

JAX: expression - RNA_Seq_BAYLOR,

Molecular Methods Description:

NuGen Ovation(R) RNA-Seq System V2 used to generate library using total RNA per manufacturer's instructions.

Analysis Description:

RNAseq data was processed with Xenome to extract human sequences. The human sequences were aligned to the hg38 genome using Bowtie2, with expression levels estimated by RSEM. RSEM estimated counts were upper quantile normalized.