

Table S1. Homology-directed repair (HDR) efficiencies of different inserts into SKI LODGE lines.

| Insert | Template size (bp) | % HDR in F1 dumpies (n) | Recipient SKI LODGE strain |
|--|---------------------------|--------------------------------|-----------------------------------|
| Blunt-strand ends, Paix protocol | | | |
| wrmScarlet | 774 | 8.57 (175) | <i>eft-3</i> |
| wrmScarlet | 774 | 9.14 (175) | <i>rab-3</i> |
| wrmScarlet | 774 | 13.04 (115) | <i>myo-3</i> |
| GFP | 944 | 11.46 (96) | <i>pie-1</i> |
| Template 1 | 1872 | 0.44 (227) | <i>rab-3</i> |
| Template 2 | 2319 | 2.08 (48) | <i>rab-3</i> |
| <i>crtc-1::wrmScarlet</i> ^a | 1534, 778 | 13.39 (112) | <i>rab-3</i> |
| <i>unc-4::wrmScarlet</i> ^a | 829, 778 | 9.56 (136) | <i>rab-3</i> |
| Single-strand ends, Dokshin protocol | | | |
| wrmScarlet | 936/696 | 13.33 (150) | <i>myo-3</i> |
| wrmScarlet | 936/696 | 26.00 (150) | <i>eft-3</i> |

^aTwo templates with overlapping sequence.