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MARMARA UNIVERSITY FACULTY of ENGINEERING COMPUTER ENGINEERING DEPARTMENT

CSE4065 – Introduction to Computational Genomics

Assignment I Report

Prepared by

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1. Project Structure

Python programming language is used to perform all operations in the project. Python's Regular Expression library "re" and CSV library "csv" are imported. Code sections are explained below:

This function aims to get input from a file. It takes the filename as an argument. If the file doesn't exist under the "res" folder it gives a standard error. There is not an extra control for that. If the file exists, it should contain all the sequence from a sample. Since it is stated that at least 5-mers should be investigated in the project description, if the file content is empty or has the length less than 5, the program raises an error and terminates. If the file contains other characters than nucleobases it also raises error and terminates. Otherwise the content of the file is returned as String.

```
complements = str.maketrans("ACTG", "TGAC")
```

This variable is declared globally to get the complements of each nucleobase by using the following function:

```
def rev_comp(sub_sequence):
    return sub_sequence.translate(complements)[::-1]
```

The operation in this function is a standard Python operation to get a sequence's reverse complement.

```
if kmer in mer_array:
           mer_array[kmer] += 1
           mer_array[kmer] = 1
        if len(mer_array) > 0:
           mer_array = {k: v for k, v in sorted(mer_array.items(), key=lambda
                       item: item[1], reverse=True)}
       for kmer in mer_array:
           if mer_array[kmer] > 1:
               revcomp = rev_comp(kmer)
               rev_comp_val = 0
               if mer_array.get(revcomp) is not None:
                   rev_comp_val = mer_array[revcomp]
               csv_writer.writerow([k, kmer, mer_array[kmer], revcomp,
                                   rev_comp_val])
   mer_array.clear()
file.close()
```

In the main function, a dictionary is declared with origins of samples as key and file contents as values.

Another dictionary "mer_array" is declared to hold the k-mers and their frequency.

For each file content, starting from 5-mers, each k-mers frequency is added to mer_array. Then this mer_array is sorted according to their values in descending order. Finally all resulst for each file stored in csv files.

For some memory issues, each k-mer is written to file with its reverse complement in its section and mer_array is cleared for the next iteration. Since results are too long, they are stored in csv files and will not be shown in this document.

2. Comparison of 2 Samples

There are distinct k-mers which appear in sequence from the patient form Nepal. These are:

| K-mer | Frequency | RevComp | Frequency |
|------------|-----------|------------|-----------|
| TAAAGTGA | 2 | TCACTTTA | 0 |
| TCAATAAA | 2 | TCACTTTA | 3 |
| TTCAATAA | 2 | TTATTGAA | 3 |
| TTCAATAAA | 2 | TTTATTGAA | 2 |
| TTTCAATAA | 2 | TTATTGAAA | 2 |
| TTTCAATAAA | 2 | TTTATTGAAA | 1 |

There are distinct k-mers which appear in sequence from the patient form Wuhan. These are:

| K-mer | Frequency | RevComp | Frequency |
|-------------|-----------|-------------|-----------|
| AAAAAA | 6 | TTTTTTT | 2 |
| AAAAAAA | 5 | TTTTTTT | 1 |
| AAAAAAAA | 4 | TTTTTTTT | 0 |
| AAAAAAAA | 3 | TTTTTTTTT | 0 |
| AAAAAAAAAA | 2 | TTTTTTTTTT | 0 |
| AAAGGTTTA | 2 | TAAACCTTT | 1 |
| AACAAAGTG | 2 | CACTTTGTT | 1 |
| AAGGTTTAT | 2 | ATAAACCTT | 0 |
| AATAGCT | 2 | AGCTATT | 3 |
| AATGACAAA | 2 | TTTGTCATT | 0 |
| ACAAAGTG | 2 | CACTTTGT | 2 |
| ACCTTCC | 2 | GGAAGGT | 1 |
| AGCTTCT | 2 | AGAAGCT | 11 |
| AGGTTTAT | 2 | ATAAACCT | 2 |
| AGTGCTATC | 2 | GATAGCACT | 1 |
| ATACCTTC | 2 | GAAGGTAT | 0 |
| ATAGCTT | 2 | AAGCTAT | 4 |
| ATTTTAATA | 2 | TATTAAAAT | 2 |
| CAAAGTGAC | 2 | GTCACTTTG | 0 |
| CATGTGAT | 2 | ATCACATG | 0 |
| CCATGTGA | 2 | TCACATGG | 0 |
| CCCATG | 2 | CATGGG | 3 |
| CCTTCCC | 2 | GGGAAGG | 0 |
| CTTAGGAG | 2 | CTCCTAAG | 0 |
| GCTTCTT | 2 | AAGAAGC | 6 |
| GGTTTATAC | 2 | GTATAAACC | 1 |
| GTGCTATC | 2 | GATAGCAC | 1 |
| GTTTATAC | 2 | GTATAAAC | 3 |
| TAAAGGTTT | 2 | AAACCTTTA | 0 |
| TAAAGGTTTA | 2 | TAAACCTTTA | 0 |
| TAATAGC | 2 | GCTATTA | 5 |
| TACCTTCC | 2 | GGAAGGTA | 0 |
| TAGTAGT | 2 | ACTACTA | 7 |
| TCAACAAA | 2 | TTTGTTGA | 4 |
| TCCCC | 2 | GGGGA | 4 |
| TCTTAGGA | 2 | TCCTAAGA | 1 |
| TTAAAGGT | 2 | ACCTTTAA | 1 |
| TTAAAGGTT | 2 | AACCTTTAA | 0 |
| TTAAAGGTTT | 2 | AAACCTTTAA | 0 |
| TTAAAGGTTTA | 2 | TAAACCTTTAA | 0 |
| TTAATAGC | 2 | GCTATTAA | 1 |
| TTAGGAG | 2 | CTCCTAA | 0 |
| TTAGTAG | 2 | CTACTAA | 10 |
| TTCAACAA | 2 | TTGTTGAA | 3 |
| TTCTTAGGA | 2 | TCCTAAGAA | 0 |
| TTTCAACA | 2 | TGTTGAAA | 1 |
| TTTTAATA | 2 | TATTAAAA | 2 |

There are common values with both different k-mer frequencies and different reverse complement frequencies in each file. These values are:

| K-mer | Freq. In Nepal | Freq. In Wuhan | Revcomp | Freq. in Nepal | Freq. in Wuhan |
|-------|----------------|----------------|---------|----------------|----------------|
| AAGGT | 45 | 46 | ACCTT | 52 | 53 |
| ACCTT | 52 | 53 | AAGGT | 45 | 46 |
| ATAAA | 58 | 57 | TTTAT | 74 | 75 |
| ATAGC | 20 | 21 | GCTAT | 44 | 45 |
| GCTAT | 44 | 45 | ATAGC | 20 | 21 |
| TTAAA | 94 | 95 | TTTAA | 90 | 91 |
| TTTAA | 90 | 91 | TTAAA | 94 | 95 |
| TTTAT | 74 | 75 | ATAAA | 58 | 57 |

There are common values with only different k-mer frequencies. These values are:

| K-mer | Freq. in Nepal | Freq. in Wuhan | Revcomp | Freq. in Nepal | Freq. in Wuhan |
|----------|----------------|-------------------|----------|----------------|-------------------|
| AAAAA | 56 | 64 | TTTTT | 61 | 61 |
| AAAAA | 2 | 9 | TTTTTT | 6 | 6 |
| AAAGG | 44 | 45 | CCTTT | 44 | 44 |
| AAAGGT | 17 | 18 | ACCTTT | 22 | 22 |
| AAAGGTT | 7 | 8 | AACCTTT | 2 | 2 |
| AAAGGTTT | 2 | 3 | AAACCTTT | 2 | 2 |
| AACAA | 98 | 99 | TTGTT | 102 | 102 |
| AACAAA | 29 | 30 | TTTGTT | 28 | 28 |
| AACAAAG | 10 | 11 | CTTTGTT | 6 | 6 |
| AACAAAGT | 3 | 4 | ACTTTGTT | 1 | 1 |
| AAGGTT | 18 | 19 | AACCTT | 11 | 11 |
| AAGGTTT | 5 | 6 | AAACCTT | 5 | 5 |
| AAGGTTTA | 3 | 4 | TAAACCTT | 2 | 2 |
| AATAA | 43 | 42 | TTATT | 72 | 72 |
| AATAAA | 16 | 15 | TTTATT | 27 | 27 |
| AATAAAG | 4 | 3 | CTTTATT | 8 | 8 |
| AATAG | 32 | 33 | CTATT | 66 | 66 |
| AATAGC | 6 | 7 | GCTATT | 15 | 15 |
| AATGA | 49 | 50 | TCATT | 37 | 37 |
| AATGAC | 9 | 10 | GTCATT | 8 | 8 |
| AATGACA | 4 | 5 | TGTCATT | 3 | 3 |
| AATGACA | 2 | 3 | TTGTCATT | 1 | 1 |
| ACAAA | | | TTTGT | | |
| | 87 | 89 | | 88 | 88 |
| ACAAAA | 19 | 20 | TTTTGT | 32 | 32 |
| ACAAAAA | 4 | 5 | TTTTTGT | 9 | 9 |
| ACAAAG | 23 | 24 | CTTTGT | 15 | 15 |
| ACAAAGT | 6 | 7 | ACTTTGT | 7 | 7 |
| ACCTTC | 11 | 12 | GAAGGT | 16 | 16 |
| AGAAT | 48 | 49 | ATTCT | 58 | 58 |
| AGAATG | 12 | 13 | CATTCT | 15 | 15 |
| AGAATGA | 2 | 3 | TCATTCT | 2 | 2 |
| AGCTT | 44 | 45 | AAGCT | 51 | 51 |
| AGCTTC | 4 | 5 | GAAGCT | 14 | 14 |
| AGGAG | 24 | 25 | CTCCT | 8 | 8 |
| AGGAGA | 6 | 7 | TCTCCT | 3 | 3 |
| AGGTT | 50 | 51 | AACCT | 39 | 39 |
| AGGTTT | 19 | 20 | AAACCT | 12 | 12 |
| AGGTTTA | 5 | 6 | TAAACCT | 5 | 5 |
| AGTAG | 23 | 24 | CTACT | 59 | 59 |
| AGTAGT | 5 | 6 | ACTACT | 16 | 16 |
| AGTAGTG | 2 | 3 | CACTACT | 4 | 4 |
| AGTGC | 39 | 40 | GCACT | 36 | 36 |
| AGTGCT | 16 | 17 | AGCACT | 6 | 6 |
| AGTGCTA | 4 | 5 | TAGCACT | 4 | 4 |
| AGTGCTAT | 3 | 4 | ATAGCACT | 2 | 2 |
| ATAAAG | 15 | 14 | CTTTAT | 19 | 19 |
| ATAAAGT | 4 | 3 | ACTTTAT | 7 | 7 |
| ATACC | 24 | 25 | GGTAT | 24 | 24 |
| ATACCT | 11 | 12 | AGGTAT | 7 | 7 |
| ATACCTT | 4 | 5 | AAGGTAT | 1 | 1 |
| ATAGCT | 6 | 7 | AGCTAT | 11 | 11 |
| ATCCC | 2 | 3 | GGGAT | 7 | 7 |
| ATGAC | 38 | 39 | GTCAT | 28 | 28 |
| ATGACA | 15 | 39 16 | TGTCAT | 14 | 26 14 |
| ATGACA | 7 | 8 | TTGTCAT | 4 | 4 |
| ATGACAA | , | 0 | TIGICAL | 4 | 4 |

| ATGTG | 48 | 49 | CACAT | 36 | 36 |
|----------|----|-----|----------|-----|---------------|
| ATGTGA | 13 | 14 | TCACAT | 12 | 12 |
| ATGTGAT | 4 | 5 | ATCACAT | 4 | 4 |
| | | | | · · | |
| ATTTT | 76 | 77 | AAAAT | 70 | 70 |
| ATTTTA | 25 | 26 | TAAAAT | 22 | 22 |
| ATTTTAA | 8 | 9 | TTAAAAT | 10 | 10 |
| ATTTTAAT | 2 | 3 | ATTAAAAT | 3 | 3 |
| CAAAA | 60 | 61 | TTTTG | 97 | 97 |
| CAAAAA | 14 | 15 | TTTTTG | 22 | 22 |
| CAAAG | 45 | 46 | CTTTG | 60 | 60 |
| CAAAGT | 12 | 13 | ACTTTG | 18 | 18 |
| CAAAGTG | 5 | 6 | CACTTTG | 4 | 4 |
| CAAAGTGA | 2 | 3 | TCACTTTG | 1 | 1 |
| CAACA | 74 | 75 | TGTTG | 97 | 97 |
| CAACAA | 28 | 29 | TTGTTG | 22 | 22 |
| | - | | | | |
| CAACAAA | 7 | 8 | TTTGTTG | 6 | 6 |
| CAACAAAG | 3 | 4 | CTTTGTTG | 0 | 0 |
| CAATA | 29 | 28 | TATTG | 60 | 60 |
| CAATAA | 7 | 6 | TTATTG | 17 | 17 |
| CAATAAA | 4 | 3 | TTTATTG | 7 | 7 |
| CATGT | 40 | 41 | ACATG | 50 | 50 |
| CATGTG | 11 | 12 | CACATG | 10 | 10 |
| CATGTGA | 4 | 5 | TCACATG | 2 | 2 |
| CCATG | 20 | 21 | CATGG | 27 | 27 |
| CCATGT | 7 | 8 | ACATGG | 10 | 10 |
| CCATGTG | 3 | 4 | CACATGG | 4 | 4 |
| CCCAT | 7 | | ATGGG | 19 | 19 |
| | | 8 | | l l | |
| CCCCA | 5 | 6 | TGGGG | 7 | 7 |
| CCTTC | 21 | 22 | GAAGG | 25 | 25 |
| CCTTCC | 3 | 4 | GGAAGG | 2 | 2 |
| CTATC | 18 | 19 | GATAG | 13 | 13 |
| CTATCC | 2 | 3 | GGATAG | 0 | 0 |
| CTTAG | 28 | 29 | CTAAG | 21 | 21 |
| CTTAGG | 6 | 7 | CCTAAG | 6 | 6 |
| CTTAGGA | 2 | 3 | TCCTAAG | 1 | 1 |
| CTTCT | 56 | 57 | AGAAG | 63 | 63 |
| CTTCTT | 25 | 26 | AAGAAG | 21 | 21 |
| CTTCTTA | 5 | 6 | TAAGAAG | 1 | 1 |
| CTTCTTAG | 2 | 3 | CTAAGAAG | 1 | <u>'</u> 1 |
| GAATG | 29 | 30 | CATTC | 33 | 33 |
| | - | | | | |
| GAATGA | 3 | 4 | TCATTC | 8 | 8 |
| GACAA | 52 | 53 | TTGTC | 47 | 47 |
| GACAAA | 15 | 16 | TTTGTC | 12 | 12 |
| GACAAAA | 2 | 3 | TTTTGTC | 2 | 2 |
| GACAAAAA | 2 | 3 | TTTTTGTC | 0 | 0 |
| GAGAA | 31 | 32 | TTCTC | 21 | 21 |
| GAGAAT | 6 | 7 | ATTCTC | 6 | 6 |
| GATTT | 48 | 49 | AAATC | 37 | 37 |
| GATTTT | 17 | 18 | AAAATC | 12 | 12 |
| GATTTTA | 5 | 6 | TAAAATC | 2 | 2 |
| GCTATC | 5 | 6 | GATAGC | 1 | 1 |
| | | 27 | GAAGC | | |
| GCTTCT | 26 | | | 24 | 24 |
| GCTTCT | 7 | 8 | AGAAGC | 14 | 14 |
| GGAGA | 18 | 19 | TCTCC | 9 | 9 |
| GGAGAA | 5 | 6 | TTCTCC | 4 | 4 |
| GGTTT | 54 | 55 | AAACC | 42 | 42 |
| GGTTTA | 16 | 17 | TAAACC | 15 | 15 |
| GGTTTAT | 4 | 5 | ATAAACC | 4 | 4 |
| GGTTTATA | 2 | 3 | TATAAACC | 1 | 1 |
| GTAGT | 44 | 45 | ACTAC | 38 | 38 |
| GTAGTG | 16 | 17 | CACTAC | 9 | 9 |
| GTAGTGC | 5 | 6 | GCACTAC | 3 | 3 |
| GTAGTGC | 2 | 3 | | | |
| | / | . ა | AGCACTAC | 0 | 0 |

| GTGAT | F2 | E2 | ATCAC | 27 | 27 |
|--|--------------------------------------|--------------------------------------|--|-------------------------------------|-------------------------------------|
| GTGAT | 52 10 | 53 11 | ATCAC AATCAC | 27 8 | 27 8 |
| GTGATT | 2 | 3 | AAATCAC | 4 | 4 |
| | | | | * | |
| GTGCT | 53 | 54 | AGCAC | 22 | 22 |
| GTGCTA | 15 | 16 | TAGCAC | 8 | 8 |
| GTGCTAT | 5 | 6 | ATAGCAC | 3 | 3 |
| GTTTA | 68 | 69 | TAAAC | 56 | 56 |
| GTTTAT | 23 | 24 | ATAAAC | 13 | 13 |
| GTTTATA | 5 | 6 | TATAAAC | 6 | 6 |
| TAAAGG | 12 | 13 | CCTTTA | 7 | 7 |
| TAAAGGT | 4 | 5 | ACCTTTA | 4 | 4 |
| TAAAGGTT | 2 | 3 | AACCTTTA | 0 | 0 |
| TAAAGT | 17 | 16 | ACTTTA | 25 | 25 |
| TAAAGTG | 4 | 3 | CACTTTA | 0 | 0 |
| TAATA | 44 | 45 | TATTA | 68 | 68 |
| TAATAG | 11 | 12 | CTATTA | 22 | 22 |
| TACCT | 35 | 36 | AGGTA | 28 | 28 |
| TACCTT | 15 | 16 | AAGGTA | 11 | 11 |
| TACCTTC | | | GAAGGTA | | |
| | 4 | 5 | AGCTA | 4 | 40 |
| TAGCT | 39 | 40 | | 40 | |
| TAGCTT | 8 | 9 | AAGCTA | 12 | 12 |
| TAGGA | 16 | 17 | TCCTA | 28 | 28 |
| TAGGAG | 5 | 6 | CTCCTA | 2 | 2 |
| TAGGAGA | 3 | 4 | TCTCCTA | 1 | 1 |
| TAGTA | 23 | 24 | TACTA | 66 | 66 |
| TAGTAG | 4 | 5 | CTACTA | 25 | 25 |
| TAGTG | 51 | 52 | CACTA | 45 | 45 |
| TAGTGC | 16 | 17 | GCACTA | 9 | 9 |
| TAGTGCT | 5 | 6 | AGCACTA | 2 | 2 |
| TAGTGCTA | 3 | 4 | TAGCACTA | 0 | 0 |
| TAGTGCTAT | 2 | 3 | ATAGCACTA | 0 | 0 |
| TATAC | 28 | 29 | GTATA | 25 | 25 |
| TATACC | 5 | 6 | GGTATA | 5 | 5 |
| TATACCT | 4 | 5 | AGGTATA | 2 | 2 |
| TATACCTT | 2 | 3 | AAGGTATA | 0 | 0 |
| TATCC | 8 | 9 | GGATA | 8 | 8 |
| | | _ | | | |
| TCAAC | 59 | 60 | GTTGA | 62 | 62 |
| TCAACA | 20 | 21 | TGTTGA | 29 | 29 |
| TCAACAA | 9 | 10 | TTGTTGA | 10 | 10 |
| TCAAT | 43 | 42 | ATTGA | 36 | 36 |
| TCAATA | 11 | 10 | TATTGA | 15 | 15 |
| TCAATAA | 3 | 2 | TTATTGA | 5 | 5 |
| TCTTA | 57 | 58 | TAAGA | 34 | 34 |
| TCTTAG | 10 | 11 | CTAAGA | 7 | 7 |
| TCTTAGG | 3 | 4 | CCTAAGA | 3 | 3 |
| TGACA | 64 | 65 | TGTCA | 48 | 48 |
| TGACAA | 16 | 17 | TTGTCA | 17 | 17 |
| TGACAAA | 7 | 8 | TTTGTCA | 4 | 4 |
| TGATT | 56 | 57 | AATCA | 43 | 43 |
| TGATTT | 17 | 18 | AAATCA | 20 | 20 |
| TGATTT | 6 | 7 | AAAATCA | 5 | 5 |
| | 2 | | | | |
| TGATTTTA | , | 3 | TAAAATCA | 0 | 0 |
| | | 20 | T4004 | 0.4 | |
| TGCTA | 65 | 66 | TAGCA | 24 | 24 |
| TGCTA TGCTAT | 65 20 | 21 | ATAGCA | 10 | 10 |
| TGCTA TGCTAT TGCTATC | 65 20 3 | 21 4 | ATAGCA GATAGCA | 10 | 10 1 |
| TGCTA TGCTAT TGCTATC TGTGA | 65 20 3 45 | 21 4 46 | ATAGCA GATAGCA TCACA | 10 1 39 | 10 1 39 |
| TGCTA TGCTAT TGCTATC | 65 20 3 | 21 4 | ATAGCA GATAGCA TCACA ATCACA | 10 | 10 1 39 8 |
| TGCTA TGCTAT TGCTATC TGTGA | 65 20 3 45 | 21 4 46 | ATAGCA GATAGCA TCACA | 10 1 39 | 10 1 39 |
| TGCTA TGCTAT TGCTATC TGTGA TGTGAT | 65 20 3 45 18 | 21 4 46 19 | ATAGCA GATAGCA TCACA ATCACA | 10 1 39 8 | 10 1 39 8 |
| TGCTA TGCTAT TGCTATC TGTGA TGTGAT TTAAAG | 65 20 3 45 18 20 | 21 4 46 19 21 | ATAGCA GATAGCA TCACA ATCACA CTITAA | 10 1 39 8 25 | 10 1 39 8 25 |
| TGCTA TGCTATC TGCTATC TGTGA TGTGAT TTAAAG TTAAAGG TTAAAT | 65 20 3 45 18 20 2 | 21 4 46 19 21 3 | ATAGCA GATAGCA TCACA ATCACA CTTTAA CCTTTAA ATTAA | 10 1 39 8 25 2 | 10 1 39 8 25 2 |
| TGCTA TGCTAT TGCTATC TGTGA TGTGAT TTAAAG TTAAAGG | 65 20 3 45 18 20 2 | 21 4 46 19 21 3 74 | ATAGCA GATAGCA TCACA ATCACA CTTTAA CCTTTAA | 10 1 39 8 25 2 59 | 10 1 39 8 25 2 59 |

| TTAGGA | 3 | 4 | TCCTAA | 9 | 9 |
|----------|----|----|----------|----|----|
| TTAGTA | 8 | 9 | TACTAA | 26 | 26 |
| TTATA | 48 | 49 | TATAA | 59 | 59 |
| TTATAC | 10 | 11 | GTATAA | 10 | 10 |
| TTATACC | 3 | 4 | GGTATAA | 1 | 1 |
| TTATACCT | 2 | 3 | AGGTATAA | 0 | 0 |
| TTCAAC | 25 | 26 | GTTGAA | 23 | 23 |
| TTCAACA | 4 | 5 | TGTTGAA | 9 | 9 |
| TTCAAT | 13 | 12 | ATTGAA | 10 | 10 |
| TTCAATA | 3 | 2 | TATTGAA | 5 | 5 |
| TTCTT | 96 | 97 | AAGAA | 82 | 82 |
| TTCTTA | 27 | 28 | TAAGAA | 14 | 14 |
| TTCTTAG | 6 | 7 | CTAAGAA | 2 | 2 |
| TTCTTAGG | 2 | 3 | CCTAAGAA | 0 | 0 |
| TTTAAT | 27 | 28 | ATTAAA | 25 | 25 |
| TTTAATA | 6 | 7 | TATTAAA | 5 | 5 |
| TTTAATAG | 2 | 3 | CTATTAAA | 2 | 2 |
| TTTAGTA | 3 | 4 | TACTAAA | 7 | 7 |
| TTTATA | 13 | 14 | TATAAA | 20 | 20 |
| TTTATAC | 2 | 3 | GTATAAA | 5 | 5 |
| TTTCAAC | 7 | 8 | GTTGAAA | 6 | 6 |
| TTTCAAT | 6 | 5 | ATTGAAA | 2 | 2 |
| TTTCAATA | 3 | 2 | TATTGAAA | 2 | 2 |
| TTTTA | 89 | 90 | TAAAA | 79 | 79 |
| TTTTAA | 34 | 35 | TTAAAA | 33 | 33 |
| TTTTAAT | 8 | 9 | ATTAAAA | 8 | 8 |

There are common values with only different reverse complement frequencies. These values are:

| K-mer | Freq. in Nepal | Freq. in Wuhan | Revcomp | Freq. in Nepal | Freq. in Wuhan |
|-----------|----------------|-------------------|-----------|----------------|-------------------|
| AAAAT | 70 | 70 | ATTTT | 76 | 77 |
| AAAATC | 12 | 12 | GATTTT | 17 | 18 |
| AAAATCA | 5 | 5 | TGATTTT | 6 | 7 |
| AAACC | 42 | 42 | GGTTT | 54 | 55 |
| AAACCT | 12 | 12 | AGGTTT | 19 | 20 |
| AAACCTT | 5 | 5 | AAGGTTT | 5 | 6 |
| AAACCTTT | 2 | 2 | AAAGGTTT | 2 | 3 |
| AAATC | 37 | 37 | GATTT | 48 | 49 |
| AAATCA | 20 | 20 | TGATTT | 17 | 18 |
| AAATCAC | 4 | 4 | GTGATTT | 2 | 3 |
| AAATCACA | 2 | 2 | TGTGATTT | 0 | 1 |
| AACCT | 39 | 39 | AGGTT | 50 | 51 |
| AACCTT | 11 | 11 | AAGGTT | 18 | 19 |
| AACCTTT | 2 | 2 | AAAGGTT | 7 | 8 |
| AAGAA | 82 | 82 | TTCTT | 96 | 97 |
| AAGAAG | 21 | 21 | CTTCTT | 25 | 26 |
| AAGAAGC | 6 | 6 | GCTTCTT | 1 | 2 |
| AAGAAGCT | 5 | 5 | AGCTTCTT | 0 | 1 |
| AAGAAGCTA | 2 | 2 | TAGCTTCTT | 0 | 1 |
| AAGCT | 51 | 51 | AGCTT | 44 | 45 |
| AAGCTA | 12 | 12 | TAGCTT | 8 | 9 |
| AAGCTAT | 4 | 4 | ATAGCTT | 1 | 2 |
| AAGGTA | 11 | 11 | TACCTT | 15 | 16 |
| AATCA | 43 | 43 | TGATT | 56 | 57 |
| AATCAC | 8 | 8 | GTGATT | 10 | 11 |
| AATCACA | 2 | 2 | TGTGATT | 0 | 1 |
| ACATG | 50 | 50 | CATGT | 40 | 41 |
| ACATGG | 10 | 10 | CCATGT | 7 | 8 |
| ACCTTT | 22 | 22 | AAAGGT | 17 | 18 |

| ACCTTTA | 4 | 4 | TAAAGGT | 4 | 5 |
|-------------------|--------|----|-----------|---------|----------|
| ACTAC | 38 | 38 | GTAGT | 44 | 45 |
| ACTACT | 16 | 16 | AGTAGT | 5 | 6 |
| ACTACTA | 7 | 7 | TAGTAGT | 1 | 2 |
| | | | | | |
| ACTTTA | 25 | 25 | TAAAGT | 17 | 16 |
| ACTTTAT | 7 | 7 | ATAAAGT | 4 | 3 |
| ACTTTATT | 4 | 4 | AATAAAGT | 1 | 0 |
| ACTTTATTG | 2 | 2 | CAATAAAGT | 1 | 0 |
| ACTTTG | 18 | 18 | CAAAGT | 12 | 13 |
| ACTTTGT | 7 | 7 | ACAAAGT | 6 | 7 |
| AGAAG | 63 | 63 | CTTCT | 56 | 57 |
| AGAAGC | 14 | 14 | GCTTCT | 7 | 8 |
| AGAAGCT | 11 | 11 | AGCTTCT | 1 | 2 |
| AGAAGCTA | 2 | 2 | TAGCTTCT | 0 | 1 |
| AGCAC | 22 | 22 | GTGCT | 53 | 54 |
| AGCACT | 6 | 6 | AGTGCT | 16 | 17 |
| AGCACTA | 2 | 2 | TAGTGCT | 5 | 6 |
| AGCTA | 40 | 40 | TAGCT | 39 | 40 |
| | | | | | |
| AGCTATT | 11 | 11 | ATAGCT | 6 | 7 |
| AGCTATT | 3 | 3 | AATAGCT | 1 | 2 |
| AGCTATTA | 2 | 2 | TAATAGCT | 0 | 1 |
| AGGTA | 28 | 28 | TACCT | 35 | 36 |
| AGGTAT | 7 | 7 | ATACCT | 11 | 12 |
| AGGTATA | 2 | 2 | TATACCT | 4 | 5 |
| ATAAAC | 13 | 13 | GTTTAT | 23 | 24 |
| ATAAACC | 4 | 4 | GGTTTAT | 4 | 5 |
| ATAAACCT | 2 | 2 | AGGTTTAT | 1 | 2 |
| ATAGCA | 10 | 10 | TGCTAT | 20 | 21 |
| ATAGCAC | 3 | 3 | GTGCTAT | 5 | 6 |
| ATAGCACT | 2 | 2 | AGTGCTAT | 3 | 4 |
| ATCAC | 27 | 27 | GTGAT | 52 | 53 |
| ATCACA | 8 | 8 | TGTGAT | 18 | 19 |
| ATCACAT | 4 | 4 | ATGTGAT | 4 | 5 |
| ATGGG | 19 | 19 | CCCAT | 7 | 8 |
| ATGGG | 3 | 3 | CCCCAT | | 1 |
| | | | | 0 | <u>-</u> |
| ATTAA | 59 | 59 | TTAAT | 73 | 74 |
| ATTAAA | 25 | 25 | TTTAAT | 27 | 28 |
| ATTAAAA | 8 | 8 | TTTTAAT | 8 | 9 |
| ATTAAAAT | 3 | 3 | ATTTTAAT | 2 | 3 |
| ATTCT | 58 | 58 | AGAAT | 48 | 49 |
| ATTCTC | 6 | 6 | GAGAAT | 6 | 7 |
| ATTGA | 36 | 36 | TCAAT | 43 | 42 |
| ATTGAA | 10 | 10 | TTCAAT | 13 | 12 |
| ATTGAAA | 2 | 2 | TTTCAAT | 6 | 5 |
| CACAT | 36 | 36 | ATGTG | 48 | 49 |
| CACATG | 10 | 10 | CATGTG | 11 | 12 |
| CACATGG | 4 | 4 | CCATGTG | 3 | 4 |
| CACTA | 45 | 45 | TAGTG | 51 | 52 |
| CACTAC | 9 | 9 | GTAGTG | 16 | 17 |
| CACTACT | 4 | 4 | AGTAGTG | 2 | 3 |
| CACTACT | 4 | 4 | CAAAGTG | 5 | 6 |
| CACTITIG | 2 | 2 | ACAAAGTG | 1 | 2 |
| | | | | | |
| CATGG | 27 | 27 | CCATG | 20 | 21 |
| CATGGG | 3 | 3 | CCCATG | 1 | 2 |
| CATTC | 33 | 33 | GAATG | 29 | 30 |
| CATTCT | 15 | 15 | AGAATG | 12 | 13 |
| CATTCTC | 2 | 2 | GAGAATG | 0 | 1 |
| CCTAA | 37 | 37 | TTAGG | 16 | 17 |
| | _ | 6 | CTTAGG | 6 | 7 |
| CCTAAG | 6 | U | | | |
| | 6 3 | 3 | TCTTAGG | 3 | 4 |
| CCTAAG | | | | 3 44 | 4 45 |
| CCTAAG CCTAAGA | 3 | 3 | TCTTAGG | | |

| CTAAC | 04 | 04 | CTTAC | 20 | 20 |
|--|---|---|--|--|--|
| CTAAGA | 21 | 21 | CTTAG | 28 | 29 |
| CTAAGA | 7 | 7 | TCTTAG | 10 | 11 |
| CTAAGAA | 2 | 2 | TTCTTAG | 6 | 7 |
| CTACT | 59 | 59 | AGTAG | 23 | 24 |
| CTACTA | 25 | 25 | TAGTAG | 4 | 5 |
| CTACTAA | 10 | 10 | TTAGTAG | 1 | 2 |
| CTACTAAA | 3 | 3 | TTTAGTAG | 0 | 1 |
| CTACTAAAA | 2 | 2 | TTTTAGTAG | 0 | 1 |
| CTATT | 66 | 66 | AATAG | 32 | 33 |
| CTATTA | 22 | 22 | TAATAG | 11 | 12 |
| CTATTAA | 9 | 9 | TTAATAG | 5 | 6 |
| CTATTAAA | 2 | 2 | TTTAATAG | 2 | 3 |
| CTCCT | 8 | 8 | AGGAG | 24 | 25 |
| CTCCTA | 2 | 2 | TAGGAG | 5 | 6 |
| CTTTAA | 25 | 25 | TTAAAG | 20 | 21 |
| | | _ | | - | |
| CTTTAT | 19 | 19 | ATAAAG | 15 | 14 |
| CTTTATT | 8 | 8 | AATAAAG | 4 | 3 |
| CTTTATTG | 2 | 2 | CAATAAAG | 1 | 0 |
| CTTTG | 60 | 60 | CAAAG | 45 | 46 |
| CTTTGT | 15 | 15 | ACAAAG | 23 | 24 |
| CTTTGTT | 6 | 6 | AACAAAG | 10 | 11 |
| GAAGC | 24 | 24 | GCTTC | 26 | 27 |
| GAAGCT | 14 | 14 | AGCTTC | 4 | 5 |
| GAAGCTA | 2 | 2 | TAGCTTC | 0 | 1 |
| GAAGG | 25 | 25 | CCTTC | 21 | 22 |
| GAAGGT | 16 | 16 | ACCTTC | 11 | 12 |
| GAAGGTA | 4 | 4 | TACCTTC | 4 | 5 |
| | | | | | |
| GATAG | 13 | 13 | CTATC | 18 | 19 |
| GCACT | 36 | 36 | AGTGC | 39 | 40 |
| GCACTA | 9 | 9 | TAGTGC | 16 | 17 |
| GCACTAC | 3 | 3 | GTAGTGC | 5 | 6 |
| GCTATT | 15 | 15 | AATAGC | 6 | 7 |
| GCTATTA | 5 | 5 | TAATAGC | 1 | 2 |
| GGAAGG | 2 | 2 | CCTTCC | 3 | 4 |
| GGATA | 8 | 8 | TATCC | 8 | 9 |
| GGGAT | 7 | 7 | ATCCC | 2 | 3 |
| GGGGA | 4 | 4 | TCCCC | 1 | 2 |
| GGTAT | 24 | 24 | ATACC | 24 | 25 |
| GGTATA | 5 | 5 | TATACC | 5 | 6 |
| GTATA | 25 | 25 | TATAC | 28 | 29 |
| GTATAA | 10 | 10 | TTATAC | 10 | 11 |
| | | | | | |
| GTATAAA | 5 | 5 | TTTATAC | 2 | 2 |
| GTATAAAC | 3 | 3 | GTTTATAC | 1 | |
| GTCAT | 28 | 28 | ATGAC | 38 | 39 |
| GTCATT | 8 | 8 | AATGAC | 9 | 10 |
| GTCATTC | 2 | 2 | GAATGAC | 0 | 1 |
| GTTGA | 62 | 62 | TCAAC | 59 | 60 |
| GTTGAA | 23 | 23 | TTCAAC | 25 | 26 |
| GTTGAAA | 6 | 6 | TTTCAAC | 7 | 8 |
| GTTGAAAA | 3 | 3 | TTTTCAAC | 0 | 1 |
| TAAAA | 70 | 70 | TTTTA | 89 | 90 |
| TAAAAT | 79 | 79 | 11117 | 09 | |
| TAAAATC | 79 22 | 79 22 | ATTTTA | 25 | 26 |
| IAAAAIG | | | ATTTTA | | 26 6 |
| | 22 2 | 22 | ATTTTA GATTTTA | 25 5 | 6 |
| TAAAC | 22 2 56 | 22 2 56 | ATTTTA GATTTTA GTTTA | 25 5 68 | 6 69 |
| TAAAC TAAACC | 22 2 56 15 | 22 2 56 15 | ATTTTA GATTTTA GTTTA GGTTTA | 25 5 68 16 | 6 69 17 |
| TAAACC TAAACC TAAACCT | 22 2 56 15 5 | 22 2 56 15 5 | ATTTTA GATTTTA GTTTA GGTTTA AGGTTTA | 25 5 68 16 5 | 6 69 17 6 |
| TAAAC TAAACC TAAACCT TAAACCTT | 22 2 56 15 5 | 22 2 56 15 5 | ATTTTA GATTTTA GTTTA GGTTTA AGGTTTA AAGGTTTA | 25 5 68 16 5 3 | 6 69 17 6 4 |
| TAAACC TAAACCT TAAACCT TAAACCTT TAAACA | 22 2 56 15 5 2 34 | 22 2 56 15 5 2 34 | ATTTTA GATTTTA GTTTA GGTTTA AGGTTTA AAGGTTTA TCTTA | 25 5 68 16 5 3 | 6 69 17 6 4 58 |
| TAAACC TAAACCT TAAACCTT TAAACCTT TAAACAACTT TAAGA | 22 2 56 15 5 2 34 14 | 22 2 56 15 5 2 34 | ATTITA GATTITA GITTA GGTTTA AGGTTTA AAGGTTTA TCTTA TTCTTA | 25 5 68 16 5 3 57 27 | 6 69 17 6 4 58 28 |
| TAAAC TAAACCT TAAACCT TAAACCTT TAAACCTT TAAGA TAAGAA TACTA | 22 2 56 15 5 2 34 14 66 | 22 2 56 15 5 2 34 14 66 | ATTITA GATTITA GATTITA GITTA GGTTTA AGGTTTA AAGGTTTA TCTTA TTCTTA TAGTA | 25 5 68 16 5 3 57 27 23 | 6 69 17 6 4 58 28 |
| TAAAC TAAACCT TAAACCTT TAAACCTT TAAGA TAAGAA TACTA TACTAA | 22 2 56 15 5 2 34 14 66 26 | 22 2 56 15 5 2 34 14 66 26 | ATTITA GATTITA GATTITA GITTA GGTTTA AGGTTTA AAGGTTTA TCTTA TTCTTA TAGTA TTAGTA | 25 5 68 16 5 3 57 27 23 8 | 6 69 17 6 4 58 28 24 9 |
| TAAAC TAAACCT TAAACCT TAAACCTT TAAACCTT TAAGA TAAGAA TACTA | 22 2 56 15 5 2 34 14 66 | 22 2 56 15 5 2 34 14 66 | ATTITA GATTITA GATTITA GITTA GGTTTA AGGTTTA AAGGTTTA TCTTA TTCTTA TAGTA | 25 5 68 16 5 3 57 27 23 | 6 69 17 6 4 58 28 |

| TACTAAAAT | 2 | 2 | ATTTTAGTA | 0 | 1 |
|-----------|-----|-----|-----------|----|---------------|
| TAGCA | 24 | 24 | TGCTA | 65 | 66 |
| TAGCAC | 8 | 8 | GTGCTA | 15 | 16 |
| TAGCACT | 4 | 4 | AGTGCTA | 4 | 5 |
| TATAA | 59 | 59 | TTATA | 48 | 49 |
| TATAA | 20 | 20 | TTTATA | 13 | 14 |
| | | | | | |
| TATAAAC | 6 | 6 | GTTTATA | 5 | 6 |
| TATTA | 68 | 68 | TAATA | 44 | 45 |
| TATTAA | 17 | 17 | TTAATA | 15 | 16 |
| TATTAAA | 5 | 5 | TTTAATA | 6 | 7 |
| TATTAAAA | 2 | 2 | TTTTAATA | 1 | 2 |
| TATTAAAAT | 2 | 2 | ATTTTAATA | 1 | 2 |
| TATTG | 60 | 60 | CAATA | 29 | 28 |
| TATTGA | 15 | 15 | TCAATA | 11 | 10 |
| TATTGAA | 5 | 5 | TTCAATA | 3 | 2 |
| TATTGAAA | 2 | 2 | TTTCAATA | 3 | 2 |
| TCACA | 39 | 39 | TGTGA | 45 | 46 |
| TCACAT | 12 | 12 | ATGTGA | 13 | 14 |
| TCACATG | 2 | 2 | CATGTGA | 4 | 5 |
| TCATT | 37 | 37 | AATGA | 49 | 50 |
| TCATTC | 8 | 8 | GAATGA | 3 | 4 |
| TCATTCT | 2 | 2 | AGAATGA | 2 | 3 |
| | | | TAGGA | | |
| TCCTA | 28 | 28 | | 16 | 17 |
| TCCTAA | 9 | 9 | TTAGGA | 3 | 4 |
| TCTCC | 9 | 9 | GGAGA | 18 | 19 |
| TCTCCT | 3 | 3 | AGGAGA | 6 | 7 |
| TGGGG | 7 | 7 | CCCCA | 5 | 6 |
| TGGGGA | 2 | 2 | TCCCCA | 0 | 1 |
| TGTCA | 48 | 48 | TGACA | 64 | 65 |
| TGTCAT | 14 | 14 | ATGACA | 15 | 16 |
| TGTCATT | 3 | 3 | AATGACA | 4 | 5 |
| TGTTG | 97 | 97 | CAACA | 74 | 75 |
| TGTTGA | 29 | 29 | TCAACA | 20 | 21 |
| TGTTGAA | 9 | 9 | TTCAACA | 4 | 5 |
| TTAAAA | 33 | 33 | TTTTAA | 34 | 35 |
| TTAAAAT | 10 | 10 | ATTTTAA | 8 | 9 |
| TTATT | 72 | 72 | AATAA | 43 | 42 |
| TTATTG | 17 | 17 | CAATAA | 7 | 6 |
| | | | - | | |
| TTATTGA | 5 | 5 | TCAATAA | 3 | 2 |
| TTATTGAA | 3 | 3 | TTCAATAA | 2 | 1 |
| TTATTGAAA | 2 | 2 | TTTCAATAA | 2 | 1 |
| TTCTC | 21 | 21 | GAGAA | 31 | 32 |
| TTCTCC | 4 | 4 | GGAGAA | 5 | 6 |
| TTCTCCT | 2 | 2 | AGGAGAA | 0 | 1 |
| TTGTC | 47 | 47 | GACAA | 52 | 53 |
| TTGTCA | 17 | 17 | TGACAA | 16 | 17 |
| TTGTCAT | 4 | 4 | ATGACAA | 7 | 8 |
| TTGTT | 102 | 102 | AACAA | 98 | 99 |
| TTGTTG | 22 | 22 | CAACAA | 28 | 29 |
| TTGTTGA | 10 | 10 | TCAACAA | 9 | 10 |
| TTGTTGAA | 3 | 3 | TTCAACAA | 1 | 2 |
| TTTATT | 27 | 27 | AATAAA | 16 | 15 |
| TTTATTG | 7 | 7 | CAATAAA | 4 | 3 |
| TTTATTGA | 3 | 3 | TCAATAAA | 2 | <u>3</u> 1 |
| | | | | | |
| TTTATTGAA | 2 | 2 | TTCAATAAA | 2 | 1 00 |
| TTTGT | 88 | 88 | ACAAA | 87 | 89 |
| TTTGTC | 12 | 12 | GACAAA | 15 | 16 |
| TTTGTCA | 4 | 4 | TGACAAA | 7 | 8 |
| TTTGTT | 28 | 28 | AACAAA | 29 | 30 |
| TTTGTTG | 6 | 6 | CAACAAA | 7 | 8 |
| | | | TCAACAAA | 1 | 2 |
| TTTGTTGA | 4 | 4 | TCAACAAA | 1 | |
| | 97 | 97 | CAAAA | 60 | 61 |

| TTTTGTC | 2 | 2 | GACAAAA | 2 | 3 |
|---------|----|----|---------|----|----|
| TTTTT | 61 | 61 | AAAAA | 56 | 64 |
| TTTTTG | 22 | 22 | CAAAAA | 14 | 15 |
| TTTTTGT | 9 | 9 | ACAAAAA | 4 | 5 |
| TTTTTT | 6 | 6 | AAAAA | 2 | 9 |
| TTTTTTG | 2 | 2 | CAAAAA | 0 | 1 |
| TTTTTTT | 2 | 2 | AAAAAA | 0 | 6 |

According to these results, there are some distinct values in each sample, and there are some common values with different frequencies.