Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:04:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716726.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_SRR9716726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716726.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:04:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,131,721
Mapped reads	991,750 / 87.63%
Unmapped reads	139,971 / 12.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,699 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	24,903 / 2.2%
Duplication rate	1.68%
Clipped reads	993,529 / 87.79%

2.2. ACGT Content

Number/percentage of A's	15,399,066 / 26.61%
Number/percentage of C's	10,658,102 / 18.42%
Number/percentage of T's	17,783,915 / 30.73%
Number/percentage of G's	14,029,077 / 24.24%
Number/percentage of N's	698 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.2056

2.4. Mapping Quality

Mean Mapping Quality	44.35

2.5. Mismatches and indels

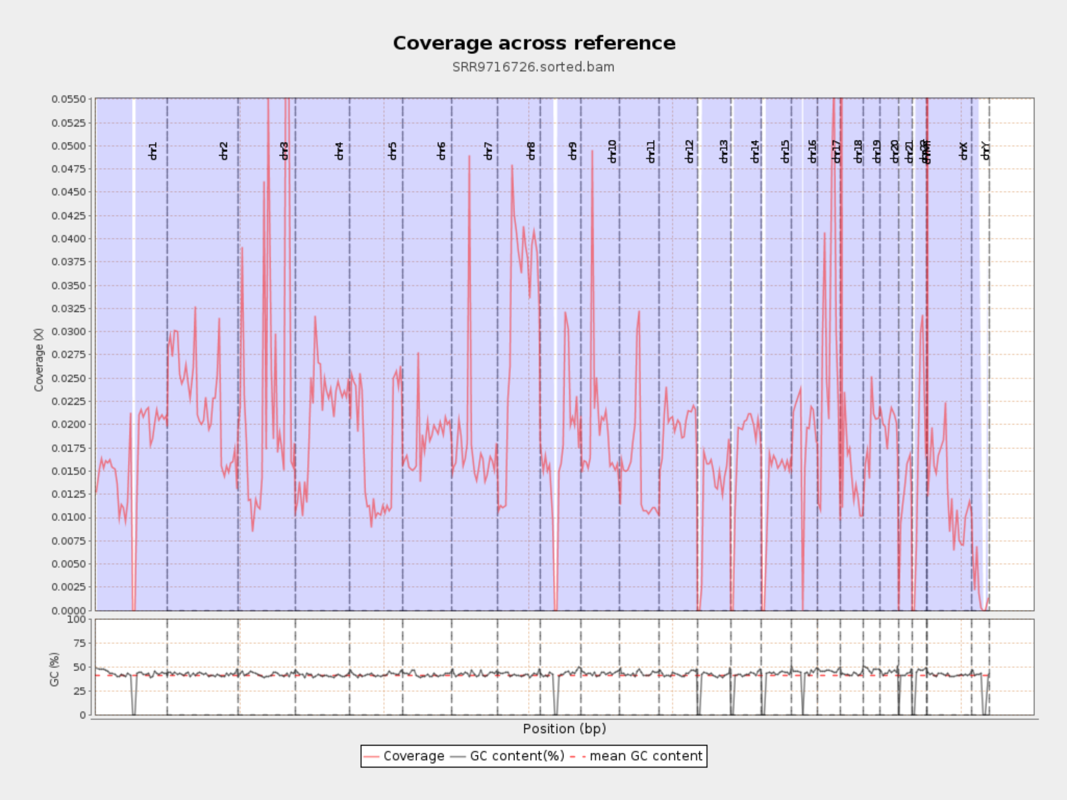
General error rate	0.51%
Mismatches	289,087
Insertions	4,225
Mapped reads with at least one insertion	0.42%
Deletions	10,817
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.21%

2.6. Chromosome stats

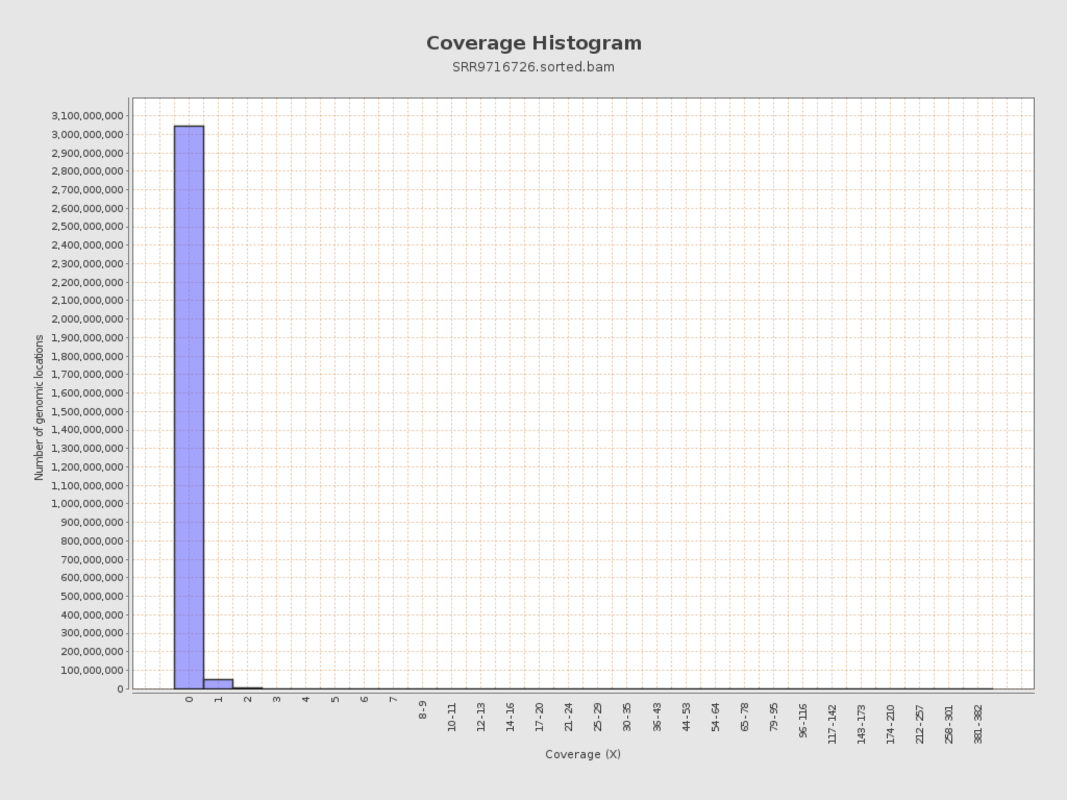
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3961301	0.0159	0.2472
chr2	243199373	5507545	0.0226	0.2313
chr3	198022430	4879216	0.0246	0.1834
chr4	191154276	4037037	0.0211	0.1593
chr5	180915260	3055732	0.0169	0.1383
chr6	171115067	3145953	0.0184	0.15
chr7	159138663	2841622	0.0179	0.4291

chr8	146364022	4640201	0.0317	0.2243
chr9	141213431	2368760	0.0168	0.1497
chr10	135534747	2668423	0.0197	0.3056
chr11	135006516	2089001	0.0155	0.1493
chr12	133851895	2693720	0.0201	0.1704
chr13	115169878	1464488	0.0127	0.1188
chr14	107349540	1800301	0.0168	0.1388
chr15	102531392	1328042	0.013	0.1257
chr16	90354753	1680930	0.0186	0.1522
chr17	81195210	2329476	0.0287	0.1845
chr18	78077248	1428680	0.0183	0.2159
chr19	59128983	1122785	0.019	0.2592
chr20	63025520	1265314	0.0201	0.1651
chr21	48129895	584717	0.0121	0.1212
chr22	51304566	840416	0.0164	0.1348
chrMT	16571	18988	1.1459	1.3143
chrX	155270560	2004038	0.0129	0.1366
chrY	59373566	131255	0.0022	0.0637

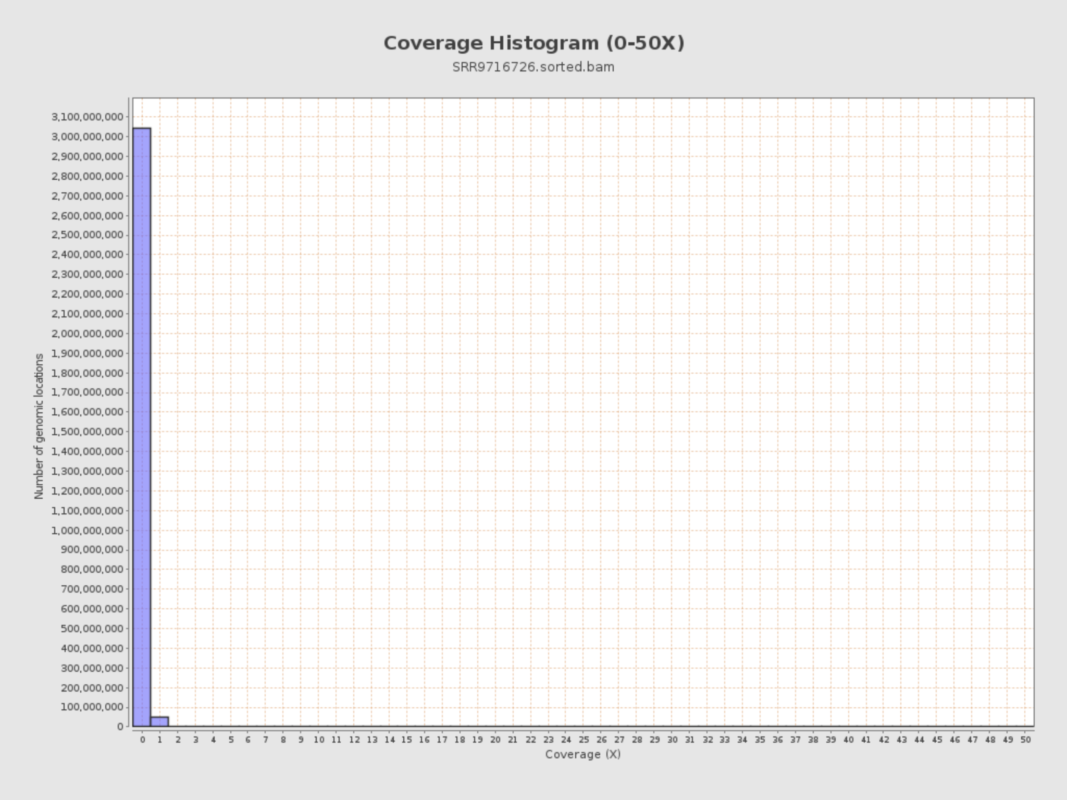
3. Results : Coverage across reference



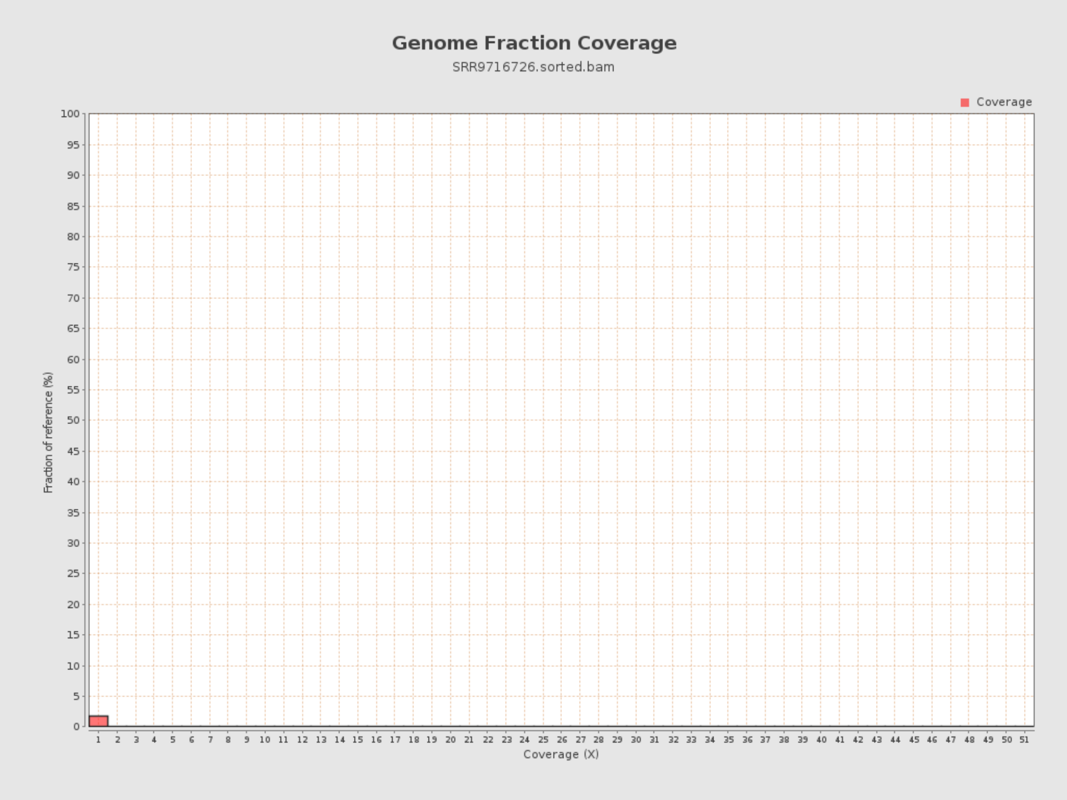
4. Results : Coverage Histogram



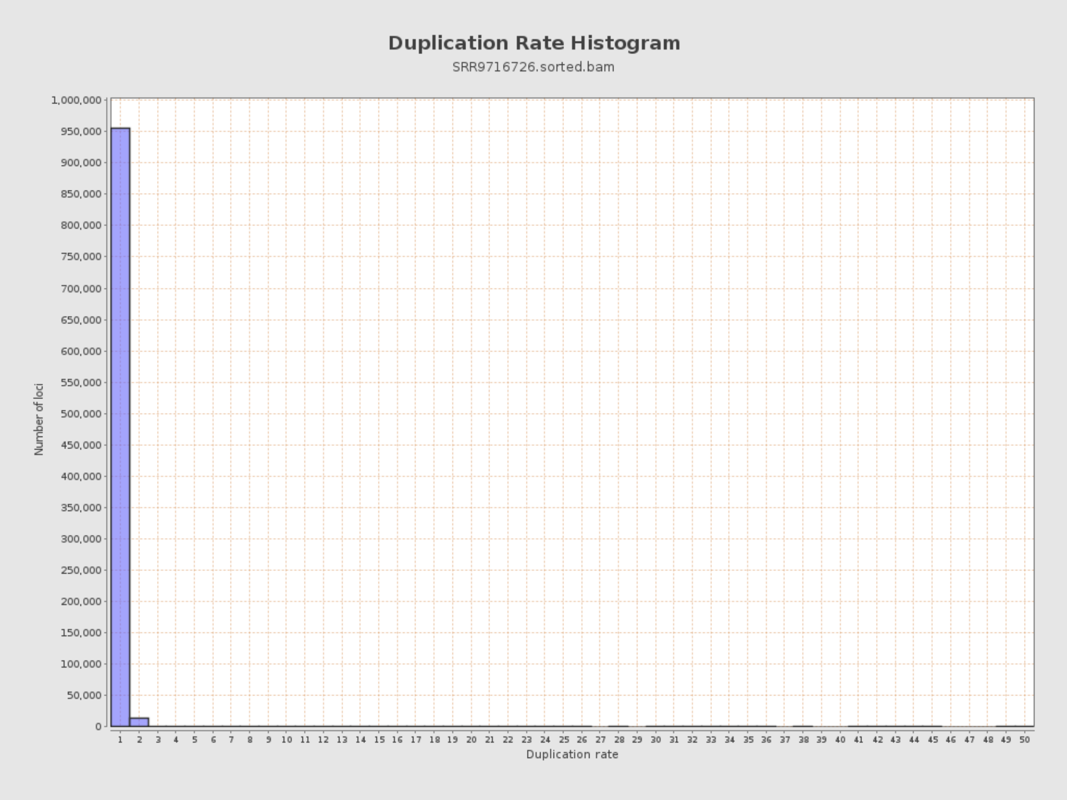
5. Results : Coverage Histogram (0-50X)



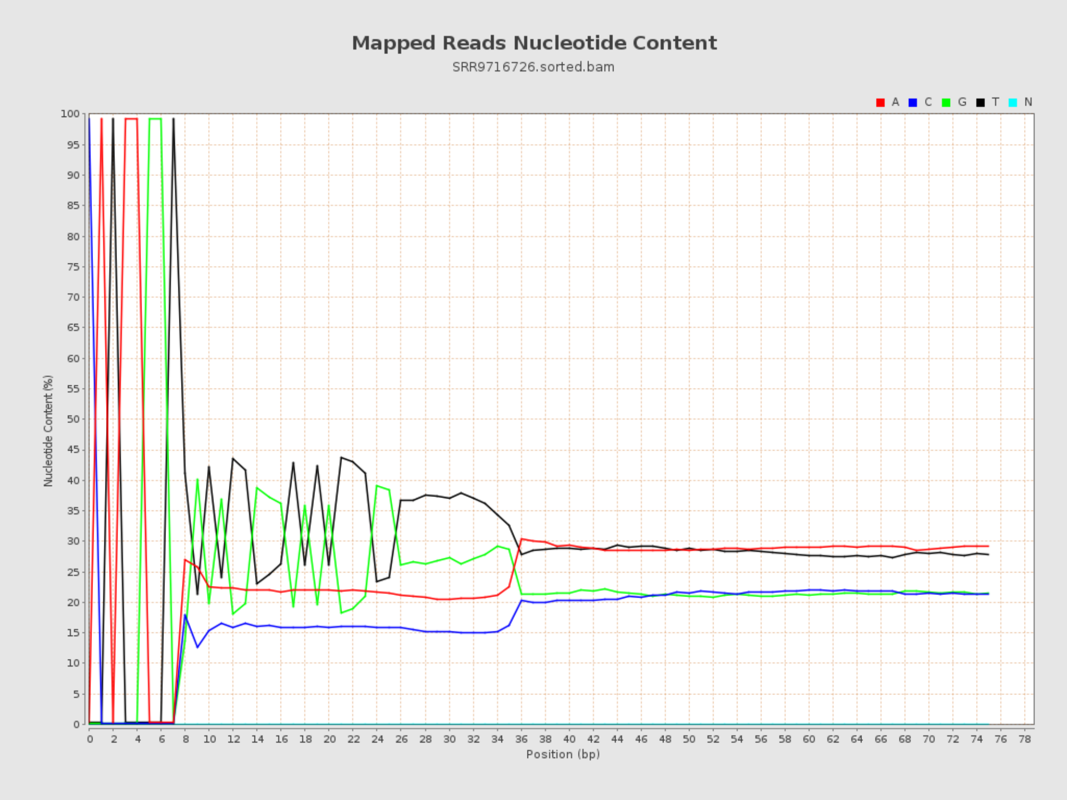
6. Results : Genome Fraction Coverage



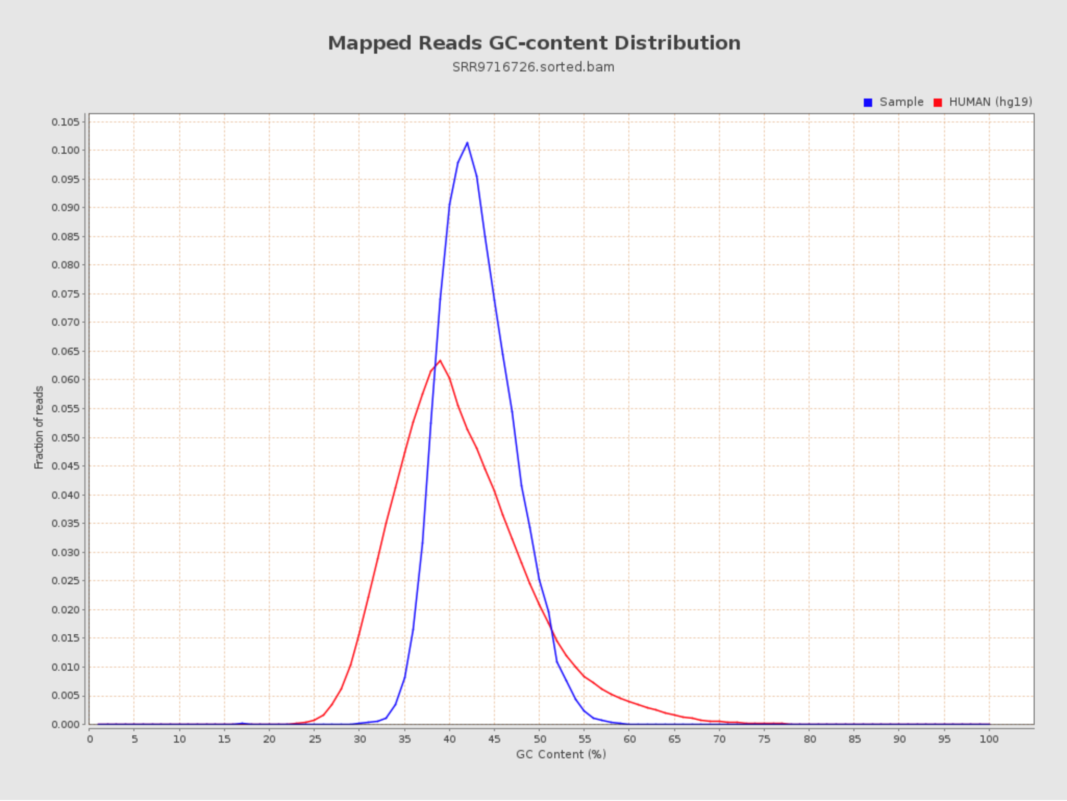
7. Results : Duplication Rate Histogram



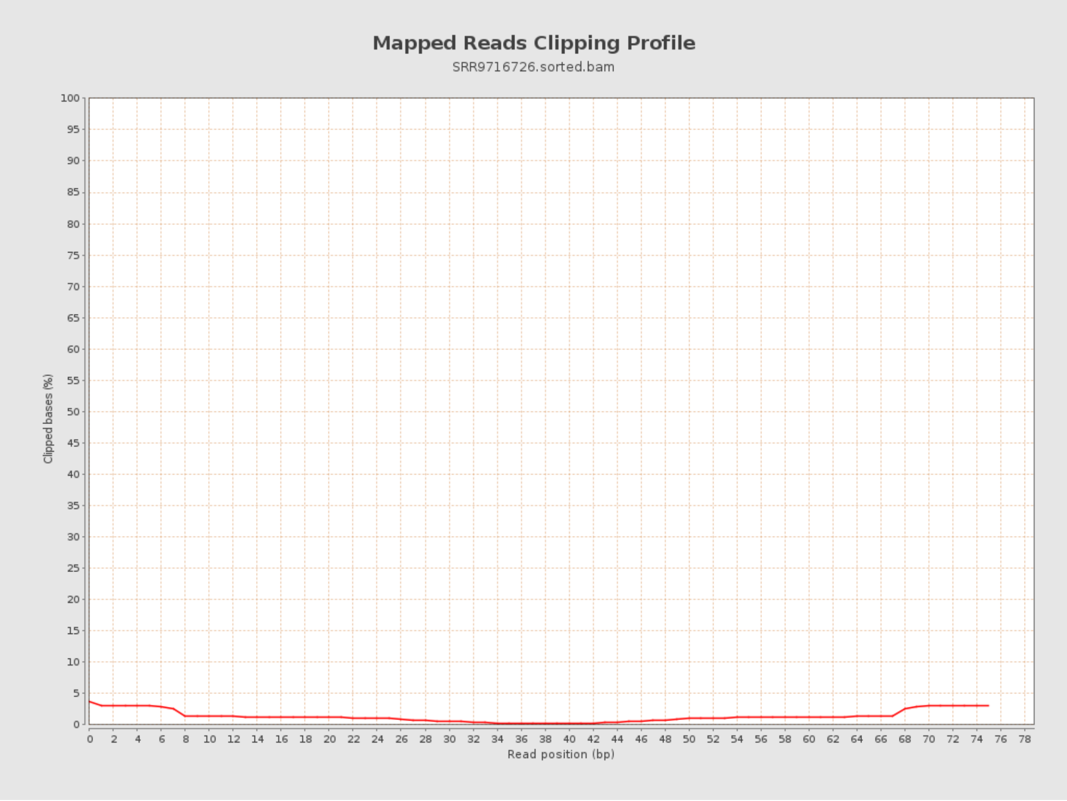
8. Results : Mapped Reads Nucleotide Content



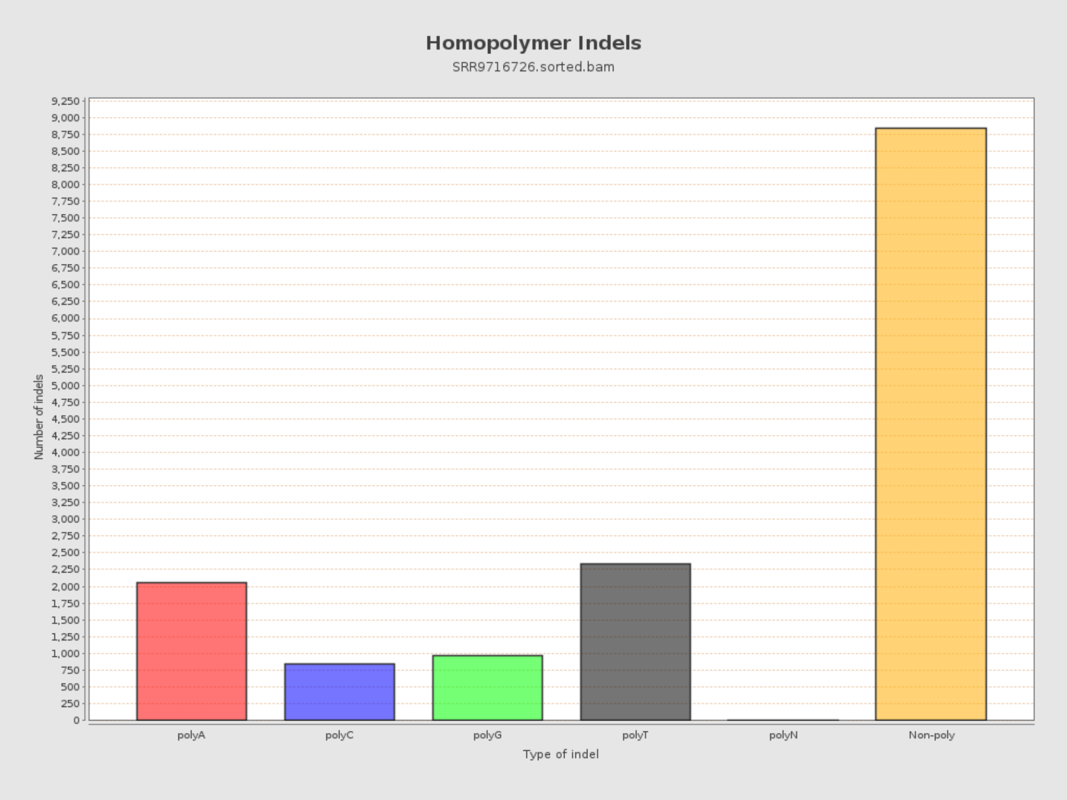
9. Results : Mapped Reads GC-content Distribution



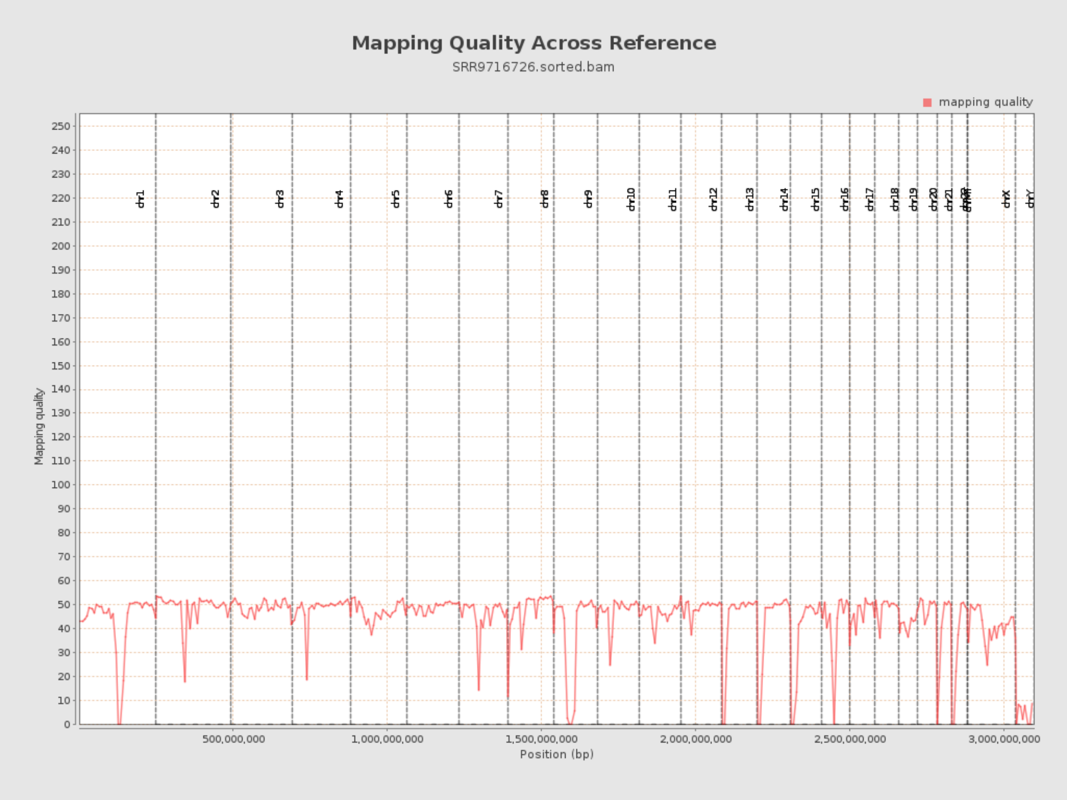
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram