A

Gene Ontology (GO)	Depletion	p-value	Number of genes
Cell proliferation	dMes-4	2.24E-08	88
	Beaf32	9,18E-08	78
Cell-death	dMes-4	6.24E-05	57
	Beaf32	1.90E-08	54
Nucleoside triphosphate metabolic process	dMes-4	~1	
	Beaf32	~1	

B

Factor	Consensus	Enrichment (E-value)
Beaf32	CGATA	1^{e}-60
DREF	TATCGATA	1^{e}-59

Figure S4. dMes-4 and Beaf32 co-regulate specific Gene Ontologies

A. Examples of gene ontologies enriched among the differentially expressed genes as measured by DGE-Seq in Beaf32-KD or Mes4-KD compared to control cells and as identified through DGE-Seq (threshold for DE genes p-value < 1e-3).

B. The 4,120 Beaf32 peaks identified by ChIP-Seq (see Figure 1A) harbor two consensus motifs that are recognized by Beaf32 and DREF, in agreement with the involvement of both factors in co-regulating specific gene ontologies (GO) including the cell cycle (see panel A; see Expanded Table E1)(Emberly et al., 2008). Also indicated are the associated E-values as obtained by motif searches through MEME (see Methods).