**Supplemental data**

**Fig. S1.** Inflammation and matrix remodeling markers were different in mRNA levels between sham and CLP.

**Fig. S2.** No significant differences were shown in circulating cytokines between two treatment groups.

**Fig. S3.** Cell cycle regulation, proliferation and pro-fibrosis markers were different in mRNA levels between sham and CLP.

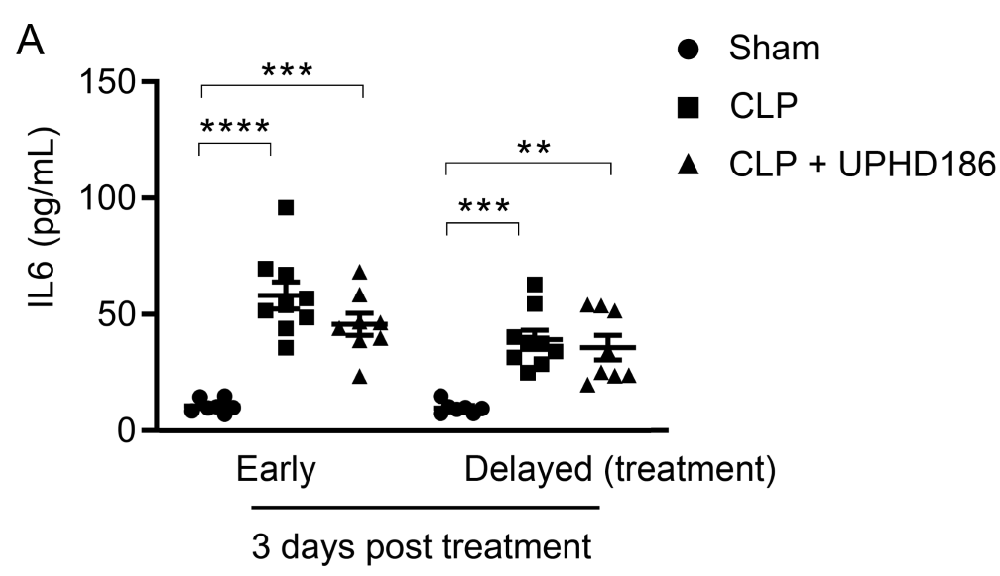
**Table. S1.** Primers for quantitative polymerase chain reaction.

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**Fig. S1.** Inflammation and matrix remodeling markers were different in mRNA levels between sham and CLP. Markers with statistically significant differences between sham and CLP + vehicle at treatment-day-3 are shown. Presented are dot plot figures with group mean ± SD of key mediators involved in inflammation (*traf1, traf2, icam*) and matrix remodeling (*lox, loxl1*). N = 6 ~ 8 for each group. \**P <* 0.05, \*\**P <* 0.01, \*\*\**P <* 0.001. Abbreviations: *icam*, intercellular adhesion molecule; *lox*, lysyl oxidase; *loxl1*, lysyl oxidase homolog 1; *traf,* tumor necrosis factor receptor associated factor.



**Fig. S2.** No significant differences were seen in circulating cytokines between two treatment groups. A. dot plots of interleukin (IL) 6. N = 7 ~ 9 each group. \*\**P <* 0.01, \*\*\**P <* 0.001, \*\*\*\**P <* 0.0001. Abbreviation: Trt, UPHD186 treatment.

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**Fig. S3.** Cell cycle regulation, proliferation and pro-fibrosis markers were different in mRNA levels between sham and CLP. Significant markers that had statistically significant differences between sham and CLP + vehicle at CLP-day-14 are shown. Presented are dot plot figures with group mean ± SD of key mediators involved in cell cycle arrest (*cdkn1a*), proliferation (*ki67*), and fibrosis (*col1a1, plod2, fsp1*). N = 9~12 for each group. \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001, \*\*\*\*P < 0.0001. Abbreviations: *cdkn1a*, cyclin-dependent kinase inhibitor 1a; *col1a1*, collagen type I alpha 1 chain; *fsp1*, fibroblast-specific protein 1; *ki67*, Ki-67; *plod2*, procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2.

**Table. S1.** Primers for quantitative polymerase chain reaction

|  |  |  |
| --- | --- | --- |
| ***Gene*** | **Primer (5' to 3')** | |
| Forward | Reverse |
| ***ccl20*** | GCCTCTCGTACATACAGACGC | CCAGTTCTGCTTTGGATCAGC |
| ***cdkn1a*** | TAGGACTCAACCGTAATATCCCGAC | AAGAGCAGCAGATCACCAGATTAAC |
| ***col1a1*** | GGTATGCTTGATCTGTATCTGCCAC | CCTCGACTCCTACATCTTCTGAGTT |
| ***fsp1*** | ACTTGGACAGCAACAGGGACA | GGGCTCCTTATCTGGGCAGC |
| ***gapdh*** | GTCAAGCTCATTTCCTGGTATGACAA | GGATAGGGCCTCTCTTGCTAGT |
| ***icam*** | GTGATGCTCAGGTATCCATCCA | CACAGTTCTCAAAGCACAGCG |
| ***ki67*** | CTGGTTGTTACTGAAGAGCCCATAC | CTTAACTGTCCTTGGTTGGTTCCTC |
| ***kim1*** | AAACCAGAGATTCCCACACG | GTCGTGGGTCTTCCTGTAGC |
| ***lox*** | CCACAGCATGGACGAATTCA | AGCTTGCTTTGTGGCCTTCA |
| ***loxl2*** | GATCTTCAGCCCCGATGGA | CAAGGGTTGCTCTGGCTTGT |
| ***nfkb*** | GGAGGCATGTTCGGTAGTGG | CCCTGCGTTGGATTTCGTG |
| ***plod2*** | GATGTTCGTTTCTGGTGGAAATTGG | TAAAGCAGAAAGACATGAGCTTCCC |
| ***traft1*** | CACTGCCAAGTATGGTTACAAGT | GGTTGTTCTGGTCAAGTAGCAT |
| ***traft2*** | TTCGGCCTTTCCAGATAACGC | ACTCCGTCAGCAGGAATGGGC |