Supplementary figure 5

(a) Kaplan Meier curves of patients stratified by expression of common mouse and human SRAS pathways, Translation Factors (Wikipathways), GPCRs, Class B Secretin-like (Wikipathways), PLCG2_30 (Static Module), and RAN_17 (Static Module) in 4 independent clinical datasets. The red and blue lines indicates high and low fingerprint scores respectively (b) P-value of Kaplan Meier estimator of patients stratified by expression of common mouse and human SRAS pathways in 4 independent clinical datasets, relative to a background of randomly selected pathways from the full pathway fingerprint, (c) common genes relative to a background of randomly selected genes from expression chip (only single dataset shown), and (d) common SRAS pathways relative to a background of randomly selected human SRAS pathways. A red dot indicates the p-value, the red cone is a bean plot representing the distribution of p-values from 1000 randomly selected sets of pathways or genes. The blue line indicates a p-value of 0.05.

Supplementary figure 6: An overlay of the Kaplan-Meier survival curves for patients stratified by expression of common mouse and human SRAS pathways, Translation Factors (Wikipathways), GPCRs, Class B Secretin-like (Wikipathways), PLCG2_30 (Static Module), and RAN_17 (Static Module) in 4 independent clinical datasets. The red and blue lines indicate high and low fingerprint scores respectively. The P-values for these datasets are as follows: GSE10358, p < 0.008; GSE1159, p < 0.0009; GSE14468, p < 0.008; GSE12417, p < 0.086.