Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:36:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231757.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_SRR6231757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:36:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,873,475
Mapped reads	5,414,405 / 92.18%
Unmapped reads	459,070 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,018 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	802,595 / 13.66%
Duplication rate	6.04%
Clipped reads	1,694,190 / 28.84%

2.2. ACGT Content

Number/percentage of A's	95,401,489 / 25.37%
Number/percentage of C's	68,588,573 / 18.24%
Number/percentage of T's	102,791,395 / 27.34%
Number/percentage of G's	109,104,563 / 29.02%
Number/percentage of N's	82,688 / 0.02%
GC Percentage	47.26%

2.3. Coverage

Mean	0.1215

Standard Deviation	64.5799

2.4. Mapping Quality

Mean Mapping Quality	46.94

2.5. Mismatches and indels

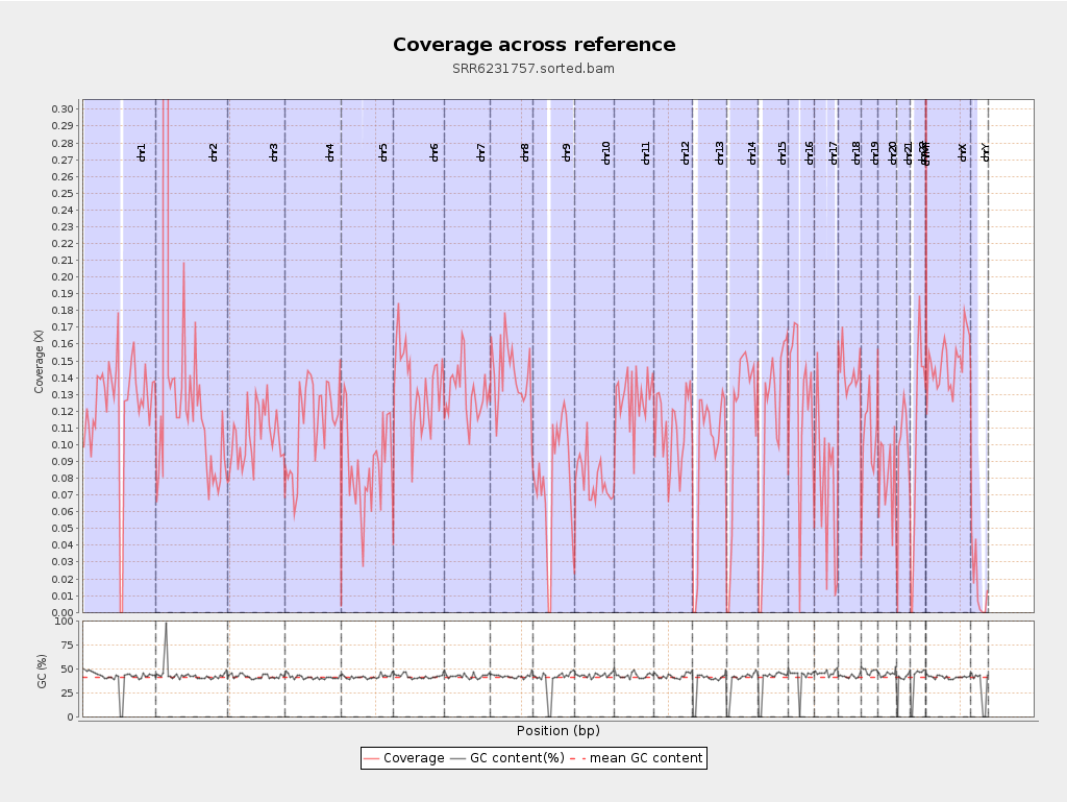
General error rate	0.6%
Mismatches	2,218,335
Insertions	23,342
Mapped reads with at least one insertion	0.43%
Deletions	77,154
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.14%

2.6. Chromosome stats

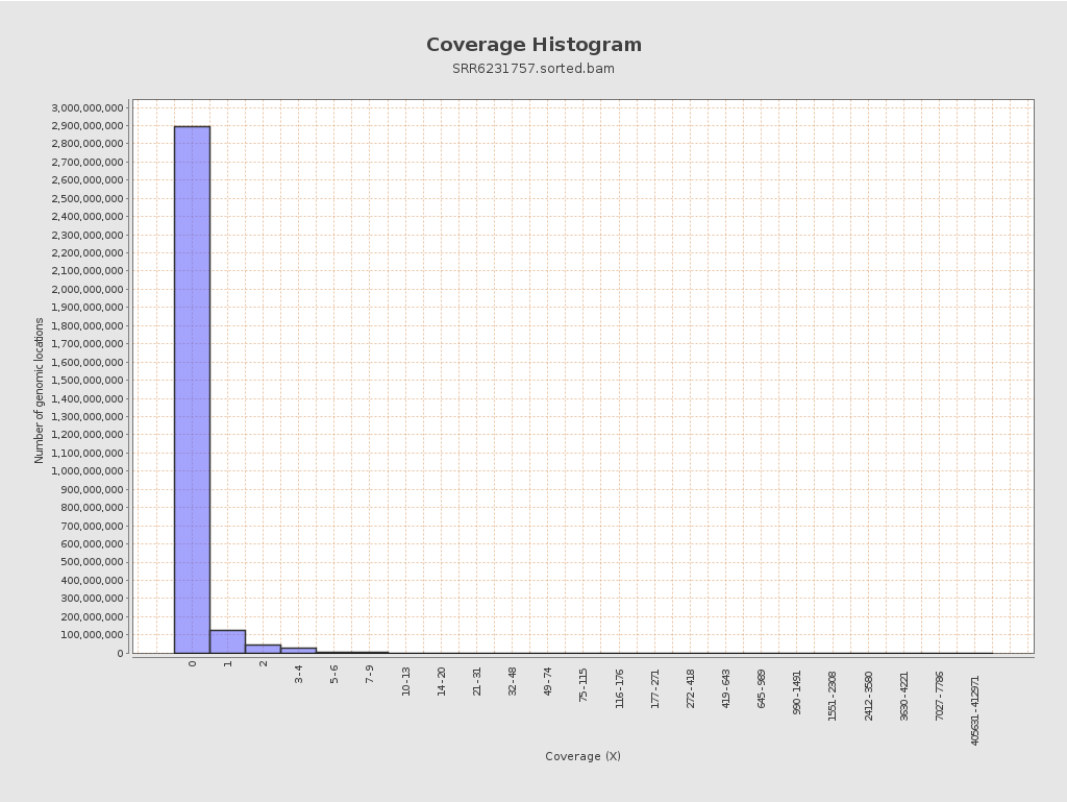
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	30732137	0.1233	1.1269
chr2	243199373	59620310	0.2451	230.3919
chr3	198022430	20757628	0.1048	0.5066
chr4	191154276	21793747	0.114	0.5779
chr5	180915260	15685345	0.0867	0.4631
chr6	171115067	23218635	0.1357	0.6596
chr7	159138663	20915050	0.1314	1.1155

chr8	146364022	20617417	0.1409	0.7822
chr9	141213431	11197817	0.0793	0.7043
chr10	135534747	10673218	0.0787	0.6091
chr11	135006516	17190425	0.1273	0.9691
chr12	133851895	14610506	0.1092	0.5303
chr13	115169878	11055762	0.096	0.4879
chr14	107349540	12318830	0.1148	0.6524
chr15	102531392	11341097	0.1106	0.534
chr16	90354753	11216084	0.1241	0.6094
chr17	81195210	6364735	0.0784	0.5971
chr18	78077248	11212089	0.1436	1.6512
chr19	59128983	6337180	0.1072	0.8712
chr20	63025520	5081020	0.0806	0.4927
chr21	48129895	4598622	0.0955	0.5864
chr22	51304566	5528958	0.1078	0.5466
chrMT	16571	7537	0.4548	0.9708
chrX	155270560	23133615	0.149	0.6901
chrY	59373566	891639	0.015	0.2815

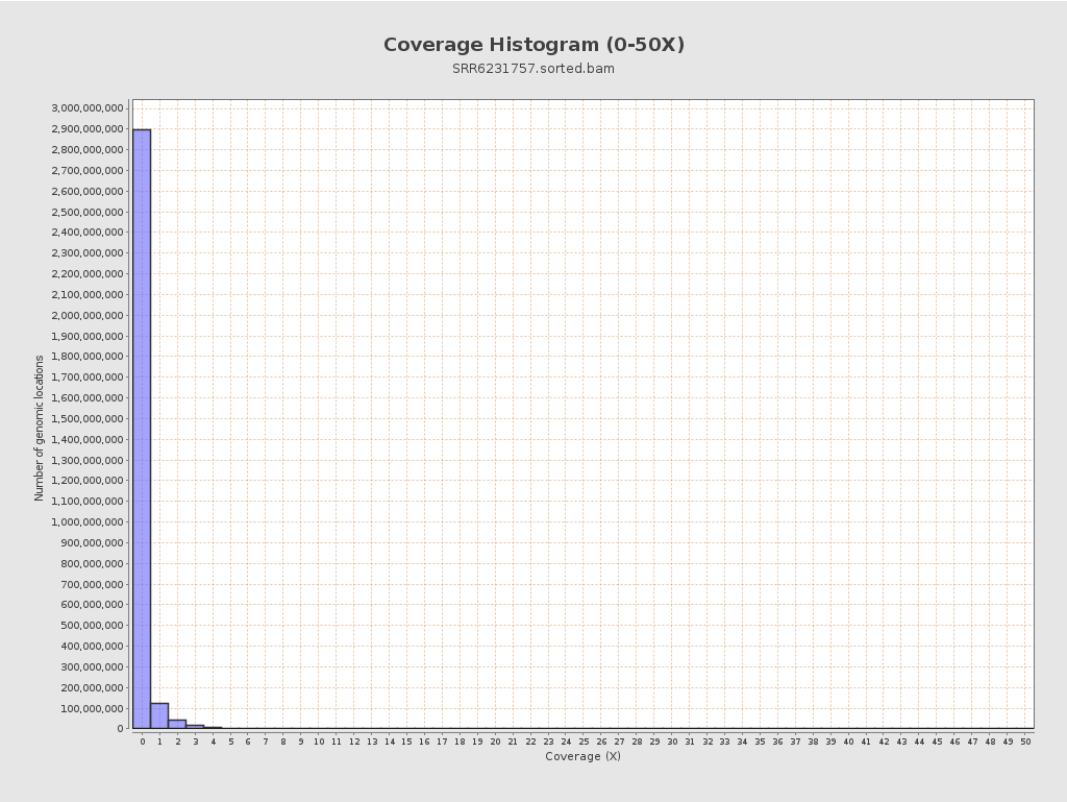
3. Results : Coverage across reference



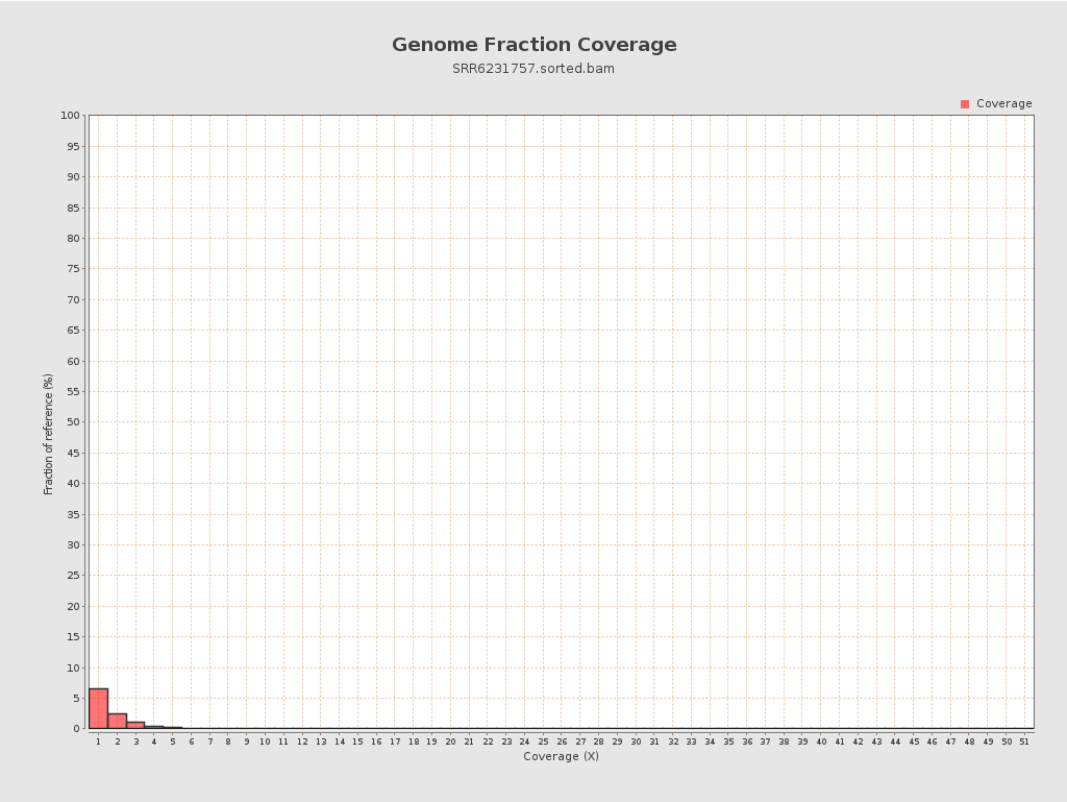
4. Results : Coverage Histogram



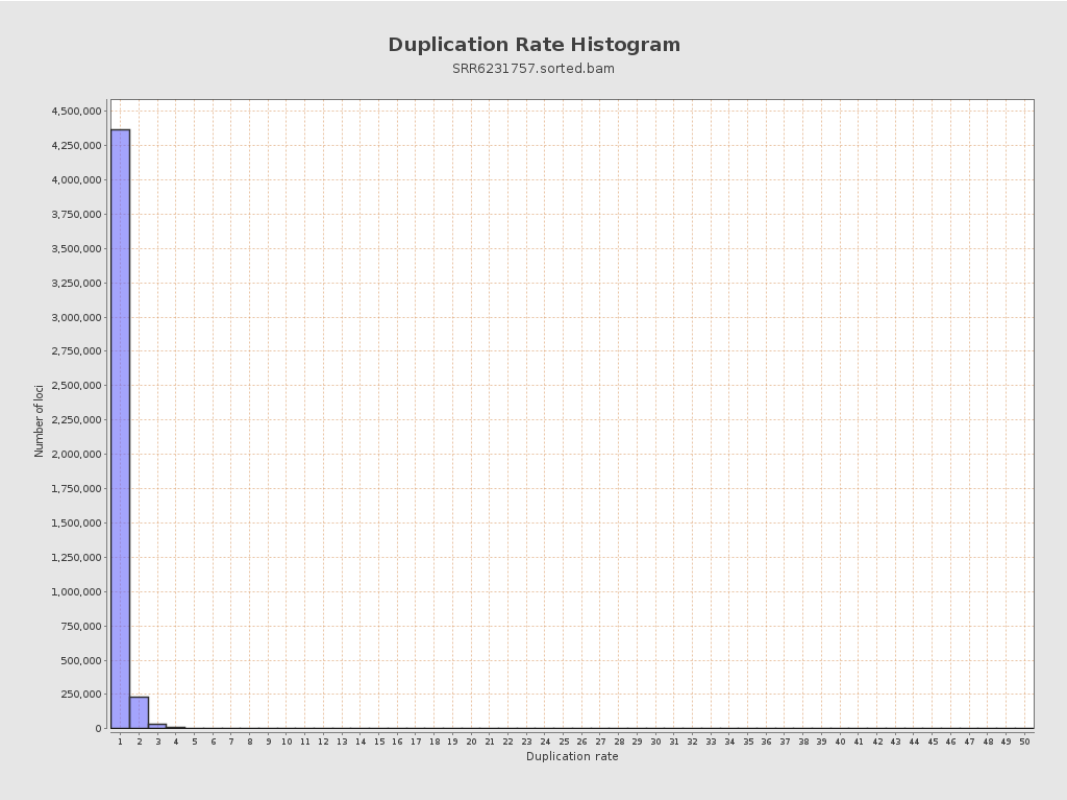
5. Results : Coverage Histogram (0-50X)



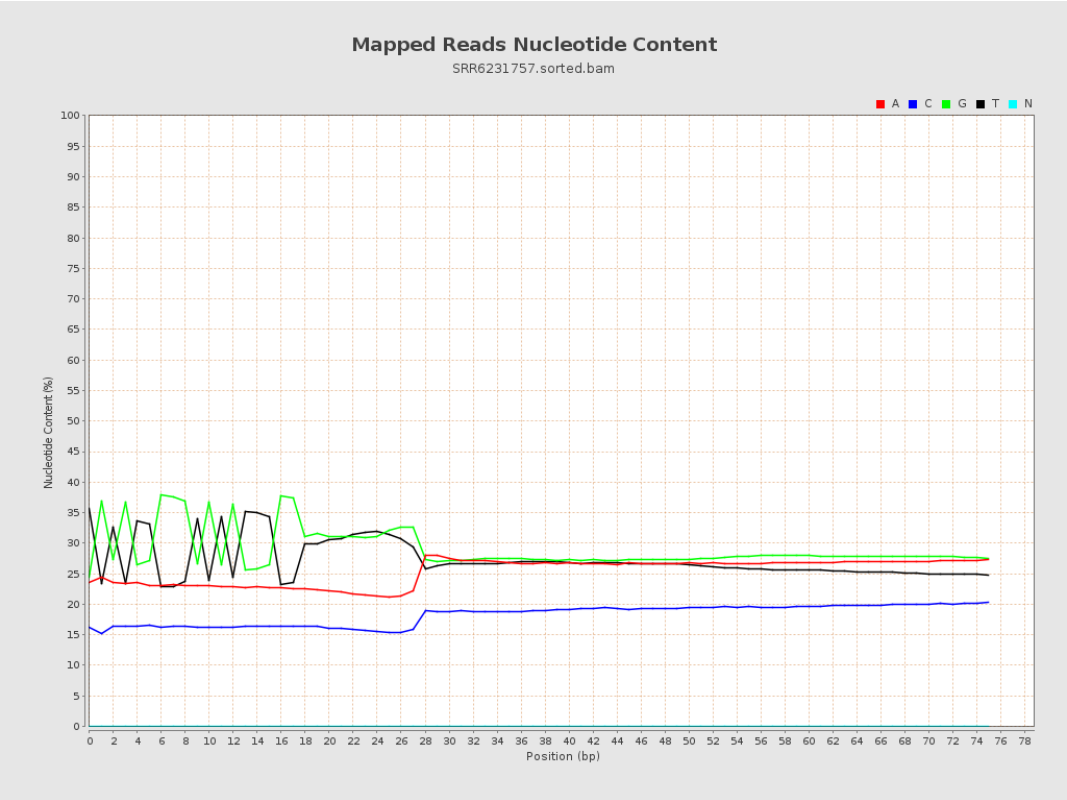
6. Results : Genome Fraction Coverage



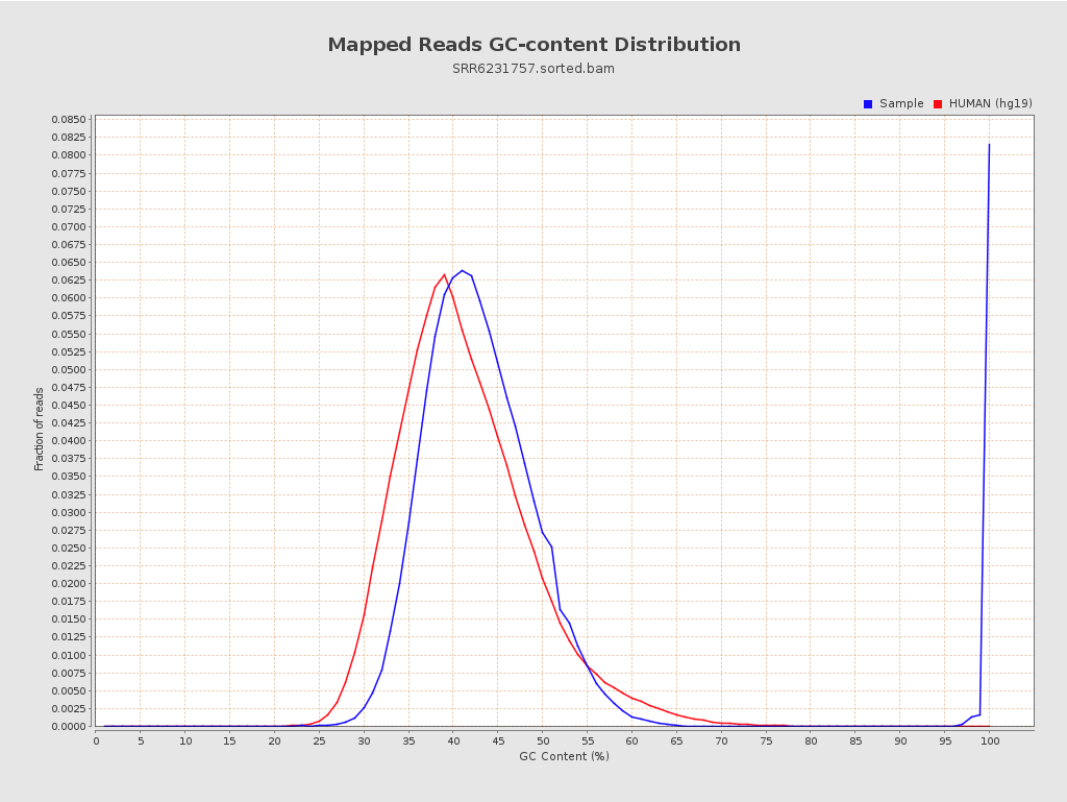
7. Results : Duplication Rate Histogram



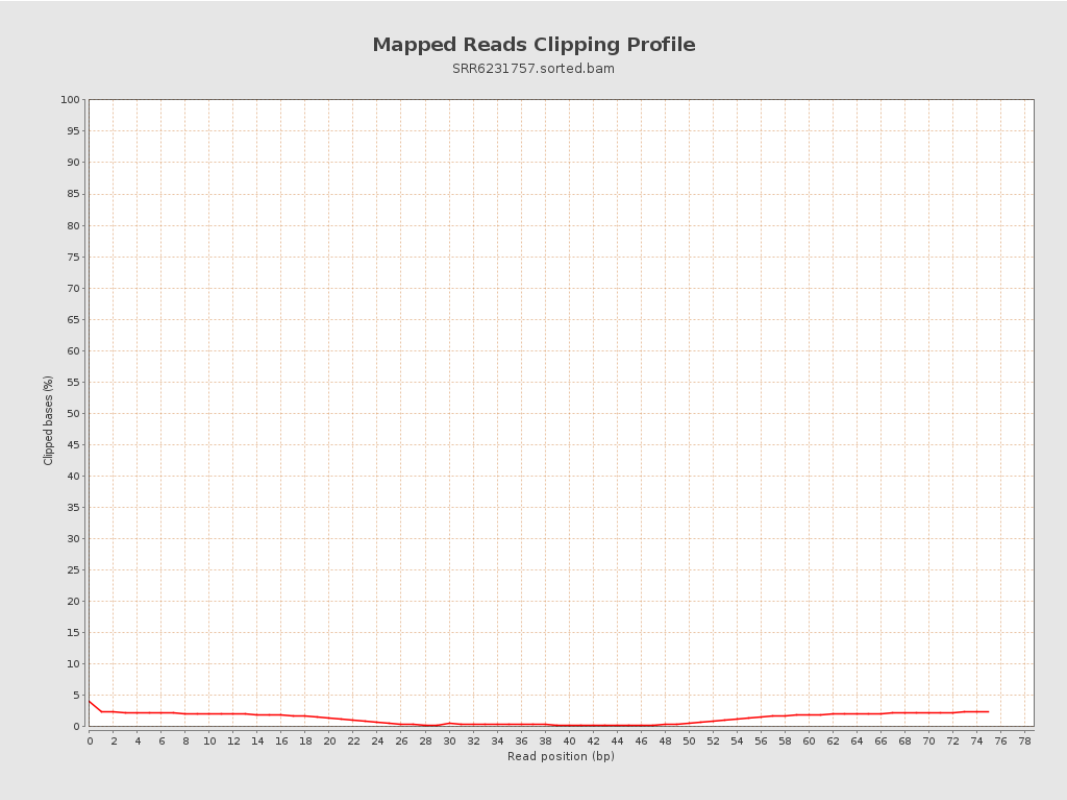
8. Results : Mapped Reads Nucleotide Content



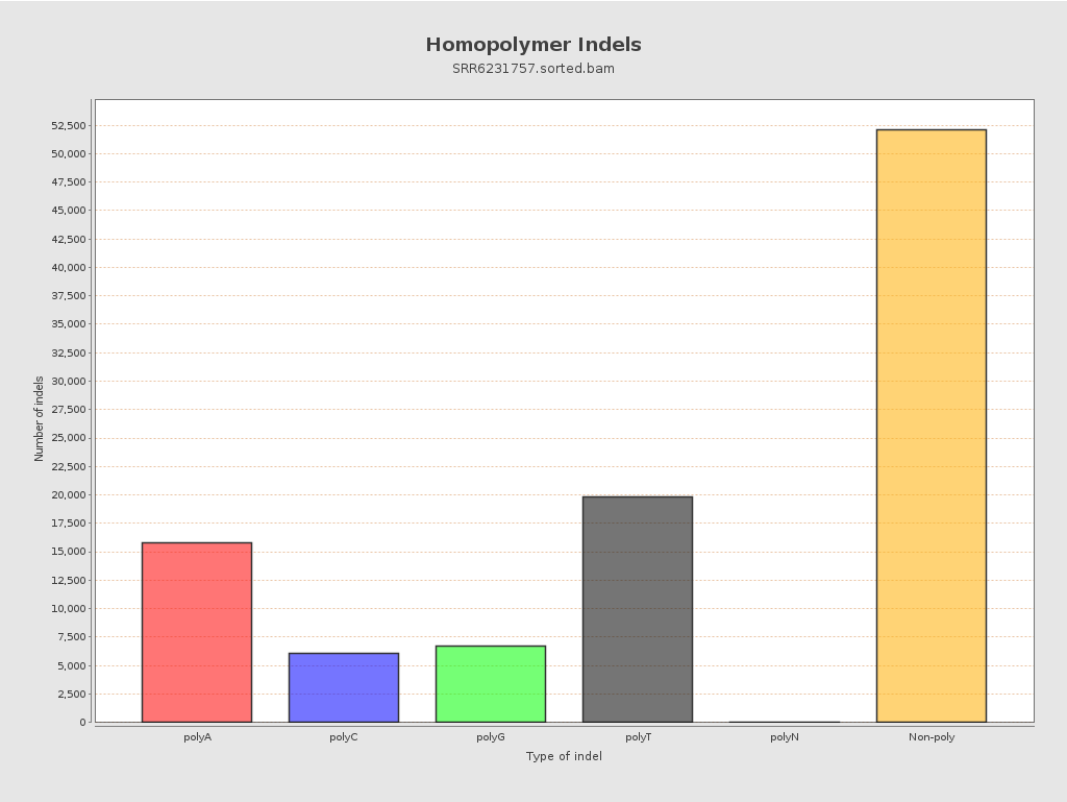
9. Results : Mapped Reads GC-content Distribution



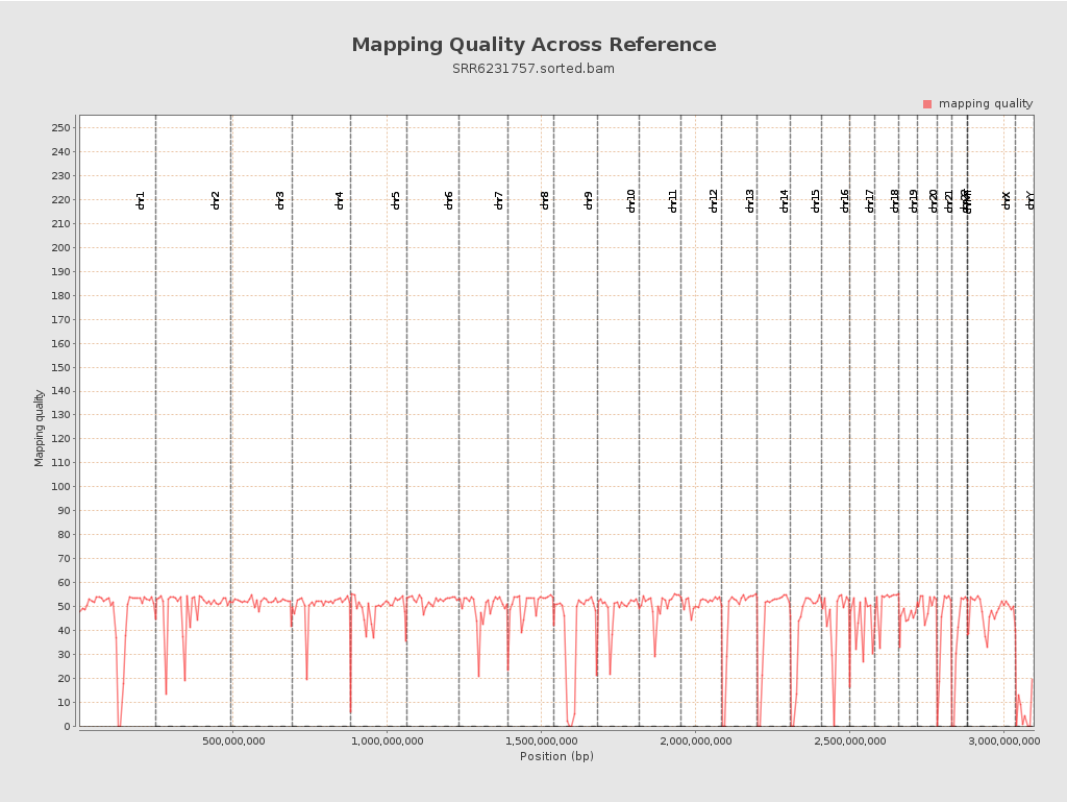
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram