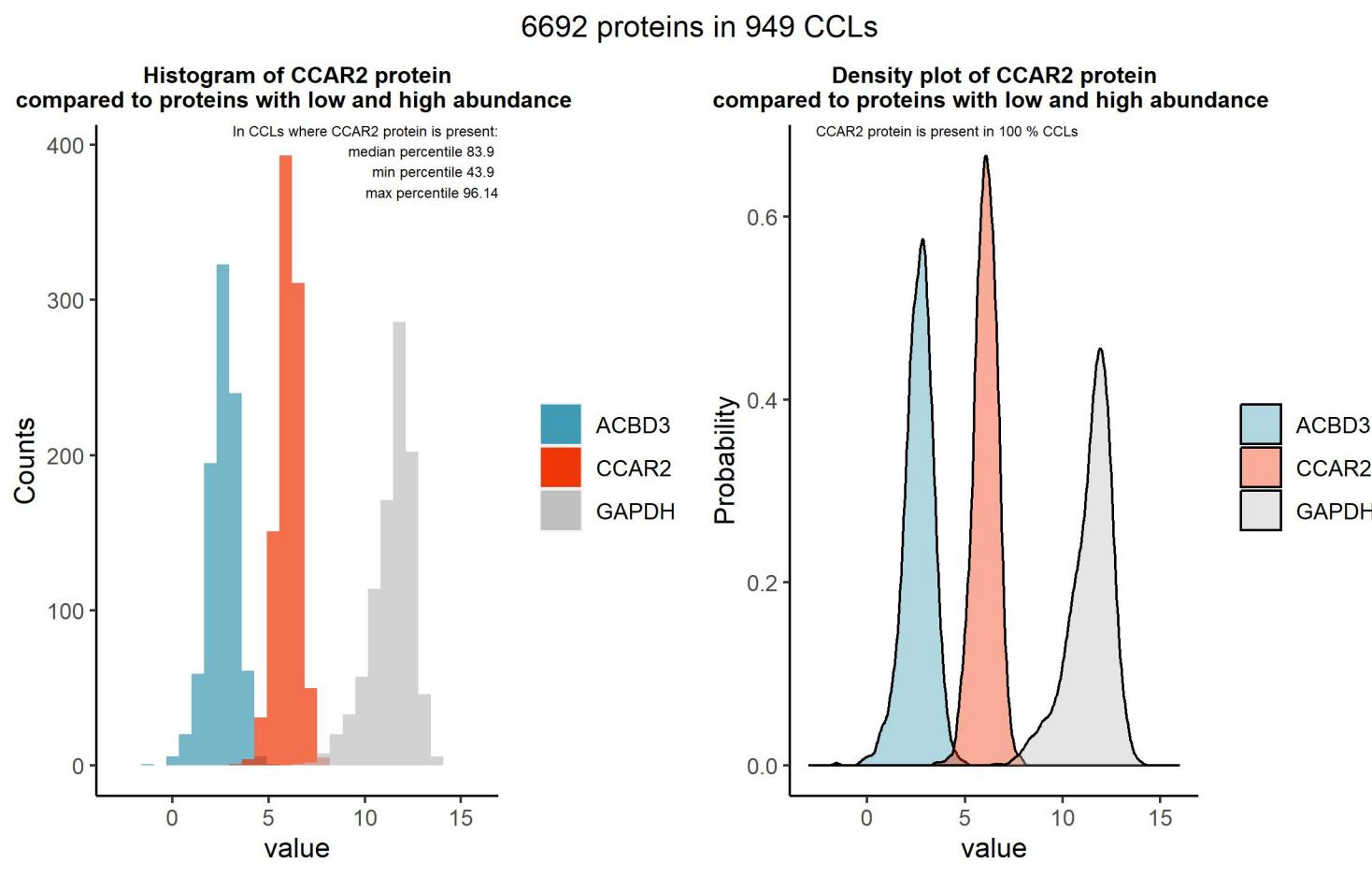


CCAR2

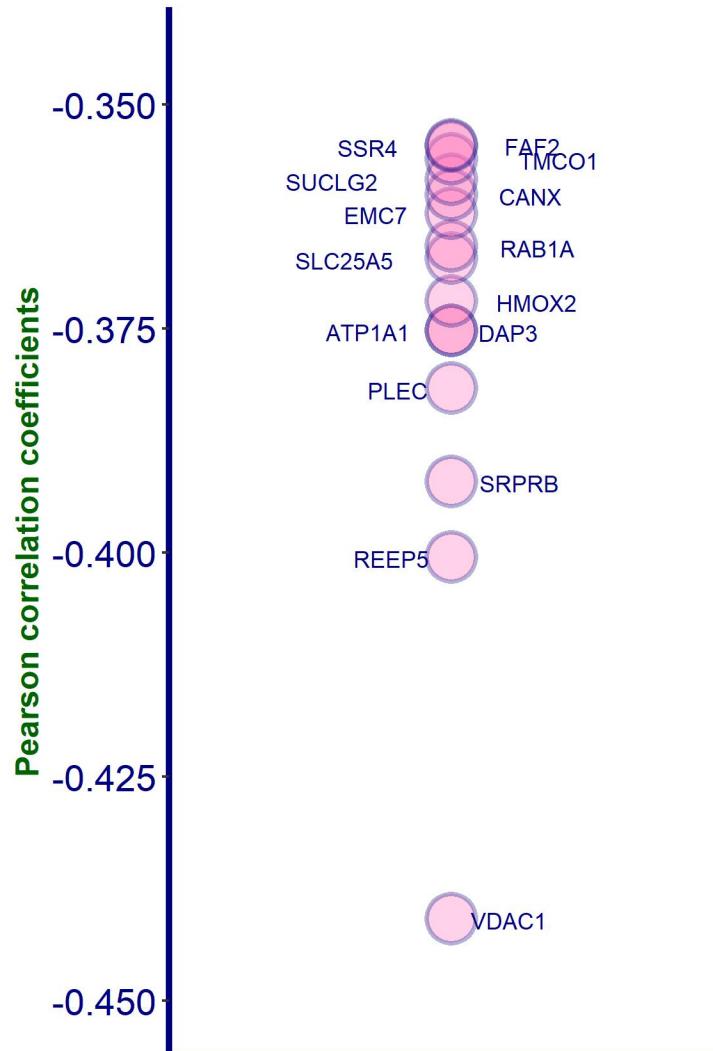
Protein name: CCAR2 ; UNIPROT: Q8N163 ; Gene name: cell cycle and apoptosis regulator 2

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

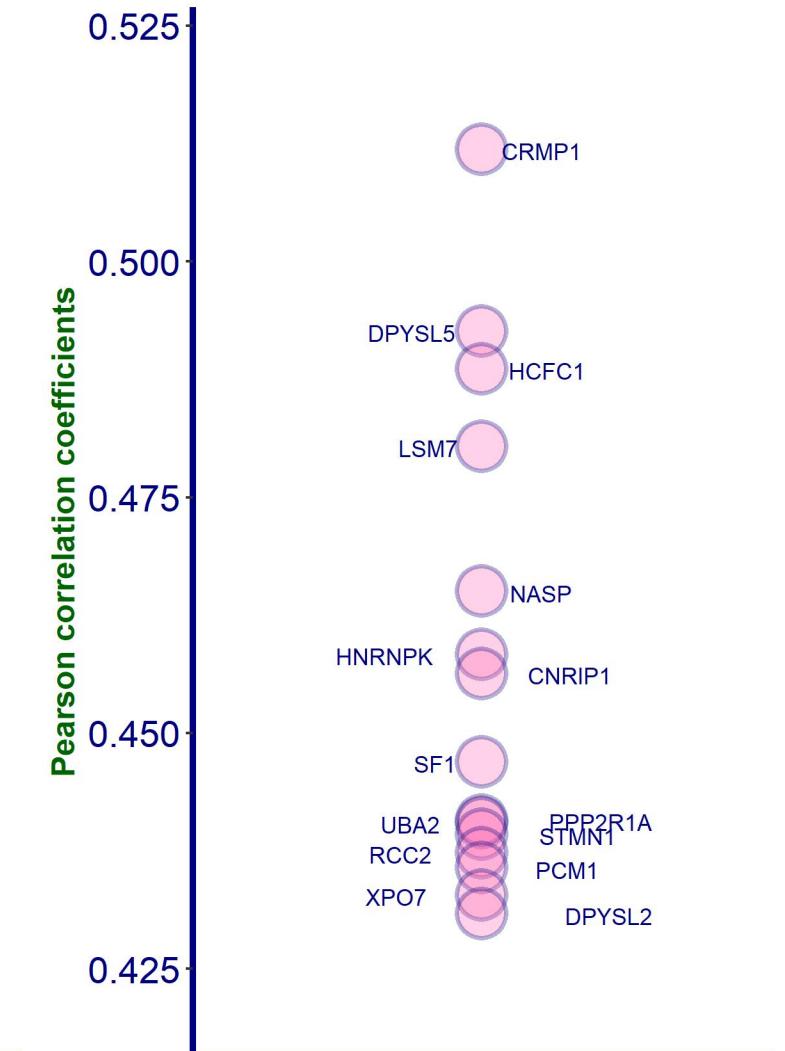
Sanger Institute Protein Database 1 (DB1), protein presence is certain



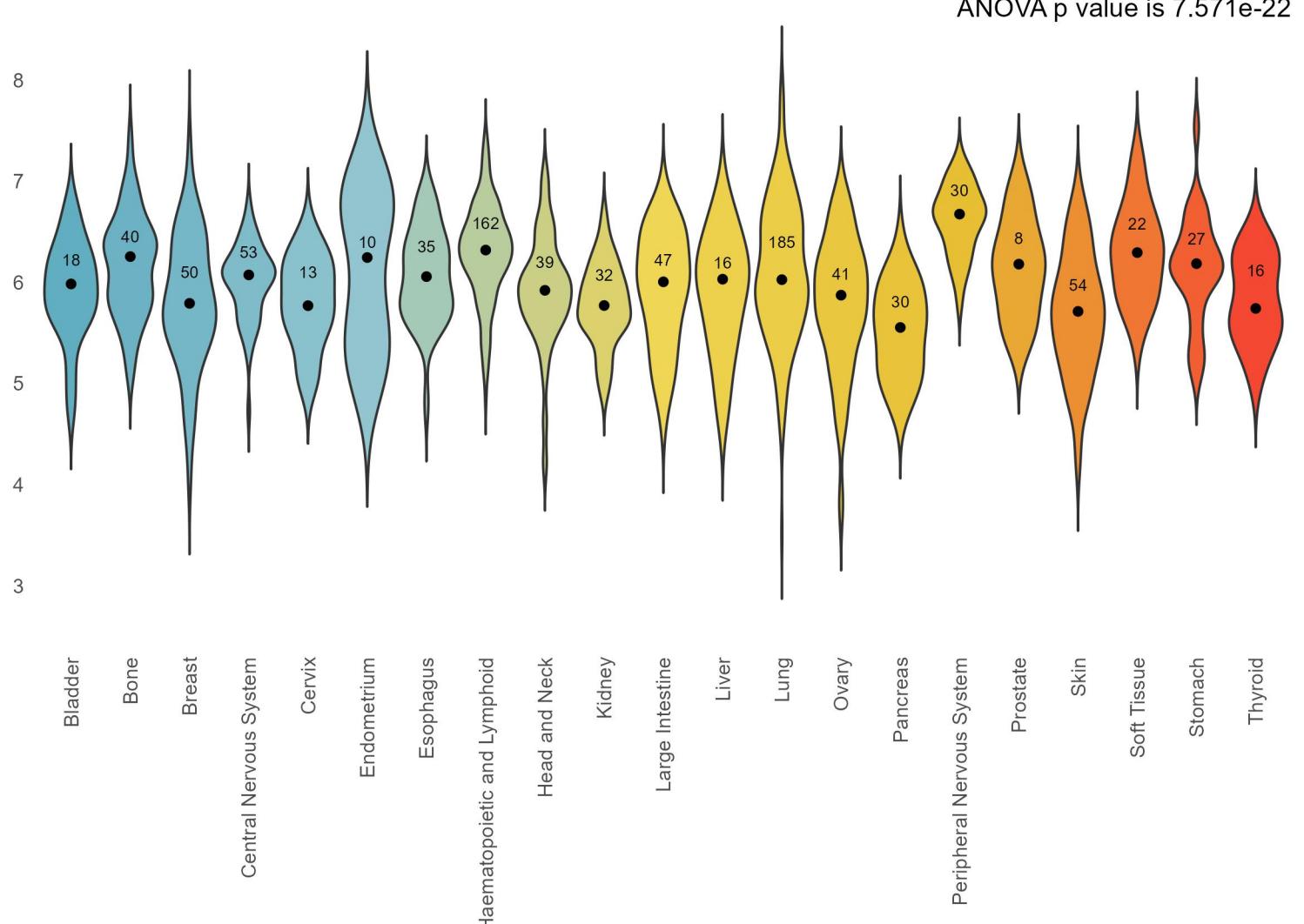
Top negative correlations of CCAR2 protein, DB1



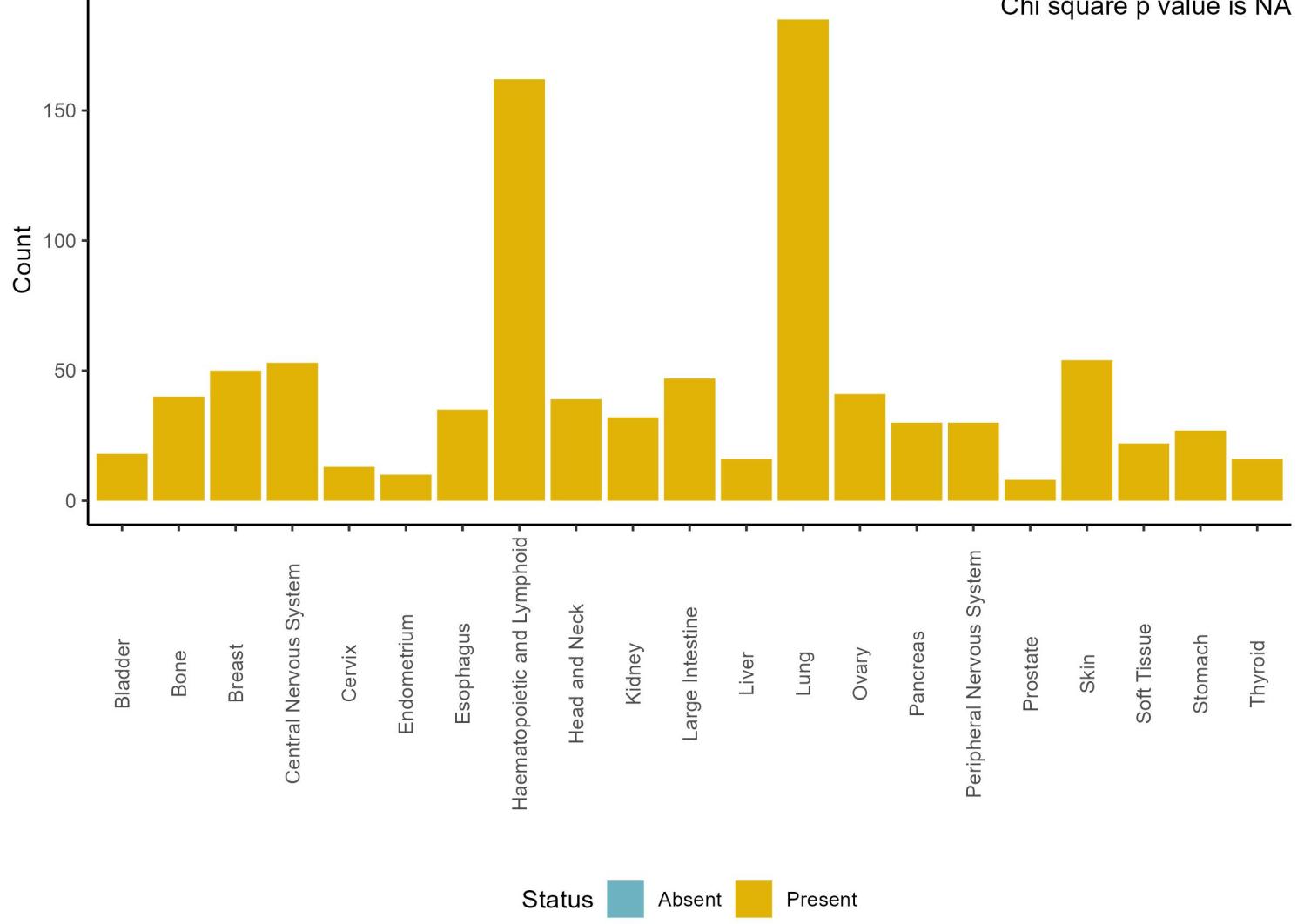
Top positive correlations of CCAR2 protein, DB1



Amount of CCAR2 protein, number of CCLs where it is present by tissue, DB1



Present and absent CCAR2 protein counts by tissue, DB1

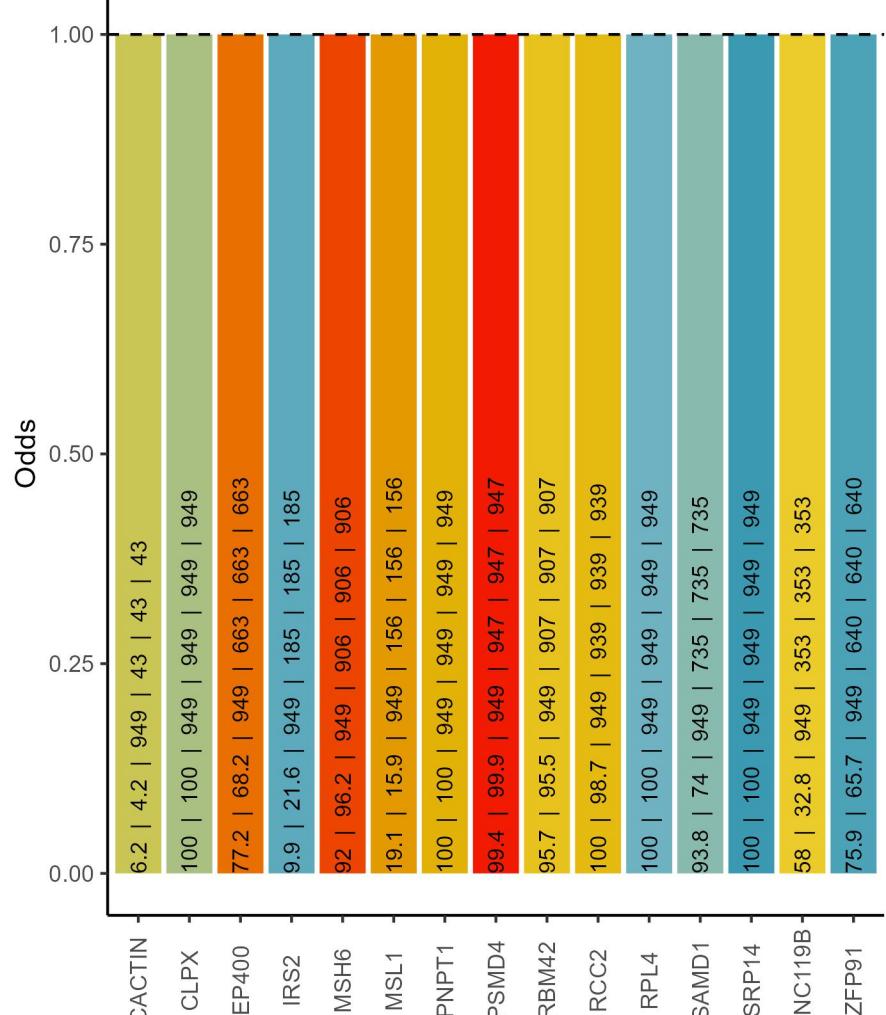


Cooccurrence with CCAR2 protein, DB1

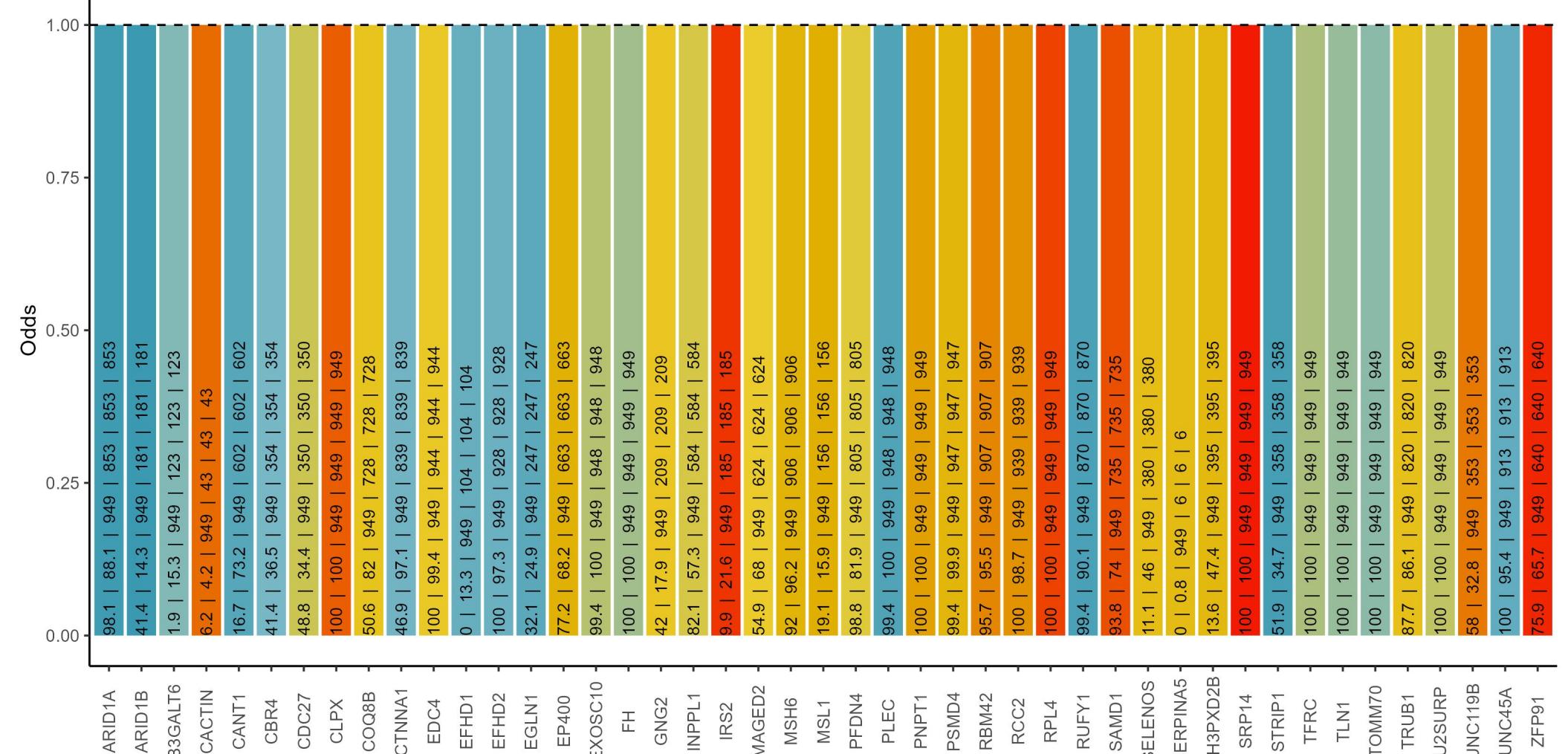
% of CCAR2 in blood cancers: 100 ; % of CCAR2 in solid cancers: 100

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of CCAR2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

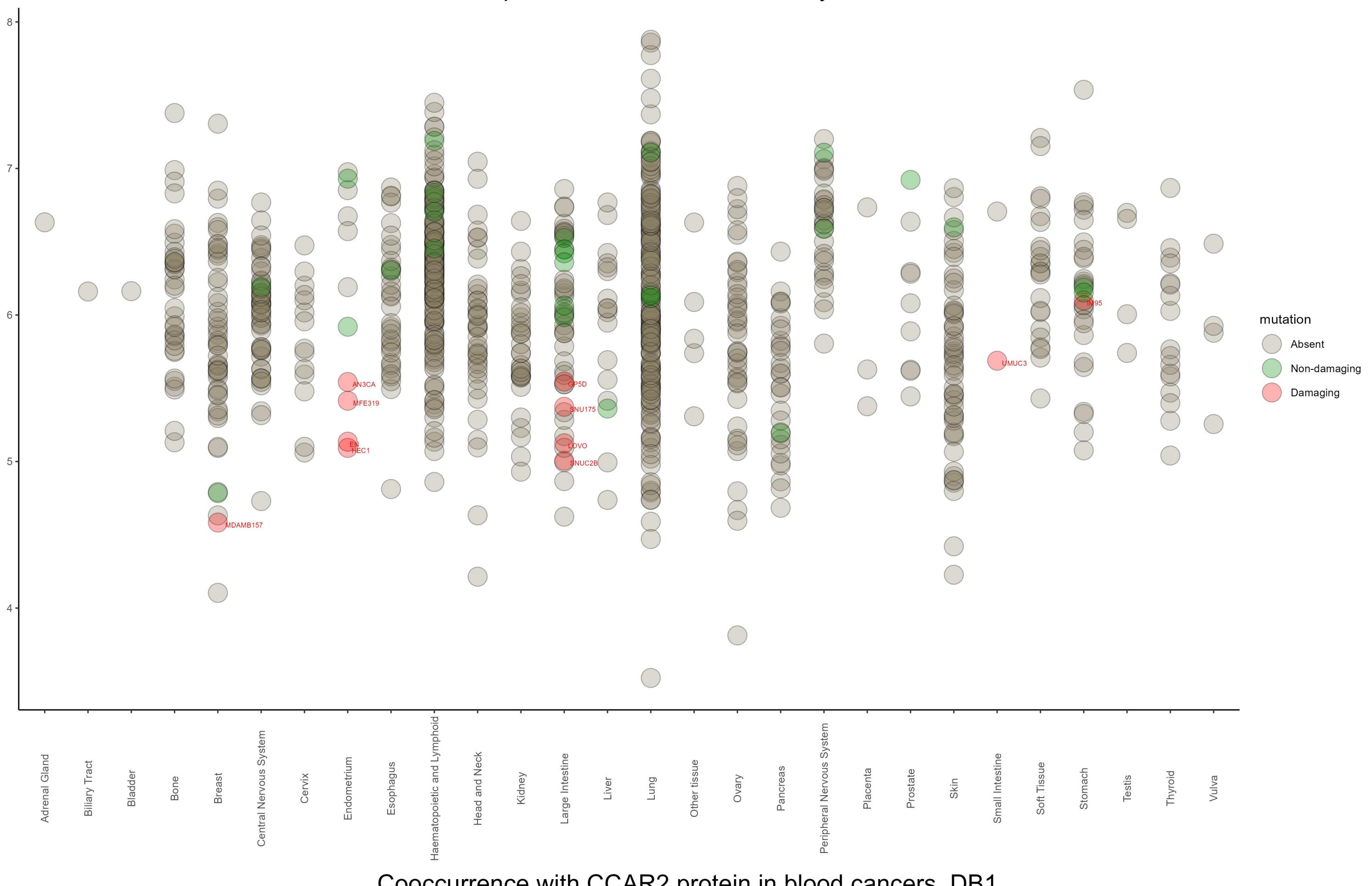
Negative cooccurrence



Positive cooccurrence



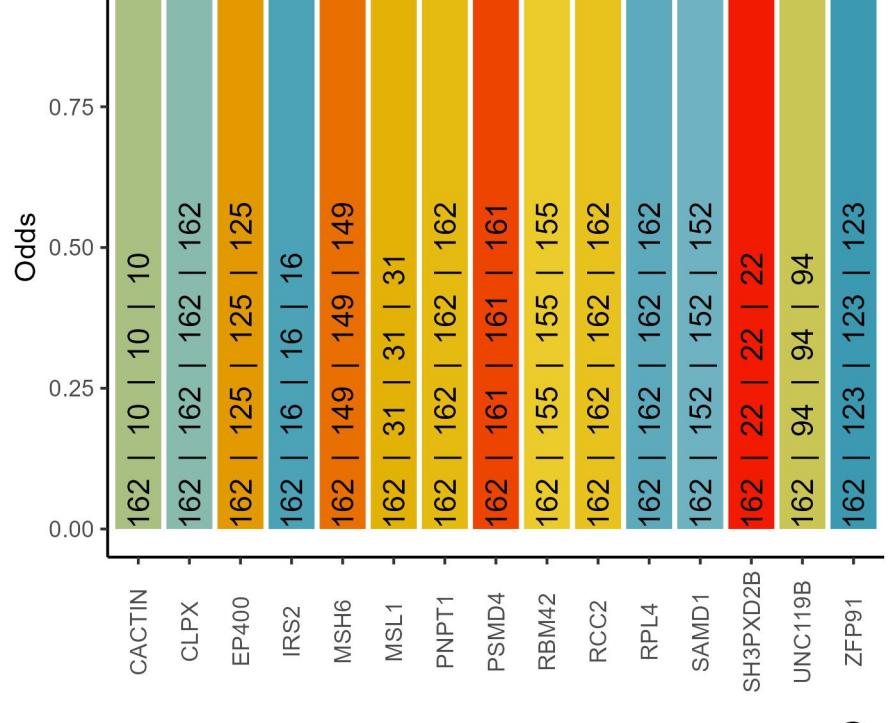
Amount of CCAR2 protein and mutation status by tissue, DB1



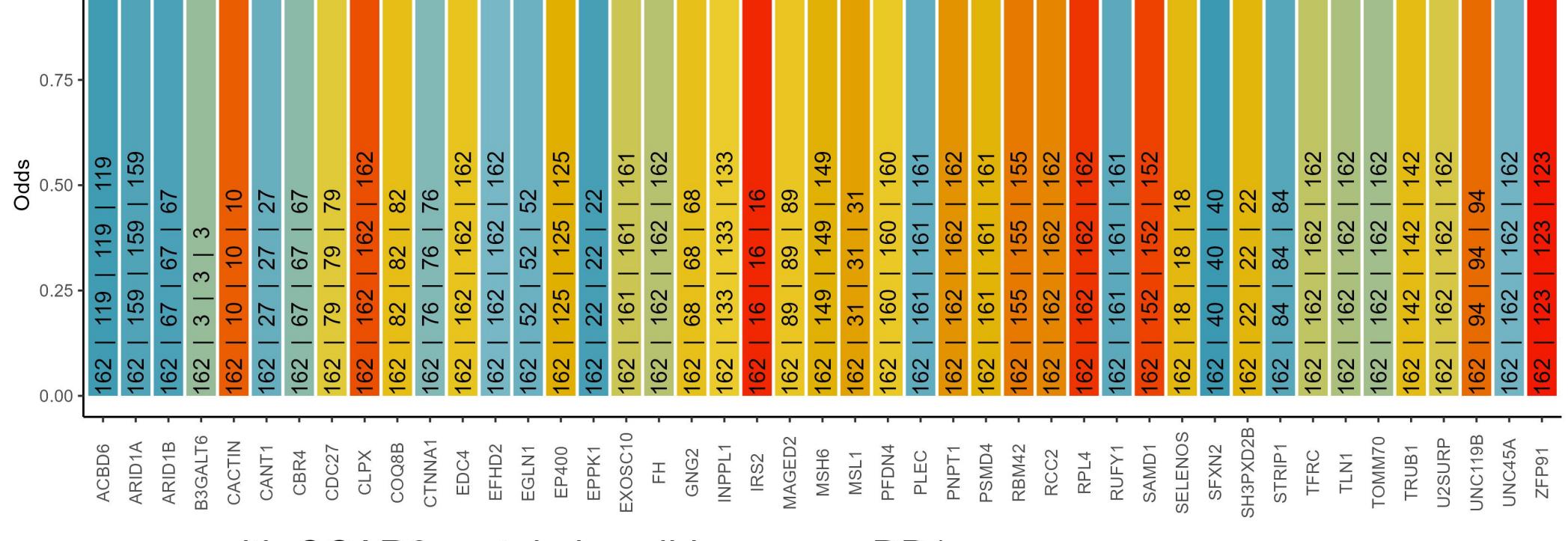
Cooccurrence with CCAR2 protein in blood cancers, DB1

The text in the bars: incidence of CCAR2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

Negative cooccurrence



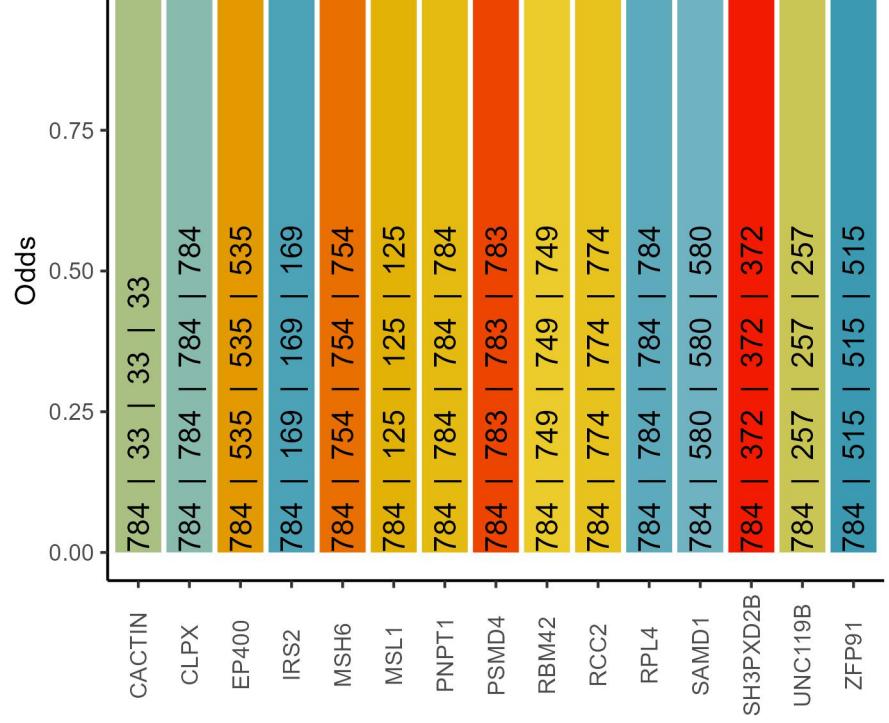
Positive cooccurrence



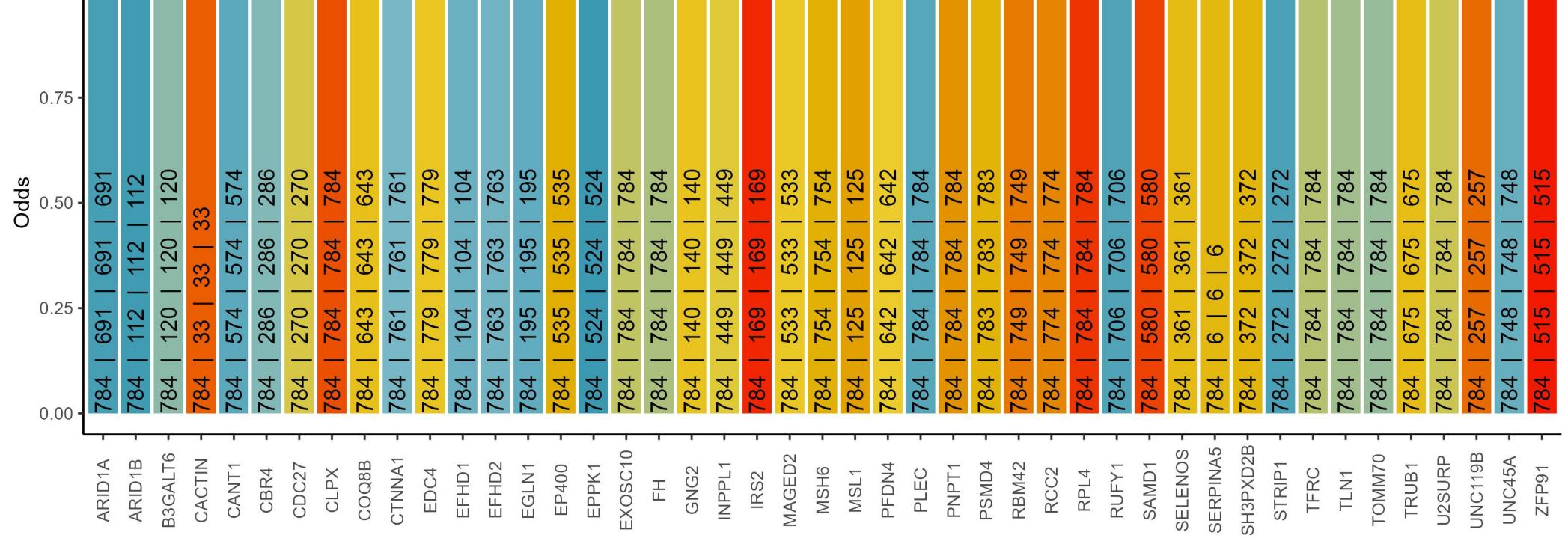
Cooccurrence with CCAR2 protein in solid cancers, DB1

The text in the bars: incidence of CCAR2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

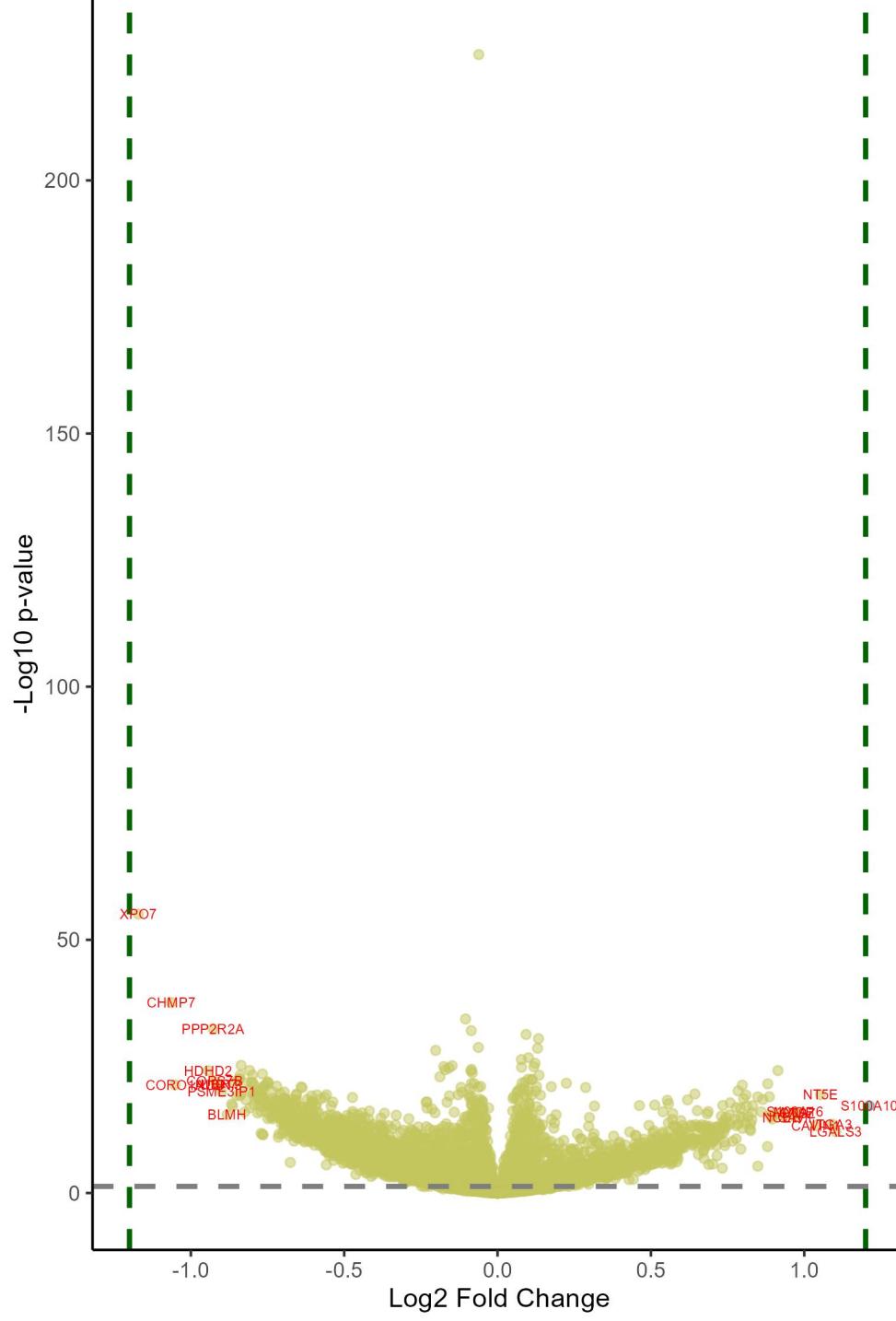
Negative cooccurrence



Positive cooccurrence

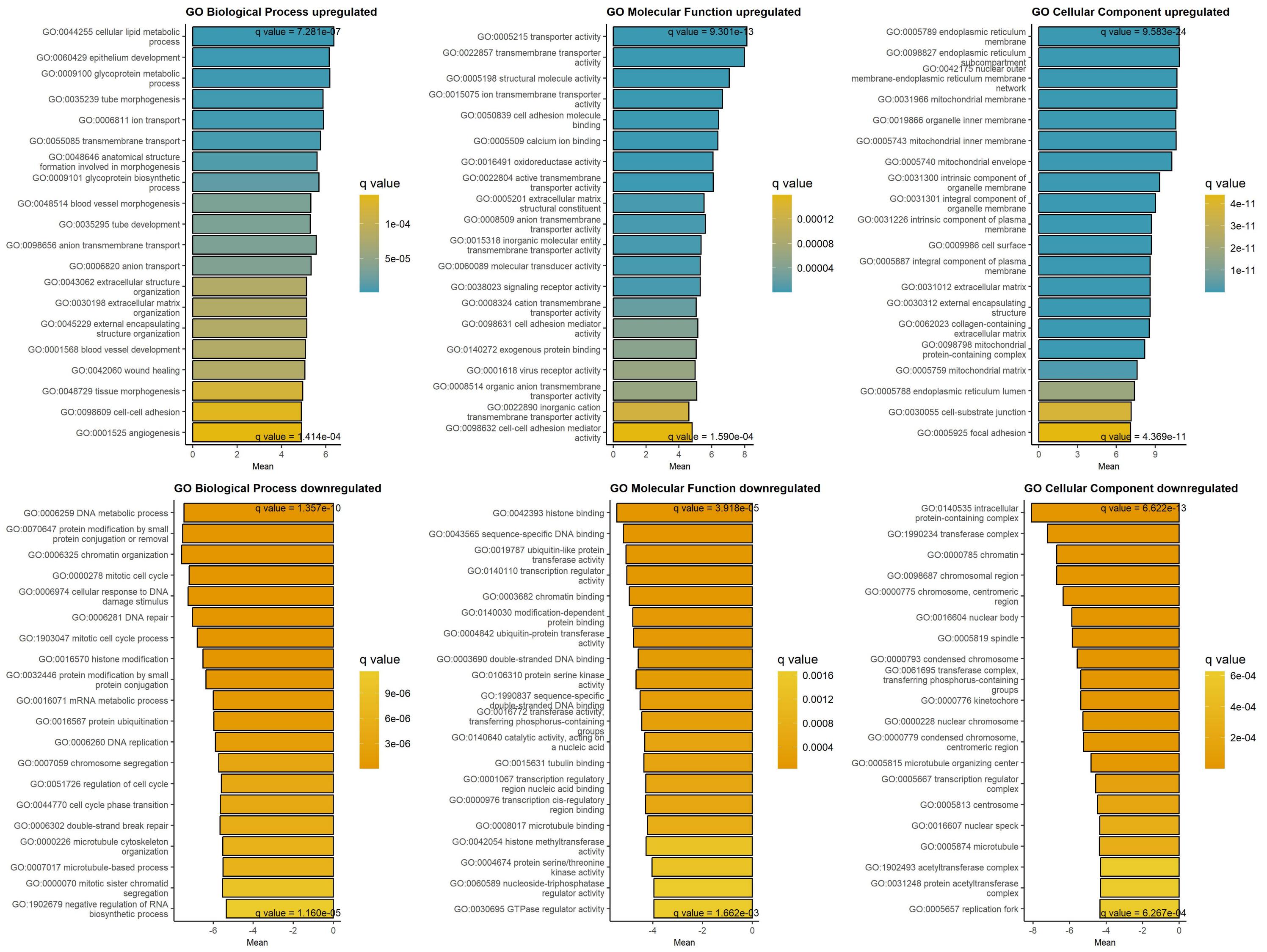


Downregulated at low/absent CCAR2 Upregulated at low/absent CCAR2

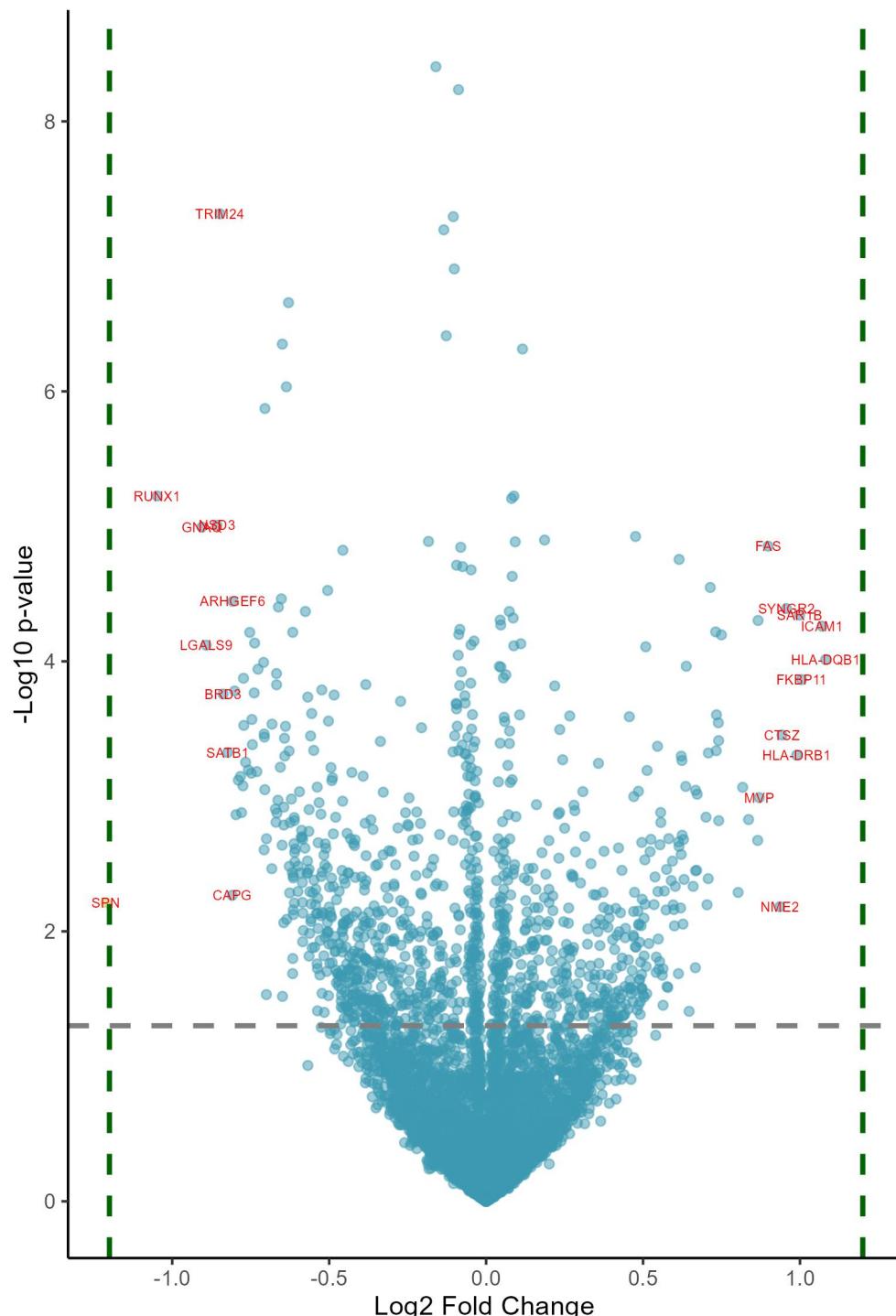


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.17	1.80e-52	XPO7	exportin 7	1.21	2.16e-16	S100A10	S100 calcium binding protein A10
-1.06	4.01e-35	CHMP7	charged multivesicular body protein	1.1	8.11e-12	LGALS3	galectin 3
-1.05	5.54e-20	CORO1A	coronin 1A	1.09	4.06e-13	ITGA3	integrin subunit alpha 3
-0.94	1.68e-22	HDHD2	haloacid dehalogenase like hydrolas	1.05	2.62e-18	NT5E	5'-nucleotidase ecto
-0.93	4.04e-30	PPP2R2A	protein phosphatase 2 regulatory su	1.04	7.46e-13	CAVIN1	caveolae associated protein 1
-0.92	1.23e-20	COPS7B	COP9 signalosome subunit 7B	0.98	5.02e-15	CTSZ	cathepsin Z
-0.91	5.81e-20	NUDT3	nudix hydrolase 3	0.97	2.22e-14	CAV1	caveolin 1
-0.91	4.86e-20	UBR7	ubiquitin protein ligase E3 compone	0.97	2.45e-15	S100A16	S100 calcium binding protein A16
-0.9	8.23e-19	PSME3IP1	proteasome activator subunit 3 inte	0.96	3.07e-15	MYOF	myoferlin
-0.88	8.15e-15	BLMH	bleomycin hydrolase	0.94	2.42e-14	NCEH1	neutral cholesterol ester hydrolase
-0.87	1.11e-16	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.93	5.56e-15	ITGA2	integrin subunit alpha 2
-0.86	2.40e-16	SEPTIN6	septin 6	0.91	1.68e-22	WFS1	wolframin ER transmembrane glycopro
-0.86	2.68e-20	SMAD4	SMAD family member 4	0.91	3.58e-15	CAVIN3	caveolae associated protein 3
-0.85	3.52e-18	SNRNP27	small nuclear ribonucleoprotein U4/	0.9	1.33e-14	CD59	CD59 molecule (CD59 blood group)
-0.85	7.09e-21	POLA2	DNA polymerase alpha 2, accessory s	0.9	4.56e-14	EGFR	epidermal growth factor receptor
-0.84	4.85e-21	PDE6D	phosphodiesterase 6D	0.89	9.60e-15	DSG2	desmoglein 2
-0.84	1.15e-21	ELP3	elongator acetyltransferase complex	0.89	9.22e-15	PPIC	peptidylprolyl isomerase C
-0.84	4.17e-18	GINS2	GINS complex subunit 2	0.89	5.89e-18	RAB32	RAB32, member RAS oncogene family
-0.84	1.53e-18	MAPRE2	microtubule associated protein RP/E	0.88	3.52e-20	FNDC3B	fibronectin type III domain contain
-0.84	2.66e-23	KDM3B	lysine demethylase 3B	0.88	3.93e-09	GNG12	G protein subunit gamma 12
-0.82	2.73e-15	PBK	PDZ binding kinase	0.86	1.72e-17	SDC4	syndecan 4
-0.82	2.79e-20	ARHGEF7	Rho guanine nucleotide exchange fac	0.86	2.54e-15	ADAM9	ADAM metallopeptidase domain 9
-0.82	2.01e-17	PM20D2	peptidase M20 domain containing 2	0.85	1.42e-05	KRT18	keratin 18
-0.81	3.51e-19	SCAF8	SR-related CTD associated factor 8	0.85	6.13e-18	HM13	histocompatibility minor 13
-0.81	1.68e-22	GTF2E2	general transcription factor IIIE su	0.83	2.12e-16	DCBLD2	discoidin, CUB and LCCL domain cont
-0.81	4.77e-16	ACYP1	acylphosphatase 1	0.83	3.54e-15	P4HA2	prolyl 4-hydroxylase subunit alpha
-0.8	1.91e-20	HAT1	histone acetyltransferase 1	0.83	6.49e-14	EPHA2	EPH receptor A2
-0.8	1.15e-21	CXXC1	CXXC finger protein 1	0.83	5.23e-12	TGM2	transglutaminase 2
-0.8	2.68e-20	GINS4	GINS complex subunit 4	0.83	3.56e-13	SQOR	sulfide quinone oxidoreductase

GAGE analysis on upregulated and downregulated proteins at low/absent CCAR2 protein, DB1

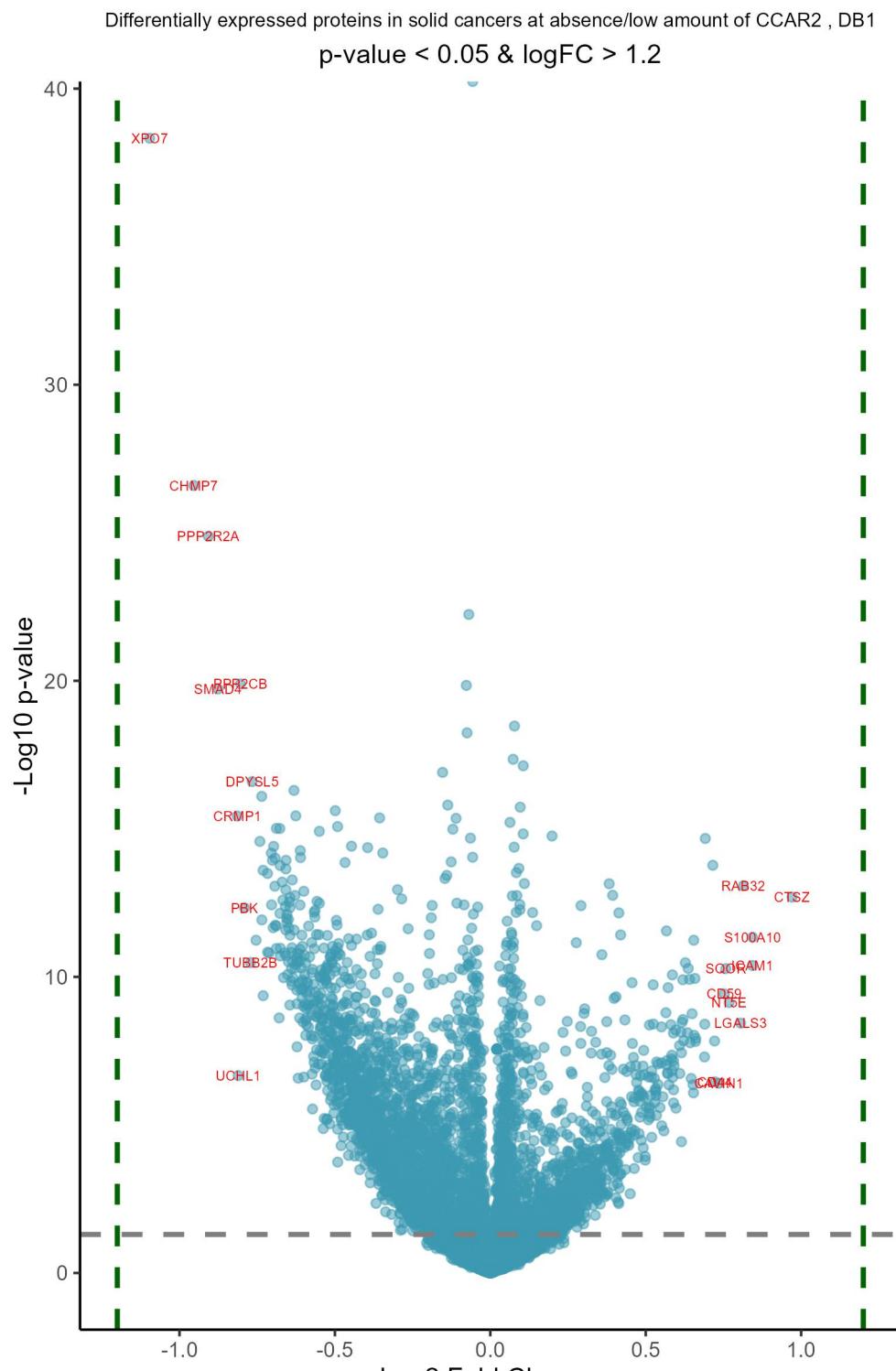


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent CCAR2 Upregulated in blood cancers at low/absent CCAR2

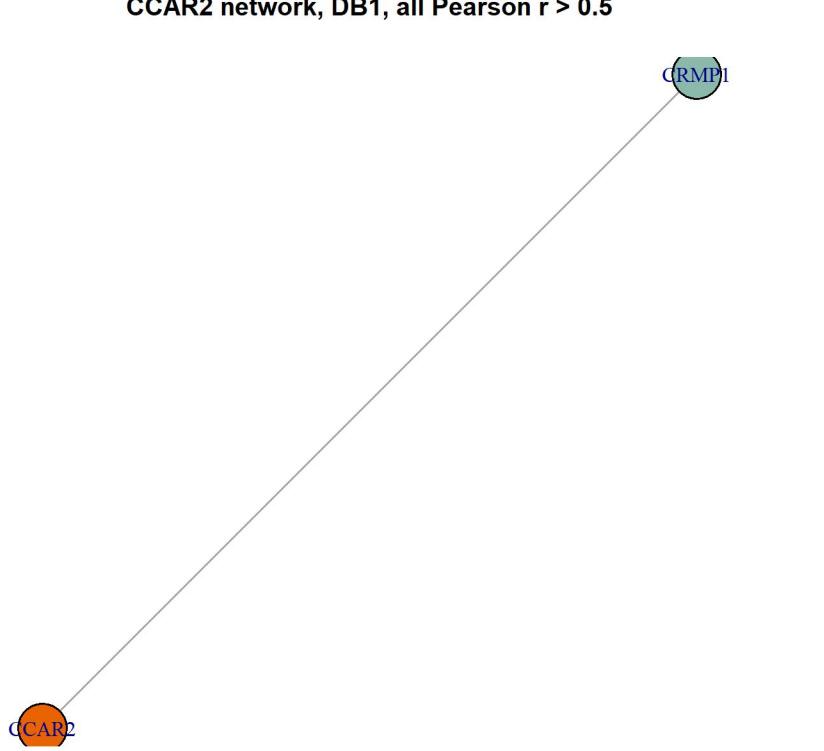
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.21	9.79e-02	SPN	sialophorin	1.08	1.09e-02	HLA-DQB1	major histocompatibility complex, c
-1.05	2.58e-03	RUNX1	RUNX family transcription factor 1	1.07	8.30e-03	ICAM1	intercellular adhesion molecule 1
-0.91	3.74e-03	GNAQ	G protein subunit alpha q	1.01	1.30e-02	FKBP11	FKBP prolyl isomerase 11
-0.89	9.09e-03	LGALS9	galectin 9	1	7.74e-03	SAR1B	secretion associated Ras related GT
-0.86	3.74e-03	NSD3	nuclear receptor binding SET domain	0.99	2.50e-02	HLA-DRB1	major histocompatibility complex, c
-0.85	6.75e-05	TRIM24	tripartite motif containing 24	0.96	7.47e-03	SYNGR2	synaptogyrin 2
-0.84	1.47e-02	BRD3	bromodomain containing 3	0.94	2.16e-02	CTSZ	cathepsin Z
-0.82	2.46e-02	SATB1	SATB homeobox 1	0.94	1.02e-01	NME2	NME/NM23 nucleoside diphosphate kin
-0.81	9.02e-02	CAPG	capping actin protein, gelsolin lik	0.9	3.96e-03	FAS	Fas cell surface death receptor
-0.81	7.02e-03	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan	0.87	3.81e-02	MVP	major vault protein
-0.8	1.43e-02	PTK7	protein tyrosine kinase 7 (inactive	0.87	7.88e-03	SAMHD1	SAM and HD domain containing deoxyn
-0.8	4.39e-02	DDAH2	dimethylarginine dimethylaminohydro	0.87	5.52e-02	LGALS3	galectin 3
-0.79	3.21e-02	ITGA5	integrin subunit alpha 5	0.84	4.63e-02	IRF4	interferon regulatory factor 4
-0.78	3.08e-02	PC	pyruvate carboxylase	0.82	3.45e-02	IKZF3	IKAROS family zinc finger 3
-0.78	4.35e-02	LCP2	lymphocyte cytosolic protein 2	0.8	8.78e-02	JCHAIN	joining chain of multimeric IgA and
-0.77	3.43e-02	CELF2	CUGBP Elav-like family member 2	0.75	8.46e-03	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.77	1.29e-02	TCF12	transcription factor 12	0.74	4.66e-02	NCEH1	neutral cholesterol ester hydrolase
-0.77	1.97e-02	IGLL1	immunoglobulin lambda like polypept	0.74	2.25e-02	LSR	lipolysis stimulated lipoprotein re
-0.77	2.69e-02	LEF1	lymphoid enhancer binding factor 1	0.74	1.93e-02	ASNS	asparagine synthetase (glutamine-hy
-0.76	2.93e-02	FLI1	Fli-1 proto-oncogene, ETS transcrip	0.73	1.82e-02	SLC25A13	solute carrier family 25 member 13
-0.75	8.45e-03	VRK3	VRK serine/threonine kinase 3	0.73	2.43e-02	DTD1	D-aminoacyl-tRNA deacylase 1
-0.75	2.99e-02	GPX7	glutathione peroxidase 7	0.73	8.45e-03	MYO5A	myosin VA
-0.75	1.89e-02	PECAM1	platelet and endothelial cell adhes	0.71	6.08e-03	ALDH1B1	aldehyde dehydrogenase 1 family mem
-0.74	2.31e-02	MAP1A	microtubule associated protein 1A	0.71	2.46e-02	SEL1L	SEL1L adaptor subunit of ERAD E3 ub
-0.74	1.46e-02	ZNF22	zinc finger protein 22	0.71	7.73e-02	ISG20	interferon stimulated exonuclease g
-0.74	9.09e-03	PDLIM2	PDZ and LIM domain 2	0.7	9.97e-02	STOM	stomatin
-0.73	2.95e-02	IRAK4	interleukin 1 receptor associated k	0.7	4.50e-02	NFKB2	nuclear factor kappa B subunit 2
-0.73	1.19e-02	BRD1	bromodomain containing 1	0.67	3.71e-02	SIL1	SIL1 nucleotide exchange factor
-0.71	1.13e-02	NECTIN2	nectin cell adhesion molecule 2	0.67	7.29e-02	JUNB	JunB proto-oncogene, AP-1 transcript



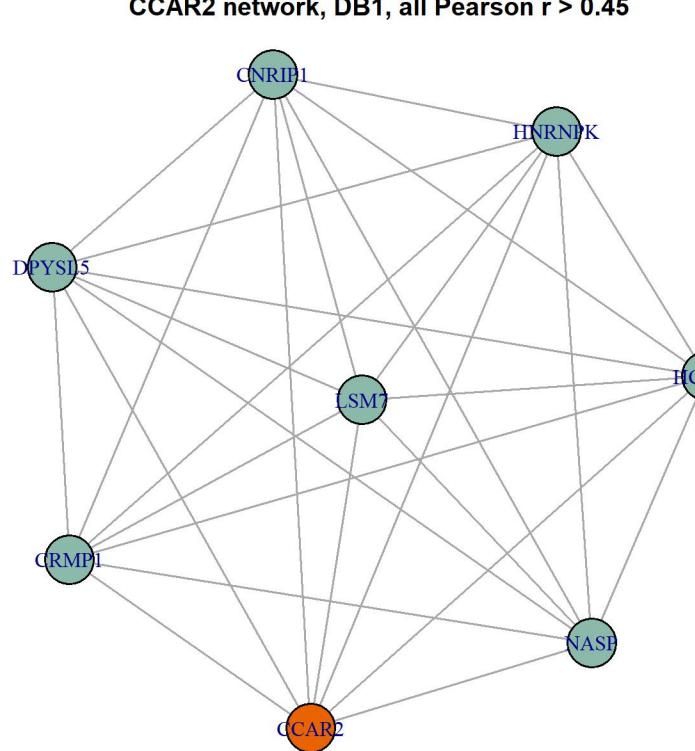
Downregulated in solid cancers at low/absent CCAR2 Upregulated in solid cancers at low/absent CCAR2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.1	1.05e-35	XPO7	exportin 7	0.97	1.86e-11	CTSZ	cathepsin Z
-0.95	4.19e-24	CHMP7	charged multivesicular body protein	0.84	2.32e-10	S100A10	S100 calcium binding protein A10
-0.91	1.74e-22	PPP2R2A	protein phosphatase 2 regulatory su	0.84	1.36e-09	ICAM1	intercellular adhesion molecule 1
-0.88	1.39e-17	SMAD4	SMAD family member 4	0.81	8.76e-12	RAB32	RAB32, member RAS oncogene family
-0.81	1.11e-13	CRMP1	collapsin response mediator protein	0.81	5.70e-08	LGALS3	galectin 3
-0.81	1.60e-06	UCHL1	ubiquitin C-terminal hydrolase L1	0.77	1.48e-08	NT5E	5'-nucleotidase ecto
-0.8	1.19e-17	PPP2CB	protein phosphatase 2 catalytic sub	0.76	1.65e-09	SQOR	sulfide quinone oxidoreductase
-0.79	3.47e-11	PBK	PDZ binding kinase	0.75	8.24e-09	CD59	CD59 molecule (CD59 blood group)
-0.77	1.13e-09	TUBB2B	tubulin beta 2B class IIb	0.74	2.67e-06	CAVIN1	caveolae associated protein 1
-0.77	1.12e-14	DPYSL5	dihydropyrimidinase like 5	0.72	2.42e-06	CD44	CD44 molecule (Indian blood group)
-0.75	2.82e-10	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.72	1.83e-07	TGM2	transglutaminase 2
-0.74	5.05e-13	PDCL	phosducin like	0.72	2.26e-12	ADGRE5	adhesion G protein-coupled receptor
-0.74	3.12e-14	ELP3	elongator acetyltransferase complex	0.69	4.13e-13	MAGT1	magnesium transporter 1
-0.74	7.59e-11	UBR7	ubiquitin protein ligase E3 compone	0.69	6.07e-08	HLA-B	major histocompatibility complex, c
-0.73	3.10e-12	HDHD2	haloacid dehalogenase like hydrolas	0.69	4.61e-07	CAVIN3	caveolae associated protein 3
-0.73	9.42e-09	BLMH	bleomycin hydrolase	0.66	1.54e-07	STOM	stomatin
-0.72	3.82e-12	GIT1	GIT ArfGAP 1	0.66	1.90e-07	RAC2	Rac family small GTPase 2
-0.72	5.99e-10	PSME3IP1	proteasome activator subunit 3 inte	0.66	3.04e-09	NCEH1	neutral cholesterol ester hydrolase
-0.71	6.31e-10	CBL	Cbl proto-oncogene	0.66	1.26e-07	DERL1	derlin 1
-0.7	1.05e-12	UBFD1	ubiquitin family domain containing	0.65	2.82e-10	FND3B	fibronectin type III domain contain
-0.7	3.00e-11	SCAF8	SR-related CTD associated factor 8	0.65	5.13e-06	GPRC5A	G protein-coupled receptor class C
-0.7	1.63e-12	MAPRE2	microtubule associated protein RP/E	0.65	2.99e-06	CAV1	caveolin 1
-0.7	1.29e-10	ADD2	adducin 2	0.65	3.14e-08	MRPS18C	mitochondrial ribosomal protein S18
-0.7	7.01e-13	RELCH	RAB11 binding and LisH domain, coil	0.65	1.93e-06	VAMP8	vesicle associated membrane protein
-0.69	8.98e-12	POLA2	DNA polymerase alpha 2, accessory s	0.64	2.05e-07	LPCAT2	lysophosphatidylcholine acyltransfe
-0.69	1.44e-12	TBCC	tubulin folding cofactor C	0.64	3.20e-09	HM13	histocompatibility minor 13
-0.69	1.09e-10	USP11	ubiquitin specific peptidase 11	0.64	1.64e-09	MYOF	myoferlin
-0.69	4.78e-10	PIN1	peptidylprolyl cis/trans isomerase,	0.63	1.05e-07	DSG2	desmoglein 2
-0.69	1.14e-10	CFDP1	craniofacial development protein 1	0.63	1.15e-09	RETSAT	retinol saturase

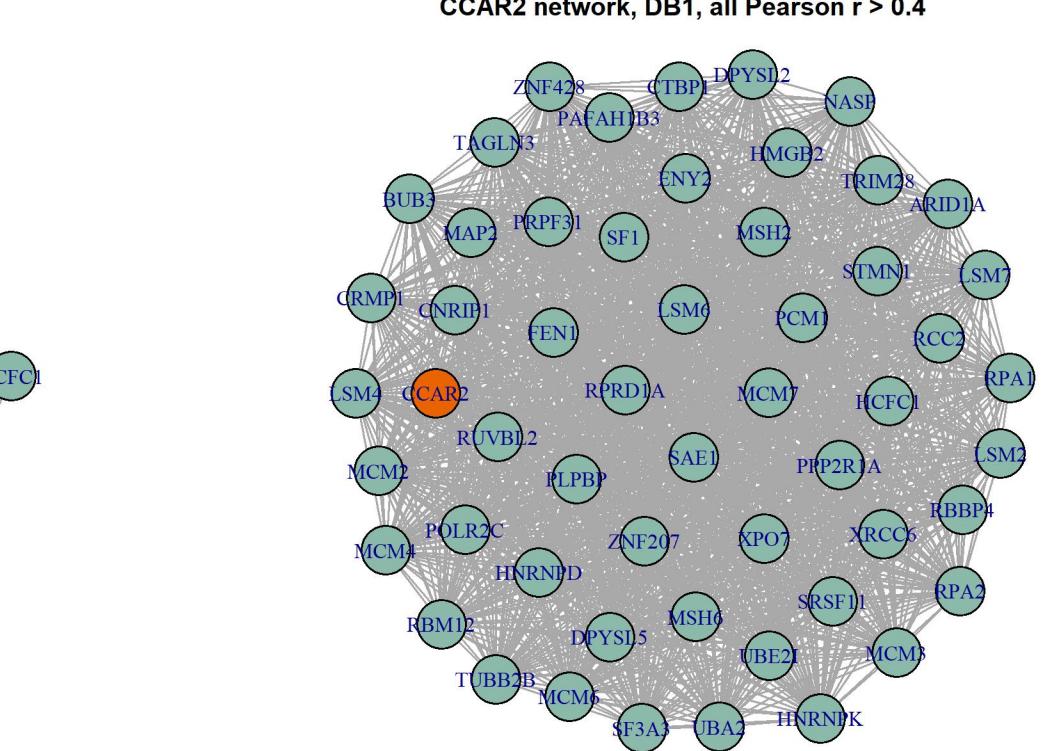
CCAR2 network, DB1, all Pearson r > 0.5



CCAR2 network, DB1, all Pearson r > 0.45



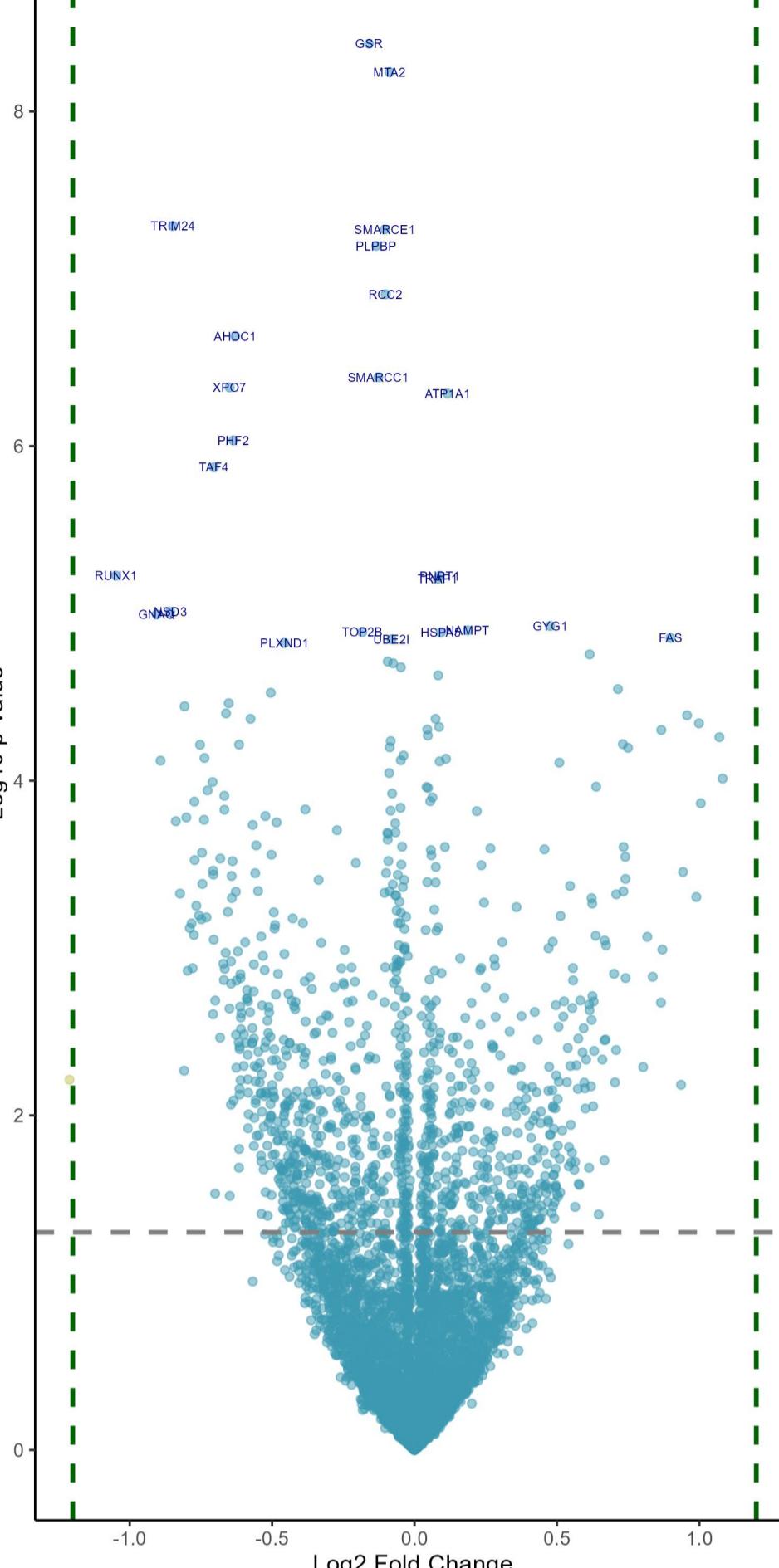
CCAR2 network, DB1, all Pearson r > 0.4



p-value < 0.05 & logFC > 1.2

Sorted by p values!

Downregulated in blood cancers at low/absent CCAR2 Upregulated in blood cancers at low/absent CCAR2

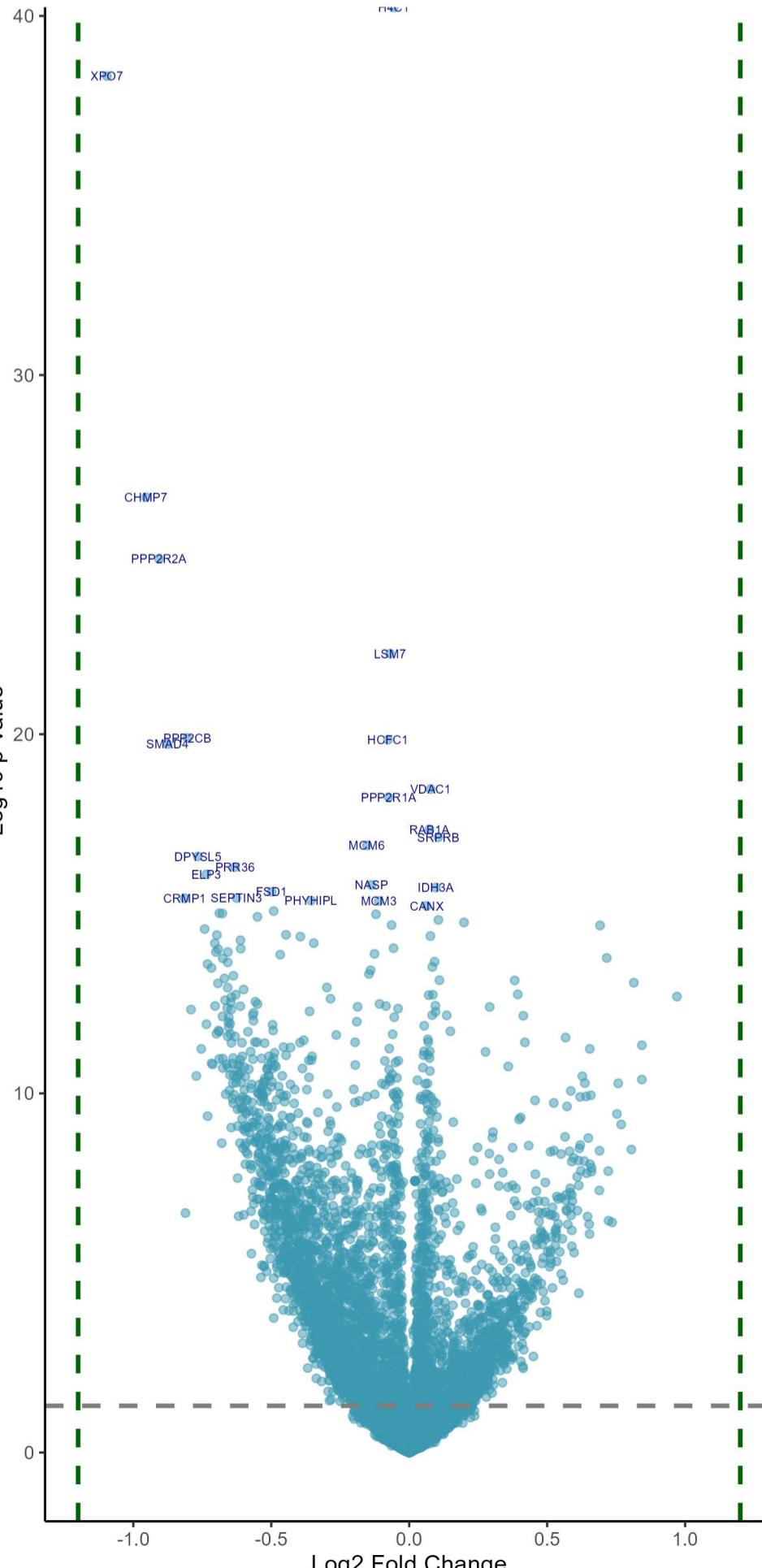


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.16	1.29e-05	GSR	glutathione-disulfide reductase	0.12	2.94e-04	ATP1A1	ATPase Na+/K+ transporting subunit
-0.09	1.29e-05	MTA2	metastasis associated 1 family memb	0.09	2.58e-03	PNPT1	polyribonucleotide nucleotidyltrans
-0.85	6.75e-05	TRIM24	tripartite motif containing 24	0.08	2.58e-03	TRAP1	TNF receptor associated protein 1
-0.1	6.75e-05	SMARCE1	SWI/SNF related, matrix associated,	0.48	3.93e-03	GYG1	glycogenin 1
-0.13	7.05e-05	PLPBP	pyridoxal phosphate binding protein	0.19	3.93e-03	NAMPT	nicotinamide phosphoribosyltransfer
-0.1	1.18e-04	RCC2	regulator of chromosome condensatio	0.09	3.93e-03	HSPA5	heat shock protein family A (Hsp70)
-0.63	1.83e-04	AHDCL1	AT-hook DNA binding motif containin	0.9	3.96e-03	FAS	Fas cell surface death receptor
-0.13	2.86e-04	SMARCC1	SWI/SNF related, matrix associated,	0.61	4.49e-03	PRKAR2A	protein kinase cAMP-dependent type
-0.65	2.94e-04	XPO7	exportin 7	0.08	5.20e-03	RRP12	ribosomal RNA processing 12 homolog
-0.64	5.13e-04	PHF2	PHD finger protein 2	0.71	6.08e-03	ALDH1B1	aldehyde dehydrogenase 1 family mem
-0.7	6.85e-04	TAF4	TATA-box binding protein associated	0.96	7.47e-03	SYNGR2	synaptogyrin 2
-1.05	2.58e-03	RUNX1	RUNX family transcription factor 1	0.07	7.47e-03	PHB2	prohibitin 2
-0.86	3.74e-03	NSD3	nuclear receptor binding SET domain	1	7.74e-03	SAR1B	secretion associated Ras related GT
-0.91	3.74e-03	GNAQ	G protein subunit alpha q	0.09	7.88e-03	LAP3	leucine aminopeptidase 3
-0.18	3.93e-03	TOP2B	DNA topoisomerase II beta	0.04	7.88e-03	HSPA9	heat shock protein family A (Hsp70)
-0.08	3.96e-03	UBE2I	ubiquitin conjugating enzyme E2 I	0.87	7.88e-03	SAMHD1	SAM and HD domain containing deoxyn
-0.46	4.00e-03	PLXND1	plexin D1	0.05	8.30e-03	PHB1	prohibitin 1
-0.09	4.72e-03	CTBP1	C-terminal binding protein 1	1.07	8.30e-03	ICAM1	intercellular adhesion molecule 1
-0.08	4.72e-03	TRIM28	tripartite motif containing 28	0.73	8.45e-03	MYO5A	myosin VA
-0.05	4.81e-03	DDX17	DEAD-box helicase 17	0.75	8.46e-03	MGAT2	alpha-1,6-mannosyl-glycoprotein 2-b
-0.5	6.20e-03	SORBS3	sorbin and SH3 domain containing 3	0.11	9.09e-03	LMAN2	lectin, mannose binding 2
-0.65	6.94e-03	ABI2	abl interactor 2	0.09	9.09e-03	PPIB	peptidylprolyl isomerase B
-0.81	7.02e-03	ARHGEF6	Rac/Cdc42 guanine nucleotide exchan	0.51	9.09e-03	ECI1	enoyl-CoA delta isomerase 1
-0.66	7.47e-03	PPP2CB	protein phosphatase 2 catalytic sub	1.08	1.09e-02	HLA-DQB1	major histocompatibility complex, c
-0.58	7.47e-03	VEZF1	vascular endothelial zinc finger 1	0.64	1.17e-02	DUS2	dihydrouridine synthase 2
-0.08	8.45e-03	HP1BP3	heterochromatin protein 1 binding p	0.04	1.17e-02	HSPE1	heat shock protein family E (Hsp10)
-0.62	8.45e-03	RANBP9	RAN binding protein 9	0.05	1.17e-02	RSL1D1	ribosomal L1 domain containing 1
-0.75	8.45e-03	VRK3	VRK serine/threonine kinase 3	0.06	1.25e-02	PES1	pescadillo ribosomal biogenesis fac
-0.09	8.46e-03	HMGB1	high mobility group box 1	0.06	1.29e-02	CANX	calnexin
-0.04	9.09e-03	U2AF2	U2 small nuclear RNA auxiliary fact	1.01	1.30e-02	FKBP11	FKBP prolyl isomerase 11
-0.74	9.09e-03	PDLIM2	PDZ and LIM domain 2	0.22	1.35e-02	SCFD1	sec1 family domain containing 1
-0.05	9.09e-03	CHD4	chromodomain helicase DNA binding p	0.73	1.82e-02	SLC25A13	solute carrier family 25 member 13
-0.89	9.09e-03	LGALS9	galectin 9	0.11	1.82e-02	SRPRB	SRP receptor subunit beta
-0.09	1.03e-02	CHAMP1	chromosome alignment maintaining ph	0.27	1.83e-02	MRPL48	mitochondrial ribosomal protein L48
-0.71	1.13e-02	NECTIN2	nectin cell adhesion molecule 2	0.46	1.84e-02	ITGA3	integrin subunit alpha 3
-0.73	1.19e-02	BRD1	bromodomain containing 1	0.06	1.84e-02	BSG	basigin (Ok blood group)
-0.08	1.22e-02	LUC7L2	LUC7 like 2, pre-mRNA splicing fact	0.06	1.91e-02	HSD17B10	hydroxysteroid 17-beta dehydrogenas
-0.67	1.24e-02	VPS28	VPS28 subunit of ESCRT-I	0.74	1.93e-02	ASNS	asparagine synthetase (glutamine-hy
0.77	1.39e-02	TCE12	transcription factor 12	0.23	2.03e-02	EMOR2A	family with sequence similarity 28

p-value < 0.05 & logFC > 1.2

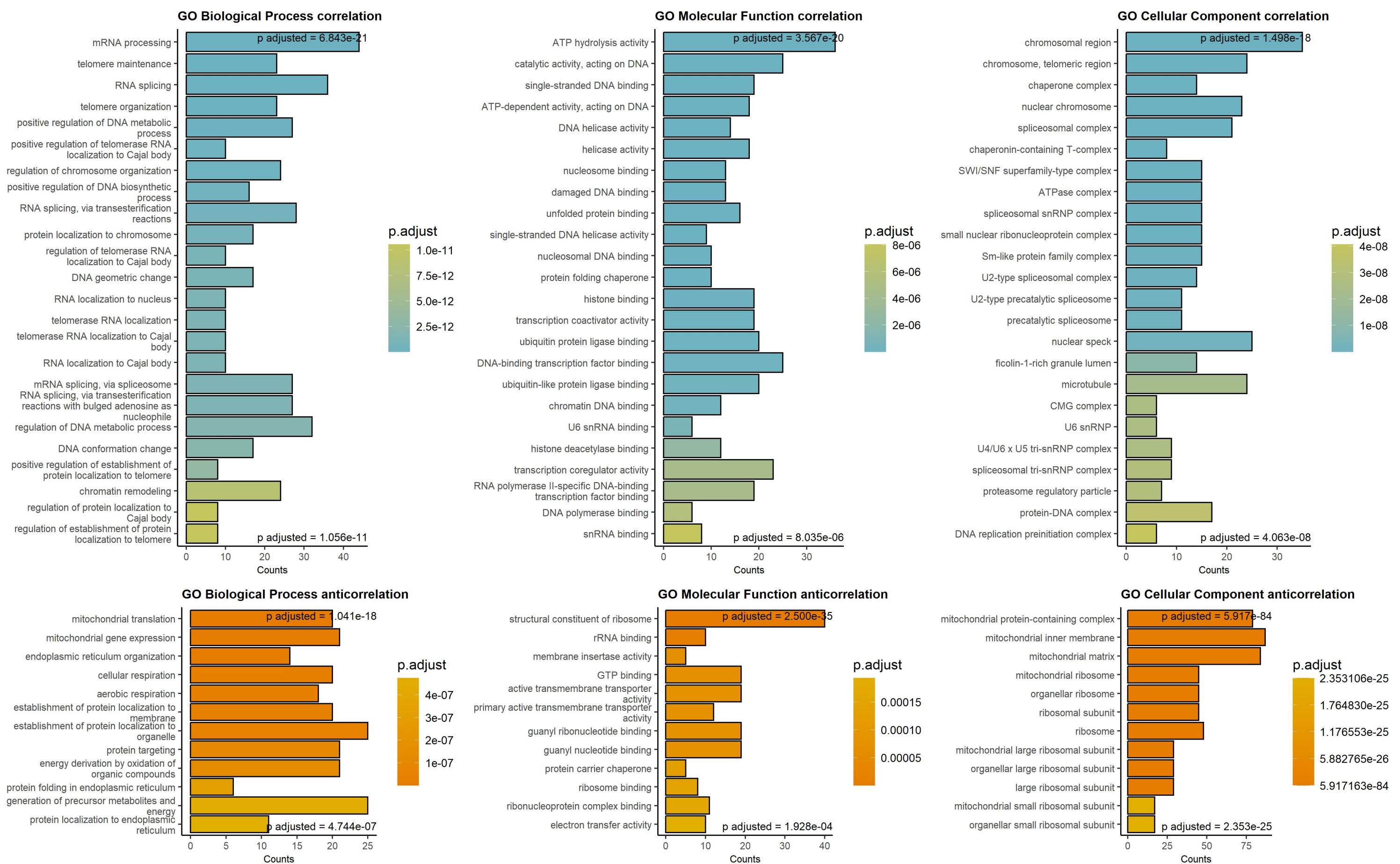
Sorted by p values!

Downregulated in solid cancers at low/absent CCAR2 Upregulated in solid cancers at low/absent CCAR2

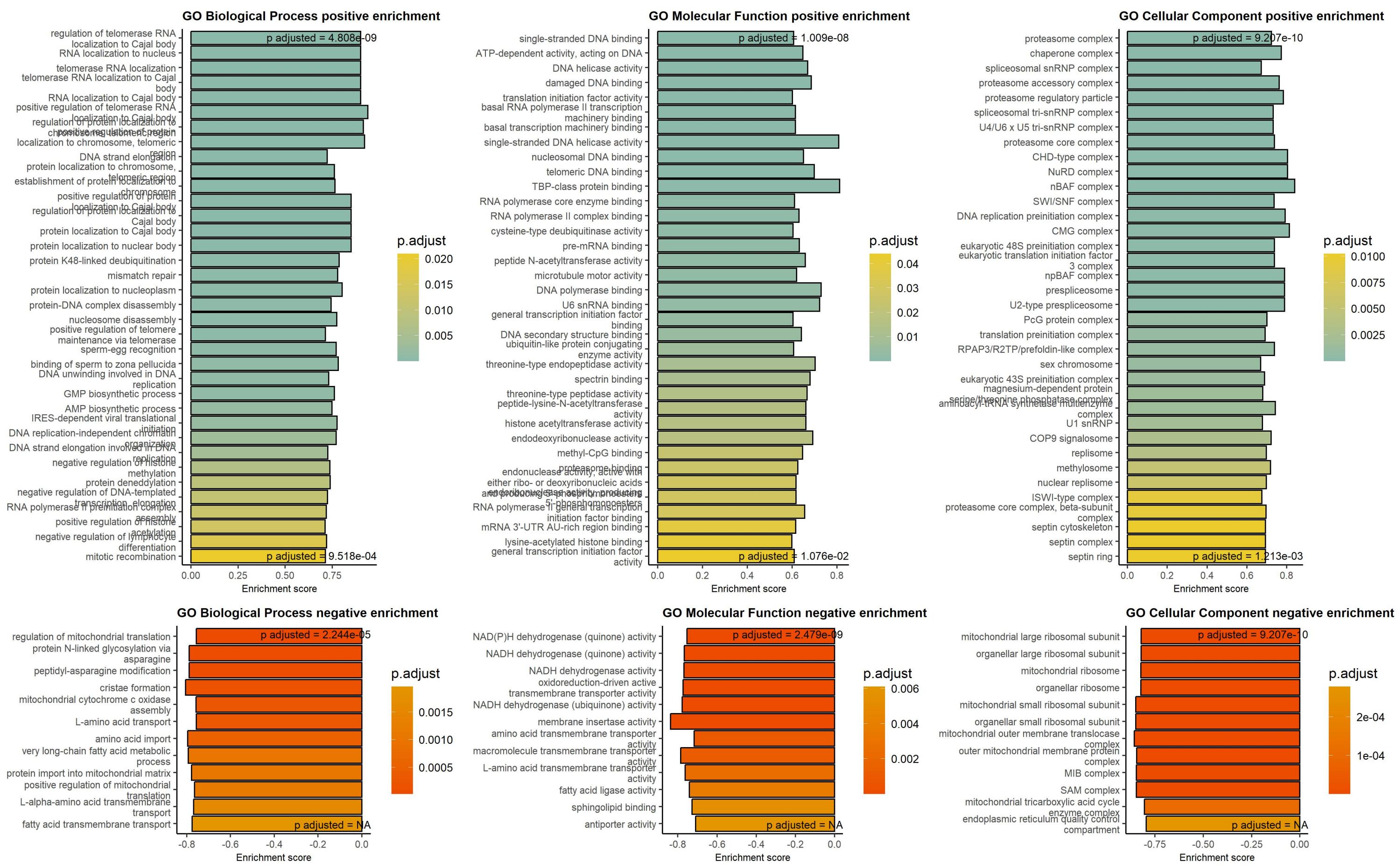


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.06	0.00e+00	H4C1	H4 clustered histone 1	0.08	2.24e-16	VDAC1	voltage dependent anion channel 1
-1.1	1.05e-35	XPO7	exportin 7	0.07	2.48e-15	RAB1A	RAB1A, member RAS oncogene family
-0.95	4.19e-24	CHMP7	charged multivesicular body protein	0.11	3.78e-15	SRPRB	SRP receptor subunit beta
-0.91	1.74e-22	PPP2R2A	protein phosphatase 2 regulatory su	0.1	6.48e-14	IDH3A	isocitrate dehydrogenase (NAD(+)) 3
-0.07	6.37e-20	LSM7	LSM7 homolog, U6 small nuclear RNA	0.06	1.61e-13	CANX	calnexin
-0.8	1.19e-17	PPP2CB	protein phosphatase 2 catalytic sub	0.11	3.18e-13	IDH3B	isocitrate dehydrogenase (NAD(+)) 3
-0.08	1.19e-17	HCFC1	host cell factor C1	0.2	3.63e-13	PLEC	plectin
-0.88	1.39e-17	SMAD4	SMAD family member 4	0.69	4.13e-13	MAGT1	magnesium transporter 1
-0.07	3.45e-16	PPP2R1A	protein phosphatase 2 scaffold subu	0.08	7.26e-13	TMED9	transmembrane p24 trafficking prote
-0.15	5.88e-15	MCM6	minichromosome maintenance complex	0.72	2.26e-12	ADGRE5	adhesion G protein-coupled receptor
-0.77	1.12e-14	DPYSL5	dihydropyrimidinase like 5	0.09	2.76e-12	LMAN2	lectin, mannose binding 2
-0.63	2.09e-14	PRR36	proline rich 36	0.08	3.64e-12	BCAP31	B cell receptor associated protein
-0.74	3.12e-14	ELP3	elongator acetyltransferase complex	0.11	7.67e-12	EMC7	ER membrane protein complex subunit
-0.14	5.82e-14	NASP	nuclear autoantigenic sperm protein	0.38	7.67e-12	SQSTM1	sequestosome 1
-0.5	8.08e-14	FSD1	fibronectin type III and SPRY domai	0.81	8.76e-12	RAB32	RAB32, member RAS oncogene family
-0.63	1.11e-13	SEPTIN3	septin 3	0.39	1.70e-11	MYO1C	myosin IC
-0.81	1.11e-13	CRMP1	collapsin response mediator protein	0.09	1.70e-11	SSR4	signal sequence receptor subunit 4
-0.36	1.22e-13	PHYH1PL	phytanoyl-CoA 2-hydroxylase interac	0.07	1.73e-11	HADHA	hydroxyacyl-CoA dehydrogenase triflu
-0.11	1.22e-13	MCM3	minichromosome maintenance complex	0.97	1.86e-11	CTSZ	cathepsin Z
-0.49	2.15e-13	MEX3A	mex-3 RNA binding family member A	0.09	3.00e-11	RPN2	ribophorin II
-0.69	2.32e-13	IRF2BP1	interferon regulatory factor 2 bind	0.29	3.07e-11	SUCLG2	succinate-CoA ligase GDP-forming su
-0.68	2.32e-13	GTF2E2	general transcription factor IIIE su	0.1	3.93e-11	OGDH	oxoglutarate dehydrogenase
-0.12	2.36e-13	MCM7	minichromosome maintenance complex	0.08	4.71e-11	ATP1A1	ATPase Na+/K+ transporting subunit
-0.55	2.69e-13	WASF1	WASP family member 1	0.14	4.71e-11	LMNA	lamin A/C
-0.06	4.13e-13	BUB3	BUB3 mitotic checkpoint protein	0.41	4.78e-11	ERGIC1	endoplasmic reticulum-golgi interme
-0.74	5.05e-13	PDCL	phosducin like	0.05	8.21e-11	CHCHD3	coiled-coil-helix-coiled-coil-helix
-0.45	7.01e-13	ELAVL3	ELAV like RNA binding protein 3	0.15	1.13e-10	RRBP1	ribosome binding protein 1
-0.7	7.01e-13	RELCH	RAB11 binding and LisH domain, coil	0.57	1.56e-10	UTRN	utrophin
-0.39	7.35e-13	SOGA3	SOGA family member 3	0.07	1.73e-10	HADHB	hydroxyacyl-CoA dehydrogenase triflu
-0.61	9.05e-13	GPSM1	G protein signaling modulator 1	0.07	2.01e-10	SSR1	signal sequence receptor subunit 1
-0.35	1.05e-12	ELAVL4	ELAV like RNA binding protein 4	0.42	2.02e-10	EHD4	EH domain containing 4
-0.7	1.05e-12	UBFD1	ubiquitin family domain containing	0.84	2.32e-10	S100A10</	

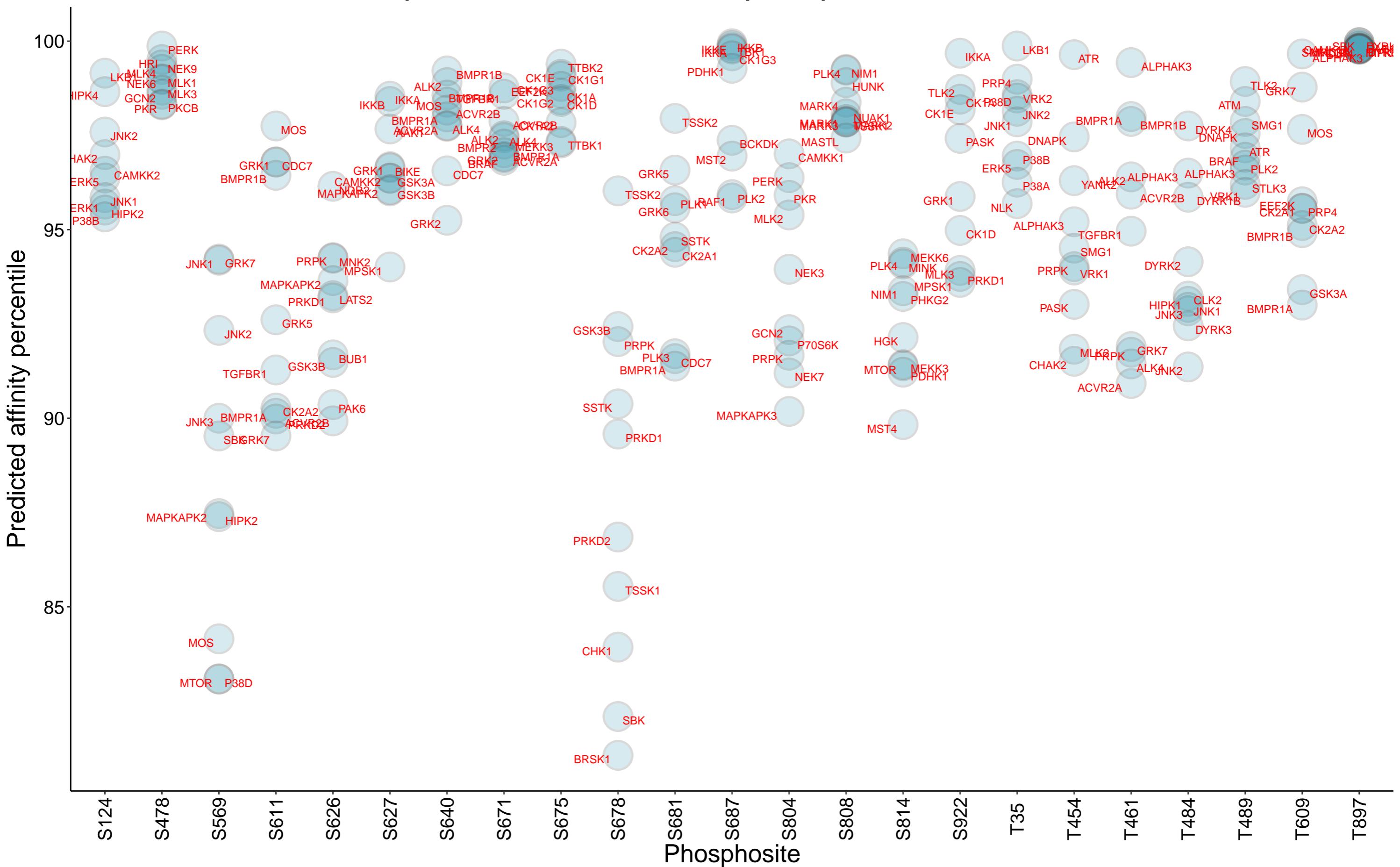
Top 250 correlation coefficients overrepresentation, CCAR2 protein, DB1



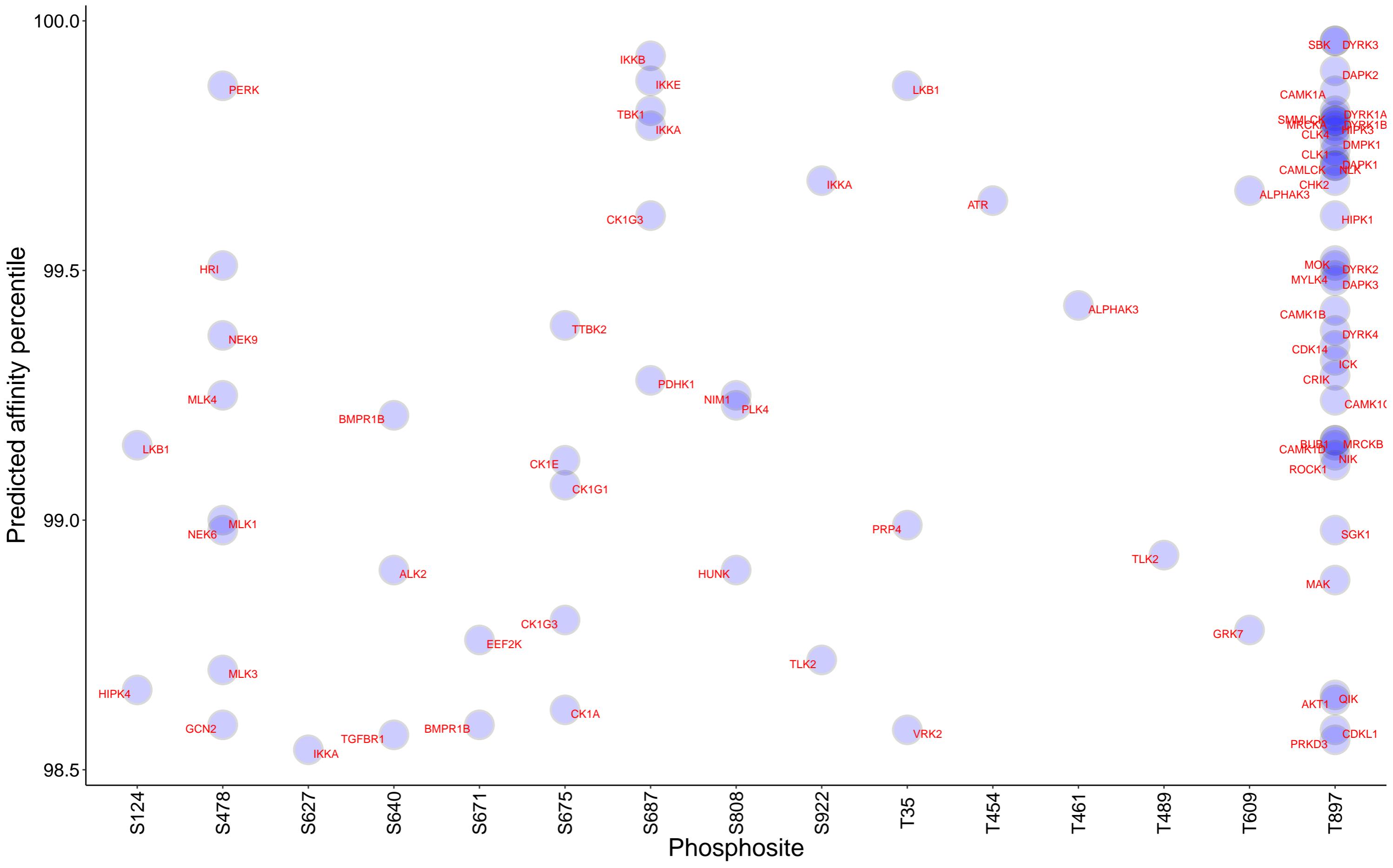
Gene Set Enrichment analysis on protein correlation coefficients, CCAR2 protein, DB1



Top 10 kinases for each phosphosite in CCAR2



Kinases with affinity greater than 98.5% to CCAR2



Top 15 positive correlation coefficients for CCAR2 protein by tissue, DB1

Beware of false positives in tissues with small number of samples

