



Additional file 3. Clustering analysis of transcript expression profiles. The hierarchical clustering is divided into 20 groups, which was further subdivided into 81 subgroups (colored lines in each cluster). These genes characterized genes investigated in this manuscript belong to the following cluster groups/subgroups: cytochrome P450 reductase (POR) 2A (Sobic.002G295100), CAS (Sobic.006G016900) and ACC oxidase (Sobic.003G197200) in 3-1; POR2C (Sobic.006G245400) in 5-2; POR2B (Sobic.007G088000) in 6-3; cytochrome P450 (CYP) 79A1 (Sobic.001G012300) and UDP-glycosyltransferase (UGT) 85B1 (Sobic.001G012400) in 8-1; nitrilase (NIT) 4B1 (Sobic.004G225000) in 10-1; CYP71E1 (Sobic.001G012200) in 12-1; HNL (Sobic.004G335500) in 13-1; NIT4B2 (Sobic.004G225100) in 15-2 and NIT4A (Sobic.004G225200) in 20-2. The number of genes in each cluster is listed in parenthesis next the cluster number. The grey field represents the span of all the expression profiles in a single cluster. The dashed line represents the concentration of dhurrin pr. mg tissue through the development in relation to the expression profiles.