Figure S8 Phylogeny of *Clostridia*-related lineages identified by the *de novo* and multi-step OTU

classification procedures. Only the OTUs present in at least 10 out of the 121 giant panda samples are

included. The prefix 'Denovo' represents the OTUs classified by the *de novo* method (highlighted by the blue

text), whereas 'GGRef' represents the OTUs classified by the reference-based approach, with numerals

representing the Greengenes' prokMSA ID (highlighted by the red text). OTUs classified by the *de novo*

method were inserted into pre-established Greengenes' phylogenetic tree in ARB. The six OTUs selected as

key phylotypes to discriminate the gut microbiota of giant pandas from that of non-panda herbivores are

highlighted in yellow. Accession numbers of reference sequences from the Greengenes' database are noted in

parentheses. The abundance range, abundance median (of only samples in which the respective OTU was detected), and the prevalence of each OTU among the 121 giant panda samples are listed in square brackets.