Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 04:47:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237595.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_SRR6237595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237595.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 04:47:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,261,141
Mapped reads	967,443 / 76.71%
Unmapped reads	293,698 / 23.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,425 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,988 / 3.33%
Duplication rate	3.2%
Clipped reads	599,100 / 47.5%

2.2. ACGT Content

Number/percentage of A's	16,148,853 / 26.88%
Number/percentage of C's	10,443,032 / 17.38%
Number/percentage of T's	18,968,859 / 31.58%
Number/percentage of G's	14,397,657 / 23.97%
Number/percentage of N's	112,429 / 0.19%
GC Percentage	41.35%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.2092

2.4. Mapping Quality

Mean Mapping Quality	43.09

2.5. Mismatches and indels

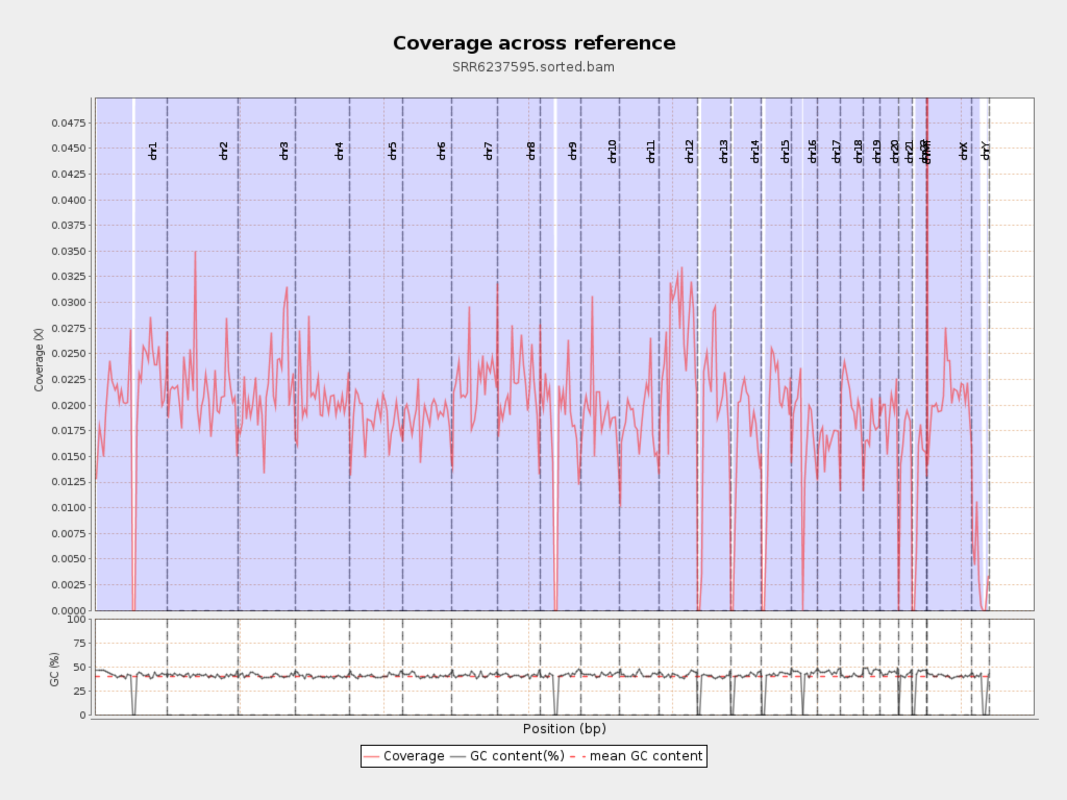
General error rate	1%
Mismatches	592,836
Insertions	5,823
Mapped reads with at least one insertion	0.6%
Deletions	22,055
Mapped reads with at least one deletion	2.25%
Homopolymer indels	48.58%

2.6. Chromosome stats

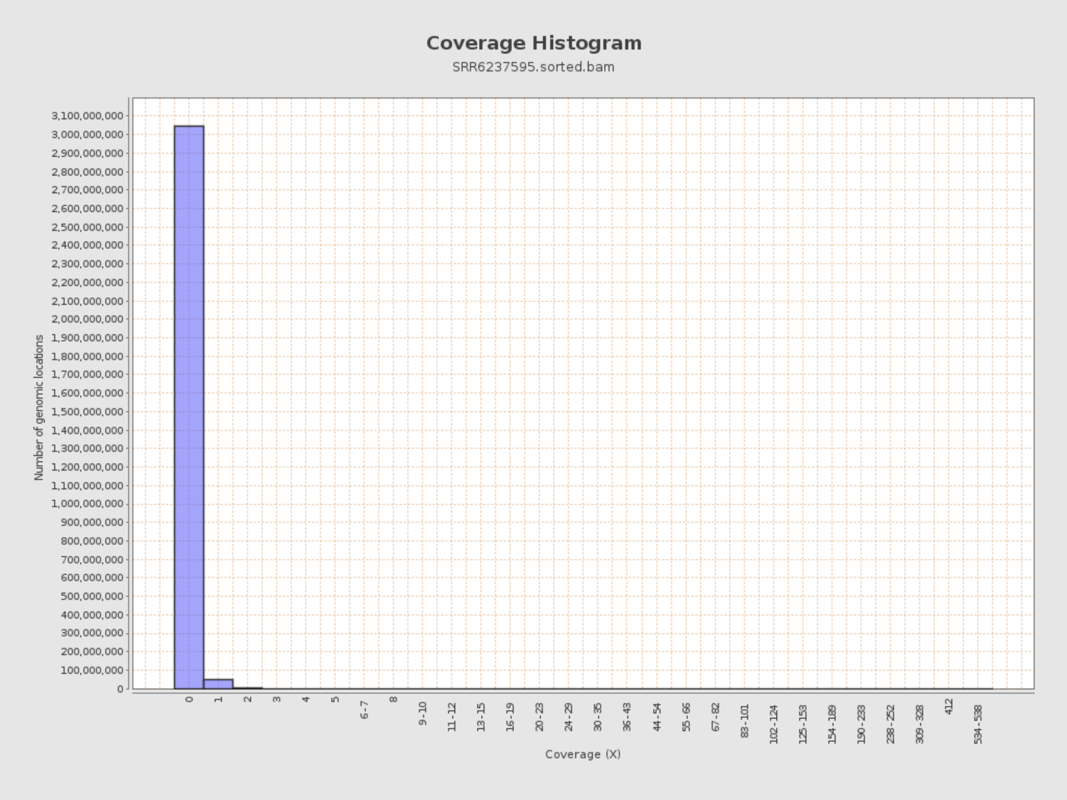
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5097029	0.0204	0.2452
chr2	243199373	5223047	0.0215	0.3143
chr3	198022430	4261795	0.0215	0.1742
chr4	191154276	3946227	0.0206	0.1719
chr5	180915260	3390025	0.0187	0.1564
chr6	171115067	3239513	0.0189	0.1886
chr7	159138663	3511485	0.0221	0.2606

chr8	146364022	3126904	0.0214	0.2164
chr9	141213431	2466644	0.0175	0.2052
chr10	135534747	2605331	0.0192	0.1923
chr11	135006516	2496835	0.0185	0.1949
chr12	133851895	3569200	0.0267	0.1973
chr13	115169878	2154363	0.0187	0.1669
chr14	107349540	1714334	0.016	0.1593
chr15	102531392	1838167	0.0179	0.1601
chr16	90354753	1491553	0.0165	0.1651
chr17	81195210	1329907	0.0164	0.156
chr18	78077248	1607801	0.0206	0.3789
chr19	59128983	1033488	0.0175	0.1886
chr20	63025520	1206297	0.0191	0.1639
chr21	48129895	742791	0.0154	0.1514
chr22	51304566	574880	0.0112	0.1221
chrMT	16571	43112	2.6017	2.1647
chrX	155270560	3234516	0.0208	0.1756
chrY	59373566	201989	0.0034	0.0873

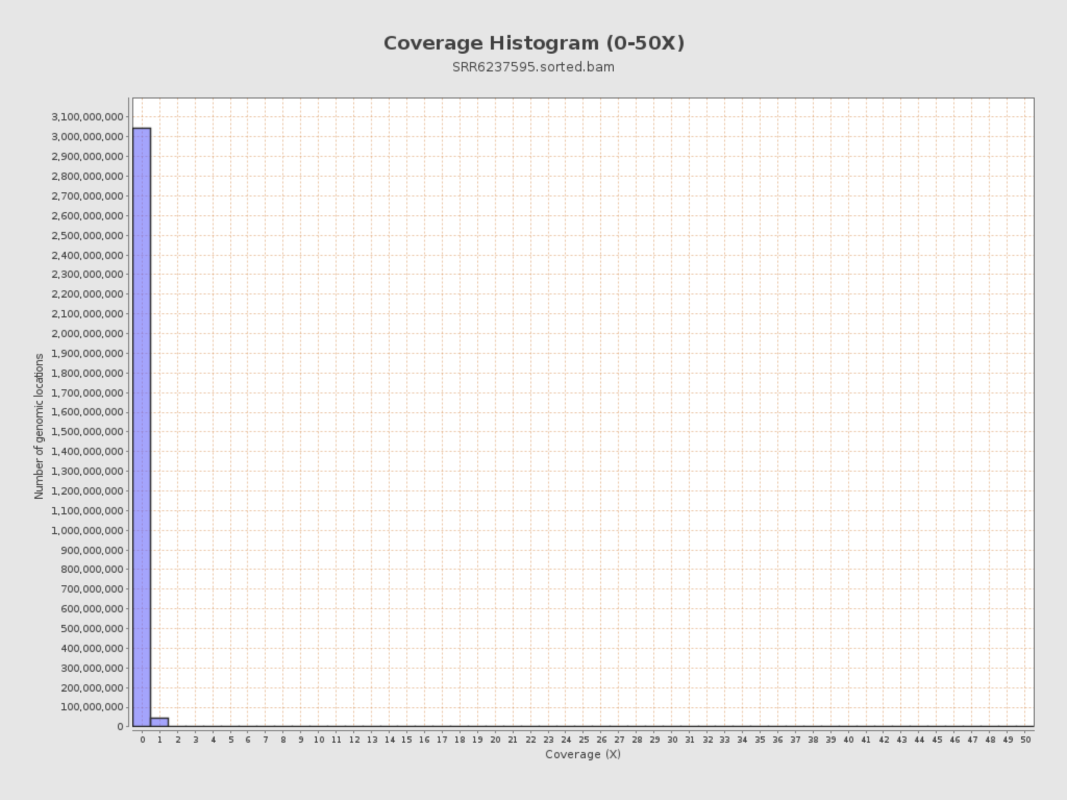
3. Results : Coverage across reference



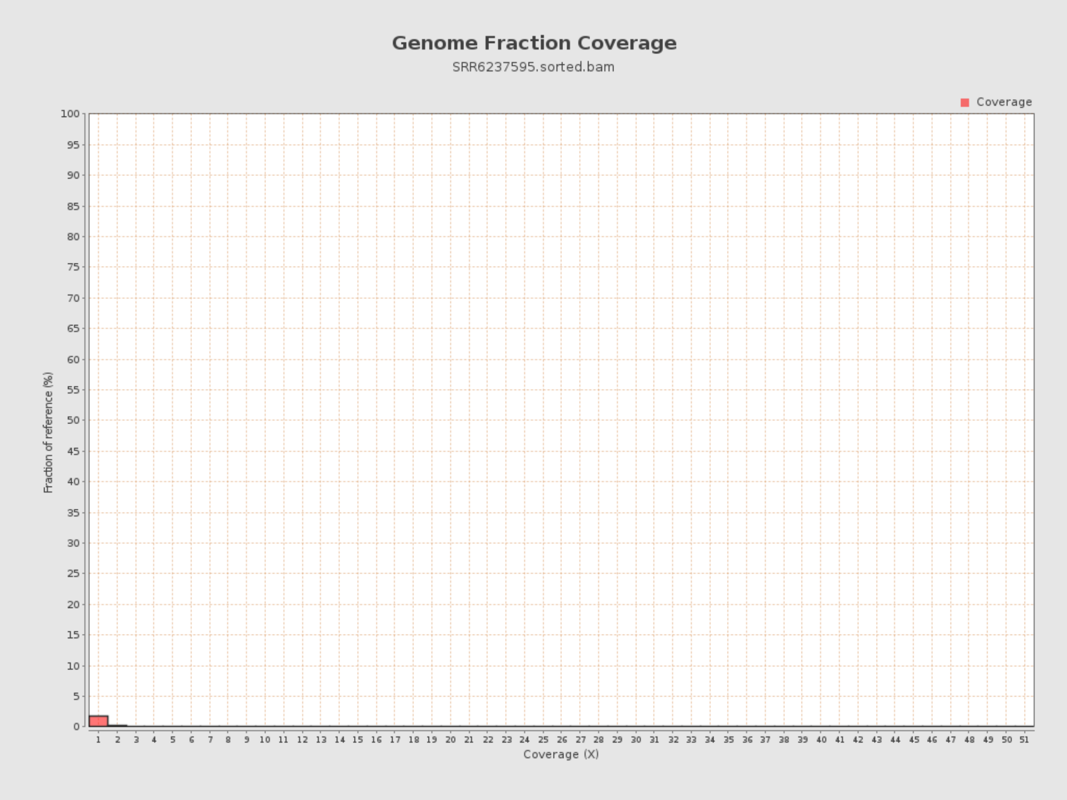
4. Results : Coverage Histogram



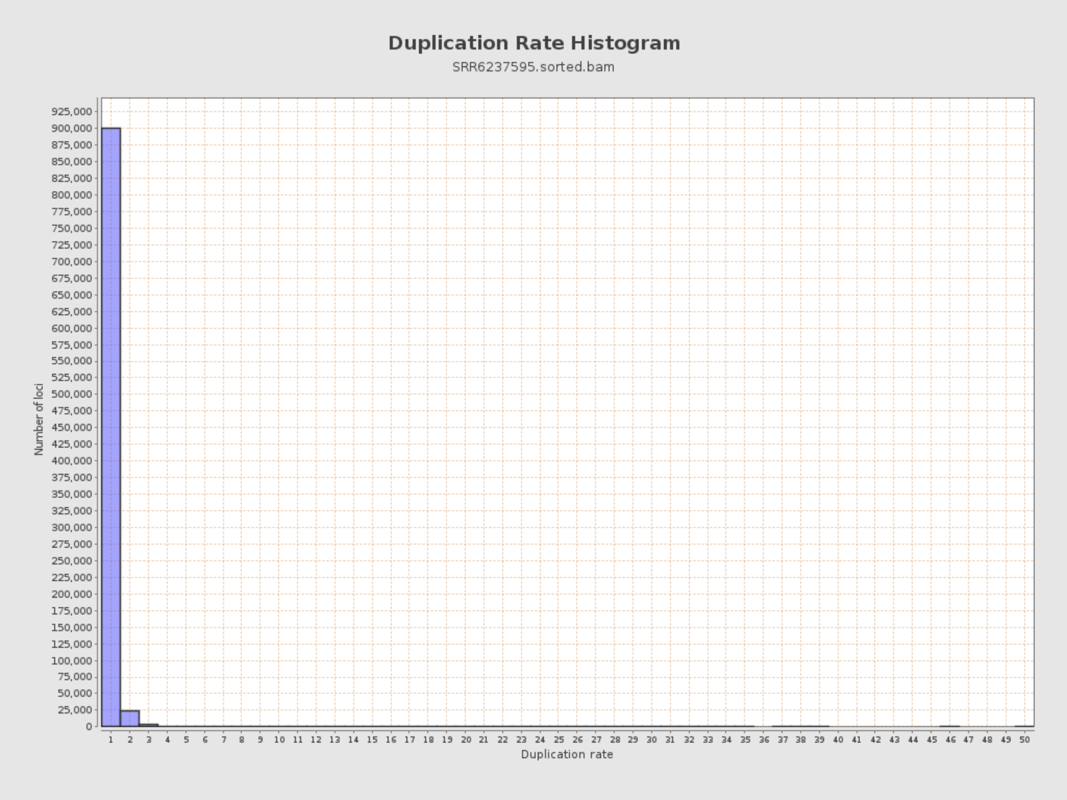
5. Results : Coverage Histogram (0-50X)



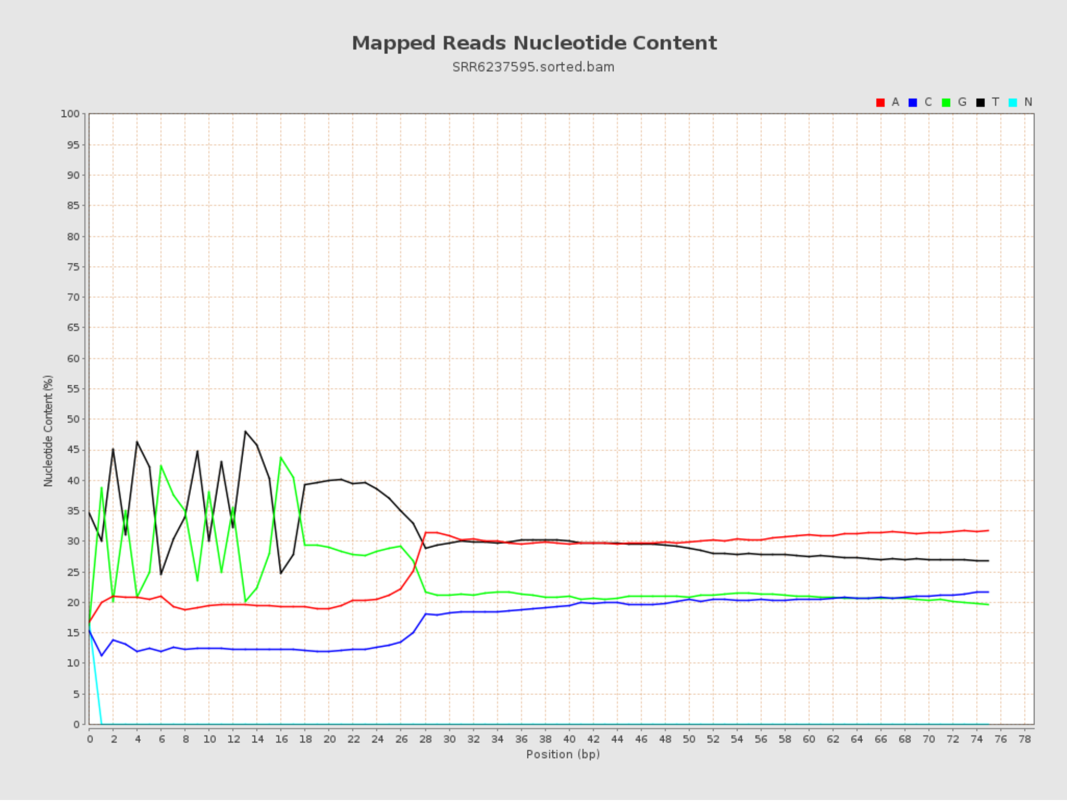
6. Results : Genome Fraction Coverage



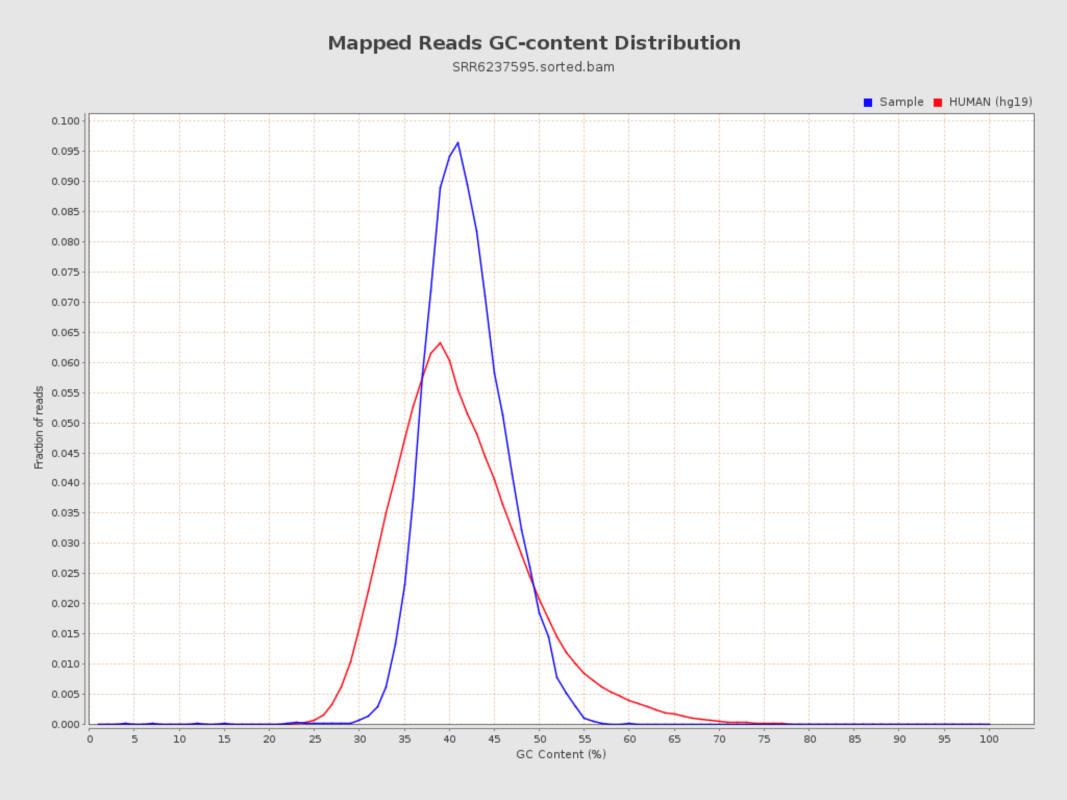
7. Results : Duplication Rate Histogram



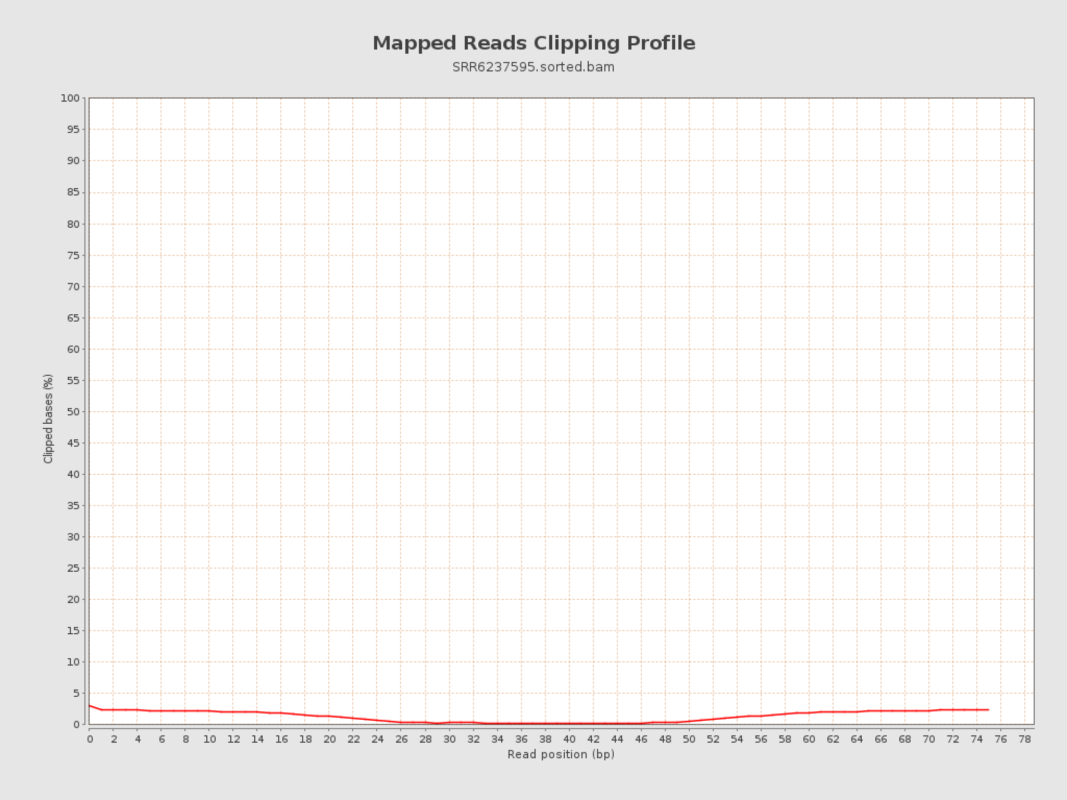
8. Results : Mapped Reads Nucleotide Content



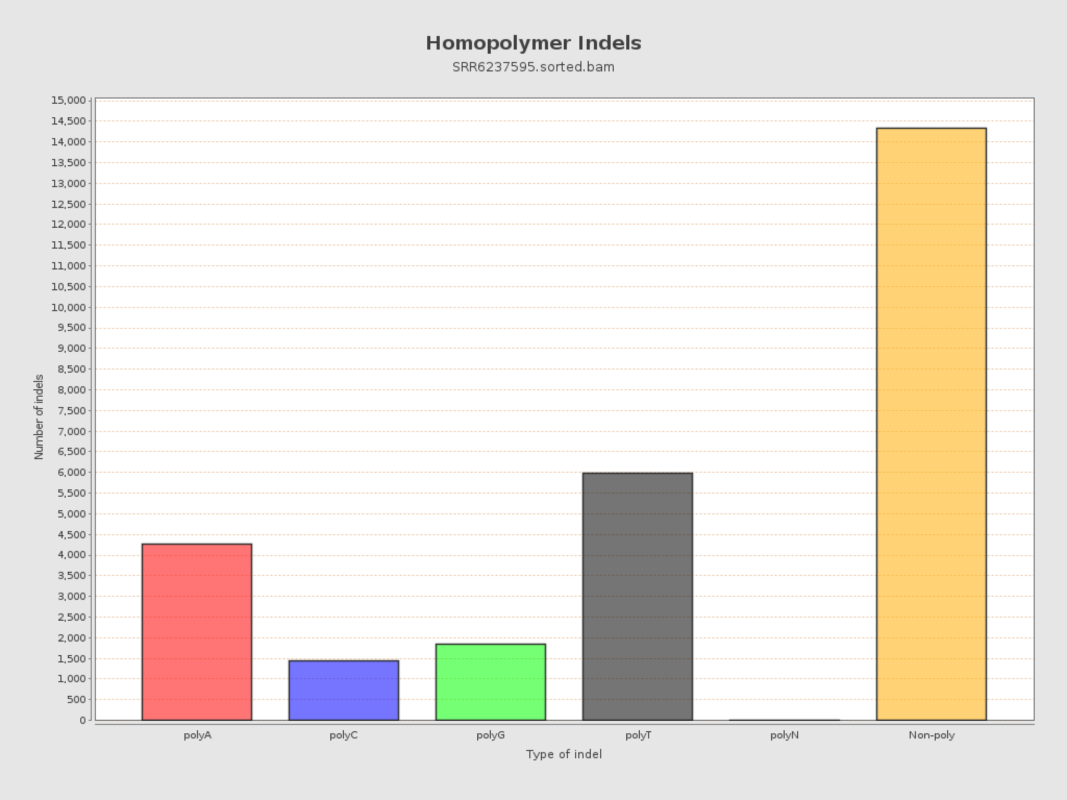
9. Results : Mapped Reads GC-content Distribution



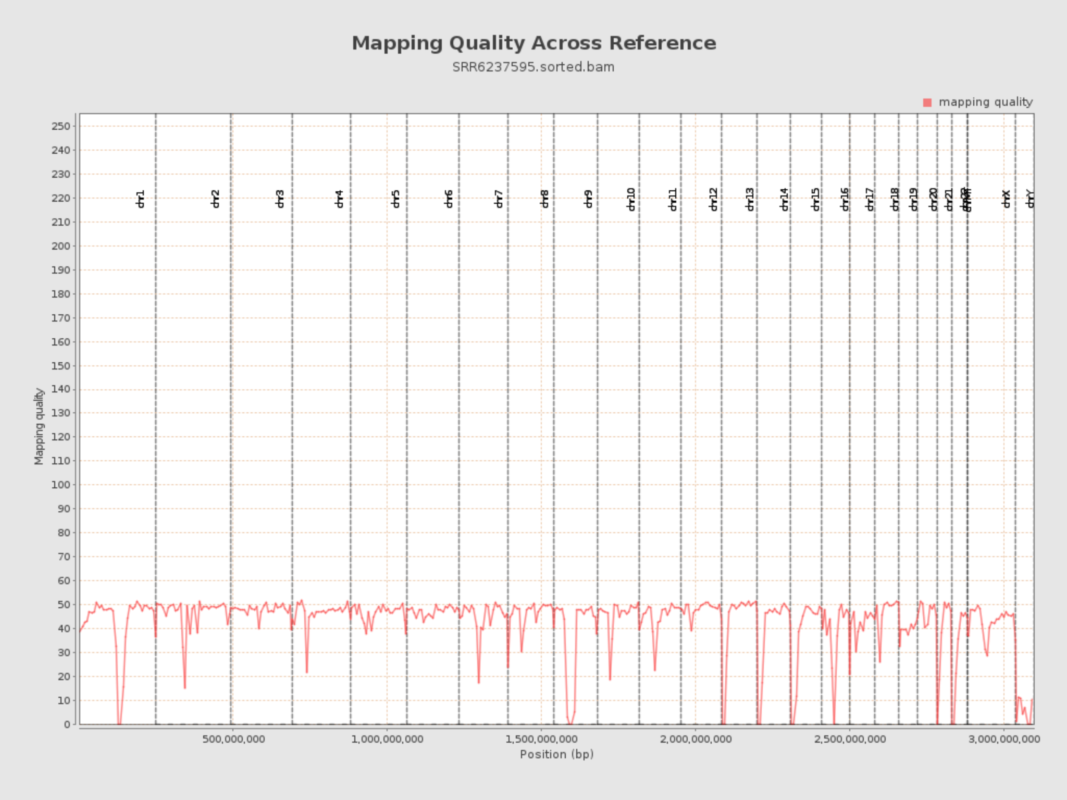
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram