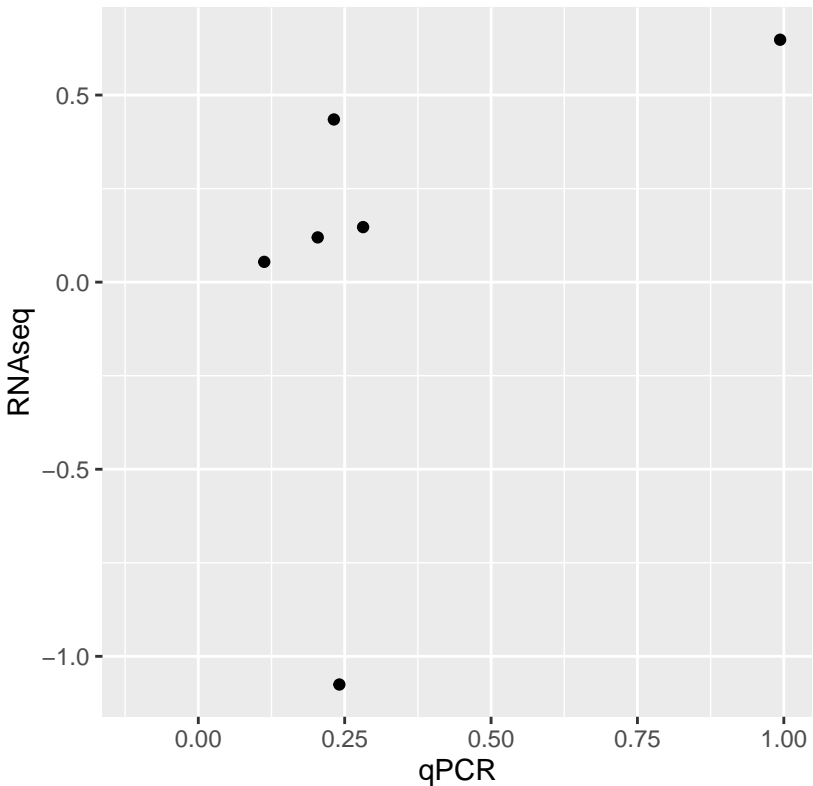


# Timepointw12 fold change, timepoint and sets

Model: Lib size normalized



(Based on data from qpcr and gene sequencing)