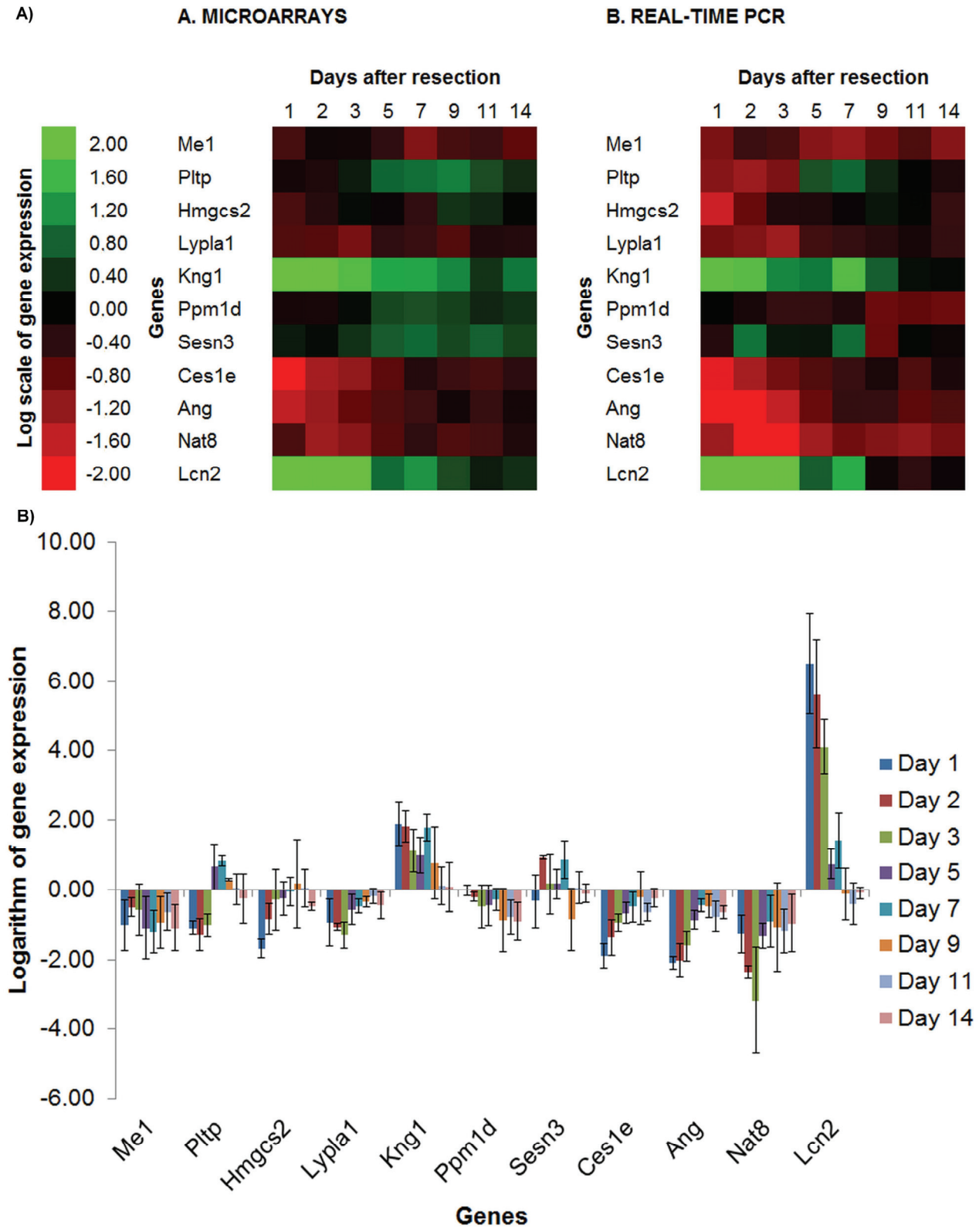

Fig. S2. Results of microarray and RT-PCR analyses and their comparison. Figure S2 displays the same data as Figure 2. Additionally it presents standard deviation error bars for the RT-PCR data. These were omitted in the Figure 2 to keep it clear. Both sections of the picture are based on log_2-transformed relative expression data. Thanks to this transformation, microarray and RT-PCR data sets can be directly compared using unified scale. The reason for using narrower y-axis span for heatmaps (**A**) than that for graphs (**B**) is that the use of full data range skewed visualisation towards black, as most of the values are far from extreme ones. Therefore the heatmap scale was limited to ±2, and exceeding values are shown with the darkest red or green colour used. **A**) Heatmaps showing gene expression patterns as quantified by both methods employed in the present study. Good overall similarity of results for majority of genes is obvious. Colours indicate direction of gene expression change (red = down- and green = upregulation; see legend). **B**) Relative gene expression as assessed by real-time RT-PCR. Log_2-transformed levels of gene expression compared to control group are shown. Values are means ± S.D. from three biological replicates run in PCR triplicates. The six presented genes showed overall time course in good accordance with microarray data. Three more genes were partially concordant and results for two genes were contradictory.