

## Supplementary Information

**Figure S1.** Representative pseudo-color plots of Lin<sup>-</sup> gated cells from 2 week-old *WT*, *Mef<sup>-/-</sup>*, *p21<sup>-/-</sup>*, *Rad50<sup>S/S</sup>*, *Rad50<sup>S/S</sup> Mef<sup>-/-</sup>* and *Rad50<sup>S/S</sup> p21<sup>-/-</sup>* mice are shown. Note that both *Rad50<sup>S/S</sup>* and *Rad50<sup>S/S</sup> p21<sup>-/-</sup>* mice exhibit a decreased percentage of c-kit Sca-1 double positive cells.

**Figure S2.** Annexin-FITC representative pseudo-color plots of LSK gated cells from 2 week-old *WT*, *Mef<sup>-/-</sup>*, *p21<sup>-/-</sup>*, *Rad50<sup>S/S</sup>*, *Rad50<sup>S/S</sup> Mef<sup>-/-</sup>* and *Rad50<sup>S/S</sup> p21<sup>-/-</sup>* mice are shown. The FITC Isotype control used to delineate the Annexin positive gate is also shown.

**Figure S3.** Ki67-FITC versus Hoechst representative pseudo-color plots of LSK gated cells from 2 week-old *WT*, *Mef<sup>-/-</sup>*, *p21<sup>-/-</sup>*, *Rad50<sup>S/S</sup>*, *Rad50<sup>S/S</sup> Mef<sup>-/-</sup>* and *Rad50<sup>S/S</sup> p21<sup>-/-</sup>* mice are shown.

**Figure S4.** Similar numbers of mature haematopoietic populations in *Rad50<sup>S/S</sup>*, *Rad50<sup>S/S</sup> p21<sup>-/-</sup>*, *Rad50<sup>S/S</sup> Mef<sup>-/-</sup>* and *Rad50<sup>S/S</sup> p27<sup>-/-</sup>* mice. (A, B and C) Flow cytometric analysis of haematopoietic tissues. The numbers of proB, preB, Immature B and myeloid cells in bone marrow (2 femurs and 2 tibias) from 4 week-old mice are depicted. Each symbol represents one animal.

**Figure S5.** Primary ear fibroblasts were treated with 60 ng/ml CPT for 2h. Etoposide was washed away and cells were allowed to recover for 2.5h. Then colcemid was added and cells were incubated for an additional 3.5h before metaphases were prepared. The percentage of cells with 0, 1 or 2 chromosome aberrations is depicted. 100 metaphases were scored per each genotype and treatment.



Figure S1

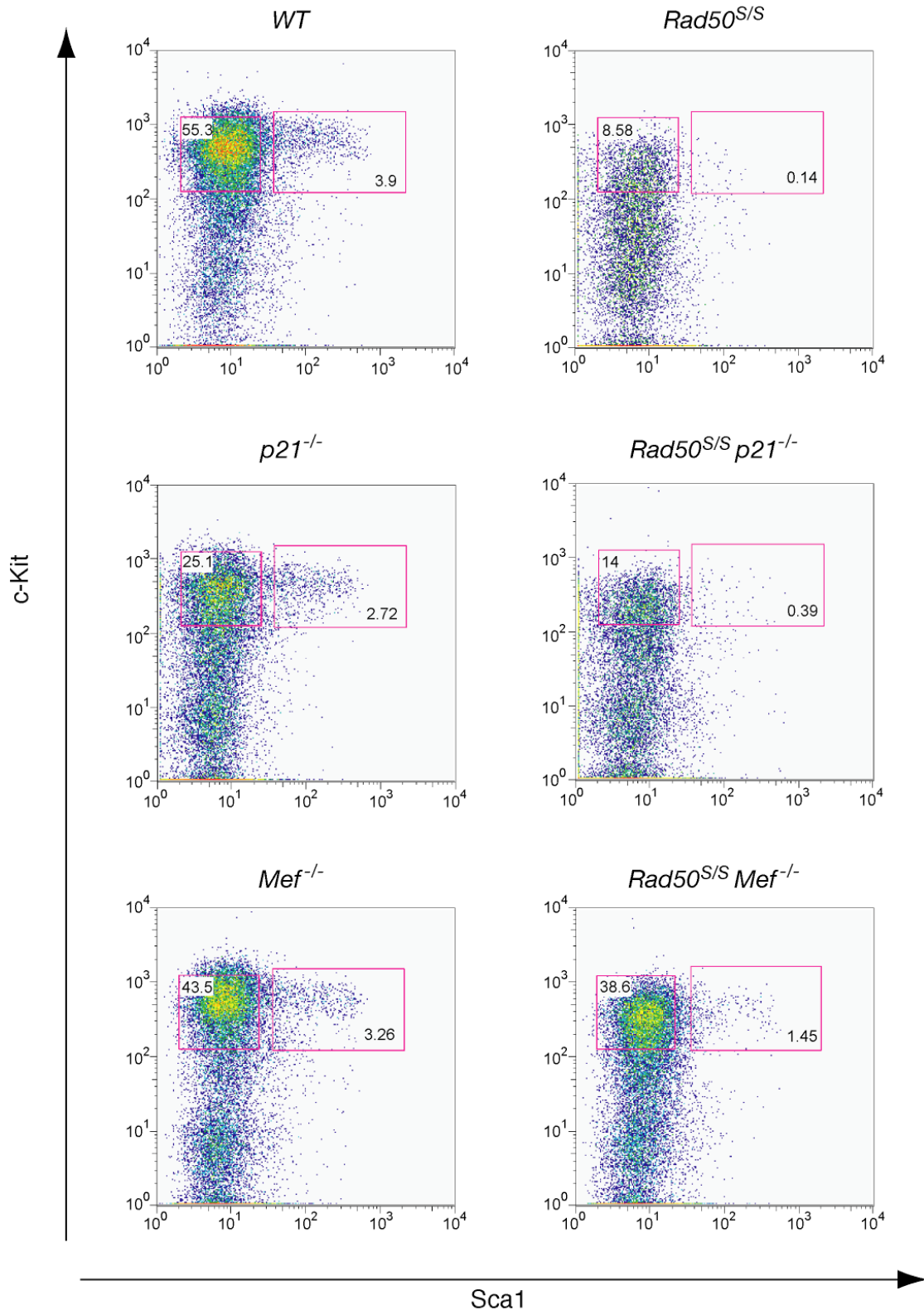


Figure S2

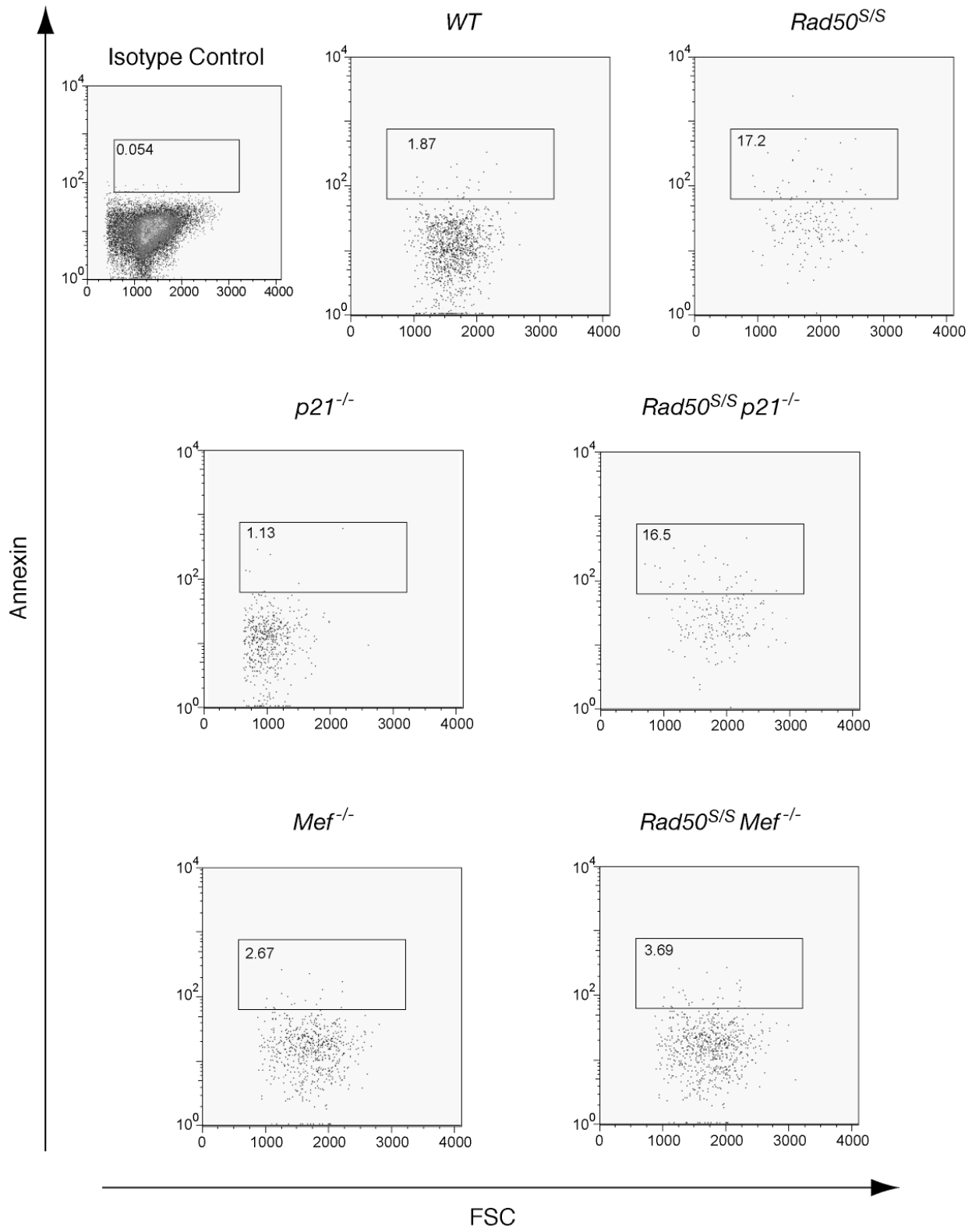
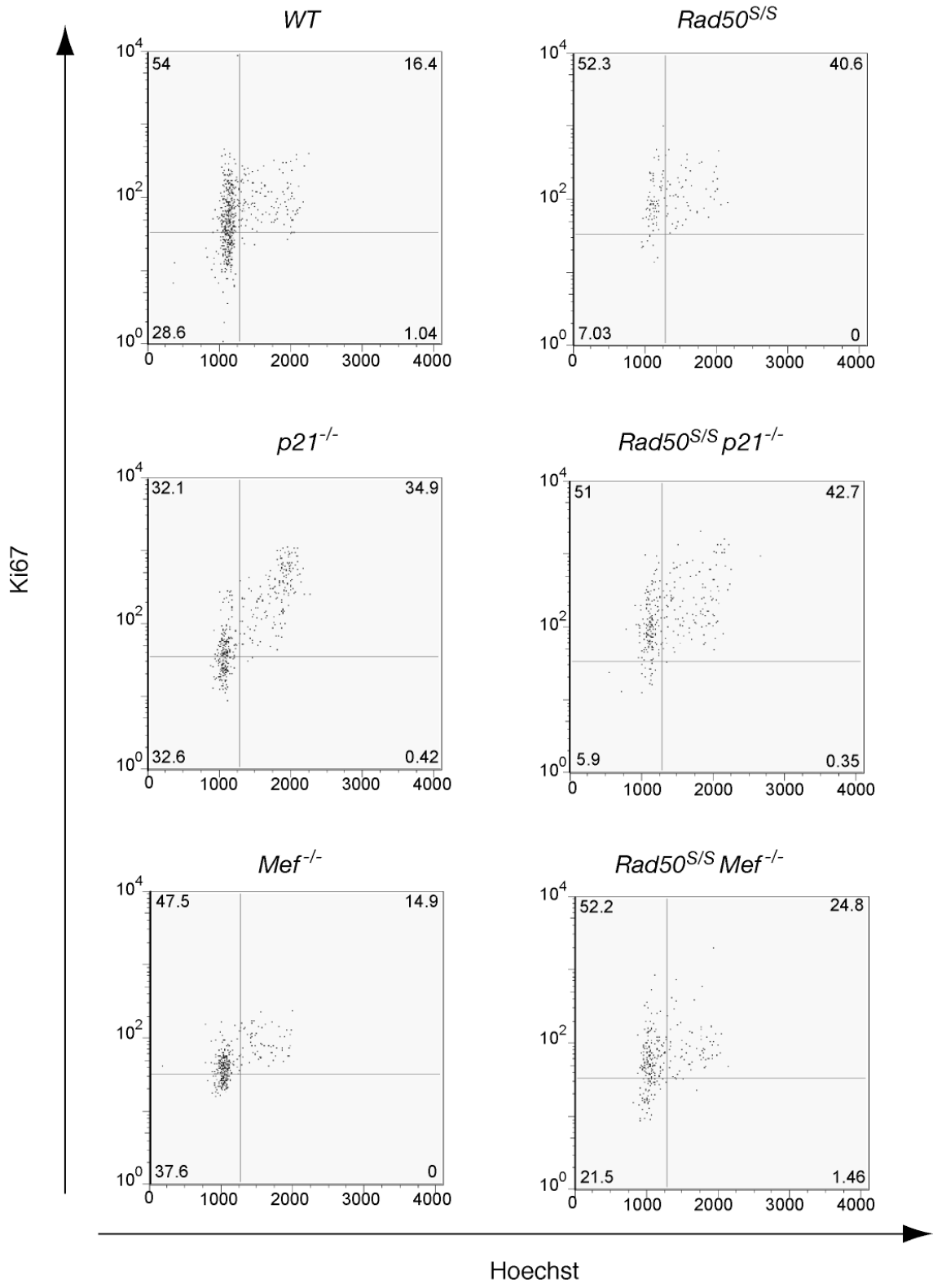
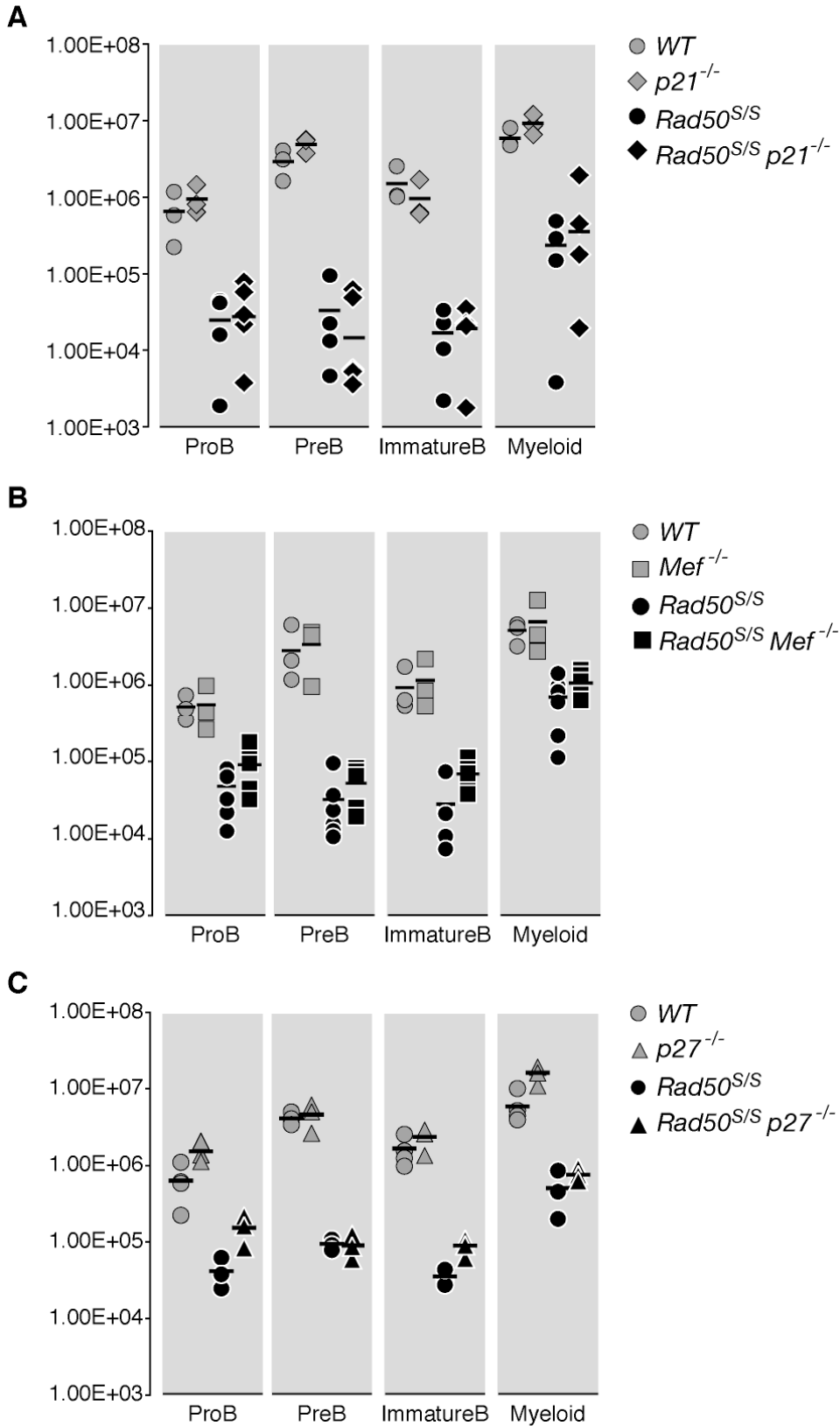


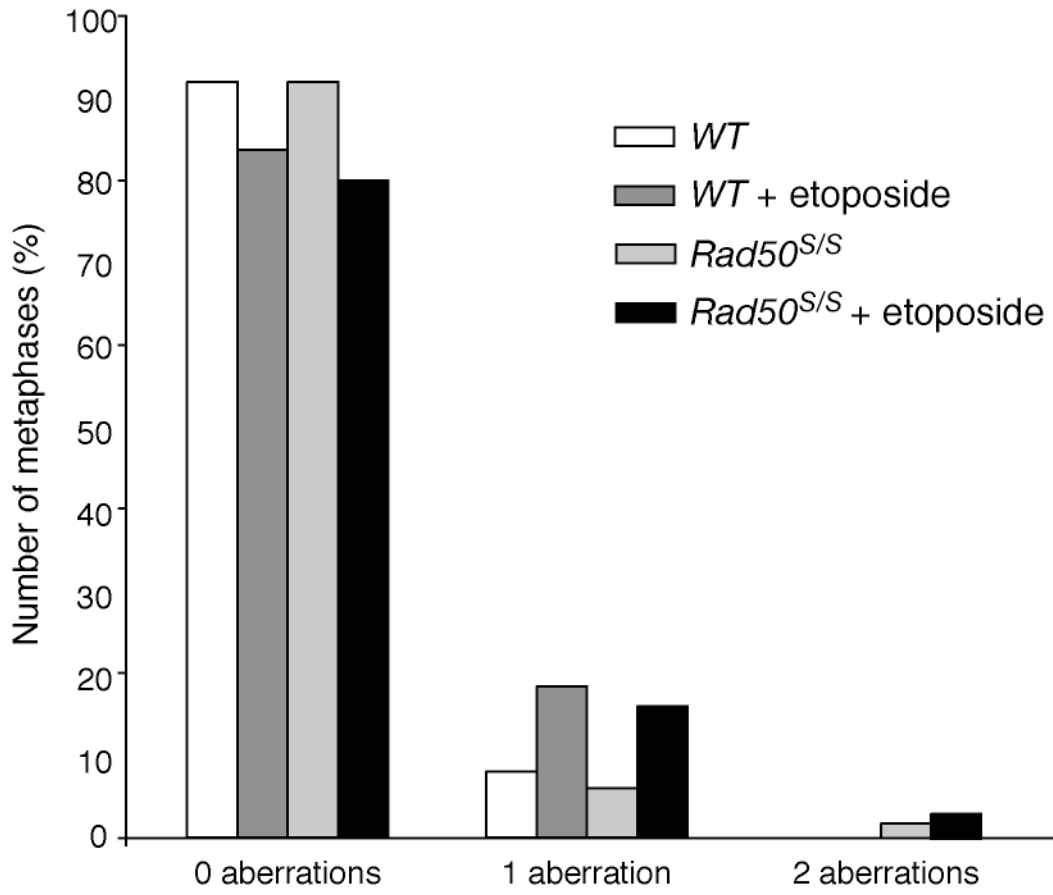
Figure S3



**Figure S4**



**Figure S5**



**Table S1.** Tumor incidence in *Rad50<sup>S/S</sup>* mice.

Genotype	<sup>1</sup> Number of mice (#)	# with malignancy	% with malignancy	Median age of tumors
<i>Rad50<sup>S/S</sup></i>	11	0	0	N/A
<i>Rad50<sup>S/S</sup> Mef<sup>-/-</sup></i>	10	3	30	2.6
<i>Rad50<sup>S/S</sup> p21<sup>+/-</sup></i>	6	3	50	13.3
<i>Rad50<sup>S/S</sup> p21<sup>-/-</sup></i>	16	6	37.5	3.1
<i>Rad50<sup>S/S</sup> p27<sup>+/-</sup></i>	7	1	14.3	14.7
<i>Rad50<sup>S/S</sup> p27<sup>-/-</sup></i>	14	5	35.7	2.9
<i>Rad50<sup>S/S</sup> Chk2<sup>-/-</sup></i>	22	17	77.3	8.3
<i>Rad50<sup>S/S</sup> Mre11<sup>ATLD1/ATLD1</sup></i>	14	12	85.7	17.2
<i>Rad50<sup>S/S</sup> Mre11<sup>+ATLD1</sup></i>	35	13	37.1	20.1

<sup>1</sup>Representative mice were submitted for complete histology