**Tuberculosis Library Workflow ( LID50532-LID50533-LID50534)**

Tuberculosis samples quantified through Qubit dsDNA HS Assay Kit and QC’d through Pulsed Field Gel Electrophoresis system. Then samples sheared at 10kb using Megaruptor device and 8-10 kb size selected with Blue pippin instrument followed by 0.45X ampure bead purification. Attached please find PacBio library protocol that has been used for this project. First step was the removal of single-stranded overhangs followed by DNA Damage Repair, End-Repair/A-tailing, Ligation of overhang barcoded adapters and sample pooling. Total of 3 pools. LID50532 (pool of 16 samples), LID50533 (pool of 10 samples), LID50534 (pool of 9 samples). After that 0.5X ampure bead clean up performed. Sequel I instrument used to sequence these 3 library pools. Libraries annealed for an hour and bounded for an hour using sequel binding kit 3.0.. Bound smrt bell complexes purified with ampure beads. The run has been set up as 10000 bp length, for 10 hours movie time. Smrt cell 1M V2 smrt cells used for each library.