

You can access the analysis options from the main Tool menu or from the tabs in MHC Analysis

MHC SFVT Analysis (Sequence Feature Variant Type Analysis), is the classical HLA loci.

Select data source:

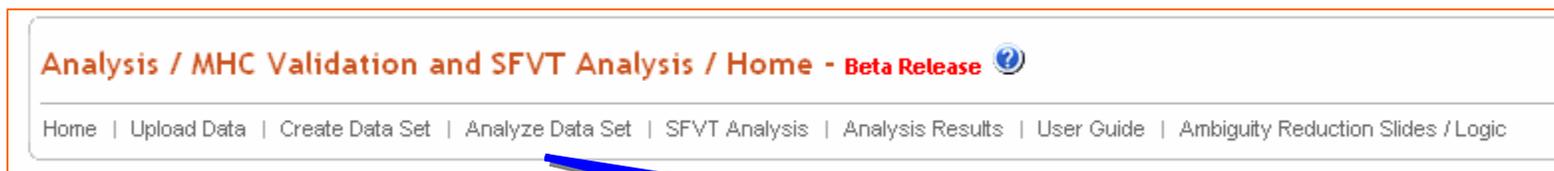
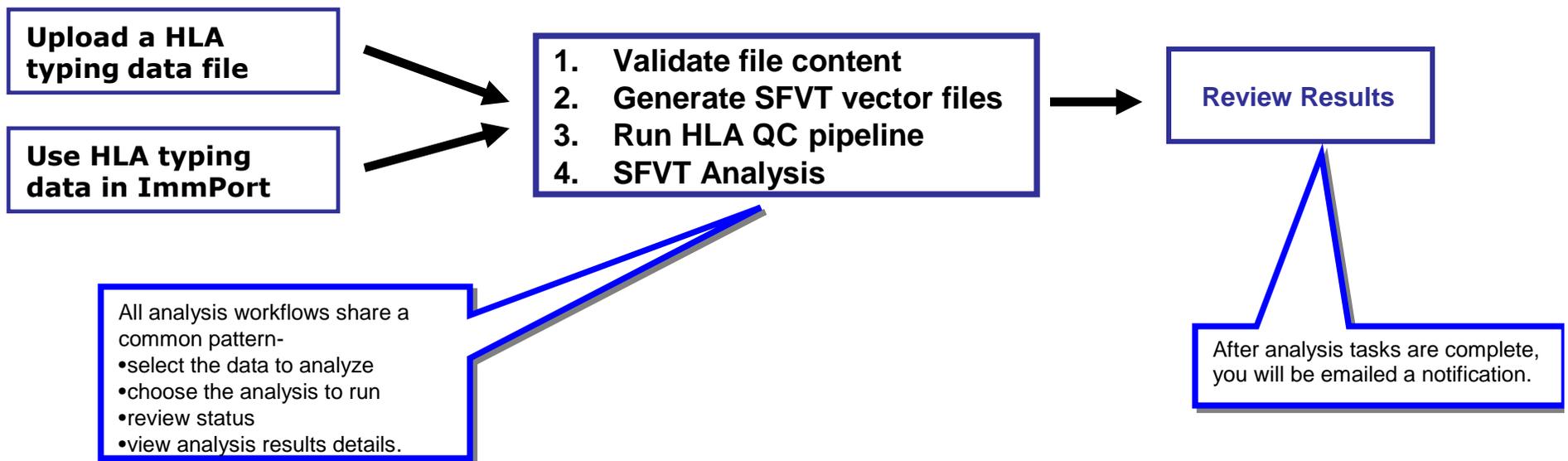
- Upload a HLA Typing File From Your Computer
- Create a HLA Data Set From ImmPort Data
- Re-analyze a HLA Data Set Previously Created in ImmPort
- Run SFVT Analysis

Next

Flow Cytometry B				
Data Management Upload Single File Upload Multiple Files View/Edit Uploaded Data Create Data Set View/Edit Data Sets	FLOCK Analyze Individual Files Analyze Data Sets	View/Edit Results FLOCK Centroid Files Cross Sample	Cross Sample Start Comparison	Help
iGenePattern (Gene expression analysis) Data Management Analysis Pipelines Analysis Modules View Results Help	Genetic Analysis B User Guide (PED) Run .PED Generation Generation Results User Guide (IGAT) Run Genetic Analysis Analysis Results	MHC Analysis B Upload Data Create Data Set Analyze Data Set SFVT Analysis Analysis Results User Guide	tagSNP Run tagSNP Results	

There are several analysis workflows supported in the MHC Analysis module and several options for data sources.

Overview of the data management and analysis options available in the MHC Analysis module



The menu tabs remind you of your options and allow you to navigate within the MHC Analysis module.

If you chose to upload a HLA typing file, you will see the following page:

Fields marked with an asterisk * are required.

Select the action *

- Validate alleles
Validation uses the [ANTTI](#) Tool to validate conformance to [IMGT/HLA version 2.8.3 nomenclature format and G- and P-Codes](#). Also, Validation converts the input file into IMGT/HLA version 3.* format since all options operate on that format.
- Validate and Generate SFVT Vector Files
- Validate and Reduce allele ambiguity
This [tool](#) was designed by Steven J. Mack et. al. and was developed with his invaluable co-operation.
The input requires the column 'Population Area' that specifies the population area ([F5](#)) associated with each row of data.
- Run [Pypop](#) HLA QC Pipeline
This pipeline validates the input file first and then runs Pypop. Please check out the '[Pypop Timings](#)' ([F5](#)).

Select the IMGT/HLA Output Version *

- Generated files will be formatted in **IMGT/HLA version 3.* format**
All the options above operate on IMGT/HLA version 3.* format and output all files in that format
- Generated files will be formatted in **IMGT/HLA version 2.* format** except for IMGT/HLA G- and P-codes
Conversion from IMGT/HLA version 3.* to version 2.* format uses the [ANTTI](#) Tool.

- ▶ The MHC Validation and SFVT Analysis tool requires a **project: "workspace"**
- ▶ It also requires a ".txt" (tab-separated text file) or a ".xls" (2003 Excel file) **HLA Typing File**.
- ▶ Please see the [User Guide](#) or contact the [help desk](#) for more information.

Select a project to store input and generated files *

HLA Typing File (.txt or .xls) *

[Download an example HLA Typing Data File \(.txt\) containing instructive errors](#)

[Download an example HLA Typing Data File \(Excel .xls\) containing instructive errors](#)

[Download the HLA Typing Data File Template \(Excel .xls\)](#)

Dataset Name *

Dataset Descriptor

NOTE: Clicking "Next" will upload the above file into the private project workspace of your chosen project, execute the action, and generate files.

1. Choose an analysis option.

2. Find your file on your computer and name the data set.

3. A pop up window displays your choices for confiraiton.



Analysis tasks can be monitored and the results downloaded.

Analysis / MHC Validation and SFVT Analysis / Create HLA Data Set / Display Submitted Request - Beta Release

Home | Upload Data | Create Data Set | Analyze Data Set | SFVT Analysis | Analysis Results | User Guide | Ambiguity Reduction Slides / Logic

Upload & Generate files → Display submitted request

Your "HLA Allele Validation" request was submitted successfully. Your analysis task ID is 3093.

Click the "Show Analysis History" button to proceed to the MHC Validation and SFVT Analysis History page. Once the task you requested is completed, you will be able to download your files.

Show Analysis History

You may monitor the status of your analysis task on the Analysis Result page..

Analysis / MHC Validation and SFVT Analysis / Analysis Results - Beta Release

Home | Upload Data | Create Data Set | Analyze Data Set | SFVT Analysis | Analysis Results | User Guide | Ambiguity Reduction Slides / Logic

This page is a list of the tasks you have submitted to the SFVT File Generation Tools. Click on a task ID to view detailed information about the task or to see the Please contact the help desk if you have any questions about the status of you analysis runs ([Contact Us](#))

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Task ID	Start Date	End Date	Task Type	Source Type	Input File	Generat. Name	Description	Status	IMGT Version
2965	2011-02-17	2011-02-17	Analyze VF	generated file	sfvt_test1_from_cp.txt	IMGT.HL. sfvt.test1 from		Error in Saving File	Release 3.00 (2010-04-01)
2965	2011-02-17	2011-02-17	Generate VF	generated file	sfvt_test_3_from_sub_IMGT.HL.	sfvt.test 3 from		Completed	Release 3.00 (2010-04-01)
2963		2011-02-17	Generate VF	generated file	sfvt_test_2_from_trp_hl	IMGT.HL. sfvt.test 2 from		Completed with V	Release 3.00 (2010-04-01)

Analysis / MHC Validation and SFVT Analysis / Analysis Results - Beta Release

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Data Set Details

SFVT Analysis Accession No: 838
 Generation Status: Completed with Validation Issues
 Data Set Name: example data from steve mask
 Description: validate
 Research Project: Test research project for v2.9.2
 Source File: [HLA Typing.xls](#)
 Source Type: uploaded file
 Source File Type: HLA Typing
 Alleles generated in format: IMGT/HLA Version 3 format (the ANTT generated file will be in the IMGT/HLA version different from that of the input file)
 IMGT Release: Release 3.00 (2010-04-01)
 SFVT Tool Information: HLA QC Pipeline (version 3.0)

The files associated with the allele validation results are:

Result Files	File name	Description	Download file
1.	Allele Validation File	Validated alleles are presented in this result file	Task-3087_Alele_validation_file.txt
2.	ANTT Validation File	The ANTT tools validation results are written to this file	Task-3087_ANTT_validation_file.txt
Summary files			
1.	Validation Summary	Summary of validation results and of any errors and exceptions	Task-3087_Alele_validation_summary.txt
2.	ANTT Validation Summary	Summary of ANTT validation results and of any errors and exceptions encountered by the ANTT tool	Task-3087_ANTT_validation_summary.txt
3.	Readme file	The files generated from the SFVT analysis task and their description	Task-3087_README.txt
Batch download files			
1.	MHC Analysis Results	Download all the above files including the source file as a single compressed archive/file	zip-file with generated name containing directory, Task-3087.Validation_result_files

An analysis task detail page allows you to review and download results.

Previous Cancel

If you chose the option to use HLA Typing data in ImmPort, the workflow is similar to the uploading your own file workflow with the additional option of choosing the locus(loci) to analyze.



Select Subjects and Experiment Samples from ImmPort projects or saved lists

You may select a previously saved subject list or choose subjects in your workspace(s).

option and then select a portion or all the records.

Accessible Projects with HLA Typing Results

ProjectID	Project Title	Project Type
3	TESTING: Bioinformatics Integration S4	RP
25	TESTING: Collaborative Projects	CP
101	CEU case subjects	RP
120	Testing GeneExp	RP
151	Research Project for ImmPort Version 1	RP

Load from selected project(s)

Saved Subject List having HLA Typing Result

ListID	List Name	List Description	Project ID
830	3378.3		68
831	3378.4		25
931	UAB AVA and 1 study 1 AVA and study 2 CNT	243	
1044	subs with hla re		266

Load from selected list(s)

Subject and Experimental Sample Data Having HLA Typing Results

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SubjectOrgAcctNum	ExpSampleAcctNum	Gender	AffectionStatus	Race	Ethnicity	AffectionPhenotype	OriginalProjTitle
SUB75387	ES108493	Male	Affected or Case	African American	Non-Hispanic	Autoimmunity	CEU case subjects
SUB75388	ES108494	Male	Affected or Case	Native Hawaiian or Pacific Islander	Native Indian	Autoimmunity	CEU case subjects

NOTE: The 'Select All' option does not add a check to the check box



Select the loci of interest

Fields marked with an asterisk * are required.

Select the action *

- Validate alleles
Validation uses the [ANIT](#) Tool to validate conformance to [IMGT/HLA version 2.8.3 nomenclature format and G- and P-codes](#). Also, Validation converts the input file into IMGT/HLA version 3.* format since all options operate on that format.
- Validate and Generate SPVT Vector Files
- Validate and Reduce allele ambiguity
This [tool](#) was designed by Steven J. Mack et. al. and was developed with his invaluable co-operation.
The input requires the column **'Population Area'** that specifies the population area ([FB](#)) associated with each row.
- Run [PyPop](#) HLA QC Pipeline
This pipeline validates the input file first and then runs PyPop. Please check out the **'PyPop Timings'** ([FB](#)).

Select the IMGT/HLA Output Version *

- Generated files will be formatted in **IMGT/HLA version 3.* format**
All the options above operate on IMGT/HLA version 3.* format and output all files in that format.
- Generated files will be formatted in **IMGT/HLA version 2.* format** except for IMGT/HLA G- and P-codes
Conversion from IMGT/HLA version 3.* to version 2.* format uses the [ANIT](#) Tool.

- The MHC Validation and SPVT Analysis tool requires a **project: "workspace"**
- It also requires a **".txt"** (tab-separated text file) or a **".xls"** (2003 Excel file) **HLA Typing File**.
- Please see the [User Guide](#) or contact the [help desk](#), for more information.

Select a project to store input and generated files *

HLA Typing File (.txt or .xls) *

[Download an example HLA Typing Data File \(.txt\) containing instructive errors](#)

[Download an example HLA Typing Data File \(Excel .xls\) containing instructive errors](#)

[Download the HLA Typing Data File Template \(Excel .xls\)](#)

Dataset Name *

Dataset Descriptor

NOTE: Clicking "Next" will upload the above file into the private project workspace of your chosen project, execute the action

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HLA Locus Name	Number of Subjects with Locus
<input type="checkbox"/> HLA-A	6
<input type="checkbox"/> HLA-B	6
<input type="checkbox"/> HLA-C	6
<input type="checkbox"/> HLA-DQA1	6
<input type="checkbox"/> HLA-DPB1	6
<input type="checkbox"/> HLA-DQA1	6
<input type="checkbox"/> HLA-DQB1	5
<input type="checkbox"/> HLA-DRB1	6
<input type="checkbox"/> HLA-DRB3	1

Sequence Feature Variant Type Analysis may be performed on data sets that have been validated and for which the Generate SFVT Vector File option was chosen.

Analysis / MHC Validation and SFVT Analysis / SFVT Analysis / Select SFVT File - Beta Release

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Select Vector File Result → Select Parameters → Display submitted request

Previous Next Cancel

Fields marked with an asterisk * are required.

The HLAVT Analysis requires a vector file result. See [User Guide](#) for more details.

Select an existing vector file generation result and then click Next*

Task ID	Start Date	End Date	Task Type	Source Type	Input File	Generat. Name	Description	Status	IMGT Version
2964	2011-02-17	2011-02-17	Generate VF	generated file	sfvt_test_3_from_sub	IMGT.HL sfvt test 3 from		Completed	Release 3.00 (2010-04-01)
2963	2011-02-17	2011-02-17	Generate VF	generated file	sfvt_test_2_from_rp_h	IMGT.HL sfvt test 2 from		Completed with V:	Release 3.00 (2010-04-01)



Data Set Details

SFVT Analysis Accession No: 846
 Generation Status: Completed with Validation Issues
 Data Set Name: HLA1_ver2_Orig_modifd.pheno.pop.txt
 Description: HLA1_ver2_Orig_modifd.pheno.pop.txt validate and gen SFVT
 Research Project: 0 revised example packages
 Source File: [HLA1_ver2_Orig_modifd.pheno.pop.txt](#)
 Source Type: uploaded file
 Source File Type: Custom HLA Typing
 Alleles generated in format: IMGT/HLA Version 3 format (the ANTT generated file will be in the IMGT/HLA version different from that of the Input file)
 IMGT Release: Release 3.00 (2010-04-01)
 SFVT Tool Information: Vector File Generator (version 3.0)

The files associated with the SFVT vector file generation results are:

Result files	File name	Description	Download file
Summary files			
1.	Validation Summary	Summary of validation results and of any errors and exceptions	Task-3098_AAllele_validation_sum
2.	Generation Summary		Task-3098_SFVT_generation_sum
3.	Readme file	The files generated from the SFVT analysis task and their description	Task-3098_README.txt
Batch download files			
1.	MHC Analysis Results	Download all the above files including the source file as a single compressed archive/file	zip-file with generated...

Previous Cancel

Cannot run SFVT analysis with no phenotype(s)

Cannot run SFVT analysis with no vector file(s)

Please note messages that indicate if your data set may not be used for SFVT Analysis.

Analysis / MHC Validation and SFVT Analysis / SFVT Analysis / Select Param

Home | Upload Data | Create Data Set | Analyze Data Set | SFVT Analysis | Analysis Results | User Guide

Select Vector File Result → Select Parameters → Display submitted request

Previous Next Cancel

You have chosen the following vector file generation task for SFVT Analysis:

Task ID: [2964](#)

Task Info: [2964

Generate VF

generated file

sfvt test 3 from sub list gen sfvt hla drb1

Completed

IMGT Release 3.00 (2010-04-01)]

Fields marked with an asterisk * are required.

- ▶ The SFVT Analysis tool requires a **project**.
- ▶ The **Dataset Name** is used to name the parameterization file generated in this workflow.
- ▶ Please see the [User Guide](#) or contact the [help desk](#) for more information.

Select a project to store generated files *

Dataset Name *

Dataset Descriptor

Select a phenotype column *

Select a statistical test *

Select Locus:*

Selected items: HLA-DRB1

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HLA Locus Name