



**Supplementary Figure S1:** Heatmap showing the eQTL LOD scores for gene expression of the probes measured in RT-qPCR. eQTL LOD profiles were calculated after correction for seed colour. *Brassica rapa* gene IDs (Bra IDs) are indicated between parentheses and the gene locations in the genome are preceded by “\_” in the gene name. The darker the intensity, the higher the LOD score. Yellow indicates a QTL effect with high transcript abundance being associated with a yellow sarson allele while blue indicates a QTL effect with high transcript abundance being associated with the pak choi allele. Red triangles indicate the positions of QTL peak markers. The black coloured tick marks at the bottom indicate the markers in the linkage map, vertical dashed lines separate linkage groups. The horizontal dotted lines separate genes.