Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:11:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004003.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_SRR6004003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004003.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:11:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,856,389
Mapped reads	2,116,037 / 74.08%
Unmapped reads	740,352 / 25.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,728 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	179,912 / 6.3%
Duplication rate	6.92%
Clipped reads	1,109,676 / 38.85%

2.2. ACGT Content

Number/percentage of A's	37,531,324 / 27.3%
Number/percentage of C's	24,213,743 / 17.61%
Number/percentage of T's	45,653,553 / 33.21%
Number/percentage of G's	30,046,078 / 21.86%
Number/percentage of N's	17,744 / 0.01%
GC Percentage	39.47%

2.3. Coverage

Mean	0.0444

Standard Deviation	0.4244

2.4. Mapping Quality

Mean Mapping Quality	46.36

2.5. Mismatches and indels

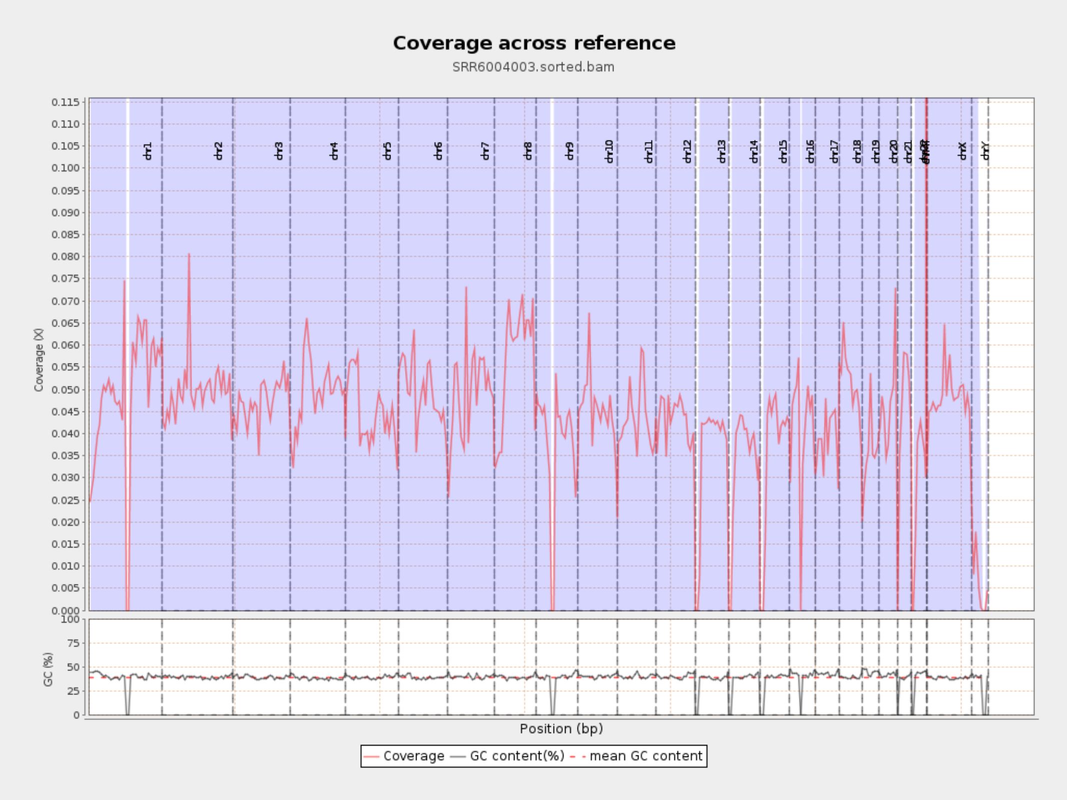
General error rate	1.08%
Mismatches	1,464,629
Insertions	12,427
Mapped reads with at least one insertion	0.58%
Deletions	45,915
Mapped reads with at least one deletion	2.14%
Homopolymer indels	49.57%

2.6. Chromosome stats

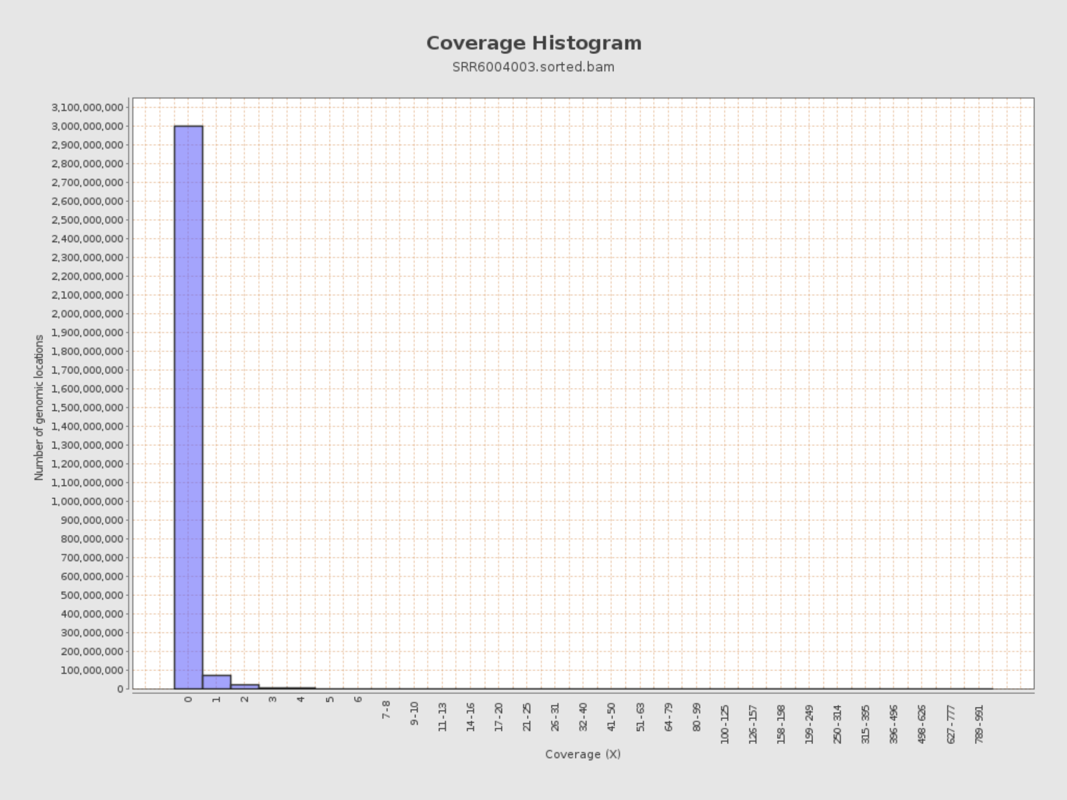
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12135548	0.0487	0.6923
chr2	243199373	12106465	0.0498	0.4937
chr3	198022430	9359345	0.0473	0.2938
chr4	191154276	9458842	0.0495	0.3124
chr5	180915260	8127460	0.0449	0.2873
chr6	171115067	8485232	0.0496	0.3424
chr7	159138663	7908175	0.0497	0.5542

chr8	146364022	8255124	0.0564	0.6805
chr9	141213431	5237674	0.0371	0.3878
chr10	135534747	6244257	0.0461	0.37
chr11	135006516	5834362	0.0432	0.386
chr12	133851895	5756099	0.043	0.2862
chr13	115169878	4006881	0.0348	0.254
chr14	107349540	3539578	0.033	0.26
chr15	102531392	3659656	0.0357	0.2569
chr16	90354753	3720170	0.0412	0.2883
chr17	81195210	3136870	0.0386	0.2852
chr18	78077248	4059943	0.052	0.7383
chr19	59128983	2137855	0.0362	0.4584
chr20	63025520	2951961	0.0468	0.2954
chr21	48129895	2130491	0.0443	0.2991
chr22	51304566	1382457	0.0269	0.2134
chrMT	16571	90864	5.4833	4.6198
chrX	155270560	7455950	0.048	0.3187
chrY	59373566	354647	0.006	0.1284

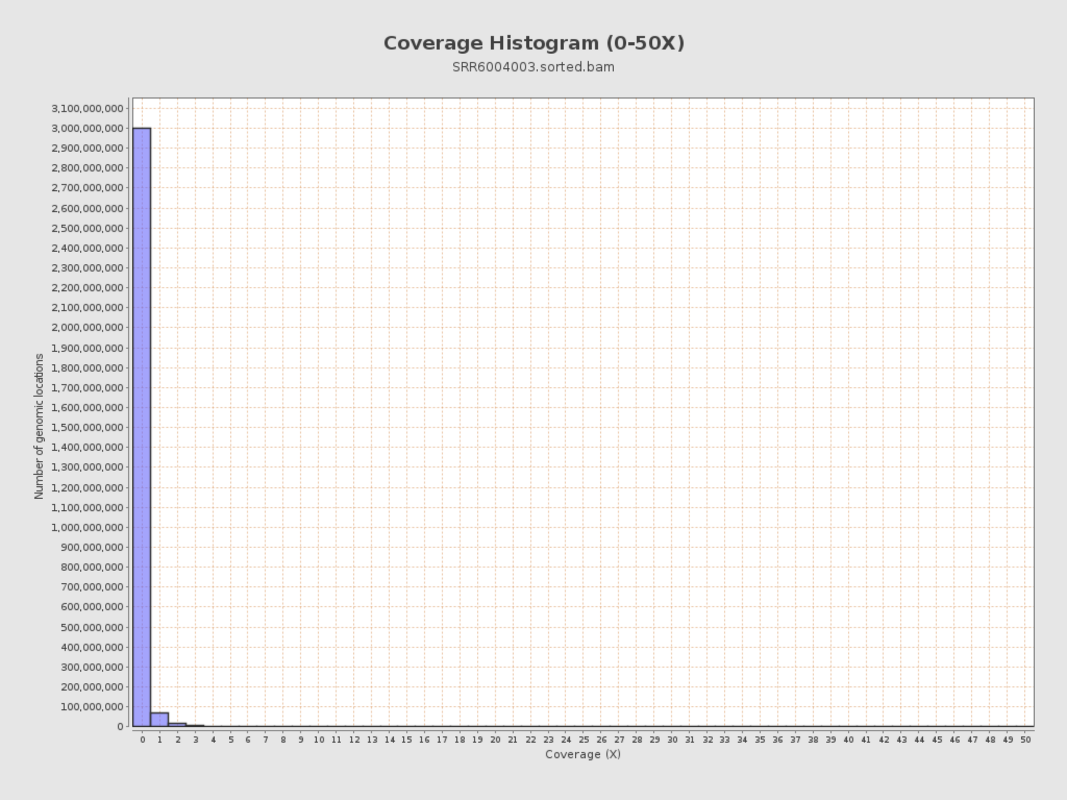
3. Results : Coverage across reference



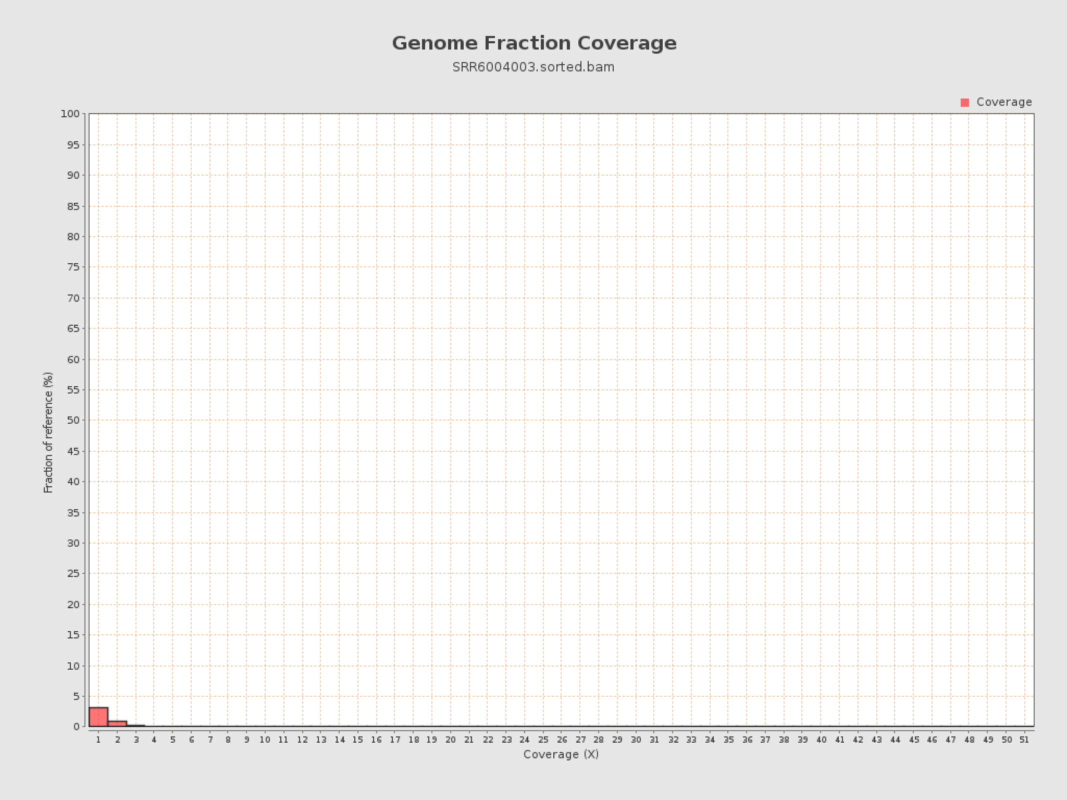
4. Results : Coverage Histogram



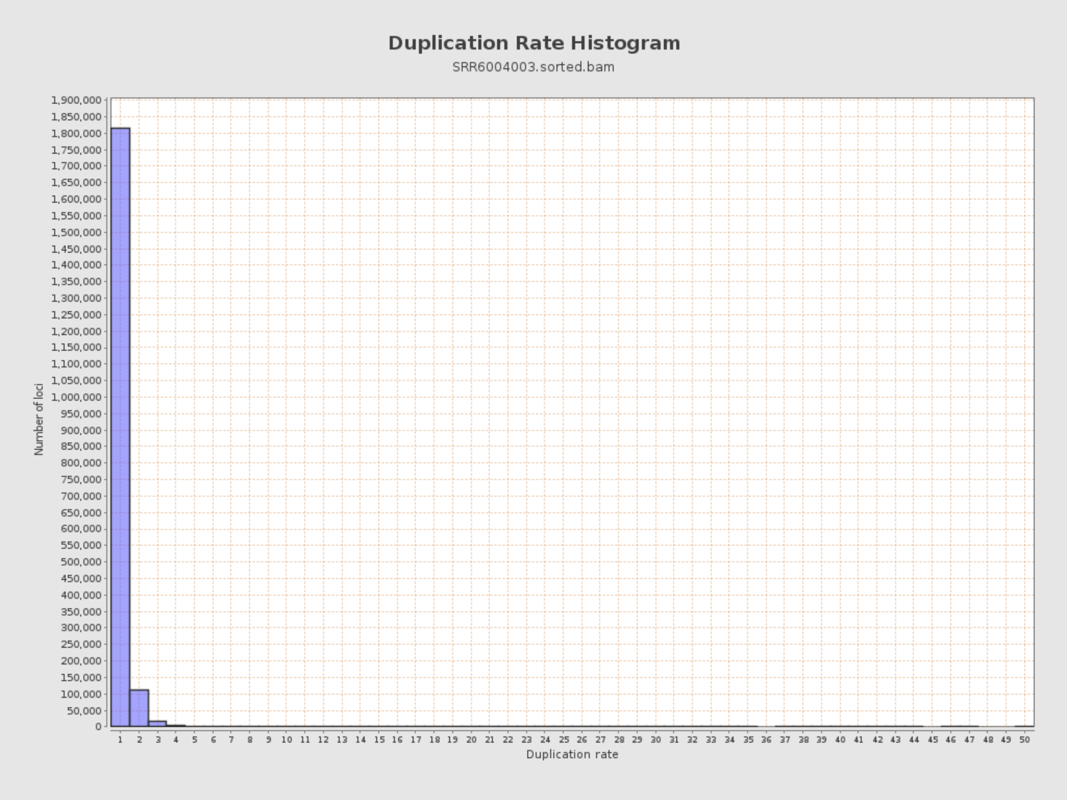
5. Results : Coverage Histogram (0-50X)



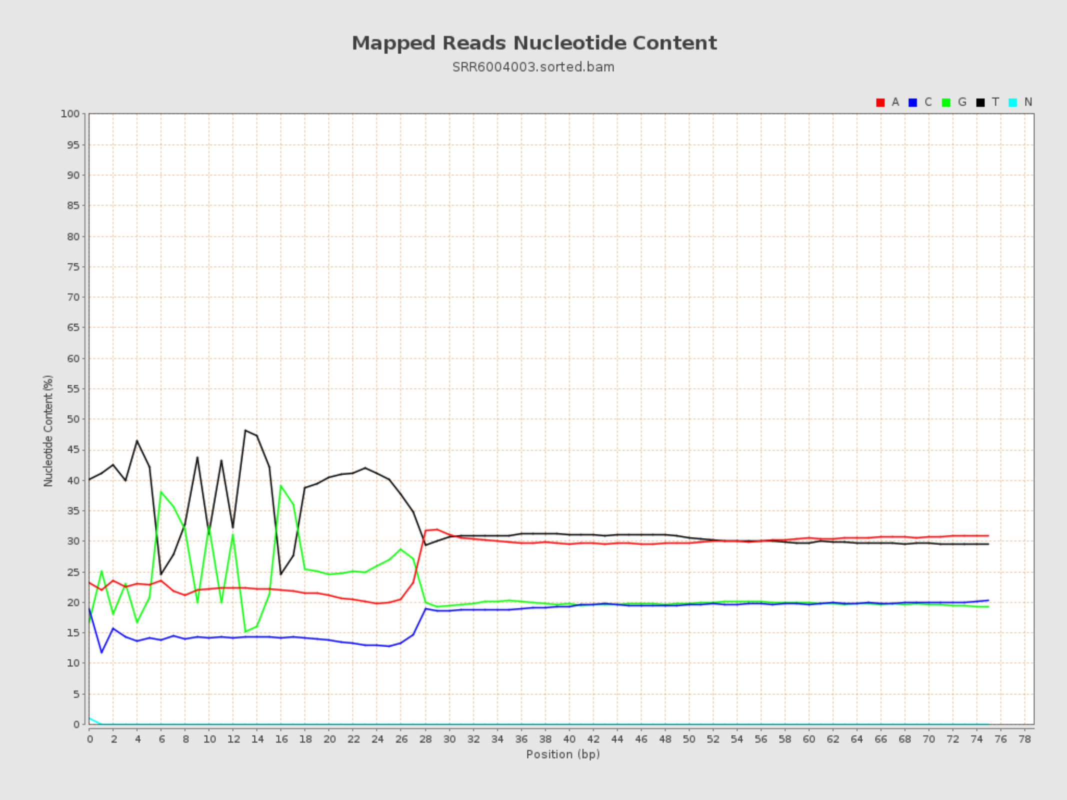
6. Results : Genome Fraction Coverage



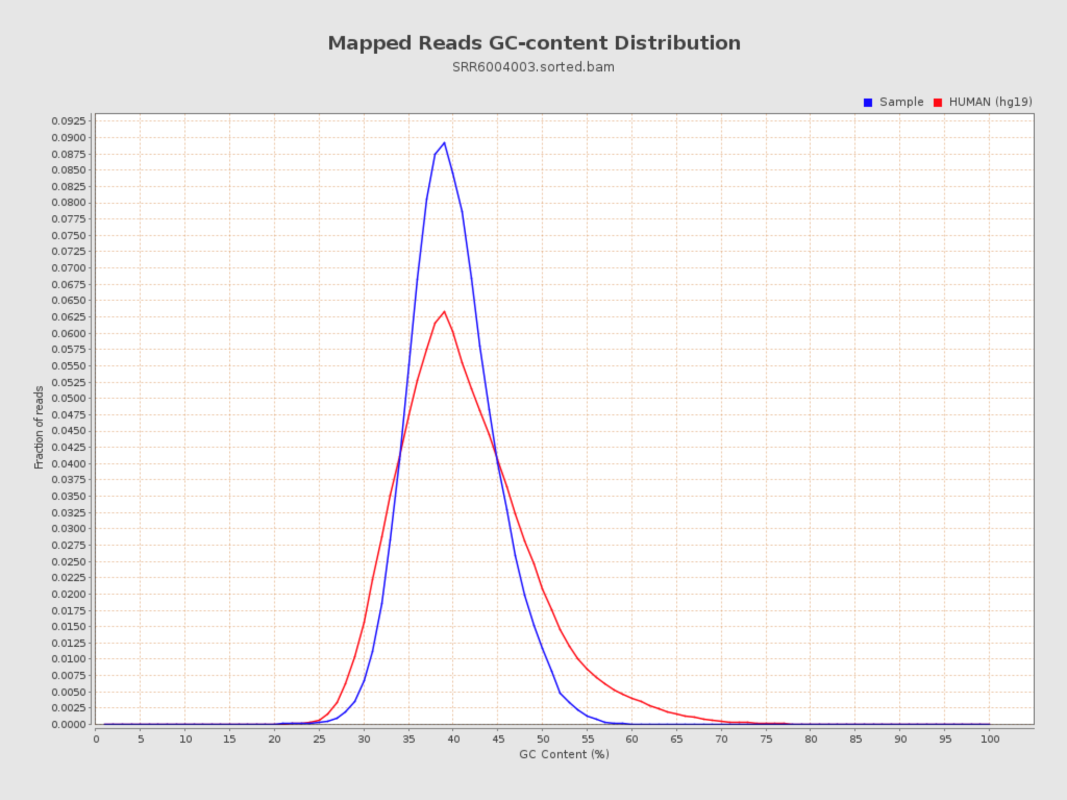
7. Results : Duplication Rate Histogram



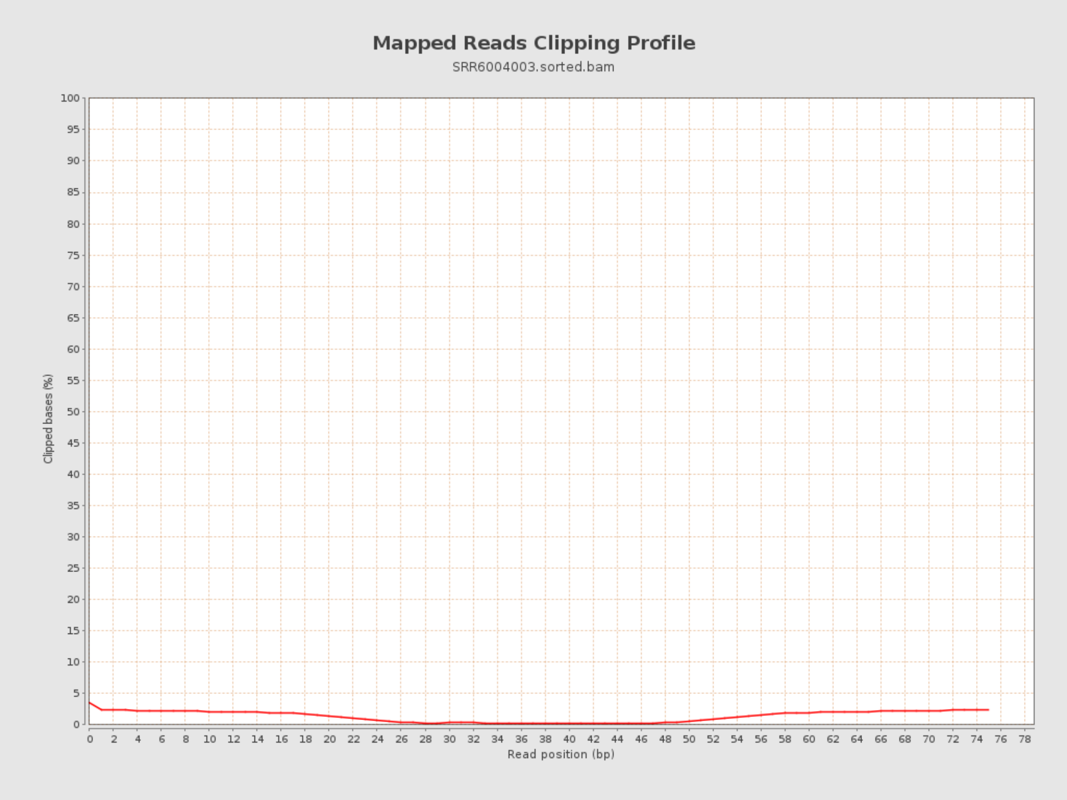
8. Results : Mapped Reads Nucleotide Content



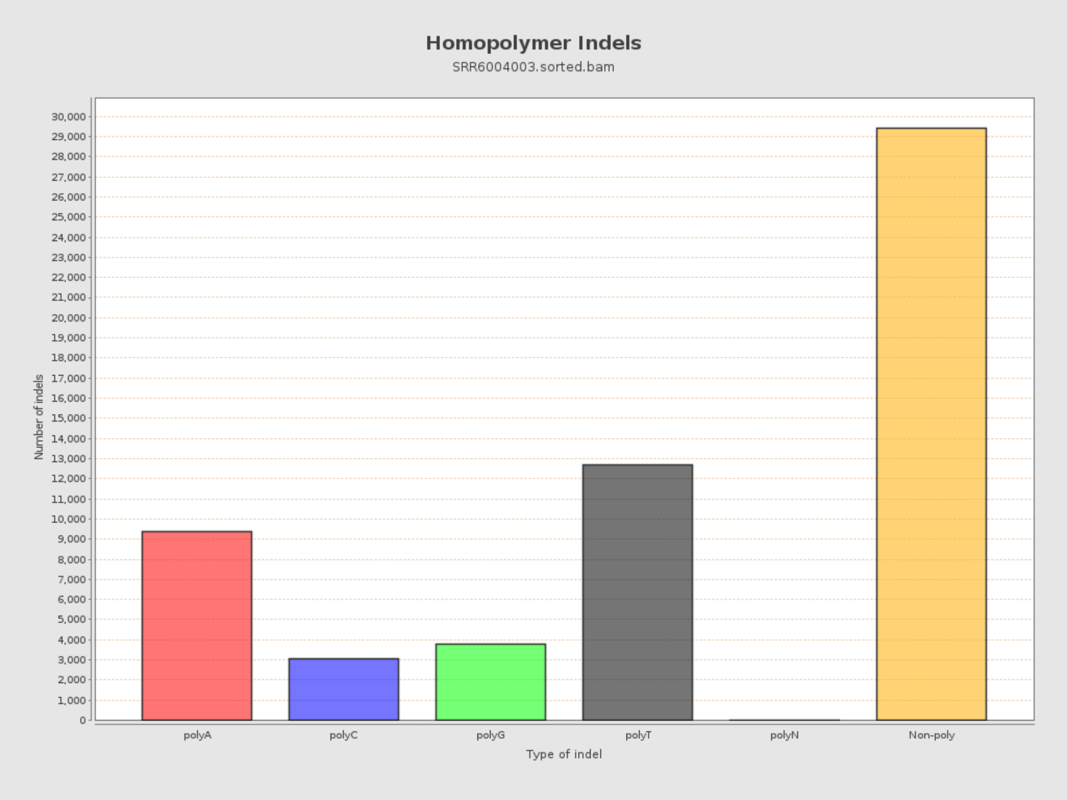
9. Results : Mapped Reads GC-content Distribution



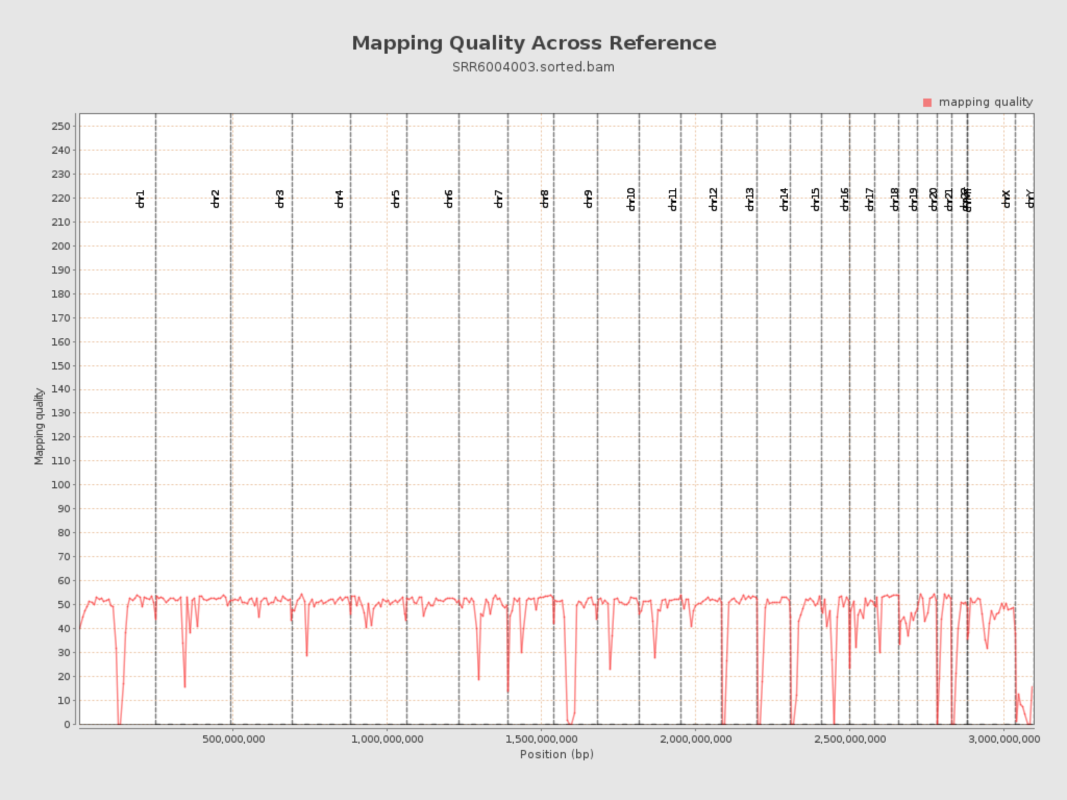
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram