RELEASE NOTES

applied
biosystems

Automated Axiom™ Analysis (AutoAX)

Updates to v1.2.1

- The artifact reduction parameter is now tuned to the specific GeneTitan camera type.

Updates to v1.2

- Best Practices with Dual Workflow has been enabled for selected arrays. When set as the default, Automated Axiom will run the Best Practices followed by Dual workflow for samples that fall within the cut off set for QC.

- Optional settings for Sample Name Mapping, Filter File, SNP List Filter, SNP Mapping File, and SNP Allele Swap are now enabled for arrays that have AxLE Export enabled.

- Option to include SNP Metrics in the AxLE SNP Map Export file.

Before use

- An Installation Checklist must be filled out and signed prior to installation of Automated Axiom software.

- Specific library files are required for Automated Axiom. Contact your local support person for more information.

- Prior to the first GTMC instrument run, set up an analysis configuration and set it as the default workflow for each array to be run. When Automated Axiom encounters that array, it automatically runs the default analysis. No user intervention is required.

- Use of AxLE template files to create AxLE Export Input files is recommended.

Software and hardware requirements

- Automated Axiom Analysis has been validated for use on Chrome. Using a different browser is not recommended, as it may result in incompatibility issues.
- GCC v6.1 [or higher]
- Linux distro installed that supports Docker version 20.10.12.
- Six or more Cores and 64GB memory.
- Systems not connected to a network require 5-10TB of local hard drive space.

Known issues and limitations

Analysis summary

- Certain probesets may be classified as Other if they contain two (2) haploid clusters and 1 or 2 diploid hom cluster(s). This may occur primarily with copy number aware genotyping probesets.

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