Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:39:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548964.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_SRR1548964 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548964.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:39:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548964.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,234,225
Mapped reads	7,207,302 / 87.53%
Unmapped reads	1,026,923 / 12.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	331,572 / 4.03%
Duplication rate	2.85%
Clipped reads	614,595 / 7.46%

2.2. ACGT Content

Number/percentage of A's	80,357,581 / 28.22%
Number/percentage of C's	61,180,508 / 21.48%
Number/percentage of T's	81,871,775 / 28.75%
Number/percentage of G's	61,390,788 / 21.56%
Number/percentage of N's	391 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.092
Standard Deviation	0.907

2.4. Mapping Quality

Mean Mapping Quality	36.67

2.5. Mismatches and indels

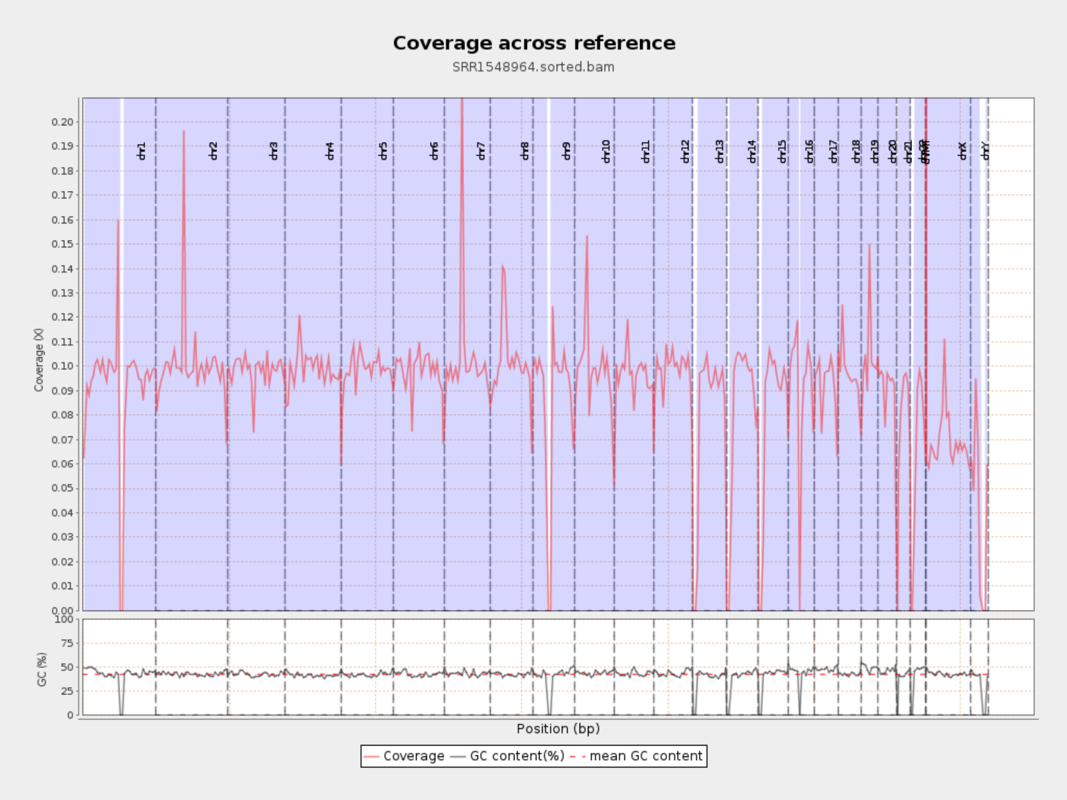
General error rate	0.32%
Mismatches	898,317
Insertions	9,733
Mapped reads with at least one insertion	0.14%
Deletions	23,009
Mapped reads with at least one deletion	0.32%
Homopolymer indels	39.05%

2.6. Chromosome stats

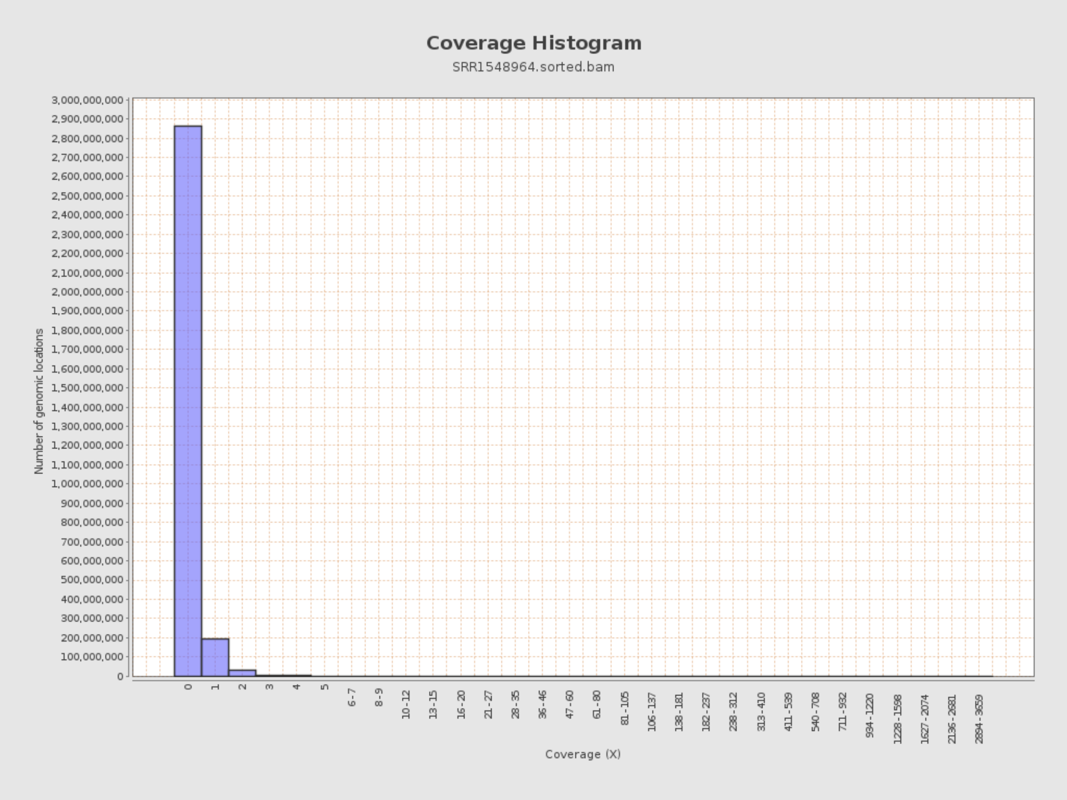
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22824688	0.0916	1.5444
chr2	243199373	24528735	0.1009	0.8816
chr3	198022430	19486934	0.0984	0.3716
chr4	191154276	18926952	0.099	0.4046
chr5	180915260	17849817	0.0987	0.3888
chr6	171115067	16770623	0.098	0.4058
chr7	159138663	16548845	0.104	1.4561
chr8	146364022	14824030	0.1013	1.8617

chr9	141213431	12155696	0.0861	0.9208
chr10	135534747	13446744	0.0992	0.6715
chr11	135006516	13026163	0.0965	0.6229
chr12	133851895	13260188	0.0991	0.4204
chr13	115169878	9137529	0.0793	0.325
chr14	107349540	8854985	0.0825	0.5218
chr15	102531392	8009935	0.0781	0.3385
chr16	90354753	7974882	0.0883	0.4628
chr17	81195210	7604498	0.0937	0.396
chr18	78077248	7659116	0.0981	1.7628
chr19	59128983	6170139	0.1044	1.5383
chr20	63025520	5699196	0.0904	0.3936
chr21	48129895	3624157	0.0753	0.4768
chr22	51304566	3179316	0.062	0.4295
chrMT	16571	12309	0.7428	1.1931
chrX	155270560	10757922	0.0693	0.514
chrY	59373566	2497454	0.0421	0.3653

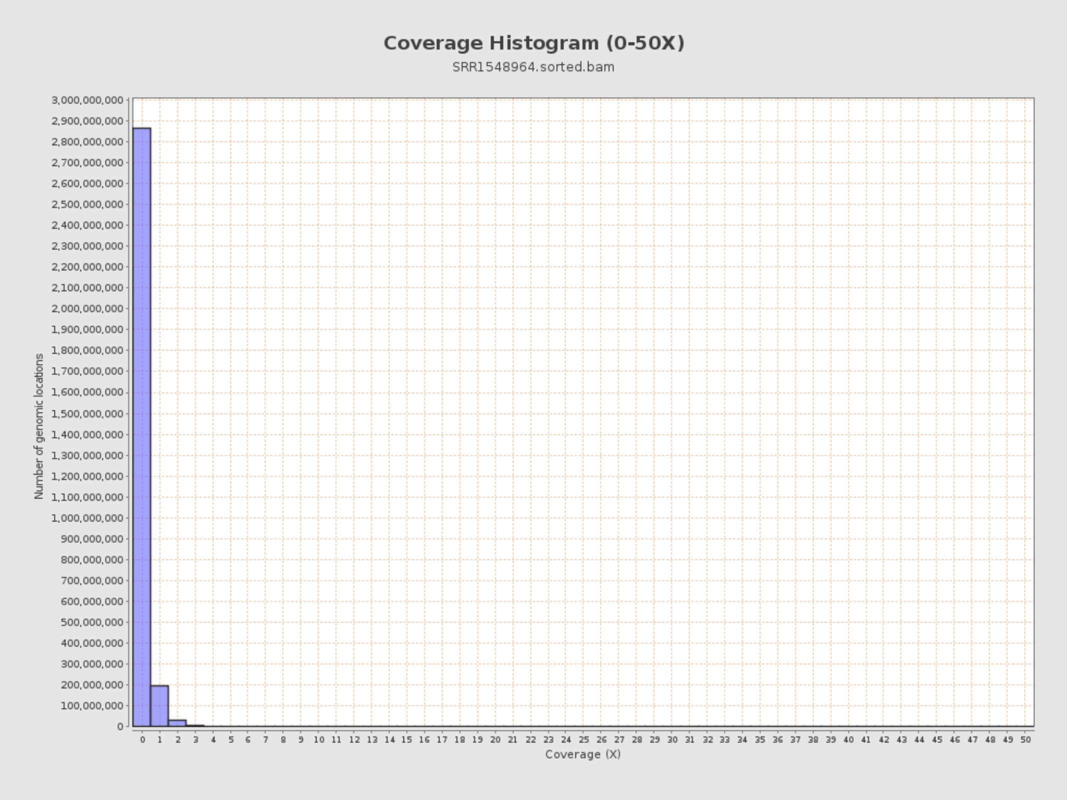
3. Results : Coverage across reference



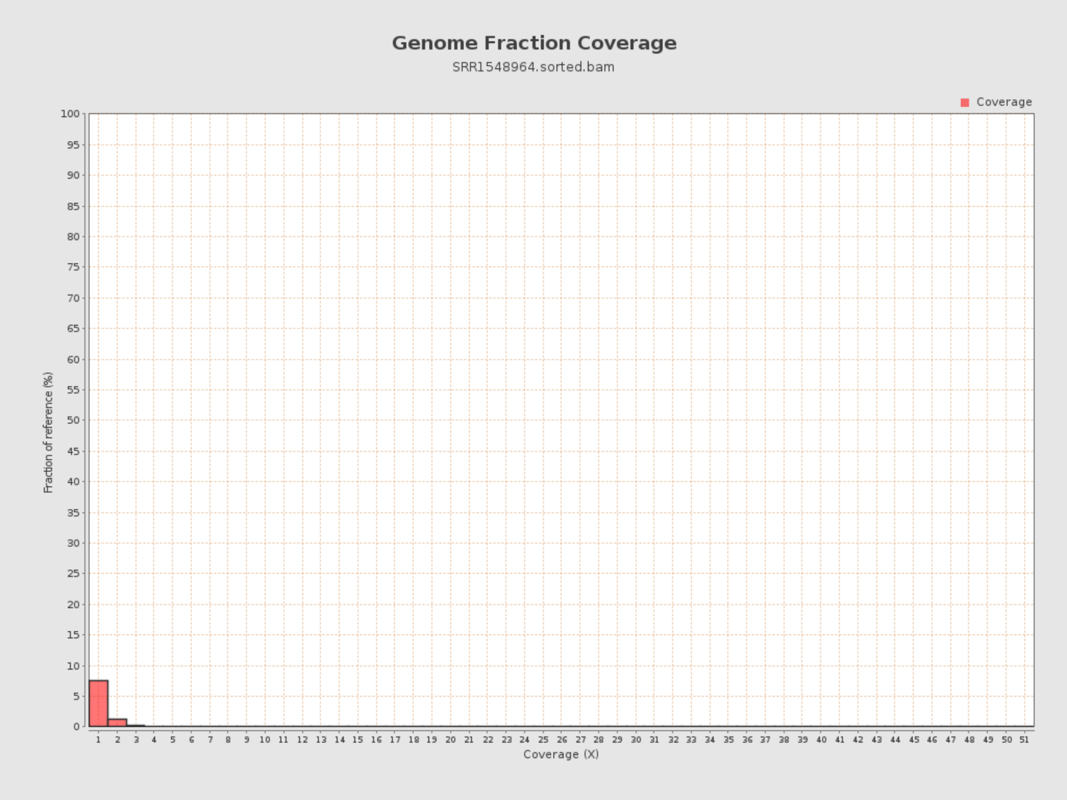
4. Results : Coverage Histogram



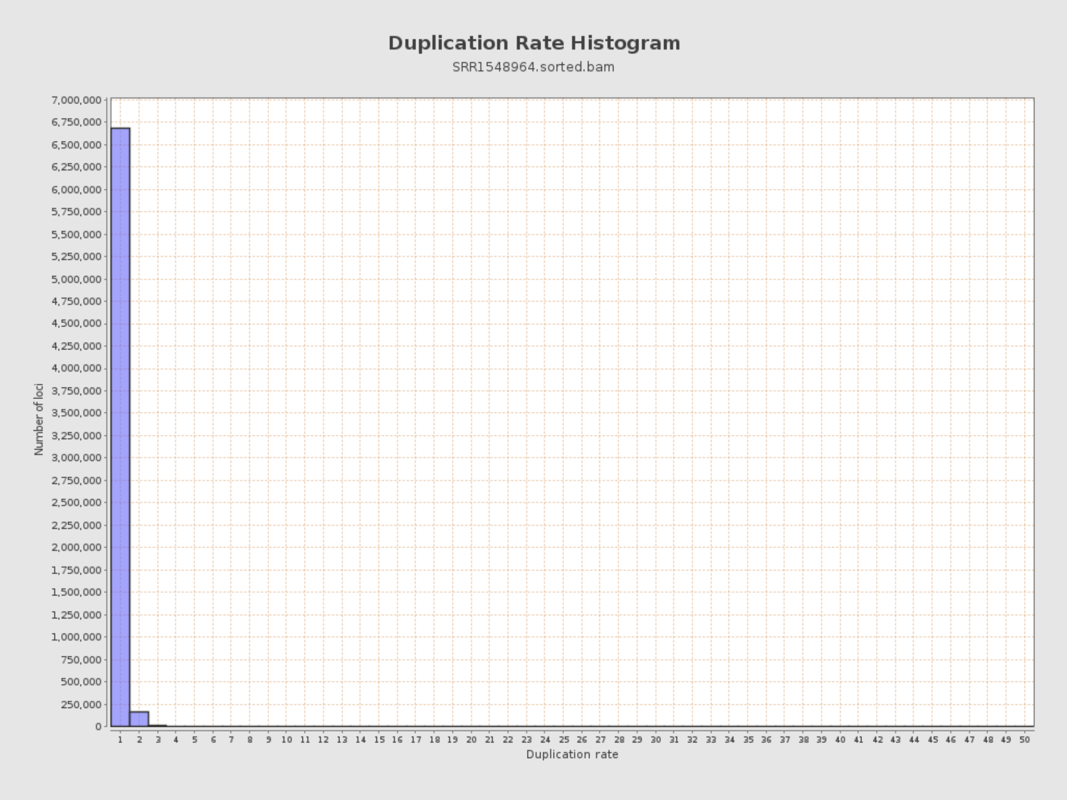
5. Results : Coverage Histogram (0-50X)



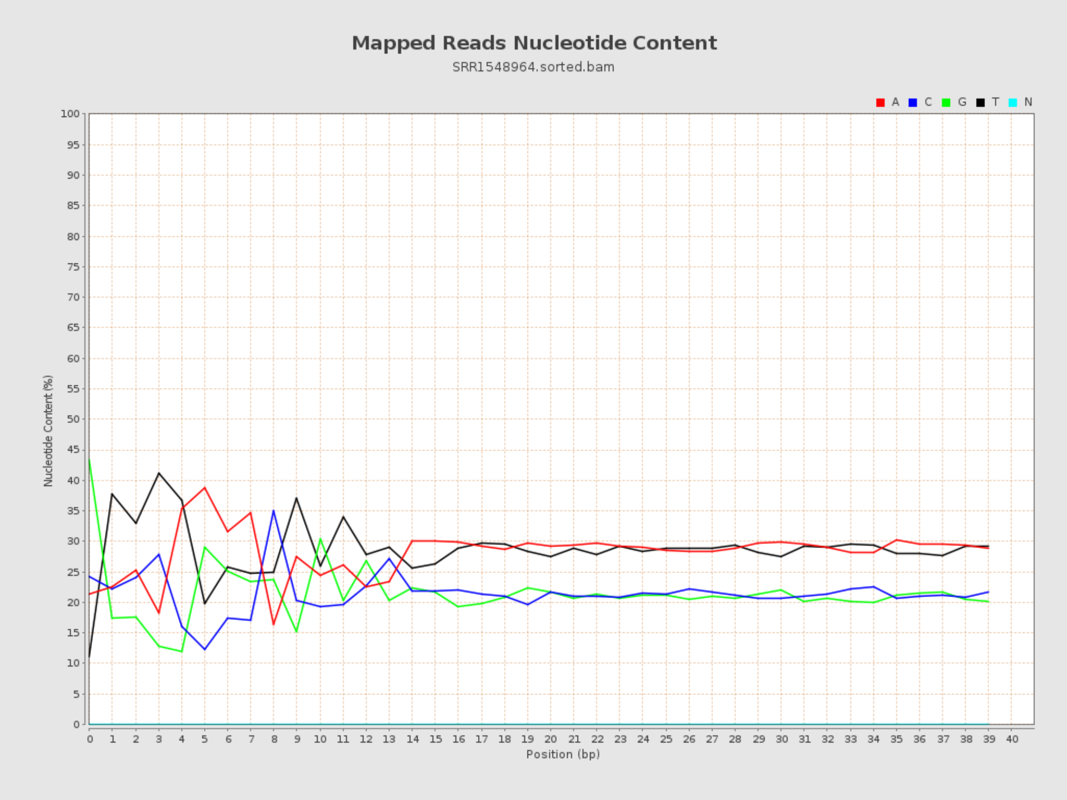
6. Results : Genome Fraction Coverage



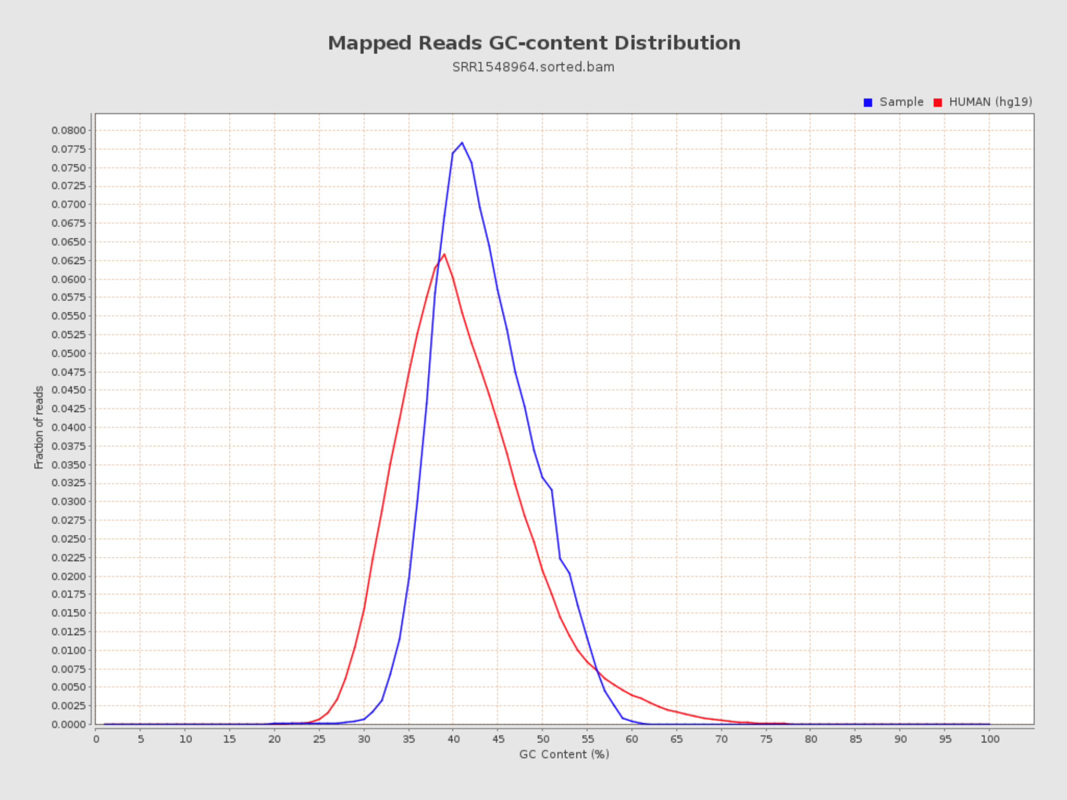
7. Results : Duplication Rate Histogram



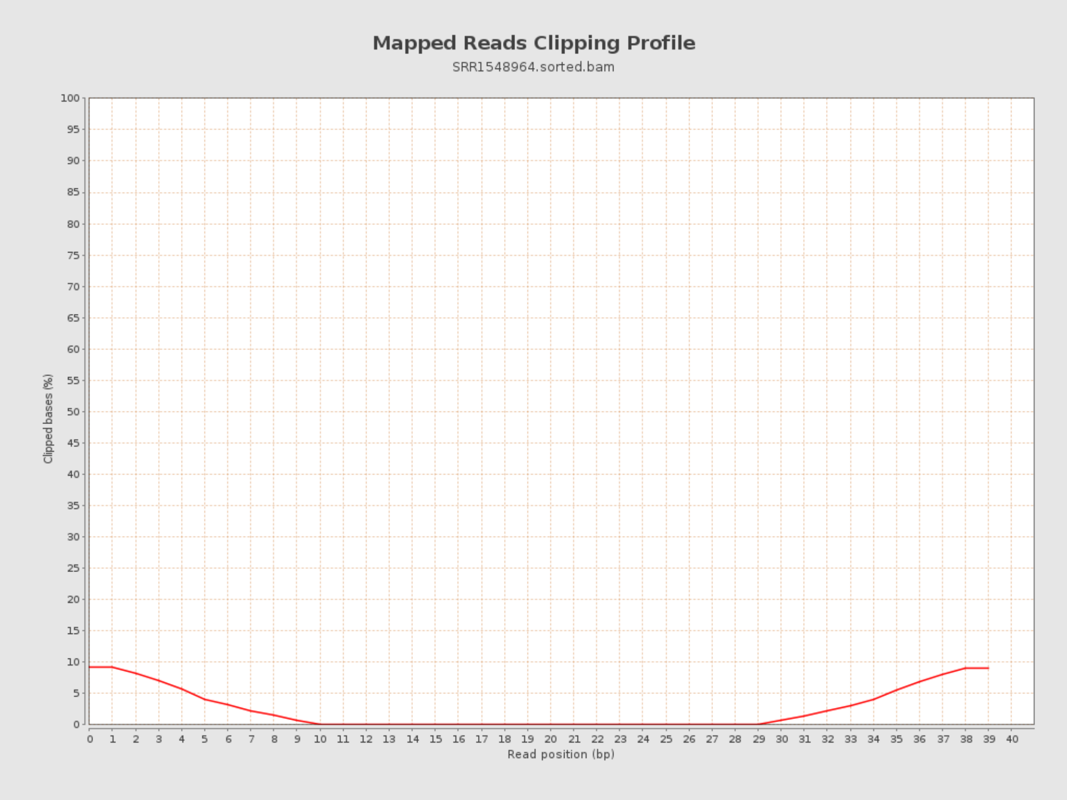
8. Results : Mapped Reads Nucleotide Content



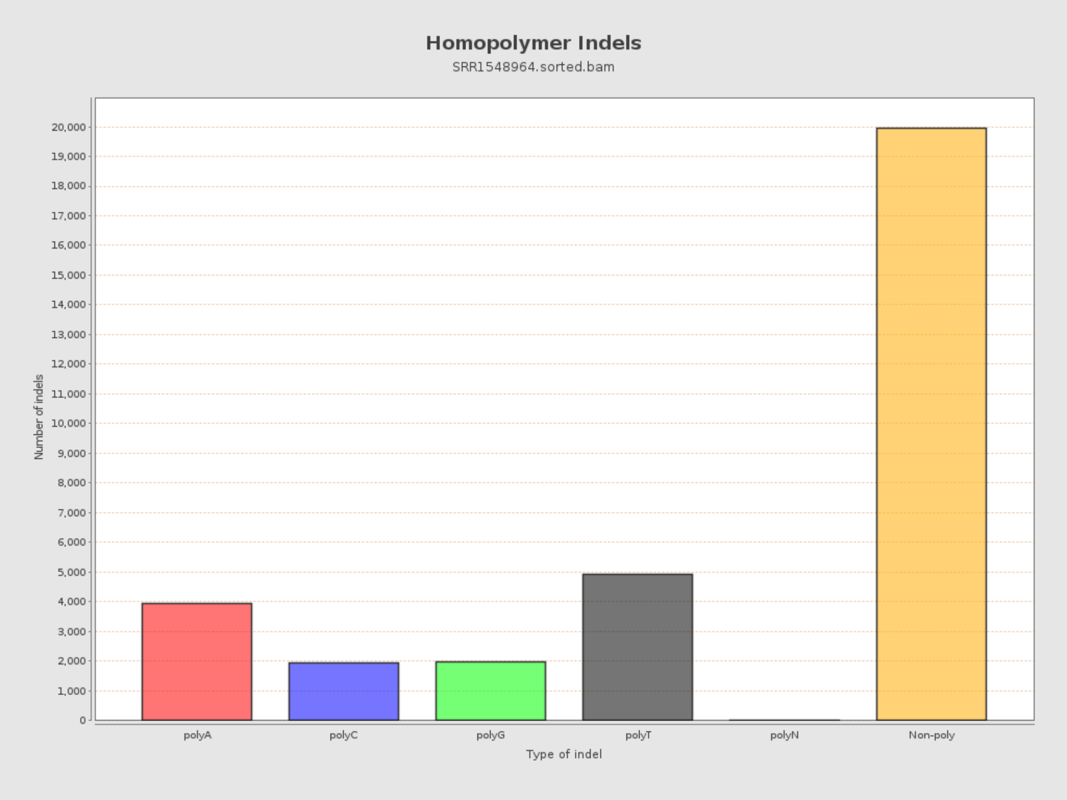
9. Results : Mapped Reads GC-content Distribution



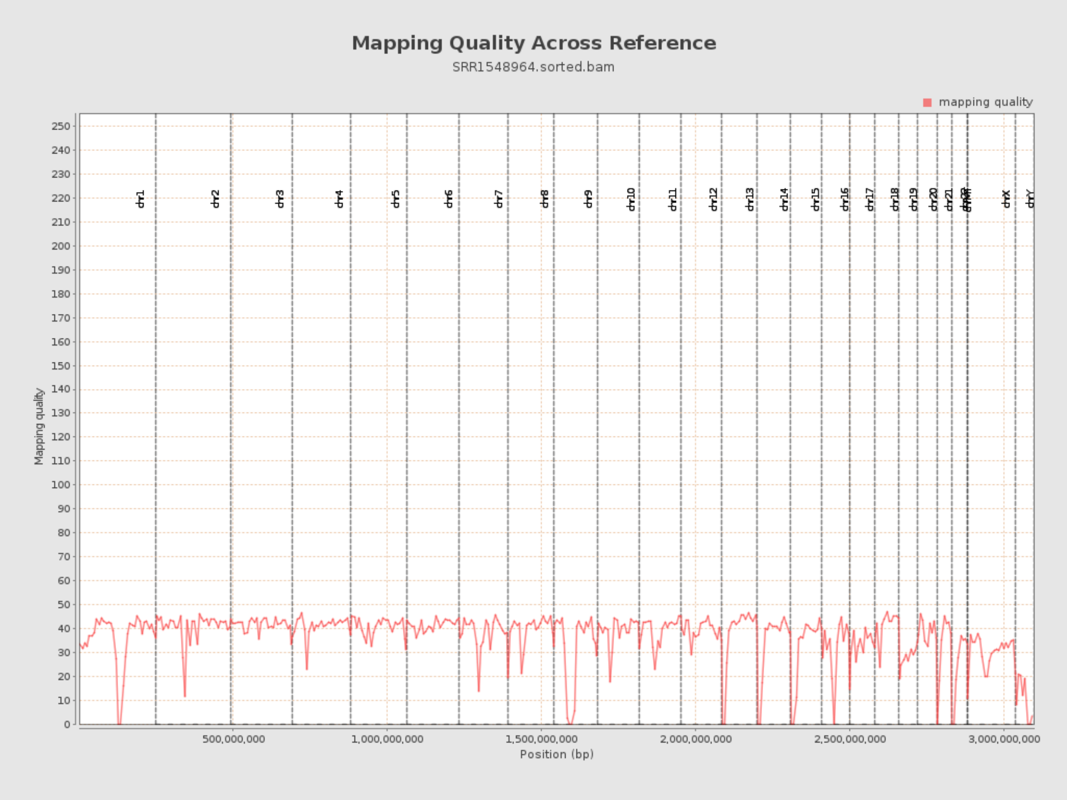
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram