GGRaSP: A R-package for selecting representative genomes using Gaussian mixture models

**Supplemental Figure**



Figure S1. **Time usage for GGRaSP**. GGRaSP runs of 100, 500, 1,000, 2,000, 3,000, or 4,000 randomly sampled genomes from the *E. coli* set was used to estimate time usage. Best-fit linear (red; r2 = 0.90) and polynomial (blue; r2 = 0.94) models were calculated and are shown.