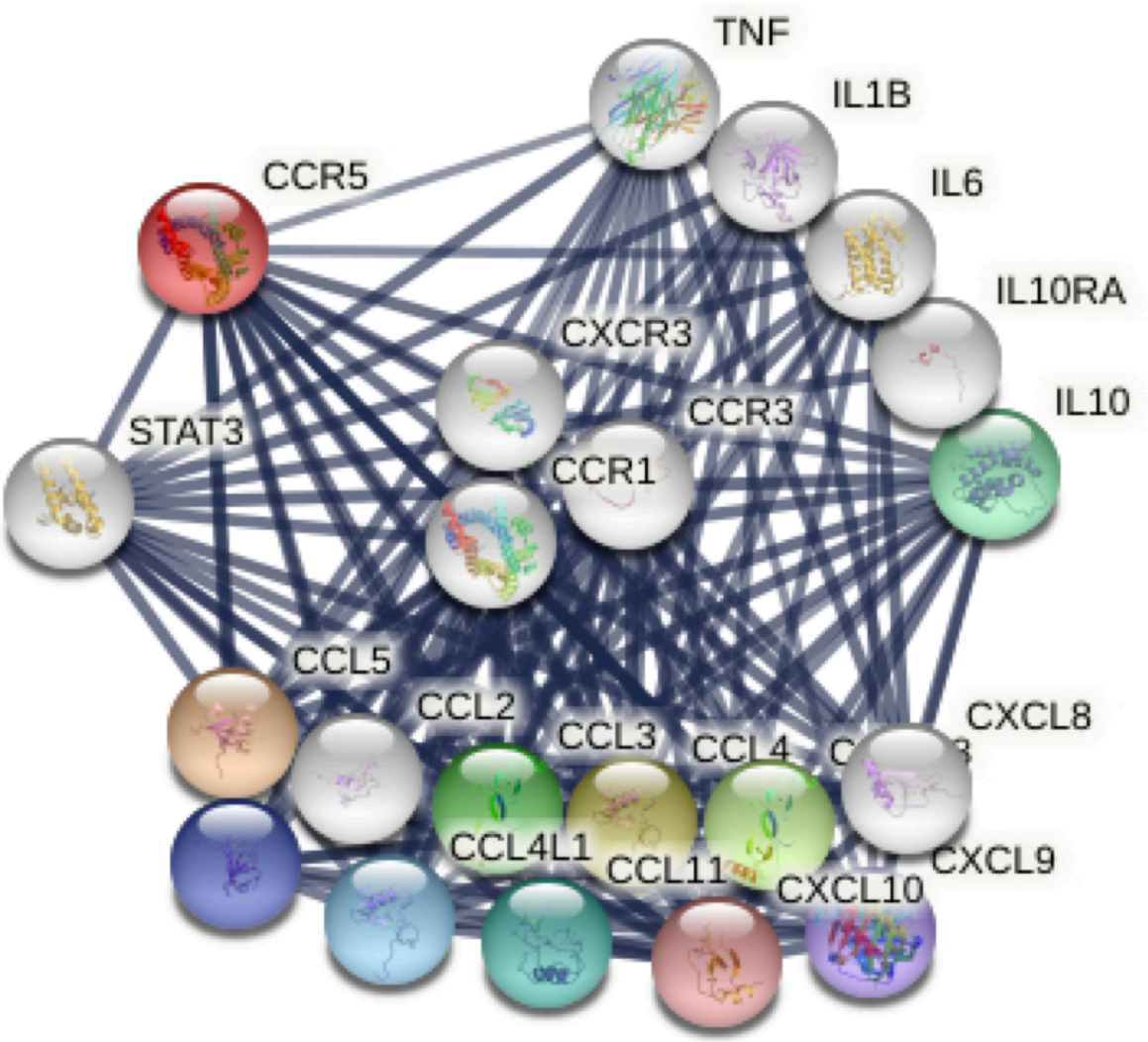


Figure S1. Protein interaction analysis of human CCR5. The schematic network was constructed by the STRING database version 11.0. This network identifies 20 *Homo sapiens* CCR5 interacting partners based on previously reported evidence.

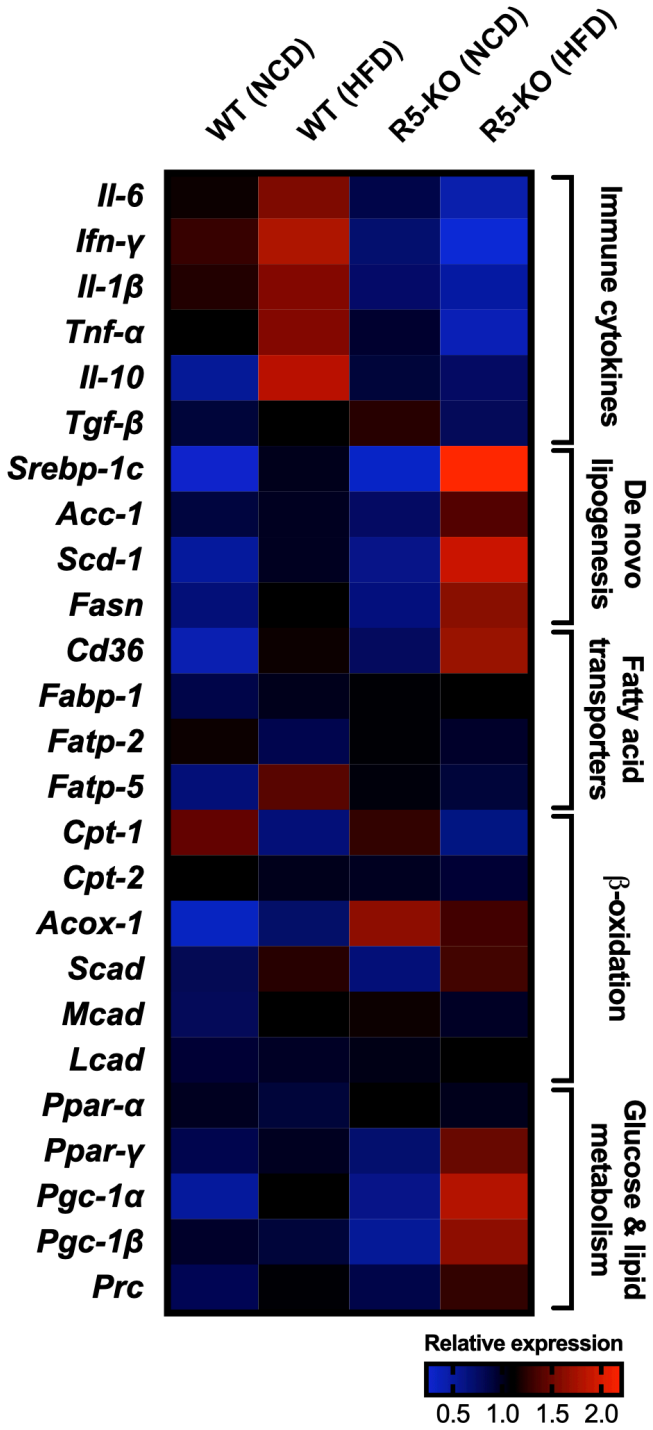


Figure S2. Gene expression profile of liver tissues from lean and obese WT versus R5-KO mice. Expression of 25 genes were analyzed by real-time PCR as described for Fig. 3 and their relative expression level was presented as a heat map. Functional groups of these genes are denoted on the right.

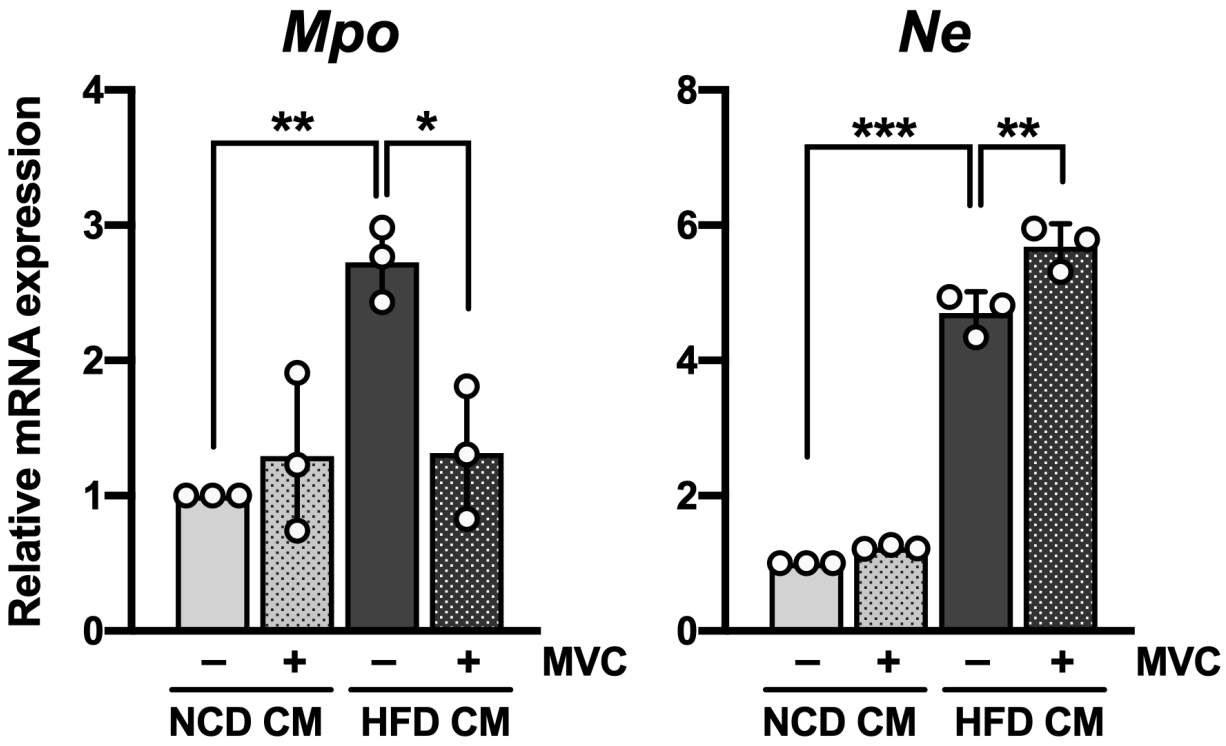


Figure S3. Fatty liver microenvironment promotes g-MDSC maturation. Primary g-MDSCs from WT mice were treated with liver-conditioned media in the presence (+) or absence (-) of MVC. The transcript levels of *Mpo* and *Ne* were analyzed as described for Fig. 4.

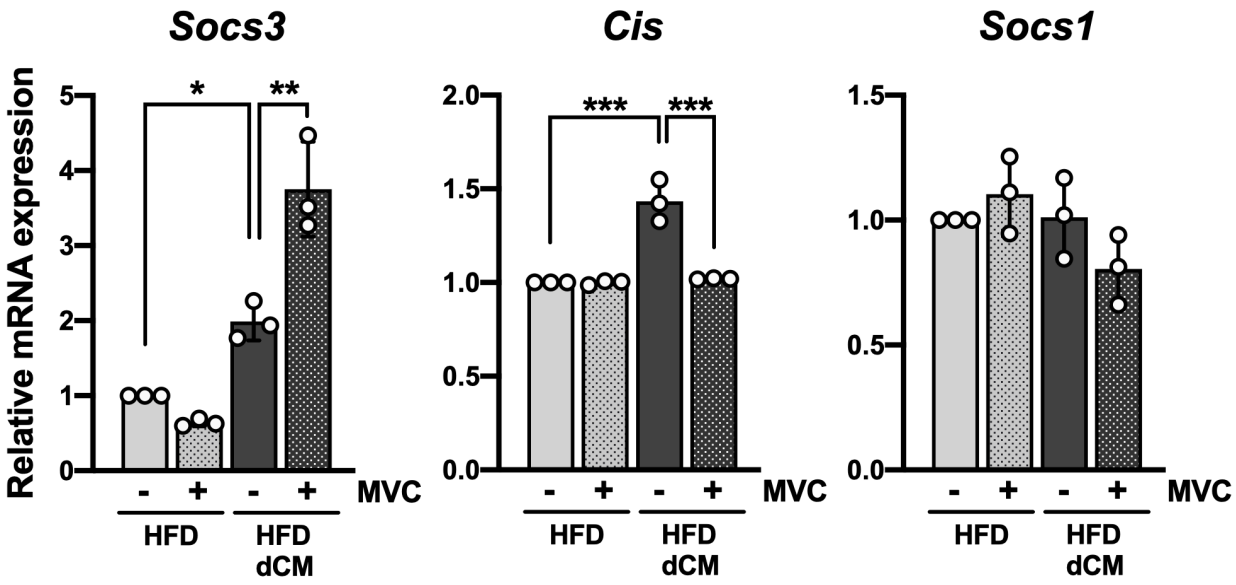


Figure S4. Distinct expression pattern of SOCS family members in fatty liver microenvironment. Primary g-MDSCs from WT mice were treated with liver-conditioned media in the presence (+) or absence (-) of MVC. The transcript levels of *Socs3*, *Cis* and *Socs1* were analyzed as described for Fig. 4.