Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:39:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524500.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_SRR10524500 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524500.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:39:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524500.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,311,791
Mapped reads	3,857,121 / 89.46%
Unmapped reads	454,670 / 10.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,348 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	236,968 / 5.5%
Duplication rate	4.62%
Clipped reads	3,859,122 / 89.5%

2.2. ACGT Content

Number/percentage of A's	58,349,648 / 26.05%
Number/percentage of C's	38,756,253 / 17.3%
Number/percentage of T's	71,090,955 / 31.74%
Number/percentage of G's	55,795,311 / 24.91%
Number/percentage of N's	6,756 / 0%
GC Percentage	42.21%

2.3. Coverage

Mean	0.0724

Standard Deviation	0.5541

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

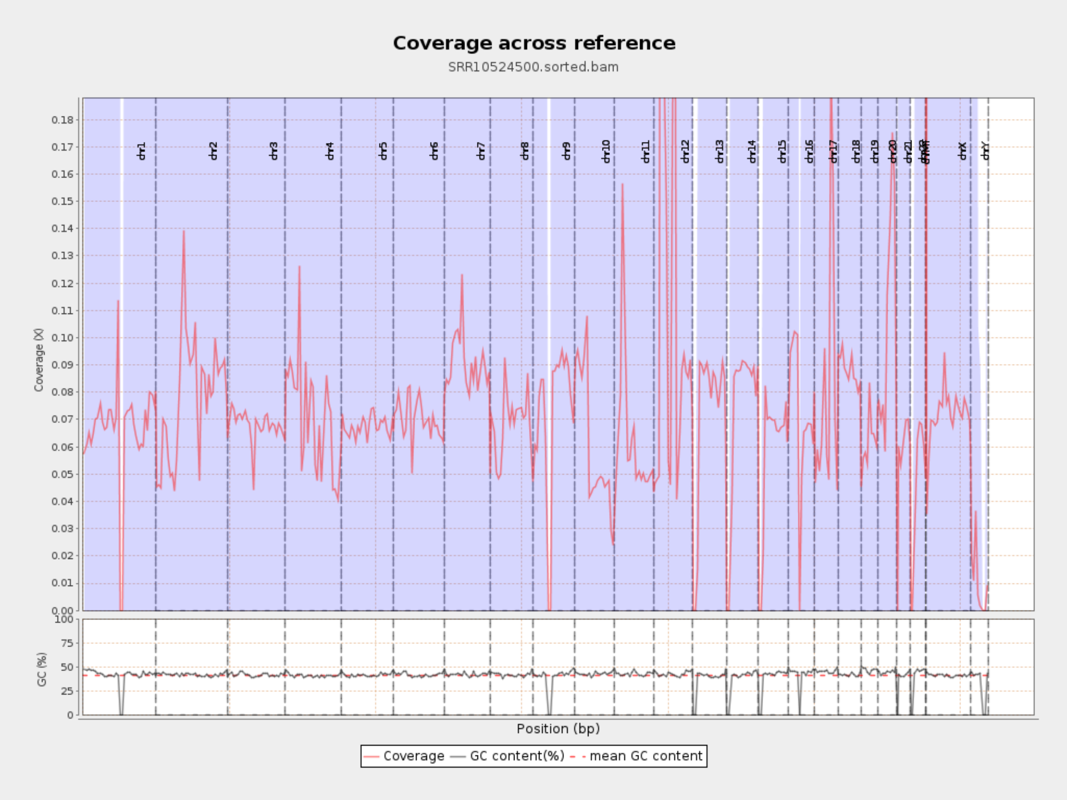
General error rate	0.49%
Mismatches	1,072,339
Insertions	15,285
Mapped reads with at least one insertion	0.39%
Deletions	35,481
Mapped reads with at least one deletion	0.91%
Homopolymer indels	42.97%

2.6. Chromosome stats

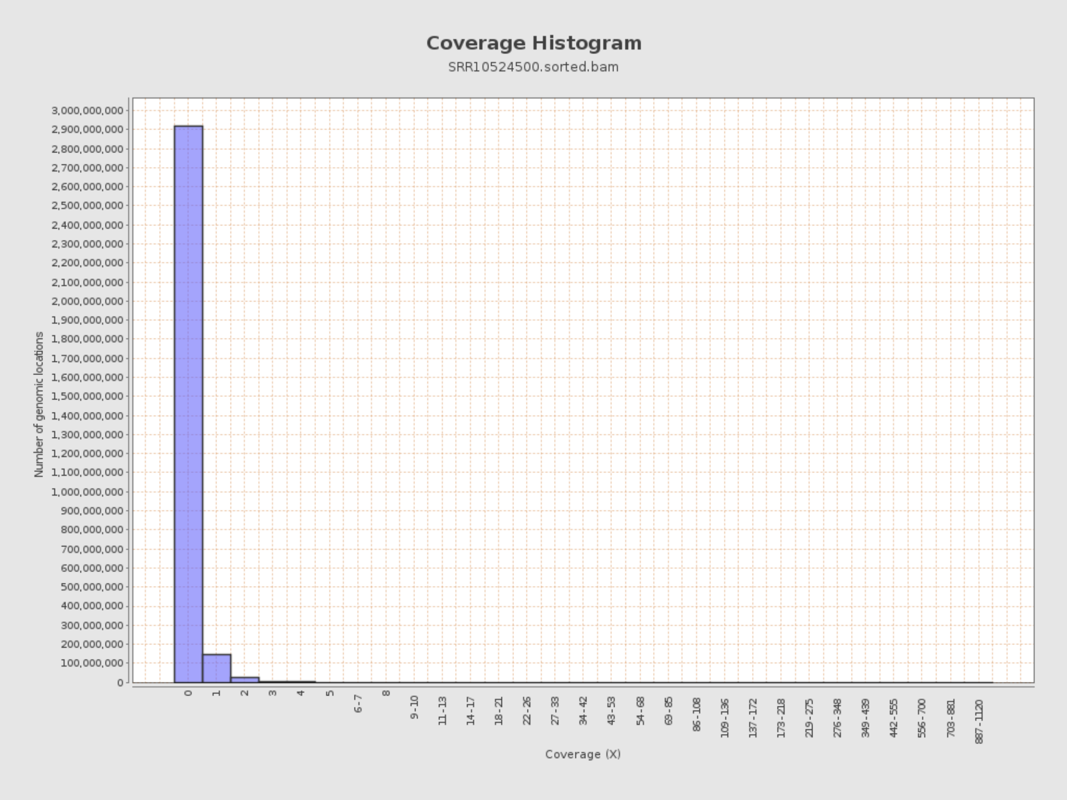
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16432892	0.0659	0.9677
chr2	243199373	19081594	0.0785	0.6346
chr3	198022430	13419603	0.0678	0.3097
chr4	191154276	13572454	0.071	0.4011
chr5	180915260	12218297	0.0675	0.3149
chr6	171115067	12029716	0.0703	0.3691
chr7	159138663	14444250	0.0908	0.7818

chr8	146364022	10041655	0.0686	0.5819
chr9	141213431	10208606	0.0723	0.5729
chr10	135534747	8173017	0.0603	0.5462
chr11	135006516	8616362	0.0638	0.4662
chr12	133851895	16298545	0.1218	0.5129
chr13	115169878	8211654	0.0713	0.3186
chr14	107349540	7863901	0.0733	0.3718
chr15	102531392	5813930	0.0567	0.2849
chr16	90354753	6349127	0.0703	0.3541
chr17	81195210	6726927	0.0828	0.3757
chr18	78077248	6889950	0.0882	1.0506
chr19	59128983	3702375	0.0626	0.7341
chr20	63025520	6949115	0.1103	0.4223
chr21	48129895	2749598	0.0571	0.3514
chr22	51304566	2312722	0.0451	0.2507
chrMT	16571	231847	13.9911	8.8719
chrX	155270560	11115109	0.0716	0.3981
chrY	59373566	604318	0.0102	0.2591

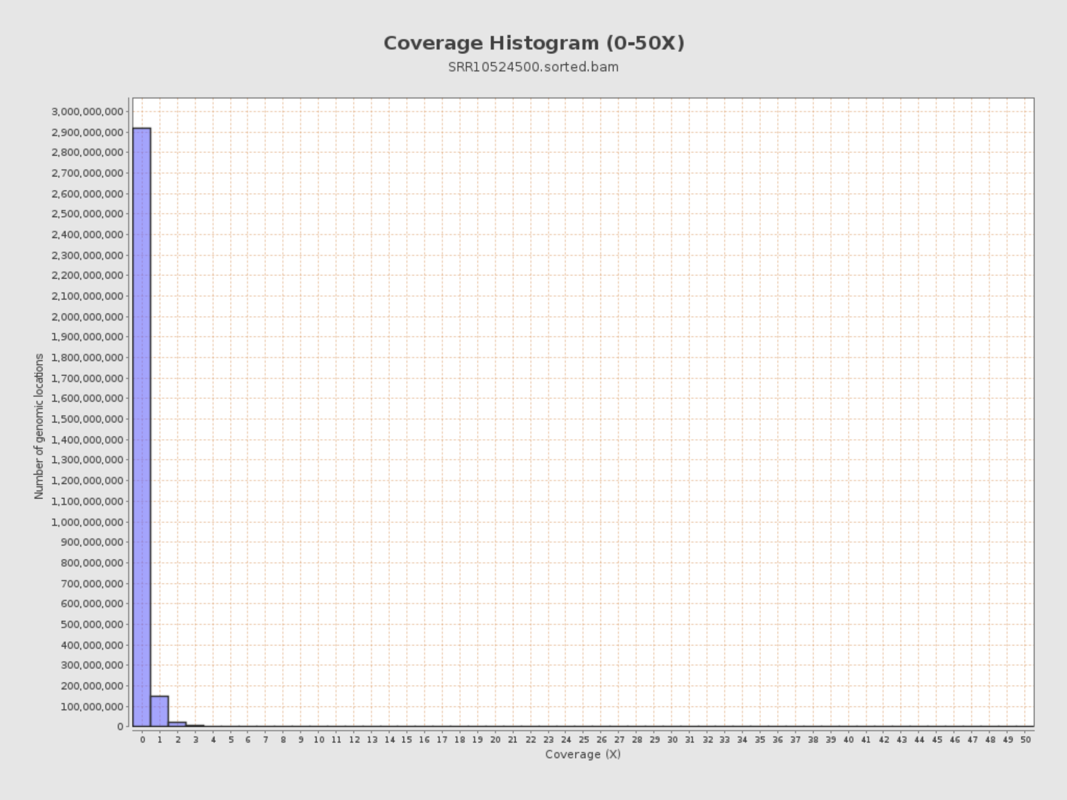
3. Results : Coverage across reference



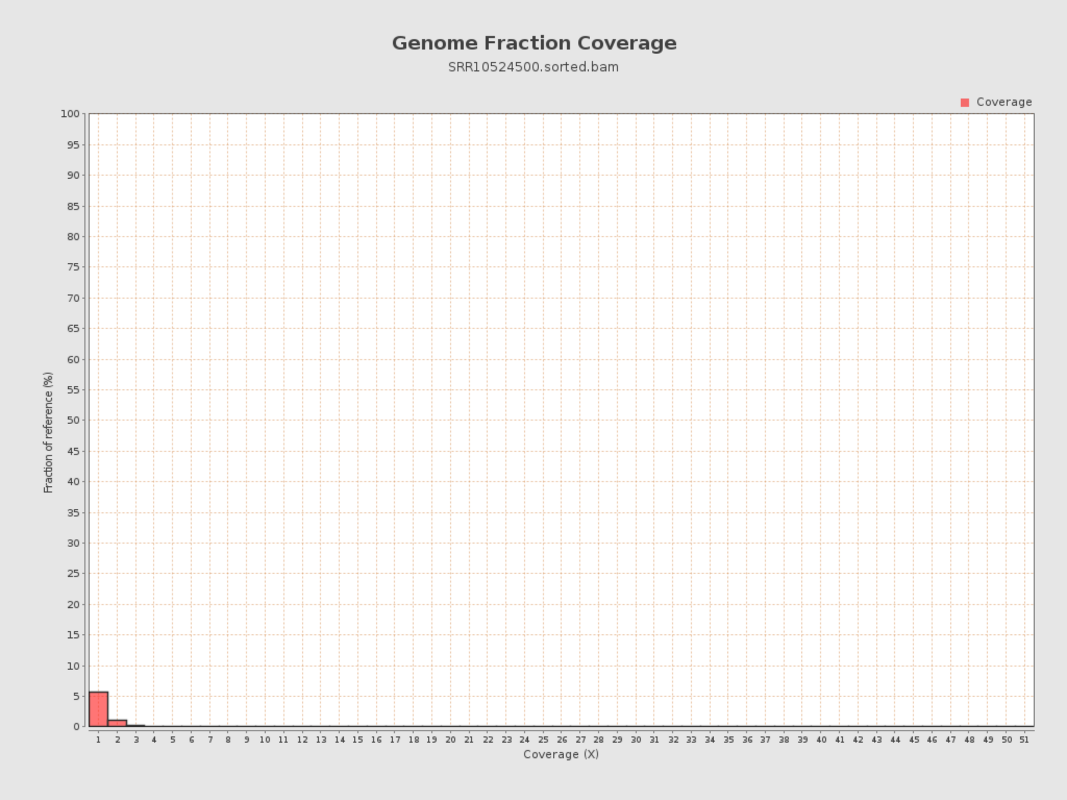
4. Results : Coverage Histogram



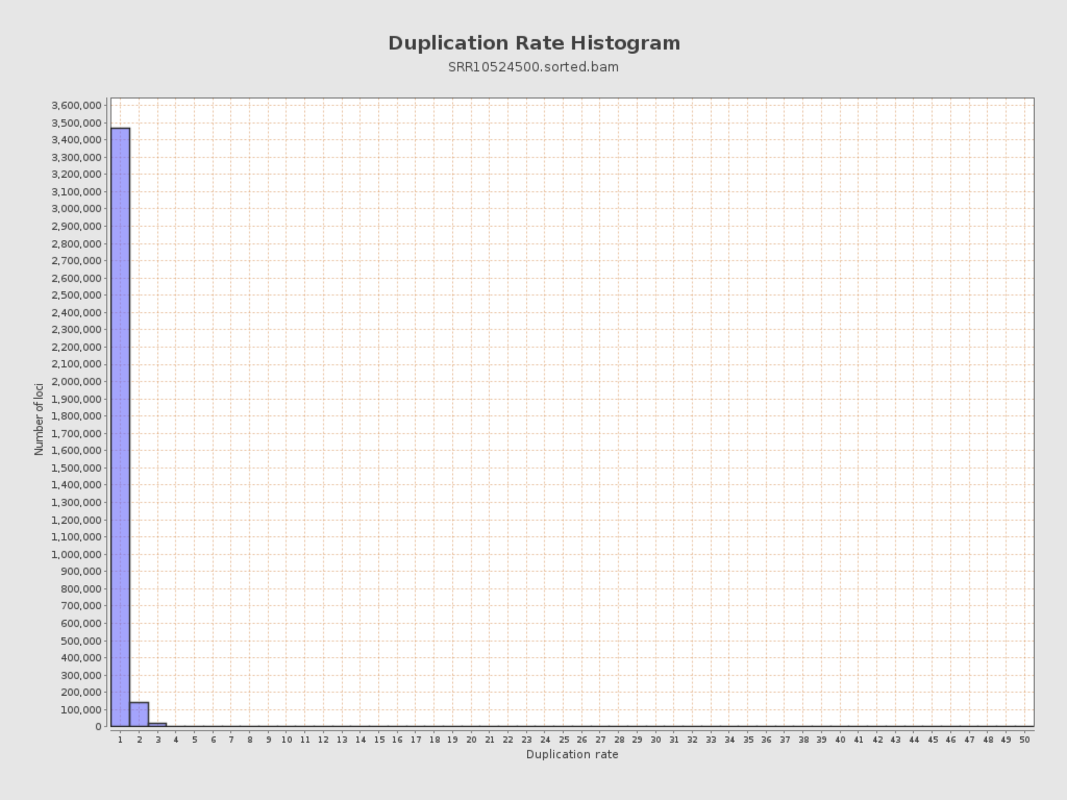
5. Results : Coverage Histogram (0-50X)



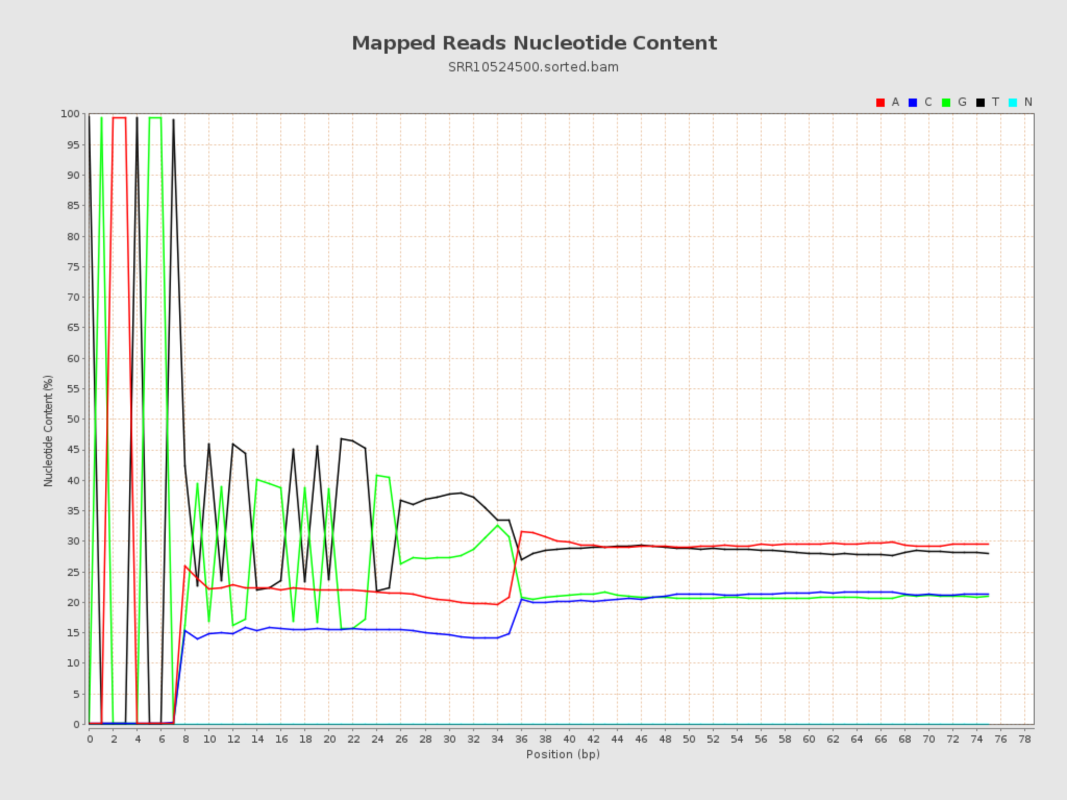
6. Results : Genome Fraction Coverage



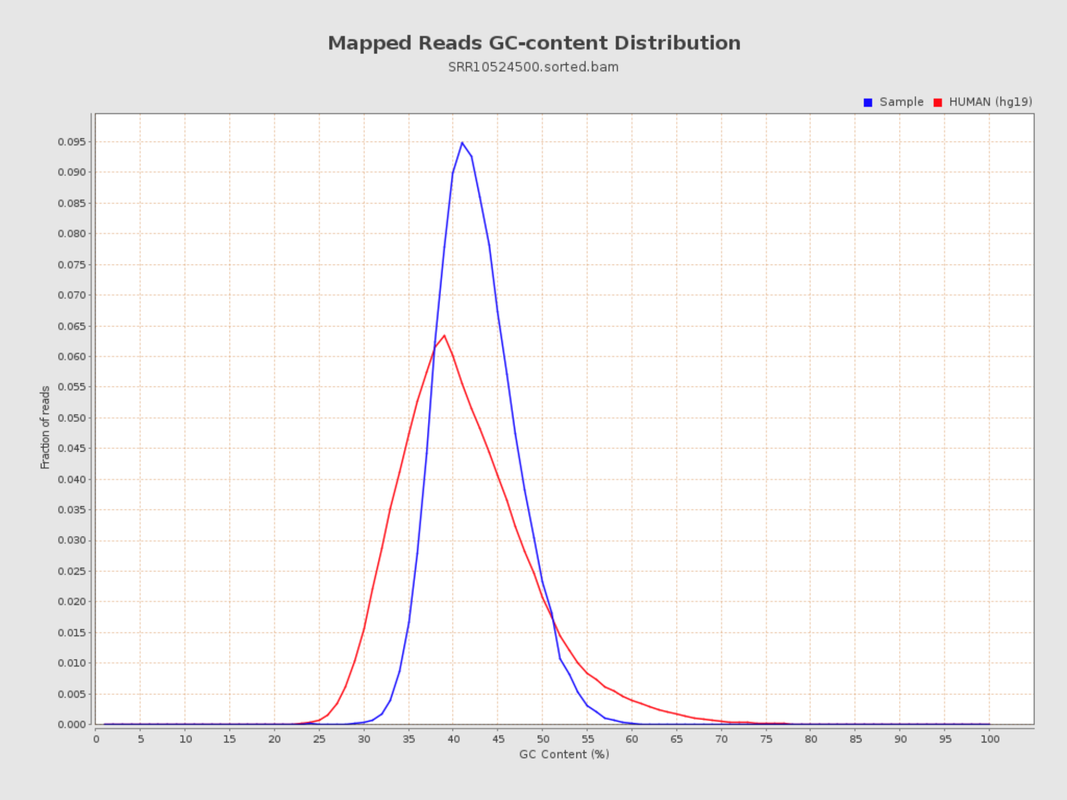
7. Results : Duplication Rate Histogram



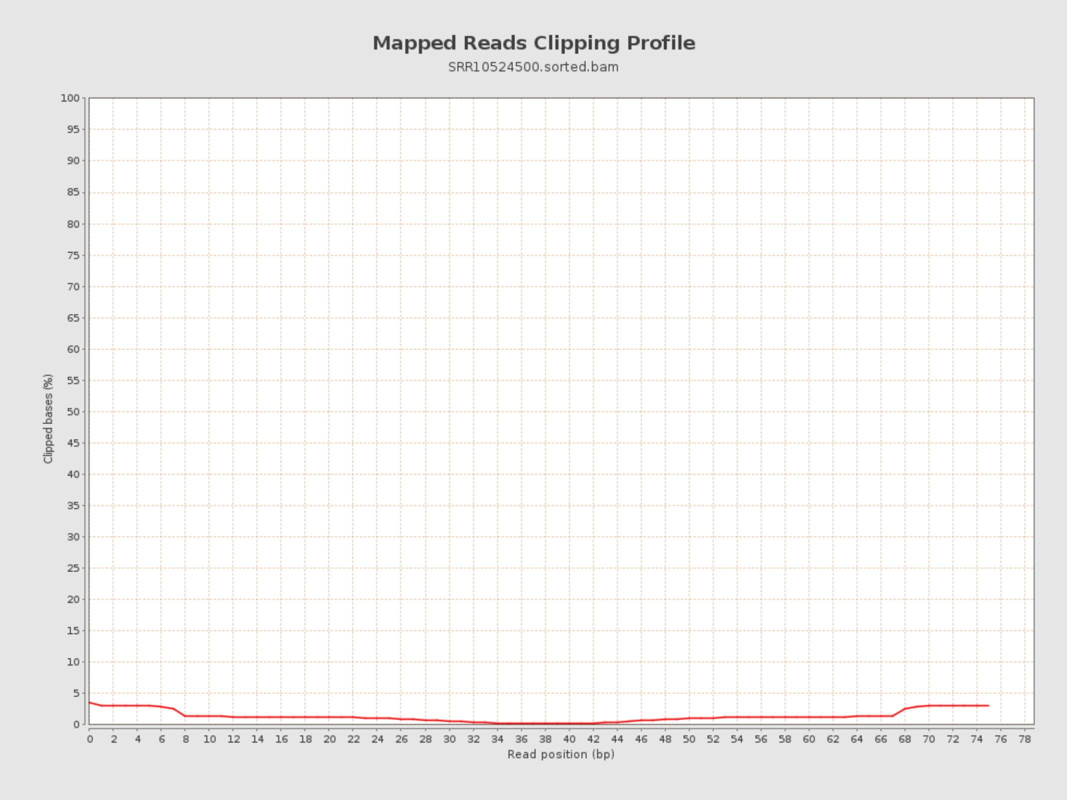
8. Results : Mapped Reads Nucleotide Content



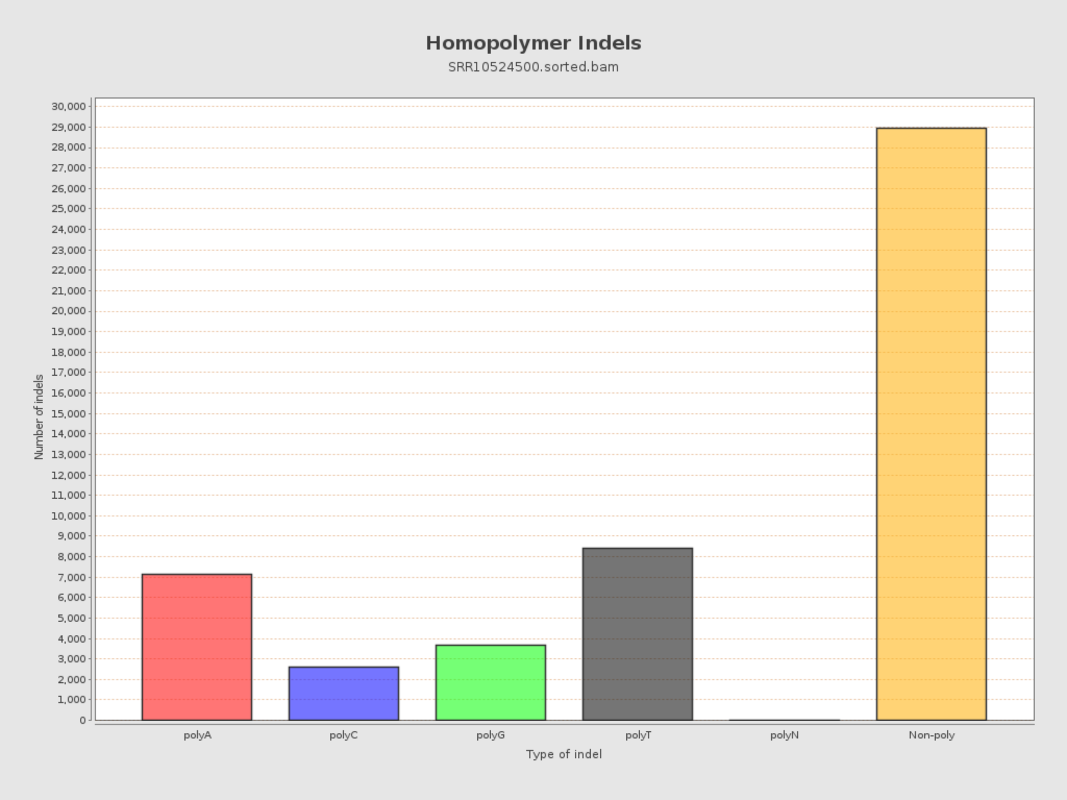
9. Results : Mapped Reads GC-content Distribution



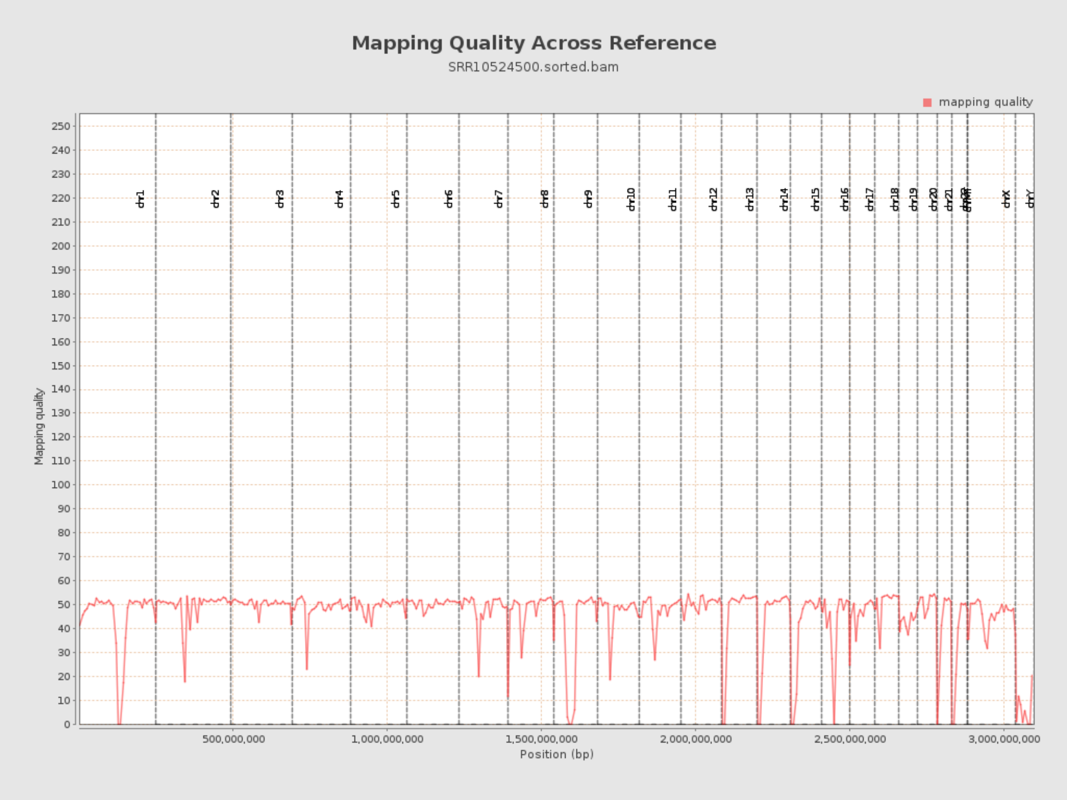
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram