Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:06:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236071.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_SRR6236071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:06:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,269,613
Mapped reads	3,791,725 / 88.81%
Unmapped reads	477,888 / 11.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,248 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	286,582 / 6.71%
Duplication rate	5.86%
Clipped reads	2,130,534 / 49.9%

2.2. ACGT Content

Number/percentage of A's	69,313,601 / 28.49%
Number/percentage of C's	45,294,204 / 18.62%
Number/percentage of T's	75,864,633 / 31.18%
Number/percentage of G's	52,829,634 / 21.71%
Number/percentage of N's	2,297 / 0%
GC Percentage	40.33%

2.3. Coverage

Mean	0.0786

Standard Deviation	0.7068

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

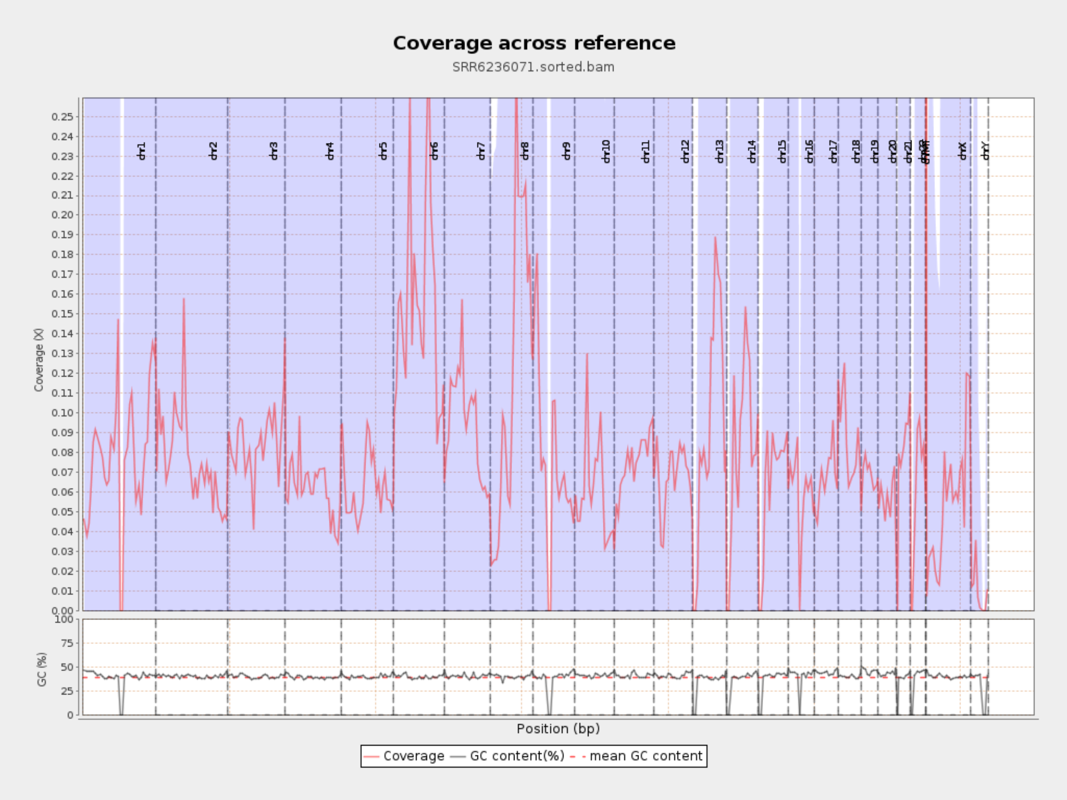
General error rate	0.79%
Mismatches	1,890,739
Insertions	17,641
Mapped reads with at least one insertion	0.46%
Deletions	76,050
Mapped reads with at least one deletion	1.98%
Homopolymer indels	44.61%

2.6. Chromosome stats

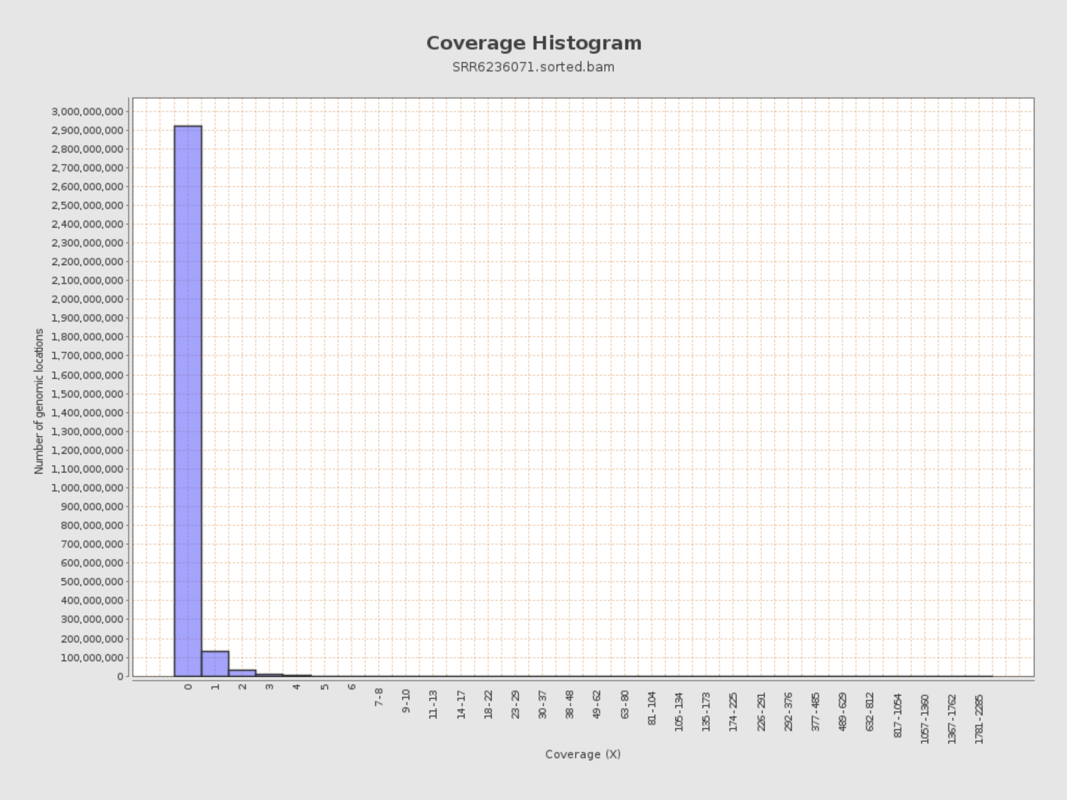
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19391246	0.0778	1.1524
chr2	243199373	18627988	0.0766	0.7181
chr3	198022430	16631962	0.084	0.3776
chr4	191154276	11827136	0.0619	0.3748
chr5	180915260	11416200	0.0631	0.3331
chr6	171115067	26791170	0.1566	0.9878
chr7	159138663	15078194	0.0947	0.8554

chr8	146364022	17961210	0.1227	1.4985
chr9	141213431	10715283	0.0759	0.5957
chr10	135534747	8143485	0.0601	0.564
chr11	135006516	10052484	0.0745	0.531
chr12	133851895	9129010	0.0682	0.3548
chr13	115169878	10903368	0.0947	0.4073
chr14	107349540	8953139	0.0834	0.4264
chr15	102531392	6454773	0.063	0.3394
chr16	90354753	5262305	0.0582	0.3731
chr17	81195210	5440072	0.067	0.3815
chr18	78077248	6823431	0.0874	1.0869
chr19	59128983	4080543	0.069	0.7966
chr20	63025520	3612685	0.0573	0.3221
chr21	48129895	3828885	0.0796	0.4155
chr22	51304566	3095805	0.0603	0.314
chrMT	16571	236265	14.2577	9.6164
chrX	155270560	8387816	0.054	0.3597
chrY	59373566	590758	0.0099	0.2337

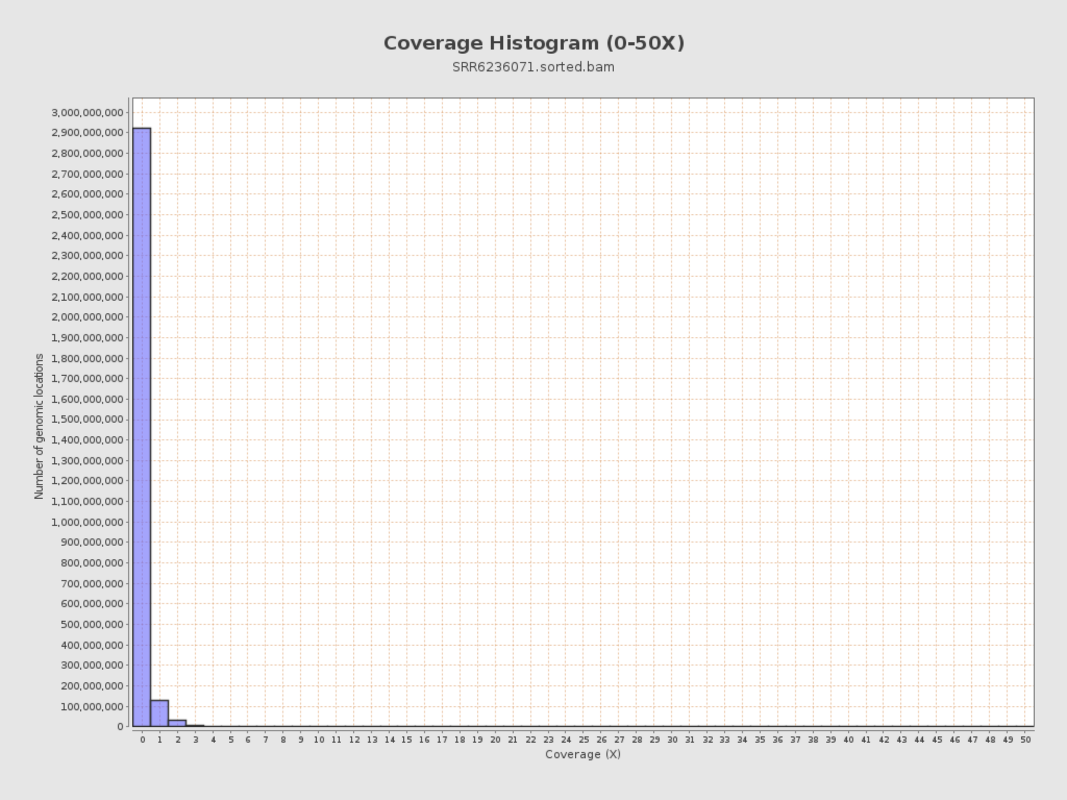
3. Results : Coverage across reference



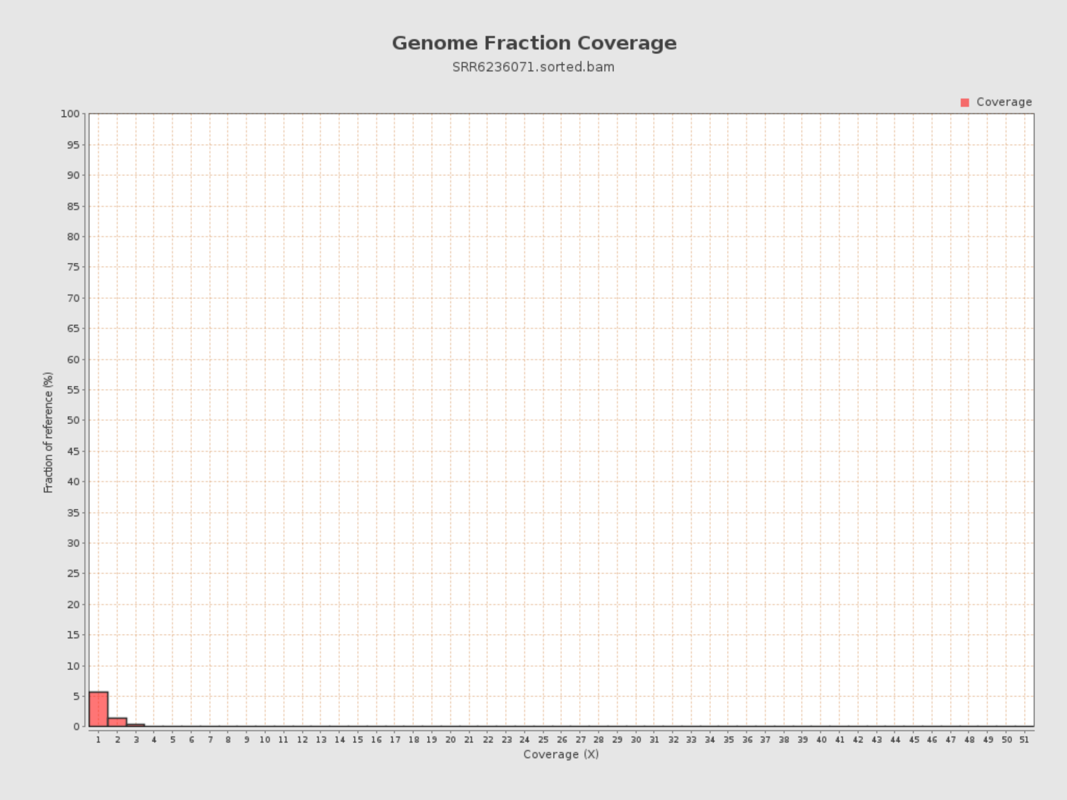
4. Results : Coverage Histogram



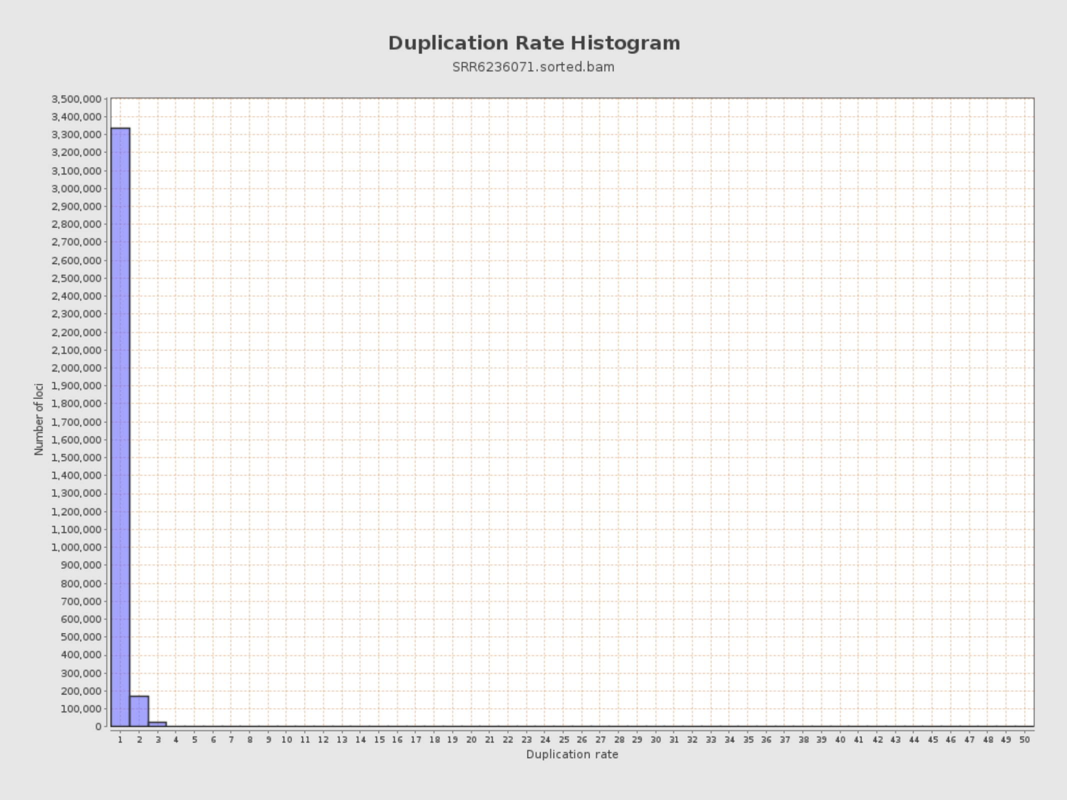
5. Results : Coverage Histogram (0-50X)



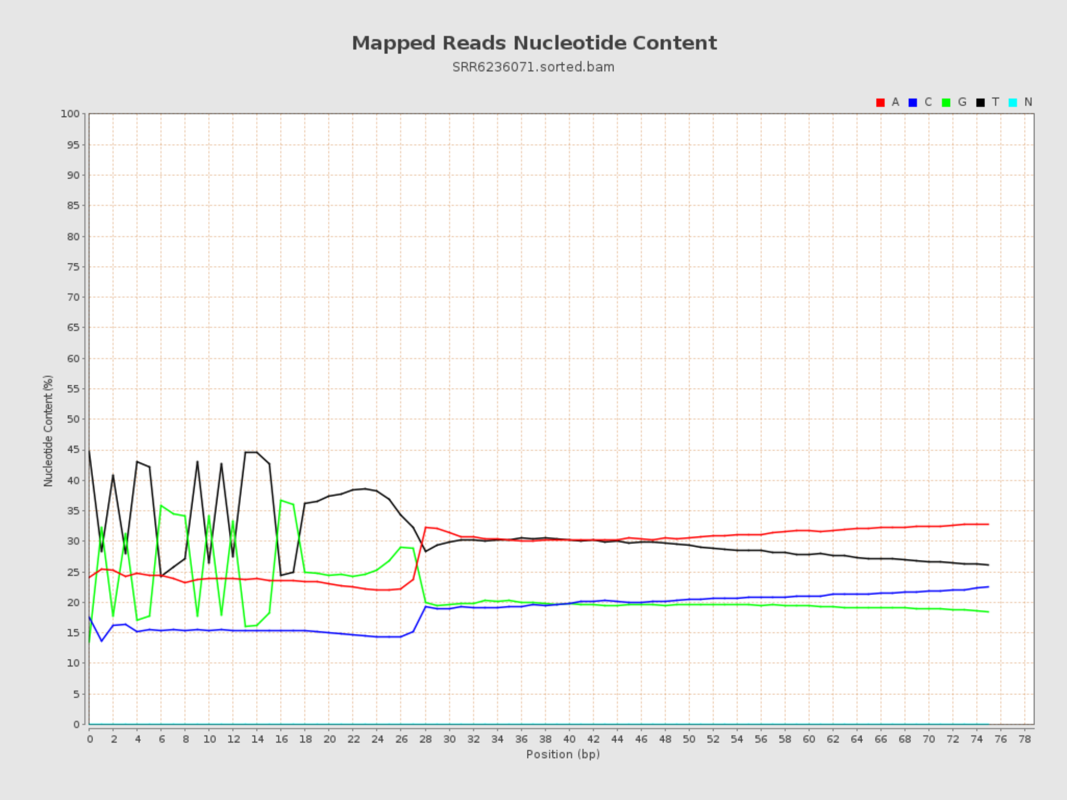
6. Results : Genome Fraction Coverage



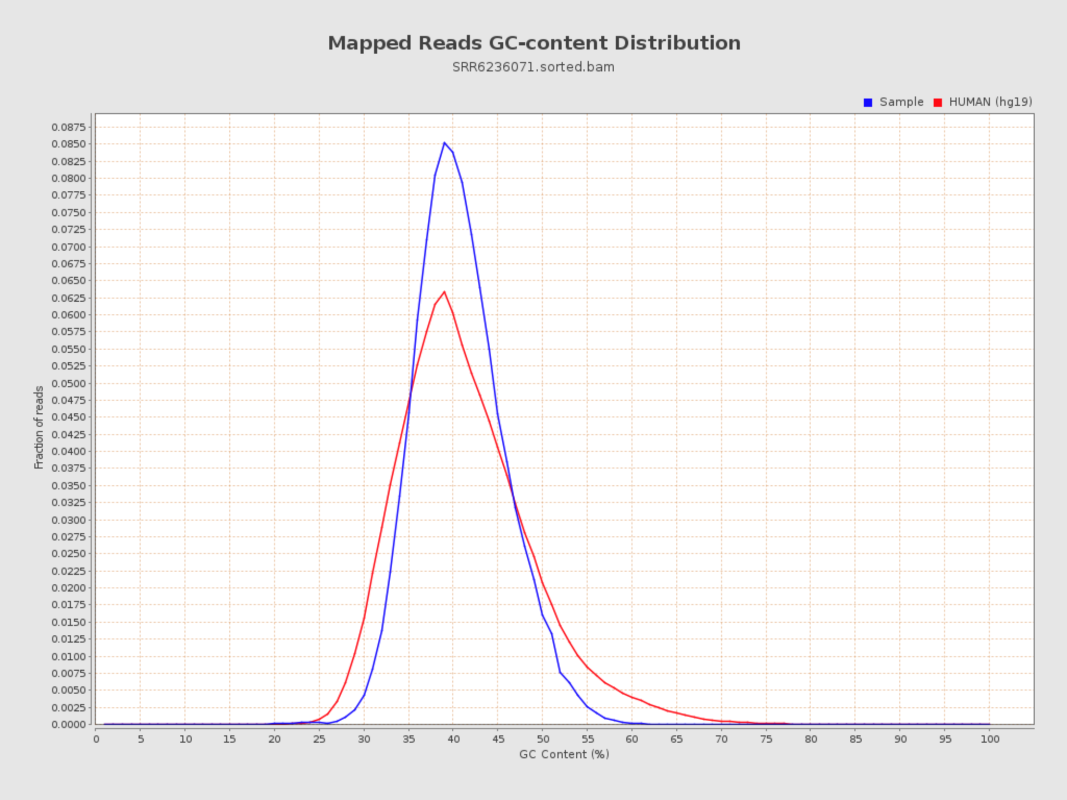
7. Results : Duplication Rate Histogram



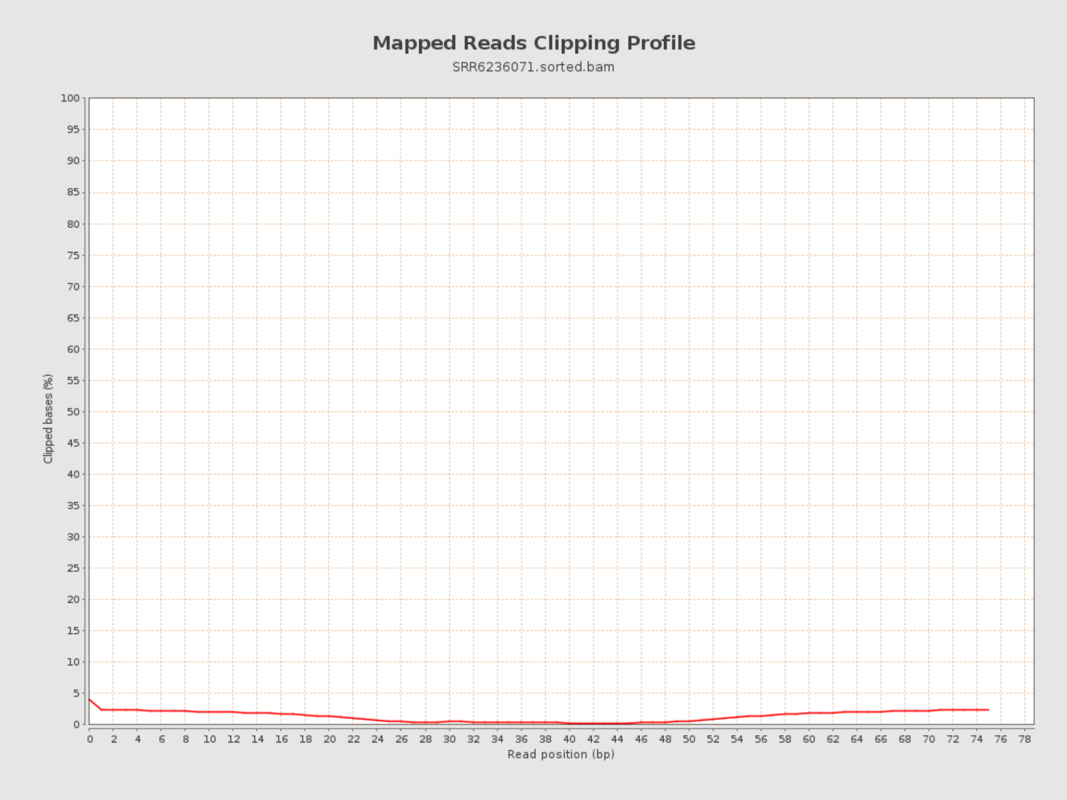
8. Results : Mapped Reads Nucleotide Content



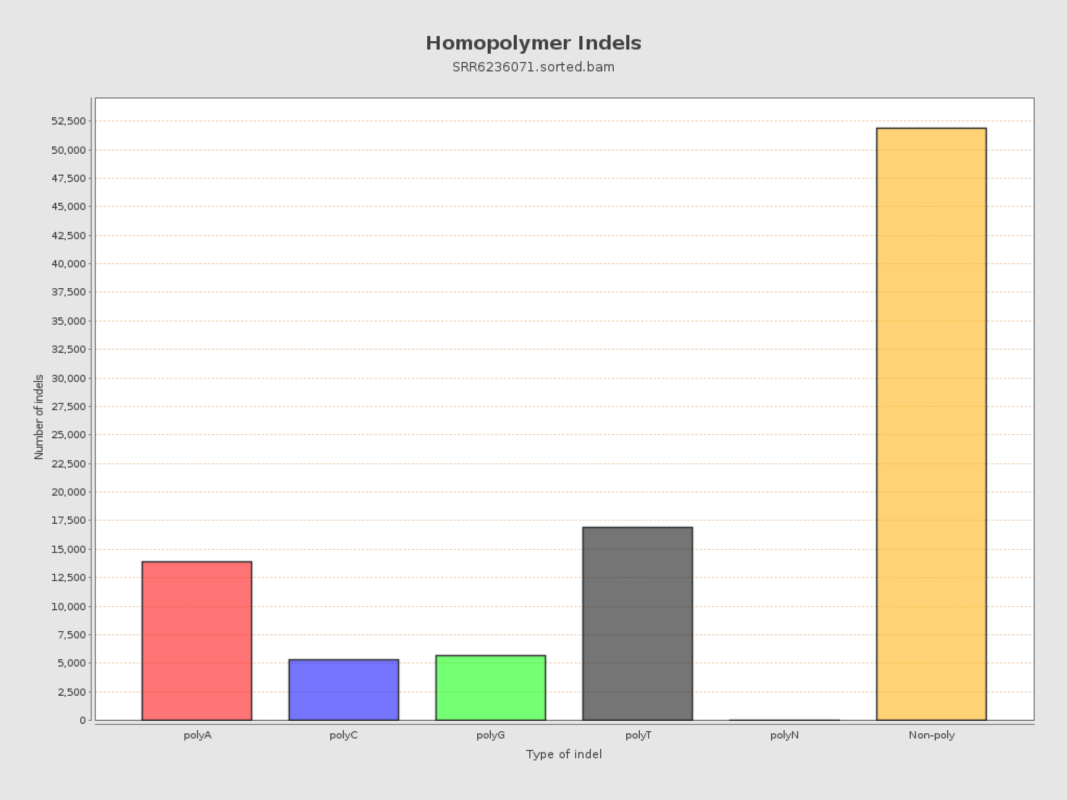
9. Results : Mapped Reads GC-content Distribution



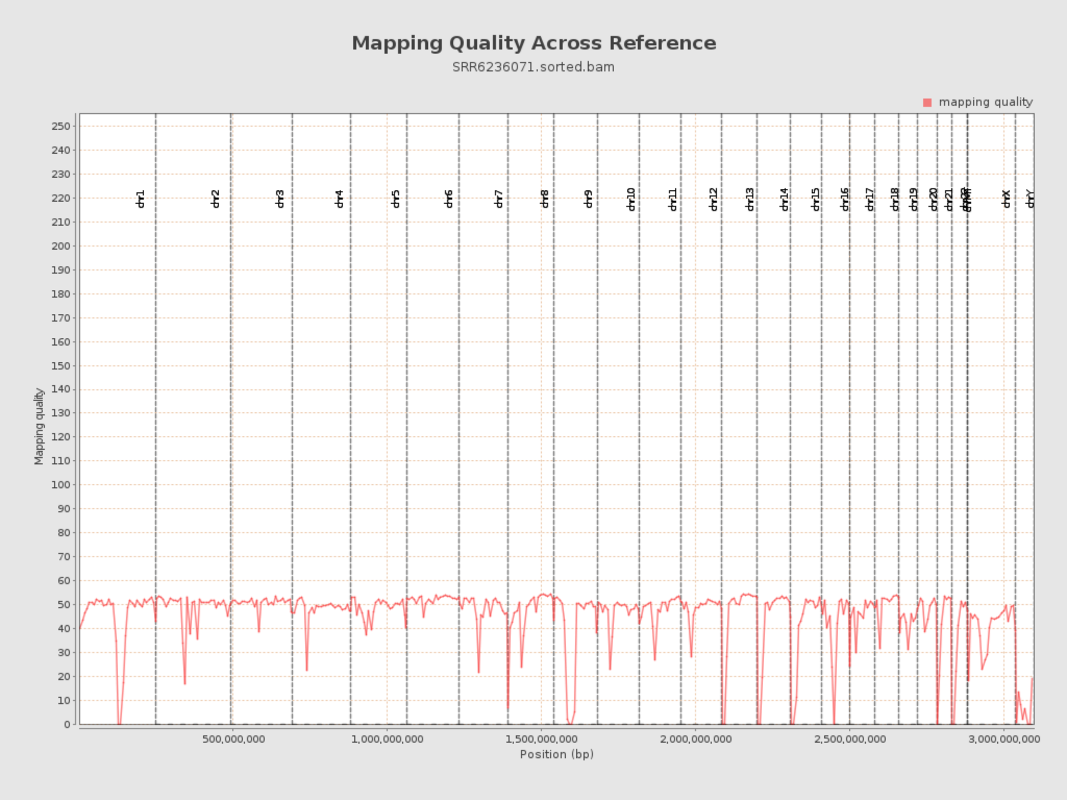
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram