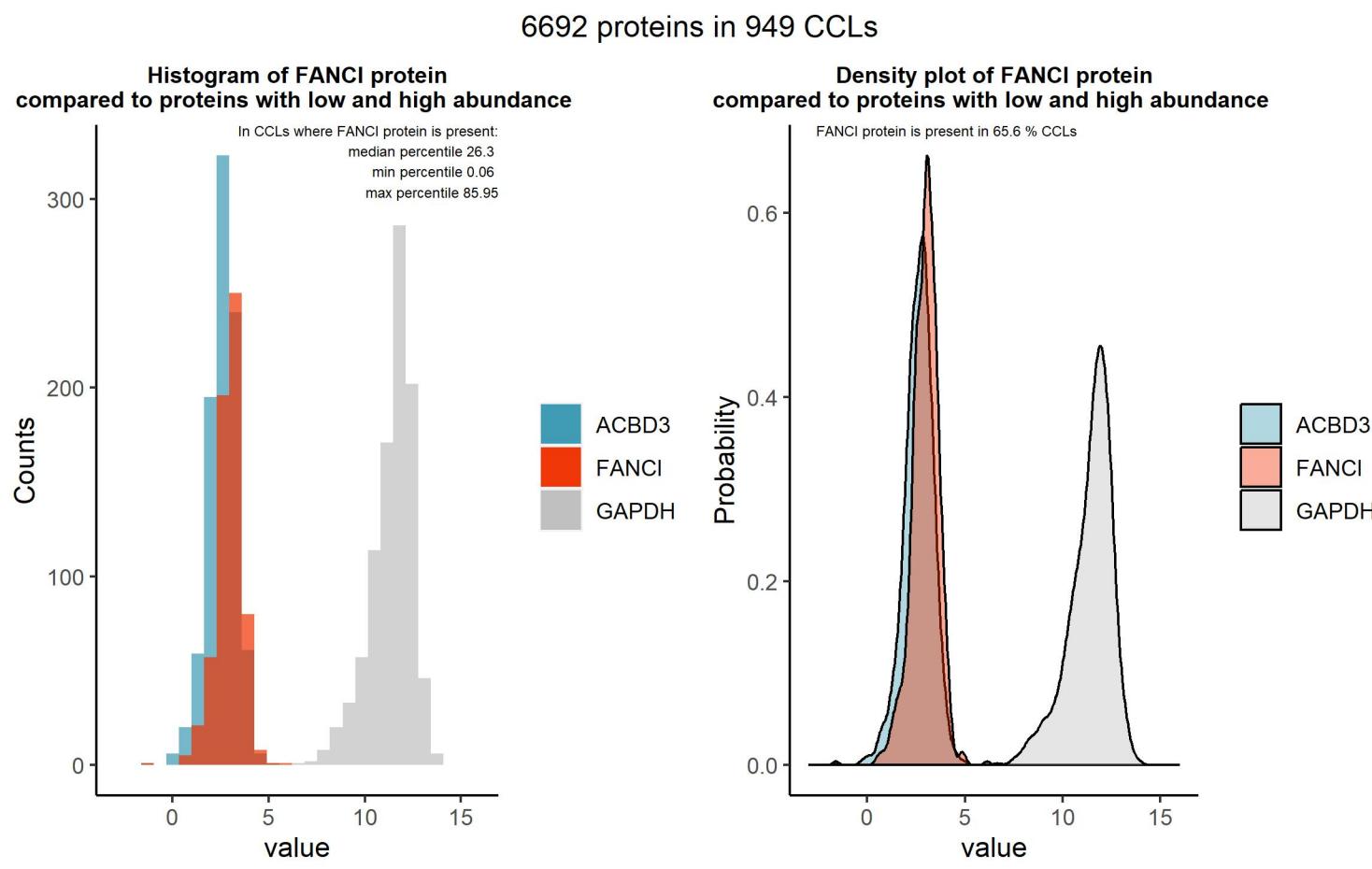


# FANCI

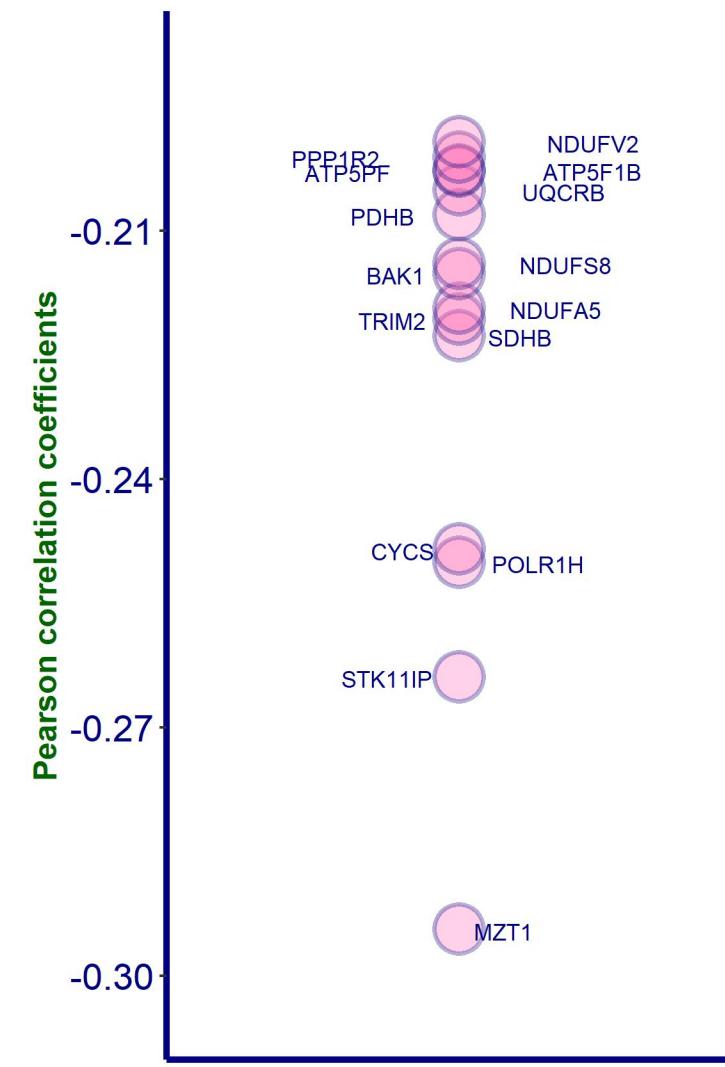
Protein name: FANCI ; UNIPROT: Q9NVI1 ; Gene name: FA complementation group I

Ligandable: Yes ; Ligandable\_by\_Chem: Yes ; Is\_enzyme: NA (<https://cansar.ai/>)

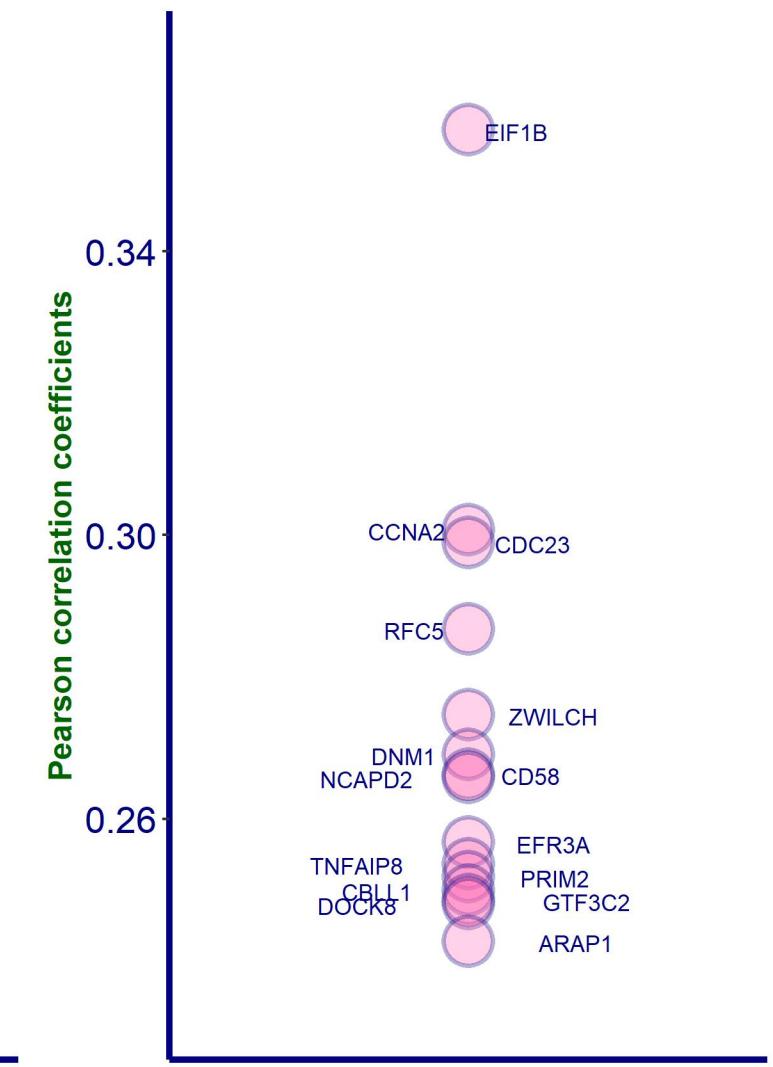
## Sanger Institute Protein Database 1 (DB1), protein presence is certain



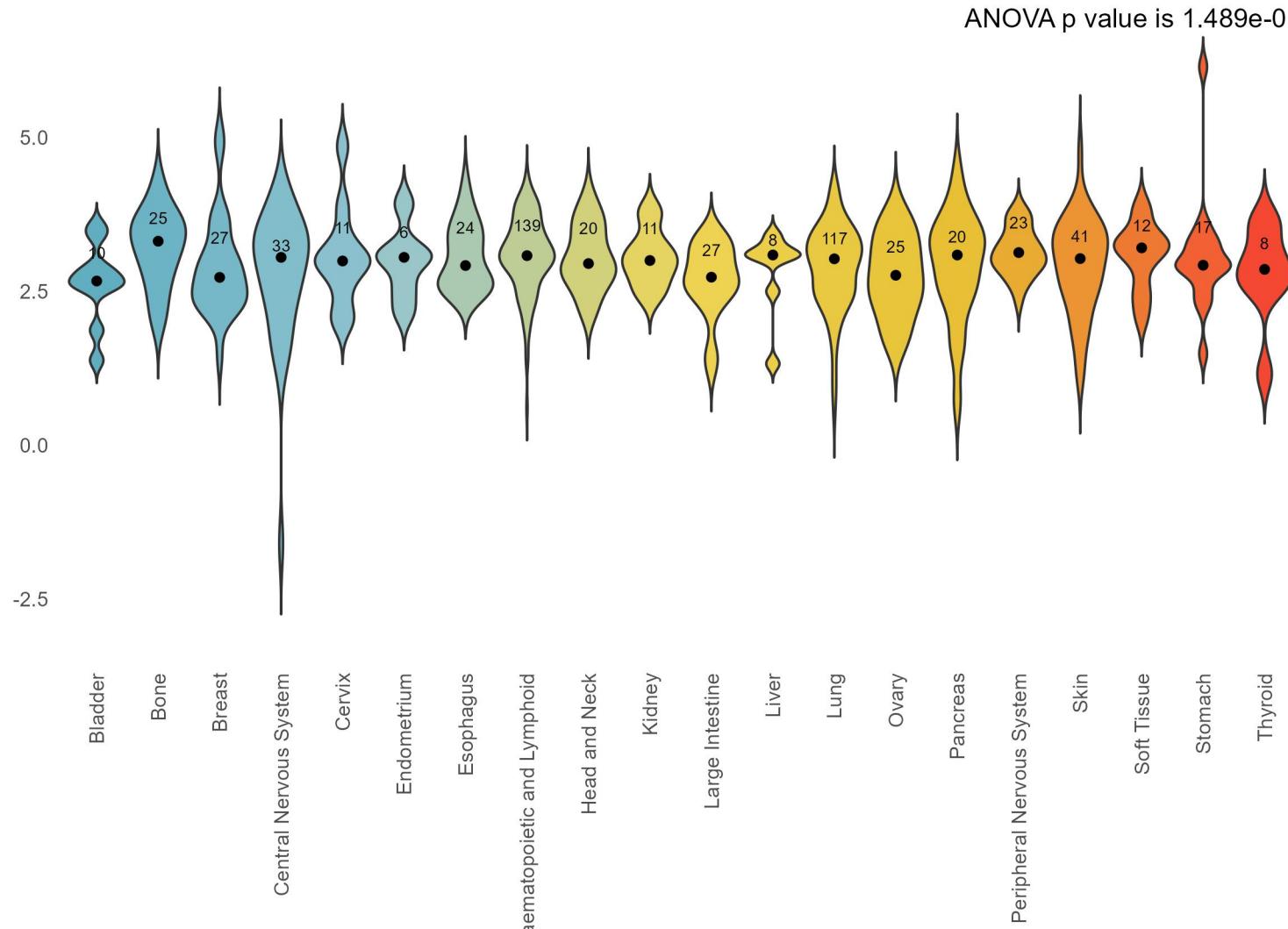
### Top negative correlations of FANCI protein, DB1



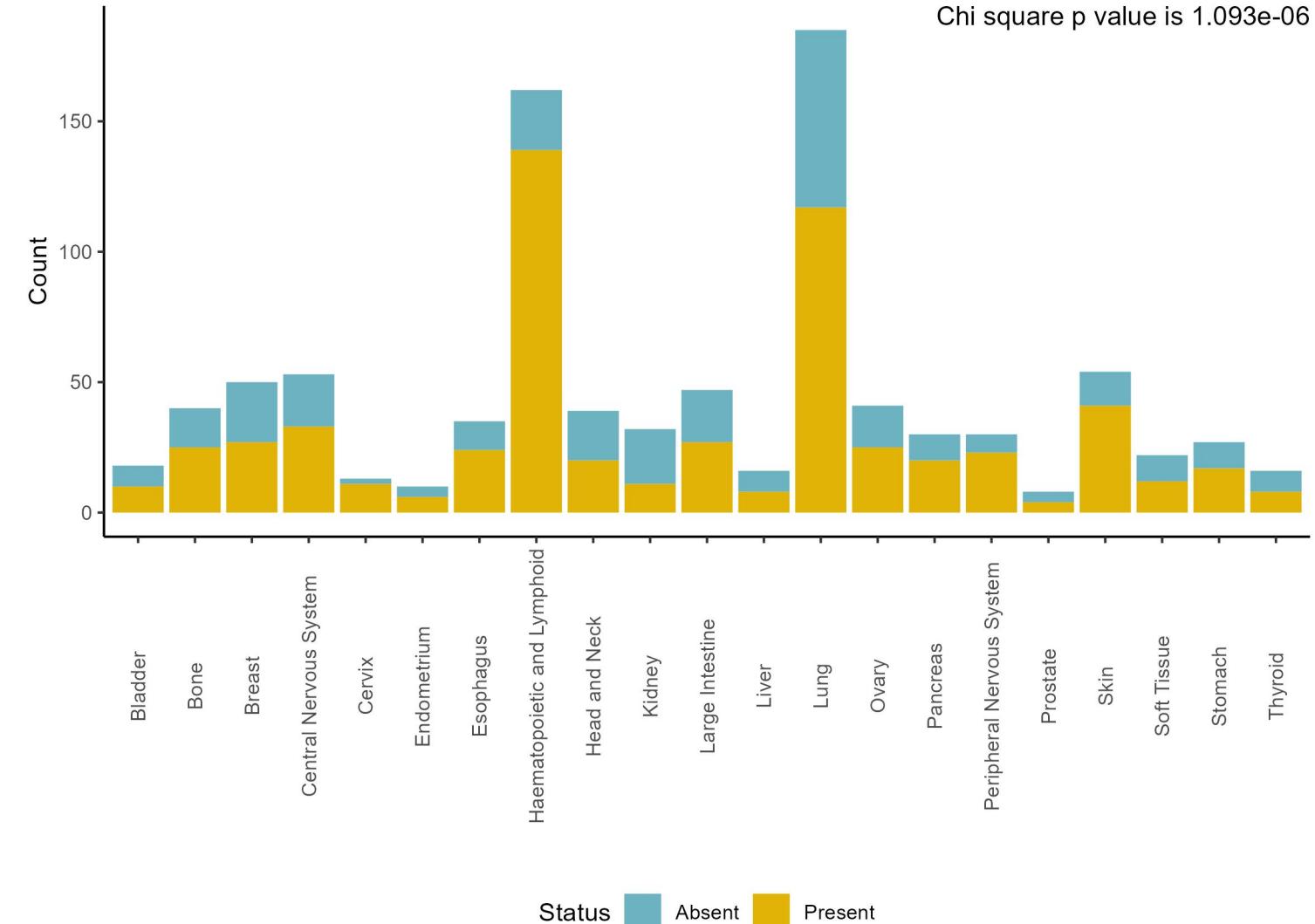
### Top positive correlations of FANCI protein, DB1



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



## Present and absent FANCI protein counts by tissue, DB1

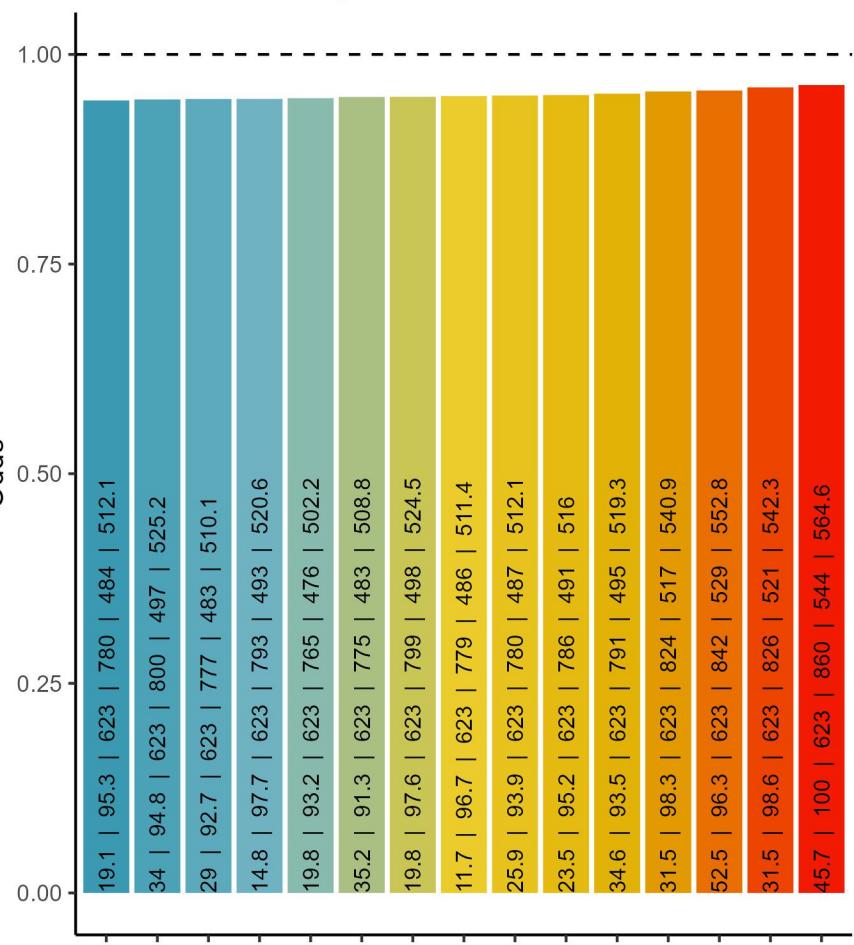


## Cooccurrence with FANCI protein, DB1

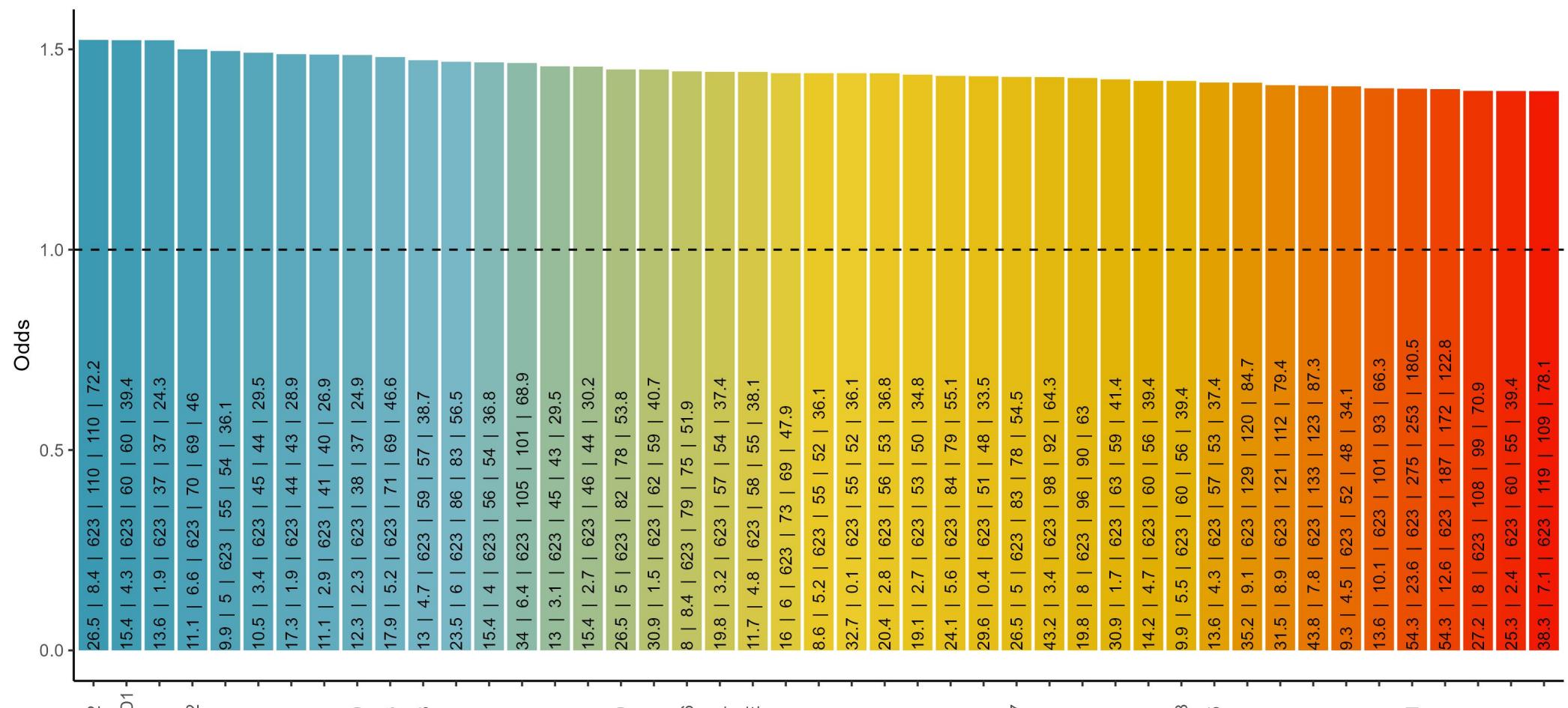
% of FANCI in blood cancers: 85.8 ; % of FANCI in solid cancers: 61.4

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

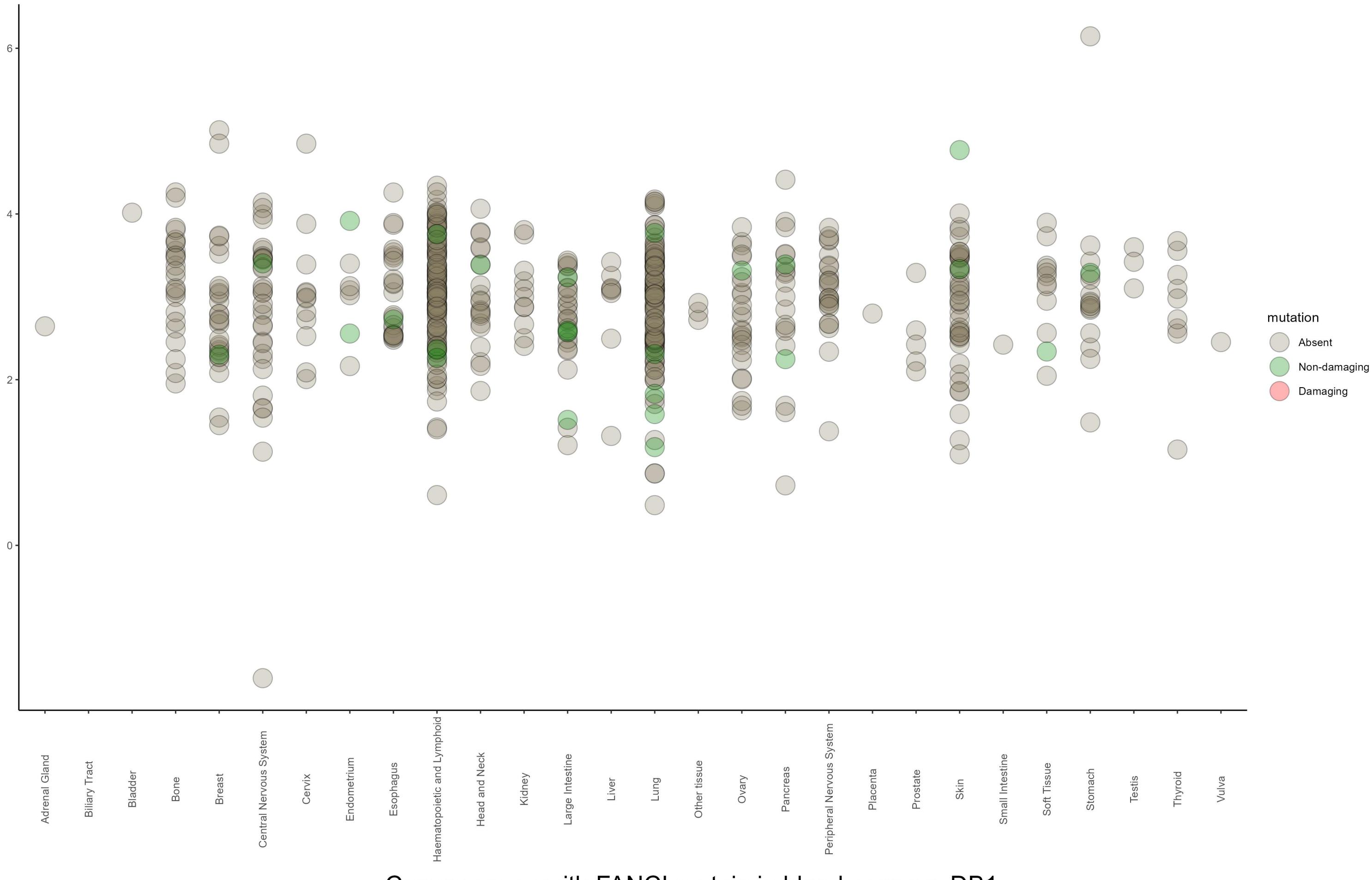
### Negative cooccurrence



### Positive cooccurrence

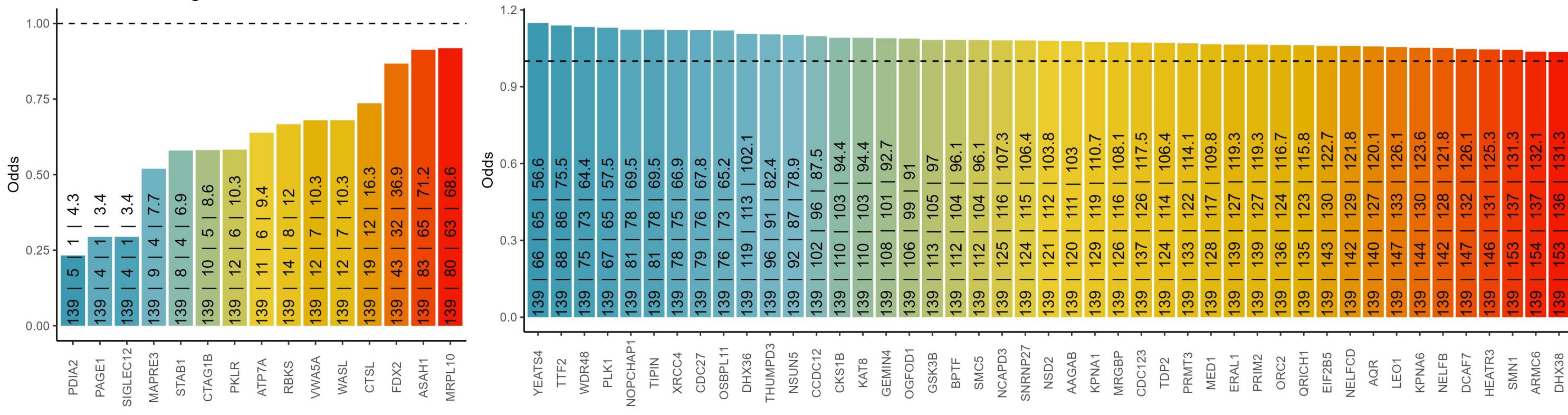


# Amount of FANCI protein and mutation status by tissue, DB1



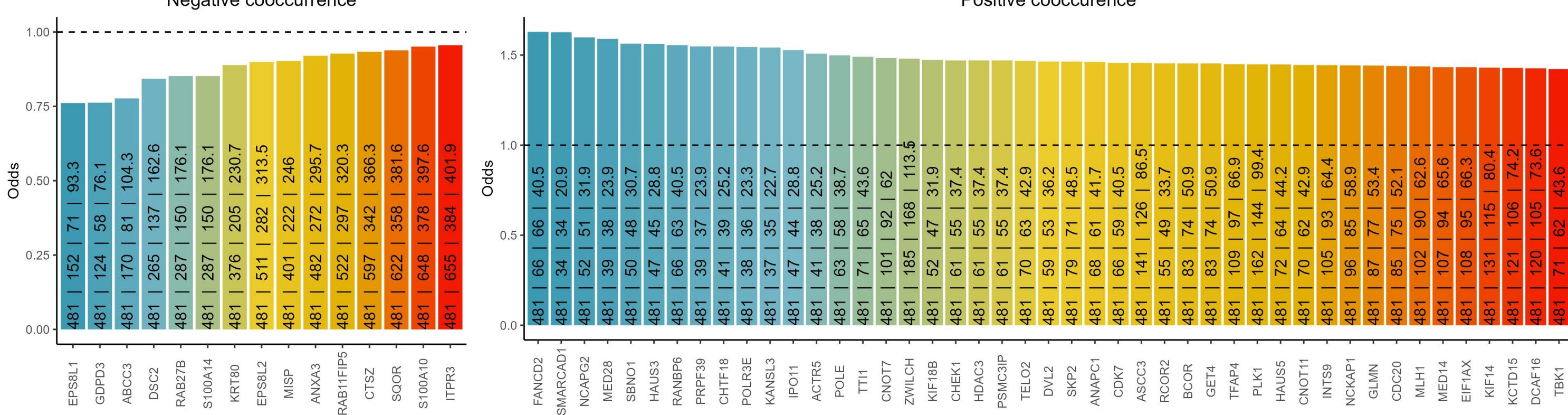
## Cooccurrence with FANCI protein in blood cancers, DB1

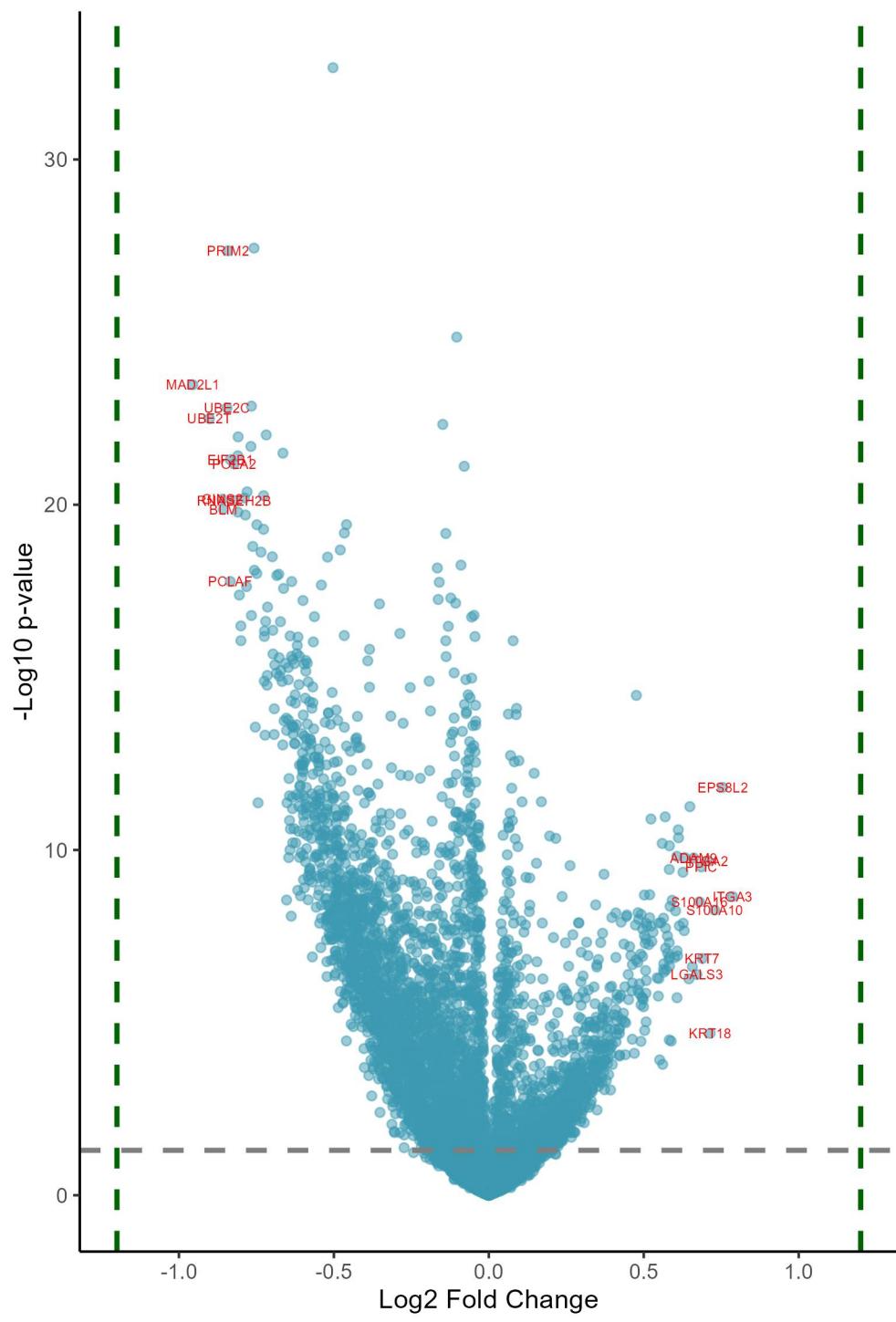
The text in the bars: incidence of FANCI | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



## Cooccurrence with FANCI protein in solid cancers, DB1

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

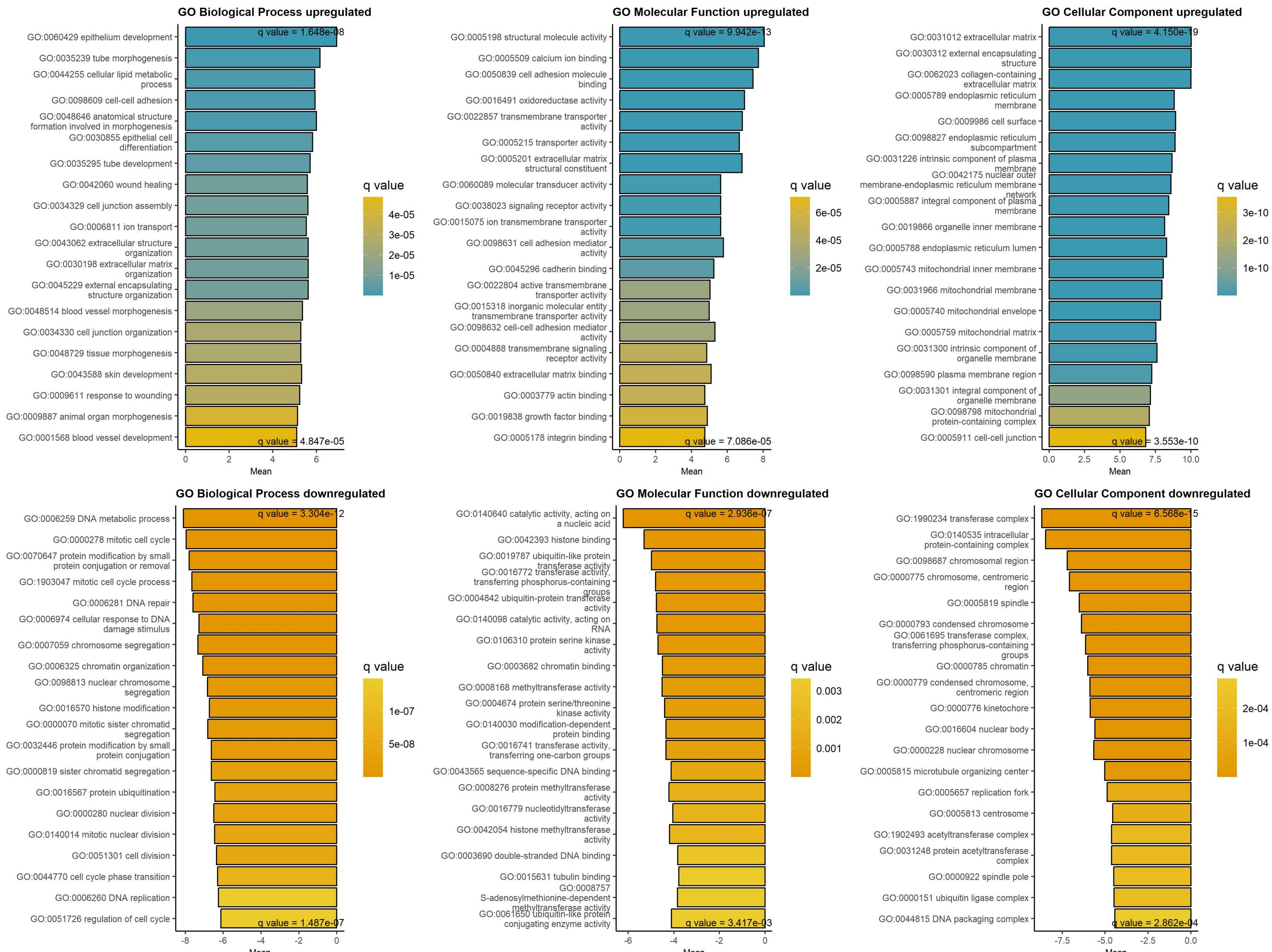


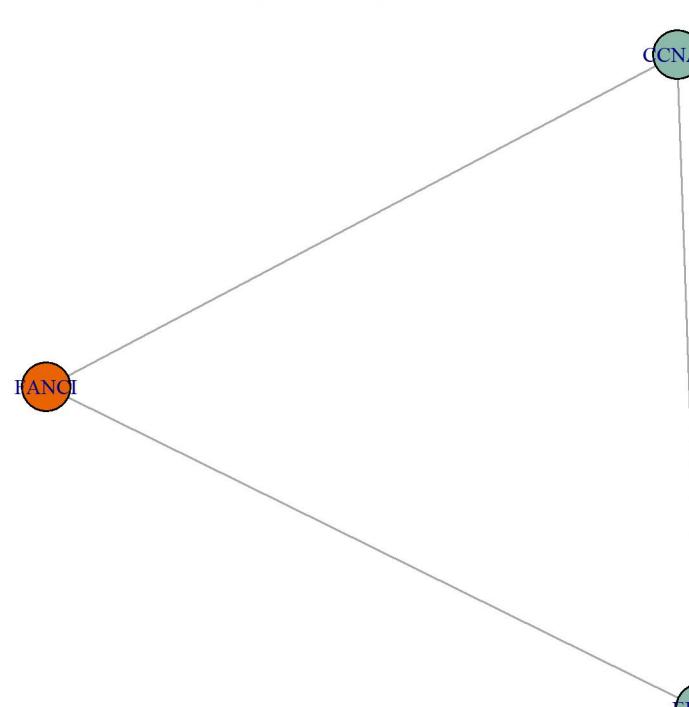
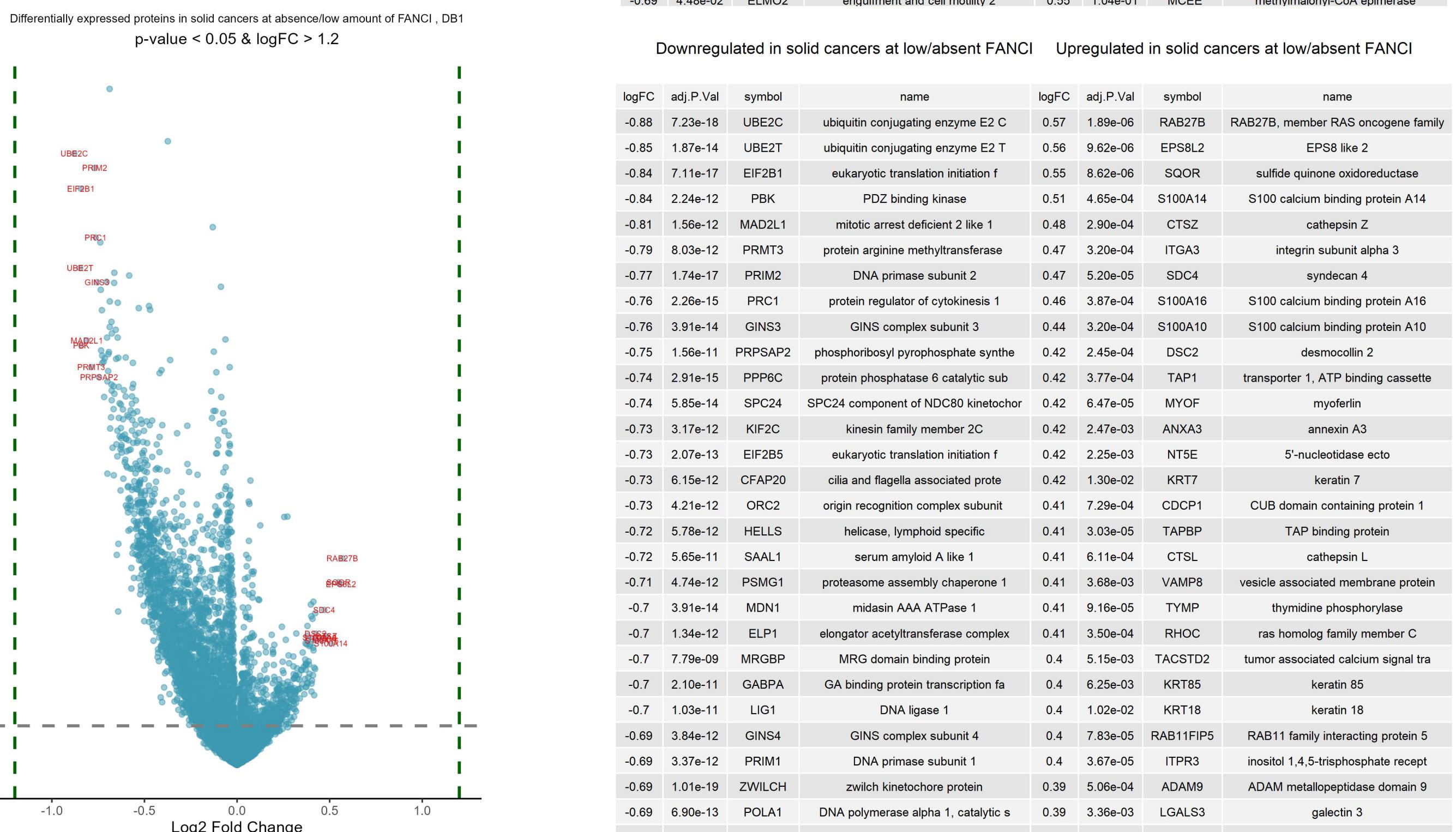
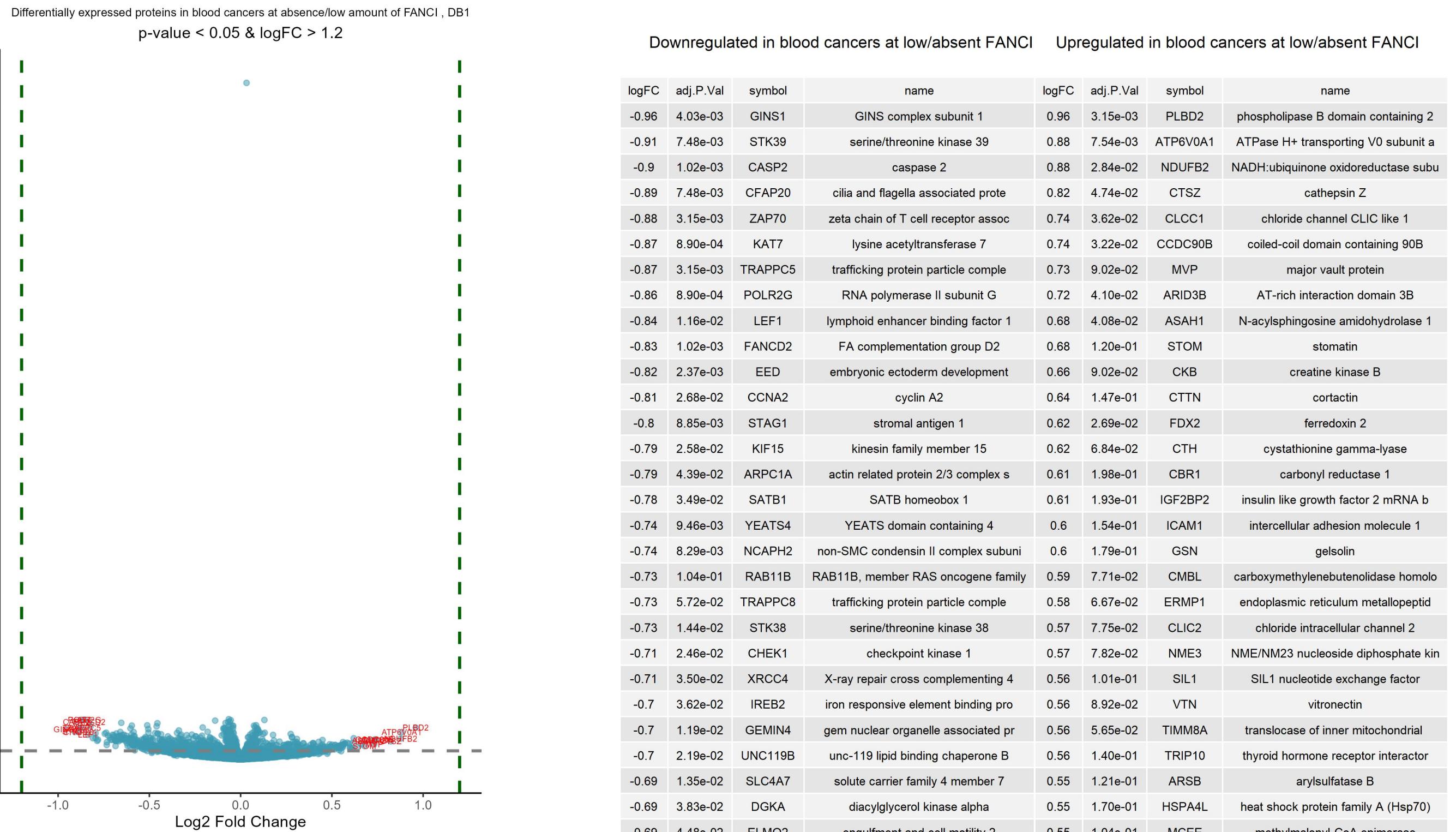


### Downregulated at low/absent FANCI Upregulated at low/absent FANCI

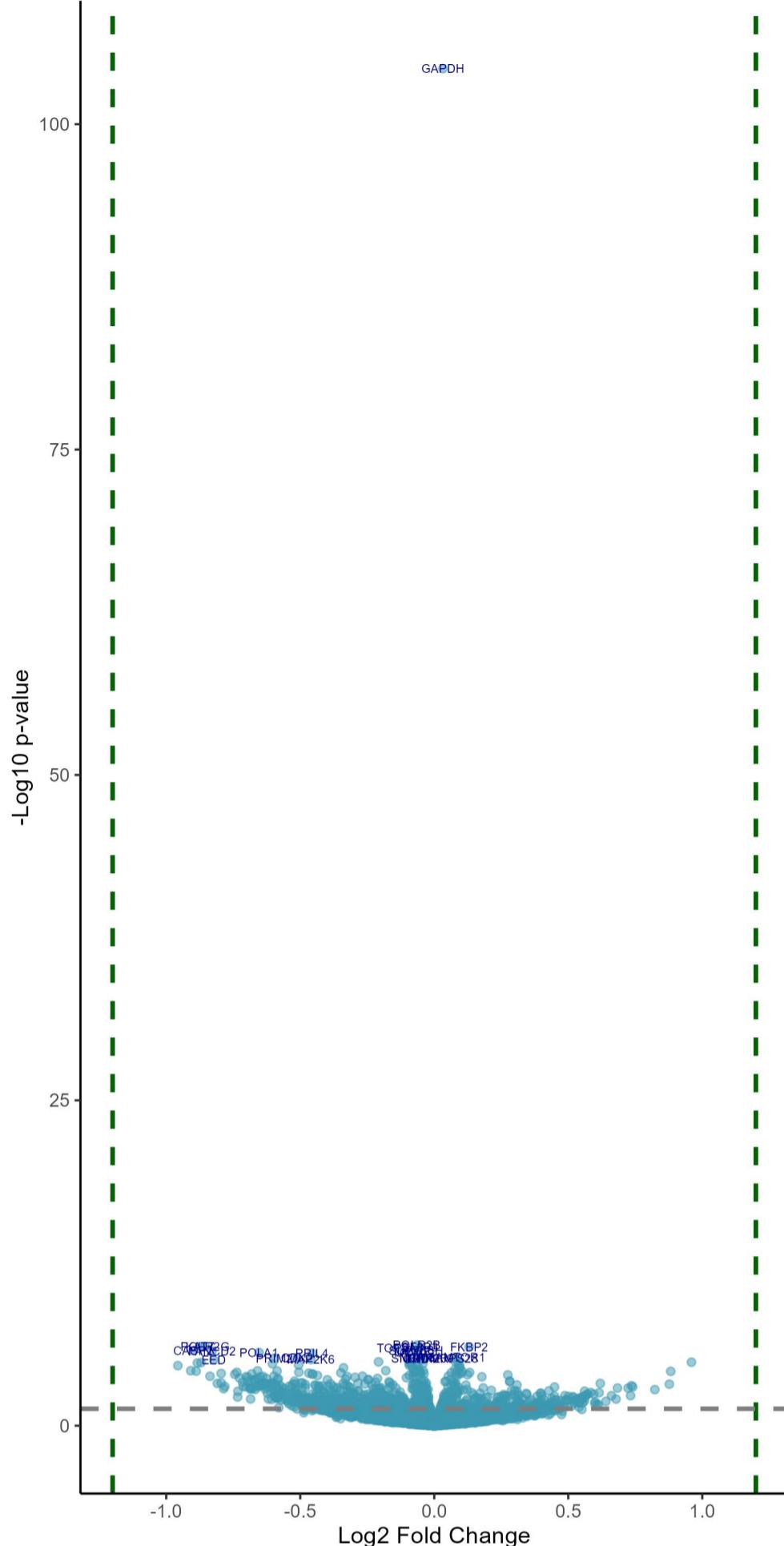
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.96	3.71e-21	MAD2L1	mitotic arrest deficient 2 like 1	0.79	2.36e-08	ITGA3	integrin subunit alpha 3
-0.9	2.37e-20	UBE2T	ubiquitin conjugating enzyme E2 T	0.75	4.19e-11	EPS8L2	EPS8 like 2
-0.86	2.08e-18	GINS2	GINS complex subunit 2	0.73	5.17e-08	S100A10	S100 calcium binding protein A10
-0.86	3.76e-18	BLM	BLM RecQ like helicase	0.71	7.46e-05	KRT18	keratin 18
-0.85	1.30e-20	UBE2C	ubiquitin conjugating enzyme E2 C	0.71	2.94e-09	ITGA2	integrin subunit alpha 2
-0.84	7.31e-25	PRIM2	DNA primase subunit 2	0.69	8.58e-07	KRT7	keratin 7
-0.83	2.54e-16	PCLAF	PCNA clamp associated factor	0.69	4.25e-09	PPIC	peptidylprolyl isomerase C
-0.83	2.05e-19	EIF2B1	eukaryotic translation initiation f	0.68	3.20e-08	S100A16	S100 calcium binding protein A16
-0.82	2.58e-19	POLA2	DNA polymerase alpha 2, accessory s	0.67	2.24e-06	LGALS3	galectin 3
-0.82	2.19e-18	RNASEH2B	ribonuclease H2 subunit B	0.66	2.43e-09	ADAM9	ADAM metallopeptidase domain 9
-0.81	1.69e-19	PRIM1	DNA primase subunit 1	0.66	1.40e-06	GNG12	G protein subunit gamma 12
-0.81	4.36e-18	PSMG1	proteasome assembly chaperone 1	0.65	1.29e-10	RAB27B	RAB27B, member RAS oncogene family
-0.81	5.98e-20	GINS3	GINS complex subunit 3	0.65	2.88e-06	CAVIN1	caveolae associated protein 1
-0.81	5.60e-16	ARMC6	armadillo repeat containing 6	0.63	2.38e-09	CTSL	cathepsin L
-0.8	3.47e-15	PRMT3	protein arginine methyltransferase	0.63	1.65e-07	PKP3	plakophilin 3
-0.8	7.81e-15	DHFR	dihydrofolate reductase	0.63	1.08e-07	EGFR	epidermal growth factor receptor
-0.79	2.02e-18	EIF2B5	eukaryotic translation initiation f	0.63	5.78e-09	CDCP1	CUB domain containing protein 1
-0.79	5.08e-18	HELLS	helicase, lymphoid specific	0.61	1.26e-07	RHOC	ras homolog family member C
-0.78	3.33e-16	TYMS	thymidylate synthetase	0.61	7.66e-10	ITPR3	inositol 1,4,5-trisphosphate receptor
-0.78	1.48e-18	POLA1	DNA polymerase alpha 1, catalytic s	0.61	4.88e-10	ITGAV	integrin subunit alpha V
-0.77	1.05e-19	GEMIN4	gem nuclear organelle associated pr	0.61	7.36e-07	JUP	junction plakoglobin
-0.77	1.30e-20	PPP6C	protein phosphatase 6 catalytic sub	0.61	5.49e-07	NT5E	5'-nucleotidase ecto
-0.77	1.89e-15	SAAL1	serum amyloid A like 1	0.61	8.84e-06	NQO1	NAD(P)H quinone dehydrogenase 1
-0.76	3.35e-17	TACC3	transforming acidic coiled-coil con	0.61	2.21e-09	NECTIN2	nectin cell adhesion molecule 2
-0.76	7.31e-25	ZWILCH	zwilch kinetochore protein	0.6	5.41e-08	SQOR	sulfide quinone oxidoreductase
-0.76	1.35e-16	KIF2C	kinesin family member 2C	0.6	8.13e-07	ANXA3	annexin A3
-0.75	1.21e-12	PBK	PDZ binding kinase	0.59	2.92e-08	RRAS	RAS related
-0.75	1.63e-16	LIG1	DNA ligase 1	0.59	1.20e-04	KRT19	keratin 19
-0.75	9.04e-18	CDK2	cyclin dependent kinase 2	0.59	4.17e-08	TPBG	trophoblast glycoprotein

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



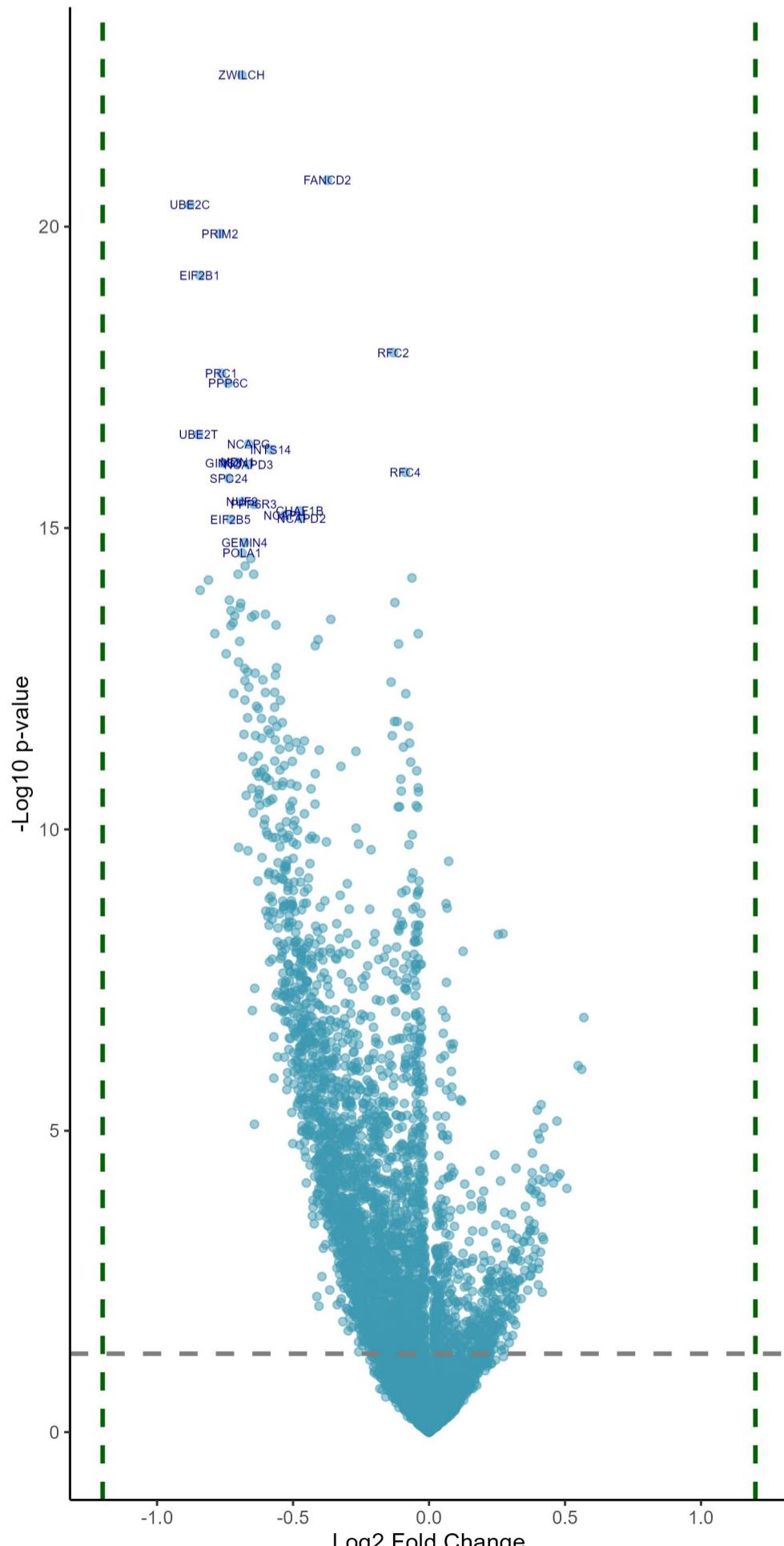


Sorted by p values!  
Downregulated in blood cancers at low/absent FANCI    Upregulated in blood cancers at low/absent FANCI



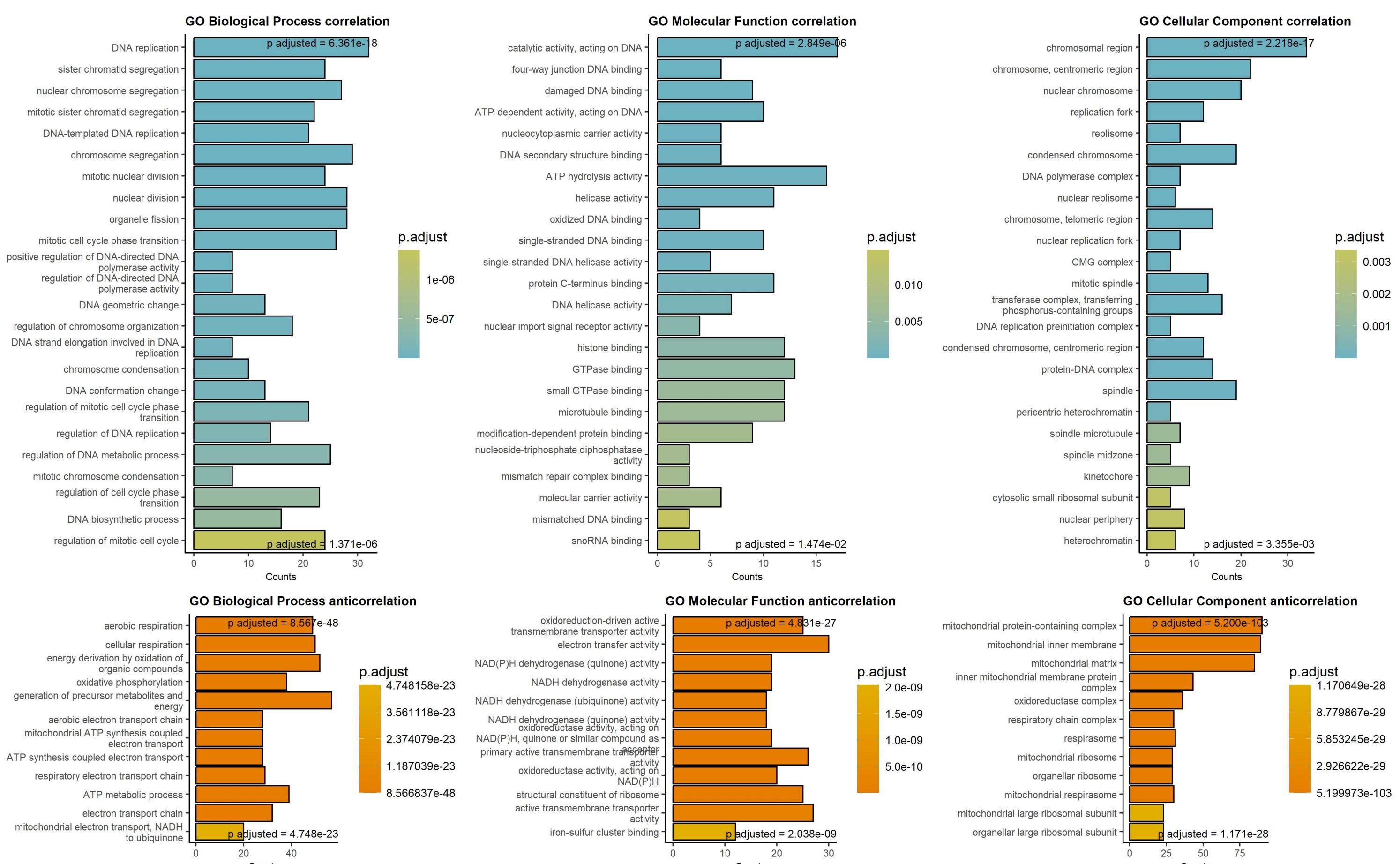
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.06	8.90e-04	POLR2B	RNA polymerase II subunit B	0.03	3.56e-101	GAPDH	glyceraldehyde-3-phosphate dehydrogenase
-0.86	8.90e-04	POLR2G	RNA polymerase II subunit G	0.13	8.90e-04	FKBP2	FKBP prolyl isomerase 2
-0.87	8.90e-04	KAT7	lysine acetyltransferase 7	0.08	2.02e-03	LAMTOR1	late endosomal/lysosomal adaptor, M
-0.05	8.90e-04	SF3B3	splicing factor 3b subunit 3	0.07	2.02e-03	MRPS28	mitochondrial ribosomal protein S28
-0.14	9.10e-04	TOP2A	DNA topoisomerase II alpha	0.08	3.01e-03	TMED9	transmembrane p24 trafficking protein
-0.06	1.02e-03	BUB3	BUB3 mitotic checkpoint protein	0.96	3.15e-03	PLBD2	phospholipase B domain containing 2
-0.9	1.02e-03	CASP2	caspase 2	0.09	3.15e-03	SDHB	succinate dehydrogenase complex iron-sulfur protein
-0.07	1.02e-03	SUPT16H	SPT16 homolog, facilitates chromatin	0.09	3.91e-03	ACO2	aconitase 2
-0.83	1.02e-03	FANCD2	FA complementation group D2	0.09	5.40e-03	PRDX5	peroxiredoxin 5
-0.65	1.18e-03	POLA1	DNA polymerase alpha 1, catalytic subunit	0.1	5.59e-03	NDUFS1	NADH:ubiquinone oxidoreductase core
-0.08	1.18e-03	MCM5	minichromosome maintenance complex	0.08	6.60e-03	NDUFS3	NADH:ubiquinone oxidoreductase core
-0.46	1.20e-03	PPIL4	peptidylprolyl isomerase like 4	0.08	7.48e-03	MRPL58	mitochondrial ribosomal protein L58
-0.06	2.02e-03	MCM7	minichromosome maintenance complex	0.88	7.54e-03	ATP6V0A1	ATPase H+ transporting V0 subunit a
-0.51	2.02e-03	CDK2	cyclin dependent kinase 2	0.1	7.54e-03	NDUFA2	NADH:ubiquinone oxidoreductase subunit 2
-0.6	2.02e-03	PRIM2	DNA primase subunit 2	0.13	8.29e-03	NDUFS6	NADH:ubiquinone oxidoreductase subunit 6
-0.04	2.02e-03	SNRNP200	small nuclear ribonucleoprotein U5	0.06	8.37e-03	TIMM44	translocase of inner mitochondrial membrane
-0.04	2.02e-03	DHX9	DExH-box helicase 9	0.1	8.85e-03	UQCRCB	ubiquinol-cytochrome c reductase bi
-0.05	2.02e-03	CHD4	chromodomain helicase DNA binding protein	0.09	9.09e-03	CYCS	cytochrome c, somatic
-0.46	2.30e-03	MAP2K6	mitogen-activated protein kinase kinase 6	0.08	9.47e-03	MRPS23	mitochondrial ribosomal protein S23
-0.82	2.37e-03	EED	embryonic ectoderm development	0.12	9.91e-03	WARS1	tryptophanyl-tRNA synthetase 1
-0.21	3.08e-03	MCMBP	minichromosome maintenance complex	0.27	1.02e-02	NDUFB1	NADH:ubiquinone oxidoreductase subunit 1
-0.09	3.15e-03	PDS5A	PDS5 cohesin associated factor A	0.05	1.16e-02	COX5B	cytochrome c oxidase subunit 5B
-0.87	3.15e-03	TRAPPC5	trafficking protein particle complex	0.08	1.16e-02	CLPP	caseinolytic mitochondrial matrix protein
-0.88	3.15e-03	ZAP70	zeta chain of T cell receptor associated	0.18	1.21e-02	MRPL49	mitochondrial ribosomal protein L49
-0.09	3.15e-03	SMC4	structural maintenance of chromosomes	0.06	1.67e-02	UBR4	ubiquitin protein ligase E3 component
-0.04	3.25e-03	PTBP1	polypyrimidine tract binding protein	0.28	2.14e-02	NDUFAF2	NADH:ubiquinone oxidoreductase complex
-0.6	3.38e-03	CDCA7	cell division cycle associated 7	0.04	2.14e-02	TUFM	Tu translation elongation factor, m
-0.09	3.81e-03	RPA1	replication protein A1	0.04	2.24e-02	HSPA9	heat shock protein family A (Hsp70)
-0.51	3.91e-03	SKP2	S-phase kinase associated protein 2	0.28	2.25e-02	MAPRE3	microtubule associated protein RP/E
-0.09	3.91e-03	BAZ1B	bromodomain adjacent to zinc finger	0.07	2.50e-02	SSR1	signal sequence receptor subunit 1
-0.96	4.03e-03	GINS1	GINS complex subunit 1	0.62	2.69e-02	FDX2	ferredoxin 2
-0.06	4.06e-03	MCM4	minichromosome maintenance complex	0.08	2.71e-02	HDLBP	high density lipoprotein binding protein
-0.06	4.44e-03	SSRP1	structure specific recognition protein	0.08	2.72e-02	ERP44	endoplasmic reticulum protein 44
-0.34	5.40e-03	UHRF1	ubiquitin like with PHD and ring finger	0.88	2.84e-02	NDUFB2	NADH:ubiquinone oxidoreductase subunit 2
-0.08	5.64e-03	CBFB	core-binding factor subunit beta	0.31	3.03e-02	STAB1	stabilin 1
-0.07	6.60e-03	MCM6	minichromosome maintenance complex	0.12	3.04e-02	CISD2	CDGSH iron sulfur domain 2
-0.07	7.31e-03	MCM2	minichromosome maintenance complex	0.06	3.04e-02	TFAM	transcription factor A, mitochondrial
-0.18	7.48e-03	NCAPD2	non-SMC condensin I complex subunit	0.74	3.22e-02	CCDC90B	coiled-coil domain containing 90B
0.91	7.48e-03	STK20	serine/threonine kinase 20	0.08	3.49e-02	DNAJ4	Dna J heat shock protein family (Hsp40)

Sorted by p values!  
Downregulated in solid cancers at low/absent FANCI    Upregulated in solid cancers at low/absent FANCI

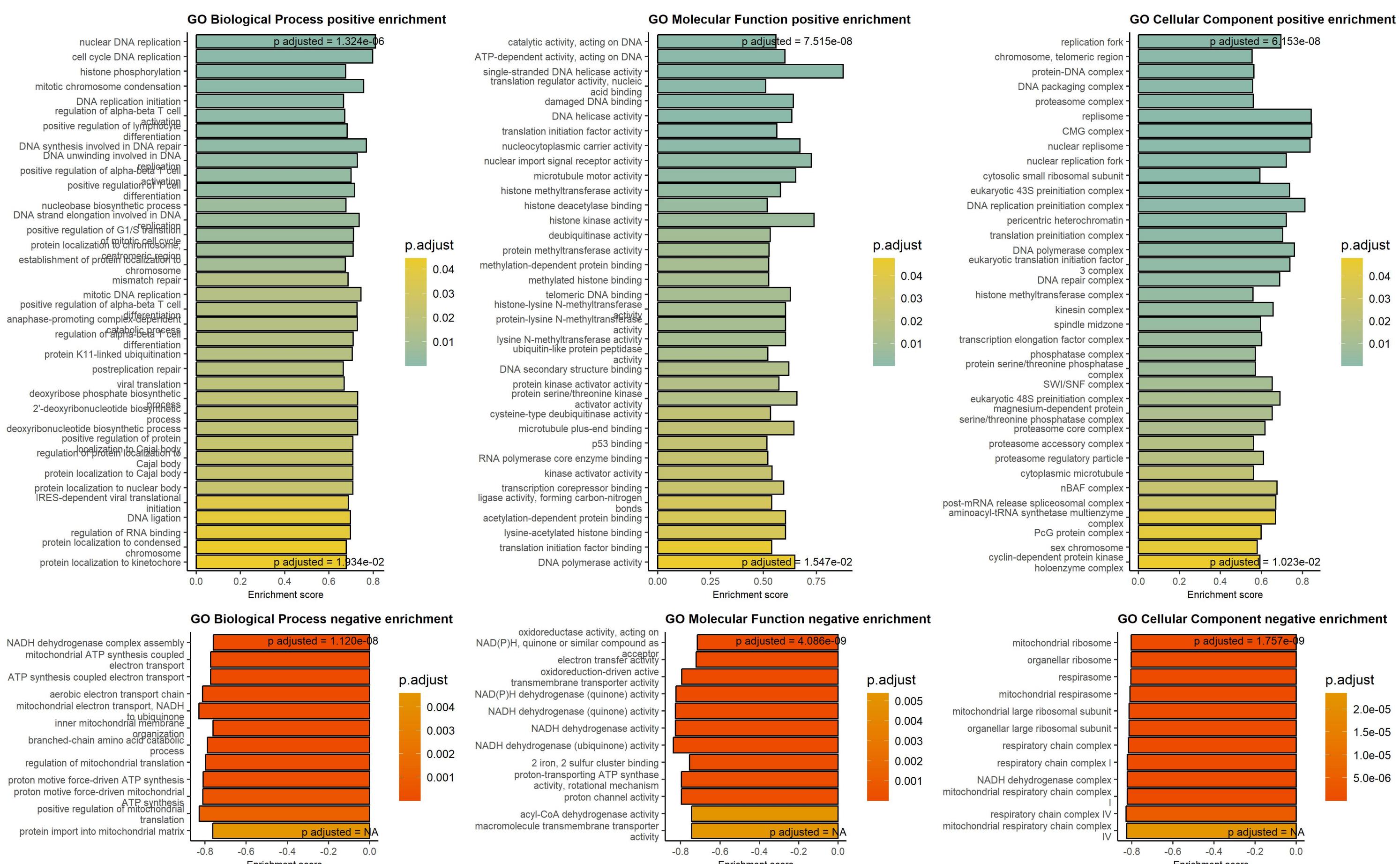


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.69	1.01e-19	ZWILCH	zwilch kinetochore protein	0.07	1.28e-08	GOLGA2	golgin A2
-0.37	3.75e-18	FANCD2	FA complementation group D2	0.06	5.16e-08	LAMTOR1	late endosomal/lysosomal adaptor, M
-0.88	7.23e-18	UBE2C	ubiquitin conjugating enzyme E2 C	0.07	5.84e-08	PGRMC2	progesterone receptor membrane component
-0.77	1.74e-17	PRIM2	DNA primase subunit 2	0.27	1.31e-07	STX4	syntaxin 4
-0.84	7.11e-17	EIF2B1	eukaryotic translation initiation factor 2B subunit 1	0.25	1.35e-07	GOLGA5	golgin A5
-0.13	1.17e-15	RFC2	replication factor C subunit 2	0.13	2.32e-07	RRBP1	ribosome binding protein 1
-0.76	2.26e-15	PRC1	protein regulator of cytokinesis 1	0.06	6.01e-07	DDRGK1	DDRGK domain containing 1
-0.74	2.91e-15	PPP6C	protein phosphatase 6 catalytic subunit	0.05	1.52e-06	GORASP2	golgi reassembly stacking protein 2
-0.85	1.87e-14	UBE2T	ubiquitin conjugating enzyme E2 T	0.06	1.88e-06	ECHS1	enoyl-CoA hydratase, short chain 1
-0.66	2.45e-14	NCAPG	non-SMC condensin I complex subunit	0.57	1.89e-06	RAB27B	RAB27B, member RAS oncogene family
-0.58	2.78e-14	INTS14	integrator complex subunit 14	0.05	3.13e-06	CNPY2	canopy FGF signaling regulator 2
-0.7	3.91e-14	MDN1	midasin AAA ATPase 1	0.09	4.28e-06	GOLGB1	golgin B1
-0.76	3.91e-14	GINS3	GINS complex subunit 3	0.08	4.34e-06	ACADVL	acyl-CoA dehydrogenase very long chain
-0.66	3.91e-14	NCAPD3	non-SMC condensin II complex subunit	0.09	5.00e-06	ZFPL1	zinc finger protein like 1
-0.09	4.93e-14	RFC4	replication factor C subunit 4	0.06	6.30e-06	LAMP1	lysosomal associated membrane protein
-0.74	5.85e-14	SPC24	SPC24 component of NDC80 kinetochore	0.04	6.92e-06	P4HB	prolyl 4-hydroxylase subunit beta
-0.69	1.35e-13	NUF2	NUF2 component of NDC80 kinetochore	0.55	8.62e-06	SQOR	sulfide quinone oxidoreductase
-0.64	1.41e-13	PPP6R3	protein phosphatase 6 regulatory subunit	0.56	9.62e-06	EPS8L2	EPS8 like 2
-0.48	1.74e-13	CHAF1B	chromatin assembly factor 1 subunit	0.08	1.03e-05	SCARB2	scavenger receptor class B member 2
-0.53	1.94e-13	NCAPH	non-SMC condensin I complex subunit	0.04	1.48e-05	DLST	dihydrolipoamide S-succinyltransferase
-0.47	2.07e-13	NCAPD2	non-SMC condensin I complex subunit	0.08	1.72e-05	ITGB1	integrin subunit beta 1
-0.73	2.07e-13	EIF2B5	eukaryotic translation initiation factor 2B subunit 5	0.06	1.87e-05	TMOD3	tropomodulin 3
-0.68	4.84e-13	GEMIN4	gem nuclear organelle associated protein	0.08	2.33e-05	HSDL2	hydroxysteroid dehydrogenase like 2
-0.69	6.90e-13	POLA1	DNA polymerase alpha 1, catalytic subunit	0.11	2.60e-05	AHNAK	AHNAK nucleoprotein
-0.66	8.23e-13	NAA25	N-alpha-acetyltransferase 25, NatB	0.12	2.74e-05	PLEC	plectin
-0.68	1.05e-12	POLR3A	RNA polymerase III subunit A	0.41	3.03e-05	TAPBP	TAP binding protein
-0.7	1.34e-12	ELP1	elongator acetyltransferase complex	0.4	3.67e-05	ITPR3	inositol 1,4,5-trisphosphate receptor
-0.64	1.34e-12	XPO5</					

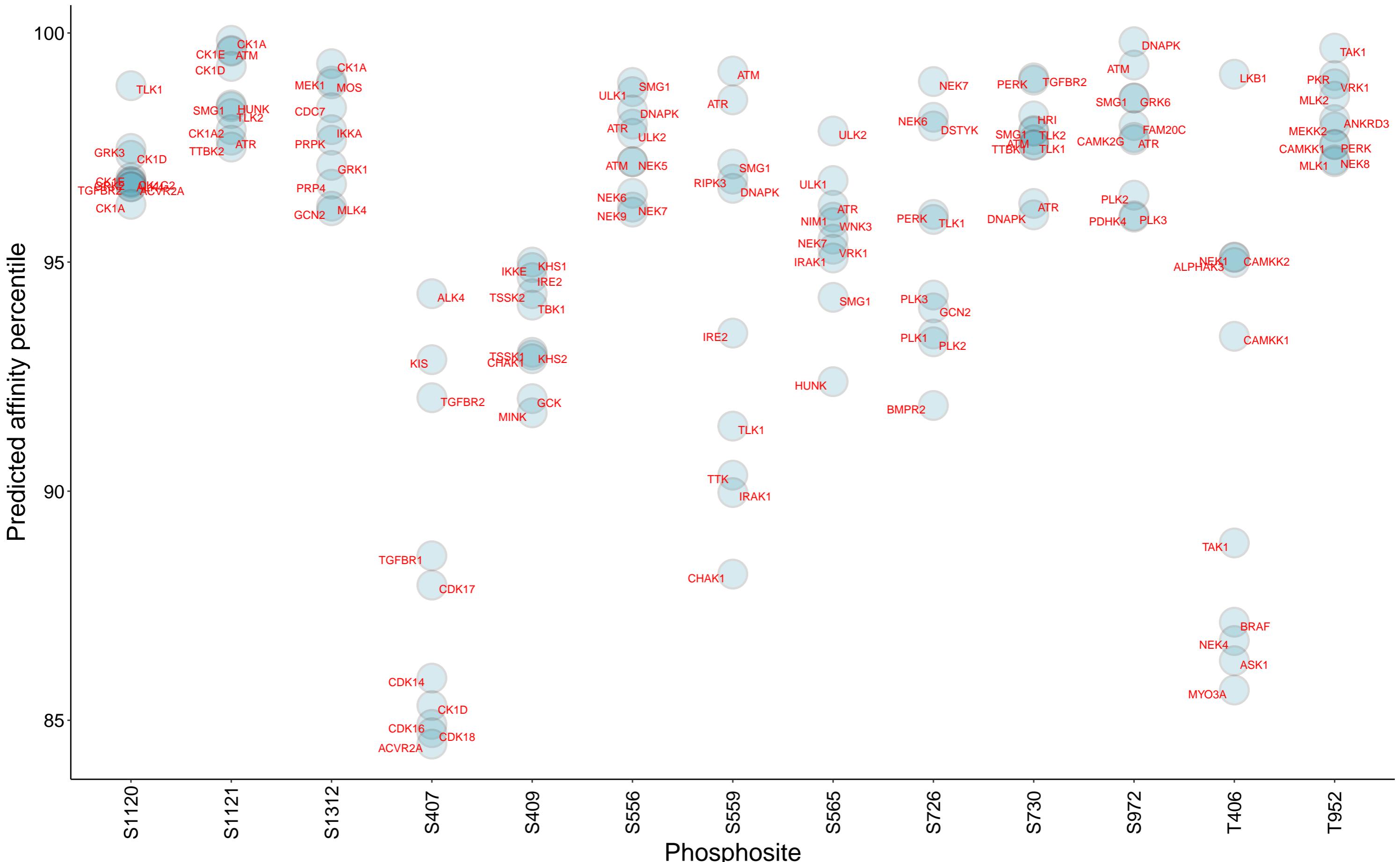
# Top 250 correlation coefficients overrepresentation, FANCI protein, DB1



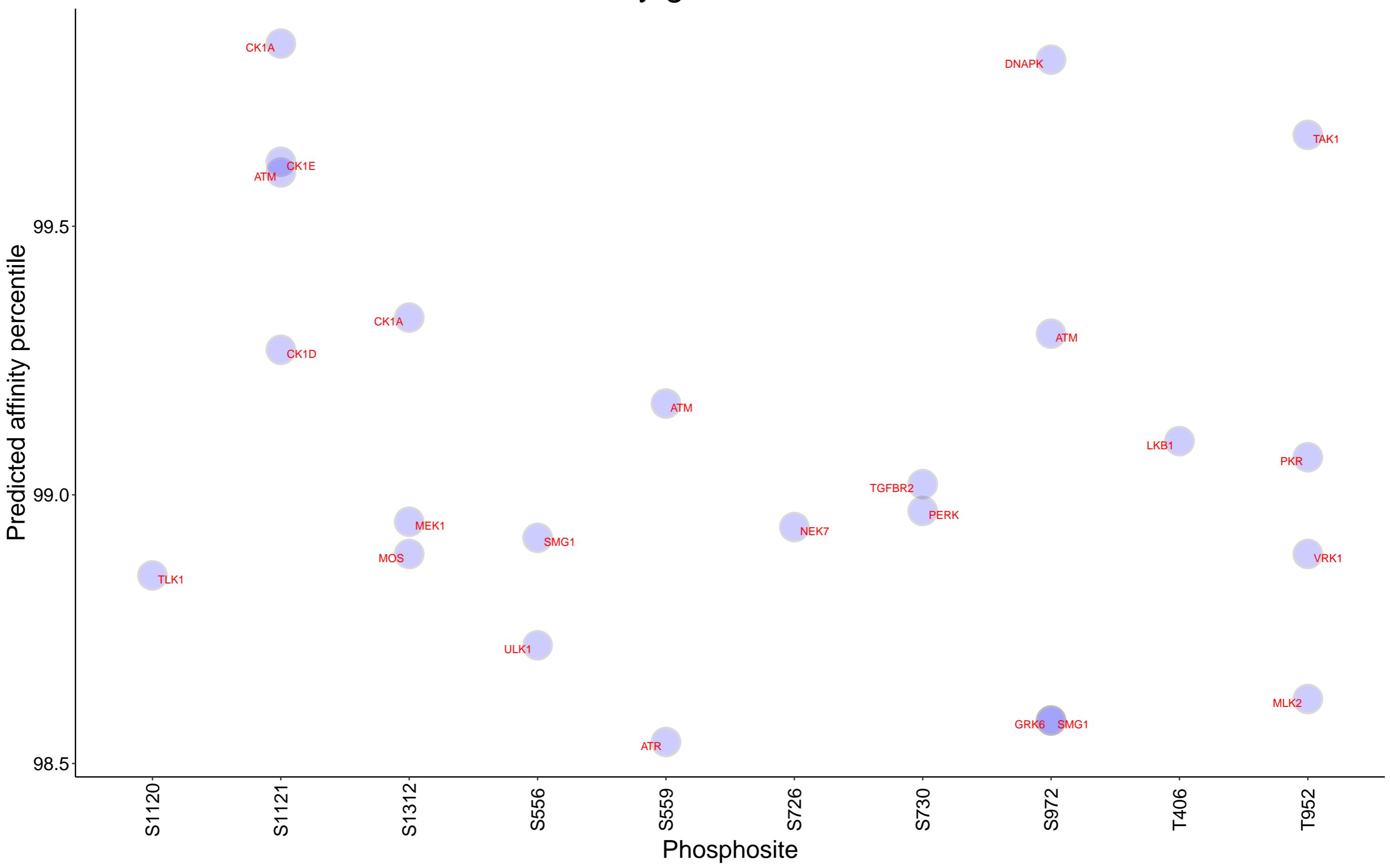
# Gene Set Enrichment analysis on protein correlation coefficients, FANCI protein, DB1



# Top 10 kinases for each phosphosite in FANCI



## Kinases with affinity greater than 98.5% to FANCI



## Top 15 positive correlation coefficients for FANCI protein by tissue, DB1

Beware of false positives in tissues with small number of samples

