

Notices

Limitations of use

For research use only. Not for use in diagnostic procedures. Unless otherwise agreed to in writing, IDT does not intend these products to be used in clinical applications and does not warrant their fitness or suitability for any clinical diagnostic use. Purchaser is solely responsible for all decisions regarding the use of these products and any associated regulatory or legal obligations.

Safety data sheets pertaining to this product are available upon request.

Safety notices



Reminder symbols call attention to minor details that may be easily overlooked and compromise the procedure resulting in decreased assay performance.



Caution symbols denote critical steps in the procedure where risk of protocol failure or damage to the product itself could occur if not carefully observed.



Stop symbols indicate where this procedure may be safely suspended and resumed at a later time without risk of compromised assay performance. Make note of these steps and plan your workflow accordingly.

Revision history

Version	Release date	Description of changes
RA-DOC-663 REV01	September 2026	Revised branding of this document and updated screenshots throughout. Included list of supported genomes. Added new document control number.
2	June 2023	Updated contact information, account information image, and target report text (RUO23-1915_001)
1	April 2021	Initial Release

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Technical support

Visit <https://www.idtdna.com/pages/support> for a helpful answers to frequently asked questions or contact us directly at applicationsupport@idtdna.com.

Introduction

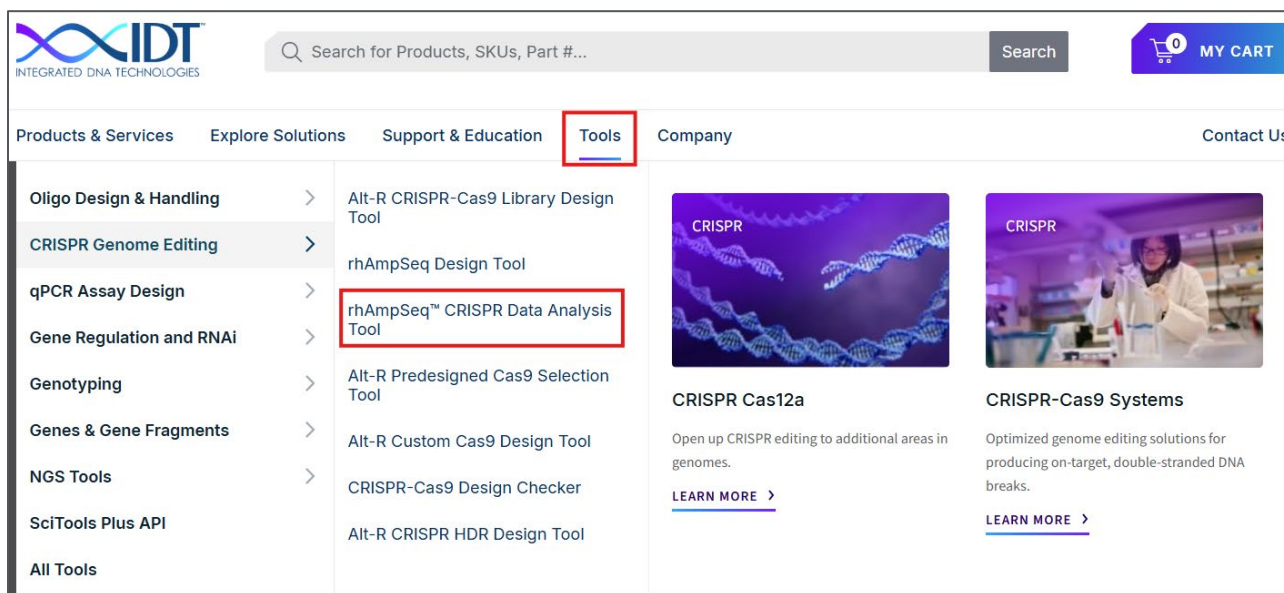
This analysis guide describes how to use the rhAmpSeq CRISPR Analysis Tool, which was designed for flexible, cloud-based interrogation of CRISPR-mediated genome editing results. This information can also be accessed in video format by viewing the [rhAmpSeq CRISPR Analysis Tool tutorial](#).

The rhAmpSeq CRISPR Analysis Tool supports the following reference genomes.

Genome Name
Bos taurus - Cow (ARS UCD1.2)
Bos taurus - Cow (ARS UMD3.1)
Caenorhabditis elegans - round worm (WBcel235)
Canis lupus familiaris – Dog (CanFam 3.1)
Danio rerio - zebrafish (GRCZ11)
Gallus gallus - Chicken (GRCg6a)
Gossypium hirsutum - Cotton (ASM98774v1)
Homo sapiens-Human (GRCh37)
Homo sapiens-human (GRCh38)
Macaca fascicularis - crab-eating macaque (macFas5)
Macaca fascicularis - crab-eating macaque (MFA1912RKSv2)
Macaca mulatta - rhesus monkey (rheMac8)
Mus musculus - Mouse (mm39)
Mus musculus-mouse (GRCm38)
Oryza sativa - Rice (IRGSP1.0)
Rattus norvegicus - rat (Rnor6)
Sus scrofa - Pig (11.1)
Vitis riparia – Grape (EGFV_Vit_rip_1.0)

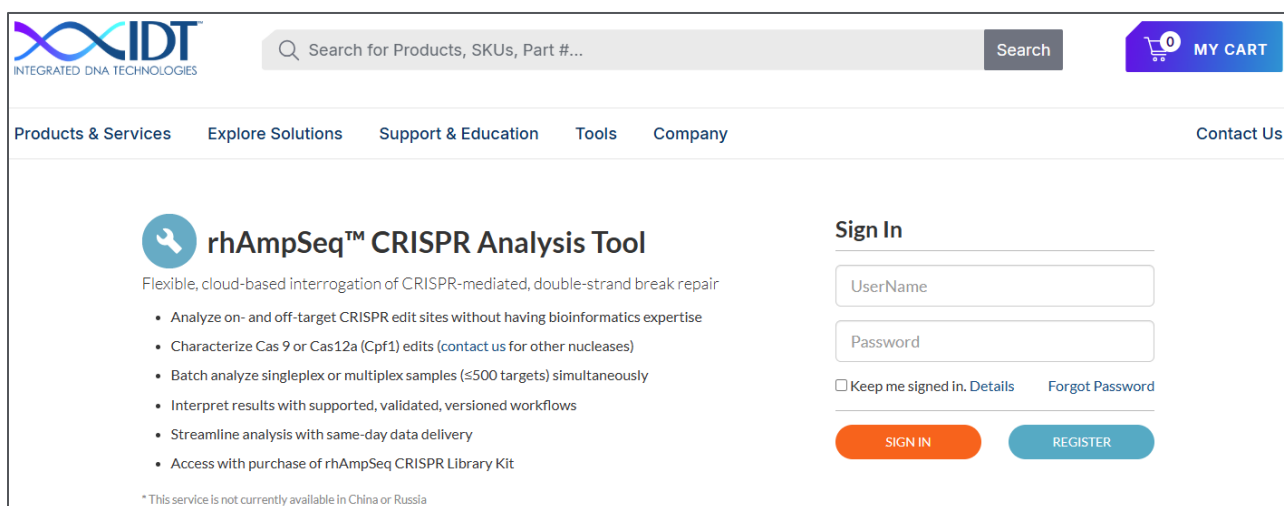
Access the rhAmpSeq CRISPR Analysis Tool

From the IDT website, go to Tools, CRISPR Genome Editing, then select the [rhAmpSeq CRISPR Analysis Tool](#).



Create an account

An IDT account provides access to the Analysis Lab page and the ability to use the rhAmpSeq CRISPR Analysis Tool.





Note: If you do not already have an IDT account, click [Register](#) to create your own account.

Once established, you will use this account login to sign in and use the rhAmpSeq CRISPR Analysis Tool. After you log in, the Analysis Lab landing page opens. If you are not already part of an analysis lab, click the Create a Lab button and give a unique name to your lab.



Analysis Lab Overview

You don't belong to any active lab. Please join or create one.

CREATE A LAB
REDEEM CREDIT
SEND INVITE
ANALYSIS TOOL

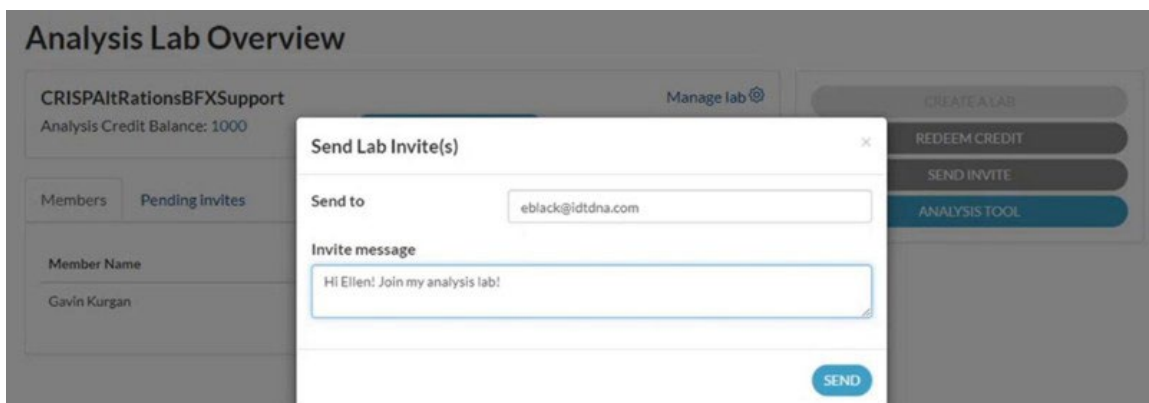


Create New Lab

Lab Name: CRISPAItRationsBFXSupport

CREATE

After creating a lab, you can invite collaborators, colleagues, and students to join your analysis lab by clicking Send Invite. Enter a list of those you want to collaborate with, and a custom message to accompany your invitation.



Analysis Lab Overview

CRISPAItRationsBFXSupport
Analysis Credit Balance: 1000

Members Pending Invites

Member Name
Gavin Kurgan

Manage lab

CREATE A LAB
REDEEM CREDIT
SEND INVITE
ANALYSIS TOOL

Send Lab Invite(s)

Send to: eblack@idtdna.com

Invite message: Hi Ellen! Join my analysis lab!

SEND



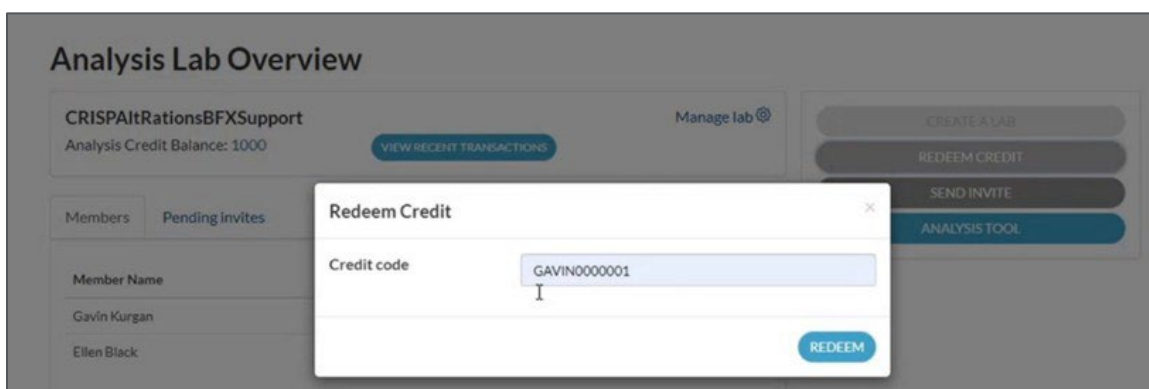
Note: You can control user privileges by setting permission levels for each invited member.

Manage your account

To use the rhAmpSeq CRISPR Analysis Tool, you will need Analysis Credits. You received a code for these credits when the order for your purchased product was invoiced. To redeem your Analysis Credits, click the gray Redeem Credit button, then enter the code. View your current balance and transaction history in the top left corner.

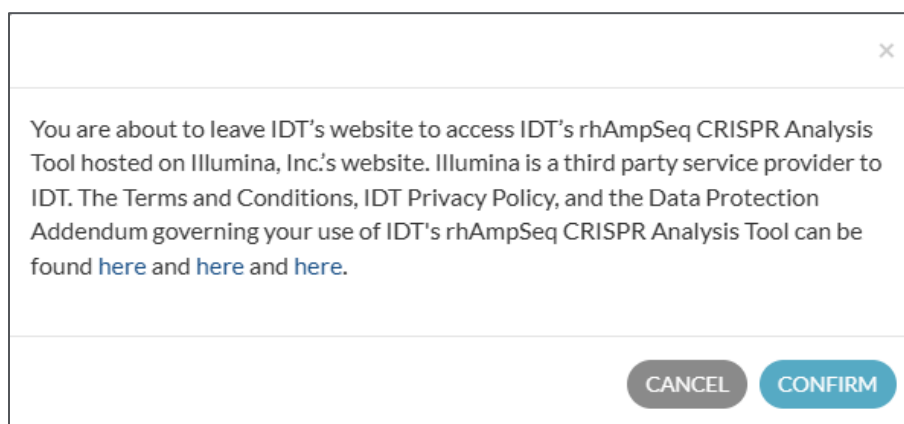


Note: Refresh the page to see the updated information on your account balance.



Start analyzing

Open the rhAmpSeq CRISPR Analysis Tool by clicking the blue Analysis Tool button. Select Confirm when prompted.



A new login page will open where you will enter your IDT account credentials again for security purposes.

Now you are ready to begin analyzing data!



Note: Since you have learned how to create and manage your account, you are ready to explore the other [tutorial videos](#) that further describe how to use the IDT rhAmpSeq CRISPR Analysis Tool.

At any point if you need help or have questions, please [contact us](#). We are here to assist you.

Upload data

Before we delve into the process of uploading data, let us review the supported data formats. Specifically, you will have to provide demultiplexed sequencing data, usually in the form of .fastq or .fastq.gz files as shown in the below image. These files contain the following attributes for each read in the sequenced sample:

- read name
- sequence
- associated quality score



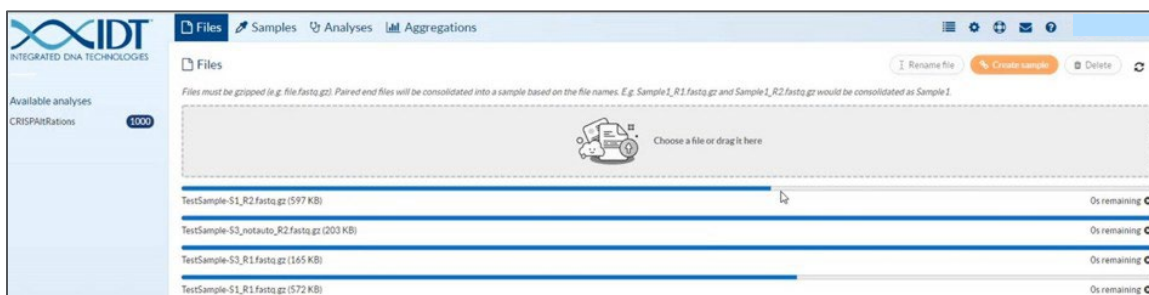
There are a few different ways to upload your data to the rhAmpSeq CRISPR Analysis Tool. You can:

- drag and drop files into the application
- upload files from a local drive
- upload files from the cloud using the Connector

For smaller file sizes, using drag-and-drop is the fastest and easiest method for uploading sequence data.

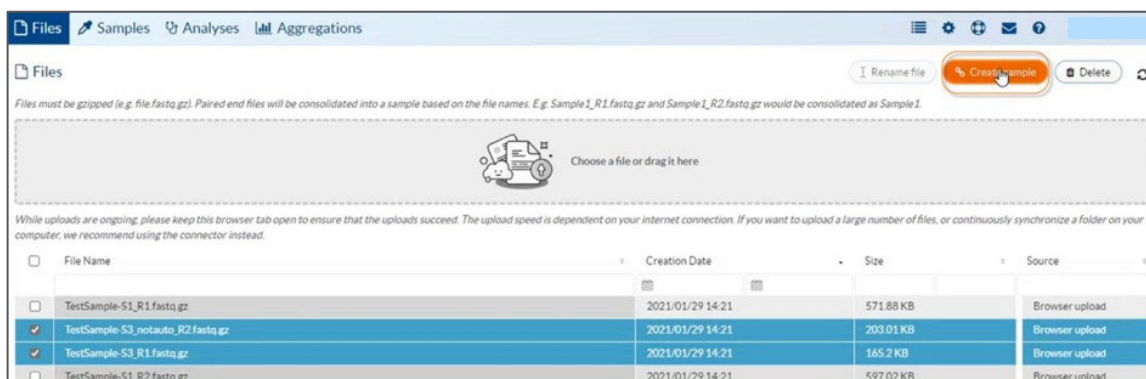
Simply navigate to the Files tab, then drag the samples you want analyzed into the open gray box in the interface as shown below.

Files are uploaded in parallel, and upon successful upload, R1/R2 files are automatically paired to create a “Sample.”



Notes:

- For drag-and-drop uploads you must stay on the upload page until the transfer is completed. Wait for the progress bars to indicate when the uploads are complete before moving to the next step.
- Alternatively, you can manually pair read data into a sample by selecting the uploaded files, then clicking the orange Create sample button.



Upload large files via connector setup

For larger files, or high-throughput applications, the drag-and-drop method may not be fast enough. Consider using the Connector setup upload feature. Navigate to the Settings page, indicated by a gear icon.



Here, you can set up the uploading of data from your local drive, or cloud storage systems. This guide will give you a high level overview of how to set up the Connector; for a more in-depth review, see the [rhAmpSeq CRISPR Analysis Tool Data Transfer Guide](#).

To start uploads from your local drive to the analysis platform, click the New button under Local Connector Settings, then specify the following:

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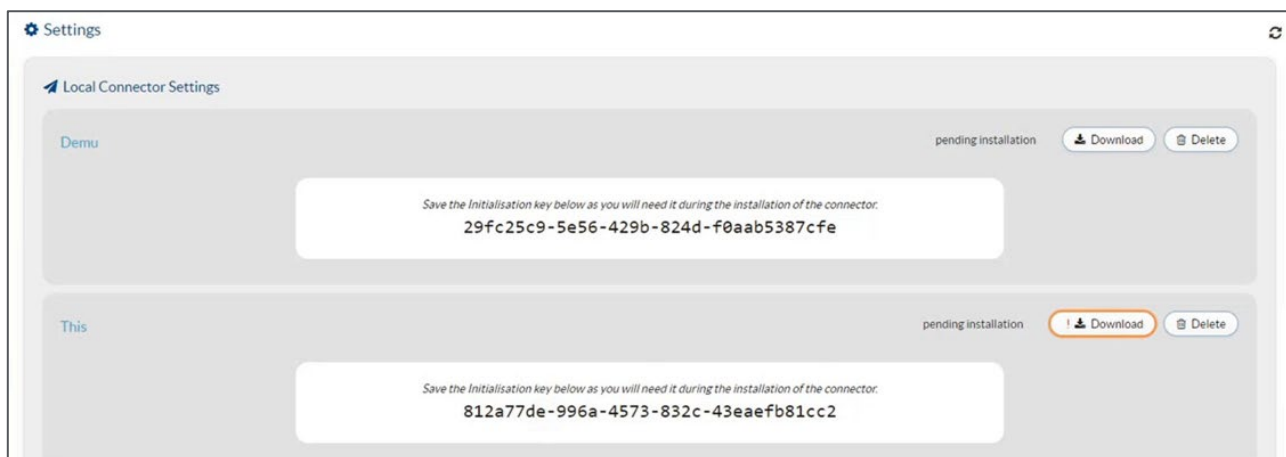
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- name of the connector
- computer's operating system
- upload/download location of your data



Save your inputs, then download and install the connector software.



Follow the on-screen installation prompts.

To start uploads from a cloud streaming scenario, click the New button under the appropriate cloud service provider that you use. The setup is the same as above (uploads from a local drive), except that some specifics for each cloud provider may differ. Reference the [rhAmpSeq CRISPR Analysis Tool Data Transfer Guide](#) for detailed instructions based on your cloud provider.

Data with multiple amplicons

If you are analyzing data with multiple amplicons in each sample, you will need to upload two 6-column

BED-formatted files specifying amplicon and guide coordinates of the genome of interest. These BED files contain the following for all targets being analyzed:

- chromosome
- start location
- stop location
- name
- strand



Important: Guide coordinates should not include the protospacer adjacent motif (PAM) but should include the correct strand information (+ or -) so that the guide is 5' to 3'.



Note: If the [rhAmpSeq Design Tool](#) was used to generate the panel, then the amplicon BED file can be found in the Design Tool dashboard, as shown below. The file “Assay_panel.bed” will work for this.

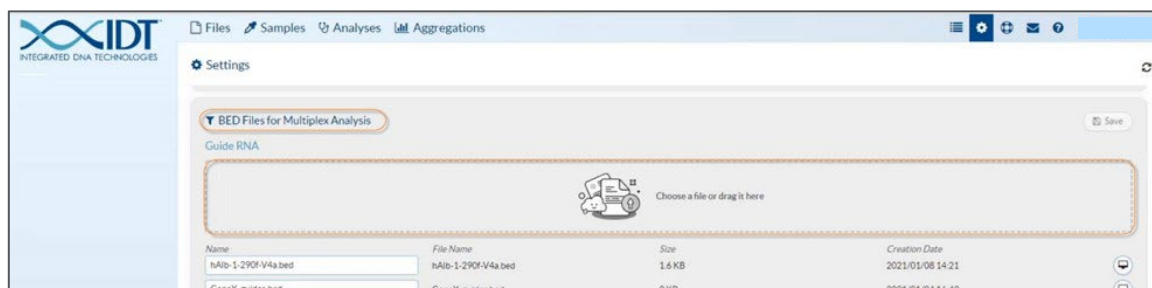
View of GeneX_guides.bed

File Name: Size: 3 KB

Creation Date: 2021/01/04 16:49

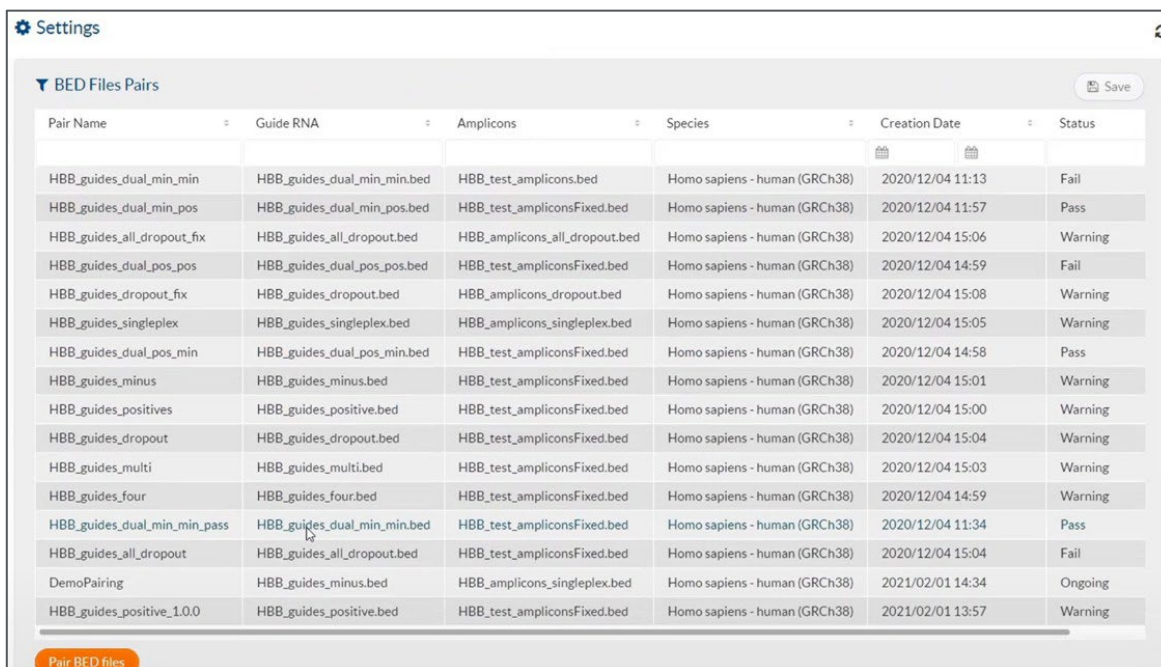
1	chr11	36573321	36573341	GeneX	0	-
2	chr1	3592654	3592674	OT1	0	-
3	chr1	16415506	16415526	OT2	0	+
4	chr1	33698343	33698363	OT3	0	+
5	chr1	34144141	34144161	OT4	0	+
6	chr1	49123705	49123725	OT5	0	-
7	chr1	52927734	52927754	OT6	0	+
8	chr1	115105040	115105060	OT7	0	-
9	chr1	154428110	154428130	OT8	0	+
10	chr1	166894026	166894046	OT9	0	-
11	chr1	183144152	183144172	OT10	0	-
12	chr1	200374008	200374028	OT11	0	-
13	chr1	206221475	206221495	OT12	0	+
14	chr10	6437025	6437045	OT13	0	-
15	chr10	106920200	106920220	OT14	0	-
16	chr10	121109396	121109416	OT15	0	-
17	chr10	125696309	125696329	OT16	0	+
18	chr11	2525645	2525665	OT17	0	+
19	chr11	12125984	12126004	OT18	0	-
20	chr11	20102285	20102305	OT19	0	+
21	chr11	57348913	57348933	OT20	0	-
22	chr11	64787970	64787990	OT21	0	-
23	chr11	103863224	103863244	OT22	0	-
24	chr12	26976538	26976558	OT23	0	+
25	chr12	49647269	49647289	OT24	0	-
26	chr12	56088641	56088661	OT25	0	+
27	chr12	57198911	57198931	OT26	0	+
28	chr12	57289518	57289538	OT27	0	+
29	chr12	74842086	74842106	OT28	0	+
30	chr12	90948235	90948255	OT29	0	-
31	chr12	106046735	106046755	OT30	0	+
32	chr12	109286629	109286649	OT31	0	-
33	chr12	124489776	124489796	OT32	0	+
34	chr13	22458937	22458957	OT33	0	+

To upload these files, use the gear icon to open the Settings page, then scroll down to find the section called “BED Files for Multiplex Analysis.” Upload your guide RNA and amplicon BED files into the specified sections by using the drag-and-drop upload method.



Quality control checking BED inputs

In order to use your BED files for multiplex analysis, the uploaded BED files need to be checked for errors. Navigate to the Settings page, then look for the “BED Files Pairs” section. This is where you QC-check your inputs to make sure they can successfully be used for analysis. To begin, select the orange Pair BED files button, as shown below.



Pair Name	Guide RNA	Amplicons	Species	Creation Date	Status
HBB_guides_dual_min_min	HBB_guides_dual_min_min.bed	HBB_test_amplicons.bed	Homo sapiens - human (GRCh38)	2020/12/04 11:13	Fail
HBB_guides_dual_min_pos	HBB_guides_dual_min_pos.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 11:57	Pass
HBB_guides_all_dropout_fix	HBB_guides_all_dropout.bed	HBB_amplicons_all_dropout.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:06	Warning
HBB_guides_dual_pos_pos	HBB_guides_dual_pos_pos.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 14:59	Fail
HBB_guides_dropout_fix	HBB_guides_dropout.bed	HBB_amplicons_dropout.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:08	Warning
HBB_guides_singleplex	HBB_guides_singleplex.bed	HBB_amplicons_singleplex.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:05	Warning
HBB_guides_dual_pos_min	HBB_guides_dual_pos_min.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 14:58	Pass
HBB_guides_minus	HBB_guides_minus.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:01	Warning
HBB_guides_positives	HBB_guides_positive.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:00	Warning
HBB_guides_dropout	HBB_guides_dropout.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:04	Warning
HBB_guides_multi	HBB_guides_multi.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:03	Warning
HBB_guides_four	HBB_guides_four.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 14:59	Warning
HBB_guides_dual_min_min_pass	HBB_guides_dual_min_min.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 11:34	Pass
HBB_guides_all_dropout	HBB_guides_all_dropout.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2020/12/04 15:04	Fail
DemoPairing	HBB_guides_minus.bed	HBB_amplicons_singleplex.bed	Homo sapiens - human (GRCh38)	2021/02/01 14:34	Ongoing
HBB_guides_positive_1.0.0	HBB_guides_positive.bed	HBB_test_ampliconsFixed.bed	Homo sapiens - human (GRCh38)	2021/02/01 13:57	Warning

You will enter:

- a unique name to reference the files being paired
- the pipeline version intended for analysis
- guide and amplicon BED files
- species these coordinates come from

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These entries will initiate the QC check on the files, which will take approximately 5–10 minutes to complete. A status message of PASS, WARNING, or FAIL will appear when the pairing is complete.

```
02/01/2021 08:20:49 PM - INFO - create:set_up_logging - Logging to bedQC.log
02/01/2021 08:20:49 PM - WARNING - columnBiasCheck:columnBiasCheck - There is only one value of {'+'} in column 5; make sure this .
02/01/2021 08:20:50 PM - INFO - create:set_up_logging - Logging to bedQC.log
```

Handling QC statuses

If a PASS status is shown, you are ready to start your analysis.

If a WARNING status is shown, double-click the pairing to understand why the paired BED files were flagged. These files will still be available for analysis; however, they should be reviewed to make sure there are no persistent problems with your experimental inputs.

If a FAIL status is shown, there is something wrong with the BED inputs that needs correction. Check the log and make the appropriate corrections in the files to reverse the failure.



Important: Once paired, BED files cannot be deleted from the analysis tool. This is to ensure they are available for previous analyses that used them. Try to provide unique and memorable names for these BED file pairs. BED file pairs may be hidden from the interface if they are no longer needed.

Analyzing singleplex experiments

If you want to screen on-target guides and conditions, you will need to know how to analyze your singleplex experiment.



Important: Make sure that data has been completely uploaded and put into samples before proceeding.

First, select your samples. Navigate to the Samples page where you will be able to see all the samples that have FASTQ files associated with them. Select the groups of samples with a single amplicon that you want to analyze. Begin the analysis by clicking Analyze Singleplex.

To start the run, you will need to associate information and parameters with the run and individual samples. This is where you will also specify the version of the CRISPAItRations software to use for the analysis.



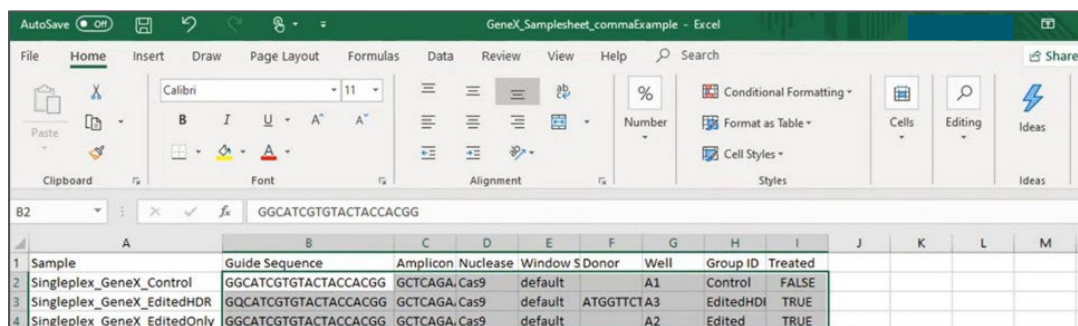
Before starting the run, provide the information highlighted by red boxes, namely the nucleotide sequences for the guide and the amplicon, 5' to 3', excluding the PAM.

Sample	Guide Sequence	Amplicon Sequence	Nuclease	Window Size	Donor
Singleplex_GeneX_Control			Cas9	default	
Singleplex_GeneX_EditedHDR			Cas9	default	
Singleplex_GeneX_EditedOnly			Cas9	default	

The additional parameters that can be configured on a run include:

- the applicable CRISPR nuclease
- window size for interrogating variants
- nucleotide sequences for HDR donors
- well position (for advanced visualizations)
- sample name
- treated vs. untreated sample

- **Tip:** You can quickly populate the same entry down an entire column at once by entering the information in the first row, then clicking the down arrow icon to the right of the field.
- **Note:** For batch runs that have a large number of samples, you will need to upload a samplesheet to provide run information. To get a template of this samplesheet, click the Export to CSV button.

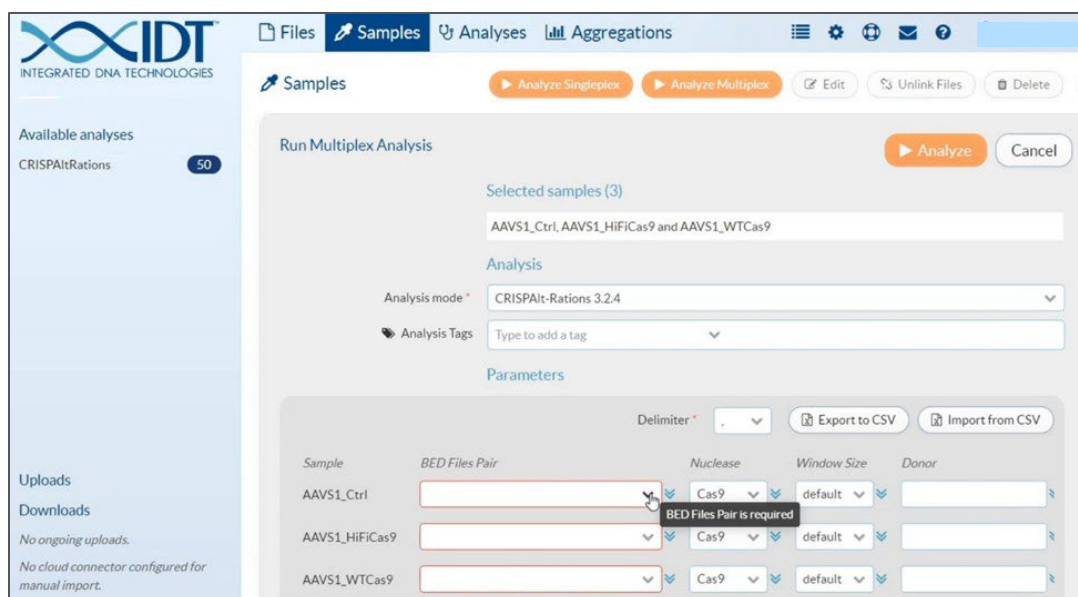


Sample	Guide Sequence	Amplicon	Nuclease	Window	Donor	Well	Group ID	Treated
Singleplex_GeneX_Control	GGCATCGTGTACTACACGG	GCTCAGA	Cas9	default		A1	Control	FALSE
Singleplex_GeneX_EditedHDR	GQCATCGTGTACTACACGG	GCTCAGA	Cas9	default	ATGGTTCTA3		EditedHDR	TRUE
Singleplex_GeneX_EditedOnly	GGCATCGTGTACTACACGG	GCTCAGA	Cas9	default		A2	Edited	TRUE

After specifying your sample information in Microsoft Excel, save and upload this file directly into the interface using the Import from CSV button.

Before starting your run, designate an “Aggregation” name, which creates a single location to interrogate all samples in the run. You can add additional metadata and unique descriptions to help label samples and experimental details for tracking results before starting the run.

Caution: When a red box highlights any of the sample information fields, you will not be able to start the run. Check the hover text on any parameter with a red box to find acceptable inputs and make corrections accordingly. When all inputs are satisfied and no red boxes appear, then you are ready to begin the run.



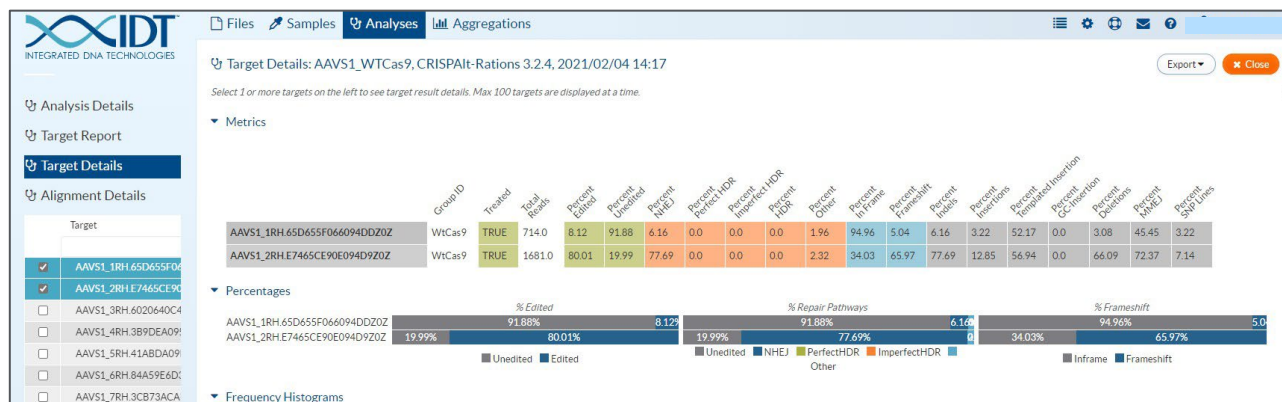
The screenshot shows the 'Run Multiplex Analysis' configuration page in the rhAmpSeq web interface. The page includes a sidebar with 'Available analyses' (CRISPRatRations) and 'Uploads/Downloads' status. The main content area shows the configuration for a multiplex analysis:

- Selected samples (3):** AAVS1_Ctrl, AAVS1_HiFiCas9, and AAVS1_WTCas9.
- Analysis mode:** CRISPRat-Rations 3.2.4.
- Analysis Tags:** A field to add tags.
- Parameters:**
 - Delimiter:** A dropdown menu.
 - Export to CSV / Import from CSV:** Buttons for file management.
 - Sample Table:** A table with columns for Sample, BED Files Pair, Nuclease, Window Size, and Donor. The 'BED Files Pair' column for AAVS1_Ctrl is highlighted with a red box, and a tooltip indicates 'BED Files Pair is required'.

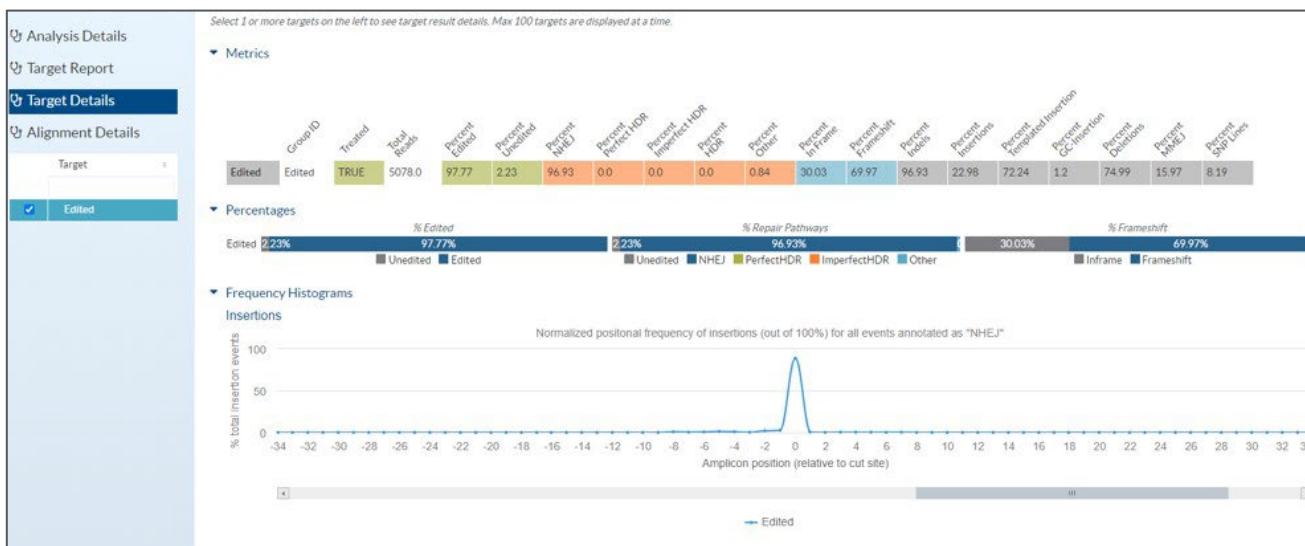
To check the status or results of a run, navigate to the Analyses page. As soon as cloud resources begin processing, a progress bar should appear. Analyses can take between 20 min–2 hr to complete.

Interpreting singleplex experiments

View your results by double-clicking the sample on the Analyses page. This opens the landing page where you will interpret the results of your experiment. View the graphics for all targets amplified in the Target Details section. You can also easily export the graphics in the interface for selected targets using the Export button in the top right corner of the page.



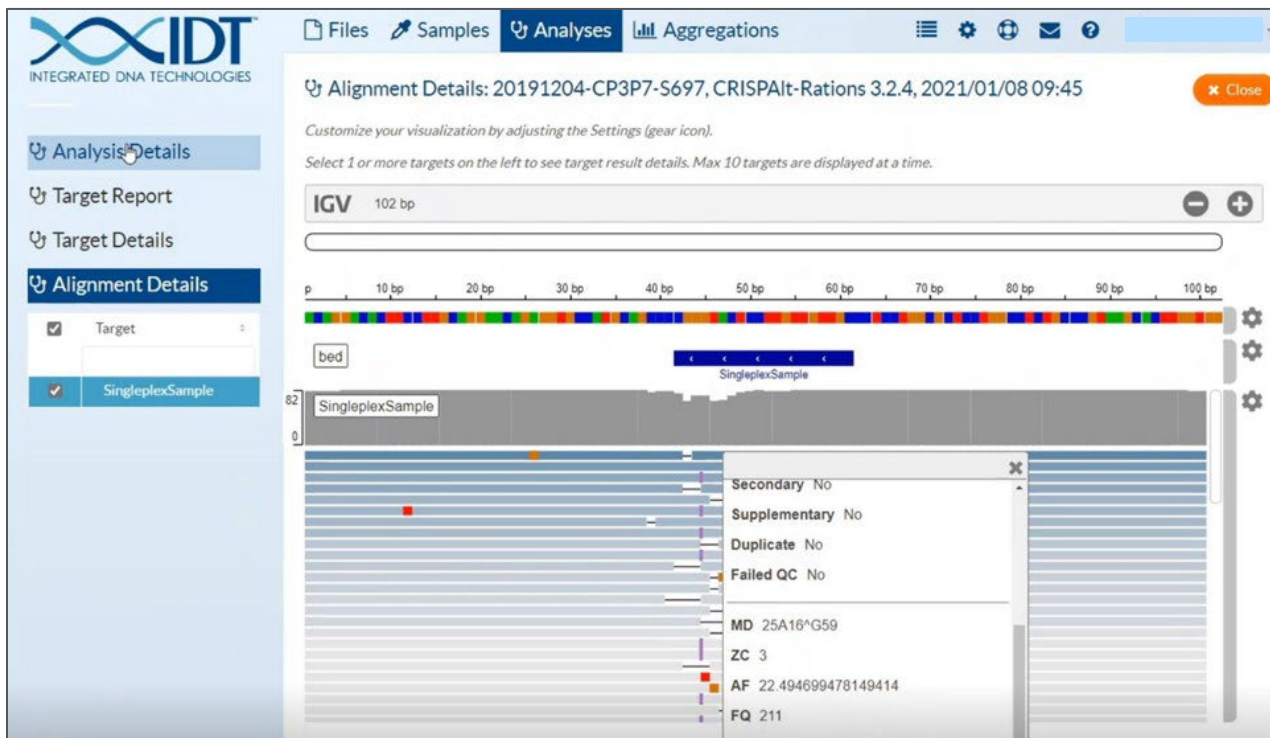
Also, on this page you will be able to find the frequency of the editing, the specific repair pathways used, and any frameshifting events that may have occurred. Dive deeper to explore the exact position of insertion and deletion events in the sequenced sample, even the size of these events. We include a frequency histogram showing the normalized positional frequency of insertions, as shown below.



Viewing allele details

Go to the Alignment Details page to view the distribution of alleles in the sequenced population using the Integrative Genomics Viewer (IGV).

Click on the event of interest to see both the frequency of the event and the read count.



For those with advanced graphical considerations, the raw data we use to render the graphics can be downloaded from the Analysis Details page in the Results section.

Analysis Details
Target Report
Target Details
Alignment Details

Guide Sequence: GGCATCGTGACTACCAGG

Amplicon Sequence: GCTCAGAATCTGTCTATGCCCAATTTTCTGTTTCATGGAATCTGCCTCCGCTAAAGTATACCCCGATGTTGTGTCACGGATTCCGCTTTGGGACAATCCTGTGAAGCTGTACCAACCAAGGCATCCACCTGCACCTGAAGCCTGGCATCTGTACTACCACGGTGGCGGGCGTCATGGGAGTTTGAGTAAGAACATTTCTCAGACC

Donor:

Well: A2

Total on-target reads: 5,078

Reads (total): 5170.0

% Merged: 98.91093

% On-target: 99.84

Nuclease: Cas9

Max Overlap: 152

Min Read Size: 60

Window Size: default

Group ID: Edited

Treated: TRUE

Species: notSpecified

% Mapped: 99.84

% QC passing: 99.45841

% Primer-dimer: 0.0

Results

File Name	Size	Format		
OUTPUT.tar.gz	821.27 KB	UNKNOWN		
SAMPLE_allSnpsTables.csv	11.74 KB	CSV		
SAMPLE_AllTargetEditing.png	11.69 KB	PNG		
SAMPLE_collapsedIndelInfo.csv	305.19 KB	CSV		
SAMPLE_deleteLocationHist.csv	8.14 KB	CSV		
SAMPLE_indel.csv	2.96 KB	CSV		
SAMPLE_insertLocationHist.csv	5.62 KB	CSV		
SAMPLE_summary.csv	704 B	CSV		
SUMMARIES.tar.gz	17.94 KB	UNKNOWN		

Results files of the targets are consultable in the Target Details menu.

On this page, you can see general sample information, as well as an assortment of other files for either viewing or downloading.

IDT
INTEGRATED DNA TECHNOLOGIES

Files
Samples
Analyses
Aggregations

Analysis Details: 20191204-CP3P7-S697, CRISPAIt-Rations 3.2.4, 2021/01/08 09:45
Close

Analysis Details
Target Report
Target Details
Alignment Detail

total on-target reads: 5,078

View of SAMPLE_collapsedIndelInfo.csv

File Name: SAMPLE_collapsedIndelInfo.csv

Size: 23.99 KB

Creation Date: 2021/01/08 09:55

freqCount	ReferenceAlignment
211	ACAGGACACTTCCTTGCAGGAACAGAGGTGCCATGCAGCCCCGGGTACTCCTTGTGTGTGCC
109	ACAGGACACTTCCTTGCAGGAACAGAGGTGCCATGCAGCCCCGGGTACTCCTTGTGTGTGCC
69	ACAGGACACTTCCTTGCAGGAACAGAGGTGCCATGCAGCCCCGGGTACTCCTTGTGTGTGCC
69	ACAGGACACTTCCTTGCAGGAACAGAGGTGCCATGCAGCCCCGG--GTACTCCTTGTGTGTGCCCTCTGGCGCTCTGGCCTCTGCCCGTAAGCACTTGGTGG
44	ACAGGACACTTCCTTGCAGGAACAGAGGTGCCATGCAGCCCCGGGTACTCCTTGTGTGTGCC
43	ACAGGACACTTCCTTGCAGGAACAGAGGTGCCATGCAGCCCCGG--

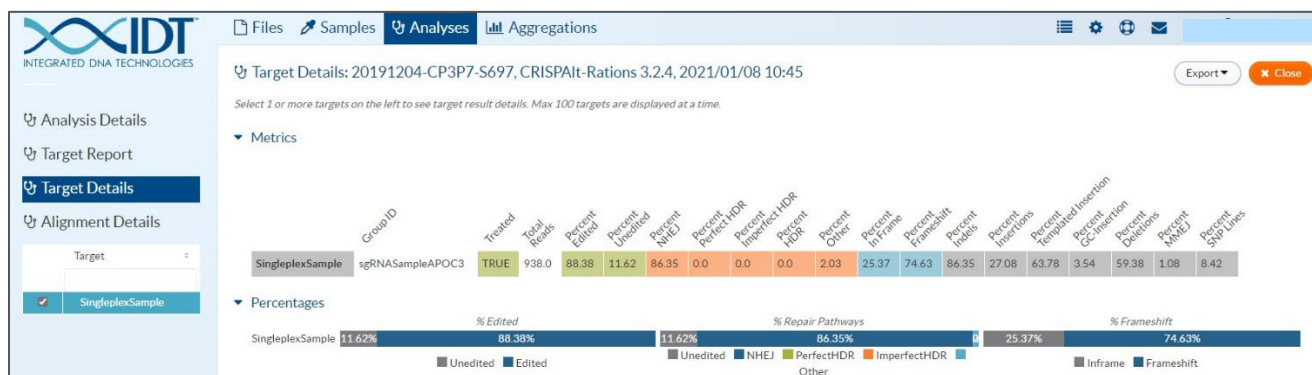
Close

Viewing the target report

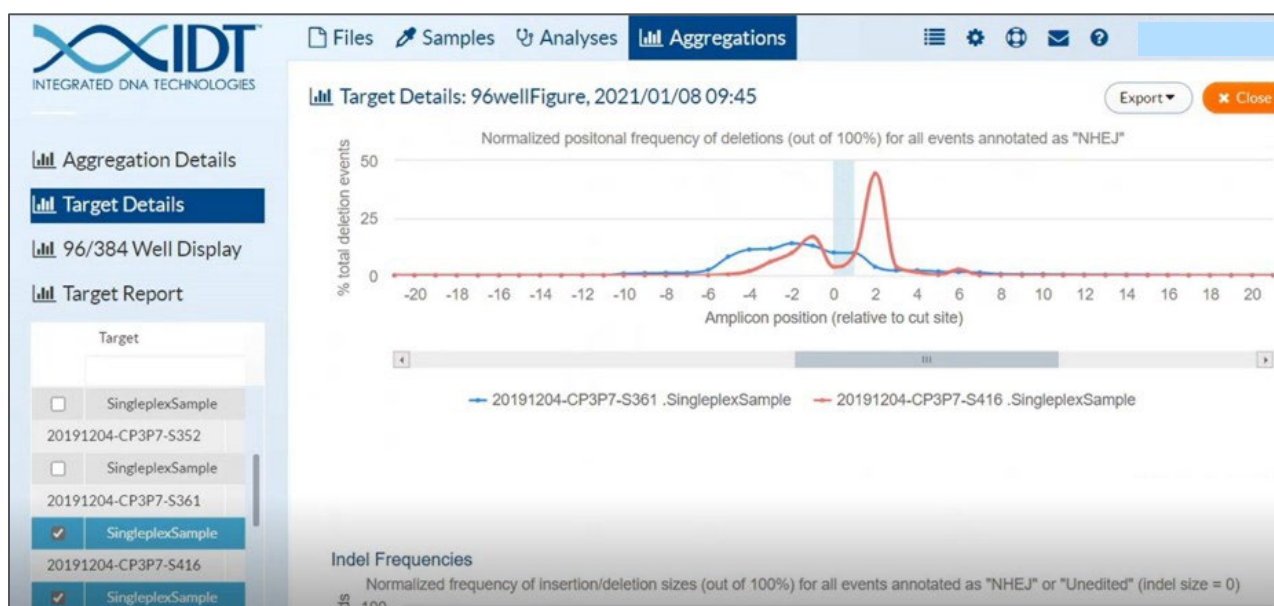
To interpret and compare results of different samples within an experiment, go to the Aggregations tab.

On the Target Report landing page, view all the samples that were aggregated for summarization. Any report that you view can easily be exported to Microsoft Excel. From the Target Report page, sort or filter the experimental results as needed, and create additional graphics in the software of your choice.

To compare a sample with another, click Target Details. On this page you will find the same graphics that were available for individual samples; however, here you can also overlay results from other relevant samples within the whole experiment.



In the graphic below, the run contained two samples with different guides, treated under the same conditions. Notice that the indel profiles of the two guides are different, as would be expected.



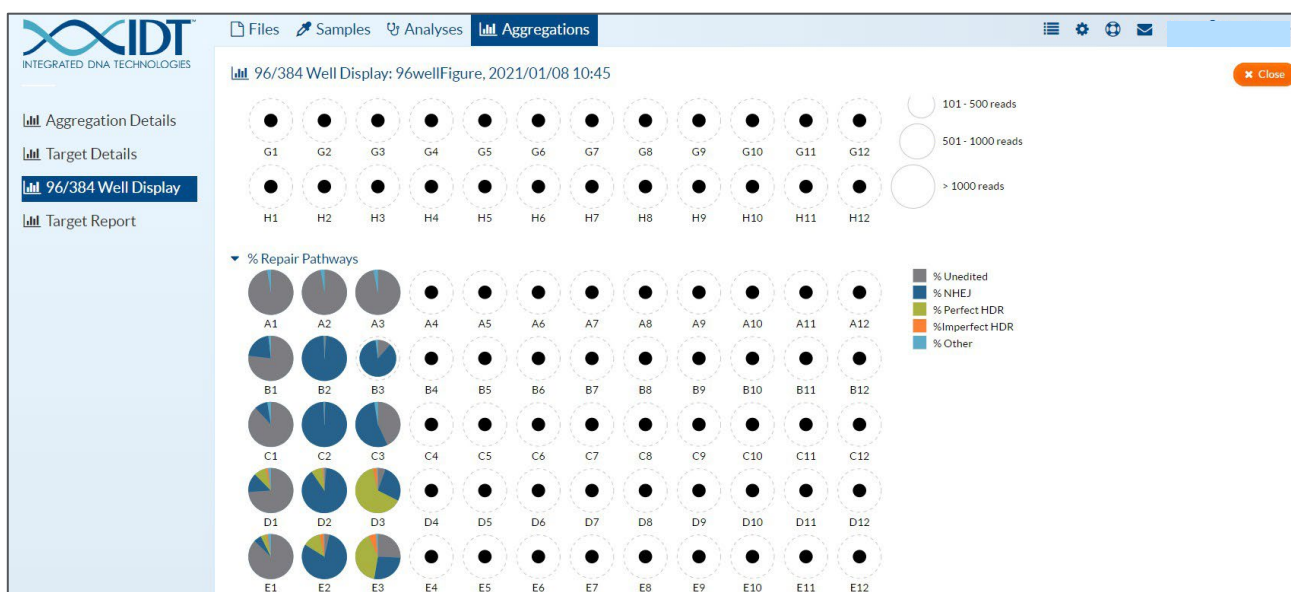
Screening guides

When screening a large number of guides under varying conditions and treatments, you can use the rhAmpSeq Analysis Tool to generate graphics in 96- or 384-well plate formats to find conditions that are optimal for your experimental goals. The graphics in 96- or 384-well plate formats are available for singleplex analyses only.

To create these graphics, simply specify the “Well” information for each singleplex sample prior to sample analysis.

Once your run is complete, go to the Aggregations tab where you can find graphics displaying the following:

- frequency of editing
- repair pathway utilization
- frameshift frequency



Analyzing multiplex experiments

The most common application for multiplex CRISPR NGS is to quantify on- and off-target editing effects of a guide. In our example, we show how to analyze samples that have multiple amplicons per sample, known as multiplexed samples.



Important: Make sure the following have been completed before proceeding.

- Data have been uploaded and created into samples

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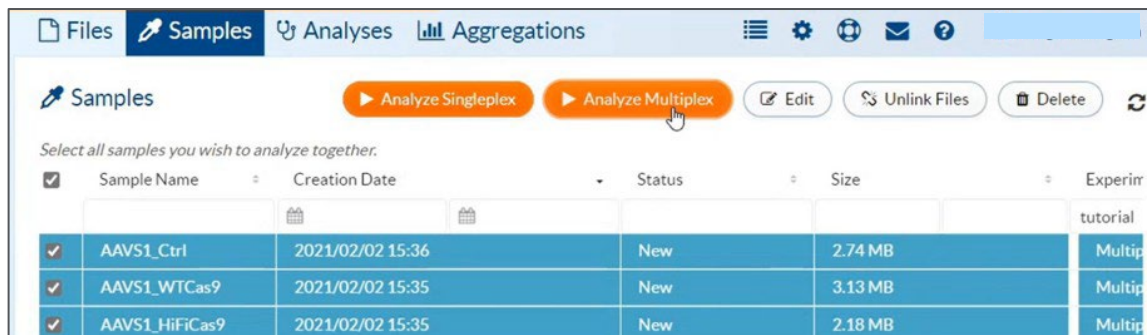
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- Guide and amplicon BED files have been uploaded and paired



Tip: For a deep dive into pairing your guide and amplicon BED files, watch the section of the rhAmpSeq CRISPR Analysis Tool video [How to quality control check multiplex file inputs](#).

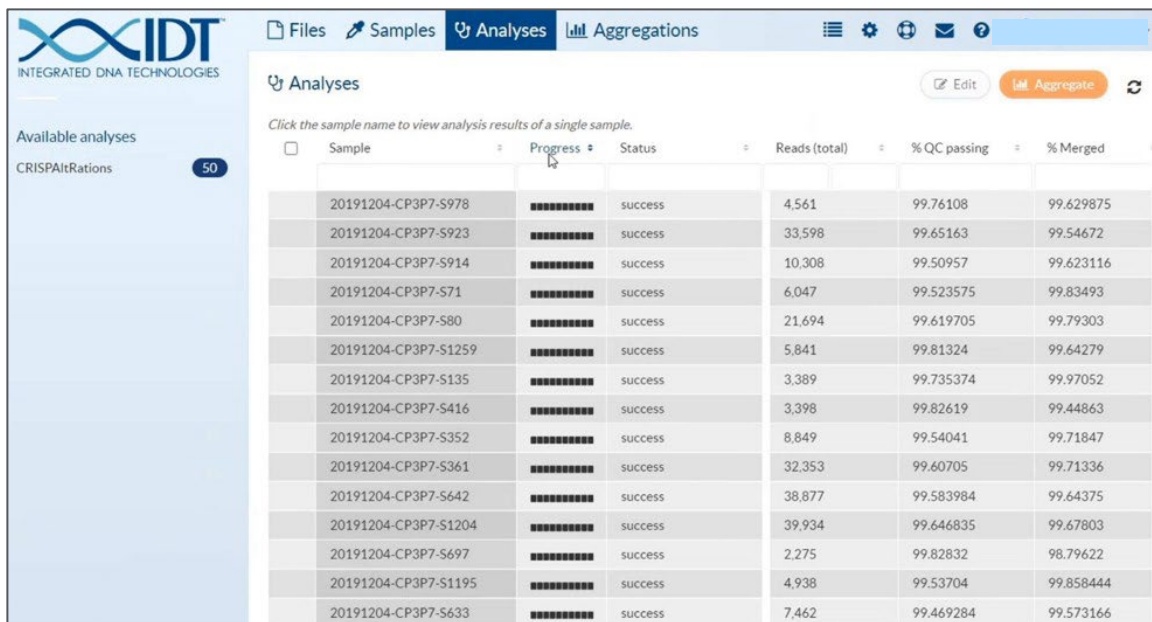
To begin, select the samples you want to analyze, then click Analyze Multiplex.



Once your data has successfully been checked for quality control, select your named guide/amplicon pairs and other relevant run information, including:

- the appropriate CRISPR nuclease
- window size for interrogating variants
- nucleotide sequences for HDR donors
- sample name information
- treated vs. untreated

Navigate to the Analyses page to check the status or results of your analysis. As soon as cloud resources begin processing, you will see the progress bar. Analyses can take anywhere from 20 min–2 hr to complete. Your turnaround time will depend on your read depth plus the number of amplicon targets being quantified per sample.



The screenshot shows the 'Analyses' tab in the IDT rhAmpSeq CRISPR Analysis Tool. On the left, there is a sidebar with 'Available analyses' and a button labeled '50'. The main area displays a table of analysis results. The table has columns for 'Sample', 'Progress', 'Status', 'Reads (total)', '% QC passing', and '% Merged'. The 'Progress' column shows a series of black bars representing the progress of each sample. The 'Status' column shows 'success' for all samples. The 'Reads (total)' column shows values ranging from 2,275 to 39,934. The '% QC passing' column shows values ranging from 99.53704 to 99.82832. The '% Merged' column shows values ranging from 98.79622 to 99.629875.

Sample	Progress	Status	Reads (total)	% QC passing	% Merged
20191204-CP3P7-S978	■■■■■■■■■■	success	4,561	99.76108	99.629875
20191204-CP3P7-S923	■■■■■■■■■■	success	33,598	99.65163	99.54672
20191204-CP3P7-S914	■■■■■■■■■■	success	10,308	99.50957	99.623116
20191204-CP3P7-S71	■■■■■■■■■■	success	6,047	99.523575	99.83493
20191204-CP3P7-S80	■■■■■■■■■■	success	21,694	99.619705	99.79303
20191204-CP3P7-S1259	■■■■■■■■■■	success	5,841	99.81324	99.64279
20191204-CP3P7-S135	■■■■■■■■■■	success	3,389	99.735374	99.97052
20191204-CP3P7-S416	■■■■■■■■■■	success	3,398	99.82619	99.44863
20191204-CP3P7-S352	■■■■■■■■■■	success	8,849	99.54041	99.71847
20191204-CP3P7-S361	■■■■■■■■■■	success	32,353	99.60705	99.71336
20191204-CP3P7-S642	■■■■■■■■■■	success	38,877	99.583984	99.64375
20191204-CP3P7-S1204	■■■■■■■■■■	success	39,934	99.646835	99.67803
20191204-CP3P7-S697	■■■■■■■■■■	success	2,275	99.82832	98.79622
20191204-CP3P7-S1195	■■■■■■■■■■	success	4,938	99.53704	99.858444
20191204-CP3P7-S633	■■■■■■■■■■	success	7,462	99.469284	99.573166

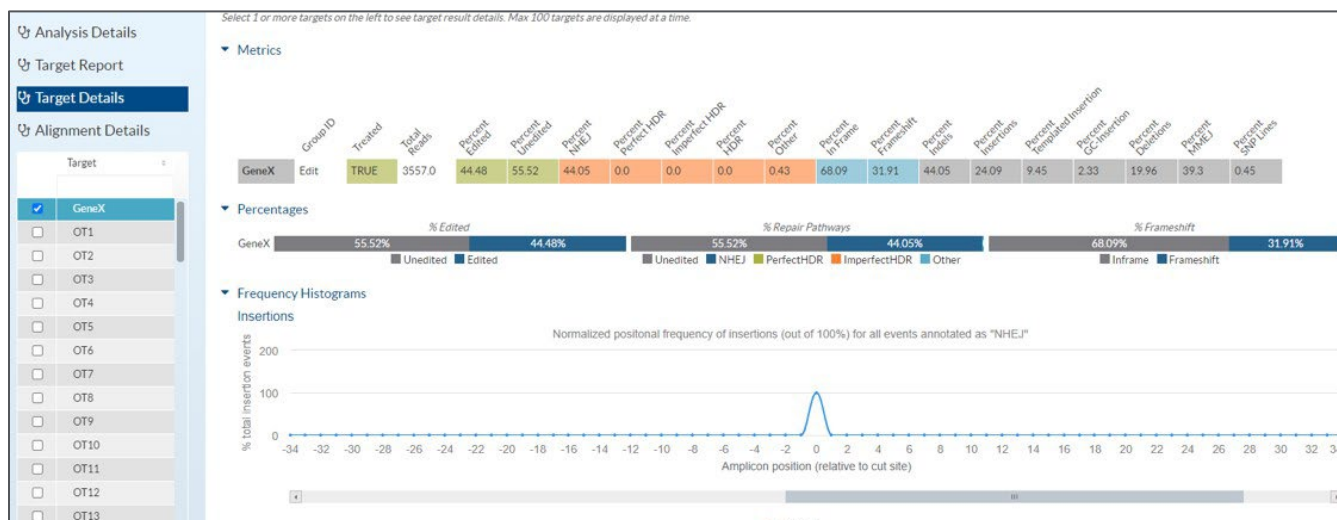
Interpreting multiplex experiments

When you have completed your analysis, the Target Details landing page displays. This page contains graphics for all amplified targets. Each target can be toggled on or off by checking or unchecking the checkboxes to the left of the targets in the table. Also, the active display on the page can easily be exported by using the Export button in the top right corner.

From the Target Details page, you can find a range of data, including:

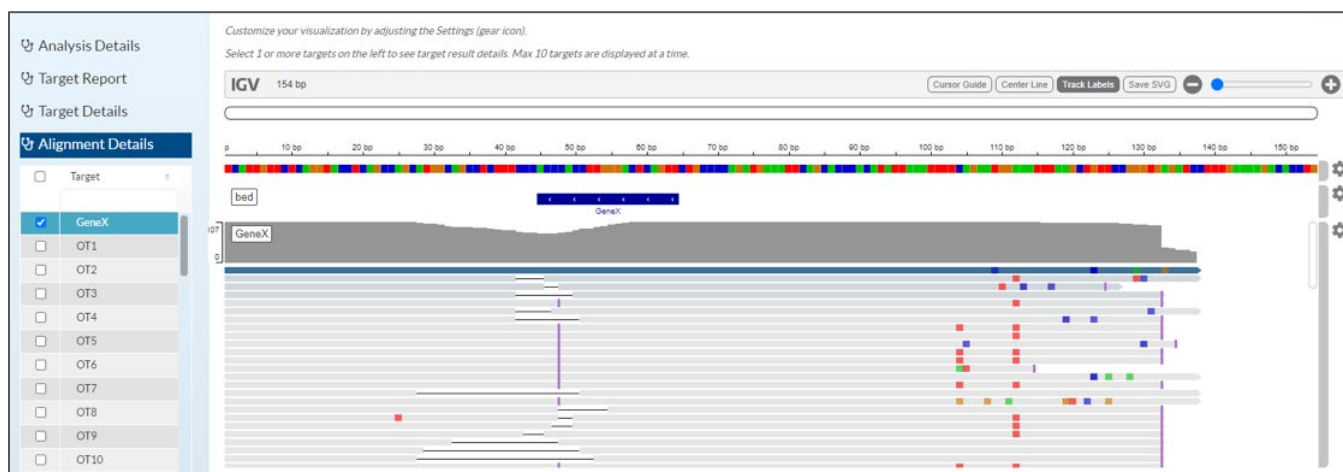
- frequency of editing
- repair pathways
- frameshifting events

Additionally, you can explore the position of any insertion and deletion event that occurred in the sequenced sample and the size of these events. We have included a frequency histogram that shows the normalized positional frequency of insertions below.



Viewing allele details

Go to the Alignment Details page to view the distribution of alleles in the sequenced population using IGV. Click on the event of interest to see both the frequency of the event and the read count.



For those with advanced graphical considerations, the raw data we use to render these graphics can be downloaded from the Analysis Details page. On this page, you can see general sample information, as well as an assortment of other files for either viewing or downloading.

Analysis Details
Target Report
Target Details
Alignment Details

Guide RNA: GeneZZ_guides.bed
Amplicons: GeneZZ_amplicons.bed
Donor:
Well: NotSpecified

Total on-target reads: 363,891
Reads (total): 364,000.0
% Merged: 99.970604
% On-target: 100.0

Nuclease: Cas9
Max Overlap: 152
Min Read Size: 60
Window Size: default
Group ID:
Treated: TRUE
Species: Homo sapiens - human (GRCh38)
% Mapped: 100
% QC passing: 99.99945
% Primer-dimer: 0.0

Results

File Name	Size	Format
OUTPUT.tar.gz	108.8 MB	UNKNOWN
SAMPLE_allSnpTables.csv	764.44 KB	CSV
SAMPLE_AllTargetEditing.png	21.41 KB	PNG
SAMPLE_collapsedIndelInfo.csv	1.29 MB	CSV
SAMPLE_deleteLocationHist.csv	344.52 KB	CSV
SAMPLE_indel.csv	21.91 KB	CSV
SAMPLE_insertLocationHist.csv	338.14 KB	CSV
SAMPLE_summary.csv	14.29 KB	CSV
SUMMARIES.tar.gz	109.36 KB	UNKNOWN

Results files of the targets are consultable in the Target Details menu.

Viewing the aggregated results

Go to the Aggregations tab to interpret and compare results of different samples within an experiment.



Files
Samples
Analyses
Aggregations

Edit
Delete
Refresh

Aggregations

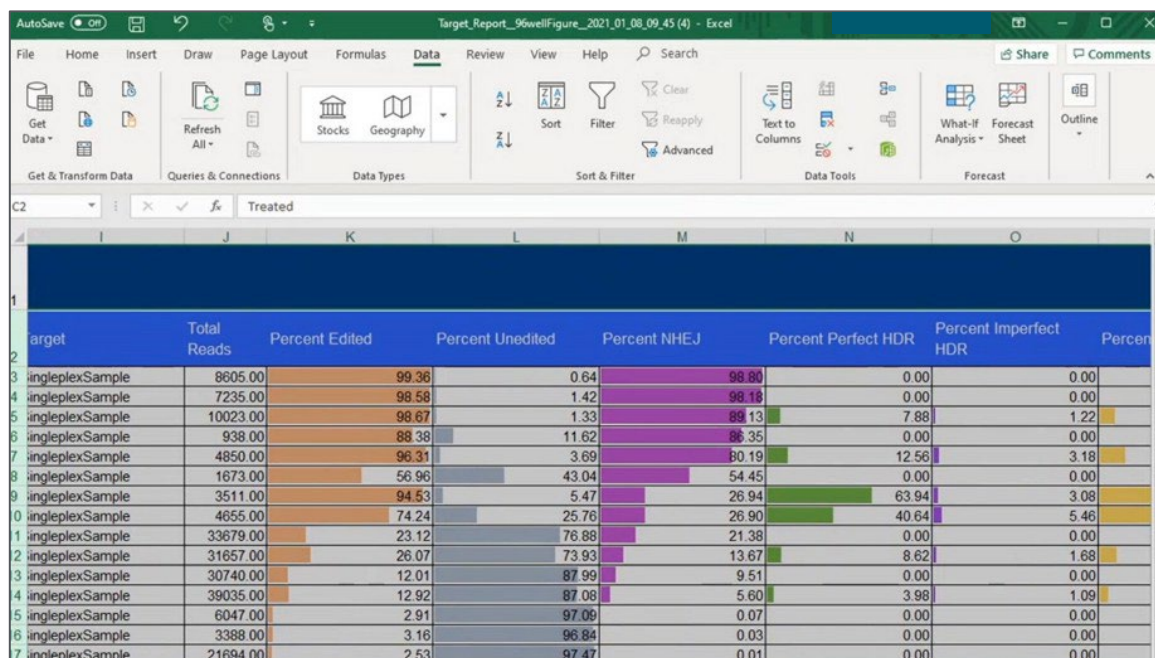
Click the name of the aggregation to view its results.

☐	Name	Creation Date	Analyses	Tags
☐	Multiplex	2021/02/02 15:48	3	Demo
	AAVS	2021/02/02 15:45	3	multiplex
	GeneXExample	2021/01/29 11:25	3	GeneX
	AAVS_Multiplex	2021/01/29 09:56	3	Demo
	MultiplexAAVS	2021/01/29 09:55	3	Demo
	RAG1_GK	2021/01/15 10:28	2	GavinKurgan
	TestNonsense	2021/01/15 09:44	8	GavinTest
	HendelLab	2021/01/14 15:37	2	HendelLab
	GavinsNonsense	2021/01/08 13:32	4	GK
	96wellFigure	2021/01/08 09:45	15	96wellFigure

On the Target Report landing page, view all the samples that were aggregated for summarization, then export this information easily to Excel. With Excel, you can easily sort or filter experimental results as needed, then render additional graphics in the software of your choice.

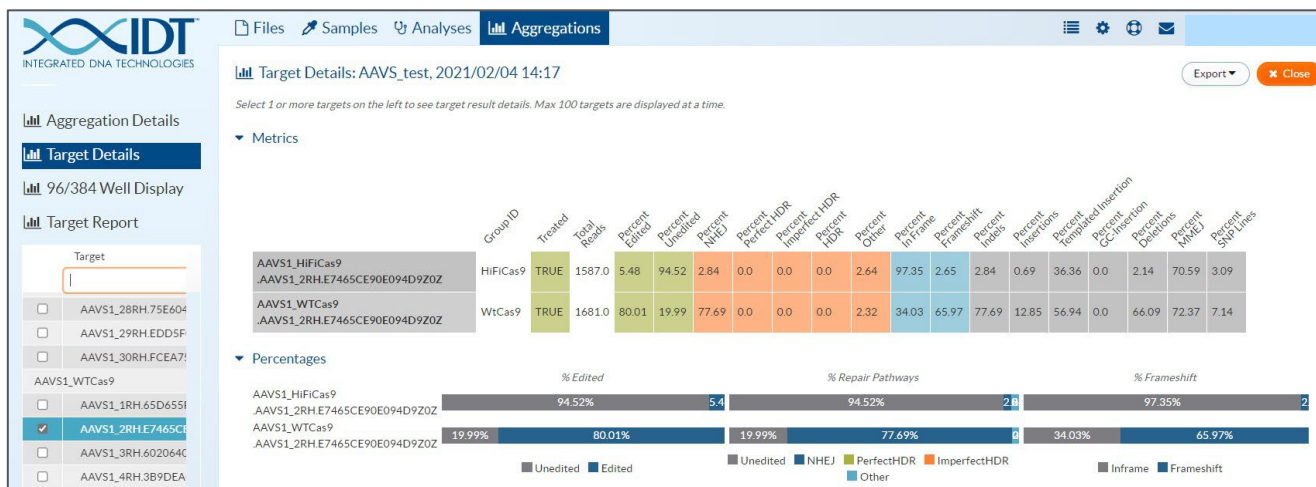
For on- and off-target editing experiments, this summary can be especially powerful for comparing treatment and control experiments. You can even use numbers in this table to implement a statistical test which can determine significant off-target effects in the experiment.

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target	Total Reads	Percent Edited	Percent Unedited	Percent NHEJ	Percent Perfect HDR	Percent Imperfect HDR	Percent
ingleplexSample	8605.00	99.36	0.64	98.80	0.00	0.00	
ingleplexSample	7235.00	98.58	1.42	98.18	0.00	0.00	
ingleplexSample	10023.00	98.67	1.33	89.13	7.88	1.22	
ingleplexSample	938.00	88.38	11.62	86.35	0.00	0.00	
ingleplexSample	4850.00	96.31	3.69	80.19	12.56	3.18	
ingleplexSample	1673.00	56.96	43.04	54.45	0.00	0.00	
ingleplexSample	3511.00	94.53	5.47	26.94	63.94	3.08	
ingleplexSample	4655.00	74.24	25.76	26.90	40.64	5.46	
ingleplexSample	33679.00	23.12	76.88	21.38	0.00	0.00	
ingleplexSample	31657.00	26.07	73.93	13.67	8.62	1.68	
ingleplexSample	30740.00	12.01	87.99	9.51	0.00	0.00	
ingleplexSample	39035.00	12.92	87.08	5.60	3.98	1.09	
ingleplexSample	6047.00	2.91	97.09	0.07	0.00	0.00	
ingleplexSample	3388.00	3.16	96.84	0.03	0.00	0.00	
ingleplexSample	21694.00	2.53	97.47	0.01	0.00	0.00	

To investigate differences between samples further, go to the Target Details page. Here, you can overlay the results of targets from different experimental samples, then export these graphics using the Export button in the top right corner. The graphics provided here are the same as when analyzing a single sample, but single samples cannot be overlaid. An example of this is shown below.



A complete video tutorial version of this guide can be viewed on the [rhAmpSeq CRISPR Analysis Tool](#) page.

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