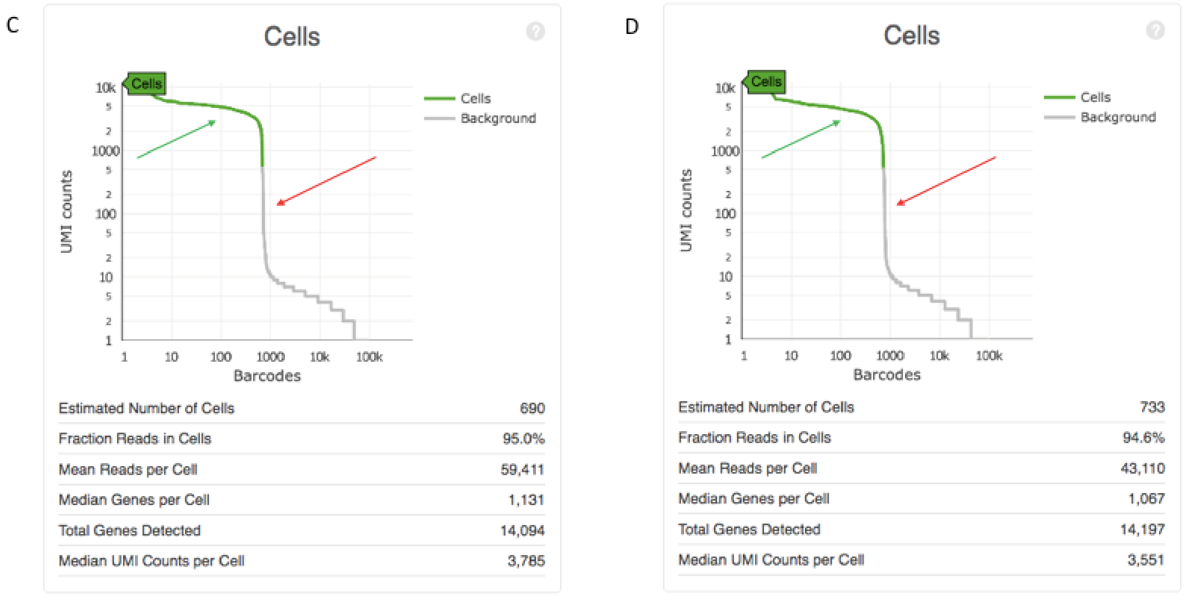

C

Estimated Number of Cells	690
Fraction Reads in Cells	95.0%
Mean Reads per Cell	59,411
Median Genes per Cell	1,131
Total Genes Detected	14,094
Median UMI Counts per Cell	3,785

D

Estimated Number of Cells	733
Fraction Reads in Cells	94.6%
Mean Reads per Cell	43,110
Median Genes per Cell	1,067
Total Genes Detected	14,197
Median UMI Counts per Cell	3,551

Figure S1. Knee plots of (A) control sample and (B) irradiated sample used for sequencing quality control analytics. Green arrows represents the 3500 UMI counts mapped back to cell barcodes. Red arrows represent the 0.001% of UMI counts not mapped back to cell barcodes.

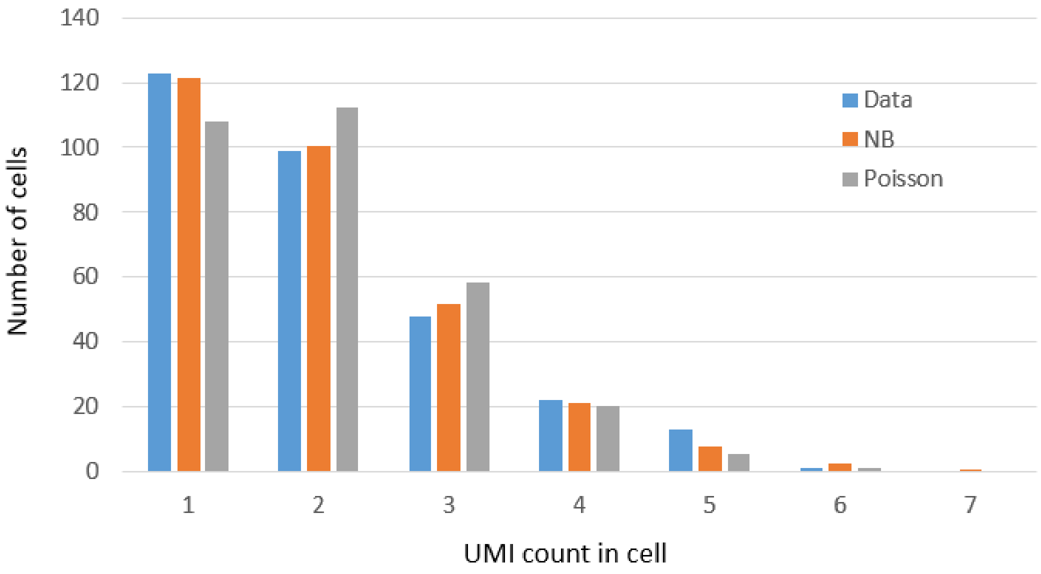

Figure S2. Distribution of UMI of PHPT1 in CD4+ cells after radiation exposure. The distribution can be fitted better with negative binomial (NB) distribution than the Poisson distribution.

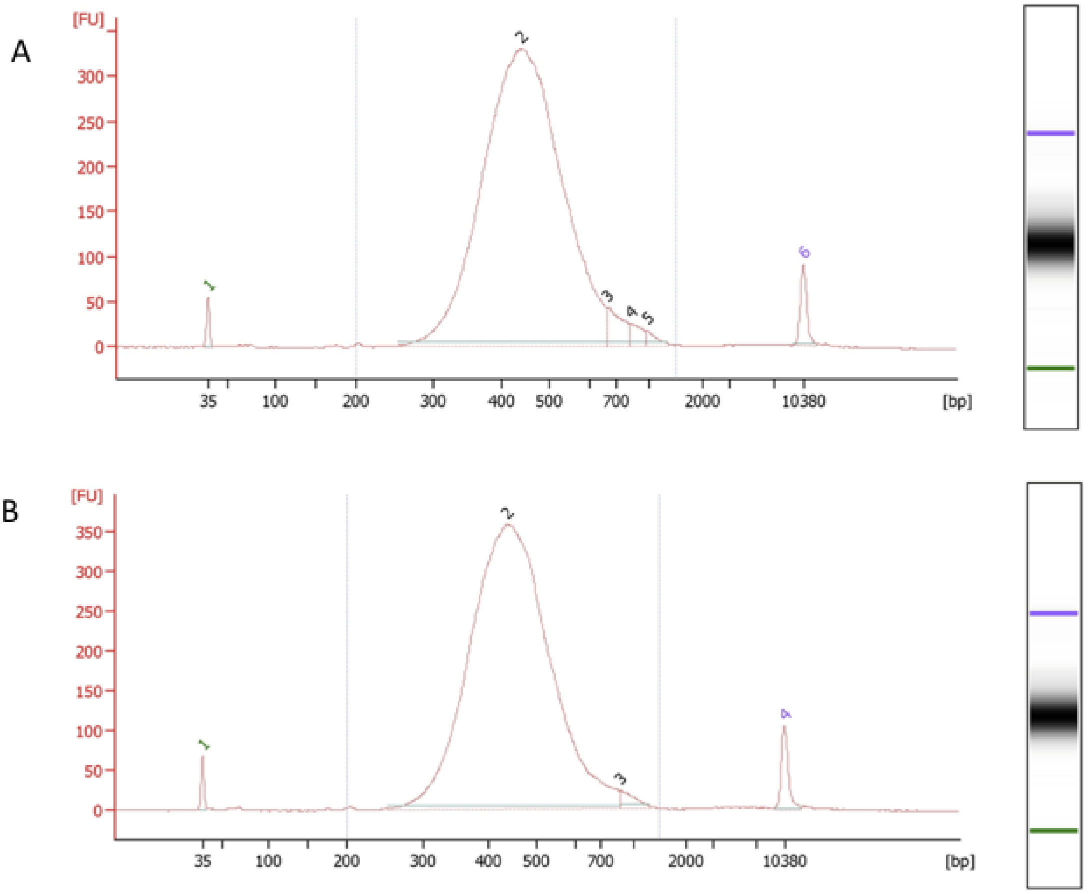

Figure S3. Average fragment size of (A) control sample and (B) irradiated sample . Average fragment size of 500bp is required for complete sequencing and identification of individual cell.