Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 03:45:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716260.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_SRR9716260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 03:45:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	455,090
Mapped reads	411,760 / 90.48%
Unmapped reads	43,330 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,297 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	6,558 / 1.44%
Duplication rate	1.15%
Clipped reads	412,998 / 90.75%

2.2. ACGT Content

Number/percentage of A's	6,445,944 / 26.51%
Number/percentage of C's	4,977,502 / 20.47%
Number/percentage of T's	7,346,188 / 30.21%
Number/percentage of G's	5,544,968 / 22.8%
Number/percentage of N's	344 / 0%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1097

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

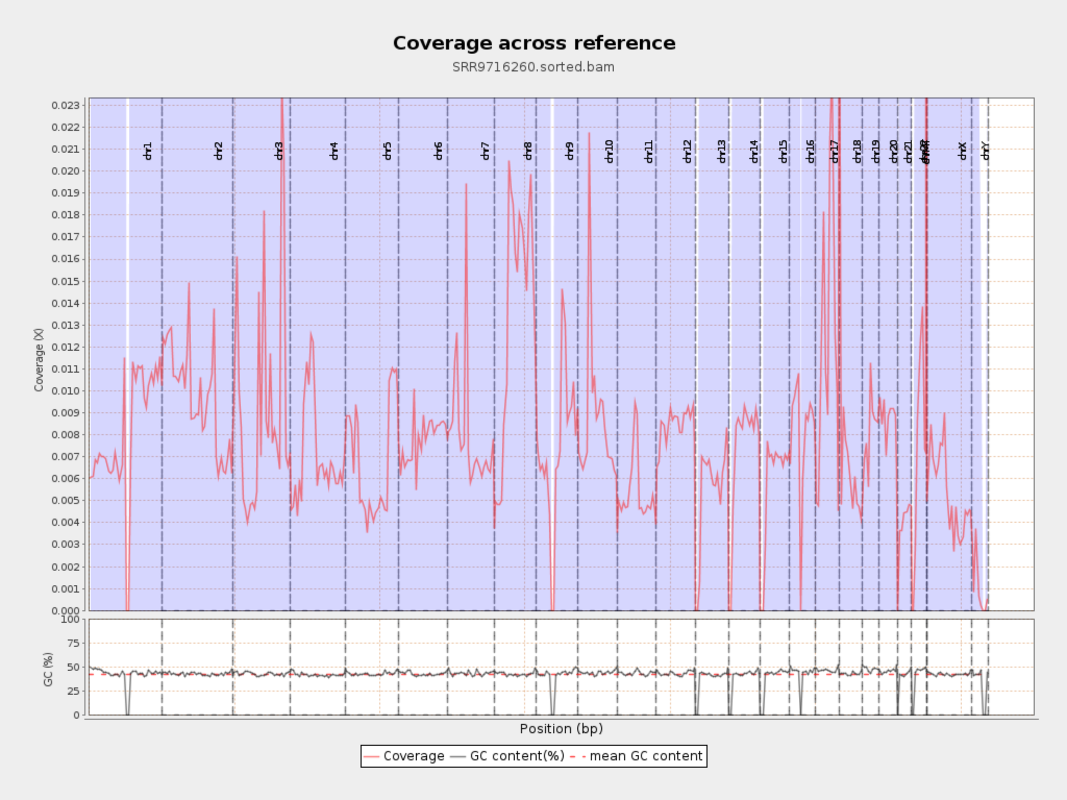
General error rate	0.51%
Mismatches	119,068
Insertions	1,862
Mapped reads with at least one insertion	0.45%
Deletions	4,285
Mapped reads with at least one deletion	1.03%
Homopolymer indels	39.08%

2.6. Chromosome stats

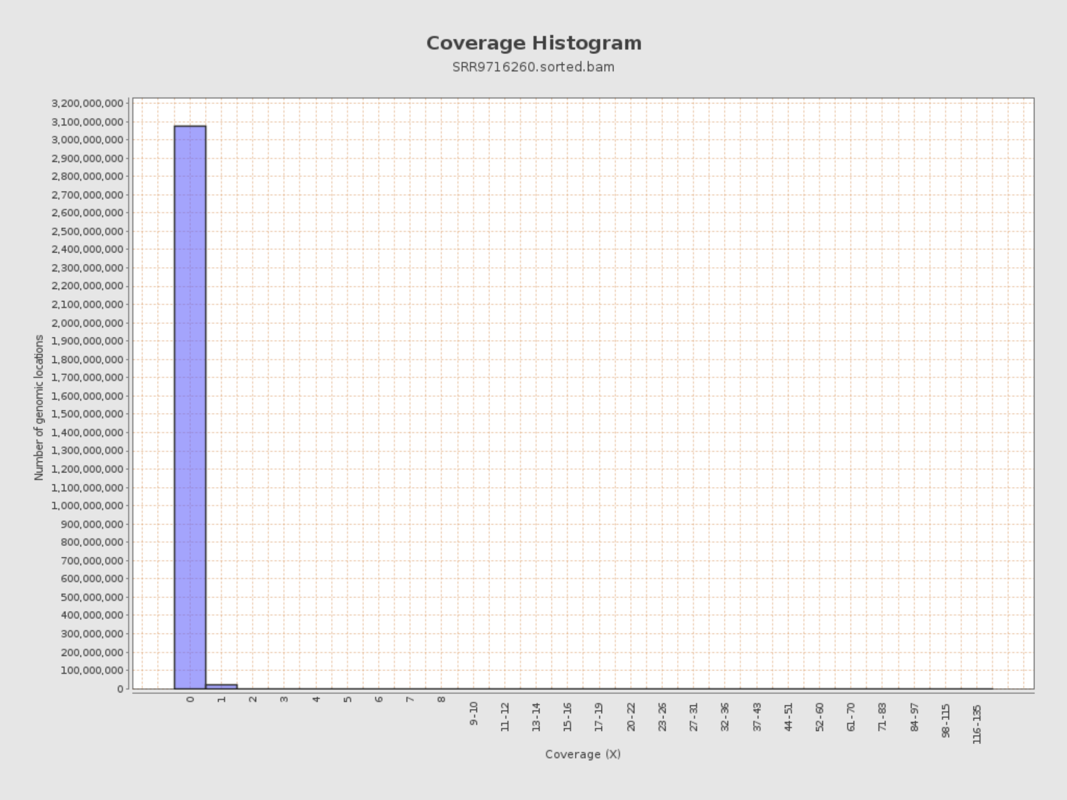
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1998267	0.008	0.1425
chr2	243199373	2392562	0.0098	0.1197
chr3	198022430	1843880	0.0093	0.1005
chr4	191154276	1351809	0.0071	0.0895
chr5	180915260	1216456	0.0067	0.0843
chr6	171115067	1336317	0.0078	0.0931
chr7	159138663	1295694	0.0081	0.1821

chr8	146364022	2006908	0.0137	0.1365
chr9	141213431	1027331	0.0073	0.0918
chr10	135534747	1178170	0.0087	0.1399
chr11	135006516	725155	0.0054	0.0799
chr12	133851895	1129327	0.0084	0.0981
chr13	115169878	624699	0.0054	0.0756
chr14	107349540	781922	0.0073	0.088
chr15	102531392	587345	0.0057	0.0783
chr16	90354753	738268	0.0082	0.0943
chr17	81195210	1012746	0.0125	0.1161
chr18	78077248	562118	0.0072	0.112
chr19	59128983	479511	0.0081	0.1308
chr20	63025520	549791	0.0087	0.0975
chr21	48129895	186112	0.0039	0.0676
chr22	51304566	363687	0.0071	0.0864
chrMT	16571	31085	1.8759	1.7126
chrX	155270560	842130	0.0054	0.0789
chrY	59373566	60337	0.001	0.0405

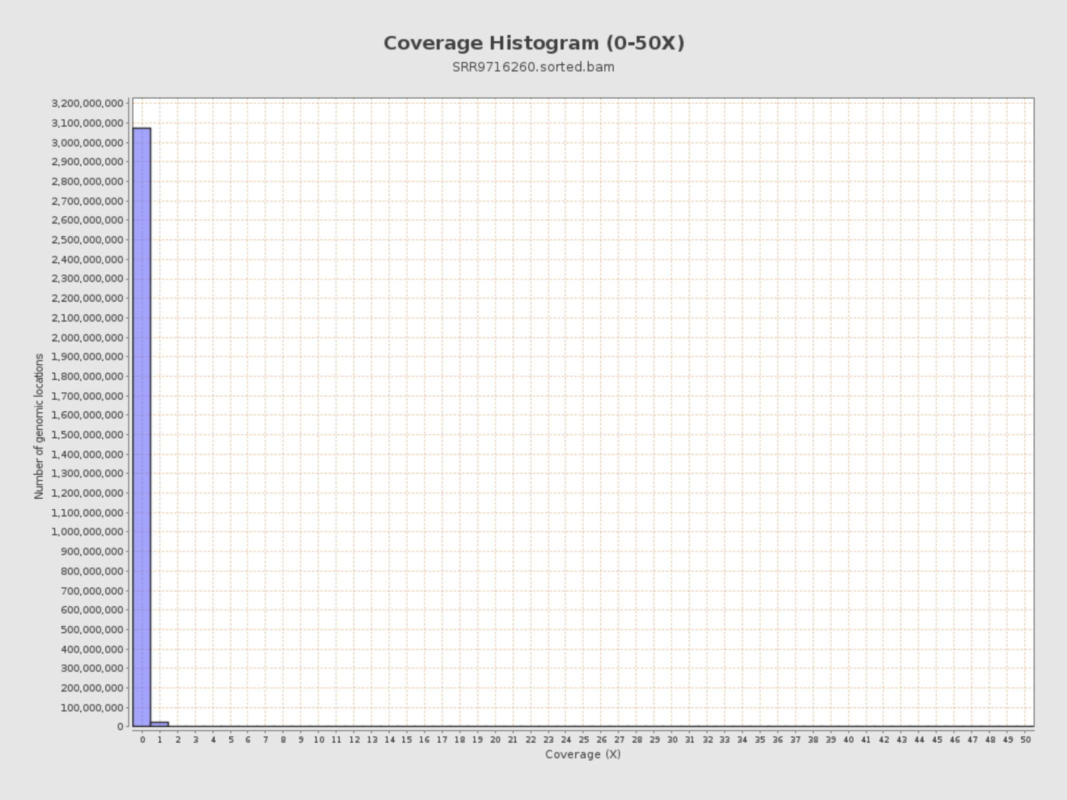
3. Results : Coverage across reference



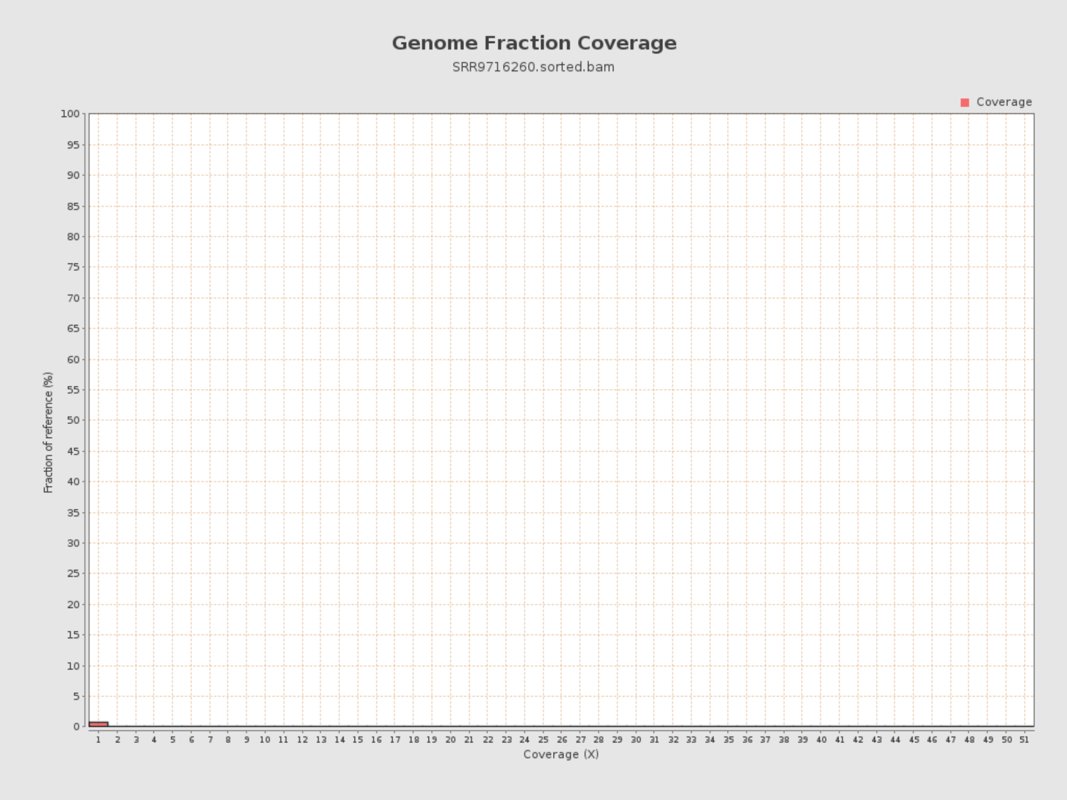
4. Results : Coverage Histogram



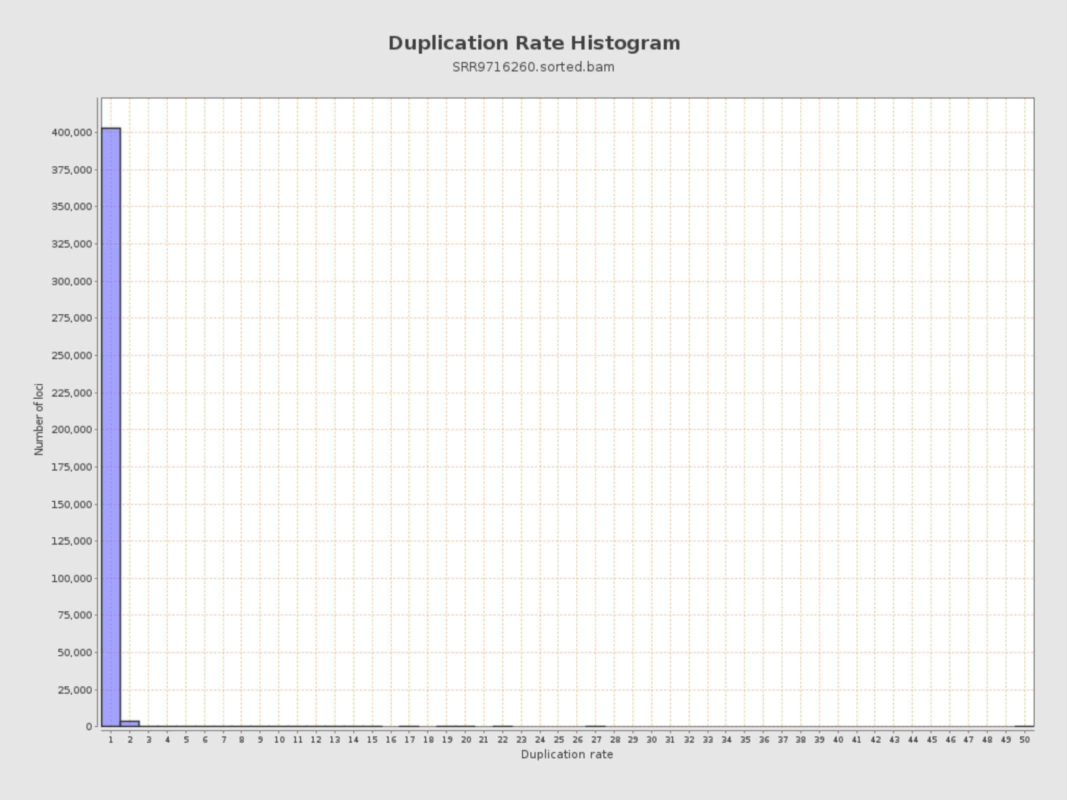
5. Results : Coverage Histogram (0-50X)



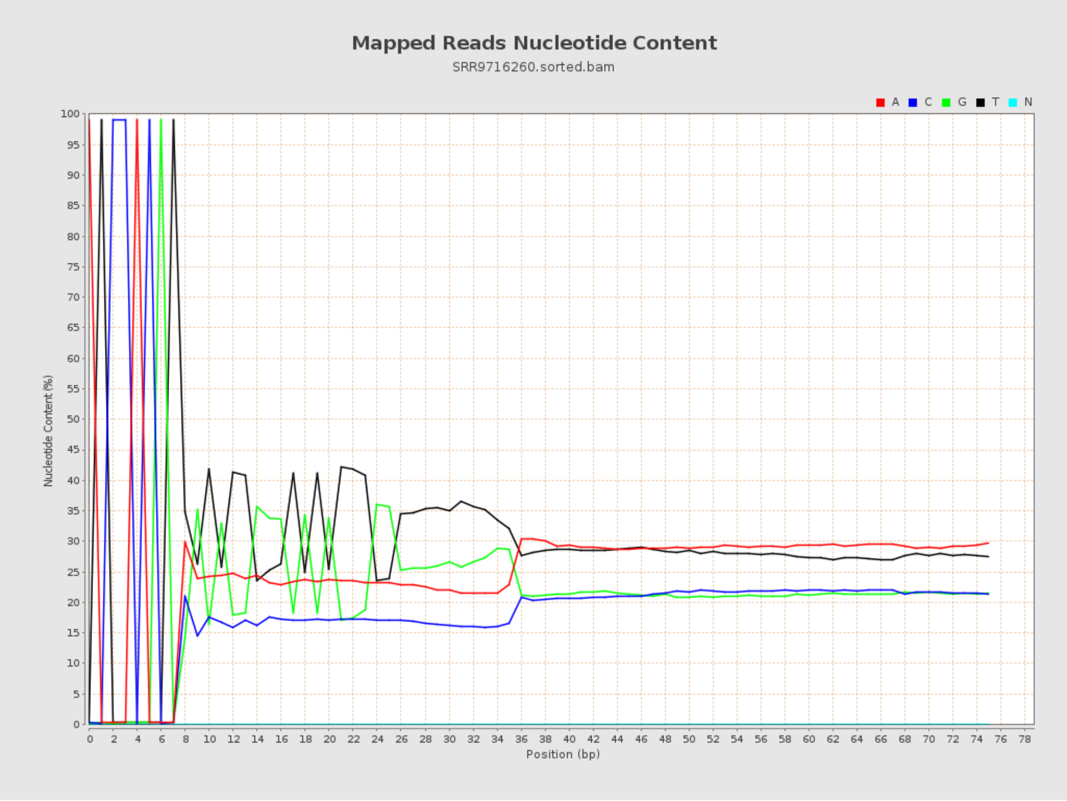
6. Results : Genome Fraction Coverage



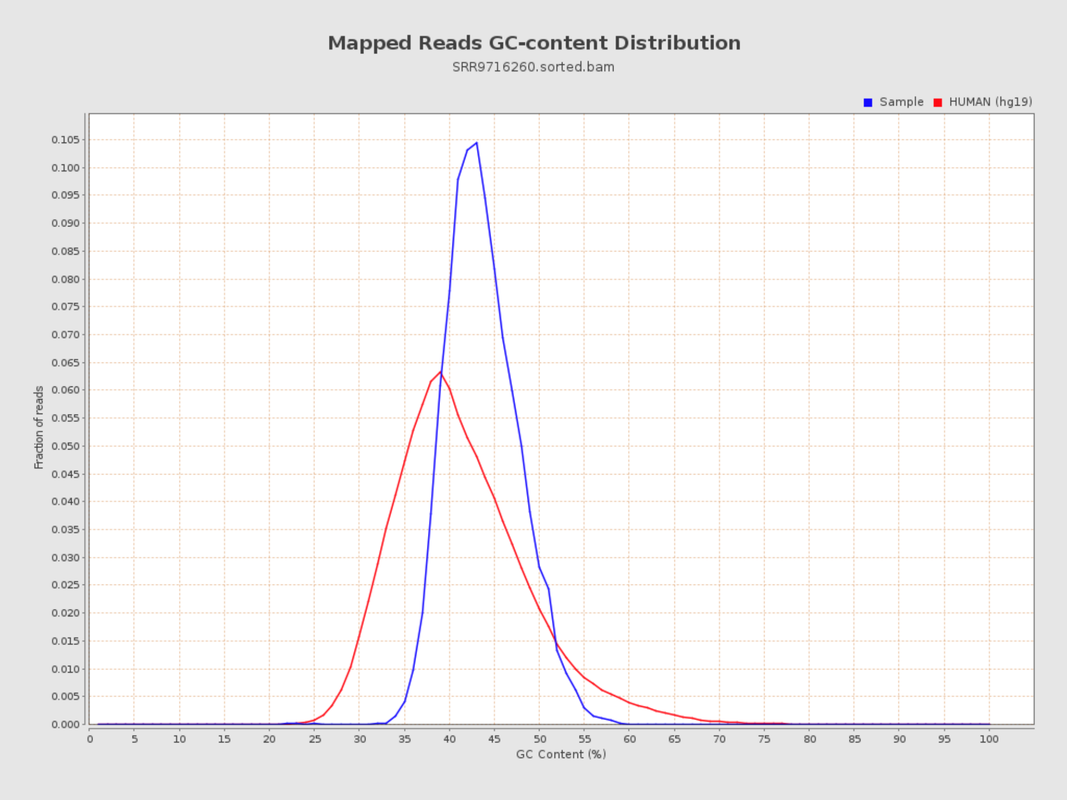
7. Results : Duplication Rate Histogram



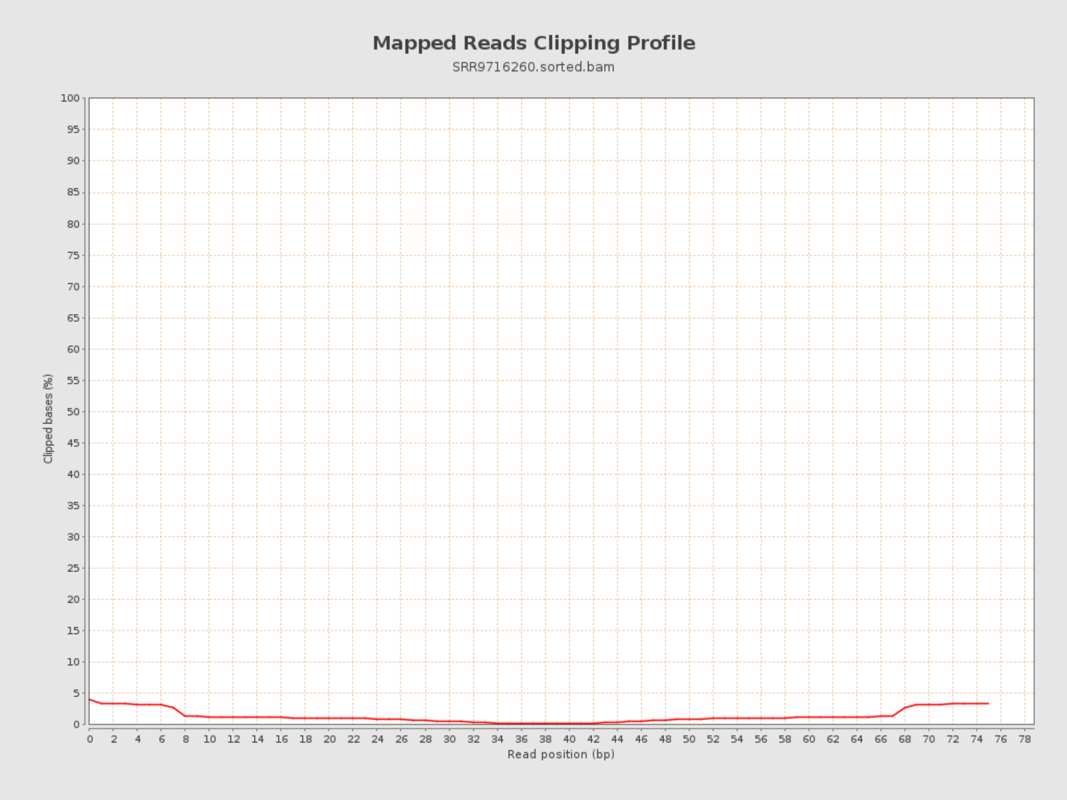
8. Results : Mapped Reads Nucleotide Content



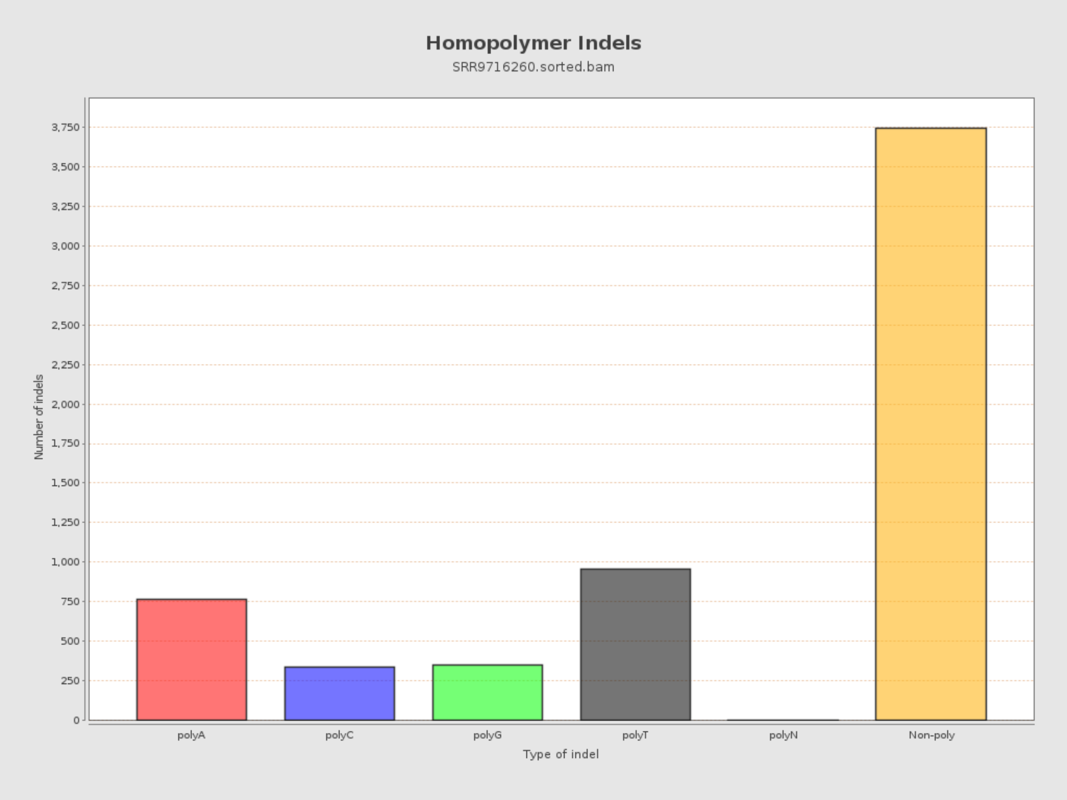
9. Results : Mapped Reads GC-content Distribution



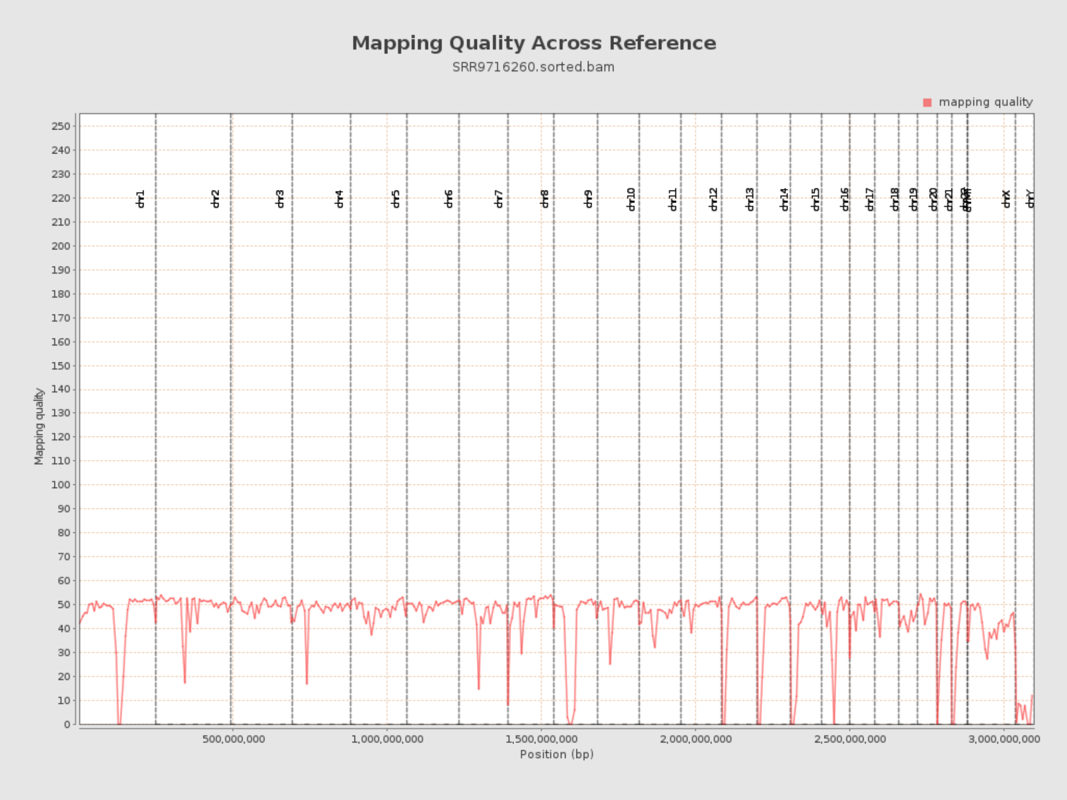
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram