



Supplementary Figure 4. Read length distributions from different vector fractions show variations in heterogeneity between production platforms. (A) Relative read abundances as a function of lengths normalized to λ DNA spike-ins from pTx/HEK293-produced vectors (top) and rBV/Sf9-produced vectors (bottom). Read lengths were binned into 10-nt intervals. The percentage of full-length genomes in full and partial capsid fractions among the pTx/HEK293-produced vectors are shown. **(B)** Illustration of how truncated self-complementary double-ITR genomes are adapted to the SMRTbell DNA loops (green) (top), and how truncated self-complementary single-ITR genomes might hypothetically be formed from oversized genomes (bottom). Oversized genomes generated by the rBV/Sf9 platform might be cleaved during the SMRT library preparation steps to yield blunt ends for adapting to the SMRTbells.