



Figure S4. Expression levels of selected genes, putatively involved in cuticle formation in sweet cherry fruit. Expression was determined in exocarp (filled symbols) and mesocarp (open symbols) during fruit development using RT-qPCR (black symbols) or RNA-seq (red symbols). Grey line indicates calculated rate of cuticle deposition (arbitrary units). Time is given in days after full bloom (DAFB). Pearson's correlation coefficients for correlation between the expression levels determined by RT-qPCR and RNA-seq were between 0.943 (*PaLTPG1*) and 0.989 (*PaATT1*); p -values $< 5 \times 10^{-8}$; $n = 16$ samples.