Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:29:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004046.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_SRR6004046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:29:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,585,237
Mapped reads	3,271,219 / 91.24%
Unmapped reads	314,018 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,012 / 1.2%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	254,067 / 7.09%
Duplication rate	5.86%
Clipped reads	1,582,633 / 44.14%

2.2. ACGT Content

Number/percentage of A's	60,662,477 / 28.02%
Number/percentage of C's	41,230,444 / 19.04%
Number/percentage of T's	66,809,687 / 30.85%
Number/percentage of G's	47,807,533 / 22.08%
Number/percentage of N's	24,356 / 0.01%
GC Percentage	41.12%

2.3. Coverage

Mean	0.07

Standard Deviation	0.657

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

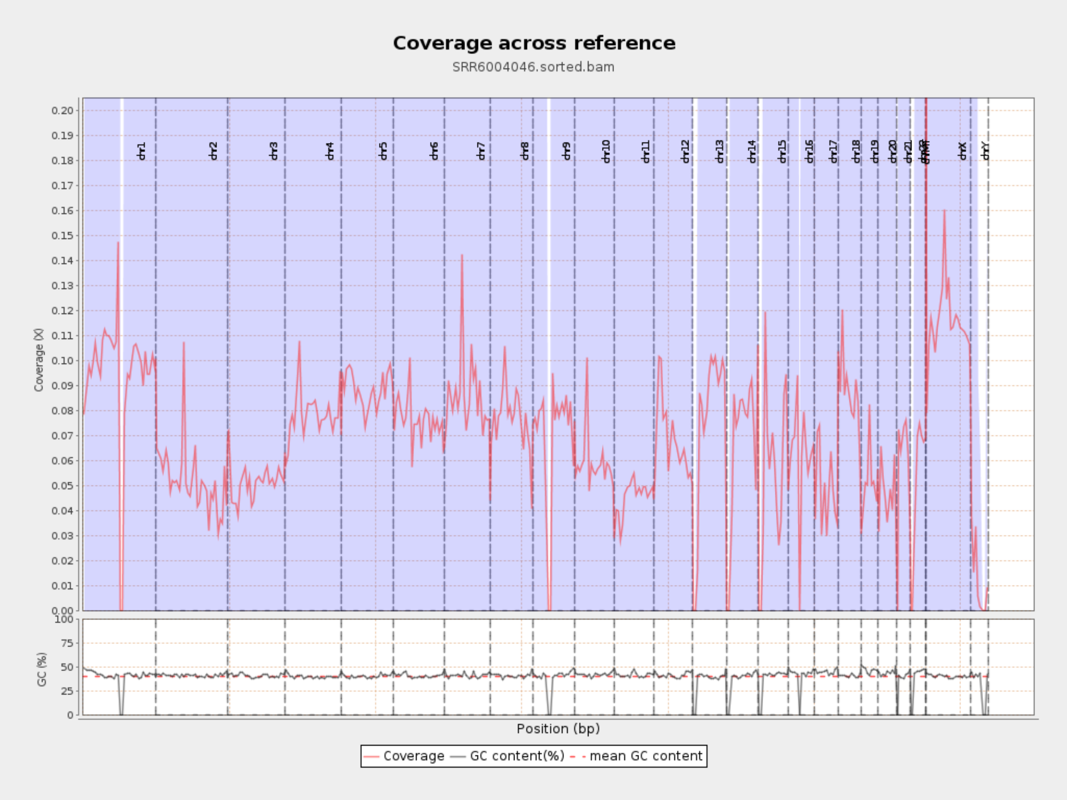
General error rate	0.78%
Mismatches	1,667,831
Insertions	15,753
Mapped reads with at least one insertion	0.48%
Deletions	54,292
Mapped reads with at least one deletion	1.64%
Homopolymer indels	46.19%

2.6. Chromosome stats

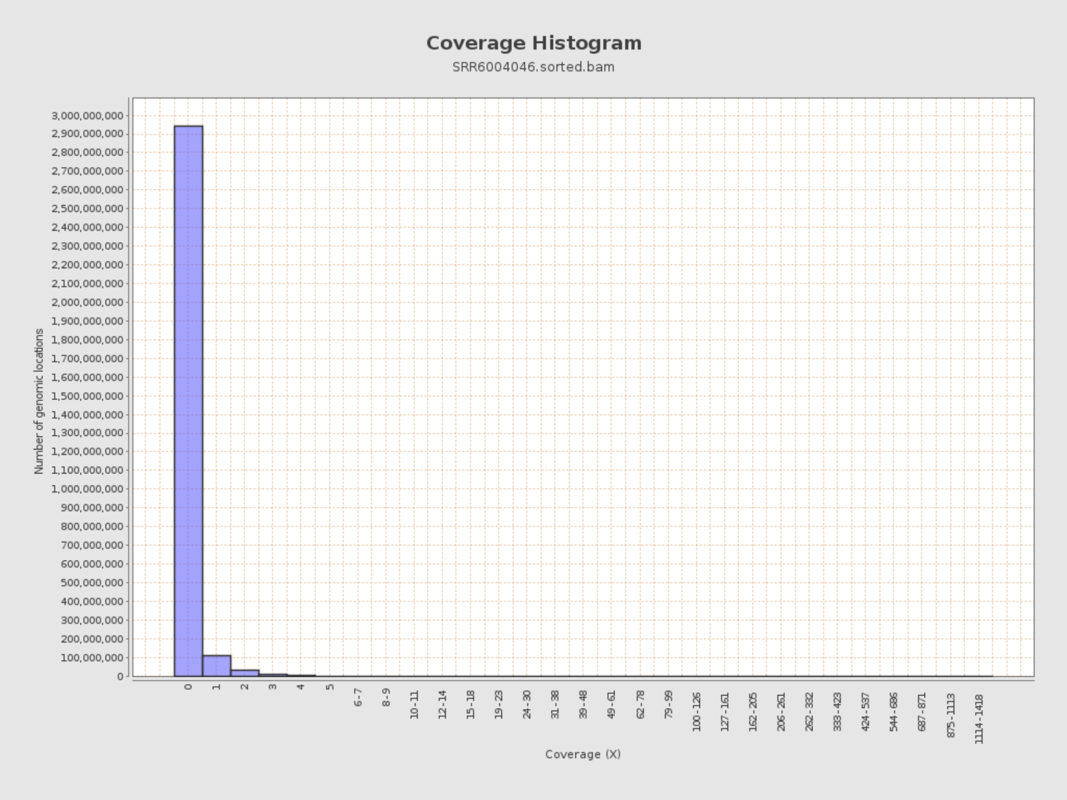
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23637734	0.0948	1.2518
chr2	243199373	12651944	0.052	0.6428
chr3	198022430	10186410	0.0514	0.3046
chr4	191154276	15073690	0.0789	0.406
chr5	180915260	15979536	0.0883	0.4046
chr6	171115067	13114853	0.0766	0.4419
chr7	159138663	13746782	0.0864	0.906

chr8	146364022	11198635	0.0765	0.9005
chr9	141213431	9747048	0.069	0.6847
chr10	135534747	7992285	0.059	0.5107
chr11	135006516	6136201	0.0455	0.4541
chr12	133851895	9201403	0.0687	0.369
chr13	115169878	8734193	0.0758	0.37
chr14	107349540	7108415	0.0662	0.4217
chr15	102531392	5571067	0.0543	0.3187
chr16	90354753	5533911	0.0612	0.4227
chr17	81195210	3936651	0.0485	0.3461
chr18	78077248	6903306	0.0884	1.3905
chr19	59128983	3069970	0.0519	0.8632
chr20	63025520	3032871	0.0481	0.3294
chr21	48129895	2861267	0.0594	0.3811
chr22	51304566	2550564	0.0497	0.2934
chrMT	16571	11399	0.6879	1.1513
chrX	155270560	17951238	0.1156	0.5479
chrY	59373566	697700	0.0118	0.233

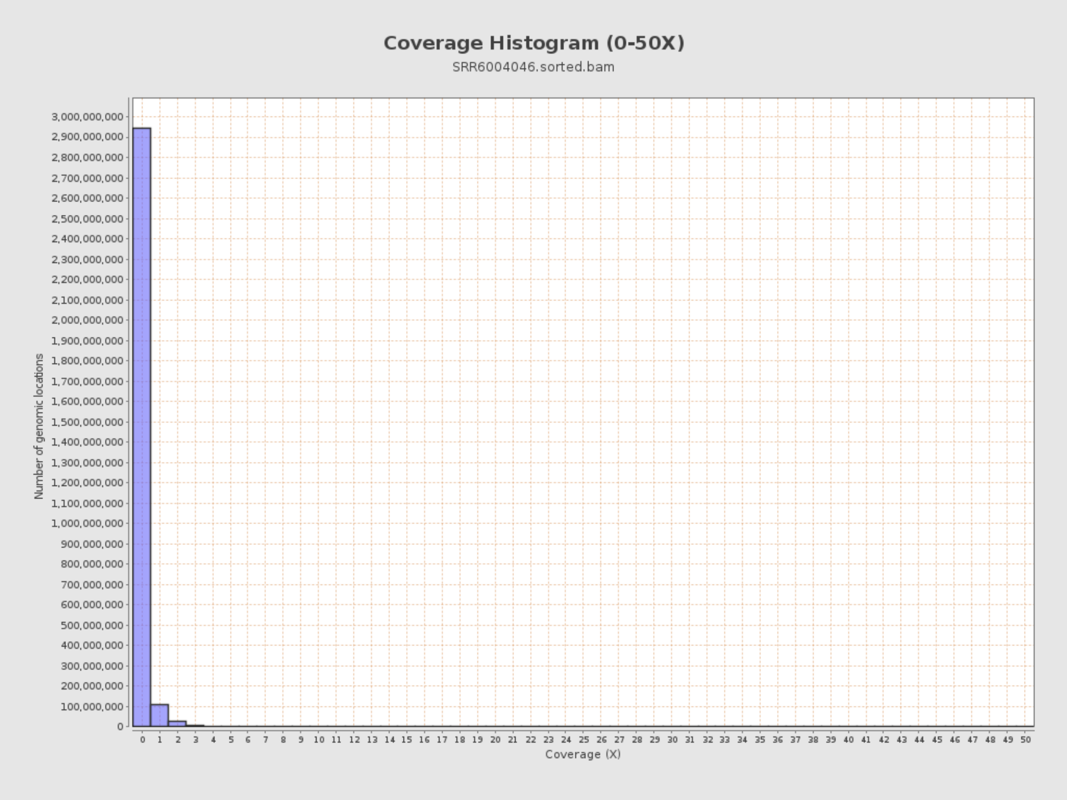
3. Results : Coverage across reference



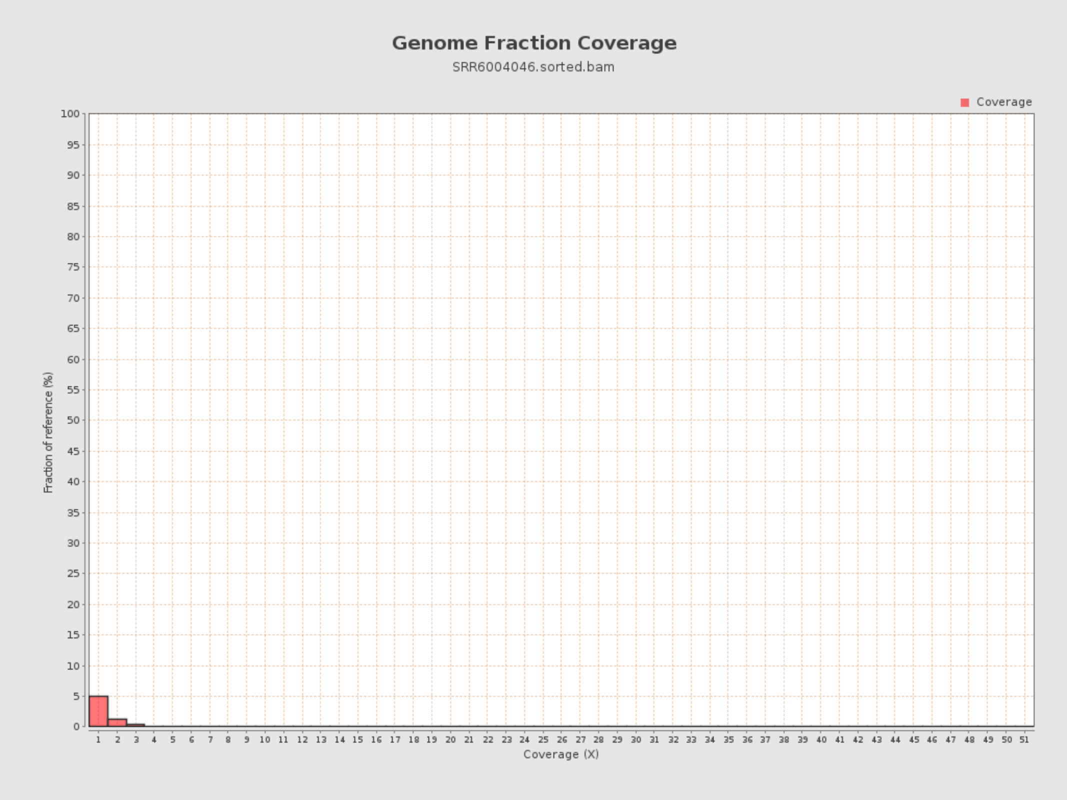
4. Results : Coverage Histogram



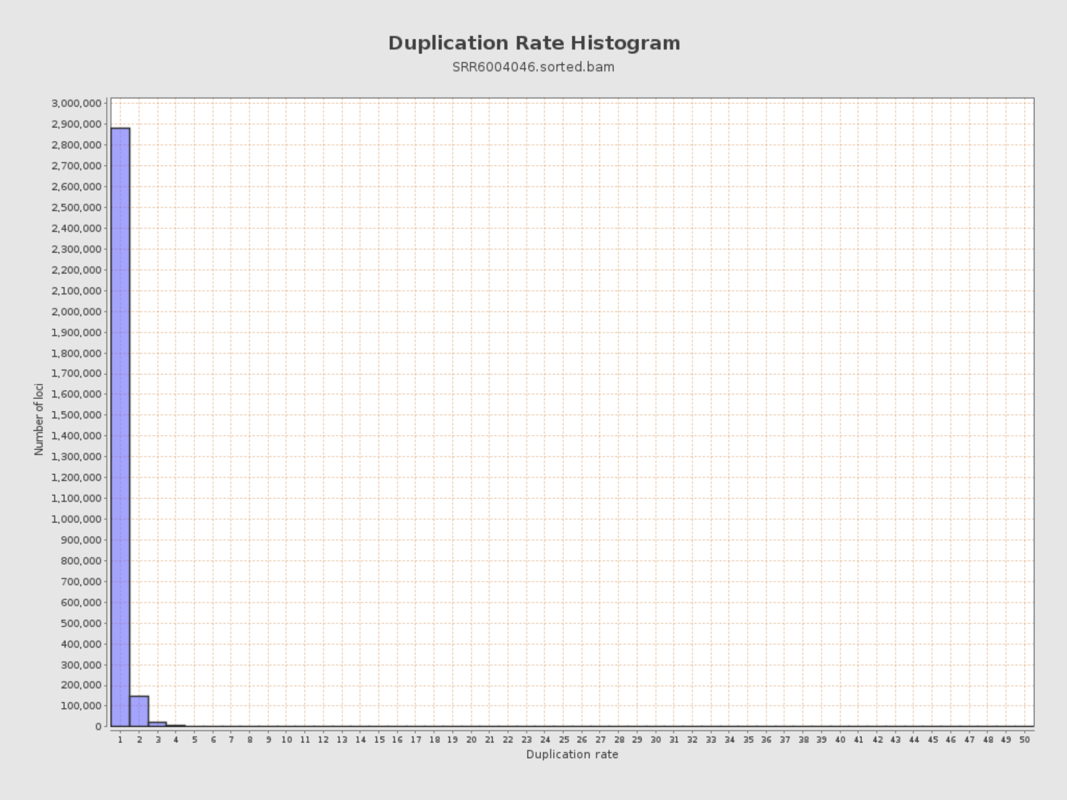
5. Results : Coverage Histogram (0-50X)



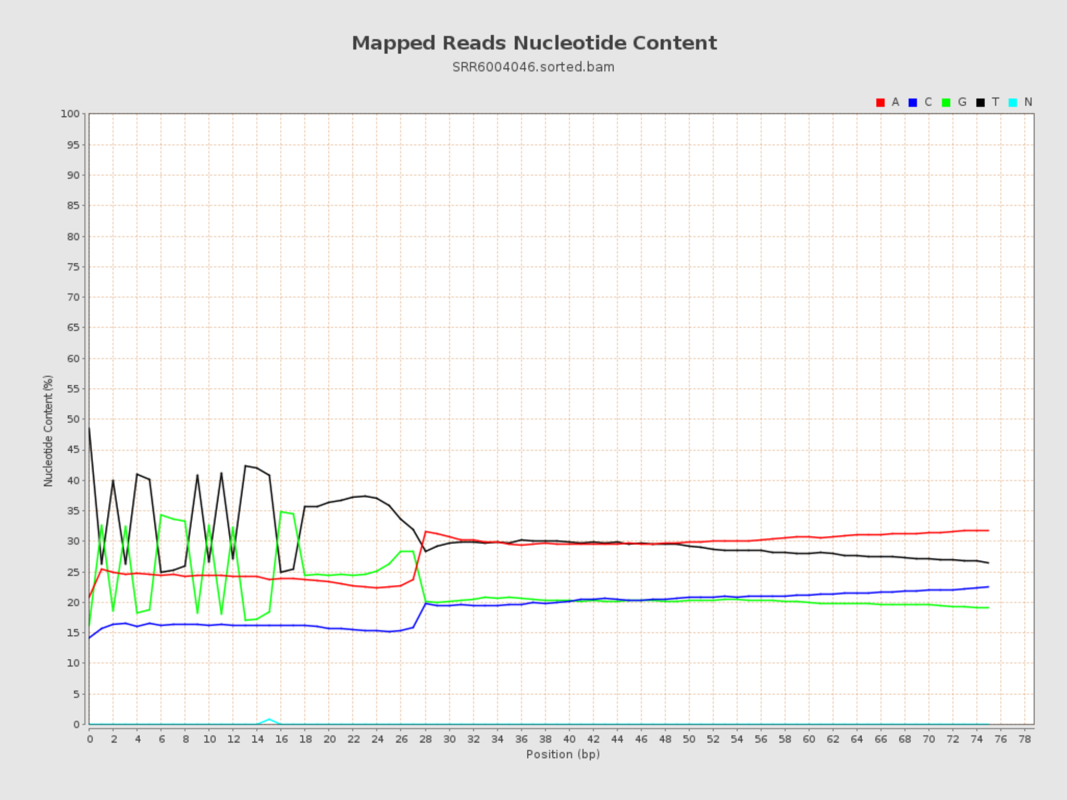
6. Results : Genome Fraction Coverage



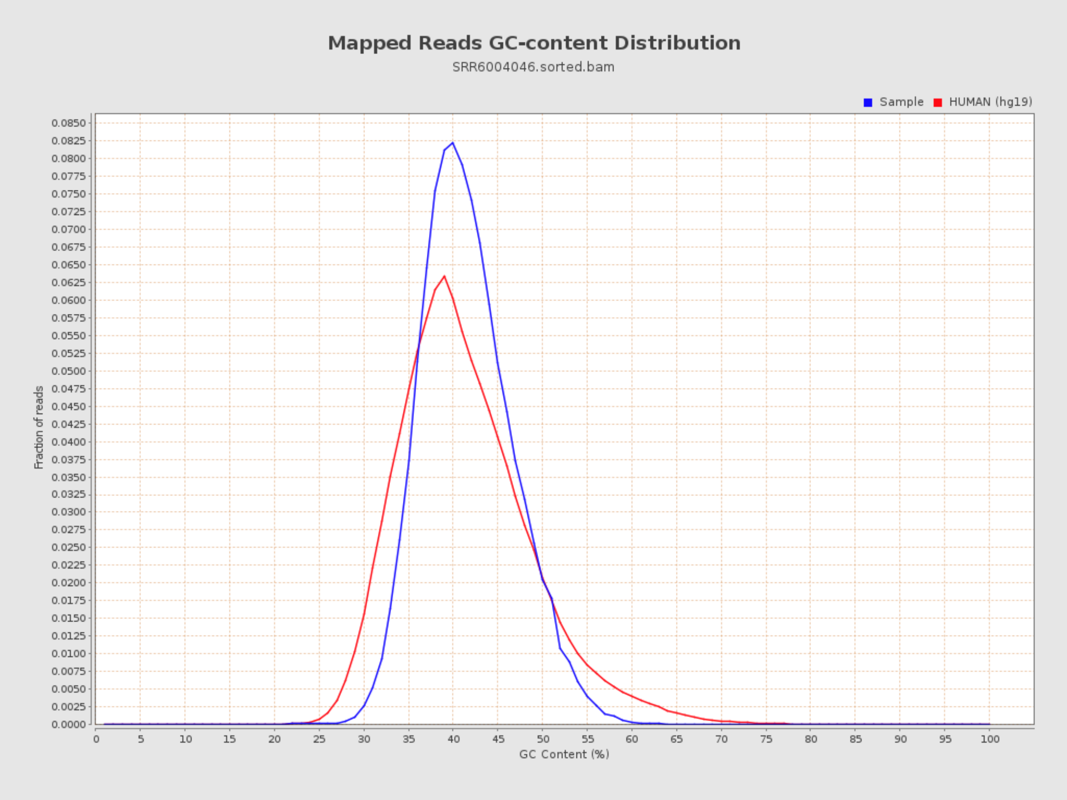
7. Results : Duplication Rate Histogram



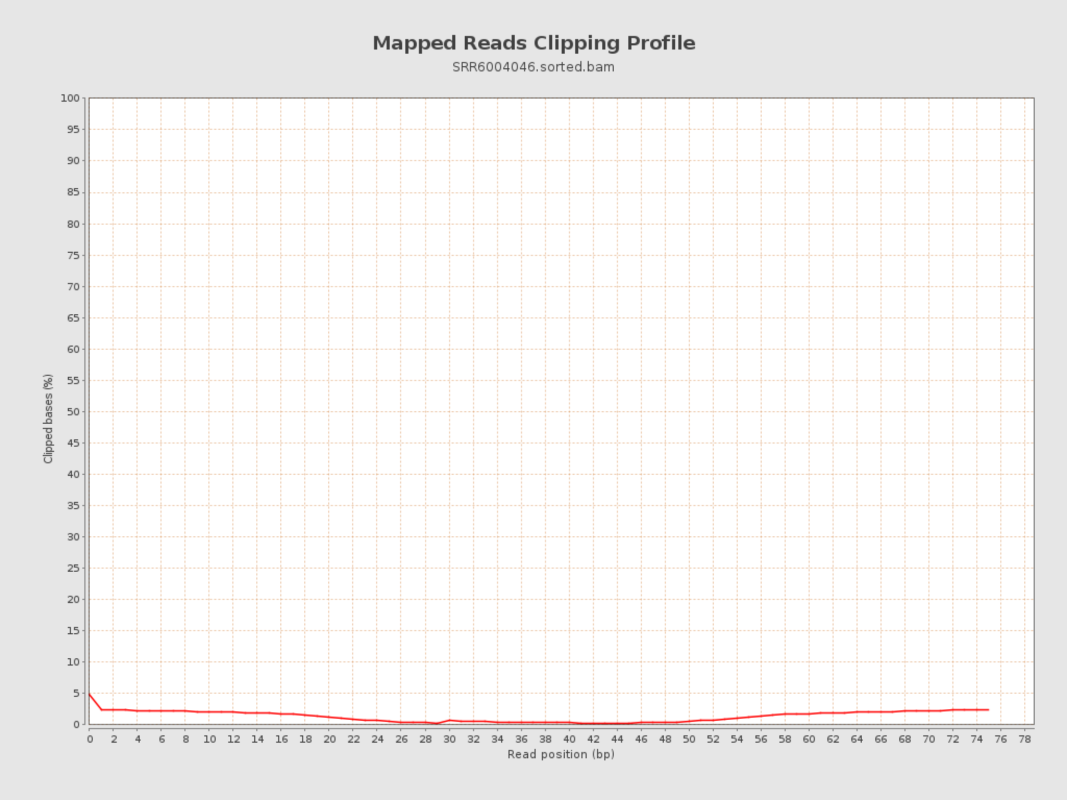
8. Results : Mapped Reads Nucleotide Content



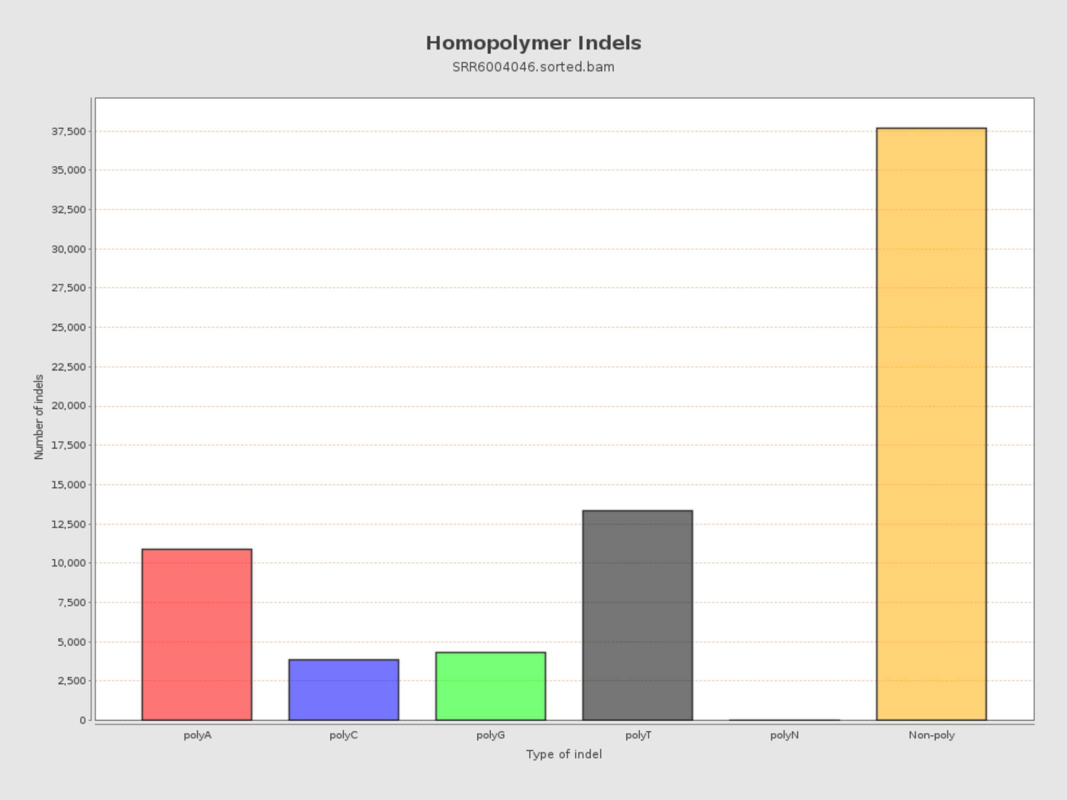
9. Results : Mapped Reads GC-content Distribution



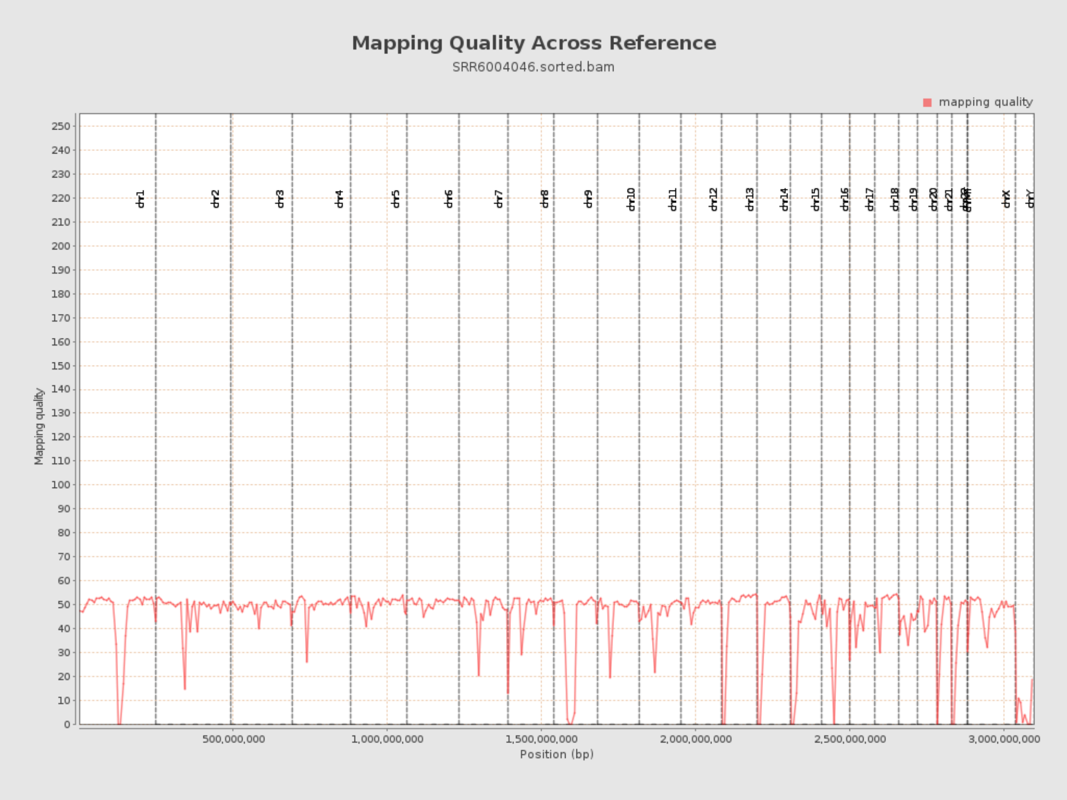
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram