**SUPPLEMENTARY FIGURES LEGENDS**

**Supplementary Figure 1. Increased tumor progression was detected 30 and 60 days after CLP.** (A) Thirty days after CLP post-sepsis mice presented increased tumor volumes. n - 10 (naïve) and n - 9 (post-sepsis). Graph is representative of two independent experiments. (B) The mortality of post-sepsis tumor bearing was higher in comparison to naïve mice. n - 10 (naïve inoculated with B16 cells), n - 9 (post-sepsis inoculated with B16 cells) or n - 7 (post-sepsis injected with vehicle). Survival curve calculated from two independent experiments. (C) After 60 days of CLP, sepsis-surviving mice showed (C) larger tumors and (D) reduced survival. n - 7 (naïve inoculated with B16 cells), n - 7 (post-sepsis inoculated with B16 cells) or n - 7 (post-sepsis injected with vehicle). All graphs are representative of two independent experiments. \* indicates p < 0.05; \*\* indicates p < 0.01; \*\*\* indicates p < 0.001.

**Supplementary Figure 2. Post-sepsis state led to increased metastatic burden.** (A) Experimental protocols. CLP indicates cecal ligation and puncture. ATB indicates ertapenem treatment. (B) Post-sepsis mice developed higher number of spontaneous lung metastasis as histologically evaluated at D+21. n - 8 (naïve) and n - 11 (post-sepsis). Data is representative of two independent experiments. (C) Post-sepsis mice died earlier than their naïve counterparts in the metastasis-associated mortality model. n - 6 per group. Graph is representative of two independent experiments. (D) Post-sepsis mice developed increased pulmonary melanoma colonization after intravenous inoculation of 30,000 cells, as measured through bioluminescence at D+18. The image depicts representative findings of each group. As the scale indicates, the redder the signal, the greater is the tumor burden. n - 6 (naïve) and n - 7 (post-sepsis). Graph is representative of two independent experiments. The horizontal red lines represent the mean and individual data are presented as scattered dot plots. \* indicates p < 0.05; \*\* indicates p < 0.01; \*\*\* indicates p < 0.001.

**Supplementary Figure 3. Post-sepsis induces the accumulation of Tregs in the spleen and lymph nodes but not within the tumor.** (A) Spleens obtained from post-sepsis mice presented increased amounts of CD4+CD25+Foxp3+ cells (Tregs) in comparison with the naïve controls. An accumulation of splenic Tregs was also detected in naïve tumor-bearing mice in comparison with naïve mice without tumor. The accumulation of Tregs was significantly higher in post-sepsis tumor-bearing animals compared to the other groups. (B) Lymph nodes from post-sepsis mice had increased number of Tregs in comparison to naïve controls. (C) No differences were noted in intratumoral Tregs percentage between post-sepsis and naïve groups. Representative dot plots of each studied group are depicted to the right of each graph. n - 5 per group. Bars indicate the means followed by the standard deviations. Data is representative of two independent experiments. \* indicates p < 0.05 compared to the naïve group without tumor. # indicates p < 0.05 compared to the post-sepsis group without tumor.

**Supplementary Figure 4. Differences in intratumoral amounts of CD3+CD4+ and CD3+CD8+ cells were not detected.** Flow cytometric analysis were conducted in tumors from post-sepsis and naïve mice at day 15 after B16 cells inoculation. No differences were detected when compared the intratumoral infiltration of (A-B) CD4+ and (C-D) CD8+ T cells subpopulations. *n* - 5 per group. ns indicates non-significant.

**Supplementary Figure 5. Expression of genes related to M1 and M2 polarization in TAM derived from naïve or post-sepsis mice.** qRT-PCR assays were conducted to evaluate gene expression of specific genes associated with M1 (Tnf and Nos2) and M2 (Arg1 and Mrc1)-polarization. Nos2 gene expression was reduced in TAM from post-sepsis mice. A trend for higher expression of Tnf, Arg1 and Mrc1 was noted. n - 4 per group. The horizontal red lines represent the mean and individual data are presented as scattered dot plots. \* indicates p < 0.05. ns indicates non-significant.

**Supplementary Figure 6. AMD3100 inhibited the ability of post-sepsis bone marrow derived macrophages to increase tumor growth**. Recipient mice injected with Post-sepsis Mφs with B16 cells (10,000 and 30,000 cells, respectively) showed increased tumor volumes at day 20 when compared to those inoculated with naïve derived Mφs. This effect was inhibited following the administration of AMD3100 to the post-sepsis Mφs recipients. n - 5 per group. \* indicates p < 0.05 in comparison to naïve Mφs group. # indicates p < 0.05 in comparison to post-sepsis Mφs + vehicle group.

**Supplementary Figure 7. Post-sepsis led to extra medullary proliferation of TAM through CXCR4/CXCL12 signaling.** (A) Post-sepsis mice presented higher amounts of TAM expressing Ki67. CXCR4/CXCL12 blockade by AMD3100 reduced Ki67 expression in TAM from post-sepsis mice. n - 5 (naïve plus vehicle), n - 5 (naïve plus AMD3100), n - 5 (post-sepsis plus vehicle) and n - 5 (post-sepsis plus AMD3100). (B) Changes in Ki67 expression were restricted to leukocytes. n - 5 (naïve plus vehicle), n - 5 (naïve plus AMD3100), n - 5 (post-sepsis plus vehicle) and n - 5 (post-sepsis plus AMD3100). (C) Representative dot plots gated in total tumor cells from naïve + vehicle, naïve + AMD3100, post-sepsis + vehicle and post-sepsis + AMD3100 groups. CXCL12 inhibition reduced the percentage of Ki67+ TAM (F4/80+). All graphs are representative of two independent experiments. The horizontal red lines represent the mean and individual data are presented as scattered dot plots. \* indicates p < 0.05; \*\* indicates p < 0.01; \*\*\* indicates p < 0.001.