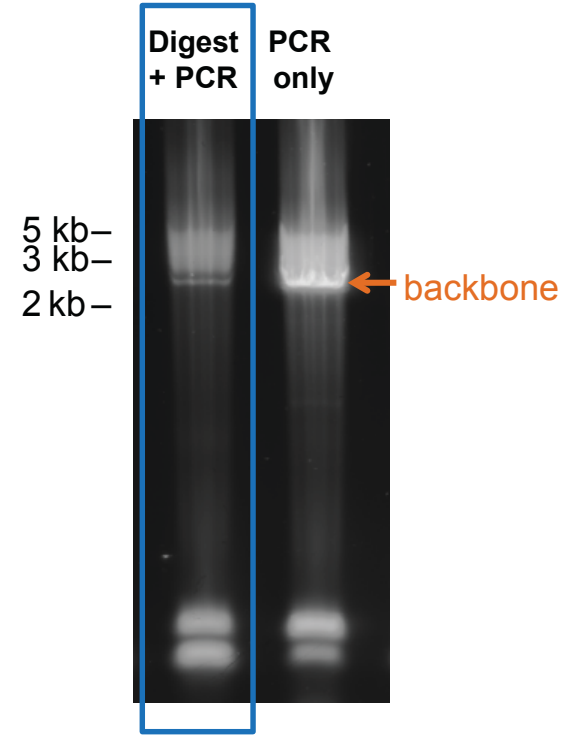
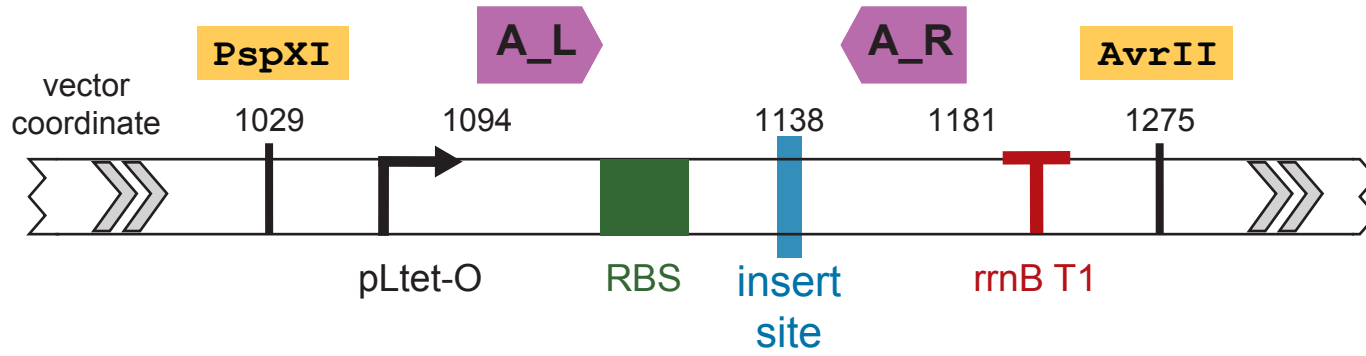
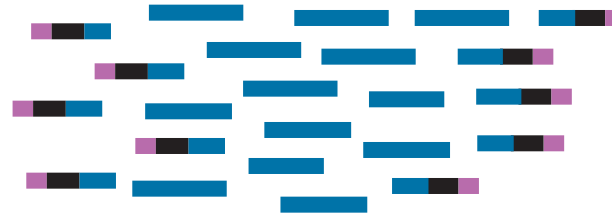


A**B**

1. Amplicons from A_L and A_R



2. Nextera tagmentation and size selection



3. Read processing:

- * Trim off backbone end if present
- * Map reads back to donor genome

