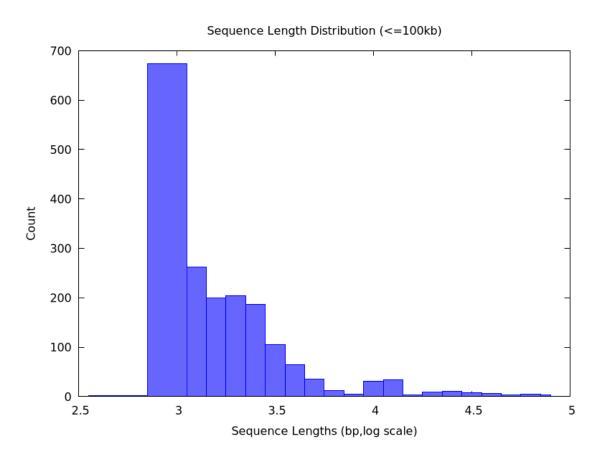
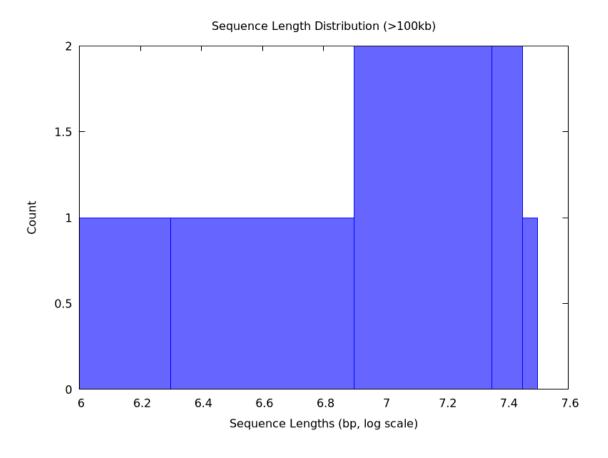
# EE282 HW#4 Figures

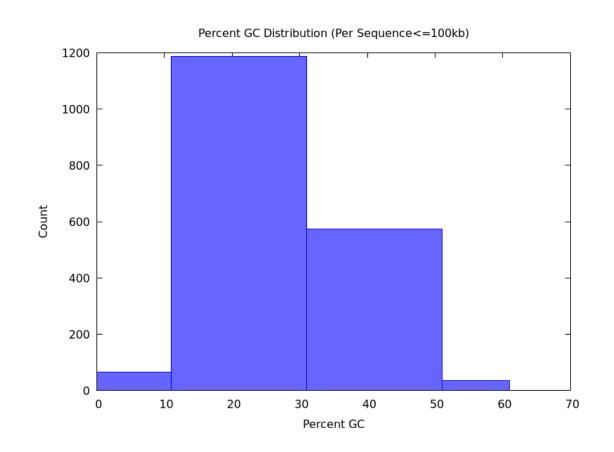
**Bobby Sims** 

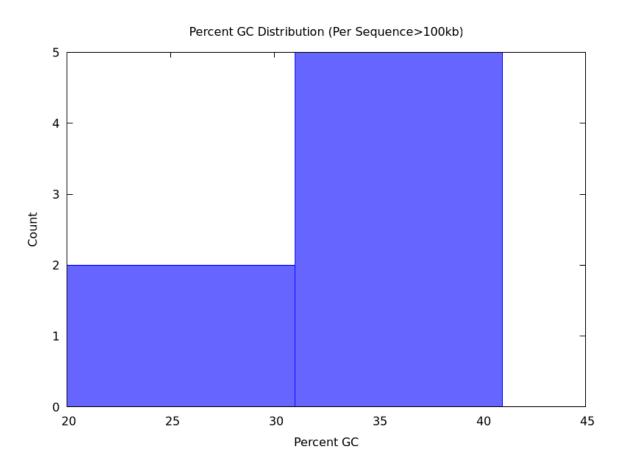
For D.Melanogaster file dmel-all-chromosome-r6.64.fasta: Sequence Length Distribution



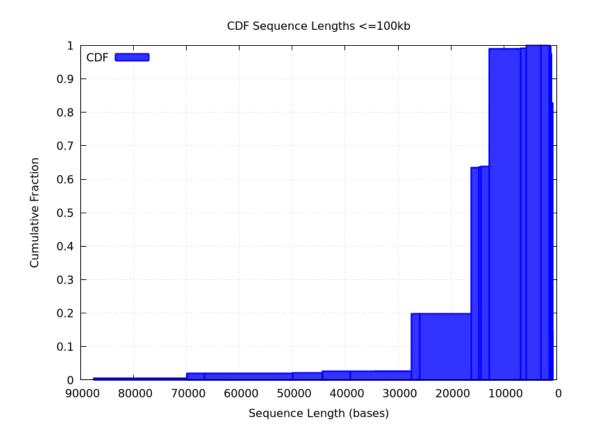


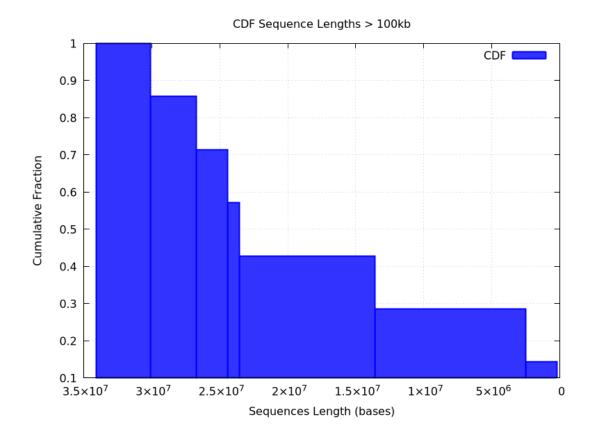
For D.Melanogaster file dmel-all-chromosome-r6.64.fasta: Percent GC% Content Distribution





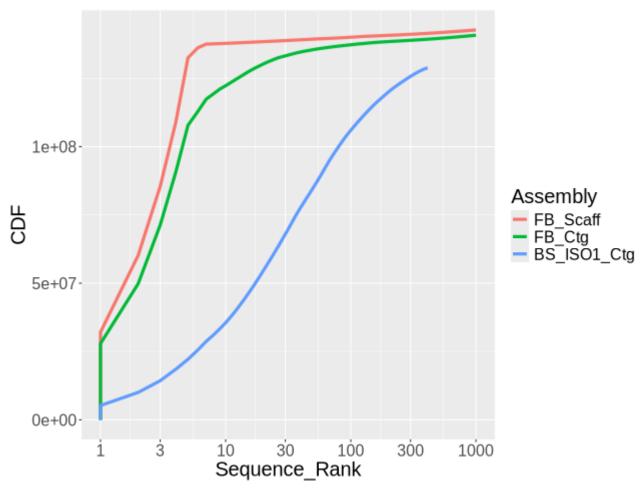
### For D.Melanogaster file dmel-all-chromosome-r6.64.fasta: Cumulative Sequence Length Distribution



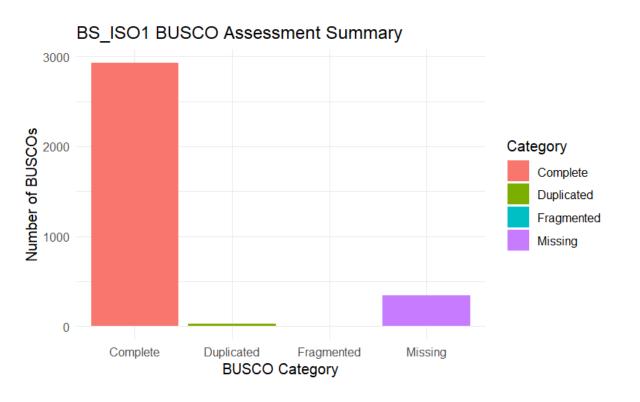


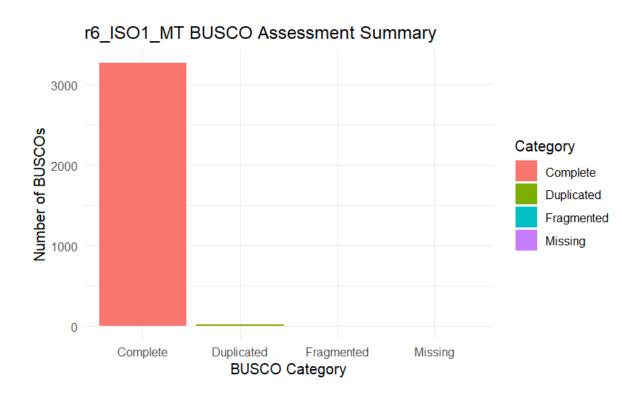
## **Contiguity Plot**

Compare fidelity of new assembly with r6\_ISO1\_MT:
r6\_ISO1\_MT Scaffold as FB\_Scaff
r6\_ISO1\_MT Contigs as FB\_Ctg
ISO1\_assembly Contigs as BS\_ISO1\_Ctg

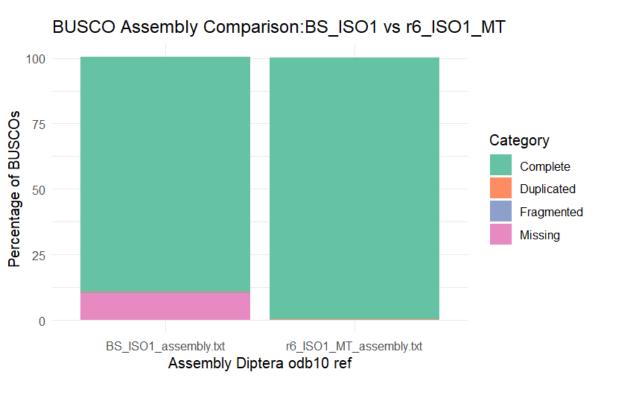


### **BUSCO** Assessment





## BUSCO Assessment Combined



Assembly	Category	Percent
BS_ISO1_assem bly.txt	Complete	89.6
BS_ISO1_assem bly.txt	Duplicated	0.4
BS_ISO1_assem bly.txt	Fragmented	0.2
BS_ISO1_assem bly.txt	Missing	10.3
r6_ISO1_MT_ass embly.txt	Complete	99.9
r6_ISO1_MT_ass embly.txt	Duplicated	0.3
r6_ISO1_MT_ass embly.txt	Fragmented	0.0
r6_ISO1_MT_ass embly.txt	Missing	0.1