Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:33:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524785.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_SRR10524785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524785.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:33:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524785.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,376,201
Mapped reads	1,244,697 / 90.44%
Unmapped reads	131,504 / 9.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,635 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	39,178 / 2.85%
Duplication rate	2.41%
Clipped reads	1,245,634 / 90.51%

2.2. ACGT Content

Number/percentage of A's	17,107,983 / 24.04%
Number/percentage of C's	14,341,453 / 20.15%
Number/percentage of T's	23,051,584 / 32.39%
Number/percentage of G's	16,664,757 / 23.41%
Number/percentage of N's	7,643 / 0.01%
GC Percentage	43.56%

2.3. Coverage

Mean	0.023

Standard Deviation	0.2096

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

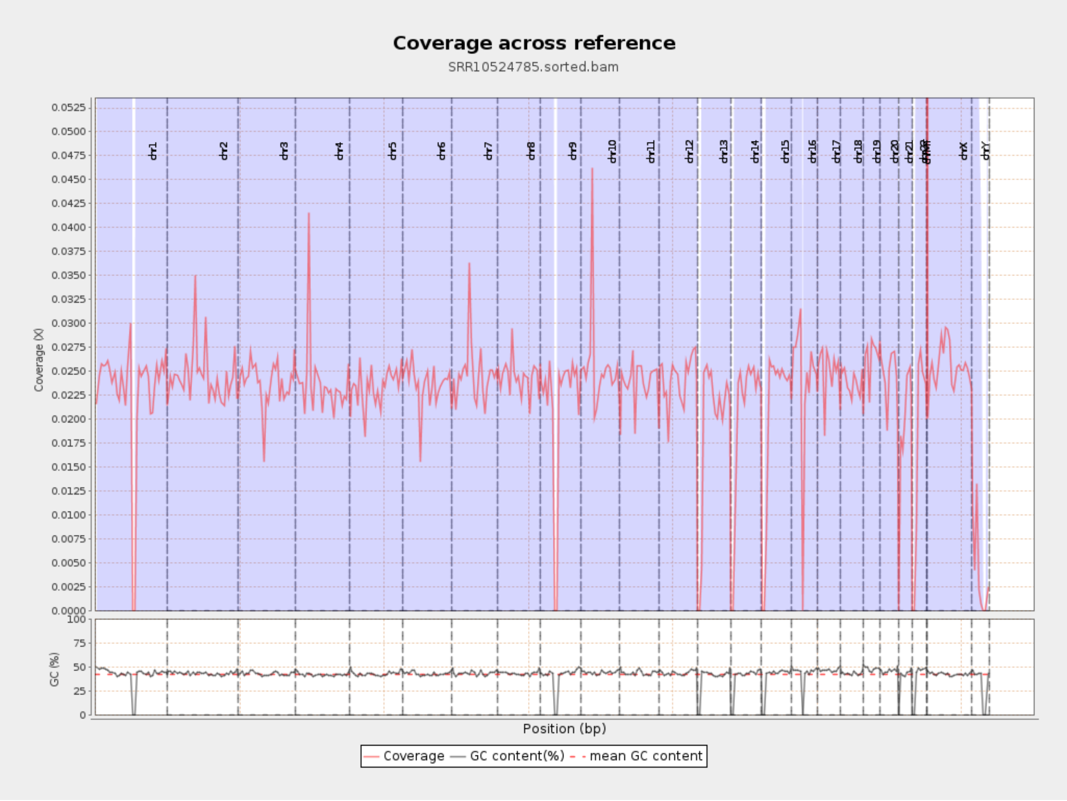
General error rate	0.53%
Mismatches	367,282
Insertions	4,584
Mapped reads with at least one insertion	0.37%
Deletions	14,461
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.46%

2.6. Chromosome stats

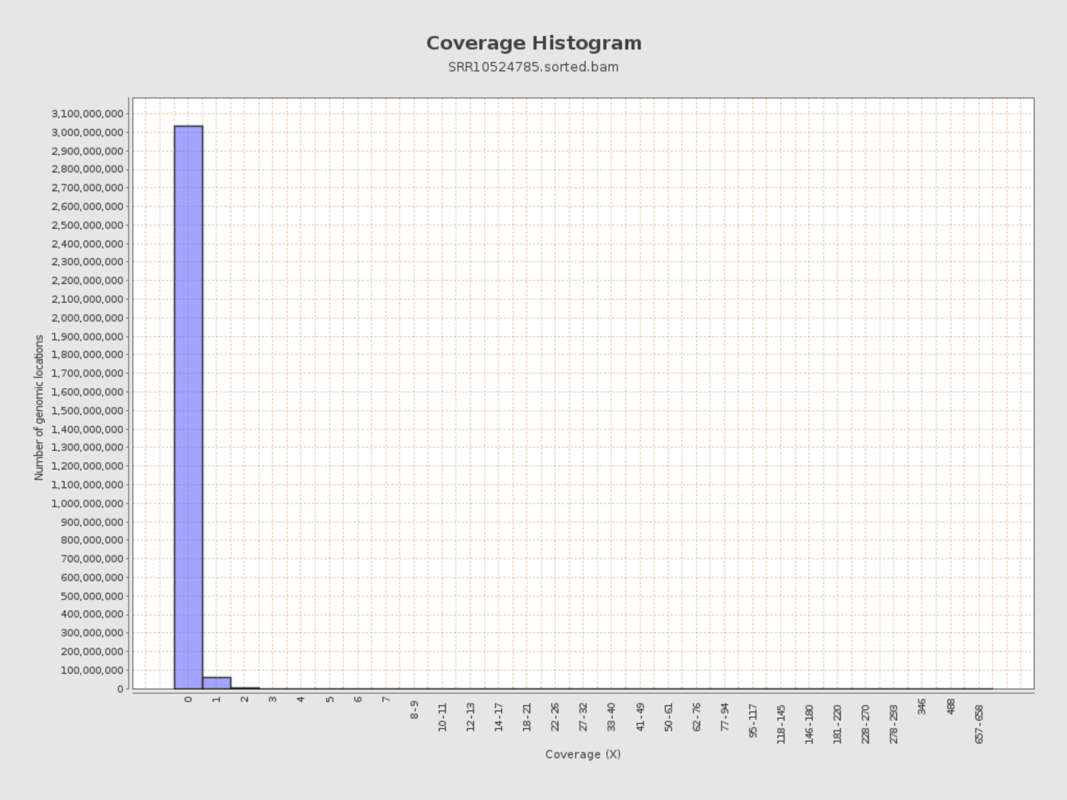
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5689028	0.0228	0.264
chr2	243199373	5954272	0.0245	0.3266
chr3	198022430	4700067	0.0237	0.1677
chr4	191154276	4551823	0.0238	0.184
chr5	180915260	4251241	0.0235	0.1659
chr6	171115067	4039242	0.0236	0.1788
chr7	159138663	3932393	0.0247	0.2584

chr8	146364022	3566470	0.0244	0.1925
chr9	141213431	3002135	0.0213	0.1844
chr10	135534747	3465128	0.0256	0.2457
chr11	135006516	3250163	0.0241	0.1941
chr12	133851895	3235978	0.0242	0.1701
chr13	115169878	2197410	0.0191	0.1495
chr14	107349540	2144629	0.02	0.1543
chr15	102531392	2059317	0.0201	0.1572
chr16	90354753	2142459	0.0237	0.18
chr17	81195210	2030893	0.025	0.1786
chr18	78077248	1858336	0.0238	0.2648
chr19	59128983	1556837	0.0263	0.2336
chr20	63025520	1538854	0.0244	0.179
chr21	48129895	923551	0.0192	0.1623
chr22	51304566	890501	0.0174	0.1432
chrMT	16571	19849	1.1978	1.3877
chrX	155270560	3963517	0.0255	0.1825
chrY	59373566	232817	0.0039	0.1101

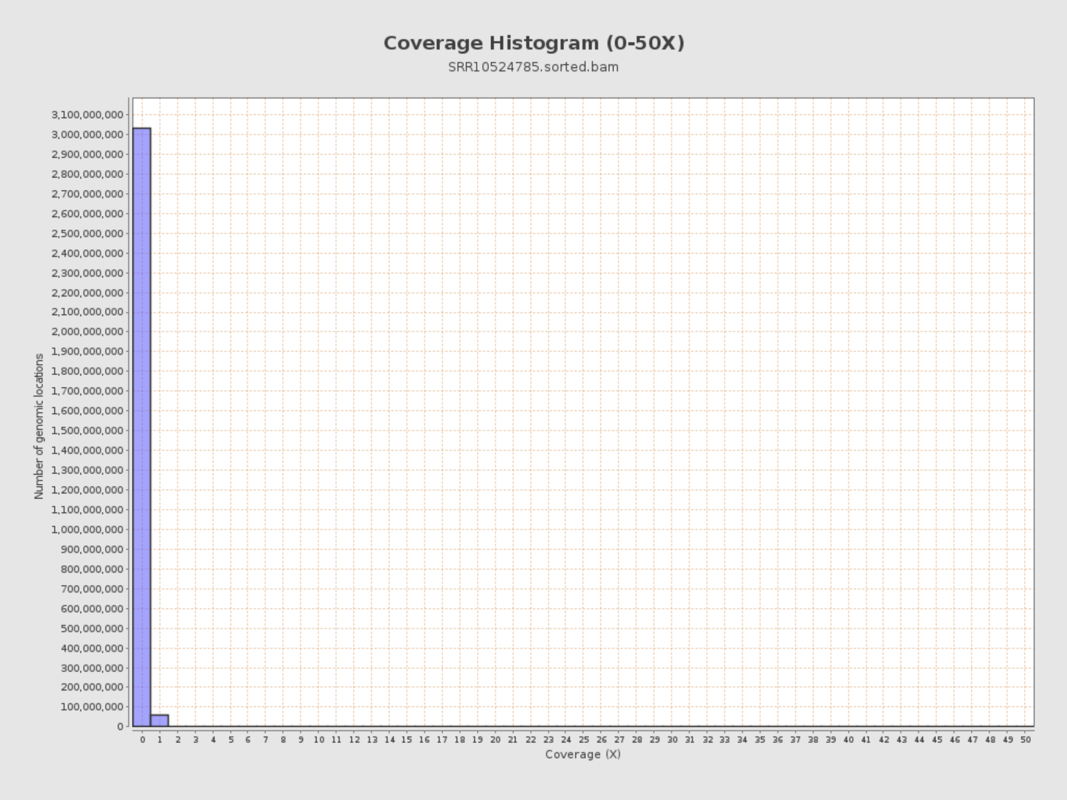
3. Results : Coverage across reference



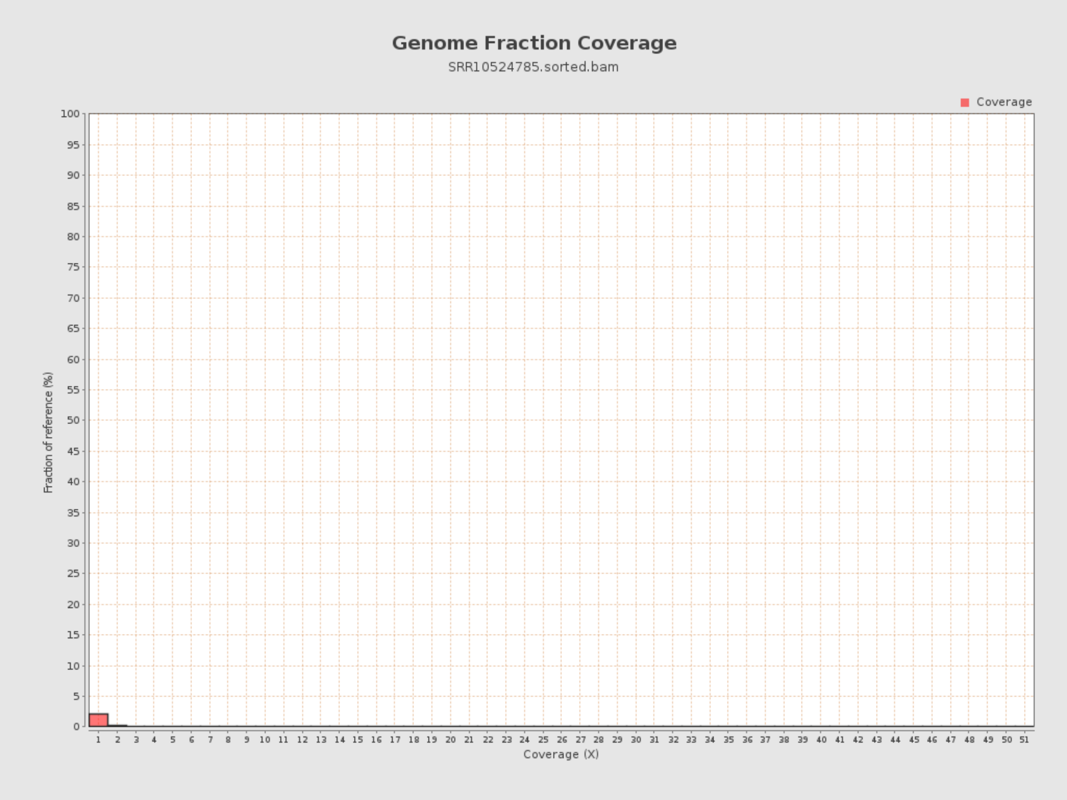
4. Results : Coverage Histogram



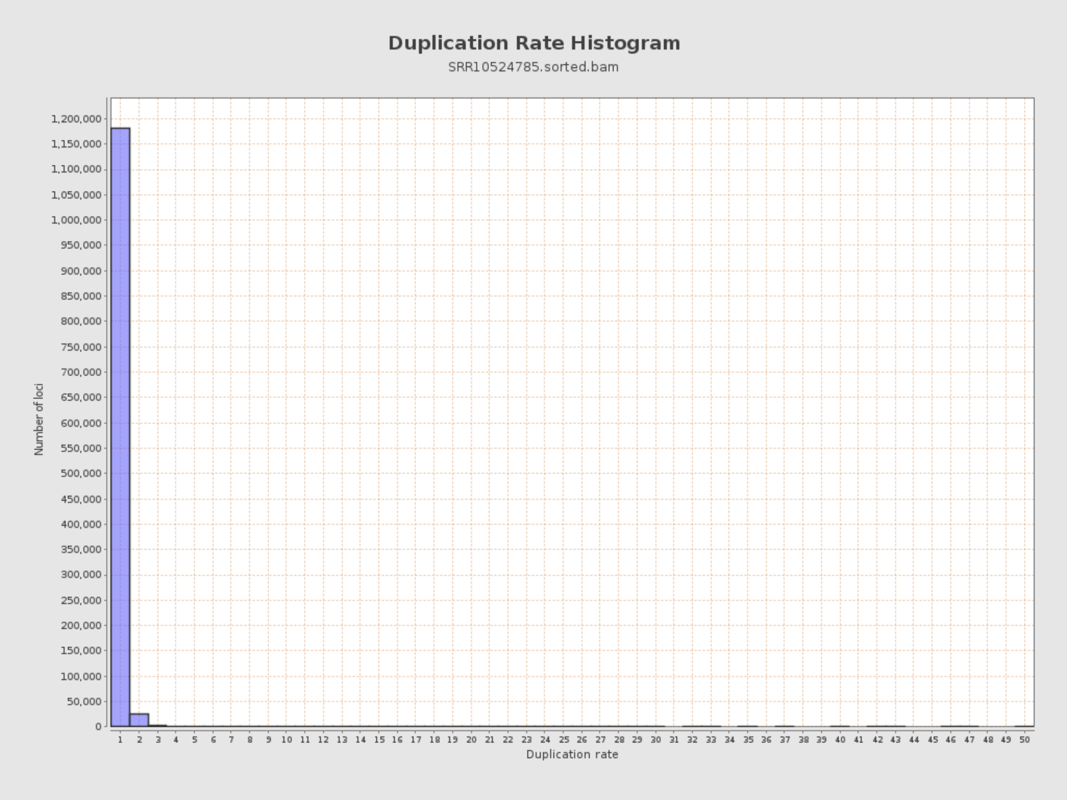
5. Results : Coverage Histogram (0-50X)



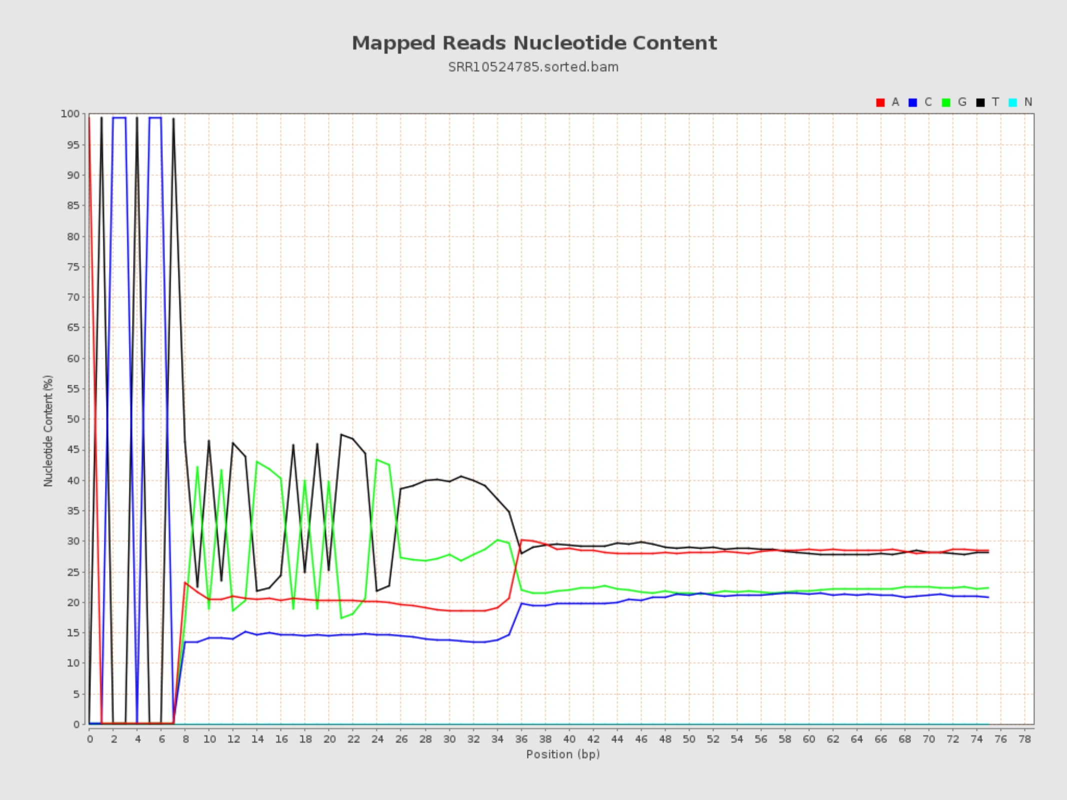
6. Results : Genome Fraction Coverage



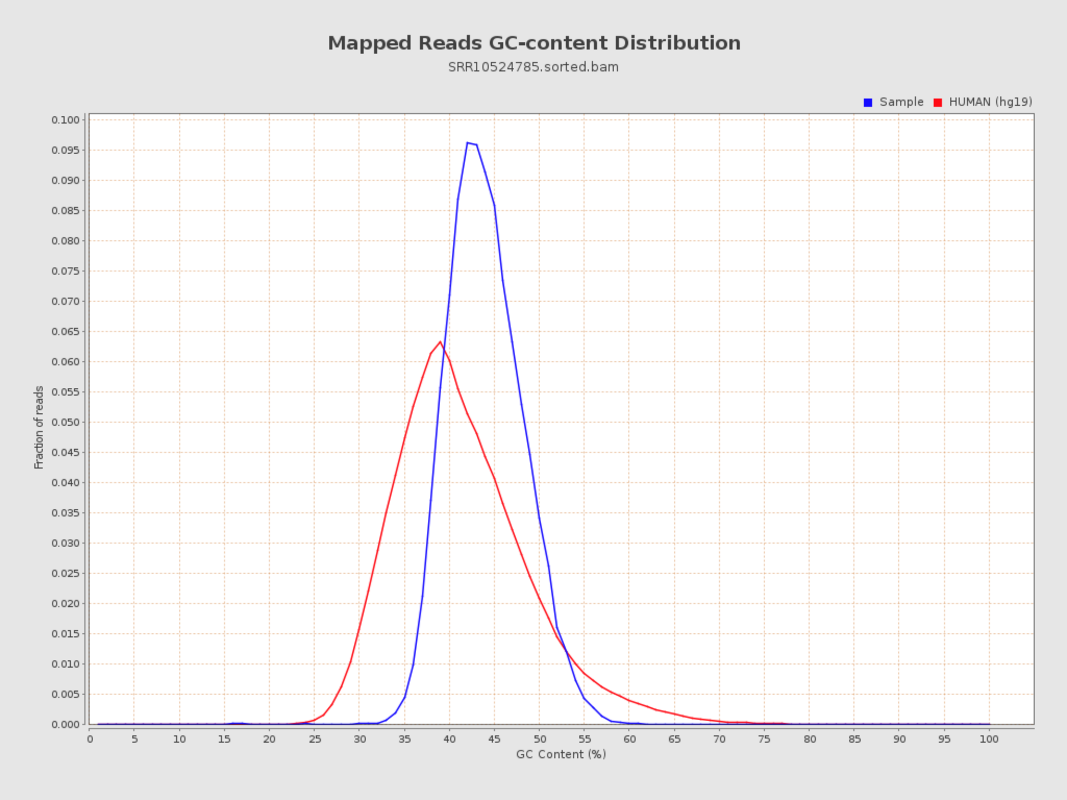
7. Results : Duplication Rate Histogram



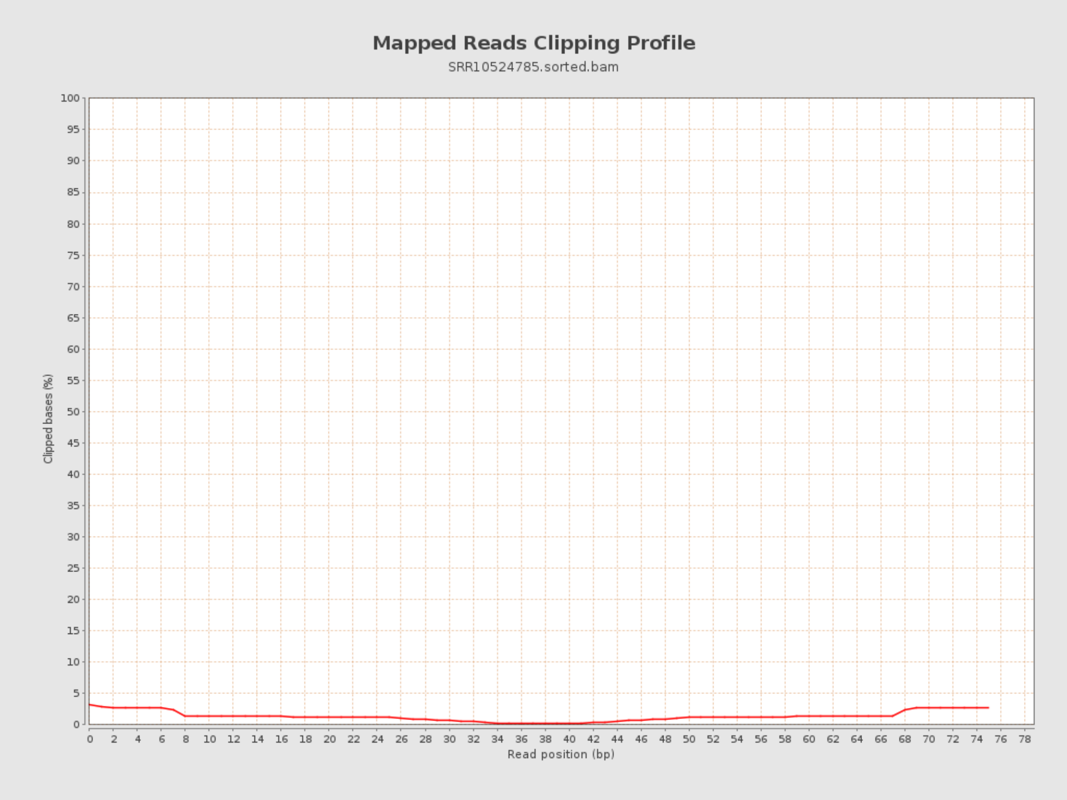
8. Results : Mapped Reads Nucleotide Content



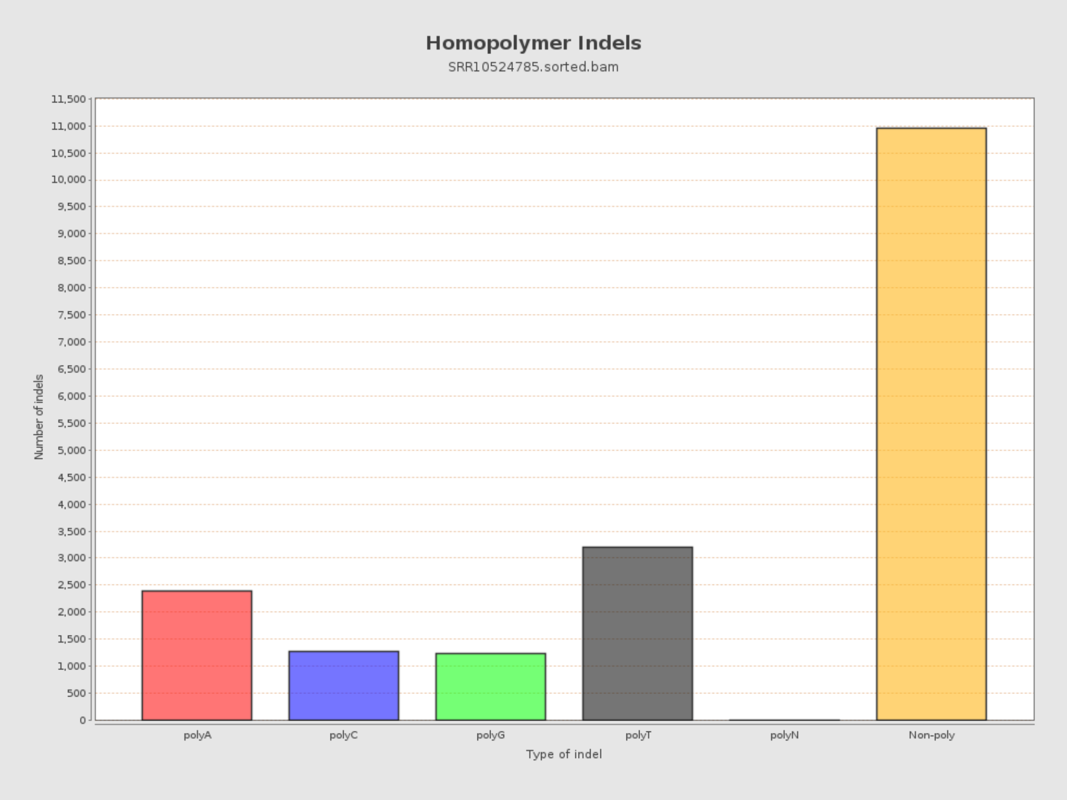
9. Results : Mapped Reads GC-content Distribution



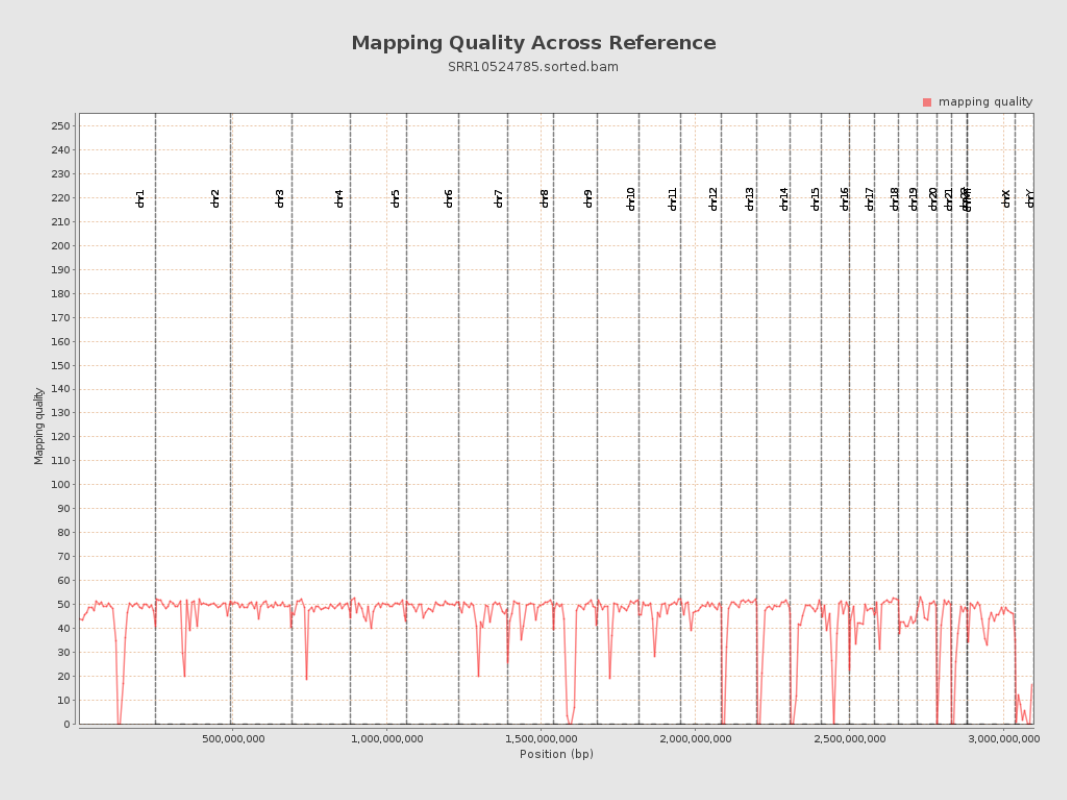
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram