Infinium Mouse Methylation BeadChip v1.0 GenomeStudio Manifest File

Release Notes

v1.0 A2

May 25, 2021

Manifest File Revision History

Revision	Date	Description of Change
v1.0 A2	April 2021	Added four manifest columns, renamed/reclassified/replaced multiple probes, updated control probe functionality for GenomeStudio, updated "Forward_Sequence" and "MFG_Change_Flag" information for certain probes
v1.0 A1	October 2020	Initial release

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Introduction

This document describe key changes to the Infinium Mouse Methylation BeadChip manifest files (.bpm and .csv formats) for different versions of the BeadChip.

I.   Manifest v1.0 A1

NEW FEATURES:

- Added 34 columns for the Mouse Methylation BeadChip. The column designations are more fully explained in the Infinium Mouse Methylation Manifest Column Headings file.

- The logic for how the IlmnID is determined is shown below in the leftmost table column and other relevant information on how the IlmnID is generated is given in the remaining columns:

IlmnID	Name	Strand_TB	Strand_CO	Infinium_Design_Type	The specific synthetic oligonucleotide probe replicate
The IlmnID is a composite of multiple information fields: the name of the probe, whether the probe targets the top or bottom strand, whether the probe targets the bisulfite converted strand or complementary strand after amplification, the Infinium probe design type, and the number of times the probe was synthesized for array representation. Example of IlmnID: **cg12345678_TC13** This probe would be a CG probe with an eight digit code that relates to the probe sequence. The following "T" indicates that the probe targets the top strand. The adjacent "C" indicates that the probe targets the strand that is initially bisulfite converted. The "1" indicates that the probe has a Type I Infinium design. The "3" indicates that the probe was synthesized three times for representation on the array The multiple fields that comprise the IlmnID are provided in the table columns to the right.	The name of the probe is determined by combining the locus target identifier, which designates the function of a given probe, with an eight digit code that relates to the probe sequence. In situations where the eight digit code has not yet been generated, standard genomic coordinates are used. Example of probe name: **cg12345678** Examples of locus target identifiers: CG probe = **cg** CAH probe = **ca** CCH probe = **cc** CTH probe = **ct** Control probe = **cl** SNP probe = **rs**	Strand_TB relates to whether the probe is designed to target the top or bottom strands of a given locus as defined by Illumina's standard designation for ambiguous SNP probes. Examples of top/bottom strand designations: Top strand = **T** Bottom strand = **B**	Strand_CO refers to whether the probe is designed to target the originally bisulfite converted DNA strand, or the strand resulting from amplification of the originally converted DNA strand. Examples of converted/uncon-verted designations: Converted strand = **C** Opposite strand = **O**	Infinium_Design_Type refers to whether the probe utilizes a Type I design that uses two attempted bead types to probe a single locus, or a Type II design that uses one attemped bead type to probe a single locus. Examples of Infinium design type designations: Infinium Type I design = **1** Infinium Type II design = **2**	This value depends on how many times a probe was synthesized for representation on the array. For instance, if the probe was synthesized three separate times, the probe generated by the first synthesis would be denoted as "1", while the probe generated from the second synthesis would be denoted as "2", and the probe generated from the third synthesis would be denoted as "3".

IMPROVEMENTS:

- None

DEFECT REPAIRS:

- None

ISSUES:

- None

II. Manifest v1.0 A2

NEW FEATURES:

- Added four columns to the manifest: "Probe_Type", "Col", "Species", and "Rep_Num".

- Human and Mouse controls renamed in manifest (for examples of functionality in mixed Human/Mouse DNA samples please see the Demo Dataset on the Mouse Methylation BeadChip Support Site).

IMPROVEMENTS:

- Recharacterized CAH, CCG, and CTH "Probe_Type" to CH.

- Replacement of a subset of mouse control probes for Bisulfite Conversion I and Bisulfite Conversion II due to suboptimal selection arising from assay design and genomic mapping.

- Negative controls updated in manifest to report as averages and standard deviations in the GenomeStudio Control Dashboard.

- Colors for Mouse and Human control probes updated for easier visualization in the GenomeStudio Control Dashboard.

DEFECT REPAIRS:

- Reclassified 32 probes that were originally defined with the incorrect "Color_Channel" information.

- Reclassfied 43 probes that were originally defined with the incorrect "Next_Base" information.

- Reclassified 400 probes that were originally defined with the incorrect "Strand_TB" strand information.

- Renamed 415 probes' IlmnID and Name (400 due to "Strand_TB" and 15 due to CH to CG reclassifications).

- Reclassified 1,253 loci that were originally defined with the incorrect "Top_Sequence" information.

- Updated "MFG_Change_Flagged" for probe types ch, rs, mu, and rp as "TRUE".

- Removed "Forward_Sequence" information for probe types rp and mu.

ISSUES:

None