Supplementary Fig. 10: Overview of abundance and position of internally deleted P-elements in hot evolved populations at generation 20. We use Sashimi plots, which usually indicate splicing in RNA-seq data, to visualize internally deleted P-elements in genomic DNA. End-points of arches are positions of deletions, and the width of the arches scales with the logarithm of the number of reads supporting a given internal deletion. Only internal deletions supported by at least three reads are shown. Vertical positions of the internal deletions have been manually adjusted to avoid overlaps. Panel at the bottom indicates the structure of the P-element, with the four ORFs shown as blue boxes. Even when conservatively assuming that no P-element insertion has more than one internal deletion, at least 87% of P-elements are full length in hot evolving populations at generation 20 (replicate 1: 87.4%; replicate 3: 90.2 %; replicate 5: 94.1%; calculated as $1 - \sum_{i=1}^{t} f_i$, where t are all internal deletions of a given replicate and f_i is the frequency of internal deletion i).