

**Table 3. Phylogenetic tree reconstruction test**

The number of complete orthologous groups and the mean fraction of correct split of ML trees for gene trees from three different kingdoms are shown. The higher value, the better the gene trees agree with the species tree. These results can be directly combined with Altenhoff and Dessimoz, 2009 (Fig. 3). FIS-Fraction of identical splits.

	Eukaryota groups		Fungi groups		Bacteria groups	
	groups	FIS [%]	groups	FIS [%]	groups	FIS [%]
phylomeDB	1977	90.2	2125	90.6	207	49.3
metaPhOrs EL=1	948	90.6	2195	89.8	191	52.9
metaPhOrs EL=2	136	91.8	1135	91.4	95	51.2
metaPhOrs EL=3	8	92.9	532	92.4	21	49