

Illumina DRAGEN COVIDSeq Pipeline Software

Release Notes

V1.3.0

For Illumina COVIDSeq Test

February 9, 2021

Introduction

This document describes at a high level the new features, defect repairs and known issues that have occurred in the software since the version 1.3.0 release.

The table below provides a high-level summary of the changes to each versions of the Illumina DRAGEN COVIDSeq Pipeline software, listing new features added, the defects that have been repaired and the critical known issues. Details for each of these versions follow the table.

I. Summary of changes between versions 1.2.2 and 1.3.0

Version	New Features	Defect Repairs	Known Issues
1.3.0	Added support for NextSeq 2000. Added support for NovaSeq 6000 S4/SP Reagent Kit v1.5	N/A	NA

II. Version 1.3.0 Release Notes

NEW FEATURES

- Added support for NextSeq 2000.
- Added support for NovaSeq 6000 S4/SP Reagent Kit v1.5.

DEFECT REPAIRS

- NA

KNOWN ISSUES

- NA

ADDITIONAL NOTES

- The final filtered consensus VCF file that corresponds to the consensus FASTA file can be found in the Logs_Intermediates/ConsensusFasta folders, and is named "filtered.vcf.gz".

The name and location of this file may change in a future software version. This file has a filtered subset of the variants found in the <sample ID>.hard-filtered.vcf.gz.