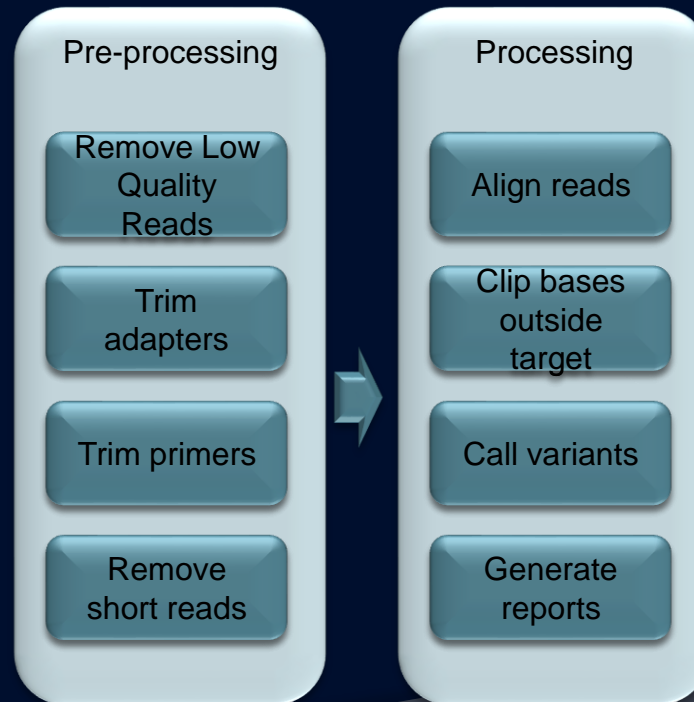# NextGENe AutoRun

- Create custom templates (optional)
- Create Job File
- Run AutoRun

Customize Default Templates

- Create custom templates
  - Save pre-installed template as new template
  - Add reference
  - Add tracks (optional)
  - Add/adjust other output report settings
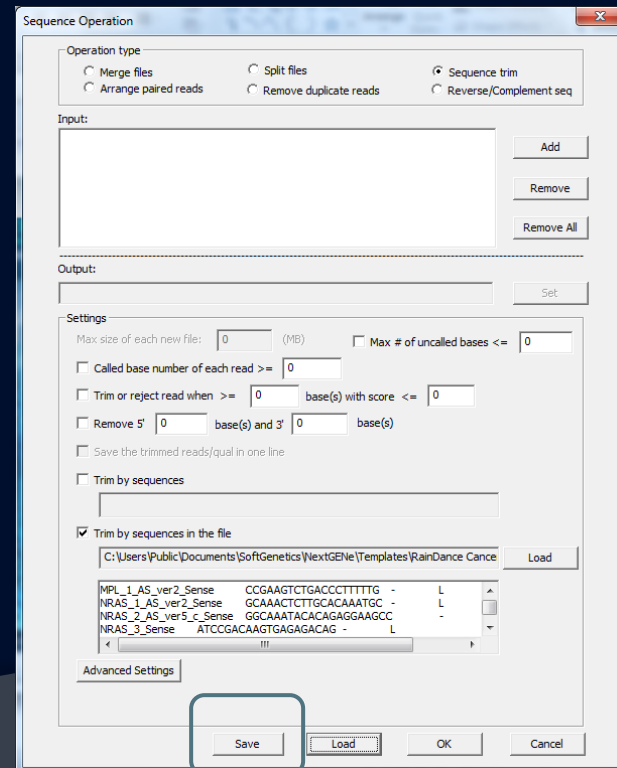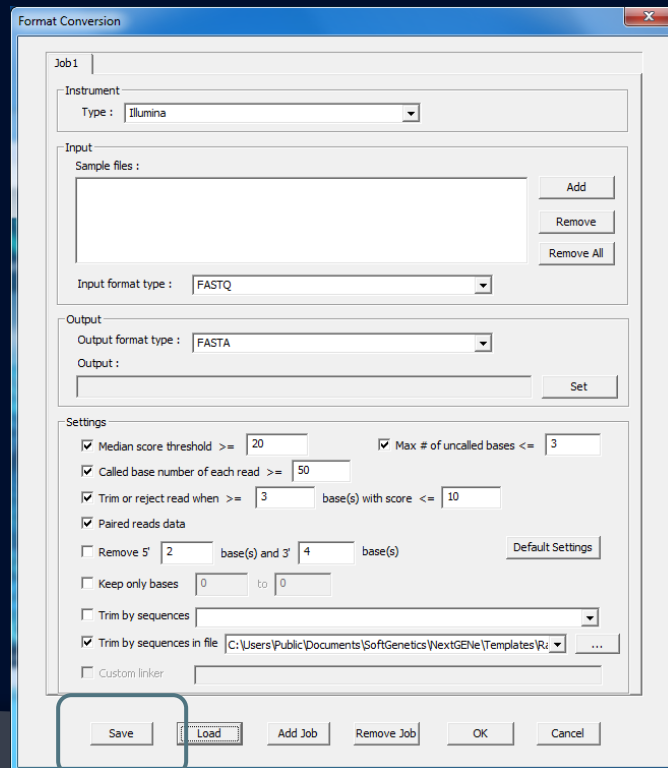
Customize Template

Pre-processing configuration	NextGENe's Tools menu
Post-processing configuration	NextGENe Viewer's report menus
Alignment/variant detection configuration	NextGENe's Project Wizard
Build template	AutoRun's Job File Editor

Pre-processing

- Remove Low Quality Reads
- Trim adapters
- Trim primers
- Remove short reads

Processing

- Align reads
- Clip bases outside target
- Call variants
- Generate reports

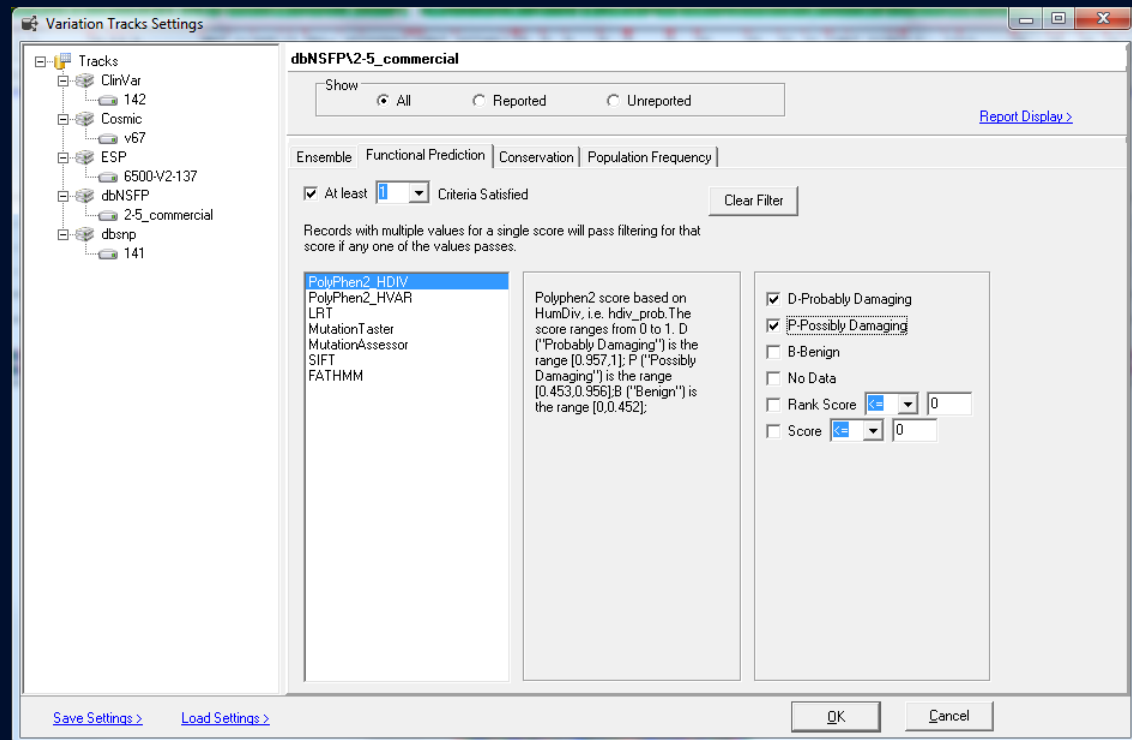# Pre-processing Configuration
(NextGENe's Tools menu)

- Format Conversion can remove low quality reads and adapters
- Sequence Operations are steps that are configured to trim adapters, remove duplicates, as well as a few other possible operations
- Make edits, and click Save

Post-processing Configuration

(NextGENe Viewer's report menus)

- ⊚ Reports like coverage, expression and variants
- ⊚ Open a project in NextGENe Viewer
- ⊚ Make edits to report settings, and click Save Settings

Alignment/Variant Detection
(NextGENe's Project Wizard)

- Alignment and variant detection sensitivity can be adjusted through the NextGENe's Project Wizard
- Post-processing configuration files can be added to the last step of the Project Wizard, or they can be added directly to the template

Build Template
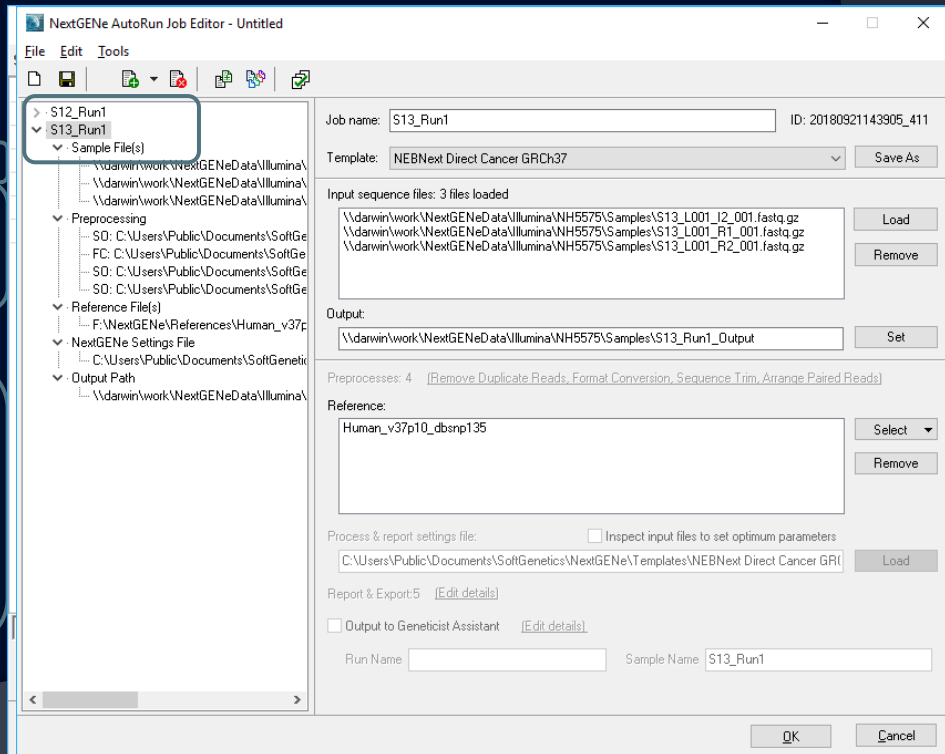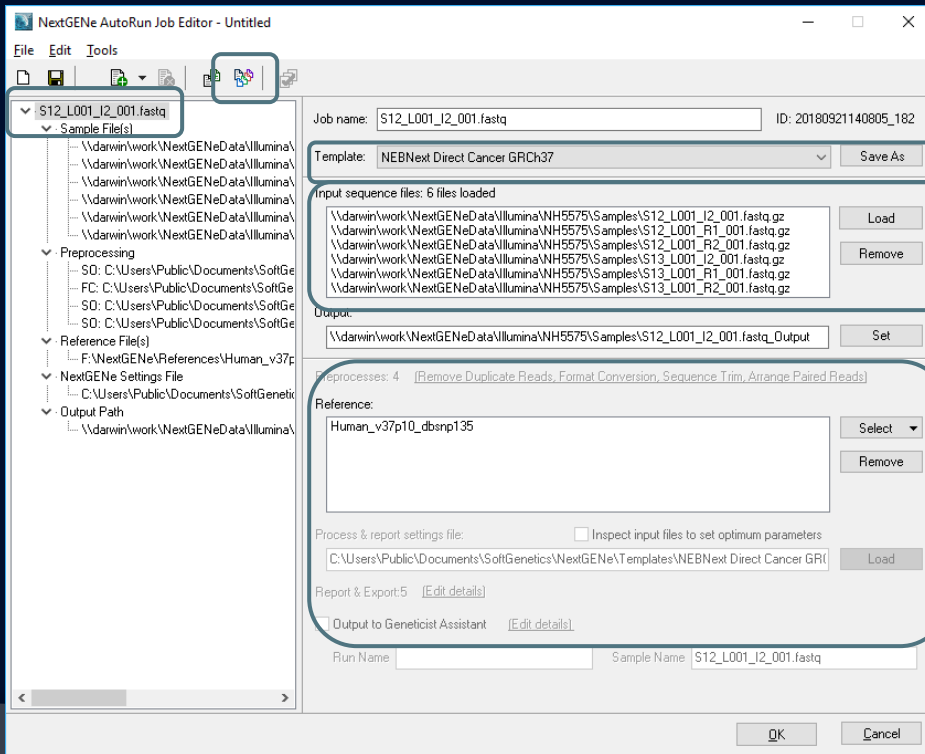## (NextGENe AutoRun's Job File Editor)

- ◉ Edit a template, or create a new template
  - • If only minor changes to a template are needed, select the template, click on Edit and Save As a new template
- ◉ Edit Preprocessing steps
  - • Select the Preprocesses link and load the Format Conversion and Sequence Operations configuration files
- ◉ Choose the alignment configuration file
- ◉ Edit Output details to add/edit report configuration files
  - • If the alignment configuration file already includes the output reports, then this step is not necessary
- ◉ Save the template
  - • When you save a new template within the NextGENe AutoRun, all configuration files are copied to the template's folder

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Next Generation Sequencing Software for Biologists
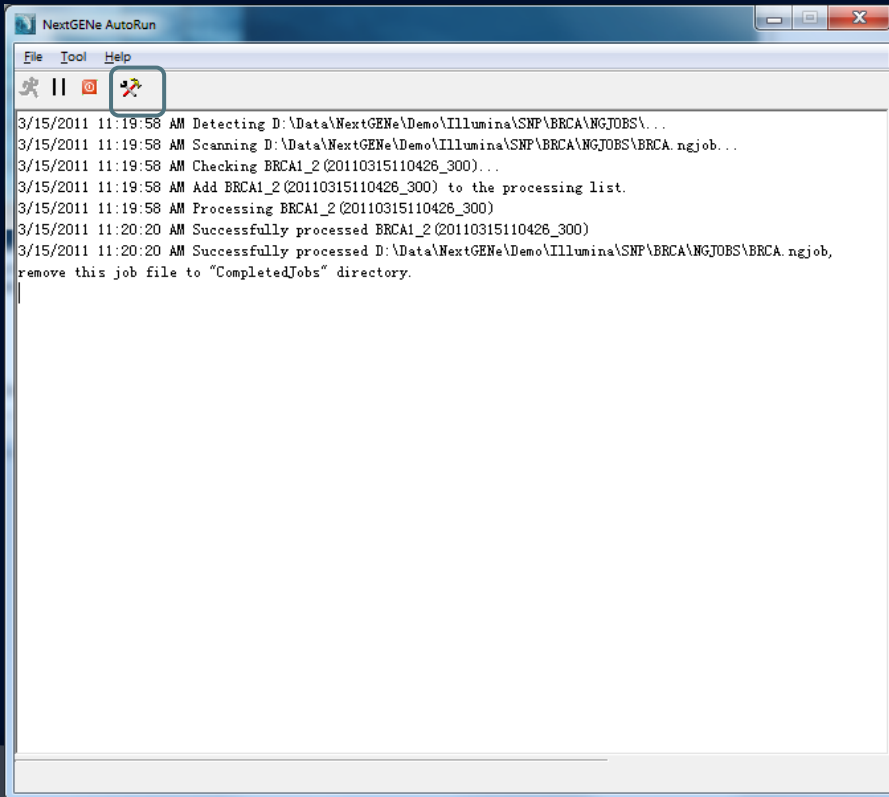
Create Job File

NextGENe AutoRun's Job File Editor)

- ◉ Add input files (multiple samples can be added)
- ◉ Select Template (optional),
  - Or add preproccesing steps, reference and process & report settings
- ◉ Group input files into Jobs
- ◉ Group Jobs can be used when multiple samples are analyzed with the same settings
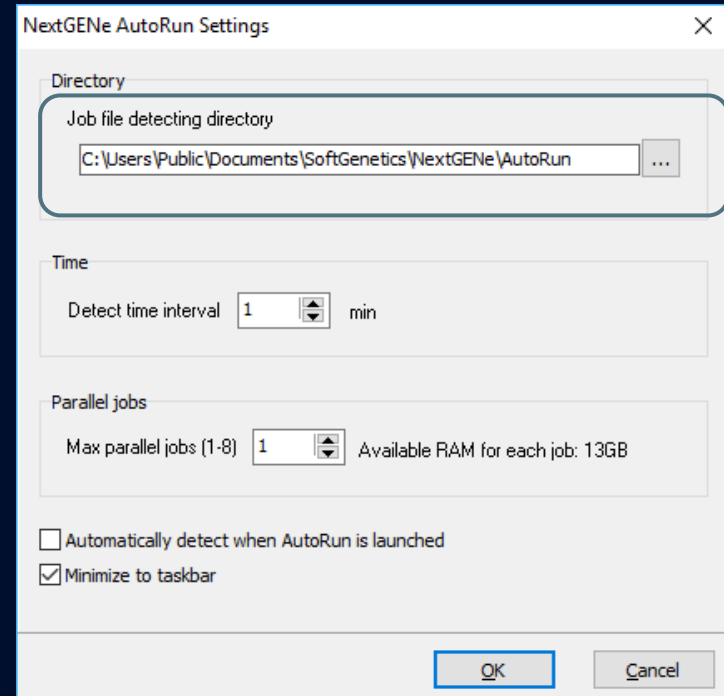
Run AutoRun

- AutoRun checks for job files in the Job file detecting directory 🛠️. When a job file is found, it is scanned for number of jobs.
- Each job within job file is checked for necessary files.
- Jobs are processed as job files become available.
- Completed job files are moved out of the queue.
- New job files can always be added to the queue.