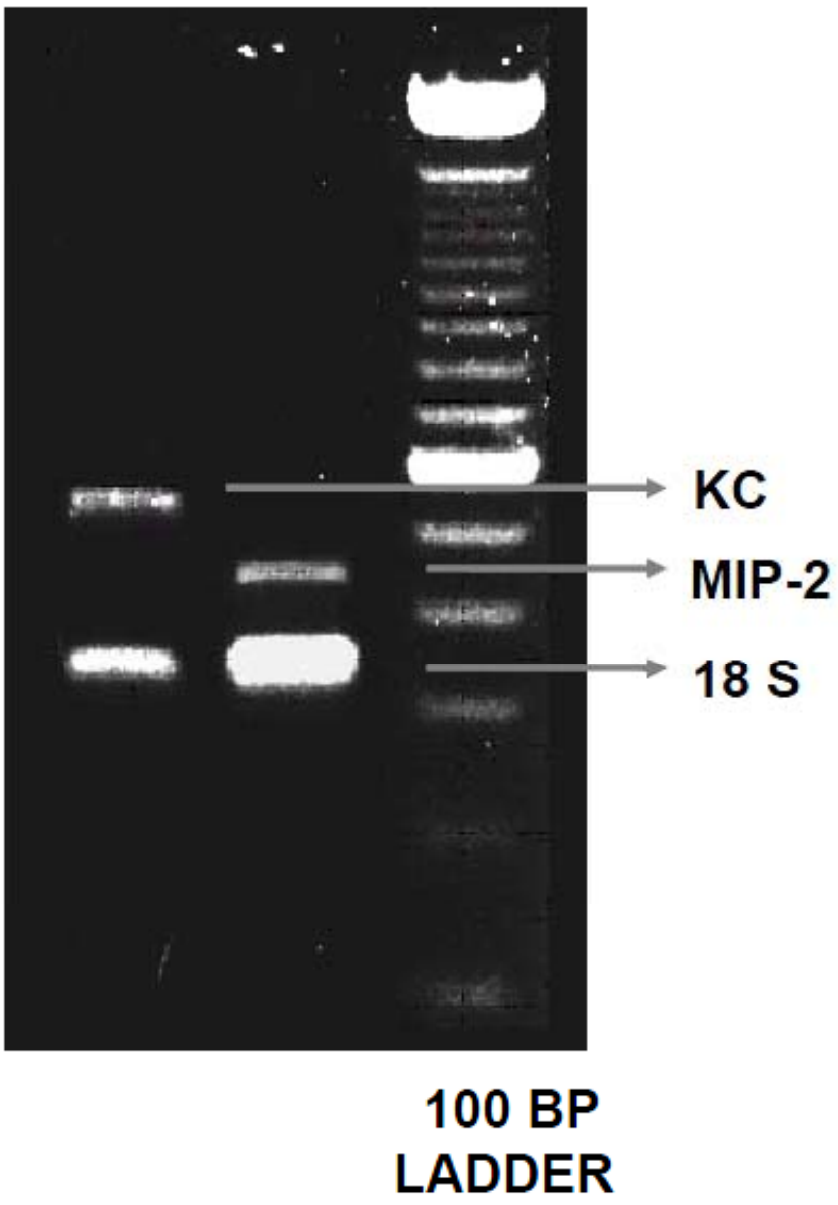
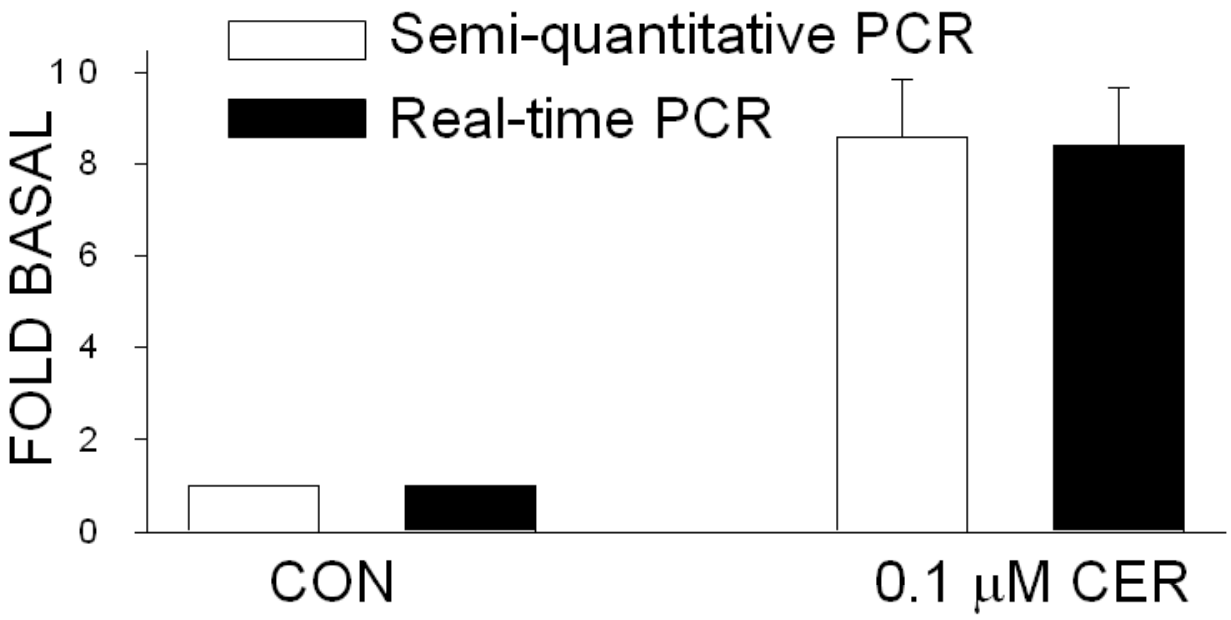
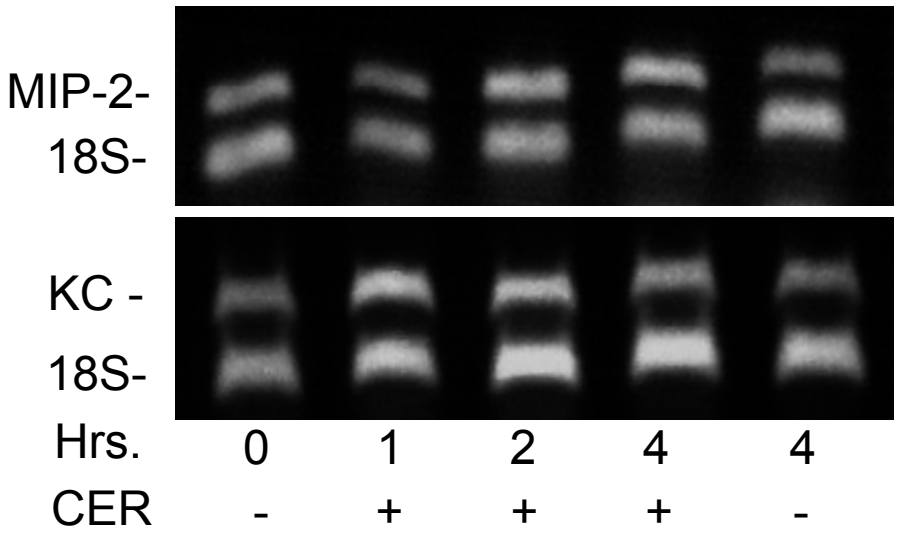


SUPPLEMENTARY FIGURE-1



SUPPLEMENTARY FIGURE-2



SUPPLEMENTARY FIGURE-3

SUPPLEMENTARY DATA:

Figure 1: Product size after amplification with PCR: cDNA prepared was mixed with KC primers and 18S primers/competimer and a PCR was done as described in materials and methods. The same was done in a second tube with the MIP-2 primers. The products were run on a TAE gel, with the product from the tube with the KC primers in the left lane, those with the MIP-2 primers in the middle lane, along with a 100 BP DNA ladder (right lane) and visualized as described in materials and methods.

Figure 2: Comparison of real-time PCR with semi-quantitative PCR using 18S as an internal standard: Samples from control acini (CON) and those treated with 100nM caerulein (CER) were run for real time PCR in duplicate (Black bars) using GAPDH and MIP-2 primers as described in materials and methods. The results calculated from these were plotted as a fold increase in MIP-2 mRNA in the caerulein treated sample over the control, and compared with the fold increase in MIP-2 as measured by semi-quantitative PCR with 18S as an internal standard (white bars) in the same samples.

Figure 3: Acini preincubated for 3 hours in HEPES ringer buffer do not upregulate KC or MIP-2 mRNA levels after stimulation with caerulein. Acini were harvested and incubated in HEPES ringer buffer as previously described (25). These were then stimulated with 100nM caerulein. Time 0 was taken as levels just before adding caerulein. Samples were collected at the indicated time points and processed as described in materials and methods.