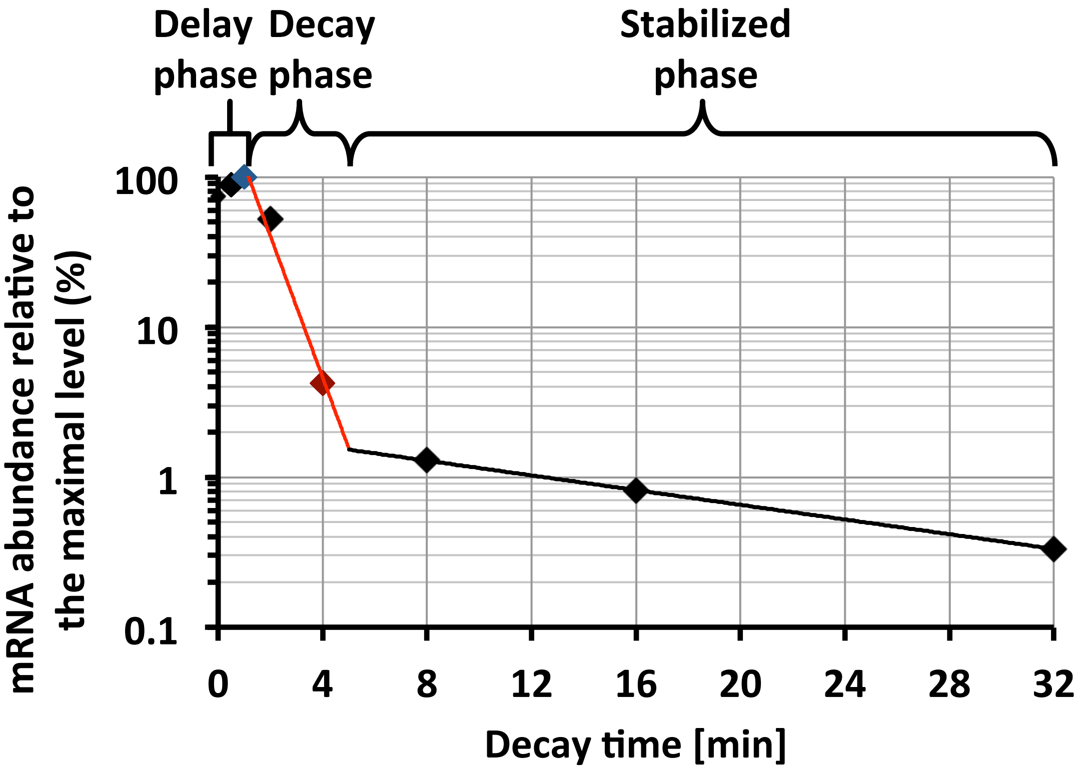

Fig. S1. mRNA decay curve. A typical mRNA decay curve includes delay, decay, and stabilized phases. The fastest mRNA degradation occurs in the decay phase. For illustration, the respective starting and ending time points of the decay phase (t_i *and* t_j) were marked as blue and red diamonds, respectively. Exponential regression of mRNA decay in the decay phase (the red line) was carried out to determine the mRNA half-life.

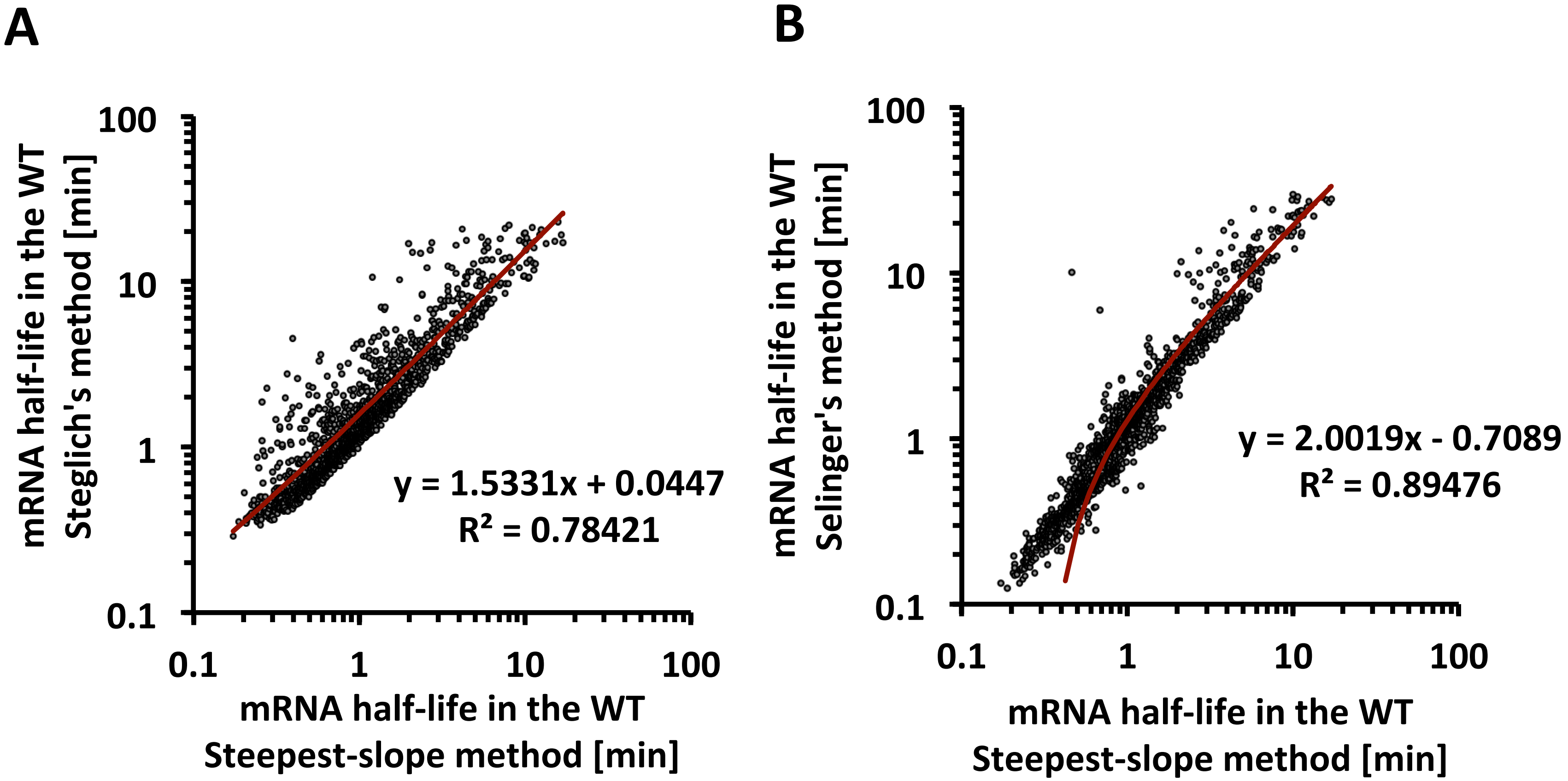

Figure S2. Comparison of three microarray-based half-life calculation methods. mRNA half-lives in the genome of *S. pyogenes* WT were calculated with steepest-slope method, Steglich's method, and Selinger's method. Results obtained from steepest-slope method were compared to those from Steglich's method (A) and Selinger's method (B).

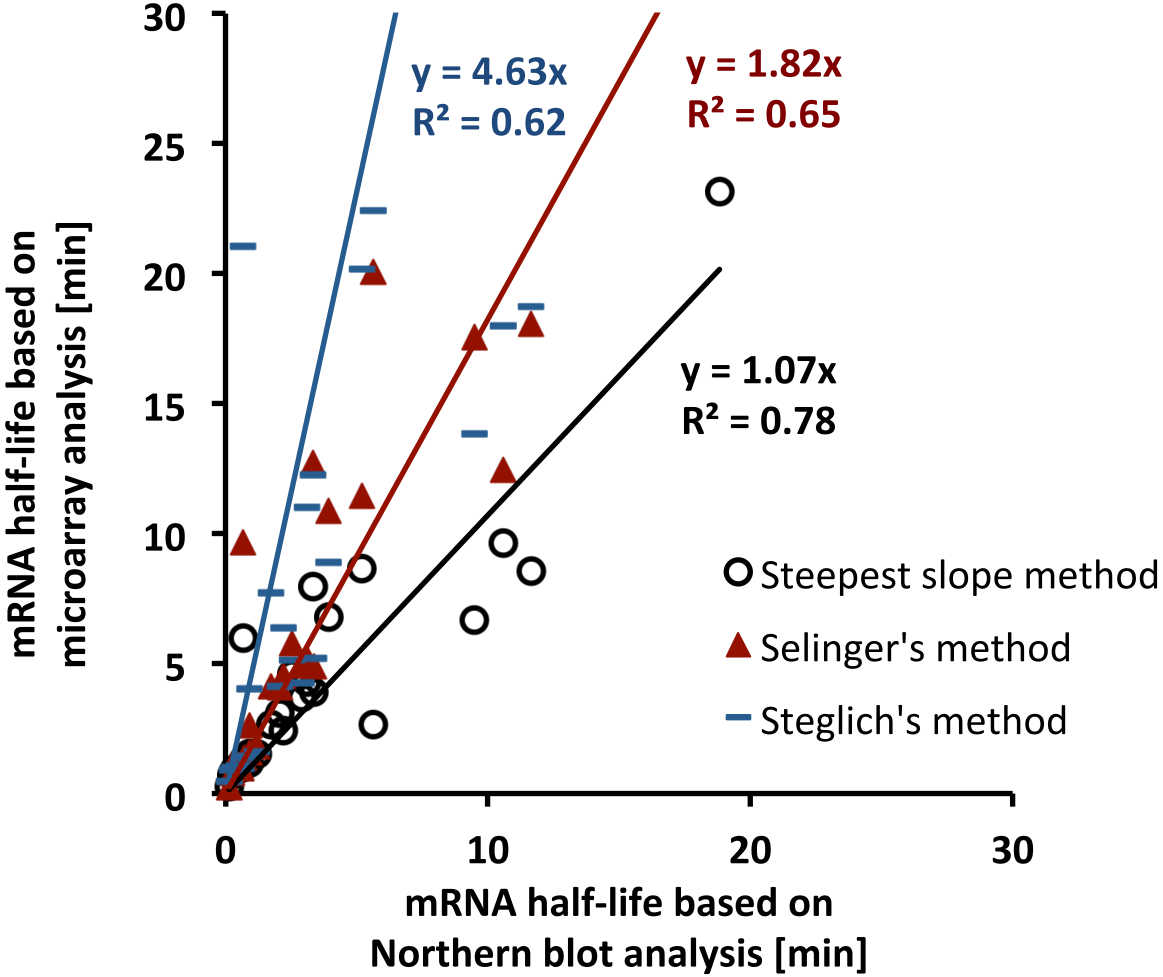

Figure S3. Evaluation of three Microarray-based methods. A total of 12 mRNAs were examined with Northern blot analysis to determine their actual half-lives. Northern blot results were compared to those obtained from three microarray-based methods, and their correlations were determined with linear regression.