



**Figure 1. Integrative Genomics Viewer (IGV) map of sequenced DNA displaying 5mC levels on *Arabidopsis* chromosome 5.**

Representative genomic region showing methylated regions of DNA on chromosome 5 from nucleotide 8,647,136 to nucleotide 8,651,646 in *Arabidopsis* samples with *Arabidopsis* RNA corresponding to genes ENODL13 and T11H3.110. Levels of 5mC at specific locations in the genome are shown with higher peaks corresponding to a higher level of 5mC detection at a given nucleotide. The coverage sections indicate the number of reads at a given position, with higher coverage of RNA indicating gene expression. The Reference Genes show known genes aligned to the *Arabidopsis* reference genome.

(Note to grader: 5mC scores will be replaced with 6mA when the appropriate tool has been identified. The region that is displayed will change to show where the 6mA markers are located)

Main critiques of original figure:

- Too busy
  - The message wasn't clear enough because we had so many tracks and were visualizing a larger region of the genome
- Unclear labels for tracks
- Methylation marks should be closer to the RNA reference genes
- The text was too small

What we changed:

- We got rid of unnecessary tracks so that we are now only showing the essentials: methylation, DNA/RNA coverage, and reference genes
  - The methylation track is now also closer to the reference genes because of this change
- We zoomed in on a smaller region of the genome to present a clearer example of methylation patterns that look fairly consistent across the genome
- We renamed the tracks and made the labels bigger so they could be read more easily.