Transcriptome profiling of ripening nectarine (*Prunus persica* L. Batsch) fruit treated with 1-MCP. *Fiorenza Ziliotto, Maura Begheldo, Angela Rasori, Claudio Bonghi, and Pietro Tonutti*

SUPPLEMENTARY DATA

Table S2. List of all probes spotted on the μPEACH 1.0 and their relative expression in the comparisons carried out in this work. In the first column, "Ctg name" refers to the peach contig number present in the database and used to synthesize the oligo probes for the μPEACH1.0 microarray, "Oligo ID" is the code assigned to each probe (4805 in total) by the manufacturer (Operon). The following six columns report the microarray experiment results: 24MCPvs24AIR (reference comparison) reports [log2 (intensity 24MCP/intensity 24AIR)]; 24AIR/T0 reports [log2 (intensity 24AIR/intensity T0)]; 72MCP/24AIR reports [log2 (intensity 72MCP/intensity 24AIR)] with relative standard deviation (std). Green is used to highlight down-regulated genes or those with a lower mRNA accumulation (log2 ratio ≤-1) for the specific comparison, red is used to highlight up-regulated genes or those with a higher mRNA accumulation (log2 ratio ≥1) for the specific comparison; and white for genes showing no differential expression (log2 ratio > -1 and < 1). The column with "Blast results" as header reports the annotation of sequence, identified using blastx algorithm to compare peach unigenes set against the non-redundant protein database. The last column ("SAM analysis") contains genes identified by SAM analysis performed as described in Material and Methods.