

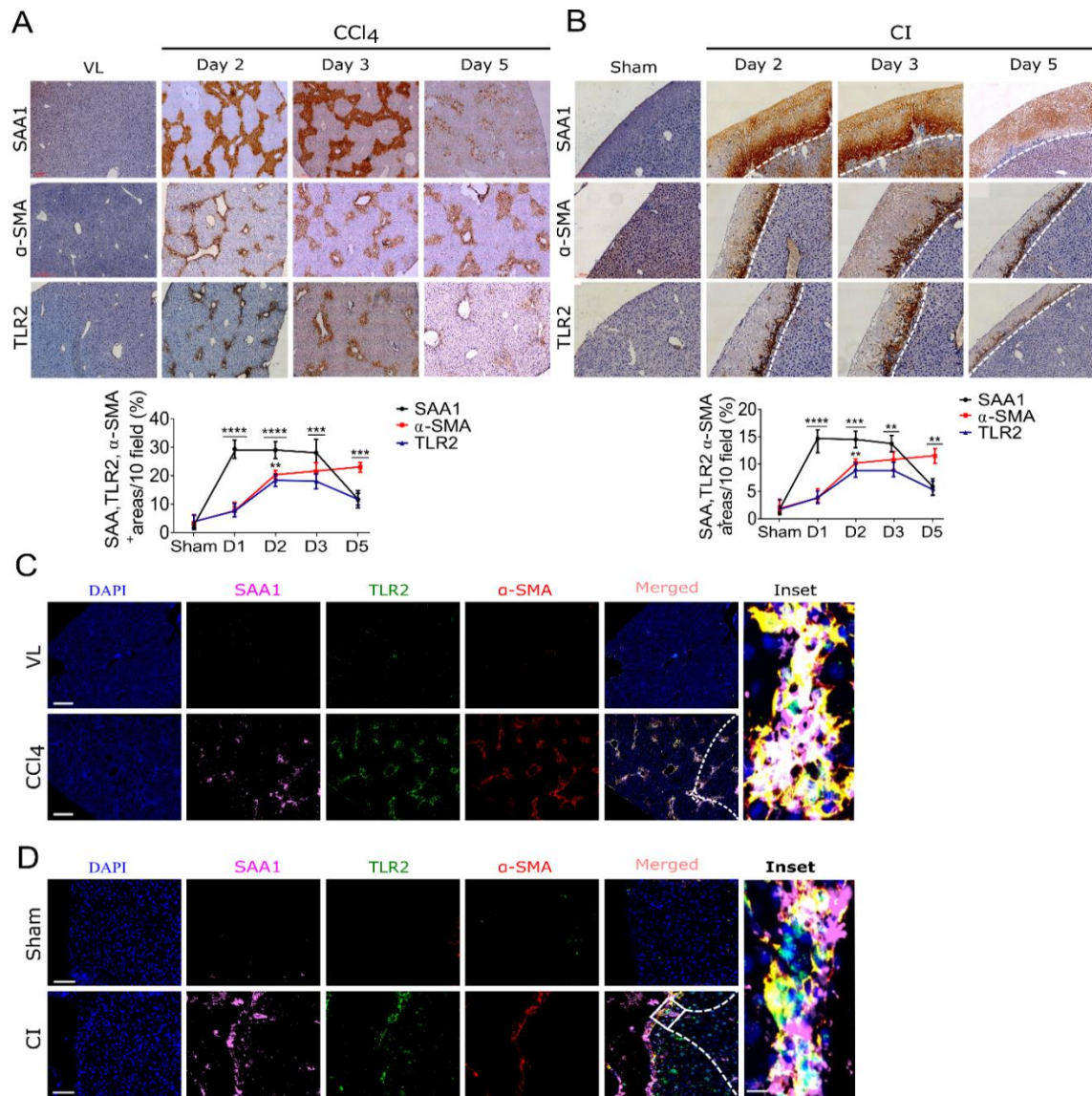
**Supplemental information**

**SAA1/TLR2 axis directs**

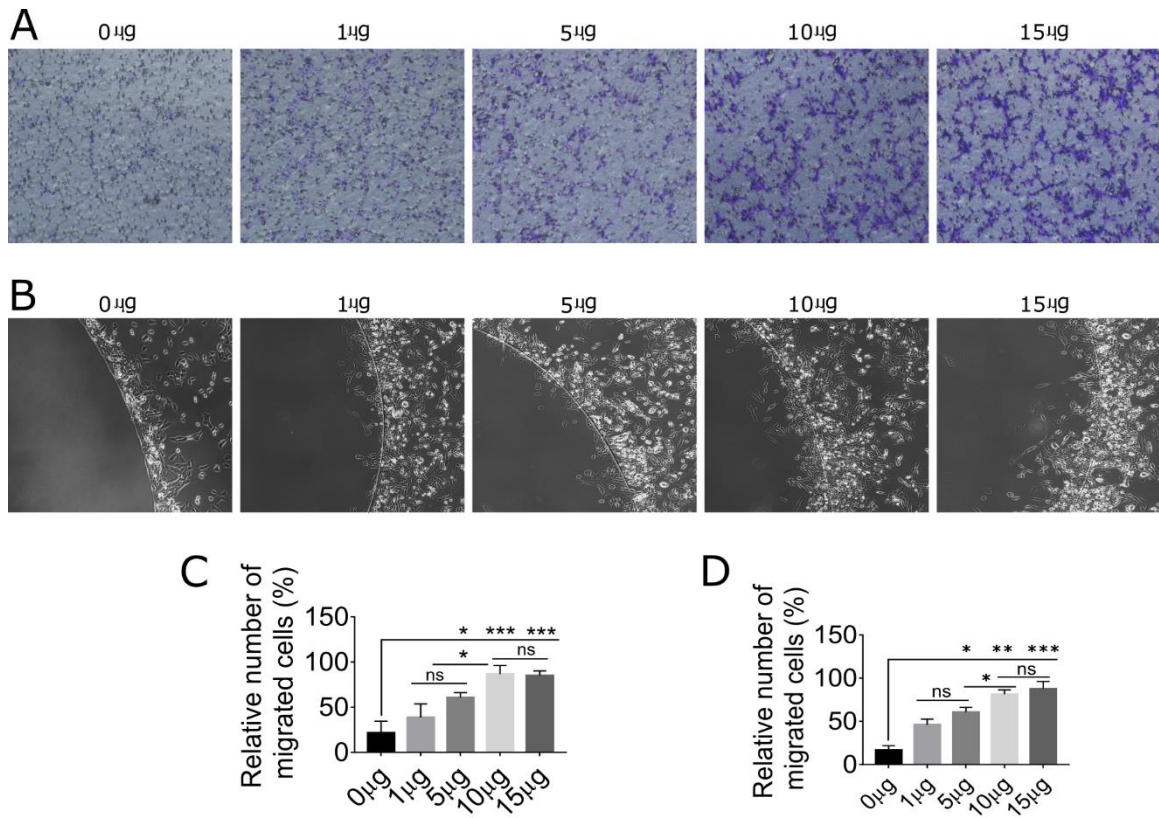
**chemotactic migration of hepatic**

**stellate cells responding to injury**

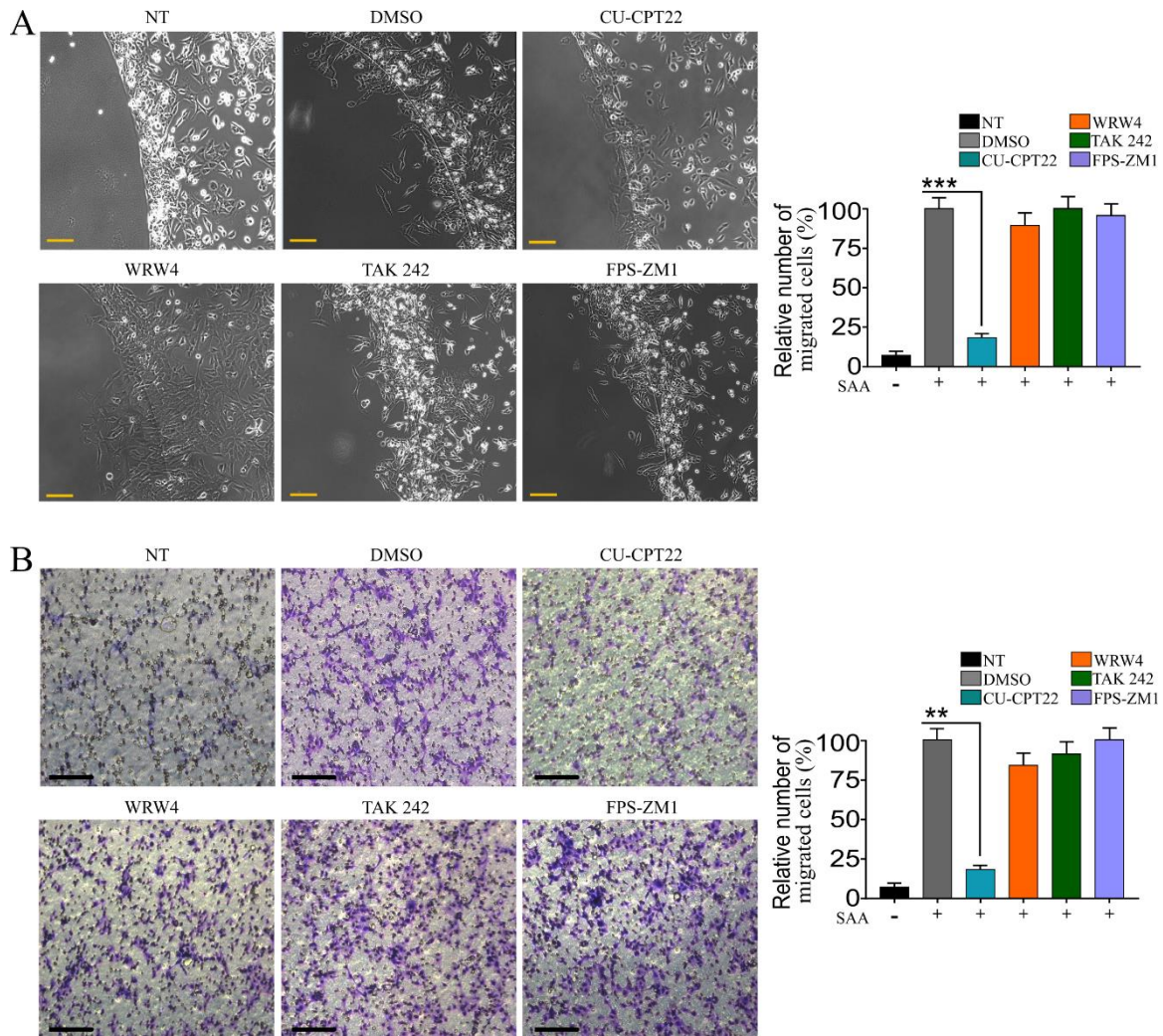
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**Figure S1. Expression and pathological relevance of SAA1, TLR2 and HSCs at injury locus, Related to Figure 2.** (A) Representative IHC staining of SAA1,  $\alpha$ -SMA and TLR2 in CCl<sub>4</sub> injury model at indicated time intervals. (B) Representative IHC staining of SAA1,  $\alpha$ -SMA and TLR2 in CI injury model at indicated time intervals. Bar graphs represent quantification of IHC positive cells/area in CCl<sub>4</sub> and CI injury model at indicated time intervals. (C and D) Confocal immunofluorescence images showing colocalization of SAA1, TLR2 and HSCs at CCl<sub>4</sub> (C) and CI injury (D) models.



**Figure S2. SAA1 mediates migration of HSCs in dose-dependent manner, Related to Figure 2.** (A) Representative Transwell migration assays showing SAA1 mediates migration of LX-2 cells in dose dependent (1-15µg) manner. (B) Representative Agarose spot migration assay showing the cells migrate under SAA1 containing spot in dose-dependent manner at indicated concentrations. (C) Quantification of Transwell migration assay. SAA1 attract LX-2 cells with maximal concentration of 10 to 15 µg/ml. (D) Quantification of agarose migration assay the maximal concentration by which SAA1 attract more numerous cells were shown at 10 to 15µg/ml.



**Figure S3. Inhibitor of TLR2 (CU\_CPT22) has blocked migration of LX-2 cells in agarose spot and Transwell assays, Related to Figure 3.** (A) Agarose spot migration assay showing LX-2 cells pretreated with different inhibitors and the effects in SAA1 induced migration. (B) Transwell migration assay showing LX-2 cells pretreated with different inhibitors and the effects in SAA1 induced migration.

**Table S1. Stealth RNAi™ siRNA sequences used for *in vivo* knockdown of SAA1, Related to Figure 1.**

SAA1-siRNA1	CAACUAUGAUGCUGCUCAA
SAA1-siRNA2	GUCCUCCUAUUAGCUCAGU
SAA1-siRNA3	GAGGAGAGGGUAAUAAACA
SAA1-siRNA4	CAUAACCUAUUGCUCUCGU
SAA1-siRNA5	GACCUCCUAUUAGCUCACA

**Table S2. siRNA sequences used to knockdown of TLR2 in HSCs, Related to STAR methods Transfection of siRNA.**

siRNA	(5'-3')	Modification
Rat-Tlr2-si-1	CAGCAGAAUCAAUACAAUAdTdT	N/A
	UAUUGUAUUGAUUCUGCUGdTdT	
Rat -Tlr2-si-2	GCCUUGACCUGUCUUUCAAdTdT	N/A
	UUGAAAGACAGGUCAAGGCdTdT	
Rat -Tlr2-si-3	GGAAAUGUAGAGACUUUCAAdTdT	N/A
	UGAAAGUCUCUACAUUUCCdTdT	
	UAAAUGUUCAAGACUGCCCdTdT	
NC	UUCUCCGAACGUGUCACGUdTdT	N/A
	ACGUGACACGUUCGGAGAAAdTdT	
FAM NC	UUCUCCGAACGUGUCACGUdTdT	5'Fam
	ACGUGACACGUUCGGAGAAAdTdT	
M/H MAPK1siRNA	UGCUGACUCCAAAGCUCUGdTdT	N/A
	CAGAGCUUUGGAGUCAGCAAdTdT	
GAPDH	GUGGAGAUUGUUGCCAUCAAdTdT	N/A
	UGAUGGCAACAAUCUCCACdTdT	

**Table S3. Primers for used in this study, Related to STAR methods Real-Time Polymerase Chain Reaction.**

Primers			Sequences	Gene ID
Species	Gene name			
Human	TLR2	Forward Reverse	gttgcaagcaggatccaaag tgtcttctgccttacttg	ID: 7097
Rat	TLR2	Forward Reverse	aggactcaagagcatcggt gcagaatggccttccctga	ID: 310553
Human	FPR2	Forward Reverse	agccaagaagcacacaggaa atccgcagaacagtgtagcc	ID: 2358
Rat	FPR2	Forward Reverse	tgctggacgtagcaaact actcgttaaggacgactgga	ID: 690158
Human	AGER	Forward Reverse	cctcaggaccaggaaccta gaggctcaccgatgatgct	ID: 177
Rat	AGER	Forward Reverse	agaaaccggtgatgaaggaca ggtgtcgttttcgccacag	ID: 81722
Human	TLR4	Forward Reverse	agacctgtccctgaaccctat cgatggacttctaaaccagcca	ID: 7099
Rat	TLR4	Forward Reverse	gaggacaatgctctggggag atgggttttaggcgcagagt	ID: 29260
Human	SR-B1	Forward Reverse	cctatccccttctatctctccg ggatgttggcatgacgatgt	ID: 949
Rat	SR-B1	Forward Reverse	gaacacgttctacacgcagc cctgcatggcctccttatcc	ID: 25073
Human	MCP-1	Forward Reverse	cagccagatgcaatcaatgcc tggatcctgaaccacttct	ID: 6347
Human	IL-8	Forward Reverse	tttgccaaggagtgctaaaga aacctctgcaccagtttc	ID: 3576
Human	RANTES	Forward Reverse	ccagcagtcgtcttgcac ctctgggtggcacacact	ID: 6352