FIGURE LEGENDS - SUPPLEMENTARY MATERIAL

Fig. S1. RNA CoMPASS analysis of c666-1.

Fig. S2. RNA CoMPASS analysis of x666-1.

Fig. S3. RNA CoMPASS analysis of CNE1.

Fig. S4. RNA CoMPASS analysis of HONE1. The presence of mycoplasma reads likely represents true contamination.

Fig. S5. RNA CoMPASS analysis of HK1.

Fig. S6. RNA CoMPASS analysis of NP460.

Fig. S7. MuLV detected in c666-1, x666-1, and NP460 cell lines.

Fig. S8. HPV-18 detected in three independent sources of CNE1 cell lines. Quantitative real-time PCR on CNE1 cells from three independent laboratories were surveyed for the presence of HPV-16 and HPV-18. All three cell lines demonstrated evidence of HPV-18 but none was infected with HPV-16. Samples were normalized to GAPDH and compared to NPC cell line c666-1 for relative viral expression.

Fig. S9. RNA CoMPASS analysis of CNE1-JPN. The presence of mycoplasma reads likely represents true contamination.

Fig. S10. Strand specific RNA-sequencing of ribodepleted RNA from CNE1, CNE1-JPN, and HONE1 cell lines reveals the majority of transcription in the sense direction. Coverage graphs are represented using a linear scale. Green coverage represents reads in both the sense and antisense strands, blue coverage represents those reads in the sense direction, and pink coverage represents those reads in the antisense direction. The y-axis represents the number of reads at each nucleotide position of the genome. Insets within the antisense coverage represent blowups of those regions with a max scale of minus 15 reads since there were so few reads. The max scale for the other coverage graphs is 1,750 reads.

Fig. S11. HPV-18 breakpoint 1-a. Homology: sequence that shares homology with both human and HPV-18 sequence.

Fig. S12. HPV-18 breakpoint 2-c.

Fig. S13. HPV-18 breakpoint 3-d. Homology: sequence that shares homology with both human and HPV-18 sequence.

Fig. S14. HPV-18 breakpoint 4-e. Homology: sequence that shares homology with both human and HPV-18 sequence.

Fig. S15. HPV-18 breakpoint 5-b. No homology: sequence that shares no homology with human or HPV-18 sequence.

Fig. S16. HPV-18 SNV analysis shows identical SNVs in HeLa cells, CNE1, and HONE1 cells. Raw reads from HeLa, CNE1, and HONE1 datasets aligned to the HPV-18 genome (NC001357) were visualized in the IGV genome browser. Coverage graphs are represented using a log scale. The y-axis represents the number of reads at each nucleotide position. Blowouts of all mismatches observed in the samples are shown in individual boxes. The nucleotide mutation coordinates and corresponding amino acid changes are represented above each respective box.

Fig. S17. Specific SNVs within CNE1 and HONE1 exhibit heterogeneity relative to HeLa cells.

Table S1. List of PCR primers.

Table S2. List of human viruses used in custom viral genome.

Table S3. Quantification of HPV-18 genes in NPC cell lines.

Fig. S1. RNA CoMPASS analysis of c666-1

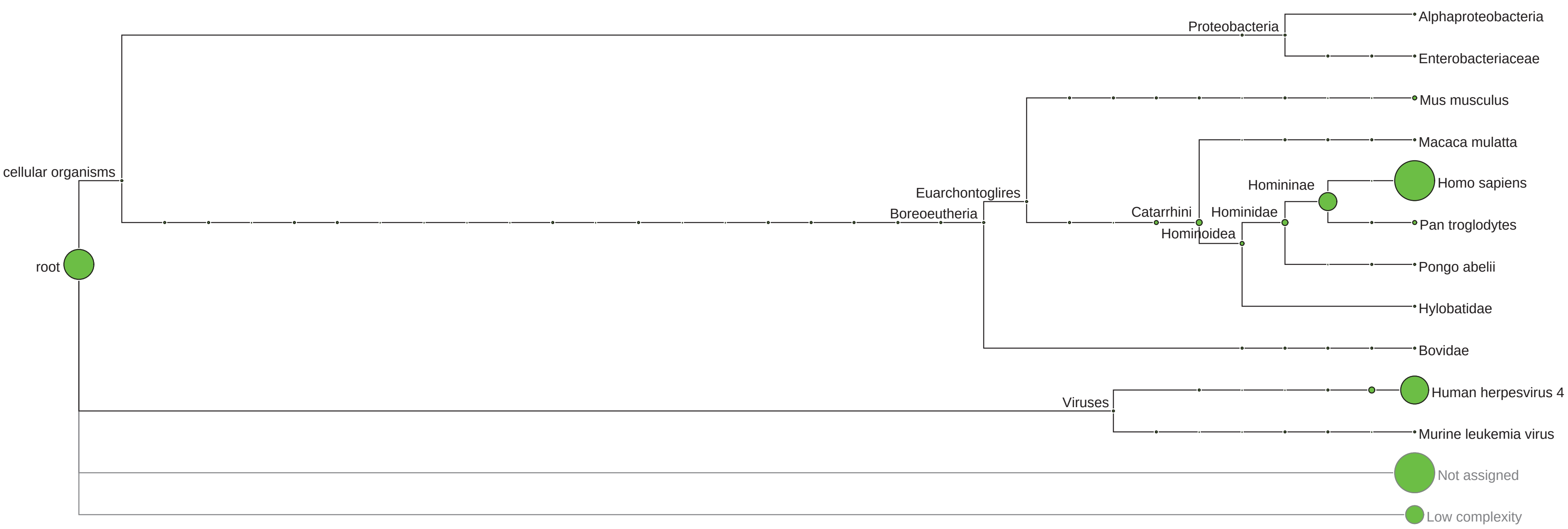

Fig. S2 RNA CoMPASS analysis of x666-1

Fig. S3 RNA CoMPASS analysis of CNE1

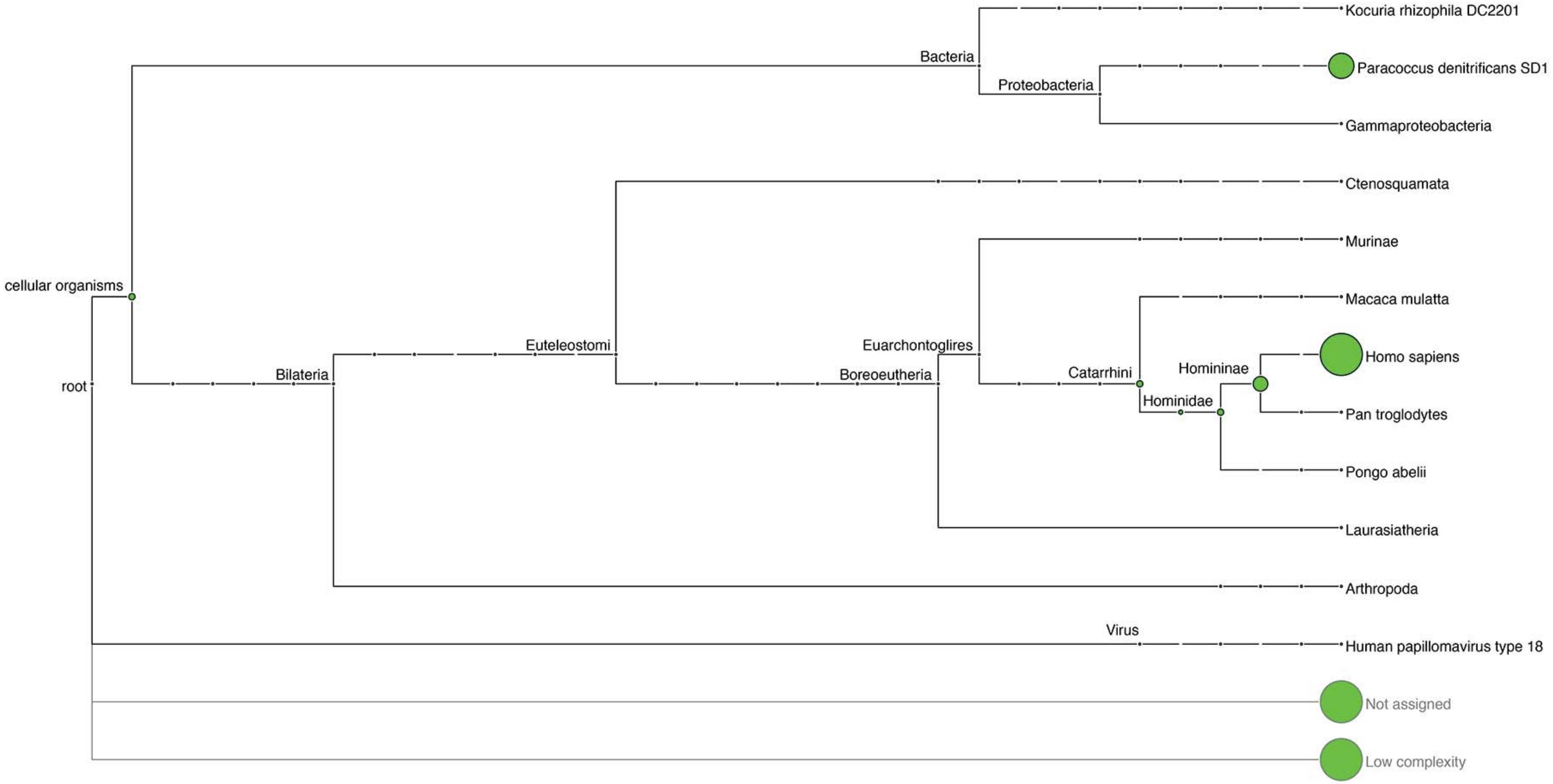

Fig.S4 RNA CoMPASS analysis of HONE1

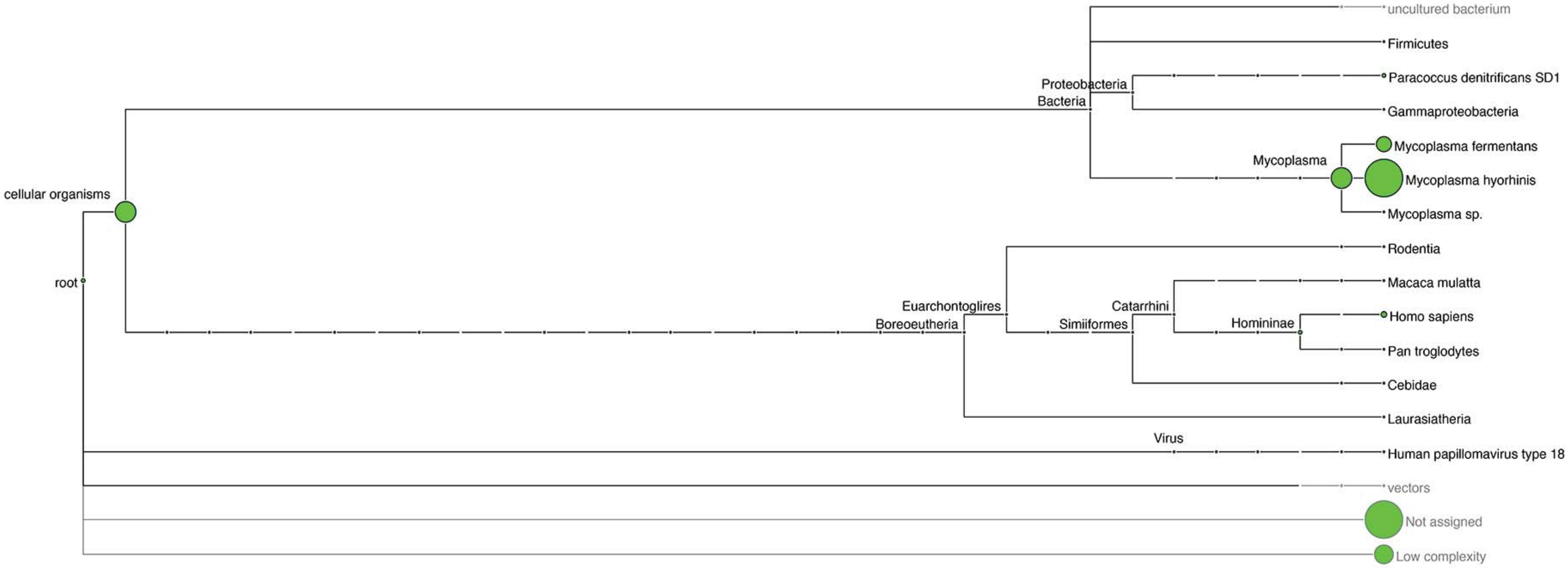

Fig. S5 RNA CoMPASS analysis of HK1

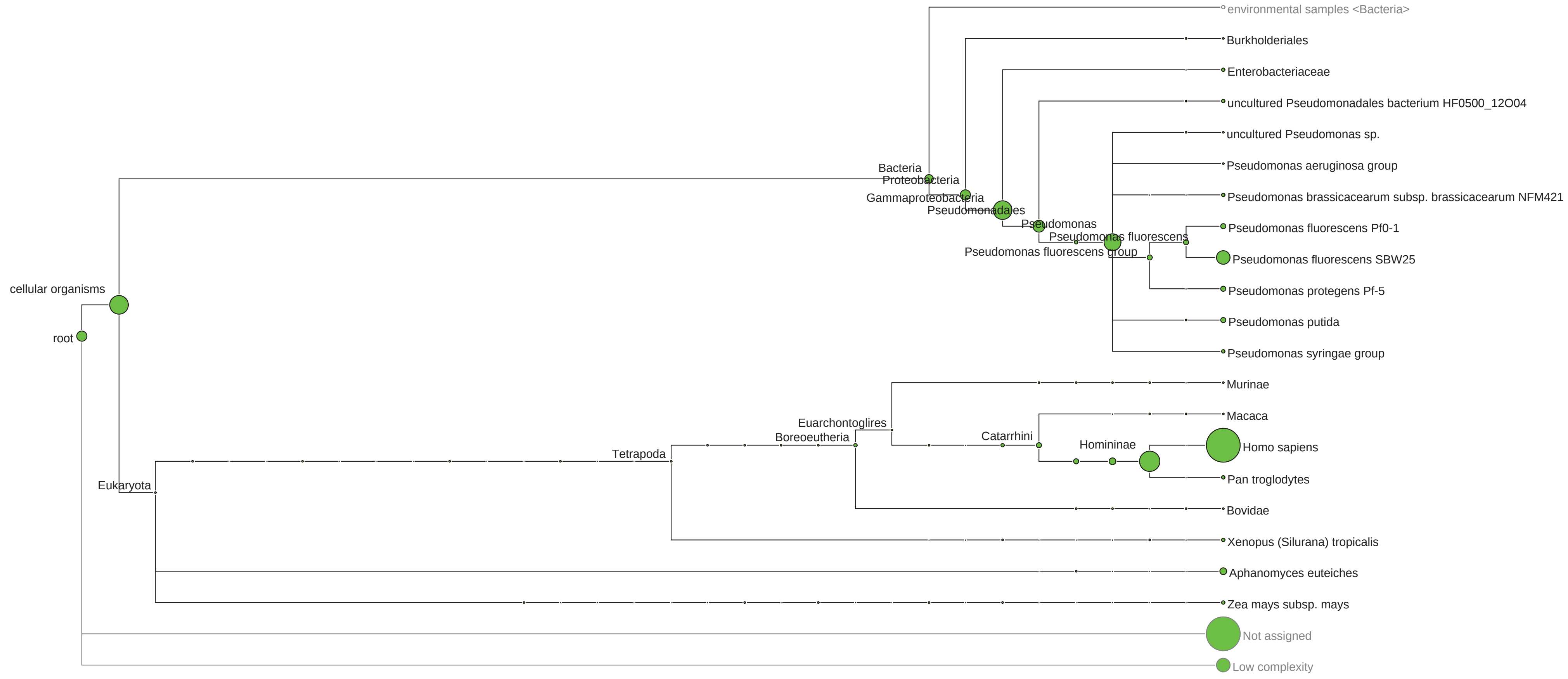

Fig. S6 RNA CoMPASS analysis of NP460

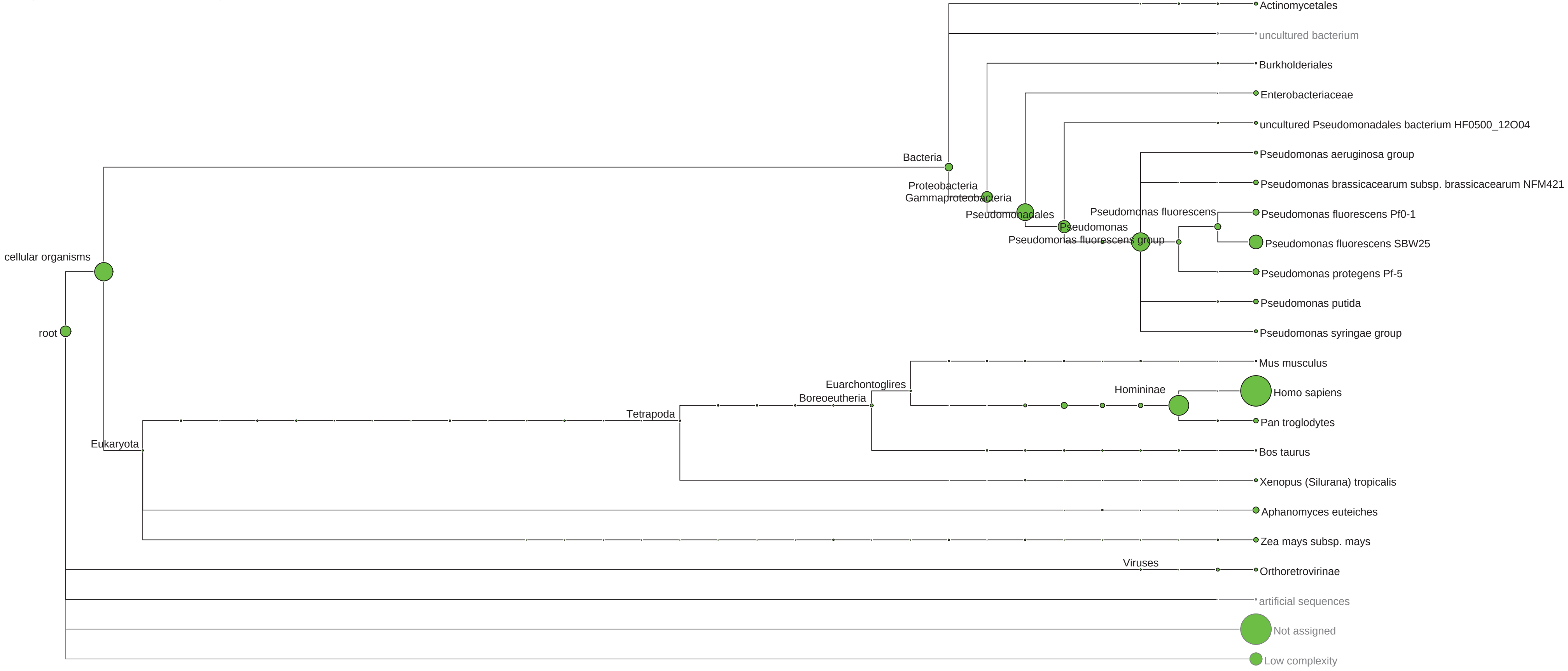

Fig. S7

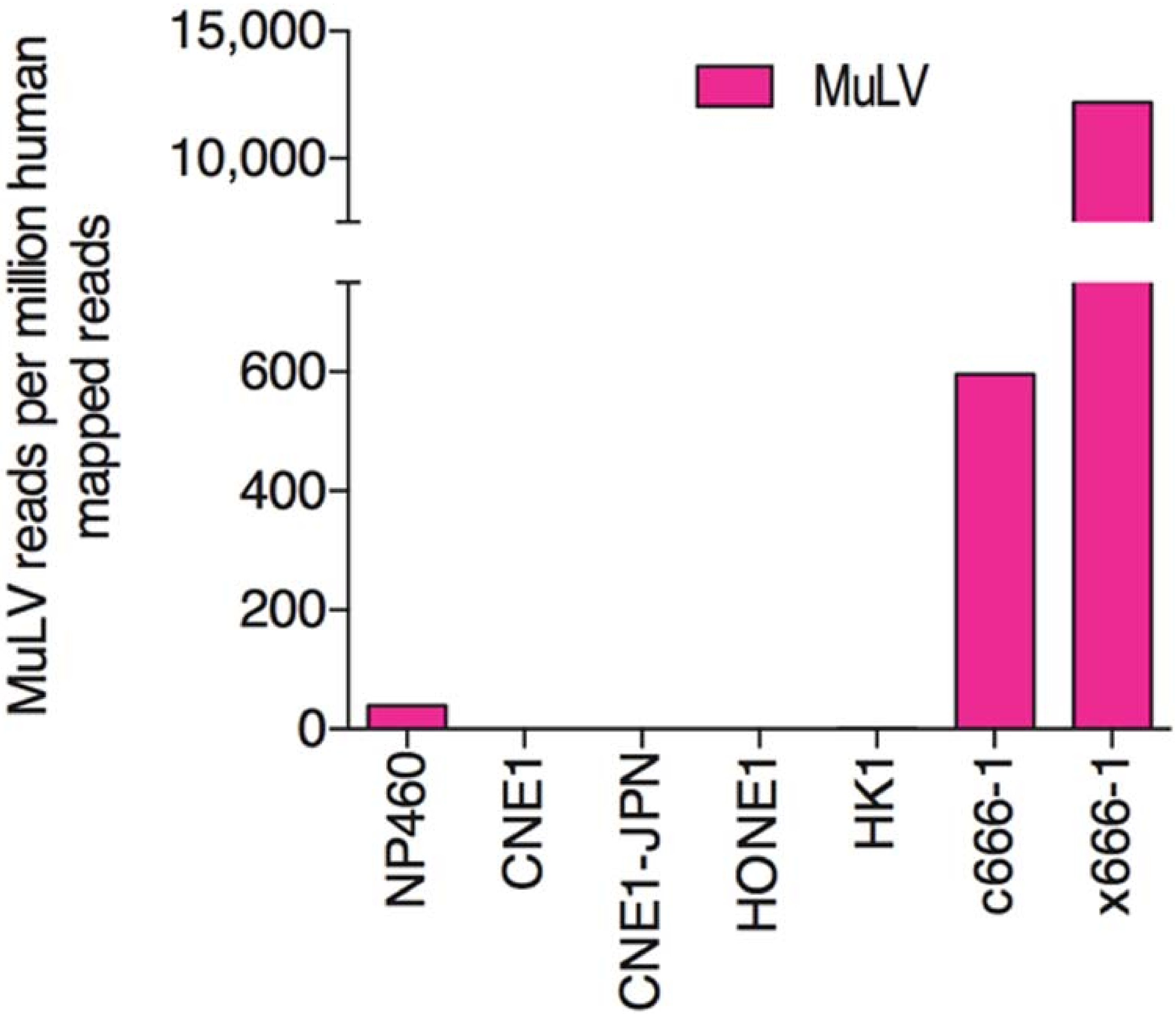
MuLV reads per million human mapped reads
15,000
10,000
600
400
200
0
MuLV
NP460
CNE1
CNE1-JPN
HONE1
HK1
c666-1
x666-1

Fig. S8

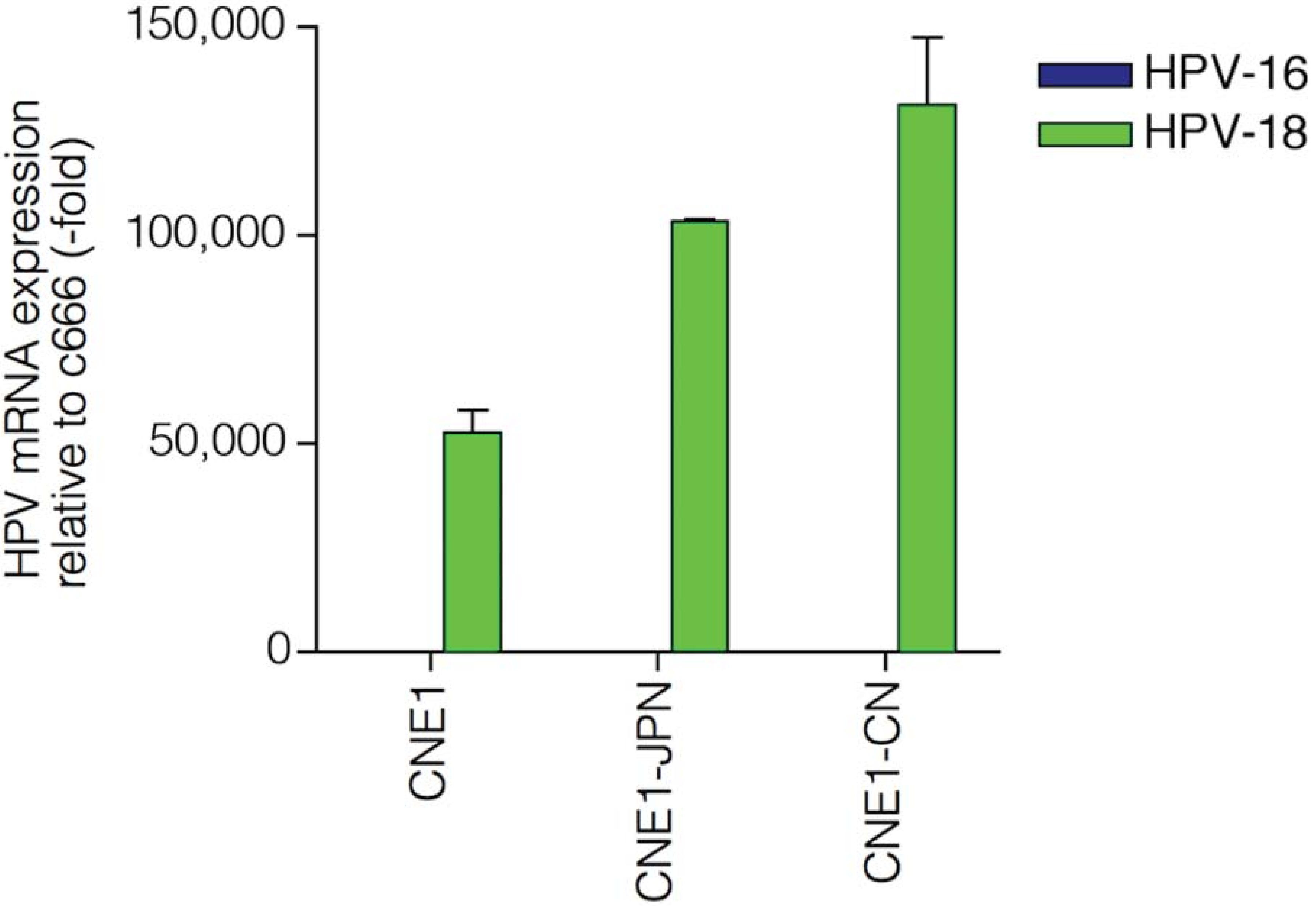
HPV mRNA expression relative to c666 (-fold)
150,000
100,000
50,000
0
HPV-16
HPV-18
CNE1
CNE1-JPN
CNE1-CN

Fig. S9 RNA CoMPASS analysis of CNE1-JPN

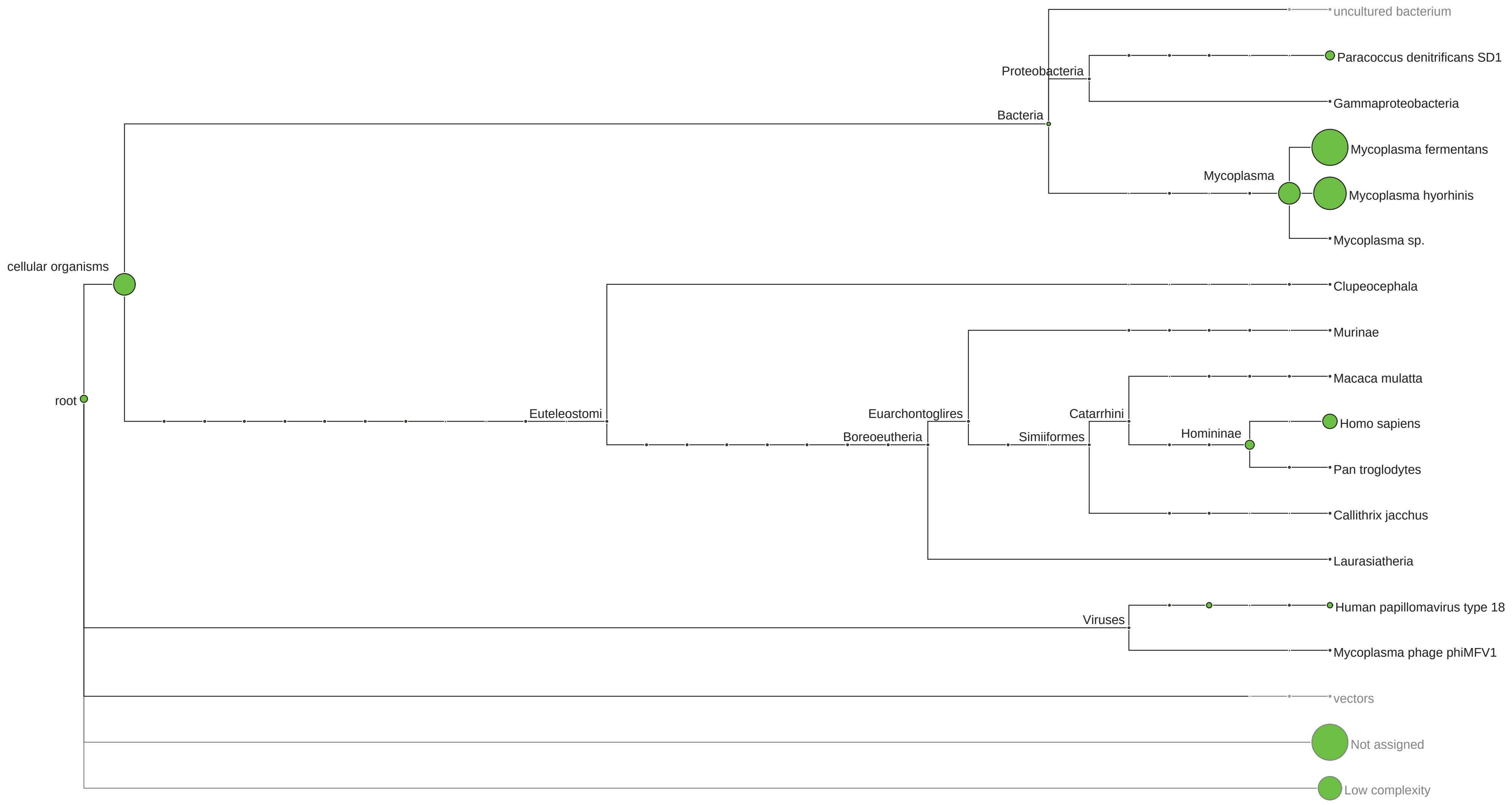

Fig. S10

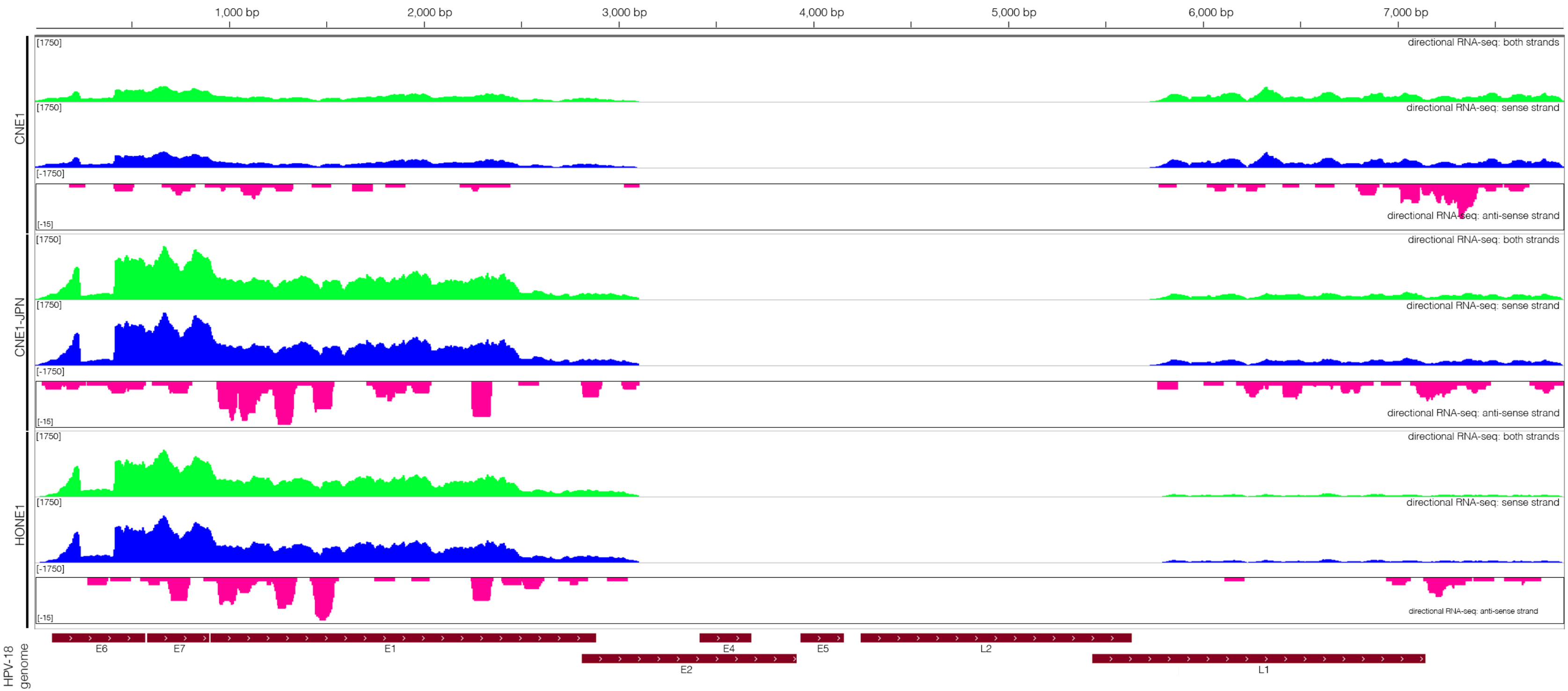
1,000 bp
2,000 bp
3,000 bp
4,000 bp
5,000 bp
6,000 bp
7,000 bp
CNE1
[1750]
directional RNA-seq: both strands
[1750]
directional RNA-seq: sense strand
[-1750]
[-15]
directional RNA-seq: anti-sense strand
CNE1-JPN
[1750]
directional RNA-seq: both strands
[1750]
directional RNA-seq: sense strand
[-1750]
[-15]
directional RNA-seq: anti-sense strand
HONE1
[1750]
directional RNA-seq: both strands
[1750]
directional RNA-seq: sense strand
[-1750]
[-15]
directional RNA-seq: anti-sense strand
HPV-18 genome
E6
E7
E1
E4
E5
L2
E2
L1

Fig. S11

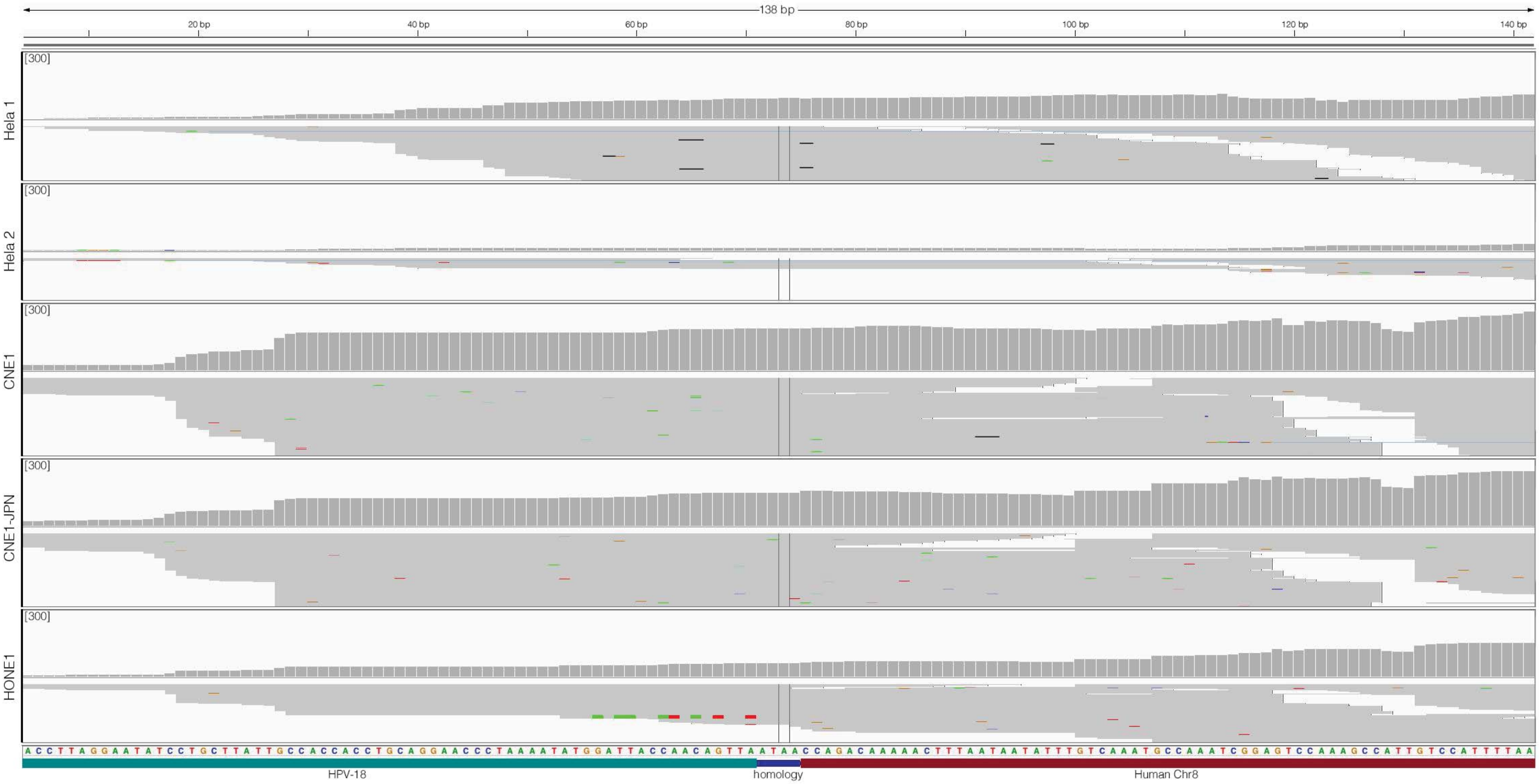
138 bp
20 bp
40 bp
60 bp
80 bp
100 bp
120 bp
140 bp
Hela 1
[300]
Hela 2
[300]
CNE1
[300]
CNE1-JPN
[300]
HONE1
[300]
ACCTTAGGAATATCCTGCTTATTGCCACCACCTGCAGGAACCCTAAAATATGGATTACCAACAGTTAATAACCAGACAAAAACTTTAATAATATTTGTCAAATGCCAAATCGGAGTCCAAAGCCATTGTCCATTTTAA
HPV-18
homology
Human Chr8

Fig. S12

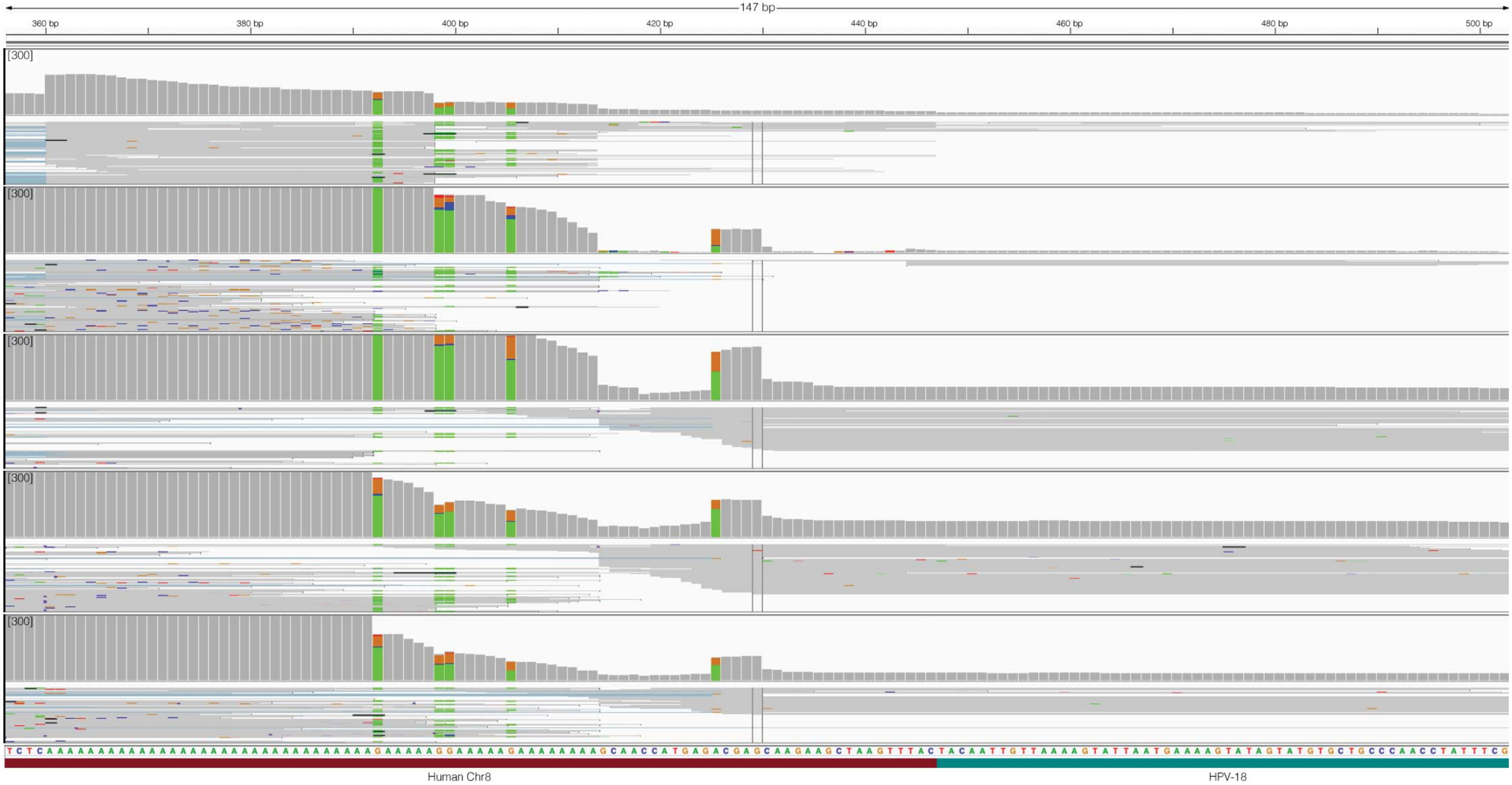
147 bp
360 bp
380 bp
400 bp
420 bp
440 bp
460 bp
480 bp
500 bp
[300]
Hela 1
Hela 2
CNE1
CNE1-JPN
HONE1
TCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAAGGAAAAAGAAAAAAAAGCAACCATGAGACGAGCAAGAAGCTAAGTTTACTACAATTGTTAAAAGTATTAATGAAAAGTATAGTATGTGCTGCCCAACCTATTTCG
Human Chr8
HPV-18

Fig. S13

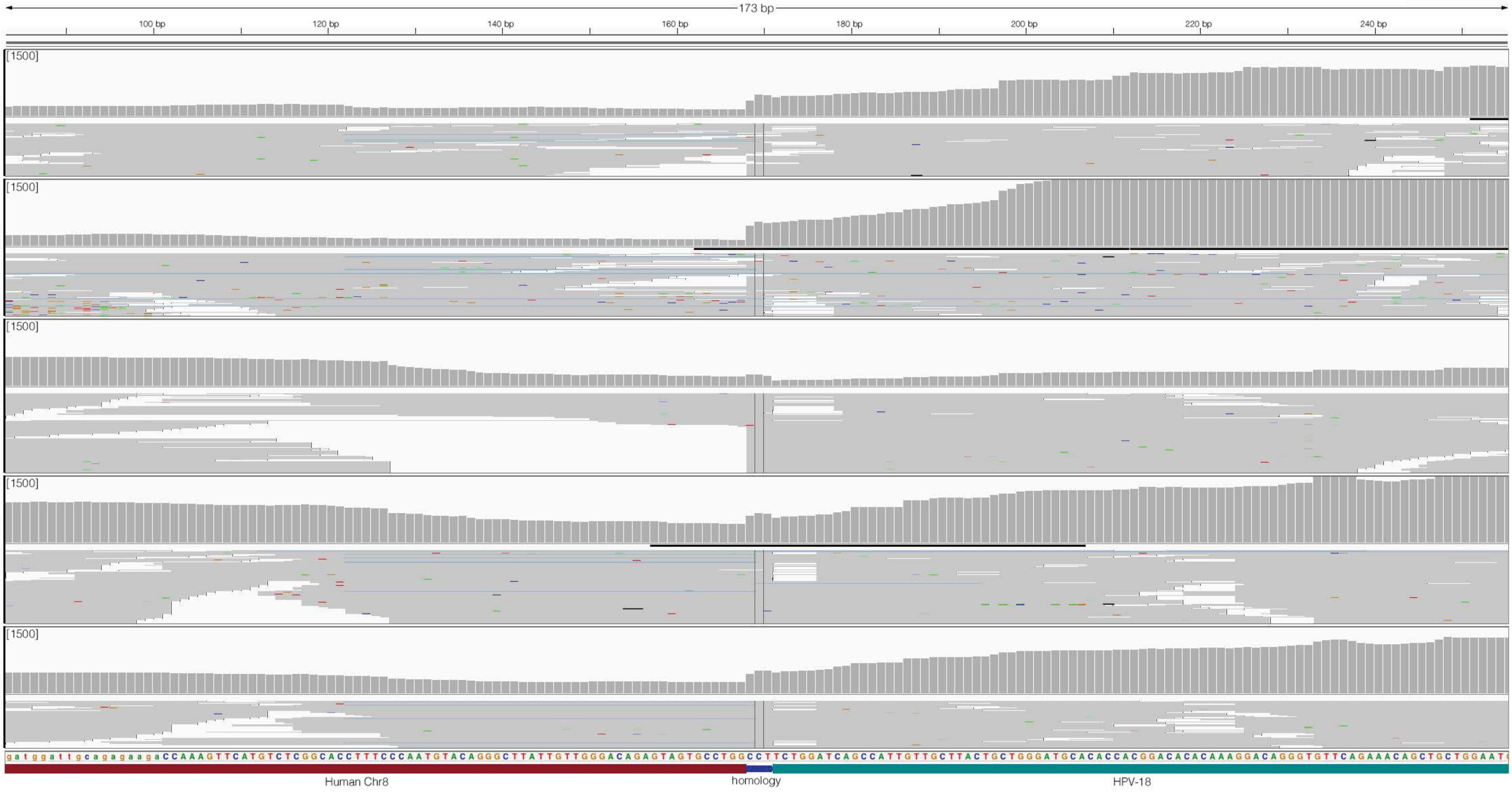
173 bp
100 bp
120 bp
140 bp
160 bp
180 bp
200 bp
220 bp
240 bp
Hela 1
[1500]
Hela 2
[1500]
CNE1
[1500]
CNE1-JPN
[1500]
HONE1
[1500]
gatggattgcagagaaagaCCAAAGTTCATGTCTCGGCACCTTTCCCAATGTACAGGGCTTATTGTTGGGACAGAGTAGTGCCTGGCCTTCTGGATCAGCCATTGTTGCTTACTGCTGGGATGCACACCACGGACACACAAAGGACAGGGTGTTCAGAAACAGCTGCTGGAAT
Human Chr8
homology
HPV-18

Fig. S14

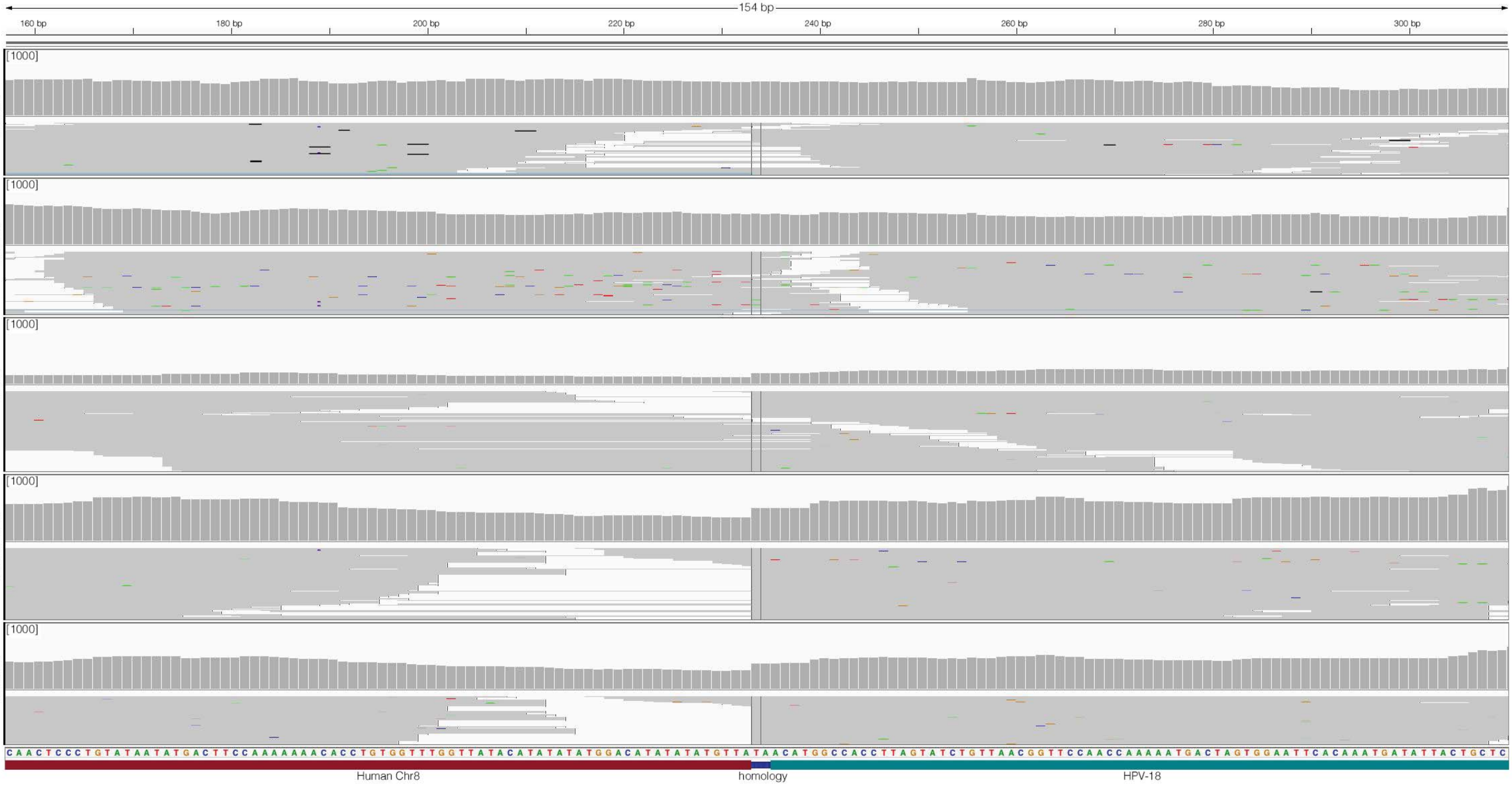
154 bp
160 bp
180 bp
200 bp
220 bp
240 bp
260 bp
280 bp
300 bp
[1000]
Hela 1
[1000]
Hela 2
[1000]
CNE1
[1000]
CNE1-JPN
[1000]
HONE1
CAACTCCCTGTATAATATGACTTCCAAAAAAACACCTGTGGTTTGGTTATACATATATATGGACATATATATGTTATAACATGGCCACCTTAGTATCTGTTAACGGTTCCAACCAAAAATGACTAGTGGAATTCACAAATGATATTACTGCTC
Human Chr8
homology
HPV-18

Fig. S15

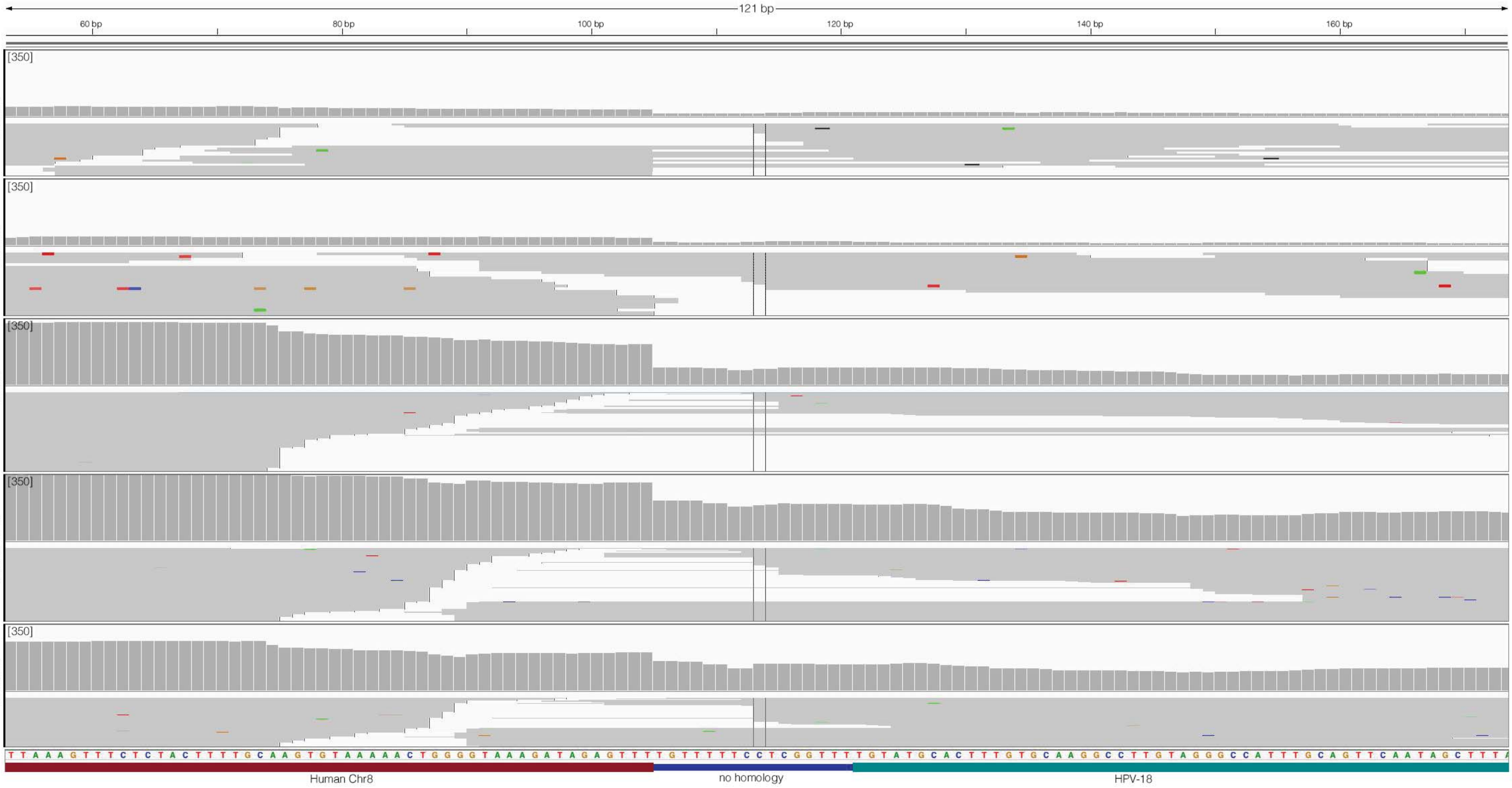
121 bp
60 bp
80 bp
100 bp
120 bp
140 bp
160 bp
Hela 1
[350]
Hela 2
[350]
CNE1
[350]
CNE1-JPN
[350]
HONE1
[350]
T T A A A G T T T C T C T A C T T T T G C A A G T G T A A A A A C T G G G G T A A A G A T A G A G T T T T G T T T T T C C T C G G T T T T G T A T G C A C T T T G T G C A A G G C C T T G T A G G G C C A T T T G C A G T T C A A T A G C T T T A
Human Chr8
no homology
HPV-18

Fig. S16

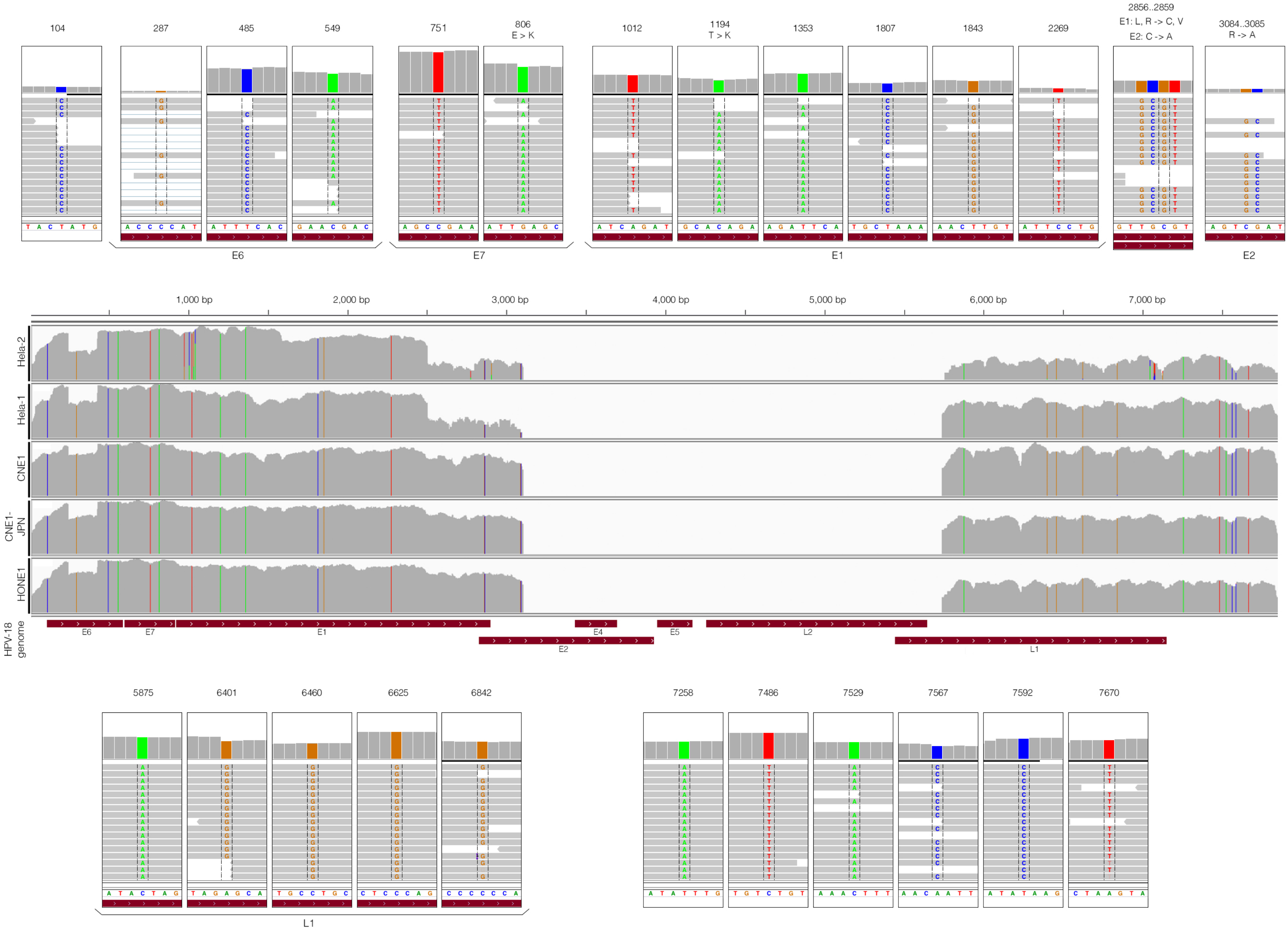
104
287
485
549
751
806
E > K
1012
1194
T > K
1353
1807
1843
2269
2856..2859
E1: L, R -> C, V
E2: C -> A
3084..3085
R -> A
T A C T A T G
A C C C C A T
A T T T C A C
G A A C G A C
A G C C G A A
A T T G A G C
A T C A G A T
G C A C A G A
A G A T T C A
T G C T A A A
A A C T T G T
A T T C C T G
G T T G C G T
A G T C G A T
E6
E7
E1
E2
1,000 bp
2,000 bp
3,000 bp
4,000 bp
5,000 bp
6,000 bp
7,000 bp
Hela-2
Hela-1
CNE1
CNE1-JPN
HONE1
HPV-18 genome
E6
E7
E1
E4
E5
L2
E2
L1
5875
6401
6460
6625
6842
7258
7486
7529
7567
7592
7670
A T A C T A G
T A G A G C A
T G C C T G C
C T C C C A G
C C C C C C A
A T A T T T G
T G T C T G T
A A A C T T T
A A C A A T T
A T A T A A G
C T A A G T A
L1

Fig. S17

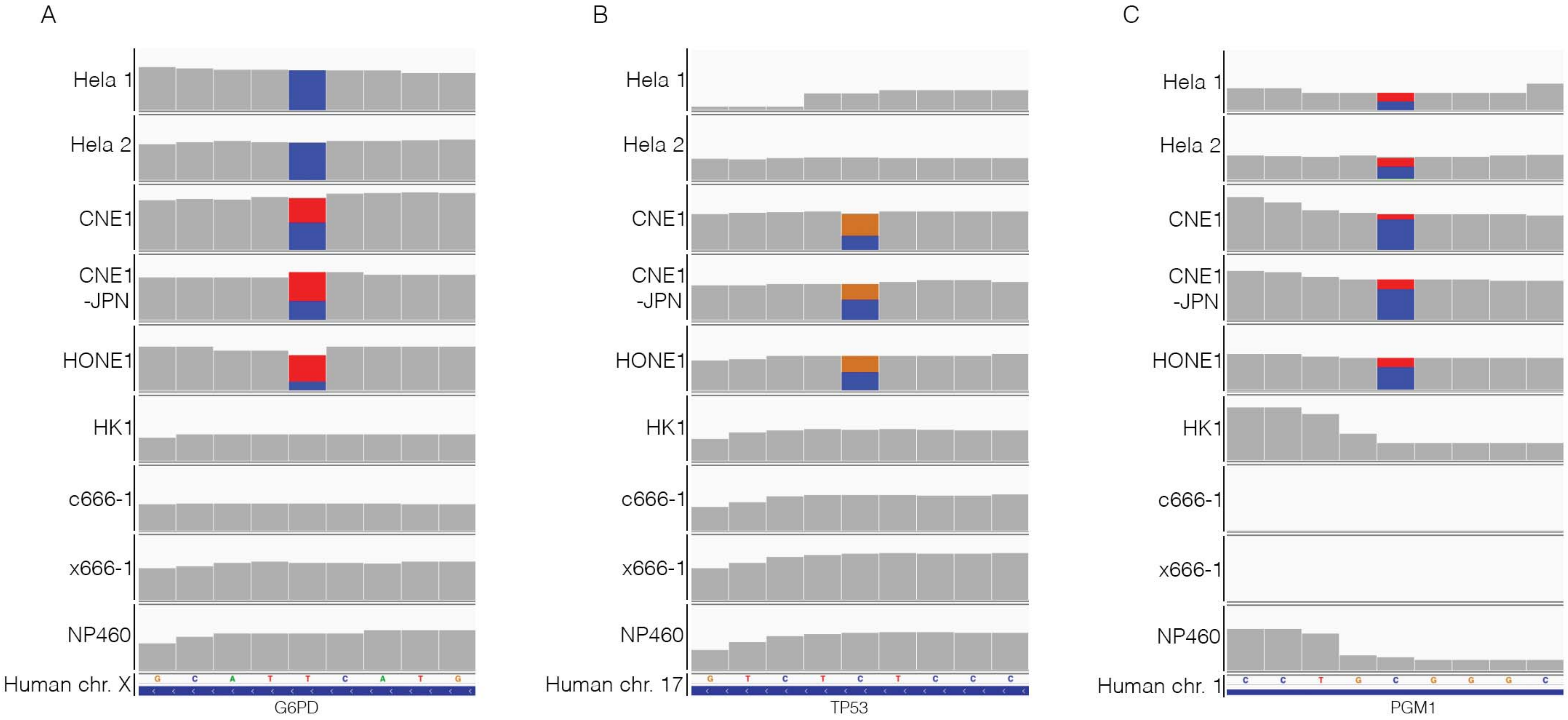
A
B
C
Hela 1
Hela 2
CNE1
CNE1 -JPN
HONE1
HK1
c666-1
x666-1
NP460
Human chr. X
G C A T T C A T G
G6PD
Human chr. 17
G T C T C T C C C
TP53
Human chr. 1
C C T G C G G G C
PGM1

Table S1 List of PCR Primers

		Forward primer	Reverse primer
GAPDH	Reference gene	5’-GAAATCCCATCACCATCTTCCAGG-3’	5’-GAGCCCCAGCCTTCTCCATG-3’
HPV-16	Reference gene	5’-TTGCAGATCATCAAGAACACGTAGA-3’	5’-CAGTAGAGATCAGTTGTCTCTGGTTGC-3’
HPV-18	Reference gene	5’-AGAGGCCAGTGCCATTCGT-3’	5’-GTTTCTCTGCGTCGTTGGAGT-3’
EBV- EBER		5’-GGACCTACGCTGCCCTAGA-3’	5’-CAGCTGGTACTTGACCGAAGA-3’

Reference for GAPDH primer: West et al, JBC 2004, Vol 279, (28): 28896-28902
Reference for HPV-16 and HPV-18 primers: Lindh et al, J ClinVirol. 2007, Vol 40, (4): 321-4

VM164A	5′-TGCCTCCTAGATCGTATTCCC-3′
VM-164B	5′-GCACTCTGTGGCATGAAGGT-3′
RB164K2	5′-TGGCTCCTCCCTCTATTATCG-3′

Primers for genotyping of the HeLa-specific L1 retrotransposon marker.

Table S2. List of human viruses used in custom viral genome.

Accession #	**Genome**
NC 001499.1	Abelson murine leukemia virus complete genome
NC 002077.1	Adeno-associated virus - 1 complete genome
NC 001401.2	Adeno-associated virus - 2 complete genome
NC 001729.1	Adeno-associated virus - 3 complete genome
NC 001829.1	Adeno-associated virus - 4 complete genome
NC 006260.1	Adeno-associated virus - 7 complete genome
NC 006261.1	Adeno-associated virus - 8 complete genome
NC 006152.1	Adeno-associated virus 5 complete genome
AF028704.1	Adeno-associated virus 6 complete genome
NC 007548.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007549.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007550.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007551.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007552.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007553.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007554.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007555.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007556.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007557.1	Adult diarrheal rotavirus strain J19 complete genome
NC 007558.1	Adult diarrheal rotavirus strain J19 complete genome
NC 012932.1	Aedes flavivirus complete genome
NC 015451.1	Aguacate virus segment L complete genome
NC 015450.1	Aguacate virus segment M complete genome
NC 015452.1	Aguacate virus segment S complete genome
NC 018459.1	Aino virus Gn-Gc-NSm gene for M polyprotein segment M genomic RNA isolate 38K
NC 018460.1	Aino virus N and NSs genes segment S genomic RNA isolate 38K
NC 018465.1	Aino virus RdRp gene for RNA-dependent RNA polymerase segment L genomic RNA isolate 38K
NC 009894.1	Akabane virus segment L complete sequence
NC 009895.1	Akabane virus segment M complete sequence

NC 009896.1	Akabane virus segment S complete sequence
NC 004355.1	Alkhurma virus complete genome
NC 010249.1	Allpahuayo virus segment L complete sequence
NC 010253.1	Allpahuayo virus segment S complete sequence
NC 010251.1	Amapari virus segment L complete sequence
NC 010247.1	Amapari virus segment S complete sequence
NC 003468.2	Andes virus segment L complete genome
NC 003467.2	Andes virus segment M complete genome
NC 003466.1	Andes virus segment S complete sequence
NC 003676.1	Apoi virus genome
NC 020808.1	Aravan virus complete genome
NC 023635.1	Arumowot virus segment L complete sequence
NC 023633.1	Arumowot virus segment M complete sequence
NC 023634.1	Arumowot virus segment S complete sequence
NC 003243.1	Australian bat lyssavirus complete genome
NC 007652.1	Avian metapneumovirus
NC 019531.1	Avian paramyxovirus 4 strain APMV-4/duck/Delaware/549227/2010 complete genome
NC 003043.1	Avian paramyxovirus 6 complete genome
NC 012534.1	Bagaza virus complete genome
NC 004211.1	Banna virus segment 1 complete sequence
NC 004201.1	Banna virus segment 10 complete sequence
NC 004200.1	Banna virus segment 11 complete sequence
NC 004198.1	Banna virus segment 12 complete sequence
NC 004217.1	Banna virus segment 2 complete sequence
NC 004218.1	Banna virus segment 3 complete sequence
NC 004219.1	Banna virus segment 4 complete sequence
NC 004220.1	Banna virus segment 5 complete sequence
NC 004221.1	Banna virus segment 6 complete sequence
NC 004204.1	Banna virus segment 7 complete sequence
NC 004203.1	Banna virus segment 8 complete sequence

NC 004202.1	Banna virus segment 9 complete sequence
NC 018382.1	Bat hepevirus complete genome
NC 017936.1	Bat sapovirus TLC58 HK complete genome
NC 010255.1	Bear Canyon virus segment L complete sequence
NC 010256.1	Bear Canyon virus segment S complete sequence
NC 007803.1	Beilong virus complete genome
NC 001538.1	BK polyomavirus complete genome
NC 001607.1	Borna disease virus complete genome
NC 002161.1	Bovine parainfluenza virus 3 complete genome
NC 001989.1	Bovine respiratory syncytial virus complete genome
NC 022039.1	Brazoran virus segment L complete sequence
NC 022038.1	Brazoran virus segment M complete sequence
NC 022037.1	Brazoran virus segment S complete sequence
NC 014373.1	Bundibugyo ebolavirus complete genome
NC 001925.1	Bunyamwera virus L segment complete sequence
NC 001926.1	Bunyamwera virus M segment complete sequence
NC 001927.1	Bunyamwera virus segment S complete sequence
NC 009026.2	Bussuquara virus complete genome
NC 012126.1	California sea lion anellovirus complete genome
NC 015374.1	Candiru virus segment L complete genome
NC 015373.1	Candiru virus segment M complete genome
NC 015375.1	Candiru virus segment S complete genome
NC 001921.1	Canine distemper virus complete genome
NC 018484.1	CAS virus segment L complete genome
NC 018481.1	CAS virus segment S complete genome
NC 001564.1	Cell fusing agent virus complete genome
NC 020805.1	Chandipura virus isolate CIN 0451 complete genome
NC 017086.1	Chaoyang virus complete genome
NC 010563.1	Chapare virus segment L complete sequence
NC 010562.1	Chapare virus segment S complete sequence

NC 004162.2	Chikungunya virus complete genome
NC 015692.1	Colobus guereza papillomavirus type 2 complete genome
NC 004181.1	Colorado tick fever virus segment 1 complete sequence
NC 004189.1	Colorado tick fever virus segment 10 complete sequence
NC 004191.1	Colorado tick fever virus segment 11 complete sequence
NC 004190.1	Colorado tick fever virus segment 12 complete sequence
NC 004182.1	Colorado tick fever virus segment 2 complete sequence
NC 004183.1	Colorado tick fever virus segment 3 complete sequence
NC 004184.1	Colorado tick fever virus segment 4 complete sequence
NC 004185.1	Colorado tick fever virus segment 5 complete sequence
NC 004186.1	Colorado tick fever virus segment 6 complete sequence
NC 004187.1	Colorado tick fever virus segment 7 complete sequence
NC 004188.1	Colorado tick fever virus segment 8 complete sequence
NC 004180.1	Colorado tick fever virus segment 9 complete sequence
NC 014372.1	Cote d'Ivoire ebolavirus
NC 005301.3	Crimean-Congo hemorrhagic fever virus segment L complete sequence
NC 005300.2	Crimean-Congo hemorrhagic fever virus segment M complete sequence
NC 005302.1	Crimean-Congo hemorrhagic fever virus segment S complete sequence
NC 008604.2	Culex flavivirus complete genome
NC 010252.1	Cupixi virus segment L complete sequence
NC 010254.1	Cupixi virus segment S complete sequence
NC 015521.1	Cutthroat trout virus complete genome
NC 001477.1	Dengue virus 1 complete genome
NC 001474.2	Dengue virus 2 complete genome
NC 001475.2	Dengue virus 3 complete genome
NC 002640.1	Dengue virus 4 complete genome
NC 005234.1	Dobrava virus segment M complete sequence
NC 005233.1	Dobrava virus segment S complete sequence
NC 005235.1	Dobrava-Belgrade virus strain DOBV/Ano-Poroia/Afl9/1999
NC 005283.1	Dolphin morbillivirus complete genome

NC 016997.1	Donggang virus complete genome
NC 004159.1	Dugbe virus segment L complete sequence
NC 004158.1	Dugbe virus segment M complete sequence
NC 004157.1	Dugbe virus segment S complete sequence
NC 020810.1	Duvenhage virus isolate 86132SA complete genome
NC 002549.1	Ebola virus - Mayinga Zaire 1976 strain Mayinga
NC 008718.1	Entebbe bat virus complete genome
NC 009527.1	European bat lyssavirus 1 complete genome
NC 009528.1	European bat lyssavirus 2 complete genome
NC 003696.1	Eyach virus segment 1 complete genome
NC 003705.1	Eyach virus segment 10 complete genome
NC 003706.1	Eyach virus segment 11 complete genome
NC 003707.1	Eyach virus segment 12 complete genome
NC 003697.1	Eyach virus segment 2 complete genome
NC 003698.1	Eyach virus segment 3 complete genome
NC 003699.1	Eyach virus segment 4 complete genome
NC 003700.1	Eyach virus segment 5 complete genome
NC 003701.1	Eyach virus segment 6 complete genome
NC 003702.1	Eyach virus segment 7 complete genome
NC 003703.1	Eyach virus segment 8 complete genome
NC 003704.1	Eyach virus segment 9 complete genome
NC 005084.2	Fer-de-lance virus complete genome
NC 010759.1	Flexal virus segment L complete sequence
NC 010757.1	Flexal virus segment S complete sequence
NC 001362.1	Friend murine leukemia virus complete genome
NC 001710.1	GB virus C/Hepatitis G virus complete genome
NC 018482.1	Golden Gate virus segment L complete genome
NC 018483.1	Golden Gate virus segment S complete genome
NC 005036.1	Goose paramyxovirus SF02 complete genome
NC 014522.1	Great Island virus segment 1 complete genome

NC 014531.1	Great Island virus segment 10 complete genome
NC 014523.1	Great Island virus segment 2 complete genome
NC 014524.1	Great Island virus segment 3 complete genome
NC 014525.1	Great Island virus segment 4 complete genome
NC 014526.1	Great Island virus segment 5 complete genome
NC 014527.1	Great Island virus segment 6 complete genome
NC 014528.1	Great Island virus segment 7 complete genome
NC 014529.1	Great Island virus segment 8 complete genome
NC 014530.1	Great Island virus segment 9 complete genome
NC 005082.1	Guanarito virus segment L complete genome
NC 005077.1	Guanarito virus segment S complete genome
NC 005218.1	Hantaan virus complete genome
NC 005219.1	Hantaan virus complete genome
NC 005222.1	Hantaan virus segment L complete genome
NC 006435.1	Hantavirus Z10 chromosome L complete genome
NC 006433.1	Hantavirus Z10 chromosome S segment complete genome
NC 006437.1	Hantavirus Z10 segment M complete genome
NC 001906.3	Hendra virus complete genome
NC 003977.1	Hepatitis B virus complete genome
NC 004102.1	Hepatitis C virus genotype 1 complete genome
NC 009823.1	Hepatitis C virus genotype 2 complete genome
NC 009824.1	Hepatitis C virus genotype 3 genome
NC 009825.1	Hepatitis C virus genotype 4 genome
NC 009826.1	Hepatitis C virus genotype 5 genome
NC 009827.1	Hepatitis C virus genotype 6 complete genome
NC 001653.2	Hepatitis delta virus complete genome
NC 001434.1	Hepatitis E virus complete genome
NC 012959.1	Human adenovirus 54 complete genome
NC 001460.1	Human adenovirus A complete genome
NC 011203.1	Human adenovirus B1 complete genome

NC 011202.1	Human adenovirus B2 complete genome
NC 001405.1	Human adenovirus C complete genome
NC 010956.1	Human adenovirus D complete genome
NC 003266.2	Human adenovirus E complete genome
NC 001454.1	Human adenovirus F complete genome
NC 001943.1	Human astrovirus complete genome
NC 007455.1	Human bocavirus complete genome
NC 012042.1	Human bocavirus 2 complete genome
NC 012564.1	Human bocavirus 3 complete genome
NC 012729.2	Human bocavirus 4 complete genome
NC 002645.1	Human coronavirus 229E complete genome
NC 006577.2	Human coronavirus HKU1 complete genome
NC 005831.2	Human coronavirus NL63 complete genome
NC 005147.1	Human coronavirus OC43 complete genome
NC 022518.1	Human endogenous retrovirus K113 complete genome
NC 012950.1	Human enteric coronavirus strain 4408 complete genome
NC 001612.1	Human enterovirus A complete genome
NC 001472.1	Human enterovirus B complete genome
NC 001430.1	Human enterovirus D complete genome
NC 004295.1	Human erythrovirus V9 complete genome
NC 001806.1	Human herpesvirus 1 complete genome
NC 001798.1	Human herpesvirus 2 complete genome
NC 001348.1	Human herpesvirus 3 complete genome
NC 007605.1	Human herpesvirus 4 Type 1
NC 009334.1	Human herpesvirus 4 Type 2
NC 006273.2	Human herpesvirus 5 strain Merlin complete genome
NC 001664.2	Human herpesvirus 6A complete genome
NC 000898.1	Human herpesvirus 6B complete genome
NC 001716.2	Human herpesvirus 7 complete genome
NC 009333.1	Human herpesvirus 8 complete genome

NC 001802.1	Human immunodeficiency virus 1 complete genome
NC 001722.1	Human immunodeficiency virus 2 complete genome
NC 004148.2	Human metapneumovirus complete genome
HPV1REF	Human papillomavirus 1
HPV2REF	Human papillomavirus 2
HPV3REF	Human papillomavirus 3
HPV4REF	Human papillomavirus 4
HPV5REF	Human papillomavirus 5
HPV6REF	Human papillomavirus 6
HPV7REF	Human papillomavirus 7
HPV8REF	Human papillomavirus 8
HPV9REF	Human papillomavirus 9
HPV10REF	Human papillomavirus 10
HPV11REF	Human papillomavirus 11
HPV12REF	Human papillomavirus 12
HPV13REF	Human papillomavirus 13
HPV14REF	Human papillomavirus 14
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HPV18REF	Human papillomavirus 18
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HPV70REF	Human papillomavirus 70
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HPV90REF	Human papillomavirus 90
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HPV153REF	Human papillomavirus 153

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HPV165REF	Human papillomavirus 165
HPV166REF	Human papillomavirus 166
HPV169REF	Human papillomavirus 169
HPV170REF	Human papillomavirus 170
NC 003461.1	Human parainfluenza virus 1 complete genome
NC 003443.1	Human parainfluenza virus 2 complete genome
NC 001796.2	Human parainfluenza virus 3 complete genome
NC 021928.1	Human parainfluenza virus 4a viral cRNA complete genome strain: M-25
NC 000883.2	Human parvovirus B19 complete genome
NC 007026.1	Human picobirnavirus RNA segment 1 complete sequence
NC 007027.1	Human picobirnavirus RNA segment 2 complete sequence
NC 001781.1	Human respiratory syncytial virus complete genome
NC 001490.1	Human rhinovirus 14 complete genome
NC 001617.1	Human rhinovirus 89 complete genome
NC 021545.1	Human rotavirus B strain Bang373 inner capsid protein (VP2) gene complete cds
NC 021544.1	Human rotavirus B strain Bang373 inner capsid protein (VP6) gene complete cds
NC 021548.1	Human rotavirus B strain Bang373 nonstructural protein (NSP2) gene complete cds
NC 021547.1	Human rotavirus B strain Bang373 nonstructural protein (NSP3) gene complete cds
NC 021550.1	Human rotavirus B strain Bang373 nonstructural protein (NSP4) gene complete cds
NC 021549.1	Human rotavirus B strain Bang373 nonstructural protein (NSP5) gene complete cds

NC 021546.1	Human rotavirus B strain Bang373 nonstructural protein 1-1 (NSP1-1) nonstructural protein 1-2 (NSP1-2) and nonstructural protein 1-3 (NSP1-3) genes complete cds
NC 021543.1	Human rotavirus B strain Bang373 outer capsid protein (VP4) gene complete cds
NC 021542.1	Human rotavirus B strain Bang373 outer capsid protein (VP7) gene complete cds
NC 021541.1	Human rotavirus B strain Bang373 RNA dependent RNA polymerase (VP1) mRNA complete cds
NC 021551.1	Human rotavirus B strain Bang373 VP3 (VP3) mRNA complete cds
NC 001436.1	Human T-lymphotropic virus 1 complete genome
NC 001488.1	Human T-lymphotropic virus 2 complete genome
NC 011800.1	Human T-lymphotropic virus 4 complete genome
NC 018629.1	Ikoma lyssavirus complete genome
NC 009028.2	Ilheus virus complete genome
NC 007357.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) complete genome
NC 007359.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) complete genome
NC 007360.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) complete genome
NC 007364.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) complete genome
NC 007358.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) segment 2 complete sequence
NC 007362.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) segment 4 complete sequence
NC 007361.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) strain A/Goose/Guangdong/1/96(H5N1)
NC 007363.1	Influenza A virus (A/Goose/Guangdong/1/96(H5N1)) strain A/Goose/Guangdong/1/96(H5N1)
NC 004905.2	Influenza A virus (A/Hong Kong/1073/99(H9N2)) complete genome
NC 004910.1	Influenza A virus (A/Hong Kong/1073/99(H9N2)) segment 1 complete sequence
NC 004911.1	Influenza A virus (A/Hong Kong/1073/99(H9N2)) segment 2 complete sequence
NC 004912.1	Influenza A virus (A/Hong Kong/1073/99(H9N2)) segment 3 complete sequence
NC 004908.1	Influenza A virus (A/Hong Kong/1073/99(H9N2)) segment 4 complete sequence
NC 004909.1	Influenza A virus (A/Hong Kong/1073/99(H9N2)) segment 6 complete sequence
NC 004907.1	Influenza A virus (A/Hong Kong/1073/99(H9N2)) segment 7 complete sequence
NC 004906.1	Influenza A virus (A/Hong Kong/1073/99(H9N2)) segment 8 complete sequence
NC 007378.1	Influenza A virus (A/Korea/426/1968(H2N2)) complete genome
NC 007375.1	Influenza A virus (A/Korea/426/68(H2N2)) segment 2 complete sequence
NC 007376.1	Influenza A virus (A/Korea/426/68(H2N2)) segment 3 complete sequence

NC 007374.1	Influenza A virus (A/Korea/426/68(H2N2)) segment 4 complete sequence
NC 007381.1	Influenza A virus (A/Korea/426/68(H2N2)) segment 5 complete sequence
NC 007382.1	Influenza A virus (A/Korea/426/68(H2N2)) segment 6 complete sequence
NC 007377.1	Influenza A virus (A/Korea/426/68(H2N2)) segment 7 complete sequence
NC 007380.1	Influenza A virus (A/Korea/426/68(H2N2)) segment 8 complete sequence
NC 007373.1	Influenza A virus (A/New York/392/2004(H3N2)) segment 1 complete sequence
NC 007372.1	Influenza A virus (A/New York/392/2004(H3N2)) segment 2 complete sequence
NC 007366.1	Influenza A virus (A/New York/392/2004(H3N2)) segment 4 complete sequence
NC 007369.1	Influenza A virus (A/New York/392/2004(H3N2)) segment 5 complete sequence
NC 007368.1	Influenza A virus (A/New York/392/2004(H3N2)) segment 6 complete sequence
NC 007367.1	Influenza A virus (A/New York/392/2004(H3N2)) segment 7 complete sequence
NC 007370.1	Influenza A virus (A/New York/392/2004(H3N2)) segment 8 complete sequence
NC 007371.1	Influenza A virus (A/New York/392/2004(H3N2)) strain A/New York/392/2004
NC 002023.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 1 complete sequence
NC 002021.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 2 complete sequence
NC 002022.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 3 complete sequence
NC 002017.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 4 complete sequence
NC 002019.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 5 complete sequence
NC 002018.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 6 complete sequence
NC 002016.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 7 complete sequence
NC 002020.1	Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 8 complete sequence
NC 002207.1	Influenza B virus RNA 4 complete sequence
NC 002208.1	Influenza B virus RNA 5 complete sequence
NC 002209.1	Influenza B virus RNA 6 complete sequence
NC 002210.1	Influenza B virus RNA 7 complete sequence
NC 002211.1	Influenza B virus RNA 8 complete sequence
NC 002205.1	Influenza B virus RNA-2 complete sequence
NC 002206.1	Influenza B virus RNA-3 complete sequence
NC 006307.1	Influenza C virus (C/Ann Arbor/1/50) segment 1 partial sequence
NC 006308.1	Influenza C virus (C/Ann Arbor/1/50) segment 2 complete sequence

NC 006309.1	Influenza C virus (C/Ann Arbor/1/50) segment 3 complete sequence
NC 006310.1	Influenza C virus (C/Ann Arbor/1/50) segment 4 complete sequence
NC 006311.1	Influenza C virus (C/Ann Arbor/1/50) segment 5 complete sequence
NC 006312.1	Influenza C virus (C/Ann Arbor/1/50) segment 6 complete sequence
NC 006306.2	Influenza C virus (C/Ann Arbor/1/50) segment 7 complete genome
NC 007906.1	Ippy virus segment L complete sequence
NC 007905.1	Ippy virus segment S complete sequence
NC 020809.1	Irkut virus complete genome
NC 007454.1	J-virus complete genome
NC 001437.1	Japanese encephalitis virus genome
NC 001699.1	JC polyomavirus complete genome
NC 005080.1	Junin virus segment L complete genome
NC 005081.1	Junin virus segment S complete genome
NC 004210.1	Kadipiro virus chromosome segment 1 complete genome
NC 004206.1	Kadipiro virus chromosome segment 10 complete genome
NC 004199.1	Kadipiro virus chromosome segment 12 complete genome
NC 004212.1	Kadipiro virus chromosome segment 2 complete genome
NC 004213.1	Kadipiro virus chromosome segment 3 complete genome
NC 004214.1	Kadipiro virus chromosome segment 4 complete genome
NC 004215.1	Kadipiro virus chromosome segment 5 complete genome
NC 004216.1	Kadipiro virus chromosome segment 6 complete genome
NC 004208.1	Kadipiro virus chromosome segment 8 complete genome
NC 004207.1	Kadipiro virus chromosome segment 9 complete genome
NC 004205.1	Kadipiro virus segment 11 complete sequence
NC 004209.1	Kadipiro virus segment 7 complete genome
NC 005064.1	Kamiti River virus complete genome
NC 006947.1	Karshi virus complete genome
NC 012533.1	Kedougou virus complete genome
NC 009238.1	KI polyomavirus Stockholm 60 complete genome
NC 009029.2	Kokobera virus complete genome

NC 004108.1	La Crosse virus segment L complete genome
NC 004109.1	La Crosse virus segment M complete genome
NC 004110.1	La Crosse virus segment S complete genome
NC 020807.1	Lagos bat virus isolate 0406SEN complete genome
NC 001608.3	Lake Victoria marburgvirus - Musoke complete genome
NC 003690.1	Langat virus complete genome
NC 004297.1	Lassa virus segment L complete sequence
NC 004296.1	Lassa virus segment S complete sequence
NC 010760.1	Latino virus segment L complete sequence
NC 010758.1	Latino virus segment S complete sequence
NC 007736.1	Liao ning virus segment 1 complete genome
NC 007745.1	Liao ning virus segment 10 complete genome
NC 007746.1	Liao ning virus segment 11 complete genome
NC 007747.1	Liao ning virus segment 12 complete genome
NC 007737.1	Liao ning virus segment 2 complete genome
NC 007738.1	Liao ning virus segment 3 complete genome
NC 007739.1	Liao ning virus segment 4 complete genome
NC 007740.1	Liao ning virus segment 5 complete genome
NC 007741.1	Liao ning virus segment 6 complete genome
NC 007742.1	Liao ning virus segment 7 complete genome
NC 007743.1	Liao ning virus segment 8 complete genome
NC 007744.1	Liao ning virus segment 9 complete genome
NC 016144.1	Lloviu virus complete genome
NC 001809.1	Louping ill virus complete genome
NC 012777.1	Lujo virus segment L complete genome
NC 012776.1	Lujo virus segment S complete genome
NC 016153.1	Luna virus segment L complete genome
NC 016152.1	Luna virus segment S complete genome
NC 018711.1	Lunk virus NKS-1 segment L complete genome
NC 018710.1	Lunk virus NKS-1 segment S complete genome

NC 004291.1	Lymphocytic choriomeningitis virus segment L complete sequence
NC 004294.1	Lymphocytic choriomeningitis virus segment S complete sequence
NC 015691.1	Macaca fascicularis papillomavirus type 2 complete genome
NC 005079.1	Machupo virus segment L complete genome
NC 005078.1	Machupo virus segment S complete genome
NC 009489.1	Mapuera virus complete genome
NC 003417.1	Mayaro virus complete genome
NC 001498.1	Measles virus complete genome
NC 007620.1	Menangle virus complete genome
NC 010277.1	Merkel cell polyomavirus complete genome
NC 007904.1	Mobala virus segment L complete sequence
NC 007903.1	Mobala virus segment S complete sequence
NC 003635.1	Modoc virus complete genome
NC 006429.1	Mokola virus complete genome
NC 001501.1	Moloney murine leukemia virus complete genome
NC 004119.1	Montana myotis leukoencephalitis virus complete genome
NC 006572.1	Mopeia Lassa reassortant 29 segment L complete genome
NC 006573.1	Mopeia Lassa reassortant 29 segment S complete genome
NC 006574.1	Mopeia virus AN20410 segment L complete genome
NC 006575.1	Mopeia virus AN20410 segment S complete genome
NC 013058.1	Morogoro virus segment L complete genome
NC 013057.1	Morogoro virus segment S complete genome
NC 021069.1	Mosquito flavivirus isolate LSFlaviV-A20-09 complete genome
NC 005339.1	Mossman virus complete genome
NC 001503.1	Mouse mammary tumor virus complete genome
NC 002200.1	Mumps virus complete genome
NC 001702.1	Murine type C retrovirus complete genome
NC 000943.1	Murray Valley encephalitis virus complete genome
NC 017937.1	Nariva virus complete genome
NC 002617.1	Newcastle disease virus B1 complete genome

NC 002728.1	Nipah virus complete genome
NC 001959.2	Norwalk virus complete genome
NC 018705.3	Ntaya virus isolate IPDIA complete genome
NC 001512.1	O nyong-nyong virus complete genome
NC 010250.1	Oliveros virus segment L complete sequence
NC 010248.1	Oliveros virus segment S complete sequence
NC 005062.1	Omsk hemorrhagic fever virus complete genome
NC 005776.1	Oropouche virus segment L complete genome
NC 005775.1	Oropouche virus segment M complete sequence
NC 005777.1	Oropouche virus segment S complete genome
NC 006430.1	Parainfluenza virus 5 complete genome
NC 010761.1	Parana virus segment L complete sequence
NC 010756.1	Parana virus segment S (small) complete genome
NC 006383.2	Peste-des-petits-ruminants virus complete genome
NC 006447.1	Pichinde virus complete genome
NC 006439.1	Pichinde virus L RNA complete genome
NC 005897.1	Pirital virus segment L complete genome
NC 005894.1	Pirital virus segment S complete sequence
NC 006579.1	Pneumonia virus of mice J3666 complete genome
NC 002058.3	Poliovirus complete genome
NC 000940.1	Porcine enteric sapovirus complete genome
NC 009640.1	Porcine rubulavirus complete genome
NC 003687.1	Powassan virus complete genome
NC 005225.1	Puumala virus segment L complete genome
NC 005223.1	Puumala virus segment M complete sequence
NC 005224.1	Puumala virus segment S complete sequence
NC 012671.1	Quang Binh virus complete genome
NC 001542.1	Rabies virus complete genome
NC 001819.1	Rauscher murine leukemia virus complete genome
NC 022630.1	Razdan virus strain LEIV-Arm2741 segment L complete sequence

NC 022631.1	Razdan virus strain LEIV-Arm2741 segment M complete sequence
NC 022632.1	Razdan virus strain LEIV-Arm2741 segment S complete sequence
NC 001803.1	Respiratory syncytial virus complete genome
NC 004161.1	Reston ebolavirus complete genome
NC 014397.1	Rift Valley fever virus segment L complete genome
NC 014396.1	Rift Valley fever virus segment M complete genome
NC 014395.1	Rift Valley fever virus segment S complete genome
NC 006296.2	Rinderpest virus (strain Kabete O) complete genome
NC 003675.1	Rio Bravo virus genome
NC 021153.1	Rodent hepacivirus isolate RHV-339 complete genome
NC 001544.1	Ross River virus complete genome
NC 011507.2	Rotavirus A segment 1 complete genome
NC 011504.2	Rotavirus A segment 10 complete genome
NC 011505.2	Rotavirus A segment 11 complete genome
NC 011506.2	Rotavirus A segment 2 complete genome
NC 011508.2	Rotavirus A segment 3 complete genome
NC 011510.2	Rotavirus A segment 4 complete genome
NC 011500.2	Rotavirus A segment 5 complete genome
NC 011509.2	Rotavirus A segment 6 complete genome
NC 011501.2	Rotavirus A segment 7 complete genome
NC 011502.2	Rotavirus A segment 8 complete genome
NC 011503.2	Rotavirus A segment 9 complete genome
NC 007547.1	Rotavirus C segment 1 complete sequence
NC 007569.1	Rotavirus C segment 10 complete sequence
NC 007573.1	Rotavirus C segment 11 complete sequence
NC 007546.1	Rotavirus C segment 2 complete sequence
NC 007572.1	Rotavirus C segment 3 complete sequence
NC 007574.1	Rotavirus C segment 4 complete sequence
NC 007570.1	Rotavirus C segment 5 complete sequence
NC 007543.1	Rotavirus C segment 6 complete sequence

NC 007544.1	Rotavirus C segment 7 complete sequence
NC 007571.1	Rotavirus C segment 8 complete sequence
NC 007545.1	Rotavirus C segment 9 complete sequence
NC 021625.1	Rotavirus F chicken/03V0568/DEU/2003 segment 1 complete sequence
NC 021629.1	Rotavirus F chicken/03V0568/DEU/2003 segment 10 complete sequence
NC 021634.1	Rotavirus F chicken/03V0568/DEU/2003 segment 11 complete sequence
NC 021626.1	Rotavirus F chicken/03V0568/DEU/2003 segment 2 complete sequence
NC 021631.1	Rotavirus F chicken/03V0568/DEU/2003 segment 3 complete sequence
NC 021630.1	Rotavirus F chicken/03V0568/DEU/2003 segment 4 complete sequence
NC 021632.1	Rotavirus F chicken/03V0568/DEU/2003 segment 5 complete sequence
NC 021635.1	Rotavirus F chicken/03V0568/DEU/2003 segment 6 complete sequence
NC 021633.1	Rotavirus F chicken/03V0568/DEU/2003 segment 7 complete sequence
NC 021628.1	Rotavirus F chicken/03V0568/DEU/2003 segment 8 complete sequence
NC 021627.1	Rotavirus F chicken/03V0568/DEU/2003 segment 9 complete sequence
NC 021590.1	Rotavirus G chicken/03V0567/DEU/2003 segment 1 complete sequence
NC 021586.1	Rotavirus G chicken/03V0567/DEU/2003 segment 10 complete sequence
NC 021587.1	Rotavirus G chicken/03V0567/DEU/2003 segment 11 complete sequence
NC 021580.1	Rotavirus G chicken/03V0567/DEU/2003 segment 2 complete sequence
NC 021581.1	Rotavirus G chicken/03V0567/DEU/2003 segment 3 complete sequence
NC 021589.1	Rotavirus G chicken/03V0567/DEU/2003 segment 4 complete sequence
NC 021583.1	Rotavirus G chicken/03V0567/DEU/2003 segment 5 complete sequence
NC 021588.1	Rotavirus G chicken/03V0567/DEU/2003 segment 6 complete sequence
NC 021585.1	Rotavirus G chicken/03V0567/DEU/2003 segment 7 complete sequence
NC 021584.1	Rotavirus G chicken/03V0567/DEU/2003 segment 8 complete sequence
NC 021582.1	Rotavirus G chicken/03V0567/DEU/2003 segment 9 complete sequence
NC 001545.2	Rubella virus complete genome
NC 006317.1	Sabia virus complete genome
NC 006313.1	Sabia virus segment L complete genome
NC 015412.1	Sandfly Sicilian Turkey virus segment L complete genome
NC 015411.1	Sandfly Sicilian Turkey virus segment M complete genome

NC 015413.1	Sandfly Sicilian Turkey virus segment S complete genome
NC 006554.1	Sapovirus C12 strain C12
NC 006269.1	Sapovirus Hu/Dresden/pJG-Sap01/DE complete genome
NC 010624.1	Sapovirus Mc10 complete genome
NC 004718.3	SARS coronavirus complete genome
NC 018466.1	Sathuperi virus Gn-Gc-NSm gene for M polyprotein segment M genomic RNA
NC 018462.1	Sathuperi virus N and NSs genes segment S genomic RNA
NC 018461.1	Sathuperi virus RdRp gene for RNA-dependent RNA polymerase segment L genomic RNA
NC 015212.1	Seal anellovirus TFFN/USA/2006 complete genome
NC 001552.1	Sendai virus complete genome
NC 005237.1	Seoul virus segment M complete sequence
NC 005236.1	Seoul virus strain 80-39 segment S complete sequence
NC 005238.1	Seoul virus strain Seoul 80-39 clone 1
NC 008719.1	Sepik virus complete genome
NC 018136.1	SFTS virus HB29 segment L complete genome
NC 018138.1	SFTS virus HB29 segment M complete genome
NC 018137.1	SFTS virus HB29 segment S complete genome
NC 018467.1	Shamonda virus Gn-Gc-NSm gene for M polyprotein segment M genomic RNA isolate Ib An 5550
NC 018464.1	Shamonda virus N and NSs genes segment S genomic RNA isolate Ib An 5550
NC 018463.1	Shamonda virus RdRp gene for RNA-dependent RNA polymerase segment L genomic RNA isolate Ib An 5550
NC 018478.1	Simbu virus Gn-Gc-NSm gene for M polyprotein segment M genomic RNA isolate SA Ar 53
NC 018477.1	Simbu virus N and NSs genes segment S genomic RNA isolate SA Ar 53
NC 018476.1	Simbu virus RdRp gene for RNA-dependent RNA polymerase segment L genomic RNA isolate SA Ar 53
NC 001669.1	Simian virus 40 complete genome
NC 006428.1	Simian virus 41 complete genome
NC 005217.1	Sin Nombre virus segment L complete sequence
NC 005215.1	Sin Nombre virus segment M complete sequence
NC 005216.1	Sin Nombre virus segment S complete sequence
NC 007013.1	Small anellovirus 1 complete genome
NC 007014.1	Small anellovirus 2 complete genome

NC 007580.2	St. Louis encephalitis virus complete genome
NC 006432.1	Sudan ebolavirus complete genome
NC 004292.1	Tacaribe virus segment L complete sequence
NC 004293.1	Tacaribe virus segment S complete sequence
NC 003996.1	Tamana bat virus genome
NC 010702.1	Tamiami virus segment L complete sequence
NC 010701.1	Tamiami virus segment S (small) complete genome
NC 015843.2	Tembusu virus strain JS804 complete genome
NC 006495.1	Thogoto virus
NC 006496.1	Thogoto virus
NC 006506.1	Thogoto virus complete genome
NC 006508.1	Thogoto virus segment 1 complete genome
NC 006507.1	Thogoto virus segment 5 complete genome
NC 006504.1	Thogoto virus segment 6 complete genome
NC 010707.1	Thottapalayam virus segment L complete sequence
NC 010708.1	Thottapalayam virus segment M complete sequence
NC 010704.1	Thottapalayam virus segment S complete sequence
NC 001672.1	Tick-borne encephalitis virus complete genome
NC 004074.1	Tioman virus complete genome
NC 014071.1	Torque teno canis virus complete genome
NC 014087.1	Torque teno douroucouli virus complete genome
NC 014072.1	Torque teno felis virus complete genome
NC 009225.1	Torque teno midi virus 1 complete genome
NC 014093.1	Torque teno midi virus 2 complete genome
NC 014097.1	Torque teno mini virus 1 complete genome
NC 014086.1	Torque teno mini virus 2 complete genome
NC 014088.1	Torque teno mini virus 3 complete genome
NC 014090.1	Torque teno mini virus 4 complete genome
NC 014089.1	Torque teno mini virus 5 complete genome
NC 014095.1	Torque teno mini virus 6 complete genome

NC 014082.1	Torque teno mini virus 7 complete genome
NC 014068.1	Torque teno mini virus 8 complete genome
NC 002195.1	Torque teno mini virus 9 complete genome
NC 014070.1	Torque teno sus virus 1 complete genome
NC 014092.2	Torque teno sus virus k2 isolate 2p complete genome
NC 014085.1	Torque teno tamarin virus complete genome
NC 015783.1	Torque teno virus complete genome
NC 002076.2	Torque teno virus 1 complete genome
NC 014076.1	Torque teno virus 10 complete genome
NC 014075.1	Torque teno virus 12 complete genome
NC 014077.1	Torque teno virus 14 complete genome
NC 014096.1	Torque teno virus 15 complete genome
NC 014091.1	Torque teno virus 16 complete genome
NC 014078.1	Torque teno virus 19 complete genome
NC 014480.2	Torque teno virus 2 complete genome
NC 014083.1	Torque teno virus 25 complete genome
NC 014079.1	Torque teno virus 26 complete genome
NC 014074.1	Torque teno virus 27 complete genome
NC 014073.1	Torque teno virus 28 complete genome
NC 014081.1	Torque teno virus 3 complete genome
NC 014069.1	Torque teno virus 4 complete genome
NC 014094.1	Torque teno virus 6 complete genome
NC 014080.1	Torque teno virus 7 complete genome
NC 014084.1	Torque teno virus 8 complete genome
NC 006319.1	Toscana virus segment L complete sequence
NC 006320.1	Toscana virus segment M complete sequence
NC 006318.1	Toscana virus segment S complete sequence
NC 020498.1	TTV-like mini virus isolate TTMV LY1 complete genome
NC 005226.1	Tula virus segment L complete sequence
NC 005228.1	Tula virus segment M complete sequence

NC 005227.2	Tula virus segment S complete genome
NC 002199.1	Tupaia paramyxovirus complete genome
NC 006551.1	Usutu virus complete genome
NC 005221.1	Uukuniemi virus complete genome
NC 005220.1	Uukuniemi virus chromosome segment M complete genome
NC 005214.1	Uukuniemi virus segment L complete sequence
NC 006998.1	Vaccinia virus complete genome
NC 001611.1	Variola virus complete genome
NC 001560.1	Vesicular stomatitis Indiana virus complete genome
NC 012735.1	Wesselsbron virus complete genome
NC 001563.2	West Nile virus complete genome
NC 009942.1	West Nile virus complete genome
NC 010703.1	Whitewater Arroyo virus segment L complete sequence
NC 010700.1	Whitewater Arroyo virus segment S complete sequence
NC 009539.1	WU Polyomavirus complete genome
NC 002031.1	Yellow fever virus complete genome
NC 005039.1	Yokose virus complete genome
NC 012532.1	Zika virus complete genome
AF221065	MuLV_DG75
	MuLV_JV
U13766	MuLV_MCF1233
HQ246218	MuLV_N417
DQ399707	XMRV_VP62

Table S3. Quantification of HPV-18 genes in NPC cell lines

Gene Name	Hela-1 (%)	Hela-2 (%)	CNE1 (%)	CNE1-JPN (%)	HONE1 (%)
E1	186.1 (15%)	1058.5 (30%)	34.4 (16%)	167.8 (22%)	164.6 (21%)
E2	1.3 (0%)	3.5 (0%)	3.1 (1%)	9.1 (1%)	11.2 (2%)
E4	0.0 (0%)	0.0 (0%)	0.0 (0%)	0.0 (0%)	0.0 (0%)
E5	0.0 (0%)	0.0 (0%)	0.0 (0%)	0.0 (0%)	0.0 (0%)
E6	294.8 (25%)	628.3 (18%)	48.5 (22%)	167.5 (21%)	181.3 (23%)
E7	658.4 (55%)	1798.5 (51%)	96.0 (43%)	393.9 (51%)	403.3 (52%)
L1	56.6 (5%)	14.9 (1%)	39.4 (18%)	37.5 (5%)	18.0 (2%)
L2	0.0 (0%)	0.0 (0%)	0.0 (0%)	0.0 (0%)	0.0 (0%)

Gene expression represented as Transcripts per Million (TPM)