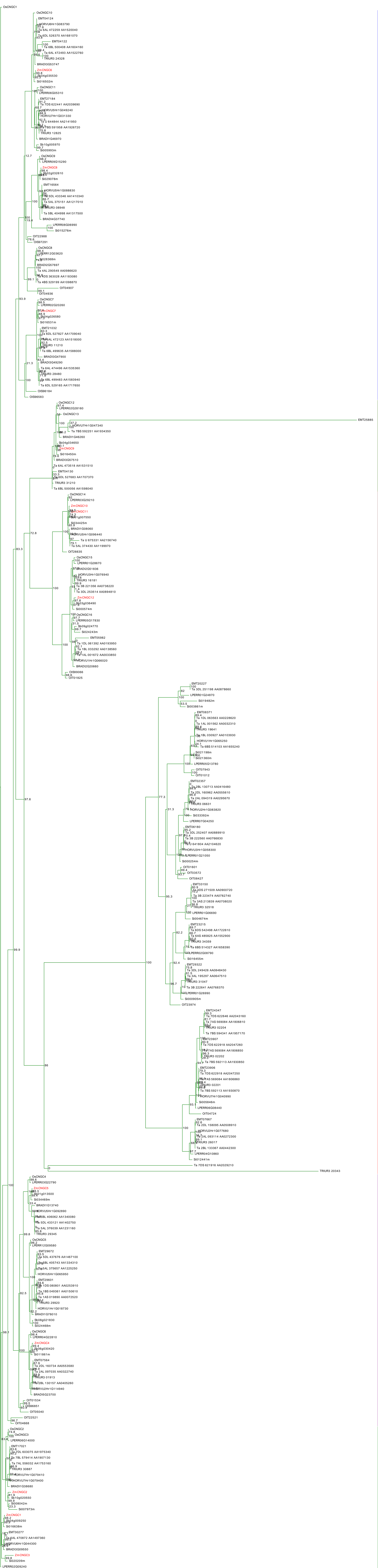


Supplemental File 4

The Maximum likelihood (ML) tree based on the maize and other 11 gramineous plants CNGCs protein sequences by using IQTREE.

The multiple alignment was performed by ClustalX program. IQTREE was used to create the Maximum likelihood (ML) with JTT+LG4 model. The tree was constructed with 1000 bootstrap replications.



III

IVa

IVb

IV

II

I