Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:00:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524965.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_SRR10524965 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524965.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:00:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524965.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	447,993
Mapped reads	419,775 / 93.7%
Unmapped reads	28,218 / 6.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,093 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	5,718 / 1.28%
Duplication rate	0.98%
Clipped reads	420,309 / 93.82%

2.2. ACGT Content

Number/percentage of A's	6,044,793 / 24.4%
Number/percentage of C's	4,662,046 / 18.82%
Number/percentage of T's	7,824,161 / 31.58%
Number/percentage of G's	6,246,245 / 25.21%
Number/percentage of N's	347 / 0%
GC Percentage	44.02%

2.3. Coverage

Mean	0.008

Standard Deviation	0.1057

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

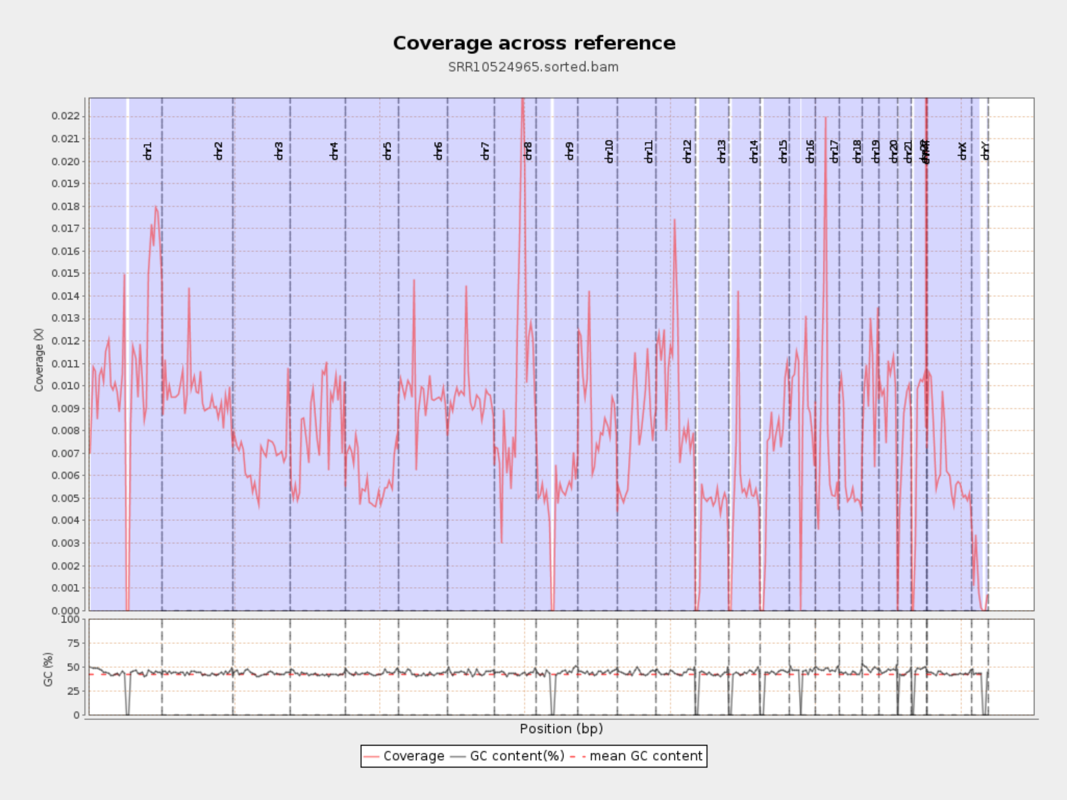
General error rate	0.48%
Mismatches	117,570
Insertions	1,304
Mapped reads with at least one insertion	0.31%
Deletions	4,888
Mapped reads with at least one deletion	1.16%
Homopolymer indels	44.2%

2.6. Chromosome stats

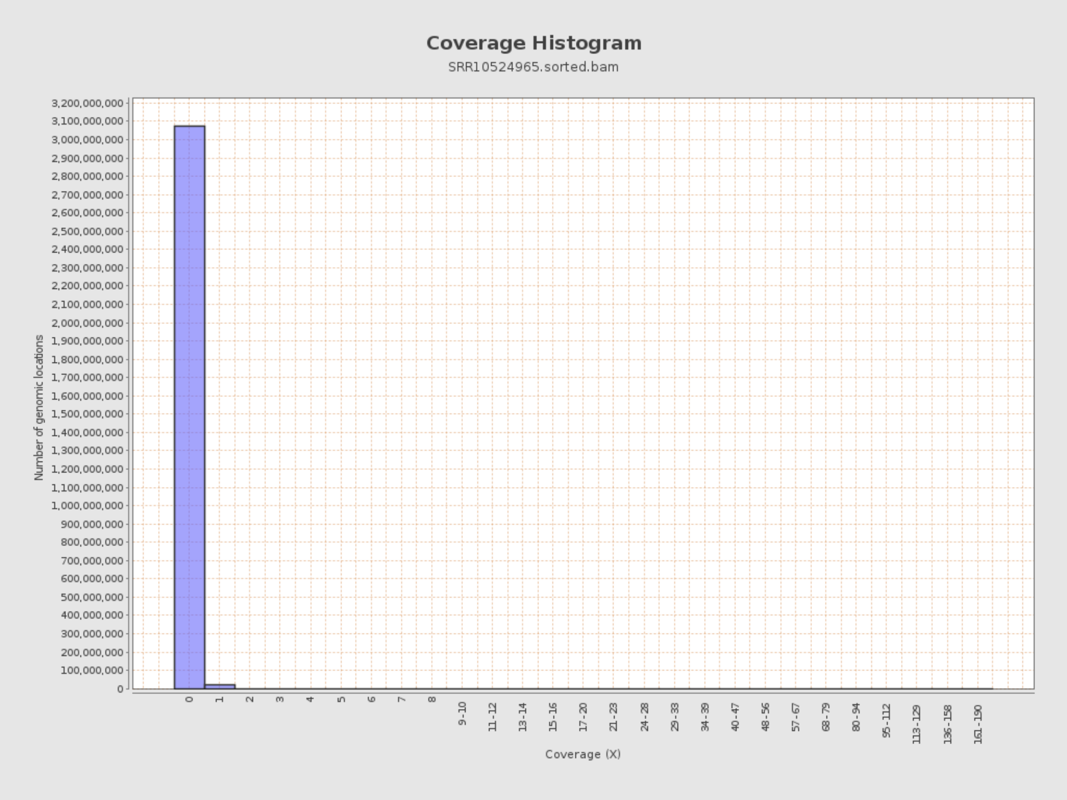
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2710770	0.0109	0.1647
chr2	243199373	2342609	0.0096	0.1169
chr3	198022430	1366989	0.0069	0.0852
chr4	191154276	1568773	0.0082	0.0939
chr5	180915260	1064281	0.0059	0.0786
chr6	171115067	1654760	0.0097	0.1131
chr7	159138663	1530517	0.0096	0.1303

chr8	146364022	1506698	0.0103	0.114
chr9	141213431	684373	0.0048	0.0821
chr10	135534747	1226819	0.0091	0.1064
chr11	135006516	1049782	0.0078	0.1
chr12	133851895	1349618	0.0101	0.1029
chr13	115169878	477860	0.0041	0.0662
chr14	107349540	573232	0.0053	0.0756
chr15	102531392	697470	0.0068	0.0873
chr16	90354753	799856	0.0089	0.0974
chr17	81195210	673296	0.0083	0.1041
chr18	78077248	484863	0.0062	0.1122
chr19	59128983	615716	0.0104	0.1236
chr20	63025520	616838	0.0098	0.1016
chr21	48129895	349978	0.0073	0.0882
chr22	51304566	355012	0.0069	0.0848
chrMT	16571	5809	0.3506	0.6086
chrX	155270560	1017871	0.0066	0.0869
chrY	59373566	62272	0.001	0.0376

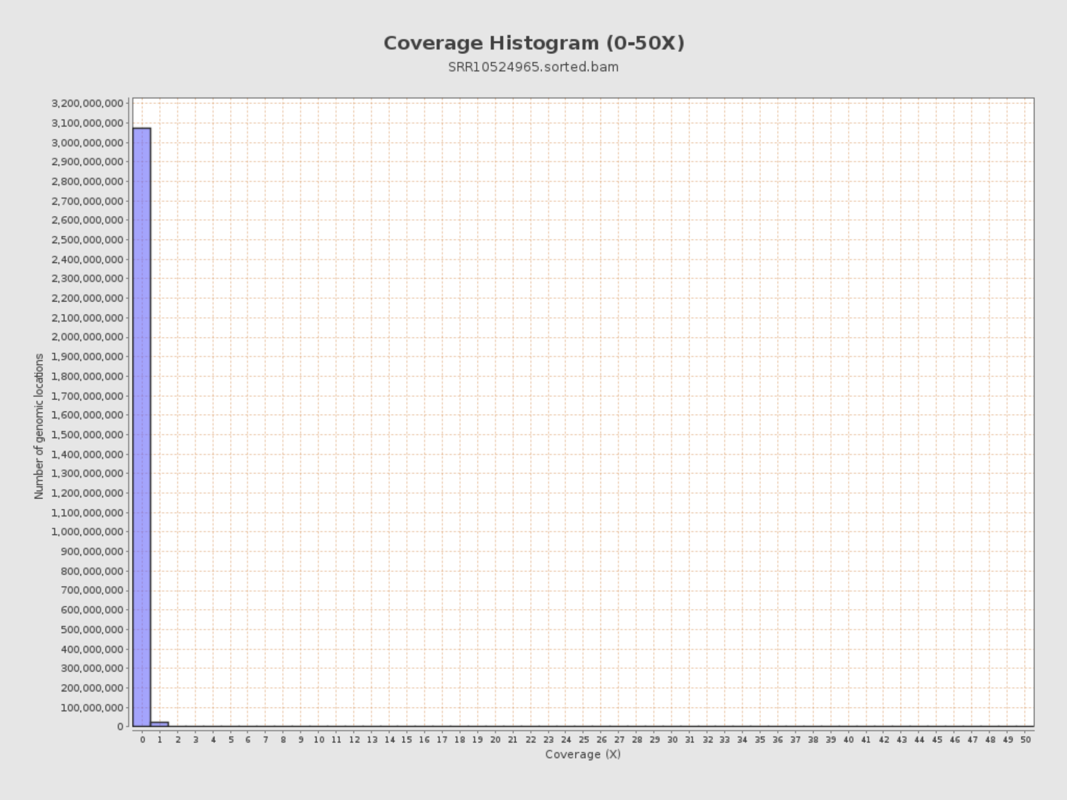
3. Results : Coverage across reference



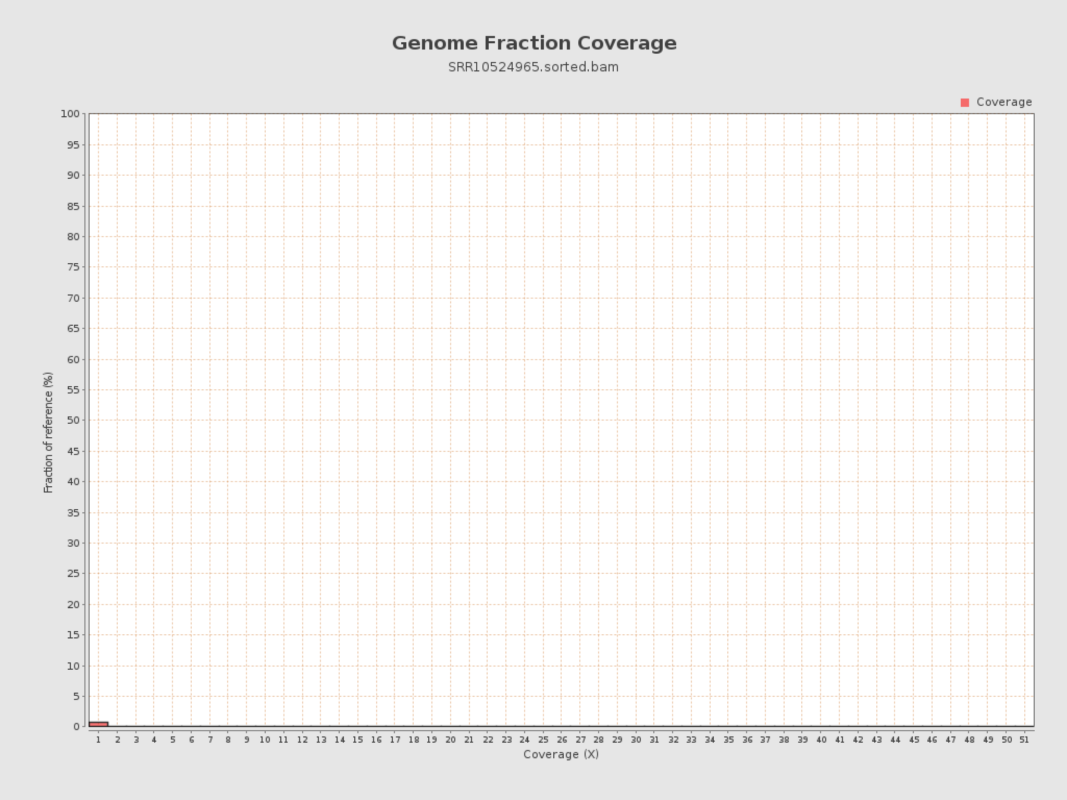
4. Results : Coverage Histogram



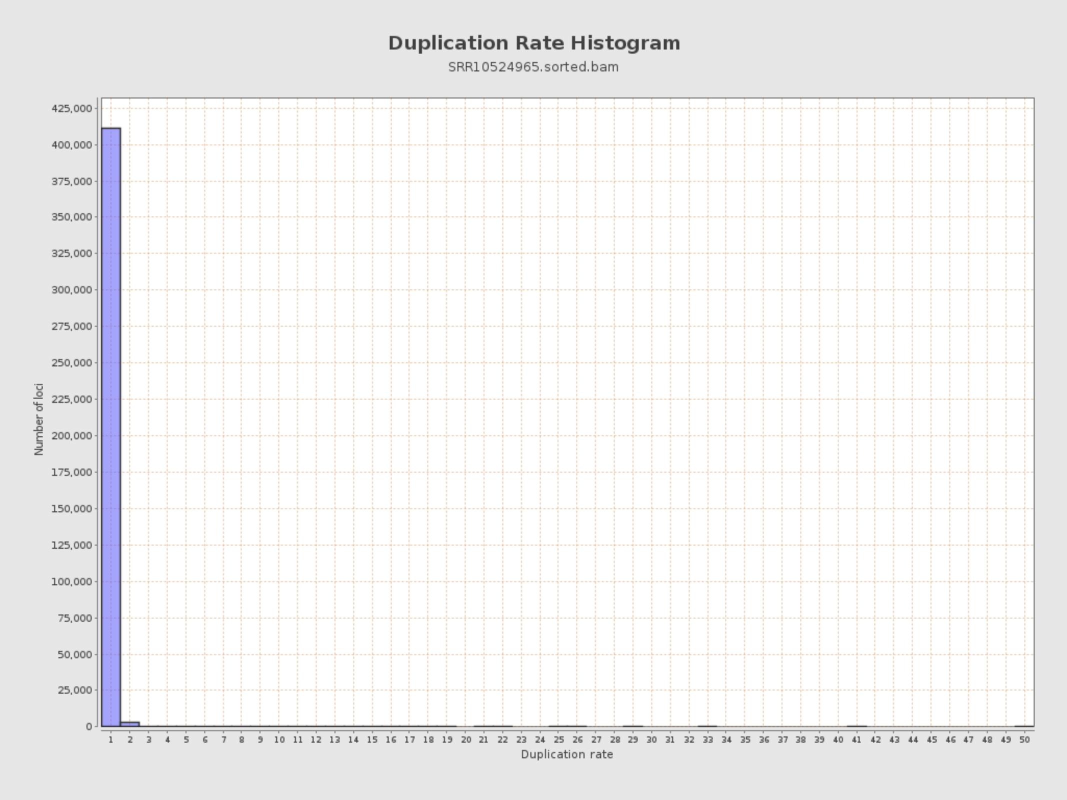
5. Results : Coverage Histogram (0-50X)



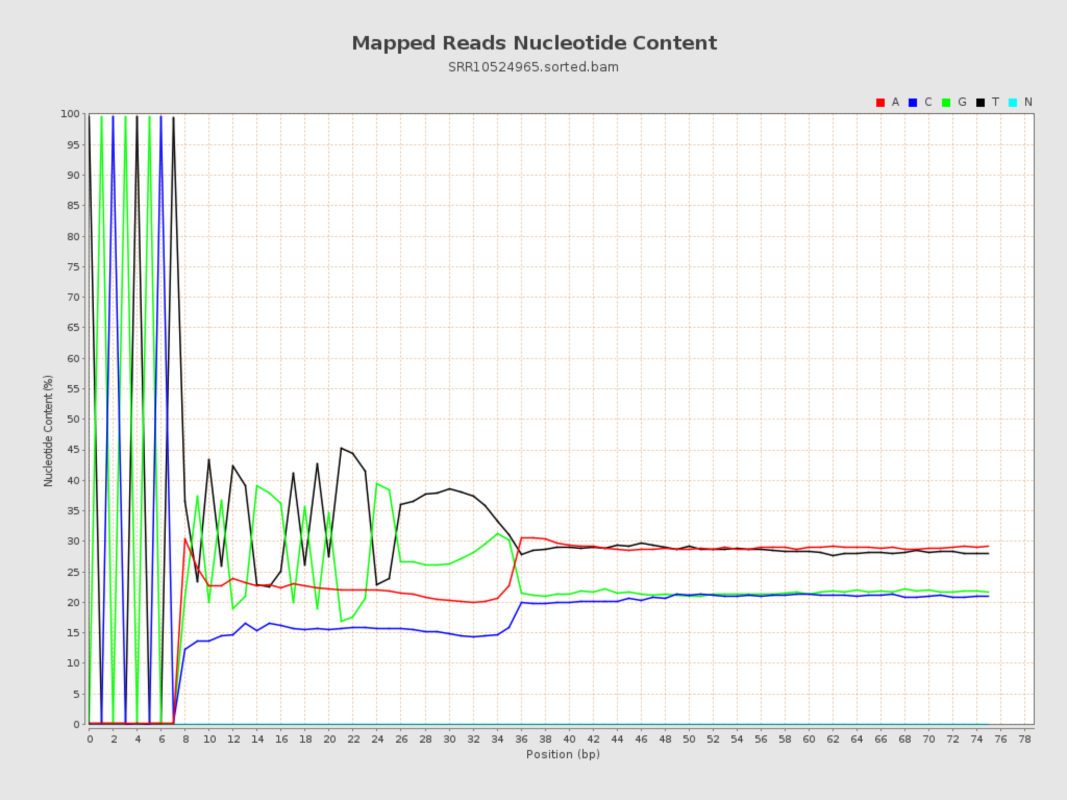
6. Results : Genome Fraction Coverage



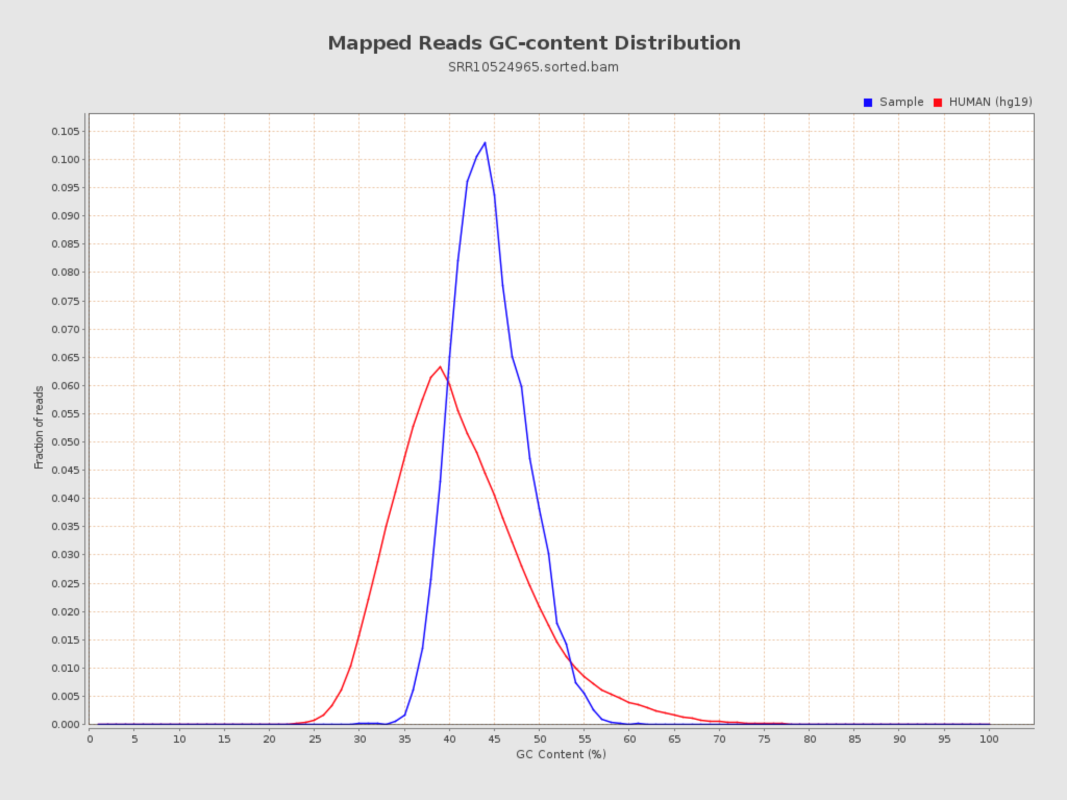
7. Results : Duplication Rate Histogram



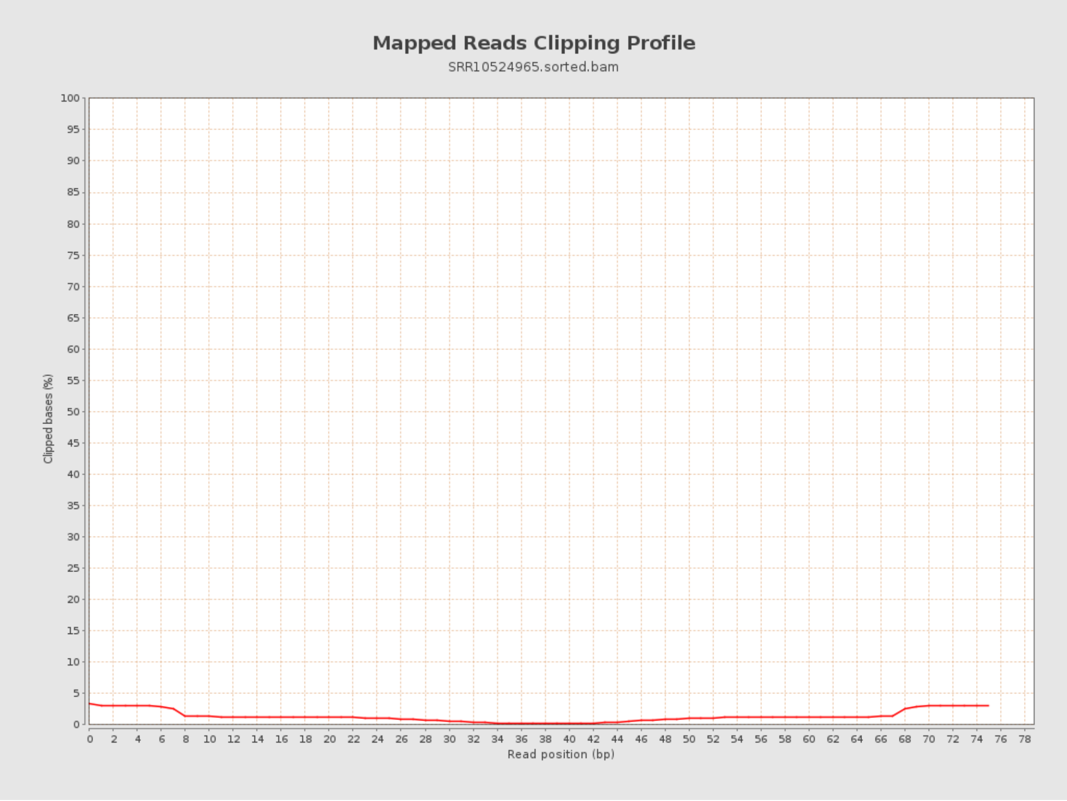
8. Results : Mapped Reads Nucleotide Content



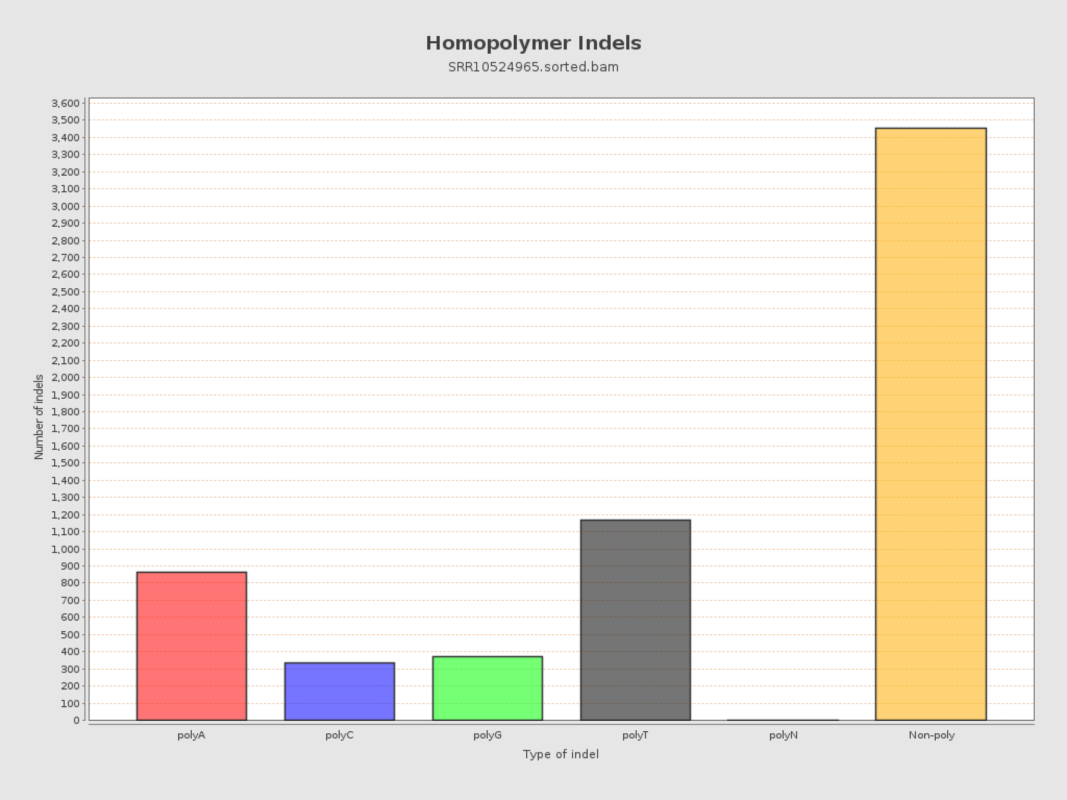
9. Results : Mapped Reads GC-content Distribution



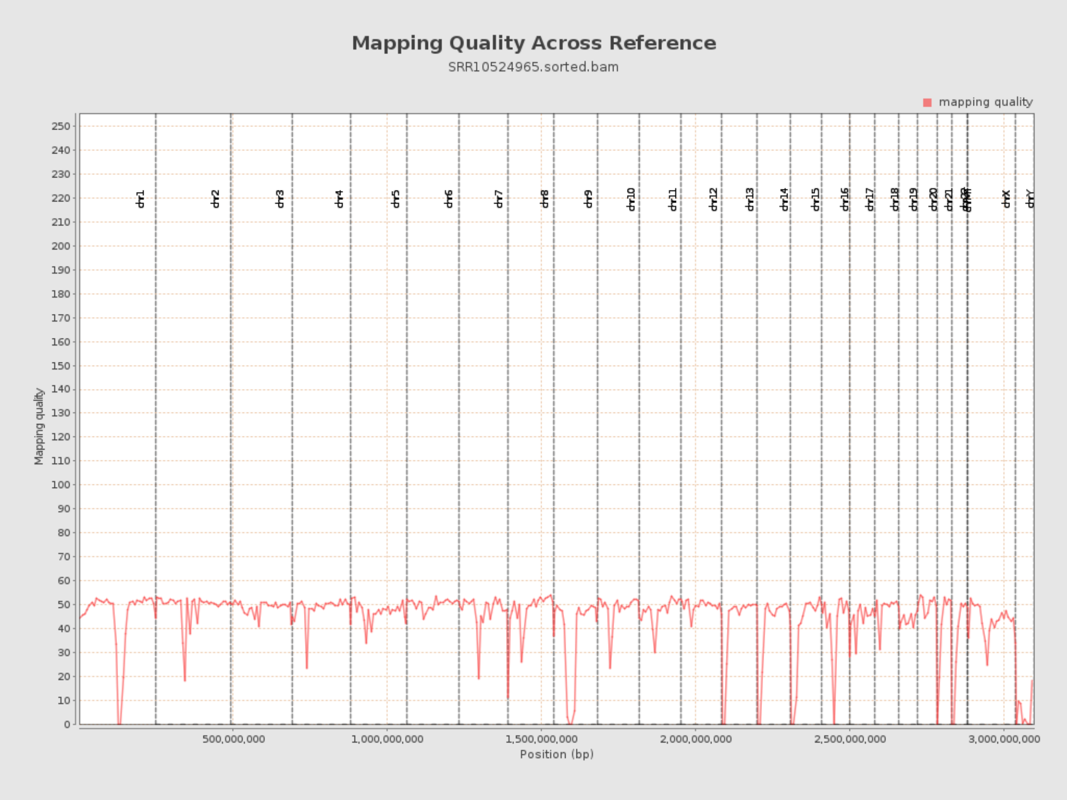
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram