



SKI LODGE line	Templates (5' → 3')	Number of Edits						
<i>myo-3p</i> Chr. I	<table style="width: 100%; border: none;"> <tr> <td style="text-align: center;">(1)</td> <td style="text-align: center;">(2)</td> </tr> <tr> <td style="text-align: center;"><i>promoter</i></td> <td style="text-align: center;"><i>tag::dpy-10 site::3'UTR</i></td> </tr> <tr> <td style="text-align: center;">2573 bp</td> <td style="text-align: center;">806 bp</td> </tr> </table>	(1)	(2)	<i>promoter</i>	<i>tag::dpy-10 site::3'UTR</i>	2573 bp	806 bp	2
(1)	(2)							
<i>promoter</i>	<i>tag::dpy-10 site::3'UTR</i>							
2573 bp	806 bp							
<i>pie-1p</i> Chr. III	<table style="width: 100%; border: none;"> <tr> <td style="text-align: center;">1166 bp</td> <td style="text-align: center;"><i>tag::dpy-10 site::3'UTR</i> 806 bp</td> </tr> <tr> <td style="text-align: center;"><i>promoter</i></td> <td></td> </tr> </table>	1166 bp	<i>tag::dpy-10 site::3'UTR</i> 806 bp	<i>promoter</i>		1		
1166 bp	<i>tag::dpy-10 site::3'UTR</i> 806 bp							
<i>promoter</i>								
<i>rab-3p</i> Chr. IV	<table style="width: 100%; border: none;"> <tr> <td style="text-align: center;">1405 bp</td> <td style="text-align: center;"><i>3'UTR</i> 732 bp</td> </tr> <tr> <td style="text-align: center;"><i>promoter::tag::dpy-10 site</i></td> <td></td> </tr> </table>	1405 bp	<i>3'UTR</i> 732 bp	<i>promoter::tag::dpy-10 site</i>		1		
1405 bp	<i>3'UTR</i> 732 bp							
<i>promoter::tag::dpy-10 site</i>								
<i>eft-3p</i> Chr. V	<table style="width: 100%; border: none;"> <tr> <td style="text-align: center;">682 bp</td> <td style="text-align: center;"><i>tag::dpy-10 site::3'UTR</i> 836 bp</td> </tr> <tr> <td style="text-align: center;"><i>promoter</i></td> <td></td> </tr> </table>	682 bp	<i>tag::dpy-10 site::3'UTR</i> 836 bp	<i>promoter</i>		1		
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<i>promoter</i>								

Figure S1. Templates used to generate SKI LODGE lines. SKI LODGE cassettes were introduced into intergenic regions on different chromosomes. Table shows templates that were used to insert SKI LODGE cassettes, and the number of CRISPR/Cas9 edits required to make the final line.