Cover Illustration: Broad taxon sampling coupled with a moderate number of genes has the power to reconstruct deep phylogenetic relationships. In this issue, Parfrey et al. test the support for major eukaryotic clades using taxon-rich analyses, including 88–451 taxa representing up to 53 of ~75 major lineages, and analyzing data from up to 16 genes. These analyses reveal remarkable consistency in supported clades, indicated by color boxes, despite varying levels of missing data (17–69%). Several major groups are both stable and strongly supported in these analyses (e.g. SAR, Rhizaria, Excavata), while the proposed supergroup “Chromalveolata” is rejected. This approach contrasts phylogenomic studies that are marked by a paucity of major eukaryotic lineages (19 or fewer). Images are of representative organisms and demonstrate the microbial nature of the majority of eukaryotic lineages. All images are from http://www.mbl.edu/microscope.