Manhattan Plot

The Manhattan plot is a common way to visualize p-values or log-odds ratios for GWAS studies across genomic coordinates.

The starting point for a Manhattan plot is a spreadsheet with SNPs on rows and p-values or log-odds ratios in a column. If beginning with p-values, you will need to convert the p-values to -$\log_{10}$(p-value).

- Select the column with p-values
- Select **Transform** form the main toolbar
- Select **Normalization & Scaling**
- Select **On Columns...**
- In the *Normalization* tab, set *Base* of the *Log(x + offset)* to **10**
- Select **OK**
- Go to **Transform > Normalization & Scaling > On Columns...** again
- Select the **Add/Mul/Sub/Div** tab
- Set *Multiply by Constant* to **-1**
- Select **OK**

The column now contains -$\log_{10}$(p-value).

We can now invoke the initial plot.

- Select **View** from the main toolbar
- Select **Genome View**

The *Genome View* tab will open. This plot will need to be configured.

- Select ( ) from the plot command bar
- Select the **Profiles** tab
- Remove any unwanted profiles
- Select **Add profile**
- Select **Column**
- Select the column with the -$\log_{10}$(p-value) or logs-odds ratio values from the drop-down menu
- Select **Value** for *Color by*
- Select **point** from the *Style* drop-down menu
- Select **OK** to add the profile
- Select **OK** to close the *Configure Plot Properties* dialog

The plot will now show a Manhattan plot (Figure 1).

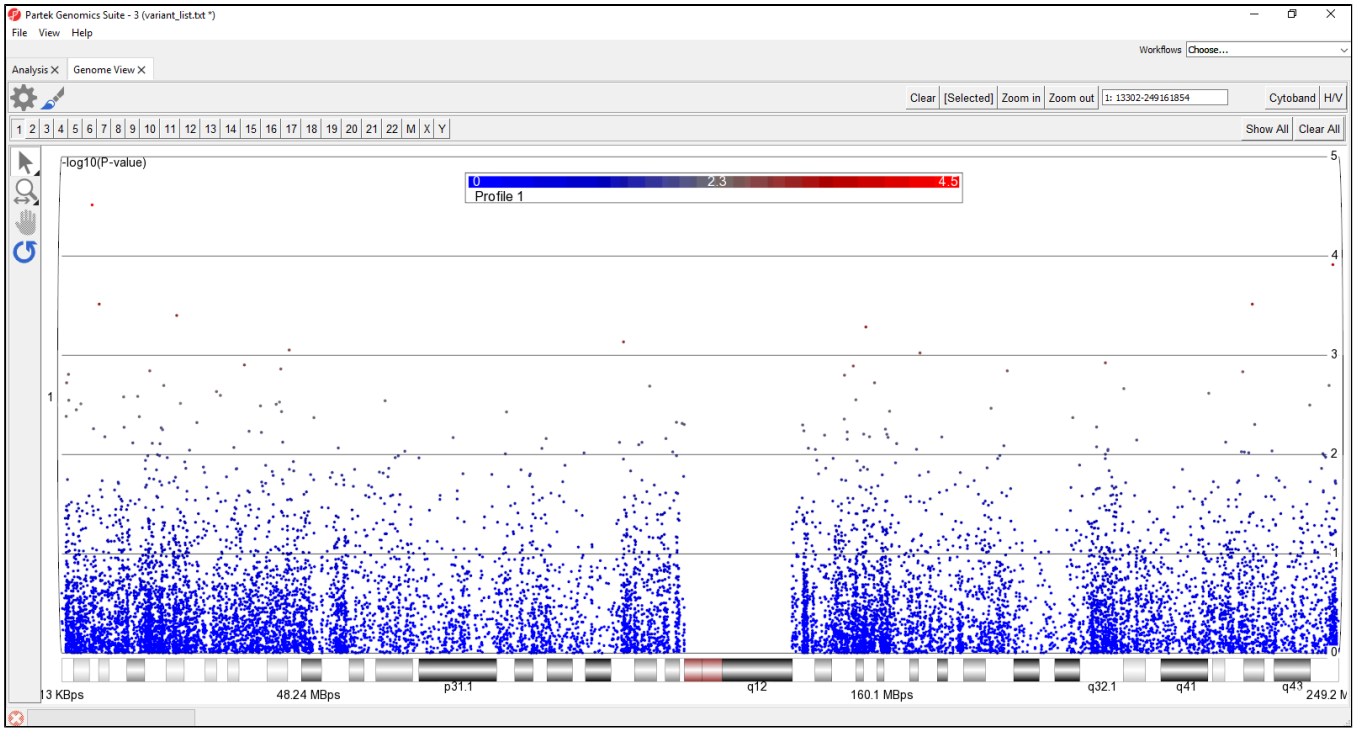

Figure 3. Customized Genome View showing genomic locations on the x-axis and -log10(P-values) of SNPs on the y-axis (Manhattten plot). Each dot represents a single SNP. The Cytoband is shown along the bottom of the plot

It is also possible to display multiple chromosomes at the same time.

- Select **Show All** in the upper-right hand corner of the plot

This displays all chromosomes vertically. We can display them horizontally for a better view.

- Select  to open the *Configure Plot* dialog
- Select **Genome in line** for *Layout*
- Select **OK**

To further improve the genome-wide view, we can remove the cytoband, remove the genomic position label, color points by chromosome, and increase point size.

- Select **Cytoband** in the upper right-hand corner
- Select 
- Select the **Axes** tab
- Deselect **Show Base Pair Labels**
- Select **Profiles**
- Select **Configure**
- Set *Color By* to a column with chromosome for each SNP/loci as a category
- Set *Shape Size* to **5.0**
- Select **OK** to close the *Configure Profile* dialog
- Select **OK** to apply changes

The plot will appear as shown (Figure 2).

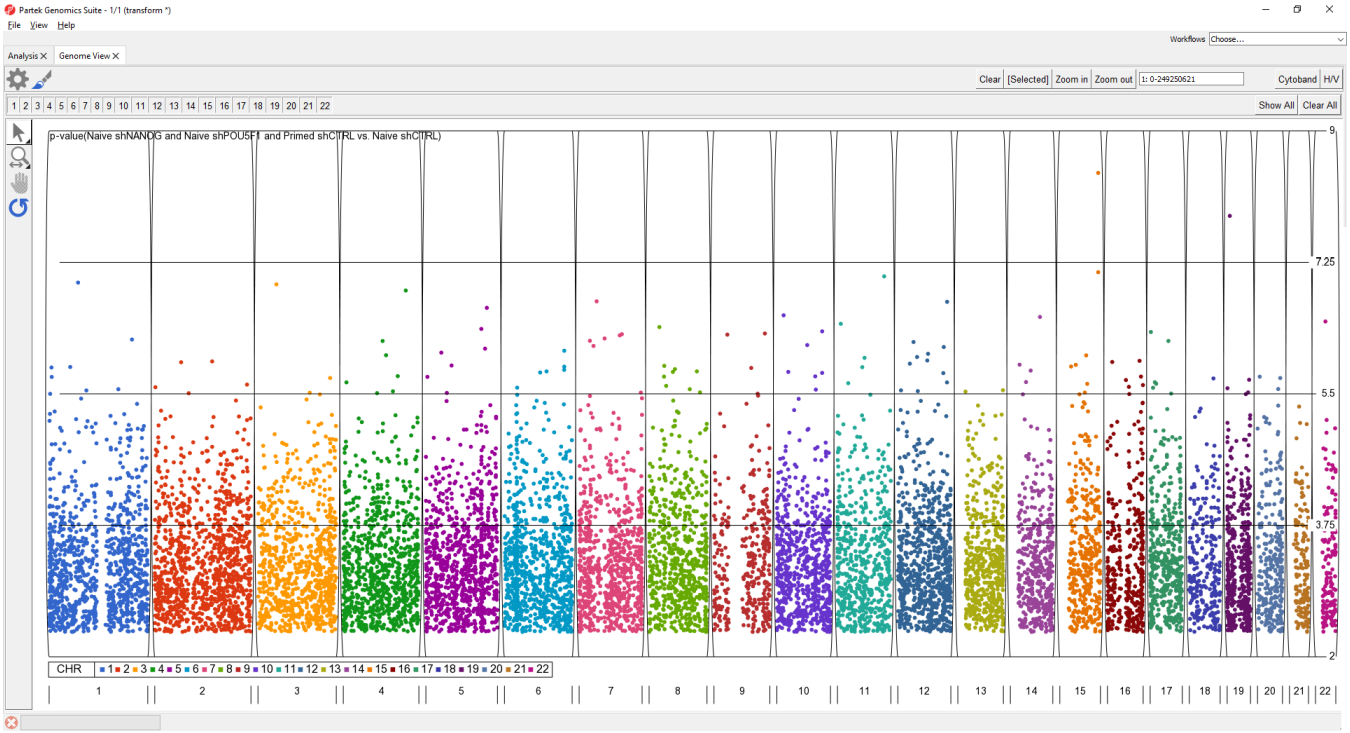

Figure 4. Full genome Manhattan plot

For details on *Genome View* see **Chapter 6: The Pattern Visualization System** in the Partek User's Manual.

Additional Assistance

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