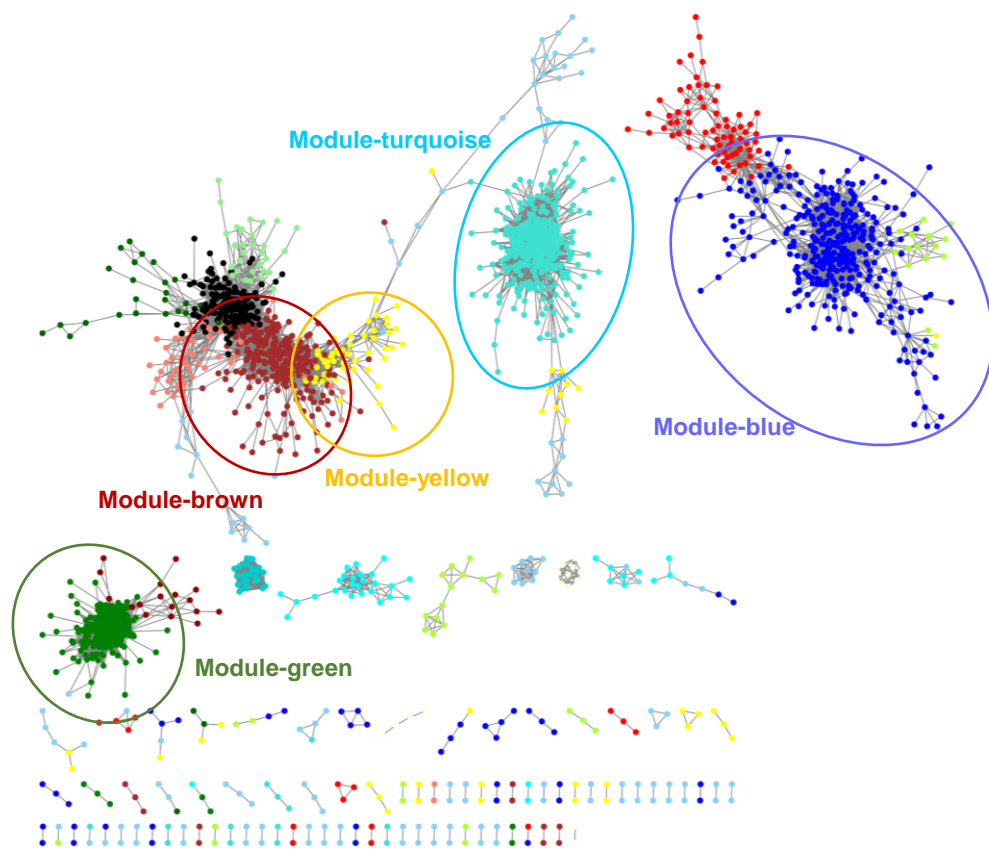


A



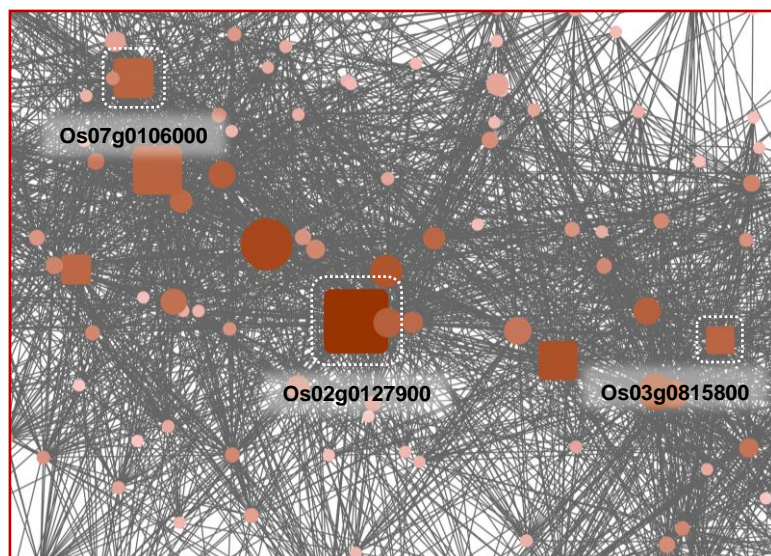
Module color / number of nodes

R value between  
ME and SLA

Module-brown / 393	-0.87 ( $p < 0.01$ )
Module-salmon / 82	-0.83 ( $p < 0.01$ )
Module-yellow / 375	-0.78 ( $p < 0.01$ )
Module-darkgreen / 40	-0.68 ( $p < 0.01$ )
Module-darkred / 42	0.68 ( $p < 0.01$ )
Module-black / 185	-0.62 ( $p < 0.01$ )
Module-palegrey / 47	-0.62 ( $p < 0.01$ )
Module-lightyellow / 45	0.62 ( $p < 0.01$ )
Module-cyan / 73	0.62 ( $p < 0.01$ )
Module-greenyellow / 142	0.60 ( $p < 0.01$ )
Module-lightgreen / 46	-0.57 ( $p < 0.05$ )
Module-green / 372	0.57 ( $p < 0.05$ )
Module-blue / 636	0.57 ( $p < 0.05$ )
Module-darkgrey / 35	0.55 ( $p < 0.05$ )
Module-red / 193	0.51 ( $p < 0.05$ )

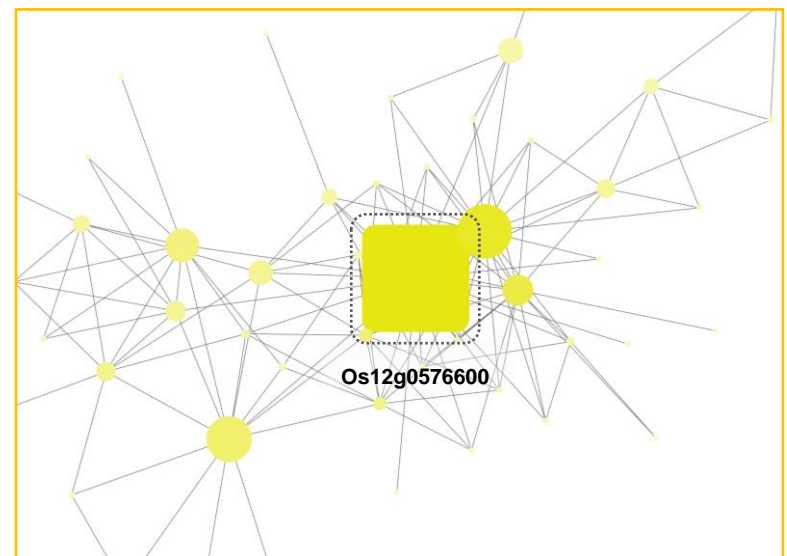
B

Module-brown



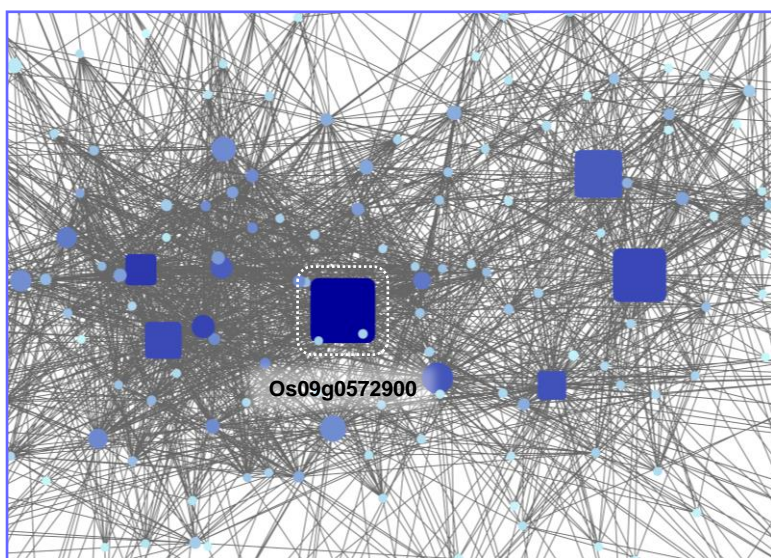
C

Module-yellow



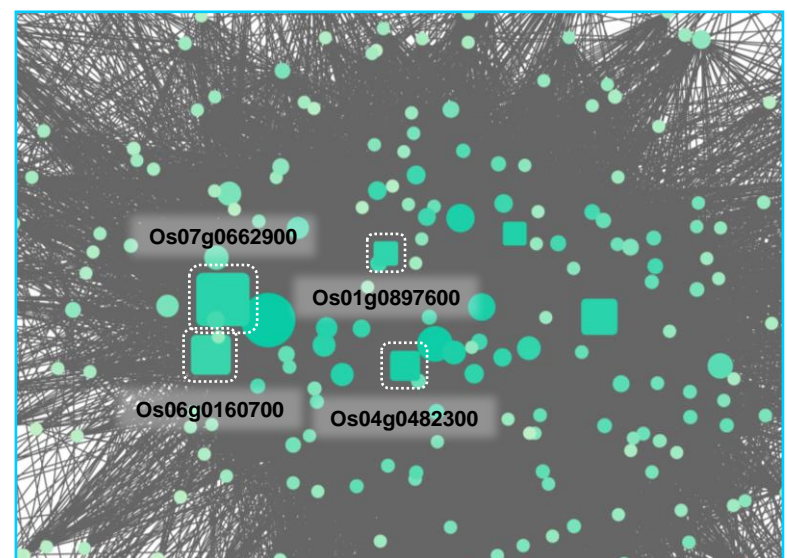
D

Module-blue



E

Module-turquoise

Weight  $\geq 0.1$ 

**Figure 7.** Co-expression network of differentially expressed genes in Koshihikari rice cultivar under control and chronic conditions.

(A) Gene co-expression network was analyzed in the differentially expressed genes (DEGs) under chronic O<sub>3</sub> conditions. The module name and its gene number were listed with top-15 highest correlation co-efficient ( $R$ ) values between module eigengene and single leaf area (SLA). In addition, the detailed network was visualized for the (B) brown, (C) yellow, (D) blue, and (E) turquoise modules. Each node represents a gene, and the shade and size of the node reflect the values of degree and Betweenness centrality, respectively. Each edge represents the connection between nodes. The square nodes are the genes that were detected as hub-gene candidates in each module.