



**Supplementary Figure 2.** A species tree showing the candidate aerolysin HGT pair from *Ixodes scapularis* and *Pseudomonas aeruginosa*, marked with blue circles on a dotted line, in the context of all other organisms whose genome has been sequenced to date. All other branches have been collapsed to the most ancestral branch that does not include either *Ixodes* or *Pseudomonas*, and include sister clades of metazoa (red), fungi (brown), plants (green), other eukaryotes (grey), bacteria (blue) and archaea (purple). A minimum of 76 gene losses (52 in prokaryotes and 24 in eukaryotes) would be necessary to explain this topology in the absence of HGT, as given by the number of visible leaves in this tree.