

Additional Figure 3

Sequence based phylogeny of Prolyl tRNA synthetase editing domains (Ybak/ProX) constructed using MEGA v5.0 using Maximum Likelihood method based on JTT matrix model. Bootstrap values indicated at the inner nodes indicate the similarity of tethered editing domains of *LmProRS* to Ala-tRNA^{Pro} type editing domains (ProX) and the standalone editing domains of *LmProRS* to Cys-tRNA^{Pro} type (Ybak).

