

FANCD2

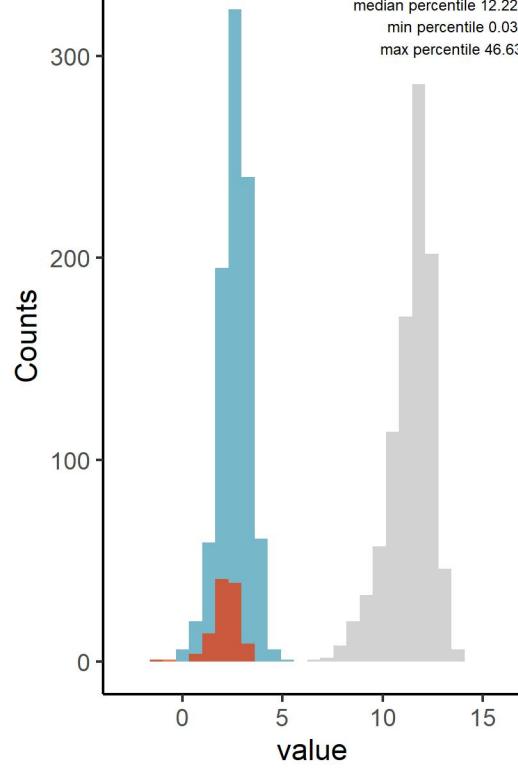
Protein name: FANCD2 ; UNIPROT: Q9BXW9 ; Gene name: FA complementation group D2

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

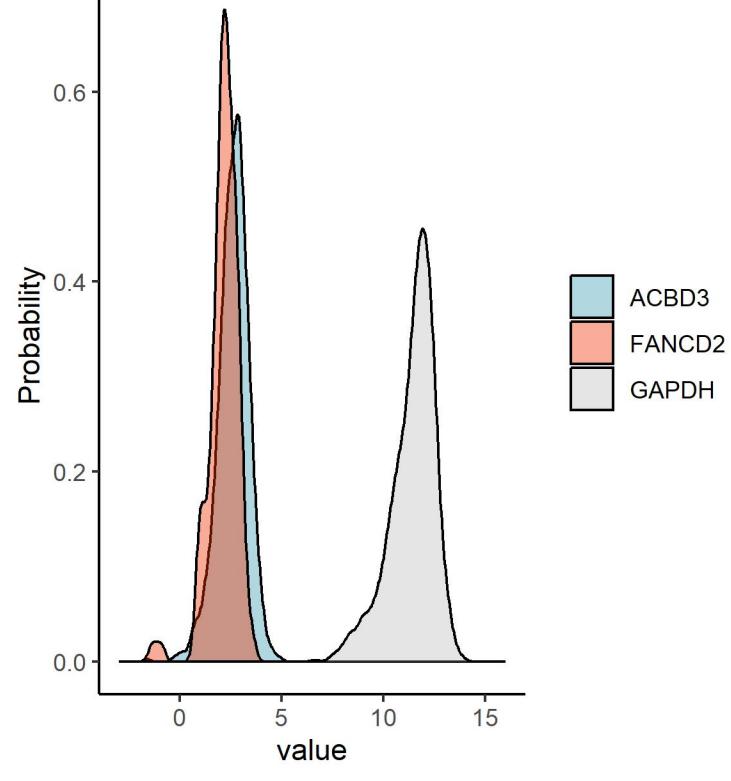
Sanger Institute Protein Database 1 (DB1), protein presence is certain

6692 proteins in 949 CCLs

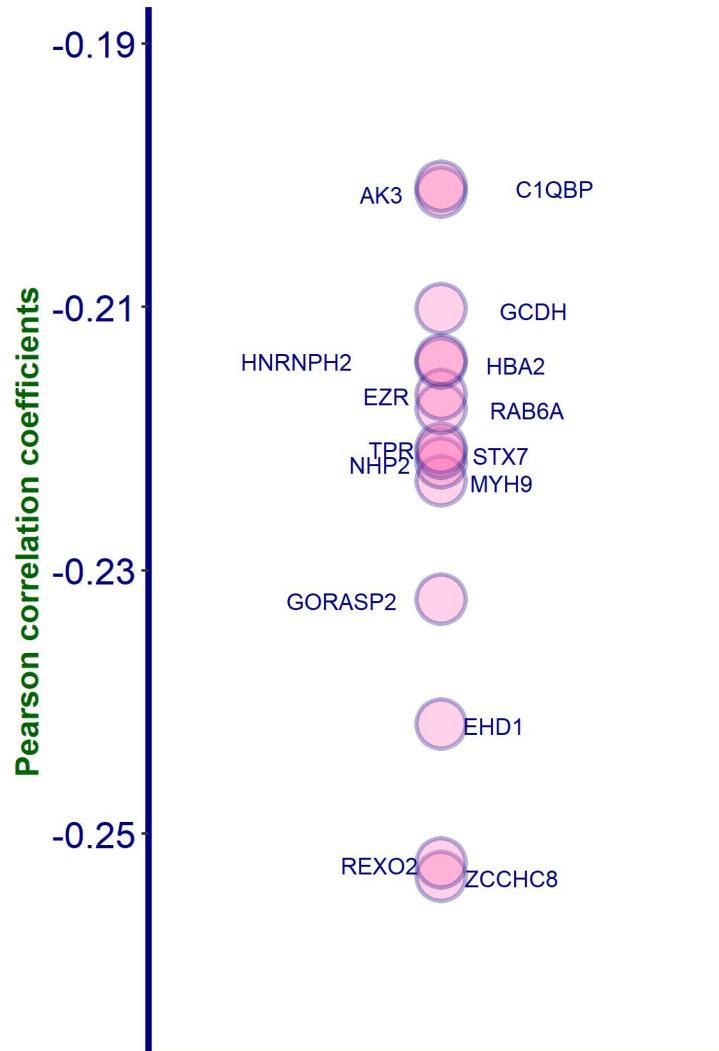
Histogram of FANCD2 protein compared to proteins with low and high abundance



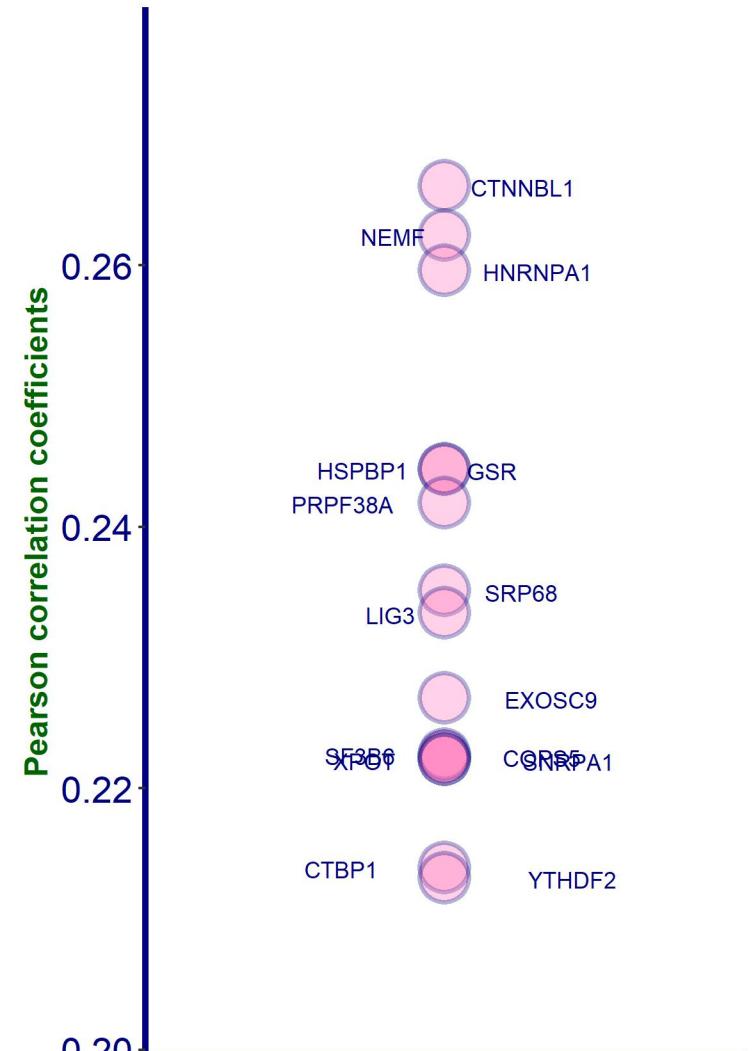
Density plot of FANCD2 protein compared to proteins with low and high abundance



Top negative correlations of FANCD2 protein, DB

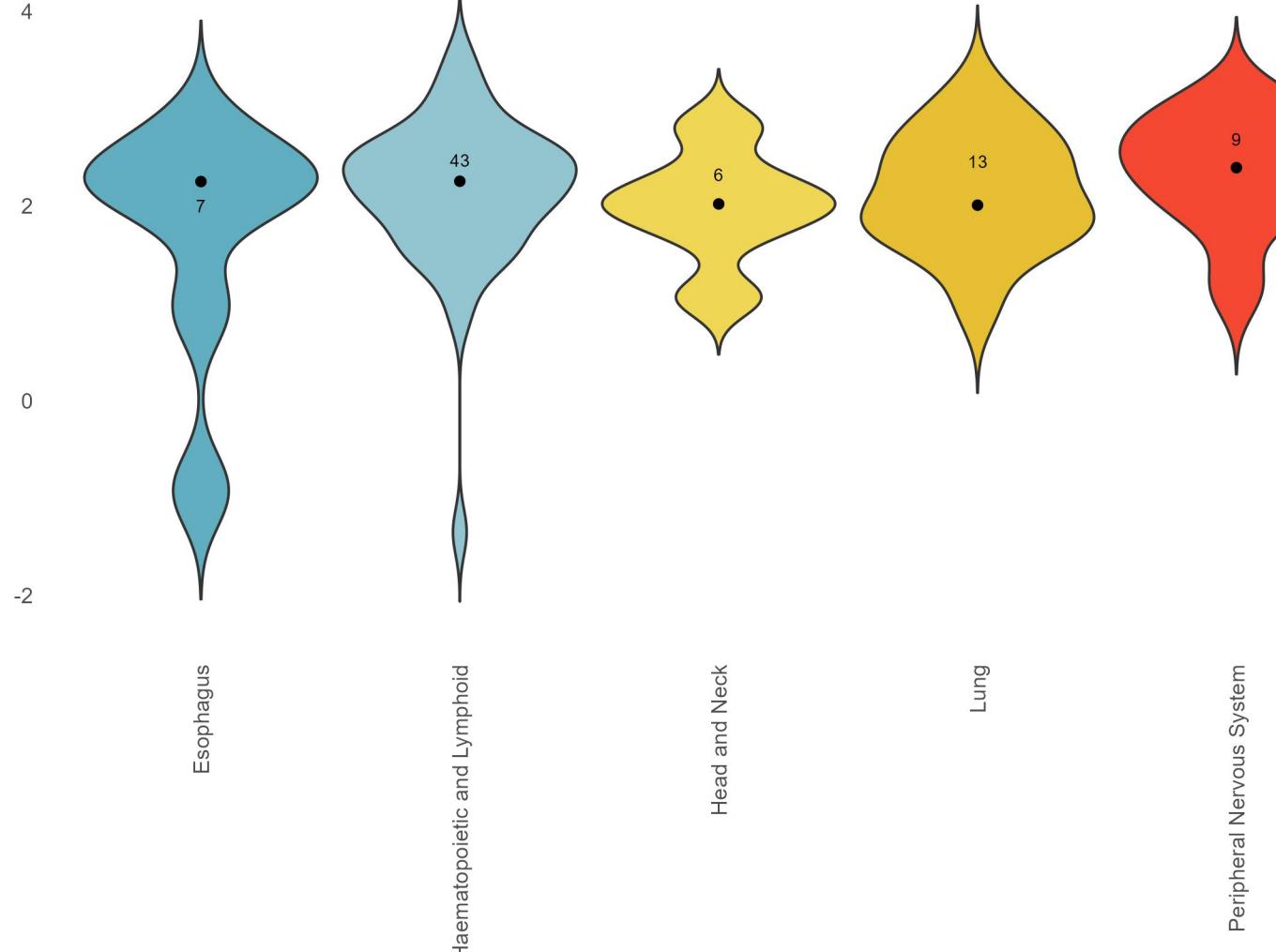


Top positive correlations of FANCD2 protein, DB



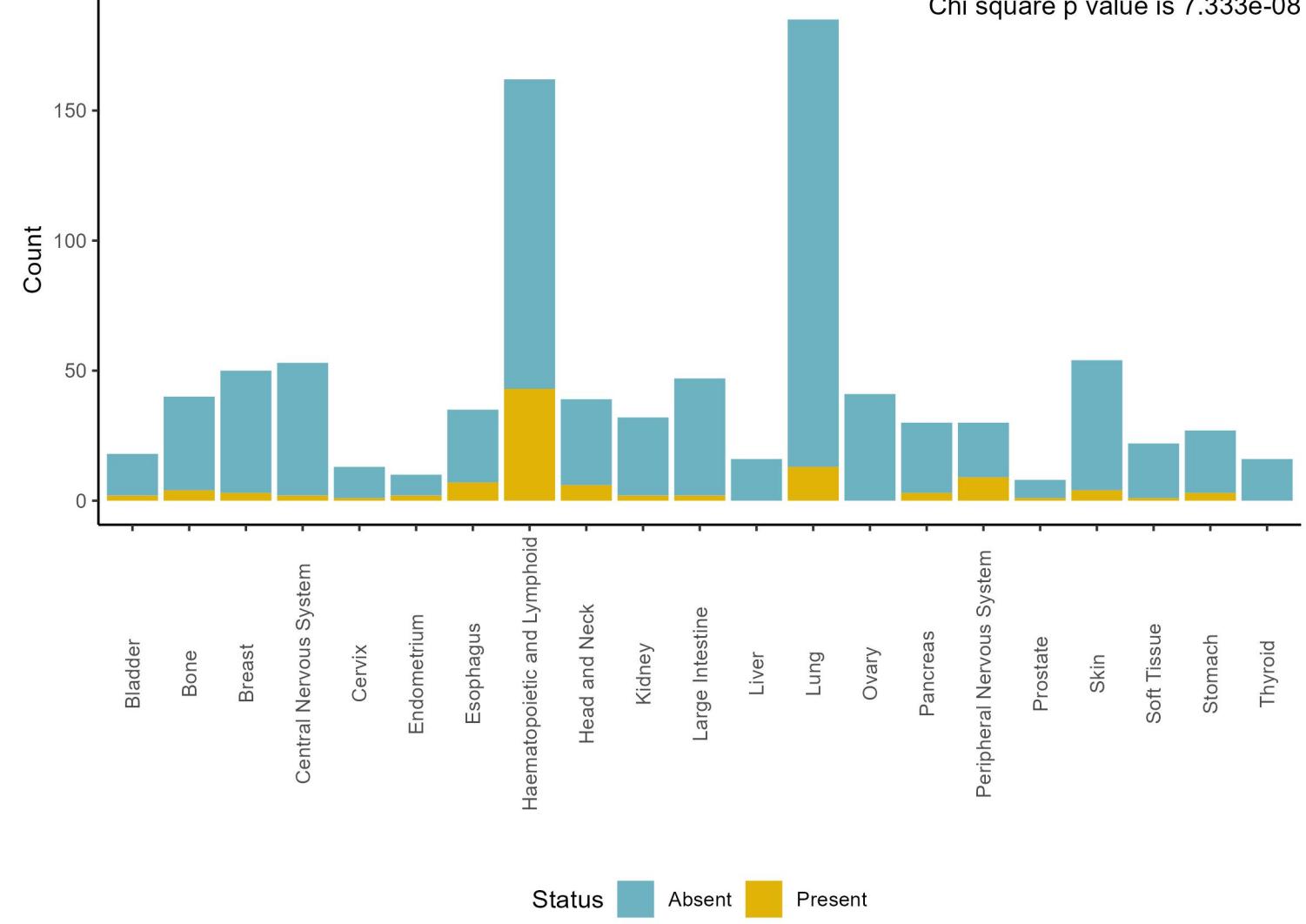
Amount of FANCD2 protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 6.577e-01



Present and absent FANCD2 protein counts by tissue, DB1

Chi square p value is 7.333e-08

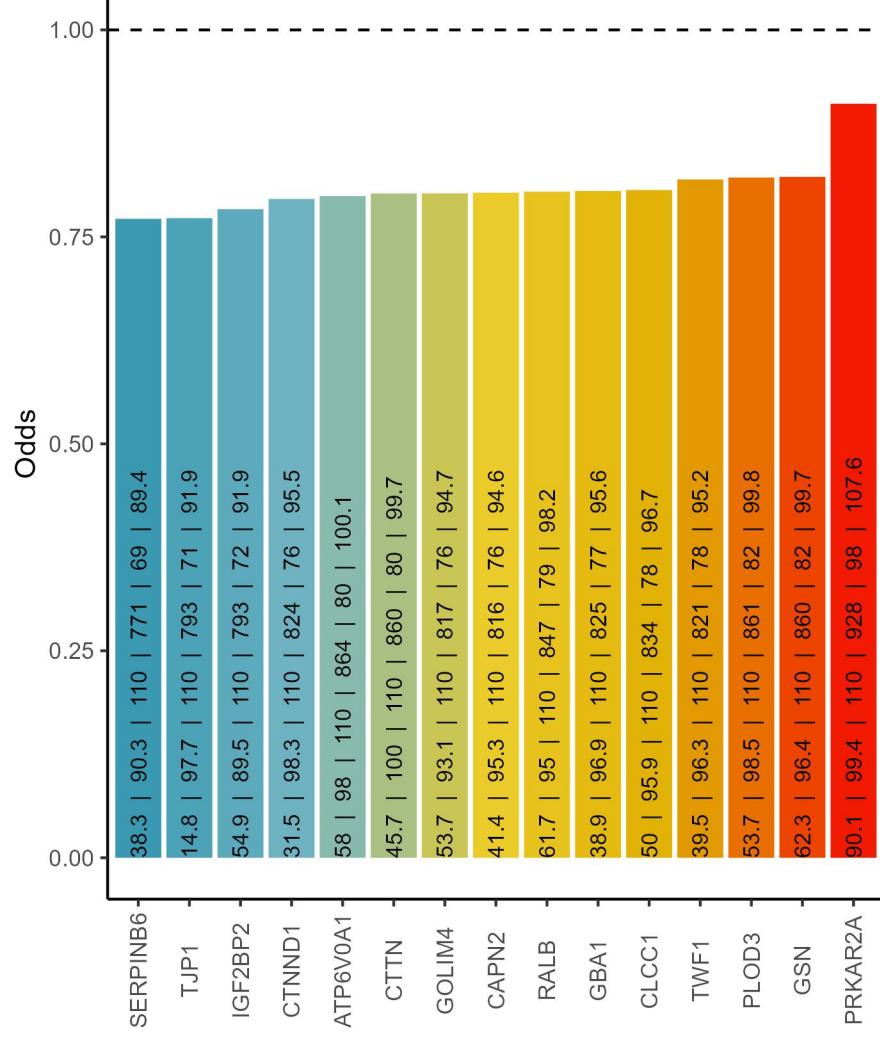


Cooccurrence with FANCD2 protein, DB1

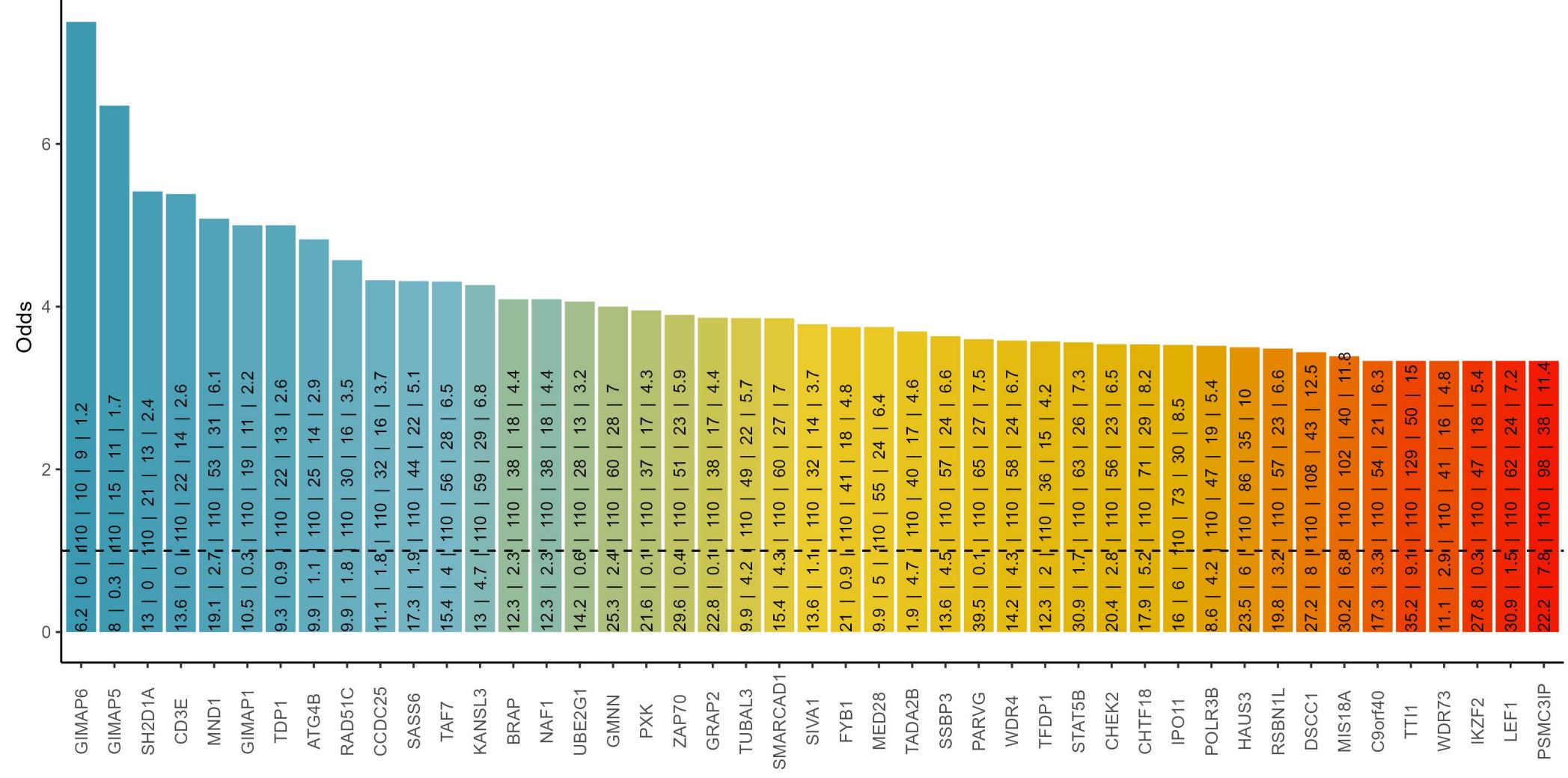
% of FANCD2 in blood cancers: 26.5 ; % of FANCD2 in solid cancers: 8.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of FANCD2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

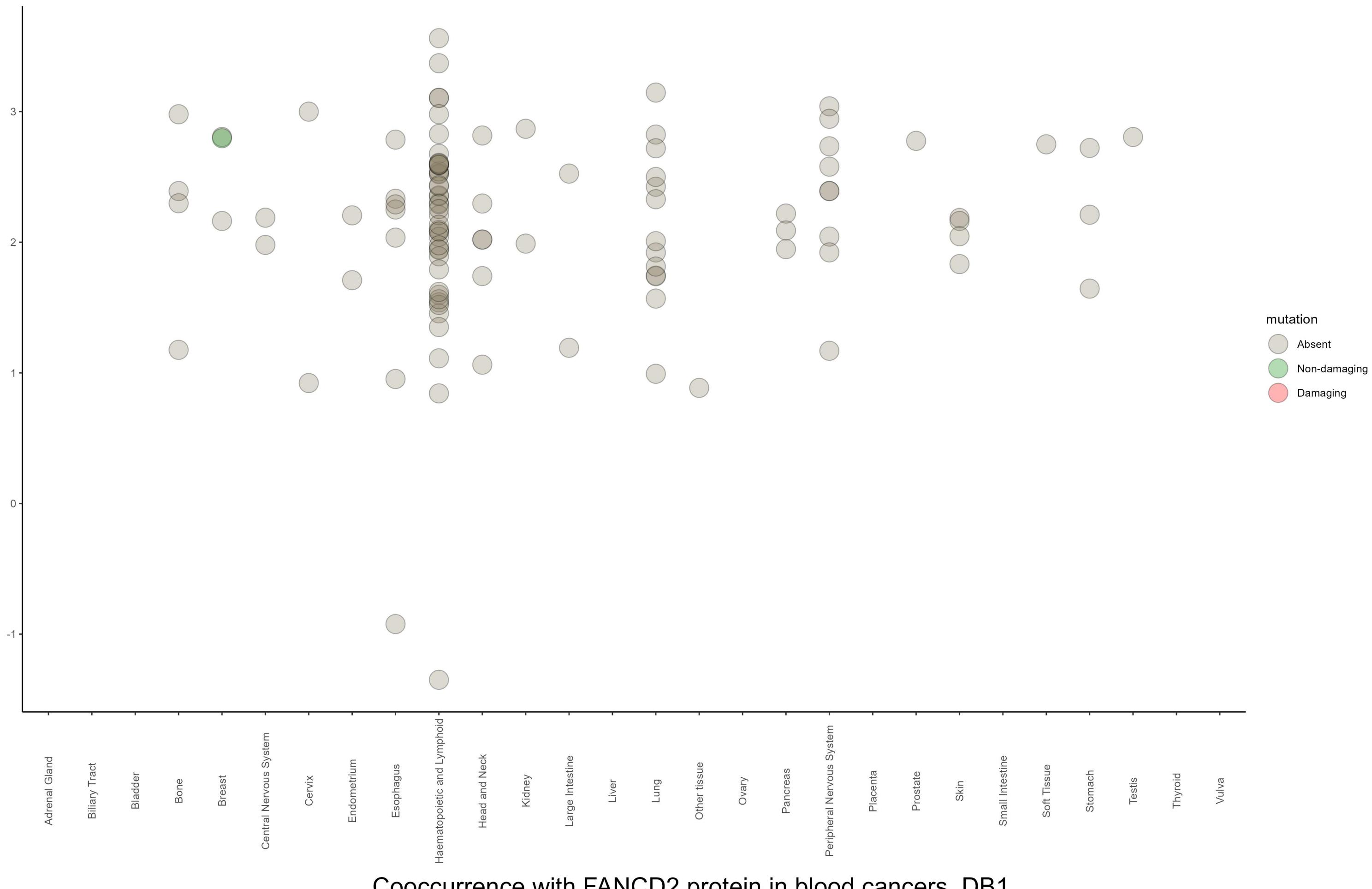
Negative cooccurrence



Positive cooccurrence

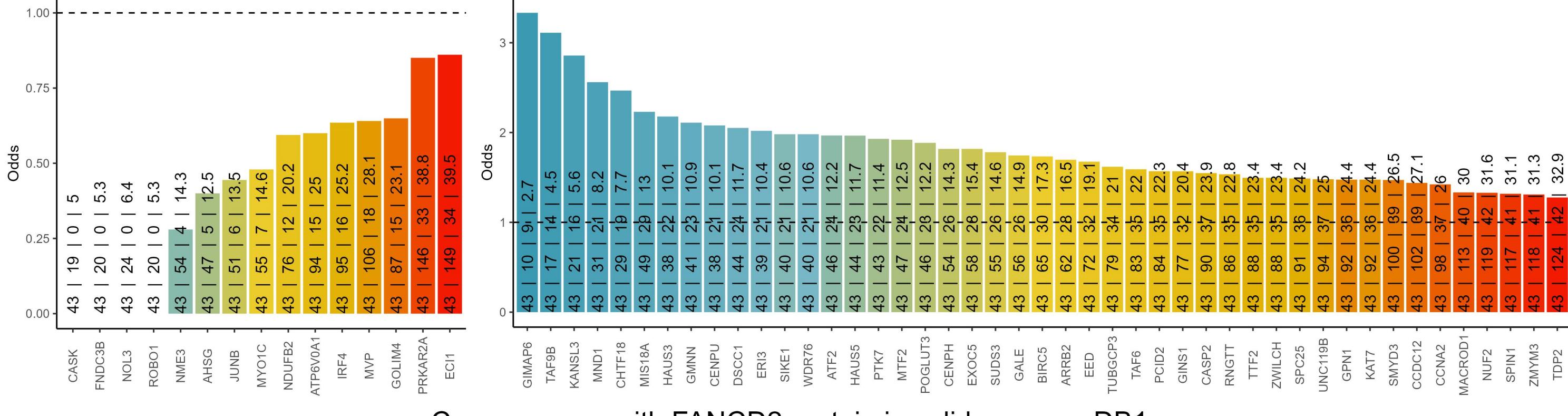


Amount of FANCD2 protein and mutation status by tissue, DB1



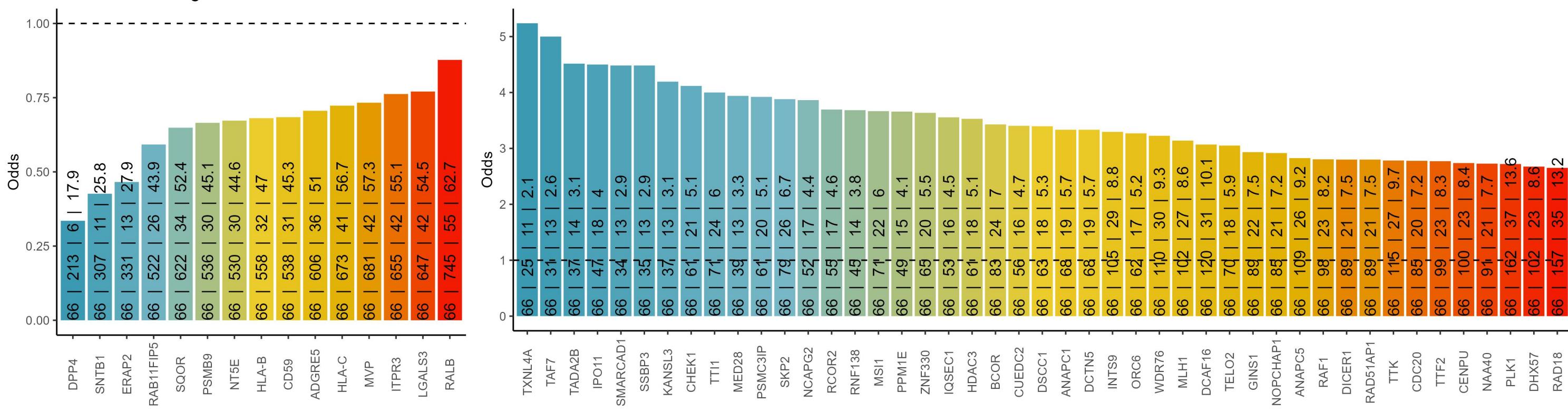
Cooccurrence with FANCD2 protein in blood cancers, DB1

The text in the bars: incidence of FANCD2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

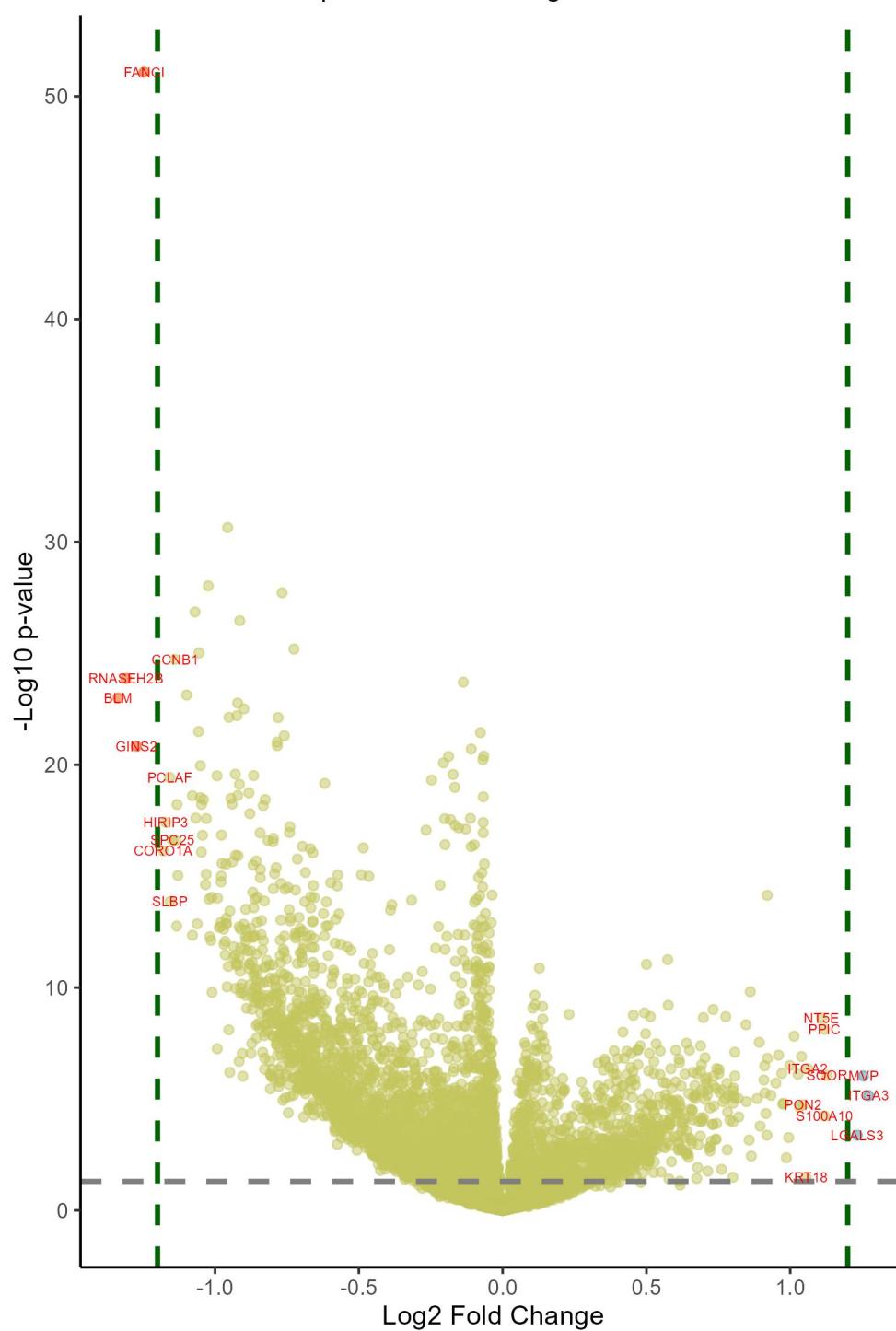


Cooccurrence with FANCD2 protein in solid cancers, DB1

The text in the bars: incidence of FANCD2 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



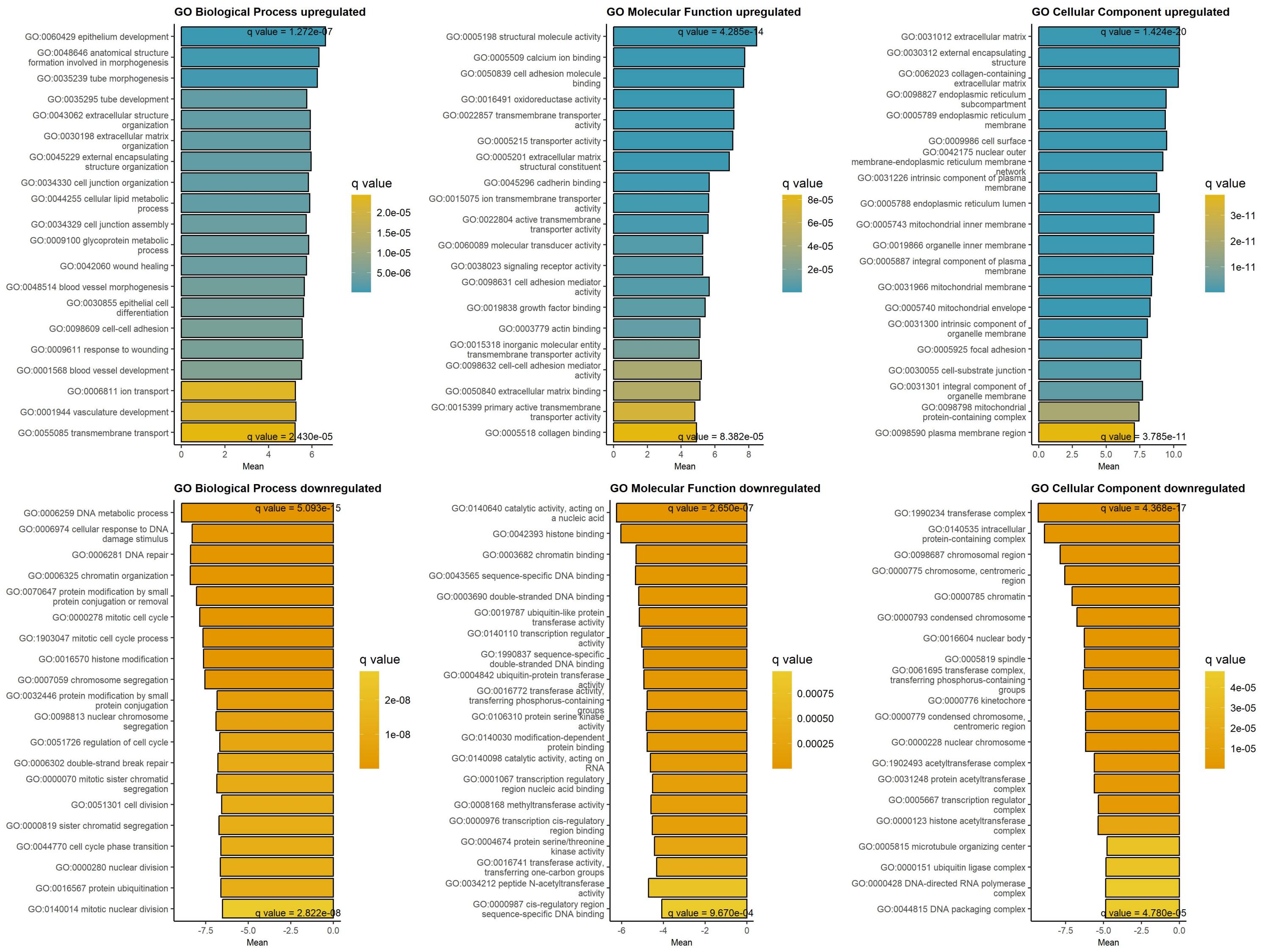
Differentially expressed proteins at absence/low amount of FANCD2 , DB1
p-value < 0.05 & logFC > 1.2



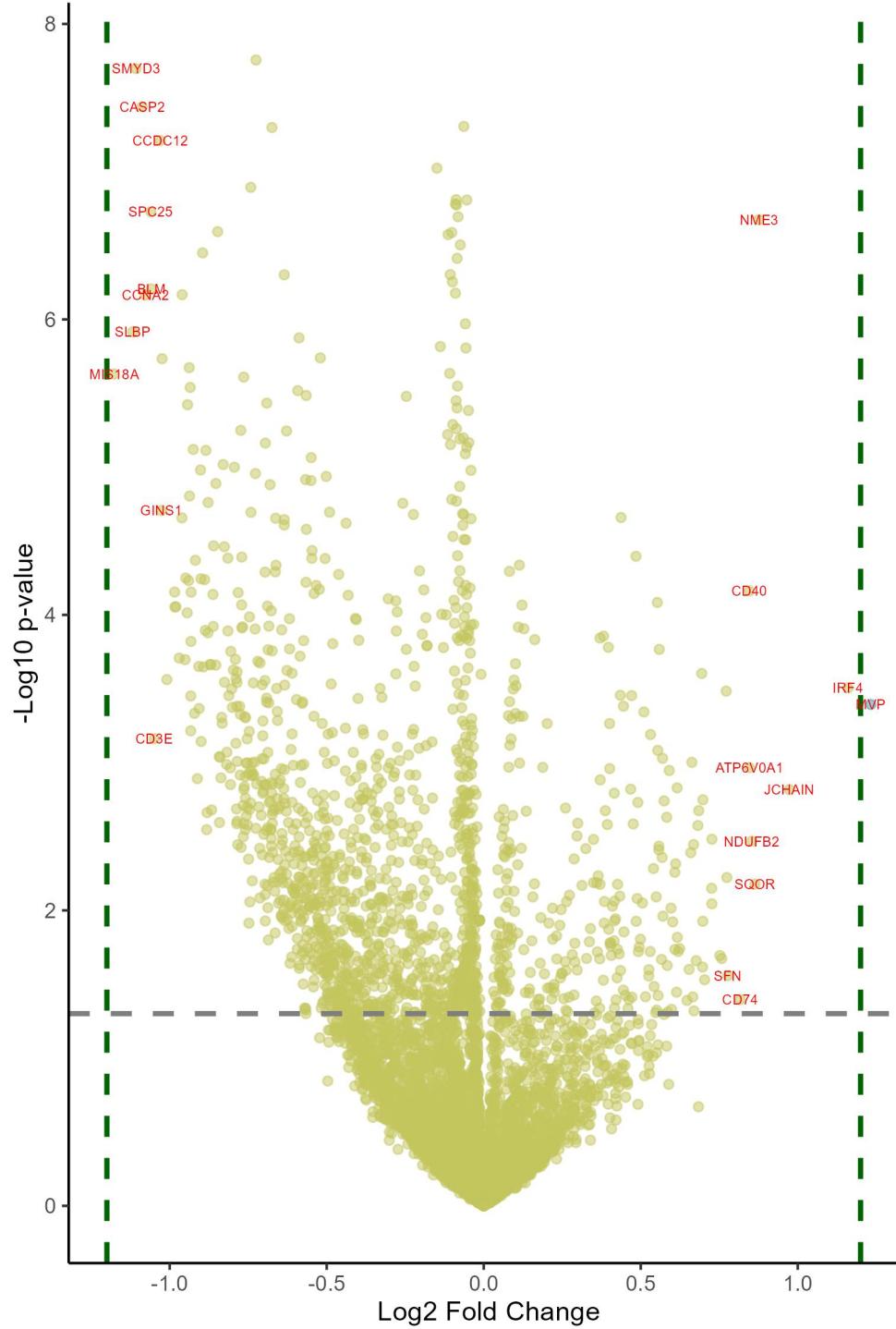
Downregulated at low/absent FANCD2 Upregulated at low/absent FANCD2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.34	4.81e-21	BLM	BLM RecQ like helicase	1.27	3.62e-05	ITGA3	integrin subunit alpha 3
-1.31	8.17e-22	RNASEH2B	ribonuclease H2 subunit B	1.25	6.19e-06	MVP	major vault protein
-1.27	3.90e-19	GINS2	GINS complex subunit 2	1.23	1.32e-03	LGALS3	galectin 3
-1.25	2.70e-48	FANCI	FA complementation group I	1.13	5.94e-06	SQOR	sulfide quinone oxidoreductase
-1.18	5.95e-15	CORO1A	coronin 1A	1.12	2.26e-04	S100A10	S100 calcium binding protein A10
-1.17	4.35e-16	HIRIP3	HIRA interacting protein 3	1.12	8.94e-08	PPIC	peptidylprolyl isomerase C
-1.16	6.78e-18	PCLAF	PCNA clamp associated factor	1.11	3.21e-08	NT5E	5'-nucleotidase ecto
-1.16	6.85e-13	SLBP	stem-loop binding protein	1.06	3.25e-06	ITGA2	integrin subunit alpha 2
-1.15	2.24e-15	SPC25	SPC25 component of NDC80 kinetochor	1.06	5.92e-02	KRT18	keratin 18
-1.14	1.24e-22	CCNB1	cyclin B1	1.04	8.31e-05	PON2	paraoxonase 2
-1.14	2.25e-15	SNRNP27	small nuclear ribonucleoprotein U4/	1.04	1.07e-06	P4HA2	prolyl 4-hydroxylase subunit alpha
-1.13	6.92e-12	DCAF16	DDB1 and CUL4 associated factor 16	1.03	9.91e-05	CAVIN1	caveolae associated protein 1
-1.13	7.91e-17	TYMS	thymidylate synthetase	1.03	5.36e-06	MYO1C	myosin IC
-1.13	6.09e-14	CFAP20	cilia and flagella associated prote	1.01	1.67e-07	ADAM9	ADAM metallopeptidase domain 9
-1.1	3.80e-21	PRIM2	DNA primase subunit 2	1	2.44e-06	CD59	CD59 molecule (CD59 blood group)
-1.08	3.79e-17	BRD2	bromodomain containing 2	0.99	1.62e-03	NCEH1	neutral cholesterol ester hydrolase
-1.08	1.60e-11	CCNA2	cyclin A2	0.99	1.01e-02	GNG12	G protein subunit gamma 12
-1.07	1.54e-24	UBE2T	ubiquitin conjugating enzyme E2 T	0.98	7.16e-05	PVR	PVR cell adhesion molecule
-1.07	3.06e-16	POLA1	DNA polymerase alpha 1, catalytic s	0.97	7.81e-05	ITGAV	integrin subunit alpha V
-1.06	5.70e-12	MAZ	MYC associated zinc finger protein	0.97	5.01e-06	EPHX1	epoxide hydrolase 1
-1.06	1.07e-19	POLA2	DNA polymerase alpha 2, accessory s	0.96	9.50e-07	RRAS	RAS related
-1.06	7.09e-23	MAD2L1	mitotic arrest deficient 2 like 1	0.95	1.18e-05	PROCR	protein C receptor
-1.05	2.35e-18	PRIM1	DNA primase subunit 1	0.93	3.55e-05	S100A16	S100 calcium binding protein A16
-1.05	4.45e-17	DHFR	dihydrofolate reductase	0.92	1.27e-06	DAG1	dystroglycan 1
-1.05	6.71e-15	TIMELESS	timeless circadian regulator	0.92	4.00e-13	RAB11FIP5	RAB11 family interacting protein 5
-1.05	7.91e-17	EIF2B1	eukaryotic translation initiation f	0.92	1.32e-03	FKBP9	FKBP prolyl isomerase 9
-1.04	1.38e-15	TACC3	transforming acidic coiled-coil con	0.92	1.83e-04	ATP1B1	ATPase Na+/K+ transporting subunit
-1.04	5.09e-17	EIF2B5	eukaryotic translation initiation f	0.91	2.86e-05	DSG2	desmoglein 2
-1.03	1.46e-13	THUMPD3	THUMP domain containing 3	0.91	2.53e-06	ITPR3	inositol 1,4,5-trisphosphate recept

GAGE analysis on upregulated and downregulated proteins at low/absent FANCD2 protein, DB1

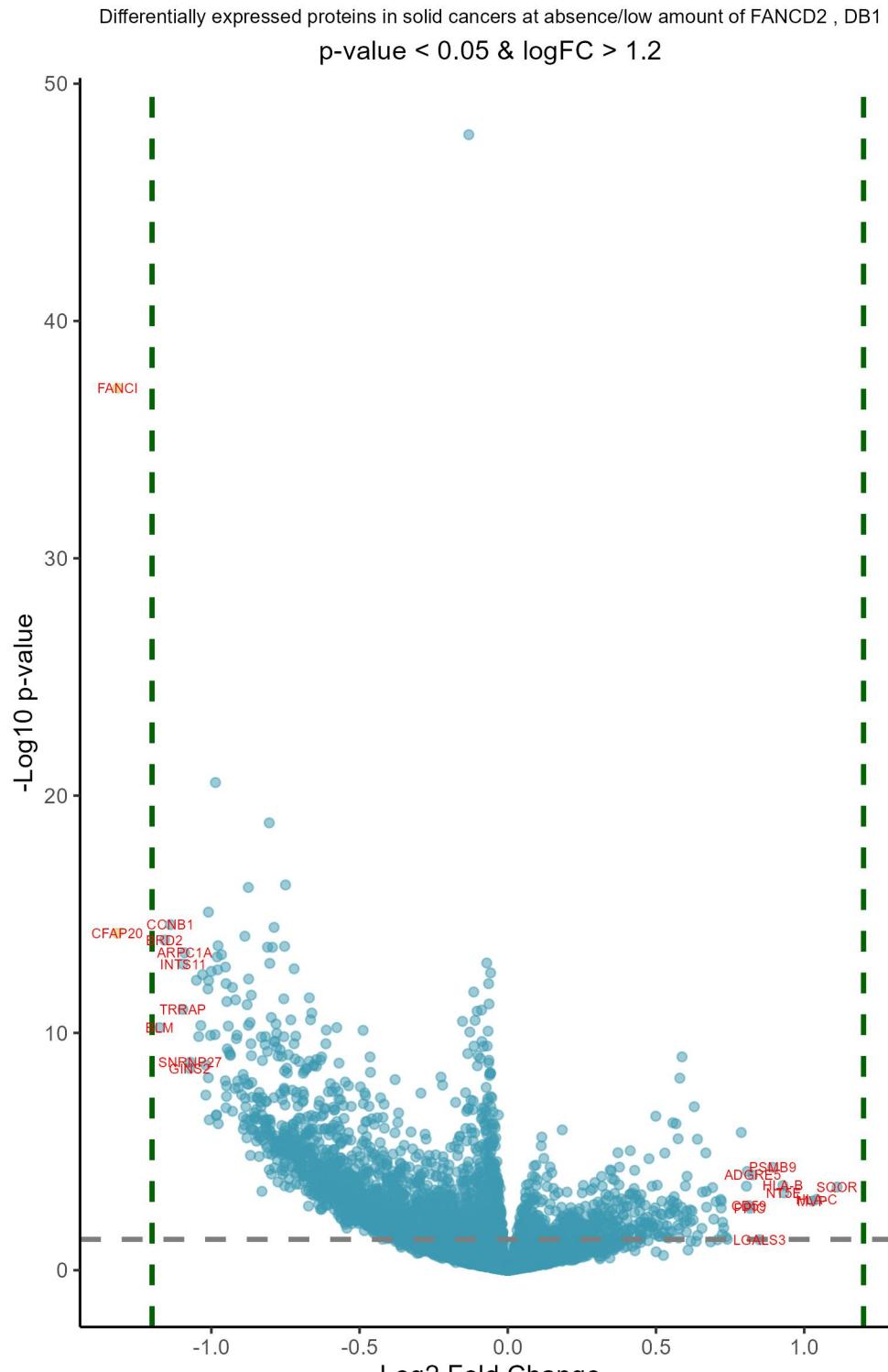


p-value < 0.05 & logFC > 1.2



Downregulated in blood cancers at low/absent FANCD2 Upregulated in blood cancers at low/absent FANCD2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.18	4.00e-04	MIS18A	MIS18 kinetochore protein A	1.23	1.03e-02	MVP	major vault protein
-1.12	2.60e-04	SLBP	stem-loop binding protein	1.16	8.67e-03	IRF4	interferon regulatory factor 4
-1.11	4.45e-05	SMYD3	SET and MYND domain containing 3	0.97	2.46e-02	JCHAIN	joining chain of multimeric IgA and
-1.09	5.57e-05	CASP2	caspase 2	0.88	8.78e-05	NME3	NME/NM23 nucleoside diphosphate kin
-1.08	1.57e-04	CCNA2	cyclin A2	0.86	5.43e-02	SQOR	sulfide quinone oxidoreductase
-1.06	8.78e-05	SPC25	SPC25 component of NDC80 kinetochor	0.85	3.94e-02	NDUFB2	NADH:ubiquinone oxidoreductase subu
-1.06	1.57e-04	BLM	BLM RecQ like helicase	0.85	1.98e-02	ATP6V0A1	ATPase H ⁺ transporting V0 subunit a
-1.05	1.49e-02	CD3E	CD3 epsilon subunit of T-cell recep	0.85	3.52e-03	CD40	CD40 molecule
-1.03	5.85e-05	CCDC12	coiled-coil domain containing 12	0.82	1.36e-01	CD74	CD74 molecule
-1.03	1.59e-03	GINS1	GINS complex subunit 1	0.78	1.04e-01	SFN	stratin
-1.02	3.41e-04	EED	embryonic ectoderm development	0.77	5.43e-02	NUCB1	nucleobindin 1
-1.01	8.06e-03	PTK7	protein tyrosine kinase 7 (inactive)	0.77	8.94e-03	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.98	3.53e-03	SUDS3	SDS3 homolog, SIN3A corepressor com	0.76	8.57e-02	PYCR1	pyrroline-5-carboxylate reductase 1
-0.98	4.03e-03	POGLUT3	protein O-glucosyltransferase 3	0.75	8.26e-02	HLA-DPB1	major histocompatibility complex, c
-0.98	4.03e-03	KIF15	kinesin family member 15	0.73	3.86e-02	EHD4	EH domain containing 4
-0.97	6.39e-03	ZAP70	zeta chain of T cell receptor assoc	0.73	5.43e-02	PRKAR2A	protein kinase cAMP-dependent type
-0.96	1.63e-03	EXOC5	exocyst complex component 5	0.73	5.43e-02	HLA-DRB3	major histocompatibility complex, c
-0.96	1.57e-04	KAT7	lysine acetyltransferase 7	0.7	1.09e-01	HLA-DQB1	major histocompatibility complex, c
-0.95	6.49e-03	MTF2	metal response element binding tran	0.7	2.69e-02	TYMP	thymidine phosphorylase
-0.95	3.17e-03	BRD3	bromodomain containing 3	0.7	5.48e-02	NIBAN1	niban apoptosis regulator 1
-0.94	4.26e-03	GALE	UDP-galactose-4-epimerase	0.7	9.46e-02	LGALS3	galectin 3
-0.94	5.24e-04	TUBGCP3	tubulin gamma complex associated pr	0.69	7.46e-03	MYO1C	myosin IC
-0.94	3.22e-03	ARRB2	arrestin beta 2	0.68	2.93e-02	EMC10	ER membrane protein complex subunit
-0.94	3.81e-04	PCID2	PCI domain containing 2	0.68	4.26e-01	LGALS1	galectin 1
-0.94	1.35e-03	BIRC5	baculoviral IAP repeat containing 5	0.68	3.36e-02	FTL	ferritin light chain
-0.93	4.57e-04	MACROD1	mono-ADP ribosylhydrolase 1	0.68	8.77e-02	HLA-DPA1	major histocompatibility complex, c
-0.93	1.37e-02	SATB1	SATB homeobox 1	0.67	1.54e-01	CTSZ	cathepsin Z
-0.93	9.41e-03	GMNN	geminin DNA replication inhibitor	0.67	4.08e-02	SPART	spartin
-0.93	5.29e-03	PARVG	parvin gamma	0.67	1.32e-01	IGF2BP2	insulin like growth factor 2 mRNA b

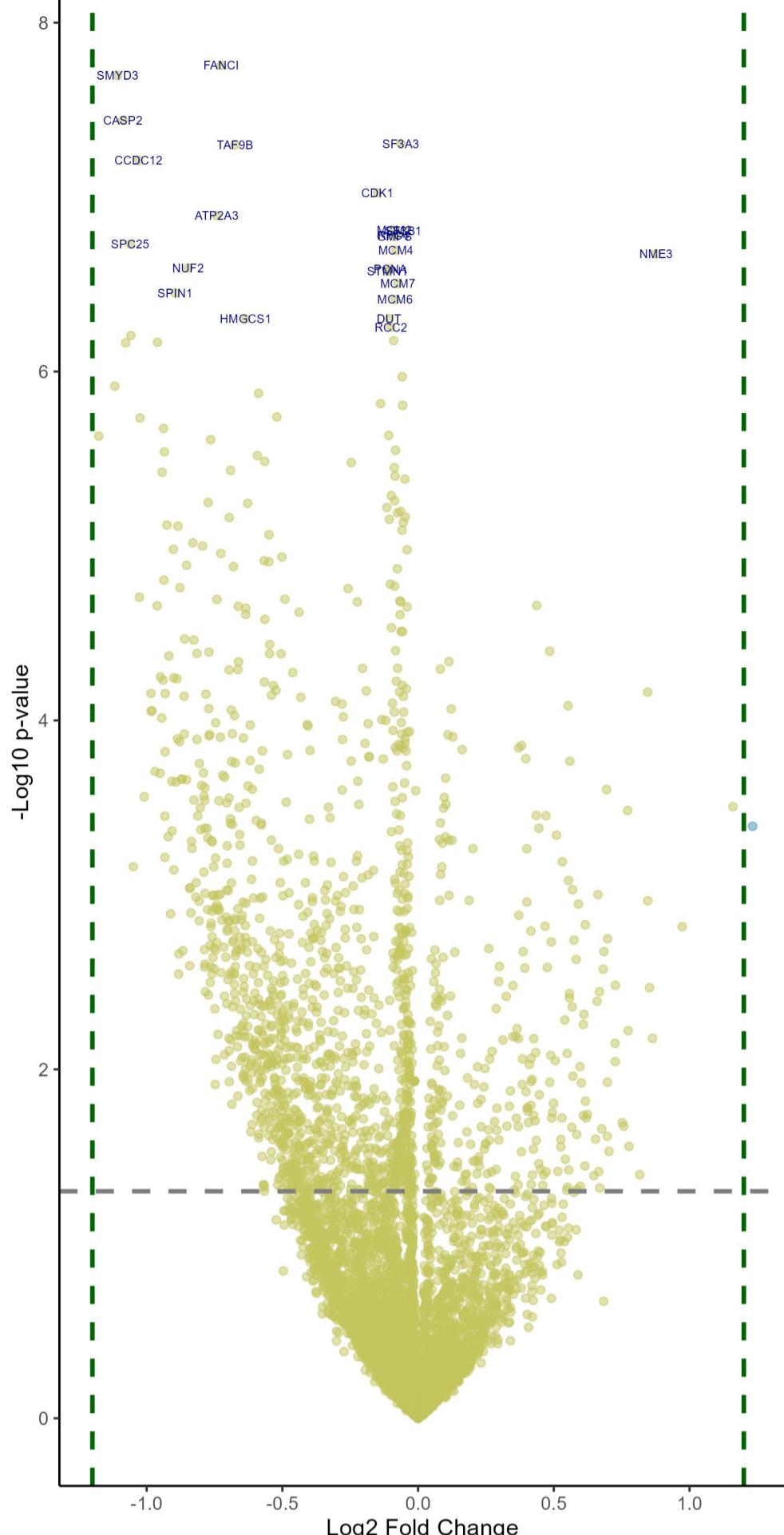


Downregulated in solid cancers at low/absent FANCD2 Upregulated in solid cancers at low/absent FANCD2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.32	3.83e-12	CFAP20	cilia and flagella associated prote	1.11	2.43e-03	SQOR	sulfide quinone oxidoreductase
-1.32	1.50e-34	FANCI	FA complementation group I	1.04	6.21e-03	HLA-C	major histocompatibility complex, c
-1.17	6.66e-09	BLM	BLM RecQ like helicase	1.03	7.07e-03	MVP	major vault protein
-1.16	6.28e-12	BRD2	bromodomain containing 2	0.93	3.79e-03	NT5E	5'-nucleotidase ecto
-1.14	2.02e-12	CCNB1	cyclin B1	0.93	2.17e-03	HLA-B	major histocompatibility complex, c
-1.	1.50e-09	TRRAP	transformation/transcription domain	0.89	5.30e-04	PSMB9	proteasome 20S subunit beta 9
-1.	3.64e-11	INTS11	integrator complex subunit 11	0.85	1.22e-01	LGALS3	galectin 3
-1.09	1.56e-11	ARPC1A	actin related protein 2/3 complex s	0.83	9.52e-04	ADGRE5	adhesion G protein-coupled receptor
-1.07	1.76e-07	GINS2	GINS complex subunit 2	0.82	1.22e-02	PPIC	peptidylprolyl isomerase C
-1.07	1.05e-07	SNRNP27	small nuclear ribonucleoprotein U4/U	0.81	9.90e-03	CD59	CD59 molecule (CD59 blood group)
-1.05	1.29e-10	PRIM2	DNA primase subunit 2	0.81	7.20e-04	PSMB8	proteasome 20S subunit beta 8
-1.04	1.34e-08	TIMELESS	timeless circadian regulator	0.81	2.27e-03	TAP1	transporter 1, ATP binding cassette
-1.04	5.71e-09	EIF2B1	eukaryotic translation initiation f	0.79	3.29e-05	RAB11FIP5	RAB11 family interacting protein 5
-1.03	8.05e-11	EZH2	enhancer of zeste 2 polycomb repres	0.74	1.18e-01	HLA-A	major histocompatibility complex, c
-1.02	1.66e-06	MLLT1	MLLT1 super elongation complex subu	0.74	1.00e-01	S100A10	S100 calcium binding protein A10
-1.02	1.32e-07	THUMPD3	THUMP domain containing 3	0.73	5.09e-02	RHOC	ras homolog family member C
-1.01	2.58e-10	SENP3	SUMO specific peptidase 3	0.72	3.36e-02	PROCR	protein C receptor
-1.01	3.90e-07	RNASEH2B	ribonuclease H2 subunit B	0.72	8.20e-02	NCEH1	neutral cholesterol ester hydrolase
-1.01	6.75e-13	WDHD1	WD repeat and HMG-box DNA binding p	0.72	7.15e-03	ITPR3	inositol 1,4,5-trisphosphate recept
-1.01	1.29e-10	MAD2L1	mitotic arrest deficient 2 like 1	0.72	1.19e-02	RRAS	RAS related
-1.01	1.21e-05	DCAF16	DDB1 and CUL4 associated factor 16	0.72	6.21e-03	CD109	CD109 molecule
-1.	1.25e-08	EIF2B5	eukaryotic translation initiation f	0.71	1.23e-01	ITGA3	integrin subunit alpha 3
-1.	6.27e-11	UBE2T	ubiquitin conjugating enzyme E2 T	0.7	7.40e-03	S100A4	S100 calcium binding protein A4
-0.99	1.19e-08	PRIM1	DNA primase subunit 1	0.69	2.66e-02	B2M	beta-2-microglobulin
-0.99	4.66e-18	NUSAP1	nucleolar and spindle associated pr	0.69	2.54e-03	FAM114A1	family with sequence similarity 114
-0.98	8.73e-06	MAZ	MYC associated zinc finger protein	0.68	1.43e-01	CD44	CD44 molecule (Indian blood group)
-0.98	8.29e-06	SINHCAF	SIN3-HDAC complex associated factor	0.67	1.11e-02	APOL2	apolipoprotein L2
-0.98	2.09e-11	SMARCD1	SWI/SNF related, matrix associated,	0.67	3.42e-03	PTPRJ	protein tyrosine phosphatase recept
-0.98	5.62e-11	POLR2G	RNA polymerase II subunit G	0.67	1.65e-04	ERAP2	endoplasmic reticulum aminopeptidas

FANCD2 network, DB1, no Pearson r > 0.3

p-value < 0.05 & logFC > 1.2

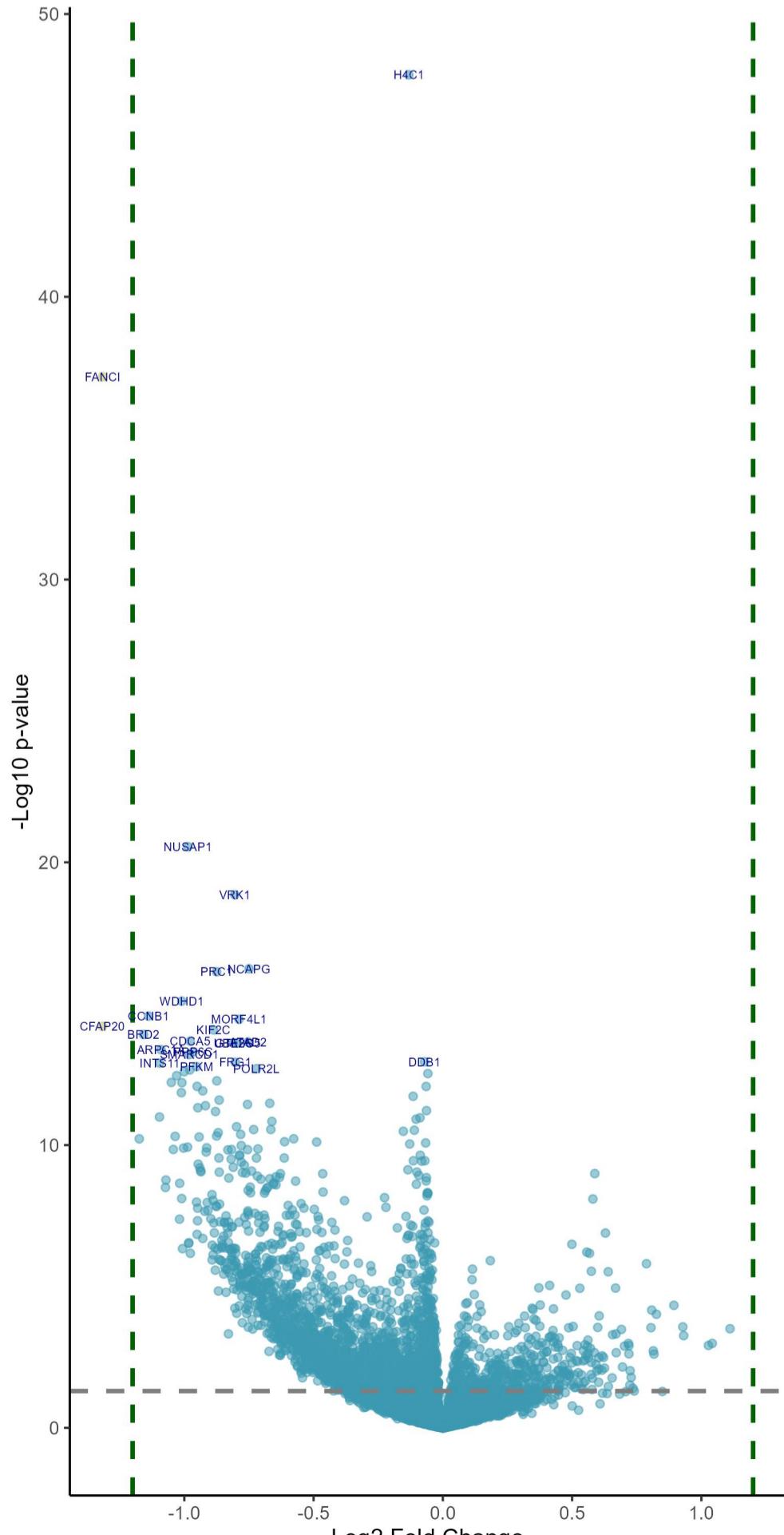


Sorted by p values!

Downregulated in blood cancers at low/absent FANCD2 Upregulated in blood cancers at low/absent FANCD2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.73	4.45e-05	FANCI	FA complementation group I	0.88	8.78e-05	NME3	NME/NM23 nucleoside diphosphate kin
-1.11	4.45e-05	SMYD3	SET and MYND domain containing 3	0.44	1.63e-03	NOL3	nucleolar protein 3
-1.09	5.57e-05	CASP2	caspase 2	0.48	2.56e-03	CARMIL1	capping protein regulator and myosi
-0.06	5.57e-05	SF3A3	splicing factor 3a subunit 3	0.11	2.77e-03	CLPP	caseinolytic mitochondrial matrix p
-0.67	5.57e-05	TAF9B	TATA-box binding protein associated	0.08	2.94e-03	MRPS28	mitochondrial ribosomal protein S28
-1.03	5.85e-05	CCDC12	coiled-coil domain containing 12	0.85	3.52e-03	CD40	CD40 molecule
-0.15	7.87e-05	CDK1	cyclin dependent kinase 1	0.55	3.88e-03	AHSG	alpha 2-HS glycoprotein
-0.74	8.59e-05	ATP2A3	ATPase sarcoplasmic/endoplasmic ret	0.12	3.99e-03	MRPL45	mitochondrial ribosomal protein L45
-0.09	8.59e-05	MCM2	minichromosome maintenance complex	0.11	4.81e-03	DNAJA3	DnaJ heat shock protein family (Hsp
-0.05	8.59e-05	SF3B1	splicing factor 3b subunit 1	0.13	4.87e-03	NDUFA2	NADH:ubiquinone oxidoreductase subu
-0.09	8.59e-05	RFC4	replication factor C subunit 4	0.38	5.14e-03	FNDC3B	fibronectin type III domain contain
-0.09	8.59e-05	GMPS	guanine monophosphate synthase	0.37	5.21e-03	ROBO1	roundabout guidance receptor 1
-1.06	8.78e-05	SPC25	SPC25 component of NDC80 kinetochor	0.16	5.26e-03	NDUFS6	NADH:ubiquinone oxidoreductase subu
-0.08	8.78e-05	MCM4	minichromosome maintenance complex	0.4	5.67e-03	CASK	calcium/calmodulin dependent serine
-0.85	9.33e-05	NUF2	NUF2 component of NDC80 kinetochore	0.56	5.75e-03	SLAMF1	signaling lymphocytic activation mo
-0.1	9.33e-05	PCNA	proliferating cell nuclear antigen	0.1	6.81e-03	MRPL13	mitochondrial ribosomal protein L13
-0.11	9.33e-05	STMN1	stathmin 1	0.69	7.46e-03	MYO1C	myosin IC
-0.07	1.04e-04	MCM7	minichromosome maintenance complex	0.1	8.08e-03	COPG1	COPI coat complex subunit gamma 1
-0.9	1.12e-04	SPIN1	spindlin 1	0.1	8.47e-03	HDLBP	high density lipoprotein binding pr
-0.08	1.17e-04	MCM6	minichromosome maintenance complex	1.16	8.67e-03	IRF4	interferon regulatory factor 4
-0.11	1.38e-04	DUT	deoxyuridine triphosphatase	0.09	8.69e-03	MRPL58	mitochondrial ribosomal protein L58
-0.64	1.38e-04	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synt	0.77	8.94e-03	JUNB	JunB proto-oncogene, AP-1 transcrip
-0.1	1.48e-04	RCC2	regulator of chromosome condensatio	0.44	9.40e-03	PLOD2	procollagen-lysine,2-oxoglutarate 5
-1.06	1.57e-04	BLM	BLM RecQ like helicase	0.47	9.40e-03	SDC1	syndecan 1
-0.09	1.57e-04	MCM5	minichromosome maintenance complex	0.08	1.01e-02	NDUFS3	NADH:ubiquinone oxidoreductase core
-0.96	1.57e-04	KAT7	lysine acetyltransferase 7	1.23	1.03e-02	MVP	major vault protein
-1.08	1.57e-04	CCNA2	cyclin A2	0.44	1.05e-02	EBI3	Epstein-Barr virus induced 3
-0.06	2.37e-04	SNRPA1	small nuclear ribonucleoprotein pol	0.51	1.12e-02	ATP1B1	ATPase Na+/K+ transporting subunit
-1.12	2.60e-04	SLBP	stem-loop binding protein	0.1	1.14e-02	NDUFS1	NADH:ubiquinone oxidoreductase core
-0.59	2.77e-04	RNASEH2B	ribonuclease H2 subunit B	0.08	1.17e-02	TMED9	transmembrane p24 trafficking prote
-0.14	3.05e-04	TOP2A	DNA topoisomerase II alpha	0.12	1.17e-02	LMAN2	lectin, mannose binding 2
-0.06	3.05e-04	RBM39	RNA binding motif protein 39	0.11	1.17e-02	UQCRCB	ubiquinol-cytochrome c reductase bi
-0.52	3.41e-04	GIMAP6	GTPase, IMAP family member 6	0.09	1.19e-02	AIFM1	apoptosis inducing factor mitochond
-1.02	3.41e-04	EED	embryonic ectoderm development	0.2	1.26e-02	MCCC2	methylcrotonyl-CoA carboxylase subu
-0.94	3.81e-04	PCID2	PCI domain containing 2	0.4	1.26e-02	DNAJB2	DnaJ heat shock protein family (Hsp
-0.11	4.00e-04	SMC4	structural maintenance of chromosom	0.53	1.42e-02	ATP2C1	ATPase secretory pathway Ca2+ trans
-1.18	4.00e-04	MIS18A	MIS18 kinetochore protein A	0.09	1.49e-02	PDIA6	protein disulfide isomerase family
-0.76	4.08e-04	TDP2	tyrosyl-DNA phosphodiesterase 2	0.08	1.61e-02	PNPT1	polyribonucleotide nucleotidyltrans
0.08	4.57e-04	HMGCR	high mobility group box 2	0.55	1.71e-02	MYO5A	myosin V/A

p-value < 0.05 & logFC > 1.2

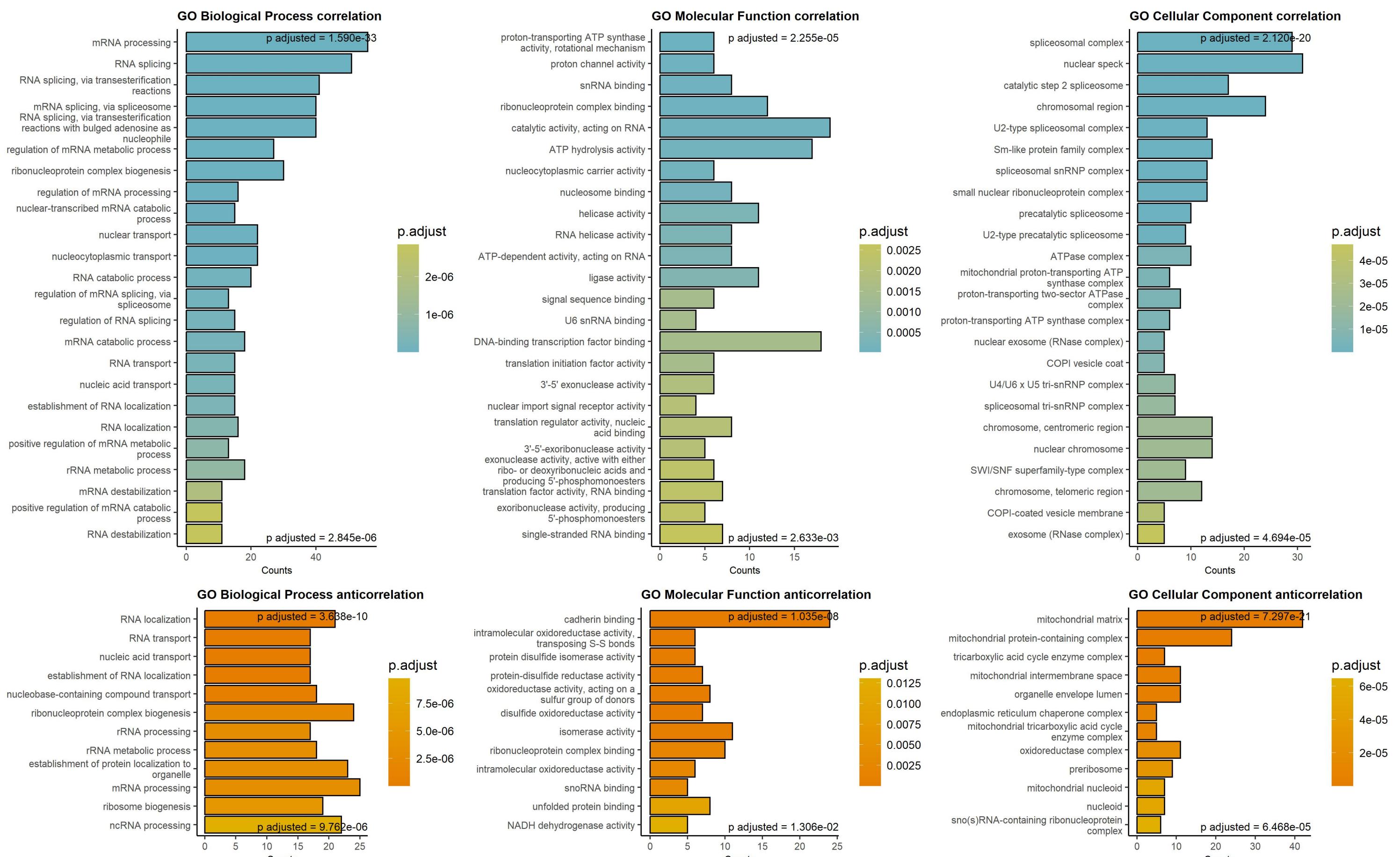


Sorted by p values!

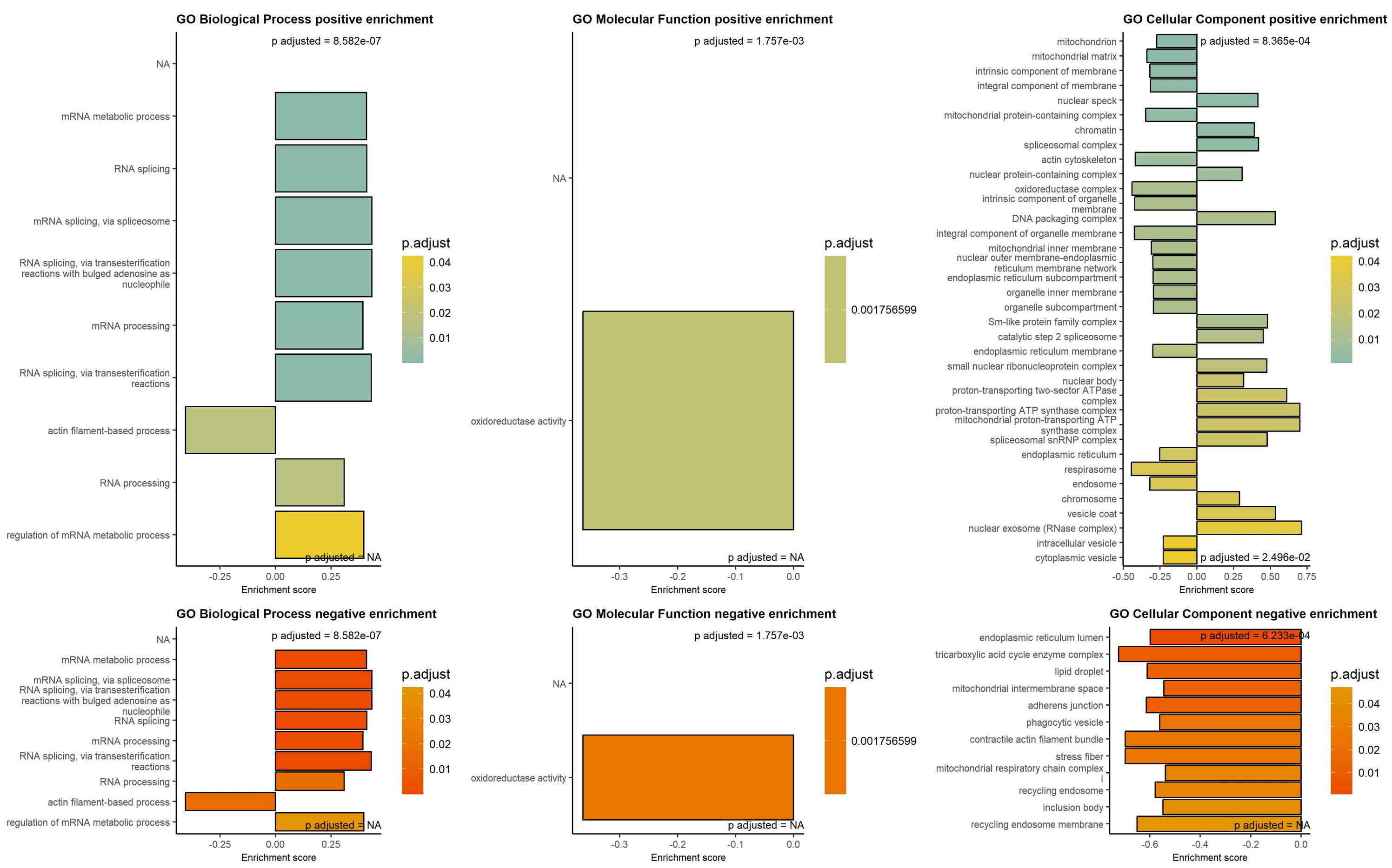
Downregulated in solid cancers at low/absent FANCD2 Upregulated in solid cancers at low/absent FANCD2

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.13	4.69e-45	H4C1	H4 clustered histone 1	0.59	6.85e-08	CD70	CD70 molecule
-1.32	1.50e-34	FANCI	FA complementation group I	0.58	4.02e-07	CPM	carboxypeptidase M
-0.99	4.66e-18	NUSAP1	nucleolar and spindle associated pr	0.63	4.20e-06	DPP4	dipeptidyl peptidase 4
-0.8	1.87e-16	VRK1	VRK serine/threonine kinase 1	0.5	9.27e-06	IL6ST	interleukin 6 cytokine family signa
-0.75	6.44e-14	NCAPG	non-SMC condensin I complex subunit	0.56	1.53e-05	CPQ	carboxypeptidase Q
-0.88	7.06e-14	PRC1	protein regulator of cytokinesis 1	0.57	1.66e-05	MUC1	mucin 1, cell surface associated
-1.01	6.75e-13	WDHD1	WD repeat and HMG-box DNA binding p	0.18	2.66e-05	SCARB2	scavenger receptor class B member 2
-1.14	2.02e-12	CCNB1	cyclin B1	0.79	3.29e-05	RAB11FIP5	RAB11 family interacting protein 5
-0.79	2.38e-12	MORF4L1	mortality factor 4 like 1	0.11	4.67e-05	DDRGK1	DDRGK domain containing 1
-1.32	3.83e-12	CFAP20	cilia and flagella associated prote	0.57	5.40e-05	CHDH	choline dehydrogenase
-0.89	4.68e-12	KIF2C	kinesin family member 2C	0.64	5.54e-05	SNTB1	syntrophin beta 1
-1.16	6.28e-12	BRD2	bromodomain containing 2	0.11	9.47e-05	MYDGF	myeloid derived growth factor
-0.98	9.66e-12	CDCA5	cell division cycle associated 5	0.41	1.39e-04	CEACAM6	CEA cell adhesion molecule 6
-0.75	9.66e-12	ATAD2	ATPase family AAA domain containing	0.37	1.62e-04	CTSS	cathepsin S
-0.81	9.66e-12	UBE2S	ubiquitin conjugating enzyme E2 S	0.67	1.65e-04	ERAP2	endoplasmic reticulum aminopeptidas
-0.79	9.66e-12	GTF3C5	general transcription factor IIIC s	0.53	1.66e-04	TYMP	thymidine phosphorylase
-1.09	1.56e-11	ARPC1A	actin related protein 2/3 complex s	0.12	2.56e-04	TMOD3	tropomodulin 3
-0.97	1.76e-11	PPP6C	protein phosphatase 6 catalytic sub	0.48	2.64e-04	NF2	NF2, moesin-ezrin-radixin like (MER
-0.98	2.09e-11	SMARCD1	SWI/SNF related, matrix associated,	0.09	4.44e-04	CLTA	clathrin light chain A
-0.07	3.55e-11	DDB1	damage specific DNA binding protein	0.09	4.81e-04	LAMTOR1	late endosomal/lysosomal adaptor, M
-0.8	3.55e-11	FRG1	FSHD region gene 1	0.14	5.19e-04	ACTN4	actinin alpha 4
-1.1	3.64e-11	INTS11	integrator complex subunit 11	0.38	5.21e-04	LOXL2	lysyl oxidase like 2
-0.95	4.64e-11	PFKM	phosphofructokinase, muscle	0.89	5.30e-04	PSMB9	proteasome 20S subunit beta 9
-0.72	5.28e-11	POLR2L	RNA polymerase II, I and III subuni	0.35	6.40e-04	ABLIM3	actin binding LIM protein family me
-0.98	5.62e-11	POLR2G	RNA polymerase II subunit G	0.43	6.65e-04	MICAL2	microtubule associated monoxygenas
-1	6.27e-11	UBE2T	ubiquitin conjugating enzyme E2 T	0.35	7.01e-04	CD99L2	CD99 molecule like 2
-0.06	7.04e-11	RAN	RAN, member RAS oncogene family	0.81	7.20e-04	PSMB8	proteasome 20S subunit beta 8
-1.03	8.05e-11	EZH2	enhancer of zeste 2 polycomb repres	0.15	8.01e-04	HSDL2	hydroxysteroid dehydrogenase like 2
-0.87	1.18e-10	MRGBP	MRG domain binding protein	0.83	9.52e-04	ADGRE5	adhesion G protein-coupled receptor
-1.05	1.29e-10	PRIM2	DNA primase subunit 2	0.6	1.06e-03	RAB27B	RAB27

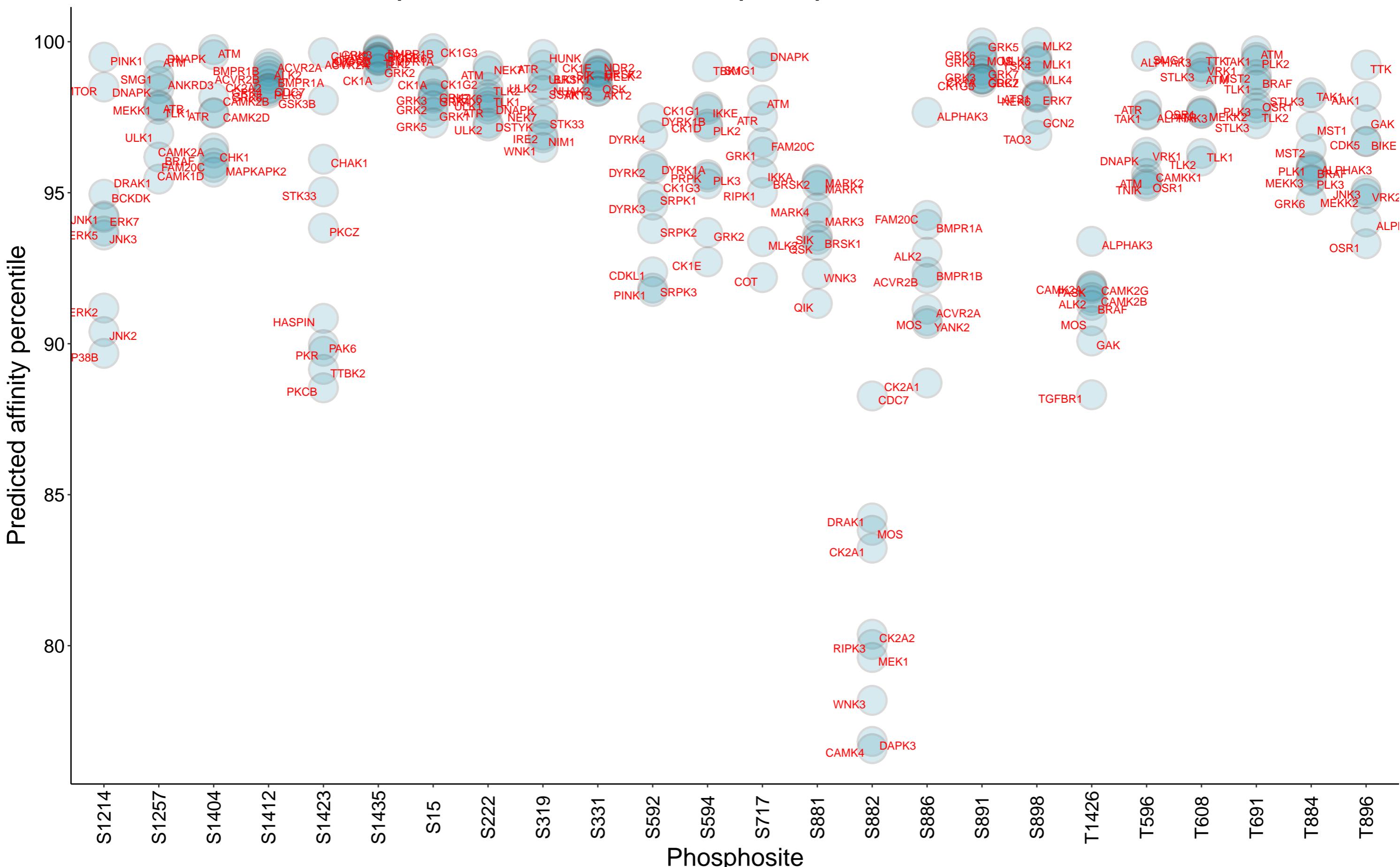
Top 250 correlation coefficients overrepresentation, FANCD2 protein, DB1



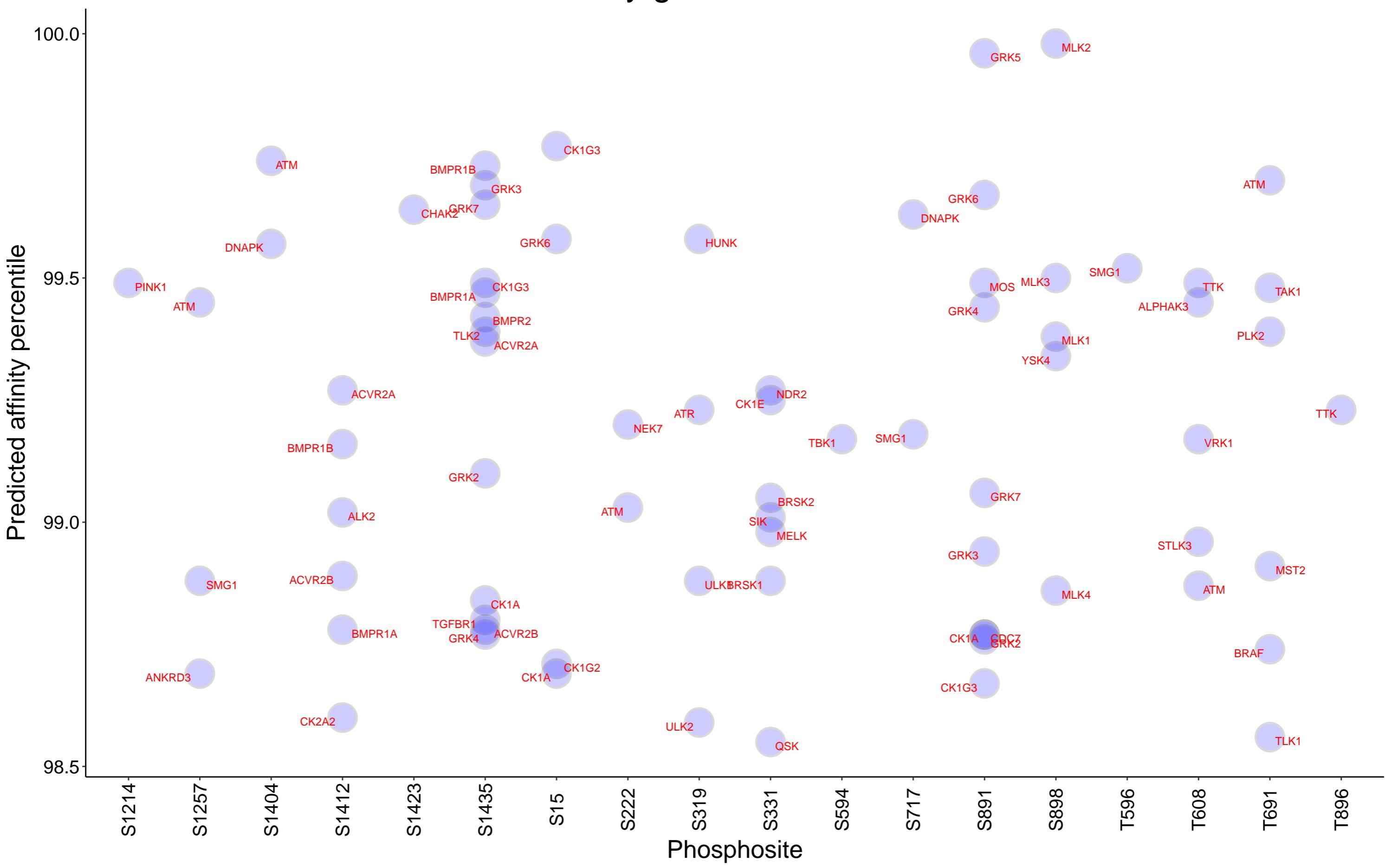
Gene Set Enrichment analysis on protein correlation coefficients, FANCD2 protein, DB1



Top 10 kinases for each phosphosite in FANCD2



Kinases with affinity greater than 98.5% to FANCD2



No sufficient paired observations in DB1 for FANCD2