**Duke/UNC/UT-Austin/EBI 1% ENCODE Array Platform Validation Tests**

For many of the initial cell lines processed including all of the Tier 1 and Tier 2 cell lines, sequencing-based results were verified by simultaneously generating microarray-based data from the same material. The microarray used was a Nimblegen tiling array that covers the 1% of the genome that was the focus of the pilot encode project.

Briefly, for each of the DNaseI HS, FAIRE, and ChIP experiments, resulting DNA libraries enriched for open chromatin or CTCF, c-Myc, or PolII binding were simultaneously prepared for sequencing and microarray experiments. Data for sequencing experiments were processed as previously described (see Methods in web pages for these corresponding tracks). Peaks of enrichment were determined within microarray data using ChIPOTle (Buck 2005) at various p-value cut-offs and with a Bonferoni correction.

Receiver Operating Curve (ROC) analysis was performed for each experiment by using the microarray-defined peaks from the pooled sample data as positively defined regions of enrichment, and by generating a corresponding set of negative regions matched in number and size to the positives that spanned microarray probes devoid of appreciable signal. For each positive and negative region, the maximum F-seq Parzen score for that region was extracted from the sequence-based experiment. Positive and negative regions were sorted by the F-seq scores and ROC Area Under the Curve (AUC) values were calculated.

Included here for each cell line and experiment are:

1. Raw data from microarray experiments in the form of pair.txt files. Note: data was independently generated for each individual replicate, but as stated above, only data from pooled sample experiments were used for ROC analysis.
2. Positive regions as determined by microarray data at different p-value cut-offs as indicated in file names (i.e. e10 -> 1 x e-10).
3. Matched negative regions.
4. ROC curves in .png format for each replicate.
5. A summary of the ROC AUC values.

Buck MJ, Nobel AB, Lieb JD. [ChIPOTle: a user-friendly tool for the analysis of ChIP-chip data](http://genomebiology.com/2005/6/11/R97" \t "_blank). Genome Biol. 2005;6(11):R97.