

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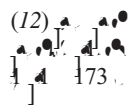
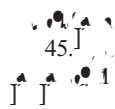
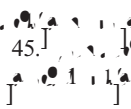
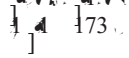
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The Genetic Legacy of Paleolithic *Homo sapien* *sapien* in Extant Europeans: A Y Chromosome Perspective

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(12)  (15) 
45. 
73. 

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

~ 1000 1-2000 3000 4000 5000 6000 7000 8000 9000 10000