

Supplementary Data 10. Phylogenetic tree based on SNPs mapping to the mitochondrial genome of Somali wild ass and domestic donkeys. Sample names in gold color represent North Africa & Eurasia donkeys while sample names in red represent Tropical Africa donkeys. A total of 953 mitochondrial SNPs were used to construct the tree. FigTree v1.4.4 (<http://tree.bio.ed.ac.uk/software/figtree/>) was used to display the tree. To make the tree more readable, the branches of the tree were transformed to be cladogram. BEAST2 software (90) was applied in this phylogenetic analysis. The parameters for generating the maximum clade credibility (MCC) tree are: HKY for site model, strict clock model for clock model (clock rate = 1), Yule model for tree priors. The phylogenetic tree was generated by Bayesian Markov chain Monte Carlo (MCMC) with 1000 simulations. Statistical support of each node was assessed by MCMC posterior probability indicated by the number aside each node. The following acronyms have been used: Ke (Kenya), Ch (China), Ni (Nigeria), Ir (Iran), Sp (Spain), Eg (Egypt), Et (Ethiopia), Ti (Tibetan), Au (Australia), and Don (the European donkey).

