Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:19:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525035.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_SRR10525035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:19:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	667,613
Mapped reads	609,613 / 91.31%
Unmapped reads	58,000 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,569 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,419 / 3.51%
Duplication rate	3.09%
Clipped reads	612,057 / 91.68%

2.2. ACGT Content

Number/percentage of A's	8,283,982 / 23.64%
Number/percentage of C's	6,794,146 / 19.39%
Number/percentage of T's	10,987,255 / 31.36%
Number/percentage of G's	8,970,061 / 25.6%
Number/percentage of N's	346 / 0%
GC Percentage	44.99%

2.3. Coverage

Mean	0.0113

Standard Deviation	0.1387

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

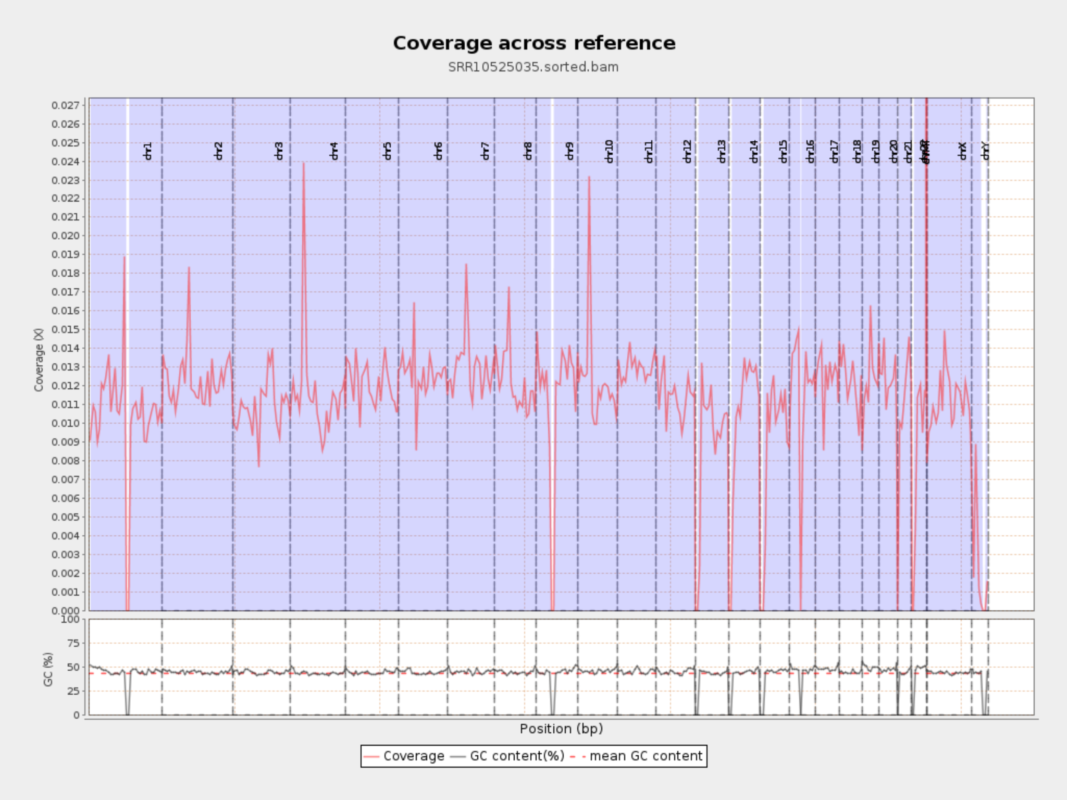
General error rate	0.53%
Mismatches	182,041
Insertions	1,949
Mapped reads with at least one insertion	0.32%
Deletions	7,233
Mapped reads with at least one deletion	1.18%
Homopolymer indels	44.31%

2.6. Chromosome stats

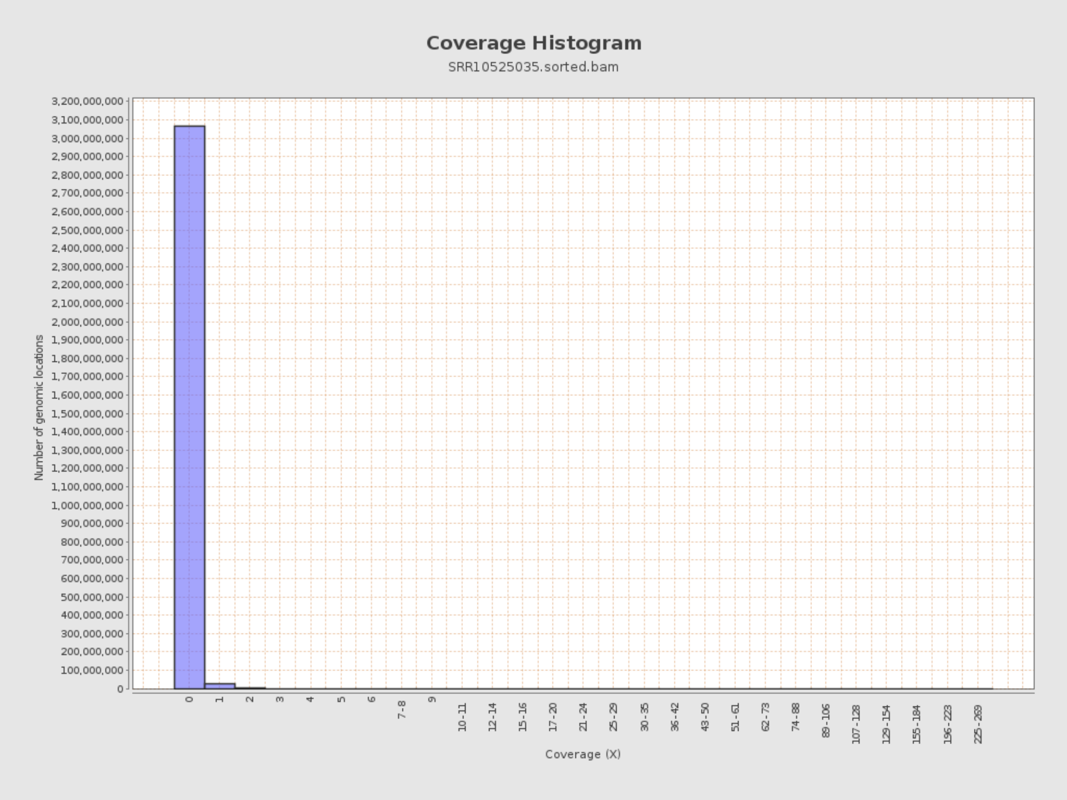
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2588441	0.0104	0.209
chr2	243199373	3026680	0.0124	0.1575
chr3	198022430	2167275	0.0109	0.1131
chr4	191154276	2212433	0.0116	0.128
chr5	180915260	2188663	0.0121	0.119
chr6	171115067	2162530	0.0126	0.1315
chr7	159138663	2079360	0.0131	0.1507

chr8	146364022	1784618	0.0122	0.1503
chr9	141213431	1565706	0.0111	0.1247
chr10	135534747	1663217	0.0123	0.1492
chr11	135006516	1748078	0.0129	0.1377
chr12	133851895	1530602	0.0114	0.1164
chr13	115169878	1011961	0.0088	0.1013
chr14	107349540	1087315	0.0101	0.1101
chr15	102531392	897897	0.0088	0.1033
chr16	90354753	1059507	0.0117	0.1203
chr17	81195210	1008439	0.0124	0.1262
chr18	78077248	957990	0.0123	0.1766
chr19	59128983	735826	0.0124	0.1601
chr20	63025520	784754	0.0125	0.122
chr21	48129895	515332	0.0107	0.1225
chr22	51304566	402905	0.0079	0.0947
chrMT	16571	2134	0.1288	0.424
chrX	155270560	1735745	0.0112	0.1197
chrY	59373566	130540	0.0022	0.0859

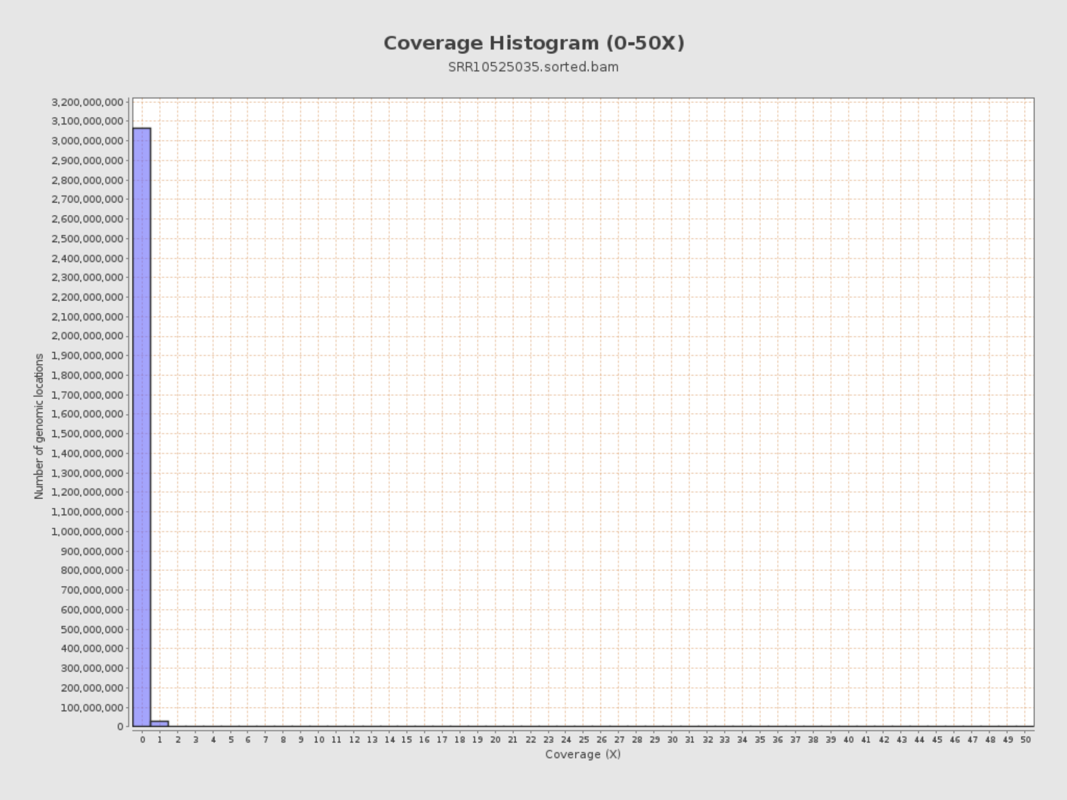
3. Results : Coverage across reference



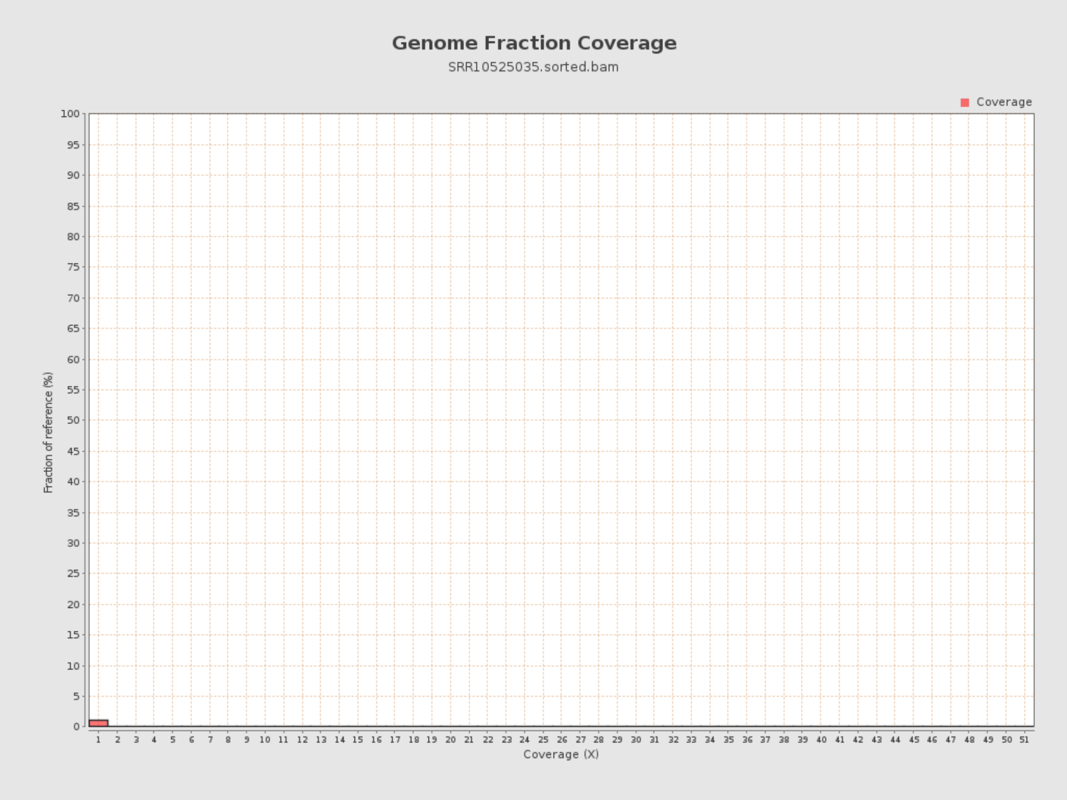
4. Results : Coverage Histogram



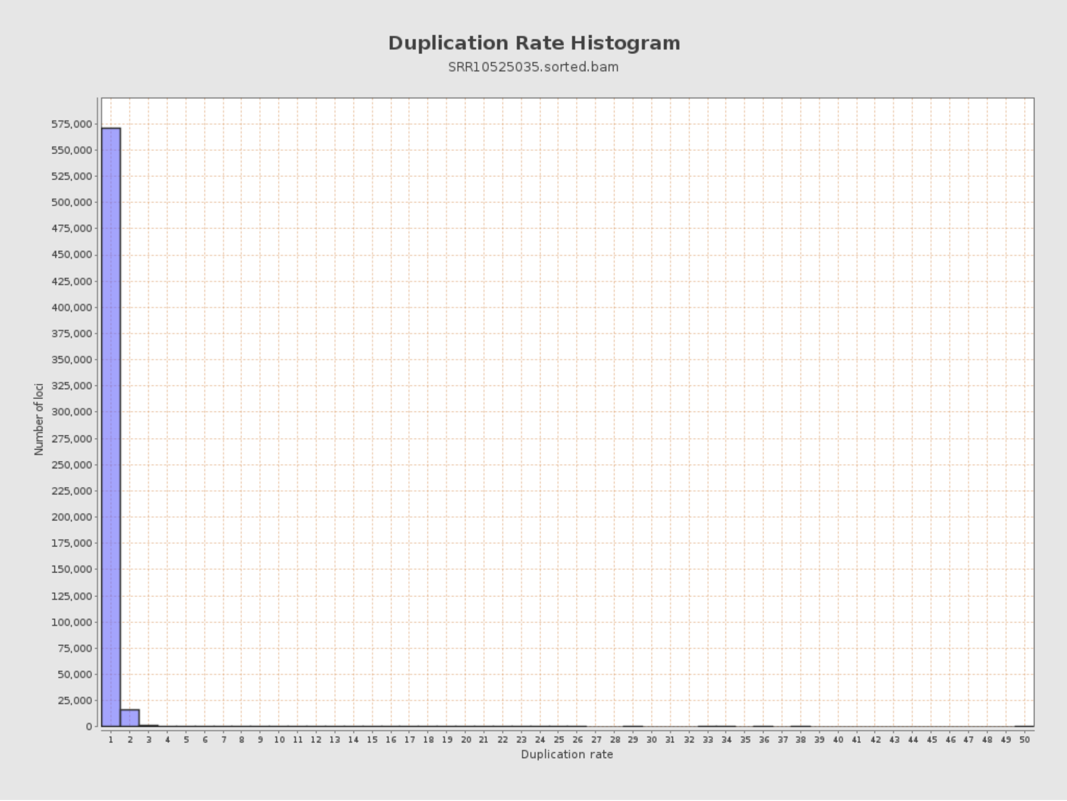
5. Results : Coverage Histogram (0-50X)



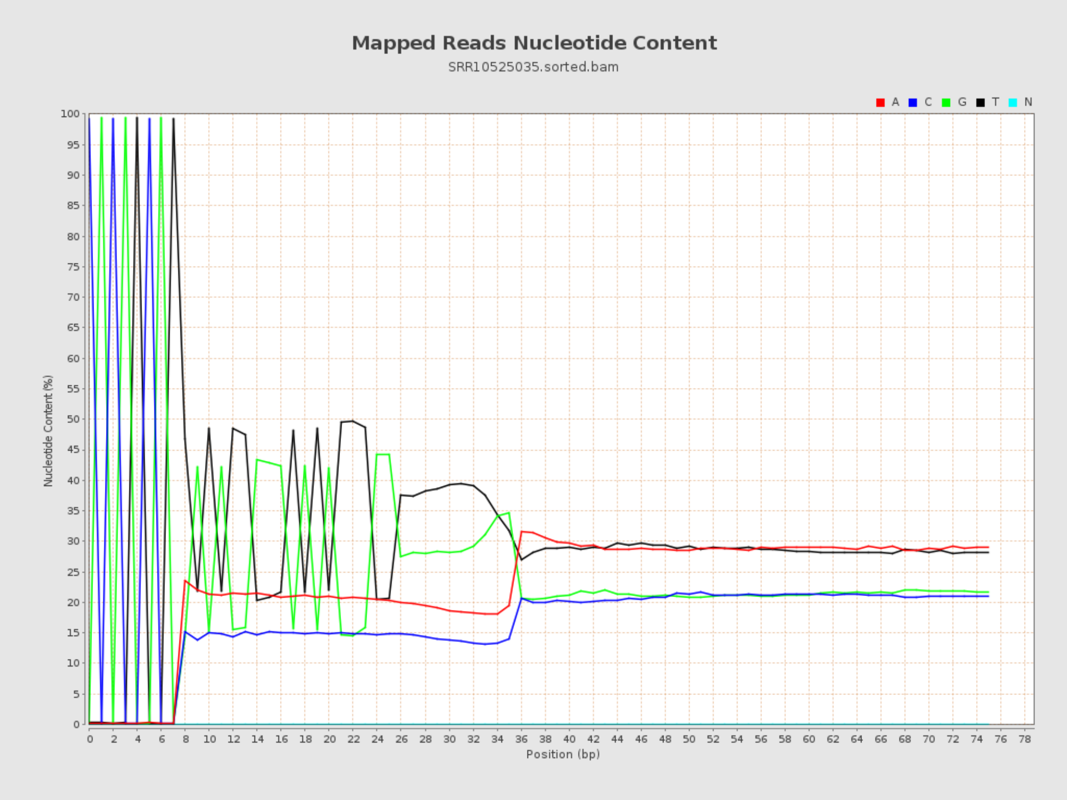
6. Results : Genome Fraction Coverage



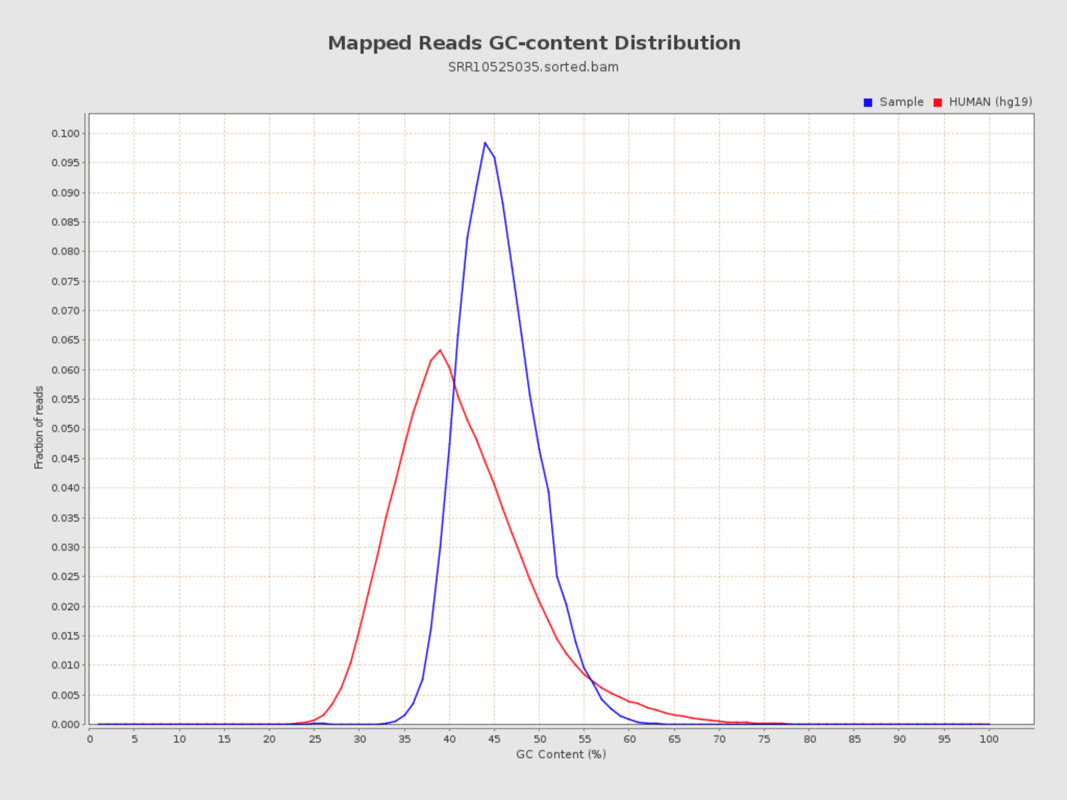
7. Results : Duplication Rate Histogram



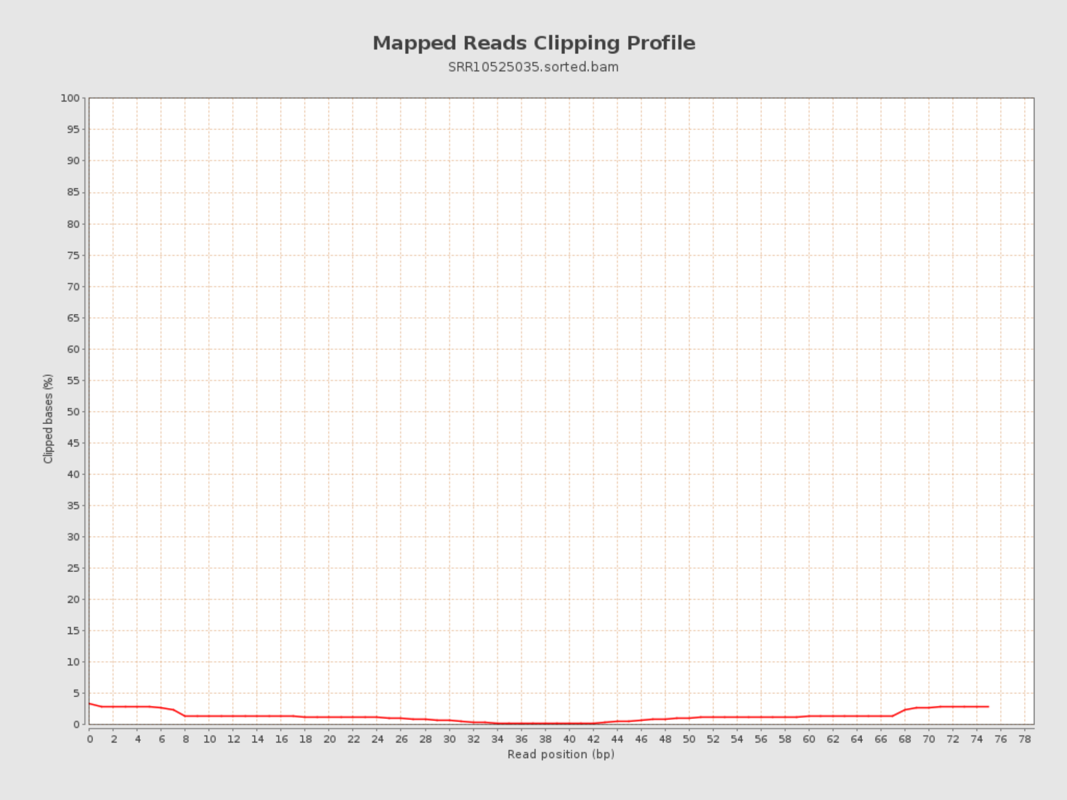
8. Results : Mapped Reads Nucleotide Content



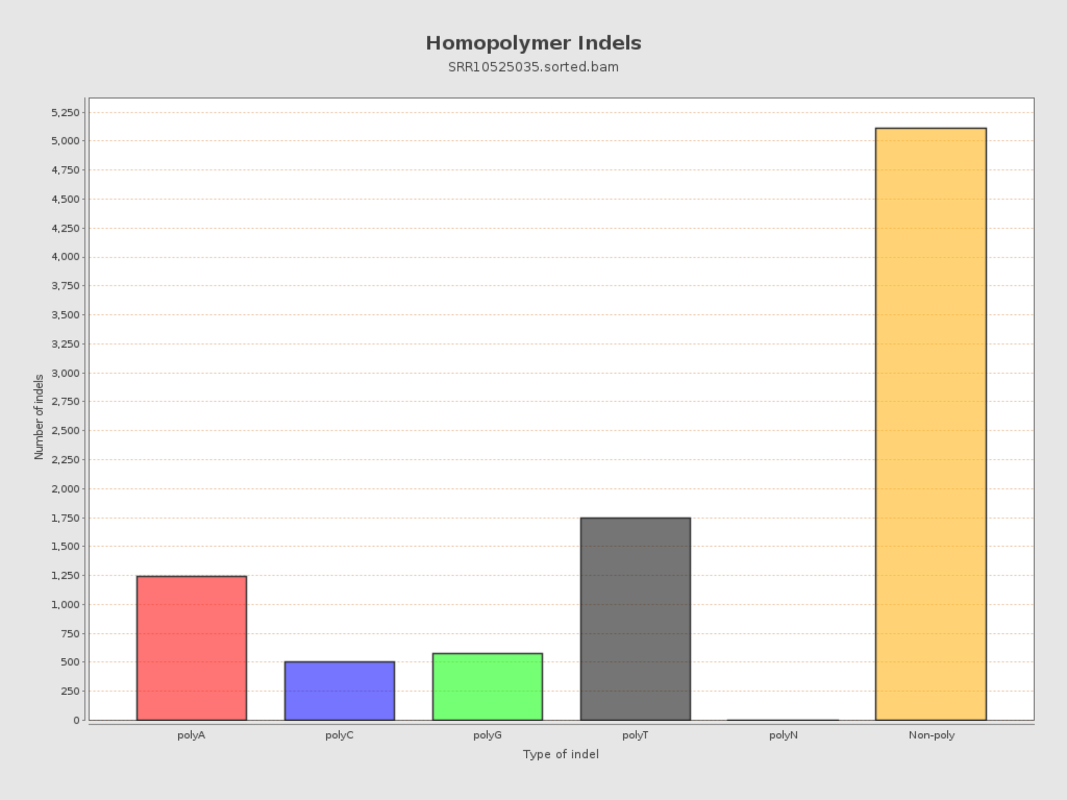
9. Results : Mapped Reads GC-content Distribution



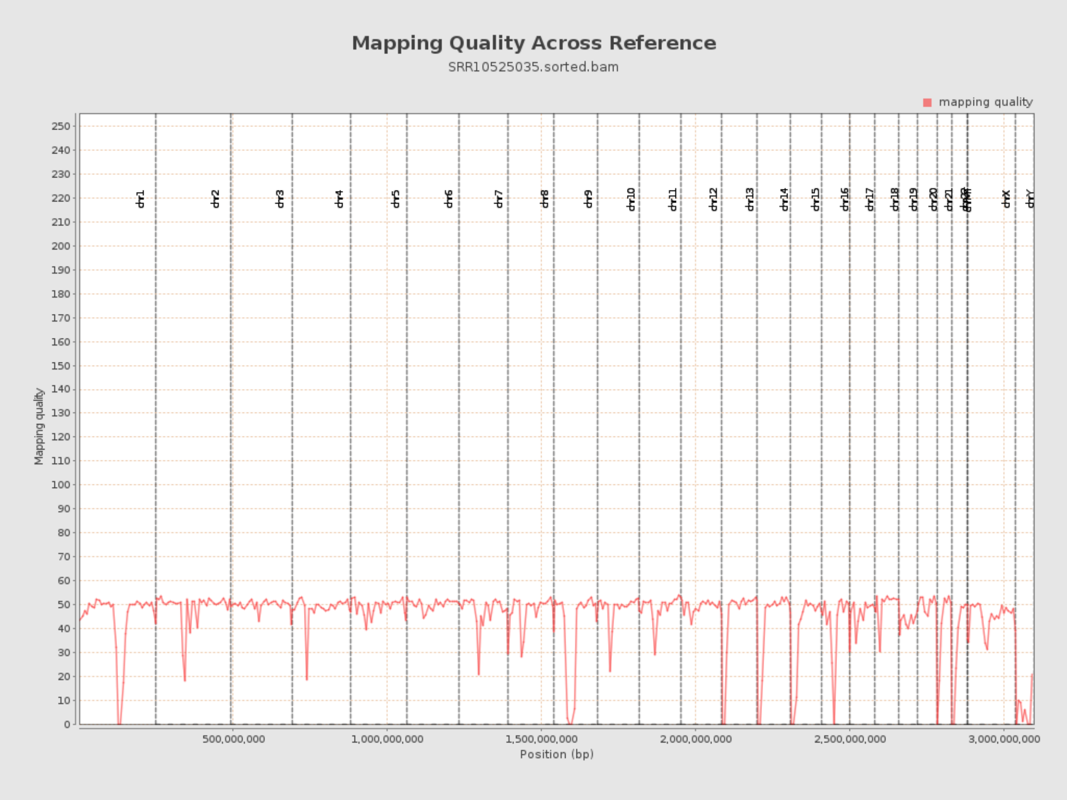
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram