MODULE TSS3:

Q1. Based on the "FlyBase Protein-Coding Genes" track, what is the coordinate of the transcription start site?

Q2. Based on the Transcription Start Sites (Celniker) (R5) track, what is the coordinate of the transcription start site?

Q3. Is the coordinate of the Transcription Start Sites (Celniker Group) (R5) prediction the same as the Combined modENCODE CAGE Read Density prediction? Remember that the Combined modENCODE CAGE Read Density track shows the density of the first base of the CAGE reads, which corresponds to the 5' end of the mRNA.

Q4. Is there an Inr motif that agrees with the other TSS predictions?

Q5. Zoom out 10x, and then zoom out another 3x. Compare the CAGE read density for the TSS that you just identified for Antp-RM, and the CAGE read densities for other positions in the region. How many positions within this region have CAGE read densities that are <u>similar to</u> the CAGE read density for the TSS of Antp-RM? Are there any Inr motifs within this 450bp region?

Q6. How many TSSs are supported by the RAMPAGE evidence track (Figure 5)?

Q7. Do all of the developmental stages shown use the same TSS?

Q8. Based on the RAMPAGE data, do you think that RNA polymerase II initiates transcription at a single site, or at multiple sites for Antp-RM (e.g., examine the RAMPAGE signal for L1 vs. L2, and 1 hr embryo vs. 2 hr embryo)?

Q9. For each developmental stage that shows RAMPAGE signal, is there a corresponding RNA-Seq signal?

Q10. According to the X-ChIP-Seq Log Likelihood Enrichment track (Figure 8), is the region immediately upstream of exon 1 enriched in RNA Pol II?