Table S6. *D* statistics of the ABBA-BABA test (Dasmahapatra *et al.* 2012; Martin *et al.* 2014) for *MC1R* and *NR6A1* loci.

Scenario	Positions of the populations in the scenario (P1-P4)[1,2]	*D* value for *MC1R*[3,4]	*D* value for *NR6A1*[4]
ABBA 1	P1: North Italian + Sardinian wild boars P2: SE European wild boars P3: All pig breeds P4: Outgroup (ancestral wild boar)	0.333	0.268
ABBA 2	P1: North Italian wild boars P2: Sardinian wild boars P3: Italian + Sardinian pig breeds P4: outgroup (ancestral wild boar)	1.000	0.715
ABBA 3	P1: Sardinian wild boars P2: North Italian wild boars P3: Italian pig breeds P4: Outgroup (ancestral wild boar)	1.000	-0.715
ABBA 4	P1: North Italian wild boars P2: Sardinian wild boars P3: Italian pig breeds P4: Outgroup (ancestral wild boar)	-1.000	0.715
ABBA 5	P1: North Italian + Sardinian wild boars P2: SE European wild boars P3: SE European pig breeds P4: Outgroup (ancestral wild boar)	0.333	0.268
BABA 1	P1: Italian + Sarda pig breeds P2: SE European pig breeds P3: All wild boar populations P4: outgroup (ancestral domestic pig)	0.335	0.184

[1] P4 is the ancestral population. The other positions (P1-P3) are those reported in the trees of Fig. S1 and indicate the direction of the introgression.
[2] Populations were grouped as follows: South-East (SE) European wild boars include wild boars sampled in Bosnia and Herzegovina, Croatia, North of Macedonia, Montenegro, Serbia and Slovenia; Italian pig breeds include Apulo-Calabrese, Casertana, Cinta Senese, Mora Romagnola and Nero Siciliano pig breeds; SE European pig breeds include Krškopolje, Black Slavonian, Turopolje, Mangalitsa, Moravka and East Balkan Swine.
[3] All domestic *MC1R* alleles were considered together in the formula for the calculation of D.
[4] Negative values indicate inverted gene flow between P2 and P1 (derived by allele frequencies in the Sarda pig breed in which the wild type alleles are absent or almost absent in the two loci)