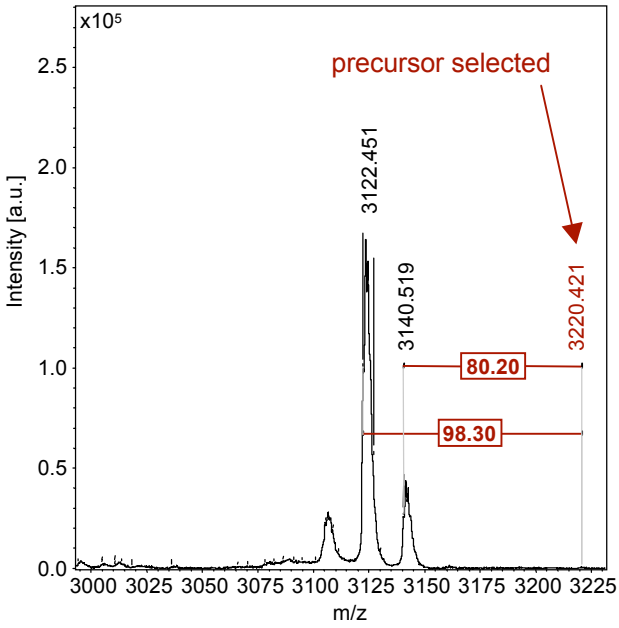
Figure S1

A



B

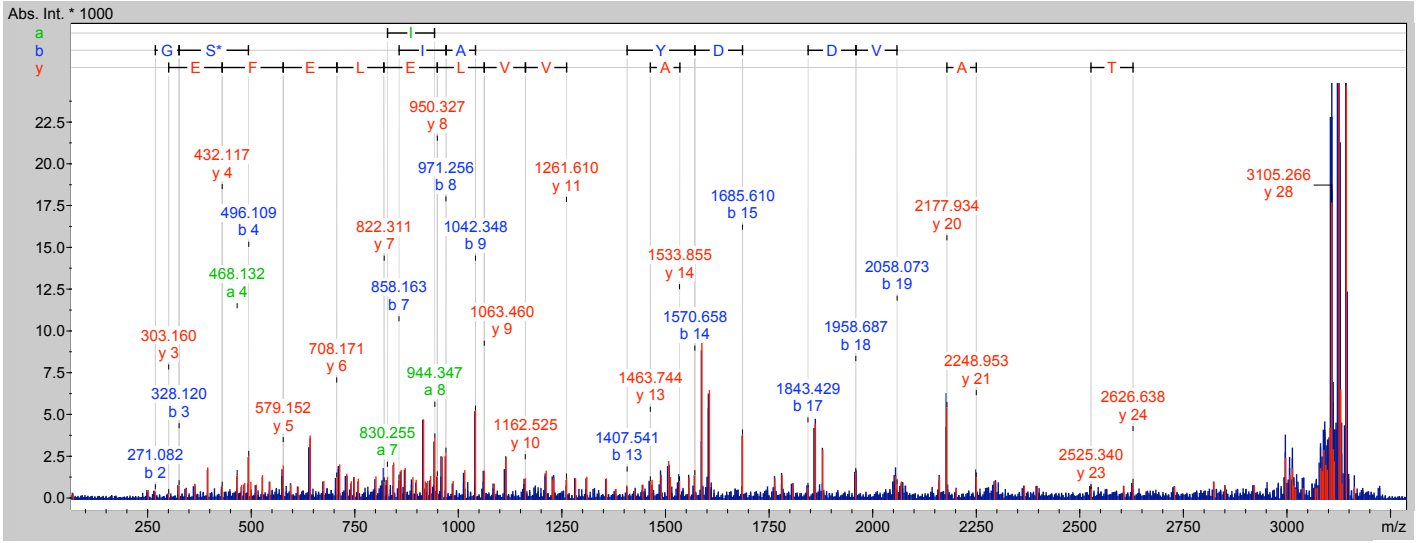


Figure S1: Identification and characterization of the phosphorylated peptide by matrix-assisted laser desorption ionization mass spectrometry (MS). ***A.*** The peptide corresponding to spot O-21 with a mass of 3220 Da showed predominant neutral mass losses of 80 Da (-HPO_3) and 98 Da (- H_3PO_4) upon laser shooting, indicating that it was singly phosphorylated. ***B.*** The corresponding MS/MS fragmentation spectrum identified the tryptic peptide to be NRGSVTYIAPPGNYDASDVVLELEFEGVK (with the unphosphorylated peptide having a mass of Mr 3140.4 Da).

Figure S2

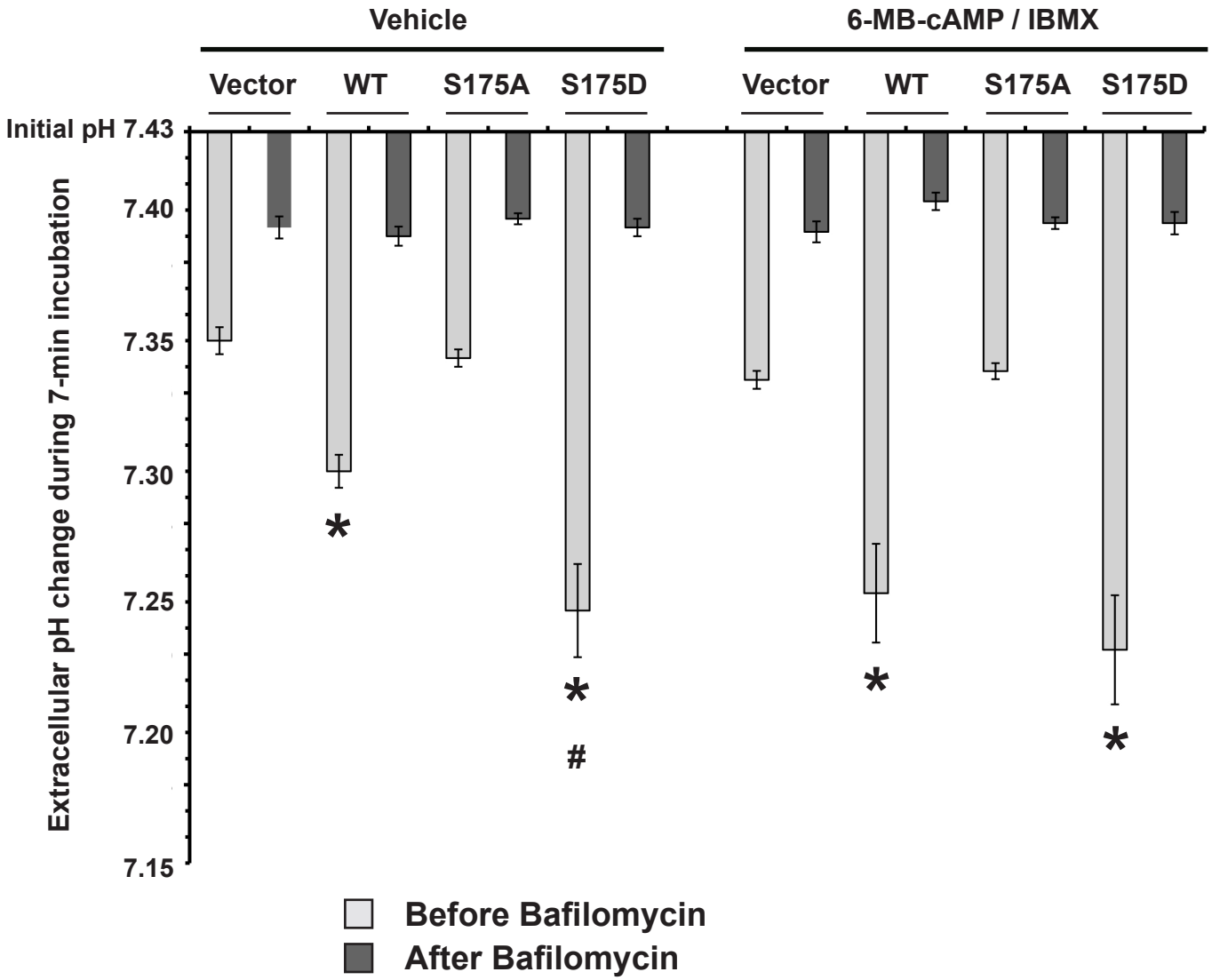


Figure S2: Extracellular pH changes measured at 37ºC (mean ± SEM) at the end of two separate 7-min incubations before (light gray) and after (dark gray) bafilomycin treatment. Each pair of bars represents one set of 6 wells that received either vehicle or 6-MB-cAMP + IBMX before the addition of bafilomycin. The starting pH of the buffer at 37ºC in all cases was 7.43. The light gray bar represents pH measurements in the third set of 7-min incubations in the absence or presence of bafilomycin. There were no significant differences between any of the pH measurements for any of the transfected cells in the presence of bafilomycin. All of the pH values after bafilomycin were significantly different from the respective untreated conditions/transfections. *, $P < 0.05$ relative to vector before bafilomycin within same treatment group; #, $P < 0.05$ relative to WT before bafilomycin within same treatment group.