Infinium HTS iSelect Methyl Custom BeadChip Manifest Column Headings

August 20, 2021

Below are detailed descriptions of the Infinium HTS iSelect Methyl Custom BeadChip manifest column headings for GenomeStudio and SeSAMe manifests.

Column heading	Description
IlmnID / Probe_ID	Unique probe identifier with four added alphabetic and numeric characters to denote top or bottom strand (T/B), converted or opposite strand (C/O), Infinium probe type (1/2), and the number of synthesis for representation of the probe on the array (1,2,3,…,n). Denoted as IlmnID in the GenomeStudio Manifest and Probe_ID in the SeSAMe Manifest.
Name	The locus target identifier (cg, ch, rp, mu, rs) followed by an eight-digit code that relates to the probe sequence. If an eight-digit code has not yet been generated, standard genomic coordinates follow the locus target identifier.
AddressA_ID / U	For Infinium I bead types, this is the Address ID for the probe specific for the A allele, which is the unmethylated allele. For Infinium II bead types, the Address ID for the probe used for both A and B alleles (ie, AddressB_ID and AlleleB_ProbeSeq columns are empty). Denoted as “AddressA_ID” in the GenomeStudio Manifest and “U” in the SeSAMe manifest.
AlleleA_ProbeSeq	The sequence of the probe identified in AddressA_ID column.
AddressB_ID / M	For Infinium I bead types, this is the address ID for the probe that is specific for the B allele, which is the methylated allele. Denoted as “AddressB_ID” in the GenomeStudio Manifest and “M” in the SeSAMe manifest.
AlleleB_ProbeSeq	For the Infinium I bead type, the sequence of the probe identified in AddressB_ID column.
Next_Base	For Infinium I probes, the actual extension base (on the probe strand) after bisulfite conversion (A or C or T).
Color_Channel	For Infinium I probes, the color channel of the “Next_Base” signal.
Col	For Infinium I probes, the color channel of the “Next_Base” signal. The red and green are abbreviated to R and G, respectively.
Probe_Type	Either cg, ch, mu, rp, or rs to denote CpG, CpH, multi-unique, repetitive element, or SNP probes. Control probes denoted in [Controls] section in the GenomeStudio Manifest and prefixed with “ctl” in the SeSAMe Manifest.
Strand_FR	The forward (F) or reverse (R) designation of the design strand. Strand_FR is dependent on the genome build used to prepare the array and manifest.
Strand_TB	Either top (T) or bottom (B) specifying whether the probe is positioned upstream (in smaller coordinates) or downstream (in greater coordinates) of the target base. Strand_TB is not dependent on the genome build used to prepare the array and manifest.
Strand_CO	Either converted (C) or opposite (O) depending on whether the probe queries the original bisulfite converted DNA strand or the opposite strand that results from amplification of the originally converted DNA stand. Strand_CO is not dependent on the genome build used to prepare the array and manifest.
Infinium_Design_Type	Infinium type I (2 probes/locus) or Infinium type II (1 probe/locus). Denoted in Roman numerals (I or II) in the GenomeStudio manifest and numbers (1 or 2) in the SeSAMe manifest.
Rep_Num	Used to distinguish multiple assays that target the same genomic site.
CHR	Chromosome containing the target base.
MAPINFO	Chromosomal coordinates of the target base.
Species	Name of the species for which a given probe was designed to target.
Genome_Build	Genome build used to derive CHR and MAPINFO for the probe.
Source_Seq	The original genomic sequence used for probe design before bisulfite conversion.
Forward_Sequence	Plus (+) strand sequences (5’-3’) flanking the target base.
Top_Sequence	Illumina’s standardized TOP strand nomenclature applied to an interrogated dinucleotide site. e.g. CpG, CpH