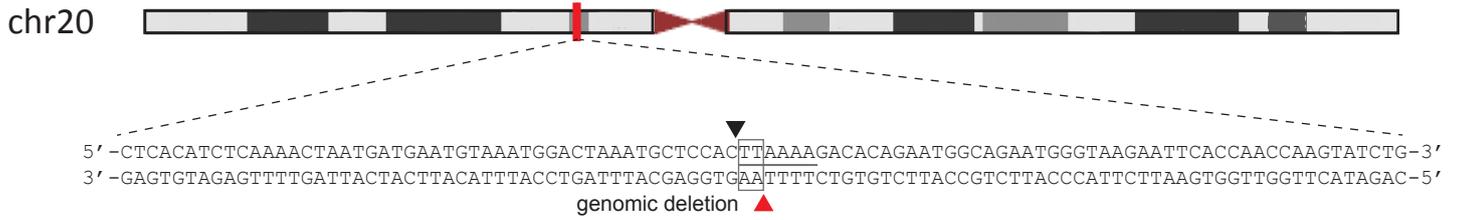# Supplemental Figure S8

A

Insertion site: chr20: 21,718,536

chr20

5'-CTCACATCTCAAAACTAATGATGAATGTAAATGGACTAAATGCTCCACTTAAAAGACACAGAATGGCAGAATGGGTAAGAATTCACCAACCAAGTATCTG-3'
3'-GAGTGTAGAGTTTTGATTACTACTTACATTTACCTGATTTACGAGGTGAATTTTCTGTGTCTTACCGTCTTACCCATTCTTAAGTGGTTGGTTCATAGAC-5'

genomic deletion ▲

Insertion structure:

5'-CTCACATCTCAAAACTAATGATGAATGTAAATGGACTAAATGCTCCAC $(A)_{96}$ AAAAGACACAGAATGGCAGAATGGGTAAGAATTCACCAACCAAGTATCTG-3'
3'-GAGTGTAGAGTTTTGATTACTACTTACATTTACCTGATTTACGAGGTG $(T)_{96}$ TTTTCTGTGTCTTACCGTCTTACCCATTCTTAAGTGGTTGGTTCATAGAC-5'
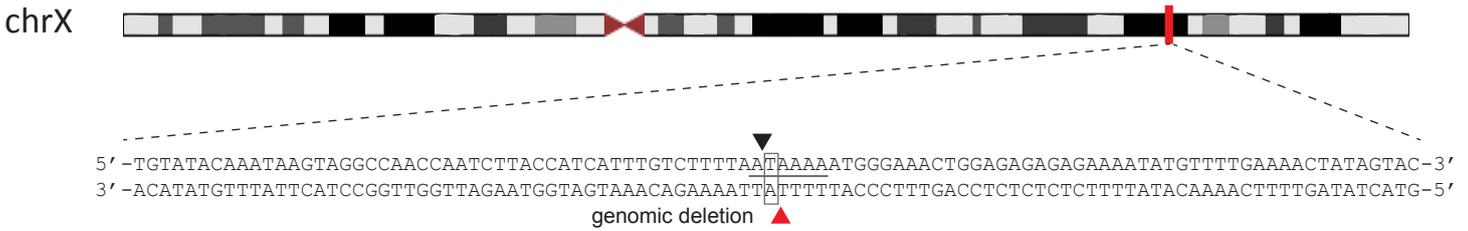
5942

TSD: none

L1 EN motif: TT/AAAA

B

Insertion site: chrX: 126,124,784

chrX

5'-TGTATACAAATAAGTAGGCCAACCAATCTTACCATCATTTGTCTTTTAATAAAAATGGGAAACTGGAGAGAGAGAAAATATGTTTTGAAAACTATAGTAC-3'
3'-ACATATGTTTATTCATCCGGTTGGTTAGAATGGTAGTAAACAGAAAATTATTTTTACCCTTTGACCTCTCTCTCTTTTATACAAAACTTTTGATATCATG-5'

genomic deletion ▲

Insertion structure:

5'-TGTATACAAATAAGTAGGCCAACCAATCTTACCATCATTTGTCTTTTAA $(A)_{61}$ AAAAATGGGAAACTGGAGAGAGAGAAAATATGTTTTGAAAACTATAGTAC-3'
3'-ACATATGTTTATTCATCCGGTTGGTTAGAATGGTAGTAAACAGAAAATT $(T)_{61}$ TTTTTACCCTTTGACCTCTCTCTCTTTTATACAAAACTTTTGATATCATG-5'
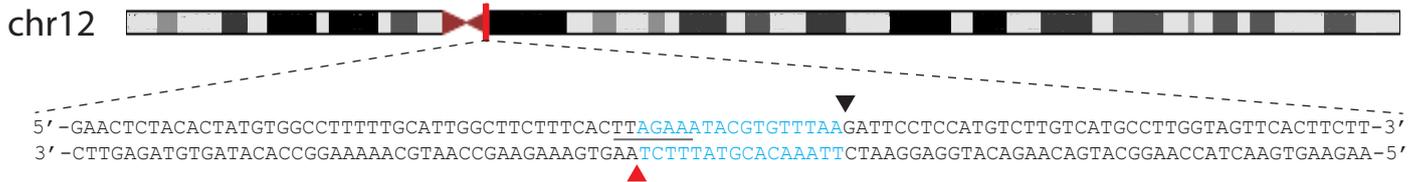
5769

TSD: none

L1 EN motif: AT/AAAA

C

Insertion site: chr12: 37,914,861

chr12

5'-GAACTCTACACTATGTGGCCTTTTTGCATTGGCTTCTTTCACTTAGAAATACGTGTTTAAGATTCCTCCATGTCTTGTCATGCCTTGGTAGTTCACTTCTT-3'
3'-CTTGAGATGTGATACACCGGAAAAACGTAACCGAAGAAAGTGAATCTTTATGCACAAATTCTAAGGAGGTACAGAACAGTACGGAACCATCAAGTGAAGAA-5'

▲

Insertion structure:

3' transduction

5'-GTGGCCTTTTTGCATTGGCTTCTTTCACTTAGAAATACGTGTTTAA $(A)_{13}$ GAAAGAAAAGAAACTTC $(A)_{28}$ AGAAATACGTGTTTAAGATTCCTCCATGTCTT-3'
3'-CACCGGAAAAACGTAACCGAAGAAAGTGAATCTTTATGCACAAATT $(T)_{13}$ CTTTCTTTTTCTTTGAAG $(T)_{28}$ TCTTTATGCACAAATTCTAAGGAGGTACAGAA-5'

5929

TSD: 16nt

L1 EN motif: TT/AGAA

Supplemental Figure S8. Structures of tumor-specific L1 insertions in ICC patients.

The chromosomal location and nucleotide position of each insertion is shown; if the insertion was located in 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. Genomic sequence deletions are boxed and labelled as such. The insertion structure is depicted below; TSDs are highlighted in blue, the L1 is depicted as rectangles, 3' UTR sequence is depicted in red, and ORF2 sequence is depicted in white. Untemplated nucleotides are so labelled. $(A)_n/(T)_n$ indicate poly(A) tail lengths. For each insertion, the TSD length and EN motif are summarized.