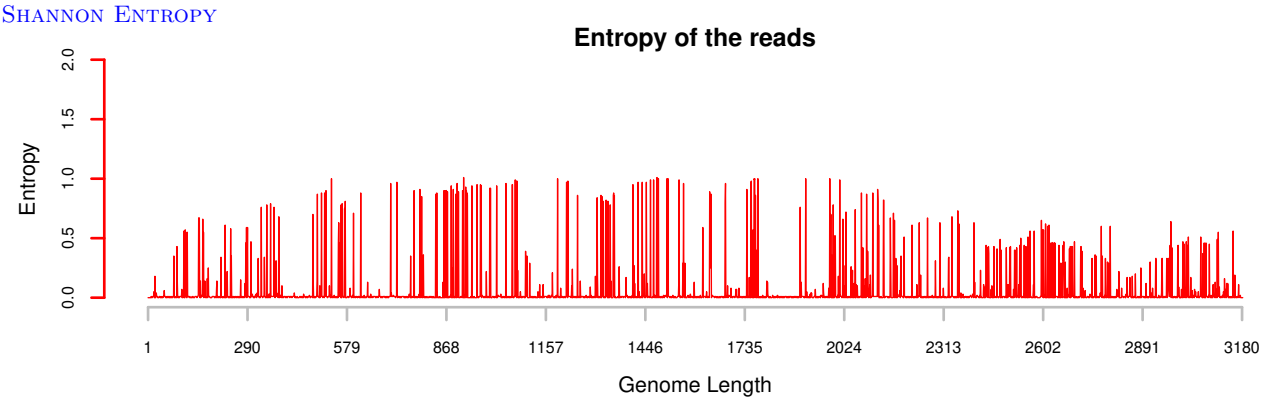
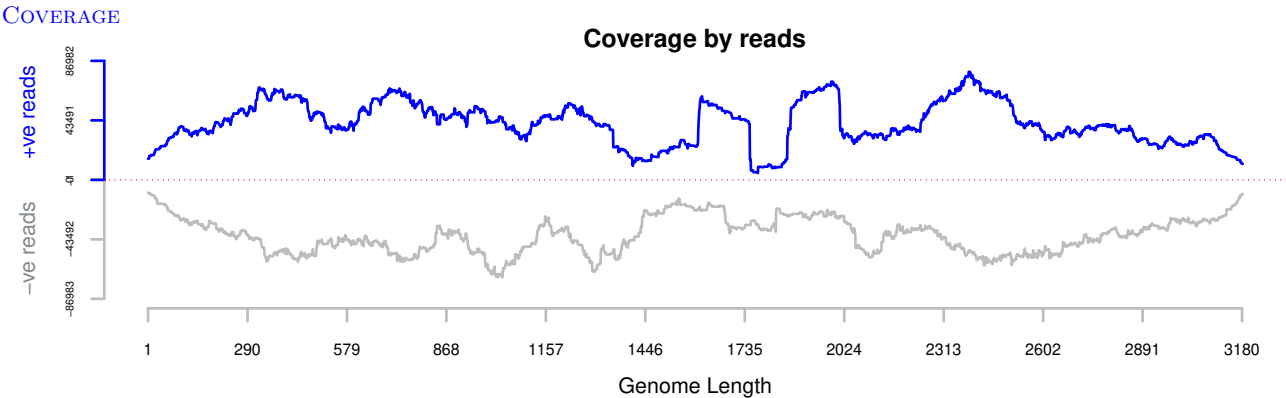


HBV-G-RYD-10

File name	HBV-G-RYD-10.sam
Ref name	KX357637.1 Hepatitis B virus isolate MK20ETH, complete genome
Ref len	3182
Program used	Tanoti Assembler 1.0
Total reads	3374730
Mapped reads	1792447 (53.11%)
Unmapped reads	1582283
Mapped loan pairs	10742
Average read length	148nt
Coverage	3182nt (100.00%)
Average depth	82075 reads/site
Average insert length	546nt



CONSENSUS SEQUENCE

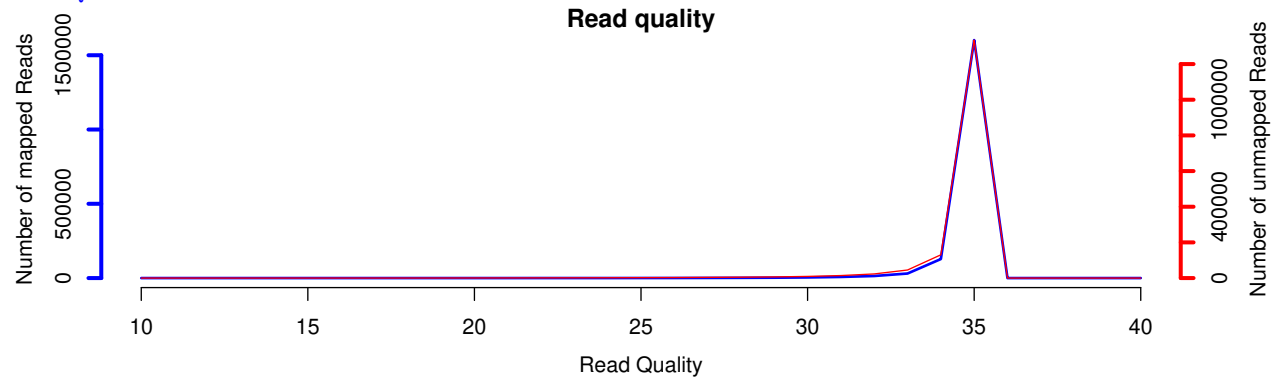
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140    ACCCTGCGCT GAACATGGAG AACATCACAT CAGGATTCCCT AGGACCCCTG CTCGTGTTAC AGGCGGGGTT
210    TTTCTTGTG ACAAGAATCC TCACAATACC GCAGAGTCTA GACTCGTGGT GGACTTCTCT CAATTTTCTA
280    GGGGGAAC TA CCGTGTGTCT TGGCCAAAAT TCGCAGTCCC CAACCTCCAA TCACTACCA ACCTCCTGTC
350    CTCCAAC TTG TCCTGGTTAT CGCTGGATGT GTCTGCGGCG TTTTATCATC TTCCTCTTCA TCCTGCTGCT
420    ATGCTCATC TTCTTGTG TTTCTCTGGA CTATCAAGGT ATGTTGCCCC TTTGTCCTCT AATTCCAGGA
490    TCTTCAACCA CCAGCACGGG ACCATGCAGA ACCTGCACGA CTCCTGCTCA AGGAACCTCT ATGTATCCCT
560    CCTGCTGCTG TACCAAAACCT TCGGACGGAA ATTGCACCTG TATTCCTATC CCATCATCCT GGGCTTTCGG
630    AAAATTCCTA TGGGAGTGGG CCTCAGCCCG TTTCTCCTGG CTCAGTTTAC TAGTGCCATT TGTTCACTGG
700    TTCGTAGGGC TTTCCCCCAC TGTTTGGCTT TCAGTTATAT GGATGATGTG GTATTGGGGG CCAAGTCTGT
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840    AACAAAACAA AAAGATGGGG TTA CTCTTTA CATTTTCATG GCTATGTCAT TGGATGTTAT GGGTCATTGC
910    CACAAGATCA CATTATACAG 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 TTGCCCGGCA ACGGCCAGGT CTGTGCCAAG TGTTTGCTGA
1190   TGCAACCCCC ACTGGCTGGG GCTTGGCCAT AGGCCATCAG CGCATGCGTG GAACCTTTGT GGTCTCCTG
1260   CCGATCCATA CTGCGGAACCT CCTAGCCGCT TGTTTTGCTC GCAGCAGGTC TGGAGCGAAA CTTATCGGGA
1330   CAGATAATTC TGTCGTTCTC TCAAGGAAAT ATACATCATT TCCATGGCTG CTAGGCTGTG CTGCCAACTG
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2170   ACTAATATGG GCCTAAAGTT CAGGCAACTA TTGTGGTTTC ACATTCTTG CCTCACTTTT GGAAGAGAAA
2240   CGGTCATAGA GTATTTGGTG TCTTTCGGAG TGTGGATTCT CACTCCTCCA GCTTATAGAC CTCCAAATGC
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3010   GATTACCCCC ACCGCACGGA GGCCTTTTGG GGTGGAGCCC TCAGGCTCAG GGCATACTAC AAACCTTGCC
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3150   AGAAACACTC ATCCTCAGGC CATGCACTGG AA

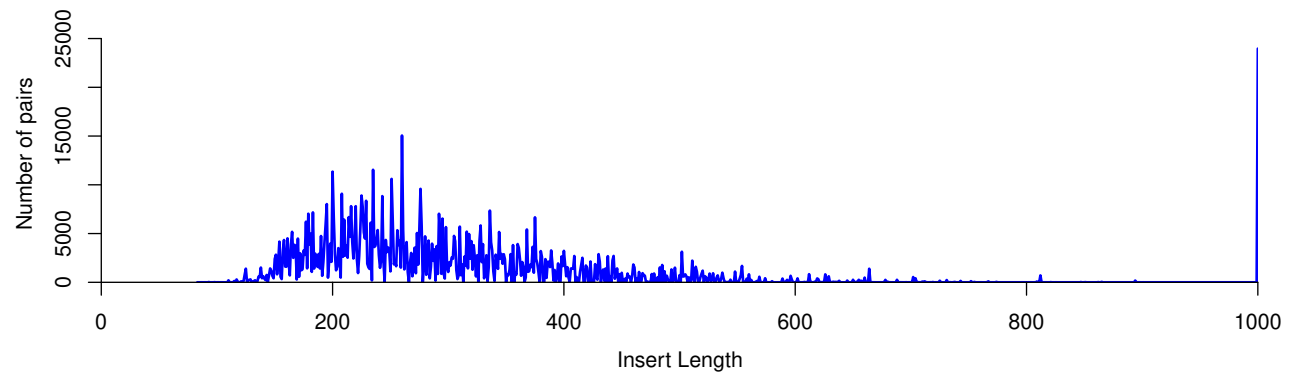
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Genome Composition	
A	732 (23.00%)
T	910 (28.60%)
G	689 (21.65%)
C	851 (26.74%)
N	0 (0.00%)
Total Nucleotides	3182
GC%	48.40

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-10.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-10
Date/Time	Mon 18 Mar 15:51:24 GMT 2019