**Figure S1**

1. Aligned to Reference Genome using TopHat
2. Assembly using Cufflinks
3. CuffCompare with Known Annotation
4. Filter Transcripts by FPKM
5. Filter Transcripts by Exon Number, Length, Genome Location, and CPC, CNCI, PLEC

**Steps:**
- Filtered RNA-seq reads
- Aligned Reads
- Assembled Reads
- Intergenic Transcripts
- High Quality Transcripts
- Long Intergenic Transcripts