Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:42:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716509.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_SRR9716509 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716509.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:42:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716509.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,502,044
Mapped reads	1,336,649 / 88.99%
Unmapped reads	165,395 / 11.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,947 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	49,938 / 3.32%
Duplication rate	2.77%
Clipped reads	1,339,303 / 89.17%

2.2. ACGT Content

Number/percentage of A's	19,615,699 / 25.56%
Number/percentage of C's	13,500,370 / 17.59%
Number/percentage of T's	24,339,967 / 31.71%
Number/percentage of G's	19,296,109 / 25.14%
Number/percentage of N's	2,134 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2529

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

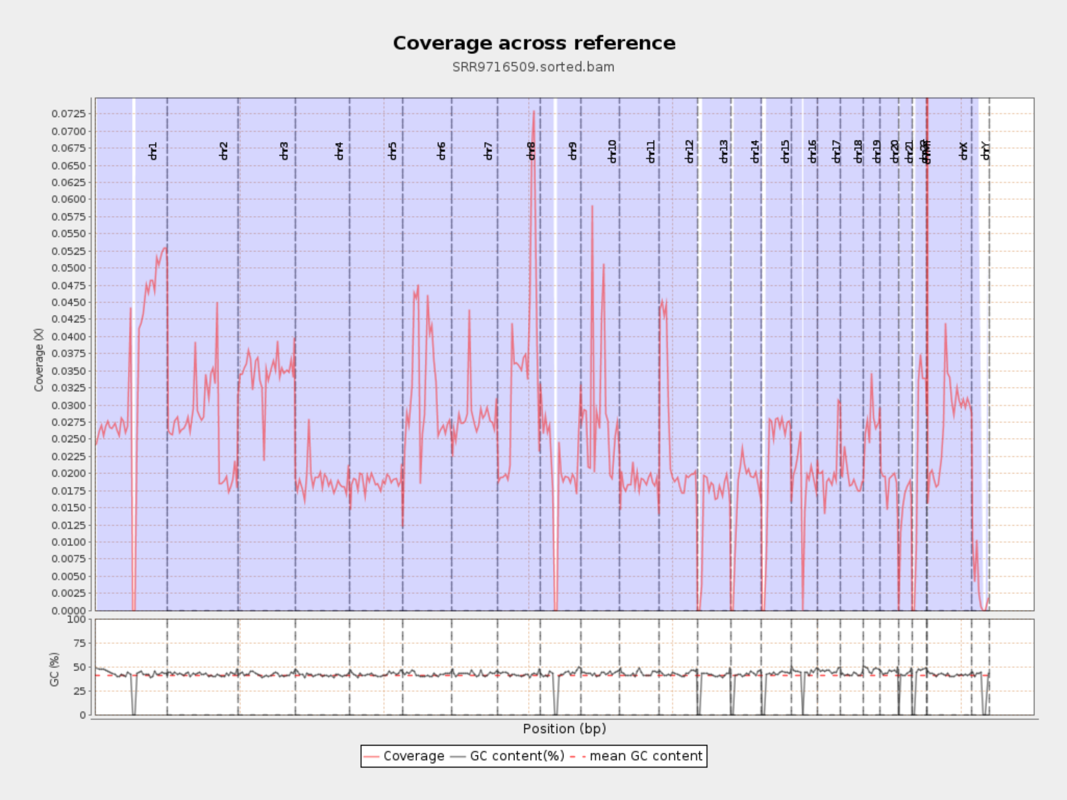
General error rate	0.51%
Mismatches	379,048
Insertions	5,224
Mapped reads with at least one insertion	0.39%
Deletions	13,114
Mapped reads with at least one deletion	0.97%
Homopolymer indels	42.29%

2.6. Chromosome stats

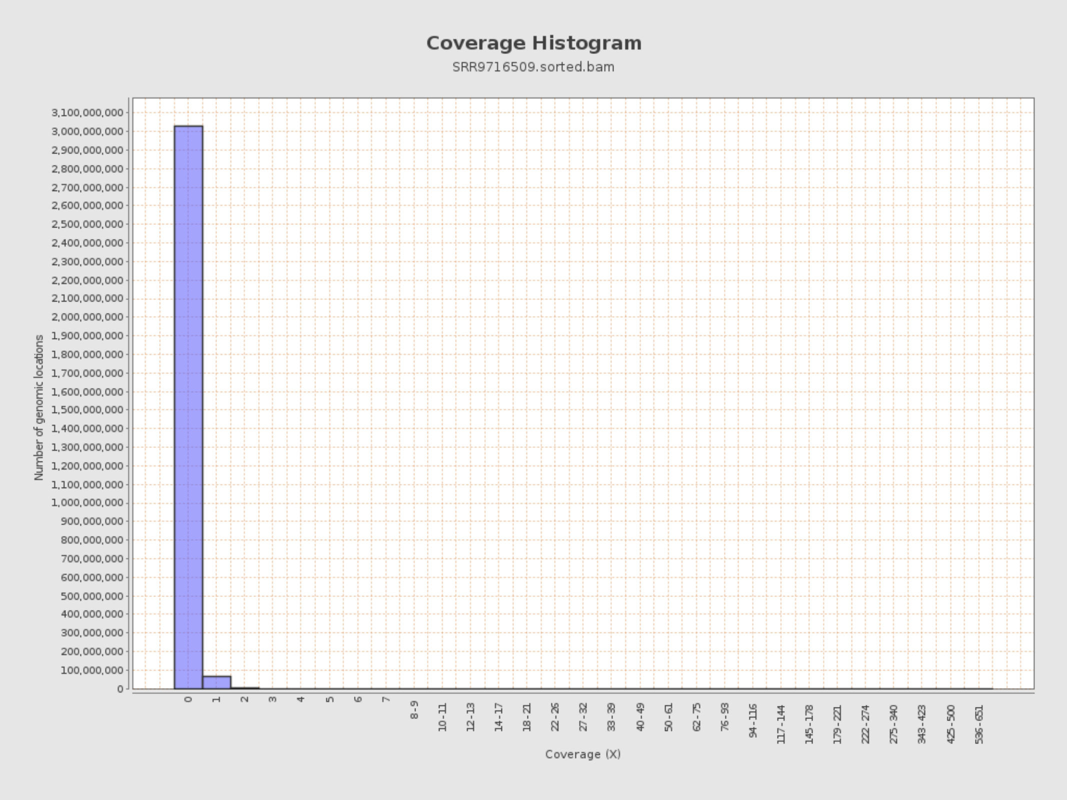
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8531383	0.0342	0.4637
chr2	243199373	6565706	0.027	0.3193
chr3	198022430	6882753	0.0348	0.2058
chr4	191154276	3638022	0.019	0.16
chr5	180915260	3422621	0.0189	0.1538
chr6	171115067	5426681	0.0317	0.2516
chr7	159138663	4532375	0.0285	0.3255

chr8	146364022	5079858	0.0347	0.2294
chr9	141213431	2851225	0.0202	0.2048
chr10	135534747	3994252	0.0295	0.2985
chr11	135006516	2550091	0.0189	0.196
chr12	133851895	3402065	0.0254	0.1775
chr13	115169878	1744784	0.0151	0.1355
chr14	107349540	1790596	0.0167	0.1529
chr15	102531392	2248145	0.0219	0.164
chr16	90354753	1638238	0.0181	0.1649
chr17	81195210	1672942	0.0206	0.1621
chr18	78077248	1499296	0.0192	0.3401
chr19	59128983	1625026	0.0275	0.3149
chr20	63025520	1177807	0.0187	0.1508
chr21	48129895	706801	0.0147	0.145
chr22	51304566	1203433	0.0235	0.1683
chrMT	16571	127197	7.6759	5.0977
chrX	155270560	4261182	0.0274	0.2037
chrY	59373566	202339	0.0034	0.0844

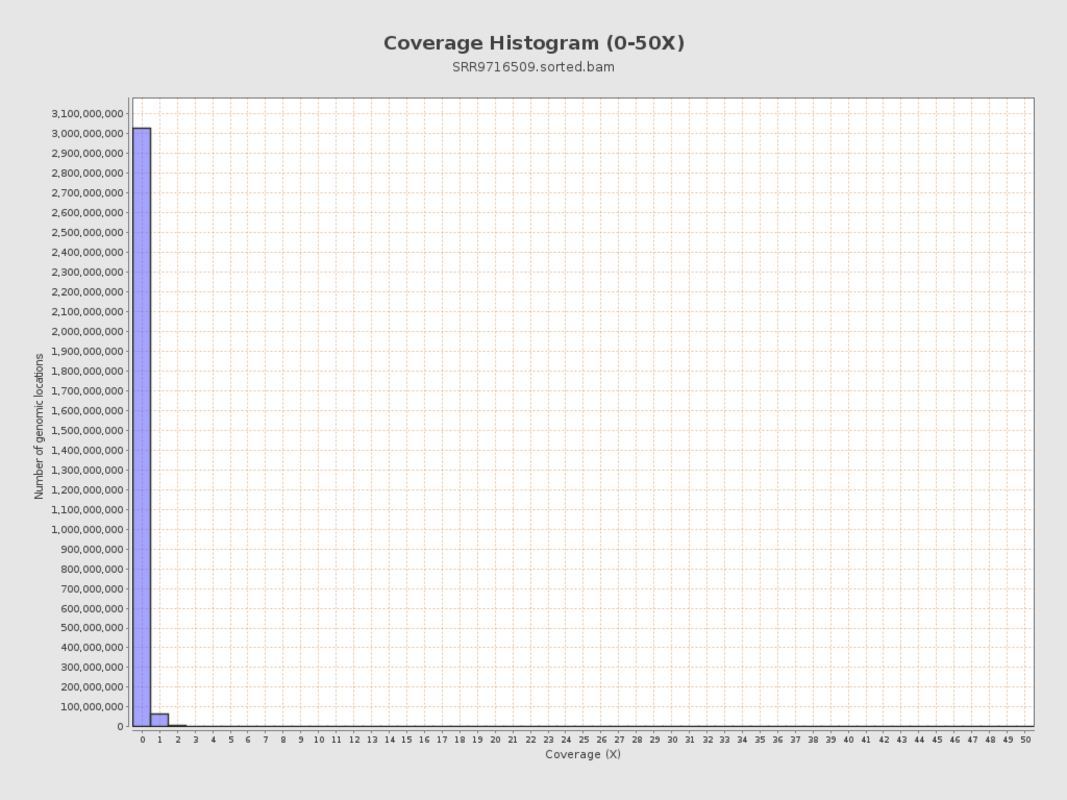
3. Results : Coverage across reference



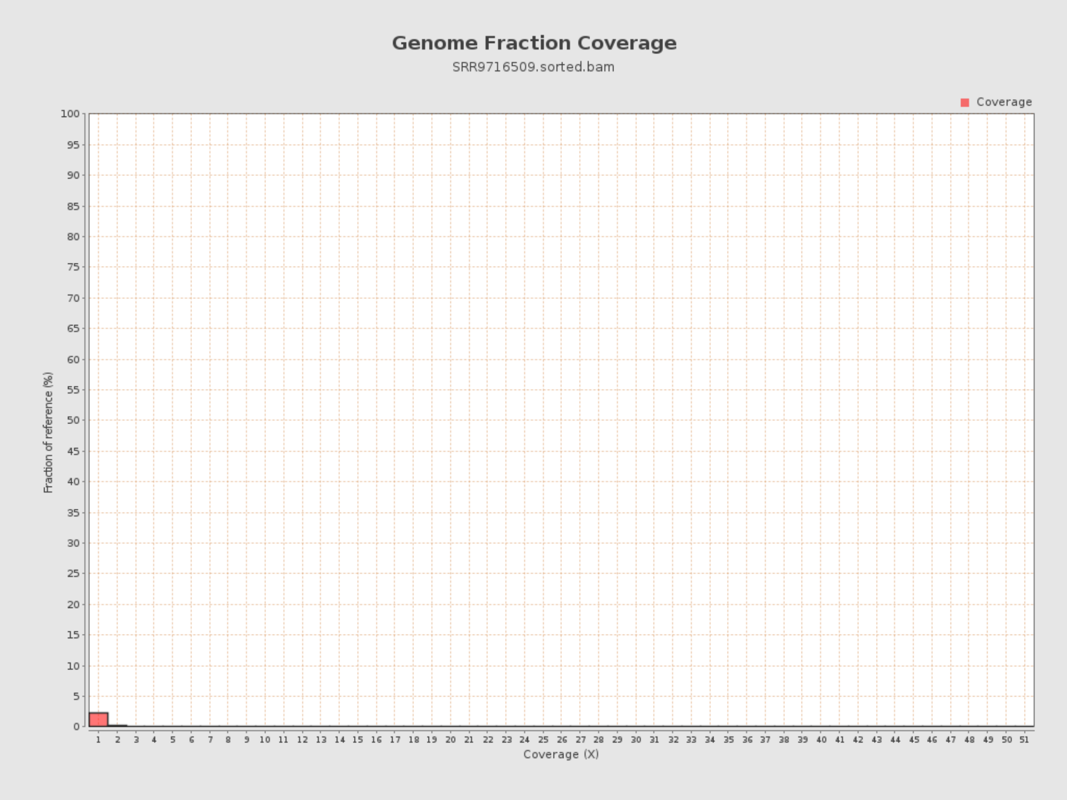
4. Results : Coverage Histogram



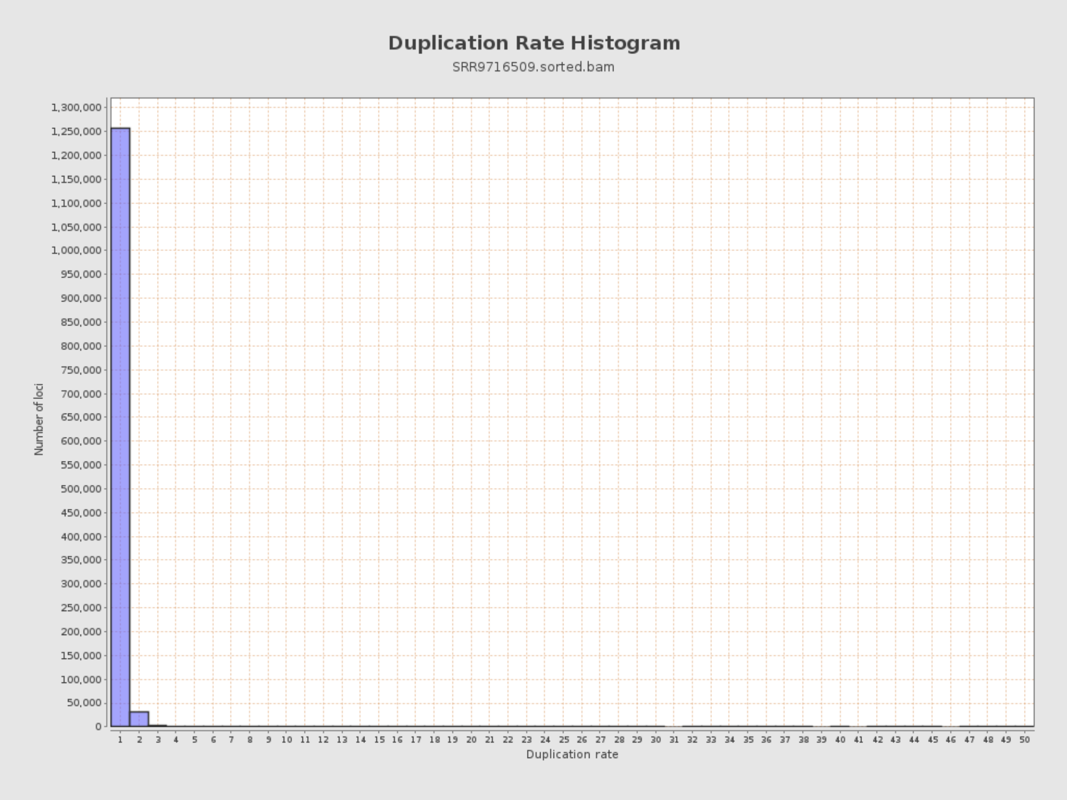
5. Results : Coverage Histogram (0-50X)



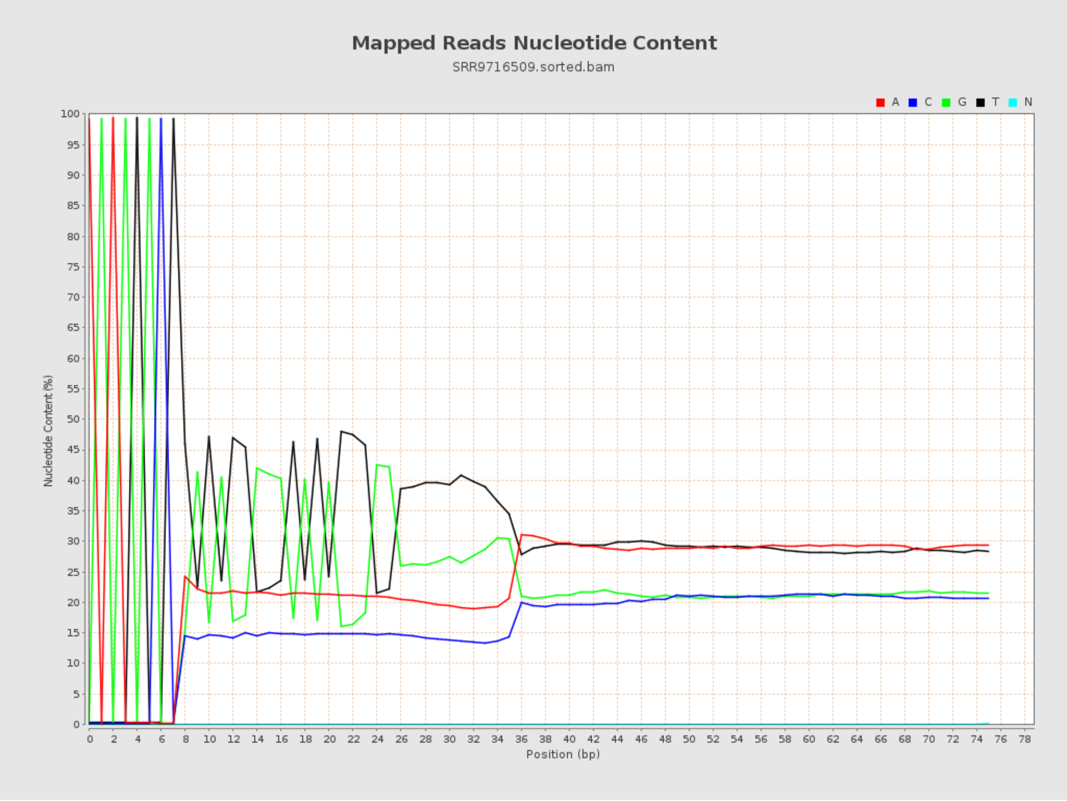
6. Results : Genome Fraction Coverage



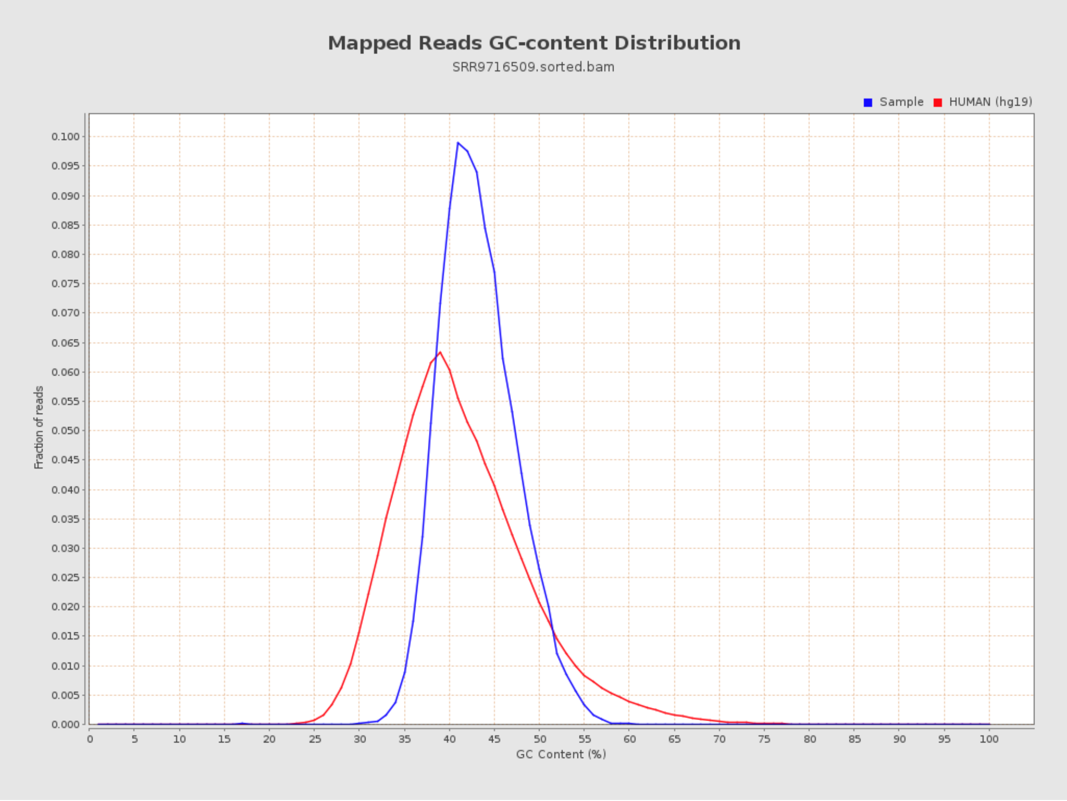
7. Results : Duplication Rate Histogram



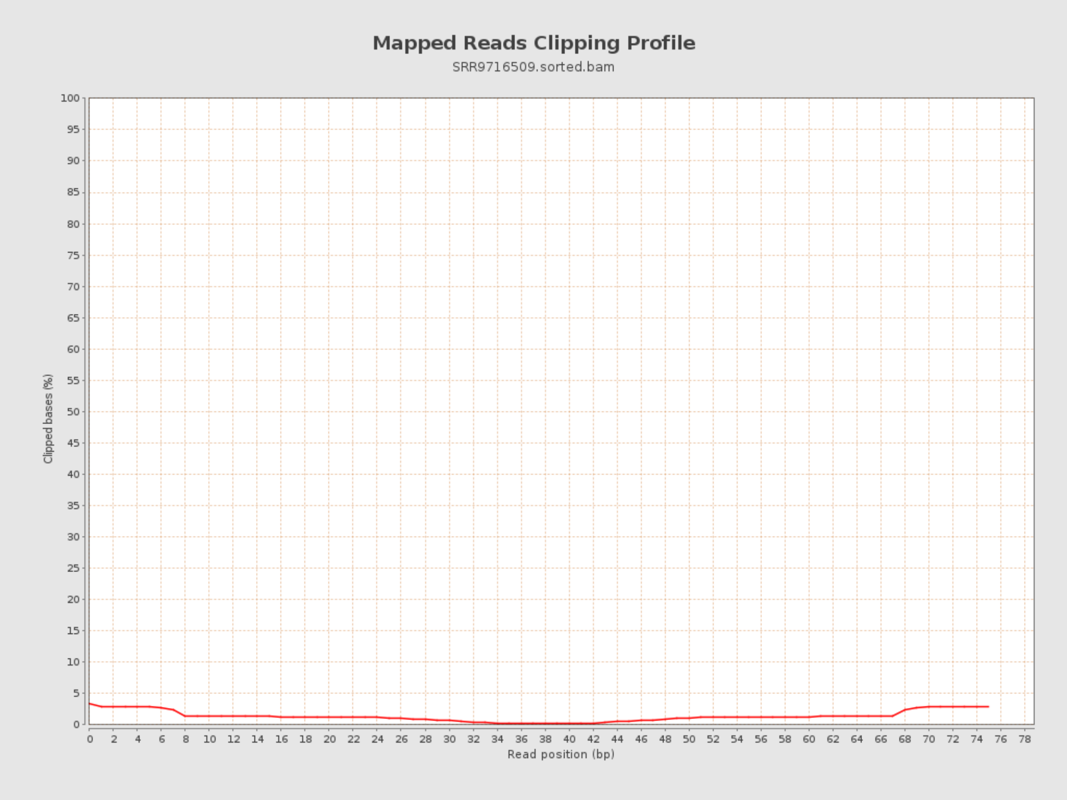
8. Results : Mapped Reads Nucleotide Content



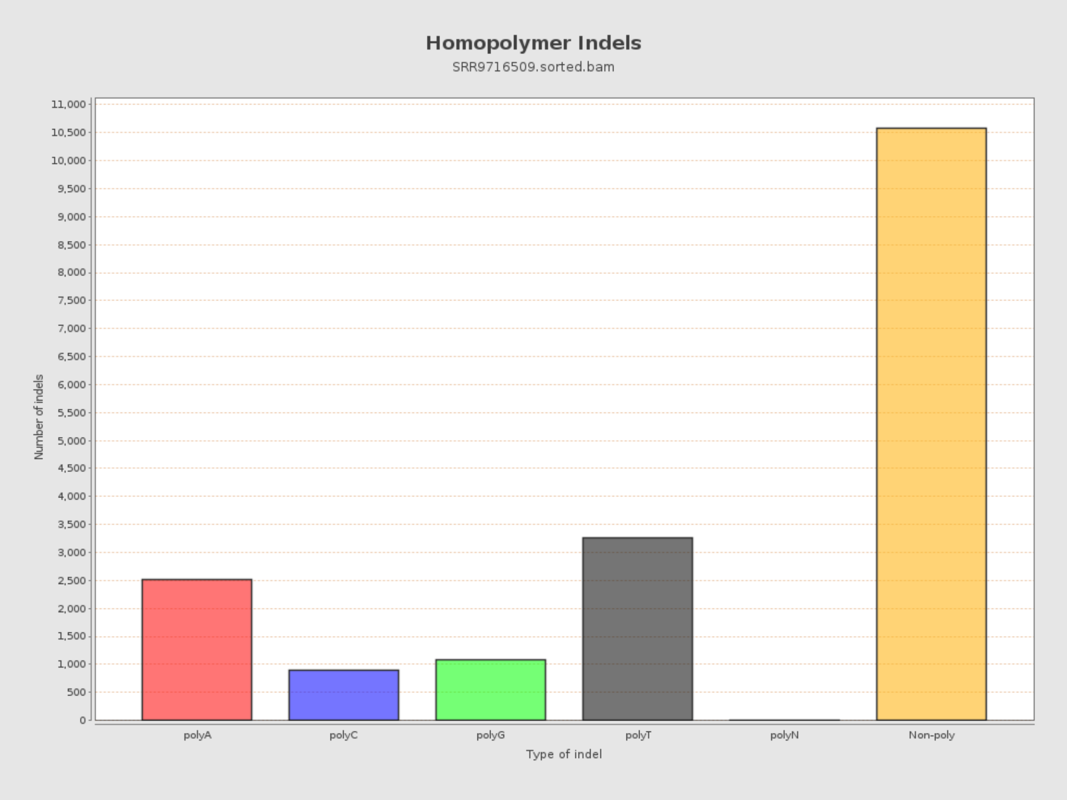
9. Results : Mapped Reads GC-content Distribution



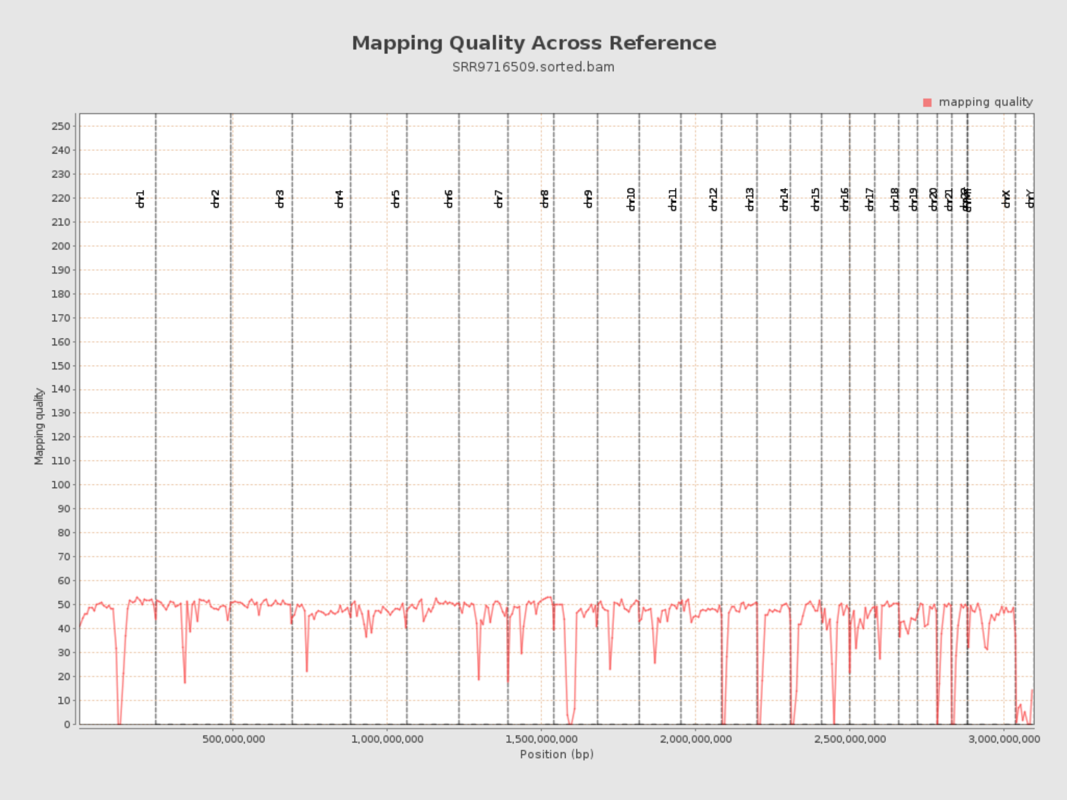
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram