

**Table S1.** Identification of bacteria family at research area.

| Phylum         | Family            | Species            | Location | Sequence region | %   | Accession  |
|----------------|-------------------|--------------------|----------|-----------------|-----|------------|
| Firmicutes     | Bacillaceae       | Bacillus sp.       | DL       | V1-V4           | 98  | AJ544784.1 |
| Firmicutes     | Planococcaceae    | Planococcus sp.    | DL       | V1-V4           | 99  | JX949541.1 |
| Firmicutes     | Planococcaceae    | Planomicrobium sp. | DL       | V1-V4           | 82  | HQ848108.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | DL       | V1-V4           | 76  | AF140014.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | DL       | V1-V4           | 99  | FJ161329.1 |
| Actinobacteria | Micrococcaceae    | Arthrobacter sp.   | DL       | V1-V4           | 99  | MH671538.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | DL       | V1-V4           | 99  | MG893114.1 |
| Firmicutes     | Planococcaceae    | Planococcus sp.    | DL       | V1-V4           | 99  | JX949541.1 |
| Actinobacteria | Cellulomonadaceae | Cellulomonas sp.   | DL       | V1-V4           | 99  | CP039291.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WA       | V1-V4           | 99  | KX946154.1 |
| Actinobacteria | Streptomyetaceae  | Streptomyces sp.   | WA       | V1-V4           | 96  | MN004813.1 |
| Actinobacteria | Micrococcaceae    | Micrococcus sp.    | WA       | V1-V4           | 100 | DQ279392.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WA       | V1-V4           | 100 | LT686077.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WA       | V1-V4           | 99  | MK542834.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WA       | V1-V4           | 100 | MK629839.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WA       | V1-V4           | 99  | MK811038.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WA       | V1-V4           | 100 | LT686077.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WE       | V1-V4           | 100 | MK811038.1 |
| Actinobacteria | Micrococcaceae    | Micrococcus sp.    | WE       | V1-V4           | 100 | DQ279392.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | WE       | V1-V4           | 96  | KC019189.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | WE       | V1-V4           | 99  | MH683132.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | WE       | V1-V4           | 90  | FR848421.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | WE       | V1-V4           | 99  | MG266315.1 |
| Firmicutes     | Bacillaceae       | Bacillus sp.       | WE       | V1-V4           | 82  | HQ848108.1 |
| Actinobacteria | Streptomyetaceae  | Streptomyces sp.   | WE       | V1-V4           | 90  | JN572690.1 |
| Firmicutes     | Staphylococcaceae | Staphylococcus sp. | WE       | V1-V4           | 100 | CP035288.1 |
| Firmicutes     | Planococcaceae    | Planococcus sp.    | DS       | V1-V4           | 82  | HQ848108.1 |
| Actinobacteria | Streptomyetaceae  | Streptomyces sp.   | DS       | V1-V4           | 99  | KX777592.1 |
| Actinobacteria | Microbacteriaceae | Microbacterium sp. | DS       | V1-V4           | 100 | DQ339613.1 |
| Firmicutes     | Planococcaceae    | Planococcus sp.    | DS       | V1-V4           | 98  | HQ202830.1 |
| Actinobacteria | Micrococcaceae    | Arthrobacter sp.   | DS       | V1-V4           | 99  | LS999985.1 |

<sup>1</sup> Location shows DL (dry lake bed), WA (wadi), WE (well), DS (desert steppe). Sequence region is variable region of 16s rDNA (V1-4). Homology rate (%) is shown as compare to the gene bank listed sequences. Accession is referred gene sequence accession number.