Arrays Analysis Command-line Interface (ACLI) Software Release Notes

v1.0.1

April 2021

Introduction

These Release Notes detail the key changes for the Arrays Analysis Command-line Interface (ACLI).

The copy-number subcommands are only intended for use with the Global Diversity Array with Enhanced PGx Content v1.0 product.

NEW FEATURES:

- None. This is the initial release

DEFECT REPAIRS:

- None. This is the initial release

KNOWN ISSUES:

- Running multiple instances in parallel on OSx will result in the following error - 'The process cannot access the file because it is being used by another process.'

- Corrupt/invalid GTC files will abort with an error instead of skipping. Customers will need to remove the corrupt/invalid GTC files before proceeding.

- In the gtc-to-vcf subcommand a mismatch between BPM and CSV manifests will not cause the command to abort with an error. Customers will need to address the mismatch before proceeding.

- For gtc-to-vcf, multi-allelic variants designed with multiple probes might not always collapsed into one variant correctly and be reported as two separate variants instead. This is especially the case when one allele is an Insertion Deletion (indel) and the other is a Single Nucleotide Variation (SNV).