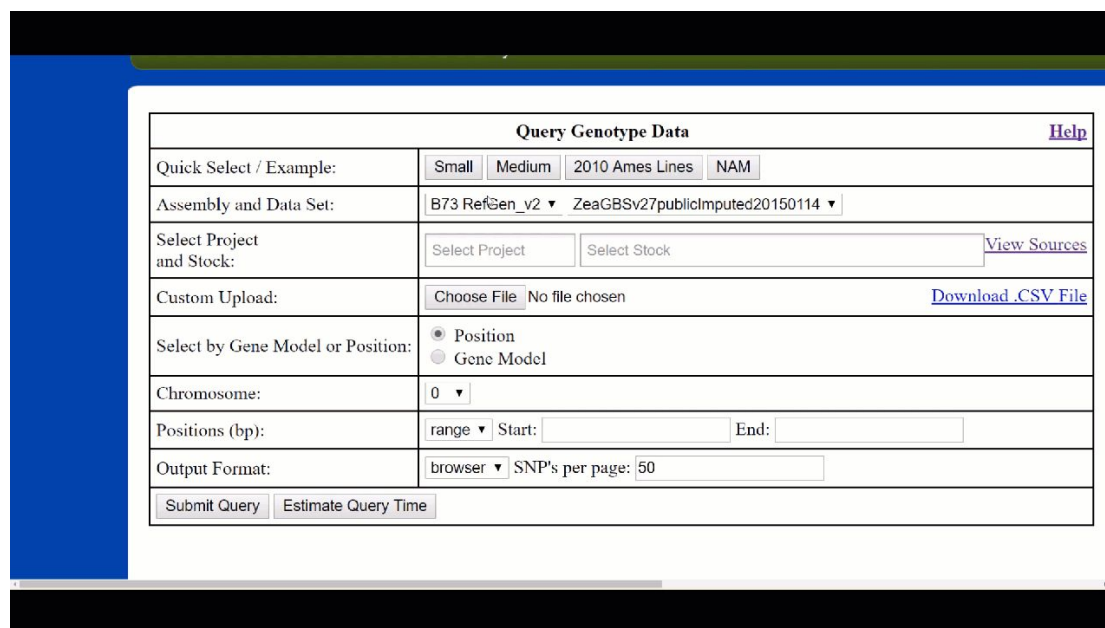


SNPiversity Step-by-Step Instructions

Step 1: Select desired assembly and data set



The screenshot shows a web form titled "Query Genotype Data" with a "Help" link in the top right corner. The form is organized into several rows, each with a label on the left and input fields on the right. The "Quick Select / Example:" row contains buttons for "Small", "Medium", "2010 Ames Lines", and "NAM". The "Assembly and Data Set:" row has two dropdown menus, the first showing "B73 RefGen_v2" and the second showing "ZeaGBSv27publicImputed20150114". The "Select Project and Stock:" row includes two text input fields labeled "Select Project" and "Select Stock", and a "View Sources" link. The "Custom Upload:" row features a "Choose File" button, the text "No file chosen", and a "Download .CSV File" link. The "Select by Gene Model or Position:" row has two radio buttons, "Position" (which is selected) and "Gene Model". The "Chromosome:" row has a dropdown menu showing "0". The "Positions (bp):" row includes a "range" dropdown, "Start:" and "End:" text input fields. The "Output Format:" row has a "browser" dropdown and "SNP's per page: 50" with a text input field. At the bottom, there are "Submit Query" and "Estimate Query Time" buttons.

Query Genotype Data		Help
Quick Select / Example:	<input type="button" value="Small"/> <input type="button" value="Medium"/> <input type="button" value="2010 Ames Lines"/> <input type="button" value="NAM"/>	
Assembly and Data Set:	<input type="text" value="B73 RefGen_v2"/> <input type="text" value="ZeaGBSv27publicImputed20150114"/>	
Select Project and Stock:	<input type="text" value="Select Project"/> <input type="text" value="Select Stock"/> View Sources	
Custom Upload:	<input type="button" value="Choose File"/> No file chosen Download .CSV File	
Select by Gene Model or Position:	<input checked="" type="radio"/> Position <input type="radio"/> Gene Model	
Chromosome:	<input type="text" value="0"/>	
Positions (bp):	<input type="text" value="range"/> Start: <input type="text"/> End: <input type="text"/>	
Output Format:	<input type="text" value="browser"/> SNP's per page: <input type="text" value="50"/>	
<input type="button" value="Submit Query"/> <input type="button" value="Estimate Query Time"/>		

The source dataset to be used for the query can be specified in the “Assembly and Data Set” section (row 2). There is one raw and one imputed data set available for each supported B73 reference genome (v2 and v3). Selecting an assembly will automatically update the available data set, as well as the projects and stocks available in step 2.

Step 2: Select project(s) and stock(s)

Query Genotype Data		Help
Quick Select / Example:	<input type="button" value="Small"/> <input type="button" value="Medium"/> <input type="button" value="2010 Ames Lines"/> <input type="button" value="NAM"/>	
Assembly and Data Set:	B73 RefGen_v2 ▾ ZeaGBSv27publicImputed20150114 ▾	
Select Project and Stock:	<input type="text" value="Select Project"/> <input type="text" value="Select Stock"/> View Sources	
Custom Upload:	<input type="button" value="Choose File"/> No file chosen Download .CSV File	
Select by Gene Model or Position:	<input checked="" type="radio"/> Position <input type="radio"/> Gene Model	
Chromosome:	0 ▾	
Positions (bp):	range ▾ Start: <input type="text"/> End: <input type="text"/>	
Output Format:	browser ▾ SNP's per page: <input type="text" value="50"/>	
<input type="button" value="Submit Query"/> <input type="button" value="Estimate Query Time"/>		

Upon selecting a dataset, a drop down menu will be populated in the “Select Project and Stock” section (row 3). This row can be used to specify desirable stocks (taxa) or projects used by the query. Upon typing, stock names with the exact match of the typed string will dynamically appear to help filter stocks.

Step 2 (alternative): Submit stocks via custom file upload

The screenshot shows a web interface titled "Query Genotype Data" with a "Help" link in the top right. The interface is organized into several rows of input fields and buttons:

- Quick Select / Example:** Includes buttons for "Small", "Medium", "2010 Ames Lines", and "NAM".
- Assembly and Data Set:** Features two dropdown menus, currently set to "B73 RefGen_v2" and "ZeaGBSv27publicImputed20150114".
- Select Project and Stock:** Contains a search box with "Imputation Test" entered, a "View Sources" link, and a secondary search box with "All Imputation Test" entered.
- Custom Upload:** Includes a "Choose File" button, the text "No file chosen", and a "Download .CSV File" link.
- Select by Gene Model or Position:** Has radio buttons for "Position" (selected) and "Gene Model".
- Chromosome:** A dropdown menu currently set to "0".
- Positions (bp):** Includes a "range" dropdown, "Start:" and "End:" input fields.
- Output Format:** A dropdown menu set to "browser" and "SNP's per page: 50".

At the bottom of the form are two buttons: "Submit Query" and "Estimate Query Time". The browser's address bar shows "example.com".

Alternatively, instead of entering stocks through the drop-down menu, one can also upload a custom file in the "Custom Upload" section (row 4). This field accepts files with .taxainfo, .stockinfo, or .csv extensions/formats. These are simply textfiles that delimit stocks by newlines. In contrast, .csv files allow the user to pin down projects and stocks (or just stocks, which degenerates into .taxainfo format). An example .csv file with comment annotations can be found on the same row under the "Download .CSV File" link. Example stocks for creating a custom file can be viewed through the "View Sources" link. **Any stocks selected through the drop-down menu in step 2 will be merged with the stocks in this file.**

Step 3: Specify genomic range by exact position

Query Genotype Data Help	
Quick Select / Example:	<input type="button" value="Small"/> <input type="button" value="Medium"/> <input type="button" value="2010 Ames Lines"/> <input type="button" value="NAM"/>
Assembly and Data Set:	B73 RefGen_v2 ▾ ZeaGBSv27publicImputed20150114 ▾
Select Project and Stock:	<div style="border: 1px solid gray; padding: 2px;"><input type="button" value="2010 Ames Lines"/> <input type="button" value="Imputation Test"/></div> <div style="display: inline-block; margin-left: 20px;"><input type="button" value="3167B"/> <input type="button" value="A131"/> <input type="button" value="All Imputation Test"/></div> View Sources
Custom Upload:	<input type="button" value="Choose File"/> example.csv Download .CSV File
Select by Gene Model or Position:	<input checked="" type="radio"/> Position <input type="radio"/> Gene Model
Chromosome:	0 ▾
Positions (bp):	range ▾ Start: <input type="text"/> End: <input type="text"/>
Output Format:	browser ▾ SNP's per page: 50
<input type="button" value="Submit Query"/> <input type="button" value="Estimate Query Time"/>	

The SNPiversity tool allows two different ways to specify the desired genomic query range. The positions in base pairs (bp) can manually be entered by selecting “Position” in the “Select by Gene Model or Position” section (row 5). The next step would be to specify the desired chromosome in the “Chromosome” section (row 6). Upon selection of a chromosome, the minimum and maximum positions of the selected chromosome will populate the “Start” and “End” fields in the “Positions (bp)” section (row 7) respectively. The user should select a subset that falls within this populated “Start” and “End” range (**typically several orders of magnitude smaller**).

Step 3 (alternative): Specify genomic range by Gene Model

Query Genotype Data Help	
Quick Select / Example:	<input type="button" value="Small"/> <input type="button" value="Medium"/> <input type="button" value="2010 Ames Lines"/> <input type="button" value="NAM"/>
Assembly and Data Set:	B73 RefGen_v2 ▾ ZeaGBSv27publicImputed20150114 ▾
Select Project and Stock:	<div style="border: 1px solid gray; padding: 2px;"><input type="button" value="2010 Ames Lines"/> <input type="button" value="Imputation Test"/></div> <div style="border: 1px solid gray; padding: 2px;"><input type="button" value="3167B"/> <input type="button" value="A131"/> <input type="button" value="All Imputation Test"/></div> View Sources
Custom Upload:	<input type="button" value="Choose File"/> example.csv Download .CSV File
Select by Gene Model or Position:	<input checked="" type="radio"/> Position <input type="radio"/> Gene Model
Chromosome:	0 ▾
Positions (bp):	range ▾ Start: <input type="text"/> End: <input type="text"/>
Output Format:	browser ▾ SNP's per page: <input type="text" value="50"/>
<input type="button" value="Submit Query"/> <input type="button" value="Estimate Query Time"/>	

Selecting the “Gene Model” option in the “Select by Gene Model or Position” section (row 5) will create a new row called “Select Gene Model and Offset”. This row allows the user to enter a desired Gene Model, and specify an offset that will be subtracted or added to the populated “Start” and “End” fields. The “Chromosome” and “Positions (bp)” section will be automatically updated to reflect the desired gene model and offset. Furthermore, a check mark(✓) will notify the user that the entered gene model is accepted by the tool. **Currently, only the first transcripts (ending in _T01) are accepted for the maize assembly.**

Step 4: Select output format and SNP's per page

Select Project and Stock:	<input type="text" value="2010 Ames Lines"/> <input type="button" value="x"/> <input type="button" value="Imputation Test"/> <input type="text" value="3167B"/> <input type="button" value="x"/> <input type="text" value="A131"/> <input type="button" value="x"/> <input type="text" value="All Imputation Test"/> <input type="button" value="x"/>	View Sources
Custom Upload:	<input type="button" value="Choose File"/> example.csv	Download .CSV File
Select by Gene Model or Position:	<input type="radio"/> Position <input checked="" type="radio"/> Gene Model	
Select Gene Model and Offset:	<input type="text" value="GRMZM2G136178_T01"/> <input checked="" type="checkbox"/> +/- (bp): <input type="text" value="2000"/>	
Chromosome:	<input type="text" value="5"/> ▾	
Positions (bp):	<input type="text" value="range"/> ▾ Start: <input type="text" value="173624110"/> End: <input type="text" value="173631497"/>	
Output Format:	<input type="text" value="browser"/> ▾ SNP's per page: <input type="text" value="50"/>	
<input type="button" value="Submit Query"/> <input type="button" value="Estimate Query Time"/>		

The last row in the table, section “Output Format” allows to specify both the output format and number of SNP’s to display per page.

Output format options are hapmap, vcf, or browser visualization (internally stored as a JSON file). The recommended way to use the tool is through the browser, since this option provides the user with the freedom to explore the data and download the results as a .csv file conveniently.

The **SNP’s per page** field is used to control the size of a typical results page digested by the browser. Some large queries can slow down the page or even cause the browser to crash, especially if a lot of stocks are selected. This field allows the user to limit the amount of work the browser needs to do in order to display a given results page.

Step 5 (optional): Estimate query time

Query Genotype Data Help	
Quick Select / Example:	<input type="button" value="Small"/> <input type="button" value="Medium"/> <input type="button" value="2010 Ames Lines"/> <input type="button" value="NAM"/>
Assembly and Data Set:	B73 RefGen_v2 ▾ ZeaGBSv27publicImputed20150114 ▾
Select Project and Stock:	<div style="border: 1px solid gray; padding: 2px;"><input type="button" value="2010 Ames Lines"/> <input type="button" value="Imputation Test"/></div> <div style="display: inline-block; margin-left: 20px;"><input type="button" value="3167B"/> <input type="button" value="A131"/> <input type="button" value="All Imputation Test"/></div> View Sources
Custom Upload:	<input type="button" value="Choose File"/> example.csv Download .CSV File
Select by Gene Model or Position:	<input type="radio"/> Position <input checked="" type="radio"/> Gene Model
Select Gene Model and Offset:	GRMZM2G136178_T01 <input checked="" type="checkbox"/> +/- (bp): <input type="text" value="2000"/>
Chromosome:	5 ▾
Positions (bp):	range ▾ Start: <input type="text" value="173624110"/> End: <input type="text" value="173631497"/>
Output Format:	browser ▾ SNP's per page: <input type="text" value="40"/>
<input type="button" value="Submit Query"/> <input type="button" value="Estimate Query Time"/>	

Having filled out all the sections, the last (optional) step before submission of the query is to estimate the time it takes to execute the query. This can be achieved by clicking on the “Estimate Query Time” button, which will spawn a box in the top-right corner of the screen summarizing the estimated time it takes to run the query.

Step 6: Submit the query

Query Genotype Data		Help
Quick Select / Example:	<input type="button" value="Small"/> <input type="button" value="Medium"/> <input type="button" value="2010 Ames Lines"/> <input type="button" value="NAM"/>	
Assembly and Data Set:	B73 RefGen_v2 ▾ ZeaGBSv27publicImputed20150114 ▾	
Select Project and Stock:	<div style="border: 1px solid gray; padding: 2px;"><input type="button" value="2010 Ames Lines"/> <input type="button" value="Imputation Test"/></div> <div style="display: inline-block; margin-left: 20px;"><input type="button" value="3167B"/> <input type="button" value="A131"/> <input type="button" value="All Imputation Test"/></div>	View Sources
Custom Upload:	<input type="button" value="Choose File"/> example.csv	Download .CSV File
Select by Gene Model or Position:	<input type="radio"/> Position <input checked="" type="radio"/> Gene Model	
Select Gene Model and Offset:	GRMZM2G136178_T01 <input checked="" type="checkbox"/> +/- (bp): 2000	
Chromosome:	5 ▾	
Positions (bp):	range ▾ Start: 173624110 End: 173631497	
Output Format:	browser ▾ SNP's per page: 40	
<input type="button" value="Submit Query"/> <input type="button" value="Estimate Query Time"/>		

Upon reviewing all the entered information, clicking the “Submit Query” button will allow the tool to double-check and verify the entered information. If successful, a loading message showing that the query is currently being processed should appear. Otherwise, an error message will appear asking the user to correct some information. The page will automatically redirect the user to the results page once the query has been completed.