Supplemental Figure 1. Sequence coverage for PiggyBac insertions identified in a clonal ES cell line. Average read numbers and 95% confidence interval are indicated with solid and dashed lines, respectively.

Supplemental Figure 2. Distribution of sequence coverage for RE based LM-PCR (RE-splink; *A*) and numbers of unique LPs identified by shear-splink (*B*) for all MMTV insertions identified in 16 MMTV-induced mouse mammary tumors.

Supplemental Figure 3. (*A*-*C*) Genome-wide density plots of MMTV insertions identified in 16 MMTV induced mammary tumors using shear-splink (unique LPs >1) or RE-splink (sequence coverage >1).

Supplemental Figure 4. Sleeping Beauty insertions, identified using the shear-splink method, with a higher number of unique LPs are significantly more often neighboring cancer relevant genes, independent of the indicated genomic distances (Wilcox test < 7.22e−20).

Supplemental Figure 5. Schematic overview of the analysis pipeline as setup for the MMTV and SB induced tumor samples.

Supplemental Figure 6. Schematic overview of the MMTV provirus.

For Southern blot analysis of MMTV insertions in clonal cell lines derived from MMTV-induced mouse mammary tumors, genomic DNA is digested with *Pst*I, blotted and hybridized with a MMTV-LTR probe, which is generated by amplifying the underlined region. The internal- and insertion specific fragments detected by the MMTV-LTR probe are indicated.