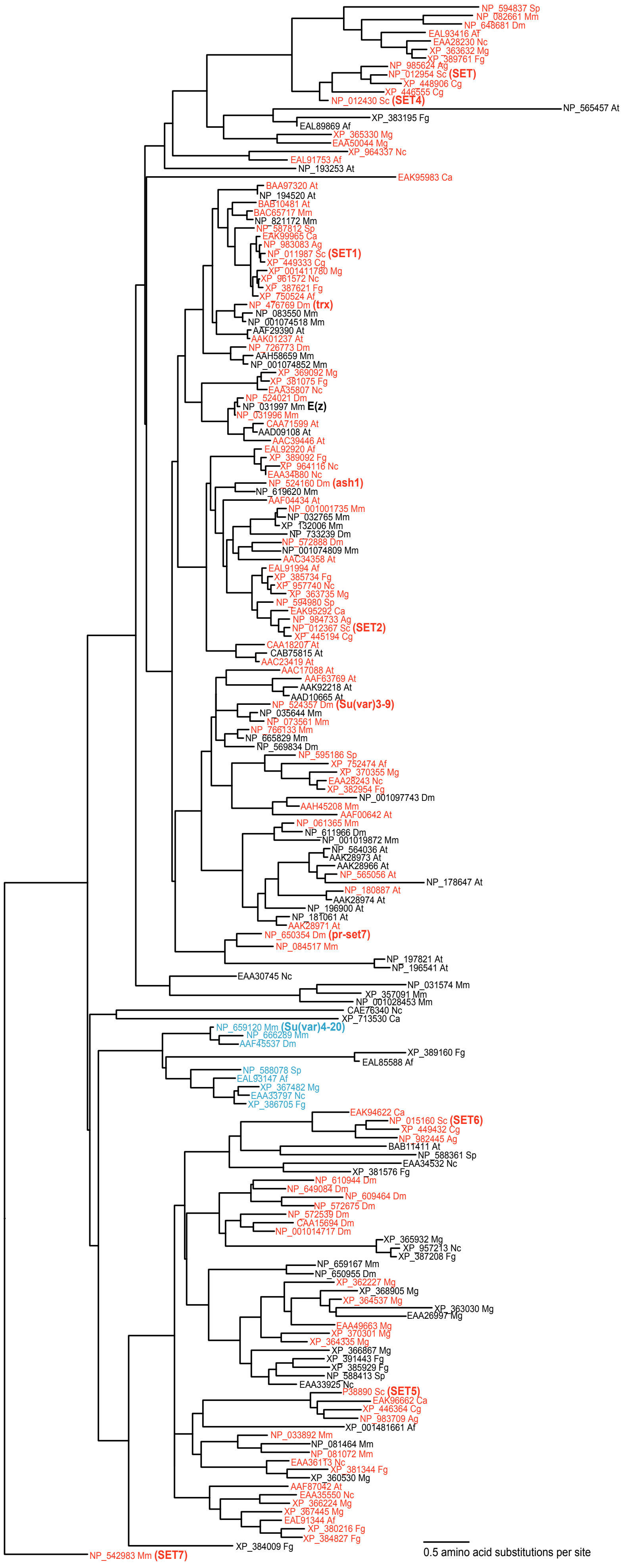

Maximum likelihood phylogeny reconstructed using 182 non-redundant SET-domain sequences. Red font indicates 113 representative sequences used to reconstruct the phylogeny shown in Fig. 1.