

analysis herein, because they are based on either completely sequenced genomes or random sequencing projects.

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dent of *S*, and in any event, is unlikely to add more than 0.01 to individual estimates of *S*. Thus, the impact of such error on our statistical analyses should be negligible.

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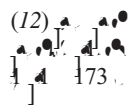
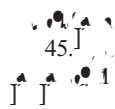
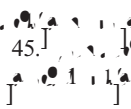
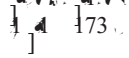
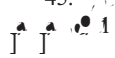

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The Genetic Legacy of Paleolithic *Homo sapien* *sapien* in Extant Europeans: A Y Chromosome Perspective

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$170 \approx 14 \cdot 12 \cdot 2 \cdot 8 \approx 19 \cdot 10$,
 $115,000 \approx 20,000$ (13). A
 $(17,000)$ (22, 23).
 $35 (14), 172 (19), 89$
 $(10), 201 (11)$.
 49
 $12 \cdot 2 (10)$
 $9, 10, 12 \cdot 2 \cdot 8$
 $11, 12 \cdot 2 \cdot 8$
 $11, 49, 8, 10$
 $16 (19)$
 $9, 10$
 11 . I. B.

$14 \approx 14 \cdot 12 \cdot 2 \cdot 8 \approx 19 \cdot 10$,
 $115,000 \approx 20,000$ (13). A
 $(17,000)$ (22, 23).
 $35 (14), 172 (19), 89$
 $(10), 201 (11)$.
 49
 $12 \cdot 2 (10)$
 $9, 10, 12 \cdot 2 \cdot 8$
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 $16 (19)$
 $9, 10$
 11 . I. B.

$1(19)$. A.
 D . A.
 (6)

... 35... D... C...
... 178,
95% A ... ~4000 ...

(14). ... A ... 178 ...
... (C)

3. ...
C ... A / 178 ...
B ...

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