Below are detailed descriptions of the Infinium MethylationEPIC Array manifest file column headings.

**IlmnID**: Unique identifier from the Illumina CG database. (The probe ID).

**Name**: The IlmnID.

**Infinium_Design_Type**: Infinium I (2 probes/locus) or Infinium II (1 probe/locus).

**Next_Base**: For Infinium I probes, the nucleotide immediately following the CpG. Blank for Infinium II.

**Color_Channel**: For Infinium I probes, the color channel of the “Next_Base” signal.

**Forward_Sequence**: Plus (+) strand (HapMap) sequence (5’-3’) flanking the CG.

**Genome_Build**: Genome Build referenced by the manifest.

**CHR**: Chromosome containing the CpG (Build 37).

**MAPINFO**: Chromosomal coordinates of the CpG (Build 37).

**SourceSeq**: The original, genomic sequence used for probe design before bisulfite conversion.

**Chromosome_36**: Chromosome containing the CpG (Build 36).

**Coordinate_36**: Chromosomal coordinates of the CpG (Build 36).

**Strand**: The Forward (F) or Reverse (R) designation of the Design Strand. *Note: in methylation manifest files, the Forward Strand = the genomic Plus (+) Strand and the Reverse Strand = the genomic Minus (-) Strand. In this context, Forward and Reverse ARE NOT EQUIVALENT to the Forward and Reverse Strand designations originating from dbSNP or as given in Infinium Genotyping manifests.

**SNP_ID**: rsid(s) of SNP(s) located in the probe. *Note: multiple listings of SNP rsid are allowed.

**SNP_DISTANCE**: Distance of SNP(s) from query base of the probe. *Note: multiple listings of the distance values are associated with rsid.

**SNP_MinorAlleleFrequency**: Minor allele frequency of SNP(s). *Note: multiple listings of the minor allele frequencies are associated with rsid.

**Random_Loci**: CpG loci chosen randomly by consortium members during the design process are marked “True”.

**Methyl27_Loci**: CpG’s carried over from the HumanMethylation27 array (92% carryover) are marked “True”.

**Methyl450_Loci**: CpG’s carried over from the HumanMethylation450 array (94% carryover) are marked “True”.

**UCSC_RefGene_Name**: Target gene name(s), from the UCSC database. *Note: multiple listings of the same gene name indicate splice variants.

**UCSC_RefGene_Accession**: The UCSC accession number(s) of the target transcript(s). Accession numbers are given in the same order as the target gene transcripts.

**UCSC_RefGene_Group**: Gene region feature category describing the CpG position, from UCSC. Features listed in the same order as the target gene transcripts.

**TSS200**: 0–200 bases upstream of the transcriptional start site (TSS).

**TSS1500**: 200–1500 bases upstream of the TSS.

**5'UTR**: Within the 5' untranslated region, between the TSS and the ATG start site.
Body = Between the ATG and stop codon; irrespective of the presence of introns, exons, TSS, or promoters.

3'UTR = Between the stop codon and poly A signal.

**UCSC_CpG_Islands_Name**: Chromosomal coordinates of the CpG Island from UCSC.

**Relation_to_UCSC_CpG_Island**: The location of the CpG relative to the CpG island. 
Shore = 0–2 kb from island.

Shelf = 2–4 kb from island.

N = upstream (5') of CpG island.

S = downstream (3') of CpG island.

**Phantom**: Classifications from the FANTOM (Functional Annotation of the Mammalian Genome) consortium as a low- or high-CpG density region associated with FANTOM 4 promoters.

**DMR**: Differentially methylated regions (experimentally determined).

DMR = Differentially Methylated Region.

CDMR = Cancer-specific Differentially Methylated Region.

RDMR = Reprogramming-specific Differentially Methylated Region.

**450k_Encoder**: Predicted enhancer elements as annotated in the original 450K design (determined by the ENCODE Consortium using informatics and the original 450K consortia members) are marked “True”.

**HMM_Island**: Hidden Markov Model Islands. Chromosomal map coordinates of computationally predicted CpG islands.

**Regulatory_Feature_Name**: Chromosomal map coordinates of the regulatory feature (determined by the ENCODE Consortium using informatics).

**Regulatory_Feature_Group**: Description of the regulatory feature referenced in “Regulatory_Feature_Name” as provided by the Methylation Consortium.

Gene_Associated

Gene_Associated_Cell_type_specific

NonGene_Associated

Promoter_Associated

Promoter_Associated_Cell_type_specific

Unclassified

Unclassified_Cell_type_specific

**DHS**: DNase I Hypersensitivity Site (experimentally determined by the ENCODE project).
Any column headers omitted from this bulletin are as described in the *Infinium Genotyping Manifest Column Headings* bulletin. Information in the methylation manifest references Genome Build 37 (HG19) unless otherwise stated.

**GenocodeBasicV12_Name**: Target gene name(s), from the basic GENECODE build. *Note: multiple listings of the same gene name indicate splice variants.

**GenocodeBasicV12_Accession**: The basic GENECODE accession number(s) of the target transcript(s). Accession numbers are given in the same order as the target gene transcripts.

**GenocodeBasicV12_Group**: Gene region feature category describing the CpG position, from basic GENECODE. Features listed in the same order as the target gene transcripts.

TSS200 = 0–200 bases upstream of the transcriptional start site (TSS).

**GenocodeCompV12_Name**: Target gene name(s), from the complete GENECODE build. *Note: multiple listings of the same gene name indicate splice variants.

**GenocodeCompV12_Accession**: The complete GENECODE accession number(s) of the target transcript(s). Accession numbers are given in the same order as the target gene transcripts.

**GenocodeCompV12_Group**: Gene region feature category describing the CpG position, from complete GENECODE. Features listed in the same order as the target gene transcripts.

TSS200 = 0–200 bases upstream of the transcriptional start site (TSS).

**DNase_Hypersensitivity_Name**: Chromosomal coordinates of the DNase hypersensitive region from ENCODE.

**DNase_Hypersensitivity_Evidence_Count**: Number of supporting experimental evidence for DNase hypersensitive region from ENCODE.

**OpenChromatin_Name**: Chromosomal coordinates of open chromatin region from ENCODE.

**OpenChromatin_Evidence_Count**: Number of supporting experimental evidence for open chromatin region from ENCODE.

**TFBS_Name**: Chromosomal coordinates of transcription factor binding site region from ENCODE.

**TFBS_Evidence_Count**: Number of supporting experimental evidence for transcription factor binding site region from ENCODE.