

How should I use these files if I am starting a new project?

Researchers should process samples according to standard protocol using the new product files.

How should I use these files if I am in the middle of a project?

There are two options for this situation. Illumina recommends that all data be reloaded into GenomeStudio to re-call all genotypes and SNP metrics using the newest revisions of the product files. Alternatively, the project can be completed using the original files. The new map positions can be updated at a later time using a downstream analysis program.

How should I use these new manifests if I am finished with my project?

Completed data can be updated to the new manifests by updating the new chromosome and base pair positions in secondary analysis (i.e., map files).

How should I use these files if I am a LIMS customer?

Note that in LIMS, the product files (.bpm, .egt, and .xml) are bound to the product in Project Manager. AutoCall will use the current file in the LIMS database for all future *.gtc file generation for a given BeadChip product. Therefore, researchers should only update Project Manager with the new product files when all projects containing the specific BeadChip product can be transitioned to the new versions. Data previously generated with the older versions should be re-queued for AutoCall.

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