Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 20:46:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236104.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_SRR6236104 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236104.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 20:46:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236104.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,803,012
Mapped reads	2,435,526 / 86.89%
Unmapped reads	367,486 / 13.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,049 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	100,747 / 3.59%
Duplication rate	2.68%
Clipped reads	1,169,769 / 41.73%

2.2. ACGT Content

Number/percentage of A's	45,540,484 / 28.42%
Number/percentage of C's	29,247,314 / 18.25%
Number/percentage of T's	49,834,507 / 31.1%
Number/percentage of G's	35,639,314 / 22.24%
Number/percentage of N's	1,563 / 0%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0518

Standard Deviation	0.573

2.4. Mapping Quality

Mean Mapping Quality	43.89

2.5. Mismatches and indels

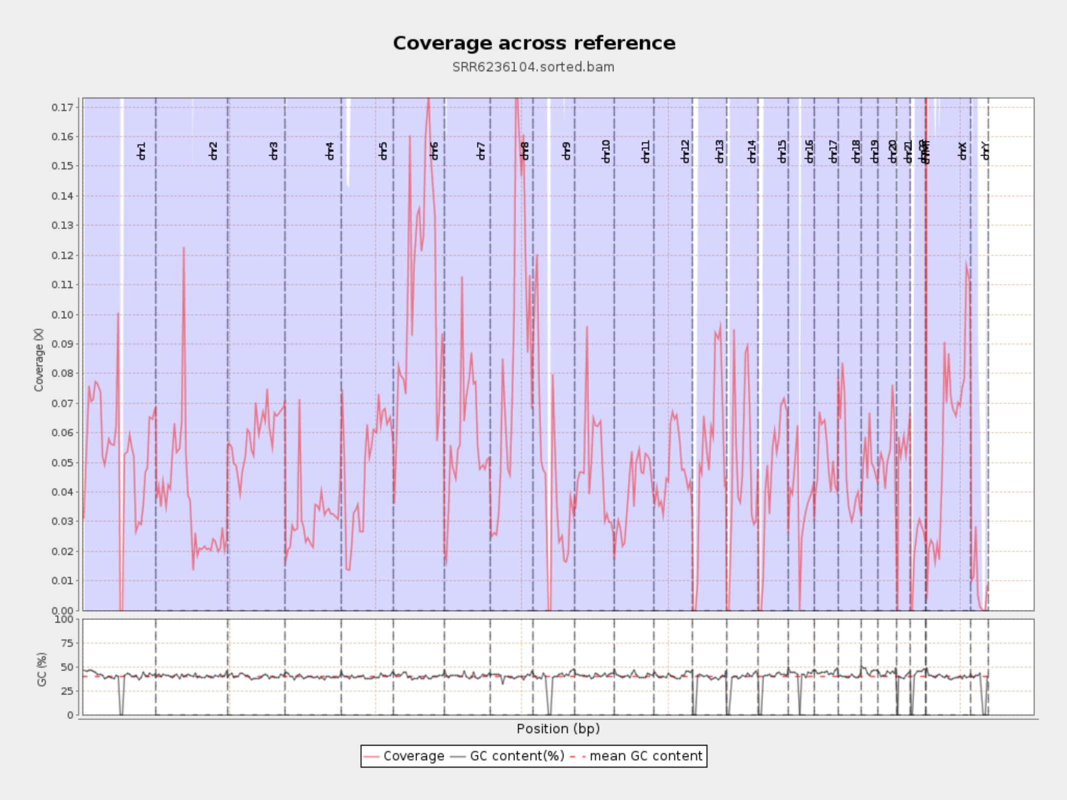
General error rate	0.82%
Mismatches	1,295,400
Insertions	13,043
Mapped reads with at least one insertion	0.53%
Deletions	48,638
Mapped reads with at least one deletion	1.97%
Homopolymer indels	45.57%

2.6. Chromosome stats

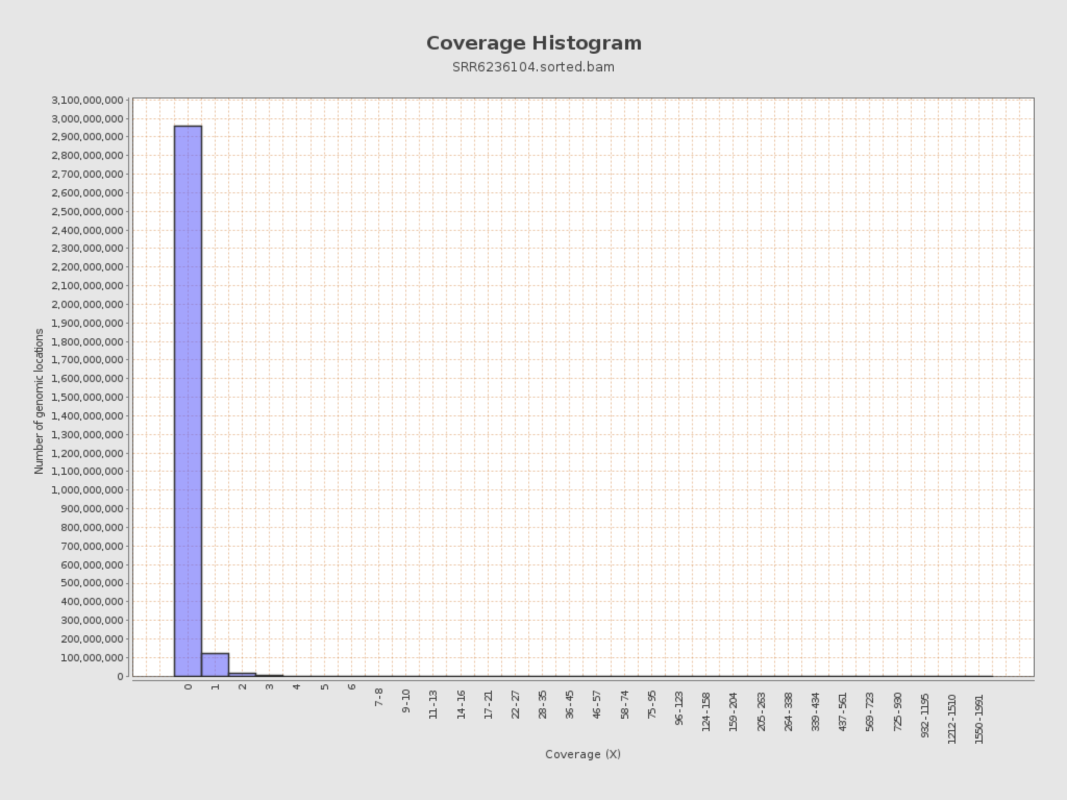
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13342917	0.0535	0.967
chr2	243199373	8868033	0.0365	0.5773
chr3	198022430	11668963	0.0589	0.2714
chr4	191154276	5983763	0.0313	0.273
chr5	180915260	8937000	0.0494	0.2557
chr6	171115067	18648871	0.109	0.5895
chr7	159138663	9222143	0.058	0.7312

chr8	146364022	12510089	0.0855	1.3128
chr9	141213431	6233996	0.0441	0.5233
chr10	135534747	6489792	0.0479	0.5021
chr11	135006516	5444540	0.0403	0.3629
chr12	133851895	6360493	0.0475	0.2629
chr13	115169878	6166772	0.0535	0.2588
chr14	107349540	5037285	0.0469	0.2865
chr15	102531392	4603464	0.0449	0.255
chr16	90354753	3208679	0.0355	0.2937
chr17	81195210	4132854	0.0509	0.329
chr18	78077248	3873630	0.0496	0.9364
chr19	59128983	2985035	0.0505	0.6511
chr20	63025520	3396658	0.0539	0.2761
chr21	48129895	2501479	0.052	0.3192
chr22	51304566	1072302	0.0209	0.1594
chrMT	16571	53538	3.2308	2.7722
chrX	155270560	9129590	0.0588	0.3235
chrY	59373566	475867	0.008	0.2301

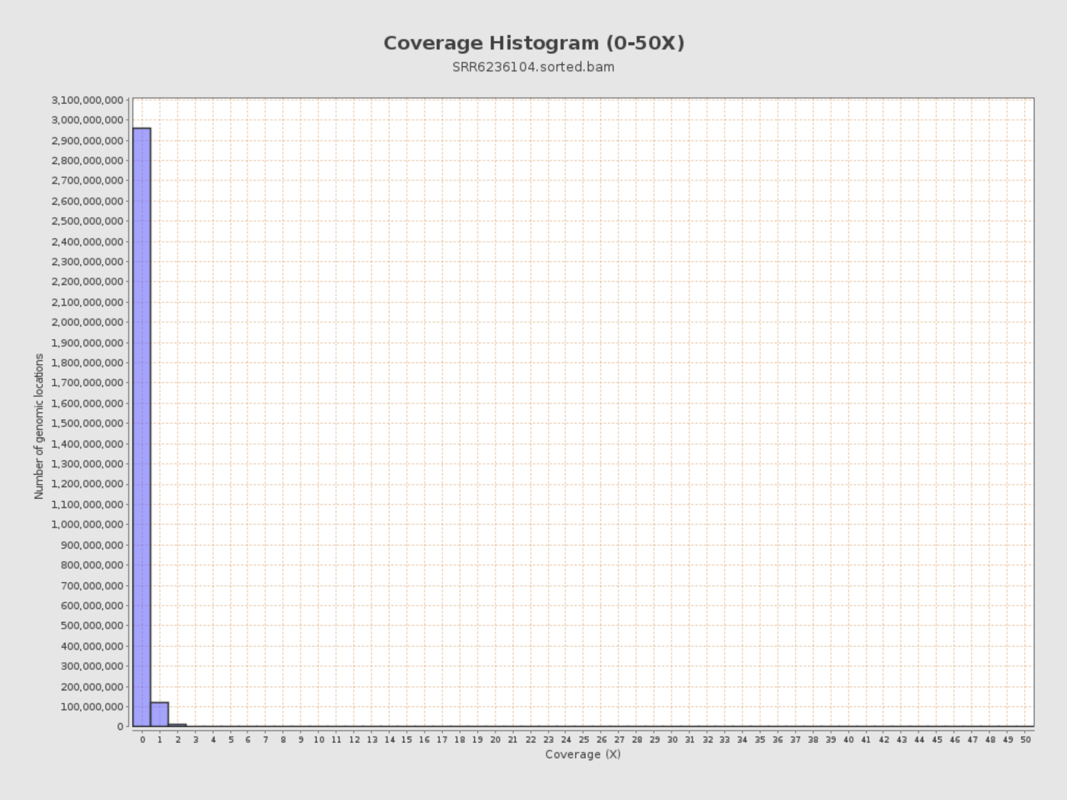
3. Results : Coverage across reference



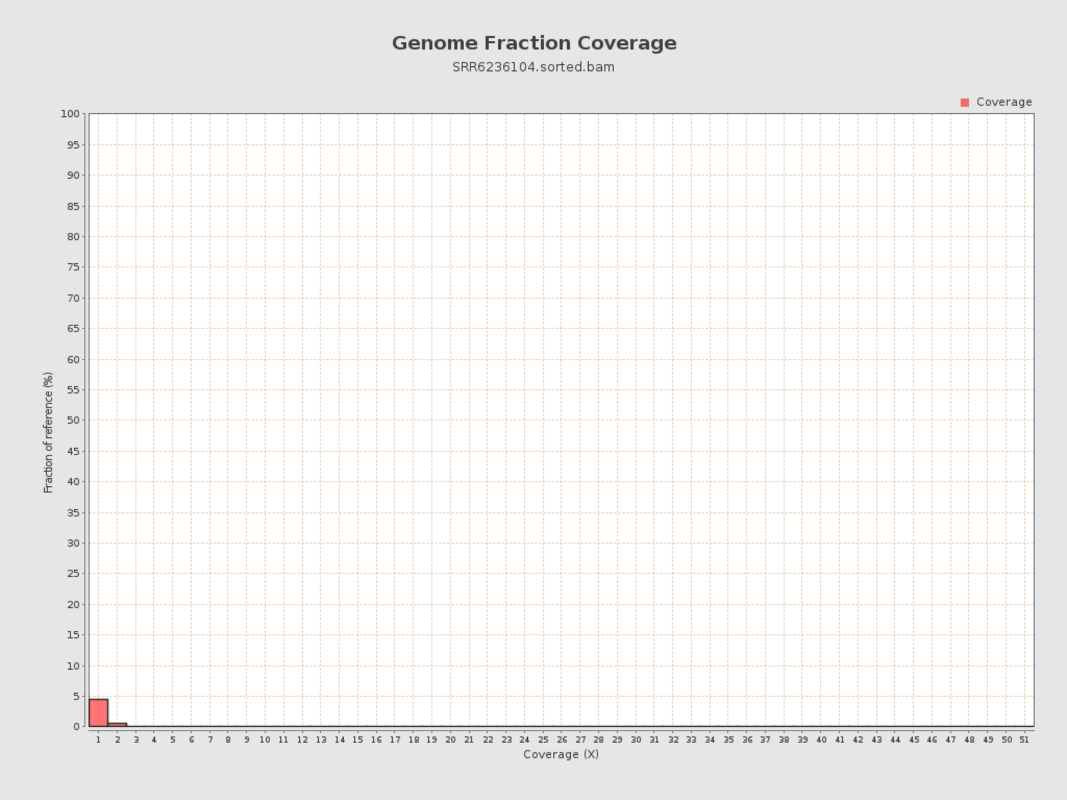
4. Results : Coverage Histogram



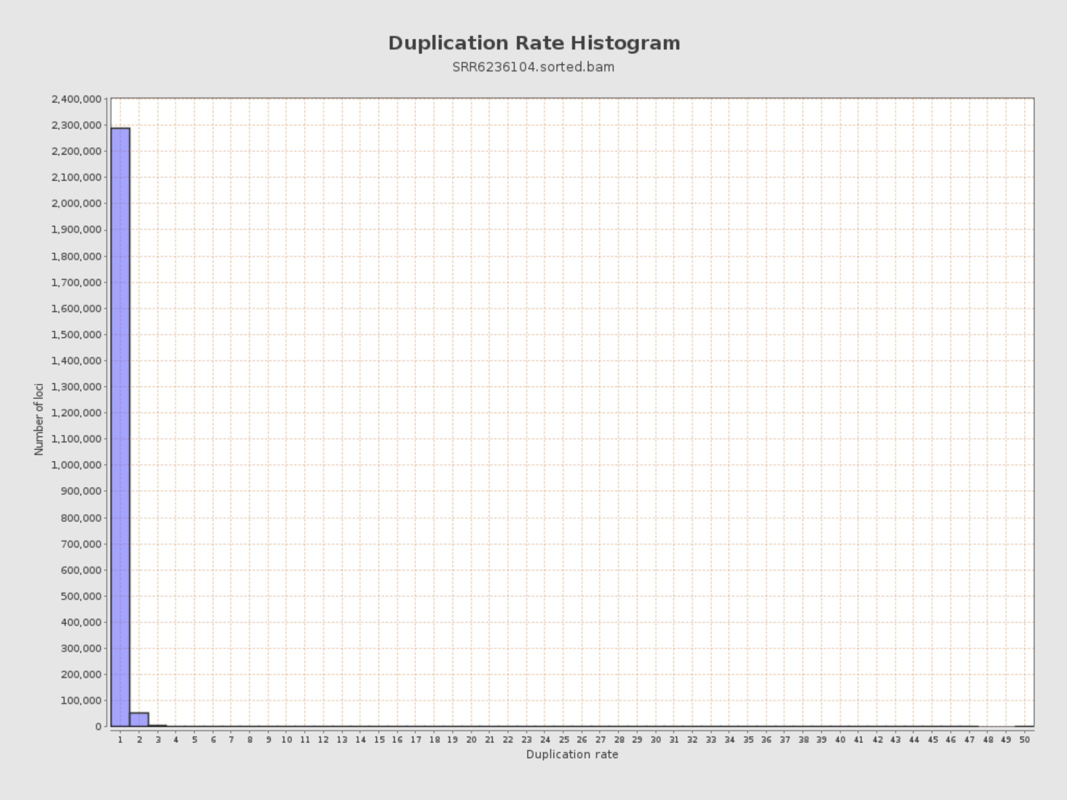
5. Results : Coverage Histogram (0-50X)



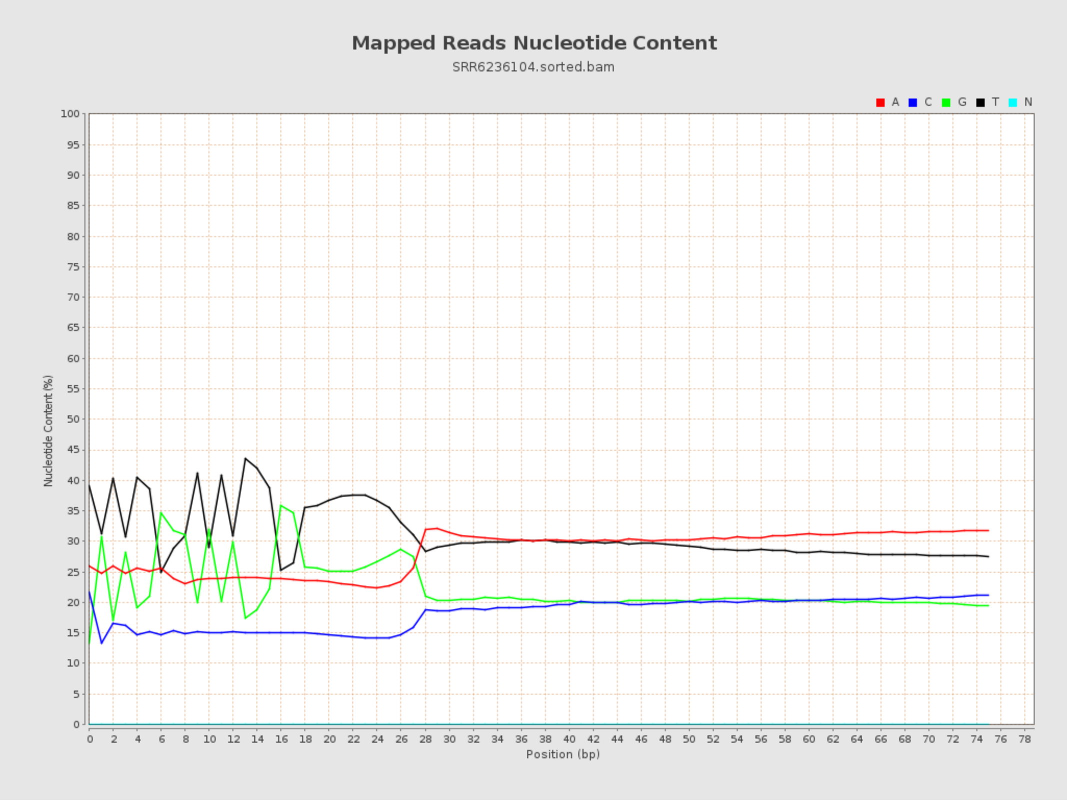
6. Results : Genome Fraction Coverage



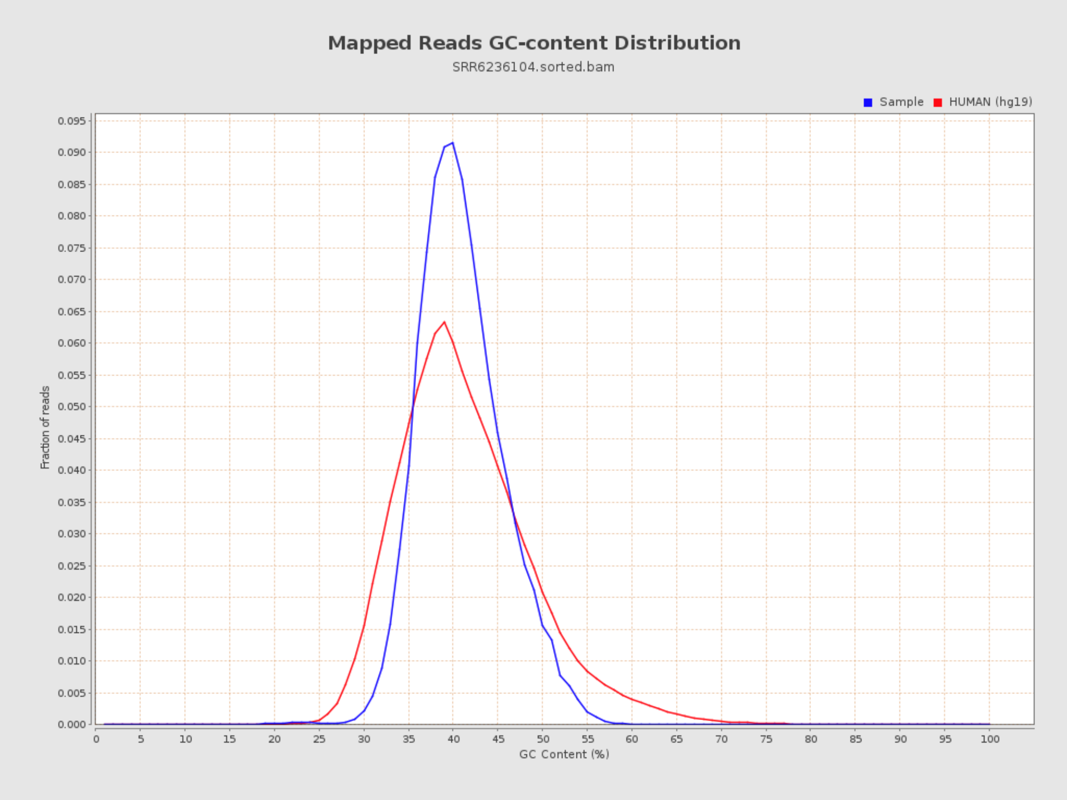
7. Results : Duplication Rate Histogram



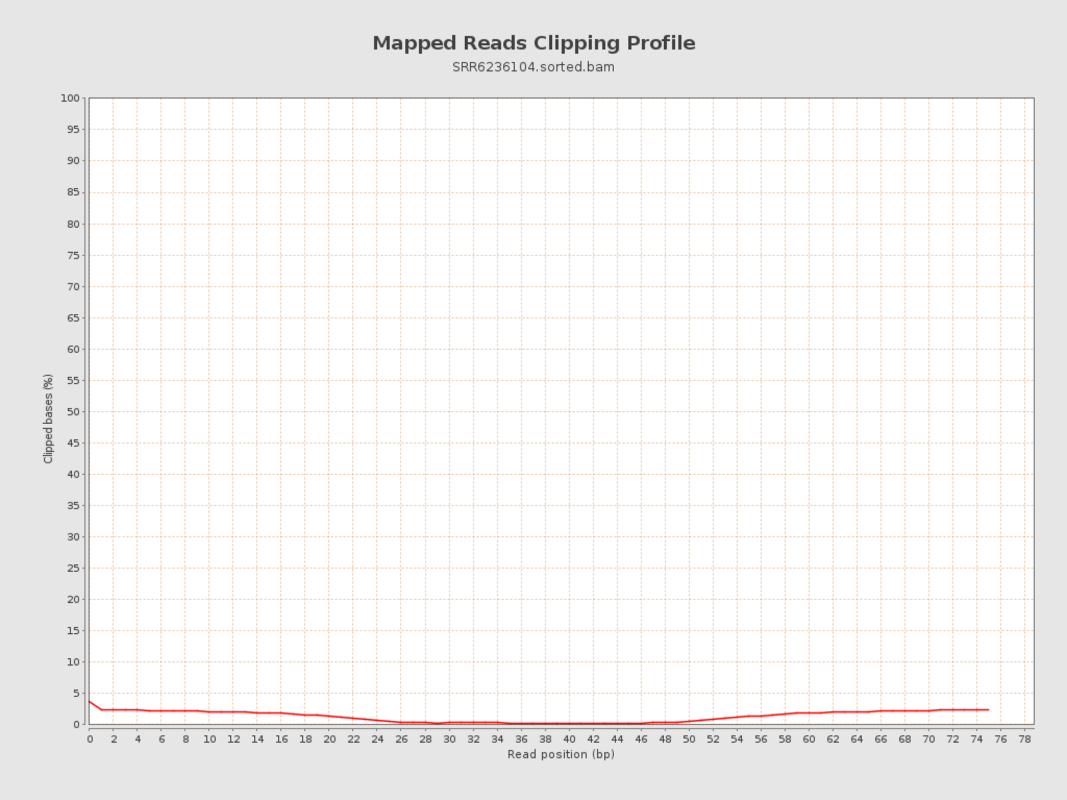
8. Results : Mapped Reads Nucleotide Content



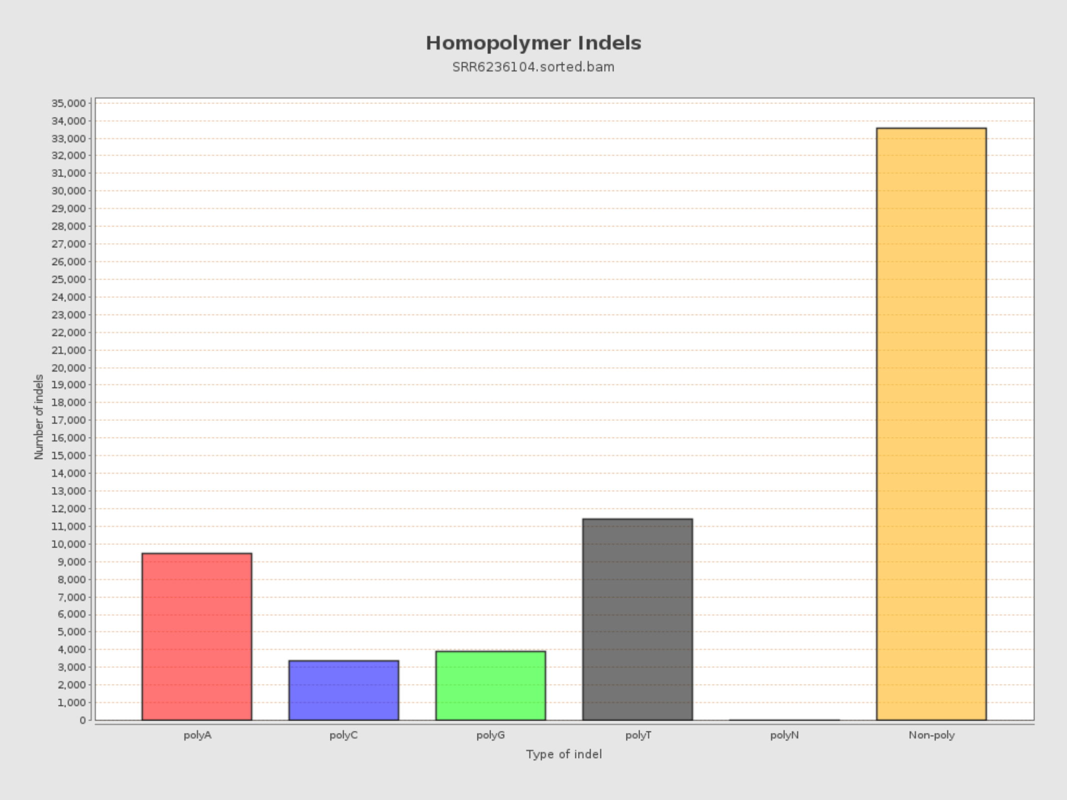
9. Results : Mapped Reads GC-content Distribution



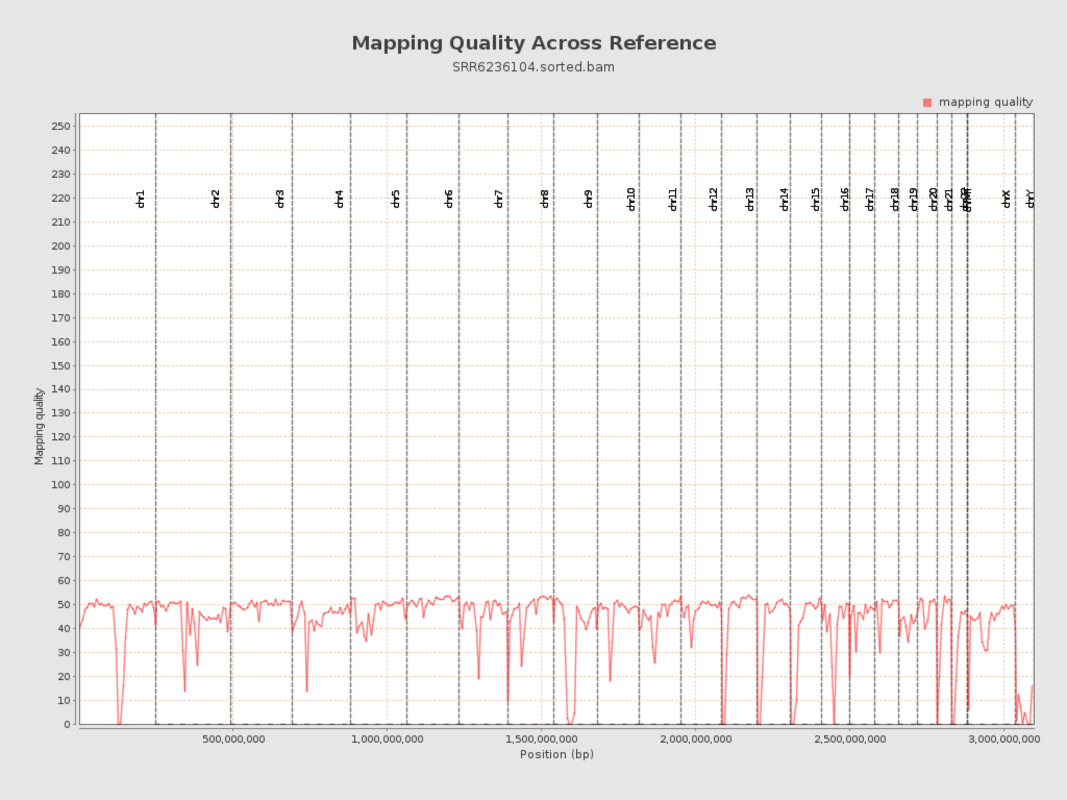
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram