**SUPPLEMENTARY MATERIAL**

**X-linked *MTMR8* diversity and evolutionary history of Sub-Saharan populations.**

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*n* – number of chromosomes

S – number of segregating sites (SNPs)

*k* – number of haplotypes

*G* – gene (haplotype) diversity

(1-*G*) – haplotype homozygosity

Θ – estimator of population mutation rate 4*Nµ* (*N* – effective population size; *µ* - mutation rate per DNA segment per generation)

Θ*π* – estimate from nucleotide diversity ([Tajima 1983](#_ENREF_13))

Θ*s* – estimate from the number of segregating sites ([Watterson 1975](#_ENREF_15))

Θ*H* – estimate from frequency of the derived alleles ([Fay, Wu 2000](#_ENREF_6))

Θ*ML* – maximum likelihood estimate by *genetree* ([Griffiths, Tavare 1994](#_ENREF_8))

Θ*k* - estimate from the number of haplotypes ([Ewens 1972](#_ENREF_4))

Θ*G* – estimator from haplotype diversity ([Zouros 1979](#_ENREF_18); [Chakraborty, Weiss 1991](#_ENREF_3))

Neutrality tests:

*D* - Tajima’s *D* statistic ([Tajima 1989](#_ENREF_14))

*Fs* – Fu’s *Fs* statistic ([Fu 1997](#_ENREF_7))

*H* – Fay and Wu’s *H* statistics ([Fay, Wu 2000](#_ENREF_6); [Zeng et al. 2006](#_ENREF_17))

Ewens- Watterson homozygosity test ([Watterson 1978](#_ENREF_16))

Slatkin exact test ([Slatkin 1994](#_ENREF_11); [Slatkin 1996](#_ENREF_12))

Chakraborty population amalgamation test ([Chakraborty 1990](#_ENREF_2))

Estimations were obtained using Arlequin V. 3.0 package ([Excoffier, Laval, Schneider 2005](#_ENREF_5)), DnaSP V.5 ([Librado, Rozas 2009](#_ENREF_10)) and *genetree*([Griffiths, Tavare 1994](#_ENREF_8))

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