

H1_JQ310712_L.l.lepida
H2_JQ310713_L.l.lepida
H3_JQ310714_L.l.lepida
H4_JQ310715_L.l.lepida
H5_JQ310716_L.l.lepida
H8_JQ310719_L.l.iberica
H8_JQ310719_L.l.iberica
H6_JQ310717_L.l.nevadensis
H7_JQ310718_L.l.nevadensis
H8_JQ310719_L.l.nevadensis
H9_JQ310720_L.l.nevadensis
H2_JQ310725_L.tangitana
H8_JQ310722_L.tangitana
H10_JQ310721_L.tangitana
H12_JQ310723_L.tangitana
H13_JQ310724_L.tangitana
H15_JQ310726_L.pater
H16_JQ310727_L.pater
H17_JQ310728_L.pater
H18_JQ310729_L.pater
H19_JQ310730_L.schreiberi
H20_JQ310731_I.monticola
H21_JQ310732_L.agilis

Figure S4 Sequence alignment from haplotypes (H1-H21) detected in locus *mk245* in each lizard species or subspecies. The accession number corresponding to each haplotype is indicated. Conserved bases are presented in grey while variable sites are highlighted with colored font. Dashes denote gaps. A microsatellite composed by six to ten GTT units is present at positions 168-197.

Figure S4 (continued)