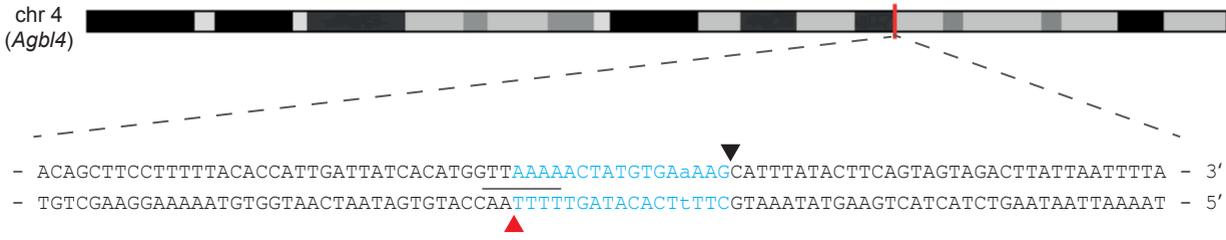


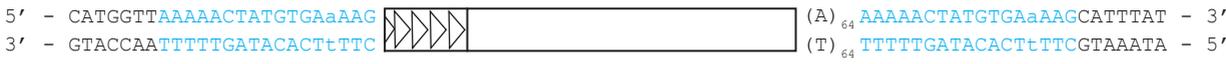
# Supplemental Figure S2

## A

Insertion site : chr 4: 111,104,716



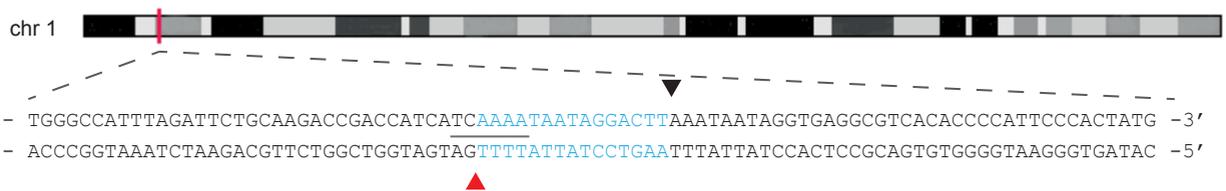
Insertion structure:



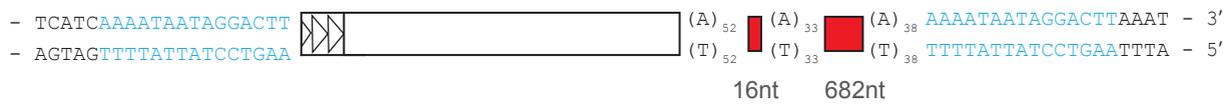
L1 subfamily:  $G_F$       Monomers: 4 + 102bp      TSD: 17nt      L1 EN motif : TT/AAAA

## B

Insertion site : chr 1: 12,998,087



Insertion structure:



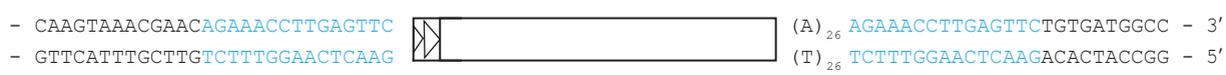
L1 subfamily:  $T_F$       Monomers: 2 + 69bp      TSD: 15nt      L1 EN motif : TC/AAAA

## C

Insertion site : chr 2: 134,994,166



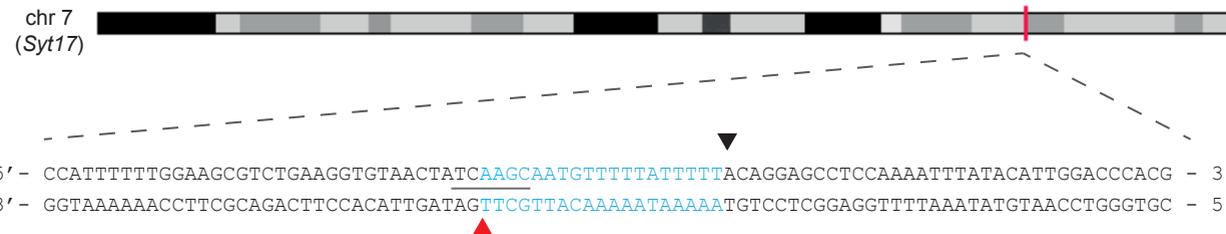
Insertion structure:



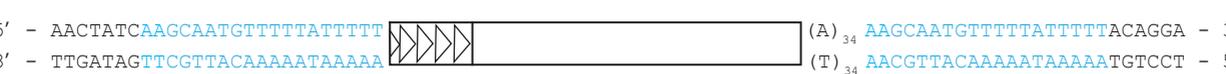
L1 subfamily:  $T_F$       Monomers: 1 + 83bp      TSD: 15nt      L1 EN motif : AC/AGAA

## D

Insertion site : chr 7: 118,392,184



Insertion structure:



L1 subfamily:  $T_F$       Monomers: 4 + 154bp      TSD: 19nt      L1 EN motif : TC/AAGC

**Supplemental Figure S2. Structures of tumor-specific L1 insertions in *Mdr2*<sup>-/-</sup> animals.**

The chromosomal location and nucleotide position of each insertion is shown; if the insertion was found within a gene, the gene name is so indicated. The genomic empty site DNA is depicted above, with the region that ultimately gave rise to the TSDs highlighted in blue. First strand endonuclease cleavage position is indicated with a red arrowhead and second strand cleavage position is indicated with a black arrowhead; the EN cleavage motif is underlined. The insertion structure is depicted below; TSDs are highlighted in blue, the L1 is shown as a white rectangle with the monomers depicted as white triangles. (A)<sub>n</sub>/(T)<sub>n</sub> indicate poly(A) tail lengths; 3' transductions are depicted as red boxes. For each insertion, the L1 subfamily, number of monomers, TSD length, and EN motif are summarized.