Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:42:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525023.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_SRR10525023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:42:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	831,487
Mapped reads	756,695 / 91.01%
Unmapped reads	74,792 / 8.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,955 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	14,537 / 1.75%
Duplication rate	1.29%
Clipped reads	758,512 / 91.22%

2.2. ACGT Content

Number/percentage of A's	11,126,035 / 25.43%
Number/percentage of C's	8,961,652 / 20.49%
Number/percentage of T's	13,233,390 / 30.25%
Number/percentage of G's	10,425,402 / 23.83%
Number/percentage of N's	441 / 0%
GC Percentage	44.32%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1585

2.4. Mapping Quality

Mean Mapping Quality	43.57

2.5. Mismatches and indels

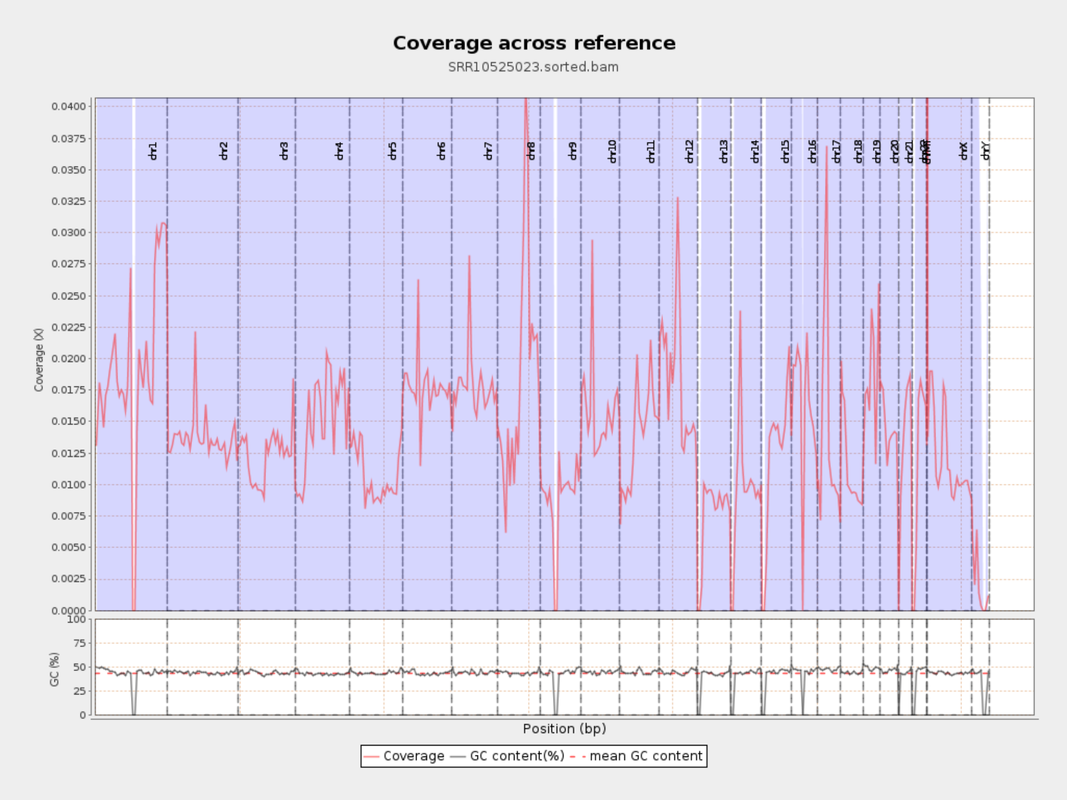
General error rate	0.52%
Mismatches	219,783
Insertions	3,169
Mapped reads with at least one insertion	0.42%
Deletions	8,808
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.32%

2.6. Chromosome stats

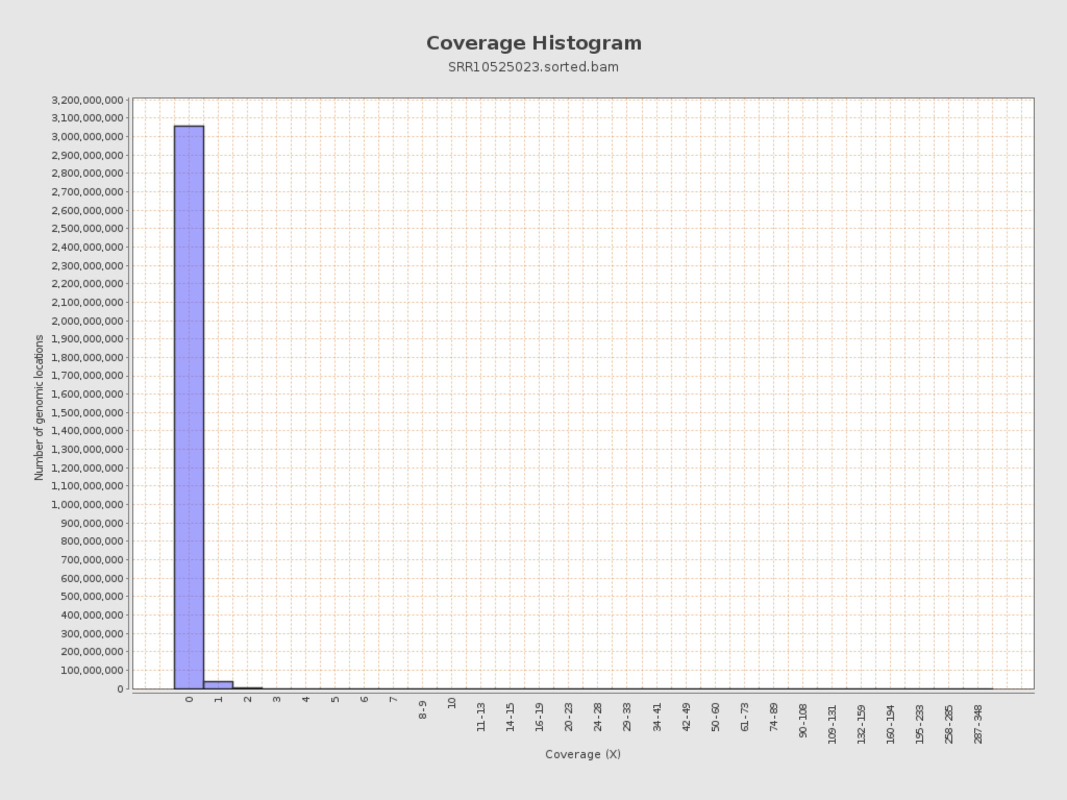
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4783729	0.0192	0.2773
chr2	243199373	3334505	0.0137	0.1646
chr3	198022430	2453212	0.0124	0.1165
chr4	191154276	2902585	0.0152	0.1334
chr5	180915260	1934772	0.0107	0.108
chr6	171115067	3021801	0.0177	0.1685
chr7	159138663	2848914	0.0179	0.2124

chr8	146364022	2752590	0.0188	0.1614
chr9	141213431	1238707	0.0088	0.1194
chr10	135534747	2162197	0.016	0.1654
chr11	135006516	1902119	0.0141	0.1451
chr12	133851895	2470276	0.0185	0.1416
chr13	115169878	866735	0.0075	0.0912
chr14	107349540	1029965	0.0096	0.1035
chr15	102531392	1259969	0.0123	0.118
chr16	90354753	1445830	0.016	0.1358
chr17	81195210	1189855	0.0147	0.152
chr18	78077248	877486	0.0112	0.1775
chr19	59128983	1108042	0.0187	0.1896
chr20	63025520	903543	0.0143	0.1251
chr21	48129895	646638	0.0134	0.1221
chr22	51304566	600648	0.0117	0.1115
chrMT	16571	14027	0.8465	1.0599
chrX	155270560	1897178	0.0122	0.1261
chrY	59373566	116249	0.002	0.0593

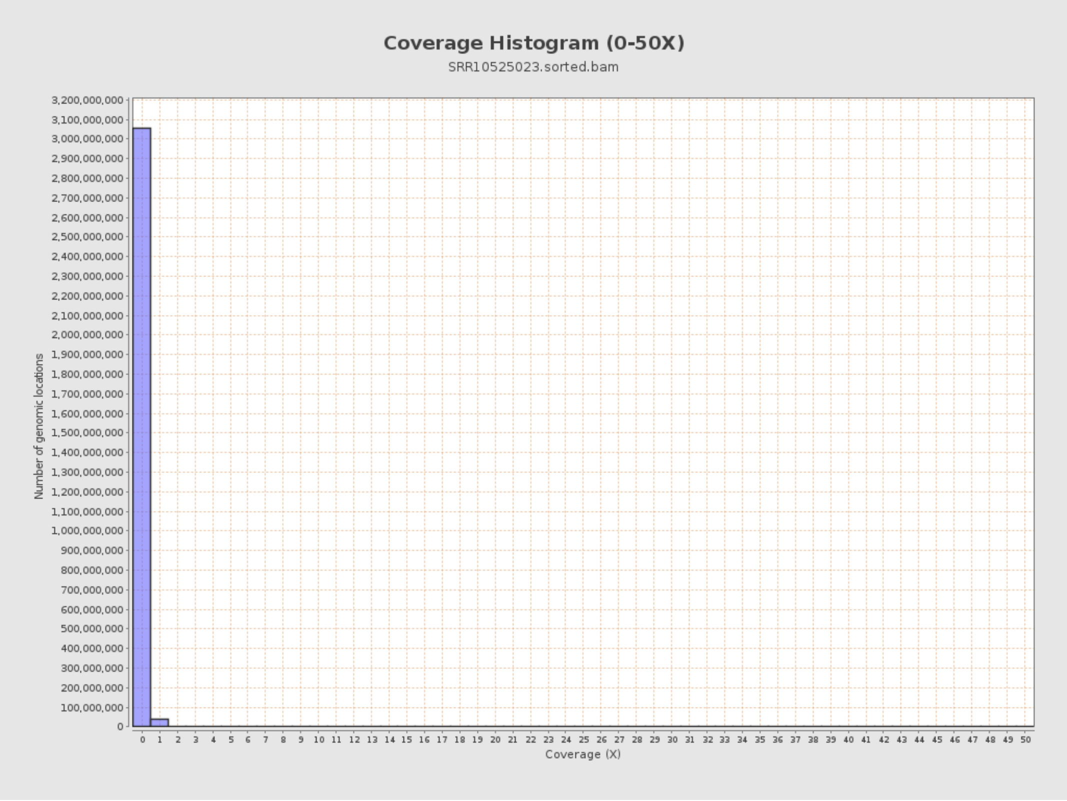
3. Results : Coverage across reference



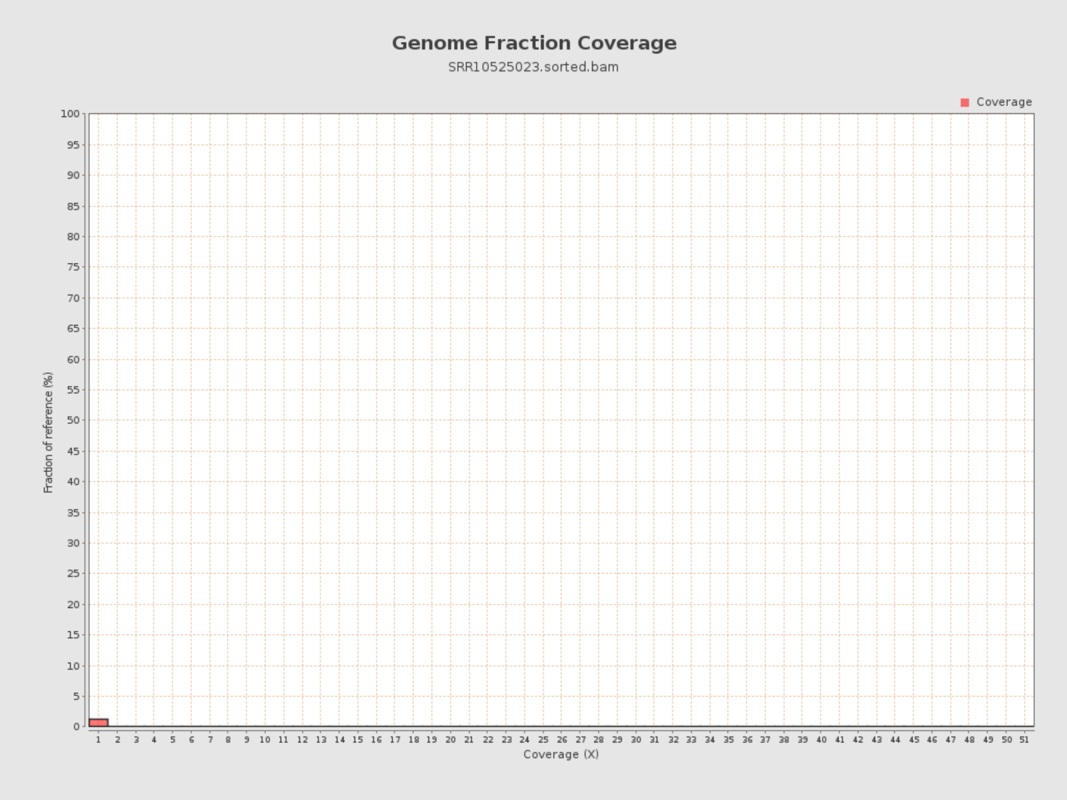
4. Results : Coverage Histogram



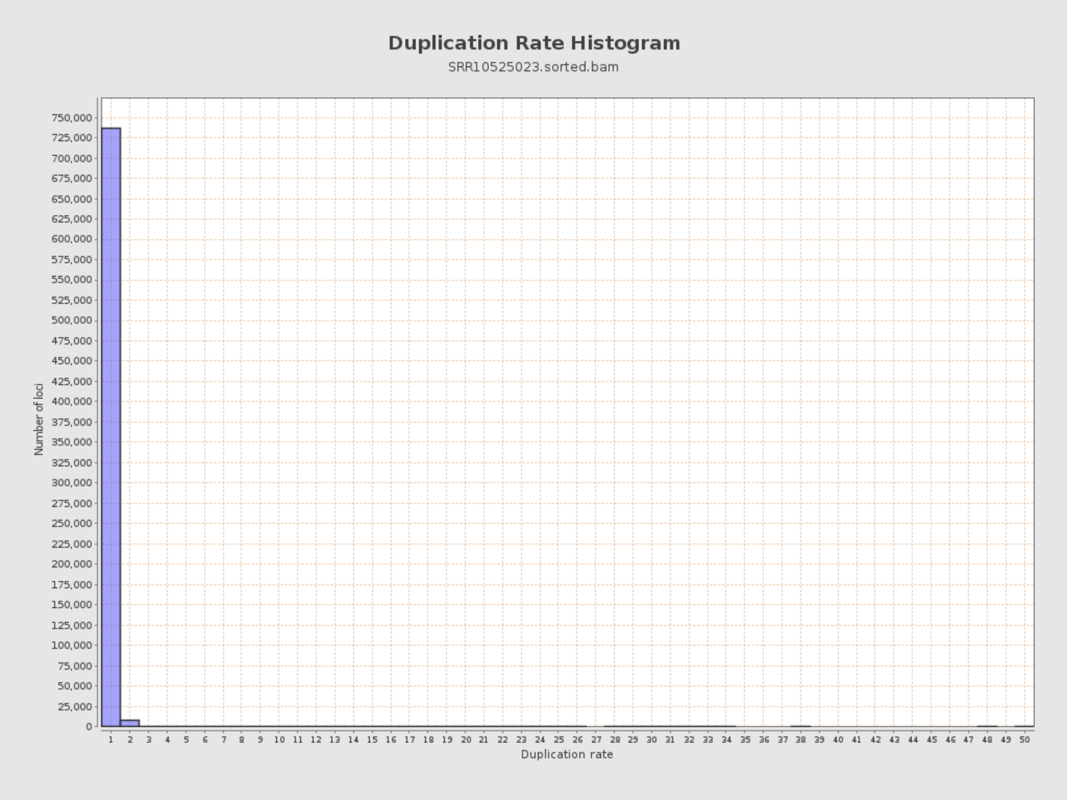
5. Results : Coverage Histogram (0-50X)



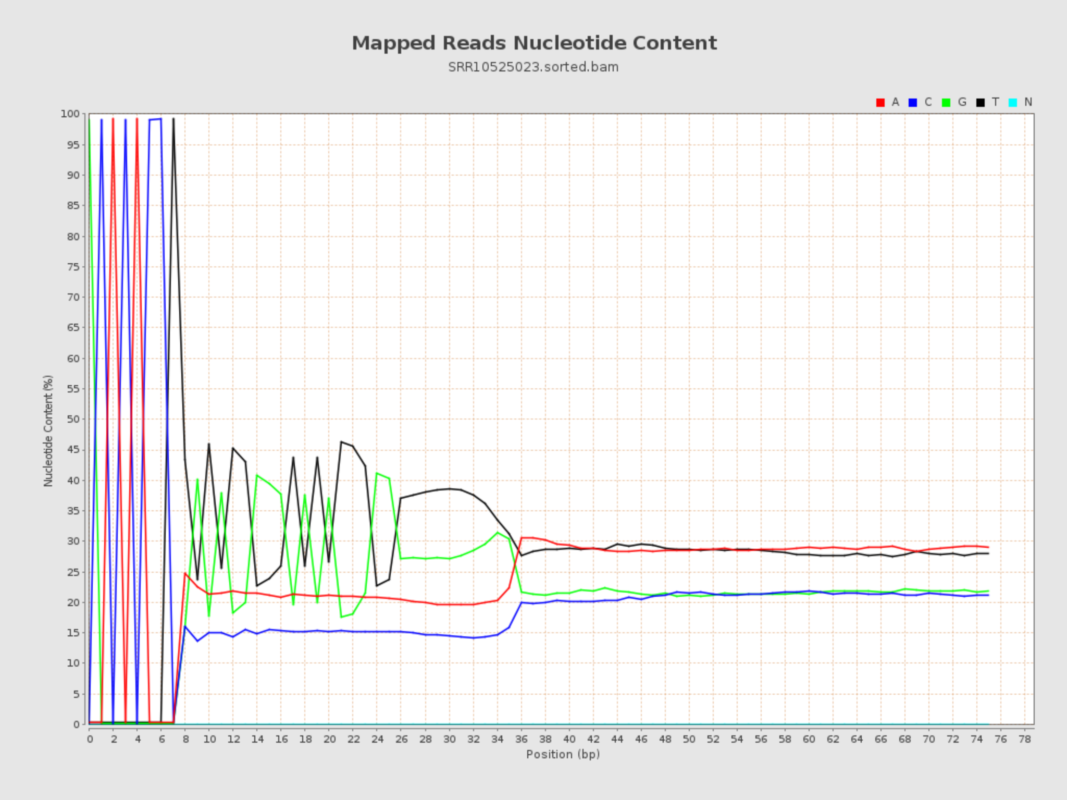
6. Results : Genome Fraction Coverage



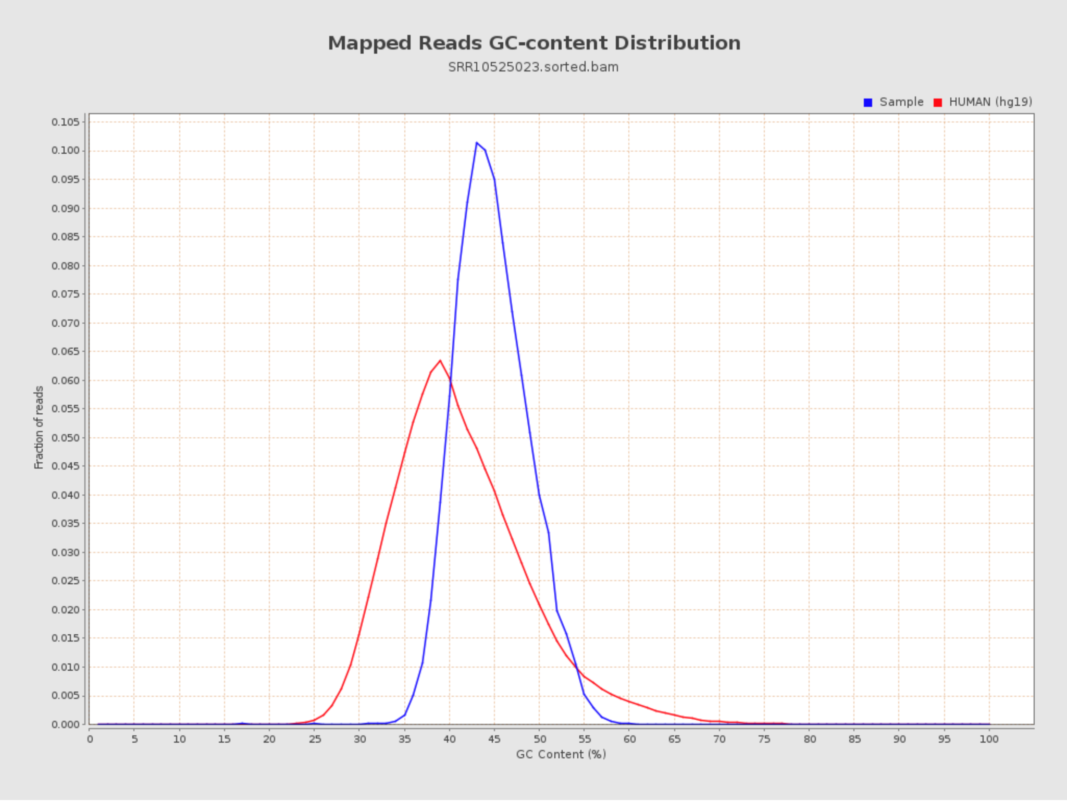
7. Results : Duplication Rate Histogram



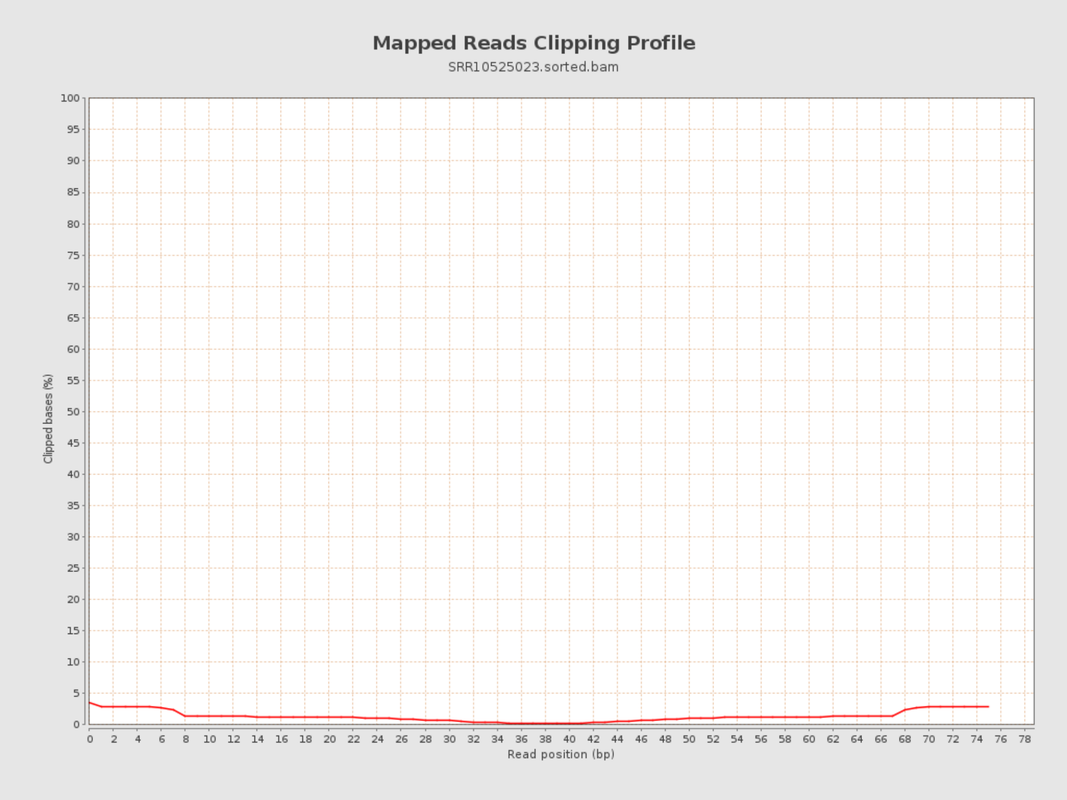
8. Results : Mapped Reads Nucleotide Content



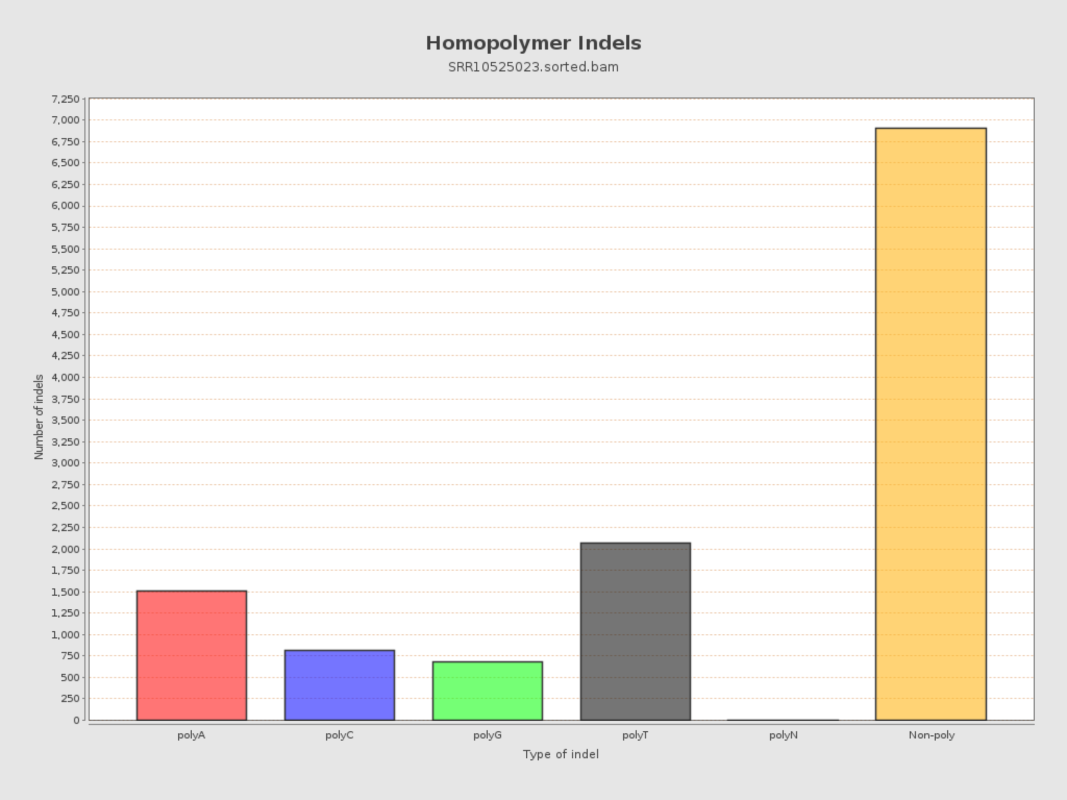
9. Results : Mapped Reads GC-content Distribution



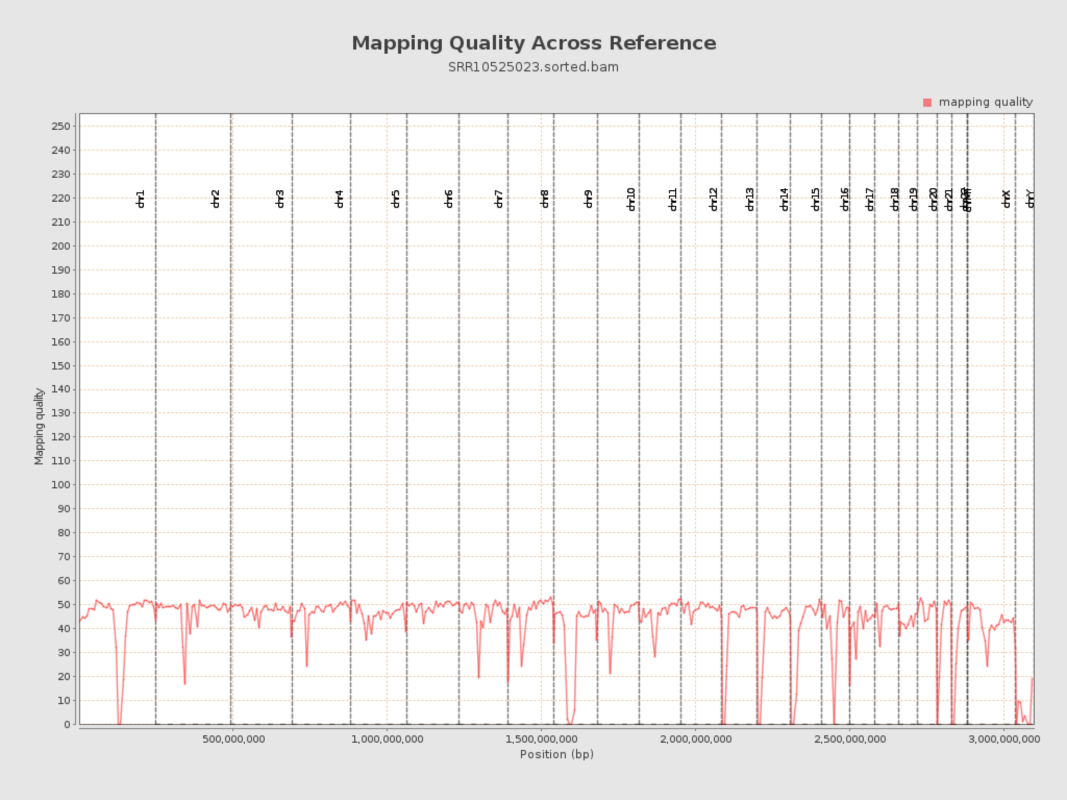
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram