Cancer Analysis Service

Informatics Pipeline Release Notes

Version 4.0.2

1. Internal workflow changes to automatic quality control outputs.
2. Stability updates.

Version 4.0.0

NEW FEATURES:

1. Upgraded Isaac to version iSAAC-SAAC00776.15.01.27
2. Isaac
    - Additional alignment attempted on reads. Now comparable to bwa-mem
3. Upgraded SV calling algorithm to Manta manta-0.23.1.
4. Upgraded CNA calling algorithm to Seneca 2.2.2.3.1.
5. Updated tumor normal variant caller Strelka to 2.0.14.1
6. Updated the annotation pipeline and annotation sources.

Version 3.0.6

1. Internal workflow changes for stability. No output or algorithmic changes.

Version 3.0.0

1. Major rework of Cancer Analysis Pipeline (CAS).
2. Released running the following packages:
    - Tumor/Normal realignment via Isaac
    - Joint Tumor/Normal small-variant caller – Strelka 2.0.14 (publically available as 1.0.12)
    - Somatic SV caller – Manta 0.18.1
    - Seneca – Somatic CNV caller
3. Changed to RefSeq using VEP v72 as the annotation engine.
4. Added b-allele plots to PDF.

Version 2.0.0

1. Initial Isaac-based release of the Cancer Analysis Pipeline.