

**Fig. S1. The resulting sequence blasting results (A) of X9 and primer efficiency curve of F1-R1 (B), F2-R2 (C) pairs.** The sequencing alignment was carried out using the Ncbi-Blast database. The plasmid subcloned with either *EZH2* variant was used as the standard DNA with fixed copies. Absolute quantification was employed in the amplification process. The slope was then calculated to deduce the primer efficiencies.

