## Infinium HumanMethylation450 Bead Chip (Illumina)

**Neuroblastoma (NBL) – Methylation**

*Protocols performed at the USC Epigenome Center.

Labeling, hybridization and scanning protocols were performed following the manufacturer's protocol using the Infinium Human Methylation450K Beadchip Kit (Illumina, San Diego, CA, #WG-314-1001).

Level 2 data contain background-corrected methylated (M) and unmethylated (U) summary intensities as extracted by the methylumi package. Non-detection probabilities (P-values) were computed as the minimum of the two values (one per allele) for the empirical cumulative density function of the negative control probes in the appropriate color channel. Background correction is performed via normal-exponential deconvolution using out-of-band probes (Triche, Jr. et al, Nucl. Acids Res 2013). Multiple-batch archives have the intensities in each of the two channels multiplicatively scaled to match a reference sample (sample with R/G ratio of normalization control probes closest to 1.0.).

Level 3 data contain derived summary measures (beta values: M/(M+U) for each interrogated locus) with annotations (based on Illumina's manifest on GEO, GPL13534) for gene symbol, chromosome (UCSC hg19, Feb 2009), and CpG/CpH coordinate (UCSC hg19, Feb 2009). Probes having a common SNP (common SNP is a SNP with Minor Allele Frequency > 1% as defined by the UCSC snp135common track) within 10bp of the interrogated CpG site or having 15bp from the interrogated CpG site overlap with a REPEAT element (as defined by RepeatMasker and Tandem Repeat Finder Masks based on UCSC hg19, Feb 2009) are masked as NA across all samples, and probes with a non-detection probability (P-value) greater than 0.05 in a given sample are masked as NA on that chip. Probes that are mapped to multiple sites on hg19 are annotated as NA for chromosome and 0 for CpG/CpH coordinate.