



Supplemental Figure 2: SAFE-plots for the survival analysis of lung adenocarcinomas. Z-like statistics from the Cox proportional hazards model were computed for all expressed genes. The shaded region represents the range of local statistics that fall in the region ($|z| > 1.96$). (A) The empirical cumulative distribution of local statistics for the 30 genes in 'Nuclear pore,' GO:0005643 is plotted (solid line) against that of a uniform distribution (dashed line). (B) Cumulative distributions are plotted for 'Nuclear membrane,' GO:0005635 using local statistics for all genes (dotted line) and for the 21 genes not present in 'Nuclear pore' (solid line). The attenuation toward uniform (dashed line) for the genes unique to the 'Nuclear membrane' suggests that only the set of genes in the nuclear pore is significant.