Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:27:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716486.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_SRR9716486 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716486.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:27:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716486.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	708,587
Mapped reads	533,638 / 75.31%
Unmapped reads	174,949 / 24.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,190 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	10,479 / 1.48%
Duplication rate	1.54%
Clipped reads	535,436 / 75.56%

2.2. ACGT Content

Number/percentage of A's	7,988,880 / 26.15%
Number/percentage of C's	5,937,489 / 19.43%
Number/percentage of T's	9,571,669 / 31.33%
Number/percentage of G's	7,052,376 / 23.08%
Number/percentage of N's	380 / 0%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0099

Standard Deviation	0.1202

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

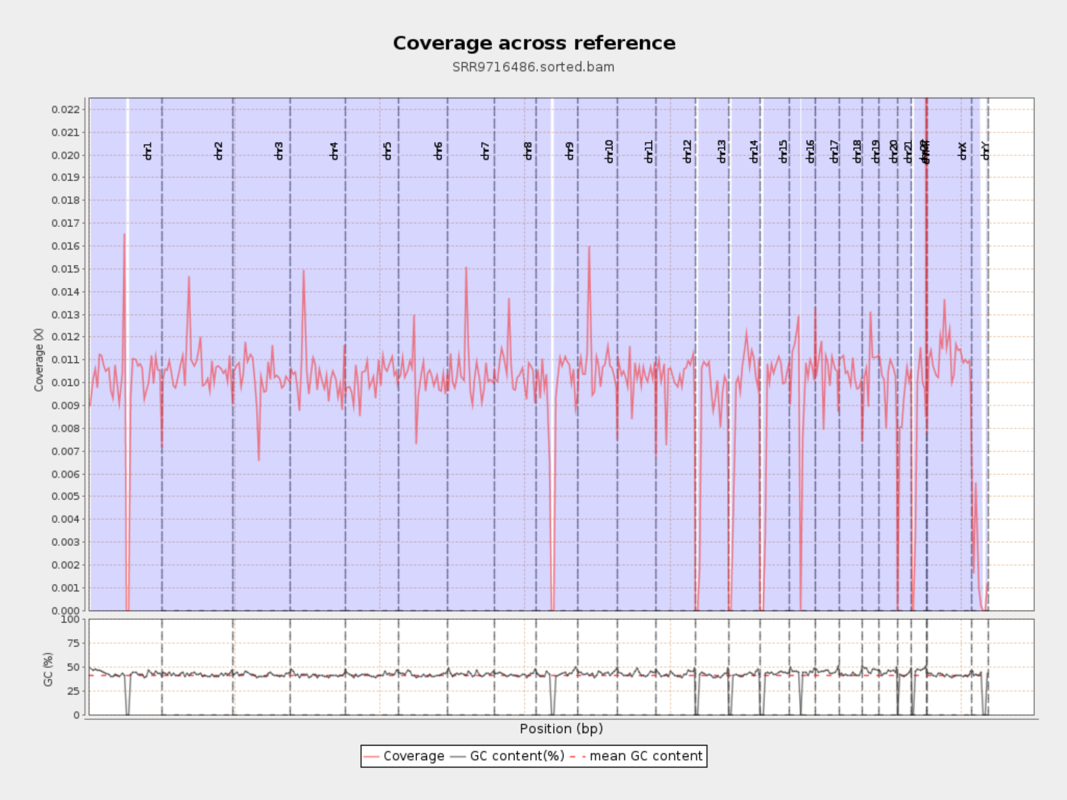
General error rate	0.52%
Mismatches	154,690
Insertions	2,196
Mapped reads with at least one insertion	0.41%
Deletions	5,653
Mapped reads with at least one deletion	1.05%
Homopolymer indels	39.02%

2.6. Chromosome stats

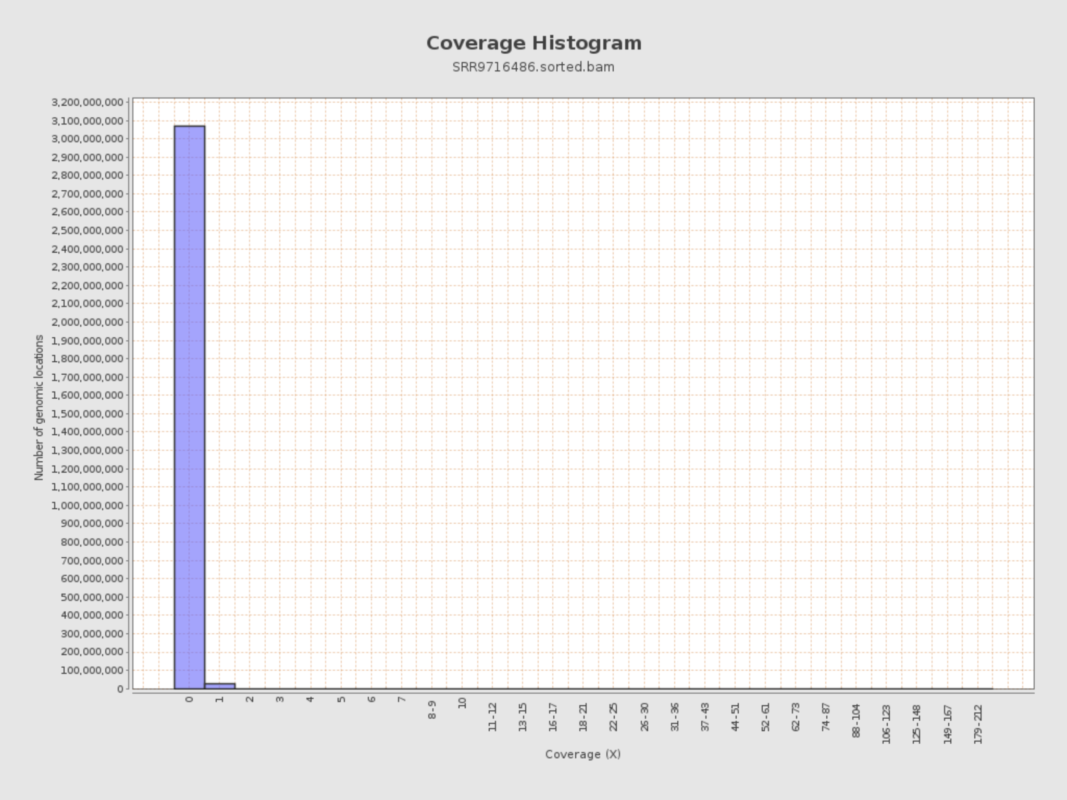
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2455173	0.0099	0.1816
chr2	243199373	2604139	0.0107	0.1358
chr3	198022430	2024861	0.0102	0.1051
chr4	191154276	1972971	0.0103	0.1093
chr5	180915260	1846707	0.0102	0.1052
chr6	171115067	1754047	0.0103	0.1115
chr7	159138663	1661605	0.0104	0.1341

chr8	146364022	1540188	0.0105	0.1212
chr9	141213431	1267333	0.009	0.1063
chr10	135534747	1470812	0.0109	0.1196
chr11	135006516	1391373	0.0103	0.1144
chr12	133851895	1379859	0.0103	0.1061
chr13	115169878	953013	0.0083	0.0943
chr14	107349540	947599	0.0088	0.0996
chr15	102531392	872218	0.0085	0.0975
chr16	90354753	890260	0.0099	0.105
chr17	81195210	847053	0.0104	0.1078
chr18	78077248	814620	0.0104	0.1454
chr19	59128983	635373	0.0107	0.1412
chr20	63025520	637724	0.0101	0.1051
chr21	48129895	408510	0.0085	0.0984
chr22	51304566	361571	0.007	0.0868
chrMT	16571	6427	0.3878	0.685
chrX	155270560	1722066	0.0111	0.1135
chrY	59373566	94207	0.0016	0.0537

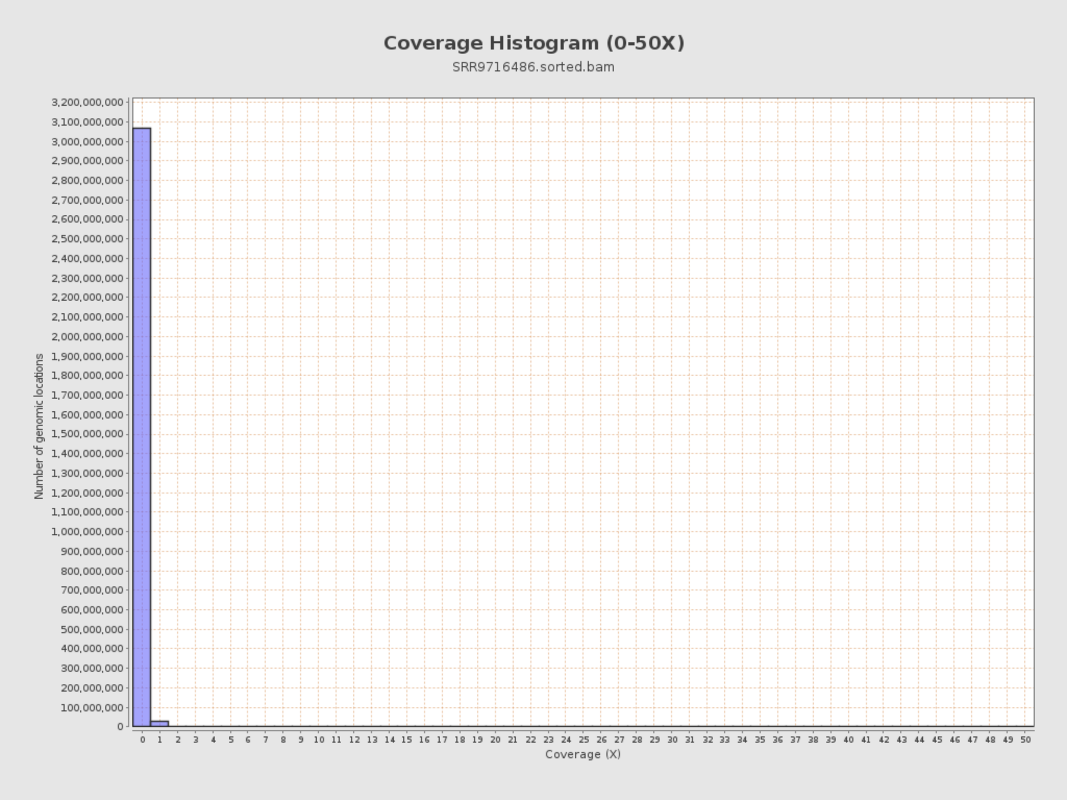
3. Results : Coverage across reference



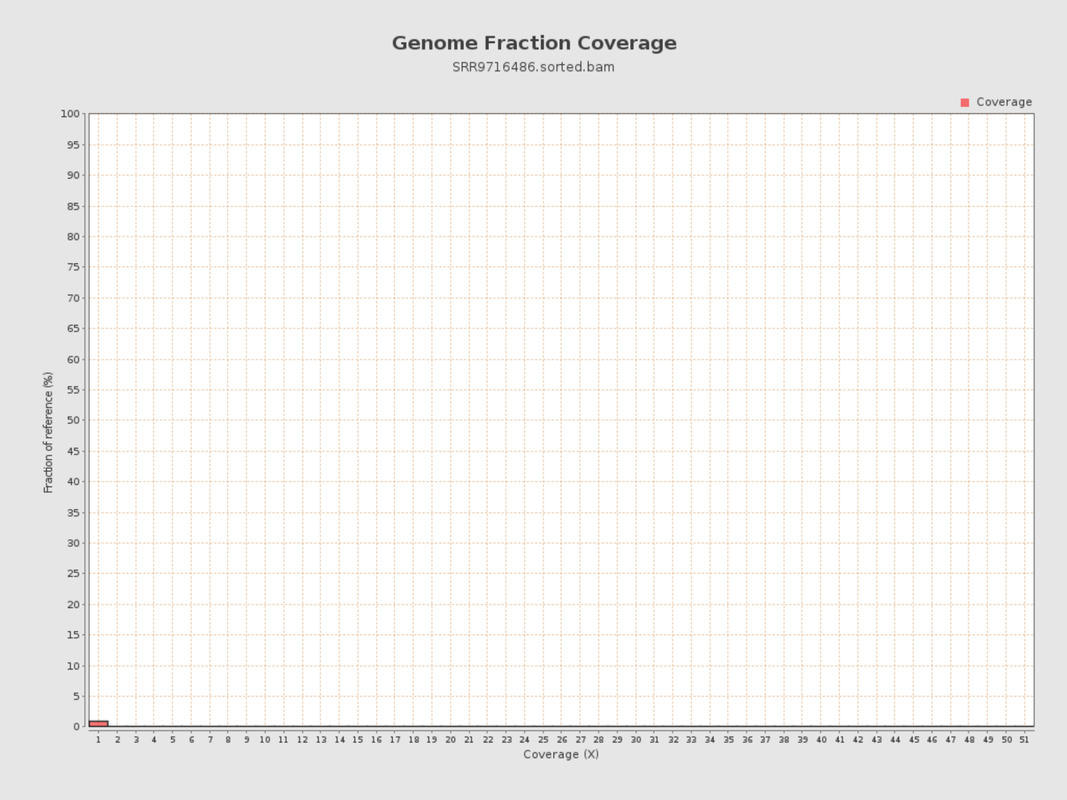
4. Results : Coverage Histogram



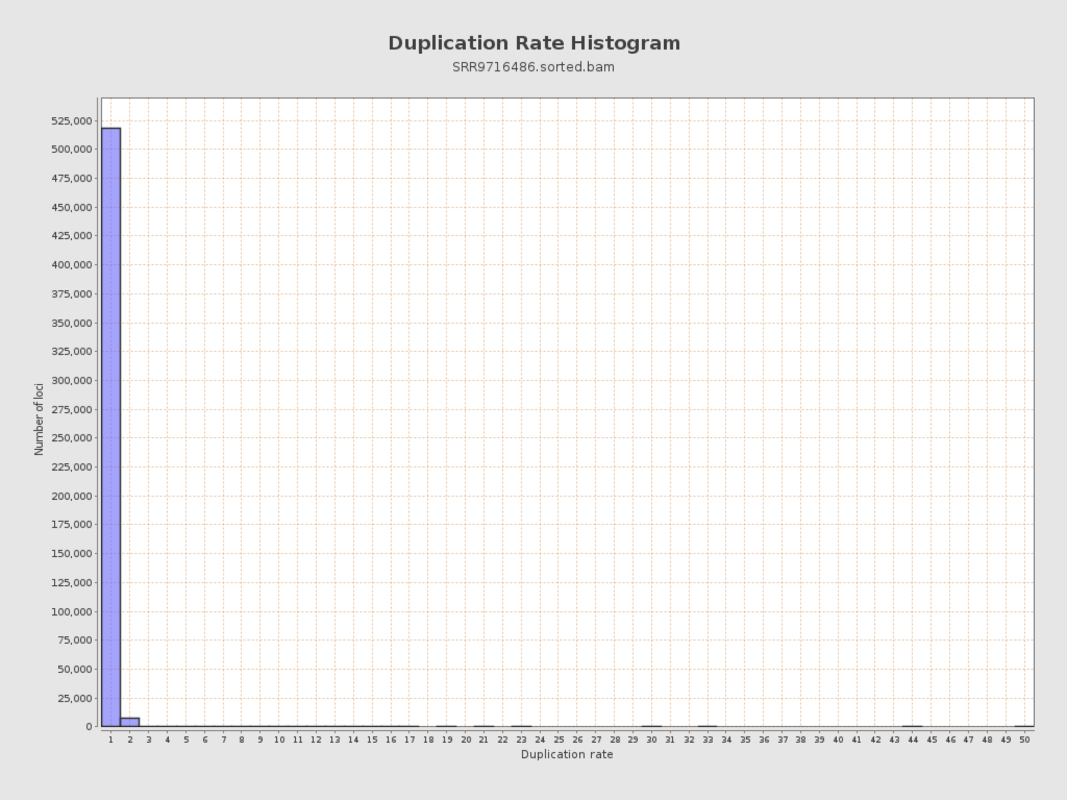
5. Results : Coverage Histogram (0-50X)



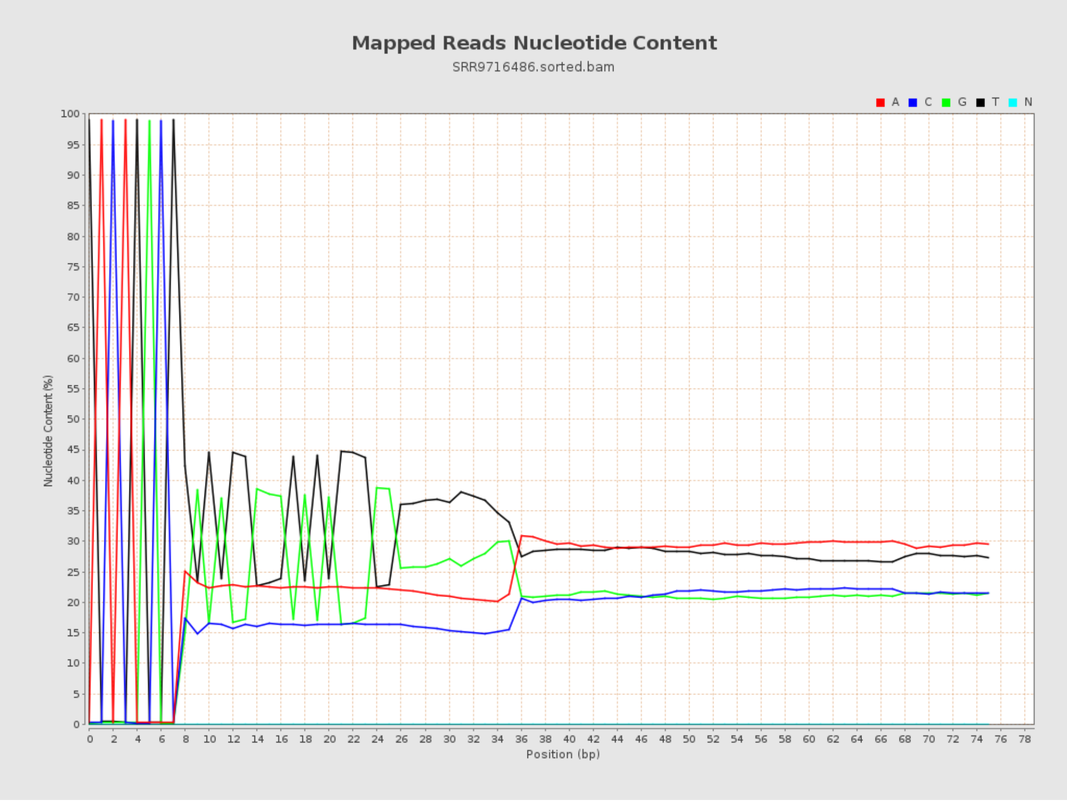
6. Results : Genome Fraction Coverage



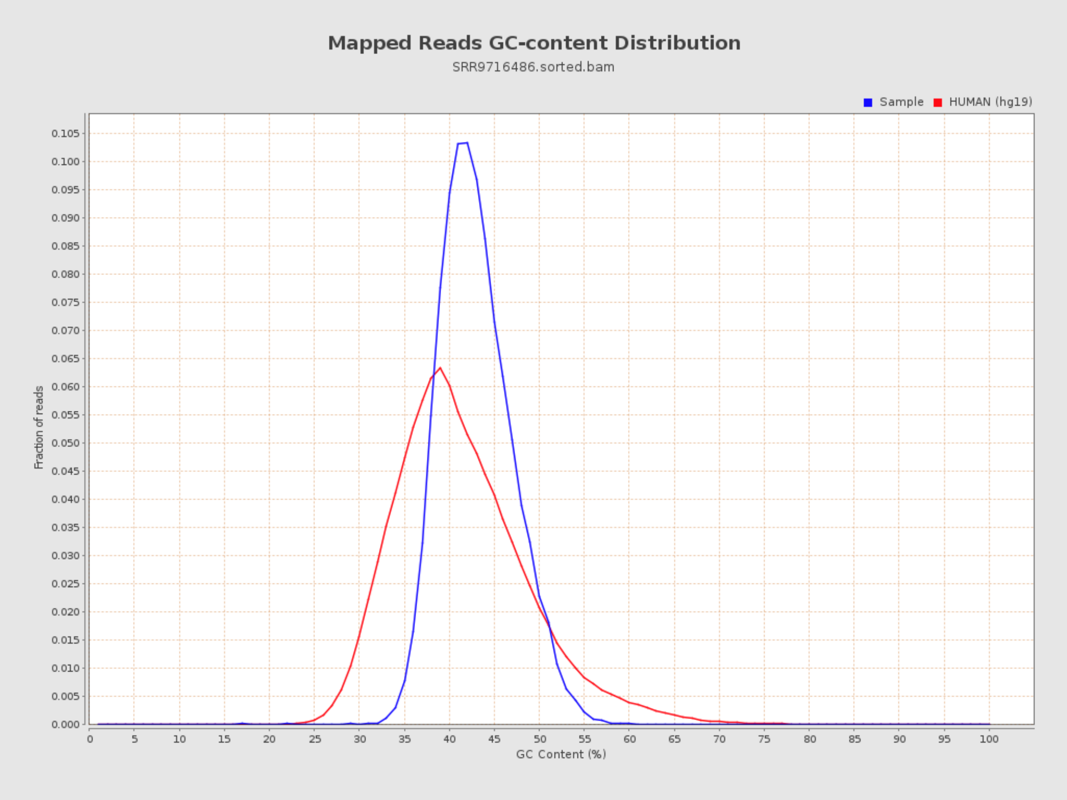
7. Results : Duplication Rate Histogram



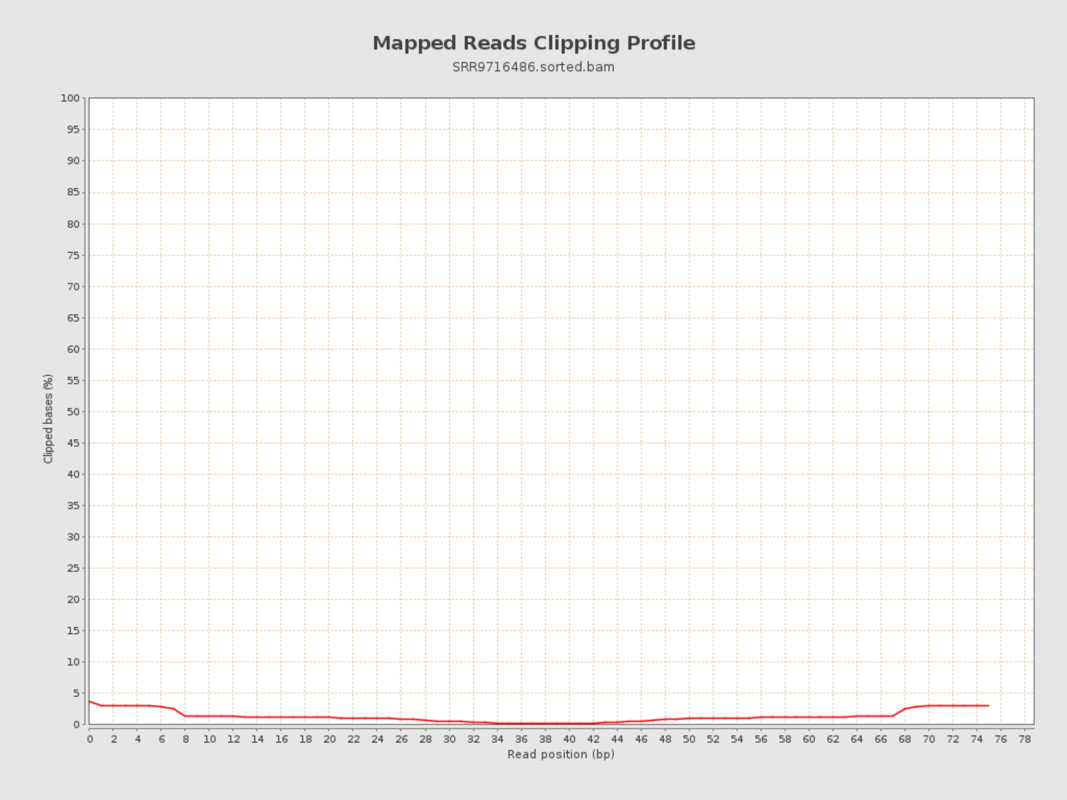
8. Results : Mapped Reads Nucleotide Content



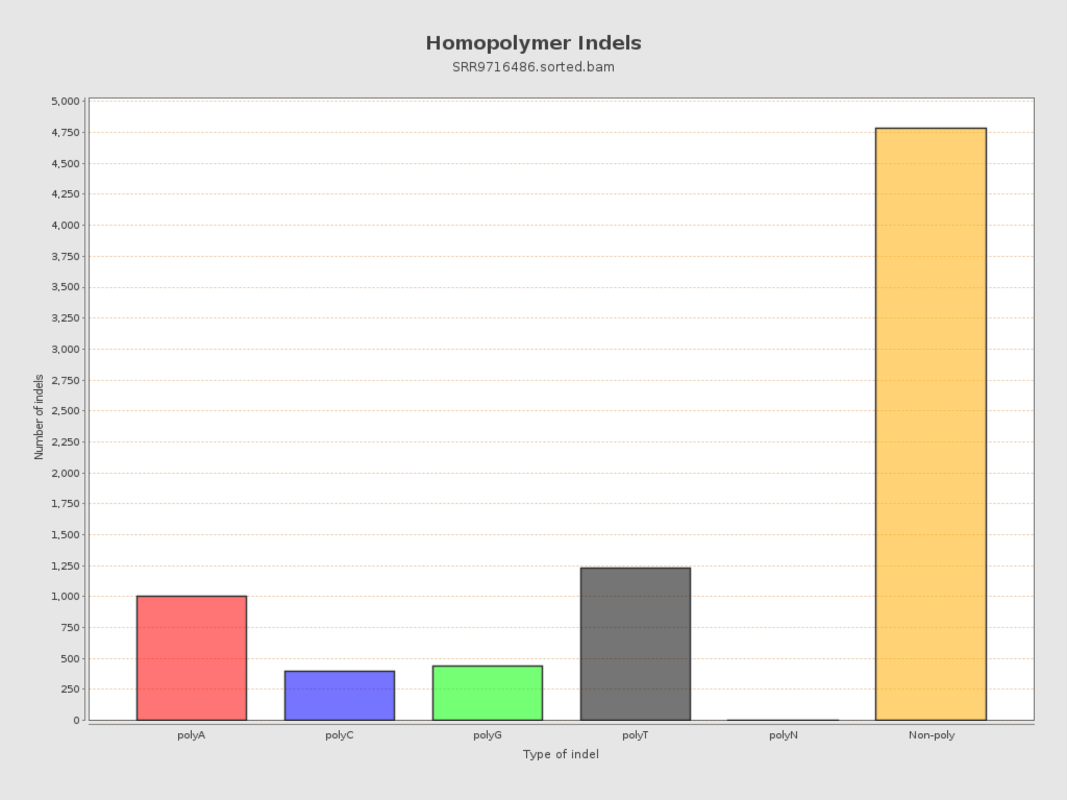
9. Results : Mapped Reads GC-content Distribution



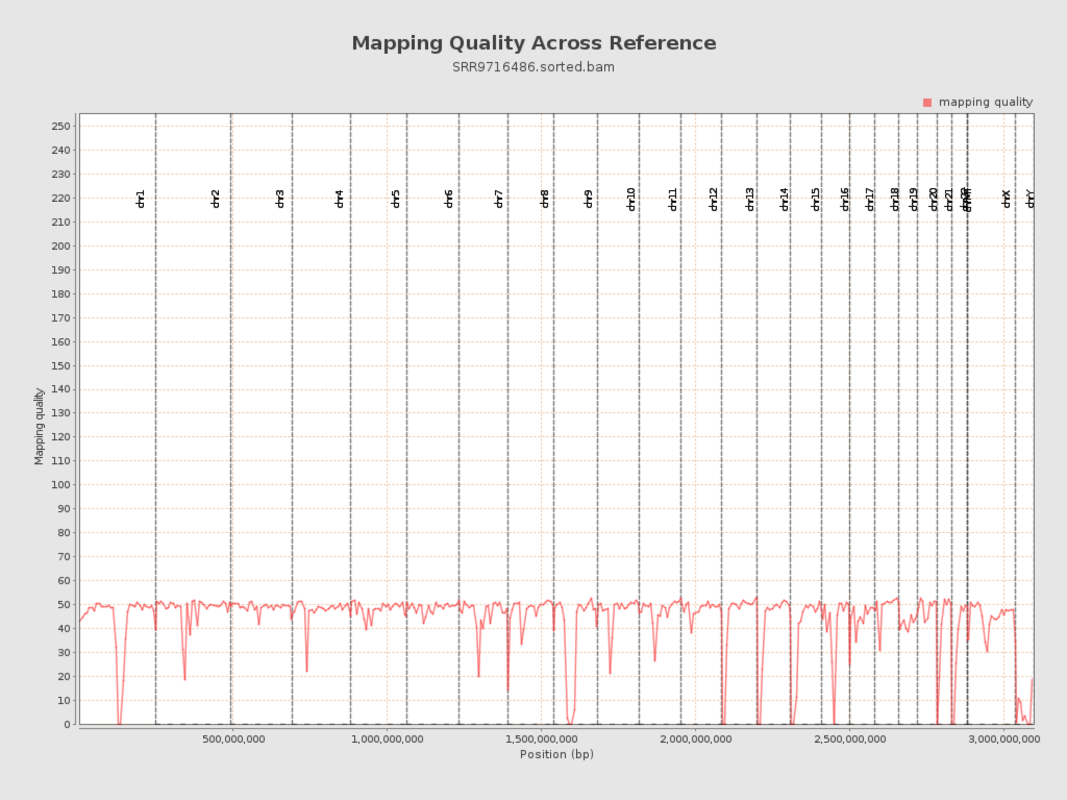
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram