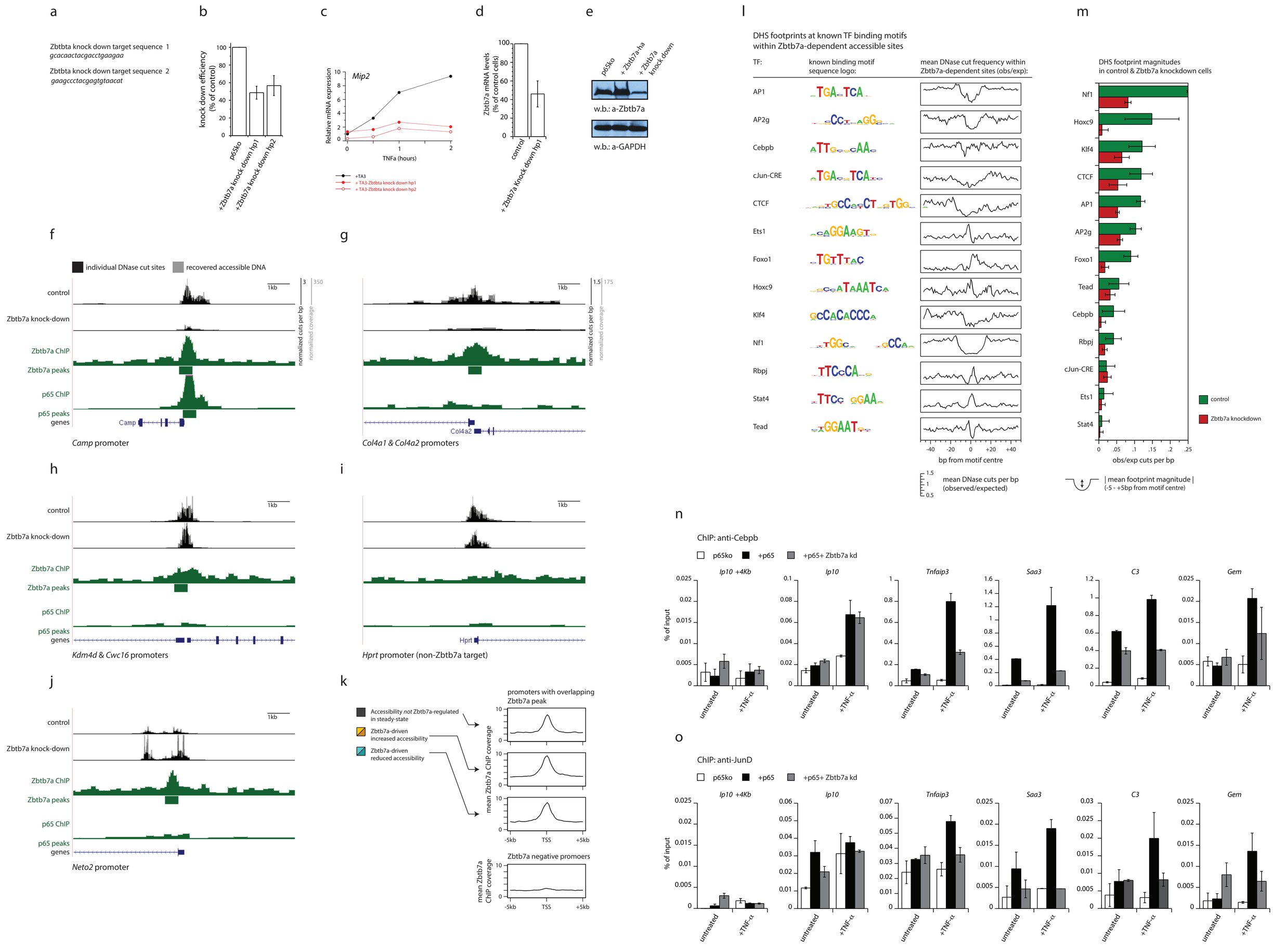
Figure S3


a
Zbtbta knock down target sequence 1
gcacaactacgacctgaagaa
Zbtbta knock down target sequence 2
gaagccctacgagtgtaacat
b
knock down efficiency (% of control)
p65ko
+Zbtb7a knock down hp1
+Zbtb7a knock down hp2
c
Mip2
Relative mRNA expression
TNFa (hours)
+TA3
+ TA3-Zbtbta knock down hp1
+ TA3-Zbtbta knock down hp2
d
Zbtb7a mRNA levels (% of control cells)
control
+ Zbtb7a knock down hp1
e
p65ko
+ Zbtb7a-ha
+ Zbtb7a knock down
w.b.: a-Zbtb7a
w.b.: a-GAPDH
l
DHS footprints at known TF binding motifs within Zbtb7a-dependent accessible sites
TF:
known binding motif sequence logo:
mean DNase cut frequency within Zbtb7a-dependent sites (obs/exp):
AP1
AP2g
Cebpb
cJun-CRE
CTCF
Ets1
Foxo1
Hoxc9
Klf4
Nf1
Rbpj
Stat4
Tead
bp from motif centre
mean DNase cuts per bp (observed/expected)
m
DHS footprint magnitudes in control & Zbtb7a knockdown cells
obs/exp cuts per bp
| mean footprint magnitude |
(-5 - +5bp from motif centre)
control
Zbtb7a knockdown
f
individual DNase cut sites
recovered accessible DNA
control
Zbtb7a knock-down
Zbtb7a ChIP
Zbtb7a peaks
p65 ChIP
p65 peaks
genes
normalized cuts per bp
normalized coverage
Camp
Camp promoter
g
Col4a2
Col4a1 & Col4a2 promoters
h
Kdm4d & Cwc16 promoters
i
Hprt
Hprt promoter (non-Zbtb7a target)
j
Neto2 promoter
k
Accessibility not Zbtb7a-regulated in steady-state
Zbtb7a-driven increased accessibility
Zbtb7a-driven reduced accessibility
promoters with overlapping Zbtb7a peak
mean Zbtb7a ChIP coverage
Zbtb7a negative promoers
-5kb
TSS
+5kb
n
ChIP: anti-Cebpb
p65ko
+p65
+p65+ Zbtb7a kd
Ip10 +4Kb
Ip10
Tnfaip3
Saa3
C3
Gem
% of input
untreated
+TNF-α
o
ChIP: anti-JunD