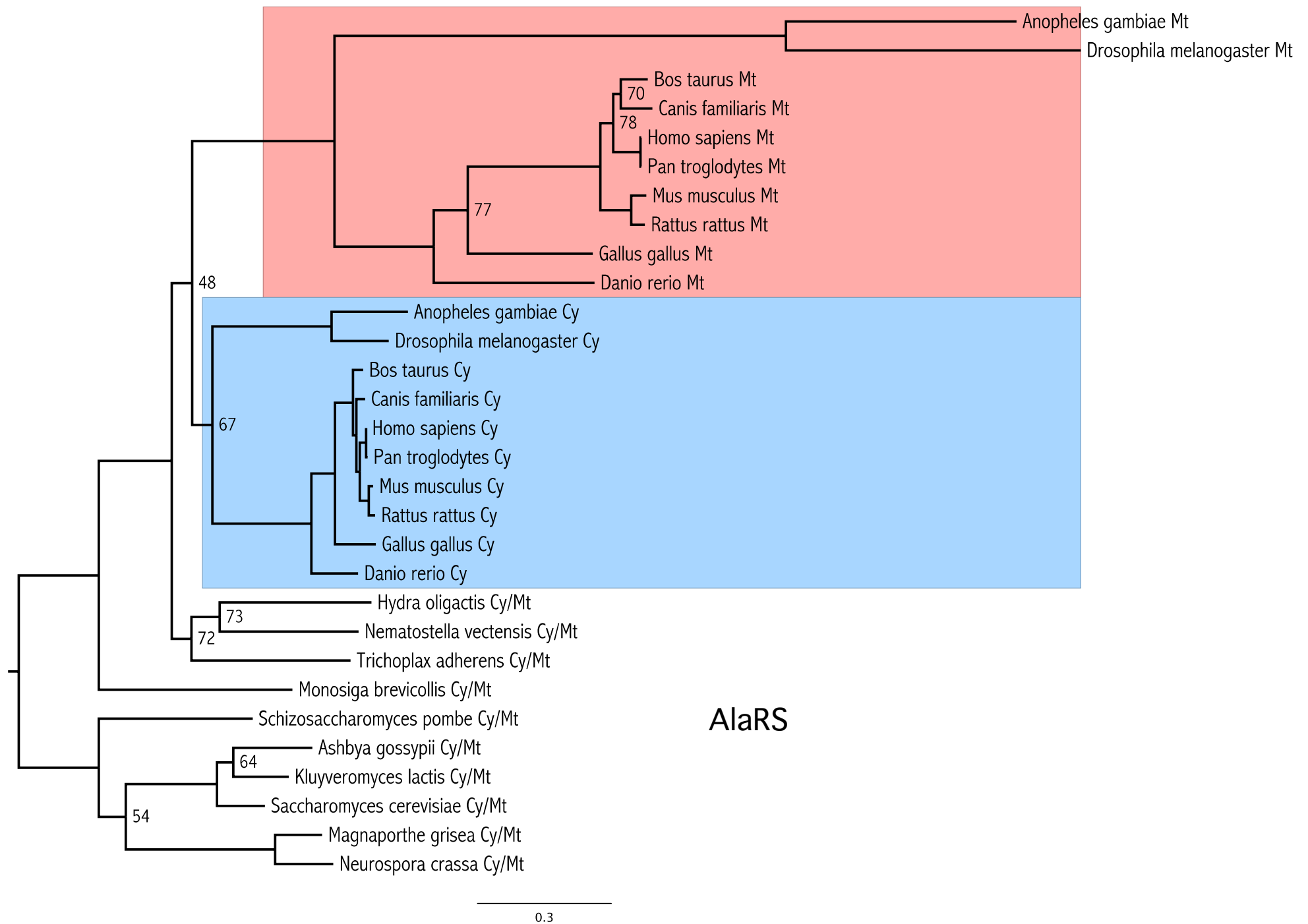
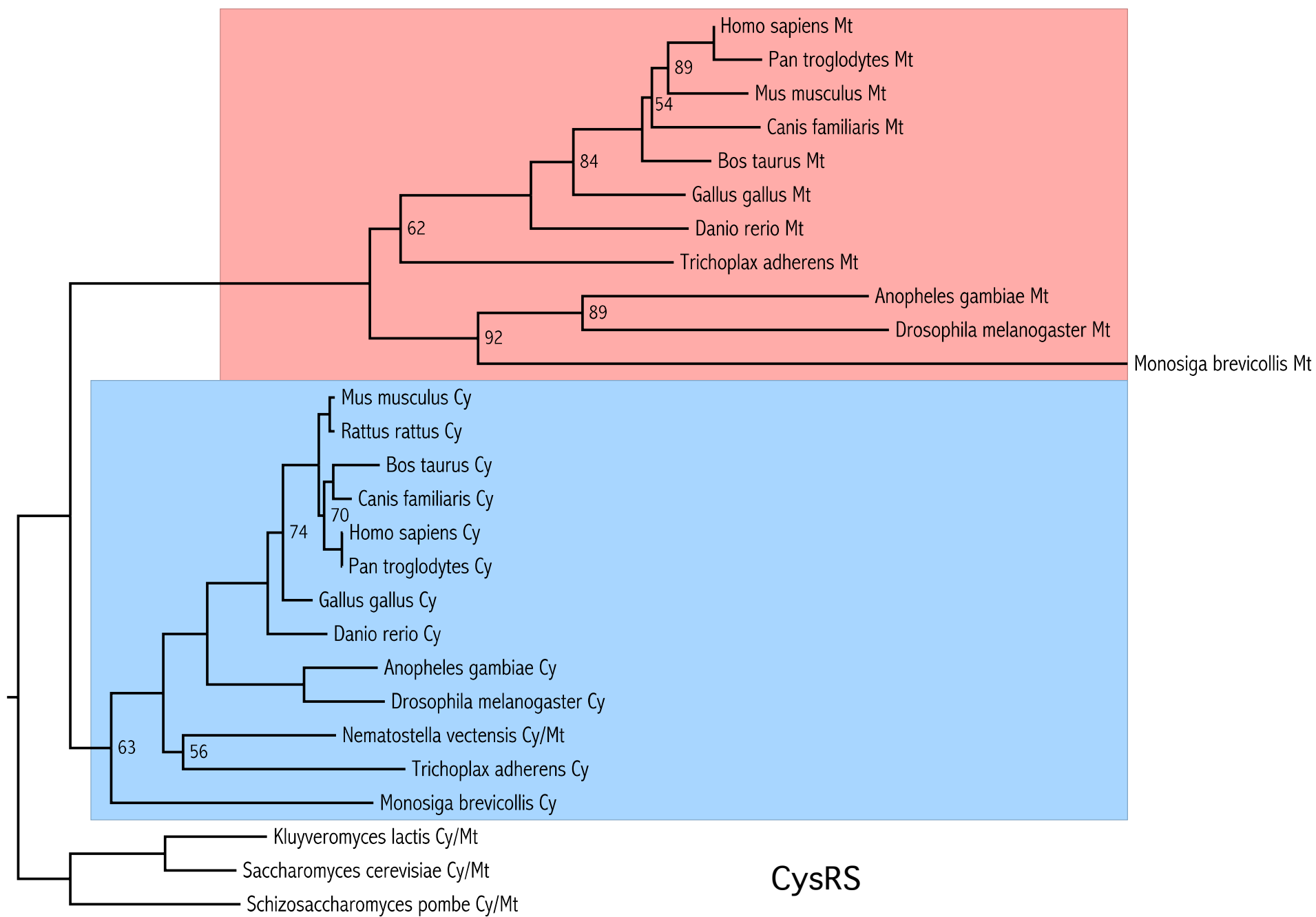


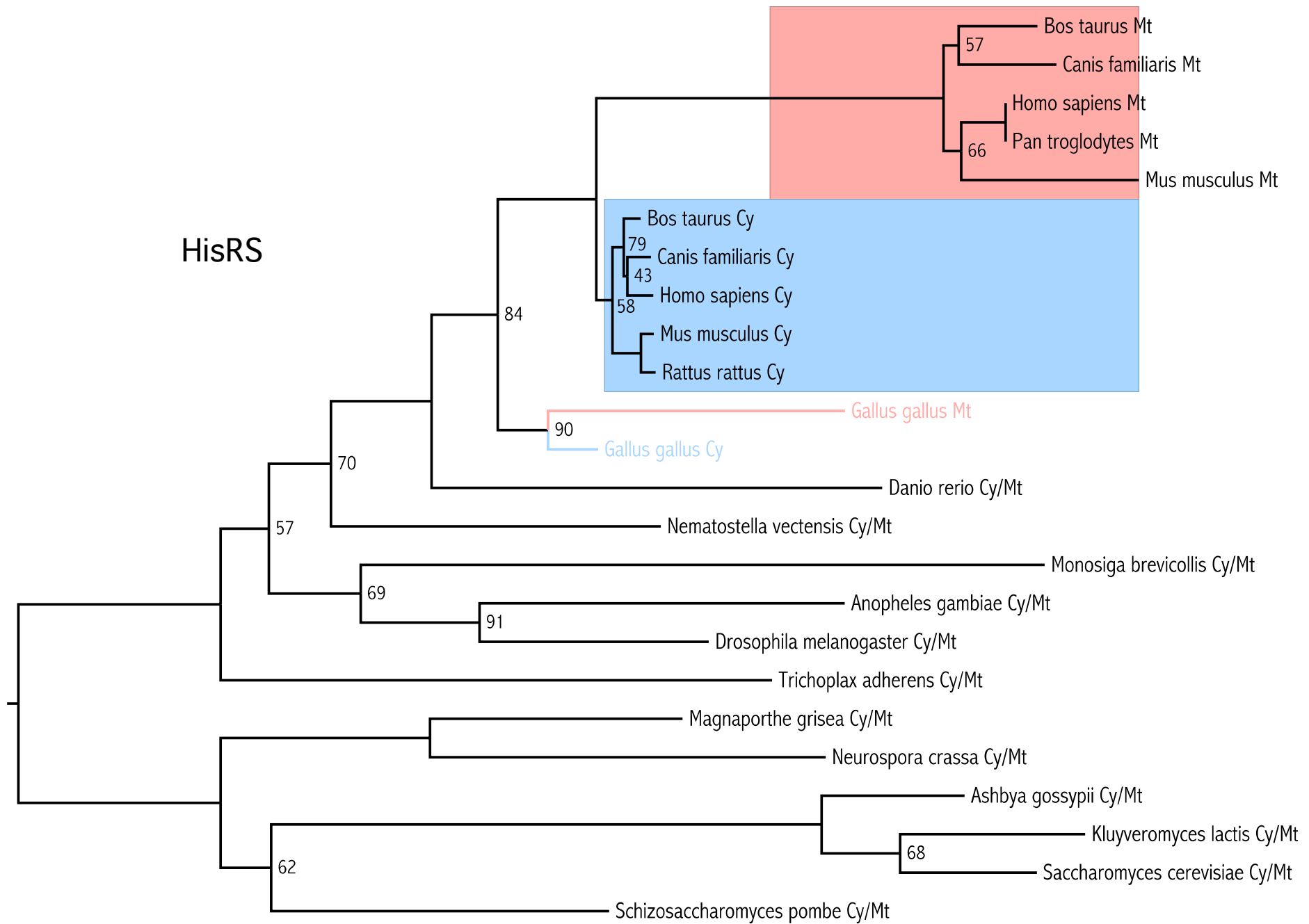
Figure S1-7. Evolution of aaRS in Metazoa and Fungi. Maximum likelihood trees for AlaRS, CysRS, HisRS, LysRS, ArgRS, ThrRS and ValRS respectively. AlaRS, CysRS, HisRS, LysRS and ThrRS were aligned using Probcons. ArgRS and ValRS were aligned using ClustalW. Numbers above nodes indicate bootstrap support < 95 from 1000 replicates. Red highlighted lineages indicate those for strictly mitochondrial aaRS genes, blue for cytosolic. Cy = cytosolic, Mt = mitochondrial, Cy/Mt = dual targeted.

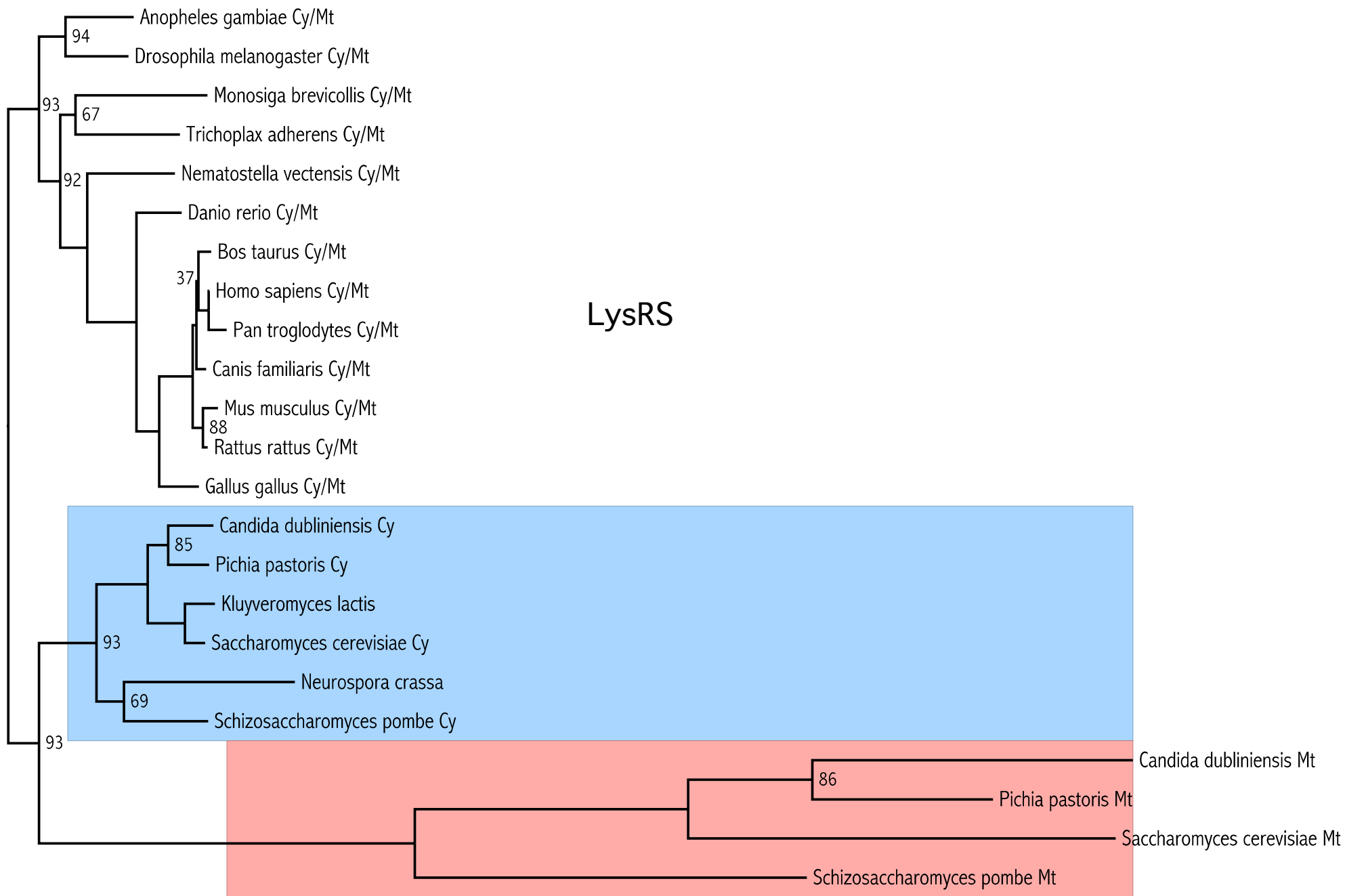




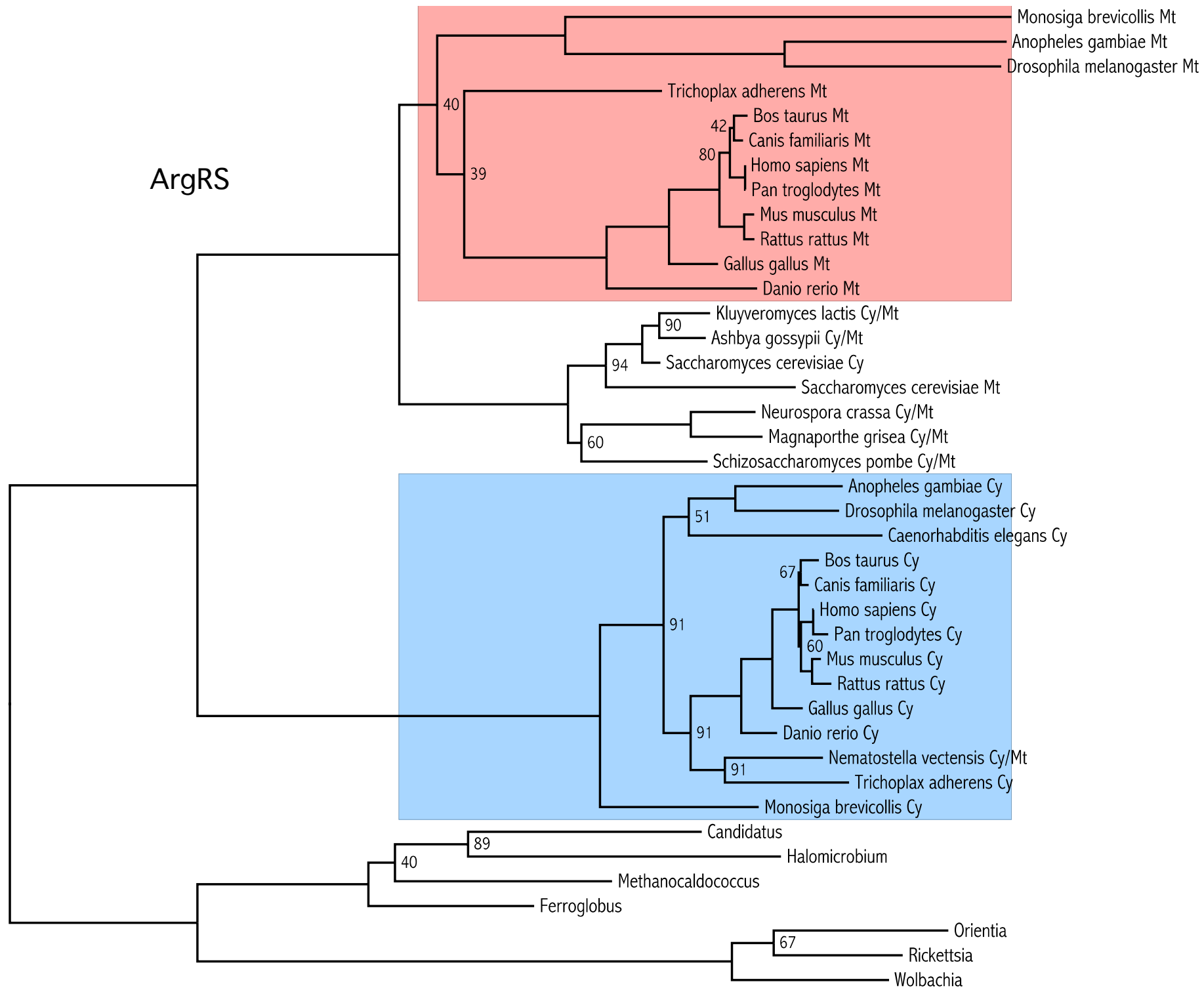
0.4

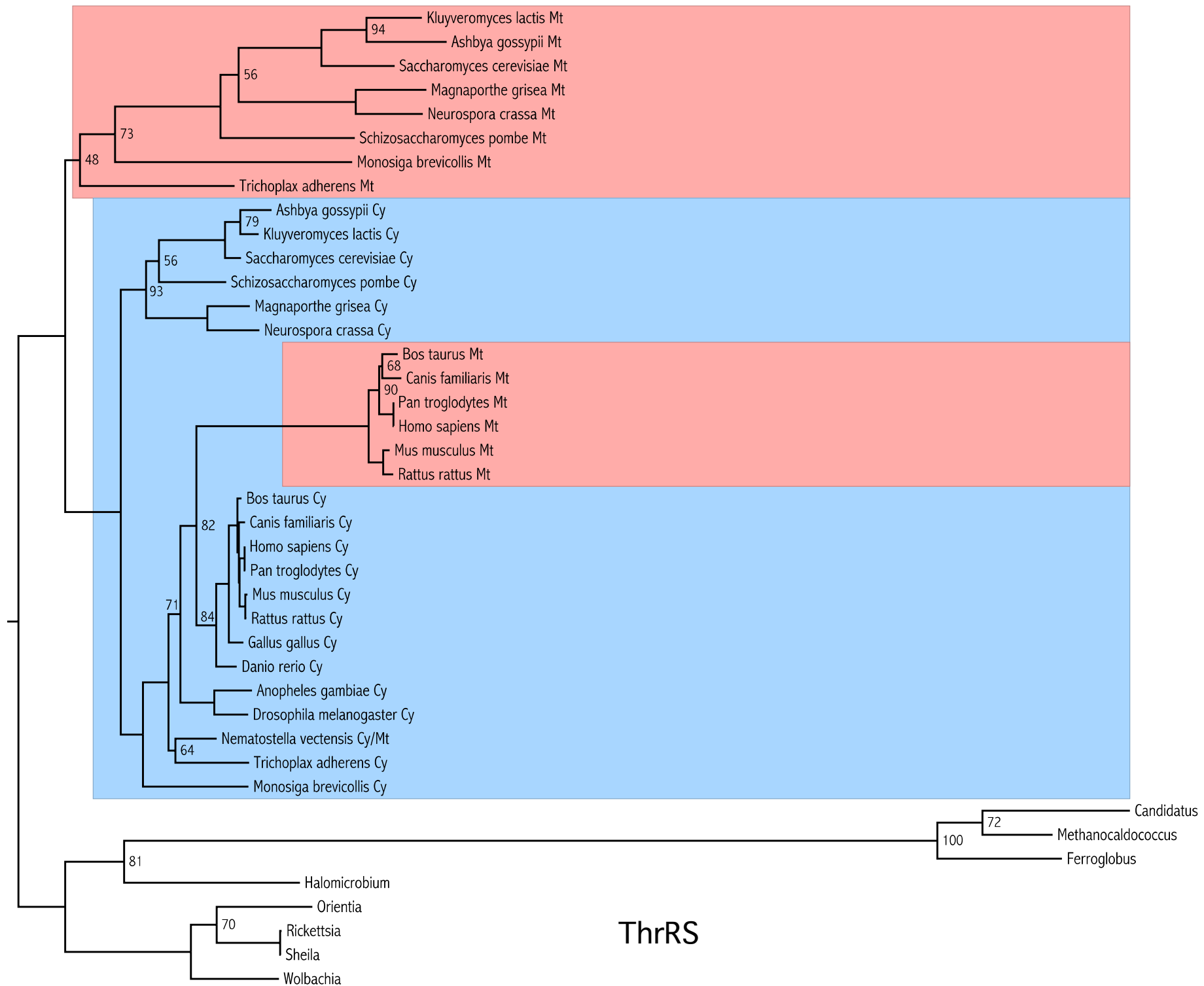
HisRS

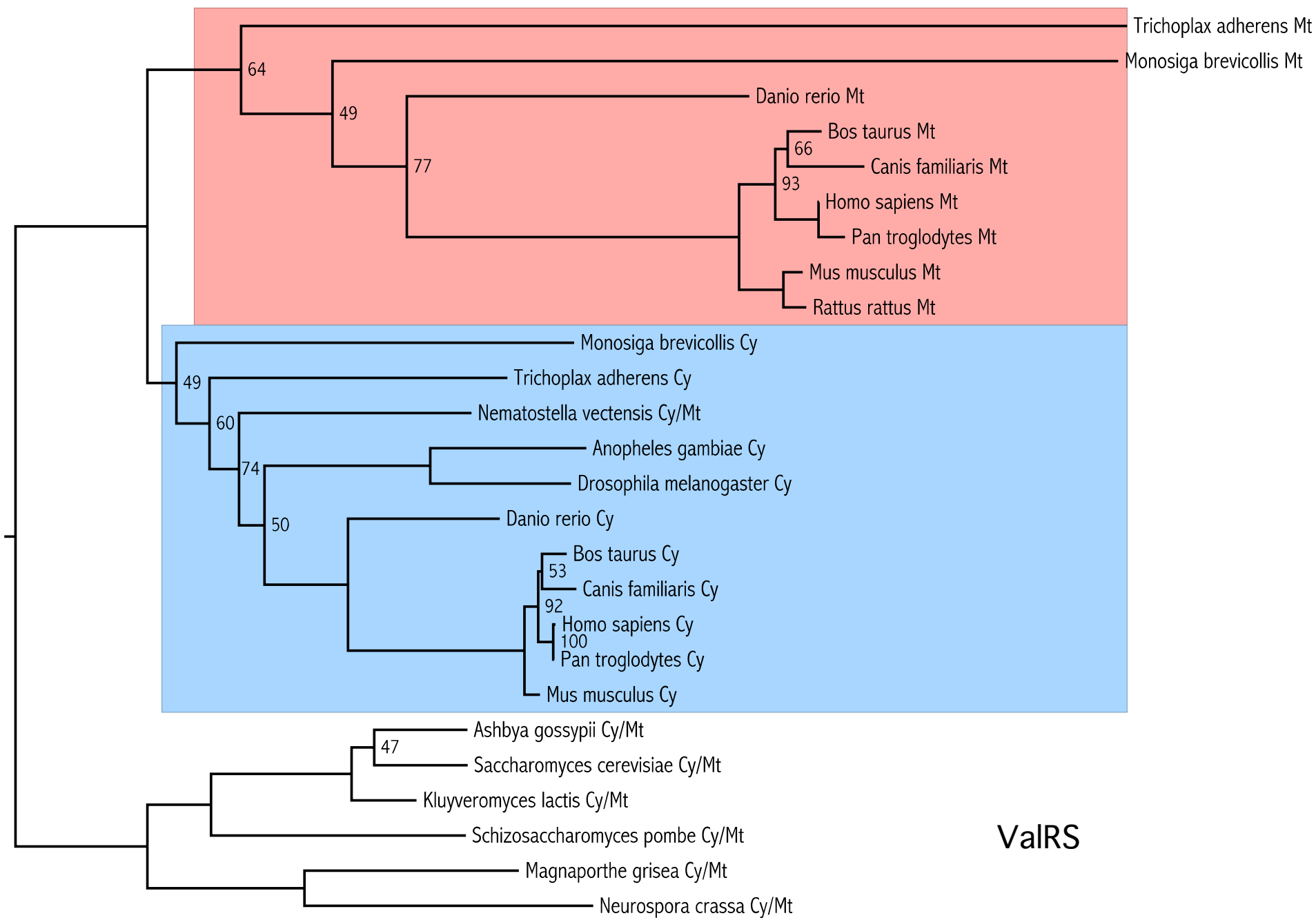




ArgRS







VaIRS