Supplementary Figure S2: Gene-metabolite co-expression network using probes with at least one eQTL (after correction for seed color). Nodes represent genes or fatty acids (FAs). Genes from different pathways are shown in different node colours, while metabolites are shown in triangle-shaped nodes in purple colour. Edges represent high absolute correlations ($|r| > 0.5$). Edges between genes within the same pathway are in blue, edges connecting genes and FAs are in green, edges connecting FAs are in purple. Edges connecting genes of different pathways have been left out to improve the visibility of the network. The shapes of gene nodes indicate *cis*-eQTLs (V-shape), *trans*-eQTLs (square) and *cis*-/*trans*-eQTLs (diamond). Node names are coded by concatenating gene name, *cis*-/*trans*-regulation (separated by "_") and linkage group (separated by "-"). For example, node "FAD2_C-5" indicates gene "FAD2", "C" for *cis*-eQTL and "5" for linkage group A05, where the *cis*-eQTL was detected. In the case of a *cis*-/trans-eQTL, "LACS2_CT-5_6" indicates gene "LACS2" and "CT-5_6" indicates a *cis*-eQTL on A05 and *trans*-eQTLs on A06. Solid lines indicate positive correlations and dotted lines indicate negative correlations. All the gene names are prefixed with "Br" because of *Brassica rapa* gene nomenclature. Multiple occurrence of the same gene name represents genes with multiple paralogues or probes.