Supporting Information:

Identification and characterization of two conserved G-quadruplex forming motifs in the Nipah virus genome and their interaction with G-quadruplex specific ligands

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**Supplementary Table S1:** Table showing Nipah virus isolate details used for the prediction of G-quadruplex forming sequences (HGQs).

| Sl. No. | Strain/Isolate Name                        | Accession Number | Length of Genome (bp) | GC% Content |
|--------|--------------------------------------------|------------------|-----------------------|-------------|
| 1      | Nipah virus                                | NC002728.1       | 18246                 | 39.88       |
| 2      | Nipah virus                                | AF212302.2       | 18246                 | 39.88       |
| 3      | Nipah virus isolate UMMC1                  | AY029767.1       | 18246                 | 39.88       |
| 4      | Nipah virus isolate UMMC2                  | AY029768.1       | 18246                 | 39.87       |
| 5      | Nipah virus isolate NV/MY/99/UM-0128        | AJ564623.1       | 18246                 | 39.87       |
| 6      | Nipah virus isolate NV/MY/99/VRI-0626       | AJ627196.1       | 18246                 | 39.89       |
| 7      | Nipah virus isolate NV/MY/99/VRI-1413       | AJ564622.1       | 18246                 | 39.88       |
| 8      | Nipah virus isolate NV/MY/99/VRI-2794       | AJ564621.1       | 18246                 | 39.87       |
| 9      | Nipah virus from Bangladesh                | AY988601.1       | 18252                 | 40.12       |
| 10     | Nipah virus isolate NIVBGD2008MANIKGONJ     | JN808857.1       | 18252                 | 40.31       |
| 11     | Nipah virus isolate NIVBGD2008RAJBARI       | JN808863.1       | 18252                 | 40.31       |
| 12     | Nipah virus isolate Ind-Nipah-07-FG from India | FJ513078.1     | 18252                 | 40.18       |

**Supplementary Table S2:** The G-quadruplex prediction result for the Nipah virus using the in-house G-quadruplex prediction tool. {1: Nipah virus (NC002728.1); 2: Nipah Virus (AF212302.2); 3: Nipah virus isolate UMMC1 (AY029767.1); 4: Nipah virus isolate UMMC2 (AY029768.1); 5: Nipah virus isolate NV/MY/99/UM-0128 (AJ564623.1); 6: Nipah virus isolate NV/MY/99/VRI-0626 (AJ627196.1); 7: Nipah virus isolate NV/MY/99/VRI-1413 (AJ564622.1); 8: Nipah virus isolate NV/MY/99/VRI-2794 (AJ564621.1); 9: Nipah virus from Bangladesh (AY988601.1); 10: Nipah virus isolate NIVBGD2008MANIKGONJ (JN808857.1); 11: Nipah virus isolate NIVBGD2008RAJBARI (JN808863.1) and 12: Nipah virus isolate Ind-Nipah-07-FG from India (FJ513078.1)}

Along with the putative G-quadruplex sequence prediction, this tool provides us with the length of the sequences, position of the sequence in the genome i.e. the start and end position and the
cC score and the cG score. The higher cG/cC score represents higher probability to G-quadruplex structure formation. The HGQ-NV-L and HGQ-NV-G chosen for further detailed analysis are highlighted in yellow the prediction table.

1. Nipah virus (NC002728.1)

| Sense Strand | # | Length (bp) | Start Position | End Position | HGQ Motifs                       | cG Score | cC Score |
|--------------|---|-------------|----------------|--------------|----------------------------------|----------|----------|
|              | 1 | 20          | 454            | 473          | GGAGAGGAGAGAGAGACAAGG            | 110      | 10       |
|              | 2 | 15          | 478            | 492          | GGAGGAGATGGAAGG                  | 90       | 0        |
|              | 3 | 18          | 892            | 909          | GGAAACTGGTATGGCAGG               | 80       | 20       |
|              | 4 | 24          | 12314          | 12337        | GGATGAGGCTAGGATCCTGAGGG          | 120      | 30       |
|              | 5 | 20          | 13151          | 13170        | GGAGAACGGGATGGAAGG               | 100      | 10       |
|              | 6 | 16          | 15080          | 15095        | GGCTATGGTGGAAGG                  | 90       | 10       |
|              | 7 | 20          | 15606          | 15625        | GGTTATCGGTATTGGAAGG              | 90       | 10       |

| Anti-sense Strand | # | Length (bp) | Start Position | End Position | HGQ Motifs                        | cG Score | cC Score |
|-------------------|---|-------------|----------------|--------------|-----------------------------------|----------|----------|
|                    | 1 | 18          | 78             | 95           | GGTCTTGGATTTTGGGAAGG              | 80       | 10       |
|                    | 2 | 18          | 399            | 416          | GGATAGGGTTTCTAGGTTG               | 90       | 10       |
|                    | 3 | 18          | 5573           | 5590         | GGGGAGGTAAAGAGGAGG                | 110      | 0        |
|                    | 4 | 22          | 8464           | 8485         | GGTTAAACGGGGTTTGGGAATTTG          | 90       | 10       |
|                    | 5 | 17          | 10334          | 10350        | GGCTGTAGGACAGGTTG                | 90       | 20       |
|                    | 6 | 25          | 14644          | 14668        | GGGACTTTGGCATCGGAGTTCCTG          | 100      | 50       |
|                    | 7 | 28          | 14948          | 14975        | GGCTTGAAGGGTTGTCTCGGATTG          | 110      | 30       |

2. Nipah Virus (AF212302.2)

| Sense Strand | # | Length (bp) | Start Position | End Position | HGQ Motifs                        | cG Score | cC Score |
|--------------|---|-------------|----------------|--------------|-----------------------------------|----------|----------|
|              | 1 | 20          | 454            | 473          | GGAGAGGAGAGGAGAGGACAAGG            | 110      | 10       |
|              | 2 | 15          | 478            | 492          | GGAGGAGATGGAAGG                  | 90       | 0        |
|              | 3 | 18          | 892            | 909          | GGAAACTGGTATGGCAGG               | 80       | 20       |
|              | 4 | 24          | 12314          | 12337        | GGATGAGGCTAGGATCCTGAGGG          | 120      | 30       |
|              | 5 | 20          | 13151          | 13170        | GGAGAACGGGATGGAAGG               | 100      | 10       |
3. Nipah virus isolate UMMC1 (AY029767.1)

### Sense Strand

| #  | Length (bp) | Start Position | End Position | HGQ Motifs                               | cG Score | cC Score |
|----|-------------|----------------|--------------|------------------------------------------|----------|----------|
| 1  | 20          | 454            | 473          | GGAGAGGAGAGGAGGACAAAGG                   | 110      | 10       |
| 2  | 15          | 478            | 492          | GGAGGAGATGGAAGG                         | 90       | 0        |
| 3  | 18          | 892            | 909          | GGAAGTCGTGGTAGGGCAGG                     | 80       | 20       |
| 4  | 24          | 12314          | 12337        | GGATGAGGCTAGGATCTCCTGAGGG               | 120      | 30       |
| 5  | 20          | 13151          | 13170        | GGAGAAGGGGATGTTAAGG                     | 100      | 10       |
| 6  | 16          | 15080          | 15095        | GGCTATGTTGGGAGGAGG                     | 90       | 10       |
| 7  | 20          | 15606          | 15625        | GGTTATCCTTGGATGGAGG                    | 90       | 10       |

### Anti-sense Strand

| #  | Length (bp) | Start Position | End Position | HGQ Motifs                               | cG Score | cC Score |
|----|-------------|----------------|--------------|------------------------------------------|----------|----------|
| 1  | 18          | 78             | 95           | GGTCTTGGAATTTGGAAGG                     | 80       | 10       |
| 2  | 18          | 399            | 416          | GGATAGGGTTCTAGGGAAGG                    | 90       | 10       |
| 3  | 18          | 5573           | 5590         | GGGAGAGGTTAAGGAGGAGG                   | 110      | 0        |
| 4  | 22          | 8464           | 8485         | GGCTATGGTGGGATTTGGAAGG                 | 90       | 10       |
| 5  | 17          | 10334          | 10350        | GGCTGTTAGGAAGGAGG                      | 90       | 20       |
| 6  | 25          | 14644          | 14668        | GGAGACTTGGCATCGGAGTTTCCCTGG            | 100      | 50       |
| 7  | 28          | 14948          | 14975        | GGCTTGAAGGTTTGTCTCGGAATTGAGG          | 110      | 30       |
4. Nipah virus isolate UMMC2 (AY029768.1)

| Sense Strand | # | Length (bp) | Start Position | End Position | HGQ Motifs                                                                 | cG Score | cC Score |
|--------------|---|-------------|----------------|--------------|----------------------------------------------------------------------------|----------|----------|
|              | 1 | 20          | 454            | 473          | GGAGAGGAGAGGAGGAGACAAGG                                                   | 110      | 10       |
|              | 2 | 15          | 478            | 492          | GGAGGAGATGGAAGG                                                           | 90       | 0        |
|              | 3 | 18          | 892            | 909          | GGAACCTGGTATGGCAGG                                                       | 80       | 20       |
|              | 4 | 24          | 12314          | 12337        | GGAAGGAGGCTAGGATCCTGAGGG                                                   | 120      | 30       |
|              | 5 | 20          | 13151          | 13170        | GGAAGACGCGGATGGTTAAGG                                                     | 100      | 10       |
|              | 6 | 16          | 15080          | 15095        | GGCTATGGTGGGAGG                                                          | 90       | 10       |
|              | 7 | 20          | 15606          | 15625        | GGAAGCGGTTGGATGGG                                                         | 90       | 10       |

| Anti-sense Strand | # | Length (bp) | Start Position | End Position | HGQ Motifs                                                                 | cG Score | cC Score |
|-------------------|---|-------------|----------------|--------------|----------------------------------------------------------------------------|----------|----------|
|                    | 1 | 18          | 78             | 95           | GGTCTGGATTTTGGAGG                                                        | 80       | 10       |
|                    | 2 | 18          | 399            | 416          | GGATAGGTTCTAGGTGG                                                        | 90       | 10       |
|                    | 3 | 18          | 5573           | 5590         | GGGAGTGAAAGGAGG                                                          | 110      | 0        |
|                    | 4 | 22          | 8464           | 8485         | GGTAACGCTGTATGGTTAAGG                                                     | 90       | 10       |
|                    | 5 | 17          | 10334          | 10350        | GGCTGAGACAGGTTG                                                         | 90       | 20       |
|                    | 6 | 25          | 14644          | 14668        | GGAGAATTTGGCAGGATCGGAGTCTGAGG                                          | 100      | 50       |
|                    | 7 | 28          | 14948          | 14975        | GGCTTGAAGGTTCGATCGGTTGAGTGTGG                                          | 110      | 30       |

5. Nipah virus isolate NV/MY/99/UM-0128 (AJ564623.1)

| Sense Strand | # | Length (bp) | Start Position | End Position | HGQ Motifs                                                                 | cG Score | cC Score |
|--------------|---|-------------|----------------|--------------|----------------------------------------------------------------------------|----------|----------|
|              | 1 | 20          | 454            | 473          | GGAGAGGAGAGGAGGAGACAAGG                                                   | 110      | 10       |
|              | 2 | 15          | 478            | 492          | GGAGGAGATGGAAGG                                                           | 90       | 0        |
|              | 3 | 18          | 892            | 909          | GGAACCTGGTATGGCAGG                                                       | 80       | 20       |
|              | 4 | 24          | 12314          | 12337        | GGAAGGAGGCTAGGATCCTGAGGG                                                   | 120      | 30       |
|              | 5 | 20          | 13151          | 13170        | GGAAGACGCGGATGGTTAAGG                                                     | 100      | 10       |
|              | 6 | 16          | 15080          | 15095        | GGCTATGGTGGGAGG                                                          | 90       | 10       |
|              | 7 | 20          | 15606          | 15625        | GGAAGCGGTTGGATGGG                                                         | 90       | 10       |

| Anti-sense Strand | # | Length (bp) | Start Position | End Position | HGQ Motifs                                                                 | cG Score | cC Score |
|-------------------|---|-------------|----------------|--------------|----------------------------------------------------------------------------|----------|----------|
|                   | 1 | 18          | 78             | 95           | GGTCTGGATTTTGGAGG                                                        | 80       | 10       |
|                   | 2 | 18          | 399            | 416          | GGATAGGTTCTAGGTGG                                                        | 90       | 10       |
|                   | 3 | 18          | 5573           | 5590         | GGGAGTGAAAGGAGG                                                          | 110      | 0        |
|                   | 4 | 22          | 8464           | 8485         | GGTAACGCTGTATGGTTAAGG                                                     | 90       | 10       |
|                   | 5 | 17          | 10334          | 10350        | GGCTGAGACAGGTTG                                                         | 90       | 20       |
|                   | 6 | 25          | 14644          | 14668        | GGAGAATTTGGCAGGATCGGAGTCTGAGG                                          | 100      | 50       |
|                   | 7 | 28          | 14948          | 14975        | GGCTTGAAGGTTCGATCGGTTGAGTGTGG                                          | 110      | 30       |
### Sense Strand

| # | Length (bp) | Start Position | End Position | HGQ Motifs | cG Score | cC Score |
|---|-------------|----------------|--------------|------------|----------|----------|
| 1 | 18          | 78             | 95           | GGTCTTGGATTGTGGAAGG | 80       | 10       |
| 2 | 18          | 399            | 416          | GGATAGGGTTCTAGGTGG  | 90       | 10       |
| 3 | 18          | 5573           | 5590         | GGAGGAGGAAAGAGGAGG  | 110      | 0        |
| 4 | 22          | 8464           | 8485         | GTGAAACCGTGTGTTGGATTG | 90       | 10       |
| 5 | 17          | 10334          | 10350        | GGCTGTAGGACAGGTGG   | 90       | 20       |
| 6 | 25          | 14644          | 14668        | GGAGACTTGGCATCGGAGTTCCTGG | 100      | 50       |
| 7 | 28          | 14948          | 14975        | GGCTTGAAGGTTGTCTCGGATTG | 110      | 30       |

### Anti-sense Strand

| # | Length (bp) | Start Position | End Position | HGQ Motifs | cG Score | cC Score |
|---|-------------|----------------|--------------|------------|----------|----------|
| 1 | 18          | 74             | 91           | GGTGGTTCTTGGATTG | 80       | 10       |
| 2 | 18          | 399            | 416          | GGATAGGGTTCTAGGTGG | 90       | 10       |
| 3 | 18          | 5573           | 5590         | GGAGGAGGAAAGAGGAGG | 110      | 0        |
| 4 | 22          | 8464           | 8485         | GTGAAACCGTGTGTTGGATTG | 90       | 10       |
| 5 | 17          | 10334          | 10350        | GGCTGTAGGACAGGTGG | 90       | 20       |
| 6 | 25          | 14644          | 14668        | GGAGACTTGGCATCGGAGTTCCTGG | 100      | 50       |
| 7 | 28          | 14948          | 14975        | GGCTTGAAGGTTGTCTCGGATTG | 110      | 30       |

### Sense Strand

| # | Length (bp) | Start Position | End Position | HGQ Motifs | cG Score | cC Score |
|---|-------------|----------------|--------------|------------|----------|----------|
| 1 | 20          | 454            | 473          | GGAGAGGAGAGGAGACAGG | 110      | 10       |

6. Nipah virus isolate NV/MY/99/VRI-0626 (AJ627196.1)

7. Nipah virus isolate NV/MY/99/VRI-1413 (AJ564622.1)
| # | Length (bp) | Start Position | End Position | HGQ Motifs                                      | cG Score | cC Score |
|---|-------------|----------------|--------------|-------------------------------------------------|----------|----------|
| 1 | 18          | 78             | 95           | GGCTTGGGATTTGGGAGGAAGG                           | 80       | 10       |
| 2 | 18          | 399            | 416          | GGTAAACGGGTGGTTGGAGTTGGG                         | 90       | 10       |
| 3 | 18          | 5573           | 5590         | GGGGAGGTAAAGAGGAGGAAGG                          | 110      | 0        |
| 4 | 22          | 8464           | 8485         | GGTAACCGGTGGTTGGAGTTGGG                         | 90       | 10       |
| 5 | 17          | 10334          | 10350        | GGCTGTAGGACAGGTTGG                              | 90       | 20       |
| 6 | 25          | 14644          | 14668        | GGGACTTTGGCATCGGAAGTTCCTGGG                     | 100      | 50       |
| 7 | 28          | 14948          | 14975        | GGCTTGAAAGGTGTCTCGGATTGAGTG                   | 110      | 30       |

8. Nipah virus isolate NV/MY/99/VRI-2794 (AJ564621.1)

| # | Length (bp) | Start Position | End Position | HGQ Motifs                                      | cG Score | cC Score |
|---|-------------|----------------|--------------|-------------------------------------------------|----------|----------|
| 1 | 20          | 454            | 473          | GGAGAGGAGAGGAGAGACAAGG                           | 110      | 10       |
| 2 | 15          | 478            | 492          | GGAGAGGAGATGGGAAGG                              | 90       | 0        |
| 3 | 18          | 892            | 909          | GGAACGTGGCTGTAGGAGG                             | 80       | 20       |
| 4 | 24          | 12314          | 12337        | GGATAGGGCTAGGTGGAGG                             | 120      | 30       |
| 5 | 20          | 13151          | 13170        | GGAACCGGGATCGGTAAGG                             | 100      | 10       |
| 6 | 16          | 15080          | 15095        | GGCTATGGGATGGAAGG                              | 90       | 10       |
| 7 | 20          | 15606          | 15625        | GGCTTATCGGATTGGAAGG                             | 90       | 10       |

| # | Length (bp) | Start Position | End Position | HGQ Motifs                                      | cG Score | cC Score |
|---|-------------|----------------|--------------|-------------------------------------------------|----------|----------|
| 1 | 18          | 78             | 95           | GGCTTGGGATTTGGGAGGAAGG                           | 80       | 10       |
| 2 | 18          | 399            | 416          | GGTAAACGGGTGGTTGGAGTTGGG                         | 90       | 10       |
| 3 | 18          | 5573           | 5590         | GGGGAGGTAAAGAGGAGGAAGG                          | 110      | 0        |
| 4 | 22          | 8464           | 8485         | GGTAAACGGGTGGTTGGAGTTGGG                         | 90       | 10       |
| 5 | 17          | 10334          | 10350        | GGCTGTAGGACAGGTTGG                              | 90       | 20       |
| 6 | 25          | 14644          | 14668        | GGGACTTTGCGATCGGAGTTGCCTGG                     | 100      | 50       |
9. Nipah virus from Bangladesh (AY988601.1)

| # | Length (bp) | Start Position | End Position | HGQ Motifs                                         | cG Score | cC Score |
|---|-------------|----------------|--------------|---------------------------------------------------|----------|----------|
| 1 | 25          | 167            | 191          | GGAAGAGATGGGAGGGCTAGTGCGG                         | 140      | 20       |
| 2 | 18          | 892            | 909          | GGAAACTGGCATGCGAGG                               | 80       | 30       |
| 3 | 20          | 13157          | 13176        | GGAGAACGGGATGGTTAAGG                              | 100      | 10       |

| # | Length (bp) | Start Position | End Position | HGQ Motifs                                         | cG Score | cC Score |
|---|-------------|----------------|--------------|---------------------------------------------------|----------|----------|
| 1 | 18          | 74             | 91           | GGTCGTTCTGGACTTGG                                  | 80       | 30       |
| 2 | 24          | 5025           | 5048         | GGAACTGAGGAAATGGATAATTTG                          | 90       | 10       |
| 3 | 18          | 5573           | 5590         | GGGGAGTGAGAGAGGAGG                                | 120      | 0        |
| 4 | 27          | 8464           | 8490         | GTAAACGGGTGTGGATTTGATGGGG                          | 120      | 10       |
| 5 | 26          | 14640          | 14665        | GGGATGCCTCAGGATTTTGGCATCGG                        | 110      | 50       |

10. Nipah virus isolate NIVBGD2008MANIKGONJ (JN808857.1)

| # | Length (bp) | Start Position | End Position | HGQ Motifs                                         | cG Score | cC Score |
|---|-------------|----------------|--------------|---------------------------------------------------|----------|----------|
| 1 | 25          | 167            | 191          | GGAAGAGATGGGAGGGCTAGTGCGG                         | 140      | 20       |
| 2 | 18          | 892            | 909          | GGAAACTGGCATGCGAGG                               | 80       | 30       |
| 3 | 20          | 13157          | 13176        | GGAGAACGGGATGGTTAAGG                              | 100      | 10       |

| # | Length (bp) | Start Position | End Position | HGQ Motifs                                         | cG Score | cC Score |
|---|-------------|----------------|--------------|---------------------------------------------------|----------|----------|
| 1 | 18          | 74             | 91           | GGTCGTTCTGGACTTGG                                  | 80       | 30       |
| 2 | 24          | 5025           | 5048         | GGAACTGAGGAAATGGATAATTTG                          | 90       | 10       |
| 3 | 18          | 5573           | 5590         | GGGGAGTGAAAGGAGGAGG                               | 110      | 0        |
| 4 | 27          | 8464           | 8490         | GTAAACGGGTGTGGATTTGATGGGG                          | 120      | 10       |
| 5 | 26          | 14640          | 14665        | GGGATGCCTCAGGATTTTGGCATCGG                        | 110      | 50       |
11. Nipah virus isolate NIVBGD2008RAJBARI (JN808863.1)

| #  | Length (bp) | Start Position | End Position | HGQ Motifs                                      | cG Score | cC Score |
|----|-------------|----------------|--------------|------------------------------------------------|----------|----------|
| 1  | 25          | 167            | 191          | GGAAGAGATGGGAGGGCTAGTGCCG                        | 140      | 20       |
| 2  | 18          | 892            | 909          | GGAAACTGGCATGGCAGG                                | 80       | 30       |
| 3  | 20          | 13157          | 13176        | GGAGAACGGGATGGTTAAGG                              | 100      | 10       |
| 4  | 18          | 18066          | 18083        | GGTTCGAAGGAGGTTTGG                                | 80       | 10       |

| #  | Length (bp) | Start Position | End Position | HGQ Motifs                                      | cG Score | cC Score |
|----|-------------|----------------|--------------|------------------------------------------------|----------|----------|
| 1  | 18          | 74             | 91           | GGTCGGTTCTGGACTTGG                               | 80       | 30       |
| 2  | 24          | 5025           | 5048         | GGAACTGAGGAAATGGGATAATGGG                       | 90       | 10       |
| 3  | 18          | 5573           | 5590         | GGGGAGGTAAAGAGGAGG                                | 110      | 0        |
| 4  | 27          | 8464           | 8490         | GGTAAACGCTTGGATTTGGATTTGATGGGG                   | 120      | 10       |
| 5  | 26          | 14640          | 14665        | GGGATGCCTCGGGATTTTGCCATCGG                       | 110      | 50       |

12. Nipah virus isolate Ind-Nipah-07-FG from India (FJ513078.1)

| #  | Length (bp) | Start Position | End Position | HGQ Motifs                                      | cG Score | cC Score |
|----|-------------|----------------|--------------|------------------------------------------------|----------|----------|
| 1  | 25          | 167            | 191          | GGAAGAGATGGGAGGGCTAGTGCCG                        | 140      | 20       |
| 2  | 18          | 892            | 909          | GGAAACTGGCATGGCAGG                                | 80       | 30       |
| 3  | 20          | 13157          | 13176        | GGAGAACGGGATGGTTAAGG                              | 100      | 10       |
| 4  | 18          | 18066          | 18083        | GGTTCGAAGGAGGTTTGG                                | 80       | 10       |

| #  | Length (bp) | Start Position | End Position | HGQ Motifs                                      | cG Score | cC Score |
|----|-------------|----------------|--------------|------------------------------------------------|----------|----------|
| 1  | 18          | 74             | 91           | GGTCGGTTCTGGACTTGG                               | 80       | 30       |
| 2  | 24          | 5025           | 5048         | GGAACTGAGGAAATGGGATAATGGG                       | 90       | 10       |
| 3  | 18          | 5573           | 5590         | GGGGAGGTAAAGAGGAGG                                | 110      | 0        |
| 4  | 27          | 8464           | 8490         | GGTAAACGCTTGGATTTGGATTTGATGGGG                   | 120      | 10       |
| 5  | 26          | 14640          | 14665        | GGGATGCCTCGGGATTTTGCCATCGG                       | 110      | 50       |
**Supplementary Table S3:** The G-quadruplex prediction results for the HGQ-NV-L and HGQ-NV-G of Nipah virus (NC002728.1) using the QGRS Mapper.

| HGQ       | Strand | Position | Length | Sequence                              | G-Score |
|-----------|--------|----------|--------|---------------------------------------|---------|
| HGQ-NV-L  | Sense  | 13151    | 20     | GGAGAACGGGATGGTTAAGG                  | 34      |
| HGQ-NV-G  | Anti-sense | 8464    | 25     | GGTAAACGGGTGTGTTGGATTGTTGGGGGG        | 34      |

**Supplementary Table S4:** The G-quadruplex prediction result for the HGQ-NV-L and HGQ-NV-G of Nipah virus (NC002728.1) using the QuadBase2.

| HGQ       | Strand | Start    | End     | Length | Sequence                              | Pattern  |
|-----------|--------|----------|---------|--------|---------------------------------------|----------|
| HGQ-NV-L  | Sense  | 13150    | 1317    | 20     | GGAGAACGGGATGGTTAAGG                  | G2L1-7   |
| HGQ-NV-G  | Anti-sense | 9758    | 9783    | 25     | CCACCCAAATCCAAAACACCGTTTAC            | C2L1-7   |

**Supplementary Figure S5:** The images below display the results obtained for G-quadruplex prediction in Nipah virus genome using the database described in the recently published paper by Lavezzo et al. (2018) The database predicts all the G-quadruplex forming sequences in the genomes of all known human viruses. Our two conserved G-quadruplex sequence, HGQ-NV-L and HGQ-NV-G were aptly predicted by this database and their conservation was also shown to be 100%. Moreover, the predicted results were in compliance with our data as only GG islands are conserved in NiV genome.
Figure S5a: The figure represents a screenshot taken for the G-quadruplex prediction results in NiV genome from the G4-virus database. The two sequences, HGQ-NV-L and HGQ-NV-G used in our study are highlighted by blue dotted box and red dotted box respectively.

Figure S5b: The figure represents a screenshot taken for the HGQ-NV-L prediction in NiV genome using the G4-virus database. The conservation was shown to be 100%. 
Figure S5c: The figure represents a screenshot taken for the HGQ-NV-G prediction in NiV genome using the G4-virus database. The conservation was shown to be 100% and this sequence is present in the anti-sense strand of the genome.

Supplementary Figure S6: The below images displays the multiple alignment of the predicted HGQs in different isolates of the Nipah virus prepared by using the MEGA7.0.26 software (1: HGQ-NV-L; 2: HGQ-NV-G; 3: HGQ-NV-1; 4: HGQ-NV-2; 5: HGQ-NV-3; 6: HGQ-NV-M1; 7: HGQ-NV-M2; 8: HGQ-NV-M3; 9: HGQ-NV-M4; 10: HGQ-NV-M5; 11: HGQ-NV-M6; 12: HGQ-NV-M7; 13: HGQ-NV-M8; 14: HGQ-NV-B1, 15: HGQ-NV-B2; 16: HGQ-NV-B3 and 17: HGQ-NV-B4.)
1. Alignment of HGQ-NV-L present in twelve isolates of Nipah Virus.

2. Alignment of HGQ-NV-G present in twelve isolates of Nipah Virus.

3. Alignment of HGQ-NV-1 present in twelve isolates of Nipah Virus.
4. Alignment of HGQ-NV-2 present in twelve isolates of Nipah Virus.

5. Alignment of HGQ-NV-3 present in twelve isolates of Nipah Virus.

6. Alignment of HGQ-NV-M1 present in eight isolates of Nipah Virus (Malaysian clade).

7. Alignment of HGQ-NV-M2 present in eight isolates of Nipah Virus (Malaysian clade).
8. Alignment of GQS-NV-M3 present in eight isolates of Nipah Virus (Malaysian clade).

| Species/Abbrev | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
|---------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. AF21302.2_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 2. AJ564621.1_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 3. AJ564622.1_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 4. AJ564623.1_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 5. AJ627196.1_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 6. AY029767.1_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 7. AY029768.1_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 8. NC002728.1_HGQ-NV-M3 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |

9. Alignment of HGQ-NV-M4 present in eight isolates of Nipah Virus (Malaysian clade).

| Species/Abbrev | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
|---------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. AF21302.2_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 2. AJ564621.1_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 3. AJ564622.1_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 4. AJ564623.1_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 5. AJ627196.1_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 6. AY029767.1_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 7. AY029768.1_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 8. NC002728.1_HGQ-NV-M4 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |

10. Alignment of HGQ-NV-M5 present in eight isolates of Nipah Virus (Malaysian clade).

| Species/Abbrev | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
|---------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. AF21302.2_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 2. AJ564621.1_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 3. AJ564622.1_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 4. AJ564623.1_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 5. AJ627196.1_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 6. AY029767.1_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 7. AY029768.1_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 8. NC002728.1_HGQ-NV-M5 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |

11. Alignment of HGQ-NV-M6 present in eight isolates of Nipah Virus (Malaysian clade).

| Species/Abbrev | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
|---------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. AF21302.2_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 2. AJ564621.1_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 3. AJ564622.1_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 4. AJ564623.1_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 5. AJ627196.1_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 6. AY029767.1_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 7. AY029768.1_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
| 8. NC002728.1_HGQ-NV-M6 | A | U | G | C | A | C | U | G | A | C | G | U | C | G | U | C | G | U | A | G | T | U | G | G | G |
12. Alignment of GQS-NV-M7 present in eight isolates of Nipah Virus (Malaysian clade).

| Species/Abbrev | Table 12.1 Alignment of GQS-NV-M7 present in eight isolates of Nipah Virus (Malaysian clade). |
|---------------|------------------------------------------------------------------------------------------|
| 1. AF21302.2  | HGQ-NV-M7                                                                                |
| 2. AJ564621.1 | HGQ-NV-M7                                                                                |
| 3. AJ564622.1 | HGQ-NV-M7                                                                                |
| 4. AJ564623.1 | HGQ-NV-M7                                                                                |
| 5. AJ627196.1 | HGQ-NV-M7                                                                                |
| 6. AY029767.1 | HGQ-NV-M7                                                                                |
| 7. AY029768.1 | HGQ-NV-M7                                                                                |
| 8. NC002728.1 | HGQ-NV-M7                                                                                |

13. Alignment of HGQ-NV-M8 present in eight strains of Nipah Virus (Malaysian clade).

| Species/Abbrev | Table 13.1 Alignment of HGQ-NV-M8 present in eight strains of Nipah Virus (Malaysian clade). |
|---------------|---------------------------------------------------------------------------------------------|
| 1. AF21302.2  | HGQ-NV-M8                                                                                  |
| 2. AJ564621.1 | HGQ-NV-M8                                                                                  |
| 3. AJ564622.1 | HGQ-NV-M8                                                                                  |
| 4. AJ564623.1 | HGQ-NV-M8                                                                                  |
| 5. AJ627196.1 | HGQ-NV-M8                                                                                  |
| 6. AY029767.1 | HGQ-NV-M8                                                                                  |
| 7. AY029768.1 | HGQ-NV-M8                                                                                  |
| 8. NC002728.1 | HGQ-NV-M8                                                                                  |

14. Alignment of HGQ-NV-B1 present in four isolates of Nipah Virus (Bangladeshi clade).

| Species/Abbrev | Table 14.1 Alignment of HGQ-NV-B1 present in four isolates of Nipah Virus (Bangladeshi clade). |
|---------------|---------------------------------------------------------------------------------------------|
| 1. AY988601.1 | HGQ-NV-B1                                                                                  |
| 2. FJ513078.1 | HGQ-NV-B1                                                                                  |
| 3. JN808887.1 | HGQ-NV-B1                                                                                  |
| 4. JN808886.3 | HGQ-NV-B1                                                                                  |

15. Alignment of HGQ-NV-B2 present in four isolates of Nipah Virus (Bangladeshi clade).

| Species/Abbrev | Table 15.1 Alignment of HGQ-NV-B2 present in four isolates of Nipah Virus (Bangladeshi clade). |
|---------------|---------------------------------------------------------------------------------------------|
| 1. AY988601.1 | HGQ-NV-B2                                                                                  |
| 2. FJ513078.1 | HGQ-NV-B2                                                                                  |
| 3. JN808887.1 | HGQ-NV-B2                                                                                  |
| 4. JN808886.3 | HGQ-NV-B2                                                                                  |

16. Alignment of HGQ-NV-B3 present in four isolates of Nipah Virus (Bangladeshi clade).

| Species/Abbrev | Table 16.1 Alignment of HGQ-NV-B3 present in four isolates of Nipah Virus (Bangladeshi clade). |
|---------------|---------------------------------------------------------------------------------------------|
| 1. AY988601.1 | HGQ-NV-B3                                                                                  |
| 2. FJ513078.1 | HGQ-NV-B3                                                                                  |
| 3. JN808887.1 | HGQ-NV-B3                                                                                  |
| 4. JN808886.3 | HGQ-NV-B3                                                                                  |
17. Alignment of HGQ-NV-B4 present in four isolates of Nipah Virus (Bangladeshi clade).

Supplementary Figure S7: Sequence logos constructed for the analyzing the conservation of the HGQs predicted in NiV using the WebLogo software. While highly conserved nucleotides are represented by a bigger letter, the large variable nucleotides represented by smaller or non-existent letters. The Sequences are either conserved in the Malaysian clade or the Bangladeshi clade and therefore, are not globally conserved. At least, one of the guanine residues essential for the G-quadruplex sequence is not globally conserved.
HGQ-NV-M6
AGUACGCUGUAAGGCCAGUGGUGGUU

HGQ-NV-M7
AAACCUGGGAUAAGGUUCAUGUGUGA

HGQ-NV-M8
CGUUGGUUGGAAUGGGAAGUUAA

HGQ-NV-B1
AGUUAGGAGAAGAGAUGGGAGGCUAGUGCGAACU

HGQ-NV-B2
AAUGGAAUCCUCGGGAUUUGGCAUCGGAGUUC

HGQ-NV-B3
CGAGGAACUGAGGAUAUGAUAUGGAAGAG

HGQ-NV-B4
UUUCGUGGUUGGAUUUGGGAAGAGU
**Supplementary Table S8:** Table showing the putative G-quadruplex forming sequences (HGQs) available in all the twelve isolates of Nipah virus and their respective sequences.

| Sl No. | HGQ Name | HGQ Sequence |
|--------|----------|--------------|
| 1      | HGQ-NV-L  | UUUAAGGAGAACGGAGUUGLUAAAGGAGUGAG |
| 2      | HGQ-NV-G  | ACAGUUGUAAAACGGUGUUUGUAGUUGGGGUGUCCAG |
| 3      | HGQ-NV-1  | GCUCGAGAACUGGUAUGGCGAGAUGAG |
| 4      | HGQ-NV-2  | UUGUCGAGGAGGUAAAGGAGGCCAGCUCCU |
| 5      | HGQ-NV-3  | ACCUCGAGCUUUGGCAUCGGAGUUGCUUCCUGGUCU |

**Supplementary Table S9:** Table showing the putative G-quadruplex forming sequences (HGQs) available in all the eight isolates of Nipah virus belonging to Malaysian clade and their respective sequences.

| Sl No. | HGQ Name | HGQ Sequence |
|--------|----------|--------------|
| 1      | HGQ-NV-M1 | GACAGGCGUCAAGGAGAGAUGGAAGGC |
| 2      | HGQ-NV-M2 | CUCAGAGGAGGCUAGGAUCCUGAGGGUGCAU |
| 3      | HGQ-NV-M3 | GUGAAGGCAUGGUGGAGAAGGAAG |
| 4      | HGQ-NV-M4 | UAUUAGGGGAUACGGUAUUUGGAAAGGUA |
| 5      | HGQ-NV-M5 | UCUUUGGCUUGAAAGGUUGCUAGGUAUGGAUGGCUU |
| 6      | HGQ-NV-M6 | AGUACAGCGUACAGACAGUGUGUGUGU |
| 7      | HGQ-NV-M7 | AAACUGGAGAGGUUGCUAGGUGUGU |
| 8      | HGQ-NV-M8 | CAGUUGGCUUUGGAGAGGUUAAAG |

**Supplementary Table S10:** Table showing the putative G-quadruplex forming sequences (HGQs) available in all the four isolates of Nipah virus belonging to Bangladesh clade and their respective sequences.

| Sl No. | HGQ Name | HGQ Sequence |
|--------|----------|--------------|
| 1      | HGQ-NV-B1 | AGUUAAGGAGAGAUGGAGCGUGCCAGCAGC |
| 2      | HGQ-NV-B2 | UAAUAGGGAUCCGCGGGAUUUGUAGCAGAGC |
| 3      | HGQ-NV-B3 | CACGAGAAGCGAAGAAGGUAUUUGGAAGA |
| 4      | HGQ-NV-B4 | UUGUCAGCGUUCGAGACUUGAGA |
**Supplementary Table S11:** Table showing the details of the predicted HGQs; the strand of Nipah virus in which it is present, the genomic location of the HGQs in the virus and the P value which represents the percentage of isolates in which the particular HGQs in conserved among the total twelve viral isolates.

| Sl No. | GQS Name     | Strand Orientation | Gene Involved                  | P Value  |
|--------|--------------|--------------------|--------------------------------|----------|
| 1      | HGQ-NV-L     | Sense Strand       | RNA dependent RNA Polymerase   | 100%     |
| 2      | HGQ-NV-G     | Anti-sense Strand  | Attachment Glycoprotein        | 100%     |
| 3      | HGQ-NV-1     | Sense Strand       | Nucleocapsid Protein           | 100%     |
| 4      | HGQ-NV-2     | Anti-sense Strand  | Matrix Protein                 | 100%     |
| 5      | HGQ-NV-3     | Anti-sense Strand  | RNA dependent RNA Polymerase   | 100%     |
| 6      | HGQ-NV-M1    | Sense Strand       | Nucleocapsid Protein           | 66.7%    |
| 7      | HGQ-NV-M2    | Sense Strand       | RNA dependent RNA Polymerase   | 66.7%    |
| 8      | HGQ-NV-M3    | Sense Strand       | RNA dependent RNA Polymerase   | 66.7%    |
| 9      | HGQ-NV-M4    | Sense Strand       | RNA dependent RNA Polymerase   | 66.7%    |
| 10     | HGQ-NV-M5    | Anti-sense Strand  | Phosphoprotein                 | 66.7%    |
| 11     | HGQ-NV-M6    | Anti-sense Strand  | Fusion Protein                 | 66.7%    |
| 12     | HGQ-NV-M7    | Anti-sense Strand  | RNA dependent RNA Polymerase   | 66.7%    |
| 13     | HGQ-NV-M8    | Anti-sense Strand  | RNA dependent RNA Polymerase   | 66.7%    |
| 14     | HGQ-NV-B1    | Sense Strand       | Nucleocapsid Protein           | 33.3%    |
| 15     | HGQ-NV-B2    | Anti-sense Strand  | Phosphoprotein                 | 33.3%    |
| 16     | HGQ-NV-B3    | Anti-sense Strand  | RNA dependent RNA Polymerase   | 33.3%    |
| 17     | HGQ-NV-B4    | Anti-sense Strand  | RNA dependent RNA Polymerase   | 33.3%    |
**Supplementary Figure S12:** CD spectra scans for the three HGQs: a. HGQ-NV-1, b. HGQ-NV-2 and c. HGQ-NV-3, in Tris-HCl buffer containing either K\(^+\), Na\(^+\), Mg\(^{2+}\) or Li\(^+\) along with the mutant of the respective GQS. The HGQ-NV-1, HGQ-NV-2 and HGQ-NV-3 are conserved in all the Nipah virus isolates but they did not show the typical signature pattern of G-quadruplex structures rather it showed a positive peak at ~280 nm. So these three HGQs were excluded from our further studies.
Supplementary Figure S13: DMS footprinting assay

The DNA substrates i.e. HGQ-NV-L-DMS and HGQ-NV-G-DMS (refer Table S18) were labeled at 5' end with the \([\gamma ^{32}\text{P}]\text{ATP\text{}}\) (Perkin-Elmer) using polynucleotide kinase (NEB). They were then subjected to Tris-HCl buffer (100 mM KCl, pH 7.4) for GQ formation and heating at 95°C for 5 min followed by slow cooling. The single-stranded DNA substrates were dissolved in Tris-HCl buffer without KCl, heated at 95°C for 5 min and snap-chilled on ice for 10 min. All the DNA substrates were then gel-purified. For the DMS footprinting assay, the purified DNA substrates, both single-stranded and GQ, were treated with 1% DMS for 5 min at room temperature and then the reaction were terminated by adding excess of calf-thymus DNA. The DNA was retrieved by ethanol precipitation which was further treated with 10% piperidine and heated at 95°C for 30 min. The DNA fragments were again ethanol precipitated thrice to remove piperidine residues and then resolved on 17% denaturing urea polyacrylamide gels at 1600V for 2.5 h in TBE buffer. The dried gels were then exposed a phosphorimaging screen and images were captured using the Fuji FLA-5000 phosphorImager.

(a) HGQ-NV-L: \(5'\text{AAGGAGACGGGATGGTAAGGAT} \ 3'\)
(b) HGQ-NV-G: \(5'\text{GTGGTAACGGTGTTGGATTTGGTGTTGGGTC} \ 3'\)
**Supplementary Figure S14.1:** ITC binding studies of TMPyP4 with HGQs-mutants. (a: HGQ-NV-Lmut; b: HGQ-NV-Gmut). The table below includes the thermodynamic parameters obtained due to interaction of the HGQ and their mutants with TMPyP4 with the help of ITC.

| Parameters       | HGQ-NV-L + TMPyP4 | HGQ-NV-L-MUT + TMPyP4 | HGQ-NV-G + TMPyP4 | HGQ-NV-G-MUT + TMPyP4 |
|------------------|-------------------|-----------------------|-------------------|-----------------------|
| $K_a 1$ (M$^{-1}$) | $1.0E8$           | $1.49E5$              | $3.32E8$          | $6.31E5$              |
| $K_a 2$ (M$^{-1}$) | $7.41E4$          | $1.53E5$              | $1.64E5$          | $2.82E5$              |

**Supplementary Figure S14.2:** ITC binding studies of Braco-19 with HGQs and their corresponding mutants. (a: HGQ-NV-L; b: HGQ-NV-Lmut; c: HGQ-NV-G; d: HGQ-NV-Gmut). The table below includes the thermodynamic parameters obtained due to interaction of the HGQ and their mutants with Braco-19 with the help of ITC.
| Parameters | HGQ-NV-L + Braco-19 | HGQ-NV-L-MUT + Braco-19 | HGQ-NV-G + Braco-19 | HGQ-NV-G-MUT + Braco-19 |
|------------|---------------------|-------------------------|---------------------|-------------------------|
| $K_a 1$ (M$^{-1}$) | 3.52E6 | 6.21E4 | 2.77E6 | 2.24E5 |
| $K_a 2$ (M$^{-1}$) | 4.58E4 | 1.35E6 | 2.73E6 | 4.45E4 |
**Supplementary Figure S15:** Taq DNA polymerase stop assay shows stalling due to the presence of a stable G-quadruplex. For the assay, the PRIMER-TPSA (Table S18) was $^{32}\text{P}$-labelled. The template DNA i.e. NV-L-TPSA or NV-G-TPSA (10nM) was incubated with the labelled primer and cold primer (15 nM) in Tris-HCl buffer (100 mM KCl, pH 7.4) and heated at 95 °C for 5 min followed by slow cooling. The increasing amounts of Braco-19 was added to the reaction mixture and incubated for 30 min at 37°C. Finally, the polymerase reactions was initiated by adding the reaction buffer (5 mM MgCl$_2$, 1.5 mg/ml BSA, and 0.2 mM dNTPs) along with the Taq DNA polymerase (NEB) at 42°C for 1 hr. The reaction was topped by the addition of formamide loading dye and samples were heated at 95°C. The samples were analyzed in 15% urea denaturing PAGE. The gel were dried and exposed to the phosphorimaging screen overnight. The image was obtained using the Fuji FLA-5000 phosphorImager.
Supplementary Figure S16: CD melting plots obtained for the HGQs on the addition of Braco-19. (a) HGQ-NV-L with Braco-19 for D/N ratio=0, D/N ratio=1, and D/N ratio=2, (b) HGQ-NV-G with Braco-19 for D/N ratio=0, D/N ratio=1, and D/N ratio=2. The $T_m$ difference between D/N ratio =1 and D/N ratio =0 is represented as $\Delta T_m1$ and the $T_m$ difference between D/N ratio =2 and D/N ratio =1 is represented as $\Delta T_m2$. Significant change in $T_m$ was also observed for both the HGQs on addition of Braco-19.
Supplementary Table S17: Dose-dependent effect of TMPyP4 on the expression of TFP bearing the HGQ sequence. Three different concentrations have been used 20 μM, 50 μM and 100 μM and we observed a gradual diminishment of fluorescence intensity with increase in ligand concentration. Thus, implicating the stabilization of the G-quadruplex sequence by the G-quadruplex binding ligand, TMPyP4.
Supplementary Table S18: List of primers, templates and other oligonucleotides used in the experiments.

| Sl. No. | Sequence Name | Sequence (5’----3’) |
|---------|---------------|---------------------|
| 1.      | HGQ-NV-L      | TTATAGGAGAACGGAAGCTGATTAAGGATGAG |
| 2.      | HGQ-NV-Lmut   | TTATAGGAGAACGGAAGCTGATTAAGGATGAG |
| 3.      | HGQ-NV-G      | ACAGTGTTAAGACGTAAGTTGATATTCGATG |
| 4.      | HGQ-NV-Gmut   | ACAGTGTTAAGACGTAAGTTGATATTCGATG |
| 5.      | HGQ-NV-L-F    | ATGAGTGTTTTGAGGAAGCAGGTATGCTATTAGAGCAG |
| 6.      | HGQ-NV-G-F    | ATGAGTGTTTTGAGGAAGCAGGTATGCTATTAGAGCAG |
| 7.      | HGQ-NV-Lmut-F | ATGAGTGTTTTGAGGAAGCAGGTATGCTATTAGAGCAG |
| 8.      | HGQ-NV-Gmut-F | ATGAGTGTTTTGAGGAAGCAGGTATGCTATTAGAGCAG |
| 9.      | HGQ-NV-RP     | CGTGTCTAGCTTTGTACAGCTCGCTCAGTCAAG |
| 10.     | HGQ-NV-PSA-FP | ATCCACTGAGTAATTCAGT |
| 11.     | HGQ-NV-PSA-RP | TTCTACTCCTGCTCAGT |
| 12.     | HGQ-NV-mut-PSA-RP | TTCTACTCCTGCTCAGT |
| 13.     | Bcl2          | AGGGGCGGCGCCGAGGAGGGAGGGAGGGAGGGAGGGAGGGAGG |
| 14.     | c-Myc         | TGAGGCTGAGGTCAGGAGG |
| 15.     | NV-L-TPSA     | AATATTTTAAGGAGAACGGAAGCTGATTAAGGATGAGCA |
| 16.     | NV-G-TPSA     | CGAAGCAGCAATTGCTATTAGTGAAGCTGCTAAAA |
| 17.     | PRIMER-TPSA   | AATATTTTAAGGAGAACGGAAGCTGATTAAGGATGAGCA |
| 18.     | HGQ-NV-L-DMS  | AATATTTTAAGGAGAACGGAAGCTGATTAAGGATGAGCA |
| 19.     | HGQ-NV-G-DMS  | AATATTTTAAGGAGAACGGAAGCTGATTAAGGATGAGCA |
Supplementary Figure S19: Full length gel images of Figure 3b showing electrophoretic gel mobility shift assay.
Lane 3 and 8 denote the mobility of the mutant counterparts of the G-quadruplex, Lane 4, 5, 6 and 7 denote the mobility of HGQs in the presence of K\(^+\), Na\(^+\), Li\(^+\) and Mg\(^{2+}\) respectively. Lane 2 represents the mobility of G-quadruplex forming sequence (positive controls): c-Myc or Bcl2. Lane 1, negative control of c-Myc or Bcl2, i.e., the mutant sequence of c-Myc or Bcl2 gene (a: HGQ-NV-L and b: HGQ-NV-G).
Supplementary Figure S20a-b: Full length gel images of Figure 6 showing Primer extension assay. This assay shows a decrease in intensity of the band with increasing concentration of TMPyP4 for both the HGQs (a1: HGQ-NV-L with TMPyP4; a2: HGQ-NV-L with TMPyP2; a3: HGQ-NV-Lmut with TMPyP4; b1: HGQ-NV-G with TMPyP4; b2: HGQ-NV-G with TMPyP2 and b3: HGQ-NV-Gmut with TMPyP4)