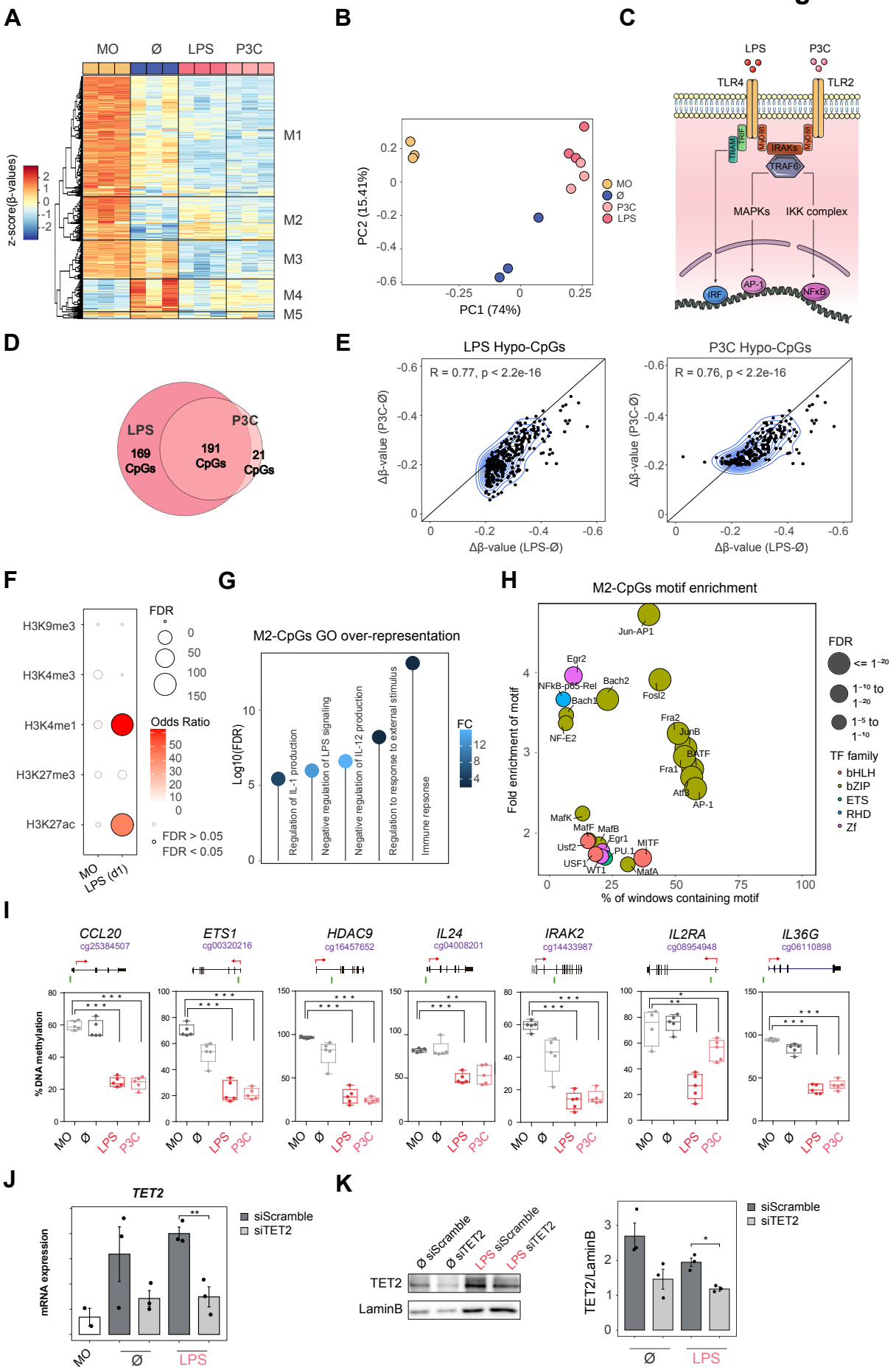
Figure S1


A
MO
Ø
LPS
P3C
z-score(β-values)
M1
M2
M3
M4
M5
B
PC2 (15.41%)
PC1 (74%)
MO
Ø
P3C
LPS
C
LPS
P3C
TLR4
TLR2
TRAM
TIRAP
MyD88
IRAKs
TRAF6
MAPKs
IKK complex
IRF
AP-1
NFκB
D
LPS
169 CpGs
191 CpGs
P3C
21 CpGs
E
LPS Hypo-CpGs
R = 0.77, p < 2.2e-16
Δβ-value (P3C-Ø)
Δβ-value (LPS-Ø)
P3C Hypo-CpGs
R = 0.76, p < 2.2e-16
Δβ-value (P3C-Ø)
Δβ-value (LPS-Ø)
F
H3K9me3
H3K4me3
H3K4me1
H3K27me3
H3K27ac
MO
LPS (d1)
FDR
0
50
100
150
Odds Ratio
50
40
30
20
10
0
FDR > 0.05
FDR < 0.05
G
M2-CpGs GO over-representation
Log10(FDR)
Regulation of IL-1 production
Negative regulation of LPS signaling
Negative regulation of IL-12 production
Regulation to response to external stimulus
Immune repsonse
FC
12
8
4
H
M2-CpGs motif enrichment
Jun-AP1
Egr2
NFkB-p65-Rel
Bach2
Bach1
Fosl2
NF-E2
Fra2
JunB
BATF
Fra1
Atf3
AP-1
MafK
MafF
MafB
Egr1
Usf2
PU.1
MITF
USF1
WT1
MafA
Fold enrichment of motif
% of windows containing motif
FDR
<= 1^-20
1^-10 to 1^-20
1^-5 to 1^-10
TF family
bHLH
bZIP
ETS
RHD
Zf
I
CCL20
cg25384507
ETS1
cg00320216
HDAC9
cg16457652
IL24
cg04008201
IRAK2
cg14433987
IL2RA
cg08954948
IL36G
cg06110898
% DNA methylation
MO
Ø
LPS
P3C
J
TET2
mRNA expression
siScramble
siTET2
MO
Ø
LPS
K
Ø siScramble
Ø siTET2
LPS siScramble
LPS siTET2
TET2
LaminB
TET2/LaminB
siScramble
siTET2
Ø
LPS