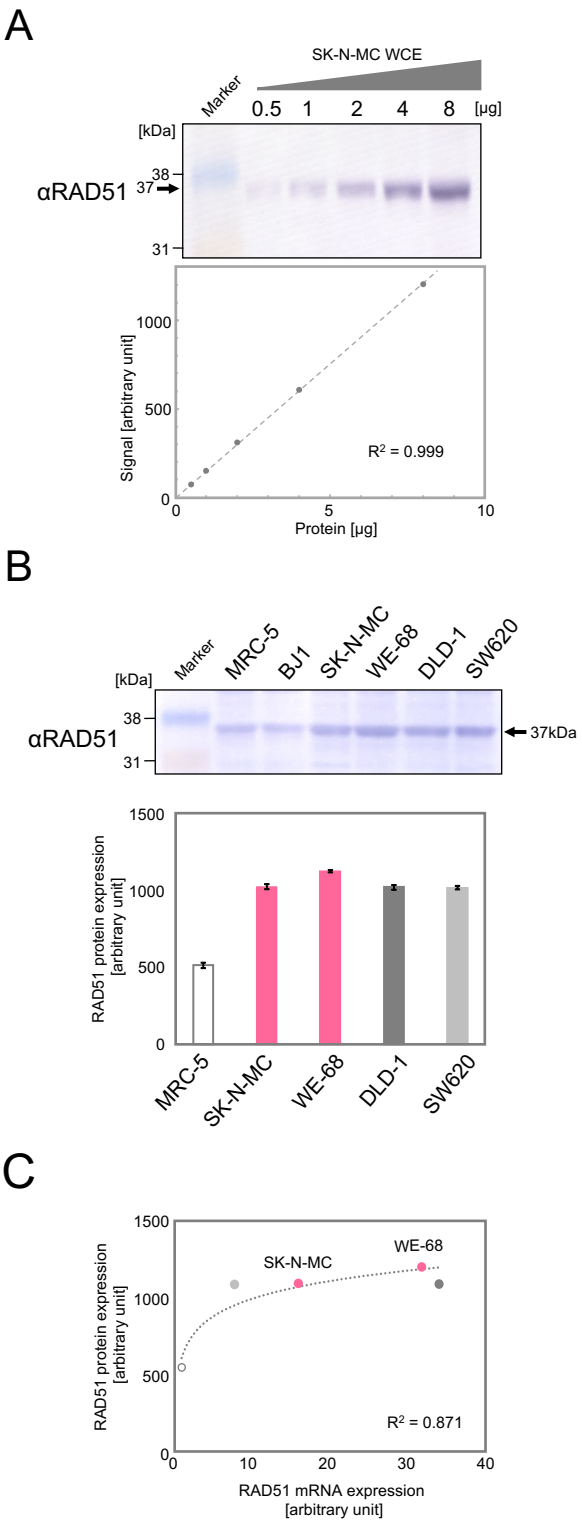


**Fig. S1. RAD51 expression in TL⁺ SK-N-MC and WE-68 Ewing sarcoma cells.**
Expression of the RAD51 protein in cells was quantitatively assessed by immunoblotting. Detection of the RAD51 antigen was linear ($R^2 = 0.99$) in this system (A). RAD51 protein expression was compared among the six representative cell lines (for details, see Materials and Methods) (B). An approximately linear ($R^2 = 0.87$) relationship was observed between RAD51 protein and mRNA expression (C).

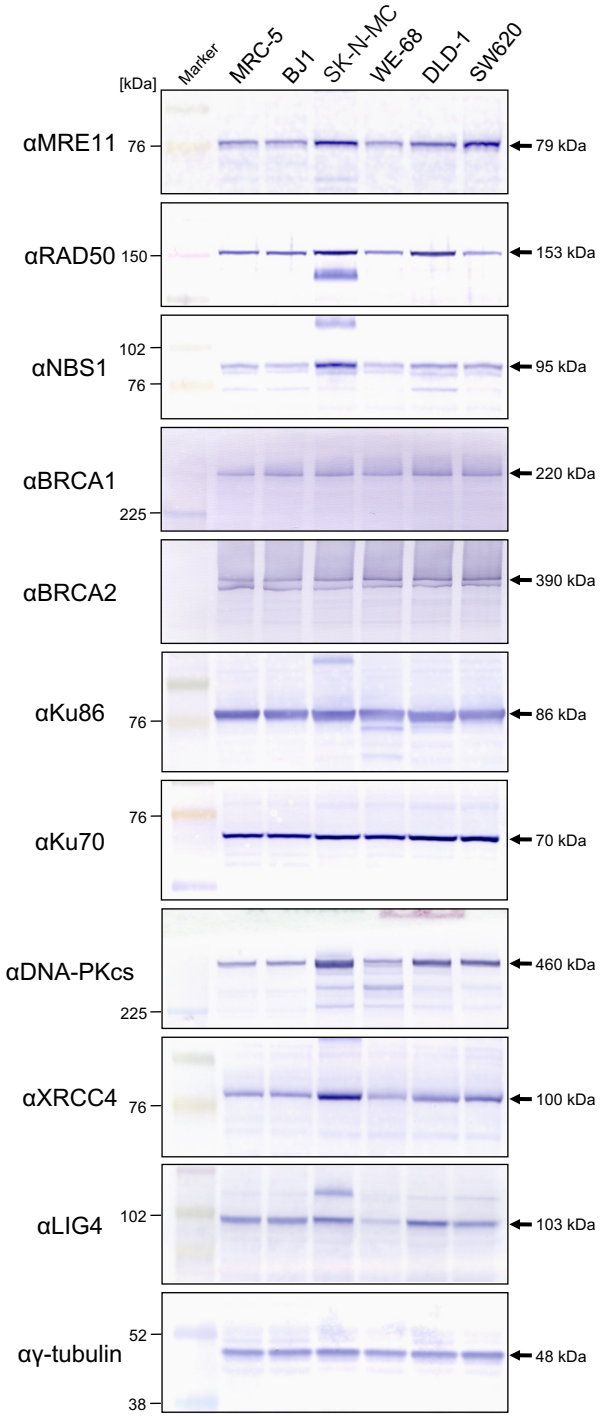


**Fig. S2. Expression of the DSBR pathway components in SK-N-MC and WE-68 cells.**

Expression of the proteins functioning in the DSBR pathways was observed using immunoblotting (for details, see Materials and Methods).

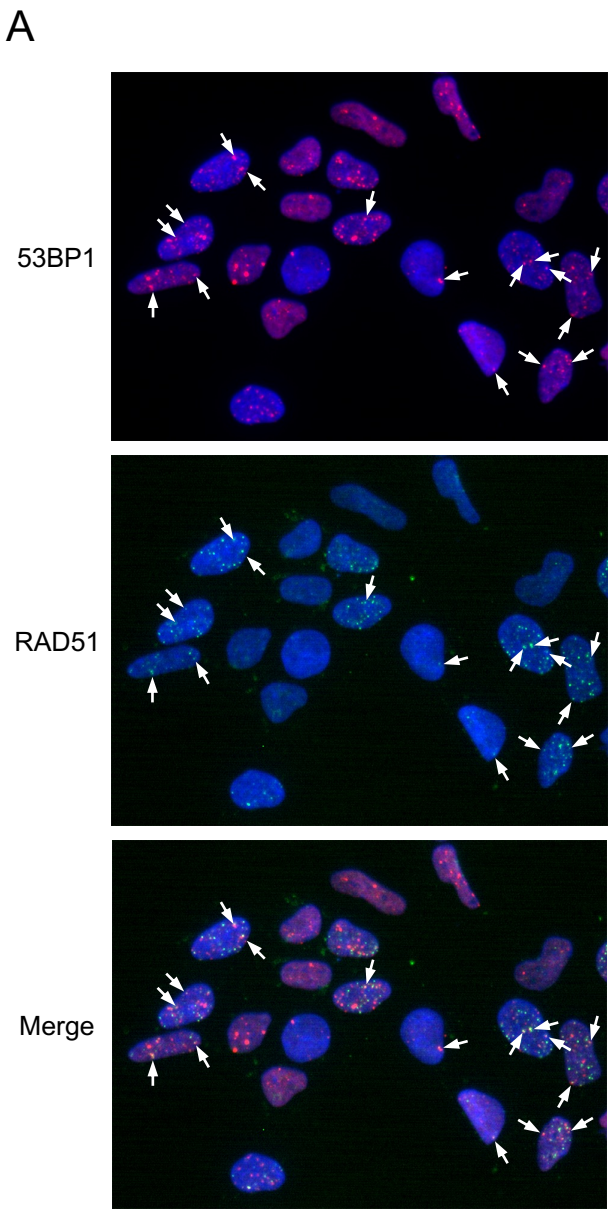


**Fig. S3. Co-localization of 53BP1 and RAD51 in Ewing sarcoma cells.**
In the magnified images of those shown in Figure 3A, 53BP1, RAD51 and 53BP1/RAD51 double positive foci in WE-68 cells, as an example, are indicated with white arrows (A). In each cell line, the ratio of 53BP1/RAD51 double -positive foci to all observed 53BP1 foci was calculated, and the results are shown in a bar chart.

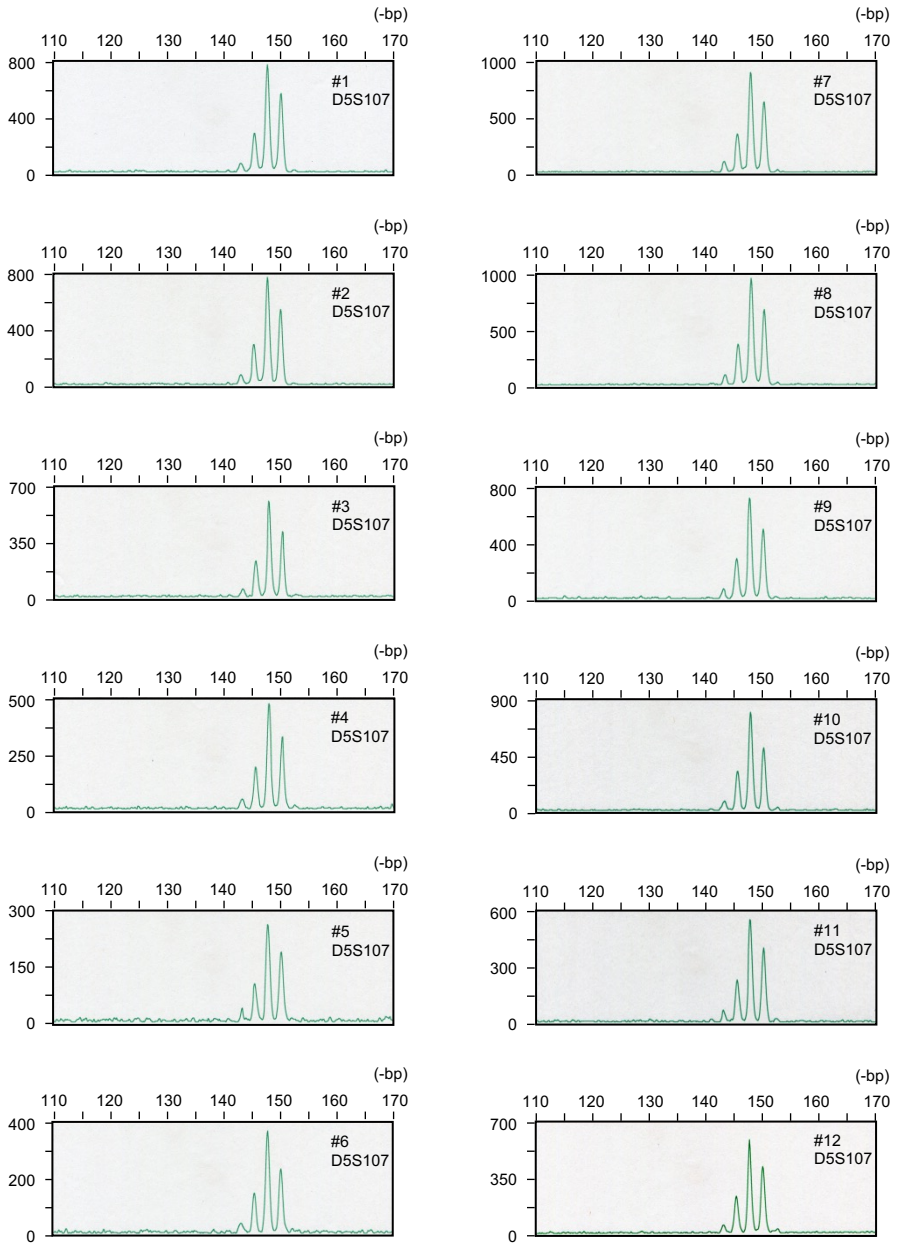


**Fig. S4. Stable dinucleotide microsatellites in WE-68 cells.**
High-resolution microsatellite analysis (see Materials and Methods) was done using subclones isolated from the WE-68 cell lines. In each subclone, several dinucleotide microsatellite sequence was analyzed. Results are compared among twelve subclones, and the representative results obtained in the D5S107 locus are shown. The x-axis corresponds to the fragment length, and the y axis to the amount of DNA fragments. Subclone names are indicated in each panel.

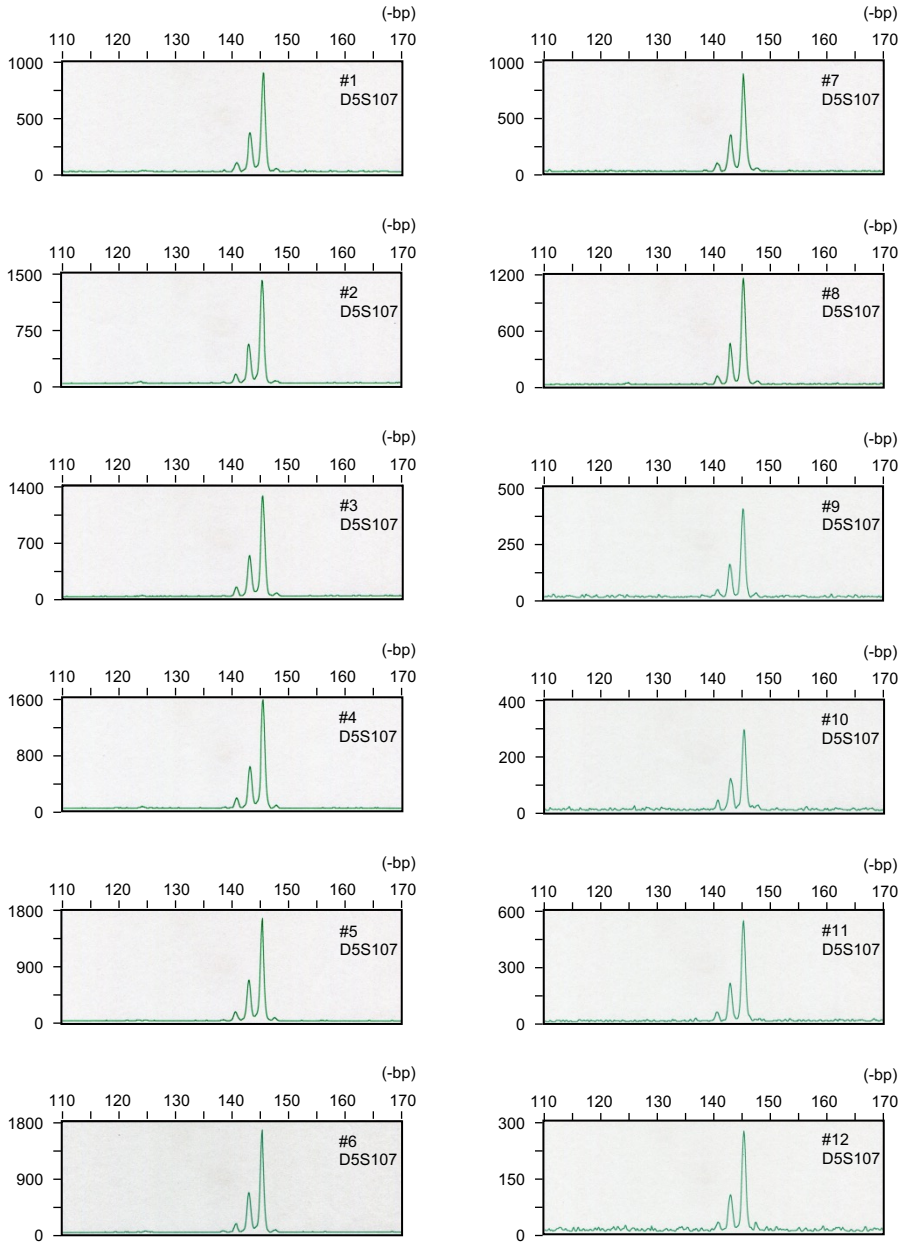


**Fig. S5. Stable dinucleotide microsatellites in SK-N-MC cells.**
High-resolution microsatellite analysis (see Materials and Methods) was similarly done using subclones isolated from the SK-N-MC cell lines. The representative results obtained in the D5S107 locus are shown. The x- and y-axes correspond to the length and the amount of DNA fragments, respectively. Subclone names are indicated in each panel.