

Estimators of the Human Effective Sex Ratio

Detect Sex Biases on Different Timescales

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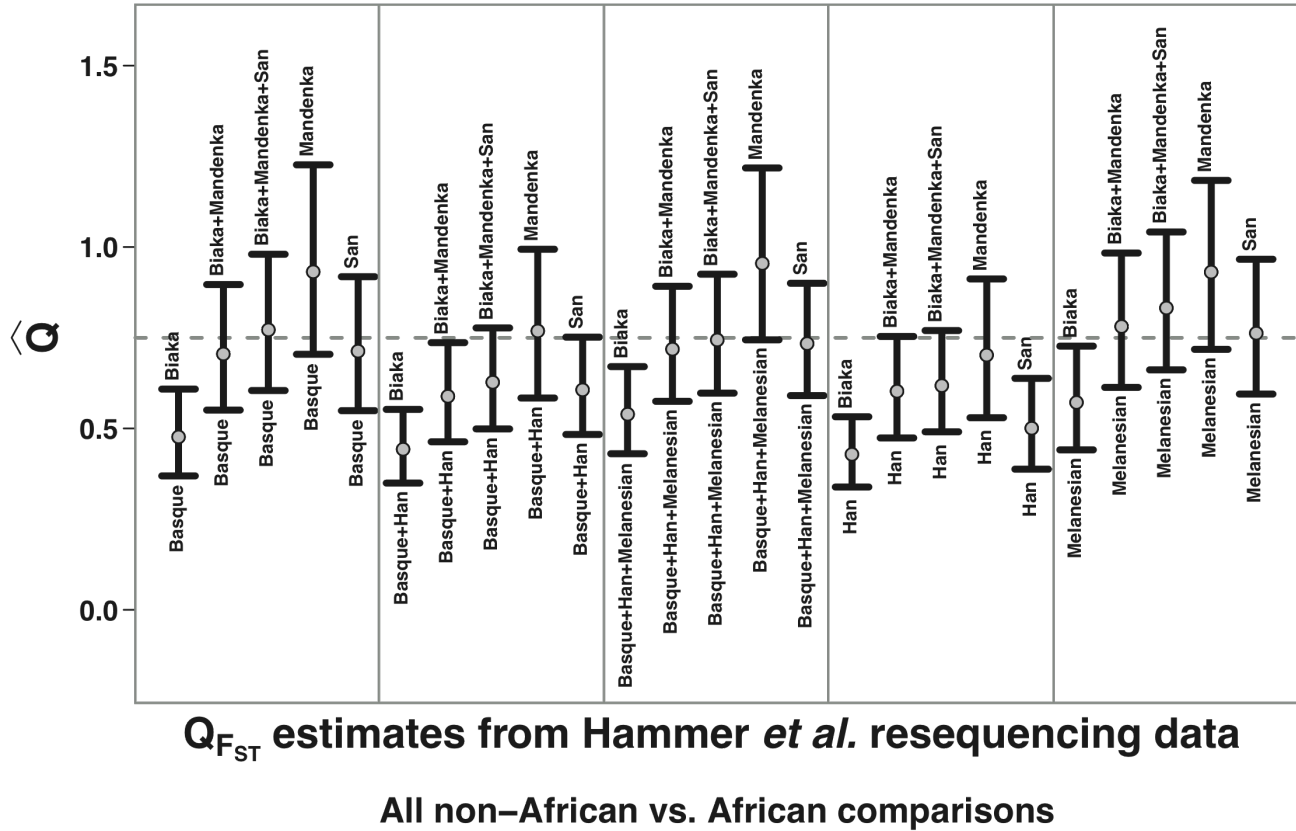
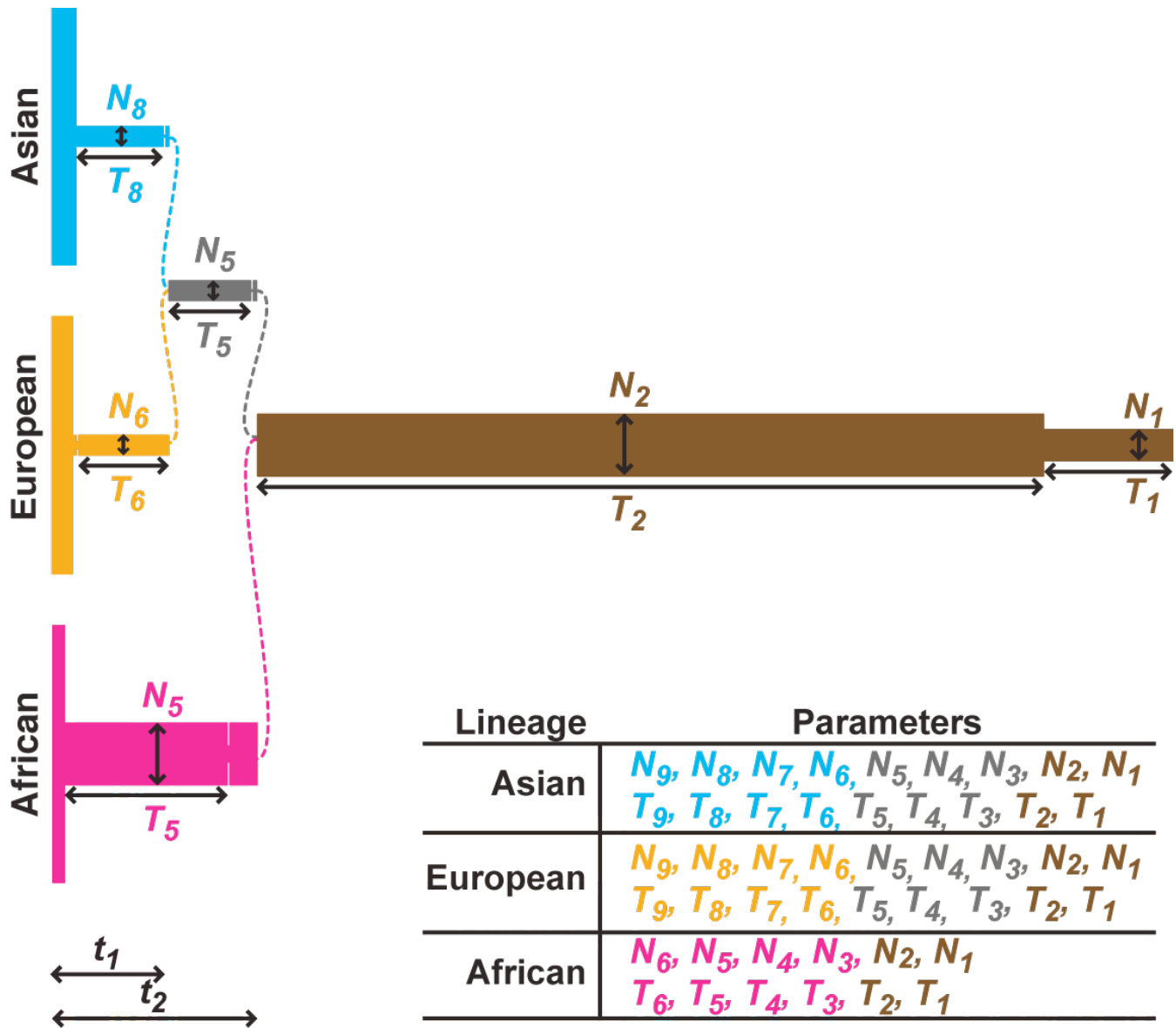


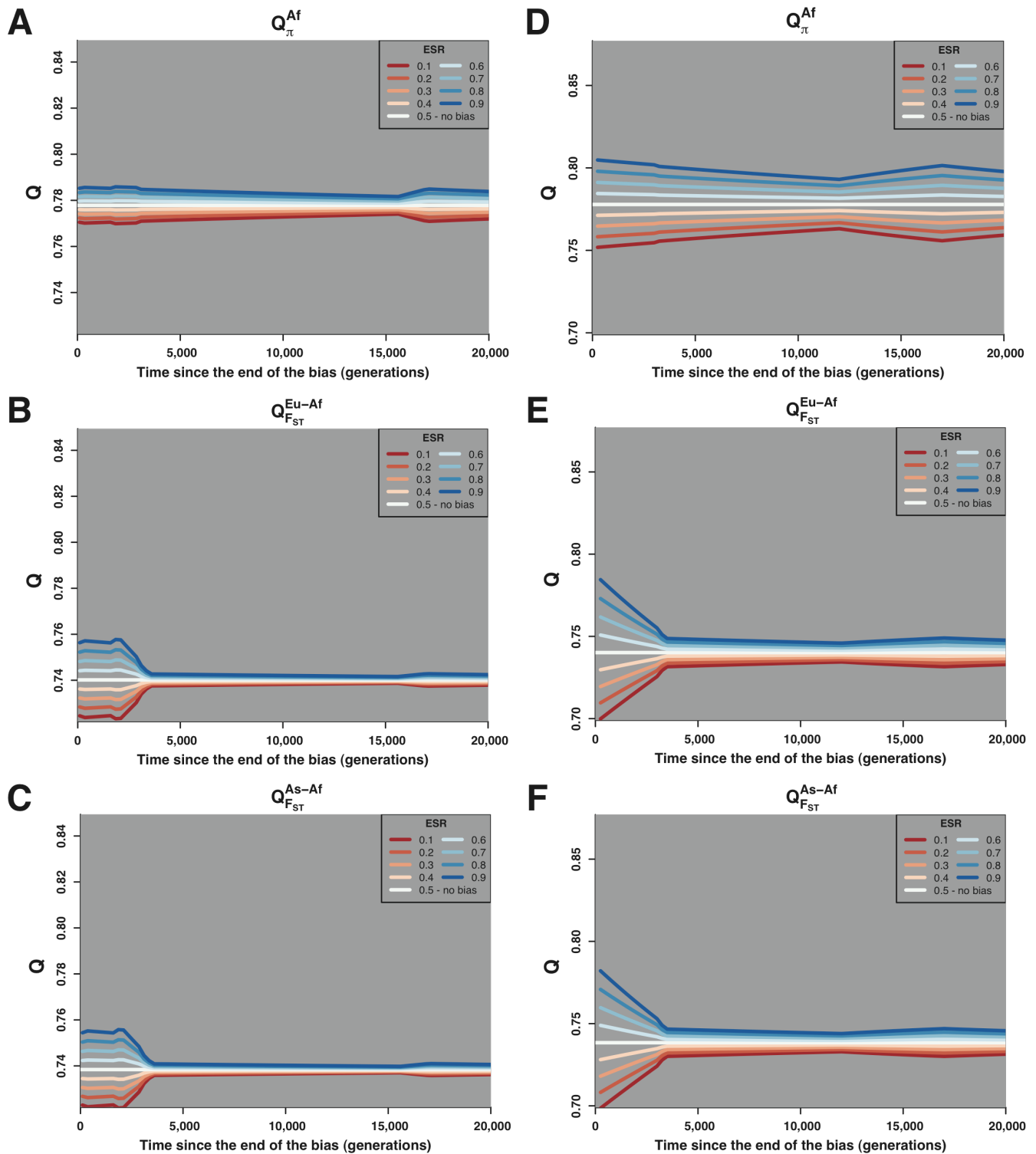
Figure S1. Estimates of  $Q_{FST}$  in the Hammer *et al.* Data Set

Nearly all comparisons between African and non-African populations are below or near the expectation of 0.75. Notable exceptions are that most comparisons to the Mandenka are higher than 0.75, and the Melanesian and Basque comparisons are higher than others. The x-axis separates the different comparisons. The two populations being compared are labeled on either end of the black bars. Black bars indicate 95% confidence intervals. The gray dashed line denotes the null expectation of 0.75.



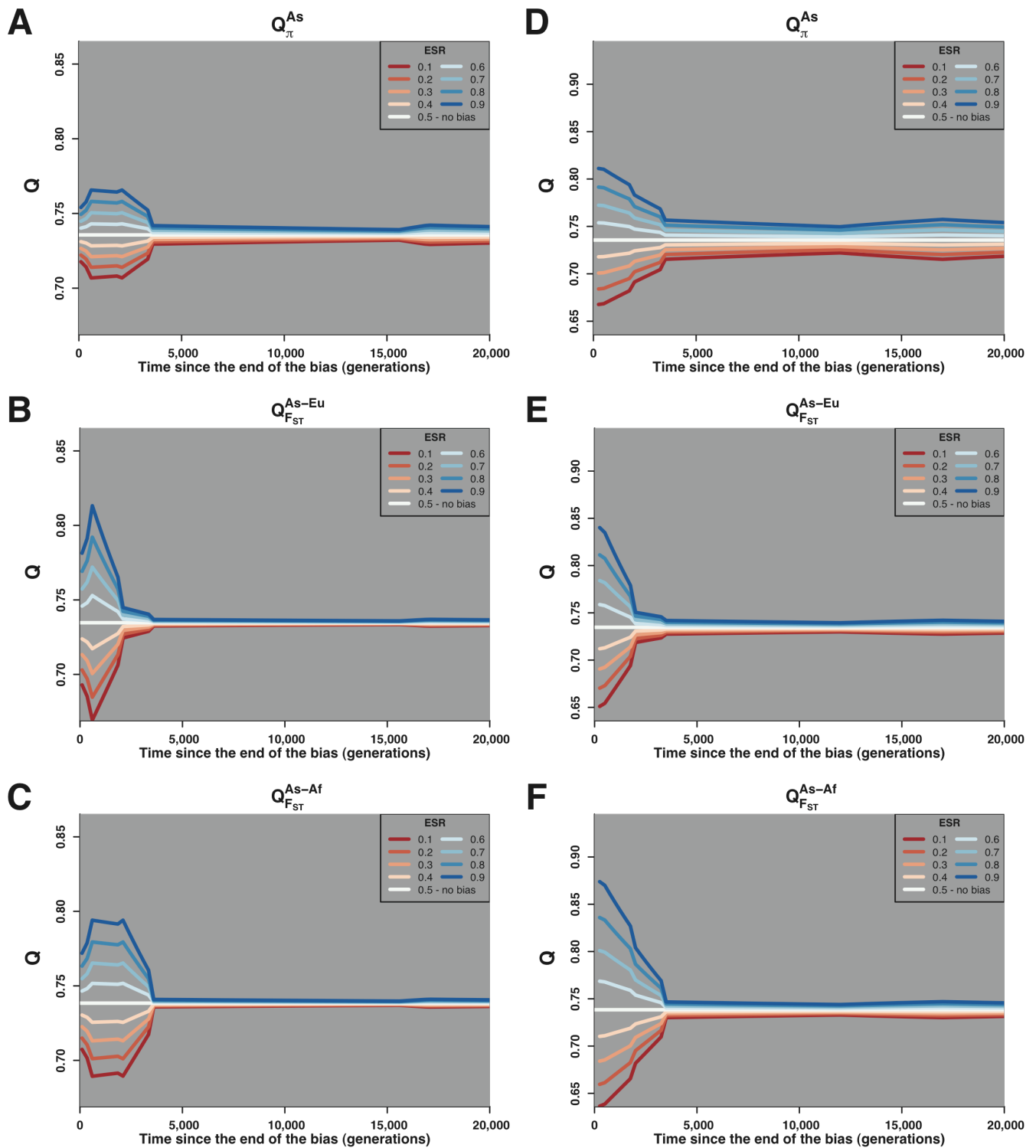
**Figure S2. Coalescent Model of Human Evolution**

Going backwards in time, the modern European (gold) and Asian (blue) populations coalesce to form the ancestral non-African population (gray). The African (pink) and non-African populations coalesce to form the ancestral human population (brown). The height of each section is proportional to the population size at that time, as taken from a best-fit model of human evolution (Schaffner *et al.* 2005). The length of each section is proportional to the number of generations spent at that population size. The coalescent history of each of the three populations is described by a set of parameters shown in the table at the bottom right. Each pair of  $N$  and  $T$  parameters corresponds to a single section of the coalescent model. Colors indicate which section each parameter is describing. Some parameters are labeled for reference. The parameters  $t_1$  and  $t_2$  are the divergence times, in generations, between the Asian & European and non-African & African populations respectively.



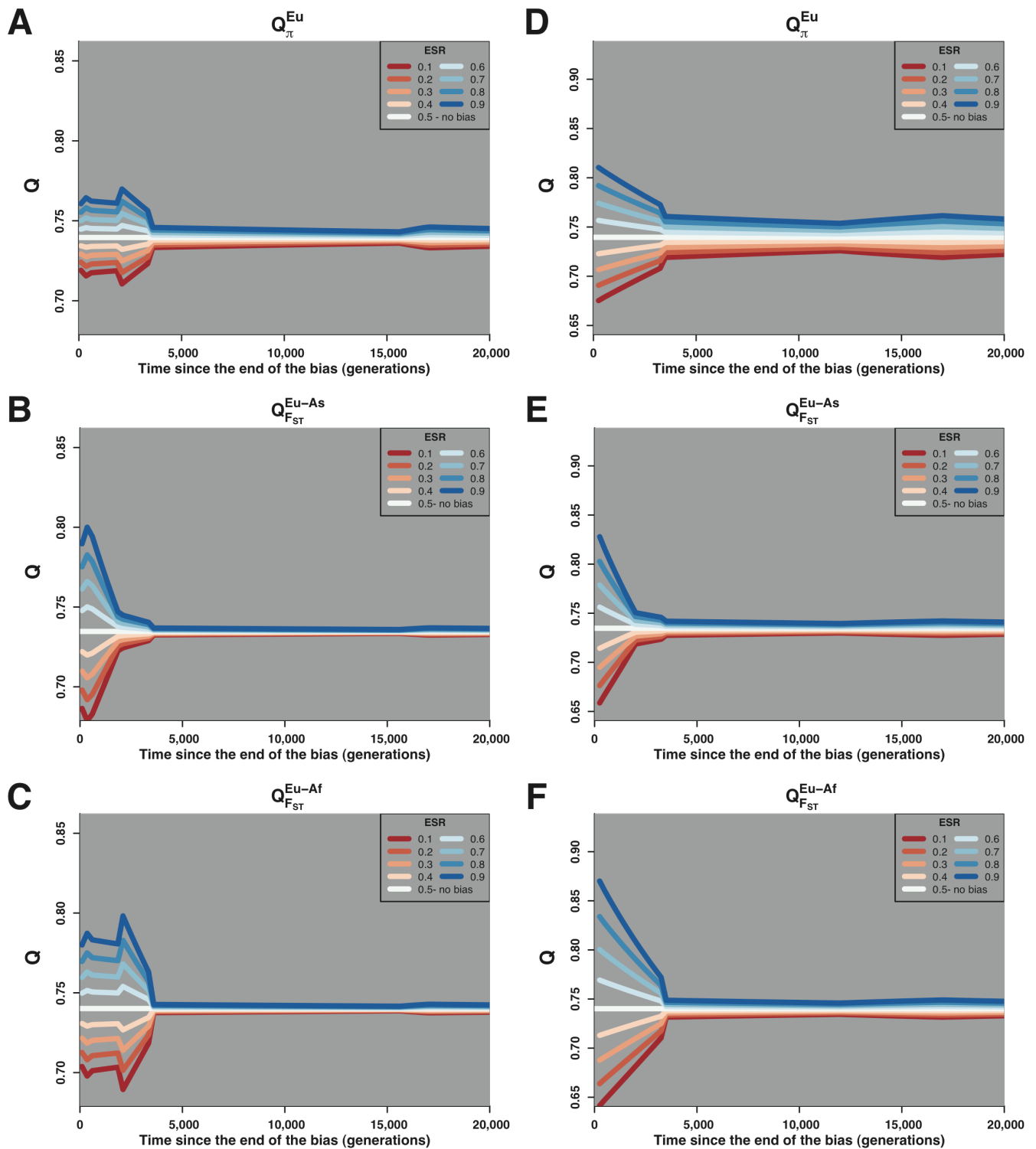
**Figure S3. Varying the Severity of the Sex Bias Introduced into Africans in the Theoretical Model**

A sex bias with the ESR denoted by the line's color was introduced into the African lineage and ended  $y$  generations ago. Each panel shows the indicated  $Q$  estimator. (A – C) A bias lasting 1,400 generations. (D – F) A bias lasting 5,000 generations.



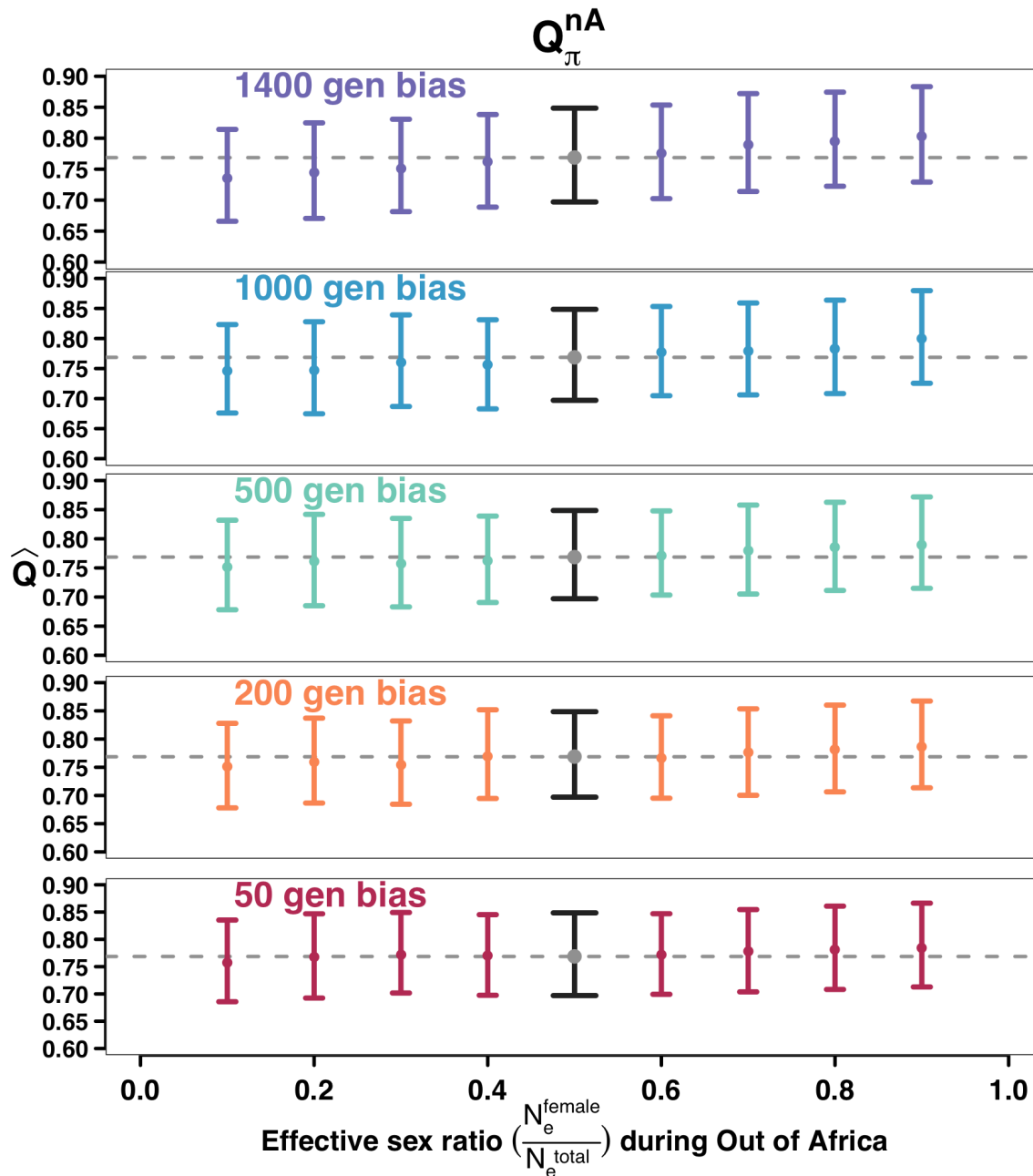
**Figure S4. Varying the Severity of the Sex Bias Introduced into Asians in the Theoretical Model**

A sex bias with the ESR given by the line's color was introduced into the Asian lineage and ended  $y$  generations ago. Each panel shows the indicated  $Q$  estimator. (A – C) A bias lasting 1,400 generations. (D – F) A bias lasting 5,000 generations.



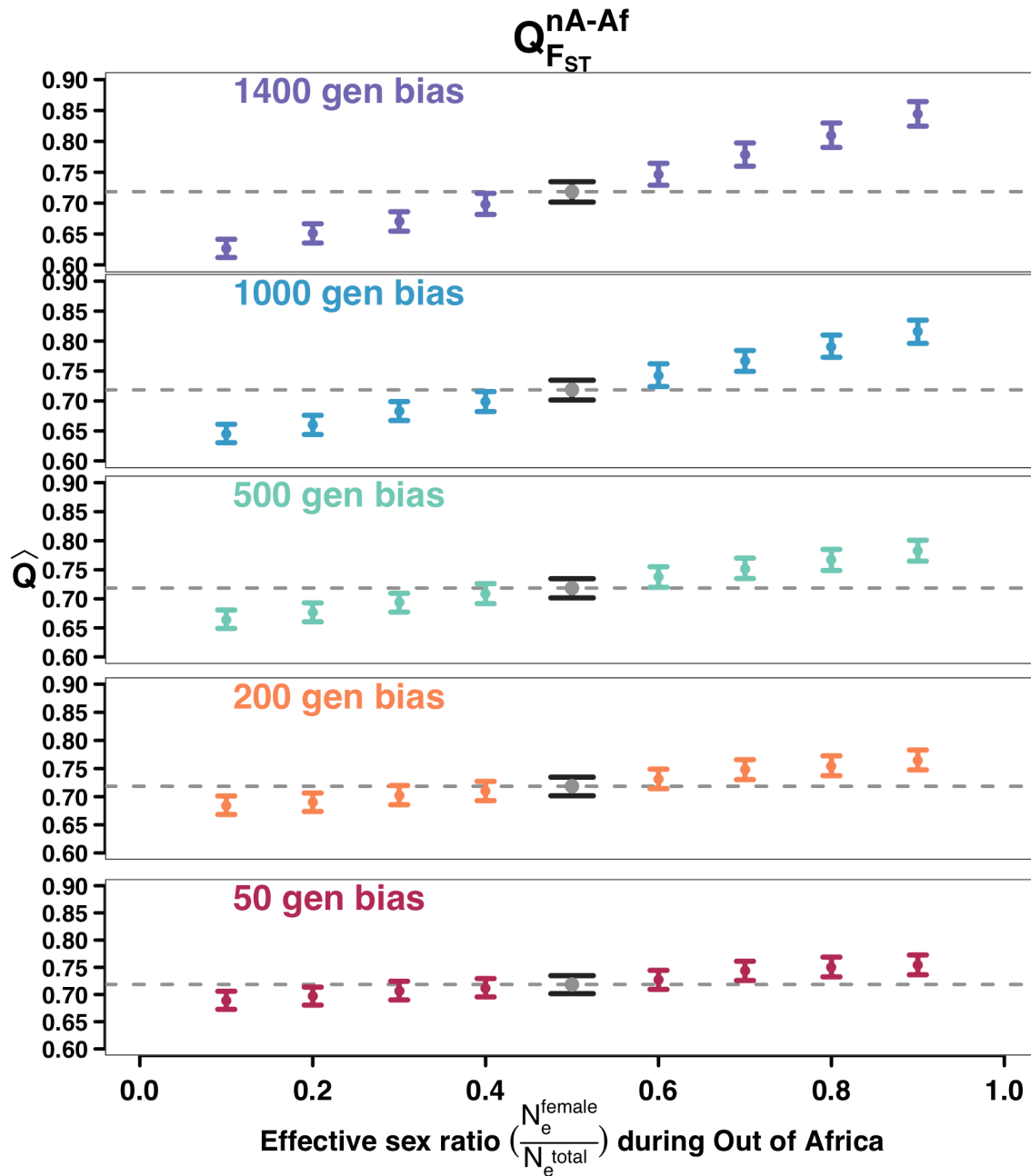
**Figure S5. Varying the Severity of the Sex Bias Introduced into Europeans in the Theoretical Model**

A sex bias with the ESR given by the line's color was introduced into the European lineage and ended  $y$  generations ago. Each panel shows the indicated  $Q$  estimator. (A – C) A bias lasting 1,400 generations. (D – F) A bias lasting 5,000 generations.



**Figure S6.  $Q_\pi$  in Non-Africans Does Not Detect Recent Sex Biases Associated with the Out of Africa Dispersal**

A bias is introduced at the start of the Out of Africa bottleneck event and persists for one of five durations (indicated by different colors; measured in generations). The bias introduced is indicated on the x-axis, measured as the proportion of females in the population. Bars indicate the 95% confidence interval around the point estimate. Black bars and gray points display the estimate of  $Q$  under no sex bias, which is higher than 0.75 due to the effects of the bottleneck. The gray dashed line corresponds to the corrected expectation when there is no sex bias.



**Figure S7. Using  $F_{ST}$  to Estimate  $Q$  for the Comparison of Non-Africans to Africans Detects Recent Sex Biases if They Are Extreme**

A bias is introduced at the start of the Out of Africa bottleneck event and persists for one of five durations (indicated by different colors; measured in generations; includes the bottleneck). The bias introduced is indicated on the x-axis, measured as the proportion of females in the population. Bars indicate the 95% confidence interval around the point estimate. Black bars and gray points display the estimate of  $Q$  under no sex bias, which is lower than 0.75 due to the effects of bottlenecks. The gray dashed line is the corrected expectation with no sex bias.

**Table S1. Parameters Used for Demographic Models, Based on Schaffner *et al.* 2005 (Table 1)**

| <i>Parameter</i>   | <i>Value Used</i>      |
|--|------------------------|
| N <sub>e</sub> ancestral <sup>b</sup>                        | 12,500                 |
| N <sub>e</sub> African <sup>b</sup>                          | 24,000                 |
| Time of ancestral expansion within Africa                    | 17,000 <sup>a</sup>    |
| Time of Out of Africa split                                  | 3,500 <sup>a</sup>     |
| N <sub>e</sub> non-African <sup>b</sup>                      | 7,700                  |
| Start time of Out of Africa bottleneck                       | 3,450                  |
| N <sub>e</sub> during Out of Africa bottleneck <sup>b</sup>  | 588                    |
| Duration of Out of Africa bottleneck                         | 50 <sup>a</sup>        |
| Start time of African bottleneck                             | 3,050 <sup>a</sup>     |
| N <sub>e</sub> during African bottleneck <sup>b</sup>        | 6,250                  |
| Duration of African bottleneck                               | 50 <sup>a</sup>        |
| Start time of African expansion due to agriculture           | 200 <sup>a</sup>       |
| Time of European/Asian split                                 | 2,000 <sup>a</sup>     |
| Start time of Asian bottleneck                               | 1,950 <sup>a</sup>     |
| N <sub>e</sub> during Asian bottleneck <sup>b</sup>          | 746                    |
| Duration of Asian bottleneck                                 | 50 <sup>a</sup>        |
| Start time of Asian expansion due to agriculture             | 400 <sup>a</sup>       |
| Start time of European bottleneck                            | 450 <sup>a</sup>       |
| N <sub>e</sub> during European bottleneck <sup>b</sup>       | 2,500                  |
| Duration of European bottleneck                              | 50 <sup>a</sup>        |
| Start time of European expansion due to agriculture          | 350 <sup>a</sup>       |
| Current N <sub>e</sub> in all three populations <sup>b</sup> | 100,000                |
| Gene conversion (initiation prob/bp) <sup>c</sup>            | 4.5 x 10 <sup>-9</sup> |
| Mutation rate  | 1.5 x 10 <sup>-8</sup> |
| Recombination rate <sup>c</sup>                              | 1.3 cM/Mb              |

<sup>a</sup> Time parameters are measured in generations before present

<sup>b</sup> These population sizes were scaled by 0.75 for the X chromosome demographic models

<sup>c</sup> These parameters are used only in the model for the coalescent simulations



**Table S2. Commands for Basic Simulation Models in ms**

Autosomal resequence data, no sex bias:

```
ms 360 8000 -t 30.00 -r 44.791040 5000 -I 3 120 120 120 -ej 0.005000 3 2 -ej 0.008750 2 1 -en  
0.000500 1 0.240000 -en 0.001000 3 0.077000 -en 0.000875 2 0.077000 -en 0.001125 2 0.077000 -en  
0.001000 2 0.025000 -en 0.004875 3 0.077000 -en 0.004750 3 0.007460 -en 0.007500 1 0.062500 -en  
0.008500 2 0.005880 -en 0.007625 1 0.240000 -en 0.008625 2 0.077000 -en 0.042500 1 0.125000
```

X-chromosomal resequence data, no sex bias:

```
ms 270 8000 -t 22.50 -r 16.796640 5000 -I 3 90 90 90 -ej 0.006667 3 2 -ej 0.011667 2 1 -en 0.000667 1  
0.240000 -en 0.001333 3 0.077000 -en 0.001167 2 0.077000 -en 0.001500 2 0.077000 -en 0.001333 2  
0.025000 -en 0.006500 3 0.077000 -en 0.006333 3 0.007460 -en 0.010000 1 0.062500 -en 0.011333 2  
0.005880 -en 0.010167 1 0.240000 -en 0.011500 2 0.077000 -en 0.056667 1 0.125000
```

Autosomal SNP data, no sex bias:

```
ms 360 1500000 -s 1 -I 3 120 120 120 -ej 0.005000 3 2 -ej 0.008750 2 1 -en 0.000500 1 0.240000 -en  
0.001000 3 0.077000 -en 0.000875 2 0.077000 -en 0.001125 2 0.077000 -en 0.001000 2 0.025000 -en  
0.004875 3 0.077000 -en 0.004750 3 0.007460 -en 0.007500 1 0.062500 -en 0.008500 2 0.005880 -en  
0.007625 1 0.240000 -en 0.008625 2 0.077000 -en 0.042500 1 0.125000
```

X-chromosomal SNP data, no sex bias:

```
ms 270 1500000 -s 1 -I 3 90 90 90 -ej 0.006667 3 2 -ej 0.011667 2 1 -en 0.000667 1 0.240000 -en  
0.001333 3 0.077000 -en 0.001167 2 0.077000 -en 0.001500 2 0.077000 -en 0.001333 2 0.025000 -en  
0.006500 3 0.077000 -en 0.006333 3 0.007460 -en 0.010000 1 0.062500 -en 0.011333 2 0.005880 -en  
0.010167 1 0.240000 -en 0.011500 2 0.077000 -en 0.056667 1 0.125000
```