Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:22:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716704.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_SRR9716704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716704.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:22:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,671,634
Mapped reads	1,498,398 / 89.64%
Unmapped reads	173,236 / 10.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,312 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	34,568 / 2.07%
Duplication rate	1.61%
Clipped reads	1,500,457 / 89.76%

2.2. ACGT Content

Number/percentage of A's	21,091,399 / 24.61%
Number/percentage of C's	18,032,175 / 21.04%
Number/percentage of T's	25,599,250 / 29.87%
Number/percentage of G's	20,974,870 / 24.48%
Number/percentage of N's	653 / 0%
GC Percentage	45.52%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2313

2.4. Mapping Quality

Mean Mapping Quality	42.55

2.5. Mismatches and indels

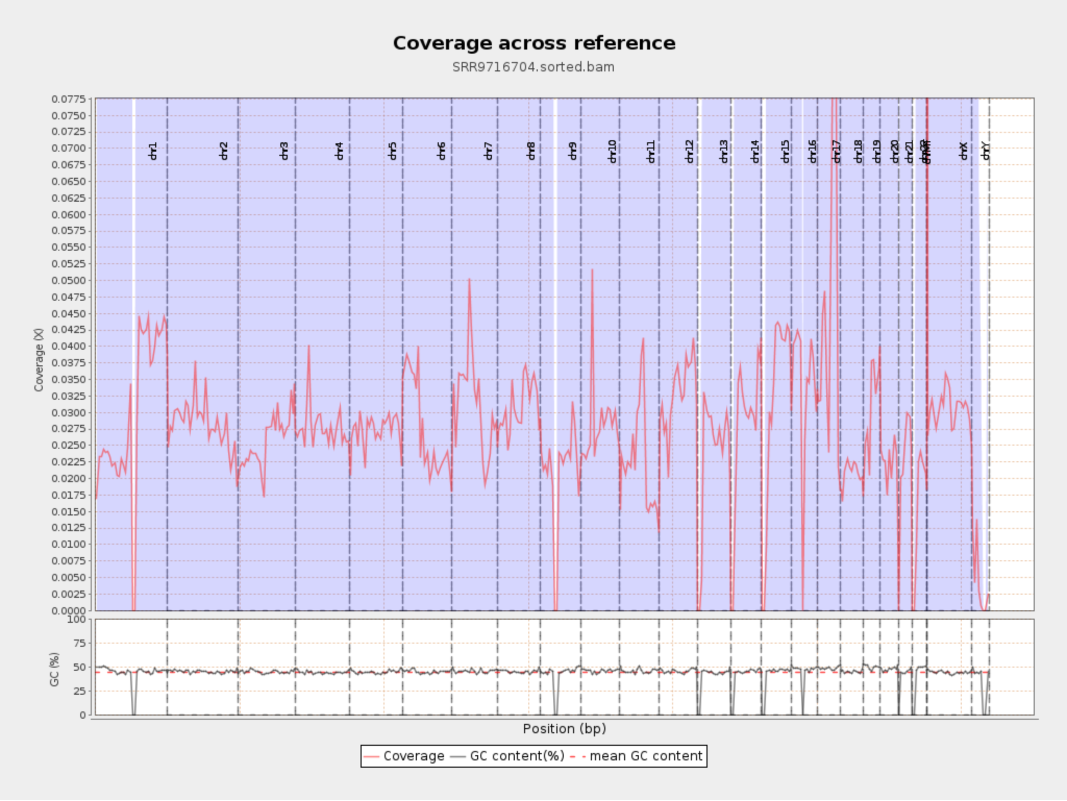
General error rate	0.53%
Mismatches	444,436
Insertions	6,043
Mapped reads with at least one insertion	0.4%
Deletions	15,819
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.11%

2.6. Chromosome stats

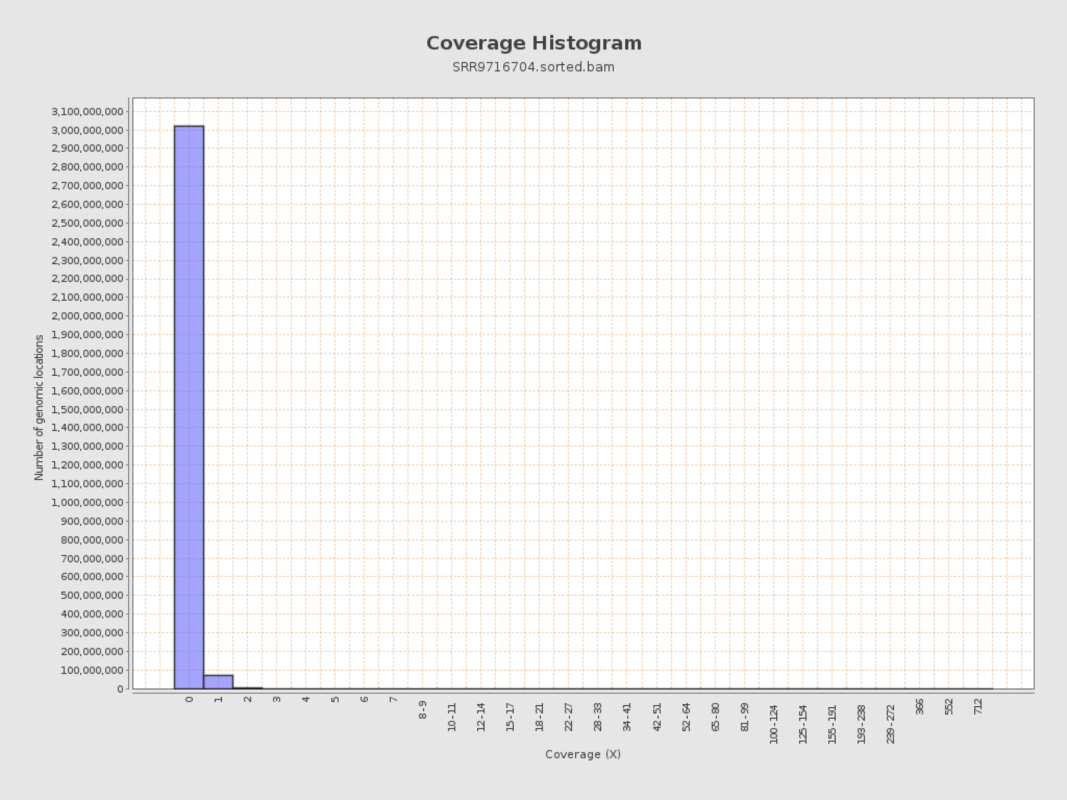
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7370443	0.0296	0.2711
chr2	243199373	6871352	0.0283	0.34
chr3	198022430	5058901	0.0255	0.1744
chr4	191154276	5313945	0.0278	0.1895
chr5	180915260	4980974	0.0275	0.1778
chr6	171115067	4723449	0.0276	0.2111
chr7	159138663	5002368	0.0314	0.3415

chr8	146364022	4537794	0.031	0.2221
chr9	141213431	2937741	0.0208	0.1784
chr10	135534747	3826477	0.0282	0.2818
chr11	135006516	3101499	0.023	0.2063
chr12	133851895	4409255	0.0329	0.197
chr13	115169878	2672633	0.0232	0.1656
chr14	107349540	2934533	0.0273	0.1846
chr15	102531392	3208842	0.0313	0.194
chr16	90354753	3022968	0.0335	0.209
chr17	81195210	3947116	0.0486	0.2507
chr18	78077248	1623340	0.0208	0.2704
chr19	59128983	1821904	0.0308	0.2683
chr20	63025520	1409737	0.0224	0.1666
chr21	48129895	1093887	0.0227	0.1719
chr22	51304566	805368	0.0157	0.1377
chrMT	16571	19303	1.1649	1.3102
chrX	155270560	4777545	0.0308	0.2016
chrY	59373566	251958	0.0042	0.1112

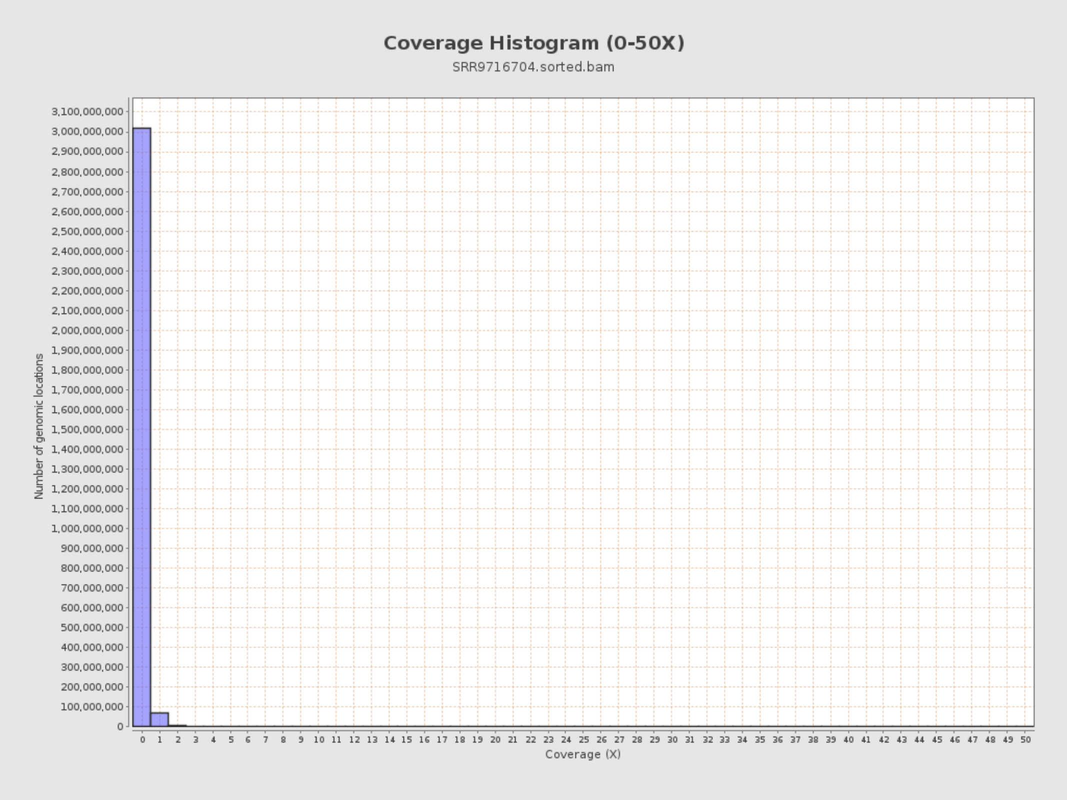
3. Results : Coverage across reference



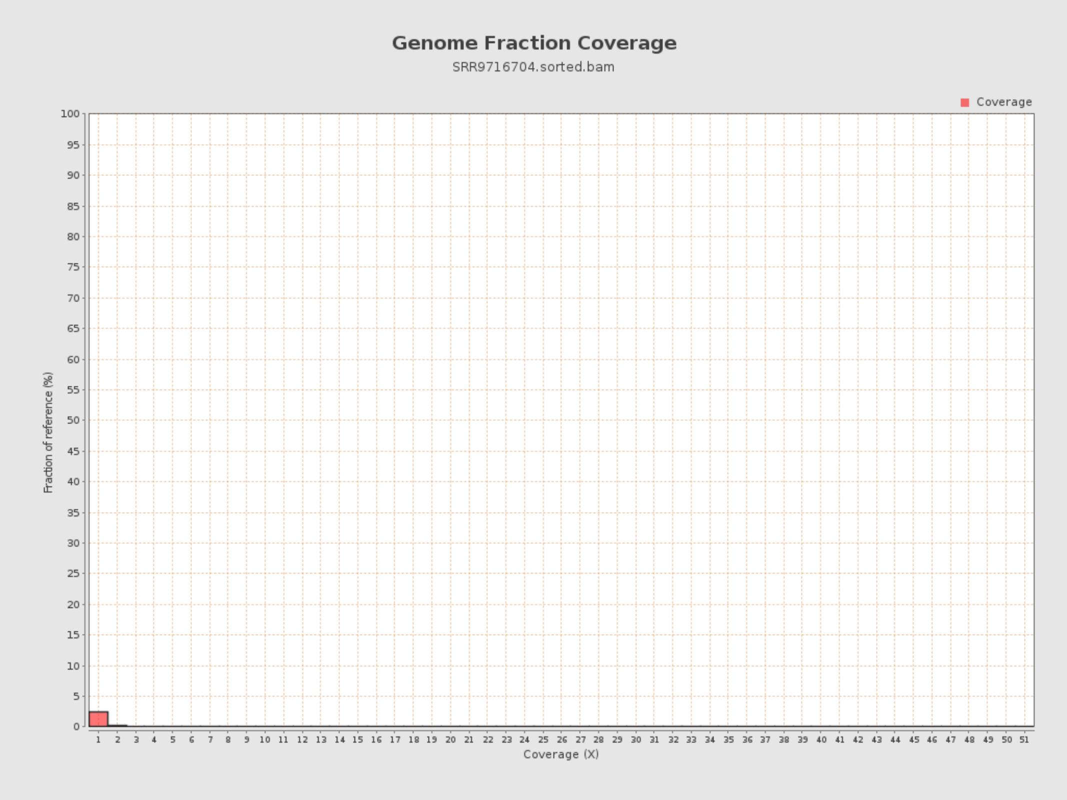
4. Results : Coverage Histogram



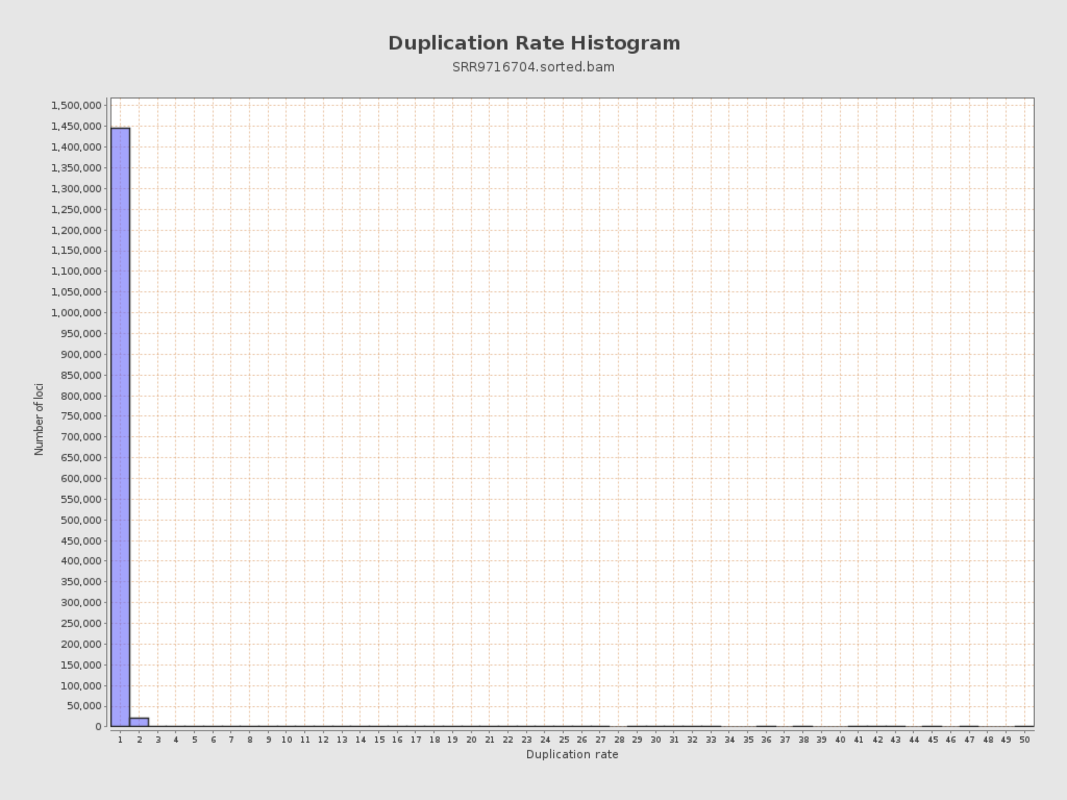
5. Results : Coverage Histogram (0-50X)



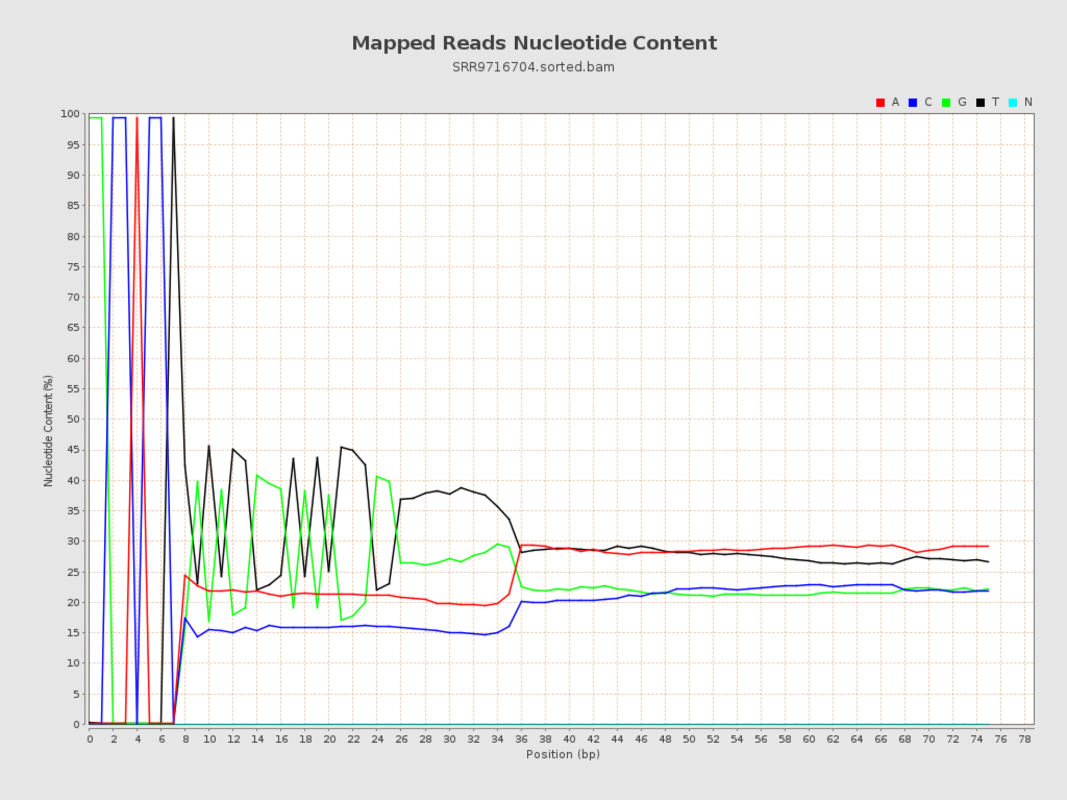
6. Results : Genome Fraction Coverage



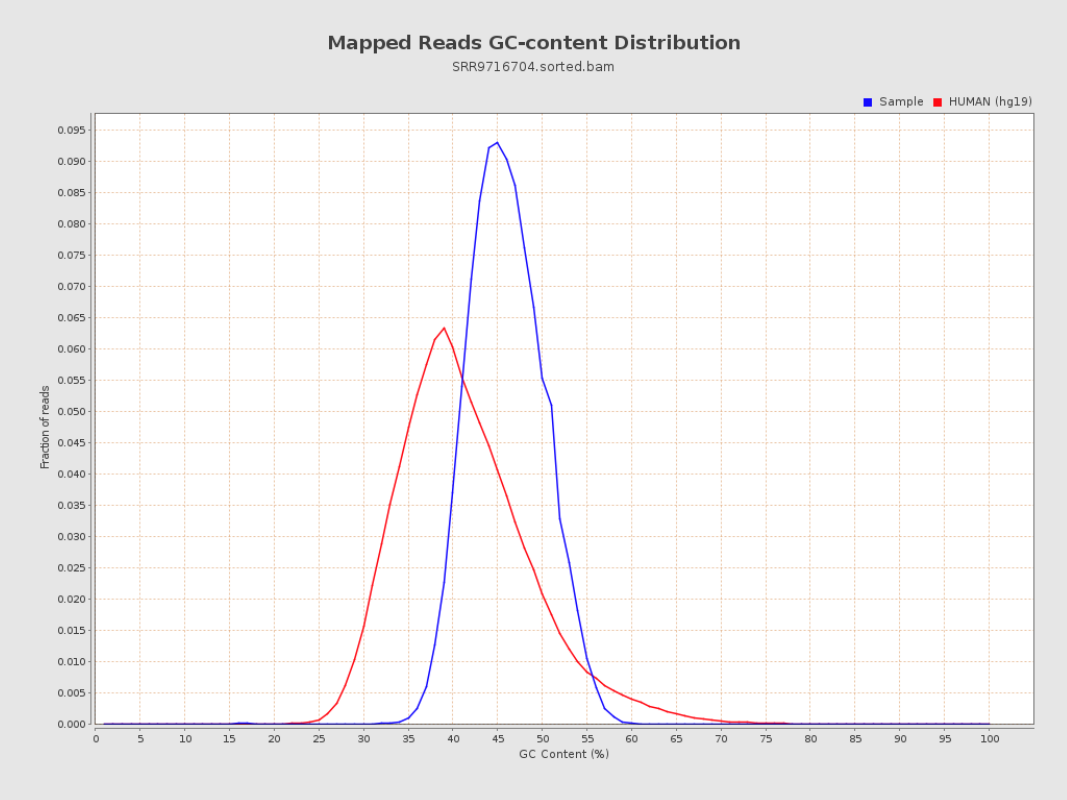
7. Results : Duplication Rate Histogram



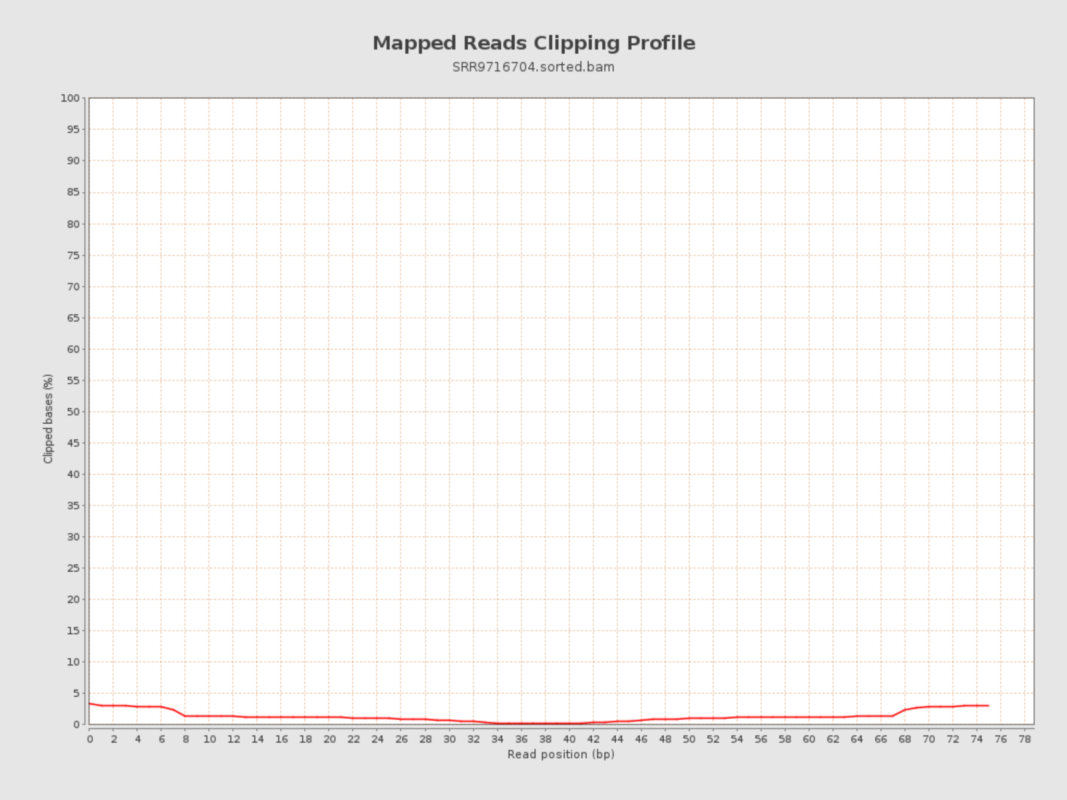
8. Results : Mapped Reads Nucleotide Content



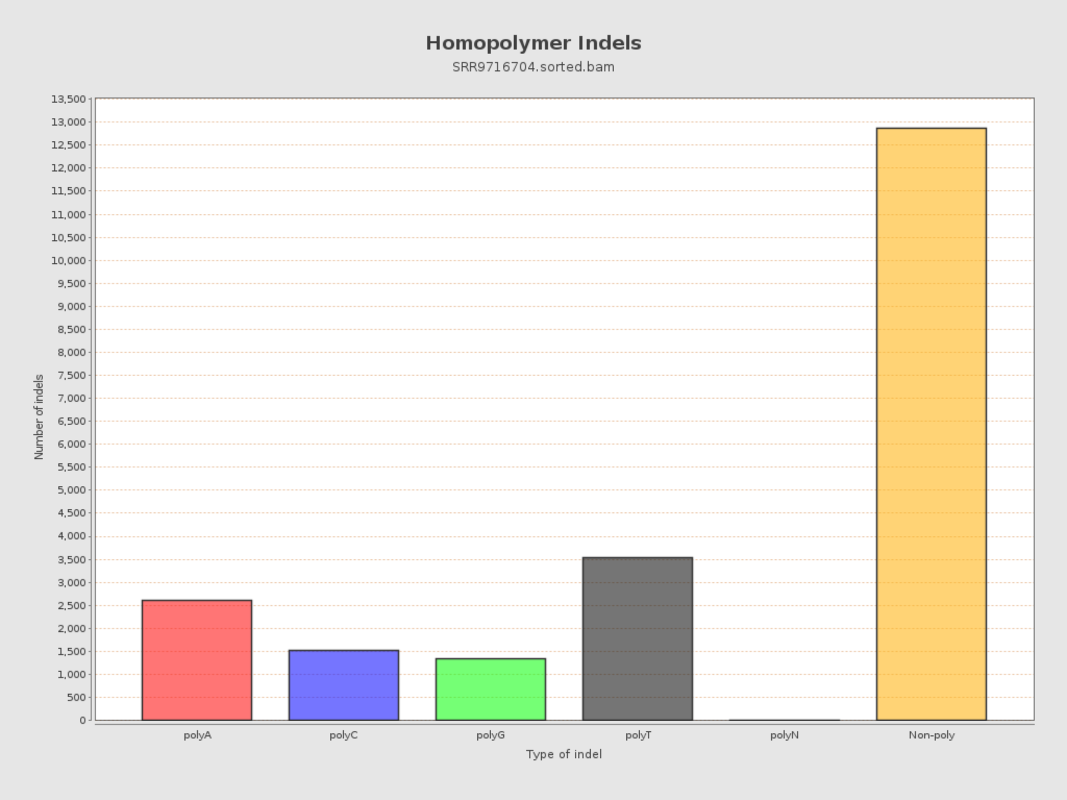
9. Results : Mapped Reads GC-content Distribution



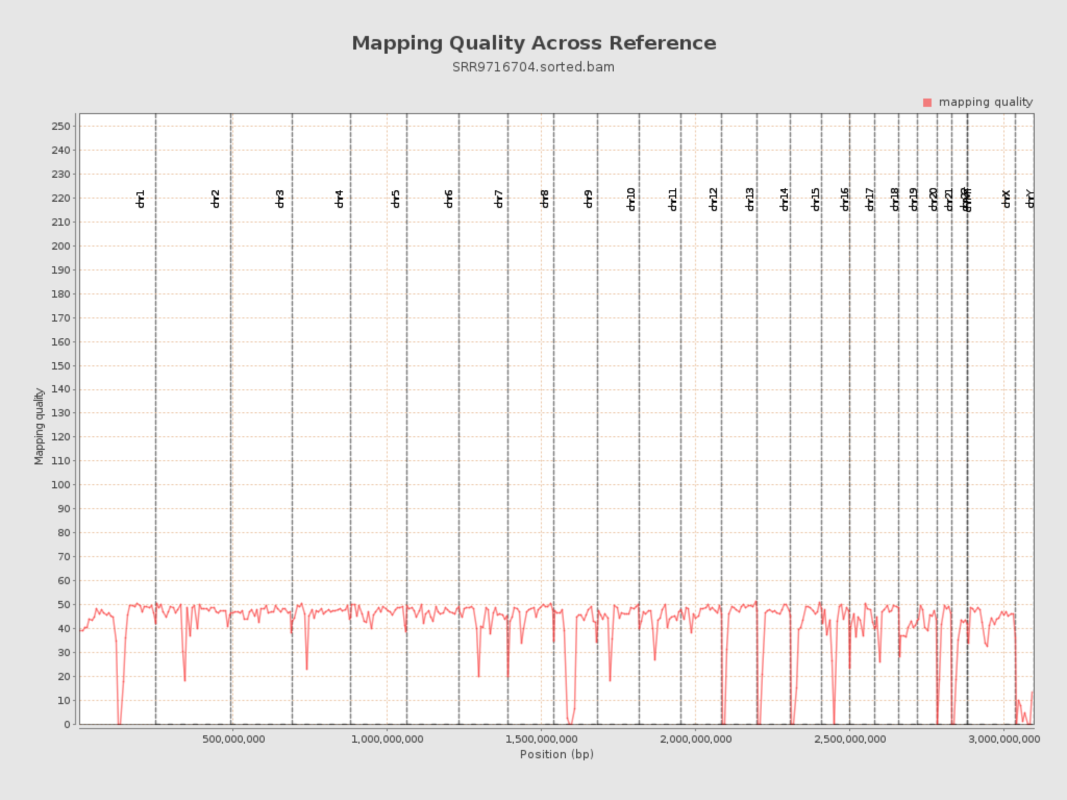
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram