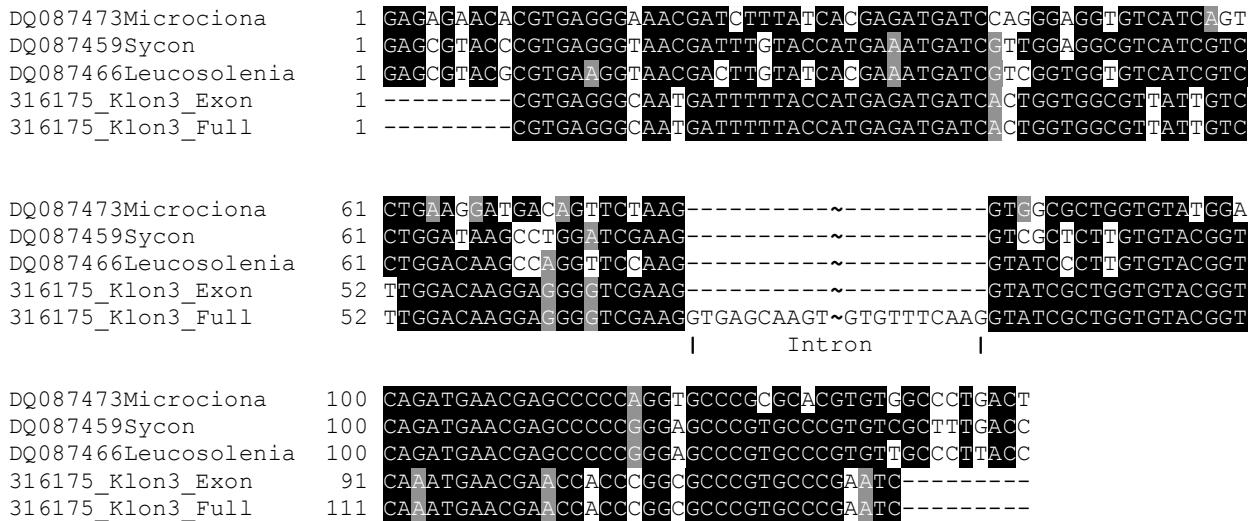


Additional Figure 1: Amino acid alignment of three sponge ATP Synthetase beta subunit sequences from Genbank (accession numbers DQ087473, DQ087459, DQ087466) and the sequence of *Leucetta chagosensis* (Specimen No. QMG 316175). Location of intron is indicated by a forward slash and * above the site. Black alignment background indicates conserved alignment positions, grey background similar chemical properties, white background variable positions with dissimilar amino acids.



Additional Figure 2: Nucleotide alignment of three sponge ATP Synthetase beta subunit sequences from Genbank (accession numbers DQ087473, DQ087459, DQ087466) and the sequence of *Leucetta chagosensis* (Specimen No. QMG 316175), the upper one contains only the exon sequence, the lower one (..._full) also 5' and 3' fragments of the phase-0 intron that follows the GT-AG rule. The missing central part of the intron is indicated by "~". Black alignment background indicates conserved alignment positions, grey and white background to indicate variable positions.