

Fig 1

A

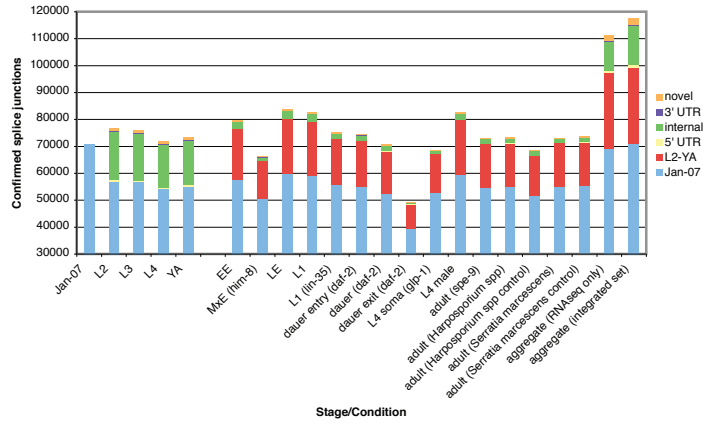
Experiment Type		Isolated Developmental Stages								Mixed Stages		
		Embryo <i>6 substages</i>	L1 <i>3 subconditions</i>	L2	L3	L4 <i>7 subconditions</i>	Adult herm. <i>8 subconditions</i>	Male <i>3 subconditions</i>	Dauer <i>7 subconditions</i>	Whole Organism	Isolated Tissues <i>21 isolates</i>	Infection <i>3 pathogens</i>
RNA-seq reads (experiments/mapped reads)	<i>polyA selected</i>	2 / 139M	2 / 111M	1 / 33M	1 / 29M	2 / 78M	4 / 195M	2 / 60M	3 / 89M			2 / 97M
	<i>small RNA selected</i>	8 / 51M	1 / 10M	1 / 10M	1 / 9M	1 / 9M	10 / 106M	1 / 12M		1 / 5M	4 / 16M	
	<i>3' UTR selected</i>	1 / 0.5M	1 / 0.2M	1 / 0.4M	1 / 0.2M	1 / 0.3M	1 / 0.1M	1 / 0.2M	4 / 0.2M	3 / 11M		
Expression Tiling Arrays	<i>experiments</i>	3	1	1	1	3	4	1			26	4
ChIP-seq, TFs	<i>factors</i>	5	7	4	6	2	1					
	<i>experiments</i>	6	8	4	6	2	1					
	<i>mapped reads</i>	81M	147M	40.1M	54M	39M	29M					
ChIP-{seq,chip}, Pol II	<i>ChIP-chip experiments</i>	3				1						
	<i>ChIP-seq experiments</i>	3	3	1	5	1	4					
	<i>mapped reads</i>	27.8M	39M	7M	68M	15M	25M					
ChIP-chip, Histone marks	<i>mark types</i>	16			12							
	<i>experiments</i>	22			17							
ChIP-chip, Chromatin	<i>factors</i>	18			2	1						
	<i>experiments</i>	31			4	1						
Nucleosome	<i>experiments</i>	1					1					
	<i>mapped reads</i>	42M					88M					

B

Inferred Genomic Elements	Representative Developmental Stages					
	Embryo	L1	L2	L3	L4	YA
Coding transcripts	35,097	35,568	32,027	34,216	34,471	33,999
TSSes	14,854	16,257	14,411	14,004	10,949	13,960
TARs	39,328	42,421	41,791	41,734	43,380	40,624
miRNAs	152	127	126	130	133	133
other ncRNAs	895	936	981	781	823	859
TF Peaks (# factors)	17,147 (5)	26,944 (7)	8,060 (4)	16,149 (6)	3,749 (2)	551 (1)

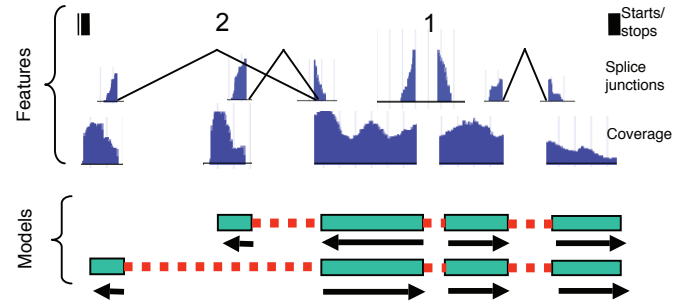
Fig 2

A

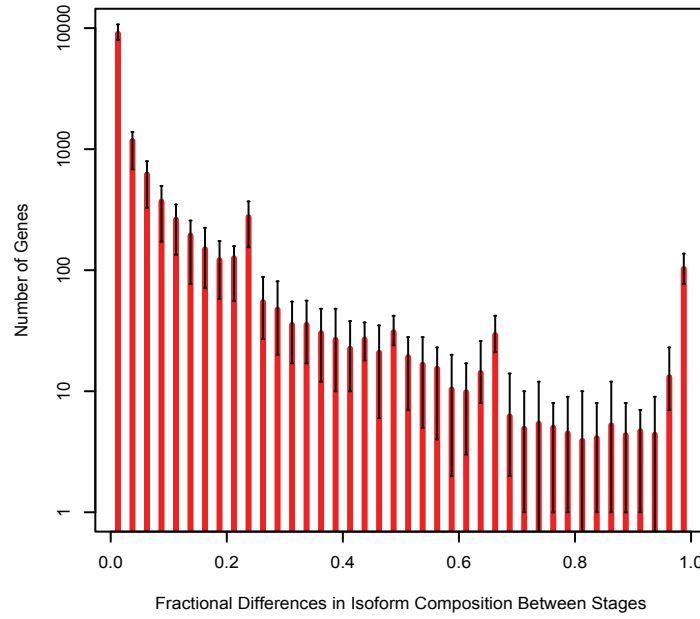


B

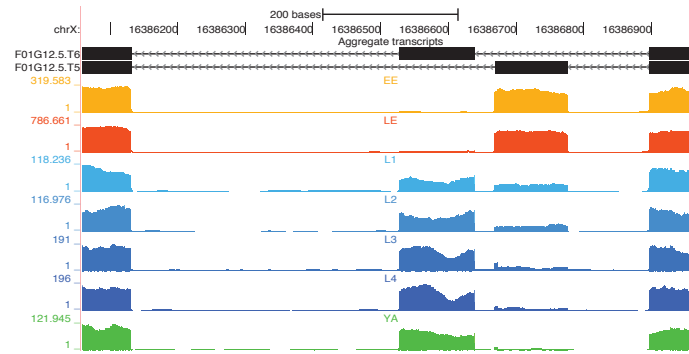
Transcript building



C



D



E

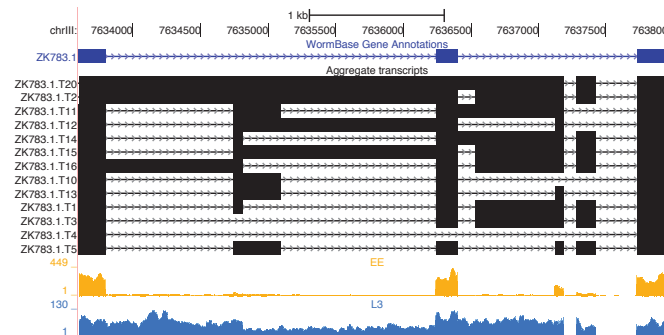


Fig 3

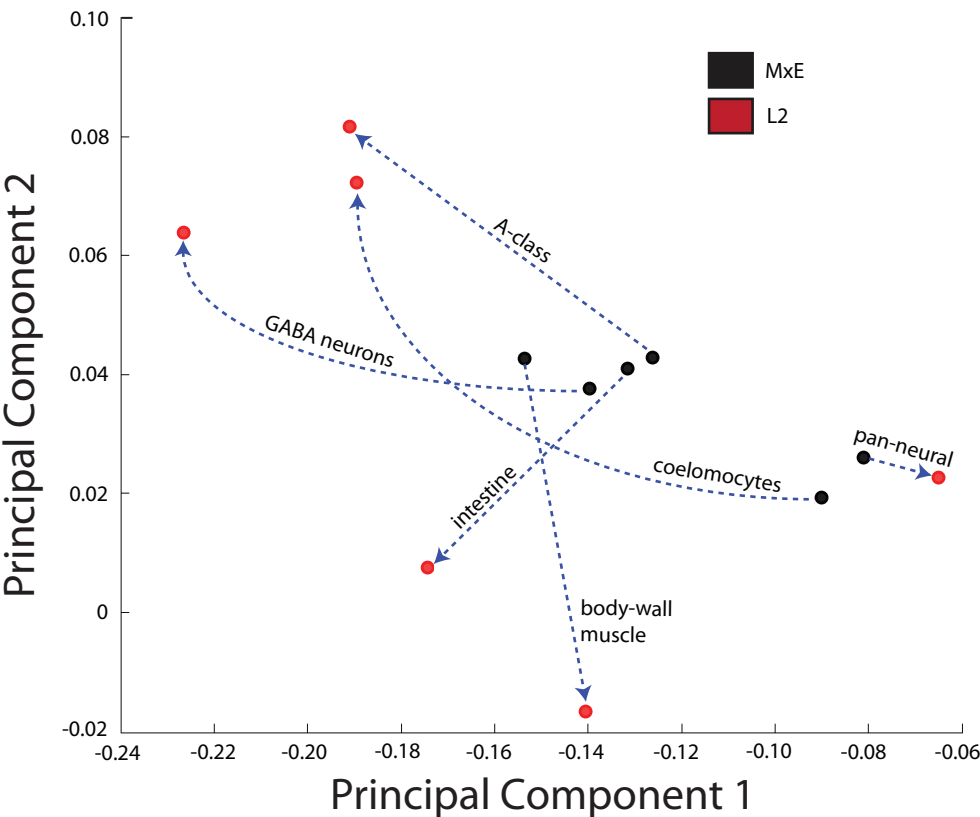
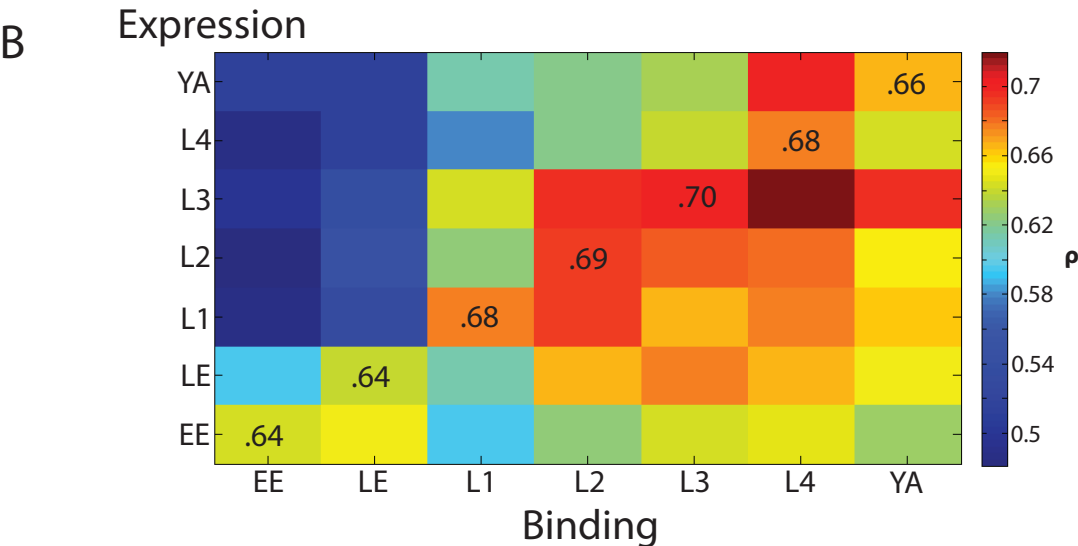
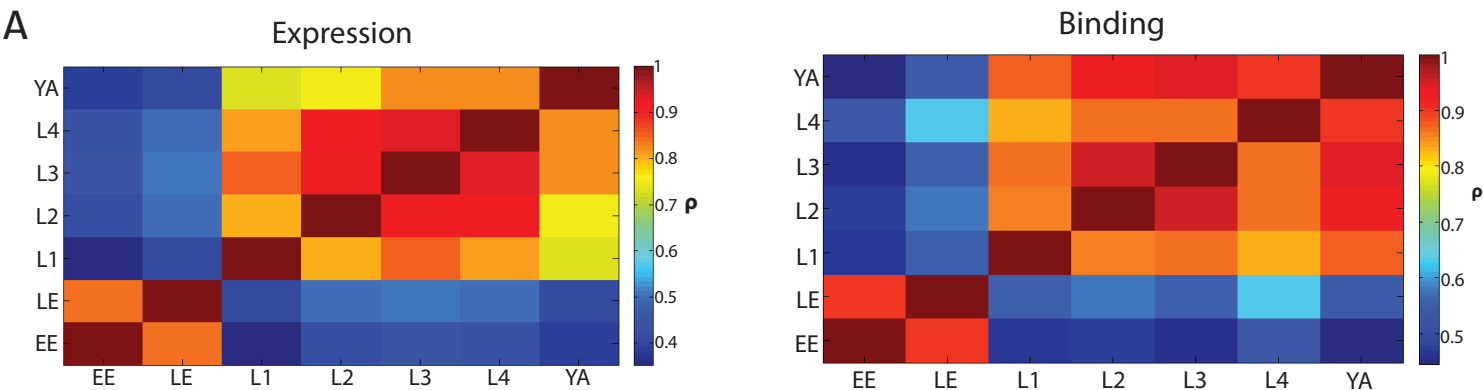
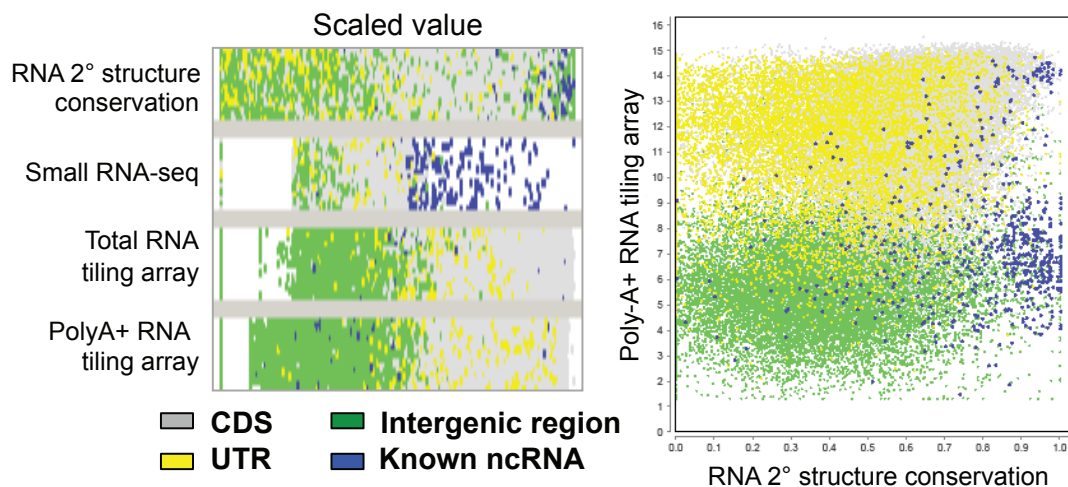
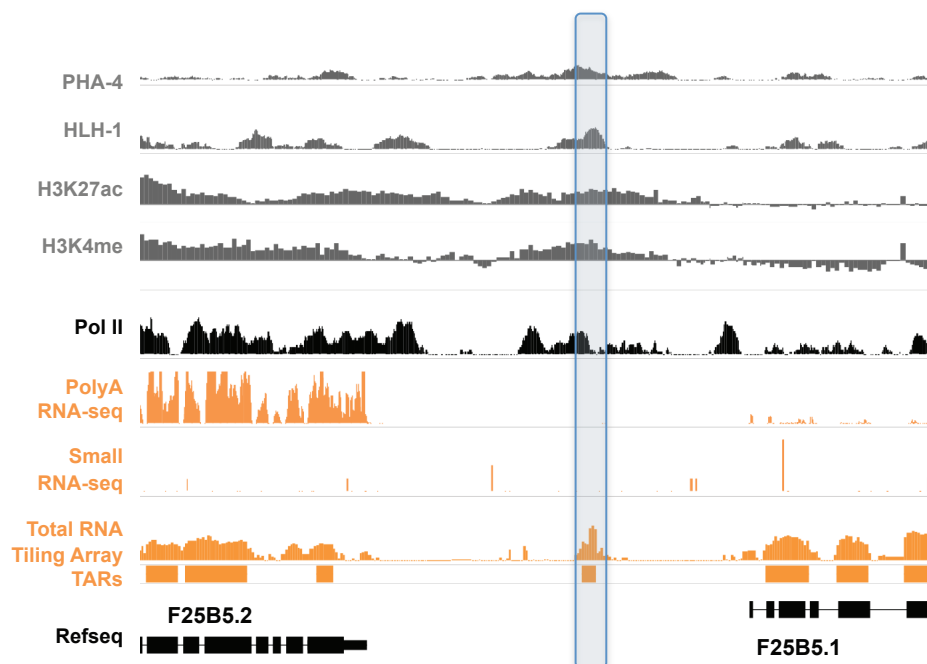


Fig 4

A



B



C

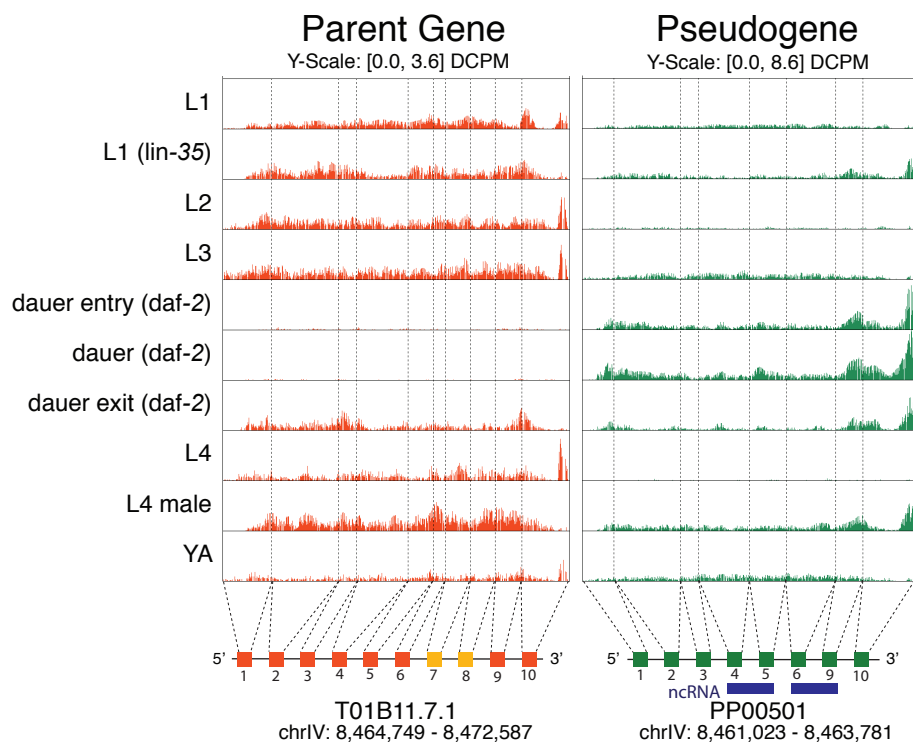
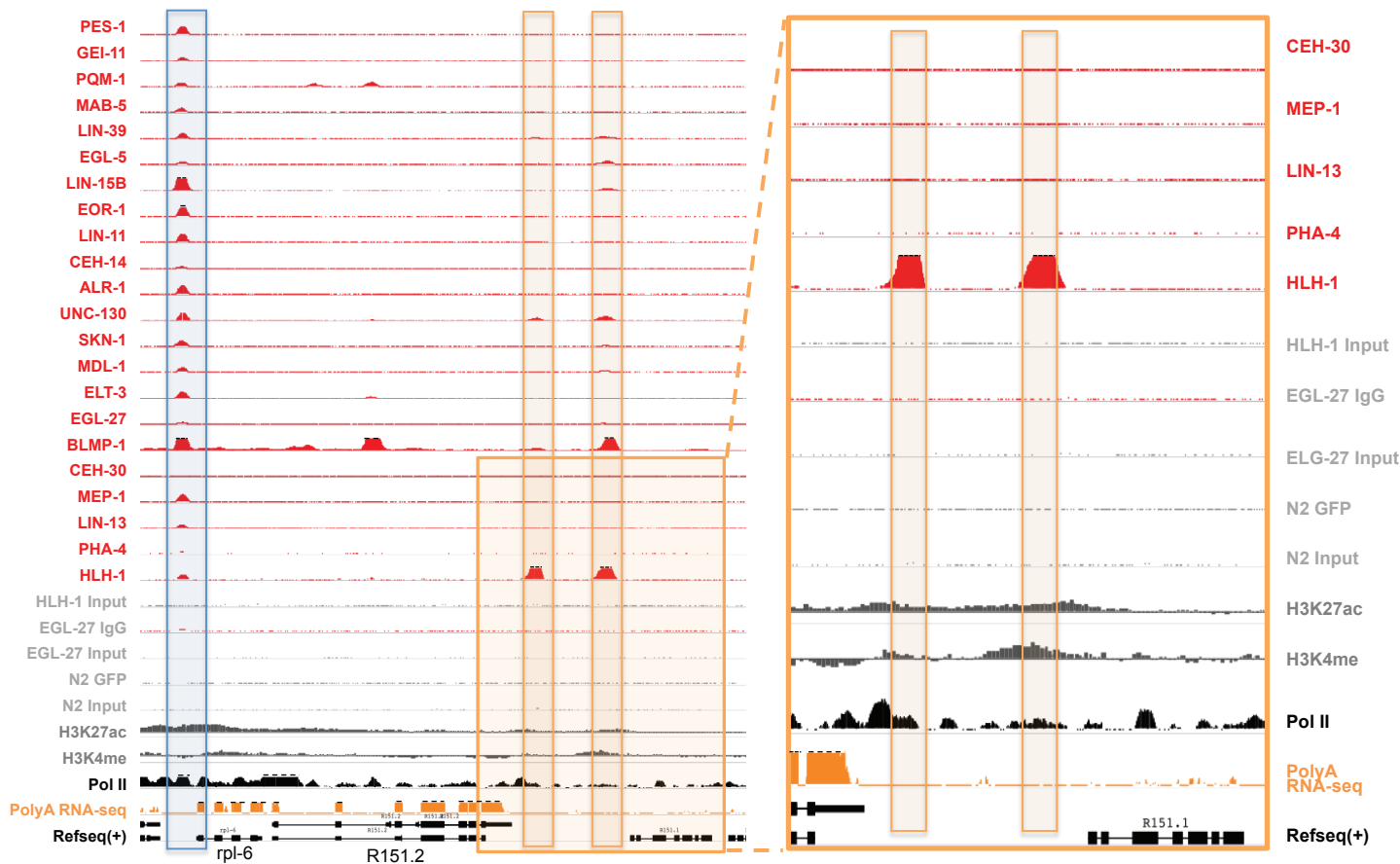


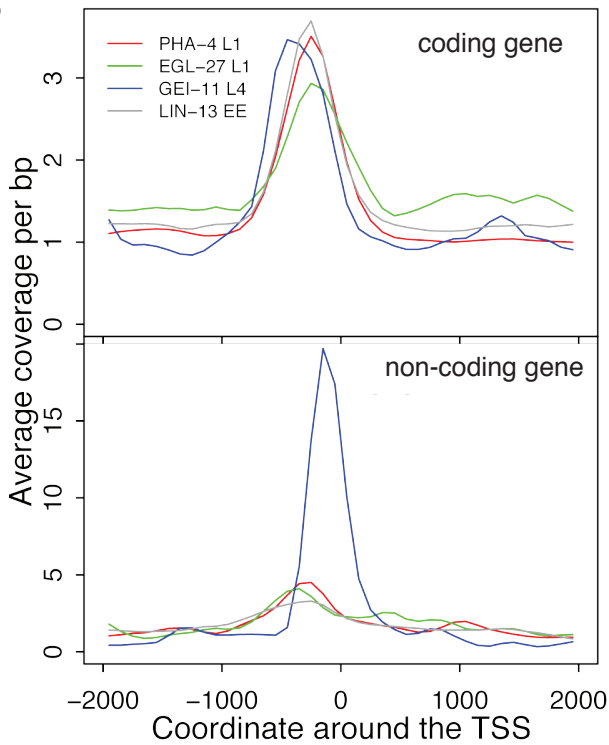
Fig 5

A

TFs: HOT binding region and specific binding regions



B



C

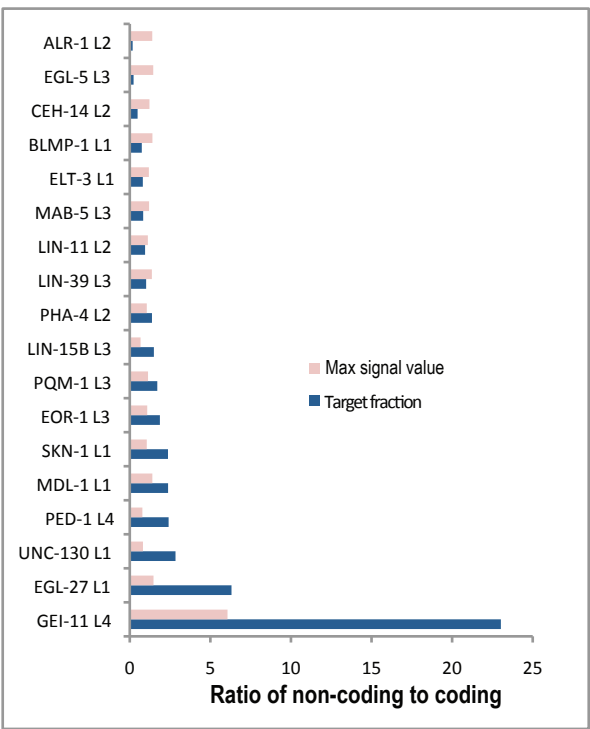


Fig 6

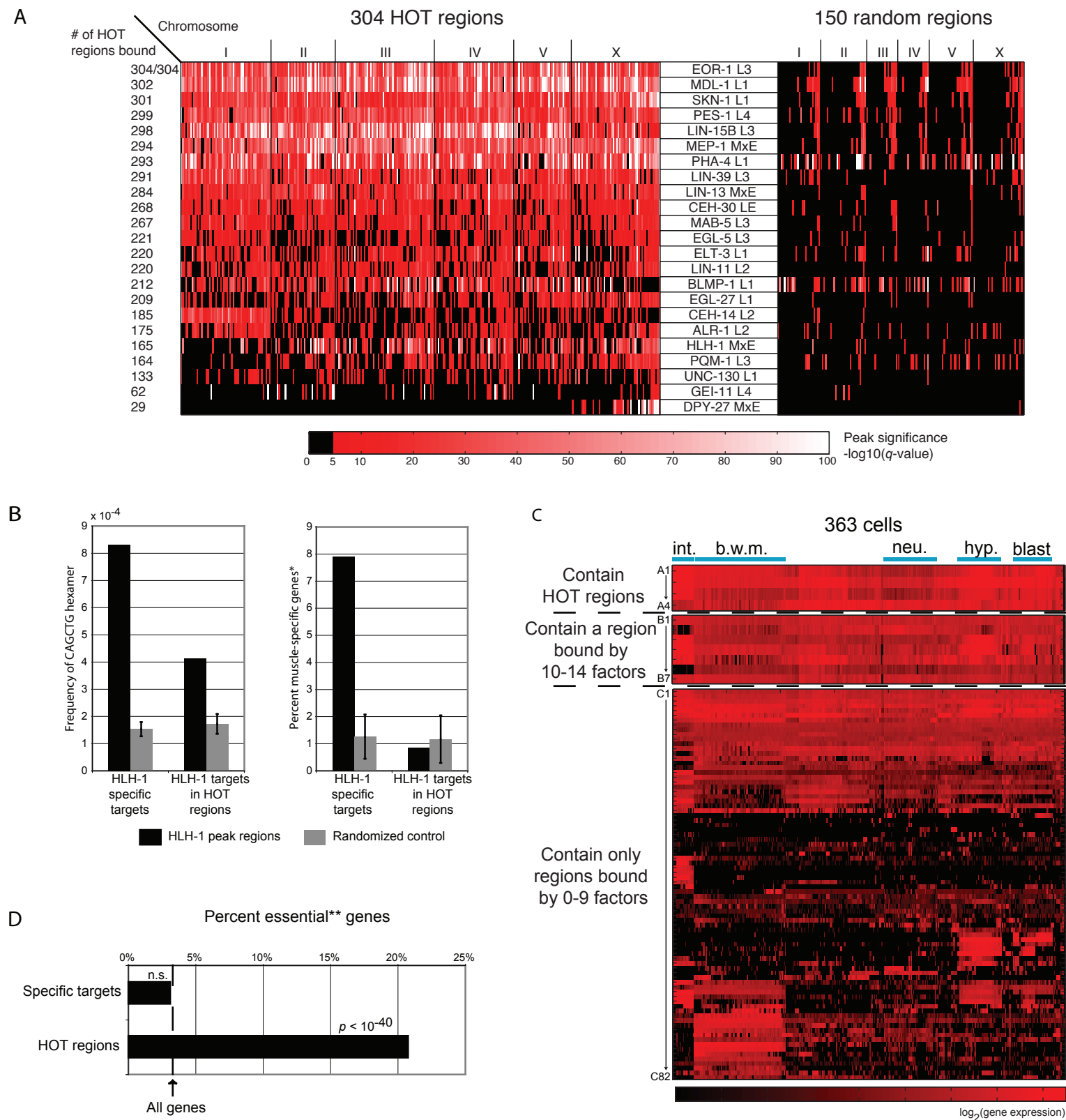


Fig 7

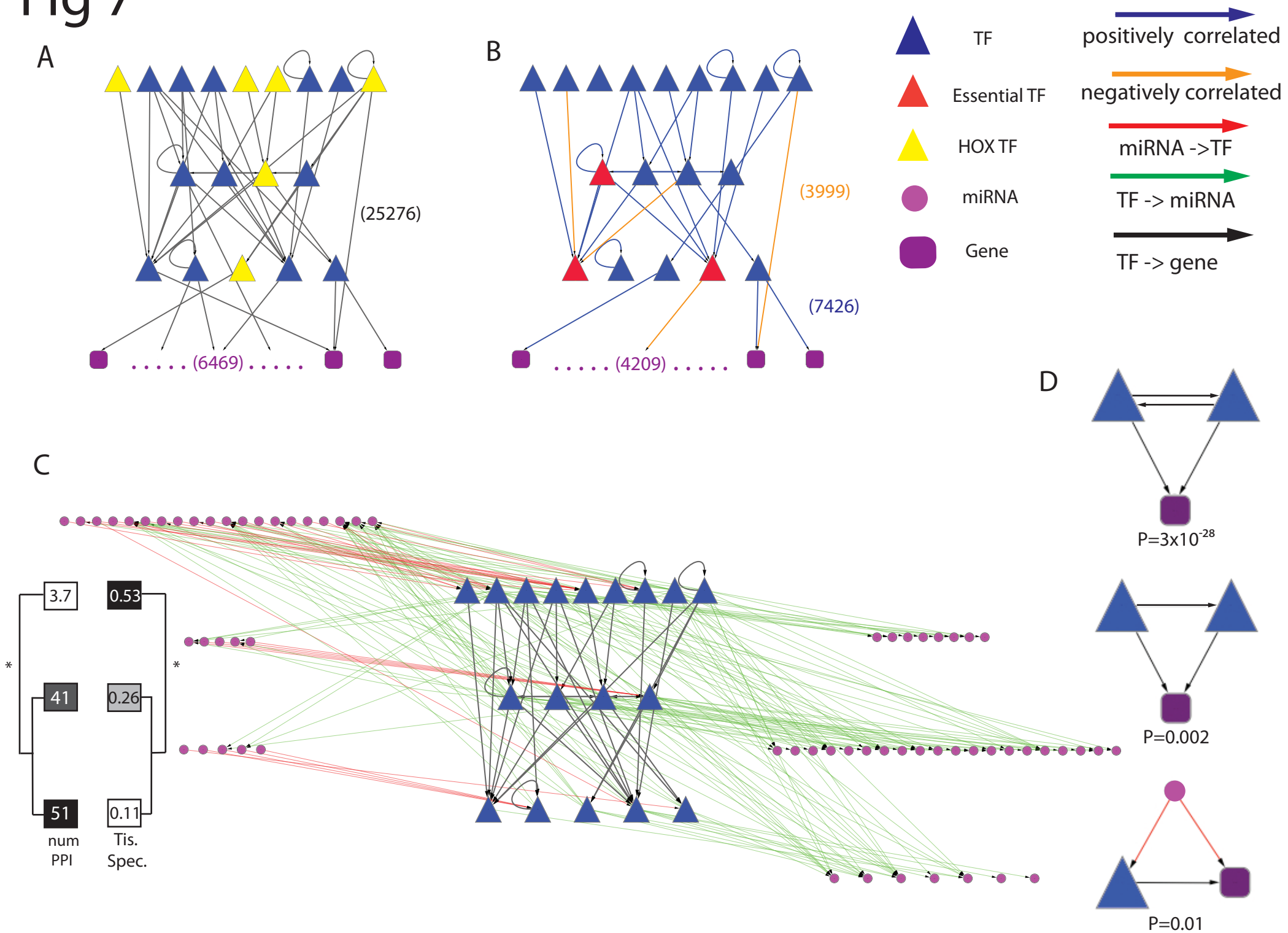


Fig 8 A

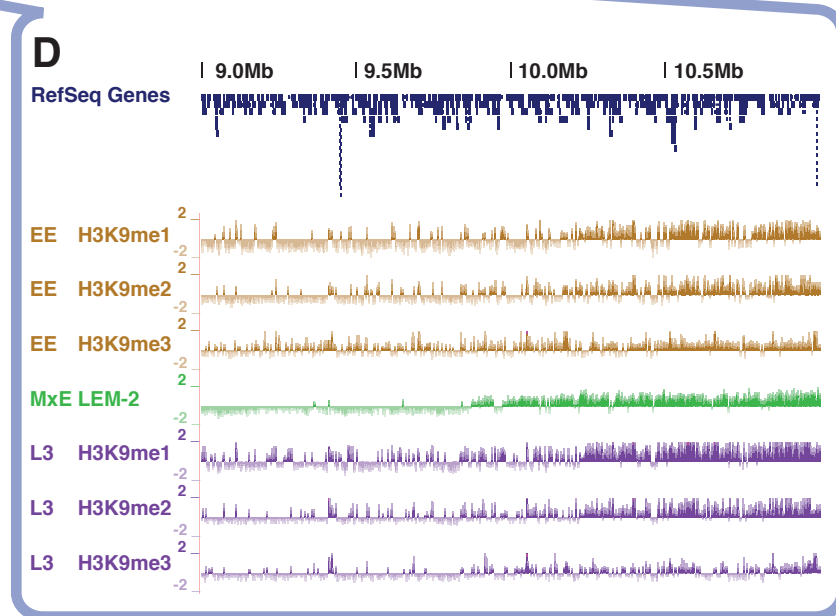
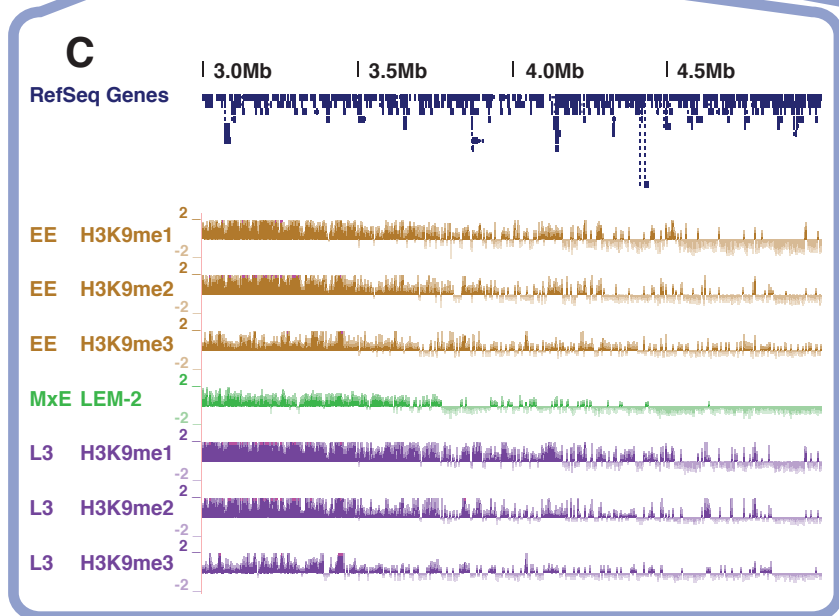
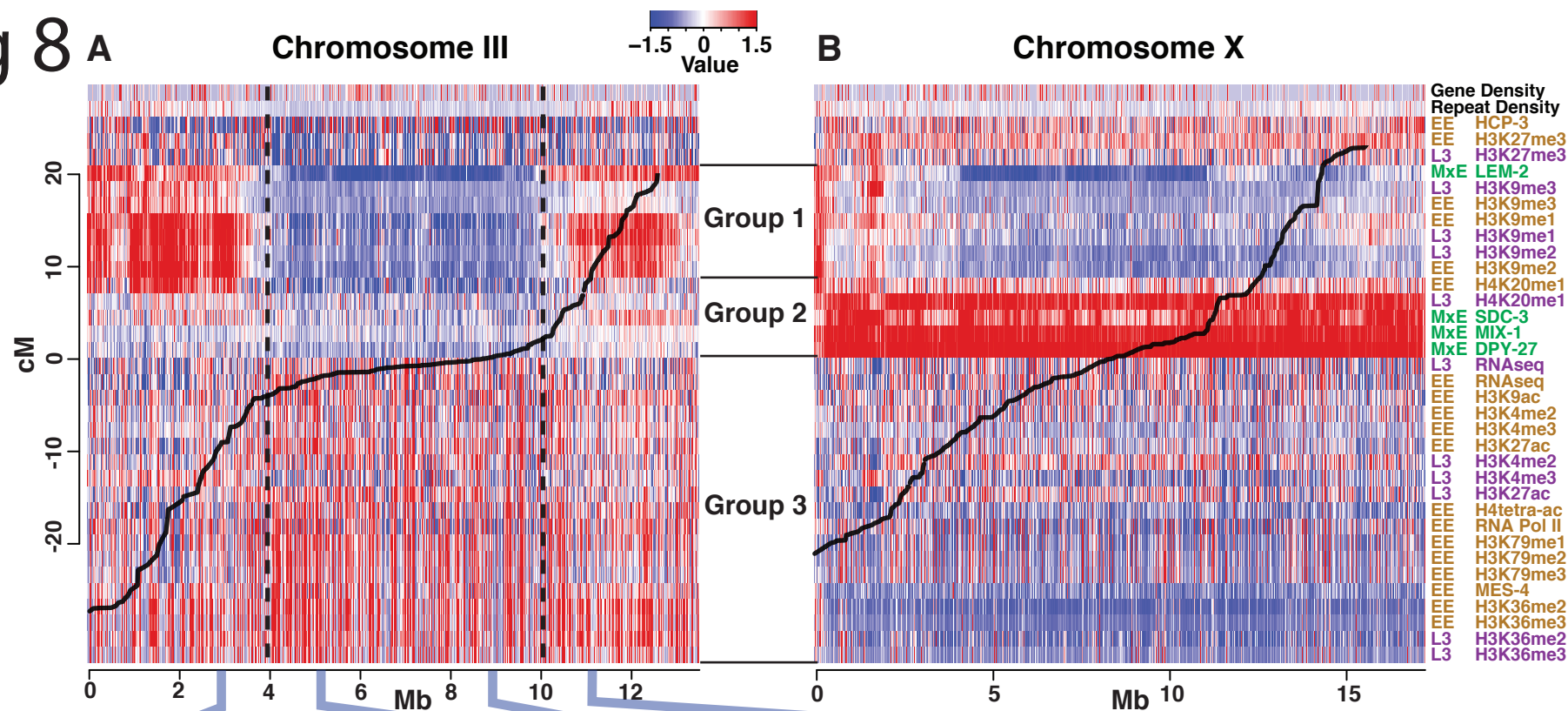
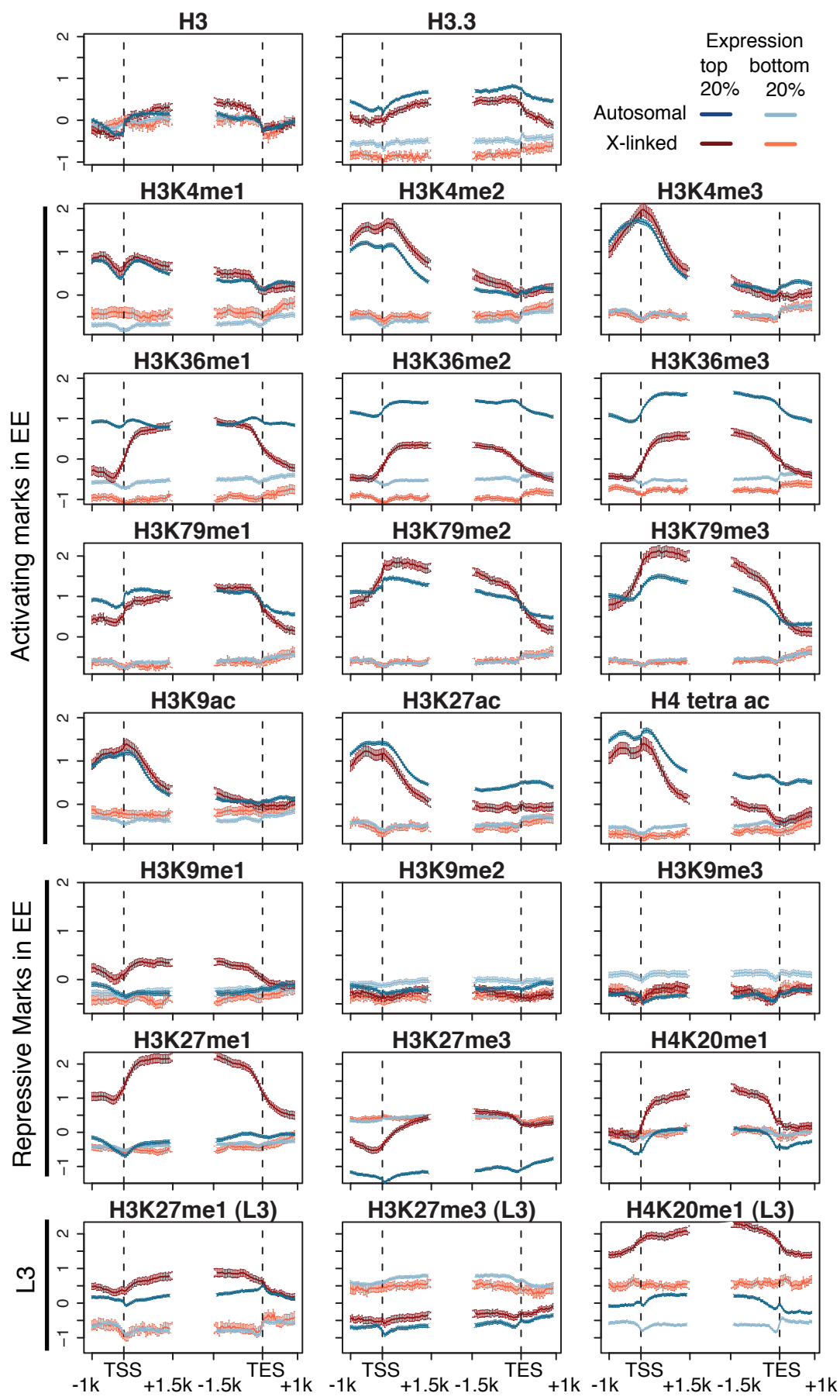
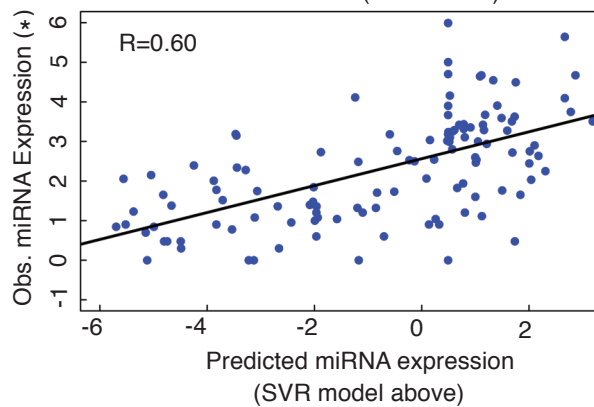
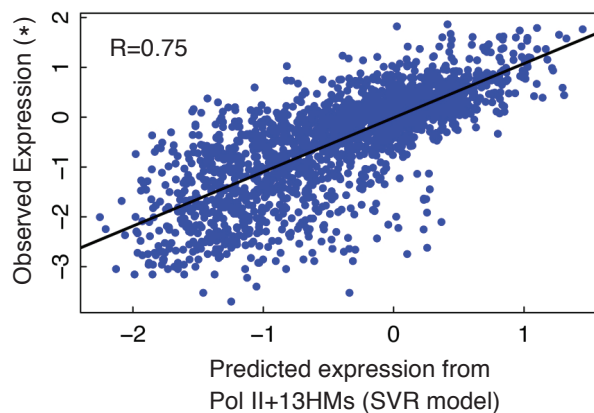
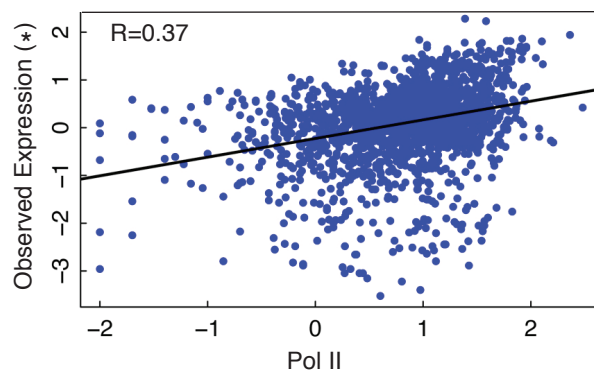
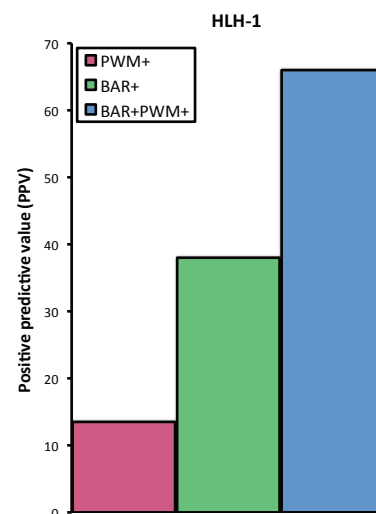
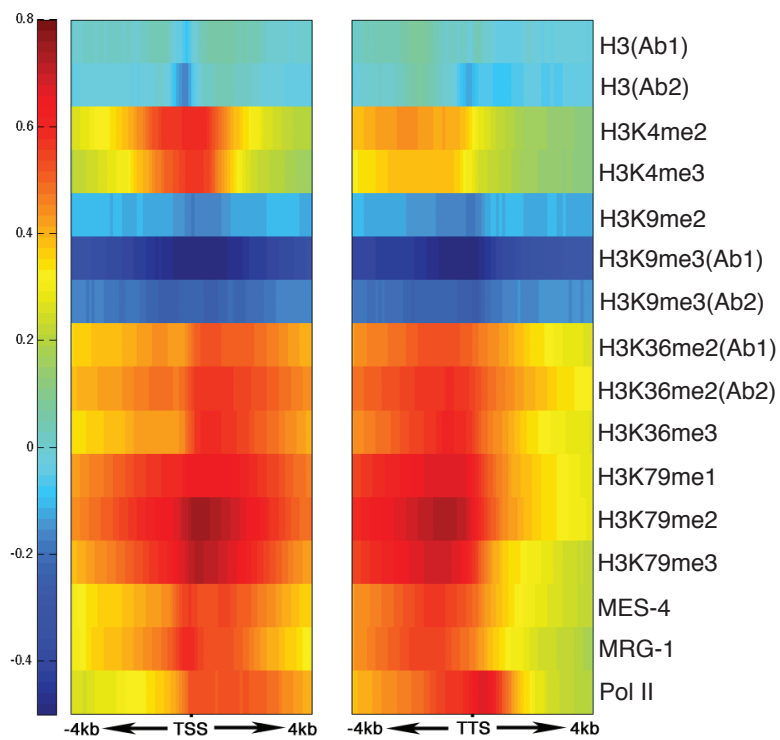
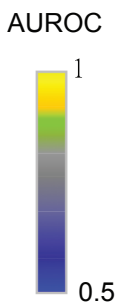


Fig 9



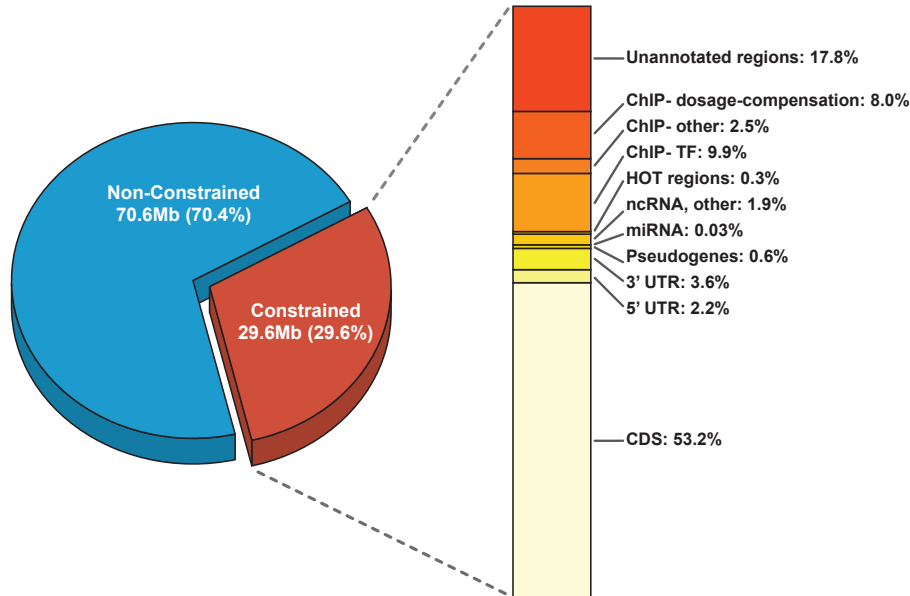
A



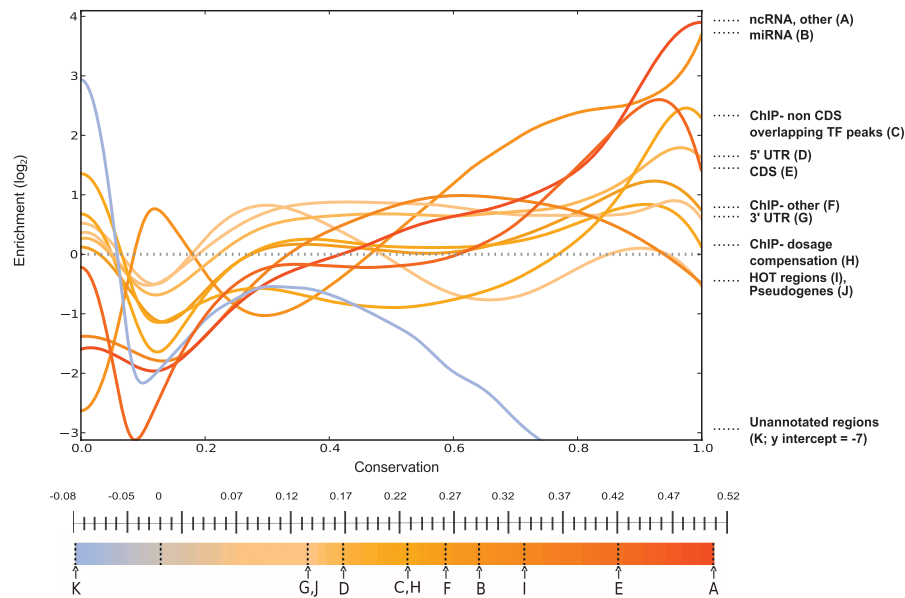
* = LOG₁₀RPKM

FIG 11

A



B



C

