



DRAGEN™ ORA Decompression v2.6.1 Software Release Notes

August 24, 2022



Introduction

These release notes detail the key changes for the DRAGEN™ ORA Decompression software v.2.6.1 which decompresses *.fastq.ora files that have been compressed using DRAGEN ORA Compression software.

Changes are relative to DRAGEN ORA Decompression software v.2.5.5. The DRAGEN ORA Decompression software v.2.5.5 is replaced with new version.

DRAGEN ORA Decompression software Installers, and User Guide are available here:
https://support.illumina.com/sequencing/sequencing_software/DRAGENDecompression.html

The v2.6.1 software package includes a binary installer that is compatible with the following Linux distributions:

- Centos 7 or later
- Ubuntu 14 or later
- Debian 8 or later
- Fedora 26 or later

New Features and command

- Default format FASTQ.GZ. By default, FASTQ.ORA files are decompressed to FASTQ.GZ.
- Decompression can occur in a streaming mode with FASTQ.ORA files located in AWS s3 or Azure Blob storage
- Added `--ora-reference` to specify your chosen path to the ora reference file if not default one. The ora reference file comes packaged in the DRAGEN ORA Decompression software, and the default location can be changed in the `ORA_REF_PATH` environment variable.
- Added `--check-ora-reference-path` to check the accessibility of the ora reference file and print its path.
- Added `-N` or `--name` to re-store original FASTQ name if it has been stored in FASTQ.ORA file
- Added `--empty-third-line` to force empty third line (line with "+" in FASTQ format)
- Added the option `-` to read FASTQ.ORA files from Standard Input
- Added the option `--quiet` for quiet mode where nothing is written to Standard Input or Standard Output
- Added information field for the option `--info` such as:
 - Whether or not the FASTQ.ORA is a paired-read interleaved file
 - Original name of the file if the info has been saved in the FASTQ.ORA file



Issue resolved

Fix for the command `orad filename.fastq.ora` that would previously work only with the option `-o` specified.

Known issues

The ora file format supports concatenation of files, e.g. with :

```
cat file1.fastq.ora file2.fastq.ora > concatenated_files.fastq.ora
```

The “`concatenated_files.fastq.ora`” is a valid ora file whose decompression will yield the concatenated contents of file1 and file2.

However, printing the file’s statistics with option `-i` on the concatenated file (`orad -i concatenated_files.fastq.ora`) will print erroneous information.