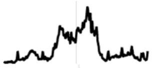
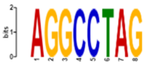
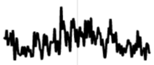
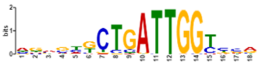
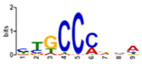
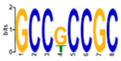
Significant motifs (E-value ≤ 0.05) identified in Trim33 ChIP seq peaks, using the program MEME

Enriched motifs similar to known transcription factors		E-value	Distribution
MYB (MA0100.2)		1.2e-22	
ZEB1 (MA0103.2)		3.0e-16	
NRF1 (MA0506.1)		5.8e-5	
Zfx (MA0146.2)		1.6e-4	
NFYB (MA0502.1)		1.4e-3	
NFYA (MA0060.2)		2.0e-2	
THAP1 (MA0597.1)		2.4e-2	
EGR1 (MA0162.2)		1.5e-2