**A**

1. **Map reads (BWA)**
2. **Generate read count matrix (FeatureCounts)**
3. **Differential expression analysis (DESeq2)**
   - **Compute coordinate coverage** (Bedtools Genomecov)
   - **Sum coordinate coverage for each 10 nt window in each gene**
   - **Compute the log₂ ratio of Δrnj/WT for each window in each gene**
   - **Identify the window with the median log₂ ratio in each gene (median window)**
   - **Normalize the log₂ ratio of the median window for all genes**
   - **Determine the absolute difference between the DESeq2 log₂ fold change and the median window log₂ ratio**
   - **Calculate the mean and standard deviation of the absolute differences of all genes**

**Genes with absolute differences <2 SDs from the mean:**
- Classify as **Fully over- or underexpressed**

**Genes with absolute differences ≥2 SDs from the mean:**
- Classify as **partially over- or underexpressed**

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**B**

**S1 Figure. Bioinformatic analysis of RNASeq data.**

A. Schematic representation of the pipeline used to differentiate fully overexpressed genes from partially overexpressed genes. B. Scatter plot representing the relationship between DESeq2 log₂ fold change and median 10 nt window log₂ ratio. The red dots indicate partially under/over expressed genes and black dots indicate fully under/over expressed genes.