



**Supplemental Figure 7.** Symmetrical sequence preferences at OmniBankII gene trap insertion sites. (A-C) Base compositions surrounding each gene trap insertion site are shown according to chromosomal cleavage offset. Insertion occurs between position -1 and 1 on the top strand (with respect to the orientation of the retroviral backbone rather than the gene trap construct components). Confirmed duplicated junction sequences are shown within the solid box. Base positions for DNA strand transfer are show by arrows. Positions showing statistically different base frequencies are highlighted. Differences of 10% are shown in grey, differences of greater than 10% are shown in blue (increased frequency) or yellow (decreased frequency). D) Base composition of insertion sites displaying

non-identical duplicated junction sequence. The most likely cleavage offset was inferred to be a 4-base offset based on the outlying T and A base preferences (shown by a dotted line). Near exclusive base compositions at position 3 and 4 are shown in orange. See supplemental text for additional discussion.