What is a sequencing library and how is it prepared?

Alt-text Figure 7 - Schematic of a typical library molecule (Illumina)

Schematic illustration of a typical library molecule in Illumina methodology. For clustering: libraries must have P5 (5’ end) and P7 (3’ end) binding regions on either end of a library. For sequencing: libraries must have sequencing primer binding regions (e.g Rd1 SP and Rd2 SP) ligated adjacent to both ends of the target DNA region. For mixing samples: libraries must have a unique index or barcodes sequence inserted between library and primer binding regions.

Alt-text Figure 8 - Bead linked transposomes simultaneously capture a fixed amount of DNA and fragment to a uniform length, whilst adding Illumina adapter sequences

Schematic illustration of a transposome. A bead-linked transposome (BLT) is represented by a circle with spike-like incrustations on its surface. These spikes bind to the library (represented by two parallel lines) binding sites forming a DNA-BLT complex.