significantly reduced RBC (**ac**) but not WBC (**ad**) or platelet counts (**ae**) in the blood of mice that had been repeatedly bled. The data in **q-ae** represent mean±s.d. from 3 independent experiments. The numbers of mice per treatment are shown in each bar in each panel. Statistical significance of differences among genotypes was assessed using a Repeated Measures one-way ANOVA with Greenhouse-Geisser correction along with Tukey's multiple comparison tests with individual variances. * indicates statistical significance relative to normal mice; # indicates statistical significance between *Scf* mutant mice and control mice after bleeding (* or # P<0.05, ** or ## P<0.01, *** P<0.001).

Supplementary video 1. HSCs are closely associated with *Tcf21*-Cre/ER-expressing stromal cells in the red pulp of the spleen. The video shows a 300 µm thick section of spleen from a *Tcf21$^{cre/ER}$; R26^{tdTomato}; α-catulin-GFP* mouse in which EMH was induced by treatment with Cy+21d G-CSF. The spleen section was stained with antibodies against c-kit (white), α-catulin-GFP (green), and DsRed (red), then cleared, imaged, and digitally reconstructed. HSCs are α-catulin-GFP$^+$c-kit$^+$. To show the spatial relationship between *α-catulin*-GFP$^+$c-kit$^+$ HSCs and Tomato$^+$ cells all channels 20-30 µm beyond the spot of interest were occasionally masked. Note that the capsule on the margin of the spleen section is highly autofluorescent.

Extended Data Table 1: Genes that are significantly (>8-fold and P<0.015) more highly expressed by *Scf*-GFP$^+$ stromal cells in spleen as compared to bone marrow. Data show mean±s.d. for log2 transformed expression values (n=3 independent samples/cell population). Maximal background expression was considered to be 6.6 (log2(100)); all expression values below this threshold were set to 6.6 for purposes of calculating fold-change. Two-tailed Student's t-tests were used to assess statistical significance. Data for bone marrow *Scf*-GFP$^+$ stromal cells are from[19].