

# FBXO5

Protein name: FBX5 ;

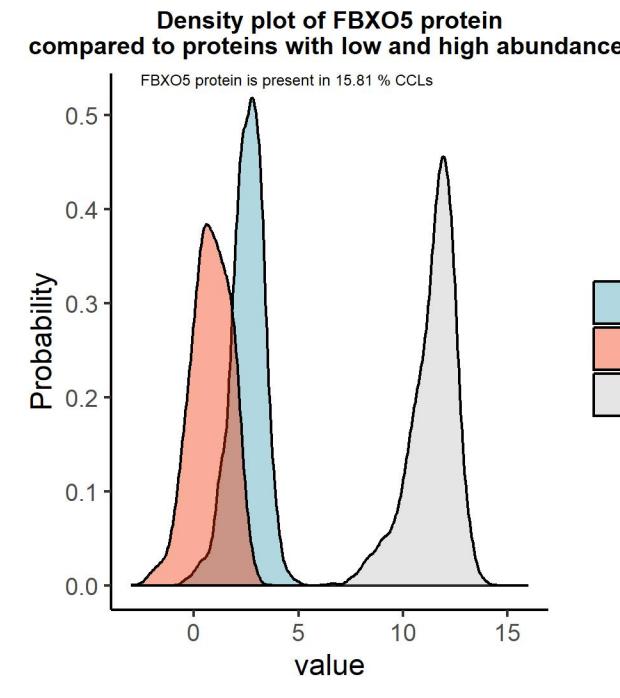
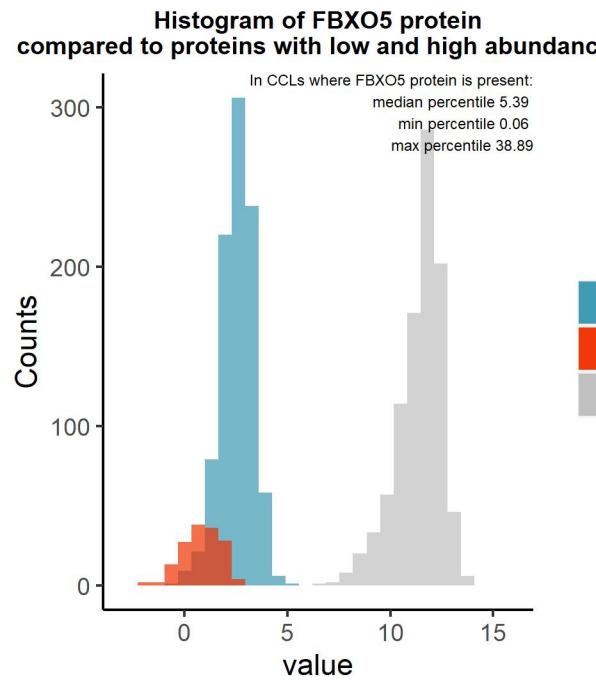
UNIPROT: Q9UKT4 ;

Gene name: F-box protein 5

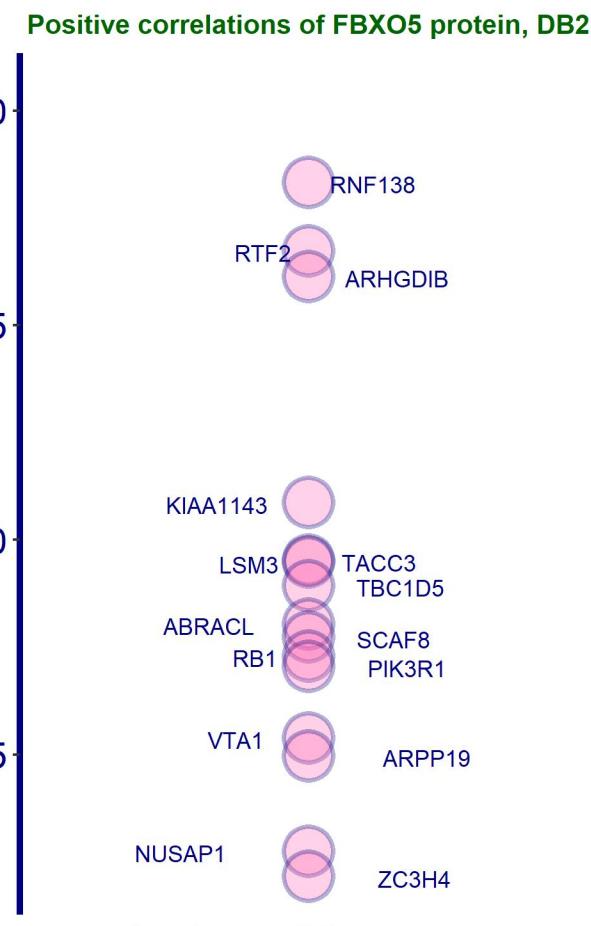
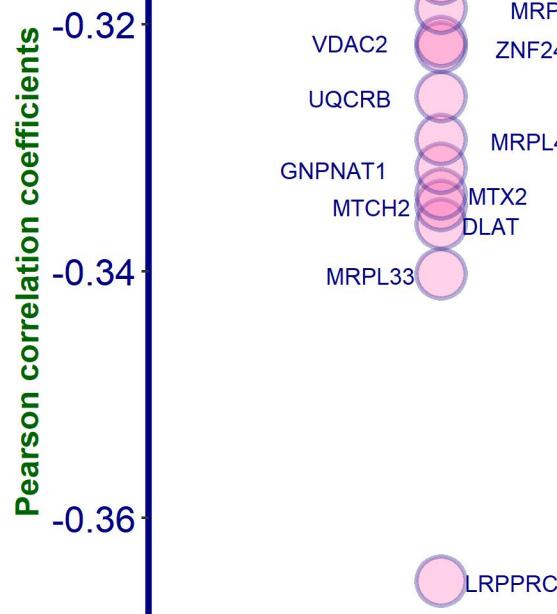
Ligandable: NA ; Ligandable\_by\_Chem: Yes ; Is\_enzyme: NA (<https://cansar.ai/>)

## Sanger Institute Protein Database 2 (DB2), protein presence is less certain

8498 proteins in same 949 CCLs

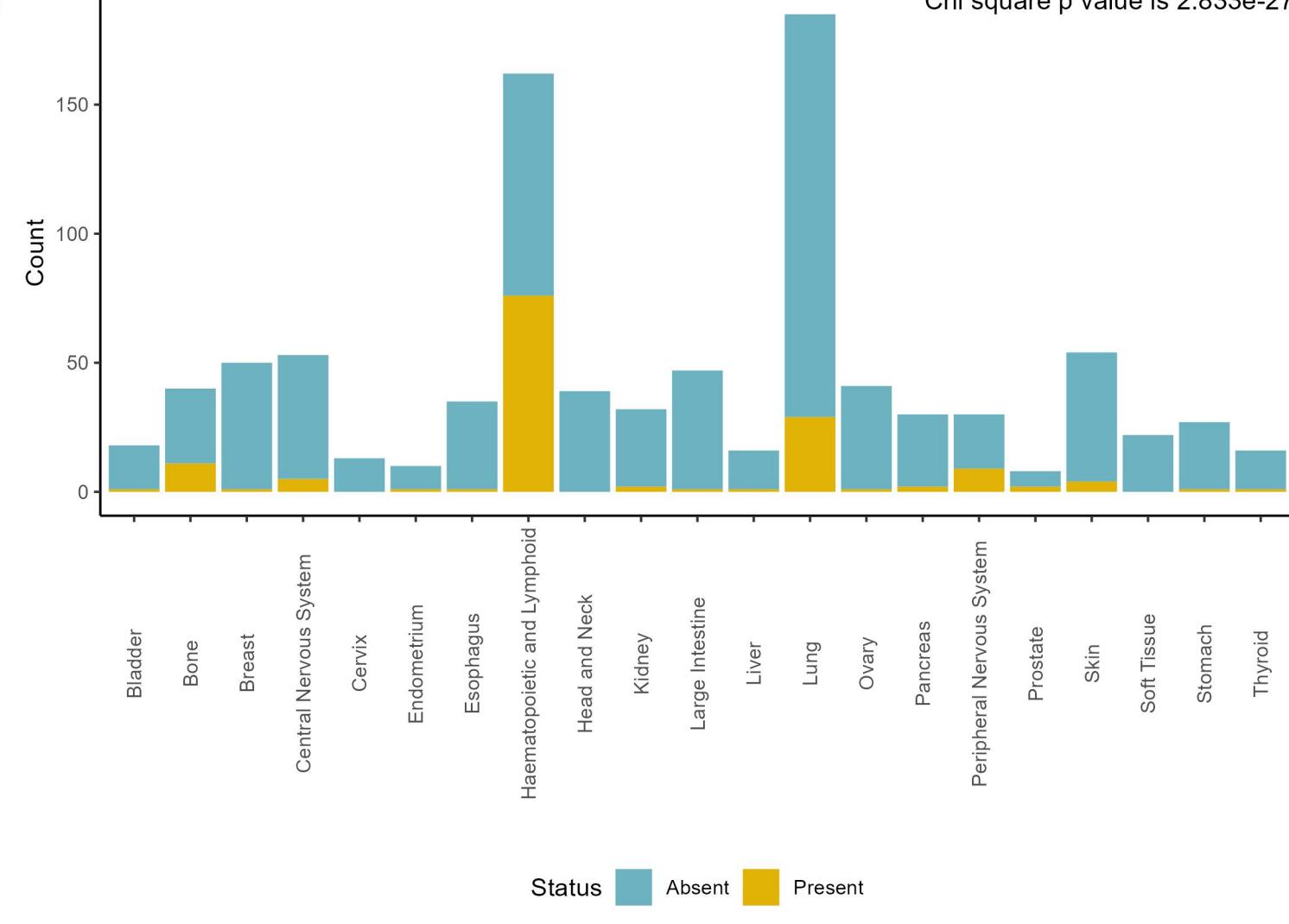
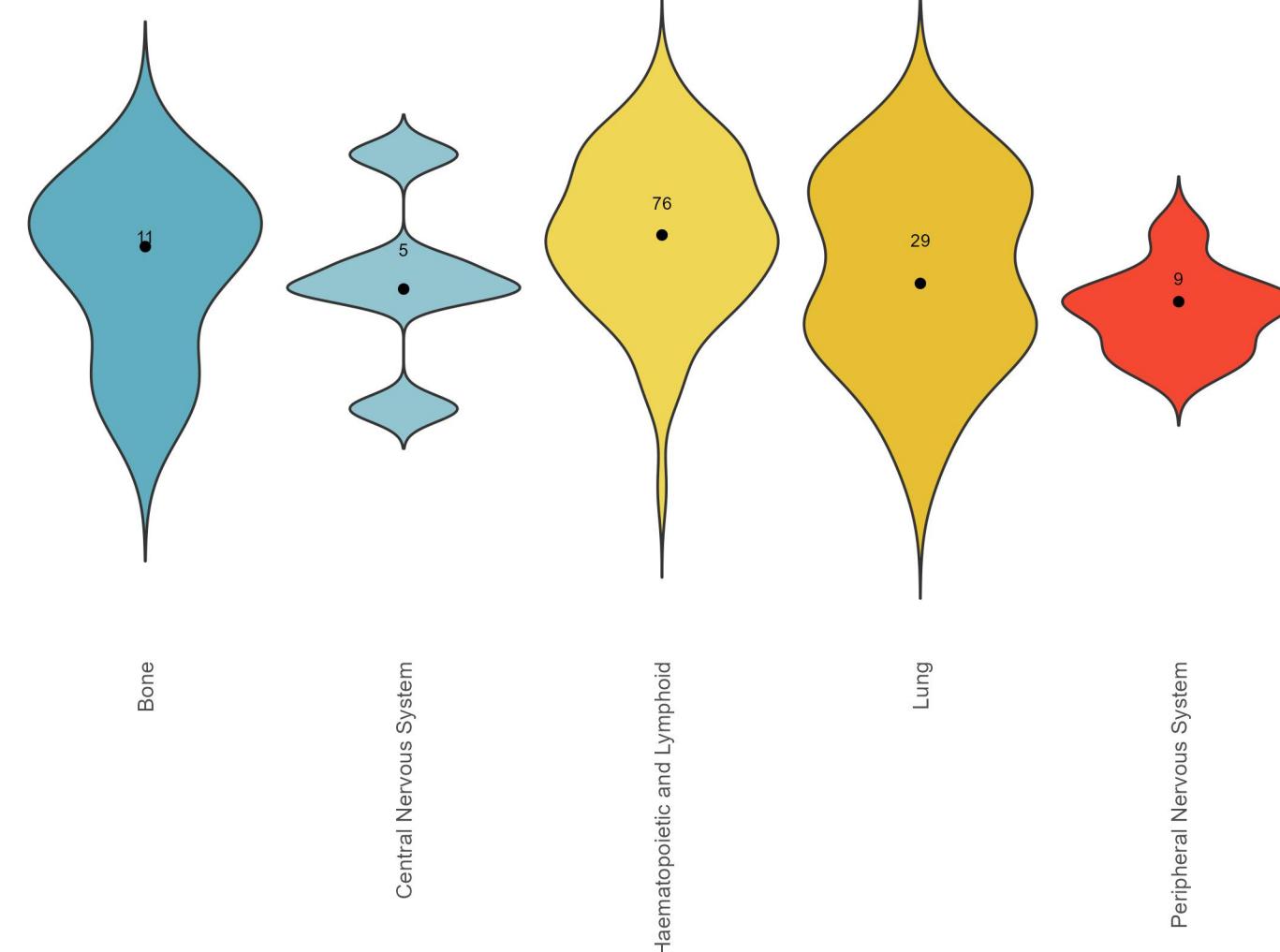


### Negative correlations of FBXO5 protein, DB2



## Amount of FBXO5 protein, number of CCLs where it is present by tissue, DB2

ANOVA p value is 4.562e-03

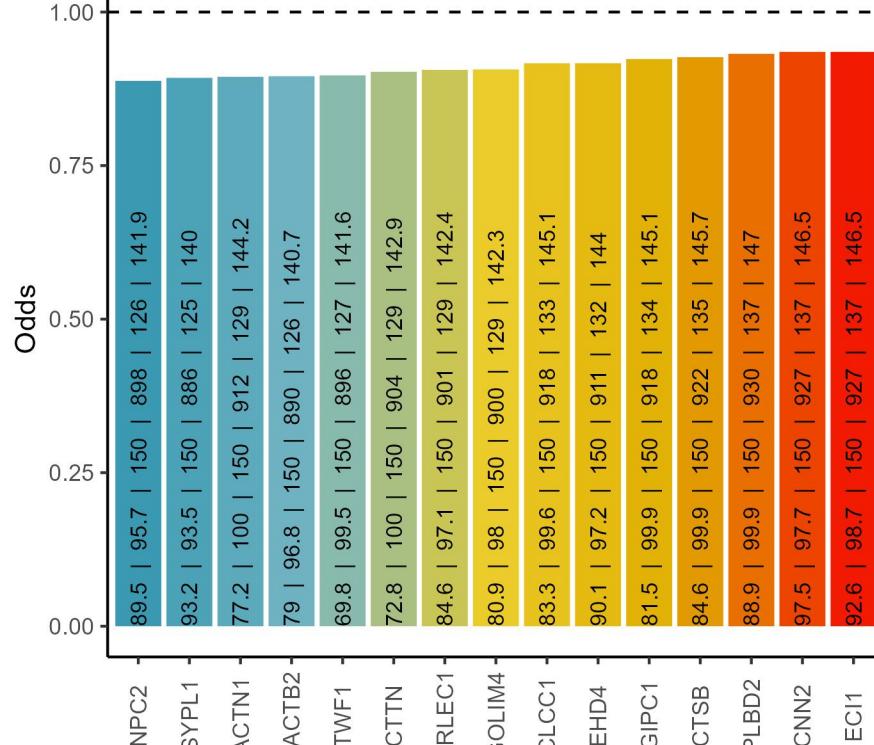


## Cooccurrence with FBXO5 protein, DB2

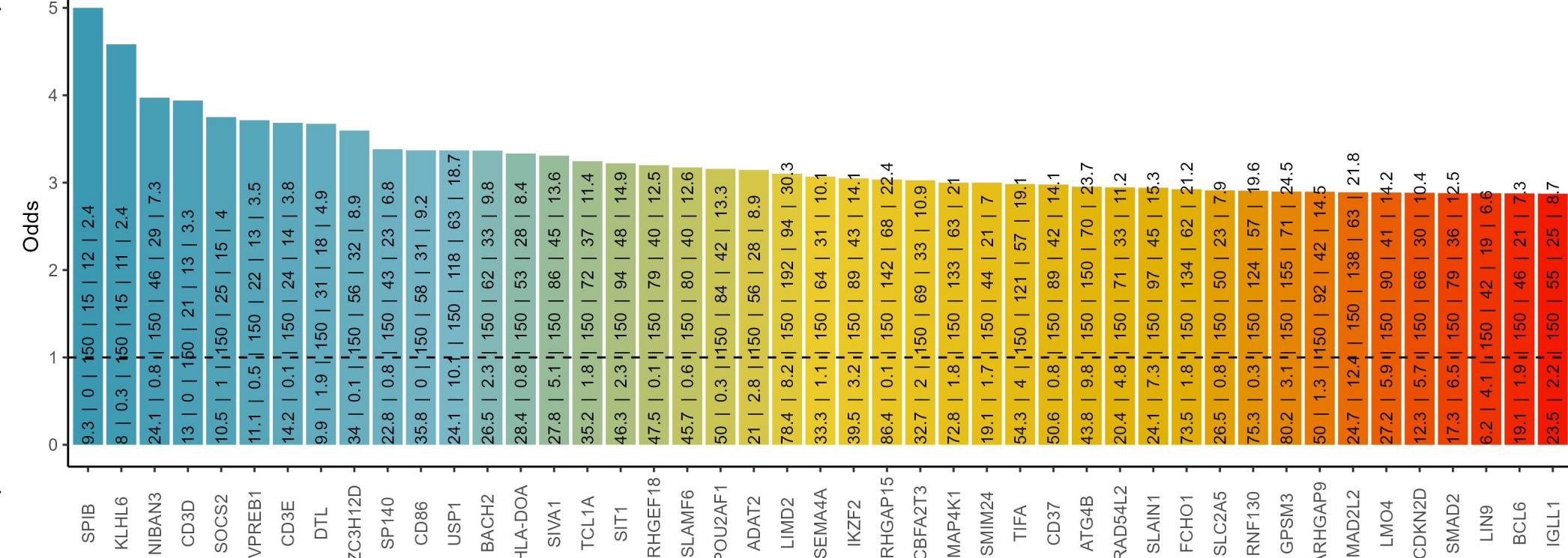
% of FBXO5 in blood cancers: 46.9 ; % of FBXO5 in solid cancers: 9.4

Text in the bars: % of Protein 2 in blood cancers | % of Protein 2 in solid cancers | incidence of FBXO5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

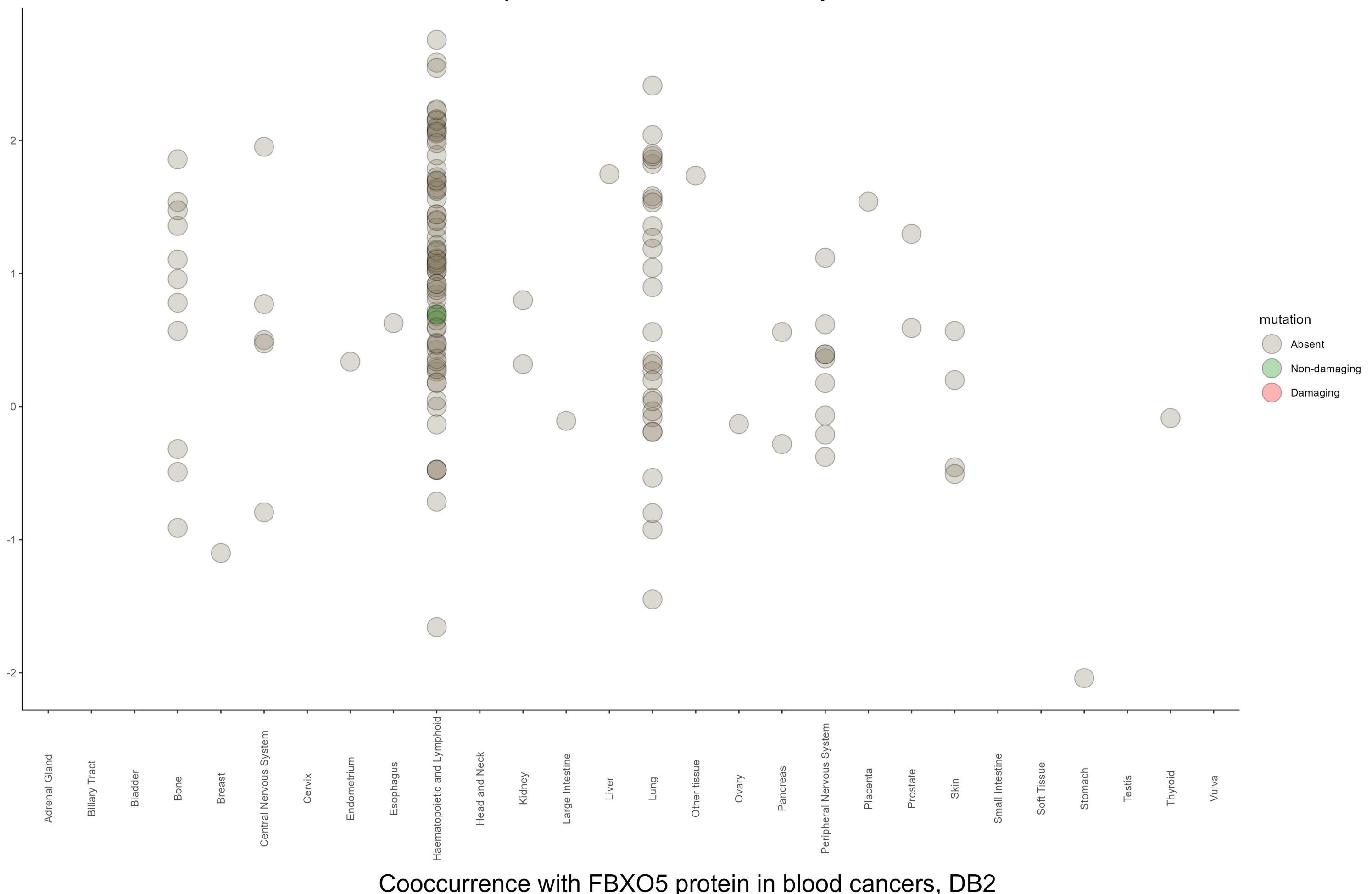
### Negative cooccurrence



### Positive cooccurrence

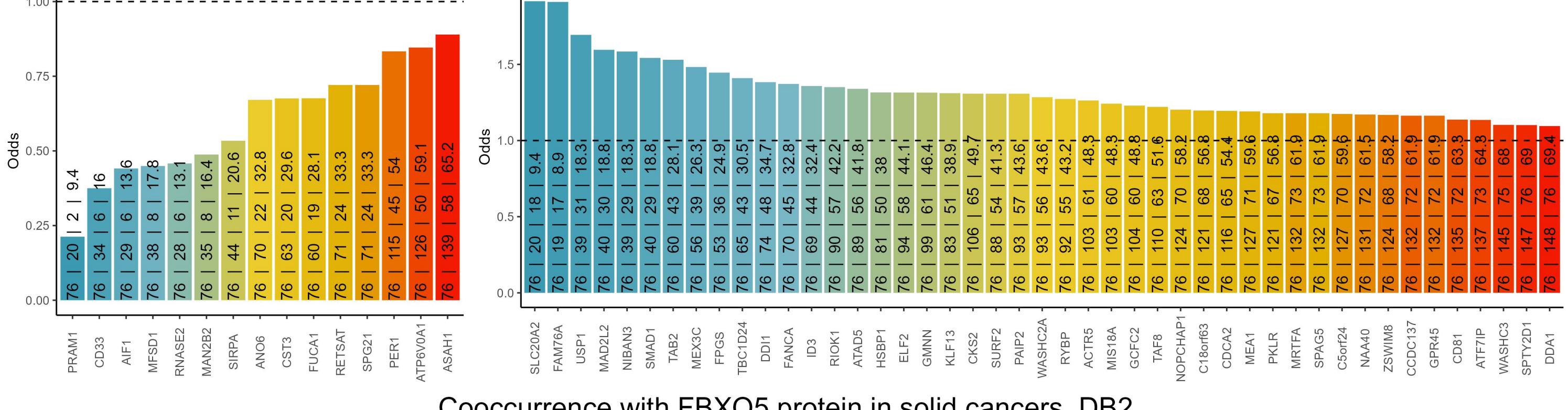


# Amount of FBXO5 protein and mutation status by tissue, DB2



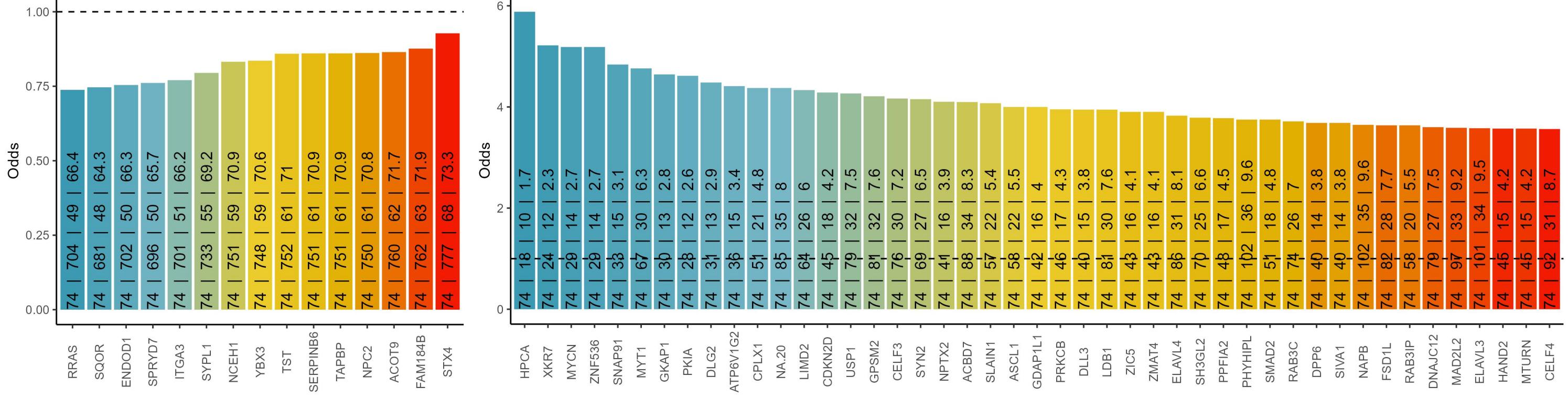
## Cooccurrence with FBXO5 protein in blood cancers, DB2

The text in the bars: incidence of FBXO5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

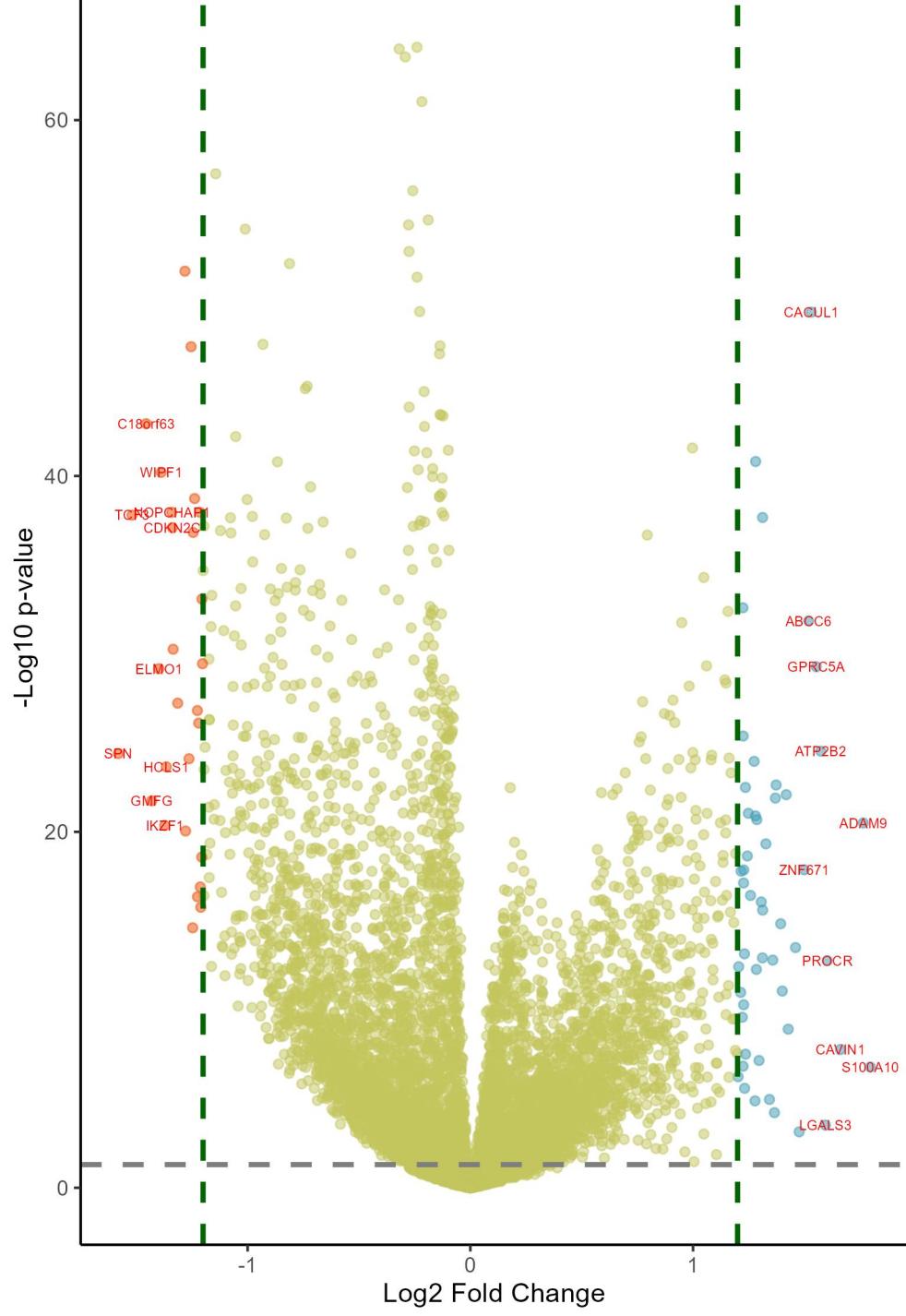


## Cooccurrence with FBXO5 protein in solid cancers, DB2

The text in the bars: incidence of FBXO5 | incidence of Protein 2 | observed cooccurrence | expected cooccurrence

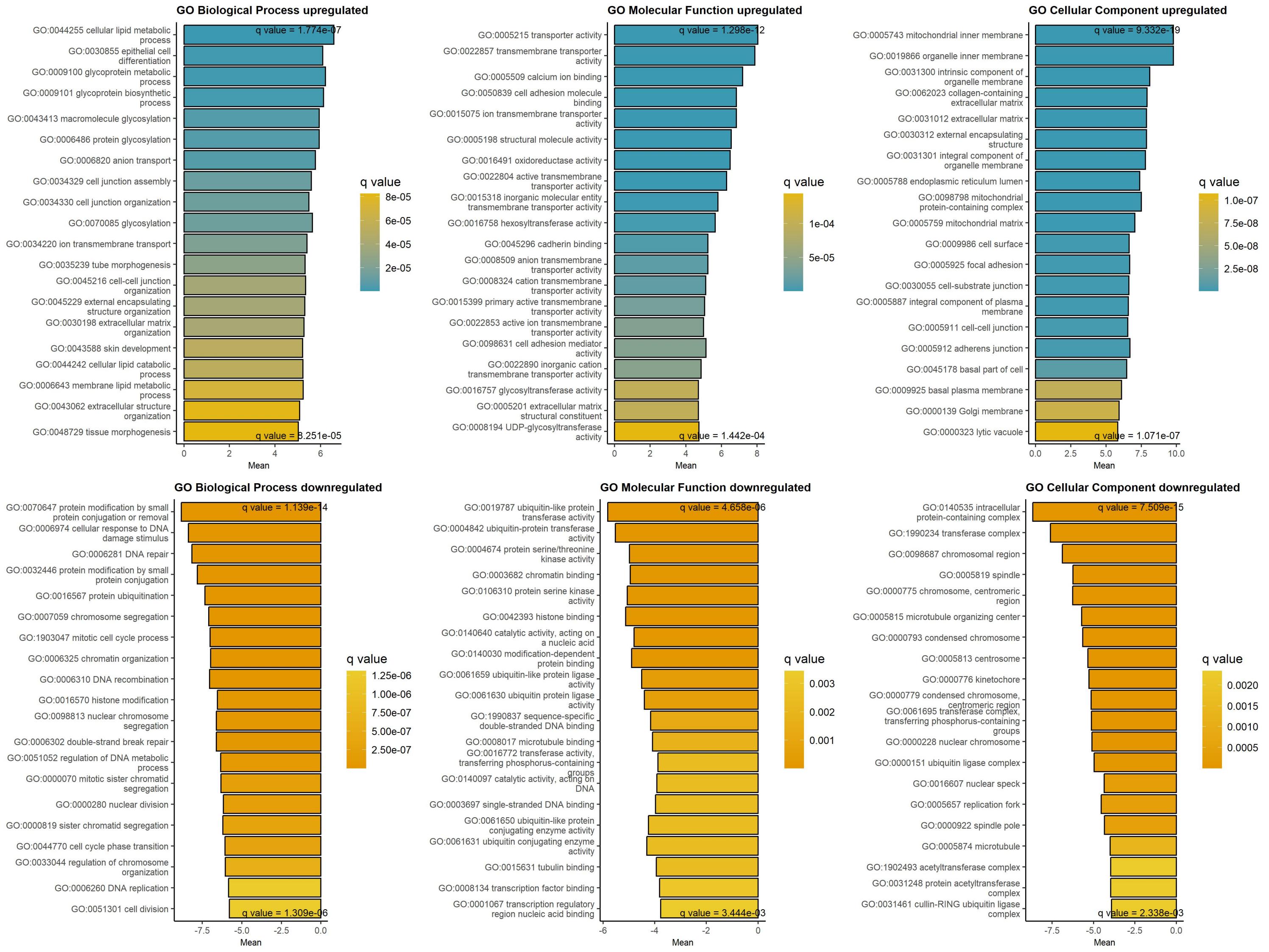


## Downregulated at low/absent FBXO5 Upregulated at low/absent FBXO5

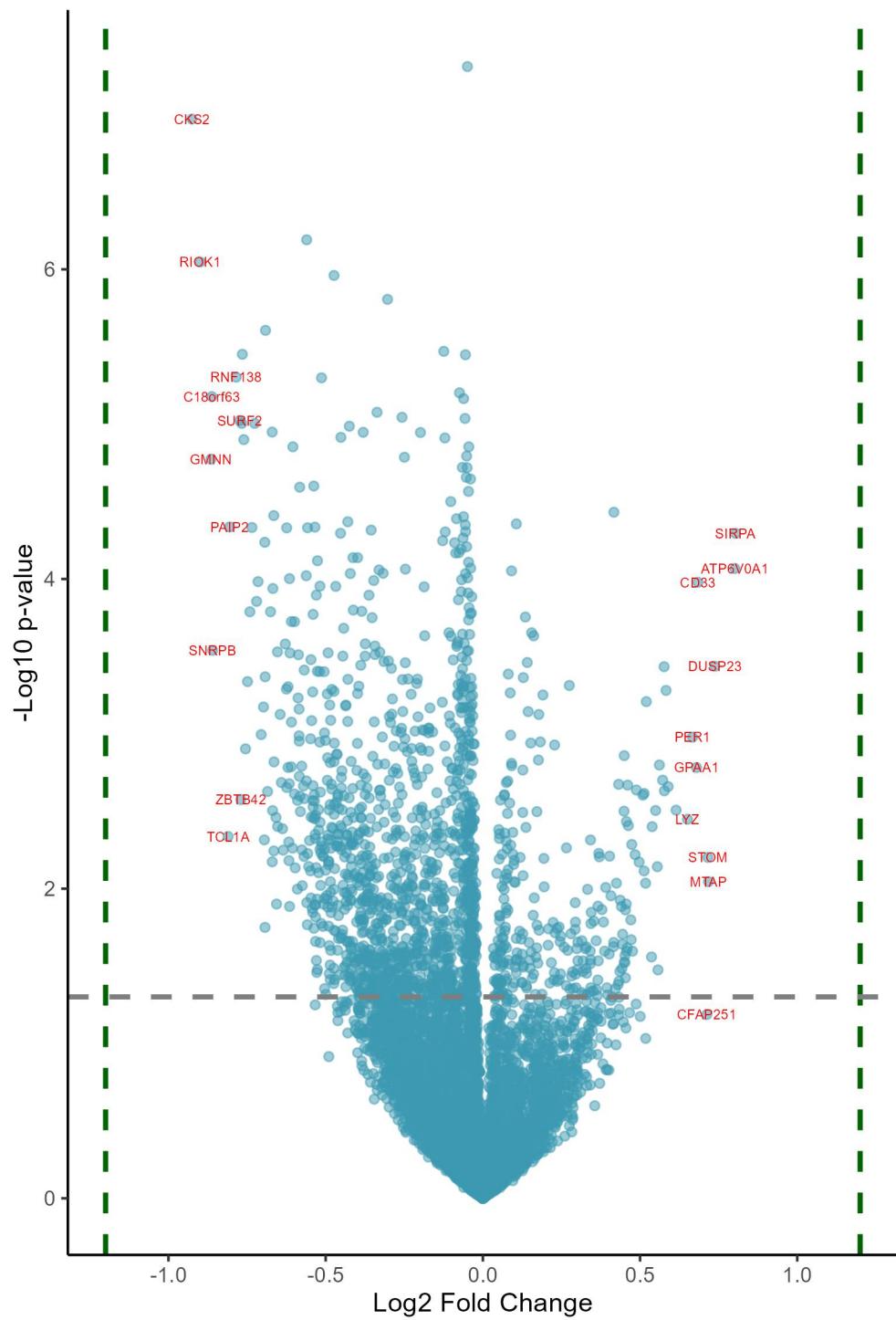


logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.58	1.34e-23	SPN	sialophorin	1.8	5.46e-07	S100A10	S100 calcium binding protein A10
-1.52	2.53e-36	TCF3	transcription factor 3	1.76	6.24e-20	ADAM9	ADAM metallopeptidase domain 9
-1.46	3.44e-41	C18orf63	chromosome 18 open reading frame 63	1.66	6.48e-08	CAVIN1	caveolae associated protein 1
-1.43	4.15e-21	GMFG	glia maturation factor gamma	1.6	1.29e-12	PROCR	protein C receptor
-1.4	4.05e-28	ELMO1	engulfment and cell motility 1	1.59	6.27e-04	LGALS3	galectin 3
-1.39	1.35e-38	WIPF1	WAS/WASL interacting protein family	1.57	1.01e-23	ATP2B2	ATPase plasma membrane Ca <sup>2+</sup> transpo
-1.37	8.53e-20	IKZF1	IKAROS family zinc finger 1	1.55	3.19e-28	GPRC5A	G protein-coupled receptor class C
-1.37	6.61e-23	HCLS1	hematopoietic cell-specific Lyn sub	1.53	3.29e-47	CACUL1	CDK2 associated cullin domain 1
-1.34	1.84e-36	NOPCHAP1	NOP protein chaperone 1	1.52	1.06e-30	ABCC6	ATP binding cassette subfamily C me
-1.34	1.05e-35	CDKN2C	cyclin dependent kinase inhibitor 2	1.5	2.00e-17	ZNF671	zinc finger protein 671
-1.33	3.64e-29	RNF138	ring finger protein 138	1.48	1.41e-03	GNG12	G protein subunit gamma 12
-1.31	2.78e-26	CARMIL2	capping protein regulator and myosi	1.46	2.63e-13	RRAS	RAS related
-1.28	1.99e-49	TYMS	thymidylate synthetase	1.43	5.43e-09	NECTIN2	nectin cell adhesion molecule 2
-1.28	1.69e-19	FGD3	FYVE, RhoGEF and PH domain containi	1.42	1.95e-21	TACSTD2	tumor associated calcium signal tra
-1.26	2.47e-23	GLCCI1	glucocorticoid induced 1	1.4	5.24e-11	EPHX1	epoxide hydrolase 1
-1.25	2.39e-45	CCNA2	cyclin A2	1.39	1.45e-14	PCLO	piccolo presynaptic cytomatrix prot
-1.25	2.35e-14	PTPRCAP	protein tyrosine phosphatase recept	1.37	6.01e-22	YAP1	Yes1 associated transcriptional reg
-1.24	1.86e-35	CORO1A	coronin 1A	1.37	2.95e-21	HMGA2	high mobility group AT-hook 2
-1.24	3.30e-37	ASF1B	anti-silencing function 1B histone	1.37	1.38e-04	ITGA3	integrin subunit alpha 3
-1.23	7.00e-26	CD300E	CD300e molecule	1.36	1.22e-12	GPX8	glutathione peroxidase 8 (putative)
-1.23	5.38e-16	MZB1	marginal zone B and B1 cell specifi	1.34	2.77e-05	NQO1	NAD(P)H quinone dehydrogenase 1
-1.22	3.26e-25	CUEDC2	CUE domain containing 2	1.33	8.30e-19	CTSL	cathepsin L
-1.22	1.84e-36	SSNA1	SS nuclear autoantigen 1	1.31	2.73e-15	GPC1	glypican 1
-1.21	1.61e-16	RCSD1	RCSD domain containing 1	1.31	3.27e-36	GGCX	gamma-glutamyl carboxylase
-1.21	1.92e-15	SASH3	SAM and SH3 domain containing 3	1.31	9.21e-13	MMP14	matrix metallopeptidase 14
-1.21	4.23e-18	GMNN	geminin DNA replication inhibitor	1.31	1.00e-15	MISP	mitotic spindle positioning
-1.21	7.47e-32	SKA3	spindle and kinetochore associated	1.3	2.46e-07	S100A16	S100 calcium binding protein A16
-1.2	2.23e-28	RNASEL	ribonuclease L	1.29	4.22e-20	RAB32	RAB32, member RAS oncogene family
-1.2	2.17e-33	TLK2	tousled like kinase 2	1.28	3.80e-12	YES1	YES proto-oncogene 1, Src family ty

## GAGE analysis on upregulated and downregulated proteins at low/absent FBXO5 protein, DB2

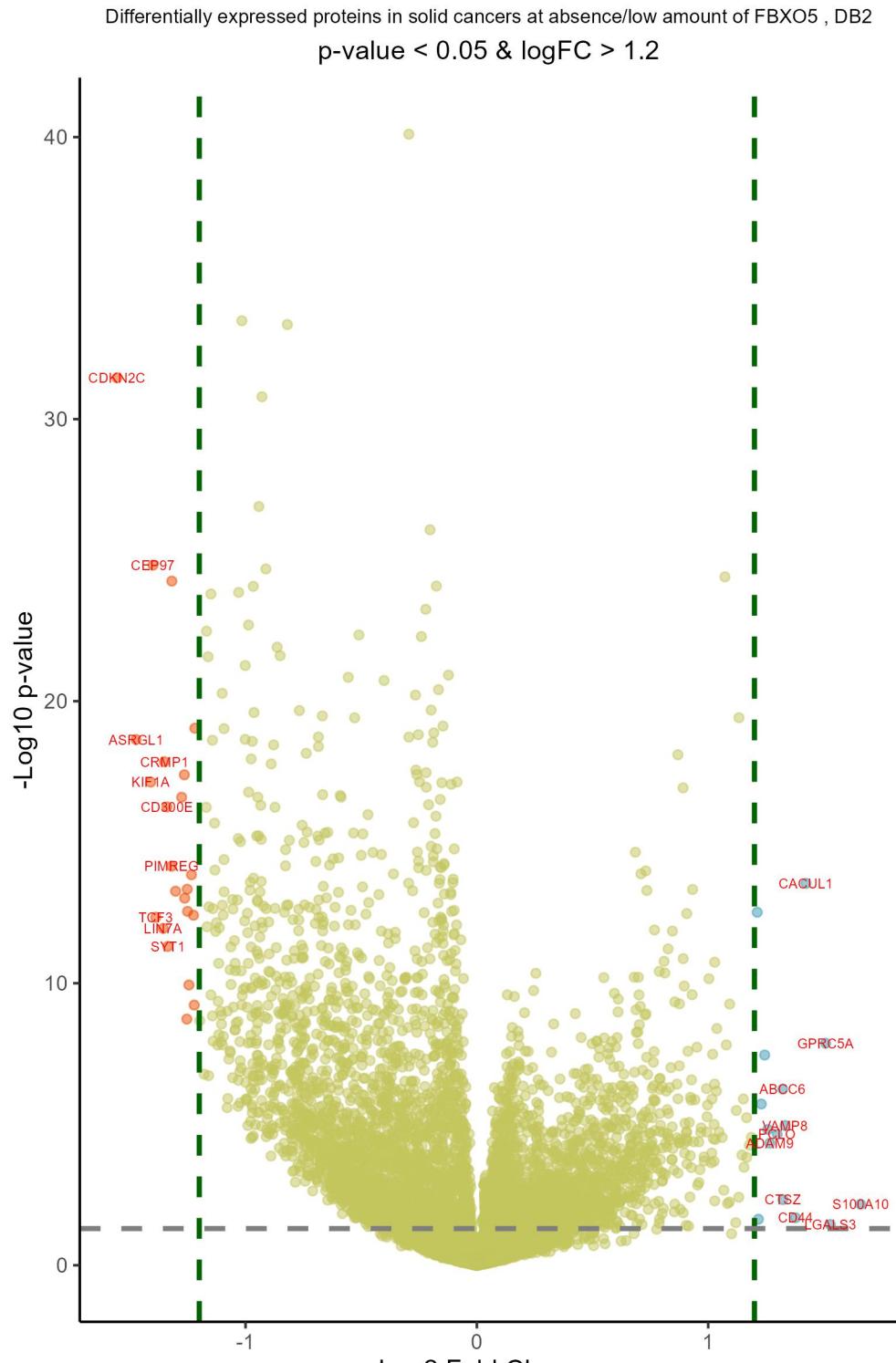


p-value &lt; 0.05 &amp; logFC &gt; 1.2



Downregulated in blood cancers at low/absent FBXO5 Upregulated in blood cancers at low/absent FBXO5

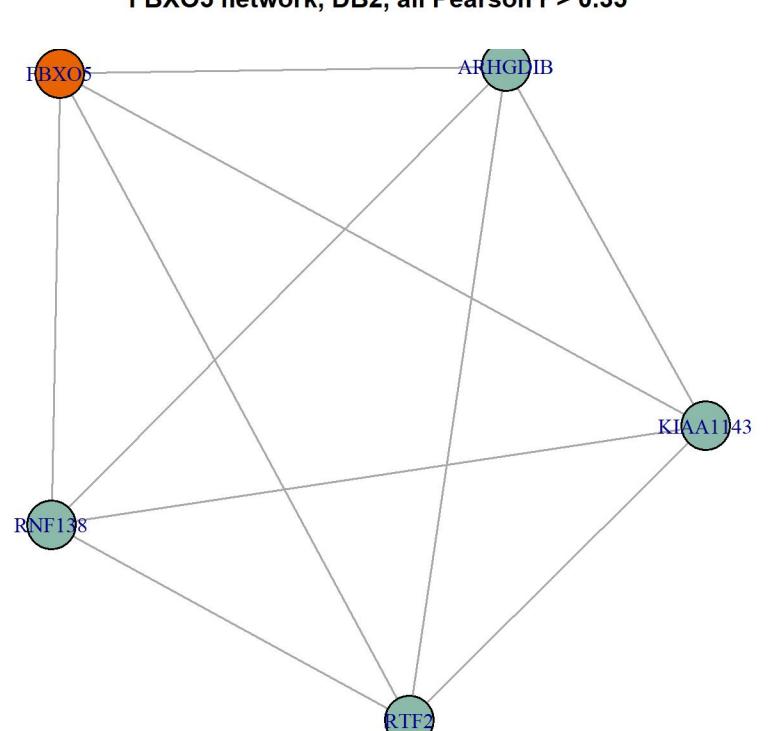
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.93	2.98e-04	CKS2	CDC28 protein kinase regulatory sub	0.8	7.19e-03	SIRPA	signal regulatory protein alpha
-0.9	1.50e-03	RIOK1	RIO kinase 1	0.8	9.74e-03	ATP6V0A1	ATPase H <sup>+</sup> transporting V0 subunit a
-0.87	4.14e-03	GMNN	geminin DNA replication inhibitor	0.74	2.10e-02	DUSP23	dual specificity phosphatase 23
-0.86	3.57e-03	C18orf63	chromosome 18 open reading frame 63	0.72	1.06e-01	MTAP	methylthioadenosine phosphorylase
-0.86	1.90e-02	SNRBP	small nuclear ribonucleoprotein pol	0.72	8.65e-02	STOM	stomatin
-0.81	7.39e-02	TCL1A	TCL1 family AKT coactivator A	0.71	2.96e-01	CFAP251	cilia and flagella associated prote
-0.81	7.19e-03	PAIP2	poly(A) binding protein interacting	0.68	1.02e-02	CD33	CD33 molecule
-0.78	3.23e-03	RNF138	ring finger protein 138	0.68	4.51e-02	GPAA1	glycosylphosphatidylinositol anchor
-0.77	3.63e-03	SURF2	surfeit 2	0.67	3.51e-02	PER1	period circadian regulator 1
-0.77	5.79e-02	ZBTB42	zinc finger and BTB domain containi	0.65	6.61e-02	LYZ	lysozyme
-0.77	3.63e-03	NOPCHAP1	NOP protein chaperone 1	0.61	6.28e-02	EPHX1	epoxide hydrolase 1
-0.77	2.71e-03	GPR45	G protein-coupled receptor 45	0.59	5.27e-02	SLC25A19	solute carrier family 25 member 19
-0.76	3.63e-03	RNF220	ring finger protein 220	0.58	2.46e-02	ASAHI	N-acylsphingosine amidohydrolase 1
-0.75	3.83e-02	MLLT11	MLLT11 transcription factor 7 cofac	0.58	5.42e-02	DUSP3	dual specificity phosphatase 3
-0.75	2.35e-02	NIBAN3	niban apoptosis regulator 3	0.58	2.10e-02	AIF1	allograft inflammatory factor 1
-0.74	1.34e-02	TSHZ2	teashirt zinc finger homeobox 2	0.57	5.03e-02	CST3	cystatin C
-0.73	7.19e-03	MAD2L2	mitotic arrest deficient 2 like 2	0.56	4.42e-02	SPG21	SPG21 abhydrolase domain containing
-0.73	3.63e-03	KCTD5	potassium channel tetramerization d	0.56	2.15e-01	BORCS8-MEF2B	BORCS8-MEF2B readthrough
-0.72	1.20e-02	TAB2	TGF-beta activated kinase 1 (MAP3K7)	0.55	9.33e-02	ZBTB48	zinc finger and BTB domain containi
-0.72	1.02e-02	MLXIPL	MLX interacting protein like	0.55	6.28e-02	PRTN3	proteinase 3
-0.71	3.47e-02	ZAP70	zeta chain of T cell receptor assoc	0.54	7.05e-02	PGPEP1	pyroglutamyl-peptidase I
-0.7	2.76e-02	DBN1	drebrin 1	0.54	1.95e-01	CSTA	cystatin A
-0.7	7.57e-02	SEPTIN1	septin 1	0.52	2.67e-02	TIMM22	translocase of inner mitochondrial
-0.69	7.74e-03	PWWP2A	PWWP domain containing 2A	0.52	3.46e-01	LGALS3	galectin 3
-0.69	1.54e-01	MZB1	marginal zone B and B1 cell specifi	0.52	1.08e-01	NIPSNAP3A	nipsnap homolog 3A
-0.69	2.29e-02	ASTN1	astrotactin 1	0.51	5.58e-02	SYNGR1	synaptogyrin 1
-0.69	2.59e-03	SPAG5	sperm associated antigen 5	0.51	9.65e-02	IL18	interleukin 18
-0.68	5.47e-02	LEF1	lymphoid enhancer binding factor 1	0.51	5.61e-02	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase
-0.68	1.34e-02	UNG	uracil DNA glycosylase	0.5	3.00e-01	LGALS1	galectin 1



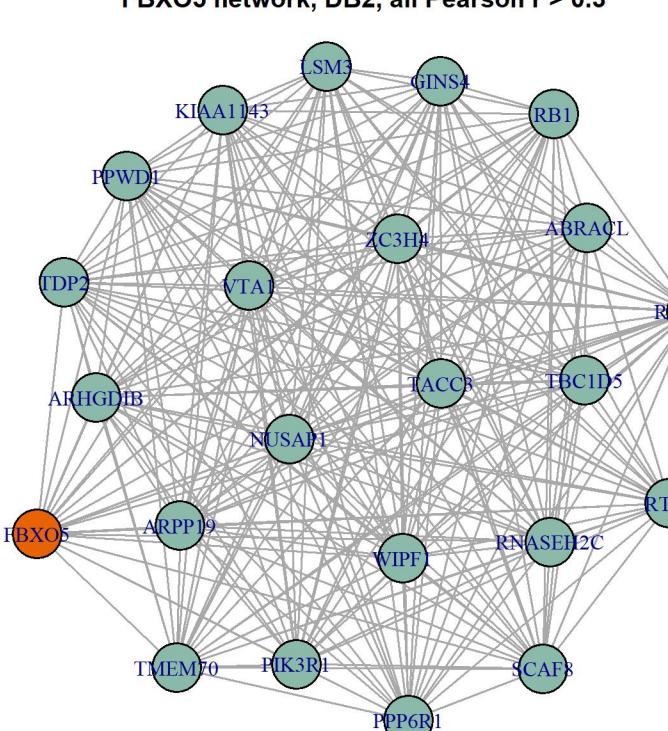
Downregulated in solid cancers at low/absent FBXO5 Upregulated in solid cancers at low/absent FBXO5

logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.56	5.74e-29	CDKN2C	cyclin dependent kinase inhibitor 2	1.66	1.73e-02	S100A10	S100 calcium binding protein A10
-1.47	4.17e-17	ASRGL1	asparaginase and isoaspartyl peptid	1.53	6.95e-02	LGALS3	galectin 3
-1.41	9.81e-16	KIF1A	kinesin family member 1A	1.51	1.94e-07	GPRC5A	G protein-coupled receptor class C
-1.4	1.39e-22	CEP97	centrosomal protein 97	1.42	1.75e-12	CACUL1	CDK2 associated cullin domain 1
-1.39	2.00e-11	TCF3	transcription factor 3	1.38	4.35e-02	CD44	CD44 molecule (Indian blood group)
-1.36	4.41e-11	LIN7A	lin-7 homolog A, crumbs cell polarit	1.33	7.02e-05	VAMP8	vesicle associated membrane protein
-1.35	2.13e-16	CRMP1	collapsin response mediator protein	1.32	1.25e-02	CTSZ	cathepsin Z
-1.34	6.12e-15	CD300E	CD300e molecule	1.32	5.38e-06	ABCC6	ATP binding cassette subfamily C me
-1.34	1.73e-10	SYT1	synaptotagmin 1	1.3	1.26e-04	PCLO	piccolo presynaptic cytomatrix prot
-1.32	4.95e-13	PIMREG	PICALM interacting mitotic regulato	1.27	2.38e-04	ADAM9	ADAM metallopeptidase domain 9
-1.32	3.85e-22	UCHL1	ubiquitin C-terminal hydrolase L1	1.26	9.14e-05	ENDOD1	endonuclease domain containing 1
-1.3	3.13e-12	SKP2	S-phase kinase associated protein 2	1.24	4.55e-07	LPCAT2	lysophosphatidylcholine acyltransfe
-1.28	2.92e-15	GPSM1	G protein signaling modulator 1	1.23	1.54e-05	TAP2	transporter 2, ATP binding cassette
-1.26	5.68e-16	TLK2	tousled like kinase 2	1.22	4.81e-02	ITGA3	integrin subunit alpha 3
-1.26	5.20e-12	C18orf63	chromosome 18 open reading frame 63	1.21	1.41e-11	KRT74	keratin 74
-1.25	3.36e-08	CRABP1	cellular retinoic acid binding prot	1.19	1.58e-04	MISP	mitotic spindle positioning
-1.25	2.76e-12	UBE2B	ubiquitin conjugating enzyme E2 B	1.18	2.76e-04	RRAS	RAS related
-1.25	1.33e-11	SEPTIN3	septin 3	1.17	6.44e-04	ATP2B2	ATPase plasma membrane Ca <sup>2+</sup> transpo
-1.24	2.92e-09	MLLT11	MLLT11 transcription factor 7 cofac	1.17	4.08e-05	TAP1	transporter 1, ATP binding cassette
-1.23	9.23e-13	NOPCHAP1	NOP protein chaperone 1	1.15	1.29e-03	ZNF671	zinc finger protein 671
-1.22	1.73e-11	SAPCD2	suppressor APC domain containing 2	1.15	1.09e-05	SP100	SP100 nuclear antigen
-1.22	1.24e-08	STMN3	stathmin 3	1.15	5.48e-04	TACSTD2	tumor associated calcium signal tra
-1.22	1.95e-17	NCAM1	neural cell adhesion molecule 1	1.13	8.77e-18	PRSS8	serine protease 8
-1.2	3.74e-08	GLCCI1	glucocorticoid induced 1	1.13	1.06e-02	SQOR	sulfide quinone oxidoreductase
-1.18	1.85e-06	CELF4	CUGBP Elav-like family member 4	1.12	2.45e-05	KRT80	keratin 80
-1.17	6.16e-15	GTSE1	G2 and S-phase expressed 1	1.12	6.11e-02	CAVIN1	caveolae associated protein 1
-1.17	1.45e-20	CDC34	cell division cycle 34, ubiquitin c	1.1	1.28e-01	LGALS1	galectin 1
-1.17	3.91e-11	ATXN7L3B	ataxin 7 like 3B	1.09	1.16e-08	SUMF1	sulfatase modifying factor 1
-1.16	9.26e-20	CKS1B	CDC28 protein kinase regulatory sub	1.09	1.48e-02	NCEH1	neutral cholesterol ester hydrolase

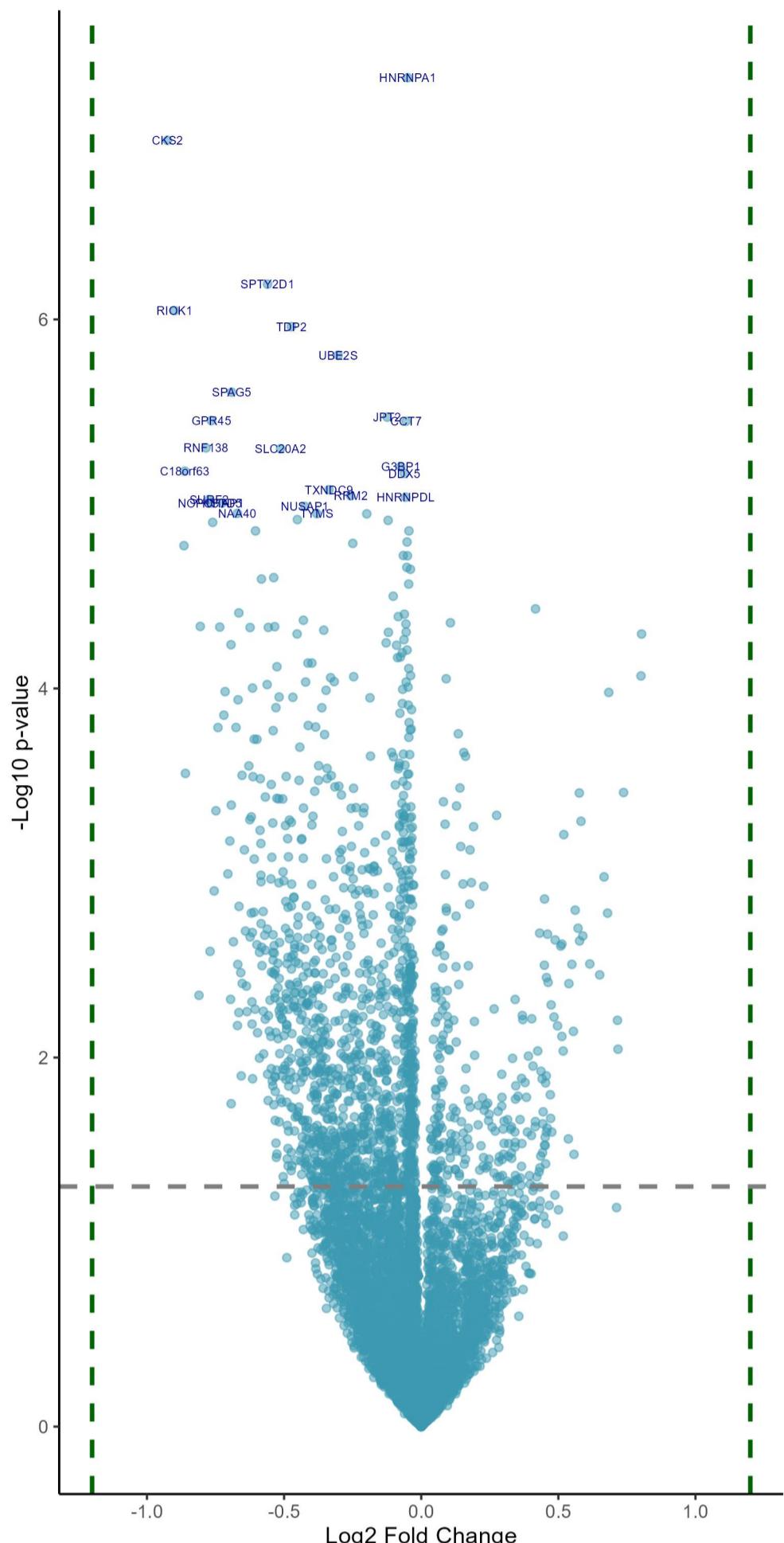
FBXO5 network, DB2, all Pearson r &gt; 0.35



FBXO5 network, DB2, all Pearson r &gt; 0.3

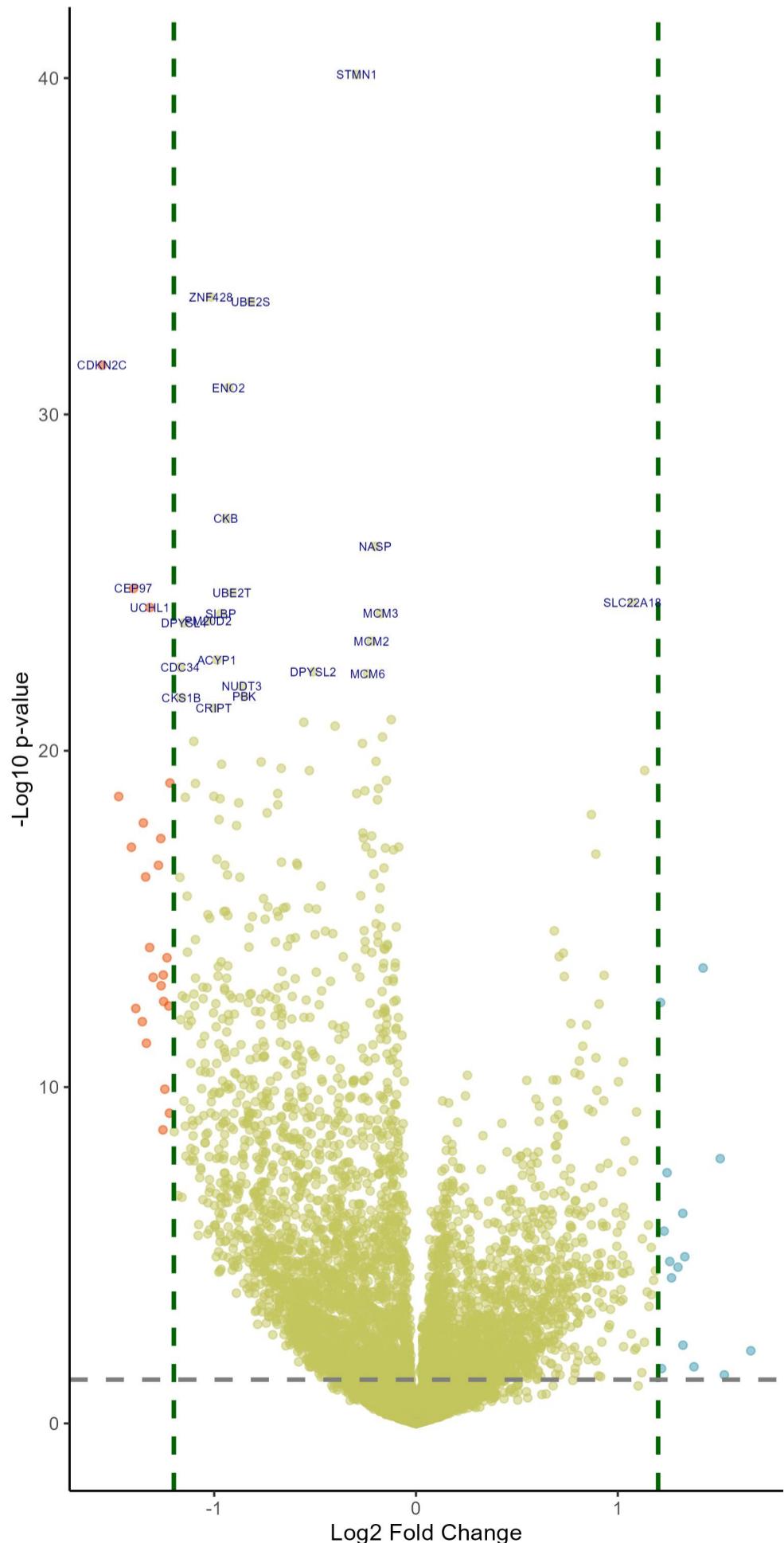


Differentially expressed proteins in blood cancers at absence/low amount of FBXO5 , DB2  
p-value < 0.05 & logFC > 1.2



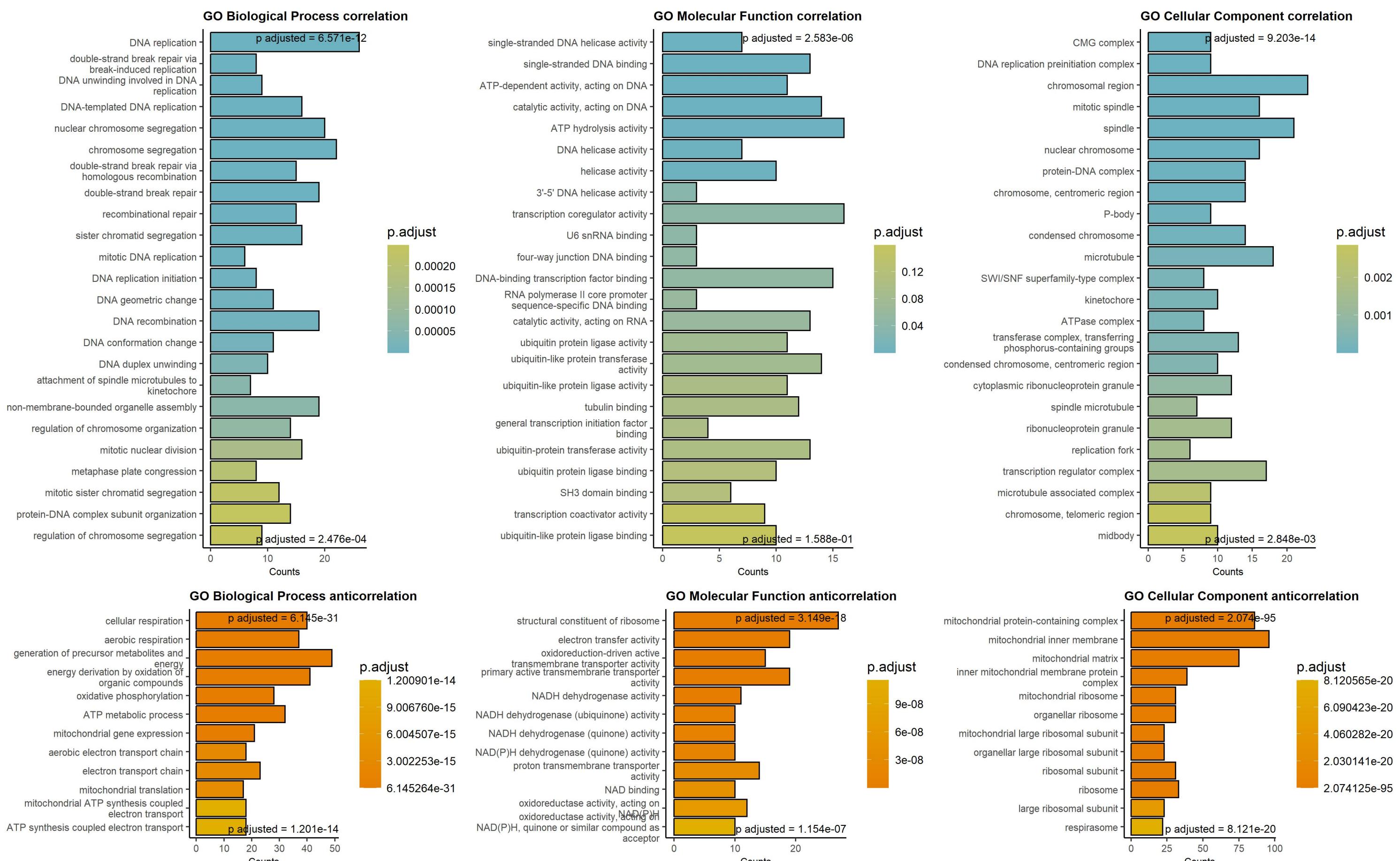
Sorted by p values!							
Downregulated in blood cancers at low/absent FBXO5				Upregulated in blood cancers at low/absent FBXO5			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.05	2.05e-04	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	0.42	7.19e-03	PRAM1	PML-RARA regulated adaptor molecule
-0.93	2.98e-04	CKS2	CDC28 protein kinase regulatory subunit 2	0.11	7.19e-03	UGGT1	UDP-glucose glycoprotein glucosyltransferase 1
-0.56	1.35e-03	SPTY2D1	SPT2 chromatin protein domain containing 2	0.8	7.19e-03	SIRPA	signal regulatory protein alpha
-0.9	1.50e-03	RIOK1	RIO kinase 1	0.8	9.74e-03	ATP6V0A1	ATPase H <sup>+</sup> transporting V0 subunit a
-0.47	1.53e-03	TDP2	tyrosyl-DNA phosphodiesterase 2	0.09	9.75e-03	CLPP	caseinolytic mitochondrial matrix peptidase
-0.3	1.87e-03	UBE2S	ubiquitin conjugating enzyme E2 S	0.68	1.02e-02	CD33	CD33 molecule
-0.69	2.59e-03	SPAG5	sperm associated antigen 5	0.14	1.39e-02	COASY	Coenzyme A synthase
-0.12	2.71e-03	JPT2	Jupiter microtubule associated homo	0.16	1.65e-02	MLEC	malectin
-0.77	2.71e-03	GPR45	G protein-coupled receptor 45	0.16	1.66e-02	RNPEP	arginyl aminopeptidase
-0.06	2.71e-03	CCT7	chaperonin containing TCP1 subunit	0.14	2.02e-02	MYDGF	myeloid derived growth factor
-0.78	3.23e-03	RNF138	ring finger protein 138	0.74	2.10e-02	DUSP23	dual specificity phosphatase 23
-0.51	3.23e-03	SLC20A2	solute carrier family 20 member 2	0.58	2.10e-02	AIF1	allograft inflammatory factor 1
-0.07	3.57e-03	G3BP1	G3BP stress granule assembly factor	0.08	2.23e-02	CLIP1	CAP-Gly domain containing linker protein
-0.86	3.57e-03	C18orf63	chromosome 18 open reading frame 63	0.13	2.29e-02	LAMTOR3	late endosomal/lysosomal adaptor, MAP62 and XPO1
-0.06	3.57e-03	DDX5	DEAD-box helicase 5	0.27	2.40e-02	ATP13A1	ATPase 13A1
-0.34	3.63e-03	TXNDC9	thioredoxin domain containing 9	0.58	2.46e-02	ASAHI	N-acylsphingosine amidohydrolase 1
-0.26	3.63e-03	RRM2	ribonucleotide reductase regulatory	0.09	2.50e-02	LAMP1	lysosomal associated membrane protein 1
-0.06	3.63e-03	HNRNPDL	heterogeneous nuclear ribonucleoprotein D-like	0.19	2.50e-02	ACADVL	acyl-CoA dehydrogenase very long chain
-0.77	3.63e-03	SURF2	surfeit 2	0.52	2.67e-02	TIMM22	translocase of inner mitochondrial membrane
-0.73	3.63e-03	KCTD5	potassium channel tetramerization domain containing 5	0.14	2.86e-02	TPP1	tripeptidyl peptidase 1
-0.77	3.63e-03	NOPCHAP1	NOP protein chaperone 1	0.18	2.93e-02	SEC23B	SEC23 homolog B, COPII coat complex
-0.42	3.63e-03	NUSAP1	nucleolar and spindle associated protein 1	0.09	3.47e-02	DNAJB11	DnaJ heat shock protein family (Hsp40) member B11
-0.67	3.63e-03	NAA40	N-alpha-acetyltransferase 40, NatD	0.67	3.51e-02	PER1	period circadian regulator 1
-0.38	3.63e-03	TYMS	thymidylate synthetase	0.18	3.66e-02	MAN2B1	mannosidase alpha class 2B member 1
-0.2	3.63e-03	GINS4	GINS complex subunit 4	0.15	3.70e-02	ARF4	ADP ribosylation factor 4
-0.45	3.63e-03	PCLAF	PCNA clamp associated factor	0.23	3.74e-02	GSTK1	glutathione S-transferase kappa 1
-0.12	3.63e-03	KPNA2	karyopherin subunit alpha 2	0.45	4.08e-02	MFSD1	major facilitator superfamily domain containing 1
-0.76	3.63e-03	RNF220	ring finger protein 220	0.18	4.29e-02	SACM1L	SAC1 like phosphatidylinositol phosphatase
-0.6	3.78e-03	SKA3	spindle and kinetochore associated	0.09	4.37e-02	M6PR	mannose-6-phosphate receptor, catiotransferrin
-0.04	3.78e-03	HSP90AB1	heat shock protein 90 alpha family	0.56	4.42e-02	SPG21	SPG21 arylhydrolase domain containing
-0.05	4.14e-03	CCT5	chaperonin containing TCP1 subunit	0.09	4.45e-02	P4HB	prolyl 4-hydroxylase subunit beta
-0.25	4.14e-03	UHRF1	ubiquitin like with PHD and ring finger	0.68	4.51e-02	GPAA1	glycosylphosphatidylinositol anchor
-0.87	4.14e-03	GMNN	geminin DNA replication inhibitor	0.13	4.58e-02	RPN2	ribophorin II
-0.07	4.44e-03	FUBP1	far upstream element binding protein 1	0.57	5.03e-02	CST3	cystatin C
-0.05	4.44e-03	CCT3	chaperonin containing TCP1 subunit	0.08	5.04e-02	TMED5	transmembrane p24 trafficking protein
-0.05	4.98e-03	RPL24	ribosomal protein L24	0.07	5.11e-02	PDHX	pyruvate dehydrogenase complex component
-0.04	4.98e-03	SFPQ	splicing factor proline and glutamine rich	0.43	5.18e-02	SMPDL3B	sphingomyelin phosphodiesterase acyl
-0.54	5.34e-03	TLE5	TLE family member 5, transcriptional	0.46	5.20e-02	FHIT	fragile histidine triad diadenosine
-0.58	5.34e-03	BMI1	PcoQ mediated genome instability 2	0.59	5.27e-02	SLC25A19	solute carrier family 25 member 19

Differentially expressed proteins in solid cancers at absence/low amount of FBXO5 , DB2  
p-value < 0.05 & logFC > 1.2

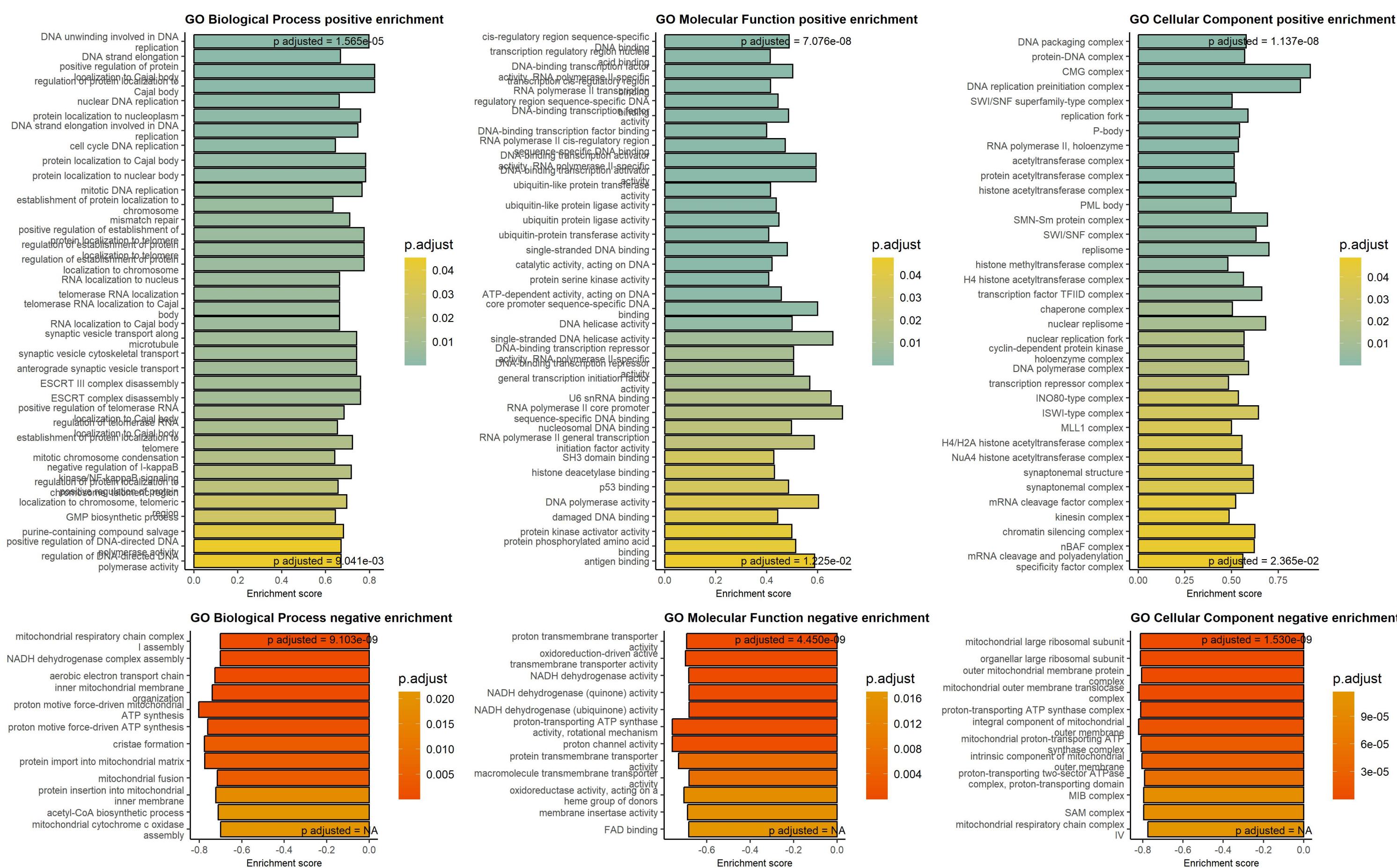


Sorted by p values!							
Downregulated in solid cancers at low/absent FBXO5				Upregulated in solid cancers at low/absent FBXO5			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.29	3.29e-37	STMN1	stathmin 1	1.07	2.96e-22	SLC22A18	solute carrier family 22 member 18
-1.02	9.07e-31	ZNF428	zinc finger protein 428	1.13	8.77e-18	PRSS8	serine protease 8
-0.82	9.23e-31	UBE2S	ubiquitin conjugating enzyme E2 S	0.87	1.25e-16	FAM83B	family with sequence similarity 83
-1.56	5.74e-29	CDKN2C	cyclin dependent kinase inhibitor 2	0.89	1.47e-15	LCN2	lipocalin 2
-0.93	2.24e-28	ENO2	enolase 2	0.69	1.80e-13	NHLRC3	NHL repeat containing 3
-0.94	1.49e-24	CKB	creatine kinase B	0.73	6.90e-13	CELSR1	cadherin EGF LAG seven-pass G-type membrane 1
-0.2	8.76e-24	NASP	nuclear autoantigenic sperm protein	0.71	8.71e-13	NECTIN4	nectin cell adhesion molecule 4
-1.4	1.39e-22	CEP97	centrosomal protein 97	1.42	1.75e-12	CACUL1	CDK2 associated cullin domain 1
-0.91	1.71e-22	UBE2T	ubiquitin conjugating enzyme E2 T	0.93	2.80e-12	ALDH3B1	aldehyde dehydrogenase 3 family member 1
-1.32	3.85e-22	UCHL1	ubiquitin C-terminal hydrolase L1	0.73	2.99e-12	MAN1B1	mannosidase alpha class 1B member 1
-0.18	5.05e-22	MCM3	minichromosome maintenance complex	1.21	1.41e-11	KRT74	keratin 74
-0.97	5.05e-22	SLBP	stem-loop binding protein	0.91	1.53e-11	MFSD10	major facilitator superfamily domain 10
-1.03	7.74e-22	PM20D2	peptidase M20 domain containing 2	0.77	5.00e-11	CENPE	centromere protein E
-1.15	8.26e-22	DPYSL4	dihydropyrimidinase like 4	0.85	5.37e-11	COX14	cytochrome c oxidase assembly factor 14
-0.22	2.72e-21	MCM2	minichromosome maintenance complex	0.83	2.04e-10	RHOF	ras homolog family member F, filopodia-associated
-0.99	9.24e-21	ACYP1	acylphosphatase 1	0.89	4.19e-10	RER1	retention in endoplasmic reticulum
-1.17	1.45e-20	CDC34	cell division cycle 34, ubiquitin c	0.81	5.07e-10	CYBA	cytochrome b-245 alpha chain
-0.51	1.87e-20	DPYSL2	dihydropyrimidinase like 2	1.03	5.37e-10	LPCAT4	lysophosphatidylcholine acyltransferase 4
-0.24	2.03e-20	MCM6	minichromosome maintenance complex	0.79	1.08e-09	ABCD1	ATP binding cassette subfamily D member 1
-0.86	4.63e-20	NUDT3	nudix hydrolase 3	0.81	1.23e-09	PIEZ01	piezo type mechanosensitive ion channel
-0.85	8.83e-20	PBK	PDZ binding kinase	0.26	1.25e-09	PICALM	phosphatidylinositol binding clathrin-associated linker protein
-1.16	9.26e-20	CKS1B	CDC28 protein kinase regulatory subunit	0.68	1.68e-09	ACOX3	acyl-CoA oxidase 3, pristanoyl
-1	1.82e-19	CRIP1	CXXC repeat containing interactor o	0.7	1.68e-09	SIAE	sialic acid acetyltransferase
-0.12	3.81e-19	TUBB	tubulin beta class I	0.55	1.72e-09	STX4	syntaxin 4
-0.56	4.41e-19	CARHSP1	calcium regulated heat stable protein	1	1.83e-09	TMEM63A	transmembrane protein 63A
-0.4	5.51e-19	SGTA	small glutamine rich tetratricopeptide repeat protein	0.9	3.15e-09	GALNT3	polypeptide N-acetylgalactosaminyltransferase 3
-0.17	1.12e-18	DNAJA1	DnaJ heat shock protein family (Hsp40) member A1	0.25	4.38e-09	TM9SF3	transmembrane 9 superfamily member 3
-1.1	1.47e-18	CDK5R2	cyclin dependent kinase 5 regulator	0.59	5.28e-09	SLC9A1	solute carrier family 9 member A1
-0.27	1.63e-18	UBA2	ubiquitin like modifier activating enzyme 2	0.93	5.84e-09	PRKCD	protein kinase C delta
-0.2	5.40e-18	MCM4	minichromosome maintenance complex	0.13	5.90e-09	RAB1A	RAB1A, member RAS oncogene family
-0.77	5.44e-18	DHPS	deoxyhypusine synthase	0.7	5.91e-09	RFT1	RFT1 homolog
-0.96	6.22e-18	ARPP19	cAMP regulated phosphoprotein 19	0.16	6.61e-09	HADHA	hydroxyacyl-CoA dehydrogenase trifunctional protein
-0.67	7.94e-18	AKR1E2	aldo-keto reductase family 1 member	0.61	7.99e-09	EPHA1	EPH receptor A1
-0.53	8.77e-18	TUBB2B	tubulin beta 2B class IIb	0.86	9.85e-09	SLC39A11	solute carrier family 39 member 11
-0.15	1.68e-17	PCNA	proliferating cell nuclear antigen	0.88	1.14e-08	SFT2D2	SFT2 domain containing 2
-1.22	1.95e-17	NCAM1	neural cell adhesion molecule 1	1.09	1.16e-08	SUMF1	sulfatase modifying factor 1
-1.09	1.97e-17	TIMELESS	timeless circadian regulator	0.71	1.37e-08	ANKRD22	ankyrin repeat domain 22
-0.19	2.71e-17	RANBP1	RAN binding protein 1	0.69	1.73e-08	NLRX1	NLR family member X1
-0.25	3.27e-17	SMC3	structural维持丝蛋白纤维	0.81	2.22e-08	RAP2B	RAP2B, member of RAP family

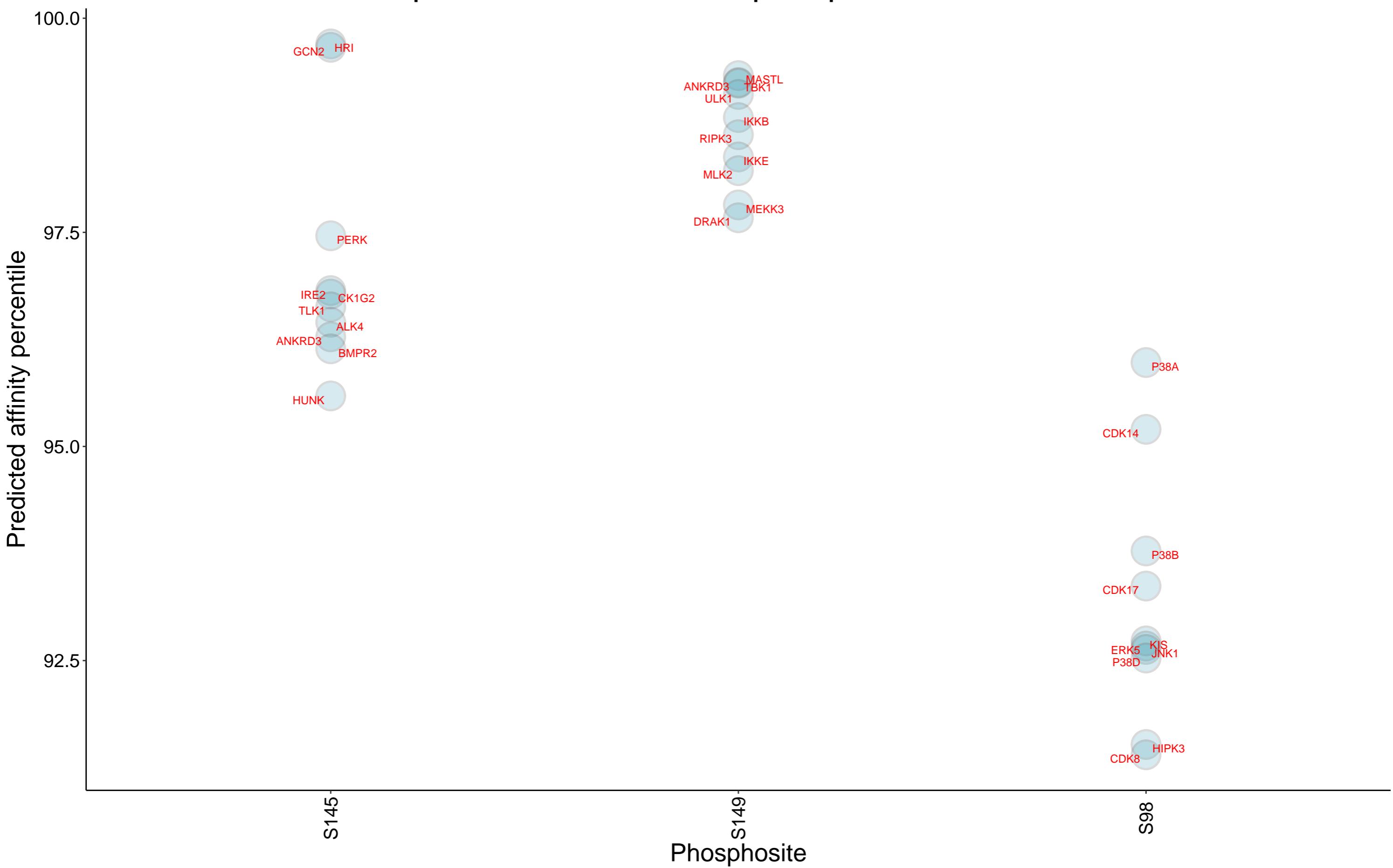
# Top 250 correlation coefficients overrepresentation, FBXO5 protein, DB2



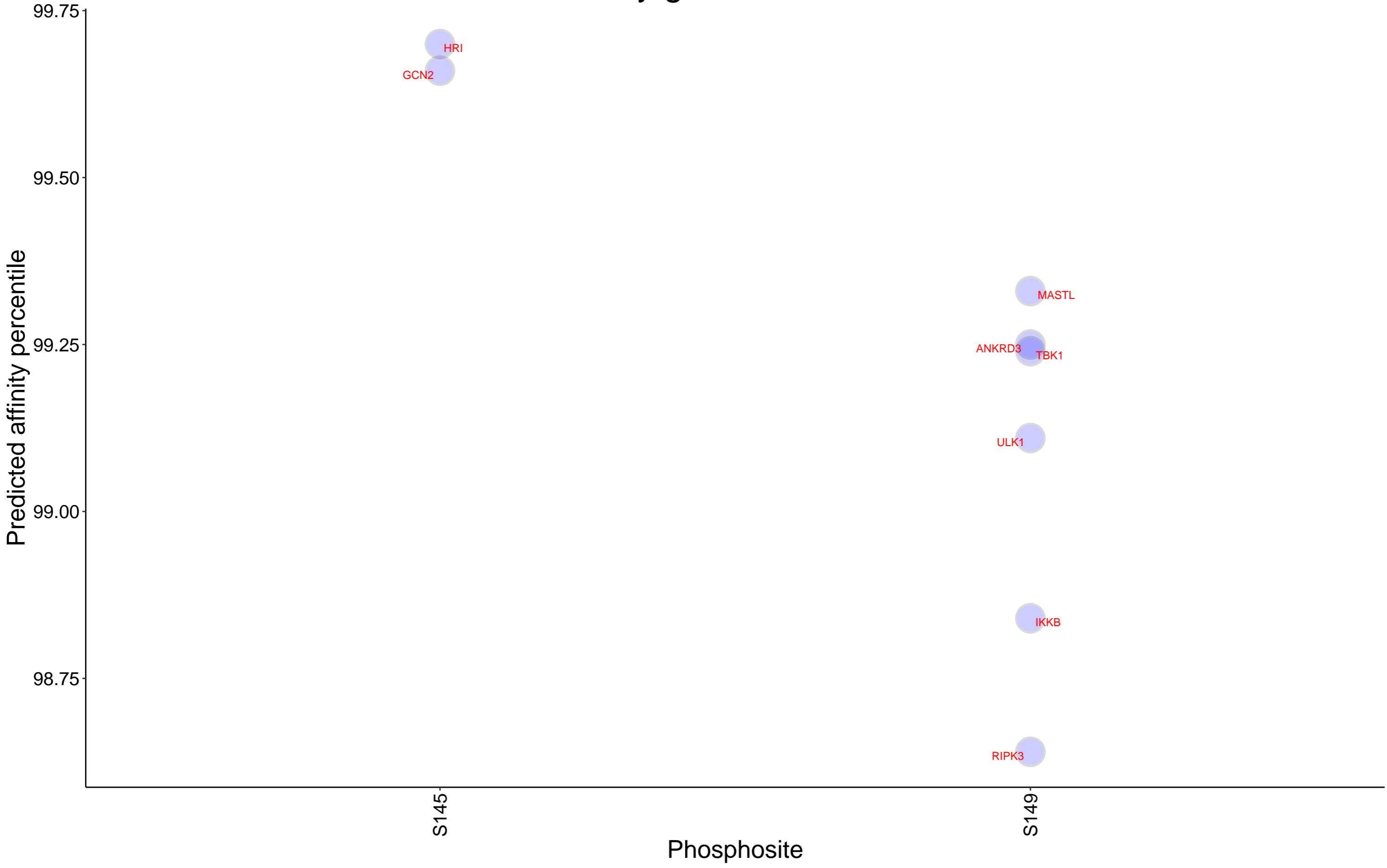
## Gene Set Enrichment analysis on protein correlation coefficients, FBXO5 protein, DB2



# Top 10 kinases for each phosphosite in FBXO5



## Kinases with affinity greater than 98.5% to FBXO5



No sufficient number of paired observations in DB2 for FBXO5