

Genomic alignment visualization showing sequence conservation and quality across a region. The top section displays multiple sequence alignments with color-coded conservation levels. Below the alignments are tracks for Conservation (0.0 to 1.0) and Quality (0.0 to 1.0). The bottom section shows a Consensus sequence. The alignment includes various identifiers such as Phyl.001021000.11-207, Phyl.001022000.11-207, and Phyl.001023000.11-207, among others. The sequence is primarily composed of nucleotide bases (A, C, G, T) with some gaps represented by dashes.