## **Supplementary information**

## High-throughput proteomic sample preparation using pressure cycling technology

In the format provided by the authors and unedited

## **Supplementary Information**

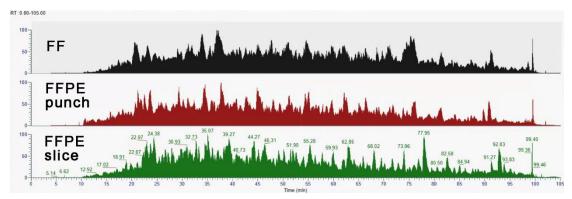
## High-throughput proteomic sample preparation using pressure cycling technology

Xue Cai<sup>1,2</sup>, Zhangzhi Xue<sup>1,2</sup>, Chunlong Wu<sup>3</sup>, Rui Sun<sup>1,2</sup>, Liujia Qian<sup>1,2</sup>, Liang Yue<sup>1,2</sup>, Weigang Ge<sup>3</sup>, Xiao Yi<sup>3</sup>, Wei Liu<sup>3</sup>, Chen Chen<sup>3</sup>, Huanhuan Gao<sup>3</sup>, Jing Yu<sup>3</sup>, Luang Xu<sup>3</sup>, Yi Zhu<sup>1,2\*</sup>, Tiannan Guo<sup>1,2\*</sup>

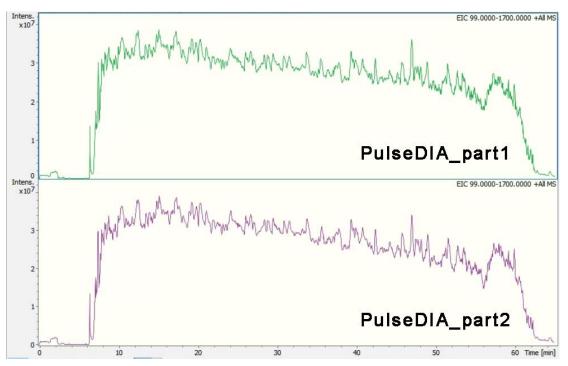
 Westlake Laboratory of Life Sciences and Biomedicine, Key Laboratory of Structural Biology of Zhejiang Province, School of Life Sciences, Westlake University, Hangzhou, Zhejiang, China;
Institute of Basic Medical Sciences, Westlake Institute for Advanced Study, Hangzhou, Zhejiang, China;

 Westlake Omics (Hangzhou) Biotechnology Co., Ltd. No.1, Yunmeng Road, Cloud Town, Xihu District, Hangzhou (310024), Zhejiang, China;

\*Correspondence: zhuyi@westlake.edu.cn; guotiannan@westlake.edu.cn



Supplementary Figure 1 | The extracted ion chromatograms for DDA-MS data of FF, FFPE punches and FFPE slices. The DDA-MS data are acquired on a nanoflow DIONEX UltiMate 3000 RSLCnano System coupled to a Q Exactive HF hybrid Quadrupole-Orbitrap with an effective LC gradient of 90 min and a total run time of 105 min.



**Supplementary Figure 2** | **The extracted ion chromatograms for PulseDIA-PASEF MS data of cancer tissues.** The PulseDIA-PASEF MS data are acquired on a nanoElute System coupled to a timsTOF Pro mass spectrometer with an effective LC gradient of 60 min and a total run time of 65 min.