Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:42:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008659.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_SRR6008659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:42:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,211,833
Mapped reads	1,989,907 / 89.97%
Unmapped reads	221,926 / 10.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,098 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	93,635 / 4.23%
Duplication rate	4.01%
Clipped reads	1,136,210 / 51.37%

2.2. ACGT Content

Number/percentage of A's	32,815,730 / 25.95%
Number/percentage of C's	23,363,617 / 18.48%
Number/percentage of T's	39,629,970 / 31.34%
Number/percentage of G's	30,587,408 / 24.19%
Number/percentage of N's	58,531 / 0.05%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.2862

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

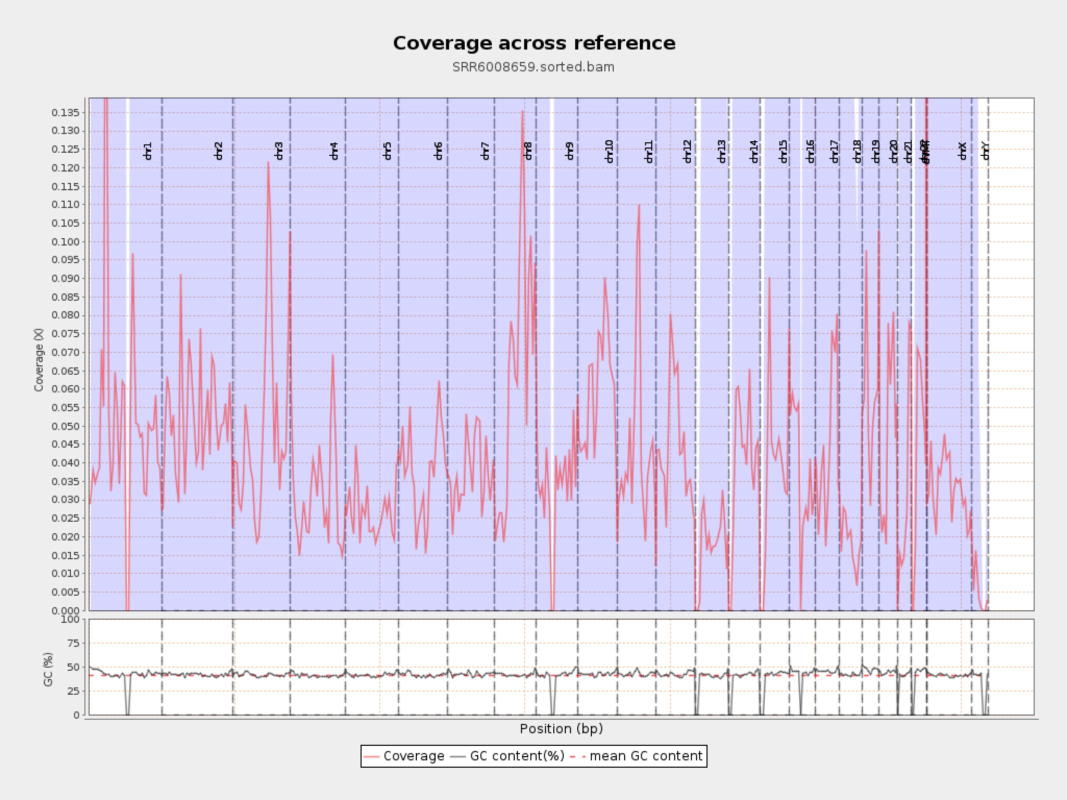
General error rate	0.78%
Mismatches	964,942
Insertions	8,503
Mapped reads with at least one insertion	0.42%
Deletions	36,409
Mapped reads with at least one deletion	1.81%
Homopolymer indels	45.27%

2.6. Chromosome stats

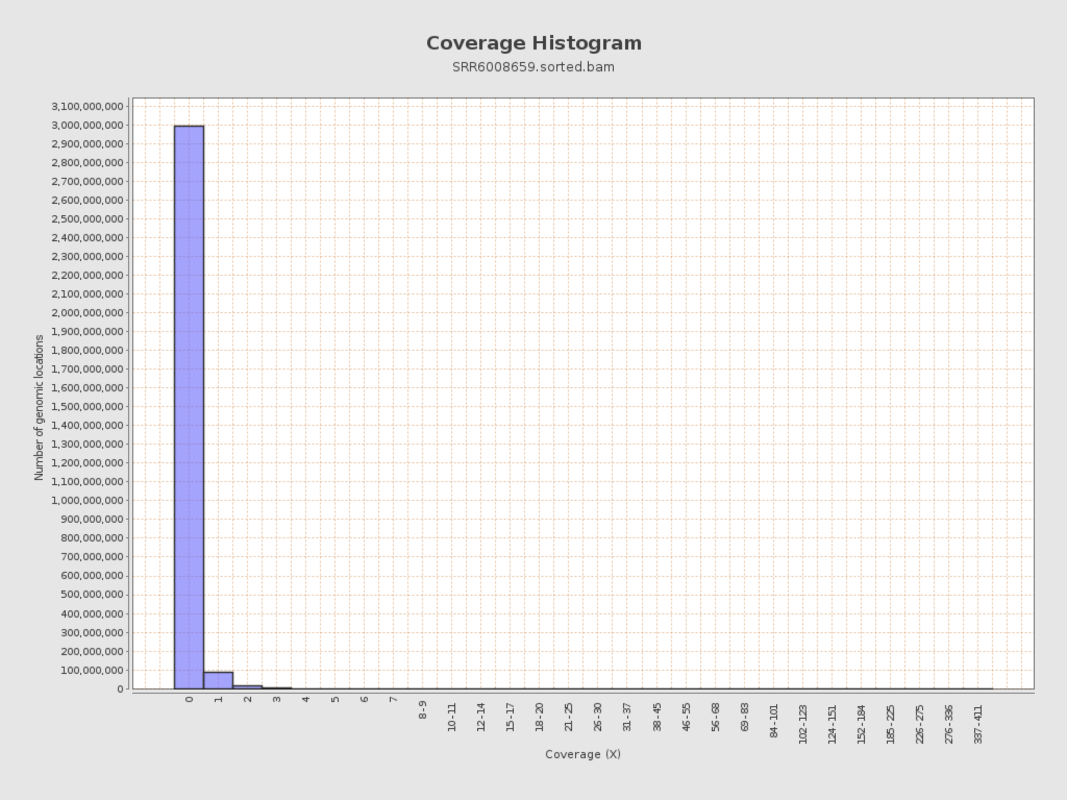
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12555117	0.0504	0.4082
chr2	243199373	12811882	0.0527	0.3325
chr3	198022430	9655577	0.0488	0.2586
chr4	191154276	5871666	0.0307	0.2147
chr5	180915260	4878350	0.027	0.1912
chr6	171115067	6543936	0.0382	0.2492
chr7	159138663	5940889	0.0373	0.327

chr8	146364022	9453486	0.0646	0.3257
chr9	141213431	4564352	0.0323	0.2746
chr10	135534747	8092140	0.0597	0.3329
chr11	135006516	5952867	0.0441	0.3078
chr12	133851895	6071062	0.0454	0.251
chr13	115169878	2013897	0.0175	0.1513
chr14	107349540	4286854	0.0399	0.2393
chr15	102531392	3848161	0.0375	0.24
chr16	90354753	3348370	0.0371	0.2646
chr17	81195210	3696069	0.0455	0.2715
chr18	78077248	1441109	0.0185	0.4001
chr19	59128983	3438851	0.0582	0.355
chr20	63025520	2919005	0.0463	0.2562
chr21	48129895	1509626	0.0314	0.2193
chr22	51304566	2101320	0.041	0.2372
chrMT	16571	37723	2.2764	2.2666
chrX	155270560	5190303	0.0334	0.2274
chrY	59373566	295688	0.005	0.1516

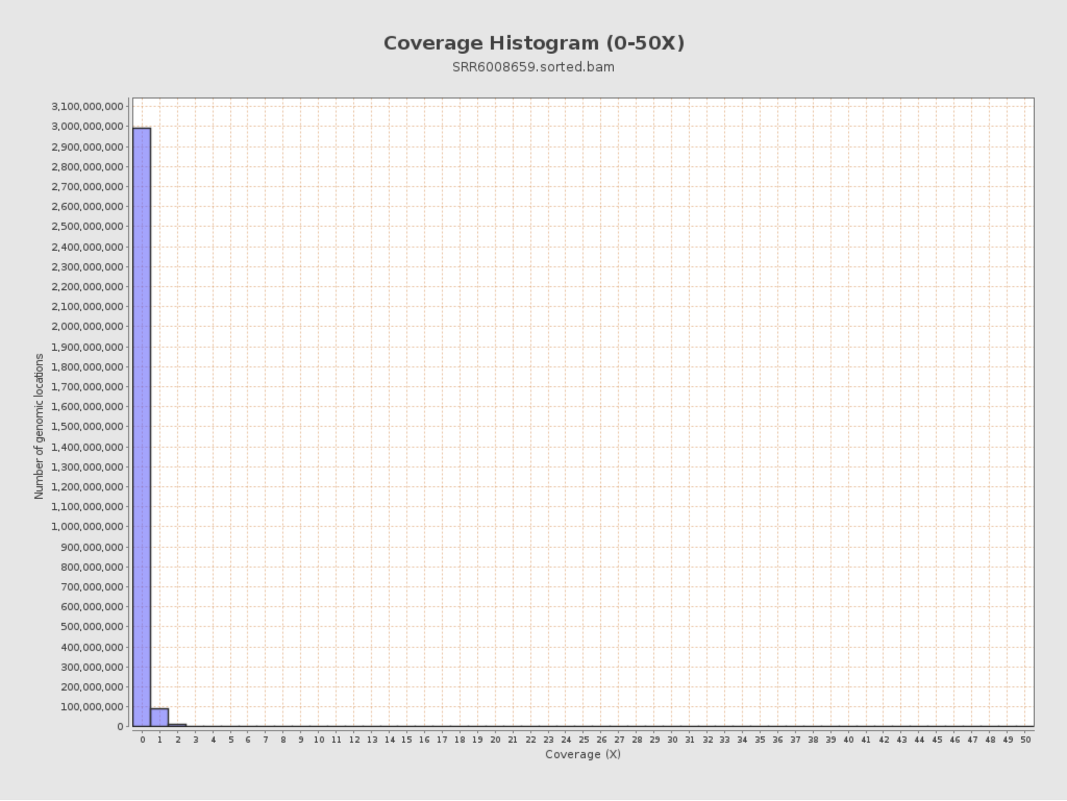
3. Results : Coverage across reference



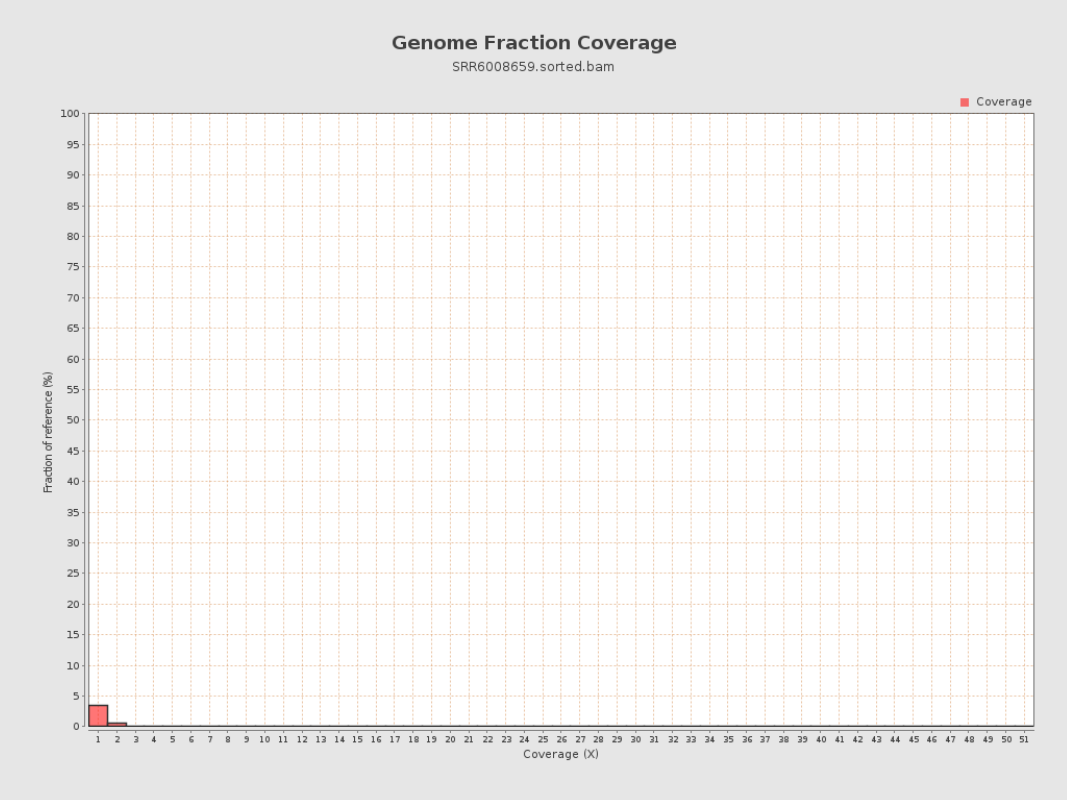
4. Results : Coverage Histogram



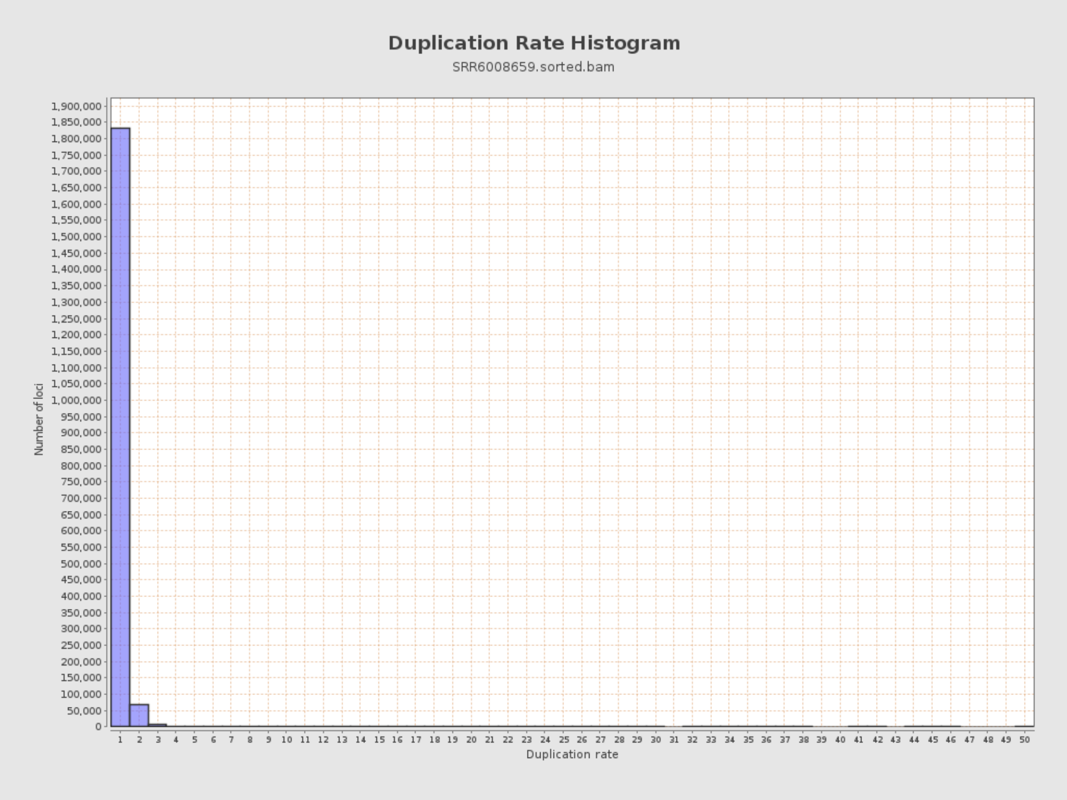
5. Results : Coverage Histogram (0-50X)



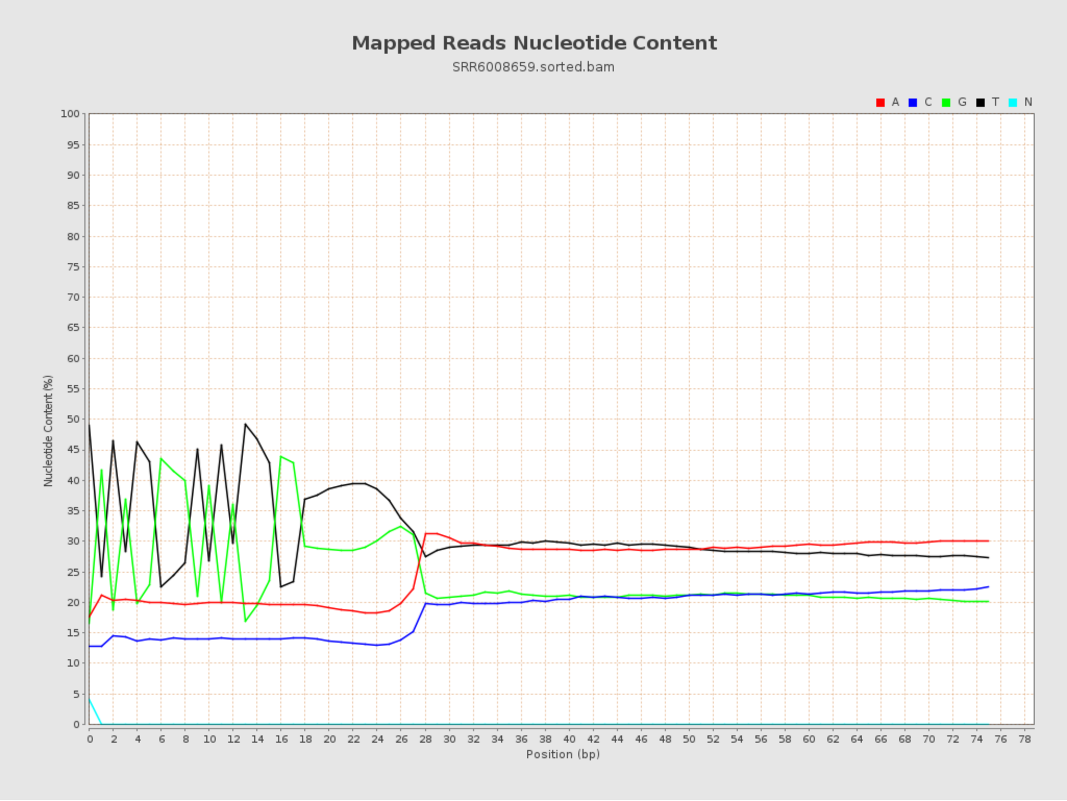
6. Results : Genome Fraction Coverage



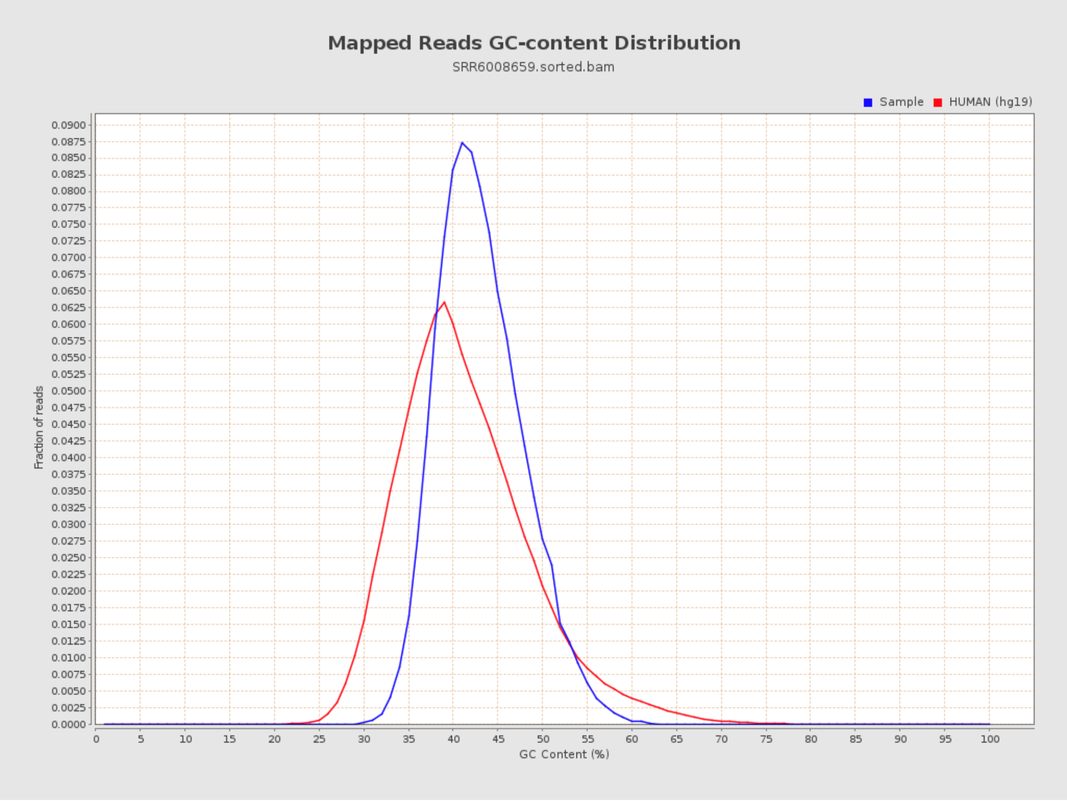
7. Results : Duplication Rate Histogram



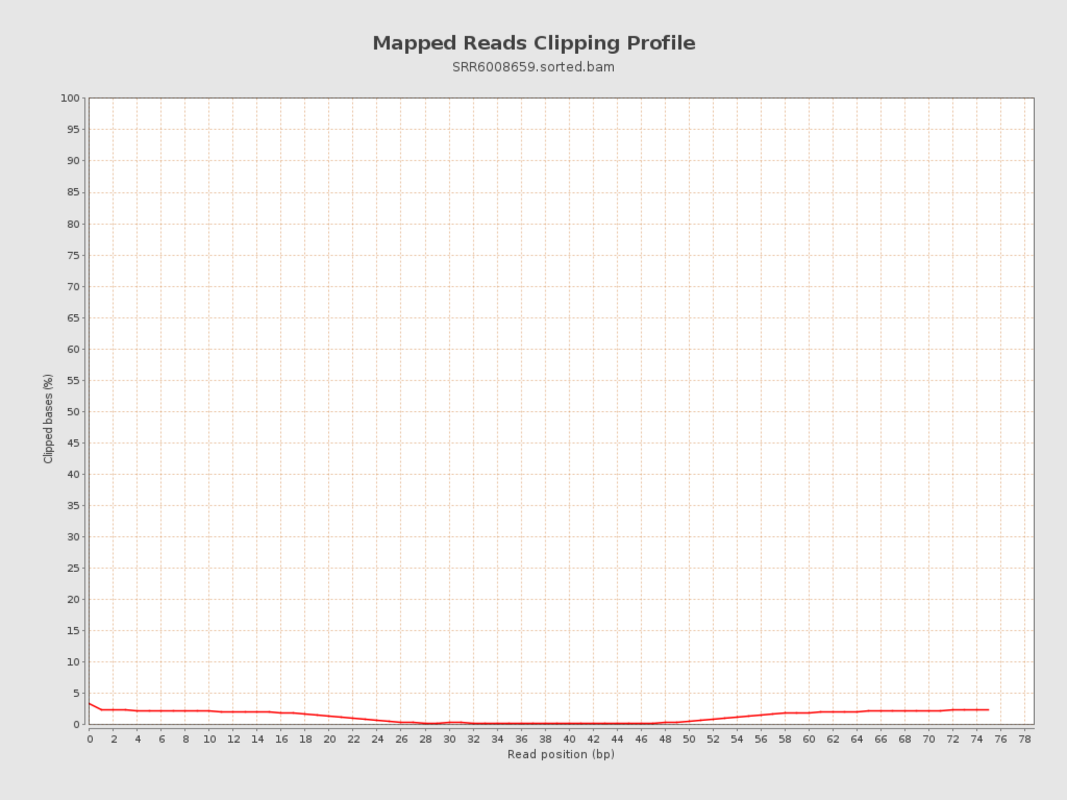
8. Results : Mapped Reads Nucleotide Content



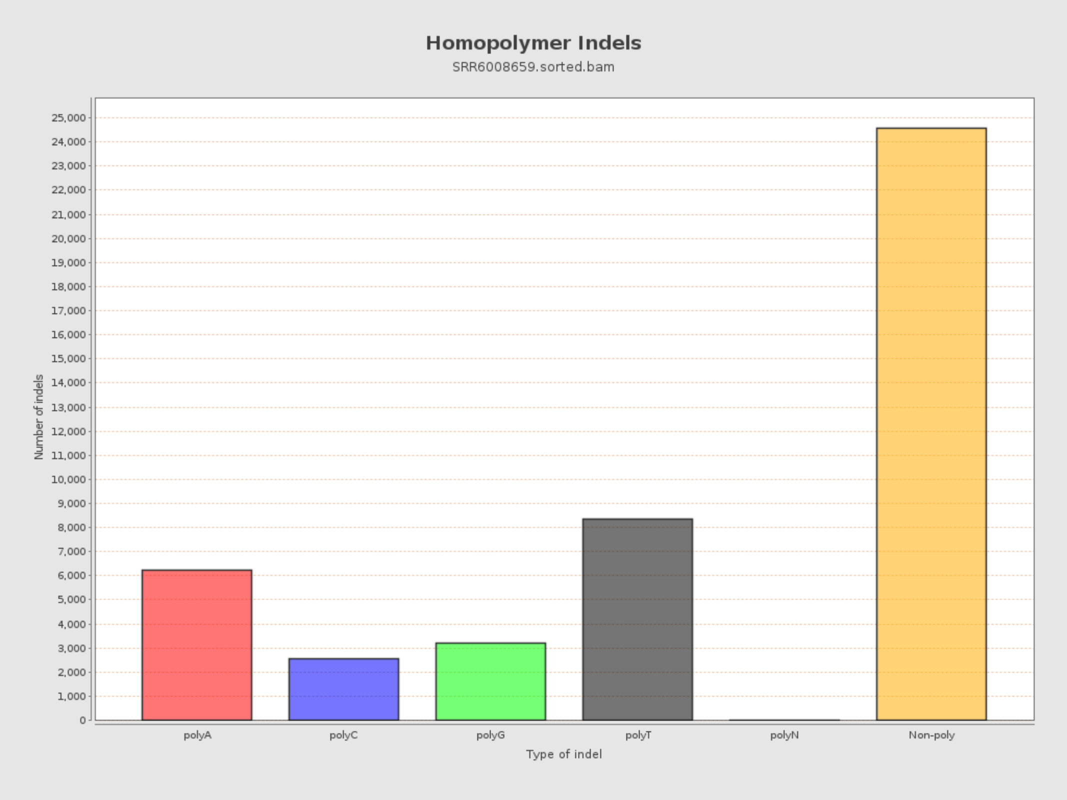
9. Results : Mapped Reads GC-content Distribution



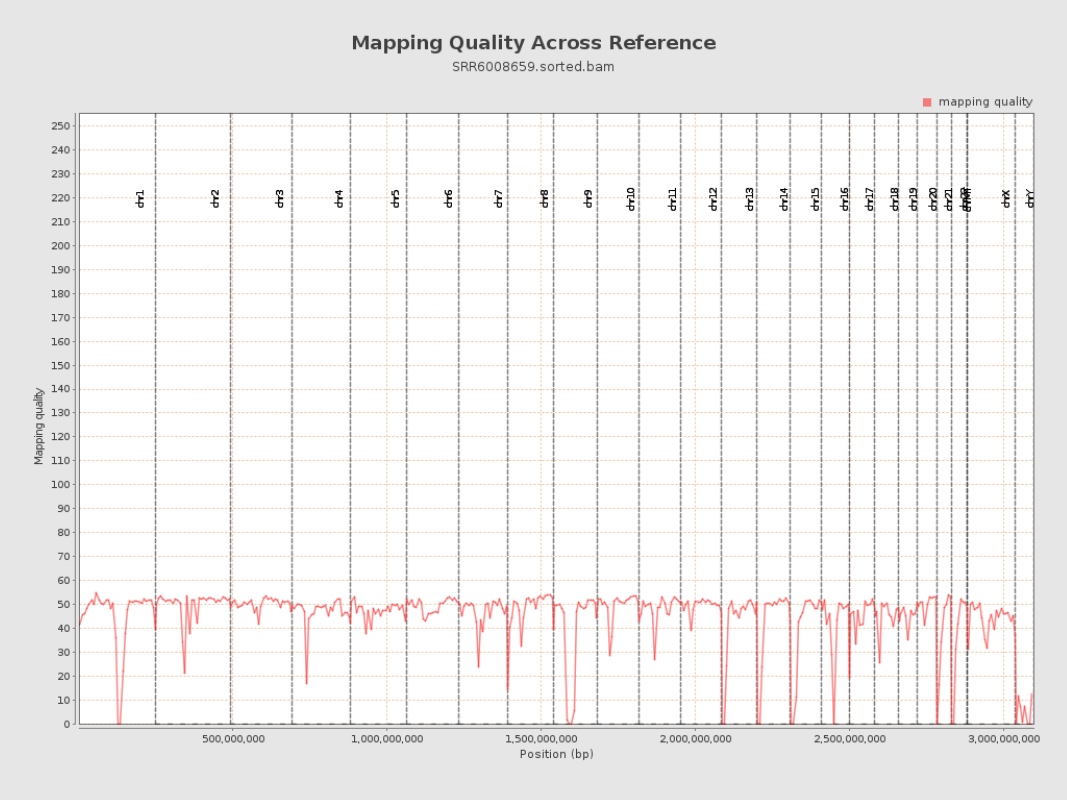
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram