

Microarray data for The Commonwealth Medical College

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4 Human cell samples

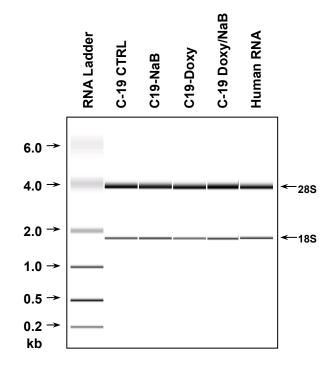




RNA was extracted and purified using Ribopure (Ambion) RNA isolation
Total RNA samples were quantitated by UV spectrophotometry (OD260/280)
Quality of Total RNA was assessed using an Agilent Bioanalyzer
First and second strand cDNA was prepared from the total RNA samples
cRNA target was prepared from the DNA template and verified on the Bioanalyzer
cRNA was fragmented to uniform size and hybridized to Agilent Human v2 GE 4x44K arrays
Slides were washed and scanned on an Agilent G2565 Microarray Scanner
Data was analyzed with Agilent Feature Extraction and GeneSpring GX v7.3.1 software packages

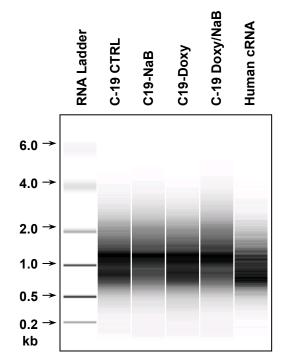


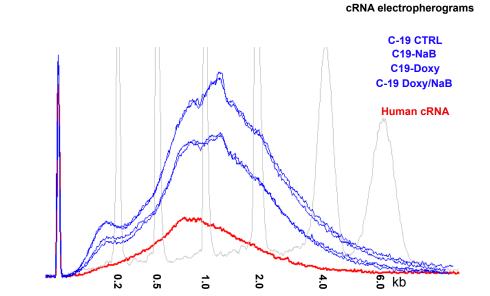






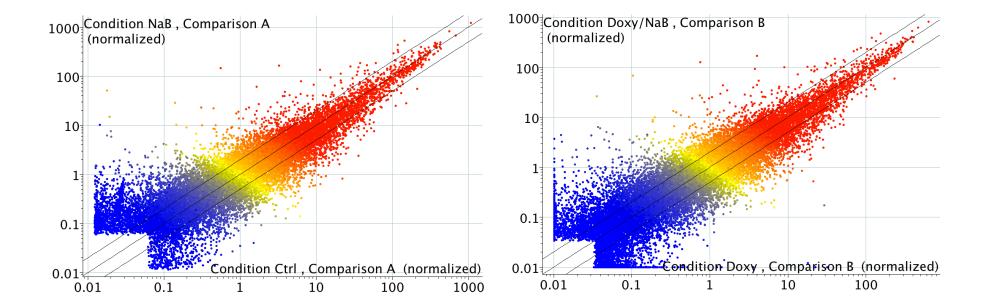






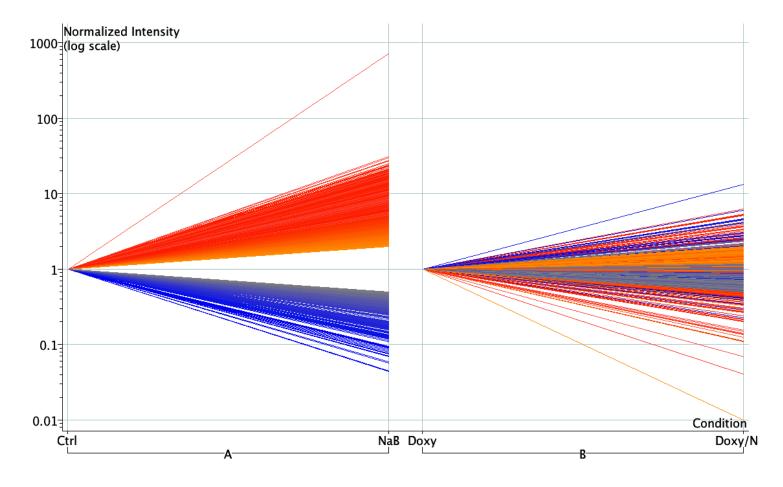






Probes above background in at least one sample per comparison (L:18,885 probes; R:22,169 probes). Intensity values are normalized to the 75th percentile intensity of each array. Diagonal lines indicate 2-fold differential expression. Red/Orange=High expression, Yellow=Medium expression, Blue=Low expression

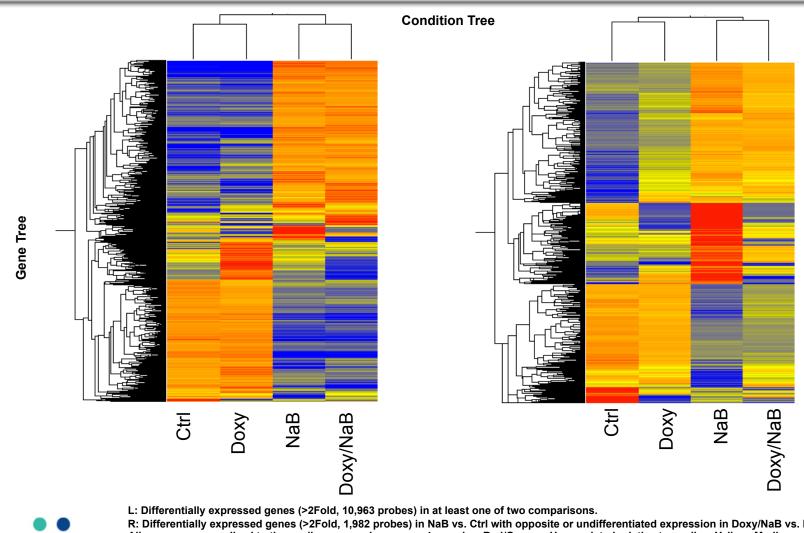




Differentially expressed (>2Fold) genes in NaB vs. Ctrl with opposite or undifferentiated expression in Doxy/NaB vs. Doxy (1,982 probes). Intensity values are normalized to the 75th percentile intensity of each array and further normalized to the control sample for each comparison. Genes are colored by the expression values in the NaB sample. Red/Orange=Up-regulated relative to Ctrl, Blue/Grey=Dn-regulated relative to Ctrl.







R: Differentially expressed genes (>2Fold, 1,982 probes) in NaB vs. Ctrl with opposite or undifferentiated expression in Doxy/NaB vs. Doxy. All genes are normalized to the median expression across 4 samples. Red/Orange=Up-regulated relative to median, Yellow=Median expression, Blue=Dn-regulated relative to median.