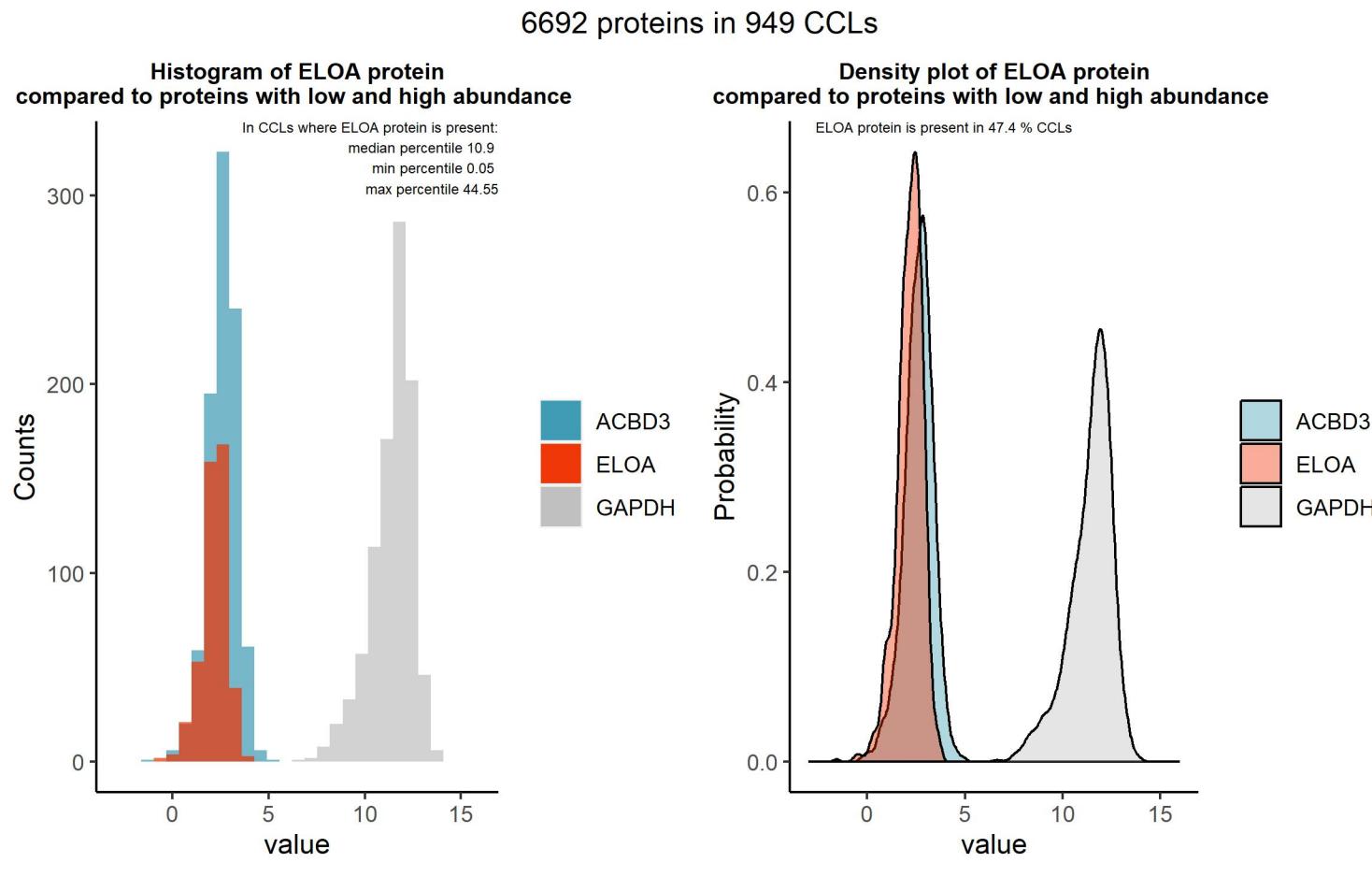


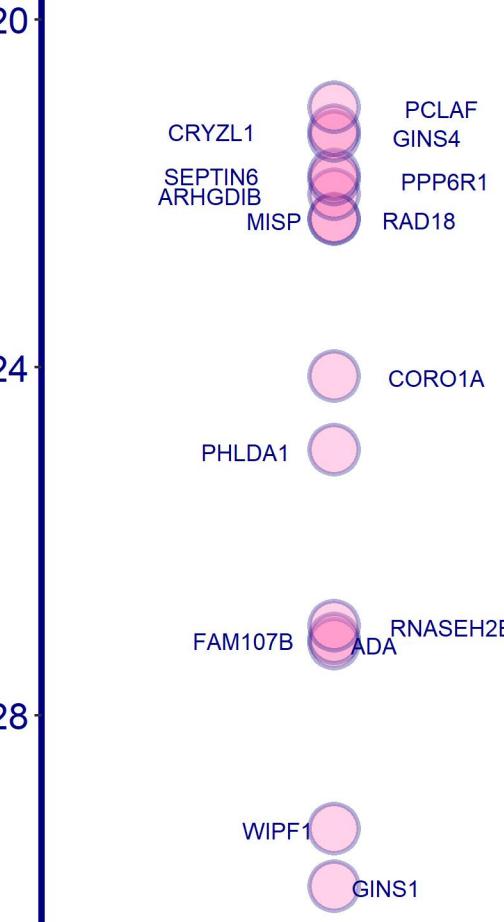
ELOA

Protein name: ELOA1 ; UNIPROT: Q14241 ; Gene name: elongin A
 Ligandable: Yes ; Ligandable_by_Chem: NA ; Is_enzyme: NA (<https://cansar.ai/>)

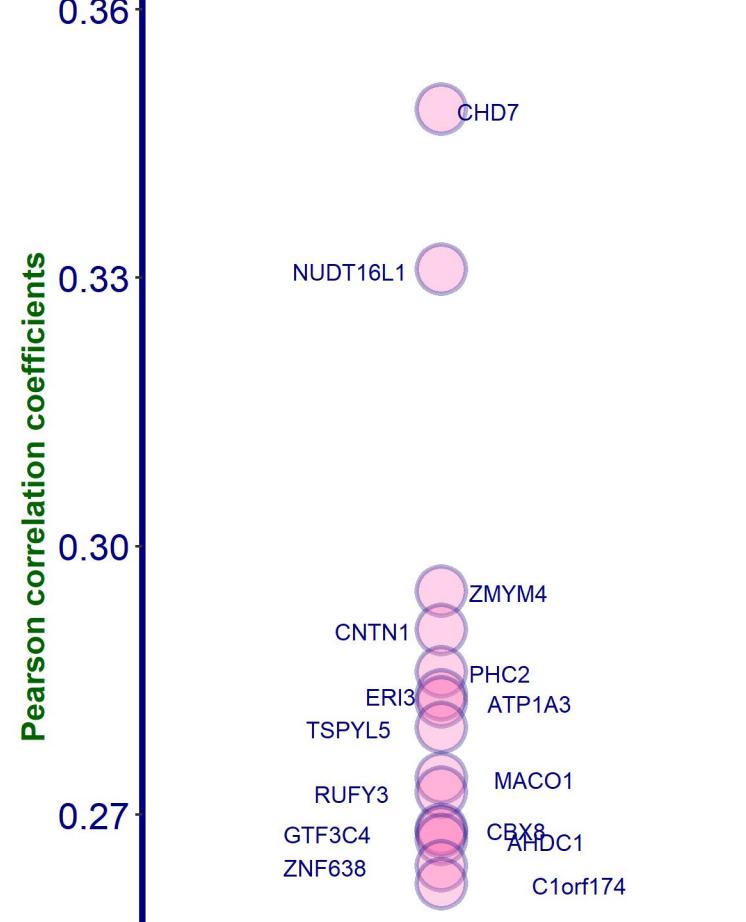
Sanger Institute Protein Database 1 (DB1), protein presence is certain



Top negative correlations of ELOA protein, DB1

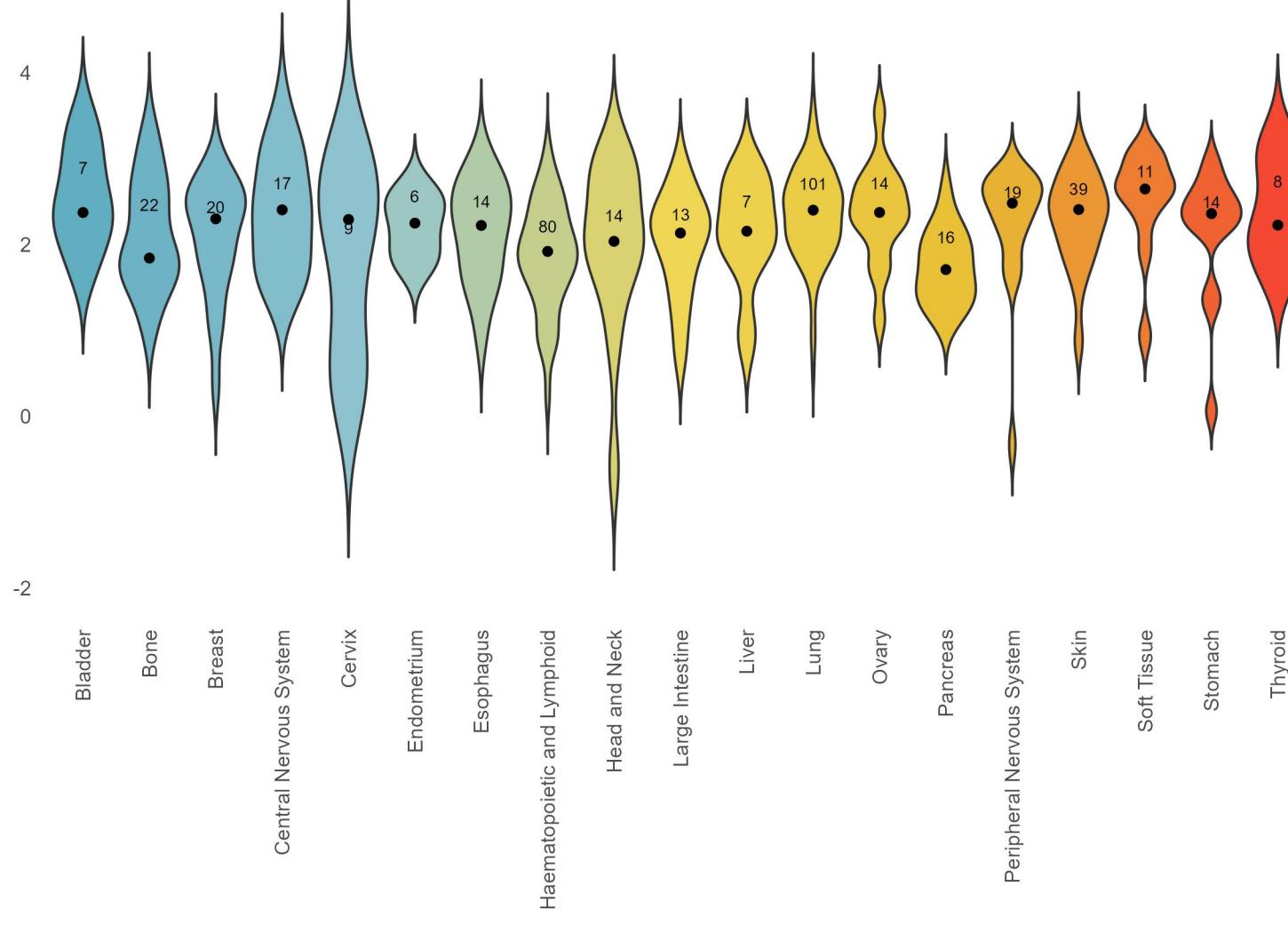


Top positive correlations of ELOA protein, DB1



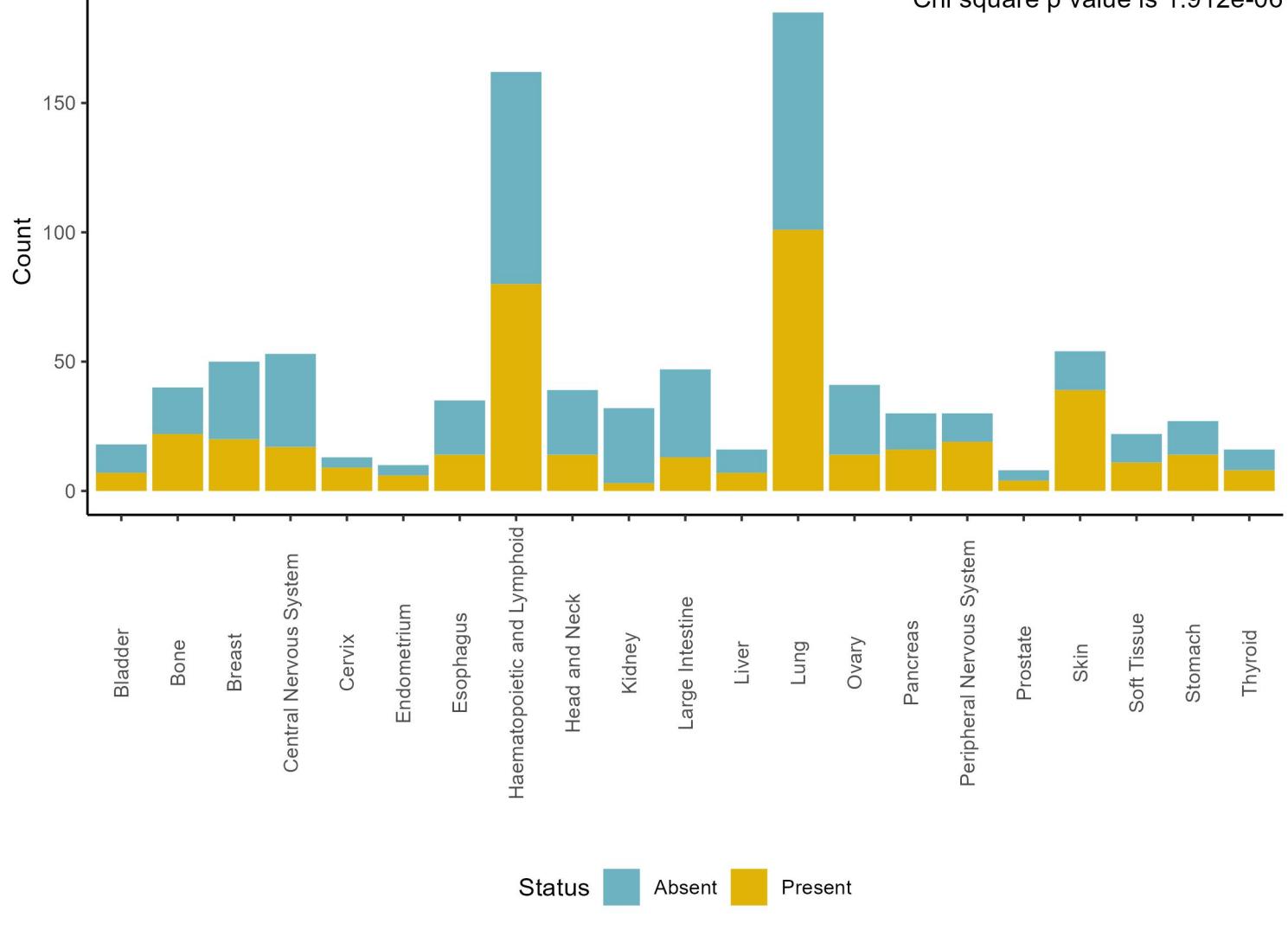
Amount of ELOA protein, number of CCLs where it is present by tissue, DB1

ANOVA p value is 1.078e-04



Present and absent ELOA protein counts by tissue, DB1

Chi square p value is 1.912e-06

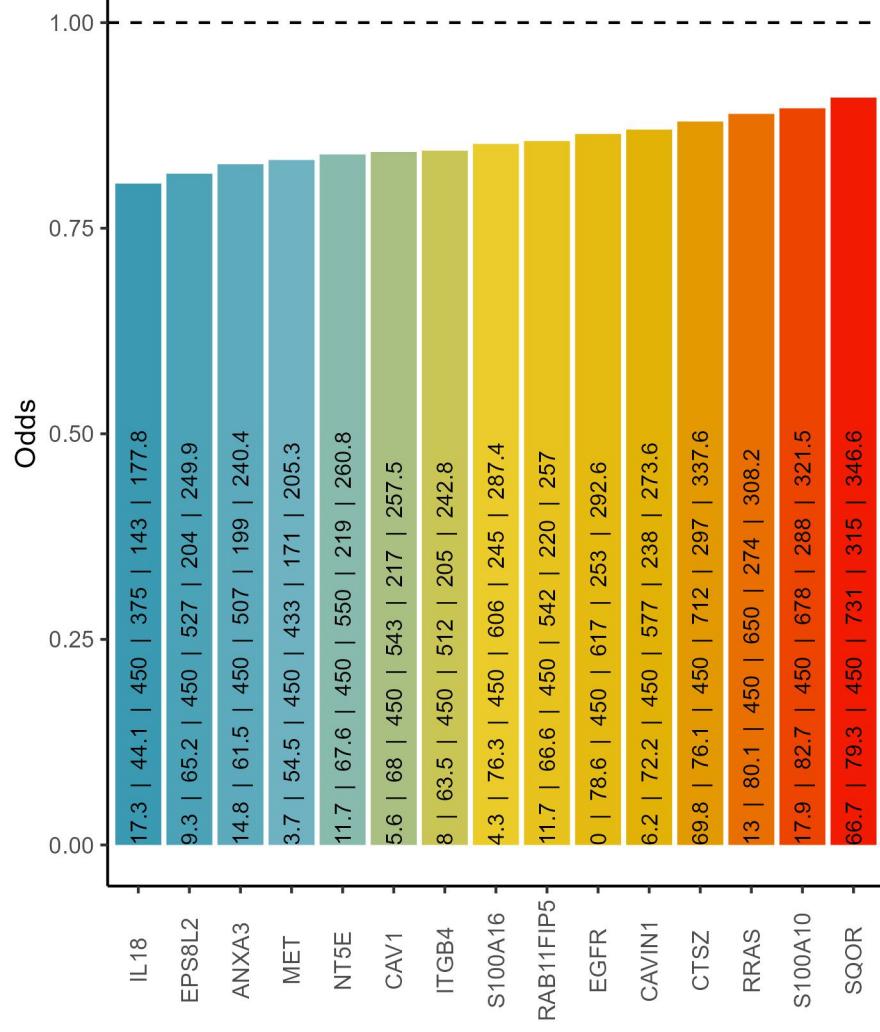


Cooccurrence with ELOA protein, DB1

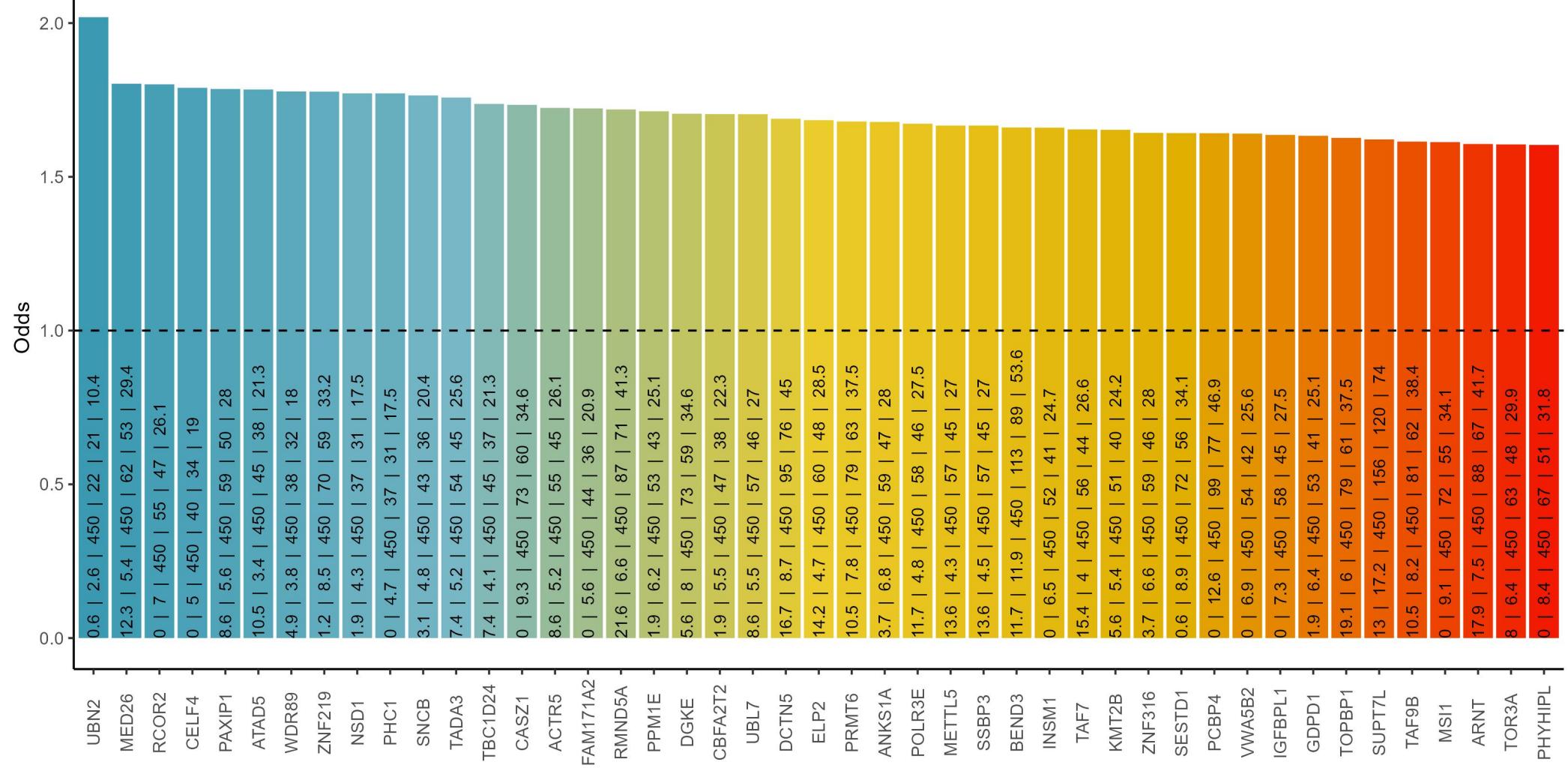
% of ELOA in blood cancers: 49.4 ; % of ELOA in solid cancers: 47.1

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

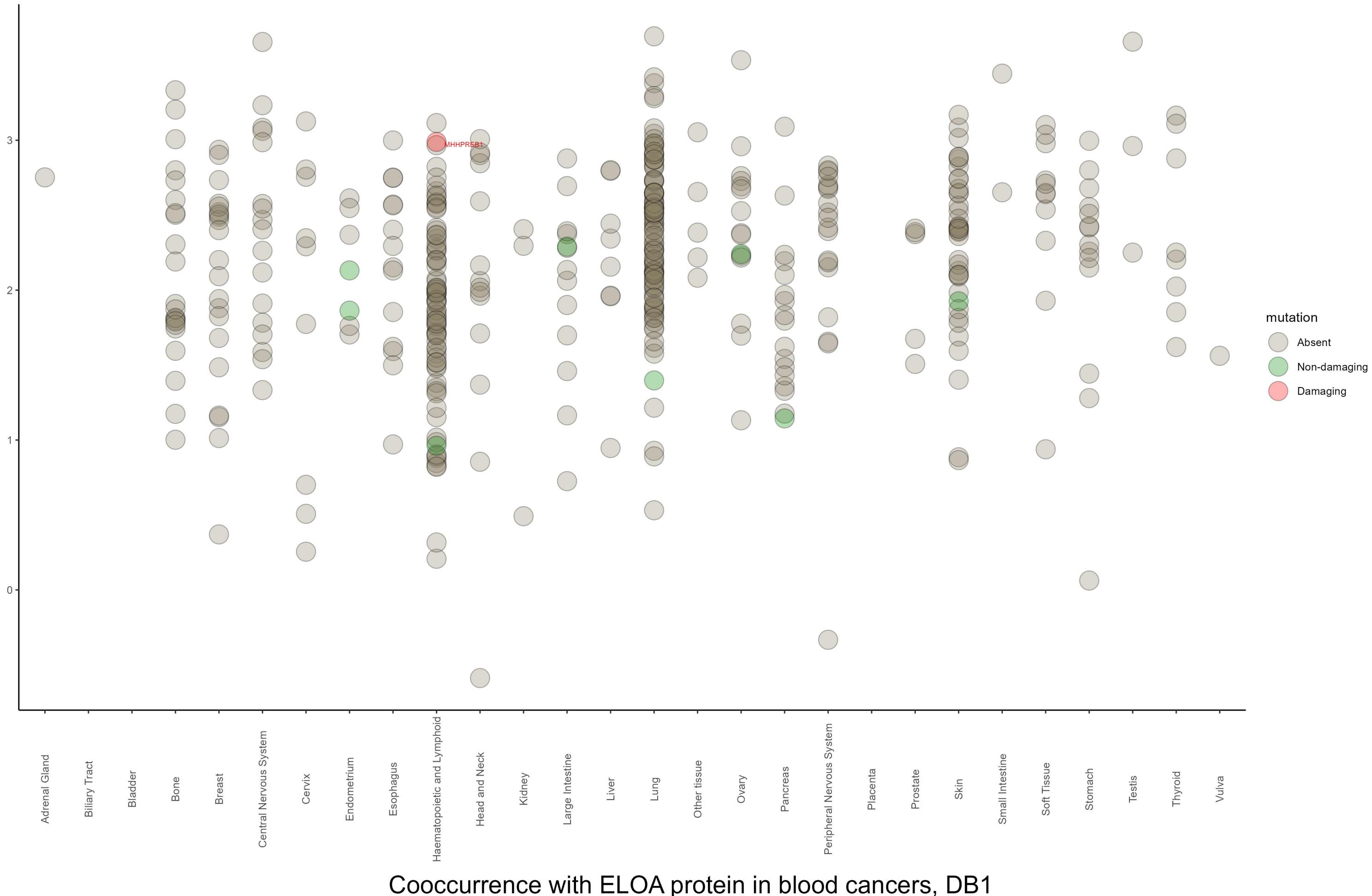
Negative cooccurrence



Positive cooccurrence

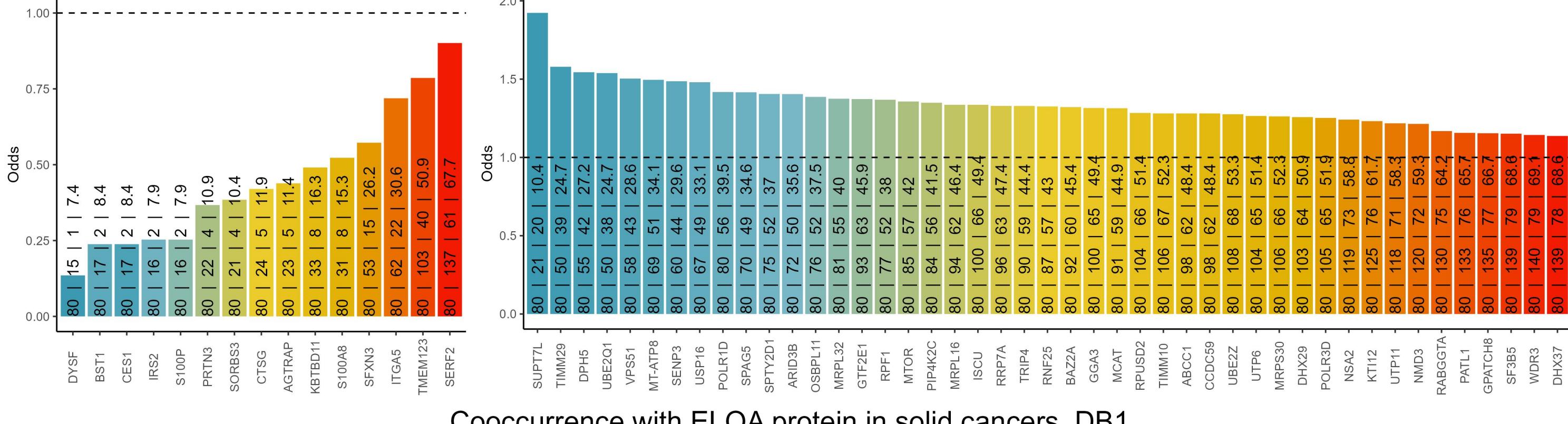


Amount of ELOA protein and mutation status by tissue, DB1



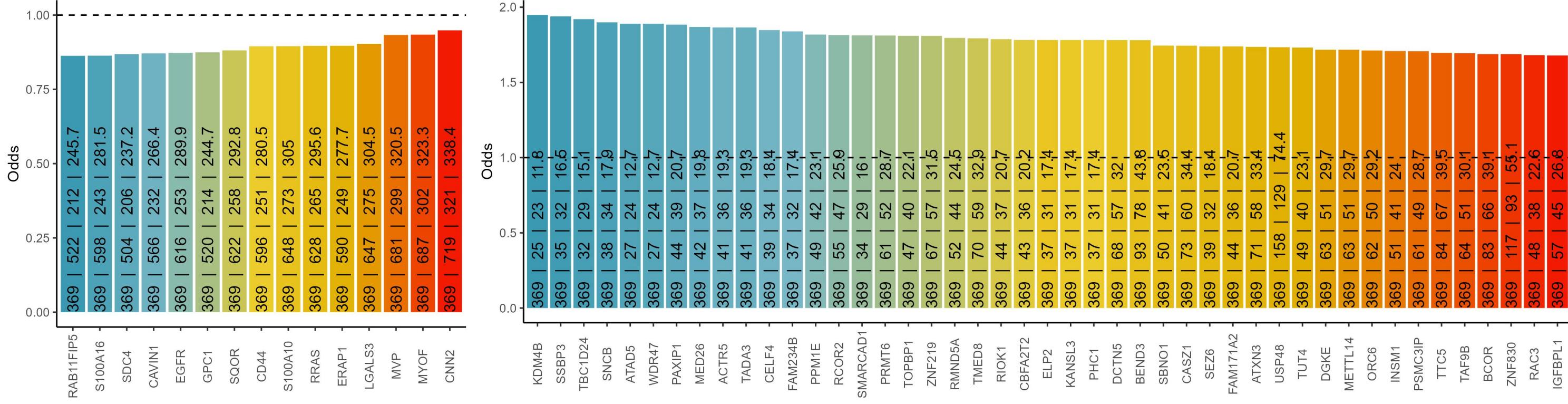
Cooccurrence with ELOA protein in blood cancers, DB1

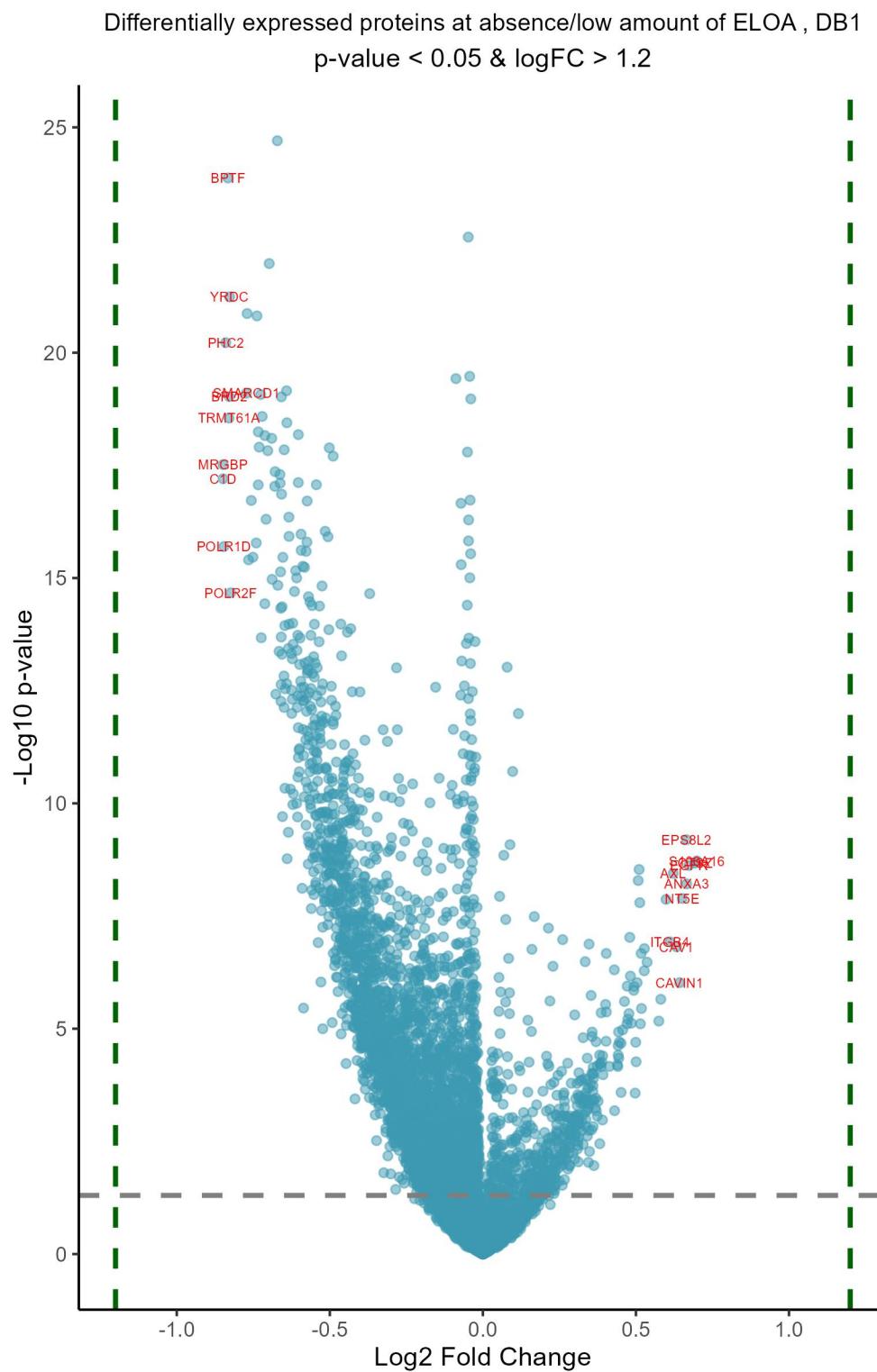
The text in the bars: incidence of ELOA | incidence of Protein 2 | observed cooccurrence | expected cooccurrence



Cooccurrence with ELOA protein in solid cancers, DB1

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

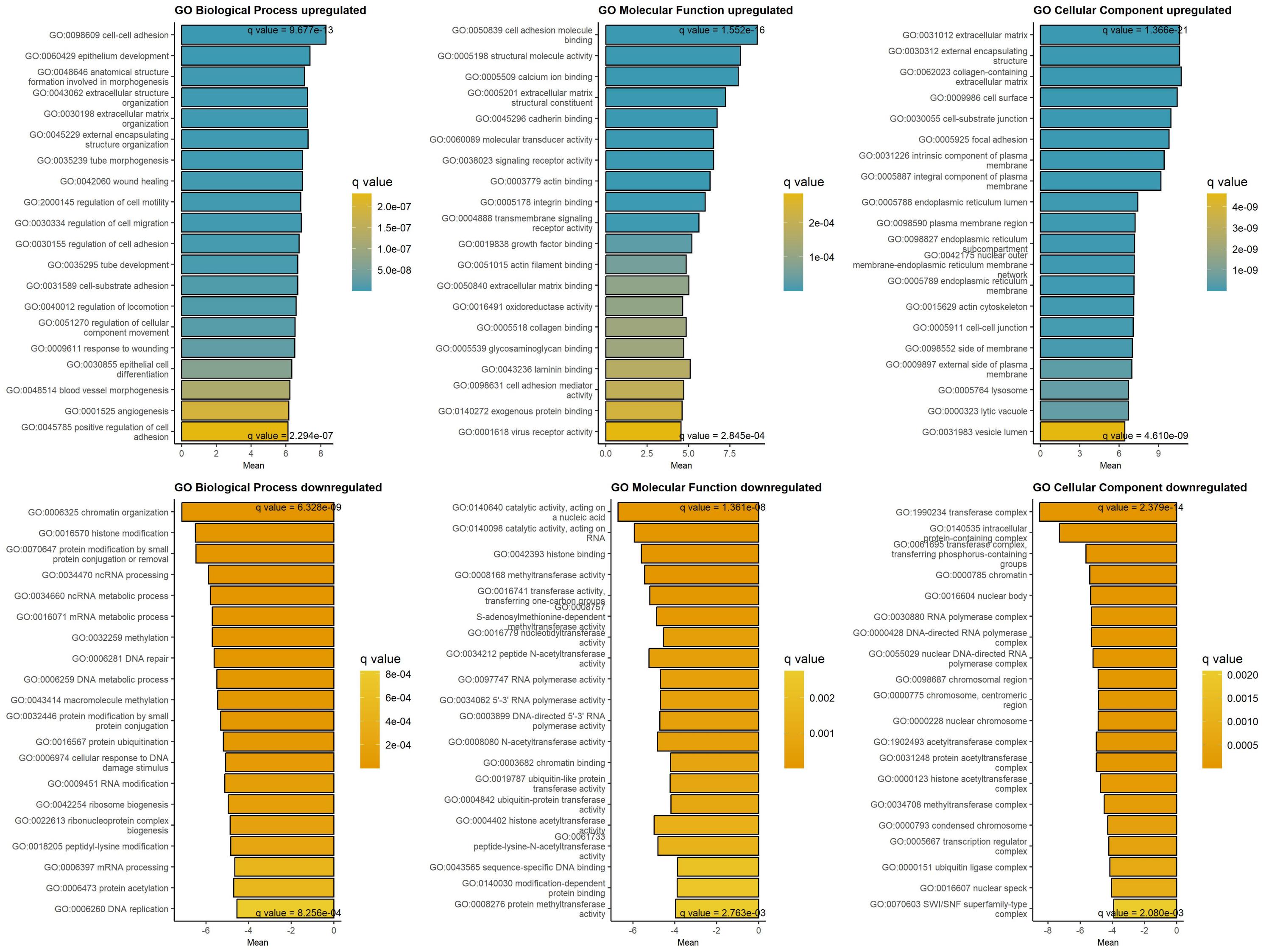


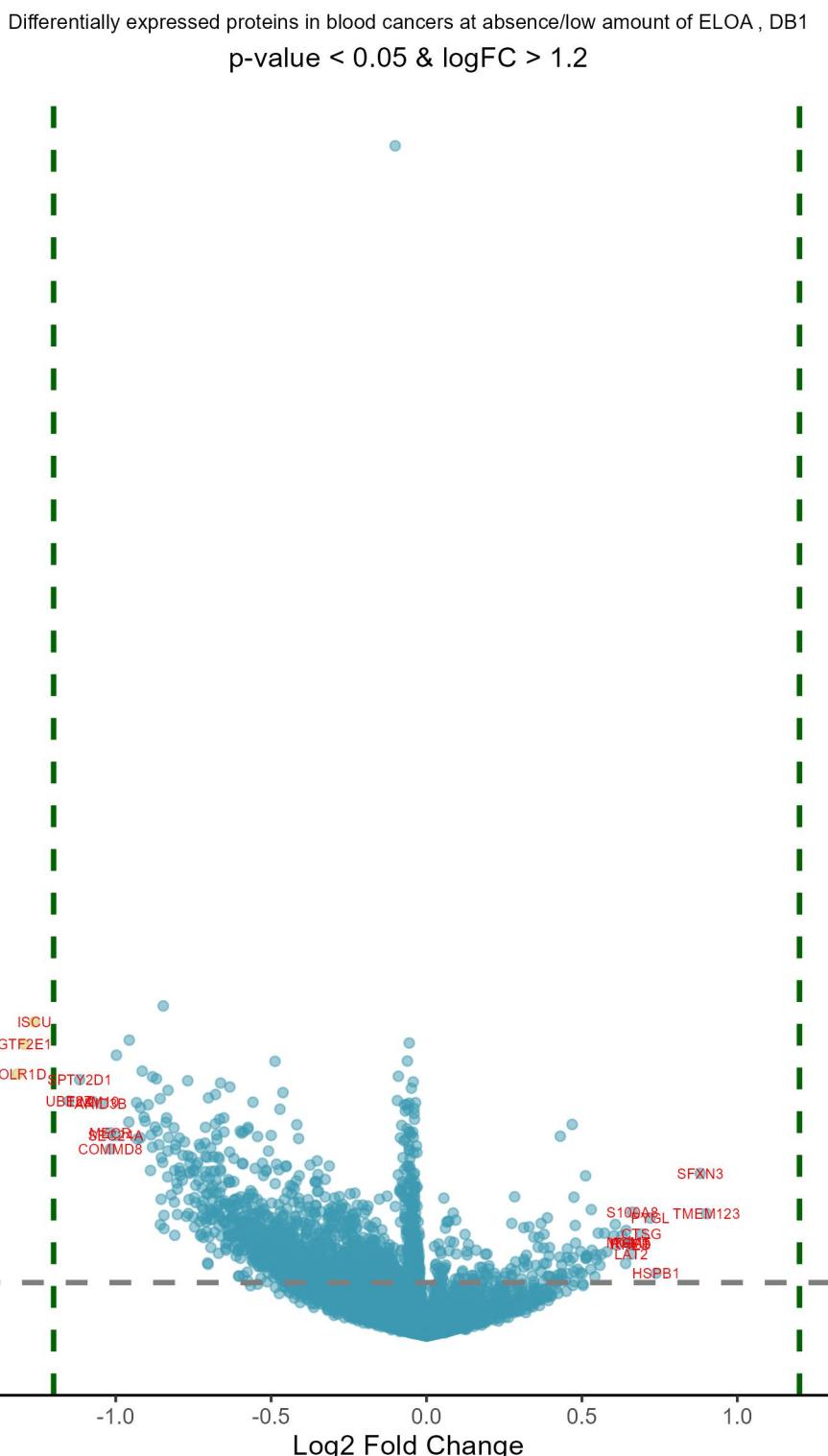


Downregulated at low/absent ELOA Upregulated at low/absent ELOA

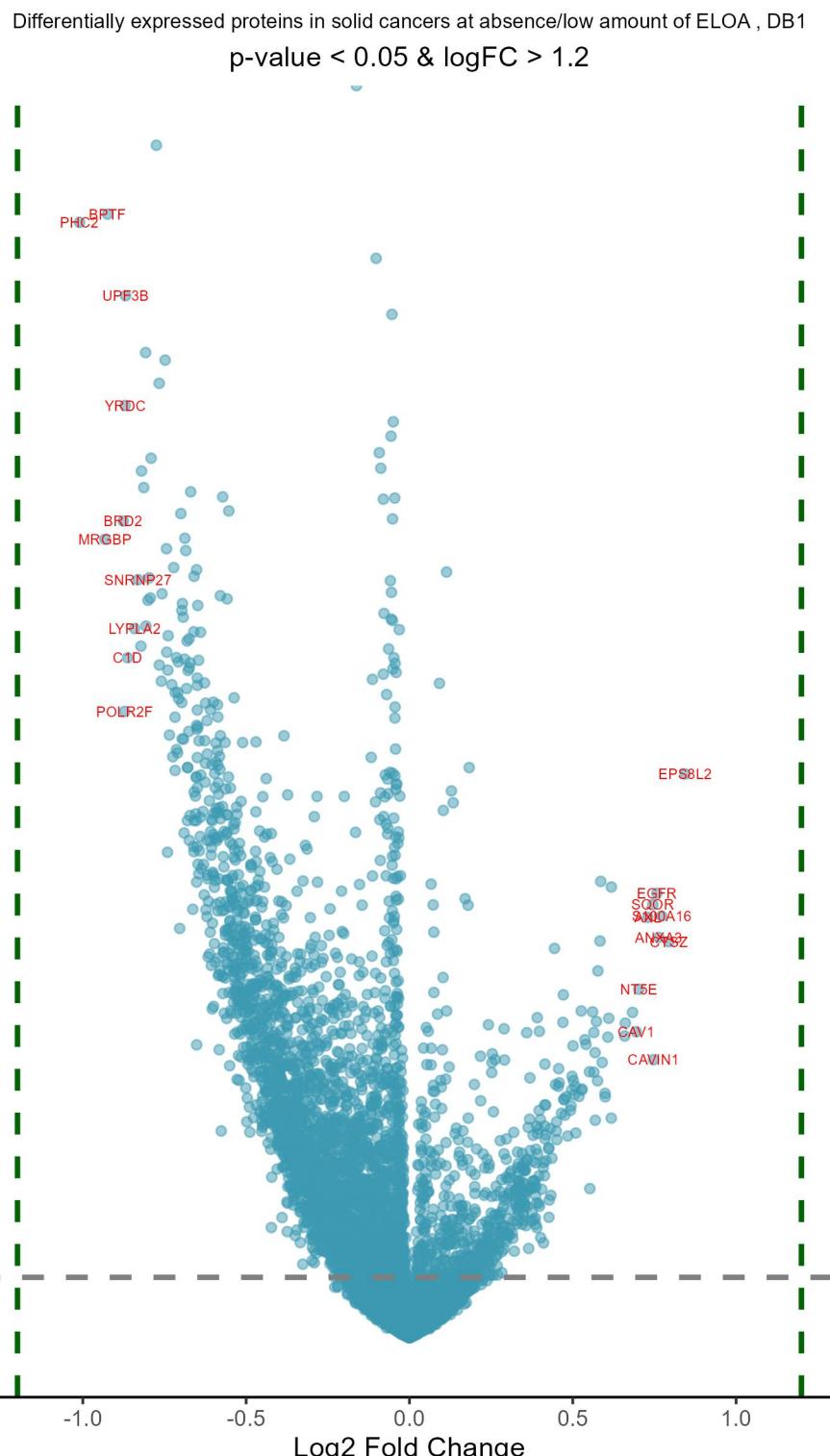
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-0.85	6.52e-16	MRGBP	MRG domain binding protein	0.7	3.01e-08	S100A16	S100 calcium binding protein A16
-0.85	1.22e-15	C1D	C1D nuclear receptor corepressor	0.69	3.29e-08	CTSZ	cathepsin Z
-0.85	2.43e-14	POLR1D	RNA polymerase I and III subunit D	0.67	3.64e-08	EGFR	epidermal growth factor receptor
-0.84	4.42e-18	PHC2	polyhomeotic homolog 2	0.67	8.50e-08	ANXA3	annexin A3
-0.83	2.94e-21	BPTF	bromodomain PHD finger transcriptio	0.67	1.23e-08	EPS8L2	EPS8 like 2
-0.83	9.87e-17	TRMT61A	tRNA methyltransferase 61A	0.65	1.64e-07	NT5E	5'-nucleotidase ecto
-0.83	3.97e-17	BRD2	bromodomain containing 2	0.64	7.15e-06	CAVIN1	caveolae associated protein 1
-0.83	6.40e-19	YRDC	yrdC N6-threonylcarbamoyltransferas	0.63	1.44e-06	CAV1	caveolin 1
-0.82	1.94e-13	POLR2F	RNA polymerase II, I and III subuni	0.62	5.28e-08	AXL	AXL receptor tyrosine kinase
-0.77	3.97e-17	SMARCD1	SWI/SNF related, matrix associated,	0.61	1.16e-06	ITGB4	integrin subunit beta 4
-0.77	1.27e-18	UPF3B	UPF3B regulator of nonsense mediate	0.6	1.71e-07	SQOR	sulfide quinone oxidoreductase
-0.77	4.32e-14	SNRNP27	small nuclear ribonucleoprotein U4/	0.58	1.49e-05	S100A10	S100 calcium binding protein A10
-0.76	3.01e-15	BUD23	BUD23 rRNA methyltransferase and ri	0.57	3.90e-05	ITGA3	integrin subunit alpha 3
-0.75	3.85e-14	LYPLA2	lysophospholipase 2	0.54	2.83e-06	KRT80	keratin 80
-0.74	2.05e-14	RPF1	ribosome production factor 1 homolo	0.53	1.56e-06	RRAS	RAS related
-0.74	1.27e-18	STEEP1	STING1 ER exit protein 1	0.53	4.15e-06	NNMT	nicotinamide N-methyltransferase
-0.73	1.50e-15	POLR2D	RNA polymerase II subunit D	0.52	2.24e-05	CAPG	capping actin protein, gelsolin lik
-0.73	1.81e-16	EZH2	enhancer of zeste 2 polycomb repres	0.52	1.93e-06	F3	coagulation factor III, tissue fact
-0.73	3.31e-16	CWC27	CWC27 spliceosome associated cyclop	0.51	4.39e-05	TGM2	transglutaminase 2
-0.73	3.97e-17	POLR3A	RNA polymerase III subunit A	0.51	1.96e-07	PPP1R13L	protein phosphatase 1 regulatory su
-0.72	1.49e-12	ACYP1	acylphosphatase 1	0.51	4.41e-08	RAB11FIP5	RAB11 family interacting protein 5
-0.72	9.60e-17	FRG1	FSHD region gene 1	0.51	7.32e-08	PHLDB2	pleckstrin homology like domain fam
-0.71	3.21e-13	ZNF593	zinc finger protein 593	0.5	7.14e-06	IL18	interleukin 18
-0.71	1.99e-16	POLR3D	RNA polymerase III subunit D	0.5	2.36e-04	CD44	CD44 molecule (Indian blood group)
-0.71	7.18e-15	SENP3	SUMO specific peptidase 3	0.5	1.00e-04	GPRC5A	G protein-coupled receptor class C
-0.7	3.55e-16	USP48	ubiquitin specific peptidase 48	0.5	9.62e-04	KRT18	keratin 18
-0.7	1.40e-19	SUGP1	SURP and G-patch domain containing	0.49	8.54e-06	GPC1	glypican 1
-0.69	2.20e-16	UTP11	UTP11 small subunit processome comp	0.49	1.01e-05	EHD2	EH domain containing 2
-0.69	1.03e-13	SSU72	SSU72 homolog, RNA polymerase II CT	0.49	4.26e-05	MYOF	myoferlin

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



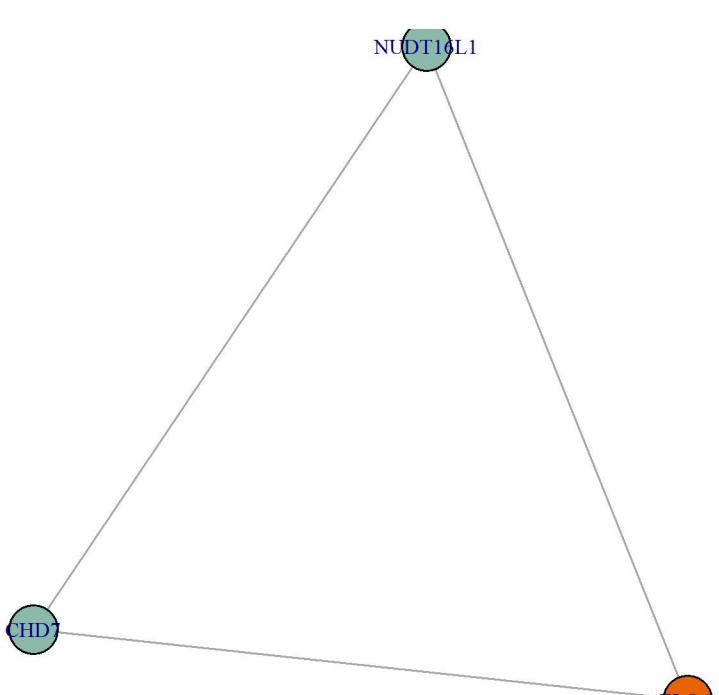


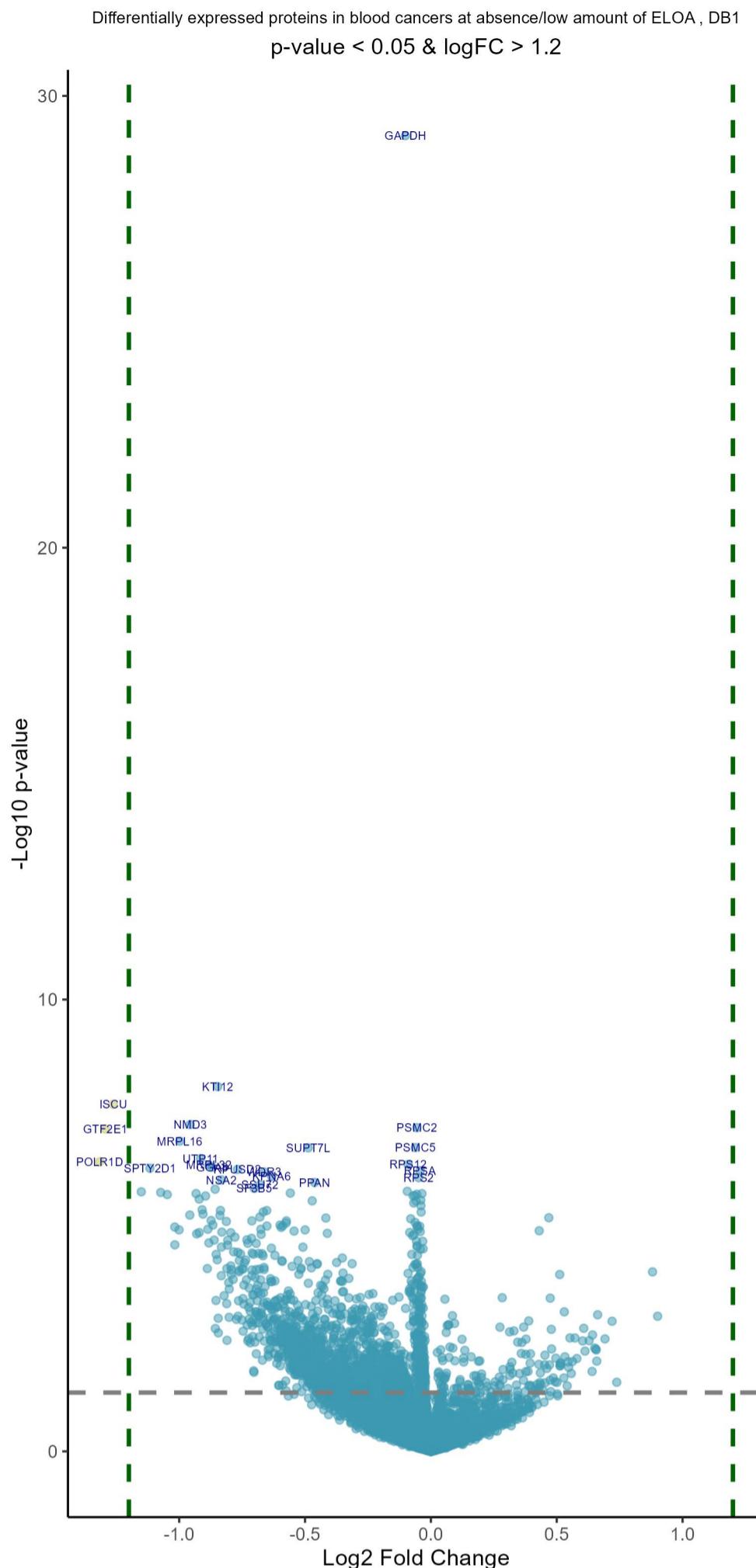
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.32	2.17e-04	POLR1D	RNA polymerase I and III subunit D	0.9	2.04e-02	TMEM123	transmembrane protein 123
-1.29	6.98e-05	GTF2E1	general transcription factor IIIE su	0.88	4.57e-03	SFXN3	sideroflexin 3
-1.26	3.47e-05	ISCU	iron-sulfur cluster assembly enzyme	0.74	1.40e-01	HSPB1	heat shock protein family B (small)
-1.15	4.00e-04	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.72	2.30e-02	PYGL	glycogen phosphorylase L
-1.12	2.25e-04	SPTY2D1	SPT2 chromatin protein domain conta	0.69	3.92e-02	CTSG	cathepsin G
-1.07	4.00e-04	TIMM10	translocase of inner mitochondrial	0.66	1.96e-02	S100A8	S100 calcium binding protein A8
-1.05	4.00e-04	ARID3B	AT-rich interaction domain 3B	0.66	7.49e-02	LAT2	linker for activation of T cells fa
-1.02	1.04e-03	MECR	mitochondrial trans-2-enoyl-CoA red	0.66	5.47e-02	RHEB	Ras homolog, mTORC1 binding
-1.02	1.82e-03	COMM8	COMM domain containing 8	0.66	5.34e-02	ITGA5	integrin subunit alpha 5
-1	1.11e-03	SEC24A	SEC24 homolog A, COPII coat complex	0.65	5.14e-02	MGMT	O-6-methylguanine-DNA methyltransferase
-1	1.13e-04	MRPL16	mitochondrial ribosomal protein L16	0.64	3.47e-02	UTRN	utrophin
-0.96	7.83e-04	PNPLA6	patatin like phospholipase domain c	0.64	1.02e-01	H1-0	H1.0 linker histone
-0.96	6.98e-05	NMD3	NMD3 ribosome export adaptor	0.63	4.11e-02	SNTB1	syntrophin beta 1
-0.93	4.00e-04	MRPS30	mitochondrial ribosomal protein S30	0.61	5.73e-02	CTBP2	C-terminal binding protein 2
-0.93	1.21e-03	TRMT61A	tRNA methyltransferase 61A	0.61	2.85e-02	SERF2	small EDRK-rich factor 2
-0.92	4.56e-04	SPAG5	sperm associated antigen 5	0.6	4.12e-02	PRTN3	proteinase 3
-0.92	1.18e-03	RCC1L	RCC1 like	0.58	7.02e-02	CLEC11A	C-type lectin domain containing 11A
-0.91	2.02e-04	UTP11	UTP11 small subunit processome comp	0.57	3.81e-02	FAM107B	family with sequence similarity 107
-0.91	6.75e-04	TRIP4	thyroid hormone receptor interactor	0.56	7.56e-02	PIK3AP1	phosphoinositide-3-kinase adaptor p
-0.91	7.61e-04	UBE2Q1	ubiquitin conjugating enzyme E2 Q1	0.56	1.08e-01	SATB1	SATB homeobox 1
-0.9	4.00e-04	DPH5	diphthamide biosynthesis 5	0.55	3.81e-02	KBTBD11	kelch repeat and BTB domain contain
-0.89	4.19e-03	ENTPD1	ectonucleoside triphosphate diphosp	0.55	9.09e-02	CPT1A	carnitine palmitoyltransferase 1A
-0.89	1.10e-03	CCDC59	coiled-coil domain containing 59	0.55	7.66e-02	H2AX	H2A.X variant histone
-0.88	1.70e-03	BABAM2	BRISC and BRCA1 A complex member 2	0.54	1.58e-01	SERPINB1	serpin family B member 1
-0.88	2.18e-04	MRPL32	mitochondrial ribosomal protein L32	0.53	6.77e-02	SYTL1	synaptotagmin like 1
-0.87	9.09e-04	PIP4K2C	phosphatidylinositol-5-phosphate 4-	0.53	1.77e-02	CES1	carboxylesterase 1
-0.87	2.25e-04	GGA3	golgi associated, gamma adaptin ear	0.53	1.24e-01	PYCARD	PYD and CARD domain containing
-0.87	1.03e-03	POLR3D	RNA polymerase III subunit D	0.52	8.15e-02	APBB1IP	amyloid beta precursor protein bind
-0.86	1.54e-03	RPF1	ribosome production factor 1 homolo	0.51	7.89e-02	SPI1	Spi-1 proto-oncogene



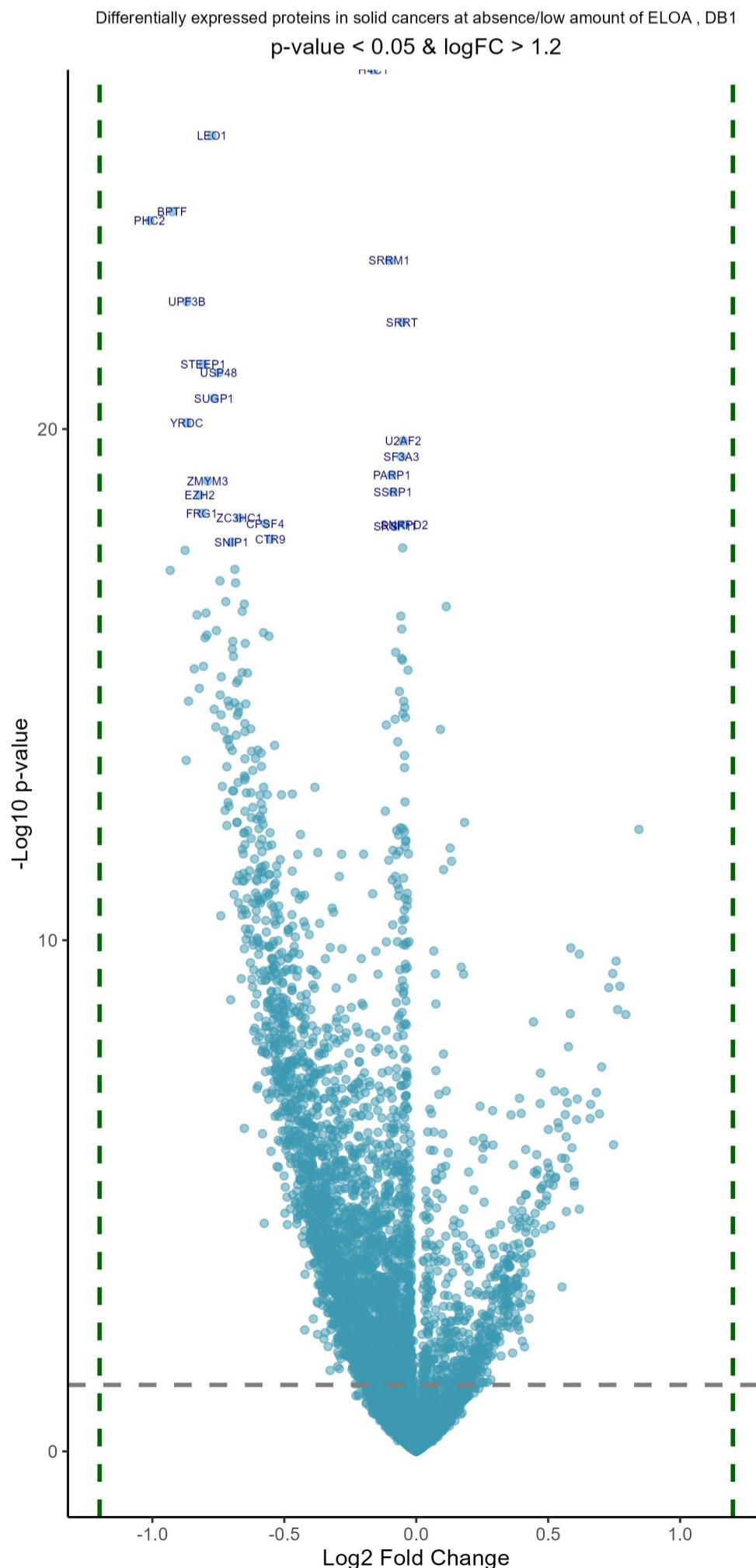
Downregulated in solid cancers at low/absent ELOA				Upregulated in solid cancers at low/absent ELOA			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
-1.01	1.11e-21	PHC2	polyhomeotic homolog 2	0.84	3.25e-11	EPS8L2	EPS8 like 2
-0.93	1.33e-15	MRGBP	MRG domain binding protein	0.79	4.61e-08	CTSZ	cathepsin Z
-0.92	9.26e-22	BPTF	bromodomain PHD finger transcriptio	0.77	1.50e-08	S100A16	S100 calcium binding protein A16
-0.88	5.83e-16	BRD2	bromodomain containing 2	0.76	3.80e-08	ANXA3	annexin A3
-0.87	2.05e-12	POLR2F	RNA polymerase II, I and III subuni	0.76	5.55e-09	EGFR	epidermal growth factor receptor
-0.87	4.17e-18	YRDC	yrdC N6-threonylcarbamoyltransferas	0.75	7.57e-06	CAVIN1	caveolae associated protein 1
-0.87	3.06e-20	UPF3B	UPF3B regulator of nonsense mediate	0.75	9.00e-09	SQOR	sulfide quinone oxidoreductase
-0.86	2.15e-13	C1D	C1D nuclear receptor corepressor	0.73	1.58e-08	AXL	AXL receptor tyrosine kinase
-0.84	6.17e-14	LYPLA2	lysophospholipase 2	0.7	3.62e-07	NT5E	5'-nucleotidase ecto
-0.83	7.80e-15	SNRNP27	small nuclear ribonucleoprotein U4/	0.69	2.22e-06	CAV1	caveolin 1
-0.82	1.31e-13	ACYP1	acylphosphatase 1	0.68	9.53e-07	ITGB4	integrin subunit beta 4
-0.82	7.23e-17	EZH2	enhancer of zeste 2 polycomb repres	0.66	1.53e-06	S100A10	S100 calcium binding protein A10
-0.81	1.56e-16	FRG1	FSHD region gene 1	0.66	2.66e-06	TGM2	transglutaminase 2
-0.81	4.02e-19	STEEP1	STING1 ER exit protein 1	0.62	4.22e-09	PPP1R13L	protein phosphatase 1 regulatory su
-0.81	5.60e-14	TRMT61A	tRNA methyltransferase 61A	0.62	9.44e-05	CD44	CD44 molecule (Indian blood group)
-0.8	1.82e-14	ZNF24	zinc finger protein 24	0.61	1.23e-06	F3	coagulation factor III, tissue fact
-0.8	7.33e-15	SMARCD1	SWI/SNF related, matrix associated,	0.61	2.81e-06	KRT80	keratin 80
-0.79	1.70e-14	POLR2D	RNA polymerase II subunit D	0.6	3.76e-05	ITGA3	integrin subunit alpha 3
-0.79	4.31e-17	ZMYM3	zinc finger MYM-type containing 3	0.6	3.23e-05	LGALS3	galectin 3
-0.77	4.03e-23	LEO1	LEO1 homolog, Paf1/RNA polymerase I	0.59	8.54e-06	NNMT	nicotinamide N-methyltransferase
-0.77	1.51e-18	SUGP1	SURP and G-patch domain containing	0.59	3.28e-09	RAB11FIP5	RAB11 family interacting protein 5
-0.77	2.84e-13	PDXP	pyridoxal phosphatase	0.58	4.46e-08	PHLDB2	pleckstrin homology like domain fam
-0.76	5.60e-13	BUD23	BUD23 rRNA methyltransferase and ri	0.58	1.62e-07	RRAS	RAS related
-0.76	1.45e-14	CWC27	CWC27 spliceosome associated cyclop	0.58	1.88e-05	CAPG	capping actin protein, gelsolin lik
-0.75	5.25e-19	USP48	ubiquitin specific peptidase 48	0.57	1.41e-06	GPC1	glypican 1
-0.74	2.07e-15	POLR3A	RNA polymerase III subunit A	0.57	1.04e-04	GPRC5A	G protein-coupled receptor class C
-0.74	1.71e-13	SMAP2	small ArfGAP2	0.57	5.56e-06	EHD2	EH domain containing 2
-0.74	9.14e-10	POLR1D	RNA polymerase I and III subunit D	0.56	2.28e-06	FHL2	four and a half LIM domains 2
-0.74	3.50e-13	OBC2	origin recognition complex subunit	0.56	1.30e-05	HLA-B	major histocompatibility complex, c

FI OA network, DB1, all Pearson $r \geq 0.3$



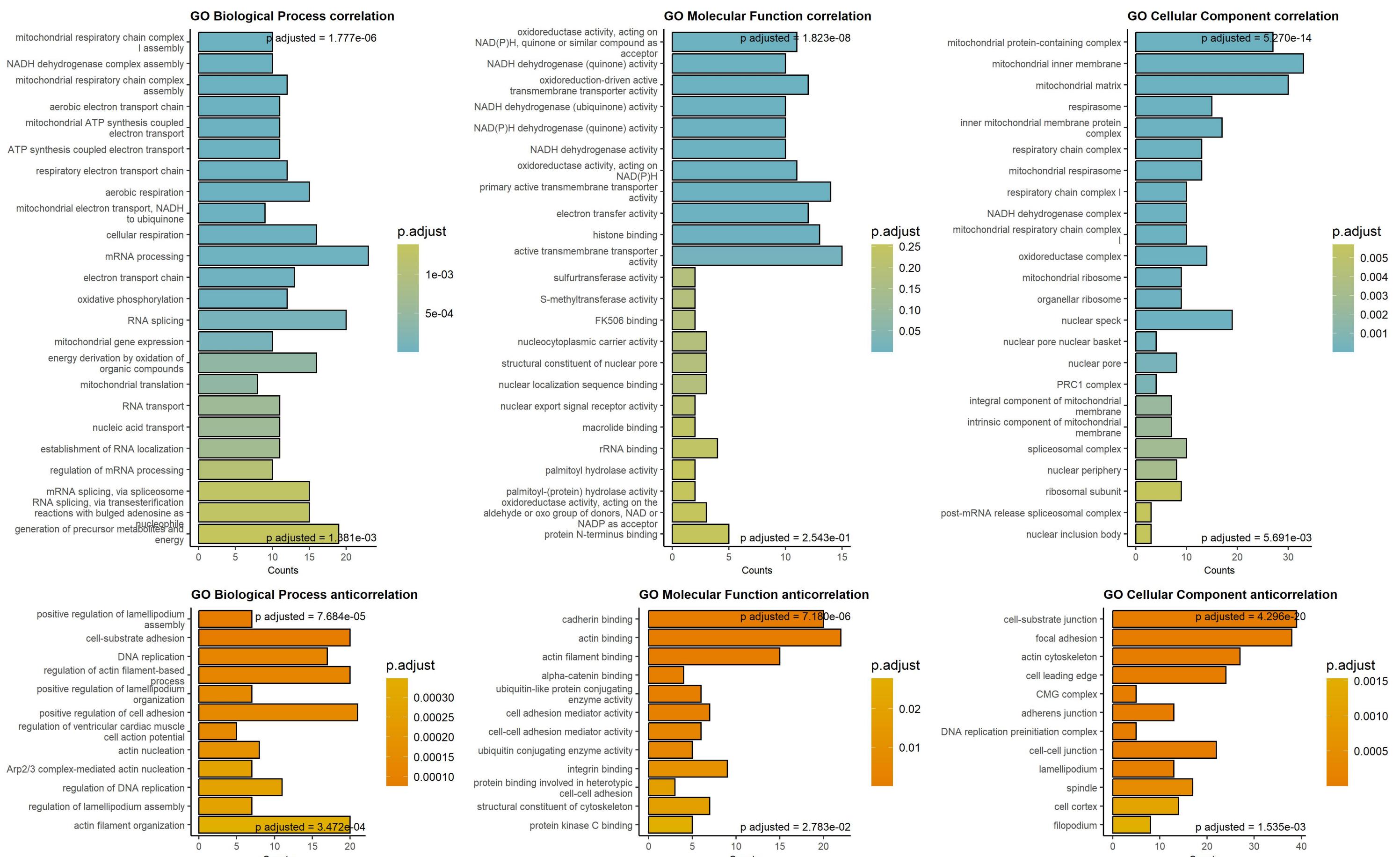


Sorted by p values!							
Downregulated in blood cancers at low/absent ELOA				Upregulated in blood cancers at low/absent ELOA			
logFC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
0.1	2.52e-26	GAPDH	glyceraldehyde-3-phosphate dehydrog	0.47	8.43e-04	DYSF	dysferlin
.85	1.88e-05	KTI12	KTI12 chromatin associated homolog	0.43	1.14e-03	IRS2	insulin receptor substrate 2
.26	3.47e-05	ISCU	iron-sulfur cluster assembly enzyme	0.88	4.57e-03	SFXN3	sideroflexin 3
.96	6.98e-05	NMD3	NMD3 ribosome export adaptor	0.51	5.00e-03	BST1	bone marrow stromal cell antigen 1
.06	6.98e-05	PSMC2	proteasome 26S subunit, ATPase 2	0.28	1.16e-02	UHRF1	ubiquitin like with PHD and ring fi
.29	6.98e-05	GTF2E1	general transcription factor IIIE su	0.47	1.17e-02	S100P	S100 calcium binding protein P
-1	1.13e-04	MRPL16	mitochondrial ribosomal protein L16	0.06	1.21e-02	RBM22	RNA binding motif protein 22
.06	1.28e-04	PSMC5	proteasome 26S subunit, ATPase 5	0.53	1.77e-02	CES1	carboxylesterase 1
.49	1.28e-04	SUPT7L	SPT7 like, STAGA complex subunit ga	0.66	1.96e-02	S100A8	S100 calcium binding protein A8
.91	2.02e-04	UTP11	UTP11 small subunit processome comp	0.09	2.01e-02	TRIR	telomerase RNA component interactin
.32	2.17e-04	POLR1D	RNA polymerase I and III subunit D	0.9	2.04e-02	TMEM123	transmembrane protein 123
.09	2.18e-04	RPS12	ribosomal protein S12	0.39	2.28e-02	RAB44	RAB44, member RAS oncogene family
.88	2.18e-04	MRPL32	mitochondrial ribosomal protein L32	0.72	2.30e-02	PYGL	glycogen phosphorylase L
.87	2.25e-04	GGA3	golgi associated, gamma adaptin ear	0.09	2.50e-02	SOD2	superoxide dismutase 2
.12	2.25e-04	SPTY2D1	SPT2 chromatin protein domain conta	0.07	2.61e-02	CTBP1	C-terminal binding protein 1
.77	2.25e-04	RPUSD2	RNA pseudouridine synthase domain c	0.07	2.62e-02	SIN3A	SIN3 transcription regulator family
.04	2.27e-04	RPSA	ribosomal protein SA	0.06	2.63e-02	MCTS1	MCTS1 re-initiation and release fac
.66	2.29e-04	WDR3	WD repeat domain 3	0.37	2.75e-02	CRMP1	collapsin response mediator protein
.63	2.71e-04	KPNA6	karyopherin subunit alpha 6	0.27	2.75e-02	SKAP2	src kinase associated phosphoprotei
.05	2.77e-04	RPS2	ribosomal protein S2	0.61	2.85e-02	SERF2	small EDRK-rich factor 2
.83	2.97e-04	NSA2	NSA2 ribosome biogenesis factor	0.48	2.92e-02	AGTRAP	angiotensin II receptor associated
.46	3.24e-04	PPAN	peter pan homolog	0.33	3.09e-02	PRAM1	PML-RARA regulated adaptor molecule
.68	3.46e-04	SSU72	SSU72 homolog, RNA polymerase II CT	0.31	3.16e-02	DACH1	dachshund family transcription fact
.07	4.00e-04	SF3B5	splicing factor 3b subunit 5	0.06	3.21e-02	PDS5A	PDS5 cohesin associated factor A
.86	4.00e-04	RRP7A	ribosomal RNA processing 7 homolog	0.64	3.47e-02	UTRN	utrophin
.09	4.00e-04	POLR2H	RNA polymerase II, I and III subuni	0.55	3.81e-02	KBTBD11	kelch repeat and BTB domain contain
.15	4.00e-04	UBE2Z	ubiquitin conjugating enzyme E2 Z	0.57	3.81e-02	FAM107B	family with sequence similarity 107
.07	4.00e-04	TIMM10	translocase of inner mitochondrial	0.69	3.92e-02	CTSG	cathepsin G
.56	4.00e-04	EIF2B2	eukaryotic translation initiation f	0.38	3.93e-02	SORBS3	sorbin and SH3 domain containing 3
.93	4.00e-04	MRPS30	mitochondrial ribosomal protein S30	0.12	3.94e-02	TOP2B	DNA topoisomerase II beta
.04	4.00e-04	RPS3A	ribosomal protein S3A	0.63	4.11e-02	SNTB1	syntrophin beta 1
.06	4.00e-04	RPL10	ribosomal protein L10	0.6	4.12e-02	PRTN3	proteinase 3
.05	4.00e-04	ARID3B	AT-rich interaction domain 3B	0.34	4.26e-02	SYNGR1	synaptogyrin 1
.06	4.00e-04	PSMC4	proteasome 26S subunit, ATPase 4	0.36	4.29e-02	CNPY3	canopy FGF signaling regulator 3
.07	4.00e-04	PARK7	Parkinsonism associated deglycase	0.08	5.00e-02	PNP	purine nucleoside phosphorylase
.9	4.00e-04	DPH5	diphthamide biosynthesis 5	0.65	5.14e-02	MGMT	O-6-methylguanine-DNA methyltransfe
.92	4.56e-04	SPAG5	sperm associated antigen 5	0.09	5.14e-02	NNT	nicotinamide nucleotide transhydrog
.04	4.68e-04	RPS20	ribosomal protein S20	0.48	5.31e-02	AZU1	azurocidin 1
.17	4.69e-04	CERBP7	CCAAT enhancer binding protein zeta	0.66	5.31e-02	ITGB5	integrin subunit alpha 5

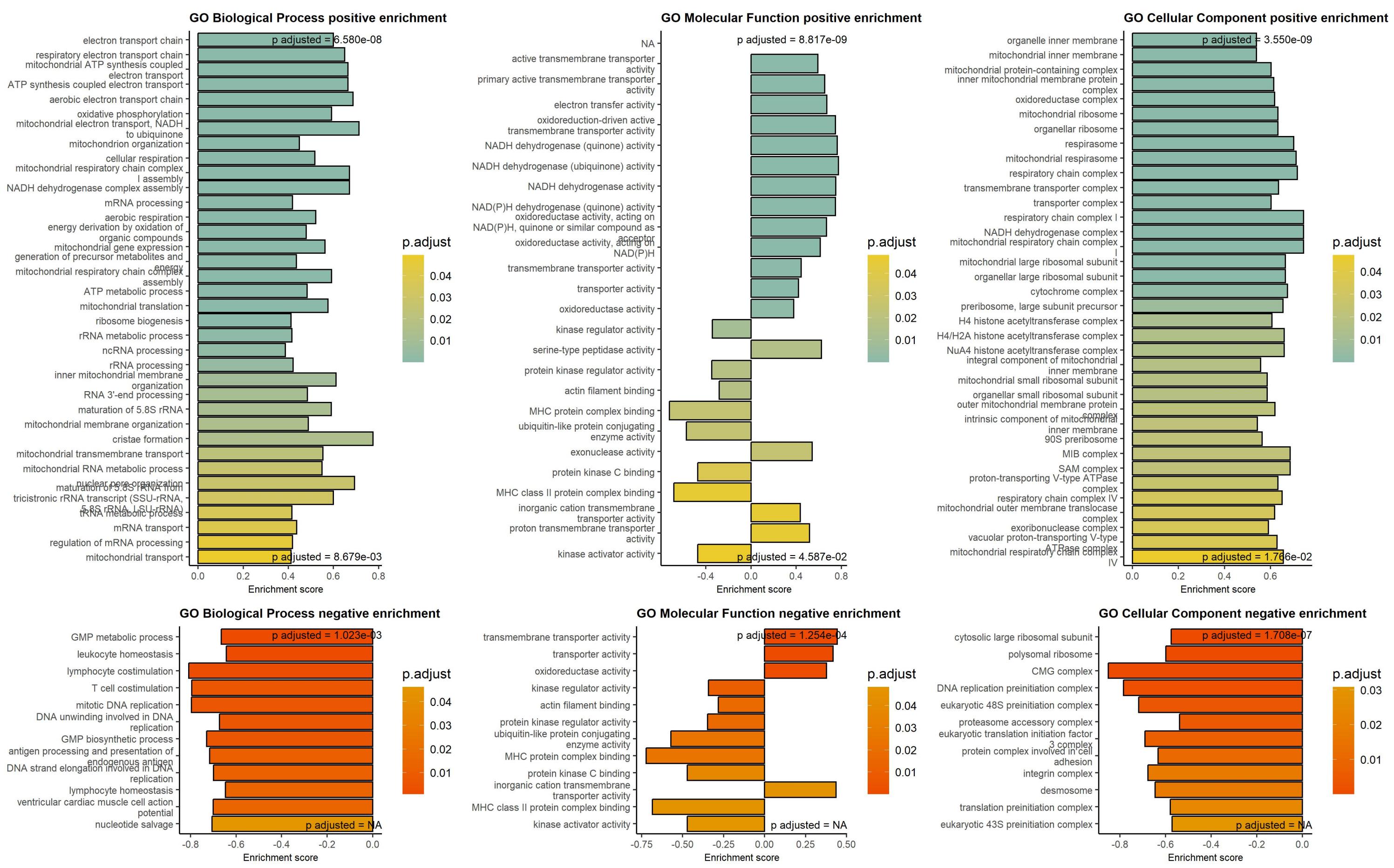


Sorted by p values!							
Downregulated in solid cancers at low/absent ELOA				Upregulated in solid cancers at low/absent ELOA			
FC	adj.P.Val	symbol	name	logFC	adj.P.Val	symbol	name
16	0.00e+00	H4C1	H4 clustered histone 1	0.11	5.80e-15	TMOD3	tropomodulin 3
77	4.03e-23	LEO1	LEO1 homolog, Paf1/RNA polymerase I	0.09	6.09e-13	MYL6	myosin light chain 6
92	9.26e-22	BPTF	bromodomain PHD finger transcriptio	0.18	2.48e-11	AHNAK	AHNAK nucleoprotein
01	1.11e-21	PHC2	polyhomeotic homolog 2	0.84	3.25e-11	EPS8L2	EPS8 like 2
1	5.56e-21	SRRM1	serine and arginine repetitive matr	0.13	6.68e-11	ITGB1	integrin subunit beta 1
87	3.06e-20	UPF3B	UPF3B regulator of nonsense mediate	0.13	1.10e-10	MYH9	myosin heavy chain 9
05	6.77e-20	SRRT	serrate, RNA effector molecule	0.1	1.56e-10	ACTN4	actinin alpha 4
81	4.02e-19	STEEP1	STING1 ER exit protein 1	0.59	3.28e-09	RAB11FIP5	RAB11 family interacting protein 5
75	5.25e-19	USP48	ubiquitin specific peptidase 48	0.07	3.72e-09	ACTBL2	actin beta like 2
77	1.51e-18	SUGP1	SURP and G-patch domain containing	0.62	4.22e-09	PPP1R13L	protein phosphatase 1 regulatory su
87	4.17e-18	YRDC	yrdC N6-threonylcarbamoyltransferas	0.76	5.55e-09	EGFR	epidermal growth factor receptor
05	8.66e-18	U2AF2	U2 small nuclear RNA auxiliary fact	0.17	7.14e-09	PLEC	plectin
06	1.64e-17	SF3A3	splicing factor 3a subunit 3	0.75	9.00e-09	SQOR	sulfide quinone oxidoreductase
09	3.50e-17	PARP1	poly(ADP-ribose) polymerase 1	0.07	9.09e-09	SPTLC1	serine palmitoyltransferase long ch
79	4.31e-17	ZMYM3	zinc finger MYM-type containing 3	0.18	9.18e-09	FLNB	filamin B
09	6.67e-17	SSRP1	structure specific recognition prot	0.77	1.50e-08	S100A16	S100 calcium binding protein A16
82	7.23e-17	EZH2	enhancer of zeste 2 polycomb repres	0.73	1.58e-08	AXL	AXL receptor tyrosine kinase
81	1.56e-16	FRG1	FSHD region gene 1	0.07	3.05e-08	IQGAP1	IQ motif containing GTPase activati
67	1.83e-16	ZC3HC1	zinc finger C3HC-type containing 1	0.76	3.80e-08	ANXA3	annexin A3
57	2.24e-16	CPSF4	cleavage and polyadenylation specif	0.58	4.46e-08	PHLDB2	pleckstrin homology like domain fam
04	2.27e-16	SNRPD2	small nuclear ribonucleoprotein D2	0.79	4.61e-08	CTSZ	cathepsin Z
08	2.29e-16	SRSF11	serine and arginine rich splicing f	0.44	6.17e-08	CNN2	calponin 2
55	3.94e-16	CTR9	CTR9 homolog, Paf1/RNA polymerase I	0.58	1.62e-07	RRAS	RAS related
7	4.31e-16	SNIP1	Smad nuclear interacting protein 1	0.1	2.14e-07	EZR	ezrin
05	5.41e-16	TARDBP	TAR DNA binding protein	0.7	3.62e-07	NT5E	5'-nucleotidase ecto
88	5.83e-16	BRD2	bromodomain containing 2	0.07	4.14e-07	RAB18	RAB18, member RAS oncogene famili
69	1.32e-15	SGF29	SAGA complex associated factor 29	0.47	4.55e-07	PDLIM1	PDZ and LIM domain 1
93	1.33e-15	MRGBP	MRG domain binding protein	0.11	9.04e-07	LASP1	LIM and SH3 protein 1
74	2.07e-15	POLR3A	RNA polymerase III subunit A	0.53	9.04e-07	MVP	major vault protein
68	2.19e-15	GTF2B	general transcription factor IIB	0.56	9.34e-07	MYOF	myoferlin
72	4.94e-15	METTL3	methyltransferase 3, N6-adenosine-m	0.68	9.53e-07	ITGB4	integrin subunit beta 4
65	5.34e-15	FNBP4	formin binding protein 4	0.09	1.02e-06	PICALM	phosphatidylinositol binding clathr
66	6.97e-15	PANK4	pantothenate kinase 4 (inactive)	0.39	1.19e-06	ERBIN	erbb2 interacting protein
8	7.33e-15	SMARCD1	SWI/SNF related, matrix associated,	0.61	1.23e-06	F3	coagulation factor III, tissue fact
83	7.80e-15	SNRNP27	small nuclear ribonucleoprotein U4/	0.57	1.41e-06	GPC1	glycan 1
06	8.00e-15	HNRNPR	heterogeneous nuclear ribonucleopro	0.47	1.47e-06	CCDC9B	coiled-coil domain containing 9B
06	1.39e-14	RUVBL1	RuvB like AAA ATPase 1	0.66	1.53e-06	S100A10	S100 calcium binding protein A10
76	1.45e-14	CWC27	CWC27 spliceosome associated cyclop	0.24	1.64e-06	MYH4	myosin heavy chain 4
59	1.52e-14	INTS11	intervening sequence 11	0.25	1.85e-06	AP2B1	beta 1,2-hydrolase domain 2

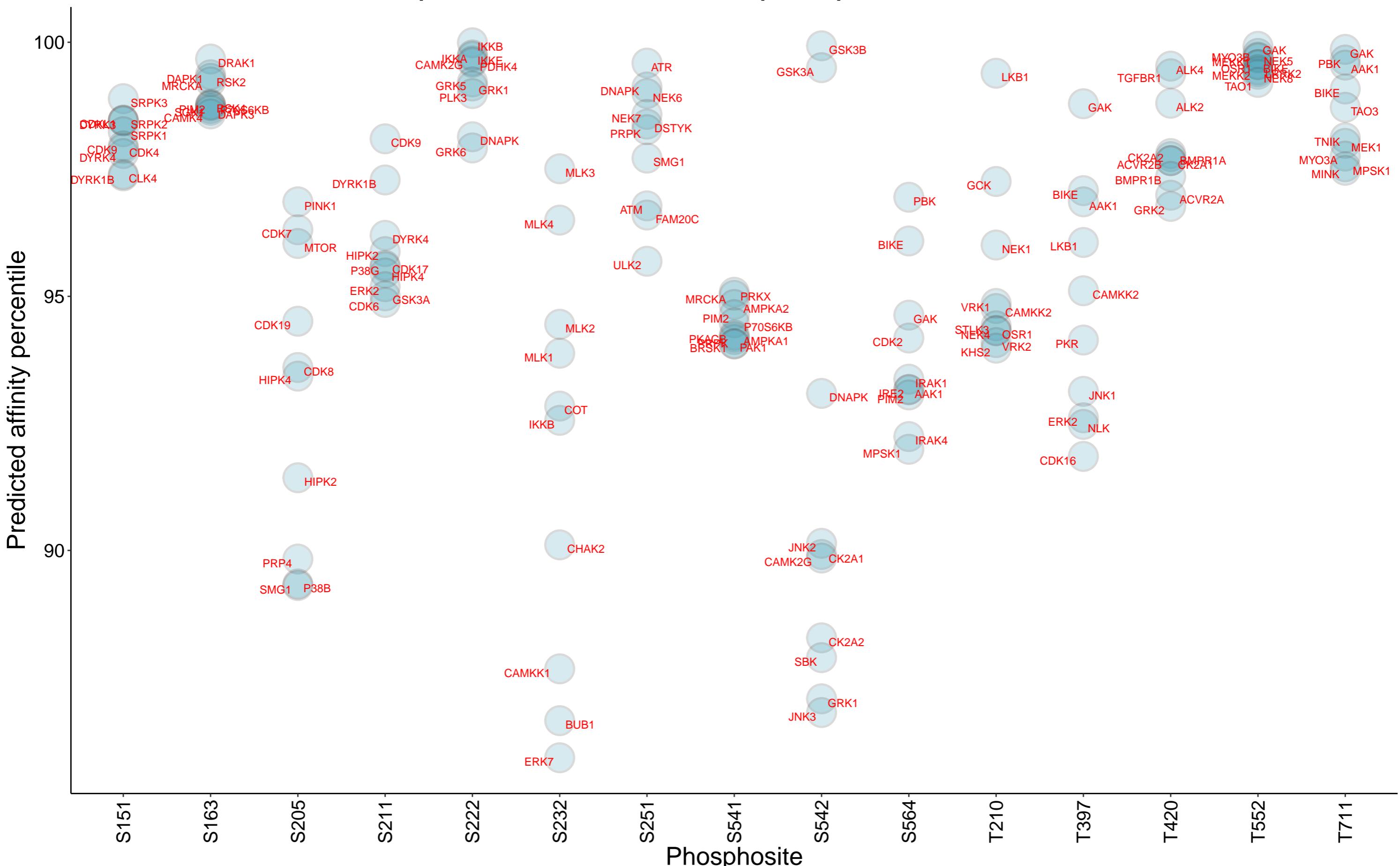
Top 250 correlation coefficients overrepresentation, ELOA protein, DB1



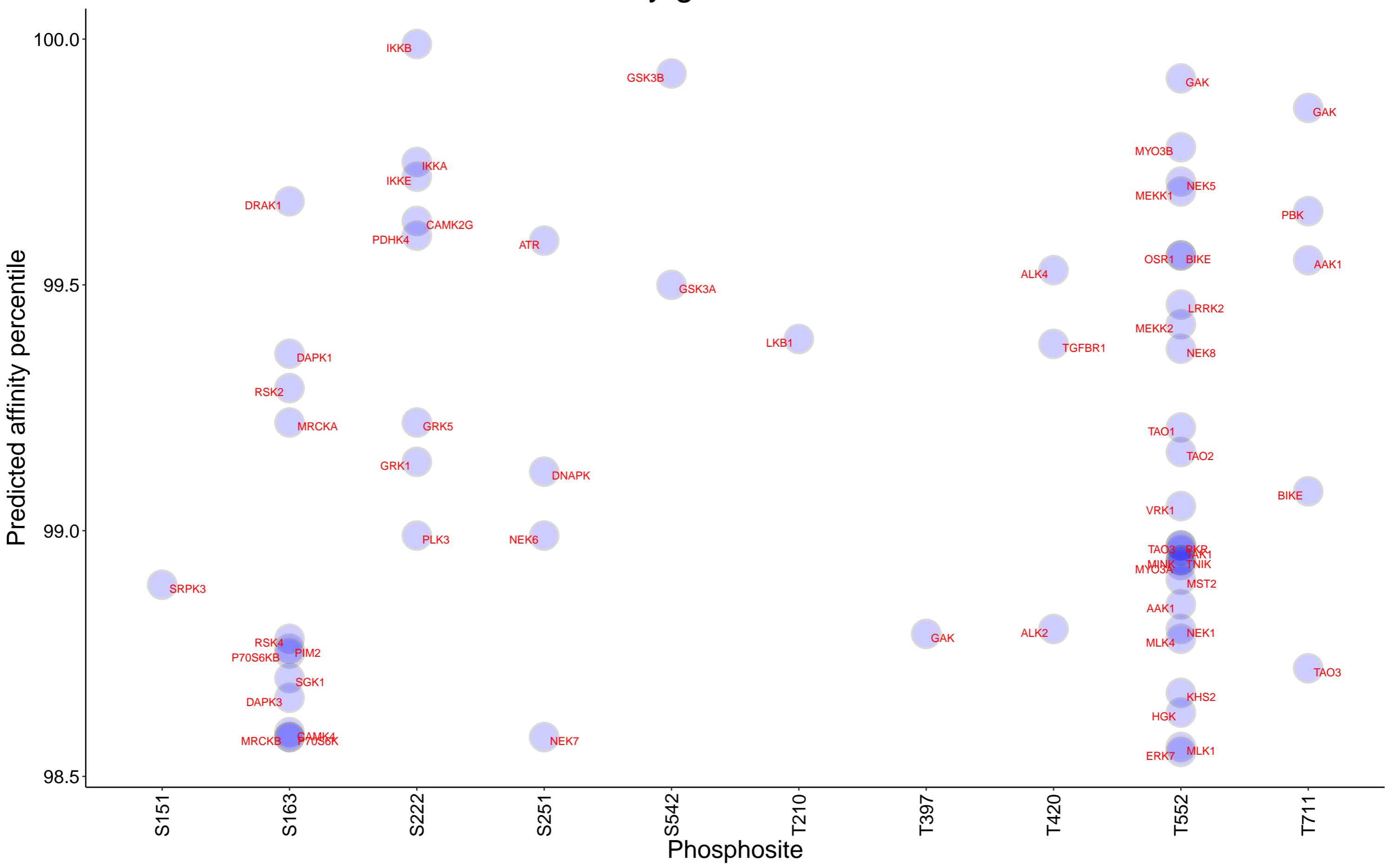
Gene Set Enrichment analysis on protein correlation coefficients, ELOA protein, DB1



Top 10 kinases for each phosphosite in ELOA



Kinases with affinity greater than 98.5% to ELOA



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

Beware of false positives in tissues with small number of samples

