**A. The qualitative comparsion of your results with Kihns and Pluznick 2017.**

Based on the number of hits, our results also indicate there are obesity induced changes to gene expression, agreeing with Kuhns and Pluznick (2017). With our Sequences 10, 8, and 9, we observe an upregulation of genes when the mice are obese. With Sequence 1, we observe a downregulation of the gene when the mice are obese. However with Sequences 2 and 6, there were minimal changes in gene regulation no matter the fatness of the mouse. This indicates Sequences 2 and 6 may not play a role in the general state of health of the mice.

**B. Answers to short answer questions 1 & 2**

1. Restricting to humans: Transcript 1: Highly similar sequences (megablast) (the optimize we used for this project) had 7 hits. With more dissimilar sequence (discontiguous megablast), there were 19 hits. With somewhat similar sequences (blastn), there were 73 hits. So the more “relaxed” our optimizing program selection was for alignment, the greater number of hits were registered for the model.  
     
   Restricting to humans: Transcript 10: Highly similar sequences (megablast) (the optimize we used for this project) had 5 hits. With more dissimilar sequence (discontiguous megablast), there were 12 hits. With somewhat similar sequences (blastn), there were 32 hits. So the more “relaxed” our optimizing program selection was for alignment, the greater number of hits were registered for the model.
2. **Hypothesis:** Greater number of hits with closer related species (eg. Greater number of hits with primates than non primates).  
   **Results:** Looking at hmmhits output: Chose Control 1 as oru RNA seq file: Primates have 3e-89.   
   Nonprimates have 2.2e-47.   
   Thus our hypothesis is supported.