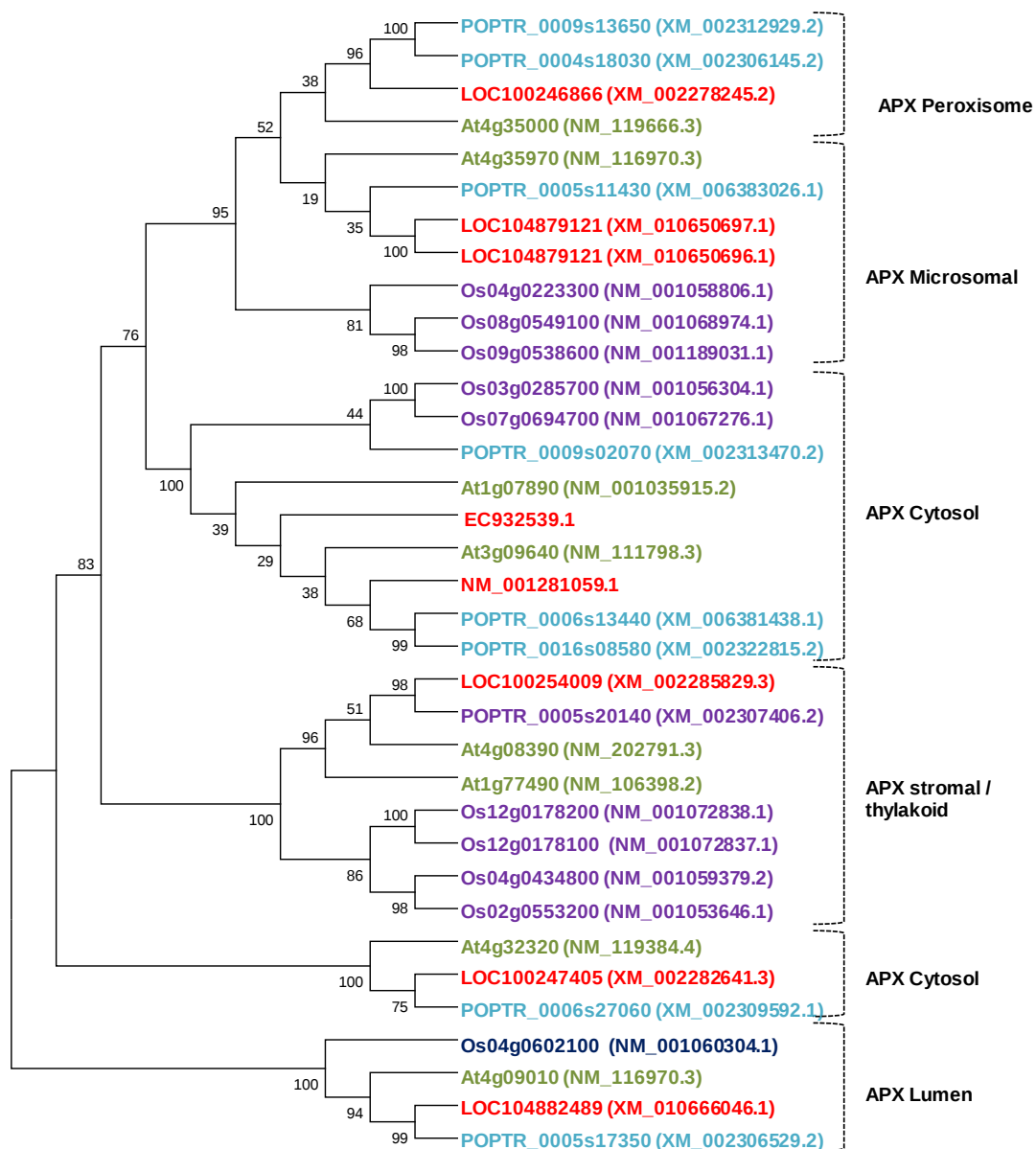
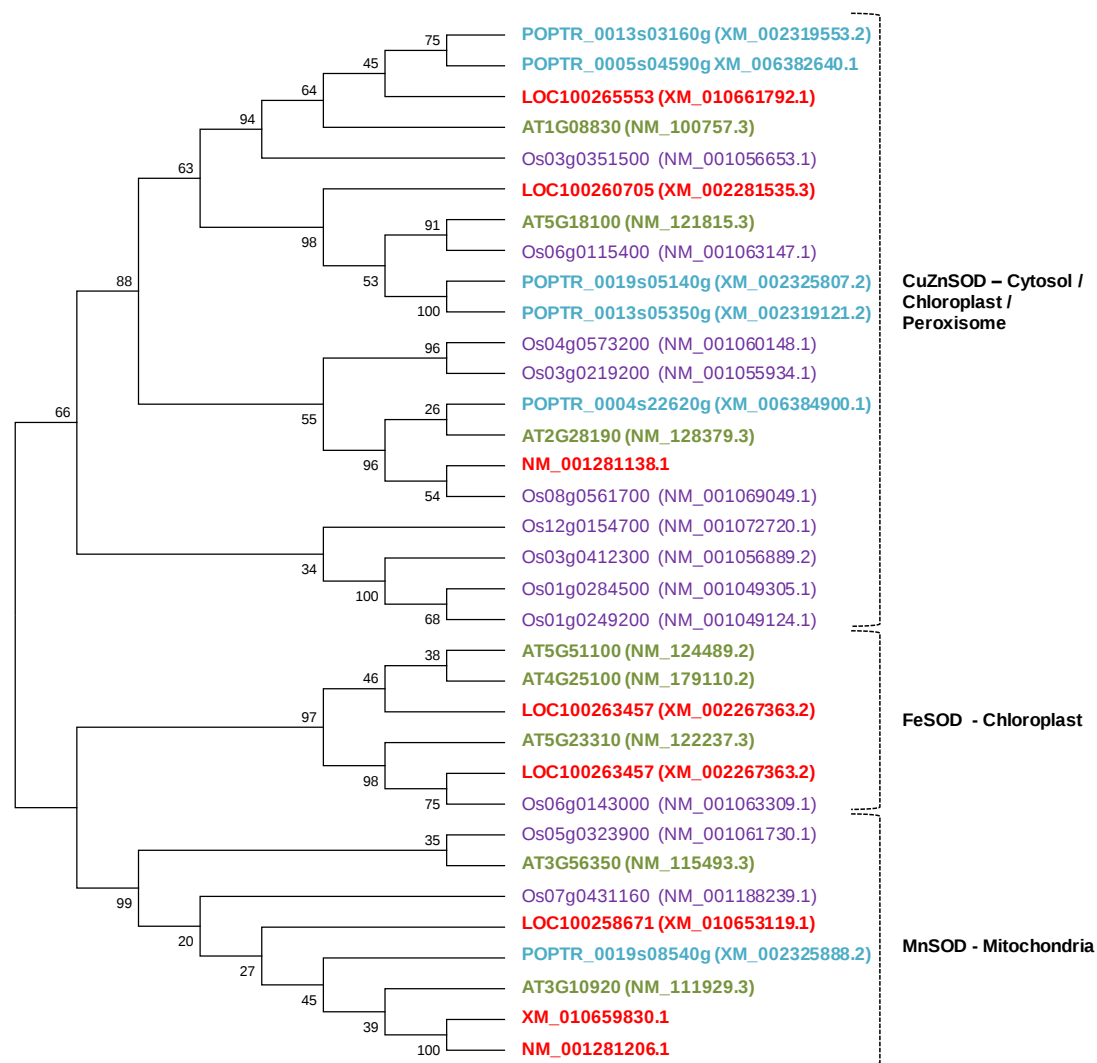


Each dendrogram was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura and Nei., 1993). The bootstrap consensus tree inferred from 500 replicates. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. Analyses were conducted in MEGA6 (Tamura et al., 2013). Species are colour coded: **Light blue** for *Populus trichocarpa*; **Purple** for *Oryza sativa* L. ssp. Japonica; **Green** for *Arabidopsis thaliana* and **Red** for *V.vinifera*. The genes used in the analysis were retrieved from NCBI. The location was hypothesized from *Arabidopsis* location annotated in NCBI database.

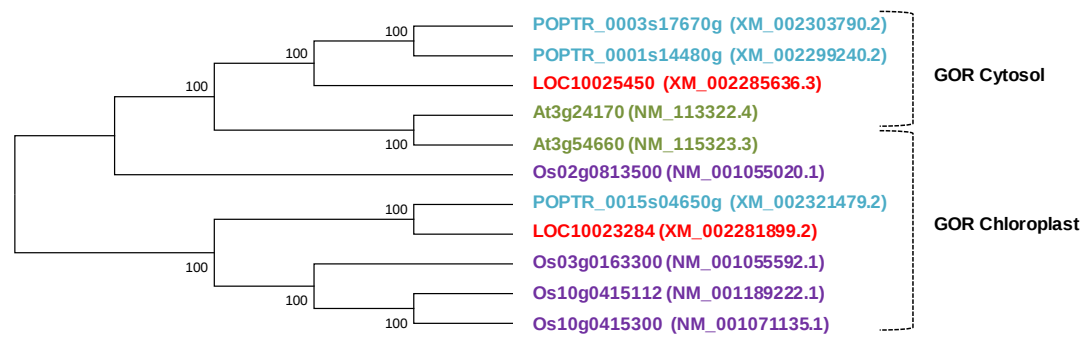
Ascorbate Peroxidase (APX) dendrogram



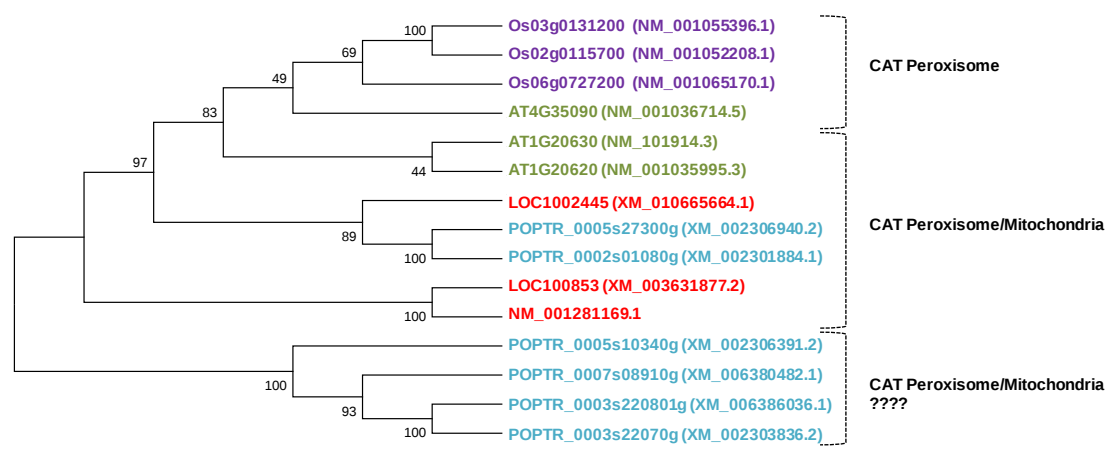
Superoxide Dismutase (SOD) dendrogram



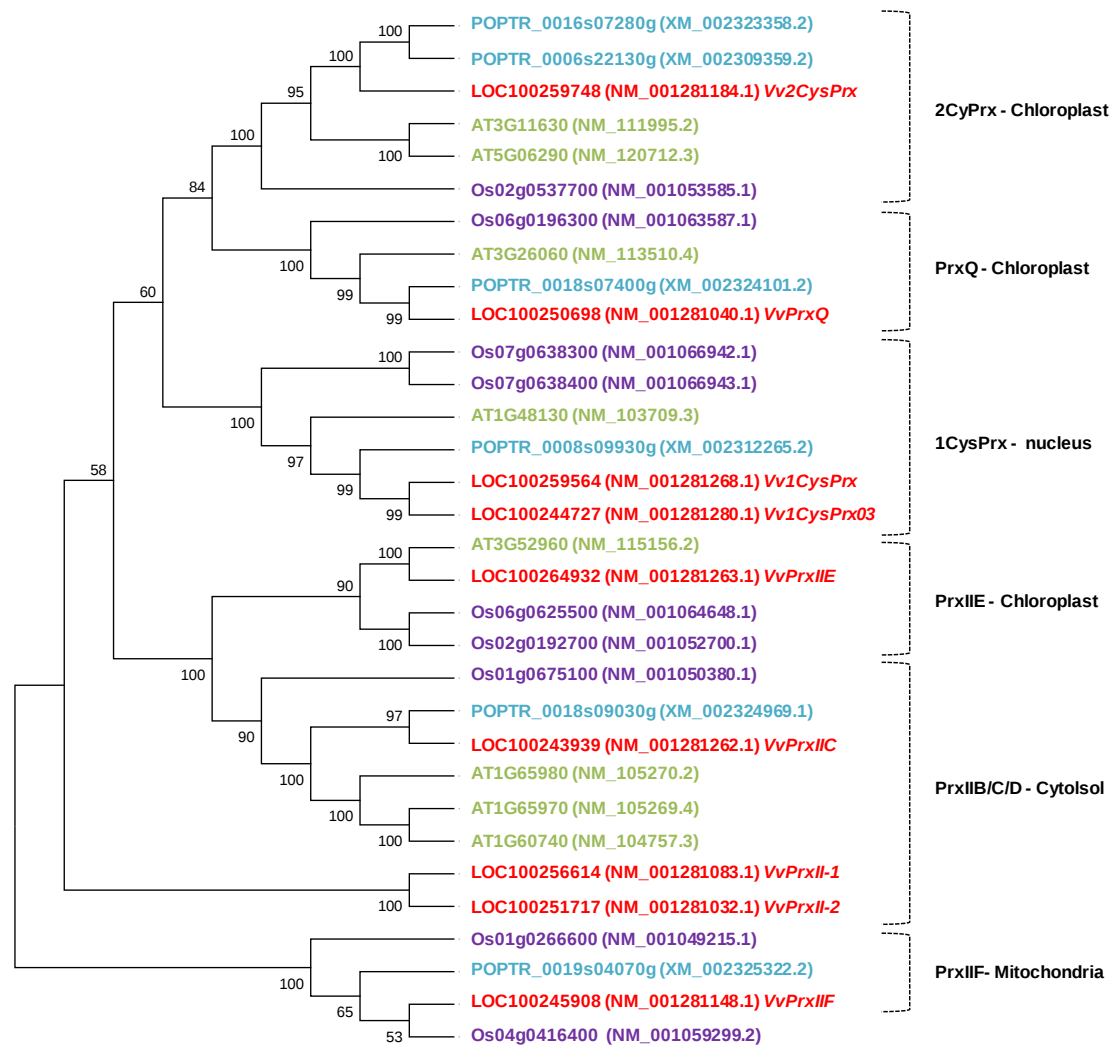
Glutathione Reductase (GOR) dendrogram



Catalase (CAT) dendrogram



Peroxiredoxin (Prx) dendrogram



Prx analysis was repeated without [Os06g0196301 \(NM_001063587.2\)](#), [POPTRDRAFT_814344 \(XM_002319807.1\)](#), [POPTRDRAFT_28808 \(XM_002327341.1\)](#) and [POPTRDRAFT_589333 \(XM_002326269.1\)](#) that were recently removed from NCBI records and had been included in the analysis performed by Vidigal et al (2013); however, there were no changes in the dendrogram's results.

SUPPLEMENTAL FIGURE 1 REFERENCES

Tamura K. and Nei M. (1993). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Molecular Biology and Evolution* 10:512-526.

Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725-2729.