

**Figure 1.** Network generation using pathway studio software version 7.1, network shows the interaction between defense related transcripts identified in chickpea after 48h post infection with Foc1.

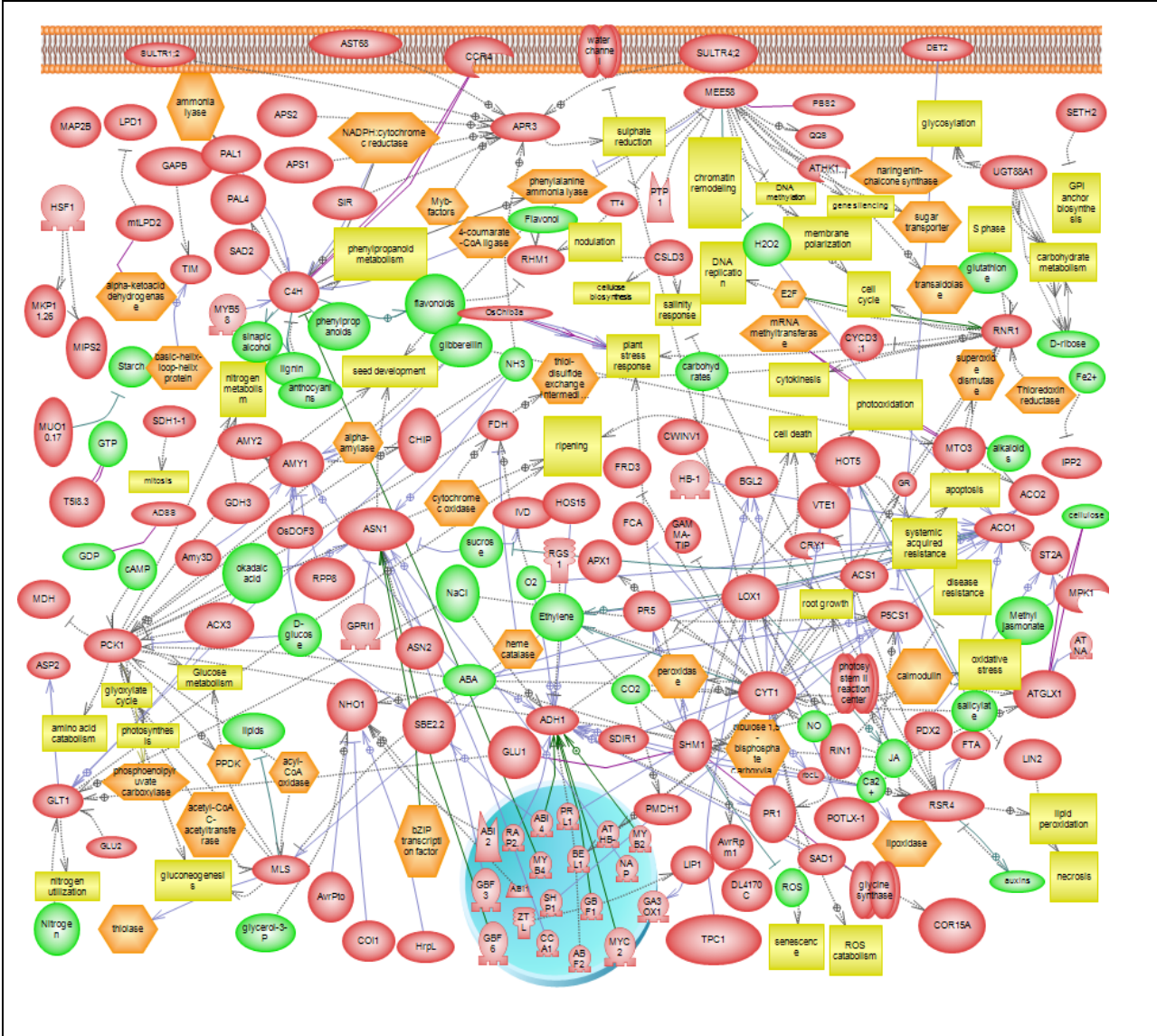


Figure2. Network generation using pathway studio software version 7.1, network shows the interaction between metabolism related transcripts identified in chickpea after 48h post infection with Foc1.

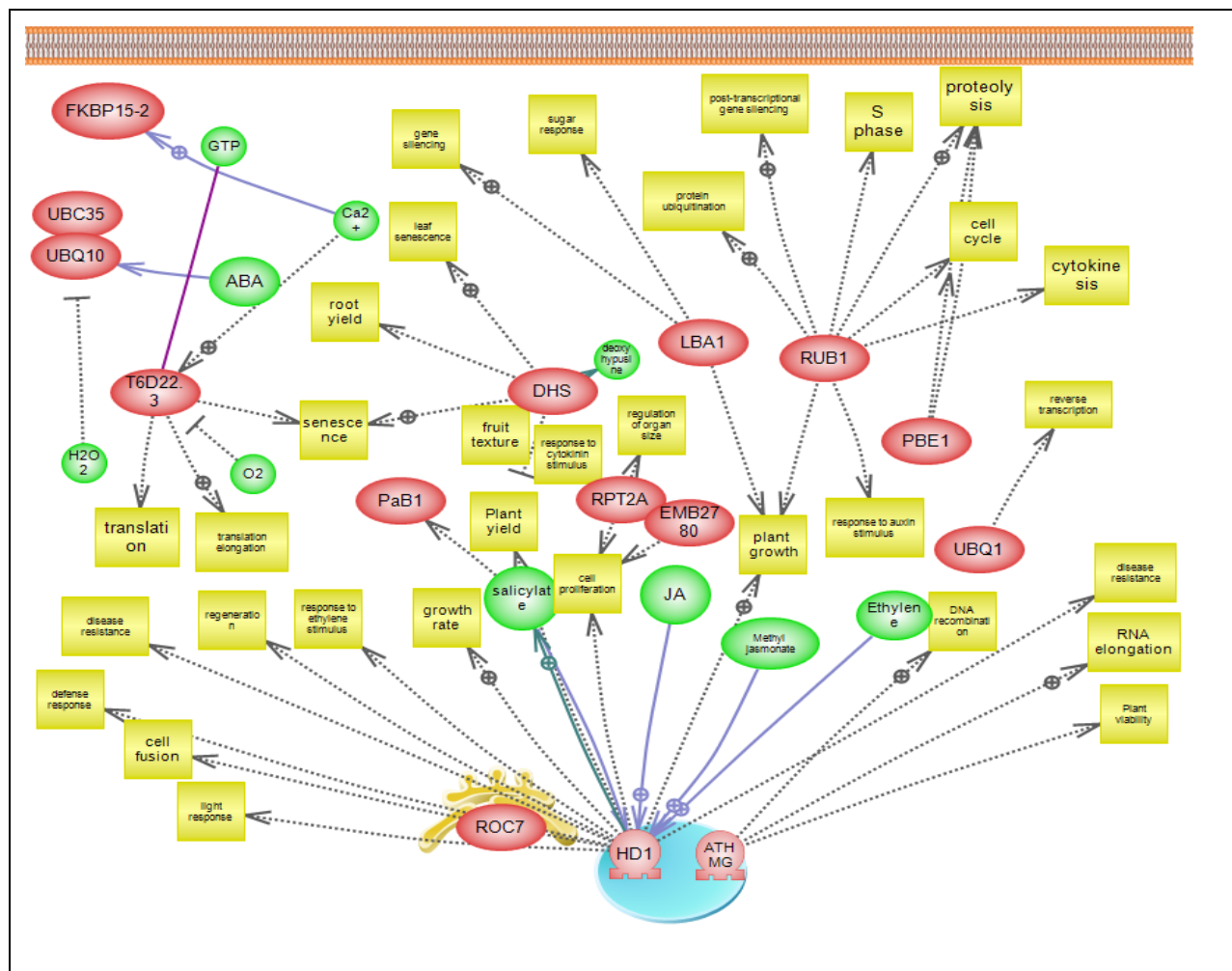
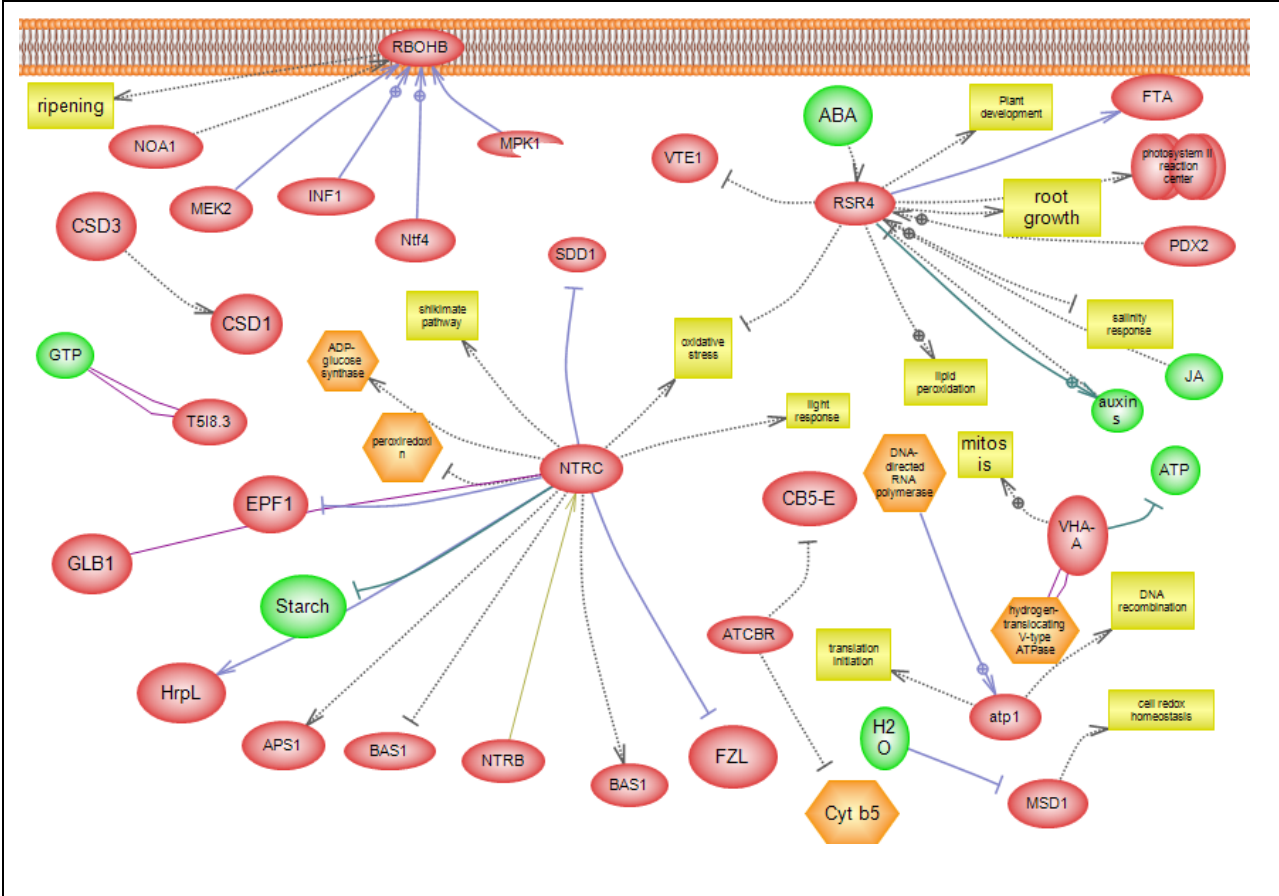


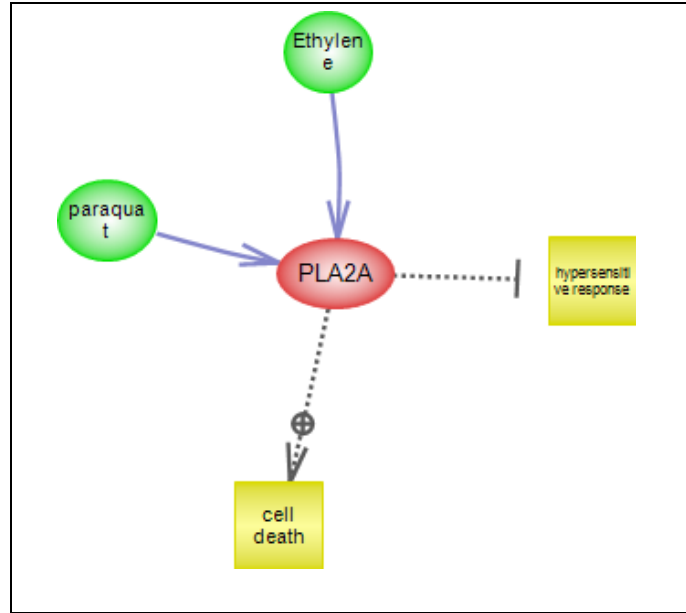
Figure3. **Network generation using pathway studio software version 7.1**, network shows the interaction between transcripts involved in protein synthesis and degradation, identified in chickpea after 48h post infection with Foc1.



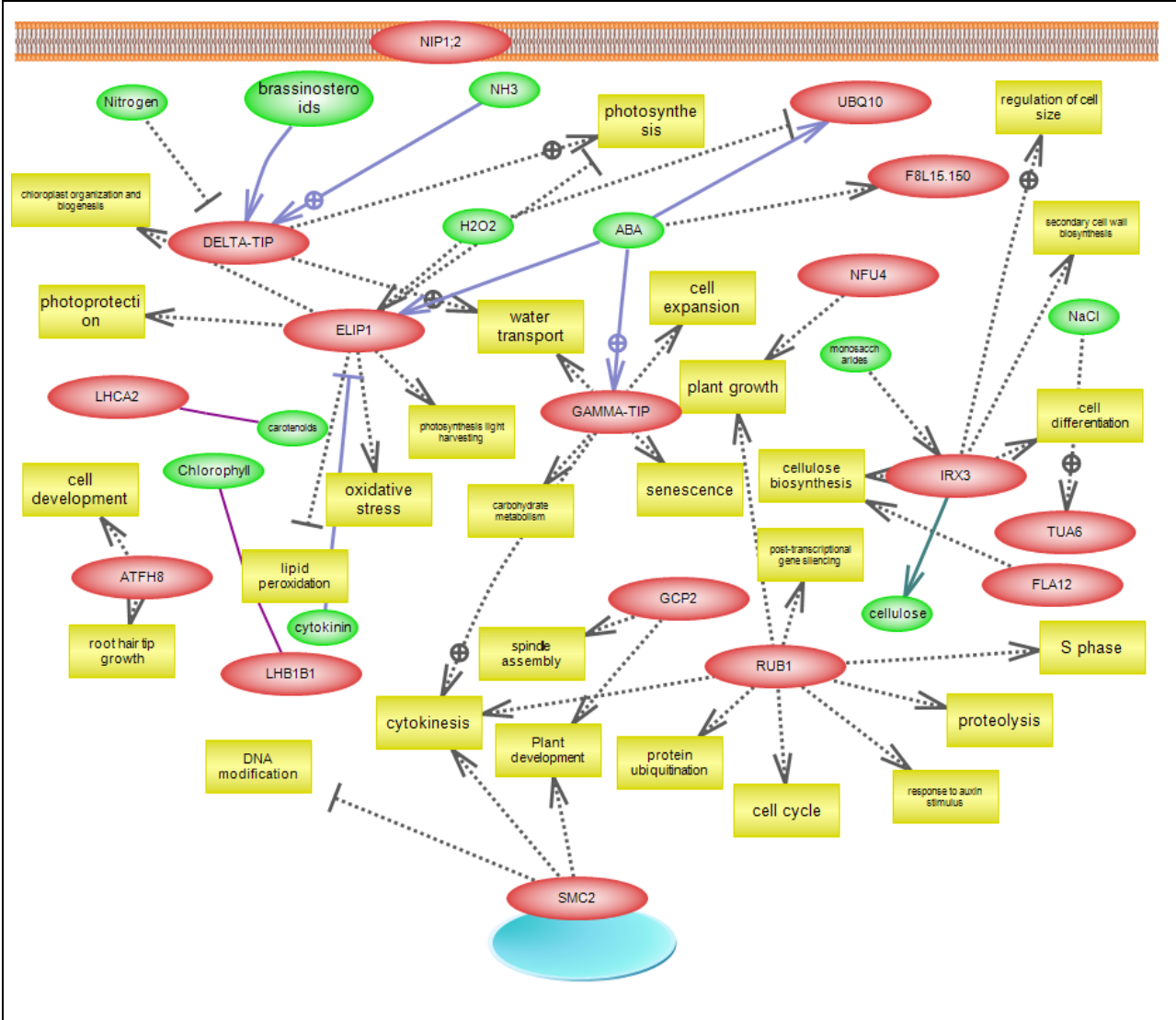
**Figure4. Network generation using pathway studio software version 7.1, network shows the interaction between transcripts involved in Reactive oxygen species generation, identified in chickpea after 48h post infection with Foc1.**



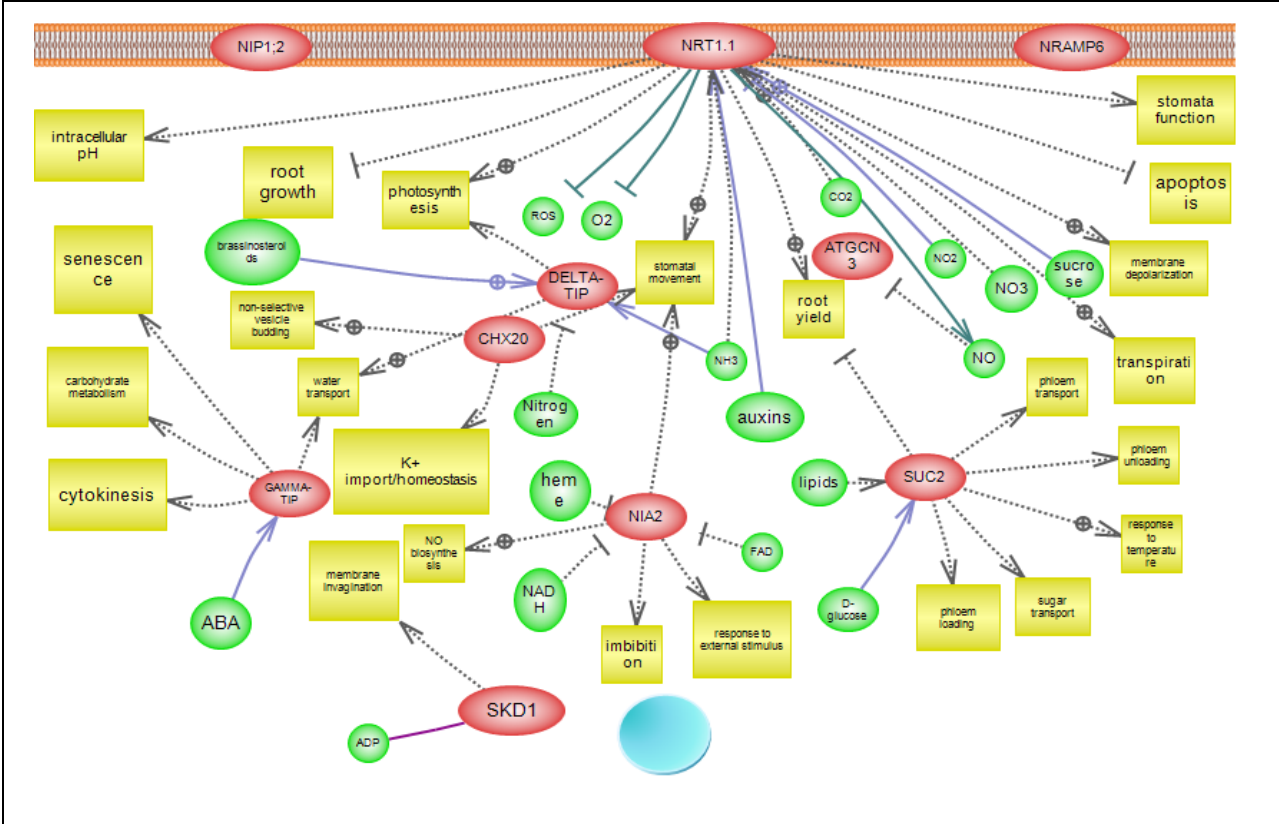




**Figure6. Network generation using pathway studio software version 7.1,** network shows the interaction between transcripts involved in storage during plant defense, identified in chickpea after 48h post infection with Foc1.



**Figure7. Network generation using pathway studio software version 7.1, network shows the interaction between structural transcripts involved in plant defense, identified in chickpea after 48h post infection with Foc1.**



**Figure8. Network generation using pathway studio software version 7.1, network shows the interaction between transport-related transcripts involved in plant defense, identified in chickpea after 48h post infection with Foc1.**