Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:55:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236086.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_SRR6236086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:55:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,432,050
Mapped reads	1,285,632 / 89.78%
Unmapped reads	146,418 / 10.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,823 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	50,013 / 3.49%
Duplication rate	3.1%
Clipped reads	603,998 / 42.18%

2.2. ACGT Content

Number/percentage of A's	23,231,673 / 27.47%
Number/percentage of C's	14,984,429 / 17.72%
Number/percentage of T's	27,298,439 / 32.28%
Number/percentage of G's	19,014,524 / 22.48%
Number/percentage of N's	44,375 / 0.05%
GC Percentage	40.2%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.265

2.4. Mapping Quality

Mean Mapping Quality	45.58

2.5. Mismatches and indels

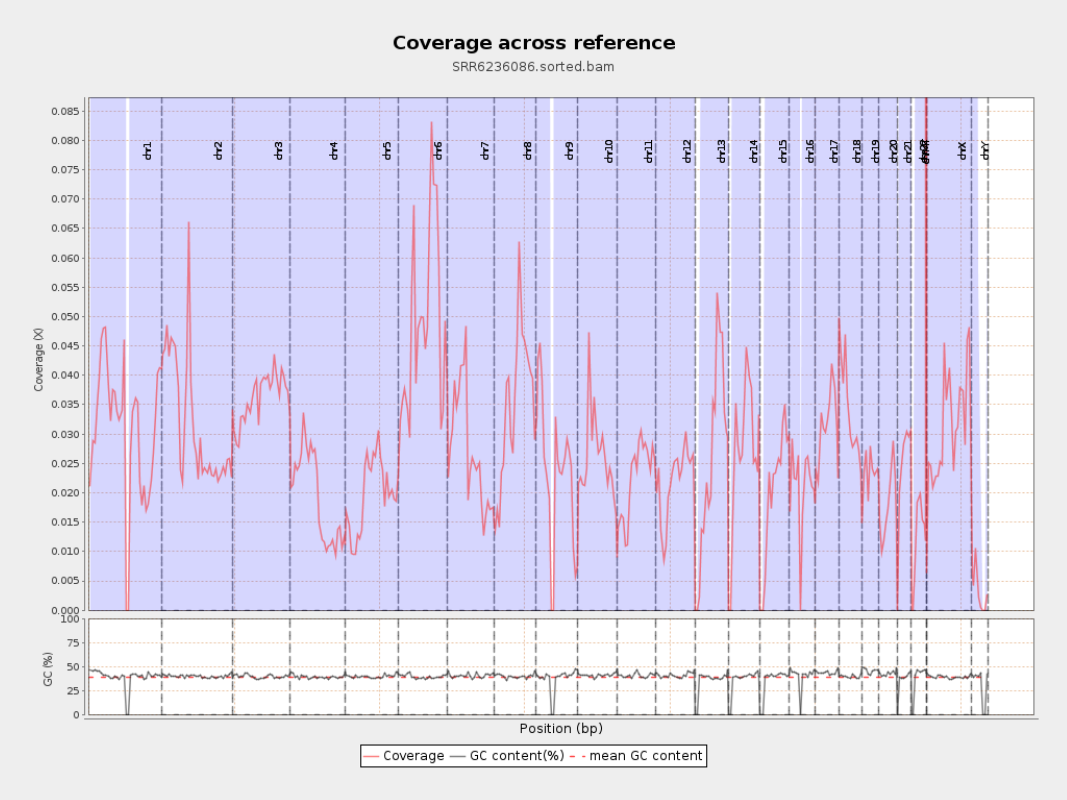
General error rate	0.79%
Mismatches	660,401
Insertions	6,086
Mapped reads with at least one insertion	0.47%
Deletions	24,238
Mapped reads with at least one deletion	1.86%
Homopolymer indels	46.49%

2.6. Chromosome stats

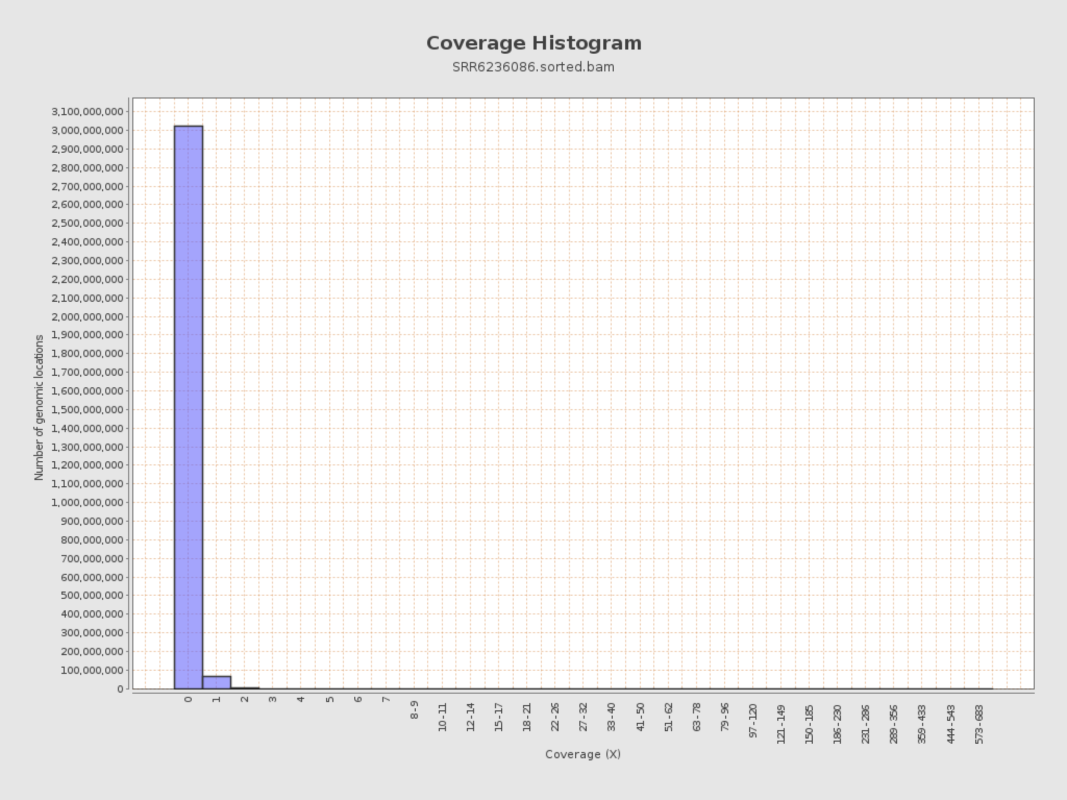
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7634045	0.0306	0.3988
chr2	243199373	7744938	0.0318	0.3118
chr3	198022430	7199217	0.0364	0.2081
chr4	191154276	3671384	0.0192	0.1644
chr5	180915260	3541882	0.0196	0.1544
chr6	171115067	8295972	0.0485	0.3113
chr7	159138663	4308572	0.0271	0.333

chr8	146364022	5101250	0.0349	0.4654
chr9	141213431	3327960	0.0236	0.2519
chr10	135534747	3563011	0.0263	0.2495
chr11	135006516	3013969	0.0223	0.1996
chr12	133851895	2942466	0.022	0.1721
chr13	115169878	2921583	0.0254	0.1747
chr14	107349540	2834217	0.0264	0.1896
chr15	102531392	2049386	0.02	0.1602
chr16	90354753	1893318	0.021	0.167
chr17	81195210	2555708	0.0315	0.2152
chr18	78077248	2672297	0.0342	0.3878
chr19	59128983	1394155	0.0236	0.2668
chr20	63025520	1116732	0.0177	0.1495
chr21	48129895	1179457	0.0245	0.1832
chr22	51304566	615740	0.012	0.1174
chrMT	16571	40489	2.4434	2.3259
chrX	155270560	4810723	0.031	0.2045
chrY	59373566	186621	0.0031	0.0894

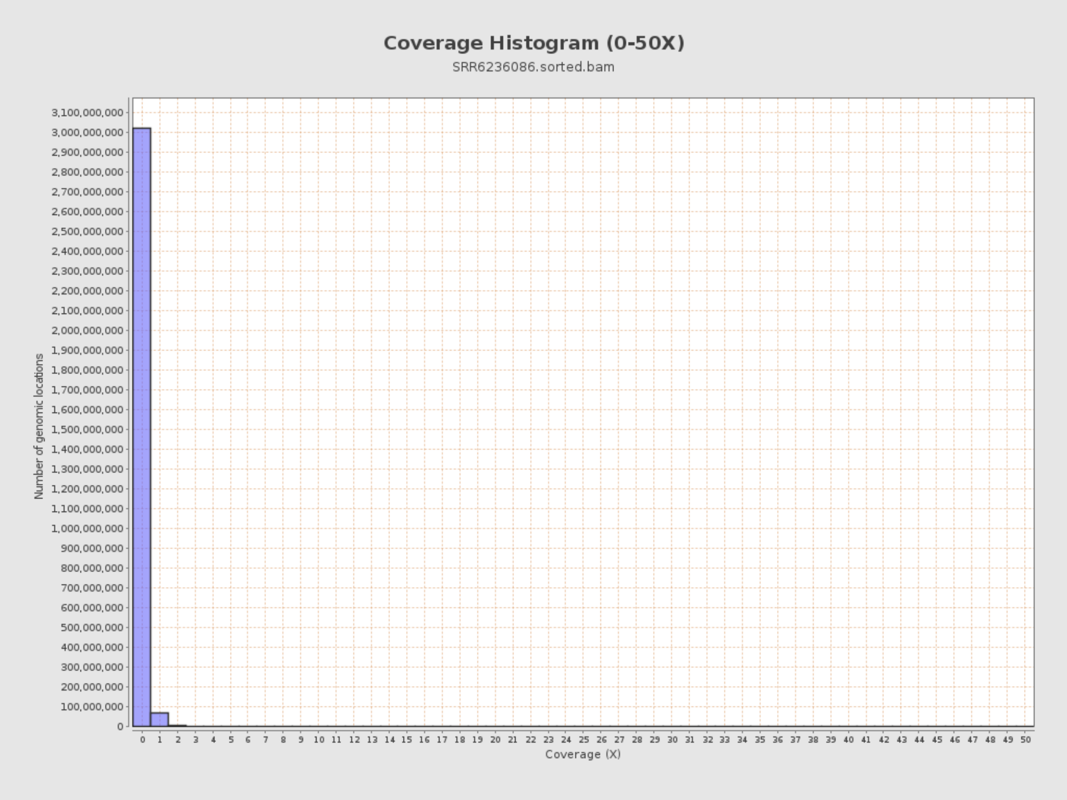
3. Results : Coverage across reference



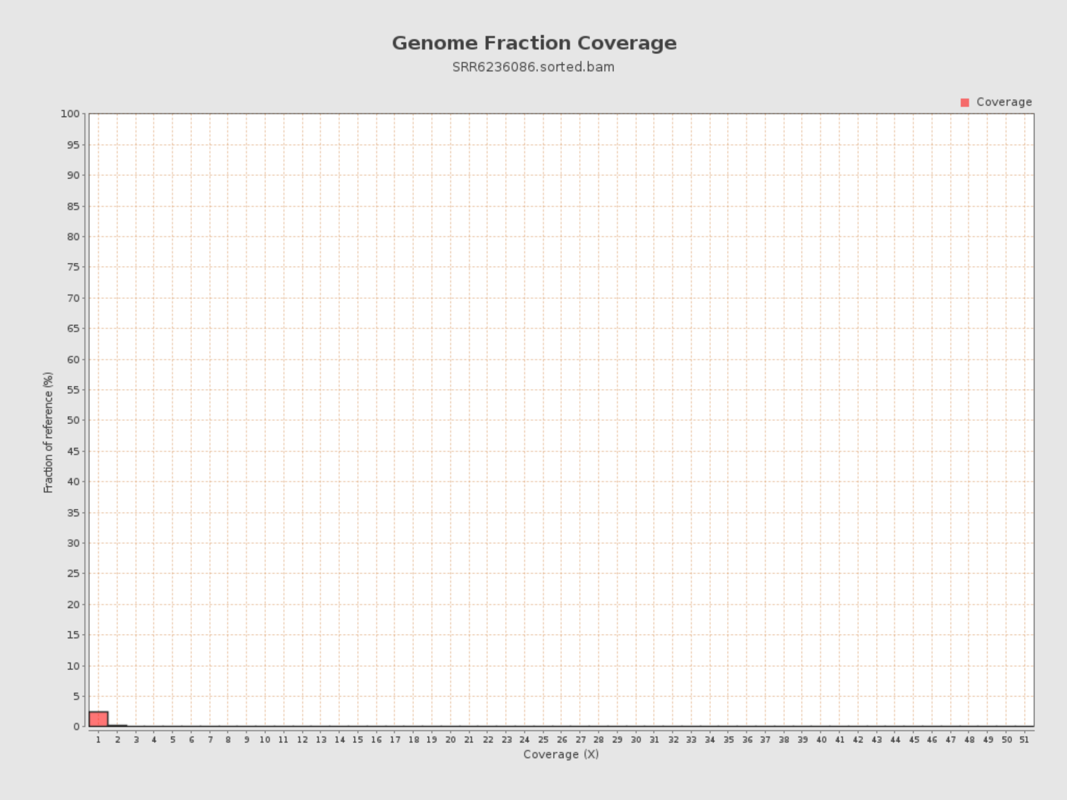
4. Results : Coverage Histogram



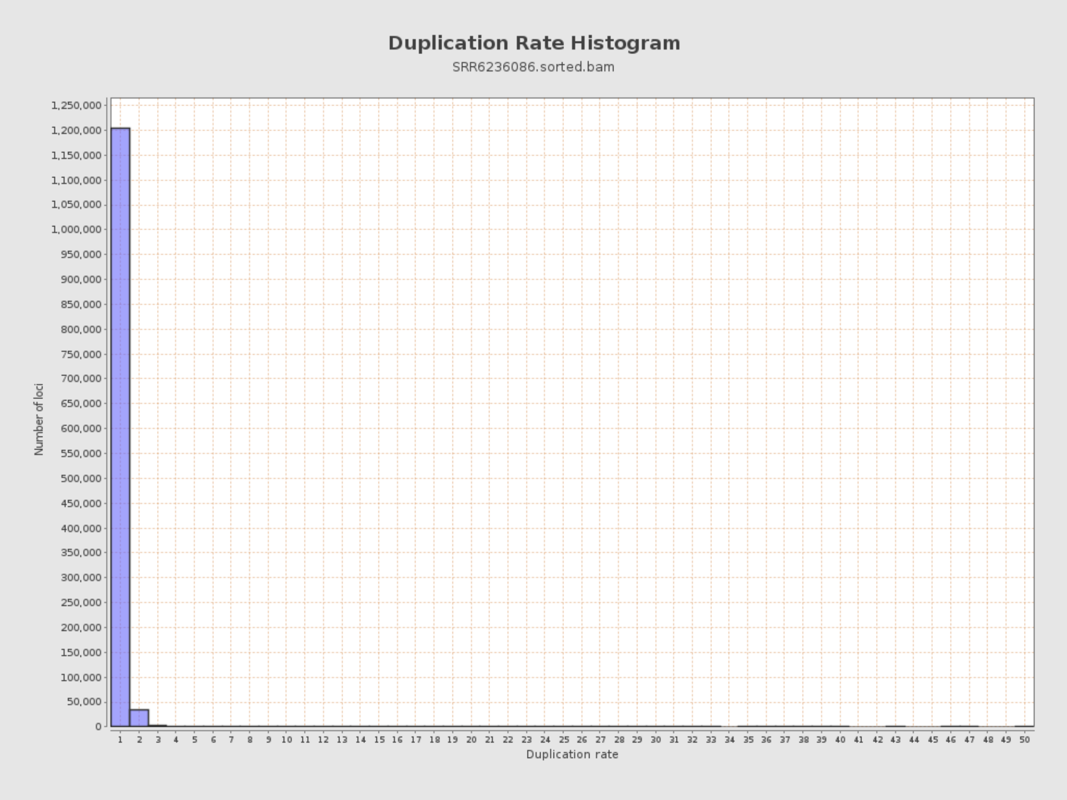
5. Results : Coverage Histogram (0-50X)



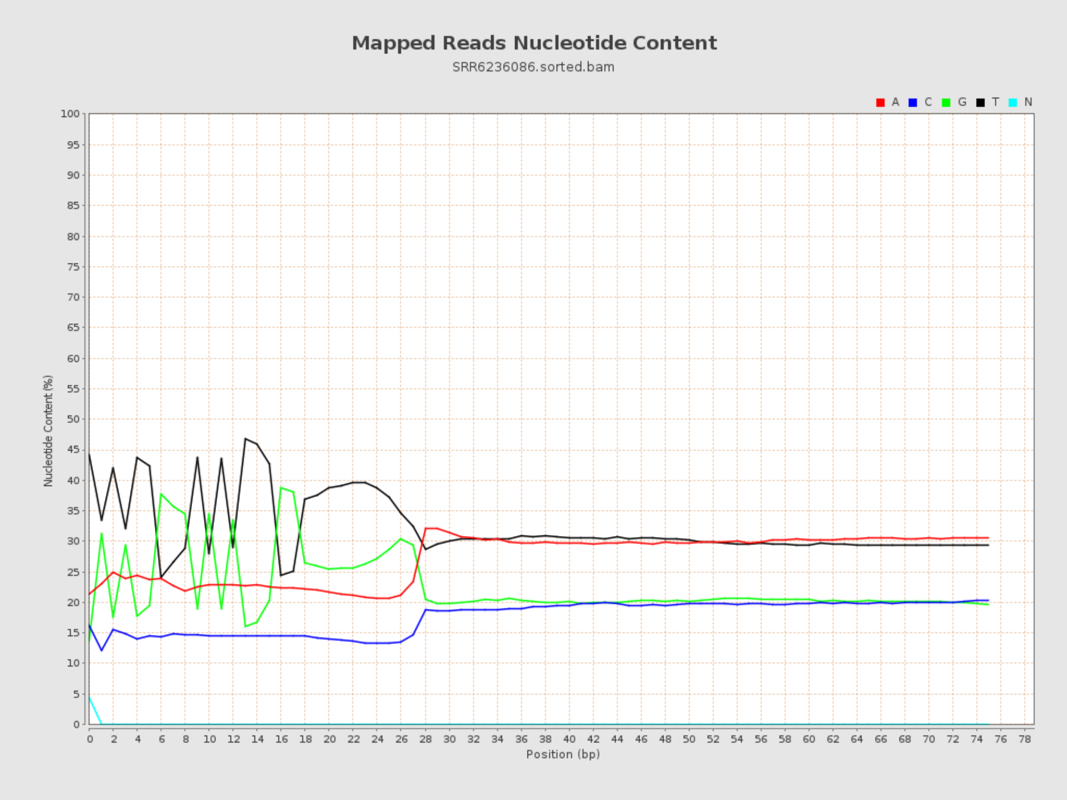
6. Results : Genome Fraction Coverage



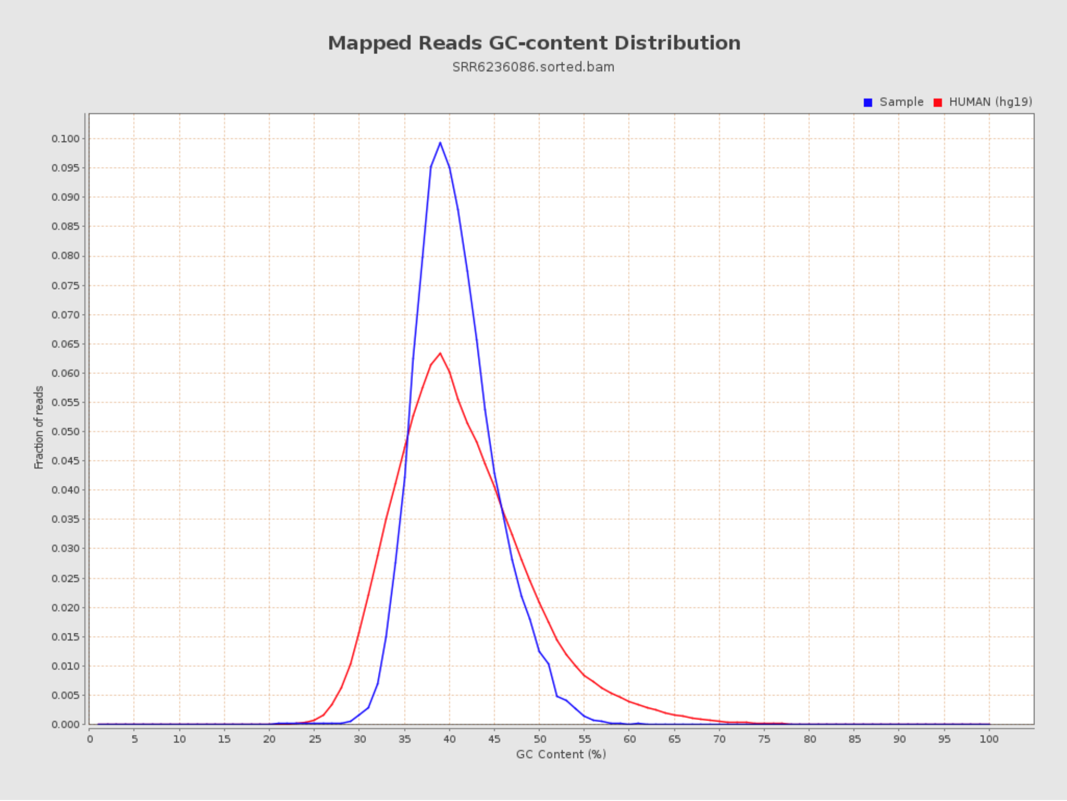
7. Results : Duplication Rate Histogram



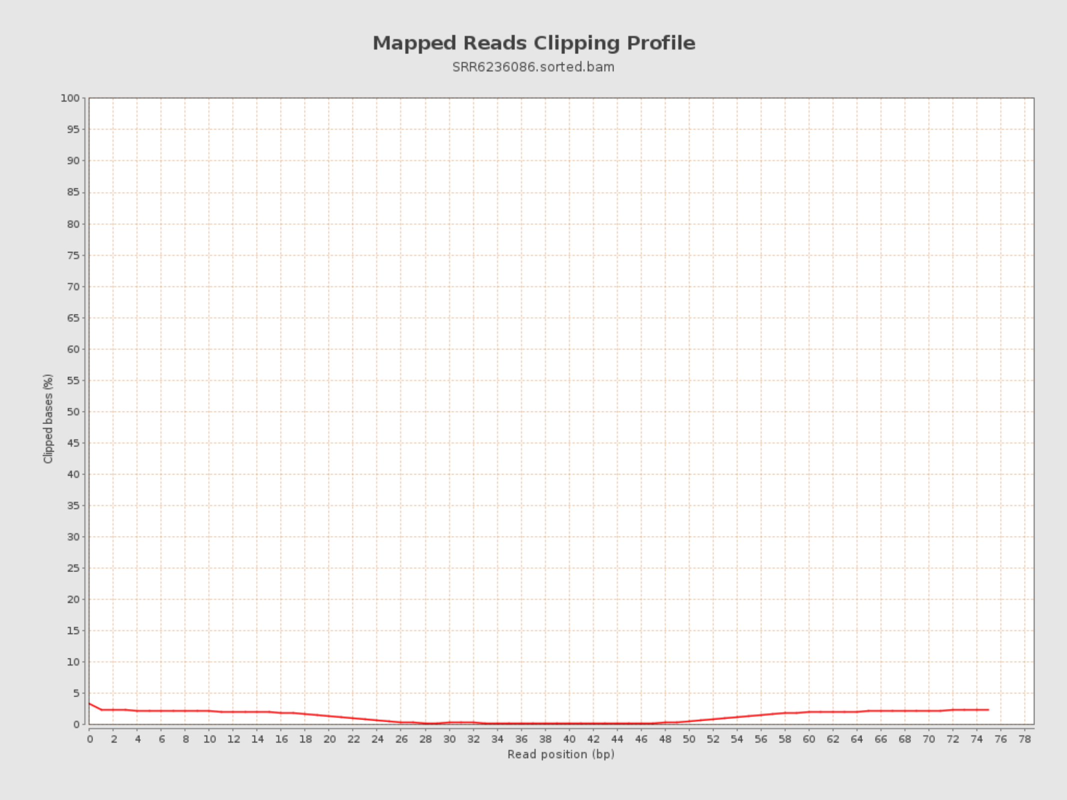
8. Results : Mapped Reads Nucleotide Content



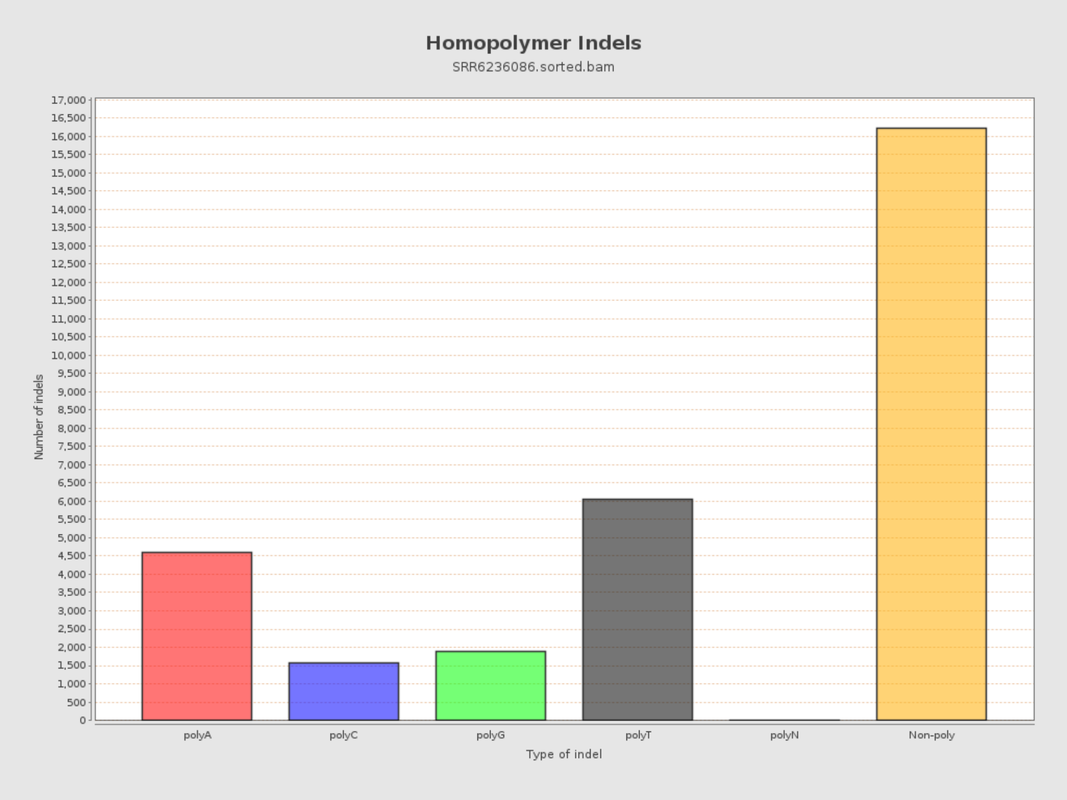
9. Results : Mapped Reads GC-content Distribution



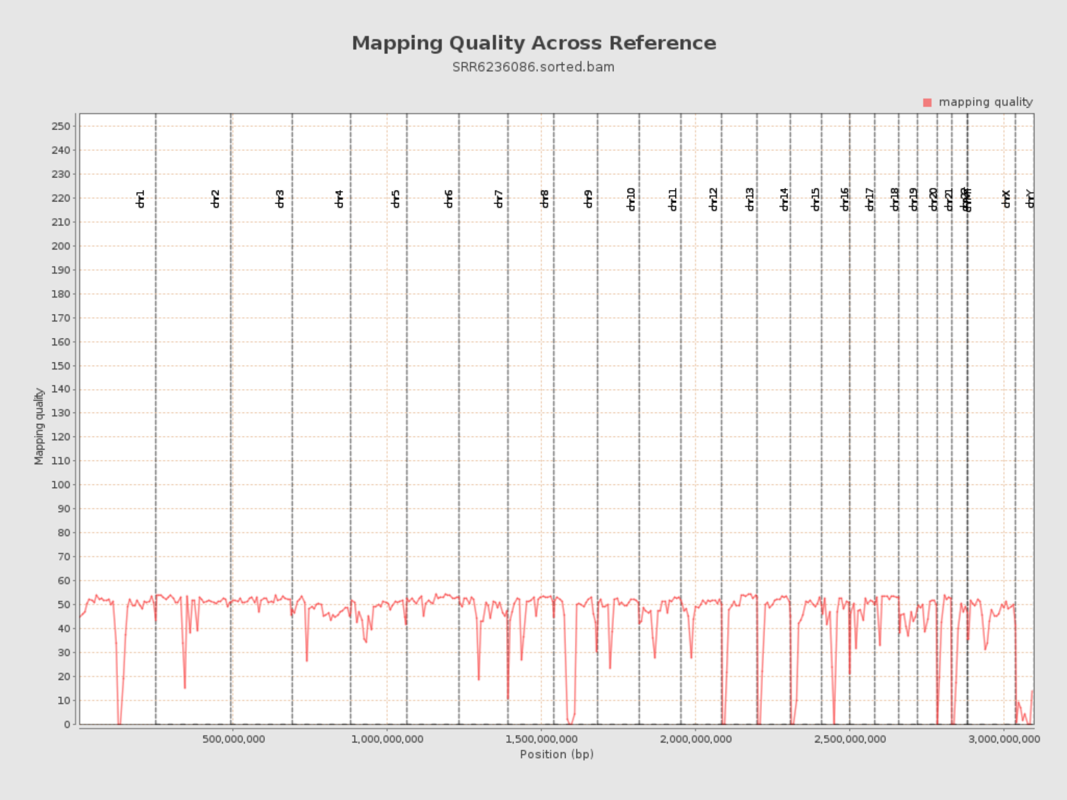
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram