

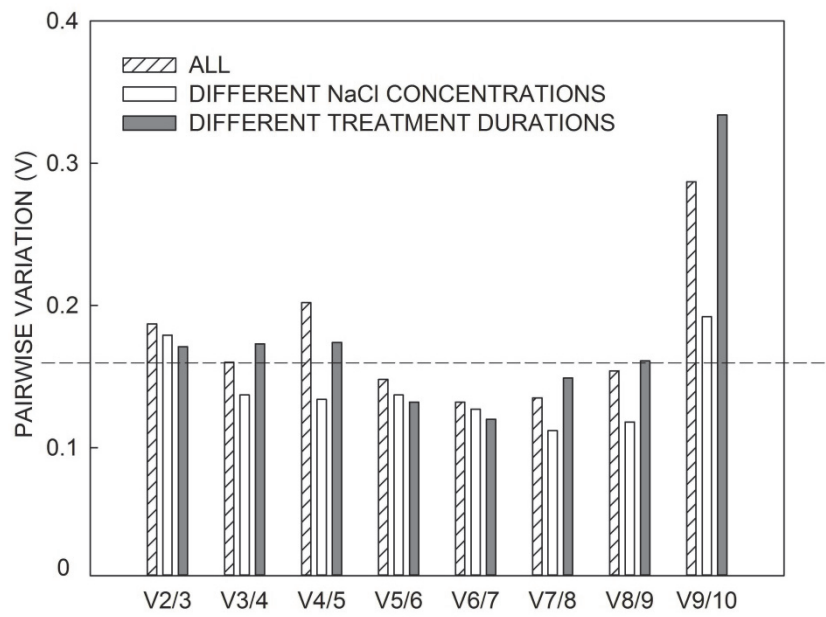


Fig. 1 Suppl. Determination of the optimal number of reference genes for normalization by pair-wise variation using *GeNorm*: 18 samples treated with different NaCl concentrations, 30 treated at different durations, and 48 represent all the samples.