Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 23:32:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231745.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_SRR6231745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 23:32:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	829,823
Mapped reads	615,748 / 74.2%
Unmapped reads	214,075 / 25.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,408 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	50,489 / 6.08%
Duplication rate	6.4%
Clipped reads	303,835 / 36.61%

2.2. ACGT Content

Number/percentage of A's	11,383,667 / 28.35%
Number/percentage of C's	6,777,798 / 16.88%
Number/percentage of T's	13,475,765 / 33.56%
Number/percentage of G's	8,509,778 / 21.2%
Number/percentage of N's	2,092 / 0.01%
GC Percentage	38.08%

2.3. Coverage

Mean	0.013

Standard Deviation	0.3373

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

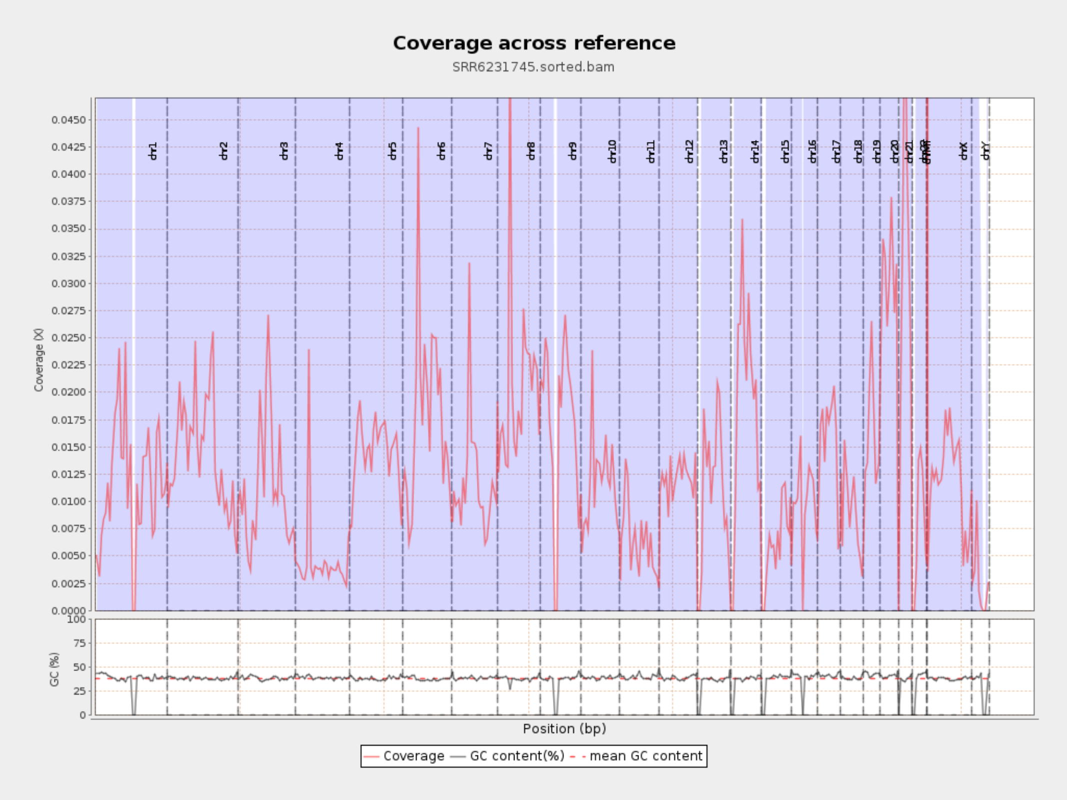
General error rate	0.91%
Mismatches	355,508
Insertions	3,925
Mapped reads with at least one insertion	0.63%
Deletions	12,880
Mapped reads with at least one deletion	2.06%
Homopolymer indels	44.33%

2.6. Chromosome stats

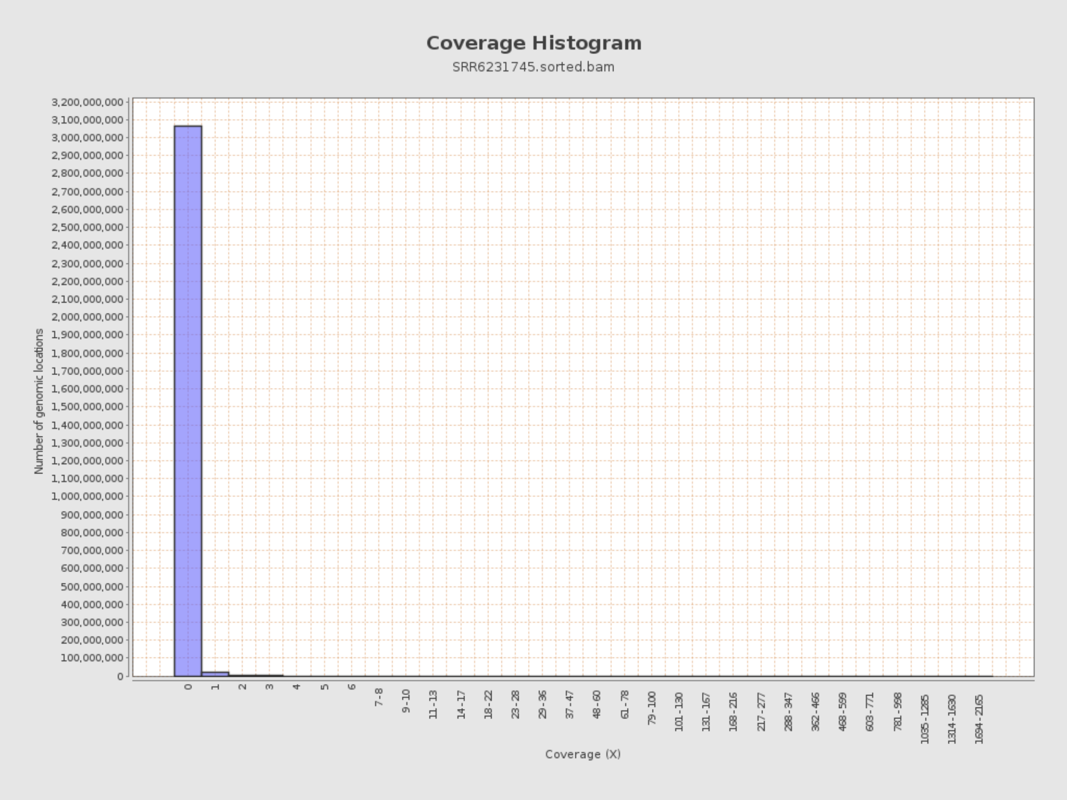
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2893166	0.0116	0.2332
chr2	243199373	3525867	0.0145	0.1892
chr3	198022430	2238606	0.0113	0.1333
chr4	191154276	878163	0.0046	0.105
chr5	180915260	2657574	0.0147	0.1564
chr6	171115067	3073643	0.018	0.1939
chr7	159138663	1859832	0.0117	0.2096

chr8	146364022	3023105	0.0207	1.346
chr9	141213431	2440582	0.0173	0.1927
chr10	135534747	1573816	0.0116	0.1625
chr11	135006516	864320	0.0064	0.1067
chr12	133851895	1622305	0.0121	0.1387
chr13	115169878	1242814	0.0108	0.1331
chr14	107349540	2007103	0.0187	0.1755
chr15	102531392	613893	0.006	0.0958
chr16	90354753	879106	0.0097	0.1298
chr17	81195210	1235388	0.0152	0.1583
chr18	78077248	702408	0.009	0.2791
chr19	59128983	966395	0.0163	0.1884
chr20	63025520	1875277	0.0298	0.219
chr21	48129895	1514741	0.0315	0.231
chr22	51304566	400471	0.0078	0.1073
chrMT	16571	79784	4.8147	4.1748
chrX	155270560	1846466	0.0119	0.1407
chrY	59373566	157484	0.0027	0.0845

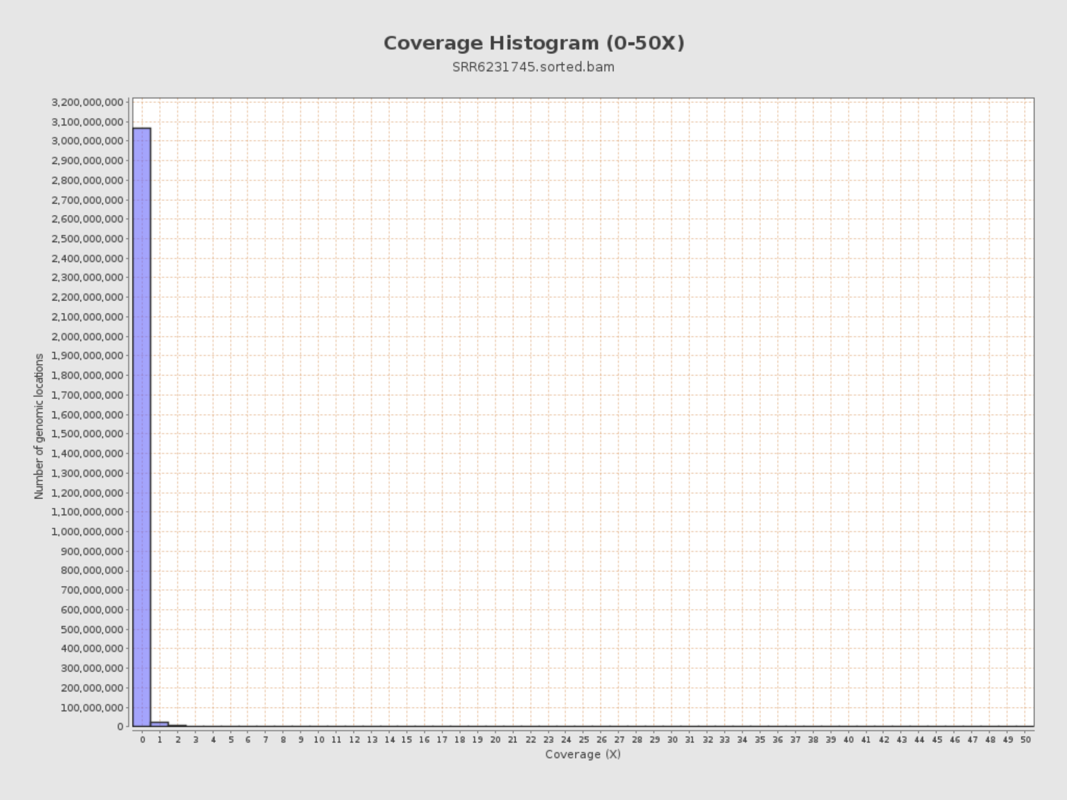
3. Results : Coverage across reference



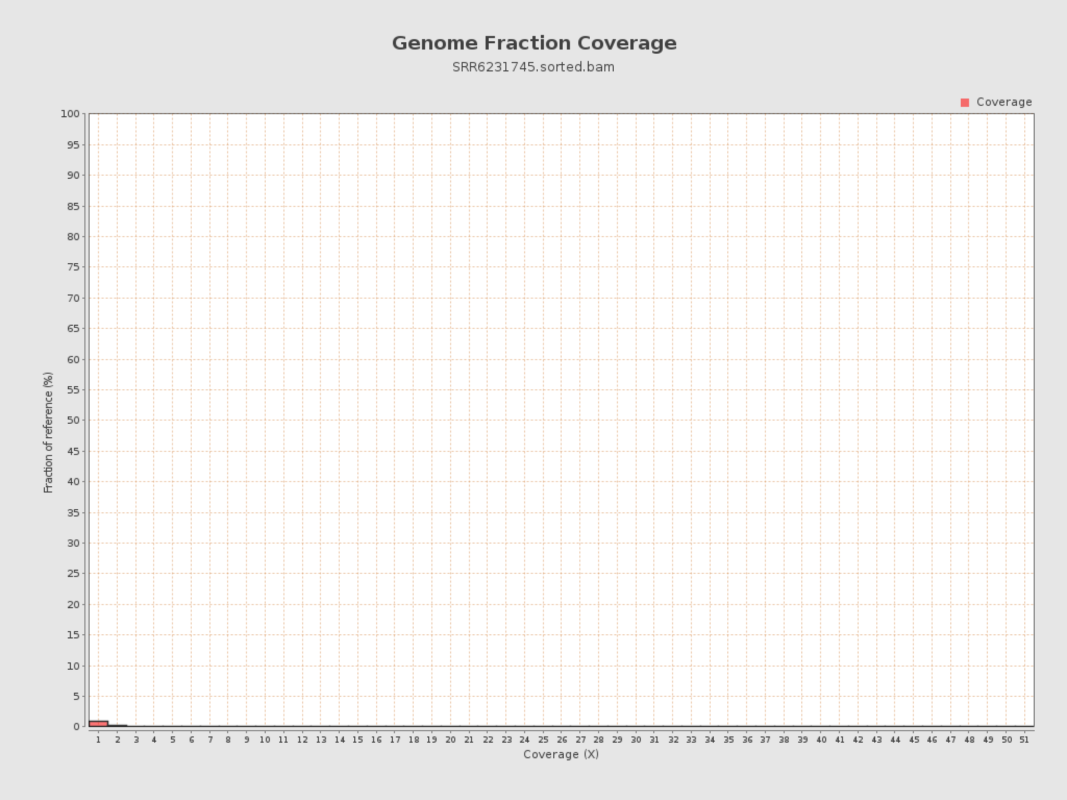
4. Results : Coverage Histogram



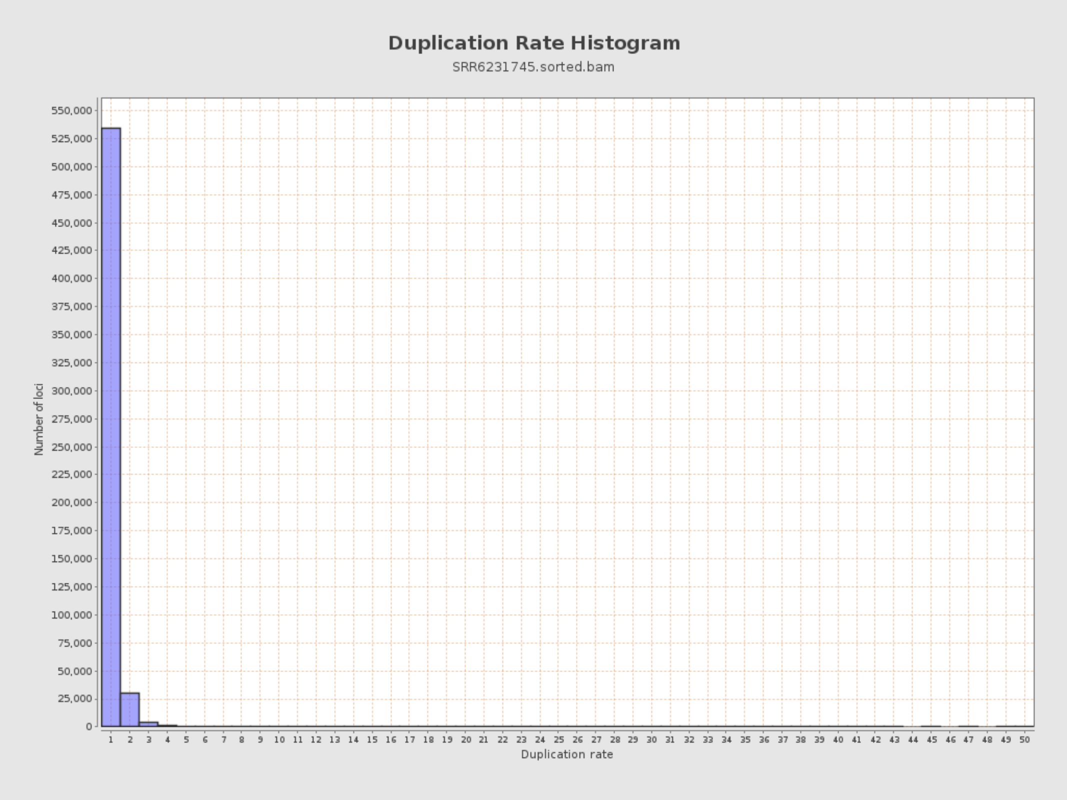
5. Results : Coverage Histogram (0-50X)



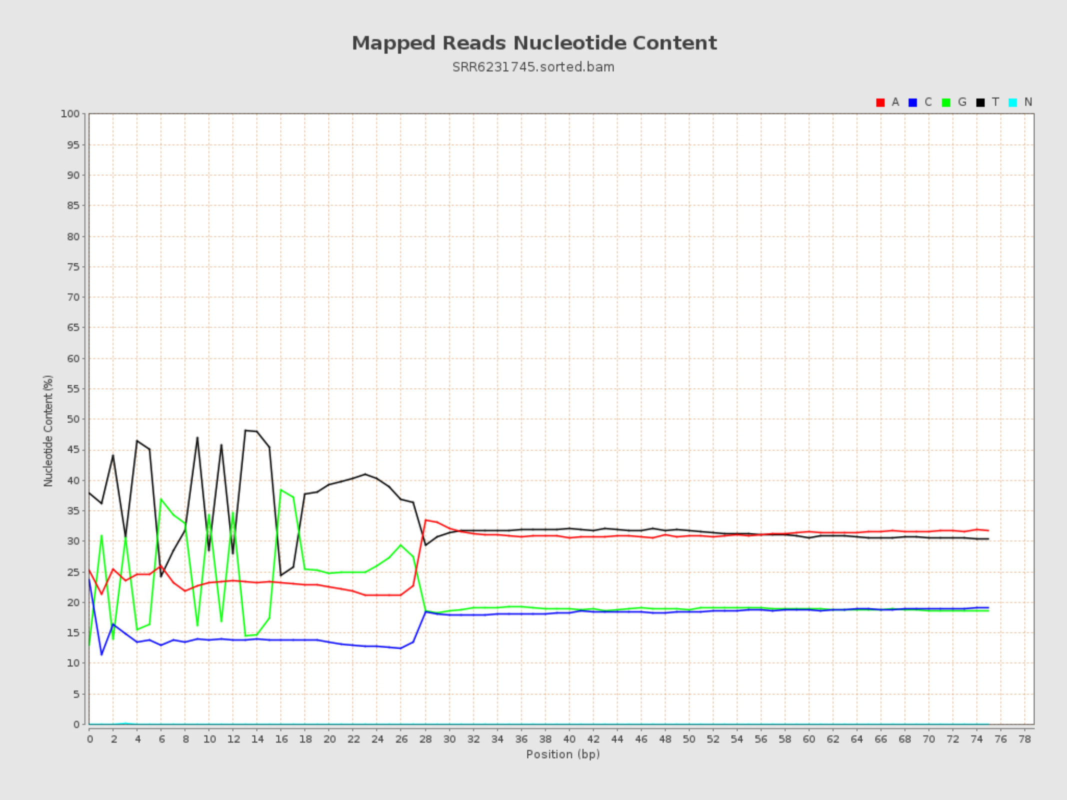
6. Results : Genome Fraction Coverage



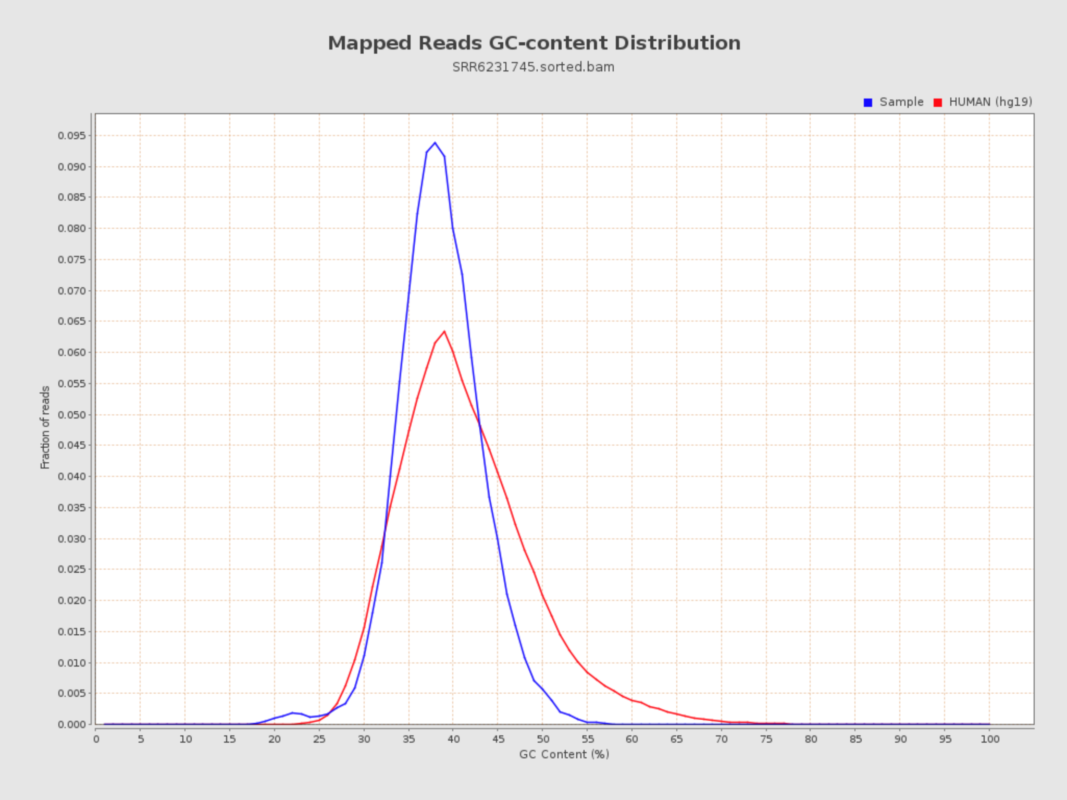
7. Results : Duplication Rate Histogram



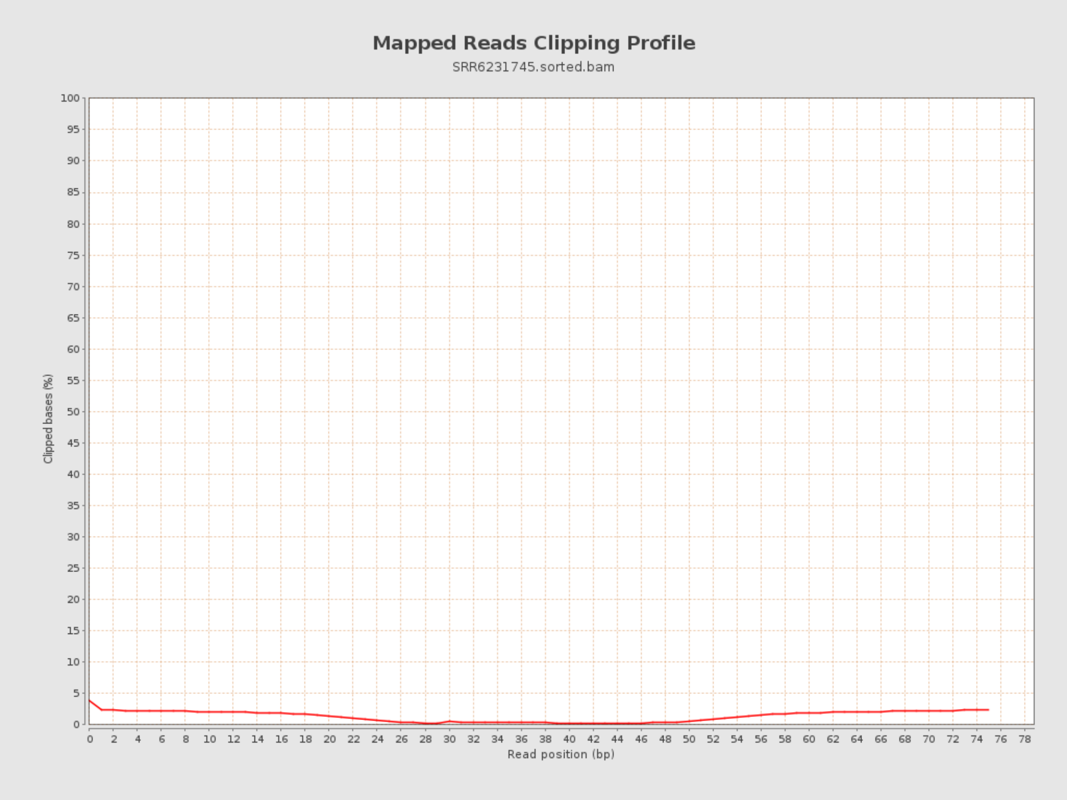
8. Results : Mapped Reads Nucleotide Content



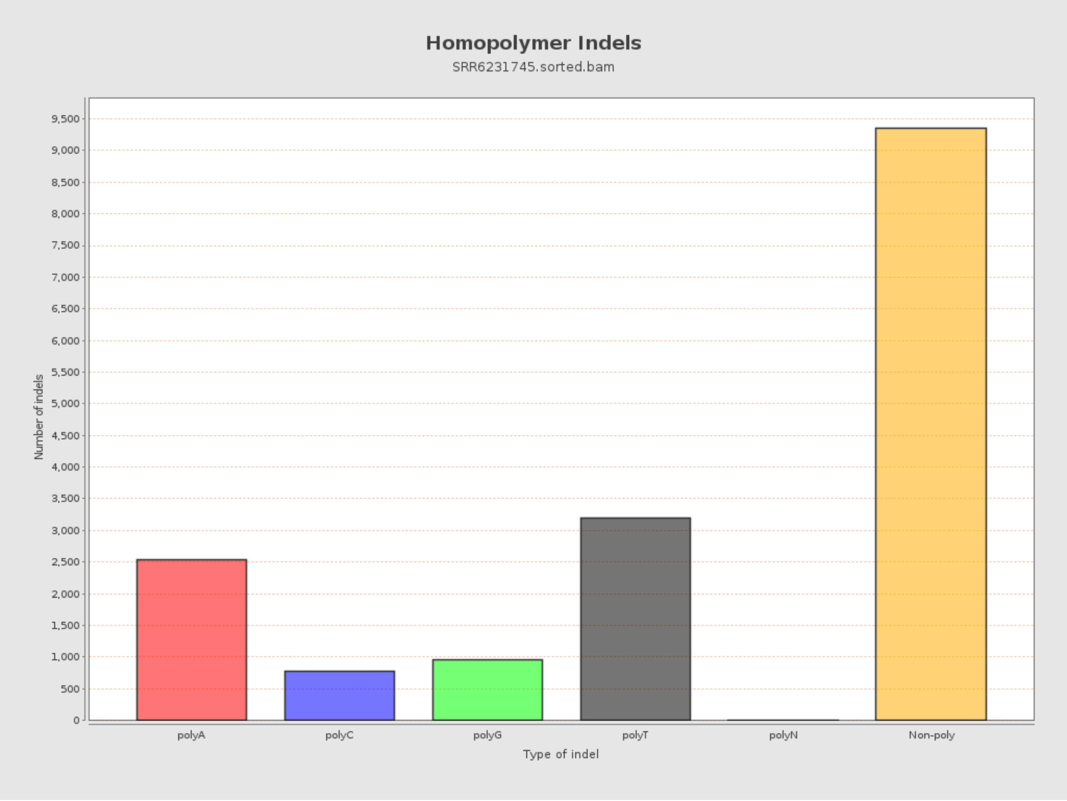
9. Results : Mapped Reads GC-content Distribution



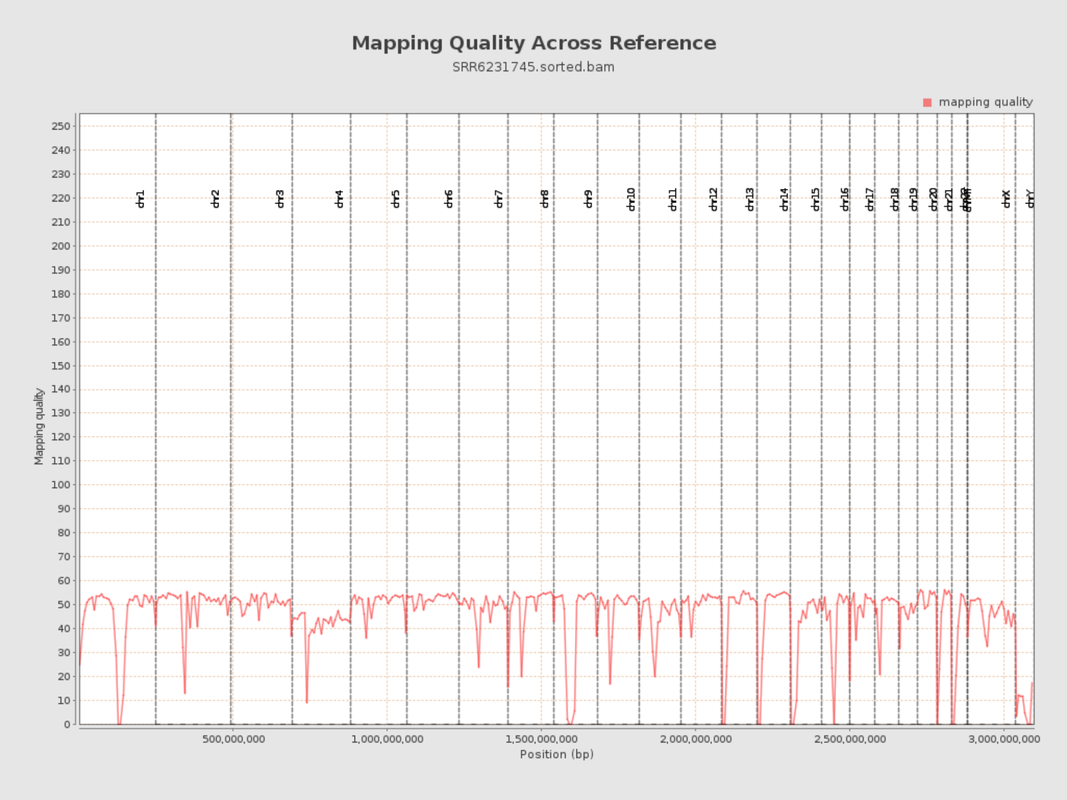
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram