Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:46:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716743.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_SRR9716743 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716743.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:46:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716743.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	589,755
Mapped reads	447,106 / 75.81%
Unmapped reads	142,649 / 24.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	749 / 0.13%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	23,742 / 4.03%
Duplication rate	4.76%
Clipped reads	447,111 / 75.81%

2.2. ACGT Content

Number/percentage of A's	5,122,165 / 21.65%
Number/percentage of C's	3,936,607 / 16.64%
Number/percentage of T's	7,663,445 / 32.39%
Number/percentage of G's	6,933,907 / 29.31%
Number/percentage of N's	372 / 0%
GC Percentage	45.95%

2.3. Coverage

Mean	0.0076

Standard Deviation	0.102

2.4. Mapping Quality

Mean Mapping Quality	43.09

2.5. Mismatches and indels

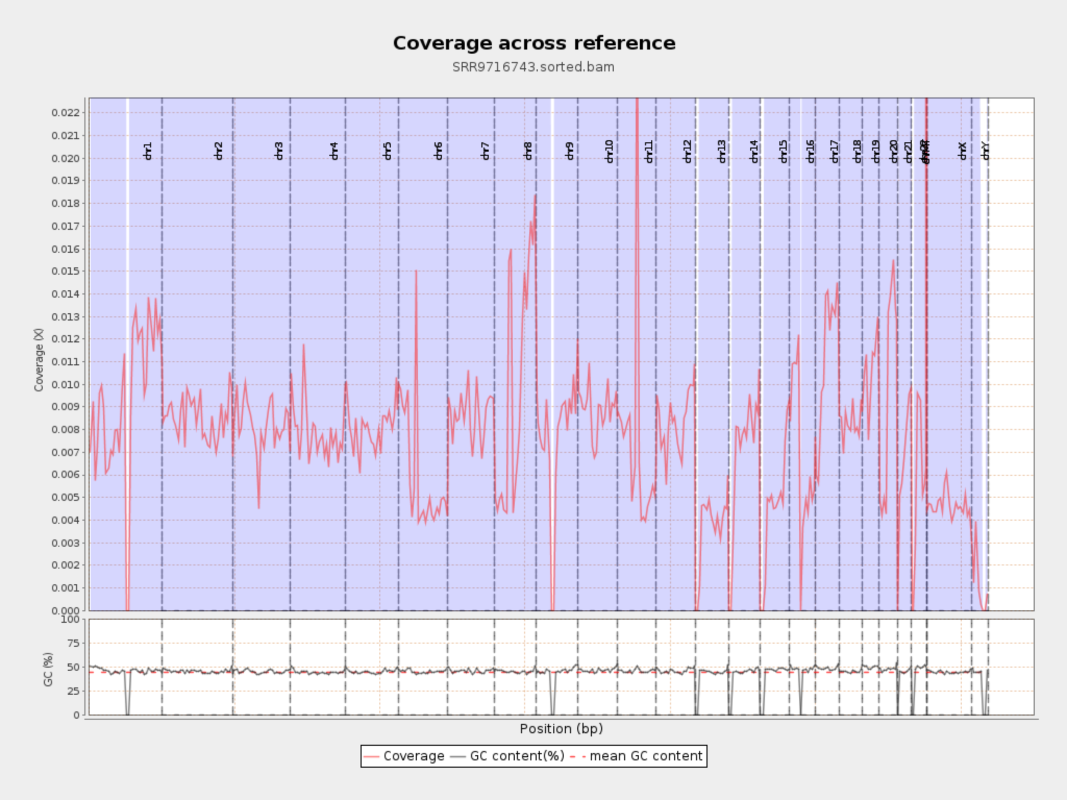
General error rate	0.67%
Mismatches	156,657
Insertions	1,325
Mapped reads with at least one insertion	0.3%
Deletions	3,411
Mapped reads with at least one deletion	0.76%
Homopolymer indels	38.79%

2.6. Chromosome stats

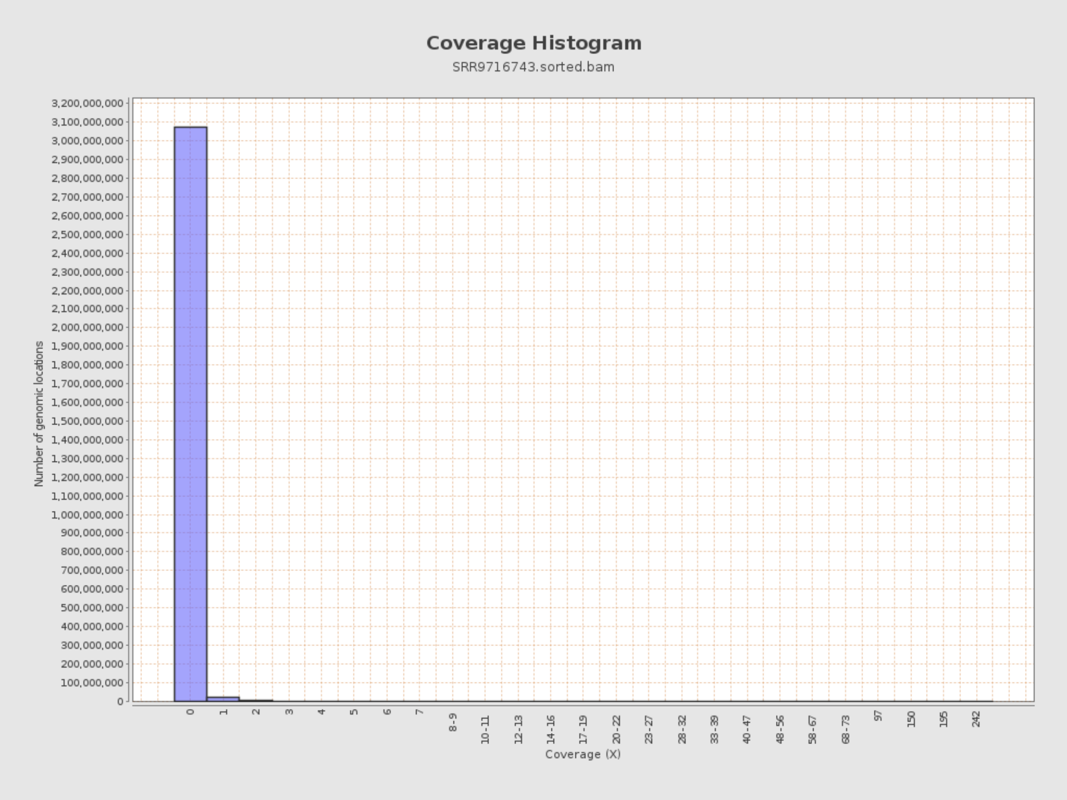
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2307731	0.0093	0.1153
chr2	243199373	2077306	0.0085	0.1376
chr3	198022430	1624311	0.0082	0.0985
chr4	191154276	1502325	0.0079	0.0978
chr5	180915260	1457854	0.0081	0.0974
chr6	171115067	1035189	0.006	0.0917
chr7	159138663	1377327	0.0087	0.1089

chr8	146364022	1474470	0.0101	0.1115
chr9	141213431	1044903	0.0074	0.0963
chr10	135534747	1198634	0.0088	0.1073
chr11	135006516	1027560	0.0076	0.099
chr12	133851895	1114452	0.0083	0.0996
chr13	115169878	413220	0.0036	0.0658
chr14	107349540	730726	0.0068	0.0902
chr15	102531392	463671	0.0045	0.0727
chr16	90354753	616614	0.0068	0.092
chr17	81195210	927276	0.0114	0.1211
chr18	78077248	645361	0.0083	0.1067
chr19	59128983	624291	0.0106	0.123
chr20	63025520	606444	0.0096	0.1083
chr21	48129895	321830	0.0067	0.0916
chr22	51304566	263831	0.0051	0.0795
chrMT	16571	16463	0.9935	1.2383
chrX	155270560	723510	0.0047	0.0748
chrY	59373566	67103	0.0011	0.0416

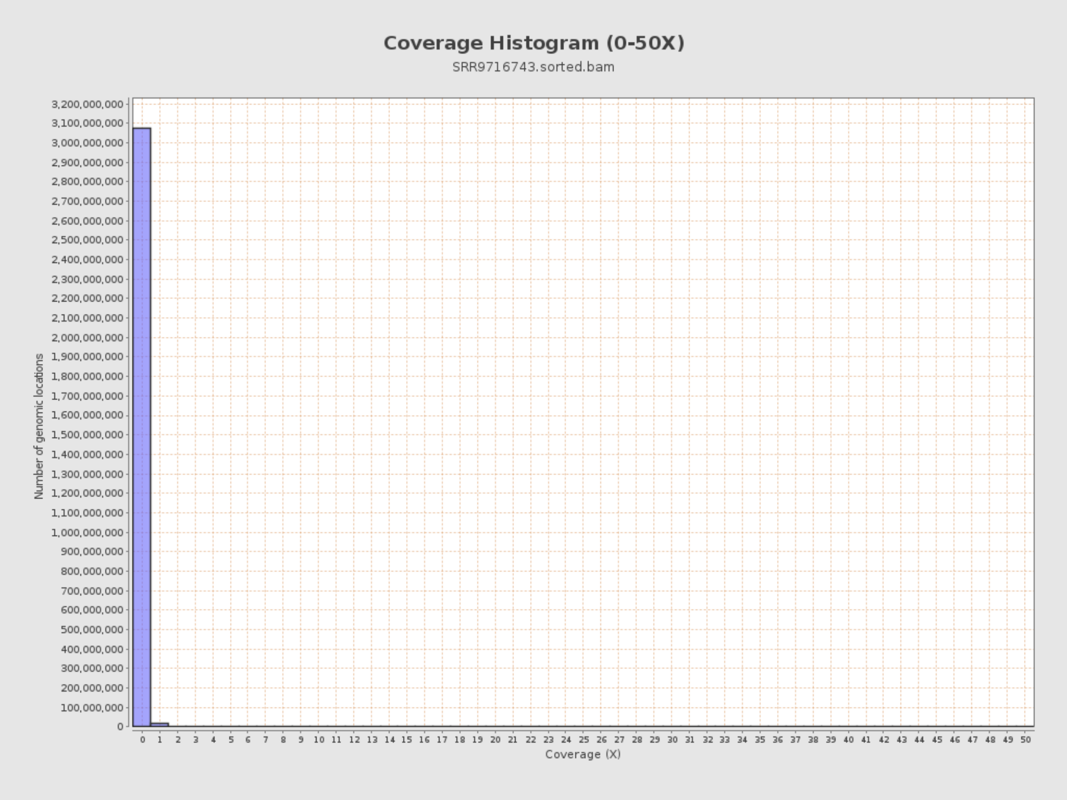
3. Results : Coverage across reference



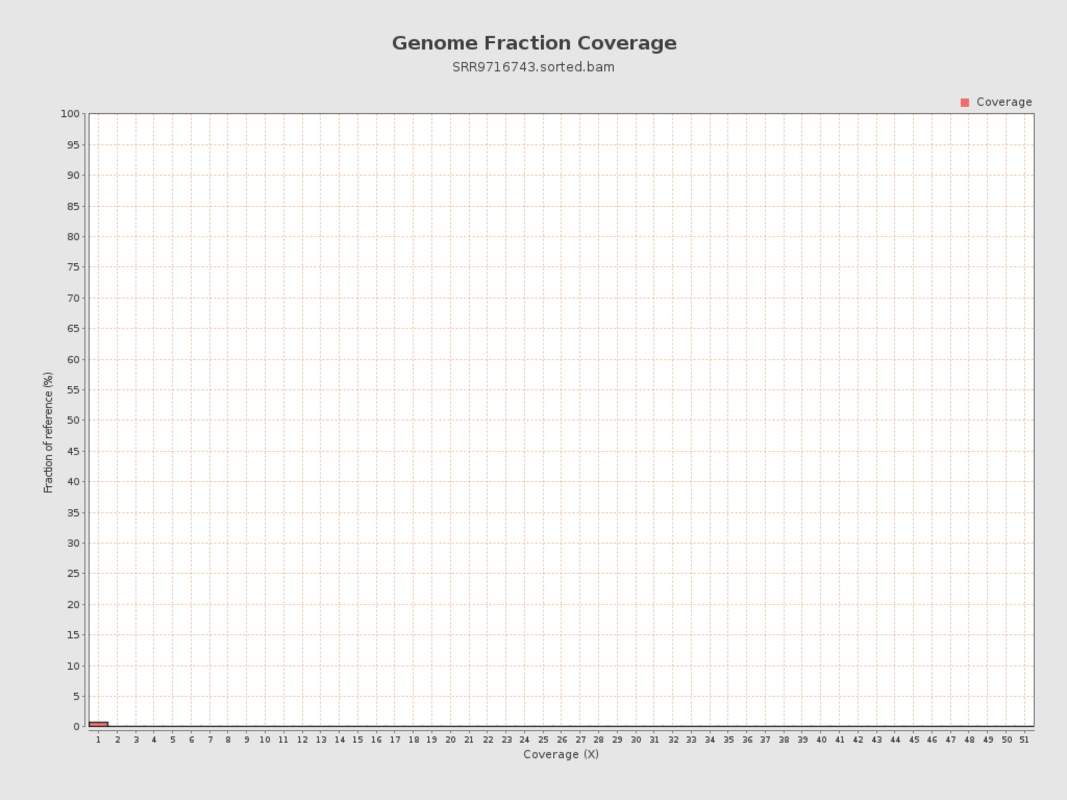
4. Results : Coverage Histogram



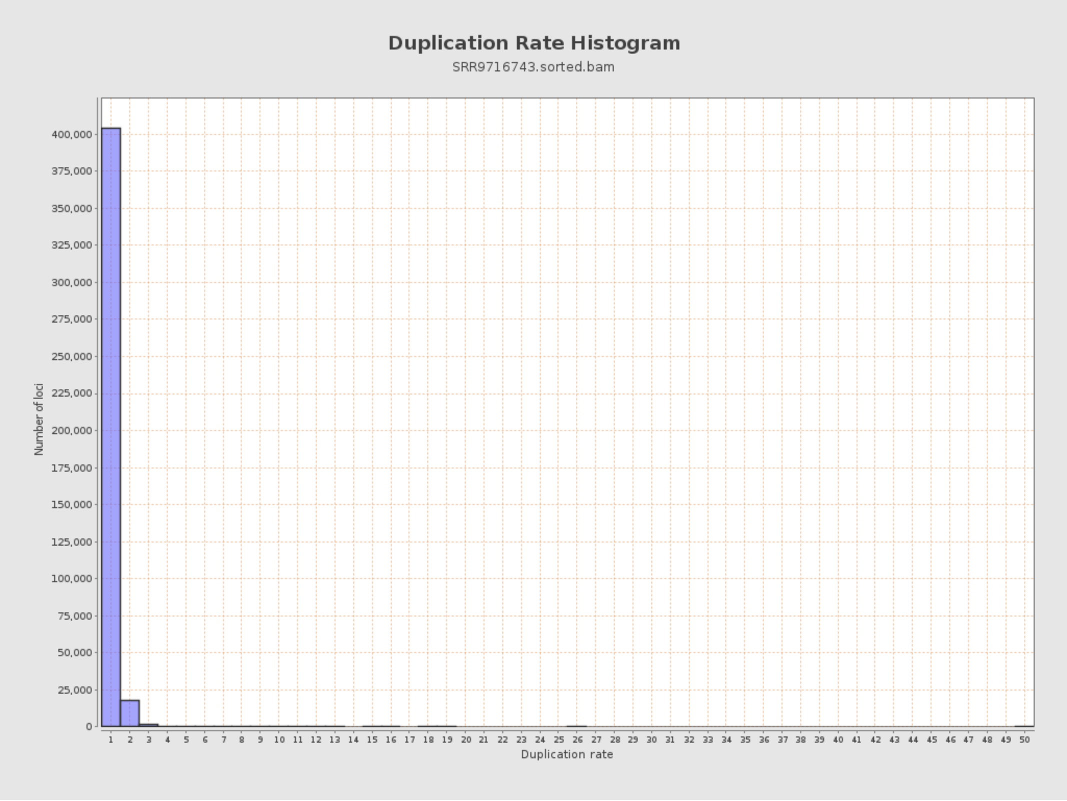
5. Results : Coverage Histogram (0-50X)



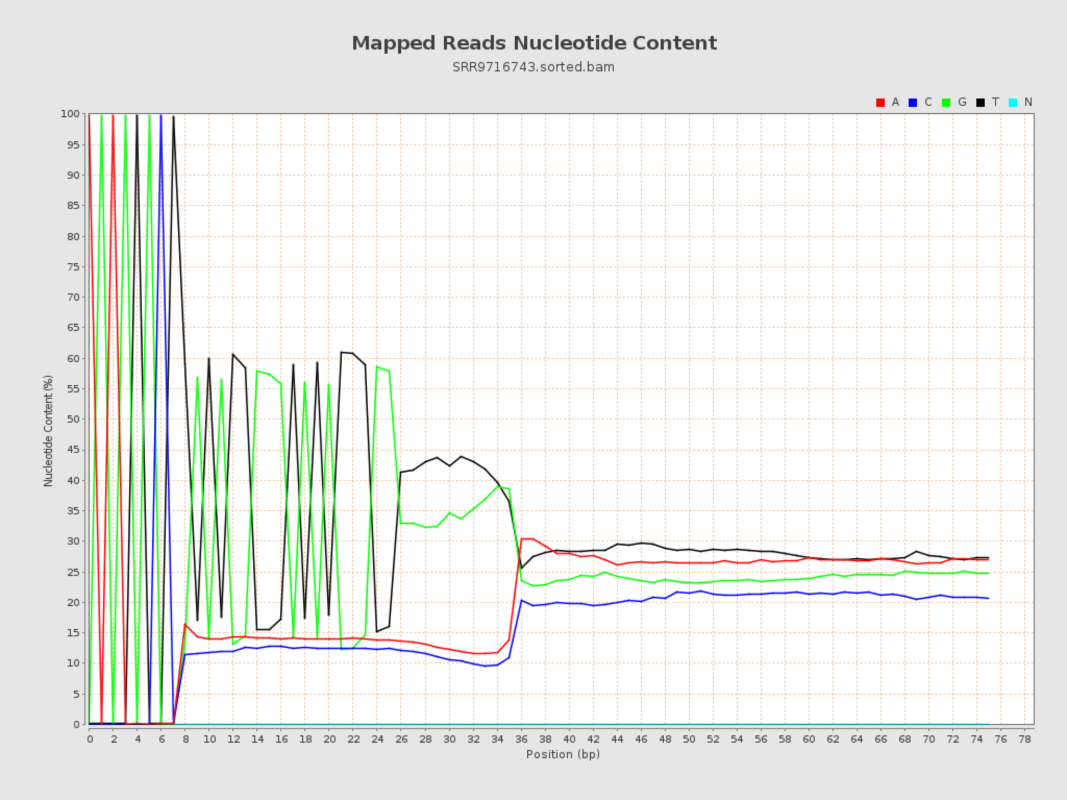
6. Results : Genome Fraction Coverage



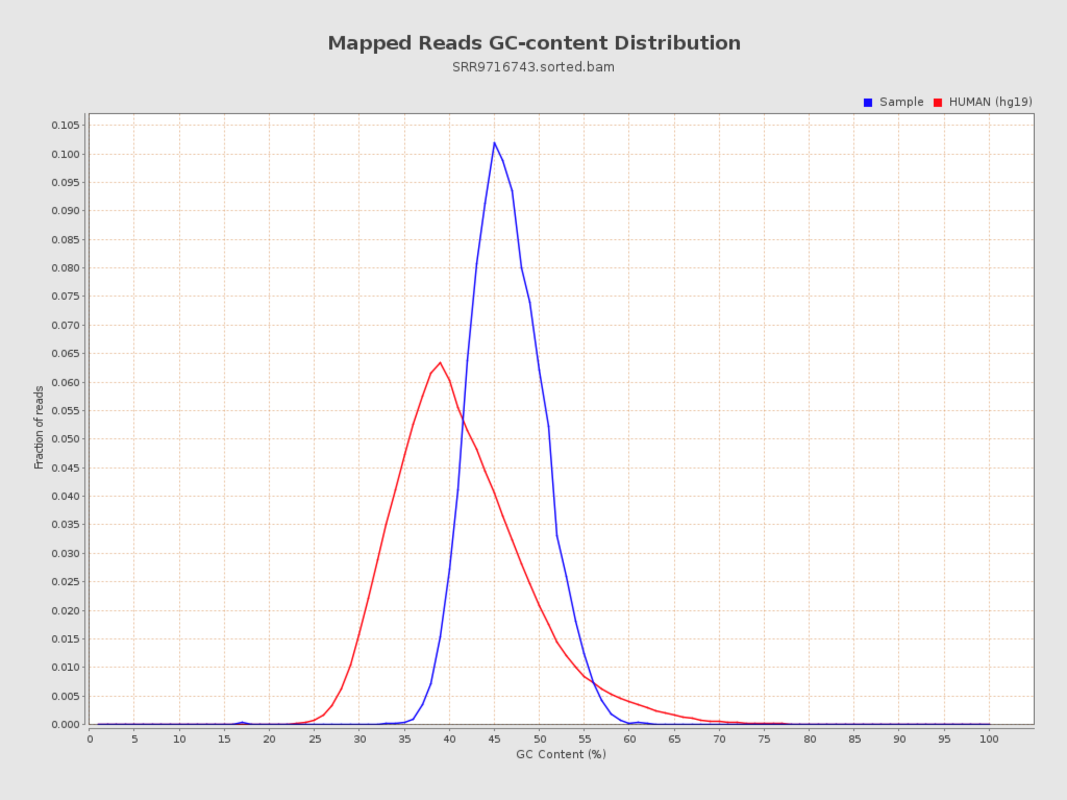
7. Results : Duplication Rate Histogram



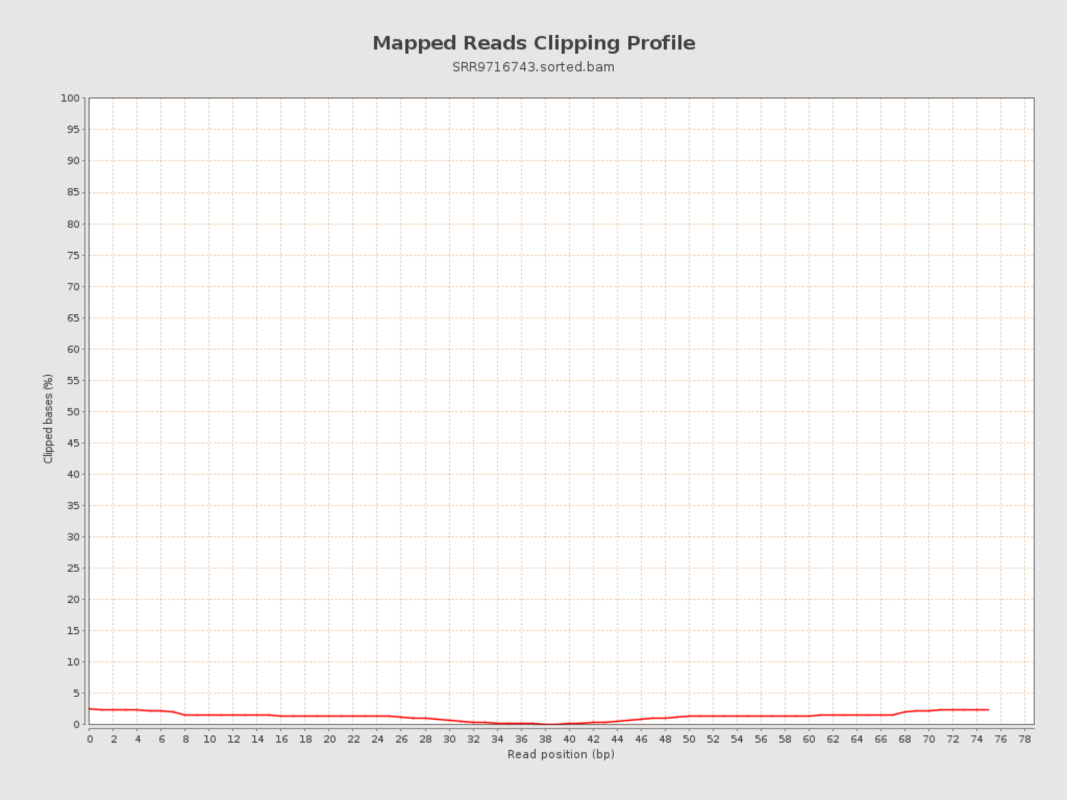
8. Results : Mapped Reads Nucleotide Content



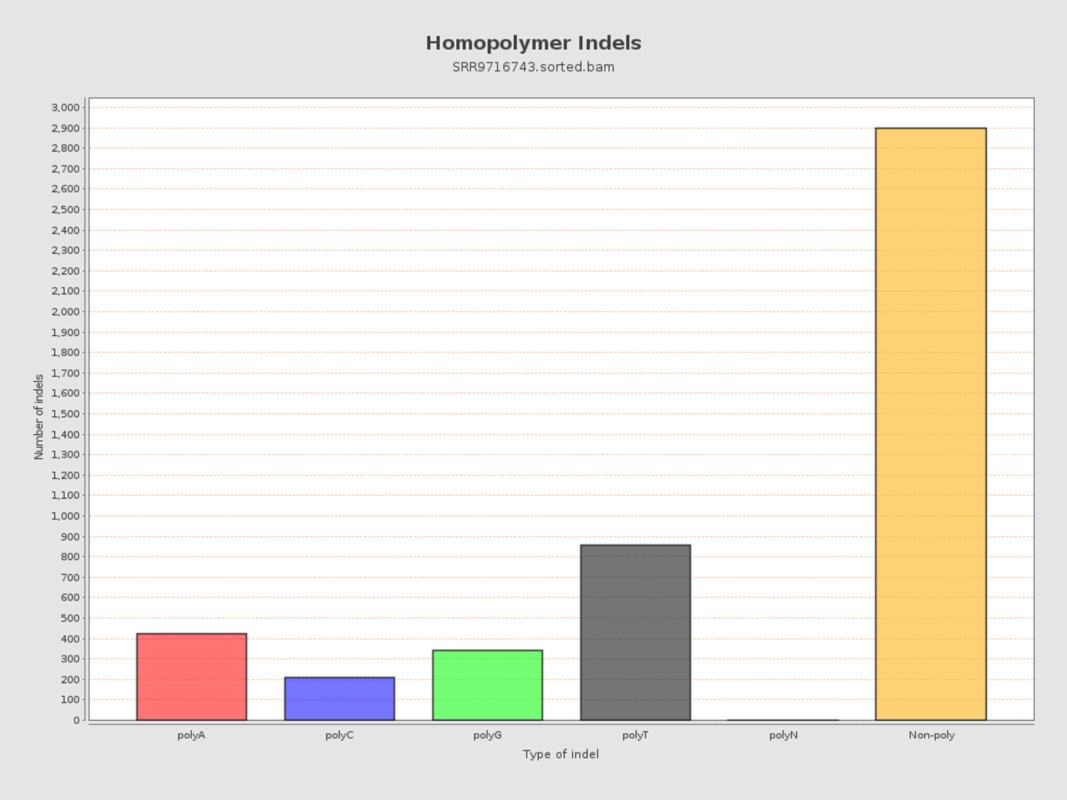
9. Results : Mapped Reads GC-content Distribution



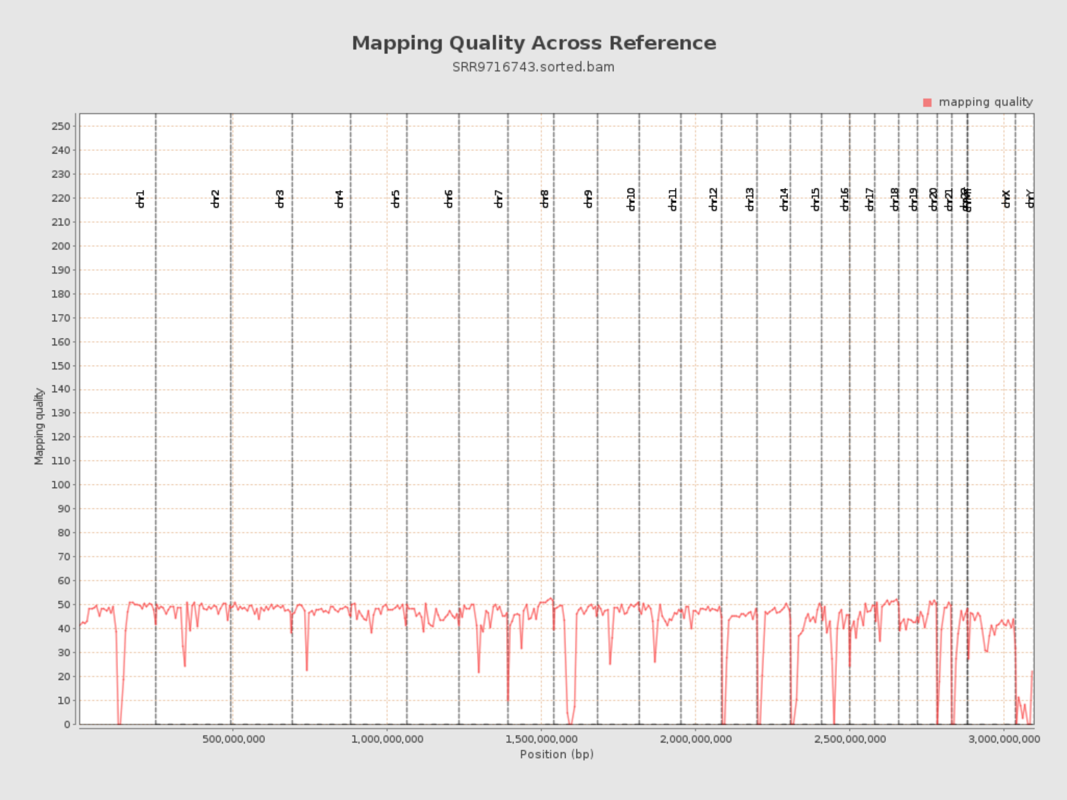
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram