

Figure S7. Maximum Likelihood tree based on a nucleotide model analysis (GTR+G+I) of a Degen1-encoded data set that lacks all serine-coding nucleotides / codons (*no-Ser1Ser2*). The six nodes of particular interest (Xenocarida, Multicrustacea, Vericrustacea, Altocrustacea, Miracrustacea, Edafopoda) are recovered, indicating that the strong signal provided by serine codons is congruent to the signal provided by codons of all other amino acids.

