

Codon optimized OvHV-2 ORF8

1 M A S P T S T L S P A A L T A L L C L A A C L G Q T P T P P T T E
ATGCTTCTC CTACCTCTAC CCGTCTCTCT GCTGCTCTGA CCGCTCTGCT GTGCTCTGGCT GCTTGTCTGG GCGAGACCCC TACCCTCTCT ACCACCGAGG
TACCGAAGAG GATGGAGATG GGACAGAGGA CGACGAGACT GCGGAGACGA CACAGACCGA CGAACAGACC CCGTCTGGGG ATGGGGAGGA TGGTGGCTCC

101 D D V I V P G H T V S P D V L K Q Q L G S G L N E E E G S I N R G P
ATGATGTGAT CGTGCCTGCC CACACCGTGT CTCACAGATGT GCTGAAGCAG CAGCTGGGCT CTGGCCTGAA TGAGGAGGAG GGCTCTATCA ATAGAGGCC
TACTACTACTA GCACGGACCG GTGTGGCACA GAGGTCTACA CACTTCTGTC GTGCACCCGA GACCCGACTT ACTCCTCTCT CCGAGATAGT TATCTCCGGG

201 M D P S A F P F R V C S A S N I G D I F R F Q T T H S C P N T K D
TATGGATCT TCTGCCTTCC CTTTCCAGAT GTGCTCTGCT TCTAACATCT GCGACATCTT CAGGTTCAG CAGTTCAGG ACCACCCACT CTTGTCTTAA CACCAAGGAT
ATACCCTAGGA AGACGGAGAG GAAAGTCTCA CACGAGACGA AGATTGTAGC CCGCTGTAGAA GTCCAAAGGT TGGTGGGTGA GAACAGGATT GTGGTTCTTA

301 K E H N E G I L L I F K E N I V P Y V F K V R K Y R K I V T T S T
AAGGAGCACA ACAGGAGGAT CCGTCTGATC TTCAGGAGA ACATCGTCCC CTACGTGTTT AAGGTGCGGA AGTACAGAAA GATCGTGACC ACCTCTACCG
TTCCTCGTGT TGCTCCCTTA GGACGACTAG AAGTCTCTCT TGTAGCACAAG TCCACCGCTT TCATGTCTTT CTAGCAGTGG TCGGATGAGG

401 V Y N G I Y S D A I T N Q H E F S K S V P H Y E A R R M D T I Y Q C
TGTACAACGG CATCTACTCT GATGCCATCA CCAACCAGCA CGAGTCTCTT AAGTCTGTGC CTCACTACGA GGCCAGAAGA ATGGATACCA TCTACCAGTG
ACATGTTGGC GTAGATGAGA CTACGGTAGT GGTGTTGCTGT GCTCAAGAGA TTCAGACAGC GAGTGTATGCT CCGTCTTCTT TACCTATGTT AGATGGTCC

501 Y N S L S L T V G G N L L A Y T D N D G Y N L T V D L Q P M D G L
CTACAACCTC CTGTCTCTGA CCGTGGGCGG CAATCTGCTT GCTTATACCG ATAACGATGG CTACAACCTG ACCGTGGATC TGCAGCTAT GGATGGCCCTG
GATGTTGAGG GACAGAGACT GGCACCCGCC GTTAGACGAC CGAATATGGC TATTGCTACC GATGTTGGAC TGGCACCTAG ACGTCCGATA CCTACCCGAC

601 S N S V R R Y N S Q P E I H A E P G W L L G G Y R R R T T V N C E
TCTAACTCCG TGAGAAGATA CAACTCTCAG CCGTGTGATC ACGTGTGAGC TGGCTGGCTG CTGGGCGGCT ACCGGAGAAG AACCCACCGT AATTGTGAGG
AGATTGAGG ACTCTTCTAT GTTGAAGAGT GGACTCTAGG TCGACTCTGG ACCACCGCAG GACCCGCGCA TGGCTCTTTC TTTGGTGGAT TTAACACTCC

701 V T D T E A R S V P P F R Y F V T N V G D T I E M S P F W S G G A N
TGACCGATAC CGAGGCTAGA TCTGTGCTCT CTTTCAGATA CTTCTGTACC AATGTGGGGC ACACATCGA GATGTCTCCA TTTTGTCTGT GCGGGCGTAA
ACTGGCTATG GCTCCGATCT AGACACGGAG GAAAGTCTAT GAAGCACTGG TTACACCCGC TGTGTTAGCT CTACAGAGGT AAAACACAGC CGCCCGGATT

801 E T E P N K E P R R T V S V L R D Y T L V D Y K D R G S R P Q P H
TGAGACAGAG CCTAATAGG AGCCTCGGAG AACAGTCTCT GTGCTGAGAG ATTACACCCCT GGTGGAATAC AAGGACAGAG GCTCTAGACT GGATGGCTAC
ACTCTGTCTC GGATTATTC TCGGAGCCTC TTGTCAGAGA CACGACTCTC TAATGTGGGA CCACCTGATG TTCCTGTCTC CGAGATCTGG AGTCCGGAGTG

901 T R I F I D K E D Y T L S W A Q Q L K N I S Y C R W A H W K S F H
ACCAGAATCT TCATCGACAA GGAGGACTAC ACCCTGTCTT GGGCTCAGCA GCTGAAGAAC ATCTCTTACT GTAGATGGGC CCACTGGAGA TCTTTCCACA
TGGTCTTAGA AGTAGCTGTT CCTCTGATG TGGACAGAA CCCGAGTCTG CACTTCTTG TAGAGAATGA CATCTACCCG GGTGACCTTC AGAAAGGTGT

1001 N A I K T E H E N S Y H F V A N D I T A S F F T P N T E A Q D V T K
ATGCTATCAA GACCGAGCAC GAGAATCCCT ACCACTTCTG GCTAATGAT ATCACCGCCA GCTTTTTCAC CCTAATACC GAGGCTCAGG ATGTGACCAA
TACGATAGTT CTGGTCTGTG CTCTTGAAGA TGGTGAAGCA TGGTGAAGCA TGGTGAAGCA TGGTGAAGCA TGGTGAAGCA TGGTGAAGCA TGGTGAAGCA

1101 T H T C L N S L I E S E M T S R L E K V N G T H V T N G S R Q Y Y
GACCCACACC TGCTGAATT CCGTGTGCTG GTCTGAGATG ACCTCCAGAC TGGAGAGGTT GAATGGCACC CACGTGACCA ATGGCTCTAG ACAGTACTAC
CTGGGTGTGG ACAGACTTAA GGGACTAGCT CAGACTCTAC TGGAGGCTG ACCTCTTCCA CTTACCGTGG GTGCAGTGGT TACCGAGATC TGTCATGATG

1201 L T N G G L L L V W Q P L V Q Q K L L N A Q D L L E A V A S K H N
CTGACCAAGC TGCTGAGGCT GCTGGTGTGG CAGCCTCTGT CAGCAGCAGA GCTGCTGAA CACTGCTGAA GCTGCTGAA CACTGCTGAA TGTGGCTTCT AAGCAACAATG
GACTGGTTAC CGCCGAGCA GCACACACCC GTCCGAGACC ACGTCTGTTT CGAGCACTTG CGAGTCTTAG ACGACTCTCG ACACCGAAGA TTCGTTGTTAC

1301 V T K P A R G R R Q R R A V S S I L I D D D V Y T A E S A L L L T Q
TGACCAAGCC TGCTGAGGCT CCGAGACAGA GAAGGCTCTG GTCTCTATC CTGATCGAGC ATGATGTGTA CACCGCTGAG TCTGCTCTG TGTGCTGCTA TGTGCTGCTA
ACTGGTTCGG ACGATCTCCG GCCTCTGTCT CTTCCCGACA CAGGAGATAG GACTAGCTGC TACTACACAT GTGGCGACTC AGACGAGAGC ACGACTGGGT

1401 I Q F A Y D M L R S Q I N T V L E E L S R A W C R E Q H R A S L M
GATCCAGTTT GCTTACGATA TGCTGAGGCT CCAGATCAAT ACCGTGTGTT AGGAGCTGTC TAGAGCTTGG TGTAGAGAGC AGCATAGAGC TTTCCCTGATG
CTAGTCTAAA CGAATCGTA ACGACTCCAG GGTCTAGTTA TGGCAGCAGC TCCCTGACAG ATCTCGAACC ACATCTCTCG TCGTATCTCG AAGGACTACT

1501 W N E L S K I N P T S V M S I Y G R P V S A K R I G D V I S V S
TGAACAGAG TGTCAAAGT CAATCTTACC TCCGTGATG CTTCCATCTA CCGCAGACCT GTGTCTGCTA AGAGAATCGG CGACGTGATC TCTGTGCTC
ACCTTGCTCG ACAGGTTCTA GTTAGGATGG AGGCACATA GGAGGTAGAT CCGCTGTGGA CACAGACGAT TCTCTTAGCC GCTGCACTAG AGACACAGAG

1601 H C V V V D Q Q S V S L H R N M R V P G R D H A H E C Y S R P P V T
ACTGTGTGGT GGTGGATCAG CAGTCTGTGT CTCTGCACAG AAACATGAGA GTGGCTGGCA GAGATCAGC TCACGAGTGT TACTCTAGAC CTCCTGTGAC
TGACACACA CCACCTAGTC GTCAGACACA GAGACGTGTC TTTGTACTCT CACGGACCGT CTCTAGTGGC AGTGTCTACA ATGAGATCTG GAGGACACTG

1701 F K F I N D S H L Y K G Q L G V N N E I L L T T T A L E V C H E N
CTTCAAGTC ATCAACGAT CCCACTGTA CAAGGCCAG CTGGCGTGA ATAATGAGT CCTGTGACC ACCACCGCTC TGGAGGTGTG TCACGAGAAT
GAGTTCAGG TAGTTCAGT GGGTGGACAT GTTCCCGACT TATTACTCTA TCGGCACTGG TGGTGGGAGG AACCTCCACAC AGTGTCTTAA

1801 T E H Y F Q G G N N M Y F Y K N Y R H V K T I P V S A V A T L D T
ACCGAGCATT ACTTTCAGG CCGCAACAAC ATGTACTTCT ACAAGAATA CCGGCACGTC AAAACCATCC CTGTGTCTGC TGTGGCTACA CTGGTACTCT
TGGCTCTAAA TGAAAGTCCC GCGTGTGTTG TACATGAAGA GTTCTTGTAT GCGCTGTGAG TTTTGGTAGG GACACAGAGC ACACCGATGT GACCTATGGA

1901 F I V L N L T L V E N I D F Q V I E L Y S R E E K R M S T V F D I E
TTATCGTGT GAATCTGACC CTGGTGGAGA ACATCGATT CAGGTGATC GAGCTGTACT CTCGGGAGGA GAAGAGAAT TCTACCGTGT TCGACATCGA
AATAGACCA CTTAGACTGG GACCACCTCT TGATAGTAAA GGTCCACTAG CTCGACATGA GAGCCCTCTT CTTCTCTTAC AGATGGCACA AGCTGTAGCT

2001 T M F R E Y N Y Y T Q R V T G L R R D L S D I A T N R N Q F V D A
GACAAATGTC CCGGAGTACA ACTACTACAC CCAGAGAGTG ACCGCGCTGA GAAGAGATCT GTCTGATATC GCCACCAACC GGAACCAAGT TGTGGATGCT
CTGTTACAAG CCGCTCATGT TGATGATGTG GGTCTCTCAC TGGCCGACT CTTCTCTAGA CAGACTATAG CCGTGGTGG CCTTGTGCAA ACACCTACGA

2101 F G T L M D D L G V V G K T V V N A V S S L A T L F S S I V T G L
TTTGGCACC TGATGGATGA TCTGGGCGTG GTGGGCAAGA CCGTGGTGAA TGCTGTGTCC TCTCTGGCTA CCTGTCTCT TCTATCTGTC ACCGCGCTGA
AAACCGTGG ACTACTACT AGACCCGAC CACCCGTTCT GGCACCACTG ACACACAGAG AGAGACCGAT GGGACAAGAG AAGATAGCAC TGGCCGACTG

2201 I N F I K N P F G G M L I F G L L A A V V I A V I L L R R R A A S F
TCAACTTCAT CAAGAATCCT TTTGGCGCA TGCTGATCTT TGGCCTGCTG GCTGCTGTGG TGATCGCTGT GATCCTGCTG CGCAGAAGGG CTGTTCTTT
AGTTGAAGTA GTTCTTAGGA AAACCGCCGT ACGACTAGAA ACCGGACGAC CGACGACACC ACTAGCGACA CTAGGACGAC GCGTCTTCCC GACGAGAAA

2301 A A N P V Q M I Y P D I Q Q I T K Q R Q E M N V E P I S K H E L D
TGCCGCTAAT CCGTGCAGA TGATCTACCC TGATATCCAG CAGATCACCA AGCAGAGACA GGAGATGAAC GTCGAGCCTA TCTTAAGCA CGAGCTGGAC
ACGGCGATTA GGGCACGCT ACTAGATGGG ACTATAGGTC GTCTAGTGGT TCGTCTGTGT CCTTACTTG CAGCTCGGAT AGAGATTCTG GCTCGACCTG

2401 R I M L A M H D Y H Q T K Q D K P D E K E G P E S G G S A N K A N
AGAATCATGC TGGCCATGCA CGATTACCAC CAGACCAAGC AGGATAAGCC TGATGAGAAG GAGGGCCCTG AGTCTGGCGG CTCTGCTAAT AAGGCTACT
TCTTAGTACG ACCGGTACGT GCTAATGGTG GTCTGGTTCC TCCTATTCGG ACTACTCTTC CTCCCGGGAC TCAGACCGCC GAGACGATTA TTCCGATTGA

2501 W L N K A K N V L R R R A G Y Q P L K R S D S T E S A A A L
GGCTGAACAA GGCCAAGAAC GTCCTGAGAA GAAGGGCAGG CTACCAGCCT CTGAAGAGGT CTGATTCTAC CGAGTCTGCT GCTGCCCTG
CCGACTTGT CCGGTCTTG CAGGACTCTT CTTCCCGTCC GATGGTCGGA GACTTCTCCA GACTAAGATG GCTCAGACGA CGACGGGAC