

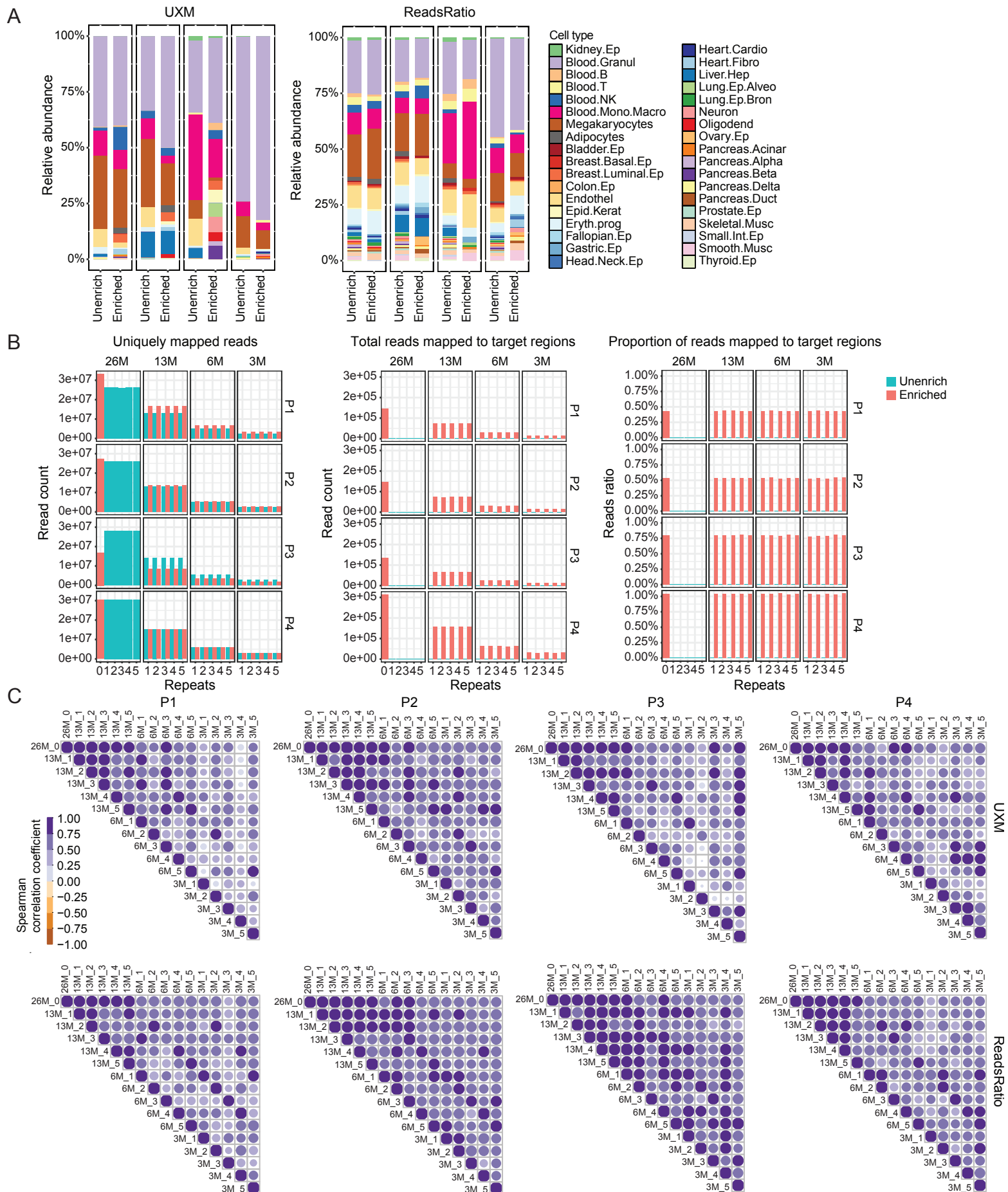


Fig S15. Performance of ReadsRatio method in target methylation sequencing data.

A. Cell type composition in paired unenrich and enriched samples. B. Subsampling analysis of unenrich and enriched samples. Each subsampling was repeated 5 times. C. Correlation of cell type composition between subsampling repeats. There is only one enriched sample in 26M group as it is the original enriched sample without down-sampling.