Table S3. PCR-RFLP and fragment analysis protocols used for the genotyping of markers at the *MC1R* and *NR6A1* genes.

Primer pair names/genes	**Genotyping method**	**Primer sequences (5'-3'): Forward and *Reverse* primers**	**Amplified region (bp)**	**PCR conditions[1]**	**Genotyping protocols/system**
MC1R_1	PCR-RFLP	CTGCACTCGCCCATGTACTA *AGCAGAGGCTGGACACCAT*	196	61/3.0	Amplicons digested with *BspH*I (c.367G = 196 bp in E^+, E^{D1} and *e*; c.367A = 154 + 42 bp in E^{D2} and E^P) [2]
MC1R_2	PCR-RFLP	GCGGGTACTGTACGTCCACAT *CCCAGCAGAGGAGGAAGAC*	154	61/3.0	Amplicons digested with *Hha*I (c.727G = 108 + 46 bp in E^+, E^{D1}, E^{D2} and E^P; c.727A = 154 bp in *e*); Amplicons digested with *Bst*UI (c.729G = 109 + 47 bp in E^+, E^{D2} and E^P; c.729A = 154 bp in E^{D1} and *e*) [2]
MC1R_indel	Fragment analysis	CACCTCTGGGAGCCATGA *GTCTGGTTGGTCTGGTTG*	168/170	55/2.5	Amplicons analysed in a capillary sequencer (ABI3100 Avant, ABI Prism)
MC1R_OA	OpenArray™ Genotyping platform	-	-	-	QuantStudioTM 12 K Flex Real-Time PCR System (Thermo Fisher Scientific) [3]
NR6A1	PCR-RFLP	GGTATCCTGAGCACCCAGTC *ACCTGGAGGACAGTGTGGAG*	203	55/2.5	Amplicons digested with *Msp*I (g.299084751C = 180 + 23 bp; g.299084751T = 203 bp) [2]
NR6A1_OA	OpenArray™ Genotyping platform	-	-	-	QuantStudioTM 12 K Flex Real-Time PCR System (Thermo Fisher Scientific) [3]

1 Annealing temperature (°C) / [$MgCl_2$] mM.
[2] Genotyping protocols were based on PCR-RFLP. Restriction enzymes used to genotype the amplified fragments are indicated together with the size of the fragments obtained after digestions and extension alleles that have the indicated PCR-RFLP patterns (Fontanesi et al. 2010, 2014).
[3] Genotyping details are reported in Muñoz *et al.* (submitted).