

FILE S1

ms commands for demographic models used in this manuscript**TRUE demographic model for Pop A, when $N_{AA} = 0.1N_A$:**

```
./ms 40 100000 -t 20.8 -r 20.8 52000 -I 3 0 0 40 0 0 -en 0 2 2 -en 0 3 0.2 -cs 5e-4 3 0.8 -ej 5e-4 3 2 -ej 5e-4 4 1 -en 0.0275 1 0.055 -
en 0.0375 1 1 -en 0.06 2 1 -ej 0.1 2 1
```

TRUE demographic model for Pop AA, when $N_{AA} = 0.1N_A$:

```
./ms 40 100000 -t 20.8 -r 20.8 52000 -I 3 0 0 40 0 -en 0 2 2 -en 0 3 0.2 -cs 5e-4 3 0.8 -ej 5e-4 3 2 -ej 5e-4 4 1 -en 0.0275 1 0.055 -
en 0.0375 1 1 -en 0.06 2 1 -ej 0.1 2 1
```

EST demographic model for Pop A when $N_{AA} = 0.1N_A$:

```
./ms 40 100000 -t 41.6 -r 41.6 52000 -eN 0.0275 0.5
```

EST demographic model for Pop AA when $N_{AA} = 0.1N_A$:

```
./ms 40 100000 -t 39.52 -r 39.52 52000 -eN 0.05 0.55
```

TRUE demographic model for Pop A, when $N_{AA} = N_A$:

```
./ms 40 100000 -t 20.8 -r 20.8 52000 -I 3 0 0 40 0 0 -en 0 2 2 -en 0 3 2 -cs 5e-4 3 0.8 -ej 5e-4 3 2 -ej 5e-4 4 1 -en 0.0275 1 0.055 -
en 0.0375 1 1 -en 0.06 2 1 -ej 0.1 2 1
```

TRUE demographic model for Pop AA, when $N_{AA} = N_A$:

```
./ms 40 100000 -t 20.8 -r 20.8 52000 -I 3 0 0 40 0 -en 0 2 2 -en 0 3 2 -cs 5e-4 3 0.8 -ej 5e-4 3 2 -ej 5e-4 4 1 -en 0.0275 1 0.055 -
en 0.0375 1 1 -en 0.06 2 1 -ej 0.1 2 1
```

EST demographic model for Pop A when $N_{AA} = N_A$:

```
./ms 40 100000 -t 41.6 -r 41.6 52000 -eN 0.0275 0.5
```

EST demographic model for Pop AA when $N_{AA} = N_A$:

```
./ms 40 100000 -t 45.76 -r 45.76 52000 -eN 0.03863636 0.45
```

Growth model estimated from the NIEHS YRI population in Lohmueller *et al.* (2010):

```
./ms 20 10000 -s $$ -r tbs $LENGTH_SEQ <$RHO_FILE -eN 0.09259575 0.5
```

Growth model estimated from the NIEHS AA population in Lohmueller *et al.* (2010):

```
./ms 20 10000 -s $$ -r tbs $LENGTH_SEQ <$RHO_FILE -eN 0.08276125 0.46,
```

where “\$\$” is the observed number of segregating sites for the locus, “\$LENGTH_SEQ” is the number of bases sequenced for the locus, and “\$RHO_FILE” is a file with the values of ρ to use.