Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:43:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716269.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_SRR9716269 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716269.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:42:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716269.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	810,634
Mapped reads	600,807 / 74.12%
Unmapped reads	209,827 / 25.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	671 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	33,110 / 4.08%
Duplication rate	4.92%
Clipped reads	600,511 / 74.08%

2.2. ACGT Content

Number/percentage of A's	6,936,715 / 21.86%
Number/percentage of C's	5,890,807 / 18.57%
Number/percentage of T's	10,285,380 / 32.42%
Number/percentage of G's	8,613,756 / 27.15%
Number/percentage of N's	640 / 0%
GC Percentage	45.72%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.123

2.4. Mapping Quality

Mean Mapping Quality	42.72

2.5. Mismatches and indels

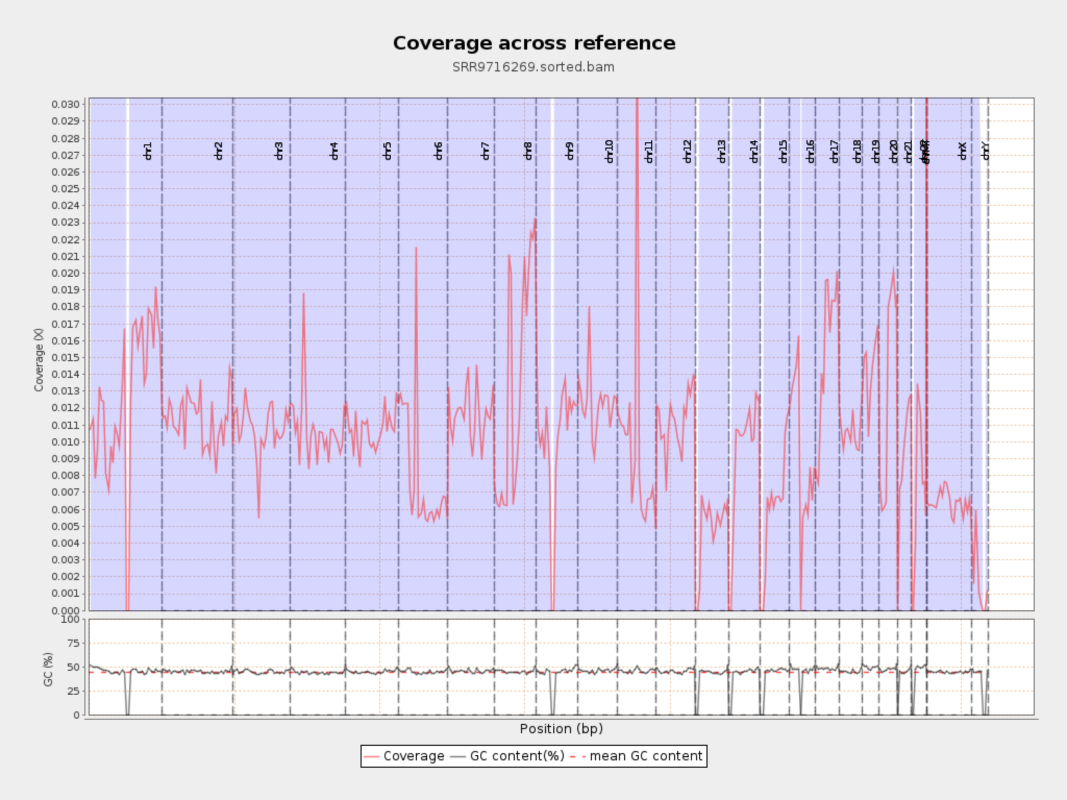
General error rate	0.7%
Mismatches	218,865
Insertions	1,761
Mapped reads with at least one insertion	0.29%
Deletions	4,960
Mapped reads with at least one deletion	0.82%
Homopolymer indels	41.35%

2.6. Chromosome stats

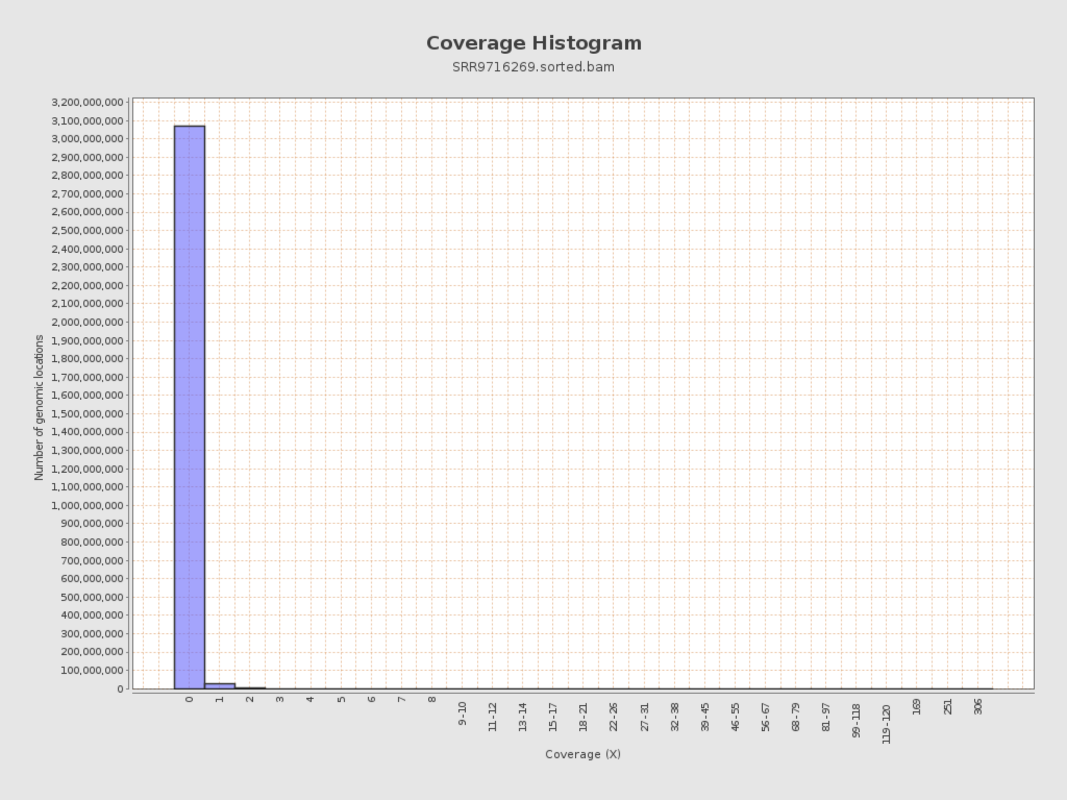
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3114575	0.0125	0.1482
chr2	243199373	2753033	0.0113	0.1726
chr3	198022430	2127333	0.0107	0.1137
chr4	191154276	2041205	0.0107	0.1173
chr5	180915260	1941653	0.0107	0.1133
chr6	171115067	1385312	0.0081	0.1097
chr7	159138663	1845727	0.0116	0.1325

chr8	146364022	1983009	0.0135	0.1315
chr9	141213431	1393594	0.0099	0.1131
chr10	135534747	1660761	0.0123	0.1342
chr11	135006516	1351807	0.01	0.117
chr12	133851895	1502091	0.0112	0.1163
chr13	115169878	546370	0.0047	0.0768
chr14	107349540	982907	0.0092	0.1049
chr15	102531392	624969	0.0061	0.0857
chr16	90354753	829411	0.0092	0.1099
chr17	81195210	1270700	0.0156	0.1435
chr18	78077248	819465	0.0105	0.1229
chr19	59128983	845690	0.0143	0.1466
chr20	63025520	825512	0.0131	0.1284
chr21	48129895	440070	0.0091	0.1089
chr22	51304566	352490	0.0069	0.0926
chrMT	16571	1051	0.0634	0.252
chrX	155270560	1000333	0.0064	0.0904
chrY	59373566	96676	0.0016	0.0545

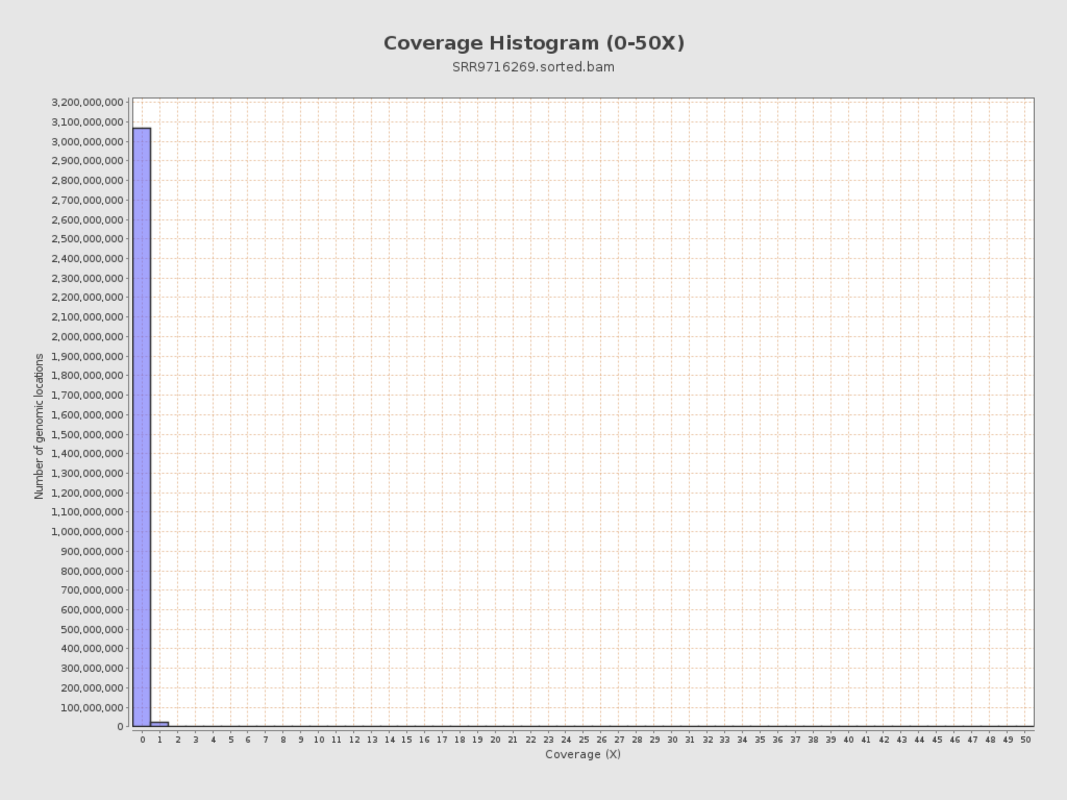
3. Results : Coverage across reference



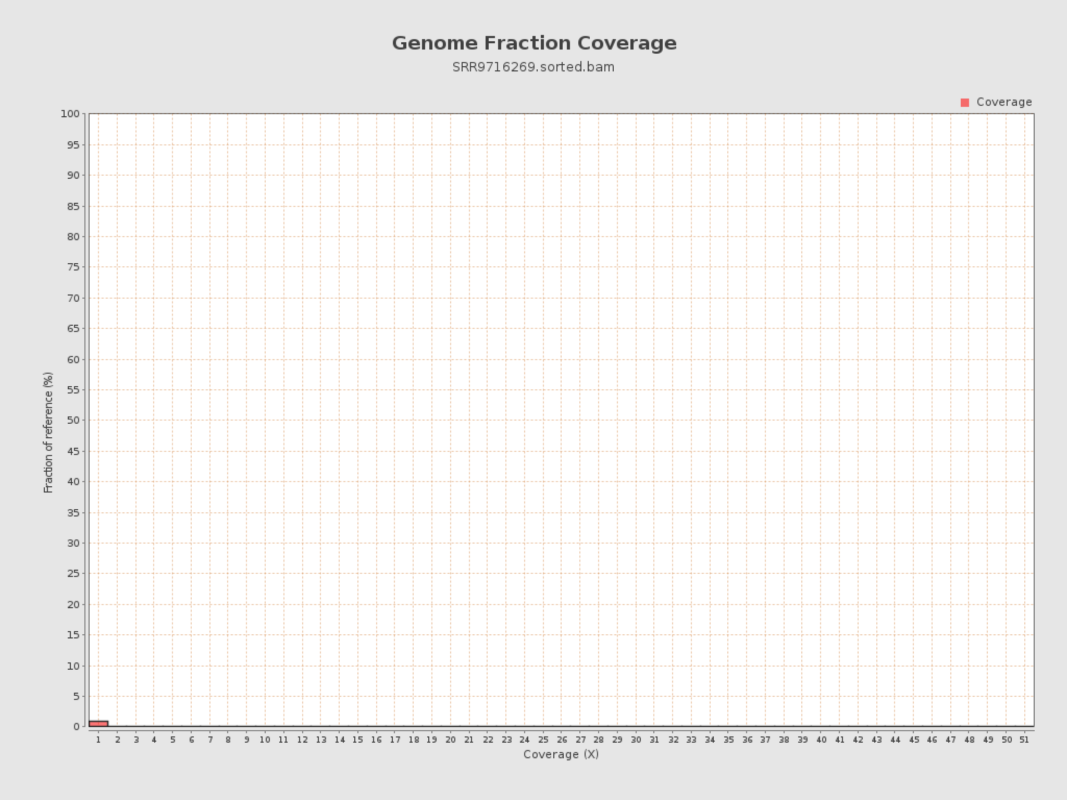
4. Results : Coverage Histogram



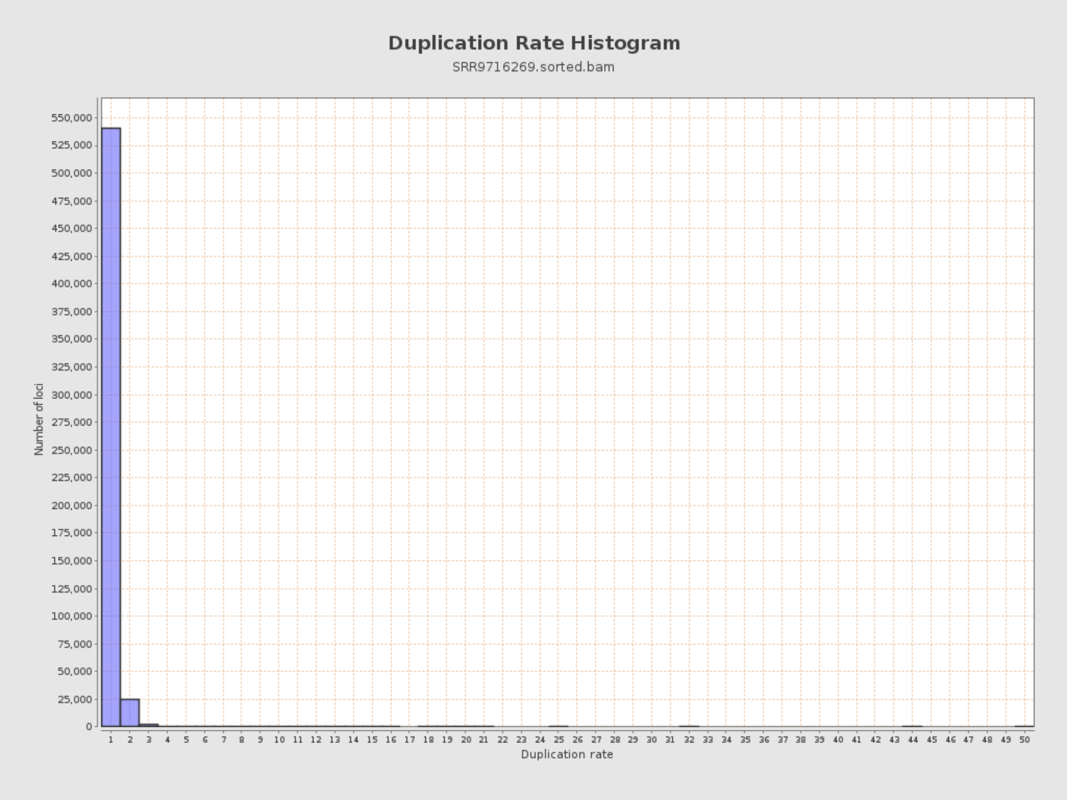
5. Results : Coverage Histogram (0-50X)



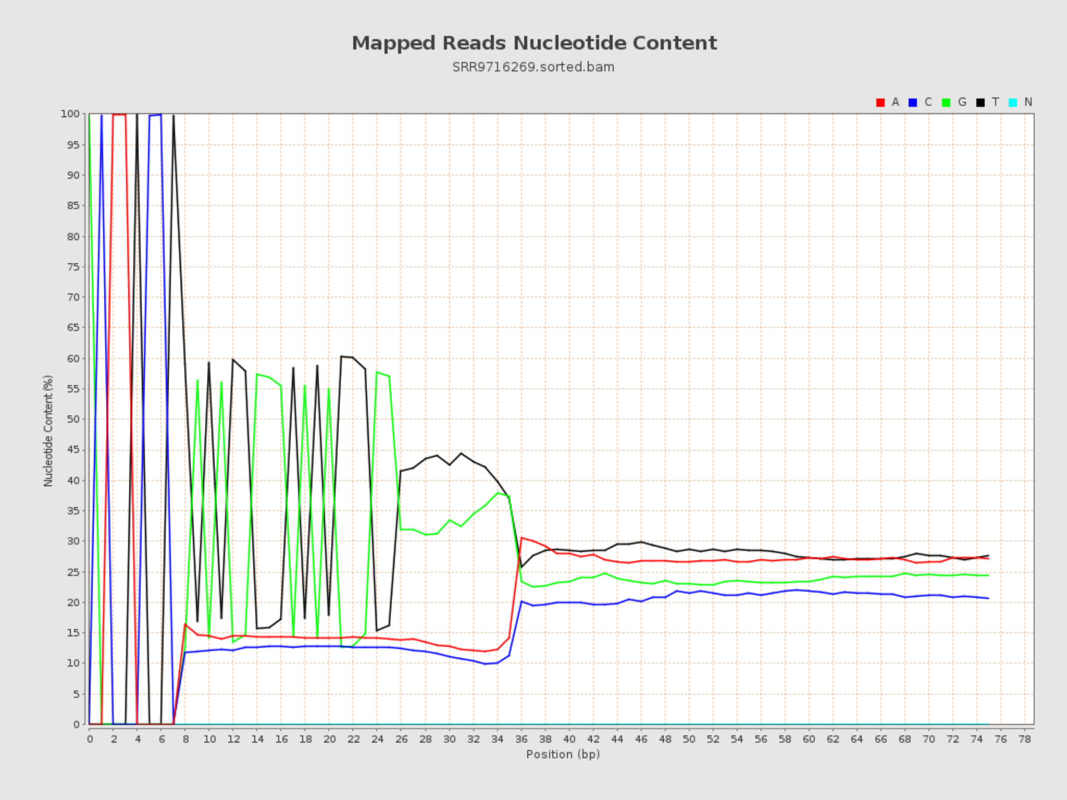
6. Results : Genome Fraction Coverage



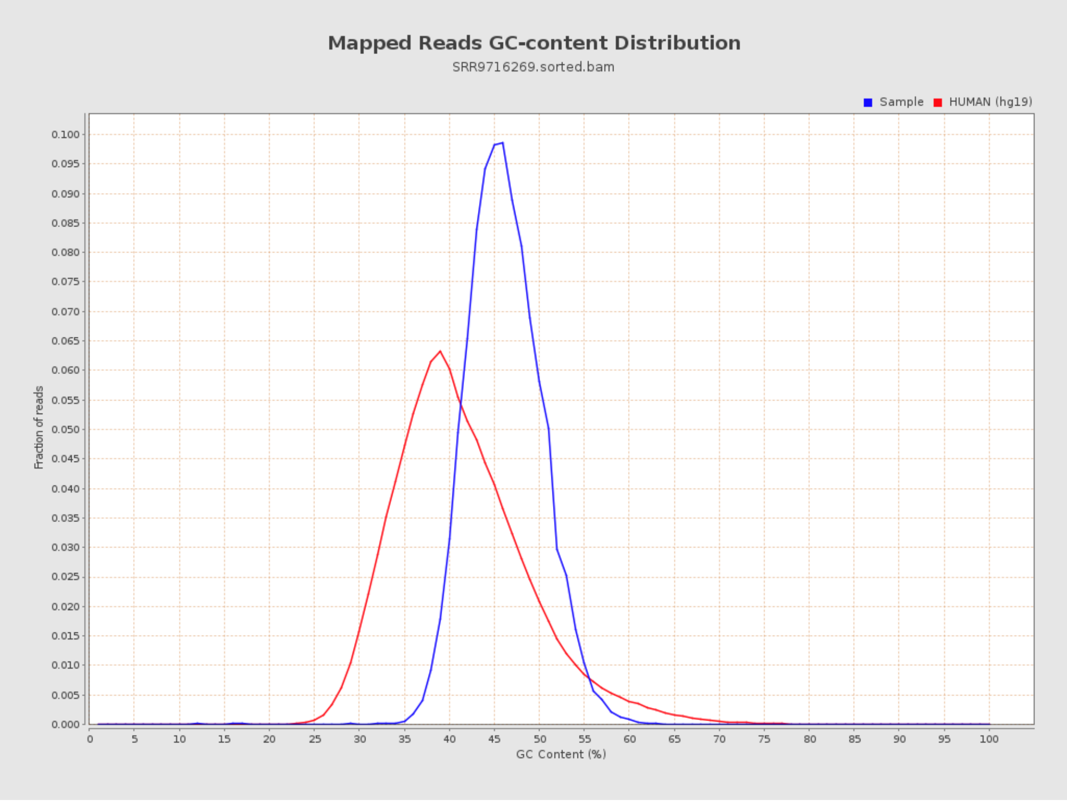
7. Results : Duplication Rate Histogram



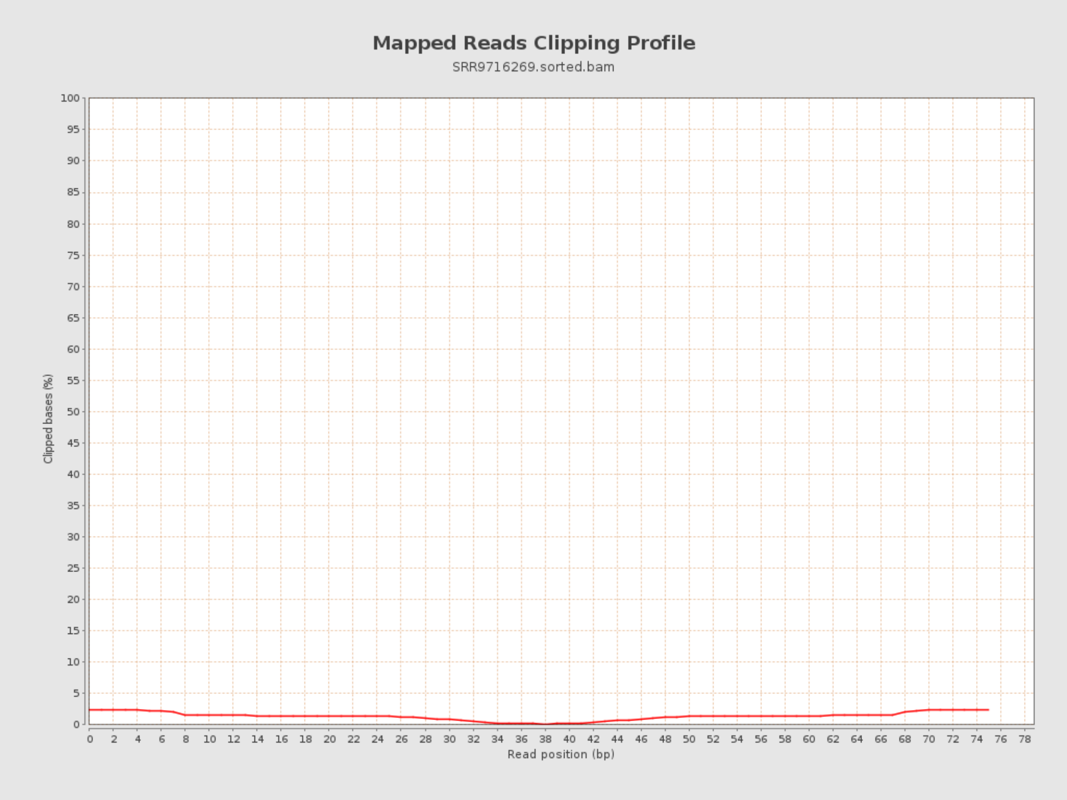
8. Results : Mapped Reads Nucleotide Content



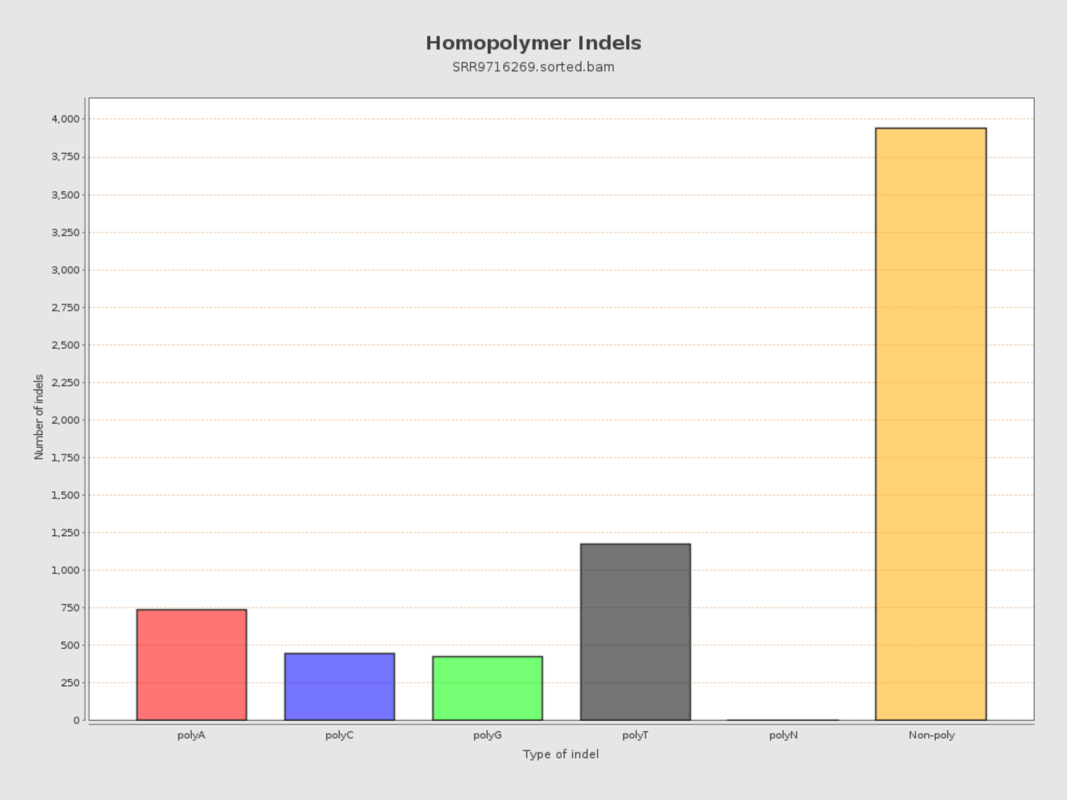
9. Results : Mapped Reads GC-content Distribution



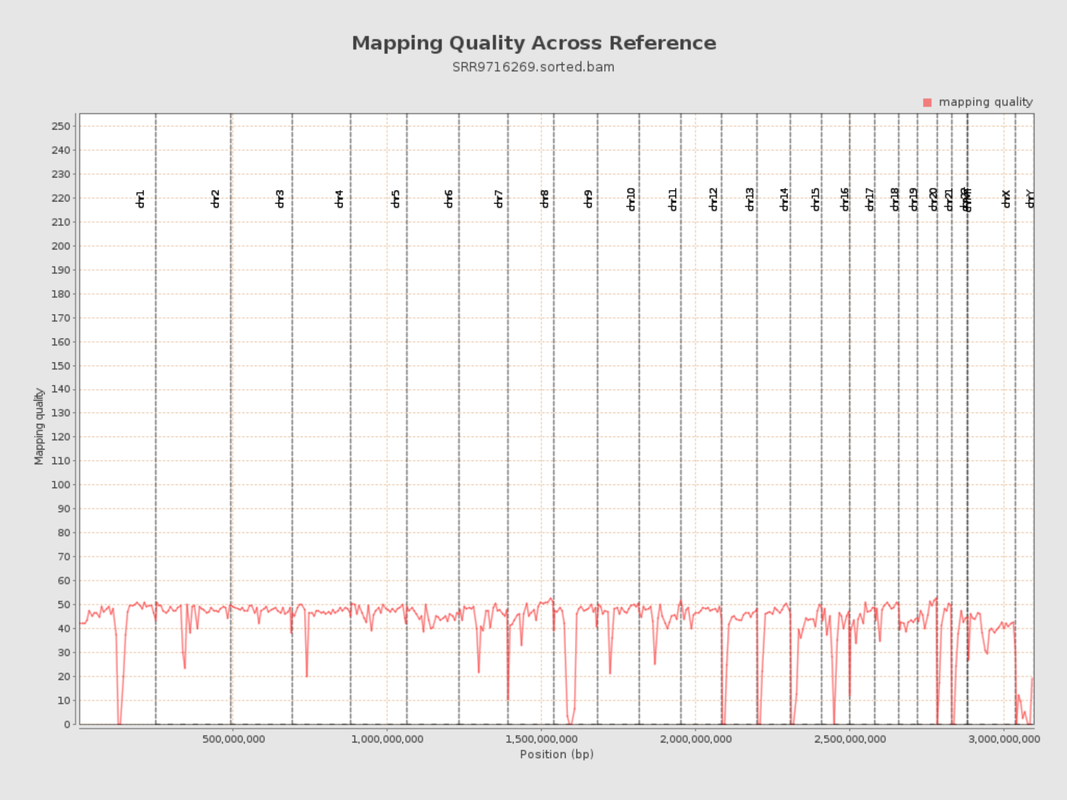
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram