Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:53:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716723.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_SRR9716723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716723.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:53:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,071,771
Mapped reads	975,566 / 91.02%
Unmapped reads	96,205 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,412 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	26,728 / 2.49%
Duplication rate	1.9%
Clipped reads	978,053 / 91.26%

2.2. ACGT Content

Number/percentage of A's	13,793,840 / 24.44%
Number/percentage of C's	11,224,307 / 19.89%
Number/percentage of T's	17,464,824 / 30.95%
Number/percentage of G's	13,945,181 / 24.71%
Number/percentage of N's	804 / 0%
GC Percentage	44.6%

2.3. Coverage

Mean	0.0182

Standard Deviation	0.2012

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Mismatches and indels

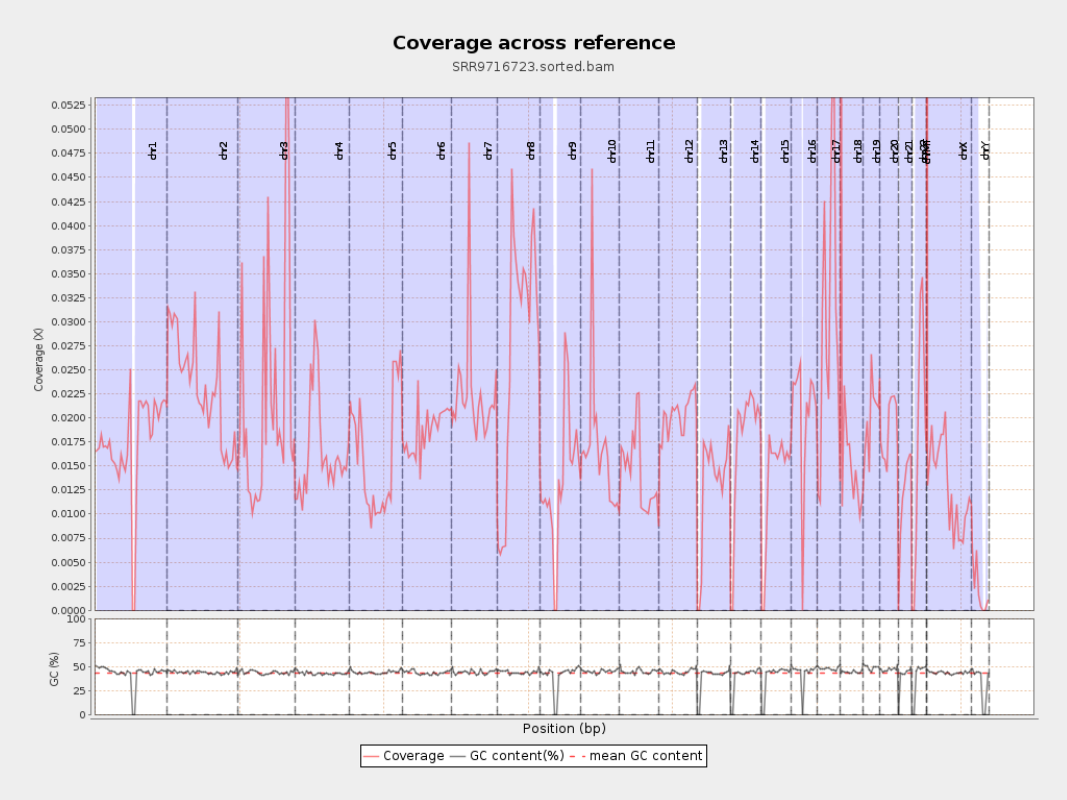
General error rate	0.51%
Mismatches	283,417
Insertions	3,616
Mapped reads with at least one insertion	0.37%
Deletions	10,583
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.98%

2.6. Chromosome stats

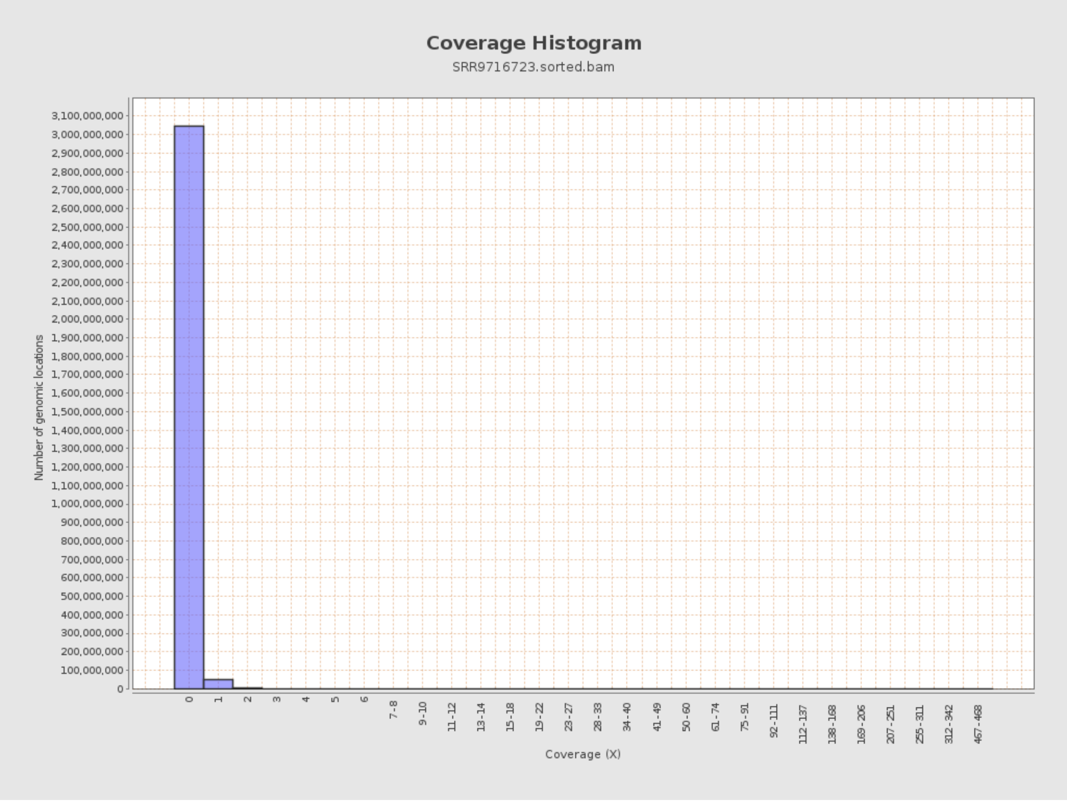
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4305833	0.0173	0.2584
chr2	243199373	5638620	0.0232	0.2499
chr3	198022430	4333040	0.0219	0.1643
chr4	191154276	3145551	0.0165	0.1419
chr5	180915260	2864549	0.0158	0.1332
chr6	171115067	3190720	0.0186	0.1527
chr7	159138663	3594136	0.0226	0.4138

chr8	146364022	4066740	0.0278	0.2197
chr9	141213431	1886810	0.0134	0.1369
chr10	135534747	2306358	0.017	0.2564
chr11	135006516	1958721	0.0145	0.1491
chr12	133851895	2711208	0.0203	0.1676
chr13	115169878	1503418	0.0131	0.1208
chr14	107349540	1871459	0.0174	0.141
chr15	102531392	1372250	0.0134	0.1262
chr16	90354753	1816051	0.0201	0.1559
chr17	81195210	2478830	0.0305	0.1898
chr18	78077248	1347956	0.0173	0.2108
chr19	59128983	1189191	0.0201	0.2513
chr20	63025520	1186199	0.0188	0.152
chr21	48129895	577500	0.012	0.1179
chr22	51304566	917041	0.0179	0.1413
chrMT	16571	72332	4.365	3.1984
chrX	155270560	1988226	0.0128	0.1343
chrY	59373566	122652	0.0021	0.0609

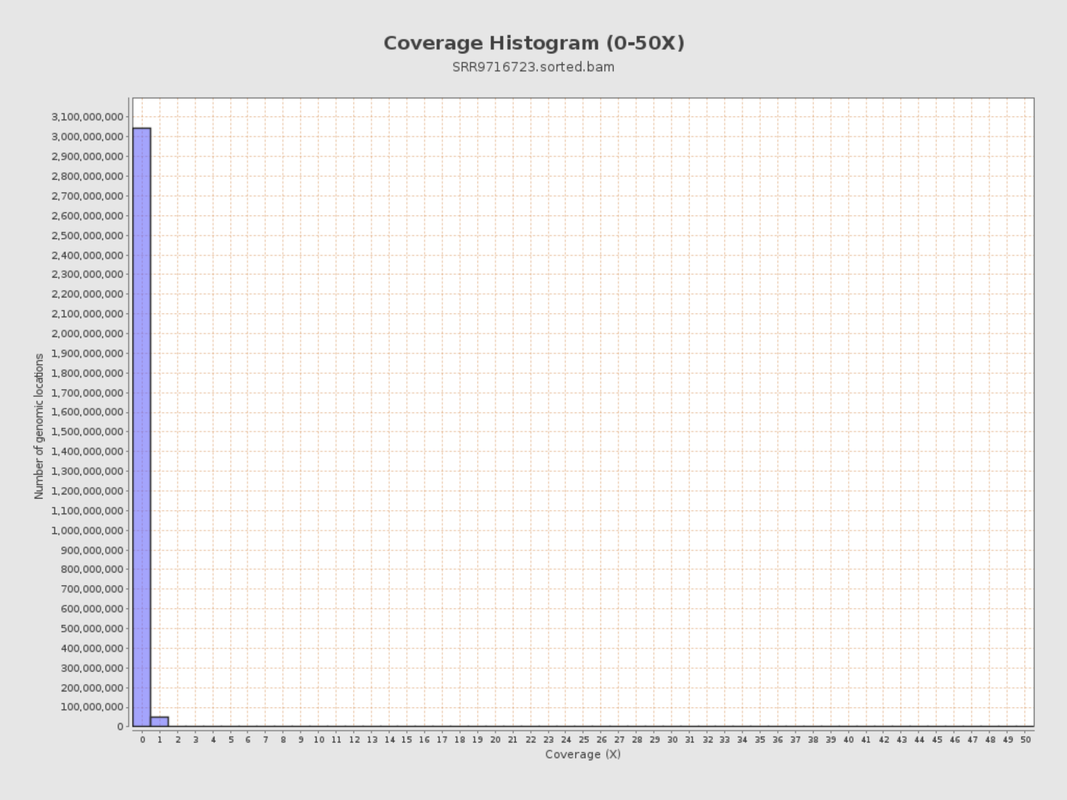
3. Results : Coverage across reference



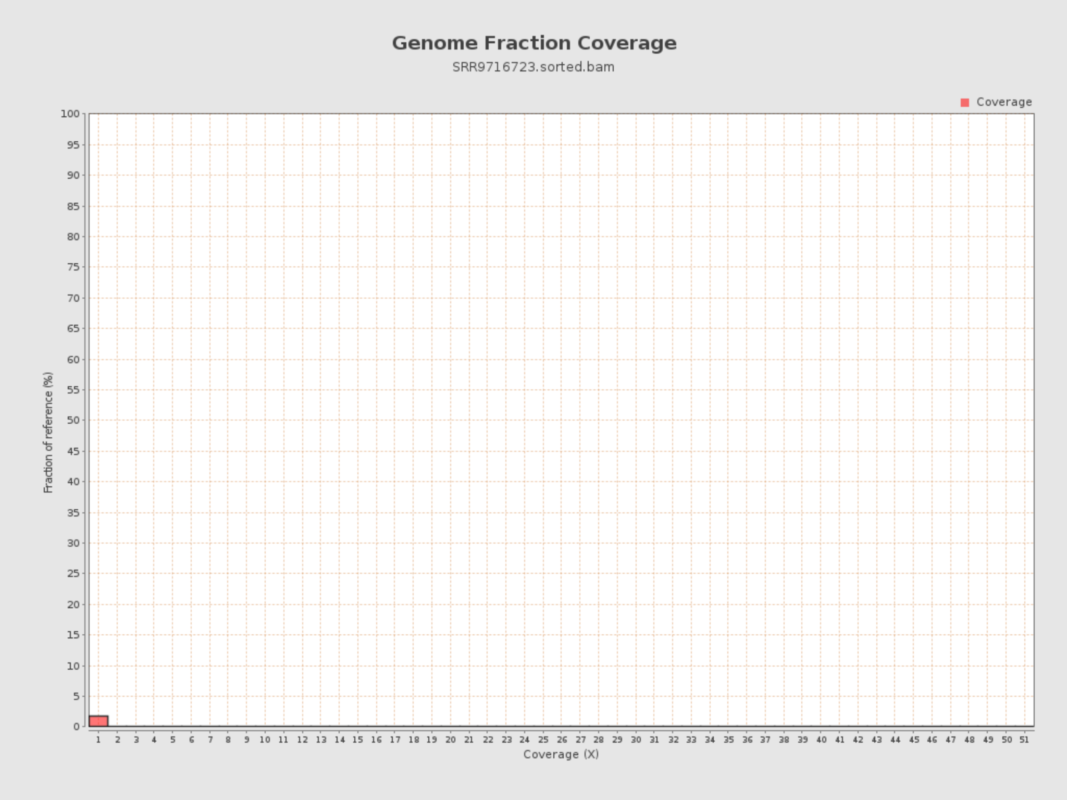
4. Results : Coverage Histogram



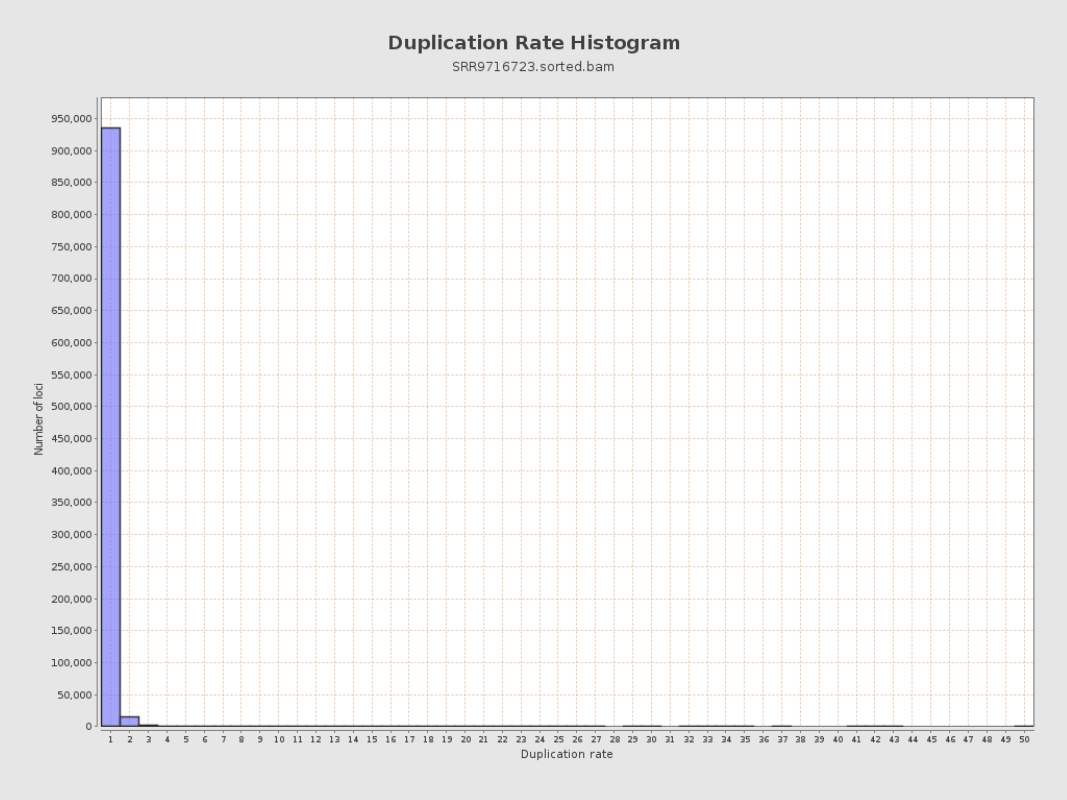
5. Results : Coverage Histogram (0-50X)



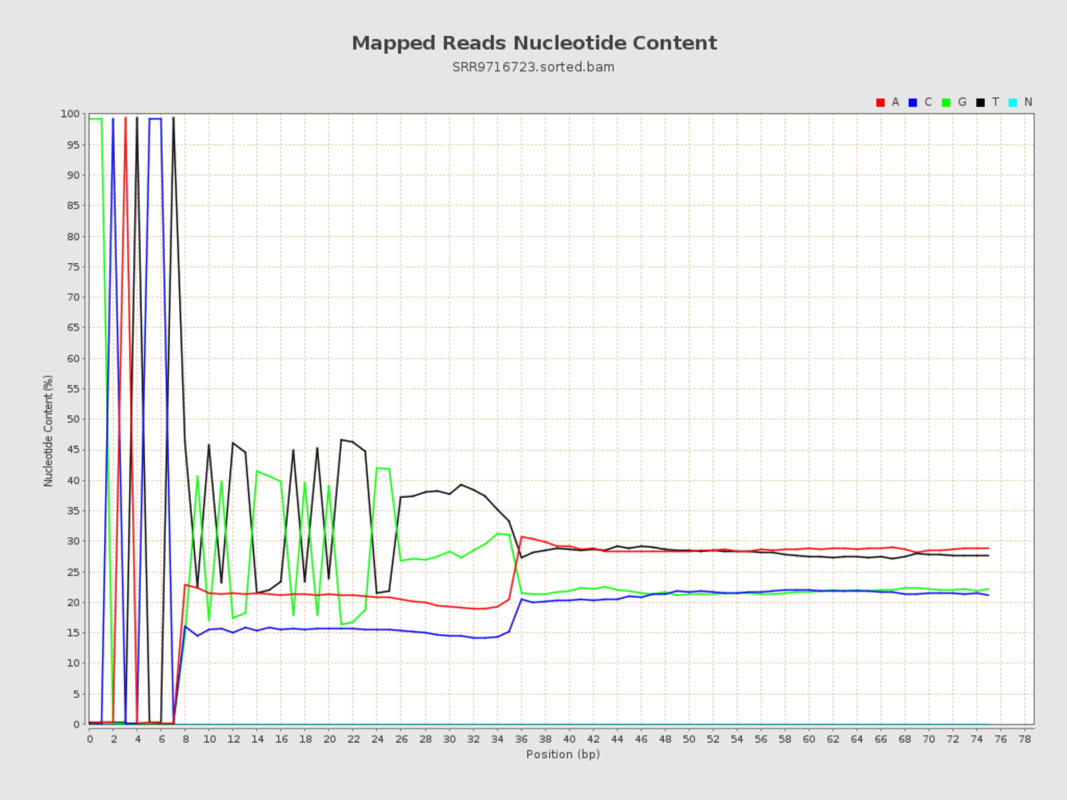
6. Results : Genome Fraction Coverage



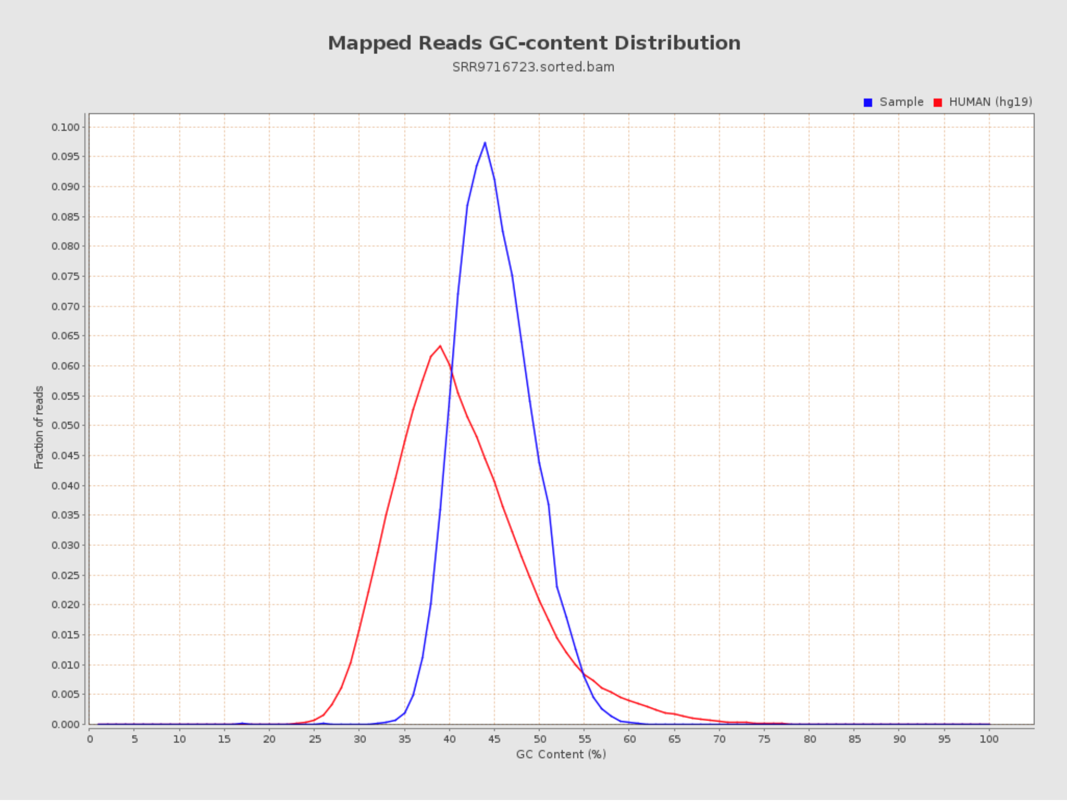
7. Results : Duplication Rate Histogram



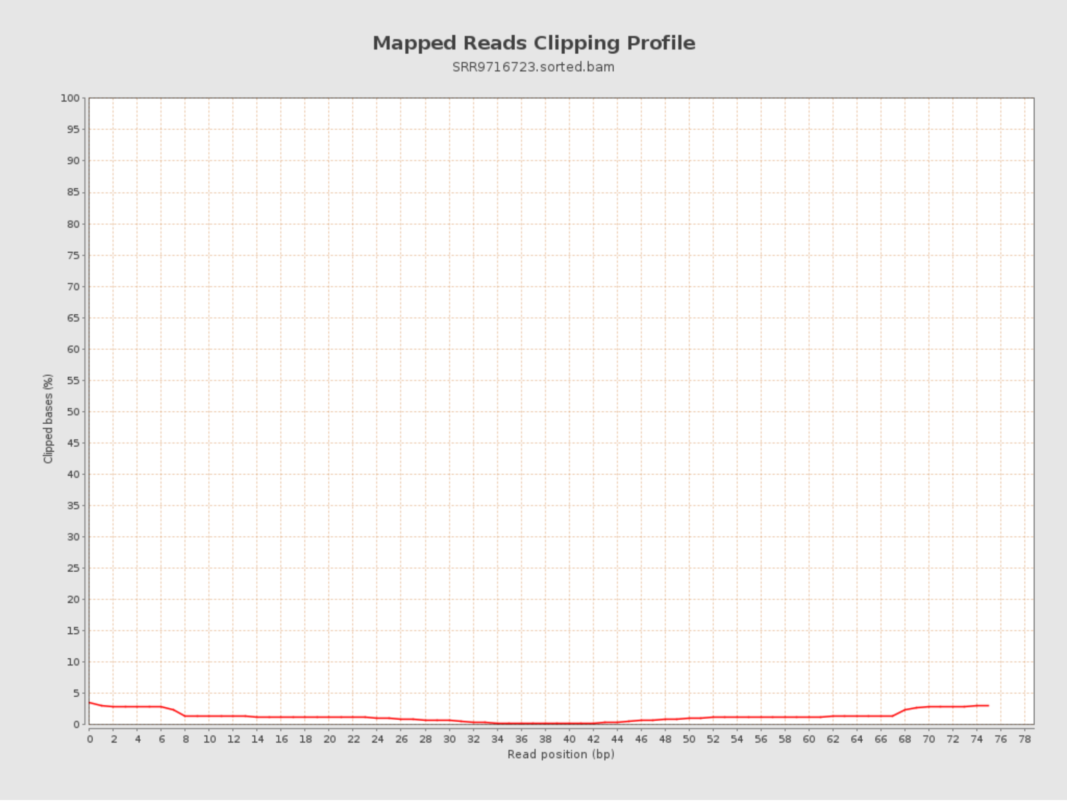
8. Results : Mapped Reads Nucleotide Content



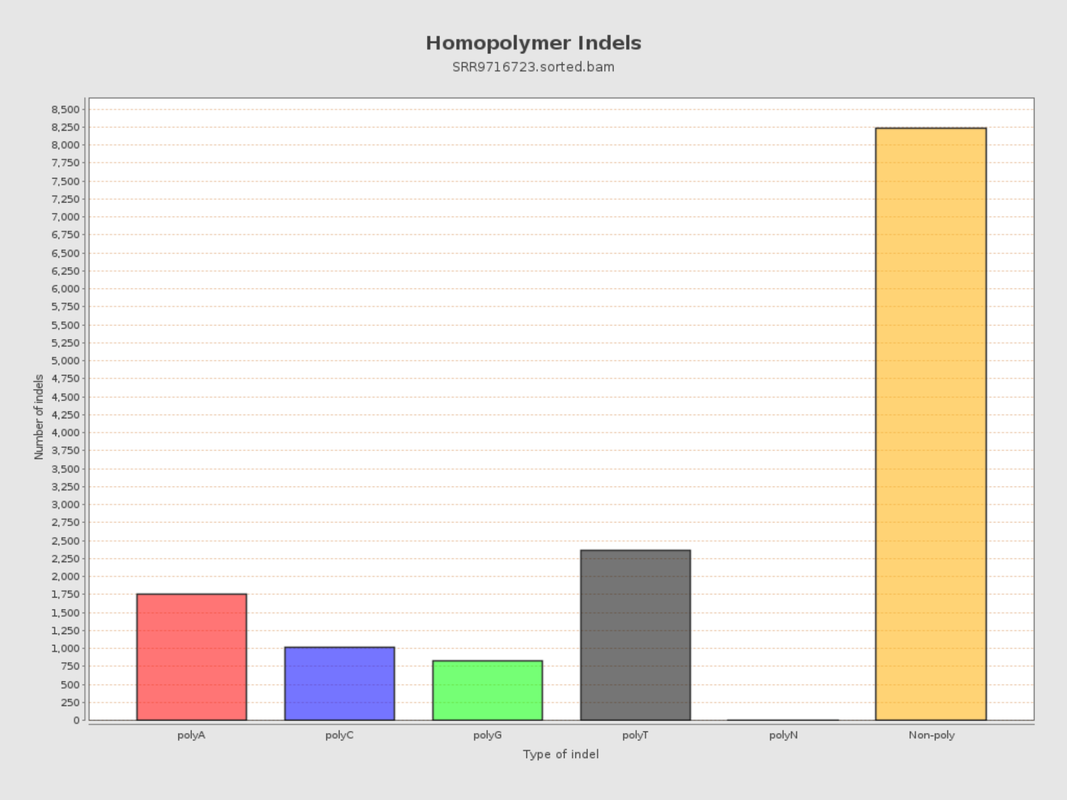
9. Results : Mapped Reads GC-content Distribution



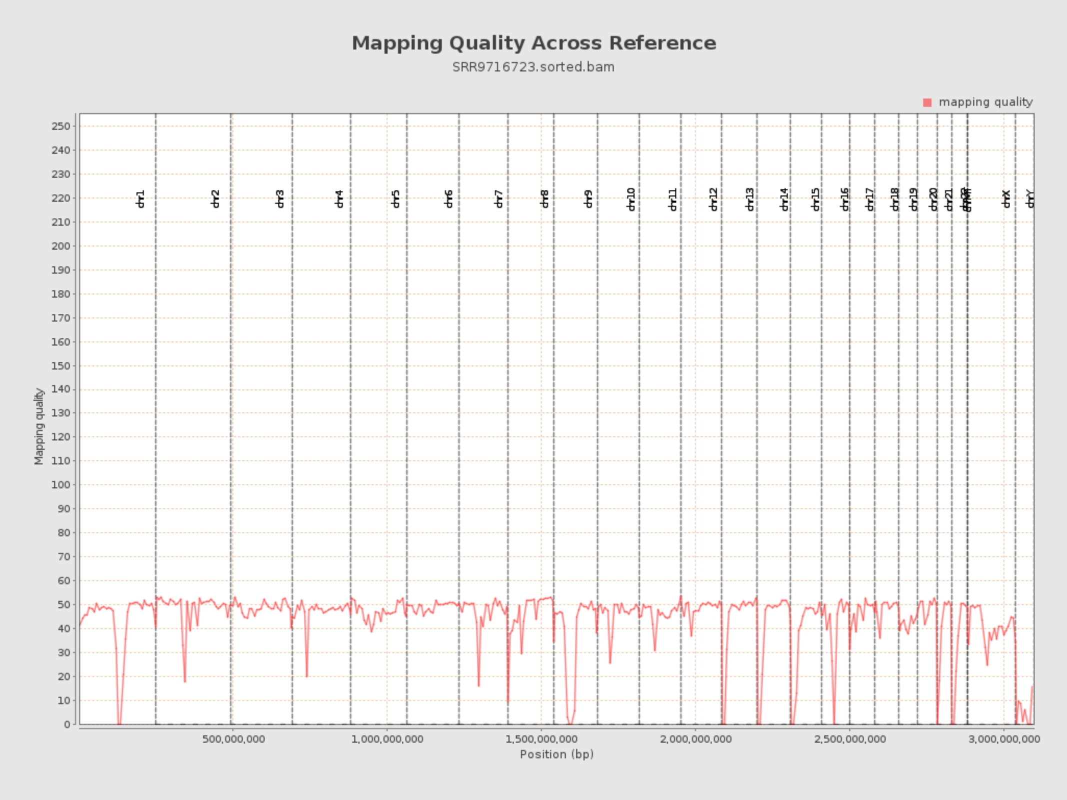
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram