**Table S5** **Nuclear *APN54* sequence diversity statistics.** Nuclear-encoded aminopeptidase (*APN54*) intron sample sizes (*N*, number of haplotypes sequenced), haplotype diversity (*h*), average number of pairwise differences (*k*), nucleotide diversity (*π*), Tajima’s *D*, Fu’s *Fs* statistic, and Ramos-Onsins and Rozas’ *R2*statistic. Standard deviations in parentheses. Boldface indicates statistically significant values. See Table 1 for sample locality abbreviations. NWP: Northwest Pacific; NEP: Northeast Pacific.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Locality | Region | *N* | *h* | *π* | *D* | *Fs* | *R2* |
| ERI | NWP | 9 | 0 | 0 | NA | NA | NA |
| KHO | NWP | 9 | 0.533 (0.172) | 0.0018 (0.0016) | 1.0320 | 1.723 | 0.267 |
| STA | NWP | 8 | 0.429 (0.169) | 0.0015 (0.0013) | 0.4142 | 1.653 | 0.214 |
| PET | NWP | 8 | 0.607 (0.164) | 0.0023 (0.0018) | 0.5846 | 0.723 | 0.210 |
| KOD | NEP | 8 | 0 | 0 | NA | NA | NA |
| COR | NEP | 8 | 0.429 (0.169) | 0.00074 (0.0008) | 0.3335 | 0.536 | 0.214 |
| JUN | NEP | 8 | 0.000 | 0 | NA | NA | NA |