Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 19:50:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236084.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_SRR6236084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 19:50:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,485,988
Mapped reads	1,285,751 / 86.52%
Unmapped reads	200,237 / 13.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,030 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	57,539 / 3.87%
Duplication rate	3.6%
Clipped reads	625,586 / 42.1%

2.2. ACGT Content

Number/percentage of A's	22,848,736 / 27.16%
Number/percentage of C's	15,072,854 / 17.92%
Number/percentage of T's	27,087,656 / 32.2%
Number/percentage of G's	19,054,844 / 22.65%
Number/percentage of N's	48,704 / 0.06%
GC Percentage	40.57%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2674

2.4. Mapping Quality

Mean Mapping Quality	45.7

2.5. Mismatches and indels

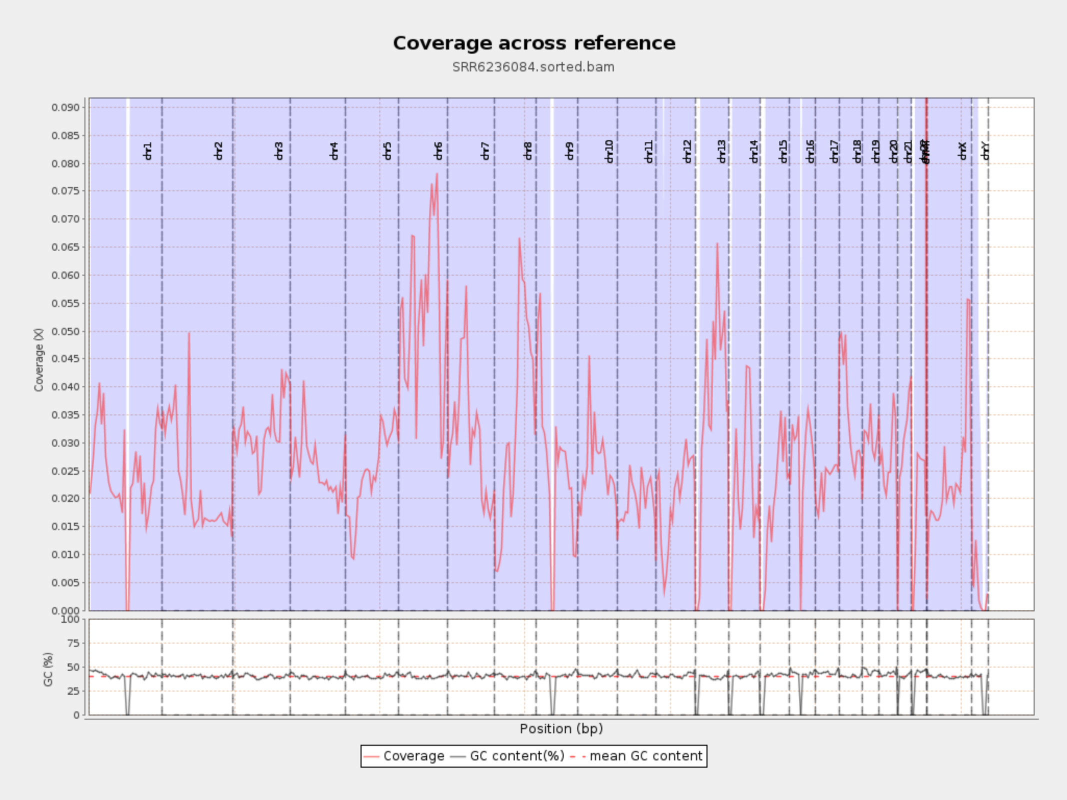
General error rate	0.83%
Mismatches	689,045
Insertions	6,152
Mapped reads with at least one insertion	0.47%
Deletions	23,266
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.91%

2.6. Chromosome stats

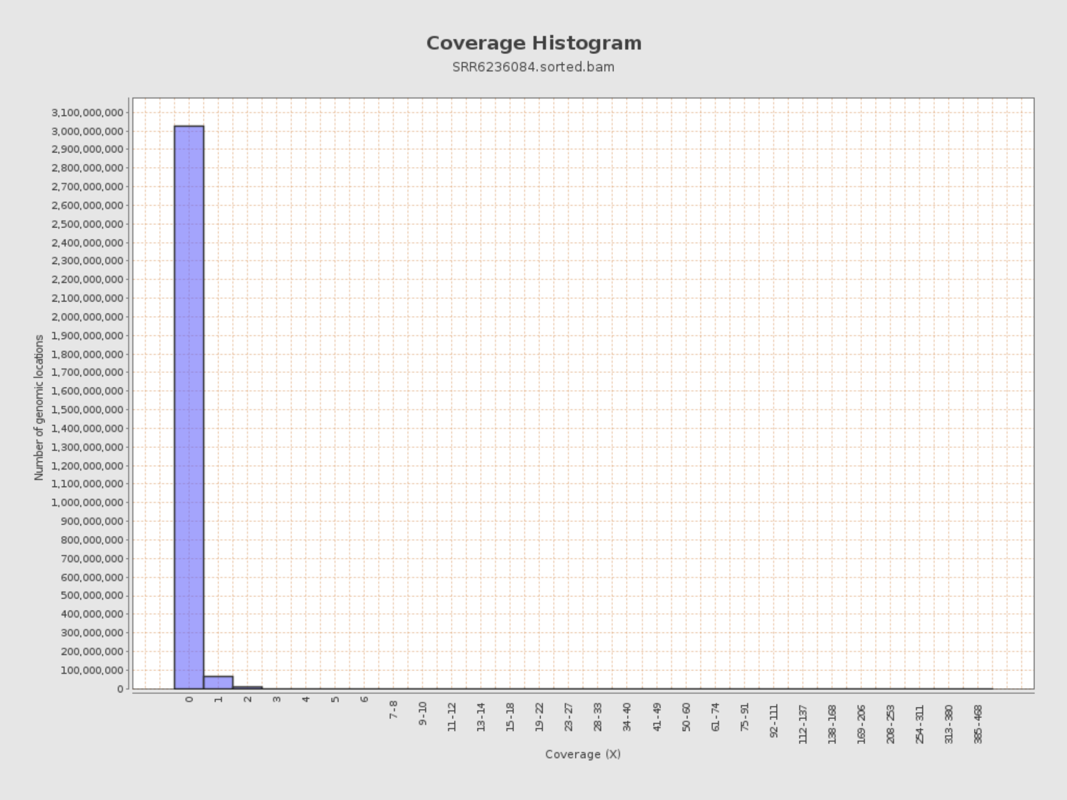
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6069256	0.0244	0.4214
chr2	243199373	5489990	0.0226	0.3076
chr3	198022430	6428895	0.0325	0.2027
chr4	191154276	4841290	0.0253	0.2025
chr5	180915260	4464758	0.0247	0.1774
chr6	171115067	9121193	0.0533	0.2982
chr7	159138663	4988740	0.0313	0.4026

chr8	146364022	4877417	0.0333	0.3435
chr9	141213431	3601728	0.0255	0.2579
chr10	135534747	3539980	0.0261	0.2549
chr11	135006516	2644804	0.0196	0.1981
chr12	133851895	2708245	0.0202	0.1668
chr13	115169878	4159788	0.0361	0.2155
chr14	107349540	2289556	0.0213	0.1727
chr15	102531392	1931026	0.0188	0.1567
chr16	90354753	2497213	0.0276	0.1978
chr17	81195210	1875237	0.0231	0.1859
chr18	78077248	2751483	0.0352	0.3769
chr19	59128983	1825109	0.0309	0.3244
chr20	63025520	1719838	0.0273	0.1903
chr21	48129895	1395863	0.029	0.2058
chr22	51304566	959012	0.0187	0.1527
chrMT	16571	43526	2.6266	2.3776
chrX	155270560	3732601	0.024	0.1876
chrY	59373566	196654	0.0033	0.1107

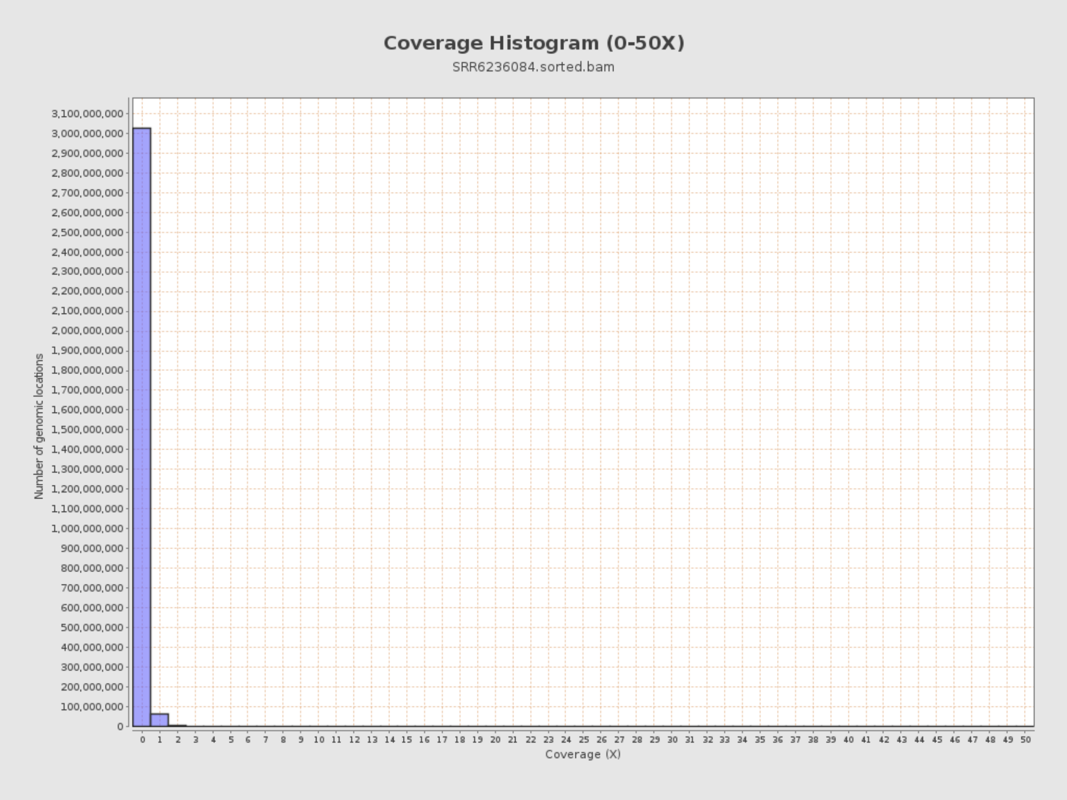
3. Results : Coverage across reference



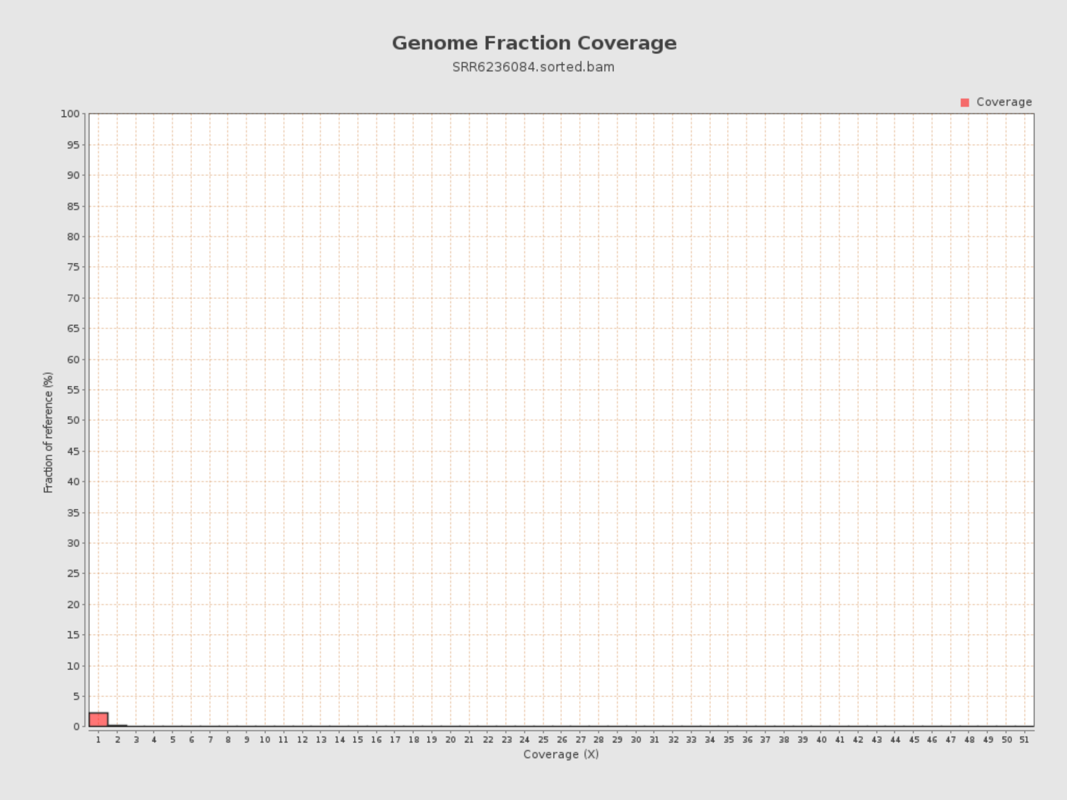
4. Results : Coverage Histogram



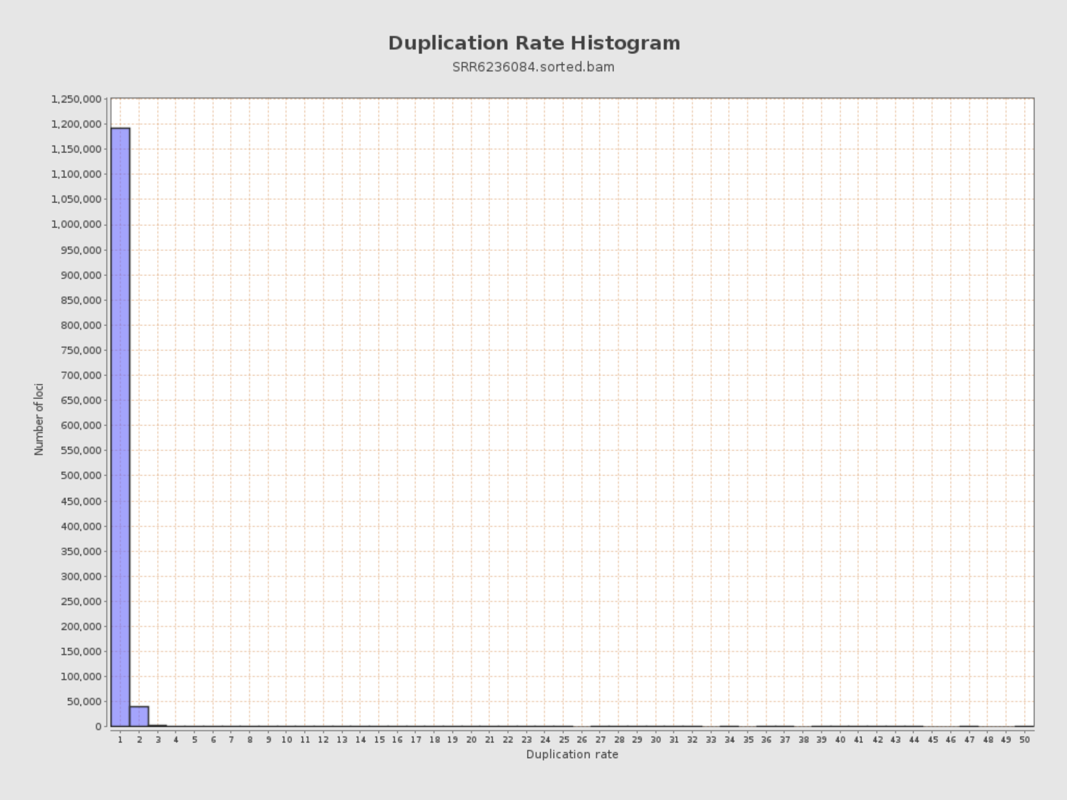
5. Results : Coverage Histogram (0-50X)



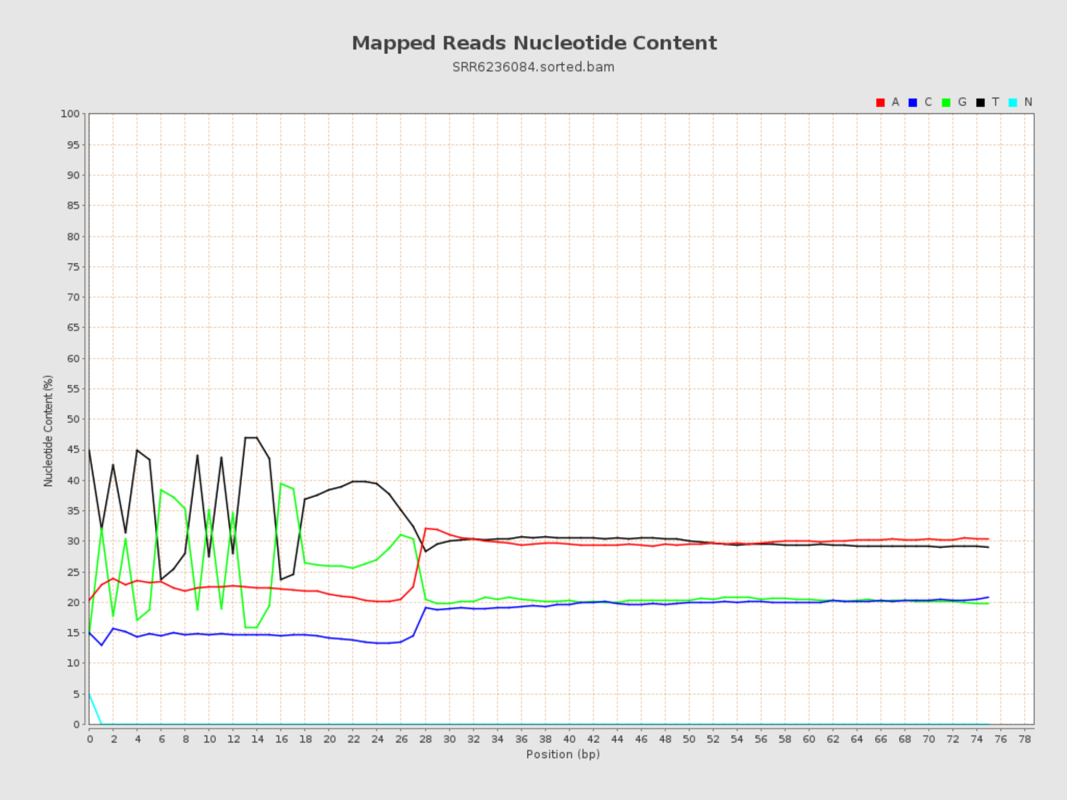
6. Results : Genome Fraction Coverage



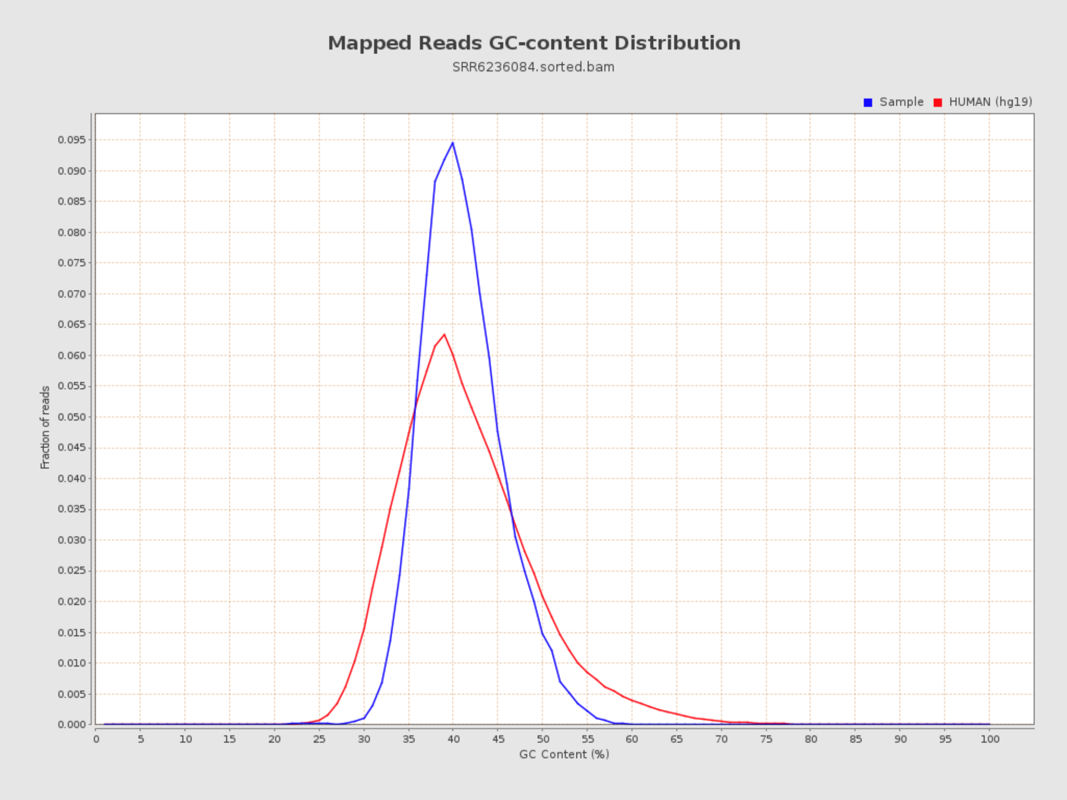
7. Results : Duplication Rate Histogram



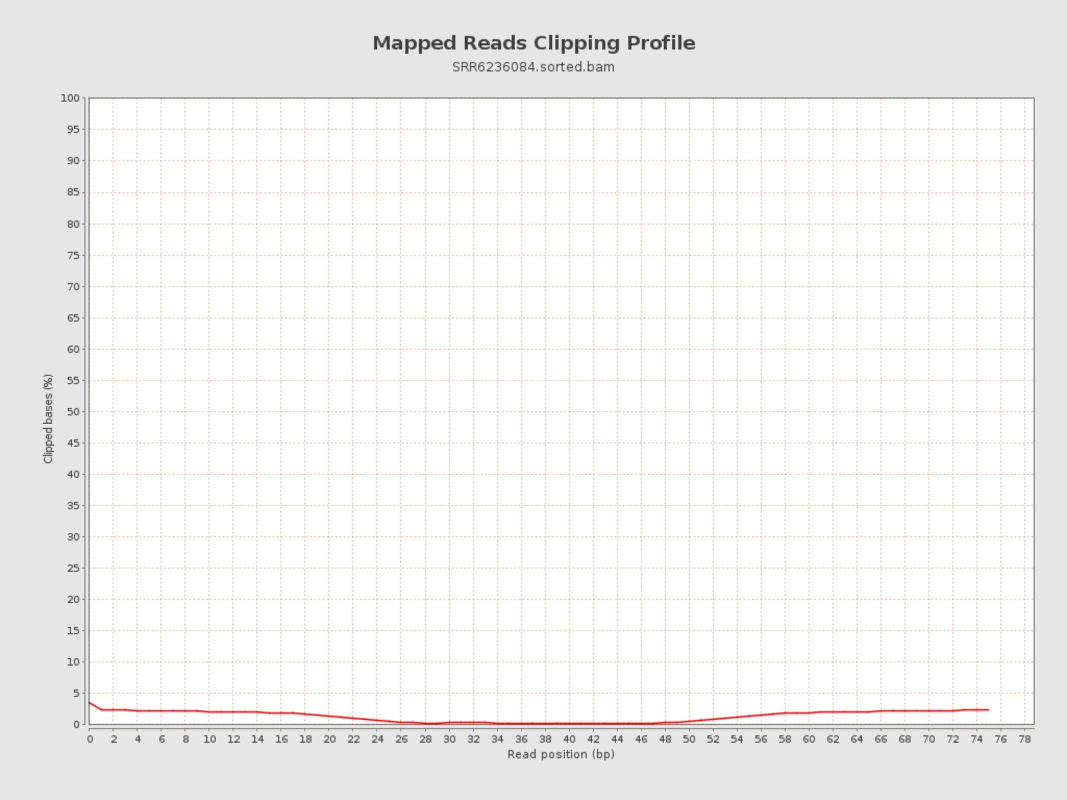
8. Results : Mapped Reads Nucleotide Content



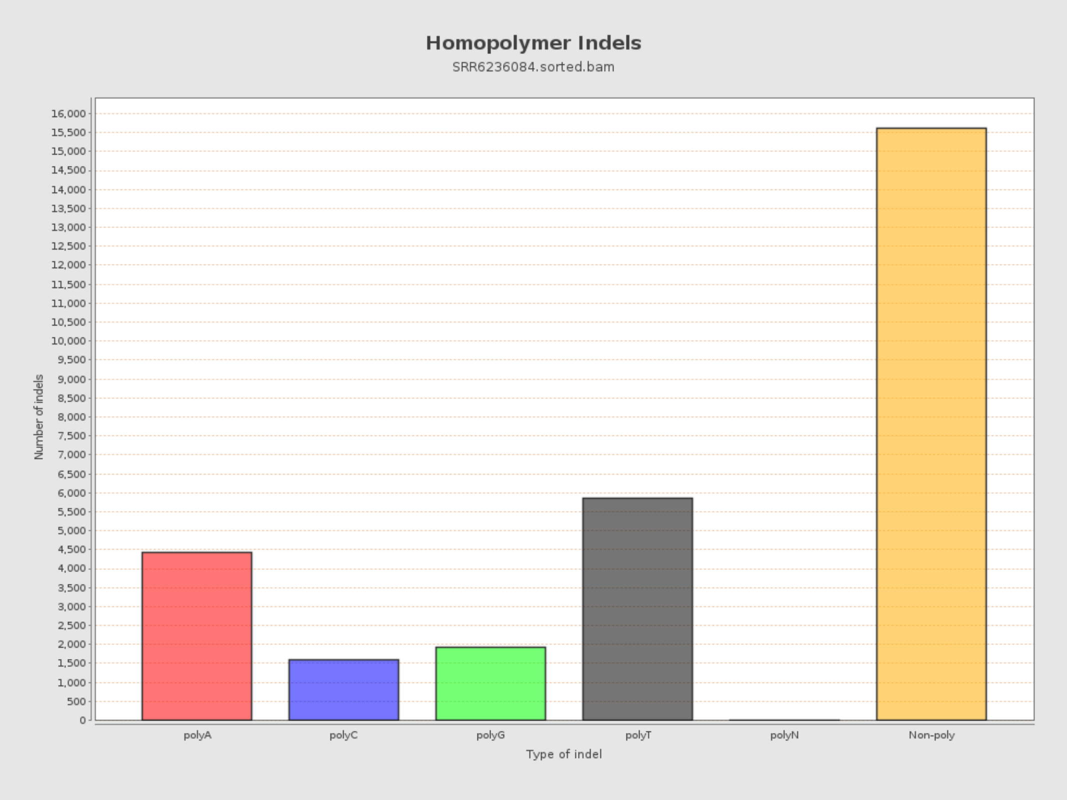
9. Results : Mapped Reads GC-content Distribution



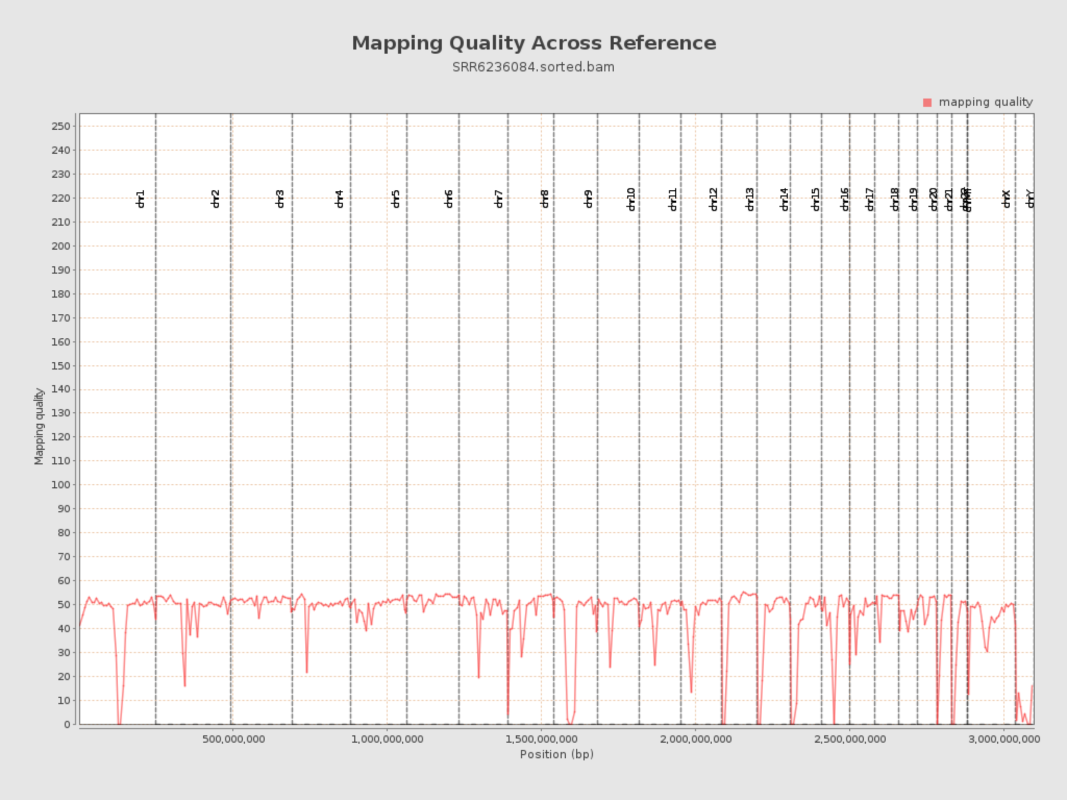
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram