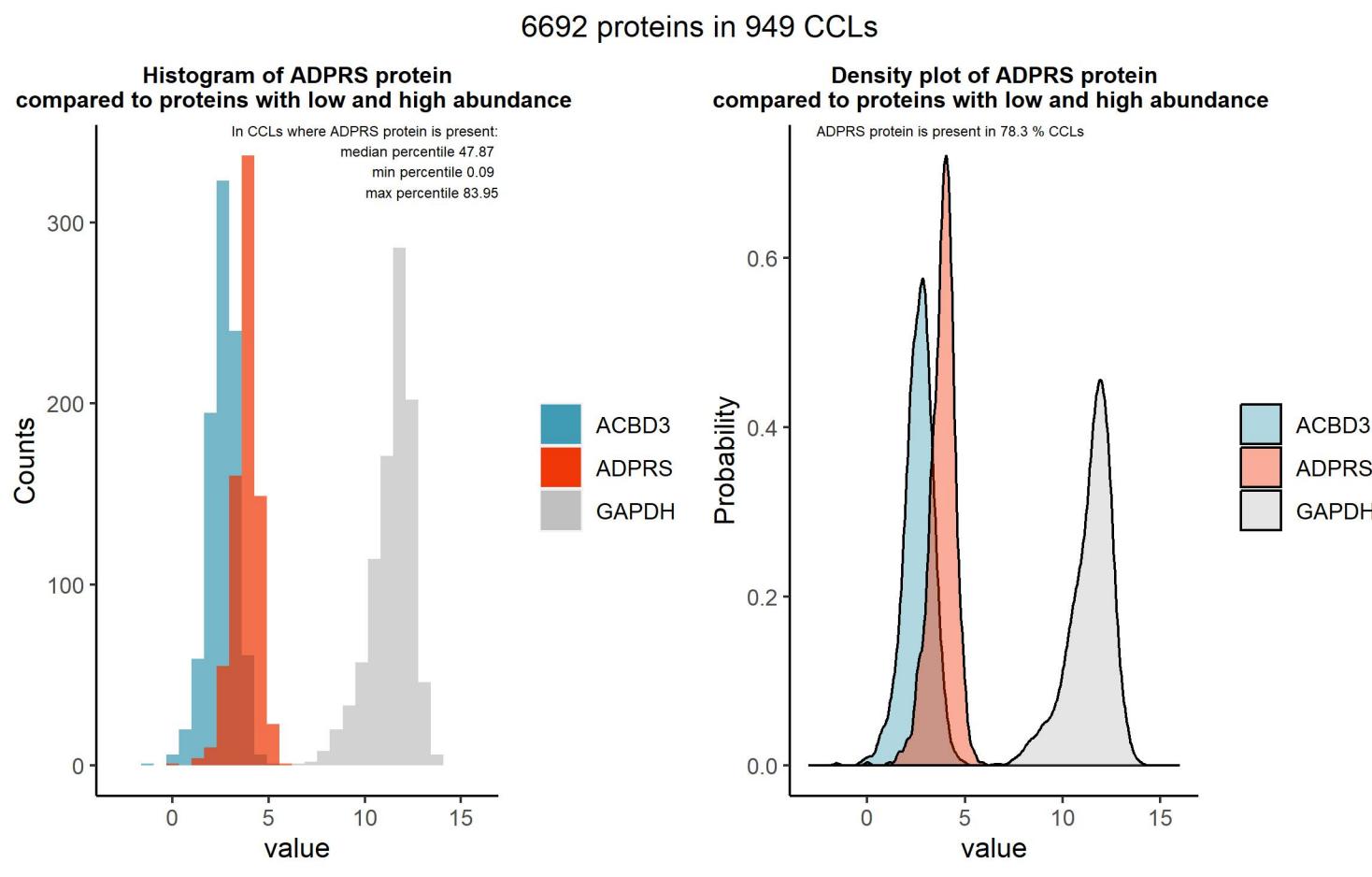


ADPRS

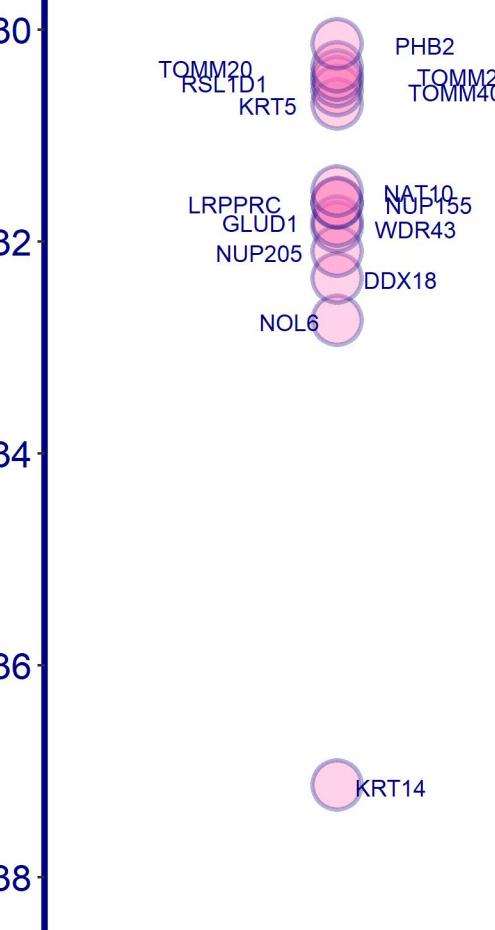
Protein name: ADPRS ; UNIPROT: Q9NX46 ; Gene name: ADP-ribosylserine hydrolase

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

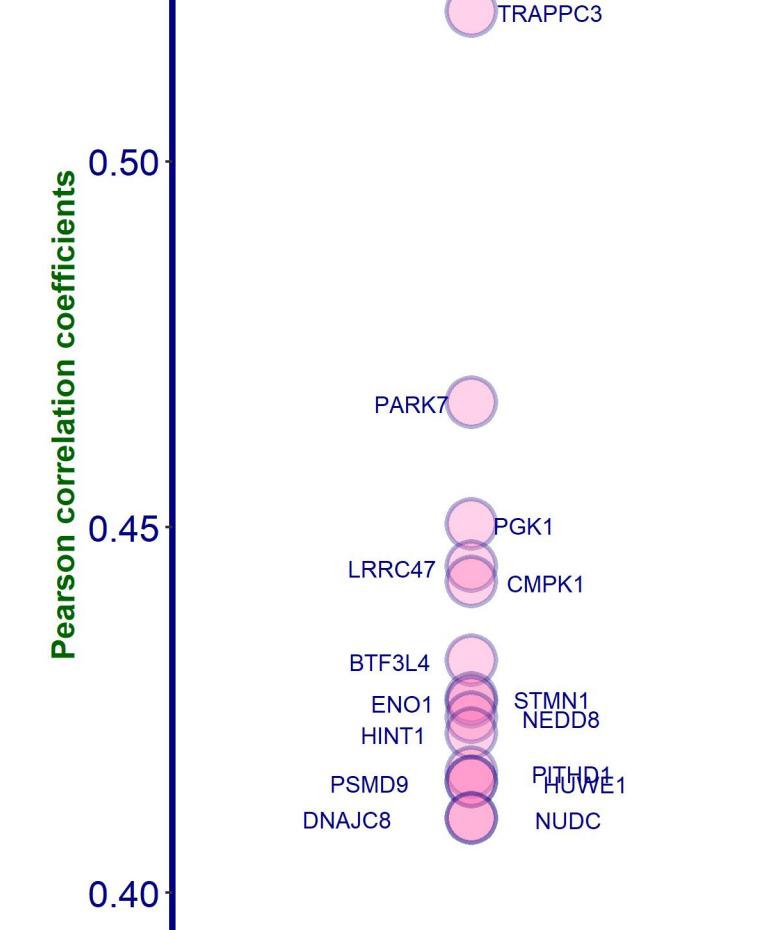
Sanger Institute Protein Database 1 (DB1), protein presence is certain



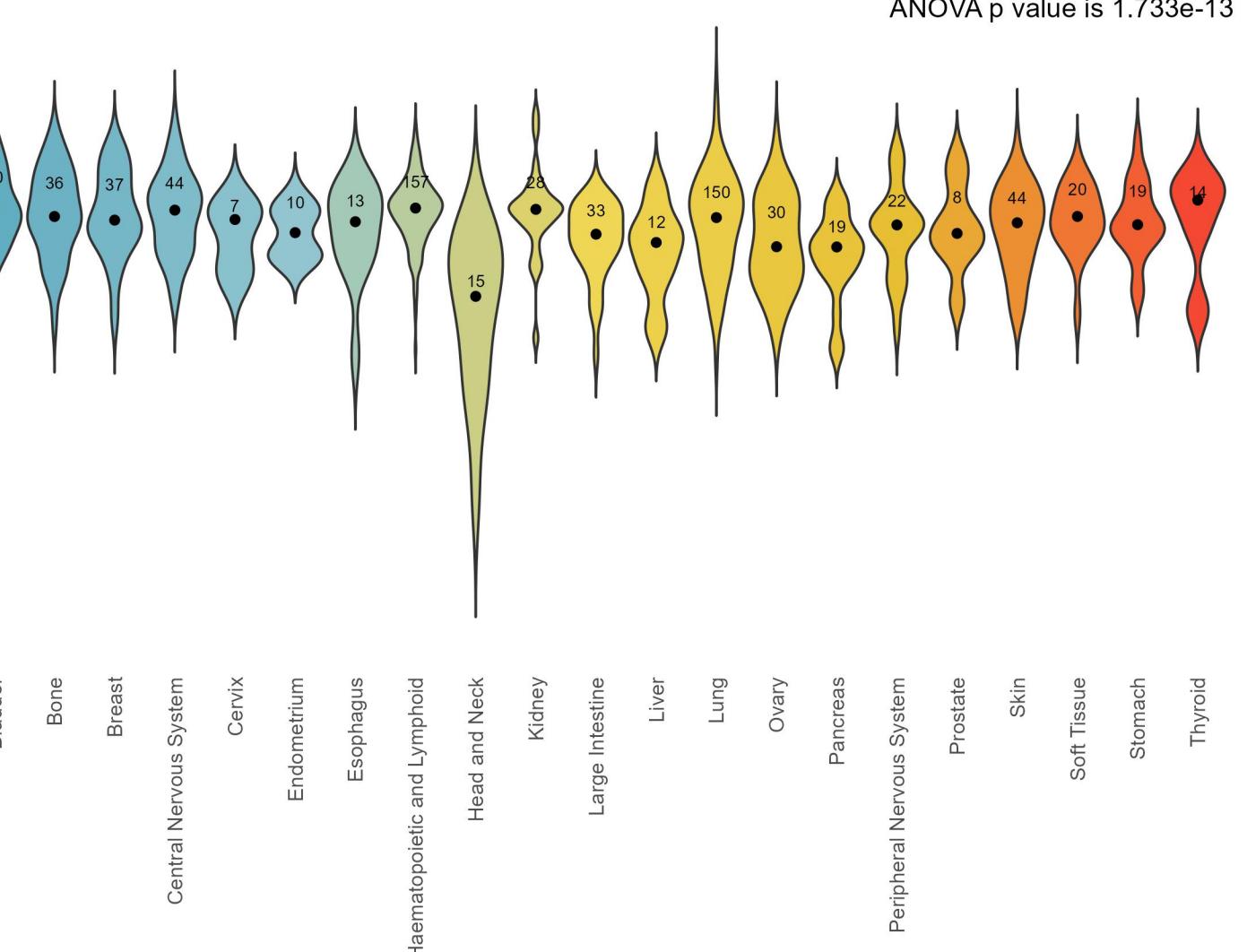
Top negative correlations of ADPRS protein, DB1



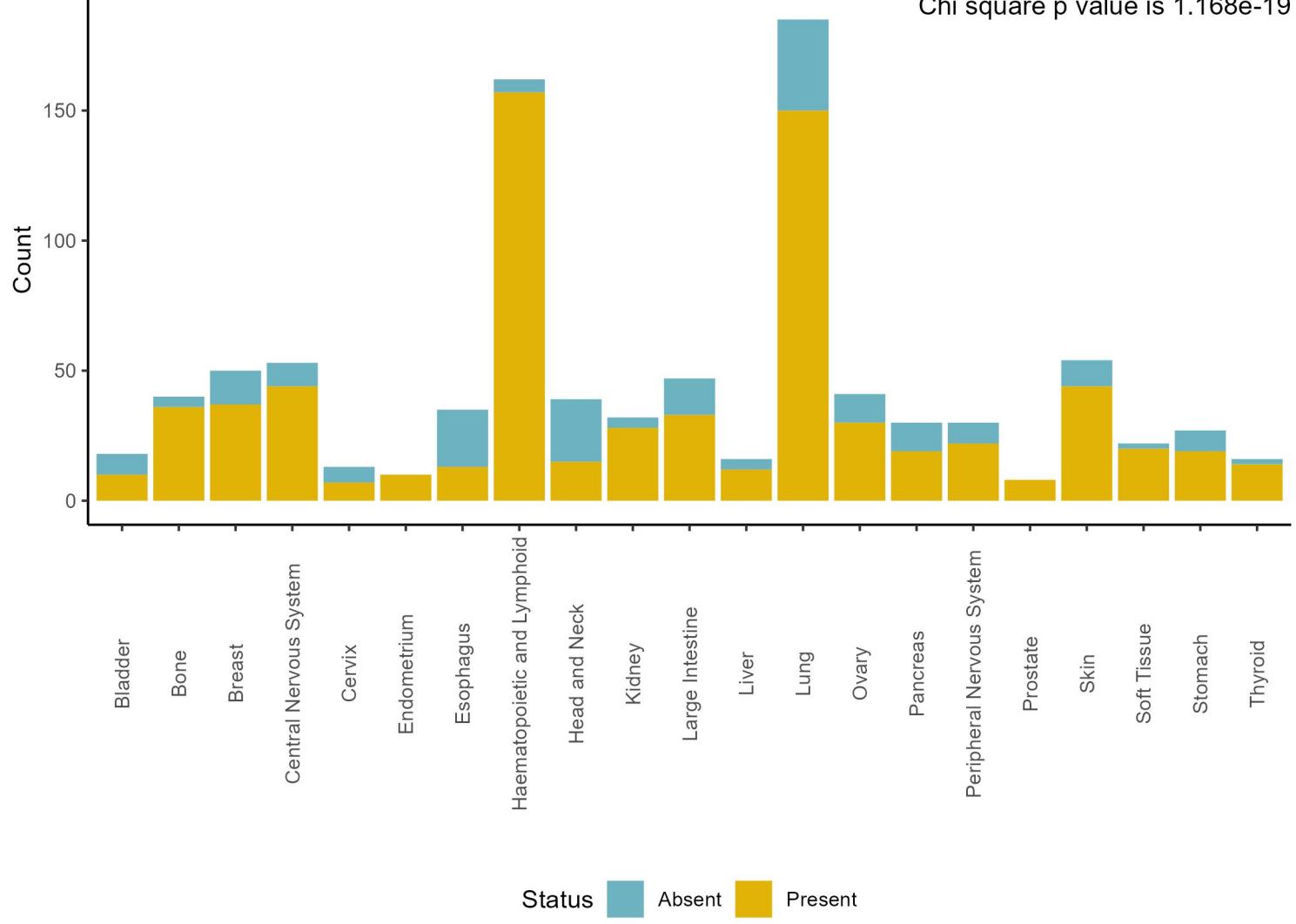
Top positive correlations of ADPRS protein, DB1



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



Present and absent ADPRS protein counts by tissue, DB1

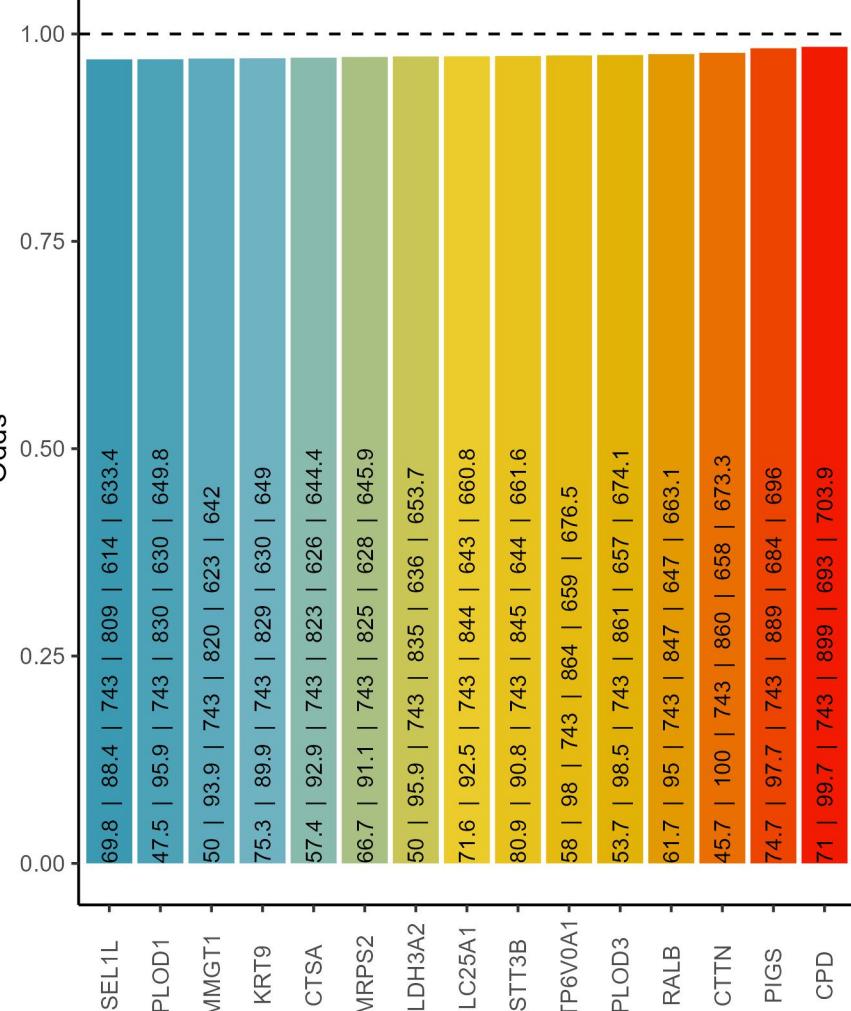


Cooccurrence with ADPRS protein, DB1

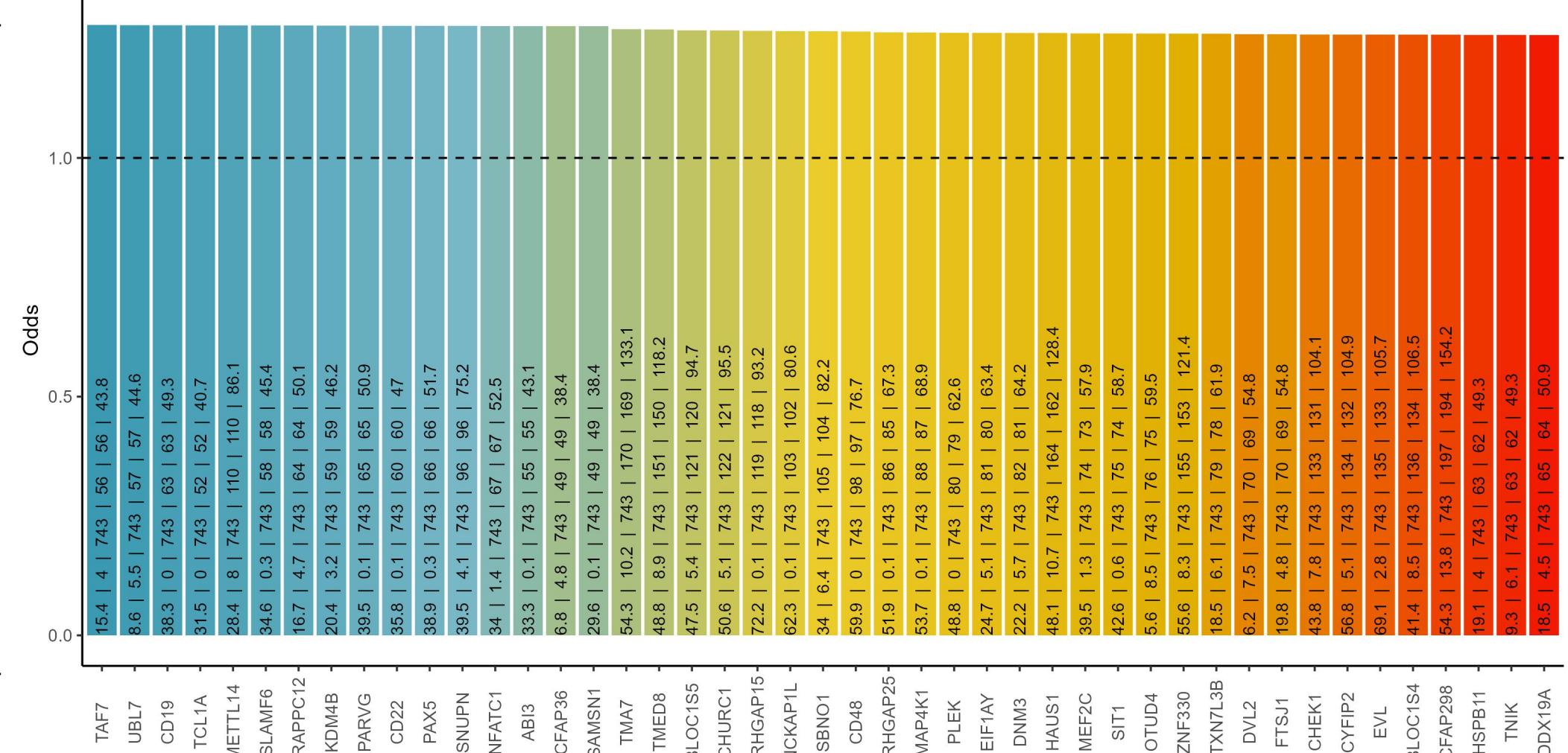
% of ADPRS in blood cancers: 96.9 ; % of ADPRS in solid cancers: 74.4

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

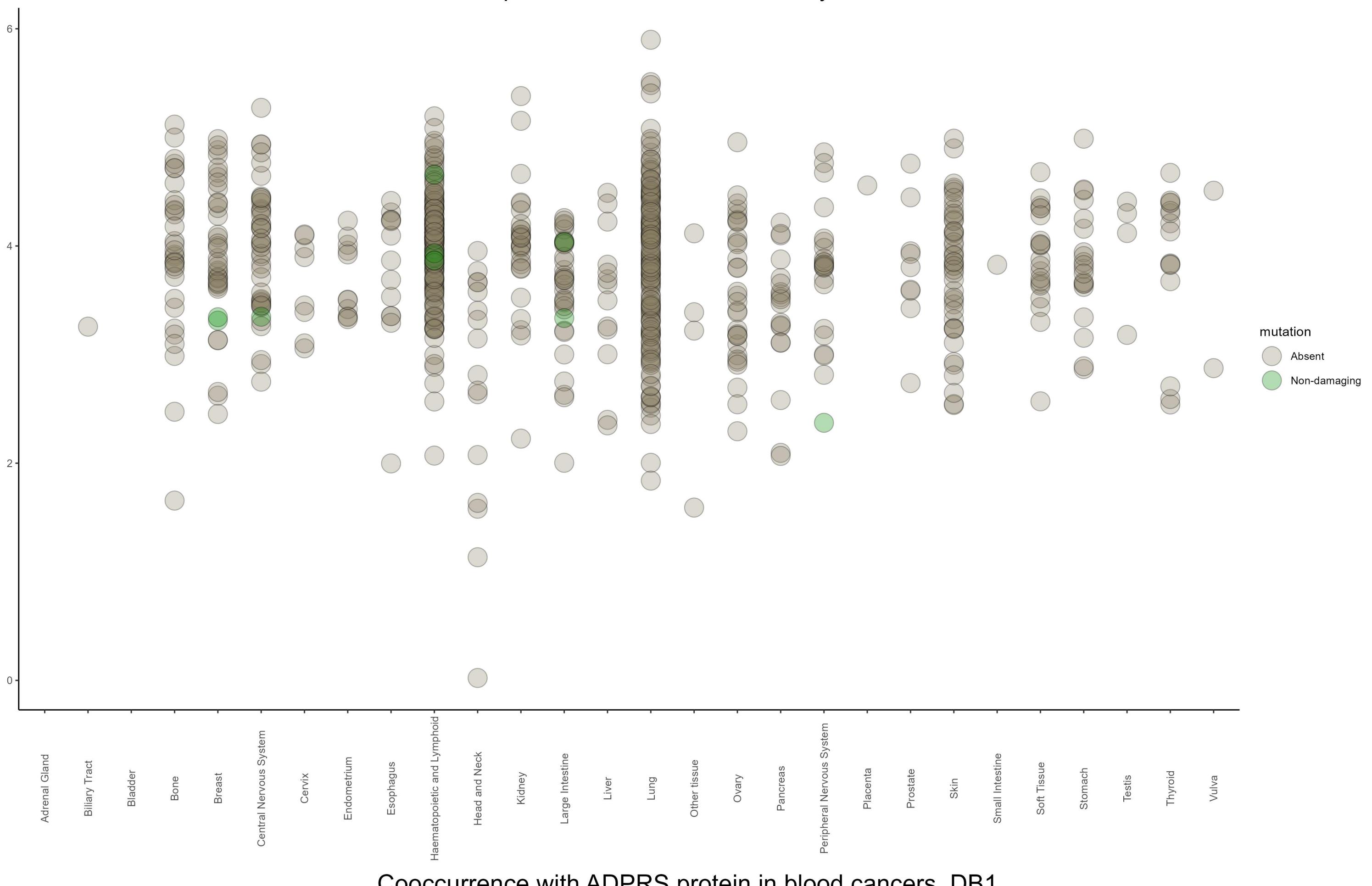
Negative cooccurrence



Positive cooccurrence



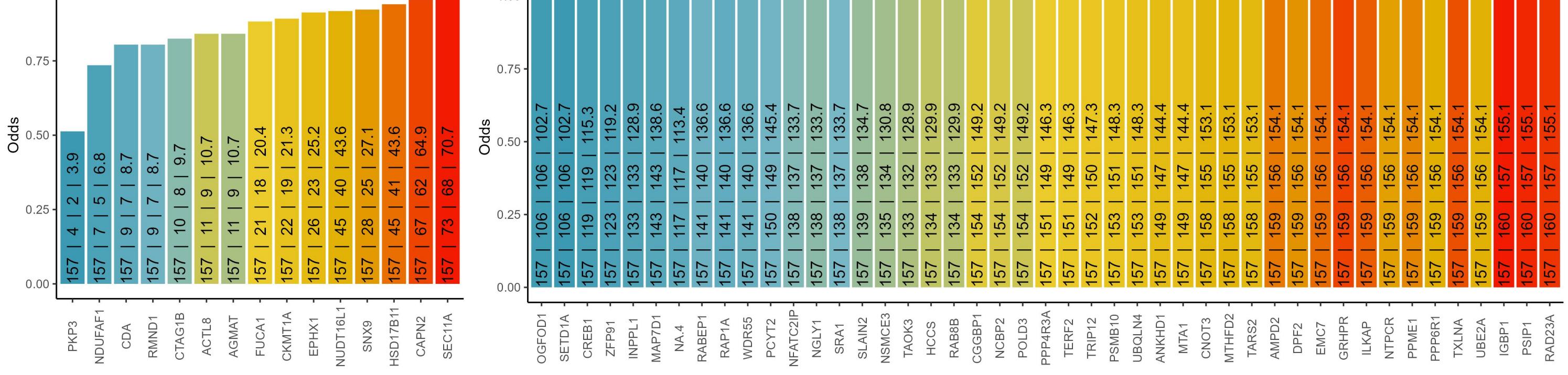
Amount of ADPRS protein and mutation status by tissue, DB1



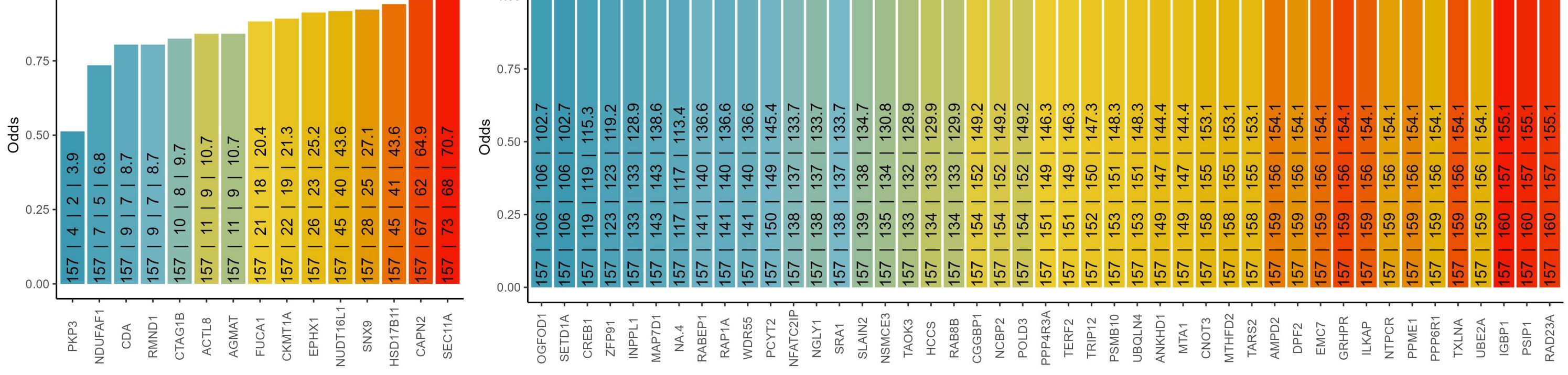
Cooccurrence with ADPRS protein in blood cancers, DB1

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

Negative cooccurrence



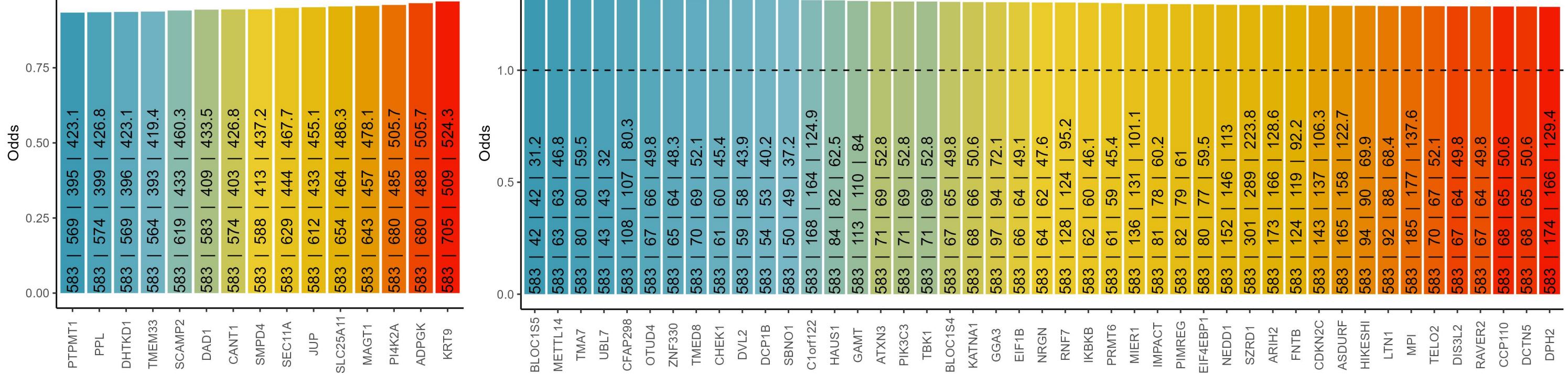
Positive cooccurrence



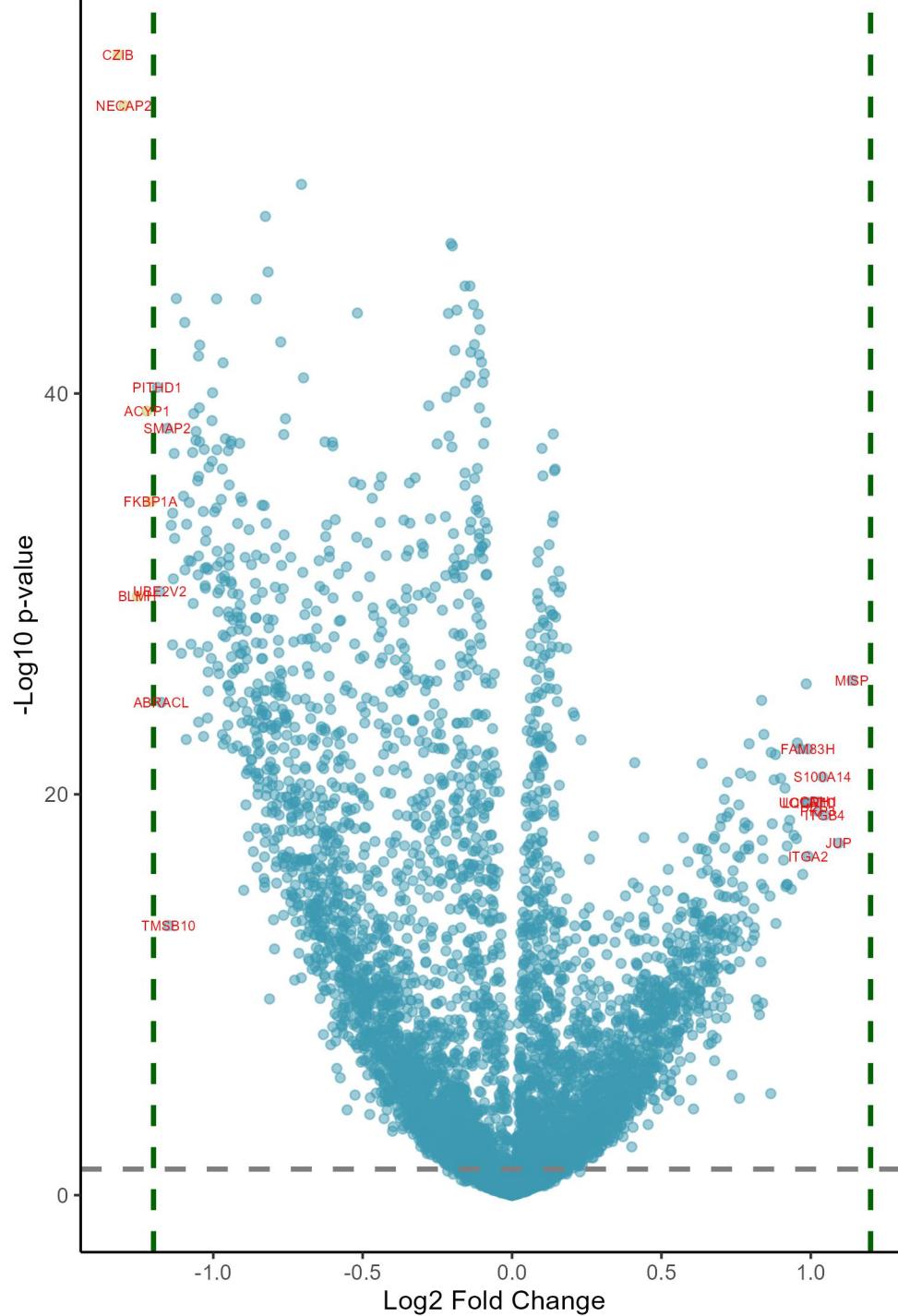
Cooccurrence with ADPRS protein in solid cancers, DB1

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

Negative cooccurrence



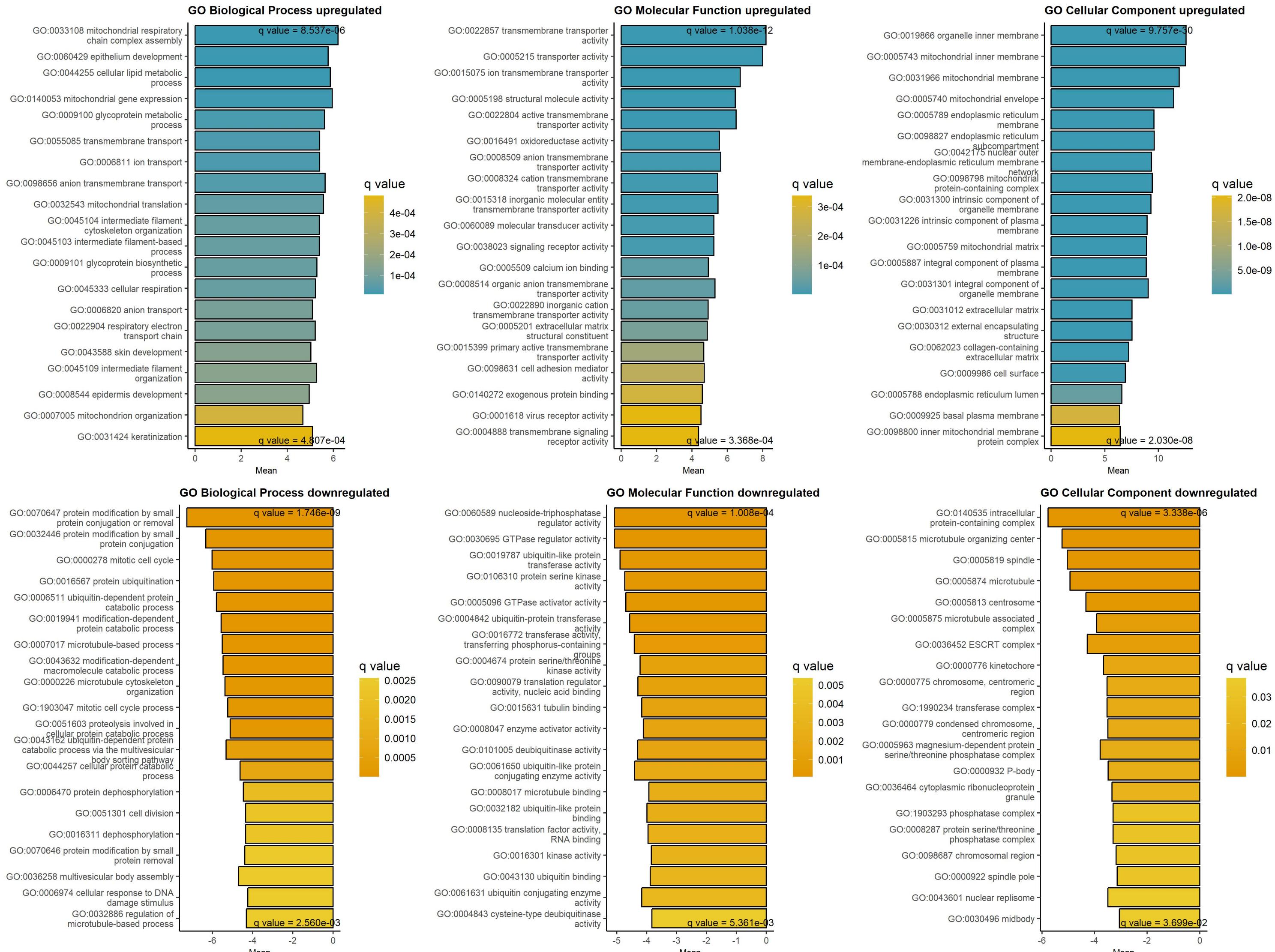
Positive cooccurrence



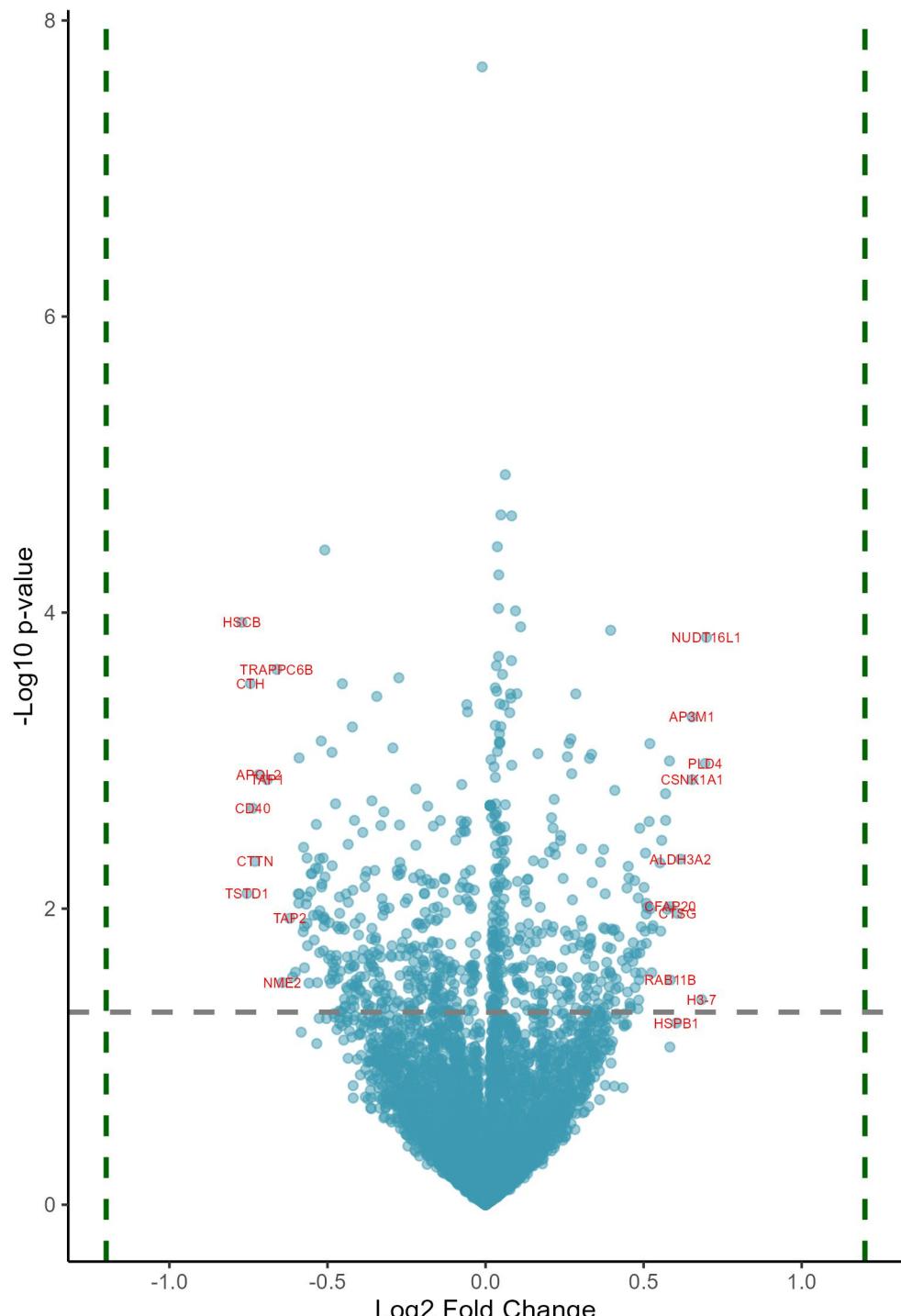
Downregulated at low/absent ADPRS Upregulated at low/absent ADPRS

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.32	4.12e-54	CZIB	CXXC motif containing zinc binding	1.14	3.68e-25	MISP	mitotic spindle positioning
-1.3	9.71e-52	NECAP2	NECAP endocytosis associated 2	1.09	2.12e-17	JUP	junction plakoglobin
-1.25	3.90e-29	BLMH	bleomycin hydrolase	1.05	9.60e-19	ITGB4	integrin subunit beta 4
-1.22	1.20e-37	ACYP1	acylphosphatase 1	1.04	1.46e-20	S100A14	S100 calcium binding protein A14
-1.21	1.77e-33	FKBP1A	FKBP prolyl isomerase 1A	1.03	2.23e-19	CDH1	cadherin 1
-1.19	9.44e-39	PITHD1	PITH domain containing 1	1.02	6.34e-19	PKP3	plakophilin 3
-1.18	2.40e-29	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.99	9.07e-17	ITGA2	integrin subunit alpha 2
-1.17	4.14e-24	ABRACL	ABRA C-terminal like	0.99	6.61e-22	FAM83H	family with sequence similarity 83
-1.15	7.82e-37	SMAP2	small ArfGAP2	0.99	2.49e-19	LCLAT1	lysocardiolipin acyltransferase 1
-1.15	1.85e-13	TMSB10	thymosin beta 10	0.99	2.49e-19	UQCRC10	ubiquinol-cytochrome c reductase, c
-1.14	2.10e-32	PPP6R1	protein phosphatase 6 regulatory subunit	0.98	5.52e-25	CDH3	cadherin 3
-1.14	7.73e-27	ENO2	enolase 2	0.97	6.63e-16	KRT17	keratin 17
-1.14	5.95e-33	COPS7B	COP9 signalosome subunit 7B	0.96	6.49e-22	LAMA5	laminin subunit alpha 5
-1.13	6.10e-30	RNF181	ring finger protein 181	0.95	3.46e-22	LAMB3	laminin subunit beta 3
-1.13	9.51e-36	DCK	deoxycytidine kinase	0.95	1.29e-17	TACSTD2	tumor associated calcium signal transducer 2
-1.13	8.60e-32	UBR7	ubiquitin protein ligase E3 compone	0.94	8.89e-18	LAD1	ladinin 1
-1.12	9.94e-43	SZRD1	SUZ RNA binding domain containing 1	0.94	3.37e-15	GPRC5A	G protein-coupled receptor class C
-1.11	1.95e-26	TMEM263	transmembrane protein 263	0.93	1.69e-18	EPB41L1	erythrocyte membrane protein band 4
-1.1	9.94e-34	PIN1	peptidylprolyl cis/trans isomerase, NIMA-like 1	0.92	3.77e-18	KRT80	keratin 80
-1.1	1.00e-41	PHPT1	phosphohistidine phosphatase 1	0.92	2.01e-15	EGFR	epidermal growth factor receptor
-1.09	2.38e-30	RPE	ribulose-5-phosphate-3-epimerase	0.92	2.90e-17	SPINT1	serine peptidase inhibitor, Kunitz type 1
-1.09	2.37e-22	NACA2	nascent polypeptide associated complex	0.92	1.98e-15	DSG2	desmoglein 2
-1.09	1.88e-32	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent	0.92	2.54e-15	PKP2	plakophilin 2
-1.08	8.82e-31	ARMC6	armadillo repeat containing 6	0.91	4.96e-20	CD9	CD9 molecule
-1.08	1.90e-33	TP53RK	TP53 regulating kinase	0.91	1.38e-16	KRT5	keratin 5
-1.07	7.23e-27	AK6	adenylate kinase 6	0.9	1.68e-20	LAMC2	laminin subunit gamma 2
-1.07	9.63e-31	HDHD2	haloacid dehalogenase like hydrolase	0.88	1.47e-13	S100A16	S100 calcium binding protein A16
-1.07	8.61e-36	RNF214	ring finger protein 214	0.88	1.22e-21	KRT6A	keratin 6A
-1.07	8.78e-29	NUDT3	nudix hydrolase 3	0.88	1.98e-20	SURF1	SURF1 cytochrome c oxidase assembly

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

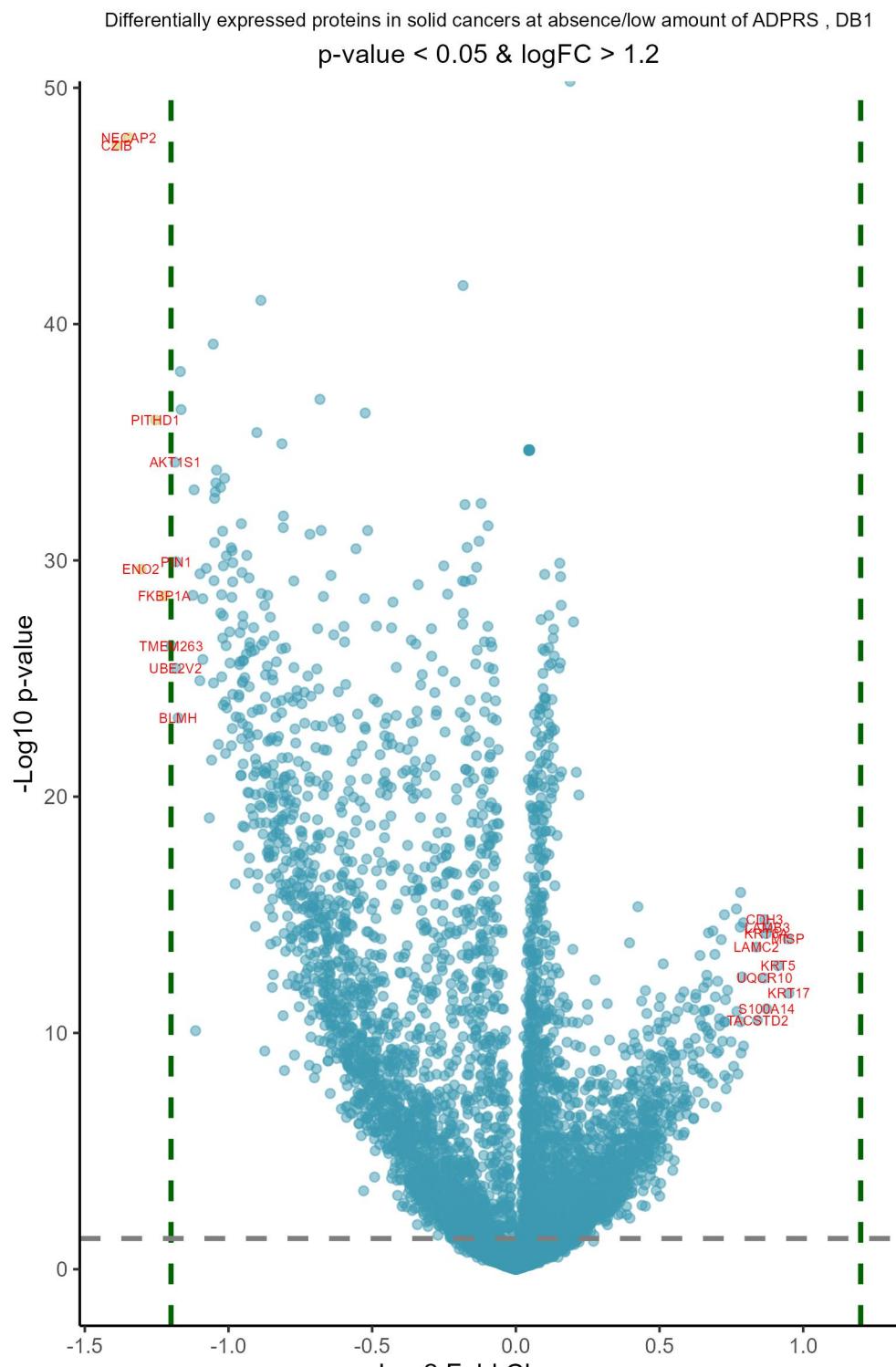


p-value < 0.05 & logFC > 1.2



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

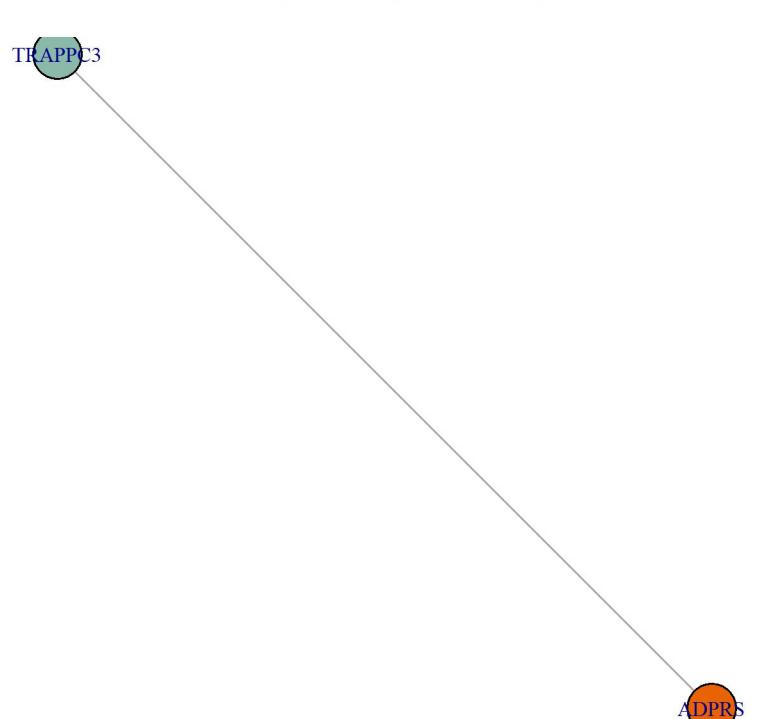
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.77	2.19e-02	HSCB	HscB mitochondrial iron-sulfur clus	0.7	2.19e-02	NUDT16L1	nudix hydrolase 16 like 1
-0.75	7.16e-02	TSTD1	thiosulfate sulfurtransferase like	0.69	2.19e-02	PLD4	phospholipase D family member 4
-0.74	2.19e-02	CTH	cystathione gamma-lyase	0.68	2.33e-01	H3-7	H3.7 histone (putative)
-0.74	2.27e-02	CD40	CD40 molecule	0.65	2.19e-02	CSNK1A1	casein kinase 1 alpha 1
-0.73	4.77e-02	CTTN	cortactin	0.65	2.19e-02	AP3M1	adaptor related protein complex 3 s
-0.72	2.19e-02	APOL2	apolipoprotein L2	0.62	4.62e-02	ALDH3A2	aldehyde dehydrogenase 3 family mem
-0.69	2.19e-02	TAP1	transporter 1, ATP binding cassette	0.61	9.21e-02	CTSG	cathepsin G
-0.66	2.19e-02	TRAPP6B	trafficking protein particle comple	0.6	2.90e-01	HSPB1	heat shock protein family B (small)
-0.64	1.97e-01	NME2	NME/NM23 nucleoside diphosphate kin	0.58	1.92e-01	RAB11B	RAB11B, member RAS oncogene family
-0.62	9.83e-02	TAP2	transporter 2, ATP binding cassette	0.58	8.47e-02	CFAP20	cilia and flagella associated prote
-0.61	1.87e-01	HLA-DQB1	major histocompatibility complex, c	0.58	3.52e-01	S100A4	S100 calcium binding protein A4
-0.6	1.77e-01	CD48	CD48 molecule	0.58	2.19e-02	POLR2G	RNA polymerase II subunit G
-0.59	7.17e-02	TRIP10	thyroid hormone receptor interactor	0.58	8.73e-02	CEP43	centrosomal protein 43
-0.59	8.09e-02	MFF	mitochondrial fission factor	0.57	2.71e-02	NCAPH2	non-SMC condensin II complex subuni
-0.59	2.19e-02	TRIP11	thyroid hormone receptor interactor	0.57	2.19e-02	KAT7	lysine acetyltransferase 7
-0.59	7.17e-02	MRPS14	mitochondrial ribosomal protein S14	0.56	3.56e-02	LYN	LYN proto-oncogene, Src family tyro
-0.58	3.11e-01	SFN	stratifin	0.55	1.14e-01	PYGL	glycogen phosphorylase L
-0.58	1.15e-01	ISG15	ISG15 ubiquitin like modifier	0.55	4.85e-02	VPS36	vacuolar protein sorting 36 homolog
-0.58	3.91e-02	MBNL1	muscleblind like splicing regulator	0.53	1.08e-01	MICAL1	microtubule associated monooxygenas
-0.57	1.08e-01	ENTPD1	ectonucleoside triphosphate diphosp	0.53	1.11e-01	MEF2D	myocyte enhancer factor 2D
-0.57	1.70e-01	MVP	major vault protein	0.53	1.78e-01	SATB1	SATB homeobox 1
-0.57	8.19e-02	NFKB2	nuclear factor kappa B subunit 2	0.52	8.70e-02	POMP	proteasome maturation protein
-0.56	4.56e-02	PSMG4	proteasome assembly chaperone 4	0.52	2.19e-02	AP1M1	adaptor related protein complex 1 s
-0.56	1.05e-01	ARID3B	AT-rich interaction domain 3B	0.52	2.75e-02	PPP4R1	protein phosphatase 4 regulatory su
-0.56	7.46e-02	ASAHI	N-acylsphingosine amidohydrolase 1	0.51	8.52e-02	KEAP1	kelch like ECH associated protein 1
-0.56	1.35e-01	NIBAN1	niban apoptosis regulator 1	0.51	8.09e-02	IPO8	importin 8
-0.56	1.97e-01	HLA-DPA1	major histocompatibility complex, c	0.51	1.31e-01	ATP6AP2	ATPase H ⁺ transporting accessory pr
-0.55	7.00e-02	LACTB	lactamase beta	0.51	9.28e-02	PXK	PX domain containing serine/threoni
-0.55	5.60e-02	VTN	vitronectin	0.51	4.25e-02	PTCD1	pentatricopeptide repeat domain 1



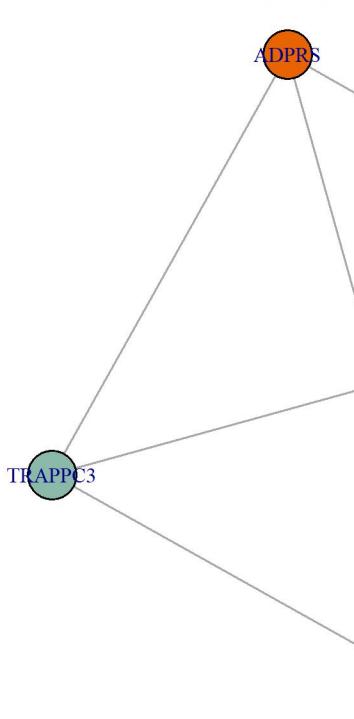
Downregulated in solid cancers at low/absent ADPRS Upregulated in solid cancers at low/absent ADPRS

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.39	4.53e-45	CZIB	CXXC motif containing zinc binding	0.95	1.21e-11	KRT17	keratin 17
-1.35	2.91e-45	NECAP2	NECAP endocytosis associated 2	0.95	7.65e-14	MISP	mitotic spindle positioning
-1.3	1.23e-28	ENO2	enolase 2	0.91	9.35e-13	KRT5	keratin 5
-1.25	6.40e-34	PITHD1	PITH domain containing 1	0.88	2.75e-14	LAMB3	laminin subunit beta 3
-1.22	1.45e-27	FKBP1A	FKBP prolyl isomerase 1A	0.87	5.12e-11	S100A14	S100 calcium binding protein A14
-1.2	1.46e-25	TMEM263	transmembrane protein 263	0.87	4.66e-14	KRT6A	keratin 6A
-1.19	4.92e-33	AKT1S1	AKT1 substrate 1	0.87	1.29e-14	CDH3	cadherin 3
-1.18	1.12e-24	UBE2V2	ubiquitin conjugating enzyme E2 V2	0.86	2.96e-12	UQCR10	ubiquinol-cytochrome c reductase, c
-1.18	6.30e-29	PIN1	peptidylprolyl cis/trans isomerase,	0.84	1.49e-10	TACSTD2	tumor associated calcium signal tra
-1.18	1.05e-22	BLMH	bleomycin hydrolase	0.84	1.65e-13	LAMC2	laminin subunit gamma 2
-1.17	8.46e-36	PHPT1	phosphohistidine phosphatase 1	0.79	1.63e-09	VAMP8	vesicle associated membrane protein
-1.17	2.76e-34	LZIC	leucine zipper and CTNNB1P1 domain	0.79	1.71e-14	SURF1	SURF1 cytochrome c oxidase assembly
-1.12	1.38e-27	ACYP1	acylphosphatase 1	0.79	2.67e-12	UXS1	UDP-glucuronate decarboxylase 1
-1.12	6.86e-32	ATOX1	antioxidant 1 copper chaperone	0.78	3.10e-09	CDH1	cadherin 1
-1.11	3.91e-10	TMSB10	thymosin beta 10	0.78	1.04e-15	DHRS7B	dehydrogenase/reductase 7B
-1.1	3.56e-24	ITPA	inosine triphosphatase	0.78	1.71e-10	KRT80	keratin 80
-1.1	1.89e-28	COPS7B	COP9 signalosome subunit 7B	0.78	2.58e-14	COL17A1	collagen type XVII alpha 1 chain
-1.09	1.86e-27	FN3KRP	fructosamine 3 kinase related prote	0.77	2.12e-08	GPRC5A	G protein-coupled receptor class C
-1.09	5.15e-25	UBR7	ubiquitin protein ligase E3 compone	0.77	6.57e-11	LPCAT2	lysophosphatidylcholine acyltransfe
-1.08	1.14e-28	PPP1R14B	protein phosphatase 1 regulatory in	0.77	4.80e-15	PTPMT1	protein tyrosine phosphatase mitoch
-1.07	1.03e-18	ABRACL	ABRA C-terminal like	0.76	1.05e-08	ITGB4	integrin subunit beta 4
-1.06	5.13e-21	LYPLA2	lysophospholipase 2	0.75	1.09e-09	LCLAT1	lysocardiolipin acyltransferase 1
-1.05	6.71e-37	NUBP2	NUBP iron-sulfur cluster assembly f	0.74	3.25e-08	JUP	junction plakoglobin
-1.05	4.38e-24	RPE	ribulose-5-phosphate-3-epimerase	0.74	9.15e-12	KRT16	keratin 16
-1.05	3.53e-28	DCK	deoxycytidine kinase	0.73	8.37e-08	BRI3BP	BRI3 binding protein
-1.05	1.55e-31	NRDC	nardilysin convertase	0.73	2.20e-11	CD9	CD9 molecule
-1.05	1.02e-29	AAMP	angio associated migratory cell pro	0.73	1.71e-10	TRIM29	tripartite motif containing 29
-1.05	8.35e-32	DOHH	deoxyhypusine hydroxylase	0.73	2.45e-08	PKP3	plakophilin 3
-1.04	3.59e-32	CASP3	caspase 3	0.73	8.11e-15	LPCAT4	lysophosphatidylcholine acyltransfe

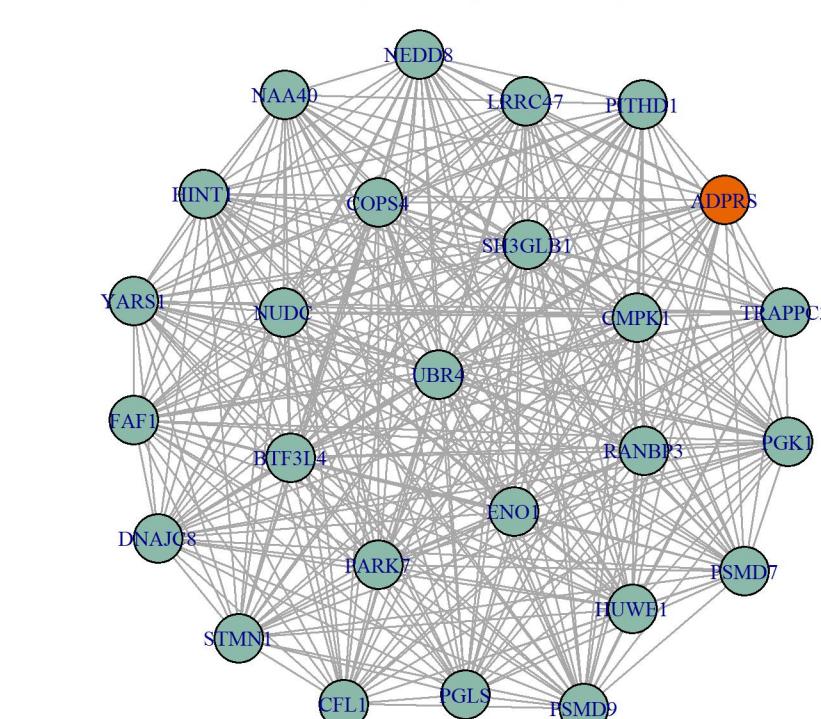
ADPRS network, DB1, all Pearson r > 0.5



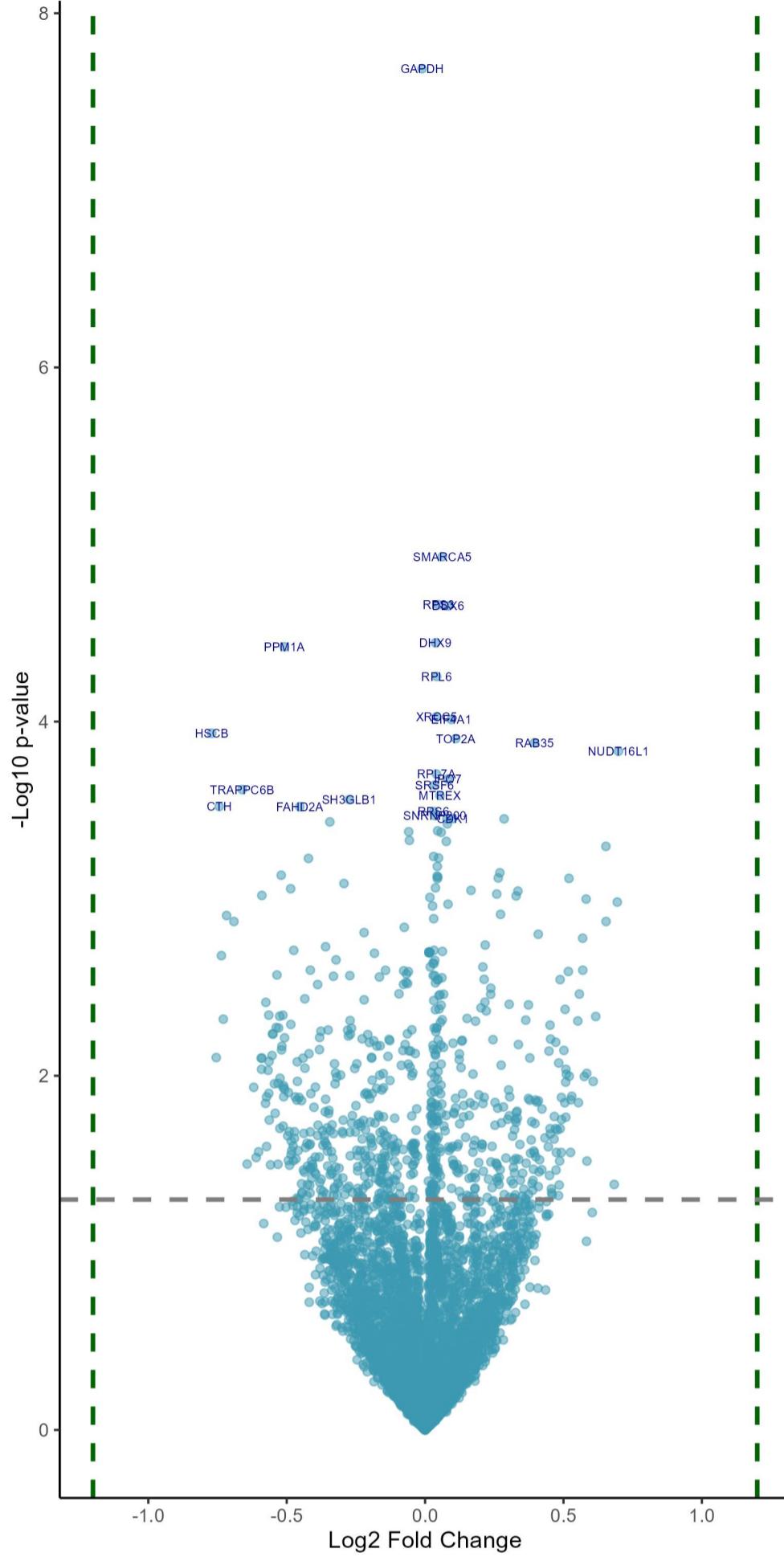
ADPRS network, DB1, all Pearson r > 0.45



ADPRS network, DB1, all Pearson r > 0.4



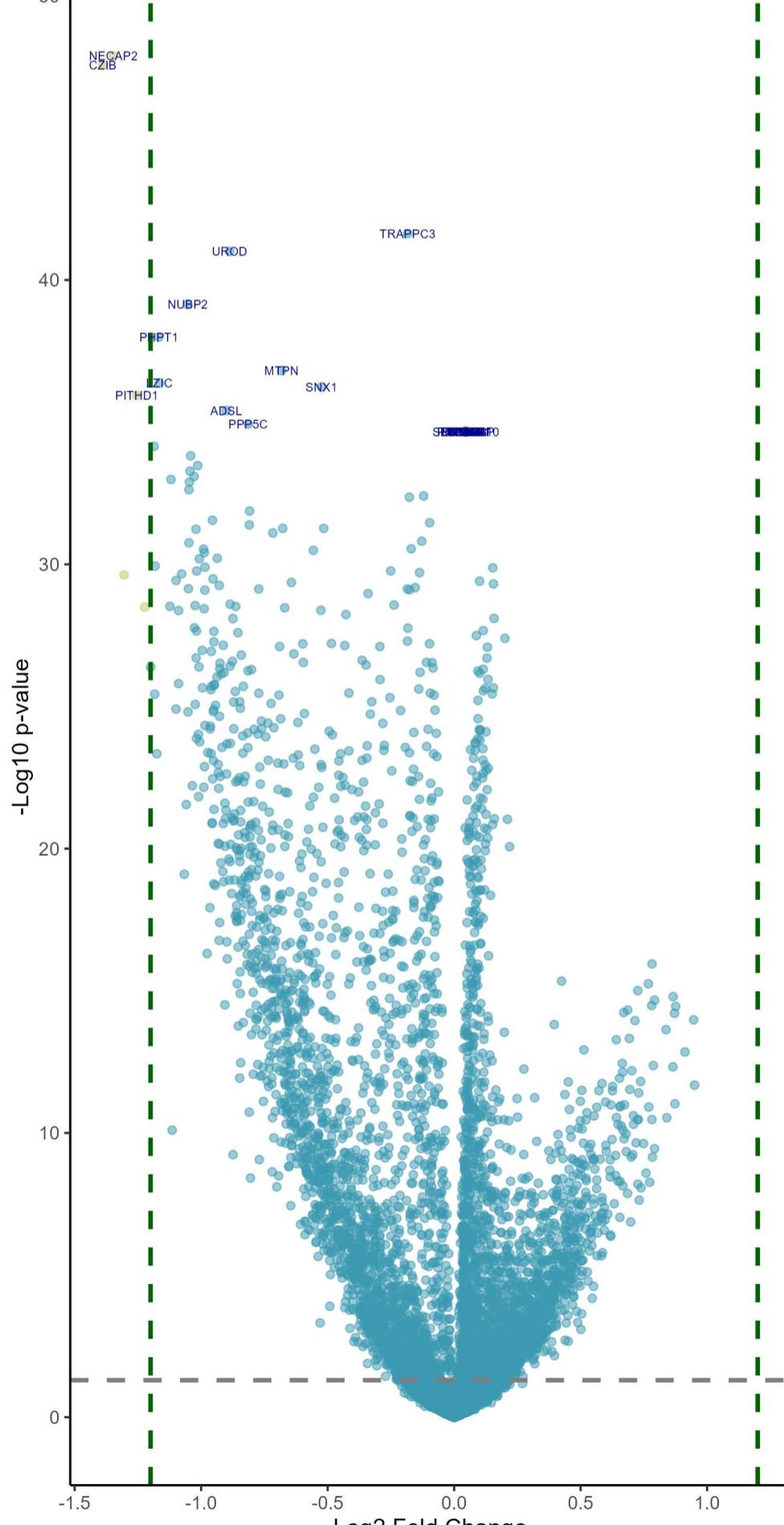
p-value < 0.05 & logFC > 1.2



Sorted by p values!

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

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.01	6.84e-05	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.06	2.19e-02	SMARCA5	SWI/SNF related, matrix associated,
-0.51	2.19e-02	PPM1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ depe	0.05	2.19e-02	RPS3	ribosomal protein S3
-0.77	2.19e-02	HSCB	HscB mitochondrial iron-sulfur clus	0.08	2.19e-02	DDX6	DEAD-box helicase 6
-0.66	2.19e-02	TRAPPC6B	trafficking protein particle comple	0.04	2.19e-02	DHX9	DExH-box helicase 9
-0.27	2.19e-02	SH3GLB1	SH3 domain containing GRB2 like, en	0.04	2.19e-02	RPL6	ribosomal protein L6
-0.74	2.19e-02	CTH	cystathione gamma-lyase	0.04	2.19e-02	XRCC5	X-ray repair cross complementing 5
-0.45	2.19e-02	FAHD2A	fumarylacetoacetate hydrolase domai	0.09	2.19e-02	EIF4A1	eukaryotic translation initiation f
-0.34	2.19e-02	CD2AP	CD2 associated protein	0.11	2.19e-02	TOP2A	DNA topoisomerase II alpha
-0.06	2.19e-02	LRRC47	leucine rich repeat containing 47	0.4	2.19e-02	RAB35	RAB35, member RAS oncogene family
-0.06	2.19e-02	HSD17B10	hydroxysteroid 17-beta dehydrogenas	0.7	2.19e-02	NUDT16L1	nudix hydrolase 16 like 1
-0.42	2.19e-02	FHIT	fragile histidine triad diadenosine	0.04	2.19e-02	RPL7A	ribosomal protein L7a
-0.52	2.19e-02	C1orf174	chromosome 1 open reading frame 174	0.08	2.19e-02	IPO7	importin 7
-0.29	2.19e-02	ATAD3B	ATPase family AAA domain containing	0.03	2.19e-02	SRSF6	serine and arginine rich splicing f
-0.49	2.19e-02	UNC119	unc-119 lipid binding chaperone	0.05	2.19e-02	MTREX	Mtr4 exosome RNA helicase
-0.59	2.19e-02	TRIP11	thyroid hormone receptor interactor	0.03	2.19e-02	RPS6	ribosomal protein S6
-0.72	2.19e-02	APOL2	apolipoprotein L2	0.04	2.19e-02	SNRNP200	small nuclear ribonucleoprotein U5
-0.69	2.19e-02	TAP1	transporter 1, ATP binding cassette	0.1	2.19e-02	CDK1	cyclin dependent kinase 1
-0.08	2.19e-02	ALDOC	aldolase, fructose-bisphosphate C	0.08	2.19e-02	BAZ1B	bromodomain adjacent to zinc finger
-0.22	2.19e-02	DFFA	DNA fragmentation factor subunit al	0.29	2.19e-02	METTL7B	methyltransferase like 7B
-0.36	2.19e-02	MTSS1	MTSS I-BAR domain containing 1	0.08	2.19e-02	PRPF8	pre-mRNA processing factor 8
-0.47	2.19e-02	FAM234A	family with sequence similarity 234	0.05	2.19e-02	RPL7	ribosomal protein L7
-0.18	2.21e-02	PML	PML nuclear body scaffold	0.06	2.19e-02	RPL3	ribosomal protein L3
-0.74	2.27e-02	CD40	CD40 molecule	0.08	2.19e-02	RPS9	ribosomal protein S9
-0.32	2.40e-02	CCS	copper chaperone for superoxide dis	0.65	2.19e-02	AP3M1	adaptor related protein complex 3 s
-0.41	2.71e-02	MTIF2	mitochondrial translational initiat	0.03	2.19e-02	RPS13	ribosomal protein S13
-0.14	2.71e-02	SEC22B	SEC22 homolog B, vesicle traffickin	0.05	2.19e-02	RPS15A	ribosomal protein S15a
-0.08	2.73e-02	MRPL45	mitochondrial ribosomal protein L45	0.04	2.19e-02	PABPC1	poly(A) binding protein cytoplasmic
-0.06	2.75e-02	ECH1	enoyl-CoA hydratase 1	0.27	2.19e-02	LONP2	ion peptidase 2, peroxisomal
-0.07	2.83e-02	PRDX5	peroxiredoxin 5	0.04	2.19e-02	NUP107	nucleoporin 107
-0.54	2.86e-02	SUMO2	small ubiquitin like modifier 2	0.05	2.19e-02	RPS16	ribosomal protein S16
-0.27	2.87e-02	NFS1	NFS1 cysteine desulfurase	0.26	2.19e-02	UHRF1	ubiquitin like with PHD and ring fi
-0.33	2.89e-02	ABRACL	ABRA C-terminal like	0.52	2.19e-02	AP1M1	adaptor related protein complex 1 s
-0.17	2.91e-02	SOD1	superoxide dismutase 1	0.04	2.19e-02	CNOT1	CCR4-NOT transcription complex subu
-0.07	3.10e-02	CARS1	cysteinyl-tRNA synthetase 1	0.04	2.19e-02	SF3B3	splicing factor 3b subunit 3
-0.06	3.13e-02	MRPL58	mitochondrial ribosomal protein L58	0.17	2.19e-02	PRPF18	pre-mRNA processing factor 18
-0.08	3.16e-02	PITHD1	PITH domain containing 1	0.34	2.19e-02	DACH1	dachshund family transcription fact
-0.39	3.16e-02	GUK1	guanylate kinase 1	0.26	2.19e-02	GPA33	glycoprotein A33
-0.09	3.56e-02	WARS1	tryptophanyl-tRNA synthetase 1	0.33	2.19e-02	RRM1	ribonucleotide reductase catalytic
0.43	3.76e-02	MRPL34	mitochondrial ribosomal protein L34	0.02	2.19e-02	TNEDSEFR	TNF receptor superfamily member 6b

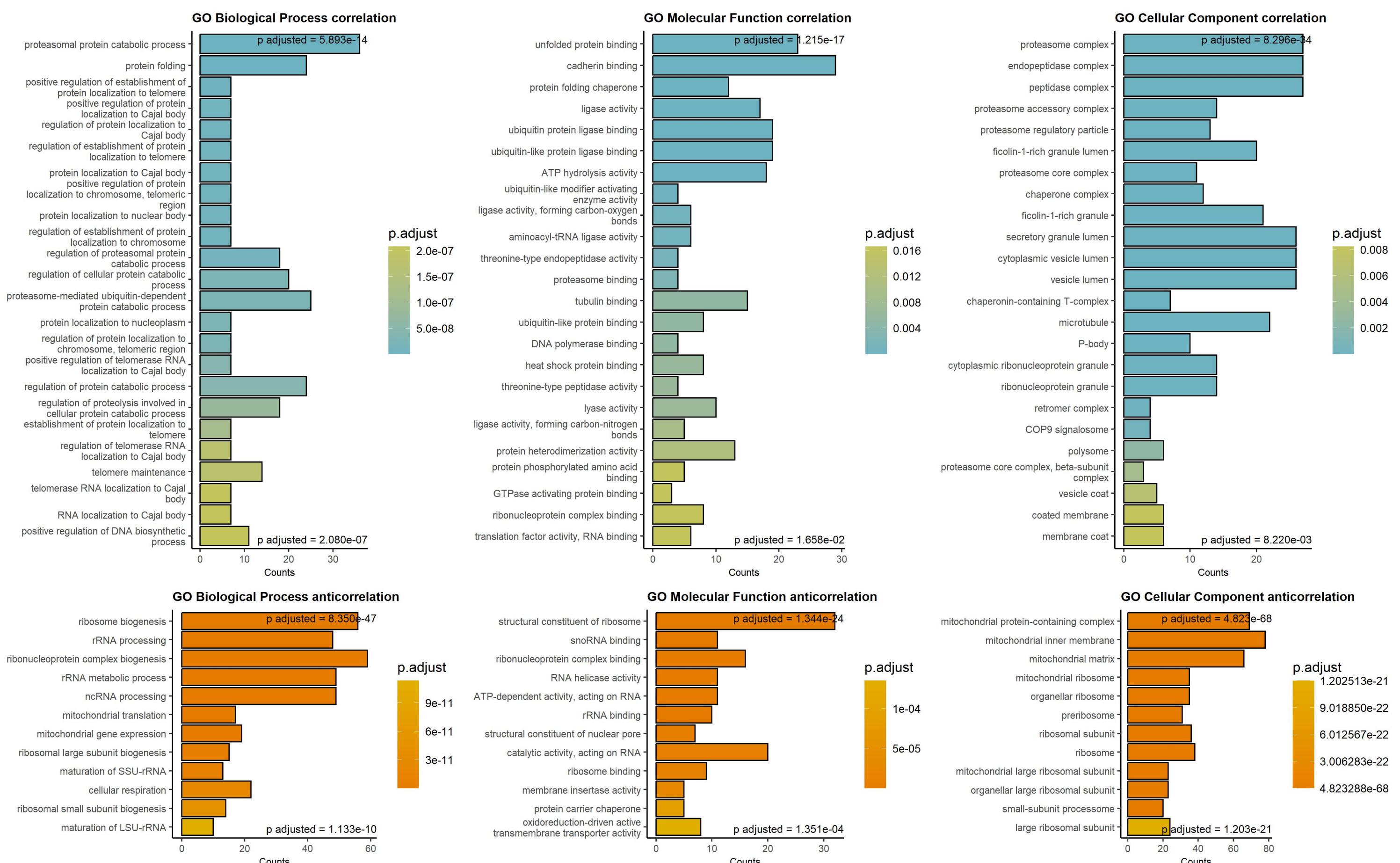
Differentially expressed proteins in solid cancers at absence/low amount of ADPRS , DB1
p-value < 0.05 & logFC > 1.2

Sorted by p values!

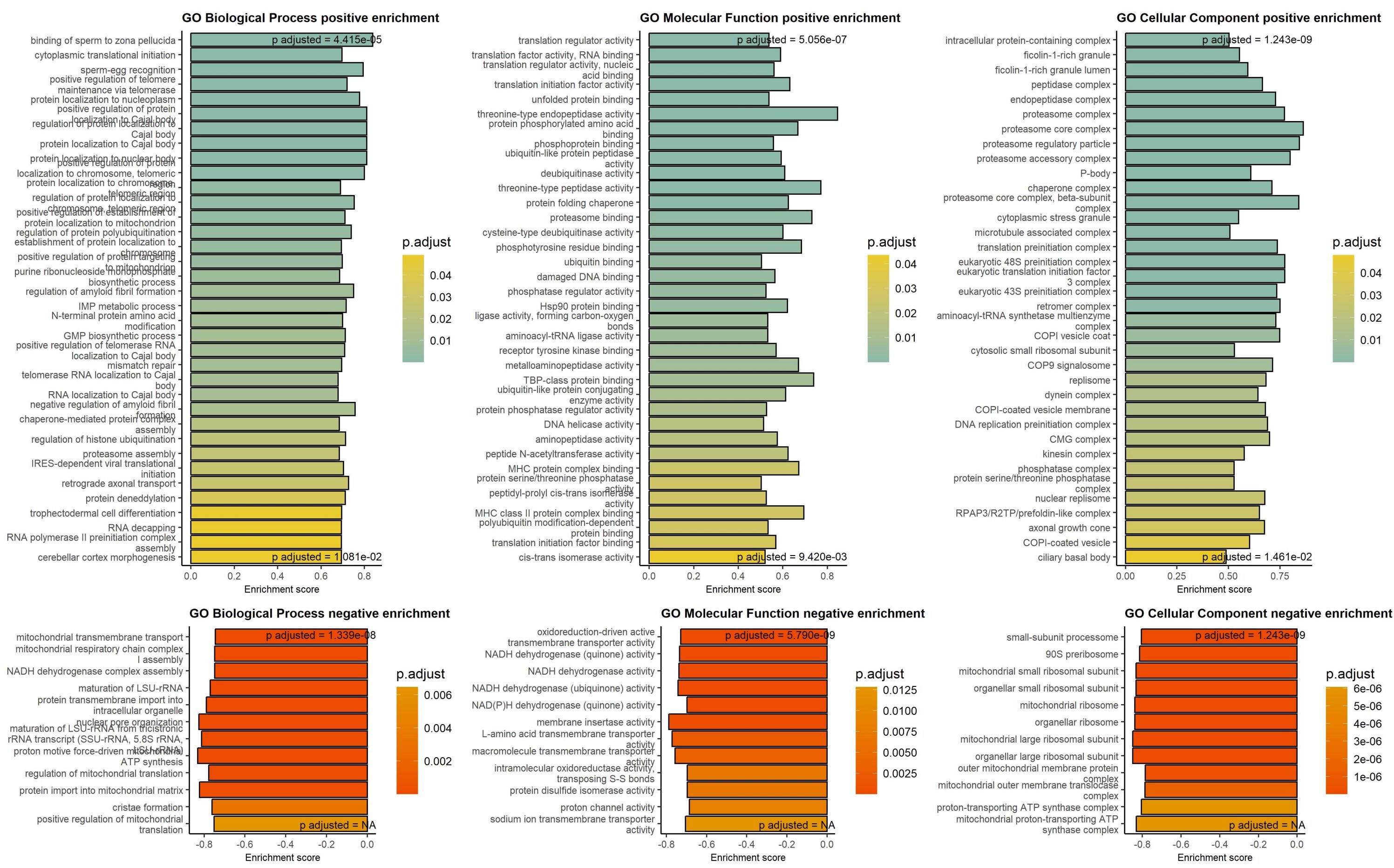
Downregulated in solid cancers at low/absent ADPRS Upregulated in solid cancers at low/absent ADPRS

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.35	2.91e-45	NECAP2	NECAP endocytosis associated 2	0.19	0.00e+00	H4C1	H4 clustered histone 1
-1.39	4.53e-45	CZIB	CXXC motif containing zinc binding	0.05	1.53e-33	PTPRCAP	protein tyrosine phosphatase recept
-0.18	3.12e-39	TRAPPC3	trafficking protein particle comple	0.05	1.53e-33	HBE1	hemoglobin subunit epsilon 1
-0.89	1.10e-38	UROD	uroporphyrinogen decarboxylase	0.05	1.53e-33	SERPINB10	serpin family B member 10
-1.05	6.71e-37	NUBP2	NUBP iron-sulfur cluster assembly f	0.05	1.53e-33	IGLL1	immunoglobulin lambda like polypept
-1.17	8.46e-36	PHPT1	phosphohistidine phosphatase 1	0.05	1.53e-33	CRYBB1	crystallin beta B1
-0.68	1.13e-34	MTPN	myotrophin	0.05	1.53e-33	ITGA2B	integrin subunit alpha 2b
-1.17	2.76e-34	LZIC	leucine zipper and CTNNBIP1 domain	0.05	1.53e-33	ACAP1	ArfGAP with coiled-coil, ankyrin re
-0.52	3.51e-34	SNX1	sorting nexin 1	0.05	1.53e-33	NCF4	neutrophil cytosolic factor 4
-1.25	6.40e-34	PITHD1	PITH domain containing 1	0.05	1.53e-33	SP140	SP140 nuclear body protein
-0.9	1.53e-33	ADSL	adenylosuccinate lyase	0.05	1.53e-33	PSTPIP1	proline-serine-threonine phosphatas
-0.81	1.53e-33	PPP5C	protein phosphatase 5 catalytic sub	0.05	1.53e-33	STAB1	stabilin 1
-1.19	4.92e-33	AKT1S1	AKT1 substrate 1	0.05	1.53e-33	SELPLG	selectin P ligand
-1.04	1.05e-32	KCMF1	potassium channel modulatory factor	0.05	1.53e-33	RCSD1	RCSD domain containing 1
-1.01	2.30e-32	ENOPH1	enolase-phosphatase 1	0.05	1.53e-33	STAT5A	signal transducer and activator of
-1.04	3.59e-32	CASP3	caspase 3	0.05	1.53e-33	CTSW	cathepsin W
-1.03	5.46e-32	SZRD1	SUZ RNA binding domain containing 1	0.05	1.53e-33	GIMAP6	GTPase, IMAP family member 6
-1.12	6.86e-32	ATOX1	antioxidant 1 copper chaperone	0.05	1.53e-33	GZMB	granzyme B
-1.05	8.35e-32	DOHH	deoxyhypusine hydroxylase	0.05	1.53e-33	HK3	hexokinase 3
-1.05	1.55e-31	NRDC	nardilysin convertase	0.05	1.53e-33	TUBA8	tubulin alpha 8
-0.12	2.54e-31	PSMD7	proteasome 26S subunit, non-ATPase	0.05	1.53e-33	CR2	complement C3d receptor 2
-0.18	2.79e-31	CAP1	cyclase associated actin cytoskelet	0.05	1.53e-33	POU2F2	POU class 2 homeobox 2
-0.81	8.42e-31	ZPR1	ZPR1 zinc finger	0.05	1.53e-33	AZU1	azurocidin 1
-0.96	1.77e-30	RAP1GDS1	Rap1 GTPase-GDP dissociation stimul	0.05	1.53e-33	CD48	CD48 molecule
-0.1	2.13e-30	PPP2R1A	protein phosphatase 2 scaffold subu	0.05	1.53e-33	SKAP2	src kinase associated phosphoprotei
-0.81	2.53e-30	DFFA	DNA fragmentation factor subunit al	0.05	1.53e-33	CCL17	C-C motif chemokine ligand 17
-0.68	3.30e-30	TXLNA	taxilin alpha	0.05	1.53e-33	ADA2	adenosine deaminase 2
-0.52	3.30e-30	SGTA	small glutamine rich tetratricopept	0.05	1.53e-33	CD3E	CD3 epsilon subunit of T-cell recep
-1.02	3.48e-30	AAMDC	adipogenesis associated Mth938 doma	0.05	1.53e-33	RNASE2	ribonuclease A family member 2
-0.72	4.67e-30	RANBP3	RAN binding protein 3	0.05	1.53e-		

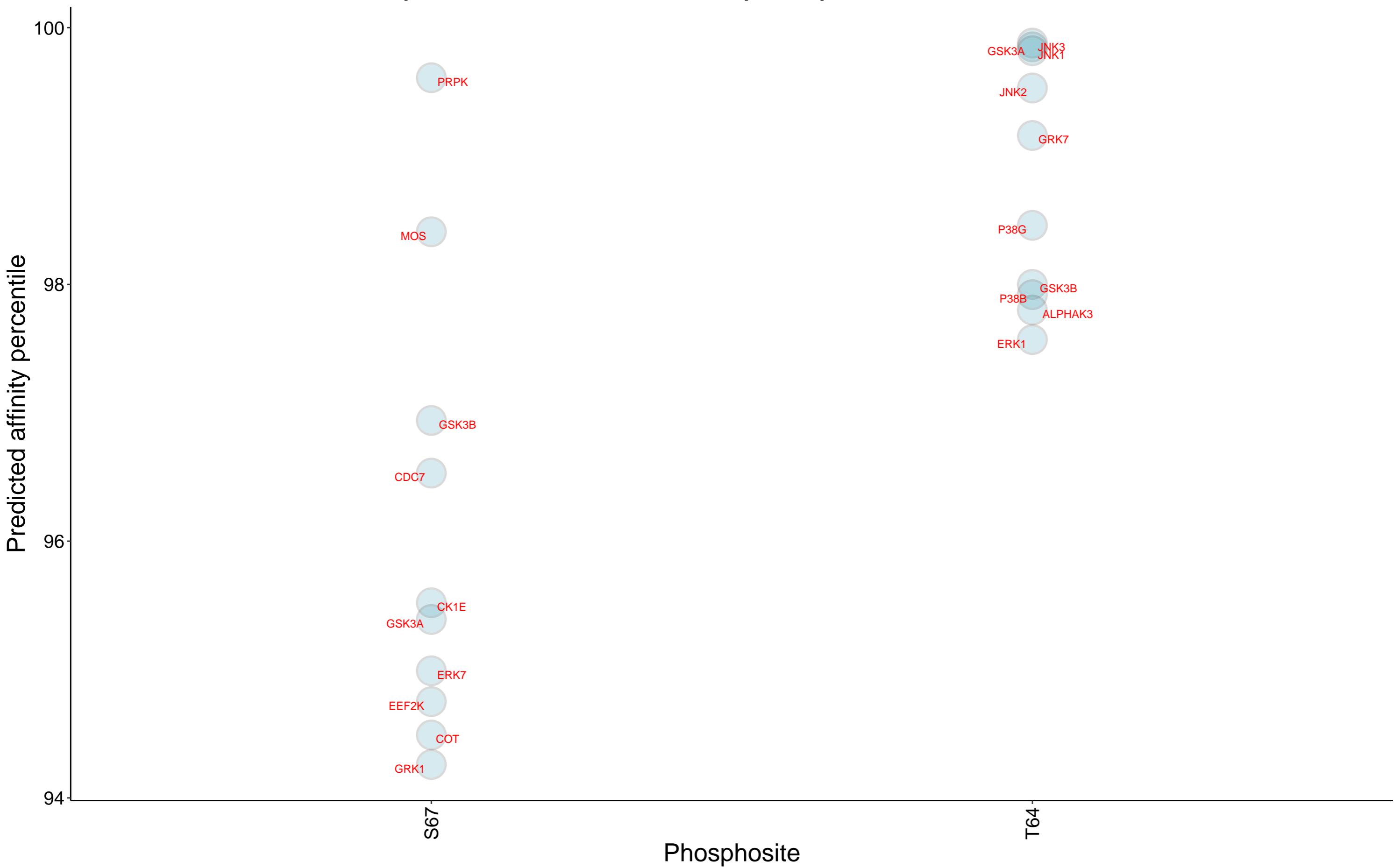
Top 250 correlation coefficients overrepresentation, ADPRS protein, DB1



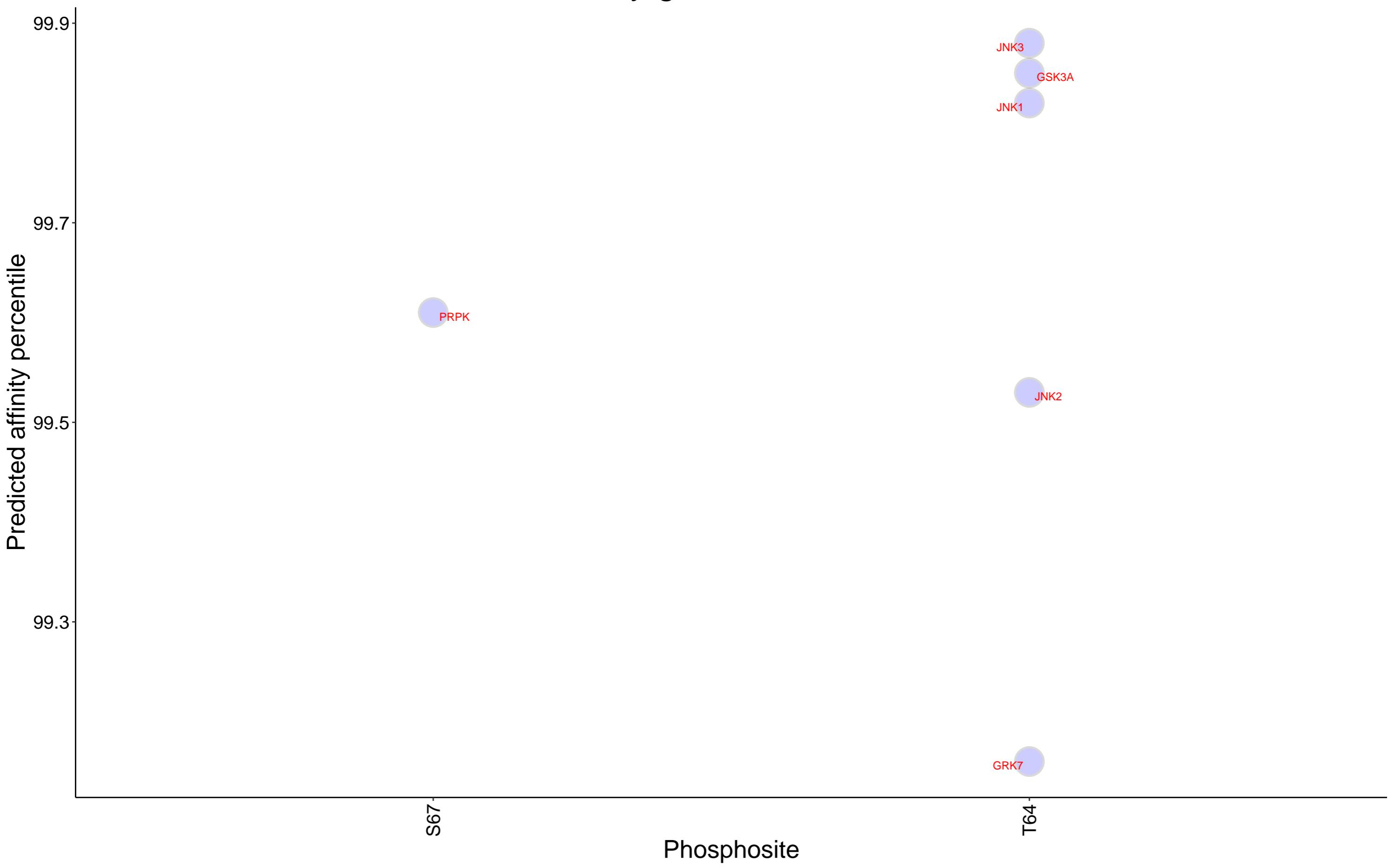
Gene Set Enrichment analysis on protein correlation coefficients, ADPRS protein, DB1



Top 10 kinases for each phosphosite in ADPRS



Kinases with affinity greater than 98.5% to ADPRS



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

Beware of false positives in tissues with small number of samples

