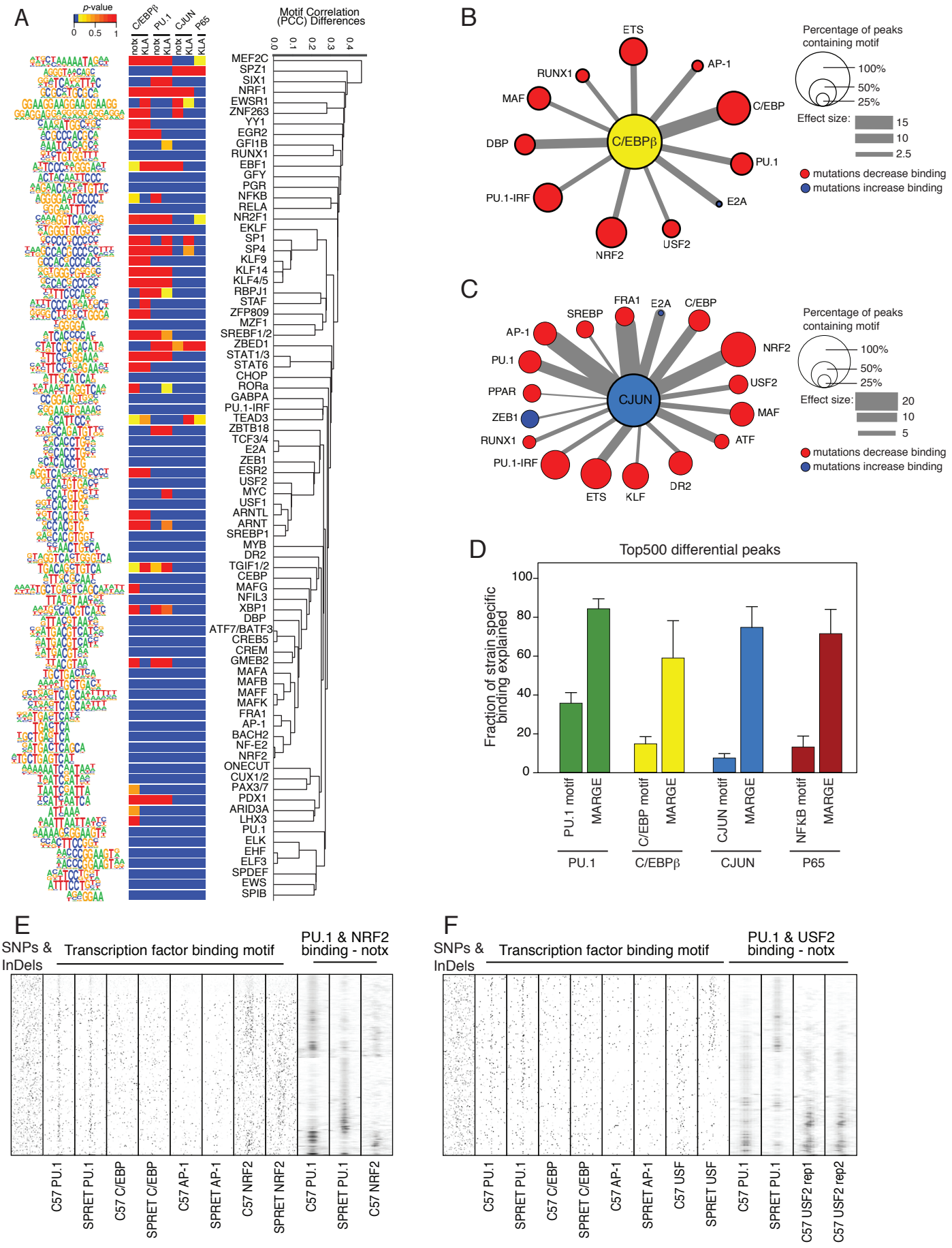
A
p-value
0 0.5 1
C/EBPβ
PU.1
CJUN
P65
notx
KLA
Motif Correlation (PCC) Differences
0.0 0.1 0.2 0.3 0.4
MEF2C
SPZ1
SIX1
NRF1
EWSR1
ZNF263
YY1
EGR2
GFI1B
RUNX1
EBF1
GFY
PGR
NFKB
RELA
NR2F1
EKLF
SP1
SP4
KLF9
KLF14
KLF4/5
RBPJ1
STAF
ZFP809
MZF1
SREBF1/2
ZBED1
STAT1/3
STAT6
CHOP
RORa
GABPA
PU.1-IRF
TEAD3
ZBTB18
TCF3/4
E2A
ZEB1
ESR2
USF2
MYC
USF1
ARNTL
ARNT
SREBP1
MYB
DR2
TGIF1/2
CEBP
MAFG
NFIL3
XBP1
DBP
ATF7/BATF3
CREB5
CREM
GMEB2
MAFA
MAFB
MAFF
MAFK
FRA1
AP-1
BACH2
NF-E2
NRF2
ONECUT
CUX1/2
PAX3/7
PDX1
ARID3A
LHX3
PU.1
ELK
EHF
ELF3
SPDEF
EWS
SPIB
B
ETS
AP-1
RUNX1
C/EBP
MAF
C/EBPβ
DBP
PU.1
PU.1-IRF
E2A
NRF2
USF2
Percentage of peaks containing motif
100%
50%
25%
Effect size:
15
10
2.5
mutations decrease binding
mutations increase binding
C
FRA1
E2A
C/EBP
SREBP
AP-1
NRF2
PU.1
USF2
PPAR
CJUN
MAF
ZEB1
ATF
RUNX1
PU.1-IRF
DR2
ETS
KLF
Percentage of peaks containing motif
100%
50%
25%
Effect size:
20
10
5
mutations decrease binding
mutations increase binding
D
Top500 differential peaks
Fraction of strain specific binding explained
100
80
60
40
20
0
PU.1 motif
MARGE
C/EBP motif
MARGE
CJUN motif
MARGE
NFκB motif
MARGE
PU.1
C/EBPβ
CJUN
P65
E
SNPs & InDels
Transcription factor binding motif
PU.1 & NRF2 binding - notx
C57 PU.1
SPRET PU.1
C57 C/EBP
SPRET C/EBP
C57 AP-1
SPRET AP-1
C57 NRF2
SPRET NRF2
C57 PU.1
SPRET PU.1
C57 NRF2
F
SNPs & InDels
Transcription factor binding motif
PU.1 & USF2 binding - notx
C57 PU.1
SPRET PU.1
C57 C/EBP
SPRET C/EBP
C57 AP-1
SPRET AP-1
C57 USF
SPRET USF
C57 PU.1
SPRET PU.1
C57 USF2 rep1
C57 USF2 rep2

Figure S4