LEGENDS TO SUPPLEMENTARY FIGURE

Supplementary FIG. 1. (a) The ssGeneFinder Webserver interface. By clicking the “Start Analysis” link, the user was guided to the genome selection page. “Salmonella Typhi” was used as the search phrase to locate *S.* Typhi genomes from the genome repository of the server. Alternatively, the user may search for a genome using its accession number or sequencing status. (b) Genome search. After selecting the required genomes, they may be added to the list of target genomes by selecting “Target genomes” in the drop-down menu and clicking “Save selection”. (c) Adding non-target genomes. Genomes for the non-target organisms were similarly added to the “Non-target genomes” using similar procedures. The ssGeneFinder Webserver automatically avoided duplicates in target and non-target genome lists, i.e. a genome cannot be a target and non-target at the same time, and otherwise the user was free to select any combination of genomes to suit the particular needs of a proposed assay. (d) Proceeding to analysis. When both target and non-target genomes have been specified, a link appears on the top status bar, allowing the user to proceed. (e) The ssGeneFinder Webserver settings page. The user was required to enter a valid email address for the results notification. (f) The results notification email. The results notification email contained the run summary and machine log file. Due to the large size of genome files and target alignments, a link was provided for the user to download all the files used and generated in the ssGeneFinder analysis. (g) The download page. In addition to the generated list of targets (shown in the box at the bottom), the download page listed all the files in the run, including also the ssGeneFinder settings file and all the genomes used. They may be downloaded to repeat the run on the user’s computer if desired.