

Figure S1: Functional pathway classification of Al-induced significantly changed proteins in (i) apical 1-cm root apex Segment 1 (and (ii) elongation/maturation Segment 2 tissues of switchgrass. Each color in the pie chart represents a pathway. The number beside the pathway indicates the number of proteins involved in that pathway. The *Arabidopsis thaliana* protein accessions annotated to these switchgrass proteins were listed in the annotated switchgrass database (*Panicum virgatum* v1.1, Phytozome v11.0). The pathways were developed using *A. thaliana* databases in Mapman.

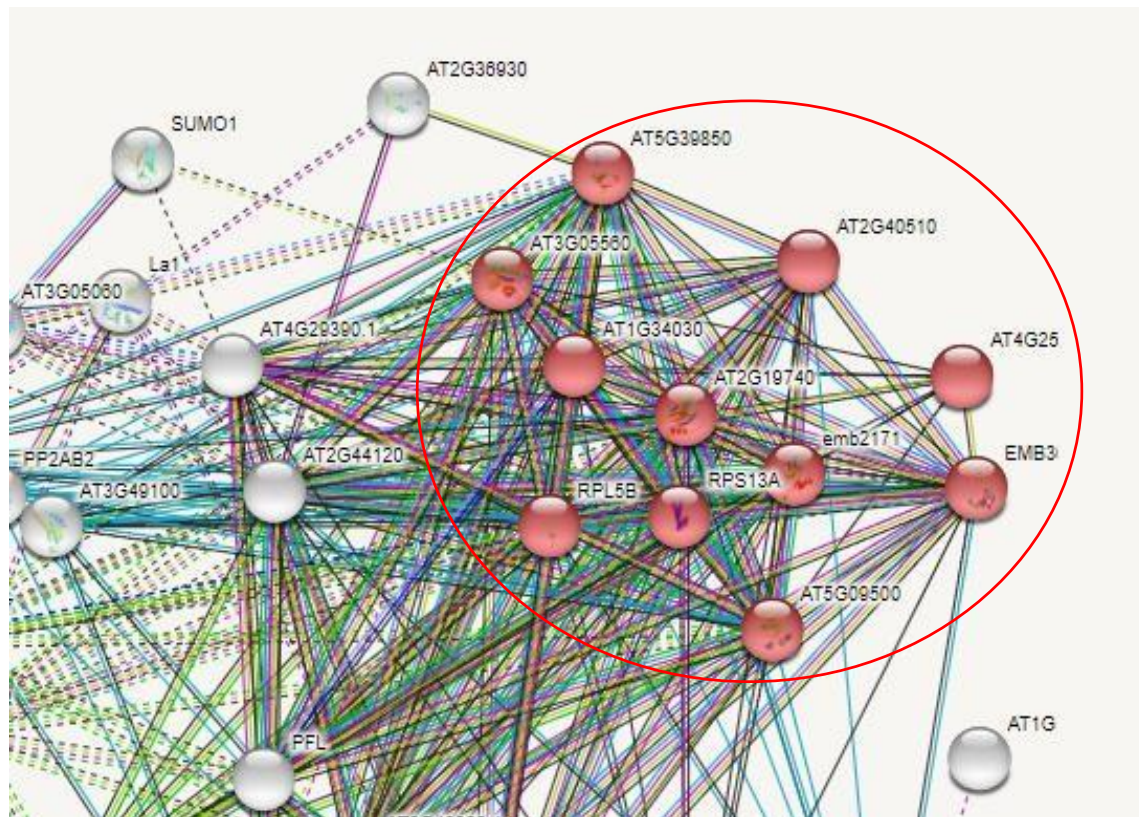


Figure S2. A STRING network of 11 switchgrass apical root tip tissue proteins involved in translation pathway and these 11 proteins showed a higher abundance level under the AI treatment condition. The association network was developed in STRING software using the homologous protein accessions from *Arabidopsis thaliana*.

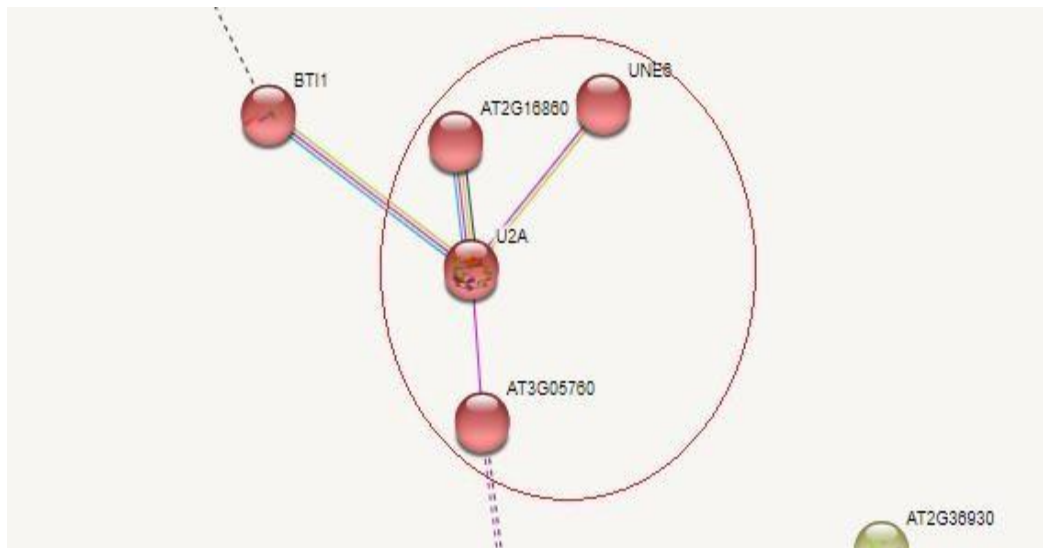


Figure S3. The STRING network involved in post transcriptional modifications occurring in 400  $\mu$ M Al-treated switchgrass apical root tips of switchgrass. The association network was developed using homologous protein accessions from *Arabidopsis thaliana*.

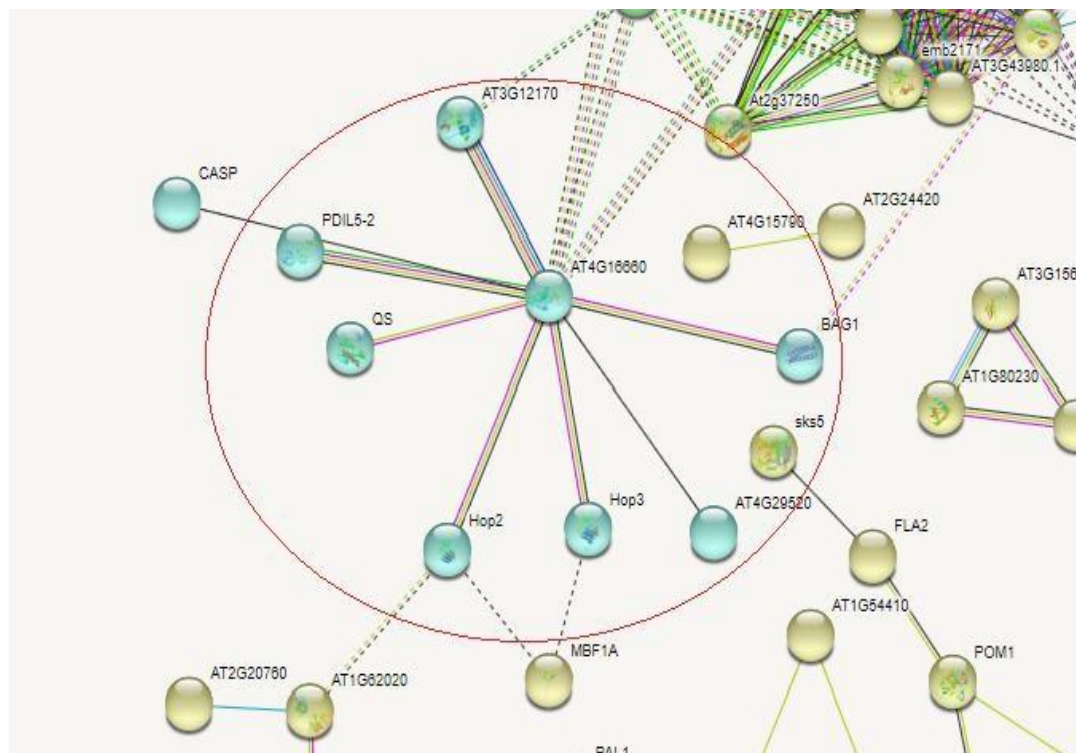


Figure S4. The STRING cluster associated with protein folding functions. These switchgrass proteins had a higher abundance level in Al-treated apical 1-cm root- tip tissues compared to non-treated control plants. The association network was developed using homologous protein accessions from *Arabidopsis thaliana*.

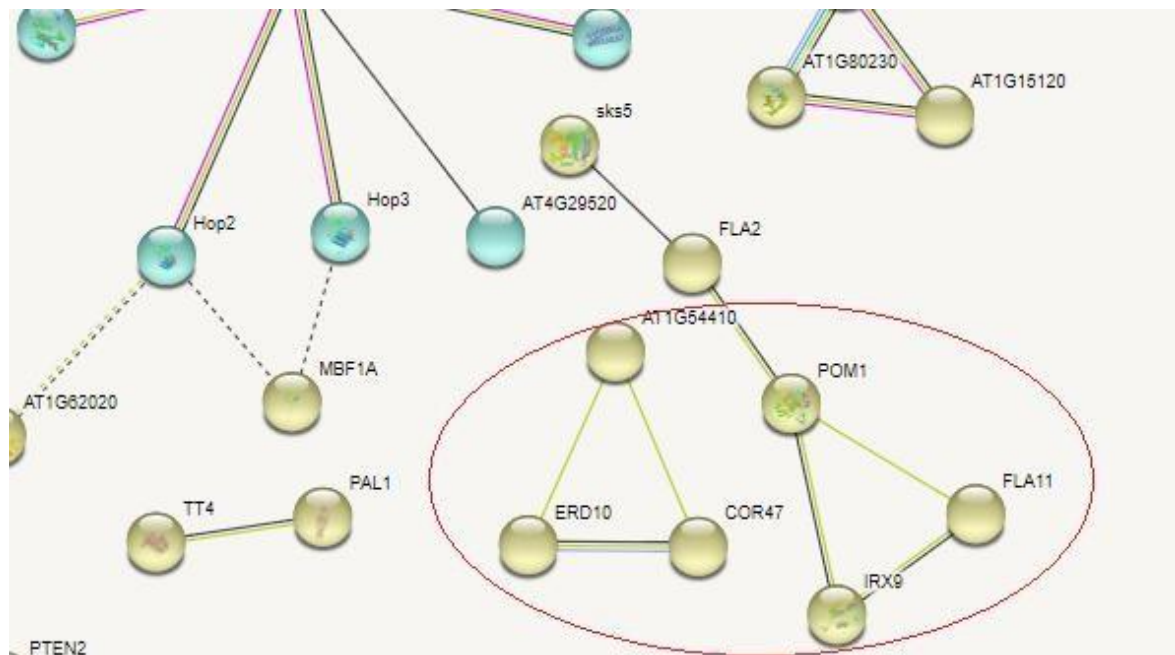


Figure S5. A STRING cluster of stress related proteins showing a higher abundance level in Al-treated apical 1-cm root tip tissues of switchgrass plants. This cluster includes dehydrins and peroxidases and other stress proteins. The association network was developed using homologous protein accessions from *Arabidopsis thaliana*.

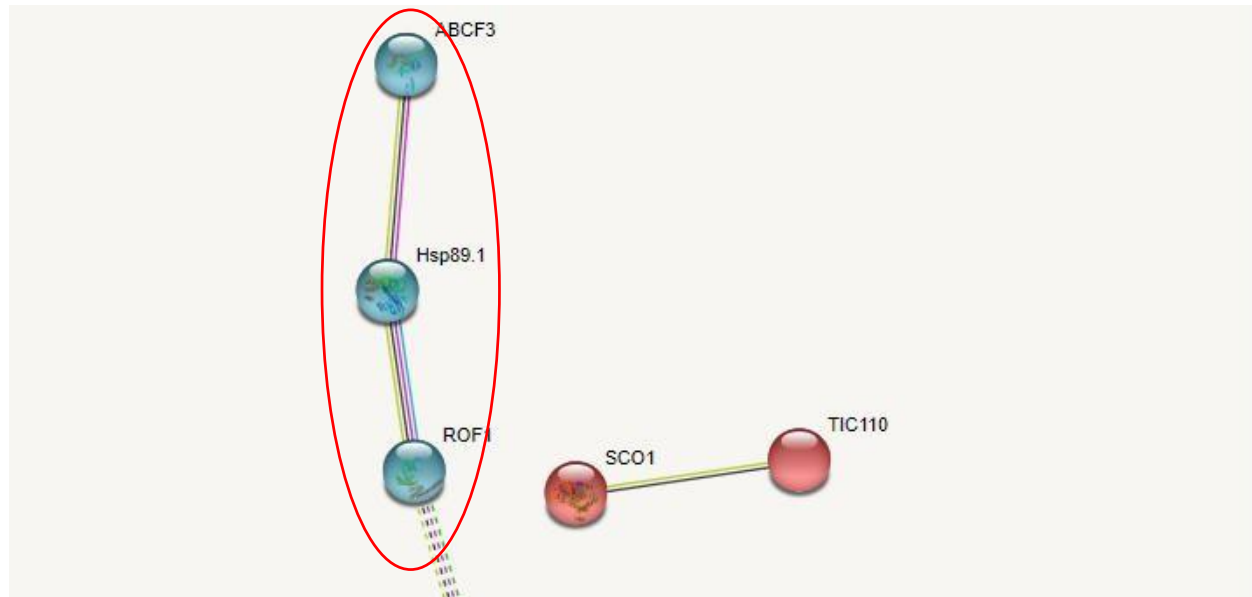


Figure S6. The STRING cluster of proteins in protein metabolic pathway. These proteins were identified at a reduced abundance level in Al-treated apical 1-cm root- tip tissues of switchgrass plants. The association network was developed using homologous protein accessions from *Arabidopsis thaliana*.

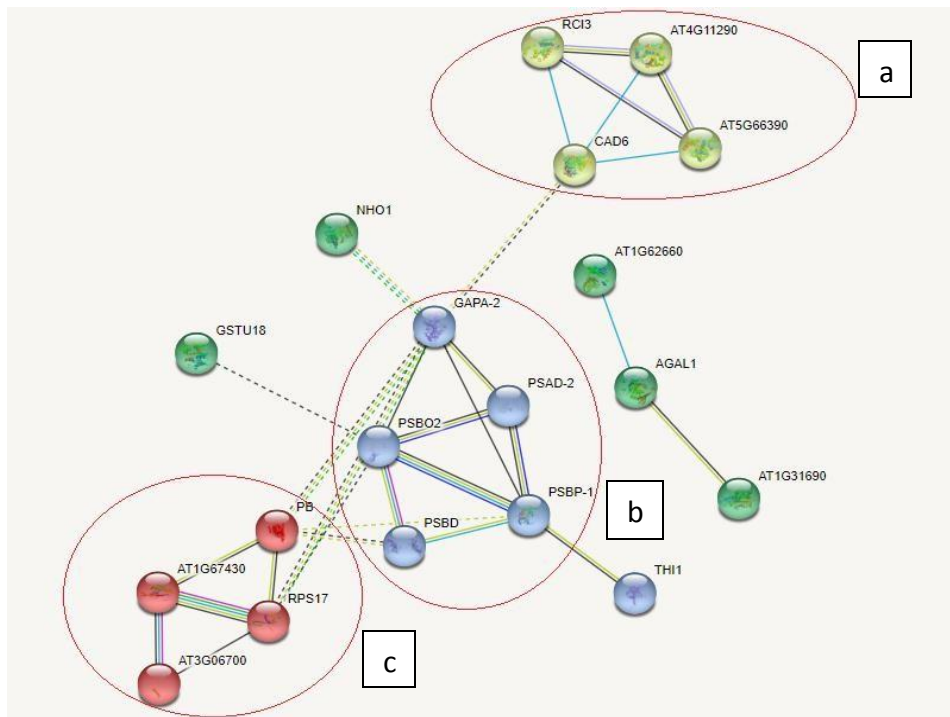


Figure S7. The STRING clusters of proteins showing significantly lower abundance levels in root elongation/maturation zones from the AI-treated to the non-treated switchgrass plants. The association network was developed using homologous protein accessions from *Arabidopsis thaliana*.

- a) A cluster of proteins involved in energy-related pathways.
- b) A cluster of proteins in the phenylpropanoid pathway.
- c) A cluster of proteins involved in protein metabolic pathways.