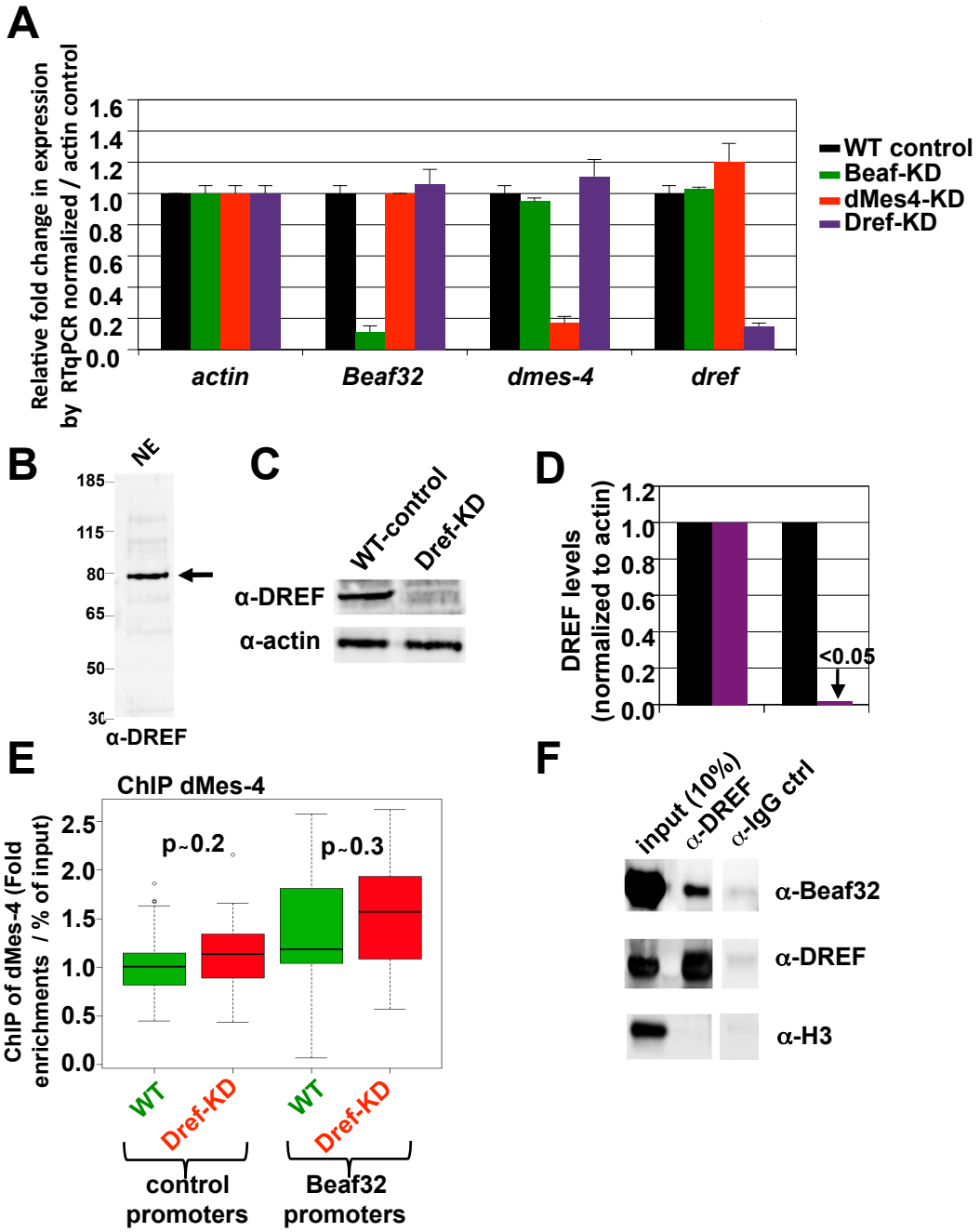
A
Relative fold change in expression by RTqPCR normalized / actin control
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
actin
Beaf32
dmes-4
dref
WT control
Beaf-KD
dMes4-KD
Dref-KD
B
NE
185
115
80
65
50
30
α-DREF
C
WT-control
Dref-KD
α-DREF
α-actin
D
DREF levels (normalized to actin)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
<0.05
E
ChIP dMes-4
ChIP of dMes-4 (Fold enrichments / % of input)
2.5
2.0
1.5
1.0
0.5
0.0
p~0.2
p~0.3
WT
Dref-KD
WT
Dref-KD
control promoters
Beaf32 promoters
F
input (10%)
α-DREF
α-IgG ctrl
α-Beaf32
α-DREF
α-H3

Figure S8. Characterization of DREF depletion

A. Graph representing the results from 3 independent RT-qPCR analyses to measure the mRNA levels of *actin*, *beaf32*, *dMes-4*, and *dref* upon knock-down of Beaf32 ('Beaf32-KD'; green bars), dMes-4 ('dMes-4-KD; red bars), DREF ('DREF-KD'; purple bars) or control ('control'; black bars). The error bar corresponds to the standard deviation of the measure. The y axis shows the relative fold change in expression normalized to *actin* control.

B. Western blotting analysis of nuclear extracts using anti-DREF antibodies. The arrow indicates the unique band detected corresponding to the molecular weight of DREF (713 AA).

C. Western blotting analysis of nuclear extracts prepared from DREF-KD or control cells using anti-DREF or anti-actin control antibodies for loading control. The efficiency of DREF-KD was confirmed by RTqPCR analysis (see panel A).

D. Quantification of DREF depletion as compared to loading control from the western blotting analysis in panel C (see Methods).

E. Box plot showing the results of ChIP performed in DREF-KD (red boxes) compared to WT-control (mock-depleted) cells (green boxes) in percent of input (y-axis) with anti- dMes-4 antibodies or IgG control, for 16 promoters harboring a Beaf32 site or not, as indicated (see Methods for a list of genes). ChIP data were analyzed by qPCR analyses in triplicates and for three independent measures normalized to three control loci (see Methods).

F. Co-immunoprecipitation experiment using anti-DREF antibodies performed in parallel with IgG control followed by western blotting analysis using anti- Beaf32, DREF or -histone H3 as loading control, compared to input nuclear extract (10% 'input').