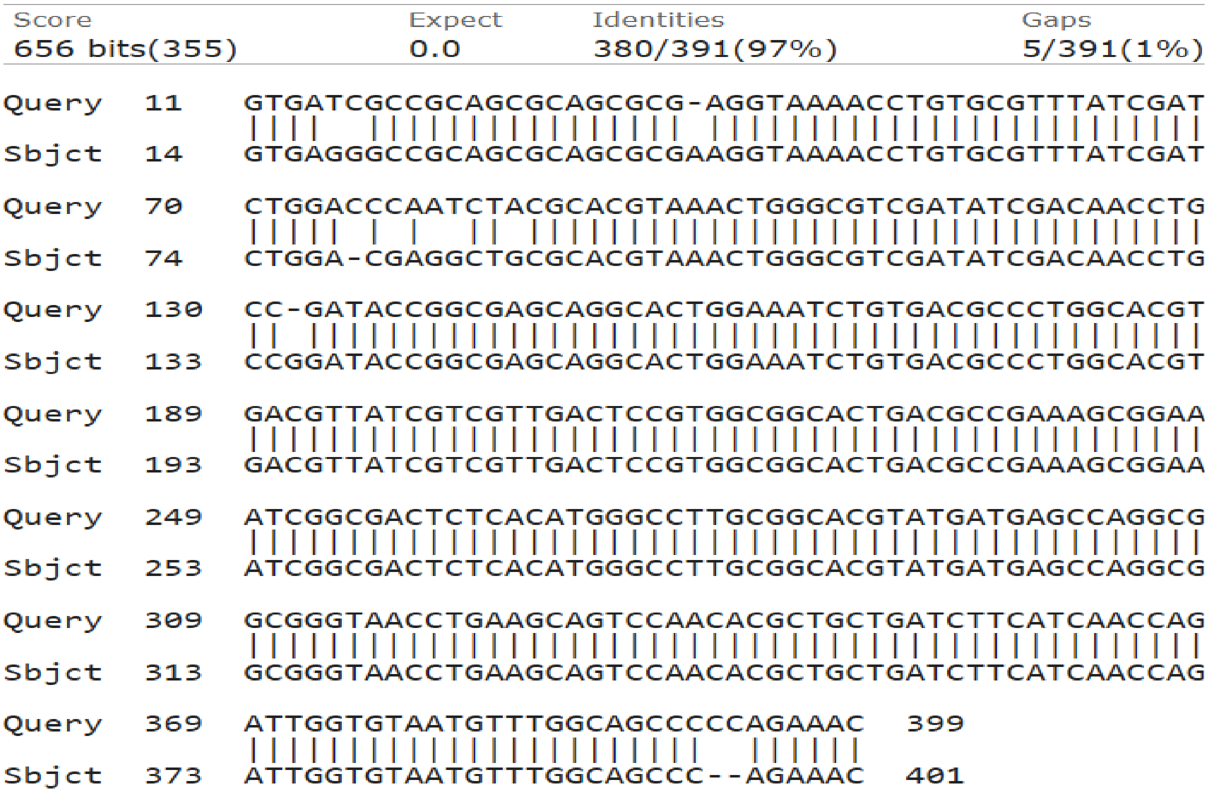
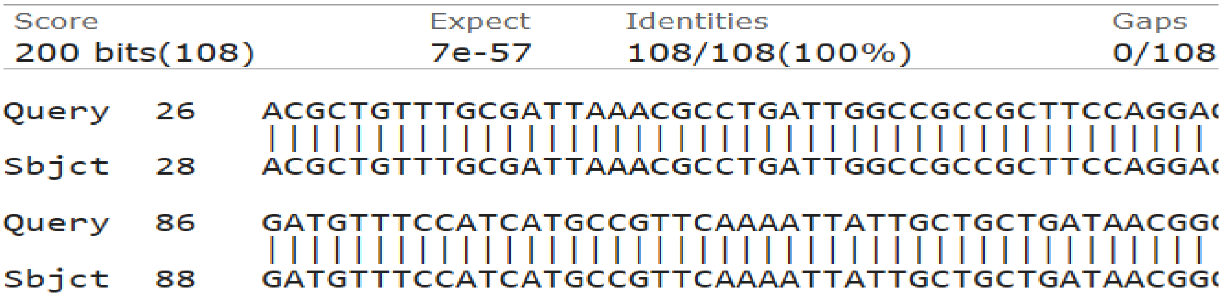
Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.

(**Query**: control strain, **Sbjct**: microgravity exposed strain). **Bacterial Strain**	**Gene/Seqence**	**Identity**	**Gap**
Escherichia coli	recA gene	381/391(97%)	4/391(1%)
Staphylococcus aureus	Dnak gene	108/108(100%)	0/108(0%)
Bacillus subtillis	16S rRNA gene.	173/173(100%)	0/173(0%)



```
Score              Expect   Identities          Gaps
656 bits(355)      0.0      380/391(97%)        5/391(1%)

Query  11   GTGATCGCCGCAGCGCAGCGCG-AGGTAAAACCTGTGCGTTTATCGAT
            ||||  |||||||||||||||| |||||||||||||||||||||||||
Sbjct  14   GTGAGGGCCGCAGCGCAGCGCGAAGGTAAAACCTGTGCGTTTATCGAT

Query  70   CTGGACCCAATCTACGCACGTAAACTGGGCGTCGATATCGACAACCTG
            ||||| | |  || ||||||||||||||||||||||||||||||||||
Sbjct  74   CTGGA-CGAGGCTGCGCACGTAAACTGGGCGTCGATATCGACAACCTG

Query  130  CC-GATACCGGCGAGCAGGCACTGGAAATCTGTGACGCCCTGGCACGT
            || |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  133  CCGGATACCGGCGAGCAGGCACTGGAAATCTGTGACGCCCTGGCACGT

Query  189  GACGTTATCGTCGTTGACTCCGTGGCGGCACTGACGCCGAAAGCGGAA
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  193  GACGTTATCGTCGTTGACTCCGTGGCGGCACTGACGCCGAAAGCGGAA

Query  249  ATCGGCGACTCTCACATGGGCCTTGCGGCACGTATGATGAGCCAGGCG
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  ATCGGCGACTCTCACATGGGCCTTGCGGCACGTATGATGAGCCAGGCG

Query  309  GCGGGTAACCTGAAGCAGTCCAACACGCTGCTGATCTTCATCAACCAG
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  313  GCGGGTAACCTGAAGCAGTCCAACACGCTGCTGATCTTCATCAACCAG

Query  369  ATTGGTGTAATGTTTGGCAGCCCCCAGAAAC  399
            |||||||||||||||||||||||  ||||||
Sbjct  373  ATTGGTGTAATGTTTGGCAGCCC--AGAAAC  401
```

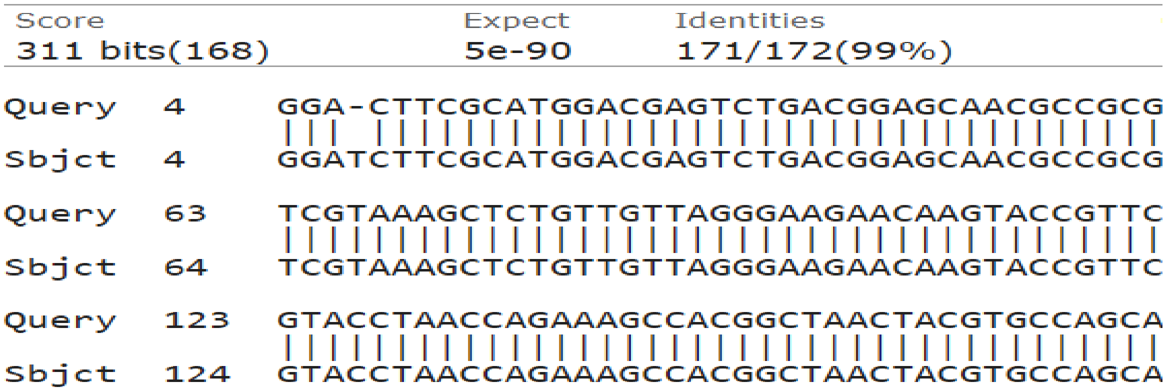


```
Score              Expect   Identities          Gaps
200 bits(108)      7e-57    108/108(100%)       0/108

Query  26   ACGCTGTTTGCGATTAAACGCCTGATTGGCCGCCGCTTCCAGGA
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  28   ACGCTGTTTGCGATTAAACGCCTGATTGGCCGCCGCTTCCAGGA

Query  86   GATGTTTCCATCATGCCGTTCAAAATTATTGCTGCTGATAACGG
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  88   GATGTTTCCATCATGCCGTTCAAAATTATTGCTGCTGATAACGG
```

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.

```
Score              Expect    Identities         Gaps
320 bits(173)      9e-93     173/173(100%)      0/173(

Query  3    GGATCTCGCATGGACGAGTCTGACGGAGCAACGCCGCGTGAGTGA
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4    GGATCTCGCATGGACGAGTCTGACGGAGCAACGCCGCGTGAGTGA

Query  63   CGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTCGAATAGG
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64   CGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTCGAATAGG

Query  123  TACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGG
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124  TACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGG
```

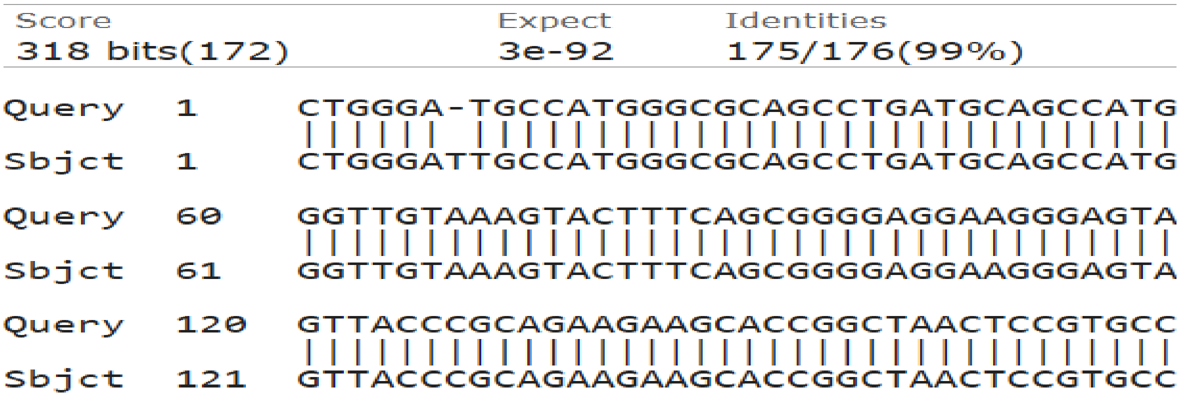
Bacillus subtillis	16S rRNA gene.	171/172(99%)	1/172(0%)



```
Score              Expect    Identities
311 bits(168)      5e-90     171/172(99%)

Query  4    GGA-CTTCGCATGGACGAGTCTGACGGAGCAACGCCGCG
            ||| |||||||||||||||||||||||||||||||||||
Sbjct  4    GGATCTTCGCATGGACGAGTCTGACGGAGCAACGCCGCG

Query  63   TCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTC
            |||||||||||||||||||||||||||||||||||||||
Sbjct  64   TCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTC

Query  123  GTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCA
            |||||||||||||||||||||||||||||||||||||||
Sbjct  124  GTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCA
```

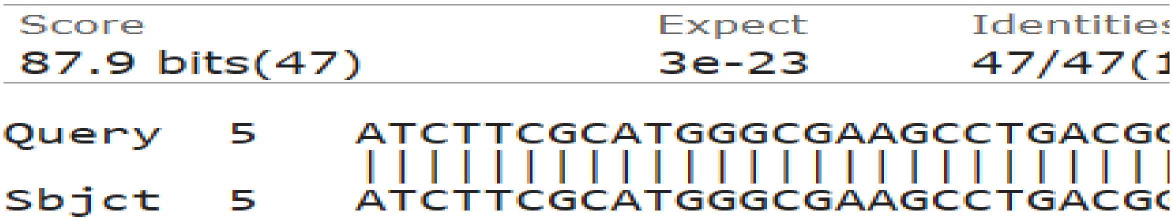
Escherichia coli	16S rRNA gene	175/176(99%)	1/176(0%)

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.



```
Score                       Expect      Identities
318 bits(172)               3e-92       175/176(99%)

Query  1     CTGGGA-TGCCATGGGCGCAGCCTGATGCAGCCATG
             |||||| |||||||||||||||||||||||||||||
Sbjct  1     CTGGGATTGCCATGGGCGCAGCCTGATGCAGCCATG

Query  60    GGTTGTAAAGTACTTTCAGCGGGGAGGAAGGGAGTA
             ||||||||||||||||||||||||||||||||||||
Sbjct  61    GGTTGTAAAGTACTTTCAGCGGGGAGGAAGGGAGTA

Query  120   GTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCC
             ||||||||||||||||||||||||||||||||||||
Sbjct  121   GTTACCCGCAGAAGAAGCACCGGCTAACTCCGTGCC
```

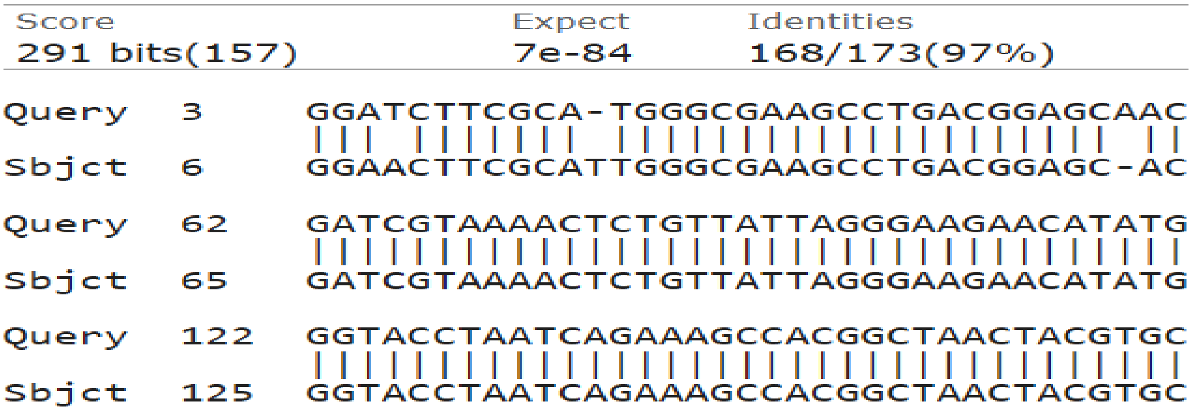
Staphylococcus aureus	16S rRNA gene	169/170(99%)	1/170(0%)



```
Score                       Expect      Identities
87.9 bits(47)               3e-23       47/47(1

Query  5     ATCTTCGCATGGGCGAAGCCTGACGC
             ||||||||||||||||||||||||||
Sbjct  5     ATCTTCGCATGGGCGAAGCCTGACGC
```

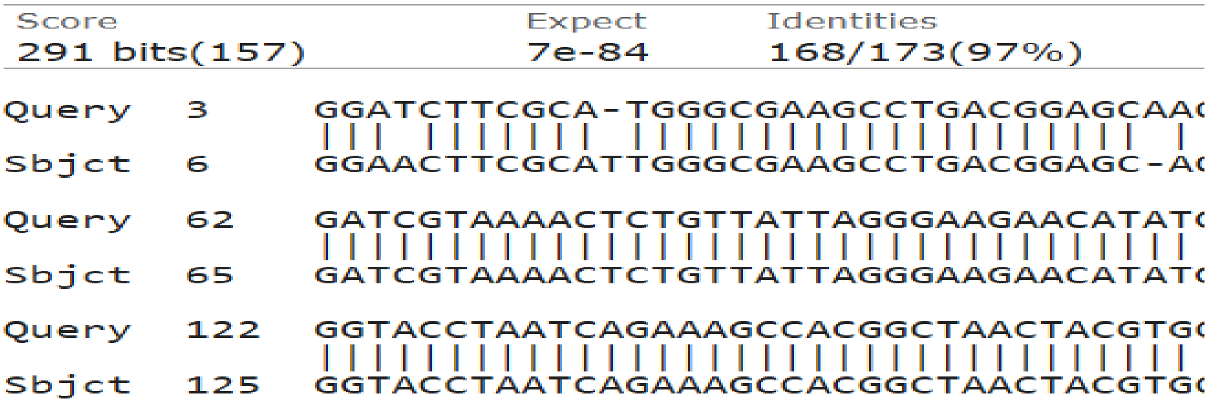
Staphylococcus aureus	16S rRNA gene	168/173(97%)	2/173(1%)

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.



```
Score              Expect     Identities
291 bits(157)      7e-84      168/173(97%)

Query  3     GGATCTTCGCA-TGGGCGAAGCCTGACGGAGCAAC
             ||| ||||||| |||||||||||||||||||| ||
Sbjct  6     GGAACTTCGCATTGGGCGAAGCCTGACGGAGC-AC

Query  62    GATCGTAAAACTCTGTTATTAGGGAAGAACATATG
             |||||||||||||||||||||||||||||||||||
Sbjct  65    GATCGTAAAACTCTGTTATTAGGGAAGAACATATG

Query  122   GGTACCTAATCAGAAAGCCACGGCTAACTACGTGC
             |||||||||||||||||||||||||||||||||||
Sbjct  125   GGTACCTAATCAGAAAGCCACGGCTAACTACGTGC
```

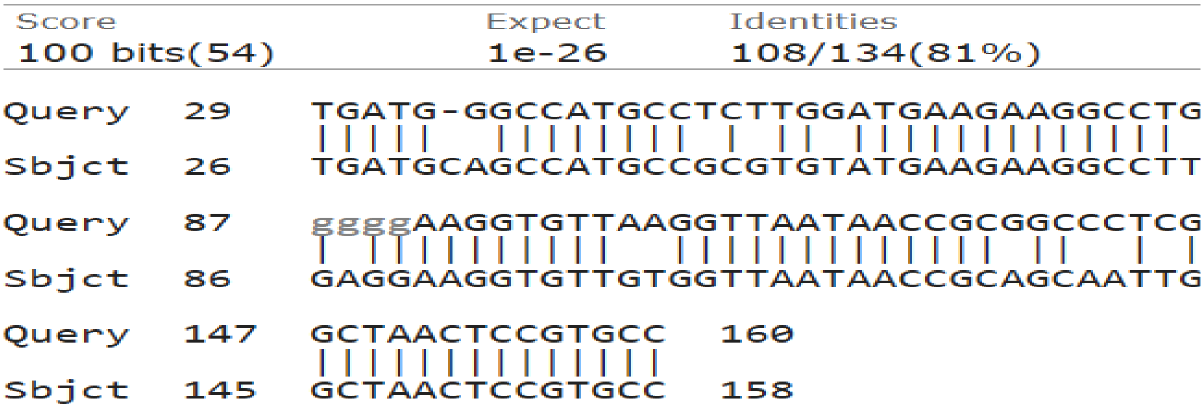
Salmonella typhimurium	16S rRNA gene	135/143(94%)	2/143(1%)



```
Score              Expect     Identities
291 bits(157)      7e-84      168/173(97%)

Query  3     GGATCTTCGCA-TGGGCGAAGCCTGACGGAGCAA
             ||| ||||||| |||||||||||||||||||| |
Sbjct  6     GGAACTTCGCATTGGGCGAAGCCTGACGGAGC-A

Query  62    GATCGTAAAACTCTGTTATTAGGGAAGAACATAT
             ||||||||||||||||||||||||||||||||||
Sbjct  65    GATCGTAAAACTCTGTTATTAGGGAAGAACATAT

Query  122   GGTACCTAATCAGAAAGCCACGGCTAACTACGTG
             ||||||||||||||||||||||||||||||||||
Sbjct  125   GGTACCTAATCAGAAAGCCACGGCTAACTACGTG
```

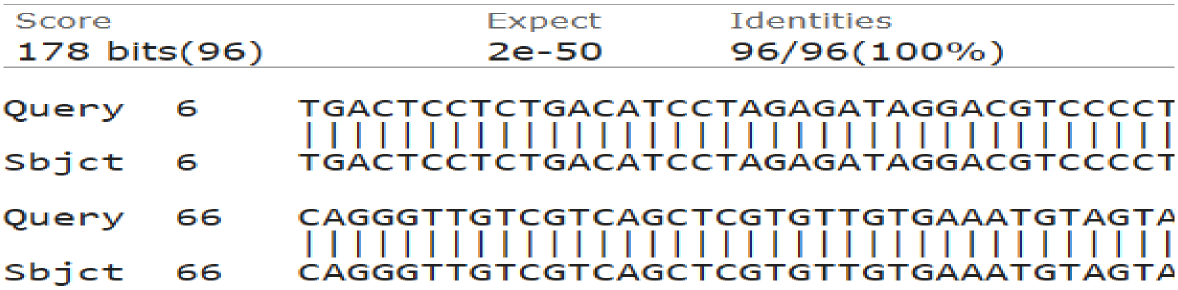
Salmonella typhimurium	16S rRNA gene	108/134(81%)	108/134(81%)

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.



```
Score                            Expect      Identities
100 bits(54)                     1e-26       108/134(81%)

Query  29    TGATG-GGCCATGCCTCTTGGATGAAGAAGGCCTG
             |||||  |||||||| | || |||||||||||||
Sbjct  26    TGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTT

Query  87    ggggAAGGTGTTAAGGTTAATAACCGCGGCCCTCG
             | ||||||||||  ||||||||||||| ||  | |
Sbjct  86    GAGGAAGGTGTTGTGGTTAATAACCGCAGCAATTG

Query  147   GCTAACTCCGTGCC   160
             ||||||||||||||
Sbjct  145   GCTAACTCCGTGCC   158
```

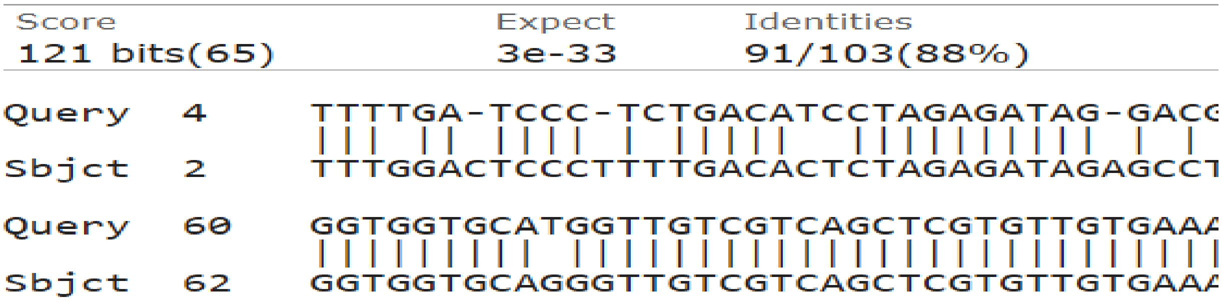
Bacillus subtillis	16S rRNA gene	96/96(100%)	0/96(0%)



```
Score                            Expect      Identities
178 bits(96)                     2e-50       96/96(100%)

Query  6     TGACTCCTCTGACATCCTAGAGATAGGACGTCCCCT
             ||||||||||||||||||||||||||||||||||||
Sbjct  6     TGACTCCTCTGACATCCTAGAGATAGGACGTCCCCT

Query  66    CAGGGTTGTCGTCAGCTCGTGTTGTGAAATGTAGTA
             ||||||||||||||||||||||||||||||||||||
Sbjct  66    CAGGGTTGTCGTCAGCTCGTGTTGTGAAATGTAGTA
```

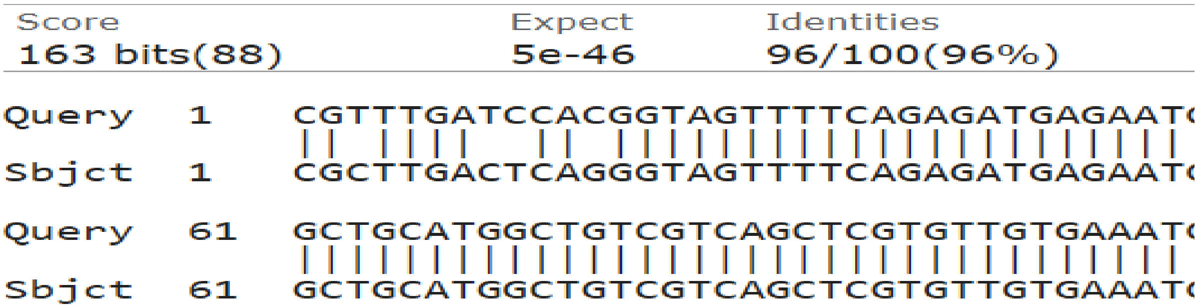
Bacillus subtillis	16S rRNA gene	91/103(88%)	4/103(3%)

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.



```
Score               Expect      Identities
121 bits(65)        3e-33       91/103(88%)

Query  4    TTTTGA-TCCC-TCTGACATCCTAGAGATAG-GAC
            ||| || |||| | |||||  |||||||||| | |
Sbjct  2    TTTGGACTCCCTTTTGACACTCTAGAGATAGAGCC

Query  60   GGTGGTGCATGGTTGTCGTCAGCTCGTGTTGTGAA
            ||||||||| |||||||||||||||||||||||||
Sbjct  62   GGTGGTGCAGGGTTGTCGTCAGCTCGTGTTGTGAA
```

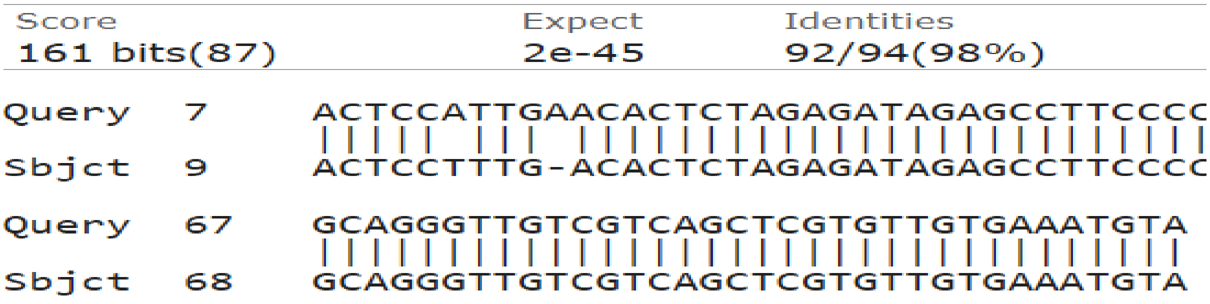
Escherichia coli	16S rRNA gene	96/100(96%)	0/100(0%)



```
Score               Expect      Identities
163 bits(88)        5e-46       96/100(96%)

Query  1    CGTTTGATCCACGGTAGTTTTCAGAGATGAGAAT
            || ||||  || ||||||||||||||||||||||
Sbjct  1    CGCTTGACTCAGGGTAGTTTTCAGAGATGAGAAT

Query  61   GCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAAT
            ||||||||||||||||||||||||||||||||||
Sbjct  61   GCTGCATGGCTGTCGTCAGCTCGTGTTGTGAAAT
```

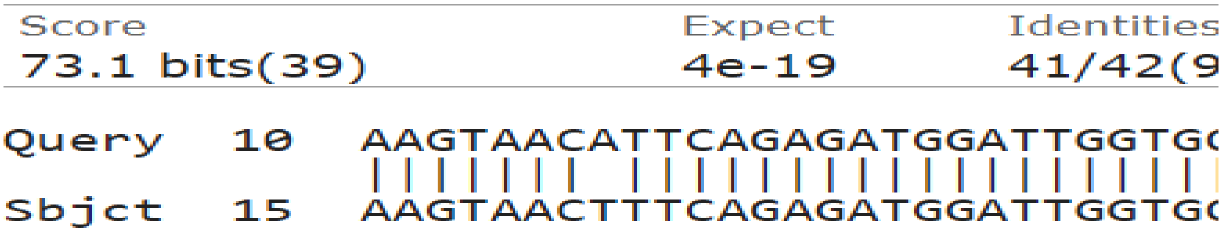
Staphylococcus aureus	16S rRNA gene	92/94(98%)	1/94(1%)

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.



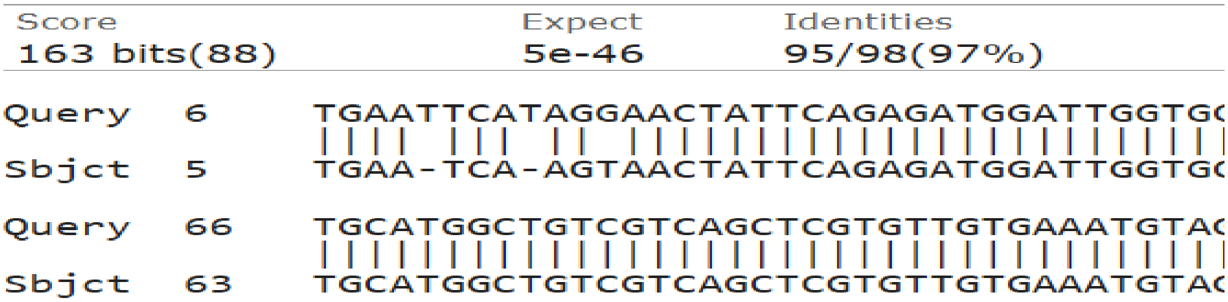
```
Score              Expect      Identities
161 bits(87)       2e-45       92/94(98%)

Query  7     ACTCCATTGAACACTCTAGAGATAGAGCCTTCCC
             ||||| ||| ||||||||||||||||||||||||
Sbjct  9     ACTCCTTTG-ACACTCTAGAGATAGAGCCTTCCC

Query  67    GCAGGGTTGTCGTCAGCTCGTGTTGTGAAATGTA
             ||||||||||||||||||||||||||||||||||
Sbjct  68    GCAGGGTTGTCGTCAGCTCGTGTTGTGAAATGTA
```

Salmonella typhimurium	16S rRNA gene	87/89(98%)	1/89(1%)



```
Score              Expect      Identities
73.1 bits(39)      4e-19       41/42(9

Query  10    AAGTAACATTCAGAGATGGATTGGTG
             ||||||| ||||||||||||||||||
Sbjct  15    AAGTAACTTTCAGAGATGGATTGGTG
```

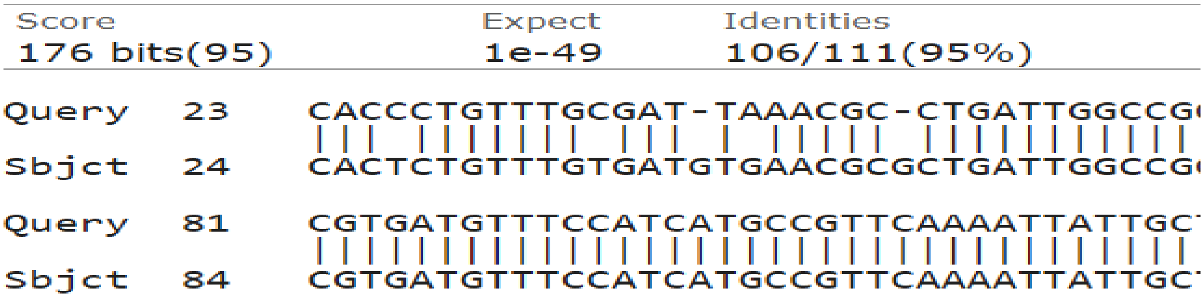
Salmonella typhimurium	16S rRNA gene	95/98(97%)	2/98(2%)



```
Score              Expect      Identities
163 bits(88)       5e-46       95/98(97%)

Query  6     TGAATTCATAGGAACTATTCAGAGATGGATTGGTG
             |||| ||| || |||||||||||||||||||||||
Sbjct  5     TGAA-TCA-AGTAACTATTCAGAGATGGATTGGTG

Query  66    TGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTA
             |||||||||||||||||||||||||||||||||||
Sbjct  63    TGCATGGCTGTCGTCAGCTCGTGTTGTGAAATGTA
```

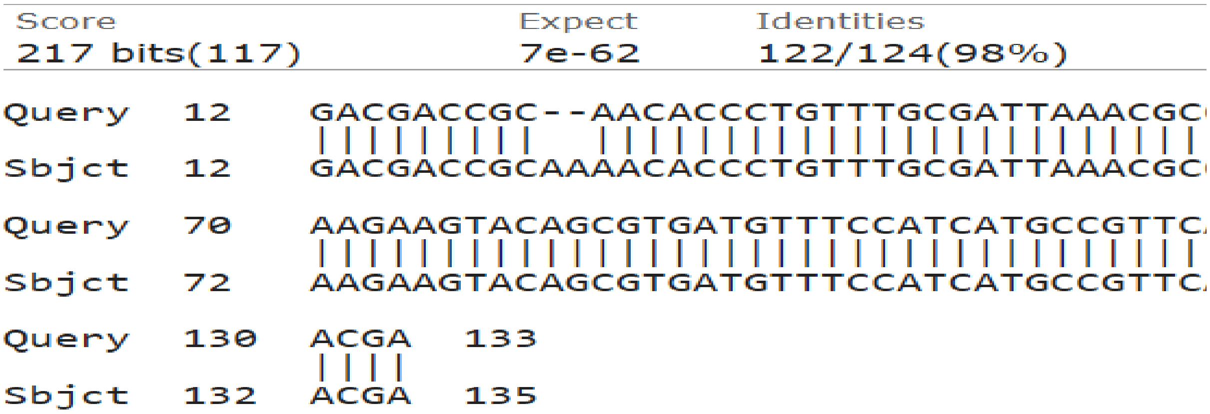
Bacillus subtillis	Dnakgene	106/111(95%)	2/111(1%)

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.



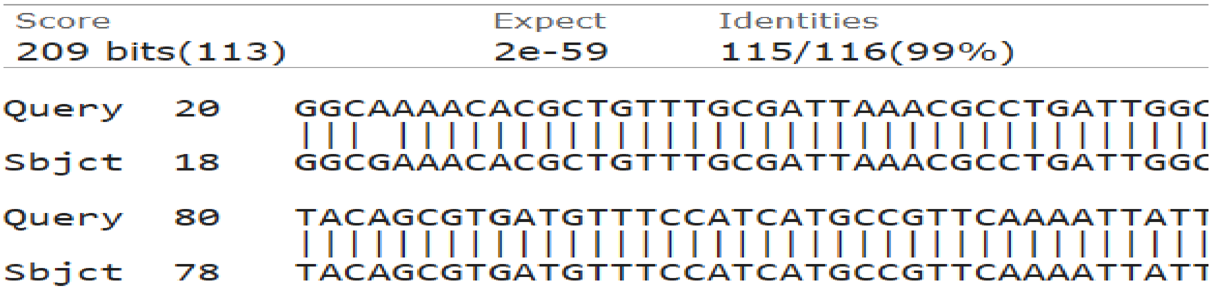
```
Score              Expect    Identities
176 bits(95)       1e-49     106/111(95%)

Query  23    CACCCTGTTTGCGAT-TAAACGC-CTGATTGGCCG
             ||| |||||| ||| | ||||| |||||||||||
Sbjct  24    CACTCTGTTTGTGATGTGAACGCGCTGATTGGCCG

Query  81    CGTGATGTTTCCATCATGCCGTTCAAAATTATTGC
             |||||||||||||||||||||||||||||||||||
Sbjct  84    CGTGATGTTTCCATCATGCCGTTCAAAATTATTGC
```

Escherichia coli	Dnakgene	122/124(98%)	2/124(1%)



```
Score              Expect    Identities
217 bits(117)      7e-62     122/124(98%)

Query  12    GACGACCGC--AACACCCTGTTTGCGATTAAACGC
             |||||||||  ||||||||||||||||||||||||
Sbjct  12    GACGACCGCAAAACACCCTGTTTGCGATTAAACGC

Query  70    AAGAAGTACAGCGTGATGTTTCCATCATGCCGTTC
             |||||||||||||||||||||||||||||||||||
Sbjct  72    AAGAAGTACAGCGTGATGTTTCCATCATGCCGTTC

Query  130   ACGA   133
             ||||
Sbjct  132   ACGA   135
```

Staphylococcus aureus	Dnakgene	136/136(100%)	0/136(0%)



```
Score              Expect    Identities
209 bits(113)      2e-59     115/116(99%)

Query  20    GGCAAAACACGCTGTTTGCGATTAAACGCCTGATTGGC
             ||| ||||||||||||||||||||||||||||||||||
Sbjct  18    GGCGAAACACGCTGTTTGCGATTAAACGCCTGATTGGC

Query  80    TACAGCGTGATGTTTCCATCATGCCGTTCAAAATTATT
             ||||||||||||||||||||||||||||||||||||||
Sbjct  78    TACAGCGTGATGTTTCCATCATGCCGTTCAAAATTATT
```

Salmonella typhimurium	Dnakgene	121/123(98%)	2/123(1%)

Table S1: Summary of BLASTN Analysis for selected bacterial strains' Sequences, depicting alignment identity and Gap percentage post-Stratospheric Exposure.

```
Score                 Expect     Identities          Ga
215 bits(116)         2e-61      121/123(98%)        2/

Query  9     GGTGAGACCGC-AACACCCTGTTTGCGATTAAACGCCTGAT
             ||| ||||||| |||||||||||||||||||||||||||||
Sbjct  9     GGT-AGACCGCAAACACCCTGTTTGCGATTAAACGCCTGAT

Query  68    GAAGAAGTACAGCGTGATGTTTCCATCATGCCGTTCAAAAT
             |||||||||||||||||||||||||||||||||||||||||
Sbjct  68    GAAGAAGTACAGCGTGATGTTTCCATCATGCCGTTCAAAAT

Query  128   GAC  130
             |||
Sbjct  128   GAC  130
```