FigS3

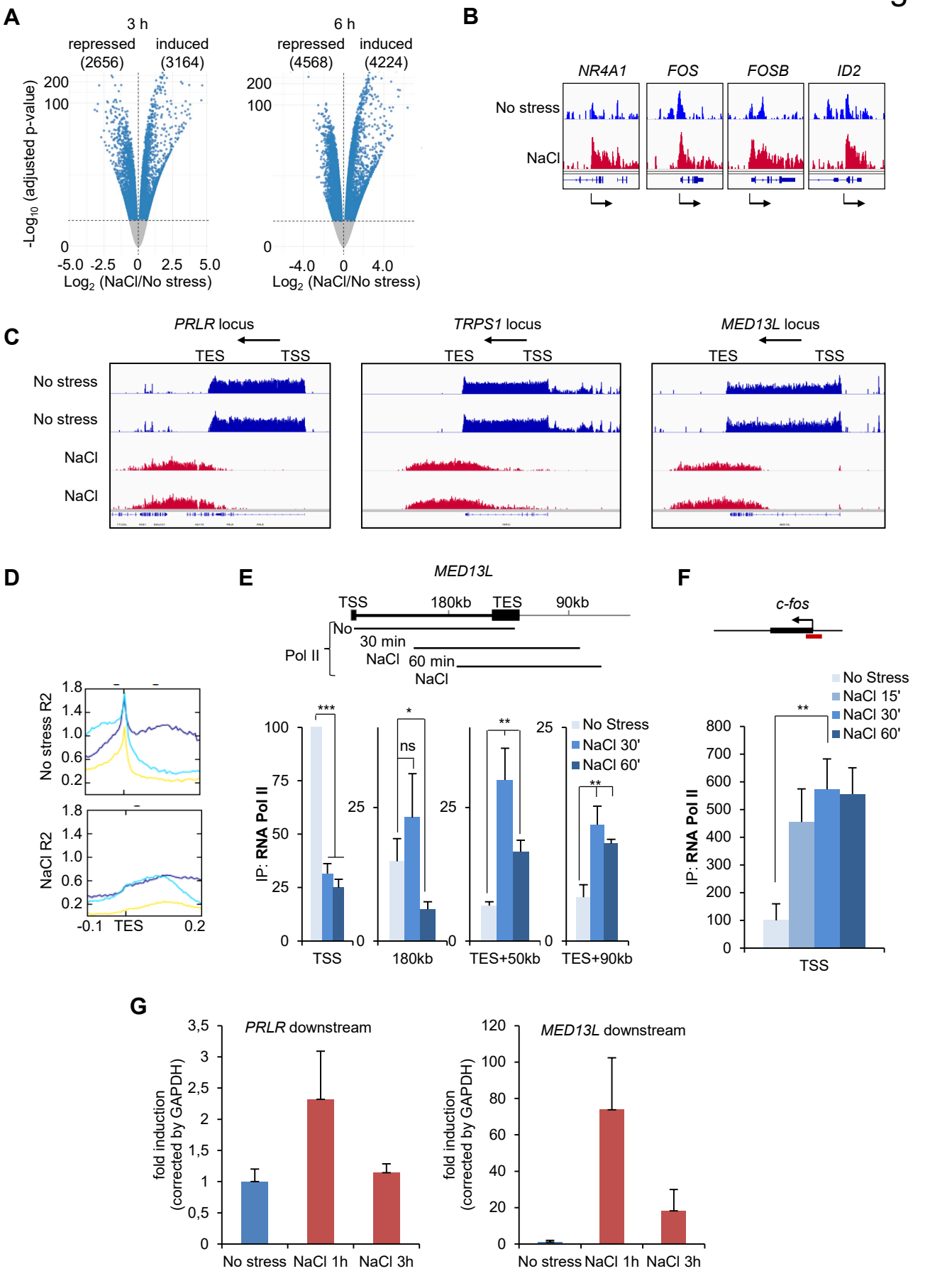
A
3 h
repressed (2656)
induced (3164)
6 h
repressed (4568)
induced (4224)
-Log10 (adjusted p-value)
Log2 (NaCl/No stress)
B
NR4A1
FOS
FOSB
ID2
No stress
NaCl
C
PRLR locus
TRPS1 locus
MED13L locus
TES
TSS
No stress
No stress
NaCl
NaCl
D
No stress R2
NaCl R2
-0.1 TES 0.2
E
MED13L
TSS
180kb
TES
90kb
No
Pol II
30 min NaCl
60 min NaCl
IP: RNA Pol II
No Stress
NaCl 30'
NaCl 60'
ns
TSS
180kb
TES+50kb
TES+90kb
F
c-fos
No Stress
NaCl 15'
NaCl 30'
NaCl 60'
IP: RNA Pol II
TSS
G
PRLR downstream
MED13L downstream
fold induction (corrected by GAPDH)
No stress
NaCl 1h
NaCl 3h

**Figure S3. Global transcriptional changes upon hyper-osmotic shock.** A) Volcano plots constructed from RNA-seq data obtained at 3 and 6 h of osmostress (110 mM NaCl). All genes that are significantly up- or down-regulated in stressed samples compared to control are highlighted as blue dots. B and C) Coverage profiles of Pol II occupancy at the indicated genes in control and 1 h NaCl-treated cells visualized using IGV (110 mM NaCl). Arrows indicate gene orientation. TSS: Transcription start site; TES: Transcription end site. D) DeepTools' k-means clustering of Pol II ChIP-seq signals of the second replicate (R2) around the TES of genes with detected Pol II run-off. E) Top: Schematic of the *MED13L* locus. The lines at the bottom represent the expected Pol II position at the indicated time based on the elongation transcription rate *in vivo*. Below: Pol II ChIP results of time course experiments across the *MED13L* locus analyzed using qPCR (SEM of N=3, * $p<0.05$, ** $p<0.005$, *** $p<0.0005$; Student's t-test). F) ChIP results of Pol II at the TSS of c-fos in response to stress at indicated times as analyzed using qPCR (SEM of N=3). G) RNA expression levels of downstream regions of *PRLR* and *MED13L* in response to stress at indicated times as analyzed using qPCR (SEM of N=3).