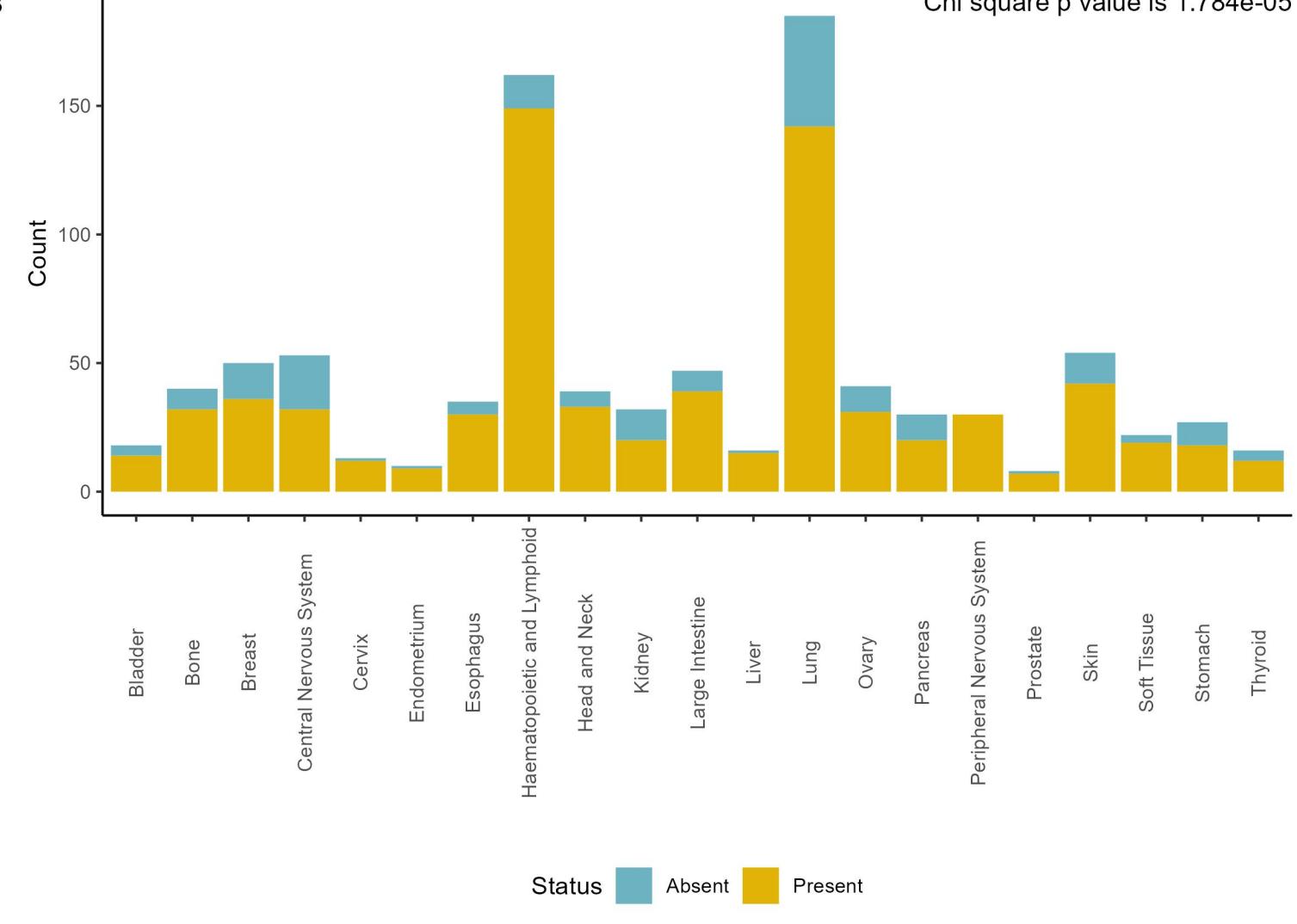
Top positive correlations of ARID2 protein, DB1



Amount of ARID2 protein, number of CCLs where it is present by tissue, DB1



Present and absent ARID2 protein counts by tissue, DB1

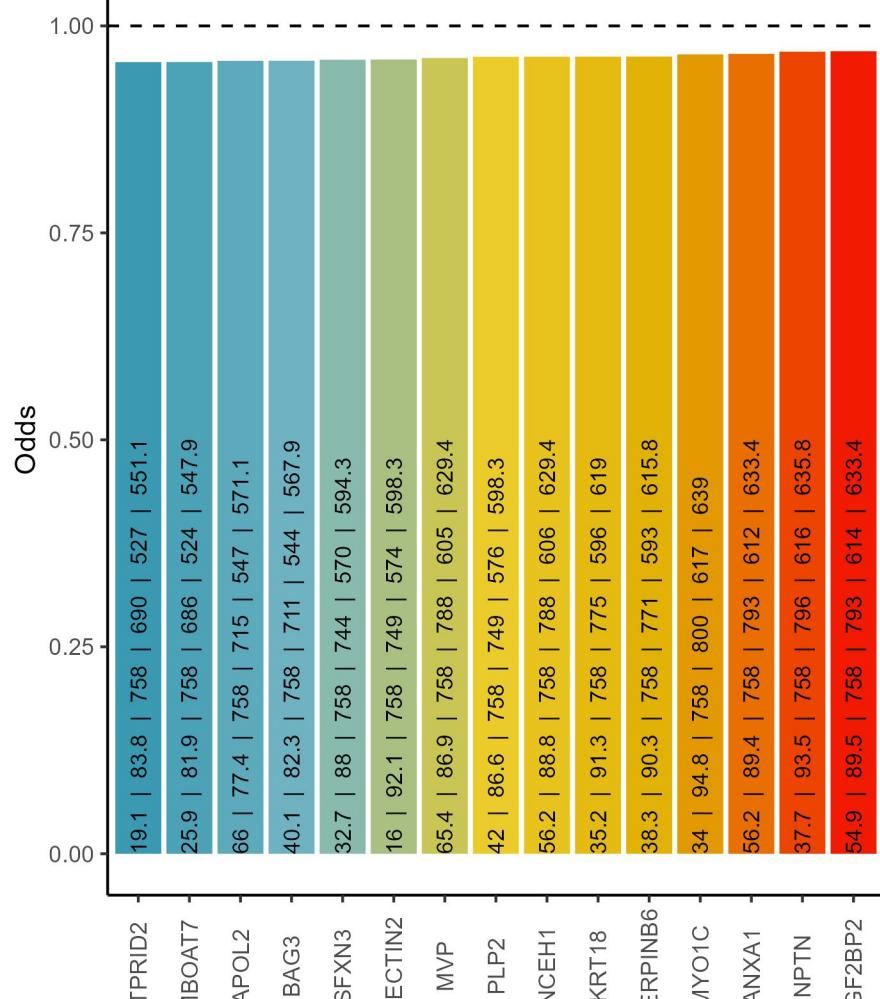


Cooccurrence with ARID2 protein, DB1

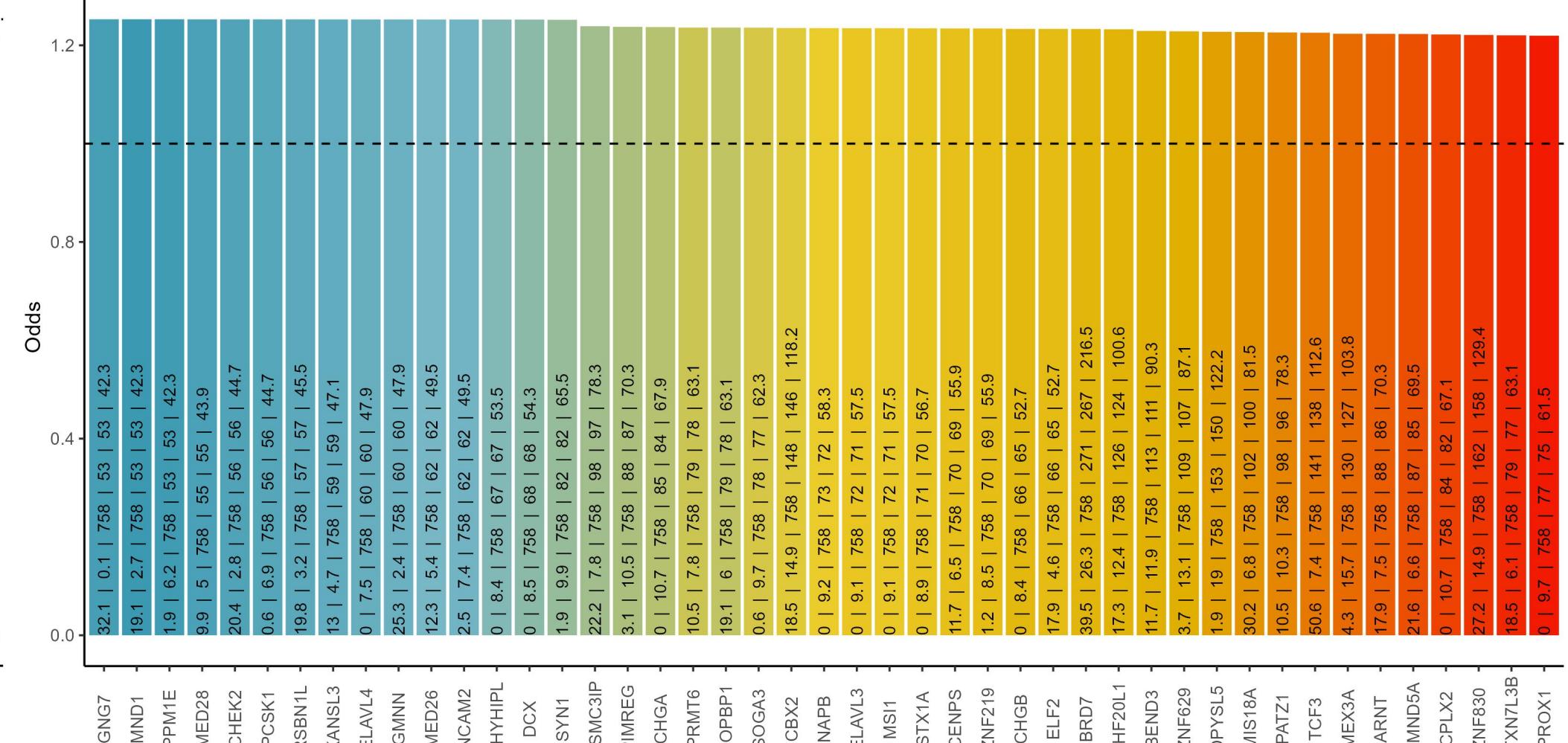
% of ARID2 in blood cancers: 92 ; % of ARID2 in solid cancers: 77.3

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of ARID2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

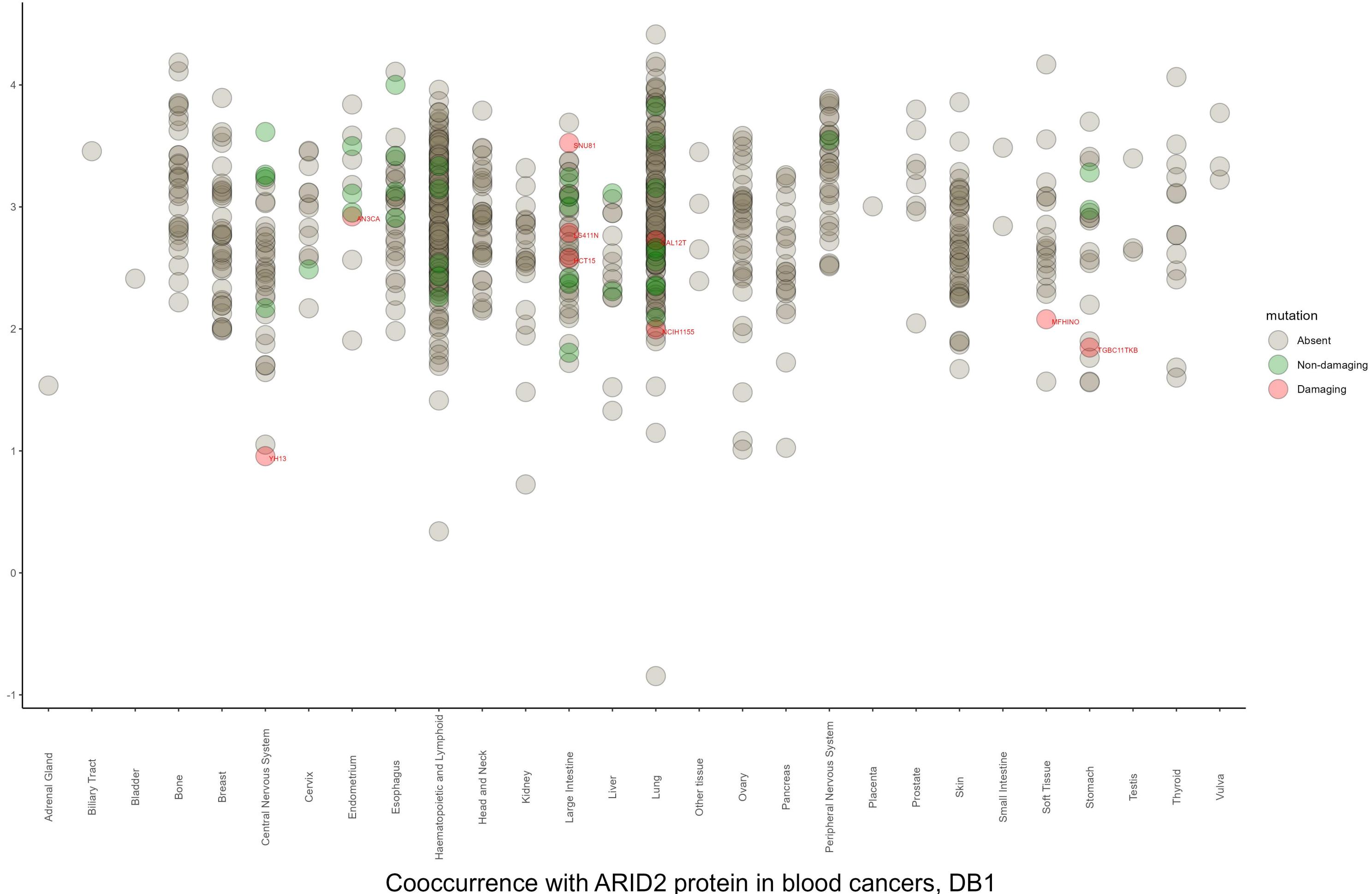
Negative cooccurrence



Positive cooccurrence

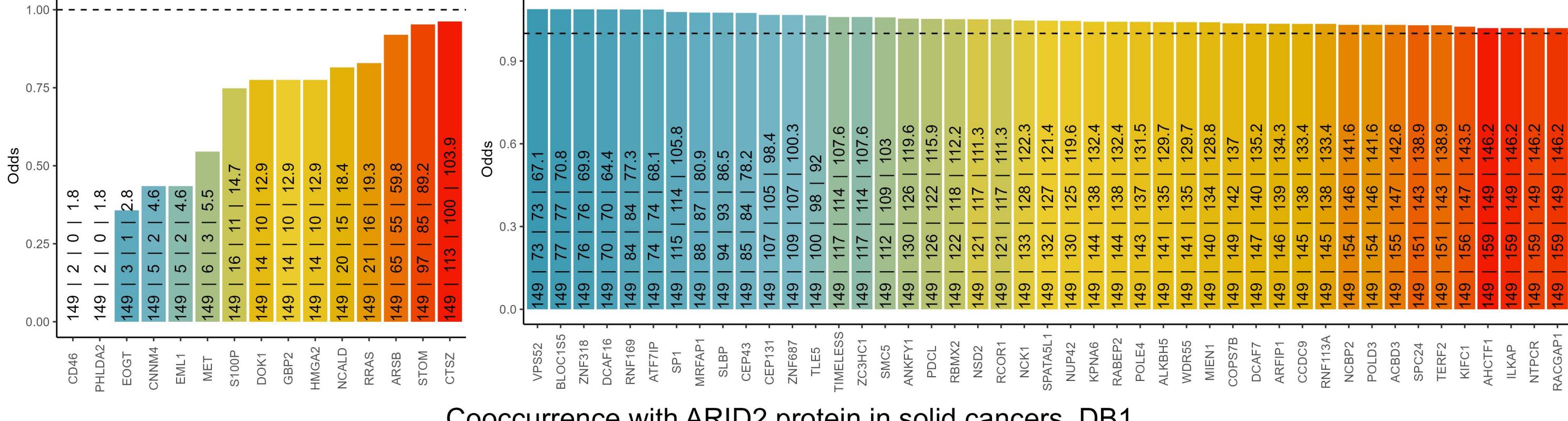


Amount of ARID2 protein and mutation status by tissue, DB1



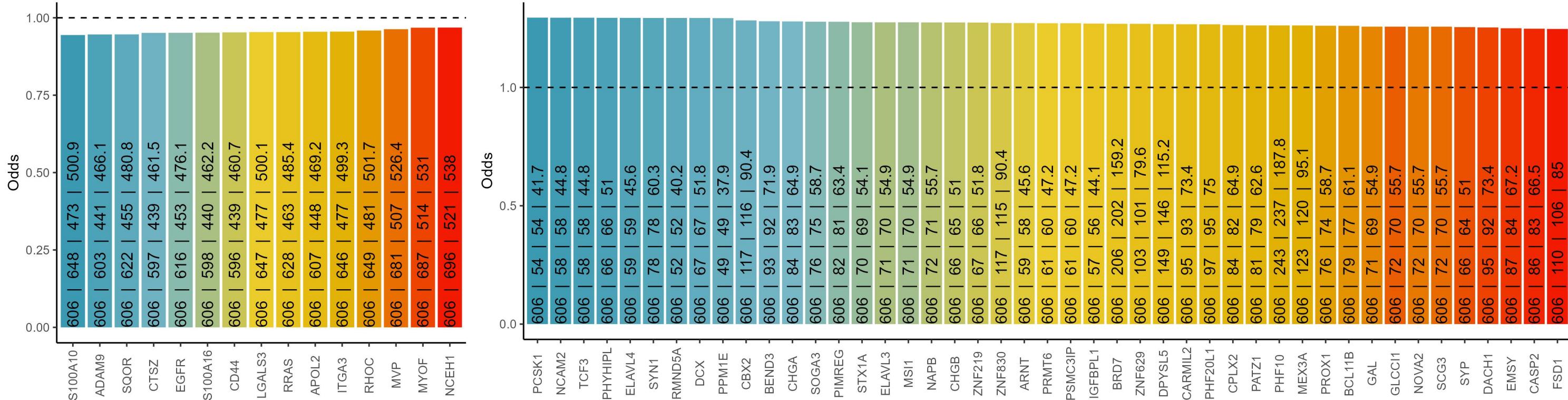
Cooccurrence with ARID2 protein in blood cancers, DB1

The text in the bars: incidence of ARID2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

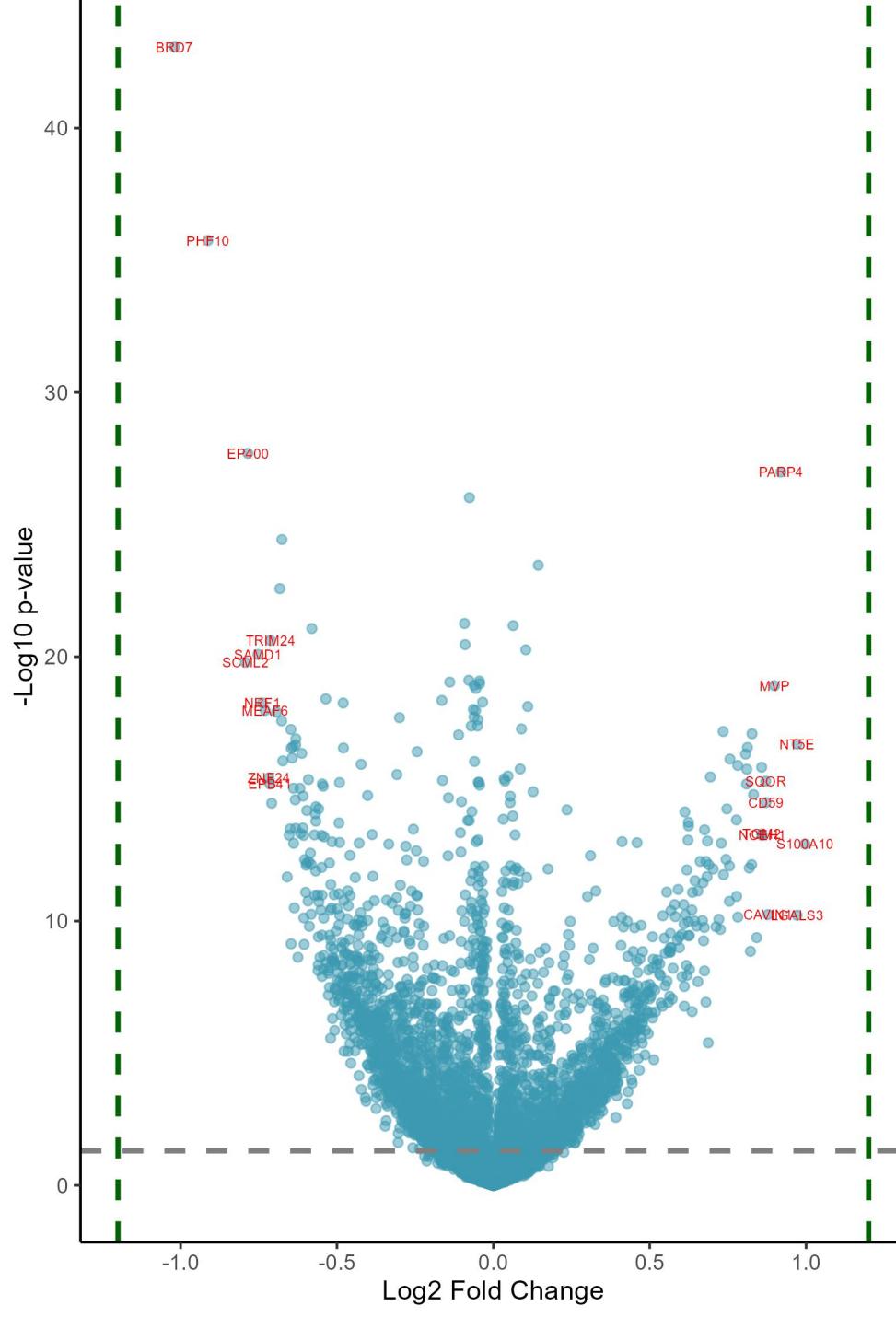


Cooccurrence with ARID2 protein in solid cancers, DB1

The text in the bars: incidence of ARID2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

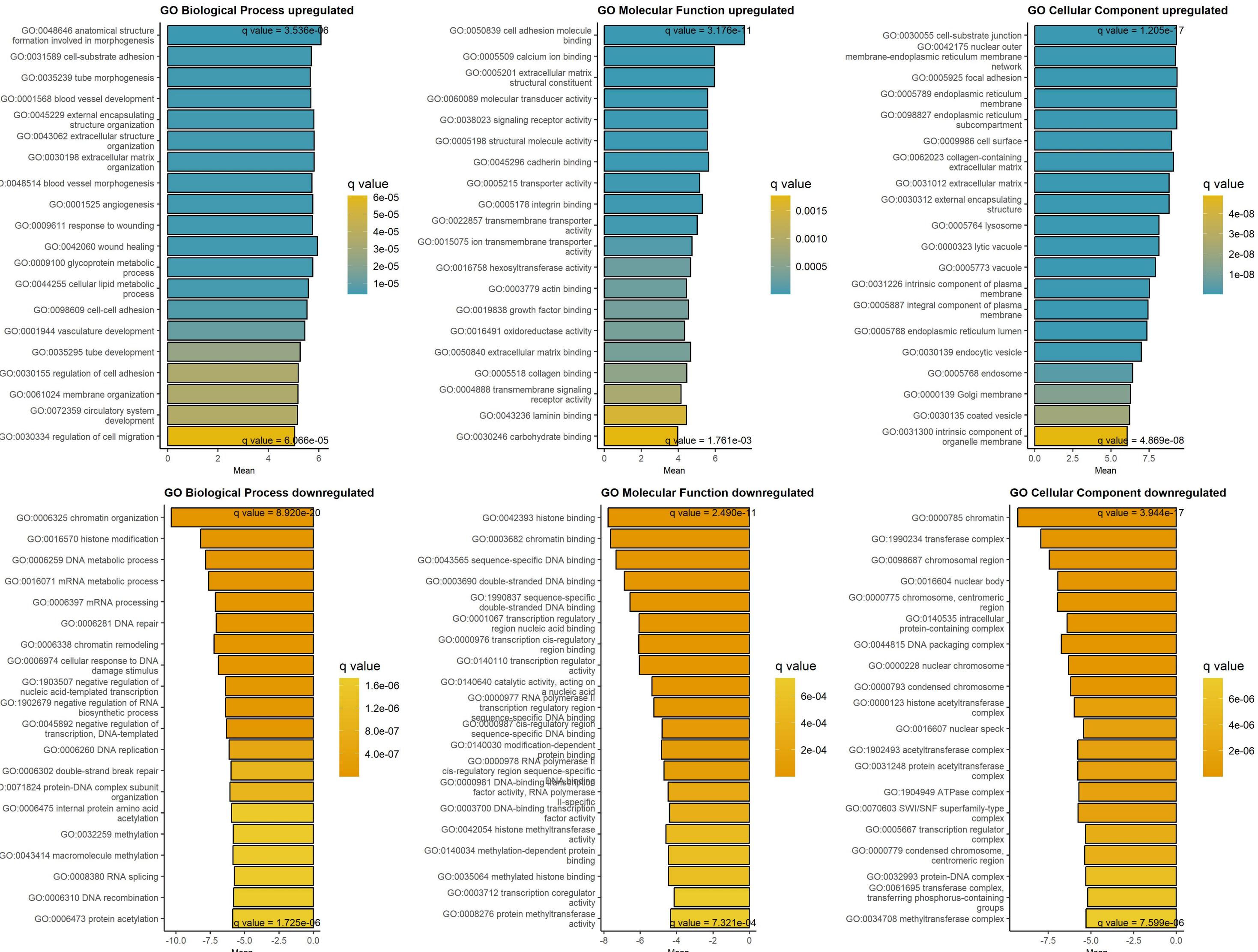


Downregulated at low/absent ARID2 Upregulated at low/absent ARID2



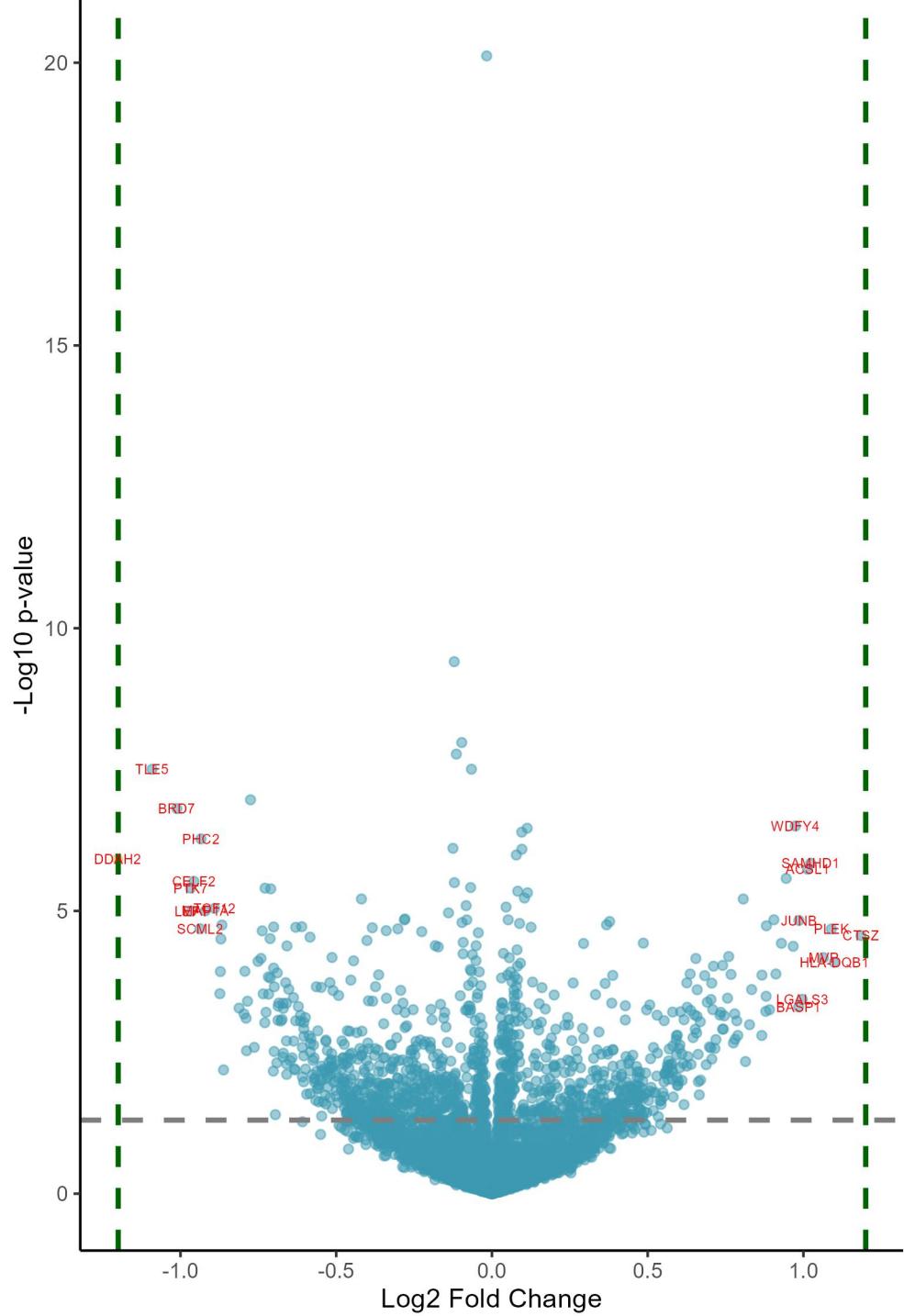
	logFC	adj.P.Val	symbol	name		logFC	adj.P.Val	symbol	name
	-1.02	2.88e-40	BRD7	bromodomain containing 7		1	5.84e-12	S100A10	S100 calcium binding protein A10
	-0.91	4.00e-33	PHF10	PHD finger protein 10		0.97	1.57e-09	LGALS3	galectin 3
	-0.79	6.38e-18	SCML2	Scm polycomb group protein like 2		0.97	2.85e-15	NT5E	5'-nucleotidase ecto
	-0.78	3.35e-25	EP400	E1A binding protein p400		0.92	1.37e-24	PARP4	poly(ADP-ribose) polymerase family
	-0.75	3.40e-18	SAMD1	sterile alpha motif domain containi		0.9	3.60e-17	MVP	major vault protein
	-0.74	1.30e-16	NRF1	nuclear respiratory factor 1		0.88	1.50e-09	CAVIN1	caveolae associated protein 1
	-0.73	2.17e-16	MEAF6	MYST/Esa1 associated factor 6		0.87	2.36e-13	CD59	CD59 molecule (CD59 blood group)
	-0.72	3.76e-14	ZNF24	zinc finger protein 24		0.87	4.66e-14	SQOR	sulfide quinone oxidoreductase
	-0.71	5.52e-14	EPB41	erythrocyte membrane protein band 4		0.86	3.04e-12	NCEH1	neutral cholesterol ester hydrolase
	-0.71	1.24e-18	TRIM24	tripartite motif containing 24		0.86	2.85e-12	TGM2	transglutaminase 2
	-0.71	2.47e-13	BRD3	bromodomain containing 3		0.86	1.63e-14	ADAM9	ADAM metallopeptidase domain 9
	-0.69	2.45e-16	ZMYM3	zinc finger MYM-type containing 3		0.84	8.64e-09	ITGA3	integrin subunit alpha 3
	-0.68	1.96e-20	DNMT3A	DNA methyltransferase 3 alpha		0.83	1.29e-13	AXL	AXL receptor tyrosine kinase
	-0.68	4.70e-16	TIMELESS	timeless circadian regulator		0.83	1.24e-15	DCBLD2	discoidin, CUB and LCCL domain cont
	-0.68	3.51e-22	ZMYM2	zinc finger MYM-type containing 2		0.83	3.07e-11	MYOF	myoferlin
	-0.67	1.01e-14	CDC45	cell division cycle associated 5		0.82	2.50e-08	CD44	CD44 molecule (Indian blood group)
	-0.66	7.88e-11	SNRNP27	small nuclear ribonucleoprotein U4/		0.82	3.94e-11	ICAM1	intercellular adhesion molecule 1
	-0.65	3.04e-12	CRMP1	collapsin response mediator protein		0.81	3.61e-15	SP100	SP100 nuclear antigen
	-0.65	1.91e-12	SUDS3	SDS3 homolog, SIN3A corepressor com		0.81	1.88e-14	NPC1	NPC intracellular cholesterol trans
	-0.65	8.96e-16	SPINDOC	spindlin interactor and repressor o		0.81	5.52e-14	RRAS	RAS related
	-0.65	1.39e-08	POLR2F	RNA polymerase II, I and III subuni		0.81	5.82e-15	FAM114A1	family with sequence similarity 114
	-0.65	3.71e-15	DPYSL5	dihydropyrimidinase like 5		0.78	1.41e-14	LACTB	lactamase beta
	-0.64	8.07e-15	MAZ	MYC associated zinc finger protein		0.78	1.80e-09	CAV1	caveolin 1
	-0.64	3.37e-15	KAT7	lysine acetyltransferase 7		0.78	3.61e-10	CTSZ	cathepsin Z
	-0.64	7.63e-14	ZCCHC3	zinc finger CCHC-type containing 3		0.78	9.46e-13	EHD2	EH domain containing 2
	-0.64	5.50e-12	SMARCD1	SWI/SNF related, matrix associated,		0.76	8.72e-15	EPS8	epidermal growth factor receptor pa
	-0.64	9.03e-10	SS18	SS18 subunit of BAF chromatin remod		0.75	3.39e-11	EPHA2	EPH receptor A2
	-0.63	1.92e-13	C5orf24	chromosome 5 open reading frame 24		0.75	5.34e-10	RHOC	ras homolog family member C
	-0.63	1.83e-12	TLE5	TLE family member 5, transcriptiona		0.75	3.93e-13	LRP10	LDL receptor related protein 10

GAGE analysis on upregulated and downregulated proteins at low/absent ARID2 protein, DB1



Differentially expressed proteins in blood cancers at absence/low amount of ARID2 , DB1

p-value < 0.05 & logFC > 1.2

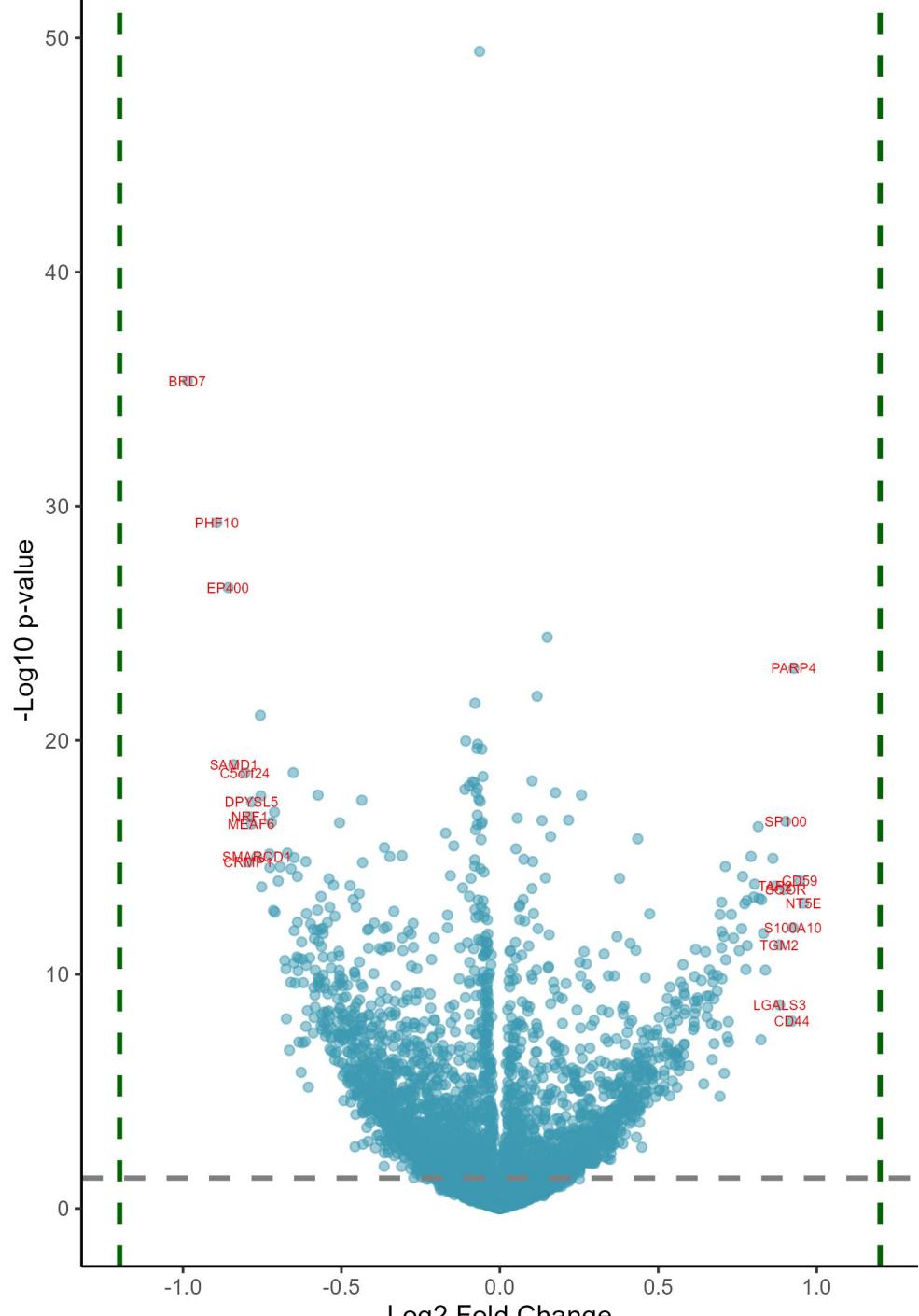


Downregulated in blood cancers at low/absent ARID2 Upregulated in blood cancers at low/absent ARID2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.2	4.75e-04	DDAH2	dimethylarginine dimethylaminohydro	1.18	2.91e-03	CTSZ	cathepsin Z
-1.09	2.97e-05	TLE5	TLE family member 5, transcriptiona	1.1	6.03e-03	HLA-DQB1	major histocompatibility complex, c
-1.01	1.14e-04	BRD7	bromodomain containing 7	1.09	2.44e-03	PLEK	pleckstrin
-0.97	1.04e-03	PTK7	protein tyrosine kinase 7 (inactive	1.06	5.39e-03	MVP	major vault protein
-0.97	1.86e-03	LEF1	lymphoid enhancer binding factor 1	1.02	5.28e-04	SAMHD1	SAM and HD domain containing deoxyn
-0.96	9.50e-04	CELF2	CUGBP Elav-like family member 2	1.01	6.38e-04	ACSL1	acyl-CoA synthetase long chain fami
-0.94	2.44e-03	SCML2	Scm polycomb group protein like 2	1	1.58e-02	LGALS3	galectin 3
-0.93	2.73e-04	PHC2	polyhomeotic homolog 2	0.99	2.28e-03	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.92	1.86e-03	MAP1A	microtubule associated protein 1A	0.98	1.86e-02	BASP1	brain abundant membrane attached si
-0.89	1.76e-03	TCF12	transcription factor 12	0.97	2.08e-04	WDFY4	WDFY family member 4
-0.87	1.38e-02	MPP1	MAGUK p55 scaffold protein 1	0.97	3.79e-03	DHRS7	dehydrogenase/reductase 7
-0.87	7.99e-03	TCF3	transcription factor 3	0.94	8.84e-04	DTD1	D-aminoacyl-tRNA deacylase 1
-0.87	3.20e-03	IGLL1	immunoglobulin lambda like polypept	0.93	3.58e-03	TYMP	thymidine phosphorylase
-0.87	2.44e-03	BCR	BCR activator of RhoGEF and GTPase	0.91	8.42e-03	CD40	CD40 molecule
-0.86	8.35e-02	RALYL	RALY RNA binding protein like	0.91	2.28e-03	PRKCD	protein kinase C delta
-0.81	1.91e-02	RUNX1	RUNX family transcription factor 1	0.89	1.93e-02	HLA-DPA1	major histocompatibility complex, c
-0.8	2.13e-02	CTSB	cathepsin B	0.88	2.44e-03	FAS	Fas cell surface death receptor
-0.79	7.99e-03	FHL1	four and a half LIM domains 1	0.88	1.44e-02	IKZF3	IKAROS family zinc finger 3
-0.79	2.38e-02	MACROD1	mono-ADP ribosylhydrolase 1	0.88	2.02e-02	ICAM1	intercellular adhesion molecule 1
-0.79	5.48e-02	PTPRF	protein tyrosine phosphatase recept	0.87	8.47e-03	ENTPD1	ectonucleoside triphosphate diphosp
-0.78	1.65e-02	FLI1	Fli-1 proto-oncogene, ETS transcript	0.87	3.81e-02	HLA-DPB1	major histocompatibility complex, c
-0.78	9.00e-05	CBX2	chromobox 2	0.83	1.22e-02	TNFRSF8	TNF receptor superfamily member 8
-0.76	5.16e-02	LGALS3BP	galectin 3 binding protein	0.83	2.81e-02	MS4A1	membrane spanning 4-domains A1
-0.75	5.89e-03	CASP2	caspase 2	0.81	6.97e-02	SERPINB9	serpin family B member 9
-0.74	5.42e-03	SPINDOC	spindlin interactor and repressor o	0.81	1.32e-03	TRAF1	TNF receptor associated factor 1
-0.74	2.54e-03	CD9	CD9 molecule	0.79	3.81e-02	CAMK2D	calcium/calmodulin dependent protei
-0.73	1.38e-02	HDAC7	histone deacetylase 7	0.79	2.52e-02	MX1	MX dynamin like GTPase 1
-0.73	2.63e-02	GPX7	glutathione peroxidase 7	0.78	4.30e-02	SQOR	sulfide quinone oxidoreductase
-0.73	1.04e-03	ZMYM2	zinc finger MYM-type containing 2	0.78	2.13e-02	SH3BP1	SH3 domain binding protein 1

Differentially expressed proteins in solid cancers at absence/low amount of ARID2 , DB1

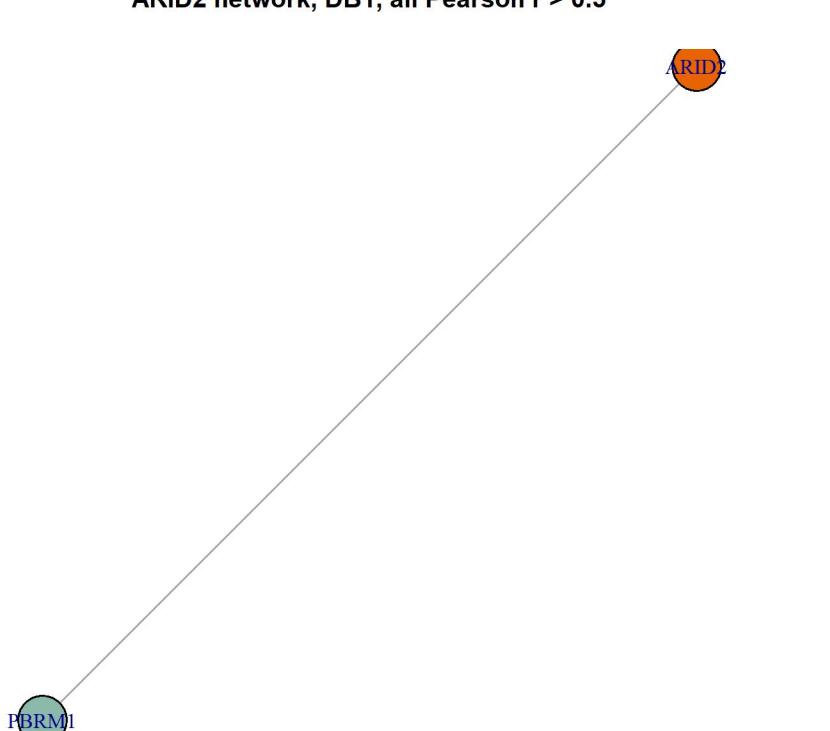
p-value < 0.05 & logFC > 1.2



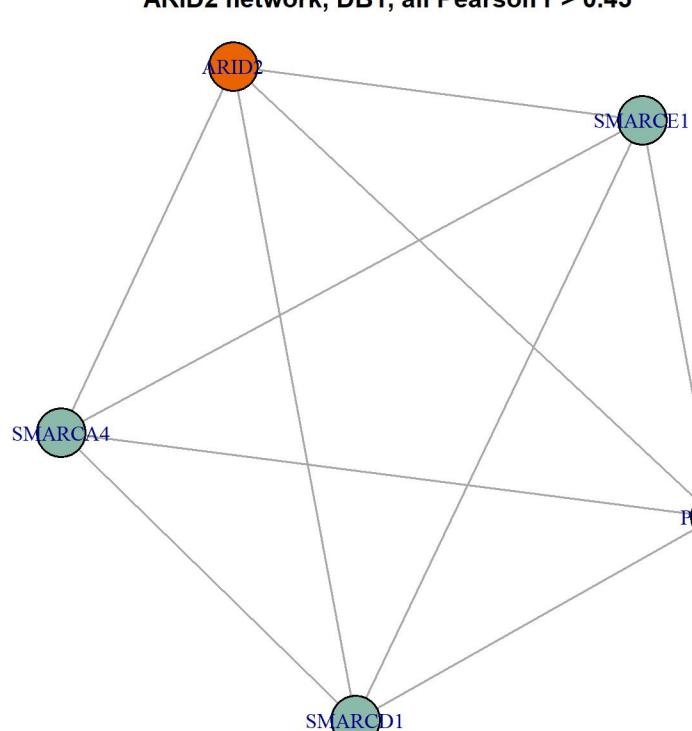
Downregulated in solid cancers at low/absent ARID2 Upregulated in solid cancers at low/absent ARID2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.99	9.98e-33	BRD7	bromodomain containing 7	0.96	5.65e-12	NT5E	5'-nucleotidase ecto
-0.89	8.47e-27	PHF10	PHD finger protein 10	0.95	7.85e-13	CD59	CD59 molecule (CD59 blood group)
-0.86	4.00e-24	EP400	E1A binding protein p400	0.93	7.96e-21	PARP4	Poly(ADP-ribose) polymerase family
-0.84	4.83e-17	SAMD1	sterile alpha motif domain containi	0.92	4.86e-11	S100A10	S100 calcium binding protein A10
-0.8	9.66e-17	C5orf24	chromosome 5 open reading frame 24	0.92	1.55e-07	CD44	CD44 molecule (Indian blood group)
-0.79	1.54e-13	CRMP1	collapsin response mediator protein	0.9	4.78e-15	SP100	SP100 nuclear antigen
-0.79	3.41e-15	NRF1	nuclear respiratory factor 1	0.9	1.66e-12	SQOR	sulfide quinone oxidoreductase
-0.78	5.54e-15	MEAF6	MYST/Esa1 associated factor 6	0.88	3.81e-08	LGALS3	galectin 3
-0.78	8.69e-16	DPYSL5	dihydropyrimidinase like 5	0.88	2.10e-10	TGM2	transglutaminase 2
-0.77	1.01e-13	SMARCD1	SWI/SNF related, matrix associated,	0.87	1.26e-12	TAP2	transporter 2, ATP binding cassette
-0.76	5.72e-19	DNMT3A	DNA methyltransferase 3 alpha	0.86	1.17e-13	PSMB9	proteasome 20S subunit beta 9
-0.75	5.46e-16	ZMYM3	zinc finger MYM-type containing 3	0.84	1.85e-09	ICAM1	intercellular adhesion molecule 1
-0.75	1.35e-12	BRD3	bromodomain containing 3	0.83	7.65e-11	AXL	AXL receptor tyrosine kinase
-0.73	8.42e-14	KIF1A	kinesin family member 1A	0.83	4.26e-12	RHOC	ras homolog family member C
-0.73	2.47e-13	SCML2	Scm polycomb group protein like 2	0.82	7.52e-07	CAVIN1	caveolae associated protein 1
-0.72	5.03e-15	CRABP1	cellular retinoic acid binding prot	0.82	3.90e-12	DCBLD2	discoidin, CUB and LCCL domain cont
-0.71	1.08e-11	EPB41	erythrocyte membrane protein band 4	0.82	6.92e-15	MVP	major vault protein
-0.71	2.28e-15	ATAD2	ATPase family AAA domain containing	0.8	1.07e-12	FAM114A1	family with sequence similarity 114
-0.71	1.22e-11	ZNF24	zinc finger protein 24	0.8	3.40e-12	NCEH1	neutral cholesterol ester hydrolase
-0.7	7.95e-13	CDC45	cell division cycle associated 5	0.79	1.01e-13	FGF2	fibroblast growth factor 2
-0.69	2.33e-13	RBM45	RNA binding motif protein 45	0.78	2.22e-10	EHD2	EH domain containing 2
-0.68	7.81e-10	CENPV	centromere protein V	0.78	4.50e-12	ADAM9	ADAM metallopeptidase domain 9
-0.67	1.67e-09	CNTN1	contactin 1	0.78	1.77e-09	HLA-B	major histocompatibility complex, c
-0.67	1.26e-07	TUBB2B	tubulin beta 2B class IIb	0.77	5.93e-12	LACTB	lactamase beta
-0.67	7.86e-14	TRIM24	tripartite motif containing 24	0.77	5.52e-13	EPS8	epidermal growth factor receptor pa
-0.66	1.89e-06	MACROH2A2	macroH2A.2 histone	0.76	5.20e-11	TAP1	transporter 1, ATP binding cassette
-0.66	5.17e-09	CSTF2T	cleavage stimulation factor subunit	0.76	3.33e-10	GBE1	1,4-alpha-glucan branching enzyme 1
-0.66	2.77e-13	KAT7	lysine acetyltransferase 7	0.74	1.14e-10	NPC1	NPC intracellular cholesterol trans
-0.65	9.66e-17	ZMYM2	zinc finger MYM-type containing 2	0.73	1.49e-11	APOL2	apolipoprotein L2

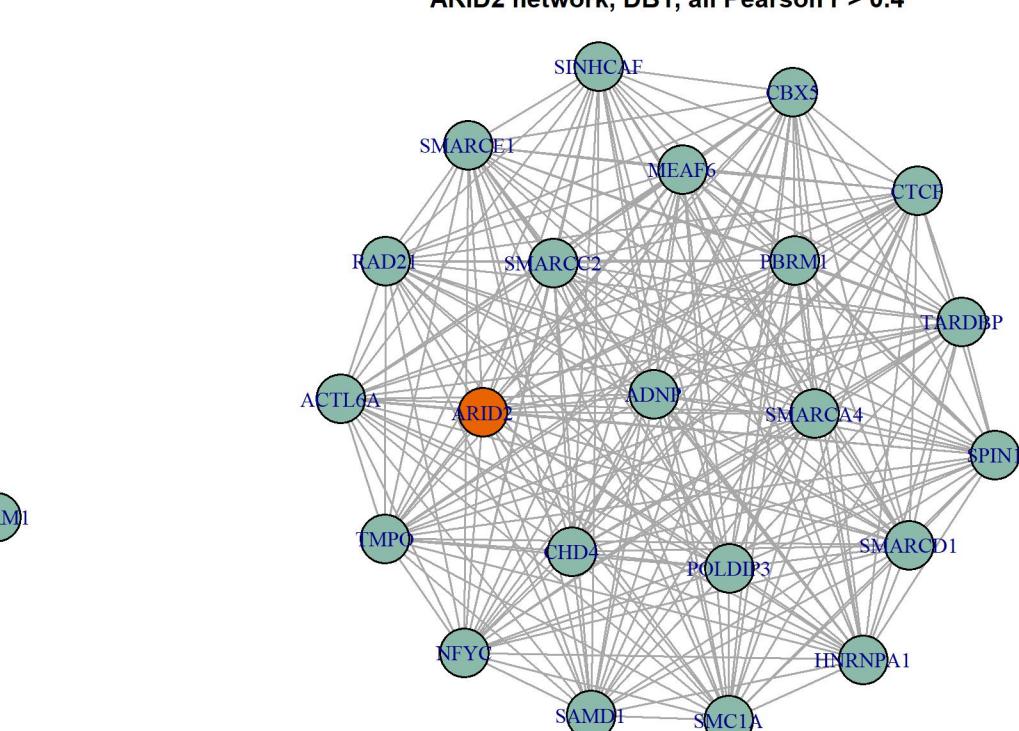
ARID2 network, DB1, all Pearson r > 0.5

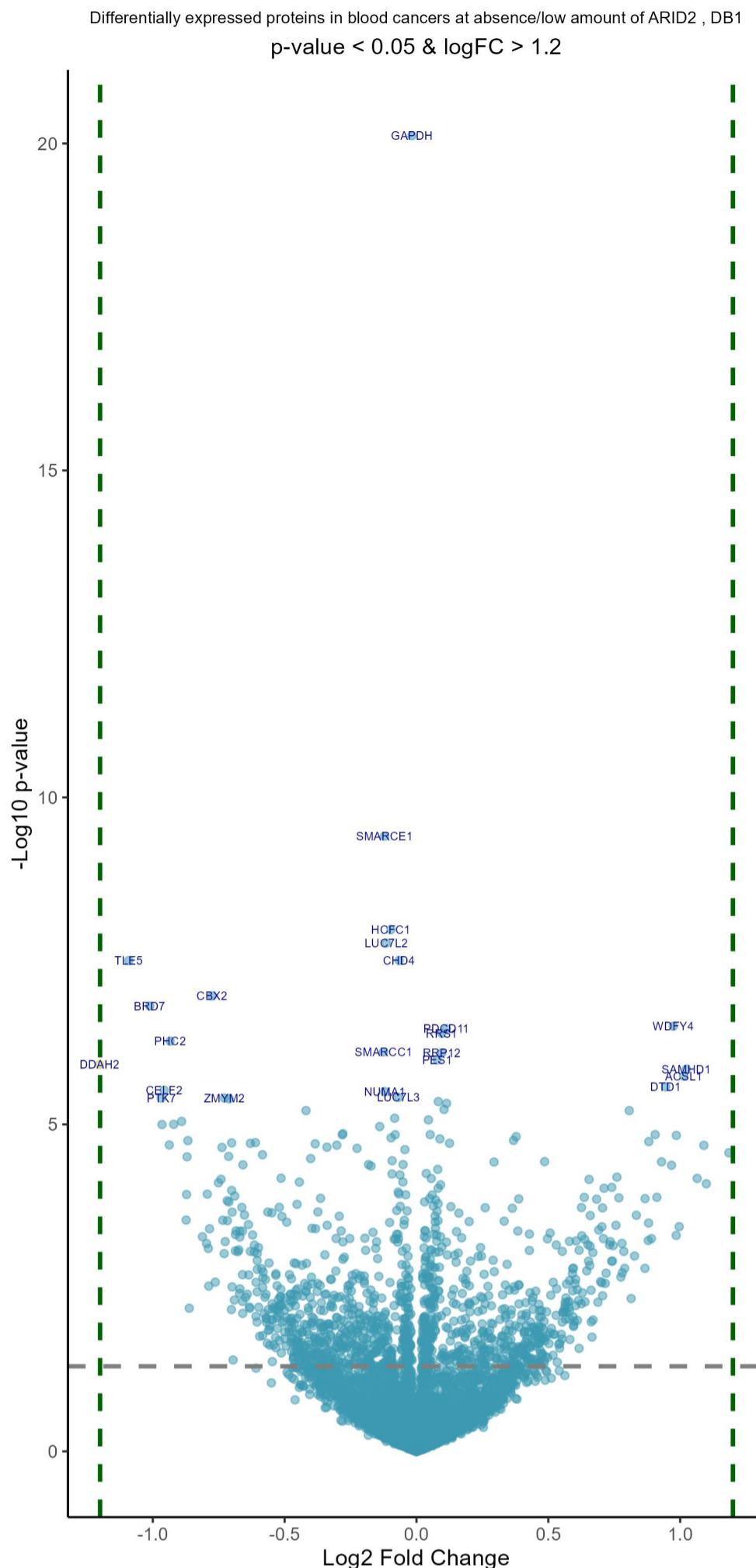


ARID2 network, DB1, all Pearson r > 0.45

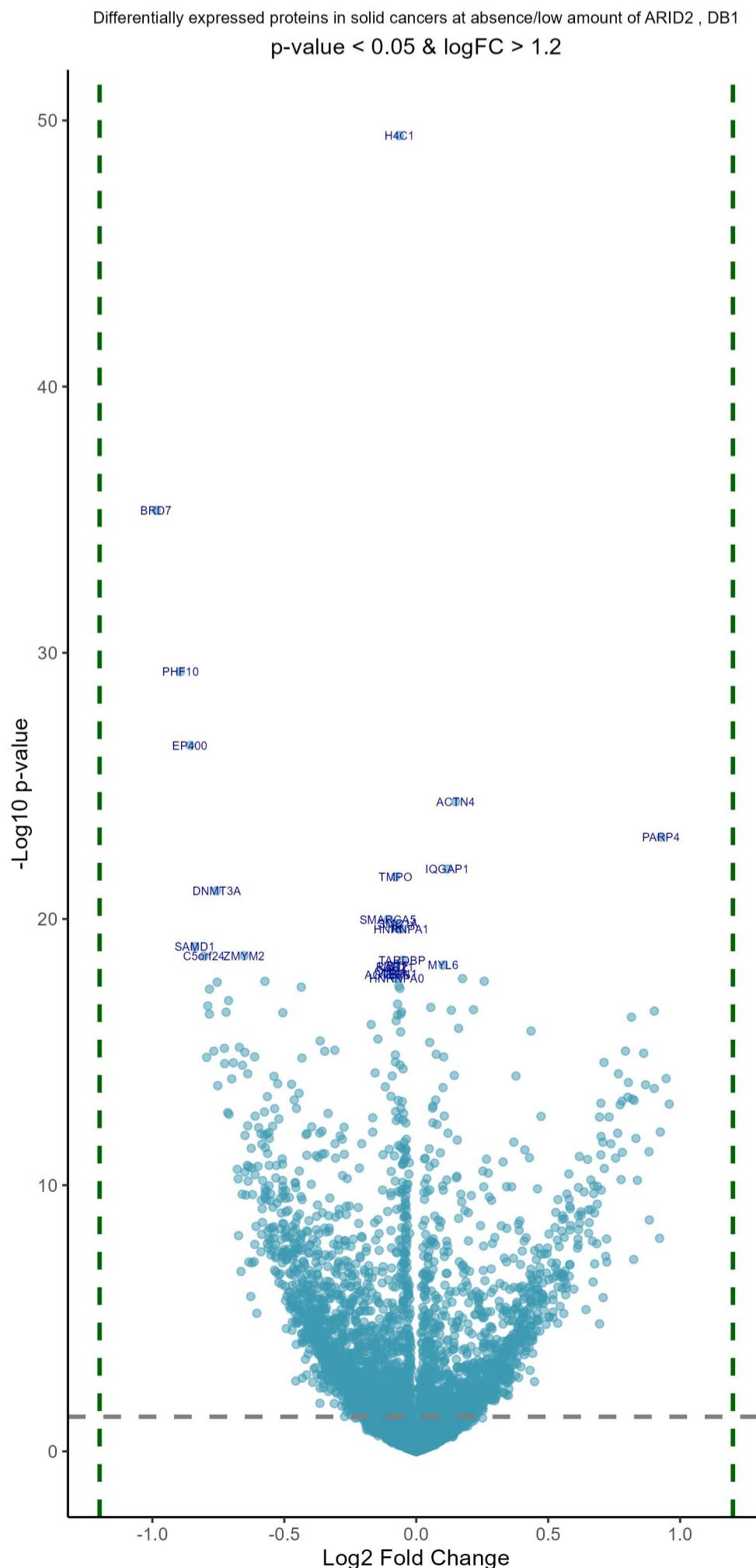


ARID2 network, DB1, all Pearson r > 0.4



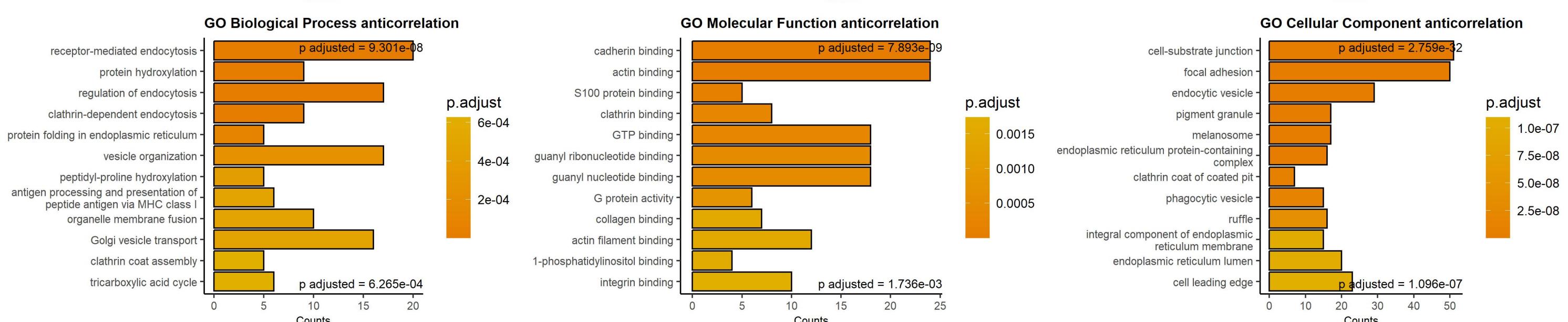
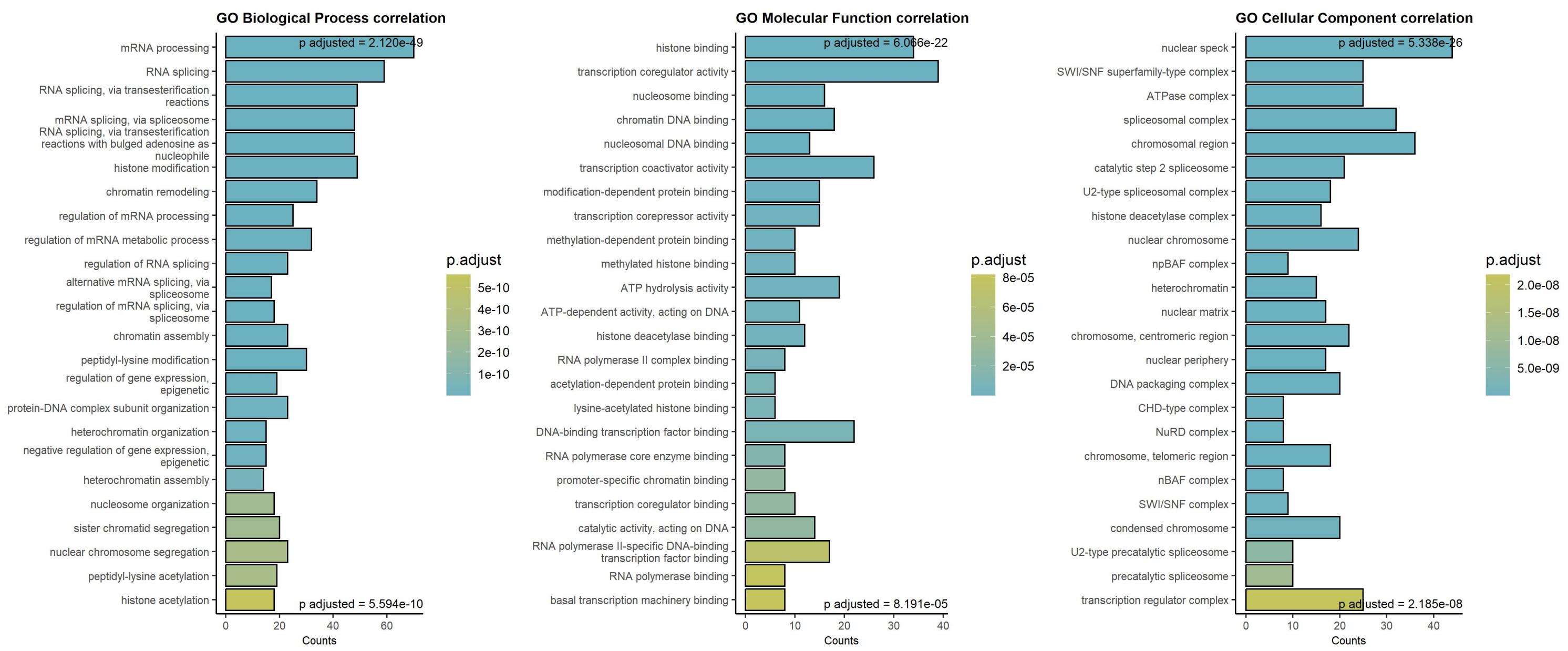


Sorted by p values!							
Downregulated in blood cancers at low/absent ARID2				Upregulated in blood cancers at low/absent ARID2			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.02	5.04e-17	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.97	2.08e-04	WDFY4	WDFY family member 4
-0.12	8.67e-07	SMARCE1	SWI/SNF related, matrix associated,	0.11	2.08e-04	PDCD11	programmed cell death 11
-0.1	1.75e-05	HCFC1	host cell factor C1	0.1	2.24e-04	RRS1	ribosome biogenesis regulator 1 hom
-0.11	2.24e-05	LUC7L2	LUC7 like 2, pre-mRNA splicing fact	0.1	3.59e-04	RRP12	ribosomal RNA processing 12 homolog
-0.07	2.97e-05	CHD4	chromodomain helicase DNA binding p	0.08	4.26e-04	PES1	pescadillo ribosomal biogenesis fac
-1.09	2.97e-05	TLE5	TLE family member 5, transcriptiona	1.02	5.28e-04	SAMHD1	SAM and HD domain containing deoxy
-0.78	9.00e-05	CBX2	chromobox 2	1.01	6.38e-04	ACSL1	acyl-CoA synthetase long chain fami
-1.01	1.14e-04	BRD7	bromodomain containing 7	0.94	8.84e-04	DTD1	D-aminoacyl-tRNA deacylase 1
-0.93	2.73e-04	PHC2	polyhomeotic homolog 2	0.08	1.10e-03	EIF5B	eukaryotic translation initiation f
-0.13	3.59e-04	SMARCC1	SWI/SNF related, matrix associated,	0.11	1.13e-03	IPO4	importin 4
-1.2	4.75e-04	DDAH2	dimethylarginine dimethylaminohydro	0.1	1.32e-03	ATP1A1	ATPase Na+/K+ transporting subunit
-0.96	9.50e-04	CELF2	CUGBP Elav-like family member 2	0.81	1.32e-03	TRAF1	TNF receptor associated factor 1
-0.12	9.55e-04	NUMA1	nuclear mitotic apparatus protein 1	0.05	1.72e-03	RPL38	ribosomal protein L38
-0.07	1.04e-03	LUC7L3	LUC7 like 3 pre-mRNA splicing facto	0.05	2.28e-03	RSL1D1	ribosomal L1 domain containing 1
-0.97	1.04e-03	PTK7	protein tyrosine kinase 7 (inactive	0.91	2.28e-03	PRKCD	protein kinase C delta
-0.73	1.04e-03	ZMYM2	zinc finger MYM-type containing 2	0.99	2.28e-03	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.71	1.04e-03	ABI2	abl interactor 2	0.38	2.32e-03	ZC2HC1A	zinc finger C2HC-type containing 1A
-0.42	1.32e-03	PATZ1	POZ/BTB and AT hook containing zinc	0.09	2.41e-03	EBNA1BP2	EBNA1 binding protein 2
-0.08	1.67e-03	HMGB2	high mobility group box 2	0.37	2.44e-03	GNL2	G protein nucleolar 2
-0.89	1.76e-03	TCF12	transcription factor 12	0.88	2.44e-03	FAS	Fas cell surface death receptor
-0.92	1.86e-03	MAP1A	microtubule associated protein 1A	0.13	2.44e-03	NIT2	nitrilase family member 2
-0.97	1.86e-03	LEF1	lymphoid enhancer binding factor 1	1.09	2.44e-03	PLEK	pleckstrin
-0.14	1.94e-03	CBX5	chromobox 5	1.18	2.91e-03	CTSZ	cathepsin Z
-0.28	2.28e-03	PBRM1	polybromo 1	0.49	3.58e-03	ACSL4	acyl-CoA synthetase long chain fami
-0.08	2.28e-03	TMPO	thymopoietin	0.93	3.58e-03	TYMP	thymidine phosphorylase
-0.28	2.28e-03	RNASEH2C	ribonuclease H2 subunit C	0.29	3.58e-03	FSD1	fibronectin type III and SPRY domai
-0.1	2.37e-03	SIN3A	SIN3 transcription regulator family	0.97	3.79e-03	DHRS7	dehydrogenase/reductase 7
-0.87	2.44e-03	BCR	BCR activator of RhoGEF and GTPase	0.08	4.27e-03	MRPL17	mitochondrial ribosomal protein L17
-0.61	2.44e-03	NFYB	nuclear transcription factor Y subu	0.04	4.86e-03	RPL5	ribosomal protein L5
-0.7	2.44e-03	SP1	Sp1 transcription factor	0.76	5.32e-03	TRMT5	tRNA methyltransferase 5
-0.63	2.44e-03	RNASEH2B	ribonuclease H2 subunit B	1.06	5.39e-03	MVP	major vault protein
-0.38	2.44e-03	KIF4A	kinesin family member 4A	0.06	5.39e-03	RARS1	arginyl-tRNA synthetase 1
-0.94	2.44e-03	SCML2	Scm polycomb group protein like 2	0.65	5.42e-03	RMDN1	regulator of microtubule dynamics 1
-0.3	2.44e-03	CTCF	CCCTC-binding factor	1.1	6.03e-03	HLA-DQB1	major histocompatibility complex, c
-0.34	2.54e-03	LZIC	leucine zipper and CTNNBIP1 domain	0.09	6.20e-03	GFM1	G elongation factor mitochondrial 1
-0.74	2.54e-03	CD9	CD9 molecule	0.74	6.70e-03	WARS2	tryptophanyl tRNA synthetase 2, mit
-0.23	2.57e-03	RNASEH2A	ribonuclease H2 subunit A	0.08	6.78e-03	LAP3	leucine aminopeptidase 3
-0.04	2.65e-03	SF3B2	splicing factor 3b subunit 2	0.71	6.78e-03	CNTRL	centriolin
-0.58	3.07e-03	KMT2D	lysine methyltransferase 2D	0.06	7.99e-03	EIF3D	eukaryotic translation initiation f

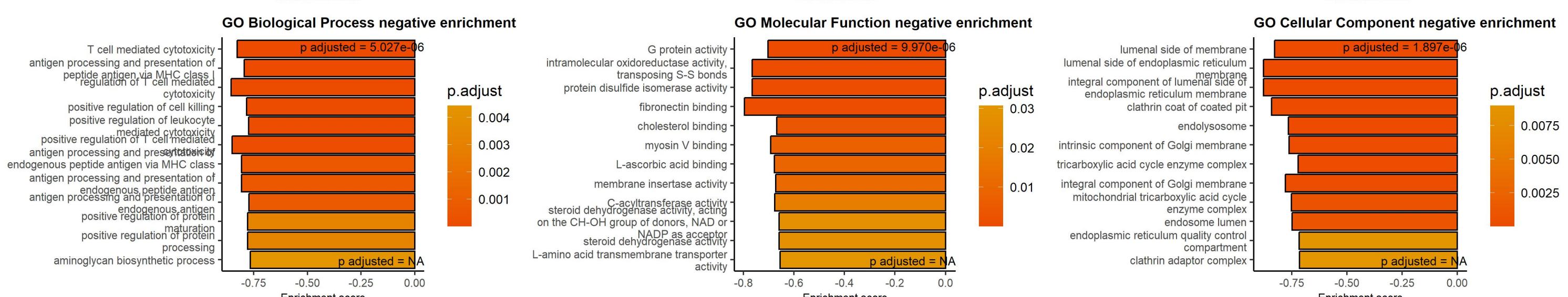
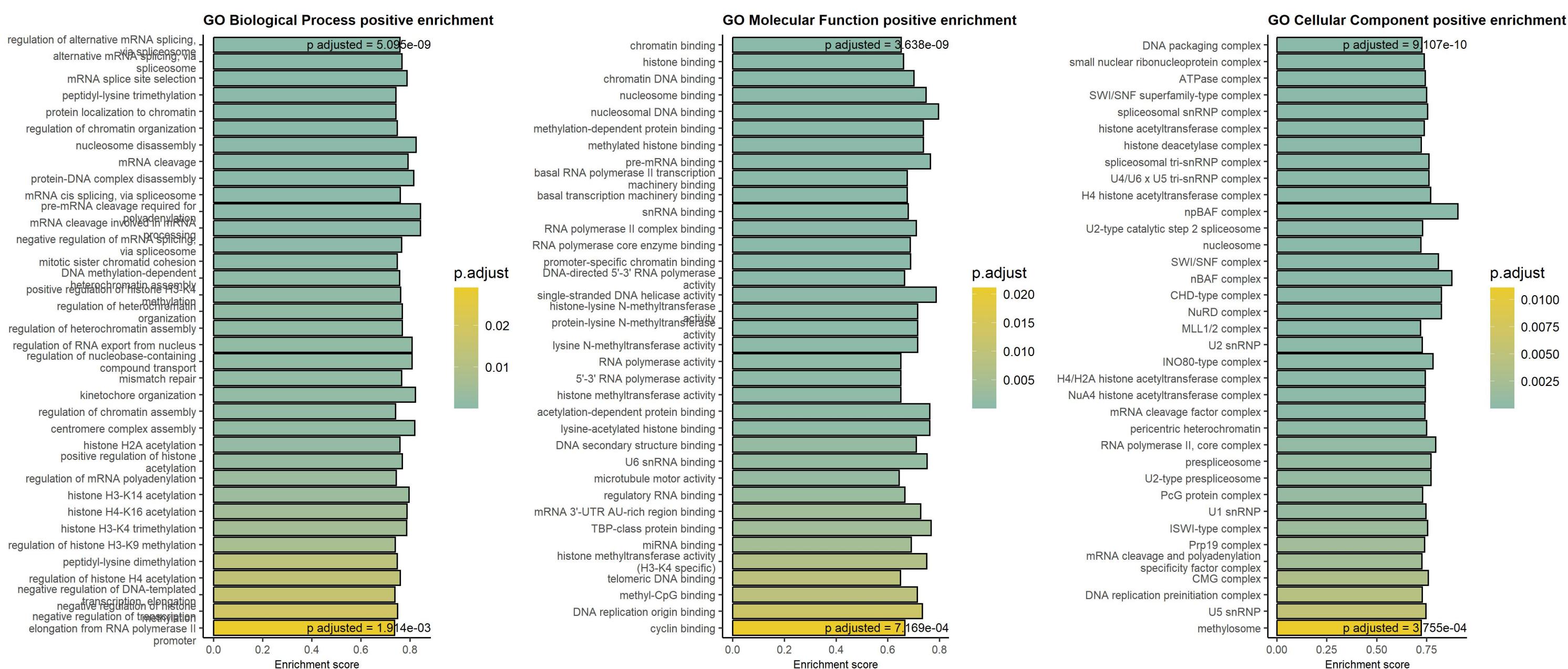


Sorted by p values!							
Downregulated in solid cancers at low/absent ARID2				Upregulated in solid cancers at low/absent ARID2			
FC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
06	1.24e-46	H4C1	H4 clustered histone 1	0.15	4.36e-22	ACTN4	actinin alpha 4
99	9.98e-33	BRD7	bromodomain containing 7	0.93	7.96e-21	PARP4	Poly(ADP-ribose) polymerase family
89	8.47e-27	PHF10	PHD finger protein 10	0.12	1.10e-19	IQGAP1	IQ motif containing GTPase activati
86	4.00e-24	EP400	E1A binding protein p400	0.1	1.89e-16	MYL6	myosin light chain 6
08	1.93e-19	TMPO	thymopoietin	0.18	4.43e-16	ACTN1	actinin alpha 1
76	5.72e-19	DNMT3A	DNA methyltransferase 3 alpha	0.26	5.20e-16	HEXB	hexosaminidase subunit beta
11	6.46e-18	SMARCA5	SWI/SNF related, matrix associated,	0.06	3.77e-15	CLTC	clathrin heavy chain
07	8.12e-18	SMC1A	structural maintenance of chromosom	0.22	4.47e-15	PLEC	plectin
07	1.13e-17	IK	IK cytokine	0.13	4.56e-15	PICALM	phosphatidylinositol binding clathr
06	1.13e-17	HNRNPA1	heterogeneous nuclear ribonucleopro	0.9	4.78e-15	SP100	SP100 nuclear antigen
84	4.83e-17	SAMD1	sterile alpha motif domain containi	0.82	6.92e-15	MVP	major vault protein
65	9.66e-17	ZMYM2	zinc finger MYM-type containing 2	0.16	1.71e-14	LMNA	lamin A/C
.8	9.66e-17	C5orf24	chromosome 5 open reading frame 24	0.44	2.11e-14	MYO1C	myosin IC
05	1.31e-16	TARDBP	TAR DNA binding protein	0.05	5.23e-14	CDC42	cell division cycle 42
09	1.93e-16	UBTF	upstream binding transcription fact	0.79	1.01e-13	FGF2	fibroblast growth factor 2
08	2.01e-16	RAD21	RAD21 cohesin complex component	0.86	1.17e-13	PSMB9	proteasome 20S subunit beta 9
.1	2.63e-16	CHD4	chromodomain helicase DNA binding p	0.08	1.26e-13	RAC1	Rac family small GTPase 1
07	3.28e-16	WBP11	WW domain binding protein 11	0.1	1.50e-13	AP2A1	adaptor related protein complex 2 s
11	3.49e-16	ACTL6A	actin like 6A	0.71	2.30e-13	RAB11FIP5	RAB11 family interacting protein 5
07	4.43e-16	HNRNPA0	heterogeneous nuclear ribonucleopro	0.77	5.52e-13	EPS8	epidermal growth factor receptor pa
57	5.20e-16	CBX2	chromobox 2	0.14	6.26e-13	MYH9	myosin heavy chain 9
75	5.46e-16	ZMYM3	zinc finger MYM-type containing 3	0.38	6.40e-13	PLIN3	perilipin 3
07	7.32e-16	PNN	pinin, desmosome associated protein	0.95	7.85e-13	CD59	CD59 molecule (CD59 blood group)
44	7.80e-16	ZNF516	zinc finger protein 516	0.8	1.07e-12	FAM114A1	family with sequence similarity 114
06	8.40e-16	SAFB	scaffold attachment factor B	0.87	1.26e-12	TAP2	transporter 2, ATP binding cassette
78	8.69e-16	DPYSL5	dihydropyrimidinase like 5	0.1	1.56e-12	TMOD3	tropomodulin 3
71	2.28e-15	ATAD2	ATPase family AAA domain containing	0.9	1.66e-12	SQOR	sulfide quinone oxidoreductase
07	3.00e-15	HCFC1	host cell factor C1	0.8	3.40e-12	NCEH1	neutral cholesterol ester hydrolase
79	3.41e-15	NRF1	nuclear respiratory factor 1	0.82	3.90e-12	DCBLD2	discoidin, CUB and LCCL domain cont
06	4.98e-15	SNRPF	small nuclear ribonucleoprotein pol	0.07	4.20e-12	AP2B1	adaptor related protein complex 2 s
72	5.03e-15	CRABP1	cellular retinoic acid binding prot	0.83	4.26e-12	RHOC	ras homolog family member C
51	5.15e-15	MEX3A	mex-3 RNA binding family member A	0.78	4.50e-12	ADAM9	ADAM metallopeptidase domain 9
06	5.54e-15	ACIN1	apoptotic chromatin condensation in	0.7	5.30e-12	DAB2	DAB adaptor protein 2
78	5.54e-15	MEAF6	MYST/Esa1 associated factor 6	0.96	5.65e-12	NT5E	5'-nucleotidase ecto
07	5.82e-15	SMC3	structural maintenance of chromosom	0.77	5.93e-12	LACTB	lactamase beta
08	9.23e-15	BUD31	BUD31 homolog	0.06	6.61e-12	RAB1A	RAB1A, member RAS oncogene family
17	1.26e-14	POLDIP3	DNA polymerase delta interacting pr	0.06	7.79e-12	ARPC4	actin related protein 2/3 complex s
06	2.25e-14	SNW1	SNW domain containing 1	0.11	1.41e-11	CALU	calumenin

Top 250 correlation coefficients overrepresentation, ARID2 protein, DB1

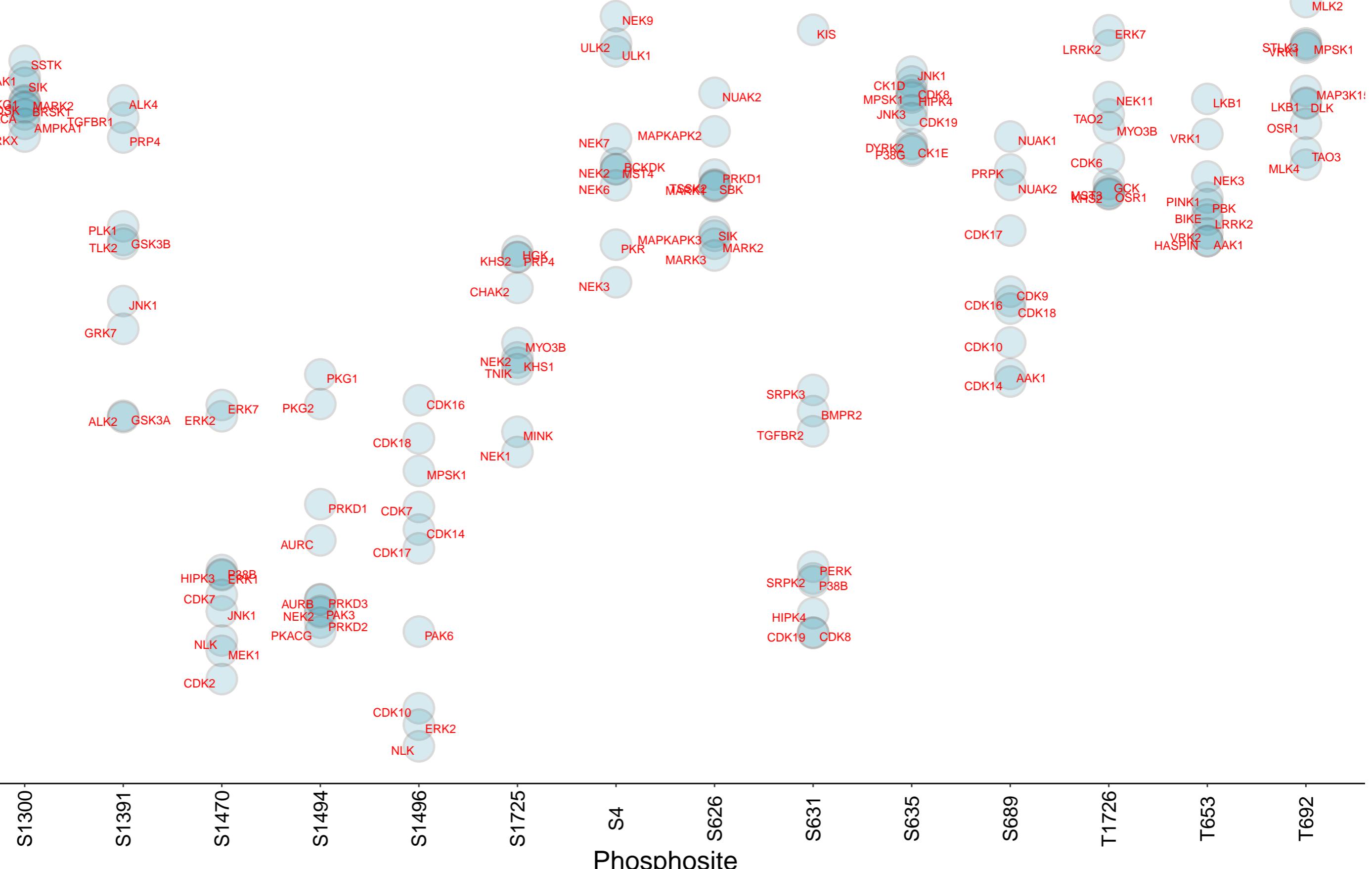


Gene Set Enrichment analysis on protein correlation coefficients, ARID2 protein, DB1



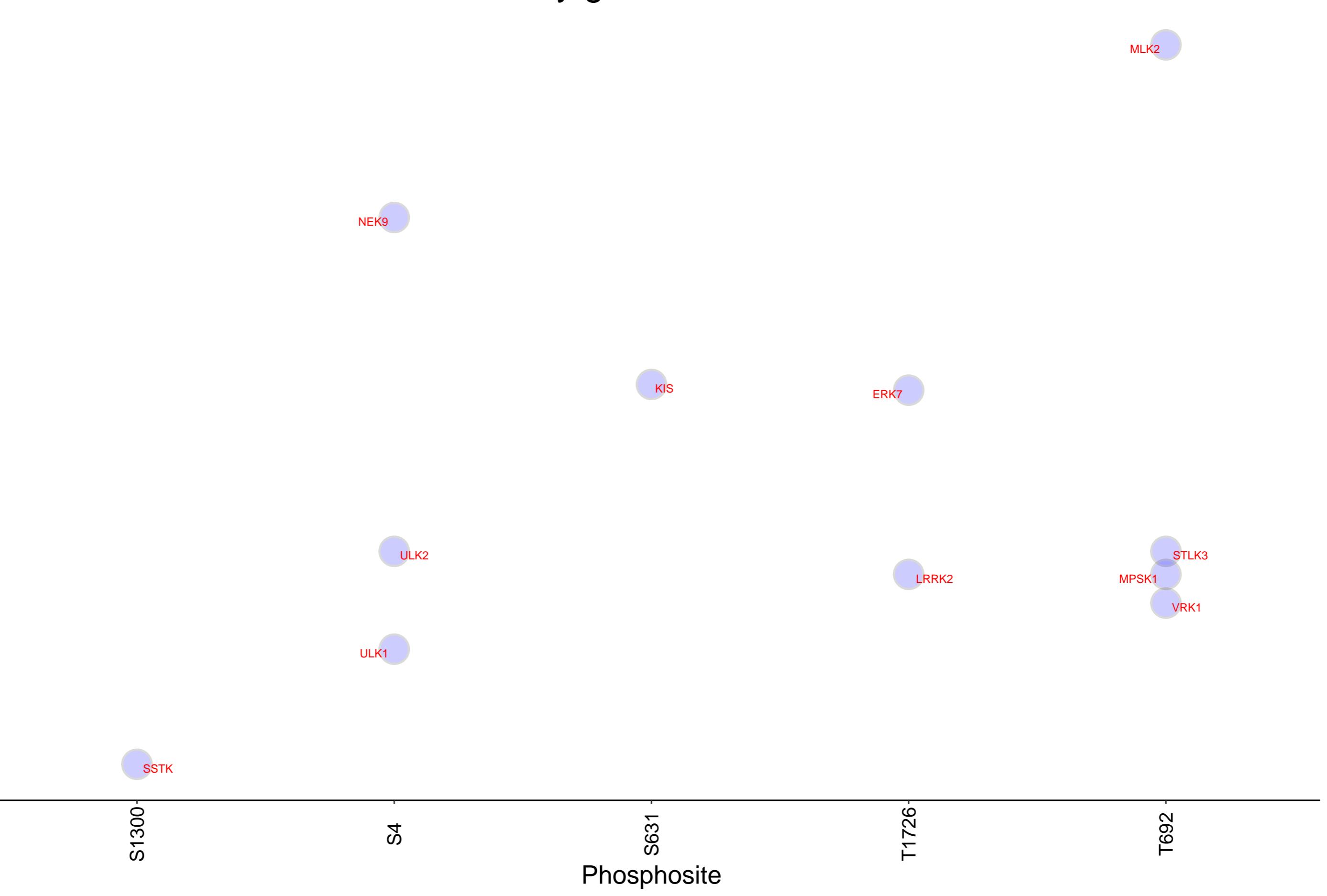
Top 10 kinases for each phosphosite in ARID2

Predicted affinity percentile



Kinases with affinity greater than 98.5% to ARID2

Predicted affinity percentile



Top 15 positive correlation coefficients for ARID2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

