

Figure S1

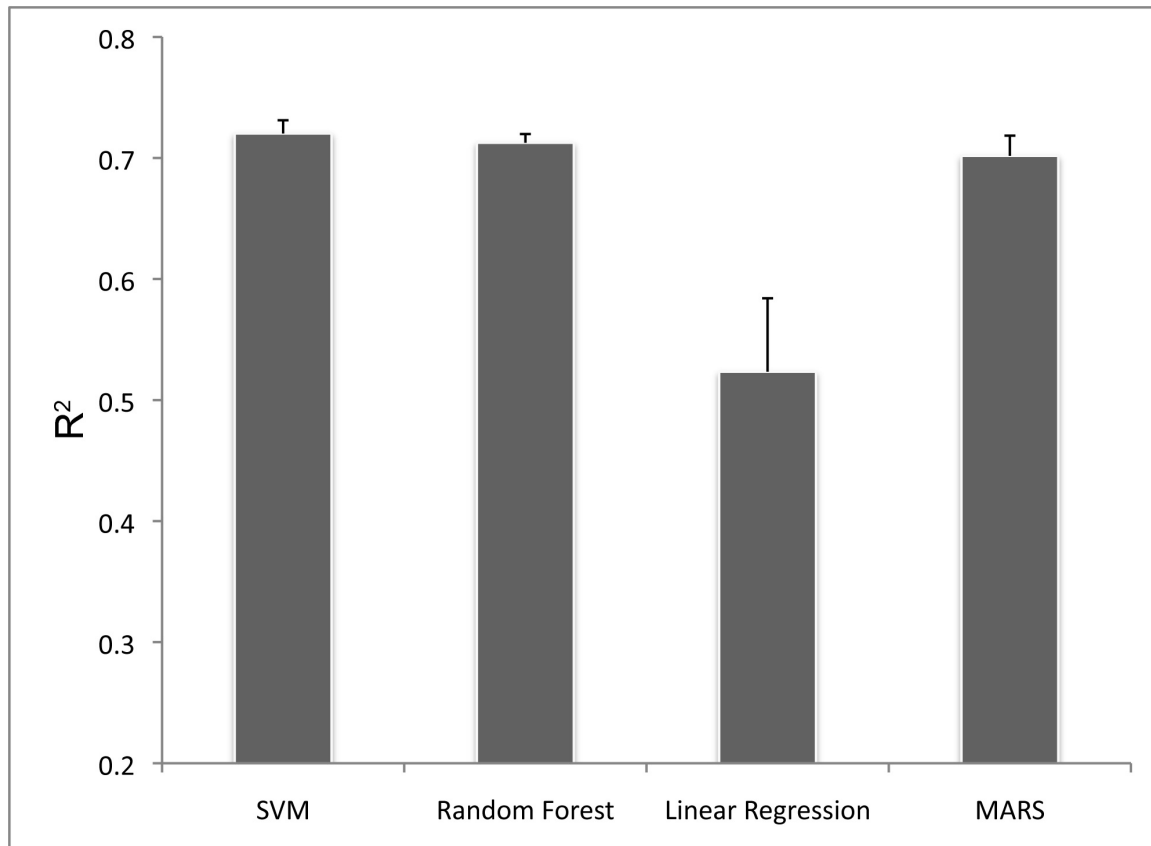


Figure S1: Predictive accuracy of different machine learning methods. The accuracy was represented as R^2 , the percentage of variation of gene expression explained by a model.

Figure S2

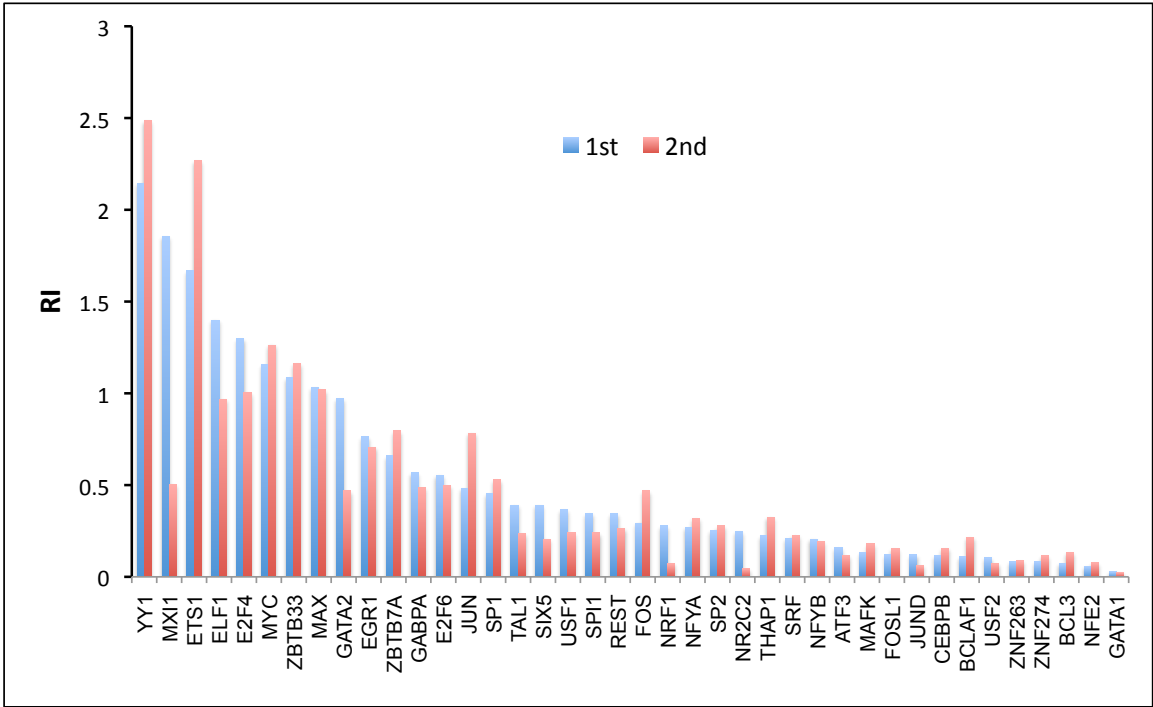


Figure S2: Relative importance of different transcription factors in models for predicting the first TSS and the second TSS of genes. Only TSSs from genes with at least two TSSs were included.

Figure S3

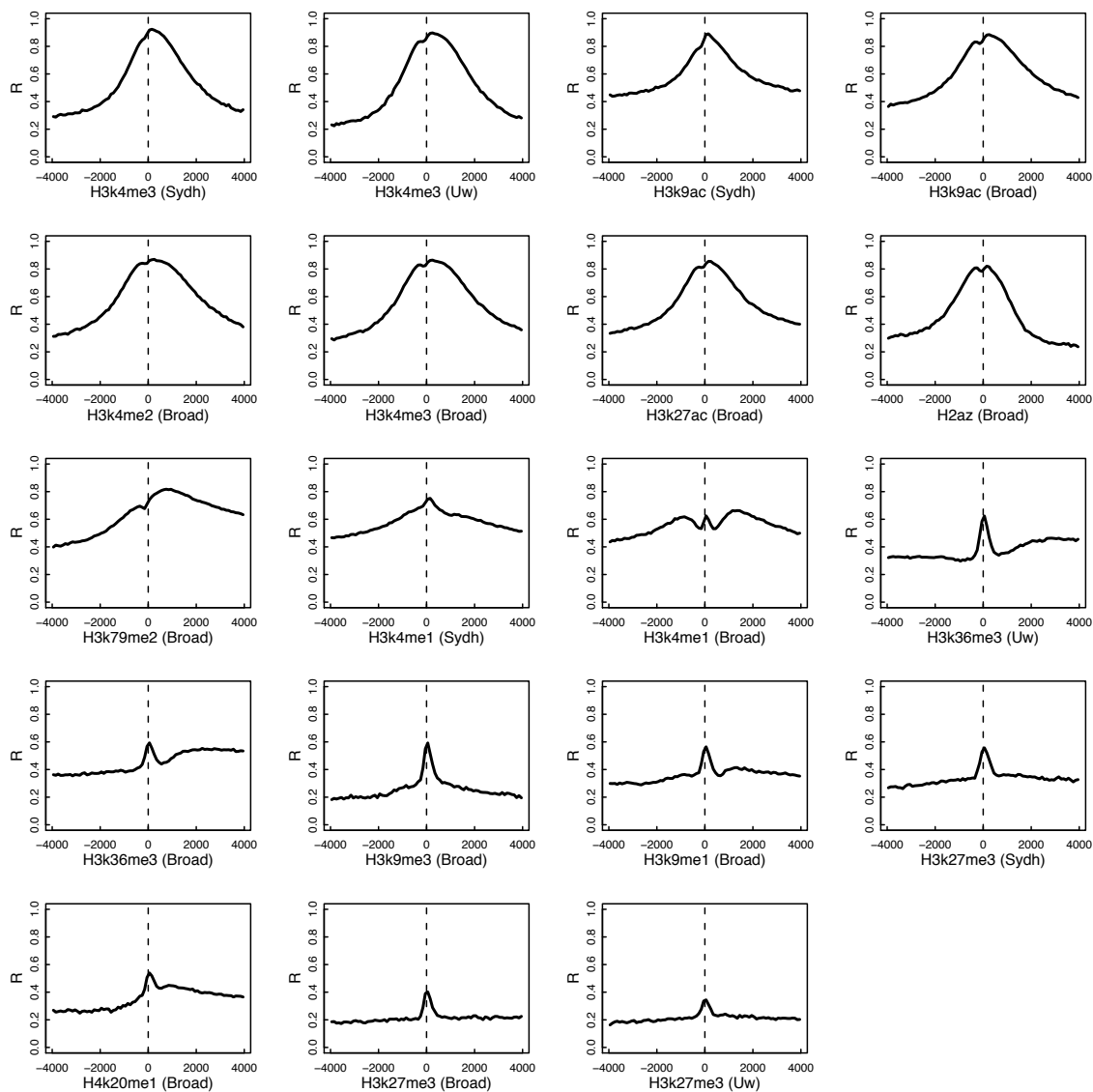


Figure S3: Accuracy of transcription factors binding signals at different positions for predicting histone modification signals. TF binding signals in 80 bins around TSS were used as predictors. The accuracy was measured as the correlation between predicted and experimental measured histone modification signals.

Figure S4

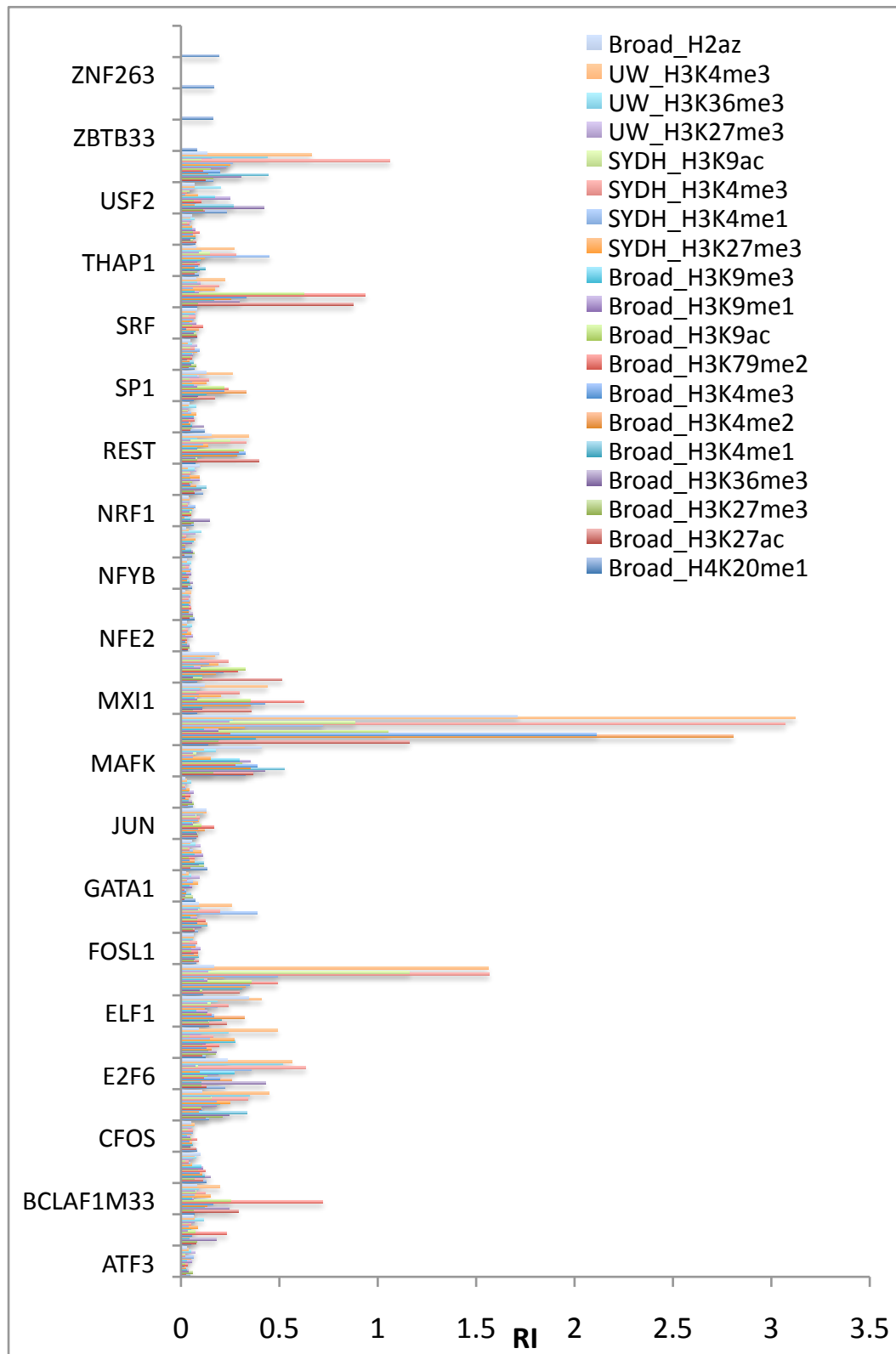


Figure S4: The relative importance of transcription factors in predicting different histone modification signals.

Figure S5

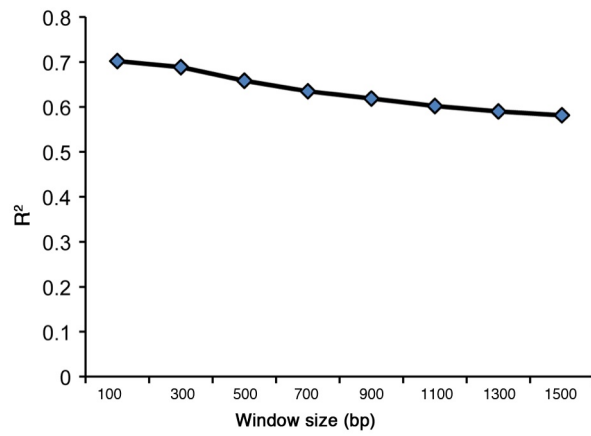


Figure S5: Predictive accuracy of the TF models using binding signals in bins of different window size. Note that TF binding signals in a narrowed DNA region around TSS achieves the highest prediction accuracy.

Legends of Supplementary Tables:

Table S1: Predictive accuracy of models with a single transcription factors. In each model, a single TF is used as variable for predicting TSS expression levels.

Table S2: Correlations between the expression level of TSSs and the binding signal of transcription factors.

Table S3: Relative importance of transcription factors in models for predicting different histone modification types.

Table S4: Predictive accuracy of five models. For each model, we calculate the fractions of variance of promoter expression levels (R^2) explained by TFSS-binding data alone (TFSS model), X data alone (X model), a combination of TFSS binding and X data (TFSS + X model), the additional variance explained by TFSS-binding data after considering the X data (TFSS|X model), and the additional variances explained by X data after considering the TFSS binding data (X|TFSS model). X can be non-specific TFs (TFNS), histone modification (HM), DNase I hypersensitivity (Dnase), FAIRE signals (FAIRE) and nucleosome occupation signals (nucleosome).

Table S5: Accuracy of TF models for predicting expression levels of TSS and transcripts measured by RNA-seq data.

Table S6: Enriched GO categories in poorly predicted genes and well predicted genes.

Table S1

TF	Category	Correlation	R2
EP300	TFNS	0.490	0.240
GTF2B	TFNS	0.703	0.495
GTF2F1	TFNS	0.710	0.505
RDBP	TFNS	0.532	0.284
SIN3A	TFNS	0.695	0.483
TAF1	TFNS	0.818	0.669
TAF7	TFNS	0.710	0.504
TBP	TFNS	0.796	0.634
ATF3	TFSS	0.454	0.206
BCL3	TFSS	0.542	0.294
BCLAF1	TFSS	0.652	0.424
CEBPB	TFSS	0.500	0.250
E2F4	TFSS	0.746	0.557
E2F6	TFSS	0.671	0.450
EGR1	TFSS	0.675	0.456
ELF1	TFSS	0.728	0.530
ETS1	TFSS	0.709	0.503
FOS	TFSS	0.616	0.379
FOSL1	TFSS	0.605	0.366
GABPA	TFSS	0.591	0.349
GATA1	TFSS	0.333	0.111
GATA2	TFSS	0.445	0.198
JUN	TFSS	0.715	0.511
JUND	TFSS	0.494	0.244
MAFK	TFSS	0.597	0.356
MAX	TFSS	0.706	0.498
MXI1	TFSS	0.696	0.485
MYC	TFSS	0.740	0.548
NFE2	TFSS	0.460	0.212
NFYA	TFSS	0.536	0.287
NFYB	TFSS	0.494	0.244
NR2C2	TFSS	0.192	0.037
NRF1	TFSS	0.557	0.311
REST	TFSS	0.648	0.420
SIX5	TFSS	0.526	0.277
SP1	TFSS	0.719	0.517
SP2	TFSS	0.582	0.339
SPI1	TFSS	0.546	0.298
SRF	TFSS	0.661	0.437
TAL1	TFSS	0.641	0.411
THAP1	TFSS	0.613	0.376
USF1	TFSS	0.618	0.381
USF2	TFSS	0.324	0.105
YY1	TFSS	0.673	0.453
ZBTB33	TFSS	0.484	0.234
ZBTB7A	TFSS	0.628	0.394
ZNF263	TFSS	0.463	0.214
ZNF274	TFSS	0.176	0.031
CHD2	ChromStr	0.609	0.371
HMG3	ChromStr	0.683	0.467
RAD21	ChromStr	0.438	0.192
SMC3	ChromStr	0.533	0.284

HDAC2	HISase	0.618	0.382
SETDB1	HISase	0.406	0.165
SIRT6	HISase	0.492	0.242
TRIM28	HISase	0.365	0.133
SMARCA4	ChromRem	0.510	0.260
SMARCB1	ChromRem	0.488	0.238
BDP1	Pol3F	0.162	0.026
BRF1	Pol3F	0.083	0.007
BRF2	Pol3F	0.388	0.151
GTF3C1	Pol3F	0.600	0.360
GTF3C2	Pol3F	0.602	0.363
POL3	Pol3F	0.100	0.010
POLR3A	Pol3F	0.402	0.162

Table S2

TF	Spearman Correlation with expression in K562
BCL3	0.579879495
BCLAF1	0.656390959
EGR1	0.684232561
ELF1	0.71985695
ETS1	0.721132114
FOSL1	0.613738577
GABPA	0.68406347
GATA2	0.594399438
MAX	0.719019881
REST	0.701587335
SPI1	0.531353679
SIX5	0.49561153
SP1	0.678316834
SP2	0.57141246
SRF	0.636612224
THAP1	0.680420082
USF1	0.64145281
YY1	0.735254489
ZBTB33	0.538487468
ZBTB7A	0.645426133
ATF3	0.416152885
E2F4	0.712098452
E2F6	0.682692116
GATA1	0.347298135
NR2C2	0.110909264
ZNF263	0.486738051
ZNF274	-0.276806238
CEBPB	0.53915908
FOS	0.637610548
JUN	0.695404394
MYC	0.71864076
JUND	0.468800166
MAFK	0.584513707
MXI1	0.686755395
NFE2	0.461795071
NFYA	0.570845358
NFYB	0.539747438
NRF1	0.48882036
TAL1	0.674164428
USF2	0.321981821

Table S3

TF	Broad H4K20me1	Broad H3K27ac	Broad H3K27me3	Broad H3K36me3	Broad H3K4me1	Broad H3K4me2	Broad H3K4me3	Broad H3K79me2	Broad H3K9ac	Broad H3K9me1	Broad H3K9me3	SYDH H3K27me3	SYDH H3K4me1	SYDH H3K4me3	SYDH H3K9ac	UW H3K27me3	UW H3K36me3	UW H3K4me3	Broad H2az
ATF3	0.044	0.026	0.060	0.039	0.027	0.025	0.016	0.032	0.018	0.053	0.028	0.049	0.063	0.021	0.020	0.073	0.049	0.036	0.027
BCL3	0.052	0.078	0.080	0.179	0.043	0.041	0.053	0.233	0.070	0.032	0.049	0.083	0.036	0.049	0.036	0.067	0.113	0.069	0.063
BCLAF1M33	0.069	0.291	0.062	0.247	0.119	0.132	0.164	0.720	0.251	0.063	0.053	0.149	0.068	0.123	0.074	0.070	0.087	0.196	0.082
CEBPB	0.128	0.112	0.069	0.150	0.117	0.105	0.092	0.124	0.083	0.111	0.100	0.053	0.047	0.037	0.019	0.054	0.078	0.066	0.096
CFOS	0.078	0.076	0.047	0.047	0.059	0.053	0.040	0.080	0.051	0.044	0.030	0.049	0.058	0.060	0.032	0.051	0.064	0.067	0.048
E2F4	0.140	0.125	0.210	0.246	0.335	0.089	0.107	0.103	0.101	0.178	0.197	0.249	0.180	0.338	0.152	0.151	0.350	0.446	0.105
E2F6	0.222	0.129	0.102	0.428	0.100	0.258	0.195	0.114	0.131	0.189	0.270	0.094	0.356	0.635	0.085	0.072	0.517	0.563	0.237
EGR1	0.124	0.106	0.175	0.180	0.134	0.152	0.129	0.192	0.108	0.125	0.277	0.271	0.144	0.161	0.043	0.096	0.239	0.492	0.091
ELF1	0.141	0.233	0.140	0.135	0.208	0.323	0.167	0.152	0.128	0.131	0.074	0.118	0.182	0.242	0.148	0.130	0.186	0.409	0.342
ETS1	0.110	0.294	0.104	0.092	0.309	0.325	0.346	0.492	0.358	0.133	0.115	0.219	0.492	1.567	1.162	0.138	0.148	1.561	0.167
FOSL1	0.075	0.090	0.063	0.066	0.087	0.085	0.062	0.086	0.052	0.098	0.051	0.073	0.070	0.081	0.040	0.048	0.061	0.063	0.062
GABP	0.084	0.067	0.061	0.103	0.131	0.131	0.080	0.122	0.079	0.080	0.044	0.075	0.388	0.199	0.089	0.086	0.093	0.259	0.089
GATA1	0.070	0.016	0.058	0.020	0.048	0.026	0.024	0.016	0.017	0.055	0.041	0.083	0.058	0.027	0.022	0.091	0.051	0.037	0.025
GATA2	0.134	0.047	0.116	0.089	0.113	0.067	0.042	0.068	0.035	0.111	0.069	0.101	0.059	0.043	0.032	0.097	0.070	0.044	0.053
JUN	0.075	0.085	0.084	0.079	0.077	0.119	0.085	0.168	0.101	0.057	0.053	0.090	0.087	0.093	0.075	0.070	0.112	0.130	0.128
JUND	0.060	0.031	0.062	0.056	0.036	0.038	0.020	0.045	0.022	0.063	0.037	0.041	0.023	0.019	0.017	0.028	0.051	0.029	0.021
MAFK	0.328	0.365	0.162	0.426	0.526	0.352	0.386	0.275	0.307	0.352	0.297	0.150	0.059	0.064	0.076	0.057	0.177	0.115	0.409
MAX	0.136	1.160	0.189	0.192	0.377	2.807	2.112	0.248	1.054	0.189	0.115	0.324	0.719	3.070	0.884	0.244	0.263	3.120	1.711
MXI1	0.081	0.356	0.060	0.105	0.108	0.354	0.427	0.627	0.353	0.080	0.068	0.201	0.088	0.296	0.076	0.091	0.093	0.438	0.119
MYC	0.082	0.513	0.105	0.058	0.104	0.177	0.216	0.287	0.326	0.099	0.062	0.189	0.139	0.239	0.092	0.098	0.120	0.171	0.194
NFE2	0.032	0.034	0.040	0.044	0.031	0.027	0.020	0.027	0.025	0.059	0.021	0.049	0.028	0.033	0.019	0.044	0.053	0.029	0.026
NFYA	0.067	0.040	0.057	0.057	0.038	0.038	0.039	0.052	0.036	0.046	0.035	0.048	0.039	0.039	0.020	0.048	0.038	0.051	0.019
NFYB	0.054	0.033	0.046	0.058	0.040	0.028	0.029	0.039	0.032	0.049	0.022	0.047	0.050	0.036	0.019	0.040	0.049	0.028	0.027
NR2C2	0.057	0.017	0.068	0.058	0.052	0.020	0.018	0.020	0.016	0.054	0.064	0.074	0.022	0.026	0.009	0.073	0.100	0.039	0.023
NRF1	0.062	0.049	0.061	0.143	0.045	0.016	0.032	0.051	0.048	0.042	0.055	0.062	0.070	0.031	0.027	0.041	0.043	0.042	0.037
PU1	0.112	0.069	0.064	0.100	0.130	0.074	0.045	0.040	0.054	0.094	0.046	0.092	0.040	0.046	0.043	0.075	0.067	0.035	0.095
REST	0.074	0.396	0.079	0.070	0.101	0.284	0.328	0.292	0.317	0.082	0.082	0.138	0.110	0.330	0.248	0.044	0.081	0.345	0.155
SIX5	0.120	0.045	0.050	0.114	0.053	0.044	0.039	0.066	0.036	0.064	0.065	0.074	0.052	0.033	0.029	0.034	0.076	0.037	0.042
SP1	0.062	0.172	0.082	0.085	0.128	0.330	0.217	0.242	0.221	0.081	0.062	0.127	0.056	0.143	0.042	0.090	0.079	0.261	0.126
SP2	0.066	0.038	0.078	0.050	0.061	0.041	0.030	0.053	0.045	0.060	0.055	0.079	0.093	0.066	0.048	0.081	0.053	0.033	0.047
SRF	0.079	0.079	0.077	0.061	0.074	0.088	0.026	0.110	0.055	0.077	0.042	0.054	0.063	0.071	0.038	0.070	0.069	0.073	0.081
TAL1	0.082	0.877	0.085	0.298	0.165	0.253	0.332	0.935	0.623	0.091	0.067	0.169	0.060	0.191	0.088	0.098	0.080	0.222	0.075
THAP1	0.087	0.068	0.081	0.093	0.122	0.068	0.085	0.094	0.066	0.081	0.096	0.117	0.448	0.280	0.146	0.088	0.100	0.269	0.075
USF1	0.071	0.076	0.059	0.046	0.070	0.071	0.060	0.095	0.060	0.070	0.054	0.054	0.047	0.043	0.027	0.051	0.066	0.046	0.053
USF2	0.232	0.117	0.111	0.420	0.267	0.068	0.073	0.102	0.061	0.250	0.171	0.083	0.021	0.028	0.042	0.063	0.201	0.069	0.069
YY1	0.163	0.125	0.164	0.304	0.442	0.137	0.196	0.112	0.149	0.229	0.237	0.247	0.261	1.061	0.102	0.155	0.439	0.662	0.134
ZBTB33	0.078	0.046	0.048	0.059	0.057	0.037	0.035	0.094	0.084	0.051	0.065	0.047	0.044	0.058	0.027	0.048	0.084	0.037	0.118
ZBTB7A	0.162	0.088	0.228	0.238	0.111	0.216	0.234	0.112	0.148	0.167	0.348	0.295	1.242	0.518	0.337	0.091	0.208	0.961	0.136
ZNF263	0.165	0.028	0.080	0.058	0.085	0.075	0.051	0.037	0.091	0.052	0.492	1.034	0.462	0.383	0.323	0.075	0.156	0.071	0.071
ZNF274	0.194	0.053	0.278	0.530	0.353	0.048	0.042	0.040	0.030	0.316	0.252	0.141	0.087	0.065	0.017	0.124	0.435	0.083	0.037

Table S4

X	TFNS		HM		Dnase		FAIRE		Nucleosome	
Model	MEAN	SD	MEAN	SD	MEAN	SD	MEAN	SD	MEAN	SD
TFSS X	0.03	0.0040	0.134	0.0067	0.166	0.0064	0.23	0.0095	0.368	0.0162
TFSS	0.703	0.0019	0.703	0.0019	0.703	0.0019	0.703	0.0019	0.703	0.0019
TFSS+X	0.735	0.0016	0.728	0.0032	0.714	0.0019	0.705	0.0020	0.663	0.0032
X	0.729	0.0007	0.646	0.0038	0.583	0.0025	0.487	0.0040	0.246	0.0123
X TFSS	0.078	0.0091	0.082	0.0081	0.01	0.0104	0.003	0.0062	0.003	0.0027

Table S5

K562	TSS (Correlation R)		Transcript (Correlation R)	
	MEAN	SD	MEAN	SD
PolyA+ RNA Whole Cell (Rep1)	0.4505	0.0220	0.5158	0.0353
PolyA+ RNA Whole Cell (Rep2)	0.4506	0.0205	0.4491	0.0502
Total RNA Chromatin (Rep1)	0.3462	0.0364	0.4513	0.0381
Total RNA Chromatin (Rep2)	0.3687	0.0188	NA	NA
PolyA+ RNA Cytosol (Rep1)	0.4592	0.0240	0.5265	0.0239
PolyA+ RNA Cytosol (Rep2)	0.4460	0.0276	0.3842	0.0467
Total RNA Nucleolus (Rep1)	0.3652	0.0191	0.4403	0.0388
Total RNA Nucleolus (Rep2)	0.3706	0.0244	NA	NA
PolyA+ RNA Nucleus (Rep1)	0.4079	0.0192	0.5376	0.0480
PolyA+ RNA Nucleus (Rep2)	0.4063	0.0176	0.4873	0.0207

Table S6

#Top 1000 genes with largest residual (y>y^)					
Annotation Cluster 1	Enrichment Score: 7.327248850749713				
Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	172	19.66	1.02E-11	1.63
GOTERM_CC_FAT	GO:0043233~organelle lumen	174	19.89	2.05E-11	1.61
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	176	20.11	2.57E-11	1.60
GOTERM_CC_FAT	GO:0031981~nuclear lumen	135	15.43	3.46E-08	1.58
GOTERM_CC_FAT	GO:0005654~nucleoplasm	83	9.49	3.01E-05	1.57
GOTERM_CC_FAT	GO:0005730~nucleolus	68	7.77	3.29E-05	1.66
Annotation Cluster 2	Enrichment Score: 6.919279843789874				
Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	26	2.97	4.52E-11	4.84
GOTERM_CC_FAT	GO:0044429~mitochondrial part	69	7.89	3.45E-08	2.00
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	53	6.06	8.31E-08	2.21
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	45	5.14	8.34E-08	2.40
GOTERM_CC_FAT	GO:0031967~organelle envelope	70	8.00	9.34E-08	1.94
GOTERM_CC_FAT	GO:0031975~envelope	70	8.00	9.98E-08	1.94
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	50	5.71	1.73E-07	2.22
GOTERM_CC_FAT	GO:0005739~mitochondrion	104	11.89	3.09E-07	1.64
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	41	4.69	5.02E-07	2.37
GOTERM_CC_FAT	GO:0044455~mitochondrial membrane part	22	2.51	4.91E-06	3.14
GOTERM_CC_FAT	GO:0031090~organelle membrane	99	11.31	5.82E-06	1.56
Annotation Cluster 3	Enrichment Score: 6.745386604603548				
Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	65	7.43	4.65E-09	2.17
GOTERM_MF_FAT	GO:0003723~RNA binding	74	8.46	4.70E-08	1.93
GOTERM_BP_FAT	GO:0006396~RNA processing	56	6.40	2.66E-05	1.79
Annotation Cluster 4	Enrichment Score: 6.433980016040818				
Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	62	7.09	8.15E-19	3.61
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	26	2.97	4.52E-11	4.84
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	27	3.09	4.47E-08	3.46
GOTERM_BP_FAT	GO:0045333~cellular respiration	22	2.51	4.80E-08	4.10
GOTERM_BP_FAT	GO:0022900~electron transport chain	22	2.51	7.72E-07	3.51
GOTERM_BP_FAT	GO:0042775~mitochondrial ATP synthesis coupled electron transport	15	1.71	7.84E-07	5.03
GOTERM_BP_FAT	GO:0042773~ATP synthesis coupled electron transport	15	1.71	7.84E-07	5.03
GOTERM_MF_FAT	GO:0016651~oxidoreductase activity, acting on NADH or NADPH	18	2.06	1.09E-06	4.10
GOTERM_CC_FAT	GO:0070469~respiratory chain	17	1.94	1.46E-06	4.22
GOTERM_CC_FAT	GO:0044455~mitochondrial membrane part	22	2.51	4.91E-06	3.14
GOTERM_MF_FAT	GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor	13	1.49	5.23E-06	5.07
GOTERM_BP_FAT	GO:0022904~respiratory electron transport chain	15	1.71	5.44E-06	4.34
GOTERM_MF_FAT	GO:0008137~NADH dehydrogenase (ubiquinone) activity	12	1.37	7.15E-06	5.40
GOTERM_MF_FAT	GO:0050136~NADH dehydrogenase (quinone) activity	12	1.37	7.15E-06	5.40
GOTERM_MF_FAT	GO:0003954~NADH dehydrogenase activity	12	1.37	7.15E-06	5.40
GOTERM_BP_FAT	GO:0006120~mitochondrial electron transport, NADH to ubiquinone	12	1.37	1.12E-05	5.16
GOTERM_CC_FAT	GO:0005747~mitochondrial respiratory chain complex I	12	1.37	1.22E-05	5.09
GOTERM_CC_FAT	GO:0030964~NADH dehydrogenase complex	12	1.37	1.22E-05	5.09
GOTERM_CC_FAT	GO:0045271~respiratory chain complex I	12	1.37	1.22E-05	5.09
GOTERM_CC_FAT	GO:0005746~mitochondrial respiratory chain	14	1.60	3.40E-05	3.96
Annotation Cluster 5	Enrichment Score: 5.678091823112668				
Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	202	23.09	6.86E-08	1.40
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	202	23.09	6.86E-08	1.40
Annotation Cluster 6	Enrichment Score: 5.577395557267241				
Category	Term	Count	%	PValue	Fold Enrichment
GOTERM_BP_FAT	GO:0006096~glycolysis	17	1.94	1.24E-09	6.63
GOTERM_BP_FAT	GO:0006007~glucose catabolic process	18	2.06	7.27E-09	5.59
GOTERM_BP_FAT	GO:0019320~hexose catabolic process	19	2.17	2.53E-08	4.90
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	19	2.17	4.25E-08	4.75
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	19	2.17	4.23E-07	4.14
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	19	2.17	7.76E-07	3.98
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	19	2.17	2.18E-05	3.19

GOTERM_BP_FAT	GO:0006006~glucose metabolic process	23	2.63	2.32E-05	2.77	0.041386251
Annotation Cluster 7	Enrichment Score: 4.047644402899908					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_CC_FAT	GO:0044429~mitochondrial part	69	7.89	3.45E-08	2.00	4.97E-05
Annotation Cluster 8	Enrichment Score: 4.033405330787139					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_BP_FAT	GO:0006396~RNA processing	56	6.40	2.66E-05	1.79	0.047353182
GOTERM_BP_FAT	GO:0008380~RNA splicing	35	4.00	2.74E-05	2.17	0.048840347
Annotation Cluster 9	Enrichment Score: 3.667522286856966					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_BP_FAT	GO:0010498~proteasomal protein catabolic process	24	2.74	1.81E-08	3.98	3.22E-05
GOTERM_BP_FAT	GO:0043161~proteasomal ubiquitin-dependent protein catabolic process	24	2.74	1.81E-08	3.98	3.22E-05
GOTERM_CC_FAT	GO:0000502~proteasome complex	17	1.94	2.70E-07	4.73	3.90E-04
GOTERM_BP_FAT	GO:0031145~anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process	17	1.94	7.01E-07	4.45	0.001249743
GOTERM_BP_FAT	GO:0051436~negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	17	1.94	7.01E-07	4.45	0.001249743
GOTERM_BP_FAT	GO:0031397~negative regulation of protein ubiquitination	18	2.06	9.37E-07	4.13	0.001669238
GOTERM_BP_FAT	GO:0051444~negative regulation of ubiquitin-protein ligase activity	17	1.94	1.10E-06	4.32	0.001956559
GOTERM_BP_FAT	GO:0051352~negative regulation of ligase activity	17	1.94	1.10E-06	4.32	0.001956559
GOTERM_BP_FAT	GO:0051437~positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle	17	1.94	1.36E-06	4.25	0.002430497
GOTERM_BP_FAT	GO:0051443~positive regulation of ubiquitin-protein ligase activity	17	1.94	2.08E-06	4.13	0.00369984
GOTERM_BP_FAT	GO:0051439~regulation of ubiquitin-protein ligase activity during mitotic cell cycle	17	1.94	2.54E-06	4.07	0.004535226
GOTERM_BP_FAT	GO:0051351~positive regulation of ligase activity	17	1.94	3.78E-06	3.96	0.006730955
GOTERM_BP_FAT	GO:0051438~regulation of ubiquitin-protein ligase activity	17	1.94	9.49E-06	3.70	0.016905834
GOTERM_BP_FAT	GO:0051340~regulation of ligase activity	17	1.94	1.58E-05	3.56	0.028196513
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	31	3.54	2.49E-05	2.32	0.04443079
GOTERM_BP_FAT	GO:0031398~positive regulation of protein ubiquitination	17	1.94	2.57E-05	3.43	0.04574429
Annotation Cluster 10	Enrichment Score: 3.426591629665715					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_BP_FAT	GO:0006412~translation	45	5.14	3.42E-08	2.48	6.09E-05
GOTERM_CC_FAT	GO:0044445~cytosolic part	28	3.20	1.18E-07	3.20	1.70E-04
Annotation Cluster 11	Enrichment Score: 3.128290217721999					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_BP_FAT	GO:0022613~ribonucleoprotein complex biogenesis	28	3.20	4.15E-06	2.70	0.007394889
GOTERM_BP_FAT	GO:0042254~ribosome biogenesis	22	2.51	4.81E-06	3.15	0.008574092
Annotation Cluster 12	Enrichment Score: 2.7763615753374977					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_CC_FAT	GO:0048770~pigment granule	19	2.17	3.42E-06	3.60	0.004928734
GOTERM_CC_FAT	GO:0042470~melanosome	19	2.17	3.42E-06	3.60	0.004928734
Annotation Cluster 13	Enrichment Score: 2.5864099999574024					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	50	5.71	5.95E-08	2.30	1.06E-04
GOTERM_BP_FAT	GO:0022402~cell cycle process	58	6.63	2.30E-05	1.78	0.041063694
Annotation Cluster 14	Enrichment Score: 2.5751066084985266					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	26	2.97	4.52E-11	4.84	8.05E-08

#Top 1000 genes with smallest residual (y<y^)

Annotation Cluster 1	Enrichment Score: 5.646202545112458					
Category	Term	Count	%	PValue	Fold Enrichment	FDR
GOTERM_CC_FAT	GO:0043233~organelle lumen	110	13.92	6.39E-08	1.65	8.99E-05
GOTERM_CC_FAT	GO:0031981~nuclear lumen	93	11.77	6.66E-08	1.75	9.37E-05
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	108	13.67	7.23E-08	1.65	1.02E-04
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	110	13.92	1.75E-07	1.62	2.47E-04
GOTERM_CC_FAT	GO:0005654~nucleoplasm	60	7.59	4.35E-06	1.85	0.006126958