

NextGENe AutoRun

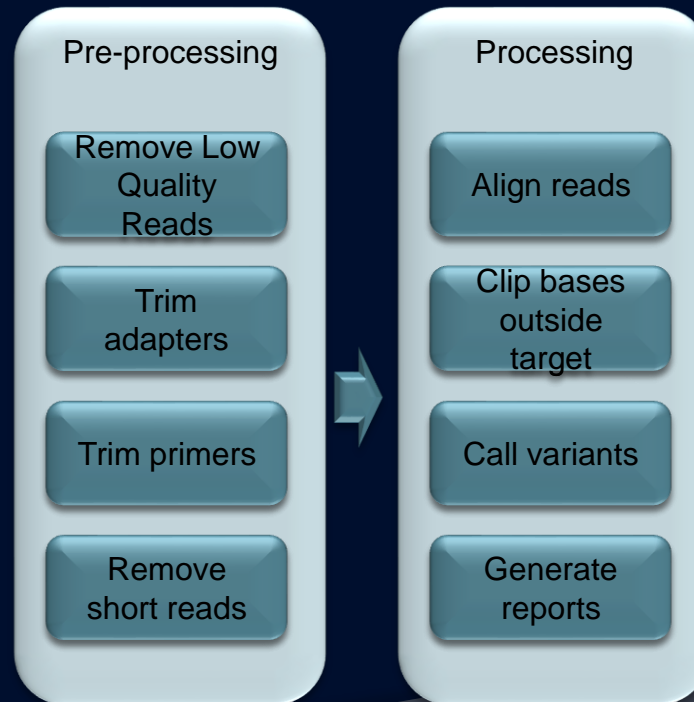
- Create custom templates (optional)
- Create Job File
- Run AutoRun

Customize Default Templates

- ① Create custom templates
 - Save pre-installed template as new template
 - Add reference
 - Add tracks (optional)
 - Add/adjust other output report settings

Customize Template

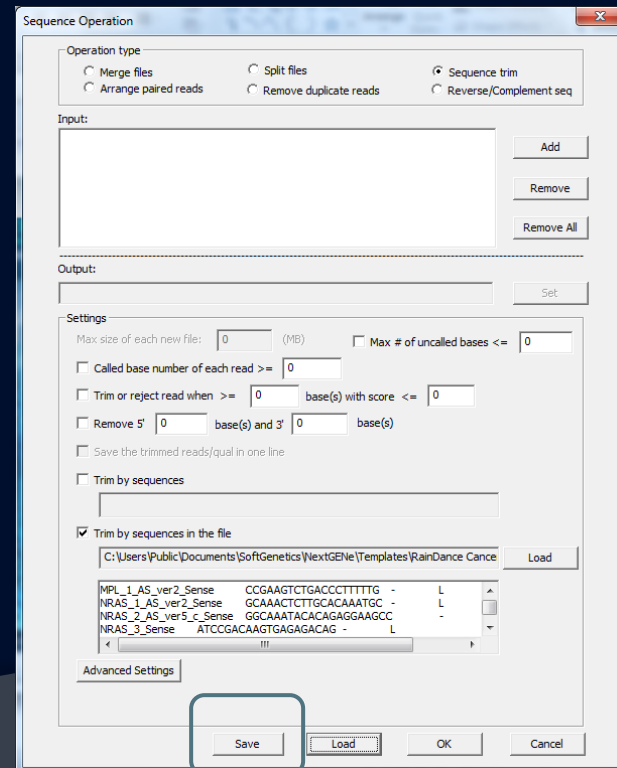
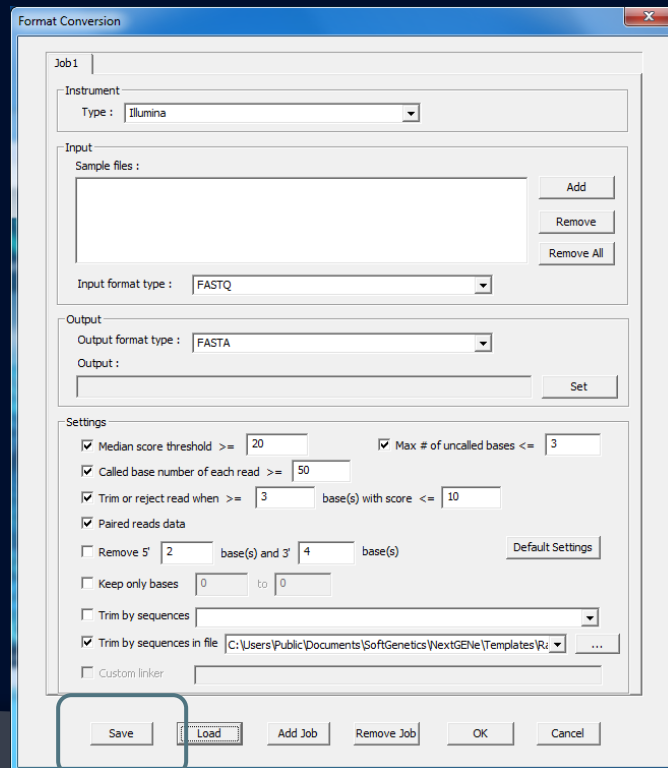
Pre-processing configuration	NextGENe's Tools menu
Post-processing configuration	NextGENe Viewer's report menus
Alignment/variant detection configuration	NextGENe's Project Wizard
Build template	AutoRun's Job File Editor



Pre-processing Configuration

(NextGENe's Tools menu)

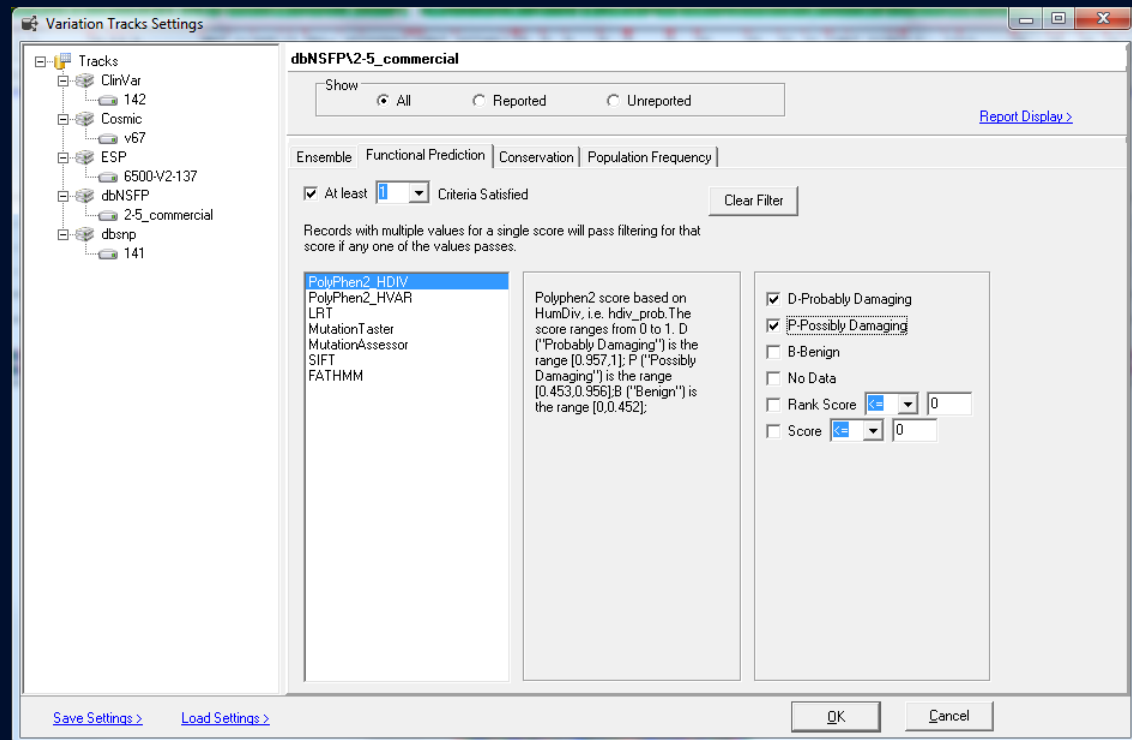
- Format Conversion can remove low quality reads and adapters
- Sequence Operations are steps that are configured to trim adapters, remove duplicates, as well as a few other possible operations
- Make edits, and click Save



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

Project Wizard - Alignment

Alignment

Reads: Allowable mismatched bases 0 (0-2)
Allowable ambiguous alignments 50

Seeds: 30 bases, move step 5 bases Inspect input files
Allowable alignments 100 (1-1000)

Overall: Matching base percentage >= 75 Detect large indels

Sample trim
 Select sequence range
from 1 bases to 30 bases
 Hide unmatched ends

Mutation filter Use original SNPs Except for homozygous Indels HomopolymerIndels

Mutation percentage <= 5 5 5
SNP allele count <= 5 5 5
Total coverage count <= 100 100 100
Balance ratios and frequency <= 0.5 0.5 0.8
80 % 80 % 80 %

File type
 Load assembled result files
 Load SAGE expression data
Extract bases from: 2 bases to: 17 bases
New sequence coverage minimum 20
 Load paired reads
Library size range: from 0 bases to 500 bases
454 Sequence:

Save matched reads Highlight anchor sequence Ambiguous gain/loss
 Detect structural variations Mismatch: 0.3 length and 50 bases
Default Settings

Save Settings Load Settings << Back Next >> Cancel Finish

Project Wizard - Post Processing

Post processing

Report Settings

Report	File Name	Set	Remove
Mutation	MR_General.ini	Set	Remove
Expression	ExpressionReport.ini	Set	Remove
Distribution	DistributionReport.ini	Set	Remove
Coverage Curve	CC_1x.ini	Set	Remove
Coverage Curve	CC_15x.ini	Set	Remove

Save summary report Add Remove All

Export Settings

Export BAM Add Remove All

Output to Genetist Assistant
GA Input

Save Settings Load Settings << Back Cancel Finish

Build Template

(NextGENe AutoRun's Job File Editor)

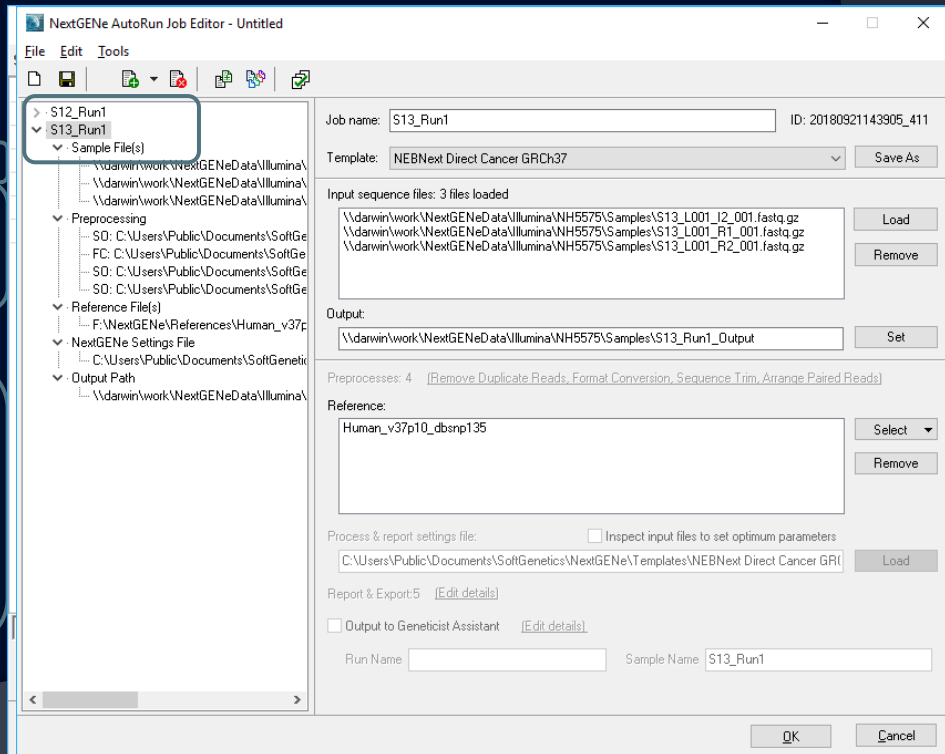
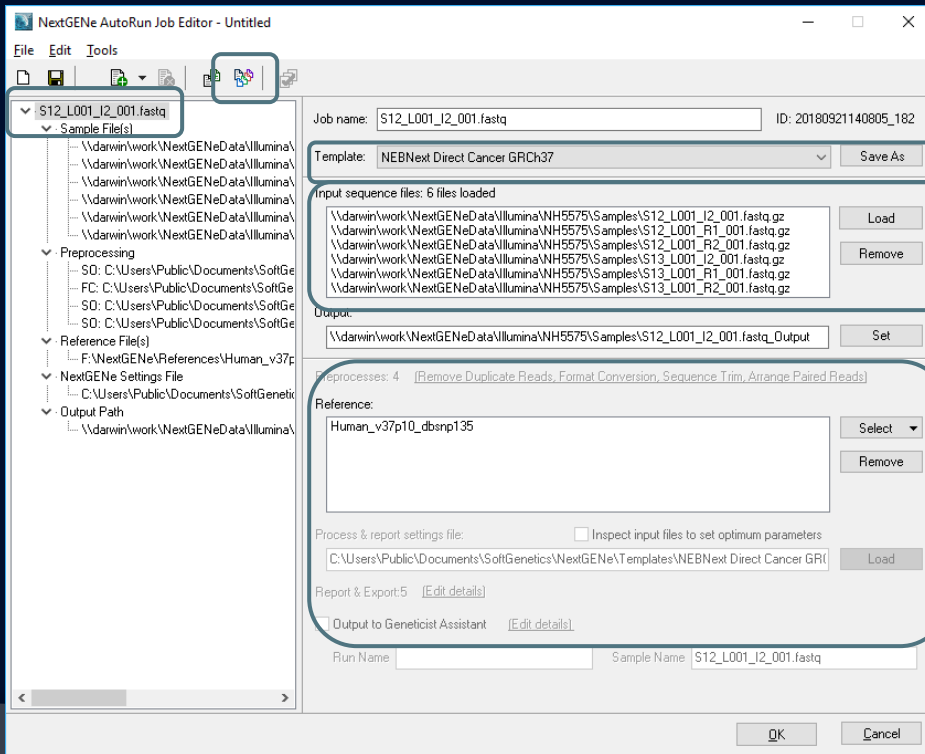
- Edit a template, or create a new template
 - If only minor changes to a template are needed, select the template, click on Edit and Save As a new template
- Edit Preprocessing steps
 - Select the Preprocesses link and load the Format Conversion and Sequence Operations configuration files
- Choose the 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

The screenshot displays the 'Job File Editor' window. At the top, there are fields for 'Job name' (Job 1) and 'ID' (20180921140805_182). Below this is a 'Template' dropdown menu set to 'Choose Template' and a 'Save' button. The 'Input sequence files' section contains an empty list box with 'Load' and 'Remove' buttons. The 'Output' section has an empty text field and a 'Set' button. The 'Preprocesses' section shows '0' and an 'Add...' button. The 'Reference' section has an empty text field, a 'Select' dropdown, and a 'Remove' button. The 'Process & report settings file' section includes a checkbox for 'Inspect input files to set optimum parameters' and a 'Load' button. The 'Report & Export' section has an 'Edit details' button. Below this is a checkbox for 'Output to Geneticist Assistant' with its own 'Edit details' button. At the bottom, there are 'Run Name' and 'Sample Name' (Job 1) fields, and 'OK' and 'Cancel' buttons.


Create Job File

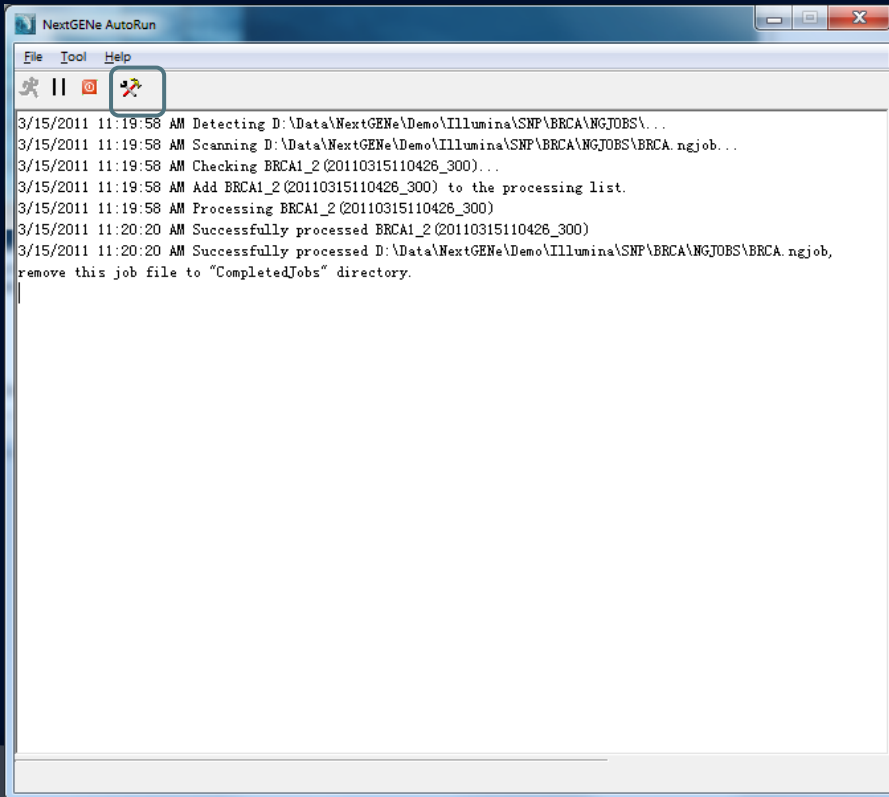
NextGENe AutoRun's Job File Editor

- Add input files (multiple samples can be added)
- Select Template (optional),
 - Or add preprocessing 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

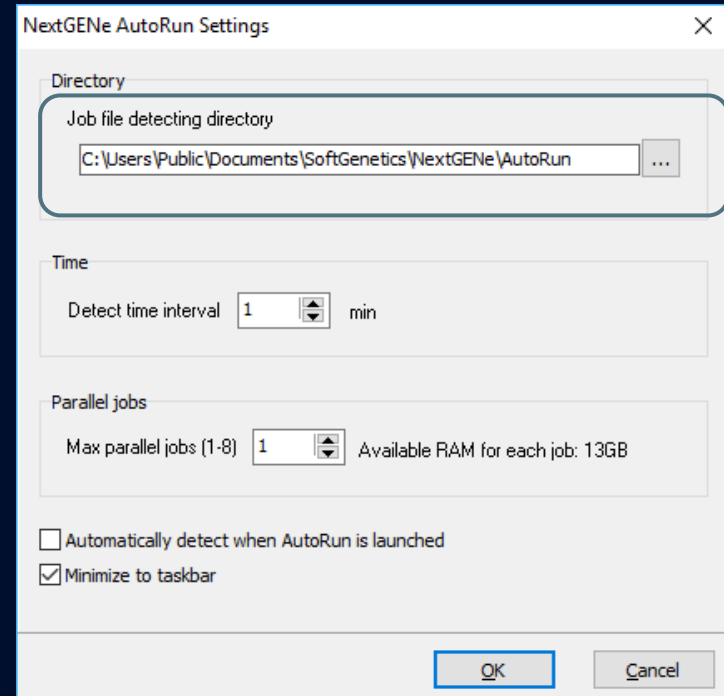


Run AutoRun

- 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.



```
3/15/2011 11:19:58 AM Detecting D:\Data\NextGENe\Demo\Illumina\SNP\BRCA\NGJOBS\...
3/15/2011 11:19:58 AM Scanning D:\Data\NextGENe\Demo\Illumina\SNP\BRCA\NGJOBS\BRCA.ngjob...
3/15/2011 11:19:58 AM Checking BRCA1_2 (20110315110426_300)...
3/15/2011 11:19:58 AM Add BRCA1_2 (20110315110426_300) to the processing list.
3/15/2011 11:19:58 AM Processing BRCA1_2 (20110315110426_300)
3/15/2011 11:20:20 AM Successfully processed BRCA1_2 (20110315110426_300)
3/15/2011 11:20:20 AM Successfully processed D:\Data\NextGENe\Demo\Illumina\SNP\BRCA\NGJOBS\BRCA.ngjob,
remove this job file to "CompletedJobs" directory.
```



NextGENe AutoRun Settings

Directory

Job file detecting directory

C:\Users\Public\Documents\SoftGenetics\NextGENe\AutoRun

Time

Detect time interval 1 min

Parallel jobs

Max parallel jobs (1-8) 1 Available RAM for each job: 13GB

Automatically detect when AutoRun is launched

Minimize to taskbar

OK Cancel