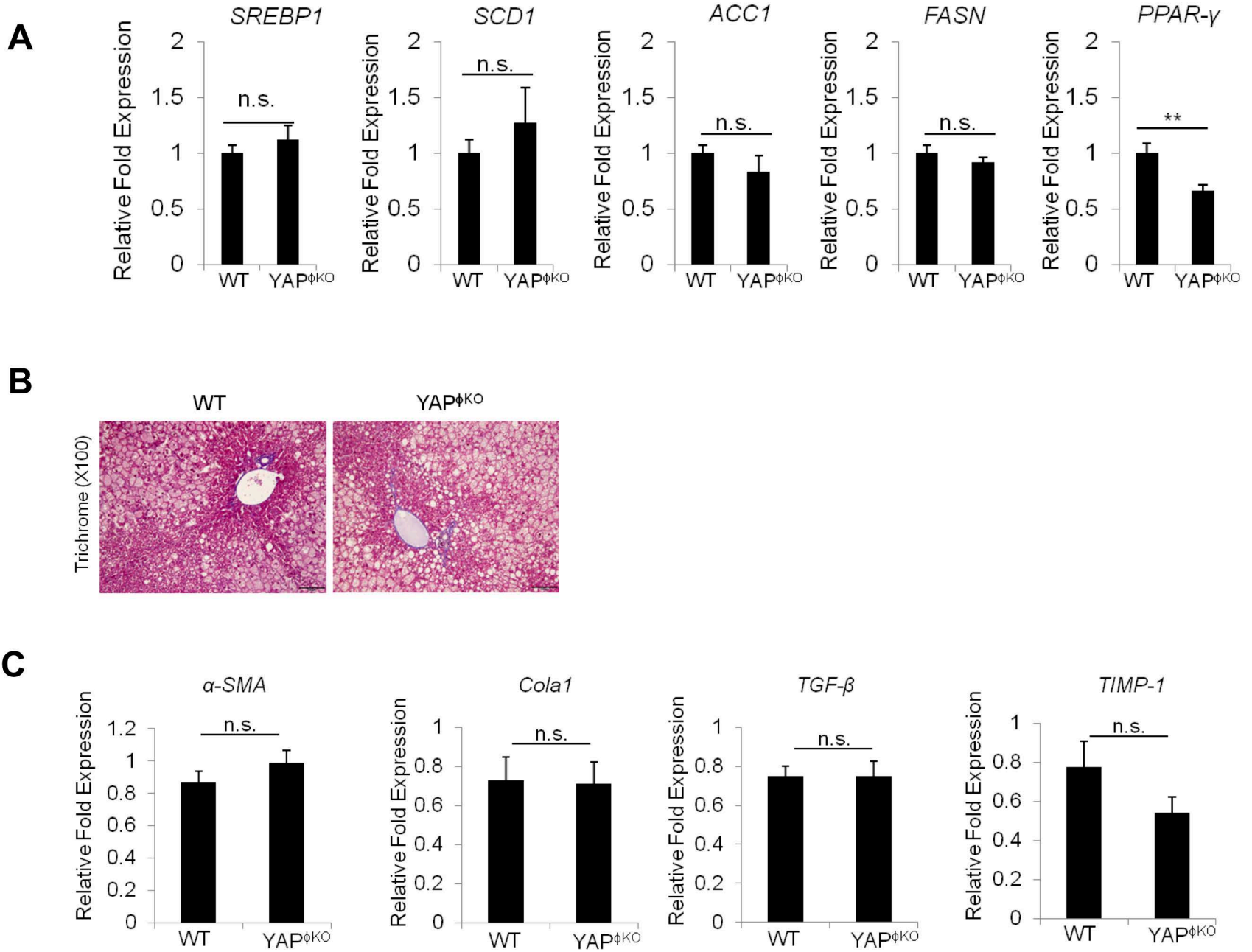
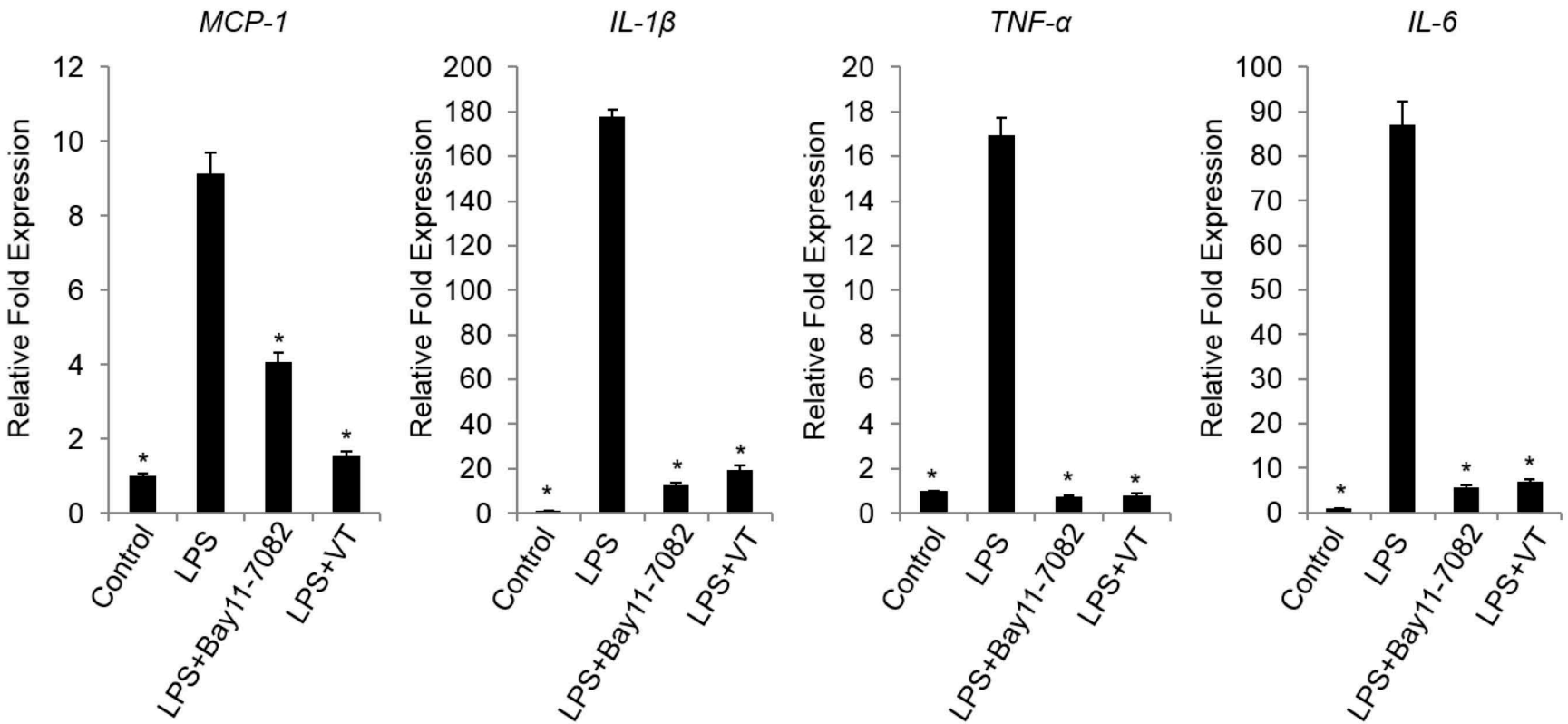
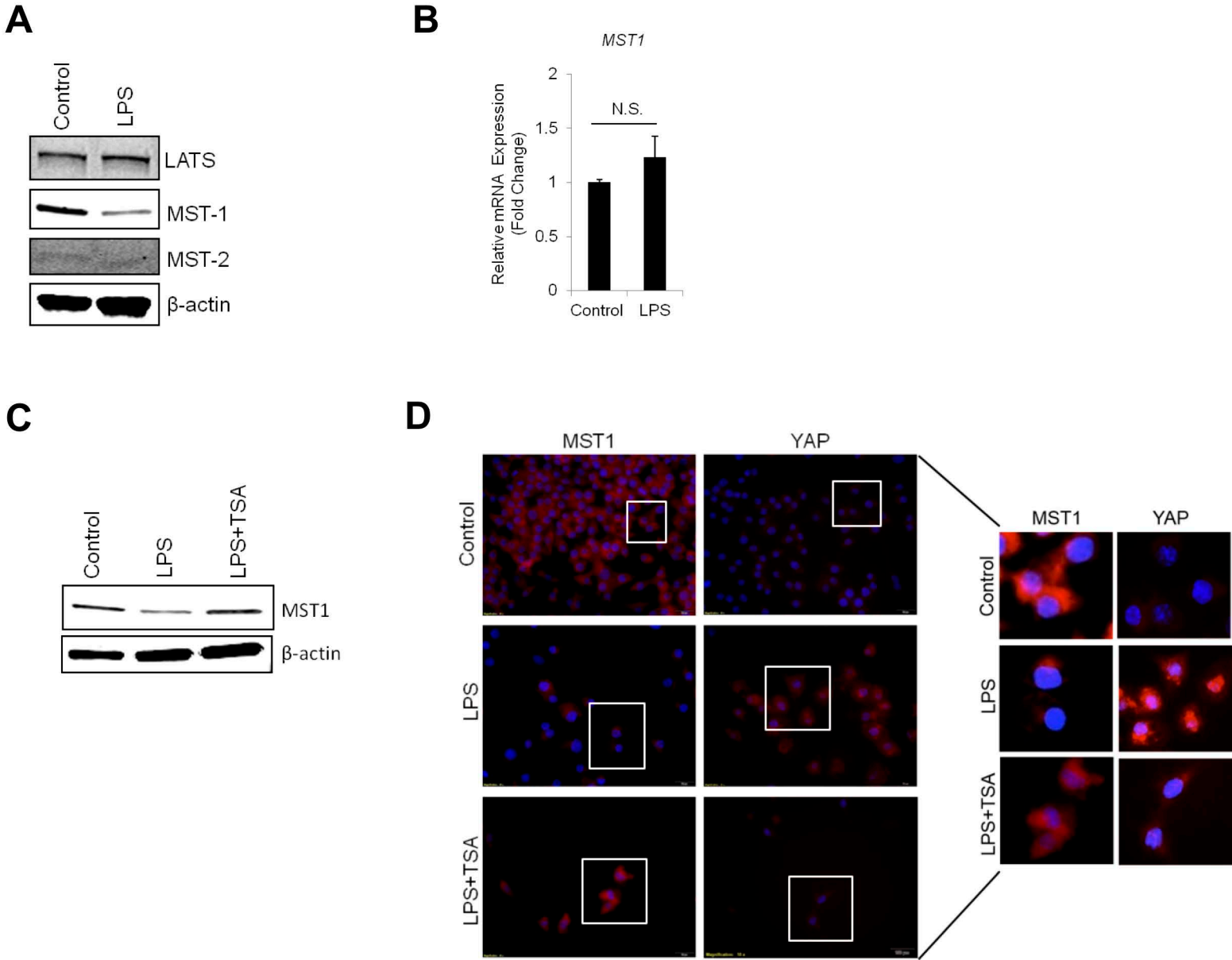
Supplementary Figure S1



Supplementary Figure S2



Supplementary Figure S3



Supplementary Table 1. DNA sequences for qRT-PCR, mouse genotyping, ChIP, EMSA and DNA-pull down assays

qRT-PCR		
Gene	Forward (5’ to 3’)	Reverse (5’ to 3’)
YAP	GGCTCTAAAGAACCCGAACC	GCAGCTGAAGAAACCACCTC
TNF-α	CCCTCACACTCAGATCATCTTCT	GCTACGACGTGGGCTACAG
IL-1β	GCAACTGTTCCTGAACTCAACT	ATCTTTTGGGGTCCGTCAAG
MCP-1	TTAAAAACCTGGATCGGAACCA	GCATTAGCTTCAGATTTACGGG
IL-6	TAGTCCTTCCTACCCCAATTTCC	TTGGTCCTTAGCCACTCCTTC
Mgl2	TGGAGCGGGAAGAGAAAAACCAGG	TCGAAGTTGTCAGCCCTGGAGTC
Retnla	CCAATCCAGCTAACTATCCCTCC	CCAGTCAACGAGTAAGCACAG
CD80	CCATGTCCAAGGCTCATTCT	TTCCCAGCAATGACAGACAG
CD86	CAGTGCTGGCAAATCAAGAA	TTGCACAGCATTCTCCAGAC
TIMP1	AGGTGGTCTCGTTGATTTCT	GTAAGGCCTGTAGCTGTGCC
Acta2	ATCATGCGTCTGGACTTGG	AATAGCCACGCTCAGTCAGG
Col1a1	GCTCCTCTTAGGGGCCACT	ATTGGGGACCCTTAGGCCAT
SREBP	ACGGCAGCCCCTGTAACGACCACTGT	TGCCAAGATGGTTCCGCCACTCACCA
SCD1	CCGGAGACCCTTAGATCGA	TAGCCTGTAAAAGATTTCTGCAAACC
FASN	AGCGGCCATTTCCATTGCCC	CCATGCCCAGAGGGTGGTTG
PPARr	GTACTGTCGGTTTCAGAAGTGCC	ATCTCCGCCAACAGCTTCTCCT
ACC1	ACTTCCCGACCAAGGACTTTG	ACAGTGGAGCTAGAATTGGAC
18S	CGCTTCCTTACCTGGTTGAT	GAGCGACCAAAGGAACCATA
Mouse genotyping		
Region	Forward (5’ to 3’)	Reverse (5’ to 3’)
LyzM	CTTGGGCTGCCAGAATTTCTC	CCCAGAAATGCCAGATTACG
TLR4	TGACCACCCATATTGCCTATAC	TGATGGTGTGAGCAGGAGAG
YAP	AGGACAGCCAGGACTACACAG	CACCAGCCTTTAAATTGAGAAC
ChIP assay		
Region	Forward (5’ to 3’)	Reverse (5’ to 3’)
YAP	ACTAAGACCTCGCCTTGTGC	GTCCCAGTTACCCACACAGG
MCP1	GCCATGGAATAAACACAGCA	GAGCGGAGTCTTCCACTCAG
TNF-α	GAGGGGAATCCTTGGAAGAC	AATTCACGGACCTCACAAGC
IL-6	TCCACCCATGTTTTAACTTTCTT	ATTGAGAATGCAAAAGGAGAAT
DNA-pull down assay		
Region	Forward (5’ to 3’)	Reverse (5’ to 3’)
WT	5’Bio/ATATCCATTGACTCATTTAATGTC	5’Bio/GACATTAAATGAGTCAATGGATAT
Mut	5’Bio/ATATCCATCATGCATTTTAATGTC	5’Bio/GACATTAAAATGCATGATGGATAT
EMSA		
Region	Forward (5’ to 3’)	Reverse (5’ to 3’)
WT	5’IRD800/GGGCCAAGTACTTTATATCCATT GACTCATTTAATGTCTCAACGACATAA	5’IRD800/TTATGTCGTTGAGACATTAAATGAGT CAATGGATATAAAGTACTTGGCCC
Cold	GGGCCAAGTACTTTATATCCATT GACTCATTTAATGTCTCAACGACATAA	TTATGTCGTTGAGACATTAAATGAGT CAATGGATATAAAGTACTTGGCCC

Supplementary Figure Legends

Supplementary Figure S1. Myeloid cell specific YAP knockout mice did not affect on lipogenesis and fibrosis. (A) qRT-PCR analysis for lipogenesis genes in the liver tissues from HFD-fed WT (n=4) and $YAP^{\phi KO}$ mice (n=6). (B) Representative images of trichrome staining of the liver tissues obtained from HFD-fed WT and $YAP^{\phi KO}$ mice (C) qRT-PCR analysis for fibrosis genes in the liver tissues from HFD-fed WT (n=4) and $YAP^{\phi KO}$ mice (n=6). The data are expressed as mean±S.E.M ***P<0.001.

Supplementary Figure S2. Comparison of inhibitory effect of NF-kB and YAP inhibitor on LPS induced inflammatory cytokines in Kupffer cells. Primary Kupffer cells were treated with verteporfin (1 μM) or Bay11-7082 (3 μM) for 1 hour followed by LPS treatment (1 μg/ml) for 6 hrs. The pro-inflammatory cytokine gene expression were measured by qRT-PCR. The data are expressed as mean±S.D. * P<0.001, compared to LPS treatment alone (p value were tested and calculated by Bonferroni-adjusted methods).

Supplementary Figure S3. LPS decreases MST1 protein in macrophages. The effect is reversed by the HDAC inhibitor Trichostatin A (TSA). (A) Raw264.7 cells were treated with LPS (1 μg/ml) for 24 hrs, and protein extracts were subjected to Western blot analysis to determine the expression of LATS, MST1, MST2. β-actin was used as the loading control. (B) LPS treatment did not alter the level of MST1 mRNA as measured by qRT-PCR. Raw264.7 cells were treated with LPS (1 μg/ml) for 24 h. (C) The HDAC inhibitor TSA reversed LPS-induced reduction of MST1 protein. Raw264.7 cells were pretreated with TSA (200 nM) for 1 hour

followed by LPS treatment (1 μg/ml) for 24 hours. (D) Immunofluorescence analysis for MST1 and YAP. Primary Kupffer cells isolated from wild type mice were pretreated with TSA (200 nM) for 1 hour followed by LPS treatment (1 μg/ml) for 24 hours. The right panels are high magnification images of the indicated square areas from the left panels (X 200).

Supplementary Methods

DNA pull down assay. DNA pull down assay was performed according to a previous report with minor modification (22). Specifically, Raw 264.7 cells were treated with LPS for 24 hours and then lysed by sonication in HKMG buffer (10 mM HEPES, pH 7.9, 100 mM KCl, 5 mM MgCl2, 10% glycerol, and 0.5% NP-40) with protease inhibitors. Cell extracts were precleared with streptavidin-agarose beads for 1 hour, and the supernatant was then incubated with 1 μg of biotinylated double-stranded oligonucleotide and 10 μg poly (dI-dC) at 4°C for overnight. The oligonucleotide sequences are: 5'-Biotin-ATATCCATTGACTCATTTAATGTC-3'(WT) and 5'-Biotin-ATATCCATCATGCATTTTA ATGTC-3' (Mutant). The biotinylated oligonucleotides and their complementary strands were annealed in TEN buffers. DNA-bound protein was collected by incubation with streptavidin-agarose beads at 4°C for 1 hour. The agarose beads were washed four times with HKMG buffer and the samples were boiled in SDS-sample buffer prior to SDS-PAGE and Western blotting for c-jun and c-fos.