How to use MochiView

1. Download MochiView from:

<http://www.johnsonlab.ucsf.edu/mochiview-downloads>

2. Install on computer, make sure you have the correct Java.

3. Import:

Fasta file:

Import – location set – format: FASTA (we use D39V)

Wig files (2 per samples)

Import – tiled set – format:WIG (decimal if importing data type for the first time)

Annotation file:

Import – location set (genes) – Format: MochiView – (annotation file should be the gene, not CDS)

4. Then create the file

Tips:

* When visualizing peak height make sure to rescale the Y-axis
* You can only copy the sequence that is visible in the window
* When searing for a gene have to type out spv\_gene#