

SUPPLEMENTAL MATERIAL

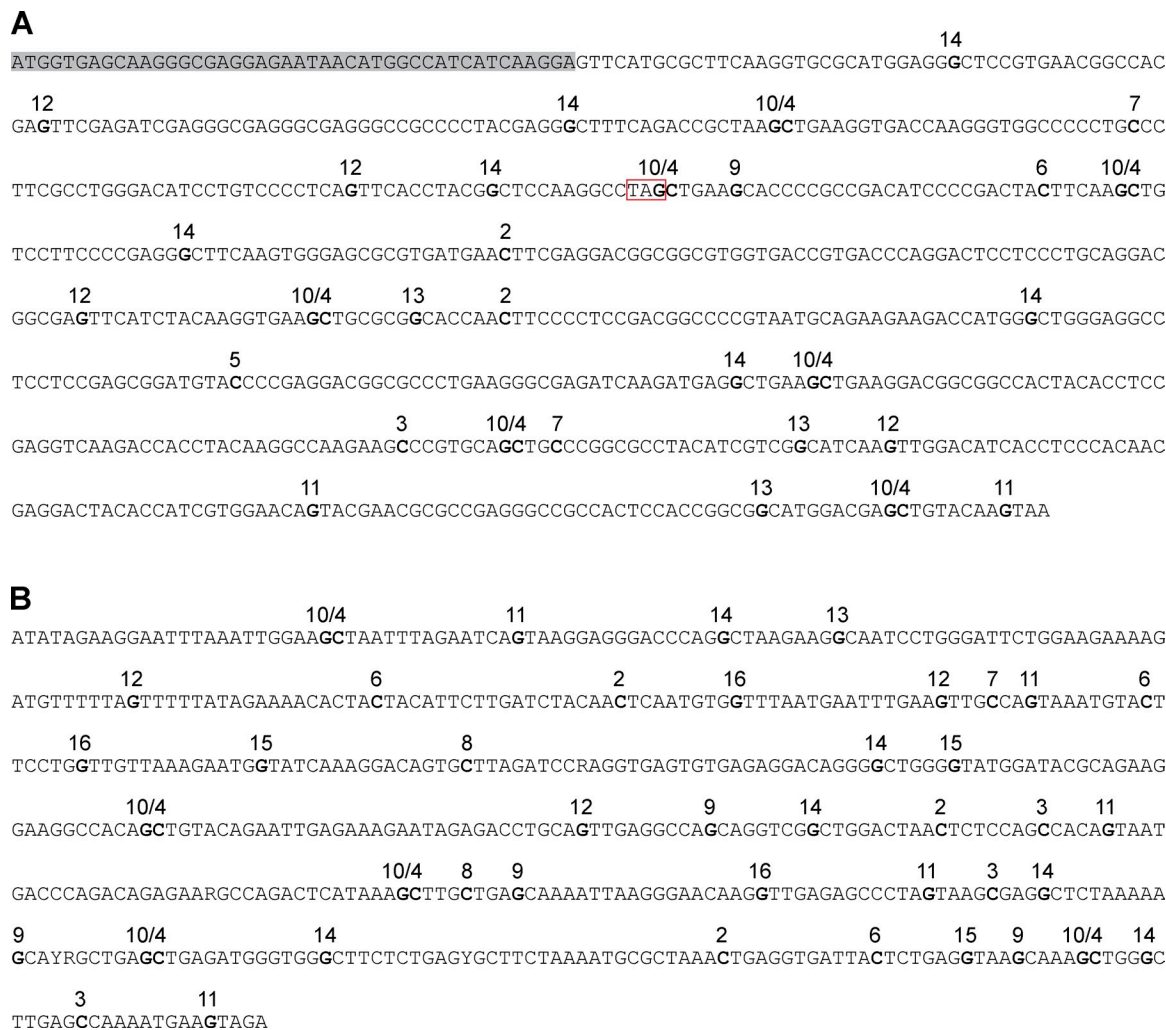
Pérez-Durán et al., <http://www.jem.org/cgi/content/full/jem.20112253/DC1>

Figure S1. mOrange^{STOP} and S μ sequences. (A) mOrange^{STOP} coding sequence. A stop codon was introduced at positions 230–233 (red box). Shaded sequence is not included in the mutation analyses. (B) PCR amplified S μ sequence analyzed by NGS. Numbers from 1 to 16 above both sequences indicate the cytosines and guanines in WRCY/RGYW hotspots as follows: AACC, AACT, AGCC, AGCT, TACC, TACT, TGCC, TGCT, AGCA, AGCT, AGTA, AGTT, GGCA, GGCT, GGTA, and GGTT (analyzed cytosines and guanines are underlined).

Tables S1 and S2 are also provided as Excel files.