Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 15:41:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524666.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_SRR10524666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524666.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 15:41:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,519,209
Mapped reads	1,408,561 / 92.72%
Unmapped reads	110,648 / 7.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,505 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	55,810 / 3.67%
Duplication rate	2.99%
Clipped reads	1,411,060 / 92.88%

2.2. ACGT Content

Number/percentage of A's	20,914,990 / 25.09%
Number/percentage of C's	15,740,795 / 18.88%
Number/percentage of T's	26,526,851 / 31.82%
Number/percentage of G's	20,161,072 / 24.19%
Number/percentage of N's	11,534 / 0.01%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.258

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

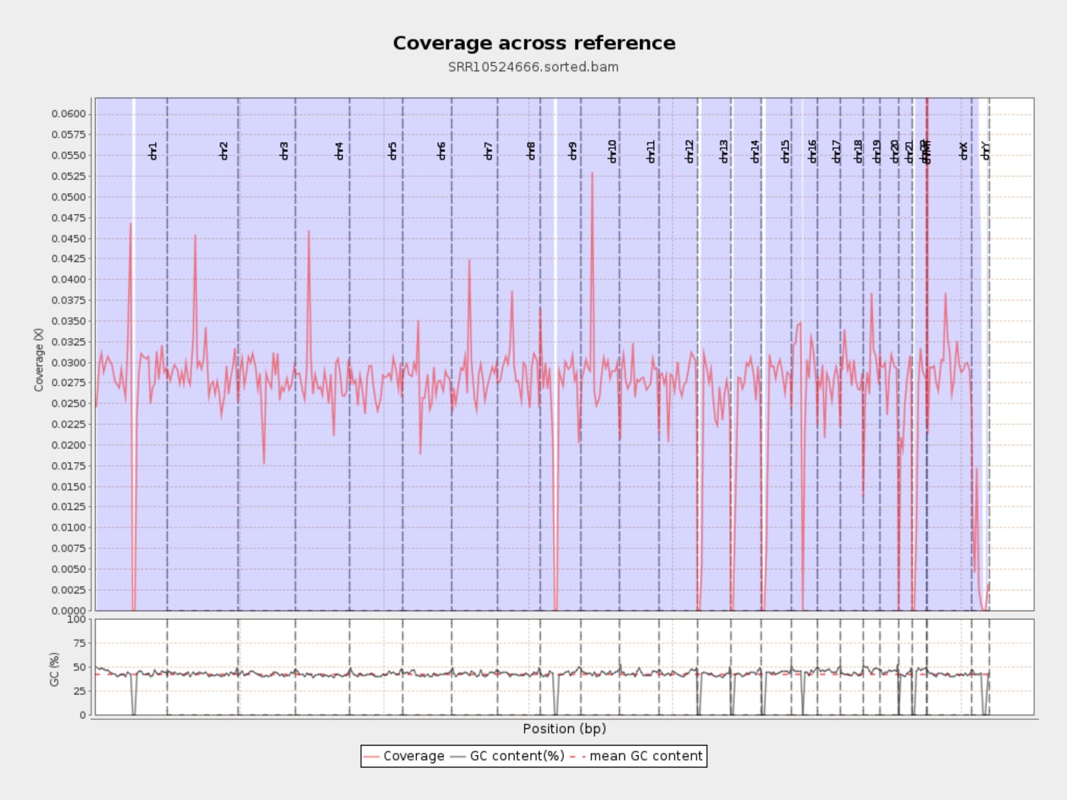
General error rate	0.51%
Mismatches	416,449
Insertions	5,964
Mapped reads with at least one insertion	0.42%
Deletions	15,607
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.41%

2.6. Chromosome stats

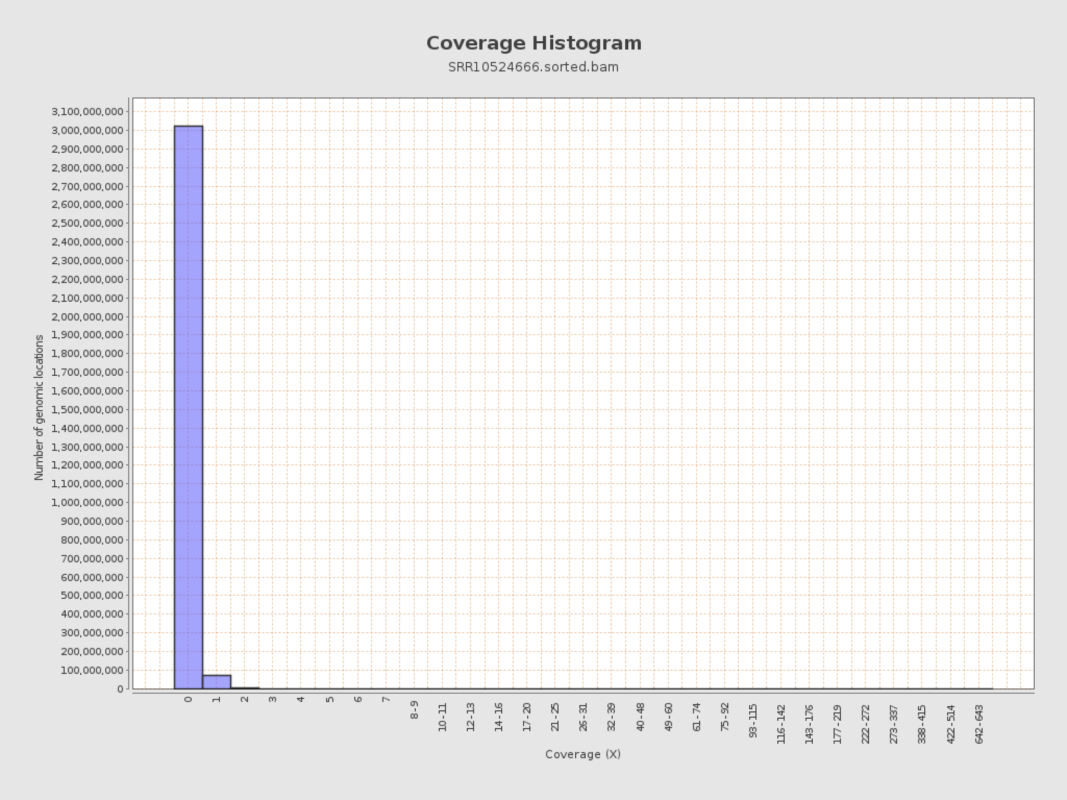
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6872058	0.0276	0.4371
chr2	243199373	7059853	0.029	0.3399
chr3	198022430	5514323	0.0278	0.1808
chr4	191154276	5403726	0.0283	0.2033
chr5	180915260	4997426	0.0276	0.1815
chr6	171115067	4726965	0.0276	0.2005
chr7	159138663	4538349	0.0285	0.3036

chr8	146364022	4261040	0.0291	0.269
chr9	141213431	3514441	0.0249	0.2183
chr10	135534747	4032787	0.0298	0.2671
chr11	135006516	3808136	0.0282	0.2277
chr12	133851895	3735422	0.0279	0.1828
chr13	115169878	2549654	0.0221	0.1616
chr14	107349540	2502747	0.0233	0.171
chr15	102531392	2385806	0.0233	0.1666
chr16	90354753	2493214	0.0276	0.1914
chr17	81195210	2195546	0.027	0.192
chr18	78077248	2268375	0.0291	0.4163
chr19	59128983	1723918	0.0292	0.3648
chr20	63025520	1795741	0.0285	0.1856
chr21	48129895	1098943	0.0228	0.1868
chr22	51304566	1017576	0.0198	0.1535
chrMT	16571	20497	1.2369	1.3402
chrX	155270560	4585149	0.0295	0.2029
chrY	59373566	278381	0.0047	0.1697

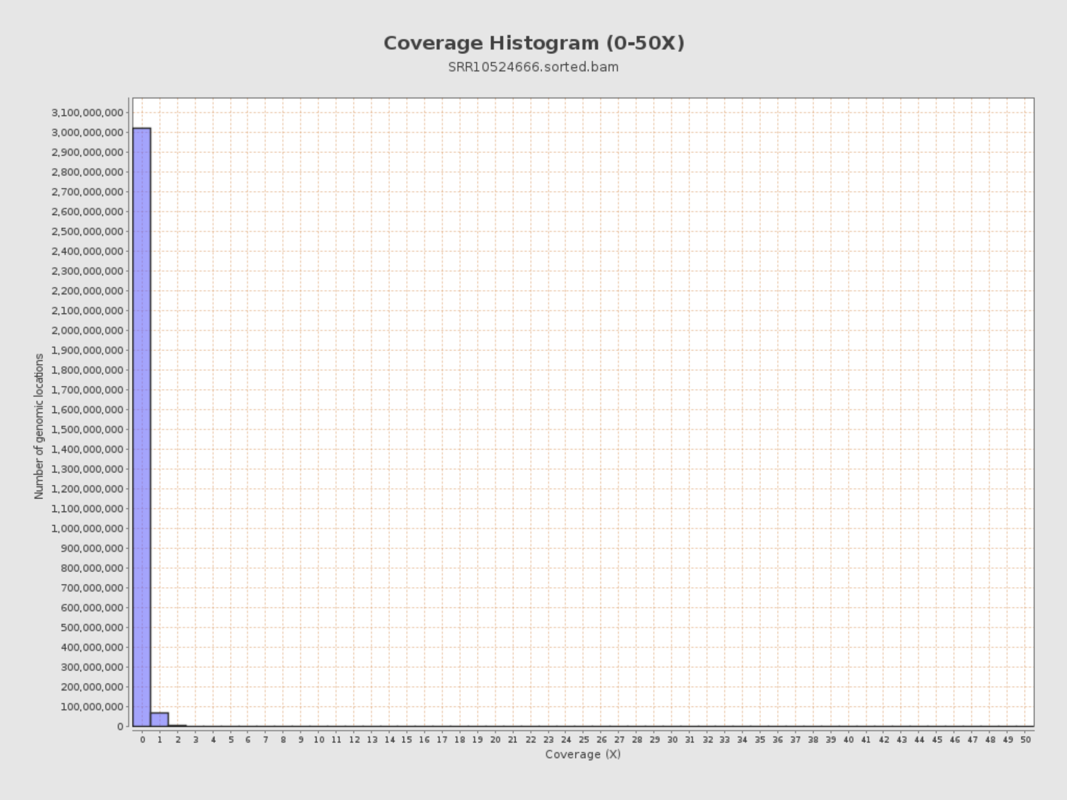
3. Results : Coverage across reference



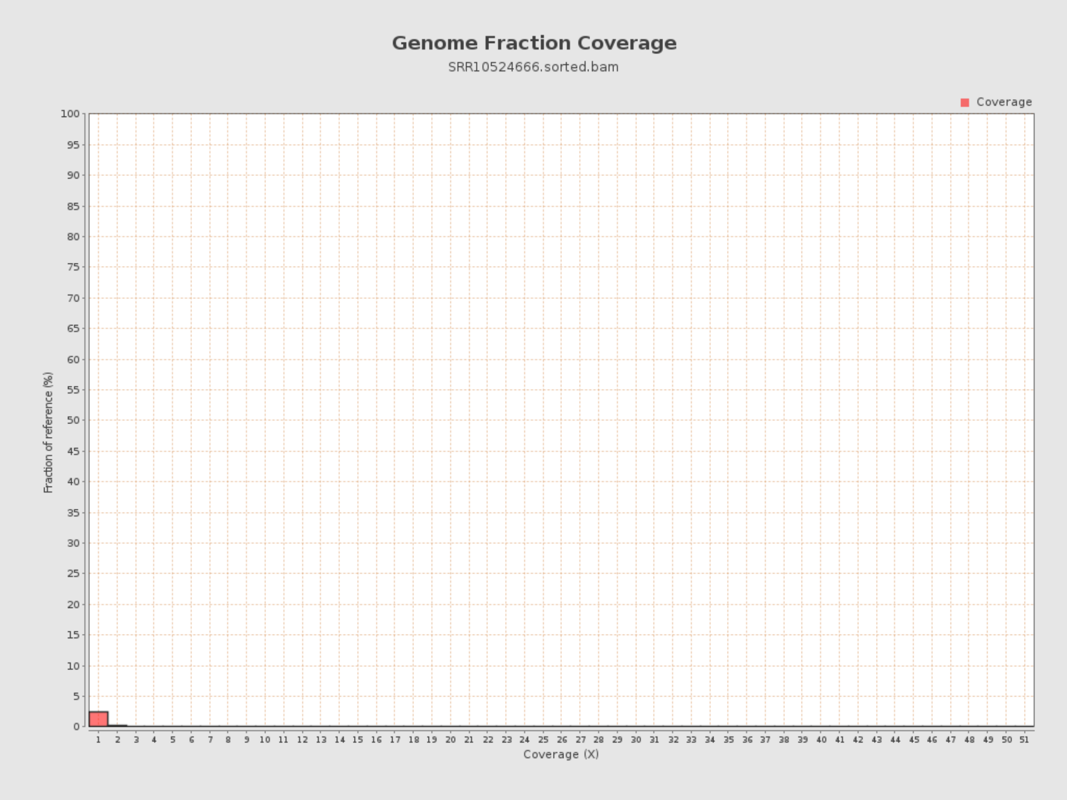
4. Results : Coverage Histogram



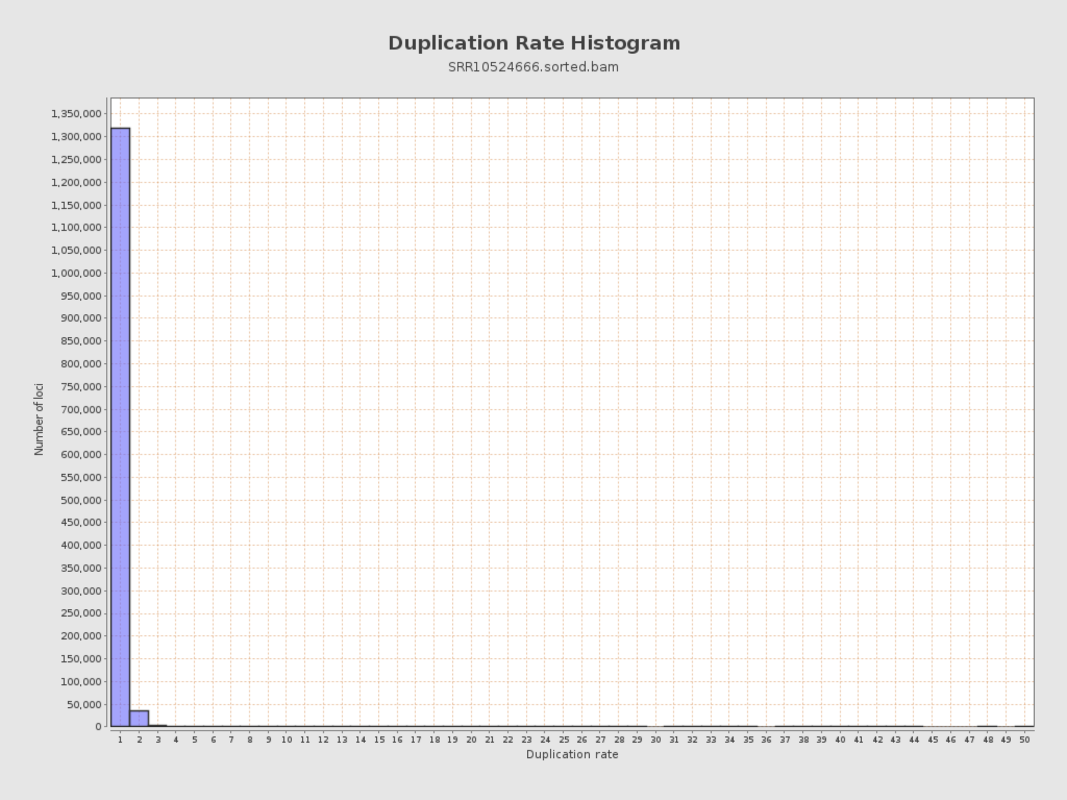
5. Results : Coverage Histogram (0-50X)



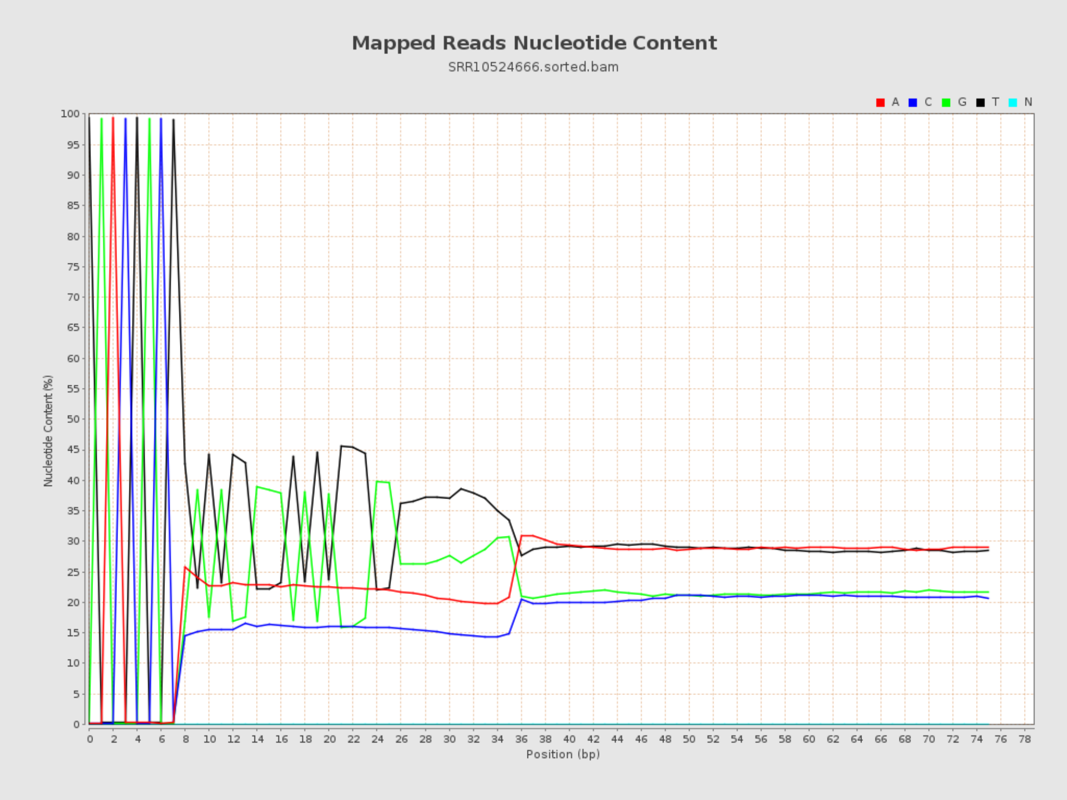
6. Results : Genome Fraction Coverage



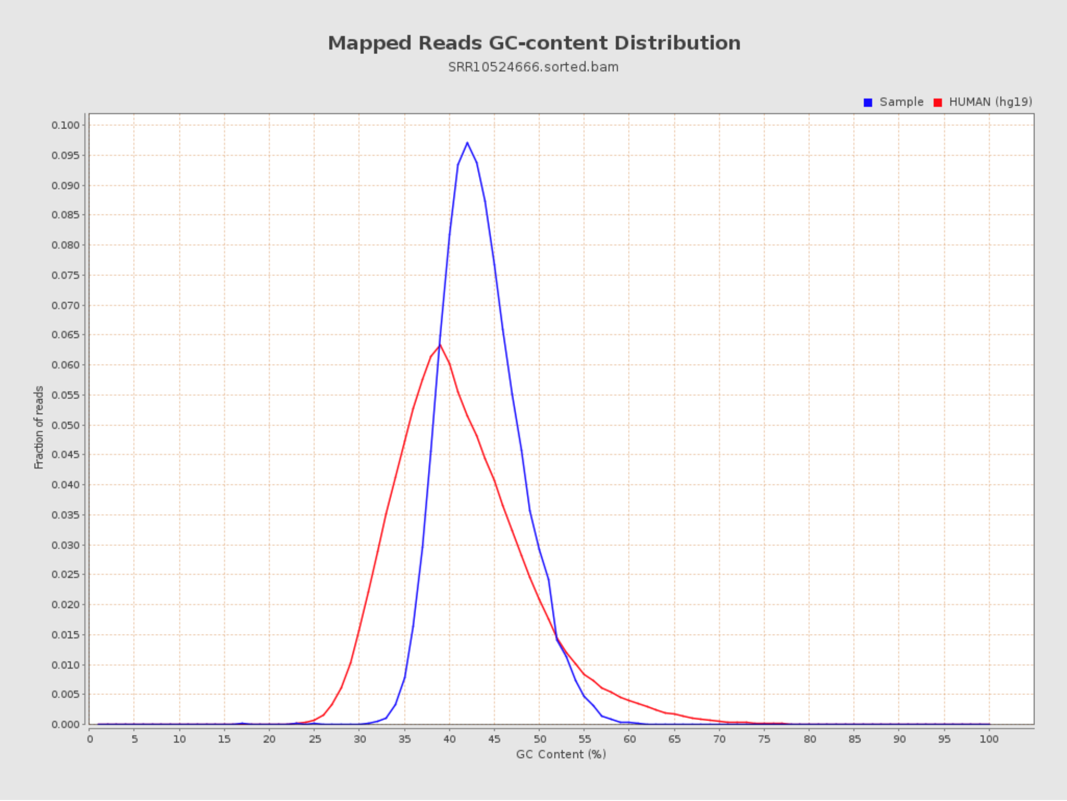
7. Results : Duplication Rate Histogram



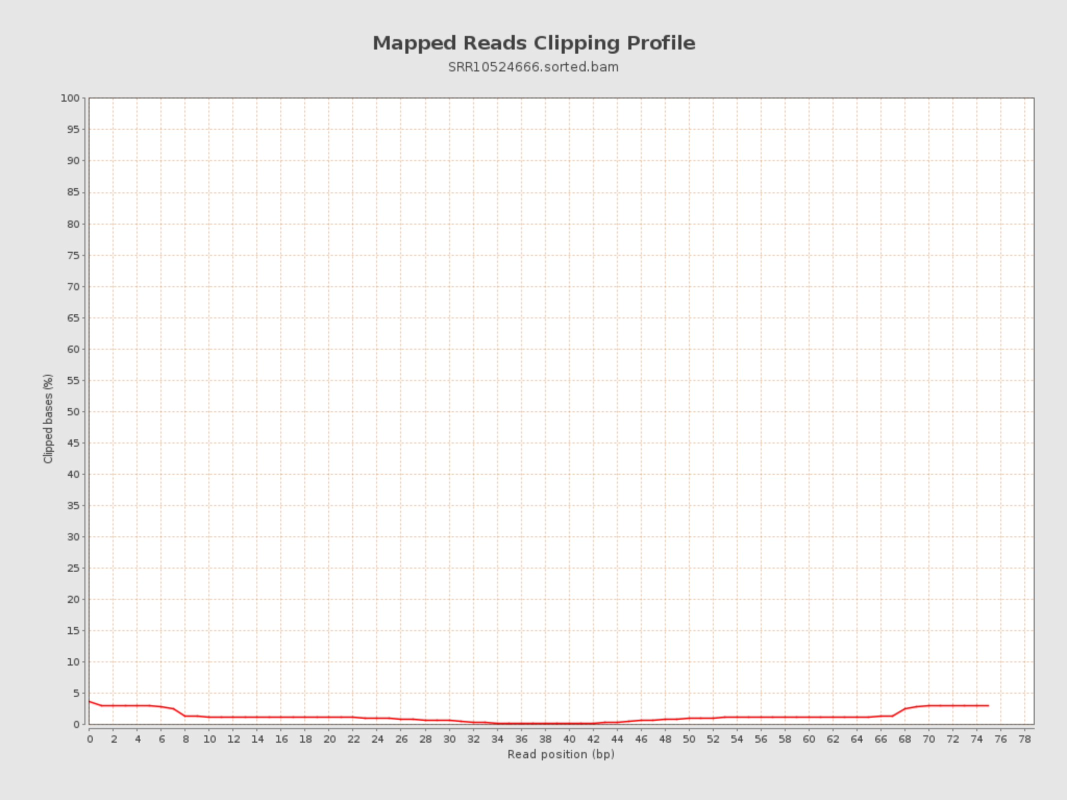
8. Results : Mapped Reads Nucleotide Content



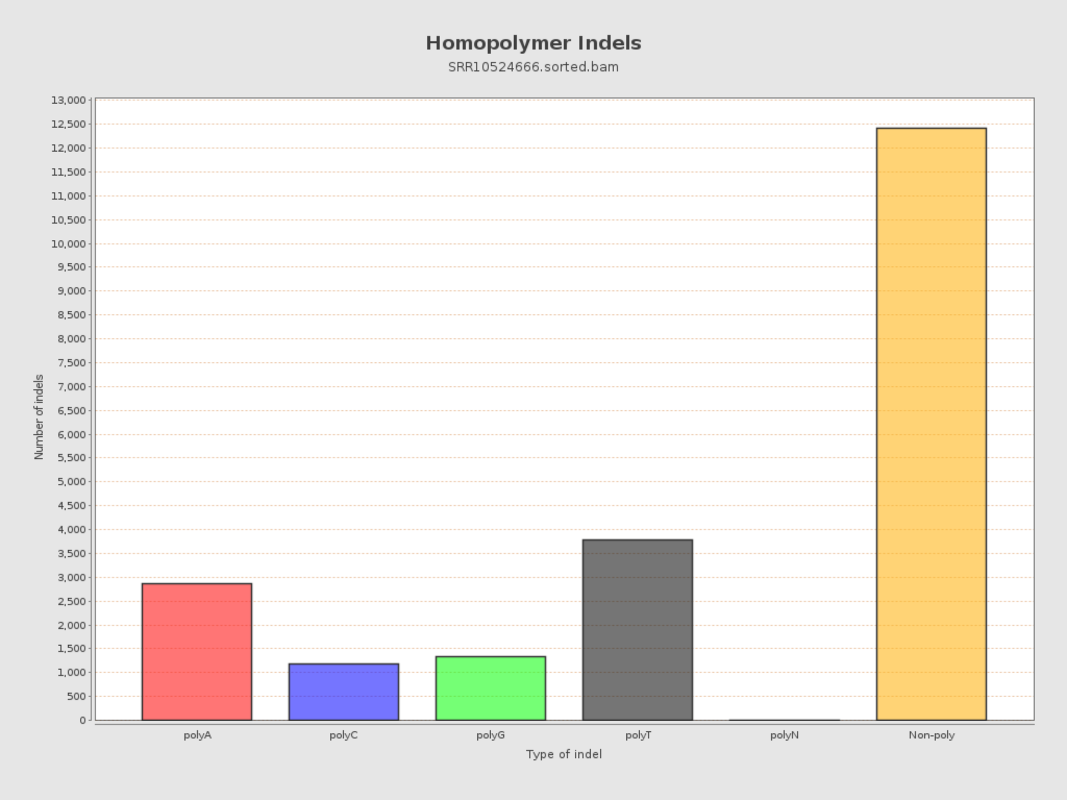
9. Results : Mapped Reads GC-content Distribution



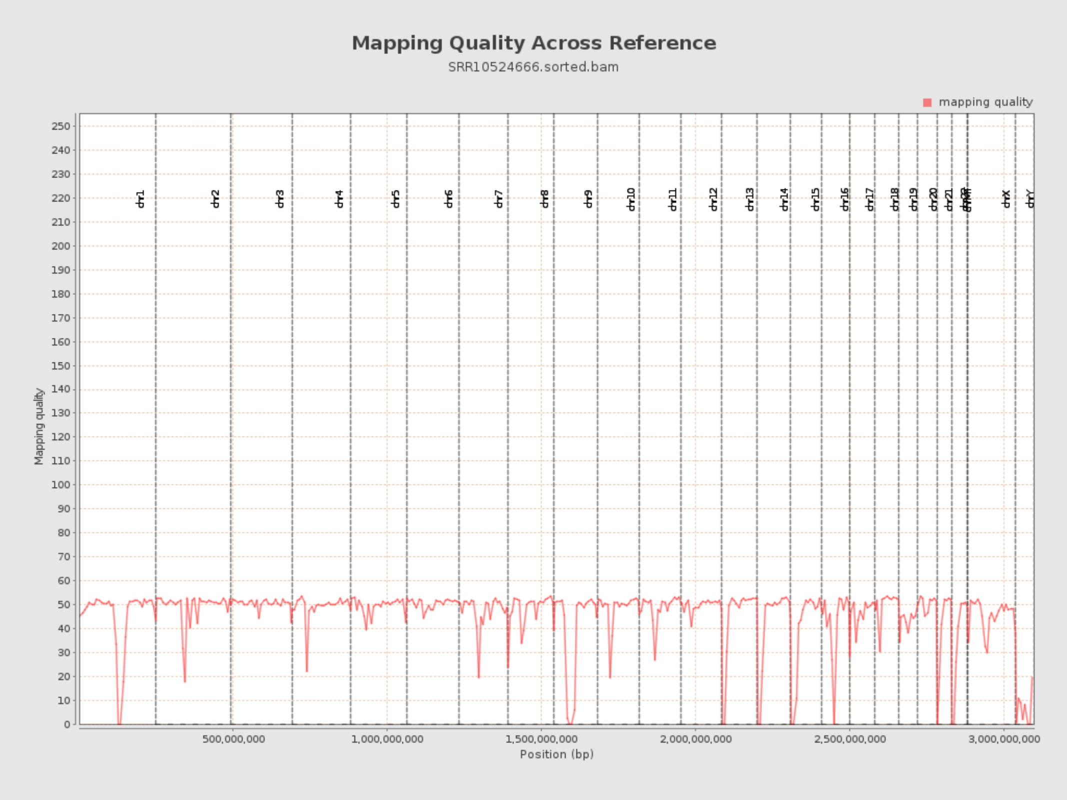
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram