Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:03:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004000.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_SRR6004000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004000.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:03:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,828,739
Mapped reads	1,438,726 / 78.67%
Unmapped reads	390,013 / 21.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,114 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	109,201 / 5.97%
Duplication rate	6.41%
Clipped reads	857,673 / 46.9%

2.2. ACGT Content

Number/percentage of A's	24,019,288 / 26.37%
Number/percentage of C's	17,230,574 / 18.92%
Number/percentage of T's	28,448,834 / 31.23%
Number/percentage of G's	21,372,527 / 23.46%
Number/percentage of N's	16,491 / 0.02%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0294

Standard Deviation	0.288

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

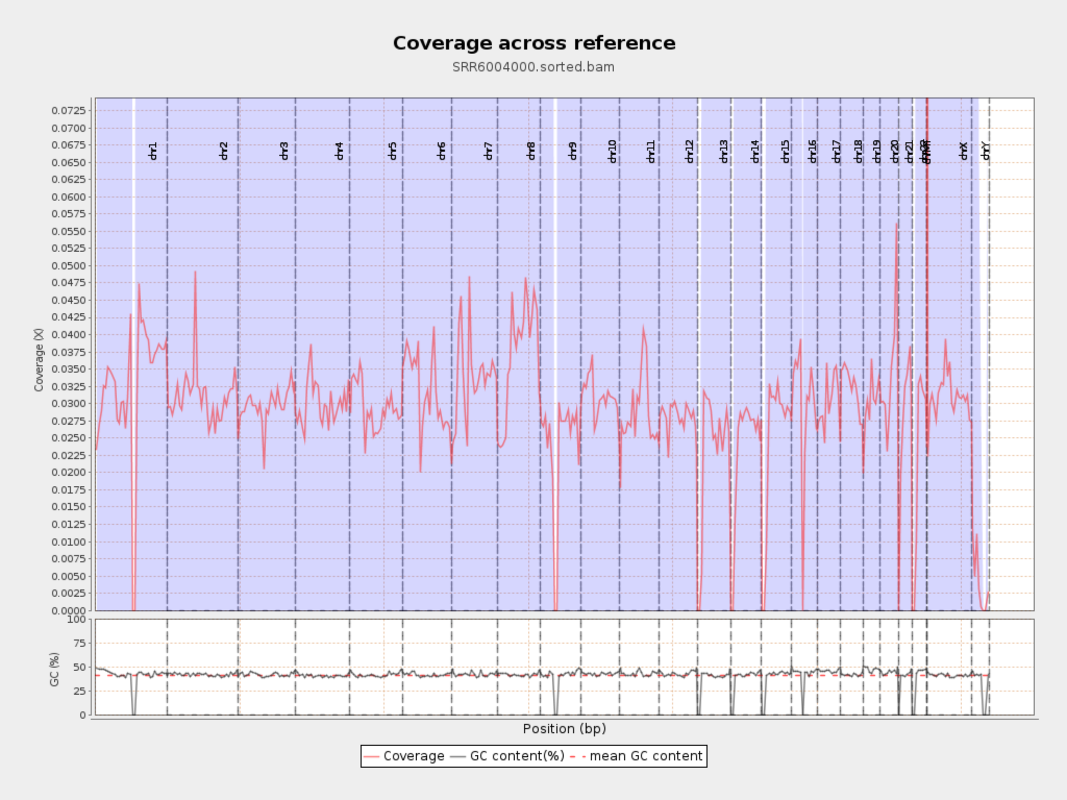
General error rate	1.02%
Mismatches	915,768
Insertions	7,348
Mapped reads with at least one insertion	0.51%
Deletions	31,402
Mapped reads with at least one deletion	2.15%
Homopolymer indels	47.02%

2.6. Chromosome stats

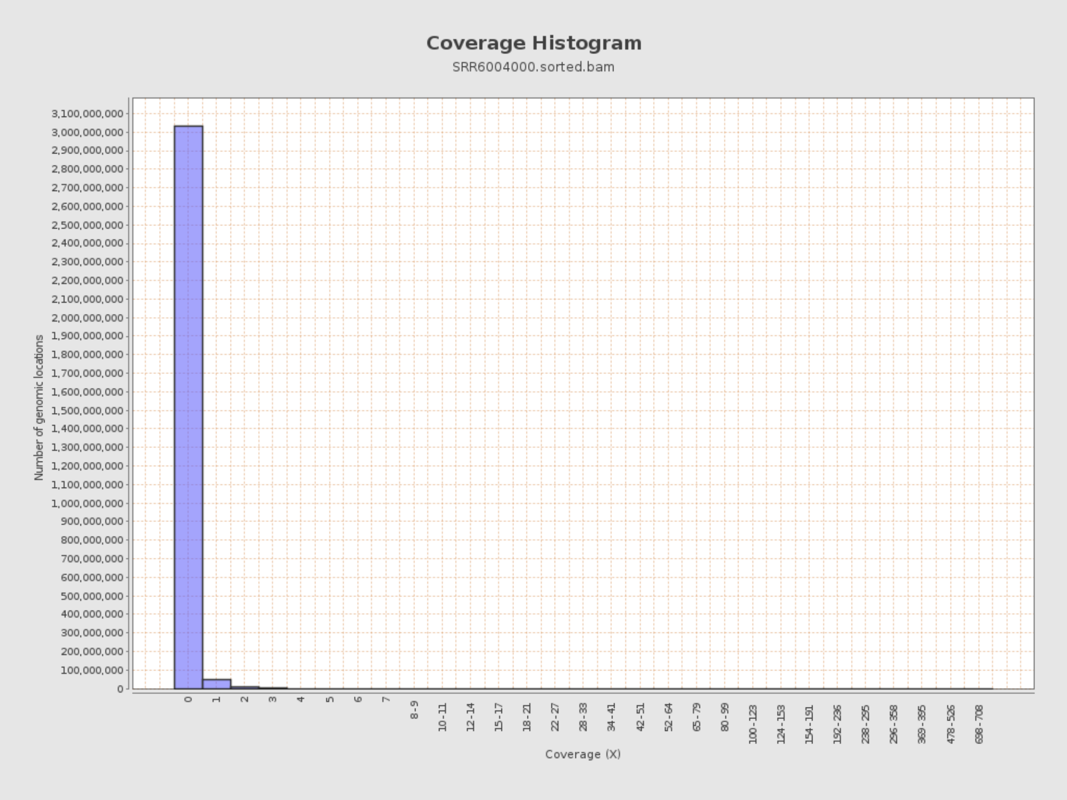
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8095333	0.0325	0.39
chr2	243199373	7578690	0.0312	0.4069
chr3	198022430	5899614	0.0298	0.2264
chr4	191154276	5750371	0.0301	0.2316
chr5	180915260	5337253	0.0295	0.2256
chr6	171115067	5454650	0.0319	0.2619
chr7	159138663	5385119	0.0338	0.403

chr8	146364022	5470024	0.0374	0.3113
chr9	141213431	3348172	0.0237	0.2438
chr10	135534747	4208116	0.031	0.2582
chr11	135006516	3894924	0.0288	0.2754
chr12	133851895	3760556	0.0281	0.2212
chr13	115169878	2606662	0.0226	0.1985
chr14	107349540	2481229	0.0231	0.2115
chr15	102531392	2510961	0.0245	0.2083
chr16	90354753	2650020	0.0293	0.2336
chr17	81195210	2459497	0.0303	0.2424
chr18	78077248	2537497	0.0325	0.3717
chr19	59128983	1804667	0.0305	0.3423
chr20	63025520	2177630	0.0346	0.2496
chr21	48129895	1329490	0.0276	0.2242
chr22	51304566	1129105	0.022	0.1962
chrMT	16571	205455	12.3985	8.2422
chrX	155270560	4829645	0.0311	0.2433
chrY	59373566	233756	0.0039	0.0878

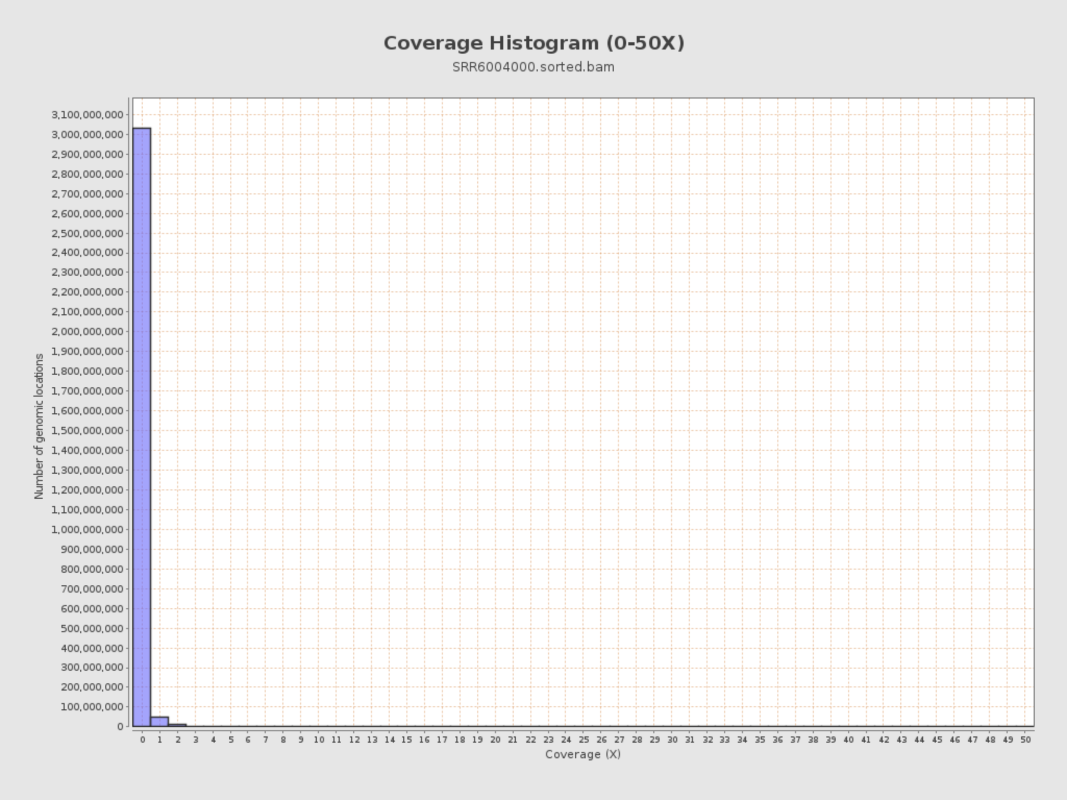
3. Results : Coverage across reference



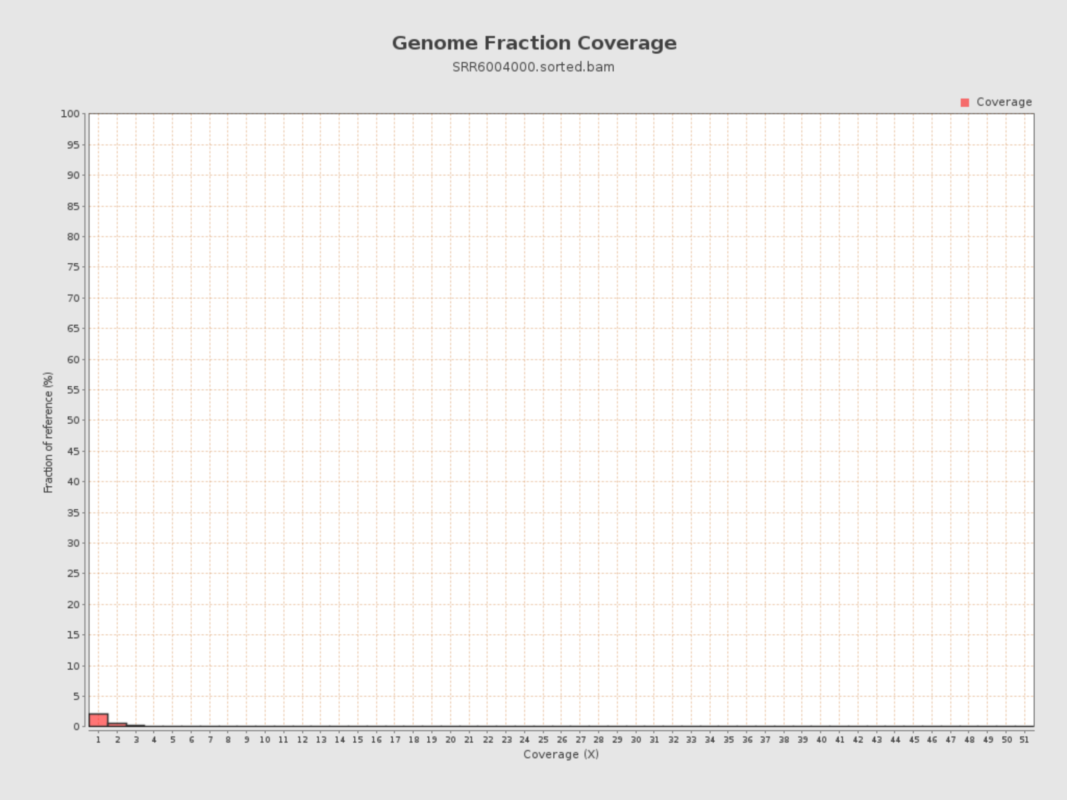
4. Results : Coverage Histogram



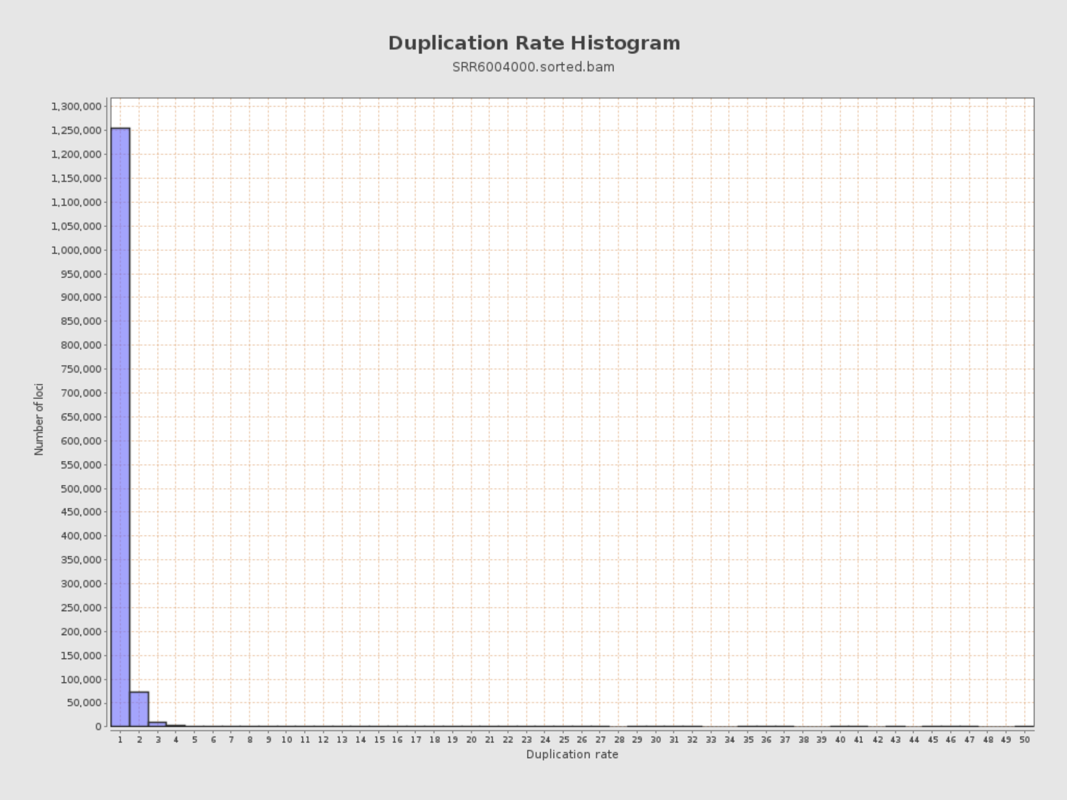
5. Results : Coverage Histogram (0-50X)



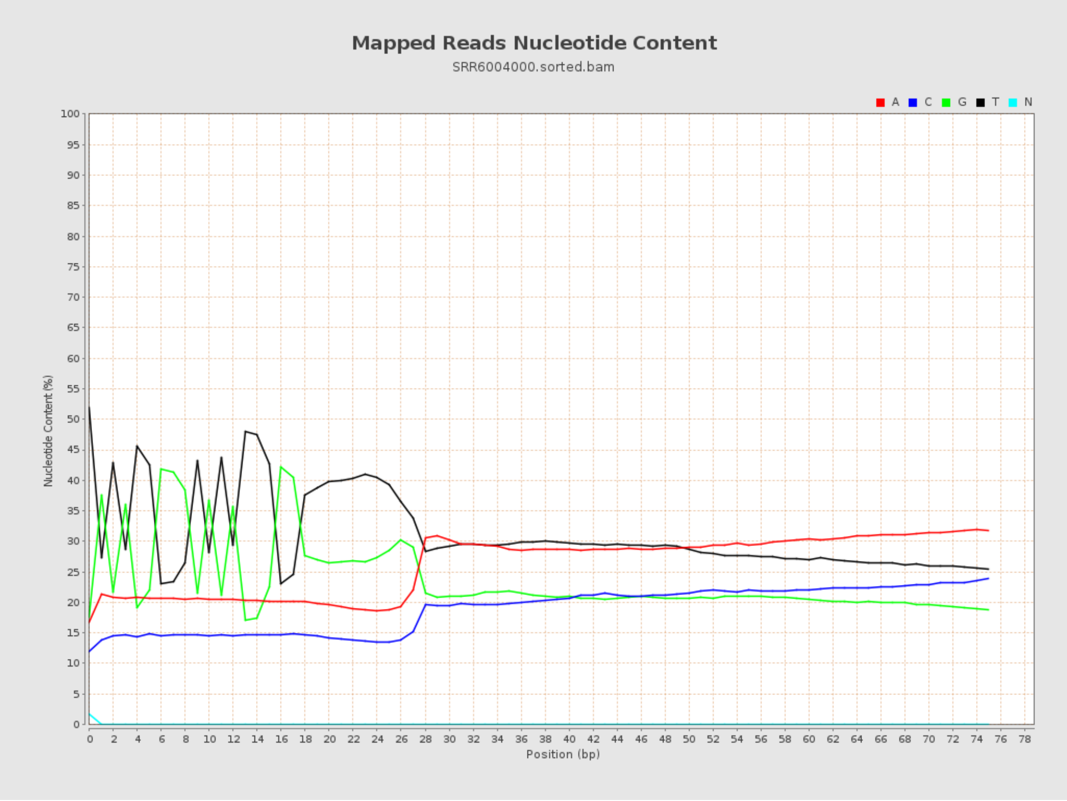
6. Results : Genome Fraction Coverage



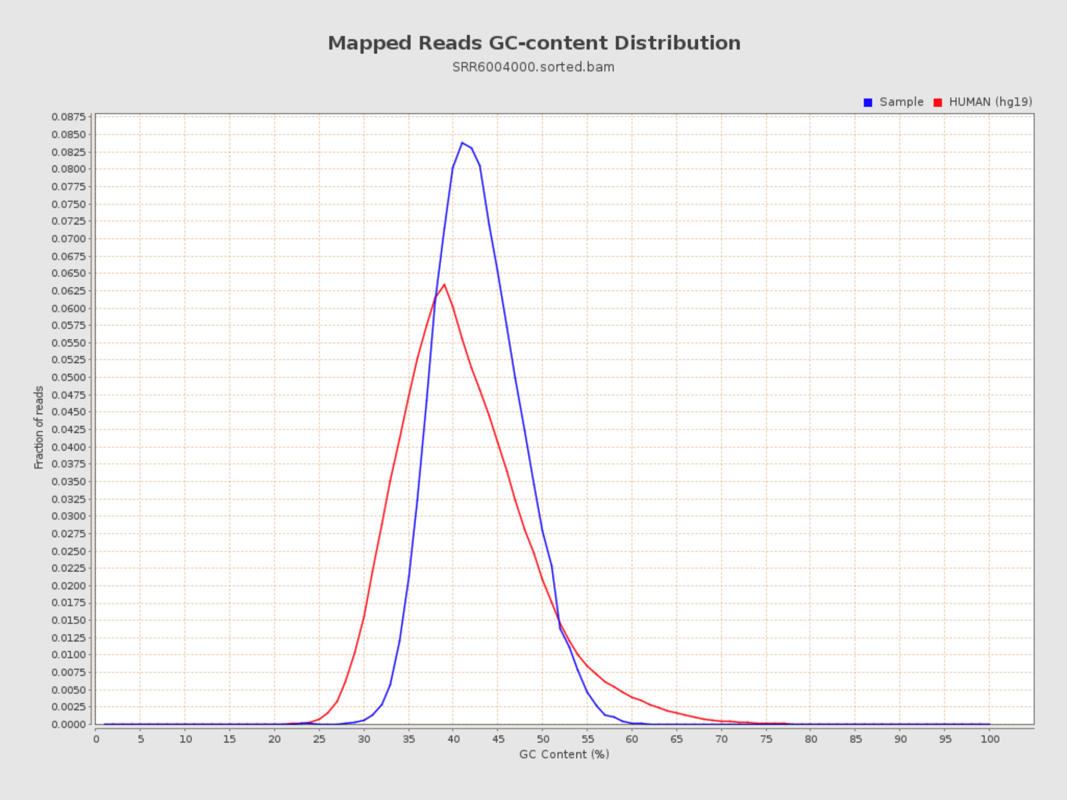
7. Results : Duplication Rate Histogram



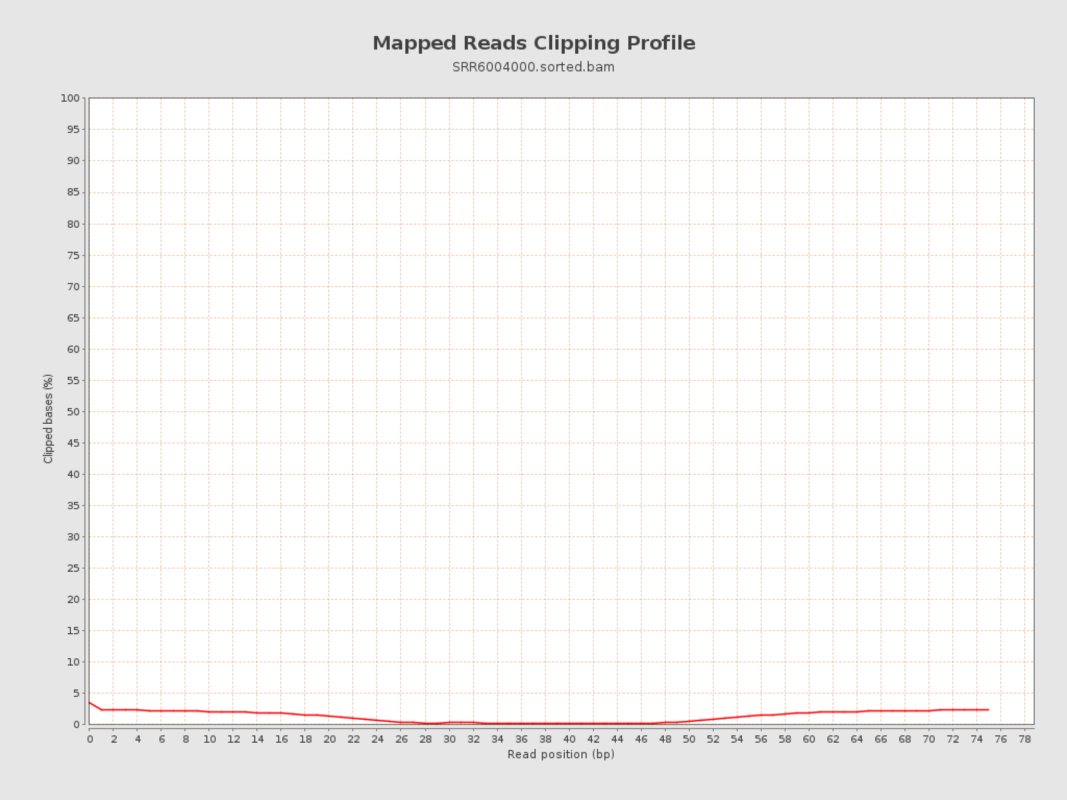
8. Results : Mapped Reads Nucleotide Content



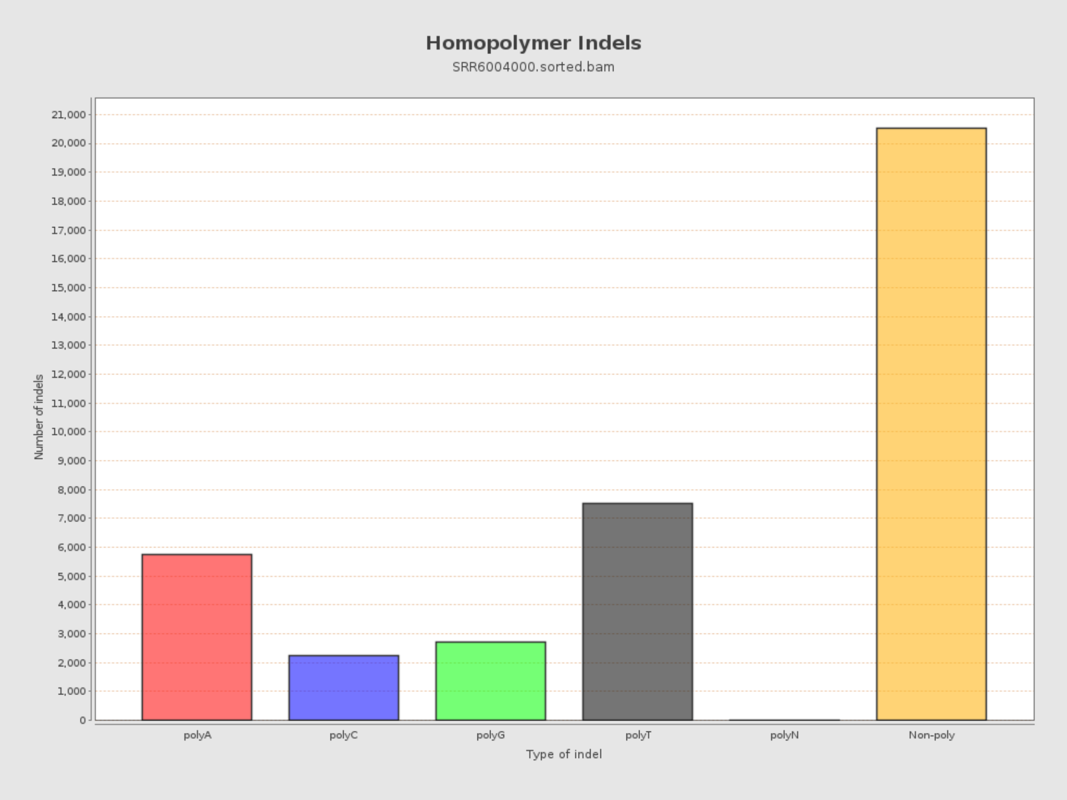
9. Results : Mapped Reads GC-content Distribution



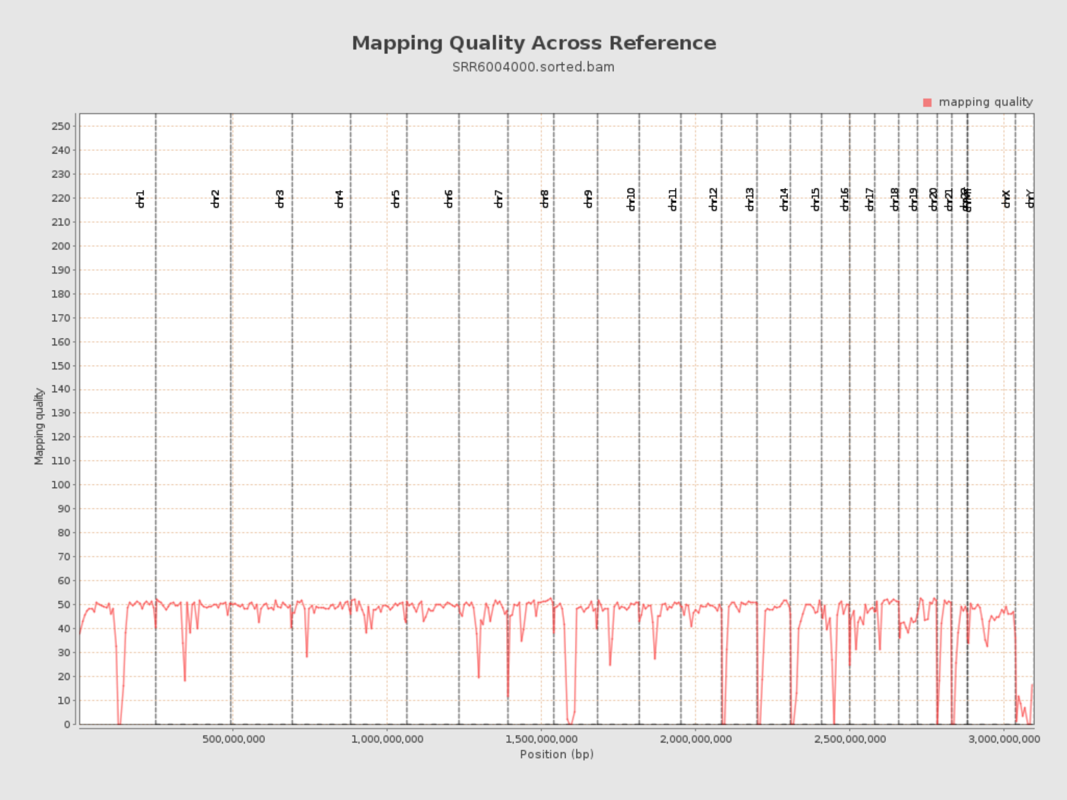
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram