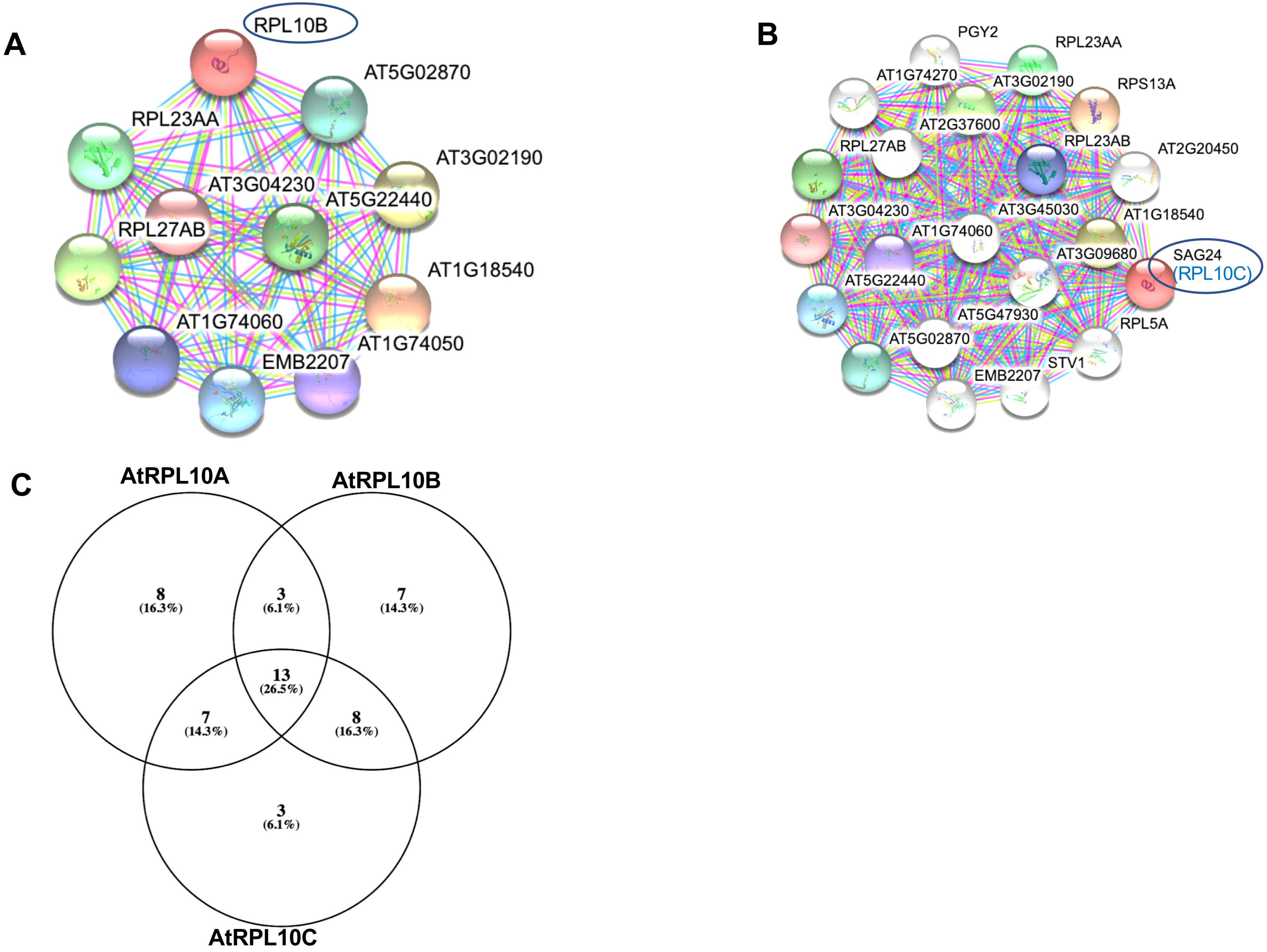

Fig. S10. *In silico* Prediction of AtRPL10A, AtRPL10B and AtRPL10C interacting proteins. (A) AtRPL10 interacting protein network. (B) AtRPL10C interacting protein network. The interactions were predicted using STRING bioinformatic tool (https://string-db.org). (C) Venn diagram showing the common and unique proteins that putatively interacts with specific RPL10 proteins. The common and unique proteins were sorted using VENNY 2.1 and the detailed list is presented in Table S3.