Table S6. Pairwise FST between *A. mexicanus* locations using and not using ENA algorithm with FreeNA.

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| --- |
| **All loci** |
| **Fst not using ENA** | **Fst not using ENA** |
| 0.264312 | 0.26159 |
| **Bootstrap resampling over loci 95% confidence interval** |
| 0.228405 | 0.224525 |
| 0.309007 | 0.305796 |

|  |  |
| --- | --- |
|  | **Per locus** |
| **Locus** | **Fst not using ENA** | **Fst not using ENA** |
| 1 | 0.352492 | 0.353243\* |
| 2 | 0.427306 | 0.419333 |
| 3 | 0.220837 | 0.221221 |
| 4 | 0.240031 | 0.243327 |
| 5 | 0.225407 | 0.212534 |
| 6 | 0.273083 | 0.273921\* |
| 7 | 0.234902 | 0.230129\* |
| 8 | 0.174466 | 0.165282 |
| 9 | 0.256044 | 0.261662\* |
| 10 | 0.263187 | 0.256983\* |

\*Null alleles detected