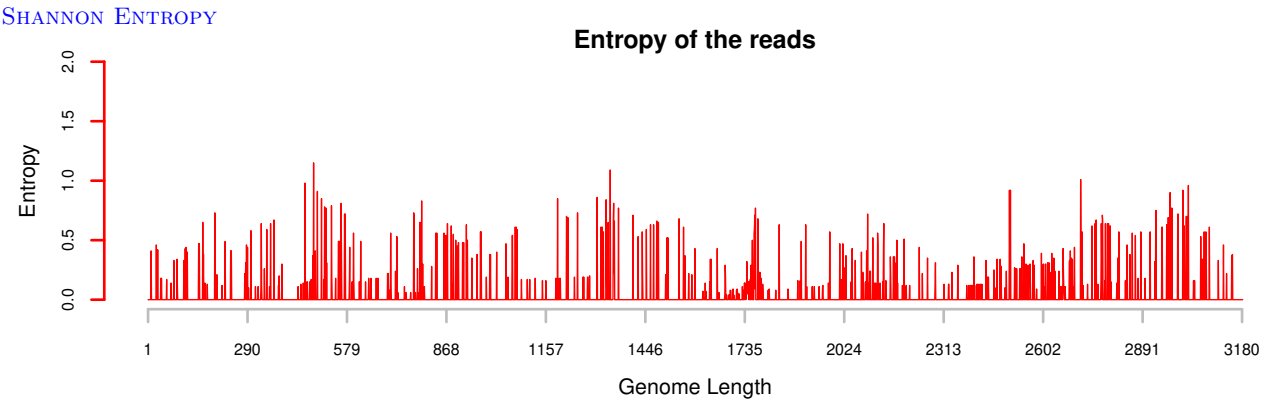
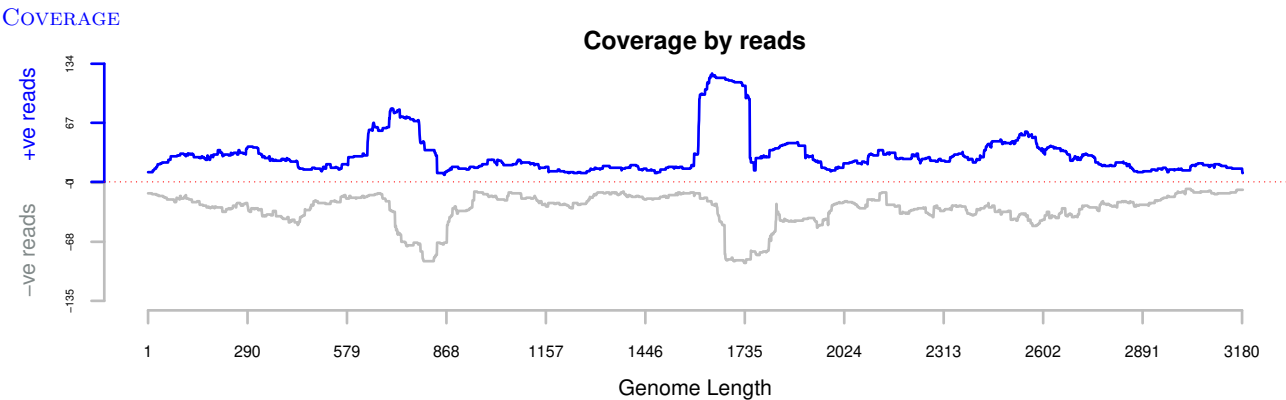


HBV-G-RYD-11

File name	HBV-G-RYD-11.sam
Ref name	KX357637.1 Hepatitis B virus isolate MK20ETH, complete genome
Ref len	3182
Program used	Tanoti Assembler 1.0
Total reads	930314
Mapped reads	1332 (0.14%)
Unmapped reads	928982
Mapped loan pairs	29
Average read length	146nt
Coverage	3182nt (100.00%)
Average depth	60 reads/site
Average insert length	0nt



# CONSENSUS SEQUENCE

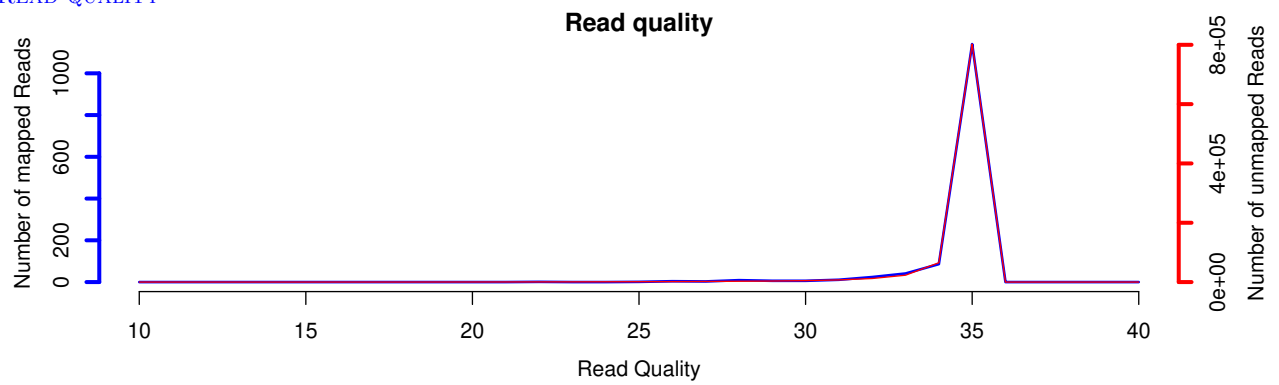
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140    ACCCTGCGCT GAACATGGAG AACATCACAT CAGGATTCCCT AGGACCCCTG CTCGCGTTAC AGGCGGGGTT
210    TTTCTTGTG ACAAGAATCC TCACAATACC GCAGAGTCTA GACTCGTGGT GGACTTCTCT CAATTTTCTA
280    GGGGGAAC TA CCGTGTGTCT TGGCCAAAAT TCGCAGTCCC CAACCTCCAA TCACTCACCA ACCTCCTGTC
350    CTCCAAC TTG TCCTGGTTAT CGCTGGATGT GTCTGCGGCG TTTTATCATC TTCCTCTTCA TCCTGCTGCT
420    ATGCTCATC TTCTTGTG TTTCTCTGGA CTATCACGGT ATGTTGCCCC TTTGTCCTCT ACTTCCAGGA
490    TCTTCAACCA CCAGCACGGG ACCATGCAGA ACCTGCACGA CTCCTGCTCA AGGAACCTCT ATGTATCCCT
560    CCTGTTGCTG TACCAAACCT TCGGACGGAA ATTGCACCTG TATTCCTATC CCATCATCCT GGGCTTTCGG
630    AAAATTCCTA TGGGAGTGGG CCTCAGCCCG TTTCTCCTGG CTCAGTTTAC TAGTGCCATT TGTTCACTGG
700    TTCGTAGGGC TTTCCCCCAC TGTTTGGCTT TCAGTTATAT GGATGATGTG GTATTGGGGG CCAAGTCTGT
770    ACGGCATCTT GAGTCCCTTT TTACCGCTGT TACCAATTTT CTTTTGTCTT TGGGTATACA TTTAAACCTT
840    AACAAAACAA AAAGATGGGG TTA CTCTTTA CATTTTCATG GCTATGTCAT TGGATGTTAT GGGTCATTGC
910    CACAAGATCA CATCATACAG AAAATCAAAG AATGTTTTAG AAAACTTCCT GTTAACAGAC CTATTGATTG
980    GAAAGTCTGT CAACGTATTG TGGGTCTTTT GGGTTTTGCT GCCCCTTTTA CACAATGTGG TTATCCTGCT
1050   TTAATGCCCT TGTATGCATG CATTCAATCT AAGCAGGCTT TCACTTTCTC GCCAACTTAC AAGGCCTTTC
1120   TGTGTAAACA ATACCTGAAC CTTTACCCCG TTGCCCGCA ACGGCCAGGT CTGTGCCAAG TGTTTGTCTG
1190   CGCAACCCCC ACTGGCTGGG GCTTGGTTAT GGGCCATCAG CGCATGCGTG GAACCTTTTT GGTCTCCTCTG
1260   CCGATCCATA CTGCGGAACCT CCTAGCCGCT TGTTTTGTCT GCAGCCGGTC TGGAGCAAAC ATTCTCGGGA
1330   CGGATAATCT TGTGTCTCTC TCCCGCAAAT ATACATCGTT TCCATGGCTG CTAGGCTGTG CTGCCAACTG
1400   GATCCTGCGC GGGACGTCCT TTGTTTACGT CCCGTGCGCG CTGAATCCCG CGGACGACCC TTCTCGGGGC
1470   CGCTTGGGAC TCTCTCGTCC CTTTCTCCGT CTGCCGTTTC GACCGACCAC GGGGCGCACC TCTCTTACG
1540   CGGACTCCCC GTCTGTGCCT TCTCATCTGC CGGACCGTGT GCACTTCGCT TCACCTCTGC ACGTCGCATG
1610   GAGACCACCG TGAACGCCCA CCAATCTTGT CCCAAGGTCT TACATAAGAG GACTCTTGA CTCTCTGTAA
1680   TGTCAACGAG CGACCTTGAG GCATACTTCA AAGACTGTTT GTTTAAAGAC TGGGAGGAGT TGGGGGAGGA
1750   GATTAGATTA AAGGTGTTT TATTAGGAGG CTGTAGGCAT AAATTGGTCT GCGCACCAGC ACCATGCAAC
1820   TTTTTCACCT CTGCCTAATC ATCTCTTGTT CATGTCCTAC TGTTCAGGCC TCCAAGCTGT GCCTTGGGTG
1890   GCTTTGGGGC ATGGACATTG ATCCTTATAA AGAATTTGGA GCTACTGTGG AGTTACTCTC GTTTTTGCCT
1960   TCTGACTTCT TTCCTTCAGT ACGAGATCTT CTAGATACCG CCTCAGCTCT ATATCGGGAA GCCTTAGAGT
2030   CTCCTGAGCA TTGTTACCTT CACCATACTG CACTCAGGCA AGCAATCTT TGCTGGGGGG AACTAATGAC
2100   TCTAGCCACC TGGGTGGGTG GTAATTTGGA AGATCCAATA TCCAGGGACC TAGTAGTCAG TTATGTTAAC
2170   ACTAATATGG GCCTAAAGTT CAGGCAACTA TTGTGGTTTC ACATTCTTG TCTCACTTTT GGAAGAGAAA
2240   CGGTCATAGA GTATTTGGTG TCTTTCGGAG TGTGGATTCT CACTCCTCCA GCTTATAGAC CACCAAATGC
2310   CCCTATCTTA TCAACACTTC CGGAGACTAC TGTTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT
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2450   AGTATTCCTT GGA CTCTATAA GGTGGGCAAC TTTACGGGGC TTTATTCTTC TACGGTTTCT GTCTTTAACC
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2590   TGTAGGCCCA CTCACAGTCA ATGAGAAAAG AAGACTACAA TTGATTATGC CTGCTAGGTT TTATCCAAAT
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2870   CAATCCTCTG GGATTCTTTC CCGACCACCA GTTGGATCCA GCCTTCAGAG CAAACACCGC AAATCCAGAT
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3010   GATTACCCCC ACCACACGGA GGCCTTTTGG GGTGGAGCCC TCAGGCTCAG GGCATACTAC AAACCTTGCC
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3150   AGAAACACTC ATCCTCAGGC CATGCACTGG AA

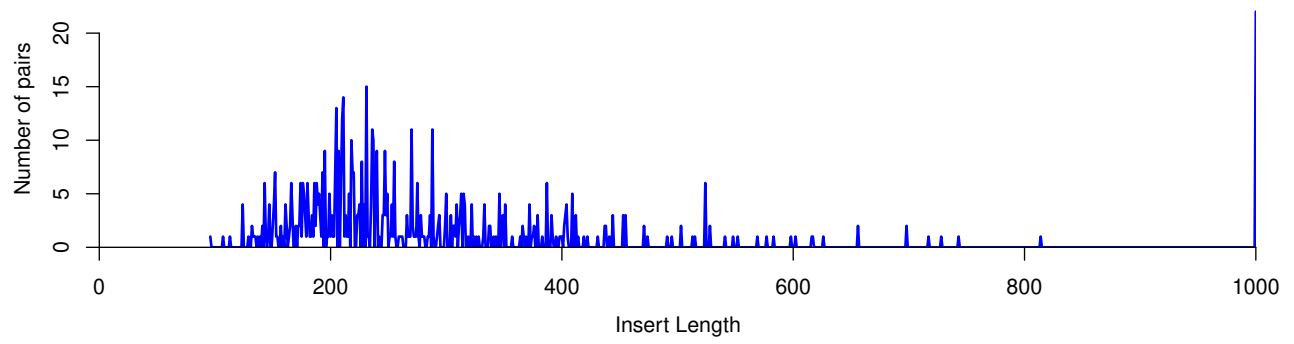
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Genome Composition	
A	725 (22.78%)
T	905 (28.44%)
G	691 (21.72%)
C	861 (27.06%)
N	0 (0.00%)
Total Nucleotides	3182
GC%	48.77

## READ QUALITY



## INSERT LENGTH DISTRIBUTION



## AMINO ACID VARIATIONS

Protein	Position	Ref AA	Consensus AA	All AAs
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Meta data	
Assembly file:	HBV-G-RYD-11.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-G-RYD-11
Date/Time	Tue 19 Mar 09:44:23 GMT 2019