Argument	Description
target.groups	A set of one or more terms that represent the target taxa. Multiple terms are to be separated by a comma and enclosed in quotation marks *i.e.* "*Taxon1,Taxon2*". This process is case-sensitive; it uses partial string matching, so the terms used must be unique *i.e.* "*Taxon1*" and "*Taxon10*" are not appropriate as the first is a subset of the second.
min.support	The minimum support (between 0-1 or 0-100 inclusive) for any clade identified during sorting (default 0), dependent on the range of support values noted in the tree file (e.g. bootstrap support, Bayesian posterior probability, or any similar measure). A node with no identified support value is treated as having a value of zero (0).
min.prop.target	The minimum proportion (between 0.0-1.0 inclusive) of target taxa to be present in a clade, out of the total target taxa in the tree (default 0.7). At 0.5, ≥ 50% of all target taxa in a tree must be in the clade; at 1.0, all target taxa in a tree must be in the clade.
in.dir	The path to the input directory containing all phylogenetic trees to be sorted. If no value is given, the function defaults to the user's current working directory.
out.dir	The output directory to be created within *in.dir*, for the trees identified during sorting to be moved or copied to. If *out.dir* is omitted, the default directory of *Sorted_Trees/* will be used. If list mode (mode="*l*") is given, this argument will be ignored, and no directory will be created. The content of *out.dir* is dependent on the *clades.sorted* parameter.
mode	Option to control whether the function will move ("*m*"), copy ("*c*") or list ("*l*") the files containing trees identified during sorting. In both move and copy modes the files will be transferred to subdirectories within *out.dir* and a list of the sorted trees will be returned. In the list mode, only the list will be returned. The type of trees sorted is dependent on the *clades.sorted* parameter.
clades.sorted	Option to control sorting for "Exclusive" ("*E*") or "Non-Exclusive" ("*NE*") clades. The default setting is to search for both types of clades, *i.e.* "*E,NE*". Sorting of "Exclusive" clades will also generate a sub-group of "All Exclusive" trees (see Supplementary Text). This argument will affect what is returned by the function and what subdirectories are created in *out.dir*.
extension	The file extension of the input phylogenetic trees (default "*.tre*").
clade.exclusivity	The minimum proportion of target taxa allowed in a "Non-Exclusive" clade, applicable only when sorting *NE* clades. The value must be ≥0.0 and <1.0. At default (0.9), ≥90% (but not 100%) of the taxa in a *NE* clade must be target taxa (*i.e.* <10% can be "interrupting" non-target taxa). Specification of 1.0 is not allowed; 1.0 implies that all (100%) taxa in a clade are target taxa (no non-target taxa allowed), thus the clade would be "Exclusive", not "Non-Exclusive".

Supplementary Figure S2. Arguments within *sortTrees* function in PhySortR.