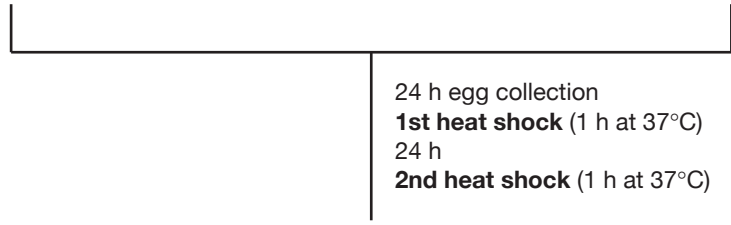


$\frac{y}{w}$; $\frac{p\{MtnBgen-gen\}}{CyO}$; $\frac{mus309^{D3}}{TM6B y^+}$ ♂♂ **X** w ; $p\{v+ 70I-Scel\}$; $\frac{mus309^{D2}}{TM2 y^+}$ ♀♀



blm -/-

$\frac{w}{w}$; $\frac{p\{MtnBgen-gen\}}{p\{v+ 70I-Scel\}}$; $\frac{mus309^{D3}}{mus309^{D2}}$ ♂ **X** $y w$ ♀♀ (on 500 μM CuSO₄)

blm +/-

$\frac{w}{w}$; $\frac{p\{MtnBgen-gen\}}{p\{v+ 70I-Scel\}}$; $\frac{mus309^{D3}}{TM2 y^+}$ ♂ **X** $y w$ ♀♀ (on 500 μM CuSO₄)

blm +/+

$\frac{w}{w}$; $\frac{p\{MtnBgen-gen\}}{p\{v+ 70I-Scel\}}$; $\frac{TM6B y^+}{TM2 y^+}$ ♂ **X** $y w$ ♀♀ (on 500 μM CuSO₄)

Figure S2
Crossing scheme for SSA analysis in blm mutant flies

For the investigation of SSA in *blm* mutants, tester constructs that are located on the 2nd chromosome were analyzed. All constructs were inserted with the help of P-elements. The tester construct transgene *p{MtnBgen-gen}* is marked with *w+*. The ratio of flies with EGFP positive abdomen per *w+* flies among the offspring was determined in all analysis tubes of the final cross for each genotype. Homozygous *blm* mutant genotypes are indicated in red. Identical analysis was also done for *p{MtnBgen*-gen}* and *p{MtnBcDNA-gen}*.