**Supplementary figure legends**

**S1.** Sanger sequencing of the region around exon 5 of *Trp53* in the four *Trp53-/-* clones C7, M20, F3 and A2. Exon 5 of *Trp53* is in red. Guide RNA sequences used to generate each clone are shown in green.

**S2**. Basal transcription of p53 target gene *Cdkn1a* was assessed in parental ID8 and two CRISPR control clones, as well as *Trp53-/-* clone M20 by quantitative reverse-transcriptase PCR, normalised to *Rpl34*. PX459 cells were selected following exposure of ID8 cells to plasmid PX459 lacking any gRNA; C3 cells were generated following transfection of ID8 with PX459 encoding guide G, but contained no *Trp53* mutation. Bars represent mean +/- s.d. (n=3) plotted relative to parental ID8.

**S3.** Sanger sequencing region around exon 3 of *Brca2* in the *Trp53-/-* clone F3, and three *Trp53-/-;Brca2-/-*. Exon 3 of *Brca2* is in red. Guide RNA sequences used to generate each clone are shown in green.

**S4.** Cells were irradiated (10Gy), fixed and stained for γH2AX and RAD51, and counterstained with DAPI. RAD51 foci were counted in up to 30 untreated and irradiated cells. Bars represented mean (+/- s.e.m.) RAD51 foci per cell relative to untreated; dotted line represents two-fold increase relative to untreated cells.

**S5.** Combined survival of mice bearing *Trp53-/-;Brca2-/-* (n=18, 6 per clone) compared to survival of mice bearing *Trp53-/-* clone F3 (n=12).

**S6.** Photograph of peritoneal dissemination and of ascites harvested from mouse bearing *Trp53-/-;Brca2-/-* tumour compared to ascites from mouse bearing parental ID8 tumour

**S7.** High magnification images of CD3 staining in lymphoid structures in *Trp53-/-;Brca2-/-* tumours presented in Fig. 5C. Bars represent 10 µm.

**S8.** Lymphoid area per tumour section and % lymphoid area per tumour section as measured using Slidepath Digital Image Hub V4.0.7 (Leica Microsystems, Milton Keynes, UK). \*;p<0.05

**S9.** CD8 staining in a lymphoid aggregate in *Trp53-/-;Brca2-/-* 2.14 tumour.

**S10.** F4/80 staining in parental ID8 and *Trp53-/-* tumours. Bars represent 100 µm. Histoscores calculation is described in Experimental Procedures. \*\*\*;p<0.001

**S11.** Full layout of murine chemokine/cytokine array presented in Figure 6A.

**S12.** Representative flow cytometry plots for Ly6C and Ly6G in tumour deposit and ascites.

**S13.** Representative flow cytometry plots for F4/80, iNOS and CD206 in ascites.

**S14.** Gating strategy for flow cytometry plots in Fig. S12 and S13.