Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 04:15:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063591.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_SRR6063591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063591.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 04:15:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,946,598
Mapped reads	5,372,266 / 90.34%
Unmapped reads	574,332 / 9.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,577 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	237,271 / 3.99%
Duplication rate	2.96%
Clipped reads	2,379,690 / 40.02%

2.2. ACGT Content

Number/percentage of A's	103,096,221 / 28.61%
Number/percentage of C's	66,382,862 / 18.42%
Number/percentage of T's	112,478,541 / 31.21%
Number/percentage of G's	78,206,309 / 21.7%
Number/percentage of N's	198,457 / 0.06%
GC Percentage	40.12%

2.3. Coverage

Mean	0.1165

Standard Deviation	0.9768

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

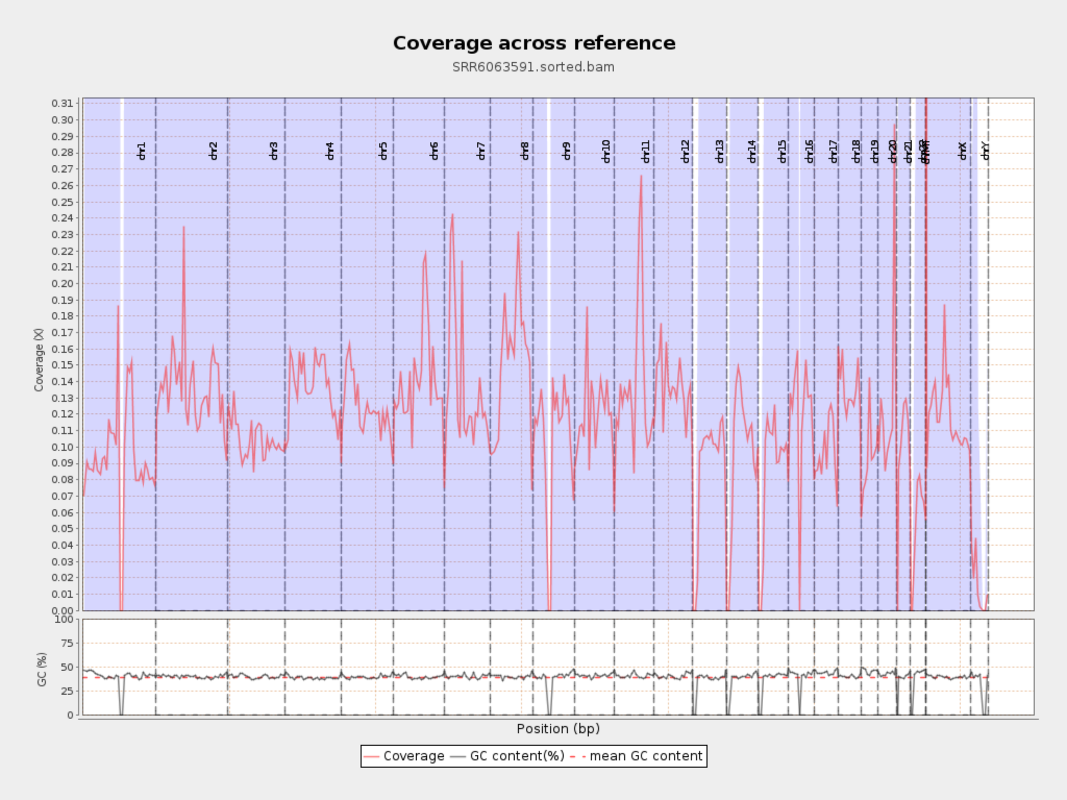
General error rate	0.9%
Mismatches	3,184,721
Insertions	29,511
Mapped reads with at least one insertion	0.54%
Deletions	113,794
Mapped reads with at least one deletion	2.09%
Homopolymer indels	45.38%

2.6. Chromosome stats

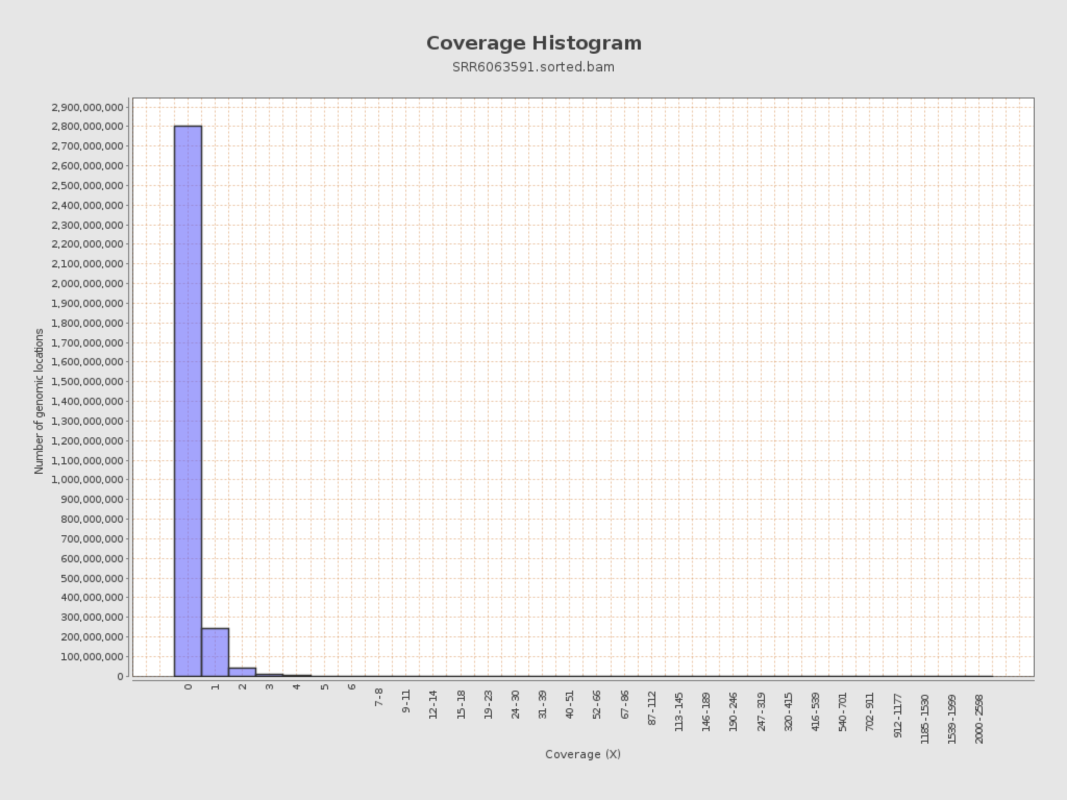
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23061942	0.0925	1.904
chr2	243199373	33133072	0.1362	1.1074
chr3	198022430	20676468	0.1044	0.3818
chr4	191154276	26337360	0.1378	0.4781
chr5	180915260	22372144	0.1237	0.4216
chr6	171115067	24271830	0.1418	0.5792
chr7	159138663	21480899	0.135	1.4109

chr8	146364022	22217141	0.1518	1.6534
chr9	141213431	14847225	0.1051	0.897
chr10	135534747	16326823	0.1205	0.8265
chr11	135006516	18513231	0.1371	0.8964
chr12	133851895	18320402	0.1369	0.4576
chr13	115169878	9971557	0.0866	0.3412
chr14	107349540	10441141	0.0973	0.4771
chr15	102531392	8585183	0.0837	0.3575
chr16	90354753	10539985	0.1167	0.555
chr17	81195210	7972236	0.0982	0.4877
chr18	78077248	10608554	0.1359	1.7552
chr19	59128983	5564936	0.0941	1.3519
chr20	63025520	8361291	0.1327	0.4731
chr21	48129895	4749777	0.0987	0.4347
chr22	51304566	2671235	0.0521	0.2583
chrMT	16571	213066	12.8578	7.6396
chrX	155270560	18450992	0.1188	0.5456
chrY	59373566	863127	0.0145	0.2848

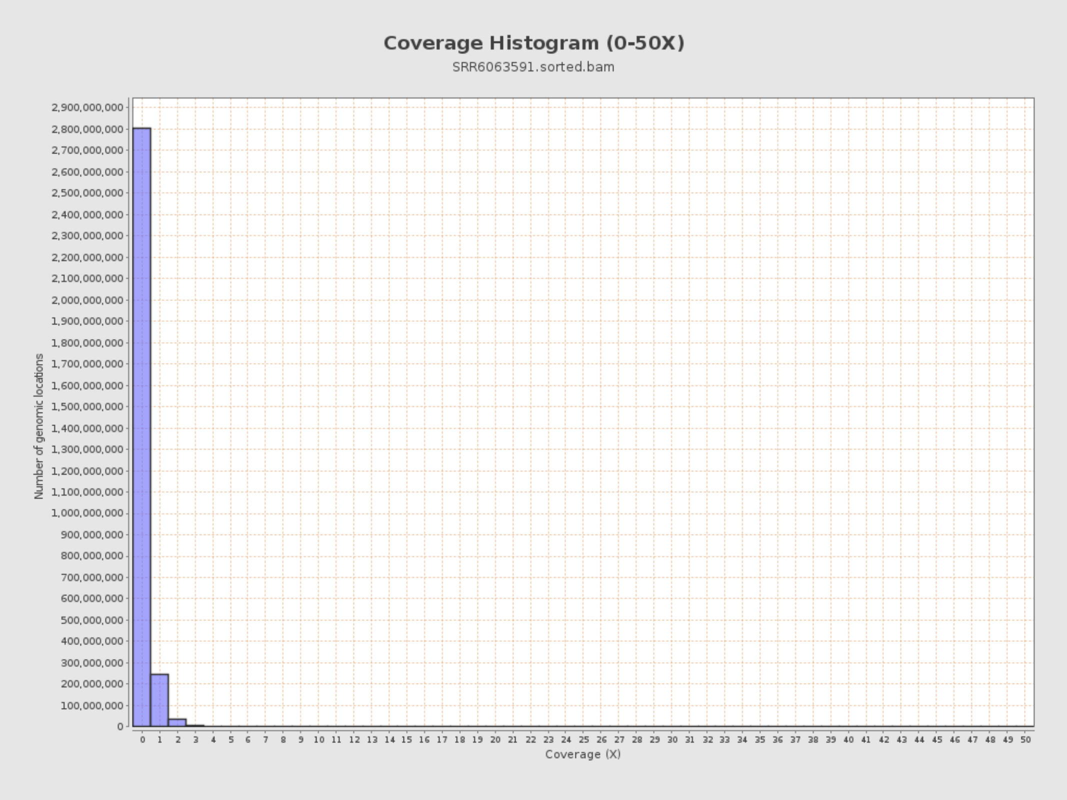
3. Results : Coverage across reference



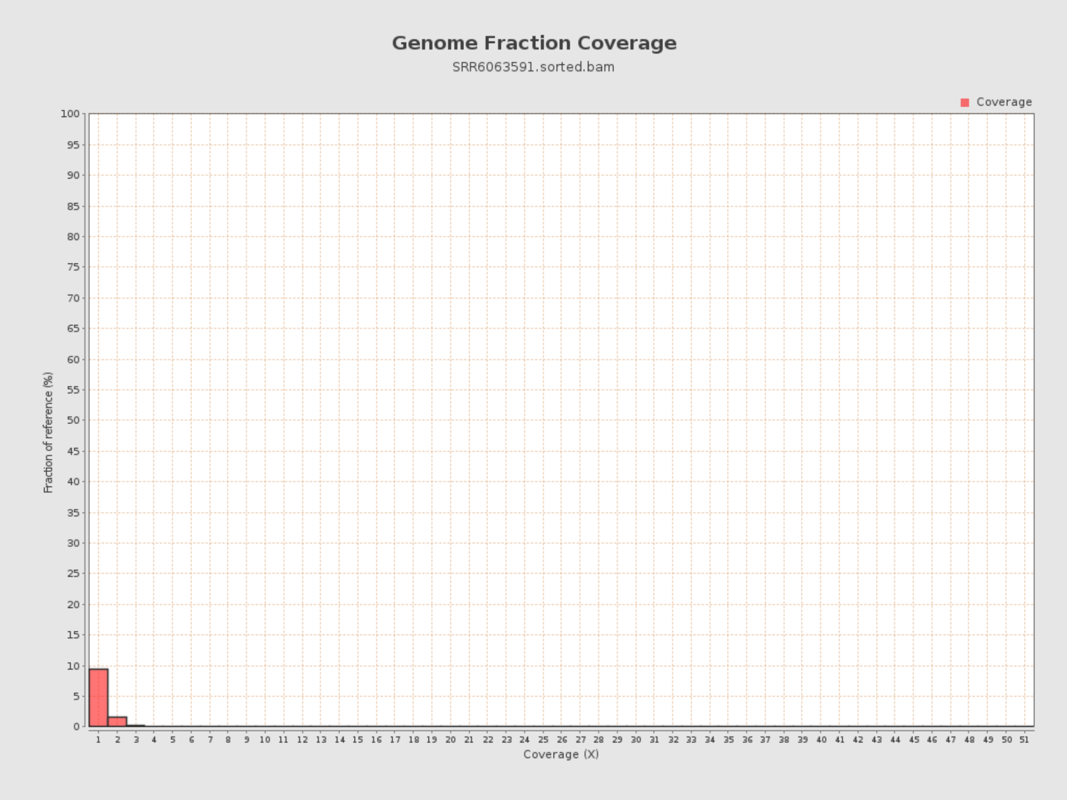
4. Results : Coverage Histogram



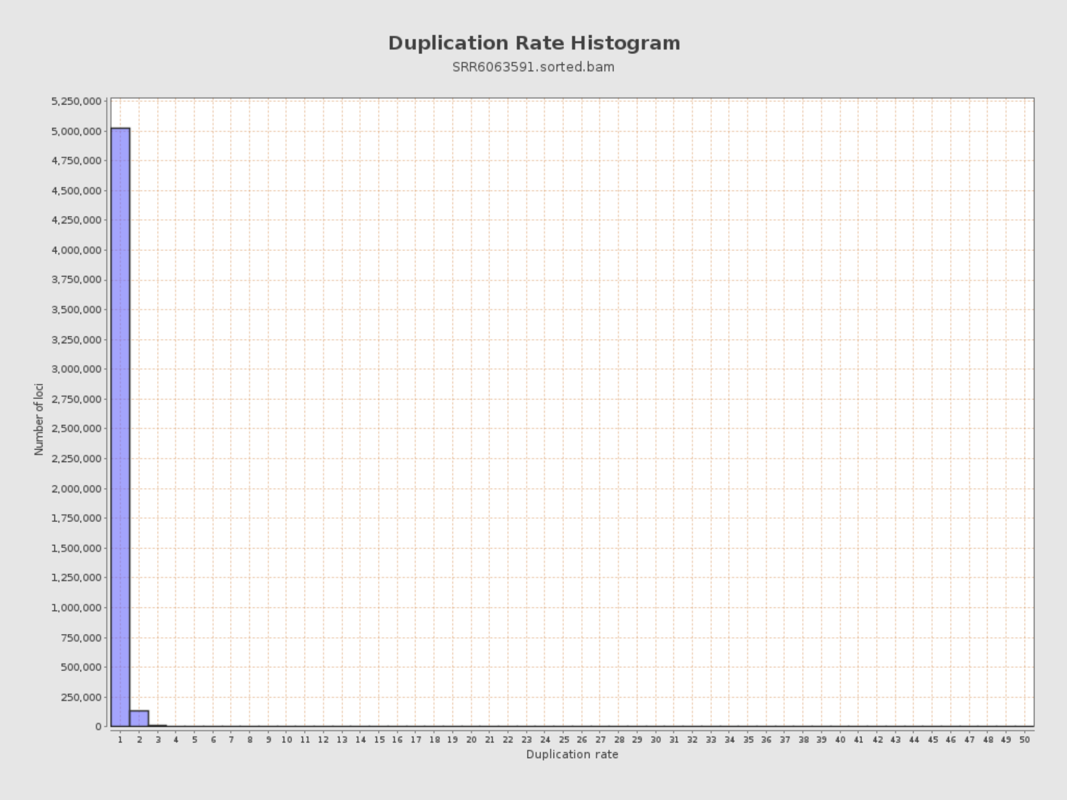
5. Results : Coverage Histogram (0-50X)



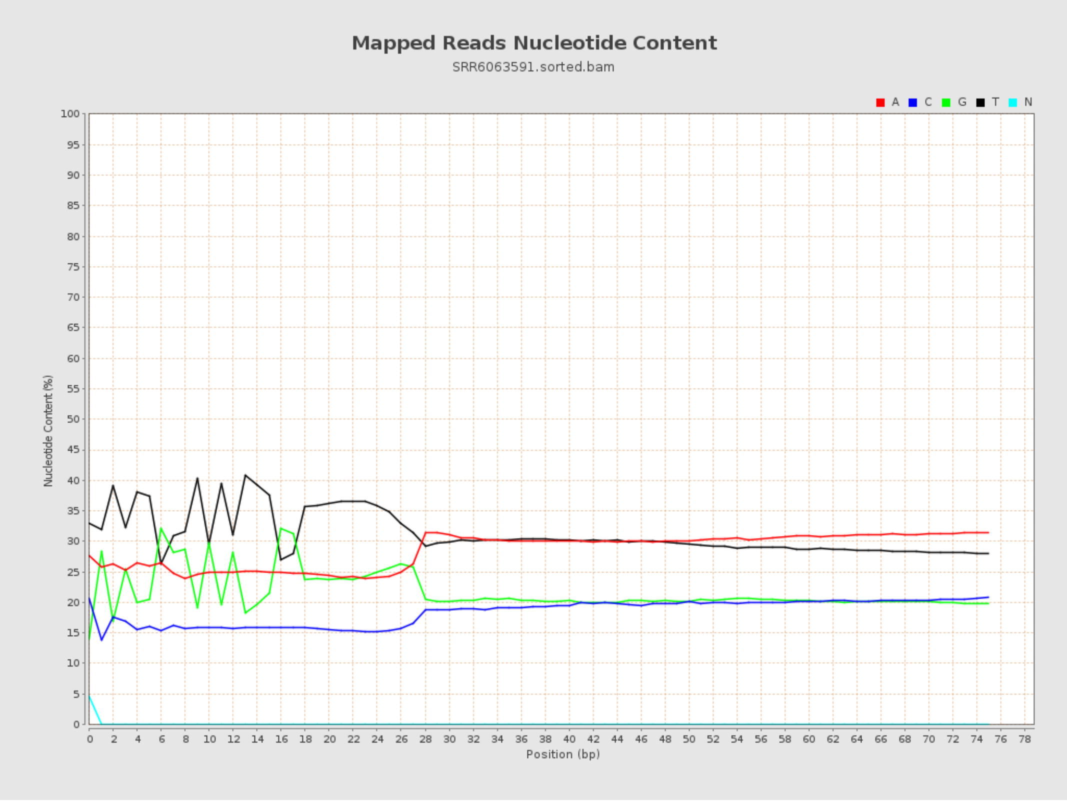
6. Results : Genome Fraction Coverage



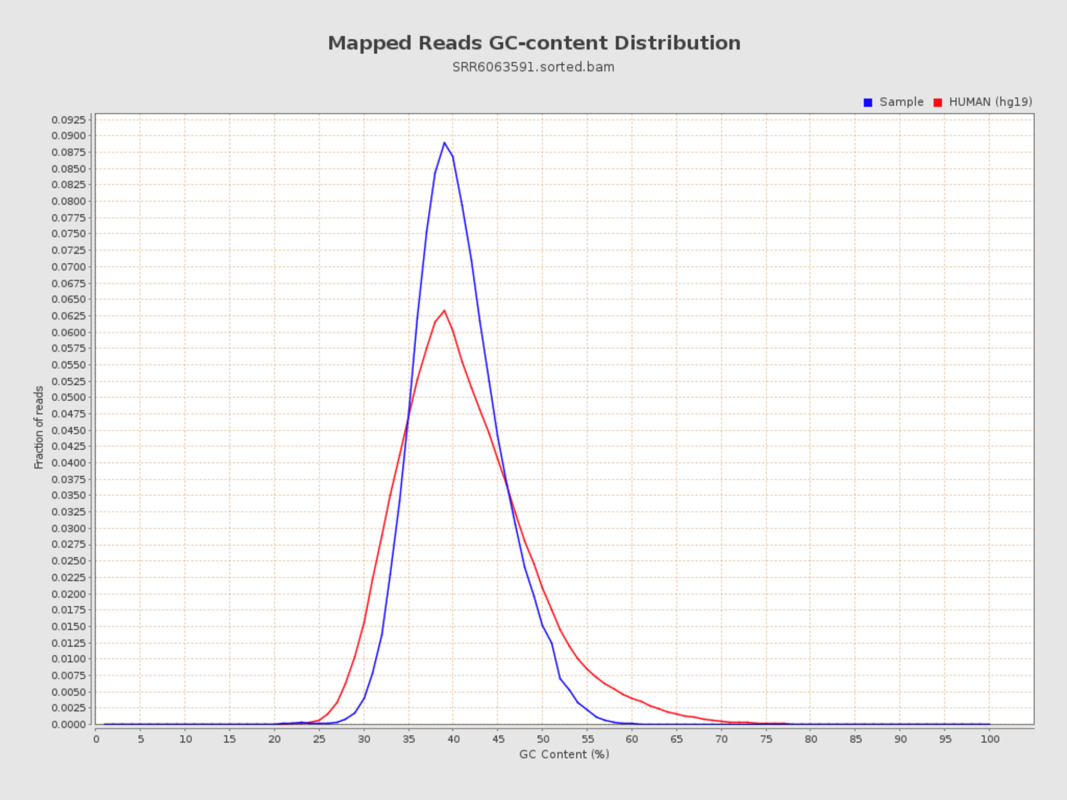
7. Results : Duplication Rate Histogram



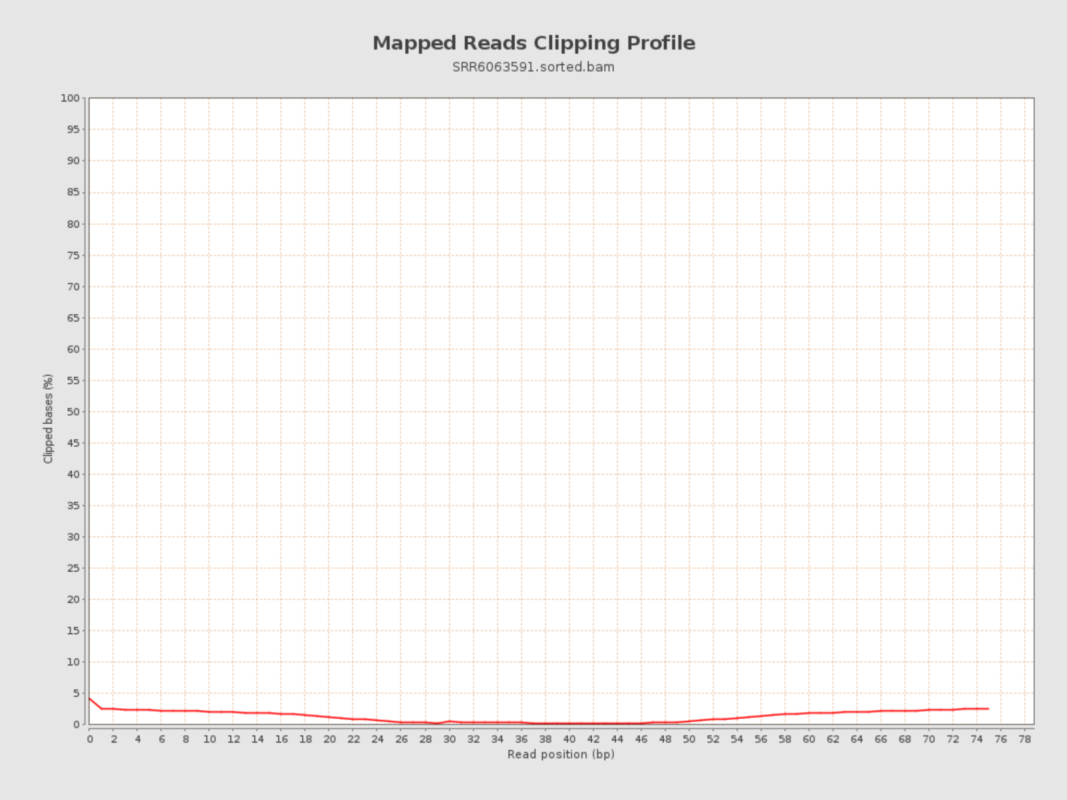
8. Results : Mapped Reads Nucleotide Content



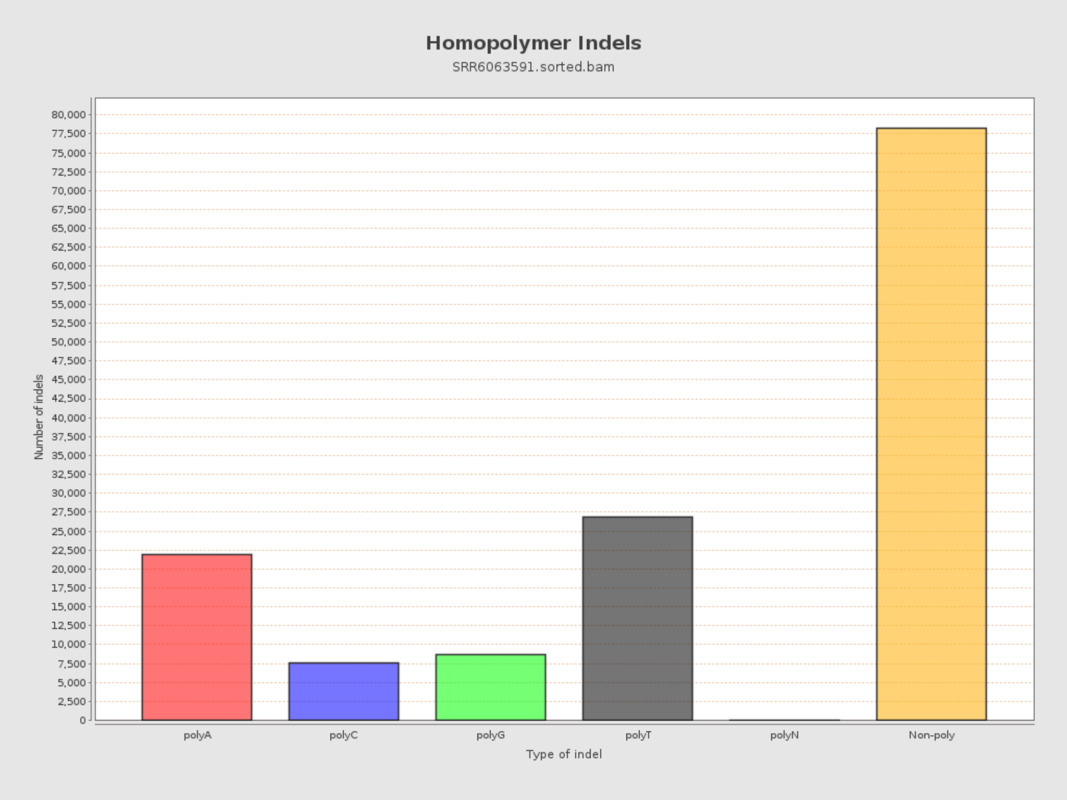
9. Results : Mapped Reads GC-content Distribution



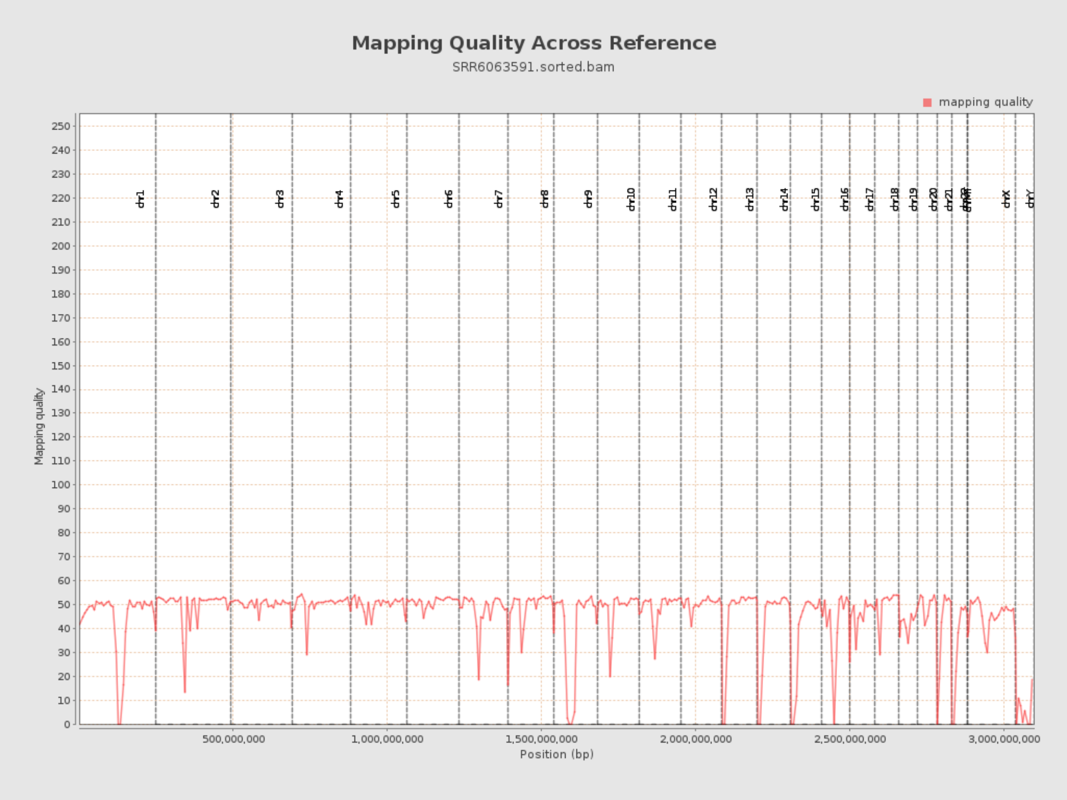
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram