

## **Exhibit 1: Statement of Work & Deliverables**

MeDIP-chip Service

## Statement of Work

- 1. Incoming genomic DNA QC and sheared DNA QC
- 2. MeDIP and quality assessment of MeDIP
- 3. Linear amplification using SIGMA WGA kit
- 4. Target preparation by labeling with Cy3/5
- 5. Array hybridization, washing, and scanning
- 6. Data extraction, analysis and summarization

## Deliverables

- 1. All raw data files derived from the Agilent Feature Extraction software
- 2. Project summary report
- 3. Analysis report files in GFF format, unless otherwise noted. These Files include:
  - Genome annotation file (including primary transcript, transcription start site, tiled region)
  - Scaled log2-ratio data
  - P-value data
  - Enrichment peak files
  - Reports listing peaks with associated transcripts and gene annotation information in MS Excel format
  - Summary of enrichment peak profiles in all samples
  - Differential enrichment peak files