Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:44:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524536.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_SRR10524536 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524536.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:44:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524536.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,919,642
Mapped reads	1,754,490 / 91.4%
Unmapped reads	165,152 / 8.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,013 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	105,049 / 5.47%
Duplication rate	4.58%
Clipped reads	1,757,646 / 91.56%

2.2. ACGT Content

Number/percentage of A's	26,423,332 / 25.65%
Number/percentage of C's	19,478,696 / 18.91%
Number/percentage of T's	32,931,715 / 31.97%
Number/percentage of G's	24,184,710 / 23.48%
Number/percentage of N's	1,403 / 0%
GC Percentage	42.38%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.3181

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

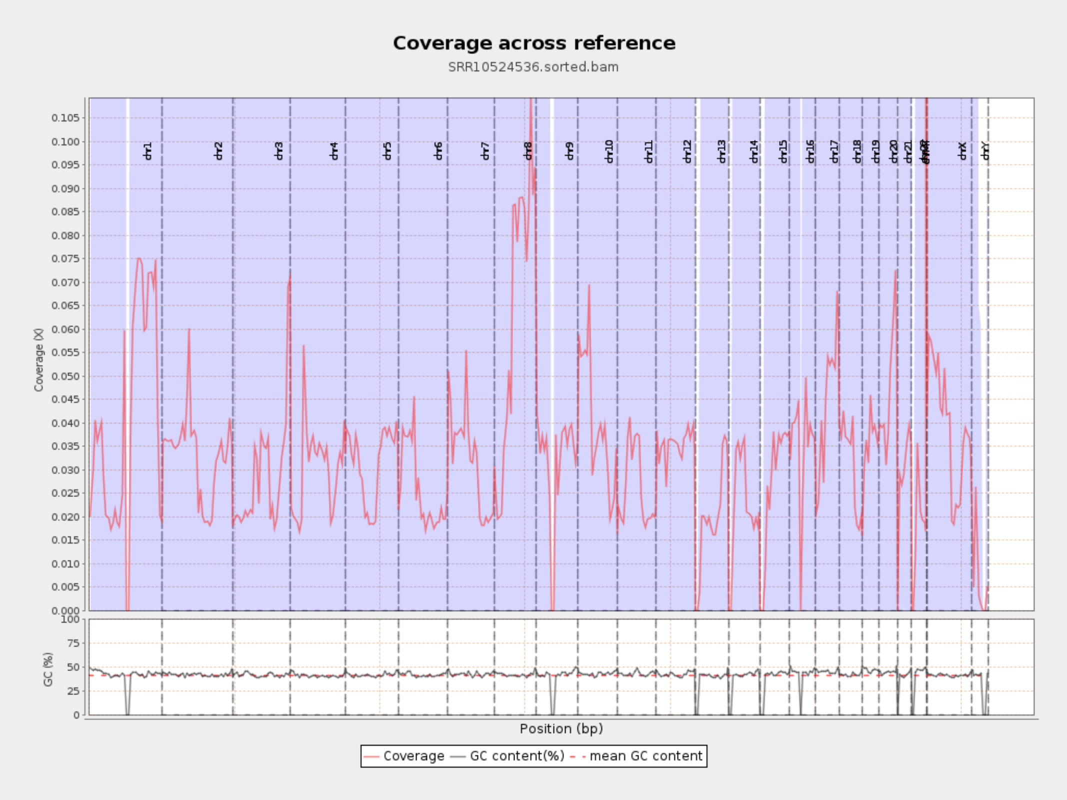
General error rate	0.53%
Mismatches	528,266
Insertions	7,259
Mapped reads with at least one insertion	0.41%
Deletions	19,523
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.33%

2.6. Chromosome stats

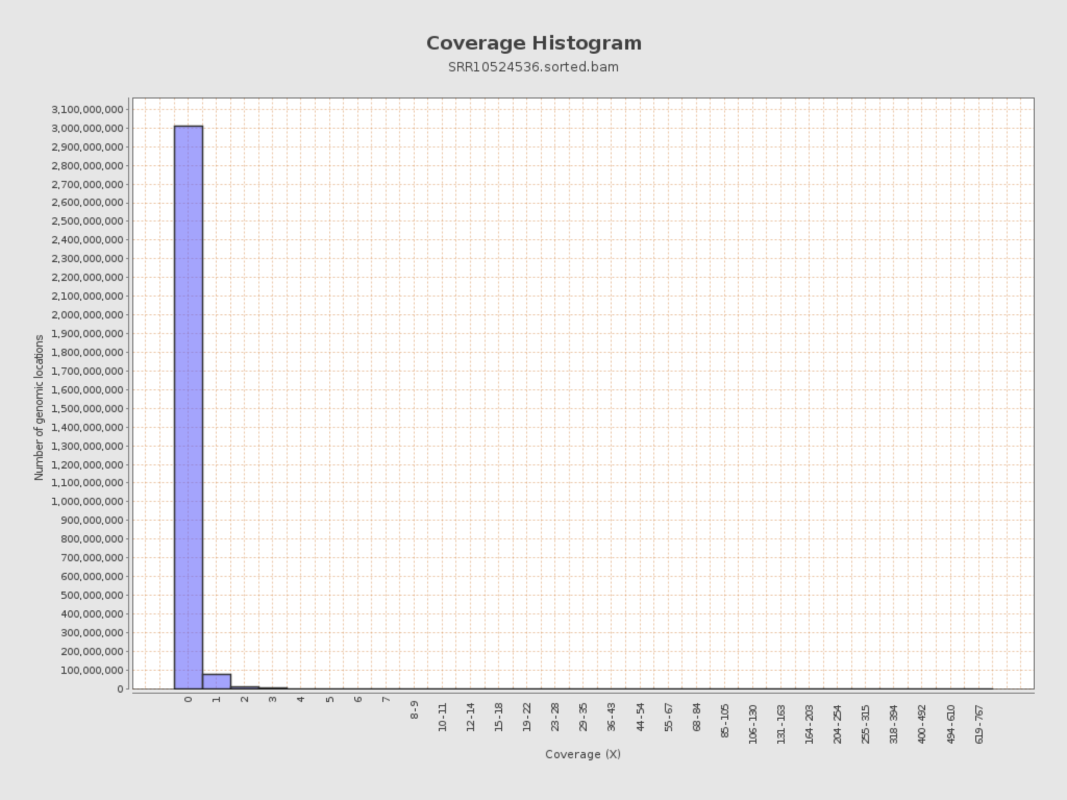
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10217775	0.041	0.6002
chr2	243199373	8074614	0.0332	0.371
chr3	198022430	5586706	0.0282	0.1924
chr4	191154276	5743314	0.03	0.2559
chr5	180915260	5682216	0.0314	0.2024
chr6	171115067	4410984	0.0258	0.2331
chr7	159138663	5090530	0.032	0.3647

chr8	146364022	9368689	0.064	0.37
chr9	141213431	4392026	0.0311	0.2663
chr10	135534747	5468302	0.0403	0.3466
chr11	135006516	3539224	0.0262	0.2719
chr12	133851895	4754924	0.0355	0.2154
chr13	115169878	2257336	0.0196	0.1601
chr14	107349540	2388571	0.0223	0.1762
chr15	102531392	2745026	0.0268	0.187
chr16	90354753	3194268	0.0354	0.2309
chr17	81195210	3641663	0.0449	0.2587
chr18	78077248	2461864	0.0315	0.4859
chr19	59128983	2118733	0.0358	0.3934
chr20	63025520	3006410	0.0477	0.2547
chr21	48129895	1417505	0.0295	0.2365
chr22	51304566	855373	0.0167	0.1453
chrMT	16571	104527	6.3078	4.57
chrX	155270560	6135139	0.0395	0.25
chrY	59373566	397041	0.0067	0.2316

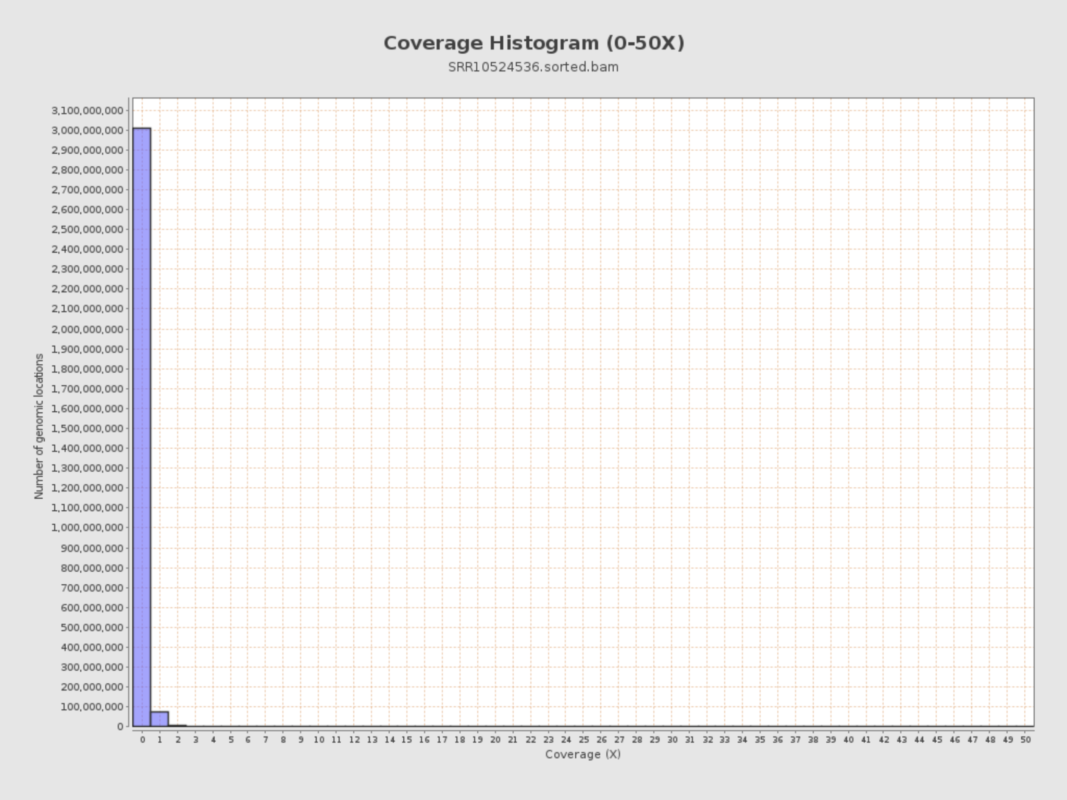
3. Results : Coverage across reference



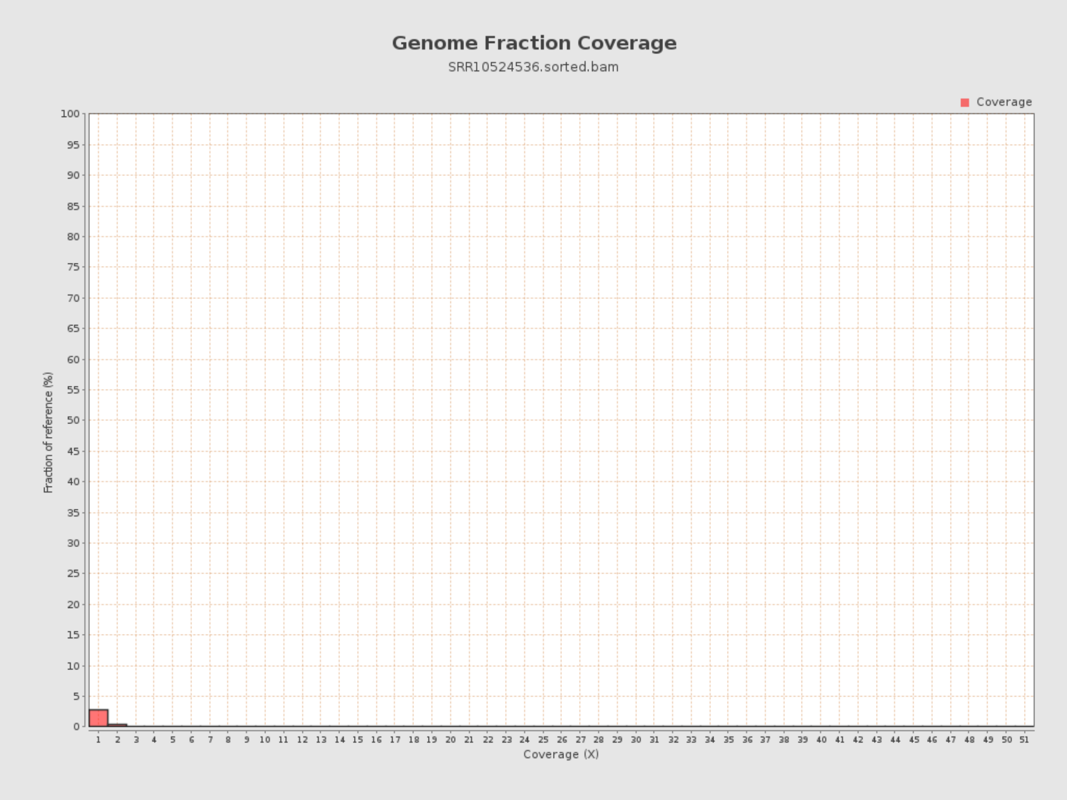
4. Results : Coverage Histogram



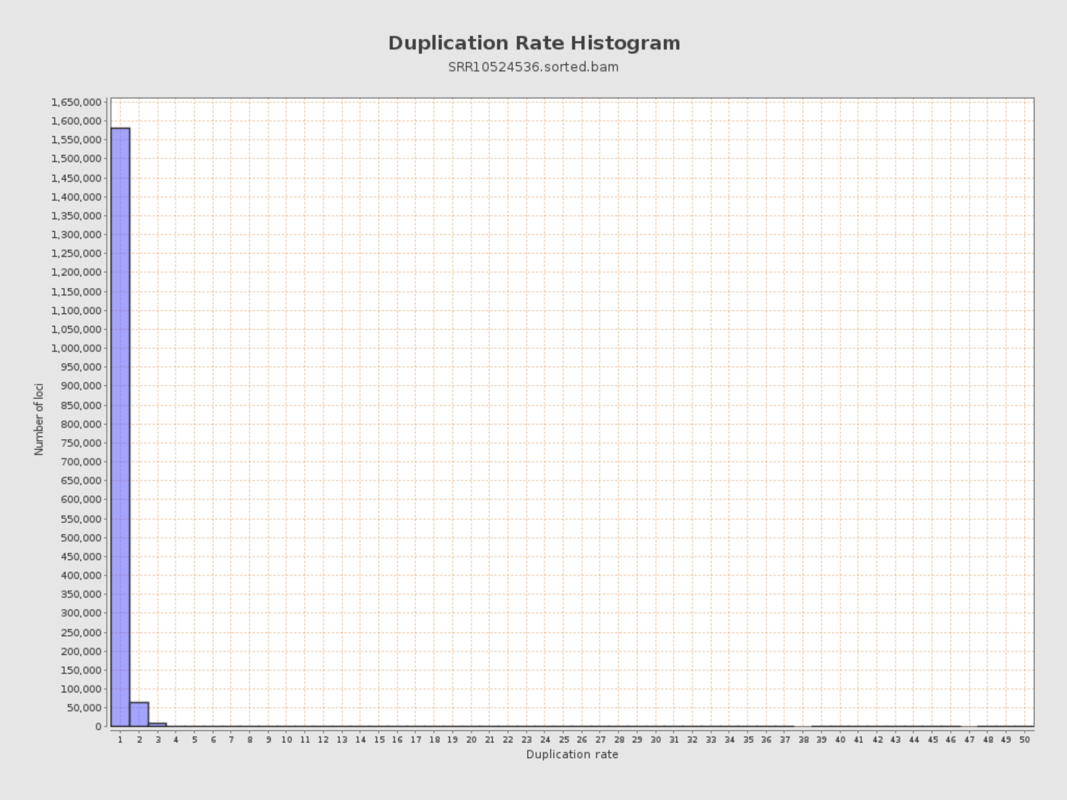
5. Results : Coverage Histogram (0-50X)



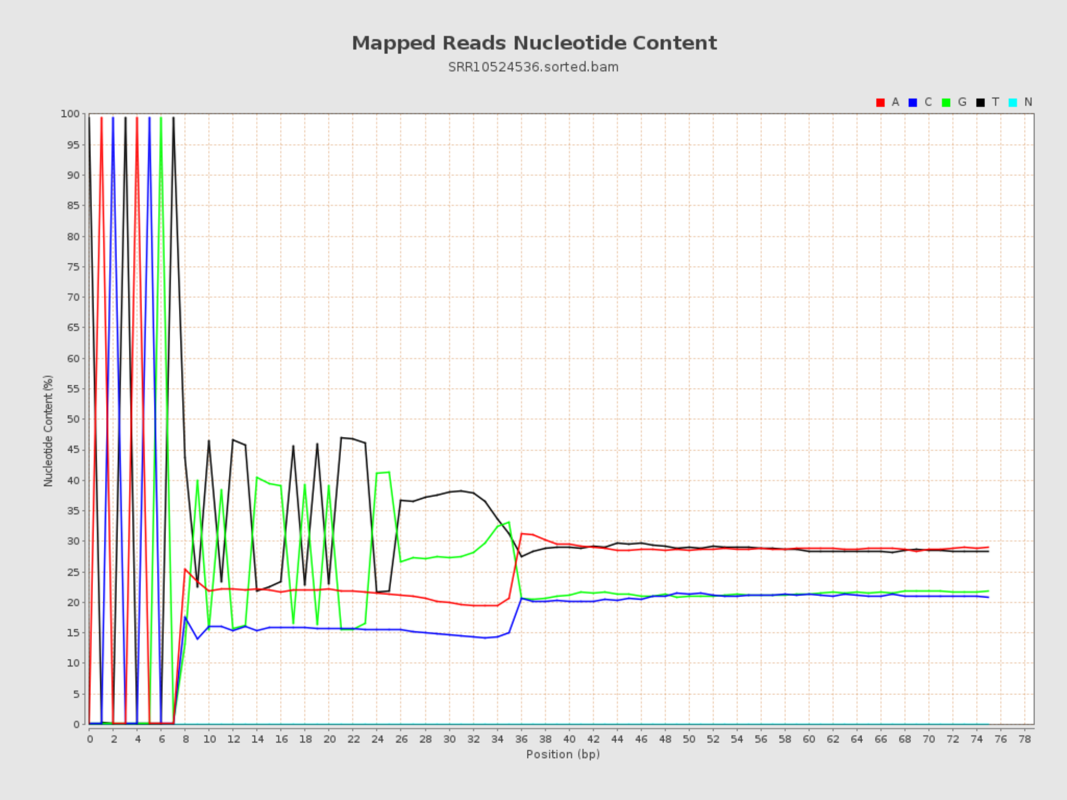
6. Results : Genome Fraction Coverage



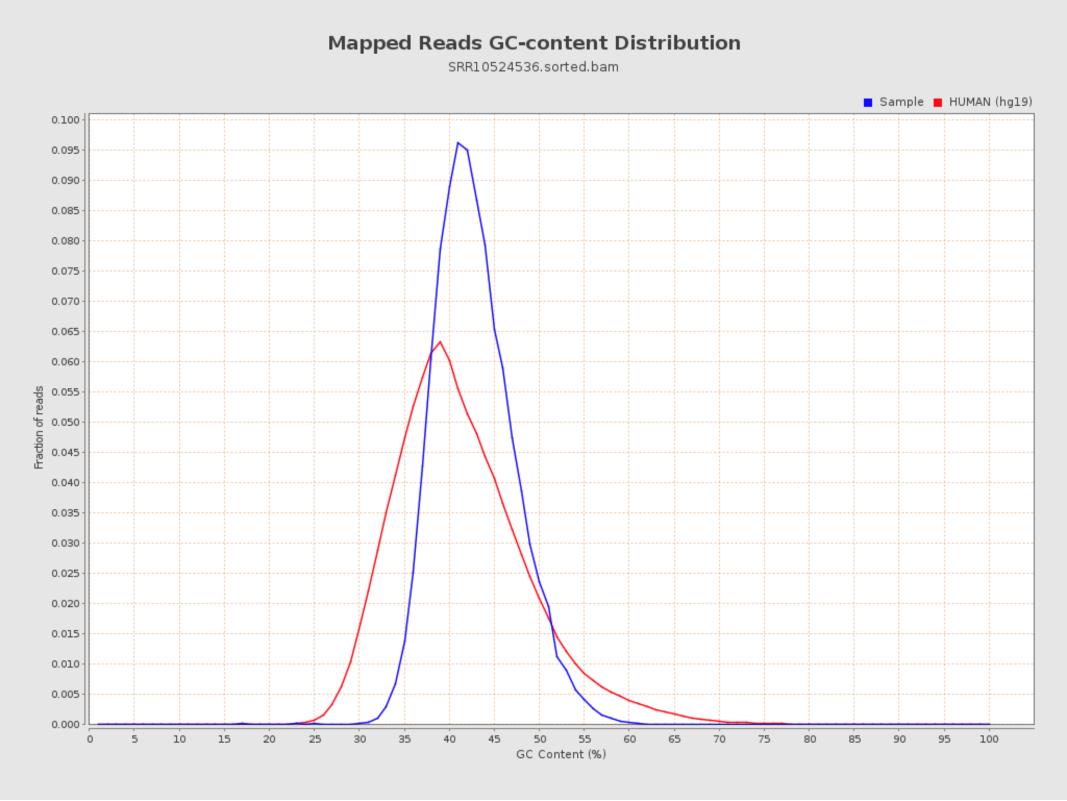
7. Results : Duplication Rate Histogram



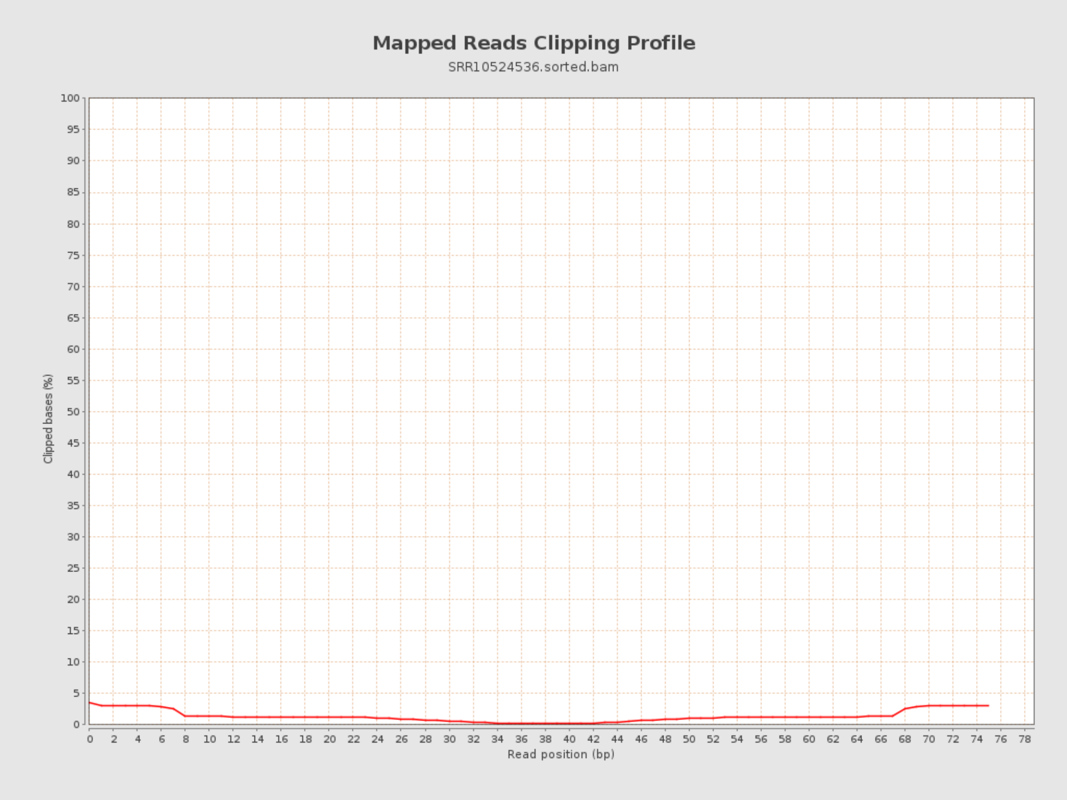
8. Results : Mapped Reads Nucleotide Content



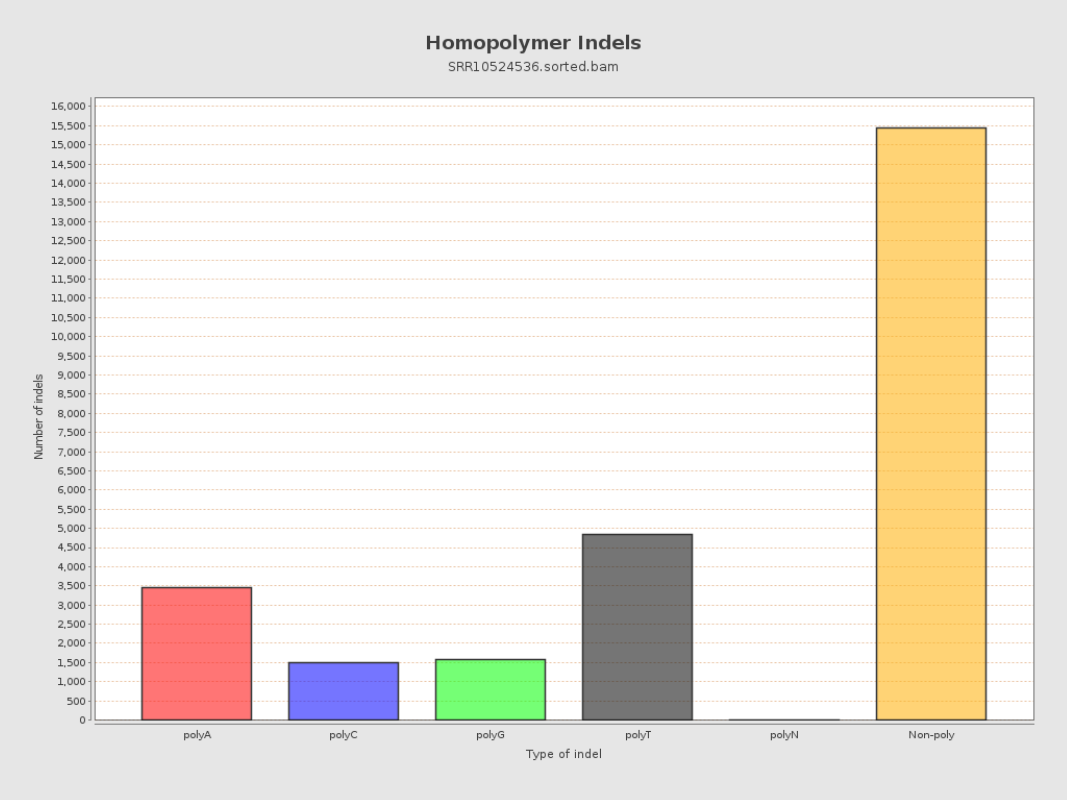
9. Results : Mapped Reads GC-content Distribution



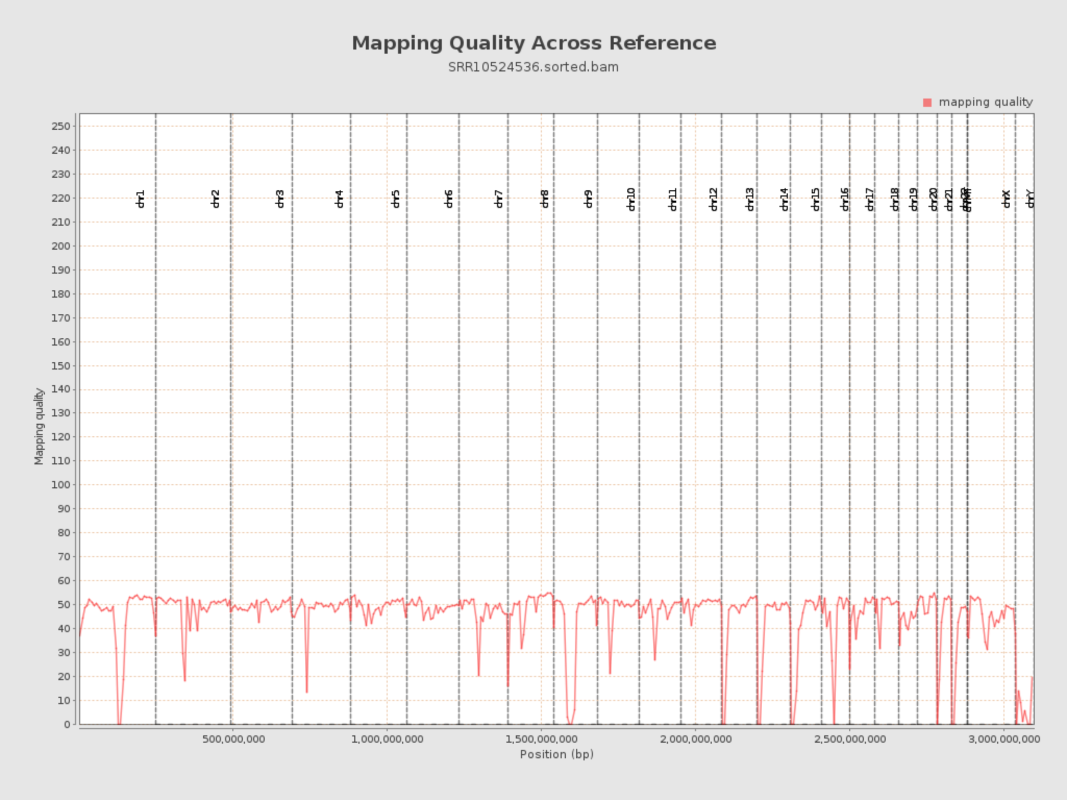
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram