

Supplemental Data

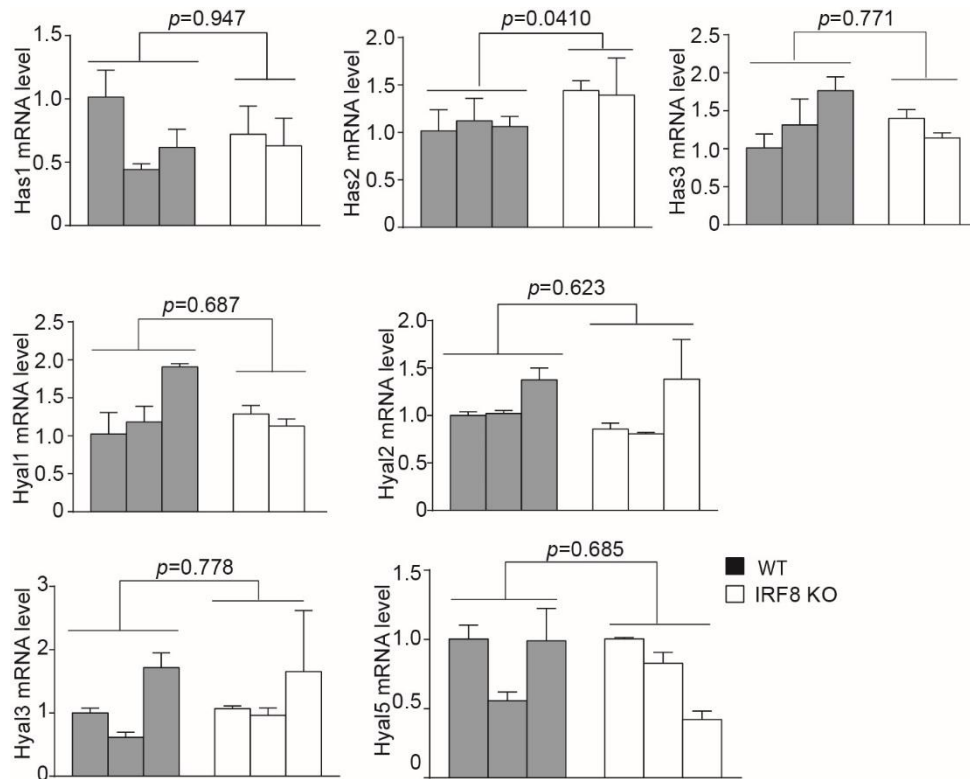


Figure S1. Expression level of hyaluronan metabolism pathway genes. Total RNA was isolated from spleens of WT (n=3) and IRF8.KO (n=2-3) mice and analyzed by real-time RT-PCR using gene-specific primer pairs as indicated. β -actin was used as internal control.

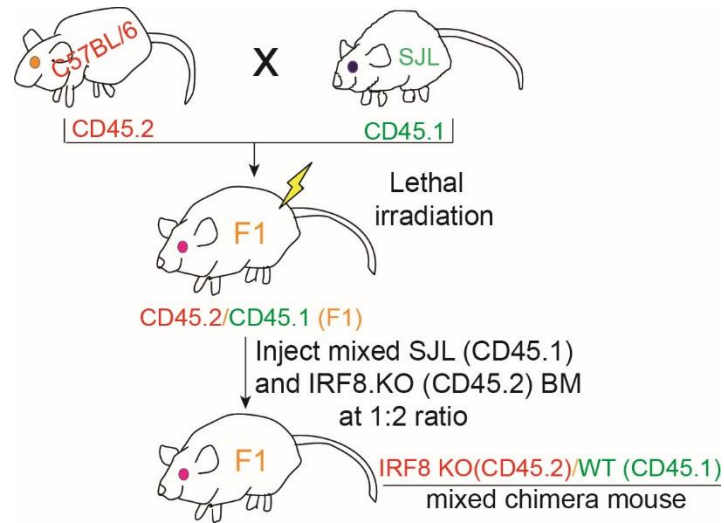


Figure S2. Scheme of creation of mixed BM chimera mice. C57BL/6 mice were crossed with SJL mice to generate F1 hybrid mice. BM cells from SJL and IRF8.KO mice were then mixed (at 1:2 or 1:5 ratio of SJL: IRF8.KO) and adoptively transferred to the lethally-radiated F1 hybrid mice to generate mixed chimera mice.

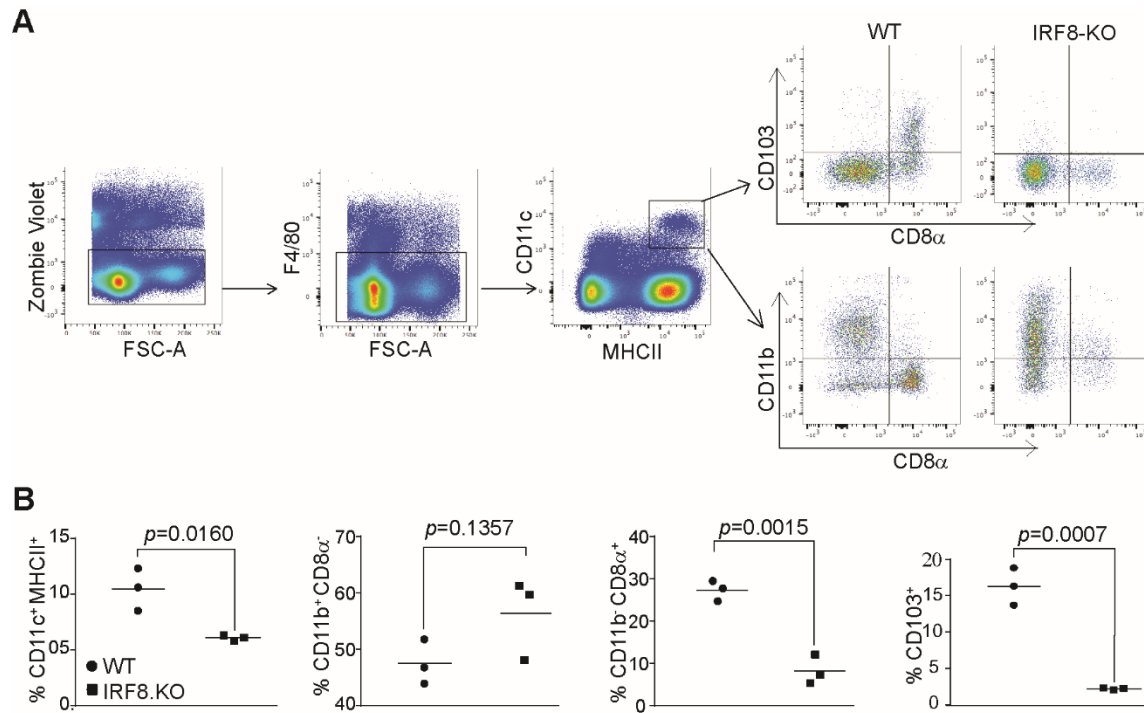


Figure S3. Myeloid cell profiles in IRF8.KO mice. **A.** Gating strategy. Peripheral blood was stained with the indicated antibodies. Live cells were gated and analyzed for F4/80⁺ cells which were then for CD11c⁺MHCII⁺ cells. The CD11c⁺MHCII⁺ myeloid cells were then analyzed for the indicated APCs. **B.** Quantification of indicated subsets of APCs in WT (n=3) and IRF8.KO (n=3) mice.

Table S1. Oligo sequences

| Primer Name | Sequence (5'→3') | Use |
|--------------------|-----------------------------------|---|
| Has1-F1 | GTGCGAGTGTGGATGAAGACC | qPCR |
| Has1-B1 | CCACATTGAAGGCTACCCAGTATC | |
| Has2-F1 | GCCATTTTCCGAATCCAAACAGAC | qPCR |
| Has2-B1 | CCTGCCACACTTATTGATGAGAACC | |
| Has3-F1 | GCTTCAGTCCAGAAACCAAAGTAGG | qPCR |
| Has3-B1 | CCTCGTTCCTCAAGAGAAACAAGG | |
| Hyal1-F1 | GCAGCAGCCAAAAACCAGTTC | qPCR |
| Hyal1-B1 | AGCAGTCAGGGAAGCCATAGTAGC | |
| Hyal2-F1 | TCACCACCTTCTACTACGACCGTC | qPCR |
| Hyal2-B1 | GCGTTCCACAGATTCCTTCAGC | |
| Hyal3-F1 | GCATTCACACCCTCTACCTGTTCTG | qPCR |
| Hyal3-B1 | TGCGGCACTCACTCCAATAGTC | |
| Hyal4-F1 | ATAGGAGAAAGTGCTGCGTTGG | qPCR |
| Hyal4-B1 | GCTGCTCTGGTCACATTGATTATG | |
| Hyal5-F1 | AAGAGTTTGAAGAGGCAGCAAGAC | qPCR |
| Hyal5-B1 | GGGCATTCTCCTTTGTAATCAGC | |
| Hyal6-F1 | GACCAAAGCGTTTATGGGGC | qPCR |
| Hyal6-B1 | TCATCATCTGGGCAACTTCCTG | |
| 15729-T | TGT GAA CTT GGT GCT TGA GG | <i>Lck-cre</i> genotyping |
| oIMR8890-T | CAG GTT CTT GCG AAC CTC AT | |
| oIMR7338-IC | CTA GGC CAC AGA ATT GAA AGA TCT | <i>Lck-cre</i> genotyping (internal control) |
| oIMR7339-IC | GTA GGT GGA AAT TCT AGC ATC ATC C | |
| Spp1-F1 | GCCTGTTTGGCATTGCCTCCTC | qPCR |
| Spp1-B1 | CACAGCATTCTGTGGCGCAAGG | |
| mSpp1CHIP-ISRE1-F2 | TTAACCCCAAGTGGCTACACG | ChIP-qPCR |
| mSpp1CHIP-ISRE1-B2 | TCATGTTGAAGTCCCCTTAAAGTAG | |
| mSpp1CHIP-ISRE2-F2 | GGATCCCTGATGCTCTTCCG | ChIP-qPCR |
| mSpp1CHIP-ISRE2-B2 | TCCTCCTCTGGTTTTGTGGT | |
| mIrf8-Q-F | GATCGAACAGATCGACAGCA | qPCR |
| mIrf8-Q-B | GCTGGTTCAGCTTTGTCTCC | |
| mIrf8-FW | CATGGCACTGGTCCAGATGTCTTCC | Irf8 whole body genotyping |
| mIrf8-wt-RV | CTTCCAGGGGATACGGAACATGGTC | |
| mIrf8-KO-RV | CGAAGGAGCAAAGCTGCTATTGGCC | |
| mIrf8exon1F | GCGCGGGCAGCGTGGGAACCGGCG | Irf8 flox genotyping |
| mIrf8exon3B | GTCACCTTCTCAAATCTGGGCTC | |
| mSpp1 ISRE-1F | TCAAATGTCATTTTCAATTTTACGAGTATTC | EMSA mSpp1- ISRE1 |
| mSpp1 ISRE-1B | GAATACTCGTGAAAATGAAATGACATTTGA | |
| mSpp1 ISRE-2F | AATGCTTTGTGTGTGTTTTCTTTTCTTCCT | EMSA mSpp1- ISRE2 |
| mSpp1 ISRE2-B | AGGAAGAAAAGGAAACACACACAAAGCATT | |
| mPD-1 ISRE-F | CTAATATTAGCAGTTTCGTTTTCCCTTTTT | EMSA mPD-1- ISRE |
| mPD-1 ISRE-B | AAAAAGGGAAAACGAACTGCTAATATTAG | |
| mβ-actin-F | ATTGTTACCAACTGGGACGACATG | qPCR |
| mβ-actin-B | CTTCATGAGGTAGTCTGTCAGGTC | |