Appendix B

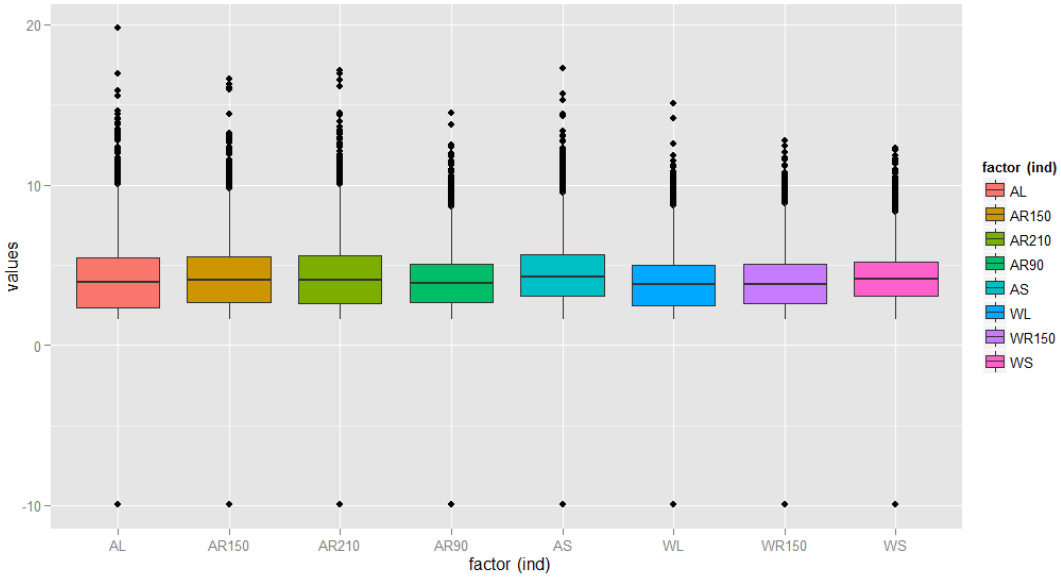

Fig. S1 The distribution of reads from the eight libraries based on sequencing data

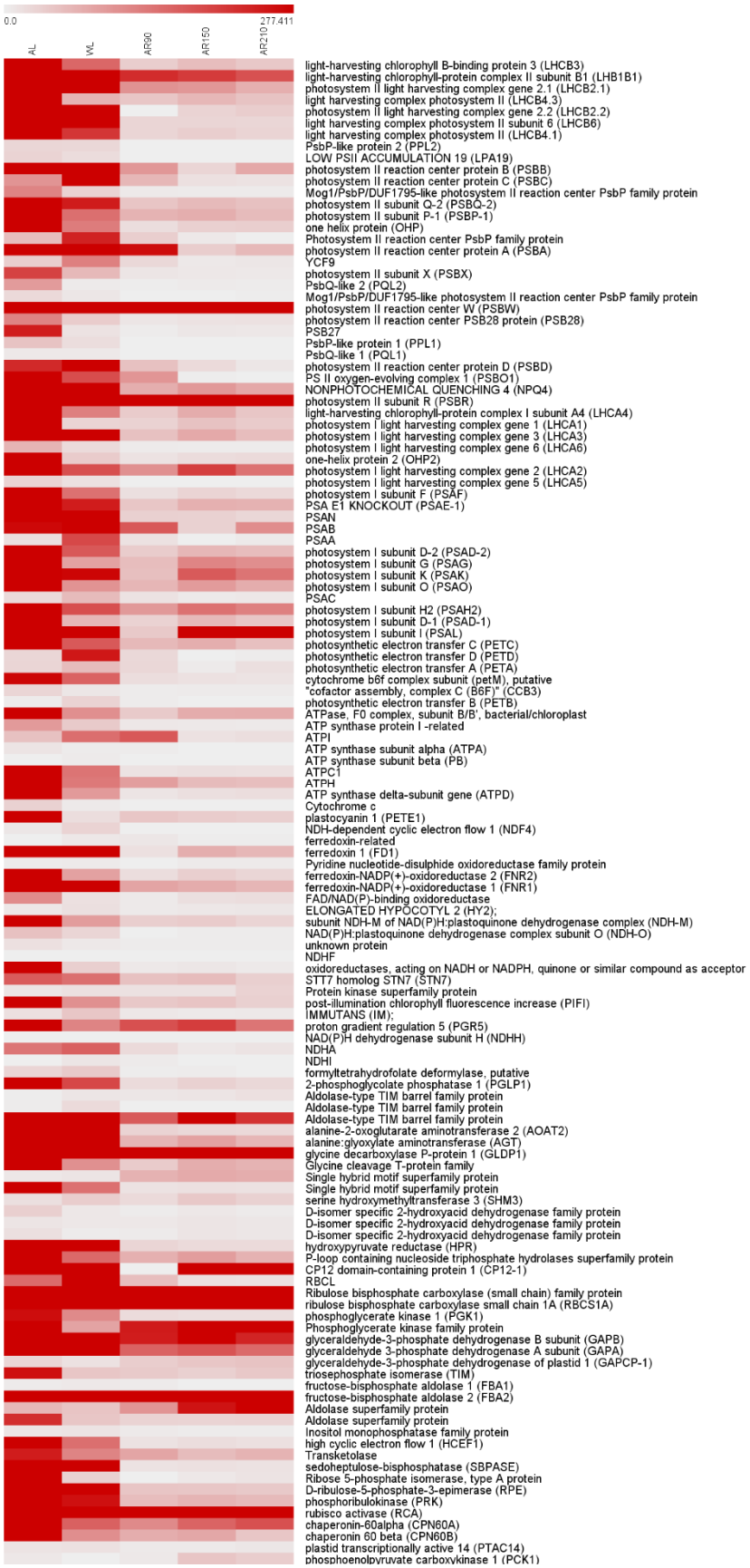

Fig. S2 The expression heat map of genes for photosynthesis in leaves and storage roots of Arg7 and W14. The bar at the top represents the FPKM intensity (log2) of these photosynthesis relevant genes.

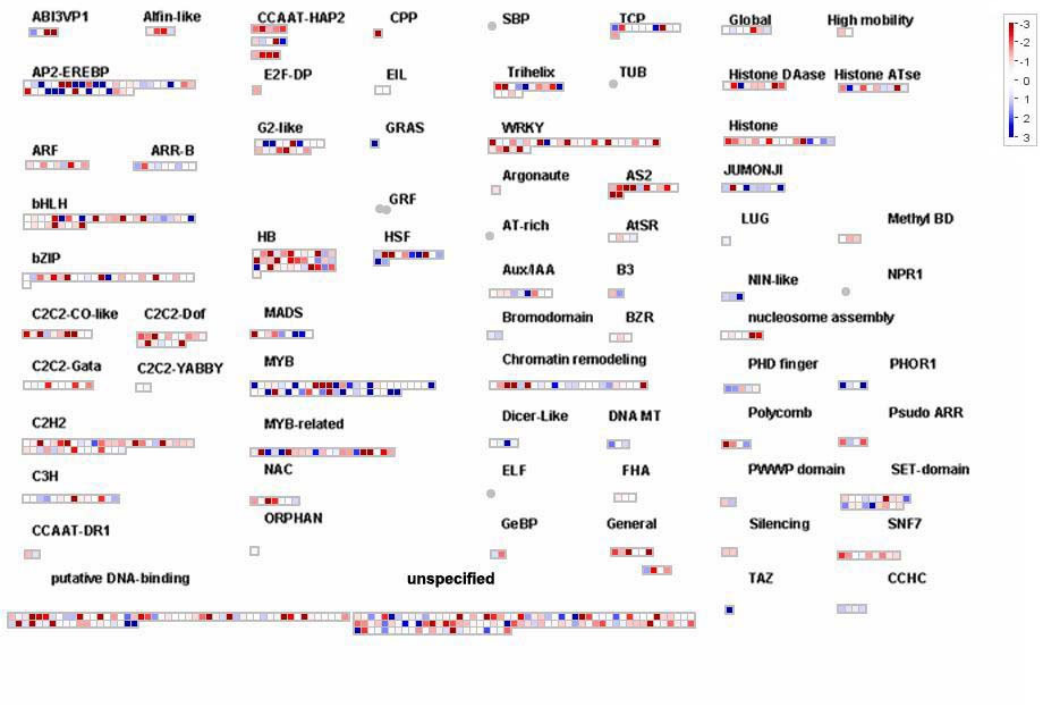

Fig. S3 Genes for transcription factors with significantly higher expression in developing stems of Arg7 than in W14. Colored rectangles correspond to the value of log2 (the FPKM of WL/AL): blue means that a gene expressed folds in W14 than Arg7, but red is converse.

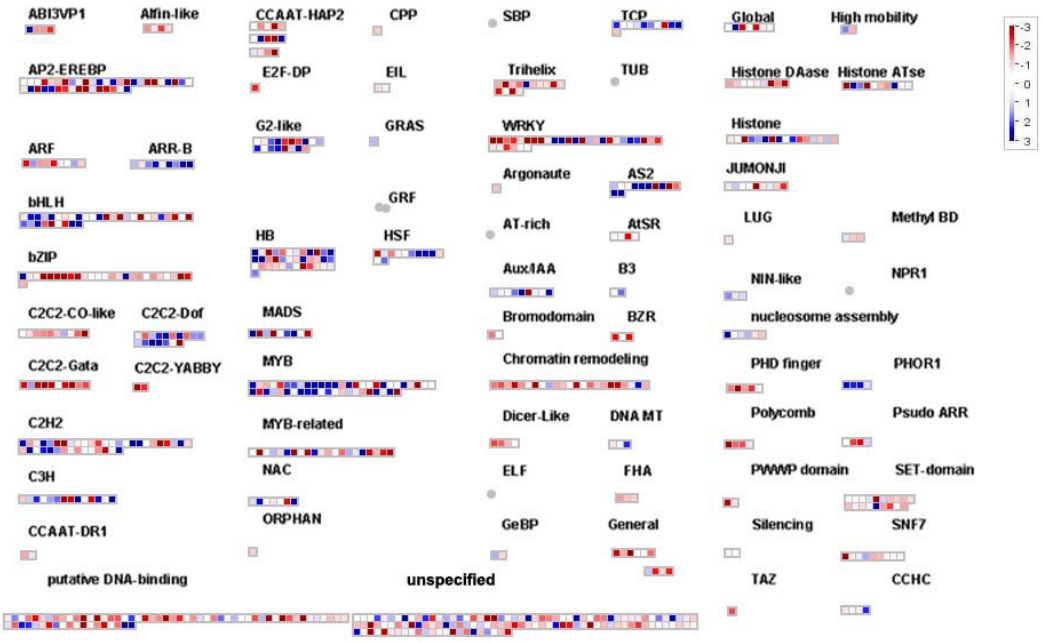

Fig. S4 Genes for transcription factors with significantly higher expression in storage roots of Arg7 than in W14. Colored rectangles correspond to the value of log2 (the FPKM of WR150/AR150): blue means that a gene expressed folds in W14 than Arg7, but red is converse.

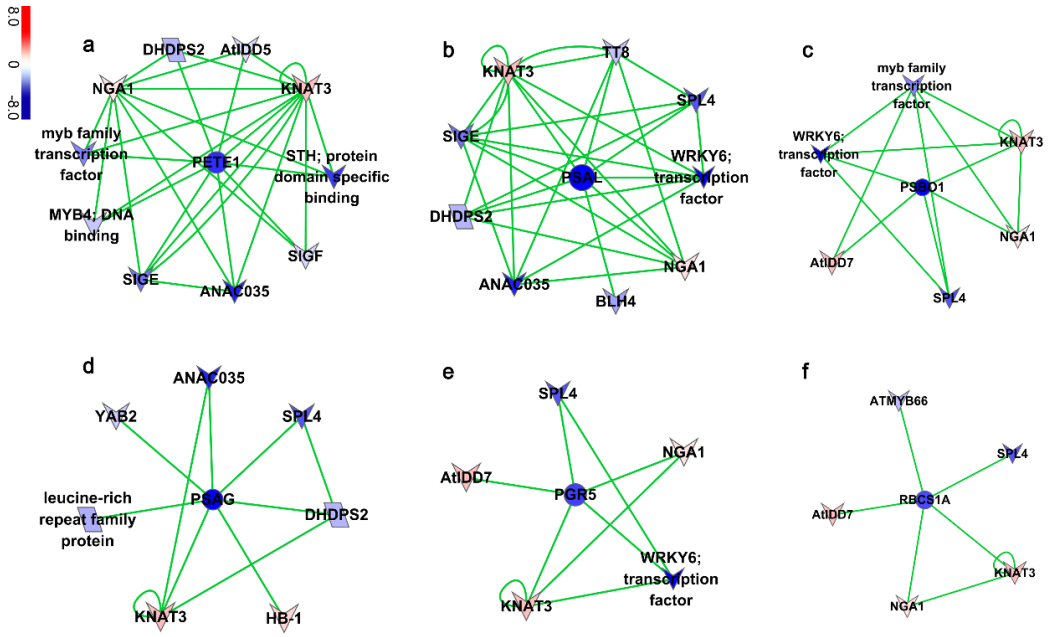

Fig. S5 Six co-expression sub-networks associated with photosynthesis inferred from MINET. Colored correspond to the value of log2 (the FPKM of WL/AL): blue means that a gene expressed folds in W14 compare to Arg7, whereas red means the converse

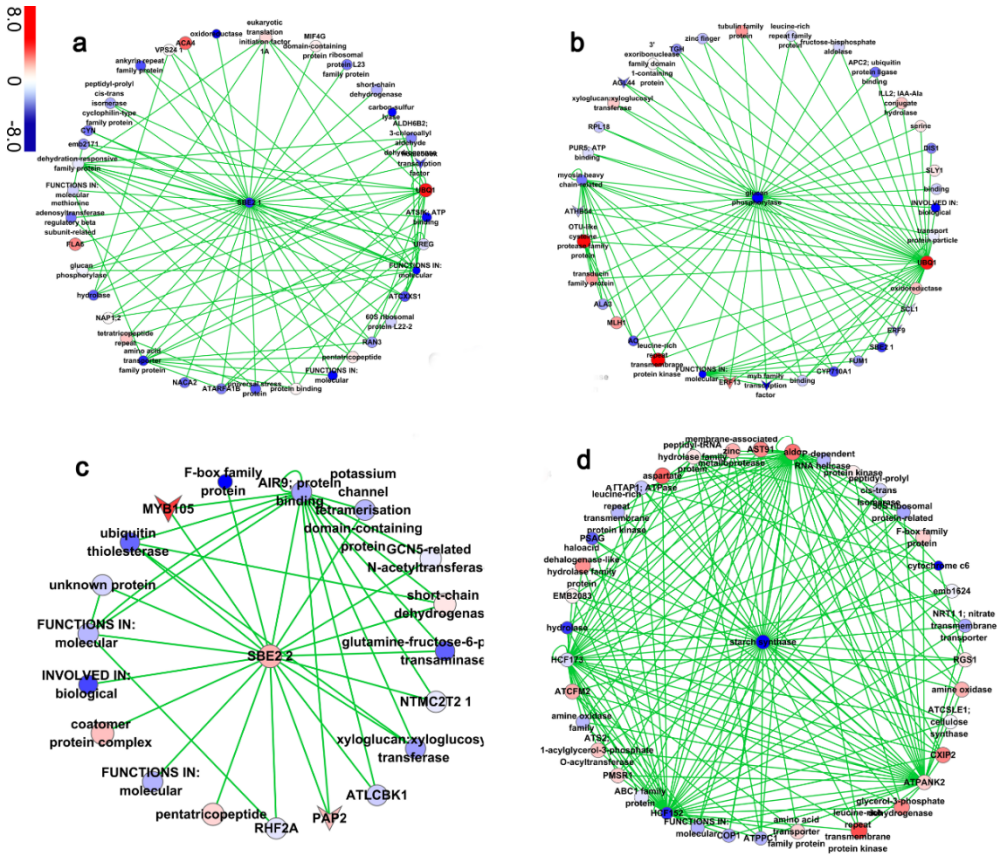

Fig. S6 Four co-expression networks associated with starch metabolism in storage roots of cassava inferred from MINET. Colored correspond to the value of log2 (the FPKM of WR150/AR150): blue means that a gene expressed folds in W14 than Arg7, whereas red means the converse