

## Haplotype and amino acid sequences list:

Detailed list of haplotype DNA sequences and amino acid variants found for the highly conserved regions for three short-fragments markers (UL18, UL22 and UL27) within the CFPV genome.

### UL18

<UL18 haplotype1, most common haplotype found all over the world; 98 nucleotides, 46 samples>

CCGTTA**A**CCCA**C**T**C**GAAGGGTCCCGTGTTCGAATTT**G**CAGAGCGCCGCTGGTACTCATTTC**C**AA**A**ACGGAGAGGATTACCCGGCGGGGTTCCAC

<UL18 amino acid sequence variable sites, only functional site variation Y/C>

RRLPVIFAVEPRRVILSVLEMSTSAAL**Y**KIRNTGPF EWVNGDRLALVPP

<UL18 haplotype2, found only in turtle from Turks and Caicos and unique individual from Portugal; 98 nucleotides, 12 samples>

CCGTT**G**ACCCAT**T**CGAAGGGTCCCGTGTTCGAATTT**G**TAGAGCGCCGCTGGTACTCATTTC**C**AA**G**ACGGAGAGAATTACCCGGCGGGGTTCCAC

<UL18 amino acid sequence variable sites, only functional site variation Y/C>

RRLPVIFAVEPRRVILSVLEMSTSAAL**C**KIRNTGPF EWVNGDRLALVPP

### UL22

<UL22 haplotype1, most common haplotype found all over the world; 132 nucleotides, 82 samples>

ATCGCTGGTCATAGACTTGCCCGTGTTCGGGGTTA**A**CCAA**A**AGATT**C**AGTGC**C**ACCAGCAGCAGCGTTTGGTT**C**GT**T**TCG**C**AAAAG**T**AT**C**AGATCC**G**AACTCTACAATATGGGTCGGAGAAAGGGCGTT

<UL22 amino acid sequence variable sites, only functional site variation D/E>

APQ**N**ATFP**P**THIVEFG**S****D**TF**A**KHEPNV**L**VR**T**ESL**V**KPANTASLL**T**SDLF**Y**PV**Q**FE

<UL22 haplotype2, found only in turtle from Turks and Caicos and unique individual from Portugal; 132 nucleotides, 13 samples>

ATCGCTGGTCATAGACTTGCCCGTGTTCGGGGTTA**A**CCAA**G**AGATT**C**AGTGC**C**ACCAGCAGCAGCGTTTGGTT**C**GT**T**TCG**C**AAAAG**T**TC**C**AGATCC**G**AACTCTACAATATGGGTCGGAGAAAGGGCGTT

<UL22 amino acid sequence variable sites, only functional site variation D/E>

APQ**N**ATFP**P**THIVEFG**S****E**TF**A**KHEPNV**L**VR**T**ESL**V**KPANTASLL**T**SDLF**Y**PV**Q**FE

### UL27

<UL27 haplotype1, most common haplotype found all over the world; 144 nucleotides, 50 samples>

CCTCCGGATGGTCGCTGGCCAA**A**GAAAACTATCTAACGTCAAAGACAAC**T**TACGGACGCTAAAAATAAAATGATGAAATCTTTACGCCACCGCGGAAACGGATACGCTCCCGTTTCGACGAGCAT**G**GCCAGTATGTATCTAG

<UL27 amino acid sequence variable sites, only functional site variations K/E and T/M>

KKAASSGWSLAK**K**KLSNVKDNFTDAK**N**MMKSLRHRGNGYAPVST**S**TASMYLDDELSTYSQ

<UL27 haplotype2, 144 nucleotides, 7 samples>

CCTCCGGATGGTCGCTGGCCAA**G**GAAAACTATCTAACGTCAAAGACAAC**T**TACGGACGCTAAAAATAAAATGATGAAATCTTTACGCCACCGCGGAAACGGATACGCTCCCGTTTCGACGAGCAT**G**GCCAGTATGTATCTAG

<UL27 amino acid sequence variable sites, only functional site variations K/E and T/M>

KKAASSGWSLAK**E**KLSNVKDNFTDAK**N**MMKSLRHRGNGYAPVST**S**TASMYLDDELSTYSQ

<UL27 haplotype3, 144 nucleotides, 18 samples>

CCTCCGGATGGTCGCTGGCCAA**A**GAAAACTATCTAACGTCAAAGACAAC**T**TACGGACGCTAAAAATAAAATGATGAAATCTTTACGCCACCGCGGAAACGGATACGCTCCCGTTTCGACGAGCA**G**GCCAGTATGTATCTAG

<UL27 amino acid sequence variable sites, only functional site variations K/E and T/M>

KKAASSGWSLAK**K**KLSNVKDNFTDAK**N**MMKSLRHRGNGYAPVST**S****M**ASMYLDDELSTYSQ







