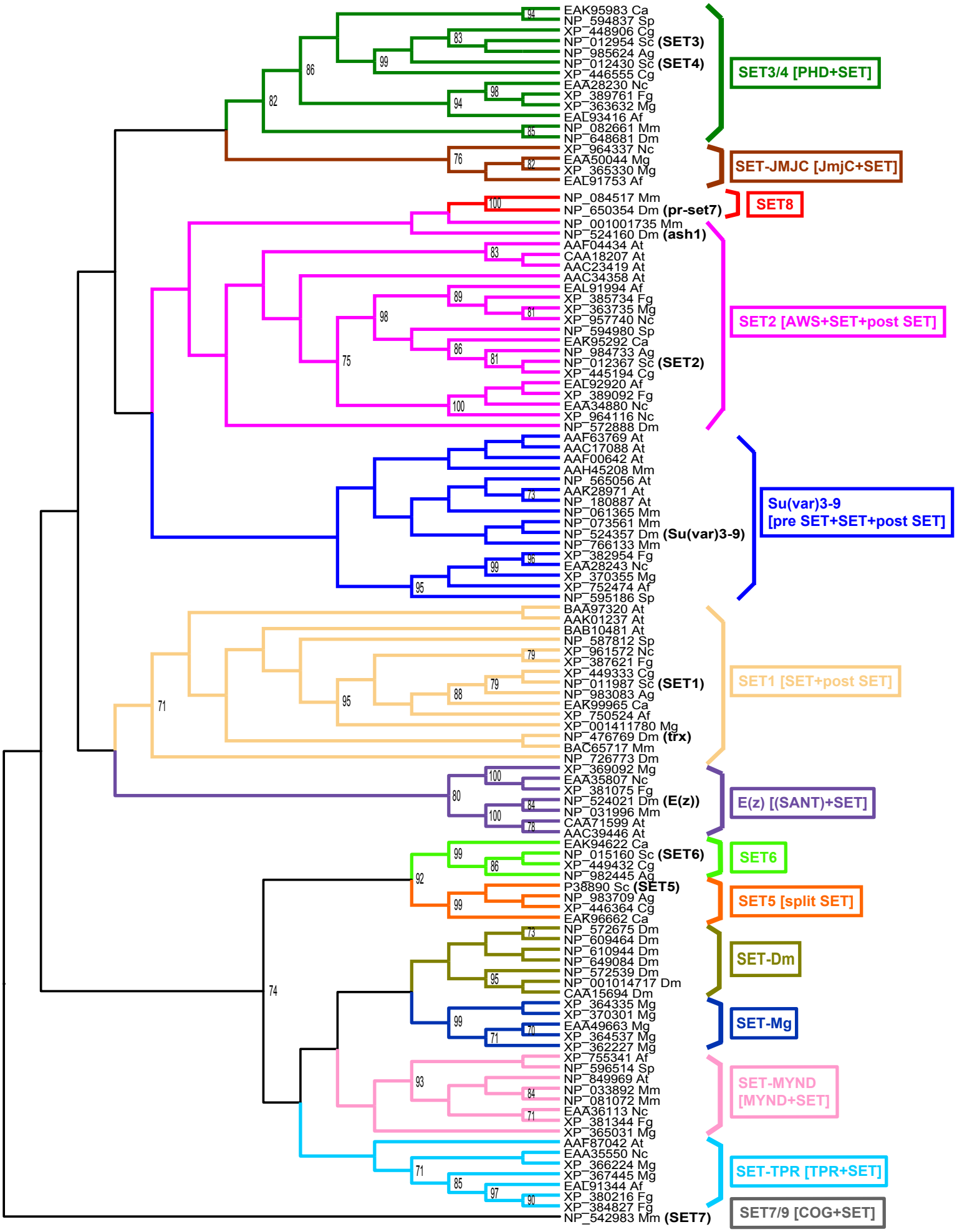

Maximum parsimony phylogeny of 113 representative SET-domain sequences. The consensus phylogeny from bootstrap analysis with 500 pseudoreplicates is shown with bootstrap values greater than 70%.