

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:07:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716904.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_SRR9716904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716904.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:07:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	560,687
Mapped reads	481,789 / 85.93%
Unmapped reads	78,898 / 14.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,203 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	7,725 / 1.38%
Duplication rate	1.1%
Clipped reads	482,031 / 85.97%

2.2. ACGT Content

Number/percentage of A's	6,015,270 / 22.45%
Number/percentage of C's	5,002,556 / 18.67%
Number/percentage of T's	8,697,136 / 32.45%
Number/percentage of G's	7,083,552 / 26.43%
Number/percentage of N's	739 / 0%
GC Percentage	45.1%

2.3. Coverage

Mean	0.0087

Standard Deviation	0.1068
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2.4. Mapping Quality

Mean Mapping Quality	39.95
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2.5. Mismatches and indels

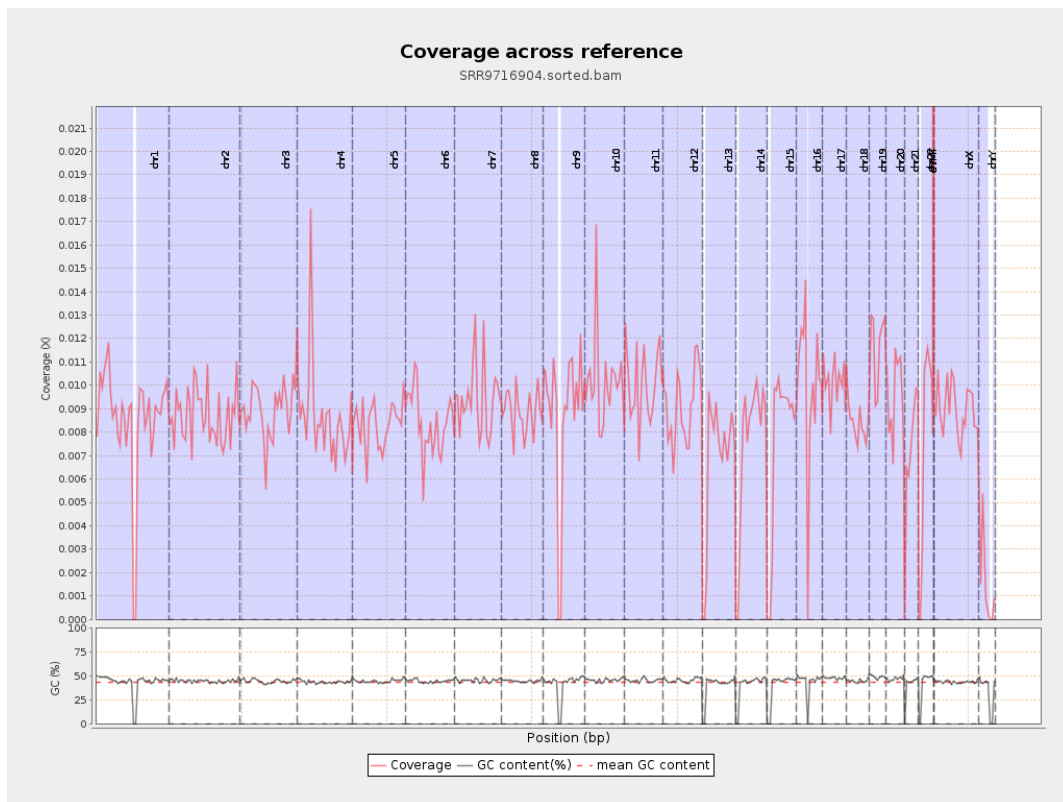
General error rate	0.55%
Mismatches	143,257
Insertions	2,061
Mapped reads with at least one insertion	0.43%
Deletions	4,644
Mapped reads with at least one deletion	0.96%
Homopolymer indels	40.3%

2.6. Chromosome stats

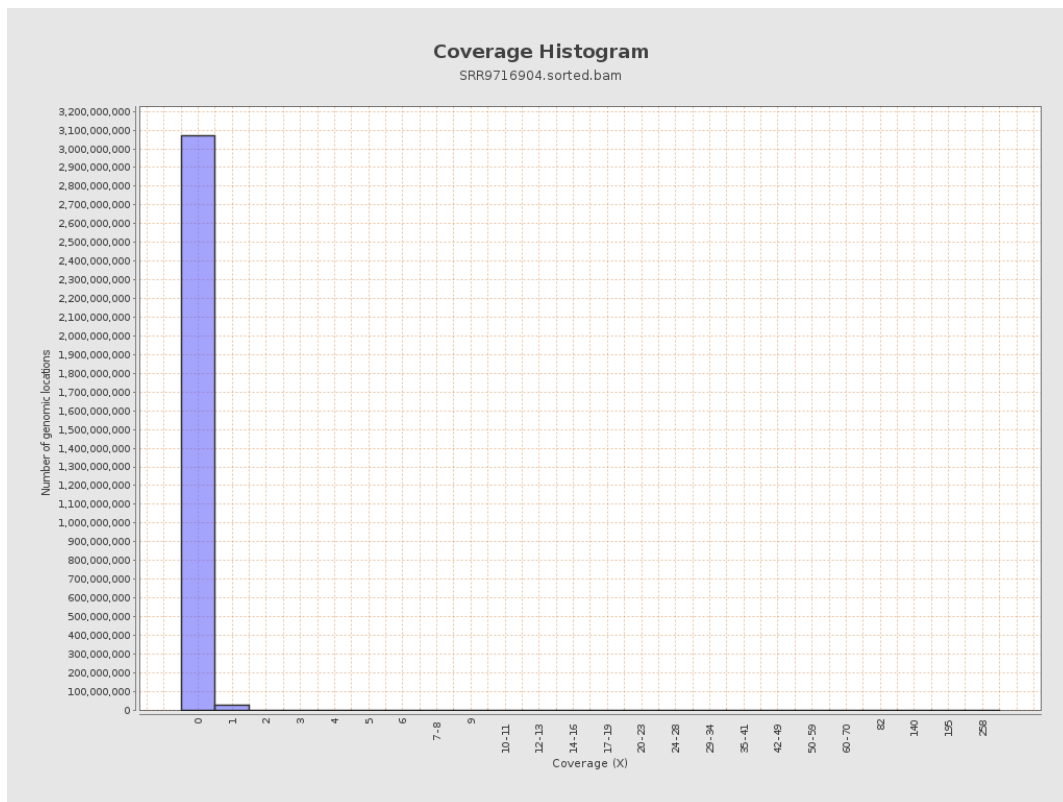
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2129146	0.0085	0.1033
chr2	243199373	2119686	0.0087	0.1435
chr3	198022430	1764679	0.0089	0.1029
chr4	191154276	1644923	0.0086	0.1031
chr5	180915260	1511175	0.0084	0.0956
chr6	171115067	1441379	0.0084	0.0985
chr7	159138663	1495560	0.0094	0.1136

chr8	146364022	1299654	0.0089	0.1022
chr9	141213431	1224130	0.0087	0.1006
chr10	135534747	1371939	0.0101	0.1238
chr11	135006516	1348090	0.01	0.1177
chr12	133851895	1211171	0.009	0.0995
chr13	115169878	781634	0.0068	0.0858
chr14	107349540	805061	0.0075	0.0914
chr15	102531392	779652	0.0076	0.0934
chr16	90354753	901432	0.01	0.1089
chr17	81195210	825486	0.0102	0.1072
chr18	78077248	657557	0.0084	0.1131
chr19	59128983	683598	0.0116	0.1238
chr20	63025520	596292	0.0095	0.1025
chr21	48129895	348450	0.0072	0.0929
chr22	51304566	376632	0.0073	0.0903
chrMT	16571	2632	0.1588	0.3944
chrX	155270560	1395441	0.009	0.1043
chrY	59373566	91580	0.0015	0.0558

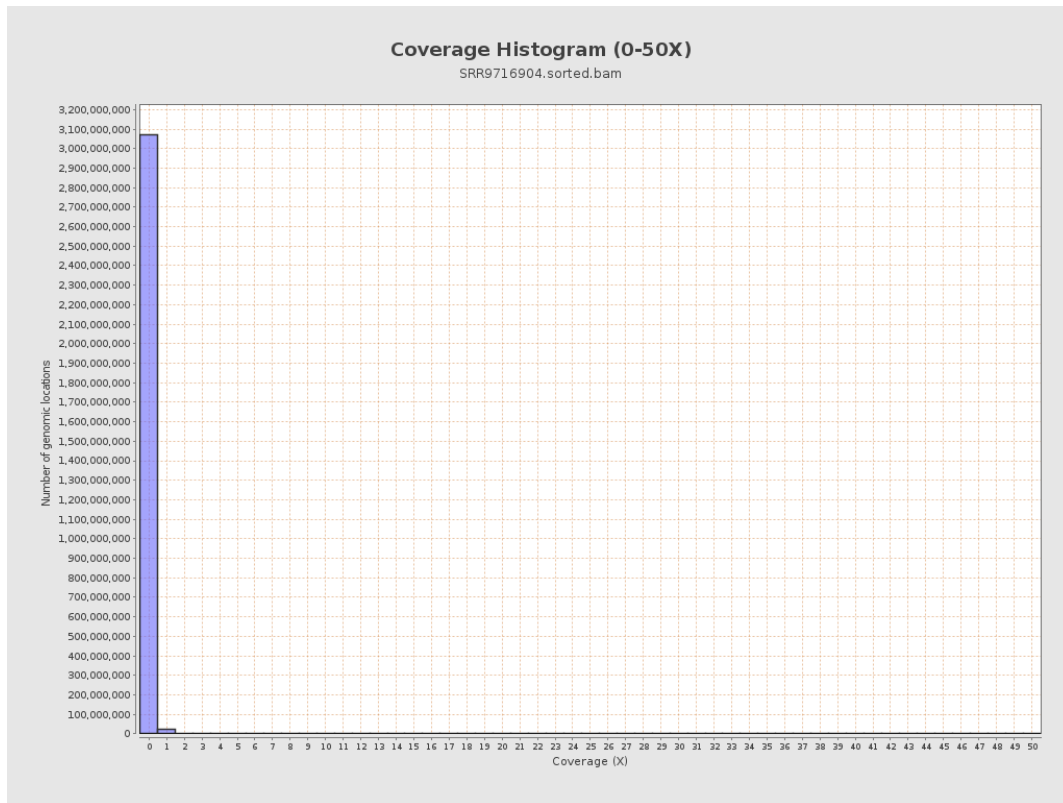
3. Results : Coverage across reference



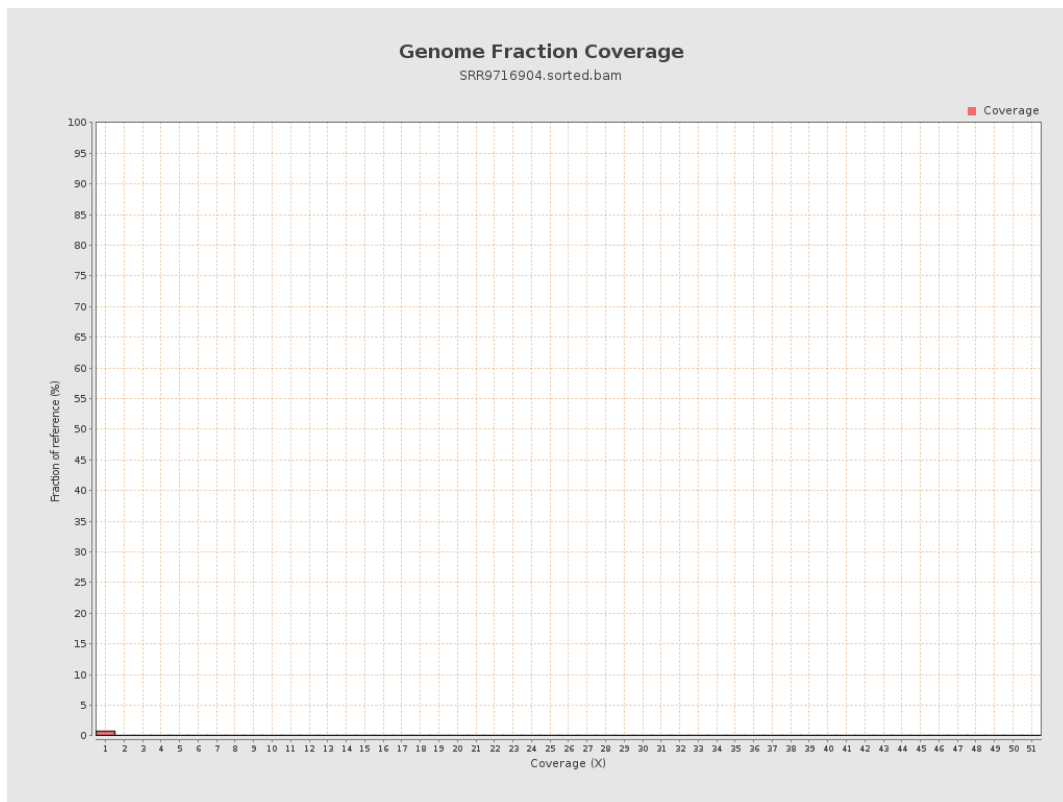
4. Results : Coverage Histogram



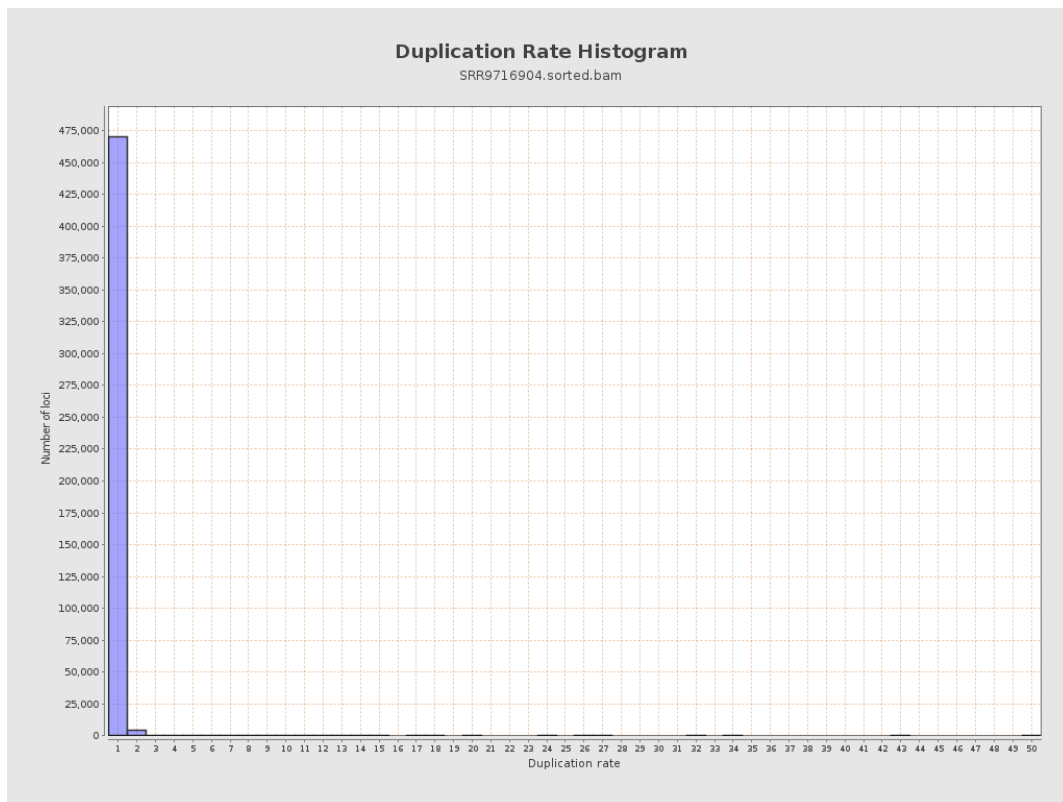
5. Results : Coverage Histogram (0-50X)



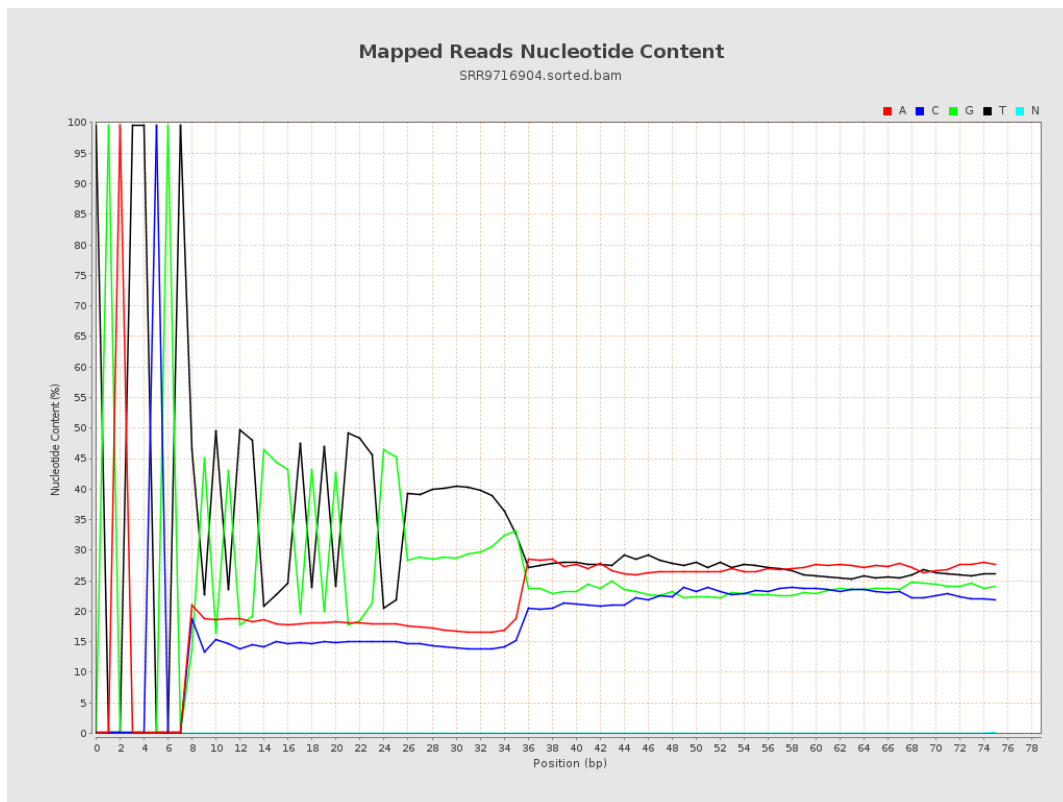
6. Results : Genome Fraction Coverage



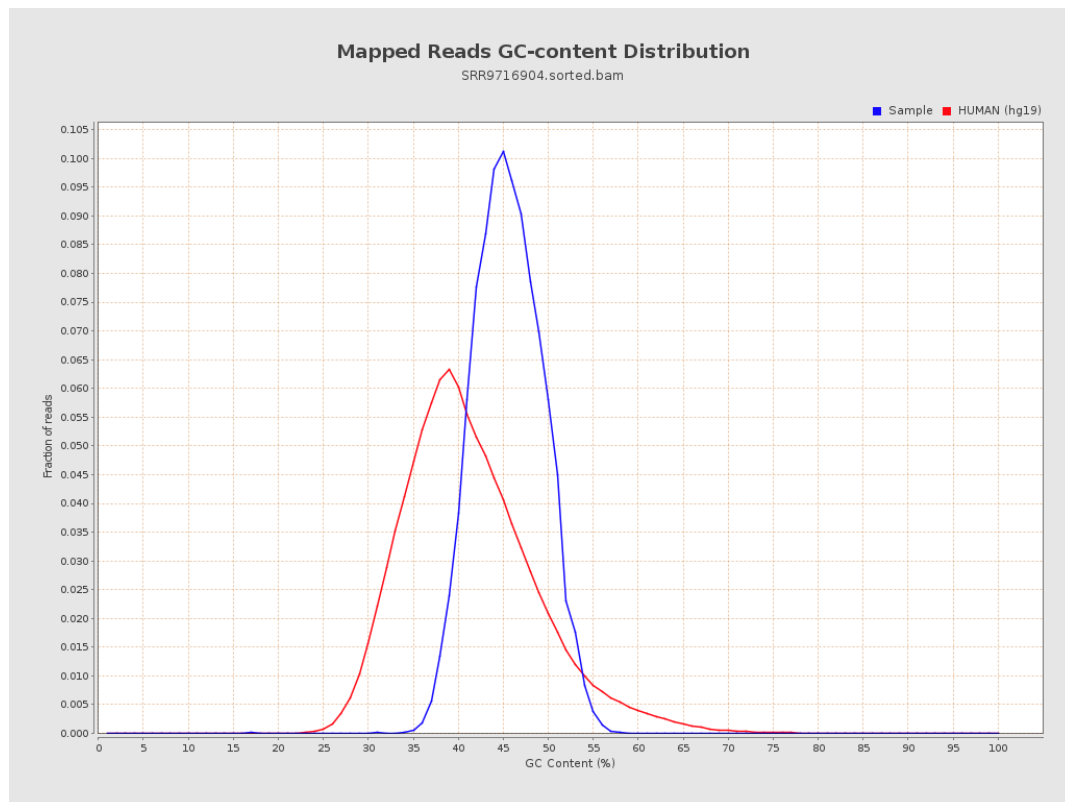
7. Results : Duplication Rate Histogram



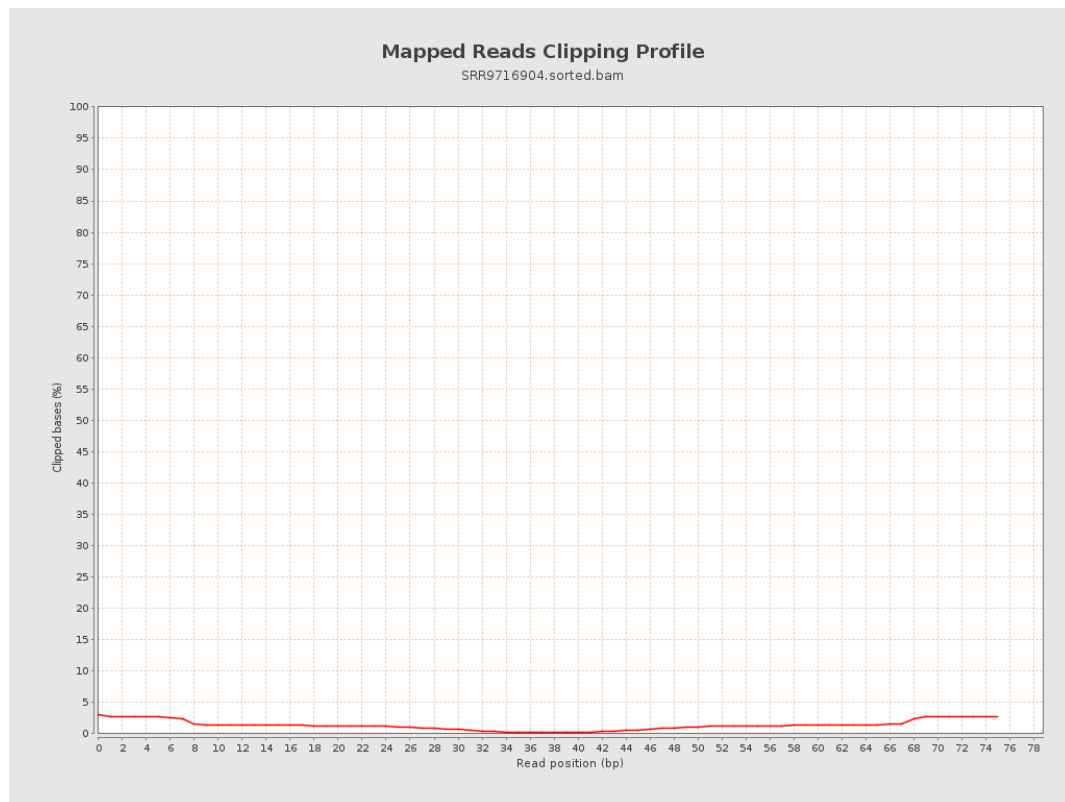
8. Results : Mapped Reads Nucleotide Content



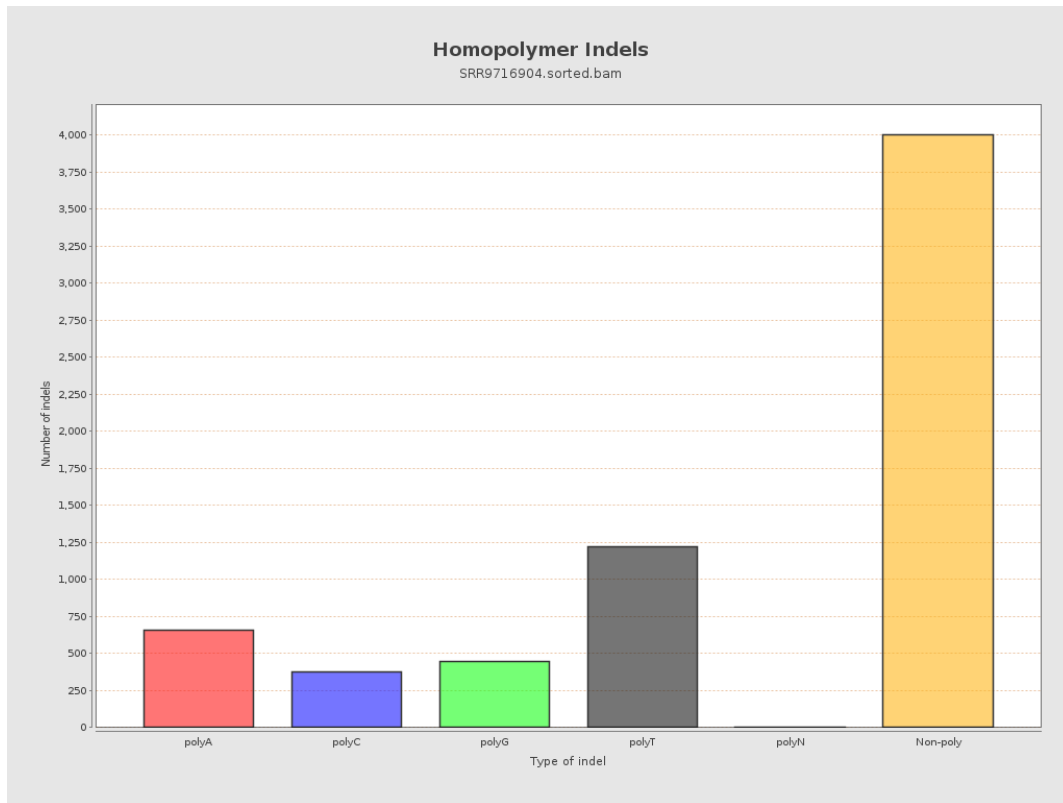
9. Results : Mapped Reads GC-content Distribution



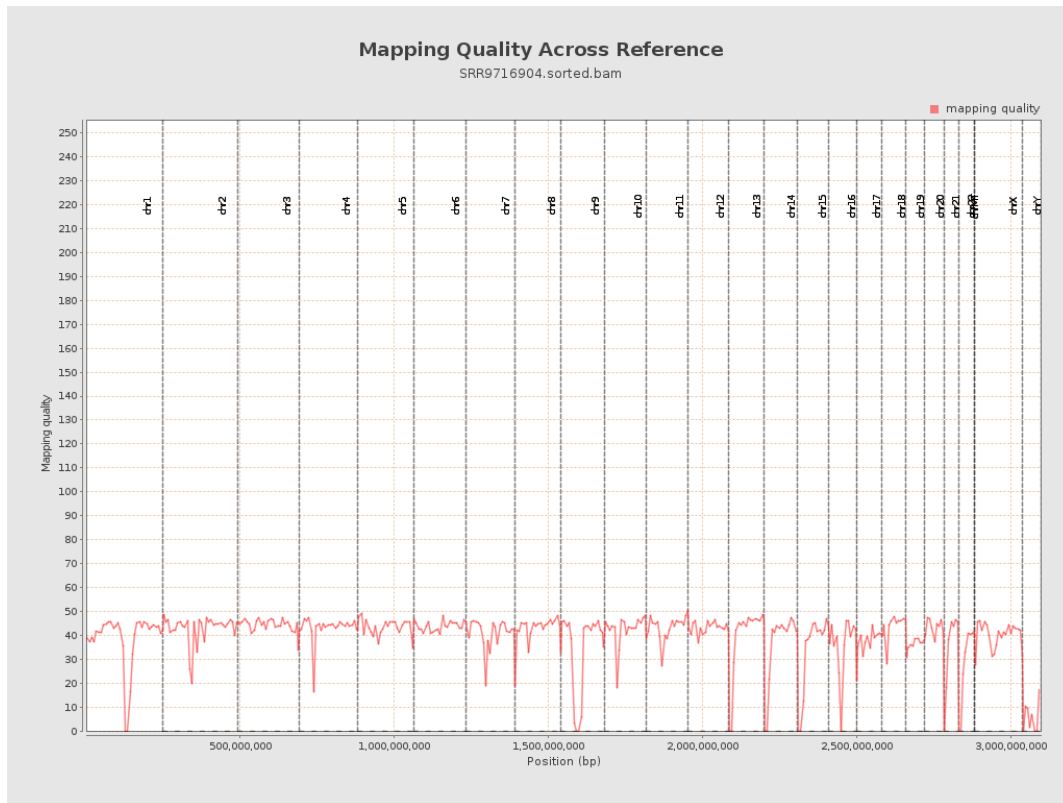
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

