

Supplementary Methods

To determine whether species differed significantly in the extent of restorative editing, Fisher's exact tests were performed to compare observed levels of restorative editing for each species pair (figure 1). A sequential Bonferroni correction used to account for multiple testing.

To predict whether an editing site within the *Octopus bimaculoides* dataset is likely to be restorative based on the frequency of editing at that site ("Frequency") and the extent of phylogenetic conservation with other cephalopods ("Conservation"), a logit model was implemented with the glm function in R, using the following command:

```
glm (Restorative ~ Conservation + Frequency, family = "binomial")
```

Estimates of the percent of transcripts that are edited at a given site in *O. bimaculoides* were taken from the original study [14], phylogenetic conservation was defined based on four different levels (see main text).

Table S1. Number of editing sites remaining after successive filters.

| Species | Nonsynonymous Edit Sites | Mapped to Outgroups | Ancestral State Inferred | Matches Edited or Unedited State |
|--|--------------------------|---------------------|--------------------------|----------------------------------|
| <i>Drosophila melanogaster</i> | 461 | 272 | 172 | 160 |
| <i>Homo sapiens</i> | 779 | 310 | 253 | 146 |
| <i>Octopus bimaculoides</i> | 50079 | 33523 | 15590 | 12903 |
| <i>Fusarium graminearum</i> ¹ | 15791 | 12064 | 5996 | 5129 |
| <i>Arabidopsis thaliana</i> | 346 | 301 | 226 | 199 |

¹*Fusarium graminearum* sites exclude one end of chromosome 1 (beginning with position 9019388) because annotated positions in that region from original study are inconsistent with currently available assembly.