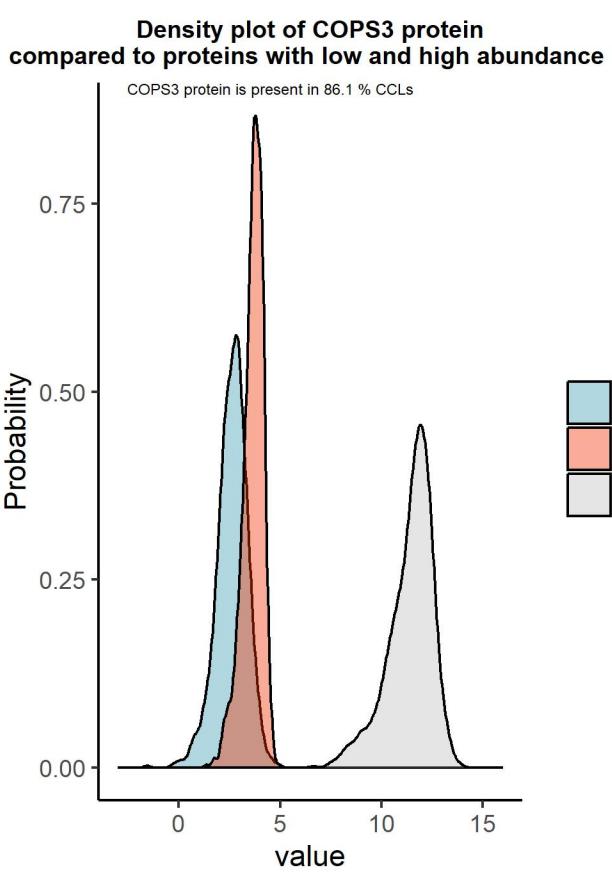
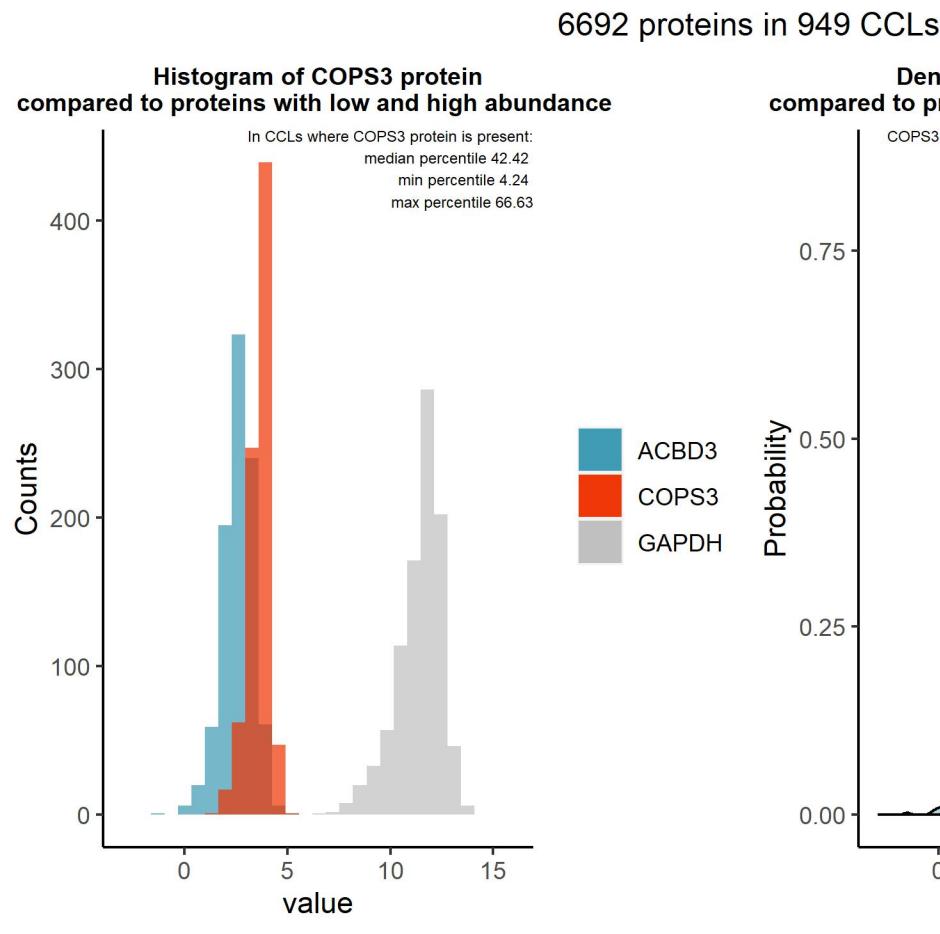


COPS3

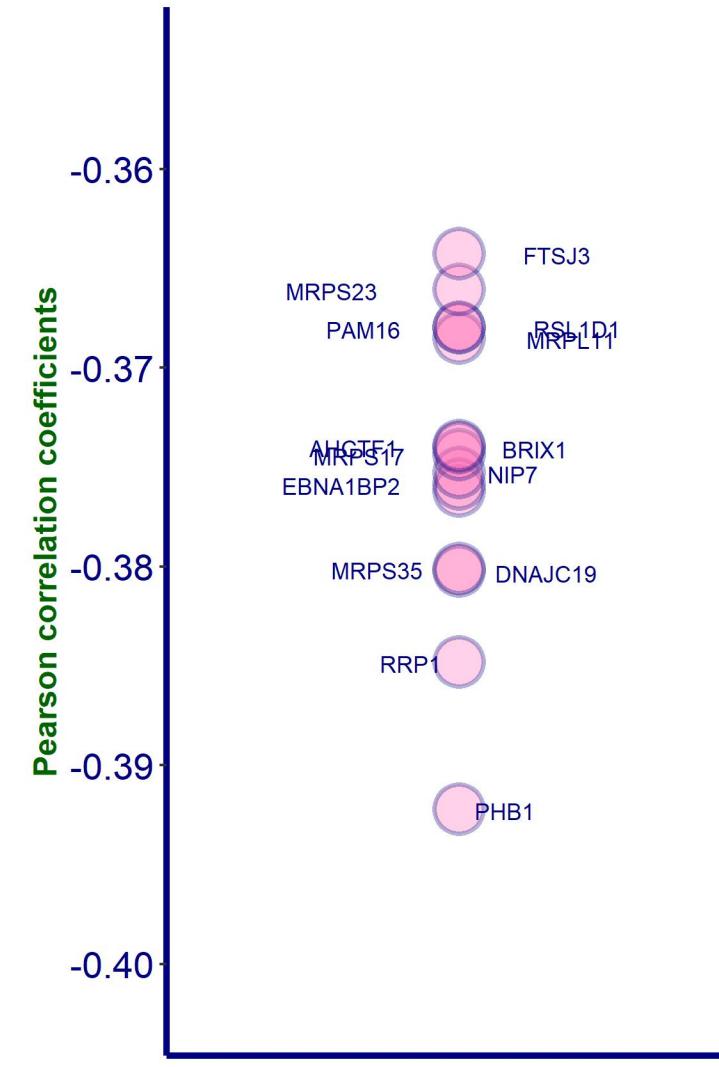
Protein name: CSN3 ; UNIPROT: Q9UNS2 ; Gene name: COP9 signalosome subunit 3

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

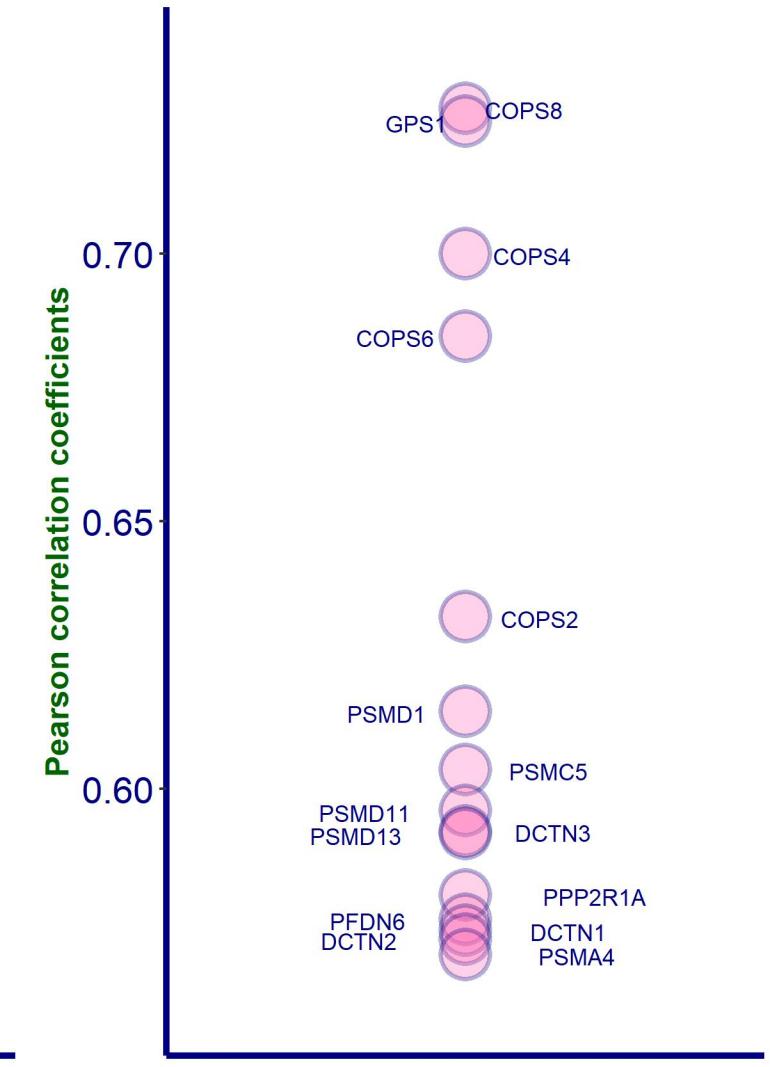
Sanger Institute Protein Database 1 (DB1), protein presence is certain



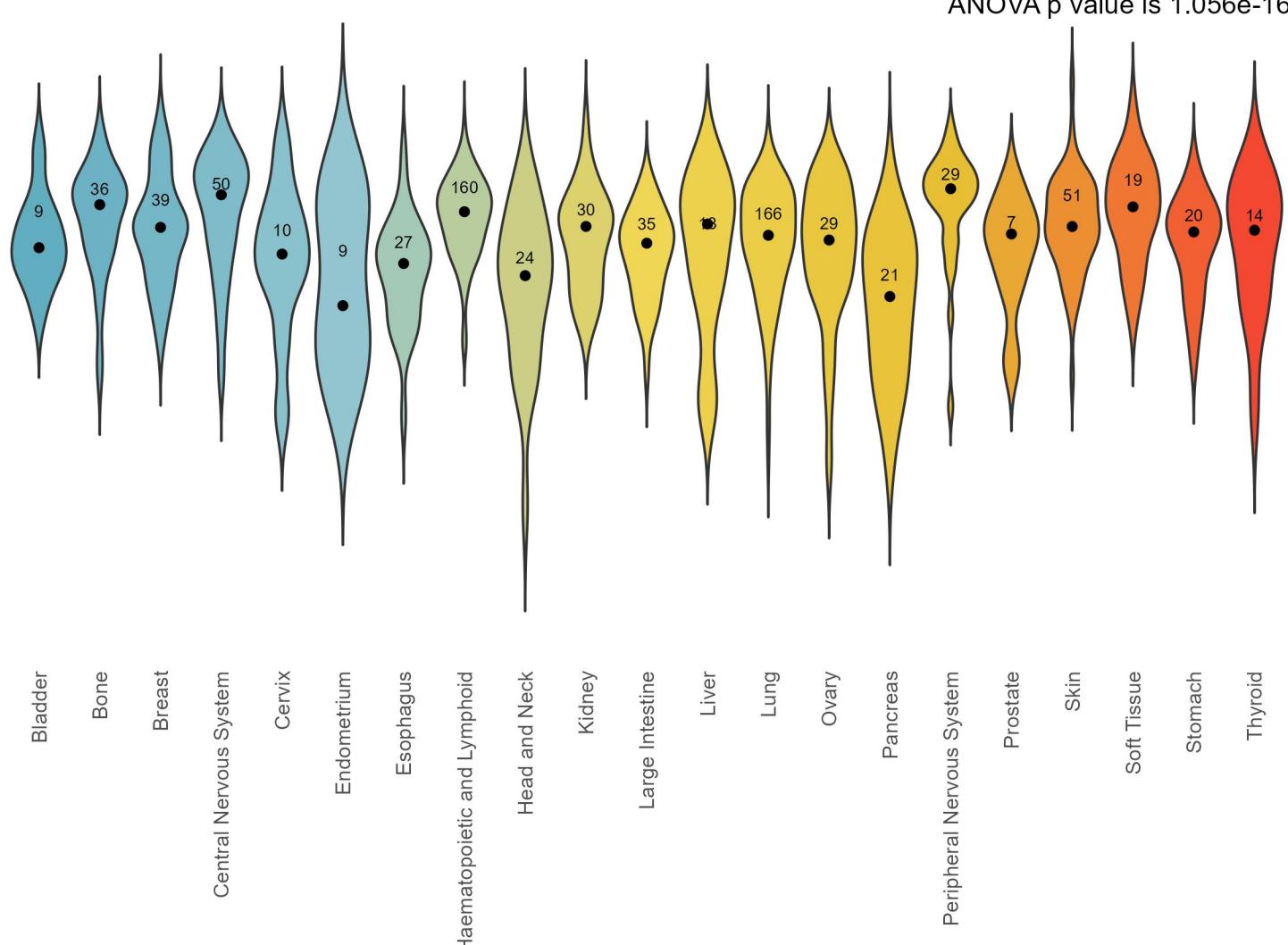
Top negative correlations of COPS3 protein, DB1



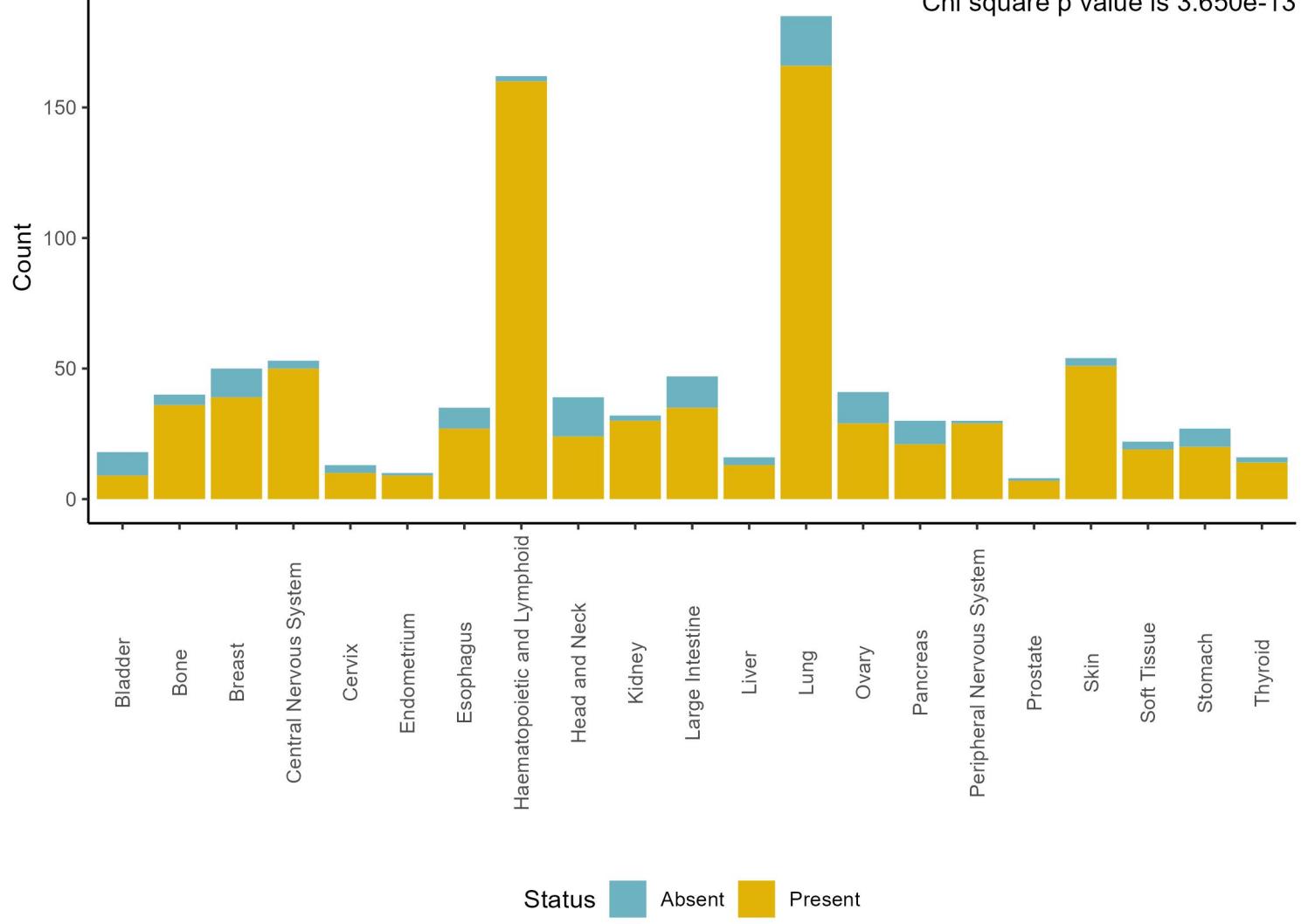
Top positive correlations of COPS3 protein, DB1



Amount of COPS3 protein, number of CCLs where it is present by tissue, DB1



Present and absent COPS3 protein counts by tissue, DB1

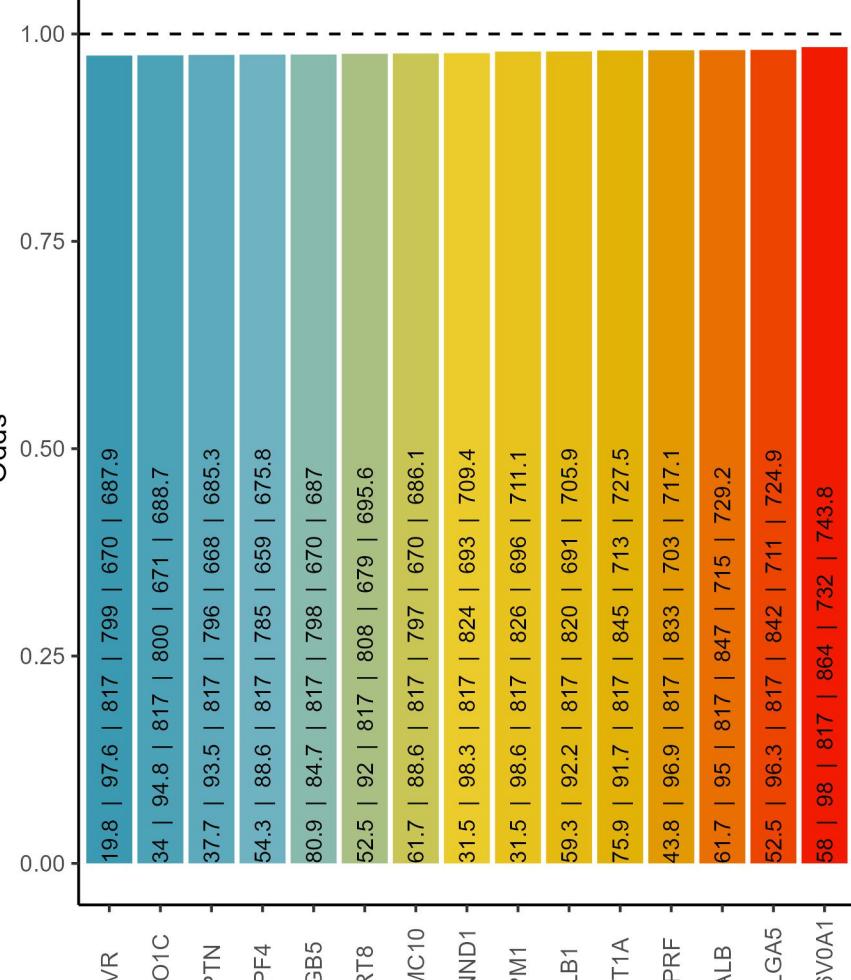


Cooccurrence with COPS3 protein, DB1

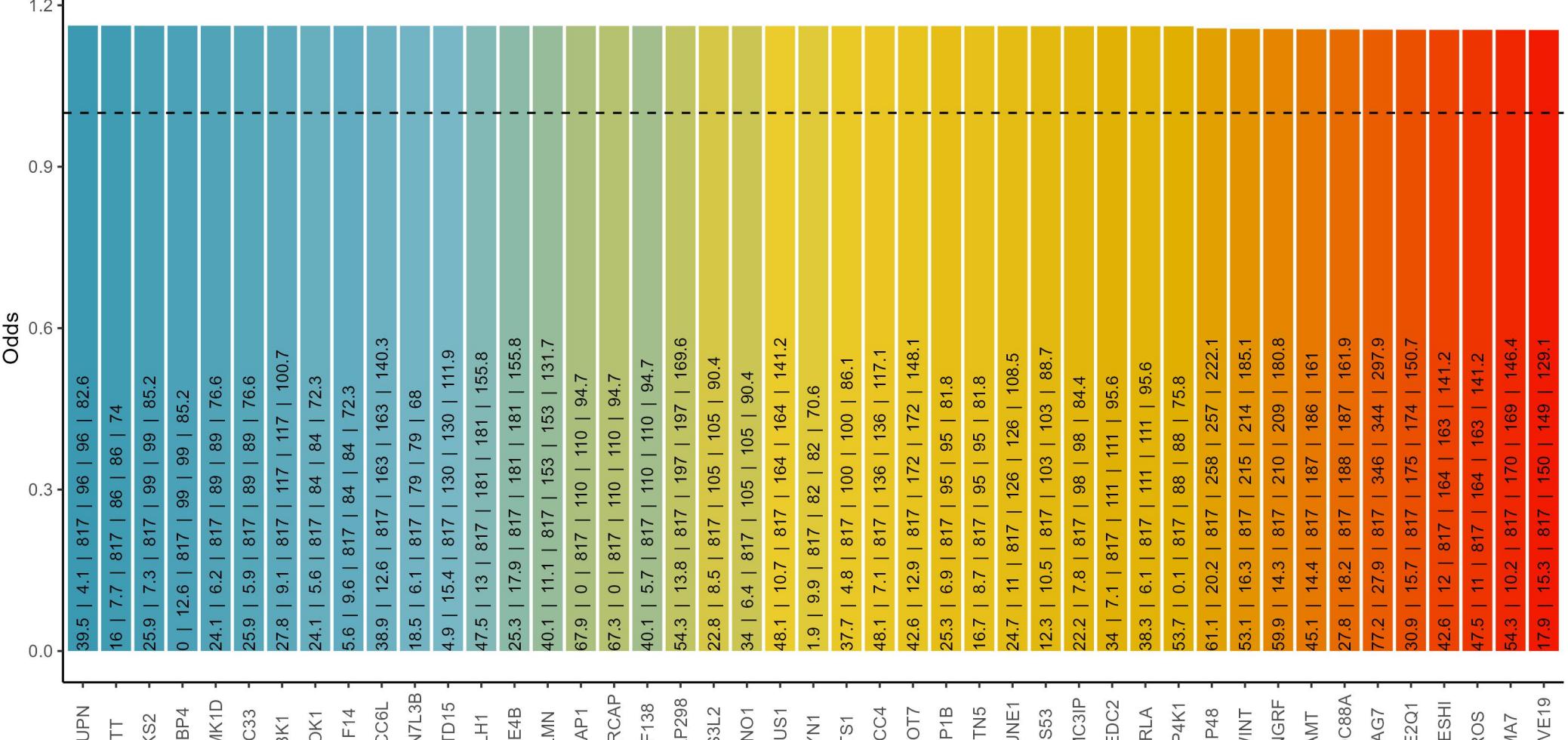
% of COPS3 in blood cancers: 98.8 ; % of COPS3 in solid cancers: 83.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of COPS3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

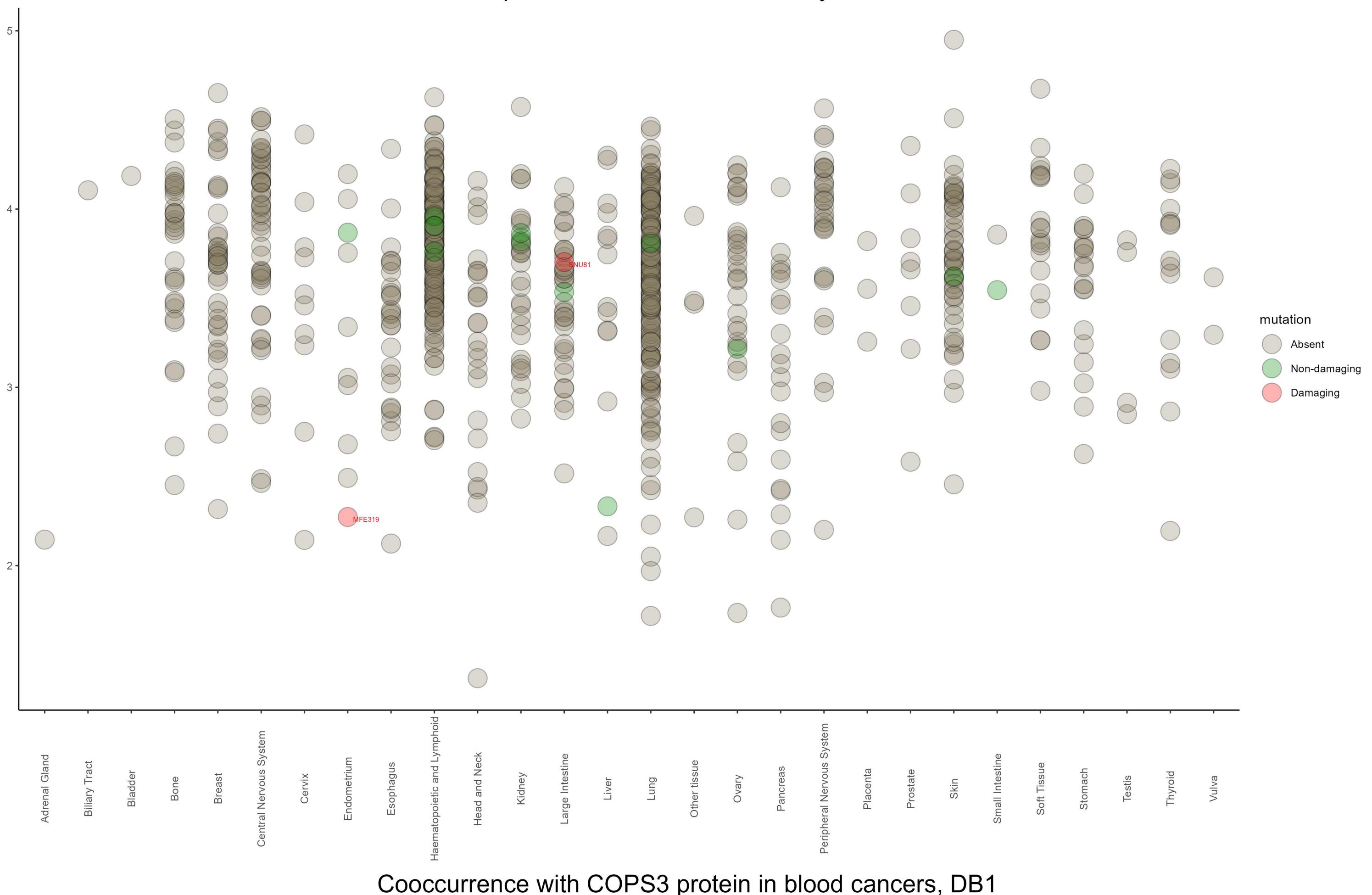
Negative cooccurrence



Positive cooccurrence



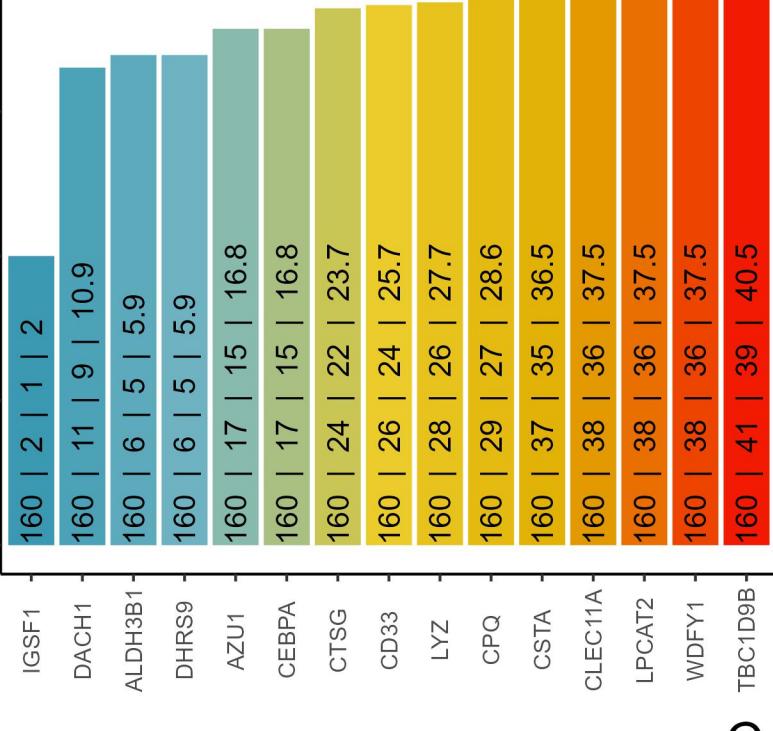
Amount of COPS3 protein and mutation status by tissue, DB1



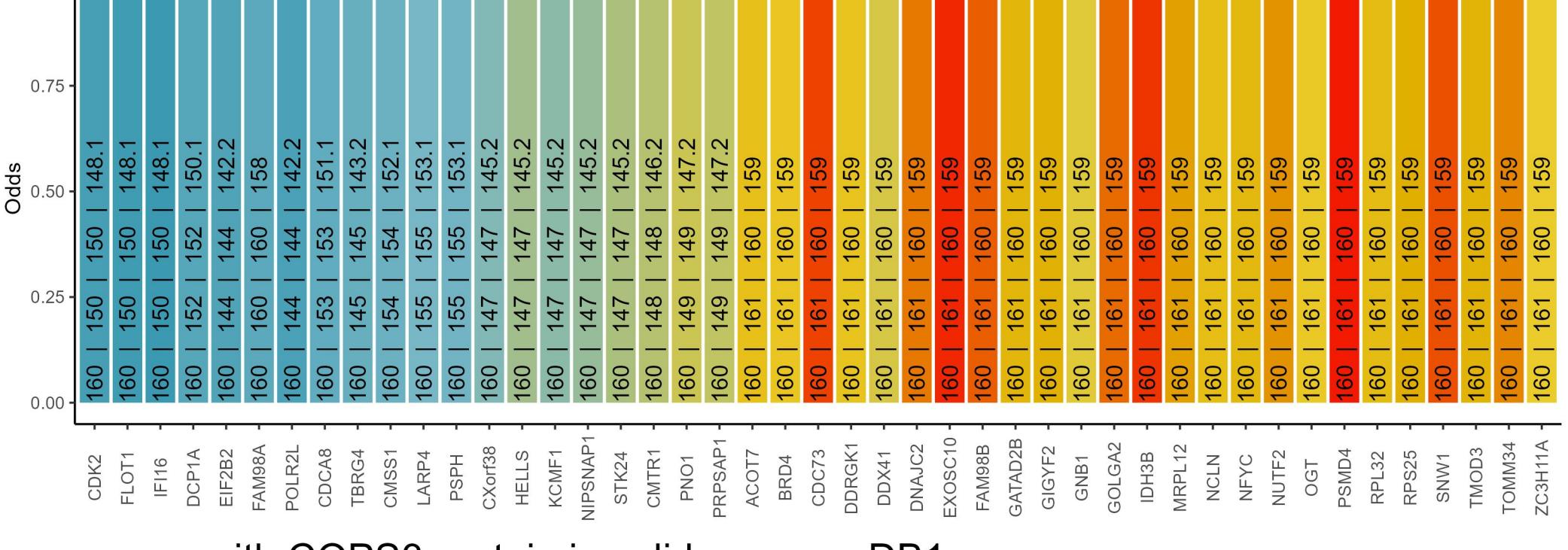
Cooccurrence with COPS3 protein in blood cancers, DB1

The text in the bars: incidence of COPS3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



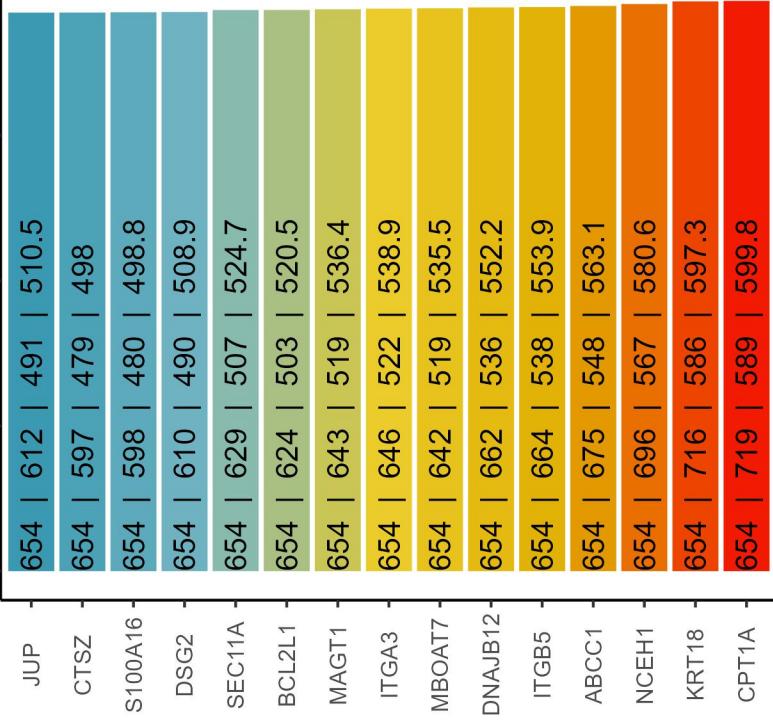
Positive cooccurrence



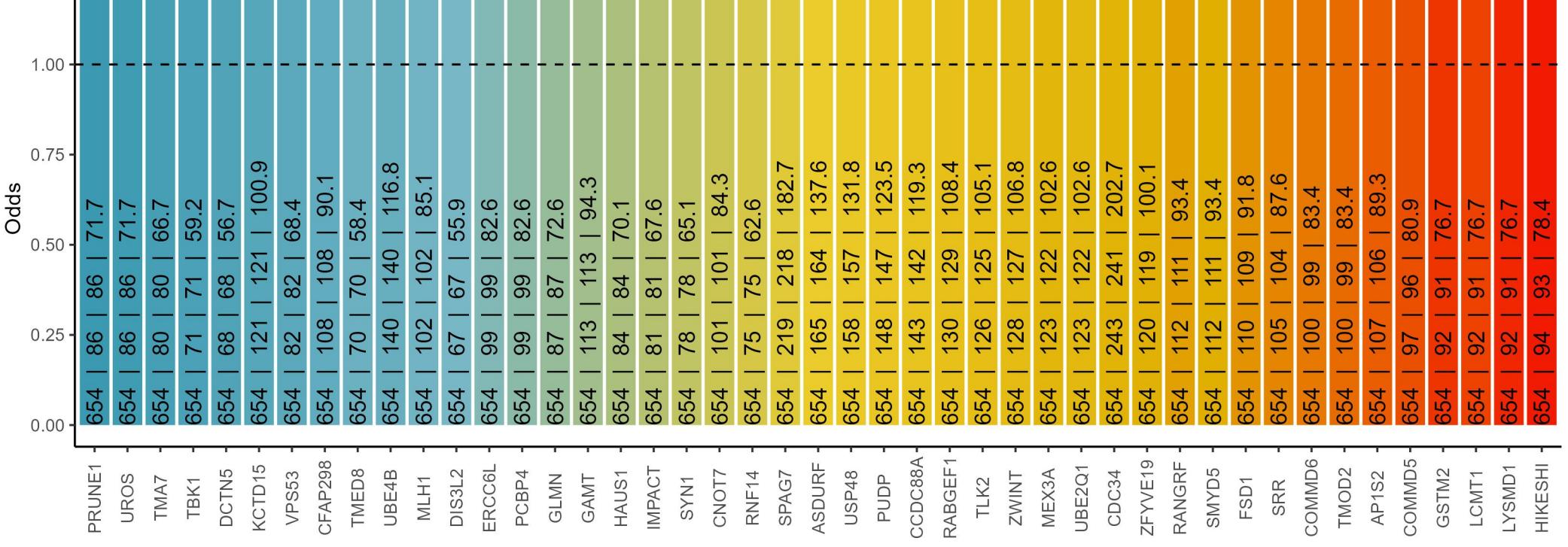
Cooccurrence with COPS3 protein in solid cancers, DB1

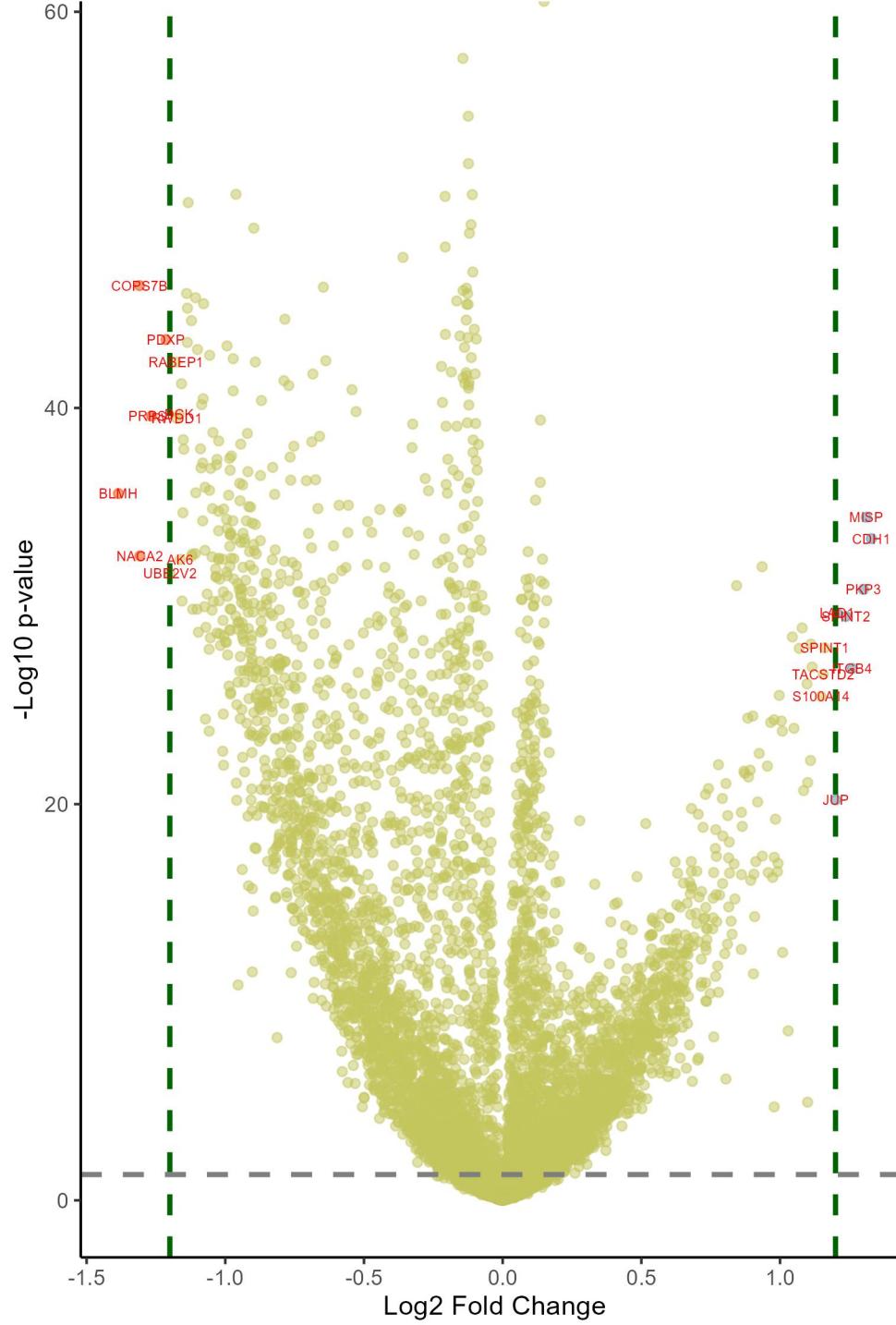
The text in the bars: incidence of COPS3 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



Positive cooccurrence

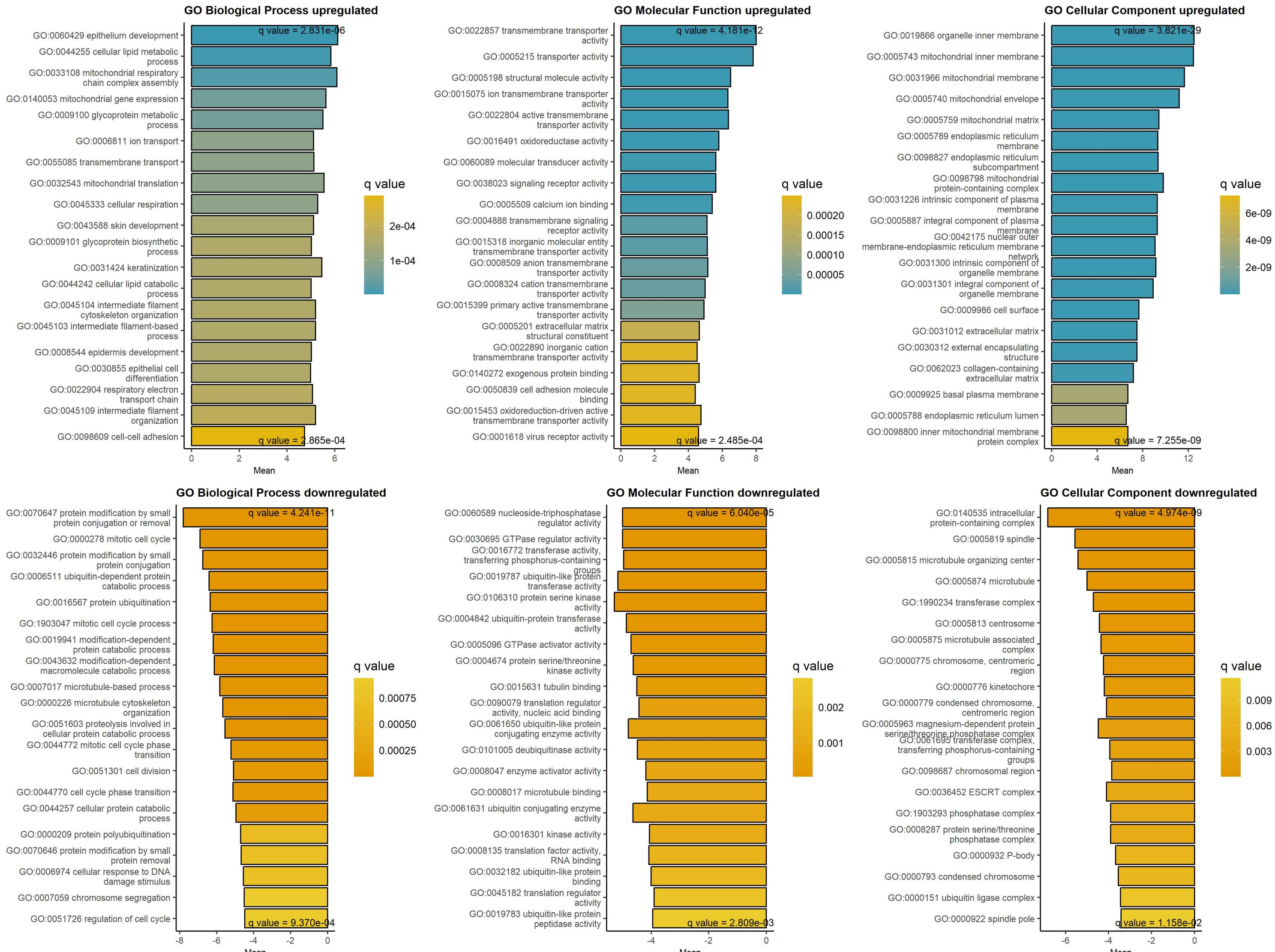


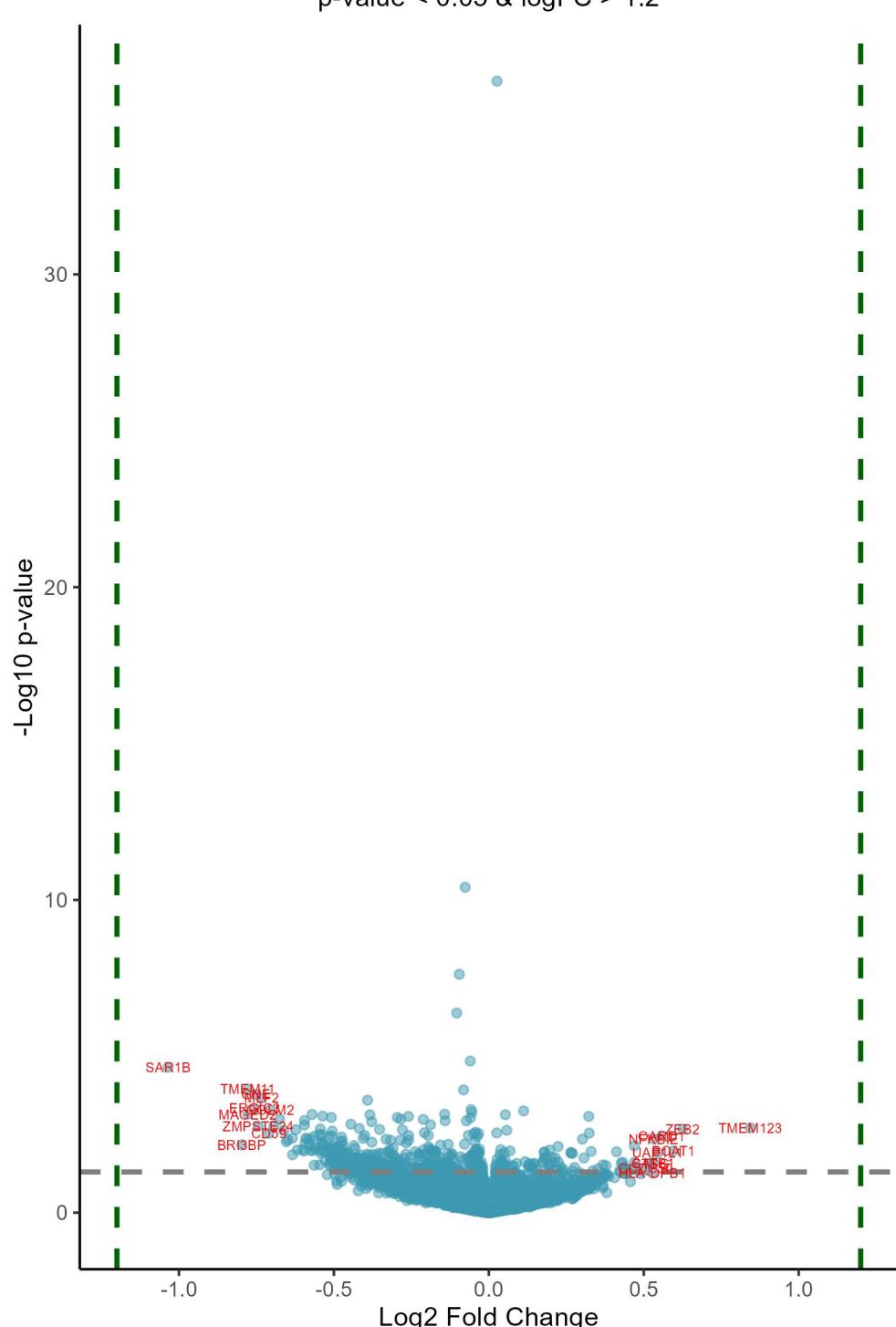


Downregulated at low/absent COPS3 Upregulated at low/absent COPS3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.39	1.12e-34	BLMH	bleomycin hydrolase	1.33	1.58e-32	CDH1	cadherin 1
-1.31	2.77e-44	COPS7B	COP9 signalosome subunit 7B	1.31	1.51e-33	MISP	mitotic spindle positioning
-1.31	1.03e-31	NACA2	nascent polypeptide associated comp	1.3	3.78e-30	PKP3	plakophilin 3
-1.27	2.46e-38	PRPS1	phosphoribosyl pyrophosphate synth	1.26	2.14e-26	ITGB4	integrin subunit beta 4
-1.21	6.55e-42	PDXP	pyridoxal phosphatase	1.24	6.94e-29	SPINT2	serine peptidase inhibitor, Kunitz
-1.2	6.65e-31	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.21	4.84e-29	LAD1	ladinin 1
-1.18	6.93e-41	RABEP1	rabaptin, RAB GTPase binding effect	1.2	5.00e-20	JUP	junction plakoglobin
-1.18	3.14e-38	RWDD1	RWD domain containing 1	1.16	2.20e-27	SPINT1	serine peptidase inhibitor, Kunitz
-1.17	2.00e-38	DCK	deoxyctydine kinase	1.16	4.10e-26	TACSTD2	tumor associated calcium signal tra
-1.16	1.47e-31	AK6	adenylate kinase 6	1.15	4.79e-25	S100A14	S100 calcium binding protein A14
-1.16	6.98e-40	CZIB	CXXC motif containing zinc binding	1.12	1.84e-26	EPCAM	epithelial cell adhesion molecule
-1.16	1.32e-29	PBK	PDZ binding kinase	1.11	1.47e-27	FAM83H	family with sequence similarity 83
-1.15	9.11e-34	NUDT3	nudix hydrolase 3	1.11	6.08e-22	PKP2	plakophilin 2
-1.15	3.29e-37	SAAL1	serum amyloid A like 1	1.1	7.19e-21	GPRC5A	G protein-coupled receptor class C
-1.15	8.93e-37	SMAP2	small ArfGAP2	1.1	2.31e-05	KRT18	keratin 18
-1.14	5.29e-44	PPP2R5D	protein phosphatase 2 regulatory su	1.1	1.19e-25	EPB41L1	erythrocyte membrane protein band 4
-1.14	8.81e-42	CHMP7	charged multivesicular body protein	1.08	1.75e-20	DSG2	desmoglein 2
-1.14	2.25e-43	DHPS	deoxyhypusine synthase	1.08	2.50e-28	LAMB3	laminin subunit beta 3
-1.13	3.19e-48	DOHH	deoxyhypusine hydroxylase	1.07	2.33e-27	RAB25	RAB25, member RAS oncogene family
-1.12	8.64e-43	RWDD4	RWD domain containing 4	1.05	1.67e-23	KRT80	keratin 80
-1.12	1.06e-31	PPP6R1	protein phosphatase 6 regulatory su	1.04	6.66e-28	CDH3	cadherin 3
-1.12	8.46e-32	ACYP1	acylphosphatase 1	1.03	8.42e-09	KRT19	keratin 19
-1.12	3.19e-29	RNF181	ring finger protein 181	1.01	1.34e-12	ITGA3	integrin subunit alpha 3
-1.11	8.09e-32	COMM2	COMM domain containing 2	1.01	2.32e-23	CDCP1	CUB domain containing protein 1
-1.11	8.21e-44	MAPK14	mitogen-activated protein kinase 14	1	7.38e-24	LAMA5	laminin subunit alpha 5
-1.11	1.04e-34	MCRIP1	MAPK regulated corepressor interact	1	4.27e-25	LAMC2	laminin subunit gamma 2
-1.1	3.19e-29	PSME3IP1	proteasome activator subunit 3 inte	0.99	6.05e-17	ITGA2	integrin subunit alpha 2
-1.1	1.85e-41	AARSD1	alanyl-tRNA synthetase domain conta	0.99	1.55e-16	KRT17	keratin 17
-1.1	3.98e-28	FKBP1A	FKBP prolyl isomerase 1A	0.98	4.28e-19	LSR	lipolysis stimulated lipoprotein re

GAGE analysis on upregulated and downregulated proteins at low/absent COPS3 protein, DB1

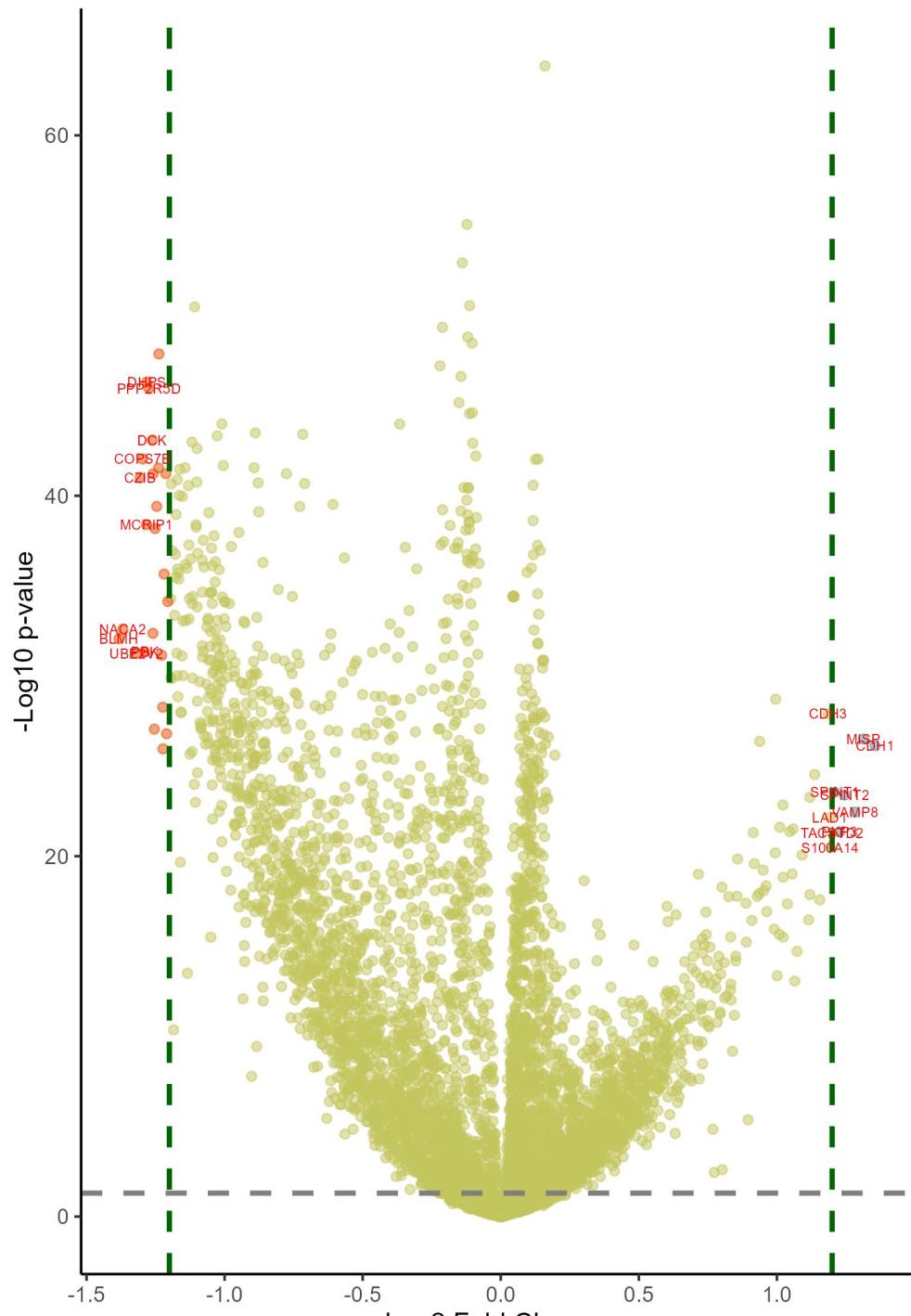




Downregulated in blood cancers at low/absent COPS3 Upregulated in blood cancers at low/absent COPS3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.03	2.12e-02	SAR1B	secretion associated Ras related GT	0.84	3.14e-01	TMEM123	transmembrane protein 123
-0.8	4.70e-01	BRI3BP	BRI3 binding protein	0.63	3.17e-01	ZEB2	zinc finger E-box binding homeobox
-0.78	8.78e-02	TMEM11	transmembrane protein 11	0.6	5.21e-01	BCAT1	branched chain amino acid transamin
-0.78	2.19e-01	MAGED2	MAGE family member D2	0.56	3.57e-01	OARD1	O-acyl-ADP-ribose deacetylase 1
-0.76	2.19e-01	ERGIC3	ERGIC and golgi 3	0.55	5.21e-01	UAP1L1	UDP-N-acetylglucosamine pyrophospho
-0.75	1.10e-01	GNE	glucosamine (UDP-N-acetyl)-2-epimer	0.53	3.88e-01	NFKBIE	NFKB inhibitor epsilon
-0.74	2.83e-01	ZMPSTE24	zinc metallopeptidase STE24	0.53	6.19e-01	SATB1	SATB homeobox 1
-0.73	1.29e-01	MLF2	myeloid leukemia factor 2	0.53	6.70e-01	HLA-DPB1	major histocompatibility complex, c
-0.71	3.50e-01	CD59	CD59 molecule (CD59 blood group)	0.52	6.19e-01	CTSG	cathepsin G
-0.71	2.19e-01	GOLM2	golgi membrane protein 2	0.51	6.40e-01	CCDC50	coiled-coil domain containing 50
-0.69	2.80e-01	RPS27L	ribosomal protein S27 like	0.49	6.70e-01	NAPRT	nicotinate phosphoribosyltransferas
-0.68	2.24e-01	MED22	mediator complex subunit 22	0.48	6.40e-01	PYCARD	PYD and CARD domain containing
-0.66	3.17e-01	SPRYD4	SPRY domain containing 4	0.47	6.19e-01	EFR3A	EFR3 homolog A
-0.65	4.28e-01	MECR	mitochondrial trans-2-enoyl-CoA red	0.47	4.88e-01	LRRC57	leucine rich repeat containing 57
-0.65	3.98e-01	MAP2K3	mitogen-activated protein kinase ki	0.46	7.46e-01	ANXA1	annexin A1
-0.63	3.88e-01	ICAM2	intercellular adhesion molecule 2	0.45	6.70e-01	SIT1	signaling threshold regulating tran
-0.63	5.31e-01	NDUFB2	NADH:ubiquinone oxidoreductase subu	0.45	6.50e-01	SNTB1	syntrophin beta 1
-0.62	3.17e-01	ERLEC1	endoplasmic reticulum lectin 1	0.44	6.40e-01	H1-1	H1.1 linker histone, cluster member
-0.62	5.21e-01	MRPS2	mitochondrial ribosomal protein S2	0.44	6.70e-01	SFXN3	sideroflexin 3
-0.6	5.21e-01	ITGB7	integrin subunit beta 7	0.44	6.70e-01	CORO1B	coronin 1B
-0.6	5.21e-01	GABARPL2	GABA type A receptor associated pro	0.44	6.39e-01	VTI1B	vesicle transport through interacti
-0.6	2.76e-01	CCDC134	coiled-coil domain containing 134	0.43	6.19e-01	SSNA1	SS nuclear autoantigen 1
-0.59	2.27e-01	MMGT1	membrane magnesium transporter 1	0.43	6.19e-01	LRCH4	leucine rich repeats and calponin h
-0.59	4.45e-01	NEU1	neuraminidase 1	0.43	6.70e-01	UTRN	utrophin
-0.59	3.88e-01	TMEM214	transmembrane protein 214	0.42	6.70e-01	INF2	inverted formin 2
-0.59	3.88e-01	KIFBP	kinesin family binding protein	0.41	5.21e-01	SHOC2	SHOC2 leucine rich repeat scaffold
-0.58	4.63e-01	ARL6IP1	ADP ribosylation factor like GTPase	0.41	7.04e-01	ENTPD1	ectonucleoside triphosphate diphosp
-0.58	3.88e-01	GYS1	glycogen synthase 1	0.39	6.84e-01	ARRB1	arrestin beta 1
-0.57	5.21e-01	ATP6V0A1	ATPase H+ transporting V0 subunit a	0.38	6.70e-01	IRFBP2	interferon regulatory factor 2 bind

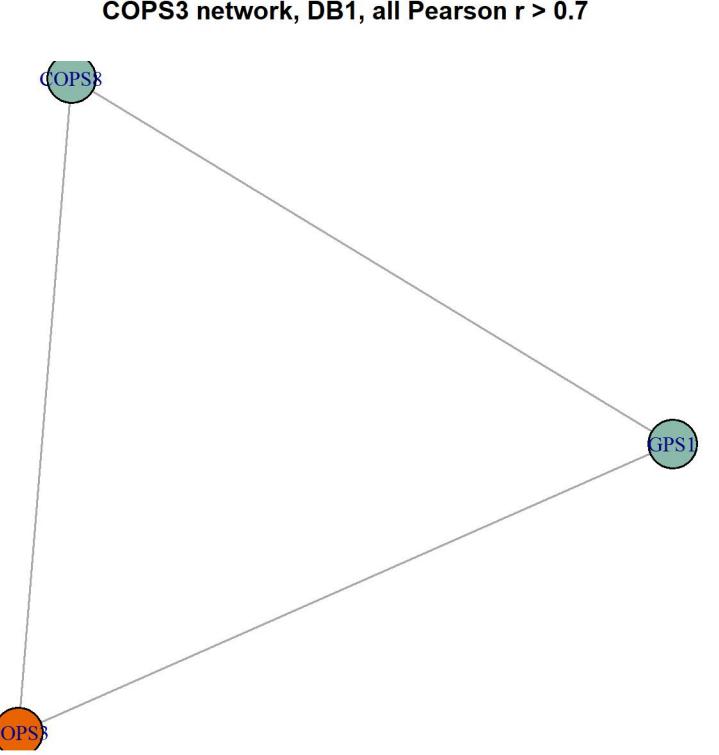
p-value < 0.05 & logFC > 1.2



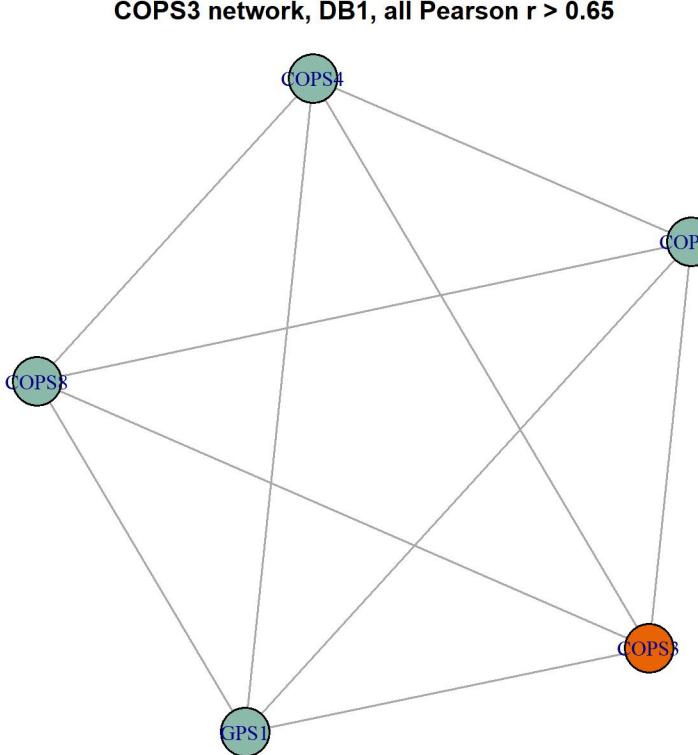
Downregulated in solid cancers at low/absent COPS3 Upregulated in solid cancers at low/absent COPS3

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.38	2.26e-31	BLMH	bleomycin hydrolase	1.36	9.88e-26	CDH1	cadherin 1
-1.37	6.90e-32	NACA2	nascent polypeptide associated comp	1.31	4.47e-26	MISP	mitotic spindle positioning
-1.32	1.36e-30	UBE2V2	ubiquitin conjugating enzyme E2 V2	1.28	3.42e-22	VAMP8	vesicle associated membrane protein
-1.31	1.69e-39	CZIB	CXXC motif containing zinc binding	1.25	4.19e-23	SPINT2	serine peptidase inhibitor, Kunitz
-1.3	2.09e-40	COPS7B	COP9 signalosome subunit 7B	1.23	3.81e-21	PKP3	plakophilin 3
-1.29	1.12e-30	PBK	PDZ binding kinase	1.21	2.91e-23	SPINT1	serine peptidase inhibitor, Kunitz
-1.28	4.01e-37	MCRIP1	MAPK regulated corepressor interact	1.2	4.46e-21	TACSTD2	tumor associated calcium signal tra
-1.28	2.48e-44	DHPS	deoxyhypusine synthase	1.19	2.62e-20	S100A14	S100 calcium binding protein A14
-1.27	5.22e-44	PPP2R5D	protein phosphatase 2 regulatory su	1.19	6.42e-22	LAD1	ladinin 1
-1.26	2.38e-41	DCK	deoxycytidine kinase	1.18	2.08e-27	CDH3	cadherin 3
-1.26	1.16e-31	AK6	adenylate kinase 6	1.16	1.64e-17	ITGB4	integrin subunit beta 4
-1.26	1.05e-39	PDXP	pyridoxal phosphatase	1.14	3.38e-24	LAMB3	laminin subunit beta 3
-1.25	1.32e-26	ENO2	enolase 2	1.12	8.74e-18	PKP2	plakophilin 2
-1.25	6.23e-37	PPM1F	protein phosphatase, Mg2+/Mn2+ depe	1.12	5.48e-23	RAB25	RAB25, member RAS oncogene family
-1.25	4.77e-38	RWDD1	RWD domain containing 1	1.11	1.92e-16	GPRC5A	G protein-coupled receptor class C
-1.24	5.61e-40	RABEP1	rabaptin, RAB GTPase binding effect	1.09	6.60e-20	KRT80	keratin 80
-1.24	8.91e-46	DOHH	deoxyhypusine hydroxylase	1.07	9.50e-15	KRT17	keratin 17
-1.23	1.74e-30	ARHGAP17	Rho GTPase activating protein 17	1.06	3.70e-13	JUP	junction plakoglobin
-1.22	9.36e-28	FKBP1A	FKBP prolyl isomerase 1A	1.06	2.63e-21	FAM83H	family with sequence similarity 83
-1.22	1.47e-25	UBE2Z	ubiquitin conjugating enzyme E2 Z	1.06	6.93e-19	EPCAM	epithelial cell adhesion molecule
-1.22	1.31e-34	SAAL1	serum amyloid A like 1	1.05	3.67e-21	LAMC2	laminin subunit gamma 2
-1.21	1.05e-39	PHPT1	phosphohistidine phosphatase 1	1.04	2.69e-17	LSR	lipolysis stimulated lipoprotein re
-1.21	2.32e-26	TMEM263	transmembrane protein 263	1.02	1.65e-15	ANXA3	annexin A3
-1.21	2.31e-33	PDCL3	phosducin like 3	1.02	1.03e-18	EPB41L1	erythrocyte membrane protein band 4
-1.2	1.65e-33	NUDT3	nudix hydrolase 3	1.02	1.41e-22	ST14	ST14 transmembrane serine protease
-1.19	2.67e-29	PRPS1	phosphoribosyl pyrophosphate synthe	1.01	2.17e-21	ITGB6	integrin subunit beta 6
-1.19	3.33e-39	APPL1	adaptor protein, phosphotyrosine in	1.01	1.17e-15	KRT5	keratin 5
-1.19	2.82e-29	LANCL1	LanC like 1	1	1.91e-13	BRI3BP	BRI3 binding protein
-1.19	8.50e-36	CCDC43	coiled-coil domain containing 43	1	3.54e-28	LAMA3	laminin subunit alpha 3

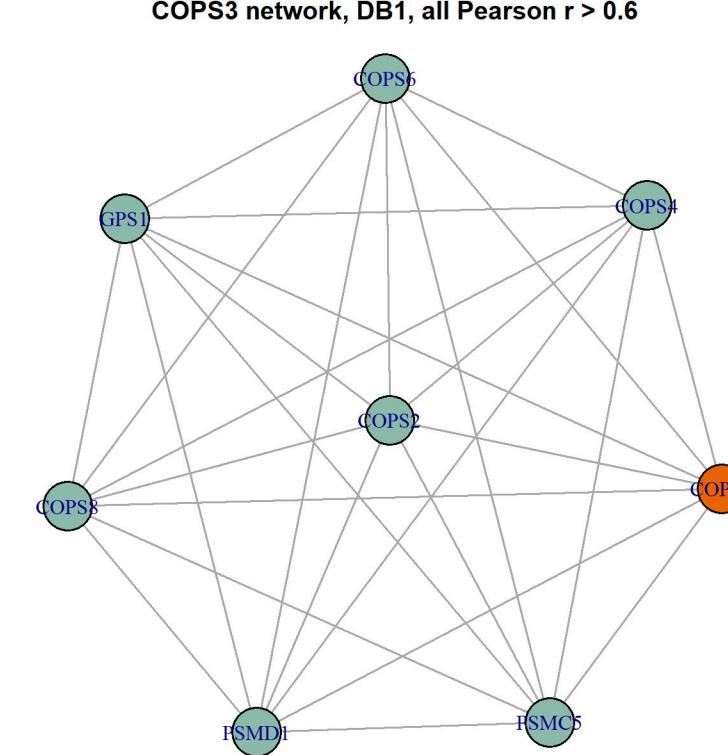
COPS3 network, DB1, all Pearson r > 0.7

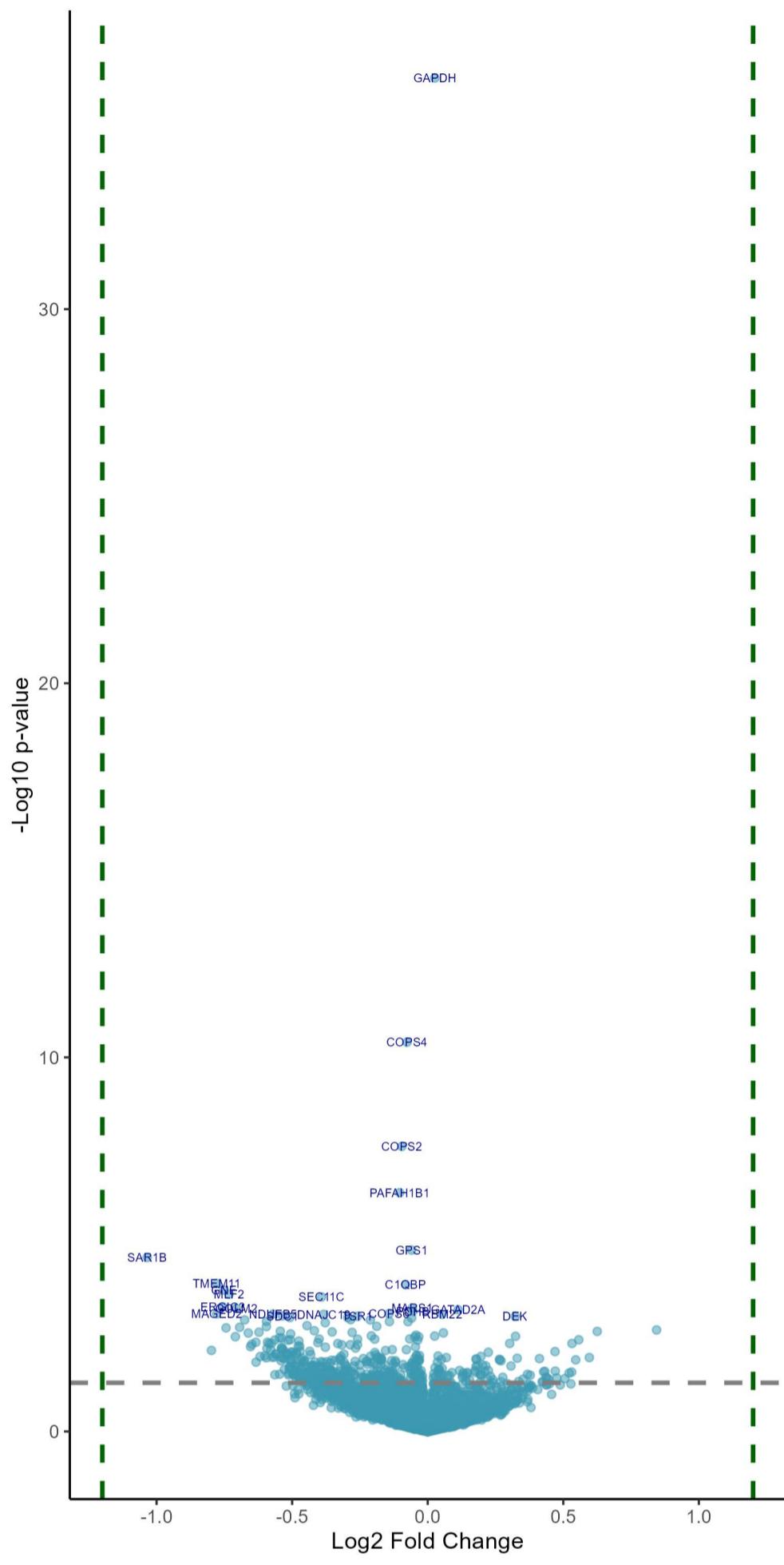


COPS3 network, DB1, all Pearson r > 0.65



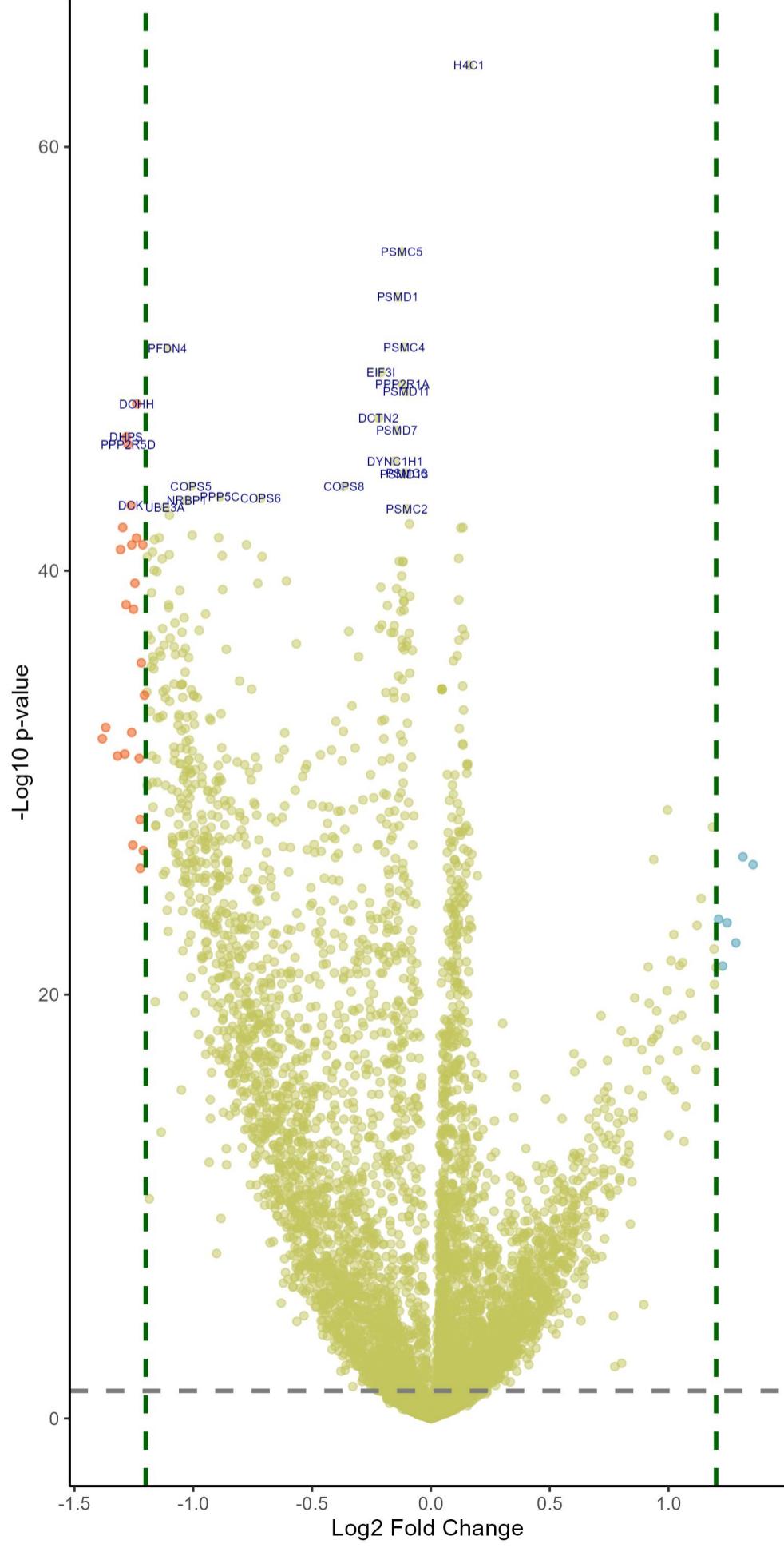
COPS3 network, DB1, all Pearson r > 0.6





Sorted by p values!

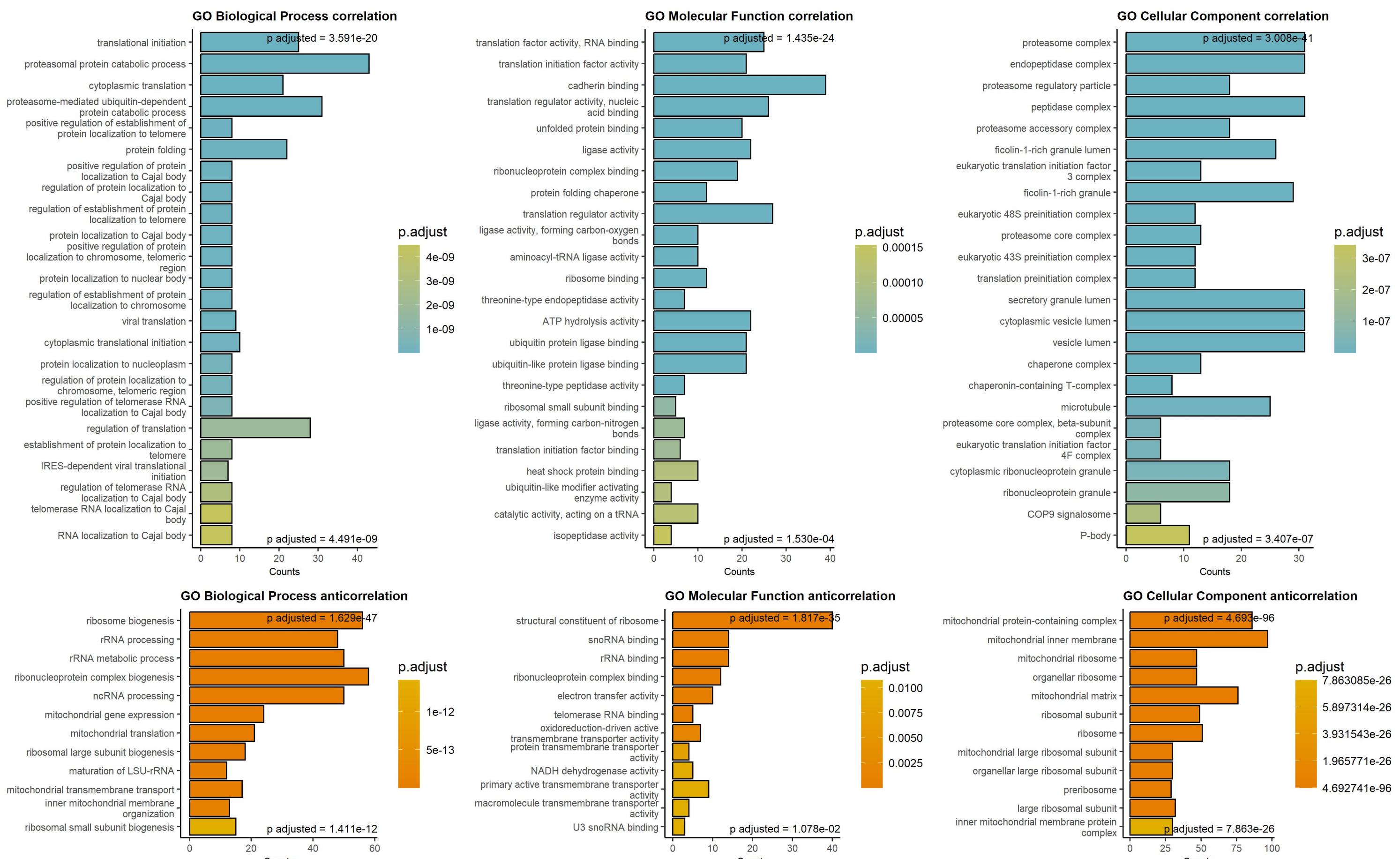
Downregulated in blood cancers at low/absent COPS3				Upregulated in blood cancers at low/absent COPS3			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.08	1.31e-07	COPS4	COP9 signalosome subunit 4	0.03	4.40e-33	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.1	5.32e-05	COPS2	COP9 signalosome subunit 2	0.11	2.19e-01	GATAD2A	GATA zinc finger domain containing protein
-0.1	5.51e-04	PAFAH1B1	platelet activating factor acetylhydrolase, secreted	0.05	2.19e-01	RBM22	RNA binding motif protein 22
-0.06	1.57e-02	GPS1	G protein pathway suppressor 1	0.32	2.19e-01	DEK	DEK proto-oncogene
-1.03	2.12e-02	SAR1B	secretion associated Ras related GT	0.84	3.14e-01	TMEM123	transmembrane protein 123
-0.78	8.78e-02	TMEM11	transmembrane protein 11	0.63	3.17e-01	ZEB2	zinc finger E-box binding homeobox
-0.08	8.78e-02	C1QBP	complement C1q binding protein	0.06	3.17e-01	IQGAP1	IQ motif containing GTPase activating protein
-0.75	1.10e-01	GNE	glucosamine (UDP-N-acetyl)-2-epimerase/lyase	0.03	3.50e-01	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1
-0.73	1.29e-01	MLF2	myeloid leukemia factor 2	0.32	3.50e-01	C3	complement C3
-0.39	1.41e-01	SEC11C	SEC11 homolog C, signal peptidase c	0.56	3.57e-01	OARD1	O-acyl-ADP-ribose deacetylase 1
-0.76	2.19e-01	ERGIC3	ERGIC and golgi 3	0.53	3.88e-01	NFKBIE	NFKB inhibitor epsilon
-0.06	2.19e-01	MARS1	methionyl-tRNA synthetase 1	0.3	3.88e-01	FCGR1	Fc gamma receptor and transporter
-0.71	2.19e-01	GOLM2	golgi membrane protein 2	0.47	4.88e-01	LRRC57	leucine rich repeat containing 57
-0.05	2.19e-01	PDHB	pyruvate dehydrogenase E1 subunit b	0.22	4.95e-01	GRK2	G protein-coupled receptor kinase 2
-0.14	2.19e-01	COPS6	COP9 signalosome subunit 6	0.04	5.21e-01	MFAP1	microfibril associated protein 1
-0.78	2.19e-01	MAGED2	MAGE family member D2	0.2	5.21e-01	LDB3	LIM domain binding 3
-0.57	2.19e-01	NDUFB5	NADH:ubiquinone oxidoreductase subunit 5	0.6	5.21e-01	BCAT1	branched chain amino acid transaminase
-0.38	2.19e-01	DNAJC19	DnaJ heat shock protein family (Hsp40) member C19	0.07	5.21e-01	MTHFD1L	methylene tetrahydrofolate dehydrogenase
-0.54	2.19e-01	SDC1	syndecan 1	0.33	5.21e-01	RAB44	RAB44, member RAS oncogene family
-0.26	2.19e-01	TSR1	TSR1 ribosome maturation factor	0.41	5.21e-01	SHOC2	SHOC2 leucine rich repeat scaffold
-0.51	2.19e-01	NAGLU	N-acetyl-alpha-glucosaminidase	0.18	5.21e-01	MGST3	microsomal glutathione S-transferase
-0.3	2.19e-01	SLC25A5	solute carrier family 25 member 5	0.18	5.21e-01	EML1	EMAP like 1
-0.06	2.19e-01	YWHAE	tyrosine 3-monooxygenase/tryptophan	0.27	5.21e-01	RAB3GAP1	RAB3 GTPase activating protein catalytic subunit
-0.28	2.24e-01	MTX1	metaxin 1	0.05	5.21e-01	PLRG1	pleiotropic regulator 1
-0.68	2.24e-01	MED22	mediator complex subunit 22	0.55	5.21e-01	UAP1L1	UDP-N-acetylglucosamine pyrophosphoryl transferase
-0.21	2.24e-01	MAGED1	MAGE family member D1	0.26	5.21e-01	SGO1	shugoshin 1
-0.59	2.27e-01	MMGT1	membrane magnesium transporter 1	0.27	5.21e-01	DOK1	docking protein 1
-0.14	2.27e-01	COPS8	COP9 signalosome subunit 8	0.04	5.31e-01	ARGLU1	arginine and glutamate rich 1
-0.07	2.27e-01	PRDX5	peroxiredoxin 5	0.2	5.72e-01	YES1	YES proto-oncogene 1, Src family tyrosine kinase
-0.38	2.36e-01	SDHAF2	succinate dehydrogenase complex assembly subunit	0.18	5.72e-01	LSM1	LSM1 homolog, mRNA degradation associated
-0.45	2.74e-01	DSG2	desmoglein 2	0.21	5.72e-01	MYL1	myosin light chain 1
-0.19	2.76e-01	TSFM	Ts translation elongation factor, m	0.31	5.72e-01	MTCH1	mitochondrial carrier 1
-0.6	2.76e-01	CCDC134	coiled-coil domain containing 134	0.18	5.72e-01	ESD	esterase D
-0.69	2.80e-01	RPS27L	ribosomal protein S27 like	0.03	5.88e-01	SF3B6	splicing factor 3b subunit 6
-0.74	2.83e-01	ZMPSTE24	zinc metallopeptidase STE24	0.05	6.05e-01	TAF15	TATA-box binding protein associated
-0.42	3.17e-01	PRAF2	PRA1 domain family member 2	0.04	6.19e-01	ZC3HAV1	zinc finger CCCH-type containing, a
-0.54	3.17e-01	MARS2	methionyl-tRNA synthetase 2, mitochondrial	0.04	6.19e-01	EIF5	eukaryotic translation initiation factor 5
-0.35	3.17e-01	PPP2R2A	protein phosphatase 2 regulatory subunit A	0.12	6.19e-01	RUFY1	RUN and FYVE domain containing 1
0.62	3.17e-01	ERPI_ECF1	endoplasmic reticulum lectin 1	0.22	6.19e-01	SLC25R2	solute carrier family 25 member R2



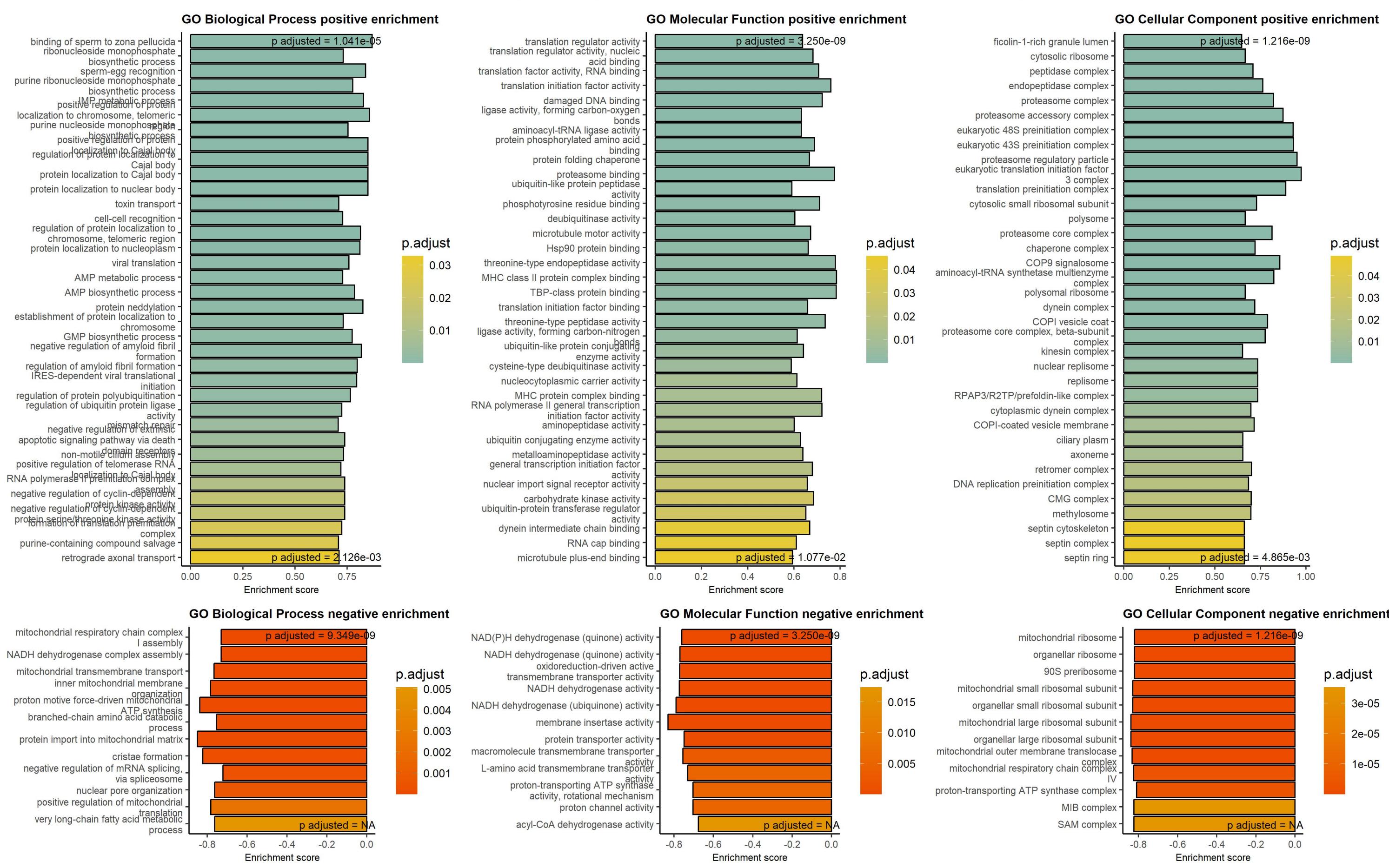
Sorted by p values!

Downregulated in solid cancers at low/absent COPS3				Upregulated in solid cancers at low/absent COPS3			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.12	1.93e-52	PSMC5	proteasome 26S subunit, ATPase 5	0.16	4.67e-61	H4C1	H4 clustered histone 1
-0.14	1.98e-50	PSMD1	proteasome 26S subunit, non-ATPase	0.13	2.09e-40	MRPL13	mitochondrial ribosomal protein L13
-0.11	3.63e-48	PSMC4	proteasome 26S subunit, ATPase 4	0.13	2.14e-40	MRPL17	mitochondrial ribosomal protein L17
-1.11	3.63e-48	PFDN4	prefoldin subunit 4	0.12	3.86e-39	MRPL11	mitochondrial ribosomal protein L11
-0.21	4.24e-47	EIF3I	eukaryotic translation initiation factor 3 subunit I	0.12	2.52e-37	MRPL43	mitochondrial ribosomal protein L43
-0.12	1.29e-46	PPP2R1A	protein phosphatase 2 scaffold subunit	0.13	4.69e-36	MRPL19	mitochondrial ribosomal protein L19
-0.1	2.53e-46	PSMD11	proteasome 26S subunit, non-ATPase	0.14	8.38e-36	MRPL41	mitochondrial ribosomal protein L41
-1.24	8.91e-46	DOHH	deoxyhypusine hydroxylase	0.12	1.36e-35	MRPL39	mitochondrial ribosomal protein L39
-0.22	3.72e-45	DCTN2	dynactin subunit 2	0.11	6.40e-35	MRPS28	mitochondrial ribosomal protein S28
-0.14	1.32e-44	PSMD7	proteasome 26S subunit, non-ATPase	0.1	1.06e-34	RPN1	ribophorin I
-1.28	2.48e-44	DHPS	deoxyhypusine synthase	0.13	1.25e-33	MRPL38	mitochondrial ribosomal protein L38
-1.27	5.22e-44	PPP2R5D	protein phosphatase 2 regulatory subunit A	0.05	1.25e-33	PTPRCAP	protein tyrosine phosphatase receptor type C
-0.15	3.02e-43	DYNC1H1	dynein cytoplasmic 1 heavy chain 1	0.05	1.25e-33	HBE1	hemoglobin subunit epsilon 1
-0.1	1.03e-42	PSMC6	proteasome 26S subunit, ATPase 6	0.05	1.25e-33	SERPINB10	serpin family B member 10
-0.11	1.08e-42	PSMD13	proteasome 26S subunit, non-ATPase	0.05	1.25e-33	IGLL1	immunoglobulin lambda like polypeptide 1
-1.01	3.67e-42	COPS5	COP9 signalosome subunit 5	0.05	1.25e-33	CRYBB1	crystallin beta 1
-0.37	3.67e-42	COPS8	COP9 signalosome subunit 8	0.05	1.25e-33	IT	

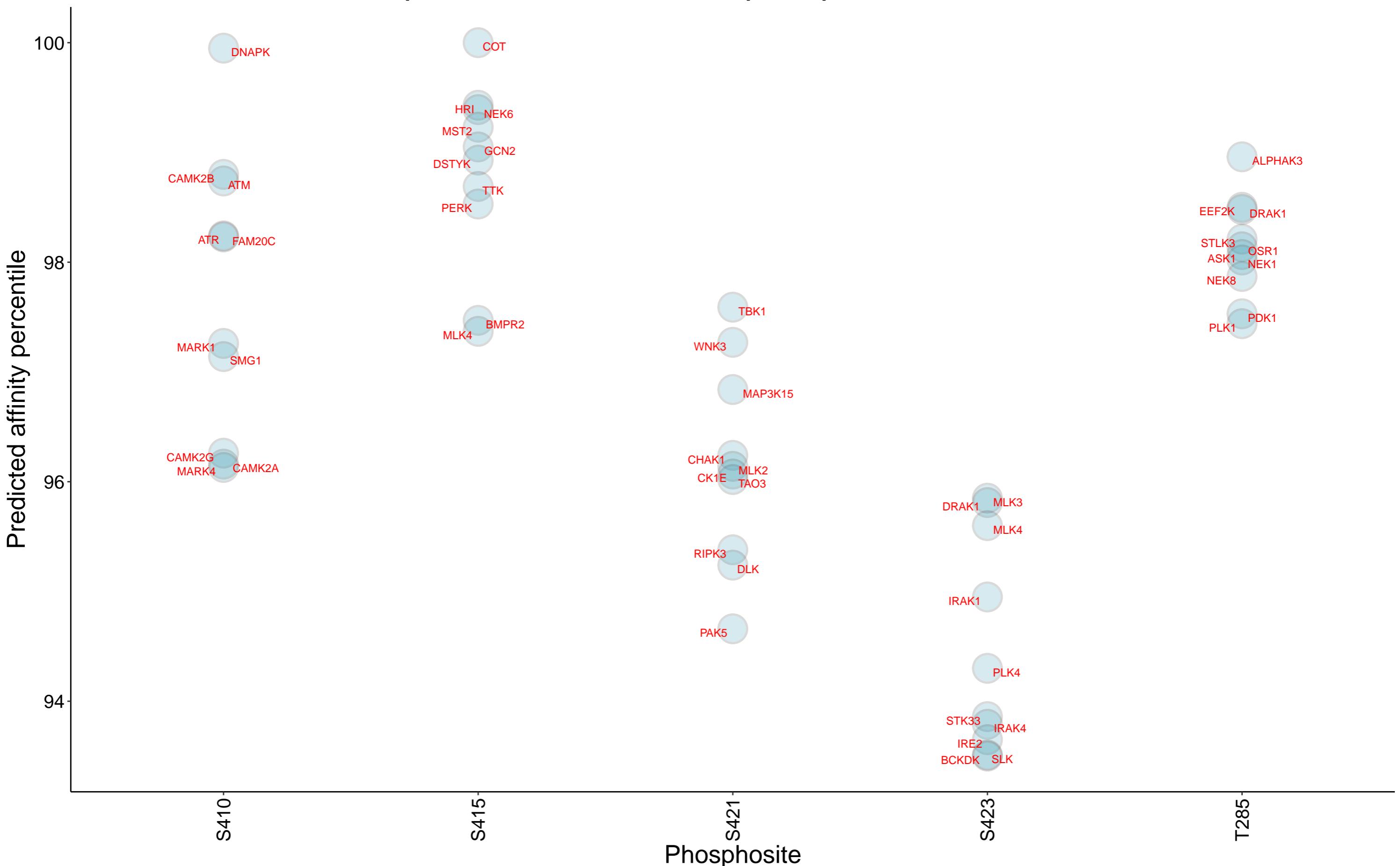
Top 250 correlation coefficients overrepresentation, COPS3 protein, DB1



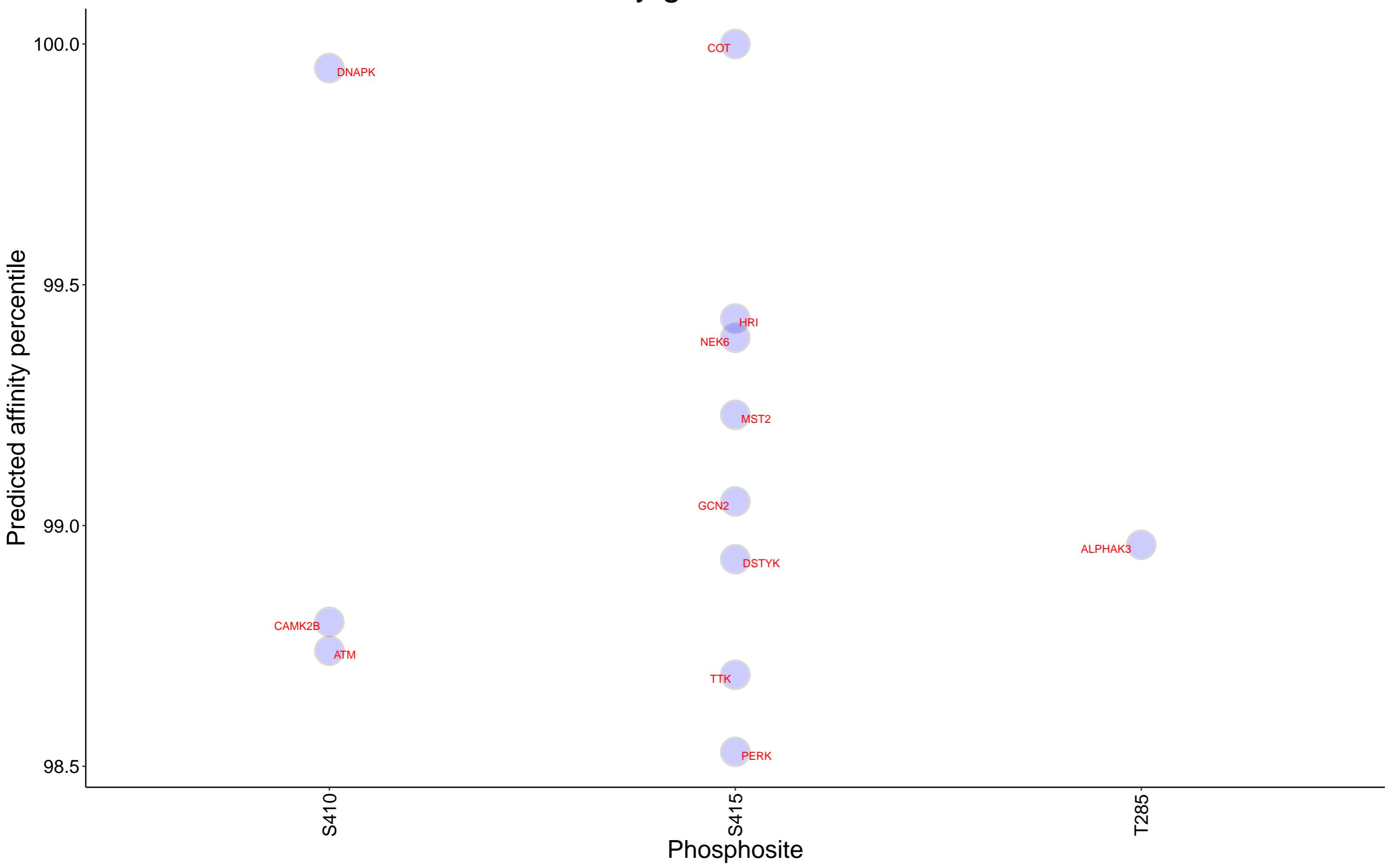
Gene Set Enrichment analysis on protein correlation coefficients, COPS3 protein, DB1



Top 10 kinases for each phosphosite in COPS3



Kinases with affinity greater than 98.5% to COPS3



Top 15 positive correlation coefficients for COPS3 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

