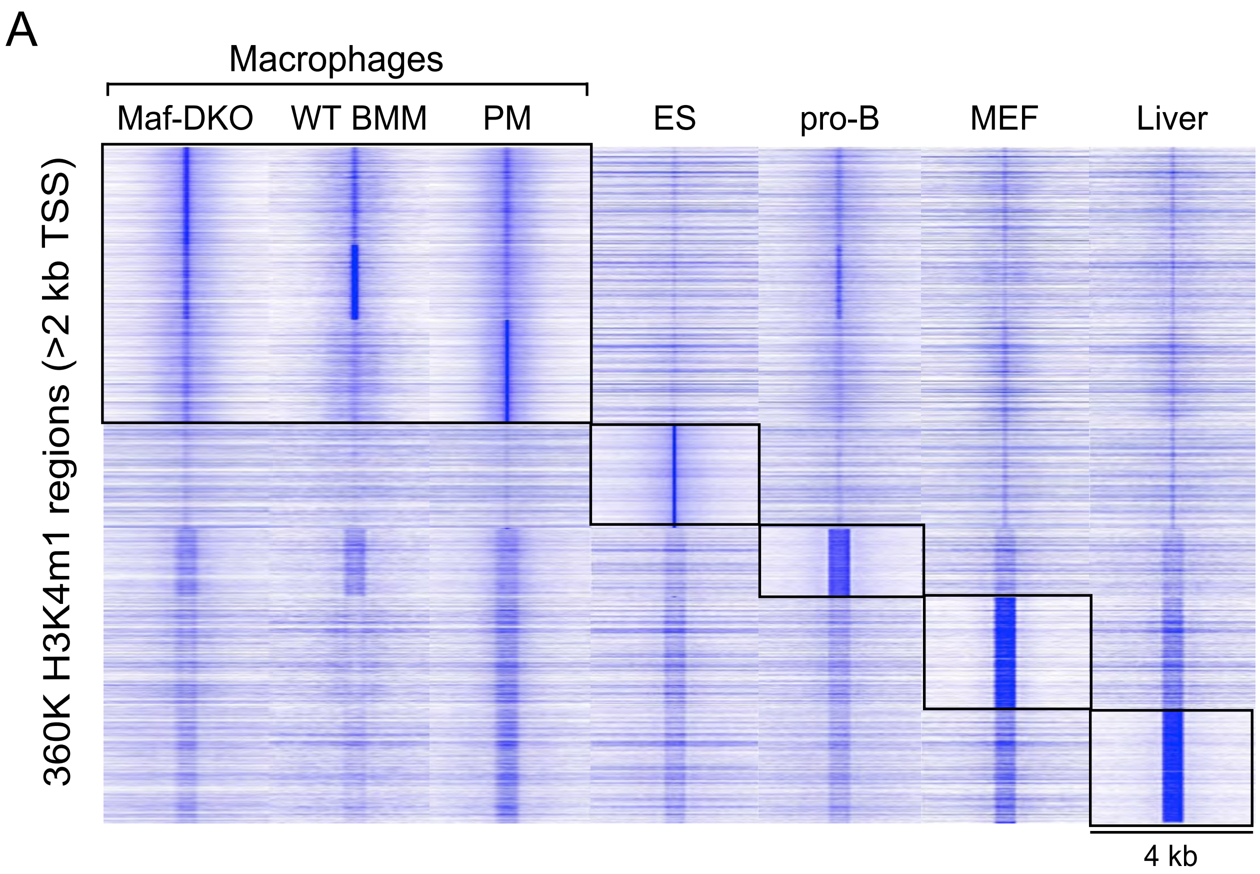
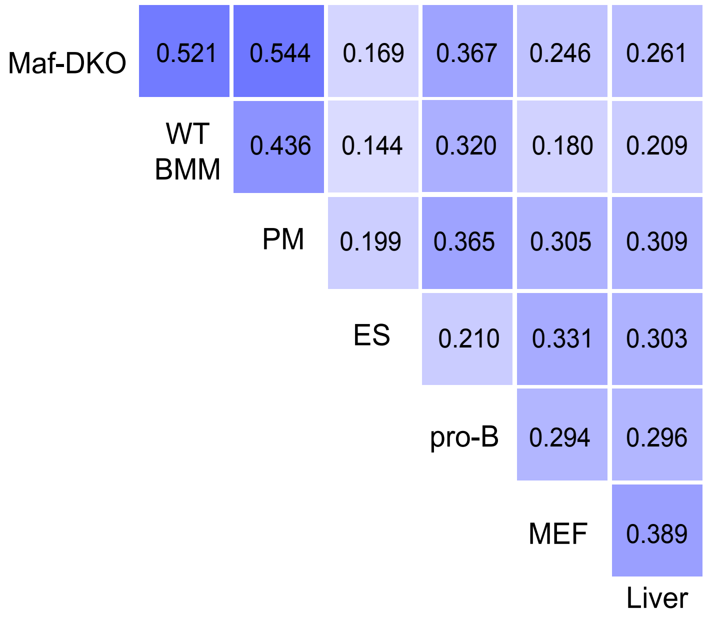
Sup. Figure 1



B

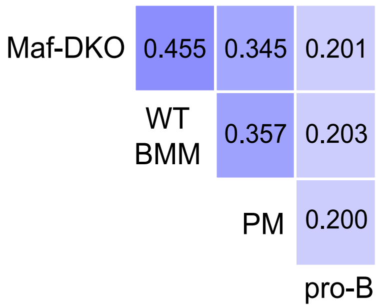
Correlation matrix: H3K4m1



	WT BMM	PM	ES	pro-B	MEF	Liver
Maf-DKO	0.521	0.544	0.169	0.367	0.246	0.261
WT BMM		0.436	0.144	0.320	0.180	0.209
PM			0.199	0.365	0.305	0.309
ES				0.210	0.331	0.303
pro-B					0.294	0.296
MEF						0.389

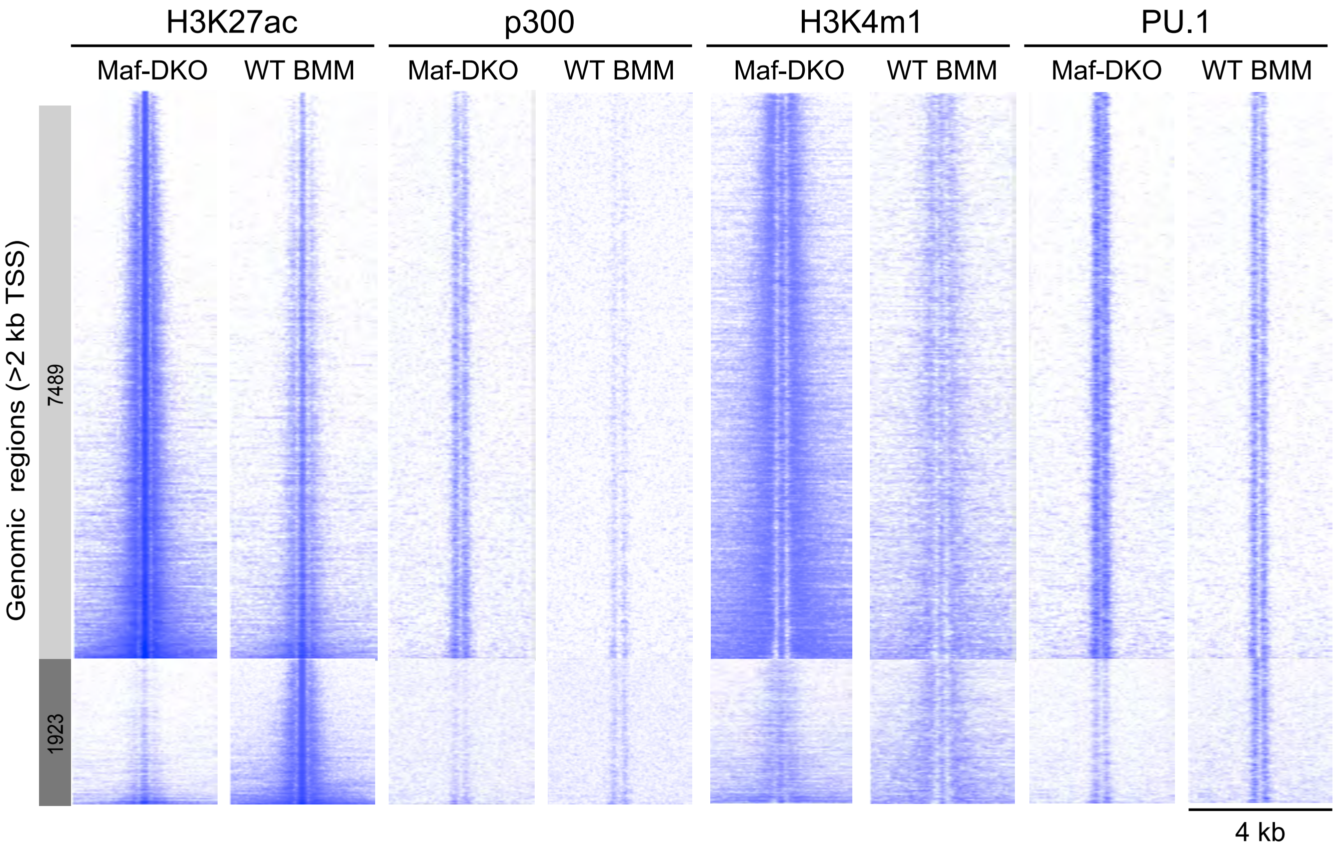
C

Correlation matrix: H3K4m1, PU.1



	WT BMM	PM	pro-B
Maf-DKO	0.455	0.345	0.201
WT BMM		0.357	0.203
PM			0.200

Sup Figure 2

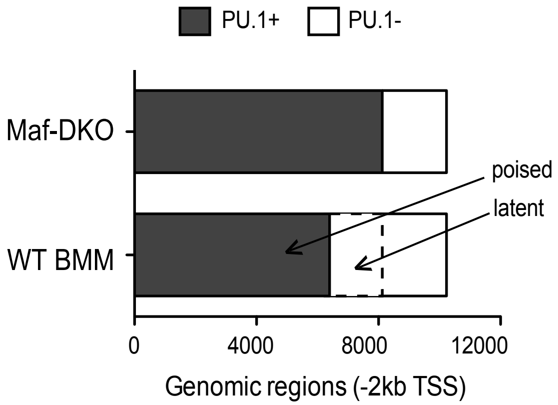

H3K27ac
p300
H3K4m1
PU.1
Maf-DKO
WT BMM
Maf-DKO
WT BMM
Maf-DKO
WT BMM
Maf-DKO
WT BMM
Genomic regions (>2 kb TSS)
7489
1923
4 kb

Sup. Figure 3

A

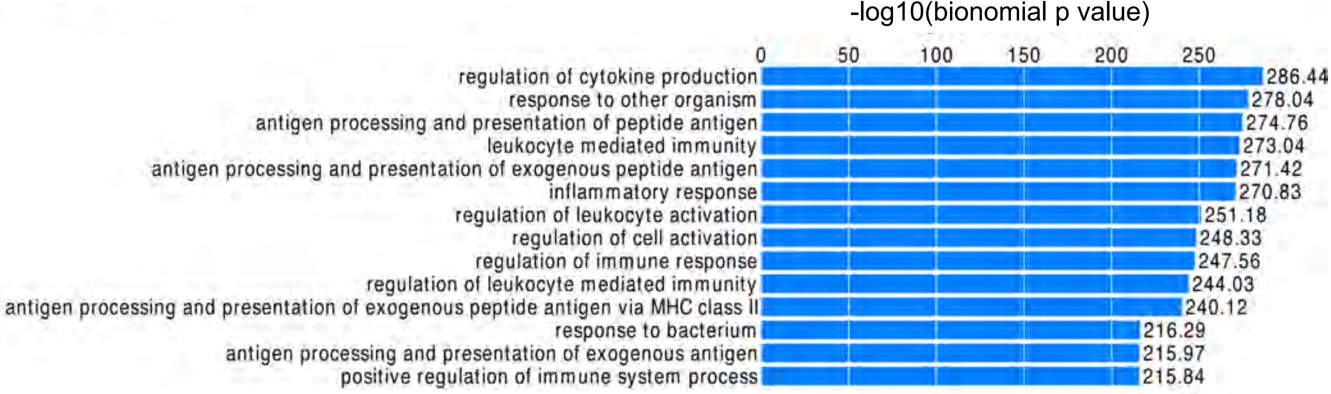
Motif	-logP value	%target/ %bkgd	Best match
	6444	53/8.3	PU.1
	6029	66/16	ETS1
	4563	68/22	PU.1-IRF
	4020	58/18	RUNX1
	3774	44/10	ATF3
	3772	47/11	AP-1
	3154	40/9.4	CEBP
	2740	41/12	CEBP:AP1
	2652	47/16	KLF5
	2640	22/3.1	JUN-AP1
	2505	42/13	MAFA
	1181	16/3.5	MAFK
	1072	16/3.9	MAFF

B

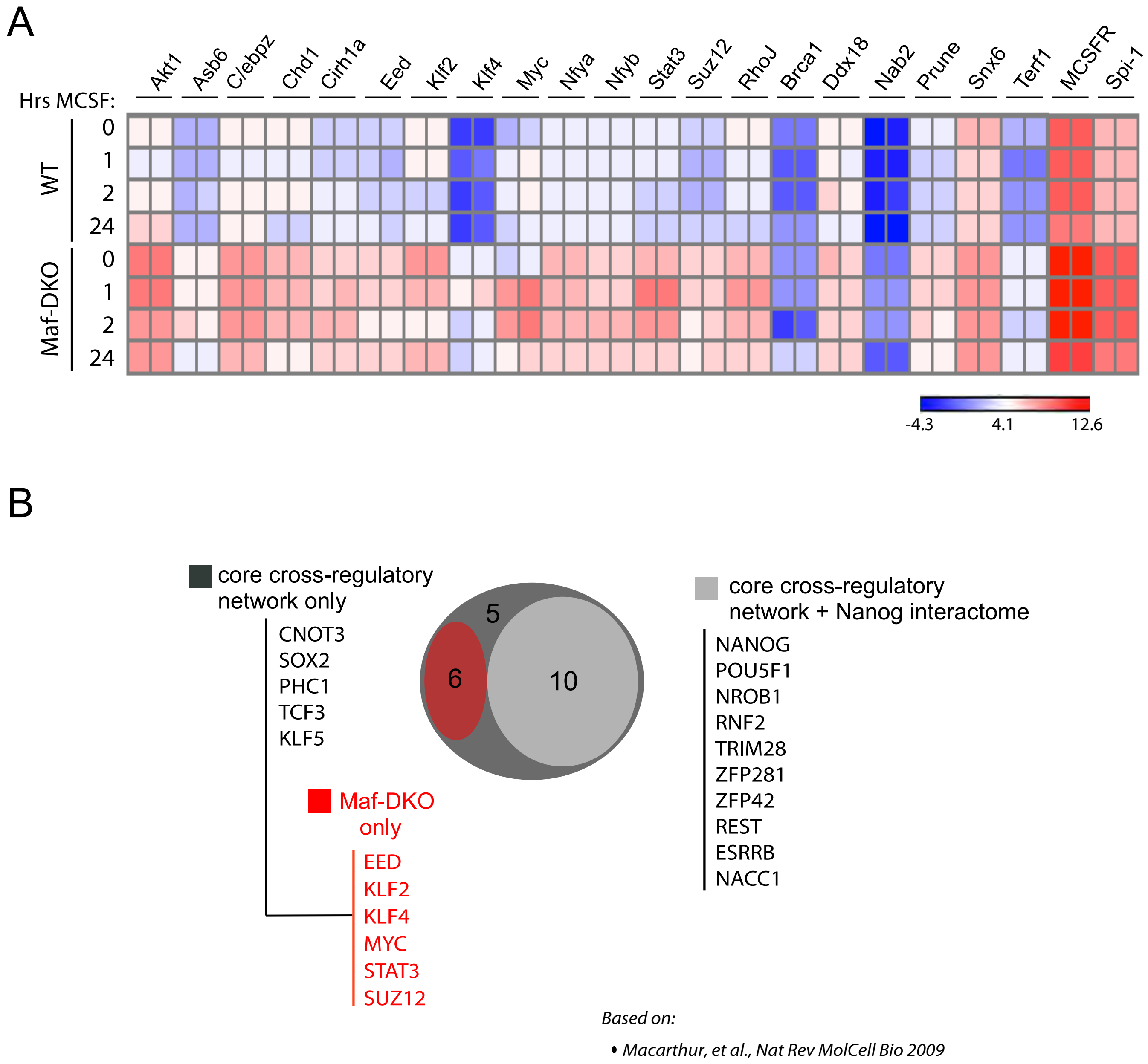


C

GO Biological process



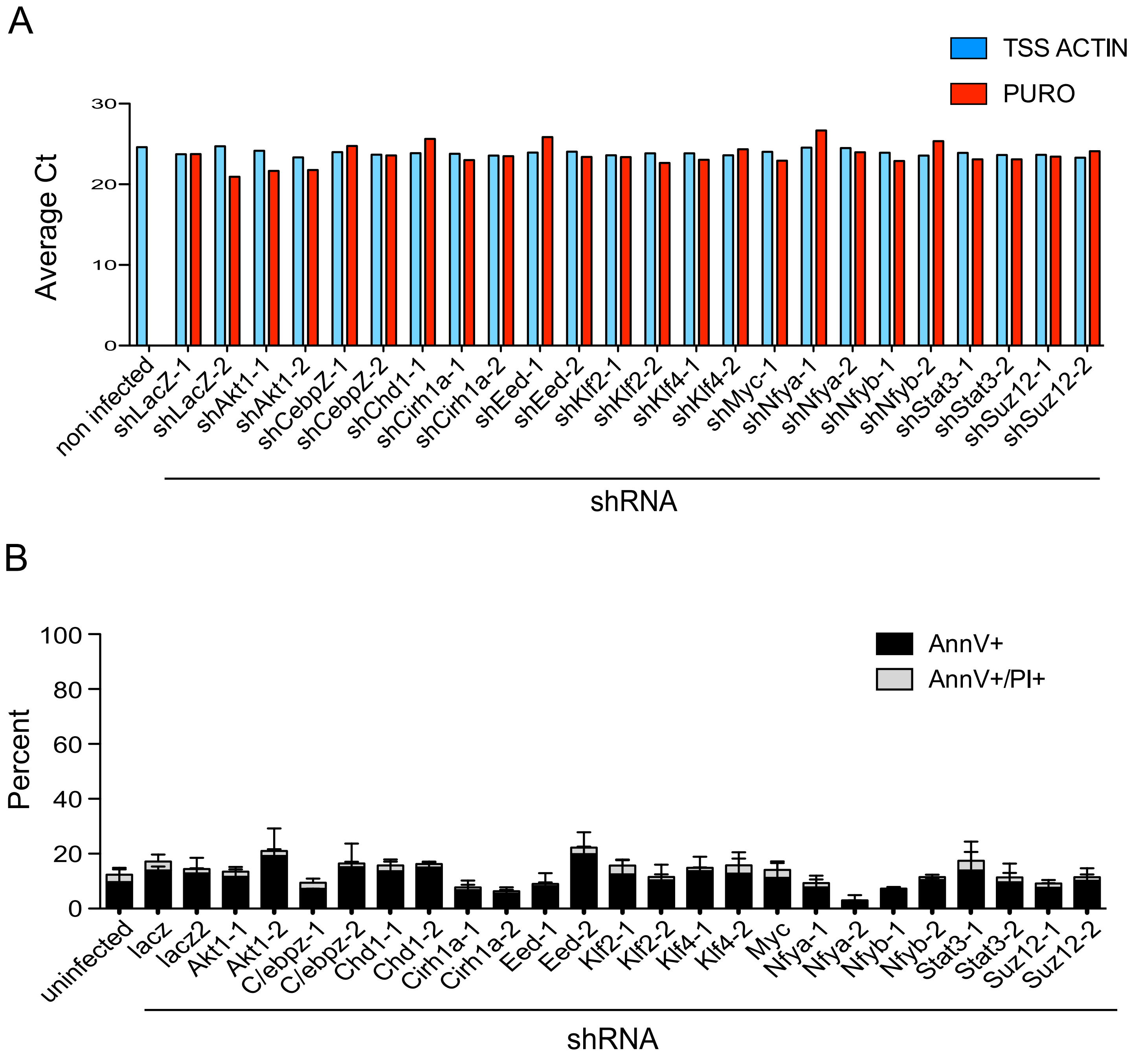
Sup. Figure 4



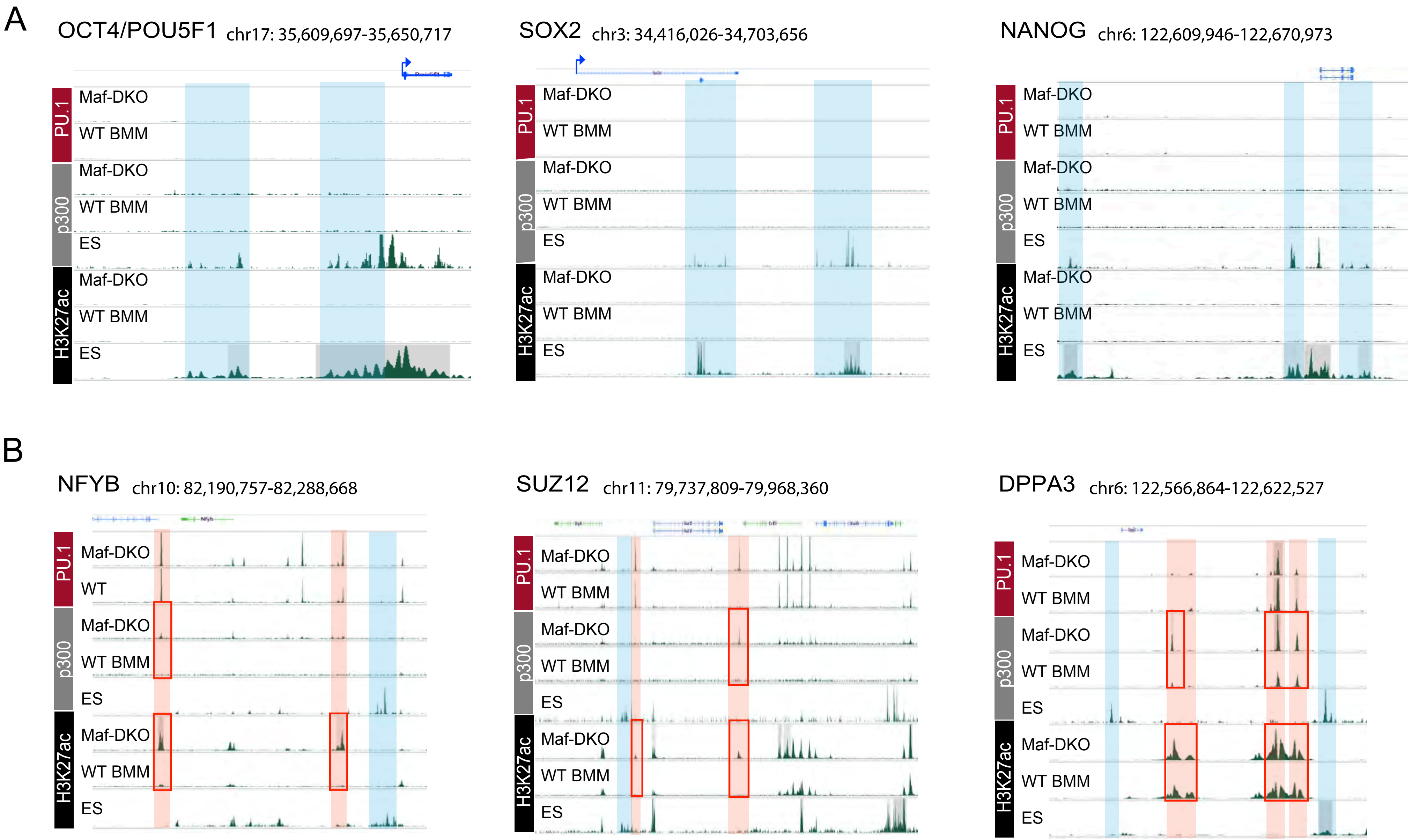
Based on:

- *Macarthur, et al., Nat Rev MolCell Bio 2009*

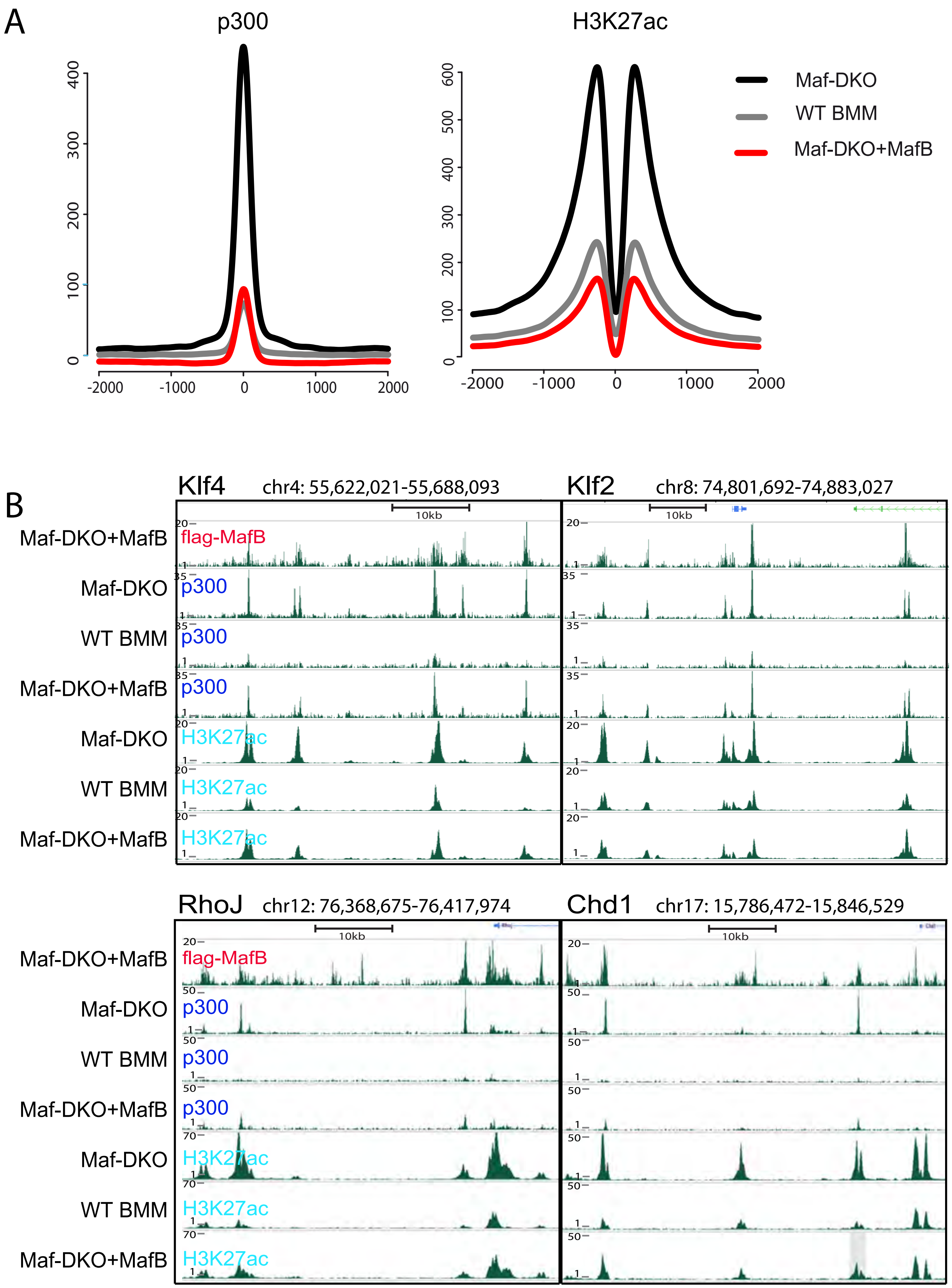
Sup. Figure 5


A
TSS ACTIN
PURO
Average Ct
30
20
10
0
non infected
shLacZ-1
shLacZ-2
shAkt1-1
shAkt1-2
shCebpZ-1
shCebpZ-2
shChd1-1
shCirh1a-1
shCirh1a-2
shEed-1
shEed-2
shKlf2-1
shKlf2-2
shKlf4-1
shKlf4-2
shMyc-1
shNfya-1
shNfya-2
shNfyb-1
shNfyb-2
shStat3-1
shStat3-2
shSuz12-1
shSuz12-2
shRNA
B
AnnV+
AnnV+/PI+
Percent
100
80
60
40
20
0
uninfected
lacz
lacz2
Akt1-1
Akt1-2
C/ebpz-1
C/ebpz-2
Chd1-1
Chd1-2
Cirh1a-1
Cirh1a-2
Eed-1
Eed-2
Klf2-1
Klf2-2
Klf4-1
Klf4-2
Myc
Nfya-1
Nfya-2
Nfyb-1
Nfyb-2
Stat3-1
Stat3-2
Suz12-1
Suz12-2
shRNA

Sup. Figure 6


A
OCT4/POU5F1 chr17: 35,609,697-35,650,717
SOX2 chr3: 34,416,026-34,703,656
NANOG chr6: 122,609,946-122,670,973
PU.1
p300
H3K27ac
Maf-DKO
WT BMM
Maf-DKO
WT BMM
ES
Maf-DKO
WT BMM
ES
B
NFYB chr10: 82,190,757-82,288,668
SUZ12 chr11: 79,737,809-79,968,360
DPPA3 chr6: 122,566,864-122,622,527
PU.1
p300
H3K27ac
Maf-DKO
WT
WT BMM
Maf-DKO
WT BMM
ES
Maf-DKO
WT BMM
ES

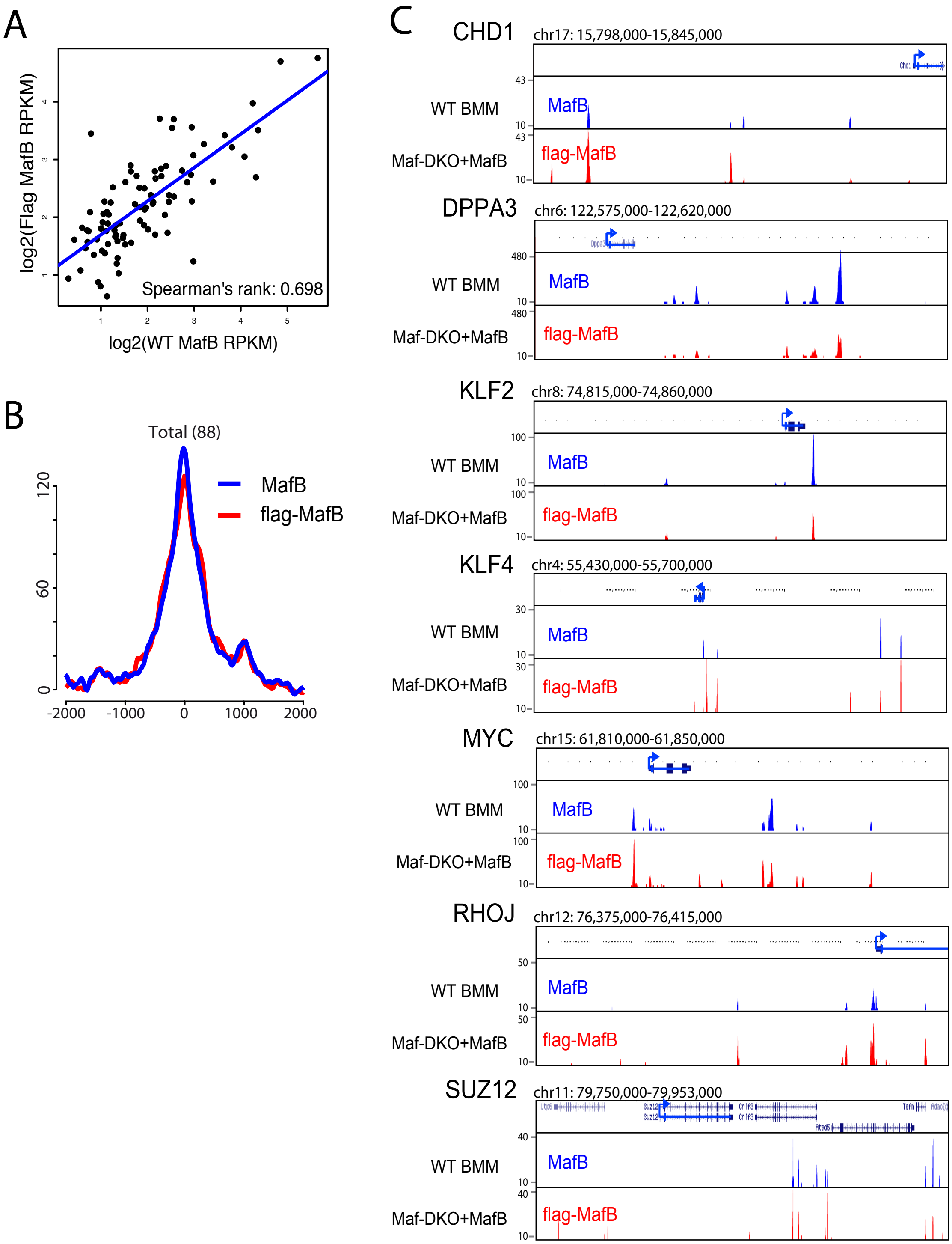
Sup. Figure 7


A
p300
H3K27ac
0
100
200
300
400
500
600
-2000
-1000
0
1000
2000
Maf-DKO
WT BMM
Maf-DKO+MafB
B
Klf4
chr4: 55,622,021-55,688,093
Klf2
chr8: 74,801,692-74,883,027
10kb
Maf-DKO+MafB
flag-MafB
Maf-DKO
p300
WT BMM
p300
Maf-DKO+MafB
p300
Maf-DKO
H3K27ac
WT BMM
H3K27ac
Maf-DKO+MafB
H3K27ac
20
35
1
RhoJ
chr12: 76,368,675-76,417,974
Chd1
chr17: 15,786,472-15,846,529
10kb
50
70

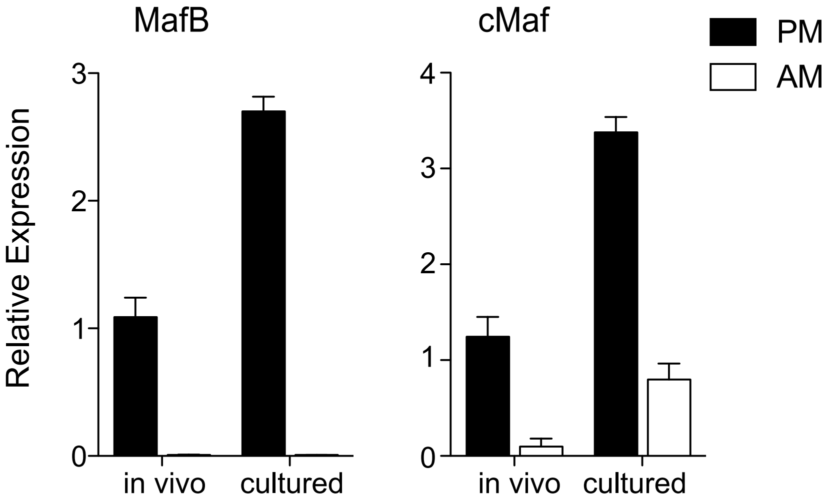
Sup. Figure 8

Motif	-logP value	%target/ %bkgd	Best match
	45.9	62/16	ETS1
	41.6	46/8.2	PU.1
	31.9	63/23	PU.1-IRF
	28.2	46/13	CEBP:AP1
	27.7	53/18	RUNX1
	26.1	41/11	CEBP
	8.2	27/12	MAFA

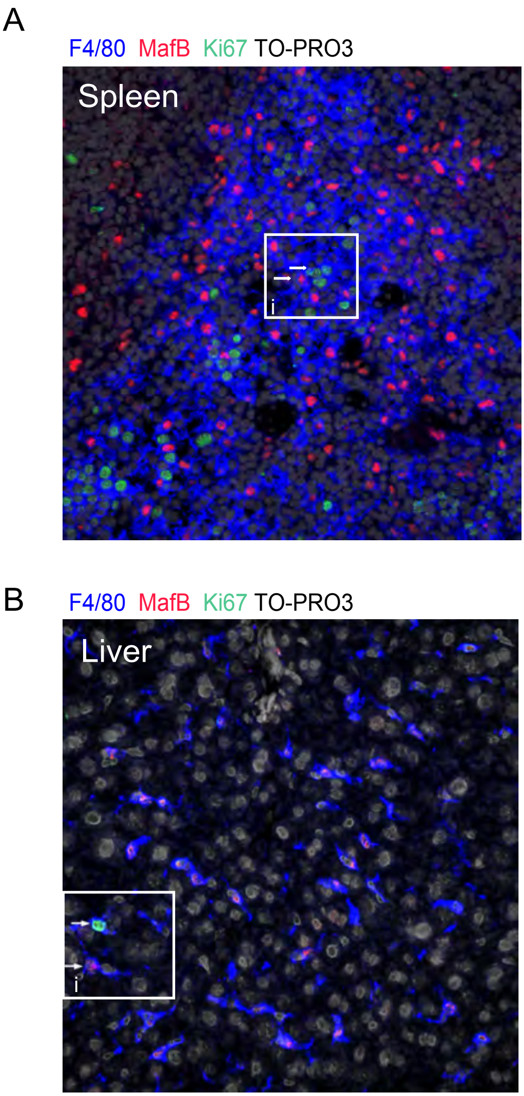
Sup. Figure 9


A
log2(Flag MafB RPKM)
log2(WT MafB RPKM)
Spearman's rank: 0.698
1
2
3
4
5
B
Total (88)
MafB
flag-MafB
0
60
120
-2000
-1000
0
1000
2000
C
CHD1
chr17: 15,798,000-15,845,000
WT BMM
Maf-DKO+MafB
MafB
flag-MafB
43
10
DPPA3
chr6: 122,575,000-122,620,000
480
10
KLF2
chr8: 74,815,000-74,860,000
100
10
KLF4
chr4: 55,430,000-55,700,000
30
10
MYC
chr15: 61,810,000-61,850,000
100
10
RHOJ
chr12: 76,375,000-76,415,000
50
10
SUZ12
chr11: 79,750,000-79,953,000
40
10

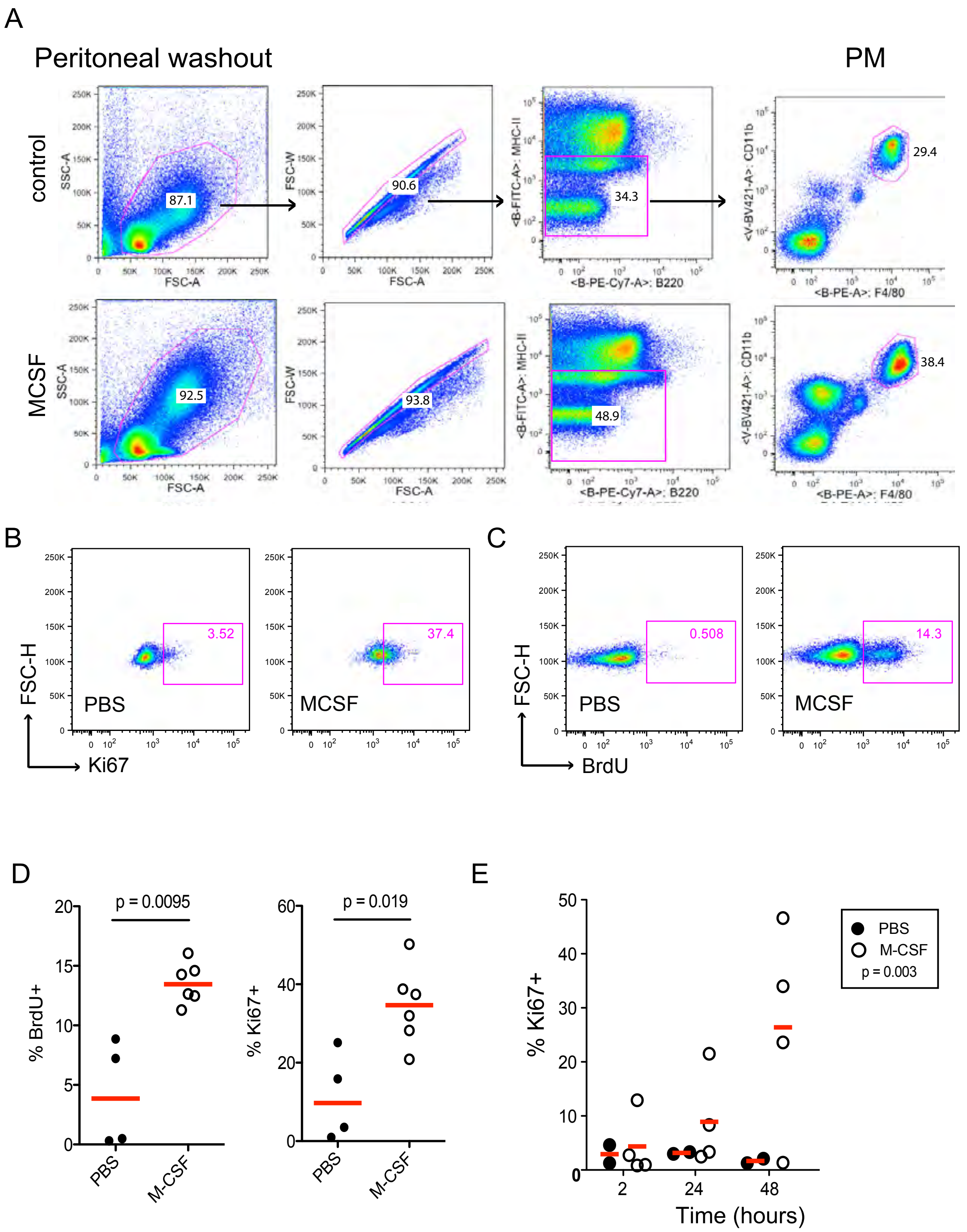
Sup. Figure 10



Sup. Figure 11



Sup. Figure 12



Sup. Figure 13