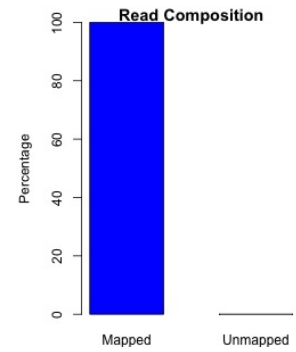


DEMO/1-MRU25010-M-MAPPED

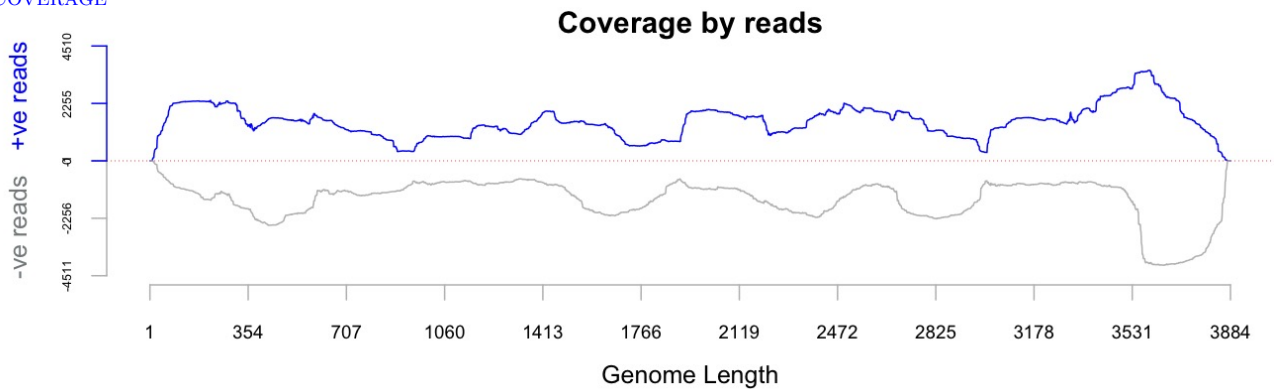
File name	demo/1-MRU25010-M-mapped.sam
Ref name	MRU25010-M
Ref len	3885
Program used	Tanoti Assembler 1.0

Total reads	42895
Mapped reads	42895 (100.00%)
Unmapped reads	0
Mapped loan pairs	0
Average read length	277nt

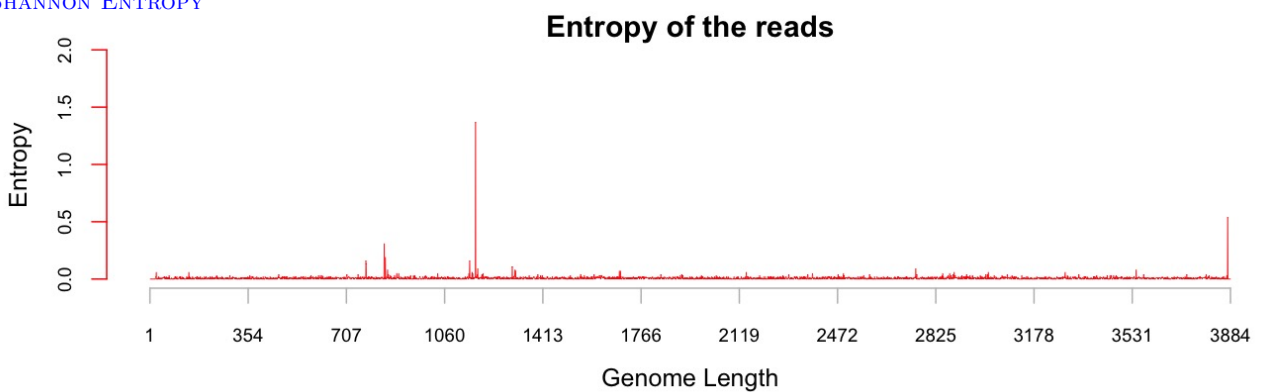
Coverage	3879nt (99.85%)
Average depth	3057 reads/site
Average insert length	37nt



COVERAGE



SHANNON ENTROPY



CONSENSUS SEQUENCE

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1      ACACAAAGAC GGTGCATTAA ATGTATGTTT TACTAACAAT TCTAATCTCG GTTCTGGTGT GTGAAGCGGT
70     TATTAGAGTG TCTCTAAGCT CCACAAGAGA AGAAACCTGT TTTGGTGACT CCACCAACCC AGAAATGATT
140    GAGAGAGCTT GGGATTCACT CAGAGAGGAG GAGATGCCAG AAGAGCTCTC TTGTTCATA TCAGGCATAA
210    GGGAGGTTAA GACCTCAAGC CAGGAATTAT ACAGGGCATT AAAAGCTATC ATTGCTGCTG ATGGCTTGAA
280    CAACATCACC TGCCATGGTA AGGATCCTGA GGACAAGATT TCTCTCATAA AGGGTCCTCC TCACAAGAAG
350    CGAGTGGGGA TAGTTCGGTG TGAGAGACGA AGAGACGCTA AGCAAGTAGG GAGAGAAACC ATGGCAGGGA
420    TTGCAATGAC AGTCCTTCCA GCCTTAGCAG TTTTGTGCTT GGCACCTGTT GTCTTTGCCG AAGACCCTCA
490    TCTTAGAAAC AGGCCAGGAA AGGGACACAA CTACATTGAC GGGATGACTC AGGAGGATGC CACATGTAAA
560    CCTGTGACAT ATGCTGGGGC ATGTAGCAGT TTTGATGTCT TGCTCGAAAA GGGAAAAATT CCCCTCTTCC
630    AGTCATACGC TCATCATAGA ACTCTACTAG AGGCCGTCCT CGACACCATT ATTGCAAAGG CTGATCCACC
700    TAGCTGTGAC CTTCAGAGTG CTCATGGGAA TCCTTGCATG AAGGAGAAAC TCGTGATGAA GACACACTGT
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910    TCCTCTCCAG GACTTATTTT GTCAGTCAAG TGAGGATGAT GGGTCAAAAA TAAAAACAAA AATGAAAAGG
980    GTCTGCGAAG TGGGAGTTCA AGCACTCAA AAGTGTGATG GCCAACTCAG CACTGCACAT GAGGTTGTGC
1050   CCTTTCAGT  ATTTAAGAAC TCAAAGAAGG TTTATCTTGA CAAGCTTGAC CTCAAGACTG AGGAAAATCT
1120   GCTACCAGAC TCATTGTGCT GCTTCGAGCA TAAGGGGAGG TATAAAGGAA AAATGGACTC TGGTCAGACA
1190   AAGAGGGAGC TCAAAAGCTT TGATATCTCT CAGTGTCCCA AGATTGGAGG GCATGGTAGC AAGAAATGTA
1260   CTGGGGAGCG AGCATTCTGC TCTGCTTATG AGTGCCTGCG TCAATACGCC AATGCCTATT GTTCACATGC
1330   TAATGGGTCA GGAATTGTAC AGATACAAAG ATCCGGGGTC TGAAGAAGC CTTTGTGTGT AGGGTATGAG
1400   AGAGTGGTTG TGAAGAGAGA GCTCTCTGCC AAGCCCATCC AGAGAGTTGA GCCTTGCACA ACTTGTATAA
1470   CCAAAATGTA GCCTCATGGA TTAATTGTCC GATCAACAGG GTTCAAGATA TCATCTGCAG TTGCTTGTGC
1540   TAGCGGAGTT TGCGTCACAG GATCGCAGAG CCCGTCTACT GAGATCACAC TCAAGTACCC AGGGATATCC
1610   CAGTCCTCTG GGGGGGACAT AGGGGTTTCA ATGGCACATG ATGATCAGTC AGTTAGCTCC AAAATAGTAG
1680   CTCACCTGCC CCCCCAGGAC CCGTCGCTAG TGCATGGCTG CATAGTGTGT GCTCATGGCT TGATAAATTA
1750   CCAGTGTACAC ACTGCTCTCA GTGCCCTTGT CGTTGTGTTC GTGTTCAGCT CTGTTGCAAT AATTTGTTTG
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1890   TTAAGTCTTT CATCAGATGG GTGTATAAGA AGATGGTTGC CAGAGTGGCA GACAATATCA ATCAAGTGAA
1960   CAGGGAATAA GGATGGATGG AAGGAGGCCA GTTAGCTCTA GGGAATCCTG CTCCTATCCC TCGTCATGCT
2030   CCAATTCCAC GTTATAGCAC ATACCTAATG CTACTATTGA TTGTCTCATA TGCATCAGCA TGTTCAGAAC
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2240   CAAACCAAGT TCCTGAAGAT AAAAAGTGTG TCAAGTGAGC TATCGTGCGG GGAGGGCCAG AGCTATTGGA
2310   CTGGGTCCTT CAGCCCCAAA TGTCTGAGCT CAAGGAGGTG CCATCTTGTG GGGGAATGTC ATGTGAATAG
2380   GTGCCGTGCT TGGAGGGACA ATGAGACTTC AGCAGAATTT TCATTTGTTG GGGAAAGCAC GACCATGCGA
2450   GAGAACAAGT GTTTTGAGCA GTGTGGAGGA TGGGATGTG GGTGTTTCAA CGTAAACCCA TCTTGCCTGT
2520   TTGTGCACAC GTATCTACAG TCAGTCAGAA AAGAGGCCCT TAGAGTTTTT AACTGCATTG ATTTGGGTGCA
2590   TAAACTTACT CTAGAGATCA CAGACTTTGA TGGCTCTGTT TCAACAATAG ACTTGGGAGC TTCATCTAGC
2660   CGTTTCACAA ACTGGGGTTC AGTTAGCCTC TCACTGGACG CAGAGGGCAT TTCAGGCTCA AATAGCTTTT
2730   CTTTCATTGA GAGCCCAGGC AAAGGGTATG CAATTGTTGA TGAGCCATTG TCAGAAATTC CTCGGCAAGG
2800   ATTCTTAGGA GAGATCAGGT GCAATTCAGA ATCTTCAGTT CTGAGTGCTC ATGAATCATG CCTTAGGGCG
2870   CCAAACTTGA TCTCATACAA ACCAATGATA GATCAGTTGG AGTGACAAAC AAATCTAATT GATCCTTTTG
2940   TAGTCTTTGA GAGGGGTTCC CTGCCACAAA CAAGGAATGA CAAAACCTTT GCAGTTTCAA AAGGGAATAG
3010   GGGTGTTCAA GCTTCTCTA AGGGCTCTGT ACAAGCTGAT CTAACCTGTA TGTTTGACAA TTTTGAGGTG
3080   GACTTCGTGG GAGCAGCCGT GTCTTGTGAT GCCGCCTTCT TGAATTTGAC AGGTTGCTAT TCATGCAATG
3150   CAGGAGCCAG AGTCTGCCTG TCTATCACAT CCACAGGAAC TGAACCTCTT TCTGCCACA ATAAGGATGG
3220   GTCTCTGCAT ATAGTTCTTC CATCAGAGAA TGAACAAAAA GATCAGTGTC AGATACTACA CTTCAGTGTA
3290   CCTGAGGTGG AGGAGGAGTT TATGTACTCT TGTGATGGAG ATGAGCGGCC TCTGTTGGTG AAAGGGACCC
3360   TGATAGCCAT TGATCCATTT GATGATAGGC GAGAAGCAGG GGGGGAATCA ACAGTTGTGA ATCCAAAATC
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3500   CTCCTAATTT GCCTGTATGT AGCATTATCA ATTGGGCTCT TTTTCCTTCT TATATATCTT GGGAGAACAG
3570   GTCTCTCTAA AATGTGGCTT GCTGCTACTA AGAAGGCCTC ATAGATCAAT ACGTGTAGAA GCAATACATA
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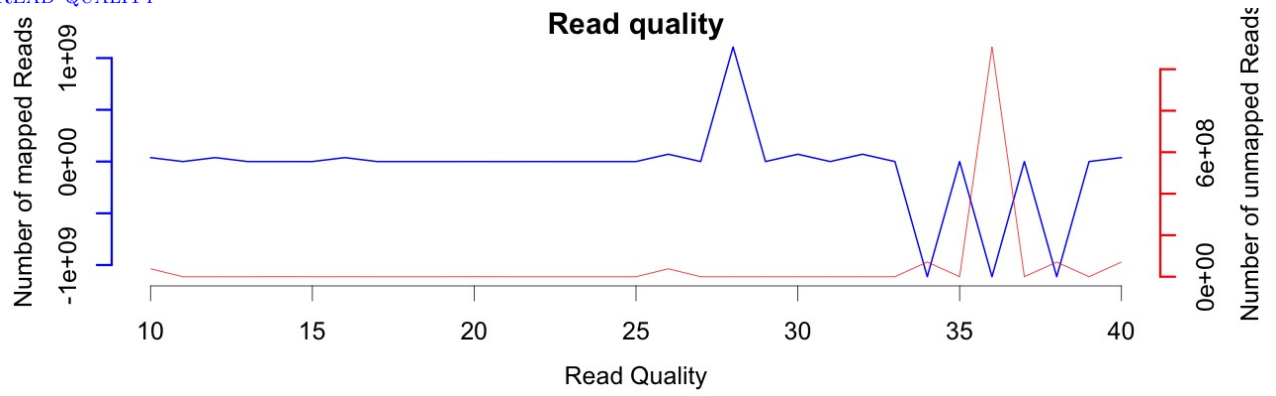
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3850      AACTAACTC TTGAAGTTG CACCGGTCTN NNNNN

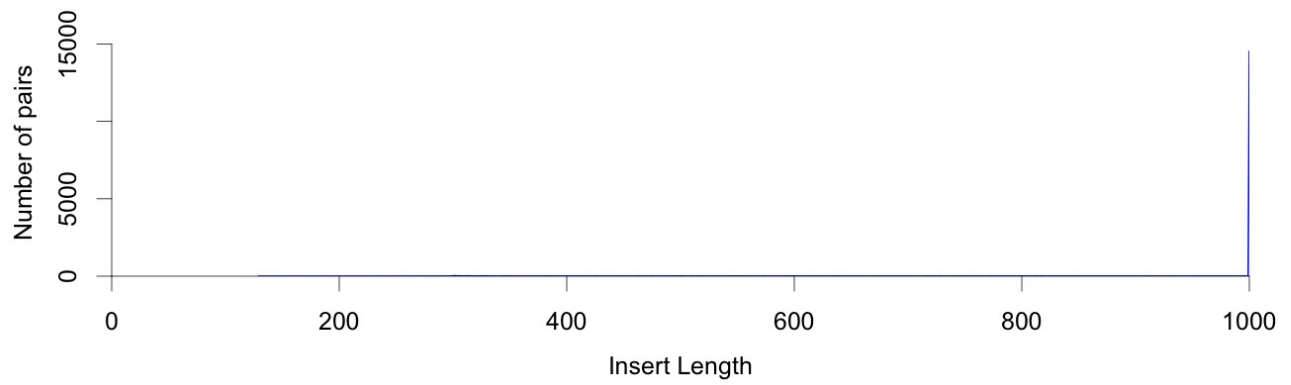
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Genome Composition	
A	1072 (27.59%)
T	1042 (26.82%)
G	975 (25.10%)
C	790 (20.33%)
N	6 (0.15%)
Total Nucleotides	3885
GC%	45.50

READ QUALITY



INSERT LENGTH DISTRIBUTION



AMINO ACID VARIATIONS

Protein	Position	Ref AA	Consensus AA	All AAs
Glycoprotein	384	T	K	K::48.77(1048) T::43.04(925) R::7.03(151)