

Supporting Information Figure S2

Revised timeline and distribution of the earliest diverged human maternal lineages in southern Africa

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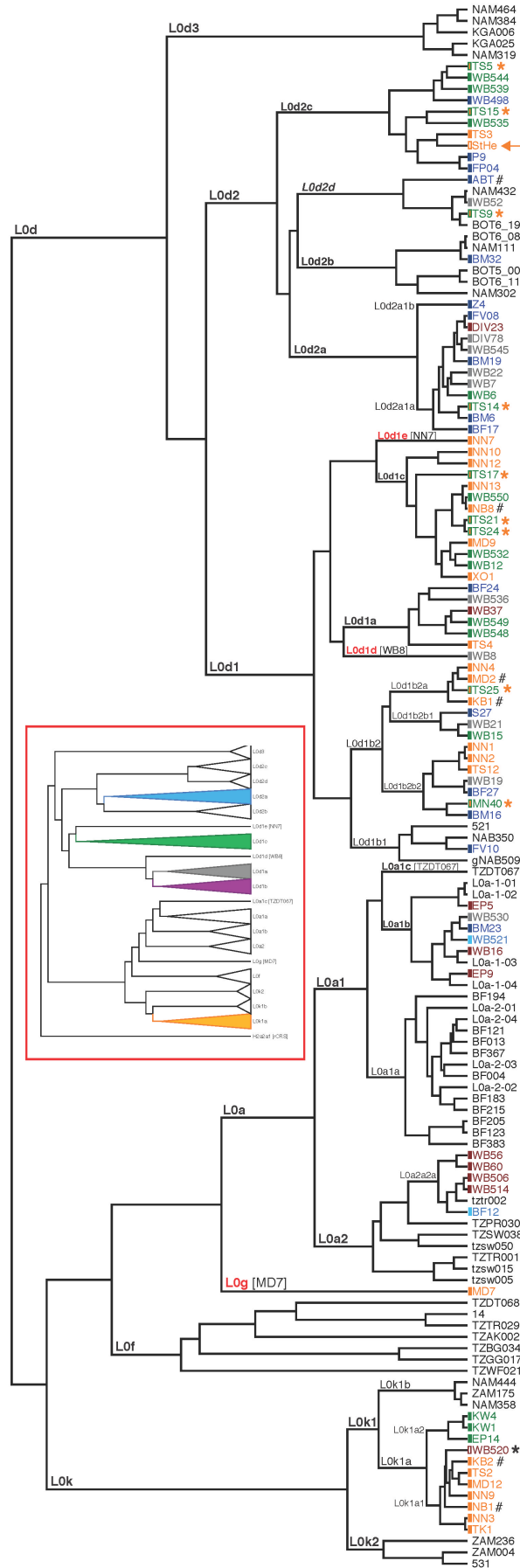


Fig. S2. Phylogeny of 139 complete mitochondrial genomes depicting the earliest diverged maternal lineages, using 15,447 bases of the coding region. The 77 novel southern African mitochondrial genomes sequenced in this study included 32 L0d1, 24 L0d2, 9 L0k1, 1 L0g and 11 L0a. Population representations are colour coded, by tip labels, as defined in Figure 1, with cultural (fill colour of rectangles) and linguistic (outline colour of rectangles) classifications indicated by rectangles next to tip labels. Co-classifications are indicated by asterisks (*); e.g. Hai//om are co-classified as culturally Bushmen (orange filled rectangles) and linguistically Nama-speakers (green rectangle outline). The previously published Khoesan skeleton assigned to L0d2c (Morris *et al.* 2014) is indicated by orange arrow. Six previously published mtDNA (Schuster *et al.* 2010) are indicated by hash marks (#). All other publicly obtained mtDNA are shown in black. Mitochondrial haplogroups according to PhyloTree Build 16 (Van Oven M and Kayser 2009) are labeled in 'black', new haplogroups proposed in previous studies are represented in 'black italic', and new haplogroups proposed in the current study are presented in 'red', noting that L0d1e could be L0d1c4. Subclades represented by single mtDNA have sample identifiers provided in square brackets ([]). The simplified tree in the inset (red box) shows the phylogeny inferred from the expanded dataset of 603 genomes; clades are collapsed with each triangle representing the relative diversity of the corresponding haplogroups and subclades.