Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:06:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716727.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_SRR9716727 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716727.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:06:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716727.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	457,292
Mapped reads	390,298 / 85.35%
Unmapped reads	66,994 / 14.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,694 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	4,722 / 1.03%
Duplication rate	0.89%
Clipped reads	390,491 / 85.39%

2.2. ACGT Content

Number/percentage of A's	6,070,770 / 26.88%
Number/percentage of C's	4,158,660 / 18.41%
Number/percentage of T's	6,937,248 / 30.72%
Number/percentage of G's	5,417,799 / 23.99%
Number/percentage of N's	295 / 0%
GC Percentage	42.4%

2.3. Coverage

Mean	0.0073

Standard Deviation	0.1003

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

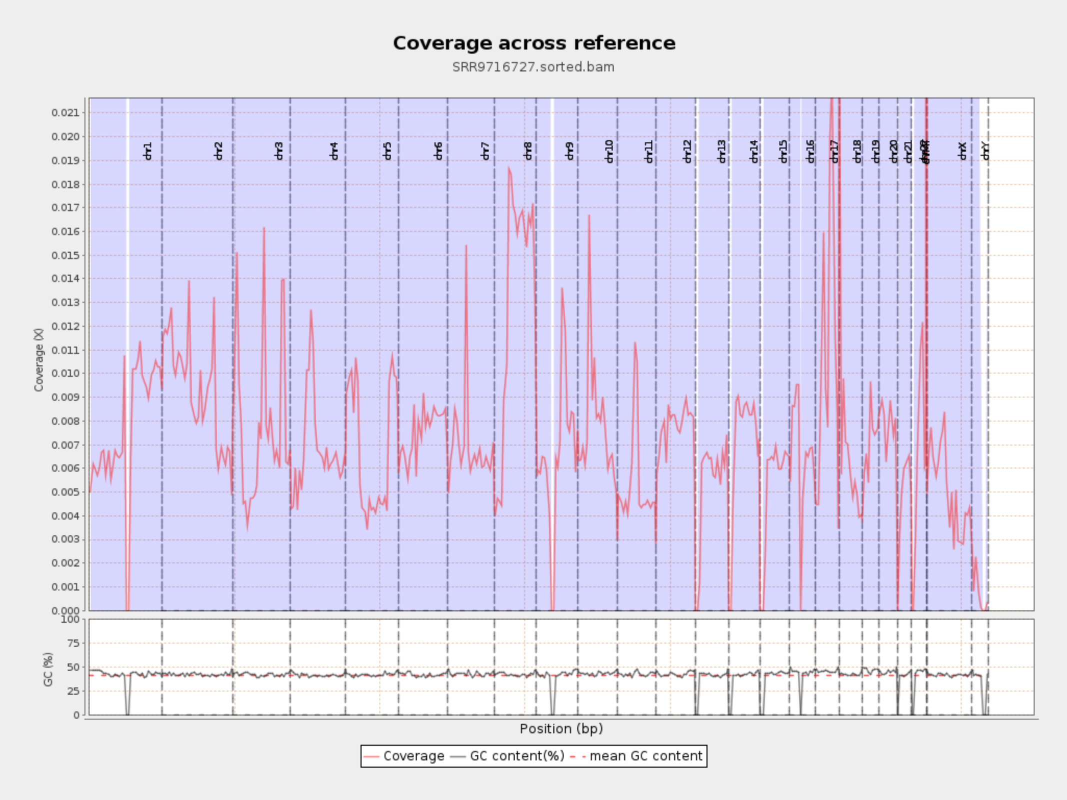
General error rate	0.51%
Mismatches	110,623
Insertions	1,878
Mapped reads with at least one insertion	0.48%
Deletions	4,065
Mapped reads with at least one deletion	1.04%
Homopolymer indels	40.03%

2.6. Chromosome stats

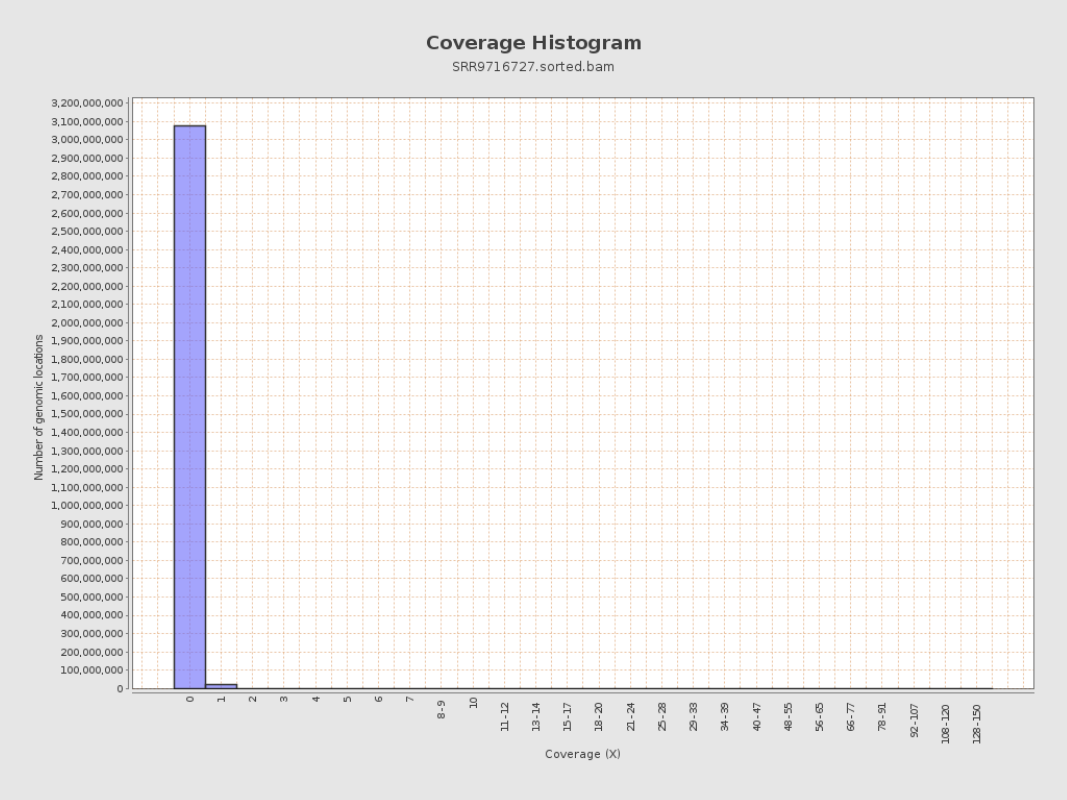
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1885399	0.0076	0.1343
chr2	243199373	2284436	0.0094	0.1195
chr3	198022430	1550270	0.0078	0.0907
chr4	191154276	1309272	0.0068	0.0854
chr5	180915260	1227663	0.0068	0.0841
chr6	171115067	1289292	0.0075	0.0911
chr7	159138663	1117891	0.007	0.1427

chr8	146364022	1938919	0.0132	0.1251
chr9	141213431	924193	0.0065	0.0869
chr10	135534747	1062819	0.0078	0.1057
chr11	135006516	716947	0.0053	0.08
chr12	133851895	1040214	0.0078	0.0909
chr13	115169878	603727	0.0052	0.0738
chr14	107349540	750023	0.007	0.0857
chr15	102531392	533440	0.0052	0.0741
chr16	90354753	597608	0.0066	0.0839
chr17	81195210	905328	0.0112	0.1091
chr18	78077248	535673	0.0069	0.1113
chr19	59128983	418475	0.0071	0.1119
chr20	63025520	491996	0.0078	0.0906
chr21	48129895	233663	0.0049	0.0714
chr22	51304566	314085	0.0061	0.0798
chrMT	16571	14989	0.9045	1.0786
chrX	155270560	800498	0.0052	0.0753
chrY	59373566	44361	0.0007	0.03

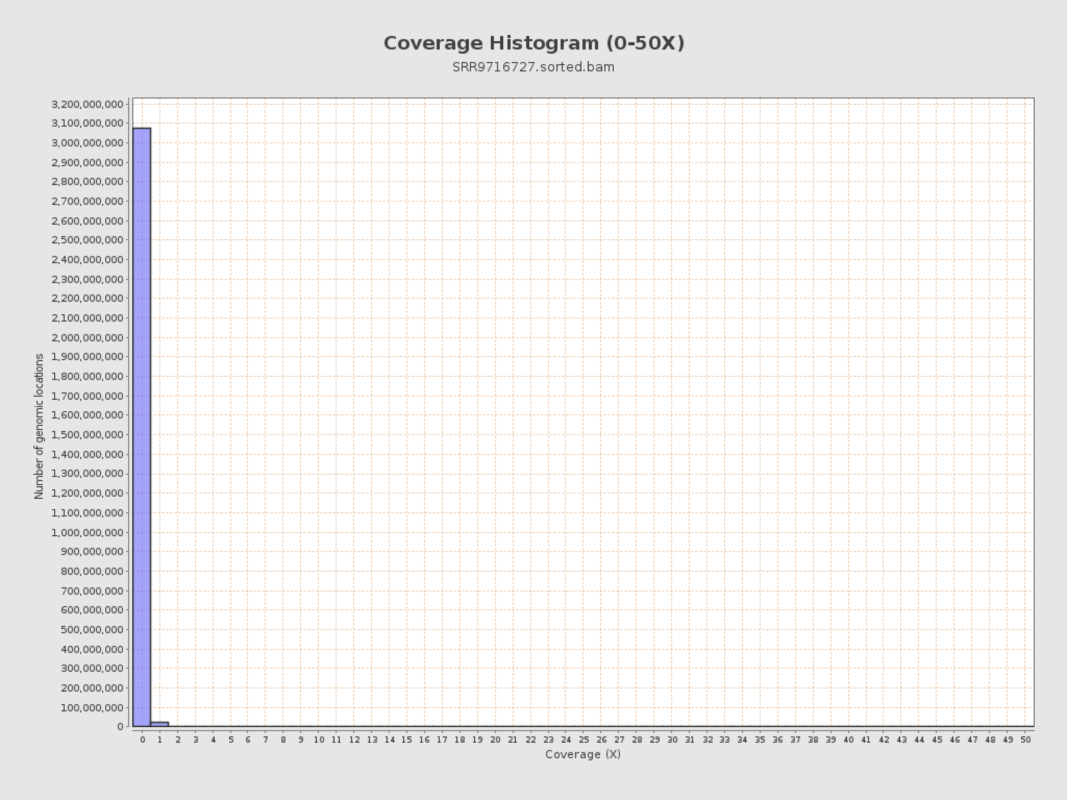
3. Results : Coverage across reference



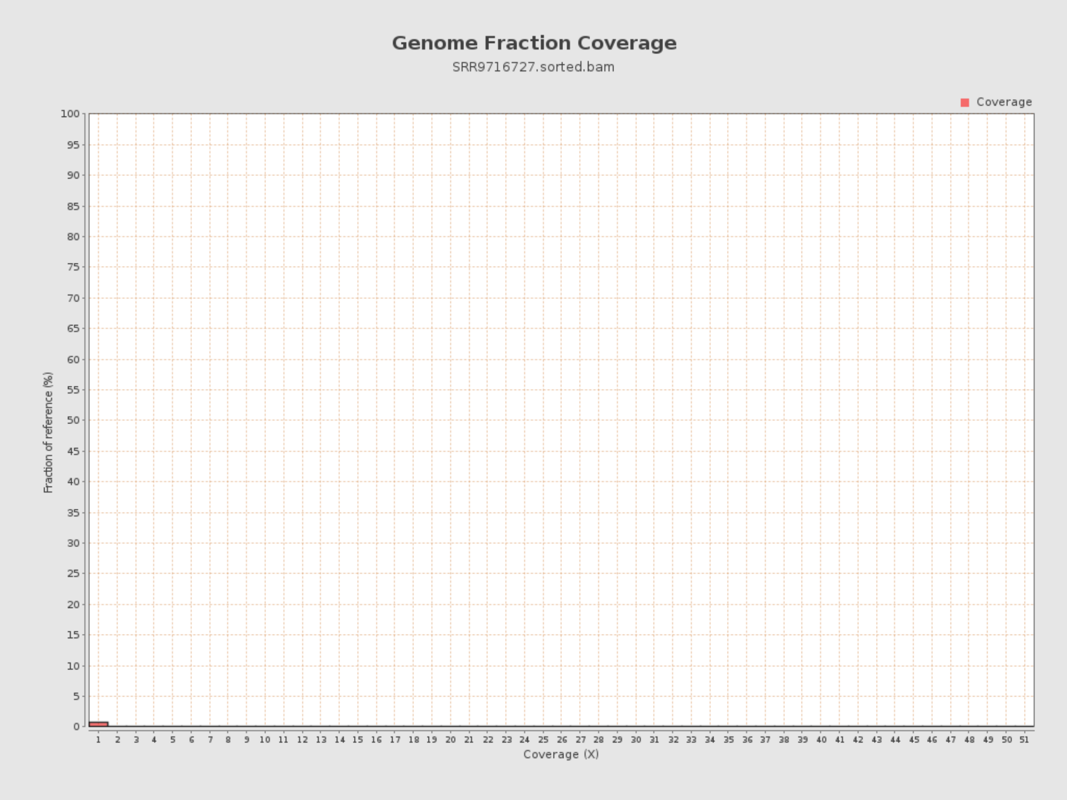
4. Results : Coverage Histogram



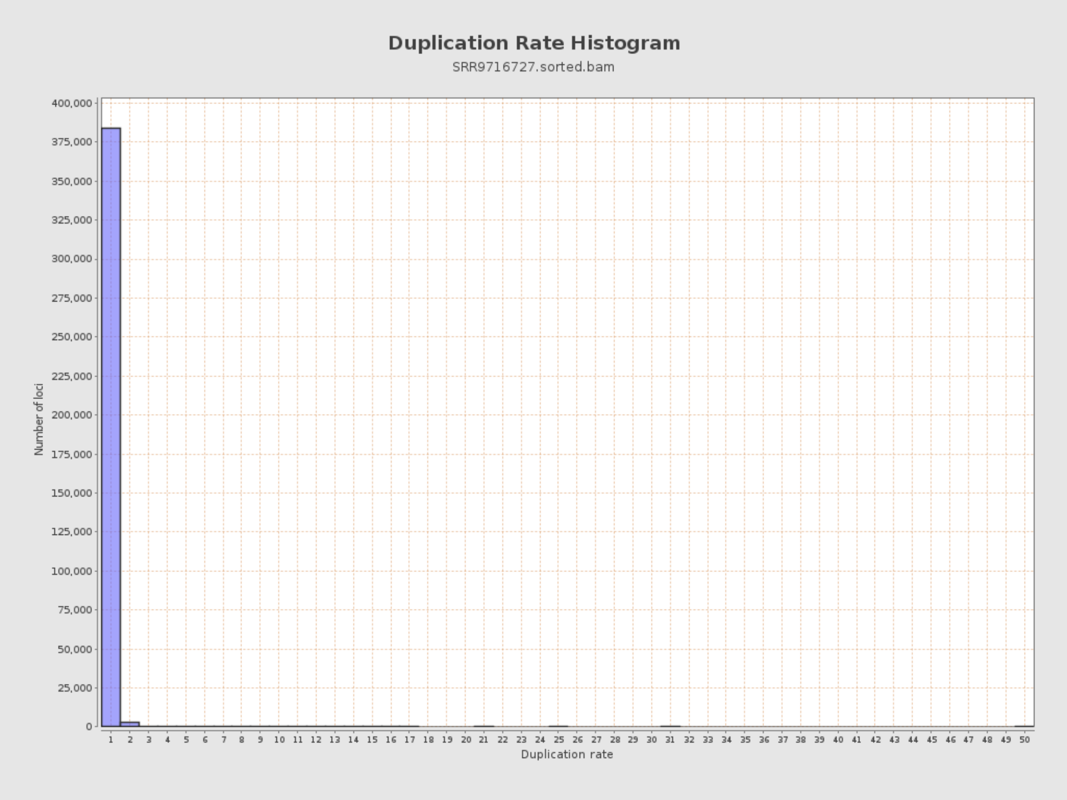
5. Results : Coverage Histogram (0-50X)



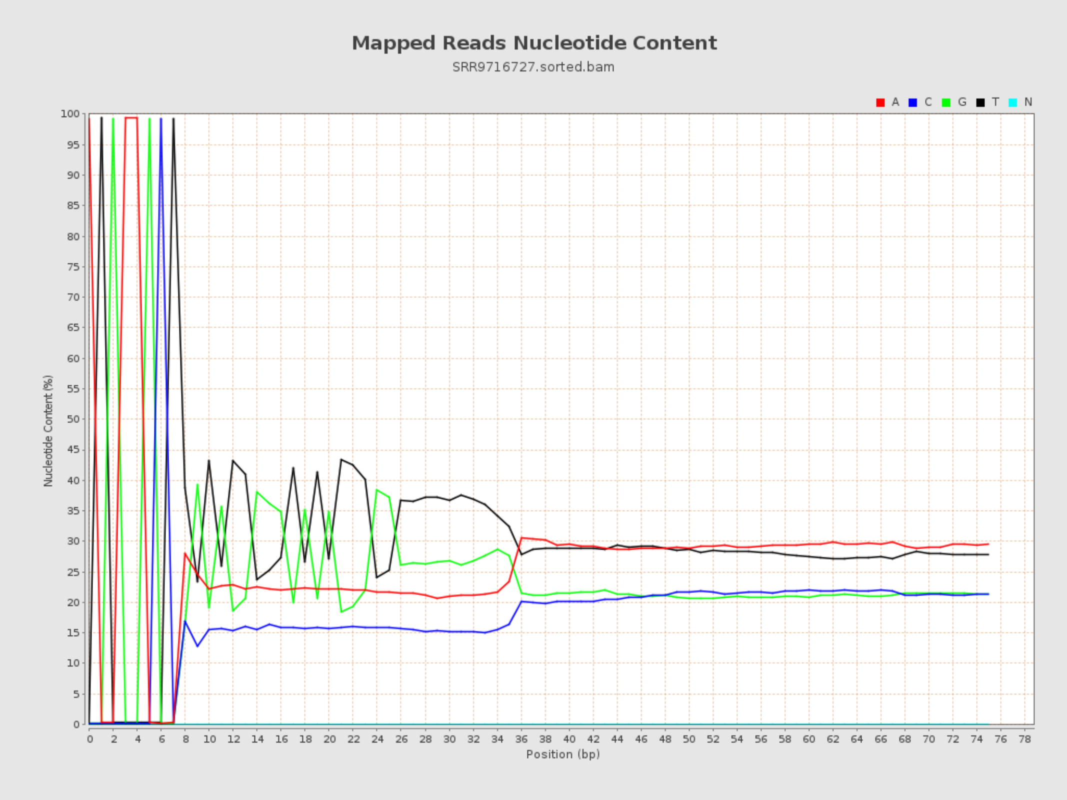
6. Results : Genome Fraction Coverage



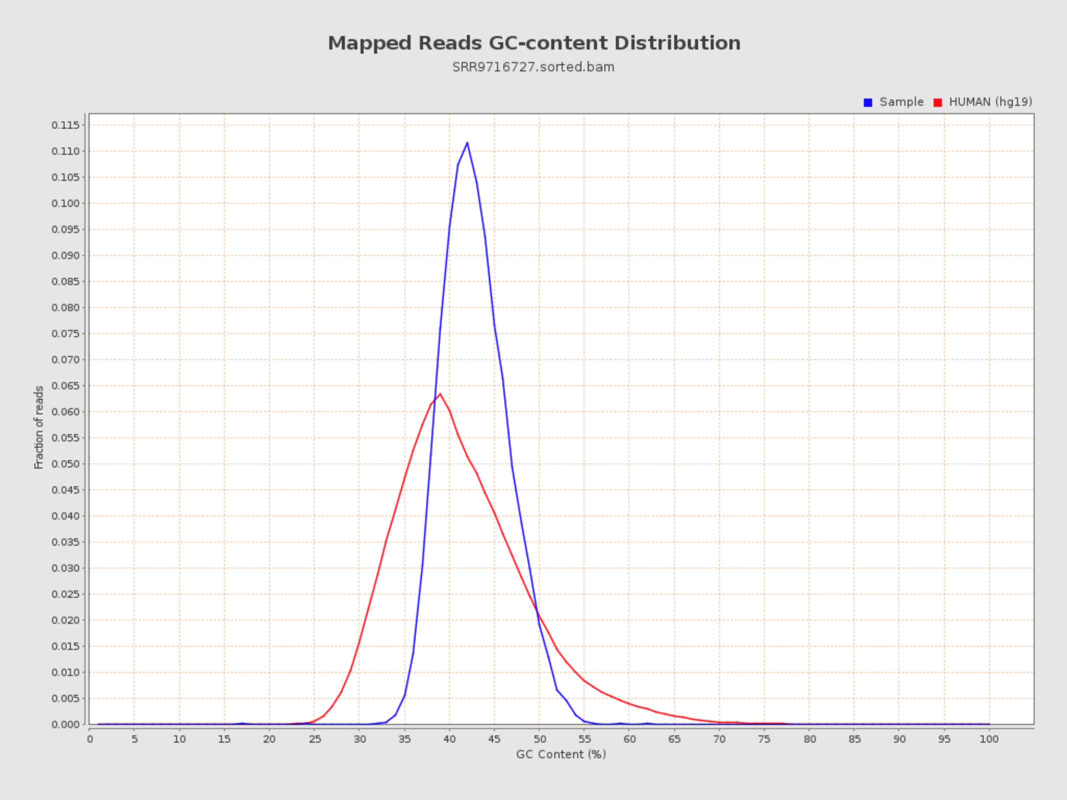
7. Results : Duplication Rate Histogram



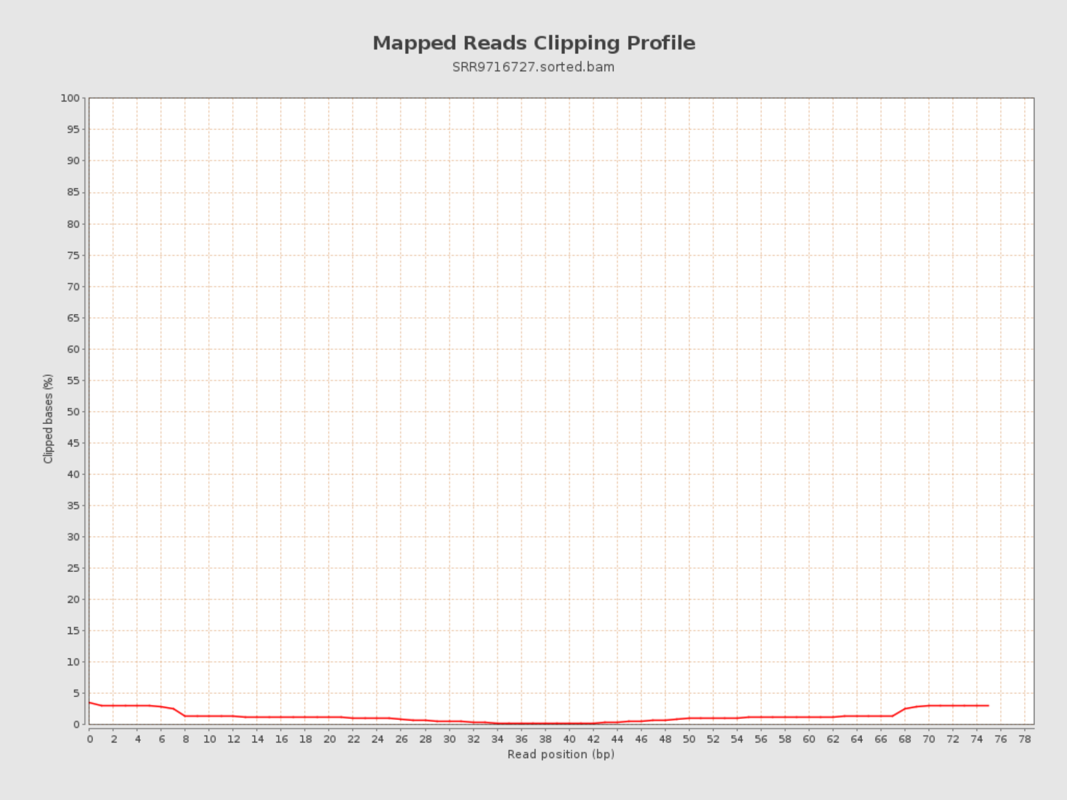
8. Results : Mapped Reads Nucleotide Content



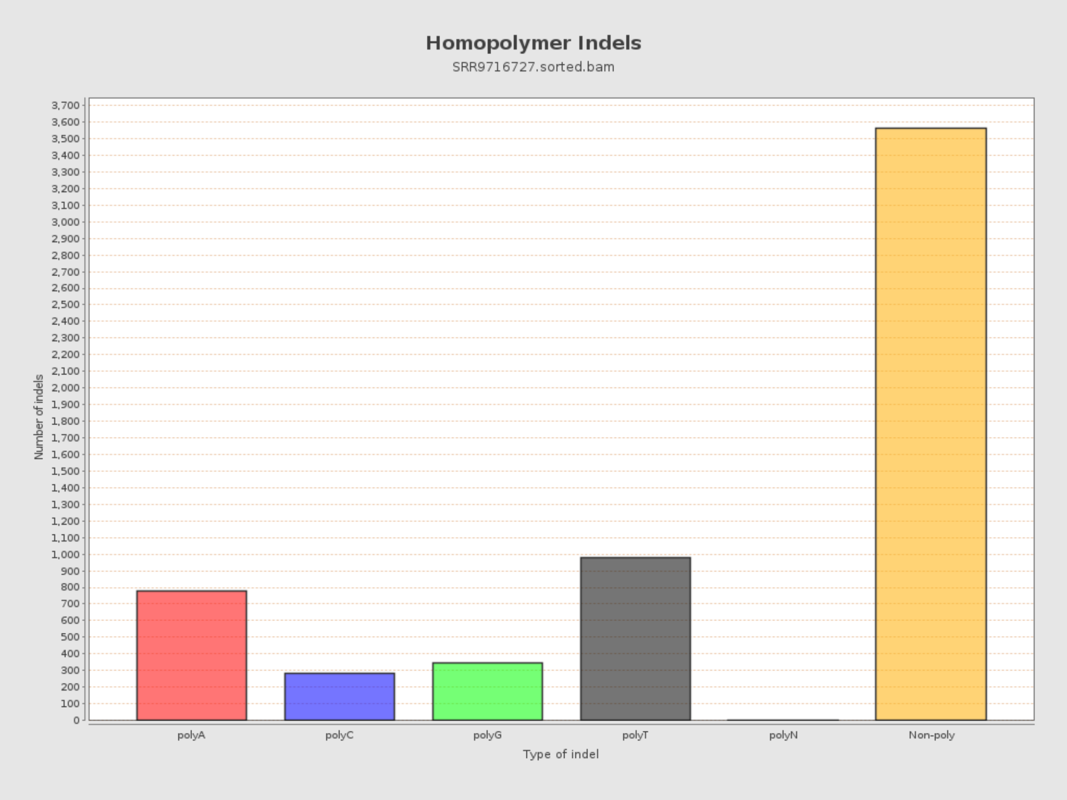
9. Results : Mapped Reads GC-content Distribution



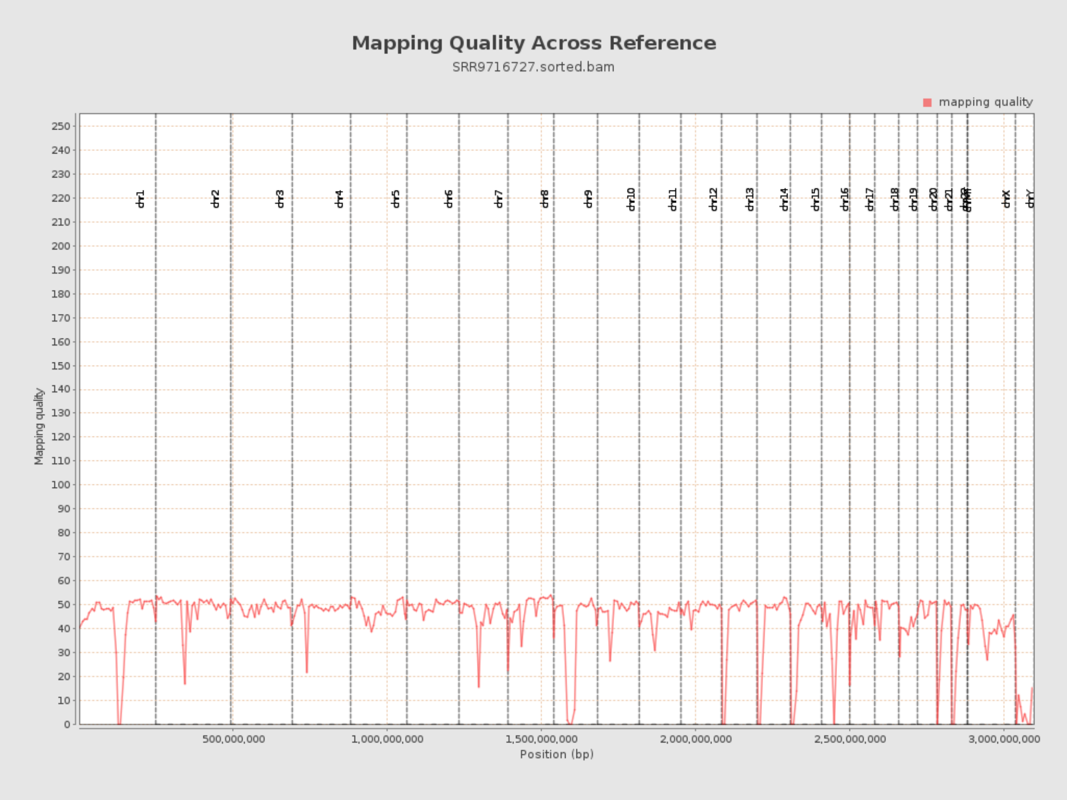
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram