SUPPLEMENTAL INFORMATION

Moving pieces in a cellular puzzle: a cryptic peptide from the scorpion toxin Ts14 activates AKT and ERK signaling and decreases cardiac myocyte contractility via dephosphorylation of phospholamban

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Supporting excel files (.xlsx)

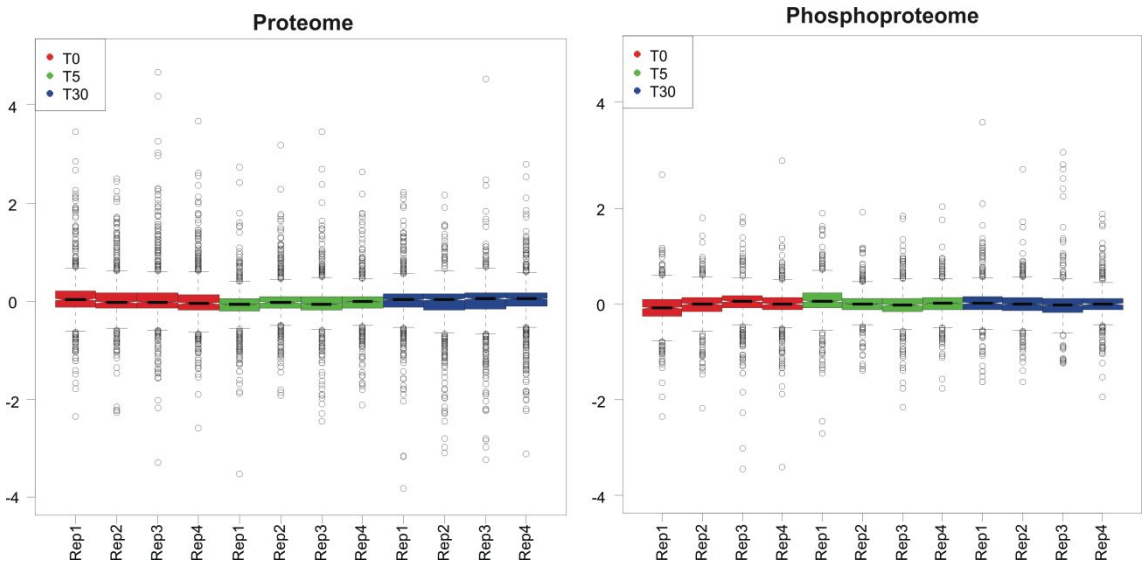

Figure S1. Box-plot of protein and phosphoprotein normalized intensity values of identified proteins in mouse cardiomyocytes Isolated mouse cardiomyocyte samples were submitted to KPP incubation during 5 (T5-in green) and 30 min (T30- in blue) before proteomics protocol. No incubation was used as control group (T0-in red). Four independent replicates (Rep) from each experimental group were analysed on mass spectrometer that result in 2049 protein groups were identified and quantified among 12 samples. Intensity values were normalized by subtracting the median at column level and mean at row level. Phosphoproteomic assessment leads us to identify and quantify 608 class I phosphopeptides (>0.75 confidence) in the 12 samples.

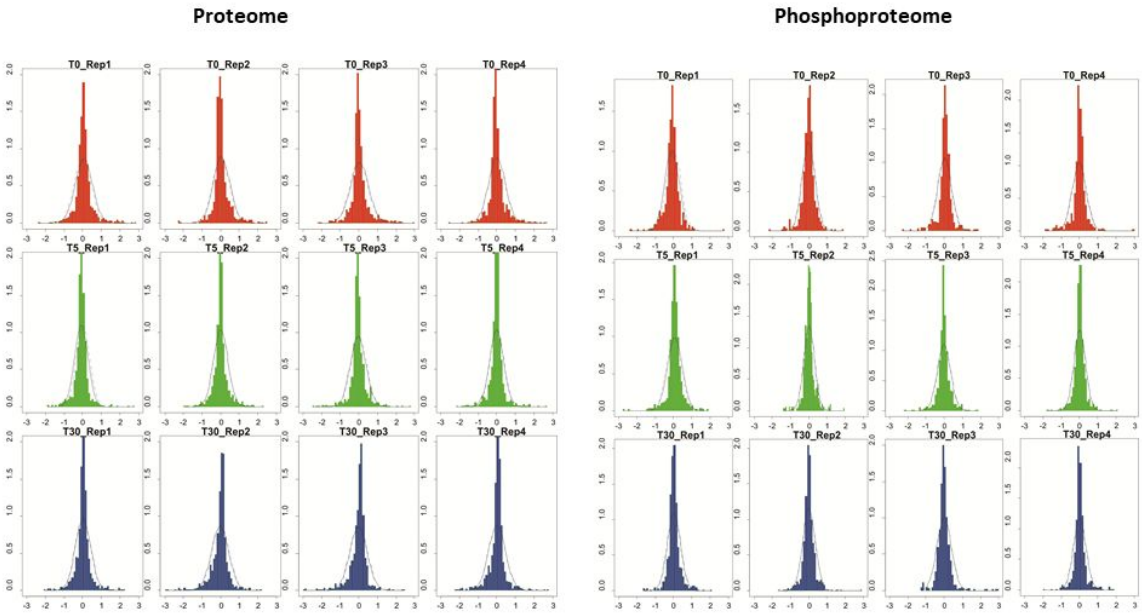

Figure S2. Histograms displayed normal distribution of protein and phosphoprotein intensity values identified in the mouse cardiomyocytes. KPP induced proteome and phosphoproteome data intensities after 5 min (T5 in green), 30 min (T30 in blue) incubation and control group (T0 in red) were normalized by subtracting median value at column and mean value at row. Intensities of phosphosites identified were also normalized by the proteome intensities when possible.

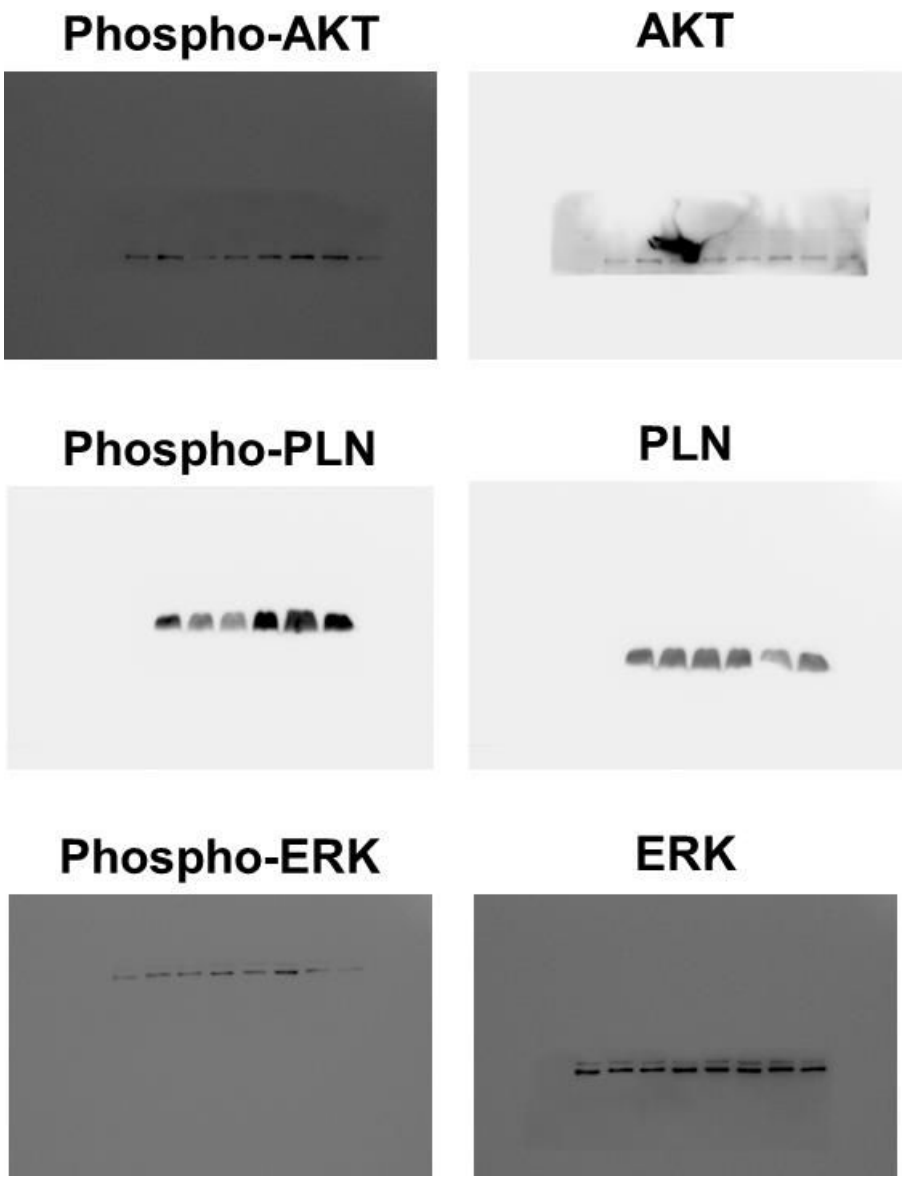

Figure S3. Western blotting. Representative photos taken from the membranes