Figure 1: Examples of bead masks to control for spatial artifacts in the raw bead data.
Figure 2: Each expression measurement in each sample is generated from the average expression estimated by a number of beads attached to the same probe. This figure shows the distribution of number of beads used.

Figure 3: Example MA plots showing the dye-specific biases associated with the two dyes used to measure gene expression.
**Figure 4:** Corrections to the distribution of the intensities of the different background-control beads. **Left:** The distribution of background intensities by control bead before correction. **Right:** The distribution of background intensities by control bead after correction. See Supplement C for details.
**Figure 5:** The distribution of “expression” levels for DASL measurements applied to genomic DNA. For details on how certain probes were removed on the basis of the divergence of their expression in gDNA from the central distribution, see text.

**qPCR vs. DASL gene ratios**

**Figure 6:** qPCR vs DASL measurements. We compared the qPCR results from five genes measured in a random subset of samples from time points two and five with those same samples from the DASL assay. The expression levels plotted are the mean ratio of each gene’s expression relative to all other measured genes in the sample. Spearman’s Rho = 0.62, p = 9.88e-10.
Figure 7: The average measurements of all 74 genes in three time points from our DASL data and a genome-wide microarray. Spearman’s Rho - 0.759 (p < 2.2e-16). Note the compression in expression ranges from the microarray data relative to the DASL data.
Figure 8: The distribution of expression values using DASL (Right) and a Nimblegen microarray (Left) confirming the dynamic compression in the microarray relative to the DASL platform.