Additional file

Additional file 7. Figure S7. Bayesian trees.

a) Bayesian (Monte Carlo–Markov chain) consensus tree displaying the relationships between 39 haplotypes of modern wild Italian *Sus scrofa* mtDNA D-loop, sequenced in this study, and previous published haplotypes, chosen as to represent the current genetic diversity of Western Eurasia. Bayesian phylogenetic tree was created using MrBayes 3.2 with the Celebes Warty Pig (*Sus celebensis*) as outgroup. Model parameters (HKY85+G+I) were identified through JModelTest 2.1. Red, orange, and grey colours distinguish the European (E1), Italian (E2), and the Asian (A), clade respectively. Numbers at relevant branch-points represent posterior probabilities.

b) Bayesian (Monte Carlo–Markov chain, created using MrBayes 3.2) consensus tree drawn using only the 80bp fragment displaying the relationships between obtained haplotypes and ancient haplotypes identified (Larson et al., 2007a). Numbers at relevant branch-points represent posterior probabilities. In blue are ancient reference sequences (Larson and Burger, 2013). The following ancient haplotypes (AH) were obtained from our sequences: AH3: 3 samples from Pompeii 79 AD and 1 samples from Sassari 2,700-1,800 BC Eneolithic; AH4: 3 samples from Campania museum, 1 sample from Tuscany museum; AH5: 1 sample from Alghero (SS) 3,500-2,700 BC Neolithic; AH6: 2 samples from Latronico (PZ) Mesolithic; AH7: 2 samples from Carbonia (CI) VII-VI sec. BC, 1 sample from Alghero (SS) I-III sec. AD Roman Age, 1 sample from Alghero (SS) XVI-XVII sec. AD, 4 samples from Sassari (SS) XI-XV sec. AD Middle Age, 1 sample from Sassari XVIII sec. AD.