

The Cancer Genome Atlas Pilot Project
Johns Hopkins University and University of Southern California
Raw Data Description

Platform: Illumina GoldenGate

Raw Data

The Illumina GoldenGate platform generates ~30 replicate measurements for each of the 1505 CpG loci on the bead array (~30 beads per locus). The software generates mean Cy3 (methylated CpG intensity) and Cy5 (unmethylated CpG intensity) intensities and standard deviations across all beads for each locus and each sample. We will provide the mean Cy3 and Cy5 values for each locus for each sample as raw data. Bead level data and standard deviations can also be provided, if desired.

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Normalized Data Description

Platform: Illumina GoldenGate

Normalized Data

The normalized DNA methylation measurement is obtained by calculating the β (beta) value, representing the ratio of the Cy3 intensity relative to Cy3 + Cy5 intensities. The beta value is contained in a range of zero to one, with low beta values suggestive of unmethylated CpG loci and high beta values indicative of methylated CpG loci. The bounded beta value obviates the need for deriving log2 derivatives of Cy3 or Cy5 intensities.

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Segmented Data Description

Platform: Illumina GoldenGate

Segmented Data

The majority of loci on the Illumina platform will be CpG islands that are normally unmethylated, and for which hypermethylation in the tumor sample will be of interest. Therefore, we will rank loci by the beta value obtained for each locus within each sample, with highly methylated loci of highest interest.