Legends to Supplementary Figures and Tables

Fig. S1. Generation of AEG-1KO mouse. A. Targeting strategy. The arrowheads indicate loxP sites. B. Southern blotting analysis to confirm genotype using the probe shown in A. C. PCR using genomic DNA. For B-C, M represents molecular weight marker. D. AEG-1 mRNA expression in different organs by Taqman Q-RT-PCR. A.U.: arbitrary unit. E. Western blot analysis for AEG-1 in the indicated organs. F. Immunohistochemistry for AEG-1 in the indicated organs.

Fig. S2. Analysis of spleen cells of adult WT and AEG-1KO mice. To examine the potential influence of IGFBP7 deficiency on the immune cell development, we analyzed the leucocyte profile in the spleens by flow cytometry. There was no significant differences between wild-type and AEG-1KO mice in the frequency of $NK1.1^{+}CD3^{-}$ natural killer cell, $CD3^{+}$ T cell or their subsets (i.e., $CD4^{+}CD3^{+}$, $CD8^{+}CD3^{+}$), $B220^{+}$ B cell, $CD11b^{+}$ myeloid cell or their subsets, including macrophage ($CD11b^{+}F4/80^{+}$), dendritic cell ($CD11b^{+}CD11c^{+}$), monocyte ($CD11b^{+}Ly6C^{high}Ly6G^{-}$), and neutrophil ($CD11b^{+}Ly6C^{low}Ly6G^{+}$).

Fig. S3. F4/80 staining for macrophages in spleen sections of aged (16 m) WT and AEG-1KO mouse. Magnification 400X.

Fig. S4. Graphical representation of quantification of F4/80 staining for macrophages in liver sections of WT and AEG-1KO mice, either untreated (naïve) or treated with DEN or DEN/PB. N=3/group. At least 9 fields were counted for each mouse section. Data represent mean ± SEM. *: $p<0.01$.

Fig. S5. Stellate cells are activated in the tumor region of WT liver. DEN-treated liver sections from WT and AEG-1KO mice were stained for α-SMA. Note increased staining for α-SMA only in the tumor of WT mouse. Magnification 200X.

Table S1. Differential count of bone marrow cells of adult WT and AEG-1KO mice. Bone marrow was collected from 8 weeks old WT and AEG-1KO mice. Bone marrow smear was made and stained. Two hundred cells were counted to obtain differential count.

Table S2. Complete blood count of peripheral blood in WT and AEG-1KO mice. Peripheral blood was collected from WT and AEG-1KO mice and analyzed for complete blood count. WBC: white blood cells; RBC: red blood cells; HCT: hematocrit; MCV: mean corpuscular volume.

Table S3. Number of liver nodules in DEN-treated WT and AEG-1KO mice.

Table S4. Liver enzyme levels in mouse sera 48 h after injection of DEN (10 μg/gm). Three WT and three AEG-1KO mice were used.

Table S5. List of differentially expressed genes identified by RNA-seq in the livers of AEG-1KO mouse *versus* WT mouse. Genes showing log2 fold-change of >1.5 or <-1.5, FDR of <0.1 and p-value of <0.01 were selected.

Table S6. Ingenuity pathway analysis of RNA-seq data that identifies upstream regulators based on changes in expression of downstream genes. Upstream regulators, IL-6, IL-1B, TNF family, IL17RA and NF-κB complex which are inhibited in AEG-1KO mice and relevant to the present studies, are highlighted in red.

Table S7. List of antibodies used in this study.