

QRIME Scene Investigation - Report

Andrew Holding & Matt Eldridge

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1 Differential binding

Here follows the analysis output for ER 45min vs ER 0min, excluding peptides with missing intensities, quantile normalization.

1.1 MA plot

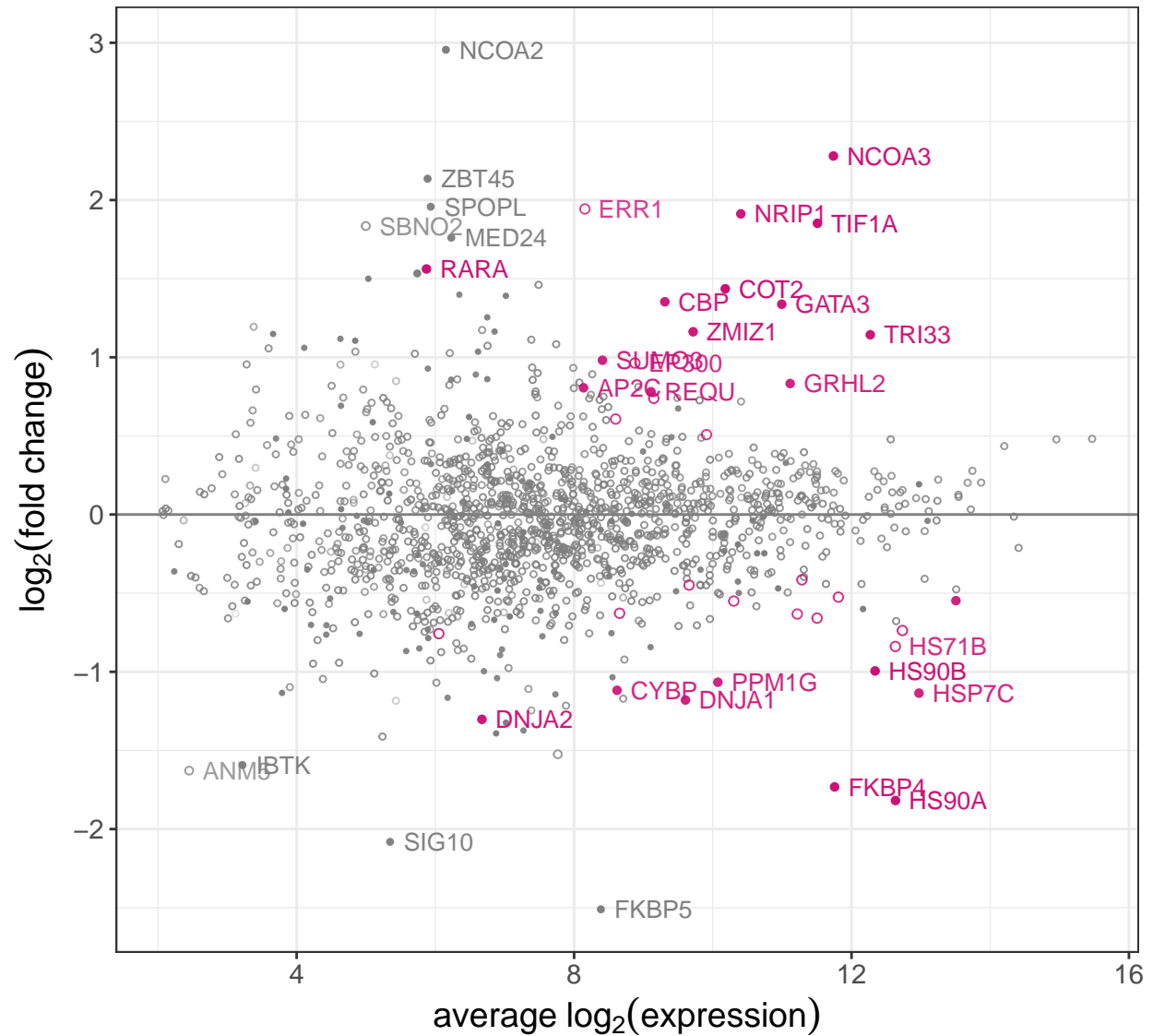
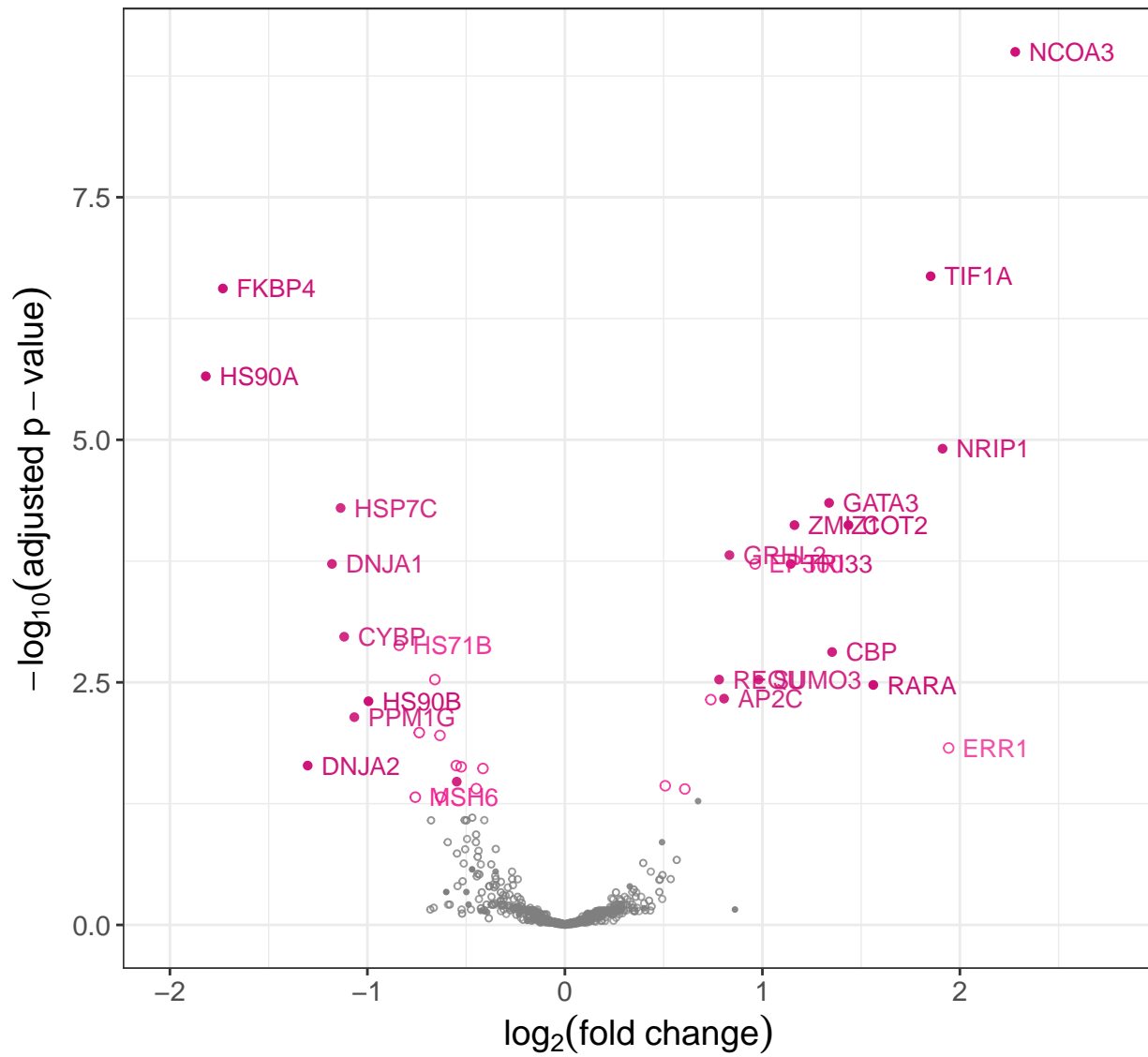


Figure 1: MA plot of the average intensity against log₂ fold change for the ER 45min vs ER 0min comparison (excluding peptides with missing intensities, quantile normalization). Top ranking differentially-bound proteins with false discovery rate below 0.05 are highlighted in pink. Open circles indicate that the protein is non-specific from the IgG control comparison.

1.2 Volcano plot



1.3 P-value histogram

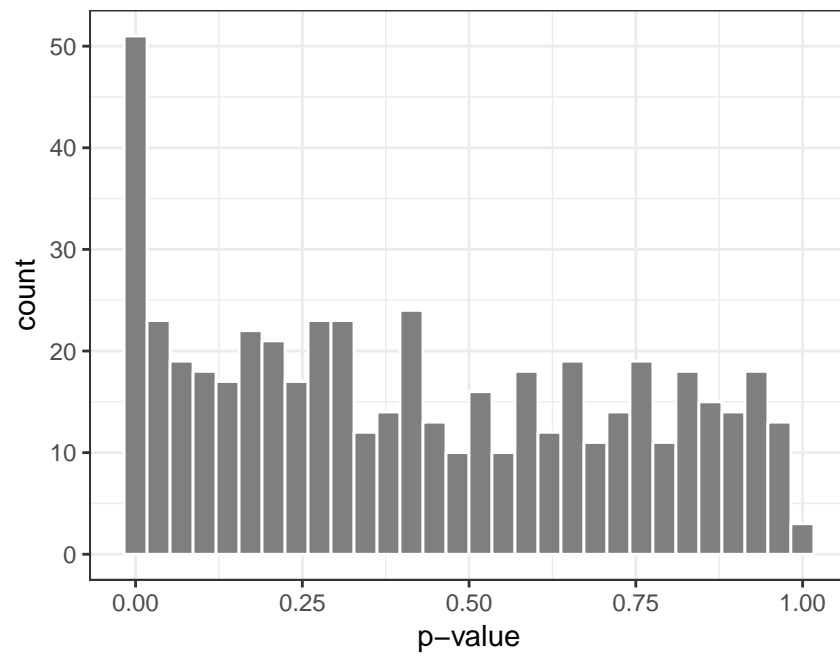


Figure 2: Histogram of p-values for the ER 45min vs ER 0min comparison (excluding peptides with missing intensities, quantile normalization)

1.4 QQ plot

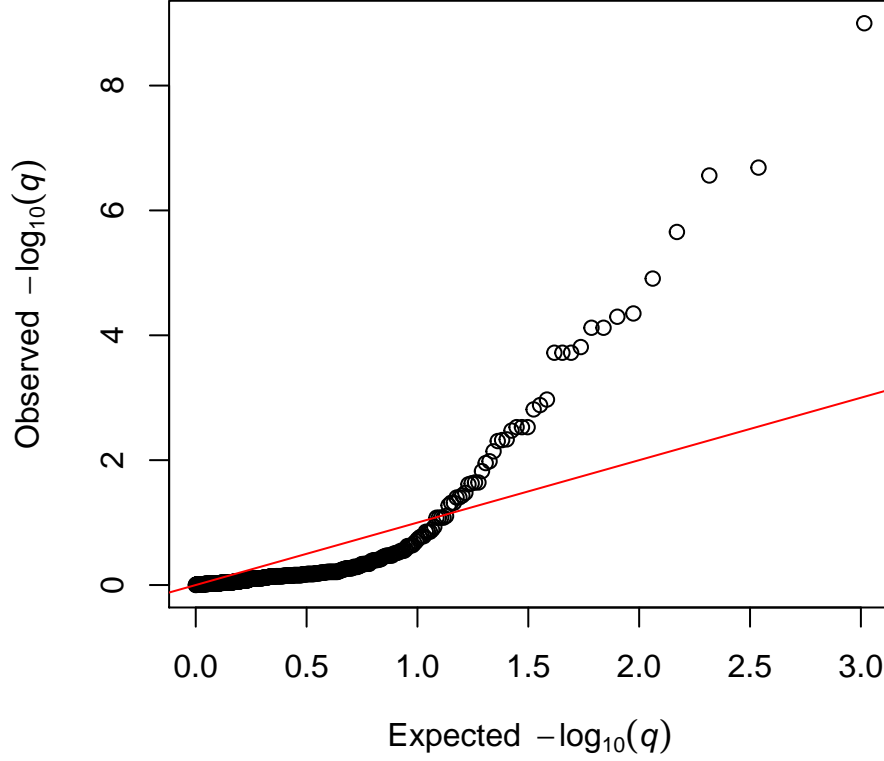


Figure 3: QQ plot of the adjusted p-values for the ER 45min vs ER 0min comparison (excluding peptides with missing intensities, quantile normalization)

2 Differential binding results tables

The following tables contain the top ranking differentially bound proteins for each comparison. Included are all proteins that reach a statistical significance of 0.05 in terms of the adjusted p-value and those with an absolute \log_2 fold change of 1 or above.

The IgG column gives the larger of the \log_2 fold changes for the two groups against the IgG control and an asterisk indicates specific binding where this \log_2 fold change is above a threshold of 1. N is the number of replicates in which the protein was observed.

In all cases, peptide intensities were quantile normalized and measurements with missing values were removed prior to summarization at the protein level.

2.1 ER 45min vs ER 0min

Protein	Gene	N	log2FC	Avg Expr	p-value	B	IgG
Q15596	NCOA2	1	2.96	6.15			2.12 *
Q13451	FKBP5	2	-2.51	8.39			2.55 *
Q9Y6Q9	NCOA3	3	2.28	11.74	1e-09	18.68	1.90 *
Q96K62	ZBT45	1	2.14	5.89			2.58 *
Q96LC7	SIG10	1	-2.08	5.35			1.79 *
Q6IQ16	SPOPL	1	1.96	5.93			1.59 *
P11474	ERR1	3	1.94	8.16	0.015	-0.99	-0.14
P48552	NRIP1	3	1.91	10.40	1.2e-05	7.81	1.56 *
O15164	TIF1A	3	1.85	11.51	2.1e-07	12.83	2.15 *
Q9Y2G9	SBNO2	1	1.83	5.00			0.09
P07900	HS90A	3	-1.82	12.63	2.2e-06	9.77	2.23 *
O75448	MED24	1	1.76	6.23			1.66 *
Q02790	FKBP4	3	-1.73	11.76	2.8e-07	12.14	1.89 *
O14744	ANM5	1	-1.63	2.45			-0.44
Q9P2D0	IBTK	1	-1.59	3.22			1.84 *
P10276	RARA	3	1.56	5.87	0.0034	0.75	2.75 *
Q15648	MED1	1	1.53	5.74			1.97 *
Q5D862	FILA2	1	-1.52	7.77			-0.29
P32242	OTX1	2	1.50	5.03			1.88 *
Q2M1P5	KIF7	1	1.46	7.49			0.71
P24468	COT2	3	1.44	10.18	7.6e-05	5.43	2.07 *
P34932	HSP74	1	-1.41	5.24			0.54
O14770	MEIS2	1	1.40	6.35			1.08 *
P61960	UFM1	1	-1.39	6.88			1.92 *
Q8N2W9	PIAS4	2	1.39	7.02			1.68 *
Q86UV5	UBP48	1	-1.37	7.27			1.36 *
Q92793	CBP	3	1.35	9.31	0.0015	1.76	1.48 *
P23771	GATA3	3	1.34	10.99	4.5e-05	6.33	1.61 *
Q9P2D7	DYH1	1	-1.32	7.02			2.63 *
O60884	DNJA2	3	-1.30	6.67	0.023	-1.51	1.76 *
Q9UBW7	ZMYM2	1	1.25	6.75			1.46 *
Q01546	K22O	2	-1.25	7.38			-1.21
O60809	PRA10	1	-1.22	7.88			-0.24
O15117	FYB	1	1.19	3.38			-1.88
P53990	IST1	1	-1.18	5.43			-4.76
P31689	DNJA1	3	-1.18	9.61	0.00019	4.08	1.20 *
O00712	NFIB	1	1.17	6.67			-0.34
Q8N283	ANR35	1	-1.17	8.71			-0.15
Q9UL15	BAG5	1	-1.16	6.18			1.11 *
Q6PHW0	IYD1	1	1.16	6.85			1.52 *
Q9ULJ6	ZMIZ1	3	1.16	9.72	7.6e-05	5.39	1.61 *
P15408	FOSL2	1	1.15	3.66			1.69 *
Q9UNE7	CHIP	2	-1.14	7.73			1.05 *
Q9UPN9	TRI33	3	1.14	12.27	0.00019	4.24	1.73 *
P11142	HSP7C	3	-1.14	12.97	5e-05	6.05	1.00 *
Q9NWS6	F118A	1	-1.13	3.79			1.60 *
Q9HB71	CYBP	3	-1.12	8.62	0.0011	2.26	1.02 *
Q8TCU4	ALMS1	1	1.12	4.63			1.44 *
O14686	KMT2D	1	1.11	7.38			0.39

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Protein	Gene	N	log2FC	Avg Expr	p-value	B	IgG	
Q7Z794	K2C1B	1	-1.11	7.34			-0.84	
Q6KC79	NIPBL	1	1.11	4.84			2.63	*
Q68E01	INT3	2	-1.10	3.90			-0.67	
Q8NFD5	ARI1B	1	1.08	7.74			0.56	
Q9Y6X2	PIAS3	2	1.07	6.75			0.71	
Q92624	APBP2	1	-1.07	6.01			0.05	
O15355	PPM1G	3	-1.07	10.07	0.0072	-0.20	1.09	*
Q8NH53	O52N1	1	1.06	4.11			1.28	*
Q13492	PICAL	1	1.06	3.60			0.12	
Q4L235	ACSF4	1	-1.05	4.38			-0.13	
O00170	AIP	2	-1.04	6.89			1.13	*
P14625	ENPL	2	1.04	4.85			-0.35	
O60244	MED14	1	1.04	6.62			1.56	*
Q15185	TEBP	1	-1.03	8.55			1.29	*
Q6P2C8	MED27	1	1.03	6.21			-0.01	
Q5VTD9	GFI1B	1	1.02	5.70			0.42	
O14929	HAT1	2	-1.01	5.12			0.70	
P08238	HS90B	3	-0.99	12.34	0.0049	0.22	2.04	*
P55854	SUMO3	3	0.98	8.41	0.003	0.96	1.13	*
Q09472	EP300	3	0.96	8.88	0.00019	4.12	0.80	
P0DMV9	HS71B	3	-0.84	12.63	0.0013	1.99	0.65	
Q6ISB3	GRHL2	3	0.83	11.12	0.00015	4.56	1.04	*
Q92754	AP2C	3	0.81	8.14	0.0046	0.38	1.15	*
Q92785	REQU	3	0.78	9.11	0.003	0.93	1.16	*
P52701	MSH6	3	-0.76	6.05	0.048	-2.50	0.97	
P63165	SUMO1	3	0.74	9.15	0.0048	0.30	0.72	
P12956	XRCC6	3	-0.74	12.73	0.01	-0.60	0.90	
P31948	STIP1	3	-0.66	11.50	0.003	0.94	0.59	
P78527	PRKDC	3	-0.63	11.22	0.011	-0.71	0.36	
Q9HAV4	XPO5	3	-0.63	8.66	0.048	-2.50	0.72	
O14497	ARI1A	3	0.61	8.60	0.04	-2.26	0.29	
Q9Y383	LC7L2	3	-0.55	10.30	0.023	-1.53	0.51	
Q13263	TIF1B	3	-0.55	13.51	0.033	-2.00	1.17	*
P09874	PARP1	3	-0.53	11.81	0.023	-1.59	0.63	
Q92925	SMRD2	3	0.51	9.91	0.037	-2.13	0.23	
P25685	DNJB1	3	-0.45	9.66	0.039	-2.22	0.60	
Q99873	ANM1	3	-0.42	11.29	0.024	-1.66	0.65	

Table 1: Top ranking differentially bound proteins from the ER 45min vs ER 0min comparison, sorted by log2 fold change.