

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:00:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716684.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_SRR9716684 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716684.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:00:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716684.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	647,873
Mapped reads	530,142 / 81.83%
Unmapped reads	117,731 / 18.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,341 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	7,715 / 1.19%
Duplication rate	1.02%
Clipped reads	531,154 / 81.98%

2.2. ACGT Content

Number/percentage of A's	7,304,531 / 24.29%
Number/percentage of C's	5,321,732 / 17.7%
Number/percentage of T's	9,522,968 / 31.67%
Number/percentage of G's	7,918,598 / 26.34%
Number/percentage of N's	229 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.116
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2.4. Mapping Quality

Mean Mapping Quality	41.94
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2.5. Mismatches and indels

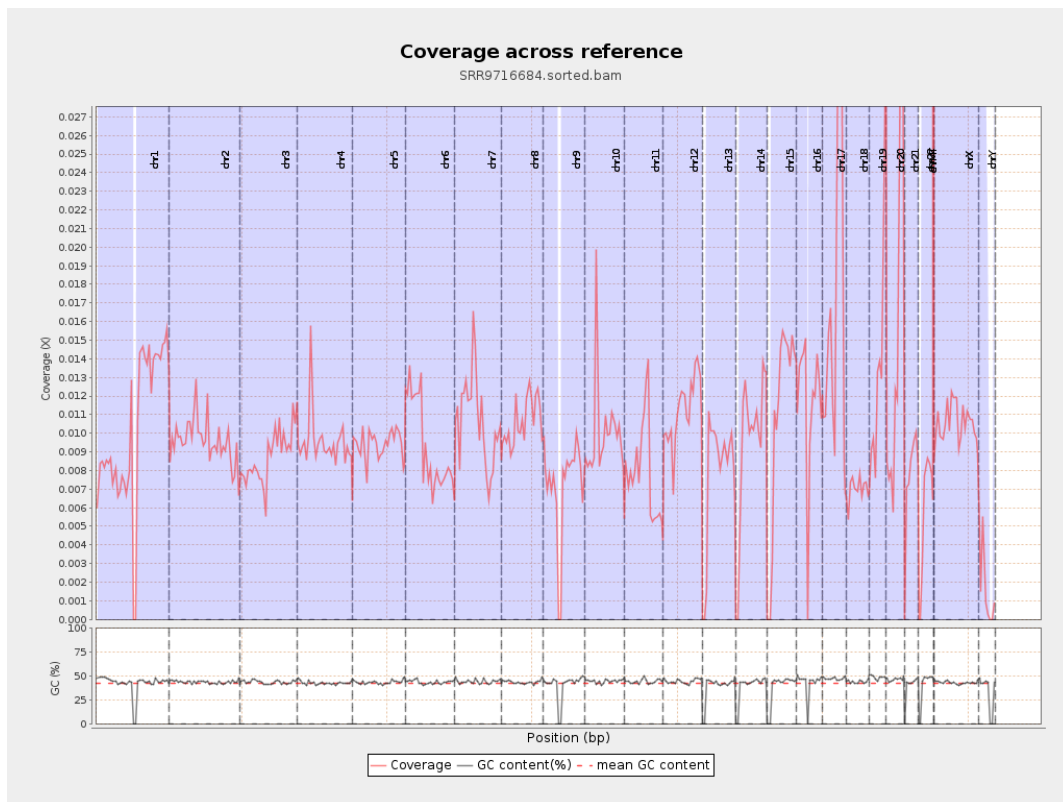
General error rate	0.54%
Mismatches	157,314
Insertions	2,204
Mapped reads with at least one insertion	0.41%
Deletions	5,744
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.76%

2.6. Chromosome stats

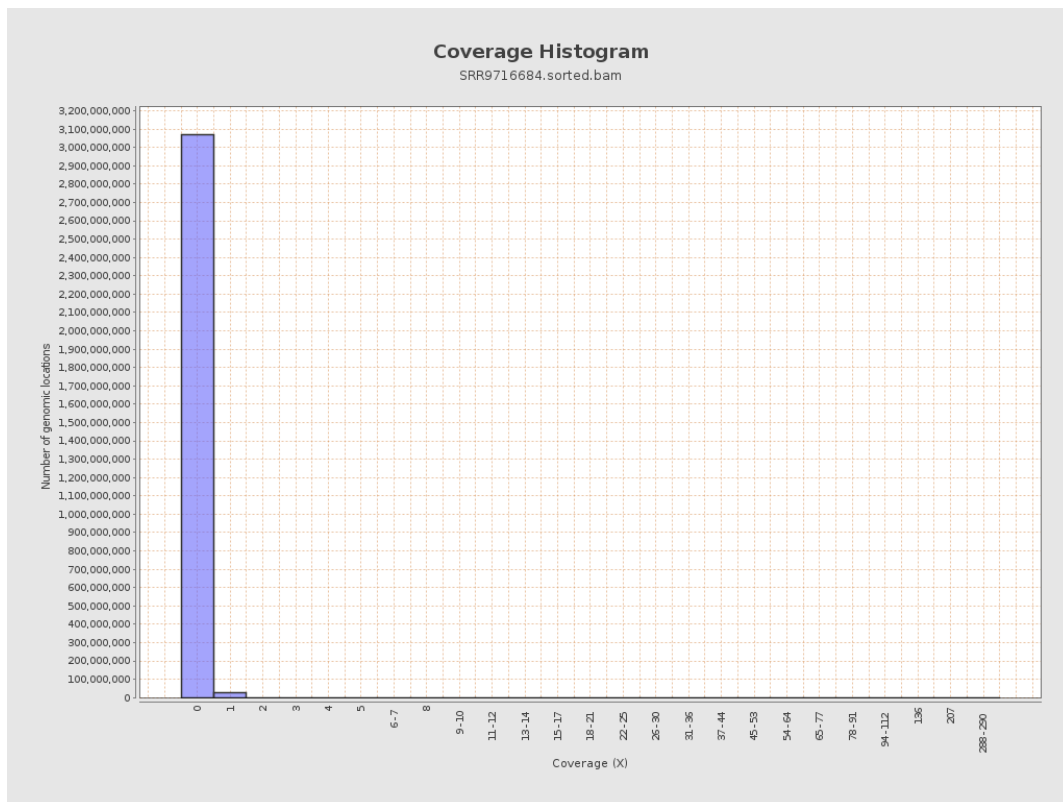
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2532393	0.0102	0.1315
chr2	243199373	2336091	0.0096	0.1536
chr3	198022430	1724590	0.0087	0.0973
chr4	191154276	1816766	0.0095	0.1047
chr5	180915260	1697629	0.0094	0.0997
chr6	171115067	1596049	0.0093	0.1059
chr7	159138663	1702522	0.0107	0.1413

chr8	146364022	1558330	0.0106	0.1164
chr9	141213431	1000668	0.0071	0.0944
chr10	135534747	1351488	0.01	0.1346
chr11	135006516	1073999	0.008	0.0998
chr12	133851895	1501376	0.0112	0.1093
chr13	115169878	898648	0.0078	0.0913
chr14	107349540	1012898	0.0094	0.1012
chr15	102531392	1118471	0.0109	0.1083
chr16	90354753	1054523	0.0117	0.1155
chr17	81195210	1353516	0.0167	0.1352
chr18	78077248	546975	0.007	0.1189
chr19	59128983	822596	0.0139	0.1418
chr20	63025520	983356	0.0156	0.1321
chr21	48129895	371059	0.0077	0.0926
chr22	51304566	288287	0.0056	0.0773
chrMT	16571	4017	0.2424	0.5505
chrX	155270560	1636451	0.0105	0.109
chrY	59373566	94545	0.0016	0.0559

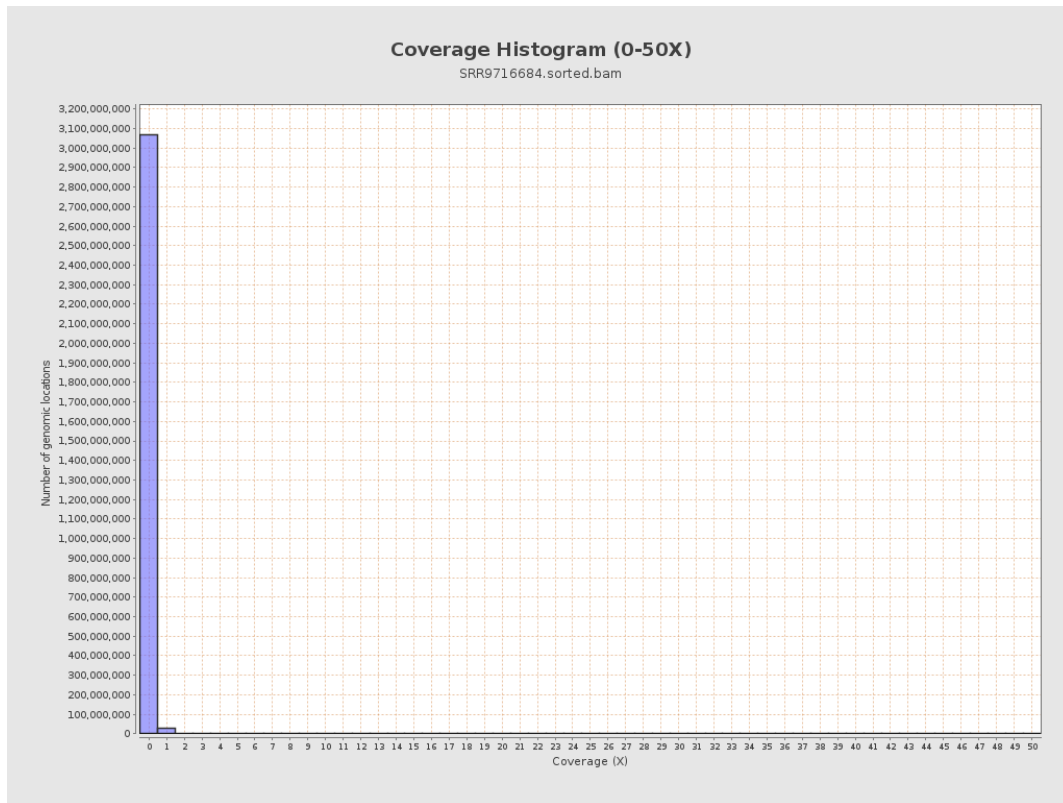
3. Results : Coverage across reference



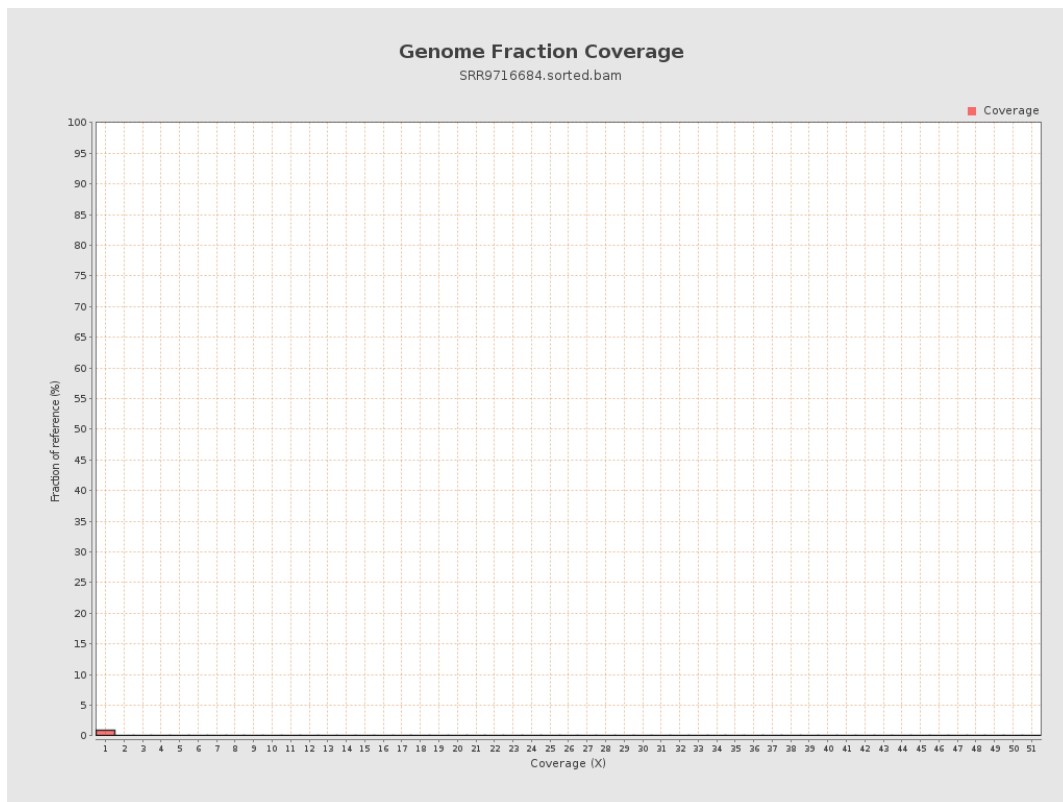
4. Results : Coverage Histogram



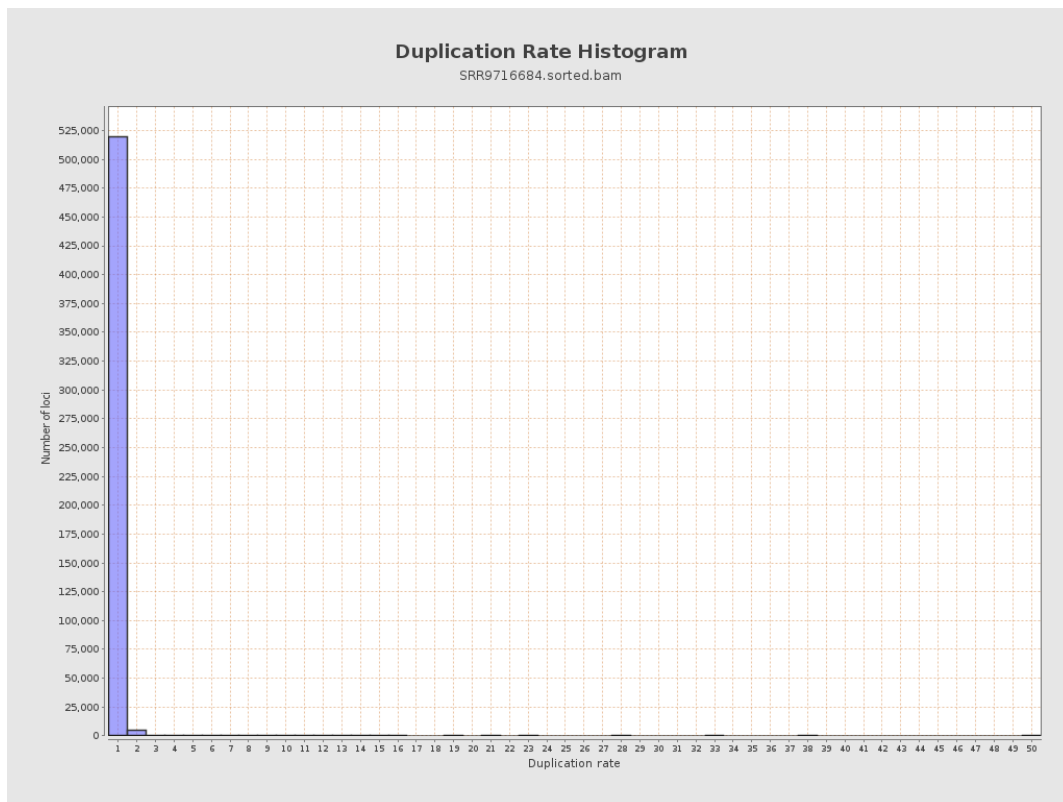
5. Results : Coverage Histogram (0-50X)



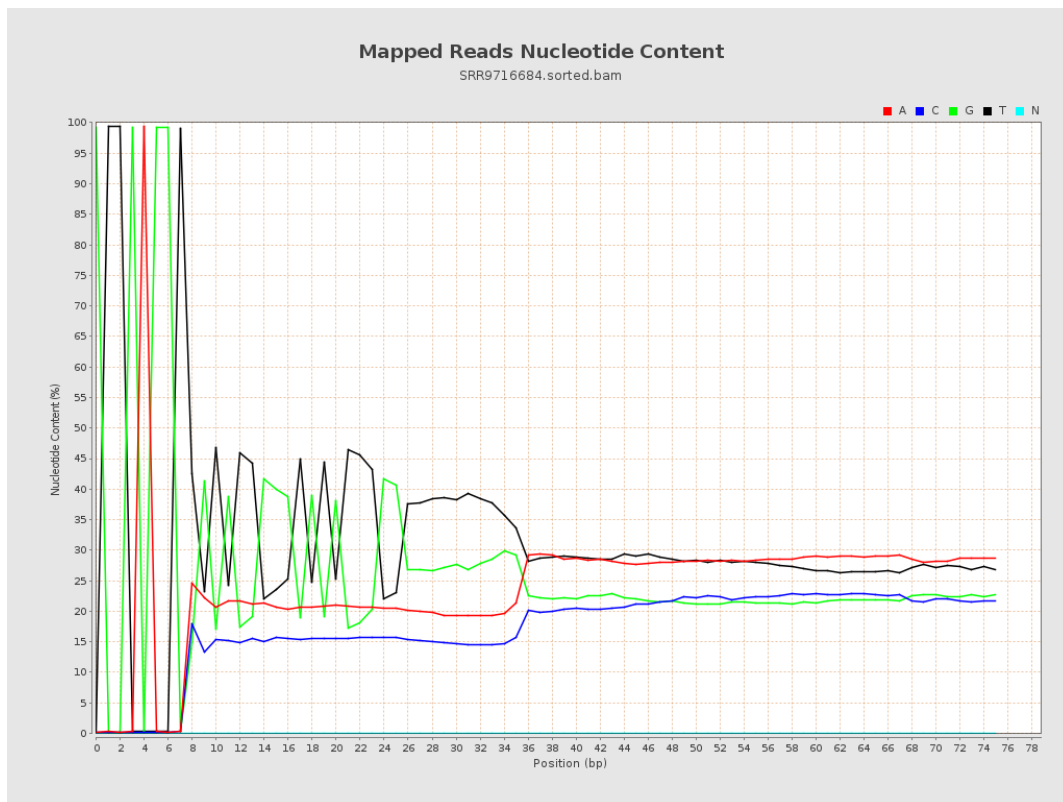
6. Results : Genome Fraction Coverage



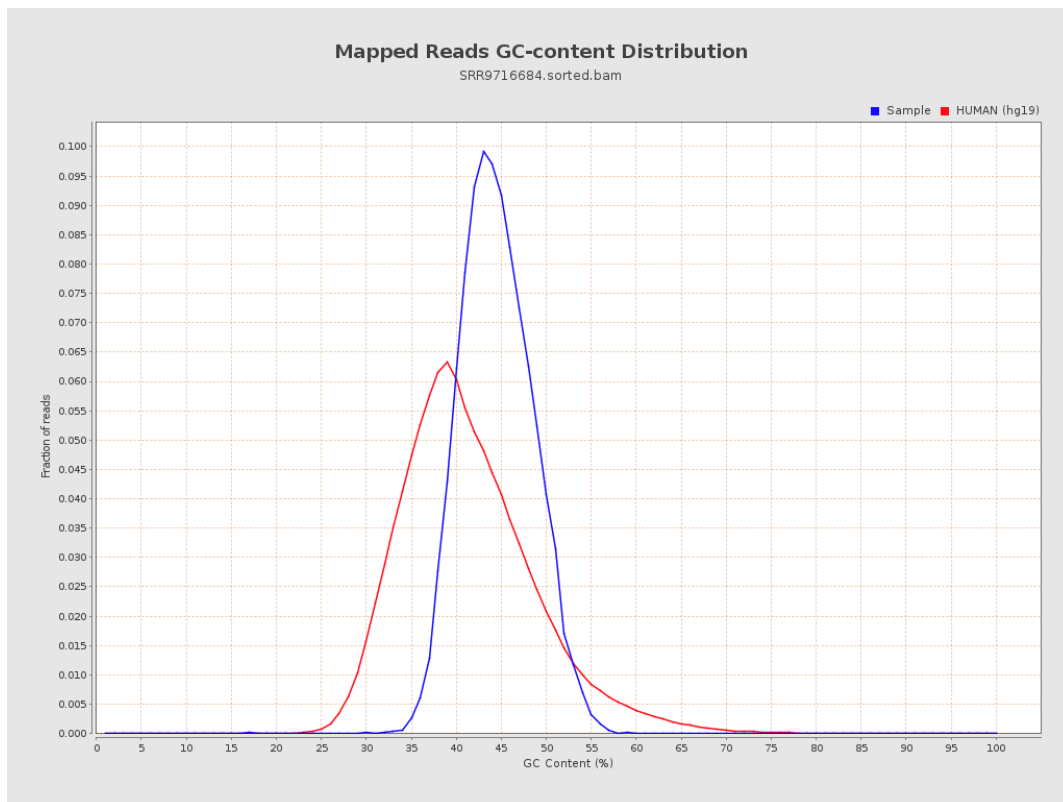
7. Results : Duplication Rate Histogram



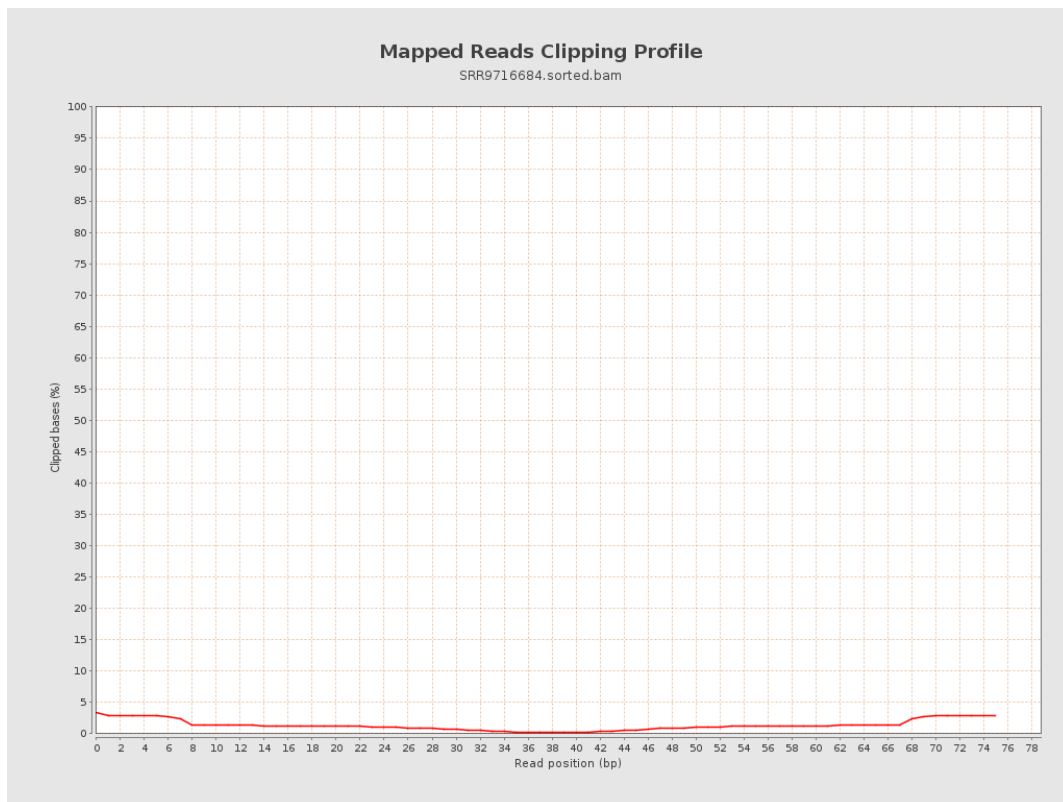
8. Results : Mapped Reads Nucleotide Content



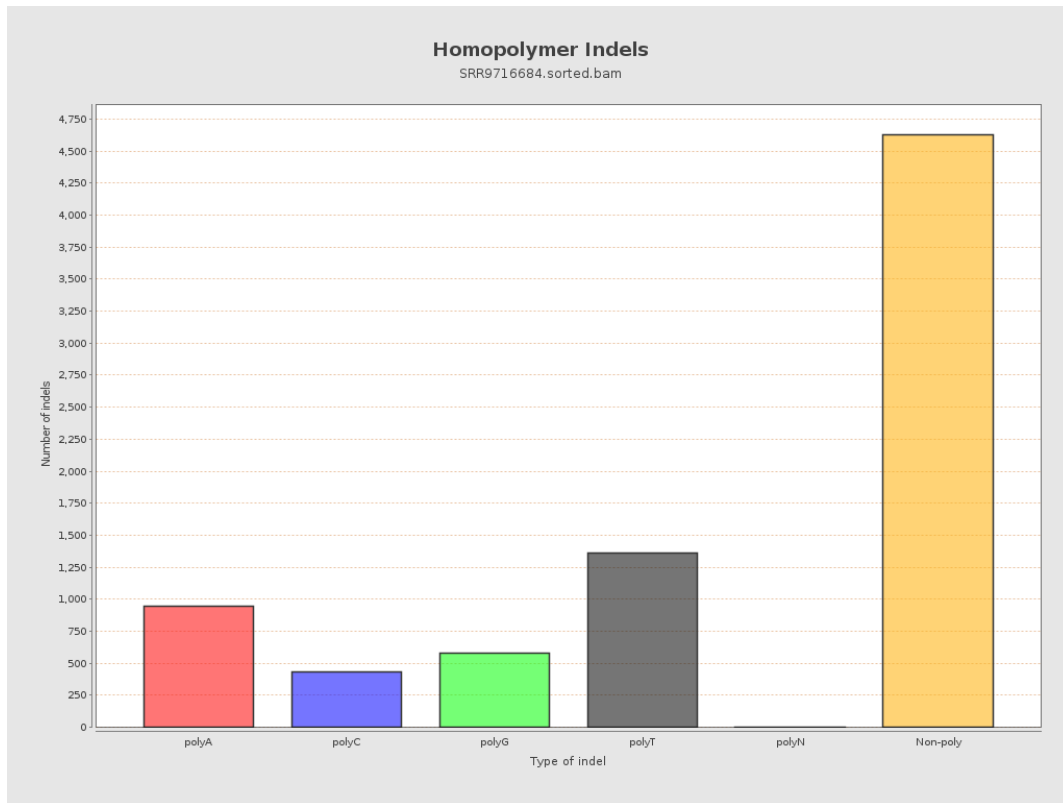
9. Results : Mapped Reads GC-content Distribution



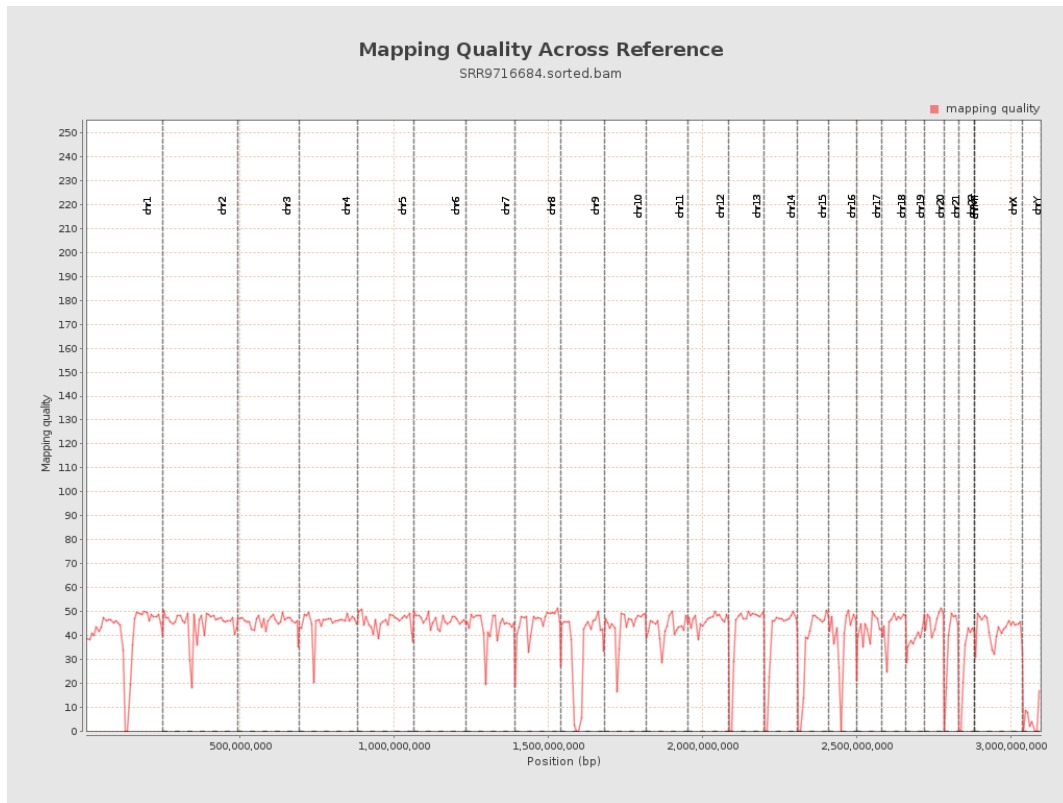
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

