

# TGex API

## Overview

TGex is an NGS Analysis, Interpretation and Reporting platform that offers a complete VCF to Reporting solution for clinics, hospitals, diagnostic companies and healthcare providers. Based on the GeneCards Suite Knowledgebase, TGex offers integrated variant prioritization, enhanced and rapid variant review and analysis, and automated reporting capabilities that allow for easy scaling of NGS operations while providing complete flexibility in customization and implementation.

This document provides information about how to upload VCF samples into TGex by way of web API.



## Create Sample

This API call allows a user/integrator to upload a VCF file and create a corresponding Sample entry in TGex. Other than the VCF file, additional metadata may be included in the Sample. Optionally, the Sample entry may be associated with an existing Subject entry (by ID).

Request URL:  [<domain> /api/createSample](https://tgex-app.genecards.org/api/createSample)

US domain: <https://tgex-app.genecards.org>

China domain: <https://tgex-app.genecards.cn>

### Post Parameters

Category	Parameter	Description	Required
Auth	ApiUserId	The API user Id	Yes
	ApiUserKey	The API user key	Yes
	CustomerAccountKey	TGex Customer account key (for integrator this should be a parameter requested from the user). If the customer account key is missing the sample will be created at the current user's account.	No
Sample	SampleSerialNumber	Sample ID, may be the same as the ID of the sample in the LIMS	Yes
	SampleSequenceDate	Date when sample was sequenced	No
	SampleTakenDate	Date when sample was taken	No
	SampleReceivedDate	Date when sample was received	No
	SampleSequenceMachineld	ID of Sequencing Machine entry as defined in customer account	No
	SampleEnrichmentKitId	ID of Enrichment Kit entry as defined in customer account. If empty the default account enrichment kit will be used.	No
	SampleType	May be one of the following: <ul style="list-style-type: none"> <li>RnaSeq</li> <li>DnaSeq</li> </ul>	No
	SampleTarget	May be one of the following: <ul style="list-style-type: none"> <li>WholeGenome</li> <li>Exome</li> <li>GenePanel</li> <li>TargetRegion</li> </ul>	No
	SampleSource	May be one of the following: <ul style="list-style-type: none"> <li>GermLine</li> <li>Tumor</li> <li>Blood</li> <li>Buccal</li> <li>Fetal</li> <li>Saliva</li> </ul>	No



		<ul style="list-style-type: none"> <li>Other</li> </ul>	
	SampleGenomeBuild	<ul style="list-style-type: none"> <li>HG19_GCRH37 - default</li> <li>GCRH38</li> </ul>	No
	SampleRelation	The sample relation, can be <ul style="list-style-type: none"> <li>Self</li> <li>Mother</li> <li>Father</li> <li>Sibling</li> <li>Twin</li> <li>MotherRelative</li> <li>FatherRelative</li> <li>Other</li> </ul>	No
	SampleNotes	Free text up to 1024 characters	No
	SampleQcData	JSON structure for QC data	NO
	SnvFile	The name of the SNV file (that is attached below)	No
	StructFile	The name of the structural variation file (that is attached below)	No
	FastQUrl	The URL to the fastQ file	No
	BamUrl	The URL to the BAM file	No
	SnvFile	The name of the uploaded SNV file	No
	StructFile	The name of the structural variation file	No
Subject	SubjectId	Unique identified for Subject. May be any string. If an existing subject exists, the sample will be associated with it.	Yes
	SubjectName	Name of subject	No
	SubjectGender	May be "M" or "F"	No
	SubjectDateOfBirth	Date of birth of subject	No
	SubjectConsanguinity	The subject consanguinity	No
	SubjectPopulationType	Population type	No
	SubjectPaternalAncestry	Paternal ancestry	No
	SubjectMaternalAncestry	Maternal ancestry	No
	SubjectFamilyHistory	The family history	No
Assignment	AssignedToUserId	The user id the sample is assigned to	No
	AssignedToFullName	The full name of the user the sample is assigned to	No
	GroupAssignment	List of groups the sample is assigned to, each list item has: <ul style="list-style-type: none"> <li>Code</li> <li>Name</li> </ul>	No
File	Files	Parameter of type File, must be .vcf or .vcf.gz	No



## Notes

- It is possible to upload more than one file as part of one API call. The example for that would be to when uploading SNV file and a Structural variation file for the same sample.
- When uploading a Structural variation file or both SNV / Structural it is required to specify which file is which at the SnvFile/StructFile fields. The value should be the file name only – without folder information.

## Response

A JSON object with the following fields

Code	success or error
Data	An optional returned data
Info	Textual message (or error message) related to the returned value

## Request Example:

Post Parameters:

```
"ApiUserId"      : "<Your API User Id>",
"ApiUserKey"     : "<Your API User Key >",
"CustomerAccountKey" : "<The customer account key>"
"SampleSerialNumber" : "SAM-00123",
"SampleSequenceDate" : '2016-05-01 08:00',
"SampleTakenDate"   : '2016-01-01 08:00',
"SampleType"       : "RndSeq",
"SampleTarget"     : "Exome",
"SampleSource"     : "Germline",
"SubjectId"       : "Subject1",
"SnvFile"         : "test.vcf"
```

File Parameter: c:\vcf\test.vcf

## Successful Response Example:

```
{ "Code": "success" }
```

## Failure Response Example:

```
{ "Code": "error", "Info": "SampleID SAM-00123 already exists" }
```



## Create Case

The create case API is used for creating a new case in TGex.

**URL:** <tgexServer>/api/CreateCase

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes
	CustomerAccountKey	TGex Customer account key (for integrator this should be a parameter requested from the user). If the customer account key is missing the sample will be created at the current user's account.	No
Case	SerialNumber	The case serial number. In case the SN is not provided it shall be automatically generated by the server	No
	Name	The case Name. In case empty it shall be assigned as the protocol name	No
	Description	The clinical description	Yes
	PhenAlleleFreq	Phenotype allele frequency. In case empty the value is taken from the protocol	No
	Phenotypes	The phenotypes to use	No
	Owner	The case doctor owner	No
	OwnerDepartment	The case doctor department	No
	GeneList	A gene list to associate with the case	No
	ProtocolId	The protocol ID to create the case from	Yes
Subject	SubjectId	An <b>existing</b> subject ID	Yes
Sample	ProbandSampleId	An <b>existing</b> main sample ID for the case	Yes
	AssociatedSamples	Array of the associated samples for the case. An example is the mother and father samples in a trio analysis. Each element in the array shall have the following fields <ul style="list-style-type: none"> <li>Relation – the sample relation</li> <li>SampleId - the sample id</li> <li>Affected – affect indication</li> </ul>	No  Yes Yes No
Assignment	AssignedToUserId	The user id that case is assigned to	No
Assignment	AssignedToFullName	The full name of the user the case is assigned to	No



#### Sample Relation valid values

- Self
- Mother
- Father
- Sibling
- Twin
- MotherRelative
- FatherRelative
- Other

#### Sample Affect valid values

- Unknown
- Affected
- Unaffected

#### Request Example:

JSON Parameters:

```
{
  "ApiUserId"      : "<Your API User Id>",
  "ApiUserKey"     : "<Your API User Key >",
  "CustomerAccountKey" : "<The customer account key>"
  "ProtocolId"     : "RG_TRIO",
  "Description"     : "Clinical Description 1",
  "PatientId"      : 'Patient1',
  "MainSampleId"   : 'Sample1',
  "AssociatedSamples" : [
    { "SampleId": "MotherSample1", "Relation": "Mother", "Affected": "Unaffected" },
    { "SampleId": "FatherSample1", "Relation": "Father", "Affected": "Unaffected" }
  ]
}
```

#### Successful Response Example:

```
{ "Code": "success", Data: { the case object } }
```

#### Failure Response Example:

```
{ "Code": "error", "Info": "MainSampleID SAM-00123 was not found" }
```



## Case Assignment

The case assignment API is used for updating the user assignment for a case

**URL:** <tgexServer>/api/CaseAssignment

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes
Case Assignment	SerialNumber	The case Serial number	Yes
	AssignedToUserId	The user id that case is assigned to	No
	AssignedToFullName	The full name of the user the case is assigned to	No

### Notes:

In case the user assignment is null, the user assignment shall be removed.

### Request Example:

JSON Parameters:

```
{
  "ApiUserId "      : "<Your API User Id>",
  "ApiUserKey"      : "<Your API User Key >",
  "SerialNumber"     : "CaseID",
  "AssignedToUserId" : "<The user id GUID>",
  "AssignedToFullName" : "John Dow",
}
```

### Successful Response Example:

```
{ "Code": "success", Data: { the case assignment object} }
```

### Failure Response Example:

```
{ "Code": "error", "Info": "Case not found" }
```



## Sample Permission

The sample assignment API is used for updating the user/group assignment for a sample

**URL:** <tgexServer>/api/SampleAssignment

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes
Sample Assignment	SerialNumber	The sample Serial number	Yes
	AssignedToUserId	The user id that case is assigned to	No
	AssignedToFullName	The full name of the user the case is assigned to	No
	GroupAssignment	List of groups the sample is assigned to, each list item has: <ul style="list-style-type: none"> <li>• Code</li> <li>• Name</li> </ul>	No

### Notes:

In case the user assignment is null, the user assignment shall be removed.

In case the group assignment is null or empty, the group assignment shall be removed

### Request Example:

JSON Parameters:

```
{
  "ApiUserId "      : "<Your API User Id>",
  "ApiUserKey"      : "<Your API User Key >",
  "SerialNumber"    : "SampleID",
  "AssignedToUserId" : "<The user id GUID>",
  "AssignedToFullName" : "John Dow",
}
```

### Successful Response Example:

```
{ "Code": "success", Data: { the sample assignment object } }
```

### Failure Response Example:

```
{ "Code": "error", "Info": "Sample not found" }
```





## Report List

The report list api is used to get new reports created on the account from a given date

**URL:** <tgexServer>/api/ReportList?startTime=xxx

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes
URL	StartTime	The start time of reports retrieval	Yes

## Report Url

The report URL api is used to download a report by the report filename returned by the report list API

**URL:** <tgexServer>/api/ReportUrl?fileName=xxx

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes
URL	FileName	The report file name to download	Yes

## Sequence machines

The sequence machine API is used to retrieve the list of sequence machines in the account

**URL:** <tgexServer>/api/SequenceMachines

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes



## Enrichment kits

The sequence machine API is used to retrieve the list of enrichment kits in the account

**URL:** <tgexServer>/api/enrichmentKits

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes

## Protocols

The sequence machine API is used to retrieve the list of protocols in the account

**URL:** <tgexServer>/api/protocols

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes

## Samples

The sequence machine API is used to retrieve the list of samples in the account

**URL:** <tgexServer>/api/samples

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes



## Patients

The sequence machine API is used to retrieve the list of patients in the account

**URL:** <tgexServer>/api/patients

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes

## Cases

The sequence machine API is used to retrieve the list of cases in the account

**URL:** <tgexServer>/api/cases

**Action:** POST

**Payload:** JSON structure

Category	Parameter	Description	Required
Auth	APIUserId	The API user Id	Yes
	APIUserKey	The API user key	Yes

