**Supplemental Table 2:** Summary of molecular diversity for two populations.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Populations | n | No. of haplo. | k(95%CI) | θS | h | π | Tajima’s D | | Fu’s FS | | Mismatch distribution | | |
| D | P | FS | P | τ (95%CI) | θ0 | θ1 |
| Control | 171 | 28 | 7.04  (4.68-10.46) | 0.77 ±0.37 | 0.91  ±0.005 | 2.15  ±1.32 | 3.16 | 0.99 | -13.22 | 0.00 | 2.29 (2.04-2.55) | 0.00 | 999 |
| RA | 201 | 31 | 7.66  (5.14-11.16) | 0.76 ±0.36 | 0.92  ±0.004 | 2.37  ±1.43 | 3.72 | 0.99 | -14.33 | 0.00 | 2.57 (2.31-2.73) | 0.00 | 999 |

Number of individuals (n); number of haplotype (No. of haplo.); average pairwise differences among individuals (*k*); number of segregating sites (*S*); haplotype diversity (*h* ± standard deviation); nucleotide diversity (π ± standard deviation) for each populations. Tajima’s *D* and Fu’s *FS*, corresponding p-value, and mismatch distribution parameter estimates for each population. D Tajima’s D estimate population expansion, Fs Fu’s Fs estimate population expansion. Values for τ, θ0, and θ1 are the age of the expansion, the population size before the expansion, and the population size after expansion, respectively, all expressed in units of mutation time.Significant p<0.05