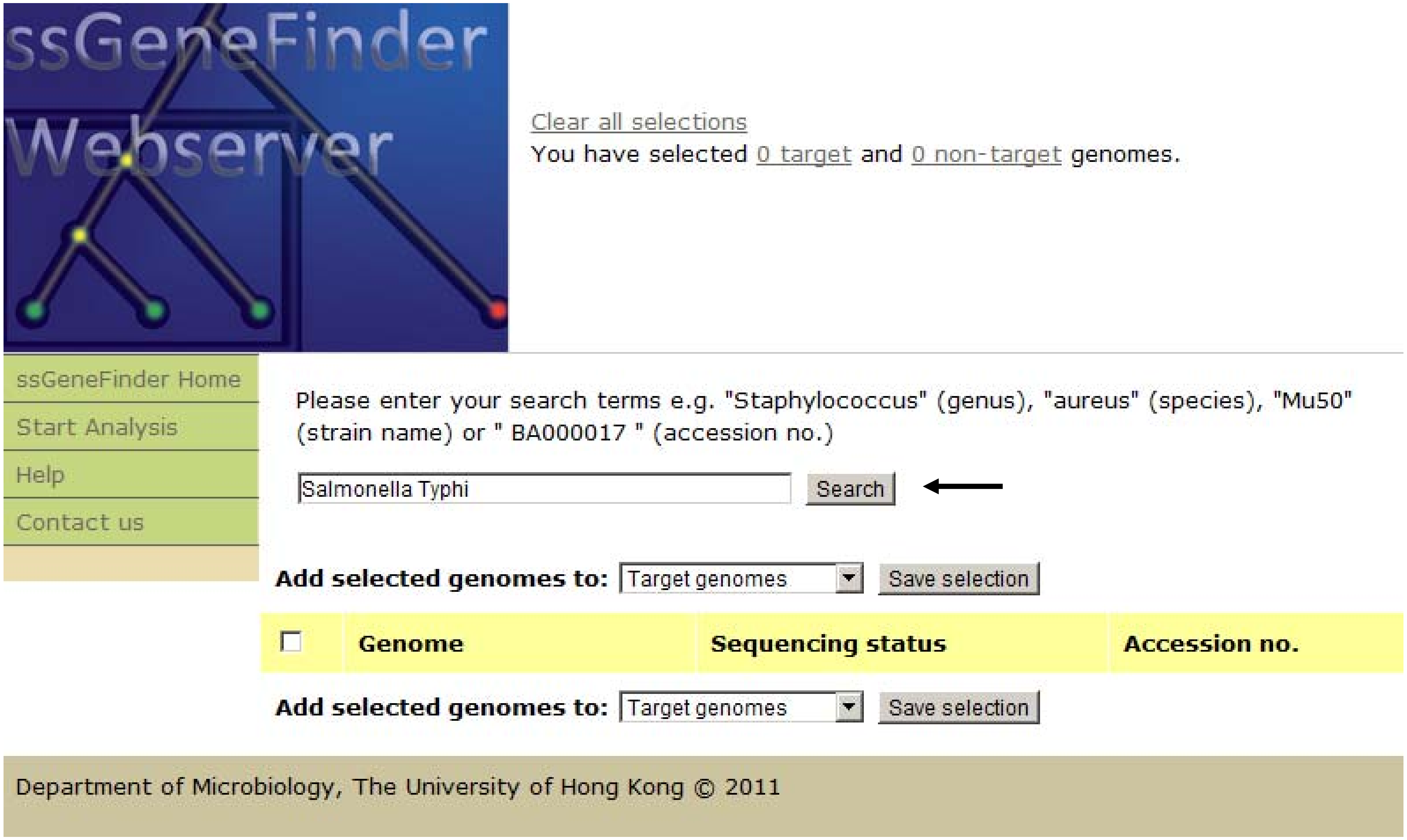
FIG. 1A



Clear all selections

You have selected 0 target and 0 non-target genomes.

Please enter your search terms e.g. "Staphylococcus" (genus), "aureus" (species), "Mu50" (strain name) or " BA000017 " (accession no.)

Salmonella Typhi

Add selected genomes to: Target genomes

☐	**Genome**	**Sequencing status**	**Accession no.**

Add selected genomes to: Target genomes

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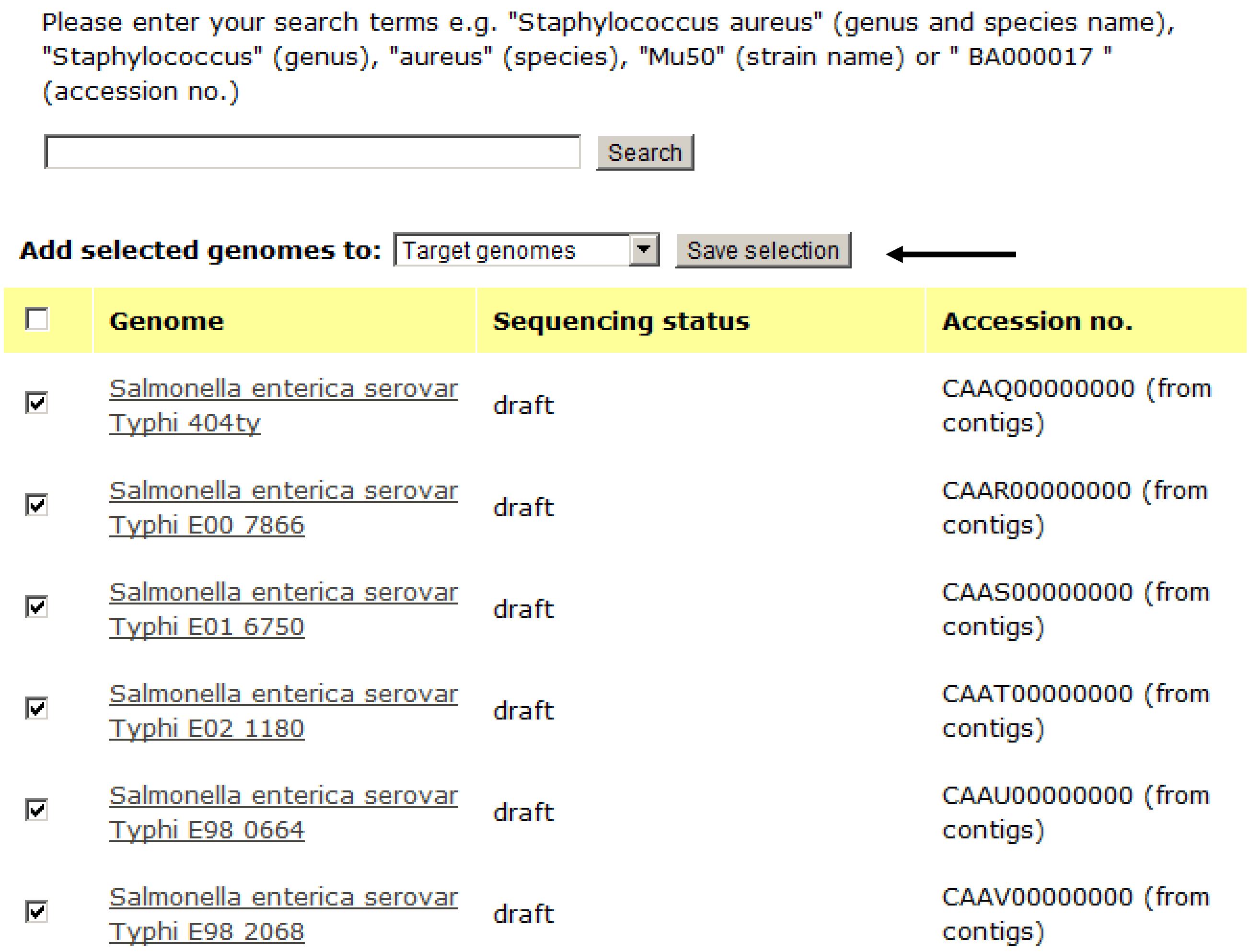
FIG. 1B

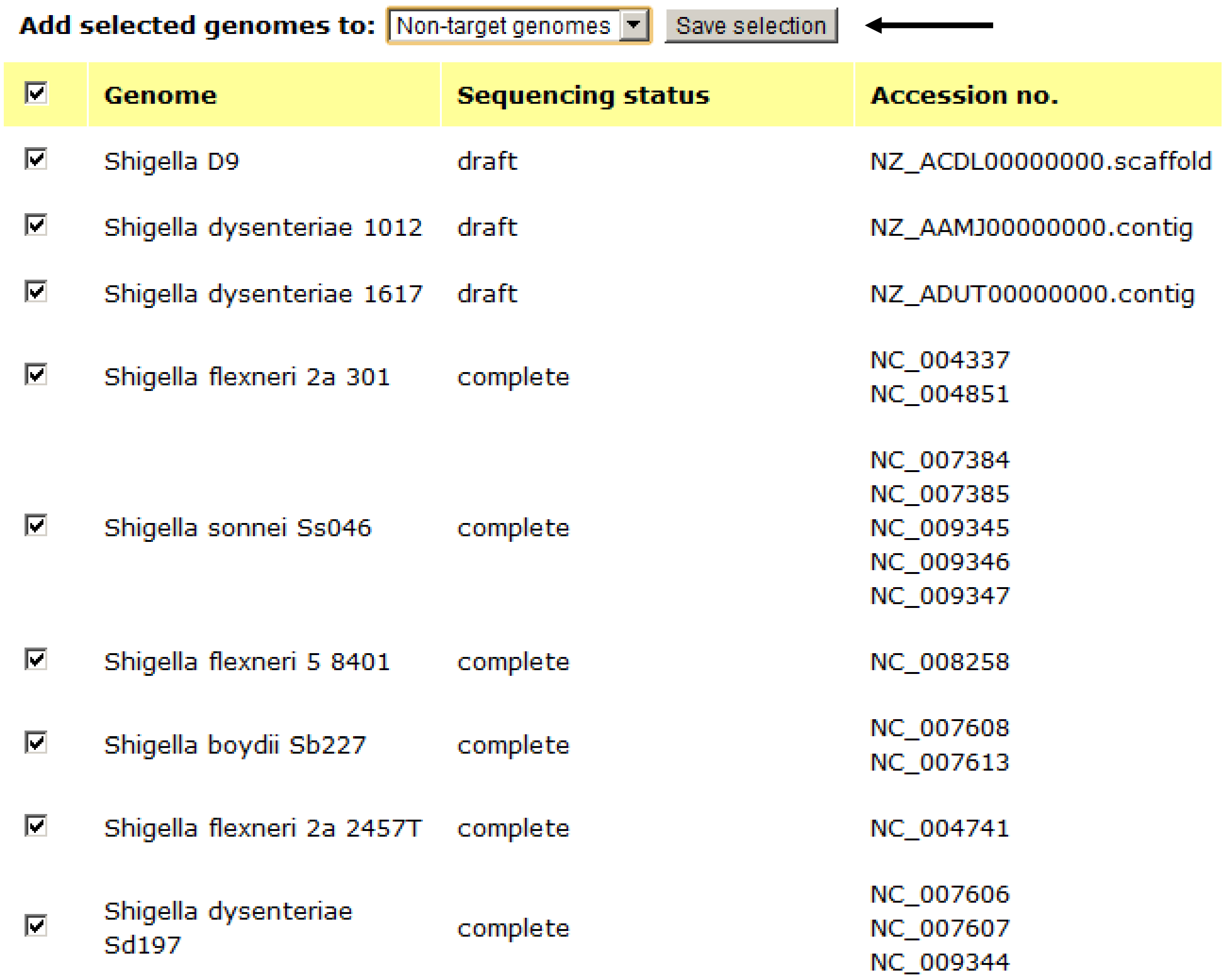


Please enter your search terms e.g. "Staphylococcus aureus" (genus and species name), "Staphylococcus" (genus), "aureus" (species), "Mu50" (strain name) or " BA000017 " (accession no.)

Add selected genomes to: Target genomes

☐	**Genome**	**Sequencing status**	**Accession no.**
☑	Salmonella enterica serovar Typhi 404ty	draft	CAAQ00000000 (from contigs)
☑	Salmonella enterica serovar Typhi E00 7866	draft	CAAR00000000 (from contigs)
☑	Salmonella enterica serovar Typhi E01 6750	draft	CAAS00000000 (from contigs)
☑	Salmonella enterica serovar Typhi E02 1180	draft	CAAT00000000 (from contigs)
☑	Salmonella enterica serovar Typhi E98 0664	draft	CAAU00000000 (from contigs)
☑	Salmonella enterica serovar Typhi E98 2068	draft	CAAV00000000 (from contigs)

FIG. 1C

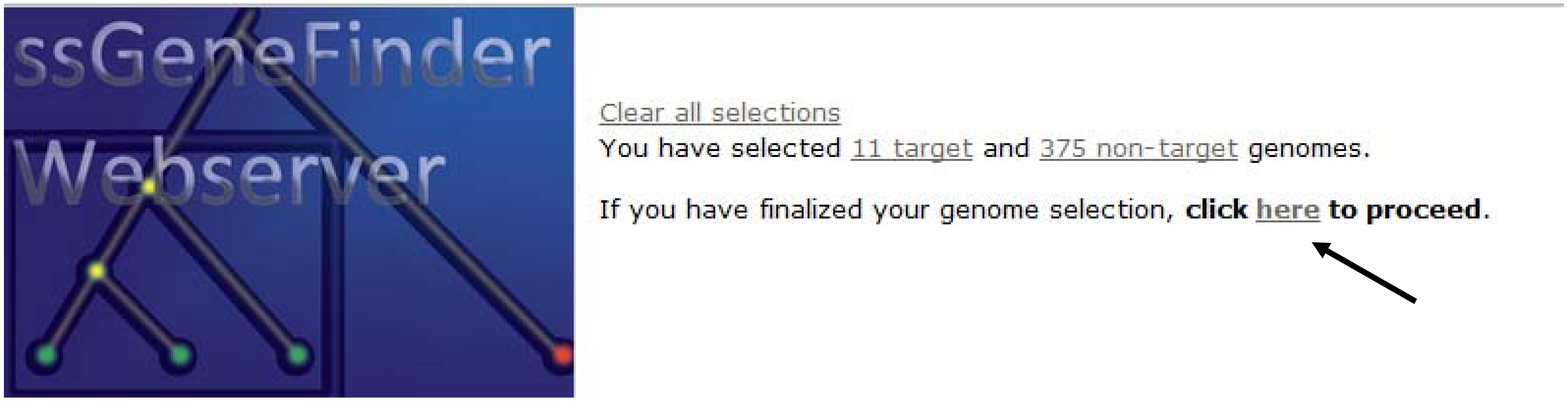


Add selected genomes to: Non-target genomes

☑	**Genome**	**Sequencing status**	**Accession no.**
☑	Shigella D9	draft	NZ_ACDL00000000.scaffold
☑	Shigella dysenteriae 1012	draft	NZ_AAMJ00000000.contig
☑	Shigella dysenteriae 1617	draft	NZ_ADUT00000000.contig
☑	Shigella flexneri 2a 301	complete	NC_004337 NC_004851
☑	Shigella sonnei Ss046	complete	NC_007384 NC_007385 NC_009345 NC_009346 NC_009347
☑	Shigella flexneri 5 8401	complete	NC_008258
☑	Shigella boydii Sb227	complete	NC_007608 NC_007613
☑	Shigella flexneri 2a 2457T	complete	NC_004741
☑	Shigella dysenteriae Sd197	complete	NC_007606 NC_007607 NC_009344

Check to select all

FIG. 1D

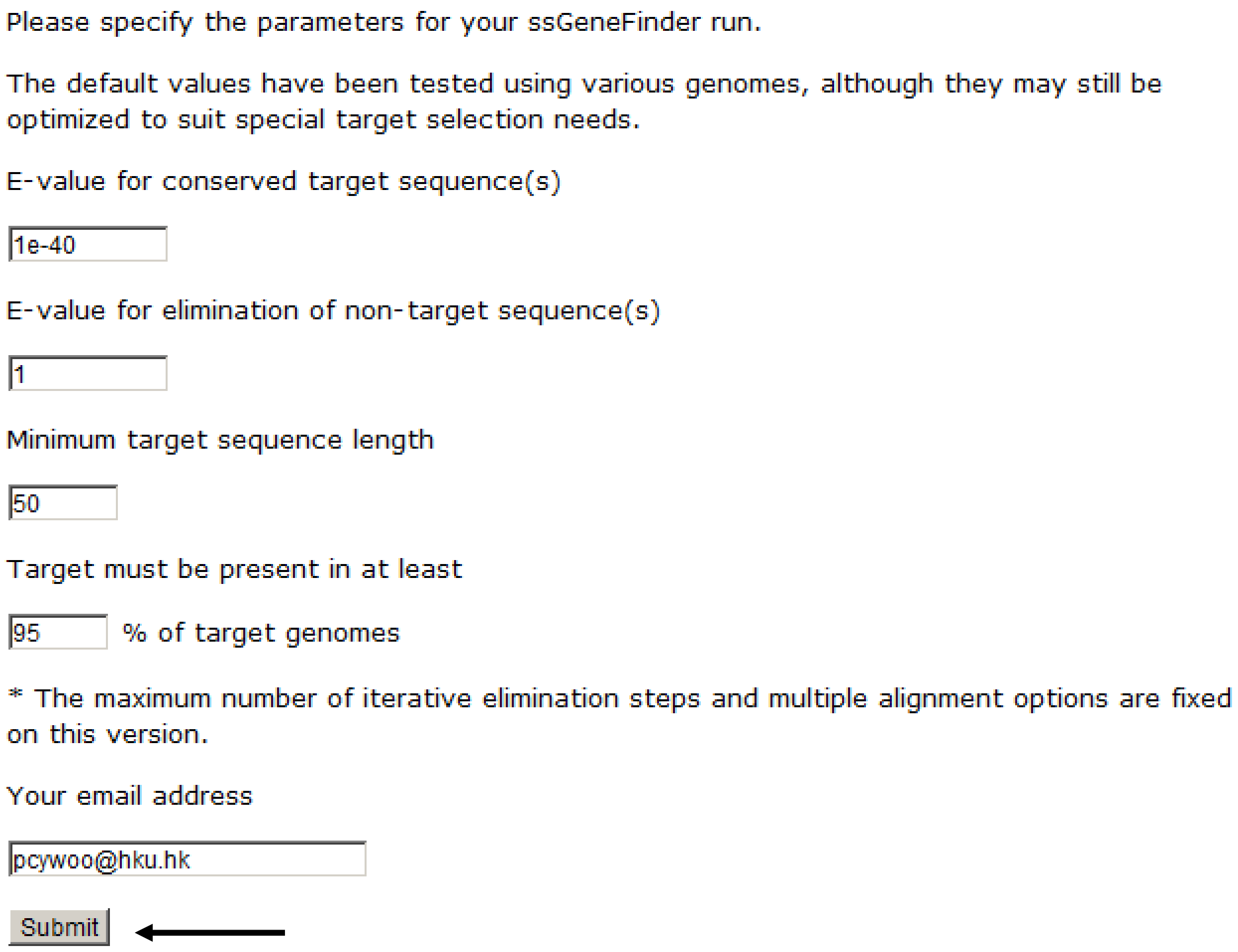


Clear all selections

You have selected 11 target and 375 non-target genomes.

If you have finalized your genome selection, **click here to proceed**.

FIG. 1E



Please specify the parameters for your ssGeneFinder run.

The default values have been tested using various genomes, although they may still be optimized to suit special target selection needs.

E-value for conserved target sequence(s)

1e-40

E-value for elimination of non-target sequence(s)

1

Minimum target sequence length

50

Target must be present in at least

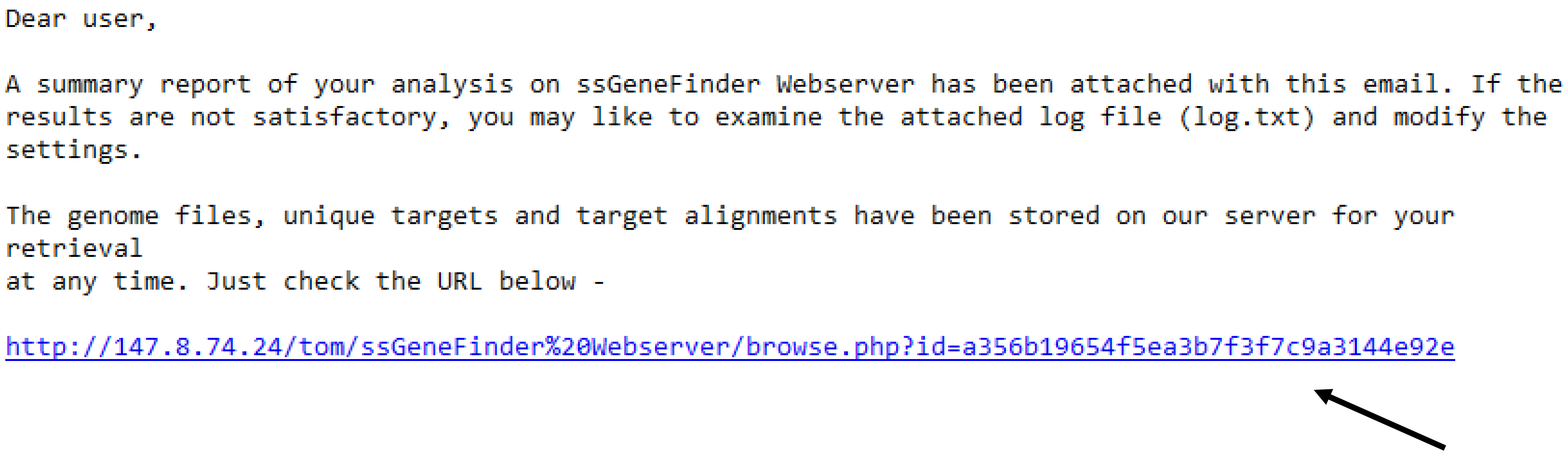
95 % of target genomes

* The maximum number of iterative elimination steps and multiple alignment options are fixed on this version.

Your email address

pcywoo@hku.hk

FIG. 1F



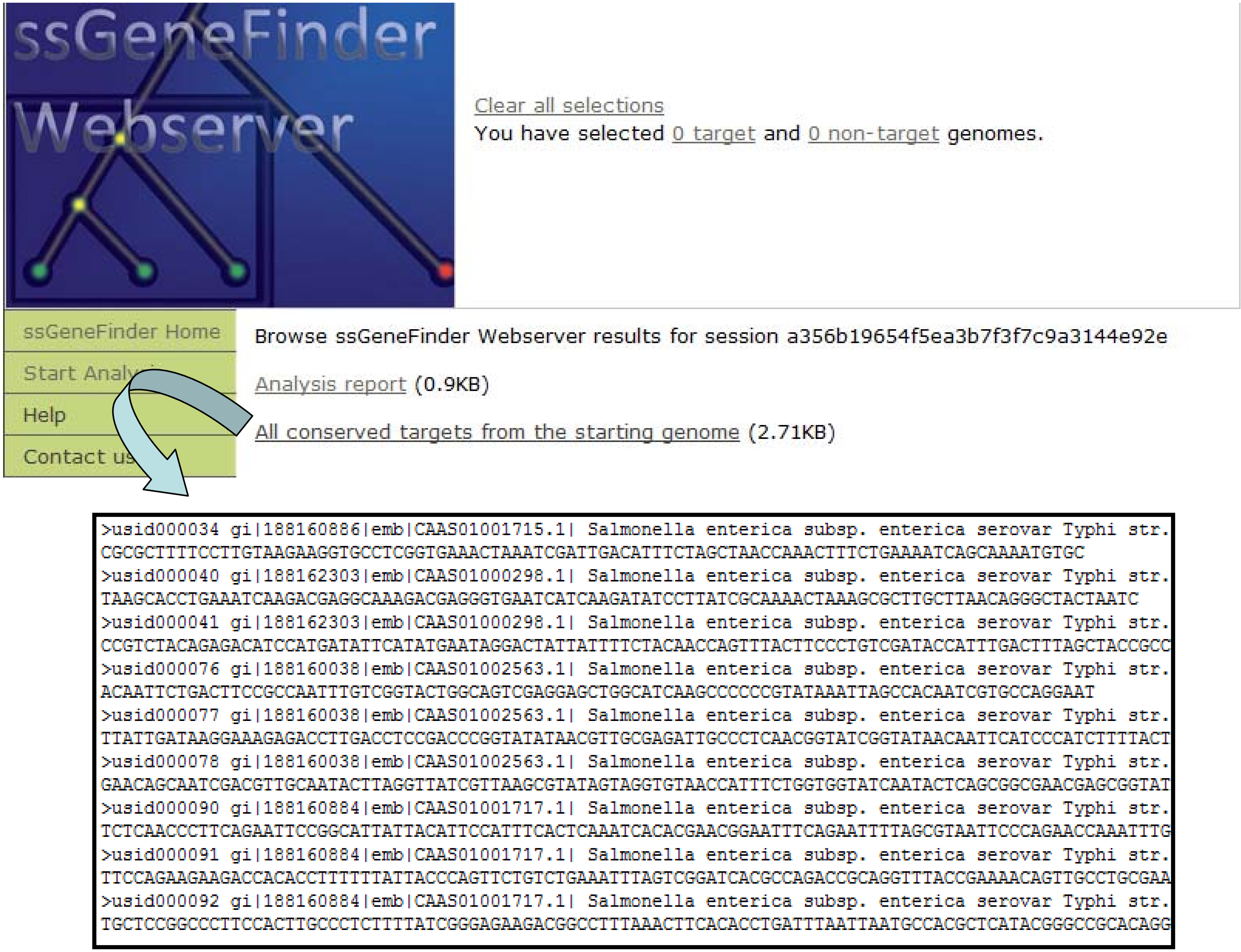
Dear user,

A summary report of your analysis on ssGeneFinder Webserver has been attached with this email. If the results are not satisfactory, you may like to examine the attached log file (log.txt) and modify the settings.

The genome files, unique targets and target alignments have been stored on our server for your
retrieval
at any time. Just check the URL below -

http://147.8.74.24/tom/ssGeneFinder%20Webserver/browse.php?id=a356b19654f5ea3b7f3f7c9a3144e92e

FIG. 1G



Clear all selections
You have selected 0 target and 0 non-target genomes.

Browse ssGeneFinder Webserver results for session a356b19654f5ea3b7f3f7c9a3144e92e

Analysis report (0.9KB)

All conserved targets from the starting genome (2.71KB)

```
>usid000034 gi|188160886|emb|CAAS01001715.1| Salmonella enterica subsp. enterica serovar Typhi str.
CGCGCTTTTCCTTGTAAGAAGGTGCCTCGGTGAAACTAAATCGATTGACATTTCTAGCTAACCAAACTTTCTGAAAATCAGCAAAATGTGC
>usid000040 gi|188162303|emb|CAAS01000298.1| Salmonella enterica subsp. enterica serovar Typhi str.
TAAGCACCTGAAATCAAGACGAGGCAAAGACGAGGGTGAATCATCAAGATATCCTTATCGCAAAACTAAAGCGCTTGCTTAACAGGGCTACTAATC
>usid000041 gi|188162303|emb|CAAS01000298.1| Salmonella enterica subsp. enterica serovar Typhi str.
CCGTCTACAGAGACATCCATGATATTCATATGAATAGGACTATTATTTTCTACAACCAGTTTACTTCCCTGTCGATACCATTTGACTTTAGCTACCGCC
>usid000076 gi|188160038|emb|CAAS01002563.1| Salmonella enterica subsp. enterica serovar Typhi str.
ACAATTCTGACTTCCGCCAATTTGTCGGTACTGGCAGTCGAGGAGCTGGCATCAAGCCCCCCGTATAAATTAGCCACAATCGTGCCAGGAAT
>usid000077 gi|188160038|emb|CAAS01002563.1| Salmonella enterica subsp. enterica serovar Typhi str.
TTATTGATAAGGAAAGAGACCTTGACCTCCGACCCGGTATATAACGTTGCGAGATTGCCCTCAACGGTATCGGTATAACAATTCATCCCATCTTTTACT
>usid000078 gi|188160038|emb|CAAS01002563.1| Salmonella enterica subsp. enterica serovar Typhi str.
GAACAGCAATCGACGTTGCAATACTTAGGTTATCGTTAAGCGTATAGTAGGTGTAACCATTTCTGGTGGTATCAATACTCAGCGGCGAACGAGCGGTAT
>usid000090 gi|188160884|emb|CAAS01001717.1| Salmonella enterica subsp. enterica serovar Typhi str.
TCTCAACCCTTCAGAATTCCGGCATTATTACATTCCATTTCACTCAAATCACACGAACGGAATTTCAGAATTTTAGCGTAATTCCCAGAACCAAATTTG
>usid000091 gi|188160884|emb|CAAS01001717.1| Salmonella enterica subsp. enterica serovar Typhi str.
TTCCAGAAGAAGACCACACCTTTTTTATTACCCAGTTCTGTCTGAAATTTAGTCGGATCACGCCAGACCGCAGGTTTACCGAAAACAGTTGCCTGCGAA
>usid000092 gi|188160884|emb|CAAS01001717.1| Salmonella enterica subsp. enterica serovar Typhi str.
TGCTCCGGCCCTTCCACTTGCCCTCTTTTATCGGGAGAAGACGGCCTTTAAACTTCACACCTGATTTAATTAATGCCACGCTCATACGGGCCGCACAGG
```