

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:06:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231718.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_SRR6231718 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231718.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:06:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231718.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	939,124
Mapped reads	467,157 / 49.74%
Unmapped reads	471,967 / 50.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,904 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	28,808 / 3.07%
Duplication rate	5.09%
Clipped reads	201,692 / 21.48%

2.2. ACGT Content

Number/percentage of A's	8,866,304 / 28.64%
Number/percentage of C's	5,387,918 / 17.4%
Number/percentage of T's	10,227,988 / 33.04%
Number/percentage of G's	6,476,673 / 20.92%
Number/percentage of N's	1,383 / 0%
GC Percentage	38.32%

2.3. Coverage

Mean	0.01

Standard Deviation	0.164
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2.4. Mapping Quality

Mean Mapping Quality	46.84
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2.5. Mismatches and indels

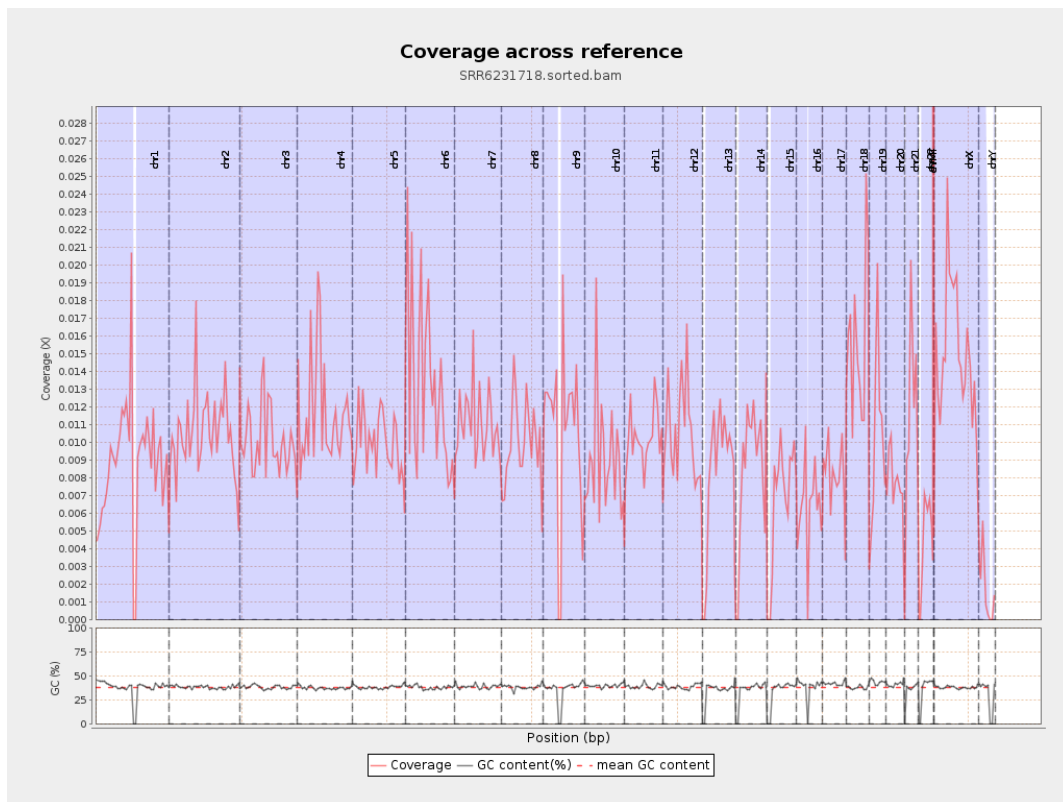
General error rate	0.83%
Mismatches	249,698
Insertions	2,896
Mapped reads with at least one insertion	0.61%
Deletions	7,951
Mapped reads with at least one deletion	1.68%
Homopolymer indels	44.85%

2.6. Chromosome stats

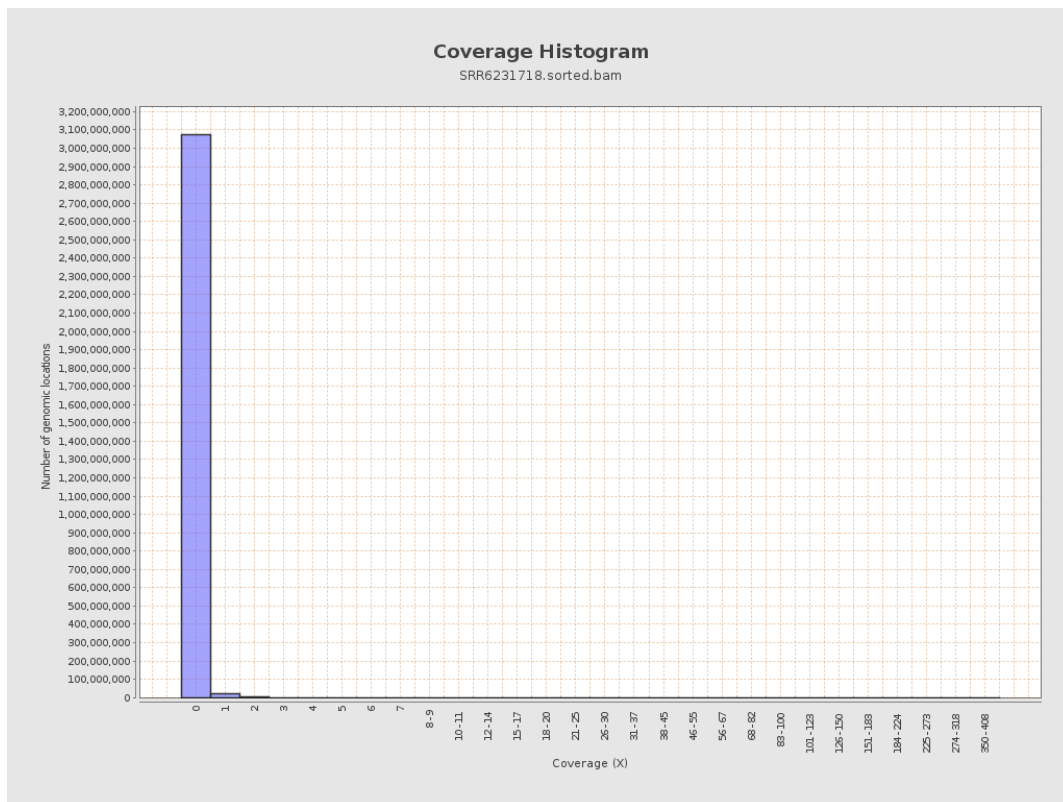
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	2207826	0.0089	0.2629
chr2	243199373	2558747	0.0105	0.1516
chr3	198022430	2008417	0.0101	0.1262
chr4	191154276	2233727	0.0117	0.1433
chr5	180915260	1806676	0.01	0.1271
chr6	171115067	2234351	0.0131	0.1817
chr7	159138663	1766495	0.0111	0.1647

chr8	146364022	1440019	0.0098	0.2708
chr9	141213431	1484960	0.0105	0.1404
chr10	135534747	1216565	0.009	0.1491
chr11	135006516	1358917	0.0101	0.1307
chr12	133851895	1401087	0.0105	0.1319
chr13	115169878	946018	0.0082	0.1167
chr14	107349540	892092	0.0083	0.118
chr15	102531392	697251	0.0068	0.1029
chr16	90354753	573147	0.0063	0.1011
chr17	81195210	656515	0.0081	0.1127
chr18	78077248	1215531	0.0156	0.2582
chr19	59128983	616279	0.0104	0.1699
chr20	63025520	490388	0.0078	0.1125
chr21	48129895	539003	0.0112	0.1371
chr22	51304566	225939	0.0044	0.0787
chrMT	16571	6584	0.3973	0.7569
chrX	155270560	2302683	0.0148	0.1608
chrY	59373566	95622	0.0016	0.0634

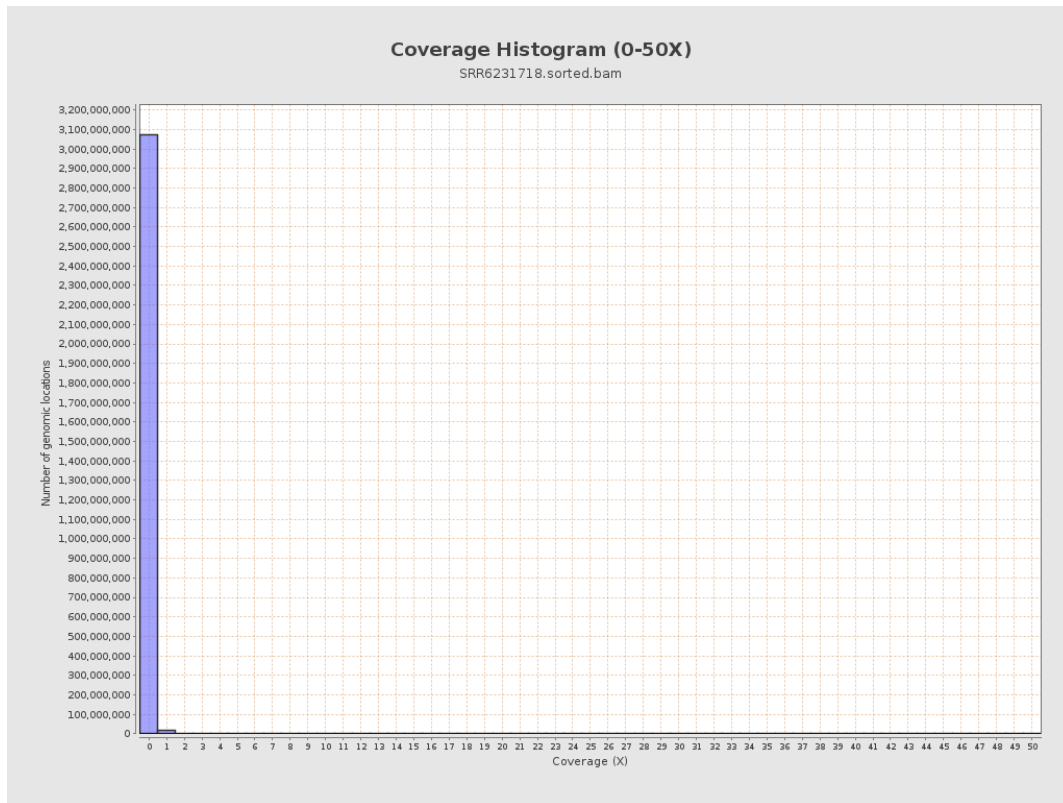
3. Results : Coverage across reference



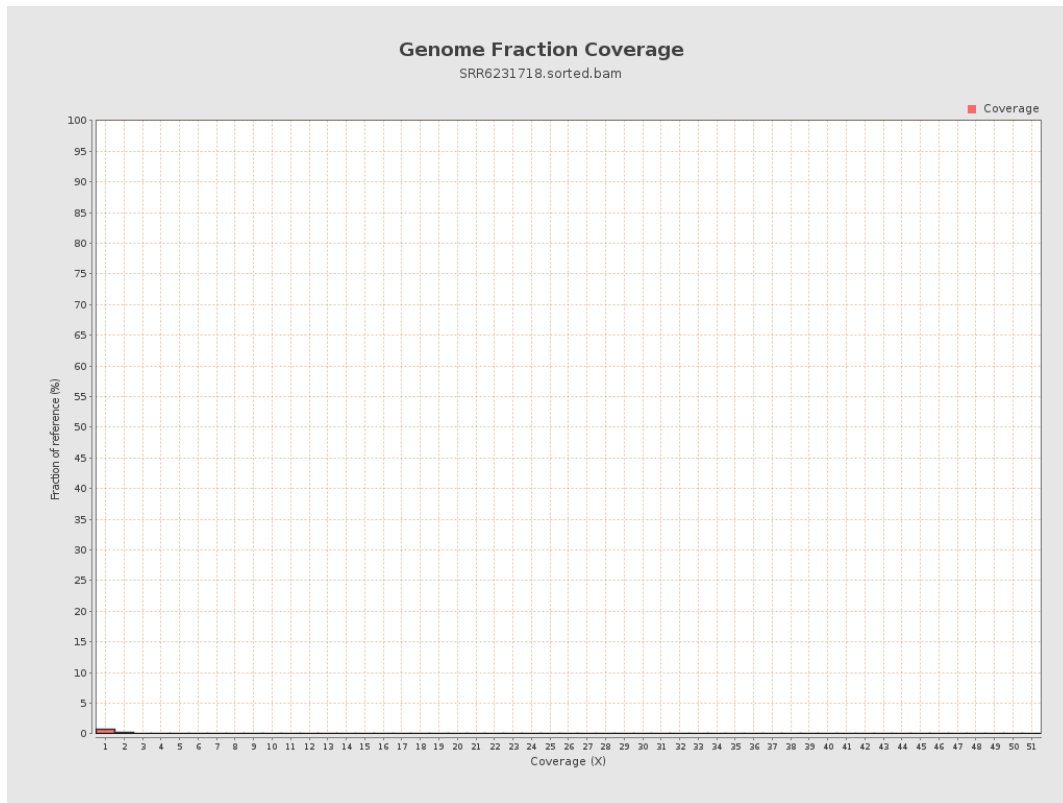
4. Results : Coverage Histogram



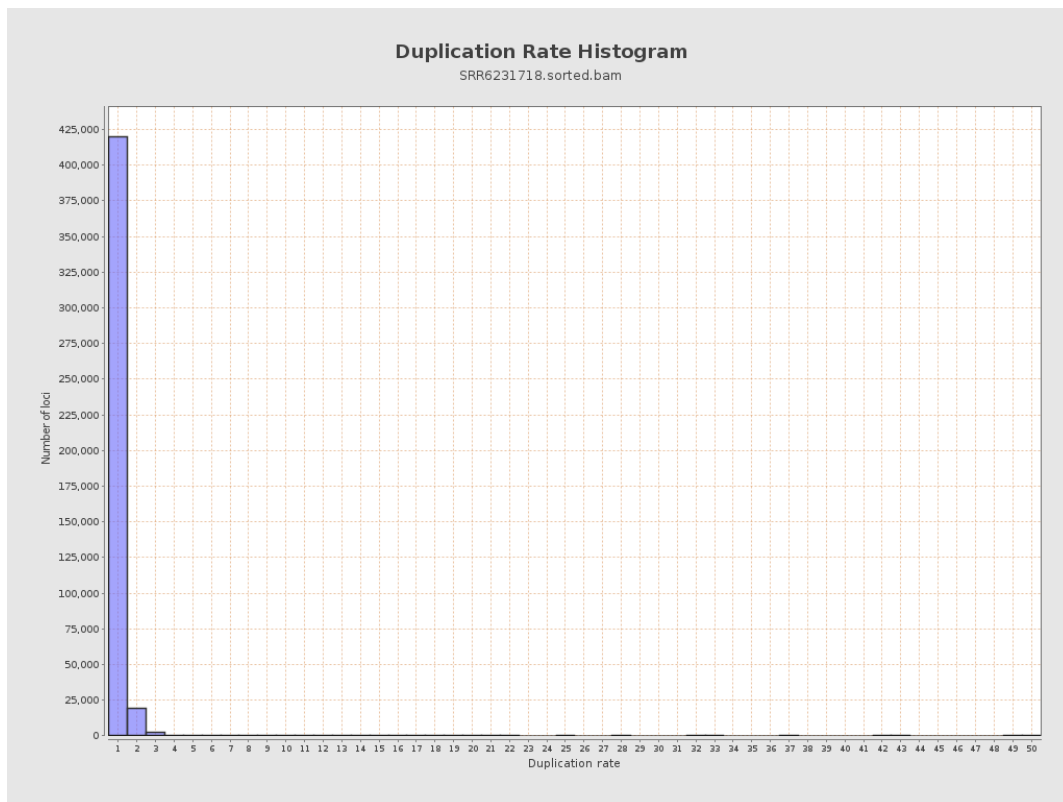
5. Results : Coverage Histogram (0-50X)



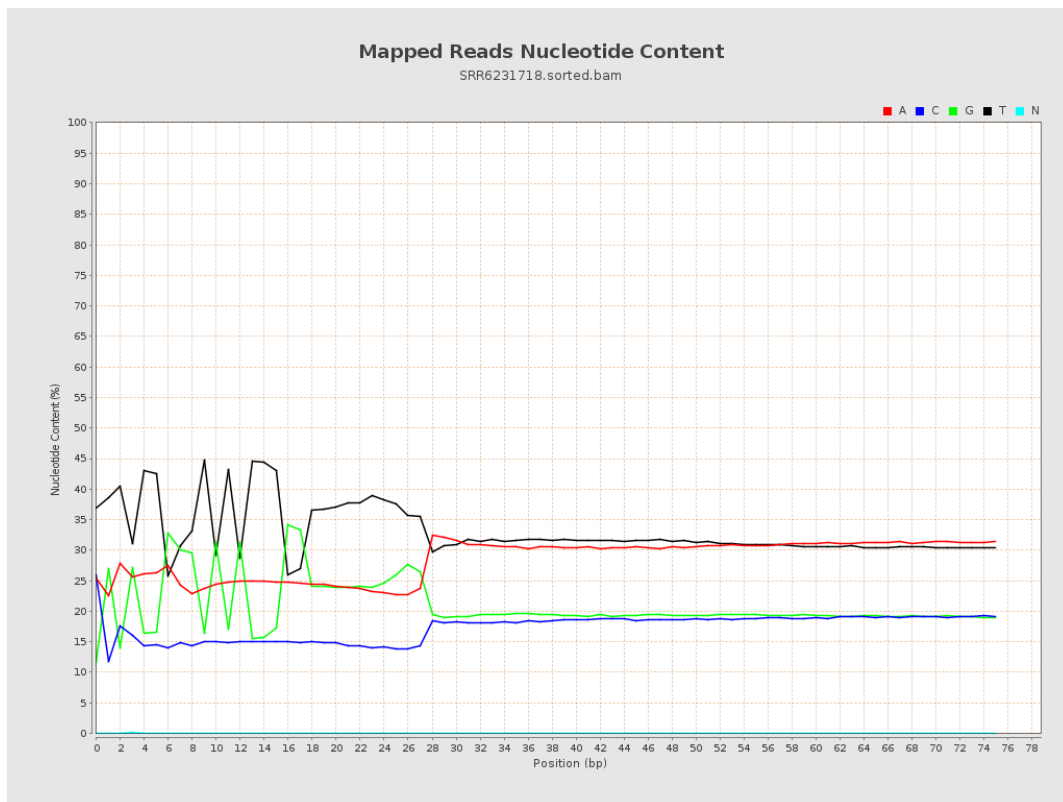
6. Results : Genome Fraction Coverage



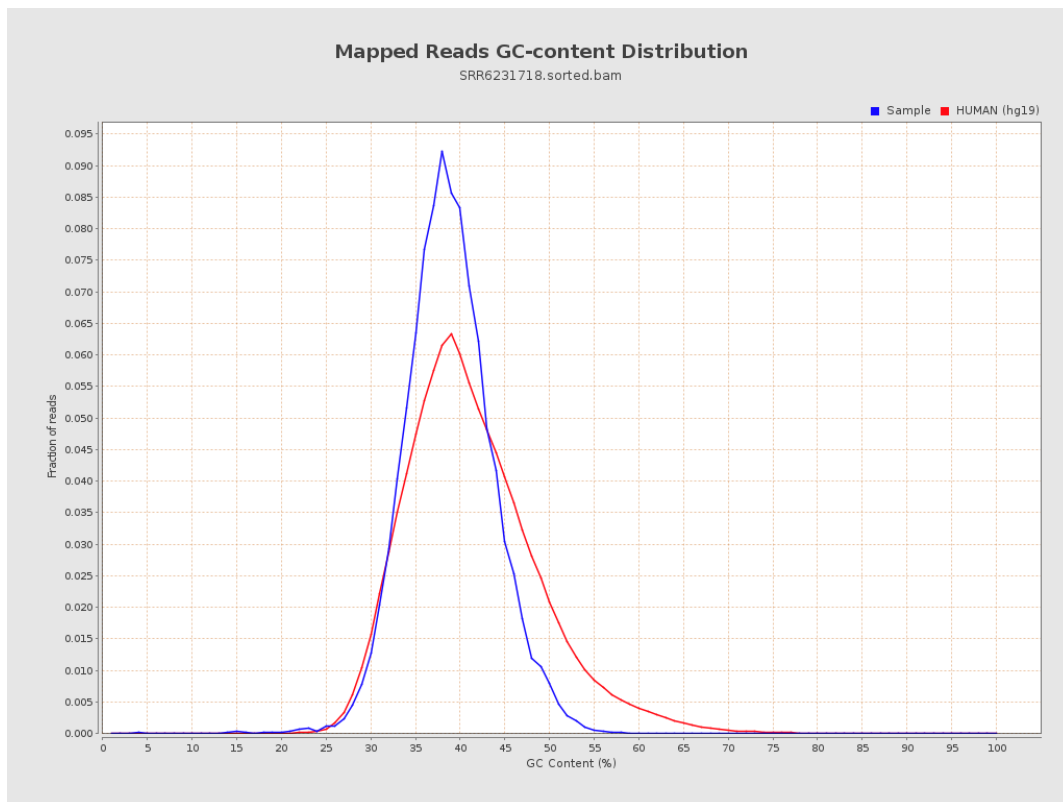
7. Results : Duplication Rate Histogram



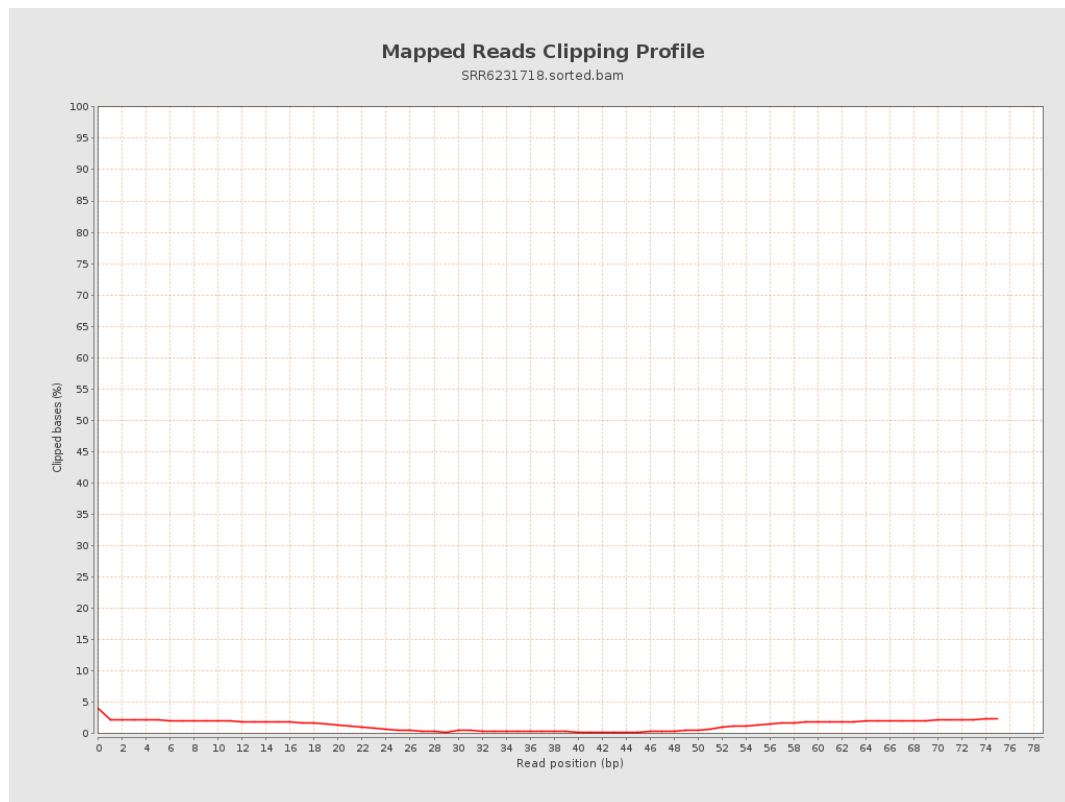
8. Results : Mapped Reads Nucleotide Content



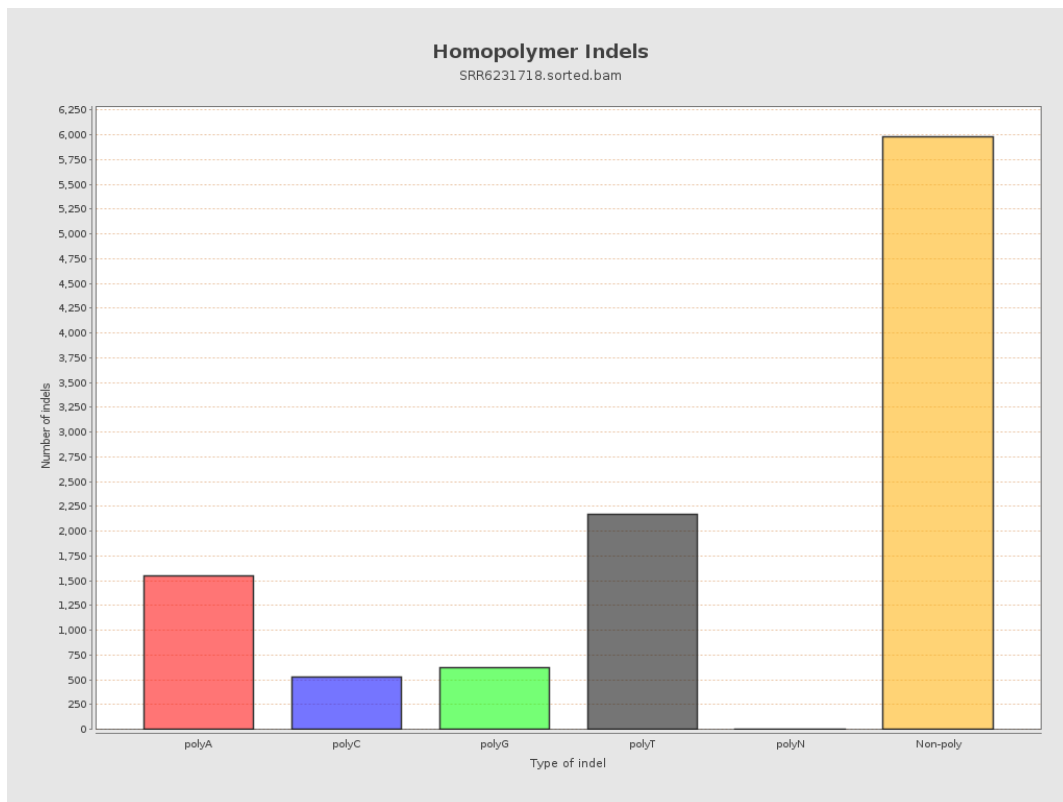
9. Results : Mapped Reads GC-content Distribution



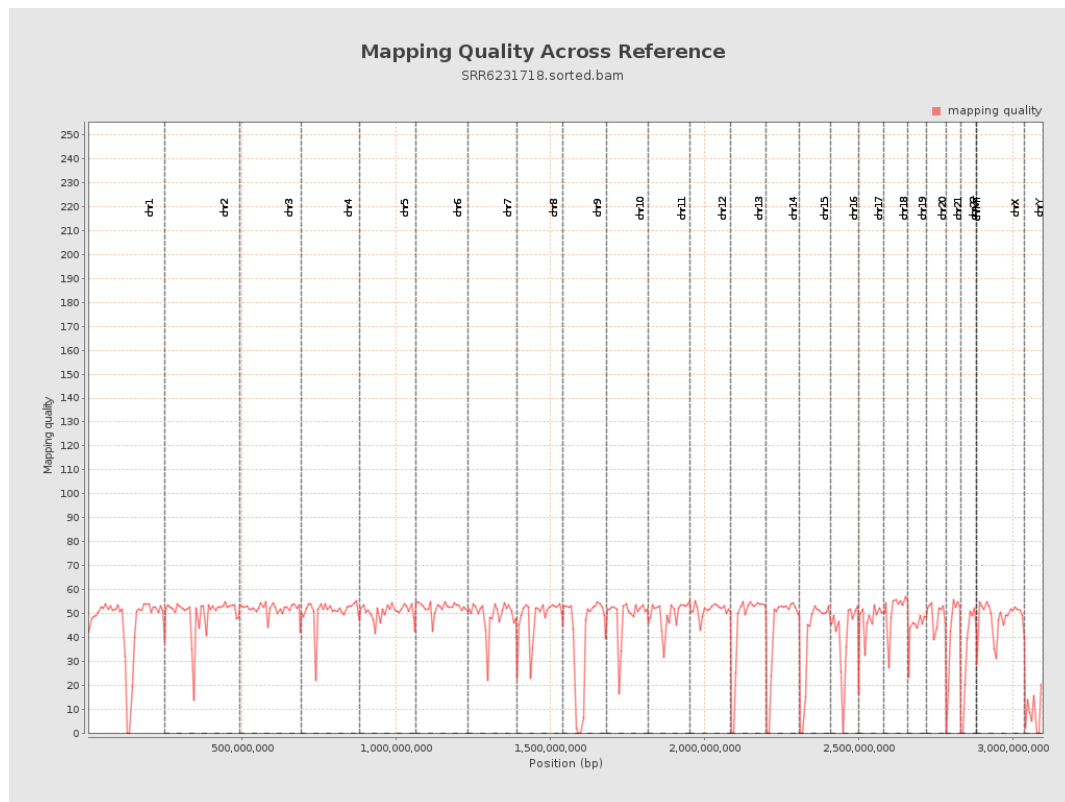
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

