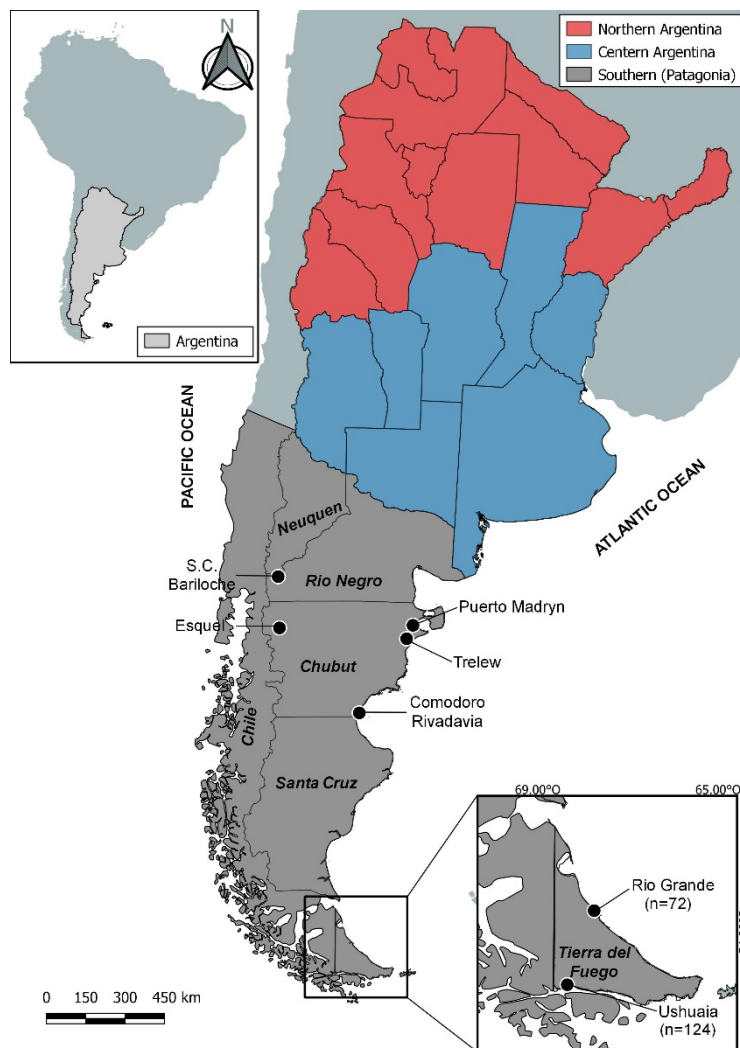
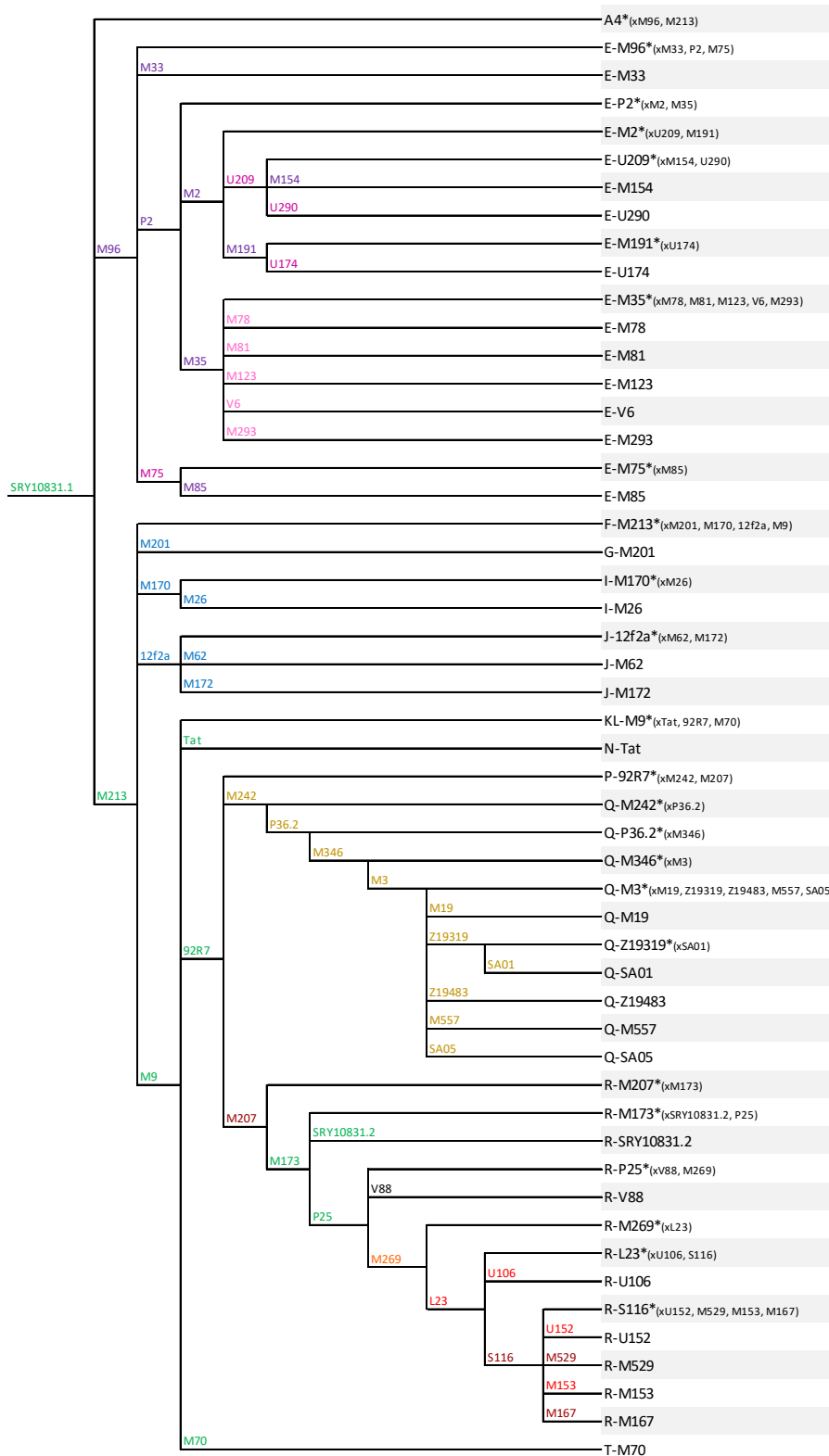


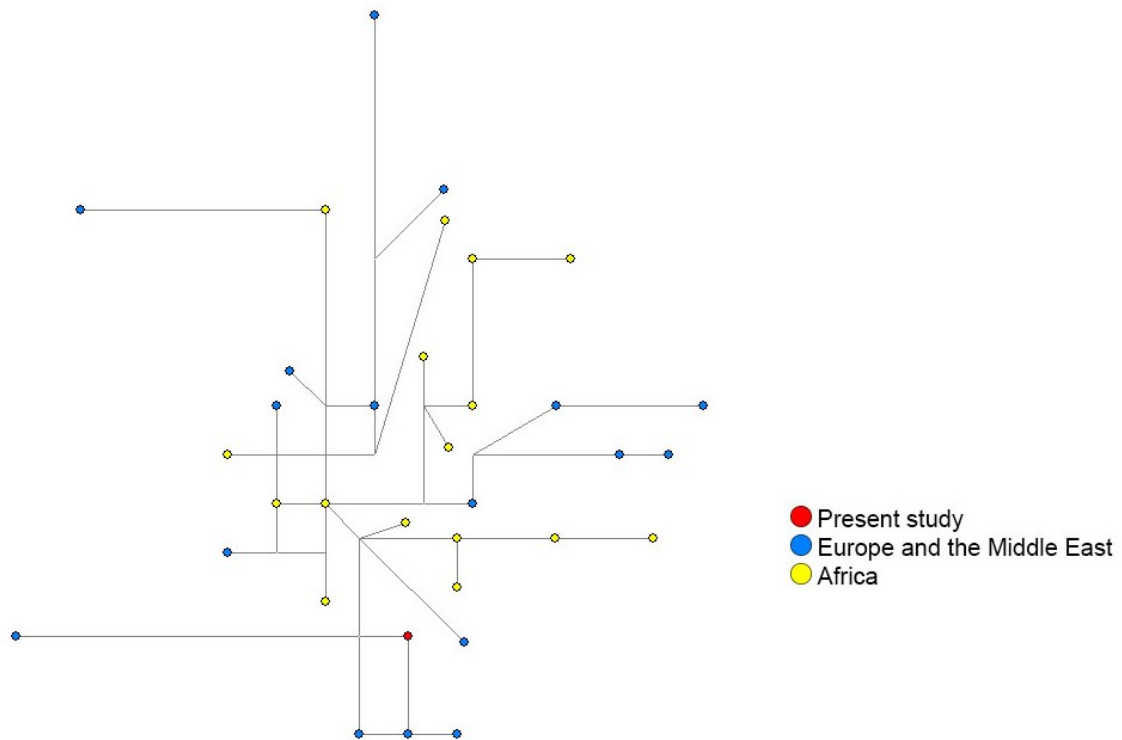
SUPPLEMENTARY FIGURES



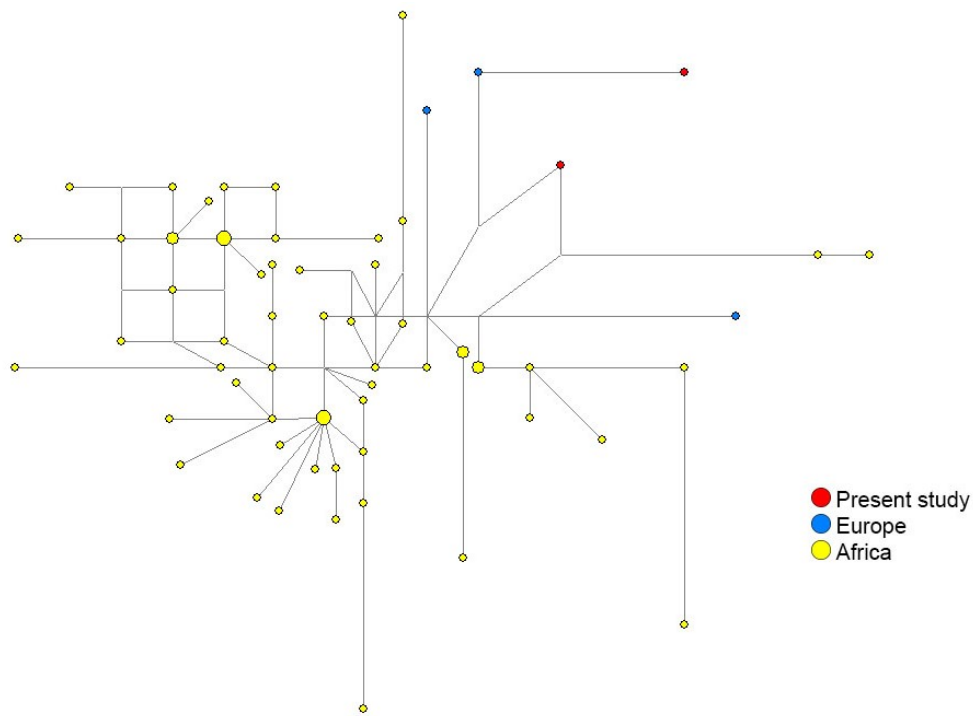
Supplementary Figure S1. Map of Argentina and the Southern tip of the American continent. The cities where the sample collections took place – Río Grande and Ushuaia - are marked in the map indicating the number of individuals participating in this study for each city.



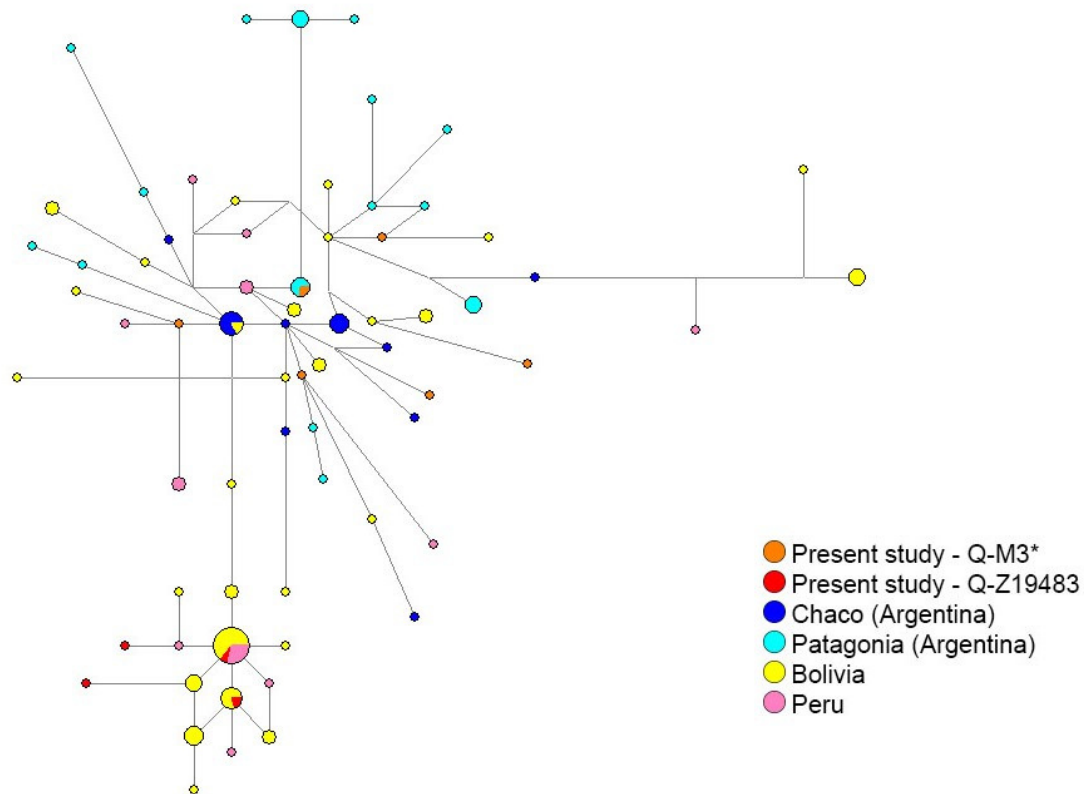
Supplementary Figure S2. Phylogenetic tree of the Y-SNPs genotyped in this study, and corresponding haplogroups. The markers are represented in different colors based on the multiplex in which they are embedded (green – Mx 1; dark pink – Mx E1; pink - Mx E2; purple – both Mx E1 and E2; blue – Mx 2; golden – Mx Q; red – Mx R1; orange – Mx R2; dark red – both Mx R1 and R2; black - singleplex).



Supplementary Figure S3. E-M35* median-joining network with 10 Y-STRs (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, and DYS439) common to all populations. In the network are included 1 sample from our dataset, 17 Eurasian (Adams et al. 2008; Boattini et al. 2013; Rębała et al. 2013; Zalloua et al. 2008), and 16 African (De Filippo et al. 2011; Larmuseau et al. 2015; Rosa et al. 2007).



Supplementary Figure S4. R-V88 median-joining network with 12 Y-STRs (DYS19, DYS385a, DYS385b, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, and DYS439) common to all populations. In the network are included 2 samples from our dataset, 3 European (Boattini et al. 2013; Di Cristofaro et al. 2018), and 62 African (Berniell-Lee et al. 2009; Di Filippo et al. 2011; Fortes-Lima et al. 2015; González et al. 2013; Larmuseau et al. 2015; Rosa et al. 2007).



Supplementary Figure S5. Haplogroup Q median-joining network with 10 Y-STRs (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, and DYS439) common to all populations. A total of 115 samples were included in the network: 6 belonging to Q-M3* and 4 belonging to Q-Z19483 from our dataset, 52 natives from Bolivia (all samples Q-M3) (Gayà-Vidal et al. 2011), 16 natives from Peru [7 samples belonging to the haplogroup Q-M3 and 9 to the haplogroup Q-M3*(xM19)] (Barbieri et al. 2017; Roewer et al. 2013), 16 natives from Chaco, Argentina, and 21 natives from Patagonia, Argentina [all samples Q-M3*(xM19)] (Roewer et al. 2013).

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