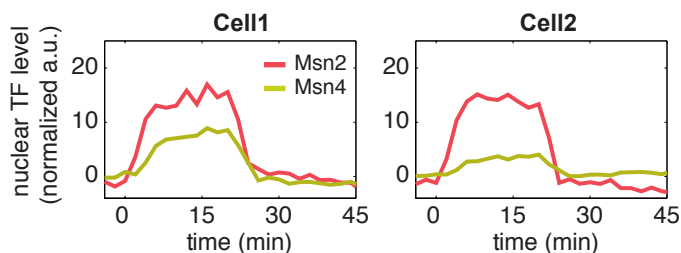
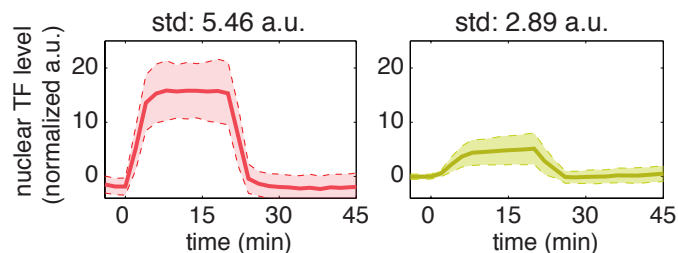


A inhibitor input

(i) single-cell time traces

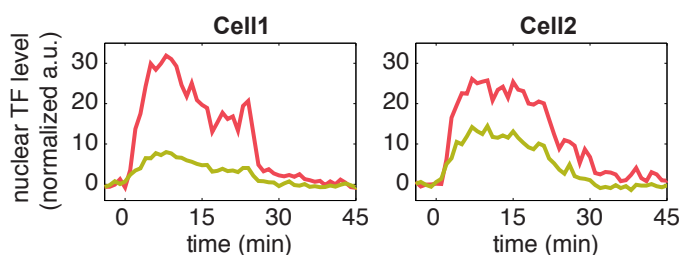


(ii) standard deviation of single-cell traces

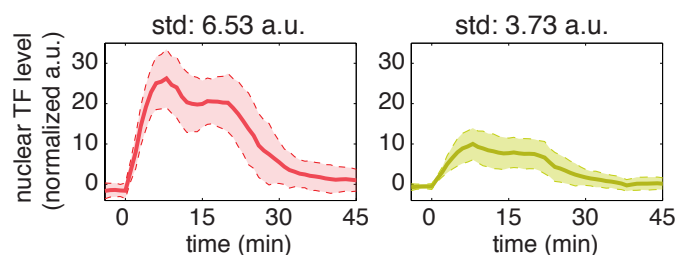


B KCl (0.5 M)

(i) single-cell time traces

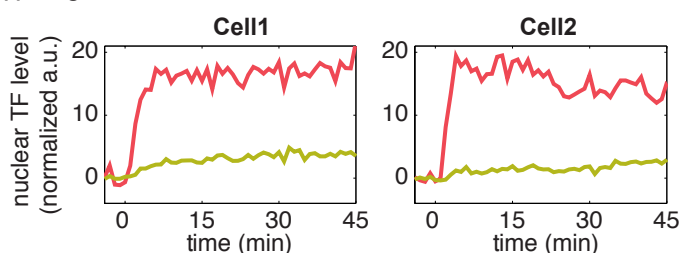


(ii) standard deviation of single-cell traces

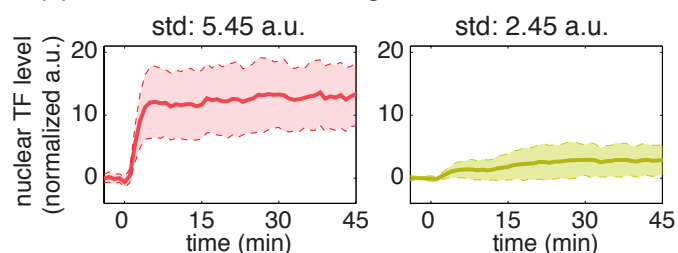


C ethanol (3%)

(i) single-cell time traces

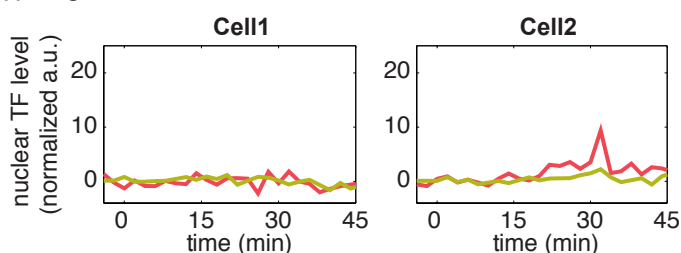


(ii) standard deviation of single-cell traces



D no stress

(i) single-cell time traces



(ii) standard deviation of single-cell traces

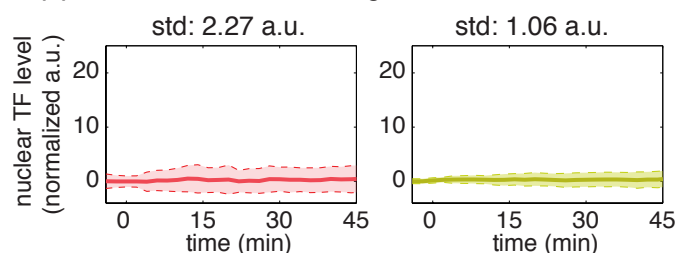


Figure 2 - figure supplement 2. Single-cell time traces of Msn2 and Msn4 after normalization of YFP and RFP fluorescence. After the YFP and RFP normalization as shown in Figure 2 - figure supplement 1, time traces of Msn2 and Msn4 nuclear translocation are plotted in the same single cells in response to (A) 20-min 1 μ M inhibitor pulse, (B) 0.5M KCl, (C) 3% ethanol, or (D) no stress. Each panel shows (i) representative single-cell time traces of Msn2 and Msn4 nuclear translocation in the same single cells; (ii) standard deviation of single-cell time traces. For each condition, the single-cell time traces and standard deviations of single cell responses are normalized so that the levels of Msn2 and Msn4 can be compared directly. In (ii), the solid curve represents the averaged time trace; the shaded region represents the standard deviation of single cell responses. The standard deviation is calculated for the peak time point of time traces for each condition and displayed above each time trace. For the condition without stress, the standard deviation is calculated for the time point used in the inhibitor condition.