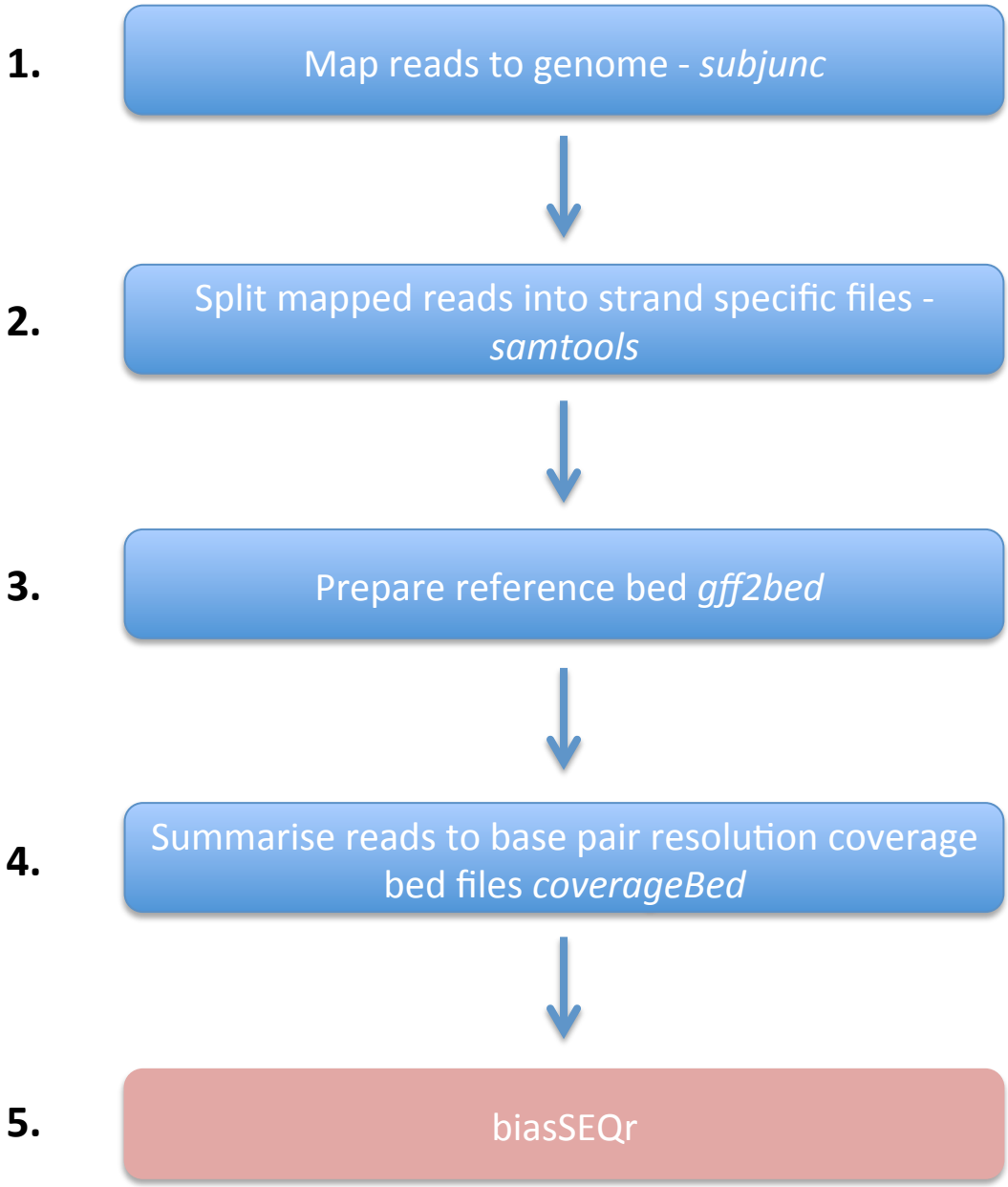
Degradome Profiler pipeline



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