

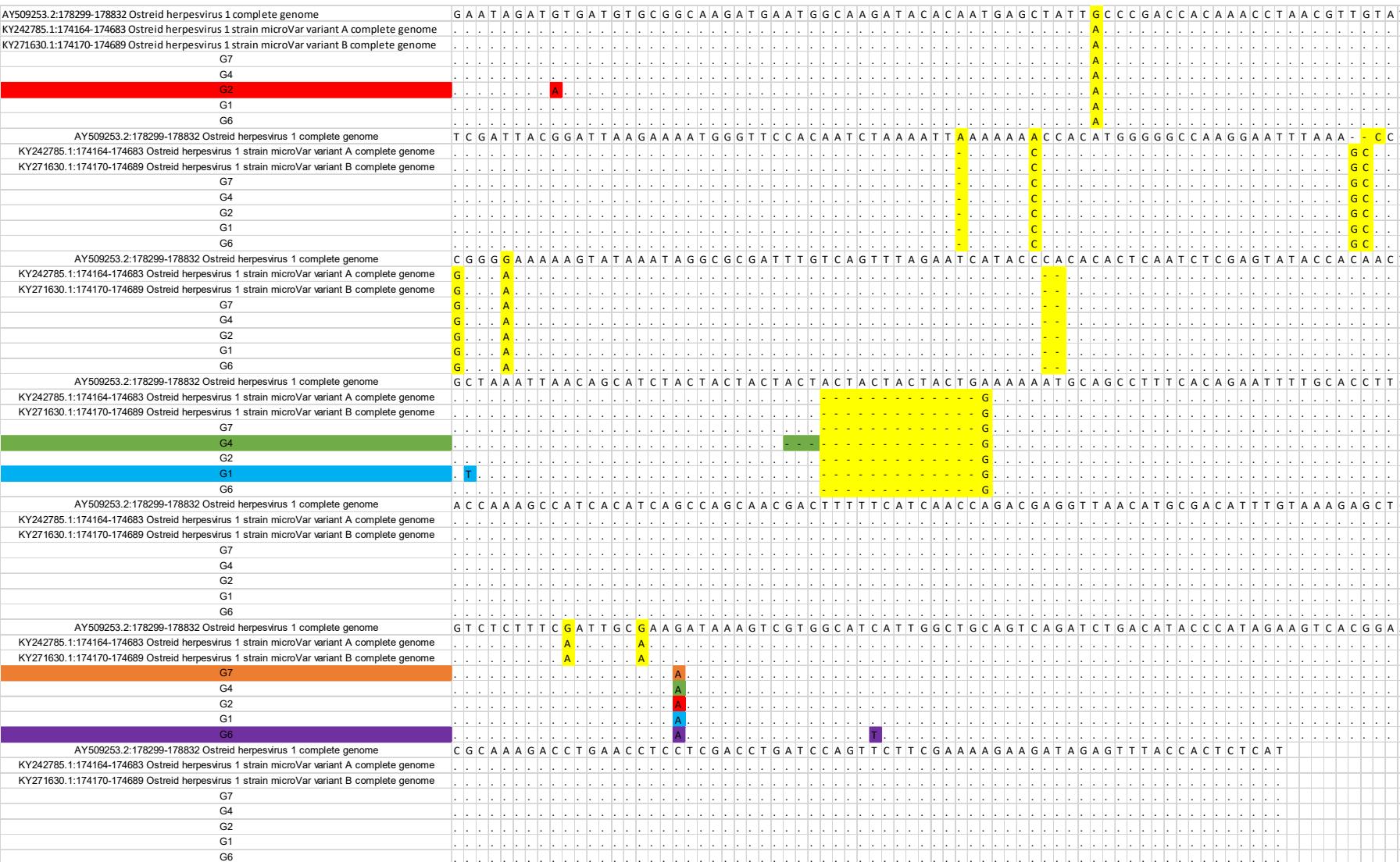
Table 1. Variants by genomic region. Not all samples yielded sequence for each region. Variants unique to a river are shown in red font highlighted in yellow.

¹ Total number of samples

² Total number of available sequences from GR-HWY-TAS

| DNA or protein sequence | Georges River (n=60) ¹ | Hawkesbury River (n=38) | Tasmania (n=2) |
|---------------------------------------|--|----------------------------|----------------|
| R1 (50-36-1) ² | G1 G2 G4 G7 | G7 | G6 |
| R2 (38-37-2) | G9 | G8 G9 | G9 |
| R3 (56-38-2) | G10 | G10 | G10 |
| R4 (50-37-0) | G11 G12 G13 G14 G15 G17 G18 G19 G20 G21 G22 G23 G24 G29 | G11 | na |
| R5 (12-29-1) | G32 G33 G34 | G31 | G34 |
| R6 (51-38-2) | G35 G36 G37 | G36 G37 | G37 |
| Concatenated R1-R2-R4-R6 (27-34-0) | V2 V3 V4 V5 V7 V8 V9 V10 V11 V12 | V1 V6 | na |
| Protein prediction R1-R2-R6 (27-34-0) | ADH | ACH | na |

Fig 1



DNA alignment

R1 (n=87): 5 groups

In yellow= mutations in common with microvariants

Common substitution A instead of G

G2(n=2) = 1 substitution A instead of G

G4 (n=8)=3 substitutions in microsatellite zone as observed on delta 15 variant

G1 (n=4)= 1 substitution T instead of C

G7(n=72)= only common substitution

G6(n=1)= substitution T instead of C

Fig 2

| | | |
|----------------|---|---|
| AY509253.2:600 | T T T T G T A A A G C T T T A T A T C T T C A A A T C C G G A A G T G T T T A A C A A C A A G A T T A C A A A A A A A T A T C A A C G G C A A T | |
| KY271630.1:580 | . | . |
| KY242785.1:580 | . | . |
| G8 | . | . |
| G9 | . | . |
| AY509253.2:600 | G T C T A A T T G T T C A T T C C C C G A T C T A C C A A A C G T G C A G T C T A C G A C G G C C C T T G C C A A T G G T A G G C T C T T C C C T G C C | |
| KY271630.1:580 | . | . |
| KY242785.1:580 | . | . |
| G8 | . | . |
| G9 | . | . |
| AY509253.2:600 | G C C A A T A G A A A T A A A C A G C A A A G G T G A T A A A T C G G T A G T T T A T C T C A G G G G T G A T G A T C A A C C A A T T G A T G T T A A C A G | |
| KY271630.1:580 | . | . |
| KY242785.1:580 | . | . |
| G8 | . | . |
| G9 | . | . |
| AY509253.2:600 | G G A A C A T A G A A T G G T A A A A G T T A C G T A T A A T G A A T A C G A T G A G C A A G A A A C G A T C A A G G T T A T T T C C T C G A C A A G G A A | |
| KY271630.1:580 | . | . |
| KY242785.1:580 | . | . |
| G8 | . | . |
| G9 | . | . |
| AY509253.2:600 | A G C A A C A A T A A A A G A T C T A C A T A A C C T A A T G A G T G T T G G T A G G G A T C T T A C A A C G G G T G T C T G C A A T A T A G A A G T A C A | |
| KY271630.1:580 | . | . |
| KY242785.1:580 | . | . |
| G8 | . | . |
| G9 | . | . |
| AY509253.2:600 | A C C G G A A T A T G G A T T C A C A C T G A G G A T A C C A G A C C C A G A C A A G T T G A A A T A A A A G T G A T A T A G A T G C A G T C T A T A G | |
| KY271630.1:580 | . | . |
| KY242785.1:580 | . | . |
| G8 | . | . |
| G9 | . | . |
| AY509253.2:600 | A C T C T T C G C T T C A A A A T A C G A C A A T A G C G A T C T A T T C G A A | |
| KY271630.1:580 | . | T |
| KY242785.1:580 | . | T |
| G8 | . | . |
| G9 | . | . |

DNA alignment

R2 (n=77)= 2 groups

In yellow= mutations in common with microvariants

G8 (n=36): 1 deletion on a T

G9 (n=41): 2 deletions on 2 A

Fig 3

| | | |
|----------|---|---|
| AY509253 | T T C T T C T C T G C C C G T G T C A T C G G T G C A T A T C T T G A T C G G C A A G G A T T C C T T A C T T C C T T G G G A C C T C T G A T T G G T A G T | |
| KY242785 | . | . |
| KY271630 | . | . |
| G 10 | . | . |
| AY509253 | G A A T C A A A A T T G C A A T T G T T T C T G A T T G T A A T T C T T C T G T A A G G T T A G C T C A G T T A A G A T T G T T T C T C T T C C A | |
| KY242785 | . | . |
| KY271630 | . | . |
| G 10 | . | . |
| AY509253 | C G T C T G T T T C T A A T G G G A G C C A T G G T G A T G A A T G A A G T T G A A A G A C G A A A A T C A A C A A A A T A T A T A G T C T T T G T A A T | |
| KY242785 | . | . |
| KY271630 | . | . |
| G 10 | . | . |
| AY509253 | A T G T C G C A G A A A A A C T A A T A G T G A A A G T A A C T T C T T G G A A T C G G T C C T C G G A G G A T A A A G T T G A C A A A G A G T G C A | |
| KY242785 | - | |
| KY271630 | - | |
| G 10 | - | |
| AY509253 | A T G A G G G G T G C C C A A A T C A C T A T C A T A T T G A T G A T T C T G A A A A G C A A T A G A A C T C T C T G C C A T G C C T G T C T C T T G G T | |
| KY242785 | - | |
| KY271630 | - | |
| G 10 | - | |
| AY509253 | T T C T T C A C G A T T A T G T A T T G T G G T T T A G C A G G G A T A A G T T C A G A T T C T T G C T C A A T C T C G C A C A C T G T T T G C T C T G T A | |
| KY242785 | - | |
| KY271630 | - | |
| G 10 | - | |
| AY509253 | G T A G A C A T A T T G A A A A A T G A A A G T G G T T T C G T A A A C T C A A A C T T T T A T T T A T G T T T T A A A A A A C A T G G T C C T A | |
| KY242785 | - | |
| KY271630 | - | |
| G 10 | - | |
| AY509253 | G T C A A A A T C T C T A T A A A A G A T G C T A A A A T A T C C A C C A G C C C G G T T A A G A C A T T G G T C T C C A C A A T A C A C A T G A T C C T | |
| KY242785 | - | |
| KY271630 | - | |
| G 10 | - | |
| AY509253 | A G A T A A T T C C C T G C C A A C A C T C T T G A T C A C A G C T C T T T C A T C G T G A T A T T A C G G G A G G G A A T T G T C G G T T G A G | |
| KY242785 | - | |
| KY271630 | - | |
| G 10 | - | |
| AY509253 | T A T C T G T C T A T C A T T G T G A T C G T A A A G G A A T G T G C A T T T A T C G C G C G A T G G T T C C T C G T G A A A A A A T C A T C A A A T T | |
| KY242785 | - | |
| KY271630 | - | |
| G 10 | - | |
| AY509253 | G T T C T A A T A C T T C G G G G C T G A A C G G T G G T A C A T T G G T A C A T C T T T A C T A T C T T T G G C A T T G A T T A T G C T T T | |
| KY242785 | . | |
| KY271630 | . | |
| G 10 | . | |
| AY509253 | T G A G T A T C G T C C A C A A G T | |
| KY242785 | . | |
| KY271630 | . | |
| G 10 | . | |

DNA alignment

R3 (n=100) : 1 group

In yellow= mutations in common with microvariants

G10 (n=100): deletions in common with microvariants and substitution C instead of T

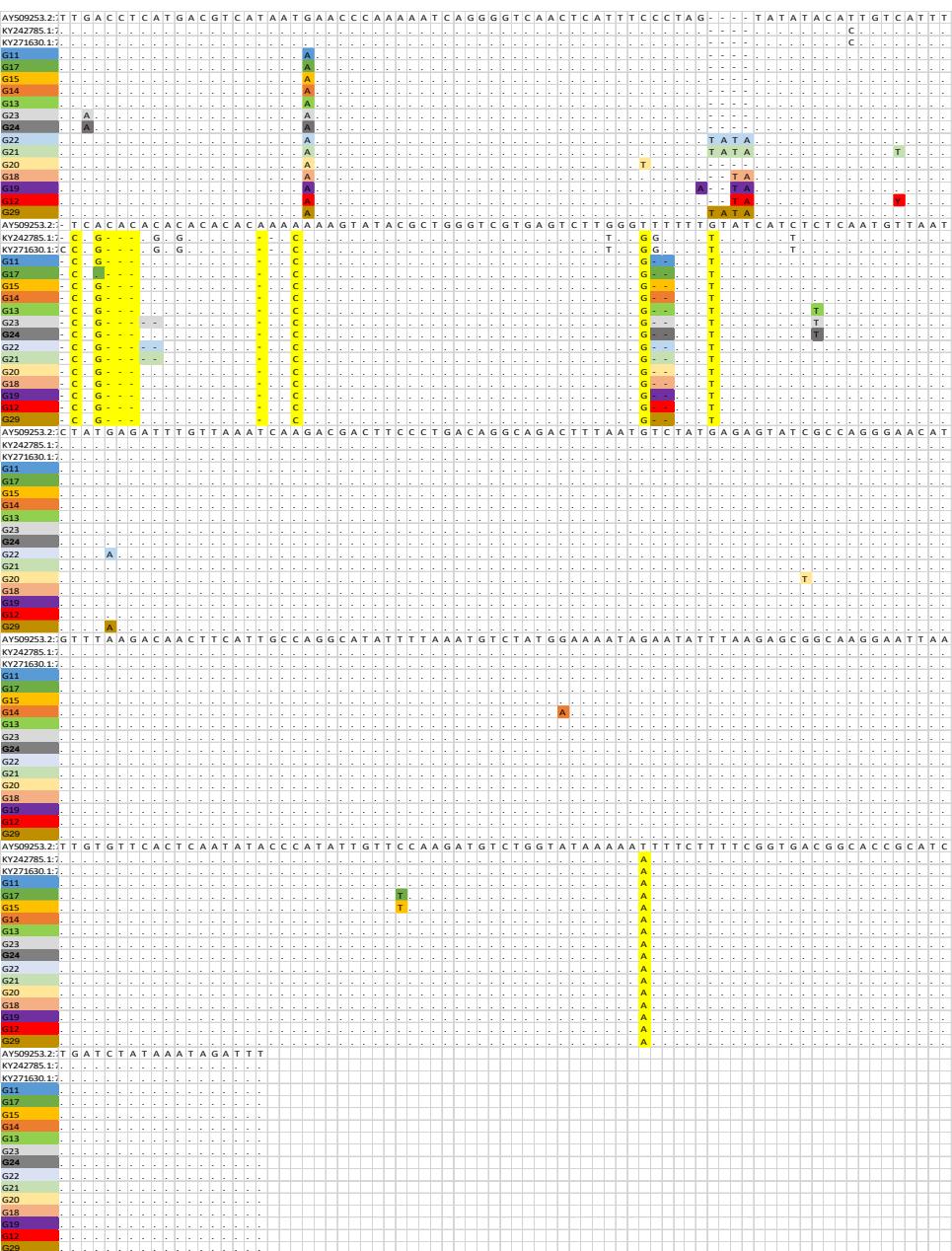


Fig 4

DNA alignment

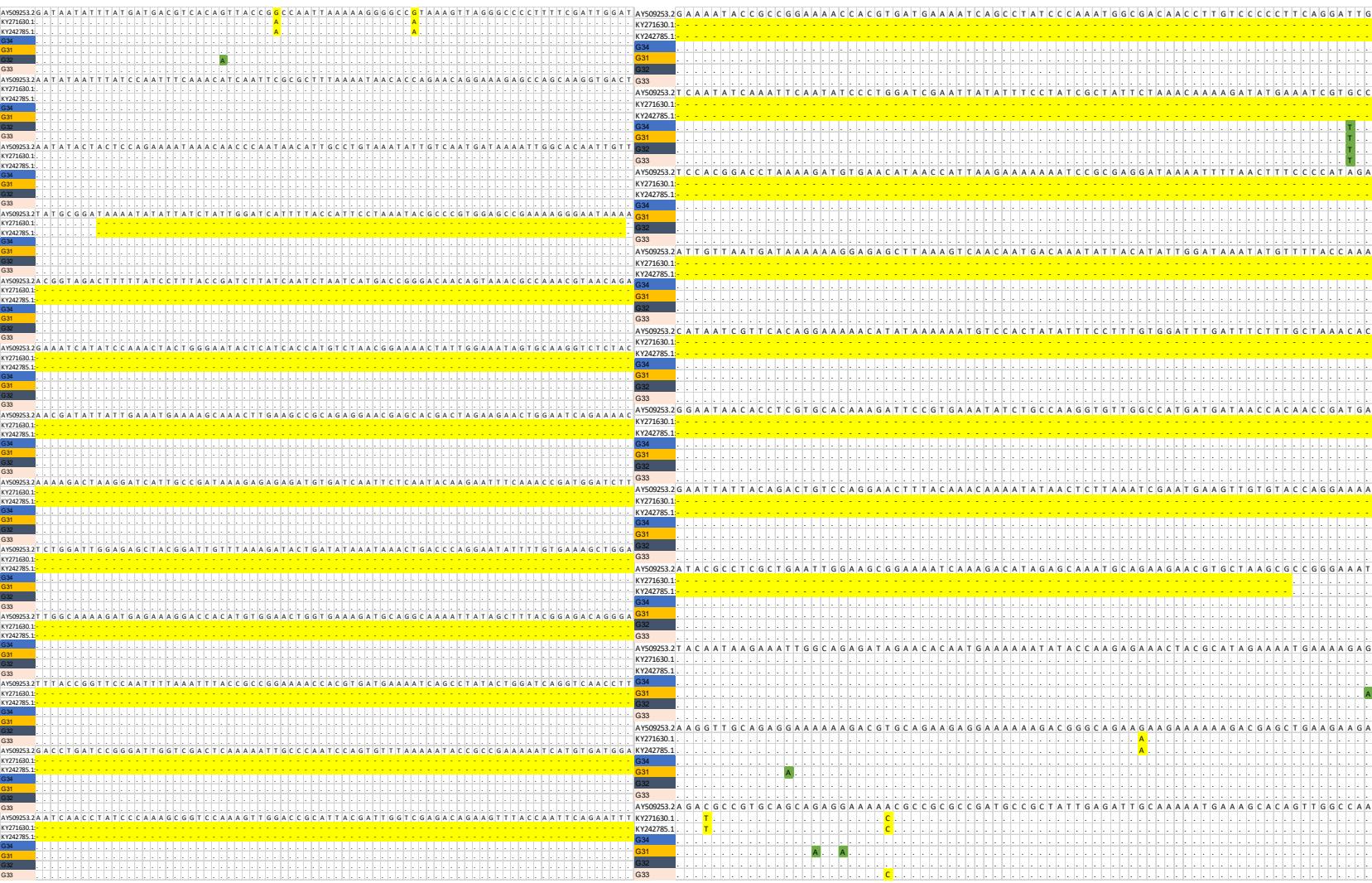
R4 (n=87): 14 groups

In yellow=mutations in common with microvariants

Common substitution A instead of G + 2 deletion on 2T

- G11 (n=56)= only mutations in common with microvariants
- G17 (n=1)= + 1 deletion on A + 1 substitution T instead of C
- G15 (n=2)= substitution T instead of C
- G14 (n=2)= substitution A instead of G
- G13 (n=5)= substitution T instead of C
- G23 (n=2)=substitution A instead of G+ 5 deletion instead of 3 + substitution T instead of C
- G24 (n=1)= substitution A instead of G+ substitution T instead of C
- G22(n=1) = insertion TATA+ 5 deletions instead of 3+ substitution A instead of G
- G21 (n=3)=insertion TATA+ substitution C instead of T+ 5 deletions instead of 3
- G20 (n=4)= subst T instead of C, subst T instead of C
- G18 (n=4)=insertion TA
- G19 (n=1)= subst A instead of G+ insertion TA
- G12 (n=4)= insertion TA + substitution T et C (Y) instead of C
- G29 (n=1)= insertion TATA+ subst A instead of G

Fig 5



DNA alignment

R5 (n=42): 4 groups

In yellow=mutations in common with microvariants

Common Substitution T instead of G

G 34 (n=11): only common mutation

G 31 (n=29): substitution A instead of G+ substitution A instead of G+ substitution A instead of G+ substitution A instead of G

G 32 (n=1): substitution A instead of G

G 33 (n=1): substitution C instead of A

Fig 6

| | |
|---|---|
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | A T G A T C A T T A T G A A A T C C A T A A T A T T A T T A C T C G C T T G G T T T T A A C A A A A A C A C A G G C G A A T A T G T T G A C C G A A T C T |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | T T G T A C T T G T C A G A A T A T G A G G G G A G T G T T G T G C T A A C A T C A T A G A C A A A A A T T T A A C G G G A T A T C C A C C T G T C A |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | A T A T T T A A C G A T T C T A C T A A A T T A C A A G A A G T A A G A T A T G T T G C C A G T G T A T G C A G C C T C A G A T C T G G A T C G T T C A A T |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | A T C A C T T G C A A T G T A A T A A C C T A C G G C A C T T A T C A T G T C A G G A T G T T T T A T C A G G T C T T A A C A T G T C C G C A T T G A T |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | T T A T A C A G A C T T C G A T A T G T G T A C G T T G G T C T T A G A G A C G C C A T A A A T T A C A A C C C A A A T A T G C A G A G G C G G T A A T G |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | G C A C C G T T T G C T T T A A T T G G C A A T A A T A A T A G T T A C A A T T A A C T T A T A A A A G A C G G T G A T A A T A T C A C C G T C G G T |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | T G T G G G T T T G G A A A T G T A G A T T T G A G C A C T G T A A A C A C C C A T G C C A G C A A A A T T G G C A G A A A T A T A A A C C T A G A T T C |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | A T G G T C G G T G T T T A C A A A C G A T A G C A A T A A G T A A T C G A G G A T G A T A T A C A G C C G T T A C A C A G A T T C A G A A T C T |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | G C C G G T G T T A T G A G A A A A T G T A A T T A A C G A G G T T A A A C C A C T T C C C C A G G A A G A T T G C A T T C A G C C C T T T G C A C C |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | |
| AY509253.2:133242-135488 Ostreid herpesvirus 1 complete genome | A A A G G A A C A G T G T A T G G A A A T A A C C T C G T T T A T G G A A G T A G A T T A C G A T G T T T C A G T A G G A C C A G G T G T T C A C A G A G A |
| KY242785.1:129838-132084 Ostreid herpesvirus 1 strain microVar variant A. | |
| KY271630.1:129844-132090 Ostreid herpesvirus 1 strain microVar variant B. | |
| G 37 | |
| G 36 | |
| G 35 | G |

DNA alignment

R6 (n=91): 3 groups

In yellow= mutations in common with microvariants

G 37 (n=54): similar to OshV-1 reference

G36 (n=36): 1 substitution C instead of G

G35 (n=1): 1 substitution G instead of A

Fig 7

Alignment of protein prediction on ORF 4

| | |
|----------|---|
| AY509253 | M Q P F T E F C T L T K A I T S A S N D F F I N Q T R L T C D I C K E L V S F D C E D K V V A S L A A V R S D I P I E V T E R K D L N L L D L I Q F F E K K I E |
| KY271630 | . |
| KY242785 | . |
| G 1 | . |
| G 2 | . |
| G 4 | . |
| G 6 | . |
| G 7 | . |
| | |
| AY509253 | F T T L |
| KY271630 | . |
| KY242785 | . |
| G 1 | . |
| G 2 | . |
| G 4 | . |
| G 6 | . |
| G 7 | . |

In yellow= mutations in common with microvariants

A = N instead of D (G 1, G2, G4, G7)

B = N instead of D + L instead of S (G6)

Fig 8

Alignment of protein prediction on ORF 43

| | |
|----------|---|
| AY509253 | M S N L F I P R S T K R A V Y D G P L P M V G S S L P P I E I N S K G D K S V V Y L R G D D Q P I D V N R E H R M V K V T Y N E Y D E Q E T I K V I F L D K K A |
| KY271630 | |
| KY242785 | |
| G 8 | |
| G 9 | |
| AY509253 | T I K D L H N L M S V G R D L T T G V C N I E V Q P E Y G F T L R I P D P D K L K Y K S D I D A V Y R L F A S K Y D N S D L F E R |
| KY271630 | |
| KY242785 | |
| G 8 | |
| G 9 | SK - |

C = synonymous mutation (G8)

D = SK- instead of FER(G9)

Alignment of protein prediction on ORF 11

| | | |
|------------|---|----|
| AY509253.2 | MDNII YPI SNI NSRFK I TPEQERASKVTNI LLQKI NNPI TLPVNI VNDKI GTI VYADKI YYLLDHTFTI PKYARGAEKG I K | |
| KY271630.1 | . | |
| KY242785.1 | . | |
| G 31 | . | |
| G 32 | . | |
| G 33 | . | |
| G 34 | . | |
| AY509253.2 | TVDFLSFTDL I NLI MTGTTVNAKRNR E I SKLLGI L I TMSNGKLLEI VQGLYNDI I EMKSKEAAEERARLEELSENKR | |
| KY271630.1 | - - - - - | |
| KY242785.1 | . | |
| G 31 | . | |
| G 32 | . | |
| G 33 | . | |
| G 34 | . | |
| AY509253.2 | LRI I ADKERDVI NSQYKNFKPMDL SGLE SYGL FKDTDI NKLTQEYFVKAGLA KDEKGPHVEL VKDAGKII AL RRQGFTGS | |
| KY271630.1 | - - - - - | |
| KY242785.1 | . | |
| G 31 | . | |
| G 32 | . | |
| G 33 | . | |
| G 34 | . | |
| AY509253.2 | NFKFTAGKP RDENQPI LDQVNLDL I RDWSTQKL PNPVFKNTAEKSCDG NQPI PKRSKVGP HYDWSRQKFTNSEFENTAGK | |
| KY271630.1 | - - - - - | |
| KY242785.1 | . | |
| G 31 | . | |
| G 32 | . | |
| G 33 | . | |
| G 34 | . | |
| AY509253.2 | PRDENQPI PNGDNLVPL QDW SI SNSI SL DRI I FPI A I LNKRYEI VPSTD LKD VNITI KK KI RED KI LTFPI EI VNDKKGE | |
| KY271630.1 | - - - - - | |
| KY242785.1 | - - - - - | |
| G 31 | . | |
| G 32 | . | |
| G 33 | . | |
| G 34 | . | |
| AY509253.2 | LKVNNNDKYYI LDKYVL PKHNRSQEKHI KNVHYI SFVDLI SLLNTGI TPRAQRFR EISAKVLAMMI TT D EELL QTVQELY | |
| KY271630.1 | - - - - - | |
| KY242785.1 | . | |
| G 31 | . | |
| G 32 | . | |
| G 33 | . | |
| G 34 | . | |
| AY509253.2 | KQNI TLKSN EVVYQE KIRLAELEAENQRHRANAEE RAKREI YNKKLAEI EHNEK I YQEKL RI ENEKRKVAA EKRRAEEE | |
| KY271630.1 | - - - - - | |
| KY242785.1 | . | |
| G 31 | . | K |
| G 32 | . | K |
| G 33 | . | |
| G 34 | . | |
| AY509253.2 | KRRAEE EKRRAEEERRRAAE EKRRAADA AI EI AKMKAQLAKELEI DVKELEN TQTLVKTNKDL DKQRAVQGRGEFI KVL | |
| KY271630.1 | K C N | |
| KY242785.1 | K C N | |
| G 31 | . | KK |
| G 32 | . | |
| G 33 | . | N |
| G 34 | . | |

Fig 9

In yellow= mutations in common with microvariants

E = similar to OsHV-1 reference (G32, G34)

F = N instead of K (G33)

G = K instead of R + K instead of L + K instead of E + K instead of E (G31)

Fig 10

Alignment of protein prediction on ORF 88a

| | |
|----------|---|
| AY509253 | M I I M K S I I L L L A W F L T K T Q A N M L T E S L Y L S E Y E G S V V L N I I D K N L N G I S T L S I F N D S T K L Q E V R Y V A S V C S L R S G S F N I T |
| KY242785 | |
| KY271630 | |
| G 35 | |
| G 36 | |
| G 37 | |
| AY509253 | C N V I T Y G T Y H V R M F L S G L N M S A F D L Y R L R Y V Y V G L R D A I N Y N P K Y A E A V M A P P F A L I G N N N I V T I K L I K D G D N I T V G C G F G |
| KY242785 | |
| KY271630 | D |
| G 35 | |
| G 36 | |
| G 37 | |
| AY509253 | N V D L S T V N T H A S K I G R N I N P R F M V G V Y T N D S N K L I E D D I Y S R Y T D S E S A G V M R K C N L N E V K T T P Q E D C I Q P F C T K G T V Y G |
| KY242785 | |
| KY271630 | |
| G 35 | |
| G 36 | |
| G 37 | |
| AY509253 | N N L V Y G S R L R C F S R T R C S Q R S R T V P Q S V P W Y I P |
| KY242785 | |
| KY271630 | |
| G 35 | |
| G 36 | |
| G 37 | |

In yellow= mutations in common with micro/microvariants

I = E instead of K (G35)

H = synonymous mutation (G36, G37)