Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:53:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063534.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_SRR6063534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063534.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:53:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,366,641
Mapped reads	2,096,338 / 88.58%
Unmapped reads	270,303 / 11.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,825 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	139,454 / 5.89%
Duplication rate	5.36%
Clipped reads	1,065,983 / 45.04%

2.2. ACGT Content

Number/percentage of A's	37,766,061 / 27.6%
Number/percentage of C's	24,904,742 / 18.2%
Number/percentage of T's	43,731,531 / 31.97%
Number/percentage of G's	30,405,328 / 22.22%
Number/percentage of N's	2,841 / 0%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0442

Standard Deviation	0.4395

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

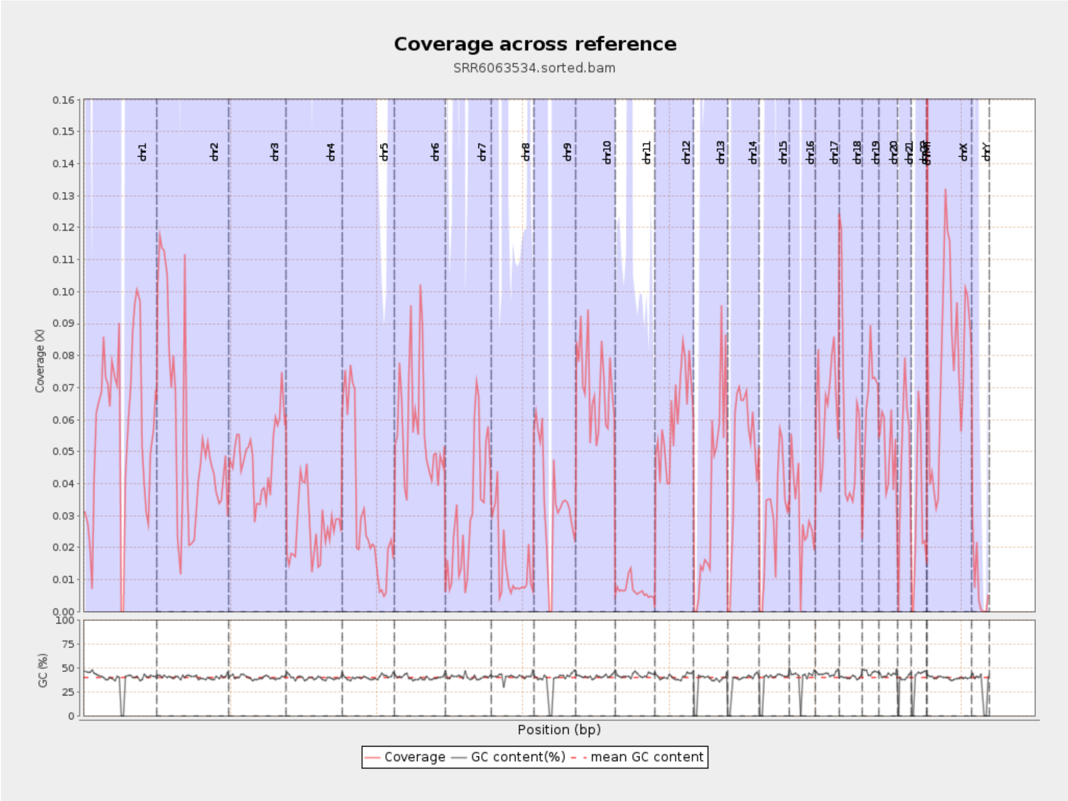
General error rate	0.81%
Mismatches	1,095,049
Insertions	10,636
Mapped reads with at least one insertion	0.5%
Deletions	40,252
Mapped reads with at least one deletion	1.9%
Homopolymer indels	46.06%

2.6. Chromosome stats

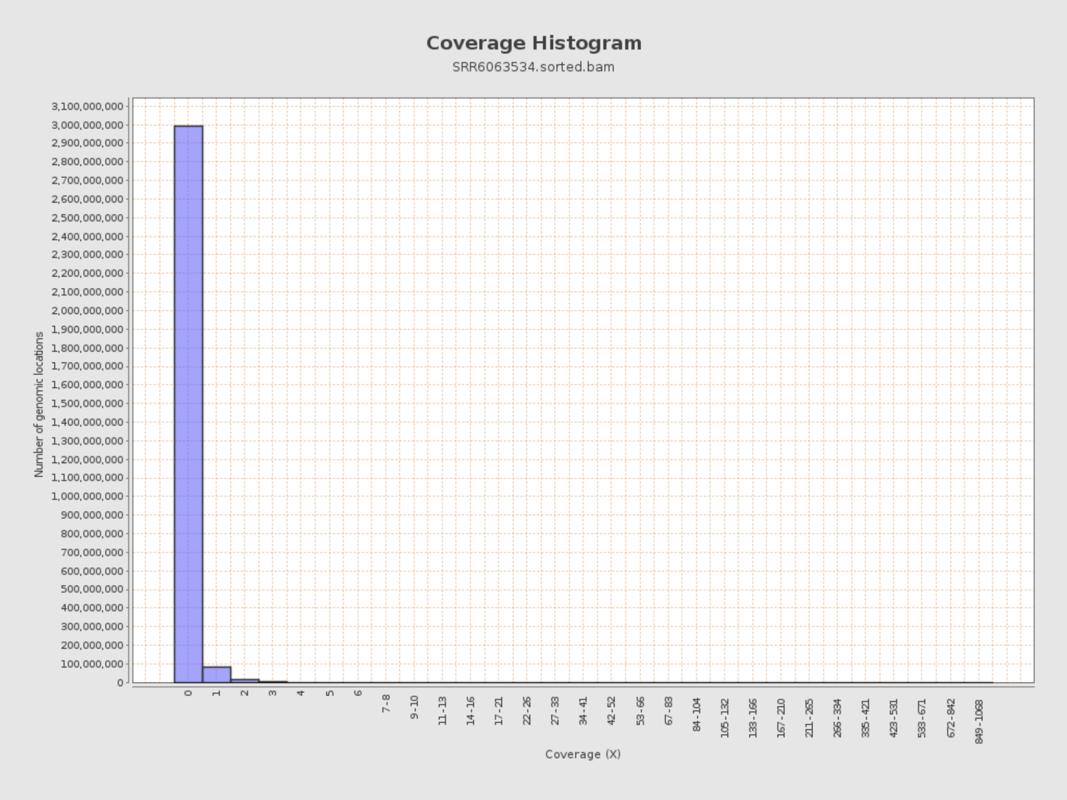
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14122383	0.0567	0.9001
chr2	243199373	13546094	0.0557	0.5914
chr3	198022430	9508508	0.048	0.2744
chr4	191154276	4966827	0.026	0.2178
chr5	180915260	5707648	0.0315	0.2254
chr6	171115067	9943969	0.0581	0.3583
chr7	159138663	4963349	0.0312	0.2534

chr8	146364022	2023536	0.0138	0.6435
chr9	141213431	4861867	0.0344	0.3676
chr10	135534747	9533191	0.0703	0.4317
chr11	135006516	904800	0.0067	0.1506
chr12	133851895	8174993	0.0611	0.3145
chr13	115169878	4225048	0.0367	0.2455
chr14	107349540	5423326	0.0505	0.2961
chr15	102531392	3008730	0.0293	0.2193
chr16	90354753	2685458	0.0297	0.2327
chr17	81195210	5350296	0.0659	0.3293
chr18	78077248	4521839	0.0579	0.5561
chr19	59128983	3918756	0.0663	0.6025
chr20	63025520	3167128	0.0503	0.2835
chr21	48129895	2267451	0.0471	0.2833
chr22	51304566	1496881	0.0292	0.2117
chrMT	16571	42773	2.5812	2.3845
chrX	155270560	12065949	0.0777	0.4301
chrY	59373566	446352	0.0075	0.2081

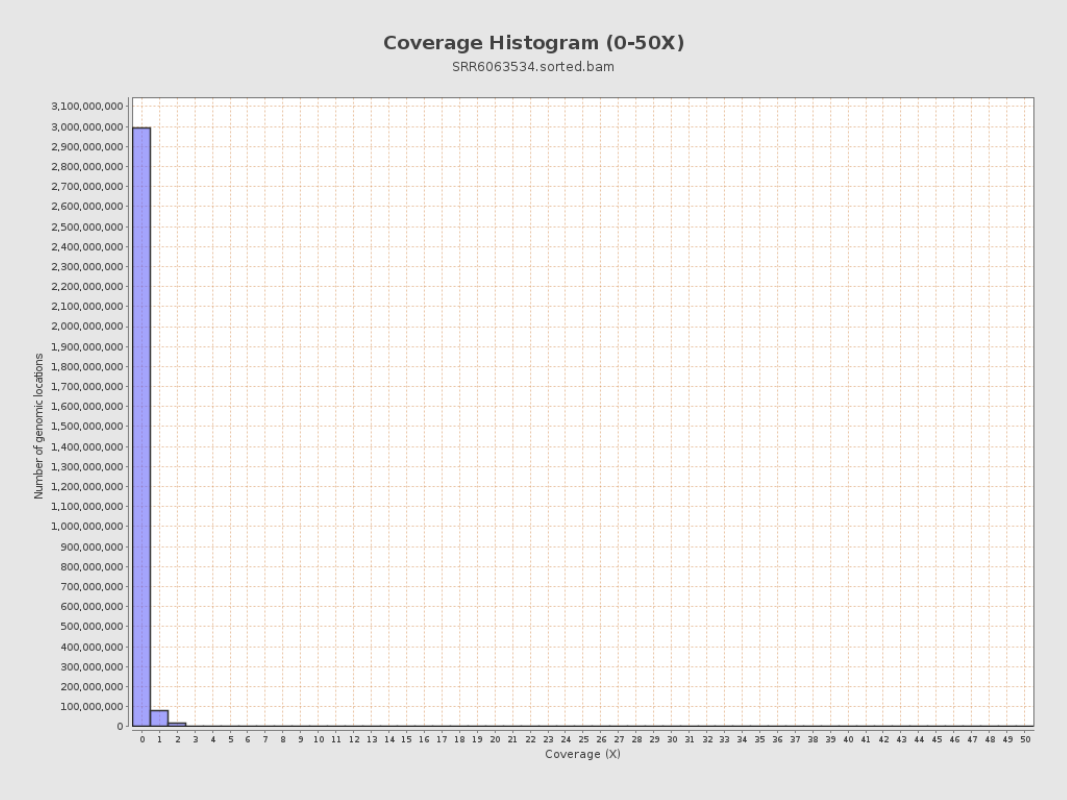
3. Results : Coverage across reference



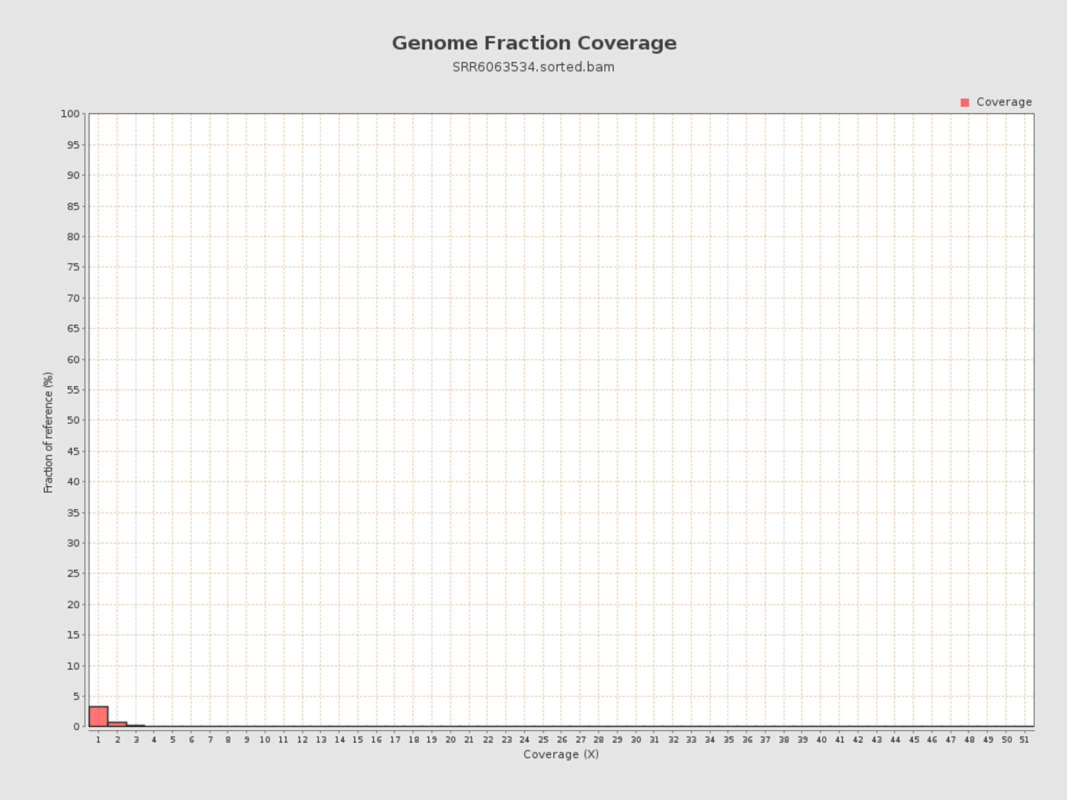
4. Results : Coverage Histogram



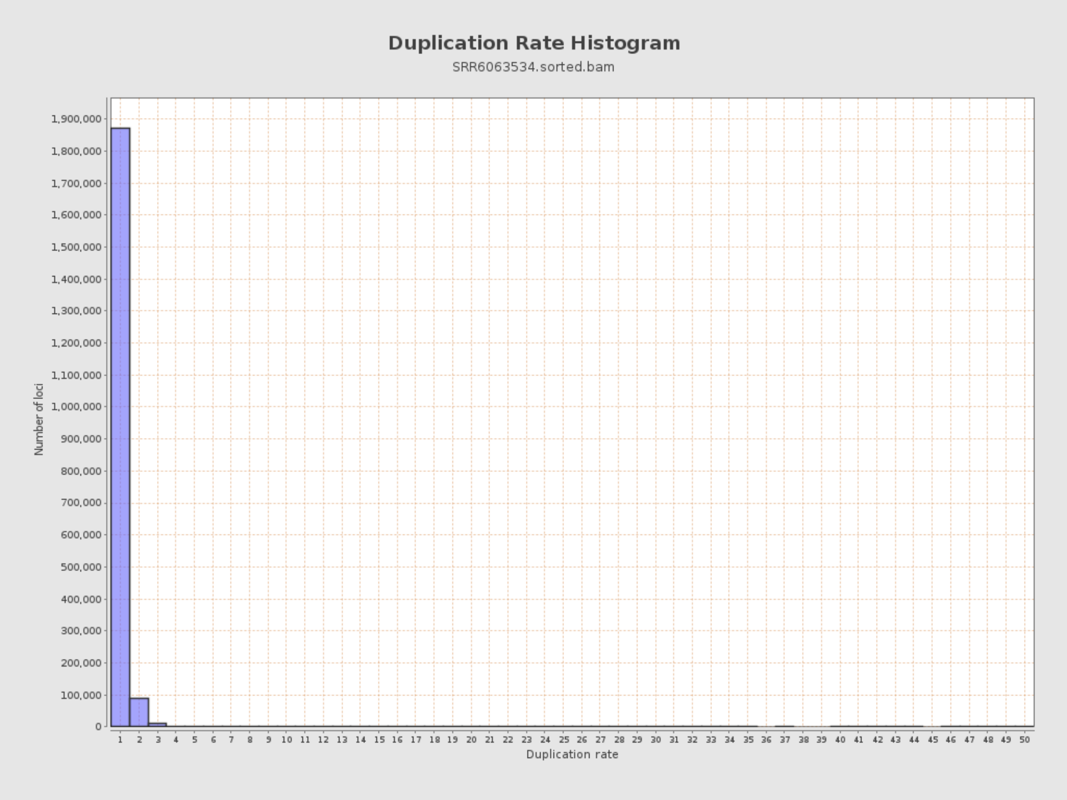
5. Results : Coverage Histogram (0-50X)



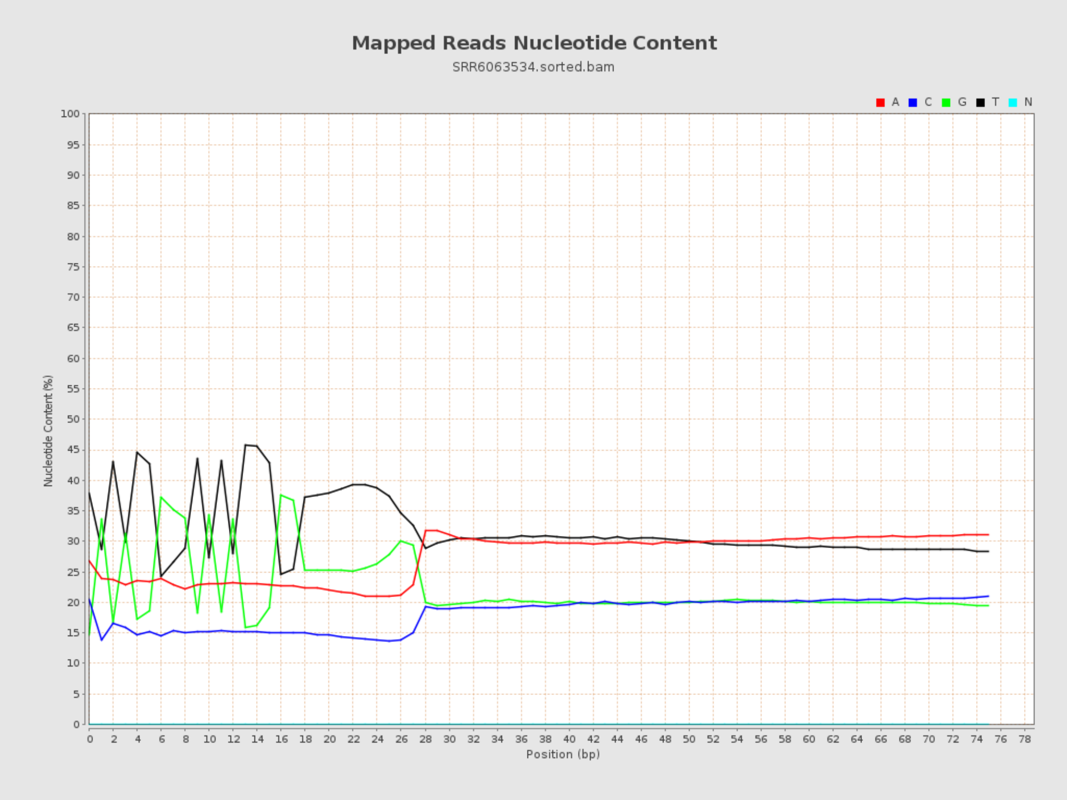
6. Results : Genome Fraction Coverage



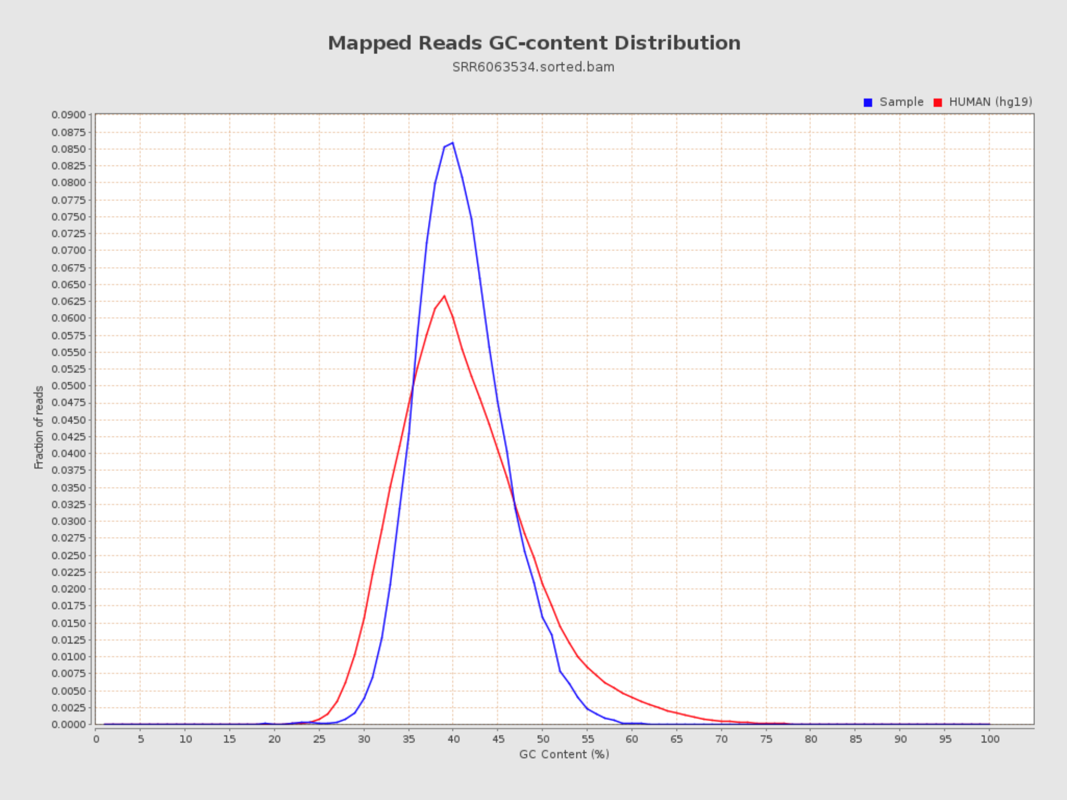
7. Results : Duplication Rate Histogram



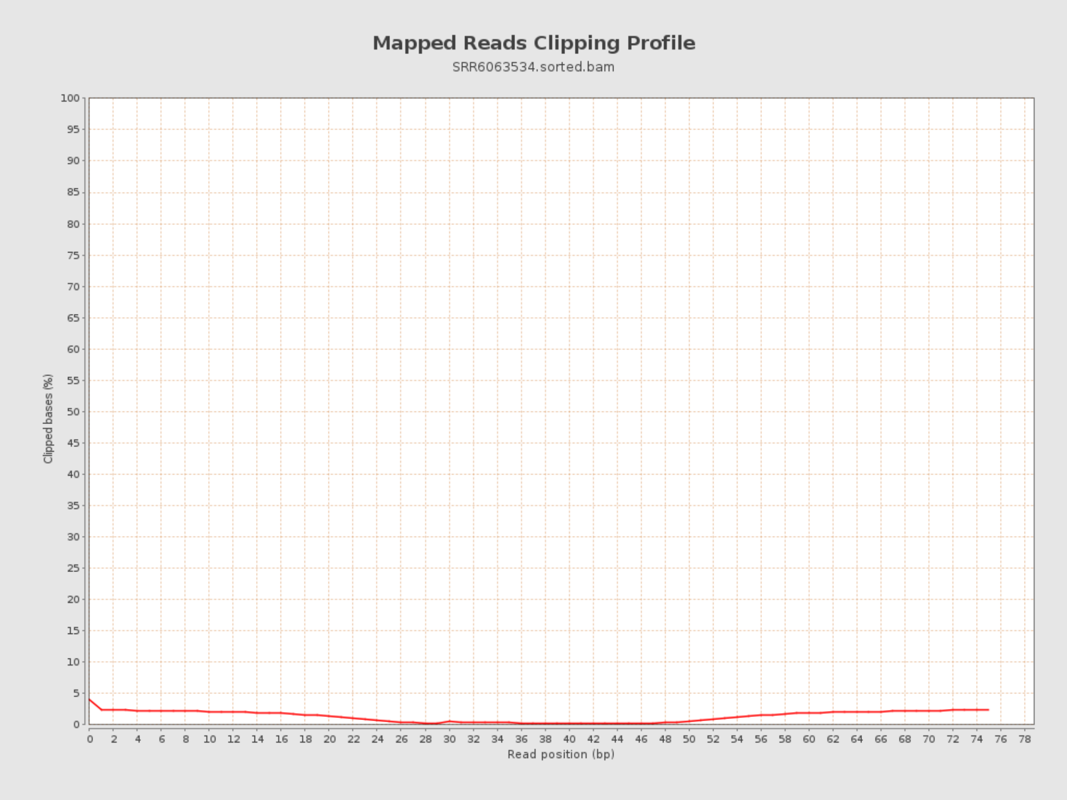
8. Results : Mapped Reads Nucleotide Content



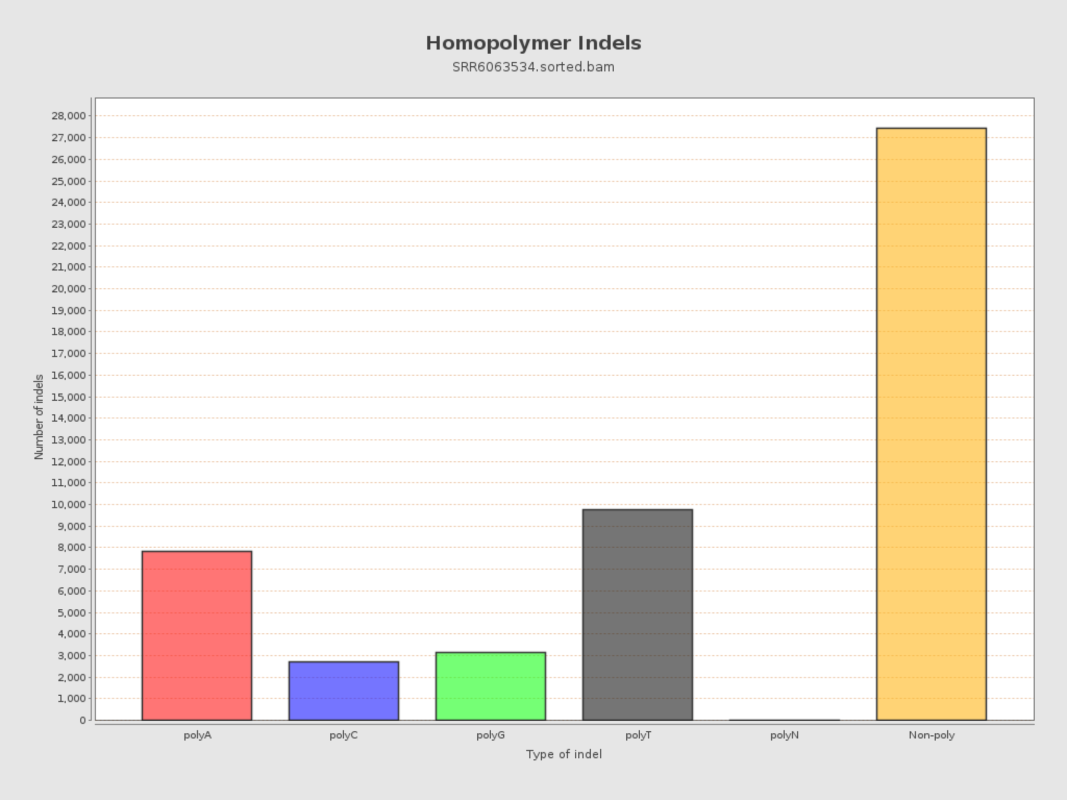
9. Results : Mapped Reads GC-content Distribution



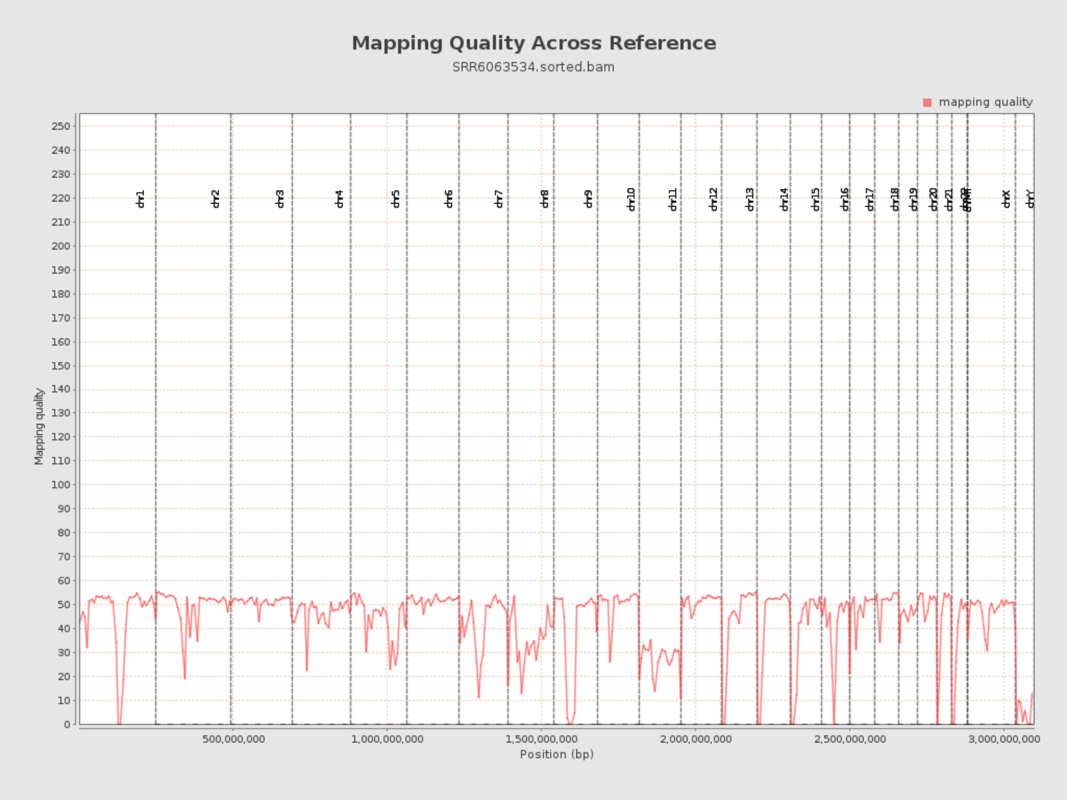
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram