

A. Crossing scheme to shuffle transgenes between landing sites using *Int** and *Int** (wildtype).

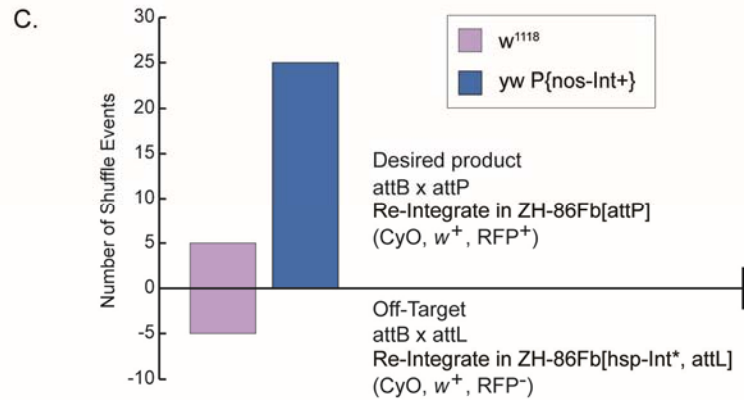
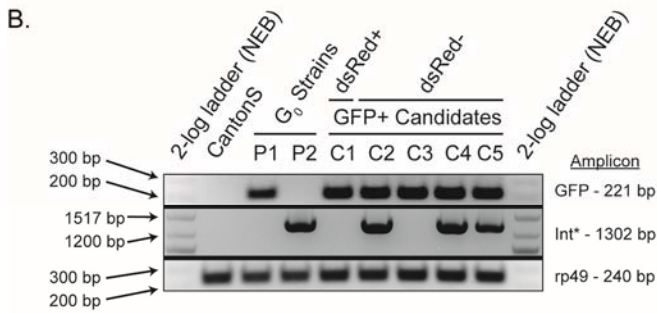
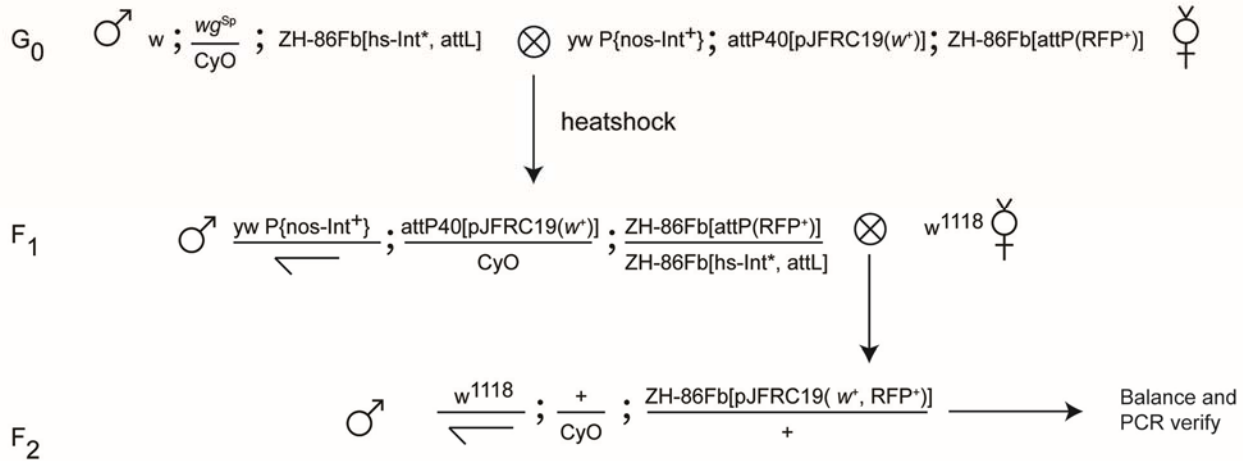


Figure S6. Genetics and integration characteristics of *Int**/*Int* transgene shuffling.

Figure S6 Genetics and integration characteristics of *Int**/*Int* transgene shuffling. (A) Crossing scheme to shuffle pJFRC2 between two autosomal landing sites. In this example, wild-type integrase is supplied by an X-linked transgene (Bischof *et al.* 2007). The movement of pJFRC19 from *attP40* (donor on *II*) to *ZH-86Fb* (receiver on *III*) was followed using the transgene's mini-white marker. Flies in the F₂ generation that carried mini-white and *CyO* carried candidate shuffle events; genetic mapping and PCR were used to confirm the presence of pJFRC19 at the receiver site. (B) Molecular characterization of selected shuffle candidates. Top – Genomic PCR confirmed the presence of GFP in five shuffle candidates (C1-C5). P1 corresponds to the maternal G₀ genotype, *w*; *attP40*[pJFRC19(*w*⁺)]; *ZH86Fb*[*attP*(*RFP*⁺)]. P2 corresponds to the paternal G₀ genotype, *w*; *wg*^{Sp}/*CyO*; *ZH86Fb*[*hs-Int**, *attL*]. Middle – Genomic PCR detected *Int** in three shuffle candidates. *Int** was not detected in candidate C1, since pJFRC19 shuffled into the receiver landing site (marked by *3xP3-DsRed*). *Int** was detected in C2, C4, and C5. This indicates that pJFRC19 re-integrated on the *hs-Int** chromosome, which is corroborated by the absence of *DsRed* expression in these flies. The *attL* sequence downstream of *hs-Int** (see Figure S1A) presented a potential re-integration target due to the relaxed integration site specificity of *Int**. The re-integration site of candidate C3 was not determined, though the lack of *DsRed* strongly suggests this was off-target. Bottom – PCR control with *rp49*. (C) Wild-type *Int* enforces canonical attP x attB recombination during transgene shuffling: Flies were scored for the presence of the *ZH-86Fb* landing site marker *3xP3-DsRed* to distinguish re-integration at the receiver site from off-target integration (see panel B). When *Int** provided both excisionase and integrase activities, half of the recovered candidates lacked *DsRed*, indicating re-integration at a site other than the receiver site. In contrast, in the presence of wild-type integrase, all candidates re-integrated at receiver landing site.