

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:21:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716463.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_SRR9716463 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716463.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:21:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716463.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	574,663
Mapped reads	521,514 / 90.75%
Unmapped reads	53,149 / 9.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,630 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	10,704 / 1.86%
Duplication rate	1.65%
Clipped reads	521,583 / 90.76%

2.2. ACGT Content

Number/percentage of A's	7,341,848 / 24.44%
Number/percentage of C's	5,818,418 / 19.37%
Number/percentage of T's	9,493,415 / 31.6%
Number/percentage of G's	7,388,090 / 24.59%
Number/percentage of N's	329 / 0%
GC Percentage	43.96%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.115
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2.4. Mapping Quality

Mean Mapping Quality	45.24
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2.5. Mismatches and indels

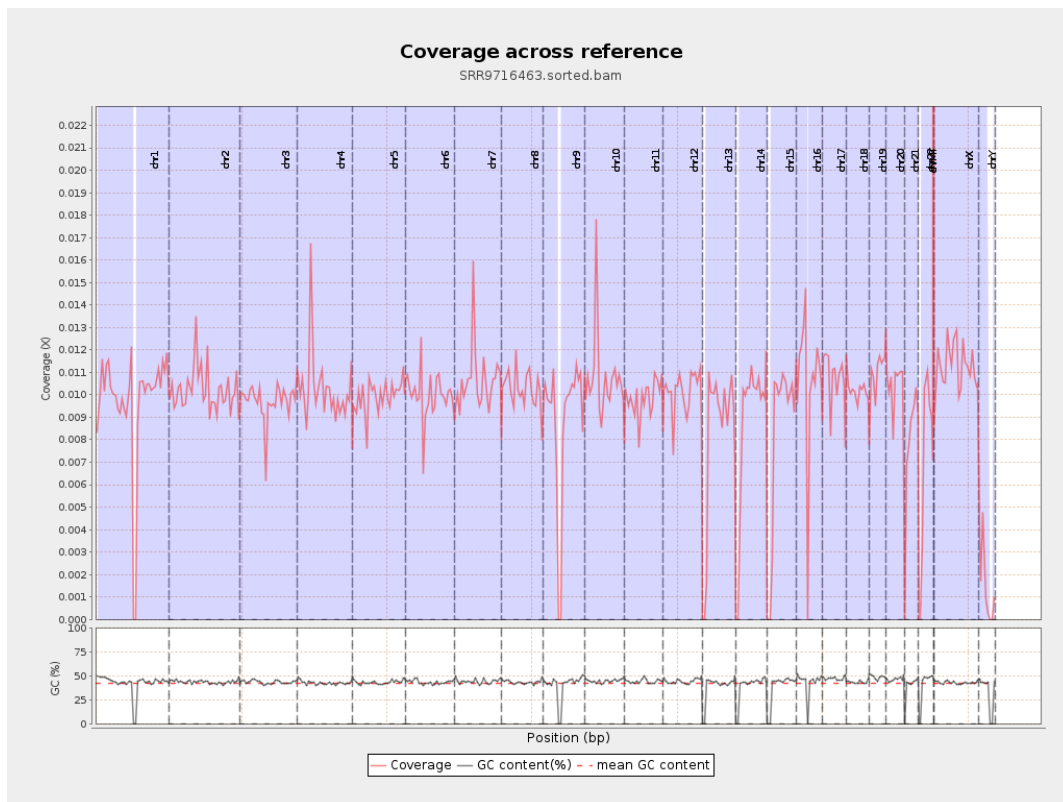
General error rate	0.51%
Mismatches	146,834
Insertions	2,372
Mapped reads with at least one insertion	0.45%
Deletions	5,995
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.48%

2.6. Chromosome stats

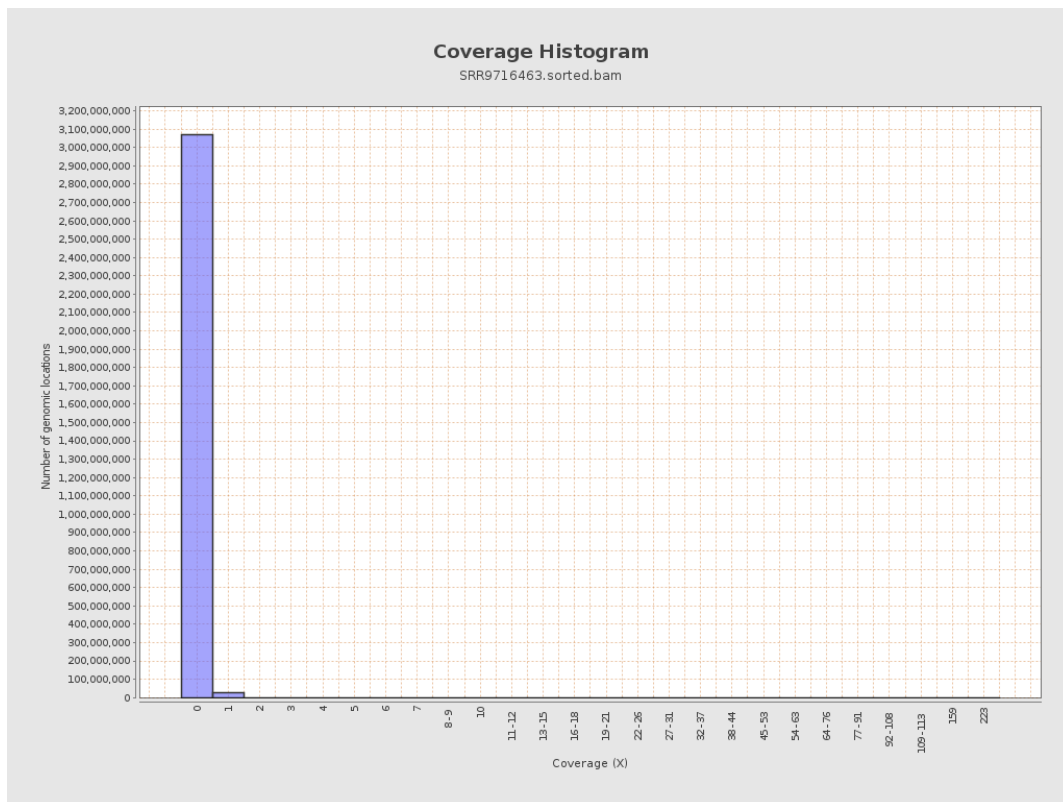
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2421475	0.0097	0.1341
chr2	243199373	2488827	0.0102	0.1441
chr3	198022430	1919933	0.0097	0.1028
chr4	191154276	1955451	0.0102	0.1088
chr5	180915260	1793535	0.0099	0.1036
chr6	171115067	1708932	0.01	0.1112
chr7	159138663	1693795	0.0106	0.1387

chr8	146364022	1499396	0.0102	0.1188
chr9	141213431	1238963	0.0088	0.1034
chr10	135534747	1449467	0.0107	0.1249
chr11	135006516	1325862	0.0098	0.1103
chr12	133851895	1358071	0.0101	0.105
chr13	115169878	943961	0.0082	0.0942
chr14	107349540	922941	0.0086	0.0972
chr15	102531392	846828	0.0083	0.0946
chr16	90354753	958446	0.0106	0.1115
chr17	81195210	865975	0.0107	0.1099
chr18	78077248	797619	0.0102	0.135
chr19	59128983	651172	0.011	0.1261
chr20	63025520	647669	0.0103	0.1063
chr21	48129895	380137	0.0079	0.0946
chr22	51304566	349222	0.0068	0.0855
chrMT	16571	1733	0.1046	0.3675
chrX	155270560	1745751	0.0112	0.1139
chrY	59373566	86600	0.0015	0.0497

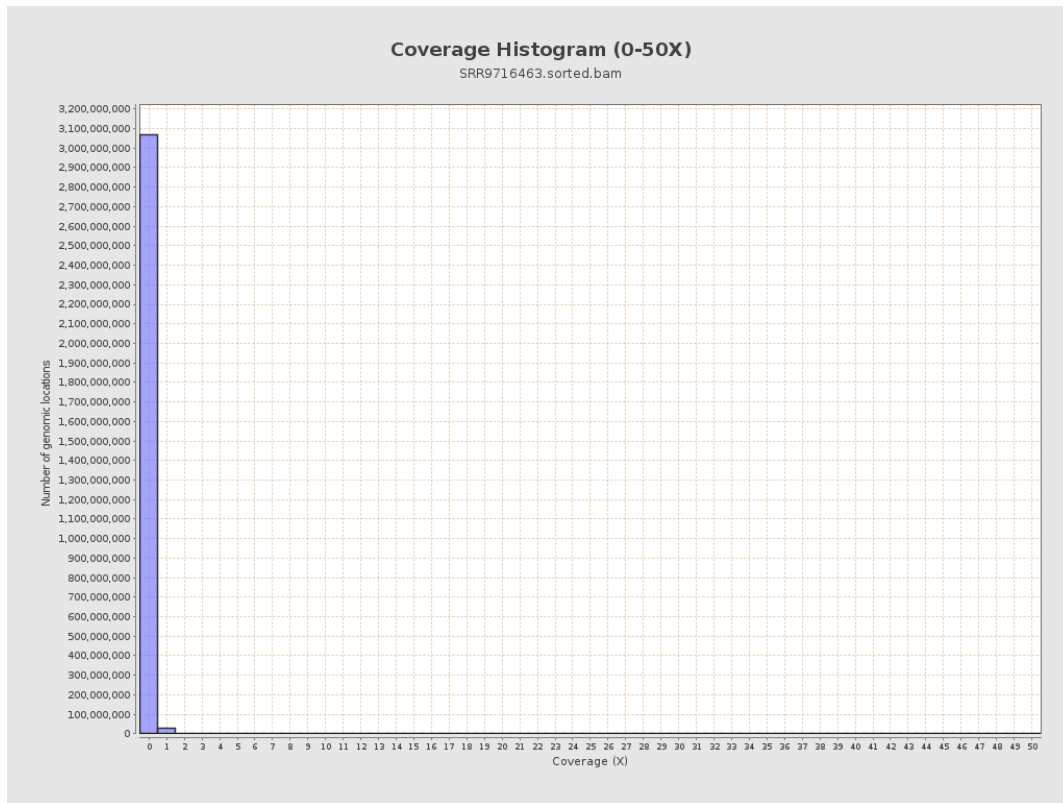
3. Results : Coverage across reference



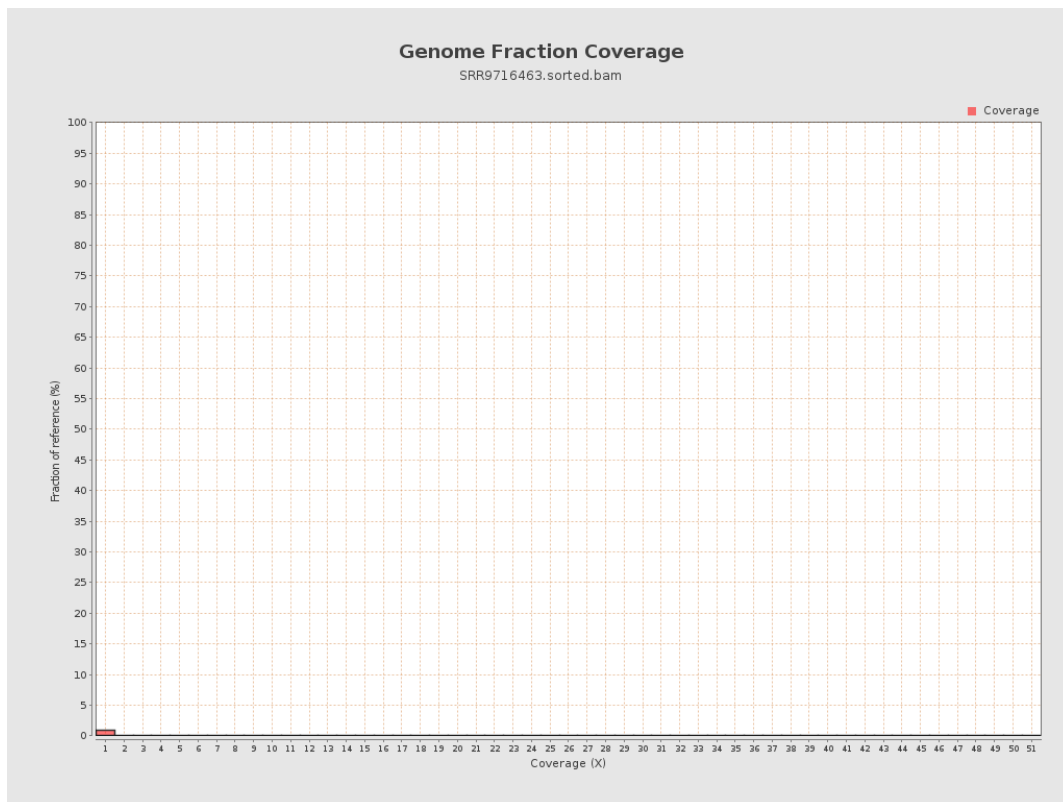
4. Results : Coverage Histogram



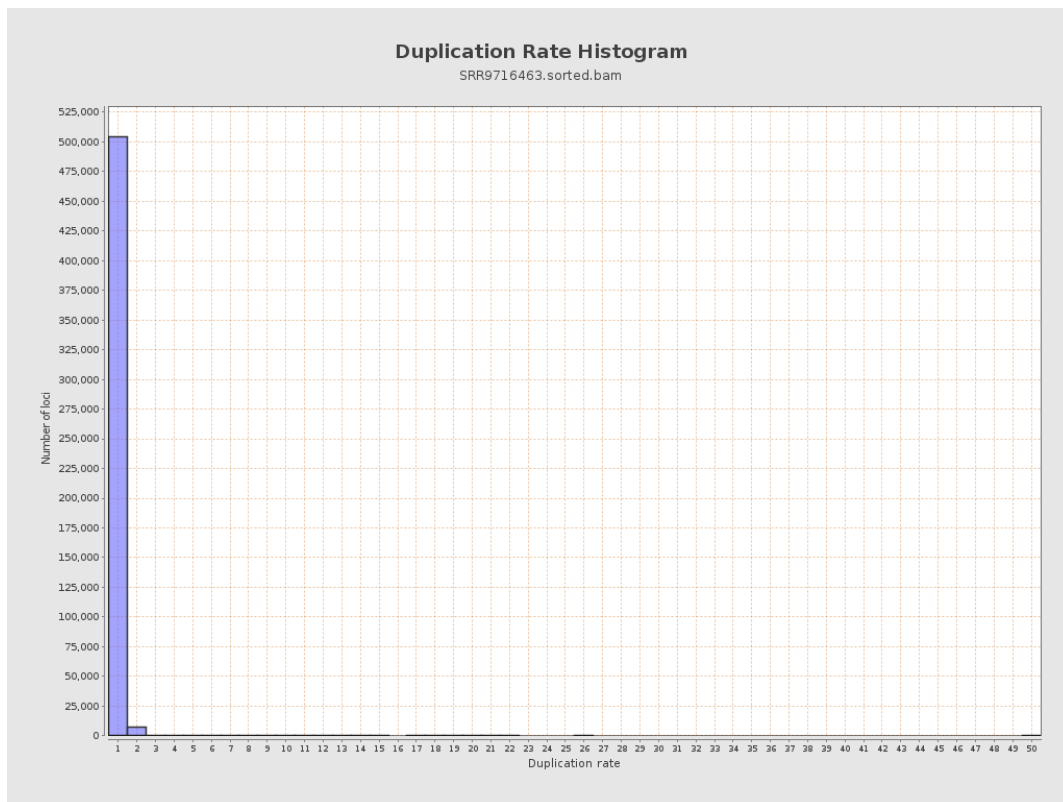
5. Results : Coverage Histogram (0-50X)



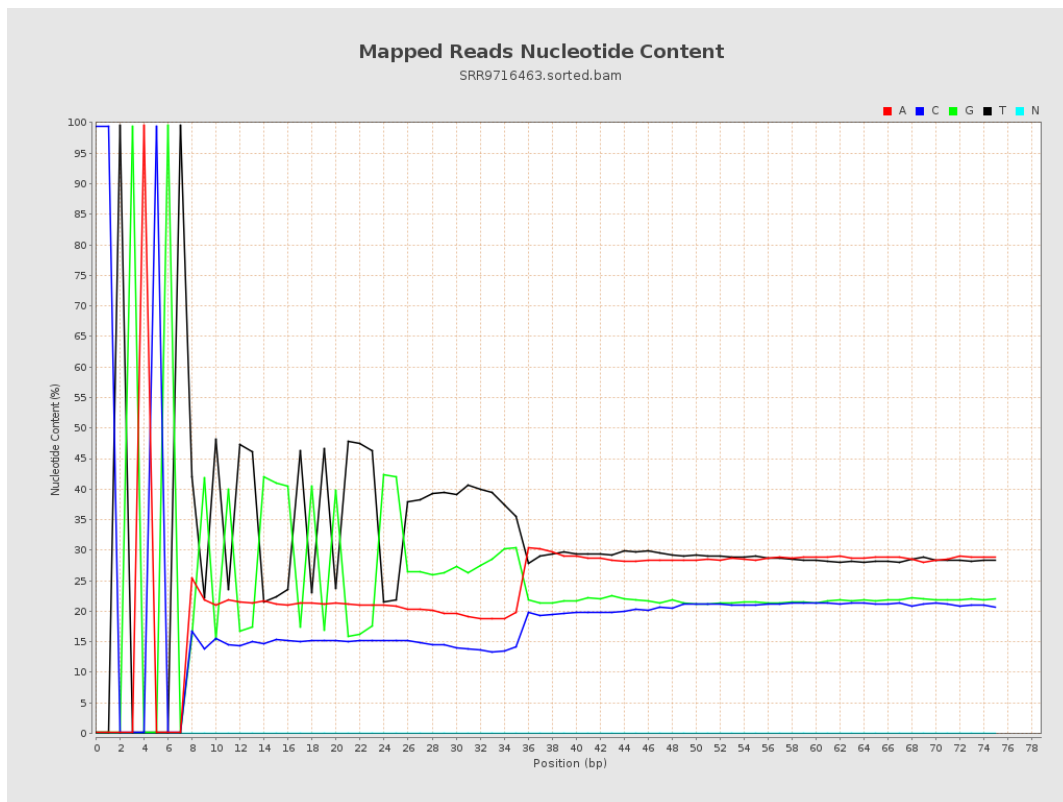
6. Results : Genome Fraction Coverage



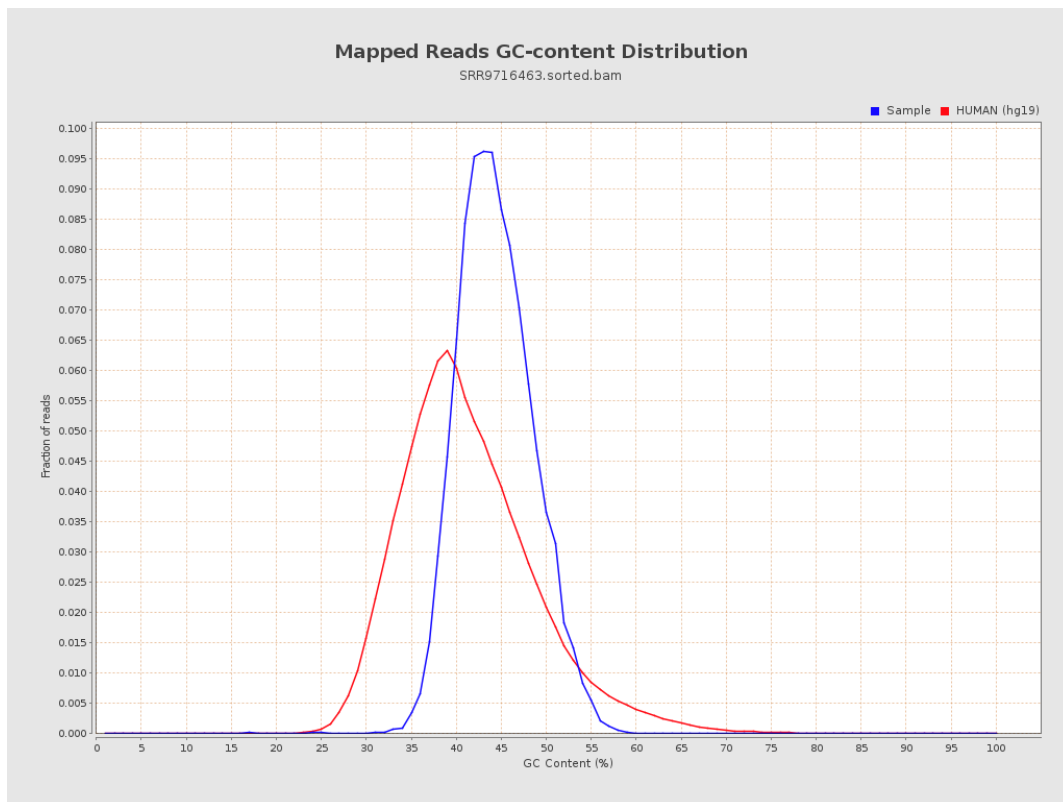
7. Results : Duplication Rate Histogram



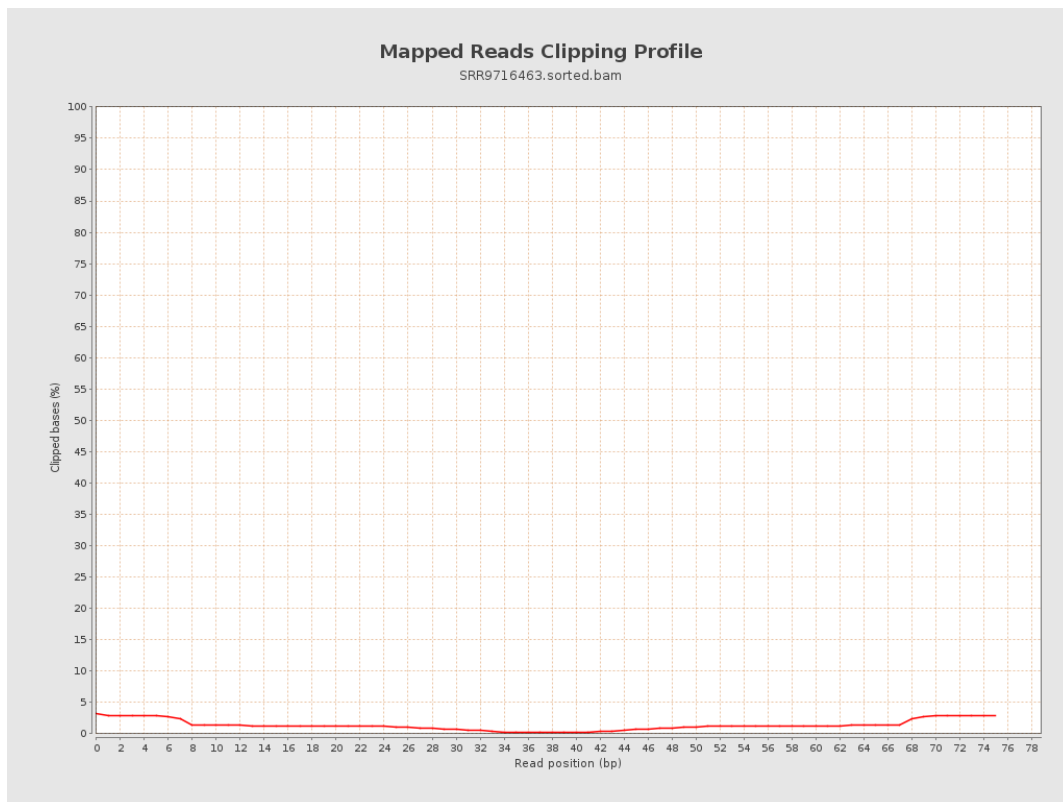
8. Results : Mapped Reads Nucleotide Content



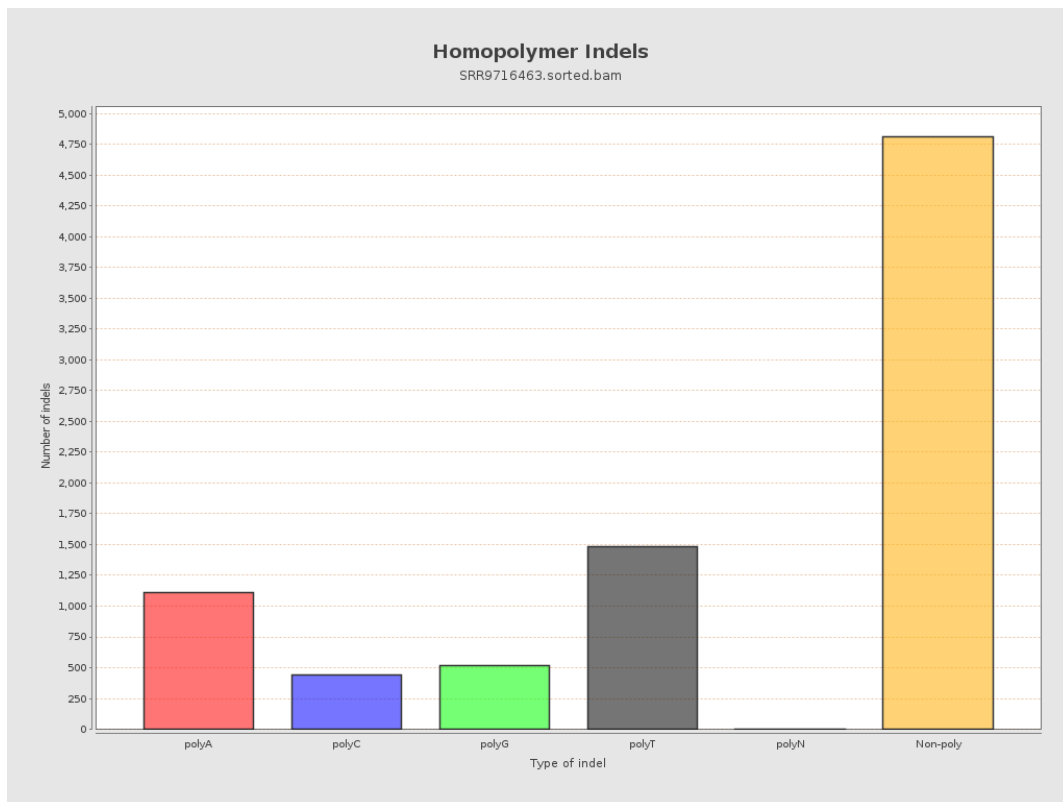
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

