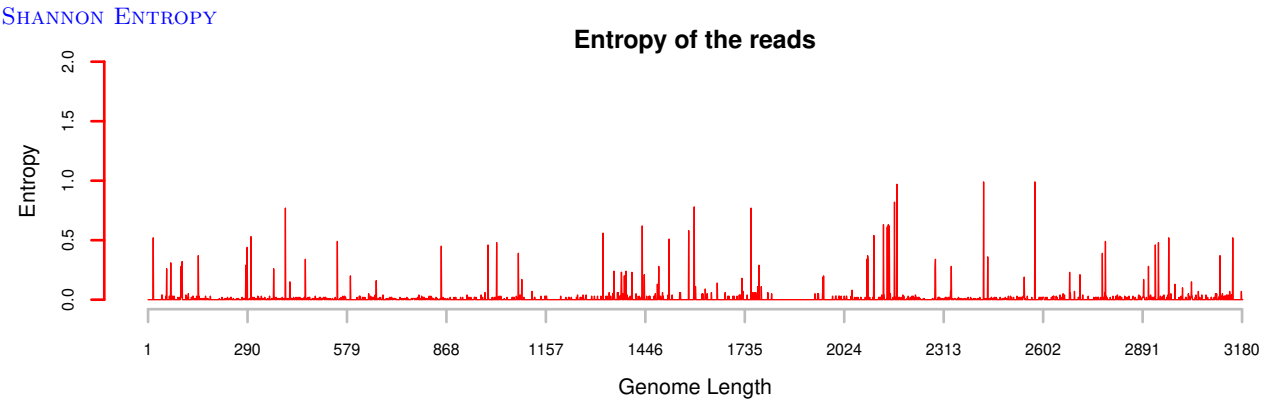
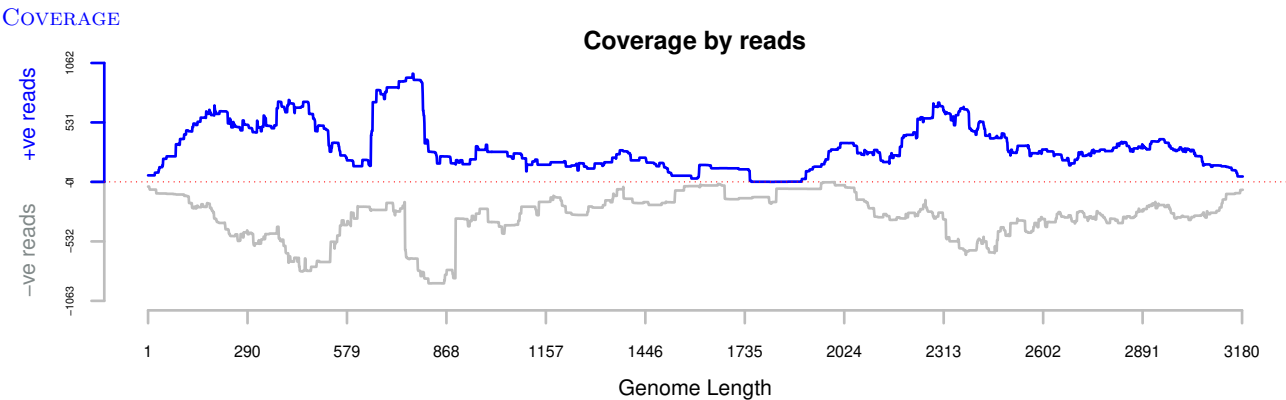


HBV-DMM-27

File name	HBV-DMM-27.sam
Ref name	KX357637.1 Hepatitis B virus isolate MK20ETH, complete genome
Ref len	3182
Program used	Tanoti Assembler 1.0
Total reads	3235628
Mapped reads	13191 (0.41%)
Unmapped reads	3222437
Mapped loan pairs	32
Average read length	146nt
Coverage	3182nt (100.00%)
Average depth	612 reads/site
Average insert length	4nt



CONSENSUS SEQUENCE

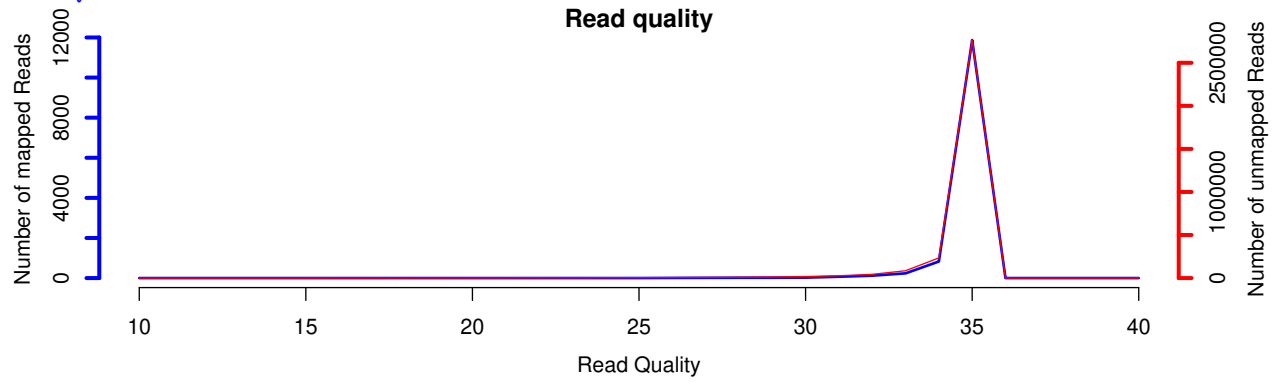
```

1      CTCCACAAC T TCCACCAA CTCTGCAAGA TCCCAGAGTG AAAGGCCTGT ATCTCCCTGC TGGTGGCTCC
70     AATTCAGGAA CAGTAAACCC TGTTCGGACC ACTGTCTCTC ACATATCGTC AATCTTCTCG AGGATTGGGG
140    ACCCTGCGCT GAACATGGAG AACATCACAT CAGGATTCCCT AGGACCCCTG CTCGTGTTAC AGGCGGGGTT
210    TTTCTTGTG ACAAGAATCC TCACAATACC GCAGAGTCTA GACTCGTGGT GGACTTCTCT CAATTTTCTA
280    GGGGGAAC TA CCGTGTGTCT TGGCCAAAAT TCGCAGTCCC CAACCTCCAA TCACTACCA ACCTCCTGTC
350    CTCTAACTTG TCCTGGATAT CGCTGGATGT GTCTGCGGCG TTTTATCATA TTCCTCTTCA TCCTGCTGCT
420    ATGCTCATC TTCTTGTG TTTCTCTGGA CTATCAAGGT ATGTTGCCCC TTTGTCCTCT AATTCCAGGA
490    TCTTCAACCA CCAGCACGGG AACATGCAGA ACCTGCACGA CTCCTGCTCA AGGAACCTCT ATGTATCCCT
560    CCTGTGCTG TACCAAACCT TCGGACGGAA ATTGCACCTG TATTCCTATC CCATCATCCT GGGCTTTCGG
630    AAAATTCCTA TGGGAGTGGG CCTCAGCCCG TTTCTCCTGG CTCAGTTTAC TAGTGCCATT TGTTCACTGG
700    TTCGTAGGGC TTTCCCCC TGTTTGGCTT TCAGTTATAT TGATGATGTG GTATTGGGGG CCAAGTCTGT
770    ACAGCATCTT GAGTCCCTTT TTACCGCTGT TACCAATTTT CTTTTGTCTT TGGGTATACA TTTAAACCTT
840    AACAAAACAA AAAGATGGGG TTAATCTTTA CATTTTCATG GCTATGTCAT TGGAAAGTTAT GGGTCATTGC
910    CACAAGATCA CATCATACAG AAAATCAAAG AATGTTTTTCG AAAACTTCCT GTTAACAGGC CTATTGATTG
980    GAAAGTCTGT CAACGTATTG TGGGTCTTTT GGGTTTTGCT GCCCCTTTTA CACAATGTGG TTATCCTGCT
1050   TTAATGCCCT TGTATGCATG TATTCAATCT AAGCAGGCTT TCACTTTCTC GCCAACTTAC AAGGCCTTTC
1120   TGTGCAAACA ATACCTGAAC CTTTACCCCG TTGCGCGGCA ACGGCCAGGT CTGTGCCAAG TGTTTGCTGA
1190   CGCAACCCCG ACTGGCTGGG GCTTGGTCAT GGGCCATCAG CGCATGCGTG GAACCTTTTT GGTCTCCTCG
1260   CCGATCCATA CTGCGGAACT CCTAGCCGCC TGTTTTGCTC GCAGCAGGTC TGGAGCAAAC ATCCTCGGGA
1330   CAGATAATC TGTTGTCTC TCCCGCAAAT ATACATCGTT TCCATGGCTG CTAGGCTGTG CTGCCAACTG
1400   GATCCTGCGC GGGACGTCTT TGTTTACGT CCCGTGCGCG CTGAATCCCG CGGACGACCC TTCTCGGGGC
1470   CGCTTGGGAC TCTCTCGTCC CTTCTCCGT CTGCCGTTT GACCGACCAC GGGGCGCACC TCTCTTACG
1540   CGGACTCCCC GTCTGTGCCT TCTCATCTGC CGGACCGGT GCACTTCGCT TCACCTCTGC ACGTCGCATG
1610   GAGACCACCG TGAACGCCA CCAATCTTGT CCCAAGGTCT TACATAAGAG GACTCTTGA CTCTCTGTAA
1680   TGTCAACGAG CGACCTTGAG GCATACTTCA AAGACTGTTT GTTTAAGGAC TGGGAGGAGT TGGGGAGGA
1750   GAATAGGTTA ATGATCTTTG TATTAGGAGG CTGTAGGCAT AAATTGGTCT GCGCACCAGC ACCATGCAAC
1820   TTTTTCACCT CTGCCTAATC ATCTCTTGTT CATGTCCTAC TGTTCAGGCC TCCAAGCTGT GCCTTGGGTG
1890   GCTTTGGGAC ATGGACATTG ATCCTTATAA AGAATTTGGA GCTACTGTGG AGTTACTCTC GTTTTTGCCT
1960   TCTGACTTCT TTCCTTCAGT ACGAGATCTT CTAGATACCG CCTCAGCTCT ATATCGGGAA GCCTTAGAGT
2030   CTCCTGAGCA TTGTTACCT CACCATACTG CACTCAGGCA AGCAATCTT TGCTGGGGGG AACTAATGAC
2100   TCTAGCCACT TGGGTGGGTG GTAATTTGGA AGATCCAATA TCCAGGGACC TAGTAGTCAG TTATGTTAAC
2170   ACTAATATGG GCCTAAAGTT CAGACAACTA TTGTGGTTTC ACATTTCTTG TCTCACTTTT GGAAGAGAAA
2240   CGGTCATAGA GTATTTGGTG TCTTTCGGAG TGTGGATTCT CACTCCTCCA GCTTATAGAC CACCAAATGC
2310   CCCTATCTTA TCAACACTTC CGGAGACTAC TGTGTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT
2380   CCCTCGCCTC GCAGACGAAG GTCTCAATCG CCGCGTCGCA GAAGATCTAA ATCTCGGGAA TCTCAATGTT
2450   AGTATTCCTT GGACTCATAA GGTGGGAAAC TTTACGGGGC TTTATTCTTC CACTGTTTCT GTCTTTAACC
2520   CTCATTGGAA AACACCCTCT TTTCTTAATA TACATTTACA CCAAGACATT ATCAAAAAAT GTGAACAATT
2590   TGTAGGCCCA CTCACAGTCA ATGAGAAAAG AAGACTGCAA TTGATTATGC CTGCTAGGTT TTATCCAAAT
2660   GTTACCAAAT ATTTGCCATT GGATAAGGGT ATTAACCTT ATTATCCAGA ACATCTAGTT AATCATTACT
2730   TCCAAACCAG ACATTATTTA CACTCTAT GGAAGGCGGG TATCTTATAT AAGAGAGAAA CAACACGTAG
2800   CGCCTCATTT TGTGGGTCAC CATATTCTTG GGAACAAGAG CTACAGCATG GGGCAGAATC TTTCCACCAG
2870   CAATCCTCTG GGATTCTTTC CCGACCACCA GTTGGATCCA GCCTTCAGAG CAAACACAGC AAATCCGGAT
2940   TGGGACTTCA ATCCCAACAA GGACACCTGG CCAGACGCCA ACAAGGTAGG AGCTGGAGCA TTGGGGCTGG
3010   GATTACCCCC ACCGCACGGA GGCCTTTTGG GGTGGAGCCC TCAGGCTCAG GGCATACTAC AAACCTTGCC
3080   AGCAAATCCG CCTCCTGCCT CCACCAATCG CCAGTCAGGA AGGCAGCCTA CCCCTCTGTC TCCACCTTTG
3150   AGAAACACTC ATCCTCAGGC CATGCACTGG AA

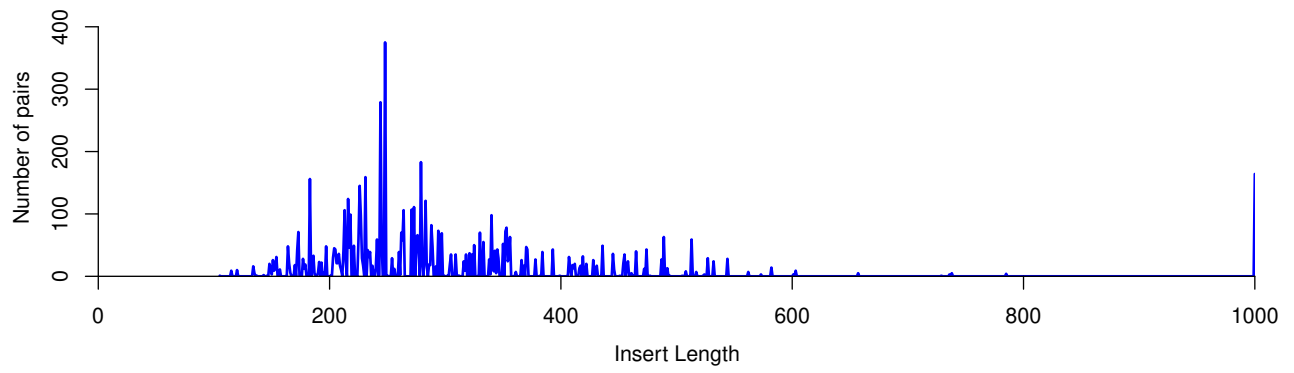
```

Genome Composition	
A	734 (23.07%)
T	903 (28.38%)
G	688 (21.62%)
C	857 (26.93%)
N	0 (0.00%)
Total Nucleotides	3182
GC%	48.55

READ QUALITY



INSERT LENGTH DISTRIBUTION



AMINO ACID VARIATIONS

Protein	Position	Ref AA	Consensus AA	All AAs
---------	----------	--------	--------------	---------

Meta data	
Assembly file:	HBV-DMM-27.sam
Annotation file:	/home3/vatt01s/Work/Project-150-HBV/Data/P150-5/Annotation/HBV.anno
Reference file:	KX357637.fa
User name	ales01a
Hostname	Alpha
Location	/home2/ales01a/HBV/P150-5/HBV-DMM-27
Date/Time	Mon 18 Mar 14:33:13 GMT 2019