PetaSuite

FE Plus – *preserve all your read data*

Overview

The **FE Plus** mode of PetaSuite enhances Functional Equivalence to preserve all the original read data that regular FE pipelines discard, in a BAM file that is **typically up to 10% smaller** than regular FE CRAM.[†]

Instantly switch quality scores back to the Original Quality Scores (OQs) in BAM or revert back to the original FASTQ using an environment variable.

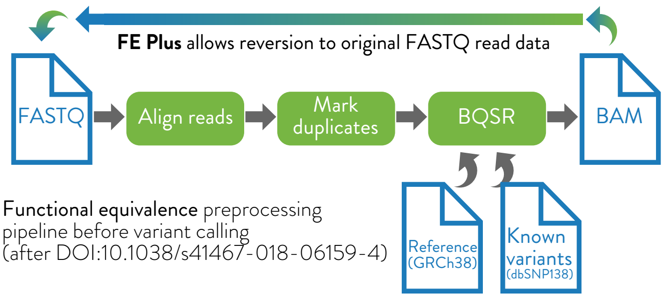
Issues with Functional Equivalence

The Functional Equivalence (FE) specification aims to harmonize variant calling across projects by establishing rules for compliant pipelines.

However, the output from FE pipelines discards original quality scores after Base Quality Score Recalibration (BQSR), and some pipelines also discard certain reads.

The FE specification will continue to be updated as improvements and innovations are made.

Thus, for reproducibility and to support future FE revisions, it is vital to ensure that all the original read data is also fully preserved, resulting in much larger CRAM files.



Functional equivalence preprocessing pipeline before variant calling (after DOI:10.1038/s41467-018-06159-4)

[†] measured on Illumina NovaSeq datasets

Preserve original read data

Instantly switch between the OQs and the BQSR quality scores using one file.

Smaller than Regular FE

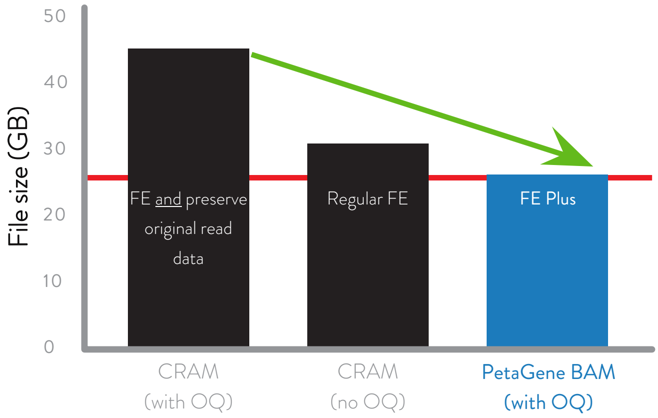
Robust, lossless, high-performance compression with full validation gives a size reduction versus FE CRAMs.

Transparent Access

Applications see a BAM file allowing transparent access to data in the original format, with preservation of the gzip representation on readback.

The Solution

FE Plus lets organizations use Functional Equivalence while also preserving all their original read data in a single BAM file that is smaller than even a regular FE CRAM, which does not preserve all the original read data.



NA12878, rep 1. NovaSeq S2: Illumina DNA PCR Free

For more information, please contact us:
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PetaGene
secure transparent compression