Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:18:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716501.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_SRR9716501 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716501.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:18:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716501.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	727,997
Mapped reads	644,790 / 88.57%
Unmapped reads	83,207 / 11.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,262 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	11,569 / 1.59%
Duplication rate	1.32%
Clipped reads	645,434 / 88.66%

2.2. ACGT Content

Number/percentage of A's	9,537,677 / 25.61%
Number/percentage of C's	7,162,916 / 19.24%
Number/percentage of T's	11,844,809 / 31.81%
Number/percentage of G's	8,691,519 / 23.34%
Number/percentage of N's	348 / 0%
GC Percentage	42.58%

2.3. Coverage

Mean	0.012

Standard Deviation	0.132

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

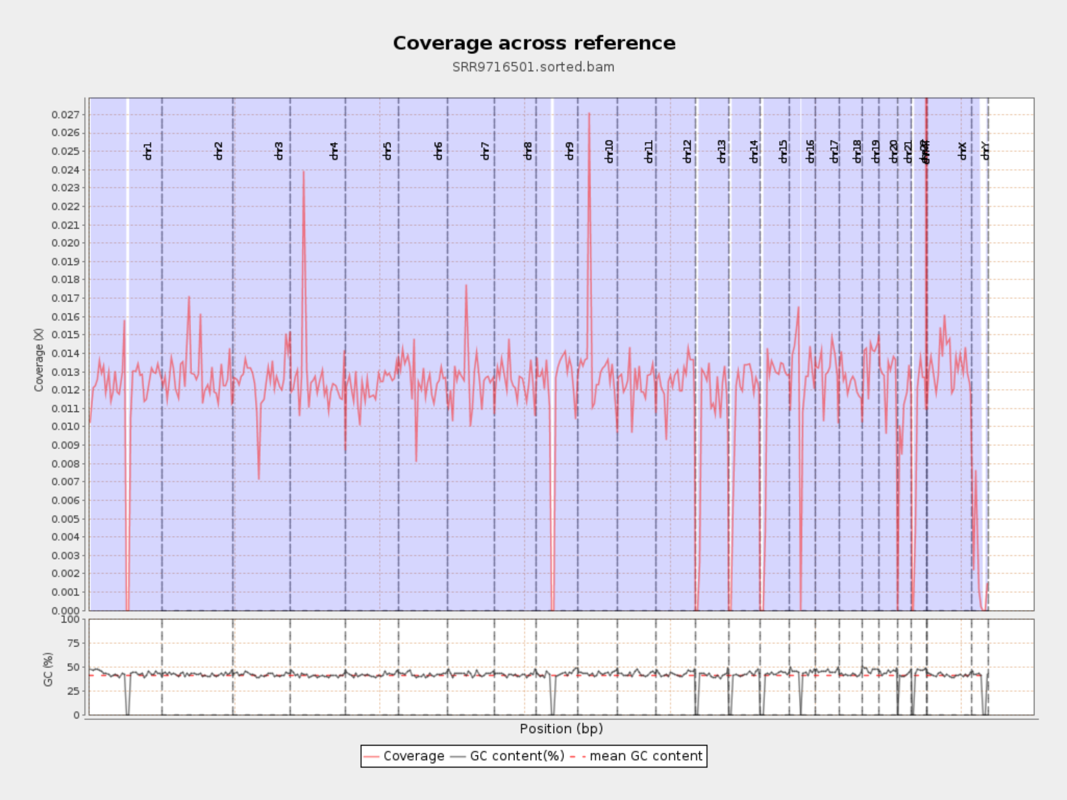
General error rate	0.53%
Mismatches	192,288
Insertions	2,544
Mapped reads with at least one insertion	0.39%
Deletions	7,503
Mapped reads with at least one deletion	1.16%
Homopolymer indels	40.21%

2.6. Chromosome stats

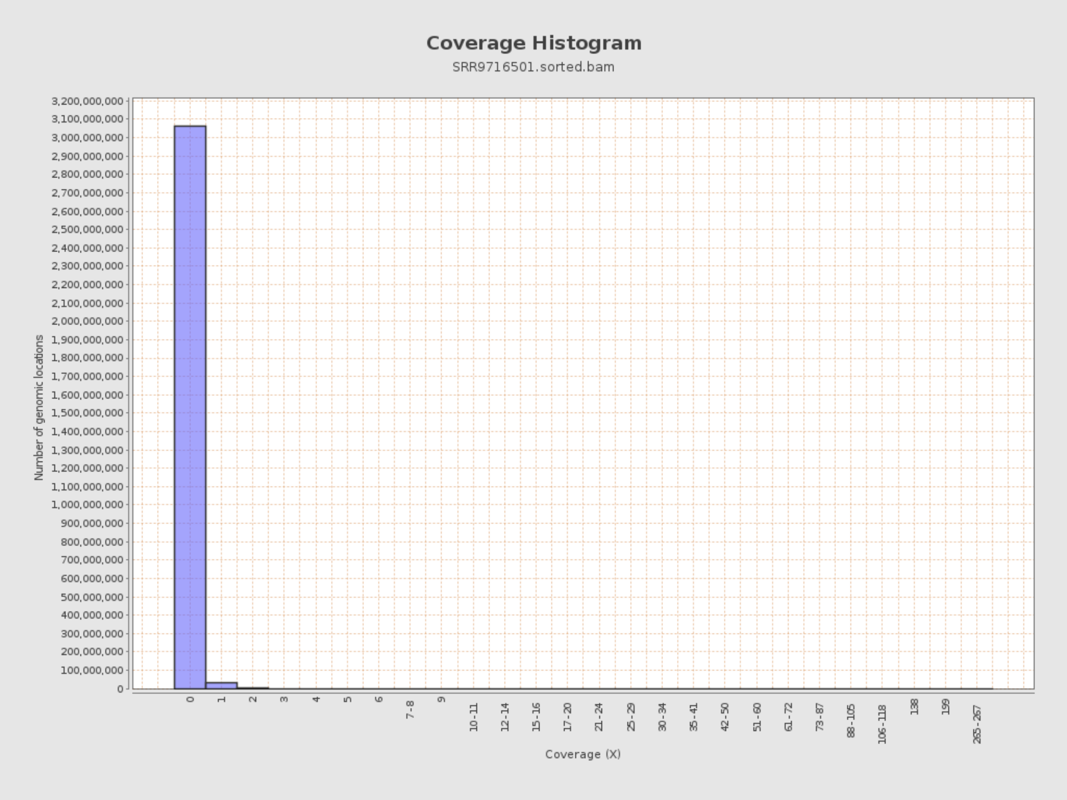
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2936496	0.0118	0.1462
chr2	243199373	3119169	0.0128	0.1696
chr3	198022430	2470687	0.0125	0.1182
chr4	191154276	2421755	0.0127	0.128
chr5	180915260	2210535	0.0122	0.1147
chr6	171115067	2148533	0.0126	0.1232
chr7	159138663	2005378	0.0126	0.1513

chr8	146364022	1831310	0.0125	0.1389
chr9	141213431	1614126	0.0114	0.1211
chr10	135534747	1840526	0.0136	0.1656
chr11	135006516	1671697	0.0124	0.1259
chr12	133851895	1678789	0.0125	0.1169
chr13	115169878	1168375	0.0101	0.105
chr14	107349540	1134618	0.0106	0.1101
chr15	102531392	1096129	0.0107	0.1085
chr16	90354753	1110930	0.0123	0.1203
chr17	81195210	1055870	0.013	0.1218
chr18	78077248	975246	0.0125	0.1647
chr19	59128983	814133	0.0138	0.1465
chr20	63025520	798114	0.0127	0.1186
chr21	48129895	484350	0.0101	0.1145
chr22	51304566	451604	0.0088	0.0982
chrMT	16571	6074	0.3665	0.6469
chrX	155270560	2077668	0.0134	0.1243
chrY	59373566	127441	0.0021	0.0789

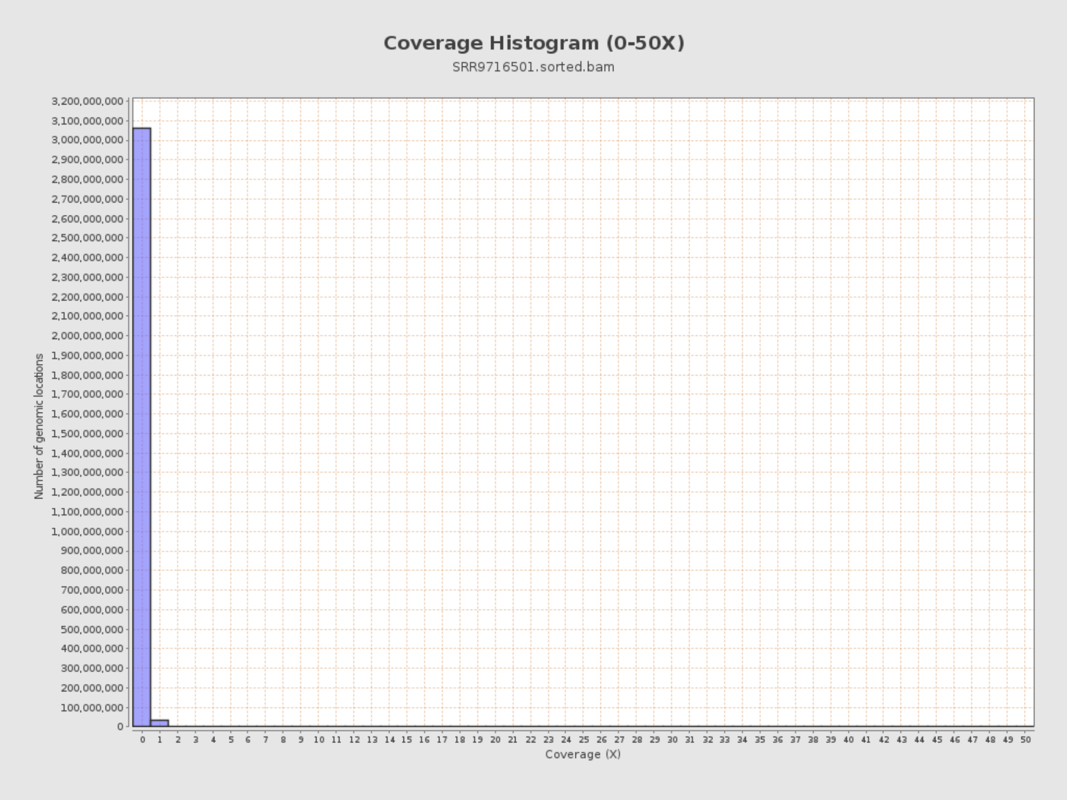
3. Results : Coverage across reference



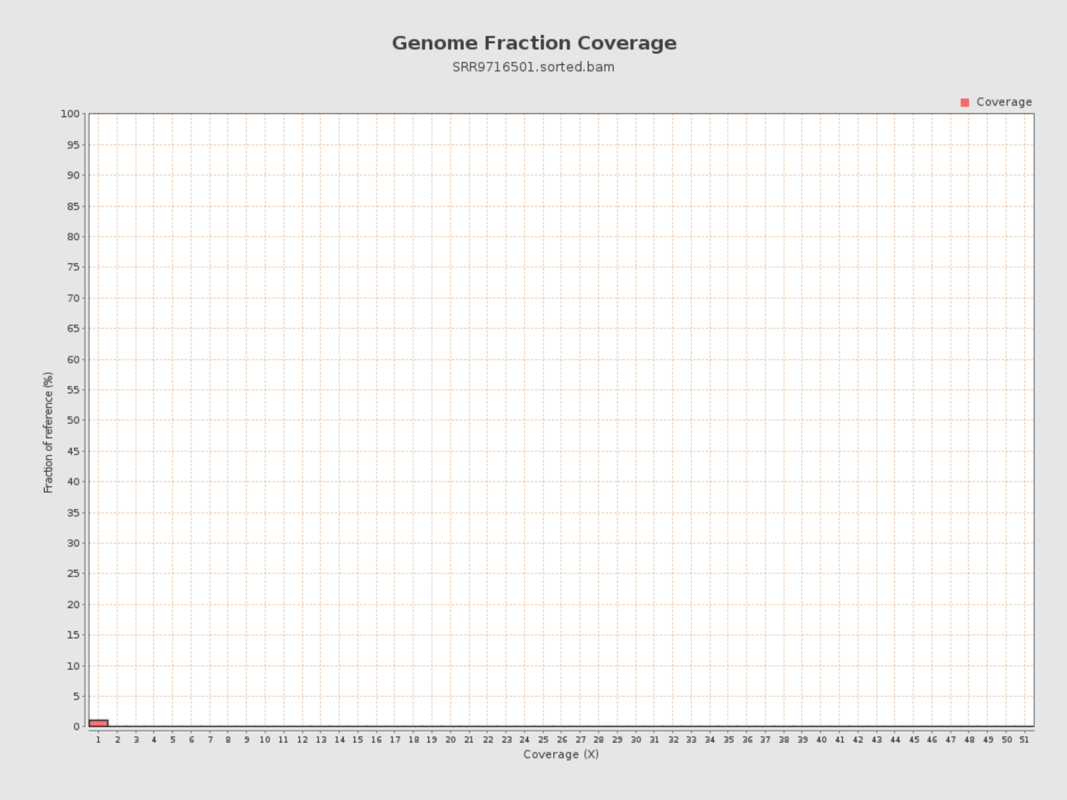
4. Results : Coverage Histogram



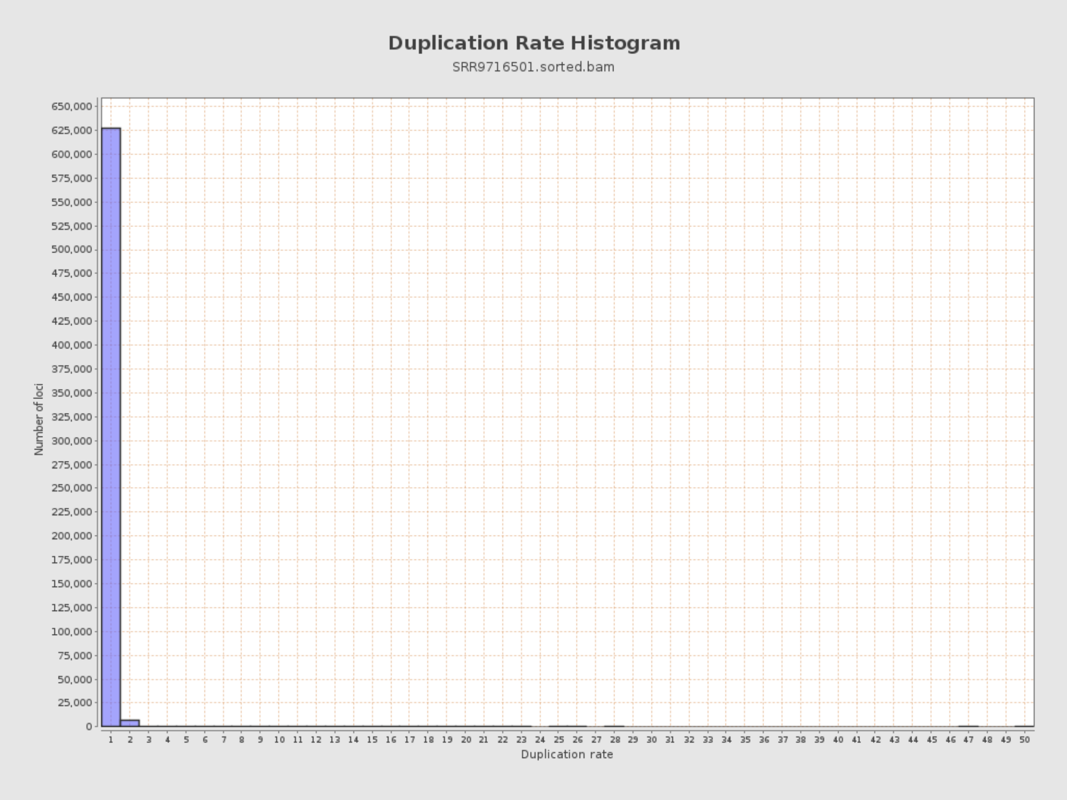
5. Results : Coverage Histogram (0-50X)



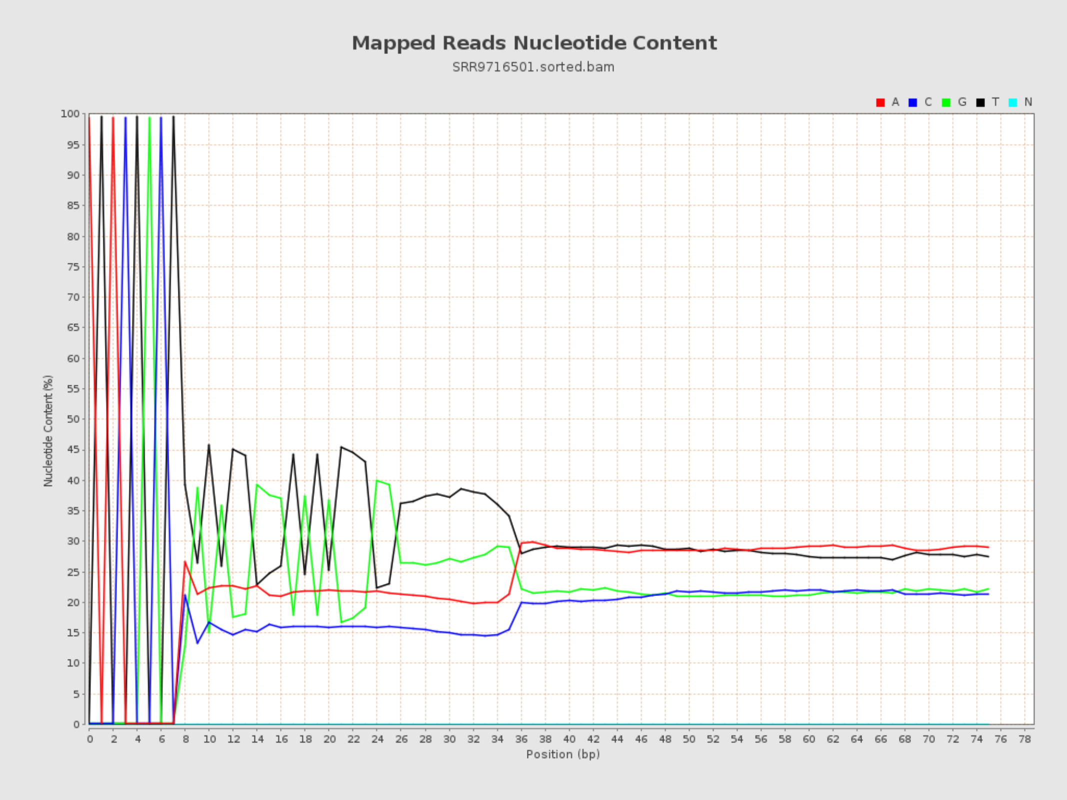
6. Results : Genome Fraction Coverage



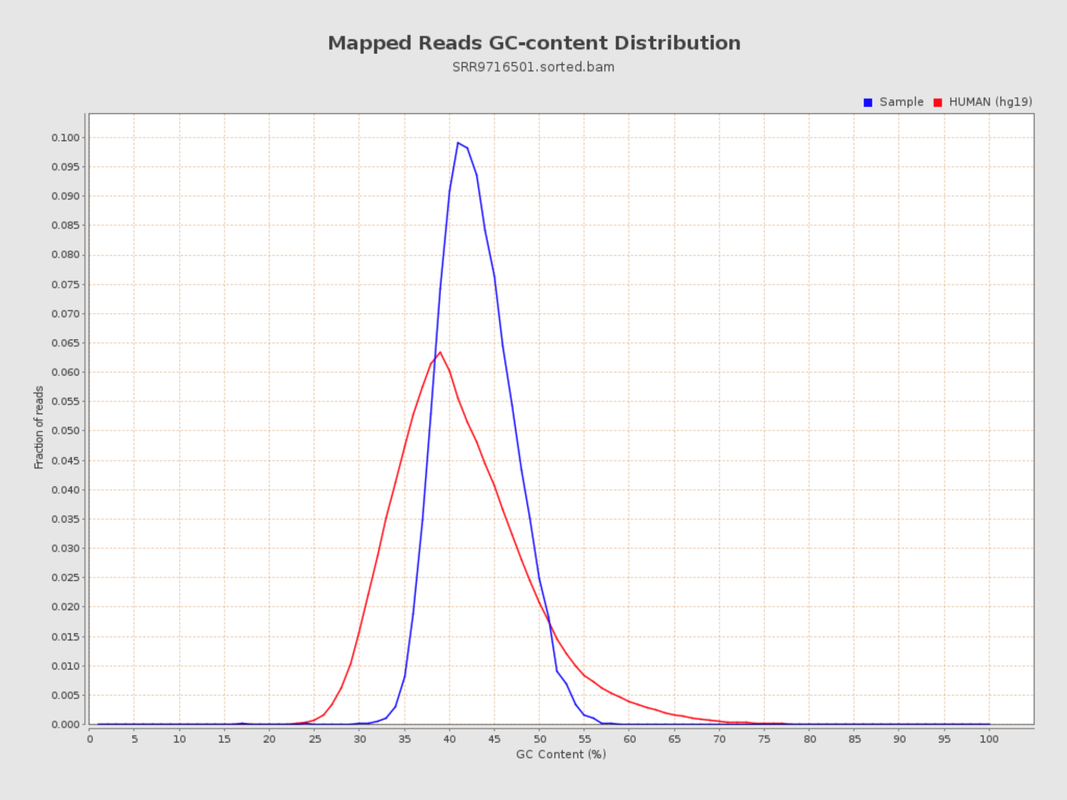
7. Results : Duplication Rate Histogram



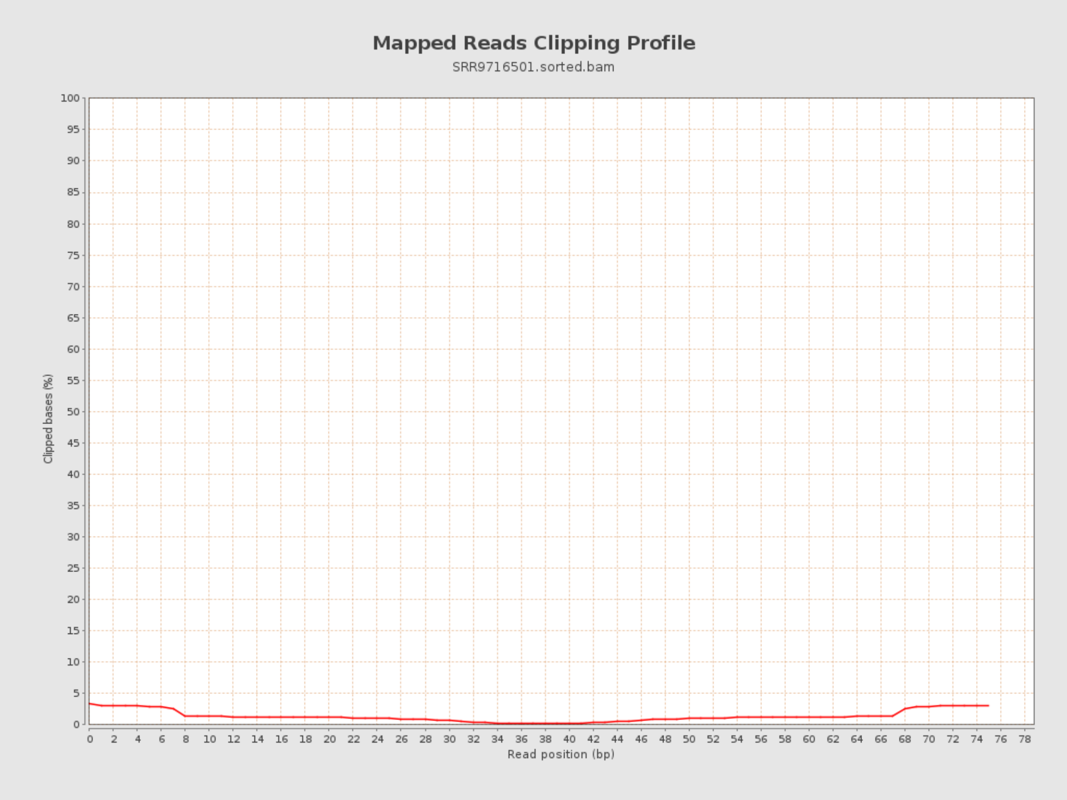
8. Results : Mapped Reads Nucleotide Content



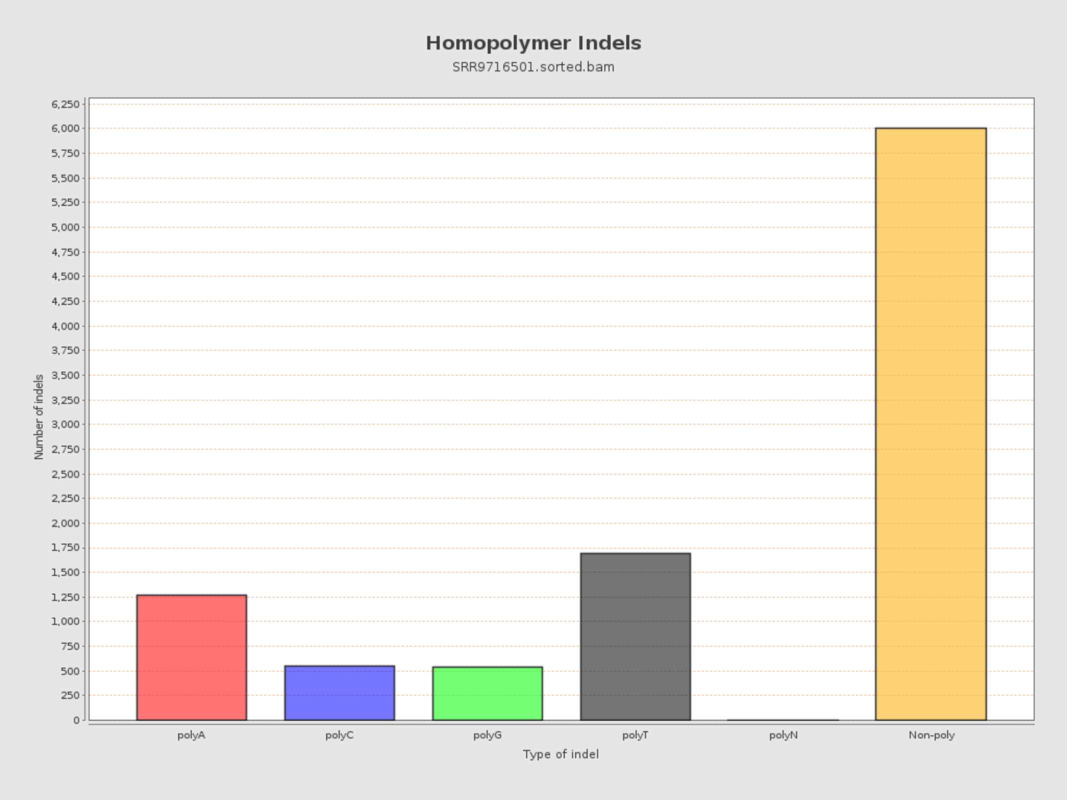
9. Results : Mapped Reads GC-content Distribution



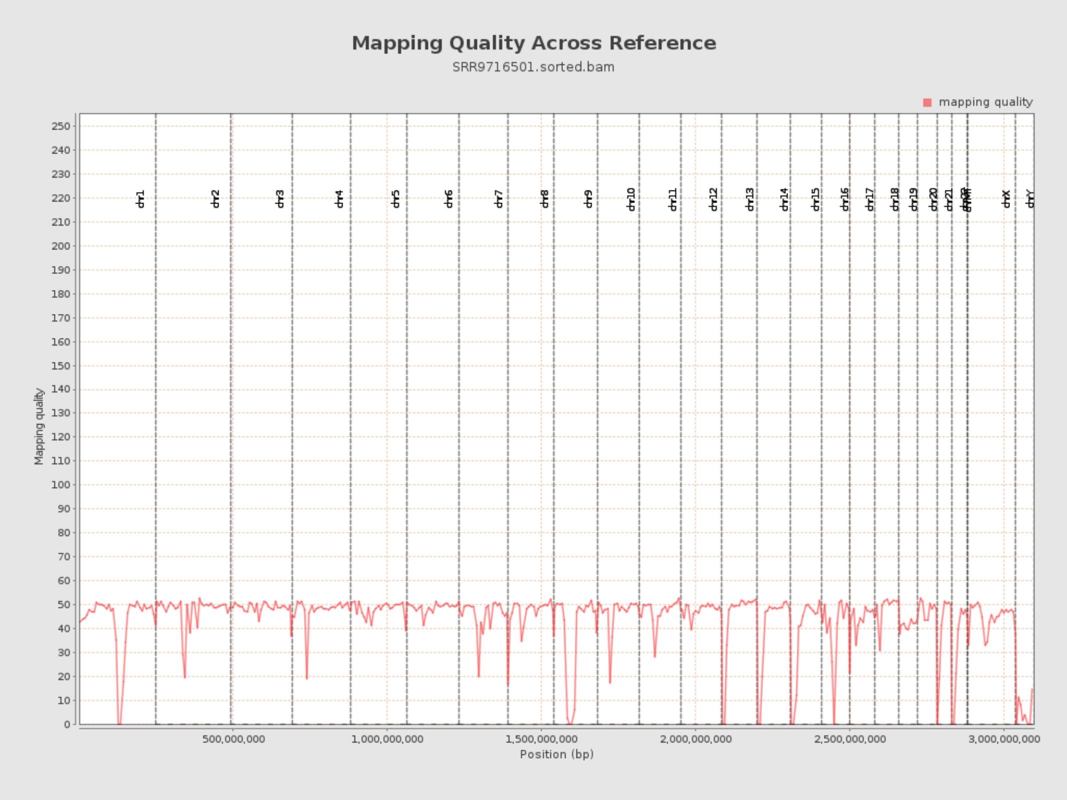
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram