

Computational Genomics: Module 7 (RNAseq Experiment Details)

Status: Released

Assay: polyA plus RNA-seq

Biosample Summary: *Homo sapiens* brain tissue female adult (66 years old)

Biosample Tissue: tissue

Description: RNA-seq of human brain tissue. The second technical replicate was performed in May 2015 and was not part of the original Lin et al. 2014 publication.

Nucleic Acid Type: polyadenylated mRNA

Size Range: 350-450 bp

Extraction Method: RNeasy Lipid Tissue Mini Kit (QIAGEN cat#74804)

Fragmentation Methods: chemical (Illumina TruSeq)

Strand Specificity: Strand-specific

Platform: Illumina HiSeq 2000, Illumina HiSeq 2500

The RNAseq data used for this week was obtained from brain tissue of an adult female at 66 years old. It contains RNA strands that range from 350-450 bp long and was meant to capture polyadenylated mRNA (transcripts). It is strand-specific data and was submitted and released on January 8th, 2015. The bam file downloaded is 4.5 gb in size. Chromosome 22 has 50818468 mapped read-segments and 1152546 unmapped read segments (samtools idxstats) in the bam file.