



Figure S3 Sequence alignment from haplotypes (H1-H19) detected in locus *mk209* 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 repetitive element composed by Gs at positions 176-185 is variable in length and is followed by a repeat of GAs, which is variable in African ocellated lizards (*L. tangitana* and *L. pater*) but not in European ocellated lizards (*Lacerta lepida nevadensis*, *L. l. iberica* and *L. l. lepida*).

Figure S3 (continued)