Supplementary Figure 2. Yoshimura et al.
Definition of JNK-dependence Index (J.I.).
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Signal log ratio was obtained for each set of experiment as \( R_{\text{caMKK7}} = \log_2 \left( \frac{I_{\text{caMKK7}+\text{JNK}}}{I_{\text{GFP}}} \right) \) and \( R_{\text{dnJNK}} = \log_2 \left( \frac{I_{\text{GFP}+\text{H2O2}}}{I_{\text{dnJNK}+\text{H2O2}}} \right) \) where \( I_{\text{caMKK7}+\text{JNK}}, I_{\text{GFP}}, I_{\text{dnJNK}+\text{H2O2}} \) and \( I_{\text{GFP}+\text{H2O2}} \) indicate normalized signal intensity of each array. Note that \( R_{\text{dnJNK}} \) was calculated so that the suppression by dnJNK is expressed as a positive value. Gene x, a given gene in the DNA microarray analysis, can be plotted in two-dimensional Euclidean space according to \( R_{\text{caMKK7}} \) and \( R_{\text{dnJNK}} \) values at the point \( (R_{\text{caMKK7}}(x), R_{\text{dnJNK}}(x)) \) where JNK-induced genes and JNK-suppressed genes are plotted in the red area and blue area, respectively. We made the assumption that the Euclidean distance of Gene x (\( D(x) \)) from the origin (0), which is calculated by square root \( (R_{\text{caMKK7}}(x)^2 + R_{\text{dnJNK}}(x)^2) \), represents the extent of Gene x induction by JNK. We multiplied \( D(x) \) with \( R_{\text{caMKK7}}(x)/R_{\text{dnJNK}}(x) \) or \( R_{\text{dnJNK}}(x)/R_{\text{caMKK7}}(x) \), whichever is less, to select those genes that are equally induced by JNK activation and suppressed by JNK inhibition. The JNK-dependence Index (J.I.) is defined by the equation as displayed at the bottom.