Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:36:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716794.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_SRR9716794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716794.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:36:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	633,241
Mapped reads	485,971 / 76.74%
Unmapped reads	147,270 / 23.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	652 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	28,548 / 4.51%
Duplication rate	5.22%
Clipped reads	485,402 / 76.65%

2.2. ACGT Content

Number/percentage of A's	5,033,438 / 19.59%
Number/percentage of C's	4,807,837 / 18.71%
Number/percentage of T's	8,614,154 / 33.53%
Number/percentage of G's	7,234,563 / 28.16%
Number/percentage of N's	445 / 0%
GC Percentage	46.88%

2.3. Coverage

Mean	0.0083

Standard Deviation	0.1068

2.4. Mapping Quality

Mean Mapping Quality	42.96

2.5. Mismatches and indels

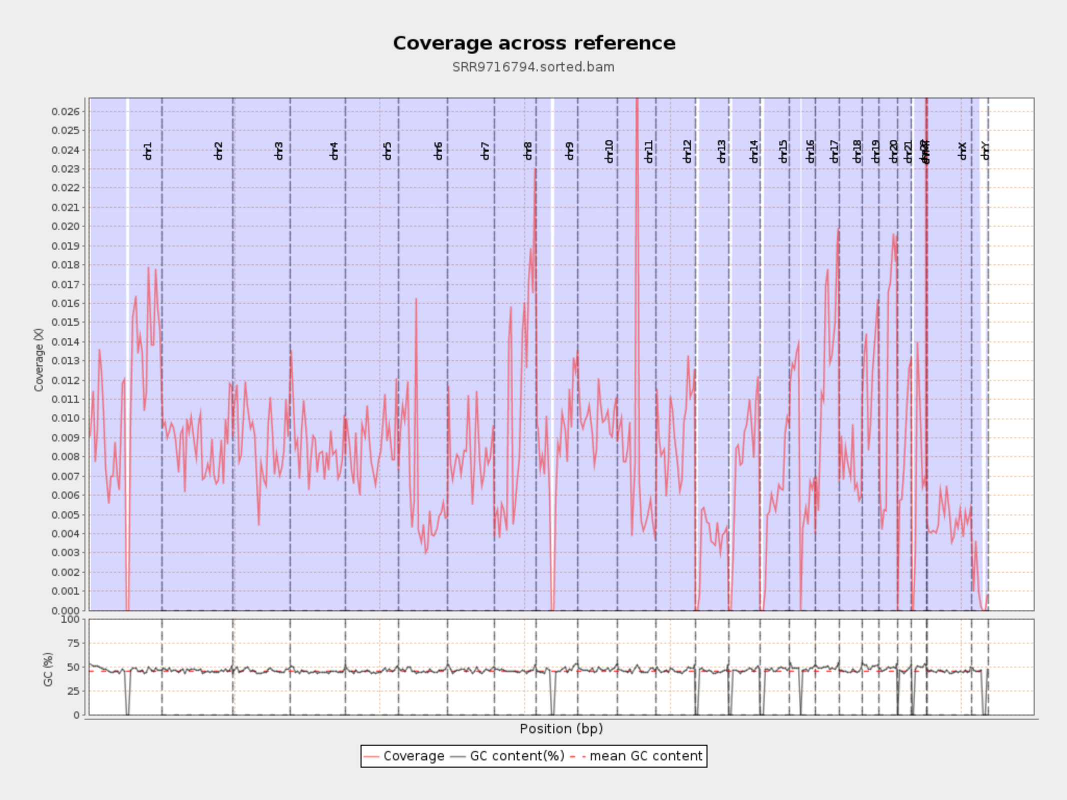
General error rate	0.66%
Mismatches	166,512
Insertions	1,635
Mapped reads with at least one insertion	0.34%
Deletions	3,623
Mapped reads with at least one deletion	0.74%
Homopolymer indels	39.67%

2.6. Chromosome stats

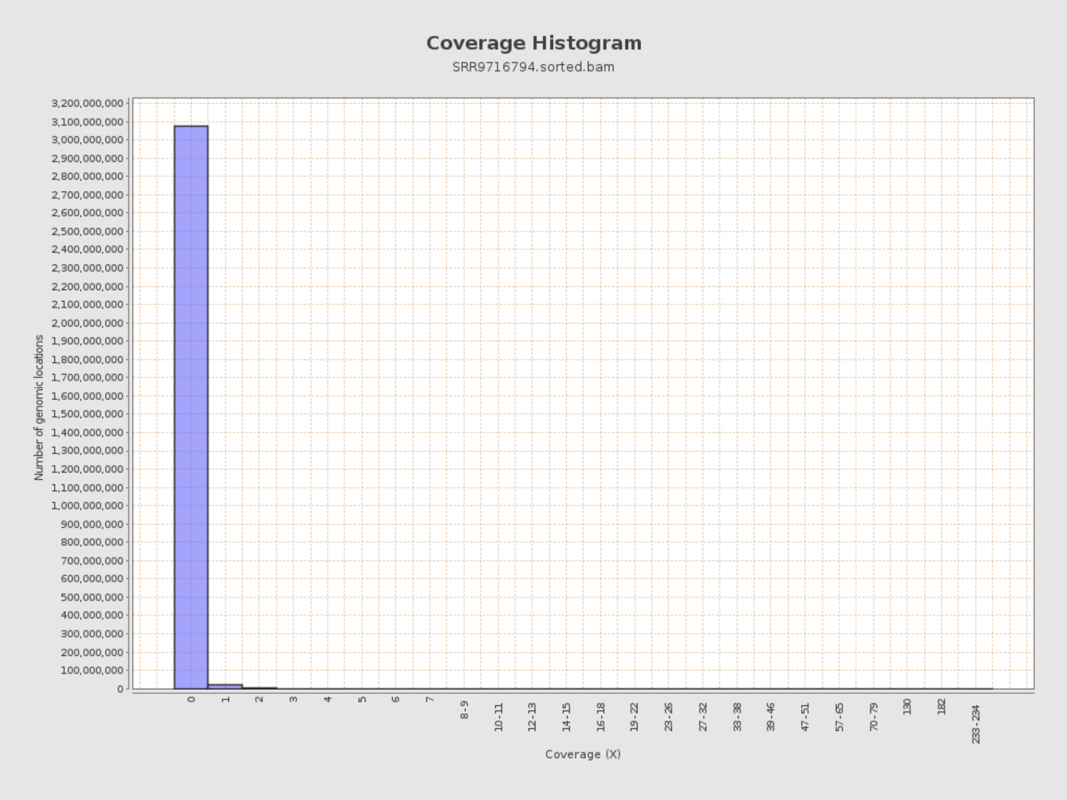
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2691853	0.0108	0.1208
chr2	243199373	2115011	0.0087	0.1377
chr3	198022430	1746802	0.0088	0.1033
chr4	191154276	1629860	0.0085	0.1028
chr5	180915260	1558915	0.0086	0.1032
chr6	171115067	1069066	0.0062	0.0932
chr7	159138663	1298297	0.0082	0.1019

chr8	146364022	1547026	0.0106	0.1159
chr9	141213431	1147109	0.0081	0.1036
chr10	135534747	1349465	0.01	0.1174
chr11	135006516	1101774	0.0082	0.1041
chr12	133851895	1253784	0.0094	0.1071
chr13	115169878	401866	0.0035	0.0665
chr14	107349540	826790	0.0077	0.0971
chr15	102531392	543383	0.0053	0.0808
chr16	90354753	731237	0.0081	0.1022
chr17	81195210	1083251	0.0133	0.1331
chr18	78077248	575256	0.0074	0.1004
chr19	59128983	742015	0.0125	0.1411
chr20	63025520	764034	0.0121	0.1286
chr21	48129895	390834	0.0081	0.1038
chr22	51304566	324068	0.0063	0.0904
chrMT	16571	11048	0.6667	1.0081
chrX	155270560	731009	0.0047	0.0756
chrY	59373566	62868	0.0011	0.0379

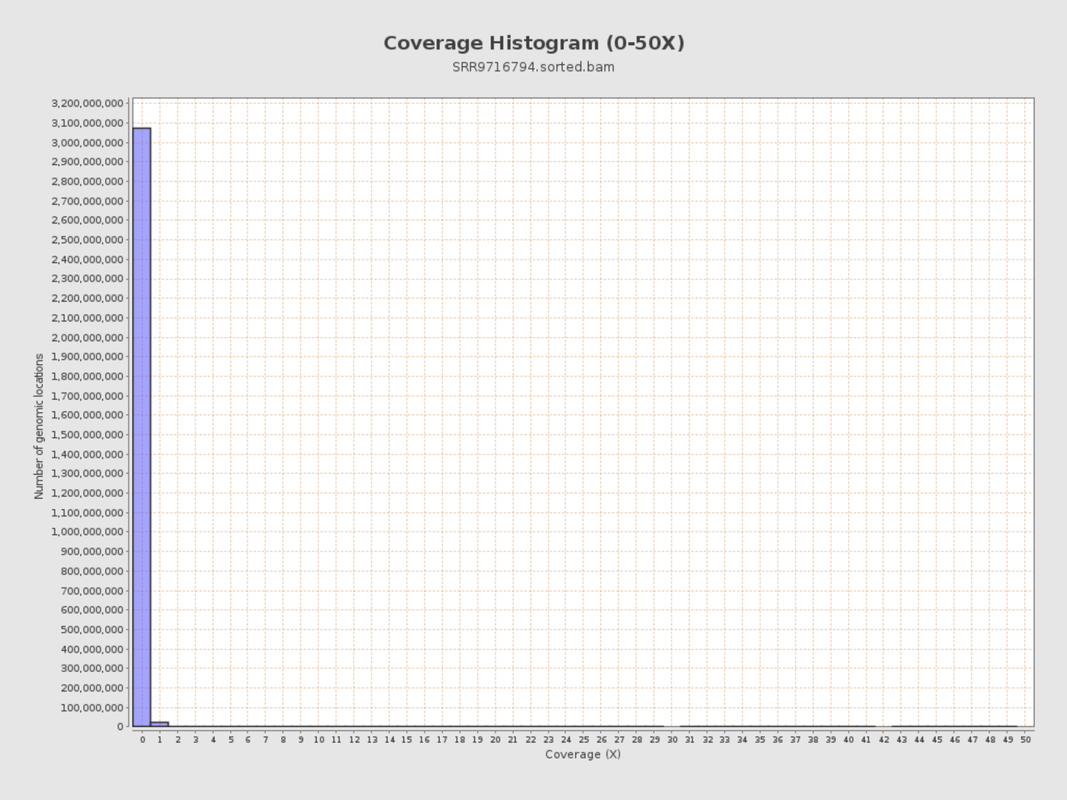
3. Results : Coverage across reference



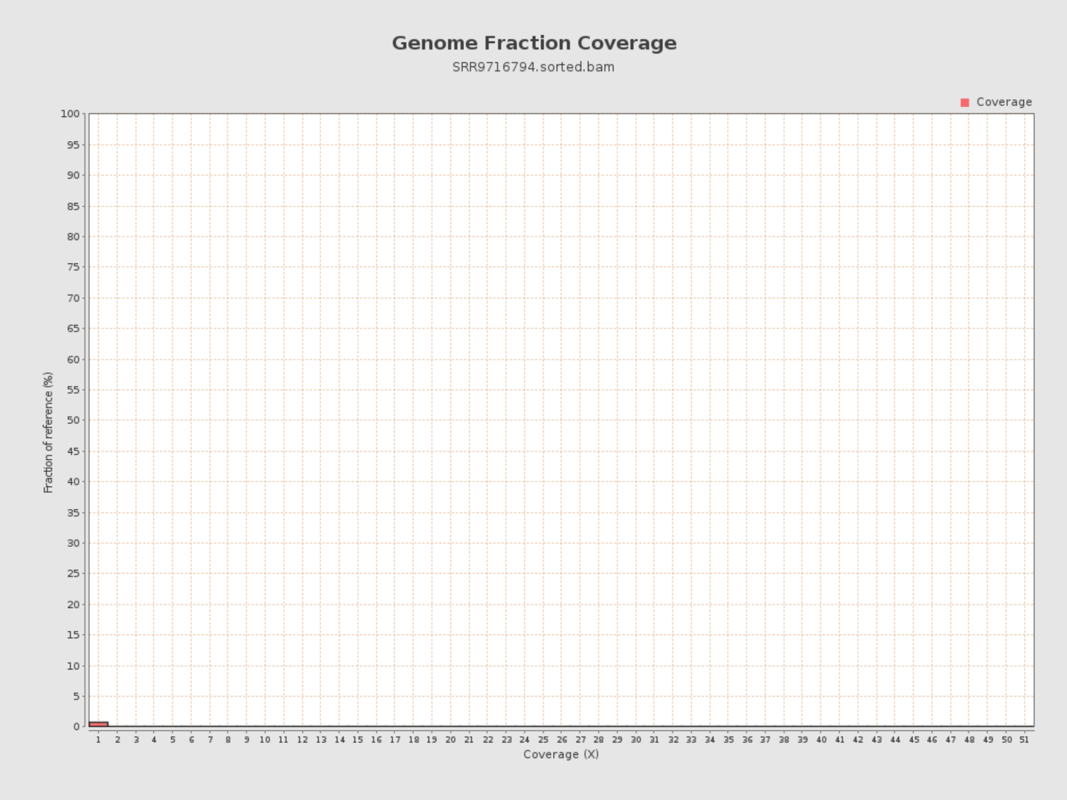
4. Results : Coverage Histogram



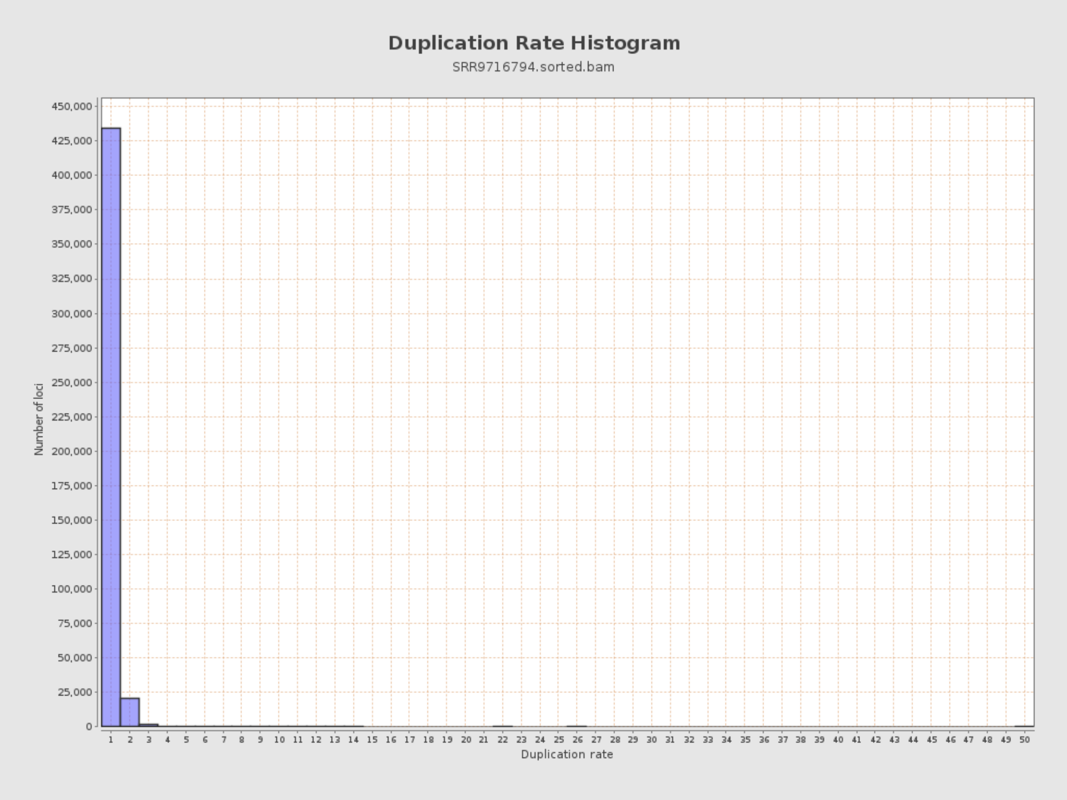
5. Results : Coverage Histogram (0-50X)



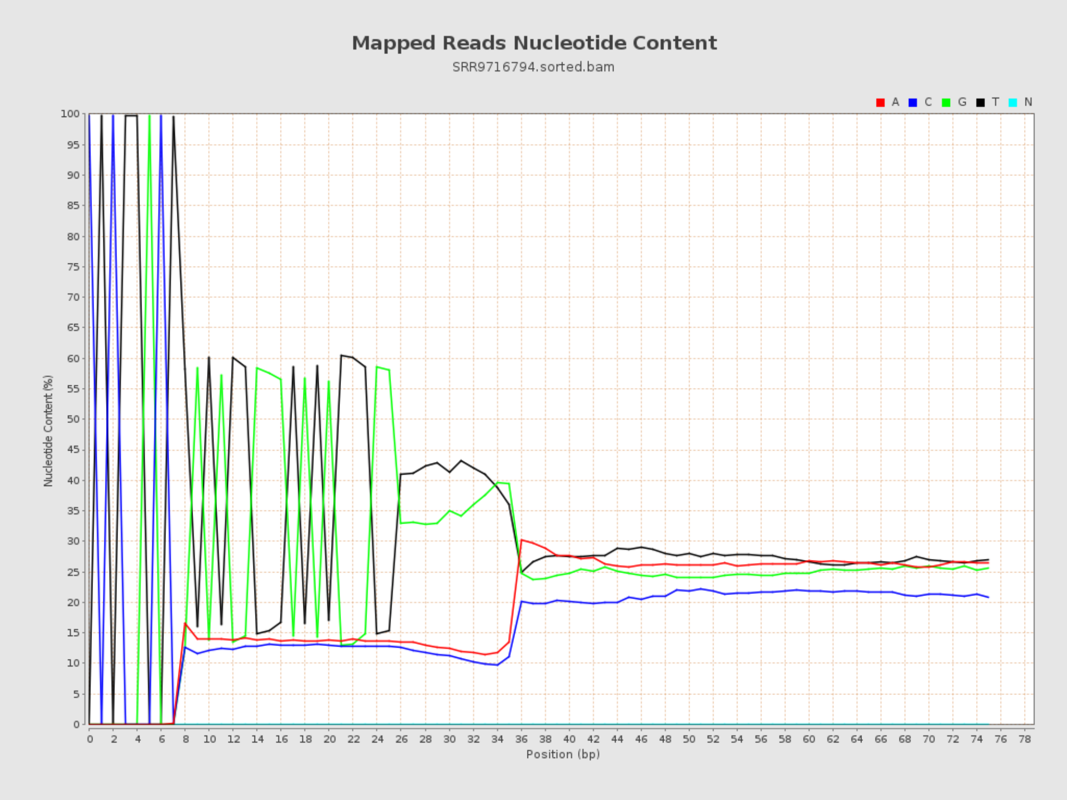
6. Results : Genome Fraction Coverage



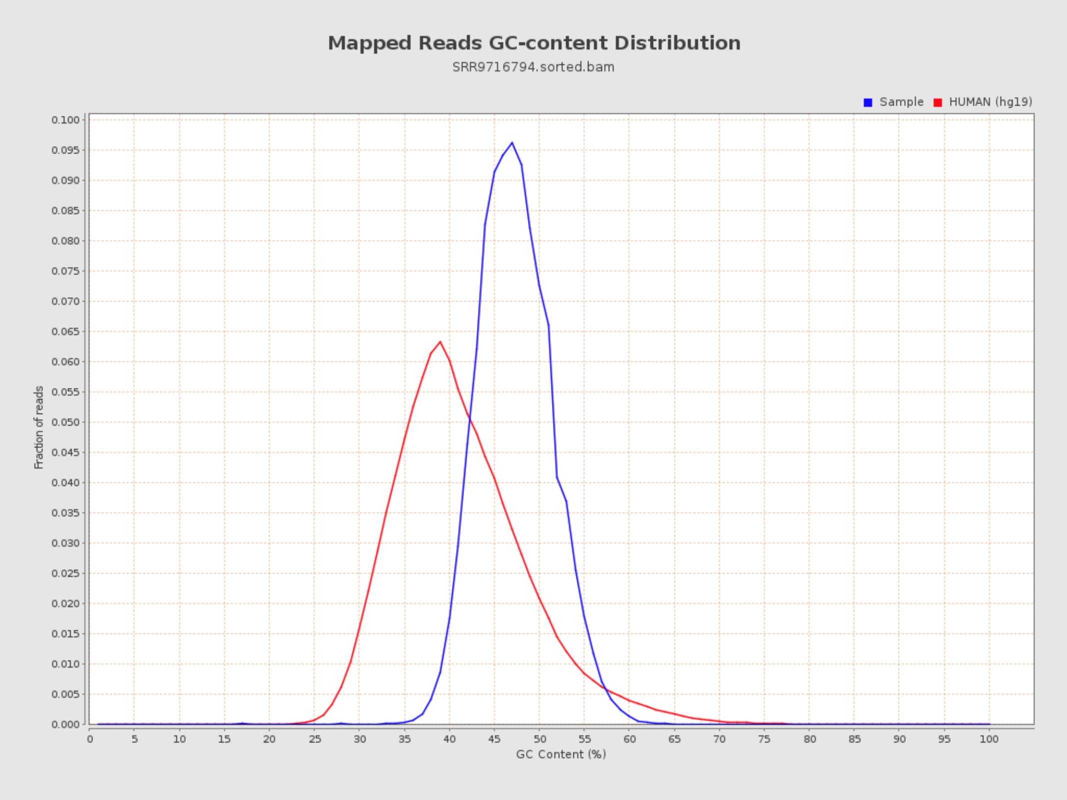
7. Results : Duplication Rate Histogram



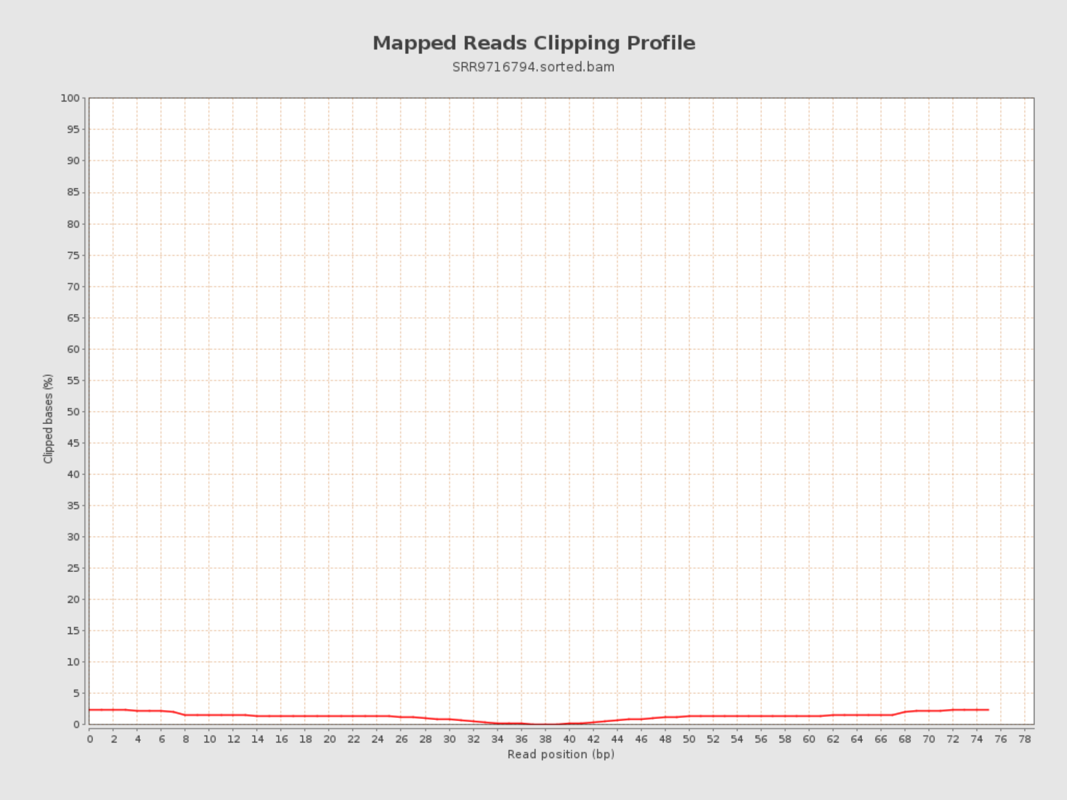
8. Results : Mapped Reads Nucleotide Content



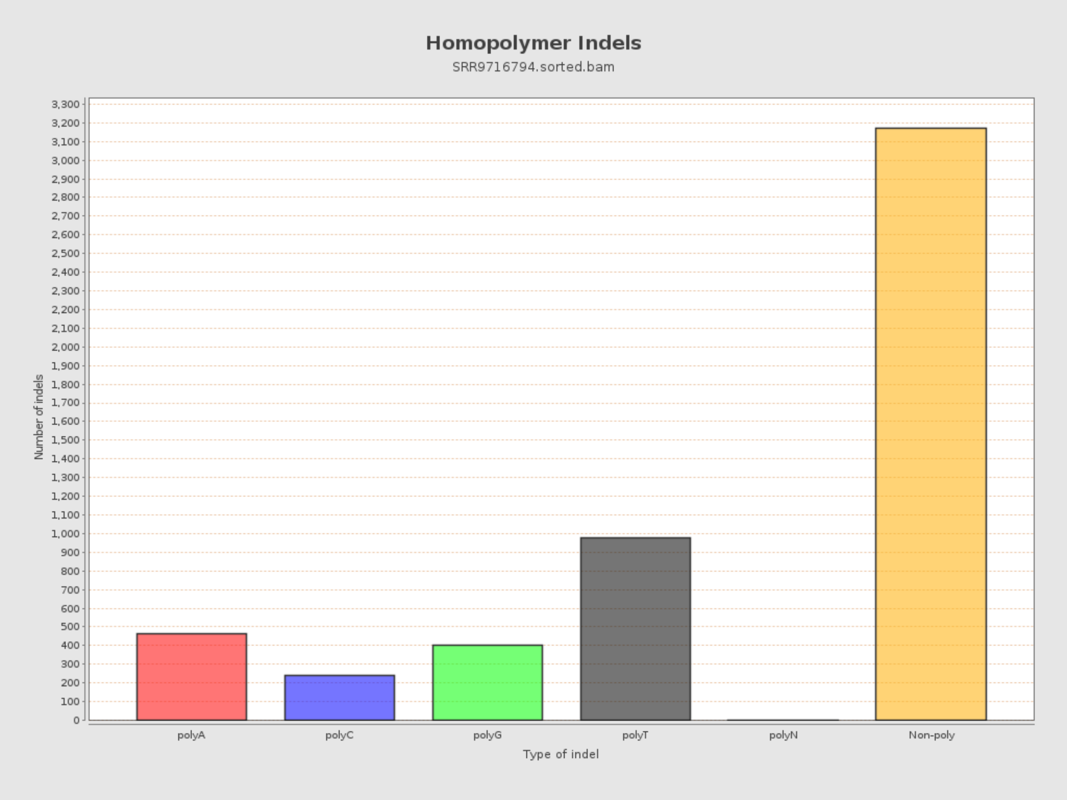
9. Results : Mapped Reads GC-content Distribution



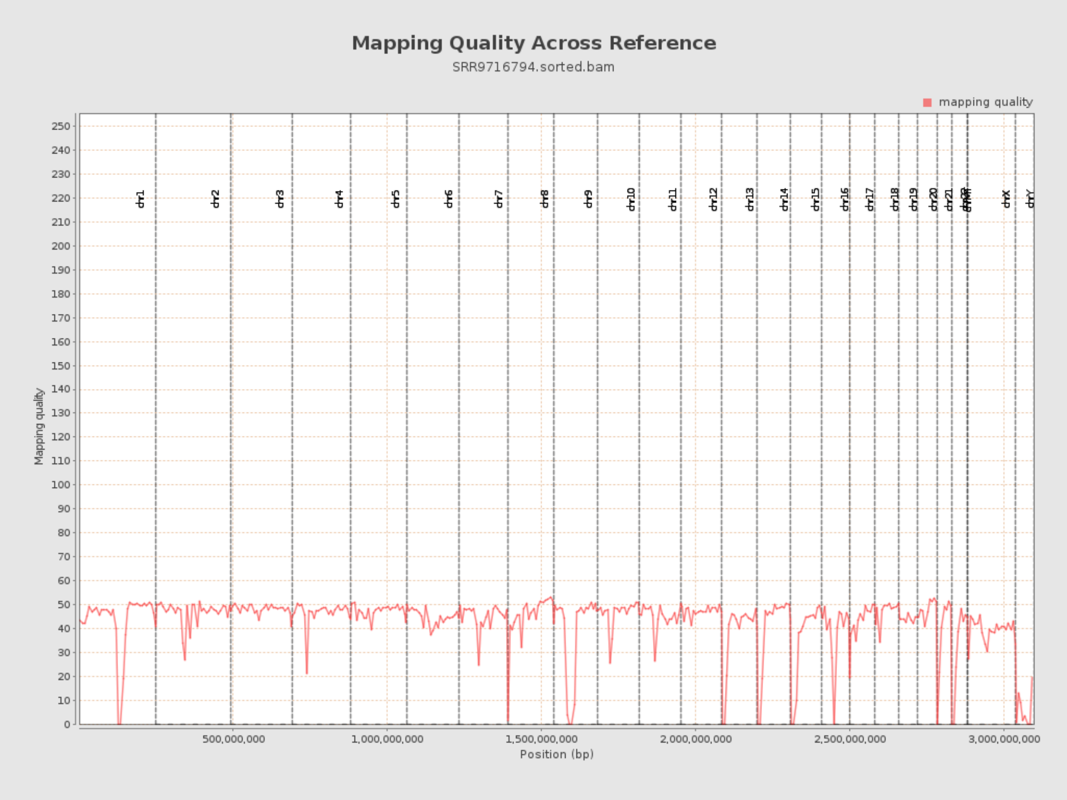
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram