

# Explicit Basic Tutorial

*“Explicit” is from the Latin: explain, unfold, extend, set forth, exhibit, disentangle*

A brief introduction to program capabilities and functions for new  
users of the Explicit software

# Table of Contents

*Note: Clicking on any level of the table of contents will take you directly to that section.*

<b>I. Begin a New Project.....</b>	<b>3</b>
A. Create a New Project .....	3
<b>II. Import OTU Data.....</b>	<b>5</b>
A. Import the OTU Data .....	5
<b>III. Import Metadata.....</b>	<b>7</b>
A. Import the Metadata.....	7
<b>IV. Save the Project .....</b>	<b>9</b>
A. Save the Project .....	9
<b>V. Adjust the Display .....</b>	<b>10</b>
A. Hierarchy, OTU, or Both .....	10
B. Counts, % of Library, % of Total .....	10
C. OTU displays .....	10
D. Hierarchy Level .....	10
E. Sort Libraries Based on a Metadata Tag (Anatomical Position) .....	11
<b>VI. Make an OTU Stacked Bar Chart.....</b>	<b>15</b>
A. Create an OTU Stacked Bar Chart of the Top 10 Most Prevalent Taxa .....	15
B. Change the Title and Label the Axes .....	18
C. Save the OTU Stacked Bar Chart as a Figure .....	19
<b>VII. Make a Pie Chart.....</b>	<b>23</b>
A. Create a Pie Chart of the Project Components .....	23
B. Make a Pie Chart with Sub-Wedges.....	26
C. Change Wedge Colors in the Pie Chart .....	29
<b>VIII. Create a Workspace .....</b>	<b>32</b>
A. Create a New Workspace.....	32
<b>IX. Apply a Filter.....</b>	<b>33</b>
A. Create a Filter .....	33
B. Set Up the Filter Parameters .....	34
<b>X. Beta Diversity (Morisita-Horn).....</b>	<b>42</b>
A. Create a Morisita-Horn Heatmap.....	42
<b>XI. Alpha Diversity .....</b>	<b>44</b>
A. Run a Good's Coverage Test .....	44
<b>XII. Two-Part Test.....</b>	<b>48</b>
A. Run a Two-Part Test .....	48
B. Set Up Filter Parameters .....	50
<b>XIII. Close the Project.....</b>	<b>62</b>

The data used in this tutorial come from an analysis of 16S ribosomal RNA gene sequences obtained from many distinct skin sites of healthy humans (Grice EA, et al. (2009) Topographical and Temporal Diversity of the Human Skin Microbiome. Science 324(5931): 1190–1192). To produce a concise tutorial, the data have been reduced from the original dataset and may not represent the findings of the original study.

## I. Begin a New Project

An Explicitet project is a single file that contains all of the OTU data, sample names (a.k.a. library names) and metadata that are to be analyzed as a unit. In other words, all data analyzed for one publication are drawn together into a single Explicitet project, independent of how many 454/Miseq runs are involved.

We will begin by creating a project and importing an OTU table. The tutorial example we have selected is based on the Human Skin Microbiome paper published by Grice, et al. This example was picked because it is relatively small and has a nice set of intuitive metadata available.

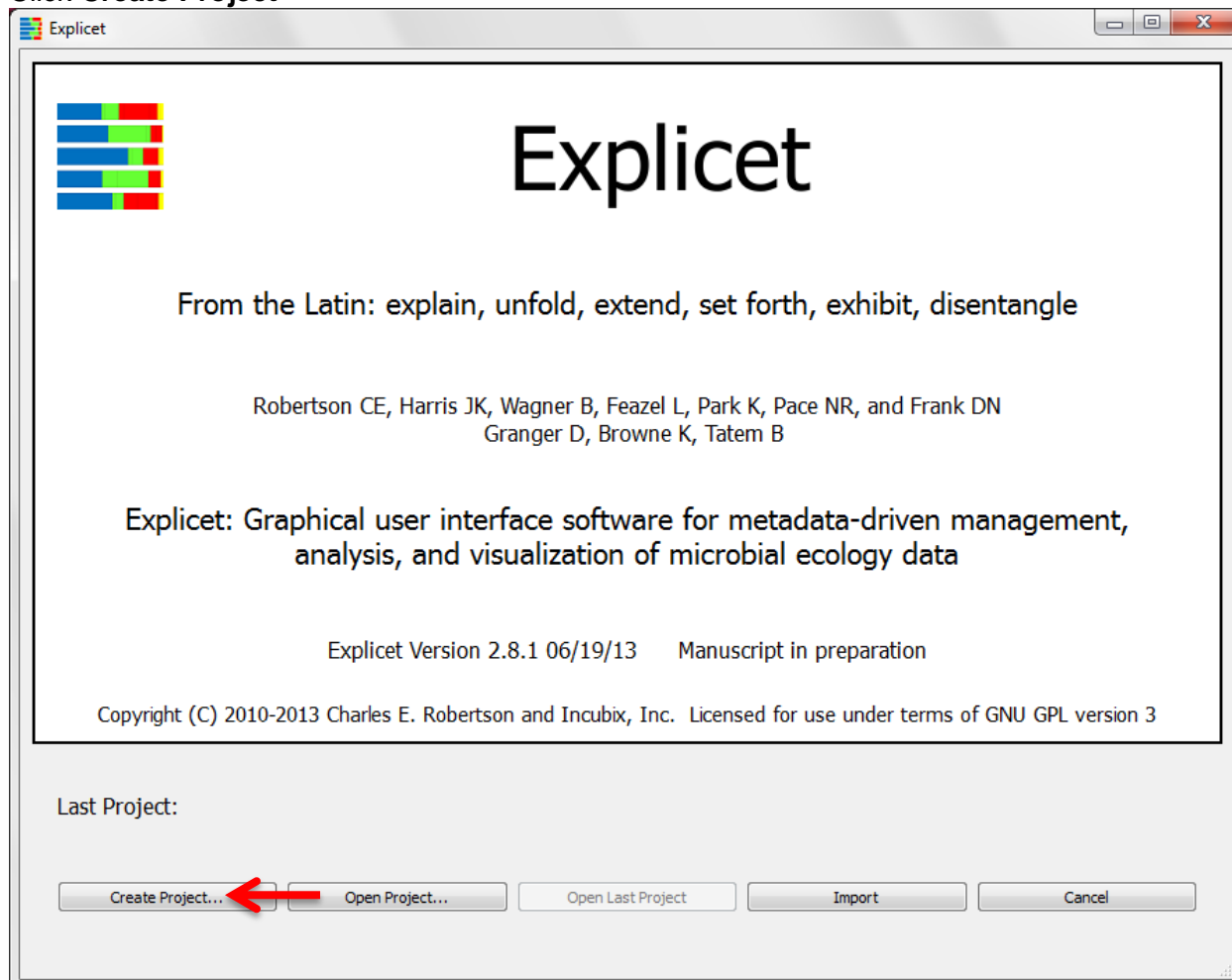
Please do not hesitate to ask questions or make suggestions via our online Explicitet forum. The Explicitet forum link can be found on our web site: [www.explicitet.org](http://www.explicitet.org).

### A. Create a New Project

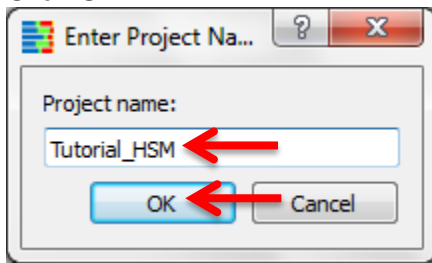
Open Explicitet

A pop-up window will open with several different options

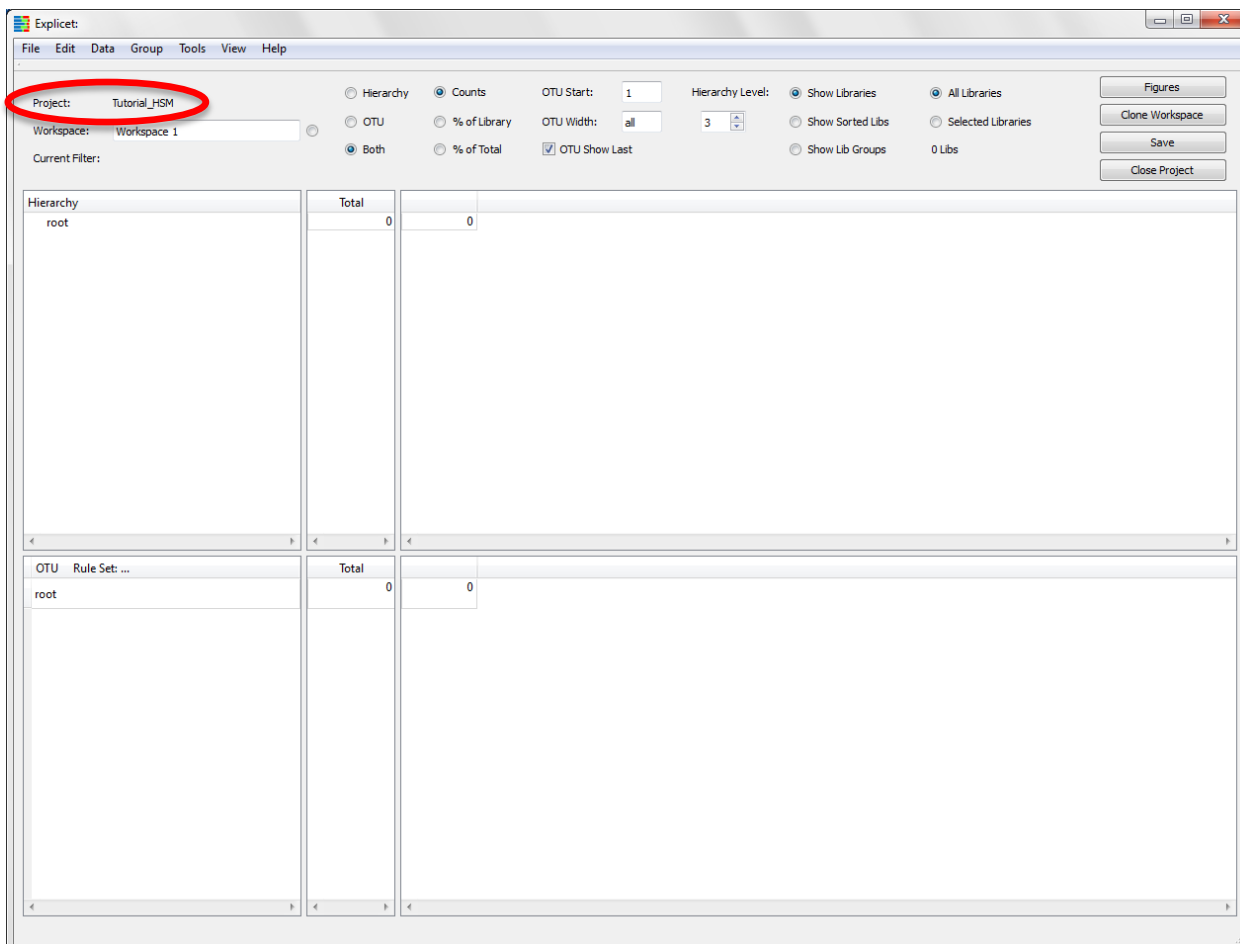
Click **Create Project**



Enter **Project Name**, "Tutorial\_HSM", when prompted  
Click **OK**



We now have a blank project in Explicitet, and the name of the current project is displayed in the upper left corner of the current workspace window.



## II. Import OTU Data

The first step in a new project is to import the data that comes out of the 16S pipeline runs into Explicit. In general, OTU tables are the most convenient form of data commonly generated by pipelines. For detailed information on how OTU tables are formatted, please see the Explicit Handbook. In short, OTU tables are a delimited file (tab-separated or comma-separated file) in which the rows are the OTUs, and the columns represent the number of each OTU seen in a given sample.

Explicit supports many other formats for importing the OTU data. For more details on the other OTU import formats, please see the Explicit Handbook. Later, we will discuss more data management tools that allow you to explore and modify subsets of the dataset without disrupting the larger project.

Now we will import the data that will belong to the new project. Once data are imported to a project, they are permanently associated with the project. Additional data can be incrementally imported to the same project. Thus, the Explicit project file can grow as a project evolves.

### A. Import the OTU Data

**File → Import → File → OTU Table Counts**

Select "Tutorial\_HSM\_OTU\_2\_Explicit"

Click **Open**

A pop-up window will open

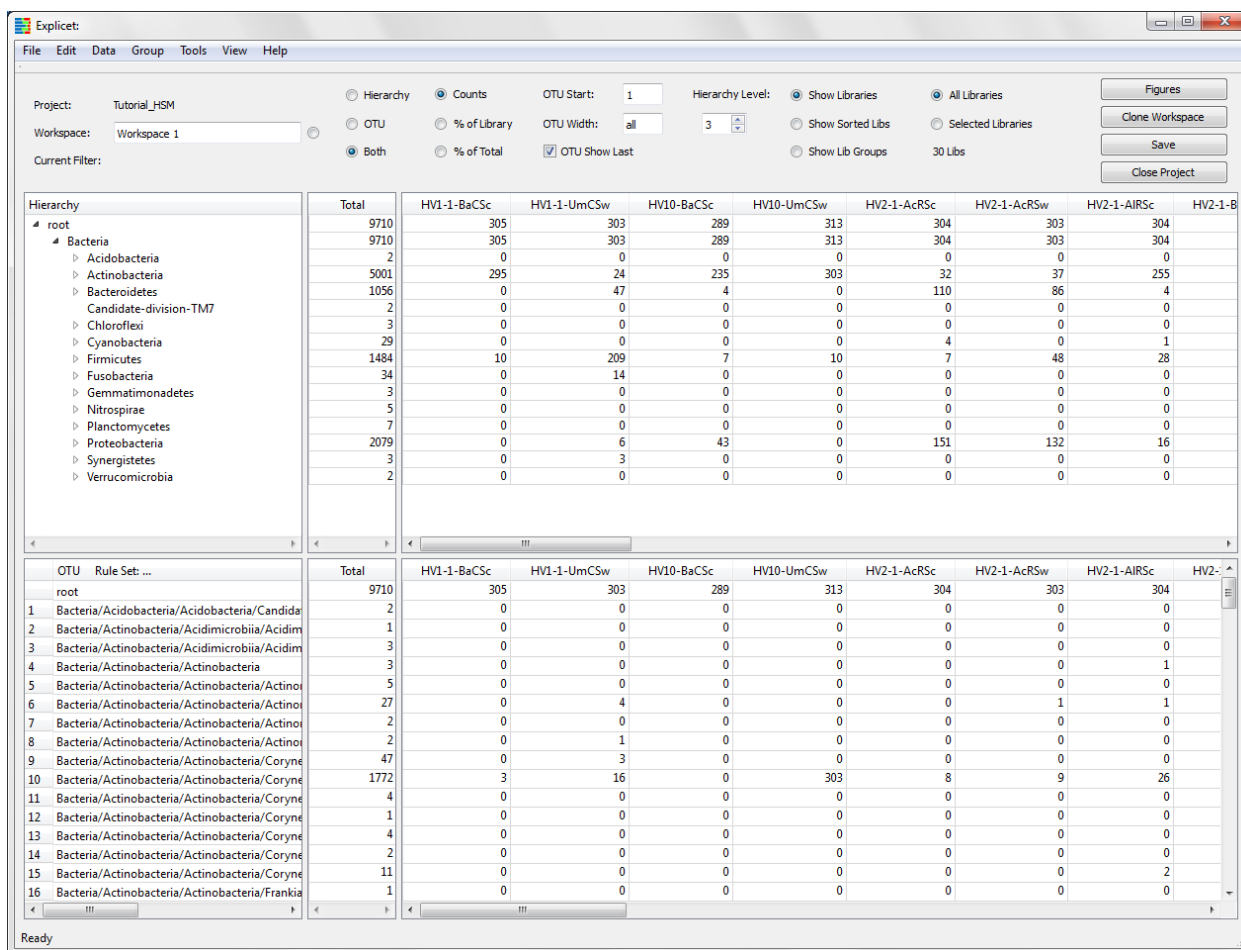
Click **Import**

A dialog box below will open

- On this dialog, Explicit tells the user how it is interpreting the rows and columns in the OTU table. The user needs to verify that Explicit has interpreted the table correctly. Note that in this case, Explicit is telling the user that it is not going to import column 2, "Total", as it will generate that sort of information itself. If Explicit gets it wrong, the user can adjust the interpretation using the provided pull down lists under **Column Type**.

	Column Name	Column Type
1	Taxonomy	OTU Name
2	Total	Do not import this column
3	HV1-1-BaCSc	Library Name and Count
4	HV10-BaCSc	Library Name and Count
5	HV2-1-BaCSc	Library Name and Count
6	HV3-1-BaCSc	Library Name and Count
7	HV4-1-BaCSc	Library Name and Count
8	HV5-BaCSc	Library Name and Count
9	HV6-1-BaCSc	Library Name and Count
10	HV7-BaCSc	Library Name and Count
11	HV8-BaCSc	Library Name and Count
12	HV9-BaCSc	Library Name and Count
13	HV1-1-UmCSw	Library Name and Count
14	HV10-UmCSw	Library Name and Count
15	HV2-1-UmCSw	Library Name and Count

The OTU data now appear in the current workspace window



### III. Import Metadata

Now we will import the metadata associated with the OTU data. Metadata refers to information about the sequence data - in this case, a description of the samples and subjects from which the sequence data were generated. In our nomenclature, a “library” represents all of the sequences generated from a single sample (multiple libraries may be generated from a given sample, for example through multiple PCR reactions, but for this tutorial we will assume a one-to-one relationship between libraries and samples). In this study, the metadata for each library includes the anatomical position, microenvironment description, sample acquisition method, and side of the body associated with each skin sample. Just like the OTU data, metadata need be imported only once (unless you choose to add more metadata) - imported metadata are also incorporated into the Explicit project file. For detailed information on how to format metadata files, please see the Explicit Handbook. In short, the metadata file is a tab-separated or comma-separated file organized by columns, generally prepared with a spreadsheet package like Microsoft Excel. The first column contains the names of the libraries in the dataset; all subsequent columns are metadata items and their values associated with each library.

#### A. Import the Metadata

**File → Import → Metadata**

Select “Tutorial\_HSM\_Metadata”

Click **Open**

A pop-up window will open

Make sure that the column containing the library name is selected

- Explicit searches all of the columns in the metadata file looking for the library names that were found when the taxonomy data were imported. In all but rare cases (e.g., when only a small portion of the sample names are present in the imported taxonomy data), Explicit will find the library column automatically.

Click **Import**

Import Metadata

Select the column which contains the Library name from 5 columns

Column	Sample Data
1 Lib	HV2-1-AcRSc
2 Anatomy	antecubital fossa
3 Symmetry	Right
4 SampleType	Scrape
5 Microenvironment	Moist

Libraries not found Libraries found

0 Libraries not found in the project for column Lib

All Libraries found

☐ Add missing libraries to the project

Metadata which does not match the Metadata in the project

☒ Check All ☐ Clear All

Metadef Name	Current Metadef Type	New Metadef Type	First Illegal Value	New Lower Bound	New Upper Bound	First New Enumerated Value	Change to new Def
--------------	----------------------	------------------	---------------------	-----------------	-----------------	----------------------------	-------------------

A new pop-up window will open which displays the imported metadata

Click **Done**

Metadata

All Libraries

Selected Libraries

30 Total Libraries

Export

Done

Defined Metadata

	Used	Name
1	30	Anatomy
2	30	Microenvironment
3	30	SampleType
4	30	Symmetry

Add ->

<- Remove

Assigned Metadata

	Library Name	Anatomy	Microenvironmen	SampleType	Symmetry
1	HV1-1-BaCSc	back	Sebaceous	Scrape	Center
2	HV1-1-UmCSw	umbilicus	Moist	Swab	Center
3	HV10-BaCSc	back	Sebaceous	Scrape	Center
4	HV10-UmCSw	umbilicus	Moist	Swab	Center
5	HV2-1-AcRSc	antecubital fossa	Moist	Scrape	Right
6	HV2-1-AcRSw	antecubital fossa	Moist	Swab	Right
7	HV2-1-AIRSc	alar crease	Sebaceous	Scrape	Right
8	HV2-1-BaCSc	back	Sebaceous	Scrape	Center
9	HV2-1-GcCSc	gluteal crease	Moist	Scrape	Center
10	HV2-1-UmCSw	umbilicus	Moist	Swab	Center
11	HV3-1-BaCSc	back	Sebaceous	Scrape	Center
12	HV3-1-RaRSw	retroauricular c...	Sebaceous	Swab	Right
13	HV3-1-UmCSw	umbilicus	Moist	Swab	Center
14	HV4-1-BaCSc	back	Sebaceous	Scrape	Center
15	HV4-1-UmCSw	umbilicus	Moist	Swab	Center
16	HV5-BaCSc	back	Sebaceous	Scrape	Center
17	HV5-UmCSw	umbilicus	Moist	Swab	Center
18	HV6-1-BaCSc	back	Sebaceous	Scrape	Center
19	HV6-1-UmCSw	umbilicus	Moist	Swab	Center

Copy

Paste

Note: Number of rows/columns to paste to must match the number of rows/columns copied. One cell may be copied then pasted to multiple cells.

Metadata Definition

Name:

Type: String that may be more than 8 characters

Upper Bound:

Optional

Lower Bound:

Optional

Status:

Enumerated Values: Optional

Add Value

Delete Value

Clear Values

Values

<New>

Add

Replace

Delete

Clear

For our example dataset, all of the library names were found in the metadata file, as indicated in the left-hand pane: i.e., the number under **Used (30)** matches the total number of libraries shown above the two panes (**30 Total Libraries**).

© 2012-2013 Charles E. Robertson and Incubix, Inc.

8

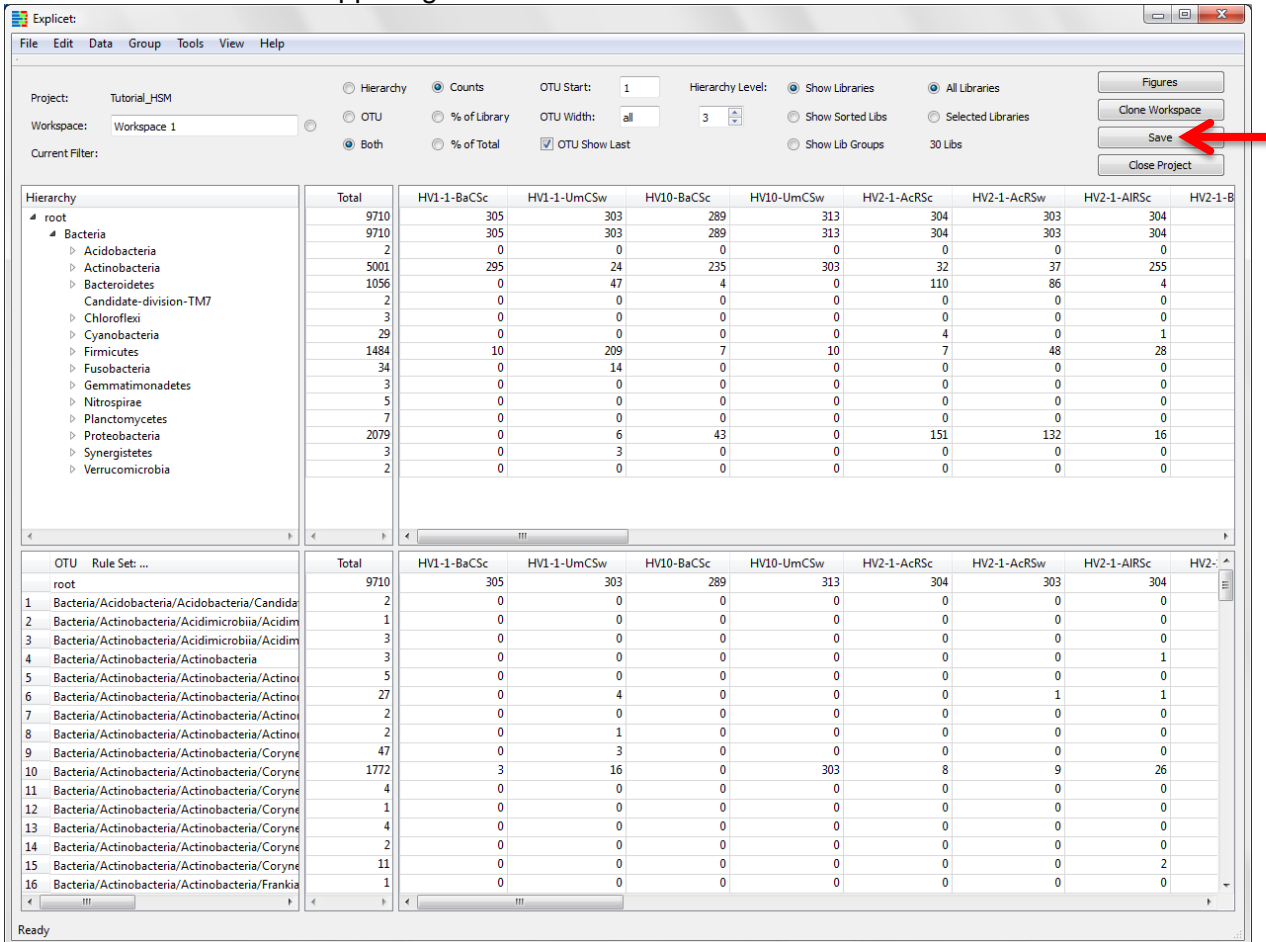


## IV. Save the Project

Now that all of the data associated with the project are imported, the file should be saved. Explicitet does not auto-save, so remember to save your project frequently!

### A. Save the Project

Click the **Save** button in upper right corner of the window



Enter desired project name and location when prompted

- The default file name is the project name with an “\_Explicitet\_Project” extension.

Click **Save**

All of the imported information is now saved within the project file.

## V. Adjust the Display

Now we will adjust the current workspace window display for ease of use (detailed demonstration on next page).

The screenshot shows a settings panel for a workspace. It includes fields for Project (Tutorial\_HSM), Workspace (Workspace 1), and Current Filter. Below these are four main sections labeled A, B, C, and D. Section A contains radio buttons for Hierarchy, OTU, and Both. Section B contains radio buttons for Counts, % of Library, and % of Total. Section C contains input fields for OTU Start (1) and OTU Width (all), and a checkbox for OTU Show Last. Section D contains a dropdown for Hierarchy Level (3). To the right of these sections are additional options: Show Libraries, Show Sorted Libs, Show Lib Groups, All Libraries, Selected Libraries, and 30 Libraries.

### A. Hierarchy, OTU, or Both

**Both** is the default

This option creates two panes on workspace screen; the upper pane shows the Hierarchy, and the lower pane shows the OTUs. The Hierarchy pane allows exploration of the dataset in a “big tree” hierarchical context, whereas the OTU pane shows a more literal view of the data from the 16S pipeline. The information in the OTU pane is used for input into the statistics and most of the plots (except for pie charts, which are graphical depictions of the Hierarchy pane).

### B. Counts, % of Library, % of Total

Select **% of Library** (**Counts** is the default)

While Counts is the default (raw sequence data counts in integers), % of Library tends to be more useful. % of Library is relative abundance, which is important since the total number of Counts received from any library is beyond our control. Using the relative abundance, or % of Library, allows us to fairly compare libraries. Otherwise, the libraries that have a very large number of counts will skew conclusions.

### C. OTU displays

These options control the manner in which the taxonomy lines are displayed on the OTU pane.

**OTU Start:** 1 is the default

This is the position (counting from one) of the first taxonomic category that the user desires to be displayed. In our tutorial example, the taxonomy lines in the OTU pane display will start with Bacteria (Bacteria is the “1<sup>st</sup> lineage level”).

Set **OTU Width** to 2 (“all” is the default)

This is the number of positions on the line to be displayed. To save space on the screen, now only 2 taxonomic levels will be displayed in the OTU taxonomy line. Taxonomies with more than 2 levels will be shown with an embedded ellipsis; for example, “Bacteria/Actinobacteria/Acidimicrobiia/Acidimicrobiales” becomes “Bacteria/Actinobacteria/.../Acidimicrobiales”.

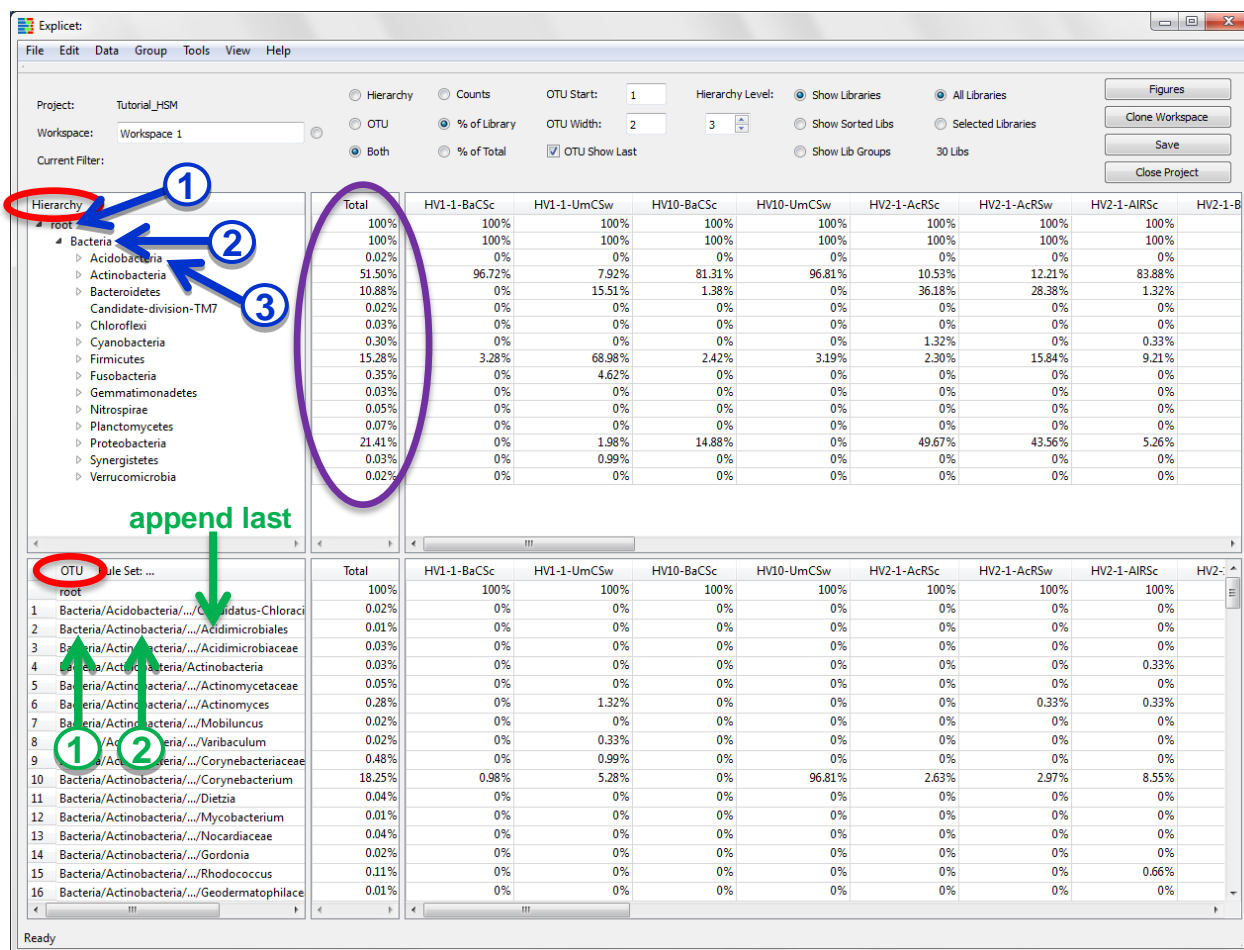
**OTU Show Last** on is the default

This option appends the last item in the taxonomic line onto a truncated OTU lineage.

### D. Hierarchy Level

**Hierarchy Level:** 3 is the default

This controls the number of taxonomic categories that will be opened on the hierarchy pane.



Since libraries are often cryptically named, it's nice to add a readable metadata tag in the view so that we have some context for the libraries we are viewing. To do this, we will sort the libraries in the view based on anatomical position.

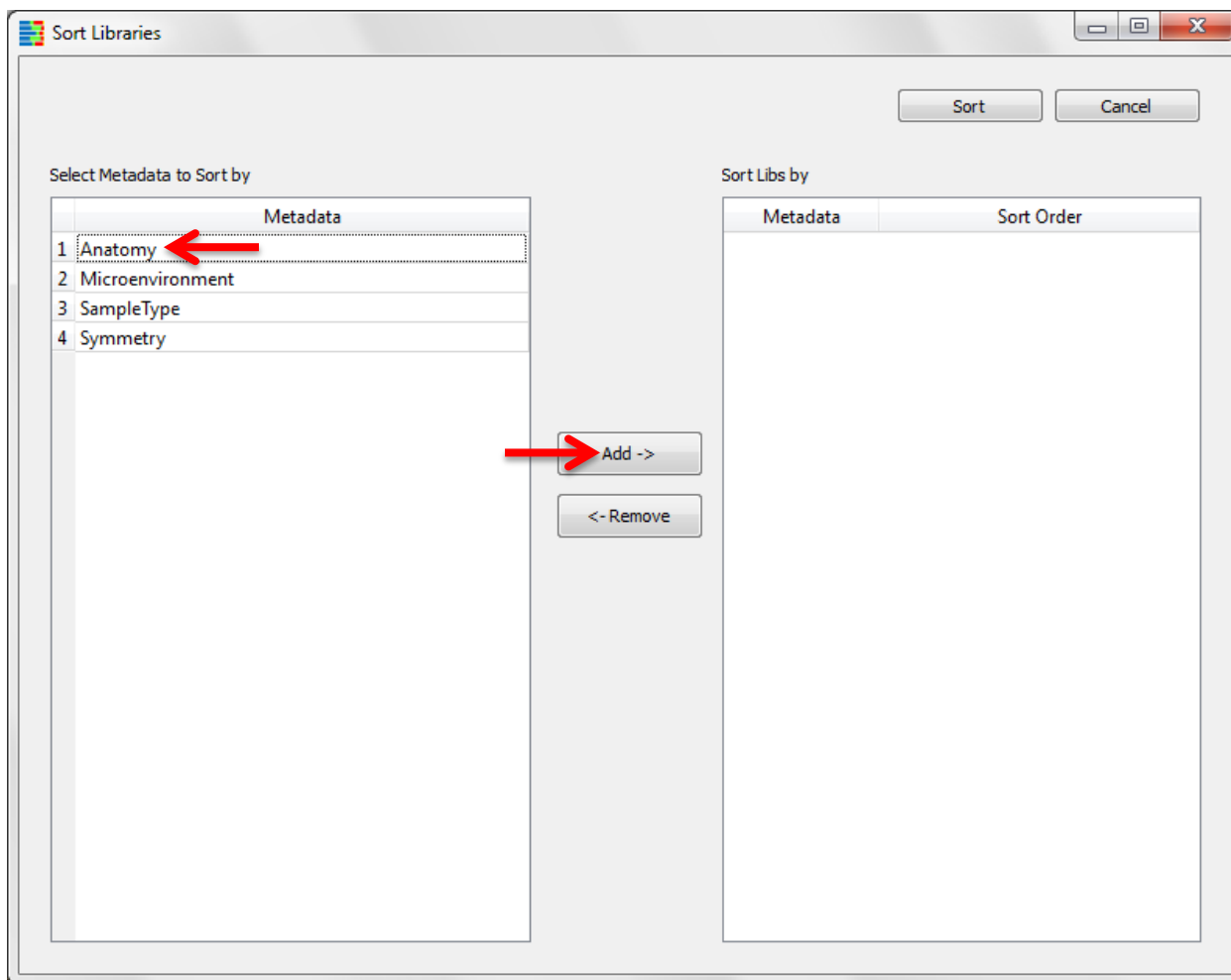
## E. Sort Libraries Based on a Metadata Tag (Anatomical Position)

### View → Sort Libraries

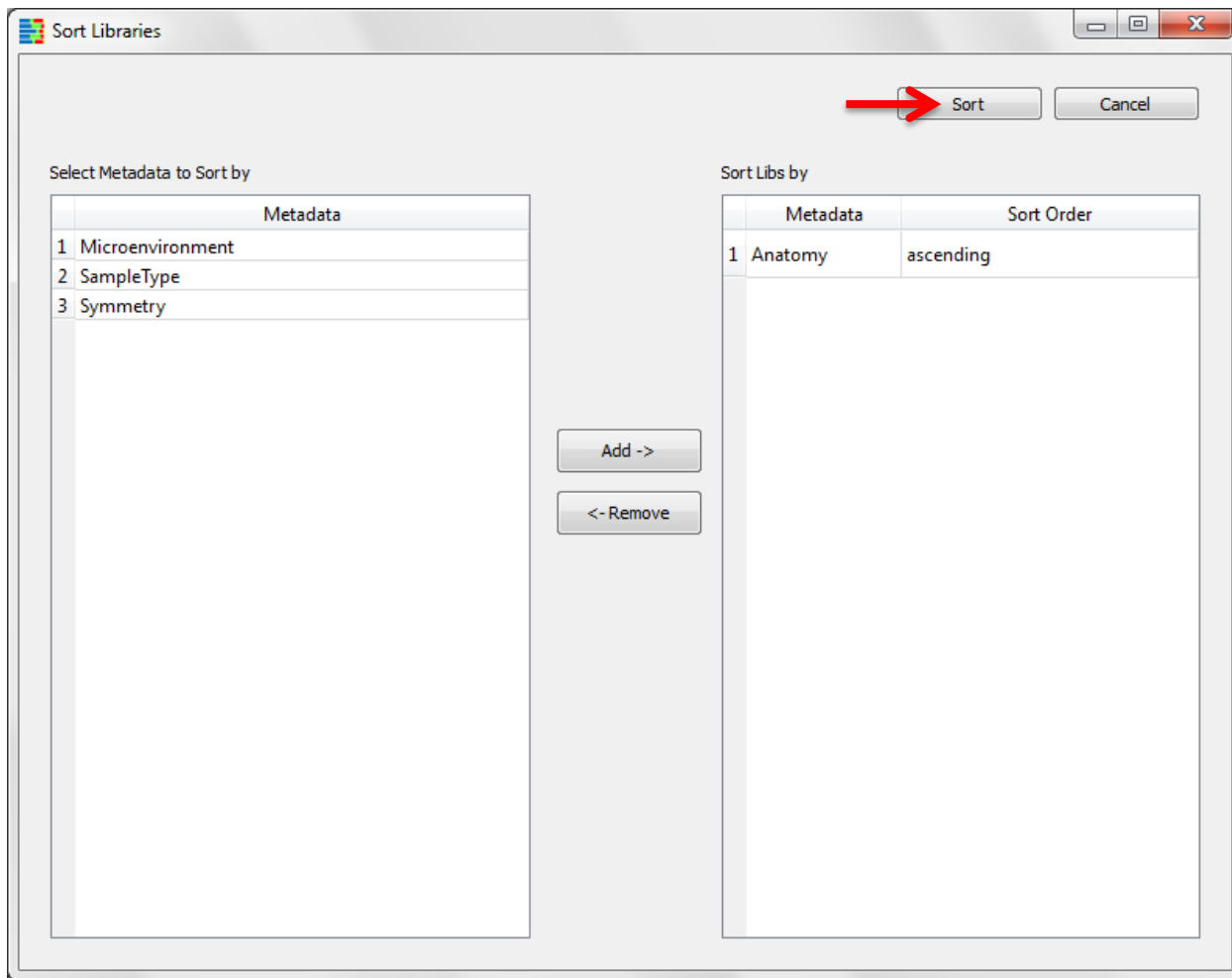
A pop-up window will open

In left panel, select **Anatomy**

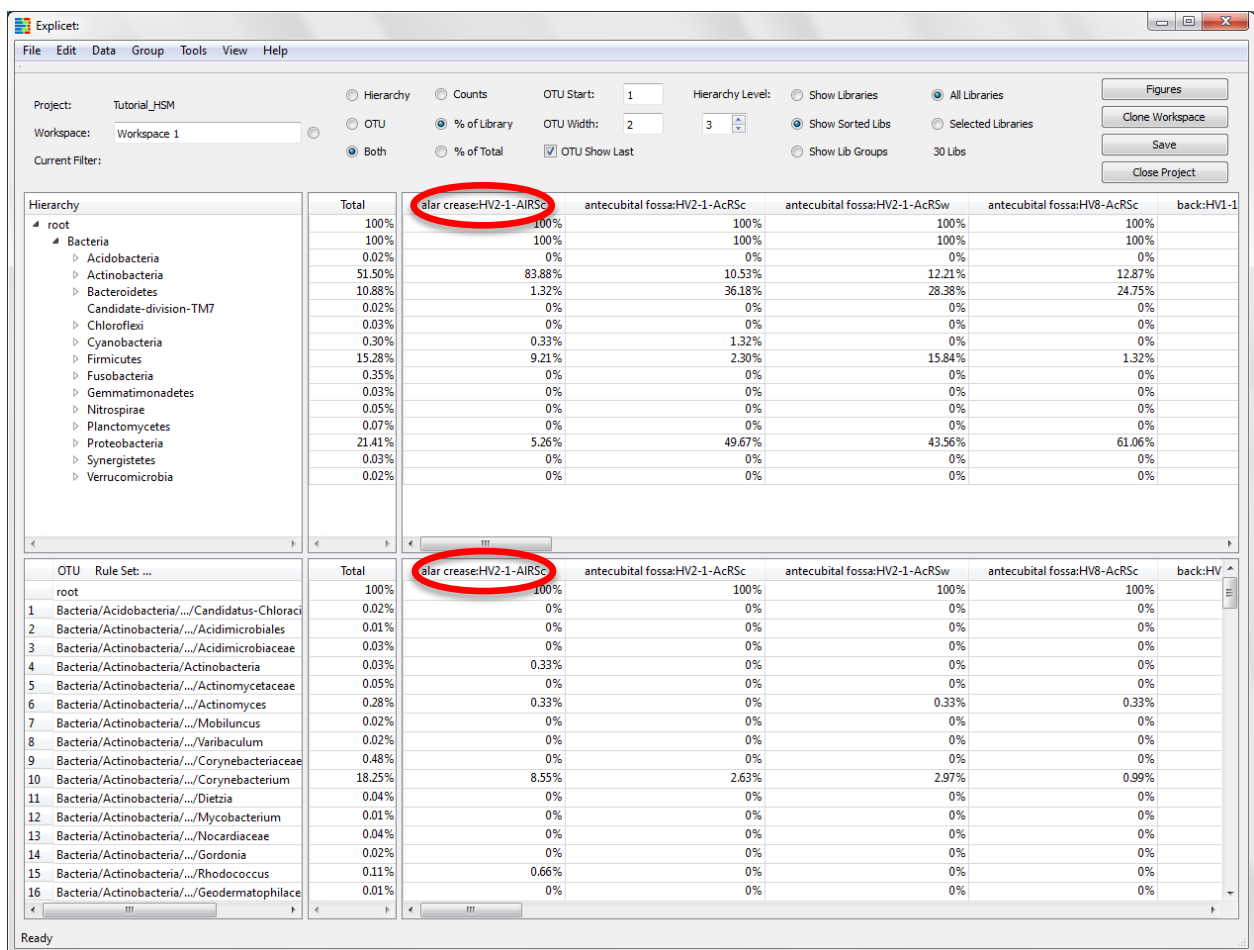
Click **Add** button between panels



Name of metadata descriptor will appear in the right panel  
Click **Sort**



Pop-up window will disappear  
Both the hierarchy and OTU tables are now sorted by anatomical position



## VI. Make an OTU Stacked Bar Chart

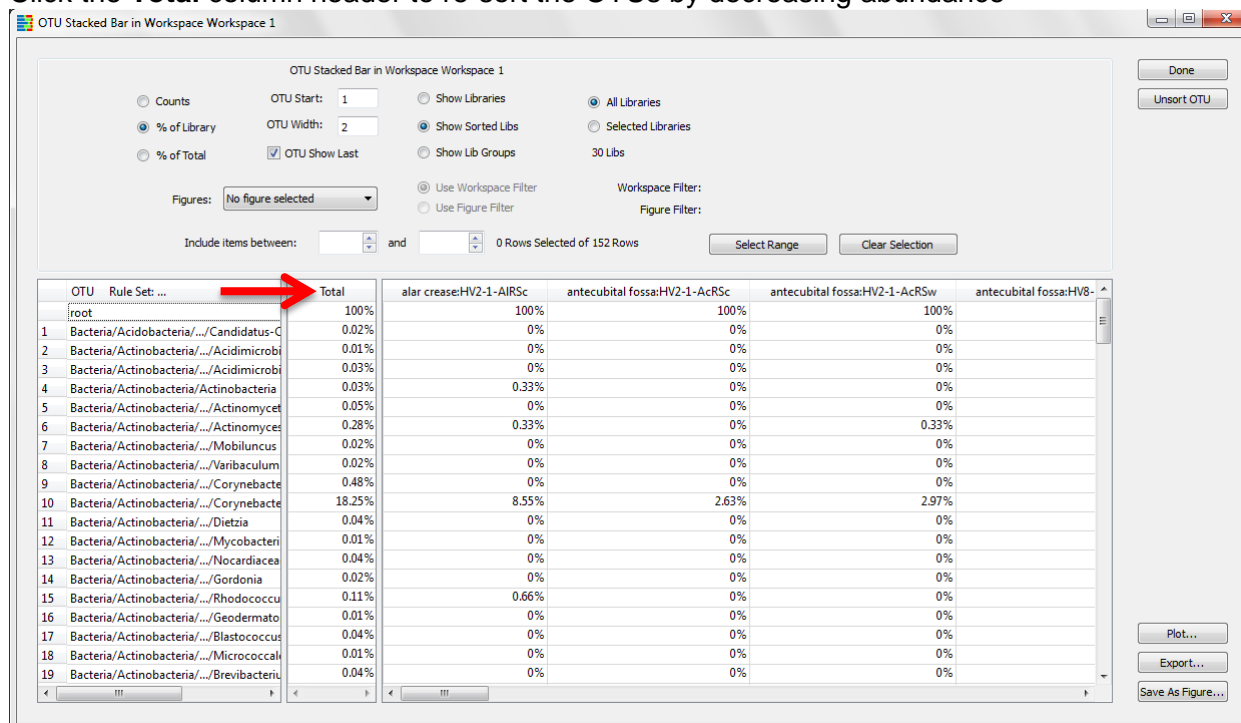
Before diving into a detailed analysis, generating an overview of the dominant organisms that exist in the dataset can be useful. One way to do this is through an OTU stacked bar chart.

### A. Create an OTU Stacked Bar Chart of the Top 10 Most Prevalent Taxa

#### Tools → Plot → OTU Stacked Bar

A new window will appear with the OTU data available in the workspace

Click the **Total** column header to re-sort the OTUs by decreasing abundance



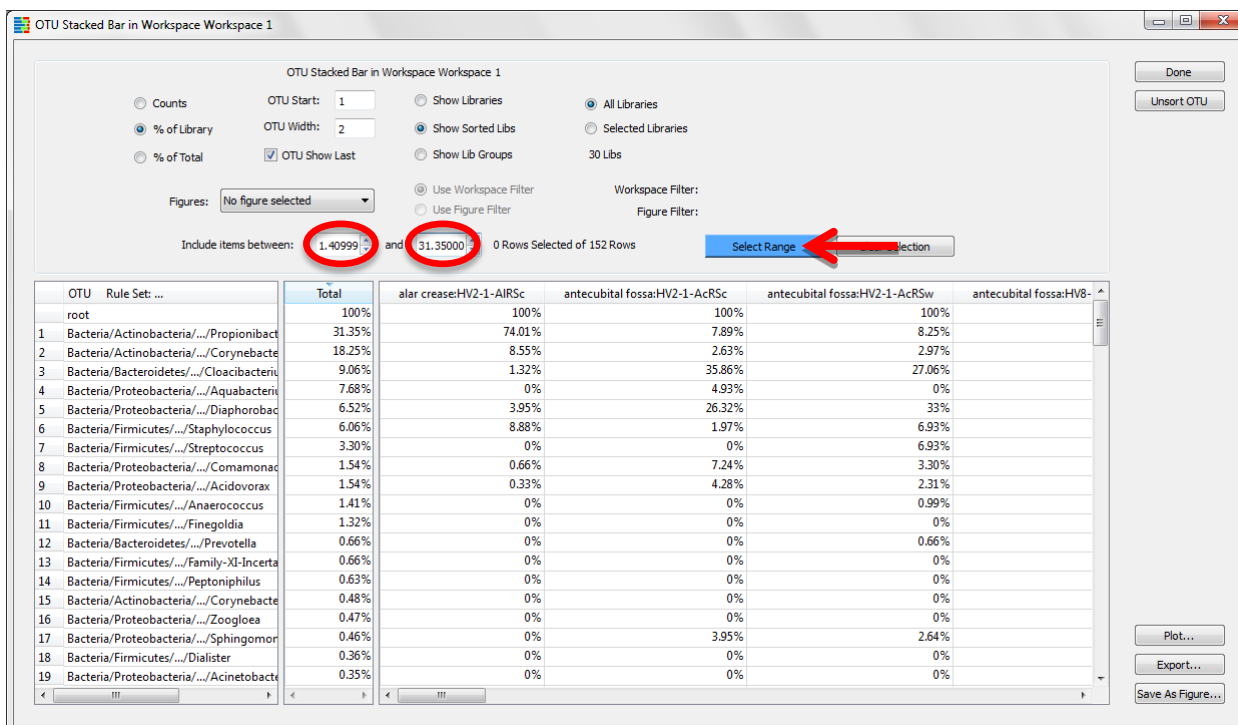
To display only the top 10 taxa in the project, note that the **Total** value of the 1<sup>st</sup> OTU in the column is 31.35

Note that the **Total** value of the 10<sup>th</sup> OTU in the column is 1.41

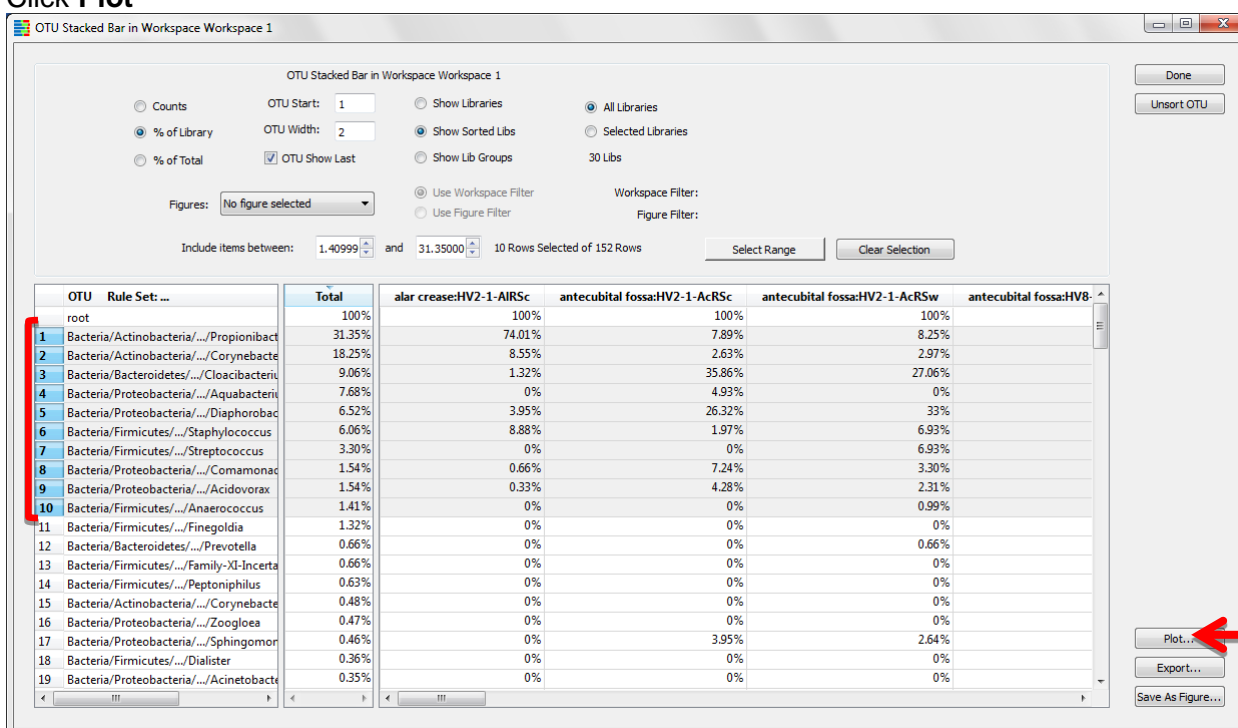
In the **Include items between** field, enter “1.41” into the first box (the lower bounding limit)

In the **Include items between** field, enter “31.35” into the second box (the upper bounding limit)

Click **Select Range**



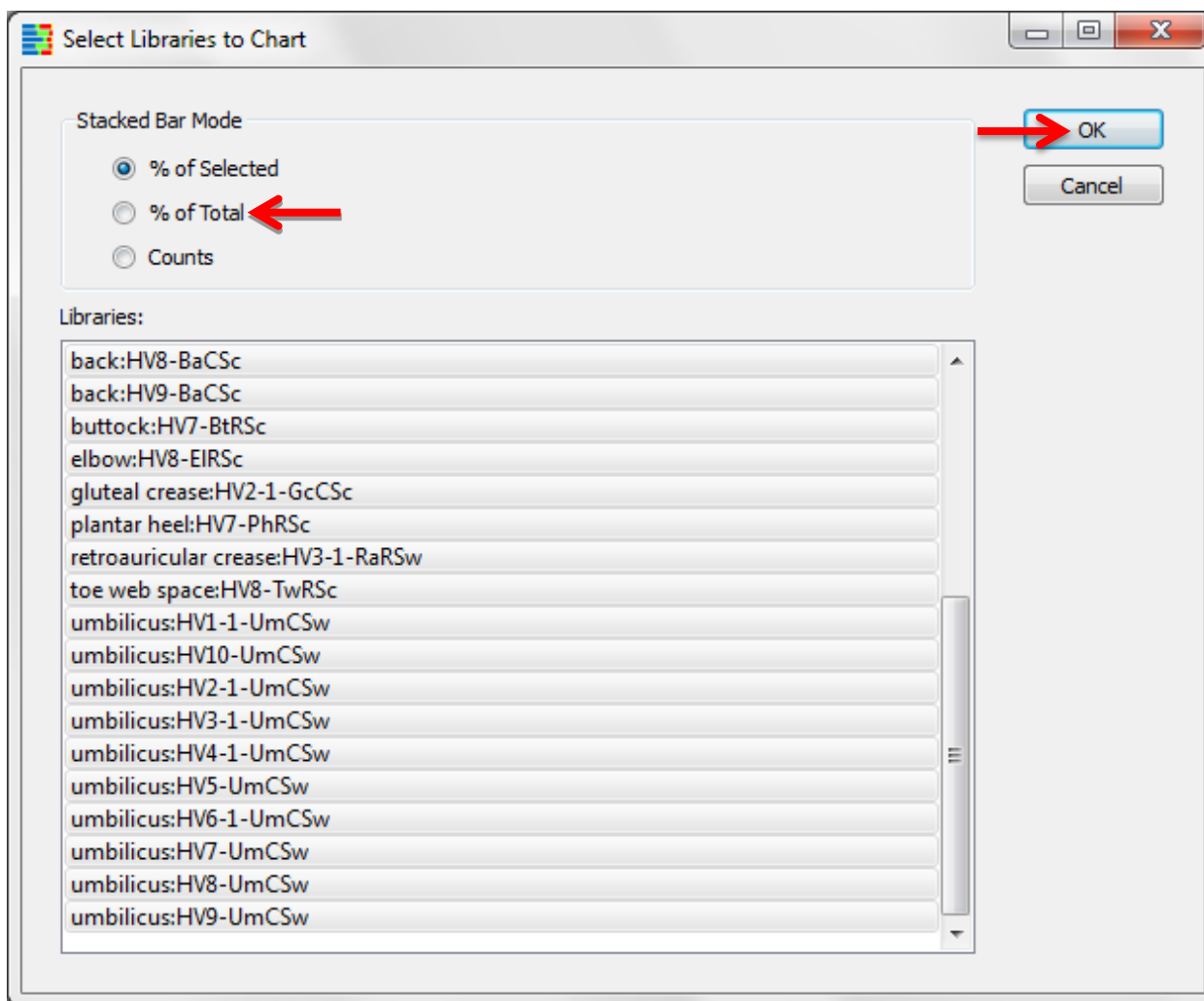
The top 10 OTUs are now highlighted  
 Click **Plot**



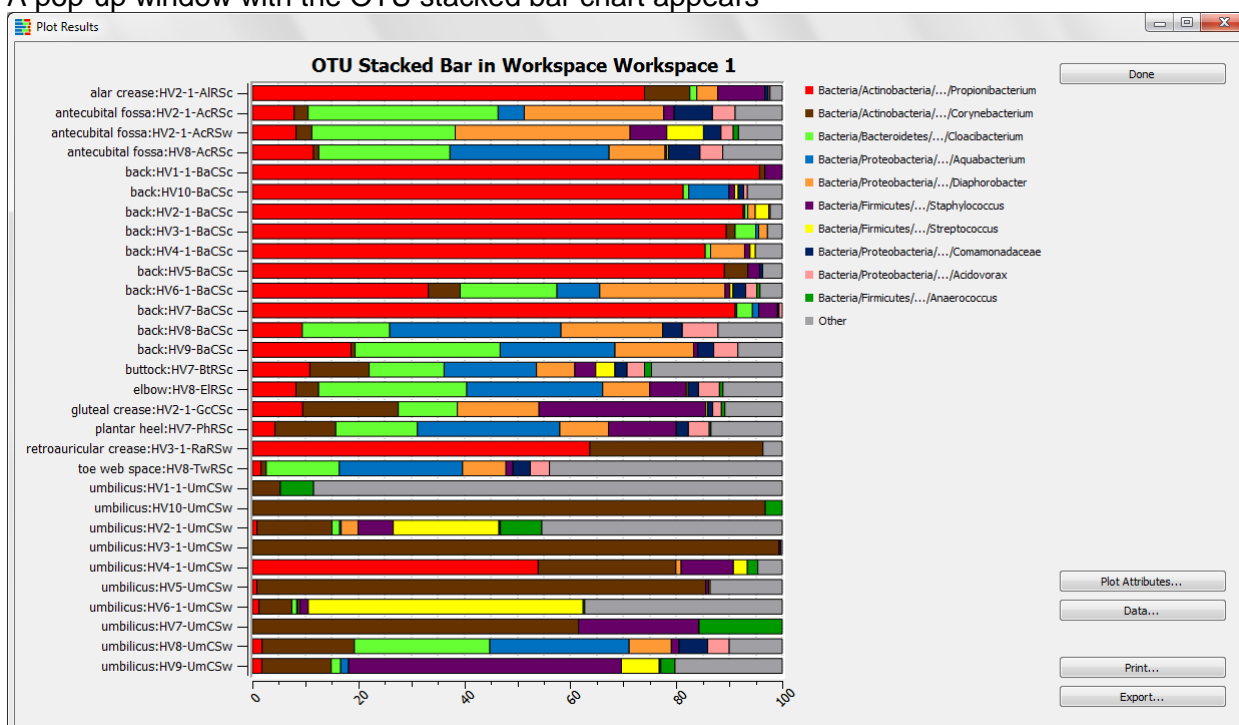
A new window will appear containing stacked bar display options

To create a stacked bar chart which displays a big picture of the project components, select **% of Total**  
 Click **OK**





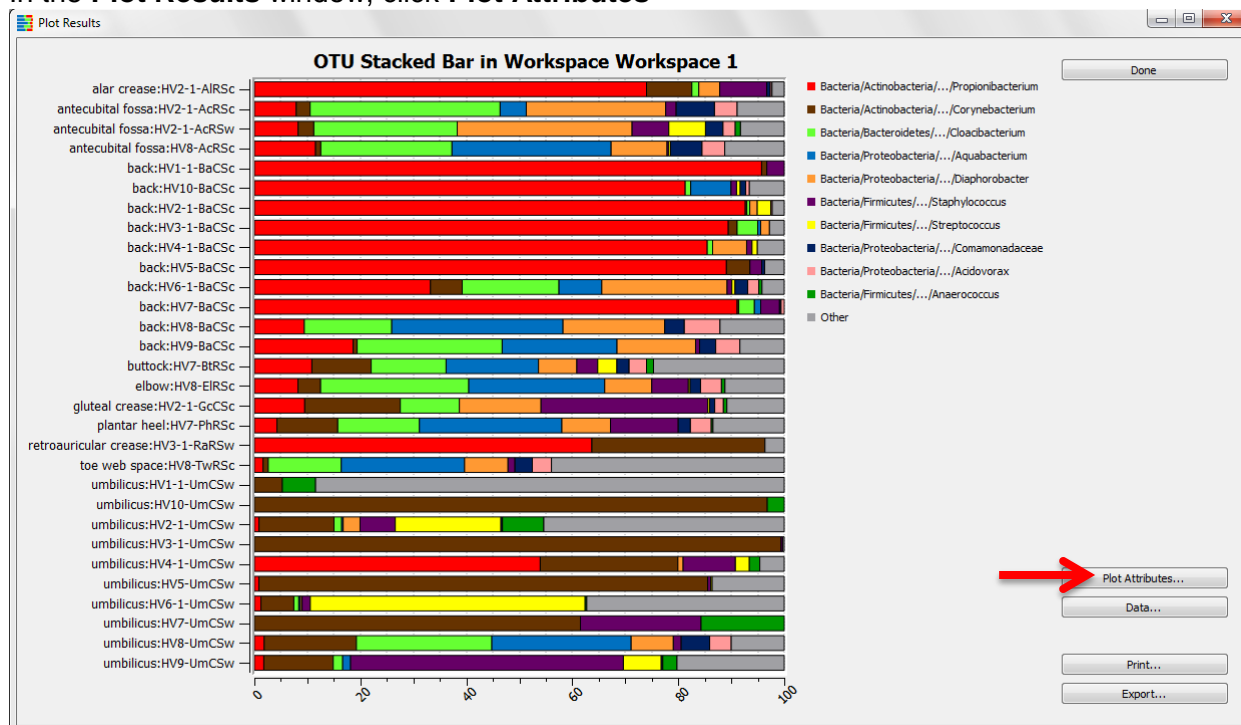
A pop-up window with the OTU stacked bar chart appears



We will now change the default title of the stacked bar chart and add axis labels.

## B. Change the Title and Label the Axes

In the **Plot Results** window, click **Plot Attributes**



A pop-up window will appear

On the **Titles/Axes** tab, enter “Top 10 Taxa” into the **Plot** field

Enter “OTU % of Total” into the **X Axis** field

Enter “Library Name” into the **Y Axis** field

Click **Save**

**Plot Attributes**

Titles/Axes   Grid   Colors   Stacked Bar   Size

Titles

Plot: Top 10 Taxa

X Axis: OTU % of Total

Y Axis: Library Name

☒ Show Library Name

X Axis

☒ Autoscale

Min Value: 0

Max Value: 100

Step Size: 0

Label Rotation: -45

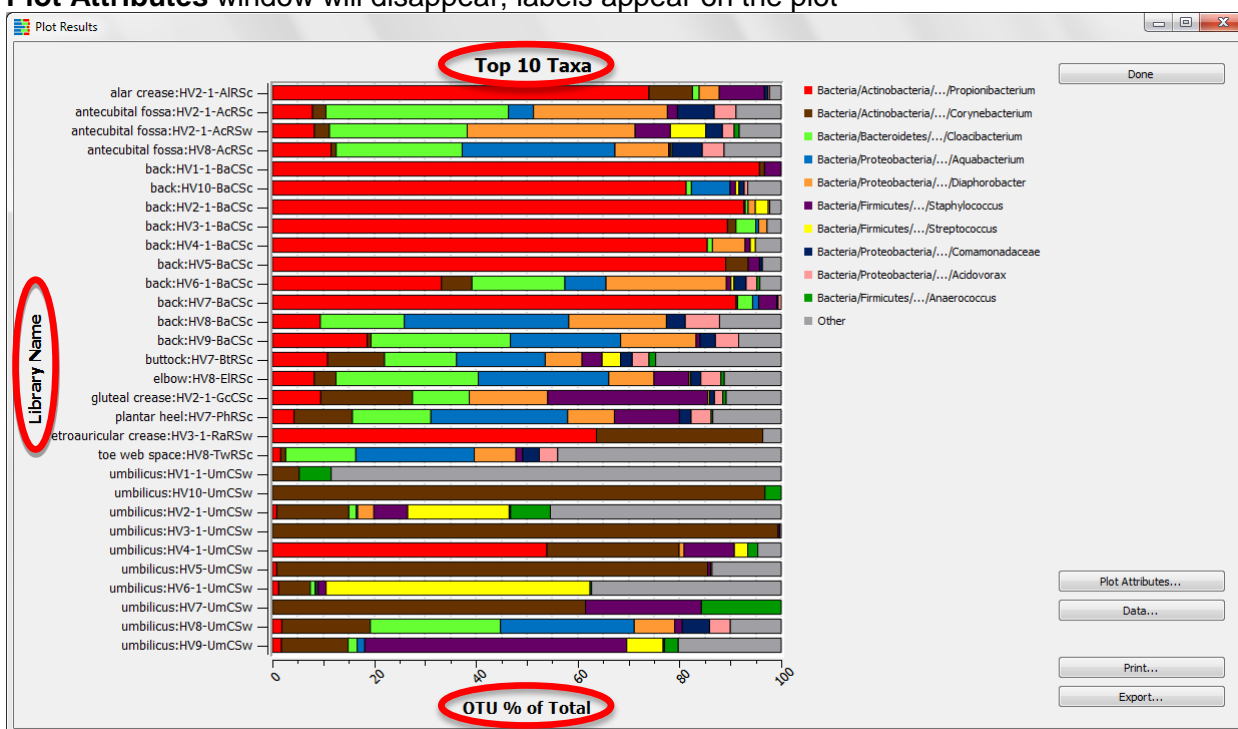
Y Axis

Label Rotation: 0

Save

Cancel

**Plot Attributes** window will disappear; labels appear on the plot

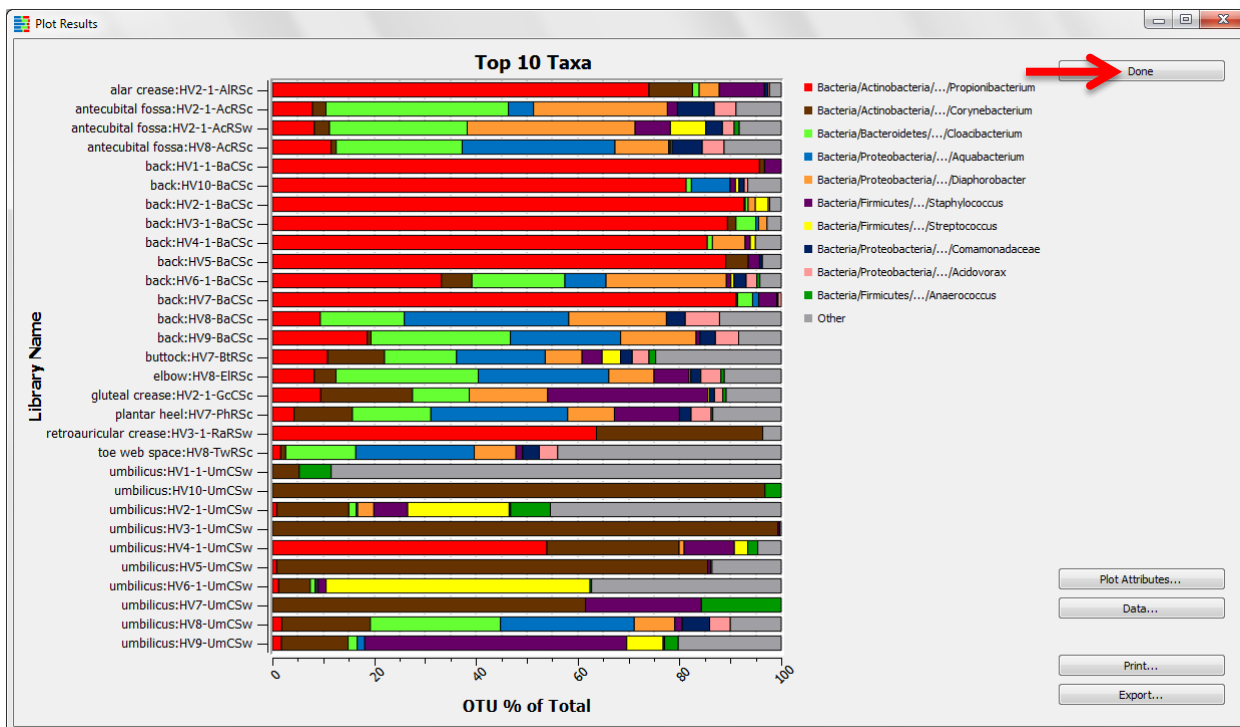


Red and brown appear to be dominant colors in this plot. According to the legend, these colors belong to the “Actinobacteria” phylum. This information may be useful in guiding us toward a hypothesis involving the dominant taxa.

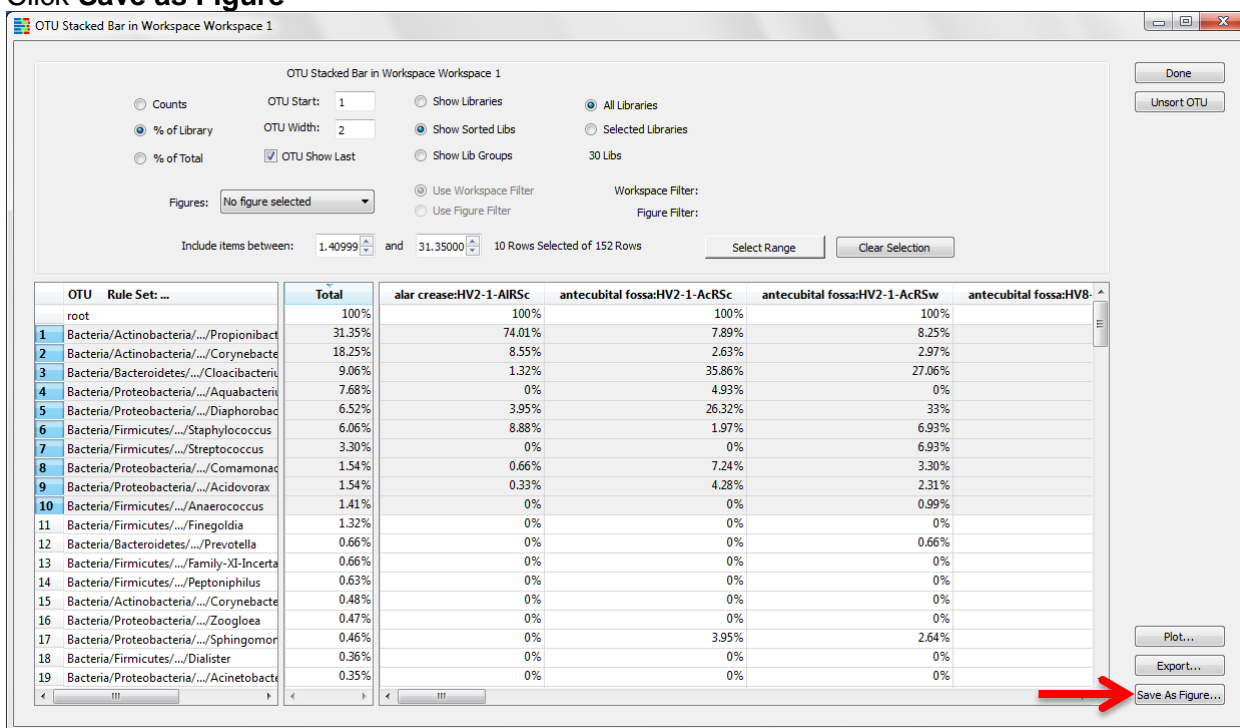
Saving figures in Explicit is easy and convenient. Figures are saved within the larger project, so they stay linked to the data from which they were created and do not create additional files on your computer.

### C. Save the OTU Stacked Bar Chart as a Figure

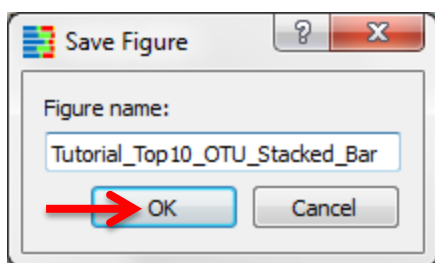
Click **Done** in the stacked bar chart **Plot Results** window



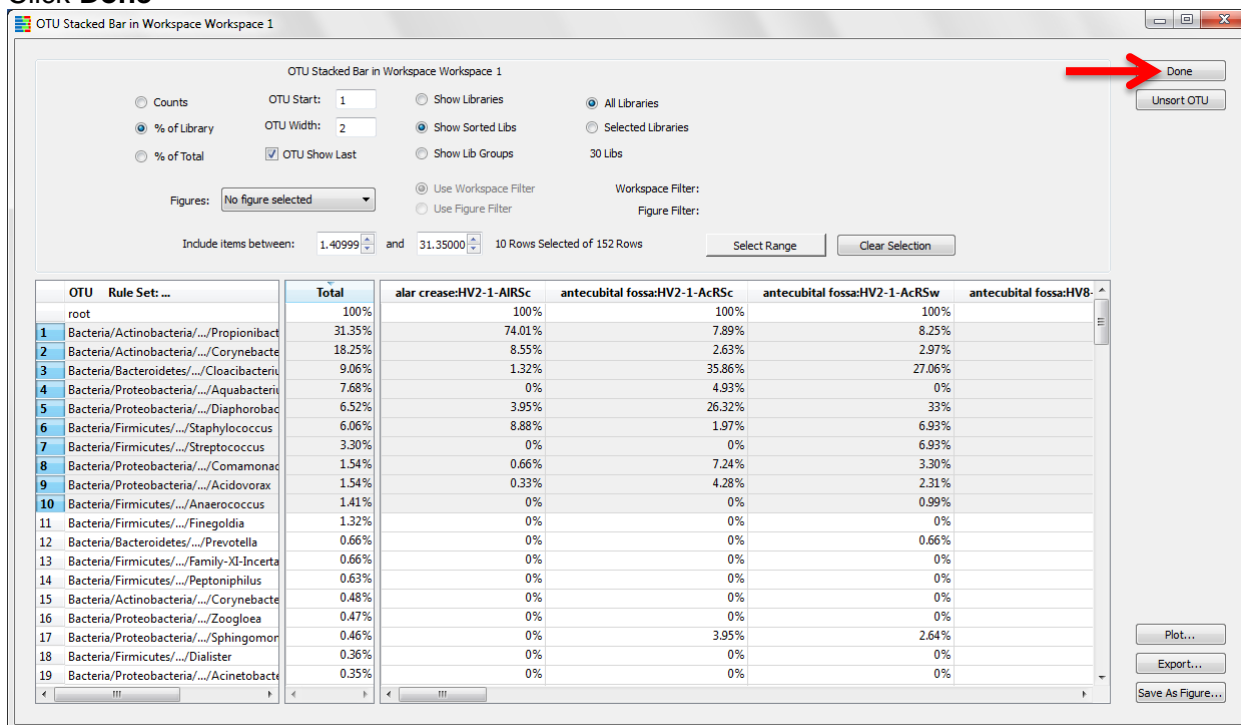
The OTU Stacked Bar setup window is back on the screen  
Click **Save as Figure**



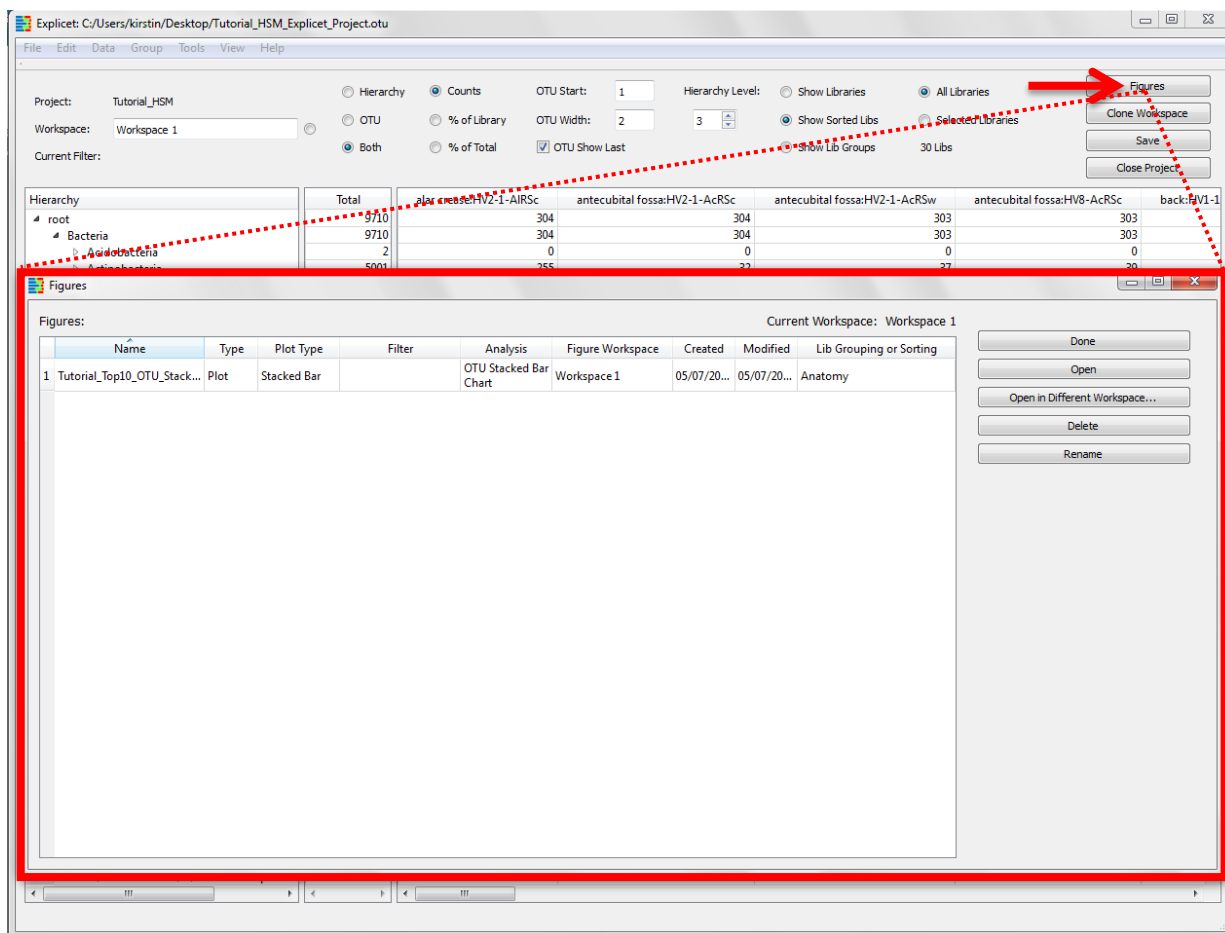
Enter stacked bar chart name in pop-up window  
Click **OK**



Click **Done**



Once saved, the stacked bar chart and associated figure data can be recalled at any point by clicking the **Figures** button on the workspace window. This provides a convenient mechanism for editing figures during manuscript preparation. Figures can also be exported in a format suitable for further modification in dedicated drawing software.



## VII. Make a Pie Chart

Another useful way to generate an overview of the organisms that exist in the dataset is through a pie chart, which allows graphical depictions of the taxonomic hierarchy.

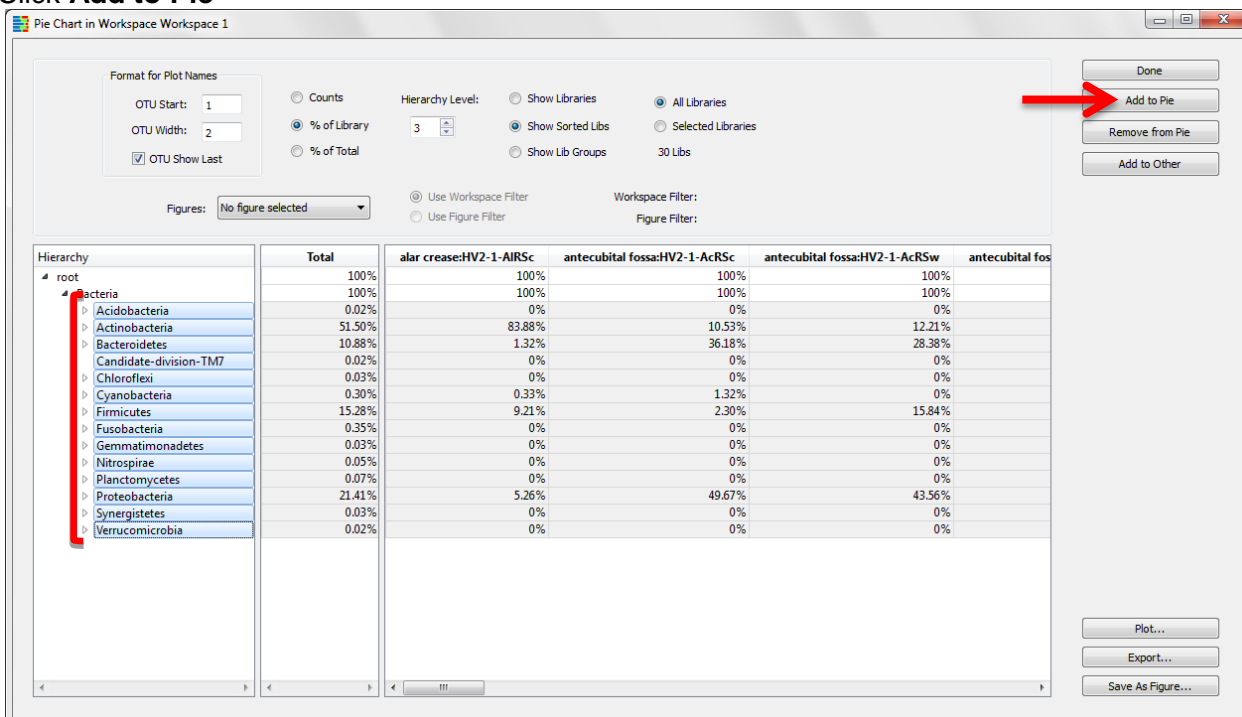
### A. Create a Pie Chart of the Project Components

#### Tools → Plot → Pie Chart

A new window will appear with the hierarchical data available in the workspace

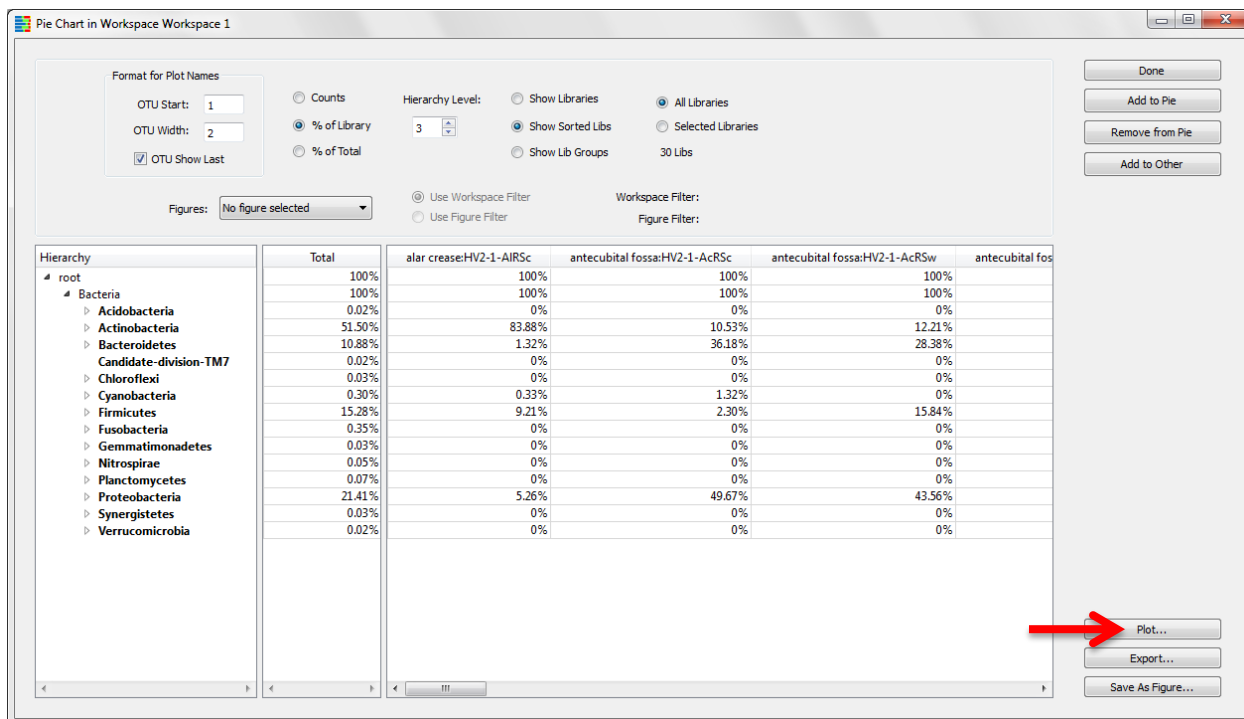
Shift-click all of the phyla in the list

Click **Add to Pie**



The selected phyla which were added to the pie are now bold

Click **Plot**

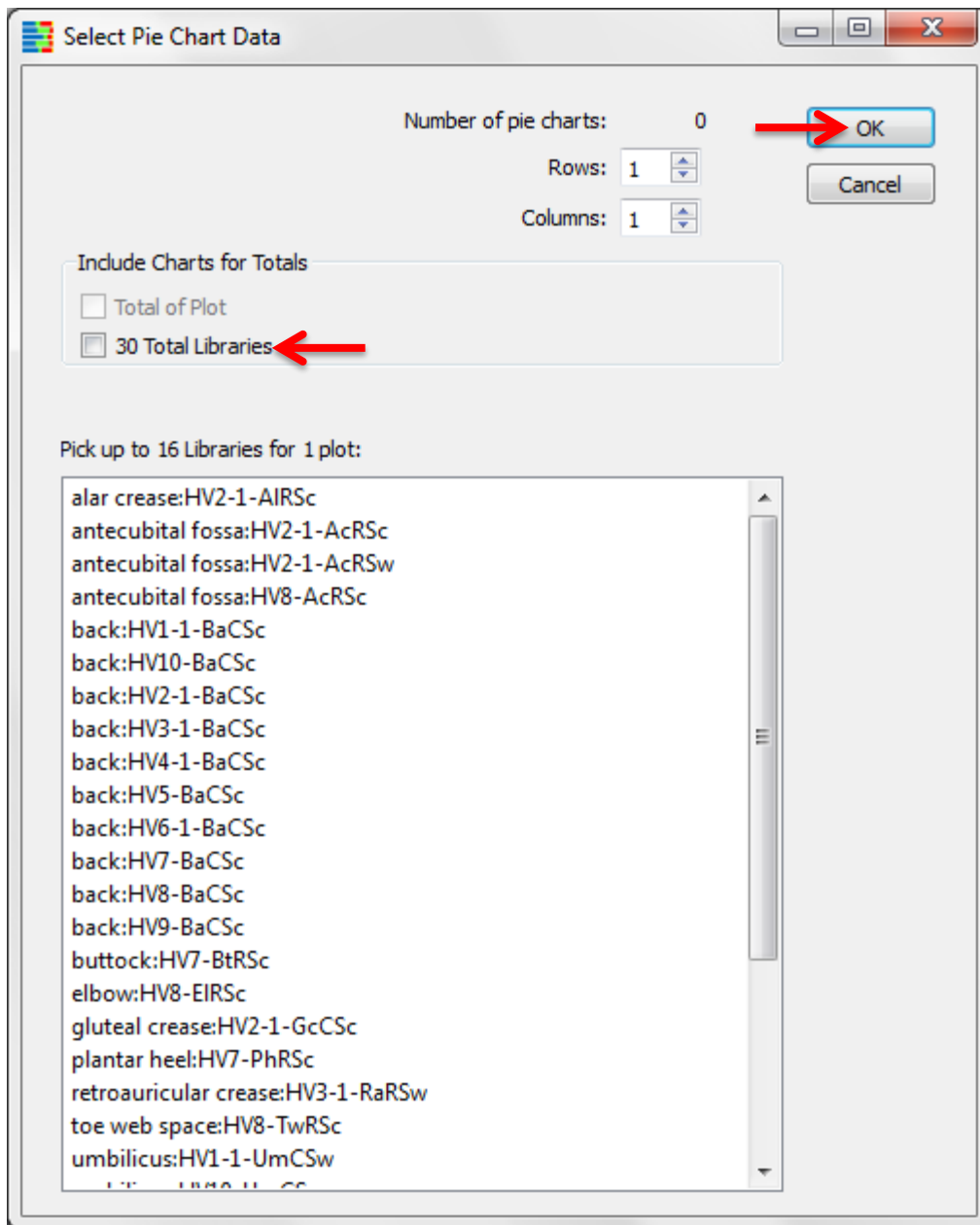


A new window will appear containing pie chart display options

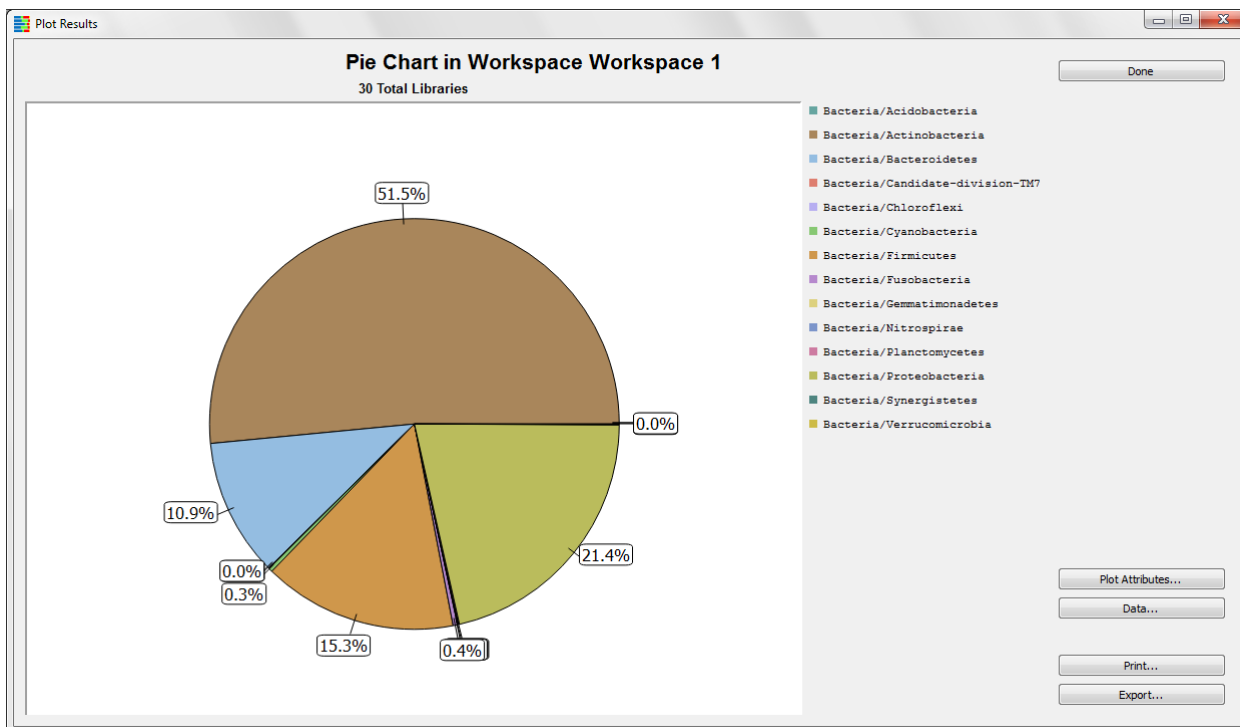
To create only a single pie chart displaying the combined libraries' data, select **30 Total Libraries**

Click **OK**





A pop-up window with the pie chart appears

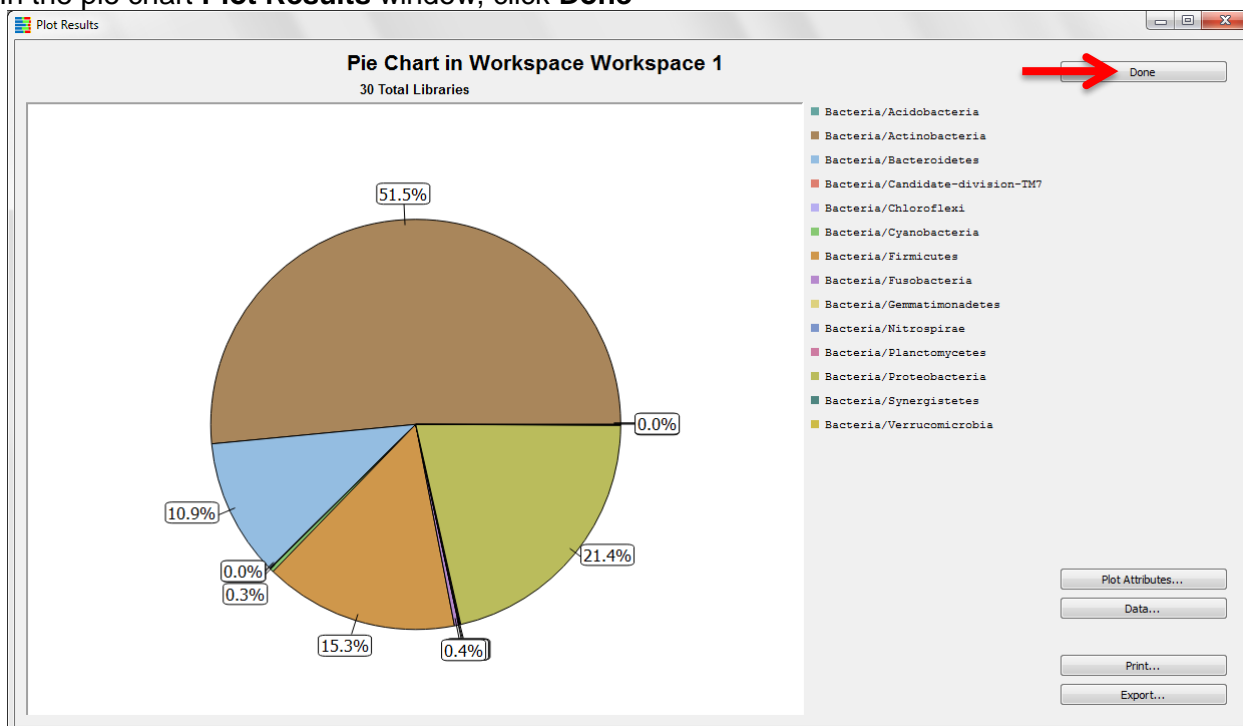


By looking at the pie chart of the phyla, it is clear that the brown wedge, Actinobacteria, is the most prevalent phylum in the data.

Additionally, we can see that the green wedge, Proteobacteria, makes up the second largest portion of the total. To visualize the classes present within the Proteobacteria phylum, we can create pie chart sub-wedges.

## B. Make a Pie Chart with Sub-Wedges

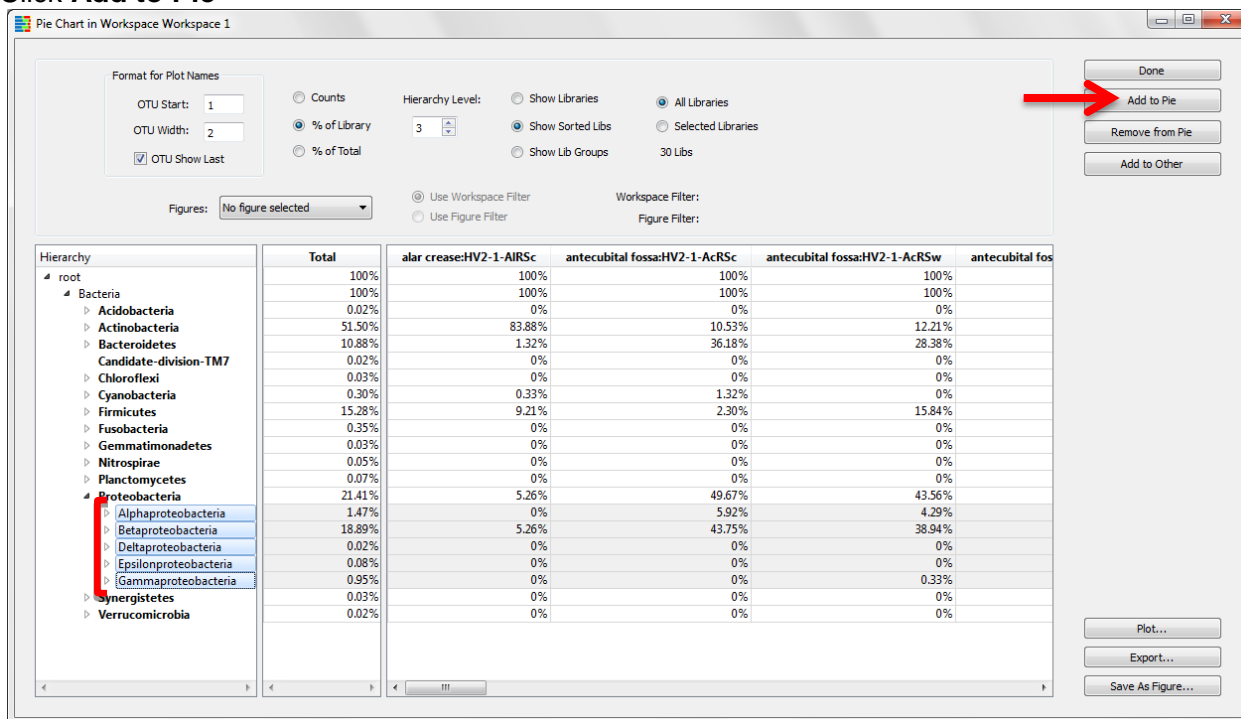
In the pie chart **Plot Results** window, click **Done**



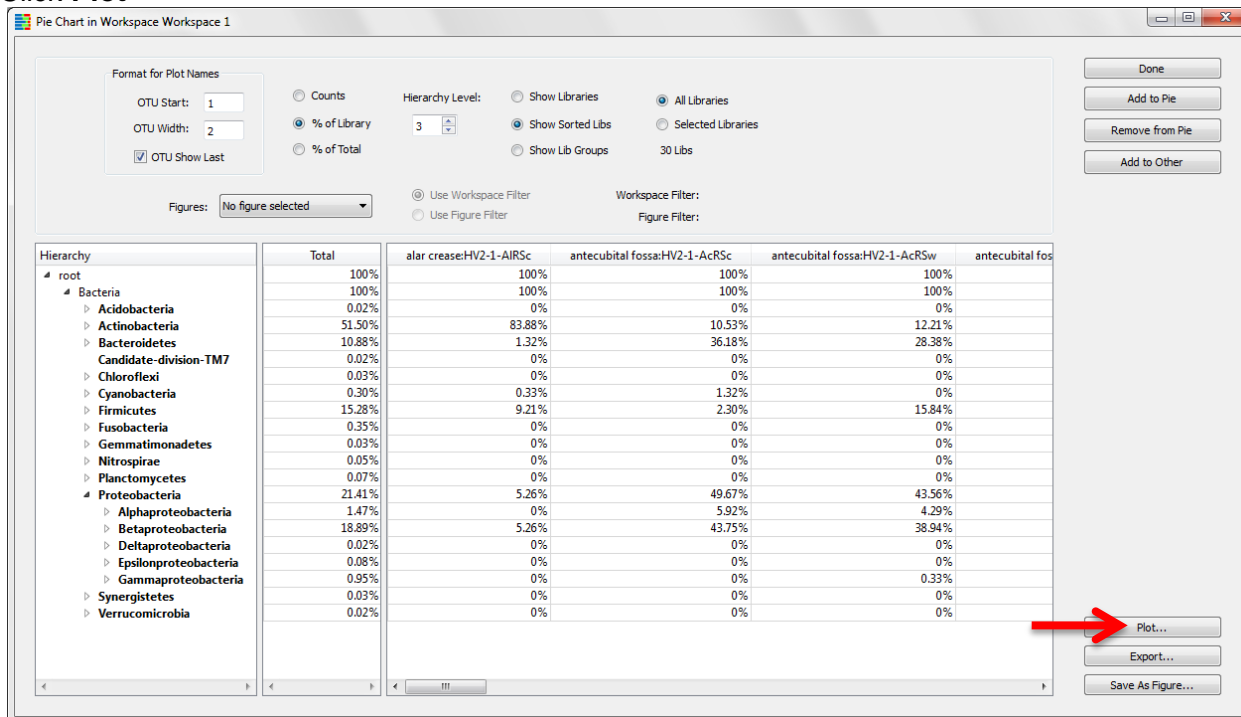
The **Taxonomy Pie Chart** setup window is back on the screen

Use the drop down arrow to the left of “Proteobacteria” to find the classes within the phylum

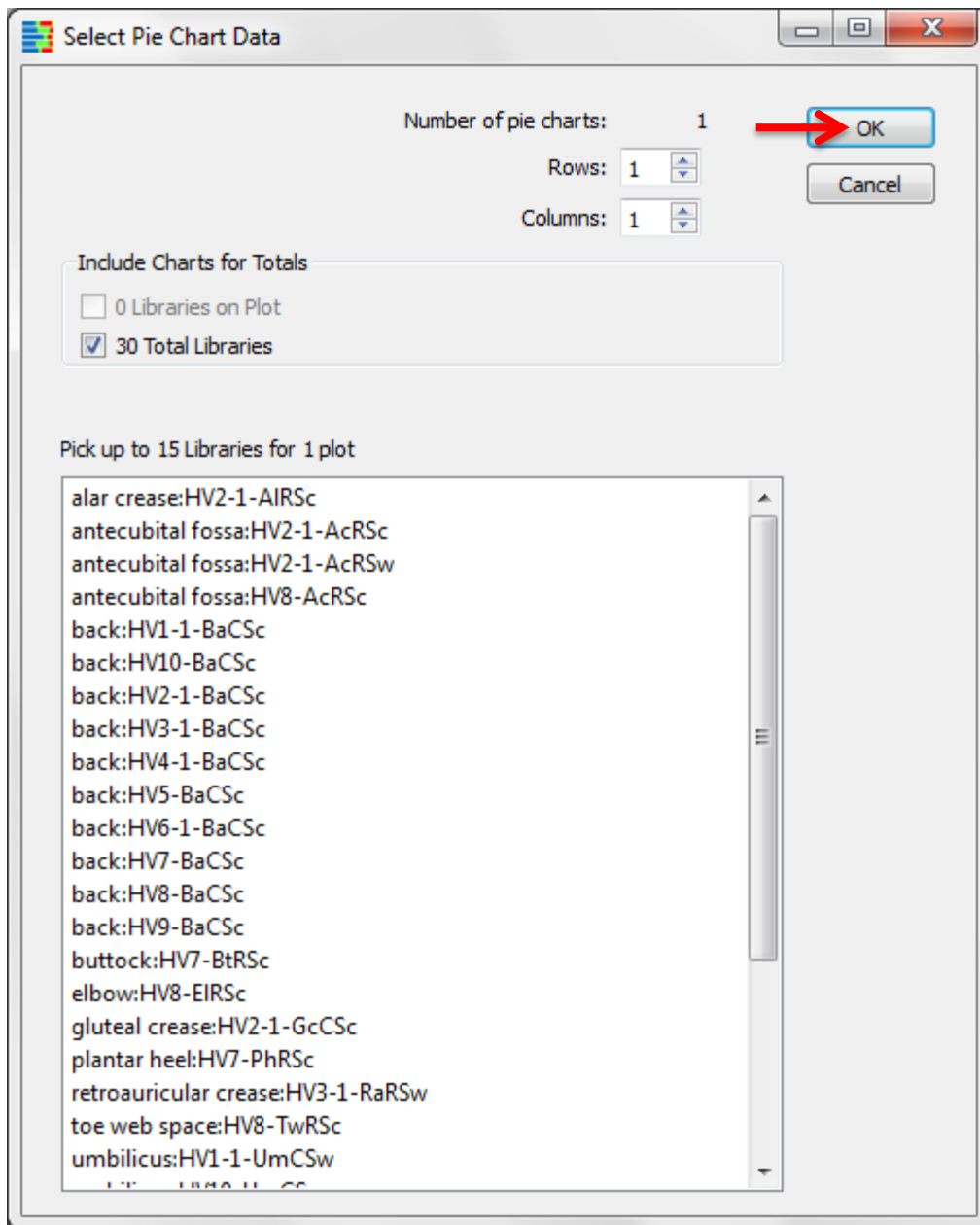
Shift-click all of the classes in the list  
Click **Add to Pie**



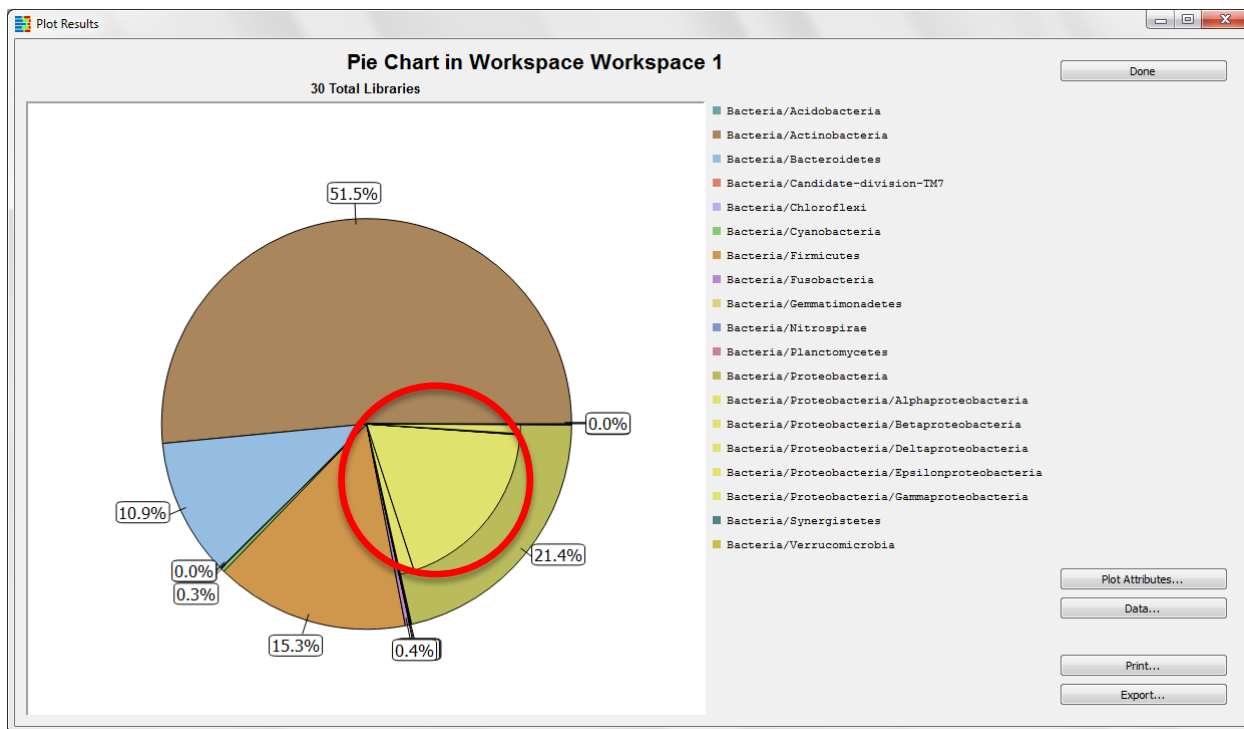
The selected classes that were added to the pie are now bold  
Click **Plot**



A new window will appear containing pie chart display options  
Again, we will create only a single pie chart displaying the combined libraries' data, so click **OK**



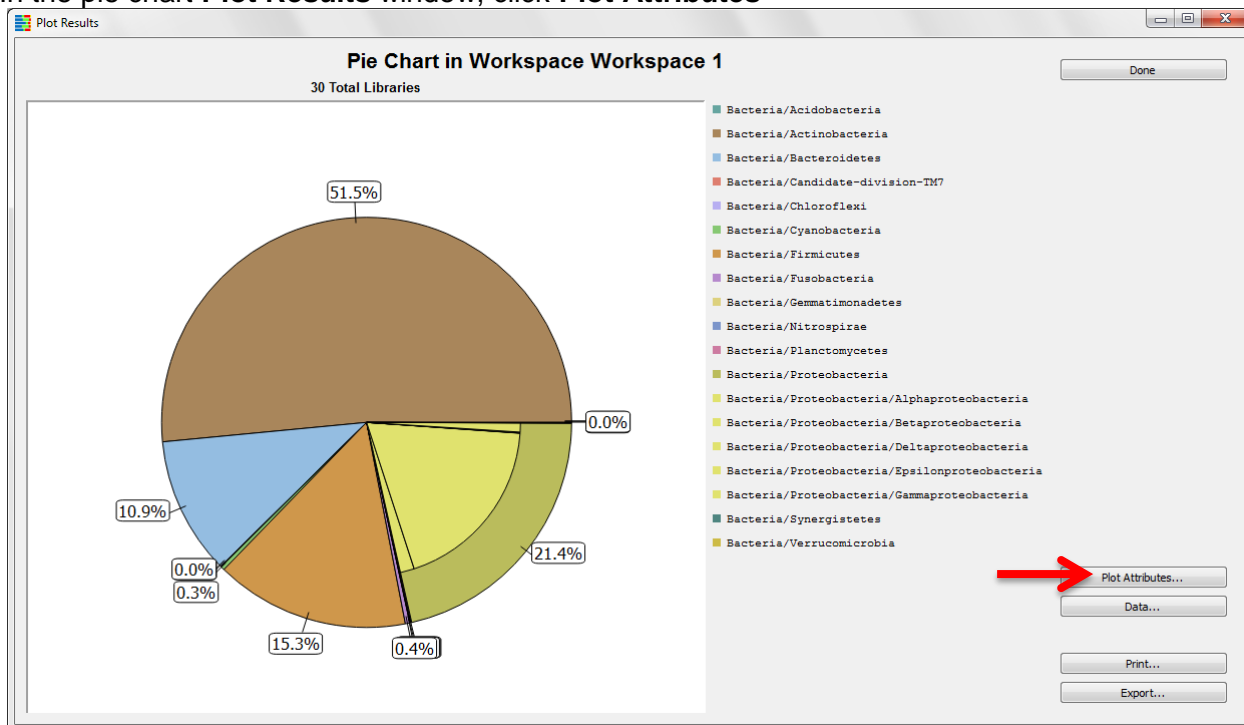
A pop-up window with the pie chart appears. We now see the classes within Proteobacteria represented as sub-wedges.



In order to better differentiate between the different classes, we can change the color of the sub-wedges.

### C. Change Wedge Colors in the Pie Chart

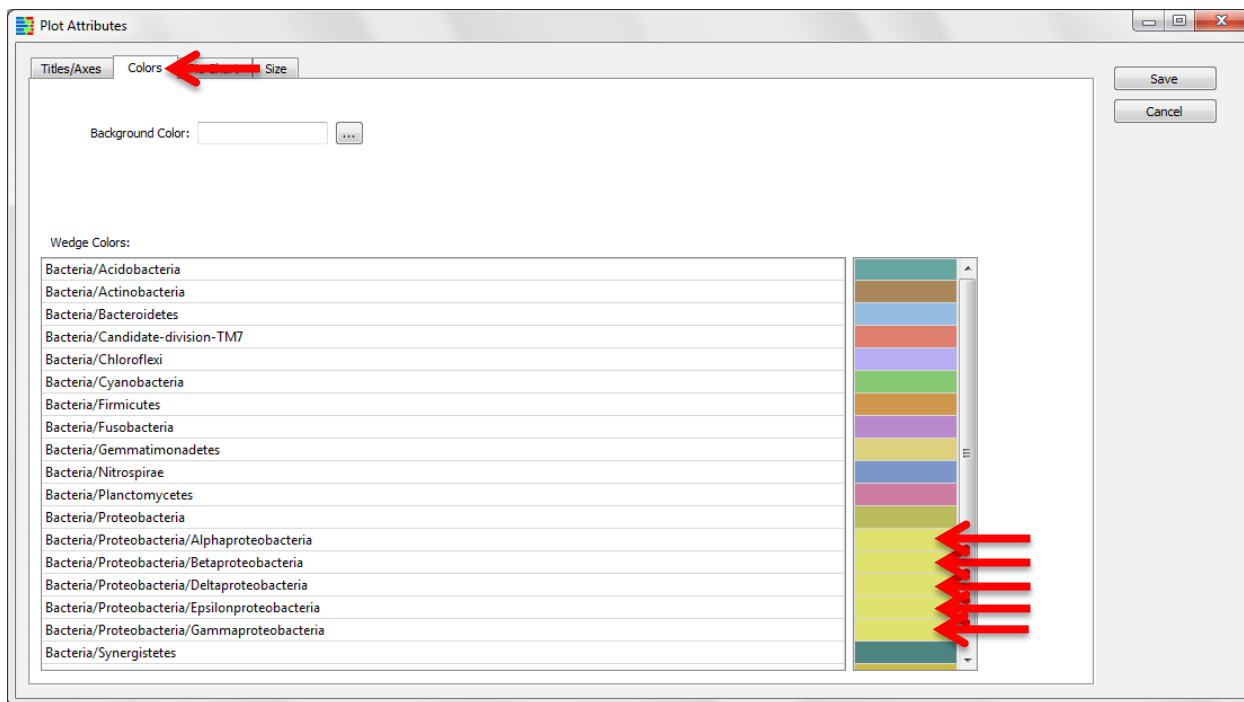
In the pie chart **Plot Results** window, click **Plot Attributes**



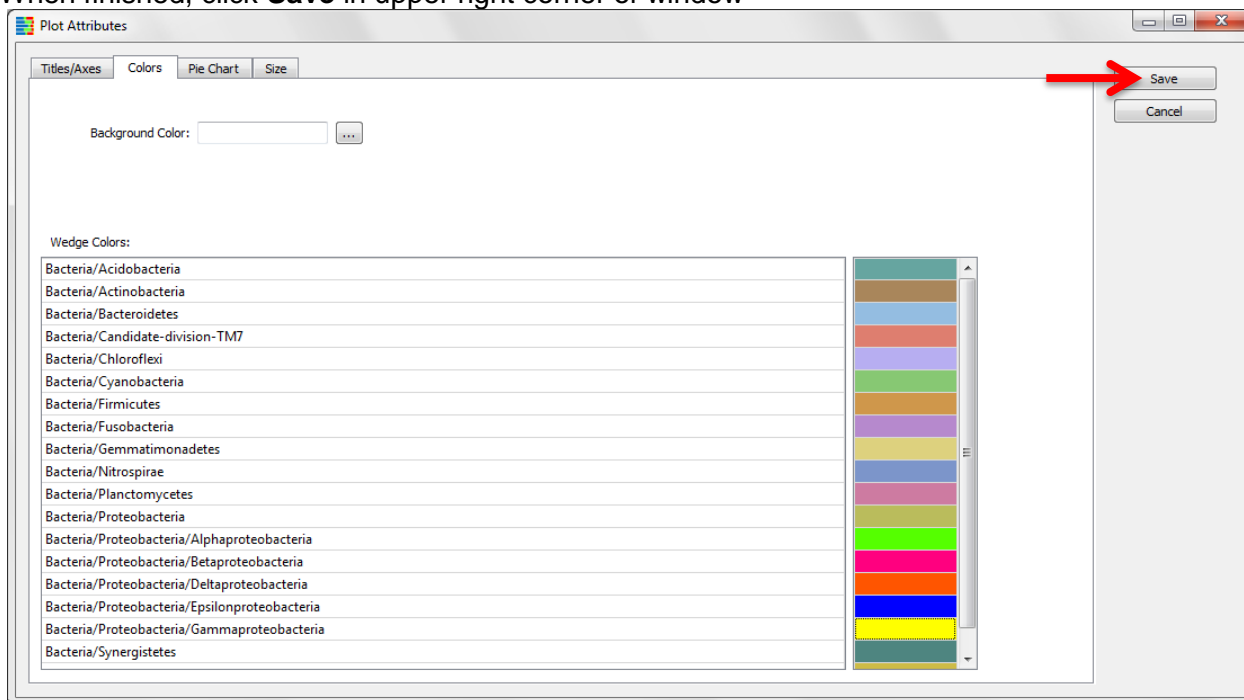
A pop-up window will appear

Click on the **Colors** tab

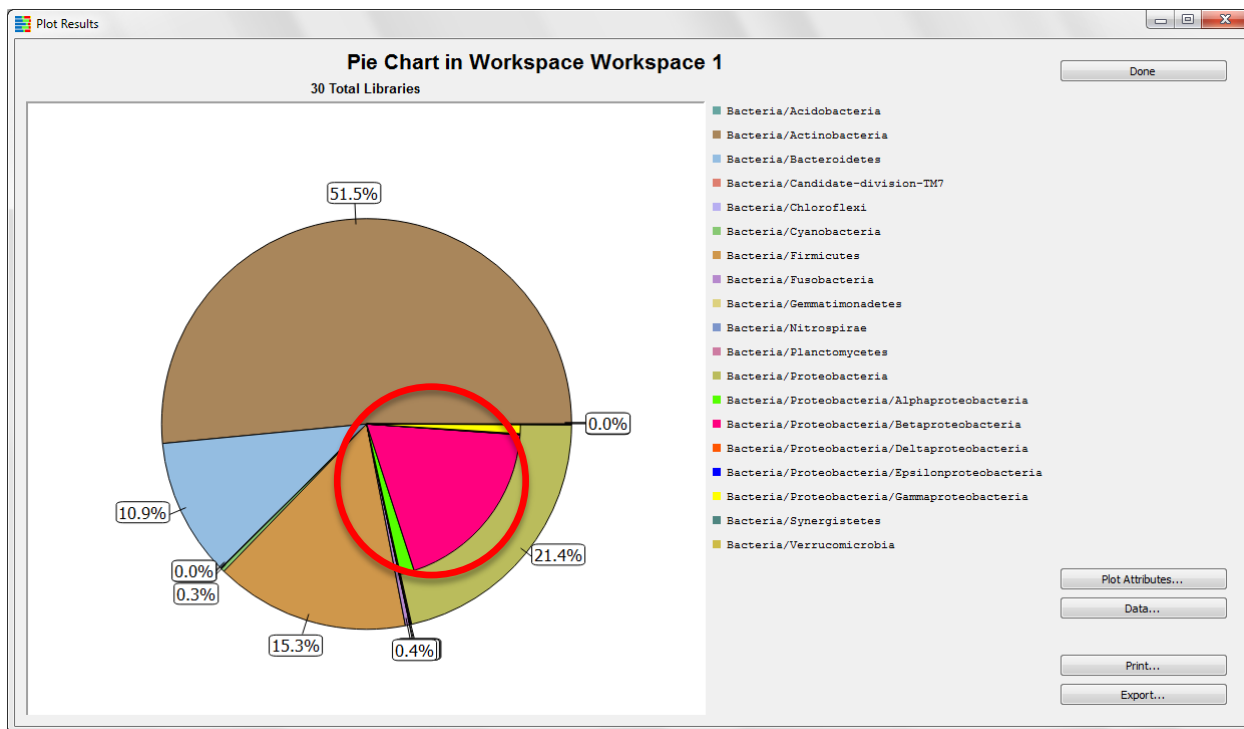
To pick a different wedge color, click on the color, and select a new color from the pop-up display



When finished, click **Save** in upper right corner of window



**Plot Attributes** window will disappear; changes will be shown on the plot



You may choose to save the pie chart as a figure. To do so, continue as shown earlier in the stacked bar chart example; close the graphics window, and select **Save As Figure** in the **Pie Chart** window.

## VIII. Create a Workspace

A workspace is a way for users to make experiments on copies or subsets of their entire data set, while keeping the original data fully intact.

Although the skin is a single organ, it harbors microbial communities that live in a range of physiologically and topographically distinct niches. The back is typically a sebaceous region, whereas the umbilicus is often a moist region of the body. Therefore, these two niches may have different taxa present. We will create a workspace for a mini-experiment to compare data from only these two anatomical positions.

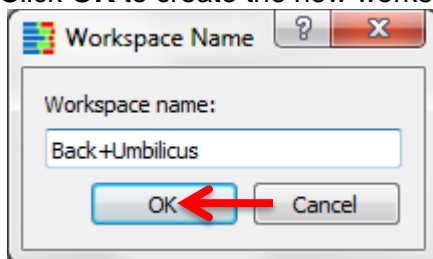
### A. Create a New Workspace

#### File → New → Workspace from Current Workspace

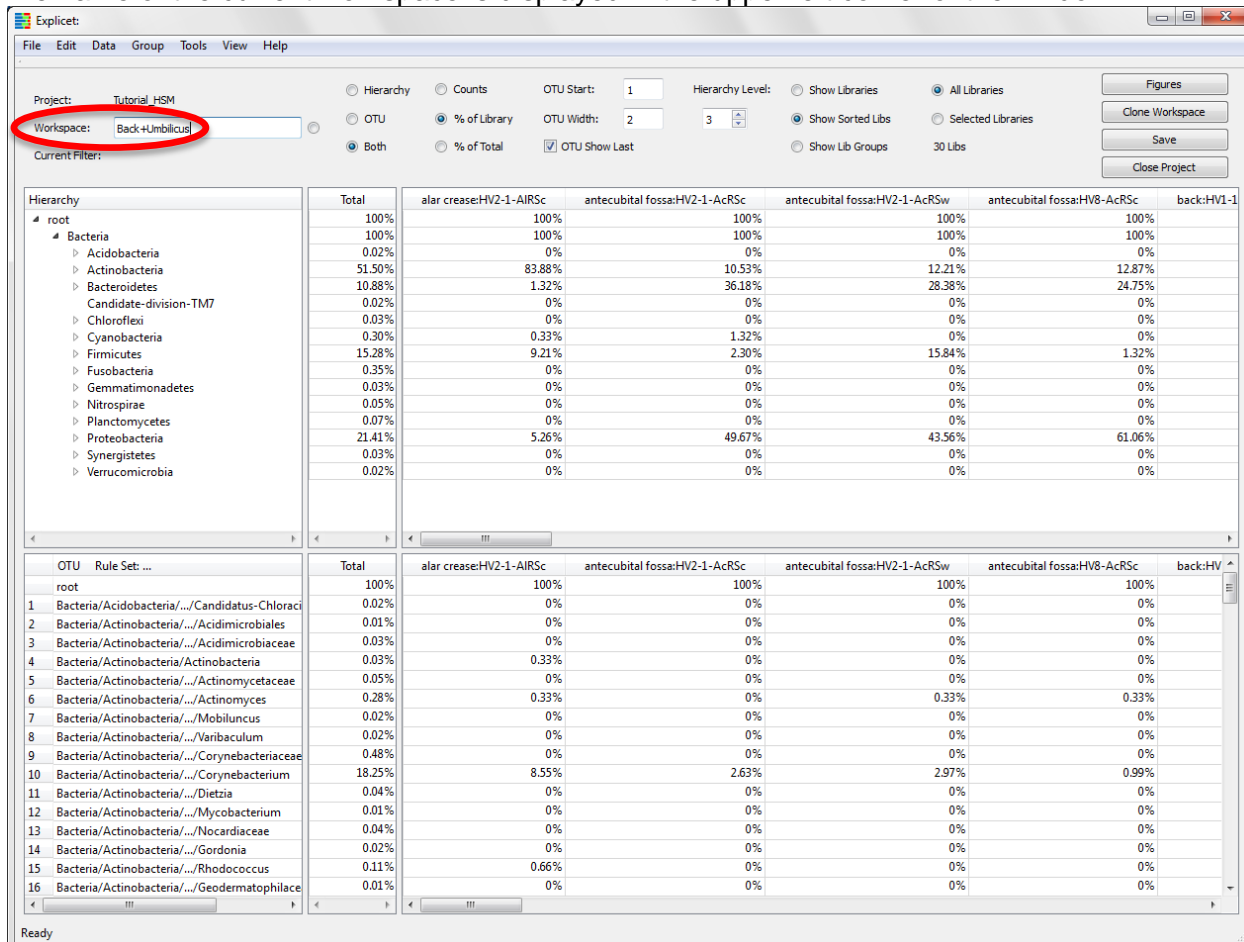
- “from Current Workspace” allows us to copy all of the display changes we’ve already made to the new workspace.

Enter desired workspace name in the pop-up window

Click **OK** to create the new workspace



The name of the current workspace is displayed in the upper left corner of the window



	Total	alar crease:HV2-1-AIRSc	antecubital fossa:HV2-1-AcRSc	antecubital fossa:HV2-1-AcRSw	antecubital fossa:HV8-AcRSc	back:HV1-1
root	100%	100%	100%	100%	100%	100%
Bacteria	100%	100%	100%	100%	100%	100%
Acidobacteria	0.02%	0%	0%	0%	0%	0%
Actinobacteria	51.50%	83.88%	10.53%	12.21%	12.87%	12.87%
Bacteroidetes	10.88%	1.32%	36.18%	28.38%	24.75%	24.75%
Candidate-division-TM7	0.02%	0%	0%	0%	0%	0%
Chloroflexi	0.03%	0%	0%	0%	0%	0%
Cyanobacteria	0.30%	0.33%	1.32%	0%	0%	0%
Firmicutes	15.28%	9.21%	2.30%	15.84%	1.32%	1.32%
Fusobacteria	0.35%	0%	0%	0%	0%	0%
Gemmatimonadetes	0.03%	0%	0%	0%	0%	0%
Nitrospirae	0.05%	0%	0%	0%	0%	0%
Planctomycetes	0.07%	0%	0%	0%	0%	0%
Proteobacteria	21.41%	5.26%	49.67%	43.56%	61.06%	61.06%
Synergistetes	0.03%	0%	0%	0%	0%	0%
Verrucomicrobia	0.02%	0%	0%	0%	0%	0%

OTU	Rule Set: ...	Total	alar crease:HV2-1-AIRSc	antecubital fossa:HV2-1-AcRSc	antecubital fossa:HV2-1-AcRSw	antecubital fossa:HV8-AcRSc	back:HV1-1
1	Bacteria/Actinobacteria/.../Candidatus-Chloraci	0.02%	0%	0%	0%	0%	0%
2	Bacteria/Actinobacteria/.../Acidimicrobiales	0.01%	0%	0%	0%	0%	0%
3	Bacteria/Actinobacteria/.../Acidimicrobiaceae	0.03%	0%	0%	0%	0%	0%
4	Bacteria/Actinobacteria/Actinobacteria	0.03%	0.33%	0%	0%	0%	0%
5	Bacteria/Actinobacteria/.../Actinomycetaceae	0.05%	0%	0%	0%	0%	0%
6	Bacteria/Actinobacteria/.../Actinomycetes	0.28%	0.33%	0%	0.33%	0.33%	0.33%
7	Bacteria/Actinobacteria/.../Molibuncus	0.02%	0%	0%	0%	0%	0%
8	Bacteria/Actinobacteria/.../Vanibaculum	0.02%	0%	0%	0%	0%	0%
9	Bacteria/Actinobacteria/.../Corynebacteriaceae	0.48%	0%	0%	0%	0%	0%
10	Bacteria/Actinobacteria/.../Corynebacterium	18.25%	8.55%	2.63%	2.97%	0.99%	0.99%
11	Bacteria/Actinobacteria/.../Dietzia	0.04%	0%	0%	0%	0%	0%
12	Bacteria/Actinobacteria/.../Mycobacterium	0.01%	0%	0%	0%	0%	0%
13	Bacteria/Actinobacteria/.../Nocardiaeae	0.04%	0%	0%	0%	0%	0%
14	Bacteria/Actinobacteria/.../Gordonia	0.02%	0%	0%	0%	0%	0%
15	Bacteria/Actinobacteria/.../Rhodococcus	0.11%	0.66%	0%	0%	0%	0%
16	Bacteria/Actinobacteria/.../Geodermatophilaceae	0.01%	0%	0%	0%	0%	0%



## IX. Apply a Filter

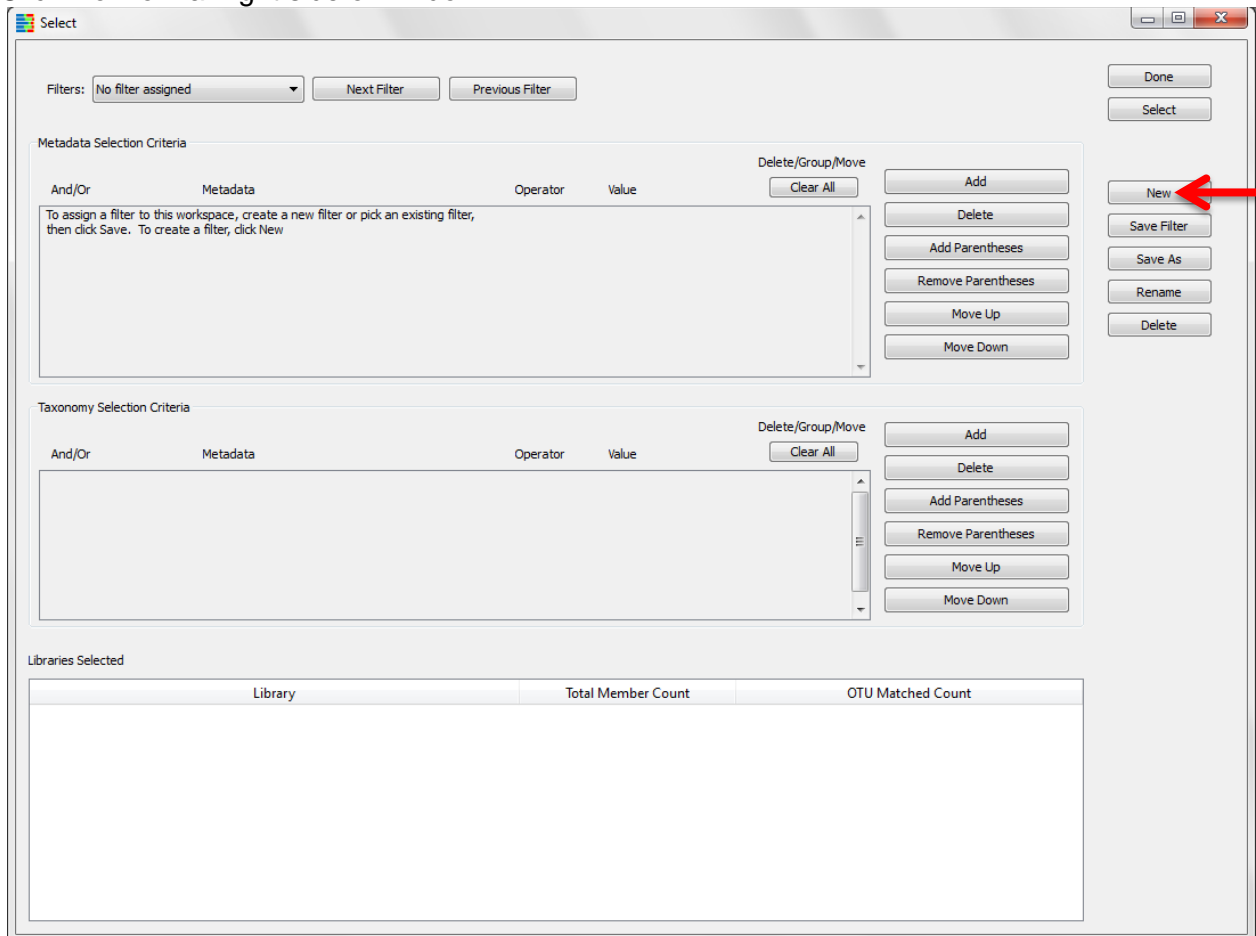
To compare data from only the back and umbilicus, we need to separate these libraries from the other body parts. This is done in Explicitet via “filters”.

### A. Create a Filter

#### Data → Select Libraries

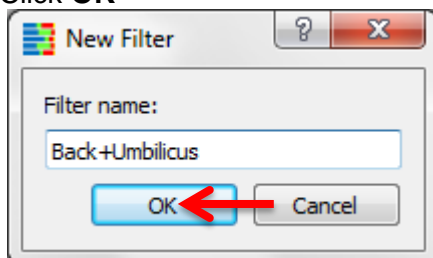
New pop-up window appears for creation of filters

Click **New** on far right side of window



Enter desired filter name in the pop-up window

Click **OK**



The filter name will appear in upper left corner of window

The screenshot shows a window titled "Select" with a toolbar at the top containing a "Filters:" dropdown menu (highlighted with a red circle and showing "Back+Umbilicus"), "Next Filter", and "Previous Filter" buttons. On the right side of the toolbar are "Done" and "Select" buttons.

Below the toolbar are two main sections for defining selection criteria:

- Metadata Selection Criteria:** This section has a table with columns "And/Or", "Metadata", "Operator", and "Value". Below the table is a text prompt: "To add a new criteria for Metadata, click Add". To the right of the table is a "Delete/Group/Move" section with a "Clear All" button and a vertical list of buttons: "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down".
- Taxonomy Selection Criteria:** This section has a similar table structure with columns "And/Or", "Metadata", "Operator", and "Value". Below the table is a text prompt: "To add a new selection criteria for Taxonomy, click Add". To the right is a "Delete/Group/Move" section with a "Clear All" button and a vertical list of buttons: "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down".

At the bottom of the window is a section titled "Libraries Selected" containing a table with three columns: "Library", "Total Member Count", and "OTU Matched Count". The table is currently empty.

Now that we have created a new filter, we need to set up the parameters to filter by. We will select for all libraries that were sampled from the “back” or “umbilicus” anatomical sites.

## B. Set Up the Filter Parameters

Click **Add** in the Metadata Criteria pane

The screenshot shows a window titled "Select" with a filter configuration interface. At the top, there's a "Filters:" dropdown menu currently set to "Back+Umbilicus", with "Next Filter" and "Previous Filter" buttons. Below this are two main sections: "Metadata Selection Criteria" and "Taxonomy Selection Criteria". Each section has a table with columns "And/Or", "Metadata", "Operator", and "Value". In the "Metadata Selection Criteria" section, the "Add" button is highlighted with a red arrow. To the right of these sections are buttons for "Delete/Group/Move" (Clear All, Add, Delete, Add Parentheses, Remove Parentheses, Move Up, Move Down) and a vertical stack of buttons: "Done", "Select", "New", "Save Filter", "Save As", "Rename", and "Delete". At the bottom, there's a "Libraries Selected" table with columns "Library", "Total Member Count", and "OTU Matched Count".

Use the first pull-down menu to select "Anatomy" (**Metadata** to filter by)  
 Use the second pull-down menu to select "contains" (filter **Operator**)  
 Enter "back" into **Value**



The screenshot shows a software window titled "Select". At the top, there is a "Filters:" dropdown menu currently set to "Back+Umbilicus", with "Next Filter" and "Previous Filter" buttons. Below this are two main sections: "Metadata Selection Criteria" and "Taxonomy Selection Criteria".

**Metadata Selection Criteria:** This section has a table with columns "And/Or", "Metadata", "Operator", and "Value". The "And/Or" column is empty. The "Metadata" column has a dropdown menu with "Anatomy" selected. The "Operator" column has a dropdown menu with "contains" selected. The "Value" column has a text input field containing "back". To the right of the table is a "Delete/Group/Move" section with a "Clear All" button and a list of action buttons: "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down". A red arrow points to the "Add" button.

**Taxonomy Selection Criteria:** This section has a similar table structure. The "And/Or" column is empty. The "Metadata" column is empty. The "Operator" column is empty. The "Value" column is empty. To the right is a "Delete/Group/Move" section with a "Clear All" button and a list of action buttons: "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down".

Below these sections is a "Libraries Selected" section with a table with three columns: "Library", "Total Member Count", and "OTU Matched Count". The table is currently empty.

On the far right of the window, there are several buttons: "Done", "Select", "New", "Save Filter", "Save As", "Rename", and "Delete".

Use the first pull-down menu to select "Or"  
 Use the second pull-down menu to select "Anatomy" (**Metadata** to filter by)  
 Use the third pull-down menu to select "contains" (filter **Operator**)  
 Enter "umbilicus" into **Value**

Select

Filters: Back+Umbilicus   Next Filter   Previous Filter

Done  
Select

### Metadata Selection Criteria

And/Or	Metadata	Operator	Value	Delete/Group/Move
	Anatomy	contains	back	<input type="checkbox"/>
or	Library	equals		<input type="checkbox"/>

Clear All   Add   Delete   Add Parentheses   Remove Parentheses   Move Up   Move Down

### Taxonomy Selection Criteria

And/Or	Metadata	Operator	Value	Delete/Group/Move
To add a new selection criteria for Taxonomy, click Add				

Clear All   Add   Delete   Add Parentheses   Remove Parentheses   Move Up   Move Down

### Libraries Selected

Library	Total Member Count	OTU Matched Count

To apply filter, click **Select** in upper right corner of window  
Click **Save Filter** on far right side of window to keep the filter

Filters: Back+Umbilicus

Next Filter

Previous Filter

Done

Select

Metadata Selection Criteria

And/Or	Metadata	Operator	Value	Delete/Group/Move
	Anatomy	contains	back	<input type="checkbox"/>
or	Anatomy	contains	umbilicus	<input type="checkbox"/>

Clear All

Add

Delete

Add Parentheses

Remove Parentheses

Move Up

Move Down

Taxonomy Selection Criteria

And/Or	Metadata	Operator	Value	Delete/Group/Move
To add a new selection criteria for Taxonomy, click Add				

Clear All

Add

Delete

Add Parentheses

Remove Parentheses

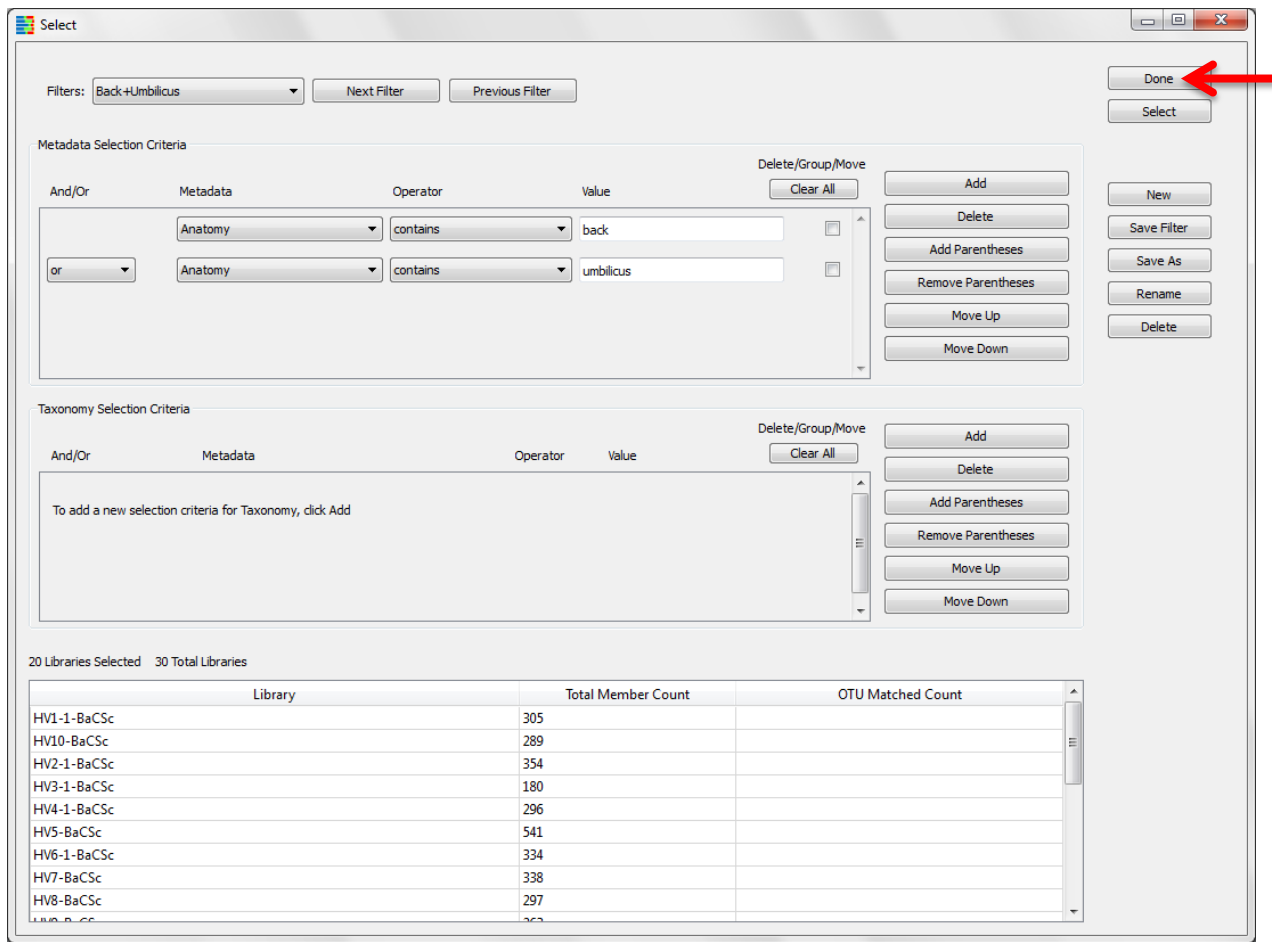
Move Up

Move Down

Libraries Selected

Library	Total Member Count	OTU Matched Count
---------	--------------------	-------------------

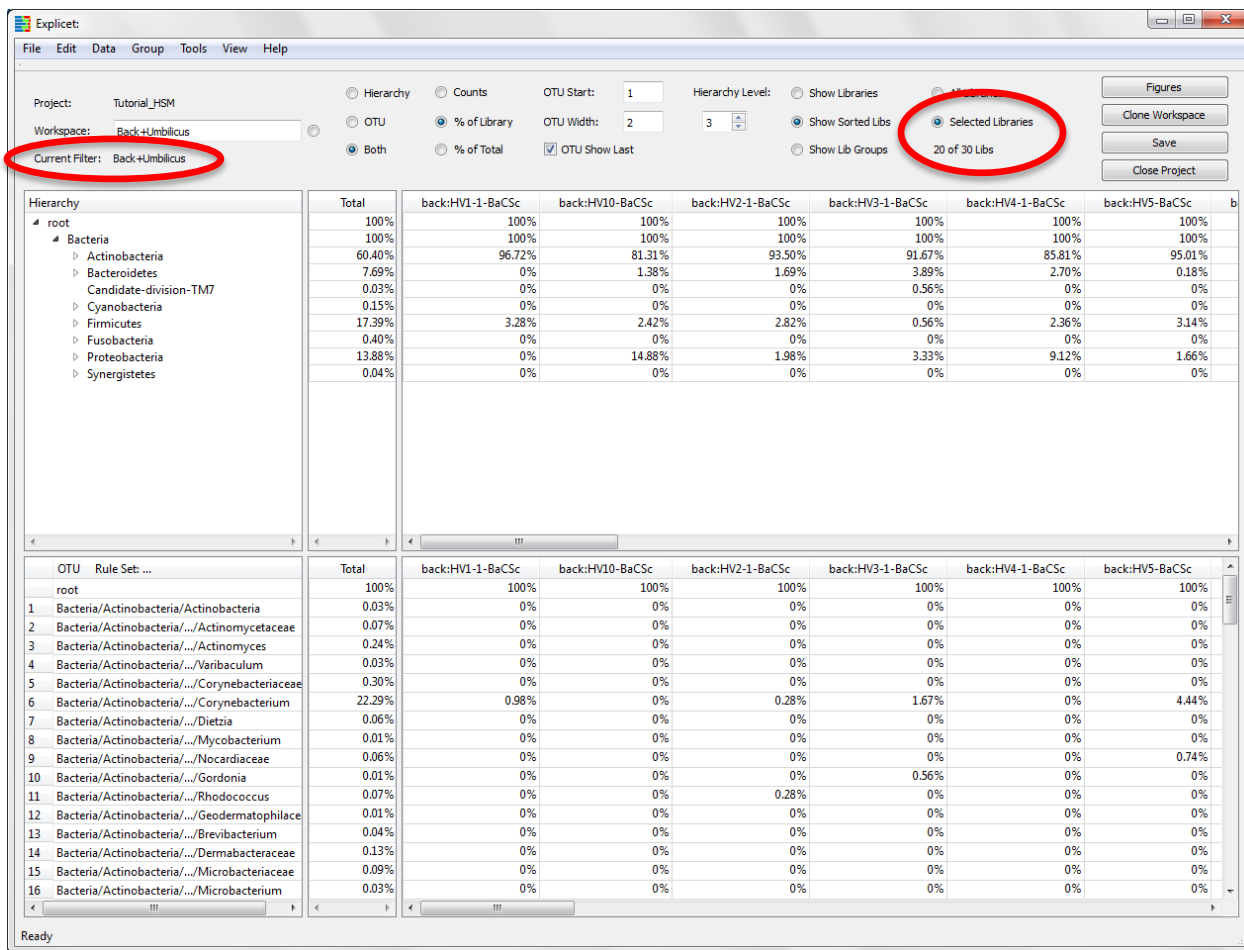
Click **Done** in upper right corner of window



Pop-up window will disappear

On the current workspace window, **Selected Libraries** is now selected, and the name of the **Current Filter** is displayed in the upper left corner of the window. The workspace window now only displays libraries from the 20 back and umbilicus samples.





## X. Beta Diversity (Morisita-Horn)

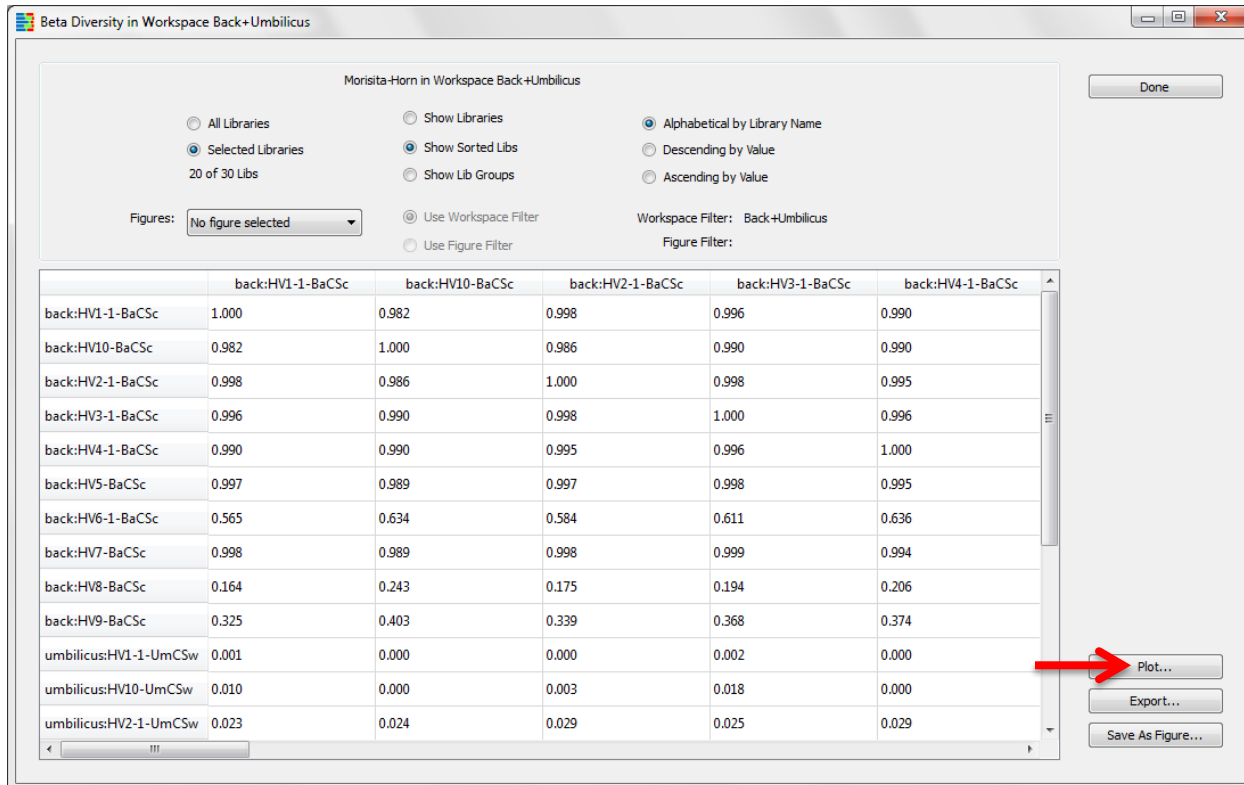
By viewing our libraries in a Morisita-Horn heatmap, we can estimate the similarity of the microbial communities present in the samples at these two anatomical positions. Morisita-Horn is an often used metric that can give insight into how similar or how different sets of samples are from each other by looking at the patterns of all of the different OTUs at the same time.

### A. Create a Morisita-Horn Heatmap

**Tools → Analyze → Beta Diversity → Morisita-Horn**

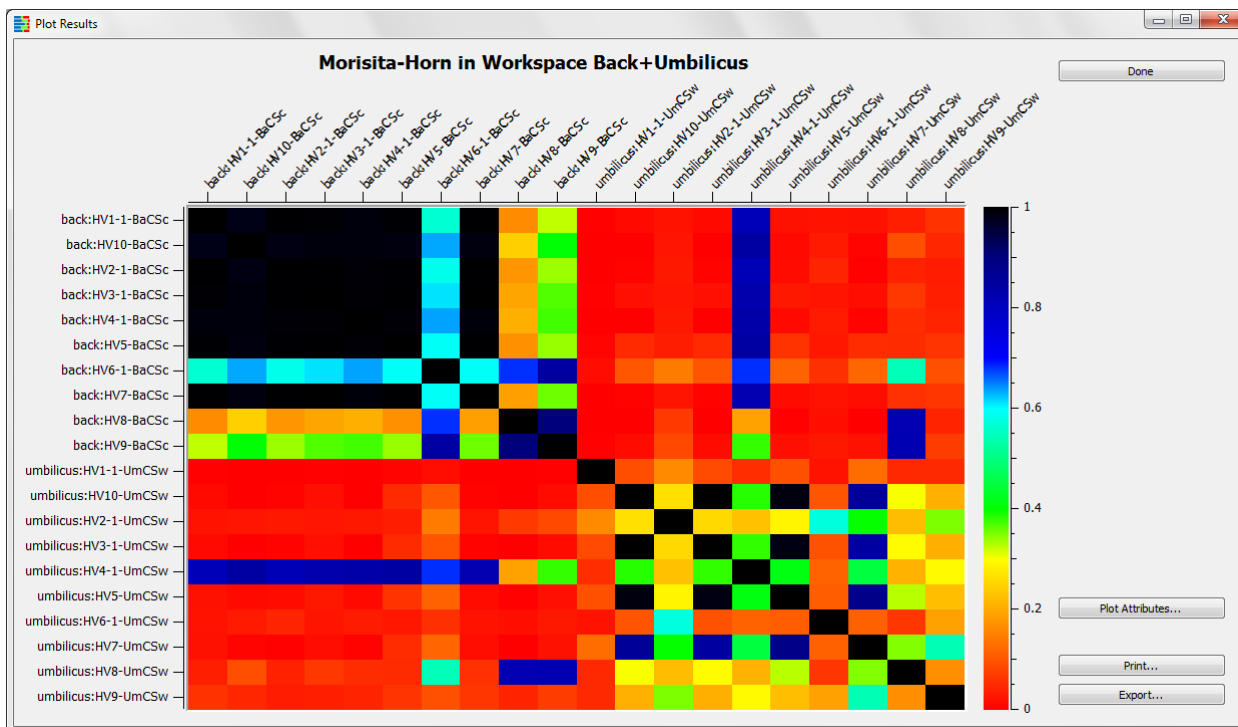
A new window will appear with a table of the sequence variant counts

Click **Plot**



A new window will appear containing the heatmap of Morisita-Horn sequence variant counts

Note: In our workspace, we have **Selected Libraries** selected, so the heatmap will only display results from our libraries of interest (only those libraries sampled from the back or umbilicus).



Anatomical positions with Morisita-Horn values near 1 (implying the samples' constituent taxonomy patterns are very *similar*) appear black. Anatomical positions with Morisita-Horn values near 0 (implying the samples' constituent taxonomy patterns are very *different*) appear red. Based on this data, the back is more similar across subjects than the umbilicus. Plot attributes allow control of plot characteristics and color usage as described earlier.

You may choose to save the Morisita-Horn heatmap as a figure. To do so, continue as shown earlier in the stacked bar chart example; close the graphics window, and select **Save As Figure** in the **OTU Heatmap** window.

## XI. Alpha Diversity

The alpha diversity statistics computed by Explicitet are generally shown in one of two ways: either as a single value calculated at the size of the smallest library (known as the rarefaction point) or as multiple values plotted as collector's curves for each library. Collector's curves are the classic way to evaluate the impact of increasing sample size (i.e., more sequencing) on the information content of the dataset. All collector's curves in Explicitet are computed with rarefaction, meaning all libraries are resampled to allow fair comparison between libraries of greatly different size. The higher the resolution of the calculations (large number of bootstrap iterations, large number of steps), the slower the computations will proceed. It is recommended that users start with the defaults and then increase as needed to get the curves to smooth out. Very large bootstrap iterations and a large number of steps may result in a run of multiple days... So, start small and work up.

The alpha diversity metrics are often quick, reliable ways to determine if samples in a dataset are sequenced adequately. Since we have a workspace set up to run mini-experiments on a subset of our data, we should make sure that the data is representative. We need to make sure that enough sequences were generated from the back and umbilicus samples to be considered representative of the anatomical position for a subject. We can test this by running an alpha diversity test called Good's Coverage.

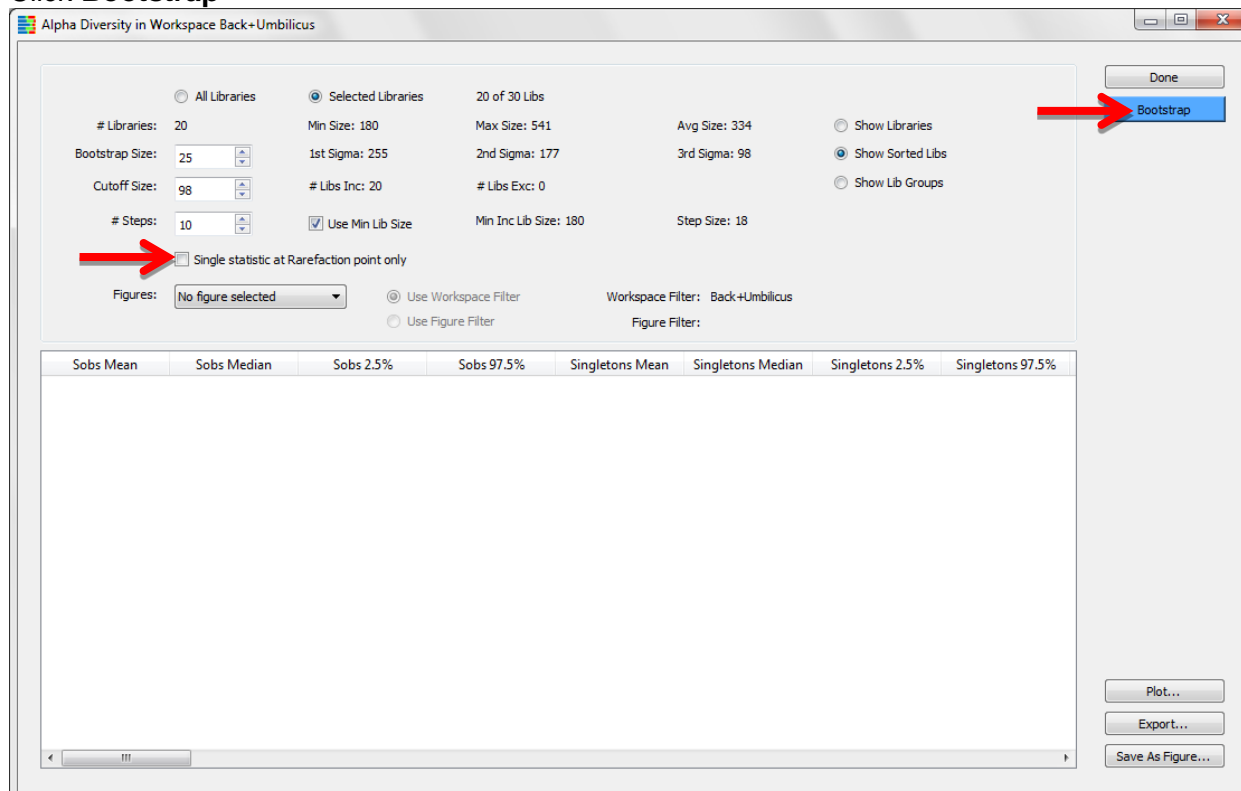
### A. Run a Good's Coverage Test

**Tools** → **Analyze** → **Alpha Diversity**

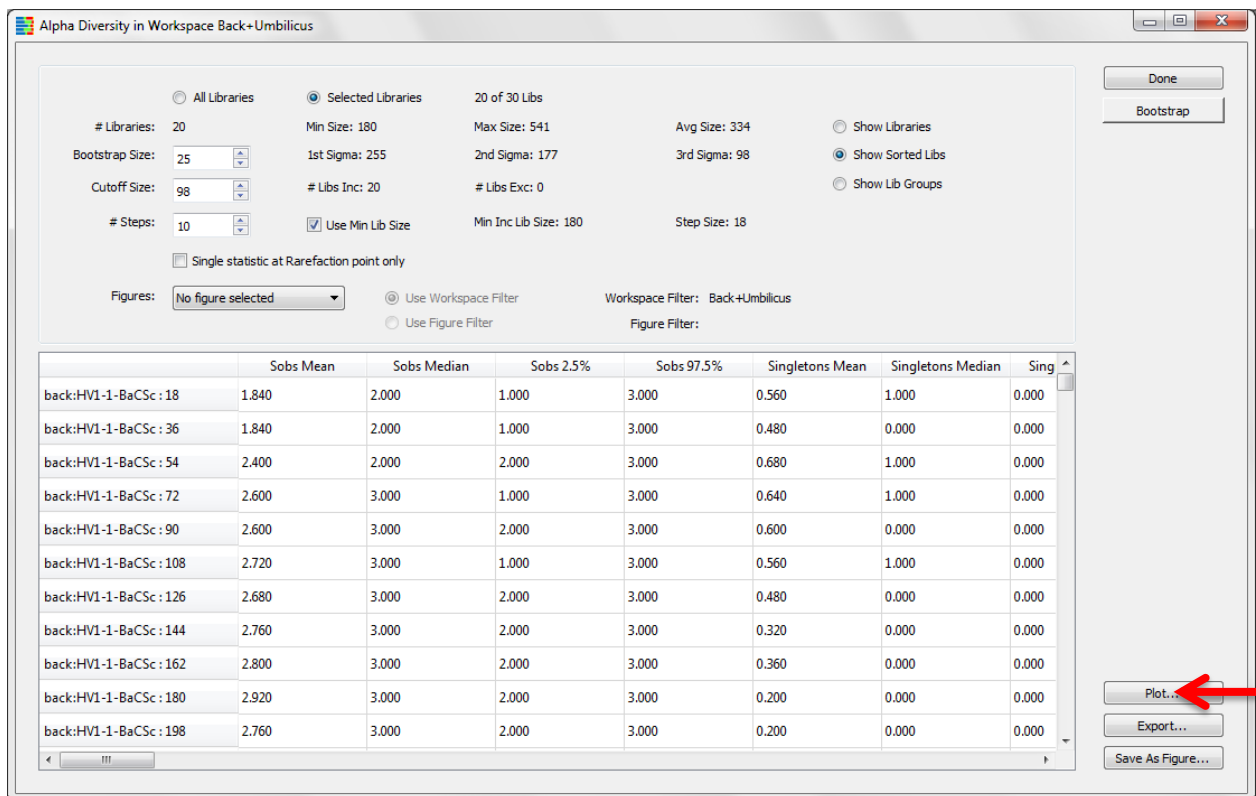
New pop-up window appears

To create curves, deselect **Single statistic at Rarefaction point only**

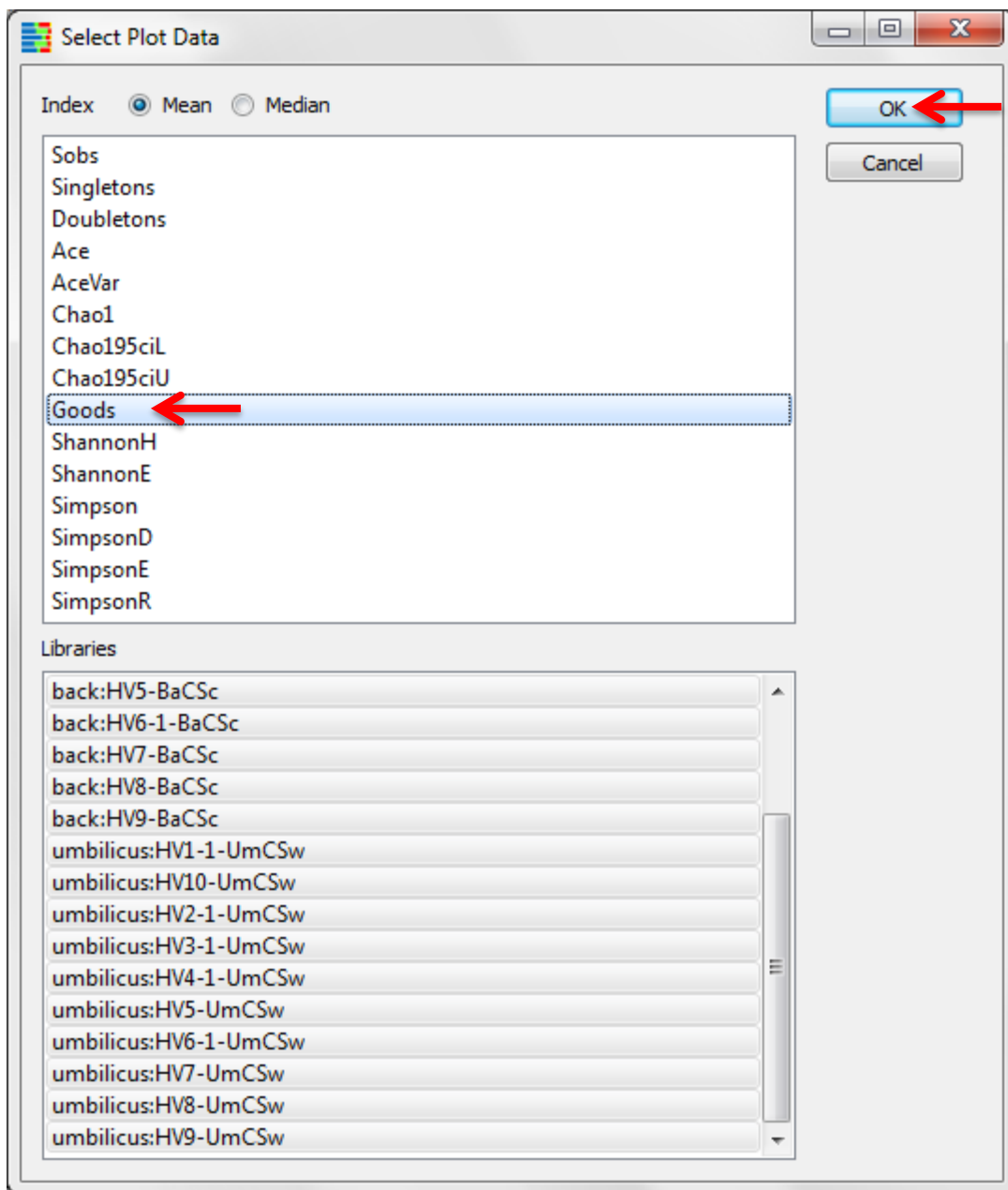
Click **Bootstrap**



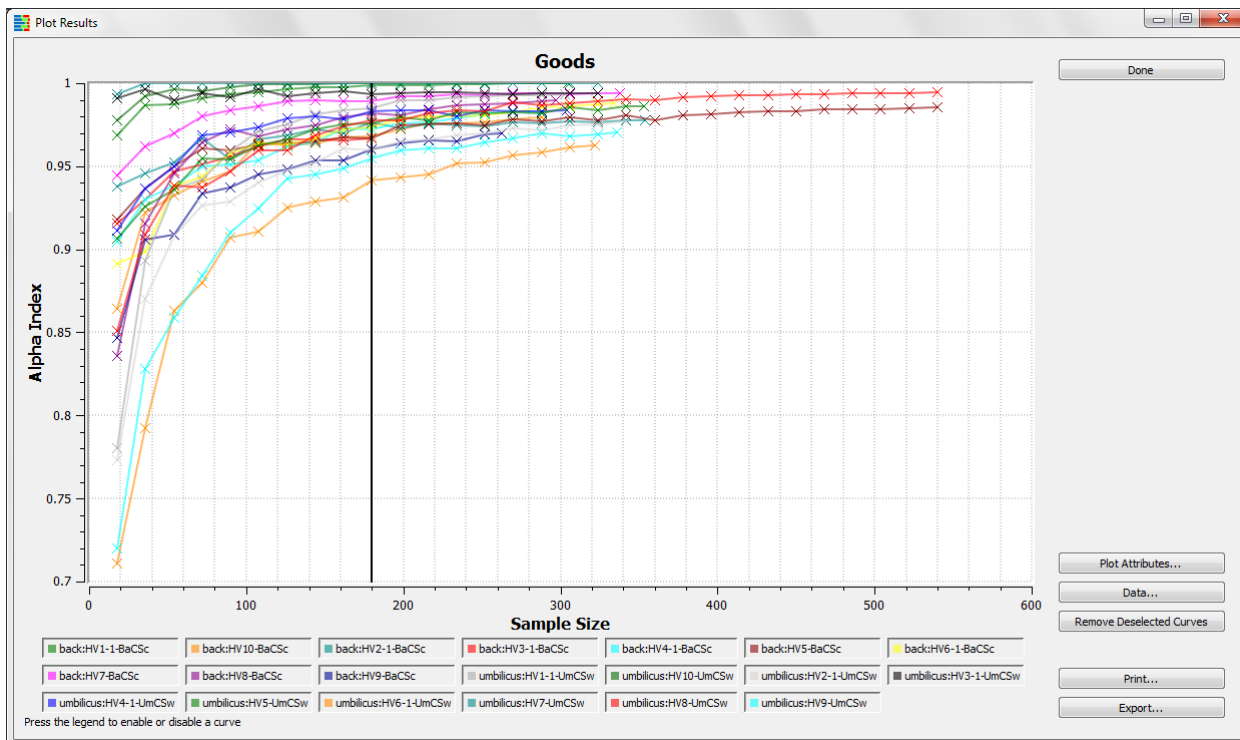
When **Bootstrap** is finished running, click **Plot**



A new pop-up window appears which lists the various alpha diversity tests  
 Select **Goods**  
 Click **OK**



A new pop-up window appears showing the Good's Coverage plot



Since the curves on the plot generally reach asymptotes, we conclude that both sites were sampled reasonably well to be considered representative of the anatomical positions.

You may choose to save your Good's Coverage plot as a figure. To do so, continue as shown earlier in the stacked bar chart example; close the graphics window, and select **Save As Figure** in the **Alpha Diversity** window.

## XII. Two-Part Test

Now that we know our data are representative, we will continue with another statistical test. A Two-Part statistical test can identify taxa that differ between two groups. We will use the Two-Part test to compare sequence counts between the back and umbilicus. The Two-Part Test is a combined statistic that examines both the proportion of the samples that contain a given OTU and the median relative abundance of the OTU across two categories. Because microbiome data often are non-normally distributed, parametric tests such as the familiar t-test may not be appropriate. Consequently, we use a non-parametric Wilcoxon test to examine percent abundance data. For more information on the Two-Part Test, please see: Wagner BD, Robertson CE, Harris JK (2011) Application of Two-Part Statistics for Comparison of Sequence Variant Counts. *PLoS ONE* 6(5): e20296.

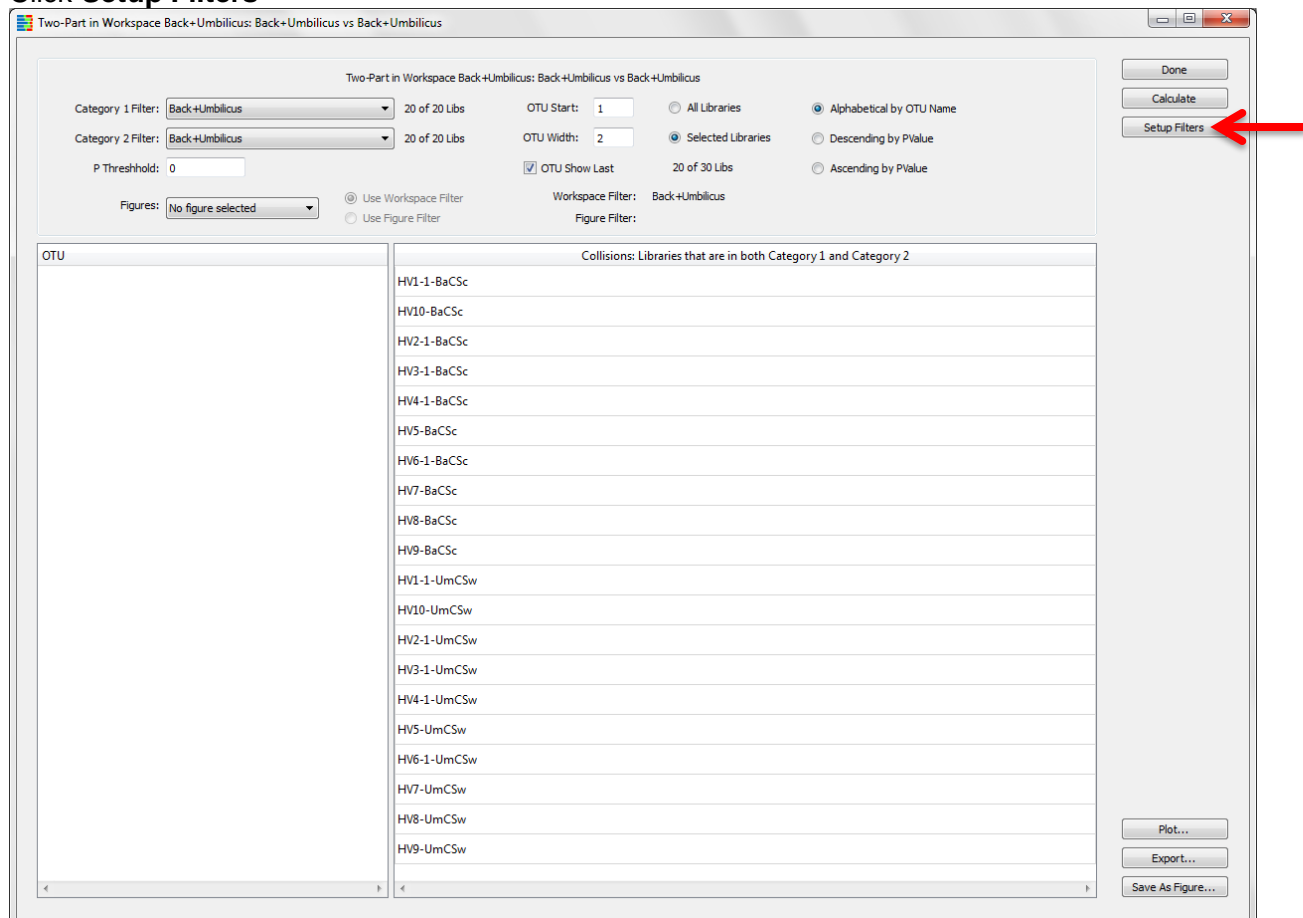
### A. Run a Two-Part Test

**Tools** → **Analyze** → **Two-Part**

A new pop-up window appears

In order to compare the back data against the umbilicus data, we need to set up individual filters for each anatomical position. To do so, we will proceed as discussed earlier in “To create a filter...”.

Click **Setup Filters**



New pop-up window appears for creation of filters

Click **New** on far right side of window



Filters: Back+Umbilicus    Next Filter    Previous Filter

Done  
Select

Metadata Selection Criteria

And/Or	Metadata	Operator	Value	Delete/Group/Move
	Anatomy	contains	back	<input type="checkbox"/>
or	Anatomy	contains	umbilicus	<input type="checkbox"/>

Clear All    Add    Delete    Add Parentheses    Remove Parentheses    Move Up    Move Down

Taxonomy Selection Criteria

To add a new selection criteria for Taxonomy, click Add

Clear All    Add    Delete    Add Parentheses    Remove Parentheses    Move Up    Move Down

20 Libs Selected of 20 Two Part Libs Selected    30 Total Libraries

Library	Total Member Count	OTU Matched Count
HV1-1-BaCSc	305	
HV10-BaCSc	289	
HV2-1-BaCSc	354	
HV3-1-BaCSc	180	
HV4-1-BaCSc	296	
HV5-BaCSc	541	
HV6-1-BaCSc	334	
HV7-BaCSc	338	
HV8-BaCSc	297	

New

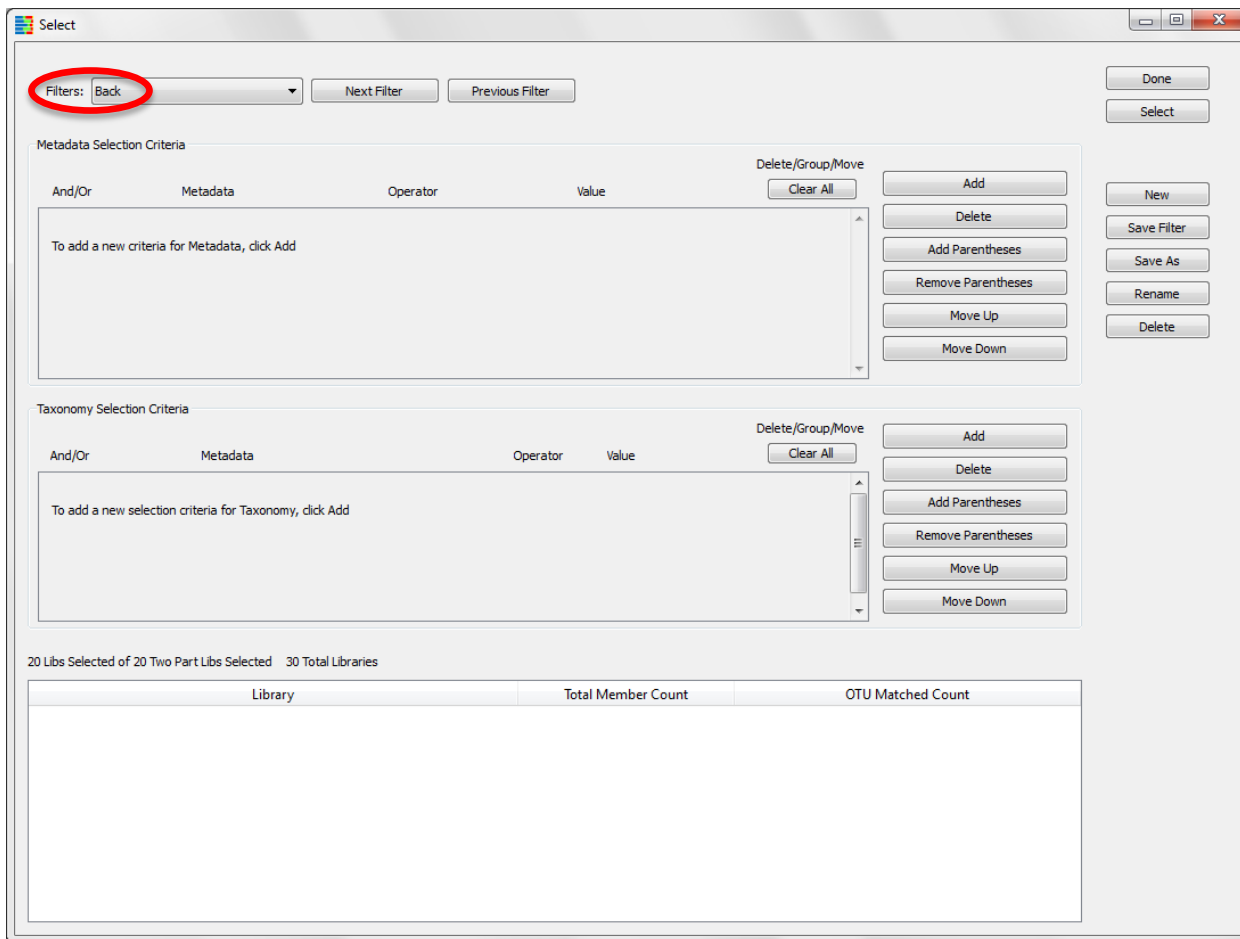
Enter desired filter name in the pop-up window  
Click **OK**

New Filter

Filter name:  
Back

OK    Cancel

The filter name will appear in upper left corner of window



Now that we have created a new filter, we need to set up the parameters to filter by. We will select for all libraries which were sampled from the “back”.

## B. Set Up Filter Parameters

Click **Add** in the **Metadata Criteria** pane

The screenshot shows the 'Select' application window. At the top, there are buttons for 'Back', 'Next Filter', and 'Previous Filter'. Below these are two main sections: 'Metadata Selection Criteria' and 'Taxonomy Selection Criteria'. Each section has a table with columns 'And/Or', 'Metadata', 'Operator', and 'Value'. To the right of each table is a 'Delete/Group/Move' section with buttons: 'Clear All', 'Add', 'Delete', 'Add Parentheses', 'Remove Parentheses', 'Move Up', and 'Move Down'. A red arrow points to the 'Add' button in the Metadata section. On the far right, there are buttons for 'Done', 'Select', 'New', 'Save Filter', 'Save As', 'Rename', and 'Delete'. At the bottom, there is a status bar showing '20 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries' and a table with columns 'Library', 'Total Member Count', and 'OTU Matched Count'.

Filters: Back Next Filter Previous Filter

Done Select

Metadata Selection Criteria

And/Or Metadata Operator Value Delete/Group/Move

Clear All Add Delete Add Parentheses Remove Parentheses Move Up Move Down

To add a new criteria for Metadata, click Add

Taxonomy Selection Criteria

And/Or Metadata Operator Value Delete/Group/Move

Clear All Add Delete Add Parentheses Remove Parentheses Move Up Move Down

To add a new selection criteria for Taxonomy, click Add

20 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries

Library	Total Member Count	OTU Matched Count
---------	--------------------	-------------------

Use the first pull-down menu to select "Anatomy" (**Metadata** to filter by)  
 Use the second pull-down menu to select "contains" (filter **Operator**)

Enter “back” into Value

The screenshot shows a window titled "Select" with a toolbar at the top containing "Filters: Back", "Next Filter", and "Previous Filter". Below this are two main sections: "Metadata Selection Criteria" and "Taxonomy Selection Criteria".

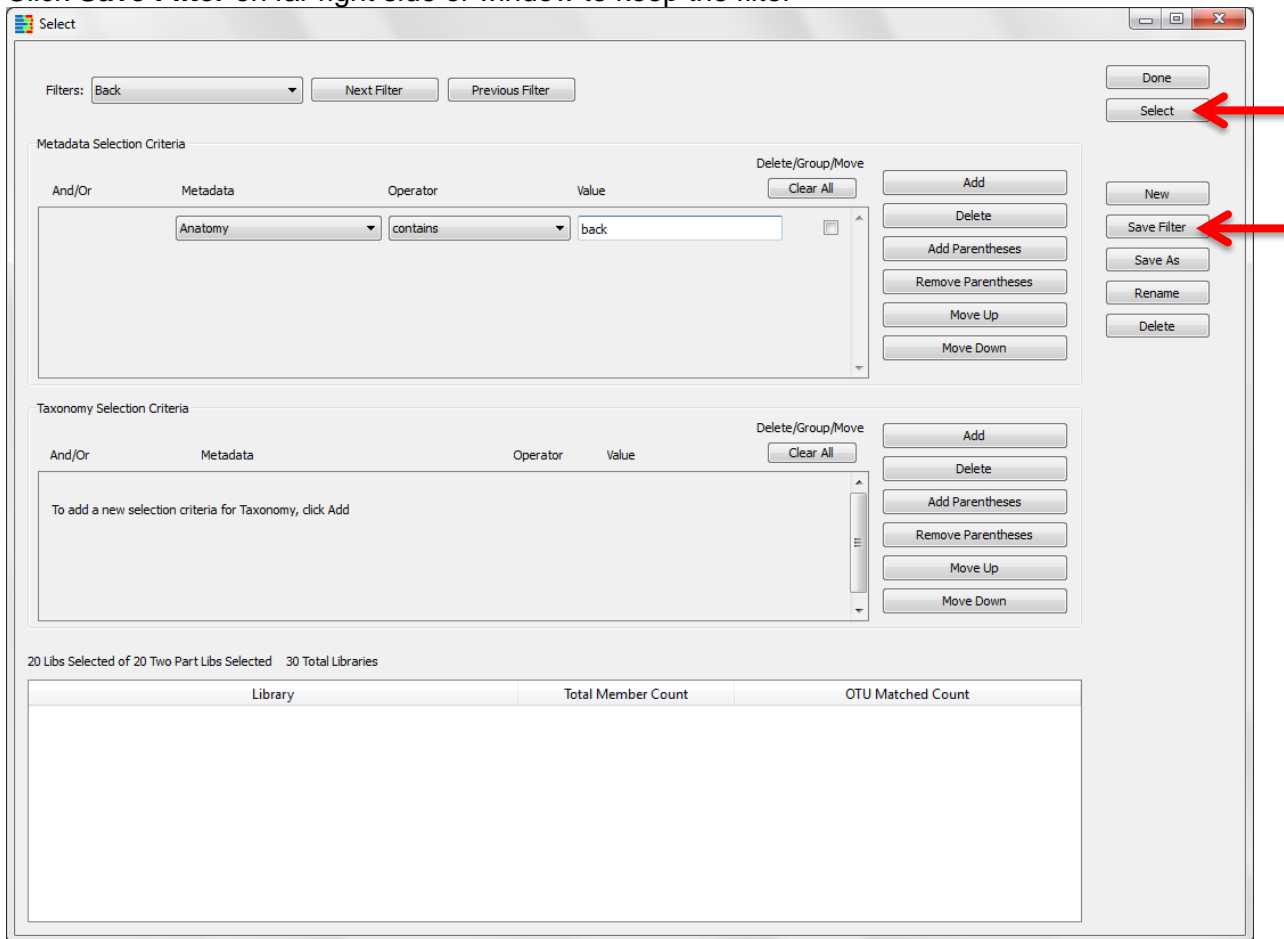
**Metadata Selection Criteria:** This section has columns for "And/Or", "Metadata", "Operator", and "Value". The "Metadata" dropdown is set to "Library", and the "Operator" dropdown is set to "equals". The "Value" field is empty. Three red arrows point to these three fields respectively. To the right of these fields are buttons for "Delete/Group/Move" (with a "Clear All" sub-button), "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down".

**Taxonomy Selection Criteria:** This section has similar columns: "And/Or", "Metadata", "Operator", and "Value". The "Value" field contains the text "To add a new selection criteria for Taxonomy, click Add". To the right are buttons for "Delete/Group/Move" (with a "Clear All" sub-button), "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down".

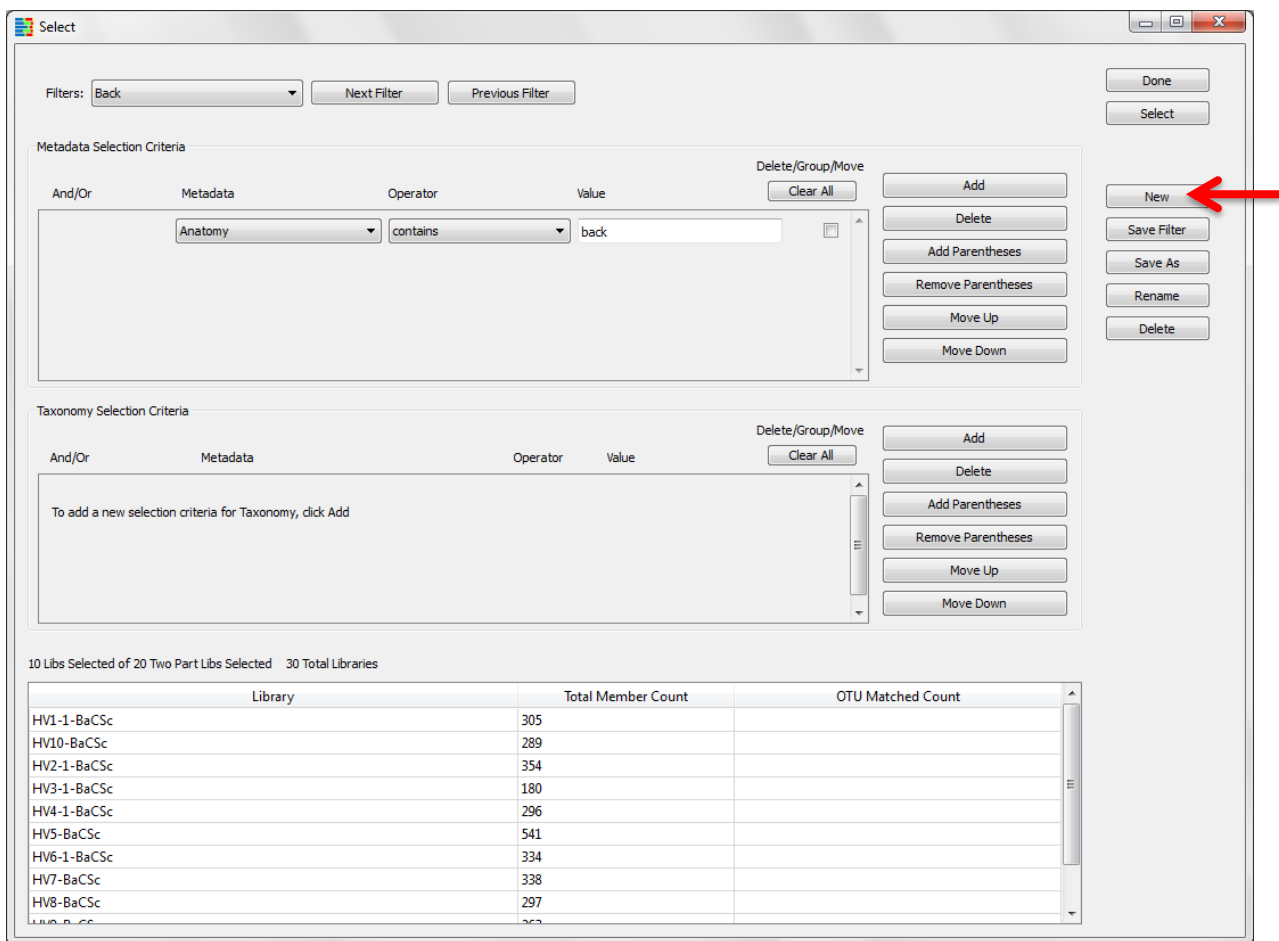
At the bottom, a status bar shows "20 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries". Below this is a table with three columns: "Library", "Total Member Count", and "OTU Matched Count". The table body is currently empty.

To apply filter, click **Select** in upper right corner of window

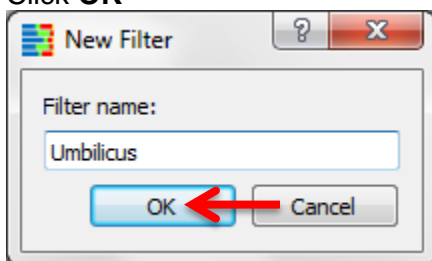
Click **Save Filter** on far right side of window to keep the filter



Now we will create a separate filter for the umbilicus  
Click **New** on far right side of window



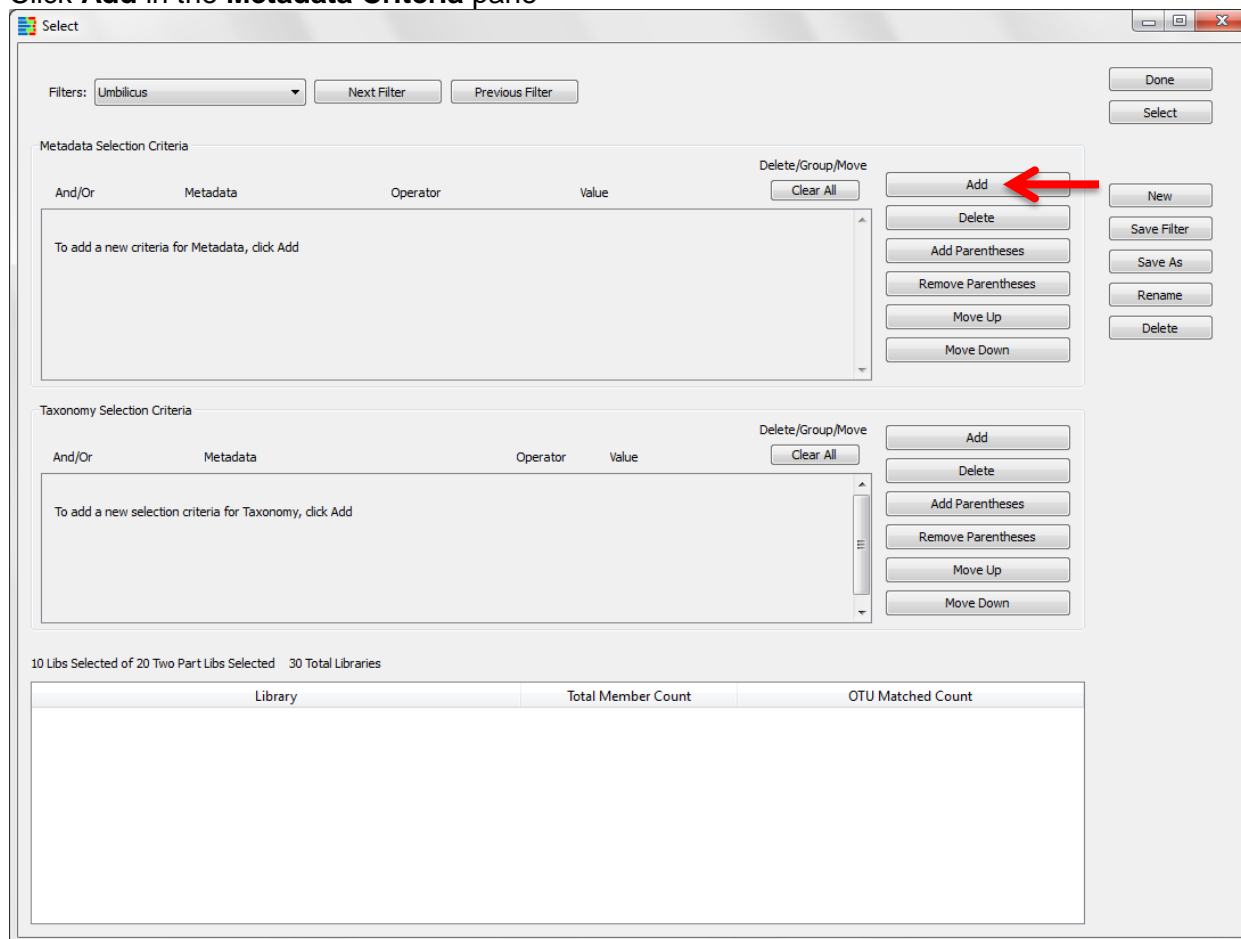
Enter desired filter name in the pop-up window  
Click **OK**



The filter name will appear in upper left corner of window.



Click **Add** in the **Metadata Criteria** pane



The screenshot shows a window titled "Select" with a toolbar at the top containing "Filters:", a dropdown menu showing "Umbilicus", and buttons for "Next Filter" and "Previous Filter". On the right side of the toolbar are "Done" and "Select" buttons.

The main area is divided into two sections: "Metadata Selection Criteria" and "Taxonomy Selection Criteria". Each section has a table with columns: "And/Or", "Metadata", "Operator", "Value", and "Delete/Group/Move".

In the "Metadata Selection Criteria" section, the "Delete/Group/Move" column contains buttons: "Clear All", "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down". A red arrow points to the "Add" button.

Below the table in the "Metadata Selection Criteria" section is a text box that says "To add a new criteria for Metadata, click Add".

The "Taxonomy Selection Criteria" section has a similar structure with a table and a text box that says "To add a new selection criteria for Taxonomy, click Add".

At the bottom of the window, there is a status bar that says "10 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries". Below this is a table with three columns: "Library", "Total Member Count", and "OTU Matched Count".

Use the first pull-down menu to select "Anatomy" (**Metadata** to filter by)  
Use the second pull-down menu to select "contains" (filter **Operator**)



Enter “umbilicus” into **Value**

The screenshot shows a window titled "Select" with a filter configuration interface. At the top, there's a "Filters:" dropdown set to "Umbilicus", with "Next Filter" and "Previous Filter" buttons. Below this is the "Metadata Selection Criteria" section, which has a table with columns: "And/Or", "Metadata", "Operator", "Value", and "Delete/Group/Move". The first row shows "Library" in the "Metadata" column, "equals" in the "Operator" column, and an empty text field in the "Value" column. Three red arrows point to these three fields respectively. To the right of the table are buttons: "Clear All", "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down". Below the Metadata section is the "Taxonomy Selection Criteria" section, which is currently empty with a message "To add a new selection criteria for Taxonomy, click Add". At the bottom, there's a status bar showing "10 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries" and a table with columns "Library", "Total Member Count", and "OTU Matched Count". On the far right, there are buttons: "Done", "Select", "New", "Save Filter", "Save As", "Rename", and "Delete".

To apply filter, click **Select** in upper right corner of window

Click **Save Filter** on far right side of window to keep the filter

The screenshot shows a software window titled "Select". At the top, there is a "Filters:" dropdown menu currently set to "Umbilicus", with "Next Filter" and "Previous Filter" buttons. Below this is the "Metadata Selection Criteria" section, which contains a table with columns "And/Or", "Metadata", "Operator", and "Value". The table has one row with "Anatomy" in the Metadata column, "contains" in the Operator column, and "umbilicus" in the Value column. To the right of the table are buttons for "Delete/Group/Move" (with a "Clear All" sub-button), "Add", "Delete", "Add Parentheses", "Remove Parentheses", "Move Up", and "Move Down". Below the metadata section is the "Taxonomy Selection Criteria" section, which has a similar layout but is currently empty, with a message "To add a new selection criteria for Taxonomy, click Add". At the bottom of the window, there is a status bar showing "10 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries" and a table with columns "Library", "Total Member Count", and "OTU Matched Count". On the far right side of the window, there is a vertical column of buttons: "Done", "Select", "New", "Save Filter", "Save As", "Rename", and "Delete". Two red arrows point to the "Select" and "Save Filter" buttons.

Filters: Umbilicus   Next Filter   Previous Filter

Metadata Selection Criteria

And/Or	Metadata	Operator	Value
	Anatomy	contains	umbilicus

Delete/Group/Move: Clear All, Add, Delete, Add Parentheses, Remove Parentheses, Move Up, Move Down

Taxonomy Selection Criteria

And/Or	Metadata	Operator	Value
To add a new selection criteria for Taxonomy, click Add			

10 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries

Library	Total Member Count	OTU Matched Count
---------	--------------------	-------------------

Buttons on the right: Done, Select, New, Save Filter, Save As, Rename, Delete

Click **Done** to return to the Two-Part test setup window

Filters: Umbilicus   Next Filter   Previous Filter

Metadata Selection Criteria

And/Or	Metadata	Operator	Value	Delete/Group/Move
	Anatomy	contains	umbilicus	<input type="checkbox"/>

Taxonomy Selection Criteria

And/Or	Metadata	Operator	Value	Delete/Group/Move
To add a new selection criteria for Taxonomy, click Add				

10 Libs Selected of 20 Two Part Libs Selected 30 Total Libraries

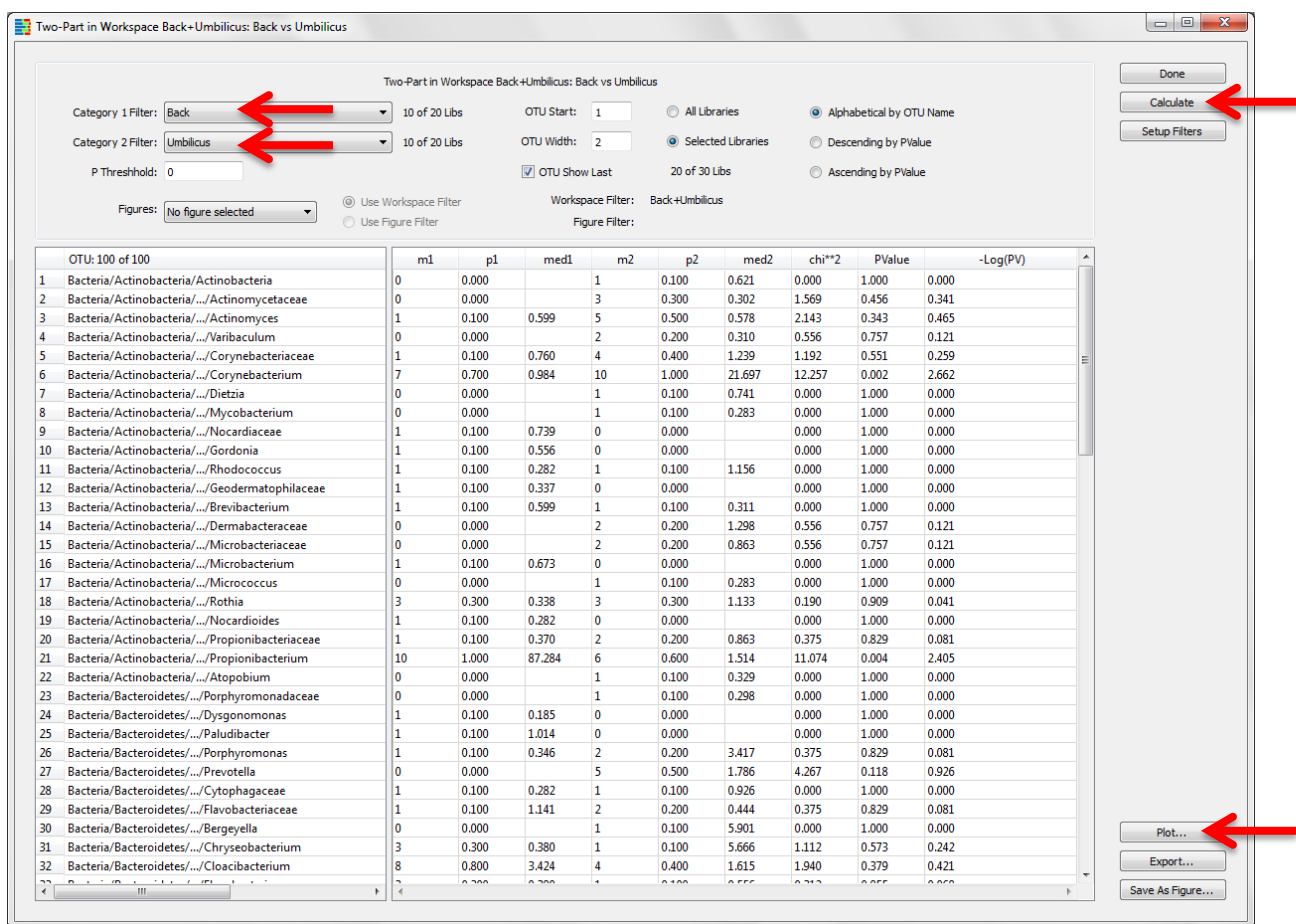
Library	Total Member Count	OTU Matched Count
HV1-1-UmCSw	303	
HV10-UmCSw	313	
HV2-1-UmCSw	346	
HV3-1-UmCSw	331	
HV4-1-UmCSw	304	
HV5-UmCSw	353	
HV6-1-UmCSw	322	
HV7-UmCSw	325	
HV8-UmCSw	540	

Select “Back” for the **Category 1 Filter**

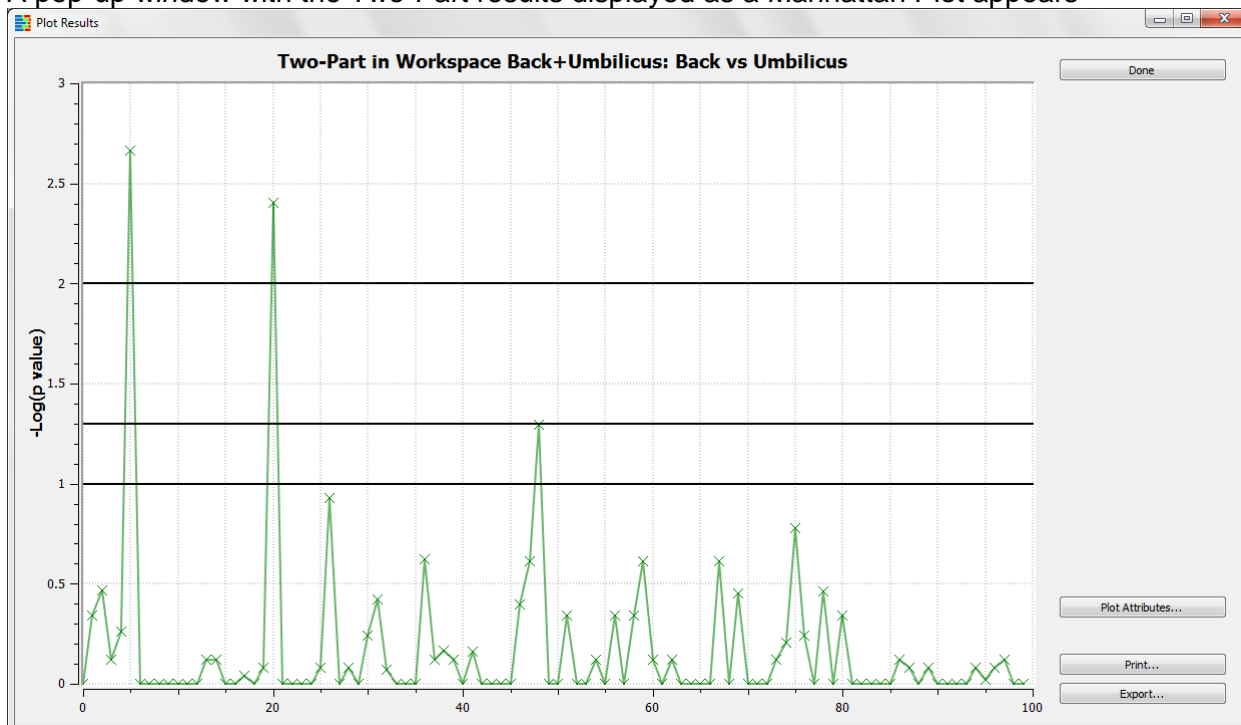
Select “Umbilicus” for the **Category 2 Filter**

Click **Calculate**

Click **Plot**



A pop-up window with the Two-Part results displayed as a Manhattan Plot appears



The Manhattan Plot displays logarithmically transformed p-values, with higher peaks representing lower (more significant) p-values. The horizontal lines represent p-values of 0.10, 0.05, and 0.01. Inclusion of the p=0.10

line is intended to highlight taxa that are approaching significance in an analysis. The x-axis represents the alphabetical position, by number, of each OTU name in the Two-Part setup dialog above.

In the Manhattan Plot, the first significant peak (position 6) corresponds to *Corynebacterium*, which have a higher proportion and relative abundance in the umbilicus samples. The second peak (position 21) represents *Propionibacterium* that is present at a higher proportion and relative abundance in the back samples. The third peak that approaches significance (position 49) represents *Anaerococcus*. This taxon is not seen in many of the libraries generated from back samples, and thus is present at higher proportion and relative abundance in the umbilicus samples.

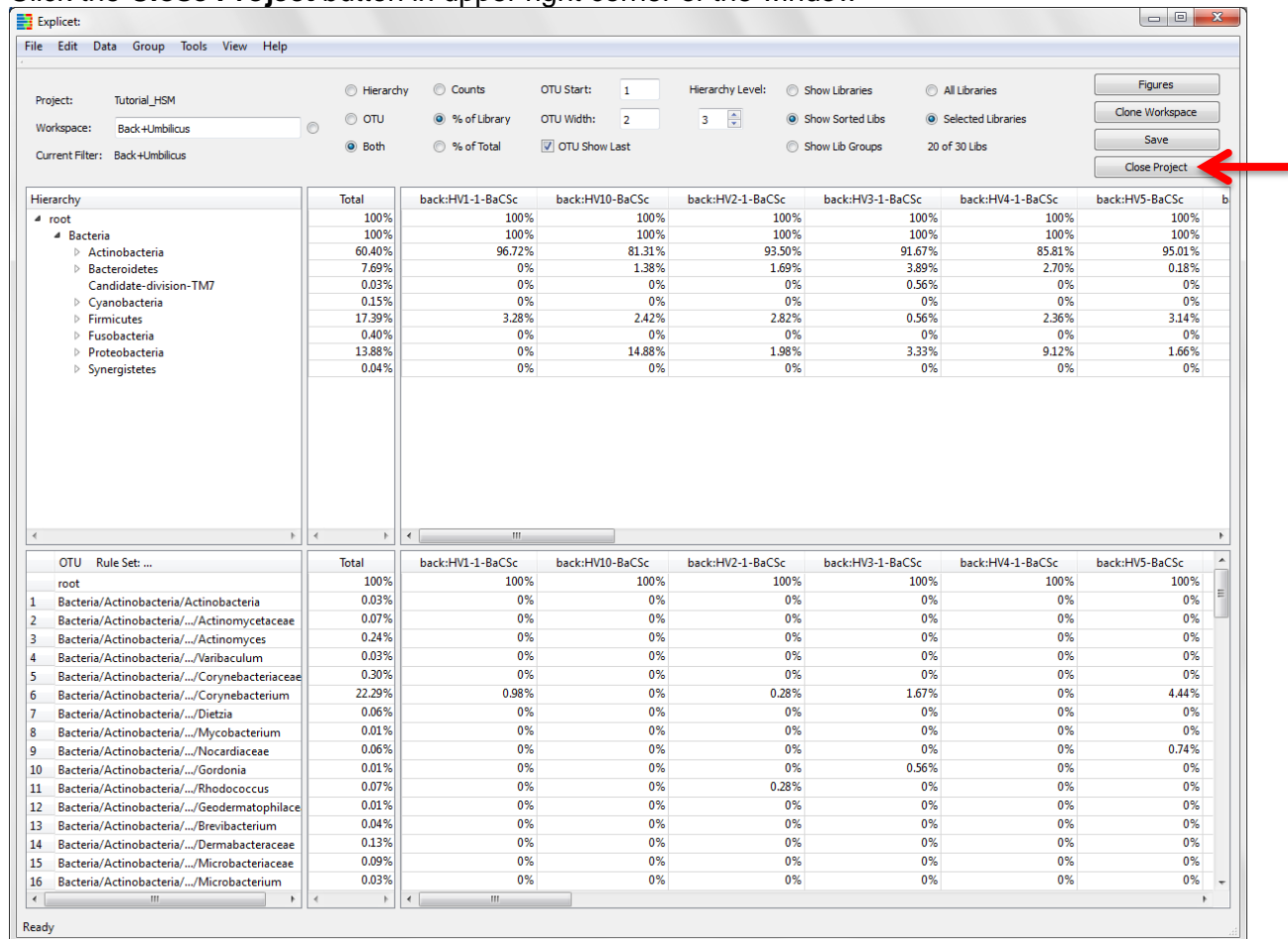
Data can be exported from the **Plot Results** window as tab delimited text using the export button (available in all graphics windows). The data incorporated for each taxon in the Two-Part statistic are summarized for each category. The number of samples with sequences belonging to an OTU within each category is designated “m”, proportion of positive libraries in a category “p”, and median relative abundance “med”.

You may choose to save the Two-Part test as a figure. To do so, continue as shown earlier in the stacked bar chart example; close the graphics window, and select **Save As Figure** in the **Two-Part** window.

This tutorial has provided a quick overview of how to use Explicit. For more complete information on Explicit capabilities, please see the Explicit Handbook. We will now save our changes and close the project.

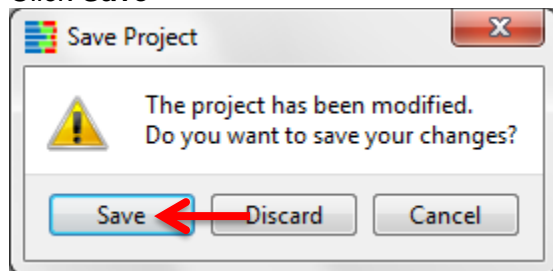
### XIII. Close the Project

Click the **Close Project** button in upper right corner of the window



A pop-up window will open

Click **Save**



The Explicitet window will close, and all of the OTU data, metadata, and figures are now saved within the project file.

Thus ends a basic overview of some functions contained in Explicitet. Please do not hesitate to ask questions or make suggestions via our online Explicitet forum. The Explicitet forum link can be found on our web site: [www.explicitet.org](http://www.explicitet.org).