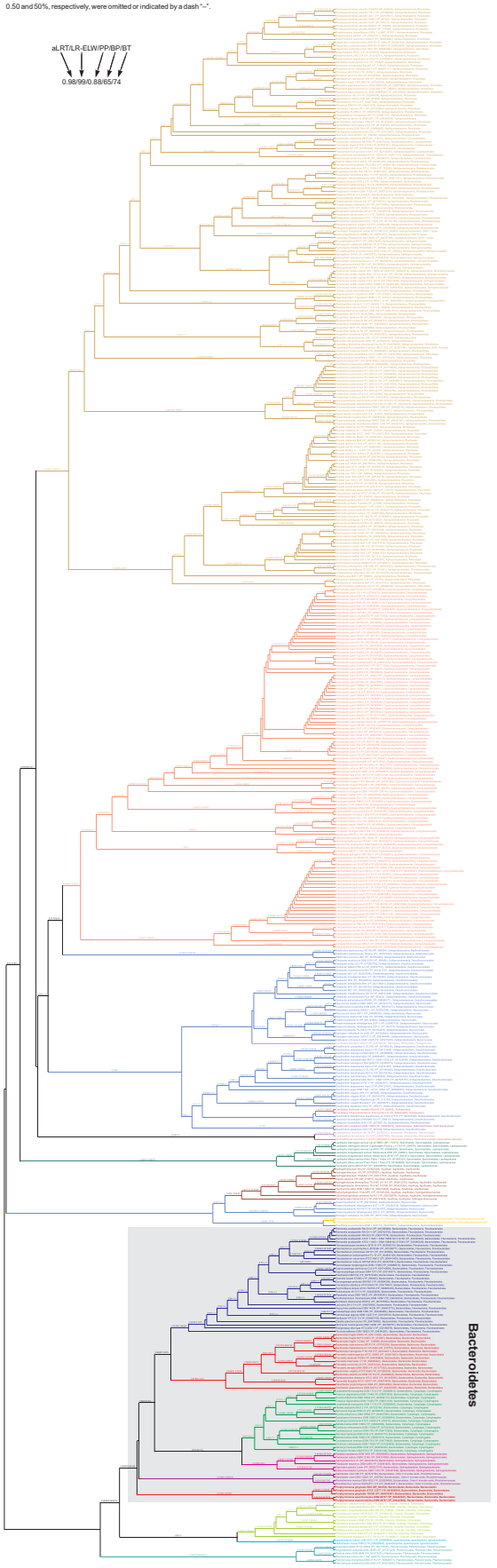Figure S2 Cladogram for 470 Fur homologs inferred in morePhyML. Members of Bacteroidetes were bolded and *Porphyromonas* taxa marked additionally red colors. Numbers at nodes in the following order correspond to: support values calculated by aLRT based on a Shimodaira-Hasegawa-like procedure (aLRT), support values based on Local Rearrangements–Expected Likelihood Weights method (LR-ELW), posterior probabilities estimated in MrBayes (PP), as well as bootstrap support values calculated in PhyML (BP) and TreeFinder (BT). Values of the posterior probabilities and bootstrap percentages lower than 0.50 and 50%, respectively, were omitted or indicated by a dash "–".