

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:29:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716177.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716177 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716177.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:29:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	433,173
Mapped reads	397,302 / 91.72%
Unmapped reads	35,871 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,110 / 1.87%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	6,796 / 1.57%
Duplication rate	1.21%
Clipped reads	404,115 / 93.29%

2.2. ACGT Content

Number/percentage of A's	7,816,796 / 24.97%
Number/percentage of C's	6,206,430 / 19.83%
Number/percentage of T's	9,924,533 / 31.71%
Number/percentage of G's	7,352,460 / 23.49%
Number/percentage of N's	2,118 / 0.01%
GC Percentage	43.32%

2.3. Coverage

Mean	0.0101

Standard Deviation	0.1339
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2.4. Mapping Quality

Mean Mapping Quality	47.42
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2.5. Mismatches and indels

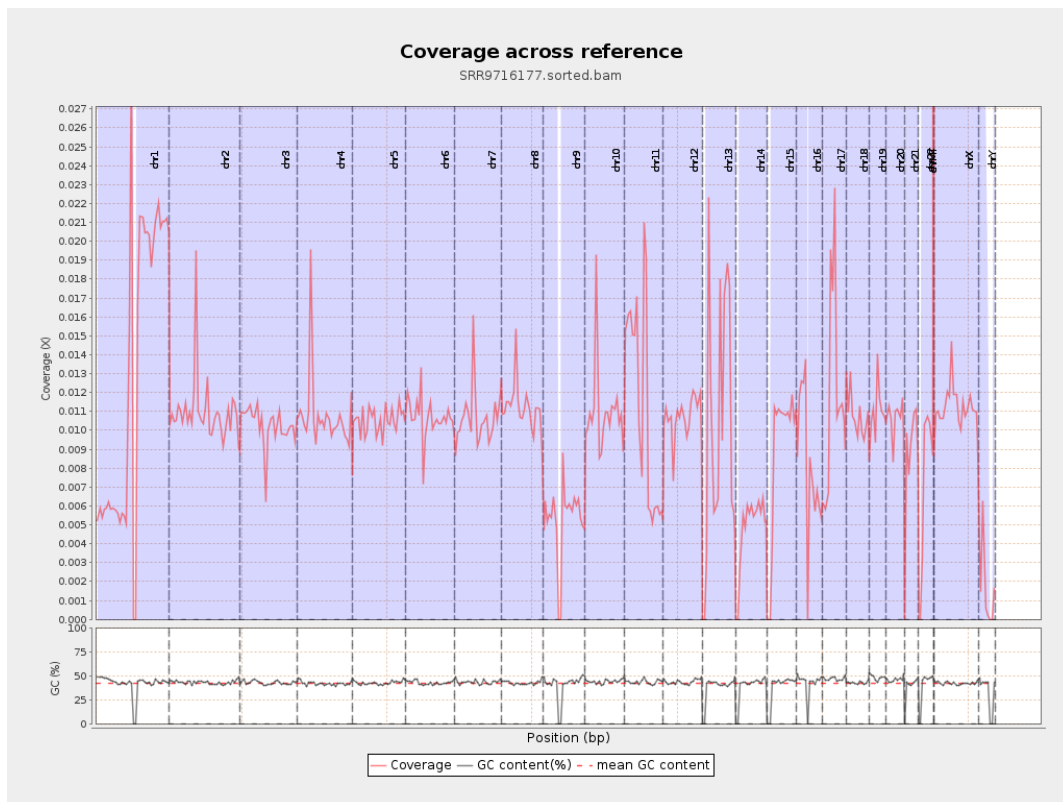
General error rate	0.67%
Mismatches	203,289
Insertions	2,774
Mapped reads with at least one insertion	0.69%
Deletions	6,974
Mapped reads with at least one deletion	1.73%
Homopolymer indels	41.58%

2.6. Chromosome stats

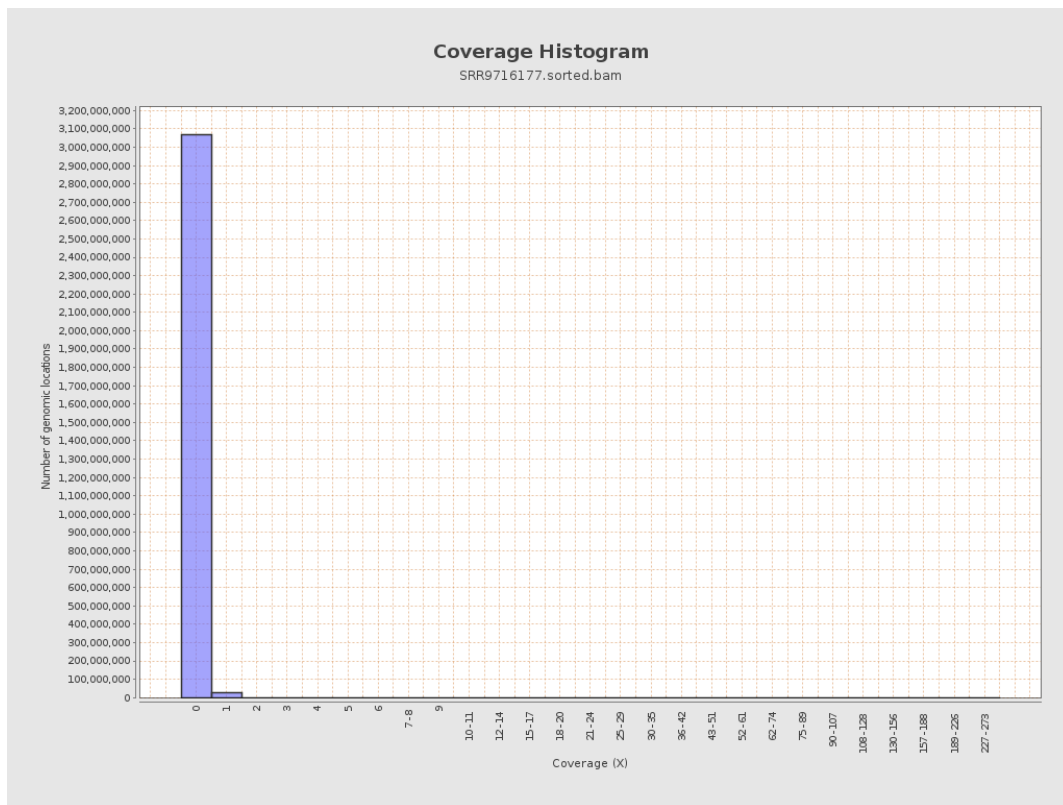
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3213118	0.0129	0.2562
chr2	243199373	2675177	0.011	0.1364
chr3	198022430	2024899	0.0102	0.104
chr4	191154276	2047892	0.0107	0.1129
chr5	180915260	1902600	0.0105	0.1057
chr6	171115067	1828740	0.0107	0.1083
chr7	159138663	1701116	0.0107	0.1506

chr8	146364022	1641199	0.0112	0.1454
chr9	141213431	747731	0.0053	0.0896
chr10	135534747	1479327	0.0109	0.1281
chr11	135006516	1524725	0.0113	0.1226
chr12	133851895	1433527	0.0107	0.1065
chr13	115169878	1161125	0.0101	0.1033
chr14	107349540	513328	0.0048	0.0754
chr15	102531392	912910	0.0089	0.0971
chr16	90354753	742424	0.0082	0.0962
chr17	81195210	979943	0.0121	0.118
chr18	78077248	841389	0.0108	0.1535
chr19	59128983	653214	0.011	0.1806
chr20	63025520	671615	0.0107	0.1094
chr21	48129895	419013	0.0087	0.1
chr22	51304566	359139	0.007	0.0864
chrMT	16571	1395	0.0842	0.3151
chrX	155270560	1742704	0.0112	0.1139
chrY	59373566	97831	0.0016	0.0638

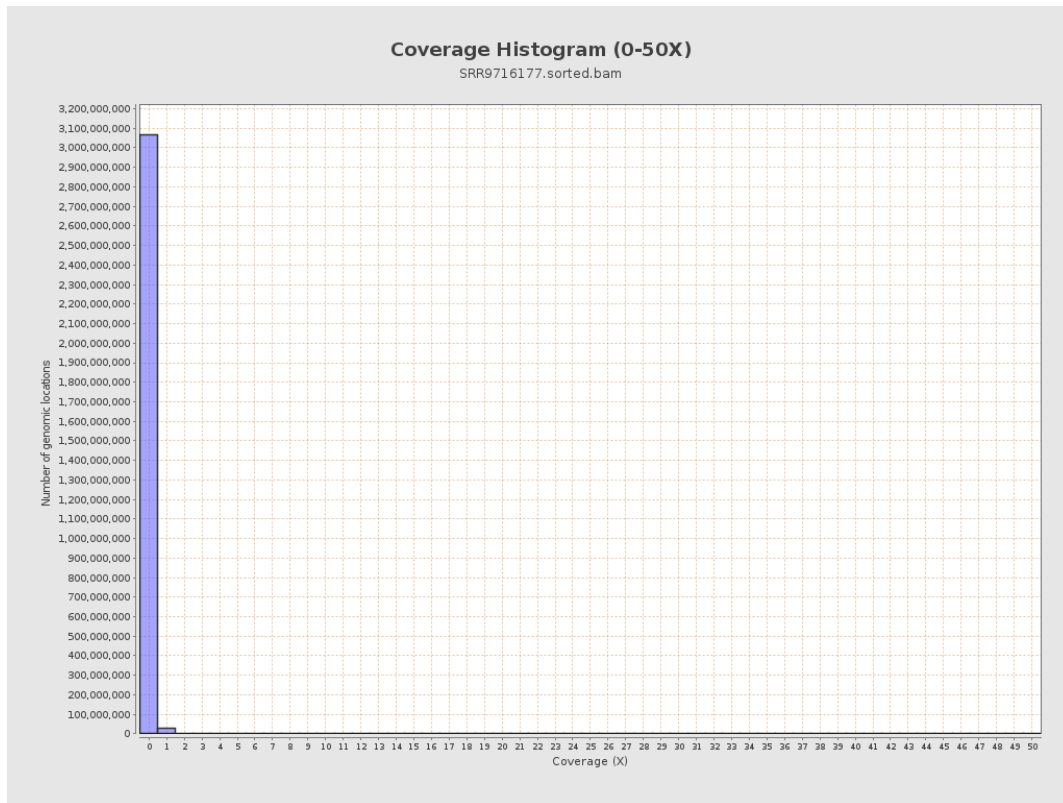
3. Results : Coverage across reference



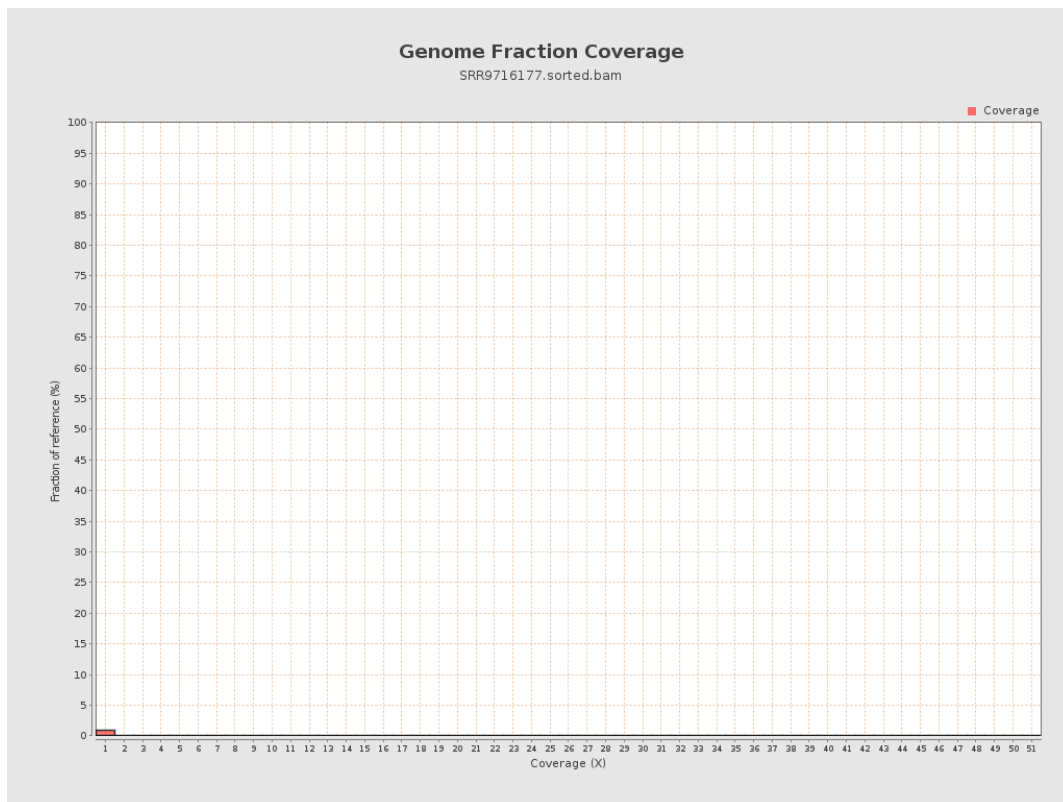
4. Results : Coverage Histogram



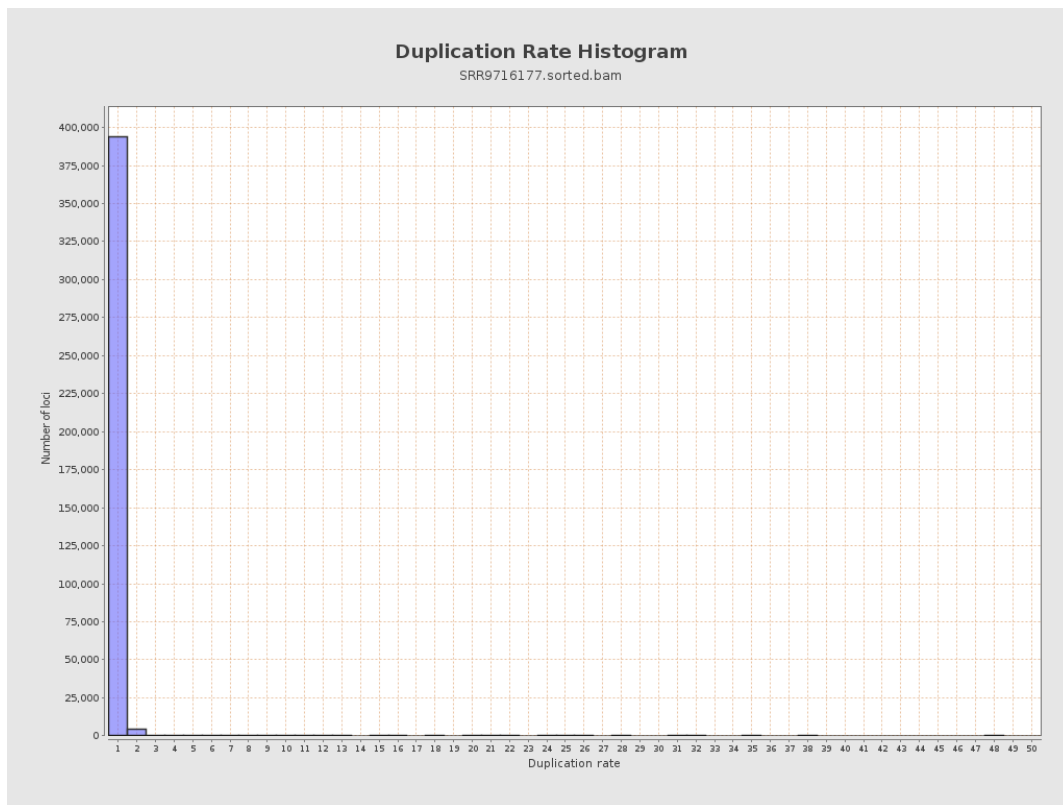
5. Results : Coverage Histogram (0-50X)



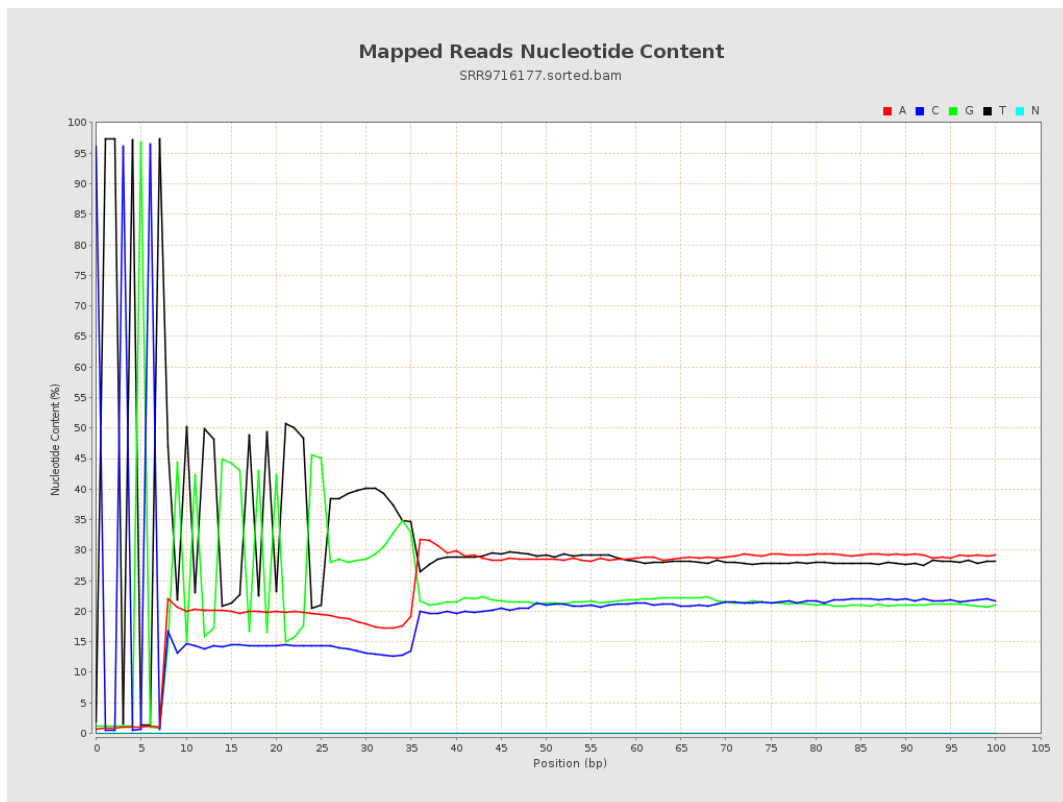
6. Results : Genome Fraction Coverage



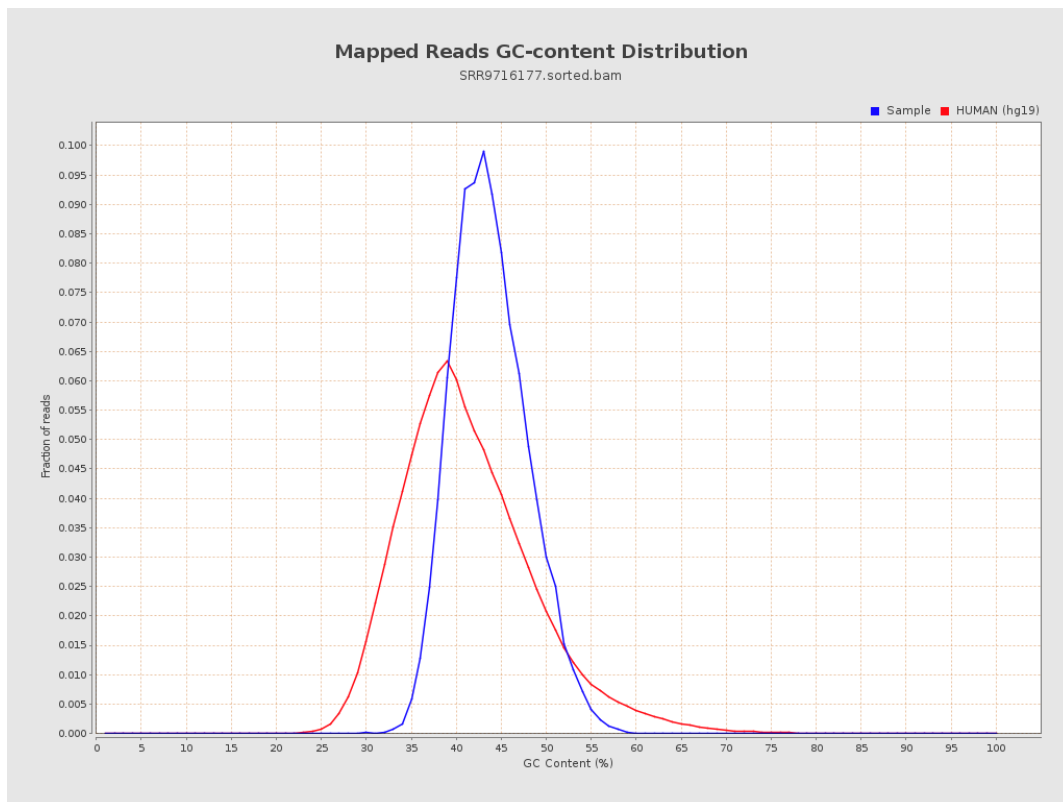
7. Results : Duplication Rate Histogram



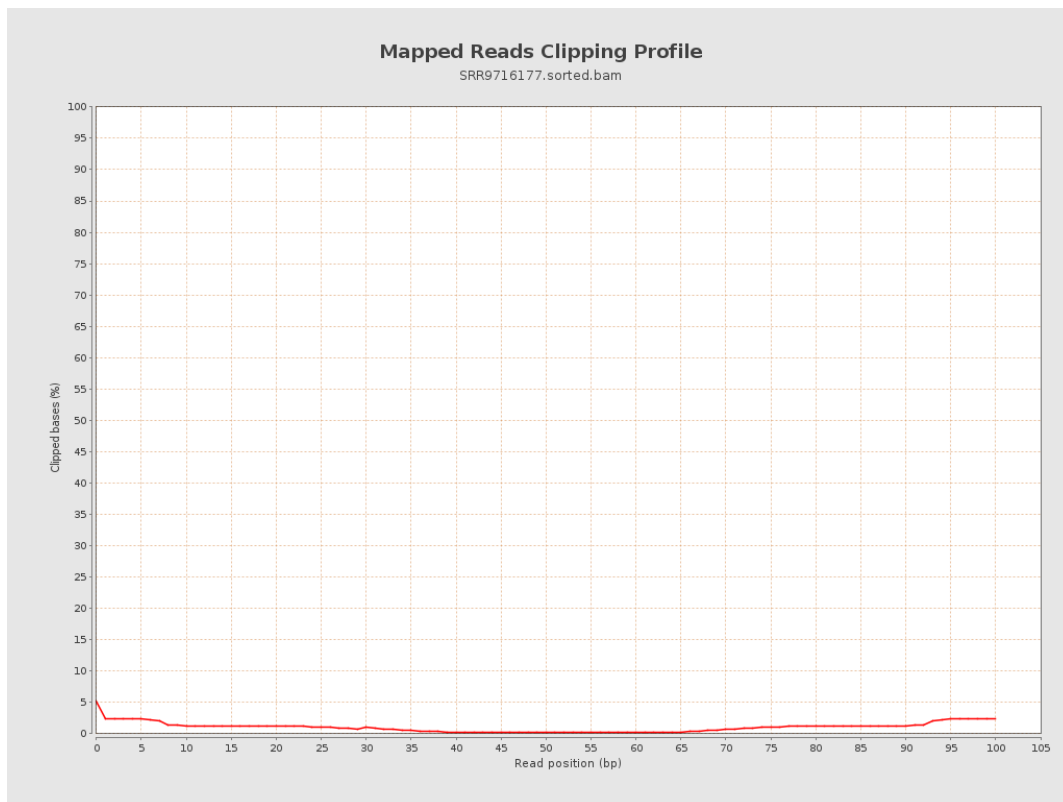
8. Results : Mapped Reads Nucleotide Content



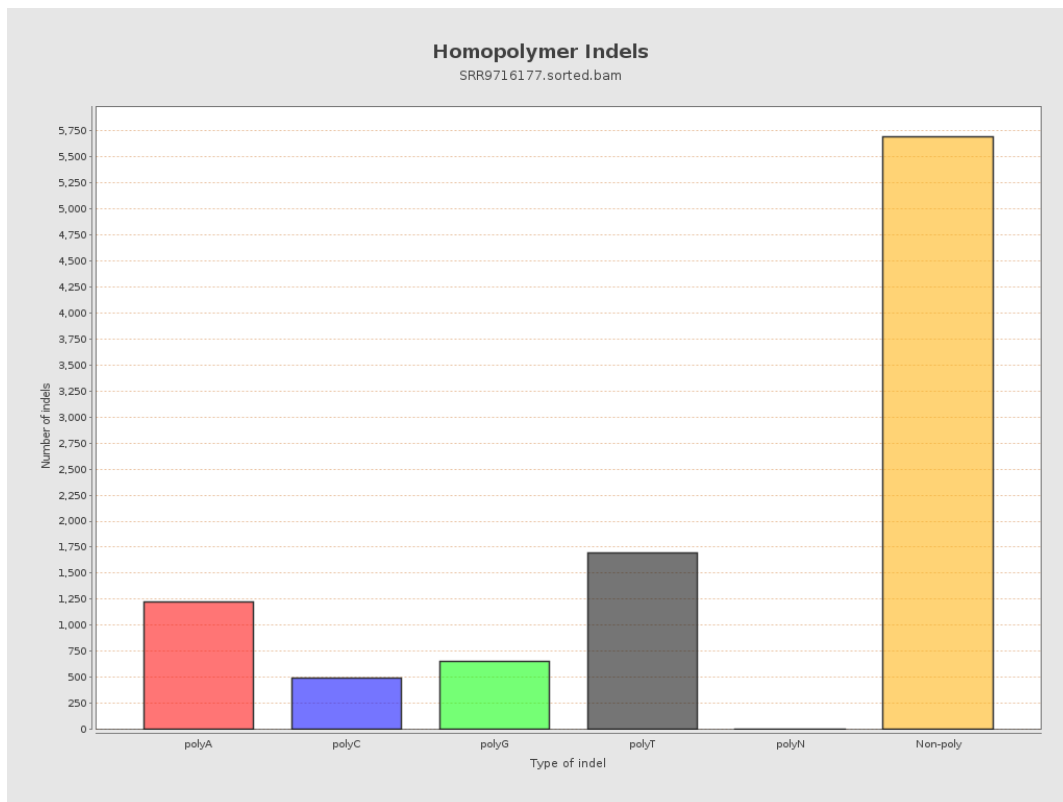
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

