Supplementary Figure legends

**Supplementary Figure 1** CTCs are more abundant in blood from the mesenteric vein than in blood from the forearm vein.

*(A)* Mononucleated cells isolated from fresh blood sampled from the mesenteric vein or the forearm vein of CRC patients were subjected to surface marker staining and FACS analysis. CTCs were defined as CD45^{dim} ESA^{+} cells. Individual paired measurements of mesenteric CTCs and forearm CTCs from the same patients are shown. *(B)* The number of forearm CTCs was positively correlated with mesenteric CTCs. *(C)* The distribution of the higher number of CTCs in PB observed in individual patients with a trend toward higher number of CTCs in IMV.

*(D)* Mononucleated cells isolated from fresh blood sampled from the forearm vein of CRC patients were subjected to surface marker staining and FACS analysis. CTCs were defined as CD45^{dim} ESA^{+} cells. Data represented the number of CTCs among stage I-IV CRC.

**Supplementary Table 1.** Clinicopathological characteristics of the patients analyzed in this study

**Supplementary Figure 2** The number of CTCs detected from forearm vein of clinical stage I/II lung cancer patients are higher than those of stages III and IV. Fresh blood sampled from forearm vein of lung cancer patients were subjected to surface marker staining and FACS analysis. CTCs, defined as CD45^{dim} ESA^{+}, are calculated in the lung cancer patients of different clinical stages.

**Supplementary Figure 3** The serum profiles of GM-CSF in mice with or without metastasis.

*(A)* In mice with (#1–3) and without (#4–6) metastases, fresh blood collected by retro-orbital sampling on the days indicated was subjected to measure serum levels of GM-CSF. Increases of GM-CSF were noted during the late phase of invasion and occurred only in mice without metastases. *(B)* An inverse trend was noted between the number of CTCs and GM-CSF.

**Supplementary Figure 4** The serum profiles of various cytokines in mice with or without metastasis.

Various cytokines were analyzed in sera collected from mice that had metastasis (#1–3) and mice that did not have metastasis (#4–6). The profiles of MIG(*A*-*B*), KC(*C*-*D*), and IL-4(*E*-*F*) possessed no specific pattern in either mouse group, nor did
the serum levels of these cytokines correlate with the increase or decrease of CTCs. (MIG: Monokine induced by gamma interferon ; KC : Chemokine (C-X-C motif) ligand 1 (CXCL1); IL-4: Interleukin 4)

**Supplementary Figure 5** Treatment with rGM-CSF decreased CTCs and inhibited metastasis.

(A) Cumulative data of CTC profiles from 10 independent experiments of recombinant GM-CSF (rGM-CSF) group or control PBS group. (B) The mice were sacrificed and dissected on day 35 to measure cecum tumor sizes (*arrows*) and quantify the number and the volume of metastatic nodules in the colon (*arrowheads*) and liver (*double arrowheads*). Metastatic lesions in the liver were confirmed by histological examination. bar = 50 µm. The sizes of tumors in the cecum (*C*), and the numbers (*D*) and volumes (*F*) of metastatic nodules were compared between the experimental and the control groups. The box plots indicate quartiles Q1 and Q3; the horizontal line in the box indicates the median and the dots represent outliers.

**Supplementary Figure 6** CT-26 cells possess receptors for IL-17A.
FACS analysis demonstrates that more than 95% of CT-26 cells possess IL-17A receptors (IL-17RA).

**Supplementary Figure 7** MMP9 is up-regulated in the inoculated tumors of IL-17A-depelting mice.
Expression of MMP9 (*A*) and MMP2 (*B*) was examined in the inoculated tumors of IL-17A depletion mice and control ones, the relative quantification (RQ) values were expressed as a fold-increase compared with MMP9 (*A*) and MMP2 (*B*) expression in isotype control mice.

**Supplementary Figure 8** GM-CSF facilitates CTC clearance by boosting host immunity.
(A) Tumor tissues were stained for iNOS and Arginase-1, representing M1 and M2 TAMs, respectively. The ratio of iNOS to Arginase-1 staining intensity, termed the M1/M2 ratio, was higher in the rGM-CSF treatments than in the control. Mean ± s.d. of 4 independent experiments is shown. Bar = 50 µm. (B) On day 35, mononucleated cells isolated from the peripheral blood of mice were subjected to FACS analysis to quantify CD8, CD4, and NK cells. Mean ± s.d. of 5 independent experiments is shown.

**Supplementary Figure 9** Expression of IL-17A was positively correlated with
MMP9 and VEGF
(A) The expression of IL-17A in tumor tissue was significantly higher than that in non-tumor tissue in CRC samples. IL-17A expression correlated with MMP9 (B) and VEGF (C) expression in CRC samples.

Supplementary Figure 10 Expression of IL-17A was higher CRC with recurrence.
Compared with CRC without recurrence, the expression of IL-17A in tumor tissue was significantly higher in tumor tissues in CRC with recurrence.

Supplementary Table 2. Pretherapy serum levels of cytokines in patients with and without recurrence