

**Table S1** chiRNA sequences used to target *yellow* and *rosy*

<b>Name</b>	<b>Target Sequence + PAM</b>	<b>Strand</b>	<b>Cleavage site</b>
YE1	GCGATATAGTTGGAGCCAGCTGG	Sense	+ 97 bp
Y5'	GGTTCAGTGTTCCGGTAATCAGG	Antisense	- 307 bp
Y3'	GGTAAACATAATCCTACACCGG	Sense	+ 4,336 bp
R1	GCACTTCACGATGTCTAACTCGG	Sense	+ 8 bp
R2	GATCCGCAACGTCGCCTGTTTGG	Sense	+ 1,843 bp

Sequences of the five different chiRNAs used to disrupt *yellow* and *rosy*. Target strand orientation is relative to the targeted gene. The site of the Cas9-generated DSB is indicated relative to the ATG translational start site of *yellow* or *rosy* (both genes have a single translational start site).