Fig. S3

(a) Scatter plots showing the relationship between log(estimated counts + 1) and log(original counts + 1) for the RESCUE, scImpute, and DrImpute methods. The x-axis represents the log(original counts + 1) and the y-axis represents the log(estimated counts + 1). The red dashed line indicates a perfect linear relationship.

(b) Box plots illustrating the percent count error for different genes (Gene911, Gene2800, Gene2973, Gene7941, Gene8742, Gene9438) using RESCUE, scImpute, and DrImpute methods. The box plots show the distribution of percent count error across different methods.

(c) A summary of the percent count error for each gene and method, showing the median, interquartile range, and whiskers.