

2.

a) In Vitro:

- SELEX-seq - a high throughput method used to identify the interactions, specificity, and affinity of proteins with specific DNA sequences. Proteins are attached to a plate. Random DNA oligonucleotides are flown over the plate. The proteins bind specifically to the DNA, the sequences that attached are then amplified and sequences to determine binding affinity.

- Advantages - quantitative binding data, no cellular components to complicate

analysis

-Disadvantages - expensive, time

- PBM - (Protein binding microarrays) a high throughput method used to identify the interactions, specificity, and affinity of proteins with specific DNA sequences. DNA is bound to surface of plate, the complementary strand is created forming a double helix, proteins marked by fluorescent probe molecules are flowed over the plate. Based the location and strength of the fluorescence, the affinity location and strength of affinity can be determined.

- Advantages - large numbers of proteins can be tracked in parallel, no cellular components to complicate analysis, quantitative binding data

-Disadvantages - expensive, time

b) In Vivo:

- ChIP-seq - (Chromatin ImmunoPrecipitation) a method used to analyze protein-DNA interactions. A DNA library is prepared, the DNA is then sequenced, and the protein interactions are then analyzed.

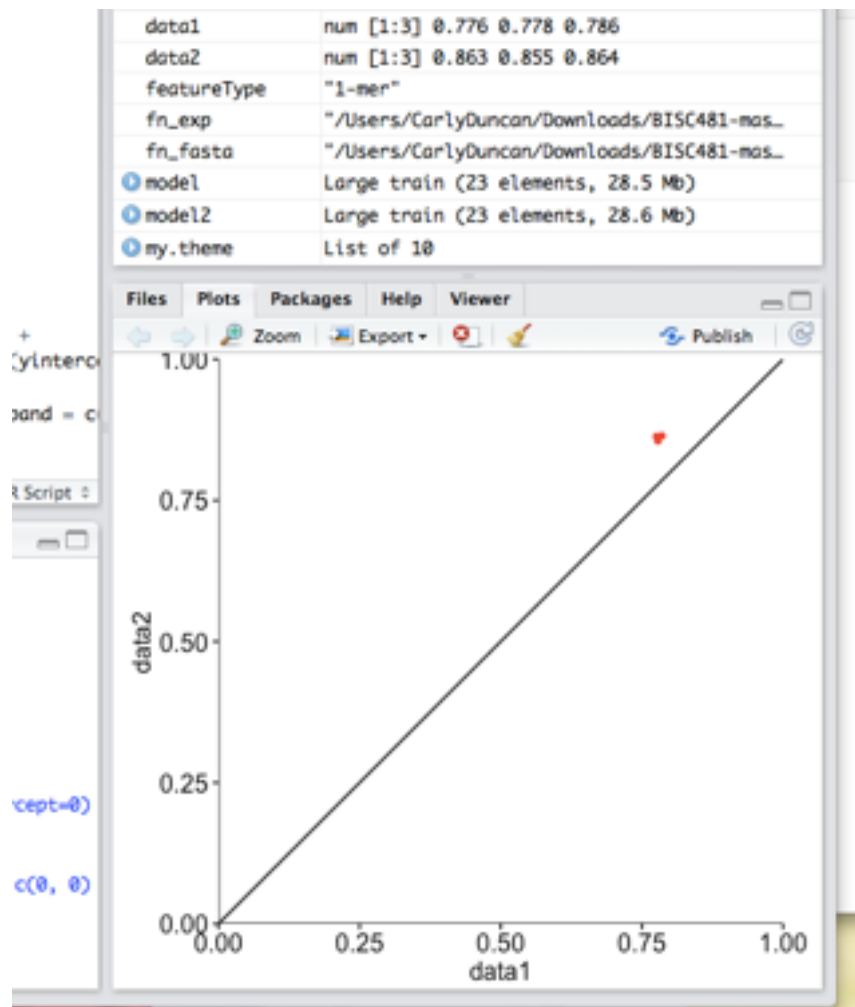
-Advantages - fast, easy, yes or no answer

-Disadvantages - only qualitative data

4.

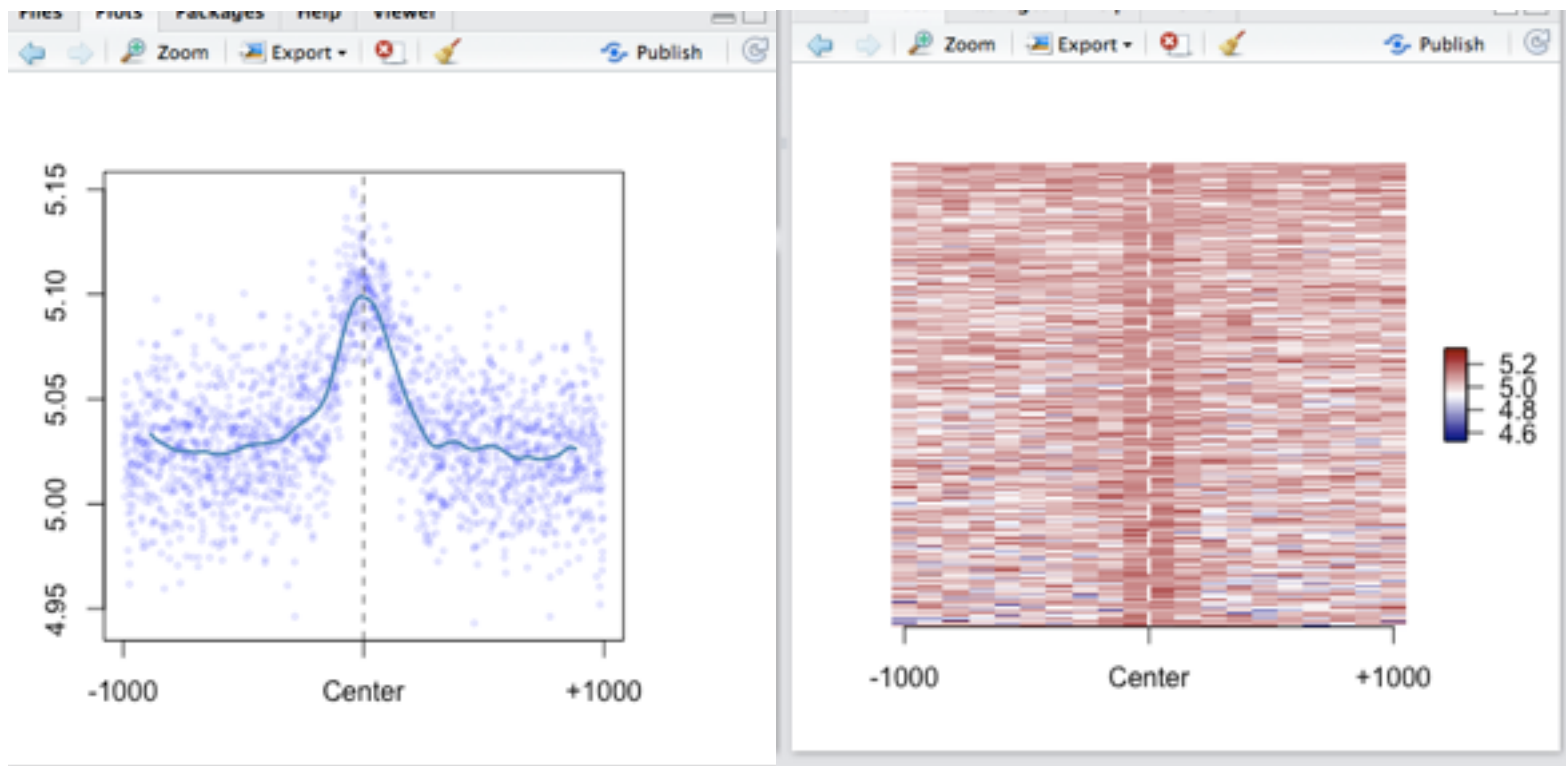
	1mer+shape	1mer
<b>Mad</b>	0.8632745	0.7757529
<b>Myc</b>	0.8554537	0.77828
<b>Max</b>	0.8643231	0.7855093

5.

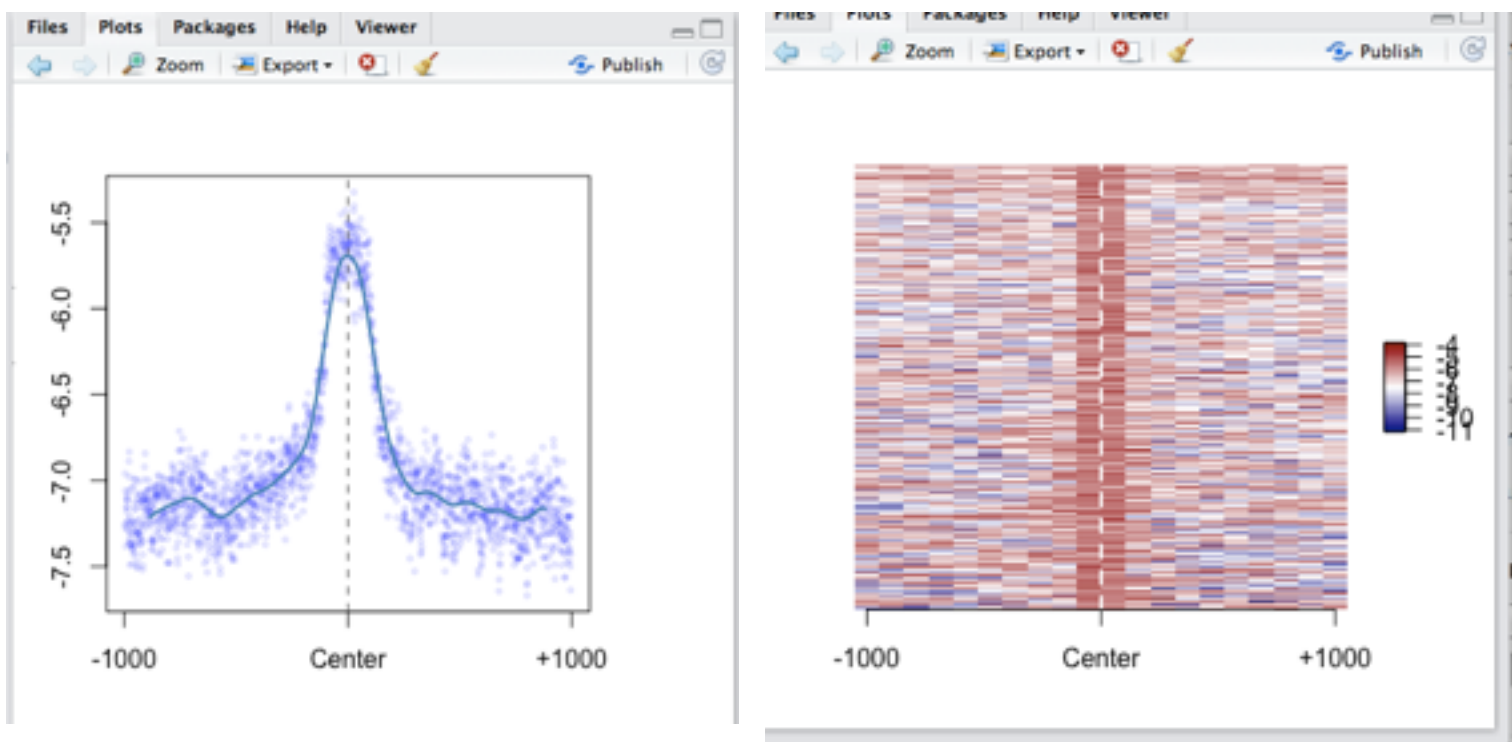


5b)  $R^2$  value for the shape model is better than that of the sequence alone. This is demonstrated by the fact that the red dots are above the line.

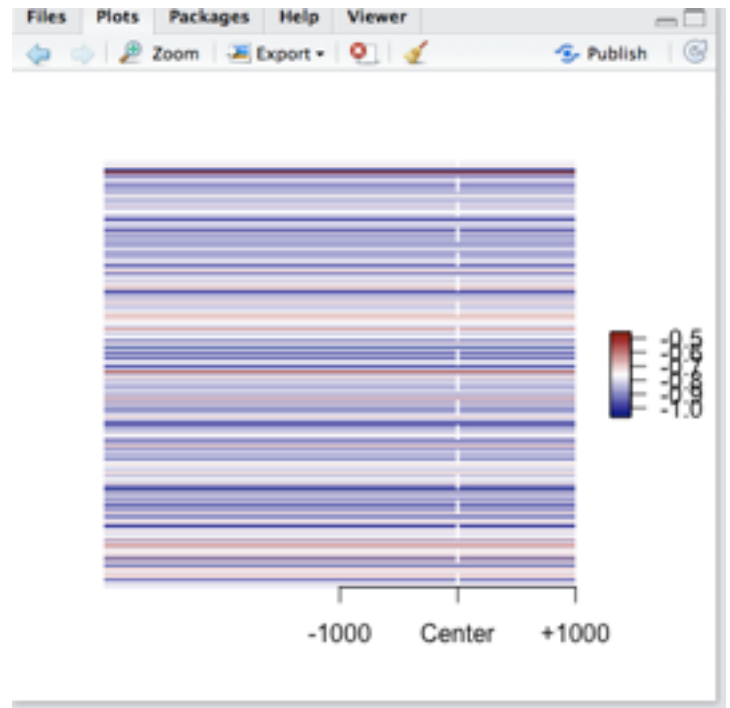
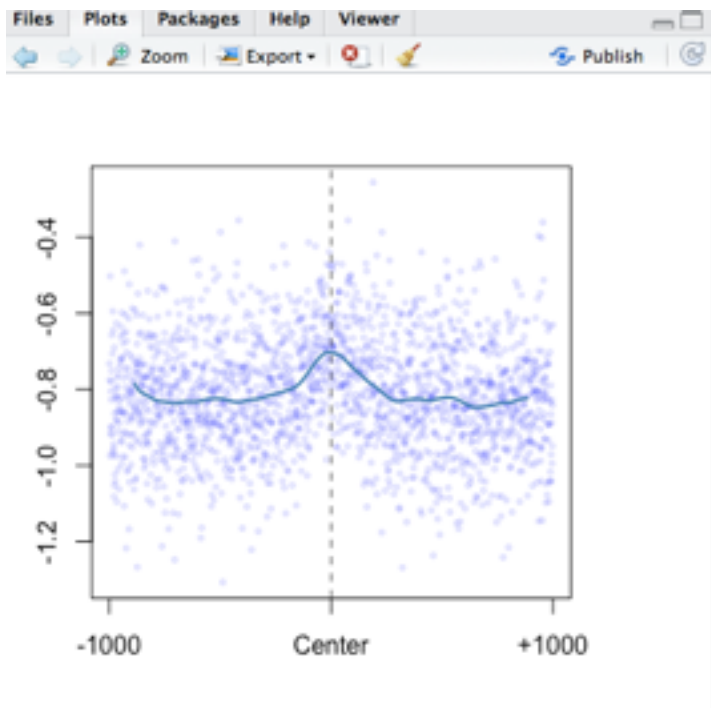
7)  
MGW Plot and Heat Shape



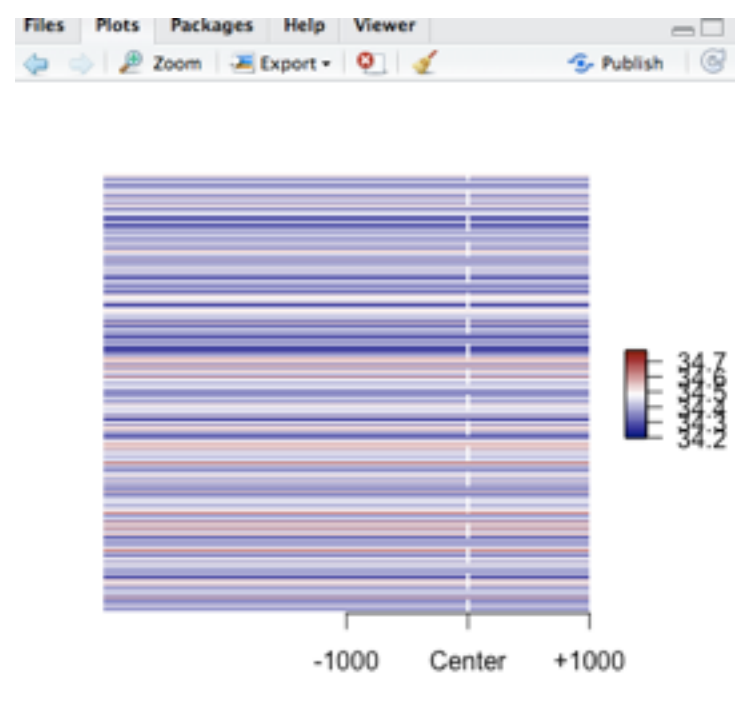
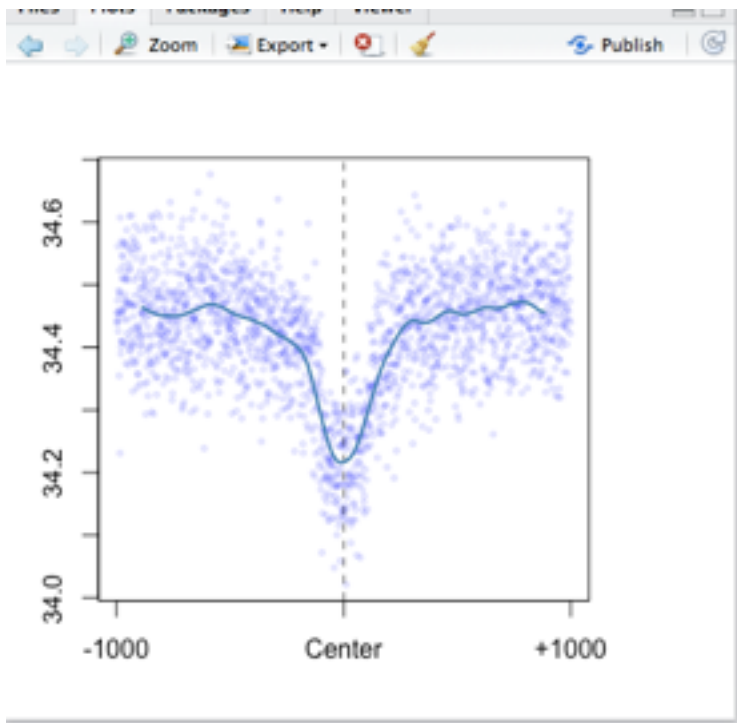
ProT Plot and Heat Shape



## Roll Plot and Heat Shape



## HeIT Plot and Heat Shape



7b) Plot Shape gives a more easily visualized result than the heat shape. Additionally, the number of bases must be changed to be a multiple of the number of bins and I had to alter it for both the Roll and the HelT in order to make heat shape plots which look very similar.

8)

1.