Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:54:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231840.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_SRR6231840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:54:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,197,186
Mapped reads	8,414,726 / 75.15%
Unmapped reads	2,782,460 / 24.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	62,586 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	573,166 / 5.12%
Duplication rate	3.17%
Clipped reads	4,053,631 / 36.2%

2.2. ACGT Content

Number/percentage of A's	160,772,546 / 28.73%
Number/percentage of C's	115,024,057 / 20.56%
Number/percentage of T's	155,876,894 / 27.86%
Number/percentage of G's	127,873,187 / 22.85%
Number/percentage of N's	44,867 / 0.01%
GC Percentage	43.41%

2.3. Coverage

Mean	0.1808

Standard Deviation	13.4477

2.4. Mapping Quality

Mean Mapping Quality	42.19

2.5. Mismatches and indels

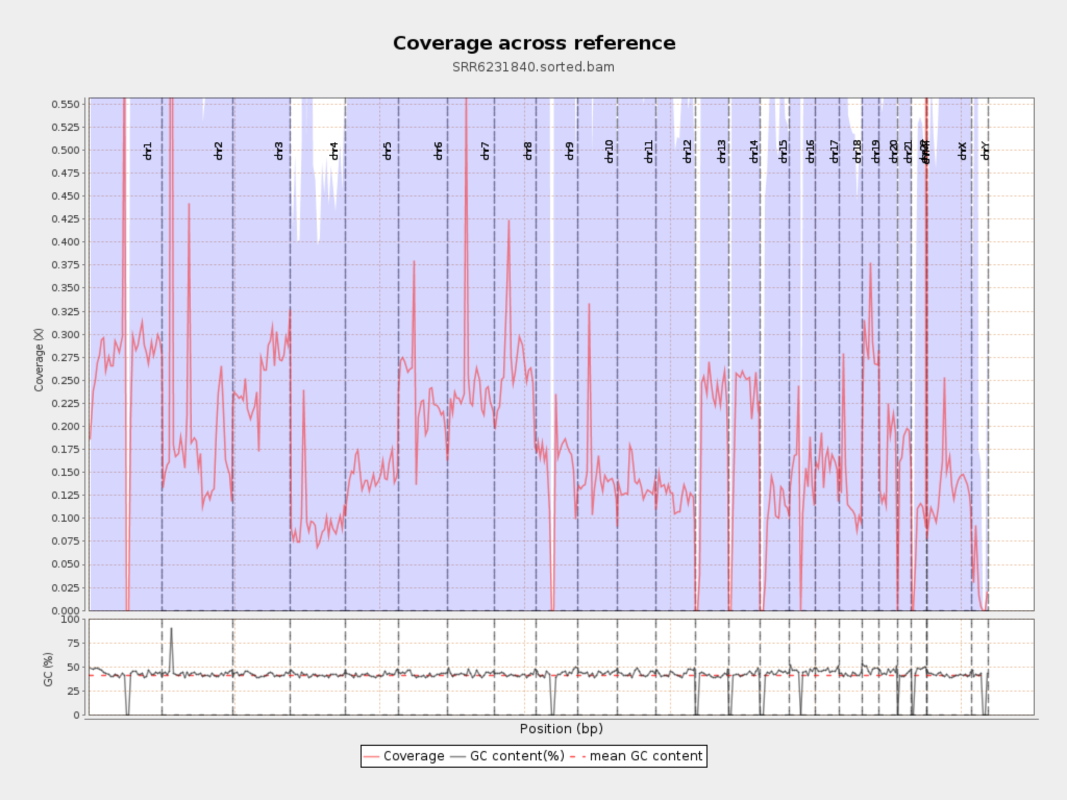
General error rate	0.66%
Mismatches	3,619,022
Insertions	44,154
Mapped reads with at least one insertion	0.52%
Deletions	125,369
Mapped reads with at least one deletion	1.47%
Homopolymer indels	44.54%

2.6. Chromosome stats

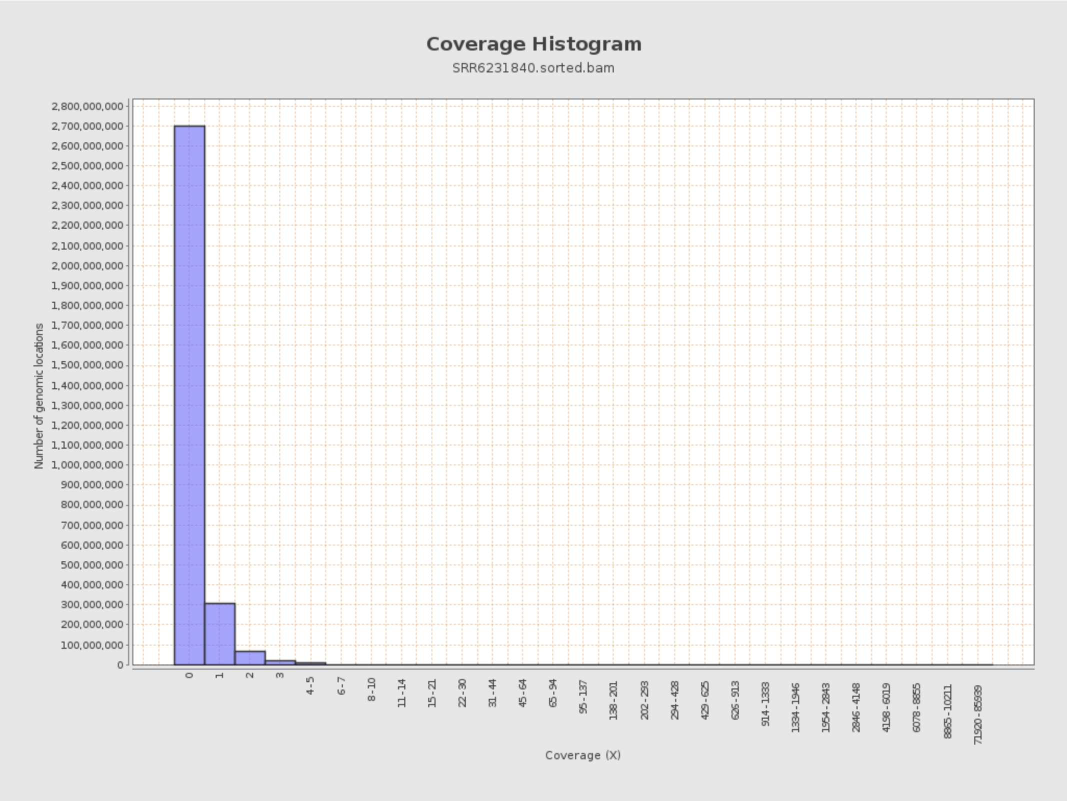
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	67367232	0.2703	7.658
chr2	243199373	49537437	0.2037	47.0194
chr3	198022430	50322700	0.2541	0.6548
chr4	191154276	18200171	0.0952	0.6949
chr5	180915260	26541763	0.1467	0.5554
chr6	171115067	40067720	0.2342	1.3672
chr7	159138663	39407806	0.2476	4.0625

chr8	146364022	38765855	0.2649	1.9272
chr9	141213431	21113568	0.1495	1.5361
chr10	135534747	20245138	0.1494	1.7351
chr11	135006516	18330645	0.1358	1.3144
chr12	133851895	16720668	0.1249	0.55
chr13	115169878	23167582	0.2012	0.5658
chr14	107349540	22003713	0.205	0.9316
chr15	102531392	9759638	0.0952	0.4027
chr16	90354753	12852393	0.1422	1.011
chr17	81195210	12962787	0.1596	0.7685
chr18	78077248	10289692	0.1318	4.0181
chr19	59128983	17253306	0.2918	4.1878
chr20	63025520	10208191	0.162	0.6987
chr21	48129895	7785241	0.1618	0.7008
chr22	51304566	3937541	0.0767	0.3368
chrMT	16571	442927	26.729	14.2054
chrX	155270560	21002788	0.1353	0.8383
chrY	59373566	1518090	0.0256	0.6181

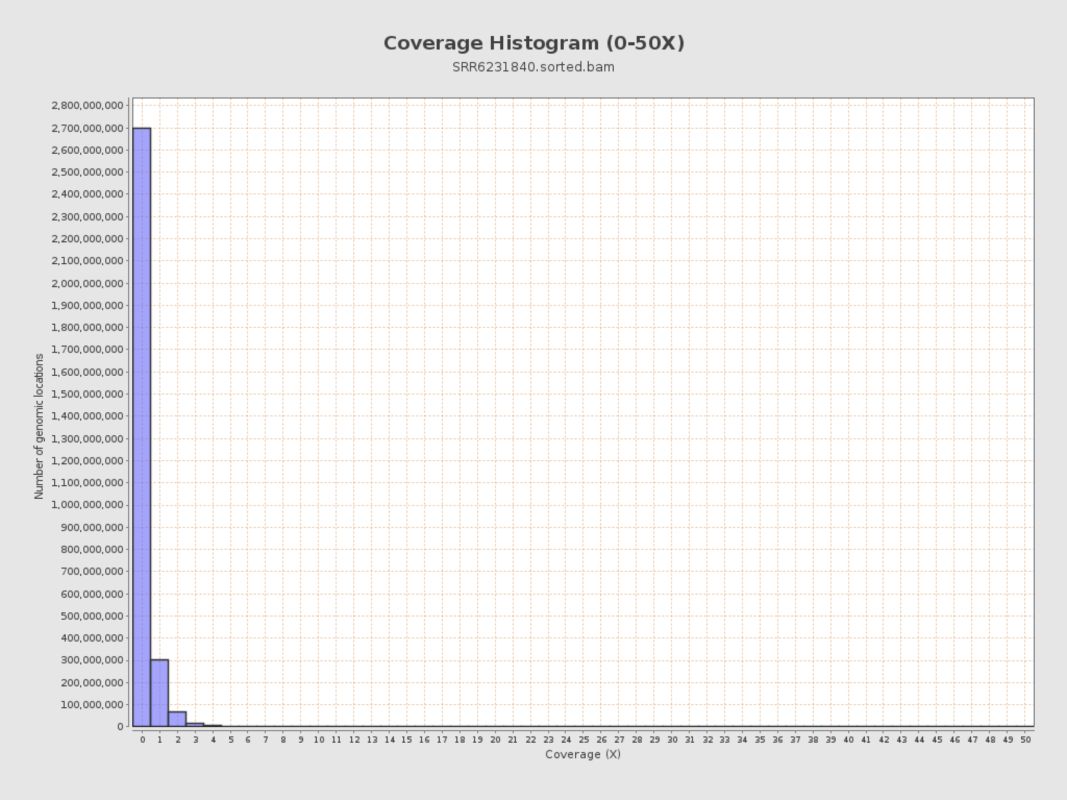
3. Results : Coverage across reference



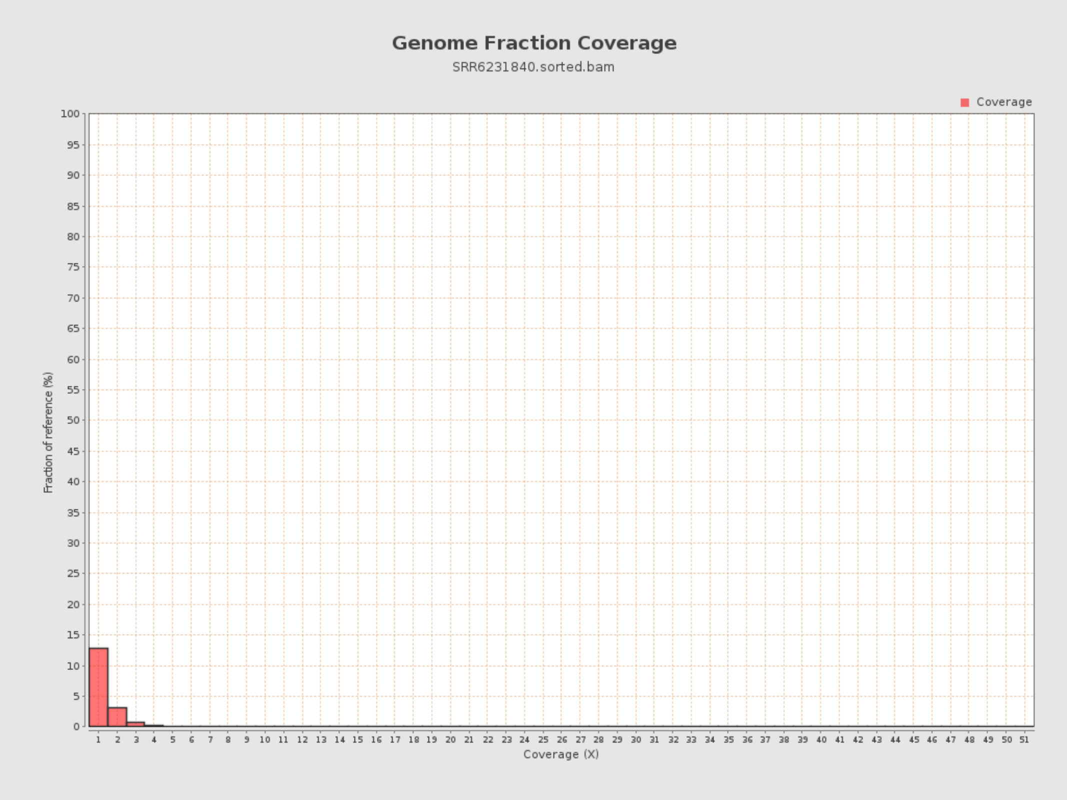
4. Results : Coverage Histogram



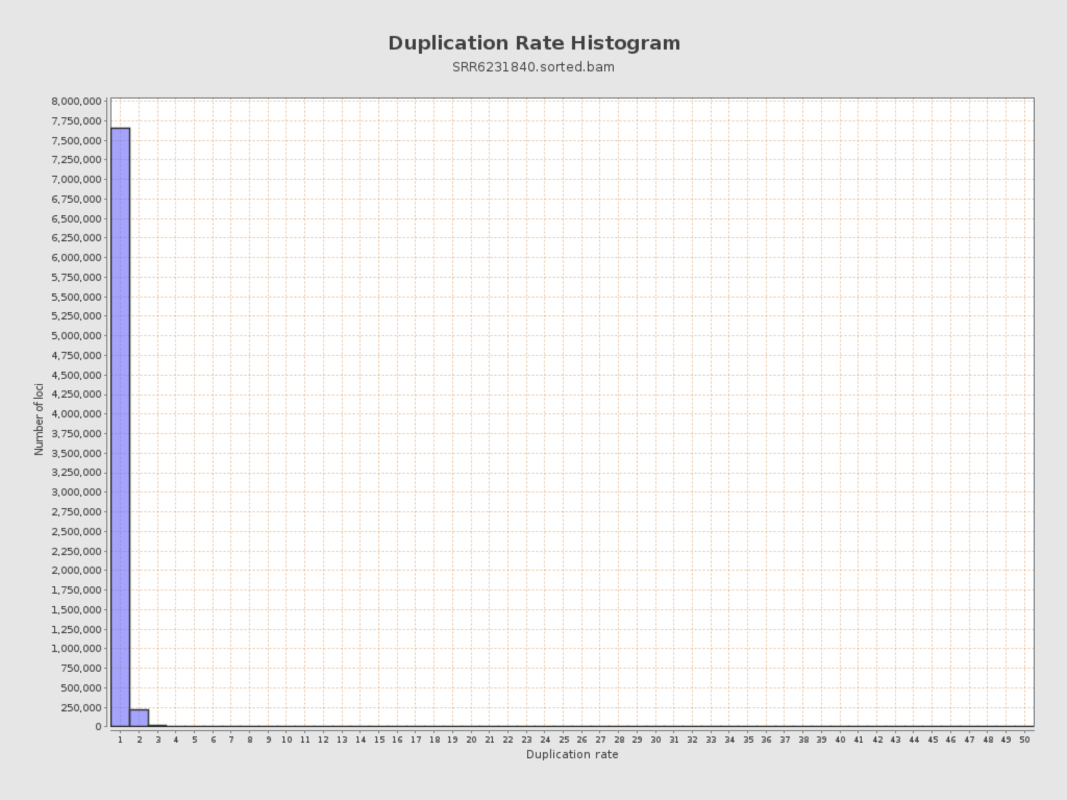
5. Results : Coverage Histogram (0-50X)



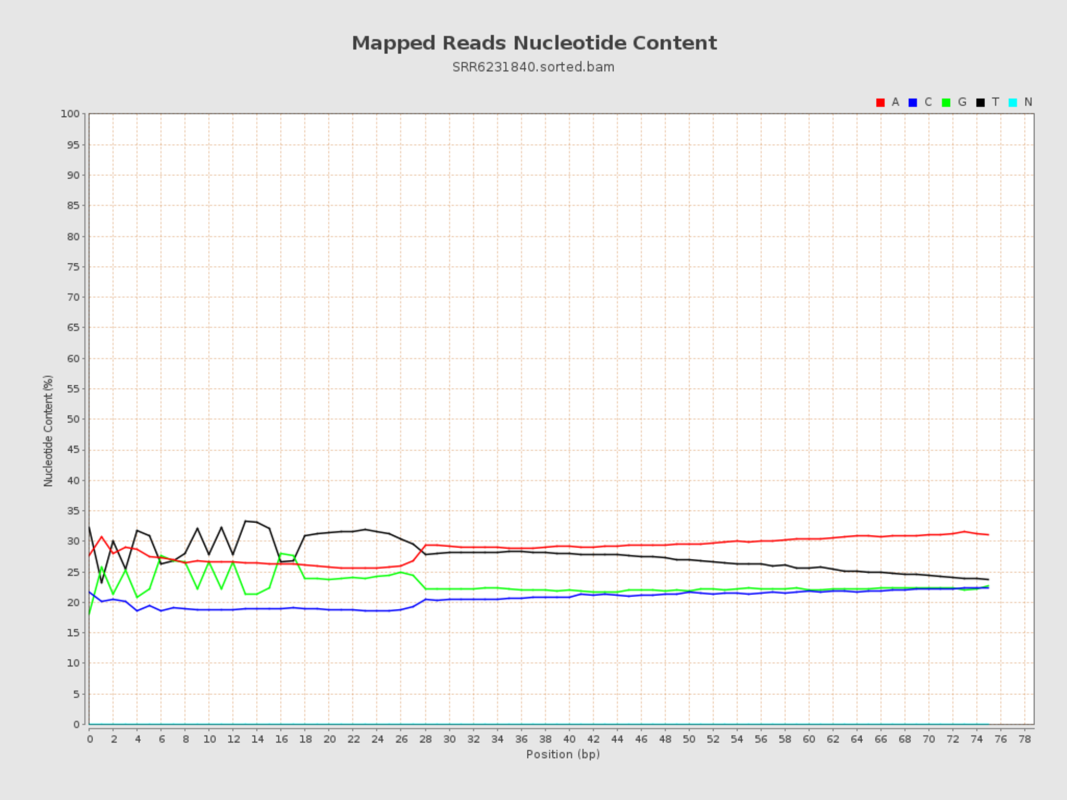
6. Results : Genome Fraction Coverage



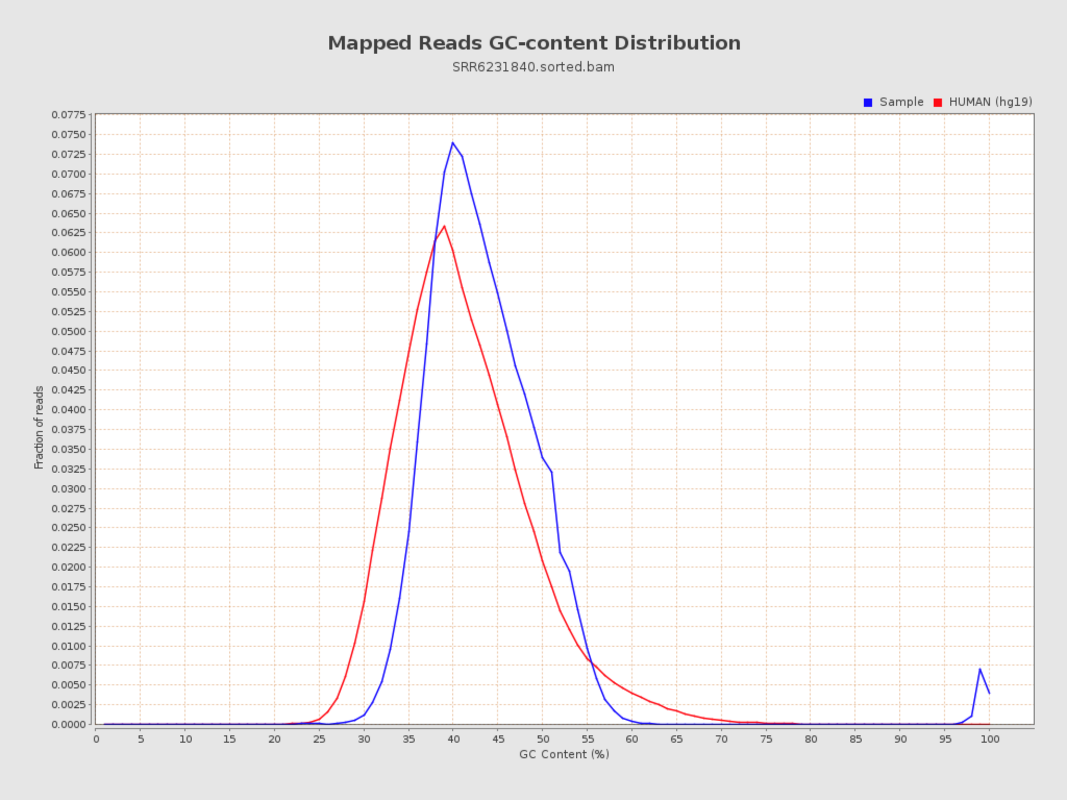
7. Results : Duplication Rate Histogram



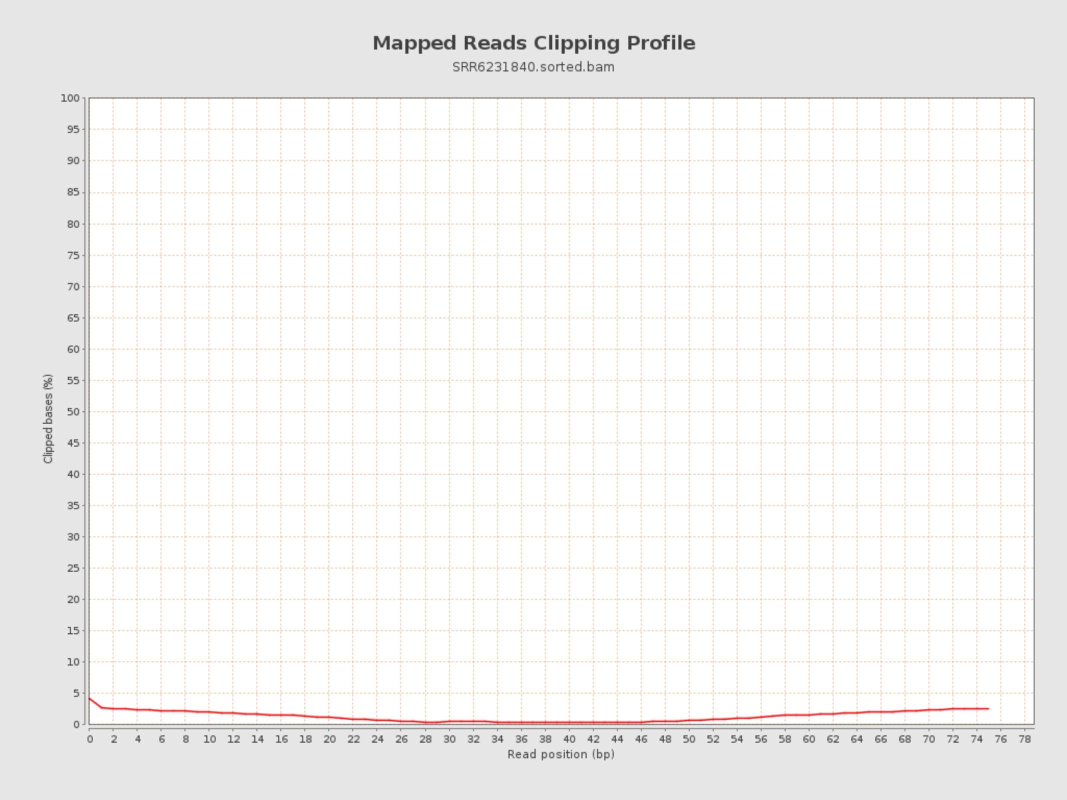
8. Results : Mapped Reads Nucleotide Content



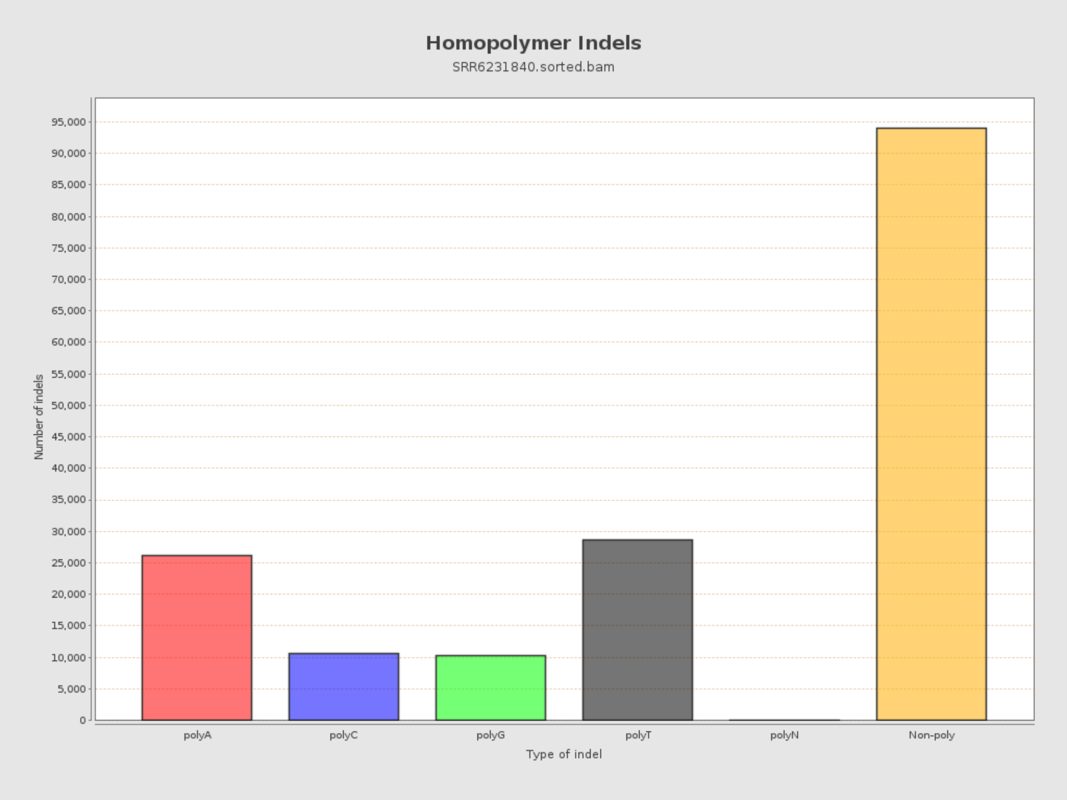
9. Results : Mapped Reads GC-content Distribution



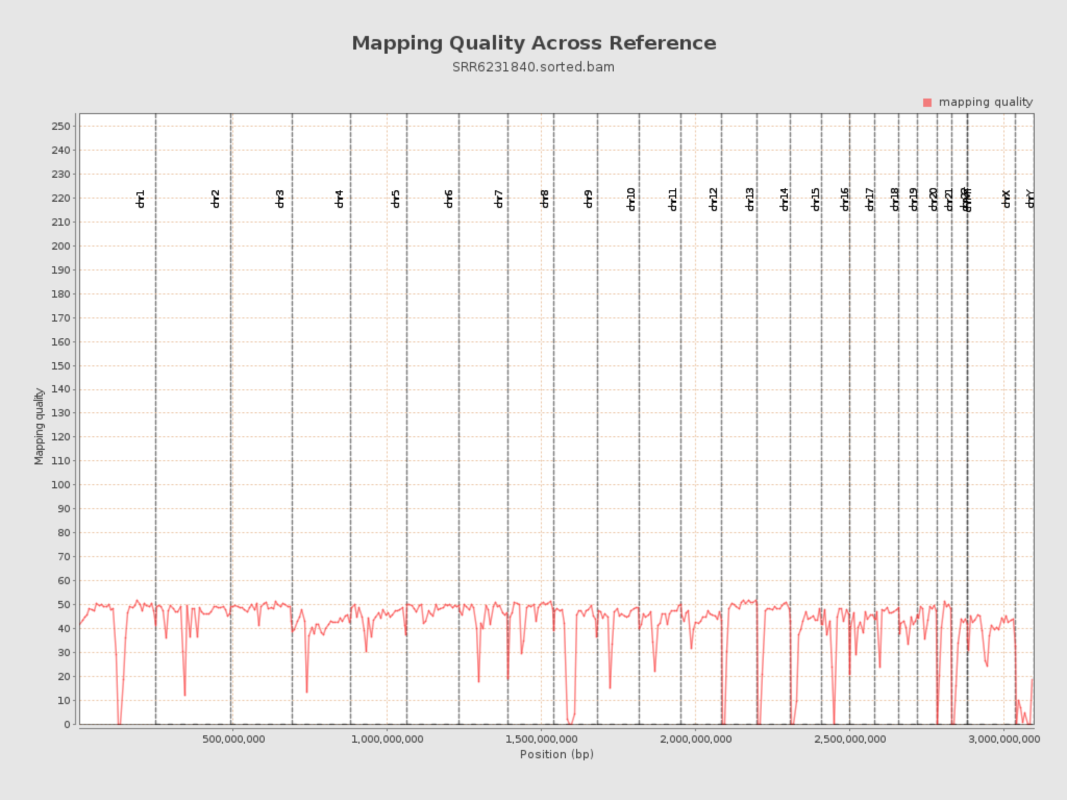
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram