Summary-

Since last meeting I finished the de novo assembly and PCR of the putative 15mb inversion on chromosome 5 (found by 3 SV programs). Both computational and empirical methods failed to confirm the inversion. As such, a step back was taken to look at the whole genome. A data driven approach was taken to study a system as it unfolds and then analyze and come to conclusions after data collection, instead of a typical hypothesis driven approach. Since last meeting, 11 additional samples have been added, 4 additional rhesus and 7 fascicularis. Samples were run through GATK best practices pipeline, SNPS were then called and filtered for further analysis. FST/TajimasD and Pi were calculated with VCF tools in sliding windows of 50kb-1.5mb. Regions of high FST will be statistically tested for correlation with SV regions in addition to being the input regions for a GO analysis. The Go analysis was performed with DAVID – using both the top 1% and bottom 1% FST regions. High FST regions primarily appeared on the X chromosome. Therefore, tests for Faster X evolution were performed. dN/dS ratios for autosomal regions were compared against the X, and between the pseudoautosomal regions. Additionally X evolution will be compared against an outgroup( Baboon). Finally , pairwise alignments between rhesus and fascicularis were made using LastZ to compare synteny between the two.

Future plans-

- •Faster X(ongoing)
- •Compare rate of diversity and divergence of Rhesus/Fascicularis compared to baboon
- •Should be less Divergence but more diversity between Rhe/fas and Baboon
- •New X polymorphisms under stronger selection
- •Further analyze SV's and Divergent region correlation
- •Overlay SV's onto pairwise alignments for each bin sizes
- ID 3 unknown Rhesus samples – use MT dna
- look to see if I recovered the obvious SVs in the dot plots
- Compare my study to those done in humans/other organisms
- Could be useful for comparing differing pathways and genomic variation between geographic groups