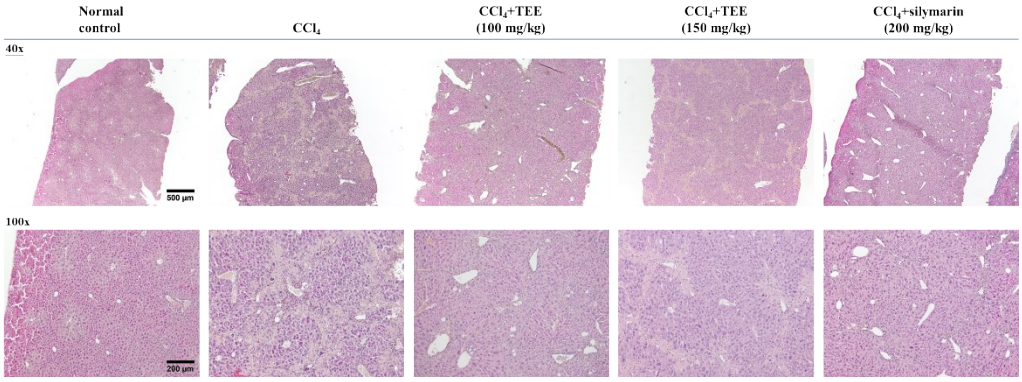
Supplementary Materials

(A)



(B)

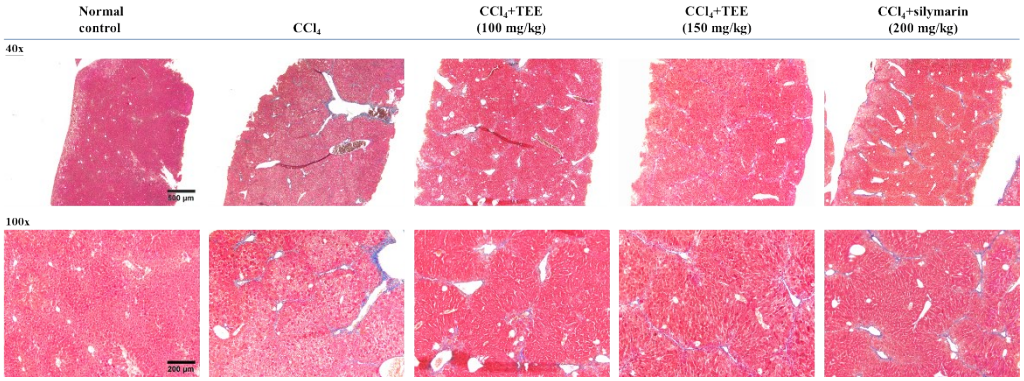
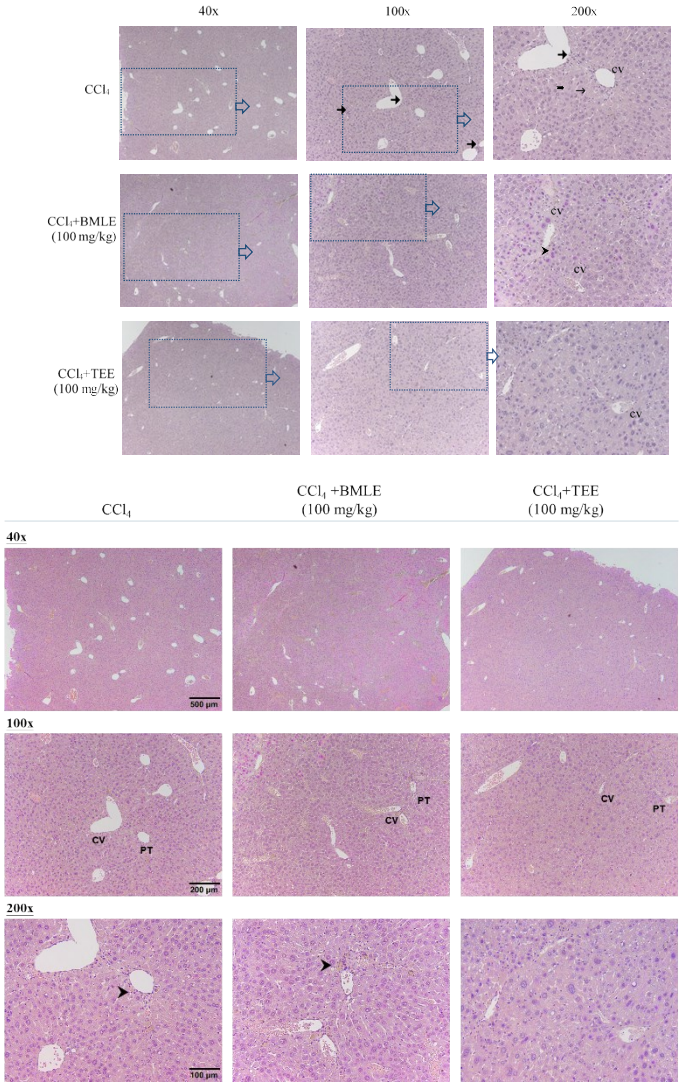
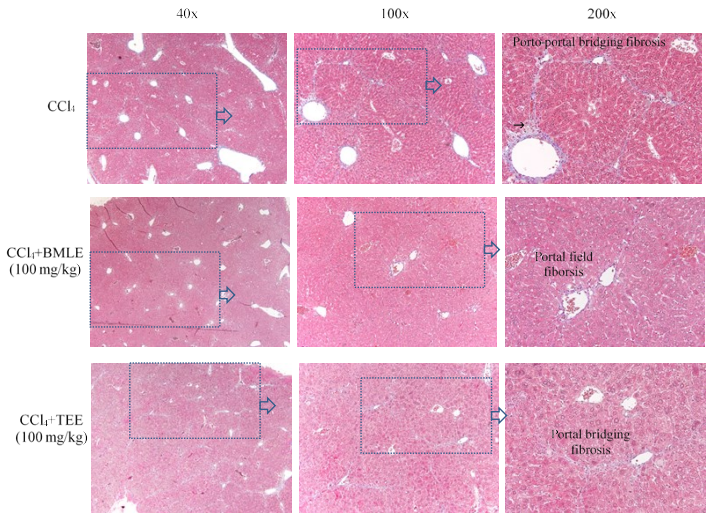


Figure S1. Lower-magnification images of Fig. 3a (A) and Fig. 3b (B).

(A)


40x
100x
200x
CCl4
CCl4+BMLE (100 mg/kg)
CCl4+TEE (100 mg/kg)
CV
CCl4
CCl4 +BMLE (100 mg/kg)
CCl4+TEE (100 mg/kg)
40x
100x
200x
PT
500 µm
200 µm
100 µm

(B)


40x
100x
200x
CCl4
CCl4+BMLE (100 mg/kg)
CCl4+TEE (100 mg/kg)
Porto-portal bridging fibrosis
Portal field fibrosis
Portal bridging fibrosis

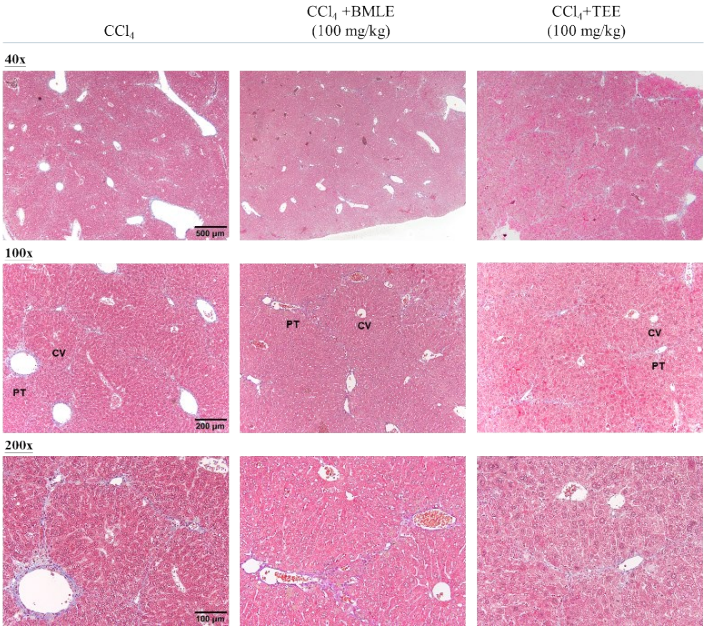


Figure S2. Conventional H&E (A) and Trichrome staining (B) of liver paraffin sections from mice treated with CCl_4, CCl_4+BMLE, and CCl_4+TEE. Original magnifications, ×40, ×100 and ×200; scale bars, 500, 200, and 100 μm, respectively. PT: portal triad; CV: central venule; dotted line area: necrosis; arrow head (⑥): inflammatory cell infiltration; arrow (•): fibrosis.

Table S1. The major triterpenoids of TEE determined by liquid chromatography-mass spectrometry

No.	Identification	m/z	RT (min)	Intensity (Counts)
1	24-O-Acetyl-cimigenol-3-O-β-D-xylopyranoside	339.2	22.13	47705
2	Methyl lucidenate P	265.1	17.36	31356
3	25-O-Acetyl cimigenol-3-O-β-D-galactoside	691.4	20.61	26694
4	Asperosaponin Ⅵ	927.5	18.38	25928
5	Quinatoside A	293.2	20.68	21743
6	1α,2α,3β,19α,23-Pentadroxyurs-12-en-28-oic acid-28-O-β-D-xylopyranoside	325.2	20.64	18708
7	Progenin	865.5	23.45	18402
8	Cimifoetiside Ⅵ	691.4	18.43	8570
9	Cimiside E	601.4	17.56	8404
10	Oleanolic acid-3-α-L-arabinofuranosyl-(1→4)-β-D-glucuronopyranoside	763.4	18.86	8034
11	3-O-α-L-Rhamnopyranosyl-(1→2)-α-L-arabinopyranosylgypsogenin	747.4	18.61	7959
12	Ganoderic acid G	265.1	15.46	7160
13	Bidentatoside Ⅰ	953.4	23.72	6790
14	Ophiopogonin C'	721.4	15.82	5862
15	Kalopanaxsaponin I	881.5	23.48	5842
16	(25R)-Ruscogenin-1-O-β-D-xylopyranosyl (1→3)-β-D-fucopyranoside	353.2	19.96	5594
17	Asperosaponin Ⅵ	927.5	17.56	5586
18	Saikosaponin E	381.2	23.19	5585
19	Deapioplatycodin D	545.3	5.24	4696
20	Malonyl-ginsenoside Rd	515.3	4.42	4505

The analytical LC-MS experiment was performed on a Waters ACQUITY UPLC I-Class system and Vion IMF QTOF MS spectrophotometry. LC-HDMSE data is acquired in resolution mode with UNIFI Scientific Information System. The mass spectrometer is operated in resolution mode with a typical resolving power of at least 40,000 FWHM (full width at half maximum) at m/z 500. All analyses are performed using positive mode ESI using a LockSpray source.