

Tencent HealthCare Omics Platform

Practical Tutorial

Product Documentation



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Visual Running Groups Submission and Management

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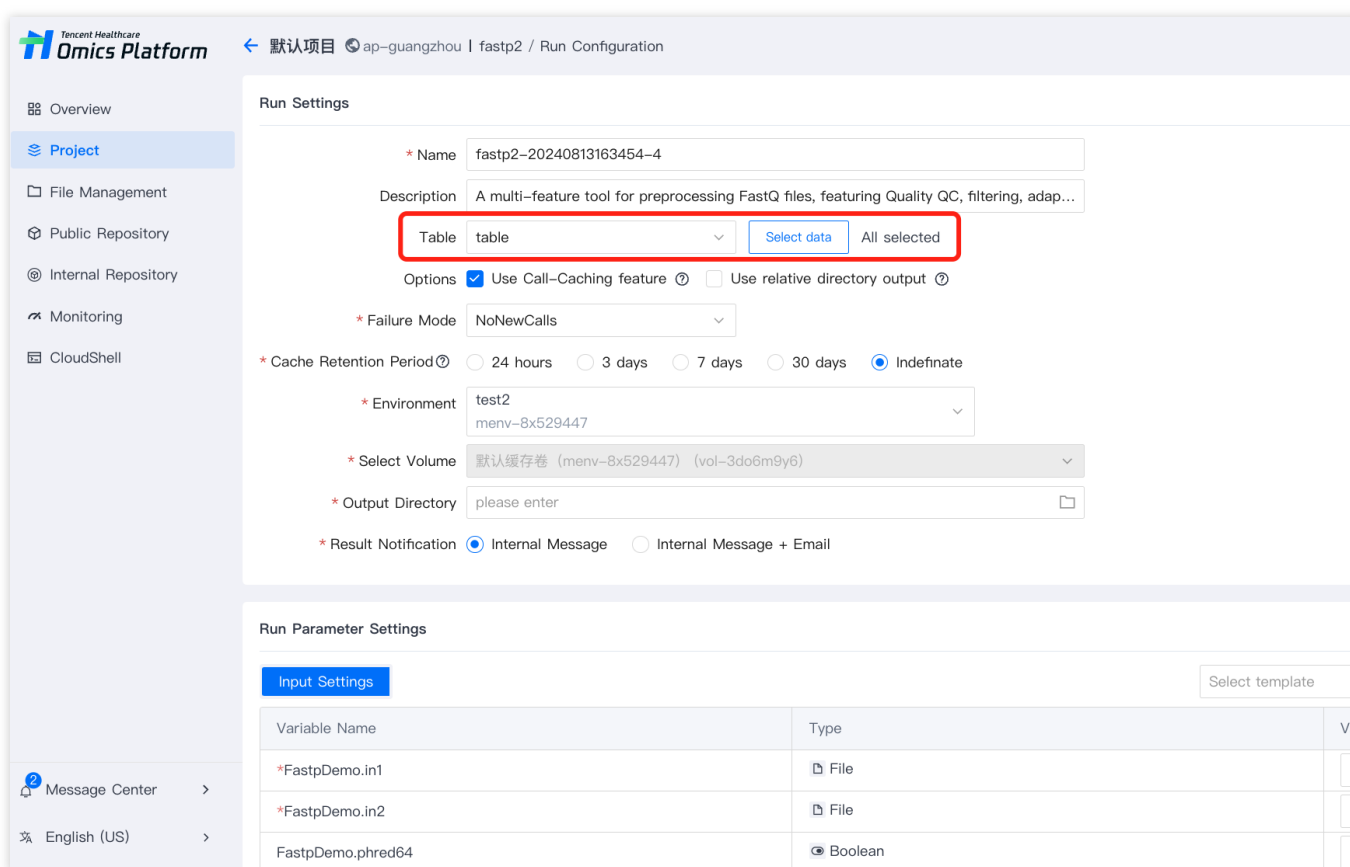
Batch running of tasks by uploading tables is supported.

Step 1: Add a New Table

For details on creating a table, see documentation: [Adding a Table](#).

Step 2: Select Table and Data

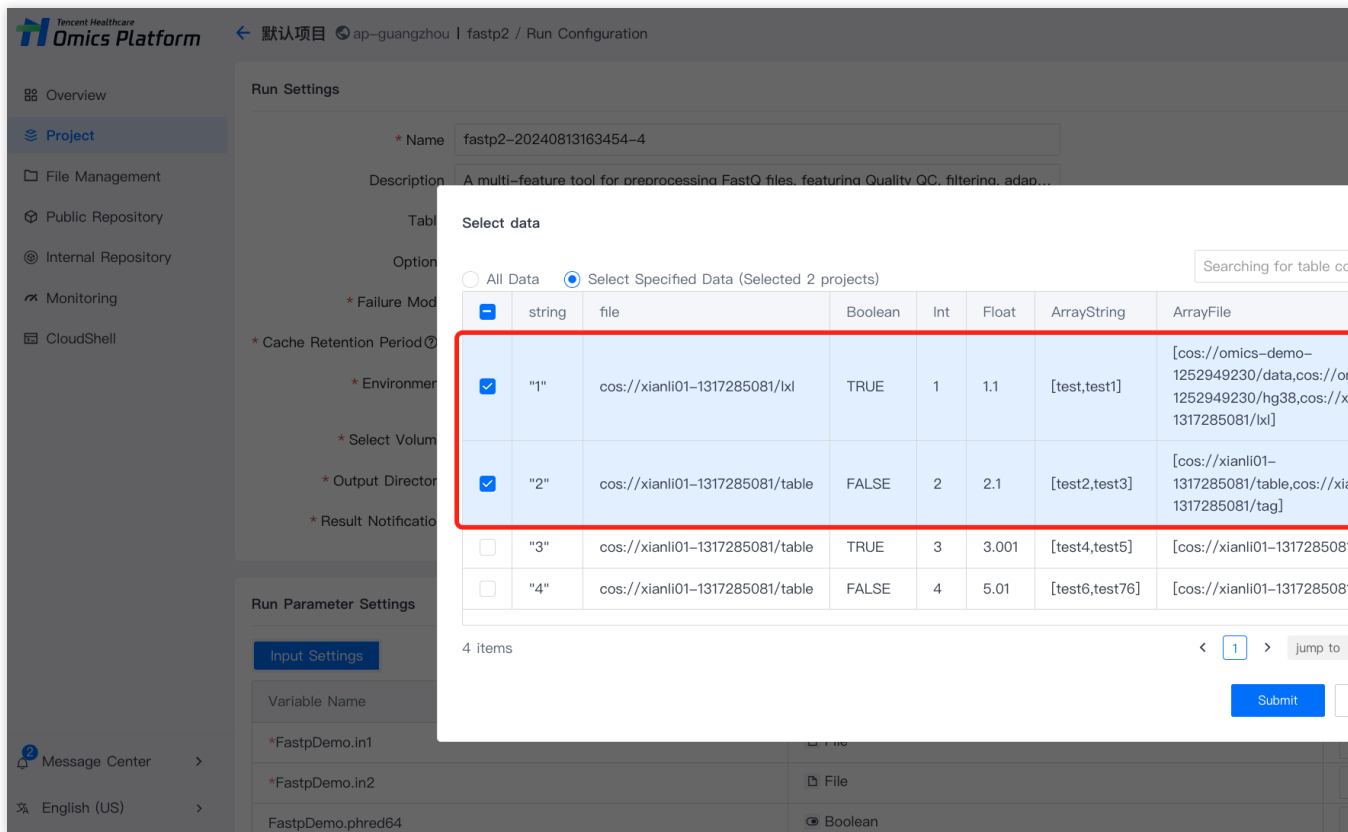
1. Select the table, all rows will be selected by default, and each row will be used to generate a run in the run group



The screenshot shows the 'Run Configuration' page in the Tencent HealthCare Omics Platform. The 'Run Settings' section includes fields for Name, Description, Table (highlighted with a red box), Options, Failure Mode, Cache Retention Period, Environment, Select Volume, Output Directory, and Result Notification. The 'Table' dropdown is set to 'table', and the 'Select data' button is highlighted. The 'All selected' option is chosen. Below, the 'Run Parameter Settings' section shows a table with columns for Variable Name, Type, and Va.

Variable Name	Type	Va
*FastpDemo.in1	File	P
*FastpDemo.in2	File	P
FastpDemo.phred64	Boolean	P

2. You can also click **Select Data** and further select the rows that need to be submitted. The input parameters that do not need to be specified by table can be filled later.



Step 3: Set the Running Parameters

1. Select appropriate running parameters. In the running parameter settings, the value corresponding to the variable name needs to match the name of the uploaded table header.

Default Project ap-guangzhou | gatk-WGS-germline-snps-indels1 / Run Configuration

Description This application uses BWA + GATK to perform Germline short variant discovery on hu...

Table table2 [Select data](#) All selected

Options Use Call-Caching feature Use relative directory output

* Failure Mode NoNewCalls

* Cache Retention Period 24 hours 3 days 7 days 30 days Indefinite

* Environment test2
menv-8x529447

* Select Volume 默认缓存卷 (menv-8x529447) (vol-3do6m9y6)

* Output Directory please enter

* Result Notification Internal Message Internal Message + Email

Run Parameter Settings

[Input Settings](#) [Select template](#)

Variable Name	Type
*PairedEndSingleSampleWorkflow.wgs_coverage_interval_list	File
*PairedEndSingleSampleWorkflow.sample_name	String
*PairedEndSingleSampleWorkflow.base_file_name	String
*PairedEndSingleSampleWorkflow.final_gvcf_base_name	String
*PairedEndSingleSampleWorkflow.flowcell_unmapped_bams	Array[File]

2. You can select a input template or manually fill in the running parameters.

Default Project | ap-guangzhou | gatk-WGS-germline-snps-indels1 / Run Configuration

* Environment: test2
 * Select Volume: 默认缓存卷 (menv-8x529447) (vol-3do6m9y6)
 * Output Directory: please enter
 * Result Notification: Internal Message Internal Message + Email

Run Parameter Settings

Input Settings

Variable Name	Type
*PairedEndSingleSampleWorkflow.wgs_coverage_interval_list	File
*PairedEndSingleSampleWorkflow.sample_name	String
*PairedEndSingleSampleWorkflow.base_file_name	String
*PairedEndSingleSampleWorkflow.final_gvcf_base_name	String
*PairedEndSingleSampleWorkflow.flowcell_unmapped_bams	Array[File]
*PairedEndSingleSampleWorkflow.unmapped_bam_suffix	String
*PairedEndSingleSampleWorkflow.wgs_calling_interval_list	File
*PairedEndSingleSampleWorkflow.haplotype_scatter_count	Int
*PairedEndSingleSampleWorkflow.break_bands_at_multiples_of	Int
*PairedEndSingleSampleWorkflow.ref_fasta	File

Select template dropdown: Published Templates, **downsampled NA12**, All Templates, downsampled NA12, + Save current page

Step 4: Run

Click **Start** in the upper right corner to start the analysis task.

Default Project ap-guangzhou | gatk-WGS-germline-snps-indels1 / Run Configuration

- Overview
- Project
- File Management
- Public Repository
- Internal Repository
- Monitoring
- CloudShell

Message Center >

English (US) >

Run Settings

*** Name**

Description

Table Select data

Options Use Call-Caching feature ? Use relative directory output ?

*** Failure Mode**

*** Cache Retention Period** 24 hours 3 days 7 days 30 days Indefinite

*** Environment**
menv-8x529447

*** Select Volume**

*** Output Directory** 📁

*** Result Notification** Internal Message Internal Message + Email

Run Parameter Settings

Input Settings
downsampled

Variable Name	Type
*PairedEndSingleSampleWorkflow.contamination_sites_ud	📁 File
*PairedEndSingleSampleWorkflow.contamination_sites_bed	📁 File
*PairedEndSingleSampleWorkflow.contamination_sites_mu	📁 File

Rerunning and Continuing Running

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1. Select the **Details** option for a running group to enter its details page.

The screenshot displays the Tencent HealthCare Omics Platform interface. On the left is a navigation sidebar with options: Overview, Project (selected), File Management, Public Repository, Internal Repository, Monitoring, and CloudShell. At the top, it shows 'Default Project' and 'Manager' for 'Guangzhou | prj-royal-aqua-flounder-582963'. The main area is divided into sections: 'Table Information' with a search bar and two table entries ('table2' and 'table'), 'Application' with three application cards ('gatk-WGS-germline-snps-indels1', 'fastp2', and 'sarek1'), and a 'Run Group' table. The 'Run Group' table has columns for 'Run Group Name', 'Application', and 'Status'. It lists seven run groups with their respective statuses: 'Completed' (green checkmark) and 'Failed' (orange exclamation mark).

Run Group Name	Application	Status
sarek1-20240709112555	sarek1 (Branch...	Completed
sarek1-20240709112421	sarek1 (Branch...	Completed
sarek1-20240709112238	sarek1 (Branch...	Completed
sarek-20240604154540	sarek (Branch...	Failed
maseq-20240415151700	maseq (Branch...	Completed
maseq-20240402190738	maseq (Branch...	Completed
maseq-20240402185000	maseq (Branch...	Failed

2. In the running list column of the running group details page, you can rerun the run groups.

Default Project Guangzhou | "sarek1-20240709112555"Run Details

Analyzing
Initializing
Computing
Completed
Failed
Terminated

<p>Name sarek1-20240709112555</p> <p>ID run-messy-navy-wildboar-527999 🔗</p> <p>Application type Private Application</p> <p>AccessMode</p> <p>Description</p> <p>Environment</p> <p>Environment ID menv-nfwniy7g 🔗</p> <p>Profile test</p> <p>Config View</p> <p>manifest View</p> <p>Nextflow Version 23.10.1</p> <p>Application File Path 🔗</p>	<p>Volume</p> <p>Volume ID vol-uab9fezx 🔗</p> <p>Mount path /vol-uab9fezx</p> <p>workdir 🔗 /vol-uab9fezx/en</p> <p>Startup path 🔗 /vol-uab9fezx/en</p> <p>Cache Duration</p>
--	---

List of Jobs of run-messy-navy-wildboar-... | ● Completed

Job name	Status	Start Time	Duratio
<p>No jobs available</p>			

🔔 Message Center >

🌐 English (US) >

3. After selecting the batch re-run option, you can choose the sub-tasks that need to be re-run. Only completed, failed, or terminated sub-tasks can be re-run.

The screenshot displays the Tencent HealthCare Omics Platform interface. The top navigation bar shows the project name 'Default Project' and location 'Guangzhou'. The left sidebar contains navigation options like 'Overview', 'Project', 'File Management', etc. The main content area is titled 'Failed' and shows a progress bar with stages: Analyzing (0), Initializing (0), Preprocessing (0), Computing (0), Archiving (0), Completed (0), Failed (0), and Terminated (1). Below this, a table lists job details such as Name, ID, Application type, and Directory. A 'Run list' section features a 'Batch Rerun' button (highlighted with a red box) and a table with columns for Run, Status, and Operation. The right side shows a 'List of Jobs of run-impossi...' with a table of job names, statuses (Completed or Terminated), and start times.

4. After the rerunning, new batch information will be generated, and the original records will not be overwritten.