**S1 Table** Gene model and predicted functional annotation based on Phytozome.

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| **Gene model** | **Locus** | **Predicted functional annotation on Phytozome** |
| *KTR2/3* | *Co-x* | *Serine/Threonine-protein kinase-like protein CCR3- related* |
| *Phvul.001G243800* | *Co-1* | Serine/Threonine-Protein Kinase-Like Protein CCR3-Related |
| *Phvul.001G244300* | *Co-AC* | Clathrin Heavy Chain (CLTC) |
| *Phvul.001G244400* | *Co-AC* | Uncharacterized protein |
| *Phvul.001G244500* | *Co-AC* | Basic Helix-Loop-Helix (bHLH) domain-containing protein with possible regulation of transcription function |
| *Phvul.001G245300* | *CoPv01CDRK* | Protein Tyrosine Kinase (Pkinase\_Tyr) // Leucine Rich Repeat N-terminal domain (LRRNT\_2) |
| *Phvul.001G246300* | *CoPv01CDRK/ PhgPv01CDRK* | Abscisic Acid Receptor PYL5 |
| *Phvul.003G109100* | *PR1a* | Pathogenesis-related protein 1 (PR1) |
| *Phvul.006G196900* | *PR1b* | Pathogenesis-related protein Bet v I family (Bet\_v\_1)) |
| *Phvul.009G256400* | *PR2* | Glucan endo-1,3-beta-D-glucosidase / Laminarinase |