

COMMD1

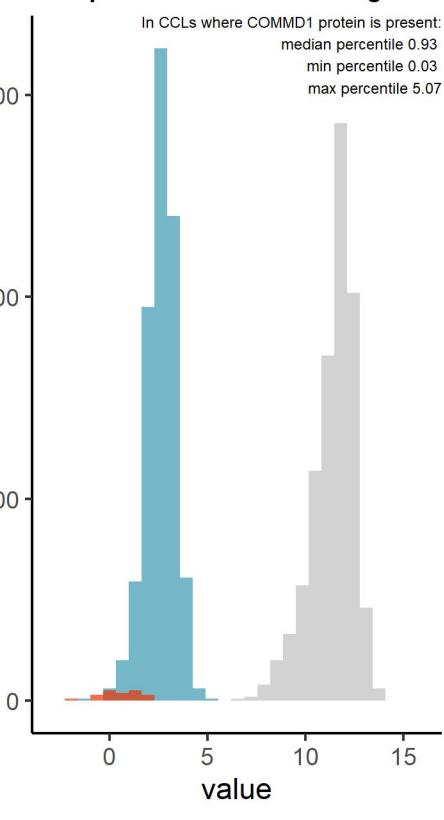
Protein name: COMMD1 ; UNIPROT: Q8N668 ; Gene name: copper metabolism domain containing 1

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

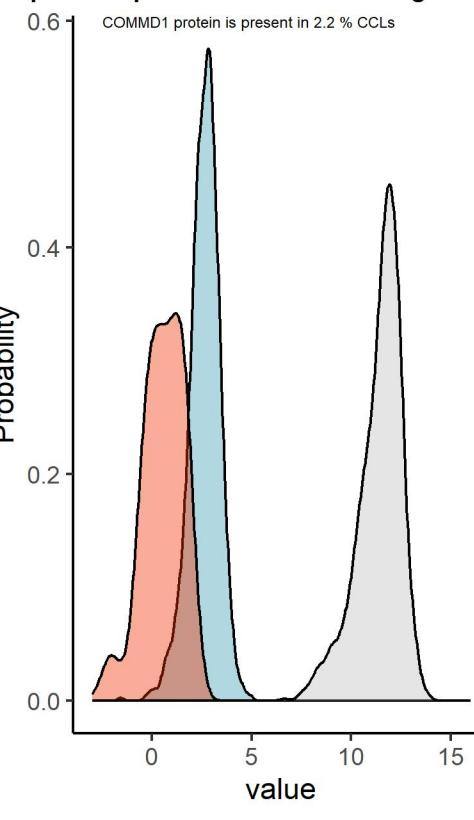
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

Histogram of COMMD1 protein compared to proteins with low and high abundance



Density plot of COMMD1 protein compared to proteins with low and high abundance



Top negative correlations of COMMD1 protein, DB1

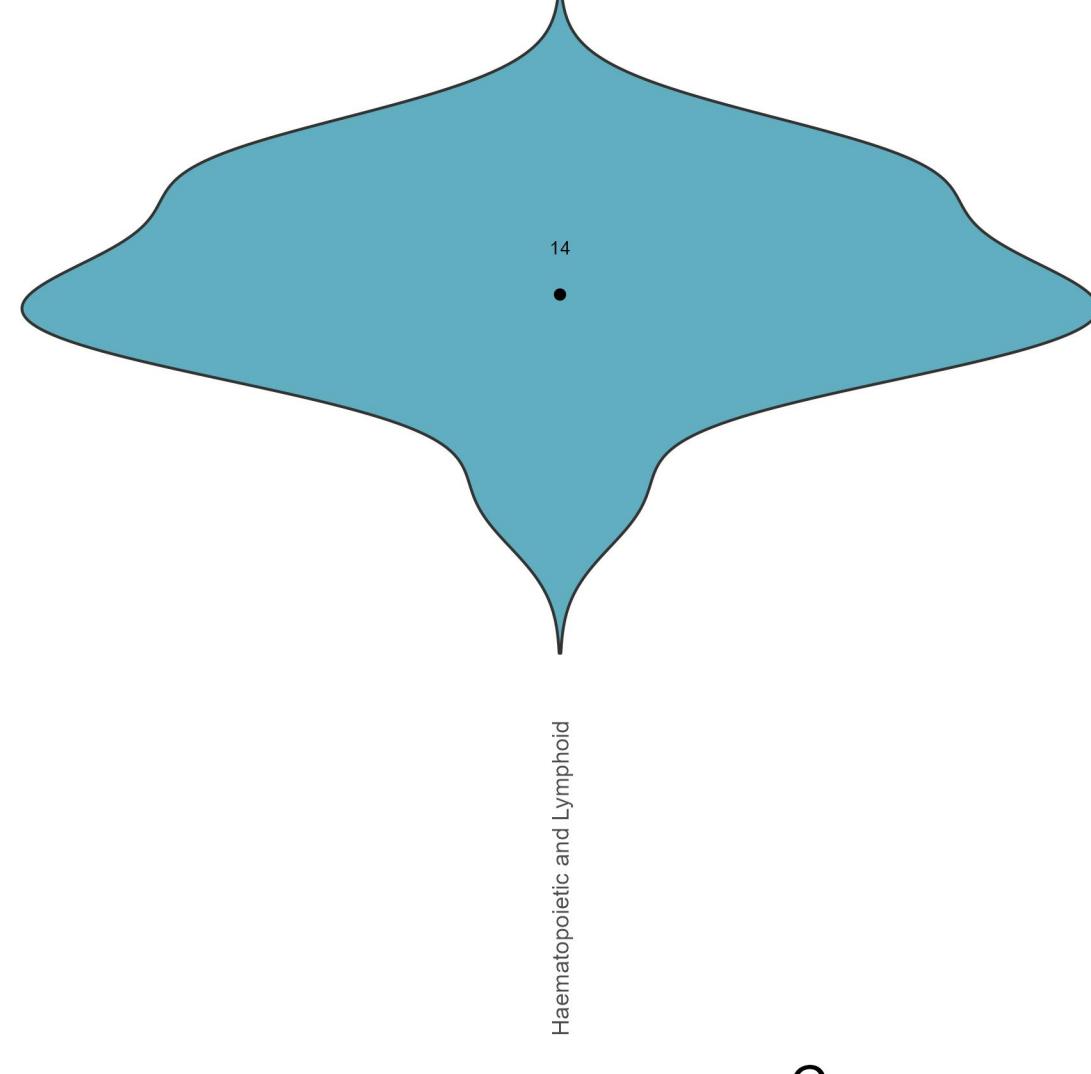
Pearson correlation coefficients

Top positive correlations of COMMD1 protein, DB1

Pearson correlation coefficients

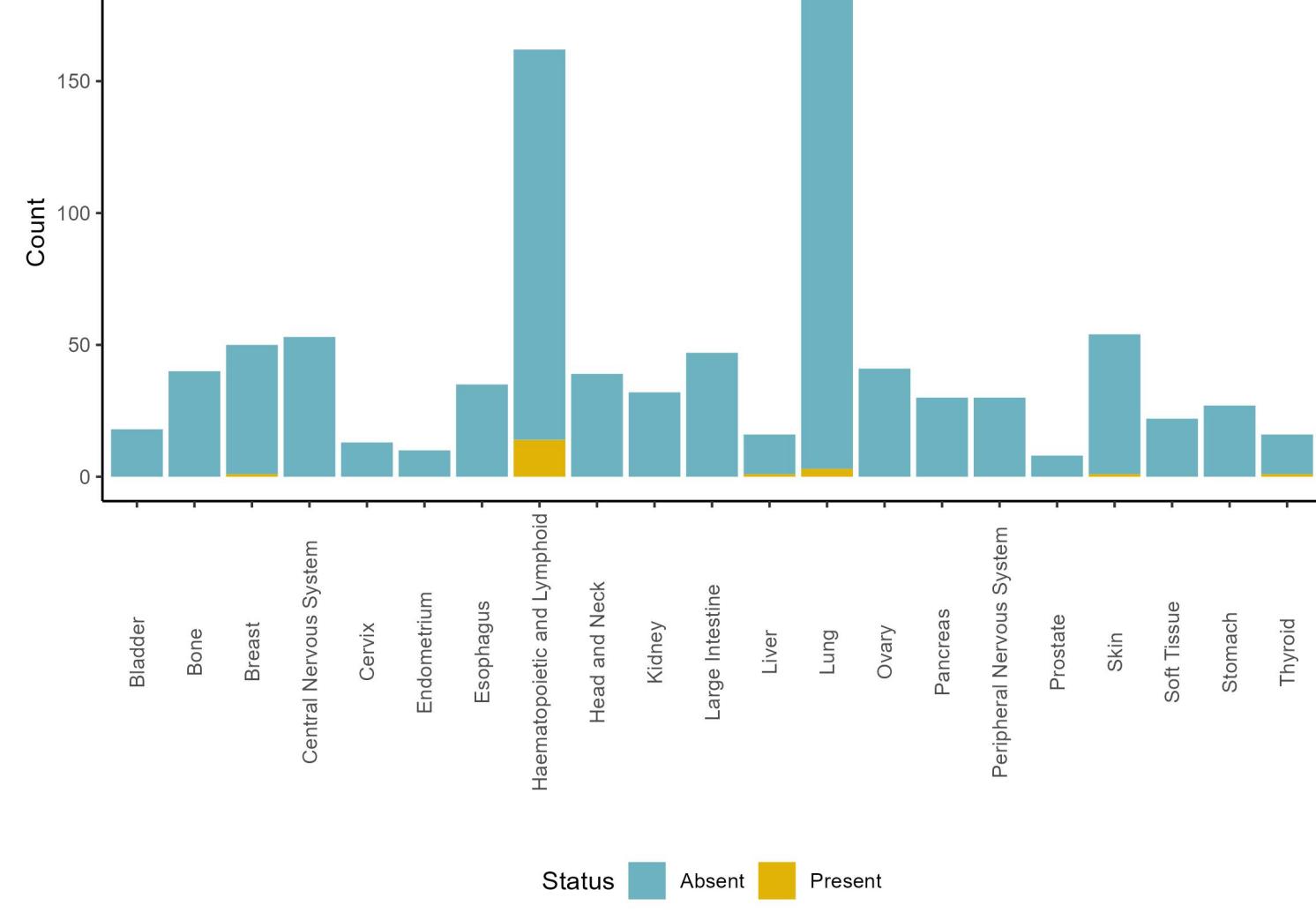
Amount of COMMD1 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 7.070e-01



Present and absent COMMD1 protein counts by tissue, DB1

Chi square p value is 2.166e-03

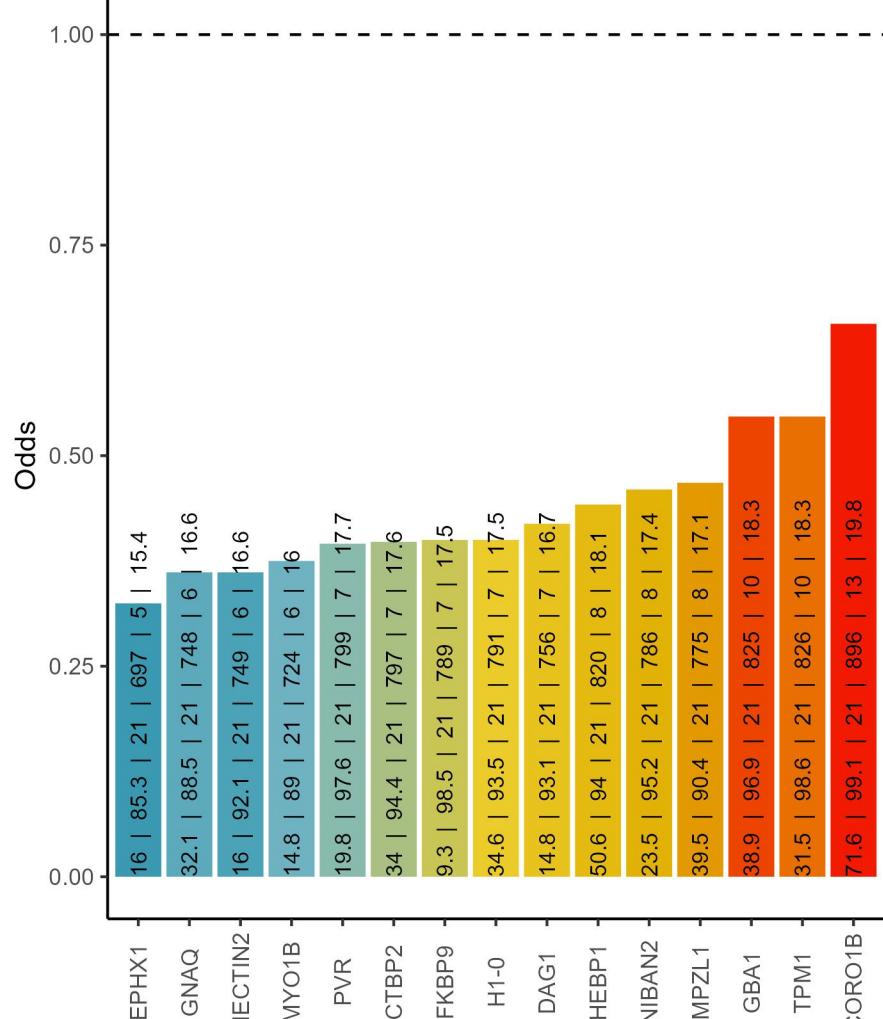


Cooccurrence with COMMD1 protein, DB1

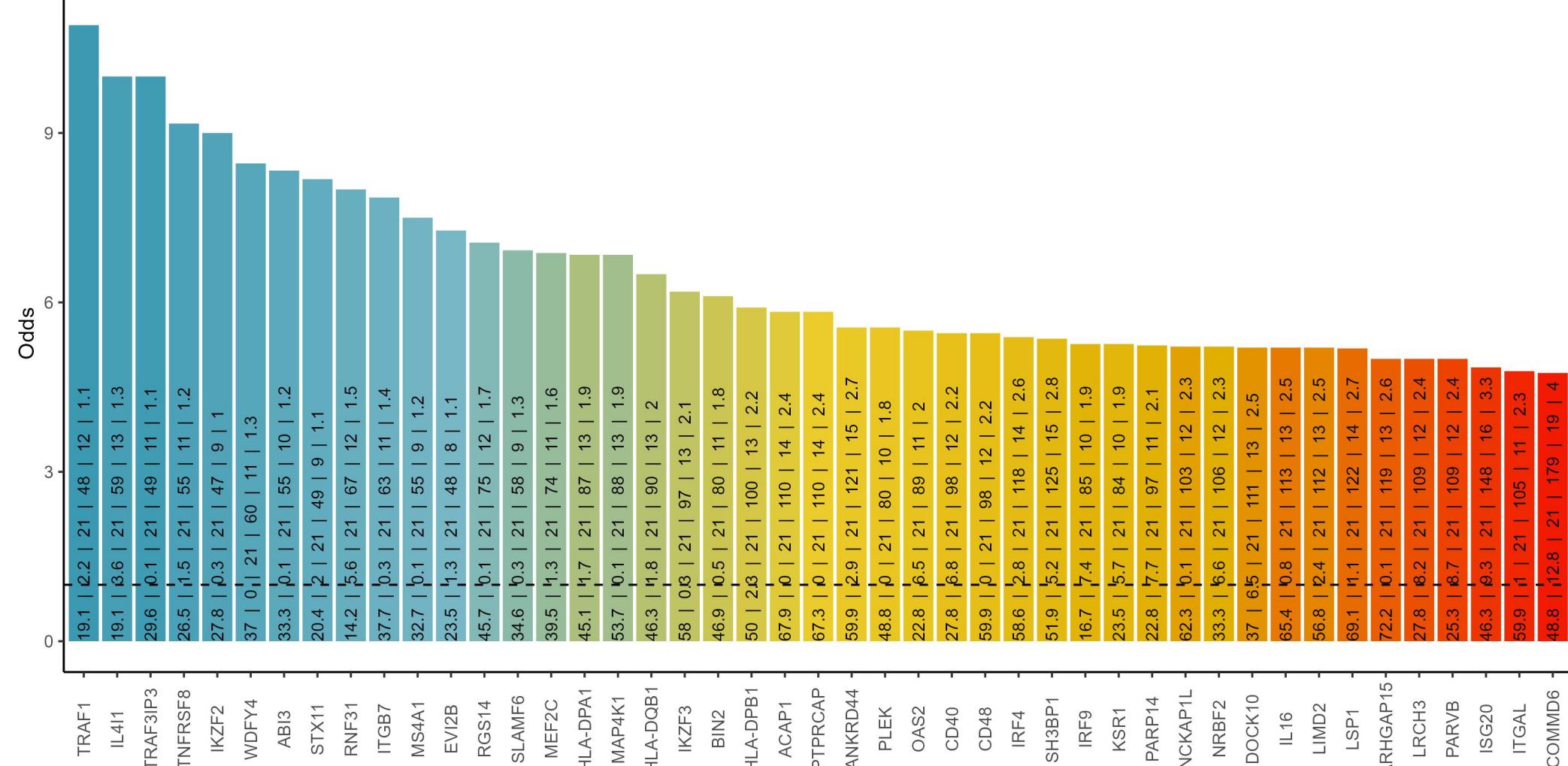
% of COMMD1 in blood cancers: 8.6 ; % of COMMD1 in solid cancers: 0.9

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of COMMD1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

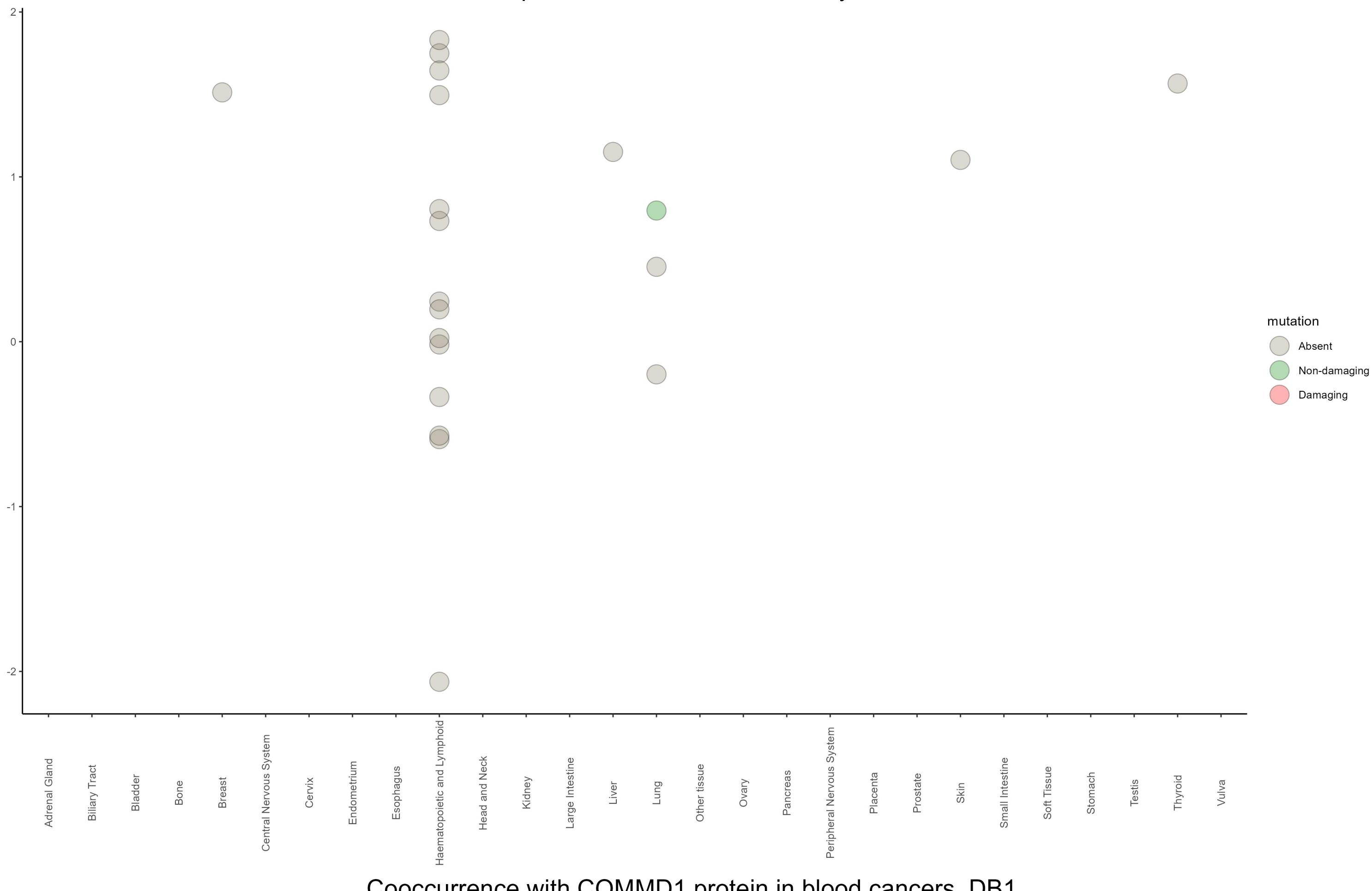
Negative cooccurrence



Positive cooccurrence

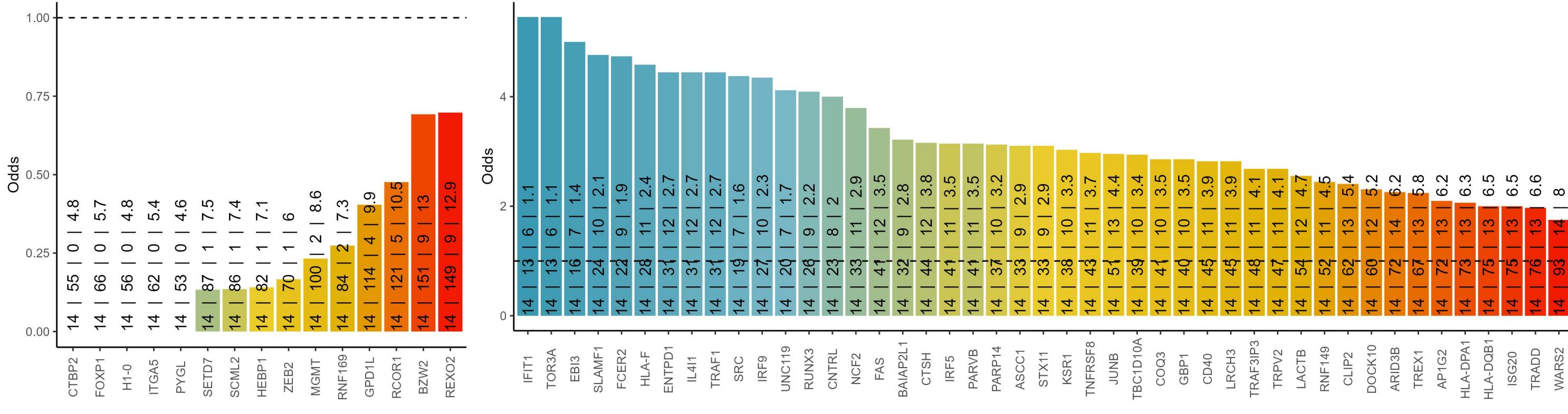


Amount of COMMD1 protein and mutation status by tissue, DB1



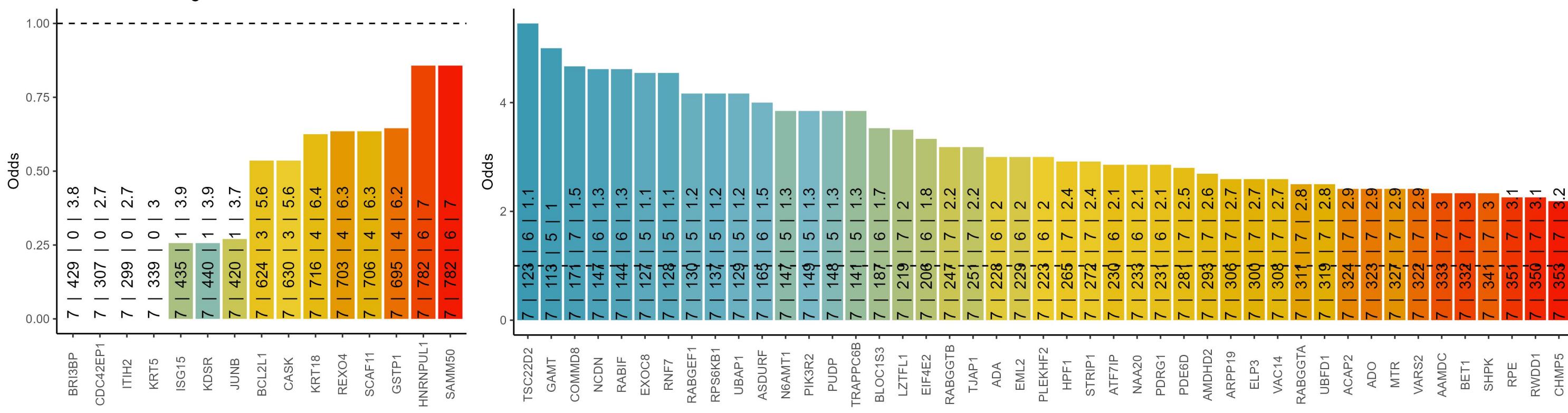
Cooccurrence with COMMD1 protein in blood cancers, DB1

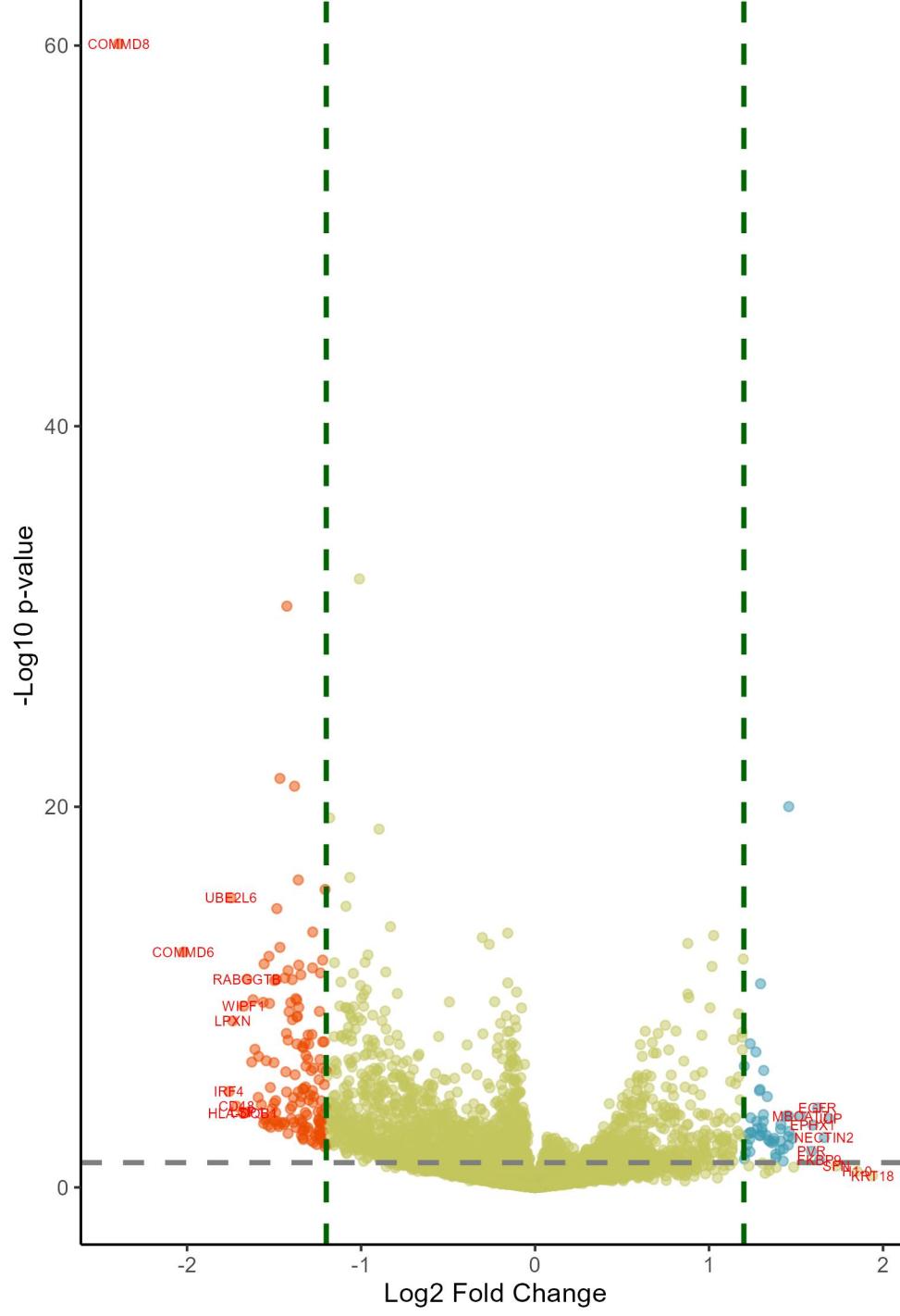
The text in the bars: incidence of COMMD1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with COMMD1 protein in solid cancers, DB1

The text in the bars: incidence of COMMD1 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

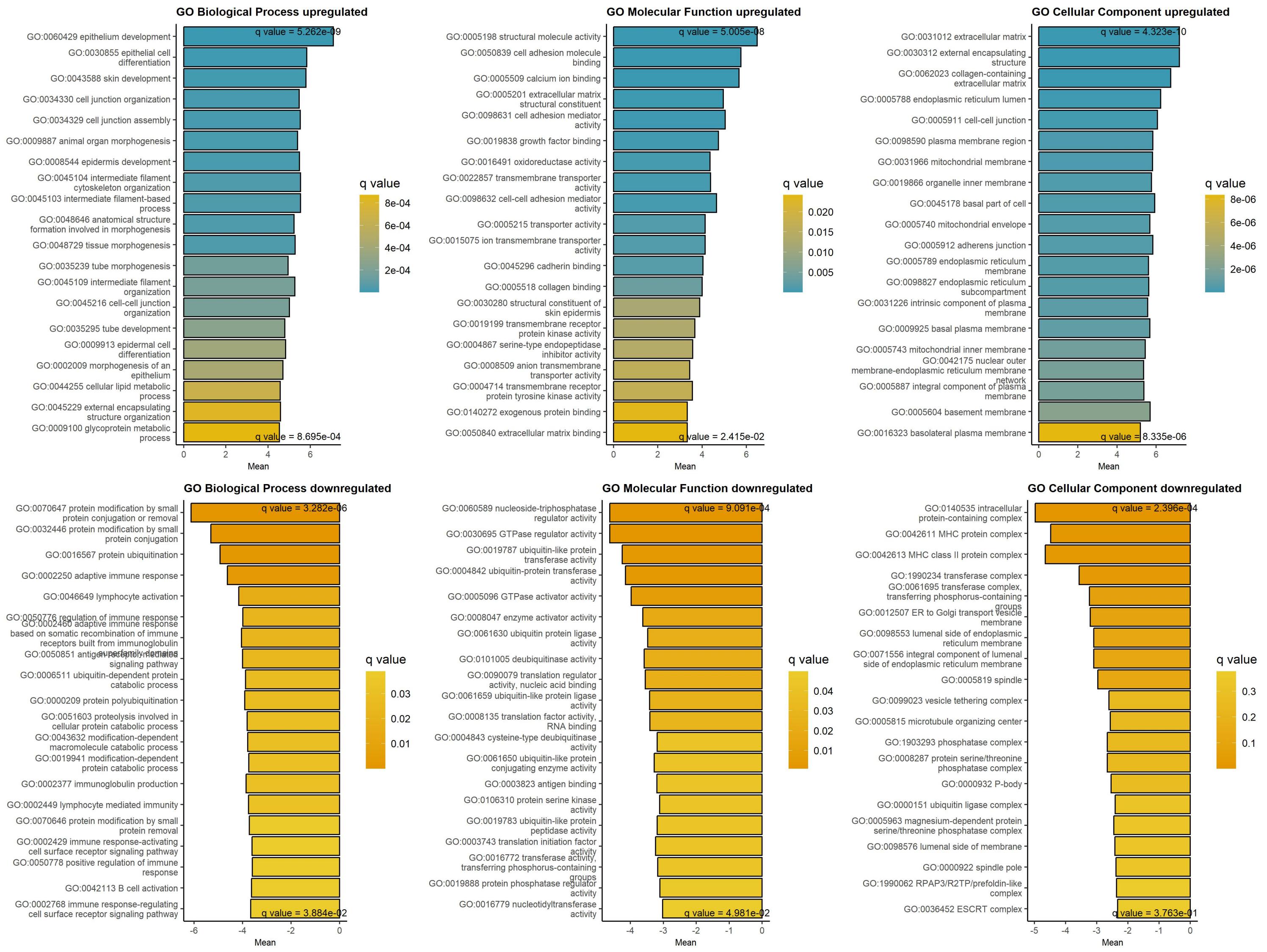




Downregulated at low/absent COMMD1 Upregulated at low/absent COMMD1

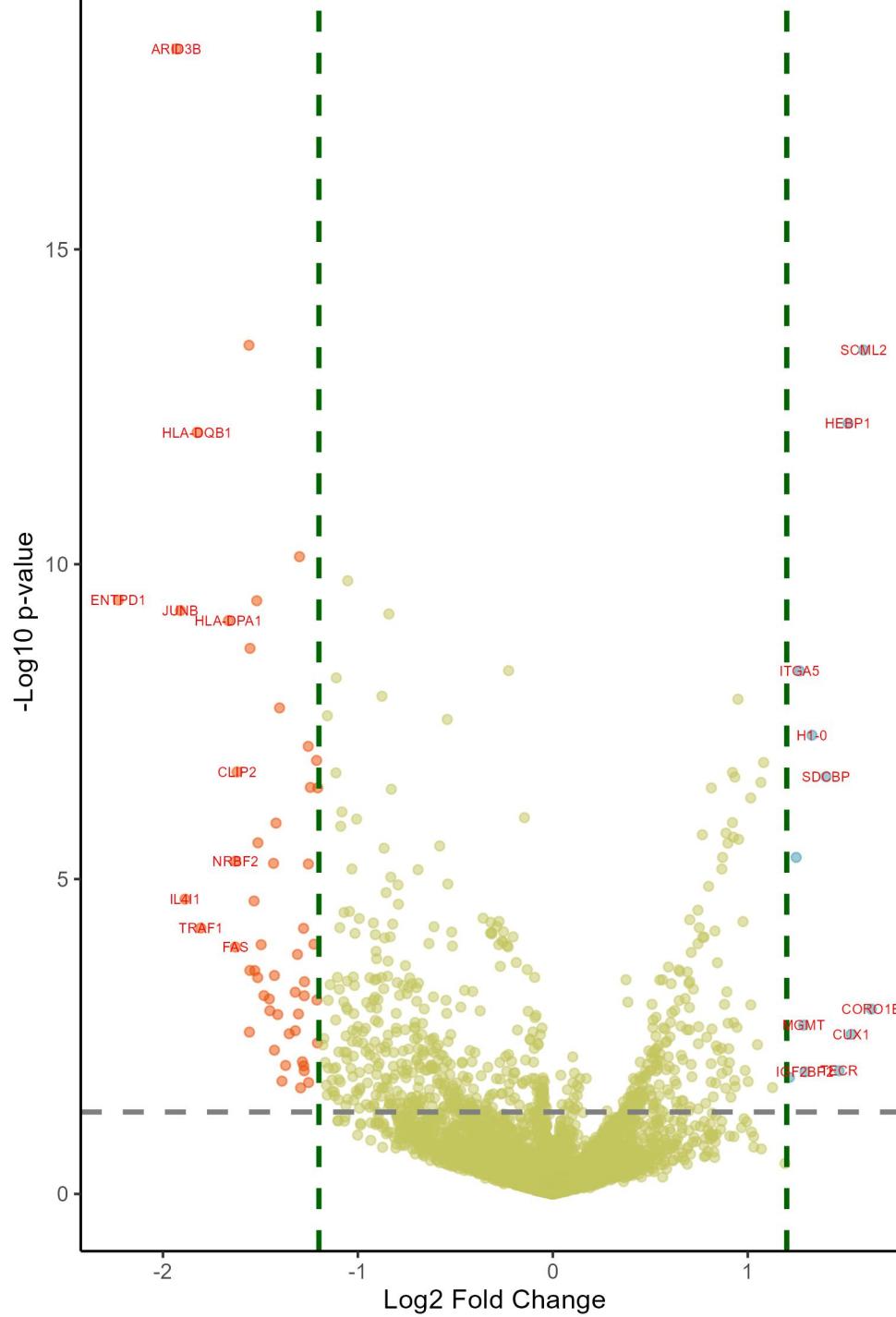
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.39	2.65e-57	COMMD8	COMM domain containing 8	1.94	4.58e-01	KRT18	keratin 18
-2.02	1.18e-10	COMMD6	COMM domain containing 6	1.85	3.27e-01	H1-0	H1.0 linker histone
-1.76	2.01e-04	IRF4	interferon regulatory factor 4	1.73	2.11e-01	SFN	stratifin
-1.75	3.13e-13	UBE2L6	ubiquitin conjugating enzyme E2 L6	1.69	2.89e-03	JUP	junction plakoglobin
-1.74	1.33e-07	LPXN	leupaxin	1.66	1.69e-02	NECTIN2	nectin cell adhesion molecule 2
-1.72	8.62e-04	CD48	CD48 molecule	1.63	1.29e-01	FKBP9	FKBP prolyl isomerase 9
-1.68	1.73e-03	HLA-DQB1	major histocompatibility complex, c	1.62	1.02e-03	EGFR	epidermal growth factor receptor
-1.67	3.09e-08	WIFP1	WAS/WASL interacting protein family	1.6	5.22e-03	EPHX1	epoxide hydrolase 1
-1.66	1.84e-09	RABGGTB	Rab geranylgeranyltransferase subun	1.59	5.96e-02	PVR	PVR cell adhesion molecule
-1.65	1.59e-03	LSP1	lymphocyte specific protein 1	1.53	2.24e-03	MBOAT7	membrane bound O-acyltransferase do
-1.63	9.61e-06	NCDN	neurochondrin	1.49	2.34e-01	KRT19	keratin 19
-1.62	1.61e-08	URI1	URI1 prefoldin like chaperone	1.48	1.82e-02	ITGA2	integrin subunit alpha 2
-1.61	2.56e-06	GIT2	GIT ArfGAP 2	1.46	9.42e-03	MYO1B	myosin IB
-1.59	3.57e-04	ARID3B	AT-rich interaction domain 3B	1.46	9.32e-18	SDC1	syndecan 1
-1.59	5.36e-06	NUDT2	nudix hydrolase 2	1.46	2.21e-03	PPL	periplakin
-1.57	7.47e-04	ISG20	interferon stimulated exonuclease g	1.46	1.55e-02	S100A16	S100 calcium binding protein A16
-1.56	2.07e-08	AVEN	apoptosis and caspase activation in	1.46	3.37e-02	PTK7	protein tyrosine kinase 7 (inactive)
-1.56	4.41e-03	PTPRCAP	protein tyrosine phosphatase recept	1.44	2.21e-03	ADAM9	ADAM metallopeptidase domain 9
-1.56	3.88e-10	STK10	serine/threonine kinase 10	1.43	4.84e-02	NIBAN2	niban apoptosis regulator 2
-1.55	3.17e-03	IL16	interleukin 16	1.43	1.40e-01	ITGA3	integrin subunit alpha 3
-1.54	8.46e-06	CELF2	CUGBP Elav-like family member 2	1.41	4.94e-03	APP	amyloid beta precursor protein
-1.54	2.91e-03	ENTPD1	ectonucleoside triphosphate diphosp	1.41	2.33e-02	HEB1	heme binding protein 1
-1.53	5.37e-03	HLA-DPA1	major histocompatibility complex, c	1.41	7.62e-03	CTBP2	C-terminal binding protein 2
-1.53	1.85e-10	RABGGTA	Rab geranylgeranyltransferase subun	1.41	5.45e-02	CORO1B	coronin 1B
-1.53	2.27e-08	ASMTL	acetylserotonin O-methyltransferase	1.39	2.41e-01	TPM1	tropomyosin 1
-1.52	1.33e-04	GMIP	GEM interacting protein	1.38	1.04e-01	DSP	desmoplakin
-1.52	6.45e-03	HLA-DPB1	major histocompatibility complex, c	1.38	7.74e-02	CAV1	caveolae associated protein 1
-1.52	2.49e-03	GMFG	glia maturation factor gamma	1.37	1.82e-02	CAV1	caveolin 1
-1.51	1.09e-03	NRBF2	nuclear receptor binding factor 2	1.37	2.30e-02	GNA11	G protein subunit alpha 11

GAGE analysis on upregulated and downregulated proteins at low/absent COMMD1 protein, DB1

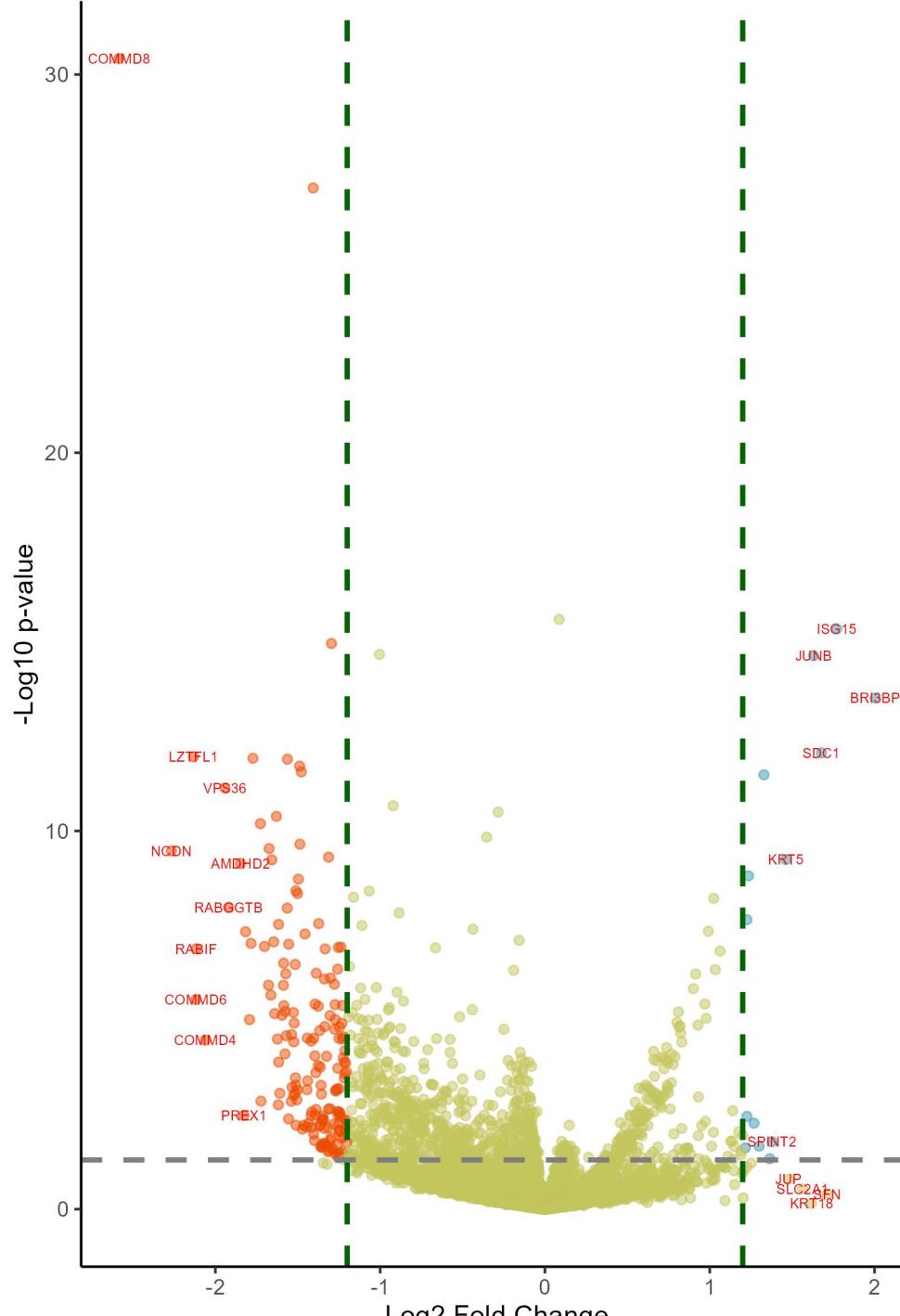


p-value < 0.05 & logFC > 1.2

Downregulated in blood cancers at low/absent COMMD1 Upregulated in blood cancers at low/absent COMMD1



logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.23	2.53e-07	ENTPD1	ectonucleoside triphosphate diphosph	1.63	4.15e-02	CORO1B	coronin 1B
-1.93	2.18e-15	ARID3B	AT-rich interaction domain 3B	1.59	6.61e-11	SCML2	Scm polycomb group protein like 2
-1.91	3.28e-07	JUNB	JunB proto-oncogene, AP-1 transcript	1.53	8.19e-02	CUX1	cut like homeobox 1
-1.89	2.13e-03	IL4I1	interleukin 4 induced 1	1.51	7.72e-10	HEBP1	heme binding protein 1
-1.82	8.92e-10	HLA-DQB1	major histocompatibility complex, c	1.47	1.96e-01	TECR	trans-2,3-enoyl-CoA reductase
-1.81	4.79e-03	TRAF1	TNF receptor associated factor 1	1.4	5.15e-05	SDCBP	syndecan binding protein
-1.66	4.02e-07	HLA-DPA1	major histocompatibility complex, c	1.33	1.50e-05	H1-0	H1.0 linker histone
-1.63	7.39e-03	FAS	Fas cell surface death receptor	1.29	2.02e-01	IGF2BP2	insulin like growth factor 2 mRNA b
-1.63	6.39e-04	NRBF2	nuclear receptor binding factor 2	1.29	6.60e-02	MGMT	O-6-methylguanine-DNA methyltransferase
-1.62	4.72e-05	CLIP2	CAP-Gly domain containing linker pr	1.27	2.05e-06	ITGA5	integrin subunit alpha 5
-1.56	6.61e-11	TSTD1	thiosulfate sulfurtransferase like	1.25	5.69e-04	SETD7	SET domain containing 7, histone ly
-1.56	7.64e-02	HLA-F	major histocompatibility complex, c	1.21	2.35e-01	CPD	carboxypeptidase D
-1.55	1.55e-02	TNFRSF8	TNF receptor superfamily member 8	1.19	7.63e-01	HSPB1	heat shock protein family B (small)
-1.55	1.03e-06	CD70	CD70 molecule	1.13	2.97e-01	PIK3AP1	phosphoinositide-3-kinase adaptor p
-1.53	2.24e-03	LACTB	lactamase beta	1.08	3.61e-05	CTBP2	C-terminal binding protein 2
-1.53	1.55e-02	CD58	CD58 molecule	1.07	6.18e-01	BZW2	basic leucine zipper and W2 domains
-1.52	2.53e-07	CD48	CD48 molecule	1.07	6.06e-05	PYGL	glycogen phosphorylase L
-1.51	1.86e-02	CD40	CD40 molecule	1.05	1.07e-01	IGF2BP1	insulin like growth factor 2 mRNA b
-1.51	3.65e-04	TREX1	three prime repair exonuclease 1	1.03	6.03e-01	REXO2	RNA exonuclease 2
-1.5	7.04e-03	FTL	ferritin light chain	1.03	5.25e-01	PYCARD	PYD and CARD domain containing
-1.48	2.92e-02	TBC1D10A	TBC1 domain family member 10A	1.02	5.25e-01	CPT1A	carnitine palmitoyltransferase 1A
-1.45	3.21e-02	CTSH	cathepsin H	1.02	3.70e-02	RBBP5	RB binding protein 5, histone lysin
-1.45	4.33e-02	PARVB	parvin beta	1.02	9.26e-05	PTK2	protein tyrosine kinase 2
-1.43	6.80e-04	ISG20	interferon stimulated exonuclease g	1	2.54e-01	ARHGAP25	Rho GTPase activating protein 25
-1.43	1.81e-02	DDX3Y	DEAD-box helicase 3 Y-linked	0.99	5.25e-01	DSP	desmoplakin
-1.43	1.22e-01	NCF2	neutrophil cytosolic factor 2	0.99	1.96e-01	IRF2BP1	interferon regulatory factor 2 bind
-1.42	2.05e-04	COMM6	COMM domain containing 6	0.98	5.25e-01	VPS36	vacuolar protein sorting 36 homolog
-1.41	4.78e-02	COQ3	coenzyme Q3, methyltransferase	0.98	4.20e-03	RNF169	ring finger protein 169
-1.4	6.36e-06	IRF4	interferon regulatory factor 4	0.97	5.25e-01	LANCL1	LanC like 1

Differentially expressed proteins in solid cancers at absence/low amount of COMMD1 , DB1
p-value < 0.05 & logFC > 1.2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.59	1.25e-27	COMM6	COMM domain containing 6	2	2.26e-11	BRI3BP	BRI3 binding protein
-2.27	8.94e-08	NCDN	neurochondrin	1.77	6.02e-13	ISG15	ISG15 ubiquitin like modifier
-2.13	6.48e-10	LZTFL1	leucine zipper transcription factor	1.71	8.00e-01	SFN	stratifin
-2.12	2.41e-04	COMM6	COMM domain containing 6	1.68	5.72e-10	SDC1	syndecan 1
-2.12	1.53e-05	RABIF	RAB interacting factor	1.63	1.92e-12	JUNB	JunB proto-oncogene, AP-1 transcript
-2.06	1.62e-03	COMM4	COMM domain containing 4	1.62	8.63e-01	KRT18	keratin 18
-1.94	2.85e-09	VPS36	vacuolar protein sorting 36 homolog	1.56	7.18e-01	SLC2A1	solute carrier family 2 member 1
-1.92	1.90e-06	RABGGTB	Rab geranylgeranyltransferase subun	1.48	5.82e-01	JUP	junction plakoglobin
-1.85	1.66e-07	AMDHD2	amidohydrolase domain containing 2	1.46	1.38e-07	KRT5	keratin 5
-1.83	5.22e-02	PREX1	phosphatidylinositol-3,4,5-trisphos	1.38	1.56e-01	SPINT2	serine peptidase inhibitor, Kunitz
-1.82	6.70e-06	STRIP1	striatin interacting protein 1	1.36	2.96e-01	BCL2L1	BCL2 like 1
-1.79	6.26e-04	TRAPP/C8	trafficking protein particle comple	1.33	1.36e-09	CDCA3	cell division cycle associated 3
-1.78	1.25e-05	PDE6D	phosphodiesterase 6D	1.3	1.83e-01	PTPMT1	protein tyrosine phosphatase mitoch
-1.77	6.48e-10	RPE	ribulose-5-phosphate-3-epimerase	1.27	7.18e-02	KIAA1522	KIAA1522
-1.73	2.03e-08	CHMP5	charged multivesicular body protein	1.25	3.47e-01	CDCA8	cell division cycle associated 8
-1.72	2.84e-02	TSC22D2	TSC22 domain family member 2	1.23	3.40e-07	CDC42EP1	CDC42 effector protein 1
-1.7	1.45e-05	UBFD1	ubiquitin family domain containing	1.23	4.02e-01	THBS1	thrombospondin 1
-1.68	1.11e-04	VAC14	VAC14 component of PIKFYVE complex	1.23	5.44e-02	KIF20A	kinesin family member 20A
-1.67	8.11e-08	TUBB2A	tubulin beta 2A class IIa	1.23	3.70e-06	SERPINB5	serpin family B member 5
-1.66	1.89e-04	ELP3	elongator acetyltransferase complex	1.22	1.97e-01	CDH1	cadherin 1
-1.66	1.38e-07	SH3PXD2B	SH3 and PX domains 2B	1.2	4.47e-01	BCAM	basal cell adhesion molecule (Luthe
-1.65	1.16e-05	BET1	Bet1 golgi vesicular membrane traff	1.2	8.42e-01	KRT19	keratin 19
-1.64	4.73e-04	SHOC2	SHOC2 leucine rich repeat scaffold	1.2	1.18e-01	LAD1	ladinin 1
-1.63	1.37e-08	PPP6R1	protein phosphatase 6 regulatory su	1.2	4.85e-01	ANXA3	annexin A3
-1.62	1.54e-03	RNF181	ring finger protein 181	1.19	2.19e-01	MISP	mitotic spindle positioning
-1.62	3.33e-02	PIK3R2	phosphoinositide-3-kinase regulator	1.19	2.55e-01	REXO4	REX4 homolog, 3'-5' exonuclease
-1.62	4.67e-06	FHOD1	formin homology 2 domain containing	1.18	1.02e-01	KDSR	3-ketodihydroinosine reductase
-1.62	4.81e-03	TJAP1	tight junction associated protein 1	1.15	6.68e-01	EGFR	epidermal growth factor receptor
-1.61	1.97e-02	DDT	D-dopachrome tautomerase	1.15	1.87e-01	EPCAM	epithelial cell adhesion molecule

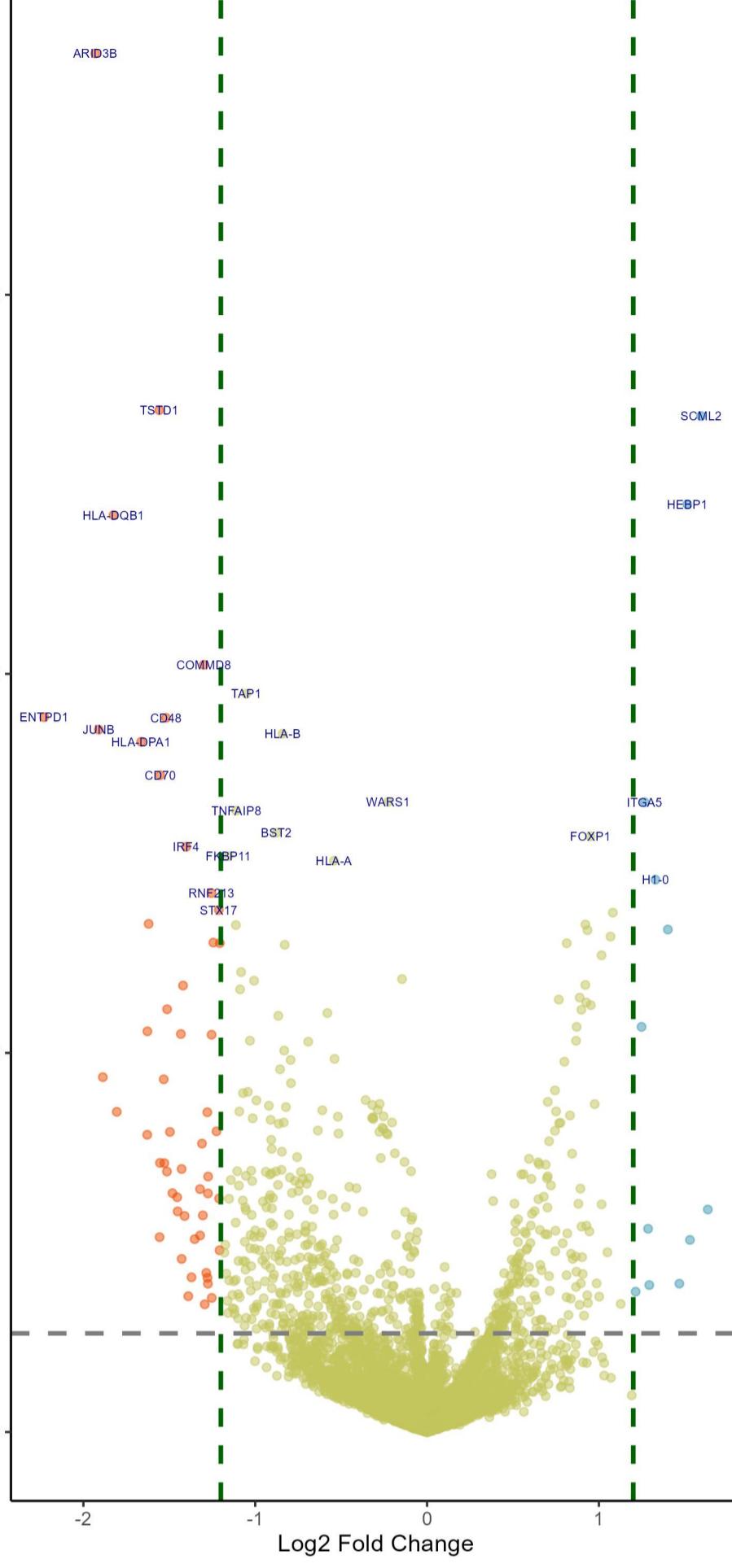
COMMD1 network, DB1, no Pearson r > 0.3

p-value < 0.05 & logFC > 1.2

Sorted by p values!

Downregulated in blood cancers at low/absent COMMD1 Upregulated in blood cancers at low/absent COMMD1

-Log10 p-value

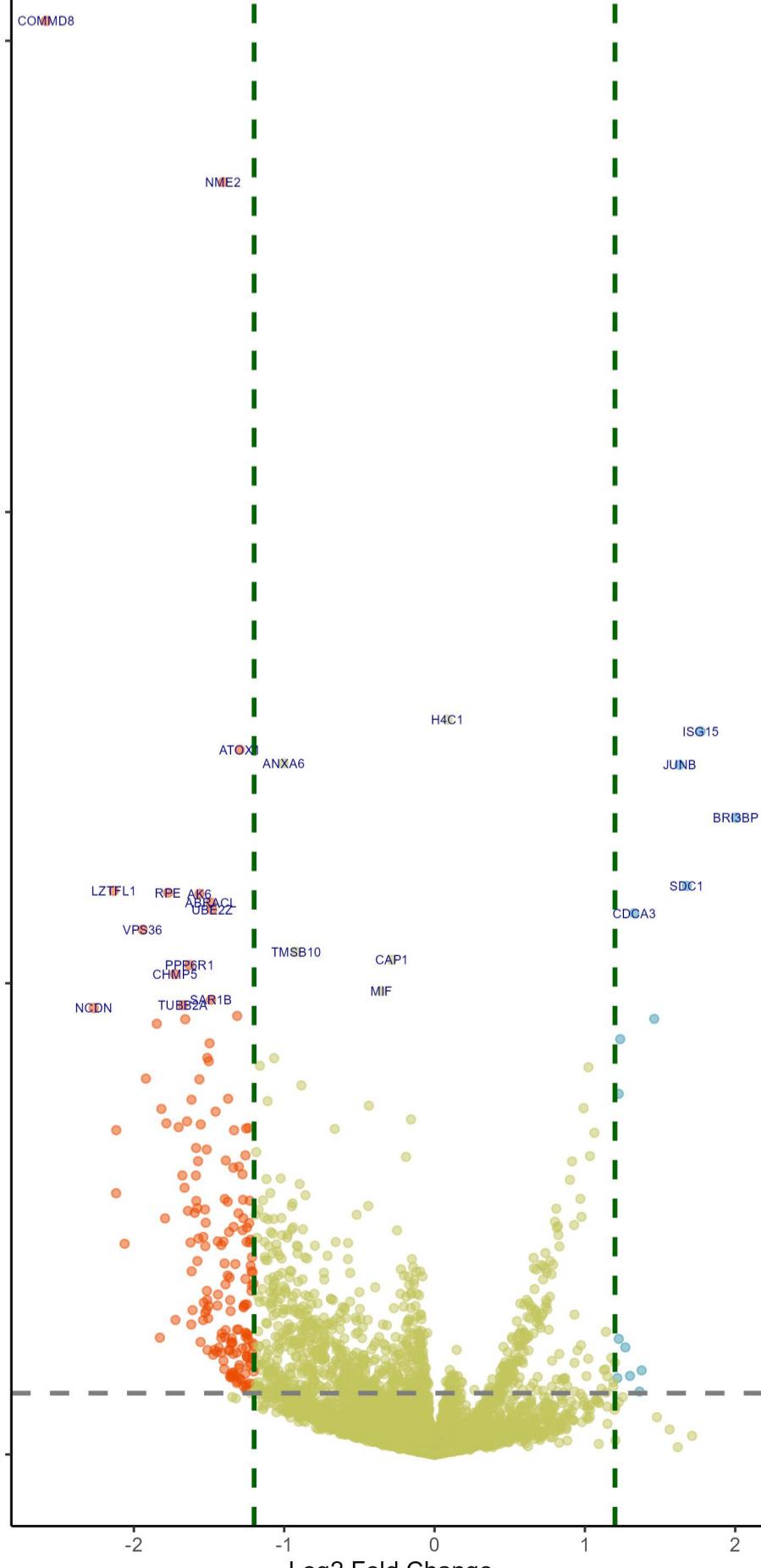


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.93	2.18e-15	ARID3B	AT-rich interaction domain 3B	1.59	6.61e-11	SCML2	Scm polycomb group protein like 2
-1.56	6.61e-11	TSTD1	thiosulfate sulfurtransferase like	1.51	7.72e-10	HEBP1	heme binding protein 1
-1.82	8.92e-10	HLA-DQB1	major histocompatibility complex, c	1.27	2.05e-06	ITGA5	integrin subunit alpha 5
-1.3	7.21e-08	COMMD8	COMM domain containing 8	0.95	4.87e-06	FOXP1	forkhead box P1
-1.05	1.52e-07	TAP1	transporter 1, ATP binding cassette	1.33	1.50e-05	H1-0	H1.0 linker histone
-2.23	2.53e-07	ENTPD1	ectonucleoside triphosphate diphosph	1.08	3.61e-05	CTBP2	C-terminal binding protein 2
-1.52	2.53e-07	CD48	CD48 molecule	0.92	4.72e-05	GALT	galactose-1-phosphate uridyltransferase
-1.91	3.28e-07	JUNB	JunB proto-oncogene, AP-1 transcript	1.4	5.15e-05	SDCBP	syndecan binding protein
-0.84	3.41e-07	HLA-B	major histocompatibility complex, c	0.93	5.15e-05	ZNF800	zinc finger protein 800
-1.66	4.02e-07	HLA-DPA1	major histocompatibility complex, c	1.07	6.06e-05	PYGL	glycogen phosphorylase L
-1.55	1.03e-06	CD70	CD70 molecule	0.81	6.79e-05	SEC24B	SEC24 homolog B, COPII coat complex
-0.23	2.05e-06	WARS1	tryptophanyl-tRNA synthetase 1	1.02	9.26e-05	PTK2	protein tyrosine kinase 2
-1.11	2.50e-06	TNFAIP8	TNF alpha induced protein 8	0.92	2.05e-04	FAIM	Fas apoptotic inhibitory molecule
-0.88	4.61e-06	BST2	bone marrow stromal cell antigen 2	0.89	2.81e-04	TESC	tescalcin
-1.4	6.36e-06	IRF4	interferon regulatory factor 4	0.77	2.92e-04	CHD7	chromodomain helicase DNA binding protein 7
-1.16	8.07e-06	FKBP11	FKBP prolyl isomerase 11	0.93	3.12e-04	DUSP23	dual specificity phosphatase 23
-0.54	8.81e-06	HLA-A	major histocompatibility complex, c	0.95	3.31e-04	ADD2	adducin 2
-1.25	2.16e-05	RNF213	ring finger protein 213	0.9	3.65e-04	FHL1	four and a half LIM domains 1
-1.21	3.47e-05	STX17	syntaxin 17	1.25	5.69e-04	SETD7	SET domain containing 7, histone lysine methyltransferase
-1.62	4.72e-05	CLIP2	CAP-Gly domain containing linker protein	0.87	5.69e-04	PCBD2	pterin-4 alpha-carbinolamine dehydratase
-1.11	4.72e-05	RFTN1	raftlin, lipid raft linker 1	0.87	7.92e-04	HSD17B11	hydroxysteroid 17-beta dehydrogenase
-1.24	6.79e-05	MECR	mitochondrial trans-2-enoyl-CoA reductase	0.8	1.38e-03	PHC2	polyhomeotic homolog 2
-1.21	6.79e-05	NT5DC1	5'-nucleotidase domain containing 1	0.74	3.05e-03	NUDT16L1	nudix hydrolase 16 like 1
-0.83	6.91e-05	FNBP1	formin binding protein 1	0.7	4.02e-03	STK3	serine/threonine kinase 3
-1.08	1.50e-04	RDH11	retinol dehydrogenase 11	0.98	4.20e-03	RNF169	ring finger protein 169
-0.15	1.81e-04	PSME2	proteasome activator subunit 2	0.75	4.79e-03	MBOAT7	membrane bound O-acyltransferase domain containing 7
-1.01	1.85e-04	PDLIM5	PDZ and LIM domain 5	0.83	5.22e-03	CLEC11A	C-type lectin domain containing 11A
-1.42	2.05e-04	COMMD6	COMM domain containing 6	0.78	5.83e-03	EIF4EBP1	eukaryotic translation initiation factor 4E-binding protein 1
-1.09	2.24e-04	ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PDZ domain containing 1	0.77	5.85e-03	DERL1	derlin 1
-1.51	3.65e-04	TREX1	three prime repair exonuclease 1	0.74	7.01e-03	ERI3	ERI3 exoribonuclease family member
-0.58	3.96e-04	B2M	beta-2-microglobulin	0.71	8.83e-03	PTGR3	prostaglandin reductase 3
-0.87	4.22e-04	COTL1	coactosin like F-actin binding protein	0.84	1.23e-02	TUBGCP3	tubulin gamma complex associated protein 3
-1.63	6.39e-04	NRBF2	nuclear receptor binding factor 2	0.59	1.40e-02	MAFG	MAF bZIP transcription factor G
-1.43	6.80e-04	ISG20	interferon stimulated exonuclease 1	0.65	1.53e-02	PAXBP1	PAX3 and PAX7 binding protein 1
-1.25	6.83e-04	FLNC	filamin C	0.65	1.59e-02	PRUNE1	prune exopolyphosphatase 1
-1.03	7.92e-04	DHRS7	dehydrogenase/reductase 7	0.69	1.60e-02	DYNC2H1	dynein cytoplasmic 2 heavy chain 1
-0.69	7.99e-04	TUBA4A	tubulin alpha 4a	0.38	1.94e-02	BAG6	BAG cochaperone 6
-0.83	1.03e-03	TIGAR	TP53 induced glycolysis regulatory	0.56	1.94e-02	CDCA7	cell division cycle associated 7
0.54	1.31e-03	ANXA6	annexin A6	0.55	1.91e-02	MADAK1	mitogen activated protein kinase kinase 1

Sorted by p values!

Downregulated in solid cancers at low/absent COMMD1 Upregulated in solid cancers at low/absent COMMD1

-Log10 p-value

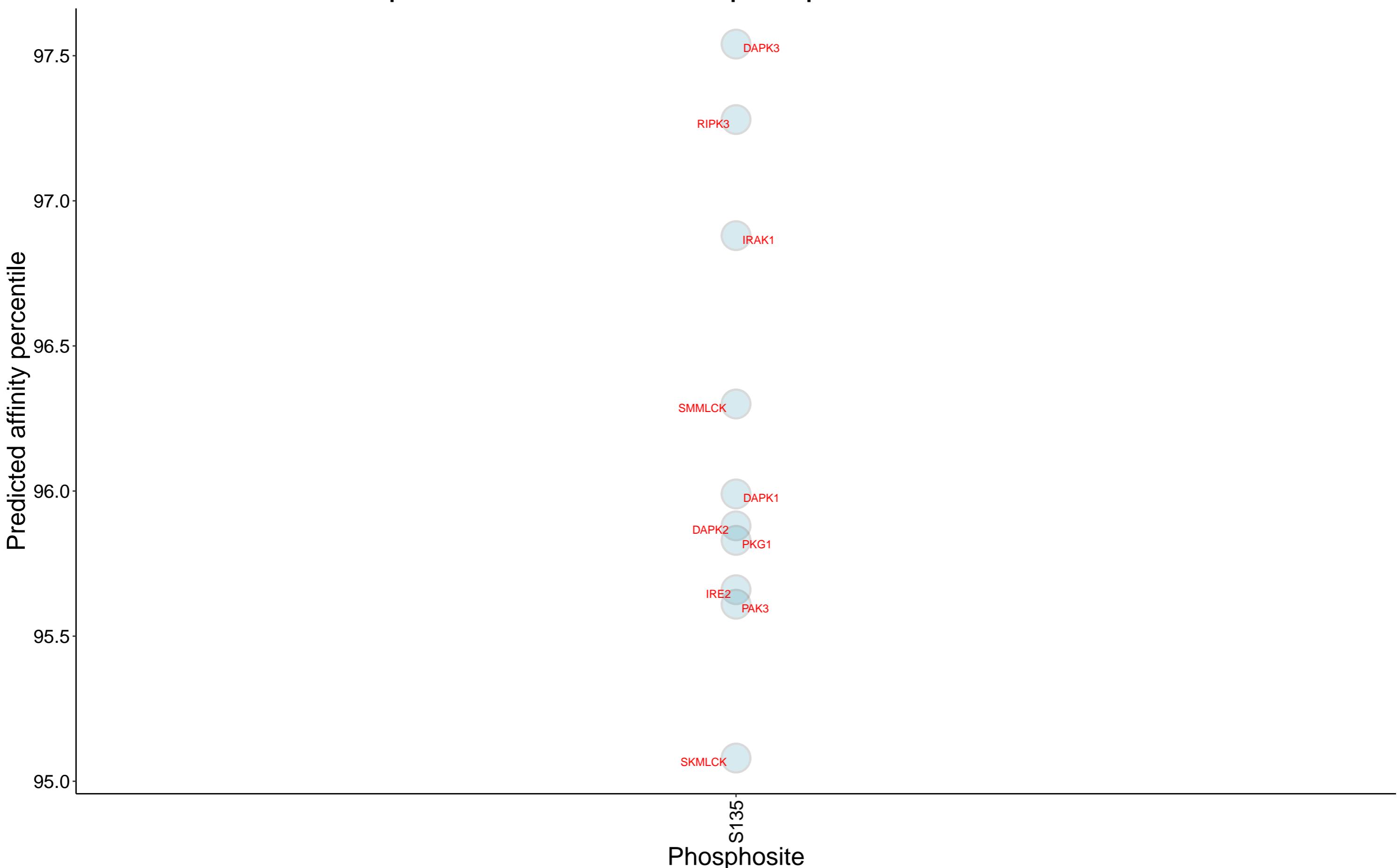


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-2.59	1.25e-27	COMMD8	COMM domain containing 8	0.09	4.24e-13	H4C1	H4 clustered histone 1
-1.41	2.21e-24	NME2	NME/NM23 nucleoside diphosphate kinase 2	1.77	6.02e-13	ISG15	ISG15 ubiquitin like modifier
-1.3	1.22e-12	ATOX1	antioxidant 1 copper chaperone	1.63	1.92e-12	JUNB	JunB proto-oncogene, AP-1 transcript
-1	1.92e-12	ANXA6	annexin A6	2	2.26e-11	BRI3BP	BRI3 binding protein
-2.13	6.48e-10	LZTFL1	leucine zipper transcription factor	1.68	5.72e-10	SDC1	syndecan 1
-1.77	6.48e-10	RPE	ribulose-5-phosphate-3-epimerase	1.33	1.36e-09	CDCA3	cell division cycle associated 3
-1.56	6.48e-10	AK6	adenylate kinase 6	1.46	1.38e-07	KRT5	keratin 5
-1.49	9.18e-10	ABRACL	ABRA C-terminal like	1.23	3.40e-07	CDC42EP1	CDC42 effector protein 1
-1.48	1.22e-09	UBE2Z	ubiquitin conjugating enzyme E2 Z	1.02	1.12e-06	TMEM65	transmembrane protein 65
-1.94	2.85e-09	VPS36	vacuolar protein sorting 36 homolog	1.23	3.70e-06	SERPINB5	serpin family B member 5
-0.92	7.95e-09	TMSB10	thymosin beta 10	0.99	6.63e-06	ITIH2	inter-alpha-trypsin inhibitor heavy chain 2
-0.28	1.11e-08	CAP1	cyclase associated actin cytoskeleton	1.06	1.71e-05	DSC2	desmocollin 2
-1.63	1.37e-08	PPP6R1	protein phosphatase 6 regulatory subunit 1	1.03	4.91e-05	ITM2B	integral membrane protein 2B
-1.73	2.03e-08	CHMP5	charged multivesicular body protein 5	0.91	5.99e-05	FAM169A	family with sequence similarity 169
-0.35	4.42e-08	MIF	macrophage migration inhibitory factor	0.9	1.32e-04	TMEM201	transmembrane protein 201
-1.49	6.48e-08	SAR1B	secretion associated Ras related GT	0.97	3.07e-04	KRT16	keratin 16
-1.67	8.11e-08	TUBB2A	tubulin beta 2A class IIa	0.81	4.40e-04	ARVCF	ARVCF delta catenin family member
-2.27	8.94e-08	NCDN	neurochondrin	0.98	6.01e-04	TRIM29	tripartite motif containing 29
-1.31	1.26e-07	FAH	fumarylacetoacetate hydrolase	0.8	7.15e-04	TOR4A	torsin family 4 member A
-1.66	1.38e-07	SH3PXD2B	SH3 and PX domains 2B	0.93	8.18e-04	ITGB6	integrin subunit beta 6
-1.85	1.66e-07	AMDHD2	amidohydrolase domain containing 2	0.82	8.57e-04	D2HGDH	D-2-hydroxyglutarate dehydrogenase
-1.5	4.04e-07	GBE1	1,4-alpha-glucan branching enzyme 1	0.81	8.94e-04	AMACR	alpha-methylacyl-CoA racemase
-1.51	7.84e-07	HS1BP3	HCLS1 binding protein 3	0.82	1.18e-03	NAT14	N-acetyltransferase 14 (putative)
-1.07	7.84e-07	CBR3	carbonyl reductase 3	0.83	1.75e-03	NECTIN1	nectin cell adhesion molecule 1
-1.5	8.85e-07	DCTD	dCMP deaminase	0.74	2.38e-03	SIGMAR1	sigma non-opioid intracellular receptor
-1.16	1.07e-06	FKBP1A	FKBP prolyl isomerase 1A	0.66	2.85e-03	MAFG	MAF bZIP transcription factor G
-1.92	1.90e-06	RABGGTB	Rab geranylgeranyltransferase subunit	0.77	3.19e-03	HGFAC	HGF activator
-1.56	1.92e-06	SERF2	small EDKR-rich factor 2	0.79	3.72e-03	ACSL5	acyl-CoA synthetase long chain family member 5
-0.89	2.50e-06	ARPC5	actin related protein 2/3 complex subunit 5	0.71	3.74e-03	MGAT5	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylgalactosaminidase
-1.37	4.58e-06	FKBP5	FKBP prolyl isomerase 5	0.72	3.91e-03	CD46	CD46 molecule
-1.62	4.67e-06	FHOD1	formin homology 2 domain containing	0.66	4		

Insufficient number of paired observations in DB1 for COMMD1

Insufficient number of paired observations in DB1 for COMMD1

Top 10 kinases for each phosphosite in COMMD1



Kinases with affinity greater than 98.5% to COMMD1

No sufficient paired observations in DB1 for COMMD1