

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:08:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716674.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_SRR9716674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716674.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:08:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,036,347
Mapped reads	3,742,407 / 92.72%
Unmapped reads	293,940 / 7.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	71,560 / 1.77%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	247,161 / 6.12%
Duplication rate	4.88%
Clipped reads	3,804,501 / 94.26%

2.2. ACGT Content

Number/percentage of A's	77,903,340 / 26.37%
Number/percentage of C's	54,891,574 / 18.58%
Number/percentage of T's	90,271,428 / 30.55%
Number/percentage of G's	72,378,244 / 24.5%
Number/percentage of N's	21,881 / 0.01%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0955

Standard Deviation	0.7256
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2.4. Mapping Quality

Mean Mapping Quality	47.62
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2.5. Mismatches and indels

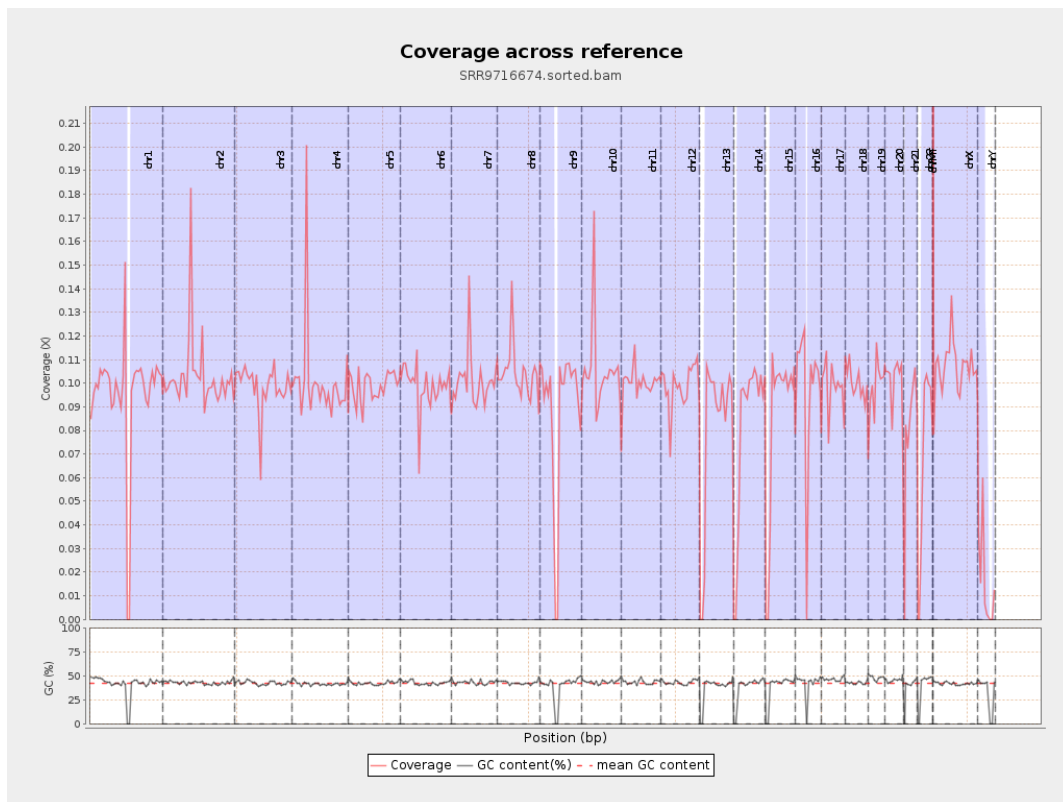
General error rate	0.67%
Mismatches	1,928,225
Insertions	26,052
Mapped reads with at least one insertion	0.68%
Deletions	71,400
Mapped reads with at least one deletion	1.88%
Homopolymer indels	42.61%

2.6. Chromosome stats

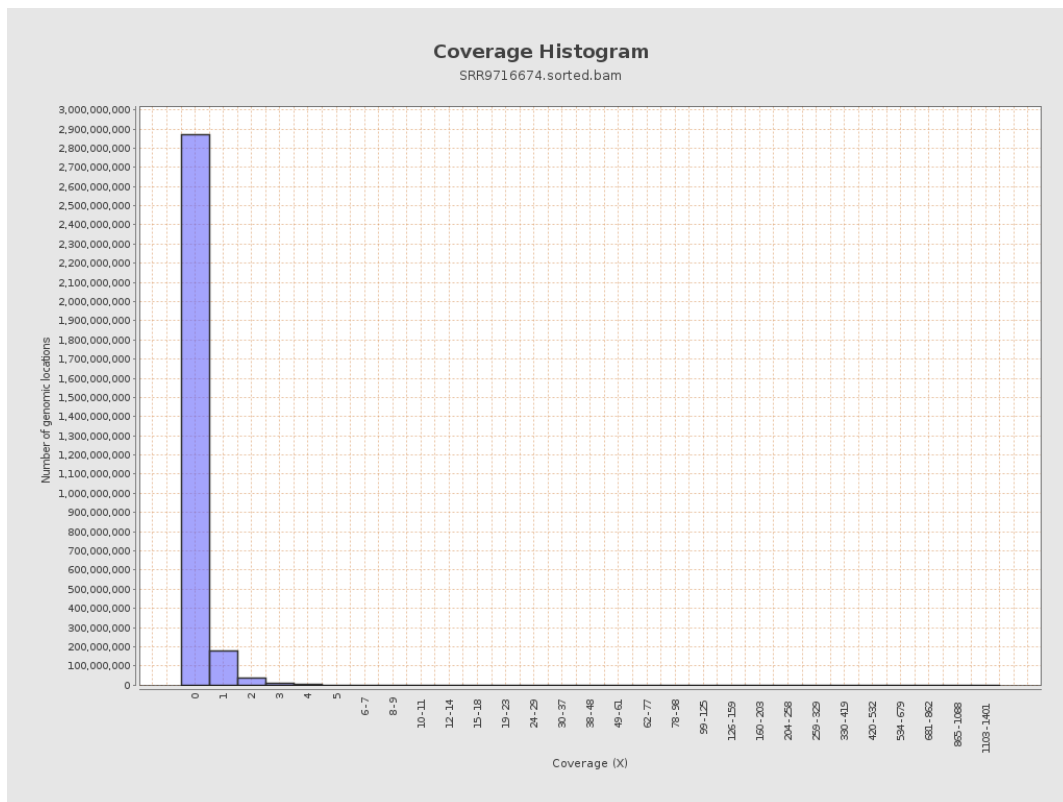
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23715892	0.0951	1.2861
chr2	243199373	25021517	0.1029	0.9099
chr3	198022430	19498573	0.0985	0.3893
chr4	191154276	19291397	0.1009	0.5936
chr5	180915260	17901429	0.0989	0.4017
chr6	171115067	16884638	0.0987	0.4551
chr7	159138663	16080507	0.101	0.9848

chr8	146364022	15191026	0.1038	0.9335
chr9	141213431	12447076	0.0881	0.659
chr10	135534747	14233358	0.105	0.8126
chr11	135006516	13554356	0.1004	0.7289
chr12	133851895	13282433	0.0992	0.3983
chr13	115169878	9279694	0.0806	0.3523
chr14	107349540	8892678	0.0828	0.4187
chr15	102531392	8547417	0.0834	0.3635
chr16	90354753	8643217	0.0957	0.4455
chr17	81195210	8048499	0.0991	0.4999
chr18	78077248	7818499	0.1001	1.1432
chr19	59128983	5863448	0.0992	0.9585
chr20	63025520	6386115	0.1013	0.4429
chr21	48129895	3919324	0.0814	0.4637
chr22	51304566	3533376	0.0689	0.3327
chrMT	16571	8103	0.489	0.8439
chrX	155270560	16628814	0.1071	0.5252
chrY	59373566	933317	0.0157	0.5101

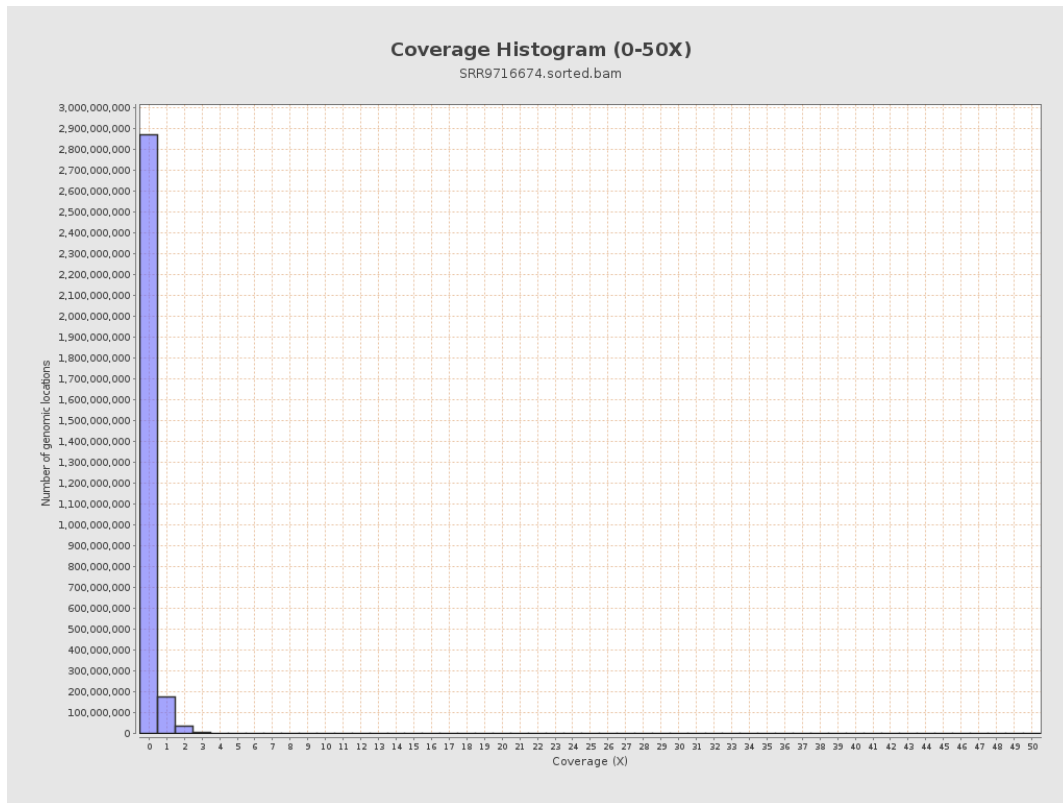
3. Results : Coverage across reference



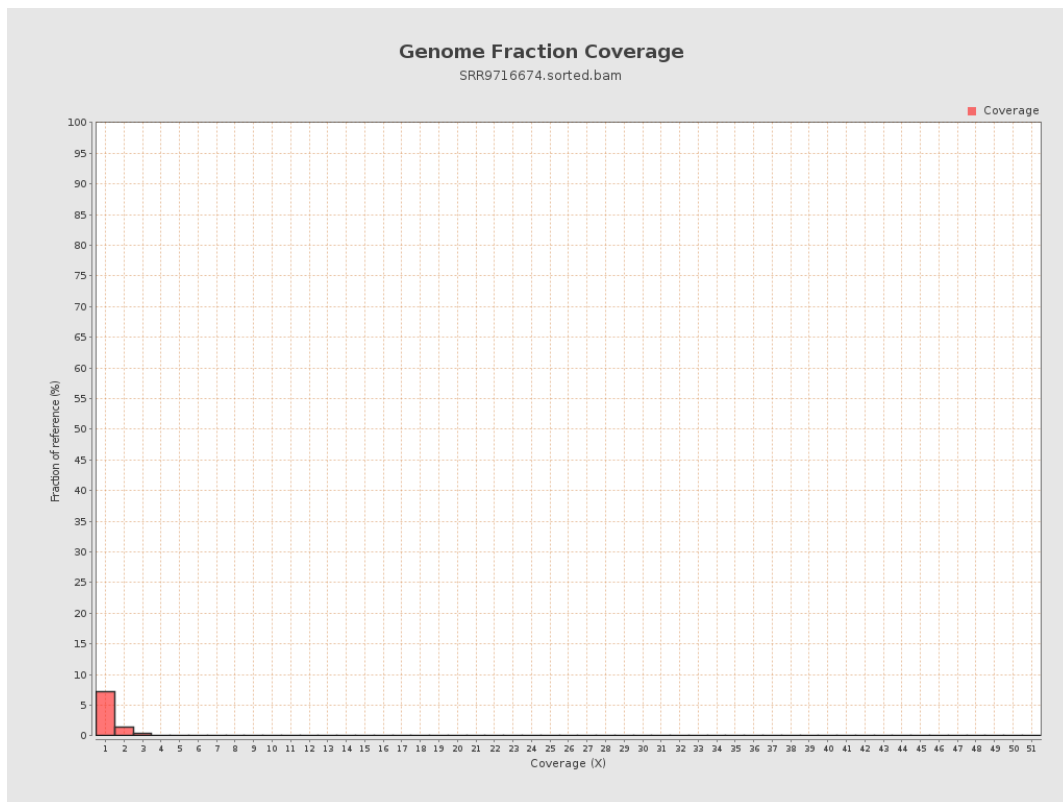
4. Results : Coverage Histogram



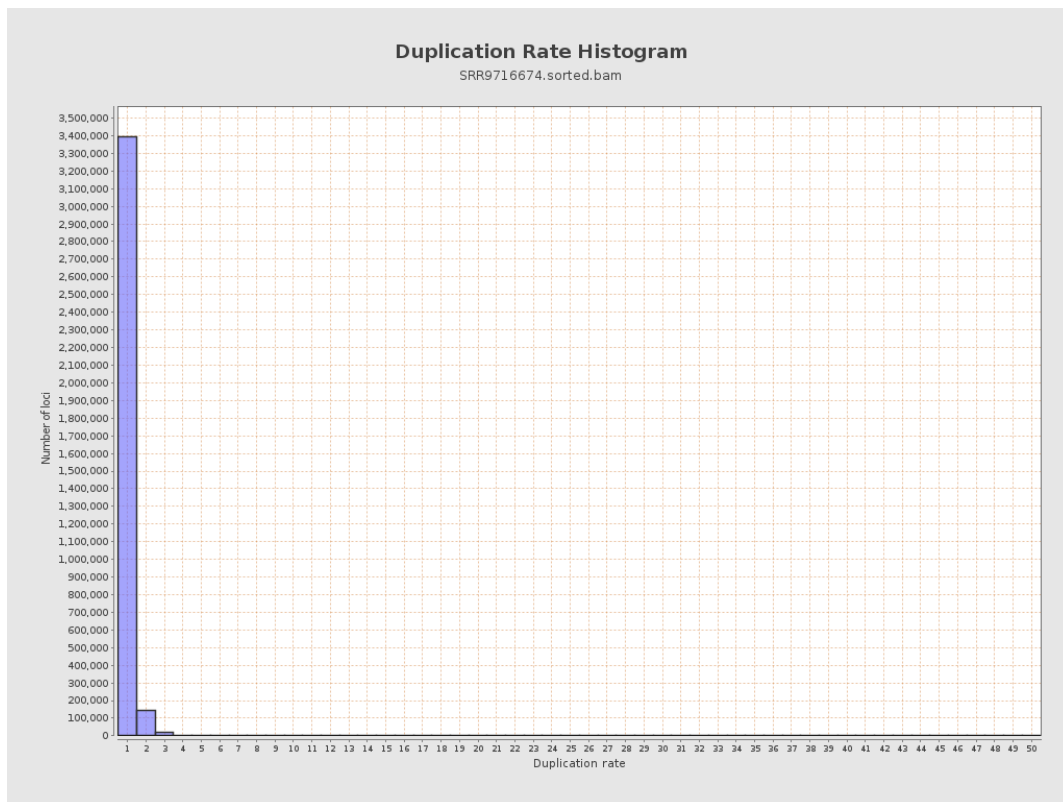
5. Results : Coverage Histogram (0-50X)



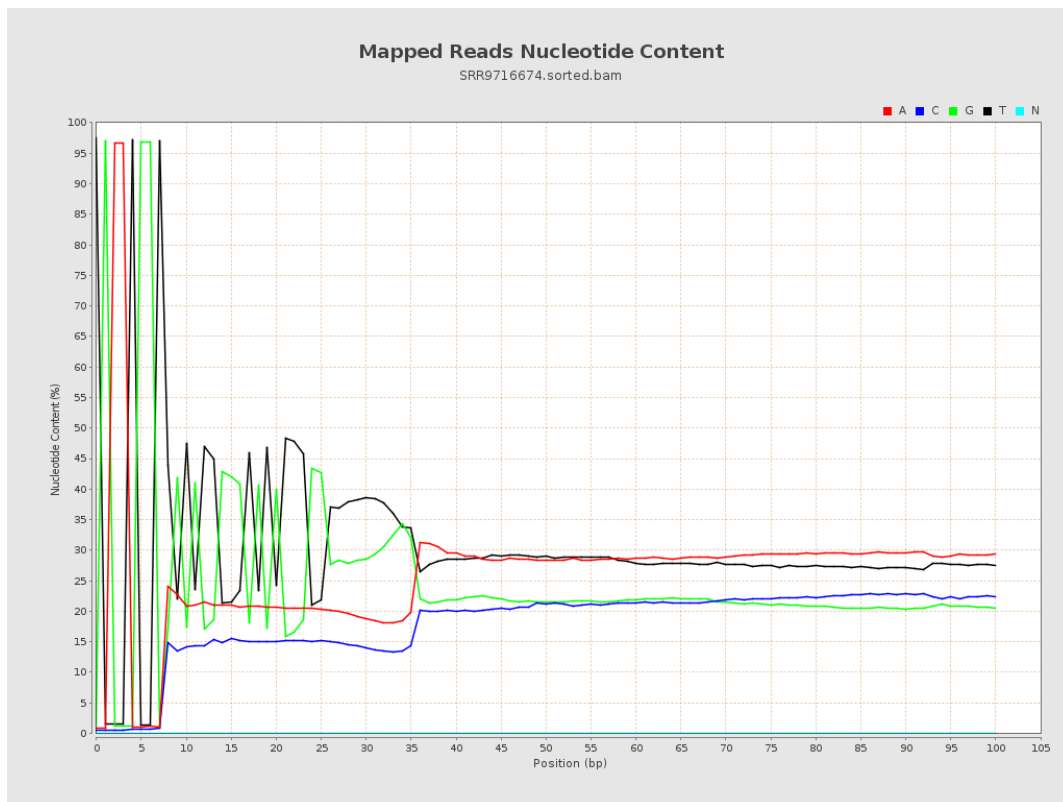
6. Results : Genome Fraction Coverage



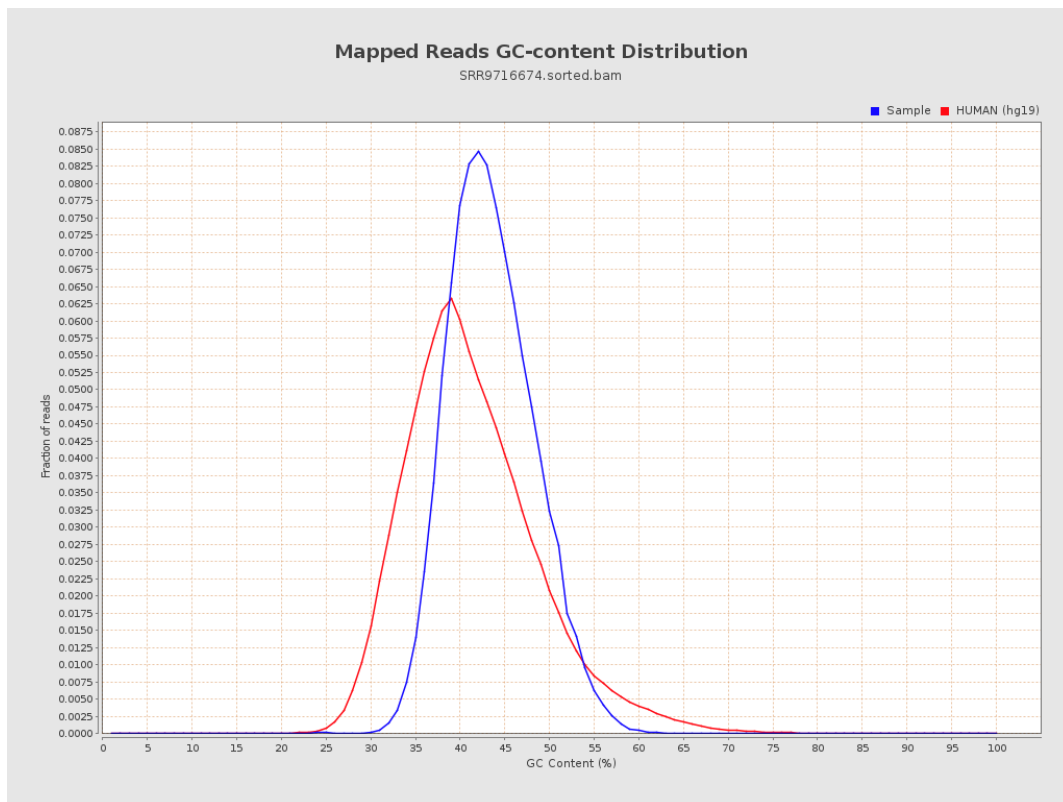
7. Results : Duplication Rate Histogram



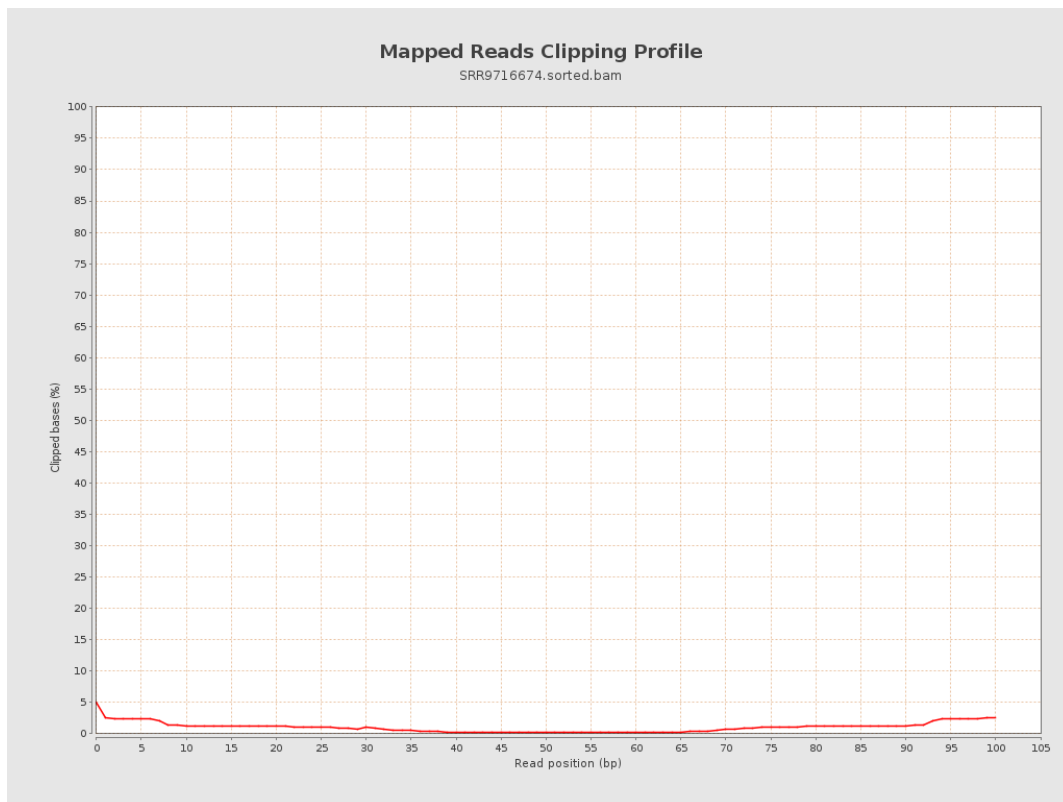
8. Results : Mapped Reads Nucleotide Content



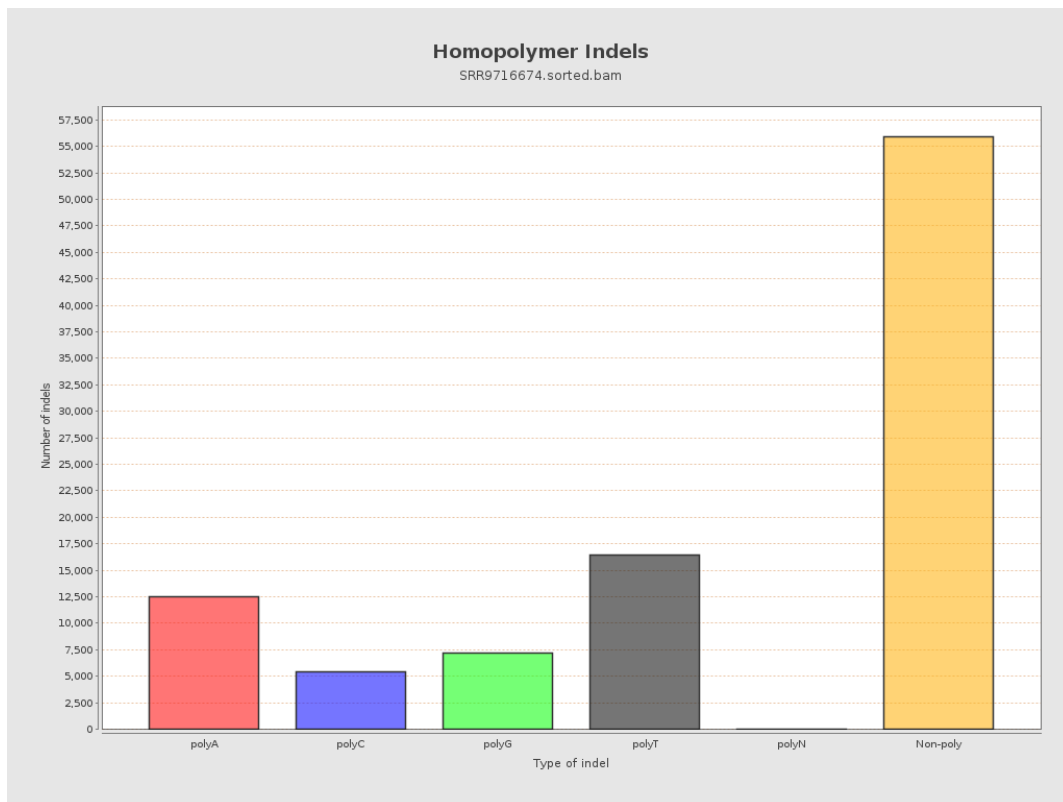
9. Results : Mapped Reads GC-content Distribution



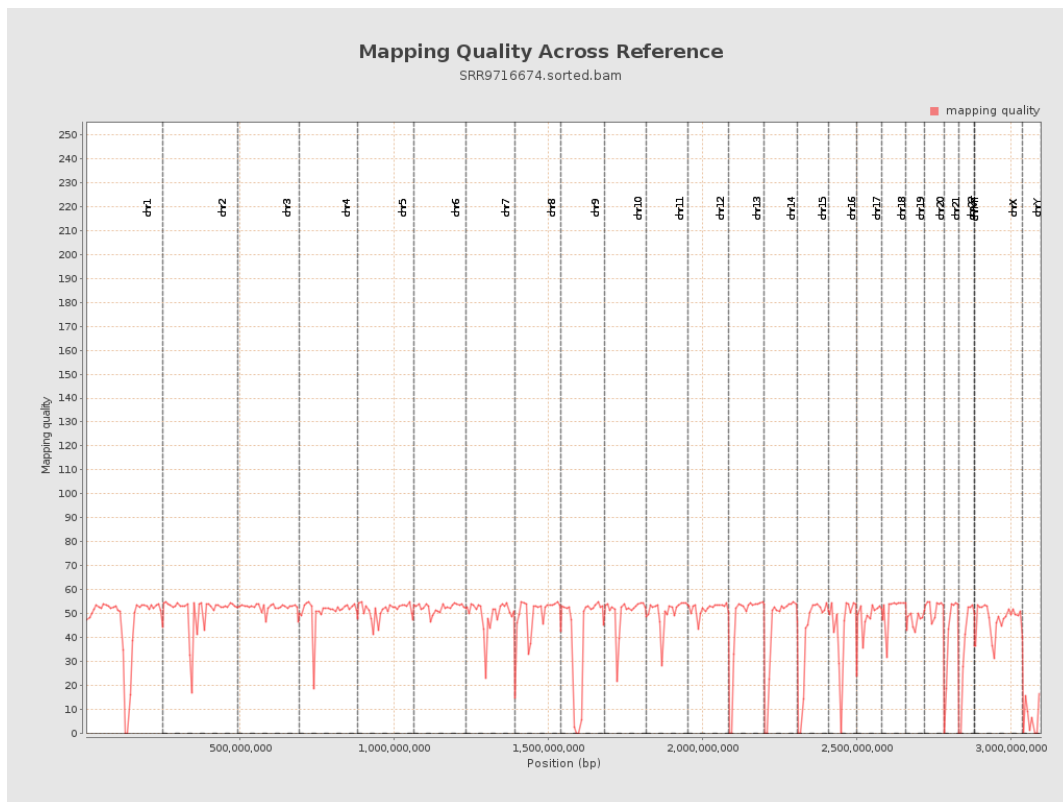
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

