

## Supplementary Table of Contents

### Supplementary Figure 1

The combinatorial nature of the regulation of acetylation by transcription factor is evident by the fact that the majority of promoters are significantly bound and regulated by multiple transcription factors in our model. Only multivariate, as opposed to univariate, models can capture this combinatorial regulation.

### Supplementary Figure 2

We capture the non-linear relationships between the binding of a transcription factor and the change in acetylation using sigmoidal curves. At low levels of binding the effect on acetylation is small, while at high levels the effect saturates at some maximal value. The midpoint of the sigmoidal function is a natural threshold for defining which promoters are genuine targets of a factor.

### Supplementary Figure 3

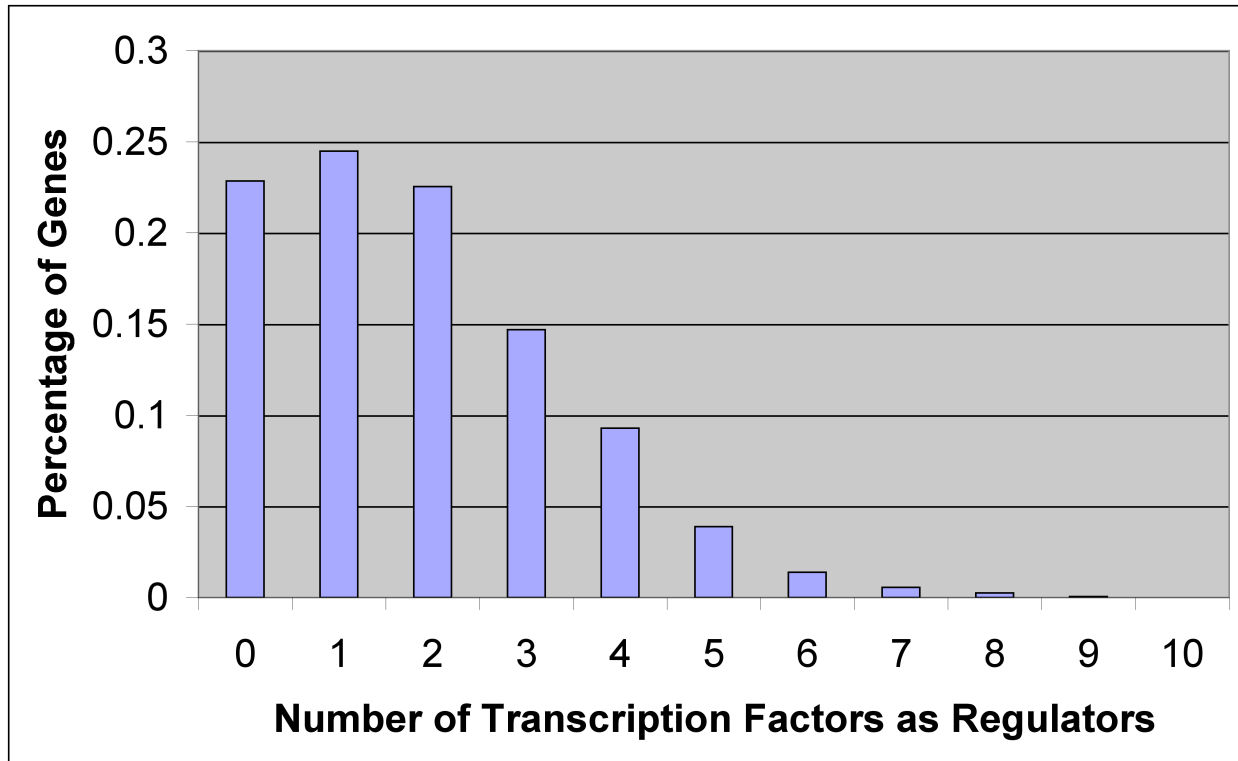
The sigmoidal function associated with each transcription actor allows us to define which promoters are targets by virtue of the fact that the binding is higher than the midpoint of the function. Based on this definition, we see that several factors act as global regulators since they bind many hundreds of genes, while other bind more limited sets of targets.

### Supplementary Figure 4

Reduction in variance (RIV) of our linear model. Our ability to model acetylation profiles in terms of transcription factor binding data is measured in terms of reduction in variance: one minus the ratio of the variance of the model residual over the variance of the acetylation measurements. A higher value of RIV indicates a better fit between our model and the observed data, with a value of one indicating perfect agreement.

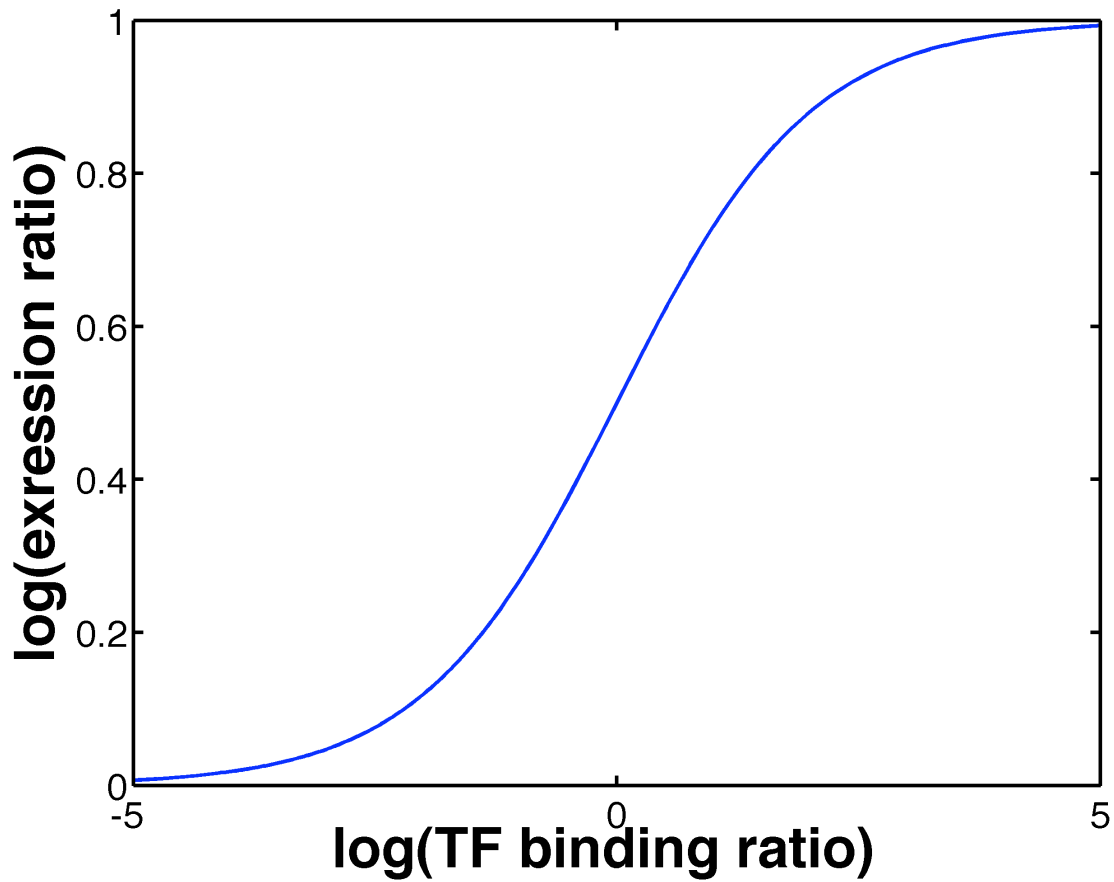
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The parameters of our model including for each transcription factor its midpoint and maximal value, along with the number of target genes.



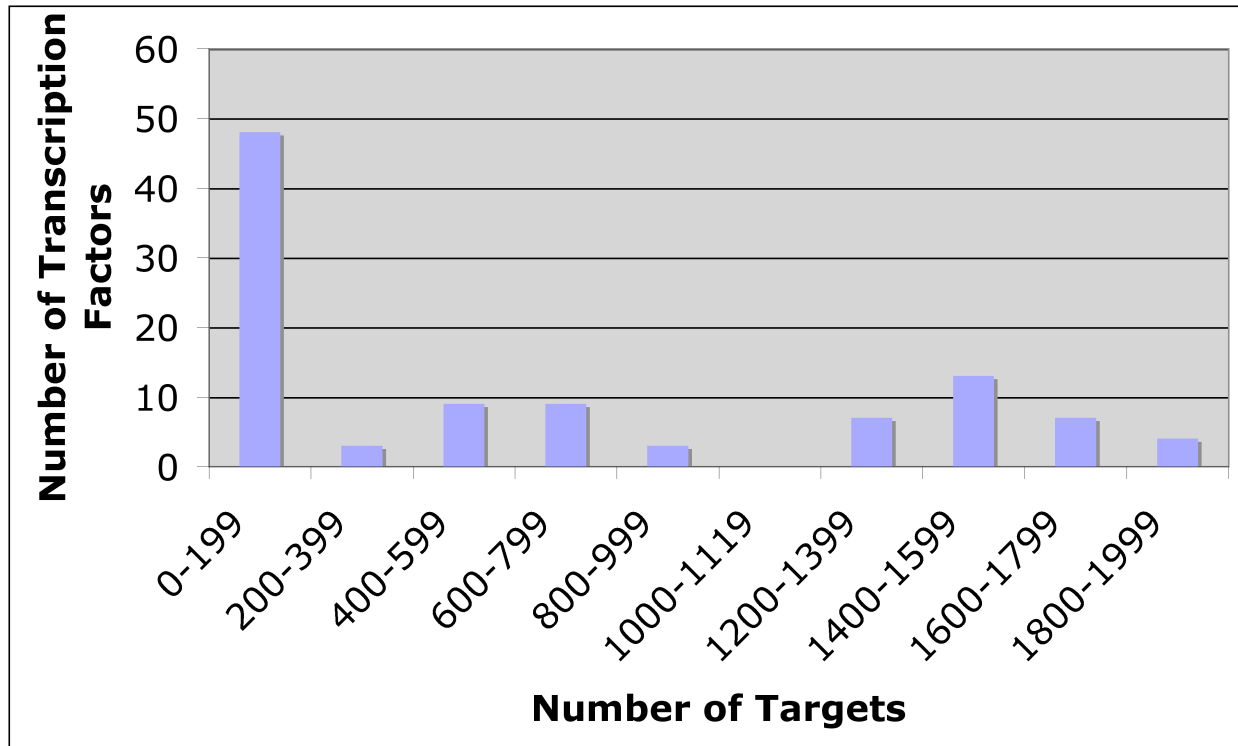
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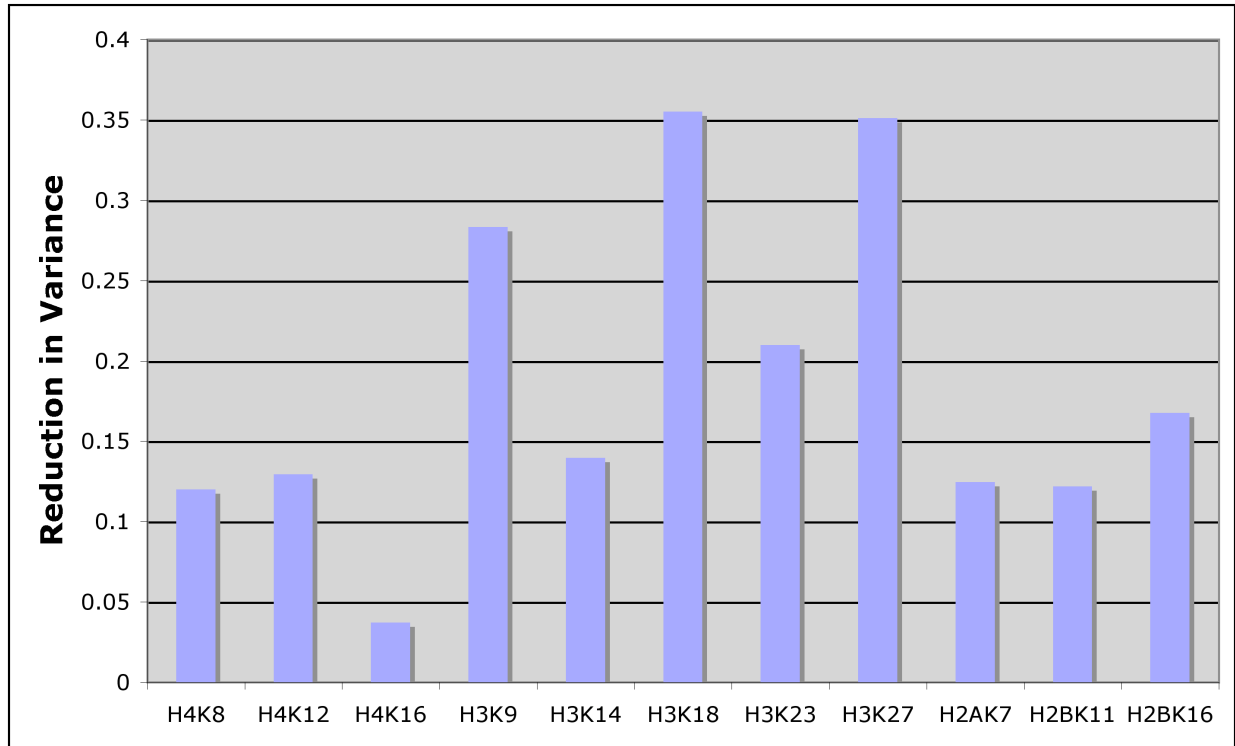
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### iK8

New Logis Coef	Knot	Genes	HAT	HDAC
SUM1	-0.7007	0.7	51	HST1, RFM1,
SPT2	0.24184	0	1536	HIF1,
RLR1	-1.4414	0	1545	
YBL054W	0.14175	0.2	754	
HIR3	0.36291	0.6	202	TAF1,
GAT3	-0.5637	1.5	23	
UME6	-0.2723	1	118	TAF10, SIN3, RPD3, RXT3, SDS3,
ABF1	0.29198	0	817	

### iK12

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	0.50273	1	92	
UME6	-0.3517	1	118	TAF10, SIN3, RPD3, RXT3, SDS3,
ABF1	0.17805	0.6	457	
SUM1	-0.4109	0.7	51	HST1, RFM1,
SPT2	0.88712	0.7	117	HIF1,
RLR1	-1.3066	0	1545	
HIR3	0.3536	0.6	202	TAF1,

### iK16

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	0.39561	0.8	102	
GAT3	-0.4047	1.2	72	

### iK9

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	0.56817	0.9	94	
HIR2	0.27309	0.2	610	
SUM1	-0.5253	0.8	37	HST1, RFM1,
MIG3	-1.7236	0	1753	
SPT2	0.31025	0	1536	HIF1,

UME6	-0.3971	1.2	90 TAF10,	SIN3, RPD3, RXT3, SDS3,
GAT3	-0.5098	1.4	41	
HIR3	1.31375	1	56 TAF1,	
RLR1	-1.1326	0	1545	
MET18	-0.8196	0	1873	
			ADA2, SPT3, SPT7, EPL1, YNG2, TAF9, TAF5, TAF14, SPT20, TAF6, TAF12, TAF1,	
GCN4	0.25478	0.5	88 NGG1,	

### iK14

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	0.62355	0.4	211	
SUM1	-0.6144	0.8	37	HST1, RFM1, SIN3, RPD3, RXT3, SDS3,
UME6	-0.908	2	25 TAF10,	
RLR1	-1.3141	0	1545	
YML081W	0.55977	0.5	153	
STP4	-1.4586	1.4	5	
SPT2	0.61004	0	1536 HIF1,	
HIR3	0.2618	0.4	404 TAF1,	
MIG2	-0.1744	0.5	132	

### iK18

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	1.363	1.6	81	
MIG3	-2.9375	0.4	72	
SPT2	0.54308	0	1536 HIF1,	
YML081W	4.20418	1.7	0	
STP4	-1.5361	0.6	148	
RLR1	-1.8647	0	1545	
HIR3	2.06146	0.4	404 TAF1,	
UME6	-0.3295	0.9	138 TAF10,	SIN3, RPD3, RXT3, SDS3,
SUM1	-0.3647	0.5	123	HST1, RFM1,
MET18	-1.3239	0	1873	
MOT2	0.38101	0.6	632	

				ADA2, SPT3, SPT7, EPL1, YNG2, TAF9, TAF5, TAF14, SPT20, TAF6, TAF12, TAF1,
GCN4	0.29708	0.4	141	NGG1,
PDC2	-0.961	0.8	11	
YBL054W	0.15372	0.2	754	
SUT1	-0.1478	0	1313	

### iK23

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	1.20952	1.3	87	
YML081W	0.39355	0.2	638	
STP4	-2.118	2	0	
UME6	-0.6639	1.5	57	SIN3, RPD3, RXT3, SDS3,
RLR1	-0.3831	0.1	1271	
HIR3	1.38515	1.1	39	TAF10, TAF1,
SNF1	0.21906	0.2	640	GCN5,
SUM1	-1.1715	2	2	HST1, RFM1,
INO4	-0.1228	0	1296	
MET18	-1.3362	0	1873	
GAT3	-0.3722	1.1	86	
SPT2	0.44367	0	1536	HIF1,

### iK27

New Logis Coef	Knot	Genes	HAT	HDAC
HIR2	0.29245	0.2	610	
FHL1	1.15026	2	71	
SUM1	-1.298	1.9	2	HST1, RFM1,
GAT3	-0.5331	1.2	72	
UME6	-0.9194	1.6	46	SIN3, RPD3, RXT3, SDS3,
RTG3	-0.2335	0	1736	
HIR3	1.66299	0.3	551	TAF10, TAF1,
RLR1	-1.378	0.3	522	
YML081W	2.28613	1.6	0	
SPT2	0.59655	0	1536	HIF1,
MET18	-0.8276	0	1873	
MIG3	-1.3357	0	1753	
STP4	-0.8791	0.6	148	



HIR1	0.12405	0	1627
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### iK7

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	0.85758	0	870	
UME6	-0.7948	1.6	46 TAF10,	SIN3, RPD3, RXT3, SDS3,
ABF1	0.39307	0.7	420	
SUM1	-0.5824	0.8	37	HST1, RFM1,
INO4	-0.1393	0	1296	
THI2	-0.9467	0	1652	
HIR3	0.10562	0.4	404 TAF1,	

### iK11

New Logis Coef	Knot	Genes	HAT	HDAC
MIG3	-1.3173	0	1753	
UME6	-0.2878	1	118 TAF10,	SIN3, RPD3, RXT3, SDS3,
HIR3	0.30588	0.4	404 TAF1,	
STP4	-1.0819	0.4	449	
YML081W	1.07315	0.2	638	
RLR1	-0.825	0	1545	
INO4	-0.108	0	1296	
GAT3	-0.4951	1.4	41	

### iH2BK16

New Logis Coef	Knot	Genes	HAT	HDAC
FHL1	0.94179	0	870	
MIG3	-1.343	0	1753	
YBL054W	0.11561	0.2	754	
UME6	-0.5275	1.3	78 TAF10,	SIN3, RPD3, RXT3, SDS3,
INO4	-0.1193	0	1296	
RTS2	0.14048	0.8	184	
NRG1	-0.6717	0.5	133	
RLR1	-1.0361	0	1545	
HIR3	1.38334	1	56 TAF1,	
SUT1	-0.1516	0	1313	
SUM1	-0.2981	0.9	30	HST1, RFM1,
GAT3	-0.646	1.2	72	

GCN4	0.19032	0.6	59	ADA2, SPT3, SPT7, EPL1, YNG2, TAF9, TAF5, TAF14, SPT20, TAF6, TAF12, TAF1, NGG1,
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