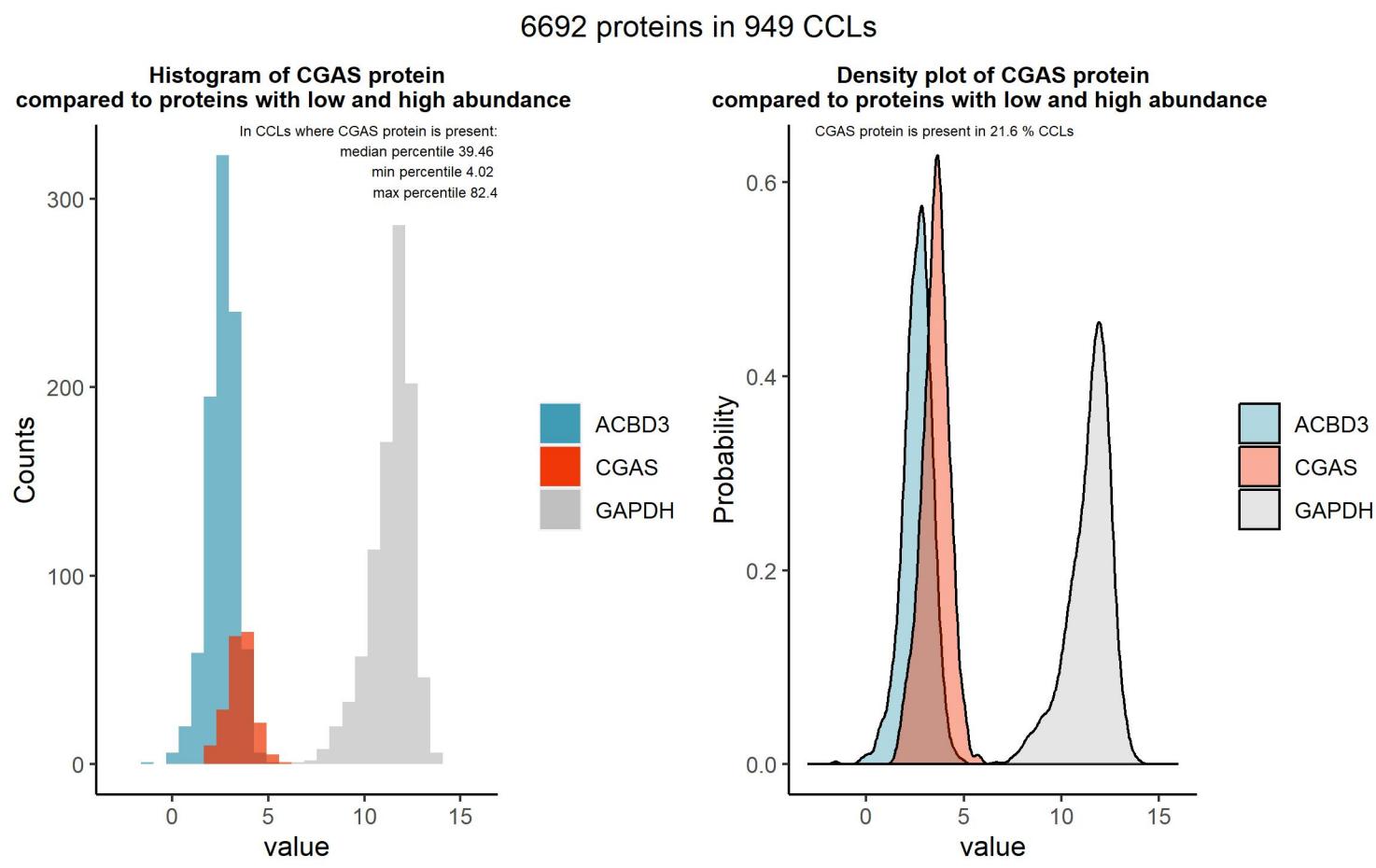


CGAS

Protein name: CGAS ; UNIPROT: Q8N884 ; Gene name: cyclic GMP-AMP synthase

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

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



Top negative correlations of CGAS protein, DB1

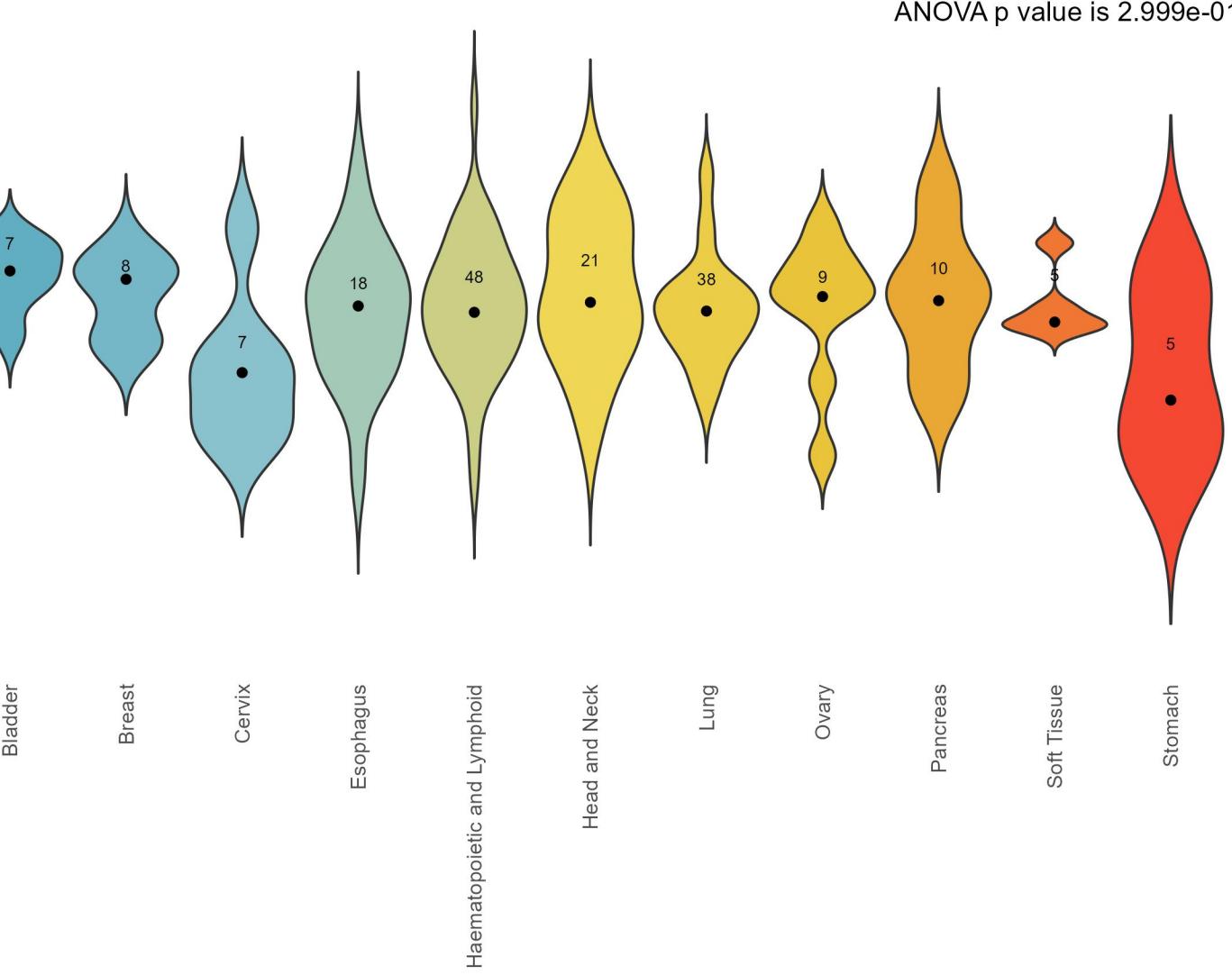
ACAD8
NQO1
AREB2
ACAT1
EPB41L
NLN
MBLAC2

DLAT
AGL

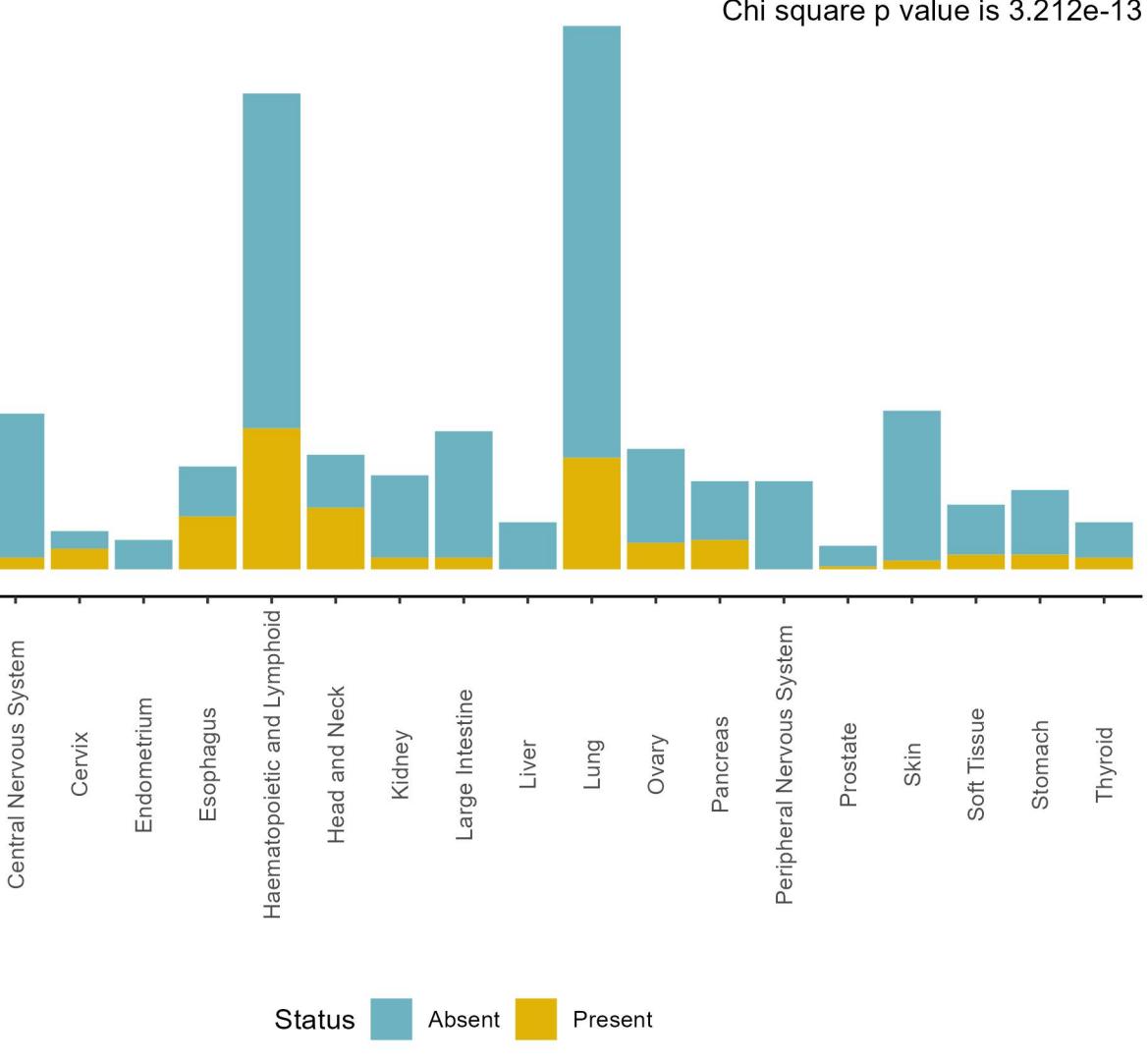
Top positive correlations of CGAS protein, DB1

GOLT1B
CDC3A
HIP1
RIF1
LTV1
POLR2I
THUMPD1
CDKAL1
INCENP
SART1
PRIM1
SPATA5L1

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



Present and absent CGAS protein counts by tissue, DB1

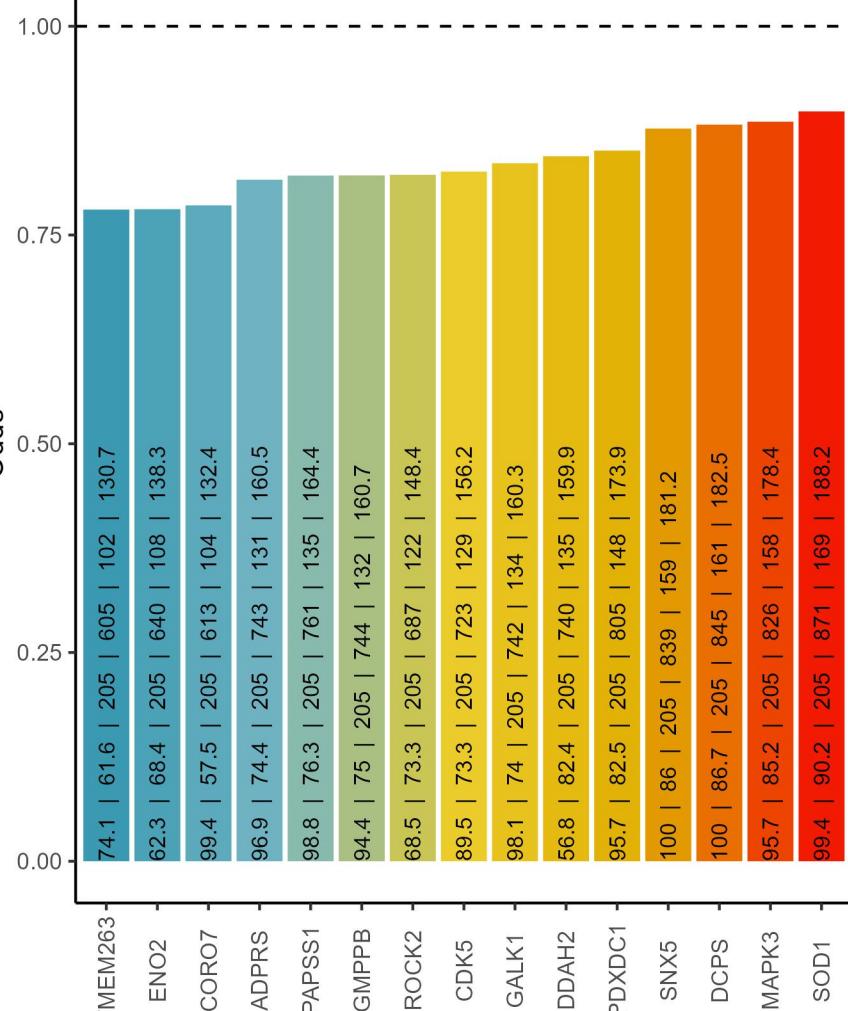


Cooccurrence with CGAS protein, DB1

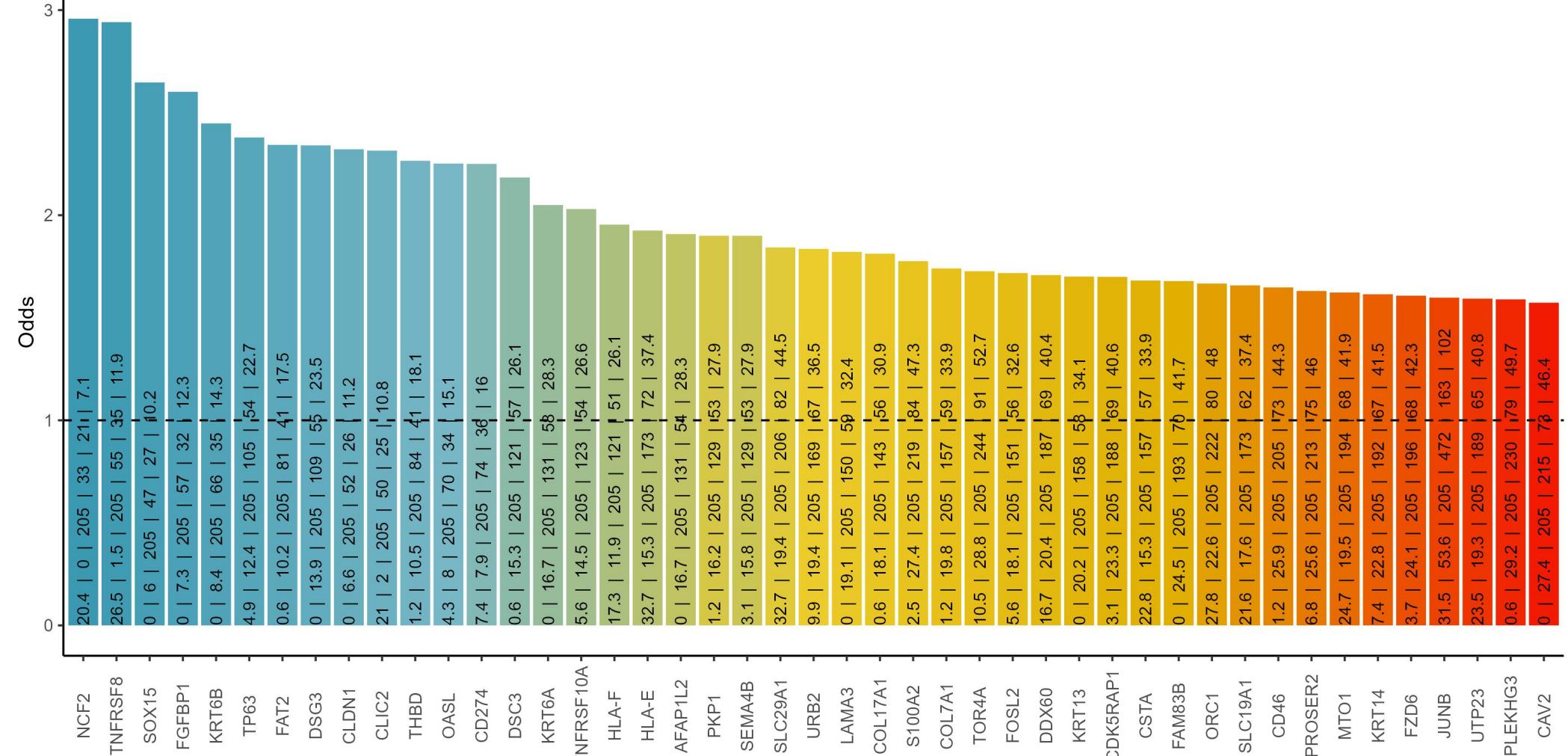
% of CGAS in blood cancers: 29.6 ; % of CGAS in solid cancers: 20

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

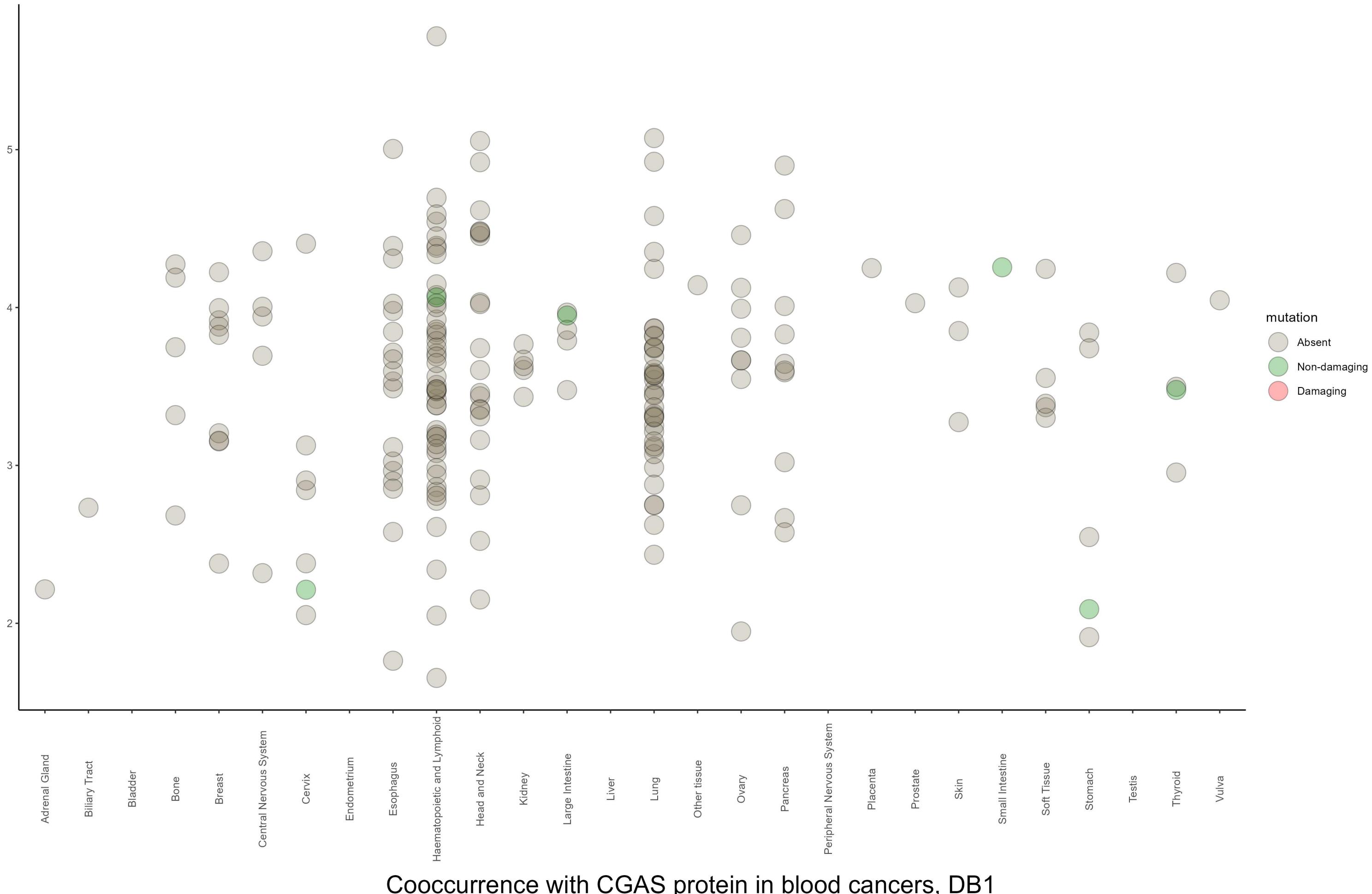
Negative cooccurrence



Positive cooccurrence

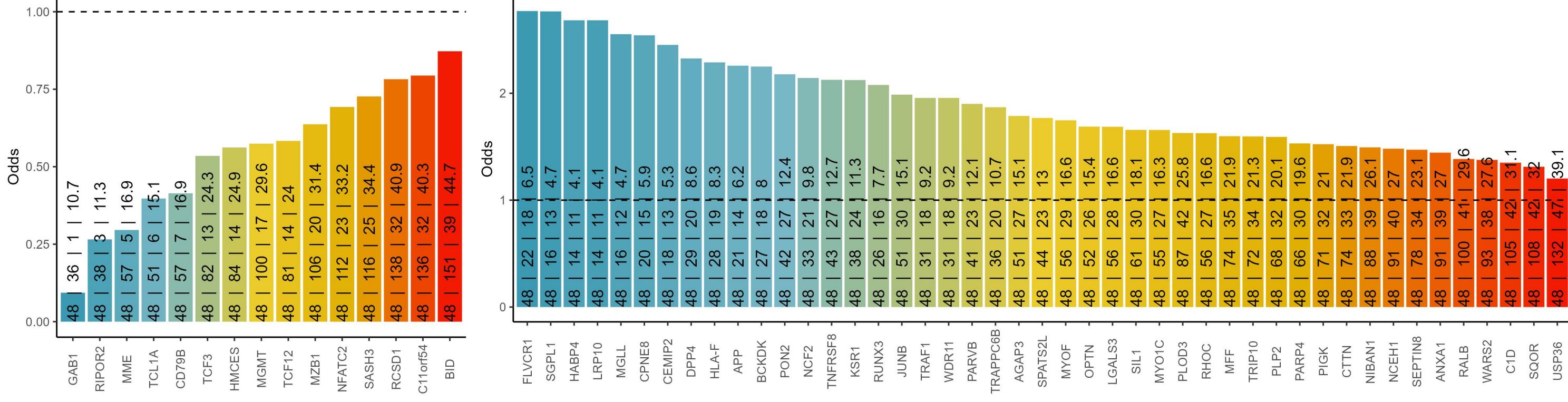


Amount of CGAS protein and mutation status by tissue, DB1



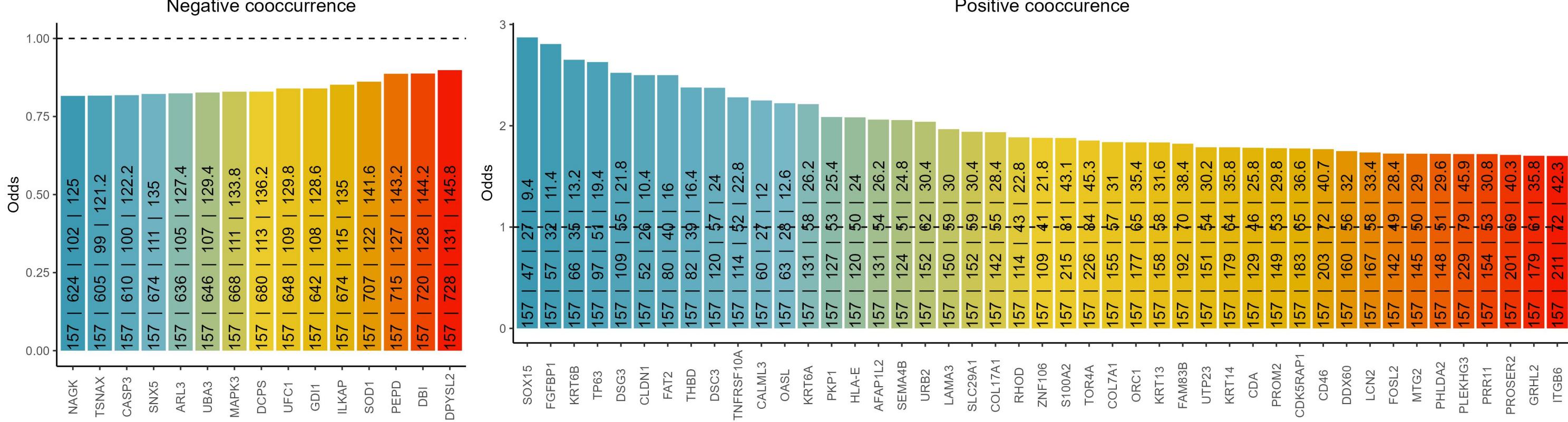
Cooccurrence with CGAS protein in blood cancers, DB1

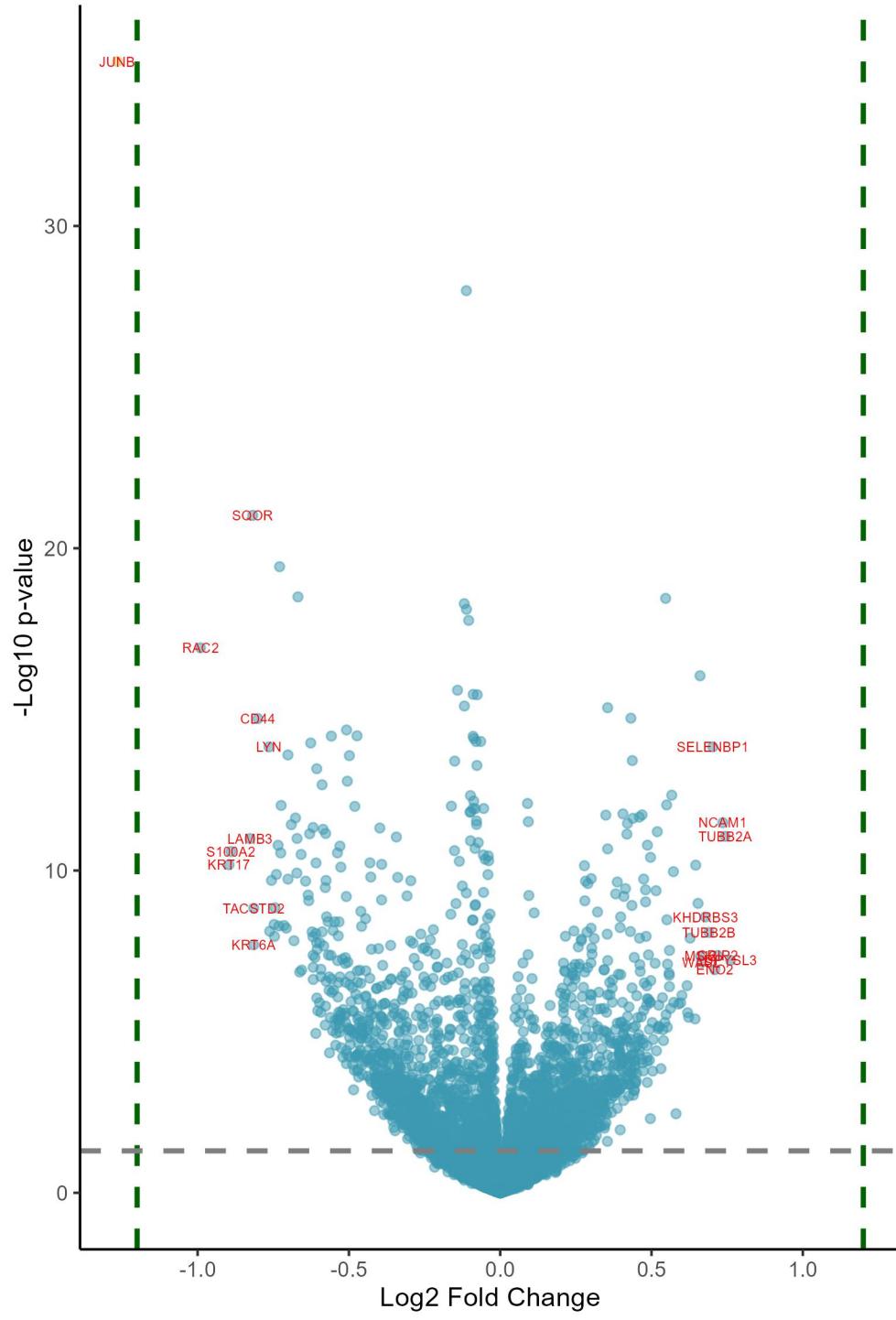
The text in the bars: incidence of CGAS | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with CGAS protein in solid cancers, DB1

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

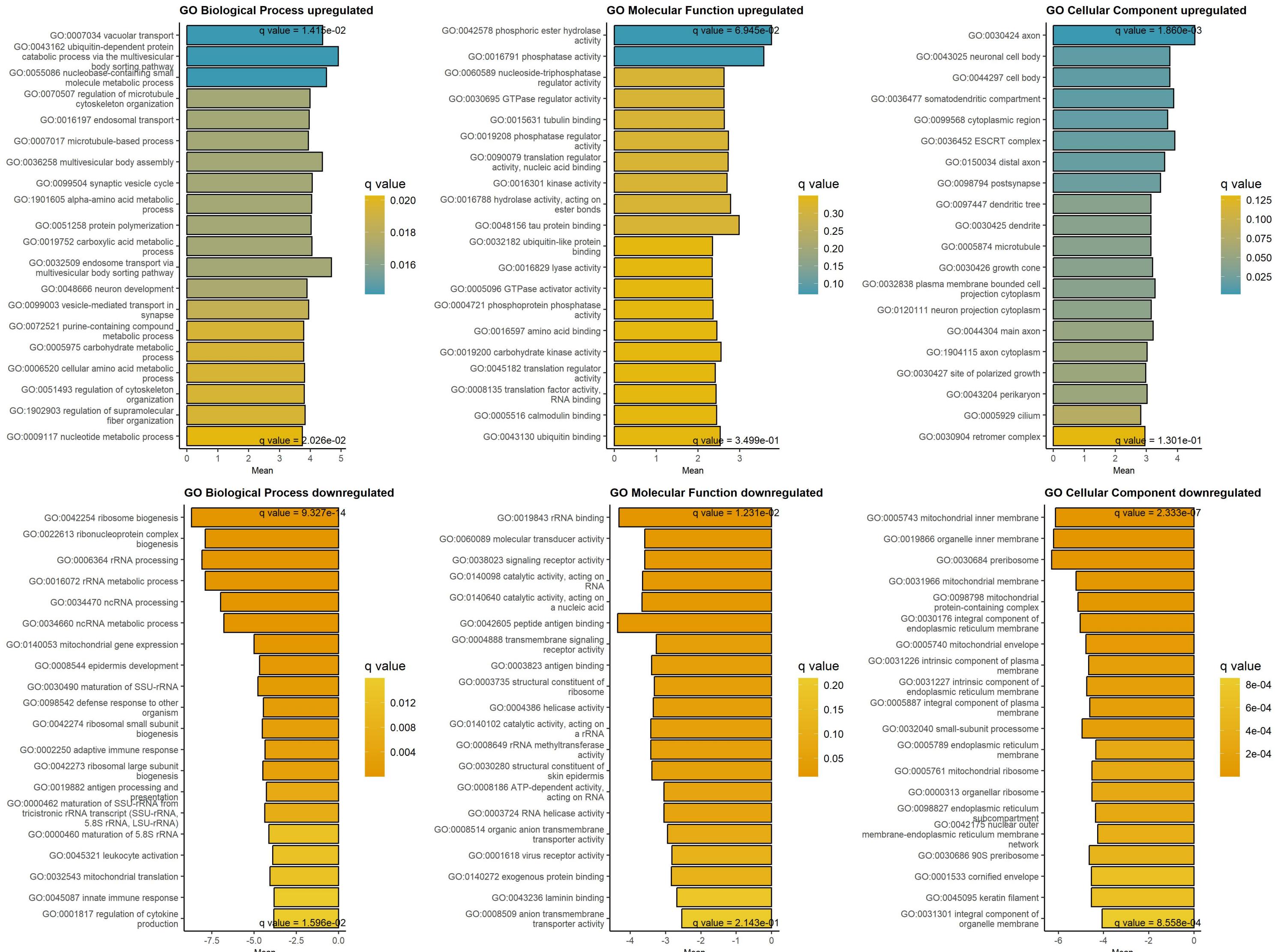


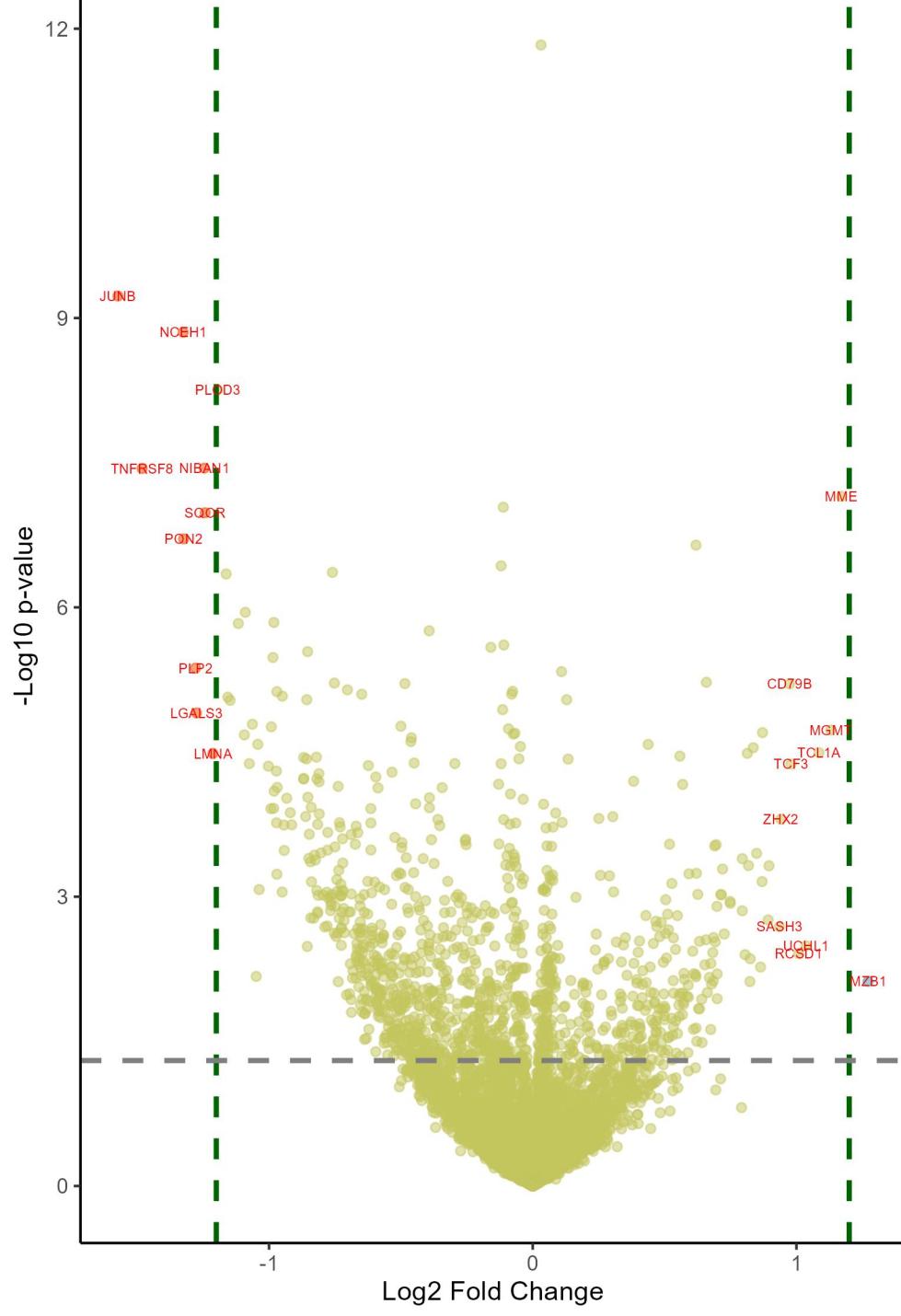


Downregulated at low/absent CGAS Upregulated at low/absent CGAS

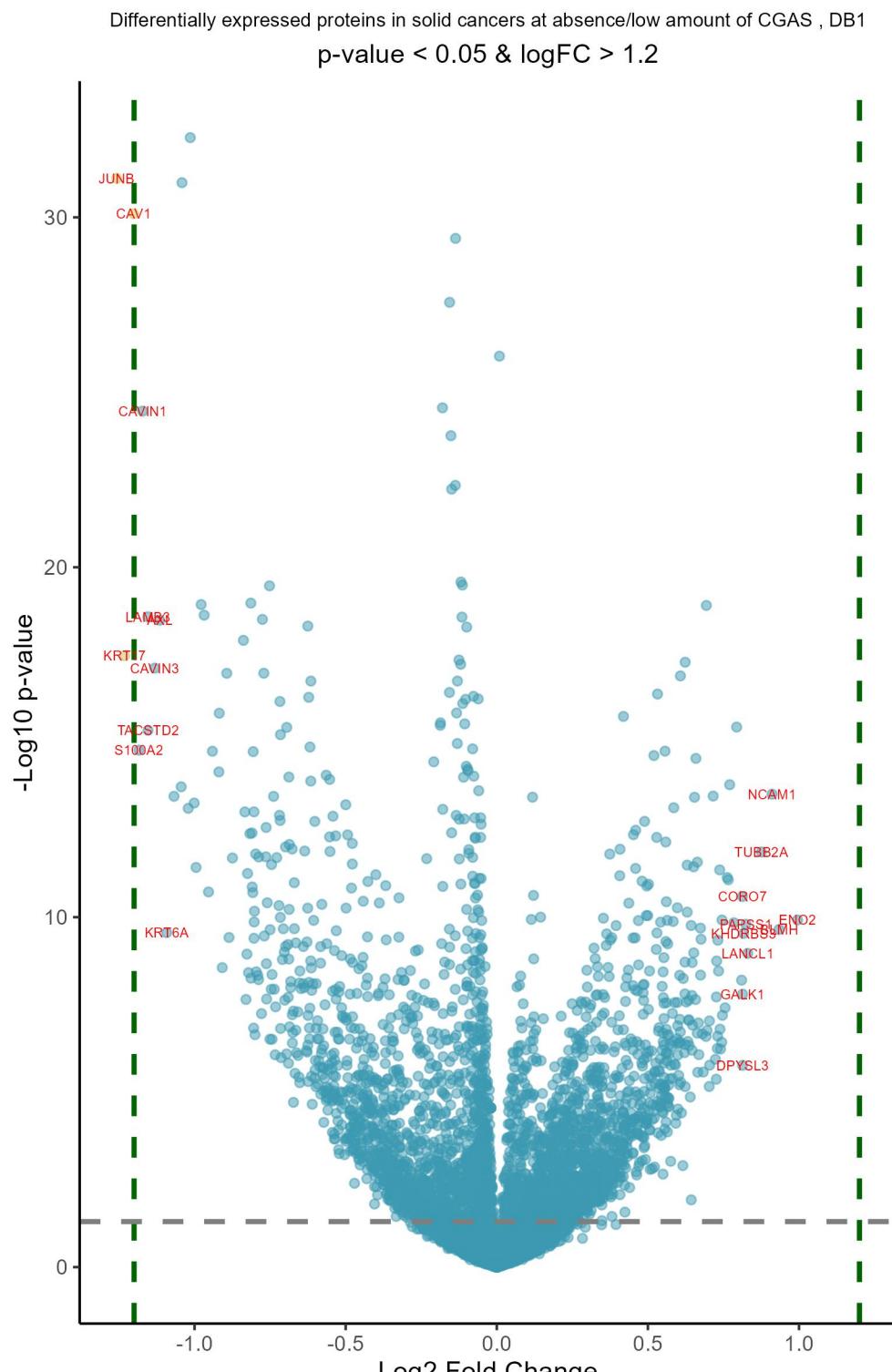
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.27	2.62e-32	JUNB	JunB proto-oncogene, AP-1 transcript	0.76	1.76e-06	DPYSL3	dihydropyrimidinase like 3
-0.99	7.44e-15	RAC2	Rac family small GTPase 2	0.74	8.27e-10	TUBB2A	tubulin beta 2A class IIa
-0.9	4.65e-09	KRT17	keratin 17	0.74	3.69e-10	NCAM1	neural cell adhesion molecule 1
-0.89	2.10e-09	S100A2	S100 calcium binding protein A2	0.72	1.30e-06	CRIP2	cysteine rich protein 2
-0.83	9.32e-10	LAMB3	laminin subunit beta 3	0.71	3.10e-06	ENO2	enolase 2
-0.82	1.58e-18	SQOR	sulfide quinone oxidoreductase	0.7	3.35e-12	SELENBP1	selenium binding protein 1
-0.81	6.90e-07	KRT6A	keratin 6A	0.69	3.24e-07	TUBB2B	tubulin beta 2B class IIb
-0.81	7.12e-08	TACSTD2	tumor associated calcium signal tra	0.68	1.26e-07	KHDRBS3	KH RNA binding domain containing, s
-0.8	6.74e-13	CD44	CD44 molecule (Indian blood group)	0.67	2.00e-06	WASL	WASP like actin nucleation promotin
-0.76	3.35e-12	LYN	LYN proto-oncogene, Src family tyro	0.66	1.36e-06	MSI2	musashi RNA binding protein 2
-0.76	3.06e-07	CAVIN3	caveolae associated protein 3	0.66	5.02e-14	MAP1A	microtubule associated protein 1A
-0.76	1.24e-08	CAV1	caveolin 1	0.65	5.27e-08	ABI2	abl interactor 2
-0.75	2.02e-07	F3	coagulation factor III, tissue fact	0.65	4.72e-09	FKBP7	FKBP prolyl isomerase 7
-0.75	4.09e-07	KRT5	keratin 5	0.64	5.64e-05	BLMH	bleomycin hydrolase
-0.74	6.94e-08	LAMC2	laminin subunit gamma 2	0.63	4.56e-07	PAPSS1	3'-phosphoadenosine 5'-phosphosulfa
-0.74	8.71e-09	ICAM1	intercellular adhesion molecule 1	0.62	5.11e-05	QPRT	quinolinate phosphoribosyltransfера
-0.73	1.42e-09	TAP2	transporter 2, ATP binding cassette	0.62	3.95e-05	TMEM263	transmembrane protein 263
-0.73	2.23e-07	AXL	AXL receptor tyrosine kinase	0.62	7.88e-06	LANCL1	LanC like 1
-0.73	4.97e-17	ADGRE5	adhesion G protein-coupled receptor	0.6	1.42e-05	TUBB4A	tubulin beta 4A class IVa
-0.73	2.26e-09	ISG15	ISG15 ubiquitin like modifier	0.6	2.18e-05	STXBP1	syntaxin binding protein 1
-0.72	1.48e-10	SP100	SP100 nuclear antigen	0.59	2.35e-05	DDAH2	dimethylarginine dimethylaminohydro
-0.71	2.17e-07	CDH3	cadherin 3	0.58	1.41e-02	ABCB6	ATP binding cassette subfamily B me
-0.71	2.54e-07	CAVIN1	caveolae associated protein 1	0.57	2.15e-05	ADPRS	ADP-ribosylserine hydrolase
-0.7	5.73e-12	TAP1	transporter 1, ATP binding cassette	0.57	7.28e-09	MAP2	microtubule associated protein 2
-0.7	1.15e-08	VAMP8	vesicle associated membrane protein	0.57	8.03e-11	APPL2	adaptor protein, phosphotyrosine in
-0.69	4.06e-10	PTPN2	protein tyrosine phosphatase non-re	0.56	3.07e-05	PDXDC1	pyridoxal dependent decarboxylase d
-0.68	5.35e-07	DSG3	desmoglein 3	0.56	9.62e-07	CDK5	cyclin dependent kinase 5
-0.68	2.83e-10	HLA-B	major histocompatibility complex, c	0.56	8.33e-06	HDHD2	haloacid dehalogenase like hydrolas
-0.67	7.98e-09	EXOSC3	exosome component 3	0.56	4.31e-06	GMPPB	GDP-mannose pyrophosphorylase B

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



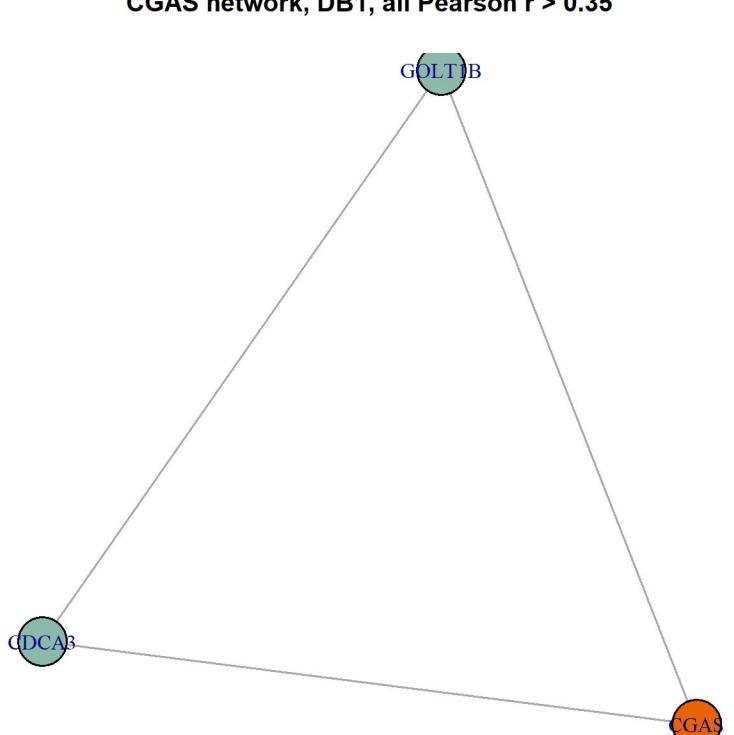


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.57	1.31e-06	JUNB	JunB proto-oncogene, AP-1 transcript	1.27	6.73e-02	MZB1	marginal zone B and B1 cell specific
-1.48	3.45e-05	TNFRSF8	TNF receptor superfamily member 8	1.17	5.89e-05	MME	membrane metalloendopeptidase
-1.33	2.33e-06	NCEH1	neutral cholesterol ester hydrolase	1.13	2.70e-03	MGMT	O-6-methylguanine-DNA methyltransferase
-1.32	1.18e-04	PON2	paraoxonase 2	1.09	3.69e-03	TCL1A	TCL1 family AKT coactivator A
-1.28	1.18e-03	PLP2	proteolipid protein 2	1.04	5.79e-02	UCHL1	ubiquitin C-terminal hydrolase L1
-1.28	2.02e-03	LGALS3	galectin 3	1.01	6.51e-02	RCSD1	RCSD domain containing 1
-1.25	3.45e-05	NIBAN1	niban apoptosis regulator 1	0.98	3.99e-03	TCF3	transcription factor 3
-1.24	6.95e-05	SQOR	sulfide quinone oxidoreductase	0.97	1.43e-03	CD79B	CD79b molecule
-1.21	3.69e-03	LMNA	lamin A/C	0.94	9.69e-03	ZHX2	zinc fingers and homeoboxes 2
-1.19	7.37e-06	PLOD3	procollagen-lysine,2-oxoglutarate 5	0.94	4.57e-02	SASH3	SAM and SH3 domain containing 3
-1.16	2.00e-04	TRIP10	thyroid hormone receptor interactor	0.9	1.93e-02	ARHGAP25	Rho GTPase activating protein 25
-1.16	1.57e-03	ANXA1	annexin A1	0.89	4.08e-02	CD38	CD38 molecule
-1.15	1.57e-03	CTTN	cortactin	0.87	2.79e-03	TCF12	transcription factor 12
-1.12	5.43e-04	MFF	mitochondrial fission factor	0.87	2.44e-02	C11orf54	chromosome 11 open reading frame 54
-1.09	2.79e-03	MYOF	myoferlin	0.86	6.73e-02	JCHAIN	joining chain of multimeric IgA and IgM
-1.09	4.68e-04	RALB	RAS like proto-oncogene B	0.85	1.59e-02	PAX5	paired box 5
-1.07	3.99e-03	RHOC	ras homolog family member C	0.84	3.39e-03	LEF1	lymphoid enhancer binding factor 1
-1.06	2.58e-03	DPP4	dipeptidyl peptidase 4	0.82	6.73e-02	CDKN2C	cyclin dependent kinase inhibitor 2
-1.05	6.73e-02	LGALS1	galectin 1	0.82	6.73e-02	ATP2A3	ATPase sarcoplasmic/endoplasmic reticulum Ca2+ channel 2A
-1.04	3.25e-03	KSR1	kinase suppressor of ras 1	0.82	1.93e-02	NFATC2	nuclear factor of activated T cells
-1.04	2.75e-02	S100A6	S100 calcium binding protein A6	0.81	3.69e-03	HMCES	5-hydroxymethylcytosine binding, ES
-1	4.10e-03	NCF2	neutrophil cytosolic factor 2	0.81	6.61e-02	MSI2	musashi RNA binding protein 2
-0.99	8.13e-03	CAPN2	calpain 2	0.79	3.61e-02	PLEKHF2	pleckstrin homology and FYVE domain containing 2
-0.99	2.62e-03	SIL1	SIL1 nucleotide exchange factor	0.79	1.71e-02	DCAF16	DDB1 and CUL4 associated factor 16
-0.98	9.57e-04	C1D	C1D nuclear receptor corepressor	0.79	3.85e-01	PHGDH	phosphoglycerate dehydrogenase
-0.98	8.13e-03	TYMP	thymidine phosphorylase	0.75	3.22e-02	SYNE2	spectrin repeat containing nuclear envelope protein
-0.98	5.43e-04	FLVCR1	FLVCR heme transporter 1	0.75	3.15e-02	UBE2J1	ubiquitin conjugating enzyme E2 J1
-0.98	6.08e-03	STOM	stomatin	0.73	4.94e-02	HIP1R	huntingtin interacting protein 1 repressor
-0.97	4.53e-03	IKBIP	IKBKB interacting protein	0.72	2.04e-02	ANKRD13A	ankyrin repeat domain 13A

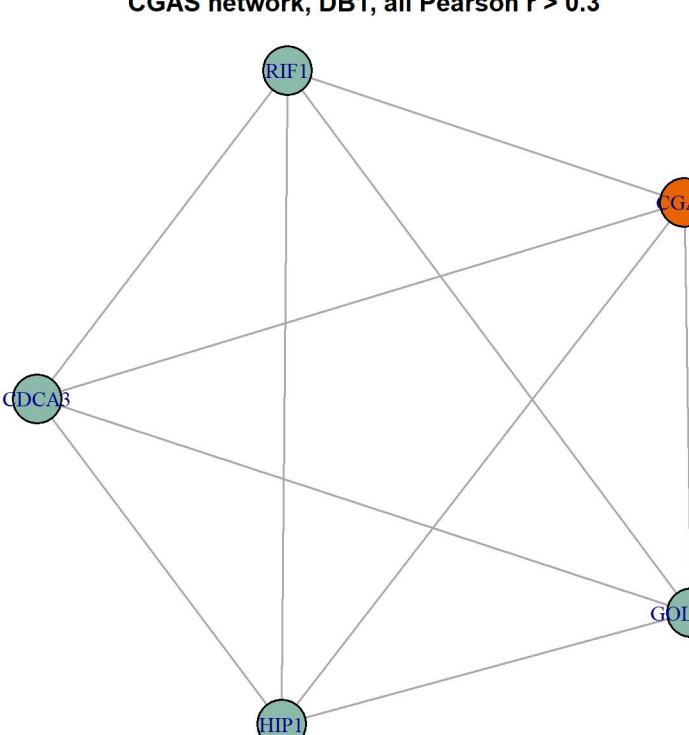


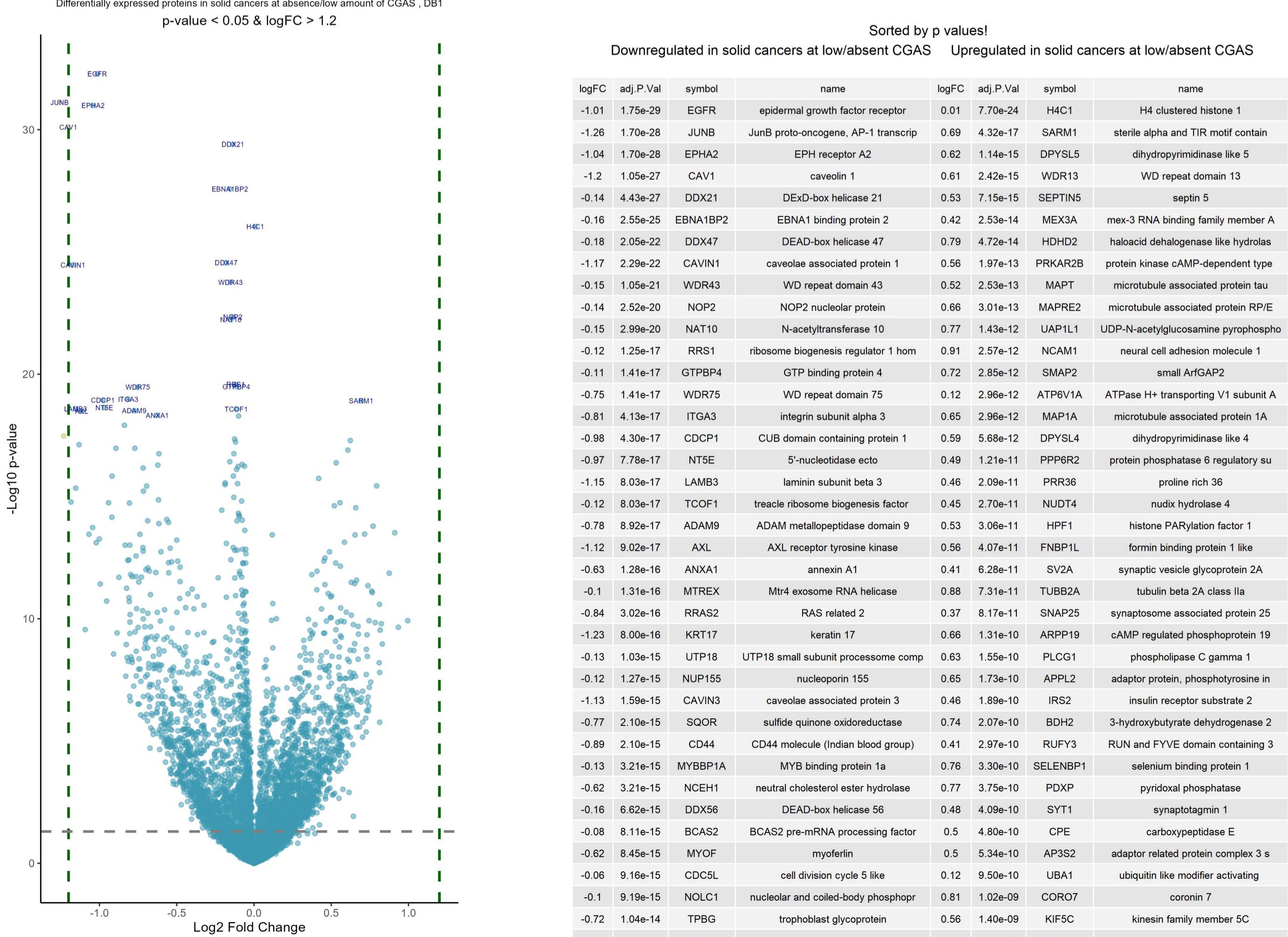
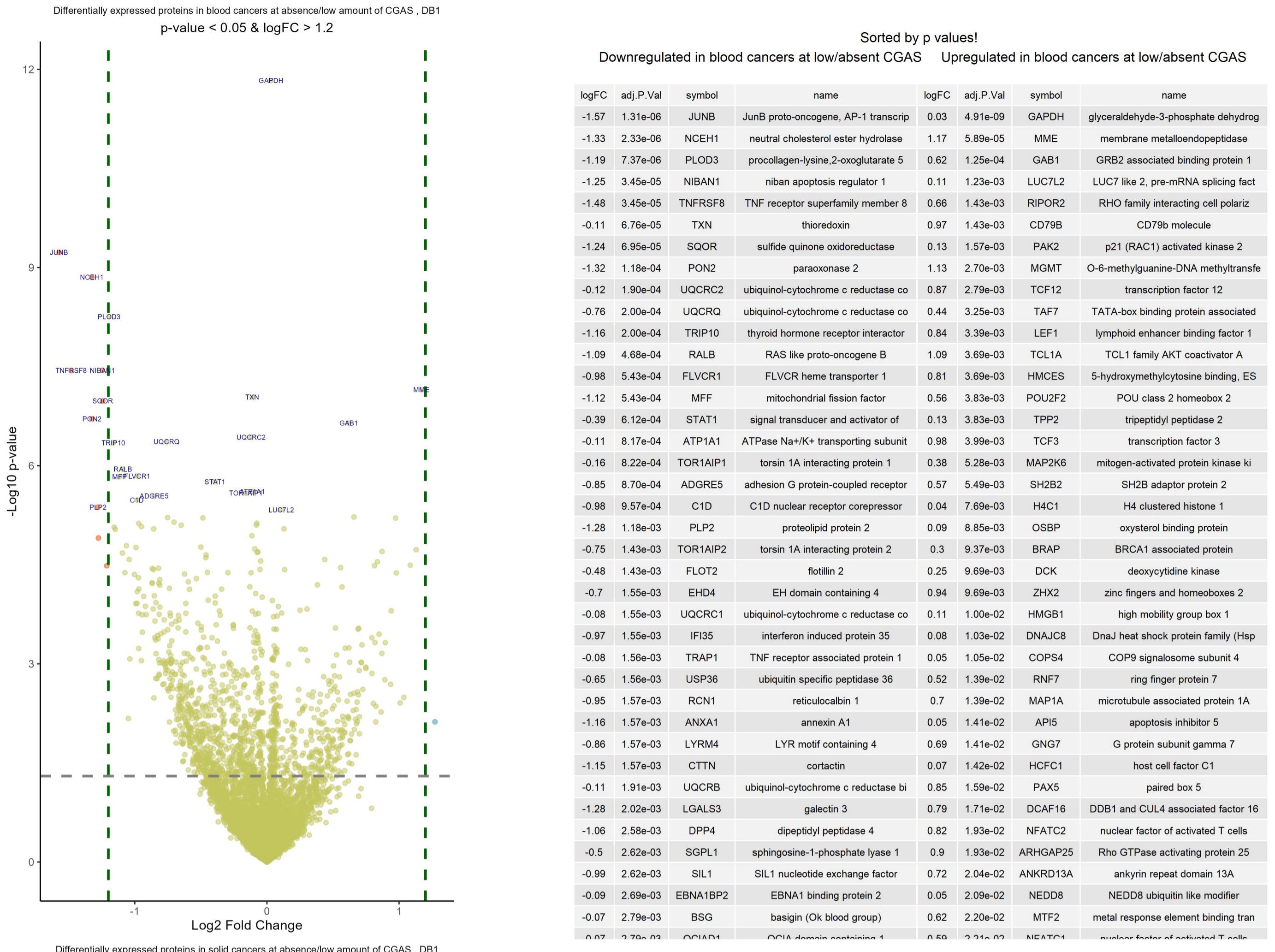
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.26	1.70e-28	JUNB	JunB proto-oncogene, AP-1 transcript	1	4.10e-09	ENO2	enolase 2
-1.23	8.00e-16	KRT17	keratin 17	0.93	7.04e-09	BLMH	bleomycin hydrolase
-1.2	1.05e-27	CAV1	caveolin 1	0.91	2.57e-12	NCAM1	neural cell adhesion molecule 1
-1.18	1.90e-13	S100A2	S100 calcium binding protein A2	0.88	7.31e-11	TUBB2A	tubulin beta 2A class IIa
-1.17	2.29e-22	CAVIN1	caveolae associated protein 1	0.83	2.76e-08	LANCL1	LanC like 1
-1.15	8.03e-17	LAMB3	laminin subunit beta 3	0.82	5.19e-09	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate sulphatase
-1.15	5.62e-14	TACSTD2	tumor associated calcium signal tra	0.82	8.91e-09	KHDRBS3	KH RNA binding domain containing, s
-1.13	1.59e-15	CAVIN3	caveolae associated protein 3	0.81	2.86e-07	GALK1	galactokinase 1
-1.12	9.02e-17	AXL	AXL receptor tyrosine kinase	0.81	1.59e-05	DPYSL3	dihydropyrimidinase like 3
-1.09	8.58e-09	KRT6A	keratin 6A	0.81	1.02e-09	CORO7	coronin 7
-1.07	2.85e-12	F3	coagulation factor III, tissue fact	0.81	1.29e-07	ADPRS	ADP-ribosylserine hydrolase
-1.04	1.62e-12	LAMC2	laminin subunit gamma 2	0.79	4.72e-14	HDHD2	haloacid dehalogenase like hydrolase
-1.04	1.70e-28	EPHA2	EPH receptor A2	0.78	4.72e-09	COMM2	COMM domain containing 2
-1.02	5.86e-12	CDH3	cadherin 3	0.77	1.43e-12	UAP1L1	UDP-N-acetylglucosamine pyrophosphorylase
-1.01	1.75e-29	EGFR	epidermal growth factor receptor	0.77	3.75e-10	PDXP	pyridoxal phosphatase
-1	4.28e-12	RAC2	Rac family small GTPase 2	0.76	3.30e-10	SELENBP1	selenophosphate binding protein 1
-0.99	1.78e-10	KRT5	keratin 5	0.76	6.24e-07	TUBB2B	tubulin beta 2B class IIb
-0.98	4.30e-17	CDCP1	CUB domain containing protein 1	0.75	9.68e-07	CAMK2D	calcium/calmodulin dependent protein kinase II
-0.97	7.78e-17	NT5E	5'-nucleotidase ecto	0.75	4.10e-09	CDK5	cyclin dependent kinase 5
-0.95	7.69e-10	GPRC5A	G protein-coupled receptor class C	0.74	4.35e-06	PDXDC1	pyridoxal dependent decarboxylase d
-0.94	1.97e-13	ZNF185	zinc finger protein 185 with LIM do	0.74	6.39e-06	TMEM263	transmembrane protein 263
-0.92	6.80e-13	ITGB4	integrin subunit beta 4	0.74	2.12e-06	CZIB	CXXC motif containing zinc binding protein
-0.92	2.09e-14	LYN	LYN proto-oncogene, Src family tyro	0.74	2.07e-10	BDH2	3-hydroxybutyrate dehydrogenase 2
-0.91	6.34e-08	DSG3	desmoglein 3	0.73	7.64e-08	GMPPB	GDP-mannose pyrophosphorylase B
-0.89	2.10e-15	CD44	CD44 molecule (Indian blood group)	0.73	1.29e-08	FKBP7	FKBP prolyl isomerase 7
-0.89	1.12e-08	SERPINB5	serpin family B member 5	0.73	3.14e-06	SH3BGRL	SH3 domain binding glutamate rich protein
-0.87	1.02e-10	PKP3	plakophilin 3	0.73	6.19e-06	MAGED2	MAGE family member D2
-0.84	3.02e-16	RRAS2	RAS related 2	0.73	4.32e-08	KLC4	kinesin light chain 4
-0.83	7.17e-12	HMGA2	high mobility group AT-hook 2	0.73	3.34e-07	TUBB4A	tubulin beta 4A class IVa

CGAS network, DB1, all Pearson r > 0.35

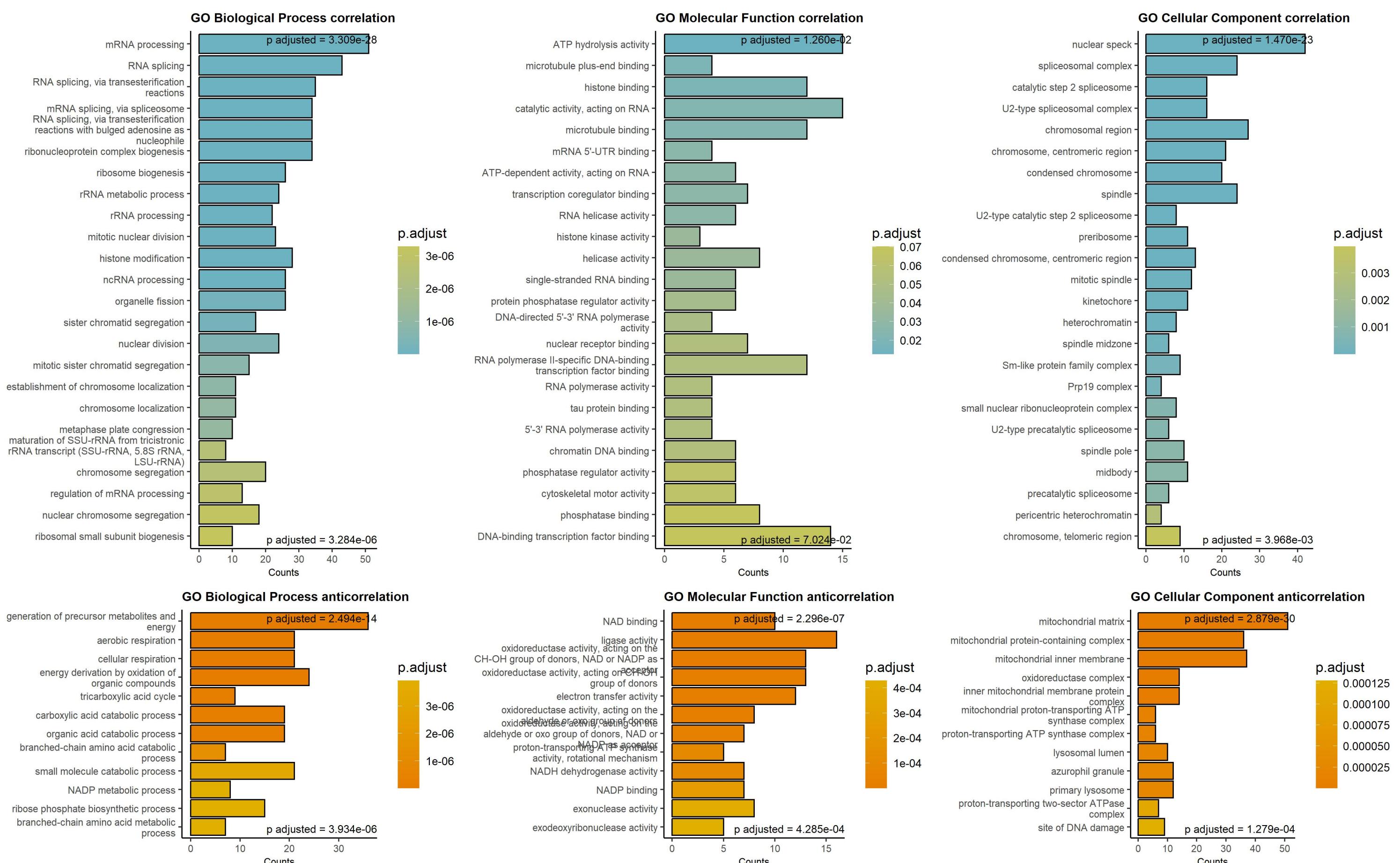


CGAS network, DB1, all Pearson r > 0.3

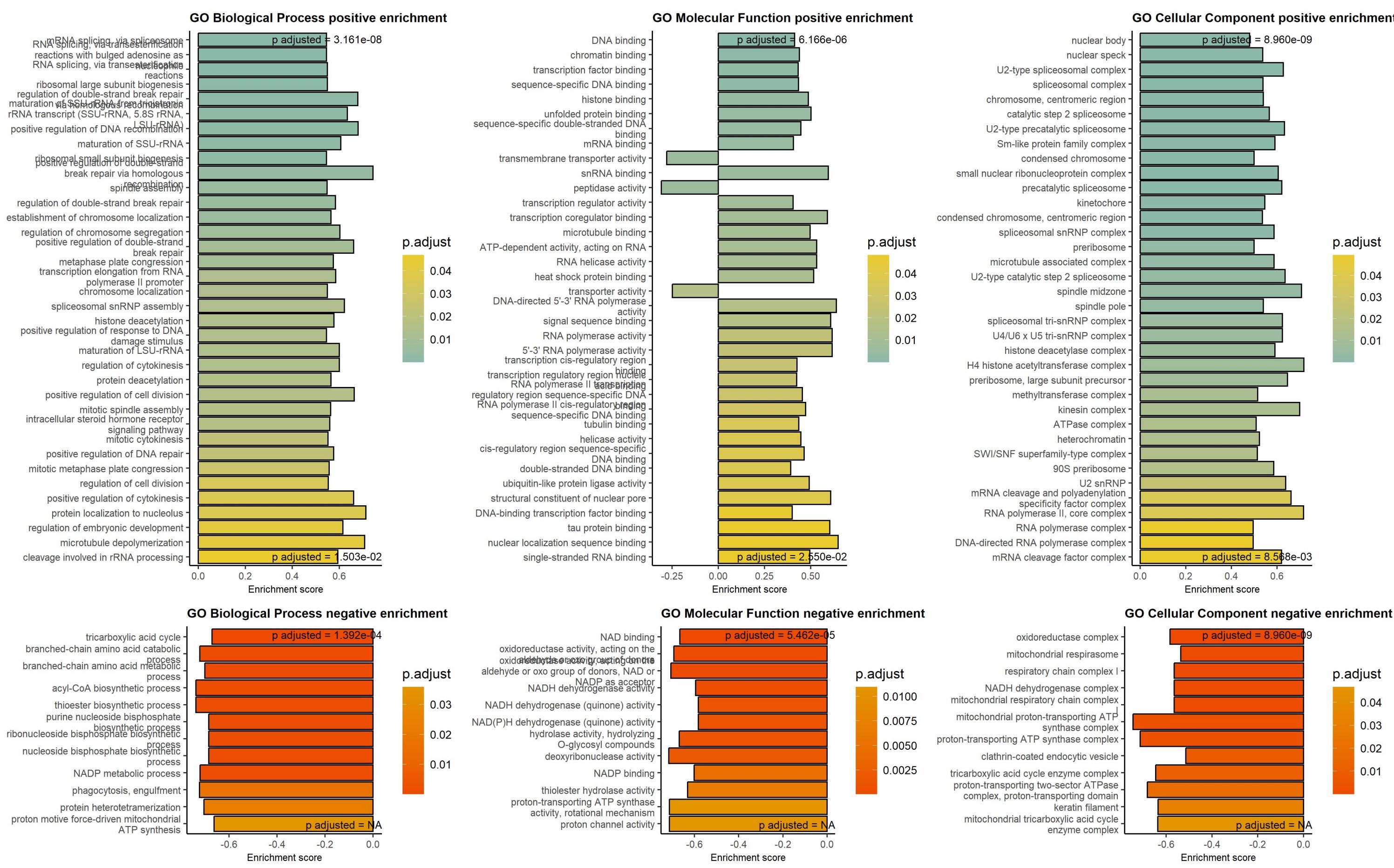




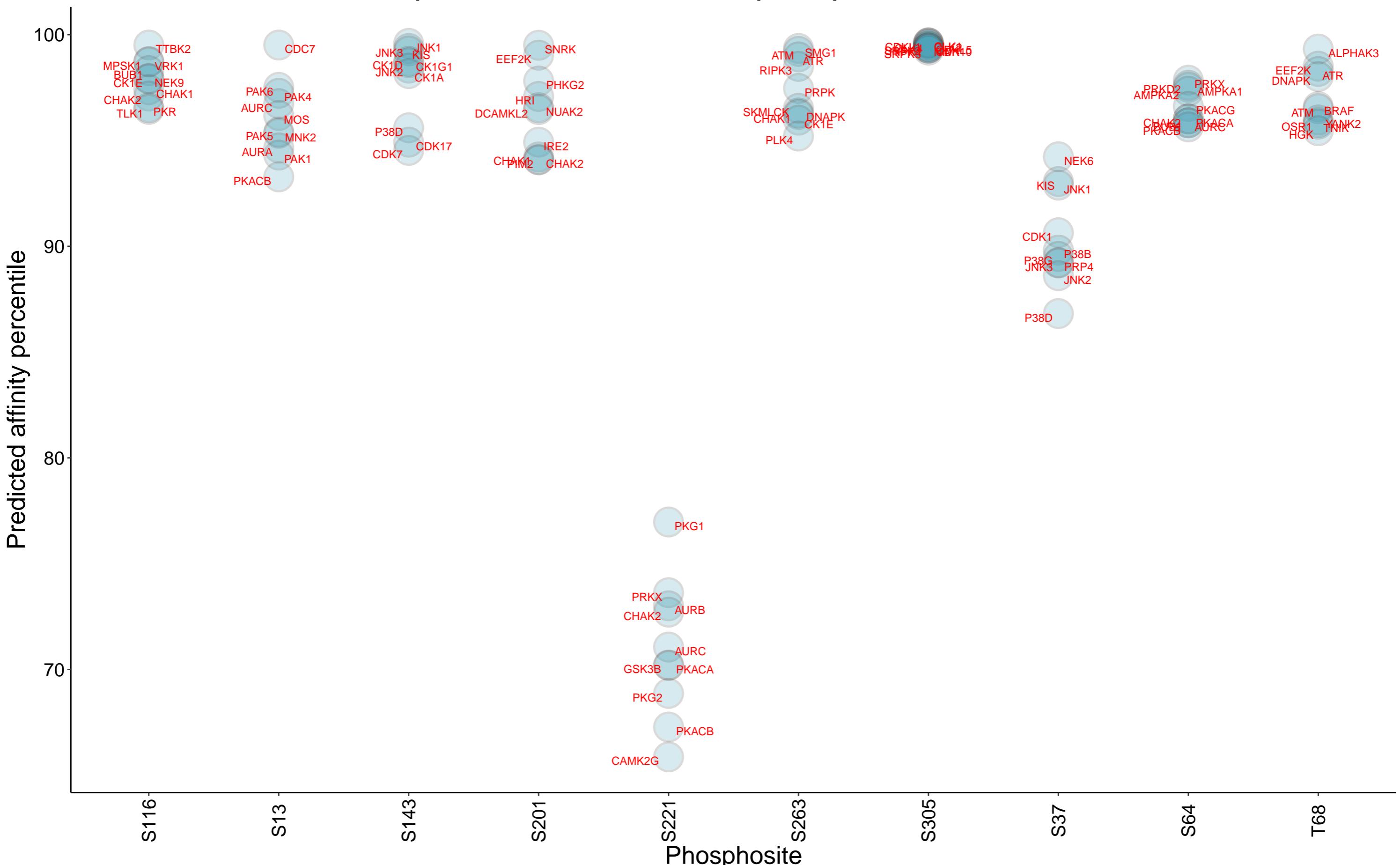
Top 250 correlation coefficients overrepresentation, CGAS protein, DB1



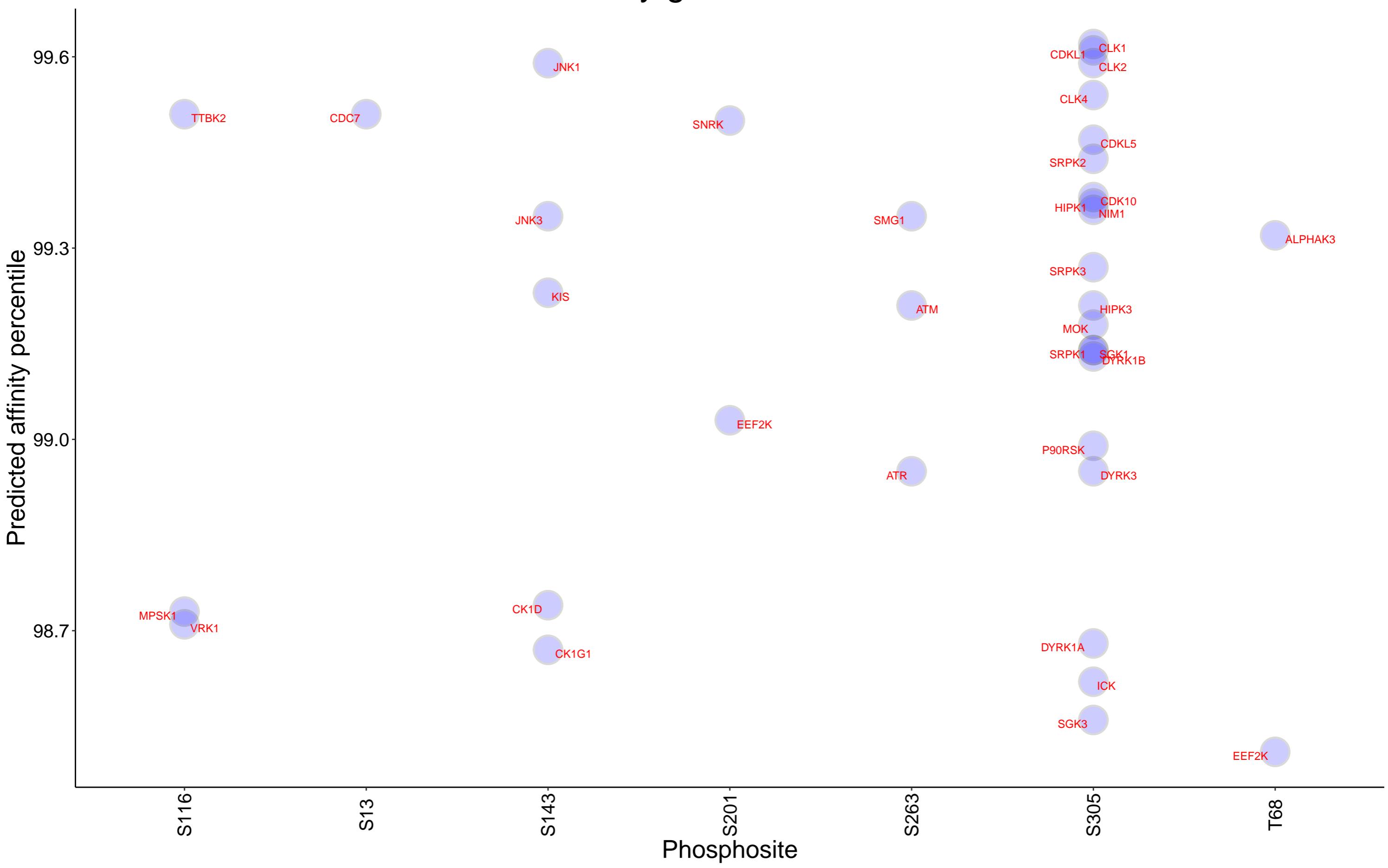
Gene Set Enrichment analysis on protein correlation coefficients, CGAS protein, DB1



Top 10 kinases for each phosphosite in CGAS



Kinases with affinity greater than 98.5% to CGAS



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

Beware of false positives in tissues with small number of samples



Cervix

Esophagus

Head and Neck