**S3 Table. Conservation among miRNA regions.** Top right in grey: p-values for the generalized linear model used to compare conservation among different miRNA regions. The model takes into account GC content: SNV density ~ GC content + miRNA region. Bottom left in white: p-values for the paired t-test comparing concatenated nucleotide diversity values of each miRNA region. Asterisks indicate p-value < 0.05.

| | Flanking 3’ | Flanking 5’ | Precursor miRNA | Mature miRNA | Seed region |
|---|---|---|---|---|---|
| Flanking 3’ | | 0.678809 | 0.029605* | 2.75E-05* | 0.000151* |
| Flanking 5’ | 0.08245 | | 0.00845* | 4.36E-06* | 2.79E-05* |
| Precursor miRNA | 8.892E-05* | 8.979E-08* | | 0.00867* | 0.030776* |
| Mature miRNA | 1.331E-07* | 6.64E-07* | 0.005981* | | 0.69483 |
| Seed region | 6.203E-05* | 1.149E-06* | 0.007482* | 0.5417 | |