**PacBio SQIIe Methods**:

The gDNA (1.7-4.8µg) was sheared using a MegaRuptor 3 system (Diagenode) to a target size of 12-16kb prior to library preparation. Sheared DNA was prepared for sequencing following the PacBio recommended procedure (PN 102-166-600 APR2022). Briefly, the DNA is treated for removal of single-stranded overhangs, damage repaired, end prepared, and ligated to a SMRTbell adapter with the SMRTbell Prep kit 3.0 (REF: 102-141-700). To target recovery of molecules ≥10 kb, SMRTbell libraries were size selected on the BluePippin system (Sage Science) using the 0.75% Agarose Dye-Free Gel Cassette (BLF7510) with the S1 Marker. Further libraries were quantified with Qubit (Thermo Fisher Scientific) and size distribution was estimated with FEMTO Pulse (Agilent Technologies) instruments. Finally, multiplexed libraries were bound to the sequencing polymerase enzyme using the Sequel II Binding Kit (REF:102-194-100) before loading at an on-plate loading concentration (OPLC) of 90pM on the PacBio Sequel IIe System (Pacific Biosciences) using the Sequel II Sequencing Kit (REF: 101-820-200) with a SMRT Cell 8M Tray (REF: 101-389-001). Sequence data was collected for a 30h movie acquisition times preceded with a 2h pre-extension time and 2h of adaptive loading. Subreads were generated using the SMRT Link v.11.1.0.166339; Chemistry Bundle: 11.1.0.154383; Params: 11.1.0; and SMRT Link v.12.0.0.177059; Chemistry Bundle: 12.0.0.172289; Params: 12.0.0.