**Table S1: Glossary of commonly encountered terminologies**

**AHE:** Anchored Hybrid Enrichment = A target enrichment method that uses in solution hybridization to capture exonic genes for phylogenomic studies.

**Adapter:**  A short piece of known DNA attached to the genomic DNA of interest to identify the sample once mixed with other samples.

**Assembly:** Assembly of fragment sequences into higher order structures based on their overlap and reference sequence, where appropriate.

**Biotinylation**: The process of attaching biotin to proteins and other macromolecules, in this case to bind the DNA regions of interest to the streptavidin magnet beads during the in solution hybridization process.

**Contig**: A contiguous stretch of DNA sequence that is the result of assembly of multiple overlapping sequence reads into a single consensus sequence.

**de Bruijn Graph:** A graph theory method for assembling a long sequence from overlapping fragments. The de Bruijn graph is a set of unique substrings (words) of a fixed length (a *k*-mer) that contain all possible words in the data set exactly once. The sequence reads are split into all possible k-mers, and overlapping k-mers are linked by edges in the graph. Reads are then mapped onto the graph of overlapping k-mers in a single pass, greatly reducing the computational complexity of genome assembly.

***de novo* Assembly:** Assembly of contigs without a reference genome.

**Exon:** A portion of a gene that is transcribed and spliced to form the final messenger RNA (mRNA). Exons contain protein-coding sequence and untranslated upstream and downstream regions (3′ UTR and 5′ UTR). Exons are separated by introns, which are sequences that are transcribed by RNA polymerase, but spliced out after transcription and not included in the mature mRNA.

**Flanking regions:** The areas immediately to the left and right of the UCE core, which are variable and, therefore, the target of UCE capture.

***K*-mer:** Nucleotide sequence of a certain length. E.g., a dinucleotide is a kmer where k=2.

**In Solution Hybridization:** Binding of biotinylated probes with denatured genomic regions of interest in the process of several hours in liquid.

**Library:** A set of nucleic acid fragments which has undergone all processing steps and is ready for actual sequencing.

**Multiplex:** A library containing various samples labelled with adapters.

**Paired-End Read:** A technology that obtains sequence reads from both ends of a DNA fragment template. The use of paired-end sequencing can greatly improve de novo sequencing applications by allowing contigs to be joined when they contain read pairs from a single template fragment, even if no reads overlap.

**Probe/bait:** A collection of oligonucleotides that will bind to specific, conserved genome regions of interest, often called baits as they can ‘fish’ out the region of interest.

**Read:** Data output from the analysis of a single fragment (sequence).

**SNP:** Single-Nucleotide Polymorphism = sequence divergence in the range of a single base.

**Target Enrichment:** Capturing genomic regions of interest by hybridization to target-specific biotinylated probes, which are then isolated by magnetic beads.

**UCE:** Ultraconserved Elements **=** highly-conserved regions within the genome that are shared among evolutionarily distant taxa.