Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:02:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231869.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_SRR6231869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231869.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:02:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,384,227
Mapped reads	4,040,408 / 92.16%
Unmapped reads	343,819 / 7.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,853 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	315,043 / 7.19%
Duplication rate	6.41%
Clipped reads	1,718,308 / 39.19%

2.2. ACGT Content

Number/percentage of A's	74,782,186 / 27.57%
Number/percentage of C's	49,736,947 / 18.34%
Number/percentage of T's	86,896,924 / 32.04%
Number/percentage of G's	59,703,820 / 22.01%
Number/percentage of N's	110,292 / 0.04%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0876

Standard Deviation	0.7809

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

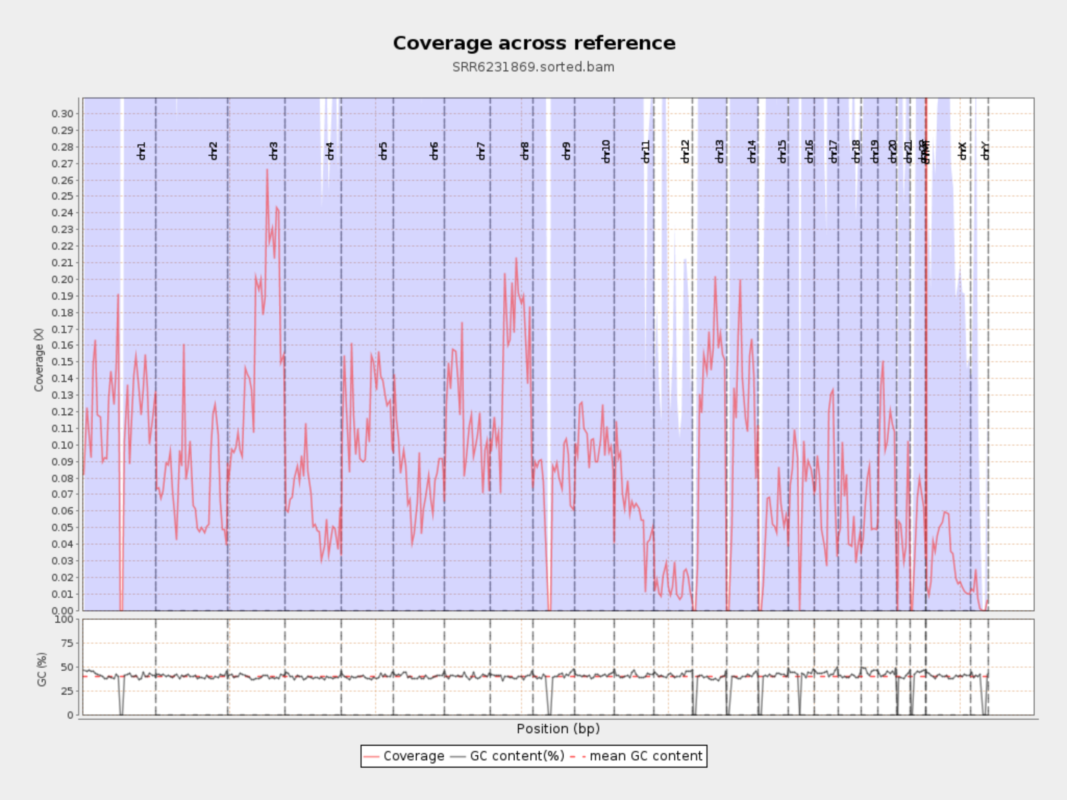
General error rate	0.62%
Mismatches	1,642,067
Insertions	18,166
Mapped reads with at least one insertion	0.45%
Deletions	60,607
Mapped reads with at least one deletion	1.48%
Homopolymer indels	45.73%

2.6. Chromosome stats

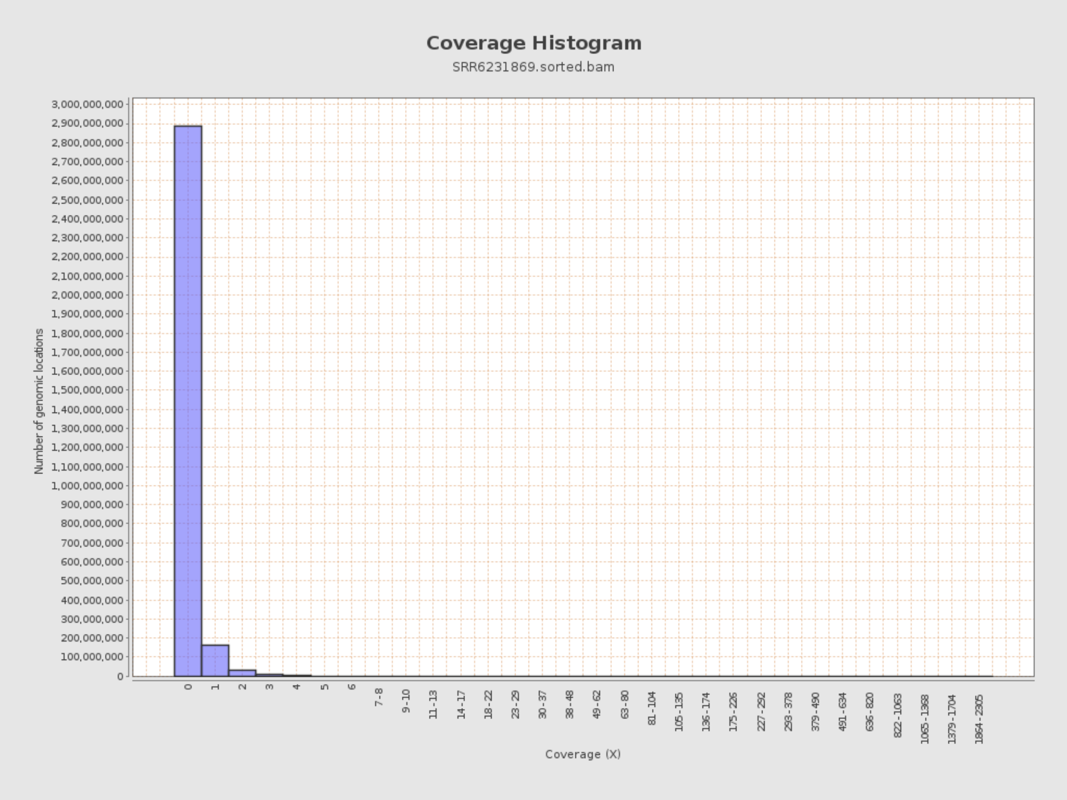
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28976394	0.1163	1.3876
chr2	243199373	18510289	0.0761	0.8662
chr3	198022430	31551593	0.1593	0.5011
chr4	191154276	11800869	0.0617	0.3422
chr5	180915260	21849670	0.1208	0.4345
chr6	171115067	13368520	0.0781	0.4091
chr7	159138663	18221192	0.1145	1.1977

chr8	146364022	22182818	0.1516	1.4946
chr9	141213431	10349699	0.0733	0.6597
chr10	135534747	13953990	0.103	0.5482
chr11	135006516	8486980	0.0629	0.5187
chr12	133851895	2122974	0.0159	0.2133
chr13	115169878	14697581	0.1276	0.4535
chr14	107349540	12294750	0.1145	0.5036
chr15	102531392	4819918	0.047	0.3094
chr16	90354753	6786670	0.0751	0.4583
chr17	81195210	6376526	0.0785	0.3905
chr18	78077248	4305949	0.0551	1.635
chr19	59128983	3489017	0.059	0.8578
chr20	63025520	7098618	0.1126	0.4632
chr21	48129895	2271699	0.0472	0.2997
chr22	51304566	2449785	0.0477	0.2614
chrMT	16571	163640	9.8751	6.2967
chrX	155270560	4741632	0.0305	0.3249
chrY	59373566	466637	0.0079	0.1517

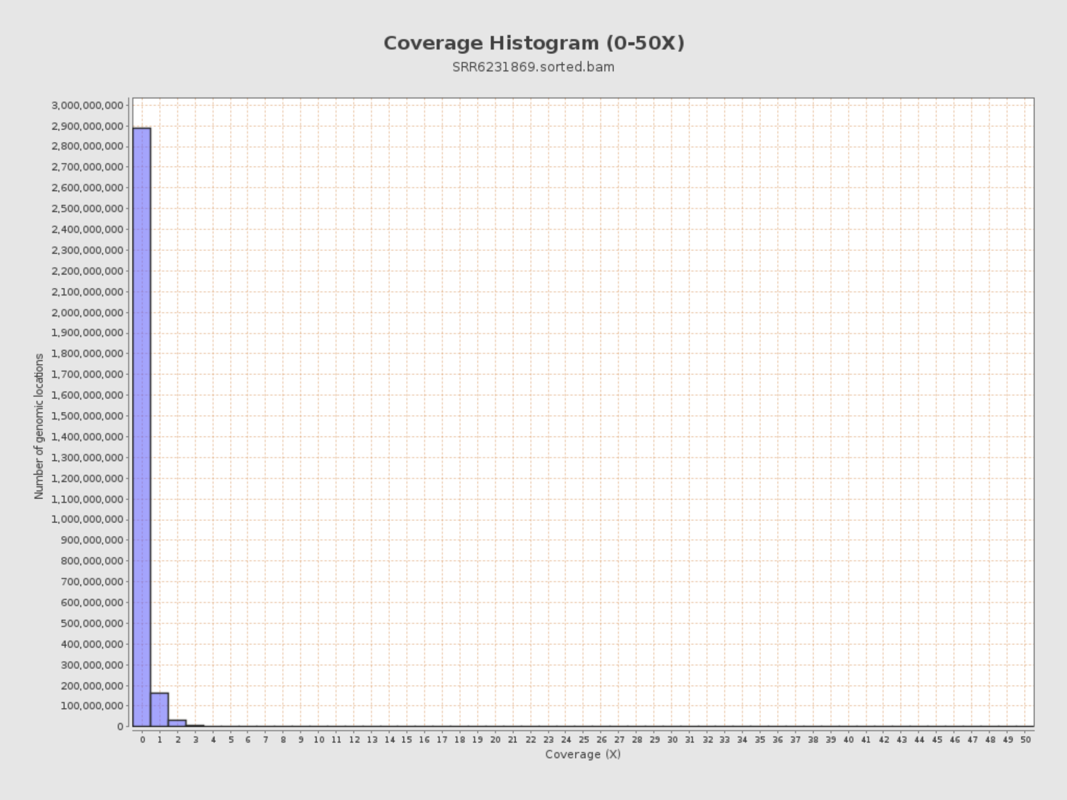
3. Results : Coverage across reference



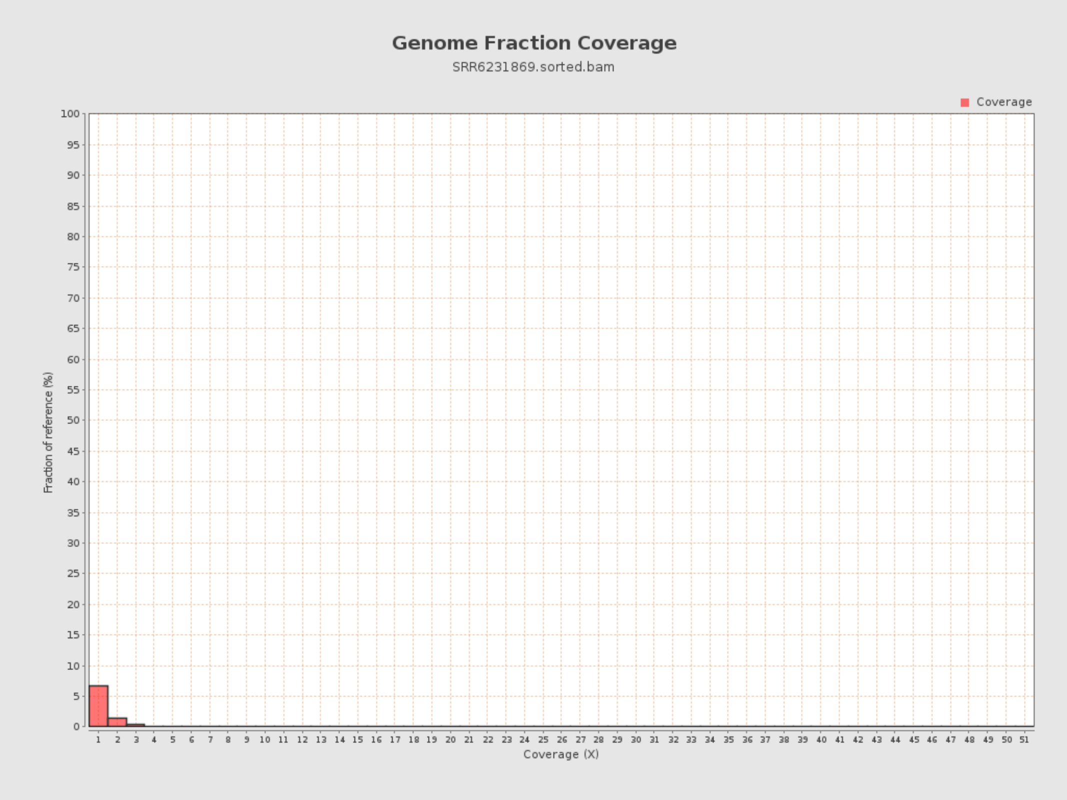
4. Results : Coverage Histogram



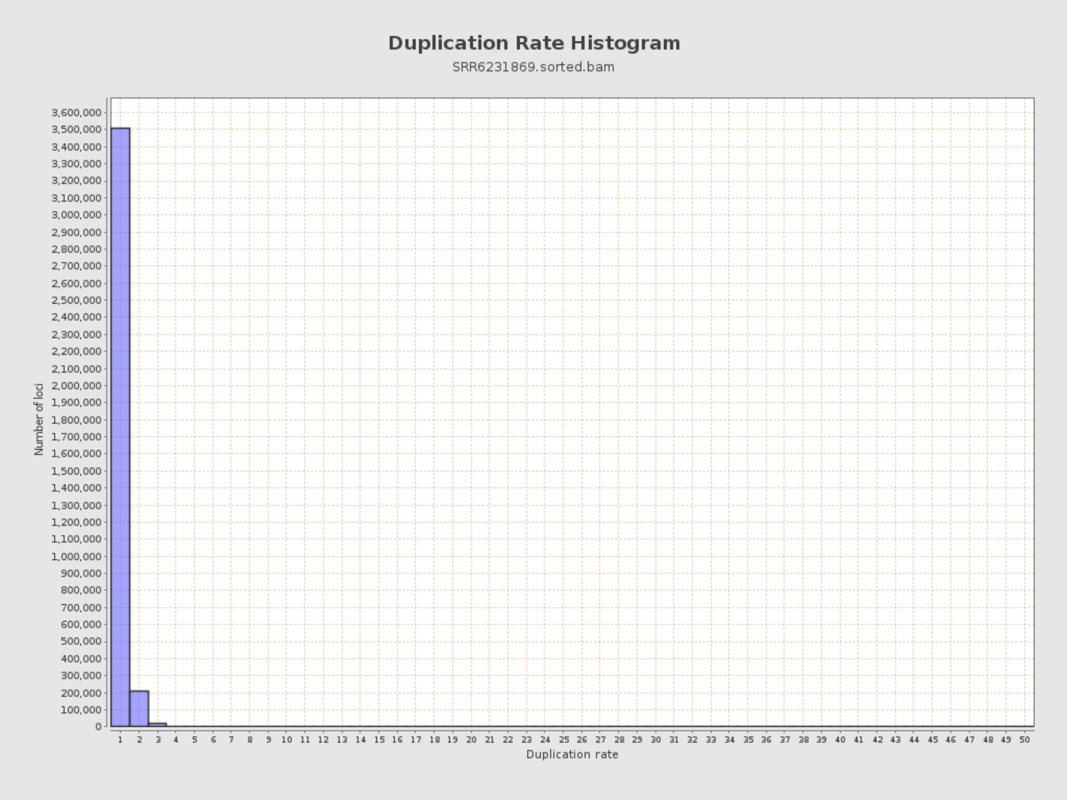
5. Results : Coverage Histogram (0-50X)



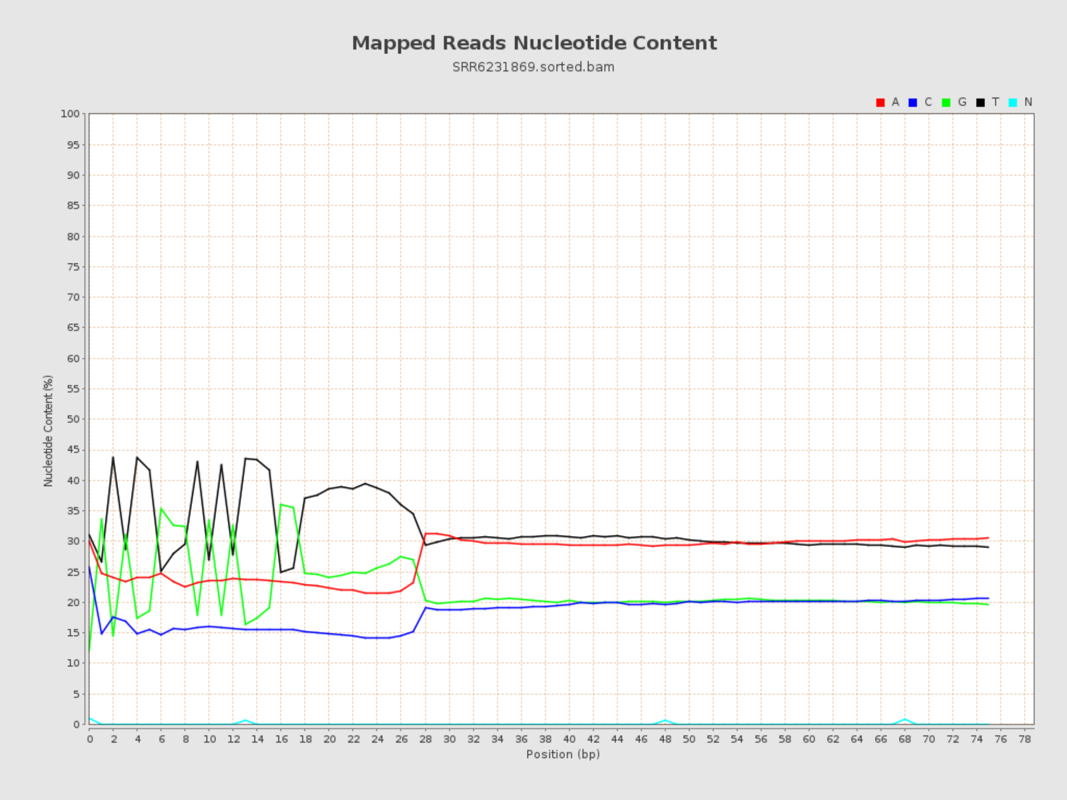
6. Results : Genome Fraction Coverage



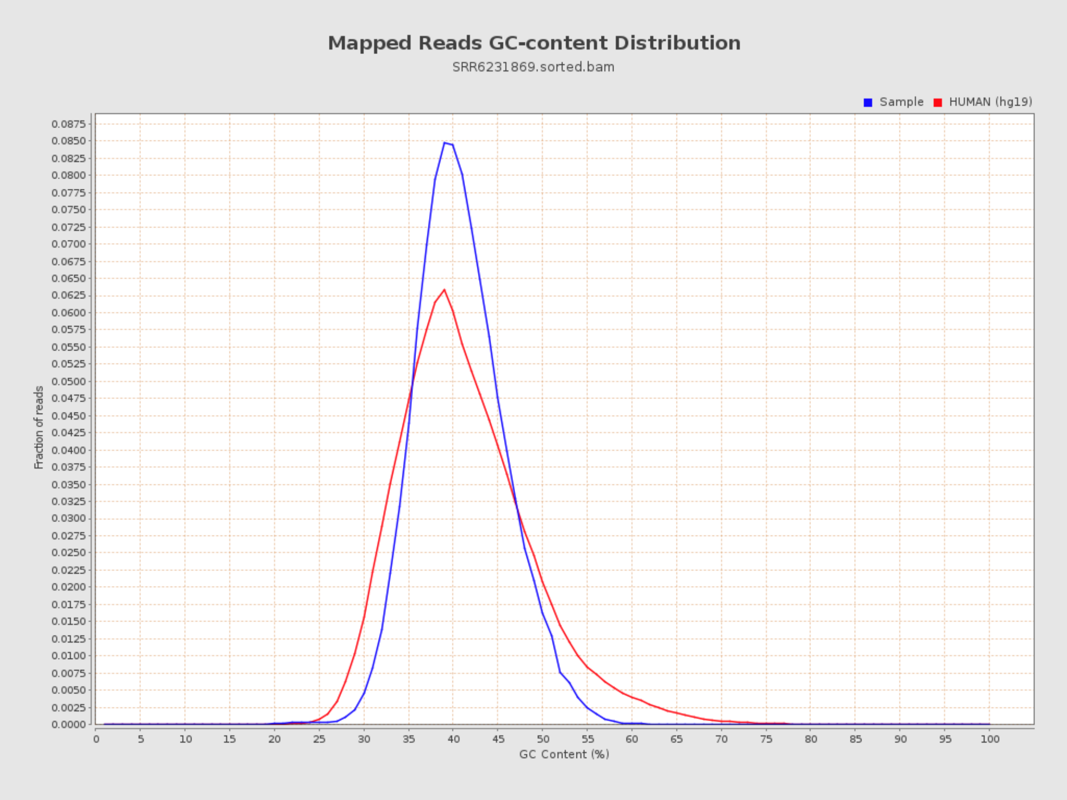
7. Results : Duplication Rate Histogram



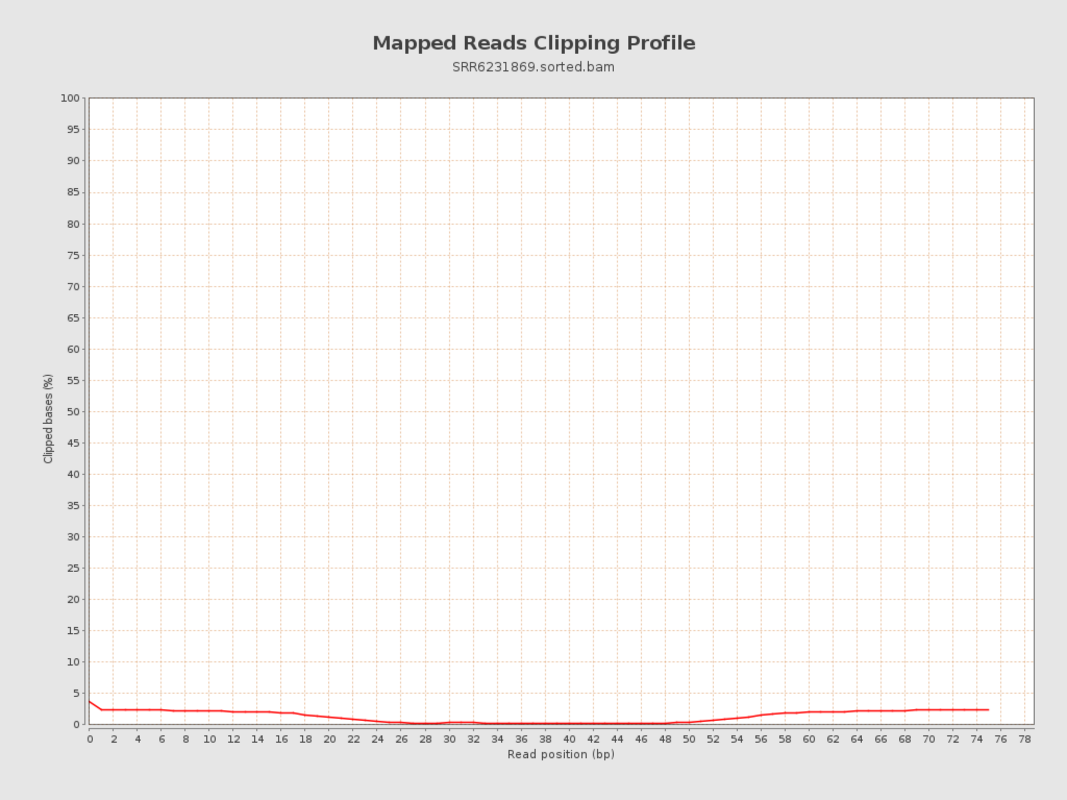
8. Results : Mapped Reads Nucleotide Content



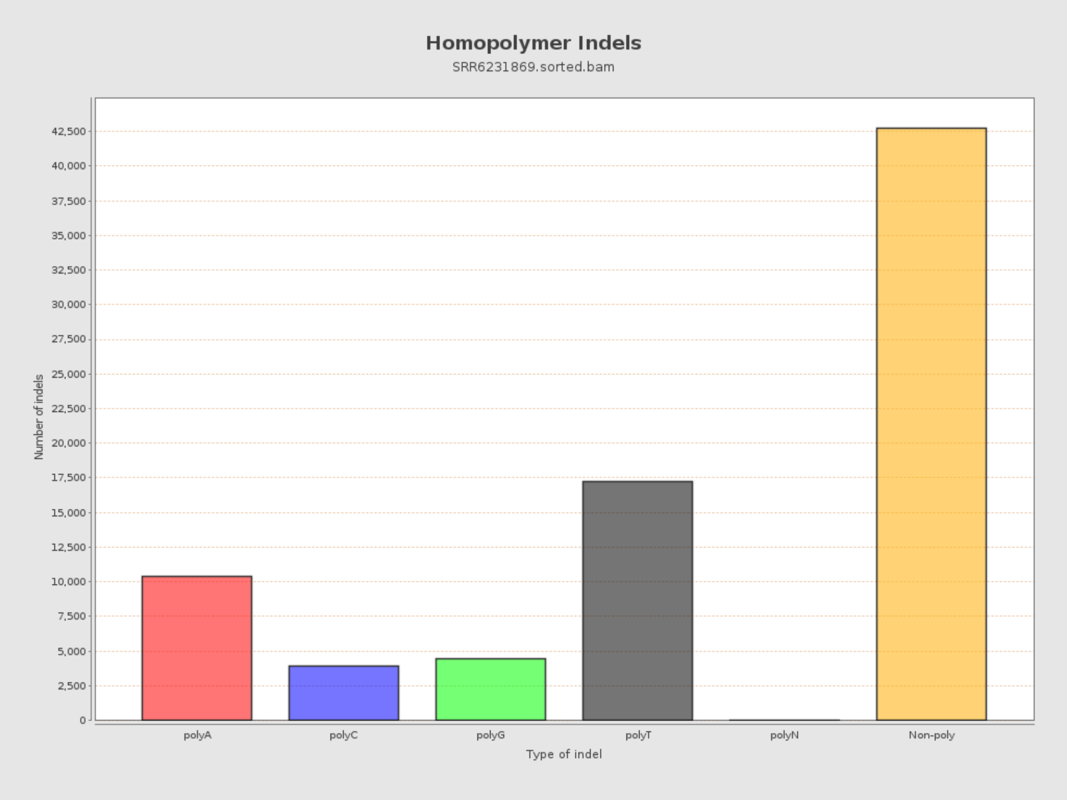
9. Results : Mapped Reads GC-content Distribution



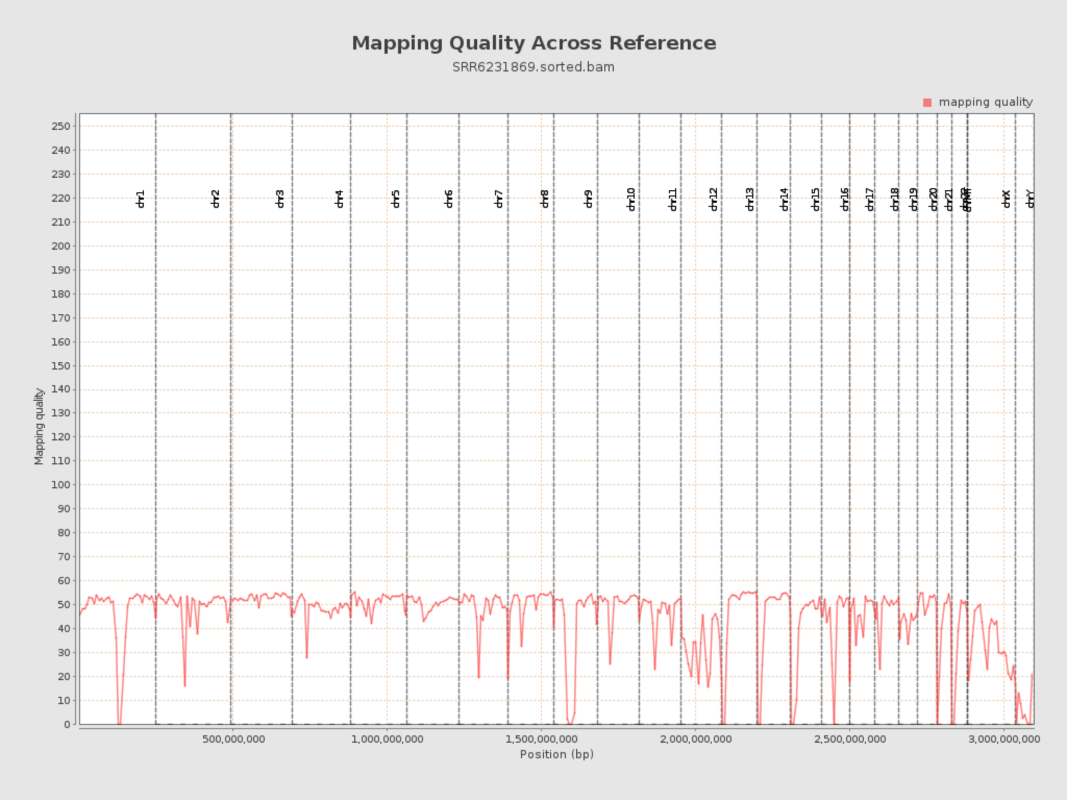
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram