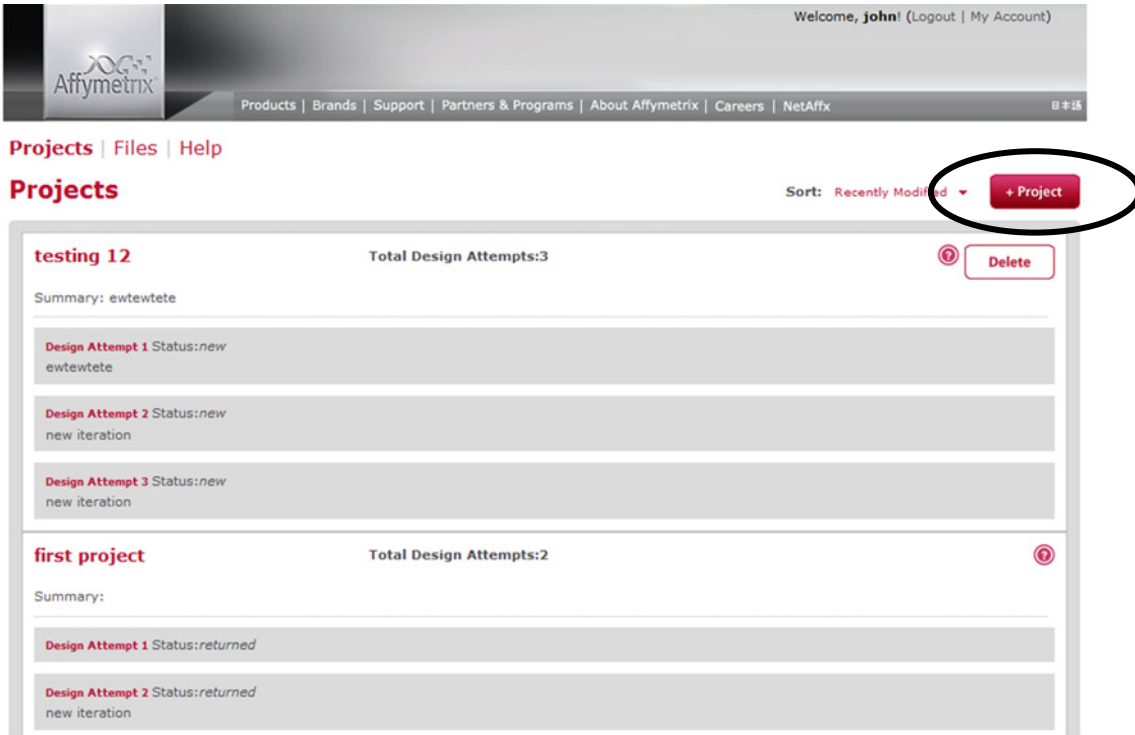


Quick Start Guide

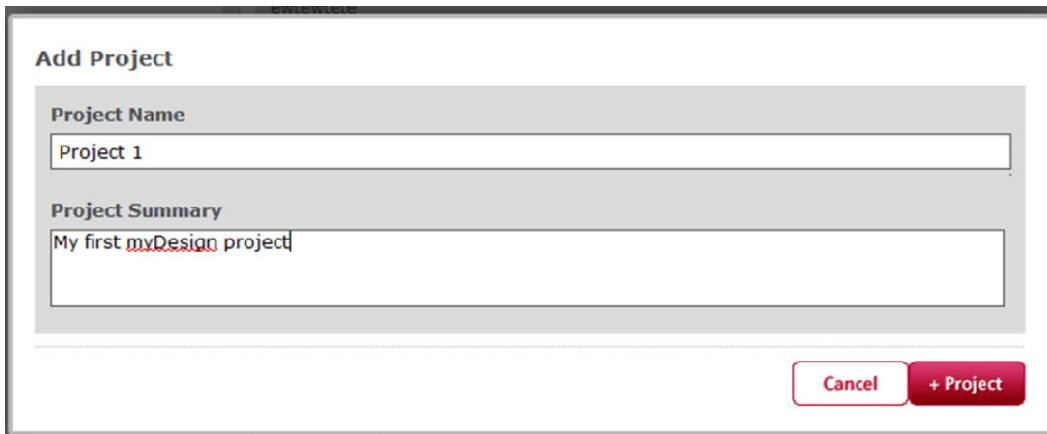
Axiom™ Design Center

1. Create a project
 - a. Click the "+ Project" button.



The screenshot shows the Affymetrix Axiom Design Center interface. At the top right, it says "Welcome, john! (Logout | My Account)". Below the navigation bar, there are links for "Projects | Files | Help". The main heading is "Projects" with a "Sort: Recently Modified" dropdown and a red "+ Project" button circled in red. Below this, there are two project cards. The first card is titled "testing 12" with "Total Design Attempts:3" and a "Delete" button. It has a summary "ewtwetete" and three design attempts, all with status "new" and "new iteration". The second card is titled "first project" with "Total Design Attempts:2" and a "Delete" button. It has a summary and two design attempts, both with status "returned" and "new iteration".

- b. Enter a project name (required) and project summary (optional).



The screenshot shows the "Add Project" form. It has two input fields: "Project Name" with the text "Project 1" and "Project Summary" with the text "My first myDesign project". At the bottom right, there are two buttons: "Cancel" and "+ Project".

2. Click the project name or "Design Attempt 1" to navigate to the project.

Welcome, **john!** (Logout | My Account)

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Projects | Files | Help

Projects Sort: Recently Modified + Project

Project 1 Total Design Attempts:1 Delete

Summary: My first myDesign project

Design Attempt 1 Status: new

3. Edit first Marker group by clicking the  icon.
 - a. (Optional): Restrict markers of interest by files.
 - i. Select the "+ File" button to select files.
 - ii. Select "change" to select a different file operator.

Marker Groups + Marker Group

Marker Group 1 Copy Delete

Marker Group Summary edit >
New Round

Step 1: Restrict Available Markers by File List (optional)

File Operation: **UNION Files** **change >**

Union Files: all the markers in the files in Set 1 are combined and the duplicates removed.

Set 1: + File

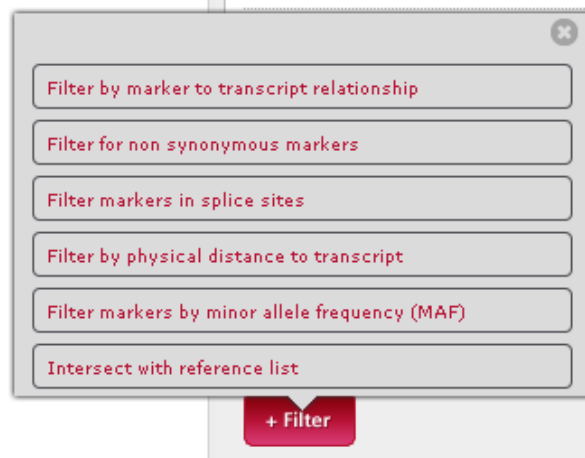
- b. Optional): Restrict markers of interest by filters.
 - i. Select "+ Filter" to choose filters of interest.

Step 2: Filter markers by Genetic and/or Annotation Information (optional)

Select the criteria to filter markers based on genetic and/or annotation information.

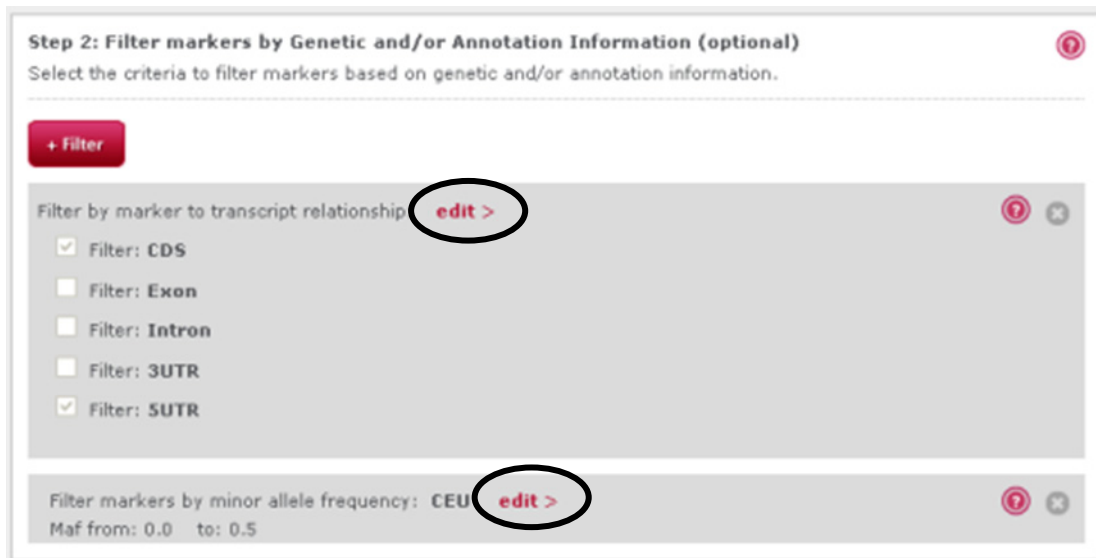
+ Filter

ii. Select filter type.

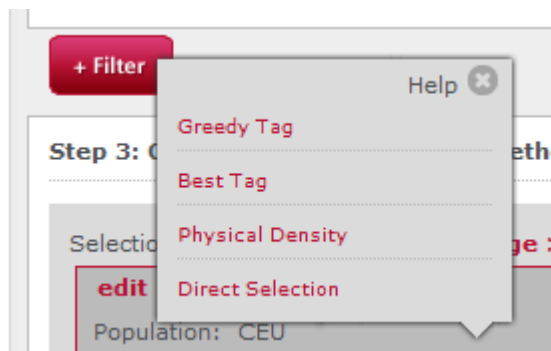
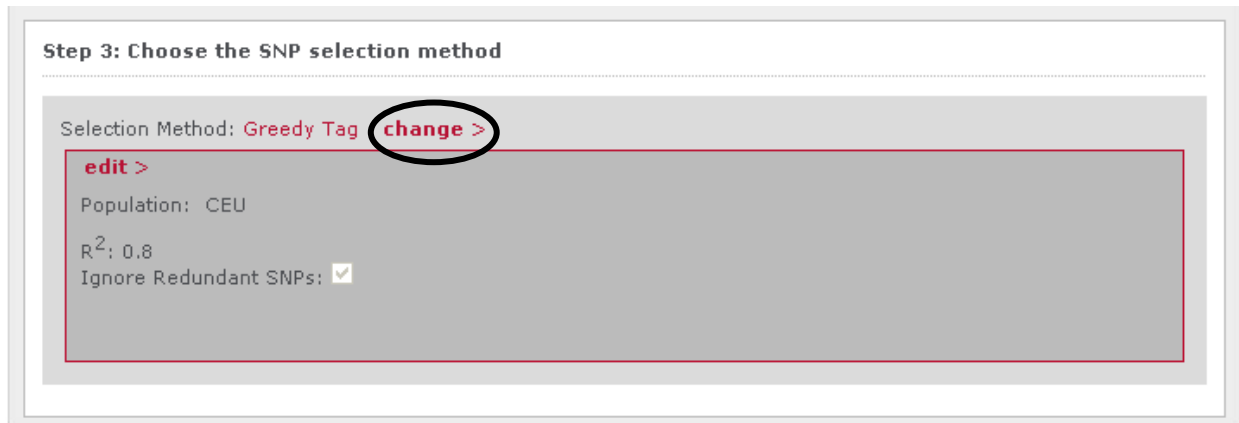


iii. Edit the parameters for the filters by clicking the appropriate "edit" links.

1. Note parameters within a filter group are combined with "OR" and across filter groups are combined with "AND."
2. The example shown below will return markers that are annotated as being in the (CDS OR the 5' UTR) AND have a minor allele frequency (MAF) between 0 and 0.5 in CEU.



- c. Choose the marker selection method by clicking the "change" link and selecting the appropriate algorithm from the pop-up menu.

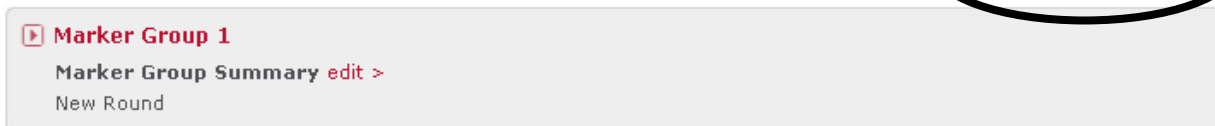


- i. Edit the parameters for the filters by clicking the appropriate "edit" links.



4. Create additional marker groups as needed by clicking the "+ Marker Group" button.

Marker Groups



5. Submit Design Attempt for processing

Project: Test Project 1 [edit >](#)
Project Summary [edit >](#)
This is a test project

Design Attempt 1

NEW | IN PROGRESS | RETURNED | FINALIZED

[Submit](#) [Copy](#) [Delete](#)

Design Attempt Summary [edit >](#)
This is a test project

Marker Groups [+ Marker Group](#)

Marker Group 1
Marker Group Summary [edit >](#)
New Round

- a. Select a population and r^2 threshold for using in calculating the coverage statistics for this design.
- b. Select "Submit" to begin the processing of the design attempt.

Submit

If you have finished defining the marker groups for this design attempt, select "Submit" to begin processing, otherwise select "Cancel" to continue defining marker groups.

You must select the population of interest and R^2 threshold for the reports summarizing the design which includes coverage estimates for the target snps.

Bioinformatics Services will contact you when your results are available in your project. If at any time you have questions about the process or your design, please email us at: Bioinformatics_services@affymetrix.com.

We look forward to working with you!

Please enter a population **ASI** and an R^2 value for your result report **0.8**

[Submit](#) [Cancel](#)

- 6. Examine results.
 - a. Design level

Design Attempt Summary

Results

Submission

[JDB-1.1.1.pdf download >](#) **Report PDF**

[JDB-1.1.1.bedfiles.zip download >](#) **Bed Files**

b. Marker group level

Marker Group 3
Marker Group Summary
New Round

Result
Click "download>" to download summary report and bed files associated with Marker Groups.

JDB-1.1.3.pdf download > **Report PDF**

7. Click "Finalize" for instructions on ordering arrays of current design.

Project: JDB-1
Project Summary

Design Attempt 1
Design Attempt Summary

NEW PENDING **RETURNED** FINALIZED

Copy **Finalize**

Results
Submission

- JDB-1.1.pdf download >
- JDB-1.1.bedfiles.zip download >

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