Filtering of RNA-Seq data using Trimmomatic (version 0.33) with default parameters
1. **Trimmomatic 0.33**
   
   Linux Centos 6

   Mapping to a given reference genome using HISAT 2 with the following modifications from the default parameters: maximum intron length (4,000); specify strand-specific information (RF); and minimum score (L, -0.1, -0.1)

2. **HISAT 2.0.2**
   
   Linux Centos 6

   Generating transcripts with Cufflinks (version 2.2.1). The default parameters were used, except for the following parameters: the minimum isoform fraction (0.05); the small anchor fraction of the spliced reads (0.05); the minimum intron length (20); the maximum intron length (4,000); the library type (fr-firststrand); the corrected frag bias; and the corrected multi-read

3. **Cufflinks 2.2.1**
   
   Linux Centos 6

   Identifying alternative splicing using ASTALAVISTA (version 4.0) with default parameters

4. **ASTALAVISTA 4.0**
   
   Linux Centos 6

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