Figure S13. In vitro nucleosome occupancy profiles (black lines), GC% (yellow lines) anchored on the summits of TSS-distal ChIP-seq peaks. For comparison, the in vivo nucleosome occupancy profiles anchored on the top one-third TSS-distal ChIP-seq peaks (strongest ChIP-seq signal; green lines; same as the green lines in Fig. S10) are also shown. Each ChIP-seq dataset is shown as a panel, alphabetically ordered by TF names.
BCL3
GM12878 – HudsonAlpha
distal

BCL3
K562 – HudsonAlpha
distal

BCLAF1
GM12878 – HudsonAlpha
distal

BCLAF1
K562 – HudsonAlpha
distal

relative distance from peak summit
in vivo
in vitro
%GC

relative distance from peak summit
in vivo
in vitro
%GC
BDP1
BDP1 – K562 – Harvard distal

BRCA1
BRCA1 – GM12878 – Stanford distal

BRF1
BRF1 – K562 – Harvard distal

BRF2
BRF2 – K562 – Harvard distal
E2F4
E2F4 – K562b – UCD
distal

E2F6
E2F6 – K562 – HudsonAlpha
distal

E2F6
E2F6 – K562b – UCD
distal

EBF1
EBF1 – GM12878 – HudsonAlpha
distal
NFYA  
NFYA – K562 – Stanford  
distal

NR2C2  
TR4 – GM12878 – UCD  
distal

NFYB  
NFYB – K562 – Stanford  
distal

NR2C2  
TR4 – K562b – UCD  
distal

relative distance from peak summit  
in vivo  
in vitro  
%GC
RAD21
RAD21 – K562 – Stanford
distal

RDBP
NELFE – K562 – Harvard
distal

REST
REST – GM12878 – HudsonAlpha
distal

REST
REST – K562 – HudsonAlpha
distal
ZZZ3
ZZZ3 – GM12878 – Harvard
distal

relative distance from peak summit

in vivo
in vitro
%GC

0 10 20 30 40 40 42 44 46 48 50

0 1000 2000

4.0 3.5 3.0 2.5 2.0 1.5 1.0