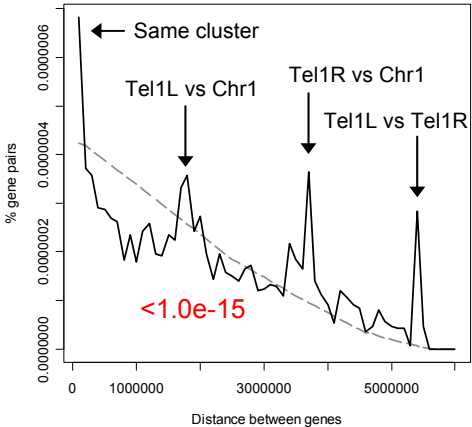


Figure S1

A Upregulated genes vs all genes



B Downregulated genes vs all genes

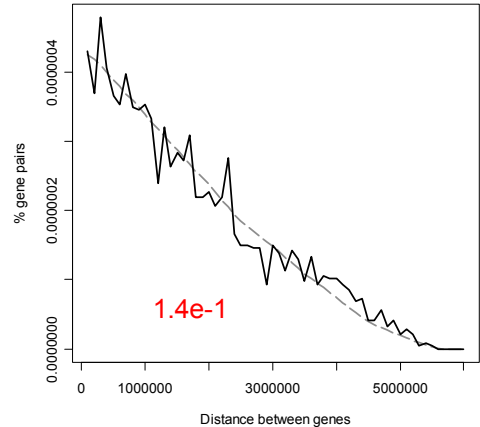


Figure S2

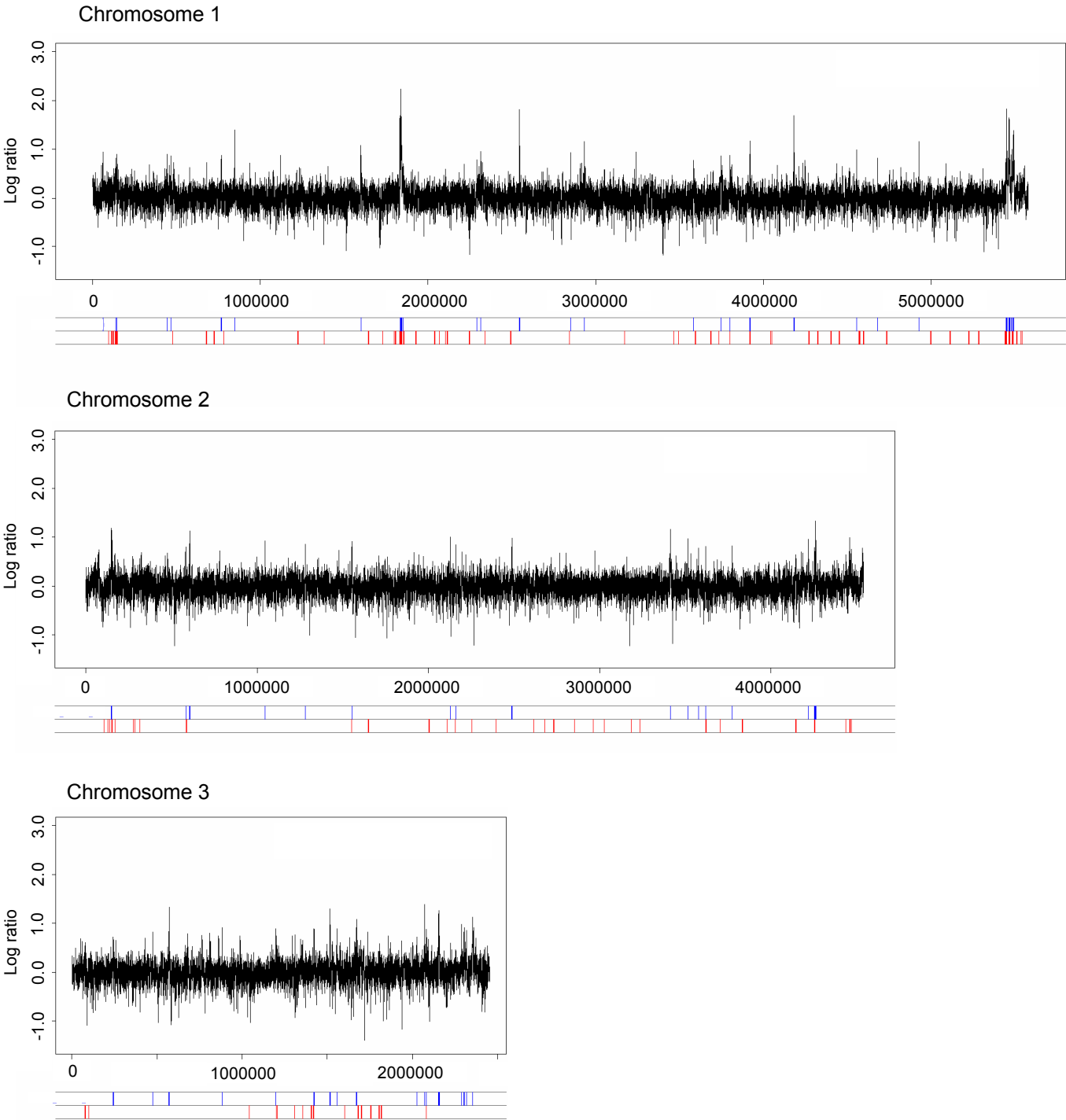
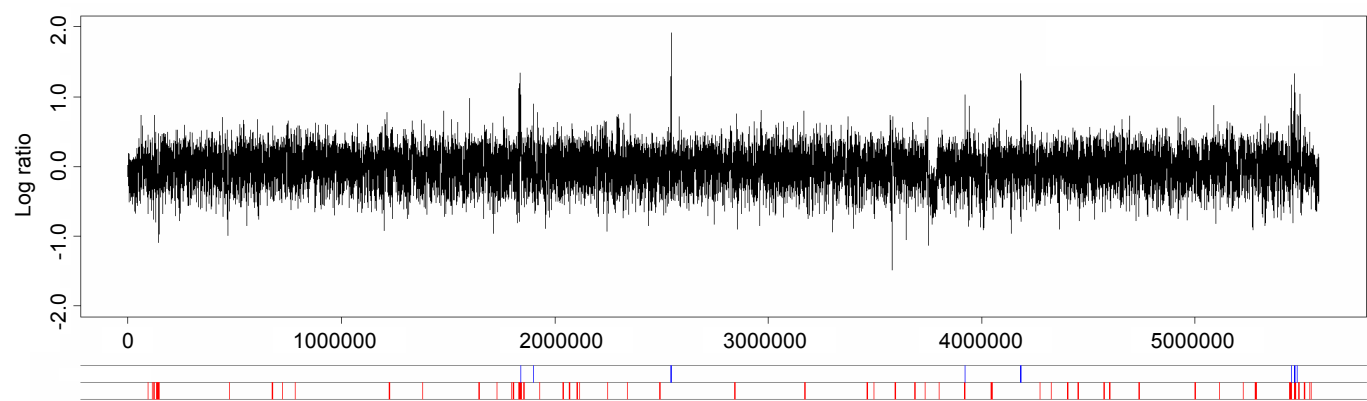
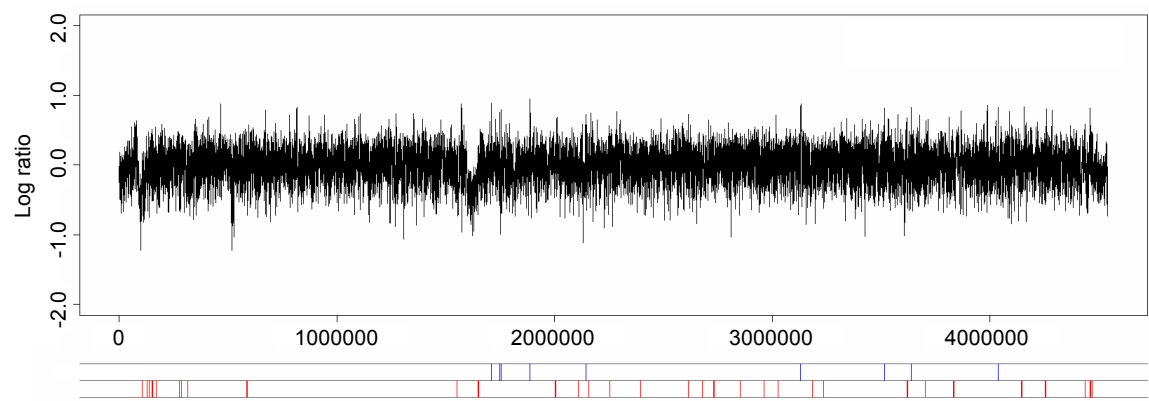


Figure S3

Chromosome 1



Chromosome 2



Chromosome 3

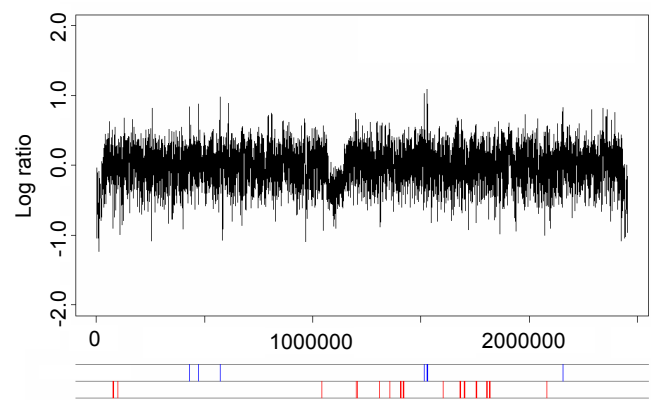


Figure S4

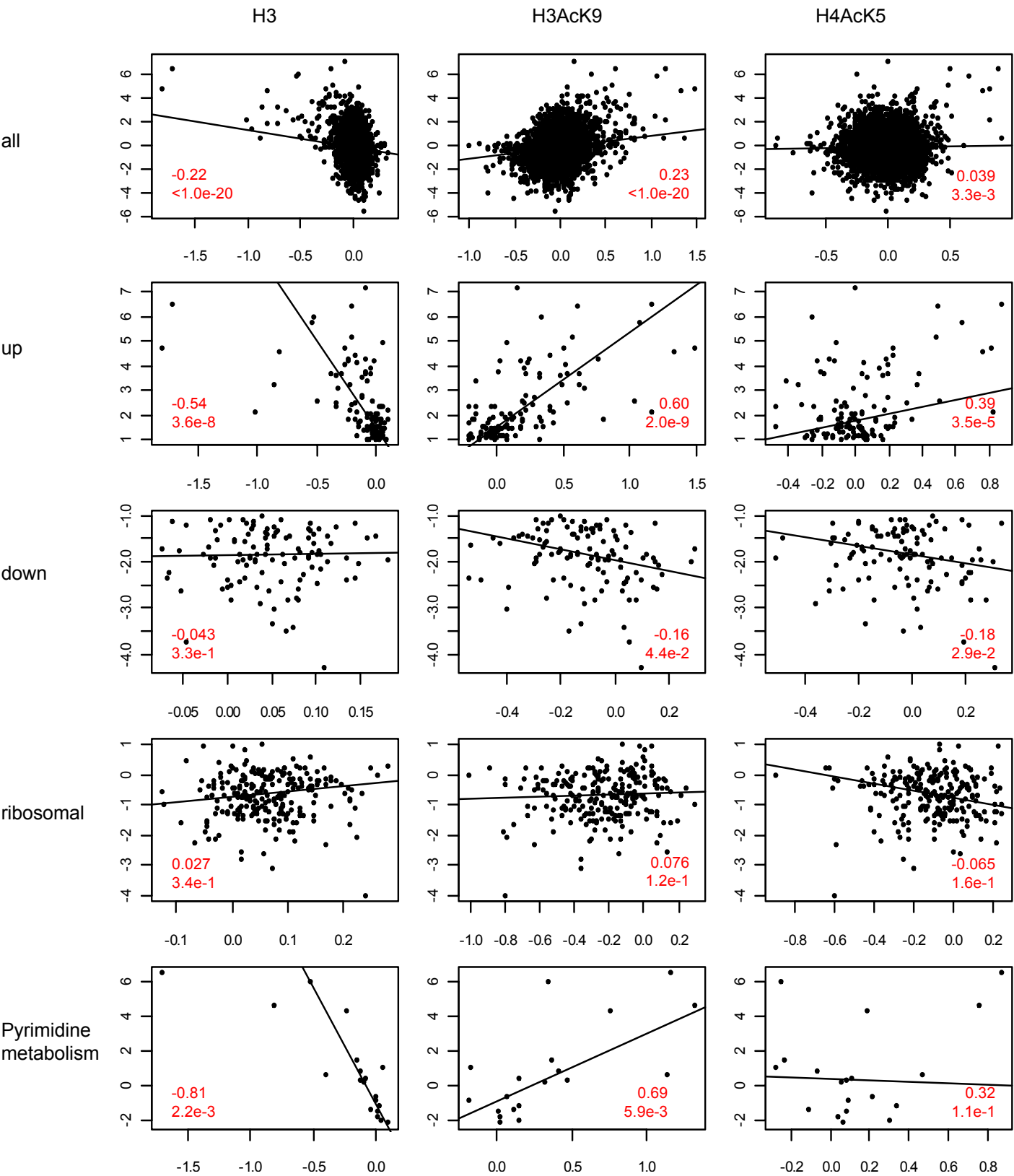


Figure S5

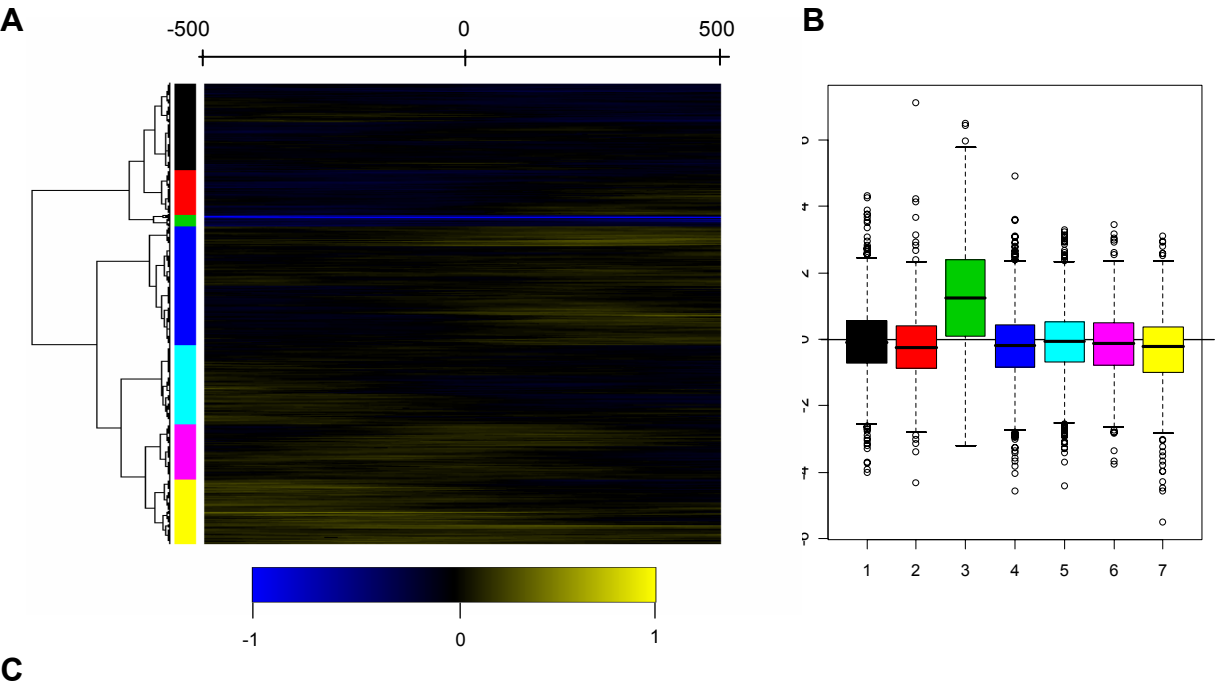


Figure S6

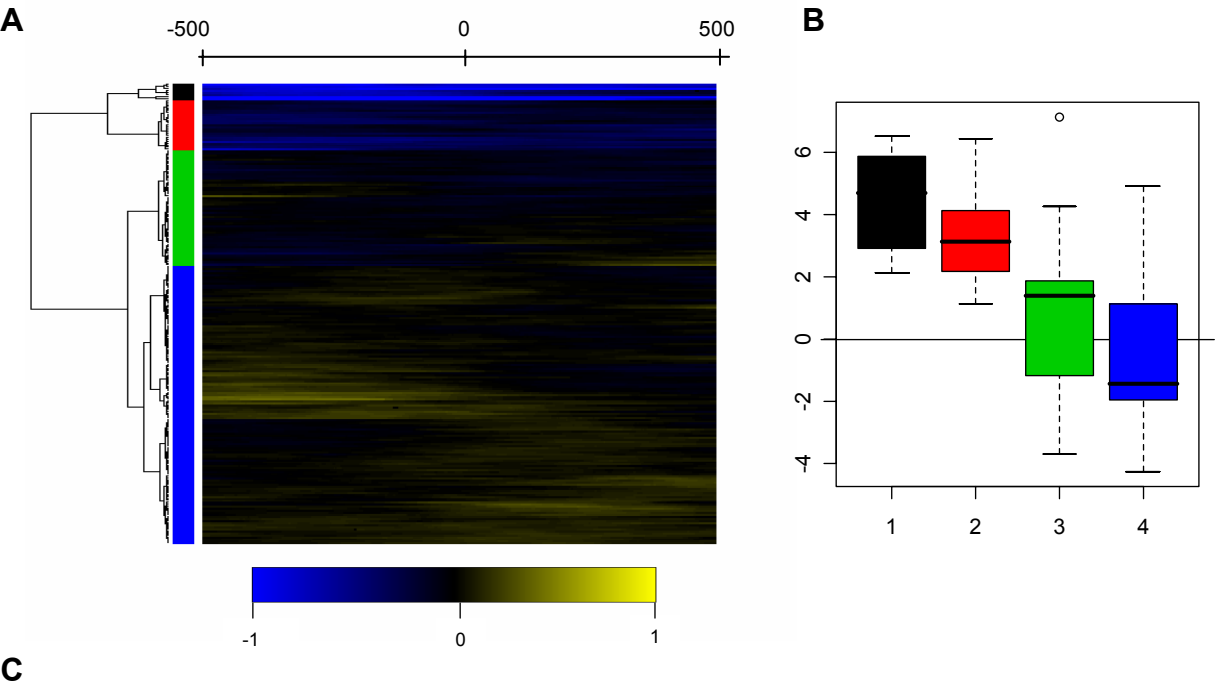
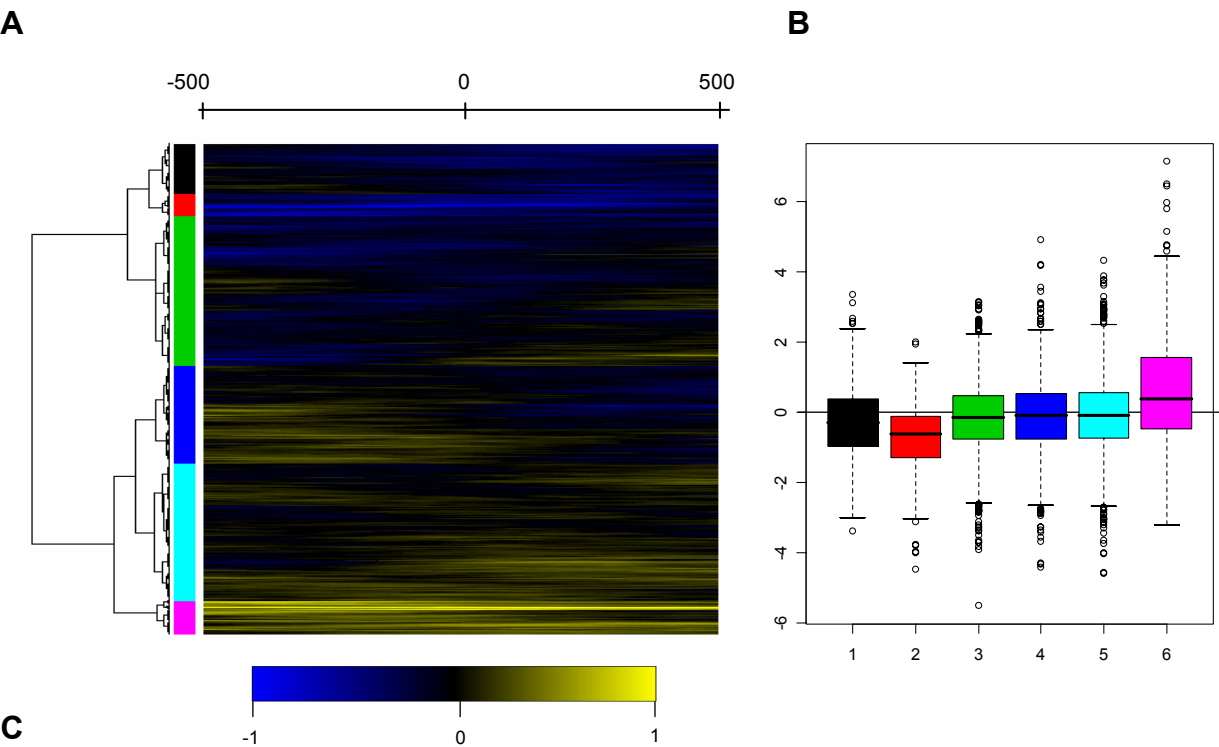


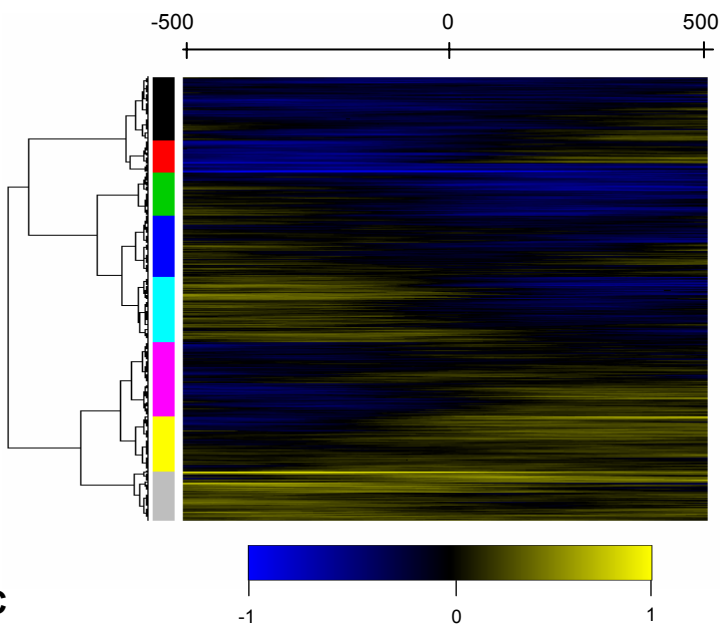
Figure S7



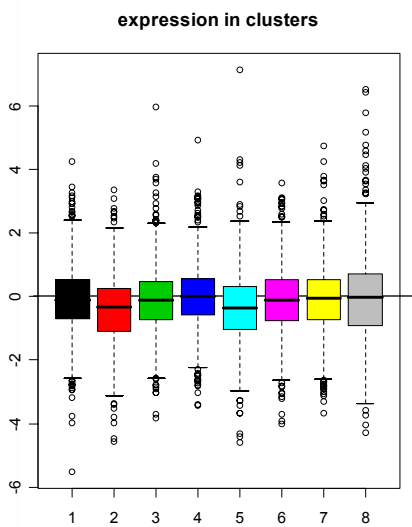
cl	Genes	Chr1	Tel1L	Tel1R	Induced	Repressed	Enriched Gene Ontology annotations
H3AcK9:1	511	1	0	1	6	18	-
H3AcK9:2	221	0	0	0	0	16	translation <1.0e-20
H3AcK9:3	1510	0	3	1	22	31	membrane-bounded organelle 9.1e-08
H3AcK9:4	995	0	5	1	23	22	cellular response to stimulus 4.1e-05 response to stress 4.3e-05
H3AcK9:5	1383	0	11	4	24	19	cell division 6.2e-06 catalytic activity 5.2e-08
H3AcK9:6	336	6	9	15	41	5	pyrimidine base metabolic process 1.1e-10 oxidoreductase activity 1.2e-05

Figure S8

A



B

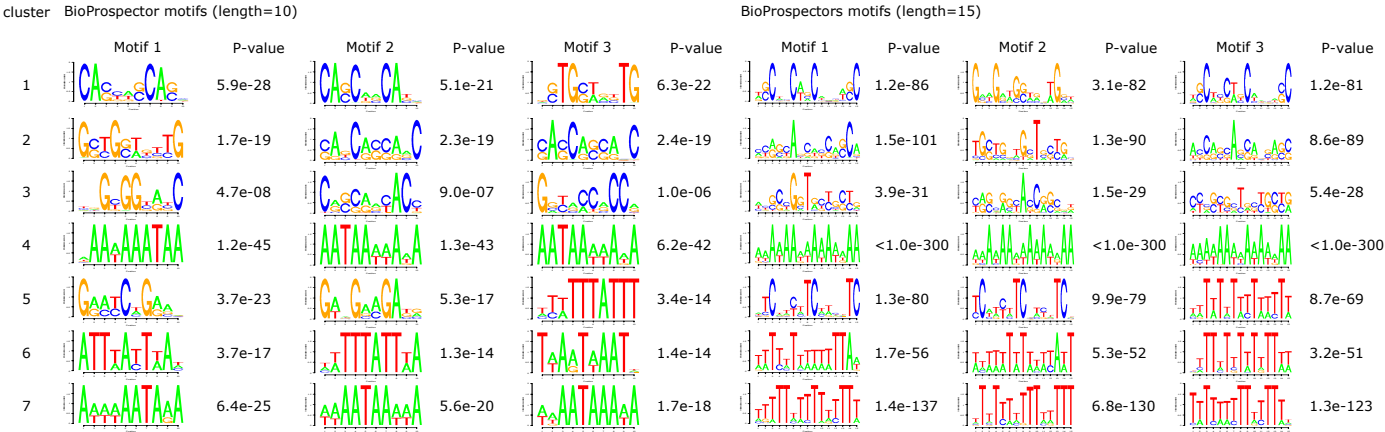


C

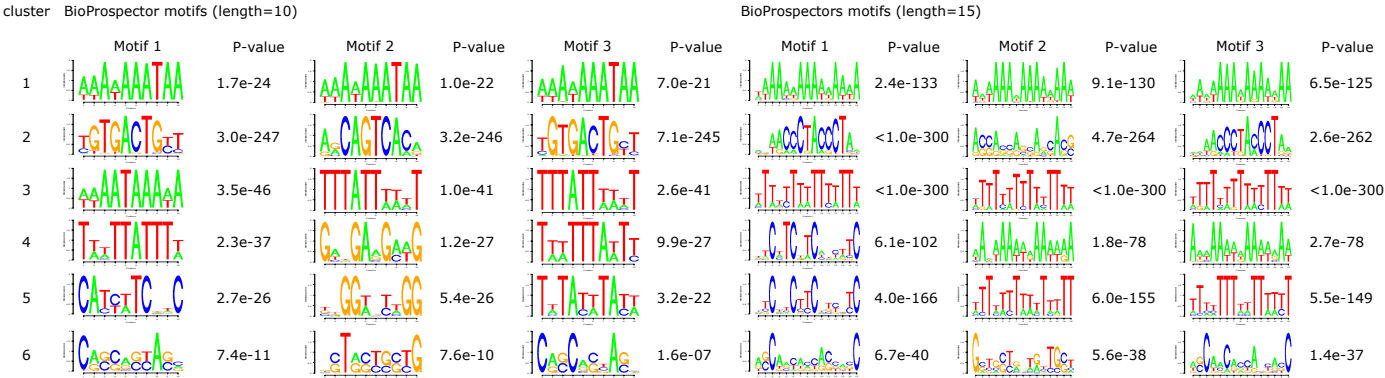
cl	Genes	Chr1	Tel1L	Tel1R	Induced	Repressed	Enriched Gene Ontology annotations
H4AcK5:1	715	0	1	4	15	17	RNA processing 5.2e-05
H4AcK5:2	349	0	3	2	4	13	translation 7.4e-06 cytosolic ribosome 3.8e-13
H4AcK5:3	482	3	6	1	14	15	-
H4AcK5:4	691	0	5	1	16	10	membrane-bounded organelle 4.3e-07 actin binding 8.7e-05
H4AcK5:5	722	0	2	2	13	18	-
H4AcK5:6	836	0	7	1	14	13	protein complex 1.2e-05
H4AcK5:7	617	0	2	3	17	9	-
H4AcK5:8	544	4	2	8	23	16	nitrogen compound metabolic proc. 4.4e-05 catalytic activity 1.5e-06

Figure S9

Clustering of TSS on difference in H3



Clustering of TSS on difference in H3AcK9



Clustering of TSS on difference in H4AcK5

