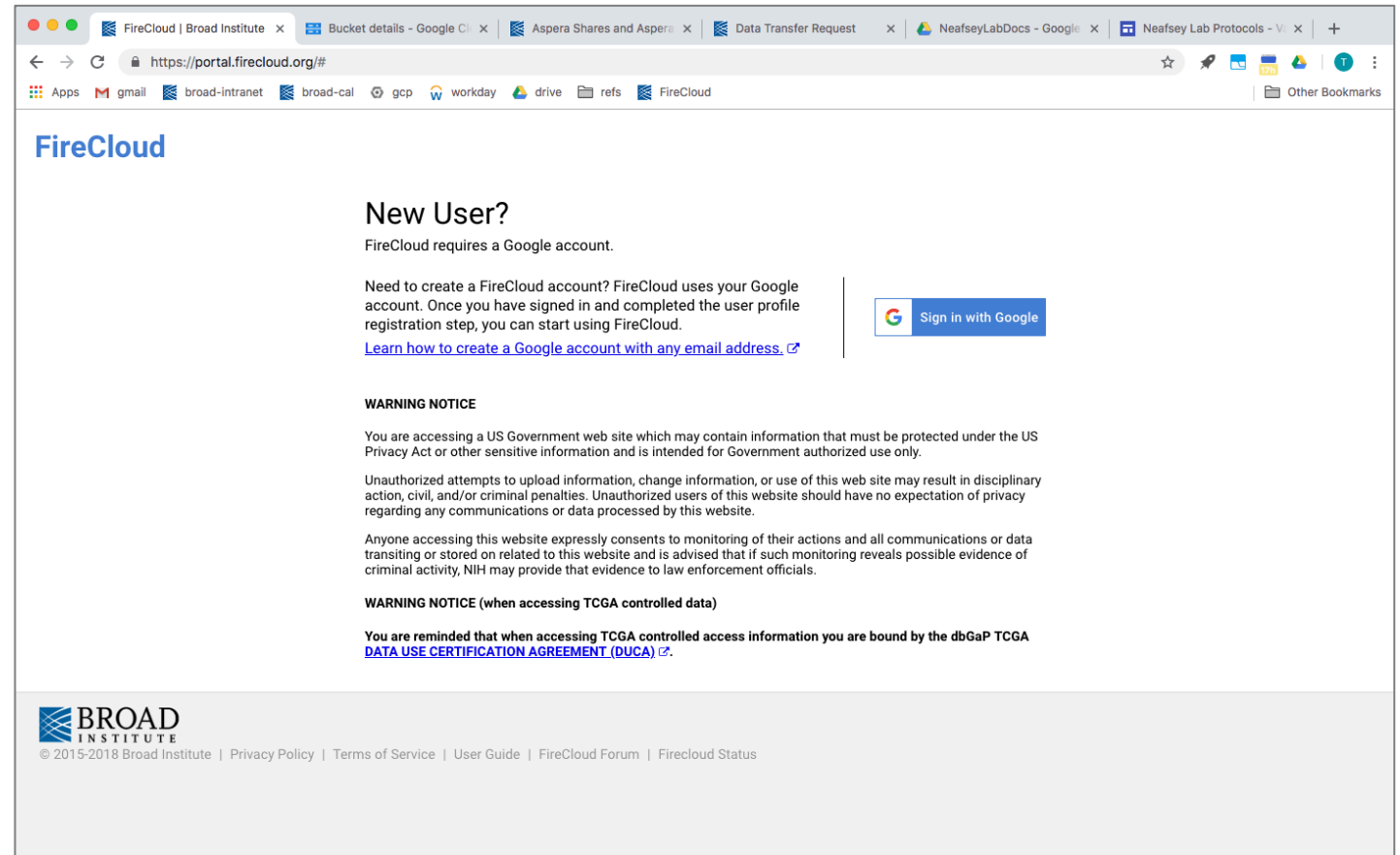


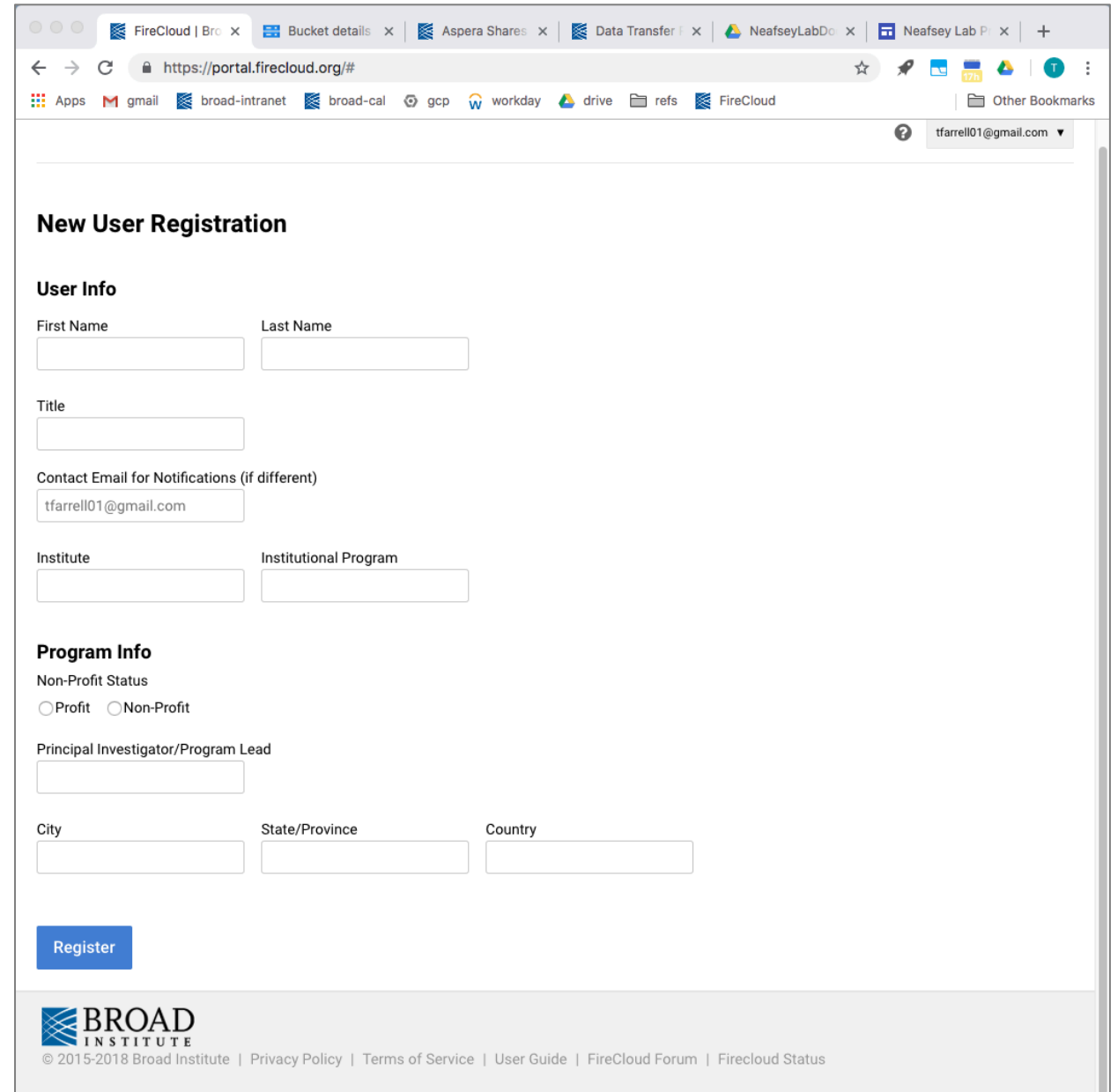
FireCloud Sign-in

- Go to portal.firecloud.org
- Click **Sign in with Google**
 - (use your Broad Institute email over a personal Google account)



FireCloud Registration

- If you are a new user, you will be directed to the registration page
- Fill out your information accordingly



The screenshot shows a web browser window with the URL <https://portal.firecloud.org/#>. The page is titled "New User Registration" and contains the following sections:

- User Info**
 - First Name:
 - Last Name:
 - Title:
 - Contact Email for Notifications (if different):
 - Institute:
 - Institutional Program:
- Program Info**
 - Non-Profit Status: ☐ Profit ☐ Non-Profit
 - Principal Investigator/Program Lead:
 - City:
 - State/Province:
 - Country:

A blue "Register" button is located below the form fields. The footer of the page features the Broad Institute logo and the following text: "© 2015-2018 Broad Institute | Privacy Policy | Terms of Service | User Guide | FireCloud Forum | Firecloud Status".

FireCloud Workspaces

- Once signed-in/registered, you should be directed your workspaces page
- Workspaces organize methods, data models (when applicable) and job monitoring in one place

The screenshot shows the FireCloud Workspaces page. The browser address bar displays <https://portal.firecloud.org/#>. The page header includes the FireCloud logo and navigation links for Workspaces, Data Library, and Method Repository. The user's email, tfarrell@broadinstitute.org, is shown in the top right corner.

On the left side, there are several filter sections:

- Tags:** A search bar and a "Collapse filters" link.
- Status:** Radio buttons for Complete, Running, and Exception.
- Access:** Radio buttons for Project Owner, Owner, Writer, Reader, and No Access.
- Publishing:** Radio buttons for Published and Un-published.
- TCGA Access:** Radio buttons for TCGA Open Access and TCGA Controlled Access.

The main content area displays a table of workspaces under the "My Workspaces (6)" tab. The table has columns for Status, Workspace, Description, Last Modified, and Access Level. The workspaces listed are:

Status	Workspace	Description	Last Modified	Access Level
✓	broad-malaria-firecloud gatk4_hc_pfalciparum-cdc	No description provided	Feb 16, 2018, 3:19 PM	Project Owner
✓	broad-malaria-firecloud gatk3_germline_snps_indels	No description provided	Oct 1, 2018, 4:41 PM	Project Owner
✓	broad-malaria-firecloud cnv_detect	Firecloud workspace for CnvDetectD2: http://bil	Mar 28, 2018, 10:58 AM	Project Owner
✓	broad-malaria-firecloud gatk4_germline_cnv	No description provided	Mar 20, 2018, 7:06 PM	Project Owner
✓	broad-malaria-firecloud gatk3_germline_snps_indels-plasmodi	gatk3_germline_snps_indels-plasmodium.wdl	Sep 28, 2018, 11:15 AM	Project Owner
✓	broad-malaria-firecloud gatk3_germline_snps_indels-anophele	No description provided	Oct 1, 2018, 12:26 PM	Project Owner

At the bottom of the table, it says "1 - 6 of 6 results (filtered from 111 total)". There are navigation links for "Prev" and "Next", and a "per page" dropdown set to 20.

The footer of the page features the Broad Institute logo and copyright information: "© 2015-2018 Broad Institute | Privacy Policy | Terms of Service | User Guide | FireCloud Forum | Firecloud Status".

FireCloud Workspaces

- When you select a workspace, the summary page looks like this
- The data models, methods and job monitoring can be found in the **Data**, **Method Configurations** and **Monitor** tabs respectively

The screenshot shows the FireCloud workspace summary page for 'broad-malaria-firecloud/gatk3_germline_snps_indels'. The page has a top navigation bar with tabs: Summary, Data, Analysis, Notebooks (BETA), Method Configurations, and Monitor. The 'Summary' tab is active. On the left, there is a green 'Complete' status box and a list of actions: Share..., Catalog Dataset..., Edit, Clone..., Lock, and Delete. The main content area is divided into three columns. The first column contains 'Workspace Access' details: Access Level (Project Owner), Workspace Owner (tfarrell@broadinstitute.org), Authorization Domain (None), and Created By (tfarrell@broadinstitute.org, September 27, 2018, 10:54 AM). The second column contains 'Project Cost' information: Estimated Monthly Storage Fee (\$1.11), Google Billing Detail (broad-malaria-firecloud), and Storage & Analysis details (Google Bucket: fc-f012e594-e4a5-4b55-849e-765ff4c987ec, Analysis Submissions: 4 Done). The third column contains 'Tags' (No tags provided), 'Description' (No description provided), and 'Workspace Attributes'. The footer includes the Broad Institute logo and copyright information (© 2015-2018 Broad Institute) along with links to Privacy Policy, Terms of Service, User Guide, FireCloud Forum, and FireCloud Status.

broad-malaria-firecloud/gatk3_germline_snps_indels

- The main workspace for malaria variant-calling is **gatk3_germline_snps_indels**
- If you select this workspace, and then click the **Method Configurations** tab, you will see 3 organism-specific template configurations:
 - anopheles : *A. gambiae*
 - pfalciparum : *P. falciparum*
 - pvivax : *P. vivax*

The screenshot shows the FireCloud portal interface. The browser address bar displays the URL: https://portal.firecloud.org/#workspaces/broad-malaria-firecloud/gatk3_germline_snps_indels/method-configs. The page title is "FireCloud Workspaces Data Library Method Repository". The user is logged in as "tfarrell@broadinstitute.org".

The workspace is "broad-malaria-firecloud/gatk3_germline_snps_indels". The "Method Configurations" tab is selected. The table below shows the configurations:

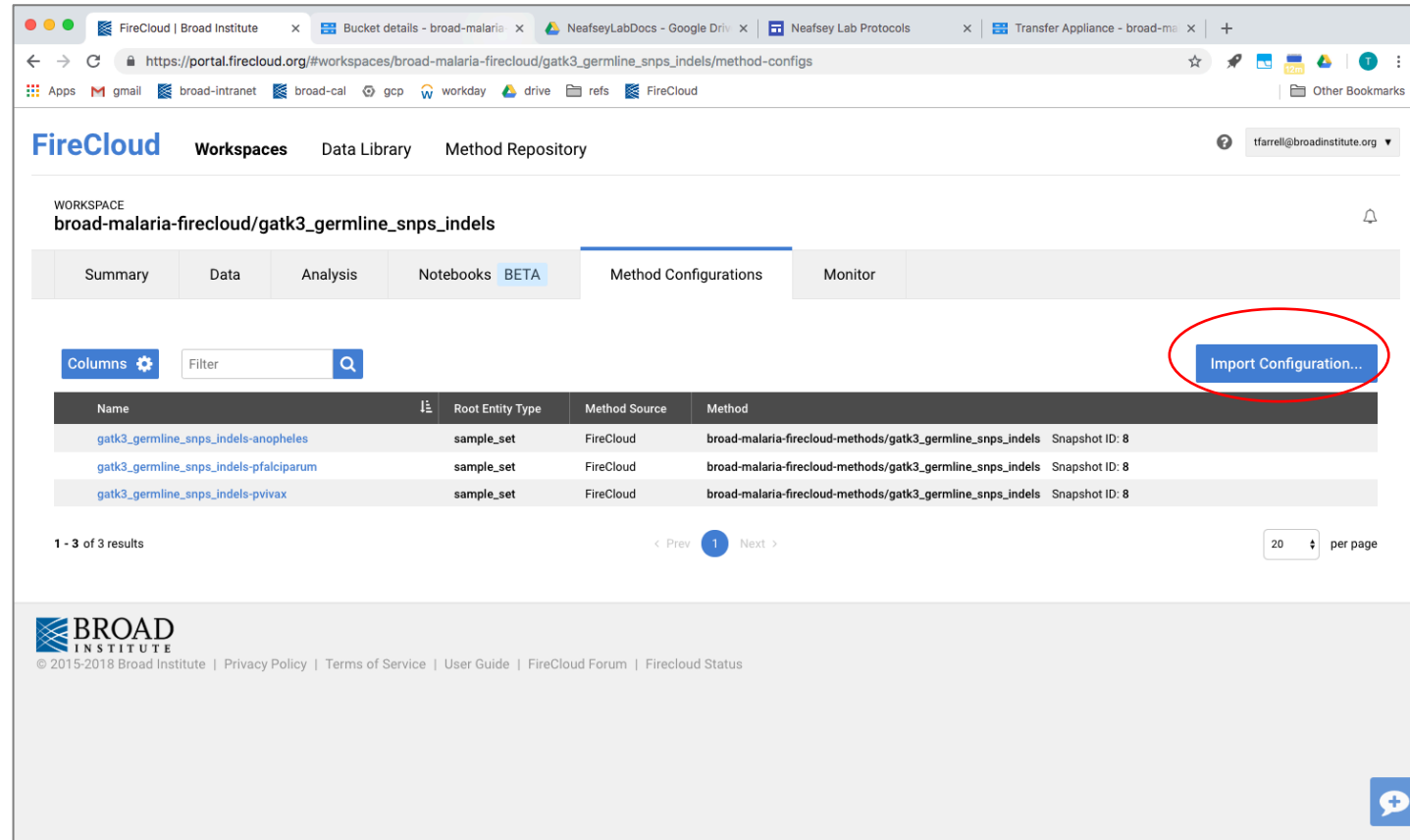
Name	Root Entity Type	Method Source	Method	Snapshot ID
gatk3_germline_snps_indels-anopheles	sample_set	FireCloud	broad-malaria-firecloud-methods/gatk3_germline_snps_indels	8
gatk3_germline_snps_indels-pfalciparum	sample_set	FireCloud	broad-malaria-firecloud-methods/gatk3_germline_snps_indels	8
gatk3_germline_snps_indels-pvivax	sample_set	FireCloud	broad-malaria-firecloud-methods/gatk3_germline_snps_indels	8

1 - 3 of 3 results

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broad-malaria-firecloud : Starting a new project analysis

- When starting a new variant-calling analysis, you'll want to create a new configuration from one of the 3 templates, depending on which organism your data was derived from
- To do this, go to the workspace **gatk3_germline_snps_indels** and the **Method Configurations** tab
- Then click on **Import Configuration...**



The screenshot shows the FireCloud portal interface. The browser address bar displays the URL: https://portal.firecloud.org/#workspaces/broad-malaria-firecloud/gatk3_germline_snps_indels/method-configs. The page title is "FireCloud | Broad Institute". The navigation bar includes "Workspaces", "Data Library", and "Method Repository". The user's email, "tfarrell@broadinstitute.org", is visible in the top right corner.

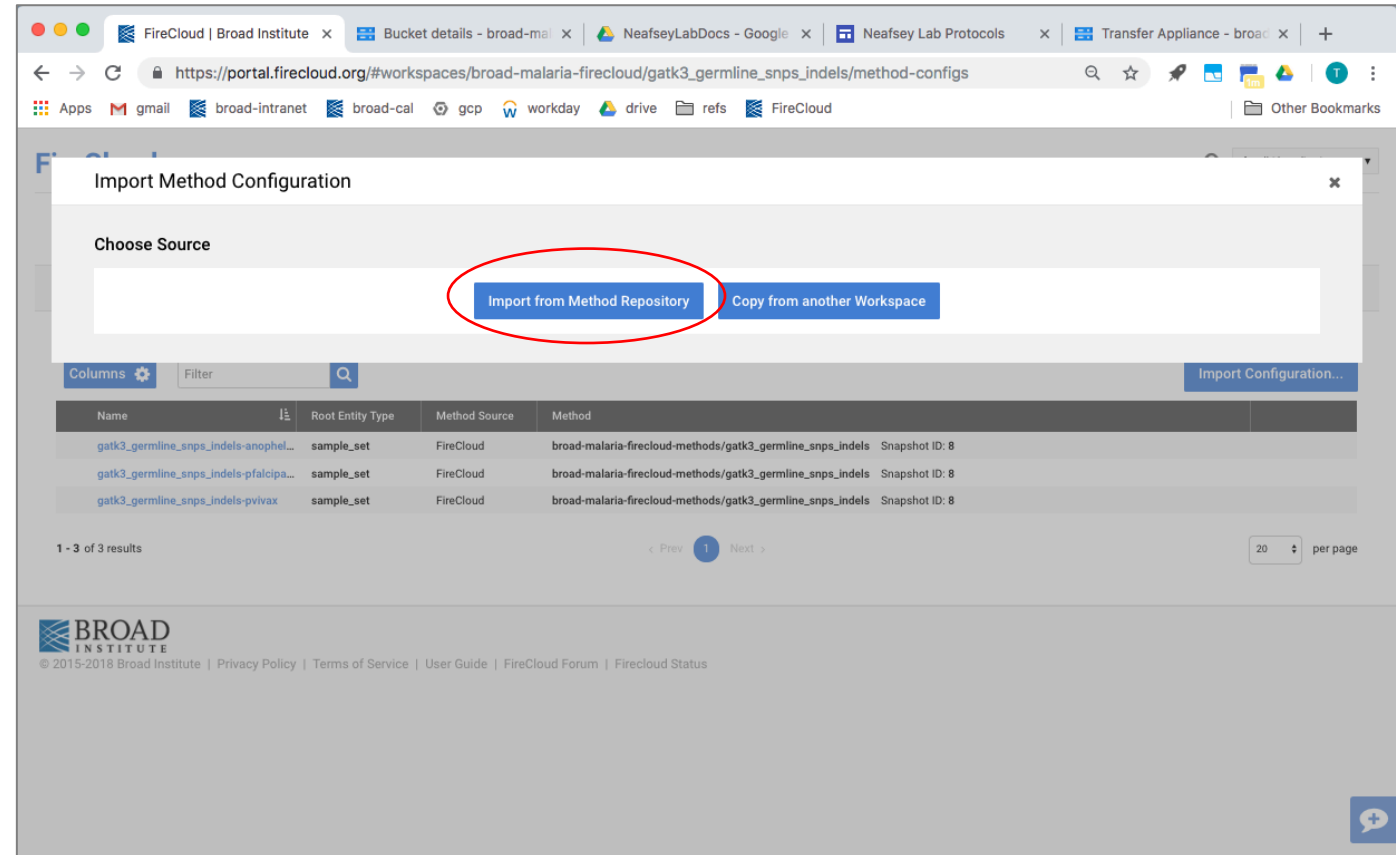
The main content area shows the workspace "broad-malaria-firecloud/gatk3_germline_snps_indels". The "Method Configurations" tab is selected, and the "Import Configuration..." button is circled in red. Below the tab, there is a table with the following data:

Name	Root Entity Type	Method Source	Method
gatk3_germline_snps_indels-anopheles	sample_set	FireCloud	broad-malaria-firecloud-methods/gatk3_germline_snps_indels Snapshot ID: 8
gatk3_germline_snps_indels-pfalciparum	sample_set	FireCloud	broad-malaria-firecloud-methods/gatk3_germline_snps_indels Snapshot ID: 8
gatk3_germline_snps_indels-pvixax	sample_set	FireCloud	broad-malaria-firecloud-methods/gatk3_germline_snps_indels Snapshot ID: 8

At the bottom of the page, the Broad Institute logo and copyright information are visible: "© 2015-2018 Broad Institute | Privacy Policy | Terms of Service | User Guide | FireCloud Forum | Firecloud Status".

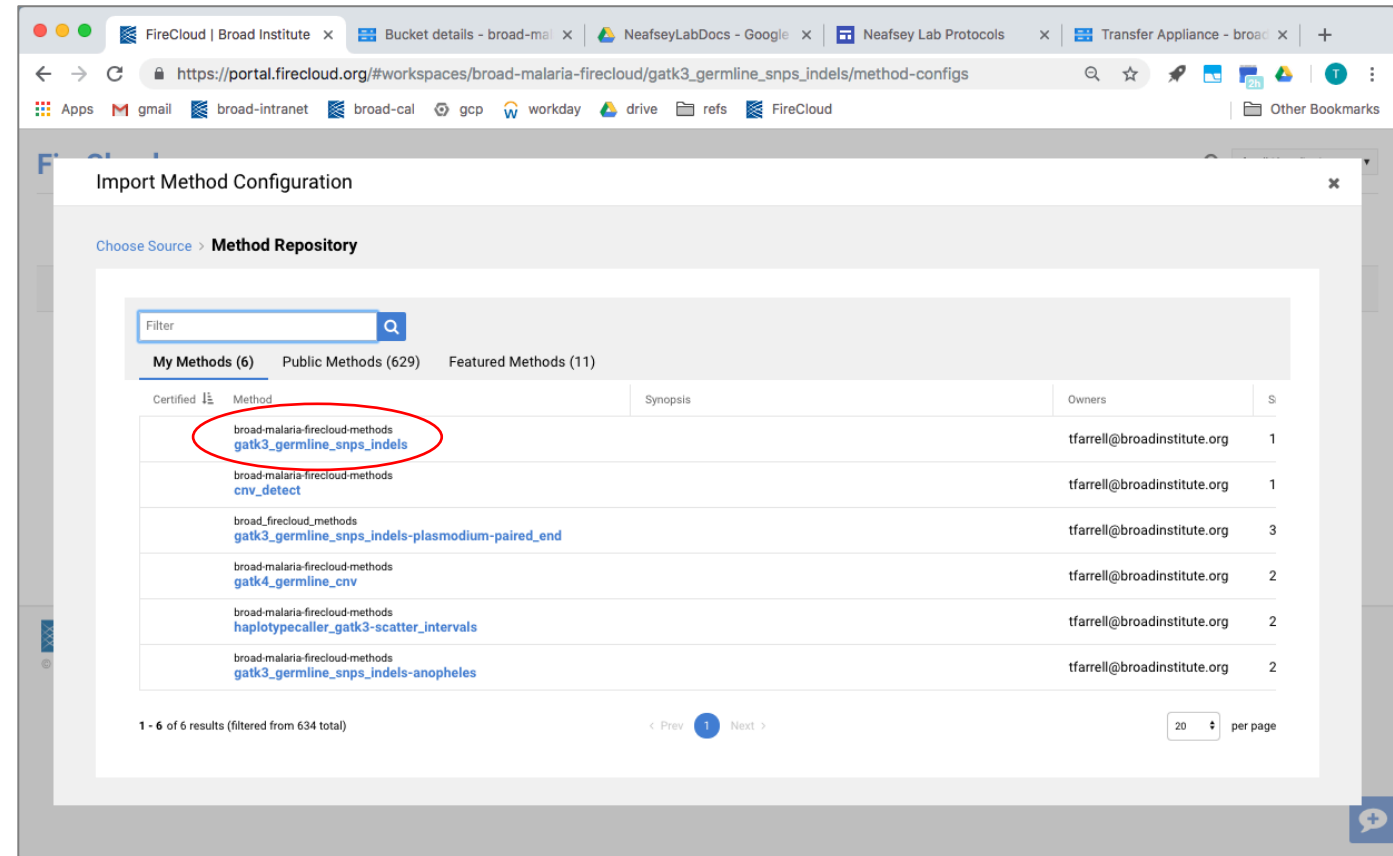
broad-malaria-firecloud : Starting a new project analysis

- Then click on **Import from Method Repository**



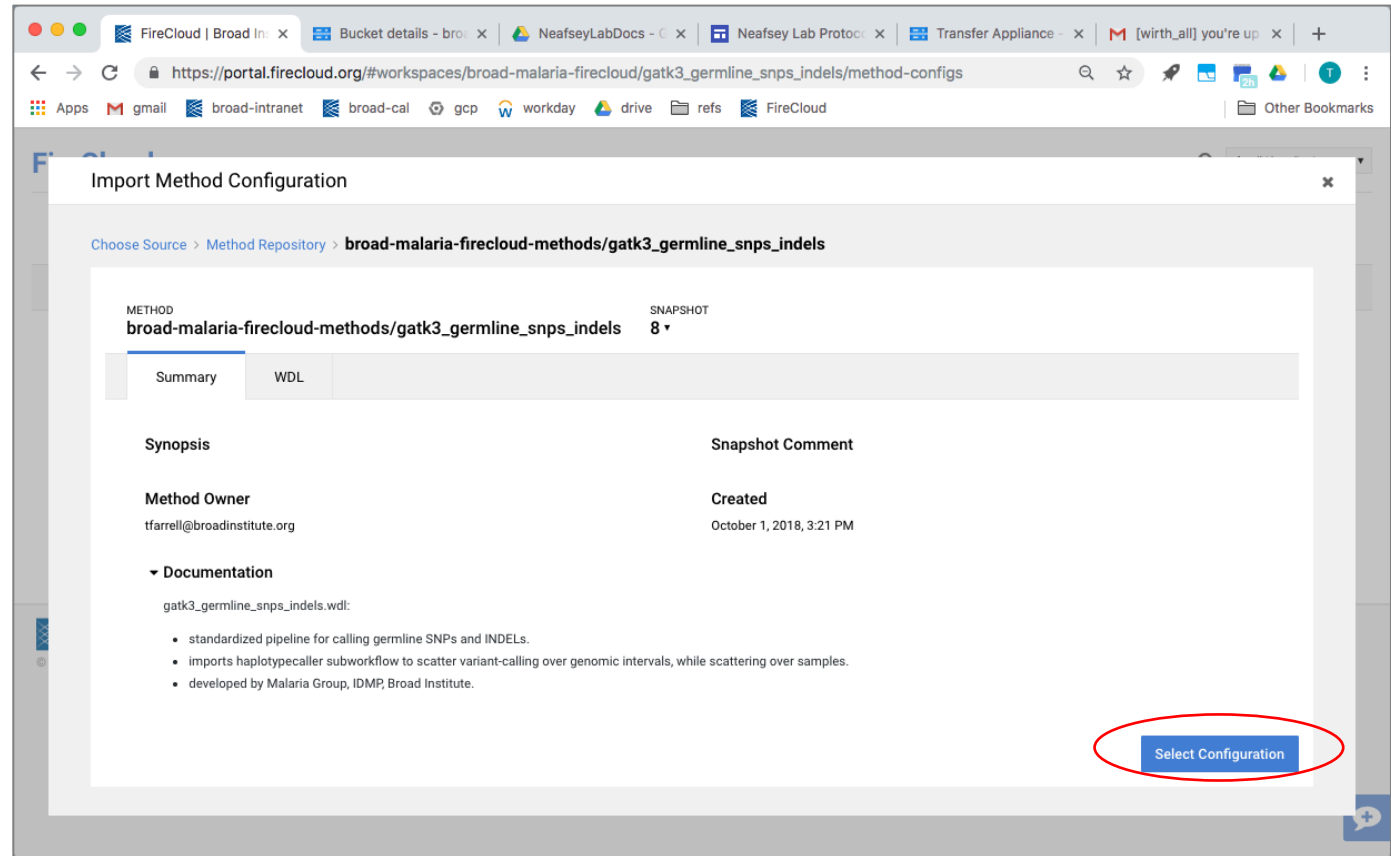
broad-malaria-firecloud : Starting a new project analysis

- You will see a list of methods in your **Methods Repository**
- Select the method **gatk3_germline_snps_indels**



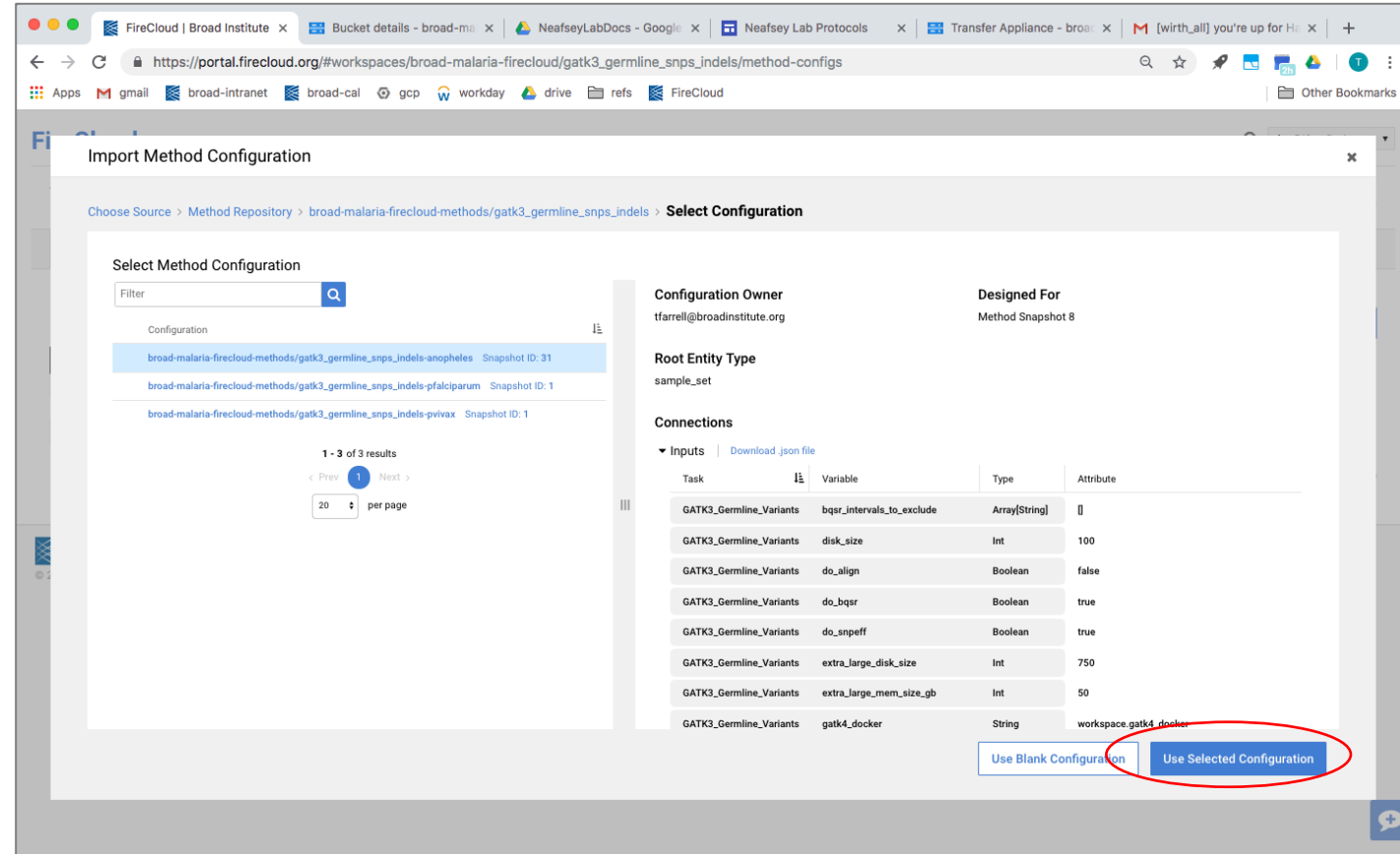
broad-malaria-firecloud : Starting a new project analysis

- You will see a summary of this method
- Then click **Select Configuration** to select one of the template configurations



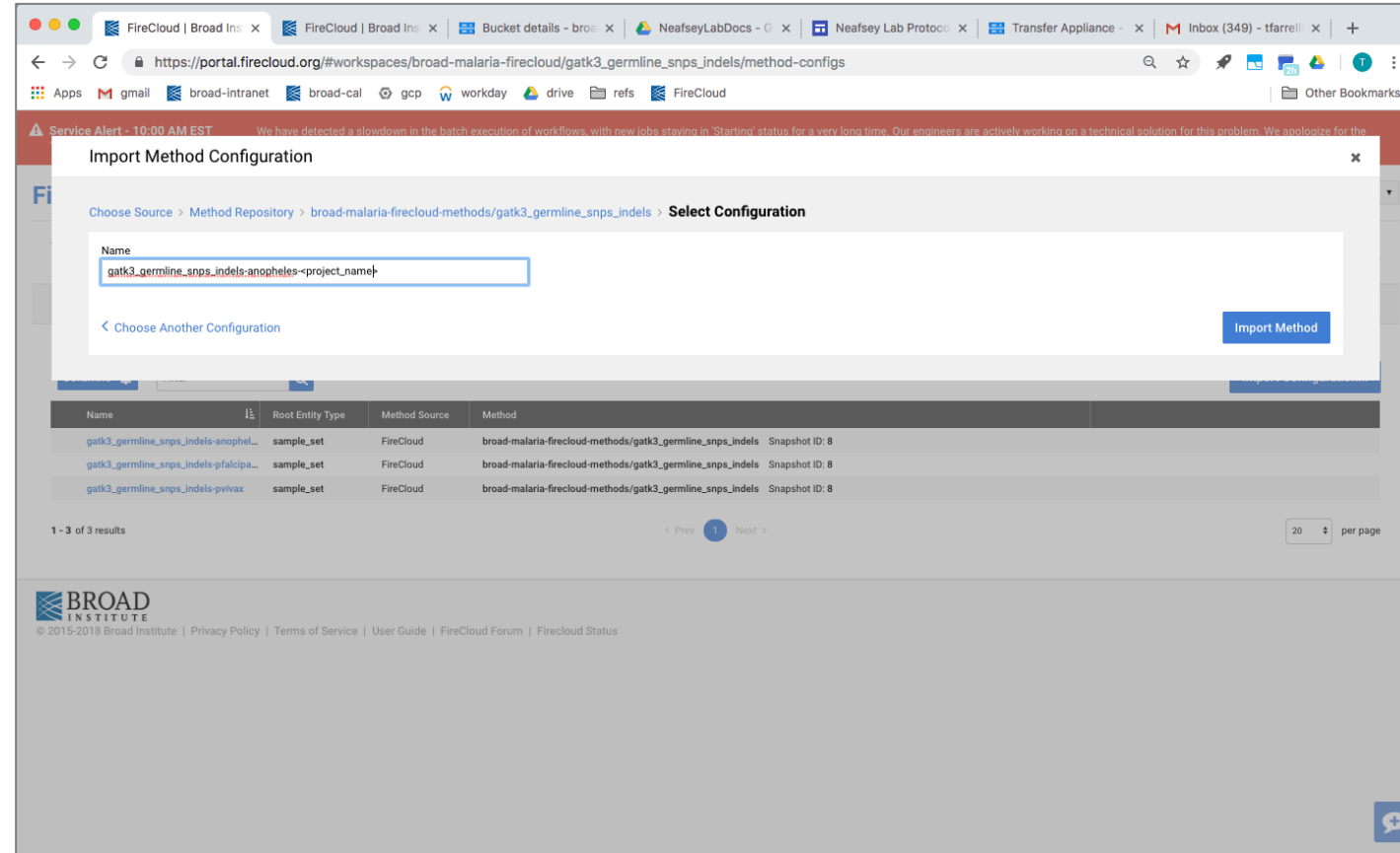
broad-malaria-firecloud : Starting a new project analysis

- You will see the list of template configs in the left panel. If you click on any of these, you will preview its values in the right panel
- Select the template config specific to your organism, and then click **Use Selected Configuration**



broad-malaria-firecloud : Starting a new project analysis

- You will then need to rename this config to make it specific to your project
 - It's recommended that you follow this convention:
gatk3_germline_snps_indels-*<organism>-<project>*
- Then click **Import Method**



broad-malaria-firecloud : Starting a new project analysis

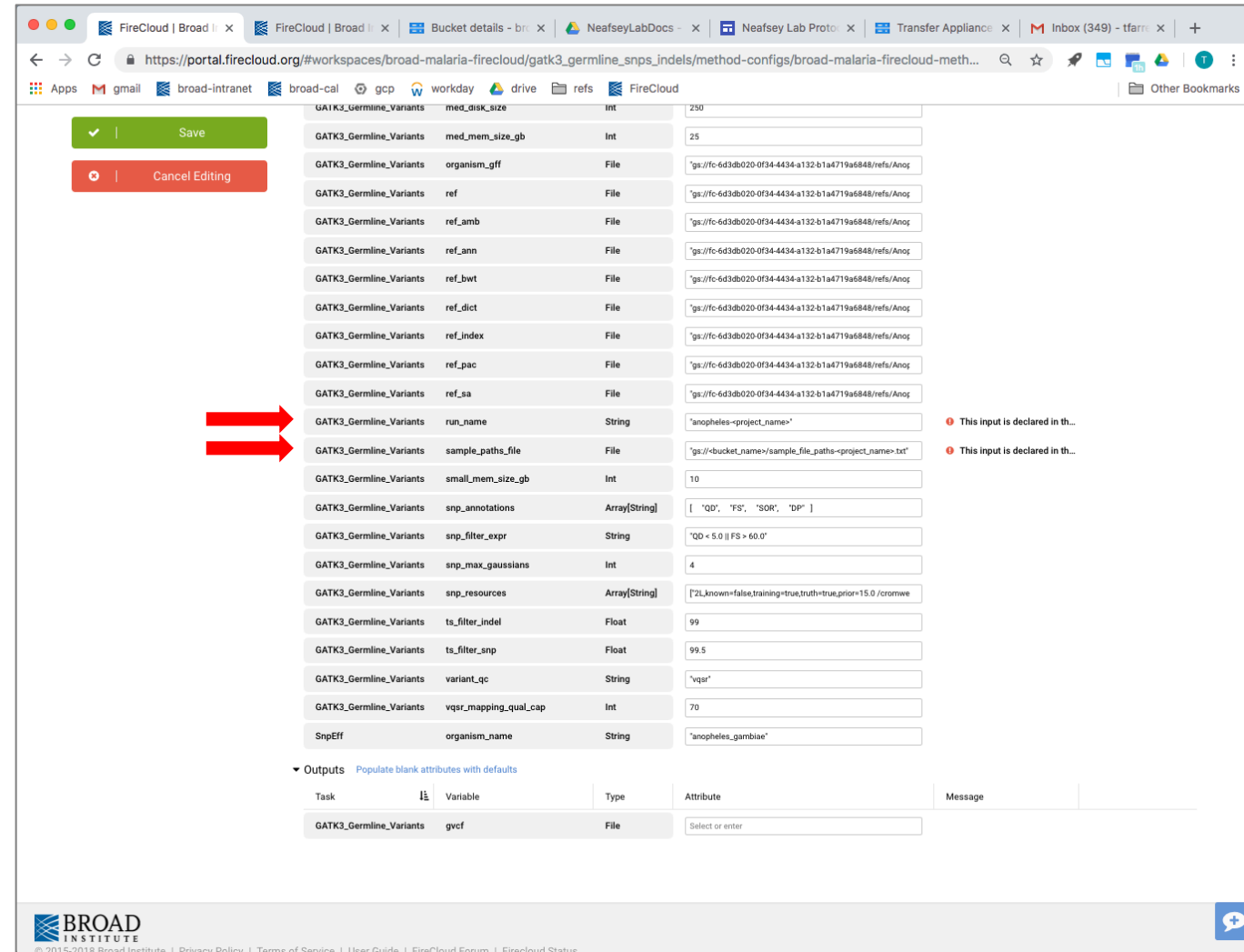
- This will create a new method config specific for your project, which will serve as a record of the config values for this run
- You can then change any of the config values as your analysis might require
- To do this, click **Edit Configuration**

The screenshot shows the FireCloud portal interface. The top navigation bar includes 'FireCloud', 'Workspaces', 'Data Library', and 'Method Repository'. The current workspace is 'broad-malaria-firecloud/gatk3_germline_snps_indels'. The 'Method Configurations' tab is active, showing a table with columns for Task, Variable, Type, Attribute, and Message. The 'Edit Configuration' button is circled in red.

Task	Variable	Type	Attribute	Message
GATK3_Germline_Variants	bqsr_intervals_to_exclude	Array[String]		
GATK3_Germline_Variants	disk_size	Int	100	
GATK3_Germline_Variants	do_align	Boolean	false	
GATK3_Germline_Variants	do_bqsr	Boolean	true	
GATK3_Germline_Variants	do_snpeff	Boolean	true	
GATK3_Germline_Variants	extra_large_disk_size	Int	750	

broad-malaria-firecloud : Starting a new project analysis

- If you don't wish to change the config values from the defaults (which follow GATK best practices), the only values that require input are **run_name** and **sample_paths_file**
- For **run_name**, this will served as the prefix for the final GVCF:
<run_name>.snpeff.g.vcf.gz
- For **sample_paths_file**, this is the Google Storage path to the tab-delimited file listing your samples and their corresponding raw data file



FireCloud | Broad | x | FireCloud | Broad | x | Bucket details - br | x | NeafseyLabDocs - x | Neafsey Lab Proto | x | Transfer Appliance | x | Inbox (349) - t | x | +

https://portal.firecloud.org/#workspaces/broad-malaria-firecloud/gatk3_germine_snps_indels/method-configs/broad-malaria-firecloud-meth...

Apps | gmail | broad-intranet | broad-cal | gcp | workday | drive | refs | FireCloud | Other Bookmarks

Save | Cancel Editing

GATK3_Germine_Variants	med_disk_size	Int	250
GATK3_Germine_Variants	med_mem_size_gb	Int	25
GATK3_Germine_Variants	organism_gff	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref_amb	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref_ann	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref_bwt	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref_dict	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref_index	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref_pac	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	ref_sa	File	'gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germine_Variants	run_name	String	'anopheles-project_name'
GATK3_Germine_Variants	sample_paths_file	File	'gs://<bucket_name>/sample_file_paths-<project_name>.txt'
GATK3_Germine_Variants	small_mem_size_gb	Int	10
GATK3_Germine_Variants	snp_annotations	Array[String]	['QD', 'FS', 'SOR', 'DP']
GATK3_Germine_Variants	snp_filter_expr	String	'QD < 5.0 FS > 60.0'
GATK3_Germine_Variants	snp_max_gaussians	Int	4
GATK3_Germine_Variants	snp_resources	Array[String]	'[?L_known=false,training=true,truth=true,prior=15.0 /cromwe
GATK3_Germine_Variants	ts_filter_indel	Float	99
GATK3_Germine_Variants	ts_filter_snp	Float	99.5
GATK3_Germine_Variants	variant_qc	String	'vqsr'
GATK3_Germine_Variants	vqsr_mapping_qual_cap	Int	70
SnpEff	organism_name	String	'anopheles_gambiae'

▼ Outputs [Populate blank attributes with defaults](#)

Task	Variable	Type	Attribute	Message
GATK3_Germine_Variants	gvcf	File	Select or enter	

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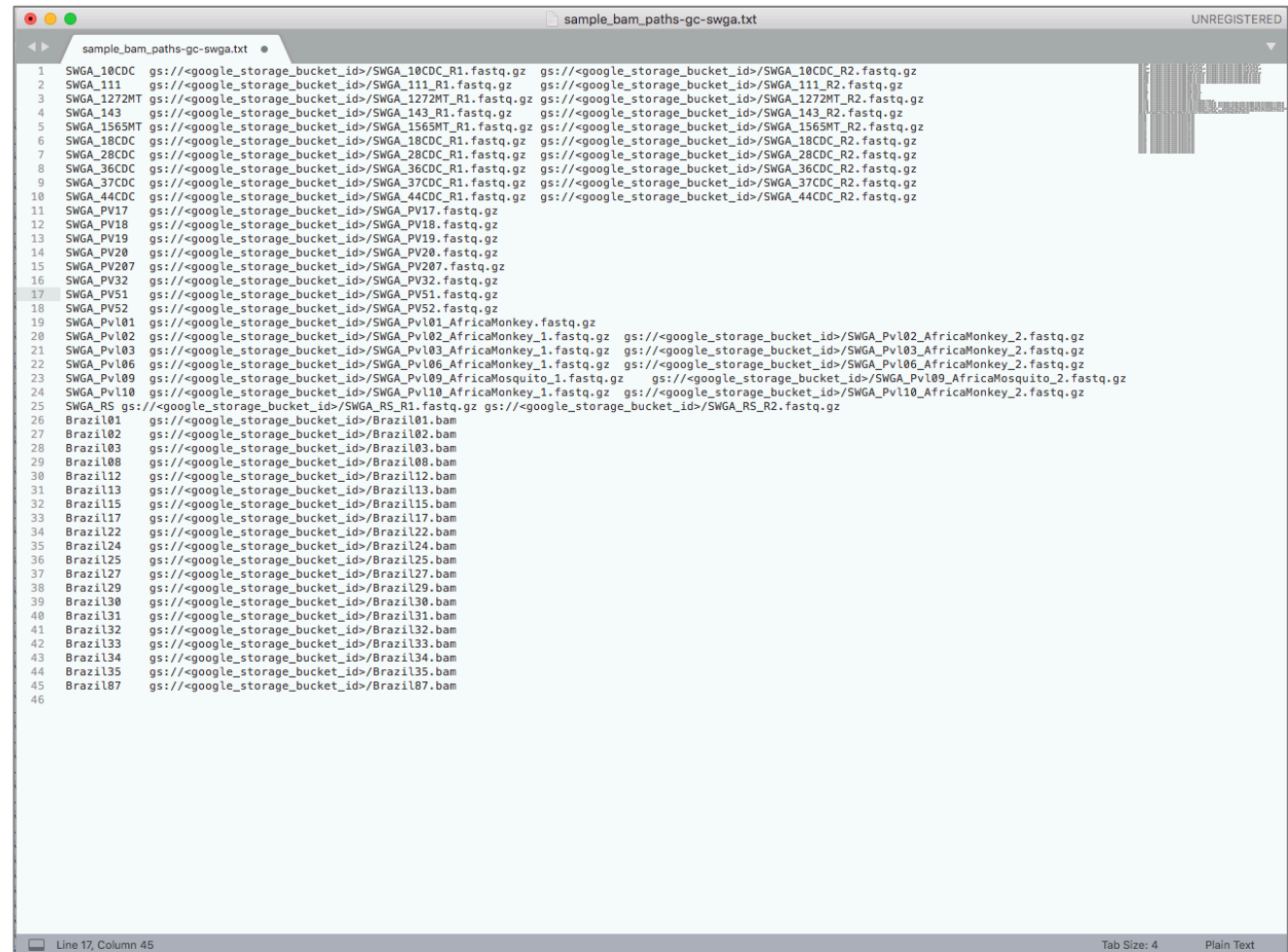
broad-malaria-firecloud : Starting a new project analysis

- Each line in your **sample_paths_file** will need to follow either of the following formats:

<sample_id> gs://<sample_id>.[bam|fastq.gz]

OR

<sample_id> gs://<sample_id>.R1.fastq.gz
 gs://<sample_id>.R2.fastq.gz



```
sample_bam_paths-gc-swga.txt
1 SWGA_10CDC gs://<google_storage_bucket_id>/SWGA_10CDC_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_10CDC_R2.fastq.gz
2 SWGA_111 gs://<google_storage_bucket_id>/SWGA_111_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_111_R2.fastq.gz
3 SWGA_1272MT gs://<google_storage_bucket_id>/SWGA_1272MT_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_1272MT_R2.fastq.gz
4 SWGA_143 gs://<google_storage_bucket_id>/SWGA_143_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_143_R2.fastq.gz
5 SWGA_1565MT gs://<google_storage_bucket_id>/SWGA_1565MT_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_1565MT_R2.fastq.gz
6 SWGA_18CDC gs://<google_storage_bucket_id>/SWGA_18CDC_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_18CDC_R2.fastq.gz
7 SWGA_28CDC gs://<google_storage_bucket_id>/SWGA_28CDC_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_28CDC_R2.fastq.gz
8 SWGA_36CDC gs://<google_storage_bucket_id>/SWGA_36CDC_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_36CDC_R2.fastq.gz
9 SWGA_37CDC gs://<google_storage_bucket_id>/SWGA_37CDC_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_37CDC_R2.fastq.gz
10 SWGA_44CDC gs://<google_storage_bucket_id>/SWGA_44CDC_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_44CDC_R2.fastq.gz
11 SWGA_PV17 gs://<google_storage_bucket_id>/SWGA_PV17.fastq.gz
12 SWGA_PV18 gs://<google_storage_bucket_id>/SWGA_PV18.fastq.gz
13 SWGA_PV19 gs://<google_storage_bucket_id>/SWGA_PV19.fastq.gz
14 SWGA_PV20 gs://<google_storage_bucket_id>/SWGA_PV20.fastq.gz
15 SWGA_PV207 gs://<google_storage_bucket_id>/SWGA_PV207.fastq.gz
16 SWGA_PV32 gs://<google_storage_bucket_id>/SWGA_PV32.fastq.gz
17 SWGA_PV51 gs://<google_storage_bucket_id>/SWGA_PV51.fastq.gz
18 SWGA_PV52 gs://<google_storage_bucket_id>/SWGA_PV52.fastq.gz
19 SWGA_Pv101 gs://<google_storage_bucket_id>/SWGA_Pv101_AfricaMonkey.fastq.gz
20 SWGA_Pv102 gs://<google_storage_bucket_id>/SWGA_Pv102_AfricaMonkey_1.fastq.gz gs://<google_storage_bucket_id>/SWGA_Pv102_AfricaMonkey_2.fastq.gz
21 SWGA_Pv103 gs://<google_storage_bucket_id>/SWGA_Pv103_AfricaMonkey_1.fastq.gz gs://<google_storage_bucket_id>/SWGA_Pv103_AfricaMonkey_2.fastq.gz
22 SWGA_Pv106 gs://<google_storage_bucket_id>/SWGA_Pv106_AfricaMonkey_1.fastq.gz gs://<google_storage_bucket_id>/SWGA_Pv106_AfricaMonkey_2.fastq.gz
23 SWGA_Pv109 gs://<google_storage_bucket_id>/SWGA_Pv109_AfricaMosquito_1.fastq.gz gs://<google_storage_bucket_id>/SWGA_Pv109_AfricaMosquito_2.fastq.gz
24 SWGA_Pv110 gs://<google_storage_bucket_id>/SWGA_Pv110_AfricaMonkey_1.fastq.gz gs://<google_storage_bucket_id>/SWGA_Pv110_AfricaMonkey_2.fastq.gz
25 SWGA_RS gs://<google_storage_bucket_id>/SWGA_RS_R1.fastq.gz gs://<google_storage_bucket_id>/SWGA_RS_R2.fastq.gz
26 Brazil101 gs://<google_storage_bucket_id>/Brazil101.bam
27 Brazil102 gs://<google_storage_bucket_id>/Brazil102.bam
28 Brazil103 gs://<google_storage_bucket_id>/Brazil103.bam
29 Brazil108 gs://<google_storage_bucket_id>/Brazil108.bam
30 Brazil112 gs://<google_storage_bucket_id>/Brazil112.bam
31 Brazil113 gs://<google_storage_bucket_id>/Brazil113.bam
32 Brazil115 gs://<google_storage_bucket_id>/Brazil115.bam
33 Brazil117 gs://<google_storage_bucket_id>/Brazil117.bam
34 Brazil122 gs://<google_storage_bucket_id>/Brazil122.bam
35 Brazil124 gs://<google_storage_bucket_id>/Brazil124.bam
36 Brazil125 gs://<google_storage_bucket_id>/Brazil125.bam
37 Brazil127 gs://<google_storage_bucket_id>/Brazil127.bam
38 Brazil129 gs://<google_storage_bucket_id>/Brazil129.bam
39 Brazil130 gs://<google_storage_bucket_id>/Brazil130.bam
40 Brazil131 gs://<google_storage_bucket_id>/Brazil131.bam
41 Brazil132 gs://<google_storage_bucket_id>/Brazil132.bam
42 Brazil133 gs://<google_storage_bucket_id>/Brazil133.bam
43 Brazil134 gs://<google_storage_bucket_id>/Brazil134.bam
44 Brazil135 gs://<google_storage_bucket_id>/Brazil135.bam
45 Brazil187 gs://<google_storage_bucket_id>/Brazil187.bam
46
```

broad-malaria-firecloud : Starting a new project analysis

- Once you've filled in your **run_name** and **sample_paths_file**, click the **Save** button
- After this step, you'll want to upload your data and then you can launch your analysis

The screenshot shows the FireCloud portal interface for configuring a GATK3_Germline_Variants analysis. The 'Save' button is highlighted with a red circle. The configuration table lists various parameters and their values.

Variable	Type	Value
GATK3_Germline_Variants large_disk_size	Int	500
GATK3_Germline_Variants large_mem_size_gb	Int	40
GATK3_Germline_Variants med_disk_size	Int	250
GATK3_Germline_Variants med_mem_size_gb	Int	25
GATK3_Germline_Variants organism_gff	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref_amb	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref_ann	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref_bwt	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref_dict	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref_index	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref_pac	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants ref_sa	File	"gs://fc-6d3db020-0f34-4434-a132-b1a4719a6848/refs/Ano...
GATK3_Germline_Variants run_name	String	"anopheles-project_name"
GATK3_Germline_Variants sample_paths_file	File	"gs://<bucket_name>/sample_file_paths-project_name.txt"
GATK3_Germline_Variants small_mem_size_gb	Int	10
GATK3_Germline_Variants snp_annotations	Array[String]	['QD', 'FS', 'SOR', 'DP']
GATK3_Germline_Variants snp_filter_expr	String	"QD < 5.0 FS > 60.0"
GATK3_Germline_Variants snp_max_gaussians	Int	4
GATK3_Germline_Variants snp_resources	Array[String]	"[2L_known=false,training=true,truth=true,prior=15.0 /cromwe
GATK3_Germline_Variants ts_filter_indel	Float	99
GATK3_Germline_Variants ts_filter_snp	Float	99.5
GATK3_Germline_Variants variant_qc	String	"vqsr"
GATK3_Germline_Variants vqsr_mapping_qual_cap	Int	70
SnEff organism_name	String	"anopheles_gambiae"

▼ Outputs [Populate blank attributes with defaults](#)

Task	Variable	Type	Attribute	Message
GATK3_Germline_Variants	gvcf	File	Select or enter	

broad-malaria-firecloud : Uploading data

FireCloud | Broad | x

FireCloud | Broad | x

Bucket details - br... x

NeafseyLabDocs - x

Neafsey Lab Proto... x

Transfer Appliance x

Inbox (349) - tfarr... x

+

https://portal.firecloud.org/#workspaces/broad-malaria-firecloud/gatk3_germline_snps_indels/method-configs/broad-malaria-firecloud-meth...

🔍 ⭐ 🚀 📄 📧 🔒 ⋮

Apps gmail broad-intranet broad-cal gcp workday drive refs FireCloud

Other Bookmarks

FireCloud

WorkspacesData LibraryMethod Repository

tfarrell@broadinstitute.org

WORKSPACE

broad-malaria-firecloud/gatk3_germline_snps_indels

🔔

SummaryDataAnalysisNotebooksBETAMethod ConfigurationsMonitor

✎

Edit Configuration

🗑

Delete

↩

Publish...

Method Configuration Name

gatk3_germline_snps_indels-anopheles-vqsr_test

Launch Analysis...

Referenced Method

Namespace: broad-malaria-firecloud-methods

Name: gatk3_germline_snps_indels

Snapshot ID: 8

Entity Type: Workflow

Source: FireCloud

Created: October 1, 2018, 3:21 PM

Owners: tfarrell@broadinstitute.org

Synopsis:

Snapshot Comment:

Documentation:

gatk3_germline_snps_indels.wdl: - standardized pipeline for calling germline SNPs and INDELs. - imports haplotypecaller subworkflow to scatter variant-calling over genomic intervals, while scattering over samples. - developed by Malaria Group, IDMP, Broad Institute.

WDL: [Expand](#)

☒ Configure inputs/outputs using the Workspace Data Model ⓘ

Entity type for input/output referencing: sample_set

FireCloud Tip

You can either change the inputs/outputs below or upload a pre-populated json file. After upload you can always edit manually.

Connections

▼ Inputs

Populate with a json file... ⓘ

Download json file

Task	Variable	Type	Attribute	Message
GATK3_Germline_Variants	bqsr_intervals_to_exclude	Array[String]	[]	
GATK3_Germline_Variants	disk_size	Int	100	
GATK3_Germline_Variants	do_align	Boolean	false	
GATK3_Germline_Variants	do_bqsr	Boolean	true	
GATK3_Germline_Variants	do_snpeff	Boolean	true	
GATK3_Germline_Variants	extra_large_disk_size	Int	750	

broad-malaria-firecloud : Launching an analysis

- Once your configuration is complete
- This will save this configuration for future. And now that it's complete, you can launch the analysis

The screenshot shows the FireCloud portal interface. The browser tabs include 'FireCloud | Broad', 'Bucket details - br...', 'NeafseyLabDocs', 'Neafsey Lab Proto...', 'Transfer Appliance', 'Inbox (349) - tfarr...', and '+'. The address bar shows the URL: https://portal.firecloud.org/#workspaces/broad-malaria-firecloud/gatk3_germline_snps_indels/method-configs/broad-malaria-firecloud-meth.... The page header includes 'FireCloud', 'Workspaces', 'Data Library', and 'Method Repository'. The user profile 'tfarrell@broadinstitute.org' is visible in the top right.

The main content area is titled 'WORKSPACE broad-malaria-firecloud/gatk3_germline_snps_indels'. It features a navigation bar with tabs: 'Summary', 'Data', 'Analysis', 'Notebooks BETA', 'Method Configurations', and 'Monitor'. The 'Method Configurations' tab is active.

On the left side, there are three buttons: 'Edit Configuration' (with a pencil icon), 'Delete' (with a trash icon), and 'Publish...' (with a share icon).

The 'Method Configuration Name' is 'gatk3_germline_snps_indels-anopheles-vqsr_test'. A red circle highlights the 'Launch Analysis...' button in the top right corner.

The 'Referenced Method' section provides details about the method configuration:

- Namespace: broad-malaria-firecloud-methods
- Name: gatk3_germline_snps_indels
- Snapshot ID: 8
- Entity Type: Workflow
- Source: FireCloud
- Created: October 1, 2018, 3:21 PM
- Owners: tfarrell@broadinstitute.org
- Synopsis:
- Snapshot Comment:
- Documentation: gatk3_germline_snps_indels.wdl: - standardized pipeline for calling germline SNPs and INDELs. - imports haplotypecaller subworkflow to scatter variant-calling over genomic intervals, while scattering over samples. - developed by Malaria Group, IDMP, Broad Institute.
- WDL: [Expand](#)

Below the method details, there is a checkbox labeled 'Configure inputs/outputs using the Workspace Data Model' which is checked. A 'FireCloud Tip' message states: 'You can either change the inputs/outputs below or upload a pre-populated json file. After upload you can always edit manually.'

The 'Connections' section shows a table of inputs:

Task	Variable	Type	Attribute	Message
GATK3_Germline_Variants	bqsr_intervals_to_exclude	Array[String]	[]	
GATK3_Germline_Variants	disk_size	Int	100	
GATK3_Germline_Variants	do_align	Boolean	false	
GATK3_Germline_Variants	do_bqsr	Boolean	true	
GATK3_Germline_Variants	do_snpeff	Boolean	true	
GATK3_Germline_Variants	extra_large_disk_size	Int	750	