Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:38:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236101.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_SRR6236101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:38:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,217,878
Mapped reads	1,697,662 / 76.54%
Unmapped reads	520,216 / 23.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,046 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	50,997 / 2.3%
Duplication rate	1.86%
Clipped reads	888,763 / 40.07%

2.2. ACGT Content

Number/percentage of A's	31,810,669 / 28.98%
Number/percentage of C's	20,423,882 / 18.61%
Number/percentage of T's	32,821,892 / 29.9%
Number/percentage of G's	24,703,834 / 22.51%
Number/percentage of N's	962 / 0%
GC Percentage	41.11%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.3743

2.4. Mapping Quality

Mean Mapping Quality	44.24

2.5. Mismatches and indels

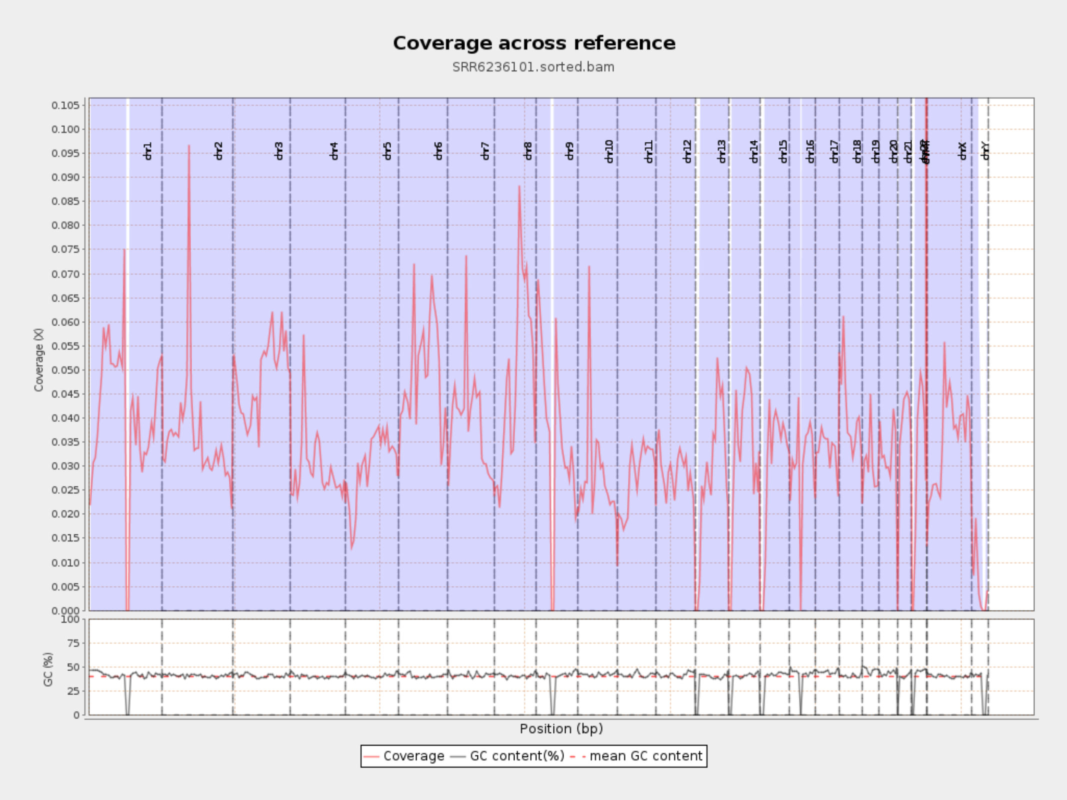
General error rate	0.85%
Mismatches	911,627
Insertions	8,825
Mapped reads with at least one insertion	0.51%
Deletions	27,819
Mapped reads with at least one deletion	1.62%
Homopolymer indels	45.47%

2.6. Chromosome stats

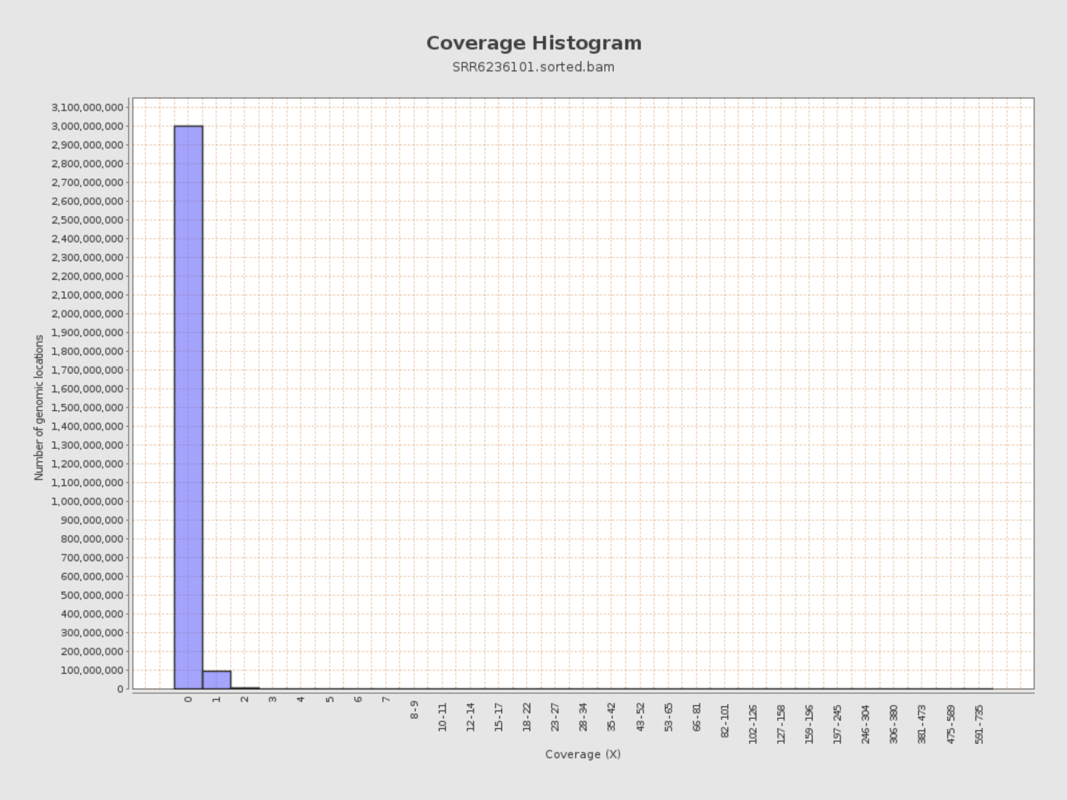
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10262758	0.0412	0.6451
chr2	243199373	8868996	0.0365	0.4573
chr3	198022430	9675617	0.0489	0.237
chr4	191154276	5636175	0.0295	0.2203
chr5	180915260	5462202	0.0302	0.1886
chr6	171115067	8396098	0.0491	0.3182
chr7	159138663	6323223	0.0397	0.4845

chr8	146364022	7063159	0.0483	0.5086
chr9	141213431	5188457	0.0367	0.3988
chr10	135534747	3846458	0.0284	0.3791
chr11	135006516	3717555	0.0275	0.2767
chr12	133851895	3862310	0.0289	0.1909
chr13	115169878	3249152	0.0282	0.1779
chr14	107349540	3470805	0.0323	0.2413
chr15	102531392	3047931	0.0297	0.1902
chr16	90354753	2757501	0.0305	0.2438
chr17	81195210	2692827	0.0332	0.2404
chr18	78077248	3240717	0.0415	0.7931
chr19	59128983	1819713	0.0308	0.4397
chr20	63025520	2073559	0.0329	0.2046
chr21	48129895	1769879	0.0368	0.2468
chr22	51304566	1524654	0.0297	0.1832
chrMT	16571	71903	4.3391	3.3089
chrX	155270560	5469872	0.0352	0.2393
chrY	59373566	317118	0.0053	0.1561

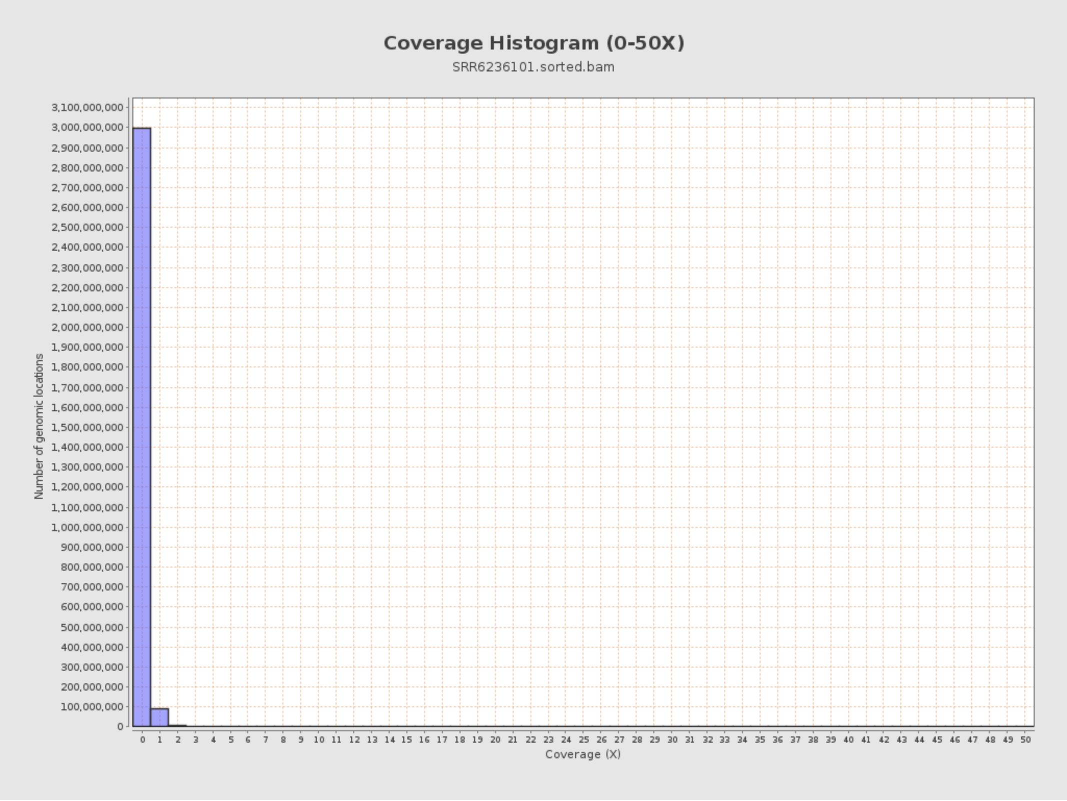
3. Results : Coverage across reference



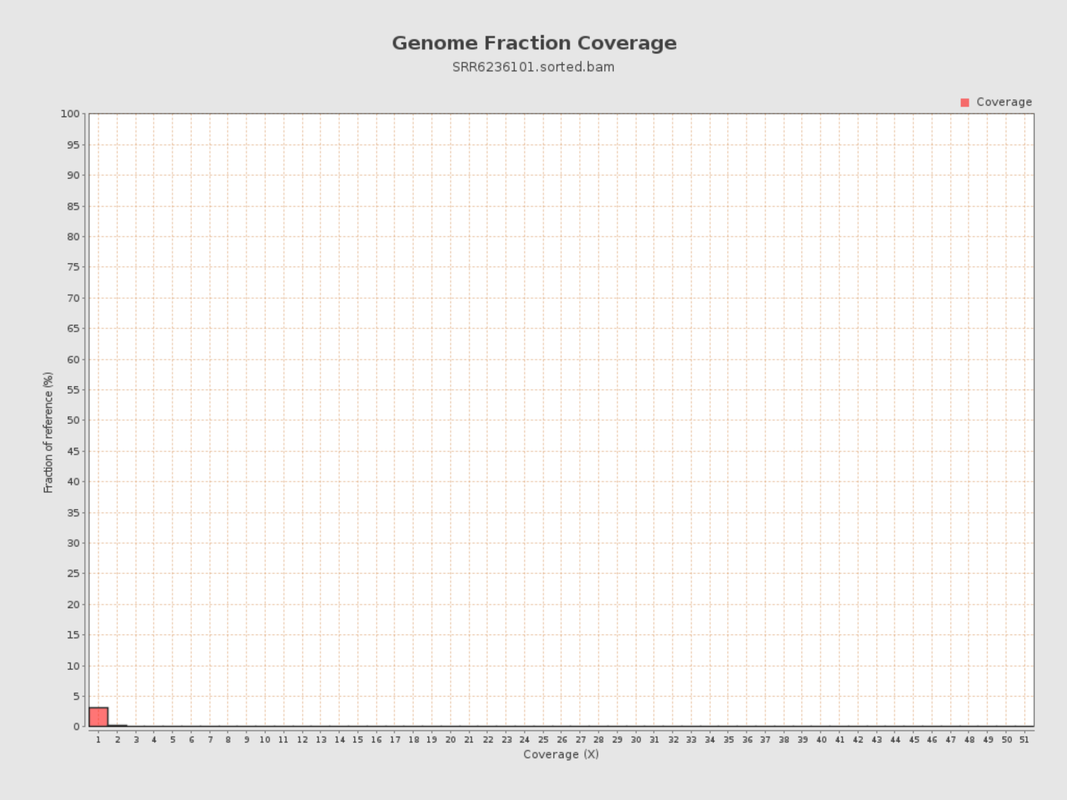
4. Results : Coverage Histogram



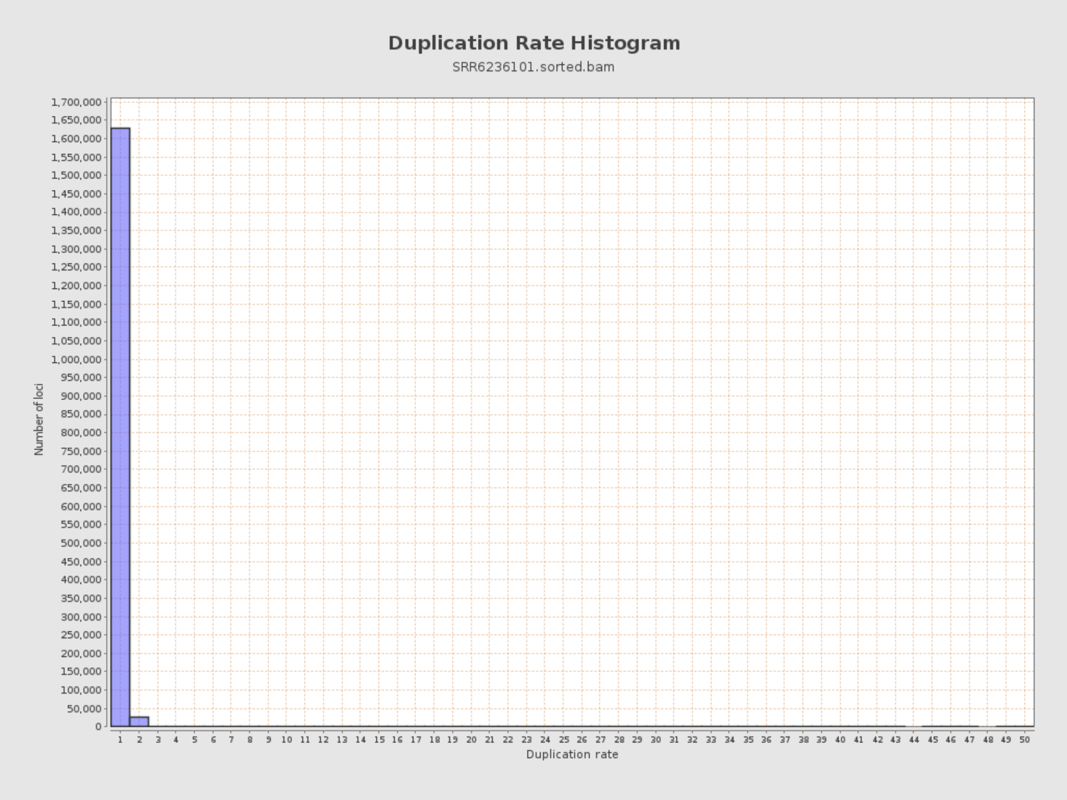
5. Results : Coverage Histogram (0-50X)



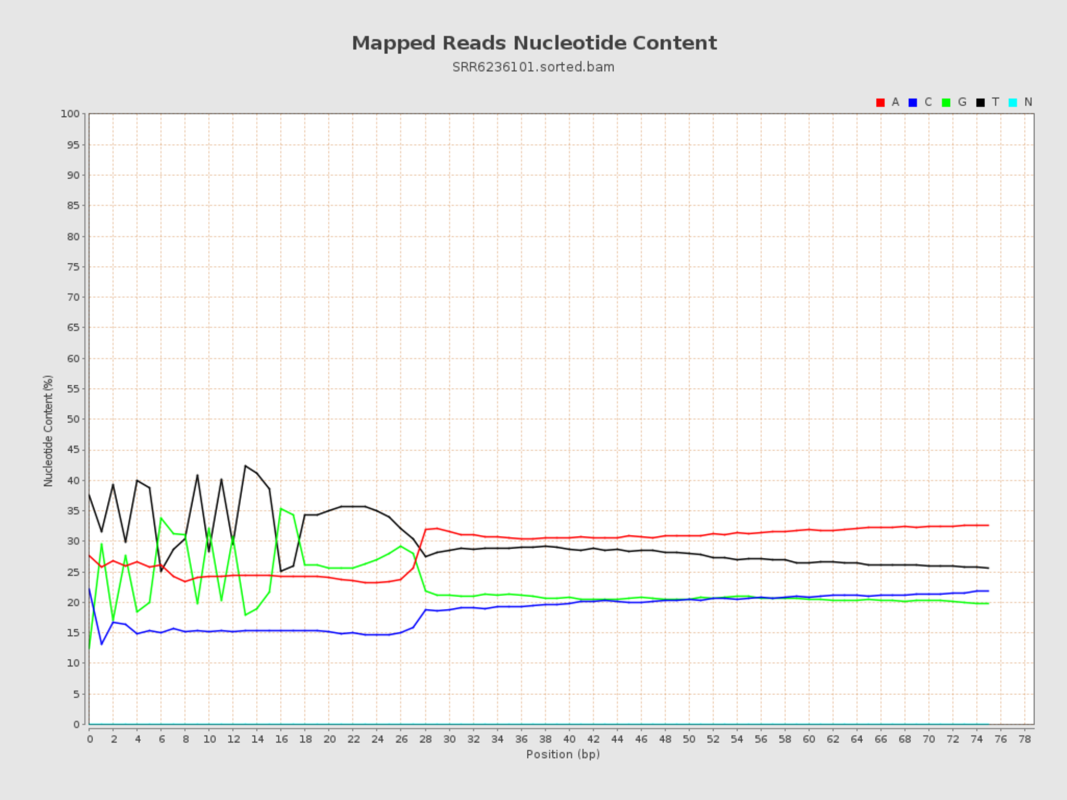
6. Results : Genome Fraction Coverage



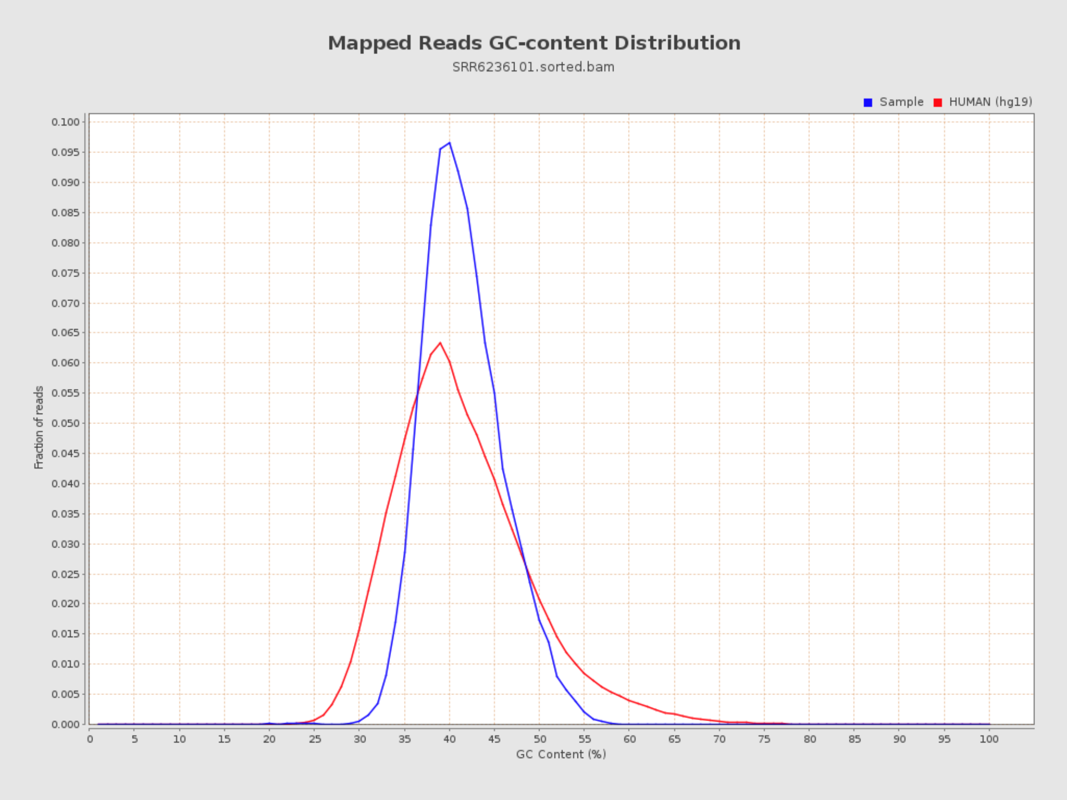
7. Results : Duplication Rate Histogram



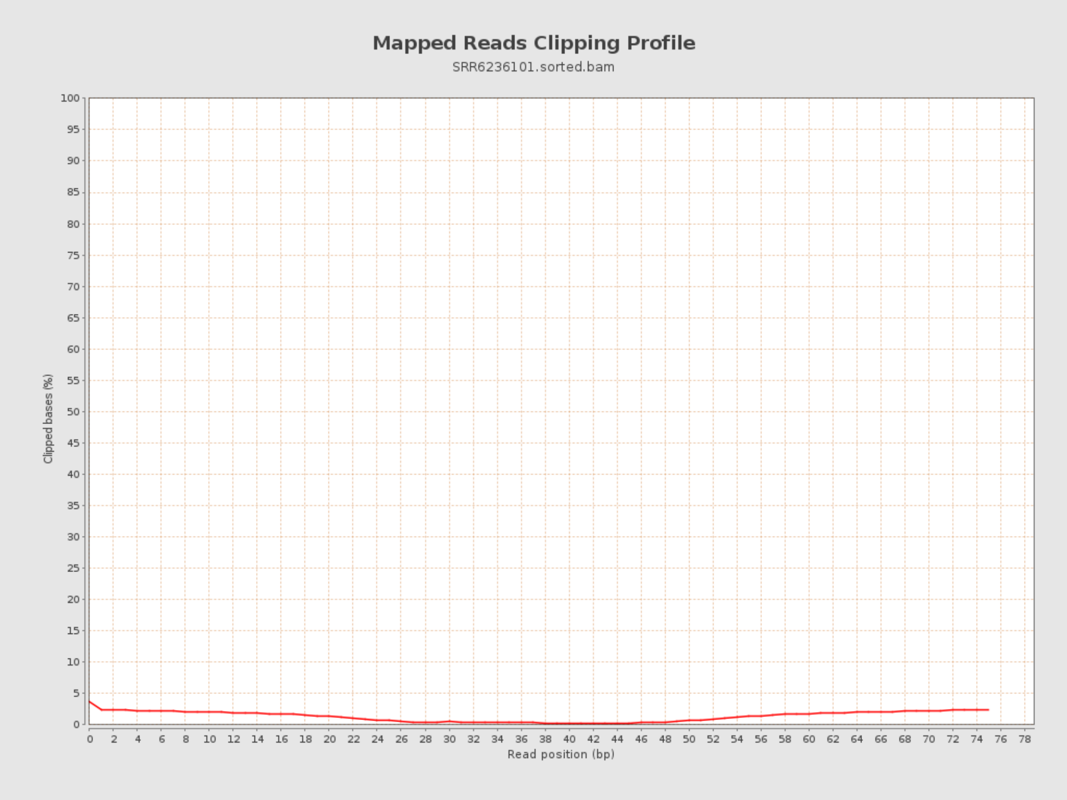
8. Results : Mapped Reads Nucleotide Content



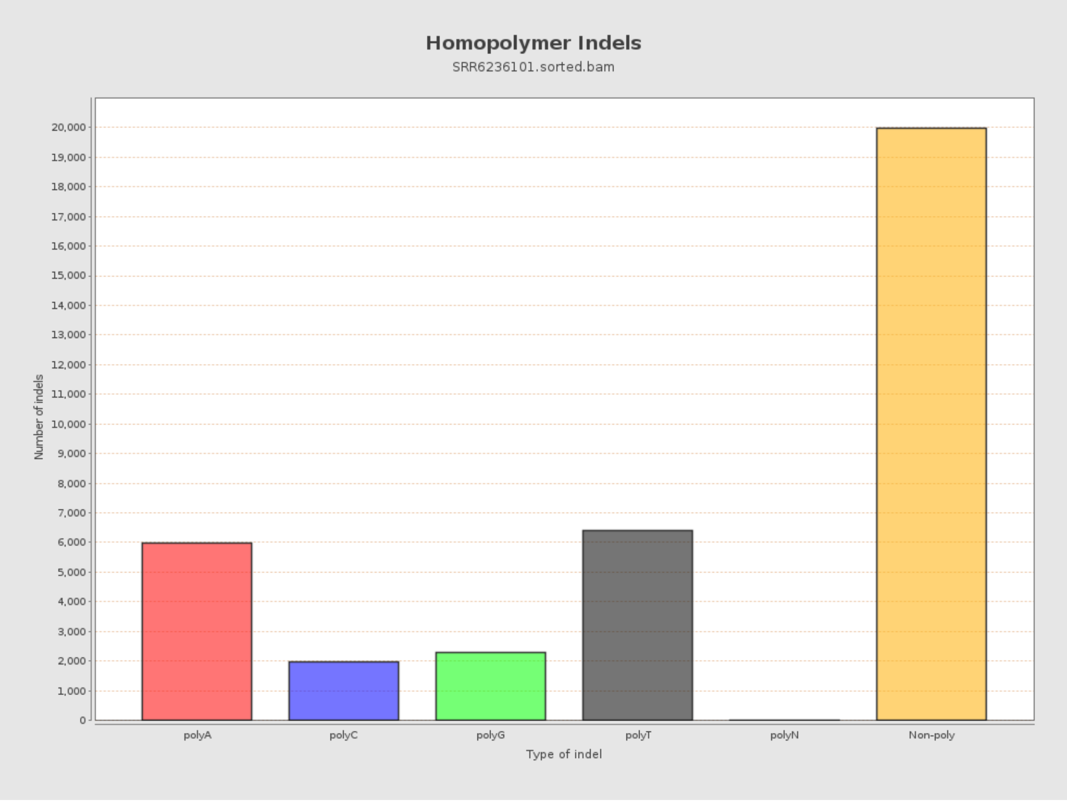
9. Results : Mapped Reads GC-content Distribution



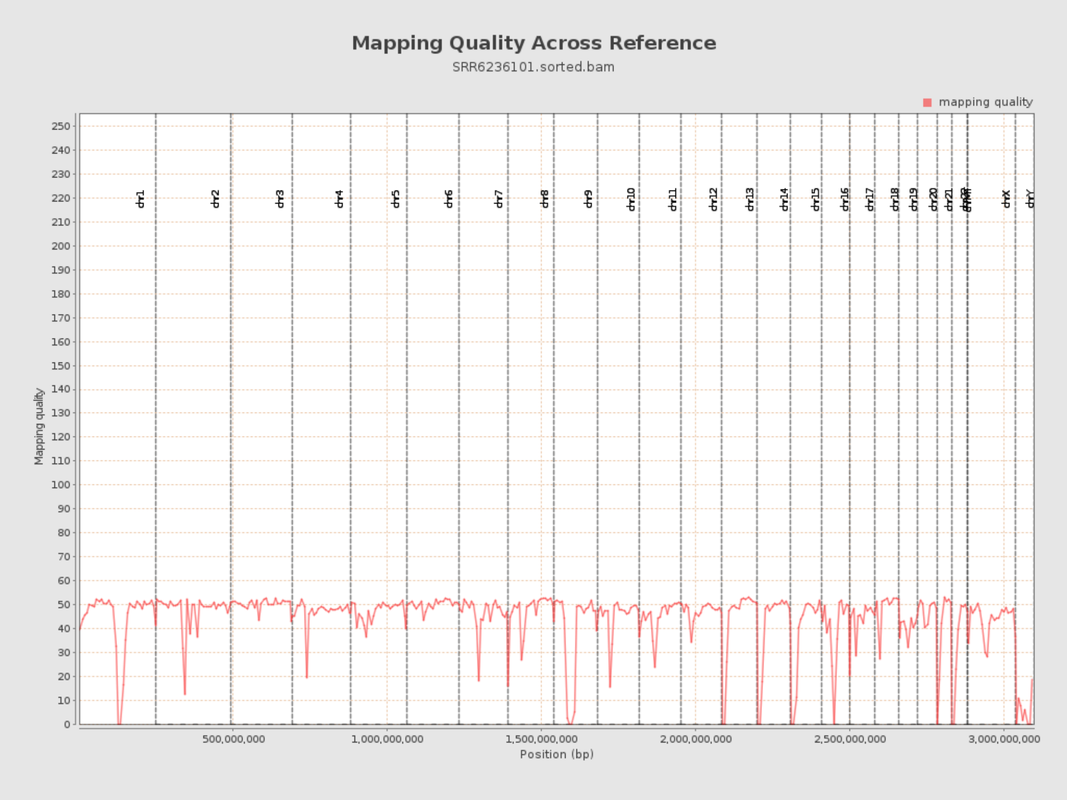
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram