

SUPPLEMENTAL MATERIAL

Saribasak et al., <http://www.jem.org/cgi/content/full/jem.20112234/DC1>



Figure S1. Location of tandems in the J_H4 intron. All J_H4 sequences that contain tandem mutations, highlighted in yellow, are aligned. WGCW hotspots are highlighted in the germline sequence in blue. $Pol\zeta^{+/+} Pol\eta^{-/-}$ and $Pol\zeta^{+/-} Pol\eta^{-/-}$ sequences are shown to base 370, as no tandems were found in bases 371–492. $Ung^{-/-}$ sequence data were only available to base 368. Wild-type sequences are displayed through base 492 to show all tandems. In wild-type sequence 12, bases 315 and 316 are not considered a tandem as base 316 is an insertion. For the two triple tandems, the first and second bases were used for the spectra analysis. Dashes represent deletions or gaps corresponding to insertions in another sequence.