**Figure S5.** Molecular characterization of new landing sites. (A) Genomic PCR verification of R11C05-LexA excision. Top – The presence of R11C05-LexA was probed using primers that bind in the LexA coding sequence. Controls that harbor the transgene (lanes 3 and 5) showed amplification, but not native attP18 or the new landing sites following treatment with Int*. (lanes 4 and 6-9). Bottom – Amplification of a region containing attP corroborates the absence of the R11C05-LexA transgene. Amplification was successful in samples with an intact attP, but fails in samples with an integrated transgene. Arrows indicate bands that were gel-extracted and sequenced. (B) To confirm the integrity of reconstituted attPs in new landing sites, the PCR products indicated in (A) were sequenced and compared to wild-type attP. The cross-over nucleotides where recombination occurs are indicated in bold. (C) Genomic location of new landing sites: Landing sites were mapped to the genome using splinkerette PCR (Potter and Luo 2010).