Supplemental Method: Use the Integrated Genome Browser (IGB) to visualize the genome-scale data sets presented in this manuscript.

The Integrated Genome Browser (http://www.bioviz.org) is one of the software packages we used to view the data sets during the data analysis process. Here we present a short guide on how to load the data sets (provided as Supplemental Dataset 1) into IGB for visualization. Other software packages, such as SignalMap (http://www.nimblegen.com) and UCSC Genome Browser (http://genome.ucsc.edu/), are also suitable. However, these softwares may require input files in a different format other than the ones provided here. Interested users should refer to the manuals of these software packages for detailed instruction.

Download the supplementary data set.

Supplemental Dataset 1 is provided in zip format and can be downloaded in the supplemental material section of this manuscript at http://www.genome.org, as well as our group's website (http://gcrg.ucsd.edu). Once downloaded, it needs to be extracted. The extracted files are organized in the following directory structure:

```
GR_suppl_dataset_1                              Top folder
     |-------- igb_quickload                    IGB quickload folder
     |                |-------- Geobacter       Analysis results folder
     |
     |-------- experimental_data                Experimental data folder
                      |-------- proteomics      Proteomics data folder
                      |-------- expression      Tiling array expression data folder
                      |-------- chip-chip       Chip-chip data folder
                      |-------- others          Oother data
```

Launch IGB.

IGB could be launched through bioviz's website (http://www.bioviz.org/igb/download.shtml). Java runtime is needed.

Configure IGB.

We provided our results as a ready-to-use IGB's quickload directory. Users need to add the igb_quickload folder as a quickload directory. Go to **File-> Preferences -> Data Sources** and click **Add** to open **Add Server** panel. Specify a friendly server name such as "Geobacter", specify the type as "QuickLoad" and specify the path to the igb_quickload directory, then click **Add**.

The URL should look similar to one of these (make sure it starts with file:///):

* A local Windows file: file:///C:/Data/GR_suppl_dataset_1/igb_quickload/
* A local Unix/Mac file: file:///home/user/GR_suppl_dataset_1/igb_quickload/

Load analysis results into IGB.

Once the quickload directory is configured, user can load the analysis results (saved as annotation files for IGB) into IGB:

1. Click the **Data Access tab** in the lower part of the IGB window.
2. Choose **Geobacter** as the species from the drop-down box and choose **Geobacter** as the genome version. Now a list of data sets, such as "experimental annotation" will appear in the **Data Sources** table at the lower left of the window and "NC_002939" will appear in the **Current Sequence** table.
3. Click a **Data Set** checkbox to start loading a data set. You also can load the genome sequence by clicking **Load all Sequence**.
4. Choose **Whole Genome** as the Load Mode for the data sets.
5. Now you can browse the data by using the sliders on top and on left to zoom and using the scrollers on bottom and on right to scroll. Information about the different tabs below can be found in the IGB manual.

Load additional experimental data into IGB.

We provided additional experimental data sets (saved as graph files for IGB) in the "experimental_data" folder. User can load them by **File -> Open**, and select the experimental data sets he wants to view in IGB. Please make sure annotation files were loaded and choose to merge the newly opened data files with the existing group.

Adjust the view

IGB provides many options to adjust the display properties of each data set, such as color, Y-Axis scale, and style. For detailed instruction, please refer to the IGB manual.