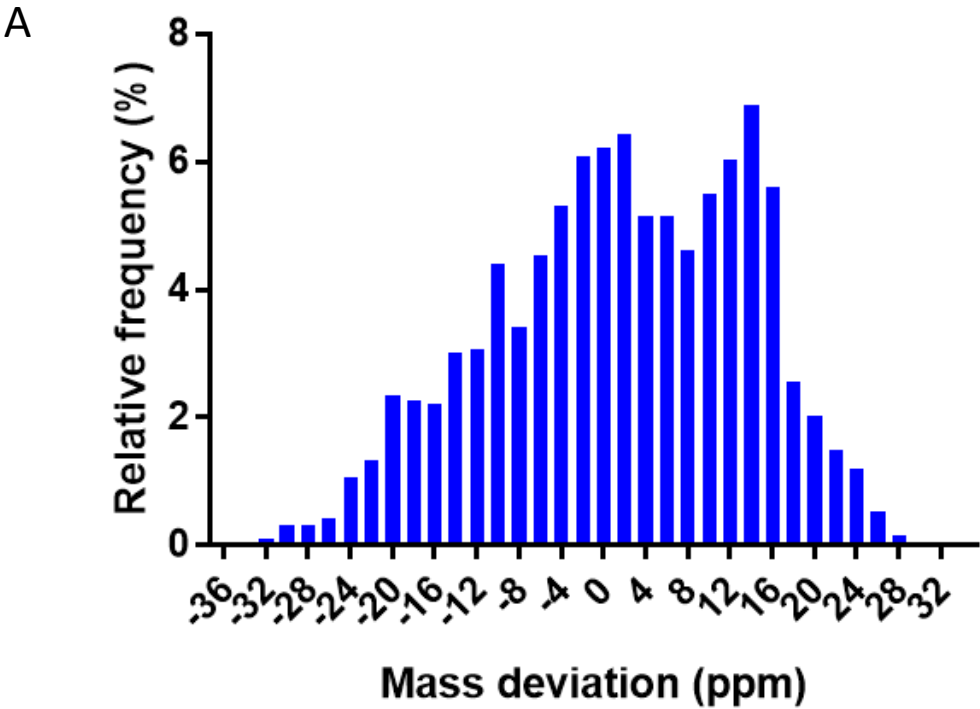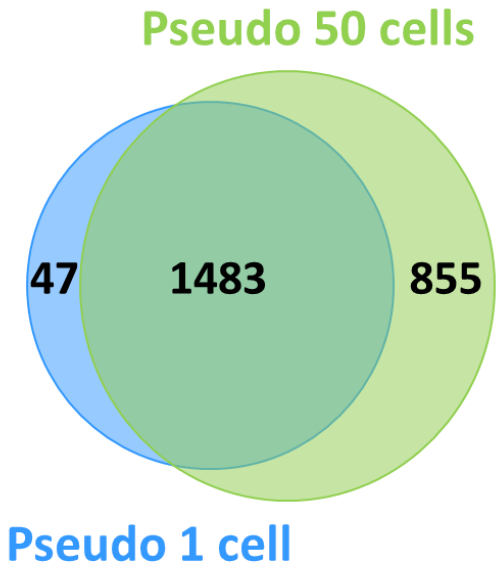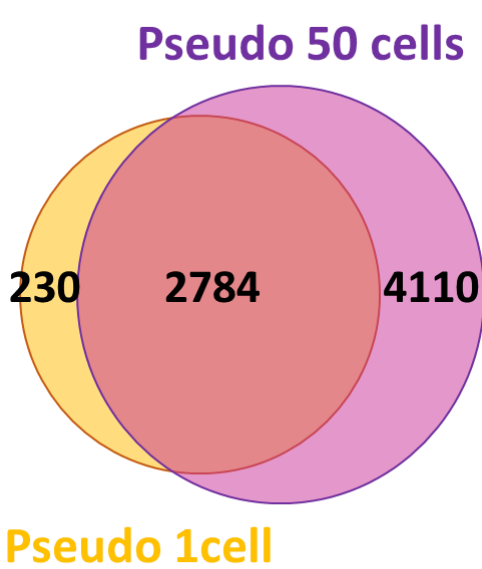**Supplementary Figure S1. Evaluation of the unique peptides and proteins identified in the pseudo single-cell by the SLB-SCP.** A) Distribution of the unique peptides identified in the single-cell samples (error rate: 1%, expect score ≤ 0.001, IPM ≥ 0.01, idotp ≥ 0.5) based on their mass deviation from the theoretical values. B) Comparison of the unique peptides and proteins identified in the pseudo single-cell samples with the pseudo 50-cells samples (bulk scale).
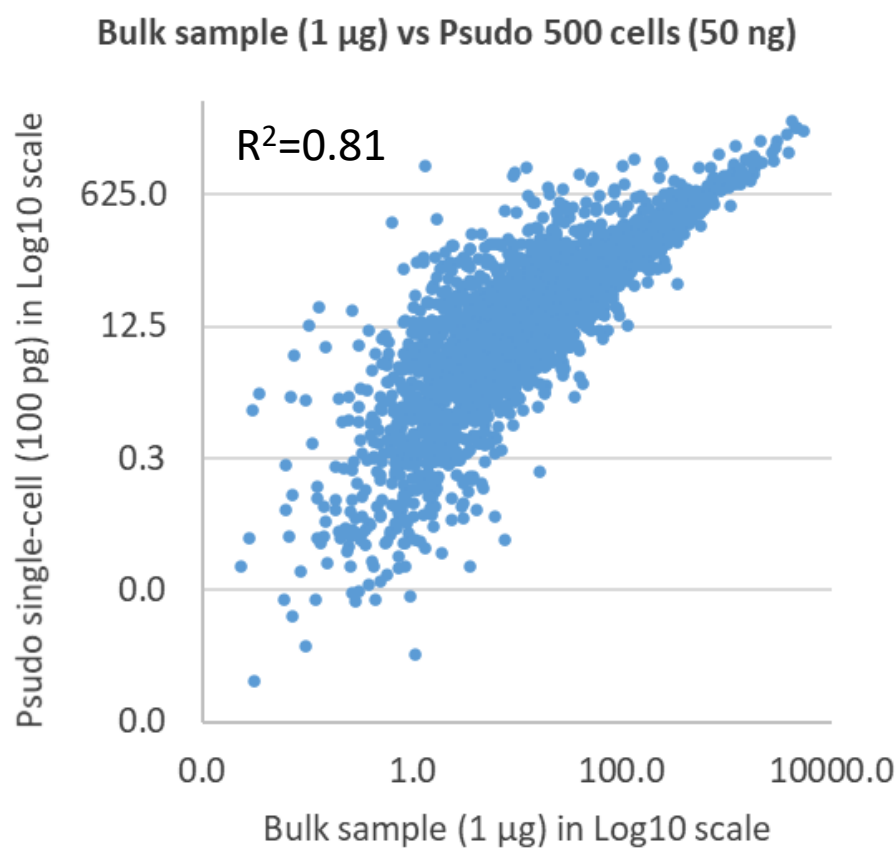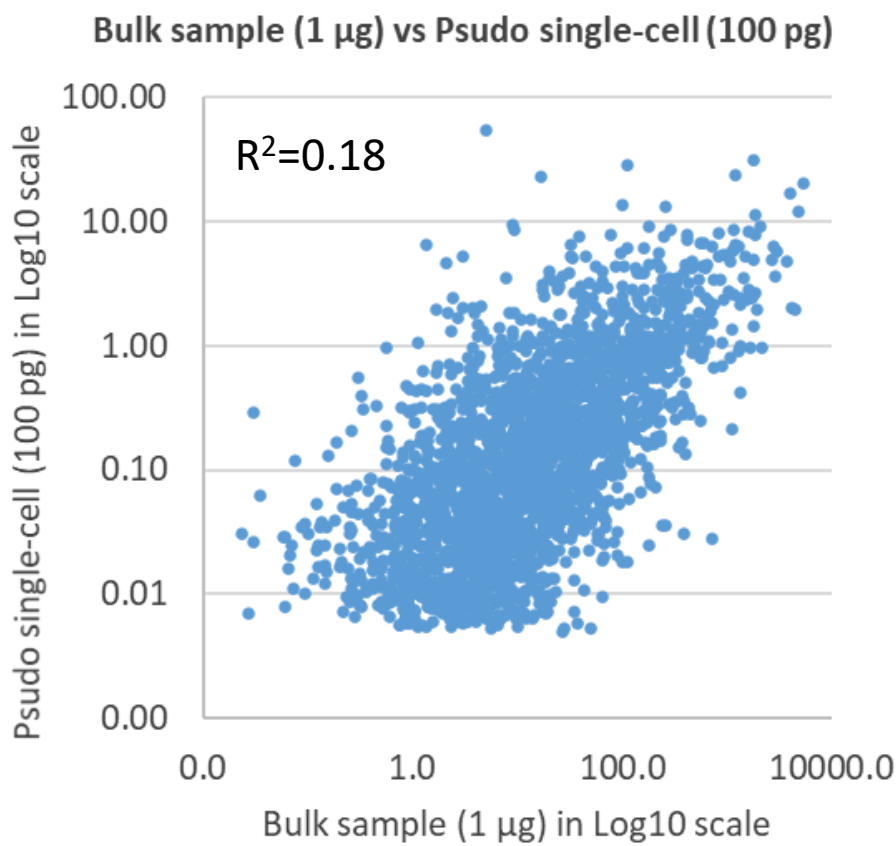
**Supplementary Figure S2. Correlation plots of protein intensity data from single-cell (100 pg) and 500-cells (50 ng) vs the bulk sample (1 µg).** A) Single-cell vs the bulk sample. B) 500-cells vs the bulk sample.



Bulk sample (1 µg) vs Psudo single-cell (100 pg)

$R^2=0.18$

Psudo single-cell (100 pg) in Log10 scale

Bulk sample (1 µg) in Log10 scale



Bulk sample (1 µg) vs Psudo 500 cells (50 ng)

$R^2=0.81$

Psudo single-cell (100 pg) in Log10 scale

Bulk sample (1 µg) in Log10 scale

**Supplementary Figure S3. Hierarchical clustering heatmap of protein intensities (IPM) for all proteins identified in the single cells of HPDE and PANC-1**