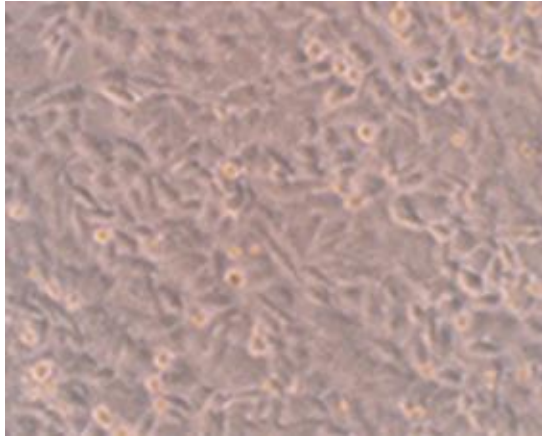
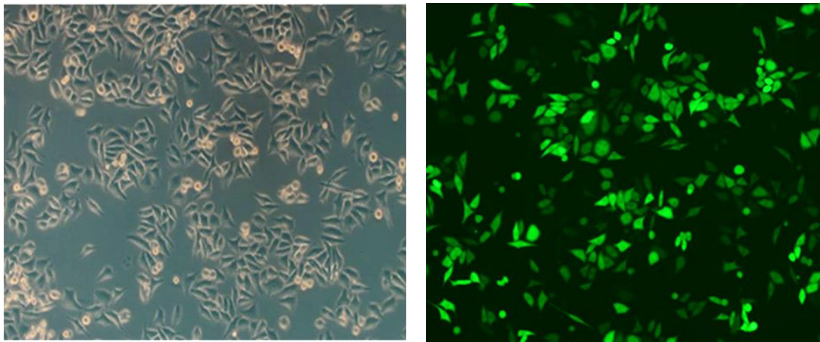


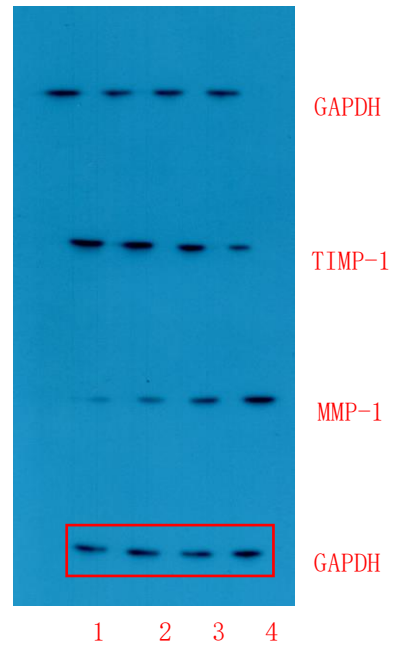
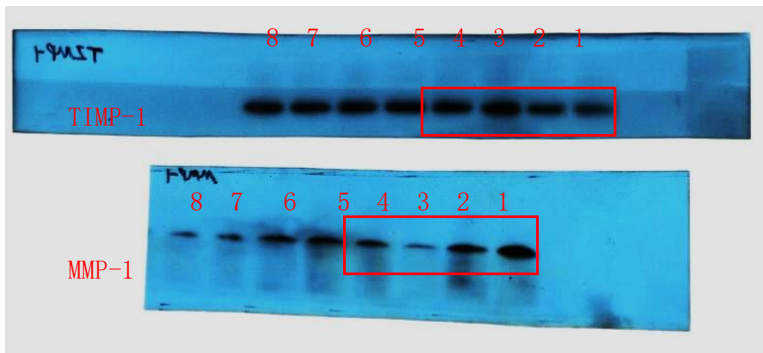
A



B



**Supplementary Figure 1. Example of cultured bone marrow MSCs and the expression of Smad7-EGFP.** (A) Example of MSCs isolated from rat bone marrow and cultured at passage 1. (B) MSCs infected with a lentiviral vector carrying Smad7-EGFP gene.



**Supplementary Figure 2. Examples of western blotting.** The cropped box areas are presented in Figure 5. Lane 1: Cirrhosis+MSC-Smad7 (21 day); Lane 2: Cirrhosis+BMSCs (21 day); Lane 3: Cirrhosis (21 day); Lane 4: Control (21day); Lane 5: Cirrhosis+MSC-Smad7 (7 day); Lane 6: Cirrhosis+BMSCs (7 day); Lane 7: Cirrhosis (7 day); Lane 8: Control (7 day).

**Supplementary Table 1.** Primer sequences for RT-PCR

| Gene         | Accession No   | F/R | Primer sequence (5' to 3')  | Location  | Size |
|--------------|----------------|-----|-----------------------------|-----------|------|
| Smad7        | AH008243.2     | F   | 5'-GGGTTTACA ACCGCAGCAGT-3' | 4032-4051 | 112  |
|              |                | R   | 5'-GCCTTGATGGAGAAACCAGG-3'  | 4143-4124 |      |
| TGFβ1        | NM_021578.2    | F   | 5'-AAACGGAAGCGCATCGAA-3'    | 269-286   | 69   |
|              |                | R   | 5'-GGGACTGGCGAGCCTTAGTT-3'  | 331-312   |      |
| Smad2        | BC127497.1     | F   | 5'-GTGTTTGCCGAGTGCCTAAGT-3' | 1114-1134 | 110  |
|              |                | R   | 5'-TTACAGCCTGGTGGGATTTTG-3' | 1223-1203 |      |
| Smad3        | NM_013095.3    | F   | 5'-GGACGCAGGCTCTCCAAAC-3'   | 802-820   | 110  |
|              |                | R   | 5'-AGGAGATGGAGACCAAAAAGG-3' | 911-891   |      |
| TIMP-1       | AY550026.1     | F   | 5'-GATTCGACGCTGTGGGAAAT-3'  | 236-255   | 107  |
|              |                | R   | 5'-AAACTCCTCGCTGCGGTTCT-3'  | 342-323   |      |
| Collagenase1 | BC133728.1     | F   | 5'-CTCCAGCGGTGGTTATGAC-3'   | 3634-3653 | 151  |
|              |                | R   | 5'-TGCTGGCTCAGGCTCTTGA-3'   | 3784-3766 |      |
| Collagenase3 | NM_032085.1    | F   | 5'-CCCTCTTATTTTGGCACAGC-3'  | 156-177   | 104  |
|              |                | R   | 5'-TGACATGGTTCTGGCTTCCAG-3' | 259-239   |      |
| α-SMA        | BC158550.1     | F   | 5'-AATGGCTCCGGGCTCTGTA-3'   | 91-109    | 106  |
|              |                | R   | 5'-TTCCAACCATCACTCCCTGG-3'  | 196-177   |      |
| TGFBR1       | BC087035.1     | F   | 5'-GCTGTGGTTGGTGTCCGATT-3'  | 831-850   | 103  |
|              |                | R   | 5'-CGTGGACAGAGCGAGTTTGAT-3' | 933-913   |      |
| MMP-1        | NM_001134530.1 | F   | 5'-CACAACAATCCTCGTTGGACC-3' | 343-363   | 104  |
|              |                | R   | 5'-AAGGCTCTCTCGATGGCGTT-3'  | 446-427   |      |
| GAPDH        | NM_017008.4    | F   | 5'-AGGGCTGCCTTCTTGTGA-3'    | 127-147   | 110  |
|              |                | R   | 5'-AACTTGCCGTGGGTAGAGTCA-3' | 236-216   |      |