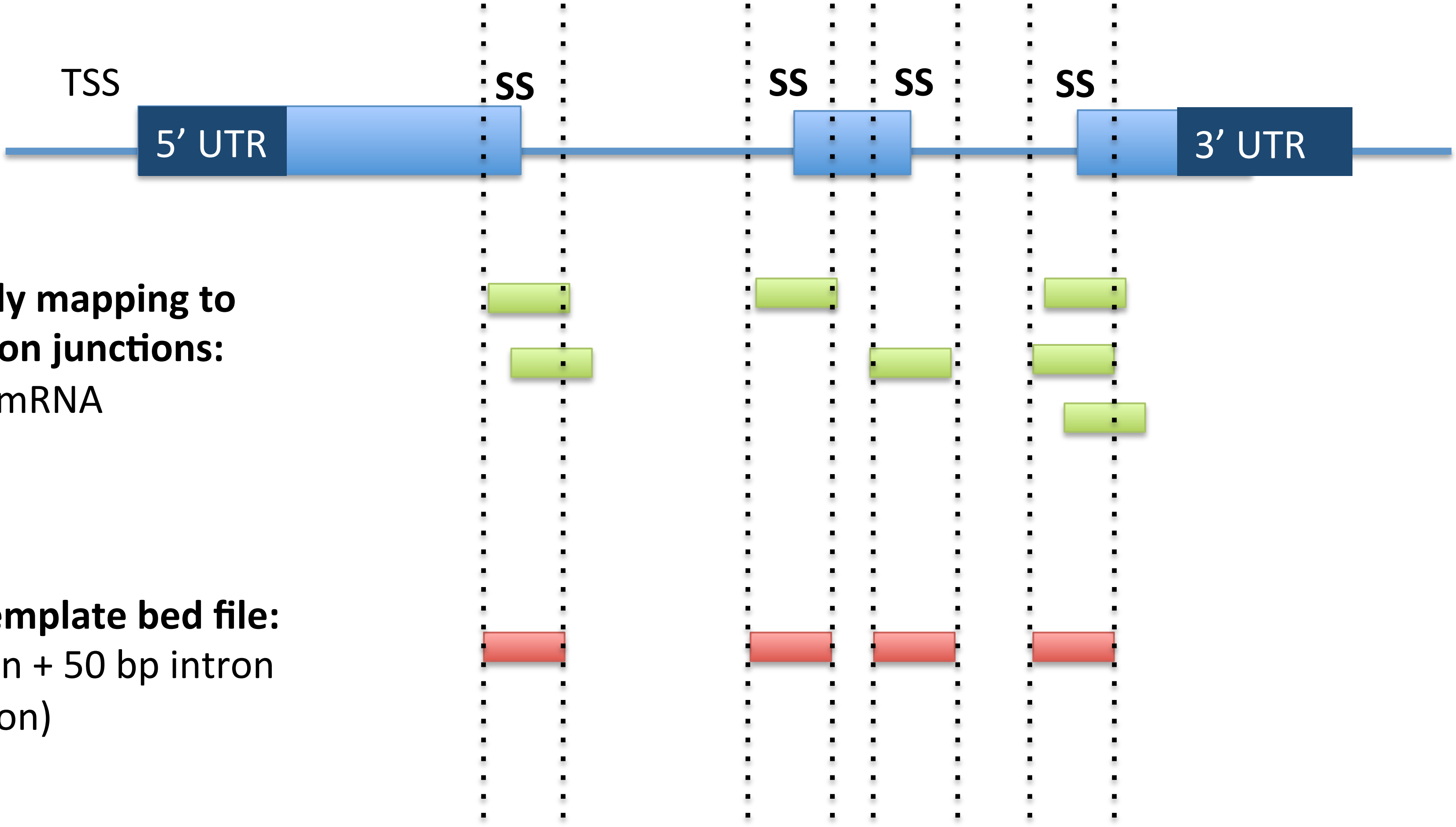
Bedtools intersect with exon-intron junction bed file



Reads only mapping to exon-intron junctions:
Only pre-mRNA

Create template bed file:
50bp exon + 50 bp intron
(at junction)

Options used with Bedtools intersect:

1. –wa outputs original read length (usual for visual display on browser)
2. -wb outputs overlapping read region (useful for counting reads rapidly in excel)
3. -f 0.51 (filters for only 100bp reads that overlap at least 51% of the target region. Should have been excellent, but discovered mapping artifacts).
4. -f 0.6 (filter for reads that have at least 60% overlap with target region. Gives more reliable outcome, but is underestimate).