Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:08:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716169.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_SRR9716169 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716169.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:08:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,167,737
Mapped reads	2,957,128 / 93.35%
Unmapped reads	210,609 / 6.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	68,315 / 2.16%
Read min/max/mean length	30 / 101 / 101.79
Duplicated reads (estimated)	117,865 / 3.72%
Duplication rate	2.71%
Clipped reads	3,023,081 / 95.43%

2.2. ACGT Content

Number/percentage of A's	59,181,436 / 26.33%
Number/percentage of C's	47,955,989 / 21.34%
Number/percentage of T's	65,286,884 / 29.05%
Number/percentage of G's	52,303,654 / 23.27%
Number/percentage of N's	26,690 / 0.01%
GC Percentage	44.61%

2.3. Coverage

Mean	0.0726

Standard Deviation	0.5742

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

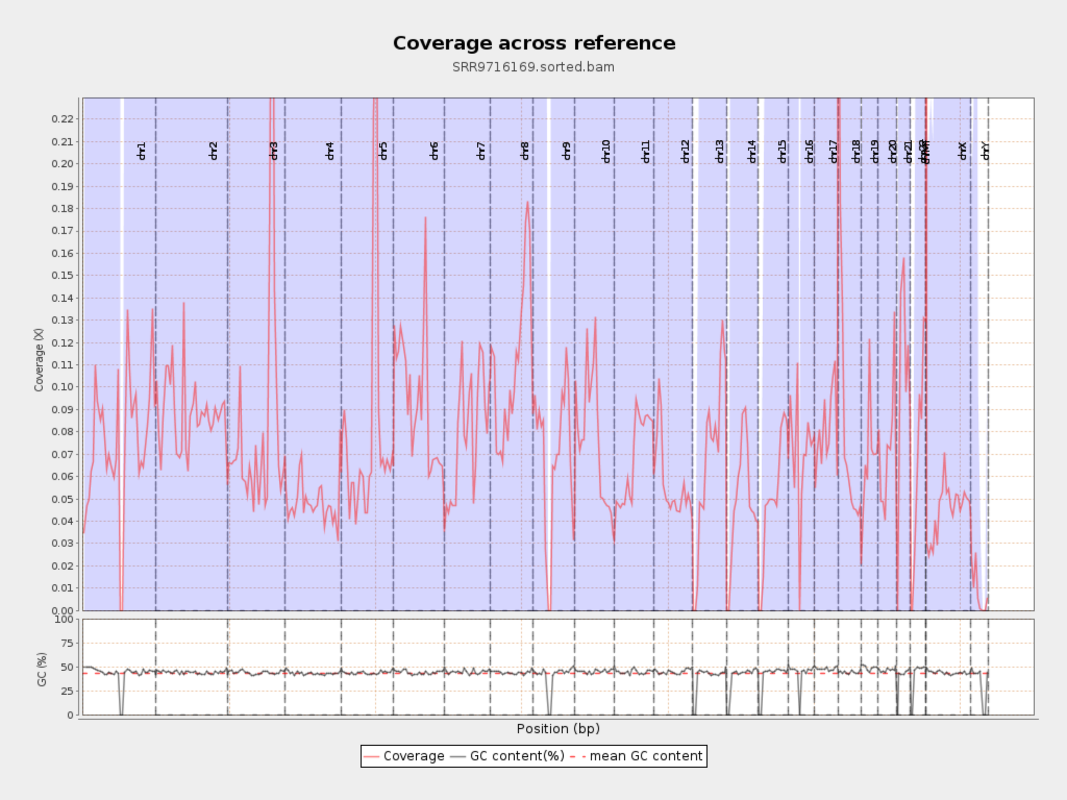
General error rate	0.78%
Mismatches	1,715,487
Insertions	17,788
Mapped reads with at least one insertion	0.59%
Deletions	46,908
Mapped reads with at least one deletion	1.56%
Homopolymer indels	40.75%

2.6. Chromosome stats

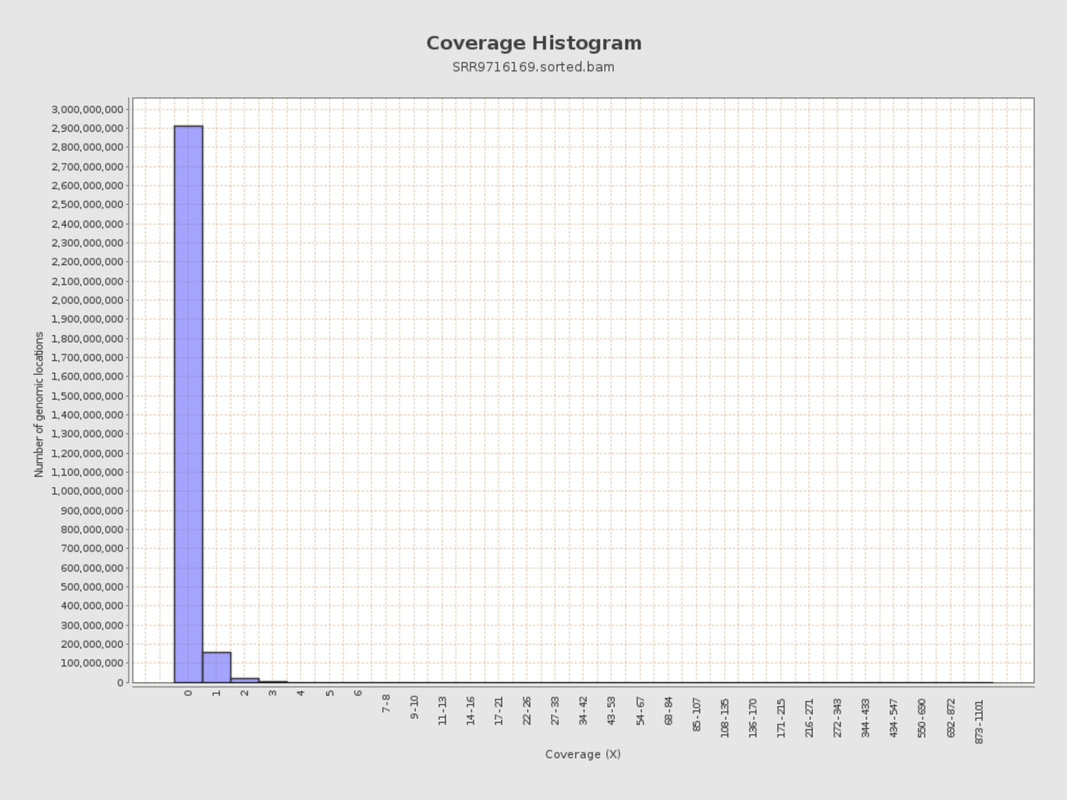
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18741585	0.0752	0.9759
chr2	243199373	21516190	0.0885	0.8742
chr3	198022430	16570384	0.0837	0.3517
chr4	191154276	9313678	0.0487	0.2809
chr5	180915260	14230145	0.0787	0.3348
chr6	171115067	16132470	0.0943	0.4369
chr7	159138663	12607446	0.0792	0.8133

chr8	146364022	16256706	0.1111	0.6718
chr9	141213431	9730318	0.0689	0.5118
chr10	135534747	10513375	0.0776	0.5662
chr11	135006516	9160356	0.0679	0.4435
chr12	133851895	7667159	0.0573	0.2829
chr13	115169878	7917786	0.0687	0.3063
chr14	107349540	5266482	0.0491	0.3067
chr15	102531392	5075607	0.0495	0.2613
chr16	90354753	6277714	0.0695	0.365
chr17	81195210	6622116	0.0816	0.4087
chr18	78077248	6803780	0.0871	1.0527
chr19	59128983	4105799	0.0694	0.7569
chr20	63025520	4617185	0.0733	0.3614
chr21	48129895	4815079	0.1	0.3931
chr22	51304566	3345732	0.0652	0.3069
chrMT	16571	67621	4.0807	3.4536
chrX	155270560	6994134	0.045	0.3295
chrY	59373566	487920	0.0082	0.2291

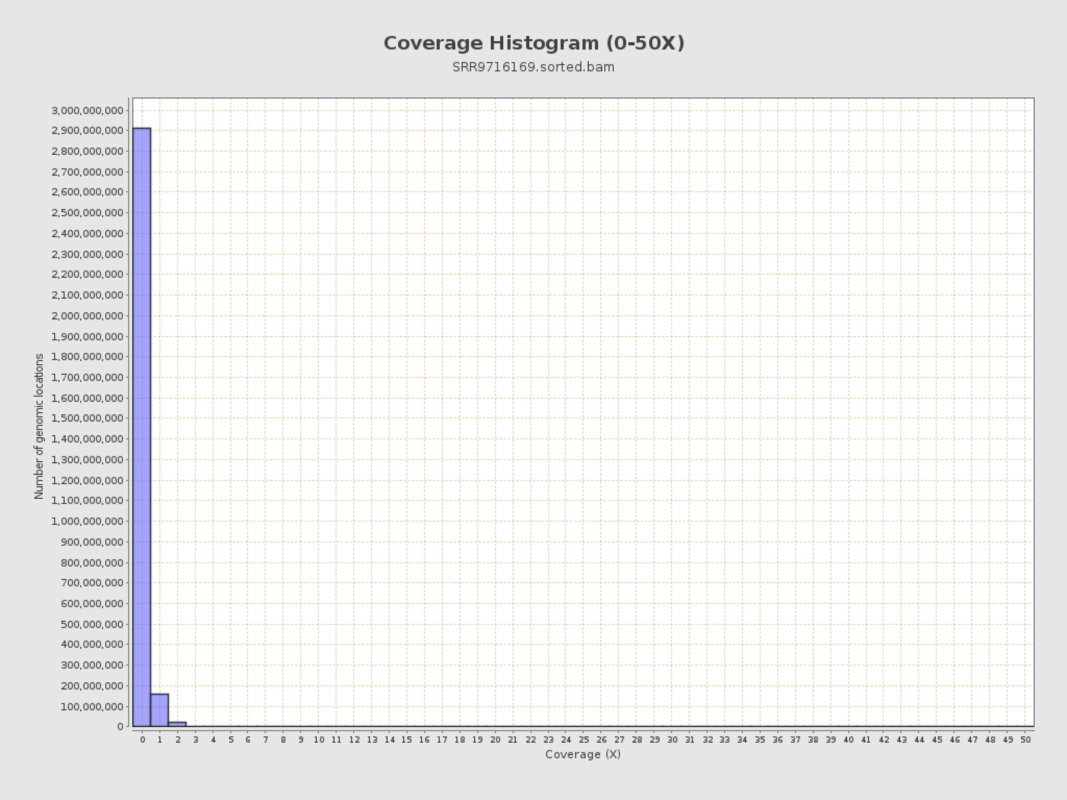
3. Results : Coverage across reference



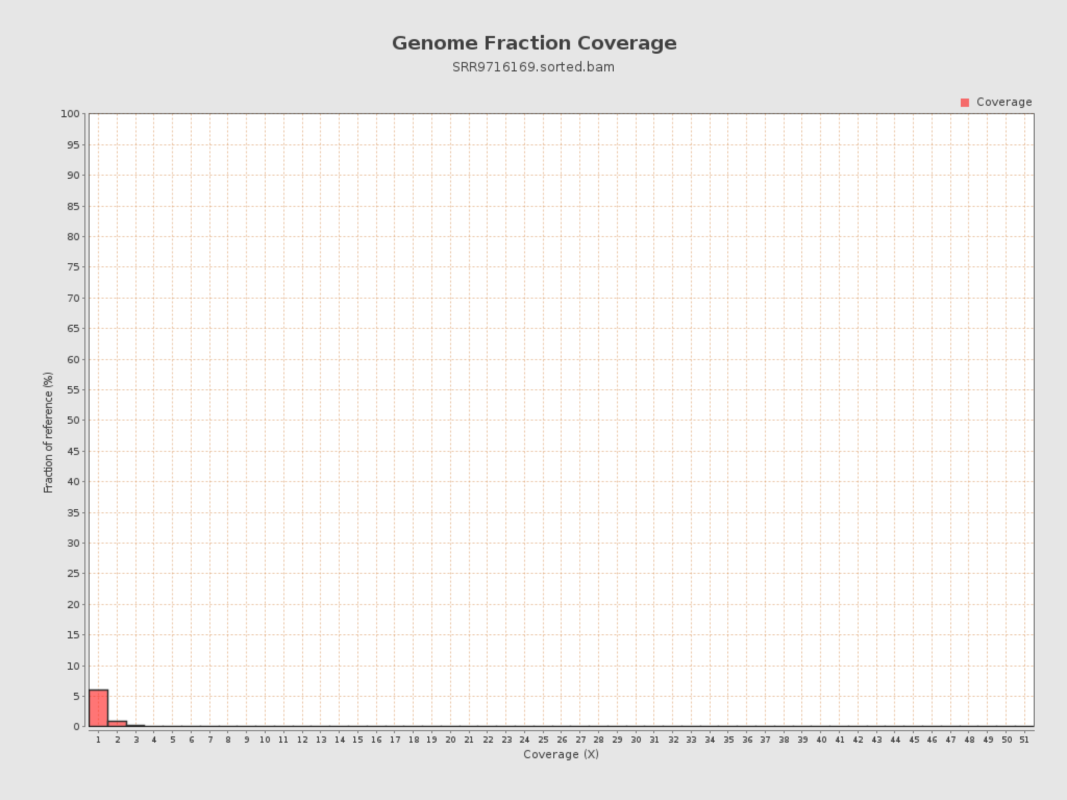
4. Results : Coverage Histogram



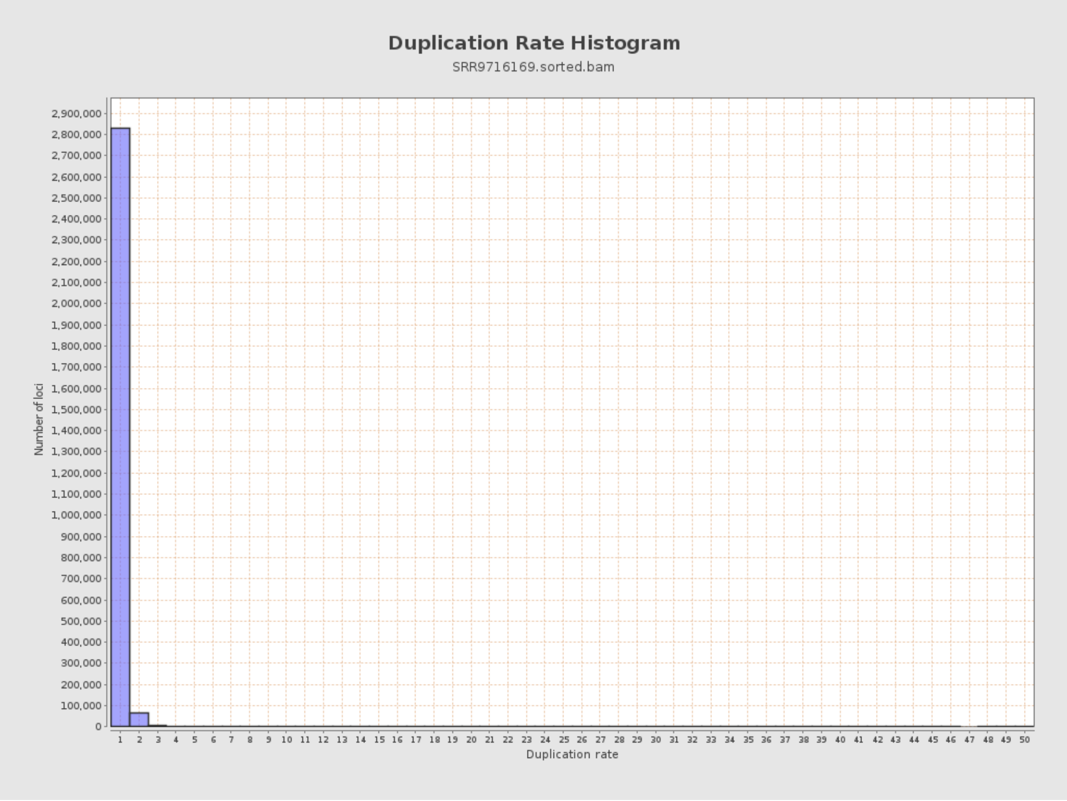
5. Results : Coverage Histogram (0-50X)



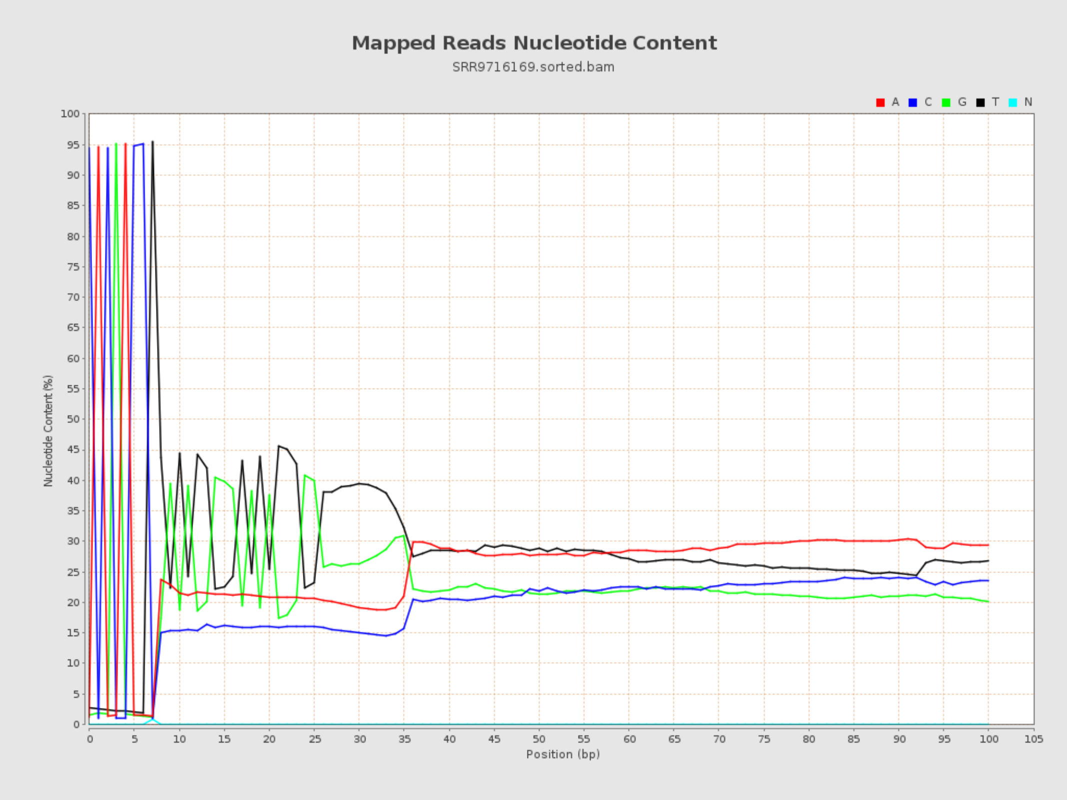
6. Results : Genome Fraction Coverage



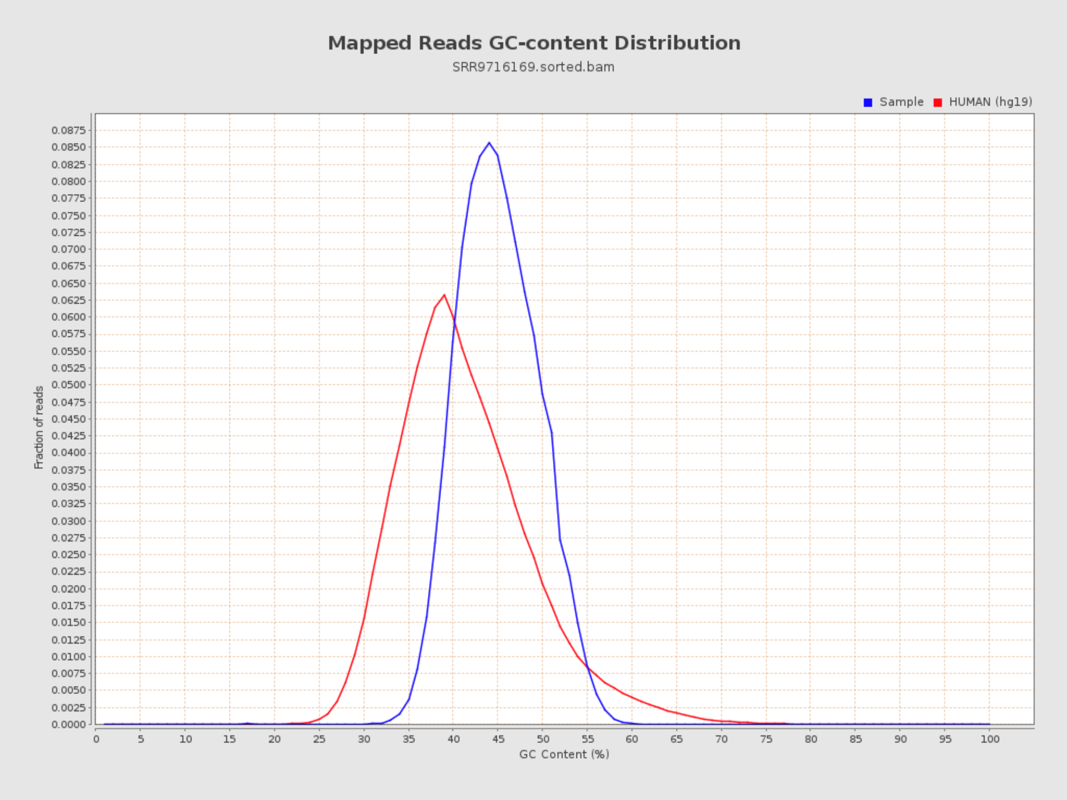
7. Results : Duplication Rate Histogram



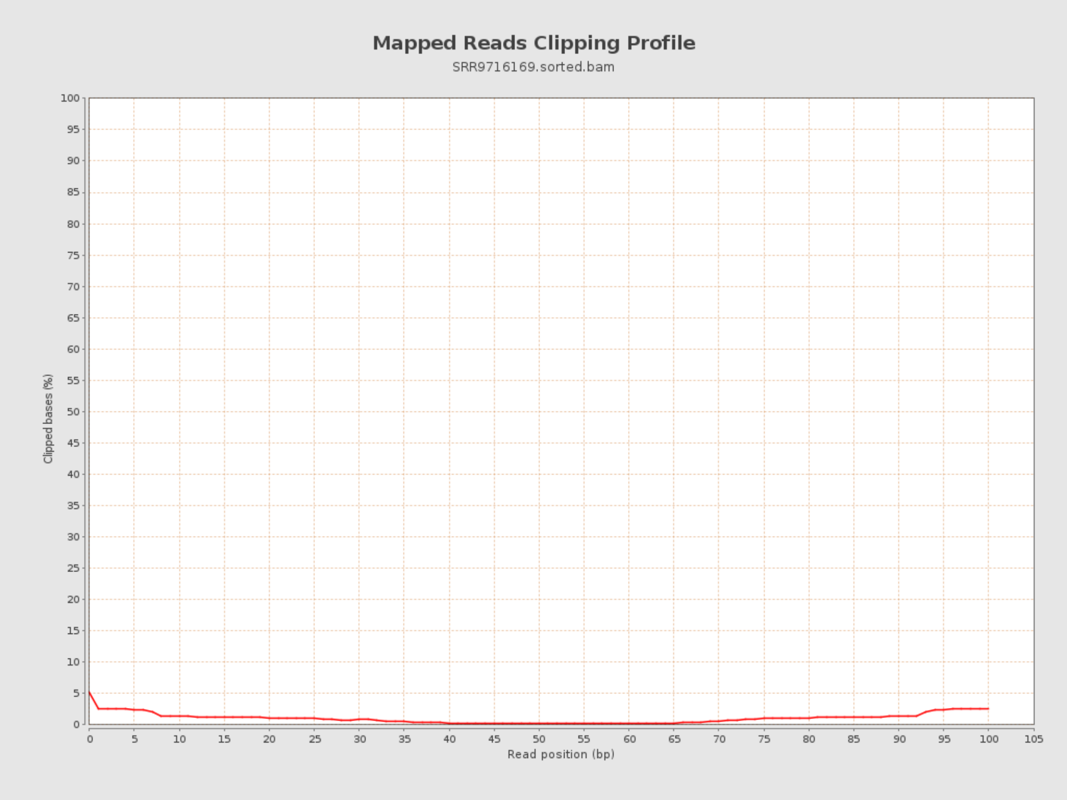
8. Results : Mapped Reads Nucleotide Content



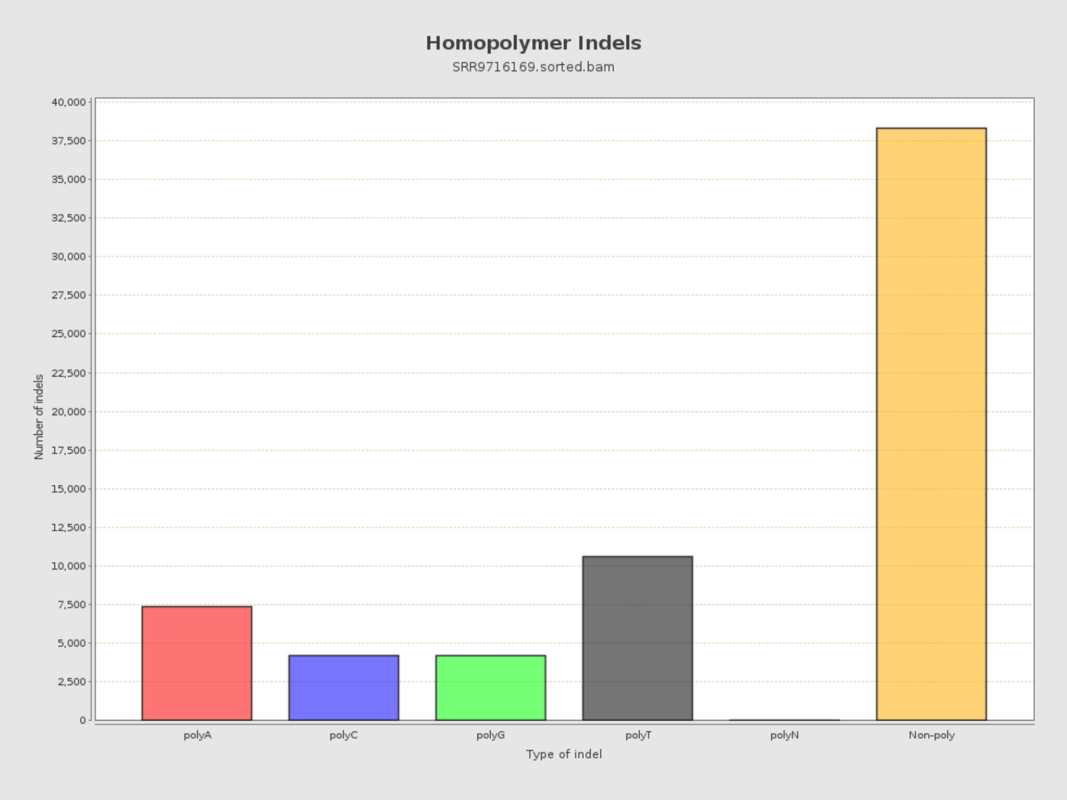
9. Results : Mapped Reads GC-content Distribution



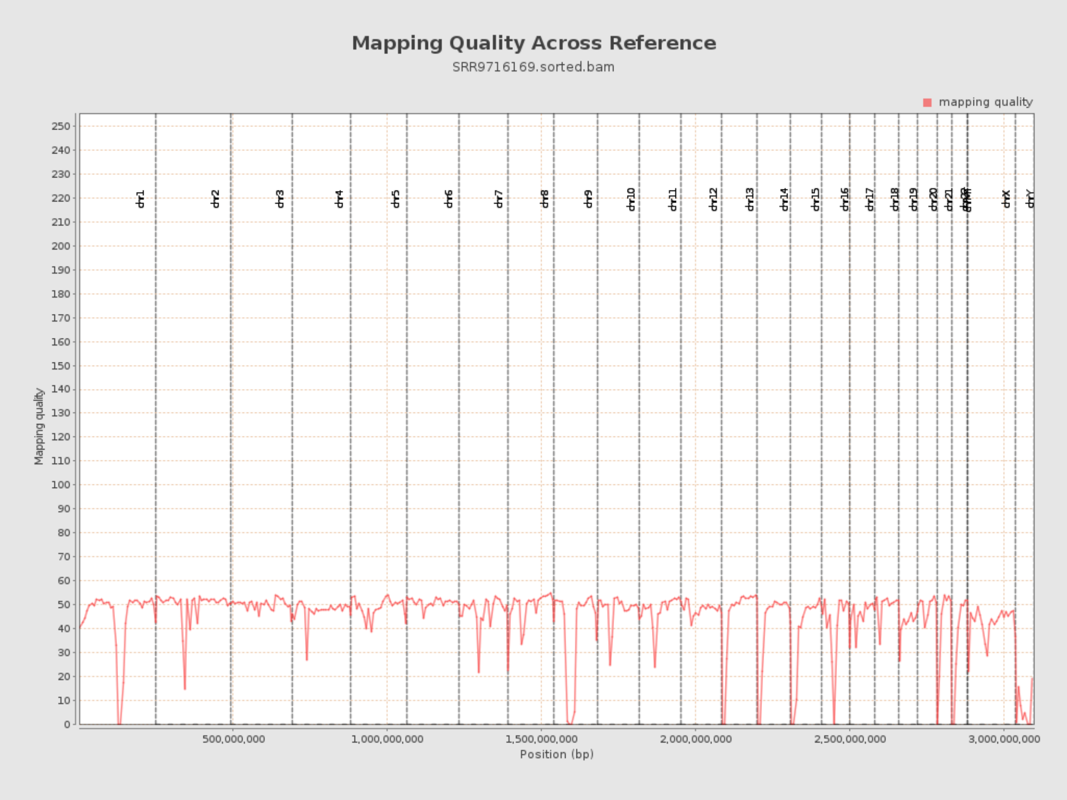
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram