Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:39:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716889.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_SRR9716889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716889.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:39:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,804,322
Mapped reads	4,153,477 / 86.45%
Unmapped reads	650,845 / 13.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,179 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	186,167 / 3.87%
Duplication rate	3.17%
Clipped reads	4,168,460 / 86.76%

2.2. ACGT Content

Number/percentage of A's	56,001,926 / 23.88%
Number/percentage of C's	45,170,976 / 19.26%
Number/percentage of T's	73,877,572 / 31.5%
Number/percentage of G's	59,466,024 / 25.36%
Number/percentage of N's	3,443 / 0%
GC Percentage	44.62%

2.3. Coverage

Mean	0.0758

Standard Deviation	0.546

2.4. Mapping Quality

Mean Mapping Quality	42.07

2.5. Mismatches and indels

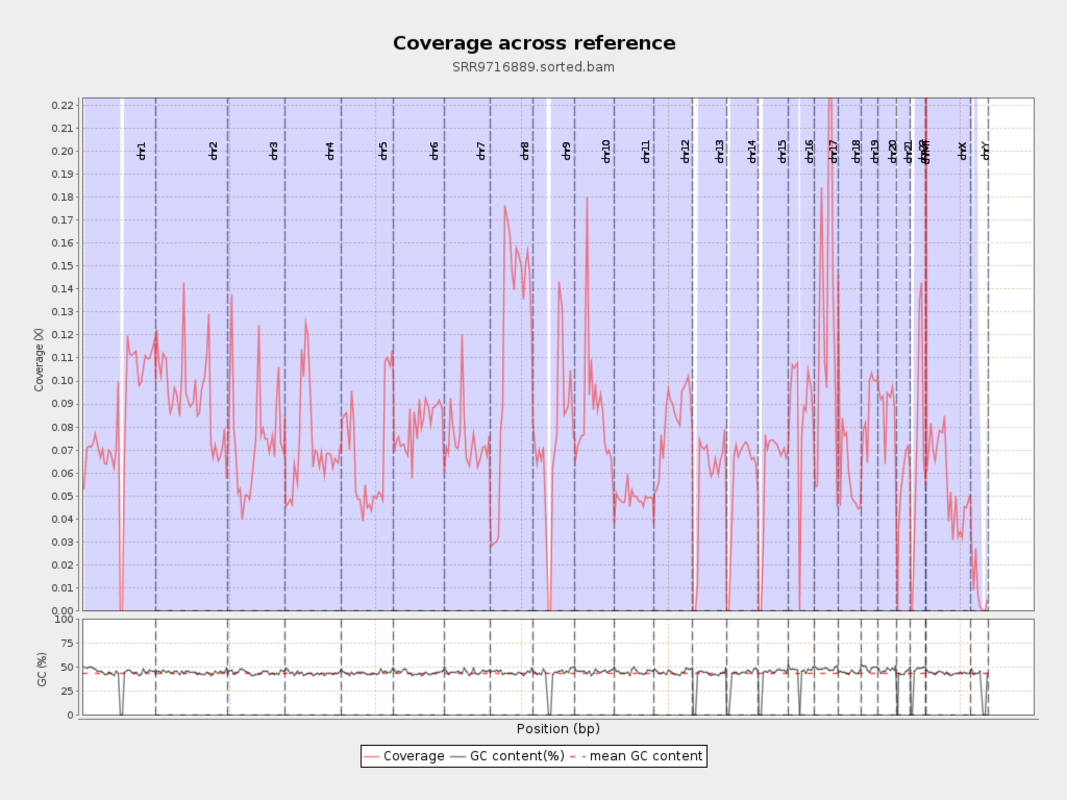
General error rate	0.53%
Mismatches	1,211,439
Insertions	13,255
Mapped reads with at least one insertion	0.32%
Deletions	43,699
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.58%

2.6. Chromosome stats

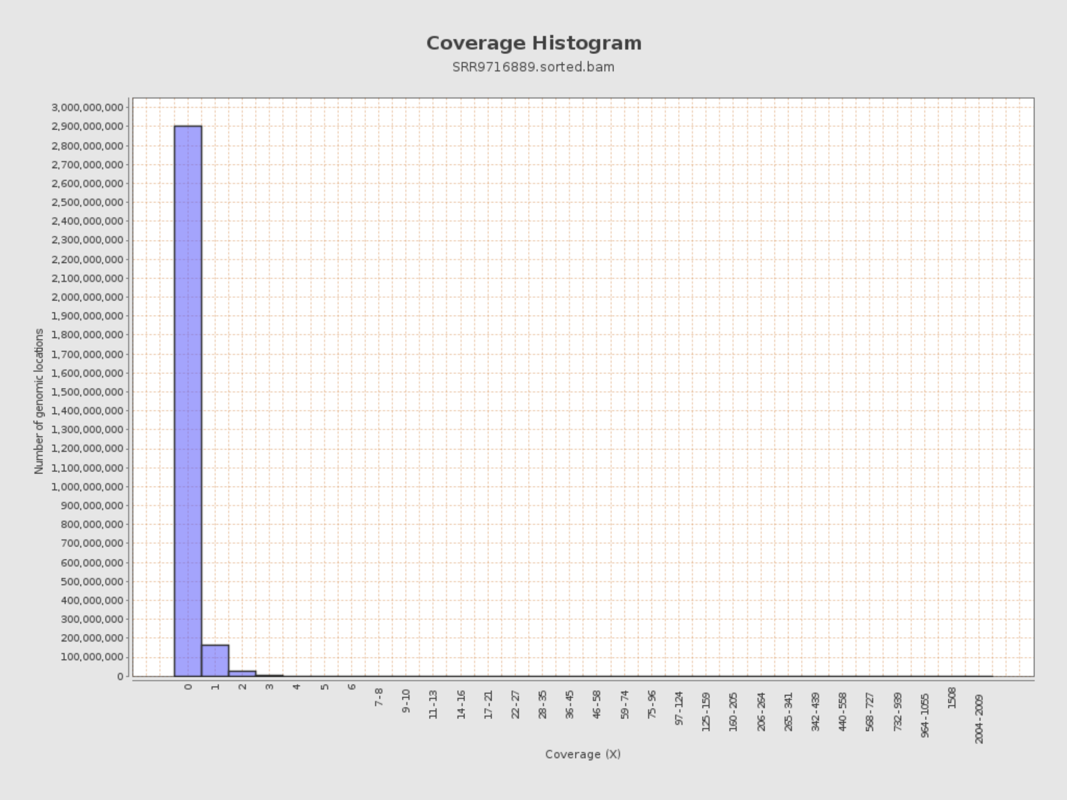
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20481180	0.0822	0.8389
chr2	243199373	22640667	0.0931	0.926
chr3	198022430	14523096	0.0733	0.3313
chr4	191154276	13736995	0.0719	0.3546
chr5	180915260	12414280	0.0686	0.3132
chr6	171115067	13762587	0.0804	0.423
chr7	159138663	11843686	0.0744	0.8282

chr8	146364022	17323099	0.1184	0.5771
chr9	141213431	10316115	0.0731	0.4266
chr10	135534747	11653481	0.086	0.6463
chr11	135006516	6602296	0.0489	0.3881
chr12	133851895	11108015	0.083	0.356
chr13	115169878	6472273	0.0562	0.2809
chr14	107349540	6213232	0.0579	0.3151
chr15	102531392	5954306	0.0581	0.2994
chr16	90354753	7723542	0.0855	0.3922
chr17	81195210	10664569	0.1313	0.4808
chr18	78077248	4854414	0.0622	0.6656
chr19	59128983	5247935	0.0888	0.7103
chr20	63025520	5560768	0.0882	0.3605
chr21	48129895	2551900	0.053	0.2954
chr22	51304566	3635964	0.0709	0.3254
chrMT	16571	11170	0.6741	0.9959
chrX	155270560	8760356	0.0564	0.3564
chrY	59373566	534064	0.009	0.2025

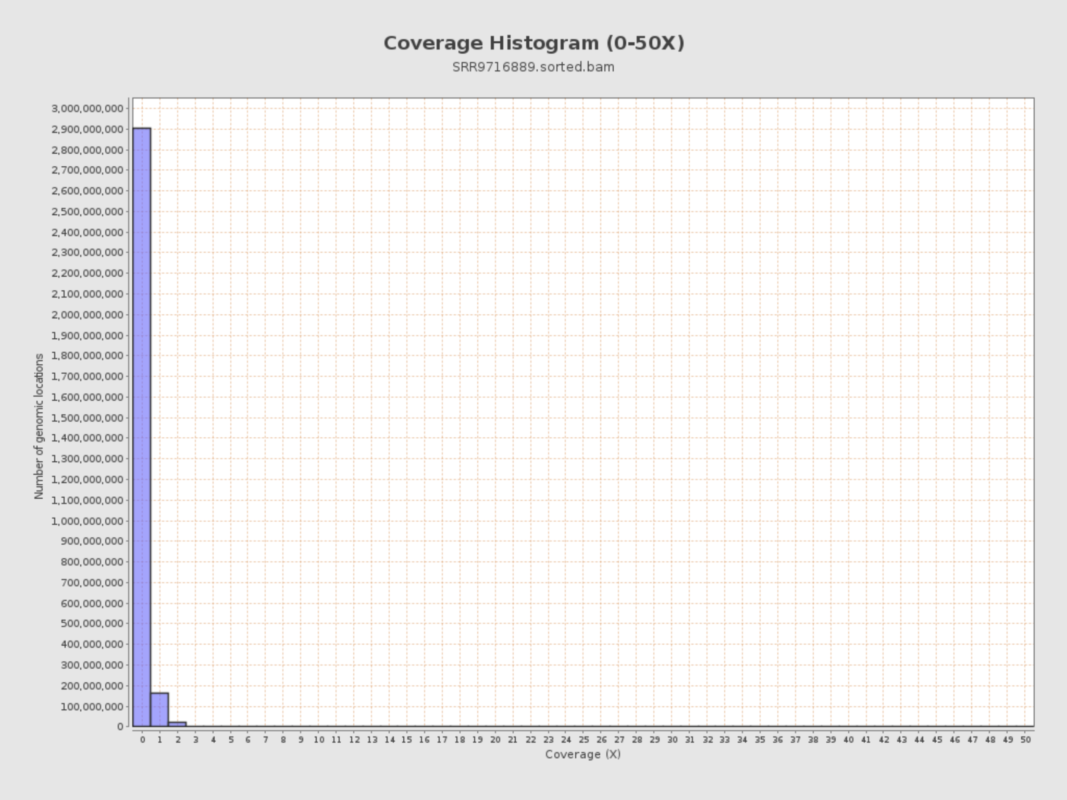
3. Results : Coverage across reference



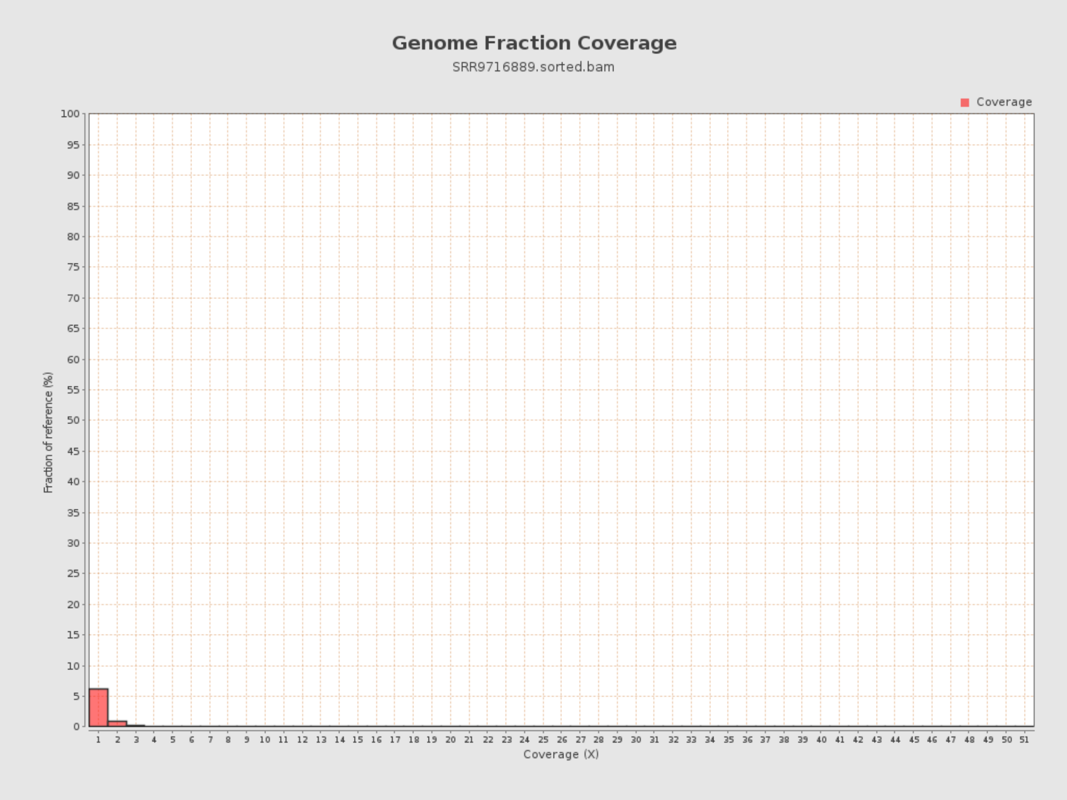
4. Results : Coverage Histogram



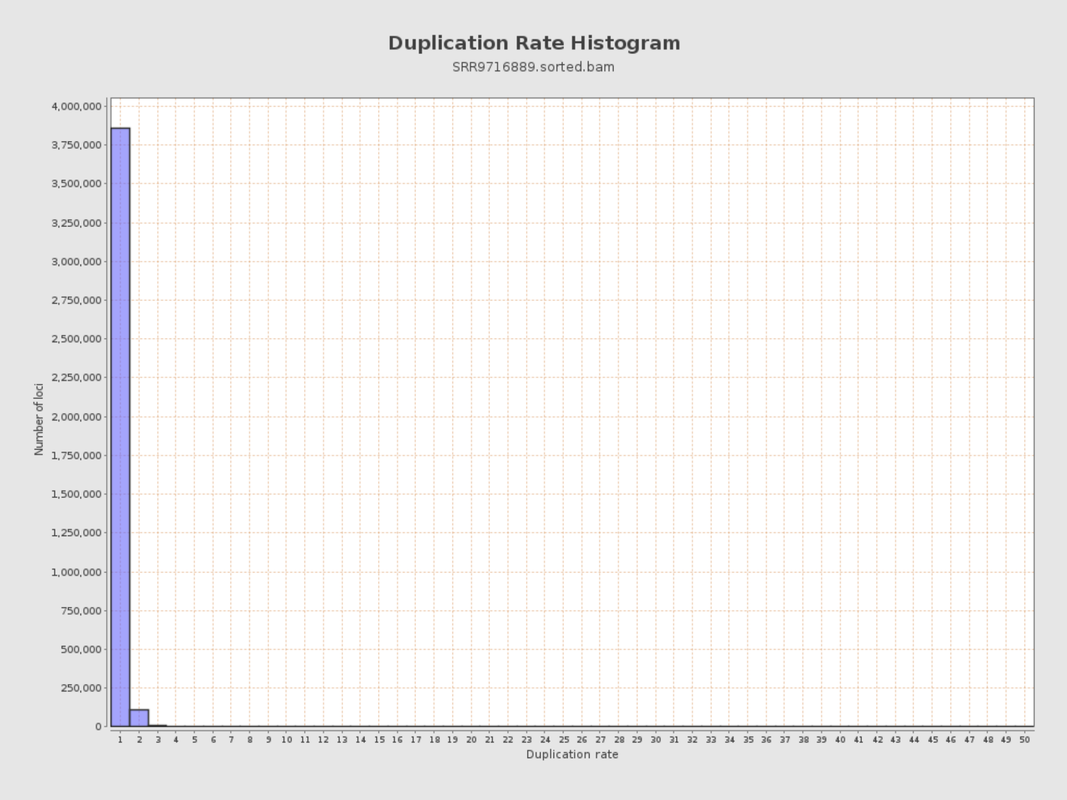
5. Results : Coverage Histogram (0-50X)



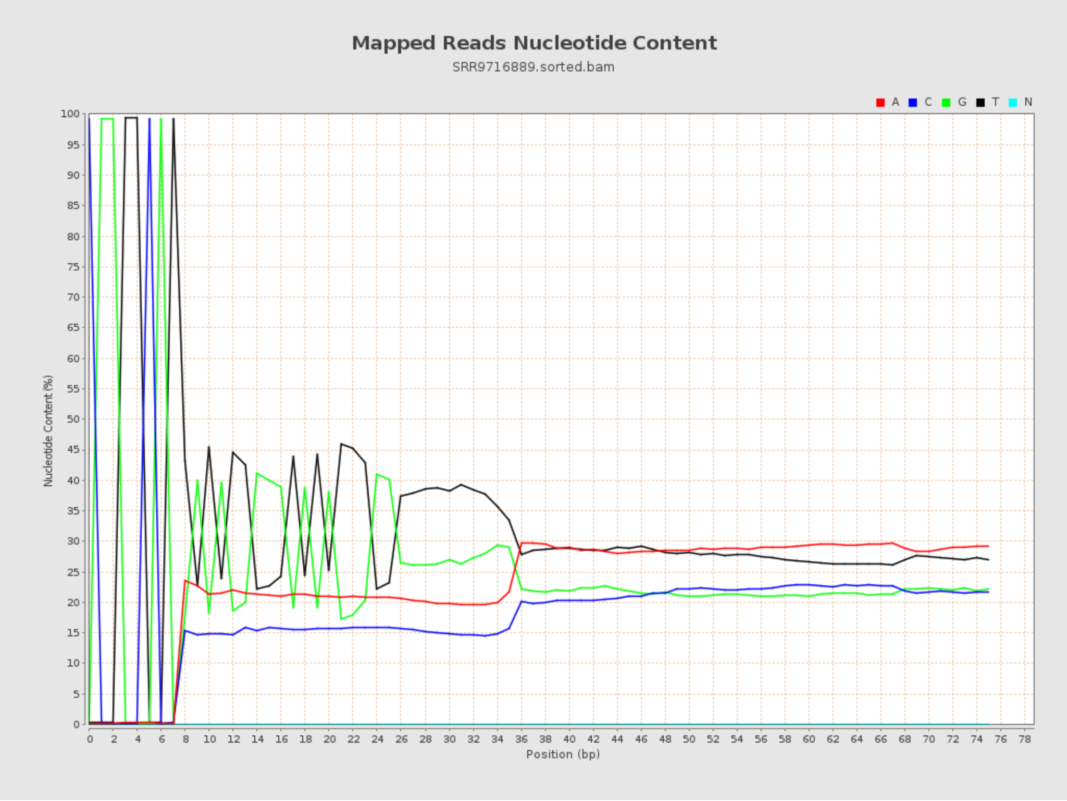
6. Results : Genome Fraction Coverage



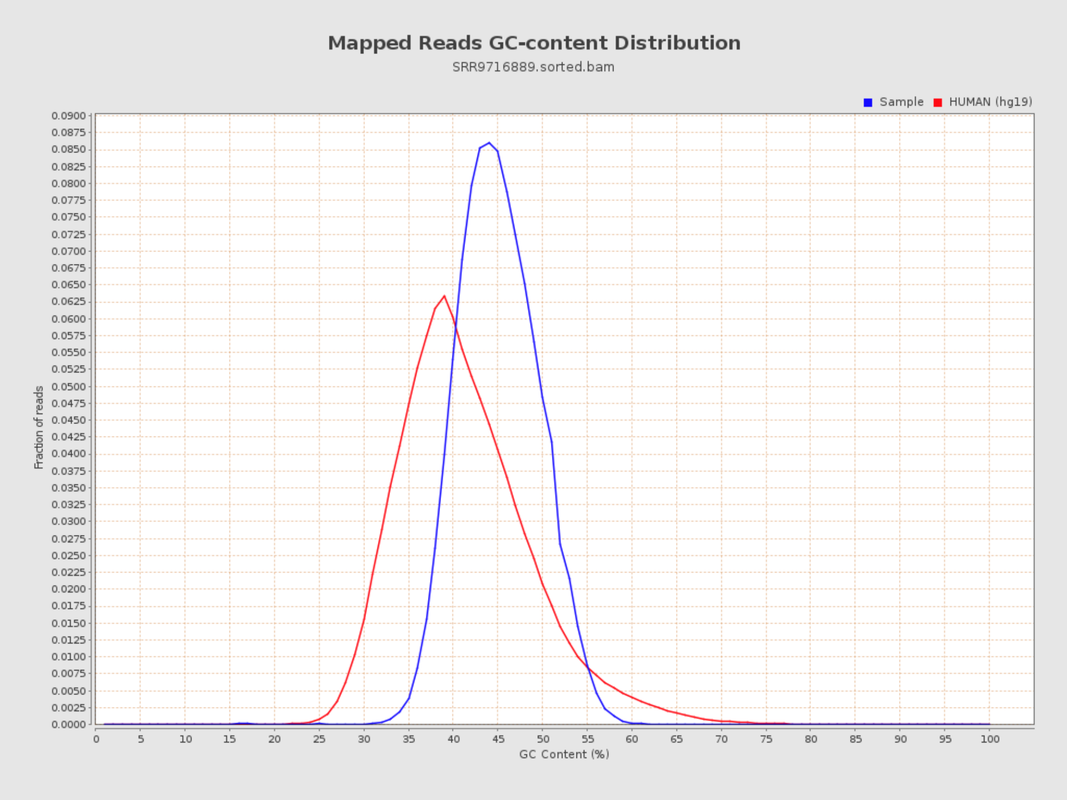
7. Results : Duplication Rate Histogram



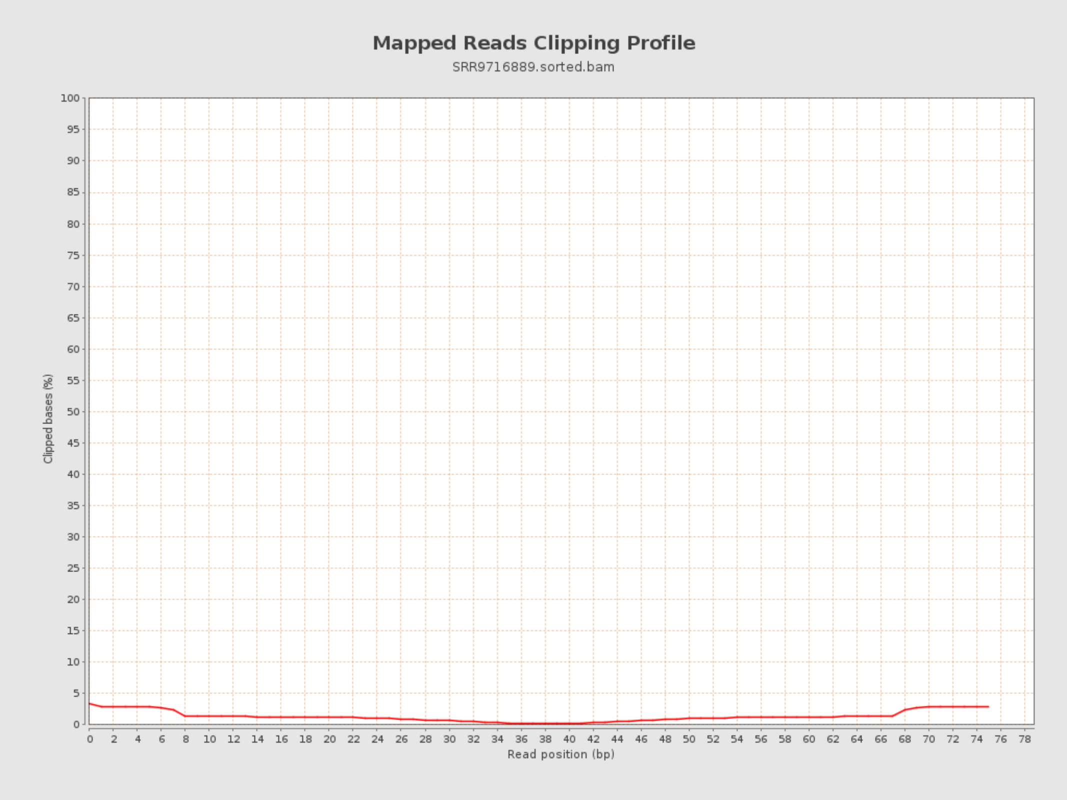
8. Results : Mapped Reads Nucleotide Content



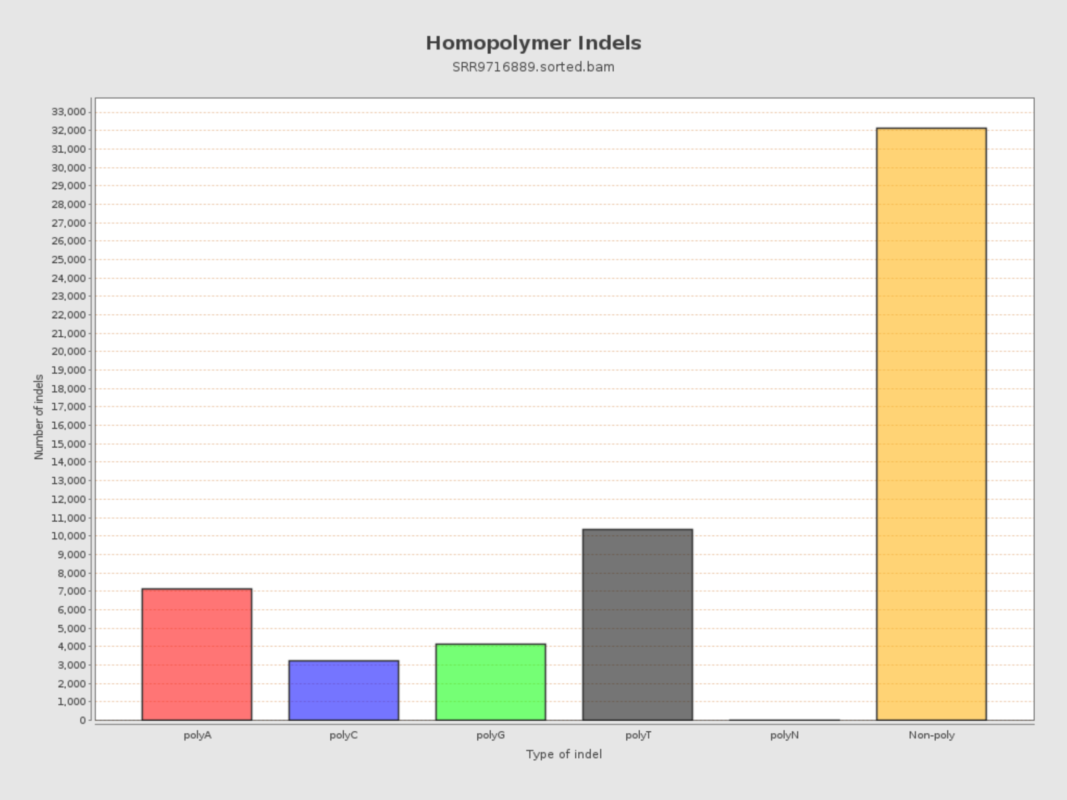
9. Results : Mapped Reads GC-content Distribution



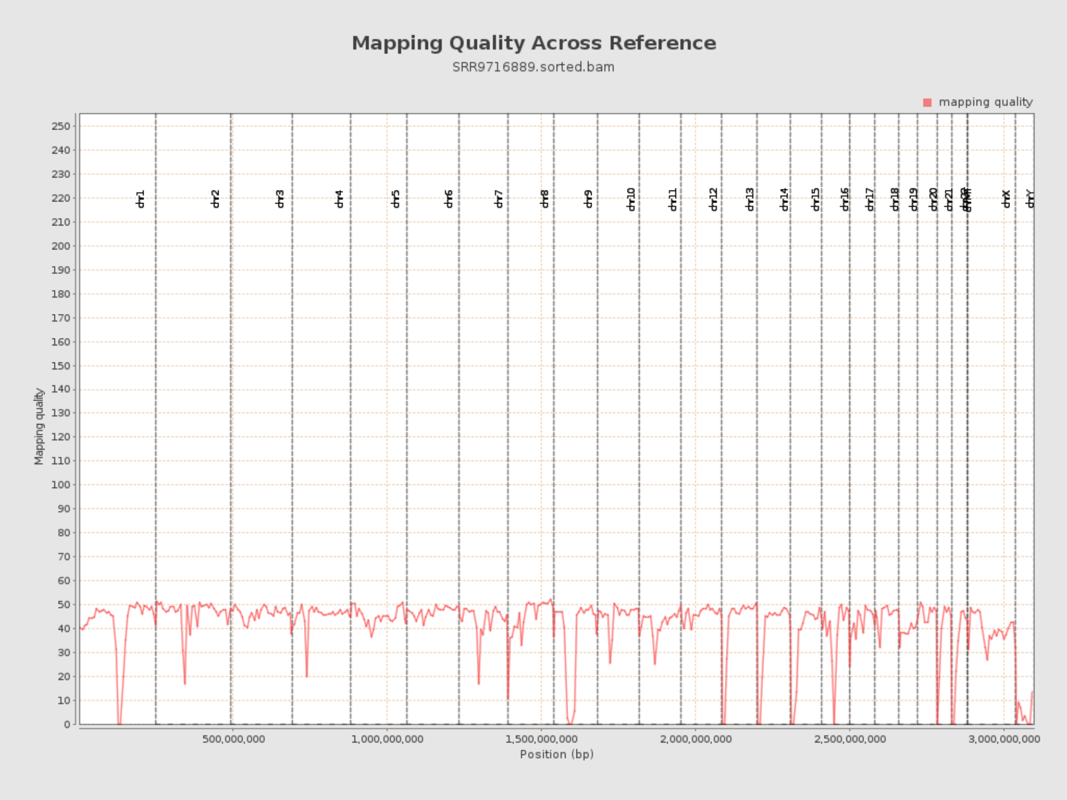
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram