

## **Description of Additional Supplementary Files**

**File name:** Supplementary Data 1

**Description:** Histones extracted from 293T cells expressing H3.3WT, H3.3K27M, H3.3K27R, EZHIP WT, EZHIP R405E, H3.3-KLP Fusion proteins were subjected to bottom-up quantitative mass-spectrometry for measurement of post-translational modifications. Relative abundances of all histone modifications as calculated using EpiProfile based on chromatographic peak are summarized.

**File name:** Supplementary Data 2

**Description:** FLAG-tagged EZHIP was expressed in 293T cells and EZHIP-associated proteins were purified using FLAG affinity purification. Immunoprecipitated material was subjected to mass-spectrometry for protein identification and quantification. Identified proteins and their quantification are summarized in the dataset.