


# Viewing a dot plot for a gene

In addition to the volcano plot showing all genes, we can view expression levels of each gene on a dot plot.

- Double-click the **Filtered feature list** data node to open the task report
- Click the **FDR step up** header in the *5uM vs. 0uM* section to sort by ascending FDR step up

In the task report table, there is a column labeled *View* with three icons    in each row.

- Select  to open a dot plot for the gene SELENOM

The dot plot for SELENOM (Figure 1) shows each sample as a point with normalized reads on the y-axis. Samples are separated and colored by treatment group.

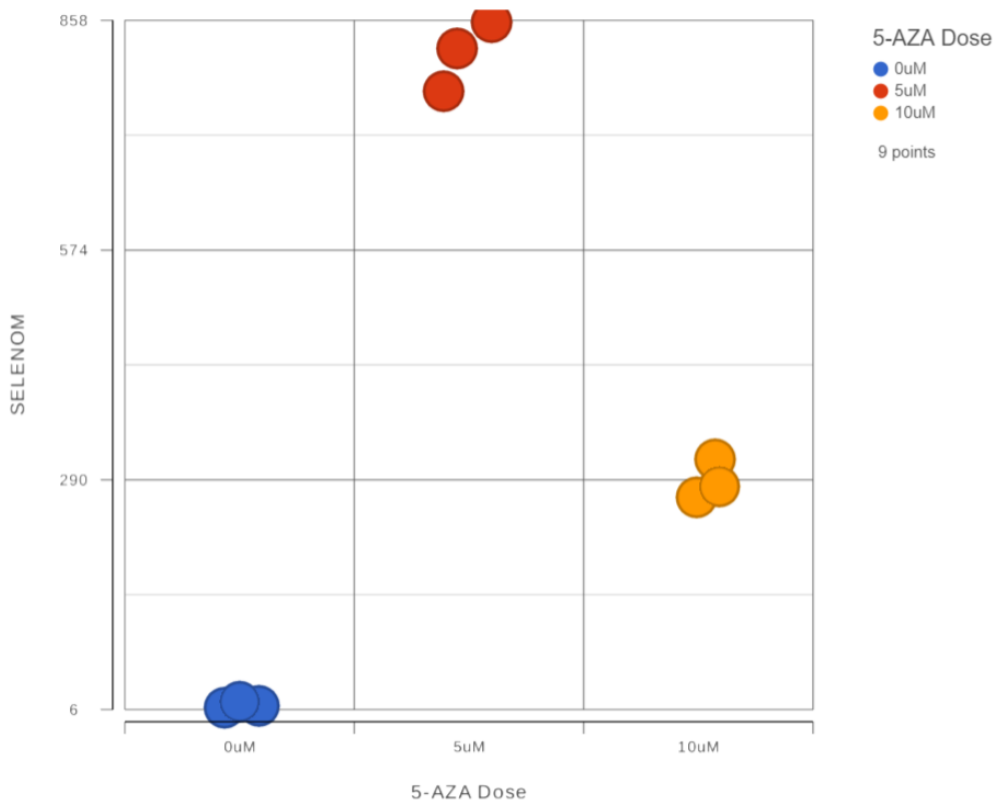




Figure 2. Dot plot for SELM

For more information about the dot plot, please see the [Dot Plot](#) user guide. To return to the DESeq2 report, switch to the browser table with filtered feature list.

In the DESeq2 report, you can select  to view additional information about the statistical results for a gene or select  to view the region in *Chromosome View*. *Chromosome View* is discussed in the next section of the tutorial.

« [Viewing DESeq2 results and creating a gene list](#) [Visualizing gene expression in Chromosome view](#) »

## Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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