Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:21:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716609.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_SRR9716609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:21:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,011,949
Mapped reads	1,870,231 / 92.96%
Unmapped reads	141,718 / 7.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	59,799 / 2.97%
Read min/max/mean length	30 / 101 / 102.07
Duplicated reads (estimated)	45,722 / 2.27%
Duplication rate	1.54%
Clipped reads	1,927,344 / 95.79%

2.2. ACGT Content

Number/percentage of A's	35,509,809 / 25.14%
Number/percentage of C's	30,760,908 / 21.78%
Number/percentage of T's	40,749,333 / 28.85%
Number/percentage of G's	34,212,066 / 24.22%
Number/percentage of N's	15,636 / 0.01%
GC Percentage	46%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.3641

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

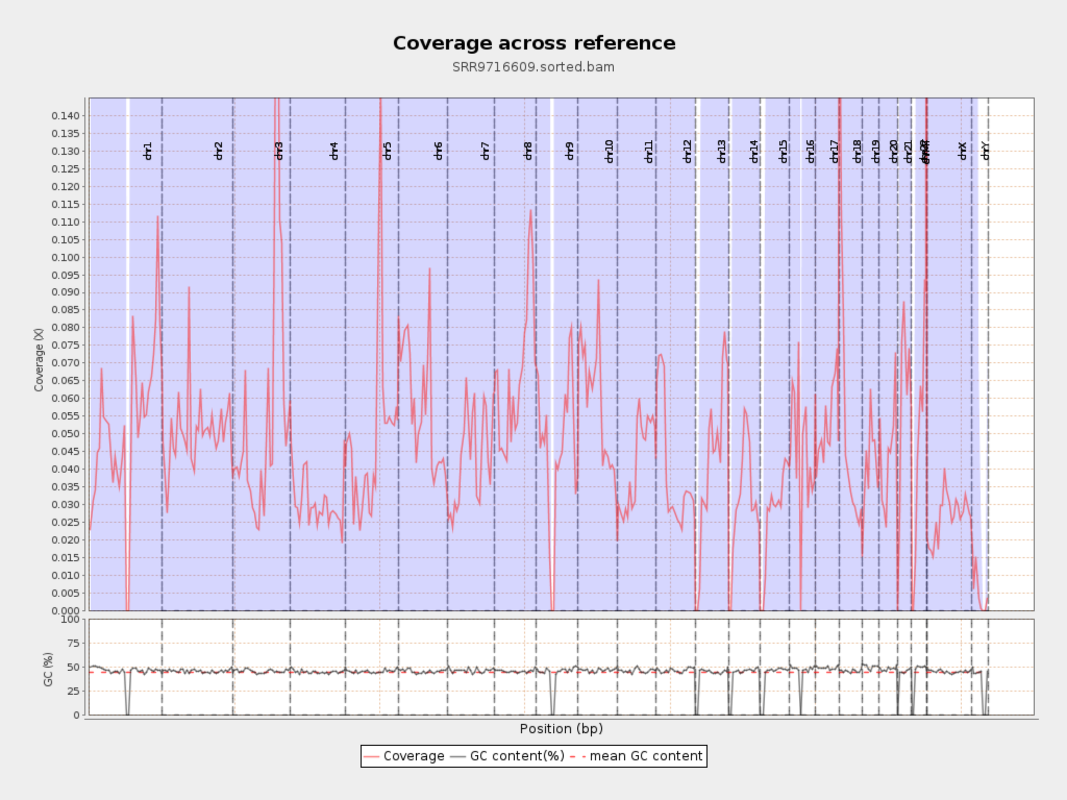
General error rate	0.8%
Mismatches	1,103,969
Insertions	12,154
Mapped reads with at least one insertion	0.64%
Deletions	28,984
Mapped reads with at least one deletion	1.53%
Homopolymer indels	40%

2.6. Chromosome stats

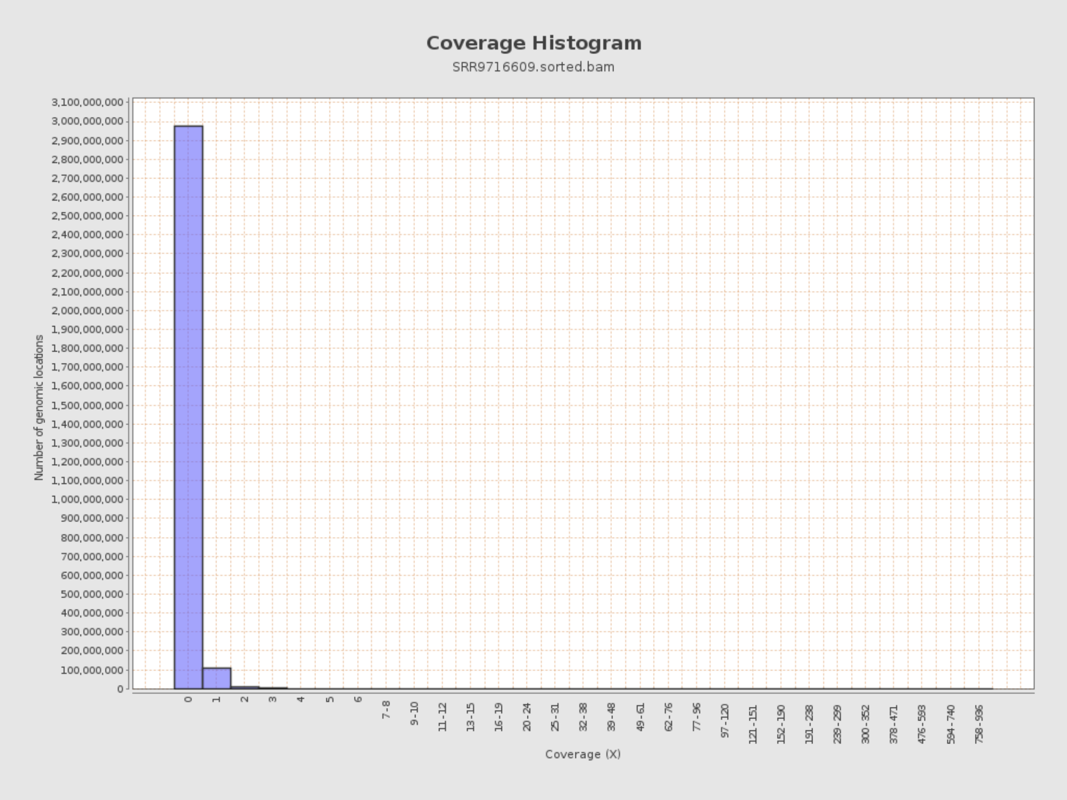
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12837096	0.0515	0.3766
chr2	243199373	12283481	0.0505	0.6608
chr3	198022430	11263514	0.0569	0.2761
chr4	191154276	5809422	0.0304	0.2025
chr5	180915260	8941202	0.0494	0.2512
chr6	171115067	9920235	0.058	0.3023
chr7	159138663	6933027	0.0436	0.4536

chr8	146364022	9827807	0.0671	0.5189
chr9	141213431	6396097	0.0453	0.3757
chr10	135534747	8116761	0.0599	0.3468
chr11	135006516	5598591	0.0415	0.3013
chr12	133851895	5200078	0.0388	0.2222
chr13	115169878	4861516	0.0422	0.2292
chr14	107349540	3317562	0.0309	0.2148
chr15	102531392	2773861	0.0271	0.1814
chr16	90354753	4007456	0.0444	0.2652
chr17	81195210	4287375	0.0528	0.2932
chr18	78077248	4125551	0.0528	0.662
chr19	59128983	2484157	0.042	0.3912
chr20	63025520	2754629	0.0437	0.2554
chr21	48129895	2809722	0.0584	0.2838
chr22	51304566	2270563	0.0443	0.246
chrMT	16571	6814	0.4112	1.0287
chrX	155270560	4161964	0.0268	0.2268
chrY	59373566	309506	0.0052	0.1389

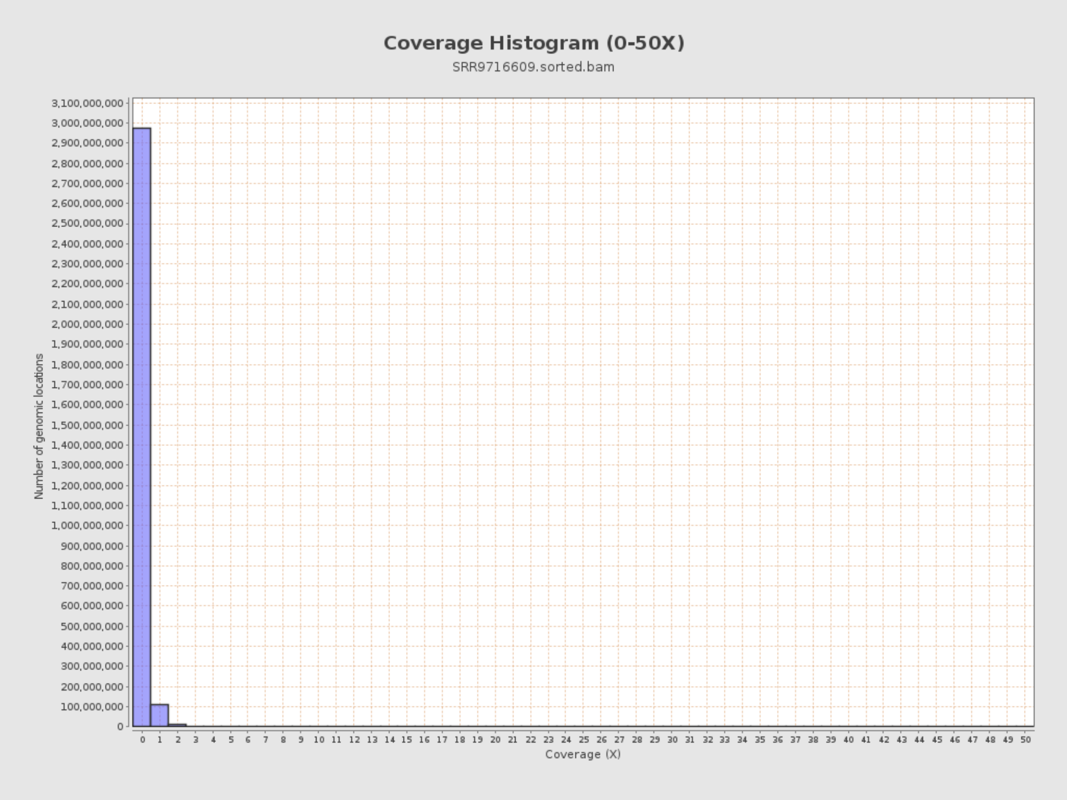
3. Results : Coverage across reference



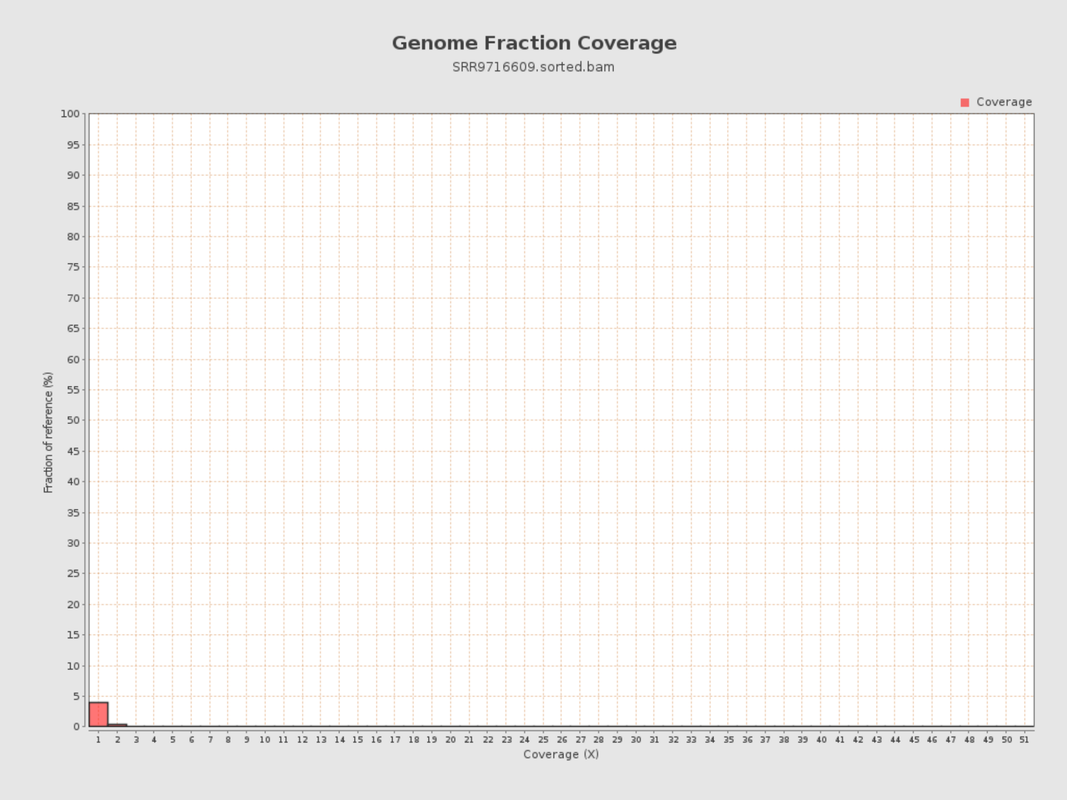
4. Results : Coverage Histogram



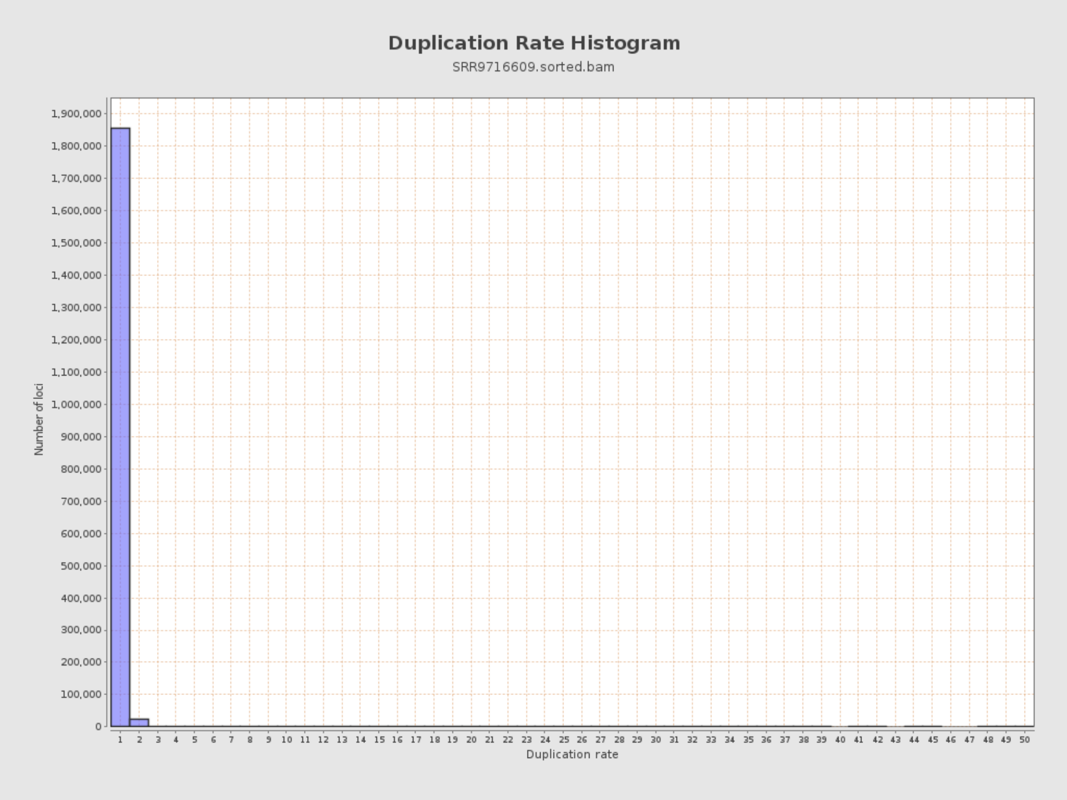
5. Results : Coverage Histogram (0-50X)



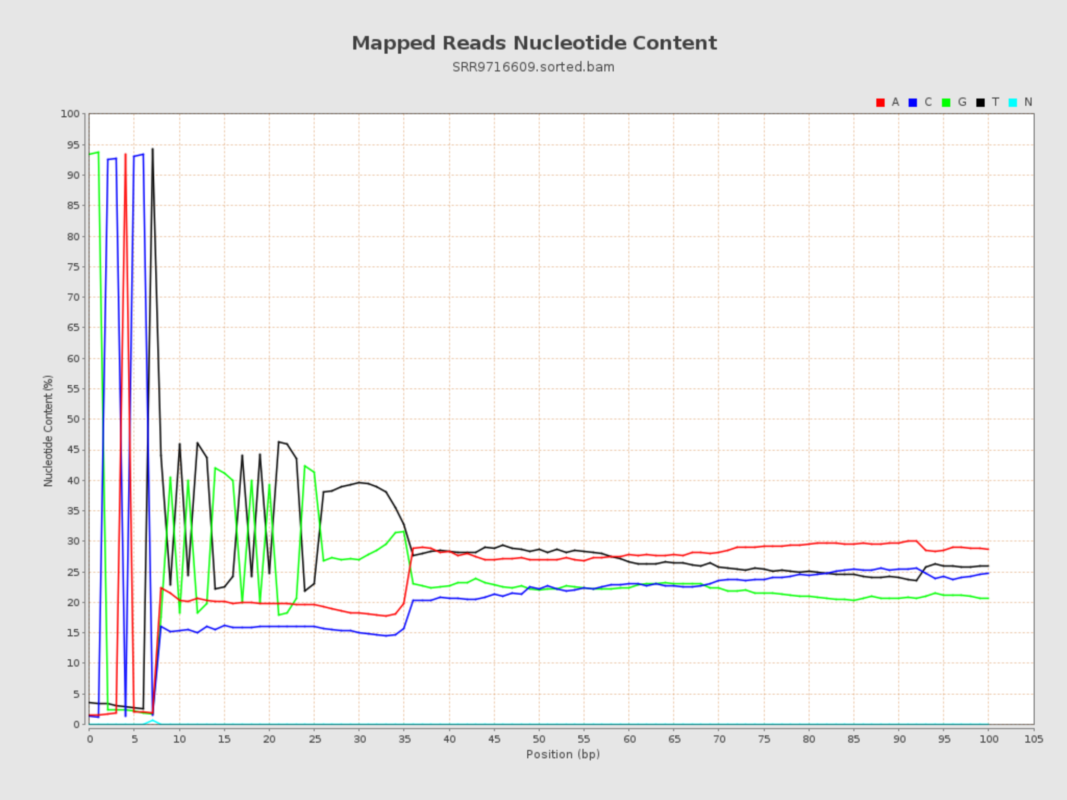
6. Results : Genome Fraction Coverage



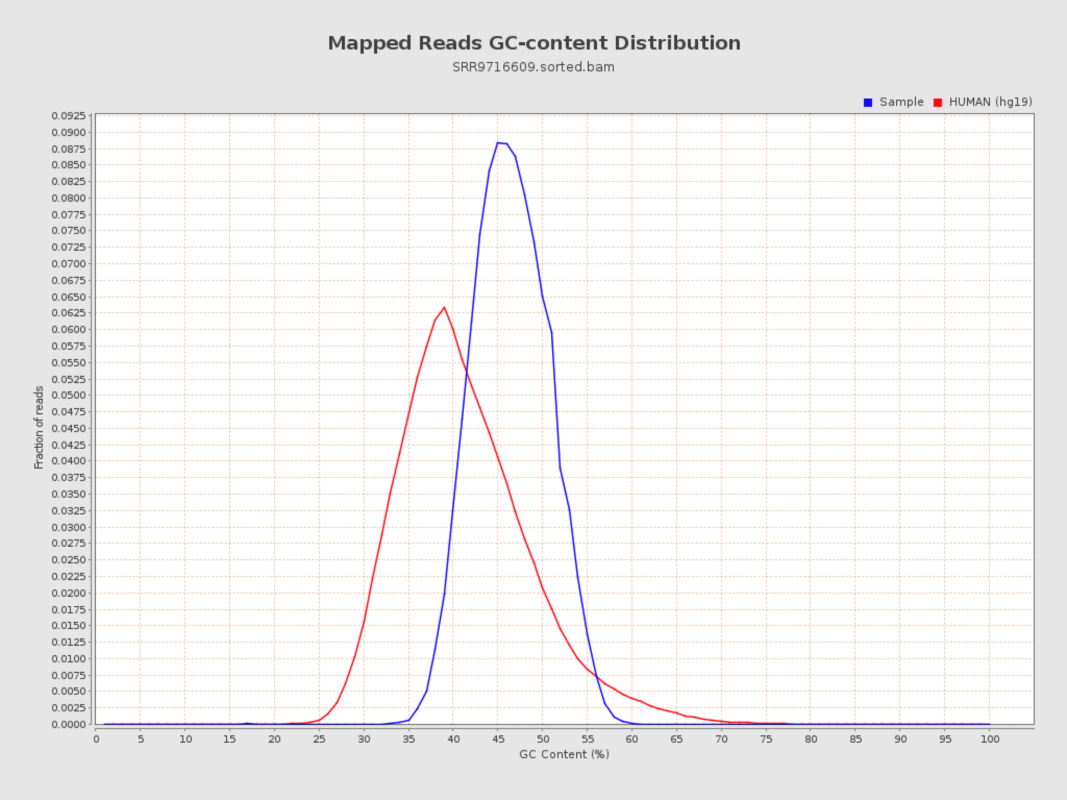
7. Results : Duplication Rate Histogram



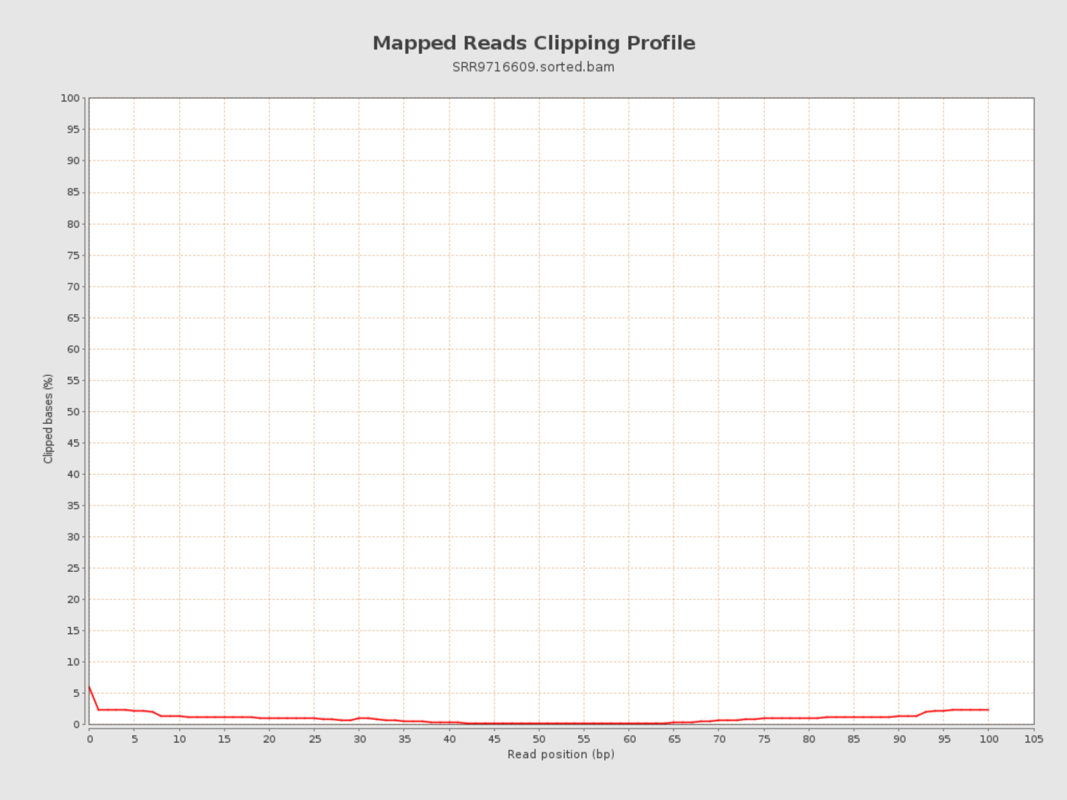
8. Results : Mapped Reads Nucleotide Content



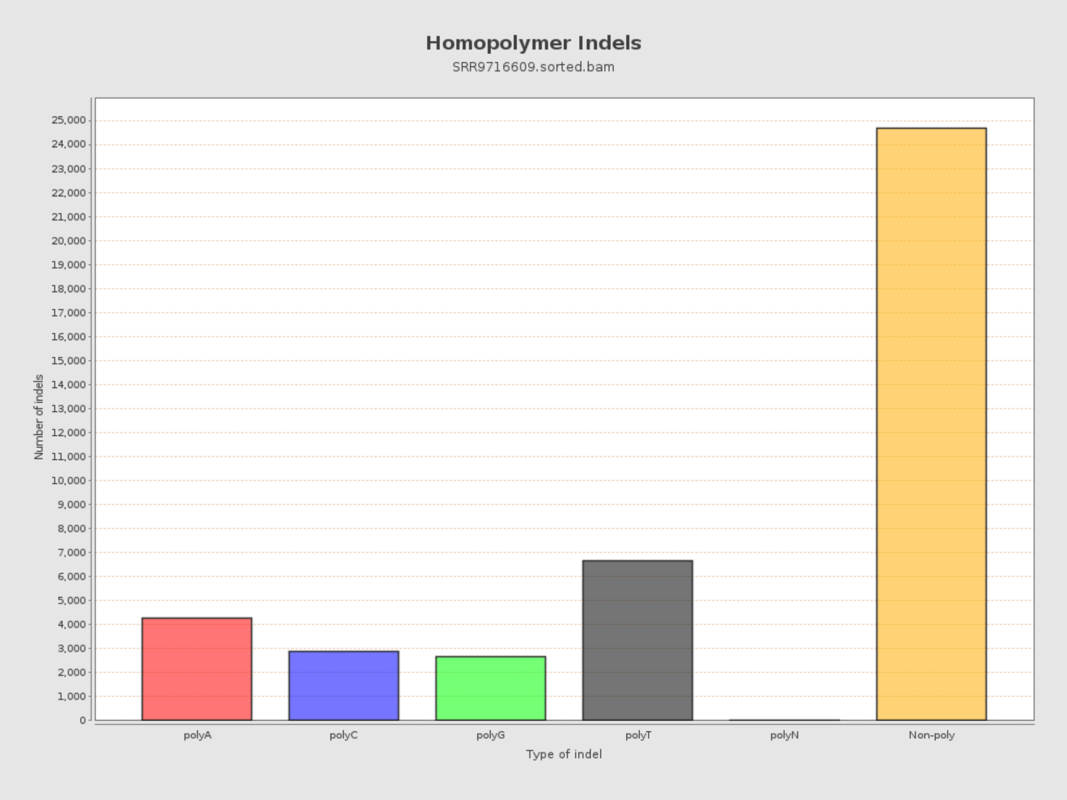
9. Results : Mapped Reads GC-content Distribution



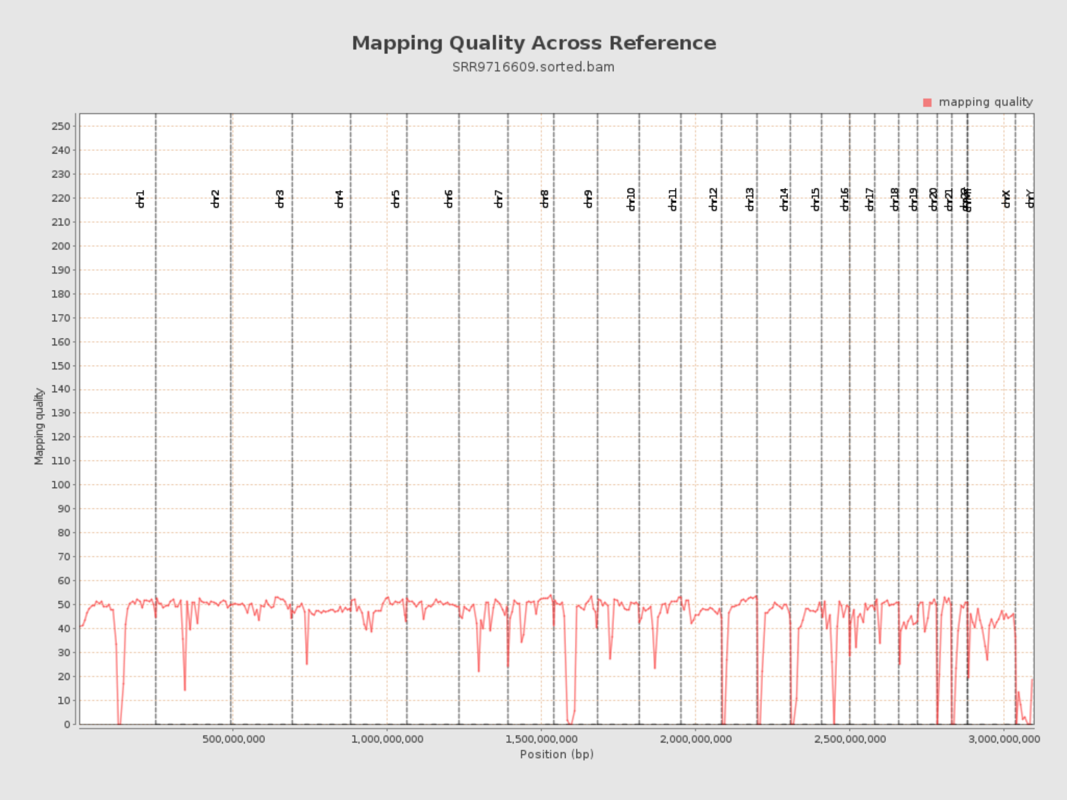
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram