

DMAP1

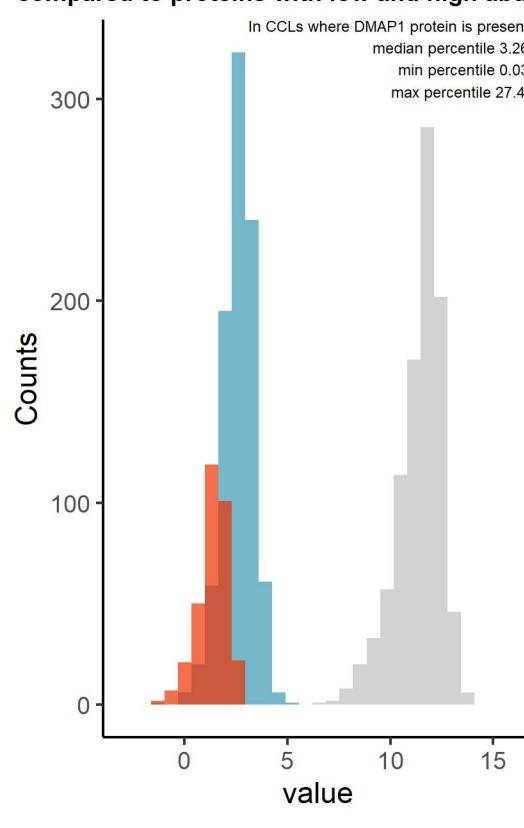
Protein name: DMAP1 ; UNIPROT: Q9NPF5 ; Gene name: DNA methyltransferase 1 associated protein 1

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

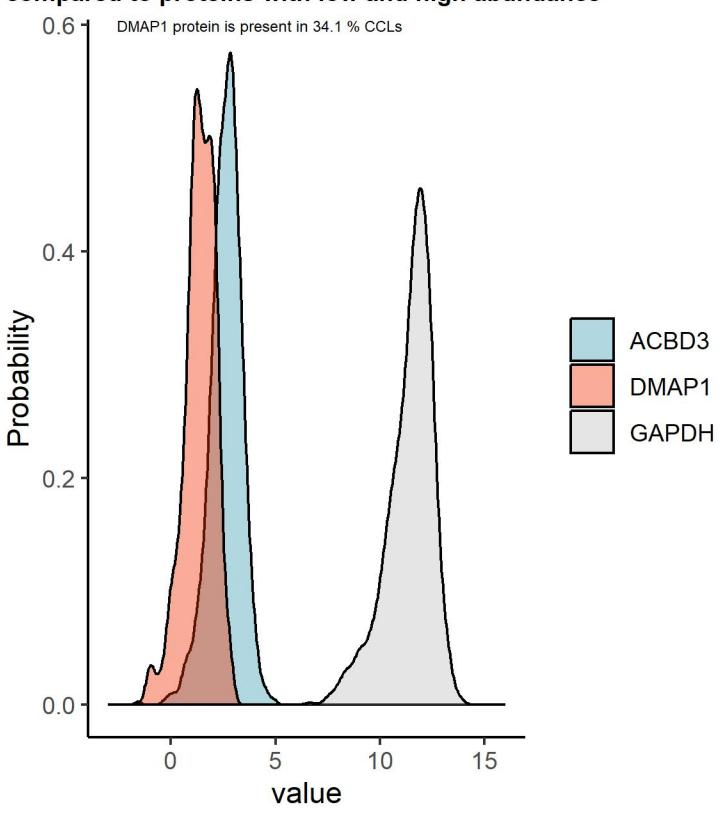
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

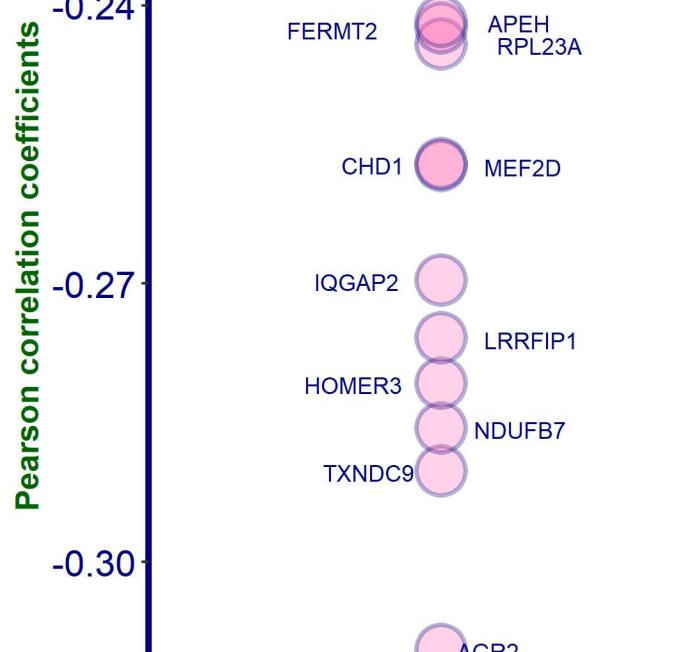
Histogram of DMAP1 protein compared to proteins with low and high abundance



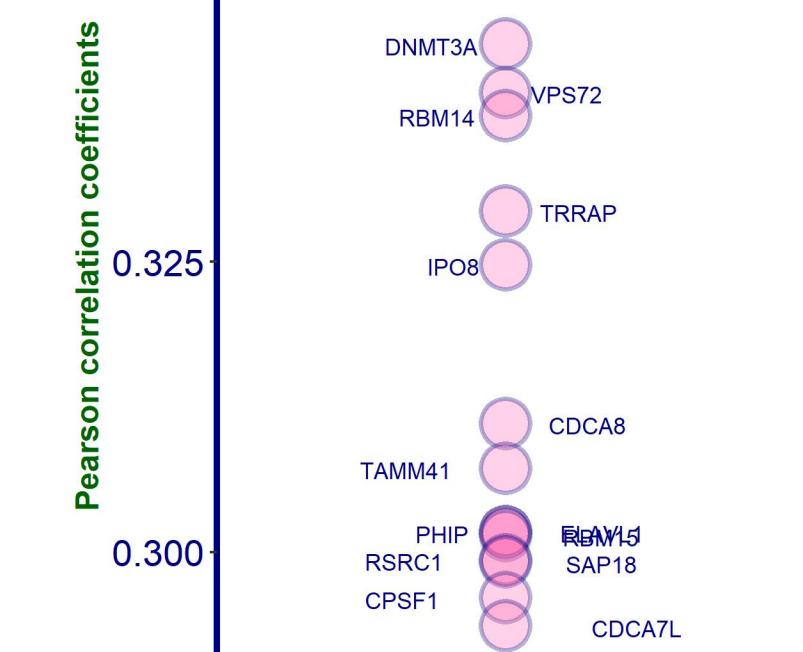
Density plot of DMAP1 protein compared to proteins with low and high abundance



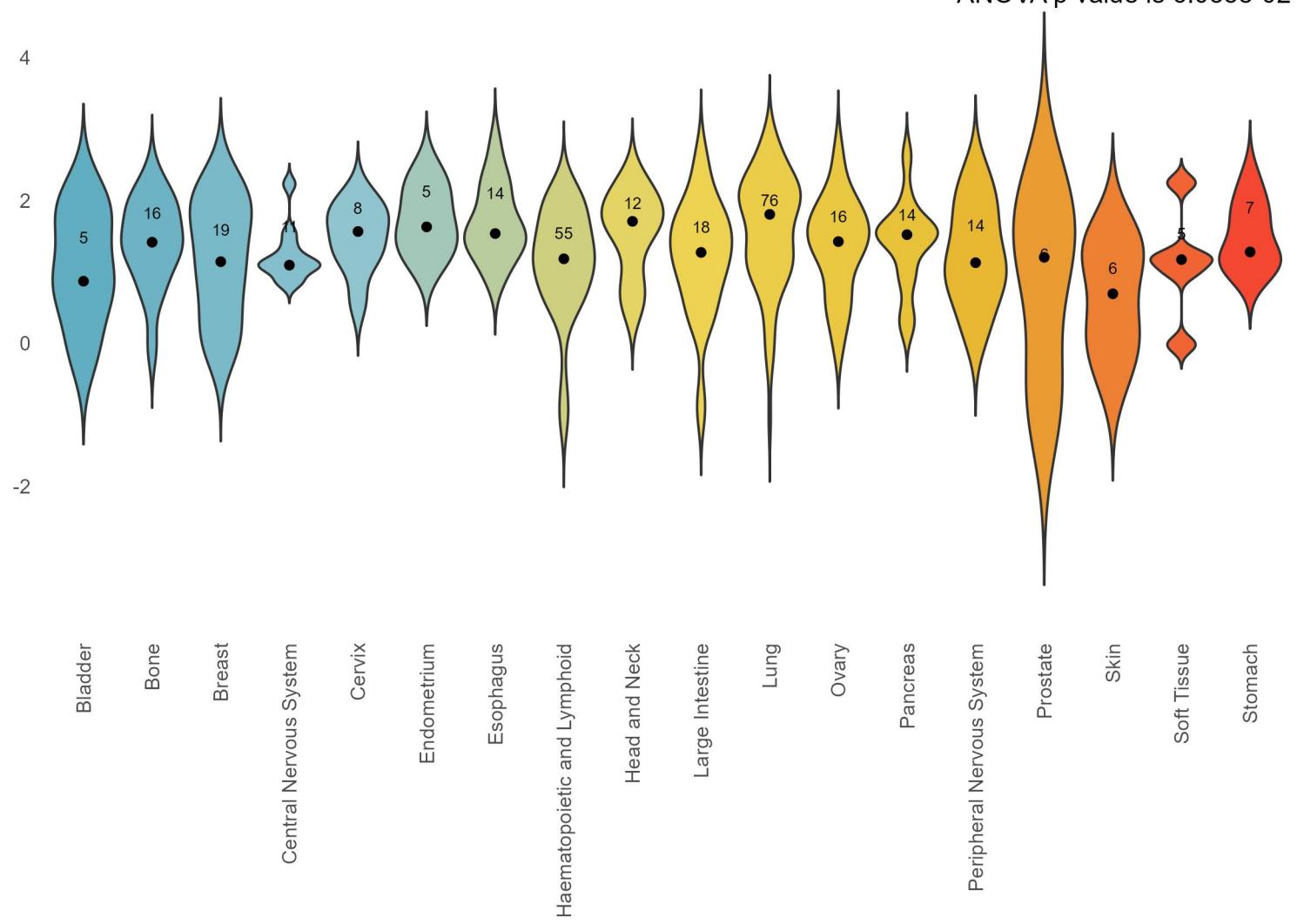
Top negative correlations of DMAP1 protein, DB1



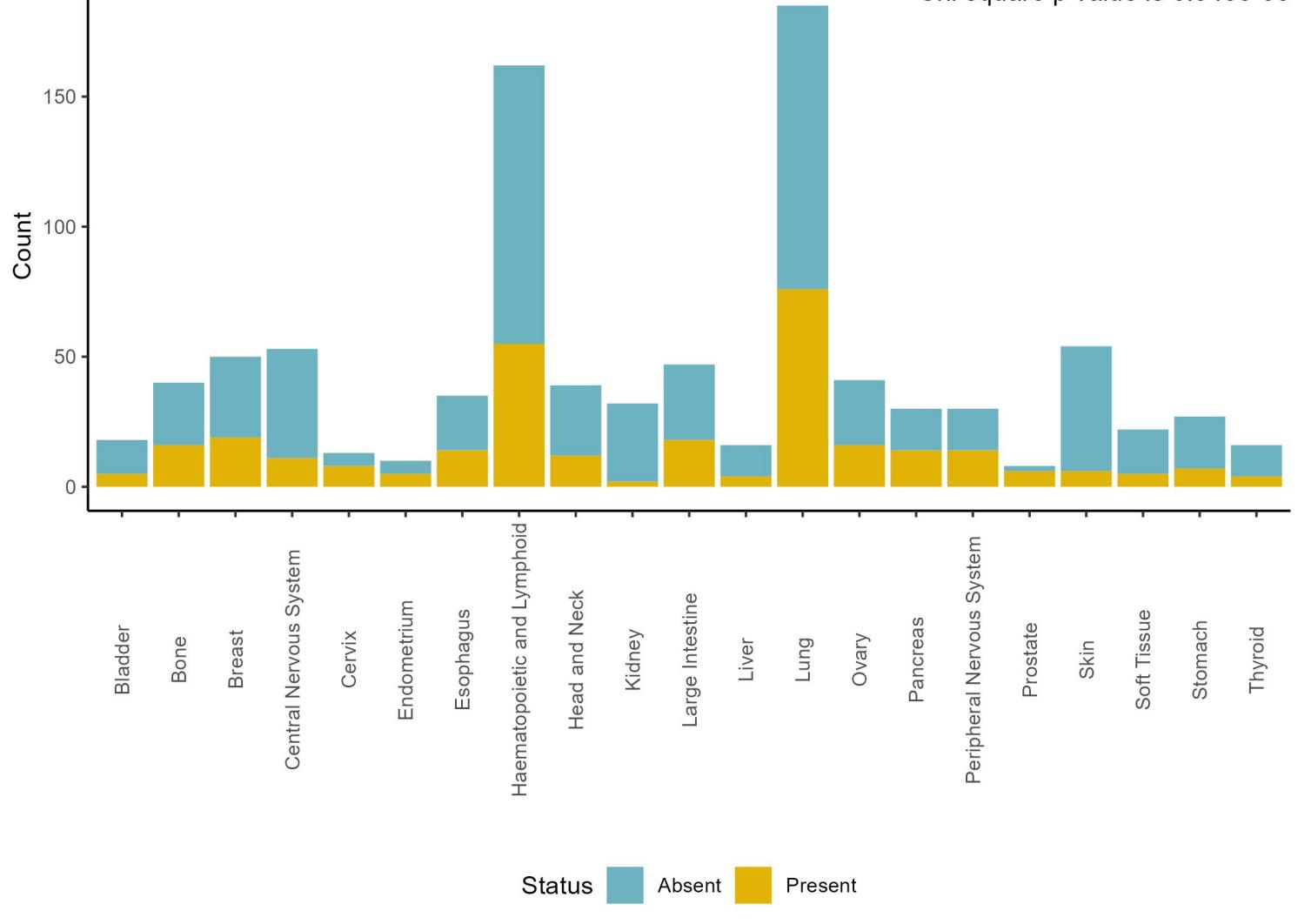
Top positive correlations of DMAP1 protein, DB1



Amount of DMAP1 protein, number of CCLs where it is present by tissue, DB1



Present and absent DMAP1 protein counts by tissue, DB1

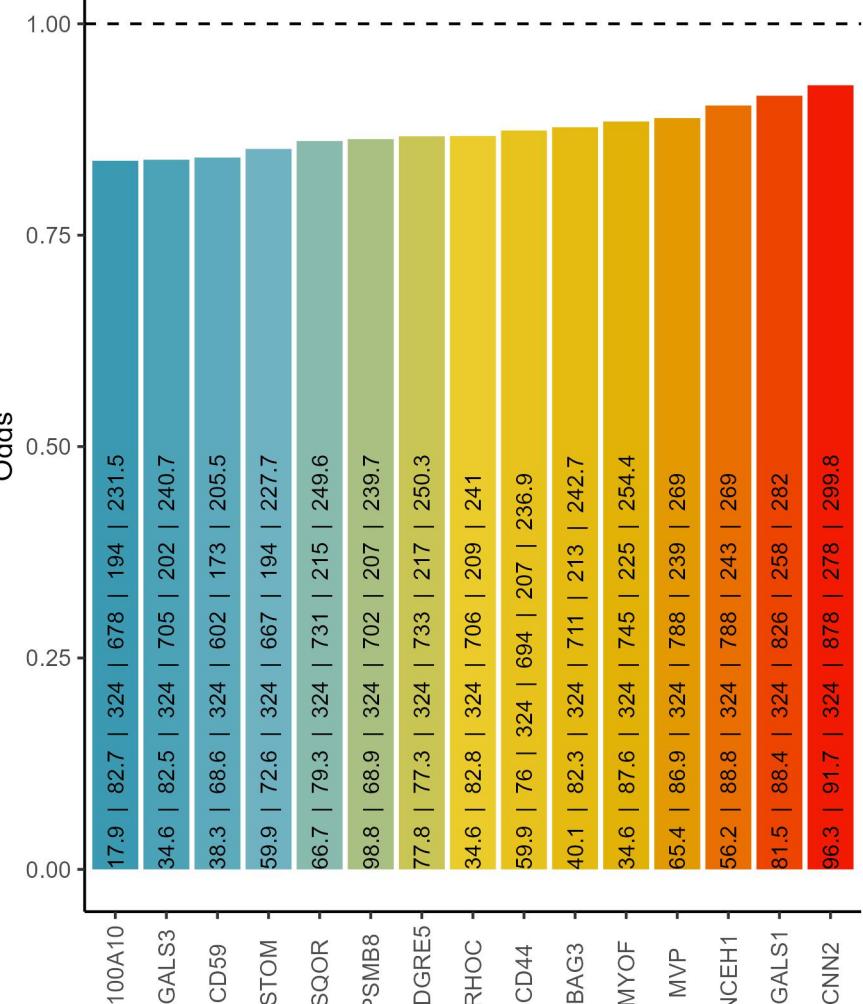


Cooccurrence with DMAP1 protein, DB1

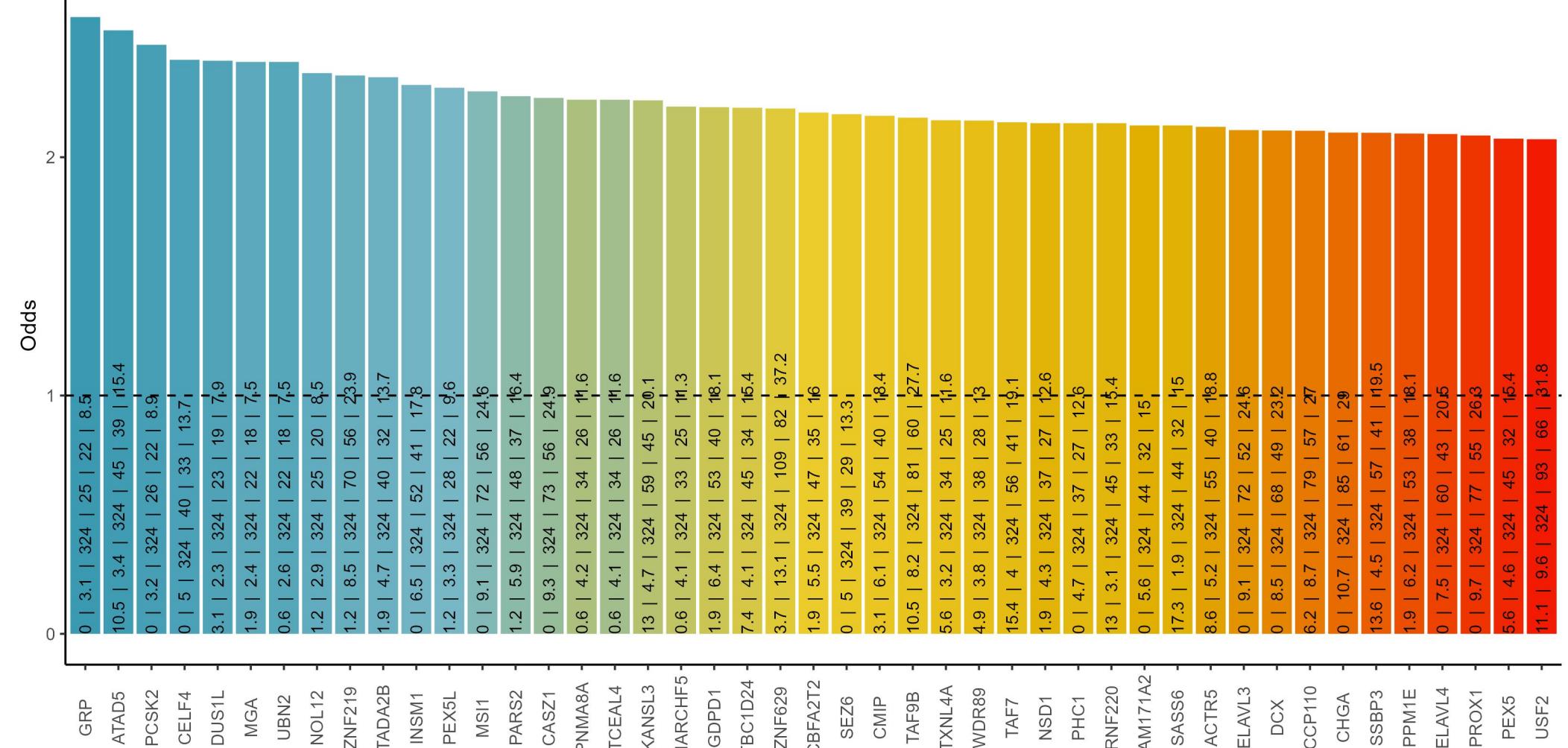
% of DMAP1 in blood cancers: 34 ; % of DMAP1 in solid cancers: 34.1

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of DMAP1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

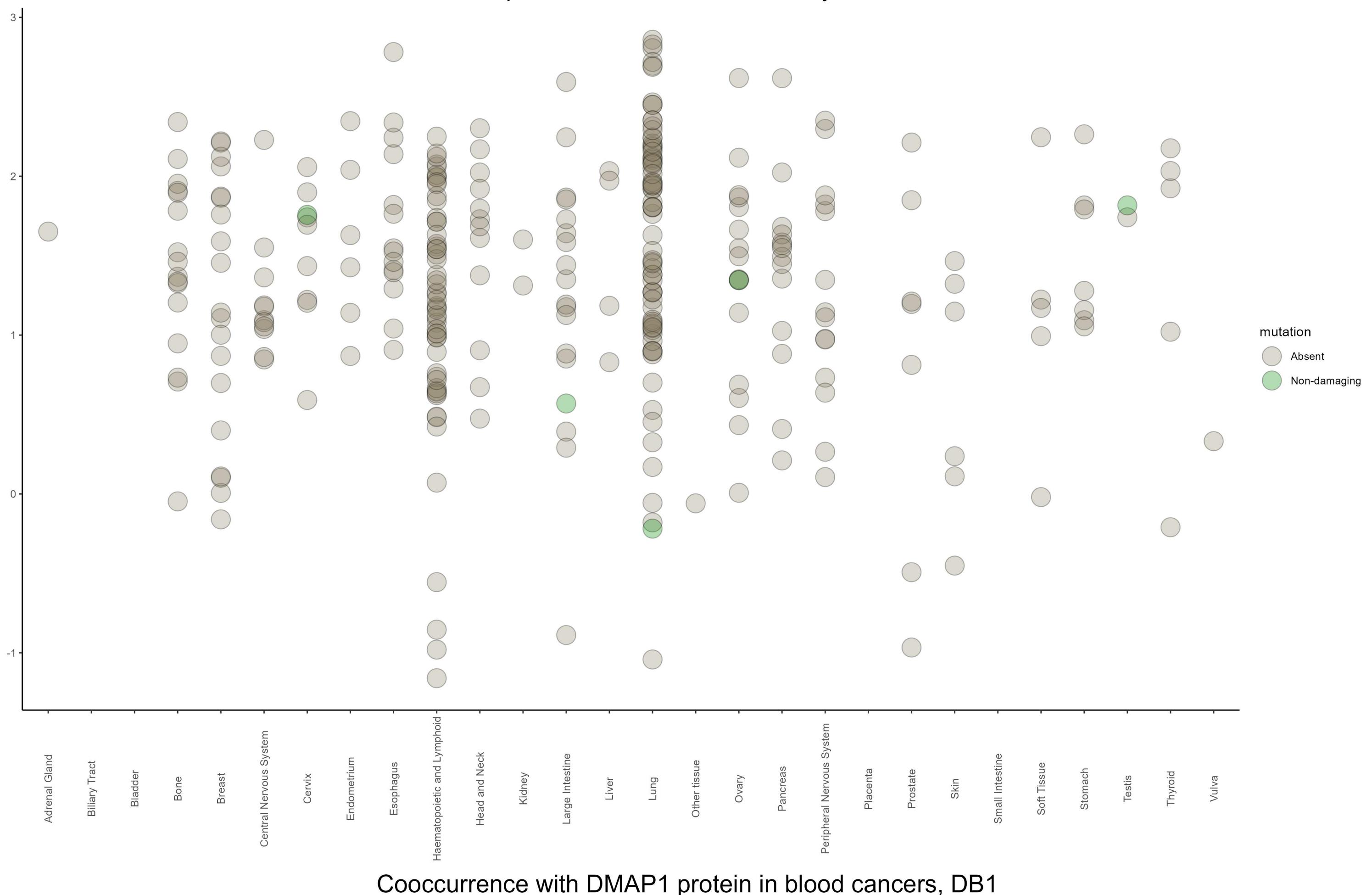
Negative cooccurrence



Positive cooccurrence

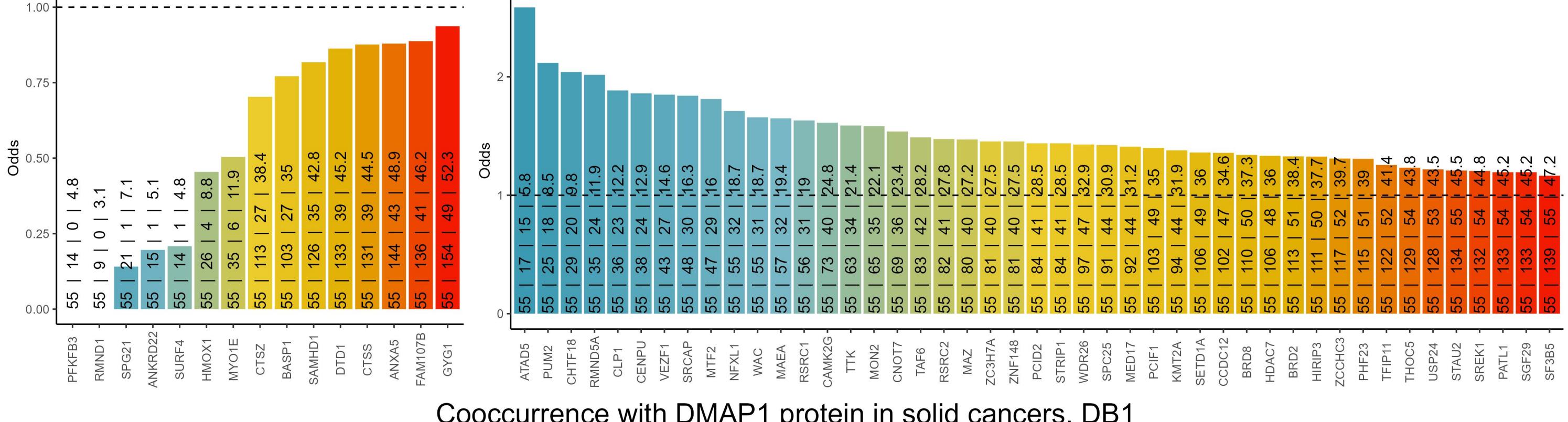


Amount of DMAP1 protein and mutation status by tissue, DB1



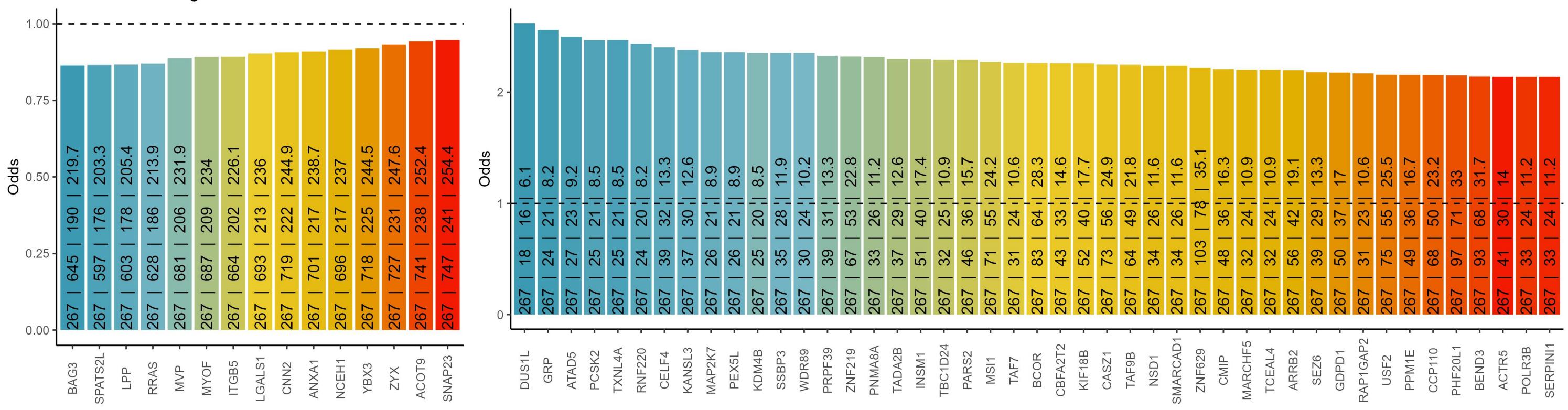
Cooccurrence with DMAP1 protein in blood cancers, DB1

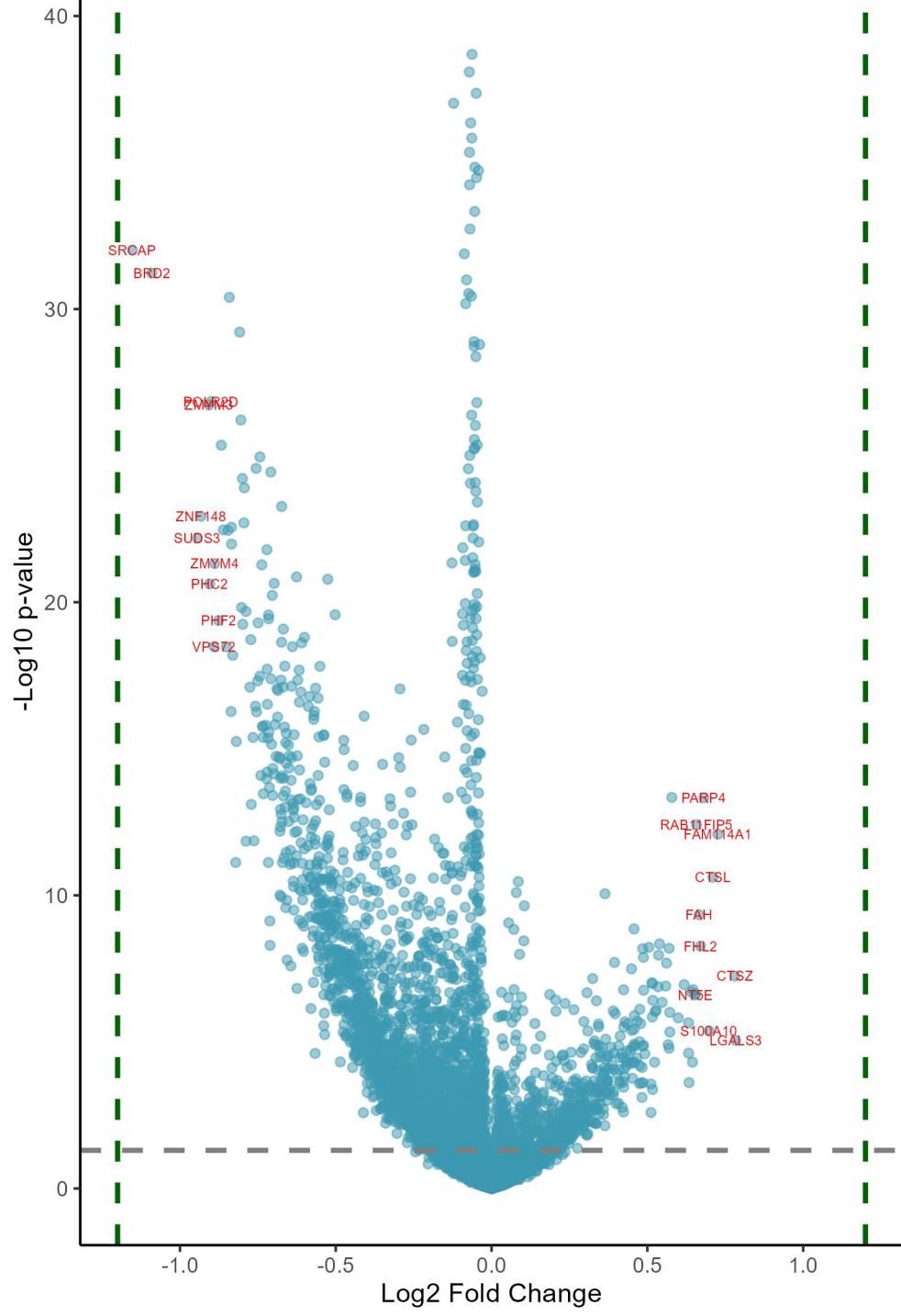
The text in the bars: incidence of DMAP1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with DMAP1 protein in solid cancers, DB1

The text in the bars: incidence of DMAP1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

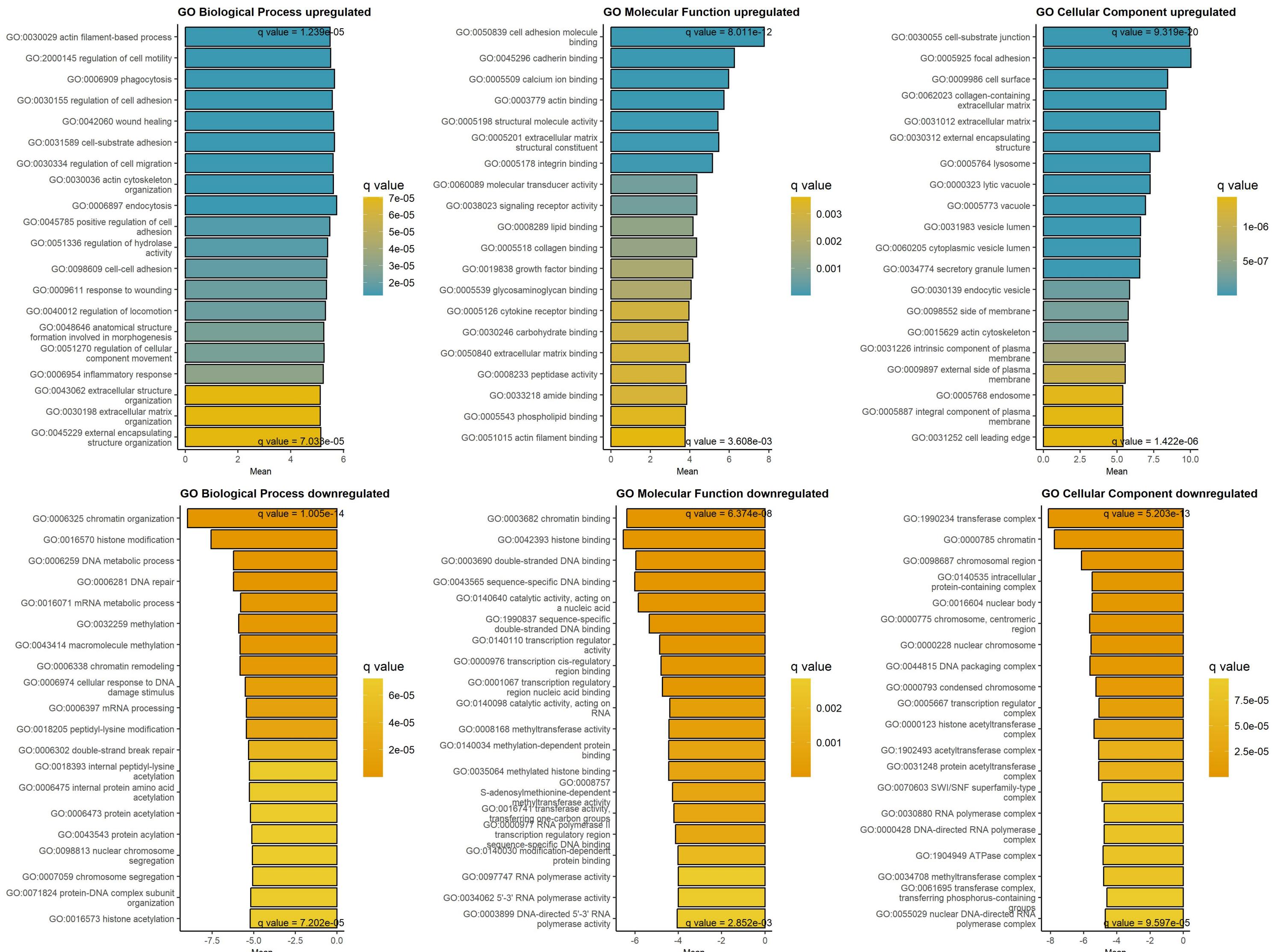




Downregulated at low/absent DMAP1 Upregulated at low/absent DMAP1

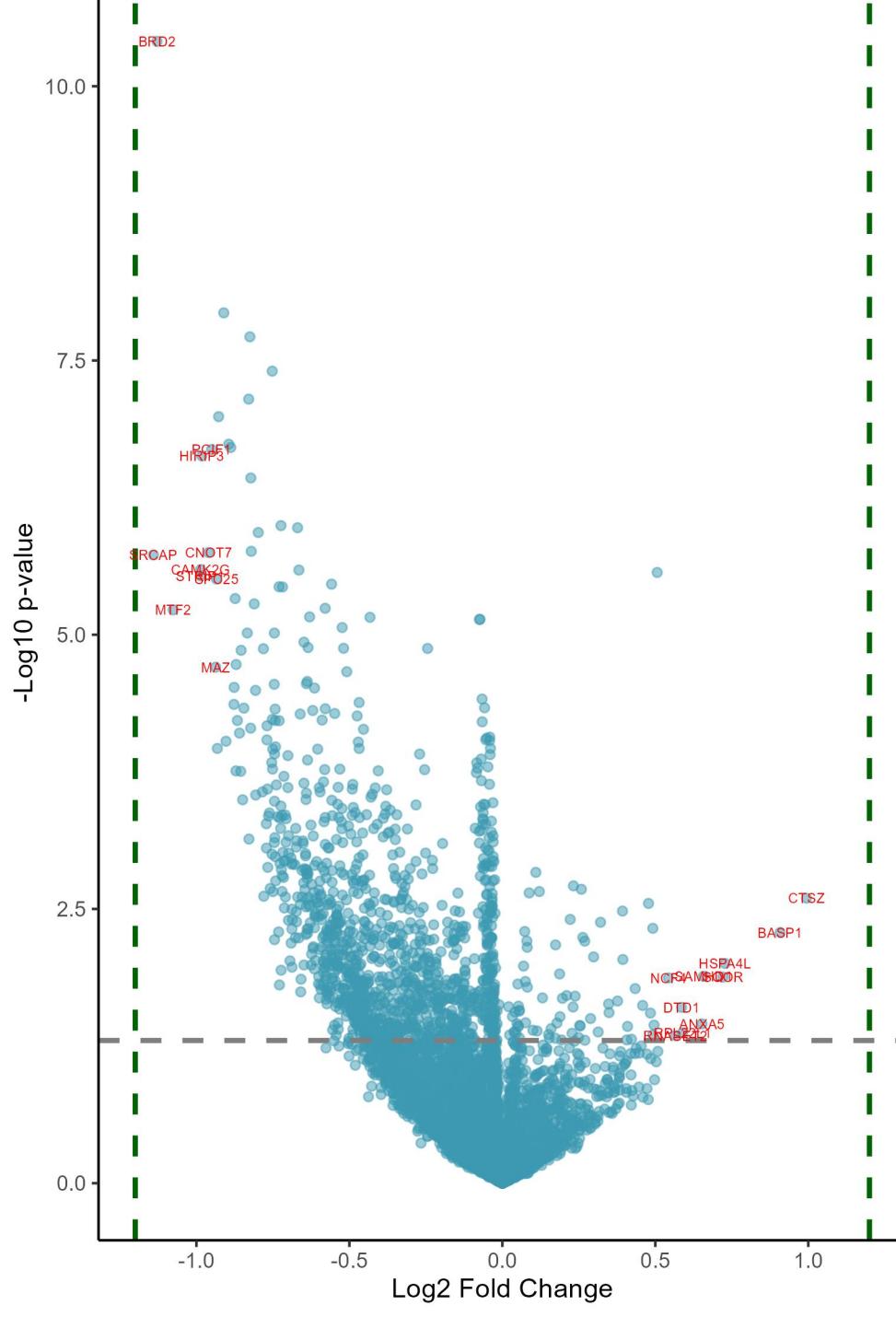
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.15	4.29e-30	SRCAP	Snf2 related CREBBP activator prote	0.78	5.18e-05	LGALS3	galectin 3
-1.09	2.32e-29	BRD2	bromodomain containing 2	0.78	5.18e-07	CTSZ	cathepsin Z
-0.94	7.26e-21	SUDS3	SDS3 homolog, SIN3A corepressor com	0.73	1.93e-11	FAM114A1	family with sequence similarity 114
-0.93	1.53e-21	ZNF148	zinc finger protein 148	0.71	4.33e-10	CTSL	cathepsin L
-0.91	4.13e-25	ZMYM3	zinc finger MYM-type containing 3	0.7	2.58e-05	S100A10	S100 calcium binding protein A10
-0.9	2.02e-19	PHC2	polyhomeotic homolog 2	0.68	1.32e-12	PARP4	Poly(ADP-ribose) polymerase family
-0.9	3.38e-25	POLR2D	RNA polymerase II subunit D	0.67	6.30e-08	FHL2	four and a half LIM domains 2
-0.89	1.99e-17	VPS72	vacuolar protein sorting 72 homolog	0.67	6.55e-09	FAH	fumarylacetoacetate hydrolase
-0.89	4.69e-20	ZMYM4	zinc finger MYM-type containing 4	0.66	9.51e-12	RAB11FIP5	RAB11 family interacting protein 5
-0.88	2.98e-18	PHF2	PHD finger protein 2	0.65	2.03e-06	NTSE	5'-nucleotidase ecto
-0.87	8.15e-24	BRD1	bromodomain containing 1	0.65	1.87e-06	SQOR	sulfide quinone oxidoreductase
-0.86	3.96e-21	TRRAP	transformation/transcription domain	0.65	1.38e-06	TGM2	transglutaminase 2
-0.85	1.99e-17	BRD3	bromodomain containing 3	0.64	2.31e-04	CD44	CD44 molecule (Indian blood group)
-0.85	4.05e-21	BPTF	bromodomain PHD finger transcriptio	0.64	1.66e-06	MVP	major vault protein
-0.84	1.25e-28	THOC5	THO complex 5	0.63	9.42e-04	LGALS1	galectin 1
-0.84	2.36e-15	PMF1	polyamine modulated factor 1	0.63	1.23e-04	CAVIN1	caveolae associated protein 1
-0.84	3.28e-21	BRD8	bromodomain containing 8	0.63	1.46e-05	RHOC	ras homolog family member C
-0.83	1.11e-20	EZH2	enhancer of zeste 2 polycomb repres	0.62	9.67e-07	ITGA5	integrin subunit alpha 5
-0.83	3.81e-17	MAZ	MYC associated zinc finger protein	0.6	1.02e-05	STOM	stomatin
-0.82	1.49e-10	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.58	1.29e-12	DAB2	DAB adaptor protein 2
-0.82	2.09e-14	SNRNP27	small nuclear ribonucleoprotein U4/	0.57	2.83e-05	CD59	CD59 molecule (CD59 blood group)
-0.81	1.76e-27	BUD13	BUD13 homolog	0.57	6.94e-06	ADAM9	ADAM metallopeptidase domain 9
-0.8	1.27e-24	TFIP11	tufetin interacting protein 11	0.57	8.79e-05	MYOF	myoferlin
-0.8	1.19e-18	SMARCD1	SWI/SNF related, matrix associated,	0.57	7.40e-08	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa
-0.8	9.08e-23	SMC6	structural maintenance of chromosom	0.57	6.92e-05	NCEH1	neutral cholesterol ester hydrolase
-0.8	3.92e-18	CCDC12	coiled-coil domain containing 12	0.56	2.08e-07	ADGRE5	adhesion G protein-coupled receptor
-0.79	2.50e-21	KAT7	lysine acetyltransferase 7	0.56	1.07e-06	NNMT	nicotinamide N-methyltransferase
-0.79	1.78e-22	MEAF6	MYST/Esa1 associated factor 6	0.55	3.42e-06	BAG3	BAG cochaperone 3
-0.79	1.58e-18	NSD3	nuclear receptor binding SET domain	0.54	5.41e-08	UPP1	uridine phosphorylase 1

GAGE analysis on upregulated and downregulated proteins at low/absent DMAP1 protein, DB1

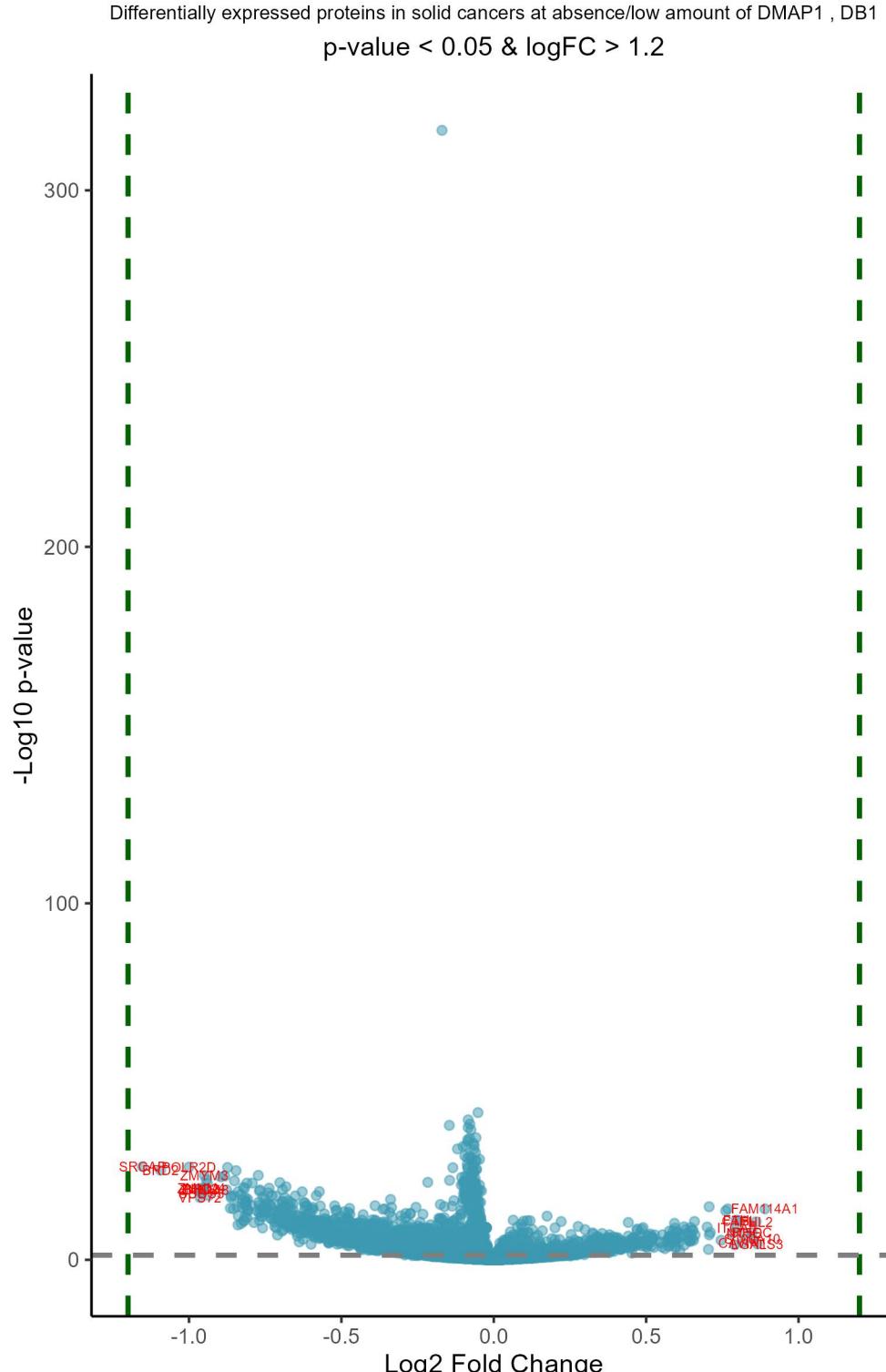


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent DMAP1 Upregulated in blood cancers at low/absent DMAP1

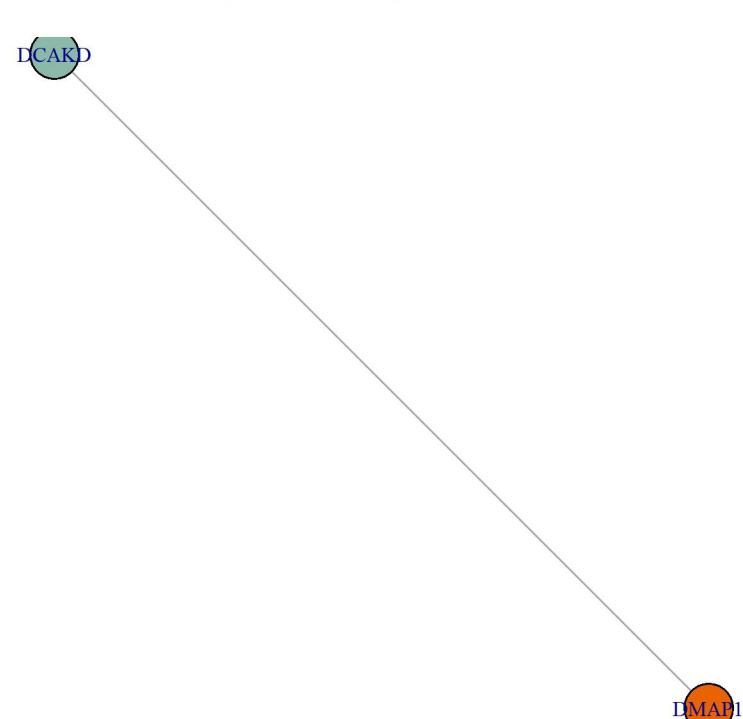


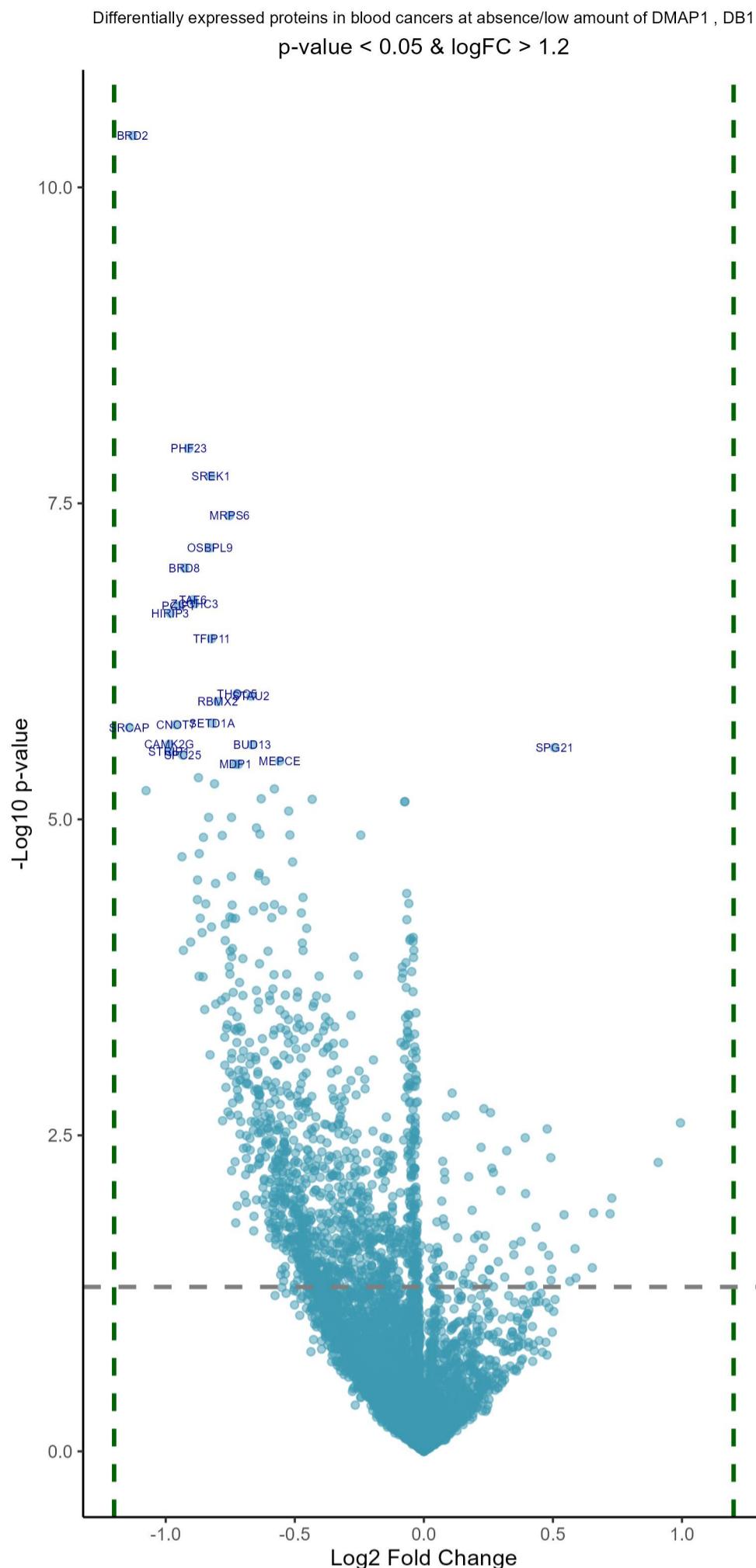
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.14	6.92e-04	SRCAP	Snf2 related CREBBP activator prote	0.99	5.14e-02	CTSZ	cathepsin Z
-1.13	1.30e-07	BRD2	bromodomain containing 2	0.91	7.50e-02	BASP1	brain abundant membrane attached si
-1.08	1.31e-03	MTF2	metal response element binding tran	0.73	1.09e-01	HSPA4L	heat shock protein family A (Hsp70)
-0.99	8.79e-04	STRIP1	striatin interacting protein 1	0.72	1.29e-01	SQOR	sulfide quinone oxidoreductase
-0.99	8.55e-04	CAMK2G	calcium/calmodulin dependent protei	0.66	1.28e-01	SAMHD1	SAM and HD domain containing deoxyn
-0.98	1.42e-04	HIRIP3	HIRA interacting protein 3	0.65	2.16e-01	ANXA5	annexin A5
-0.96	6.92e-04	CNOT7	CCR4-NOT transcription complex subu	0.59	2.35e-01	RPL22L1	ribosomal protein L22 like 1
-0.95	1.36e-04	PCIF1	phosphorylated CTD interacting fact	0.59	1.76e-01	DTD1	D-aminoacyl-tRNA deacylase 1
-0.94	2.92e-03	MAZ	MYC associated zinc finger protein	0.57	2.46e-01	RNASET2	ribonuclease T2
-0.93	8.97e-04	SPC25	SPC25 component of NDC80 kinetochor	0.54	1.30e-01	NCF4	neutrophil cytosolic factor 4
-0.93	8.55e-03	KIF15	kinesin family member 15	0.51	2.89e-01	RAB27A	RAB27A, member RAS oncogene family
-0.93	9.76e-05	BRD8	bromodomain containing 8	0.51	8.57e-04	SPG21	SPG21 abhydrolase domain containing
-0.91	2.58e-05	PHF23	PHD finger protein 23	0.5	3.25e-01	ICAM1	intercellular adhesion molecule 1
-0.9	7.87e-03	MON2	MON2 homolog, regulator of endosome	0.5	3.78e-01	CBR1	carbonyl reductase 1
-0.89	1.36e-04	TAF6	TATA-box binding protein associated	0.5	2.19e-01	CD40	CD40 molecule
-0.89	1.36e-04	ZCCHC3	zinc finger CCHC-type containing 3	0.49	2.43e-01	ALCAM	activated leukocyte cell adhesion m
-0.88	5.22e-03	MAEA	macrophage erythroblast attacher, E	0.49	7.27e-02	PRTN3	proteinase 3
-0.88	3.99e-03	CCNK	cyclin K	0.48	3.16e-01	GCA	grancalcin
-0.87	1.15e-03	KMT2A	lysine methyltransferase 2A	0.48	1.88e-01	SPR	sepiapterin reductase
-0.87	1.14e-02	SUDS3	SDS3 homolog, SIN3A corepressor com	0.48	5.46e-02	MYO1E	myosin IE
-0.87	2.82e-03	TRMT61A	tRNA methyltransferase 61A	0.48	4.66e-01	UCHL1	ubiquitin C-terminal hydrolase L1
-0.87	5.94e-03	ZNF148	zinc finger protein 148	0.47	2.99e-01	NCEH1	neutral cholesterol ester hydrolase
-0.86	7.18e-03	RBM15B	RNA binding motif protein 15B	0.47	4.14e-01	CD70	CD70 molecule
-0.86	1.14e-02	FLI1	Fli-1 proto-oncogene, ETS transcrip	0.46	4.53e-01	LMNA	lamin A/C
-0.85	2.15e-03	HDAC7	histone deacetylase 7	0.46	1.72e-01	LYZ	lysozyme
-0.85	1.69e-02	DCAF16	DDB1 and CUL4 associated factor 16	0.45	2.75e-01	ALDH2	aldehyde dehydrogenase 2 family mem
-0.84	5.37e-03	SMYD3	SET and MYND domain containing 3	0.45	2.96e-01	ASNS	asparagine synthetase (glutamine-hy
-0.83	1.73e-03	WDR26	WD repeat domain 26	0.45	4.10e-01	IGF2BP2	insulin like growth factor 2 mRNA b
-0.83	7.89e-05	OSBPL9	oxysterol binding protein like 9	0.44	2.81e-01	ENDOG	endonuclease G



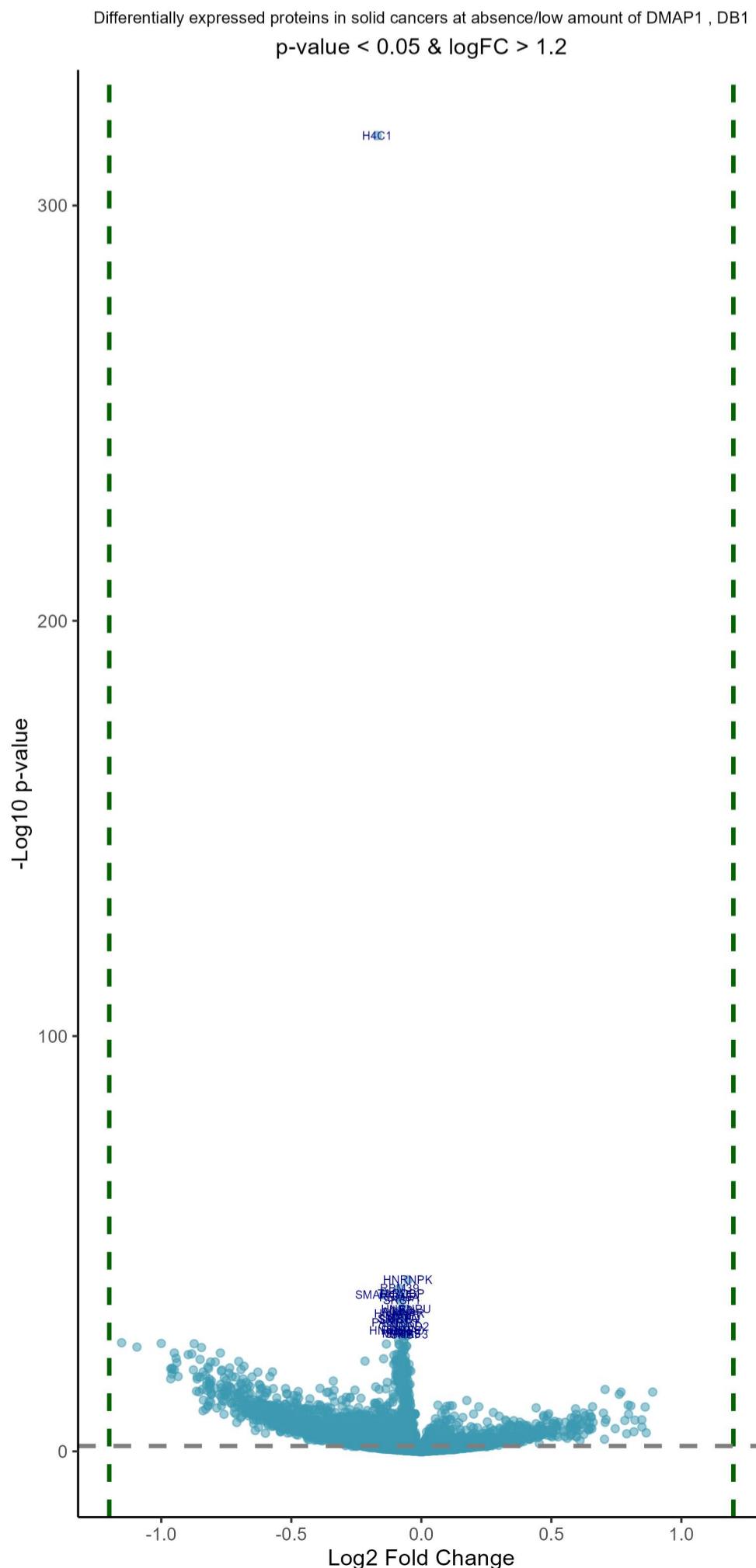
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.15	1.51e-24	SRCAP	Snf2 related CREBBP activator prote	0.89	1.56e-13	FAM114A1	family with sequence similarity 114
-1.09	1.26e-23	BRD2	bromodomain containing 2	0.86	1.45e-04	LGALS3	galectin 3
-1	2.10e-24	POLR2D	RNA polymerase II subunit D	0.86	3.62e-10	FHL2	four and a half LIM domains 2
-0.96	1.69e-16	VPS72	vacuolar protein sorting 72 homolog	0.85	8.30e-06	S100A10	S100 calcium binding protein A10
-0.96	1.03e-18	PHC2	polyhomeotic homolog 2	0.85	2.18e-07	RHOC	ras homolog family member C
-0.96	6.73e-19	ZMYM4	zinc finger MYM-type containing 4	0.82	2.54e-07	NT5E	5'-nucleotidase ecto
-0.96	1.34e-17	SUDS3	SDS3 homolog, SIN3A corepressor com	0.82	8.52e-05	CAVIN1	caveolae associated protein 1
-0.96	1.18e-18	BRD3	bromodomain containing 3	0.81	1.96e-10	CTSL	cathepsin L
-0.95	2.95e-22	ZMYM3	zinc finger MYM-type containing 3	0.8	1.23e-08	ITGA5	integrin subunit alpha 5
-0.95	1.59e-18	ZNF148	zinc finger protein 148	0.8	1.43e-10	FAH	fumarylacetoacetate hydrolase
-0.94	4.20e-21	EZH2	enhancer of zeste 2 polycomb repres	0.79	2.35e-04	CD44	CD44 molecule (Indian blood group)
-0.94	3.63e-20	TRRAP	transformation/transcription domain	0.78	2.96e-07	TGM2	transglutaminase 2
-0.94	5.06e-17	PHF2	PHD finger protein 2	0.77	1.57e-13	RAB11FIP5	RAB11 family interacting protein 5
-0.9	6.57e-22	BRD1	bromodomain containing 1	0.76	4.94e-13	PARP4	poly(ADP-ribose) polymerase family
-0.88	4.69e-22	MEAF6	MYST/Esa1 associated factor 6	0.75	1.81e-05	CTSZ	cathepsin Z
-0.88	1.69e-18	BPTF	bromodomain PHD finger transcriptio	0.71	1.77e-07	ADAM9	ADAM metallopeptidase domain 9
-0.87	2.46e-24	THOC5	THO complex 5	0.71	7.42e-07	MVP	major vault protein
-0.86	1.04e-13	PMF1	polyamine modulated factor 1	0.71	4.27e-14	DAB2	DAB adaptor protein 2
-0.86	1.83e-16	ZNF280C	zinc finger protein 280C	0.7	3.38e-03	LGALS1	galectin 1
-0.86	5.90e-17	DNMT3A	DNA methyltransferase 3 alpha	0.7	8.15e-09	PAPSS2	3'-phosphoadenosine 5'-phosphosulfa
-0.85	1.43e-13	SNRNP27	small nuclear ribonucleoprotein U4/	0.66	7.60e-07	NNMT	nicotinamide N-methyltransferase
-0.85	6.46e-17	PRPF38B	pre-mRNA processing factor 38B	0.66	3.12e-10	LPP	LIM domain containing preferred tra
-0.85	8.02e-21	SMC6	structural maintenance of chromosom	0.66	1.87e-05	CD59	CD59 molecule (CD59 blood group)
-0.85	1.59e-23	BUD13	BUD13 homolog	0.65	5.74e-08	ADGRE5	adhesion G protein-coupled receptor
-0.84	3.93e-14	GRPEL2	GrpE like 2, mitochondrial	0.65	4.54e-08	BAG3	BAG cochaperone 3
-0.84	2.40e-09	NDUFB11	NADH:ubiquinone oxidoreductase subu	0.65	8.97e-06	MYOF	myoferlin
-0.84	4.61e-18	CDCA5	cell division cycle associated 5	0.65	1.17e-08	UPP1	uridine phosphorylase 1
-0.84	1.11e-11	POLR2F	RNA polymerase II, I and III subuni	0.65	8.53e-07	EHD2	EH domain containing 2
-0.83	2.66e-17	BRD8	bromodomain containing 8	0.64	3.86e-05	S100A16	S100 calcium binding protein A16

DMAP1 network, DB1, all Pearson r > 0.35



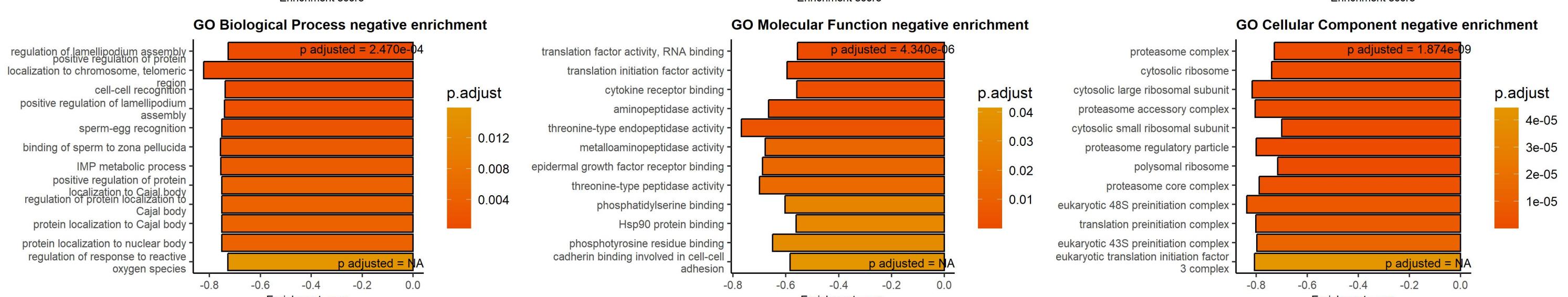
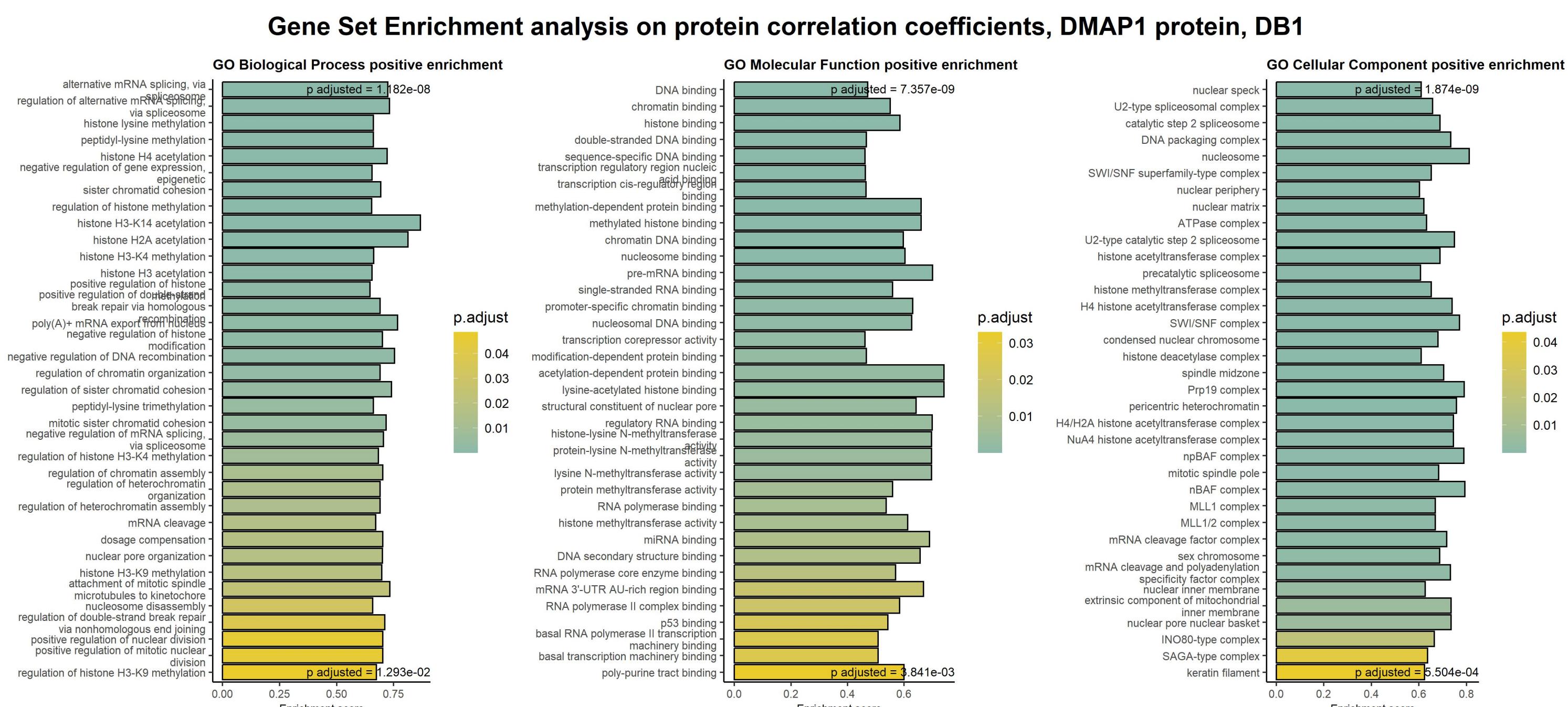
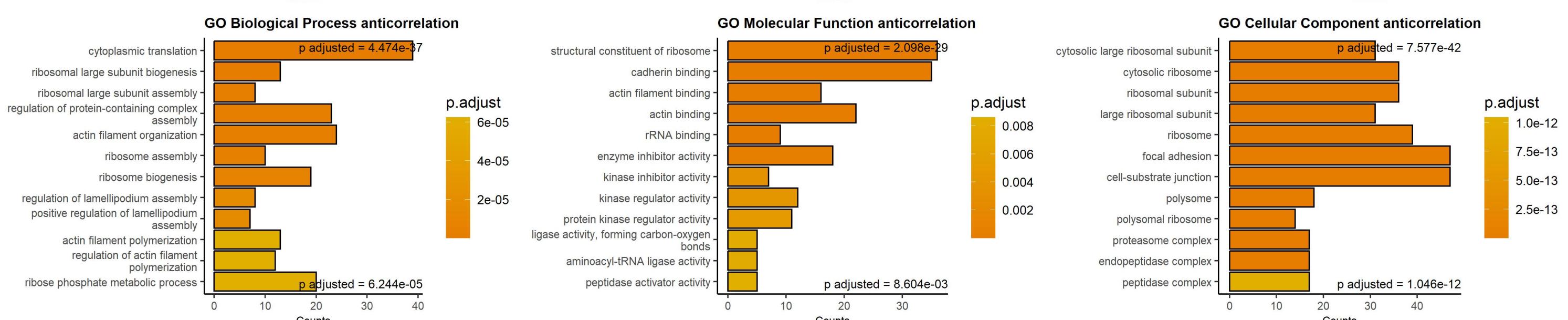
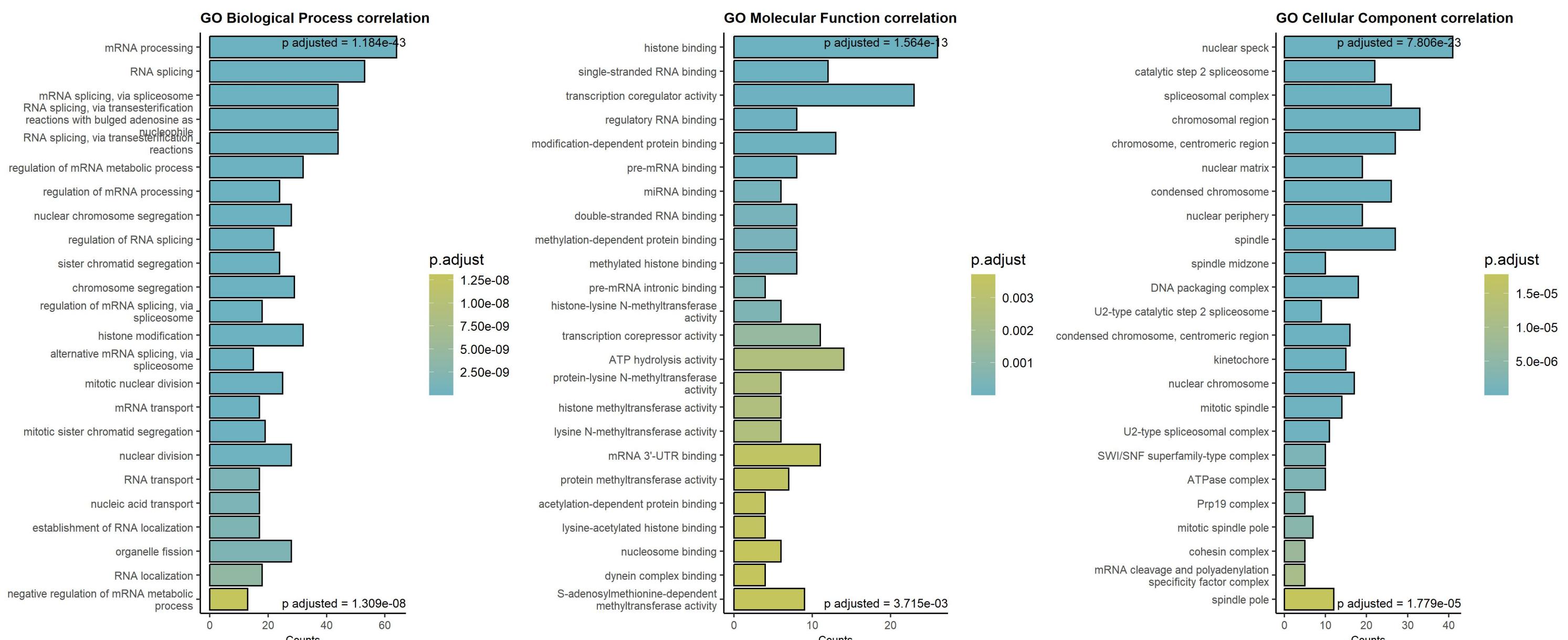


Sorted by p values!							
Downregulated in blood cancers at low/absent DMAP1				Upregulated in blood cancers at low/absent DMAP1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.13	1.30e-07	BRD2	bromodomain containing 2	0.51	8.57e-04	SPG21	SPG21 abhydrolase domain containing
-0.91	2.58e-05	PHF23	PHD finger protein 23	0.11	3.75e-02	CYC1	cytochrome c1
-0.83	3.20e-05	SREK1	splicing regulatory glutamic acid a	0.23	4.40e-02	PPID	peptidylprolyl isomerase D
-0.75	5.26e-05	MRPS6	mitochondrial ribosomal protein S6	0.26	4.65e-02	PFKFB3	6-phosphofructo-2-kinase/fructose-2
-0.83	7.89e-05	OSBPL9	oxysterol binding protein like 9	0.12	4.79e-02	UQCRH	ubiquinol-cytochrome c reductase hi
-0.93	9.76e-05	BRD8	bromodomain containing 8	0.09	4.84e-02	RAB14	RAB14, member RAS oncogene famil
-0.89	1.36e-04	TAF6	TATA-box binding protein associated	0.99	5.14e-02	CTSZ	cathepsin Z
-0.89	1.36e-04	ZCCHC3	zinc finger CCHC-type containing 3	0.48	5.46e-02	MYO1E	myosin IE
-0.95	1.36e-04	PCIF1	phosphorylated CTD interacting fact	0.39	5.94e-02	HMOX1	heme oxygenase 1
-0.98	1.42e-04	HIRIP3	HIRA interacting protein 3	0.22	6.59e-02	NDUFA9	NADH:ubiquinone oxidoreductase sub
-0.82	2.06e-04	TFIP11	tuftelin interacting protein 11	0.32	6.81e-02	ANKRD22	ankyrin repeat domain 22
-0.72	5.03e-04	THOC5	THO complex 5	0.49	7.27e-02	PRTN3	proteinase 3
-0.67	5.03e-04	STAU2	staufen double-stranded RNA binding	0.07	7.45e-02	TXN	thioredoxin
-0.8	5.19e-04	RBMX2	RNA binding motif protein X-linked	0.91	7.50e-02	BASP1	brain abundant membrane attached s
-0.82	6.92e-04	SETD1A	SET domain containing 1A, histone I	0.26	7.92e-02	IDE	insulin degrading enzyme
-0.96	6.92e-04	CNOT7	CCR4-NOT transcription complex subu	0.08	8.15e-02	UQCRB	ubiquinol-cytochrome c reductase bi
-1.14	6.92e-04	SRCAP	Snf2 related CREBBP activator prote	0.27	8.16e-02	ACP3	acid phosphatase 3
-0.99	8.55e-04	CAMK2G	calcium/calmodulin dependent protei	0.17	8.46e-02	MAN2B1	mannosidase alpha class 2B member
-0.67	8.55e-04	BUD13	BUD13 homolog	0.08	8.74e-02	PNP	purine nucleoside phosphorylase
-0.99	8.79e-04	STRIP1	striatin interacting protein 1	0.3	1.01e-01	MGLL	monoglyceride lipase
-0.93	8.97e-04	SPC25	SPC25 component of NDC80 kinetochor	0.39	1.04e-01	EPHX1	epoxide hydrolase 1
-0.56	9.39e-04	MEPCE	methylphosphate capping enzyme	0.73	1.09e-01	HSPA4L	heat shock protein family A (Hsp70)
-0.73	9.39e-04	MDP1	magnesium dependent phosphatase 1	0.07	1.12e-01	UQCRC2	ubiquinol-cytochrome c reductase co
-0.72	9.39e-04	PPP4R1	protein phosphatase 4 regulatory su	0.19	1.24e-01	SFXN1	sideroflexin 1
-0.87	1.15e-03	KMT2A	lysine methyltransferase 2A	0.66	1.28e-01	SAMHD1	SAM and HD domain containing deoxy
-0.81	1.24e-03	MED17	mediator complex subunit 17	0.72	1.29e-01	SQOR	sulfide quinone oxidoreductase
-0.58	1.31e-03	CWC27	CWC27 spliceosome associated cyclop	0.54	1.30e-01	NCF4	neutrophil cytosolic factor 4
-1.08	1.31e-03	MTF2	metal response element binding tran	0.08	1.35e-01	SNX3	sorting nexin 3
-0.63	1.42e-03	SGF29	SAGA complex associated factor 29	0.05	1.39e-01	PHB2	prohibitin 2
-0.43	1.42e-03	ATAD5	ATPase family AAA domain containing	0.08	1.43e-01	ME2	malic enzyme 2
-0.07	1.42e-03	MCM2	minichromosome maintenance complex	0.43	1.46e-01	MNDA	myeloid cell nuclear differentiatio
-0.07	1.42e-03	RFC4	replication factor C subunit 4	0.21	1.58e-01	PTPRN2	protein tyrosine phosphatase recept
-0.52	1.63e-03	CNOT2	CCR4-NOT transcription complex subu	0.24	1.59e-01	SURF4	surfeit 4
-0.83	1.73e-03	WDR26	WD repeat domain 26	0.13	1.60e-01	HSD17B4	hydroxysteroid 17-beta dehydrogenas
-0.75	1.73e-03	ZMYM3	zinc finger MYM-type containing 3	0.2	1.60e-01	RMND1	required for meiotic nuclear divisi
-0.65	2.04e-03	C11orf54	chromosome 11 open reading frame 54	0.38	1.64e-01	GYG1	glycogenin 1
-0.64	2.12e-03	PATL1	PAT1 homolog 1, processing body mRN	0.35	1.70e-01	GNG10	G protein subunit gamma 10
-0.52	2.12e-03	HDAC2	histone deacetylase 2	0.46	1.72e-01	LYZ	lysozyme
-0.24	2.12e-03	EMSY	EMSY transcriptional repressor, PRC	0.05	1.74e-01	HSPB5	heat shock protein family A (Hsp70)

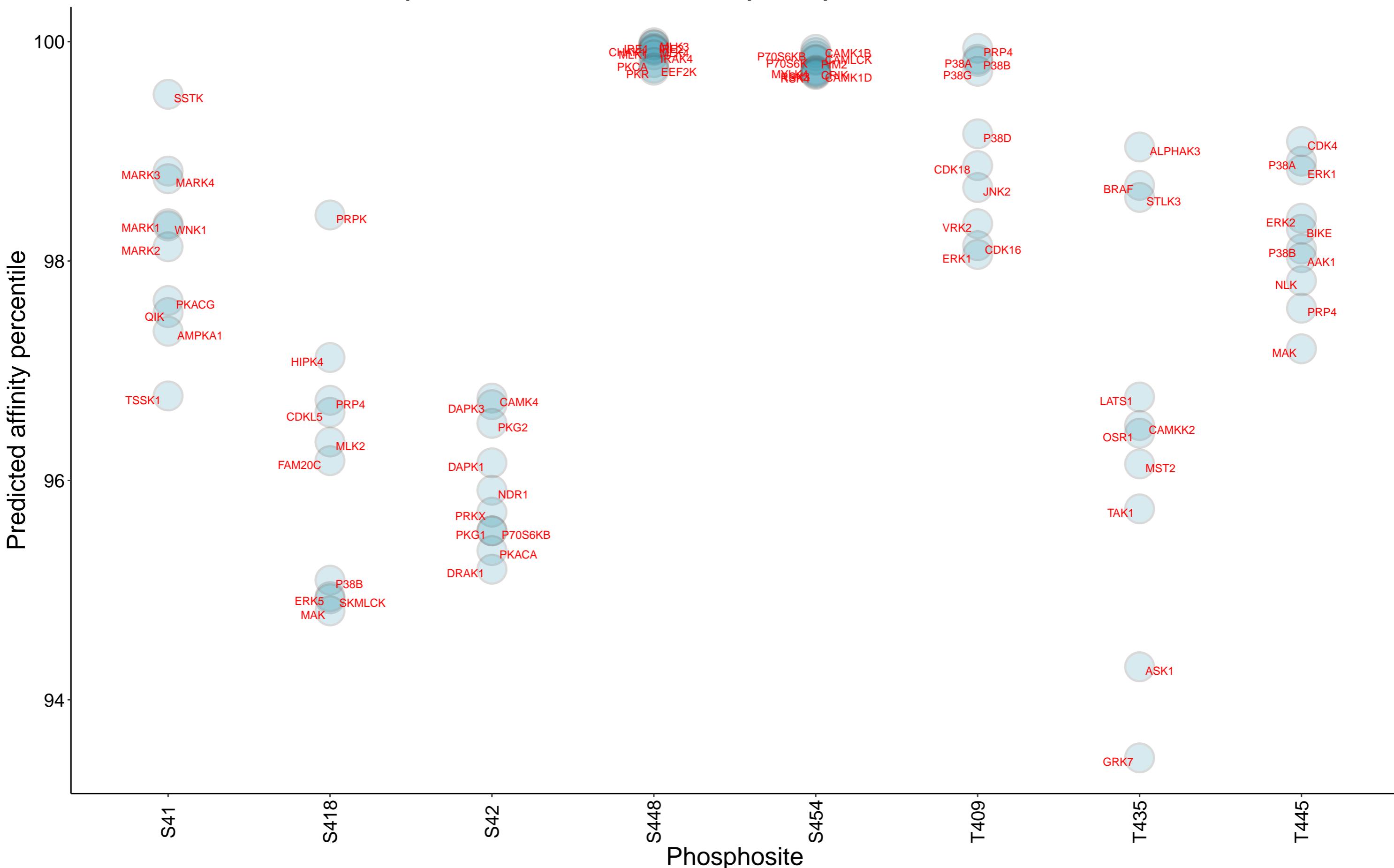


Sorted by p values!							
Downregulated in solid cancers at low/absent DMAP1				Upregulated in solid cancers at low/absent DMAP1			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.17	4.93e-314	H4C1	H4 clustered histone 1	0.71	4.27e-14	DAB2	DAB adaptor protein 2
-0.05	1.10e-38	HNRNPK	heterogeneous nuclear ribonucleopro	0.89	1.56e-13	FAM114A1	family with sequence similarity 114
-0.08	9.09e-37	RBM39	RNA binding motif protein 39	0.77	1.57e-13	RAB11FIP5	RAB11 family interacting protein 5
-0.08	1.16e-35	TARDBP	TAR DNA binding protein	0.76	4.94e-13	PARP4	Poly(ADP-ribose) polymerase family
-0.15	2.13e-35	SMARCA5	SWI/SNF related, matrix associated,	0.17	1.28e-11	ACTN1	actinin alpha 1
-0.08	7.35e-35	RBM8A	RNA binding motif protein 8A	0.8	1.43e-10	FAH	fumarylacetoacetate hydrolase
-0.07	3.02e-34	SRSF1	serine and arginine rich splicing f	0.06	1.43e-10	EEF1D	eukaryotic translation elongation f
-0.06	4.12e-32	HNRNPU	heterogeneous nuclear ribonucleopro	0.11	1.93e-10	CLIC1	chloride intracellular channel 1
-0.08	5.78e-32	ILF3	interleukin enhancer binding factor	0.81	1.96e-10	CTSL	cathepsin L
-0.09	1.14e-31	ACIN1	apoptotic chromatin condensation in	0.12	1.97e-10	ACTN4	actinin alpha 4
-0.08	3.62e-31	HNRNPR	heterogeneous nuclear ribonucleopro	0.1	2.62e-10	IQGAP1	IQ motif containing GTPase activati
-0.07	1.02e-30	SRSF7	serine and arginine rich splicing f	0.66	3.12e-10	LPP	LIM domain containing preferred tra
-0.06	3.73e-30	SFPQ	splicing factor proline and glutami	0.22	3.17e-10	AHNAK	AHNAK nucleoprotein
-0.09	4.70e-30	SMC1A	structural maintenance of chromosom	0.86	3.62e-10	FHL2	four and a half LIM domains 2
-0.1	6.82e-30	SMC3	structural maintenance of chromosom	0.44	5.59e-10	PLIN3	perilipin 3
-0.12	3.07e-29	PARP1	Poly(ADP-ribose) polymerase 1	0.59	9.19e-10	ZYX	zyxin
-0.07	3.96e-29	SRRT	serrate, RNA effector molecule	0.09	1.45e-09	MYL6	myosin light chain 6
-0.06	2.48e-28	SNRPD2	small nuclear ribonucleoprotein D2	0.28	5.94e-09	CTSB	cathepsin B
-0.09	2.29e-27	HNRNPA0	heterogeneous nuclear ribonucleopro	0.62	7.32e-09	RBPM5	RNA binding protein, mRNA process
-0.08	2.48e-27	RBM25	RNA binding motif protein 25	0.08	7.62e-09	TPD52L2	TPD52 like 2
-0.09	7.31e-27	PNN	pinin, desmosome associated protein	0.7	8.15e-09	PAPSS2	3'-phosphoadenosine 5'-phosphosulf
-0.08	1.00e-26	MATR3	matrin 3	0.09	1.05e-08	TMOD3	tropomodulin 3
-0.07	1.54e-26	SF3A3	splicing factor 3a subunit 3	0.49	1.17e-08	CAST	calpastatin
-0.05	1.68e-26	SRSF3	serine and arginine rich splicing f	0.65	1.17e-08	UPP1	uridine phosphorylase 1
-0.06	3.78e-26	U2AF2	U2 small nuclear RNA auxiliary fact	0.2	1.17e-08	PLEC	plectin
-0.06	3.78e-26	SF3B2	splicing factor 3b subunit 2	0.8	1.23e-08	ITGA5	integrin subunit alpha 5
-0.09	4.20e-25	TMPO	thymopoietin	0.59	1.34e-08	PXN	paxillin
-0.07	5.64e-25	HNRNPL	heterogeneous nuclear ribonucleopro	0.47	2.35e-08	PDLIM5	PDZ and LIM domain 5
-0.07	5.64e-25	DHX9	DExH-box helicase 9	0.49	2.71e-08	TGFB1I1	transforming growth factor beta 1 i
-1.15	1.51e-24	SRCAP	Snf2 related CREBBP activator prote	0.63	2.94e-08	YAP1	Yes1 associated transcriptional reg
-1	2.10e-24	POLR2D	RNA polymerase II subunit D	0.13	3.11e-08	ITGB1	integrin subunit beta 1
-0.87	2.46e-24	THOC5	THO complex 5	0.3	3.34e-08	SUCLG2	succinate-CoA ligase GDP-forming s
-0.09	2.65e-24	IK	IK cytokine	0.65	4.54e-08	BAG3	BAG cochaperone 3
-0.13	2.70e-24	ACTL6A	actin like 6A	0.47	5.31e-08	STK10	serine/threonine kinase 10
-0.09	3.97e-24	ILF2	interleukin enhancer binding factor	0.65	5.74e-08	ADGRE5	adhesion G protein-coupled receptor
-0.06	7.58e-24	HNRNPM	heterogeneous nuclear ribonucleopro	0.16	6.48e-08	RRBP1	ribosome binding protein 1
-0.06	7.92e-24	SF3B1	splicing factor 3b subunit 1	0.59	6.96e-08	CNN2	calponin 2
-0.07	1.09e-23	CDC5L	cell division cycle 5 like	0.58	7.96e-08	TRIP10	thyroid hormone receptor interactor
-1.00	1.20e-23	PPBP2	heterogeneous nuclear ribonucleop	0.2	1.11e-07	CHIKBP1	CH2C domain containing protein 1

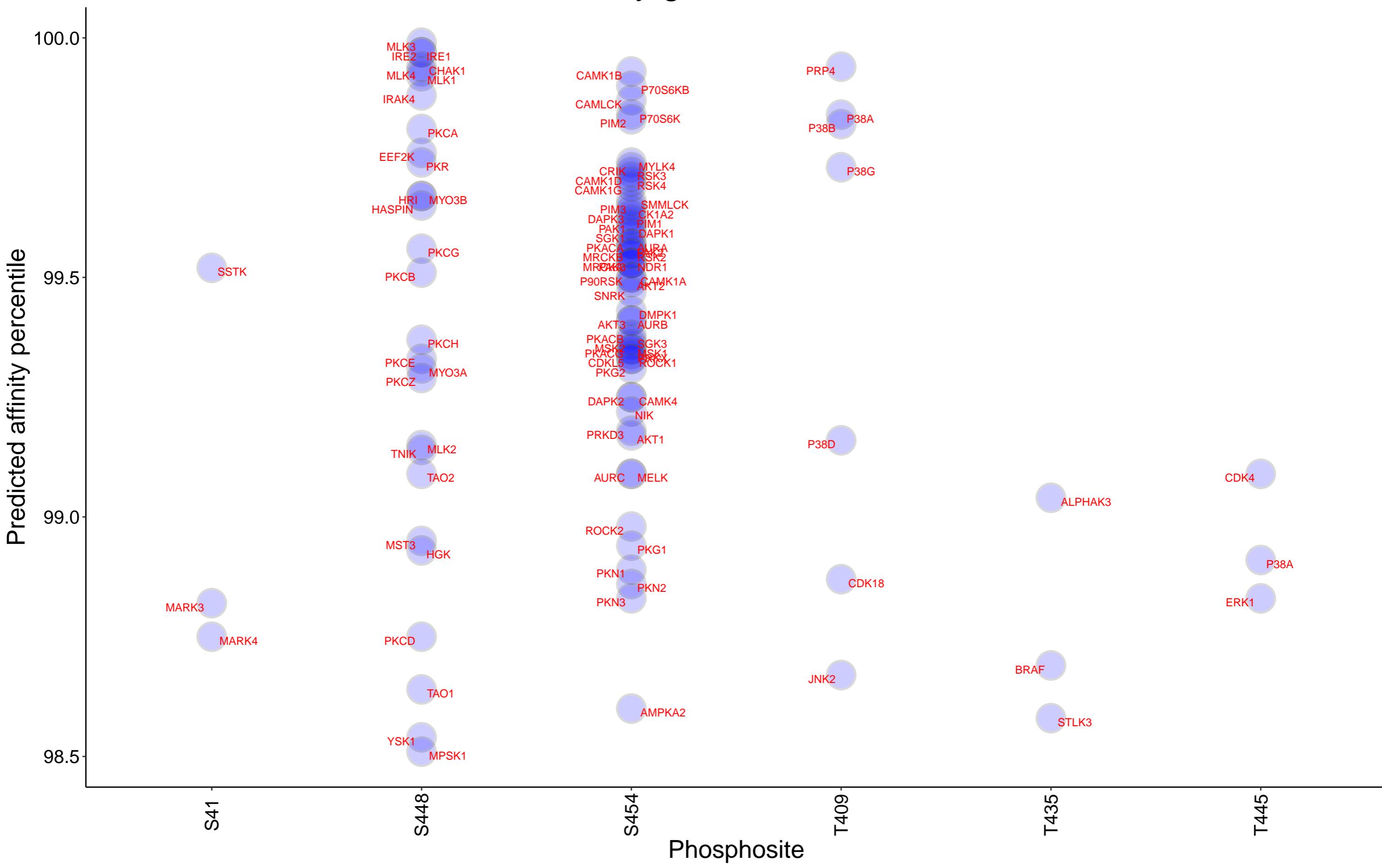
Top 250 correlation coefficients overrepresentation, DMAP1 protein, DB1



Top 10 kinases for each phosphosite in DMAP1



Kinases with affinity greater than 98.5% to DMAP1



Top 15 positive correlation coefficients for DMAP1 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

