Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 03:22:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063576.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_SRR6063576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063576.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 03:22:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,275,471
Mapped reads	3,039,824 / 92.81%
Unmapped reads	235,647 / 7.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,952 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	174,710 / 5.33%
Duplication rate	4.41%
Clipped reads	1,257,837 / 38.4%

2.2. ACGT Content

Number/percentage of A's	57,301,760 / 28.08%
Number/percentage of C's	37,946,036 / 18.6%
Number/percentage of T's	64,211,552 / 31.47%
Number/percentage of G's	44,568,775 / 21.84%
Number/percentage of N's	5,649 / 0%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0659

Standard Deviation	0.5859

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

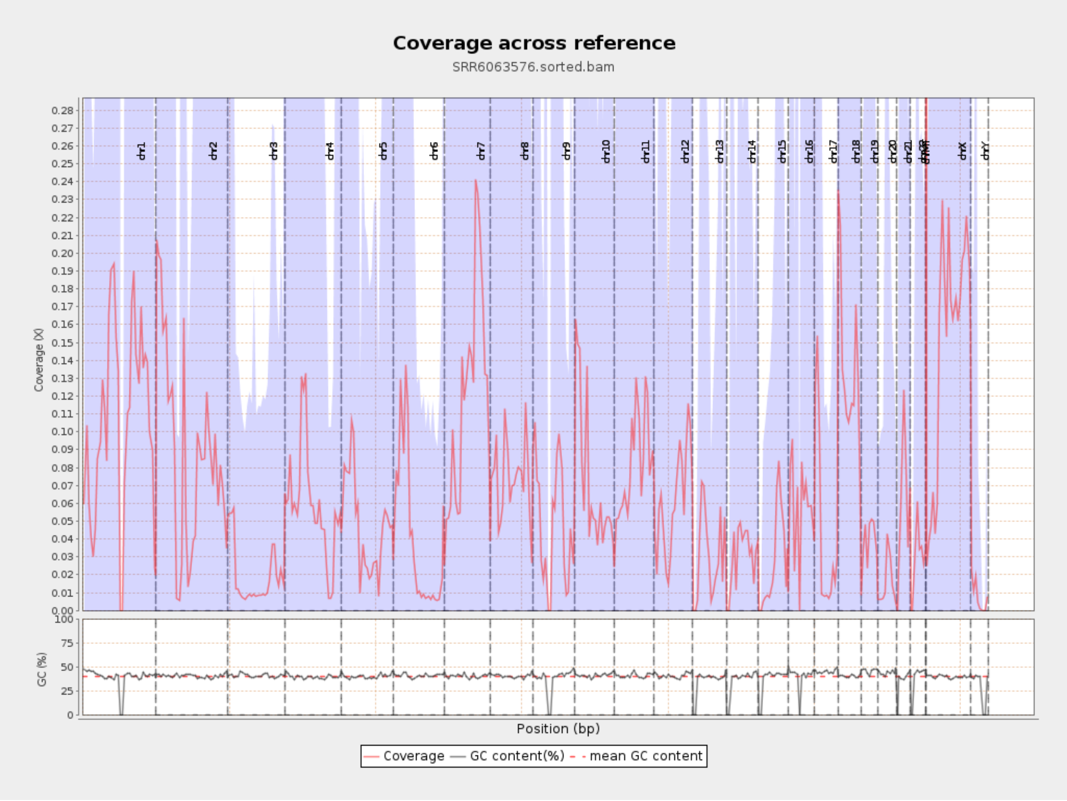
General error rate	0.73%
Mismatches	1,455,240
Insertions	13,893
Mapped reads with at least one insertion	0.45%
Deletions	47,768
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.12%

2.6. Chromosome stats

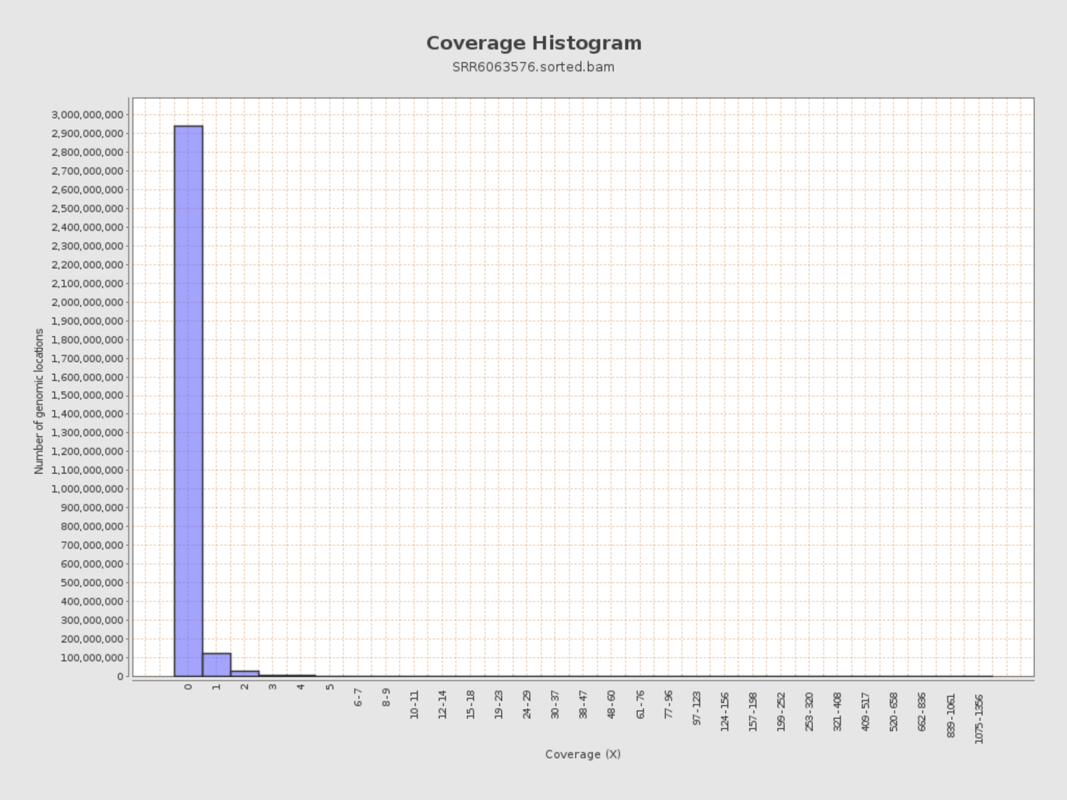
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26477714	0.1062	0.8624
chr2	243199373	21917572	0.0901	0.8843
chr3	198022430	3834141	0.0194	0.2387
chr4	191154276	11355778	0.0594	0.3188
chr5	180915260	8533459	0.0472	0.2684
chr6	171115067	6897682	0.0403	0.2655
chr7	159138663	19078218	0.1199	1.0266

chr8	146364022	10738026	0.0734	0.5781
chr9	141213431	6538343	0.0463	0.5668
chr10	135534747	9862392	0.0728	0.8705
chr11	135006516	11012624	0.0816	0.4768
chr12	133851895	8103454	0.0605	0.3246
chr13	115169878	3517767	0.0305	0.2141
chr14	107349540	3281190	0.0306	0.2849
chr15	102531392	2760528	0.0269	0.204
chr16	90354753	5083515	0.0563	0.3577
chr17	81195210	3642268	0.0449	0.3499
chr18	78077248	10635672	0.1362	0.9421
chr19	59128983	2272216	0.0384	0.7471
chr20	63025520	965828	0.0153	0.1868
chr21	48129895	2814874	0.0585	0.3259
chr22	51304566	1471130	0.0287	0.207
chrMT	16571	80055	4.831	3.9978
chrX	155270560	22793936	0.1468	0.6415
chrY	59373566	448527	0.0076	0.1694

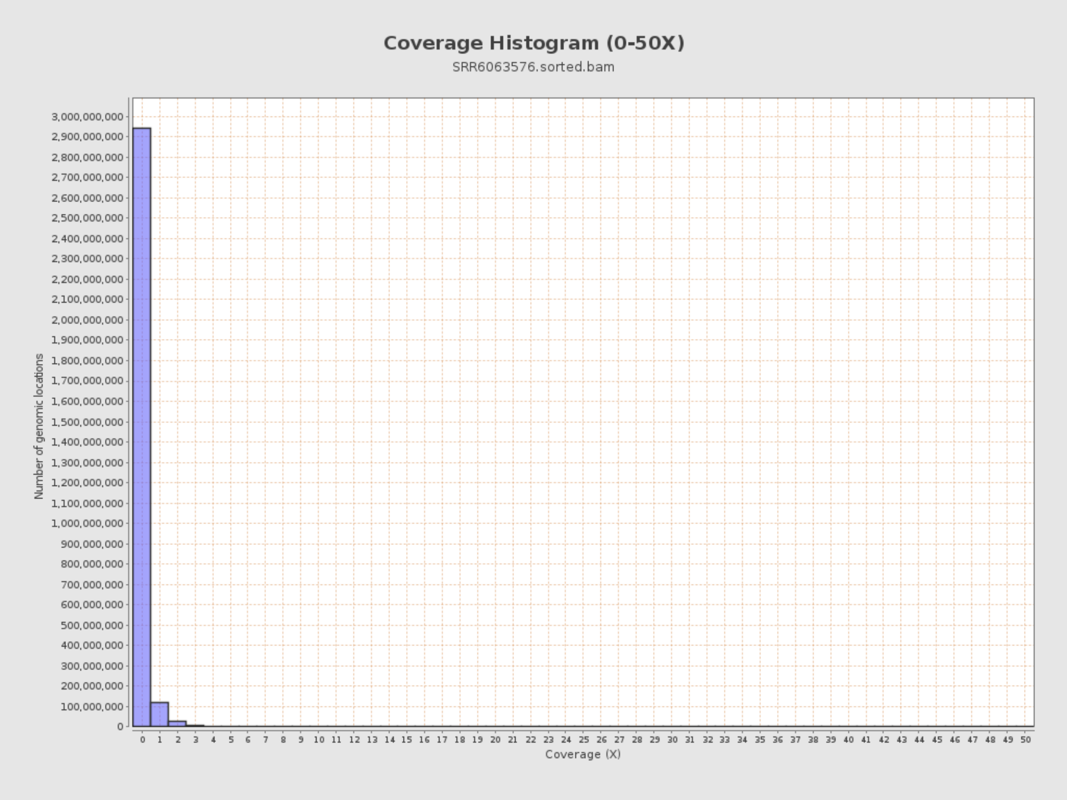
3. Results : Coverage across reference



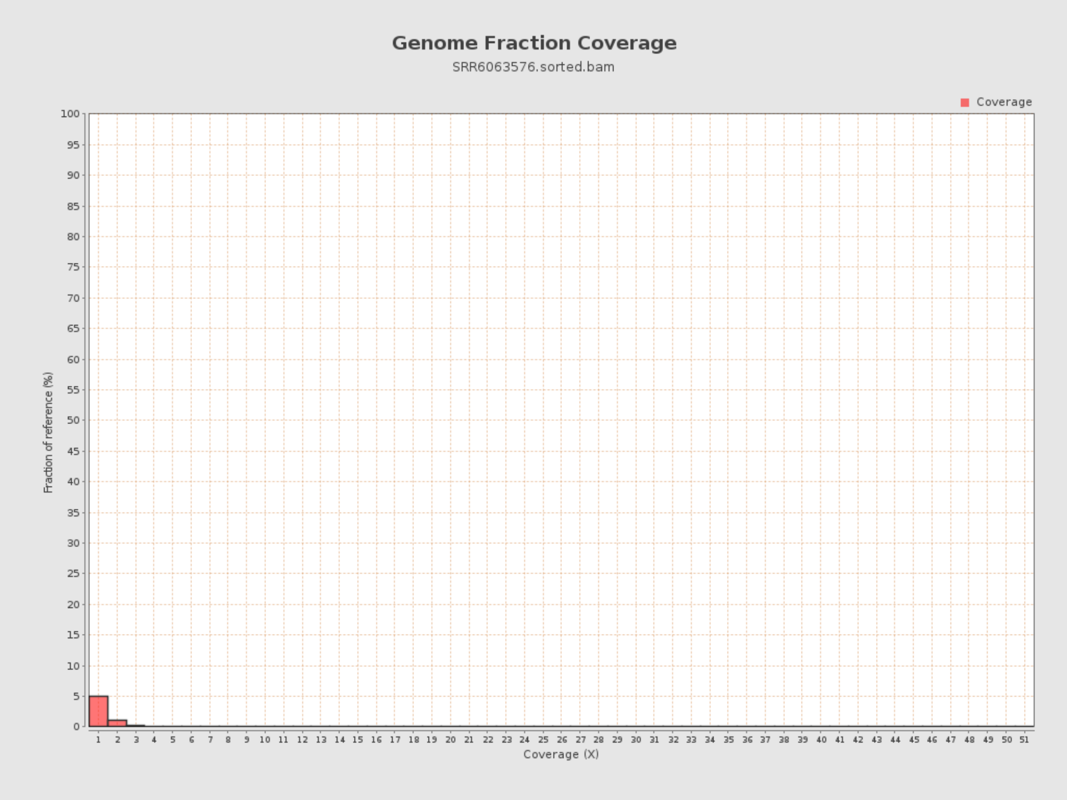
4. Results : Coverage Histogram



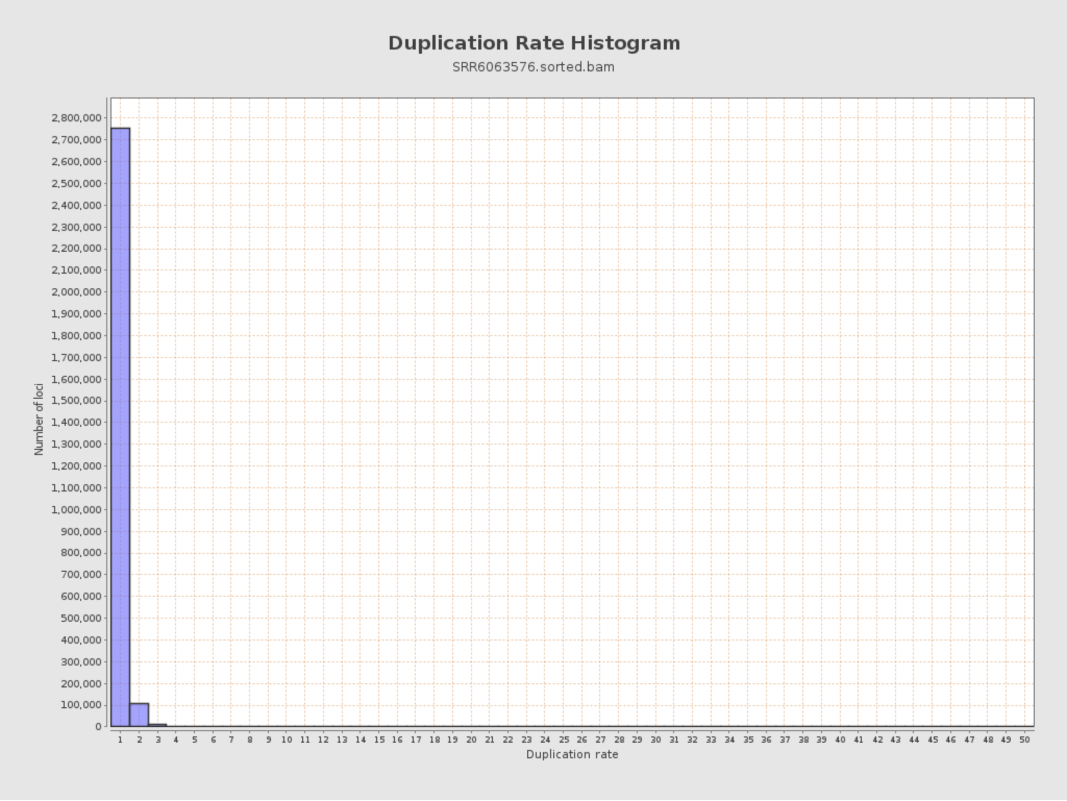
5. Results : Coverage Histogram (0-50X)



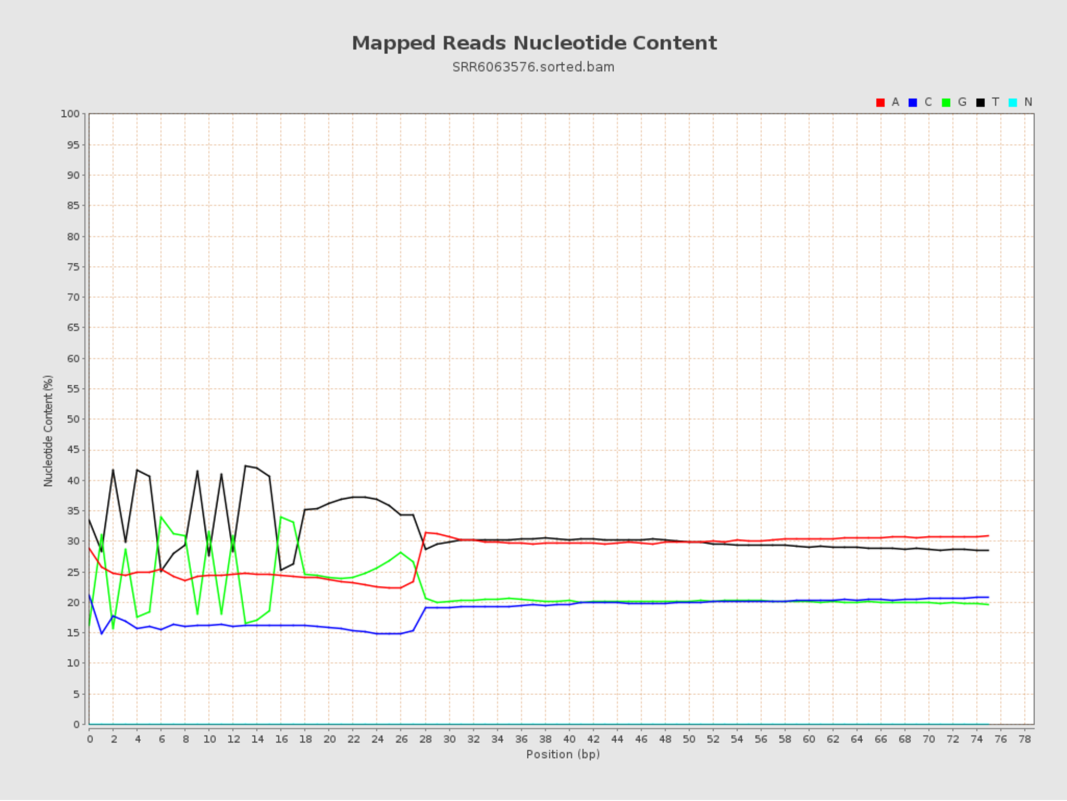
6. Results : Genome Fraction Coverage



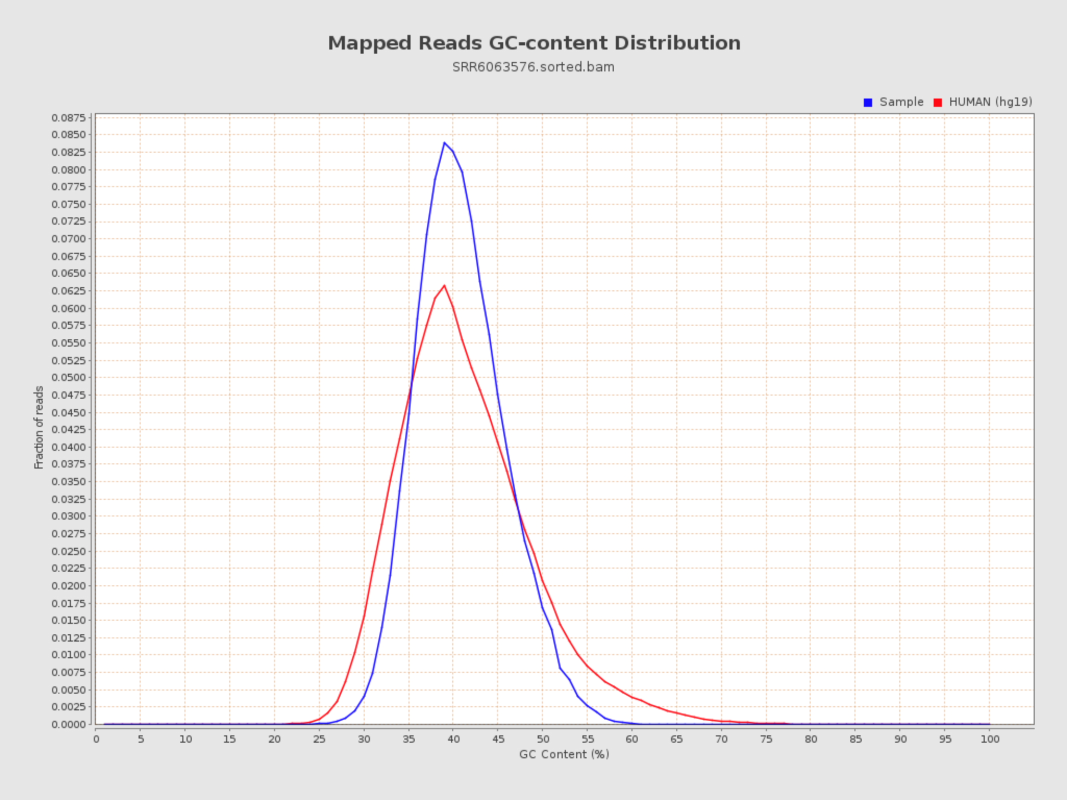
7. Results : Duplication Rate Histogram



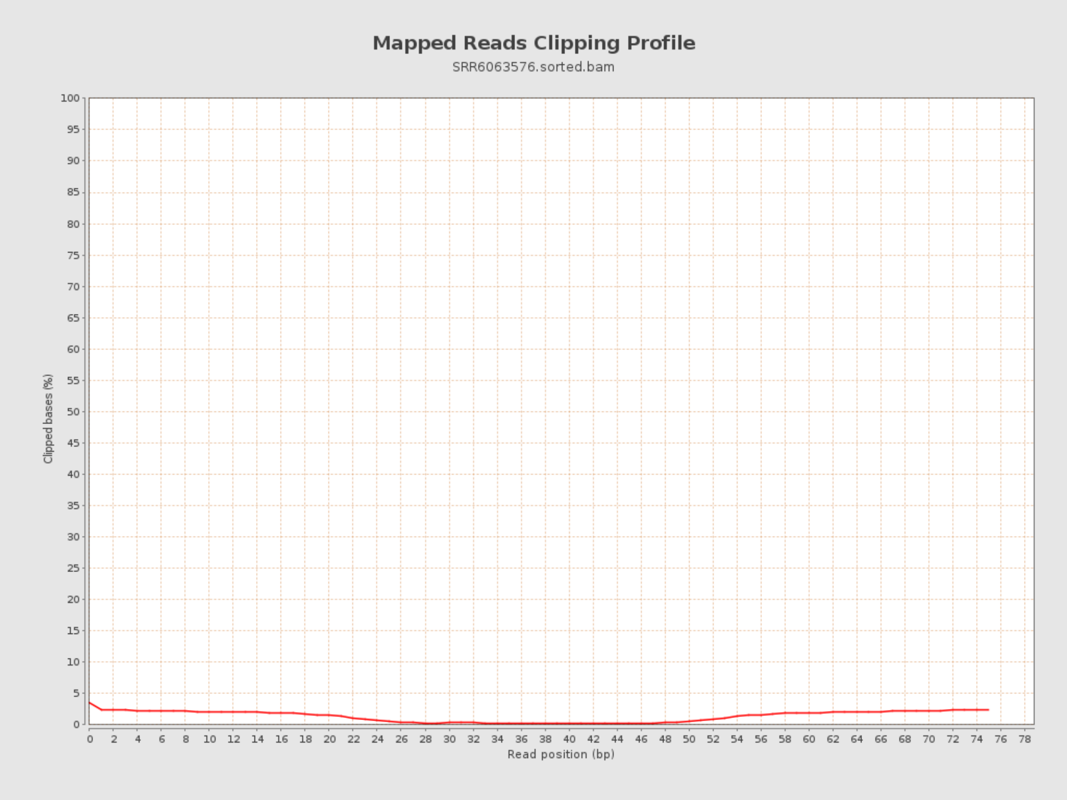
8. Results : Mapped Reads Nucleotide Content



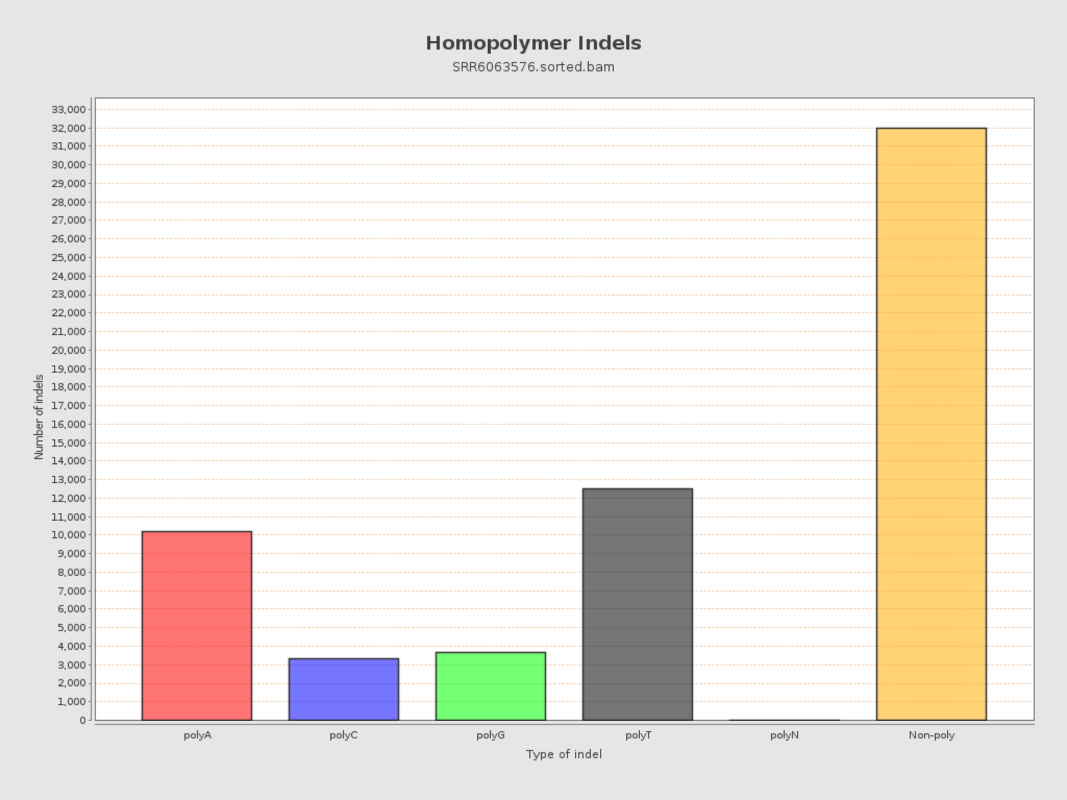
9. Results : Mapped Reads GC-content Distribution



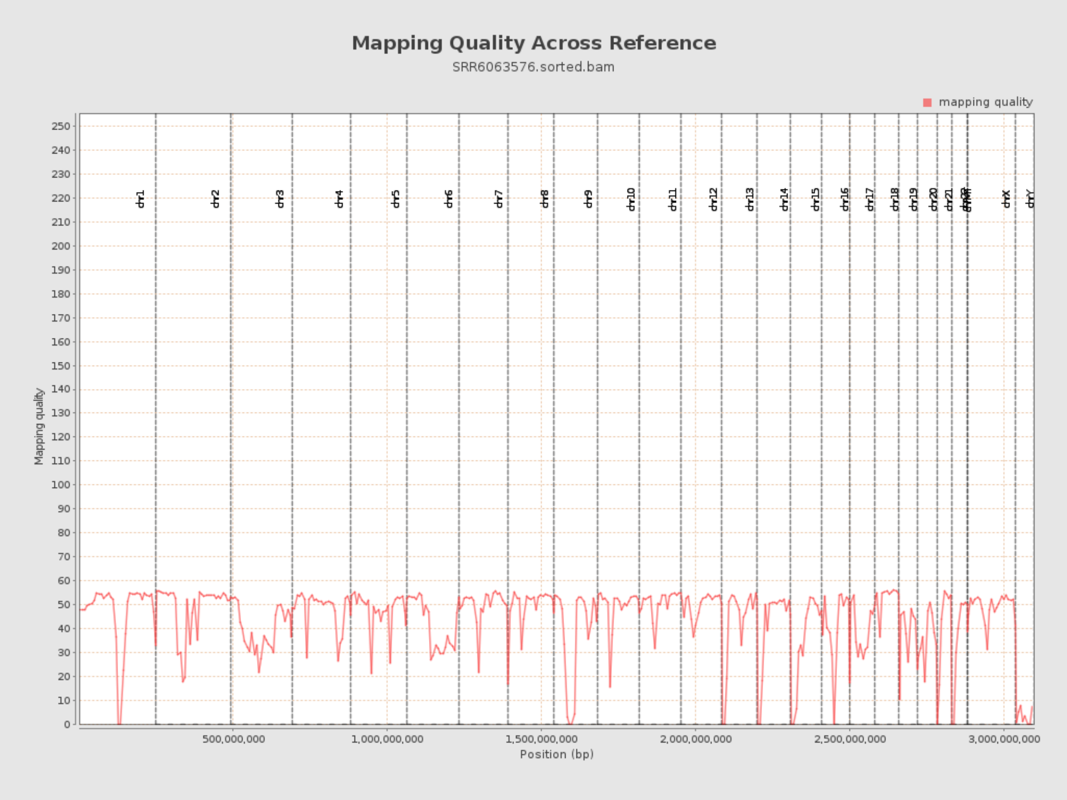
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram