

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:29:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716735.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_SRR9716735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:29:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,458,651
Mapped reads	1,345,845 / 92.27%
Unmapped reads	112,806 / 7.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,462 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	36,094 / 2.47%
Duplication rate	1.9%
Clipped reads	1,349,178 / 92.49%

2.2. ACGT Content

Number/percentage of A's	20,040,528 / 25.43%
Number/percentage of C's	16,629,398 / 21.1%
Number/percentage of T's	23,388,354 / 29.68%
Number/percentage of G's	18,749,617 / 23.79%
Number/percentage of N's	965 / 0%
GC Percentage	44.89%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2429
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2.4. Mapping Quality

Mean Mapping Quality	44.11
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2.5. Mismatches and indels

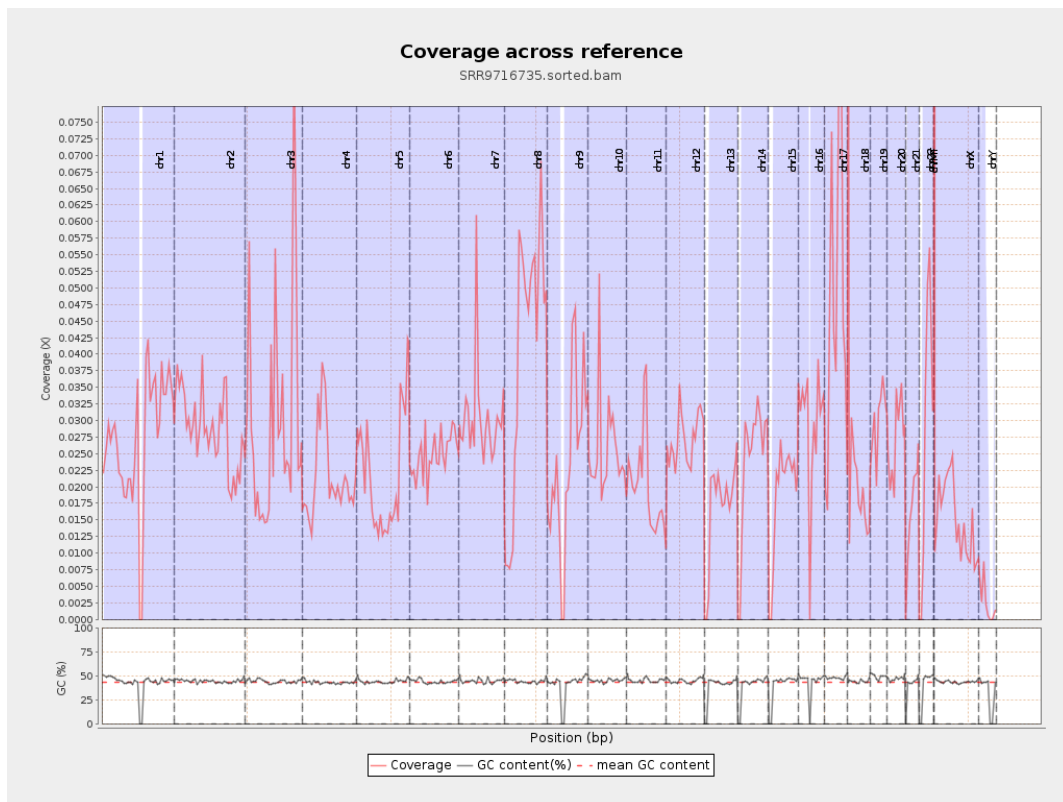
General error rate	0.5%
Mismatches	382,189
Insertions	5,777
Mapped reads with at least one insertion	0.43%
Deletions	14,366
Mapped reads with at least one deletion	1.06%
Homopolymer indels	40.55%

2.6. Chromosome stats

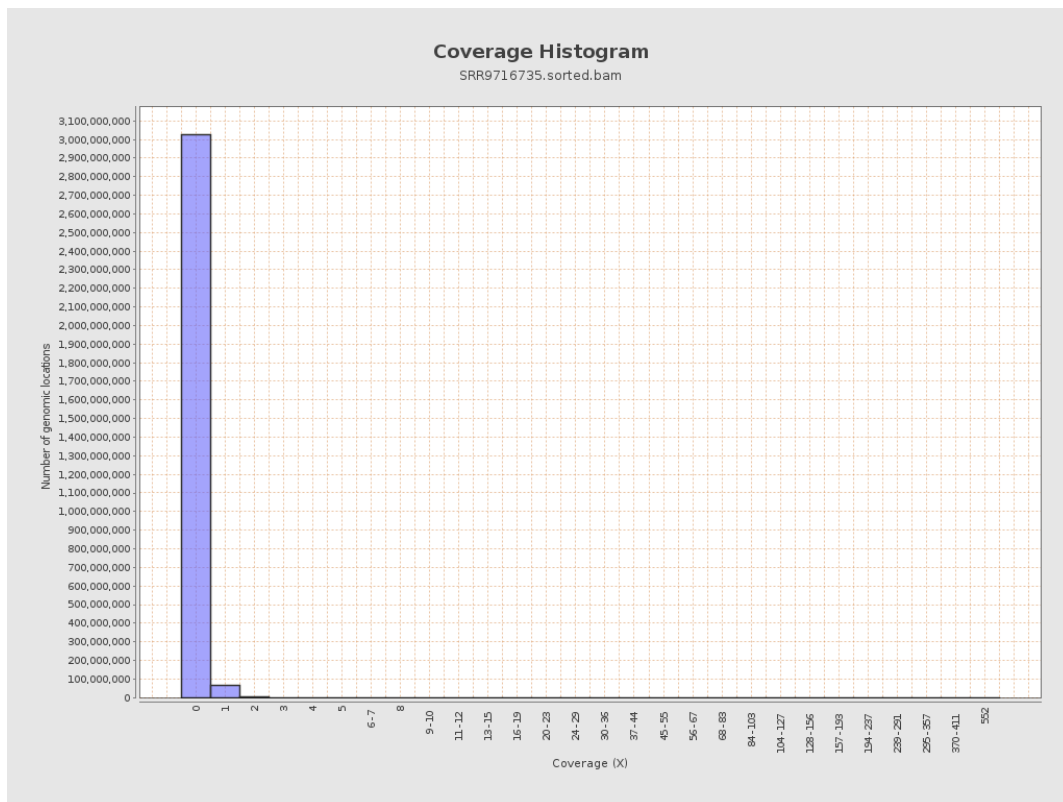
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6772127	0.0272	0.344
chr2	243199373	7007016	0.0288	0.2876
chr3	198022430	5873706	0.0297	0.1956
chr4	191154276	4100685	0.0215	0.1666
chr5	180915260	3894424	0.0215	0.1562
chr6	171115067	4244987	0.0248	0.1784
chr7	159138663	4842116	0.0304	0.4988

chr8	146364022	5977535	0.0408	0.2572
chr9	141213431	3275467	0.0232	0.1792
chr10	135534747	3457927	0.0255	0.296
chr11	135006516	2771835	0.0205	0.1823
chr12	133851895	3649347	0.0273	0.1883
chr13	115169878	1929319	0.0168	0.1377
chr14	107349540	2570396	0.0239	0.1675
chr15	102531392	1895974	0.0185	0.1474
chr16	90354753	2629761	0.0291	0.1879
chr17	81195210	3925268	0.0483	0.2458
chr18	78077248	1747845	0.0224	0.2673
chr19	59128983	1772086	0.03	0.3043
chr20	63025520	1696418	0.0269	0.1815
chr21	48129895	783432	0.0163	0.1415
chr22	51304566	1485076	0.0289	0.1828
chrMT	16571	32576	1.9658	1.8711
chrX	155270560	2339877	0.0151	0.1473
chrY	59373566	156205	0.0026	0.0744

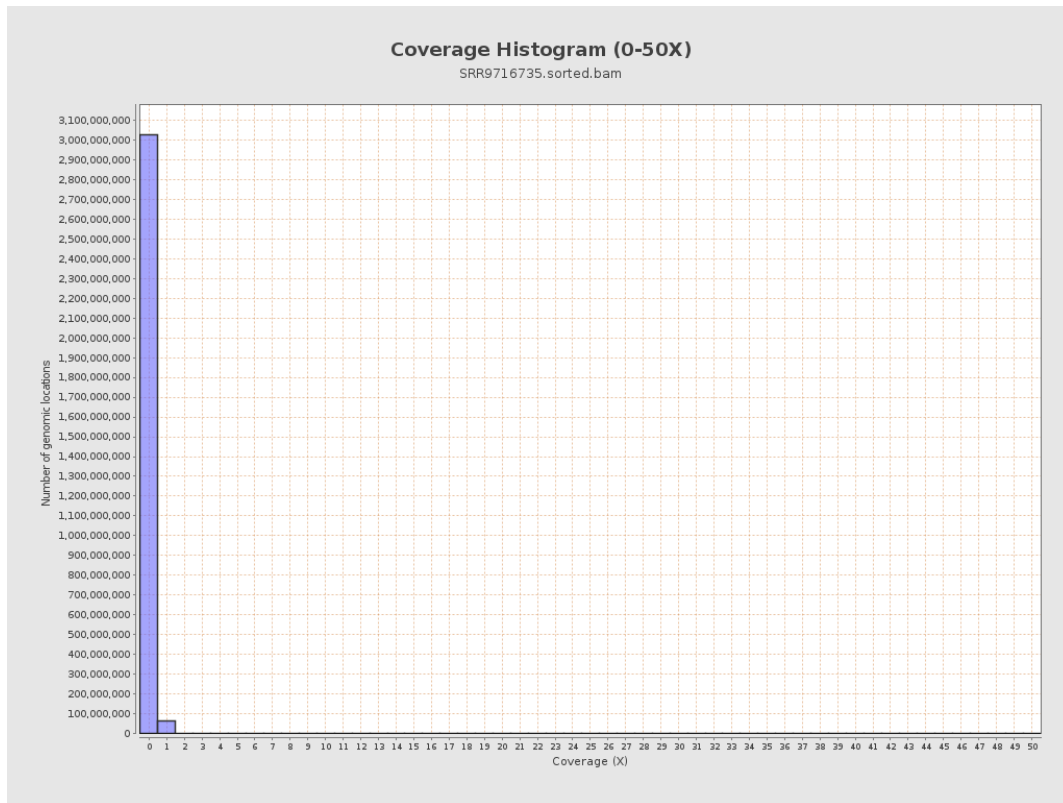
3. Results : Coverage across reference



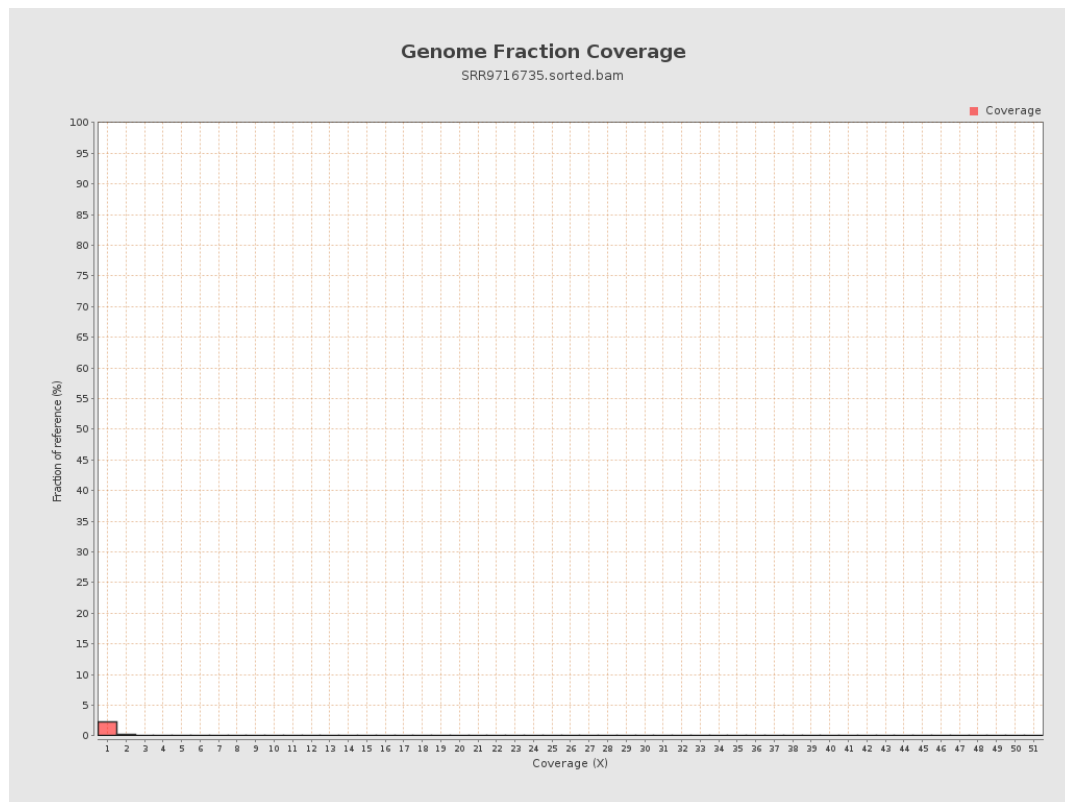
4. Results : Coverage Histogram



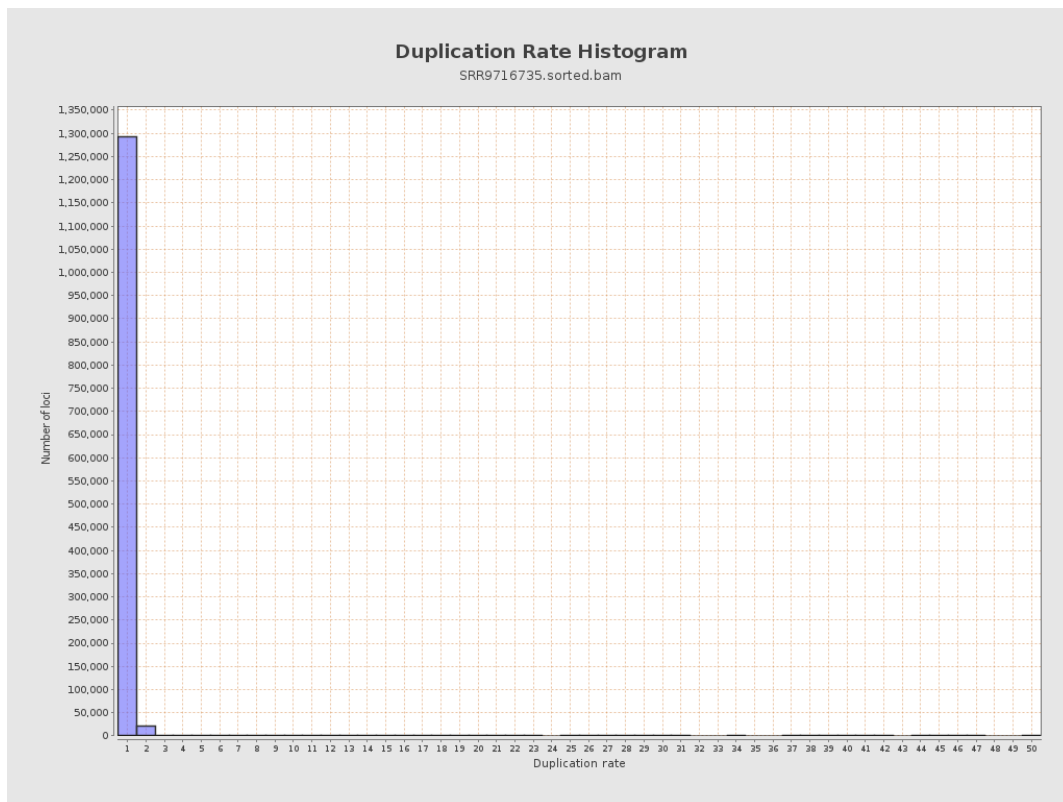
5. Results : Coverage Histogram (0-50X)



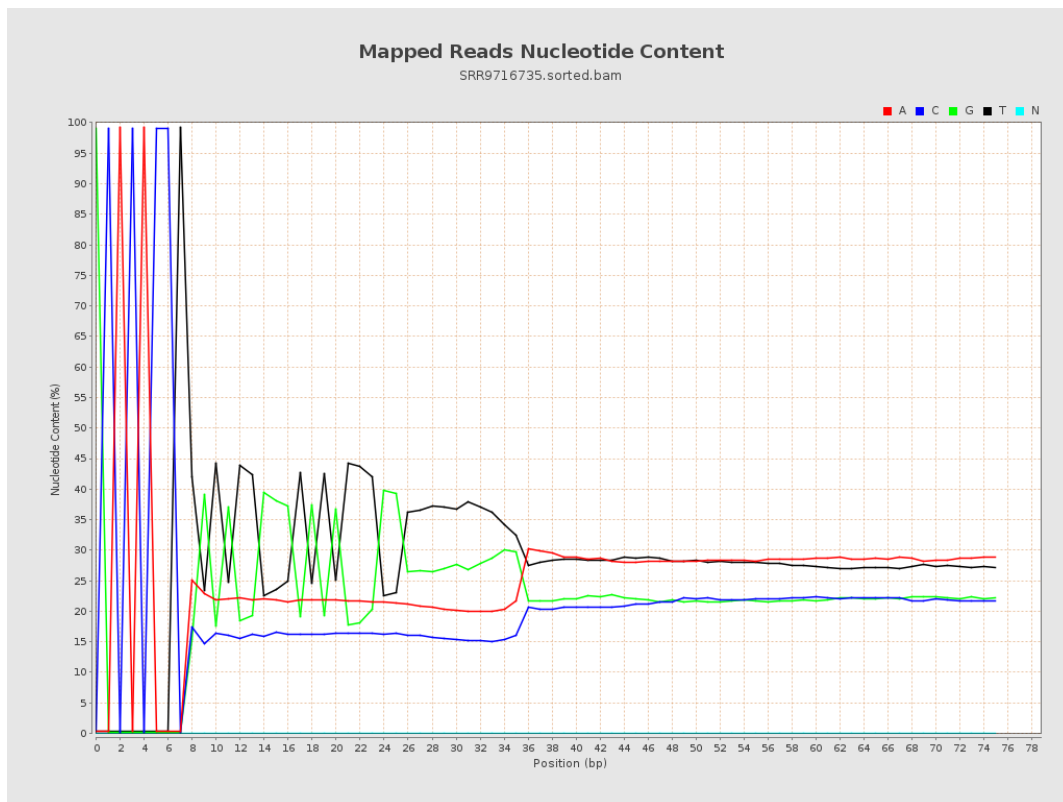
6. Results : Genome Fraction Coverage



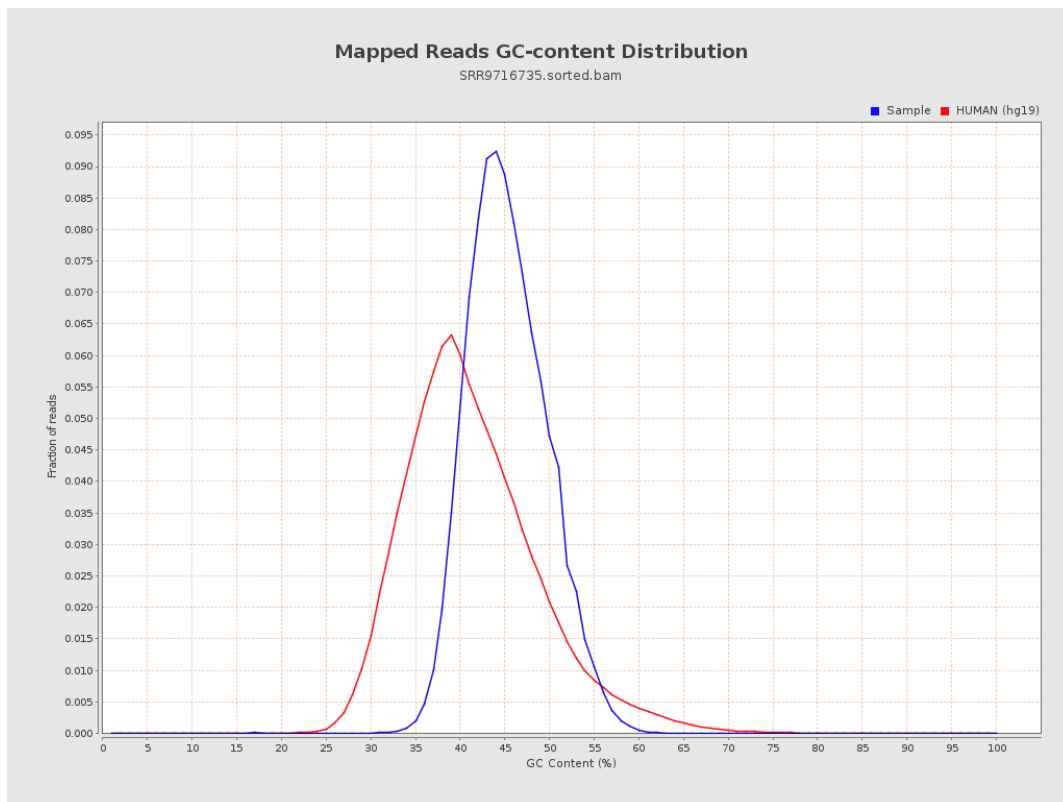
7. Results : Duplication Rate Histogram



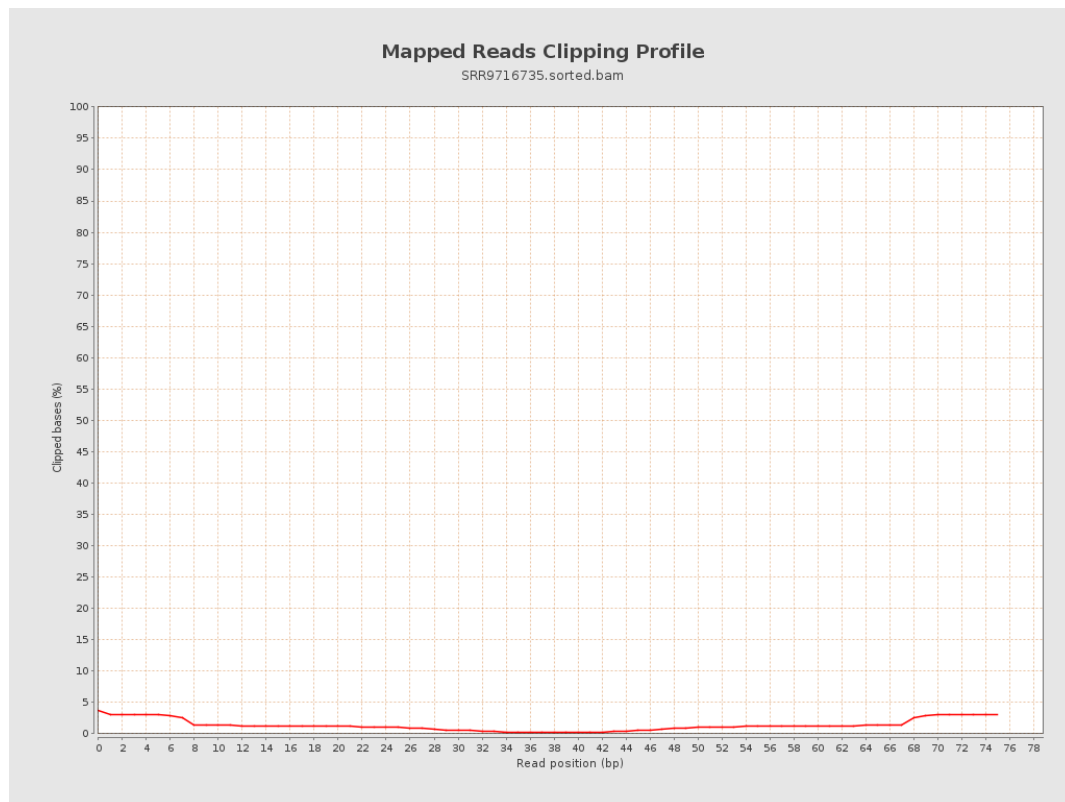
8. Results : Mapped Reads Nucleotide Content



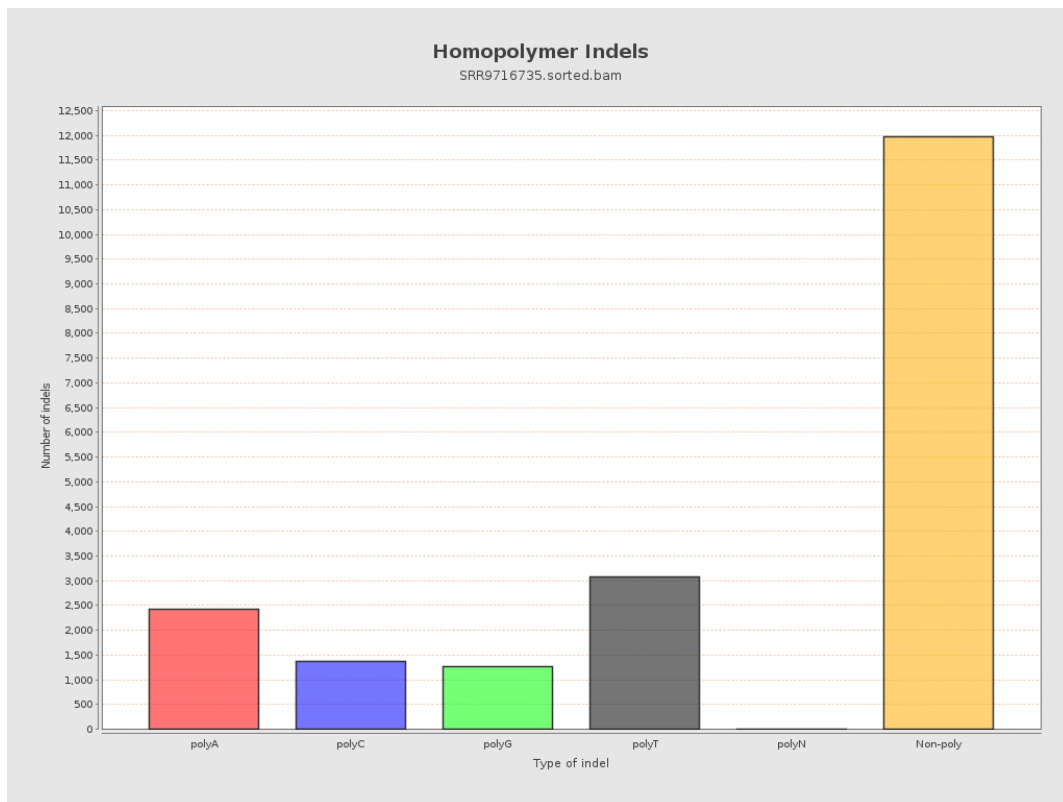
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

