Degradome Profiler pipeline

1. Map reads to genome - *subjunc*

2. Split mapped reads into strand specific files - *samtools*

3. Prepare reference bed *gff2bed*

4. Summarise reads to base pair resolution coverage bed files *coverageBed*

5. biasSEQr

Filter by length, trim ends, filter by coverage

Summarise coverage to 100 bp windows as % *stats.bin()*

Print transcriptome-wide heatmaps with *heatmap.2()*

Export csv of windowed coverage data (20,000 x 100)

Calculate average coverage per bin and plot trends

Calculate 5' vs 3' ratio per gene