Supplemental Figure S1. Quality assessment of microarray hybridization. A) The distribution of the perfect match (PM) probes for each chip. Normalization of these data relies on the assumption that the data from each chip come from the same distribution, differing only in location or scale. This plot indicates that both of these assumptions are likely to have been met. B) RNA digestion plot. Probes were ordered according to their position in the transcript and then the mean was computed for each position over all probesets. This gives some idea of the amount of RNA degradation as well as the efficiency of the second-strand synthesis step (e.g. if the intensity of the more 5' biased probes is lower, this may indicate less transcript was available to bind). Parallel lines with nearly equivalent slopes indicates that degradation between samples is nearly equivalent and consistent across the length of each transcript.