

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:26:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716734.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_SRR9716734 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716734.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:26:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716734.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	796,234
Mapped reads	737,843 / 92.67%
Unmapped reads	58,391 / 7.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,938 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	16,147 / 2.03%
Duplication rate	1.66%
Clipped reads	740,638 / 93.02%

2.2. ACGT Content

Number/percentage of A's	11,292,603 / 25.93%
Number/percentage of C's	8,899,117 / 20.44%
Number/percentage of T's	13,210,550 / 30.34%
Number/percentage of G's	10,140,849 / 23.29%
Number/percentage of N's	581 / 0%
GC Percentage	43.73%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1525
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2.4. Mapping Quality

Mean Mapping Quality	45.25
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2.5. Mismatches and indels

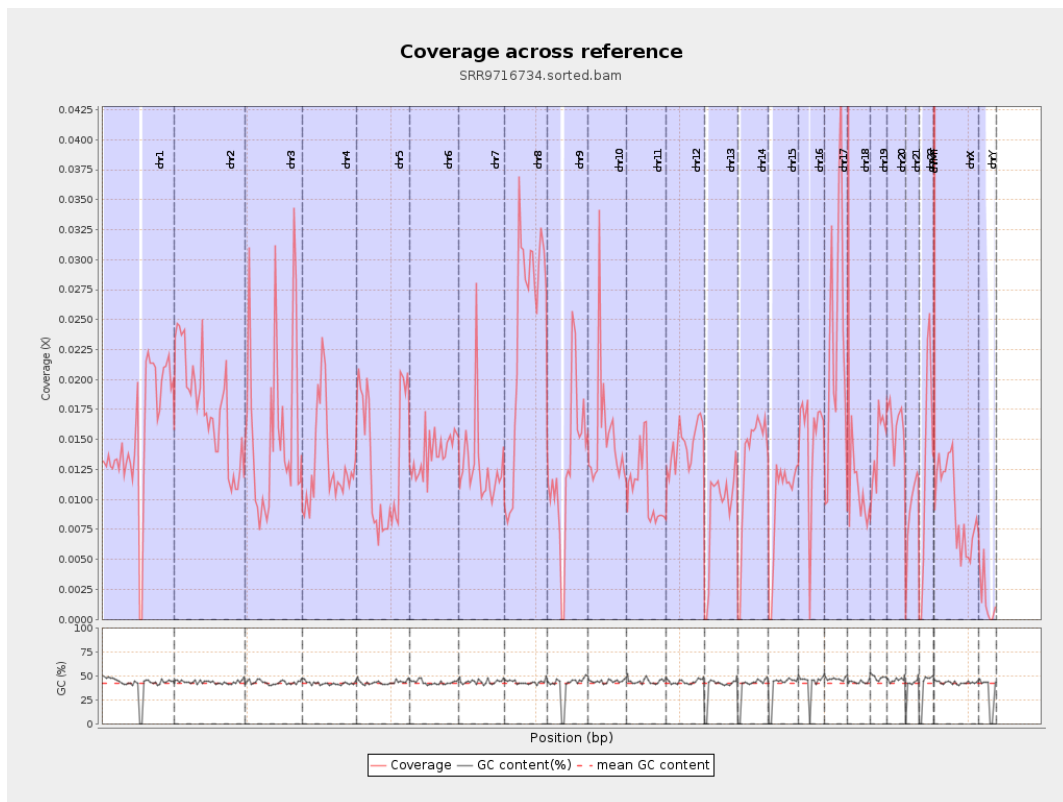
General error rate	0.49%
Mismatches	206,591
Insertions	3,012
Mapped reads with at least one insertion	0.41%
Deletions	7,473
Mapped reads with at least one deletion	1.01%
Homopolymer indels	41.35%

2.6. Chromosome stats

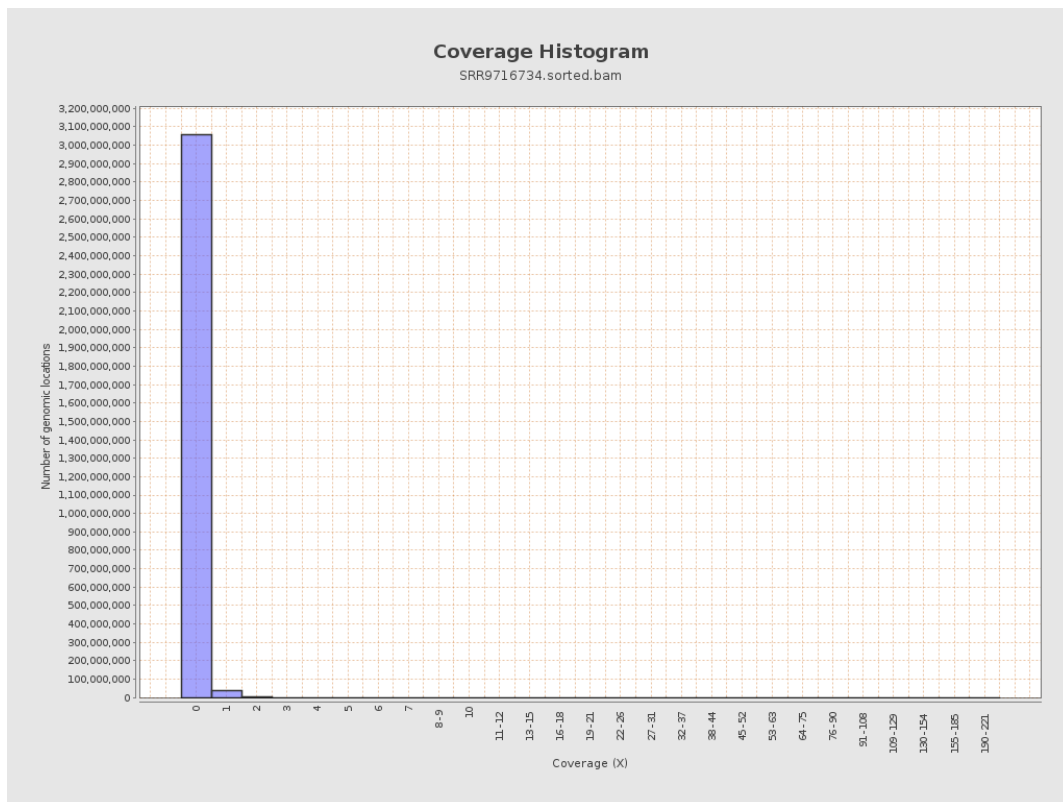
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3844272	0.0154	0.2047
chr2	243199373	4296648	0.0177	0.177
chr3	198022430	3090419	0.0156	0.1323
chr4	191154276	2479143	0.013	0.1279
chr5	180915260	2374671	0.0131	0.12
chr6	171115067	2369000	0.0138	0.1273
chr7	159138663	2036699	0.0128	0.233

chr8	146364022	3550561	0.0243	0.1926
chr9	141213431	1787774	0.0127	0.1257
chr10	135534747	2048889	0.0151	0.184
chr11	135006516	1474210	0.0109	0.1199
chr12	133851895	1948969	0.0146	0.1309
chr13	115169878	1059424	0.0092	0.1003
chr14	107349540	1401054	0.0131	0.1218
chr15	102531392	991179	0.0097	0.1027
chr16	90354753	1349446	0.0149	0.1306
chr17	81195210	1858471	0.0229	0.1619
chr18	78077248	957964	0.0123	0.1641
chr19	59128983	855730	0.0145	0.1795
chr20	63025520	1024563	0.0163	0.1353
chr21	48129895	443609	0.0092	0.1056
chr22	51304566	660590	0.0129	0.1186
chrMT	16571	95552	5.7662	4.3483
chrX	155270560	1457615	0.0094	0.108
chrY	59373566	99169	0.0017	0.0606

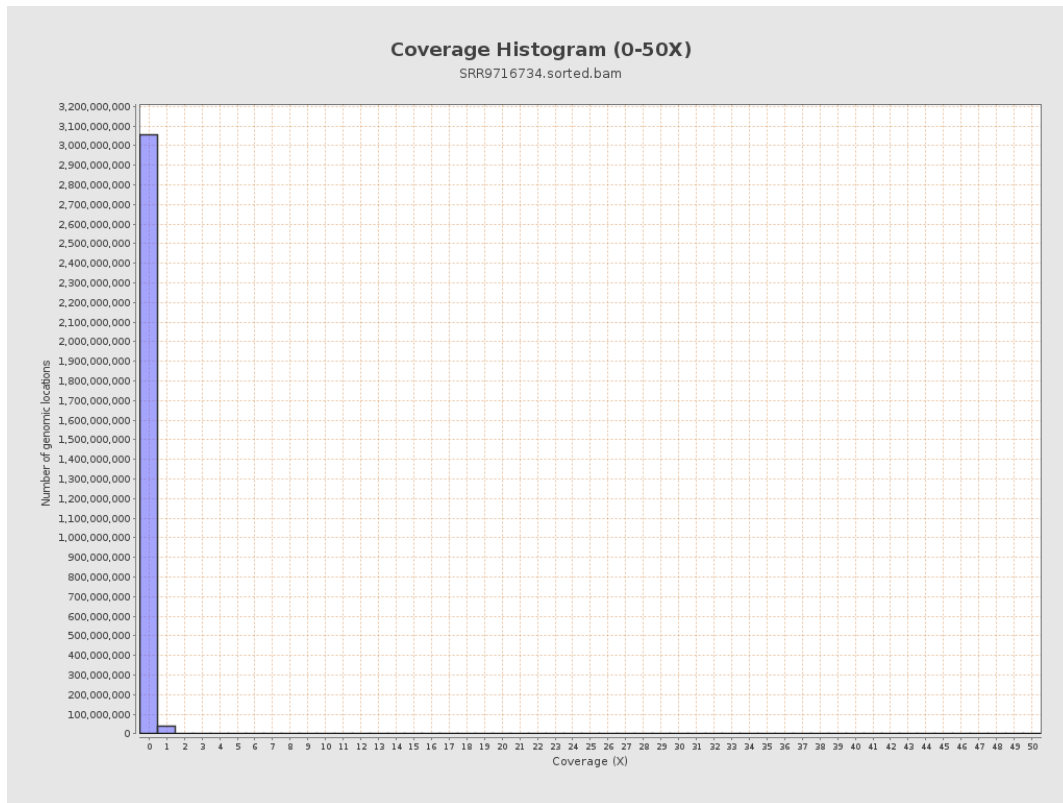
3. Results : Coverage across reference



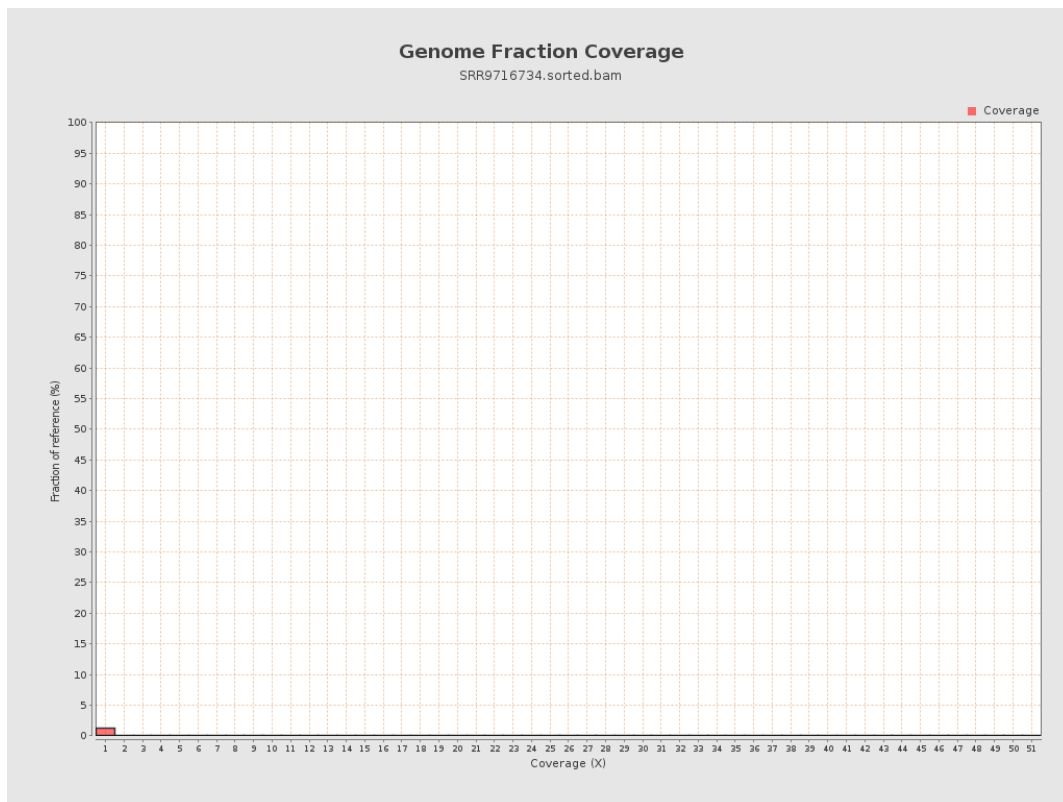
4. Results : Coverage Histogram



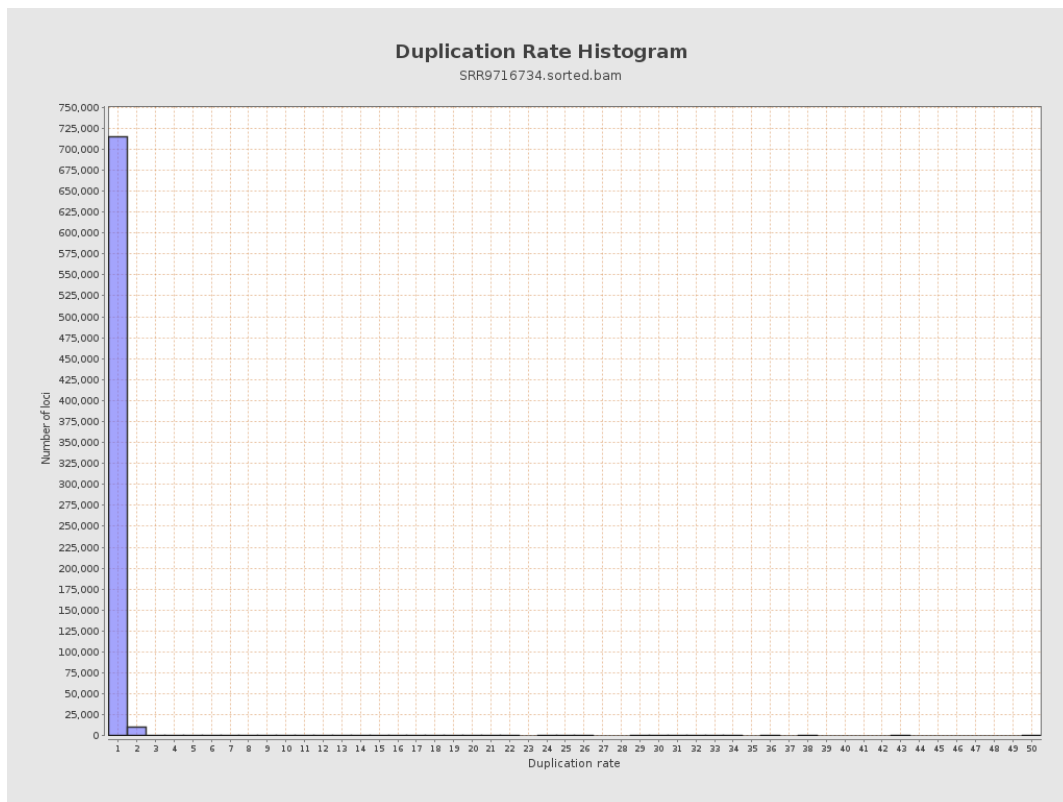
5. Results : Coverage Histogram (0-50X)



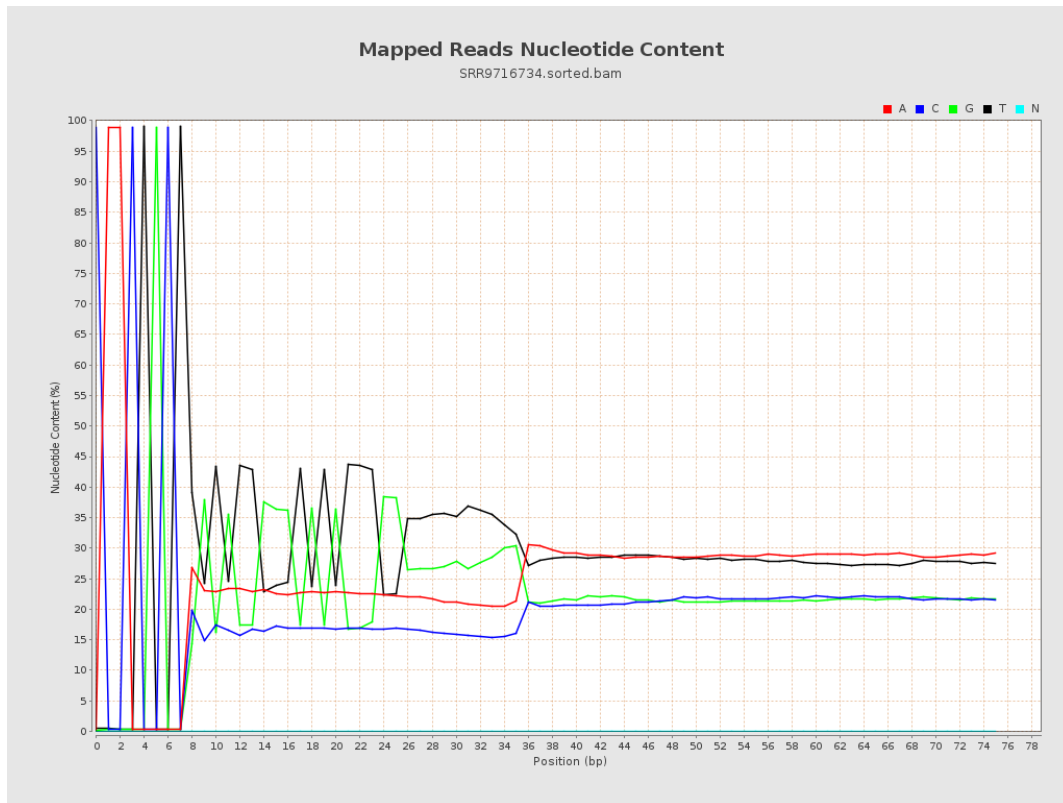
6. Results : Genome Fraction Coverage



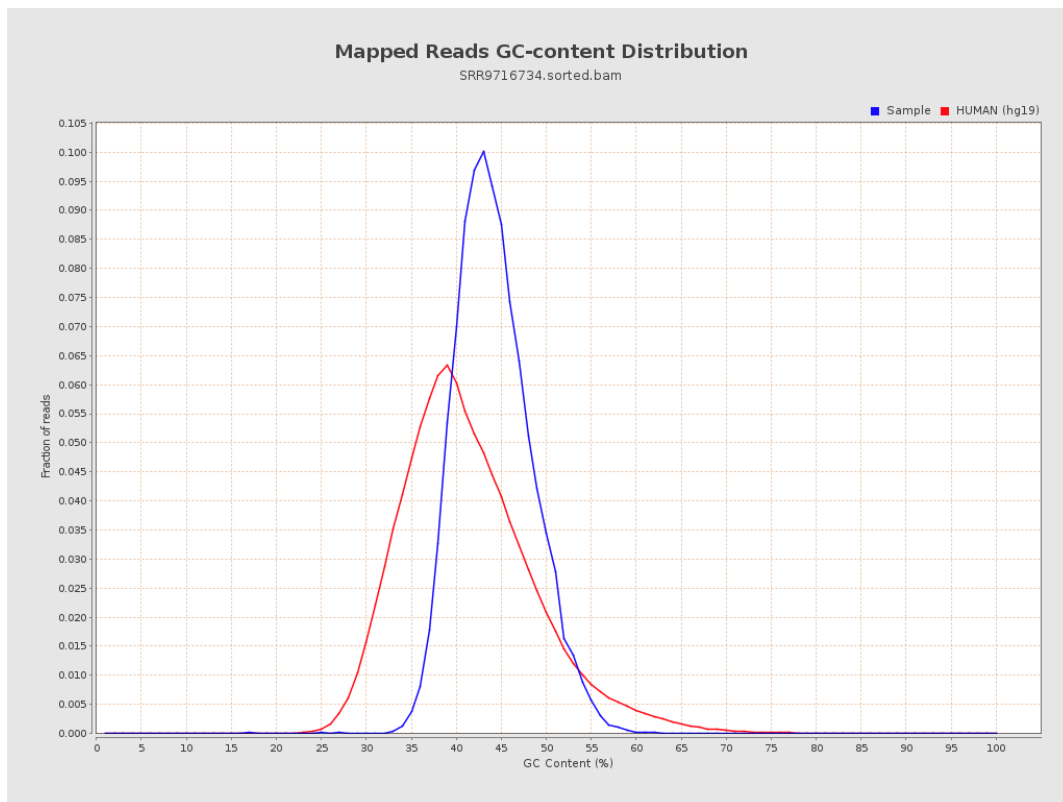
7. Results : Duplication Rate Histogram



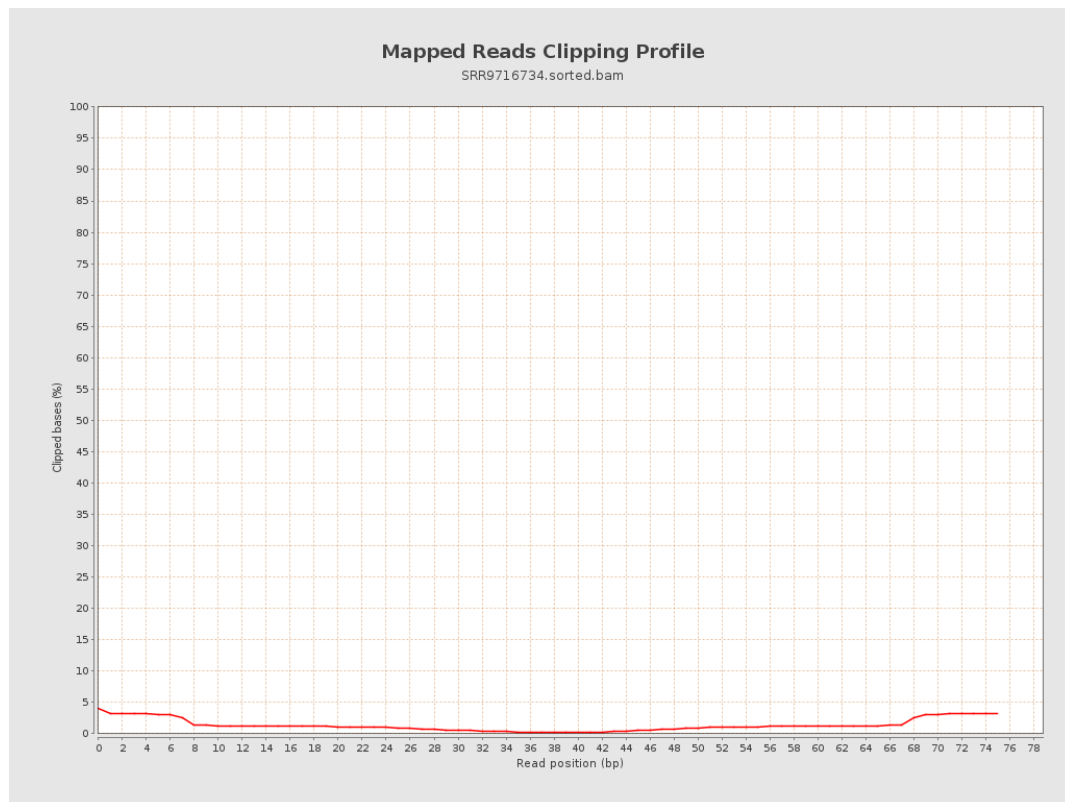
8. Results : Mapped Reads Nucleotide Content



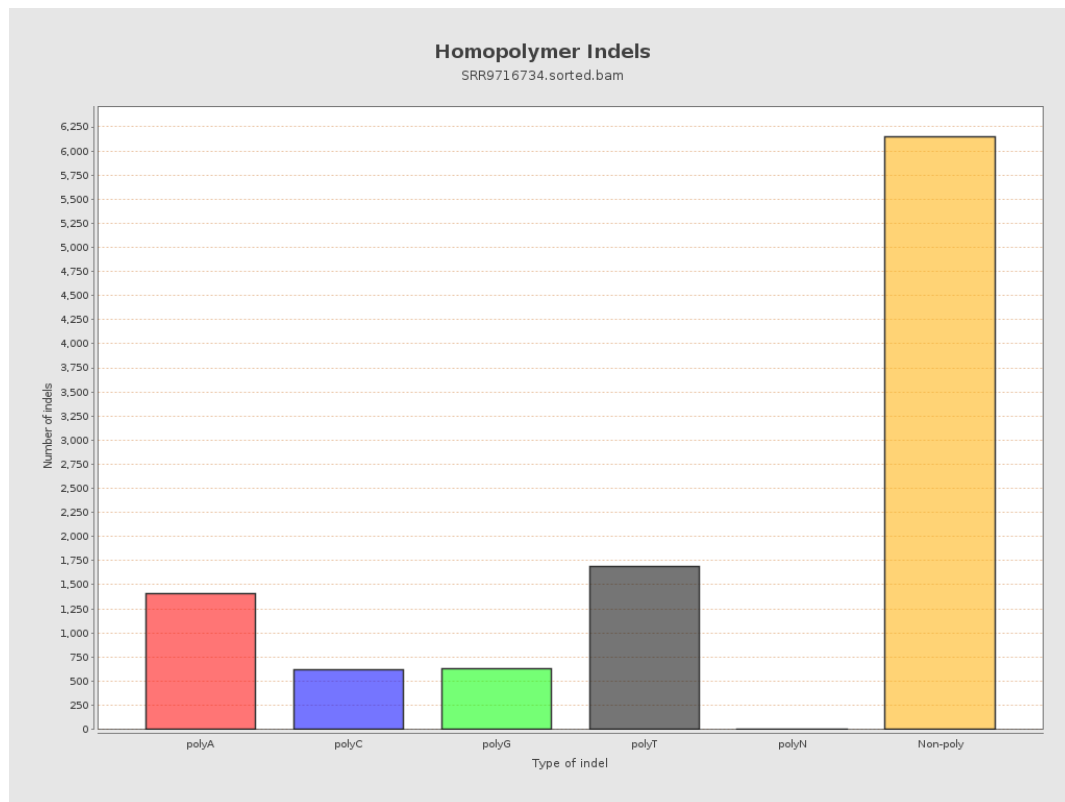
9. Results : Mapped Reads GC-content Distribution



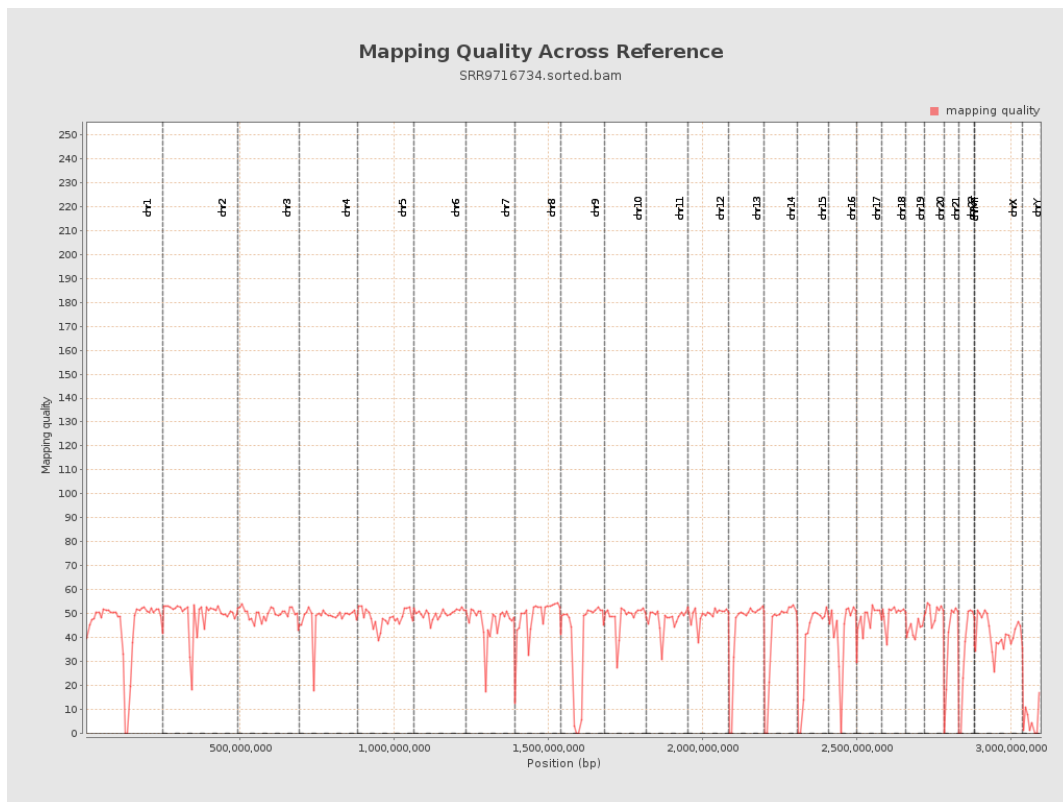
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

