Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:57:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548952.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_SRR1548952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:57:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,823,497
Mapped reads	9,458,634 / 87.39%
Unmapped reads	1,364,863 / 12.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	480,803 / 4.44%
Duplication rate	3.37%
Clipped reads	736,812 / 6.81%

2.2. ACGT Content

Number/percentage of A's	105,260,416 / 28.13%
Number/percentage of C's	80,006,131 / 21.38%
Number/percentage of T's	107,828,981 / 28.82%
Number/percentage of G's	81,052,573 / 21.66%
Number/percentage of N's	508 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.1209
Standard Deviation	1.07

2.4. Mapping Quality

Mean Mapping Quality	38.01

2.5. Mismatches and indels

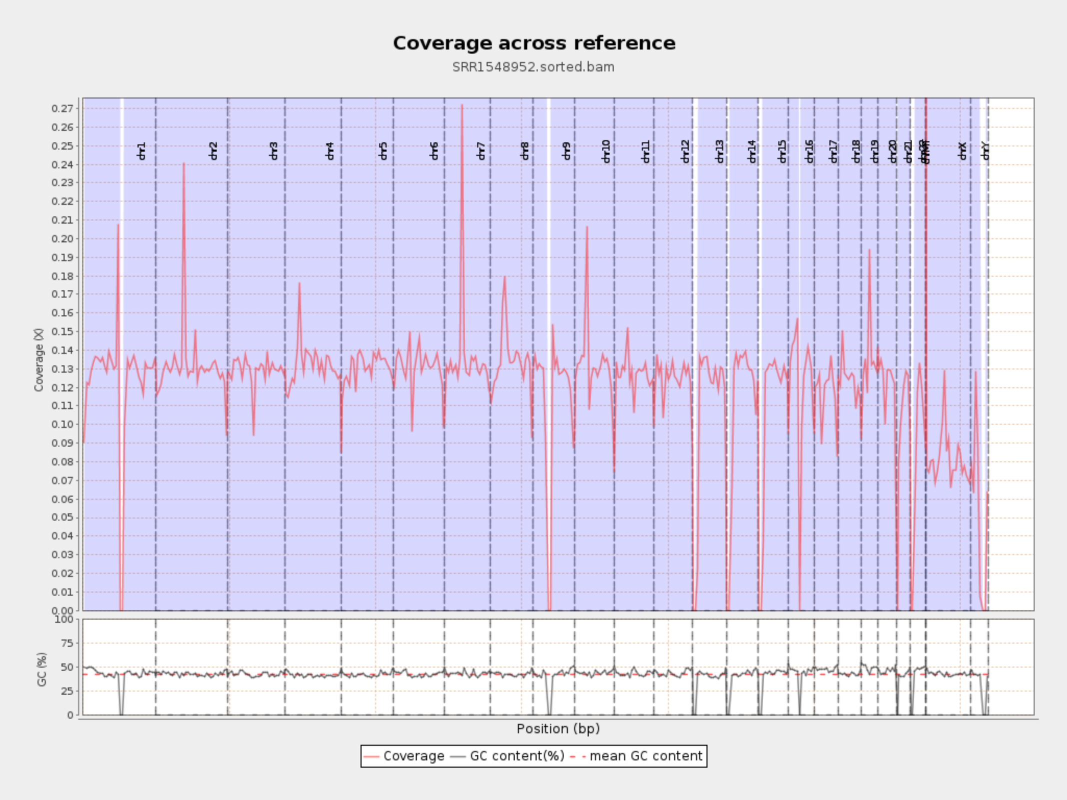
General error rate	0.3%
Mismatches	1,098,465
Insertions	11,807
Mapped reads with at least one insertion	0.12%
Deletions	27,476
Mapped reads with at least one deletion	0.29%
Homopolymer indels	39.68%

2.6. Chromosome stats

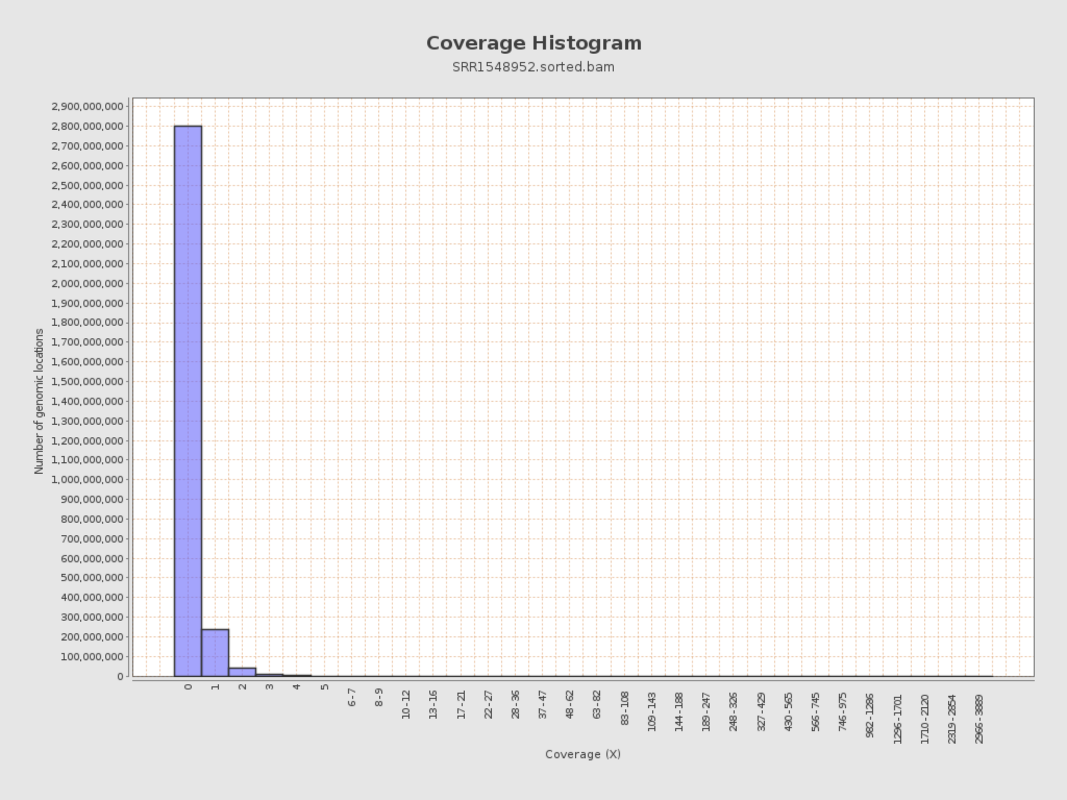
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30668279	0.123	1.9069
chr2	243199373	32160006	0.1322	1.0458
chr3	198022430	25559830	0.1291	0.4373
chr4	191154276	25304487	0.1324	0.5116
chr5	180915260	23637691	0.1307	0.4657
chr6	171115067	22506294	0.1315	0.4949
chr7	159138663	21762719	0.1368	1.7385
chr8	146364022	19618351	0.134	2.0073

chr9	141213431	15850594	0.1122	1.0757
chr10	135534747	18010062	0.1329	0.8392
chr11	135006516	17102836	0.1267	0.7427
chr12	133851895	16794494	0.1255	0.4776
chr13	115169878	12272306	0.1066	0.3888
chr14	107349540	11719873	0.1092	0.6435
chr15	102531392	10649388	0.1039	0.4025
chr16	90354753	10666925	0.1181	0.5679
chr17	81195210	9618265	0.1185	0.4595
chr18	78077248	9761905	0.125	2.0474
chr19	59128983	8064719	0.1364	1.8645
chr20	63025520	7693792	0.1221	0.4737
chr21	48129895	4782484	0.0994	0.6008
chr22	51304566	4189715	0.0817	0.4901
chrMT	16571	7528	0.4543	0.799
chrX	155270560	12653219	0.0815	0.5926
chrY	59373566	3128589	0.0527	0.4401

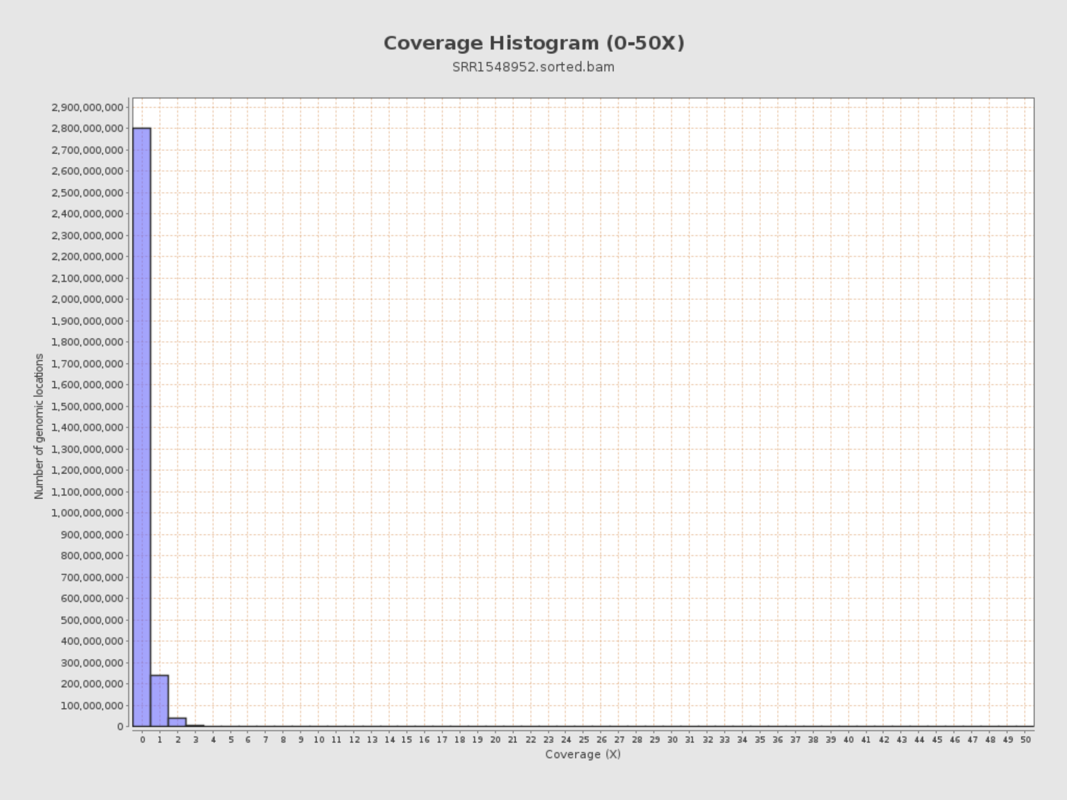
3. Results : Coverage across reference



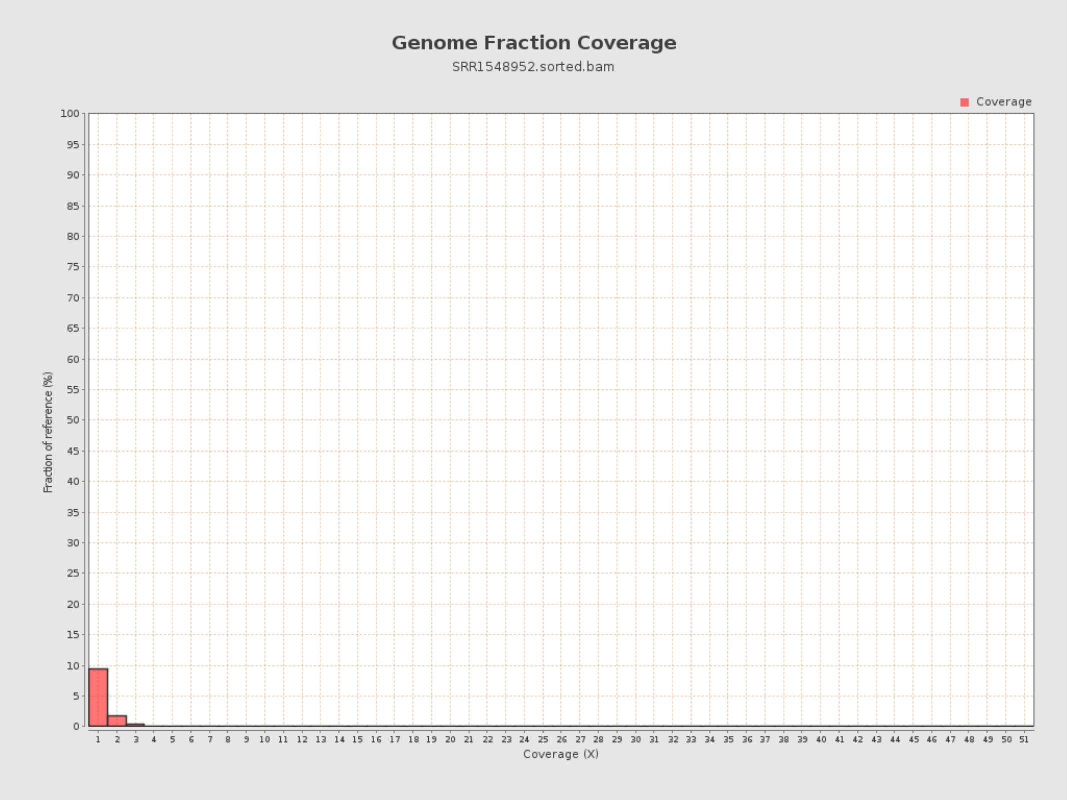
4. Results : Coverage Histogram



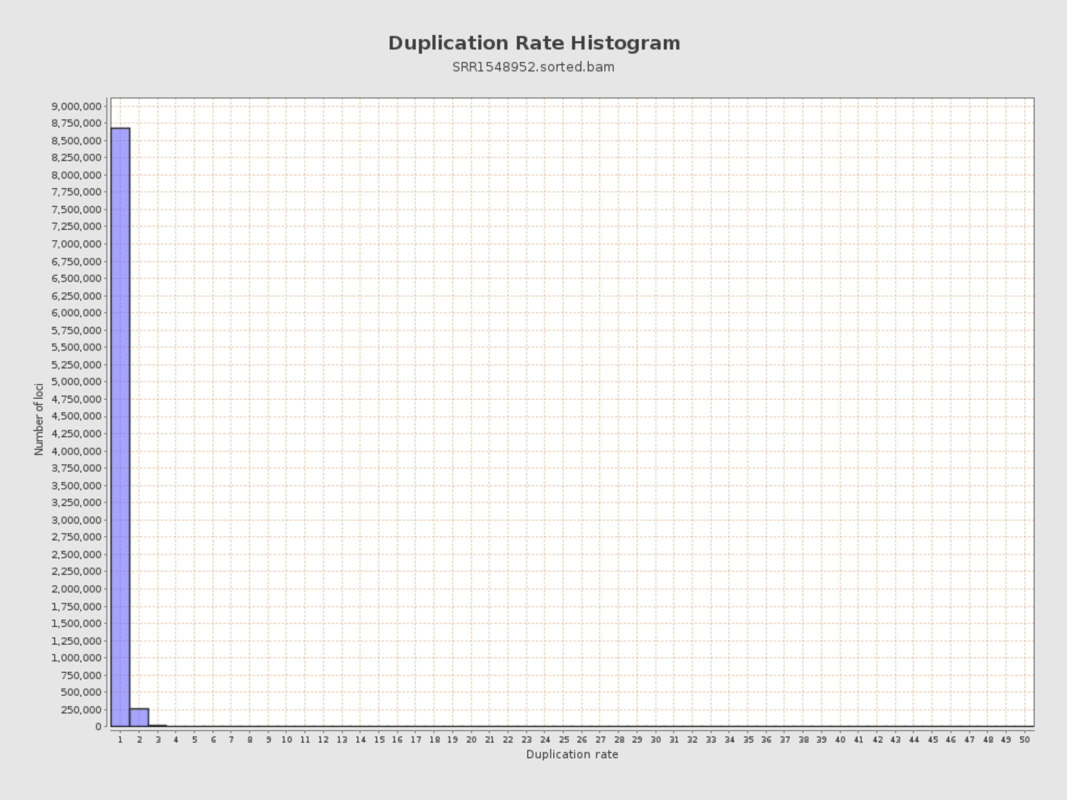
5. Results : Coverage Histogram (0-50X)



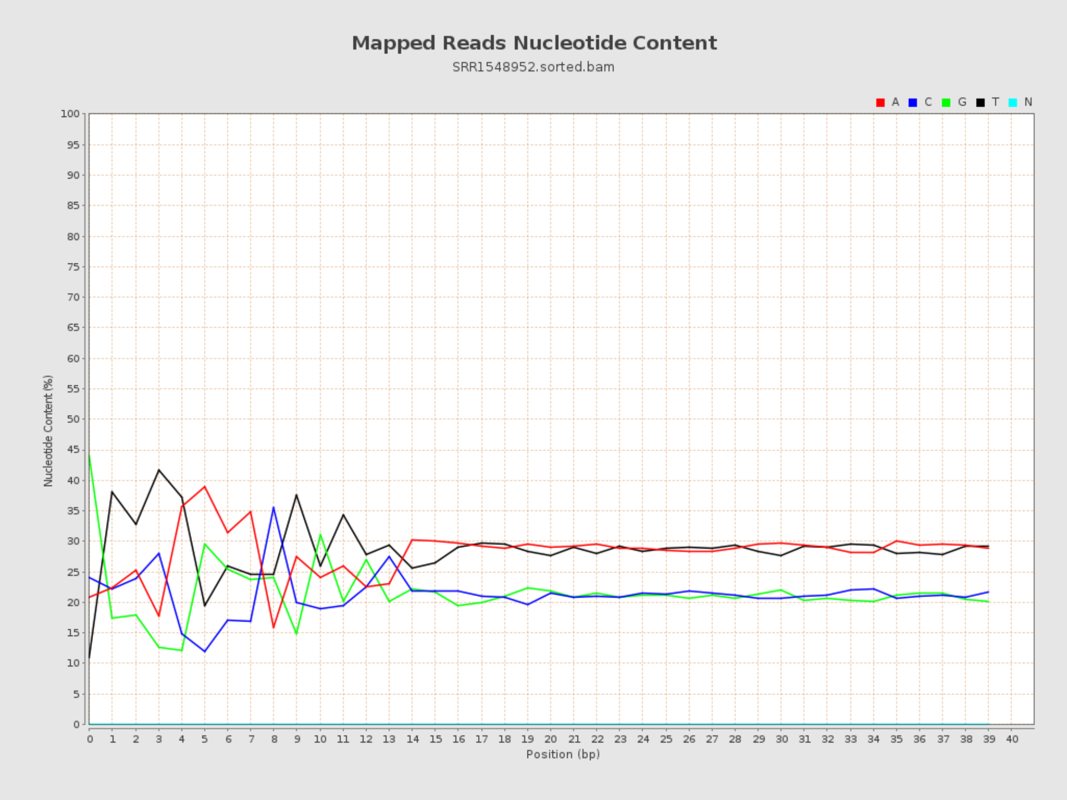
6. Results : Genome Fraction Coverage



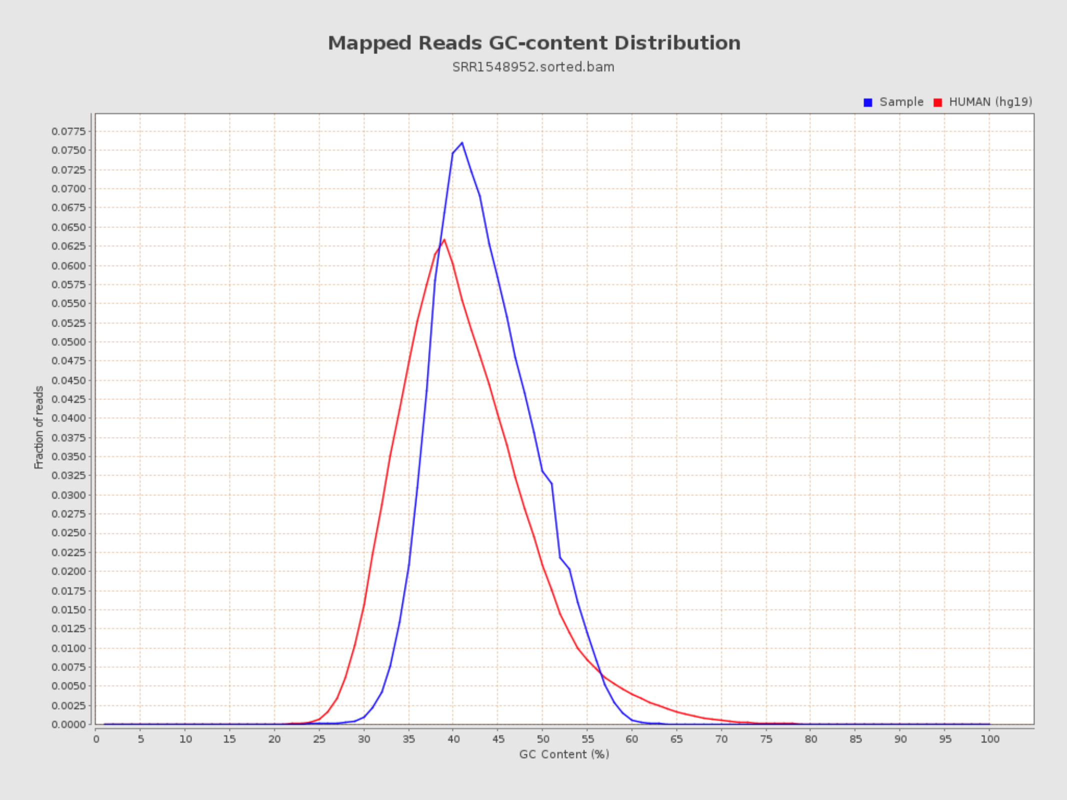
7. Results : Duplication Rate Histogram



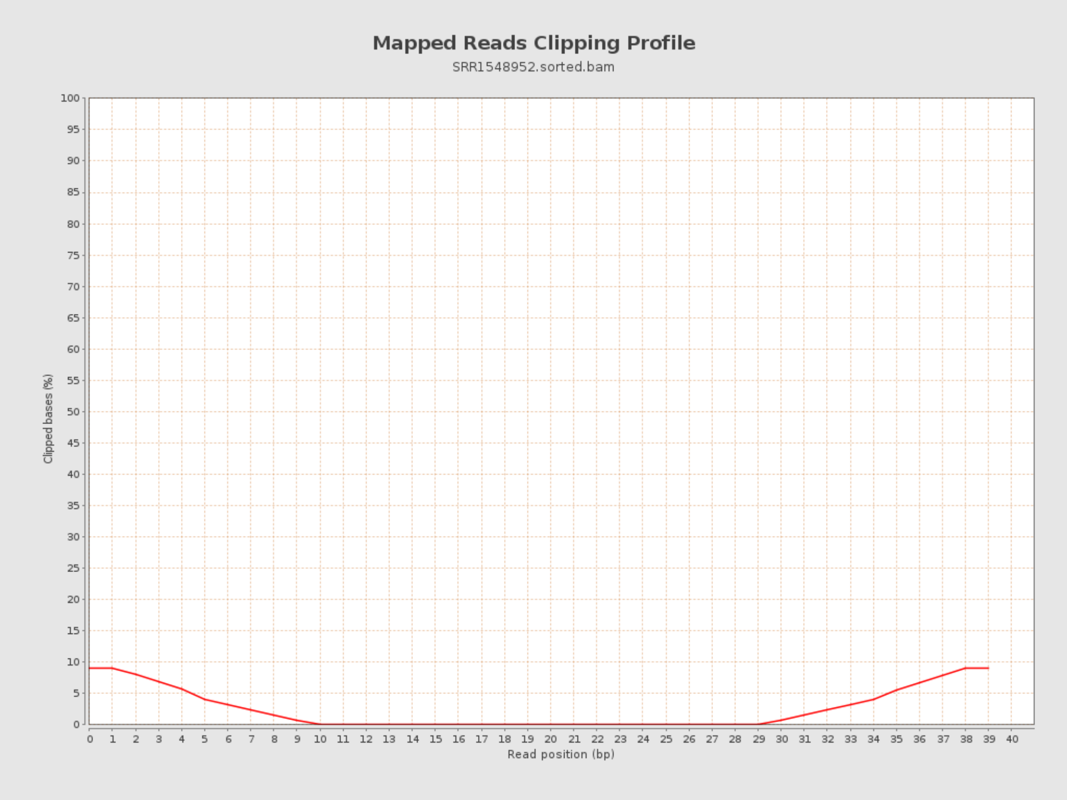
8. Results : Mapped Reads Nucleotide Content



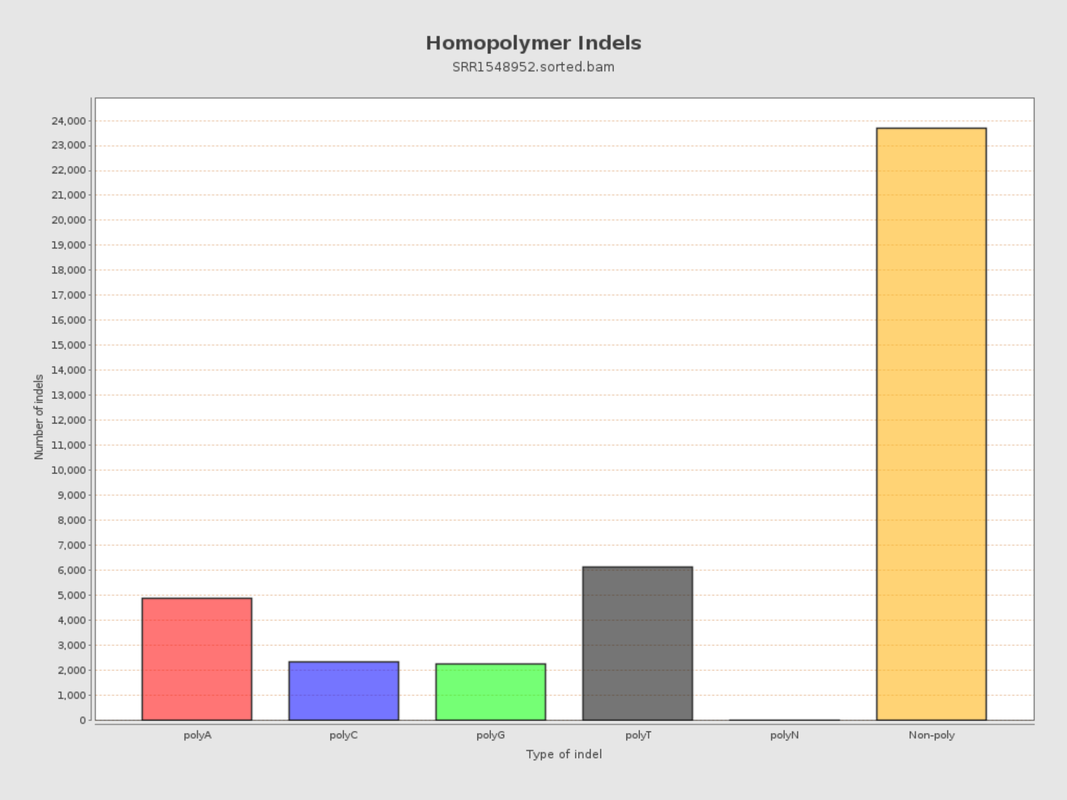
9. Results : Mapped Reads GC-content Distribution



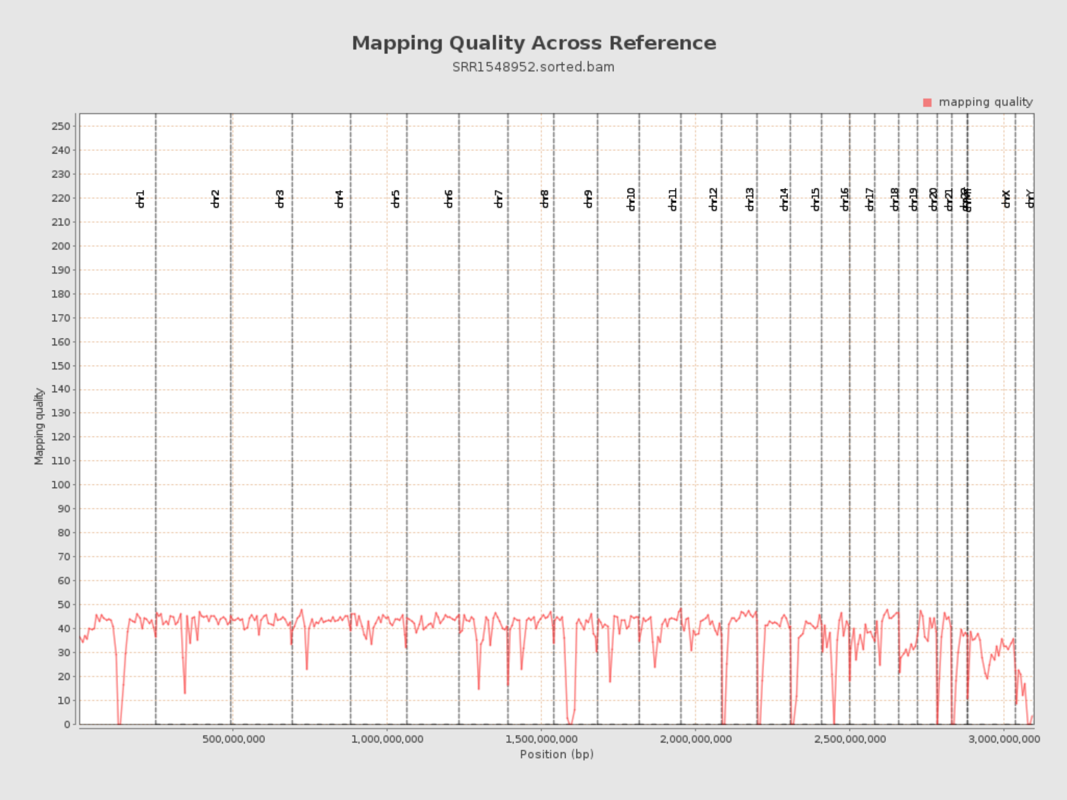
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram