Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:35:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236121.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_SRR6236121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:35:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,141,365
Mapped reads	2,744,383 / 87.36%
Unmapped reads	396,982 / 12.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,604 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	263,539 / 8.39%
Duplication rate	7.41%
Clipped reads	1,315,355 / 41.87%

2.2. ACGT Content

Number/percentage of A's	50,964,120 / 28.14%
Number/percentage of C's	32,859,826 / 18.15%
Number/percentage of T's	57,902,142 / 31.98%
Number/percentage of G's	39,355,775 / 21.73%
Number/percentage of N's	1,755 / 0%
GC Percentage	39.88%

2.3. Coverage

Mean	0.0585

Standard Deviation	0.6534

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

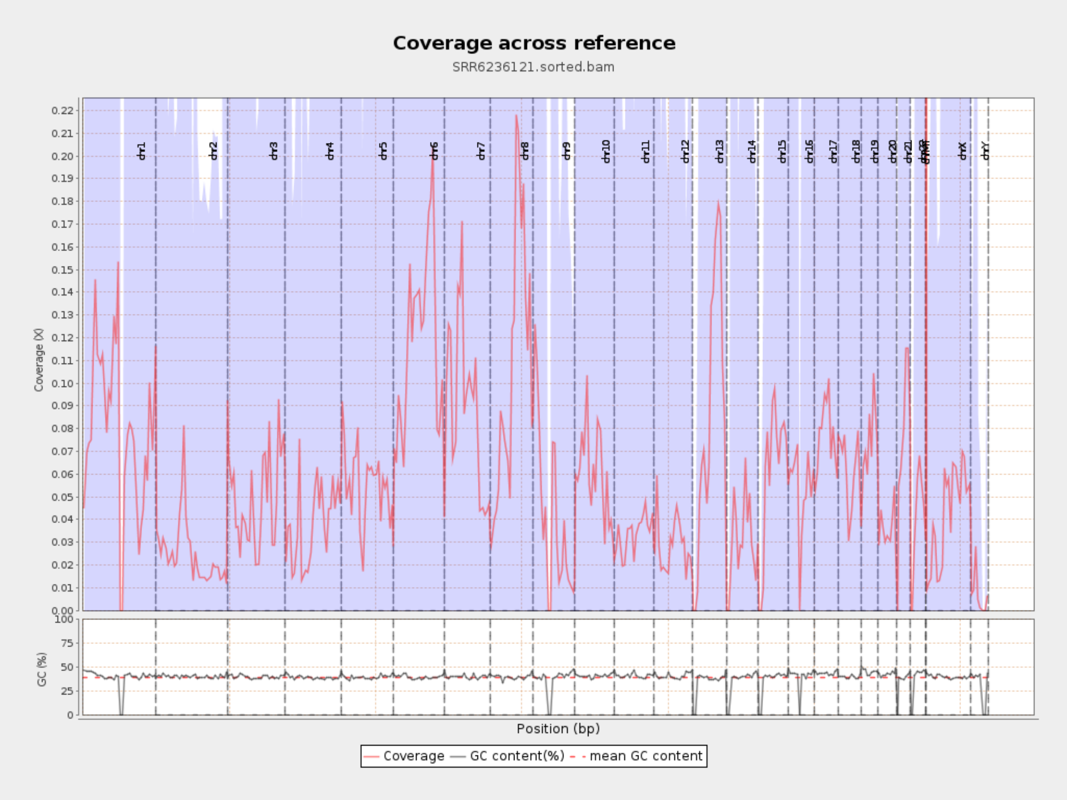
General error rate	0.77%
Mismatches	1,365,715
Insertions	13,901
Mapped reads with at least one insertion	0.5%
Deletions	53,558
Mapped reads with at least one deletion	1.93%
Homopolymer indels	46.52%

2.6. Chromosome stats

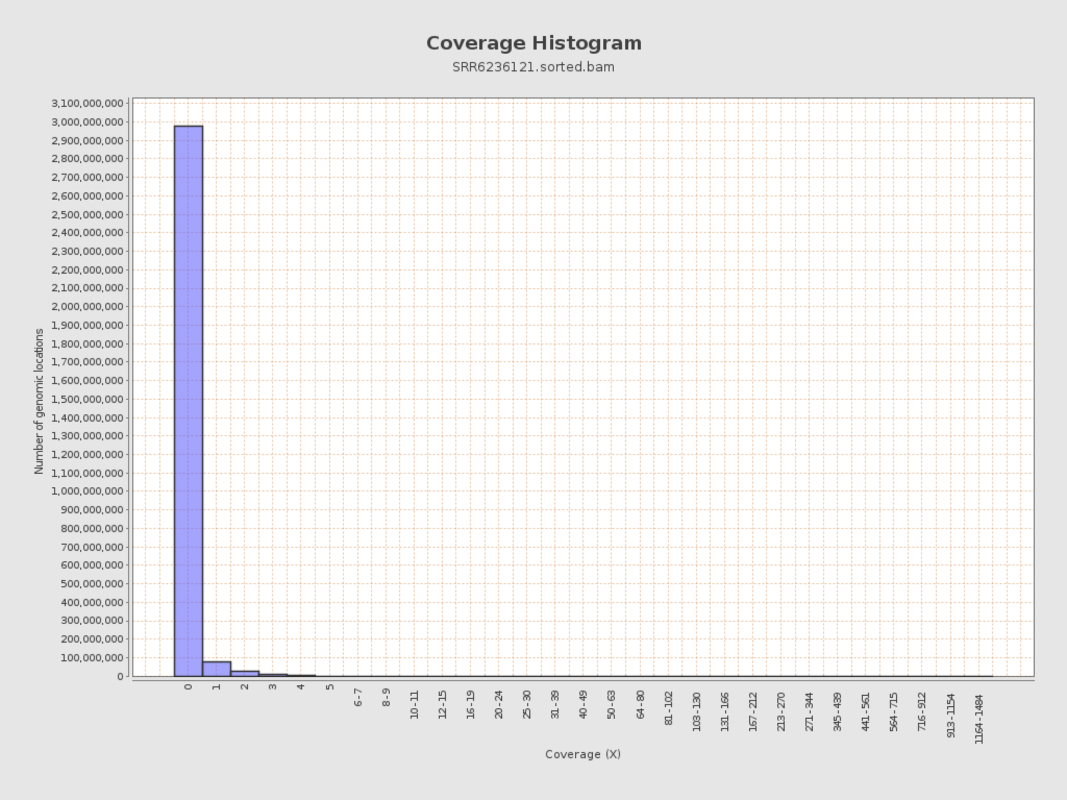
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19913008	0.0799	1.34
chr2	243199373	6112018	0.0251	0.5336
chr3	198022430	9770466	0.0493	0.3139
chr4	191154276	7255815	0.038	0.3596
chr5	180915260	10133597	0.056	0.3395
chr6	171115067	20538832	0.12	0.6391
chr7	159138663	14360945	0.0902	1.068

chr8	146364022	15764626	0.1077	1.0468
chr9	141213431	5865745	0.0415	0.4726
chr10	135534747	8054771	0.0594	0.552
chr11	135006516	4573799	0.0339	0.3635
chr12	133851895	3844007	0.0287	0.2532
chr13	115169878	10011882	0.0869	0.426
chr14	107349540	3285368	0.0306	0.2684
chr15	102531392	6203641	0.0605	0.3523
chr16	90354753	4729740	0.0523	0.3566
chr17	81195210	6264050	0.0771	0.4908
chr18	78077248	4879728	0.0625	0.951
chr19	59128983	4339416	0.0734	0.8645
chr20	63025520	2348087	0.0373	0.2825
chr21	48129895	3724299	0.0774	0.4326
chr22	51304566	2066444	0.0403	0.274
chrMT	16571	157205	9.4868	6.9935
chrX	155270560	6558827	0.0422	0.316
chrY	59373566	420794	0.0071	0.2394

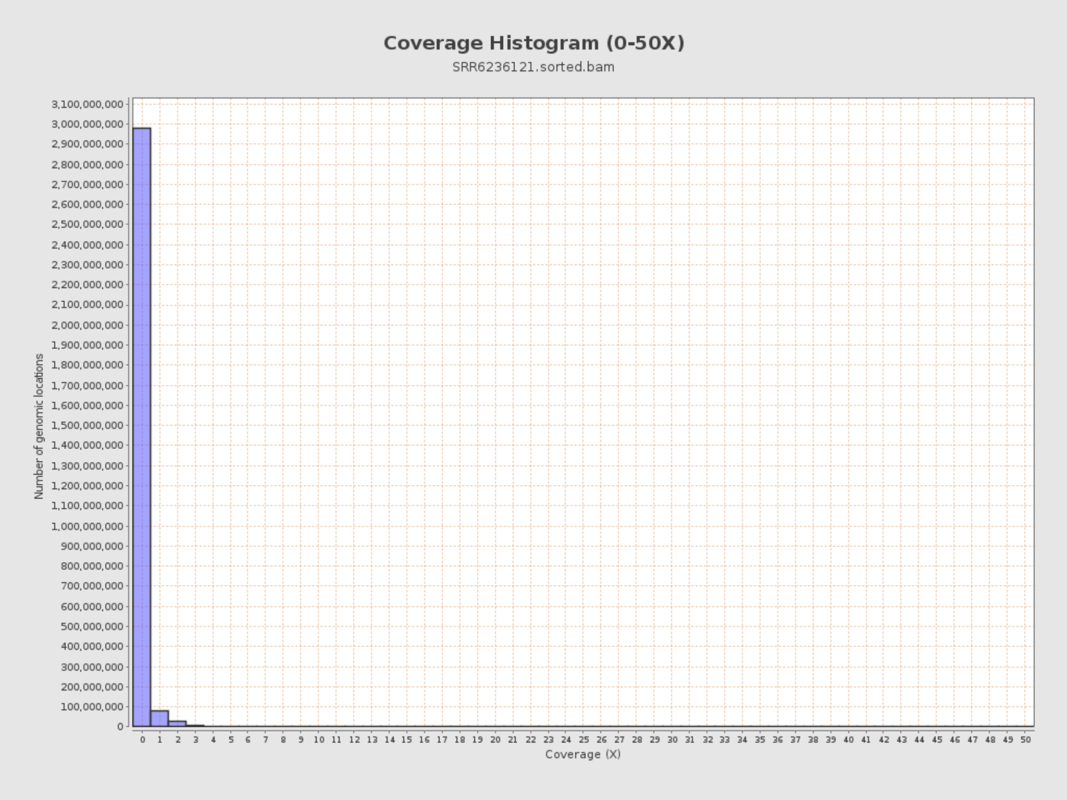
3. Results : Coverage across reference



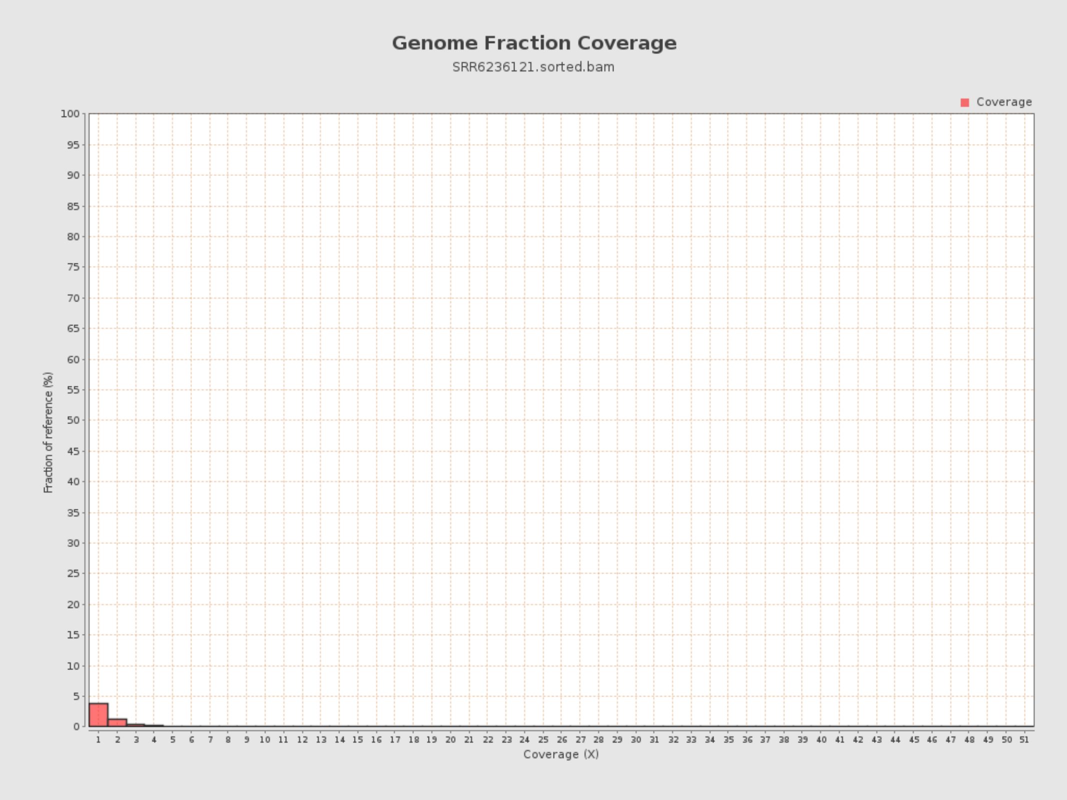
4. Results : Coverage Histogram



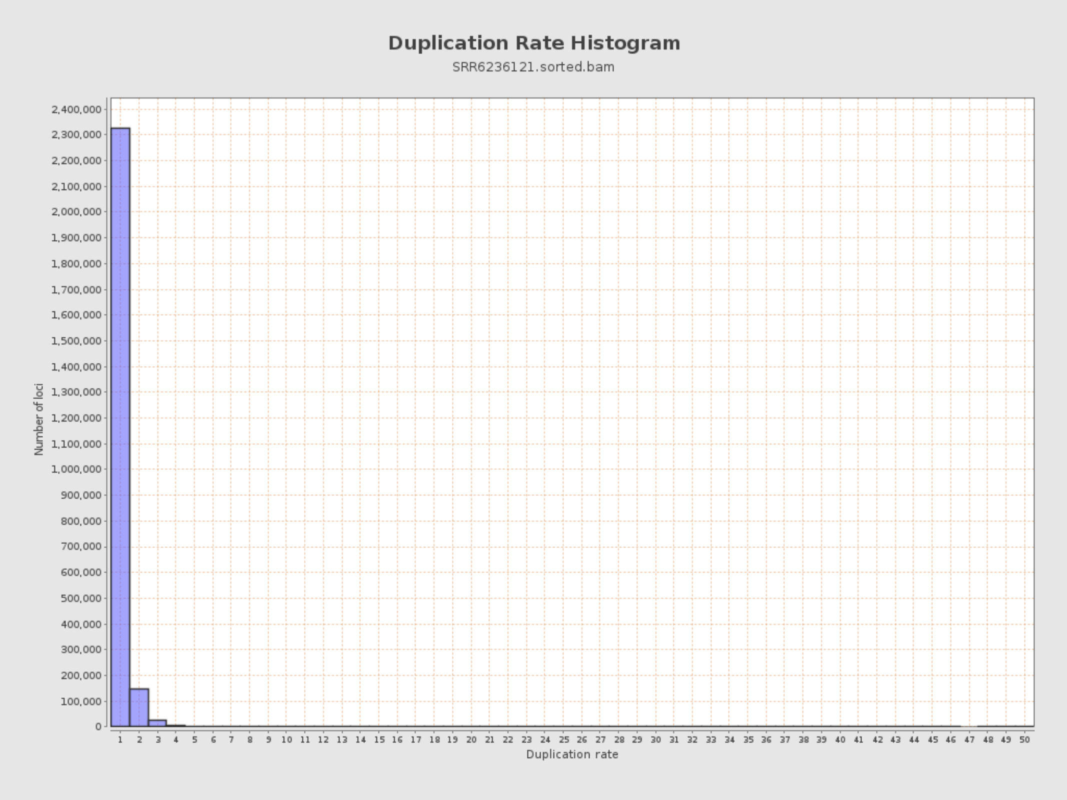
5. Results : Coverage Histogram (0-50X)



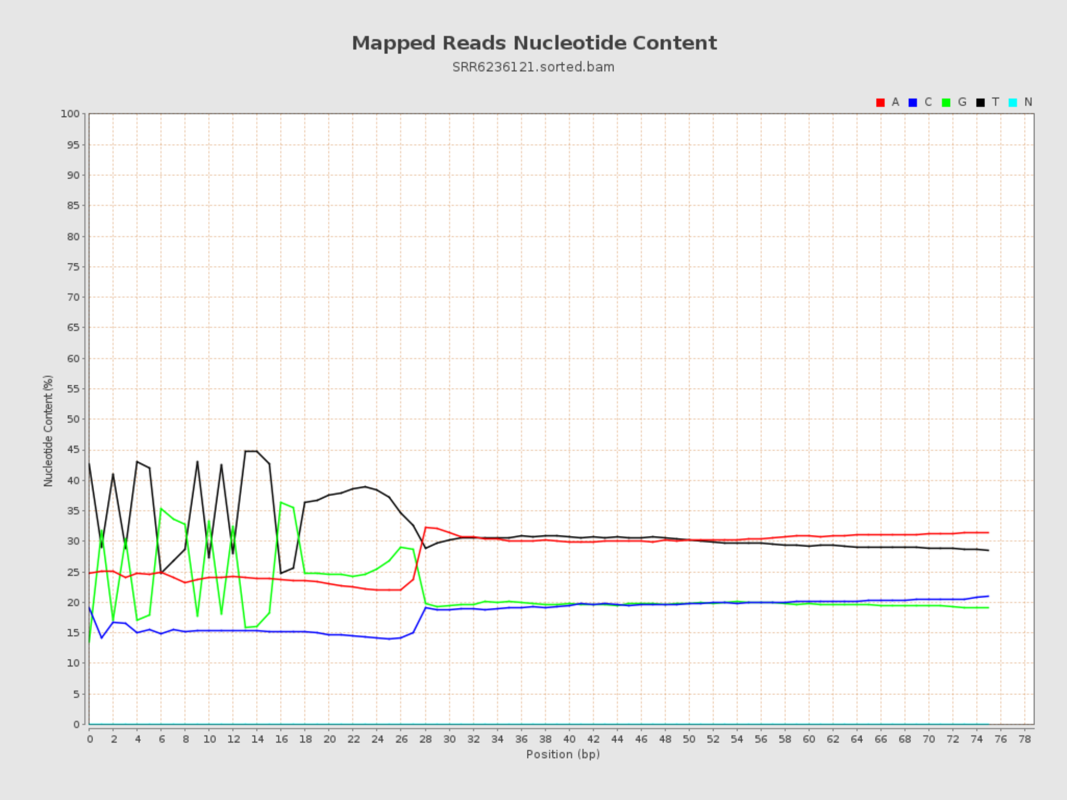
6. Results : Genome Fraction Coverage



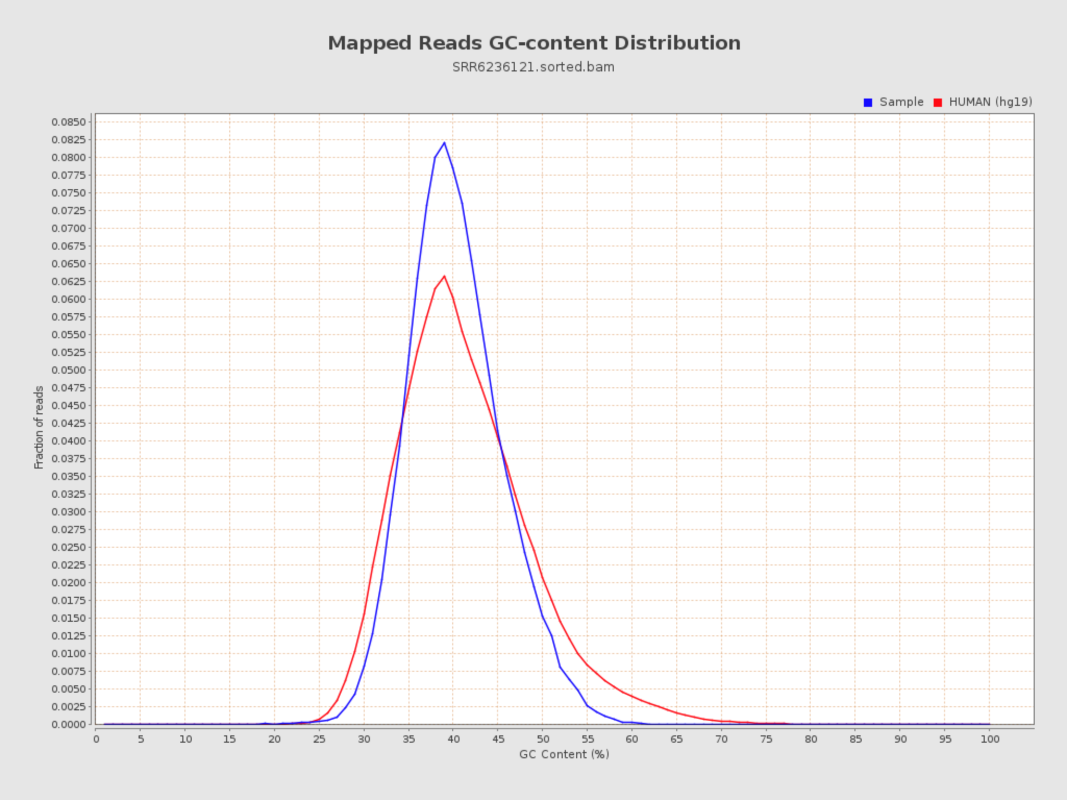
7. Results : Duplication Rate Histogram



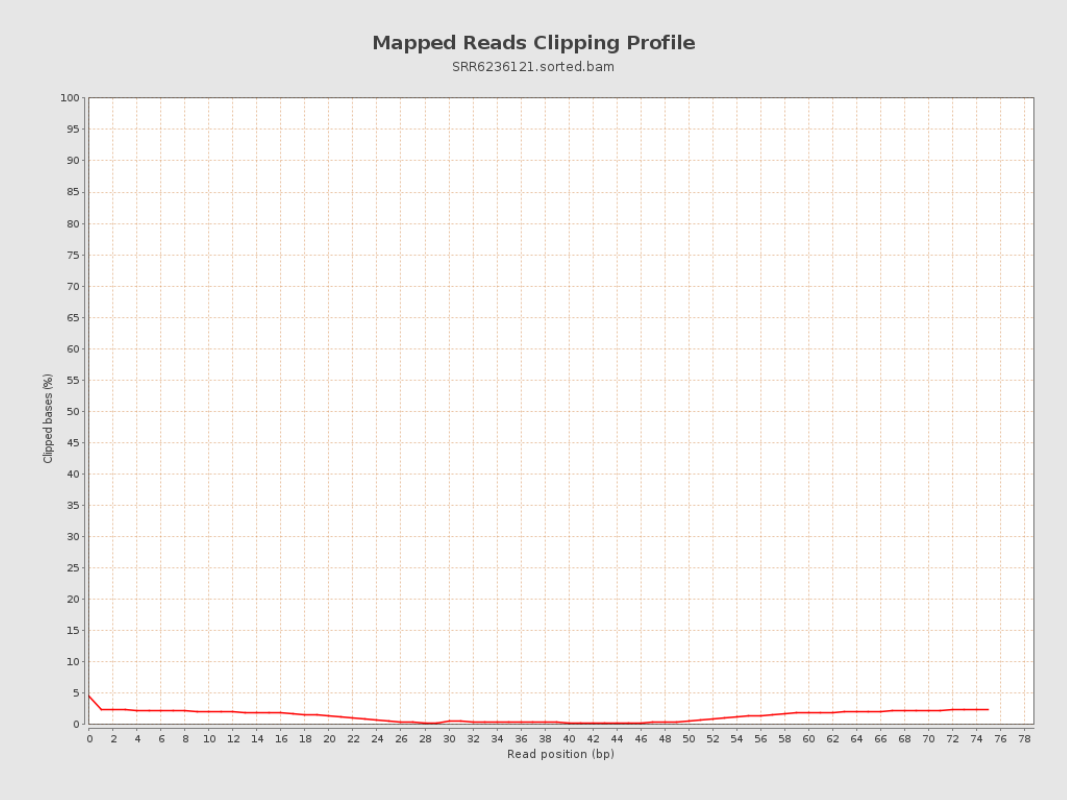
8. Results : Mapped Reads Nucleotide Content



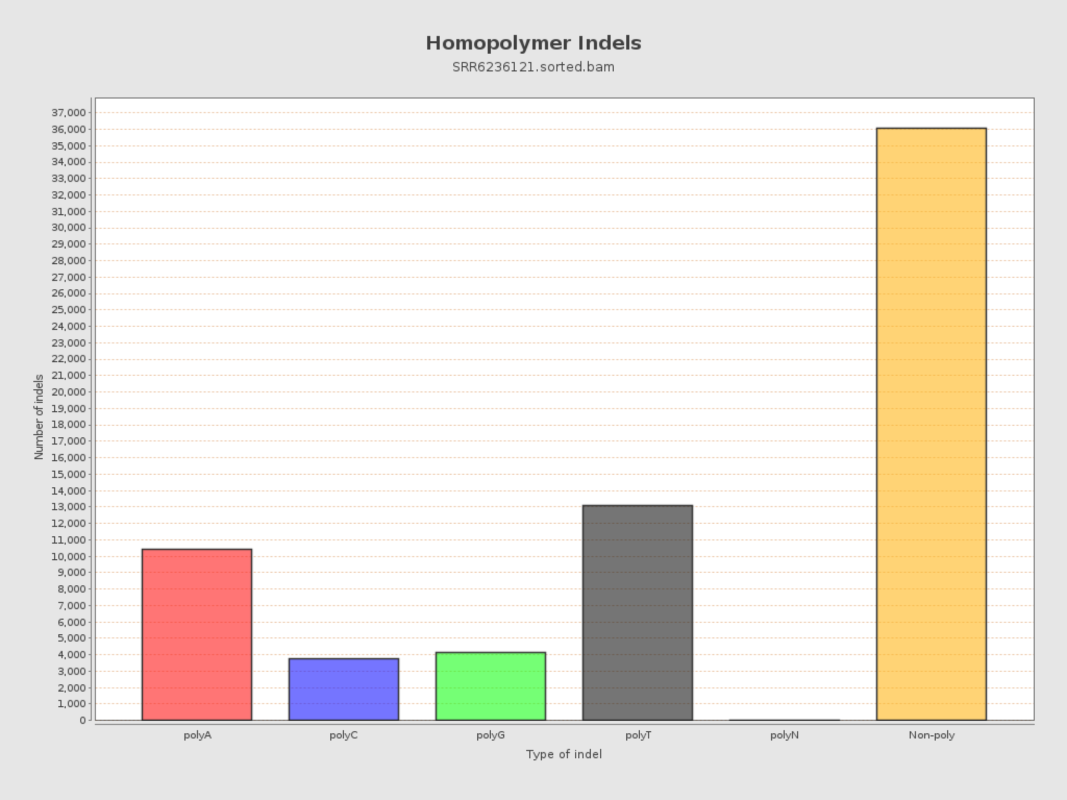
9. Results : Mapped Reads GC-content Distribution



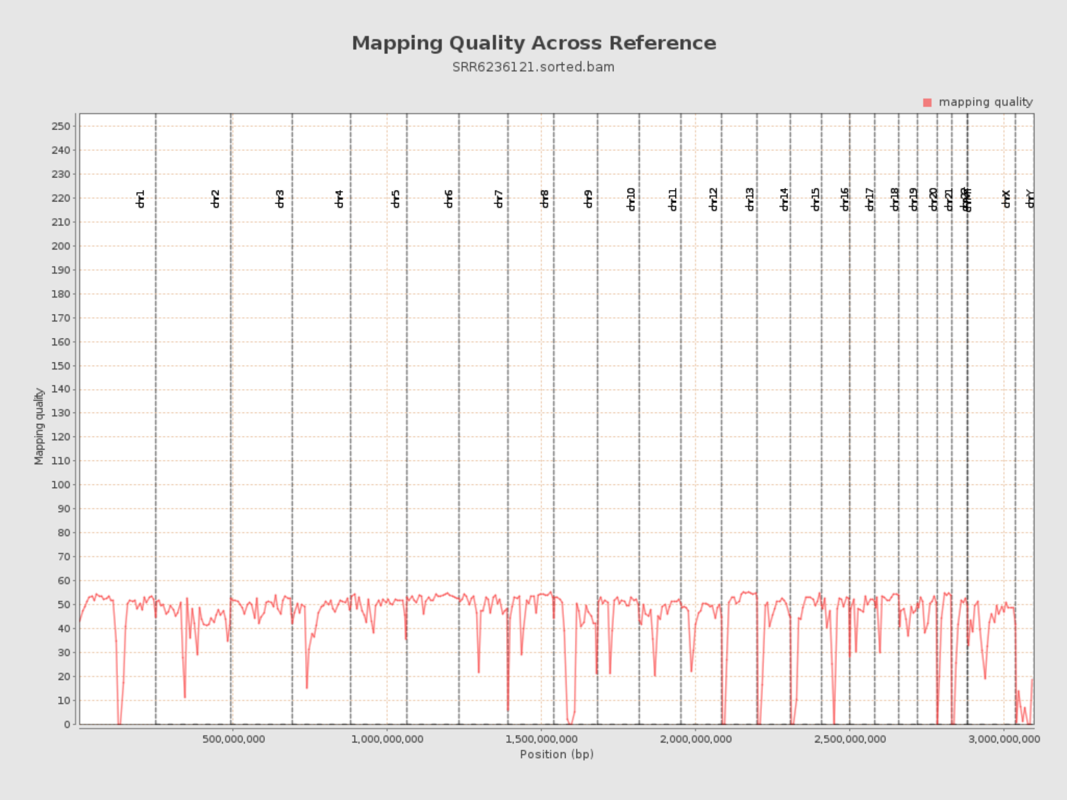
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram