*Supplementary material*

# Viral susceptibility of *Haloferax* species

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**Table S1.** *Haloferax* **strains used in the study**

| Strain | Reference |
|---|---|
| *Haloferax volcanii* H26 | [37] |
| *Haloferax* sp. s5a-1 | [29] |
| *Haloferax* sp. SP10-1 | [29] |
| *Haloferax* sp. SS9-6 | [19] |
| *Haloferax* sp. SS10-6 | [19] |
| *Haloferax* sp. SS10-7 | [19] |
| *Haloferax* sp. LR1-5 | [59] |
| *Haloferax* sp. LR1-14 | [59] |
| *Haloferax* sp. LR1-18 | [59] |
| *Haloferax* sp. LR1-19 | [59] |
| *Haloferax* sp. LR1-24 | [59] |
| *Haloferax gibbonsii* LR2-5 | [59,60] |
| *Haloferax* sp. LR2-16 | [59] |
| *Haloferax mediterranei* DSM 1411 | [76] |

**Table S2. Viruses used in the study**

Please see separate excel table

**Table S3. Underrepresented palindromic motifs in viral genomes[1]**

| | CTAG | GATC | AGCT | TGCA | CATG |
|---|---|---|---|---|---|
| HFTV1 | 0.0314 | 0.0714 | 0.2252 | 0.8473 | 0.9074 |
| HCTV-6 | 0 | 0 | 0 | 0.2976 | 0.4192 |
| HCTV-15 | 0 | 0 | 0 | 0.2976 | 0.4192 |
| HRTV-11 | 0 | 0 | 0 | 0.2742 | 0.3604 |
| HSTV-2 | 0 | 0 | 0 | 0.3023 | 0.3638 |
| HRTV-7 | 0 | 0 | 0 | 0.3291 | 0.3654 |
| HRTV-2 | 0 | 0 | 0 | 0.3091 | 0.3721 |
| HRTV-10 | 0 | 0 | n | 0.2756 | 0.3855 |
| HRTV-20 | 0 | 0 | n | 0.2959 | 0.3261 |
| HRTV-18 | 0 | 0 | n | 0.2964 | 0.3263 |
| HRTV-26 | 0 | 0 | n | 0.2764 | 0.3341 |
| HRTV-22 | 0.0067 | 0 | n | 0.2707 | 0.3146 |
| HJTV-1 | 0 | 0 | n | 0.24 | 0.3905 |
| HRTV-21 | 0 | 0 | n | 0.2565 | 0.3741 |
| HRTV-5 | 0 | 0 | n | 0.2757 | 0.3566 |
| HRTV-13 | 0 | 0 | n | 0.2604 | 0.3638 |
| HRTV-16 | 0 | 0 | n | 0.2811 | 0.3554 |
| HRTV-9 | 0 | 0 | n | 0.3411 | 0.3623 |
| HCTV-10 | 0 | 0 | n | 0.2886 | 0.3382 |
| HCTV-8 | 0 | 0 | n | 0.2886 | 0.3379 |
| HCTV-7 | 0 | 0 | n | 0.2993 | 0.3408 |
| HCTV-11 | 0 | 0 | n | 0.2994 | 0.3412 |
| HCTV-9 | 0 | 0 | n | 0.2991 | 0.3409 |

[1] Calculated as Odds Markov values where they are not zero. n represent normal frequencies. Orange color incidates the value 0.

**Table S4 Manual counting of modified DNA motifs found the genomes of viruses infecting *Hfx. gibbonsii* LR2-5**

| | CTAG [1] | GCGCTG | AYCnnnnnCTTYG | CRAAGnnnnnGRT | CCAnnnnnnRTCnC | GnGAYnnnnnnTGG |
|---|---|---|---|---|---|---|
| HFTV-1 | 2 | 0 | 2 | 0 | 3 | 9 |
| HCTV-6 | 0 | 41 | 9 | 14 | 6 | 10 |
| HCTV-15 | 0 | 41 | 9 | 14 | 6 | 10 |
| HRTV-11 | 0 | 39 | 6 | 15 | 9 | 7 |
| HSTV-2 | 0 | 37 | 8 | 14 | 8 | 6 |
| HRTV-7 | 0 | 32 | 6 | 15 | 9 | 5 |
| HRTV-2 | 0 | 36 | 8 | 15 | 8 | 9 |
| HRTV-10 | 0 | 12 | 8 | 10 | 5 | 6 |
| HRTV-20 | 0 | 14 | 11 | 11 | 7 | 6 |
| HRTV-18 | 0 | 14 | 11 | 11 | 7 | 6 |
| HRTV-26 | 0 | 16 | 12 | 9 | 7 | 4 |
| HRTV-22 | 1 | 13 | 13 | 9 | 6 | 5 |
| HJTV-1 | 0 | 9 | 9 | 10 | 4 | 9 |
| HRTV-21 | 0 | 13 | 9 | 10 | 3 | 7 |
| HRTV-5 | 0 | 10 | 5 | 11 | 5 | 7 |
| HRTV-13 | 0 | 10 | 6 | 11 | 5 | 8 |
| HRTV-16 | 0 | 10 | 6 | 10 | 2 | 7 |
| HRTV-9 | 0 | 14 | 5 | 12 | 3 | 9 |
| HCTV-10 | 0 | 10 | 5 | 10 | 5 | 7 |
| HCTV-8 | 0 | 10 | 5 | 10 | 5 | 7 |
| HCTV-7 | 0 | 10 | 6 | 10 | 5 | 7 |
| HCTV-11 | 0 | 10 | 6 | 10 | 5 | 7 |
| HCTV-9 | 0 | 10 | 6 | 10 | 5 | 7 |

[1] Modified bases are shown in bold. The color range blue to yellow is from a low number of occurrences (0) to a high number of occurrences (>30)
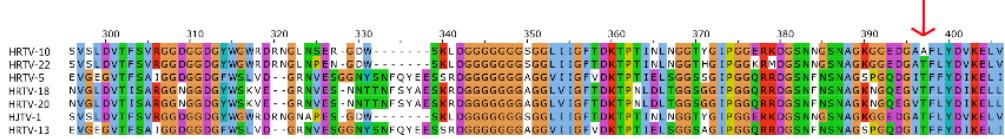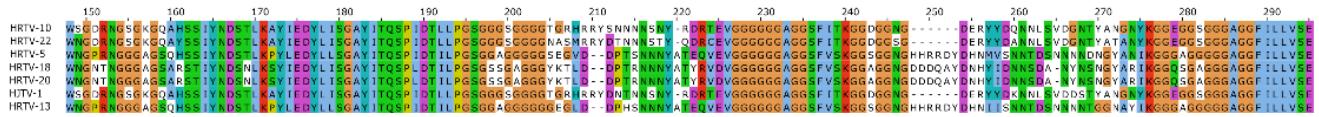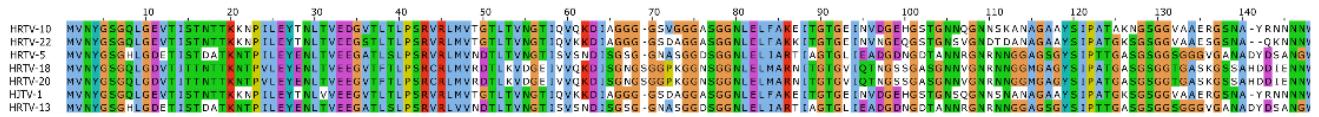
**Figure S1.** Multiple sequence alignment of adhesins belonging to the Clade 3 (see also Figure 5). Protein sequences were aligned using Clustal W. The colors correspond to the amino acid identity. The arrow indicates the T380A substitution in HRTV-10.
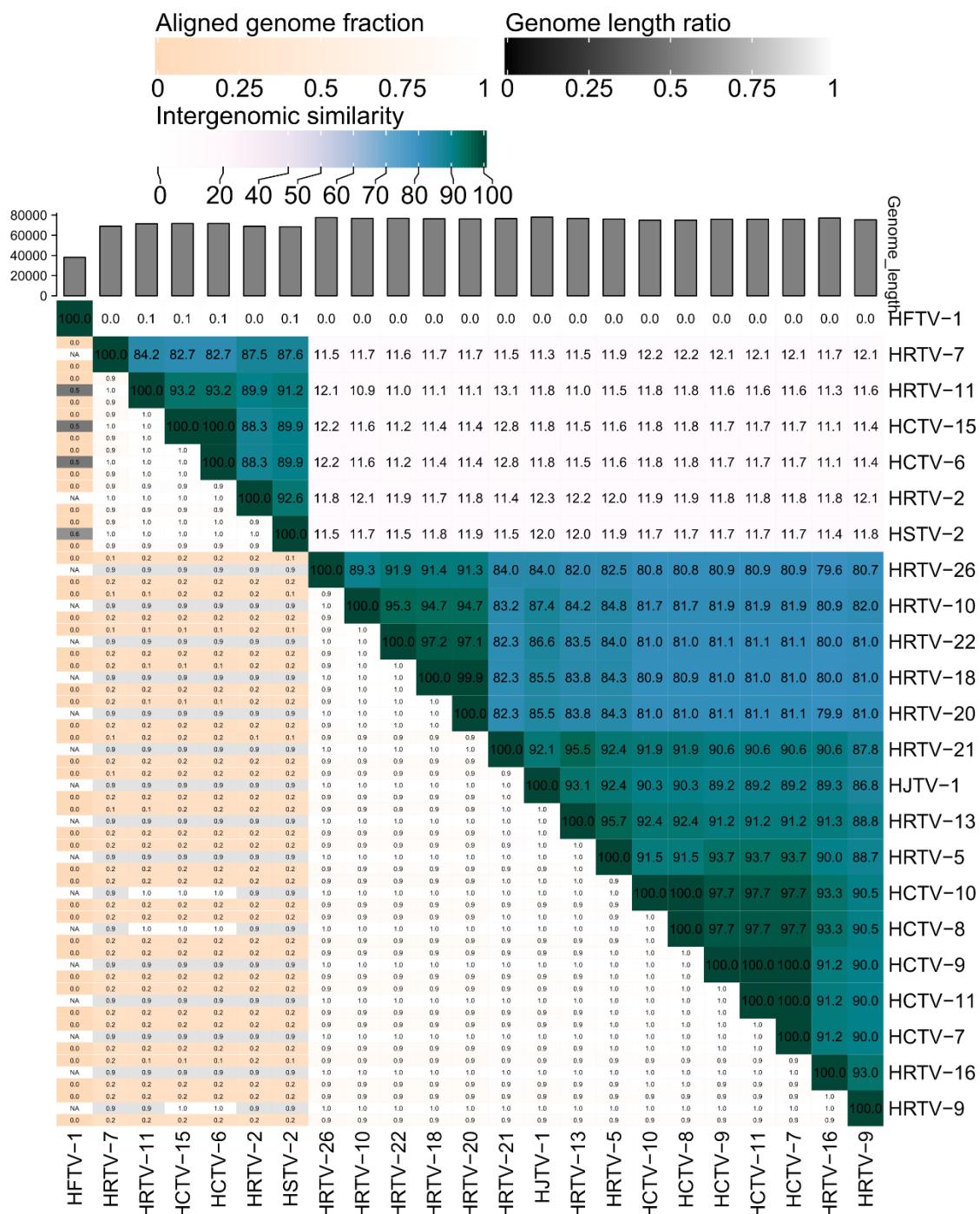
**Figure S2. VIRIDIC generated heatmap.** The right half indicates the intergenomic similarity between the viral genomes using a color gradient. Darker colors indicate higher intergenomic similarities. The left side shows three different values; the aligned genome fraction for the genome found in the row(top), genome length ratio for the genomes in this pair (middle) and the aligned genome fraction for the genome found in this column (bottom).