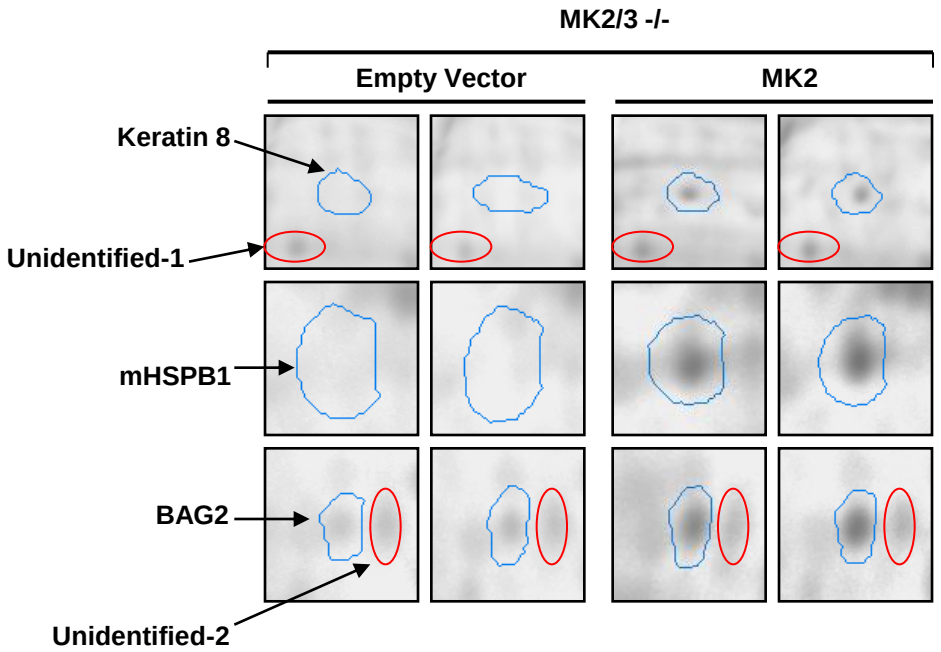
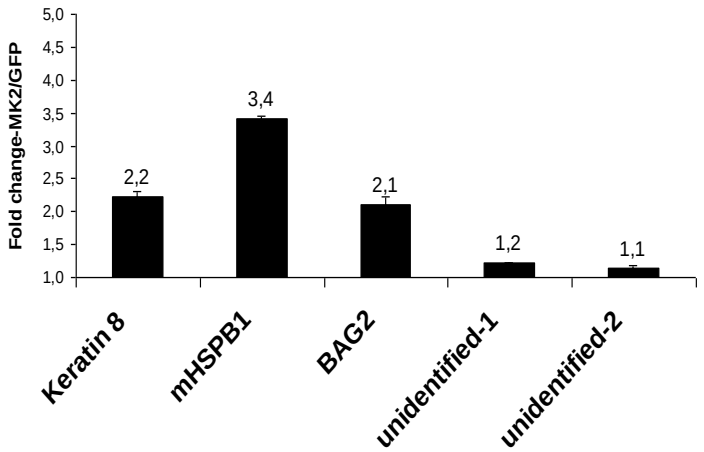
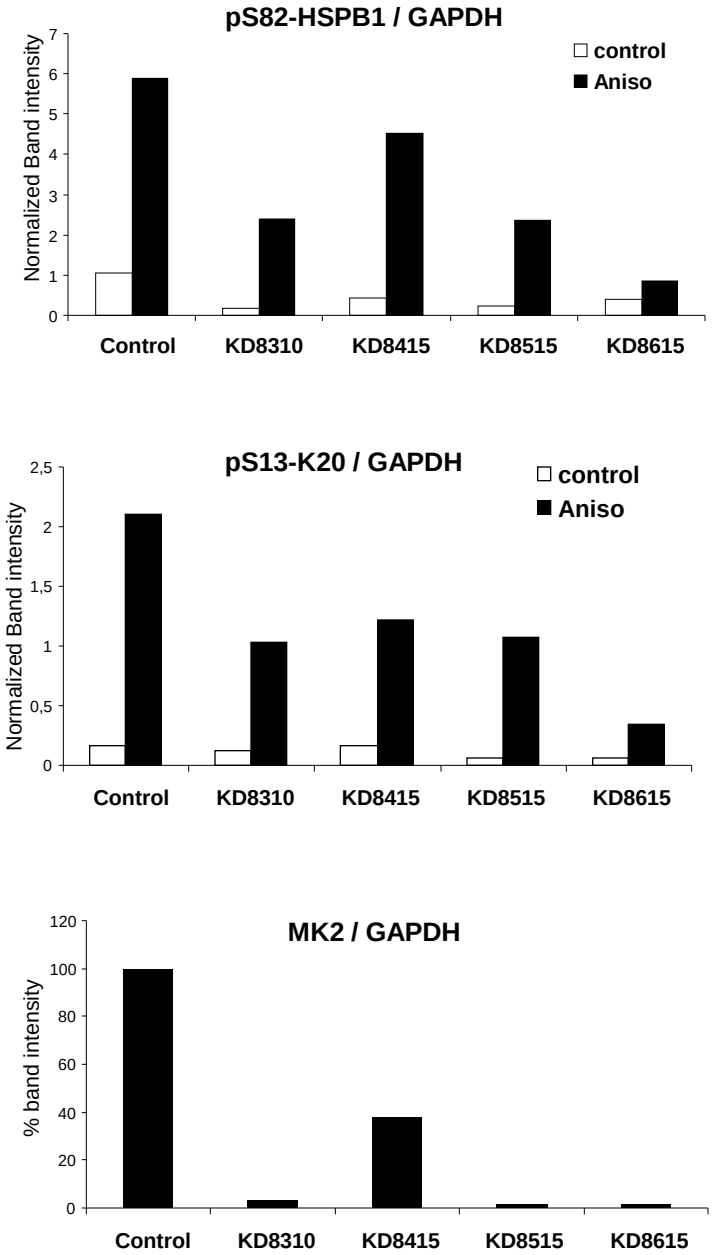
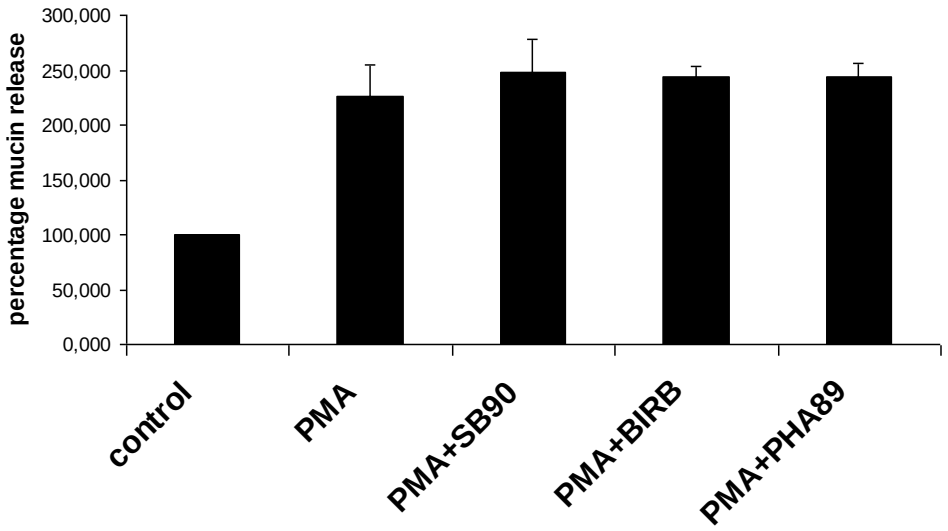




Supplementary Figure 1. Pro-Q Diamond stained spots from gel portions shown in figure 1 were quantified by TINA software (RayTest). The data is presented as fold change – MK2 by empty vector. Identified spots (mHSPB1, BAG2 and Keratin 8) are in blue and random selected spots are marked in red.



Supplementary Figure 2. Cell lines stably transduced with different MK2 shRNA constructs (KD8310, KD8415, KD8515, KD8615) and with a control shRNA were analysed for MK2 levels and anisomycin stimulated K20 S13 and Hsp27 S82 phosphorylation. Band intensities were calculated and normalised to GAPDH as described in '*materials and methods'*.



Supplementary Figure 3. Differentiated HT29-MTX cells were treated as in figure 4C and stimulated with 100ng/mL PMA (Sigma) for 30 minutes. The cells were pre-treated for 30 minutes with 5µM SB202190 (SB90), 1µM BIRB-796 (BIRB) or 25µM PHA781089 (PHA89). Mucin was quantified by ELLA and represented as percentage control