

EP400

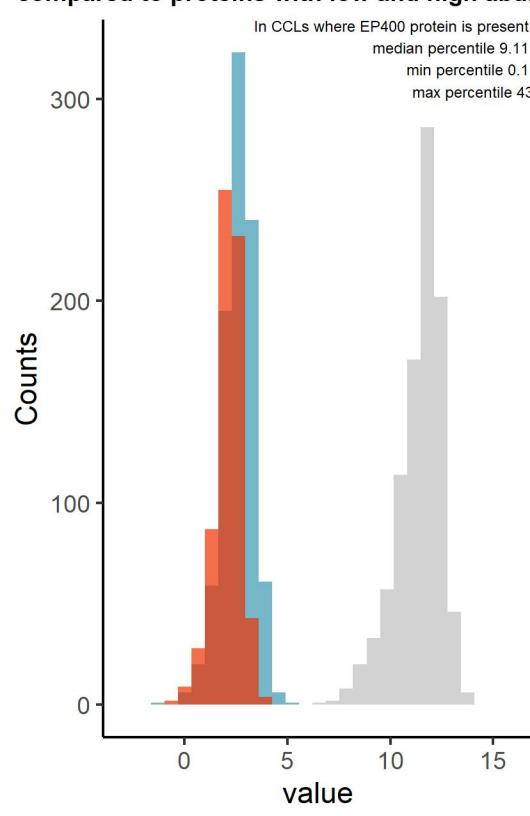
Protein name: EP400 ; UNIPROT: Q96L91 ; Gene name: E1A binding protein p400

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

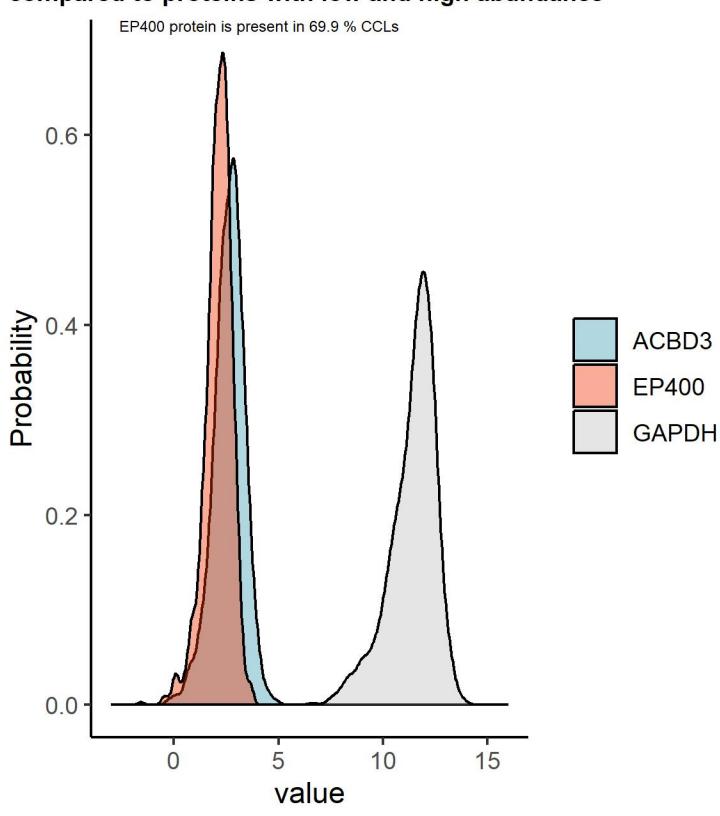
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

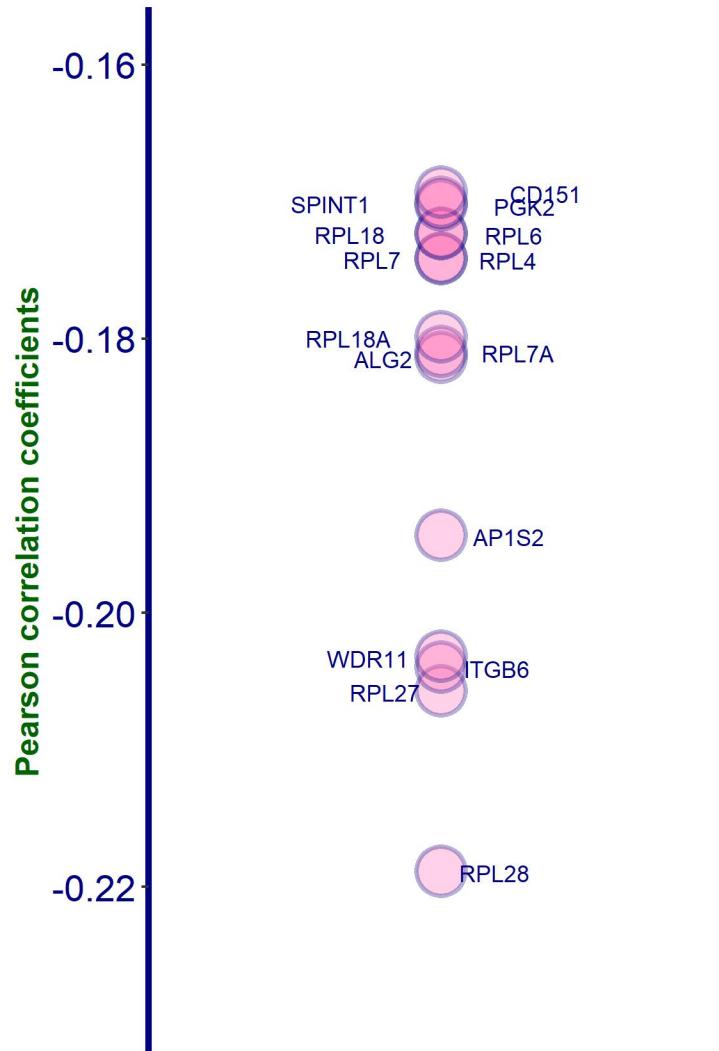
Histogram of EP400 protein compared to proteins with low and high abundance



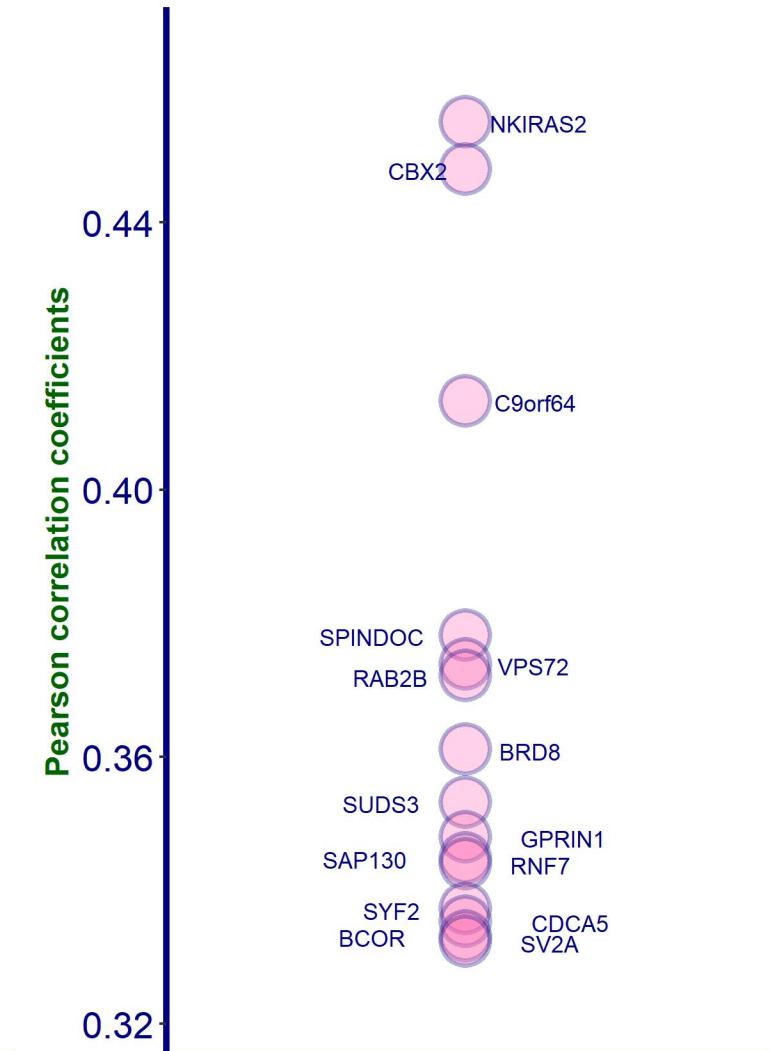
Density plot of EP400 protein compared to proteins with low and high abundance



Top negative correlations of EP400 protein, DB1

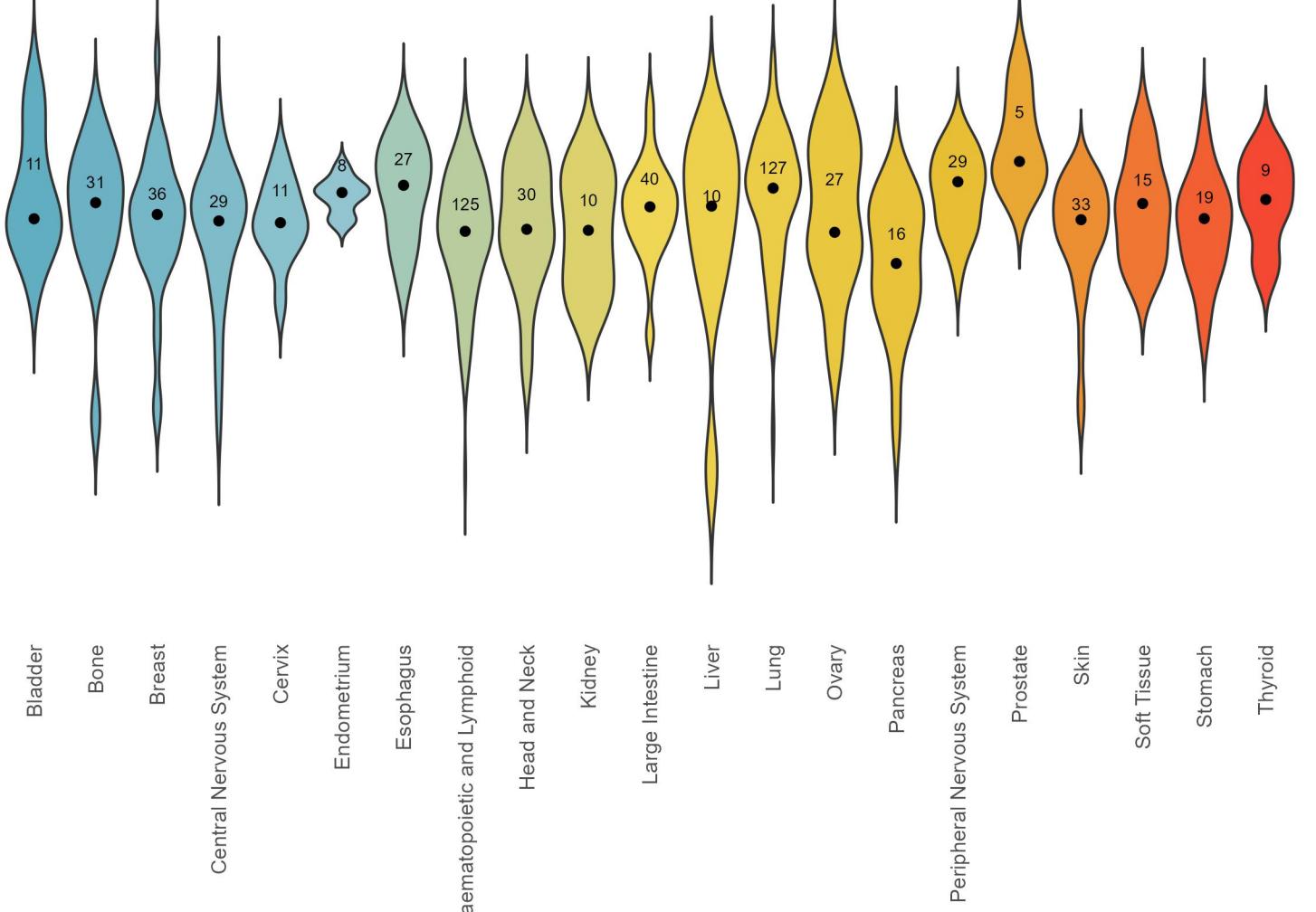


Top positive correlations of EP400 protein, DB1



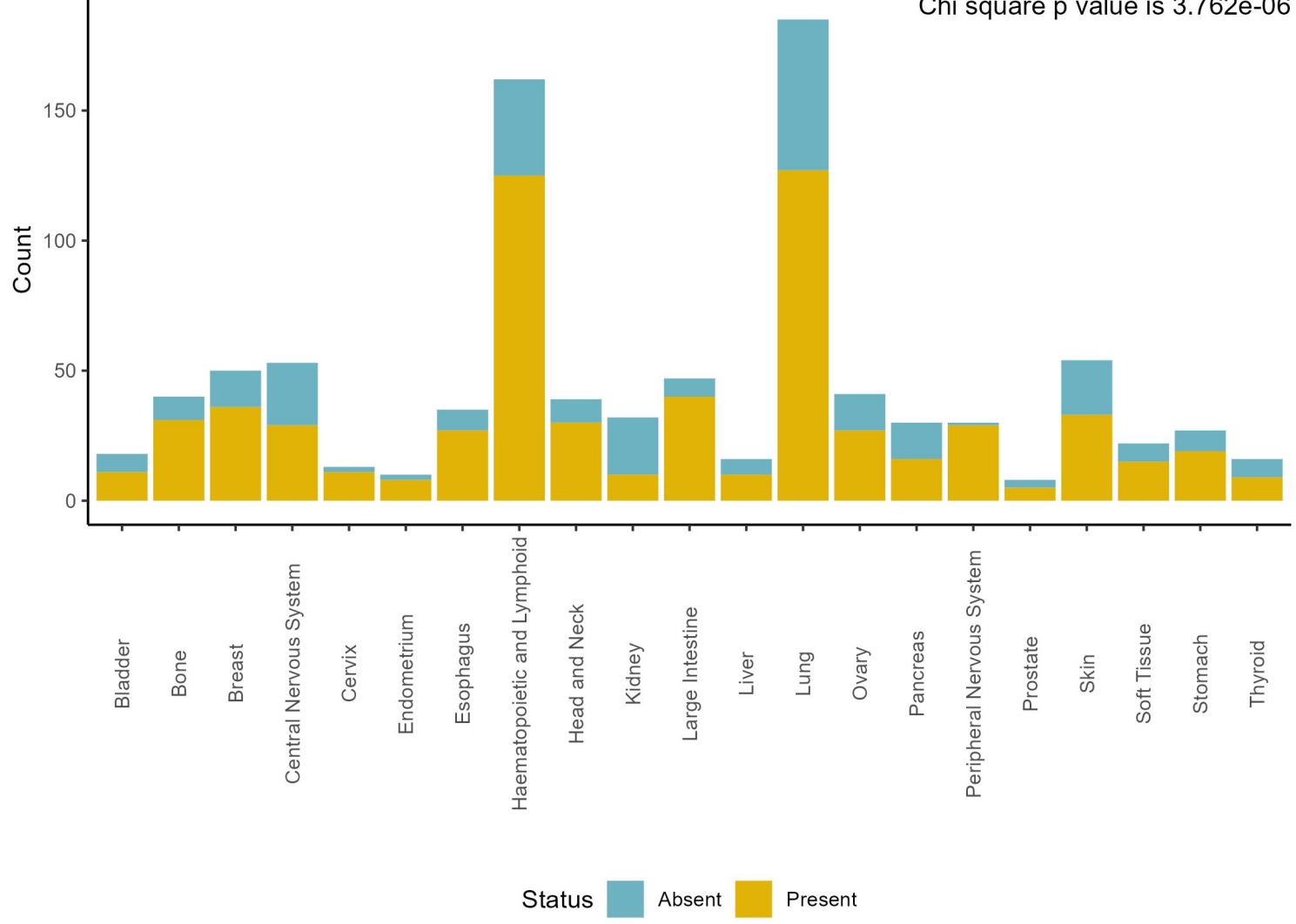
Amount of EP400 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.279e-05



Present and absent EP400 protein counts by tissue, DB1

Chi square p value is 3.762e-06

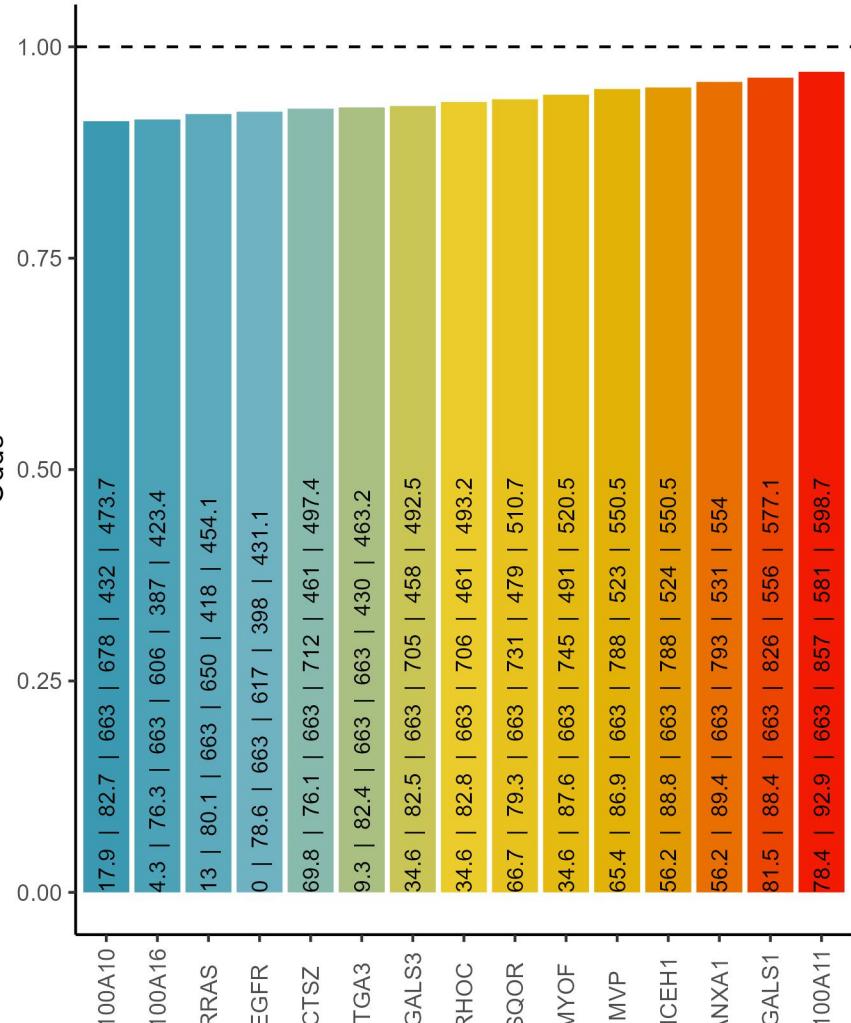


Cooccurrence with EP400 protein, DB1

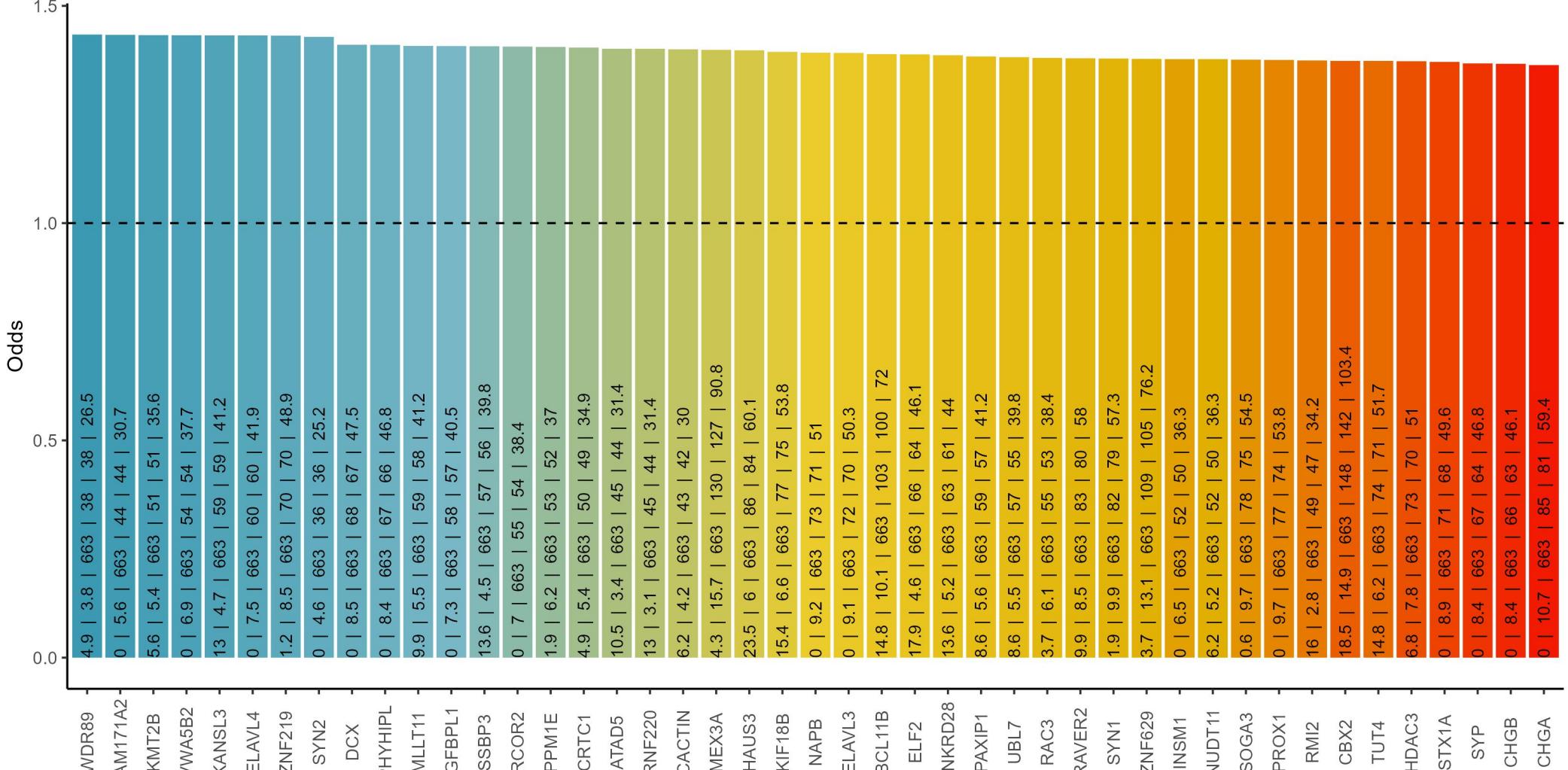
% of EP400 in blood cancers: 77.2 ; % of EP400 in solid cancers: 68.2

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of EP400 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

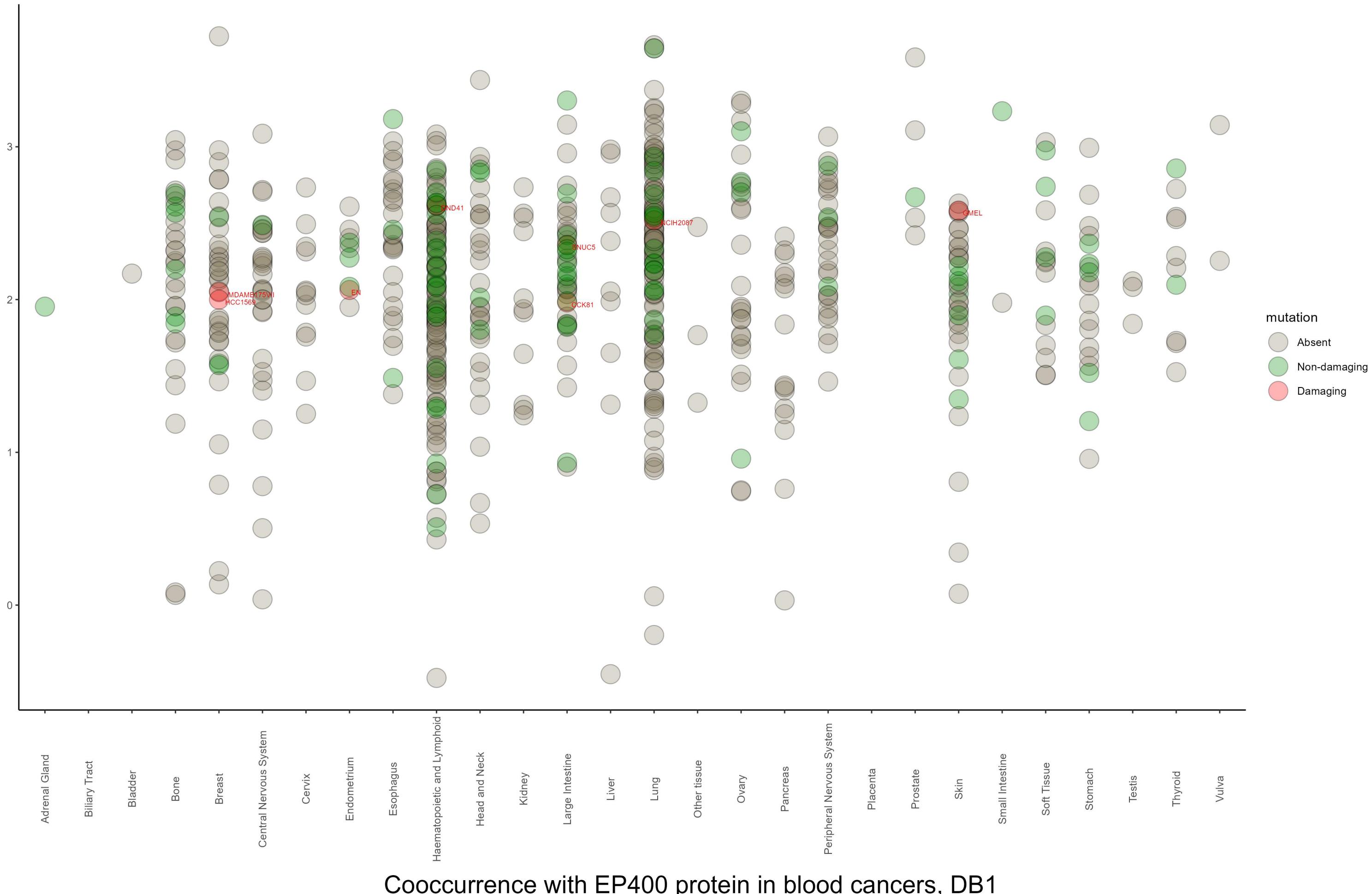
Negative cooccurrence



Positive cooccurrence

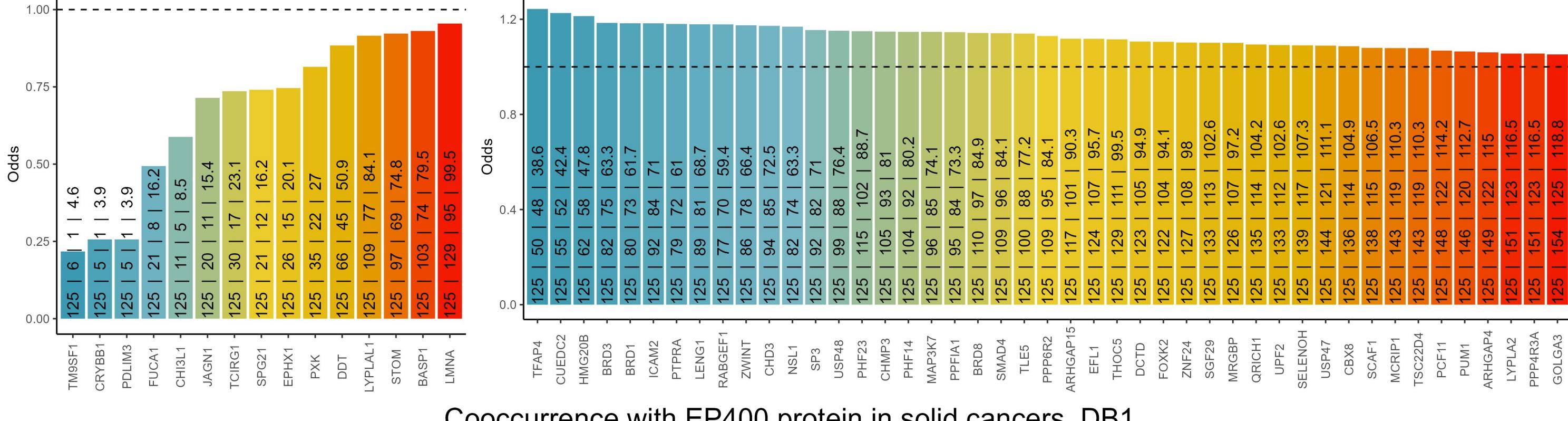


Amount of EP400 protein and mutation status by tissue, DB1



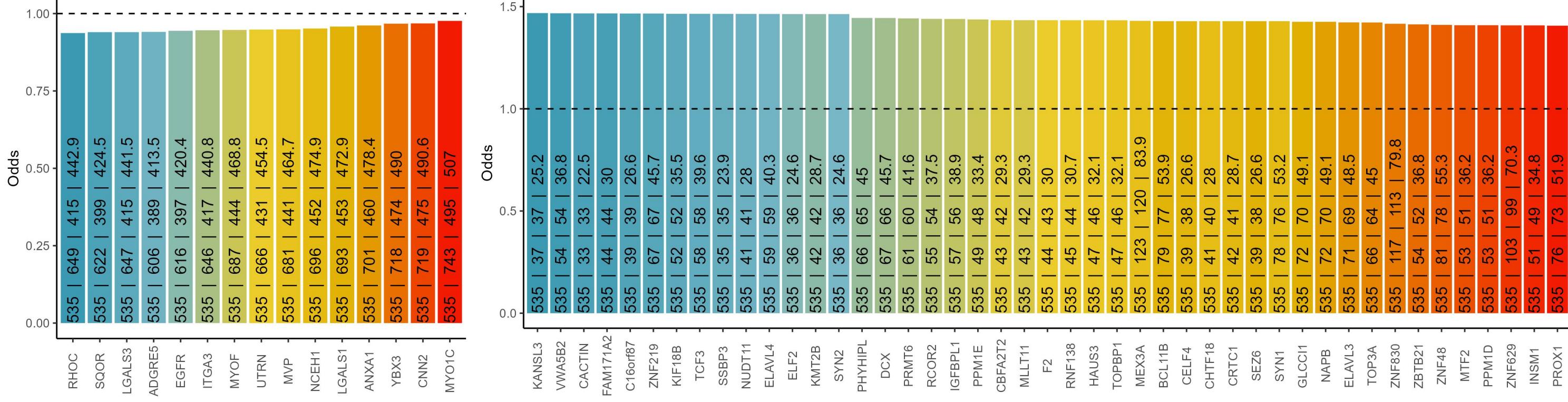
Cooccurrence with EP400 protein in blood cancers, DB1

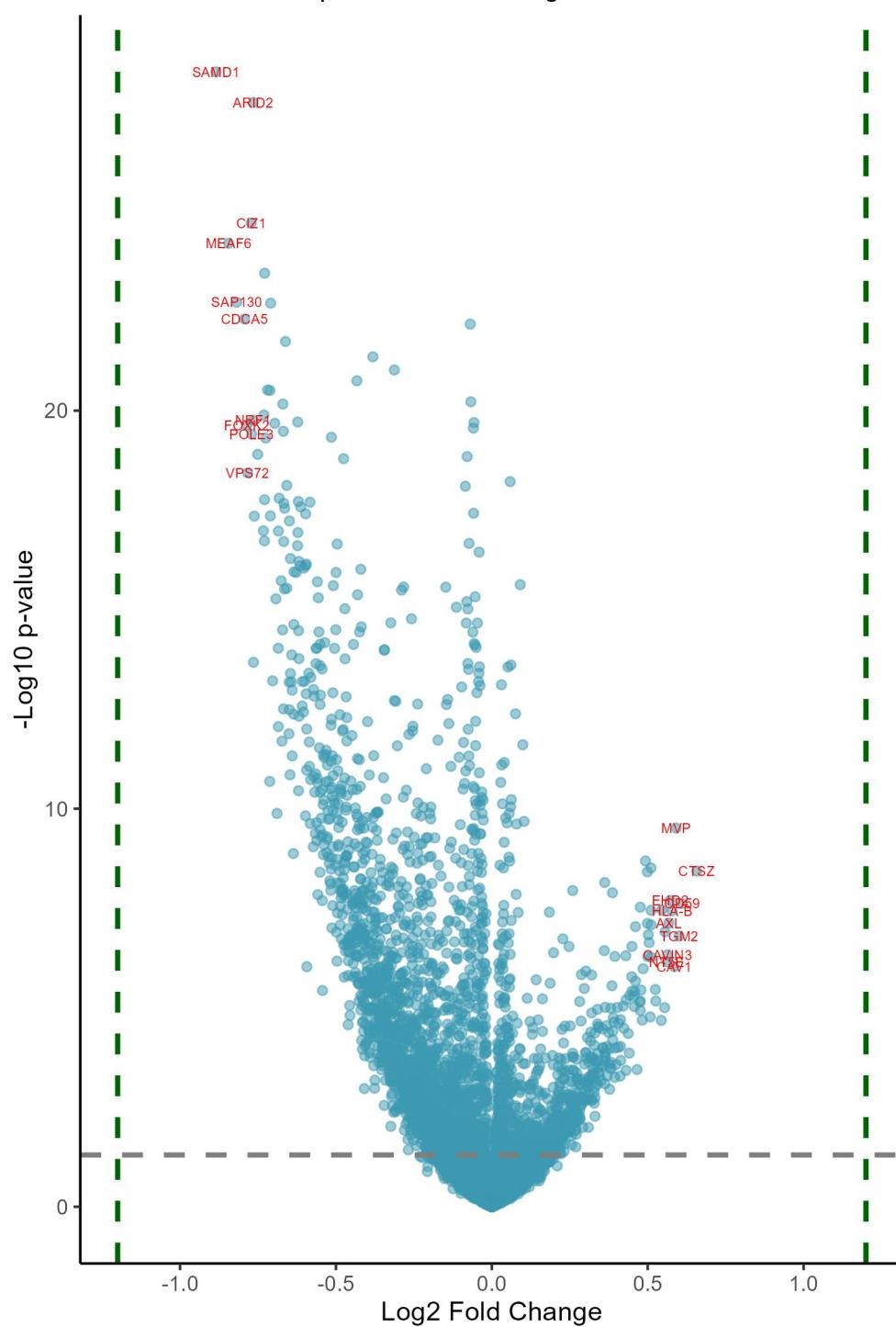
The text in the bars: incidence of EP400 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with EP400 protein in solid cancers, DB1

The text in the bars: incidence of EP400 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

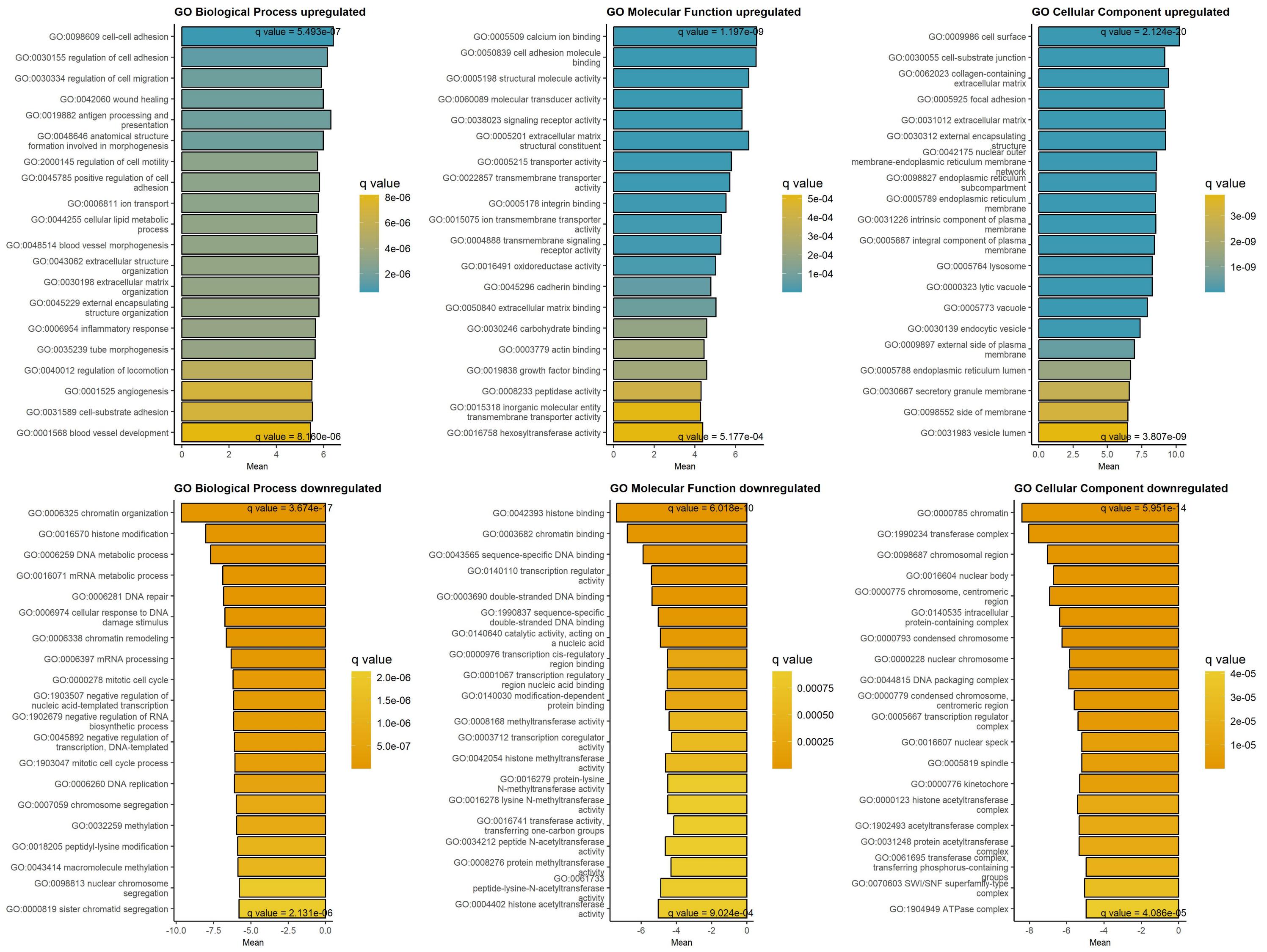




Downregulated at low/absent EP400 Upregulated at low/absent EP400

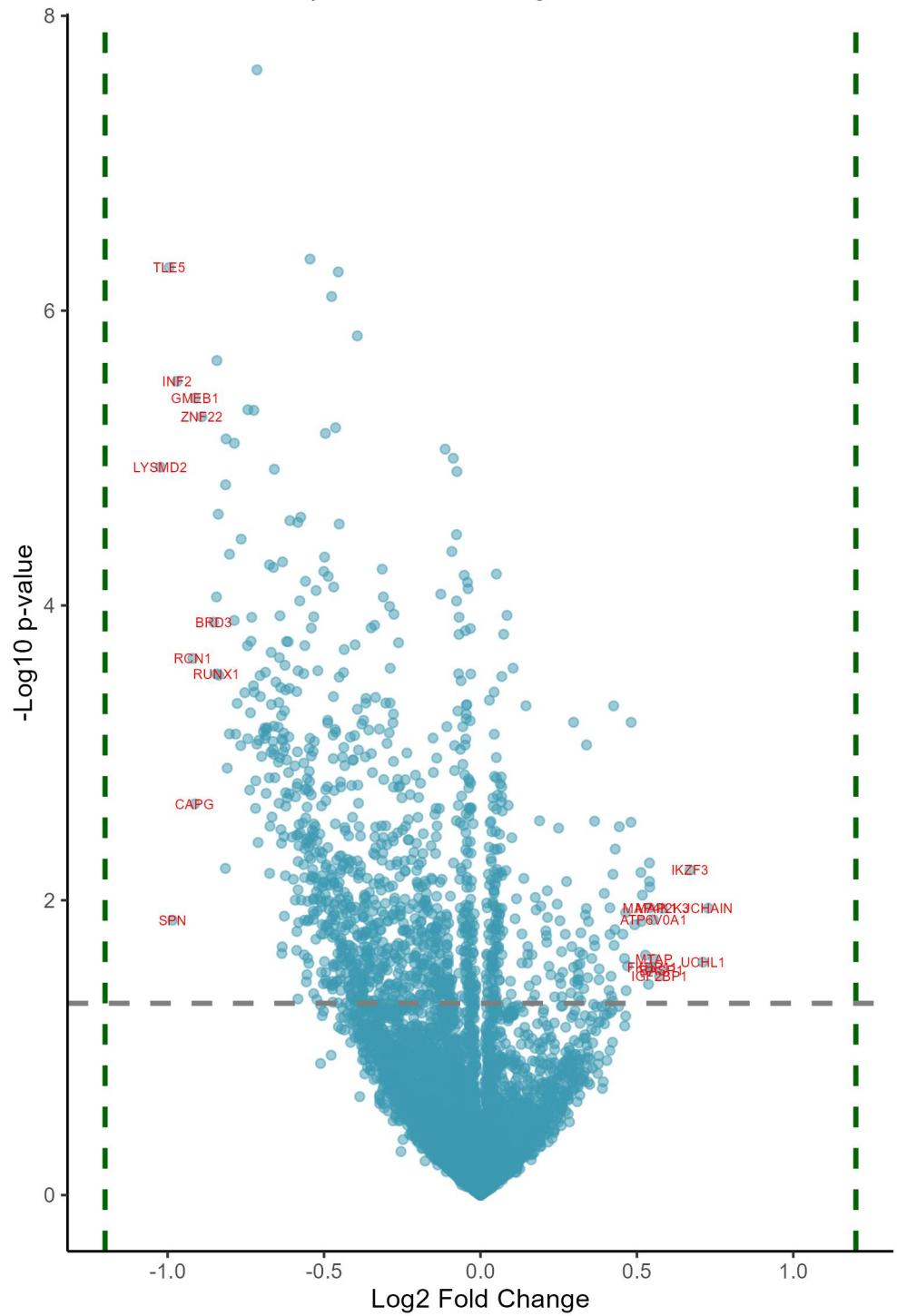
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.88	1.02e-25	SAMD1	sterile alpha motif domain containi	0.66	6.21e-08	CTSZ	cathepsin Z
-0.84	8.30e-22	MEAF6	MYST/Esa1 associated factor 6	0.61	3.33e-07	CD59	CD59 molecule (CD59 blood group)
-0.82	1.66e-20	SAP130	Sir3A associated protein 130	0.6	1.76e-06	TGM2	transglutaminase 2
-0.79	3.70e-20	CDCA5	cell division cycle associated 5	0.59	6.79e-09	MVP	major vault protein
-0.79	6.43e-18	FOXK2	forkhead box K2	0.58	8.53e-06	CAV1	caveolin 1
-0.78	7.36e-17	VPS72	vacuolar protein sorting 72 homolog	0.58	4.80e-07	HLA-B	major histocompatibility complex, c
-0.77	3.23e-22	CIZ1	CDKN1A interacting zinc finger prot	0.57	2.85e-07	EHD2	EH domain containing 2
-0.77	9.54e-18	POLE3	DNA polymerase epsilon 3, accessory	0.57	9.12e-07	AXL	AXL receptor tyrosine kinase
-0.77	5.74e-18	NRF1	nuclear respiratory factor 1	0.56	4.58e-06	CAVIN3	caveolae associated protein 3
-0.77	4.03e-25	ARID2	AT-rich interaction domain 2	0.56	6.67e-06	NT5E	5'-nucleotidase ecto
-0.76	1.25e-12	MRGBP	MRG domain binding protein	0.56	1.43e-06	STOM	stomatin
-0.76	6.33e-16	ZNF24	zinc finger protein 24	0.55	6.91e-05	LGALS3	galectin 3
-0.75	2.78e-17	NSD3	nuclear receptor binding SET domain	0.55	4.60e-07	RAB32	RAB32, member RAS oncogene family
-0.73	1.41e-15	SMARCD1	SWI/SNF related, matrix associated,	0.54	1.33e-04	CAVIN1	caveolae associated protein 1
-0.73	4.49e-18	ZMYM3	zinc finger MYM-type containing 3	0.53	4.90e-05	GPRC5A	G protein-coupled receptor class C
-0.73	2.39e-15	SCAF8	SR-related CTD associated factor 8	0.52	2.73e-05	S100A16	S100 calcium binding protein A16
-0.73	3.02e-16	NUSAP1	nucleolar and spindle associated pr	0.51	5.23e-06	SQOR	sulfide quinone oxidoreductase
-0.73	3.92e-21	SUGP1	SURP and G-patch domain containing	0.51	9.99e-07	TAP1	transporter 1, ATP binding cassette
-0.73	1.12e-17	CHAF1A	chromatin assembly factor 1 subunit	0.51	4.70e-07	HSPG2	heparan sulfate proteoglycan 2
-0.72	1.29e-18	BRD8	bromodomain containing 8	0.51	5.24e-08	PARP4	poly(ADP-ribose) polymerase family
-0.71	6.36e-10	CHRAC1	chromatin accessibility complex sub	0.51	1.11e-04	S100A10	S100 calcium binding protein A10
-0.71	1.29e-18	BRD7	bromodomain containing 7	0.5	2.45e-06	DCBLD2	discoidin, CUB and LCCL domain cont
-0.71	6.33e-16	BPTF	bromodomain PHD finger transcriptio	0.5	1.66e-06	LACTB	lactamase beta
-0.71	1.66e-20	SGF29	SAGA complex associated factor 29	0.5	4.99e-06	RRAS	RAS related
-0.7	3.27e-12	SNRNP27	small nuclear ribonucleoprotein U4/	0.5	9.29e-07	NRP1	neuropilin 1
-0.7	6.03e-18	TRIM24	tripartite motif containing 24	0.5	6.46e-08	TCIRG1	T cell immune regulator 1, ATPase H
-0.69	4.43e-14	SUDS3	SDS3 homolog, SIN3A corepressor com	0.49	3.69e-08	DAB2	DAB adaptor protein 2
-0.69	3.21e-09	POLR2K	RNA polymerase II, I and III subuni	0.49	9.55e-06	CTSL	cathepsin L
-0.68	5.87e-13	EPB41	erythrocyte membrane protein band 4	0.48	1.31e-04	ICAM1	intercellular adhesion molecule 1

GAGE analysis on upregulated and downregulated proteins at low/absent EP400 protein, DB1



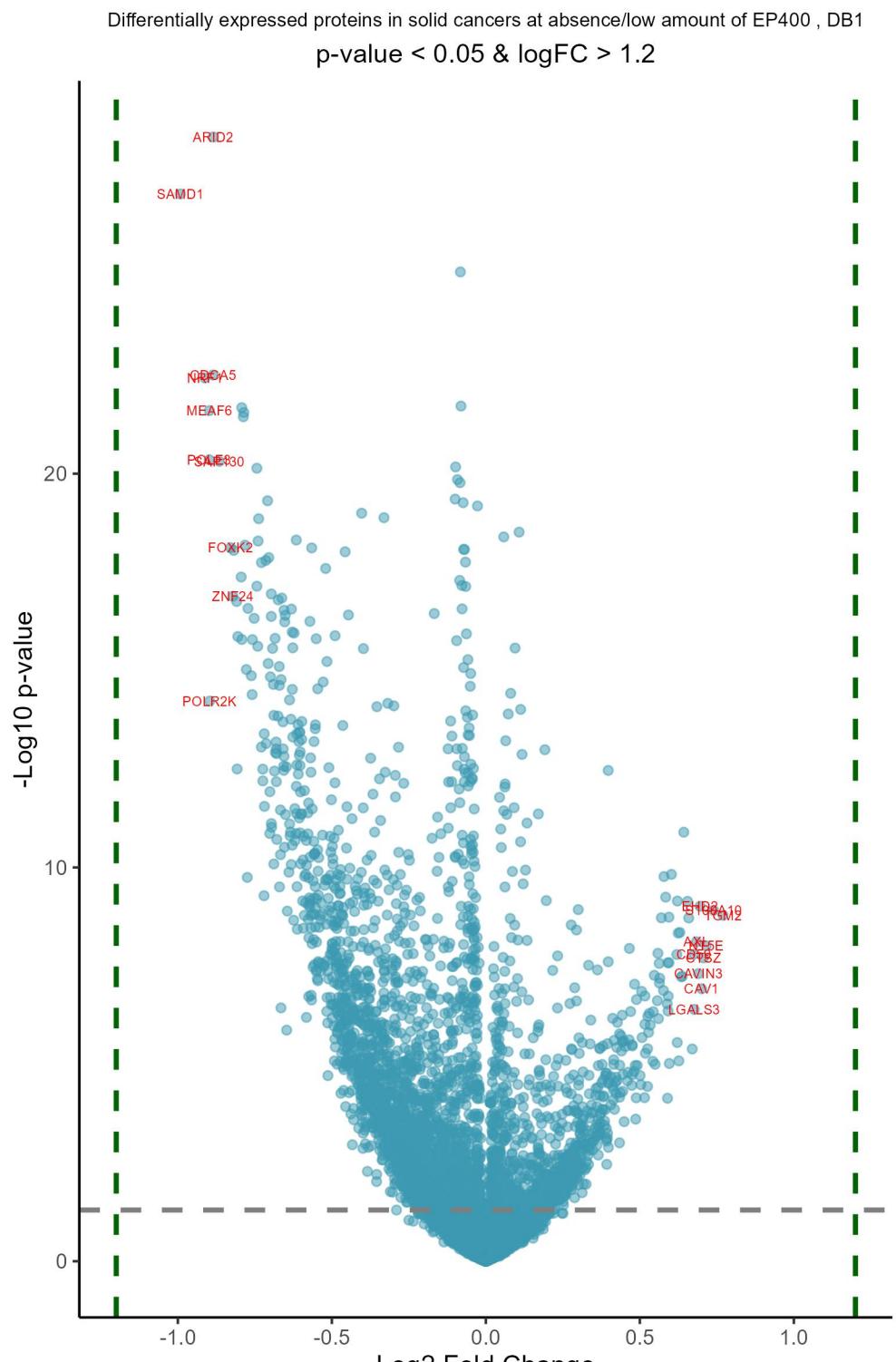
Differentially expressed proteins in blood cancers at absence/low amount of EP400 , DB1

p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent EP400 Upregulated in blood cancers at low/absent EP400

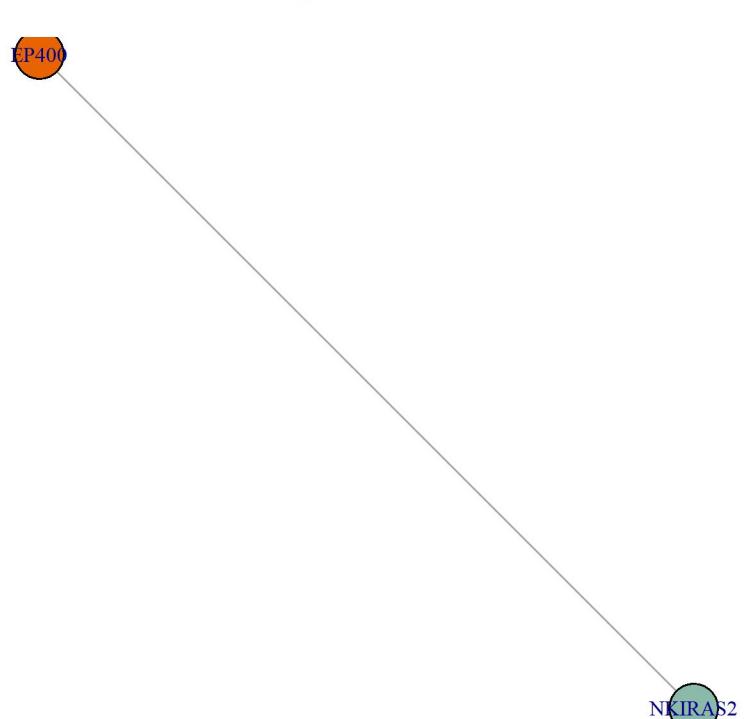
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.02	3.73e-03	LYSMD2	LysM domain containing 2	0.73	1.34e-01	JCHAIN	joining chain of multimeric IgA and
-1	7.26e-04	TLE5	TLE family member 5, transcriptional	0.71	2.01e-01	UCHL1	ubiquitin C-terminal hydrolase L1
-0.98	1.46e-01	SPN	sialophorin	0.67	1.01e-01	IKZF3	IKAROS family zinc finger 3
-0.97	2.23e-03	INF2	inverted formin 2	0.58	1.34e-01	MAP2K3	mitogen-activated protein kinase ki
-0.92	1.95e-02	RCN1	reticulocalbin 1	0.58	2.13e-01	BASP1	brain abundant membrane attached si
-0.91	5.64e-02	CAPG	capping actin protein, gelsolin lik	0.57	2.24e-01	IGF2BP1	insulin like growth factor 2 mRNA b
-0.91	2.60e-03	GMEB1	glucocorticoid modulatory element b	0.56	1.95e-01	MTAP	methylthioadenosine phosphorylase
-0.89	2.69e-03	ZNF22	zinc finger protein 22	0.55	1.45e-01	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-0.85	1.44e-02	BRD3	bromodomain containing 3	0.55	2.07e-01	FKBP11	FKBP prolyl isomerase 11
-0.84	2.18e-02	RUNX1	RUNX family transcription factor 1	0.54	1.34e-01	MAP4K1	mitogen-activated protein kinase ki
-0.84	1.19e-02	PARVG	parvin gamma	0.54	1.13e-01	DTD1	D-aminoacyl-tRNA deacylase 1
-0.84	1.81e-03	TCF20	transcription factor 20	0.54	1.09e-01	HM13	histocompatibility minor 13
-0.84	6.66e-03	LUZP1	leucine zipper protein 1	0.54	9.45e-02	ANXA5	annexin A5
-0.84	2.19e-02	ZC3HAV1L	zinc finger CCCH-type containing, a	0.54	2.12e-01	SAR1B	secretion associated Ras related GT
-0.82	9.97e-02	FSCN1	fascin actin-bundling protein 1	0.54	2.36e-01	STOM	stomatin
-0.81	4.39e-03	CHD8	chromodomain helicase DNA binding p	0.53	1.90e-01	ITGB7	integrin subunit beta 7
-0.81	3.08e-03	CIZ1	CDKN1A interacting zinc finger prot	0.52	1.23e-01	LYPLAL1	lysophospholipase like 1
-0.81	4.16e-02	GNG2	G protein subunit gamma 2	0.51	1.46e-01	LSR	lipolysis stimulated lipoprotein re
-0.8	3.29e-02	TMEM263	transmembrane protein 263	0.51	1.02e-01	RAB30	RAB30, member RAS oncogene family
-0.8	9.33e-03	C9orf78	chromosome 9 open reading frame 78	0.49	1.50e-01	IFI30	IFI30 lysosomal thiol reductase
-0.79	1.42e-02	FGD3	FYVE, RhoGEF and PH domain containi	0.48	3.13e-02	RPL7L1	ribosomal protein L7 like 1
-0.79	3.10e-03	BRD8	bromodomain containing 8	0.48	6.77e-02	SDC1	syndecan 1
-0.78	3.29e-02	UNC13D	unc-13 homolog D	0.47	2.05e-01	SAMHD1	SAM and HD domain containing deoxyn
-0.78	2.70e-02	CEP43	centrosomal protein 43	0.47	2.50e-01	PLCG2	phospholipase C gamma 2
-0.77	3.45e-02	NIPSNAP2	nipsnap homolog 2	0.46	2.99e-01	ISG20	interferon stimulated exonuclease g
-0.77	7.86e-03	KMT2A	lysine methyltransferase 2A	0.46	1.39e-01	MYO5A	myosin VA
-0.75	2.52e-02	MAZ	MYC associated zinc finger protein	0.46	3.26e-01	MS4A1	membrane spanning 4-domains A1
-0.74	1.68e-02	PHF14	PHD finger protein 14	0.46	1.94e-01	SIL1	SIL1 nucleotide exchange factor
-0.74	3.31e-02	FLI1	Fli-1 proto-oncogene, ETS transcrip	0.46	1.58e-01	RAB9A	RAB9A, member RAS oncogene family



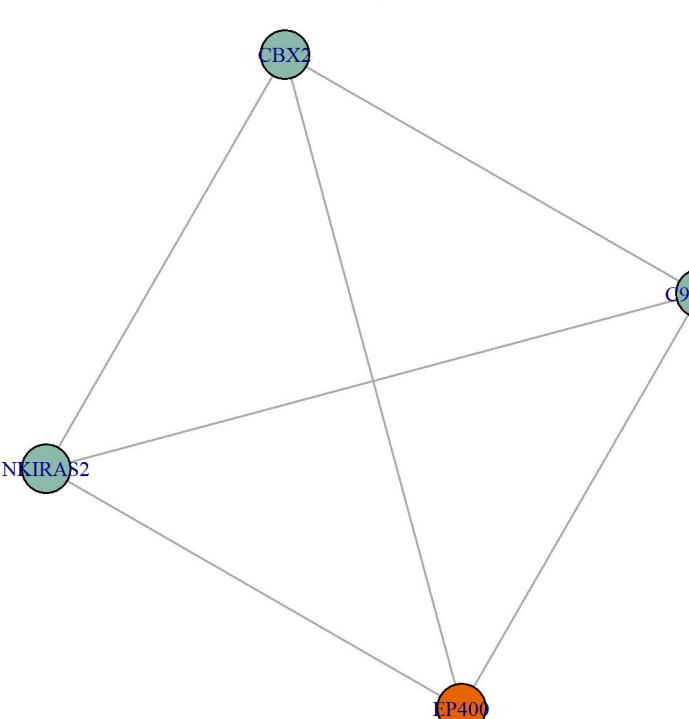
Downregulated in solid cancers at low/absent EP400 Upregulated in solid cancers at low/absent EP400

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.99	1.75e-24	SAMD1	sterile alpha motif domain containi	0.77	2.78e-08	TGM2	transglutaminase 2
-0.91	4.10e-20	NRF1	nuclear respiratory factor 1	0.74	2.16e-08	S100A10	S100 calcium binding protein A10
-0.9	2.45e-18	POLE3	DNA polymerase epsilon 3, accessory	0.72	1.37e-07	NT5E	5'-nucleotidase ecto
-0.9	1.85e-19	MEAF6	MYST/Esa1 associated factor 6	0.71	2.57e-07	CTSZ	cathepsin Z
-0.9	4.13e-13	POLR2K	RNA polymerase II, I and III subuni	0.7	1.25e-06	CAV1	caveolin 1
-0.89	4.10e-20	CDCA5	cell division cycle associated 5	0.7	1.75e-08	EHD2	EH domain containing 2
-0.89	9.37e-26	ARID2	AT-rich interaction domain 2	0.69	5.67e-07	CAVIN3	caveolae associated protein 3
-0.87	2.49e-18	SAP130	Sin3A associated protein 130	0.68	1.10e-07	AXL	AXL receptor tyrosine kinase
-0.83	1.65e-16	FOXK2	forkhead box K2	0.68	3.62e-06	LGALS3	galectin 3
-0.82	1.84e-15	ZNF24	zinc finger protein 24	0.68	2.13e-07	CD59	CD59 molecule (CD59 blood group)
-0.82	1.73e-16	NUSAP1	nucleolar and spindle associated pr	0.67	2.79e-05	CAVIN1	caveolae associated protein 1
-0.81	2.34e-15	SMARCD1	SWI/SNF related, matrix associated,	0.66	3.19e-08	RAB32	RAB32, member RAS oncogene family
-0.81	1.35e-11	MRGBP	MRG domain binding protein	0.65	1.35e-08	RHOC	ras homolog family member C
-0.81	1.38e-14	VPS72	vacuolar protein sorting 72 homolog	0.64	3.81e-10	MVP	major vault protein
-0.79	6.84e-16	NSD3	nuclear receptor binding SET domain	0.64	6.56e-07	S100A16	S100 calcium binding protein A16
-0.79	1.75e-19	SUGP1	SURP and G-patch domain containing	0.64	6.71e-07	HLA-B	major histocompatibility complex, c
-0.79	1.56e-14	SCAF8	SR-related CTD associated factor 8	0.63	6.67e-08	FHL2	four and a half LIM domains 2
-0.79	2.17e-19	SUZ12	SUZ12 polycomb repressive complex 2	0.63	5.23e-05	CD44	CD44 molecule (Indian blood group)
-0.79	1.86e-19	CIZ1	CDKN1A interacting zinc finger prot	0.62	6.93e-08	TAP1	transporter 1, ATP binding cassette
-0.78	1.51e-16	CHAF1A	chromatin assembly factor 1 subunit	0.62	1.34e-08	HSPG2	heparan sulfate proteoglycan 2
-0.78	7.64e-14	EPB41	erythrocyte membrane protein band 4	0.62	2.00e-05	GPRC5A	G protein-coupled receptor class C
-0.77	3.97e-09	CHRAC1	chromatin accessibility complex sub	0.62	2.15e-07	DCBLD2	discoidin, CUB and LCCL domain cont
-0.77	3.44e-15	PRCC	proline rich mitotic checkpoint con	0.6	3.41e-09	PARP4	poly(ADP-ribose) polymerase family
-0.76	1.07e-13	ORC2	origin recognition complex subunit	0.6	5.96e-05	LGALS1	galectin 1
-0.76	2.88e-13	POLR2D	RNA polymerase II subunit D	0.59	3.26e-07	CTSL	cathepsin L
-0.76	1.56e-14	SCML2	Scm polycomb group protein like 2	0.59	3.05e-08	RRAS	RAS related
-0.75	5.31e-15	C5orf24	chromosome 5 open reading frame 24	0.59	1.85e-06	SQOR	sulfide quinone oxidoreductase
-0.74	3.23e-18	SGF29	SAGA complex associated factor 29	0.59	3.90e-06	MMP14	matrix metallopeptidase 14
-0.74	1.08e-15	ZMYM3	zinc finger MYM-type containing 3	0.59	3.28e-07	NRP1	neuropilin 1

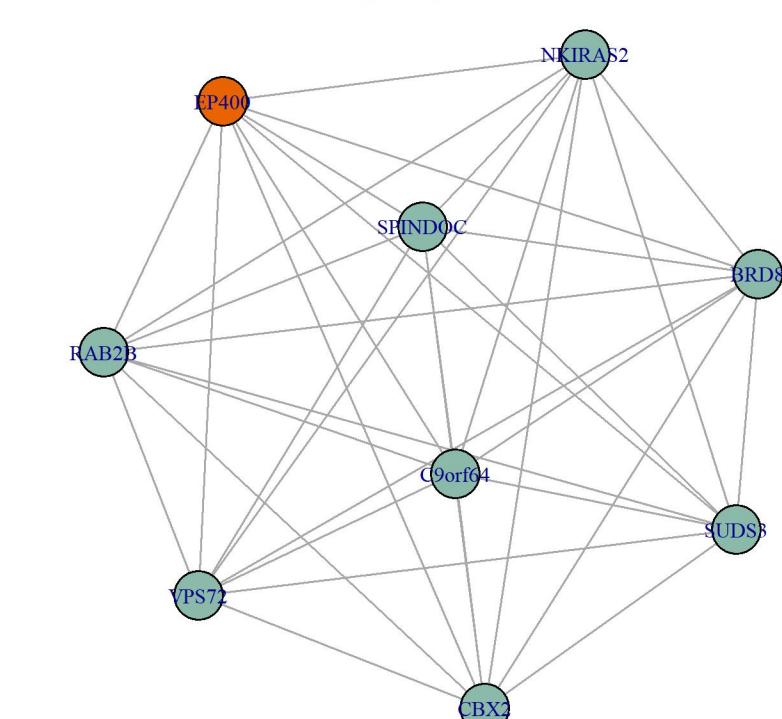
EP400 network, DB1, all Pearson r > 0.45

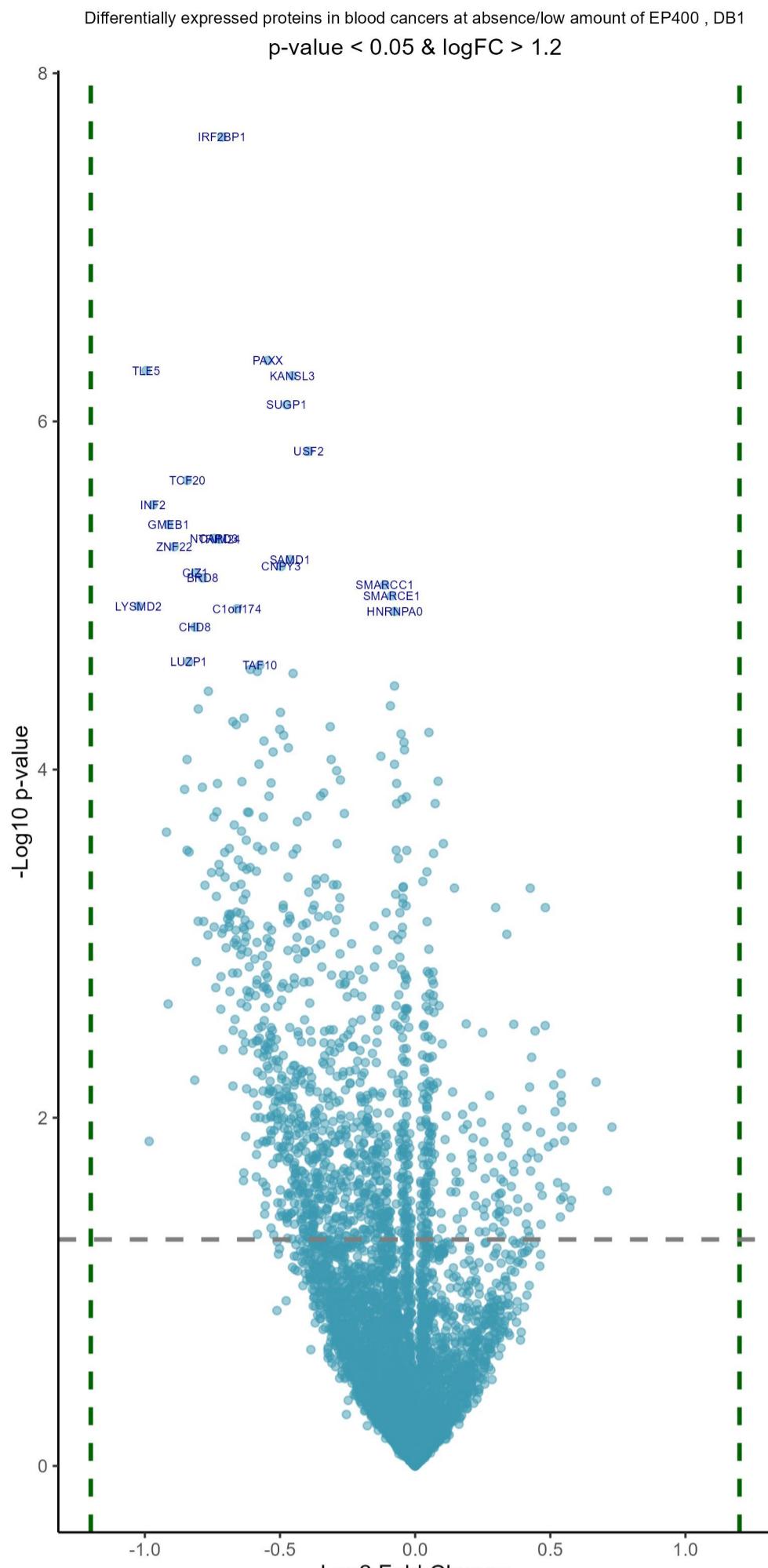


EP400 network, DB1, all Pearson r > 0.4

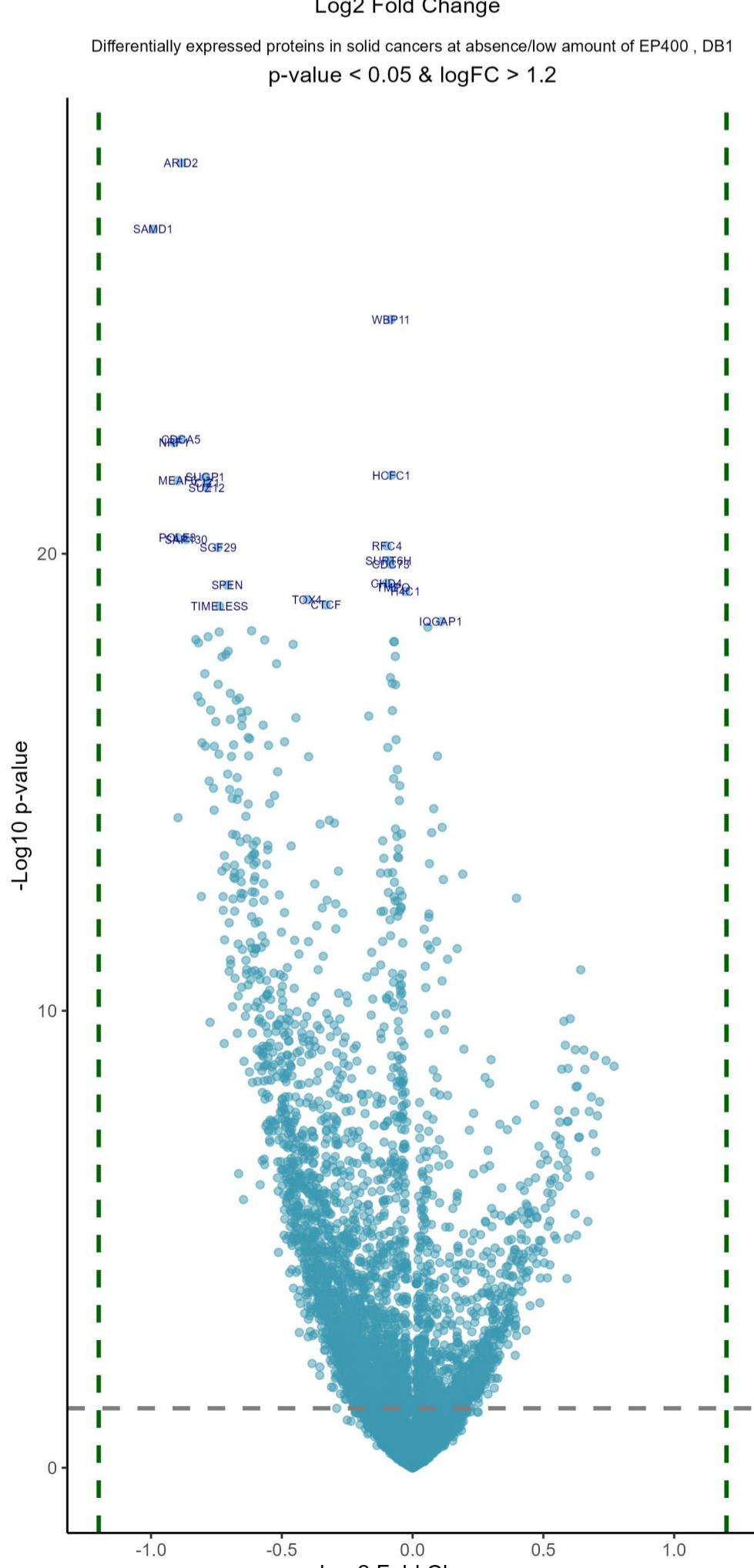


EP400 network, DB1, all Pearson r > 0.35



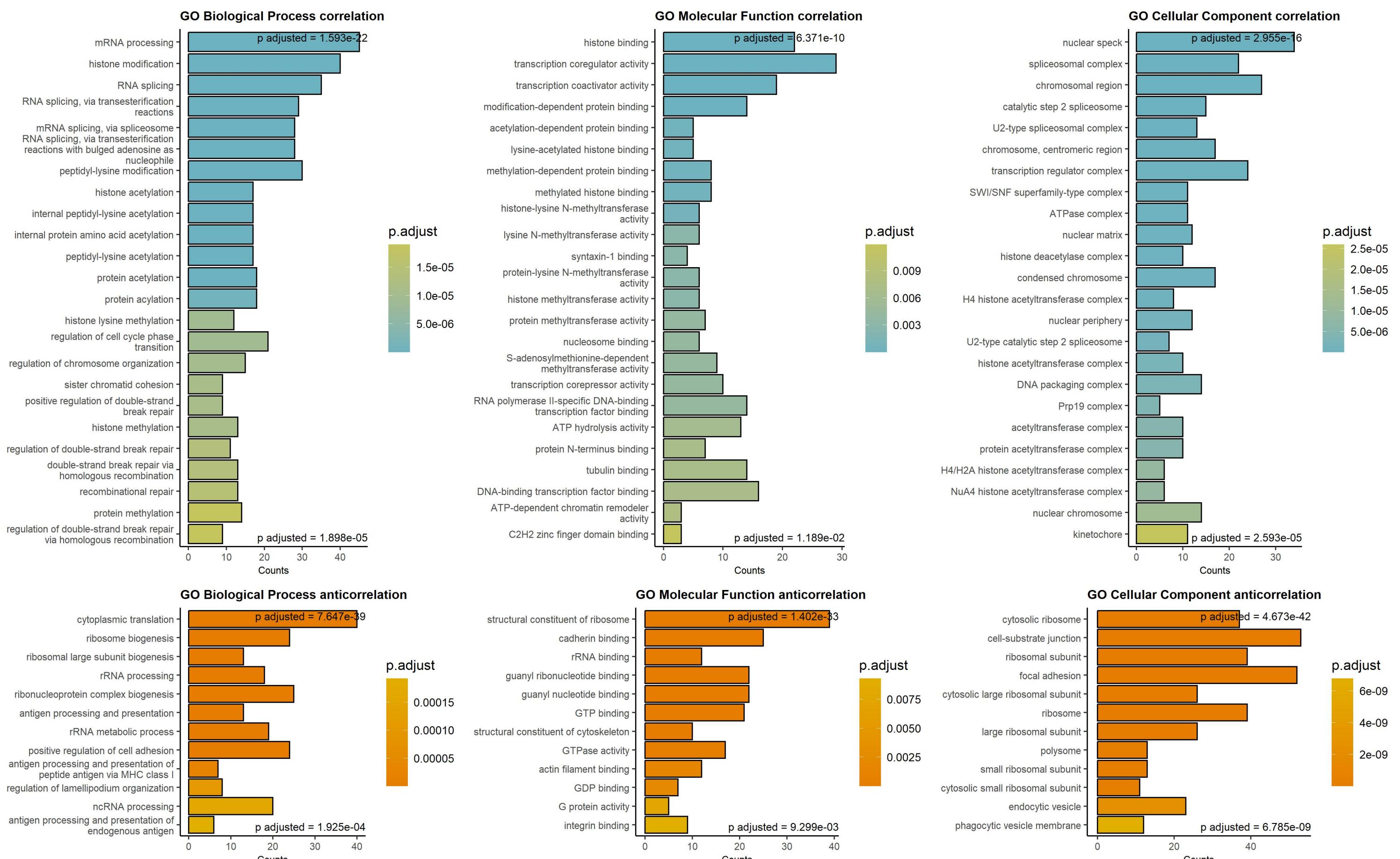


Sorted by p values!							
Downregulated in blood cancers at low/absent EP400				Upregulated in blood cancers at low/absent EP400			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.71	7.73e-05	IRF2BP1	interferon regulatory factor 2 bind	0.05	1.03e-02	FARSA	phenylalanyl-tRNA synthetase subunit
-0.54	7.26e-04	PAXX	PAXX non-homologous end joining fac	0.08	1.38e-02	CLPP	caseinolytic mitochondrial matrix p
-1	7.26e-04	TLE5	TLE family member 5, transcriptional	0.07	1.56e-02	ABCE1	ATP binding cassette subfamily E me
-0.45	7.26e-04	KANSL3	KAT8 regulatory NSL complex subunit	0.1	2.18e-02	HEATR1	HEAT repeat containing 1
-0.48	8.89e-04	SUGP1	SURP and G-patch domain containing	0.07	2.19e-02	RRP1	ribosomal RNA processing 1
-0.39	1.41e-03	USF2	upstream transcription factor 2, c-	0.04	2.52e-02	RSL1D1	ribosomal L1 domain containing 1
-0.84	1.81e-03	TCF20	transcription factor 20	0.03	2.70e-02	RPS7	ribosomal protein S7
-0.97	2.23e-03	INF2	inverted formin 2	0.15	2.70e-02	NAMPT	nicotinamide phosphoribosyltransfer
-0.91	2.60e-03	GMEB1	glucocorticoid modulatory element b	0.43	2.70e-02	PNO1	partner of NOB1 homolog
-0.74	2.63e-03	NCAPD3	non-SMC condensin II complex subunit	0.3	3.13e-02	ECPAS	Ecm29 proteasome adaptor and scatfo
-0.72	2.63e-03	TRIM24	tripartite motif containing 24	0.48	3.13e-02	RPL7L1	ribosomal protein L7 like 1
-0.89	2.69e-03	ZNF22	zinc finger protein 22	0.04	3.29e-02	EIF4G1	eukaryotic translation initiation f
-0.46	2.96e-03	SAMD1	sterile alpha motif domain containi	0.34	3.45e-02	TPD52	tumor protein D52
-0.5	3.02e-03	CNPY3	canopy FGF signalling regulator 3	0.05	3.75e-02	SND1	staphylococcal nuclease and tudor d
-0.81	3.08e-03	CIZ1	CDKN1A interacting zinc finger prot	0.04	4.55e-02	PSMD2	proteasome 26S subunit ubiquitin re
-0.79	3.10e-03	BRD8	bromodomain containing 8	0.07	4.57e-02	RRP9	ribosomal RNA processing 9, U3 smal
-0.11	3.21e-03	SMARCC1	SWI/SNF related, matrix associated,	0.05	4.58e-02	AHCY	adenosylhomocysteinase
-0.09	3.51e-03	SMARCE1	SWI/SNF related, matrix associated,	0.06	4.73e-02	RRP12	ribosomal RNA processing 12 homolog
-1.02	3.73e-03	LYSMD2	LysM domain containing 2	0.07	4.81e-02	PPIB	peptidylprolyl isomerase B
-0.66	3.73e-03	C1orf174	chromosome 1 open reading frame 174	0.05	5.16e-02	TIMM50	translocase of inner mitochondrial
-0.08	3.73e-03	HNRNPA0	heterogeneous nuclear ribonucleopro	0.07	5.22e-02	NMT1	N-myristoyltransferase 1
-0.81	4.39e-03	CHD8	chromodomain helicase DNA binding p	0.04	5.24e-02	PSMD8	proteasome 26S subunit, non-ATPase
-0.84	6.66e-03	LUZP1	leucine zipper protein 1	0.07	5.53e-02	NPEPPS	aminopeptidase puromycin sensitive
-0.57	6.66e-03	TAF10	TATA-box binding protein associated	0.09	5.72e-02	SRPRB	SRP receptor subunit beta
-0.61	6.66e-03	SGF29	SAGA complex associated factor 29	0.04	5.73e-02	RPS16	ribosomal protein S16
-0.58	6.66e-03	PHF2	PHD finger protein 2	0.05	5.84e-02	FARSB	phenylalanyl-tRNA synthetase subuni
-0.45	6.66e-03	LYPLA2	lysophospholipase 2	0.07	5.95e-02	PDCD11	programmed cell death 11
-0.08	7.59e-03	ZC3HAV1	zinc finger CCCH-type containing, a	0.19	6.70e-02	TOR3A	torsin family 3 member A
-0.77	7.86e-03	KMT2A	lysine methyltransferase 2A	0.36	6.71e-02	PKP2	plakophilin 2
-0.09	9.24e-03	SIN3A	SIN3 transcription regulator family	0.03	6.71e-02	RPS3	ribosomal protein S3
-0.8	9.33e-03	C9orf78	chromosome 9 open reading frame 78	0.48	6.77e-02	SDC1	syndecan 1
-0.5	9.46e-03	DNMT3A	DNA methyltransferase 3 alpha	0.03	6.79e-02	RPL6	ribosomal protein L6
-0.63	9.91e-03	ZNF384	zinc finger protein 384	0.44	6.89e-02	NAGLU	N-acetyl-alpha-glucosaminidase
-0.67	1.01e-02	CD5	CD5 molecule	0.25	6.98e-02	SPATA20	spermatogenesis associated 20
-0.66	1.02e-02	MEAF6	MYST/Esa1 associated factor 6	0.05	7.21e-02	PES1	pescadillo ribosomal biogenesis fac
-0.31	1.02e-02	NCOA6	nuclear receptor coactivator 6	0.04	7.24e-02	TUFM	Tu translation elongation factor, m
-0.5	1.03e-02	USP47	ubiquitin specific peptidase 47	0.06	7.35e-02	EBNA1BP2	EBNA1 binding protein 2
-0.05	1.03e-02	ENO1	enolase 1	0.1	7.48e-02	BPNT1	3'(2'), 5'-bisphosphate nucleotidas
-0.19	1.03e-02	ANKRD17	ankyrin repeat domain 17	0.03	8.20e-02	RPS18	ribosomal protein S18

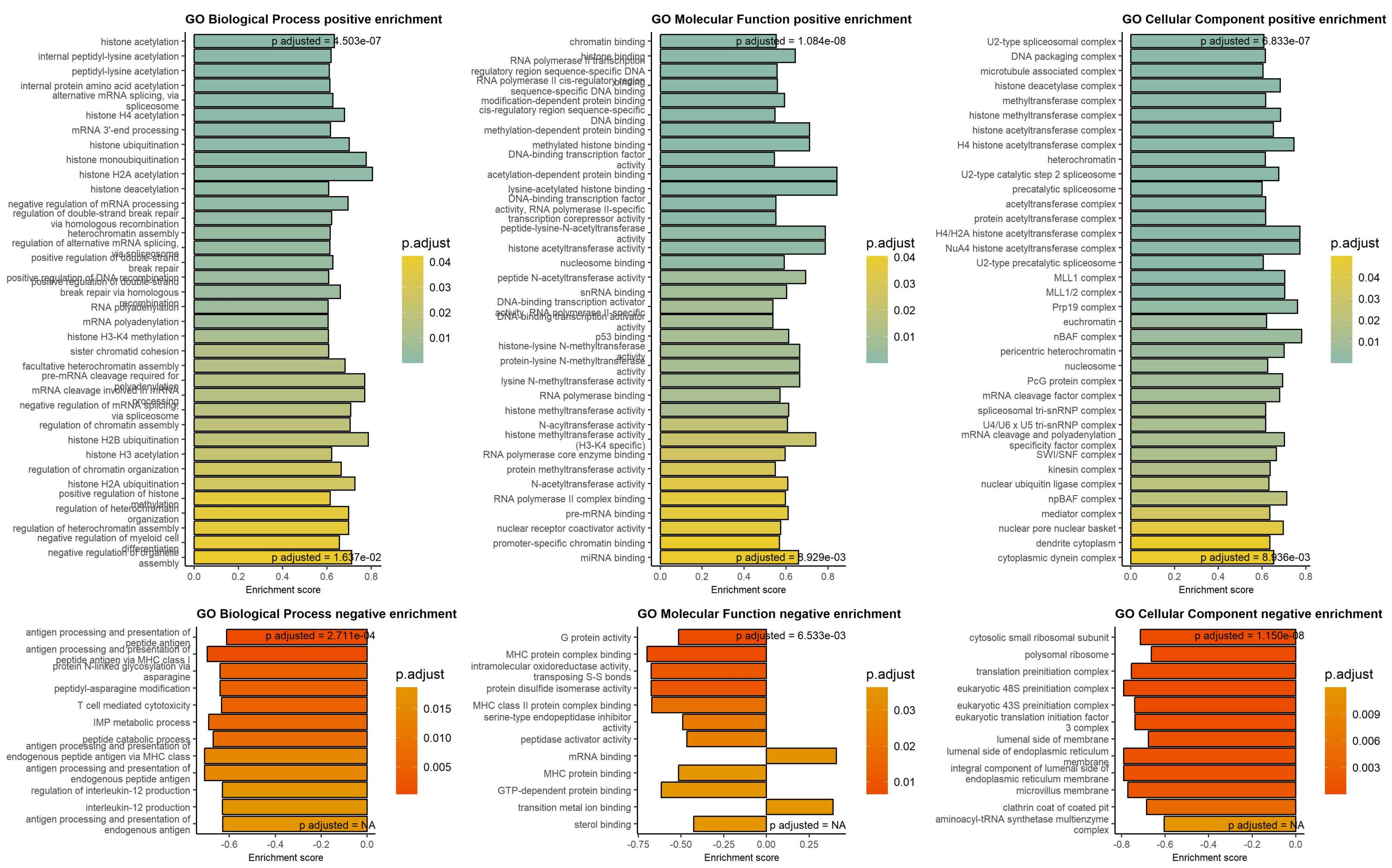


Sorted by p values!							
Downregulated in solid cancers at low/absent EP400				Upregulated in solid cancers at low/absent EP400			
FC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
39	9.37e-26	ARID2	AT-rich interaction domain 2	0.11	8.11e-17	IQGAP1	IQ motif containing GTPase activati
99	1.75e-24	SAMD1	sterile alpha motif domain containi	0.06	1.03e-16	CLTC	clathrin heavy chain
08	1.25e-22	WBP11	WW domain binding protein 11	0.09	2.41e-14	MYL6	myosin light chain 6
39	4.10e-20	CDCA5	cell division cycle associated 5	0.08	2.71e-13	ACTBL2	actin beta like 2
91	4.10e-20	NRF1	nuclear respiratory factor 1	0.11	6.46e-13	ACTN4	actinin alpha 4
08	1.75e-19	HCFC1	host cell factor C1	0.07	8.27e-13	RAC1	Rac family small GTPase 1
79	1.75e-19	SUGP1	SURP and G-patch domain containing	0.06	3.22e-12	RAB1A	RAB1A, member RAS oncogene family
9	1.85e-19	MEAF6	MYST/Esa1 associated factor 6	0.19	4.97e-12	PLEC	plectin
79	1.86e-19	CIZ1	CDKN1A interacting zinc finger prot	0.12	6.35e-12	PICALM	phosphatidylinositol binding clathr
79	2.17e-19	SUZ12	SUZ12 polycomb repressive complex 2	0.4	1.44e-11	MYO1C	myosin IC
9	2.45e-18	POLE3	DNA polymerase epsilon 3, accessory	0.06	2.83e-11	VDAC1	voltage dependent anion channel 1
37	2.49e-18	SAP130	Sin3A associated protein 130	0.06	3.32e-11	P4HB	prolyl 4-hydroxylase subunit beta
1	3.20e-18	RFC4	replication factor C subunit 4	0.04	5.86e-11	CDC42	cell division cycle 42
74	3.23e-18	SGF29	SAGA complex associated factor 29	0.09	1.04e-10	AP2A1	adaptor related protein complex 2 s
09	5.87e-18	SUPT6H	SPT6 homolog, histone chaperone and	0.06	1.21e-10	ARPC4	actin related protein 2/3 complex s
08	6.62e-18	CDC73	cell division cycle 73	0.17	1.42e-10	AHNAK	AHNAK nucleoprotein
1	1.63e-17	CHD4	chromodomain helicase DNA binding p	0.07	1.44e-10	AP2B1	adaptor related protein complex 2 s
71	1.70e-17	SPEN	spen family transcriptional repress	0.13	2.32e-10	LMNA	lamin A/C
07	1.82e-17	TMPO	thymopoietin	0.05	3.24e-10	CAPZB	capping actin protein of muscle Z-l
03	2.09e-17	H4C1	H4 clustered histone 1	0.64	3.81e-10	MVP	major vault protein
4	3.04e-17	TOX4	TOX high mobility group box family	0.11	6.14e-10	CTSD	cathepsin D
33	3.79e-17	CTCF	CCCTC-binding factor	0.05	8.36e-10	RPL27	ribosomal protein L27
74	3.86e-17	TIMELESS	timeless circadian regulator	0.13	2.73e-09	ACTN1	actinin alpha 1
62	1.19e-16	LRWD1	leucine rich repeats and WD repeat	0.09	2.93e-09	TMOD3	tropomodulin 3
74	1.22e-16	RBBP6	RB binding protein 6, ubiquitin lig	0.6	3.41e-09	PARP4	poly(ADP-ribose) polymerase family
78	1.51e-16	CHAF1A	chromatin assembly factor 1 subunit	0.58	3.79e-09	RAB11FIP5	RAB11 family interacting protein 5
33	1.65e-16	FOXP2	forkhead box K2	0.12	5.55e-09	MYH9	myosin heavy chain 9
57	1.65e-16	SFSWAP	splicing factor SWAP	0.06	6.42e-09	TMED9	transmembrane p24 trafficking prote
07	1.70e-16	SART1	spliceosome associated factor 1, re	0.58	1.11e-08	DAB2	DAB adaptor protein 2
07	1.70e-16	IK	IK cytokine	0.2	1.31e-08	GALNT2	polypeptide N-acetylgalactosaminylt
32	1.73e-16	NUSAP1	nucleolar and spindle associated pr	0.62	1.34e-08	HSPG2	heparan sulfate proteoglycan 2
46	1.83e-16	ZC3H13	zinc finger CCCH-type containing 13	0.65	1.35e-08	RHOC	ras homolog family member C
7	2.50e-16	PHF3	PHD finger protein 3	0.7	1.75e-08	EHD2	EH domain containing 2
71	2.87e-16	BRD7	bromodomain containing 7	0.3	2.07e-08	PLIN3	perilipin 3
07	3.08e-16	SMC1A	structural maintenance of chromosom	0.74	2.16e-08	S100A10	S100 calcium binding protein A10
73	3.08e-16	BRD8	bromodomain containing 8	0.77	2.78e-08	TGM2	transglutaminase 2
52	4.25e-16	RING1	ring finger protein 1	0.59	3.05e-08	RRAS	RAS related
79	6.84e-16	NSD3	nuclear receptor binding SET domain	0.57	3.16e-08	TCIRG1	T cell immune regulator 1, ATPase H
29	8.14e-16	ZNF202	zinc finger protein 202	0.29	3.19e-08	RAB26	RAB26, member RAB family

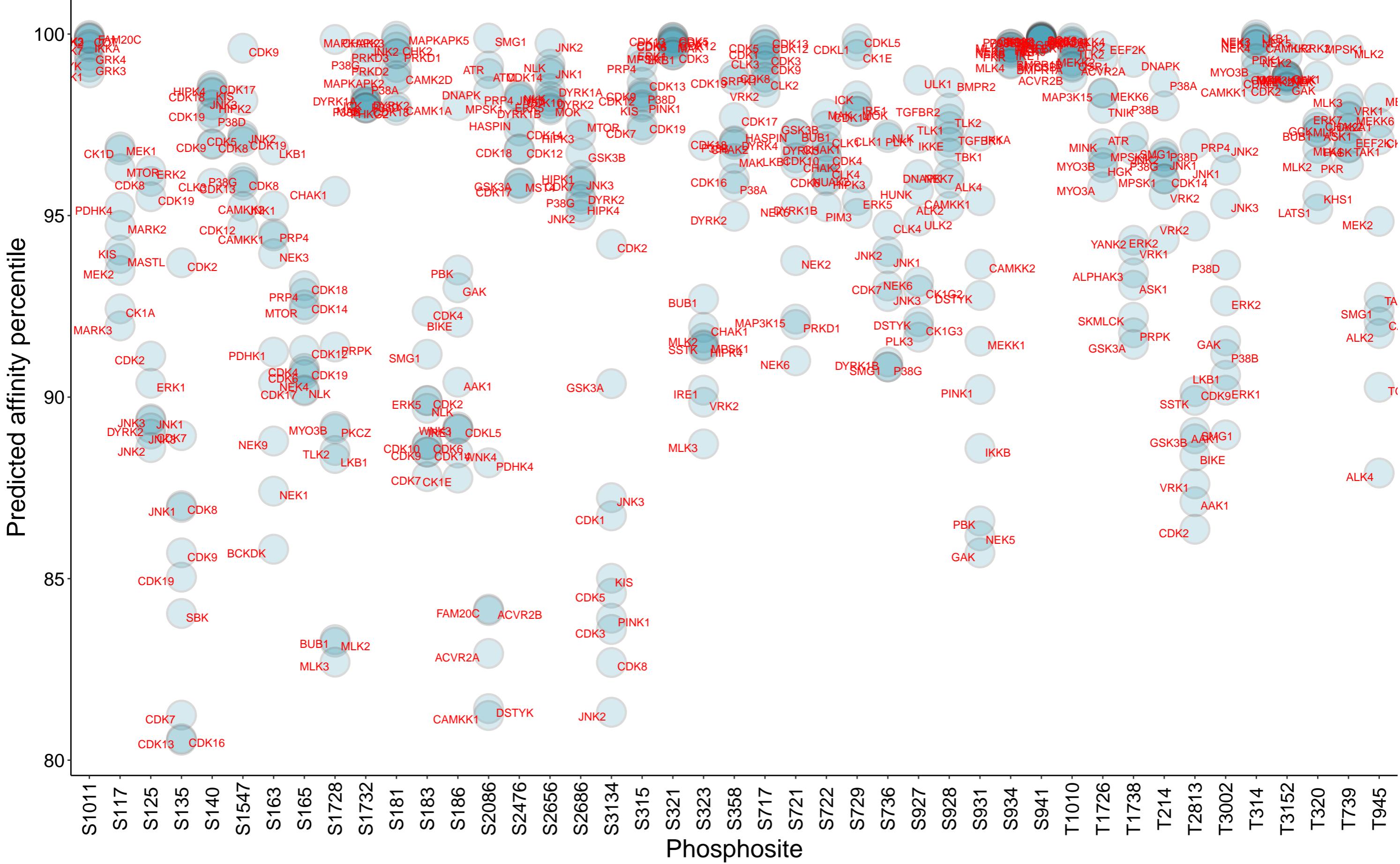
Top 250 correlation coefficients overrepresentation, EP400 protein, DB1



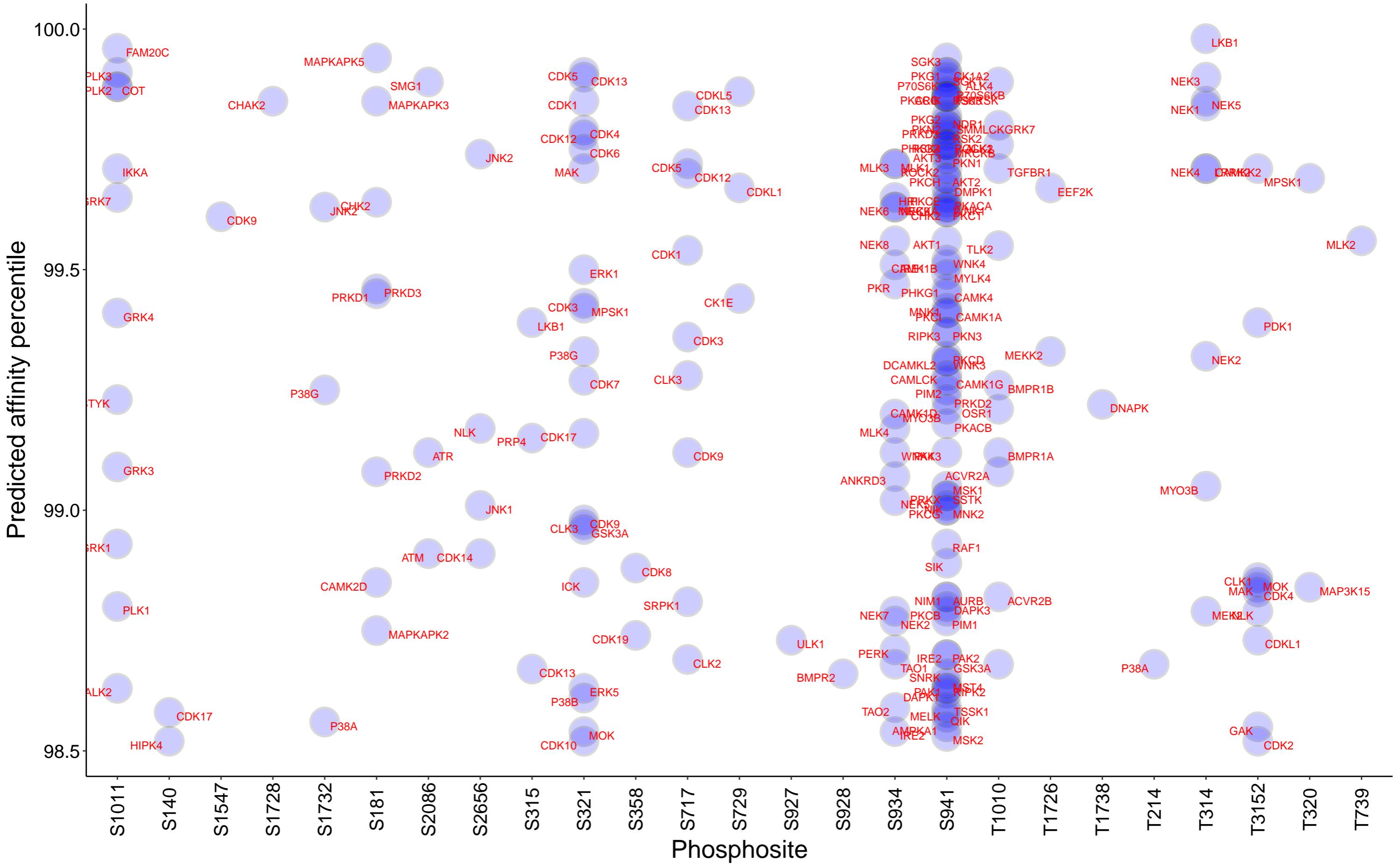
Gene Set Enrichment analysis on protein correlation coefficients, EP400 protein, DB1



Top 10 kinases for each phosphosite in EP400



Kinases with affinity greater than 98.5% to EP400



Top 15 positive correlation coefficients for EP400 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

