Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 21:41:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716561.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_SRR9716561 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716561.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 21:41:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716561.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,470,451
Mapped reads	4,058,506 / 90.79%
Unmapped reads	411,945 / 9.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,571 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	213,467 / 4.78%
Duplication rate	4%
Clipped reads	4,063,740 / 90.9%

2.2. ACGT Content

Number/percentage of A's	58,164,529 / 25.12%
Number/percentage of C's	48,528,938 / 20.96%
Number/percentage of T's	68,958,806 / 29.78%
Number/percentage of G's	55,889,833 / 24.14%
Number/percentage of N's	5,144 / 0%
GC Percentage	45.1%

2.3. Coverage

Mean	0.0748

Standard Deviation	0.4993

2.4. Mapping Quality

Mean Mapping Quality	44.3

2.5. Mismatches and indels

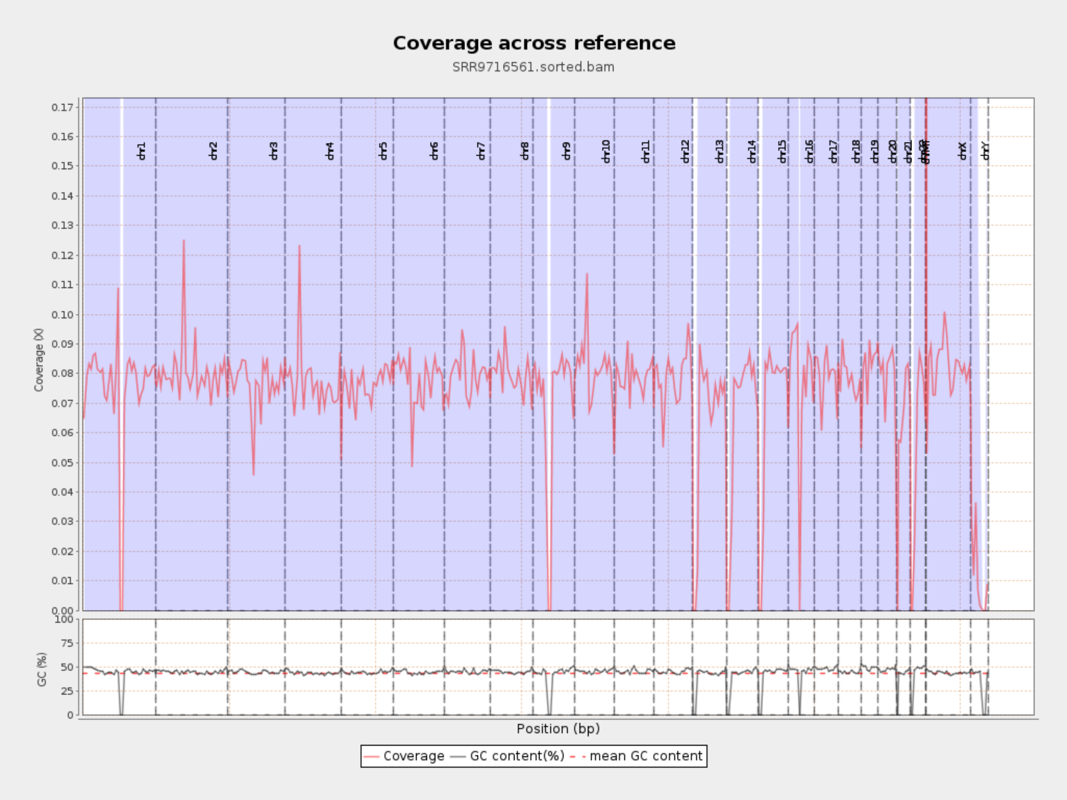
General error rate	0.5%
Mismatches	1,122,425
Insertions	15,763
Mapped reads with at least one insertion	0.39%
Deletions	35,768
Mapped reads with at least one deletion	0.88%
Homopolymer indels	40.11%

2.6. Chromosome stats

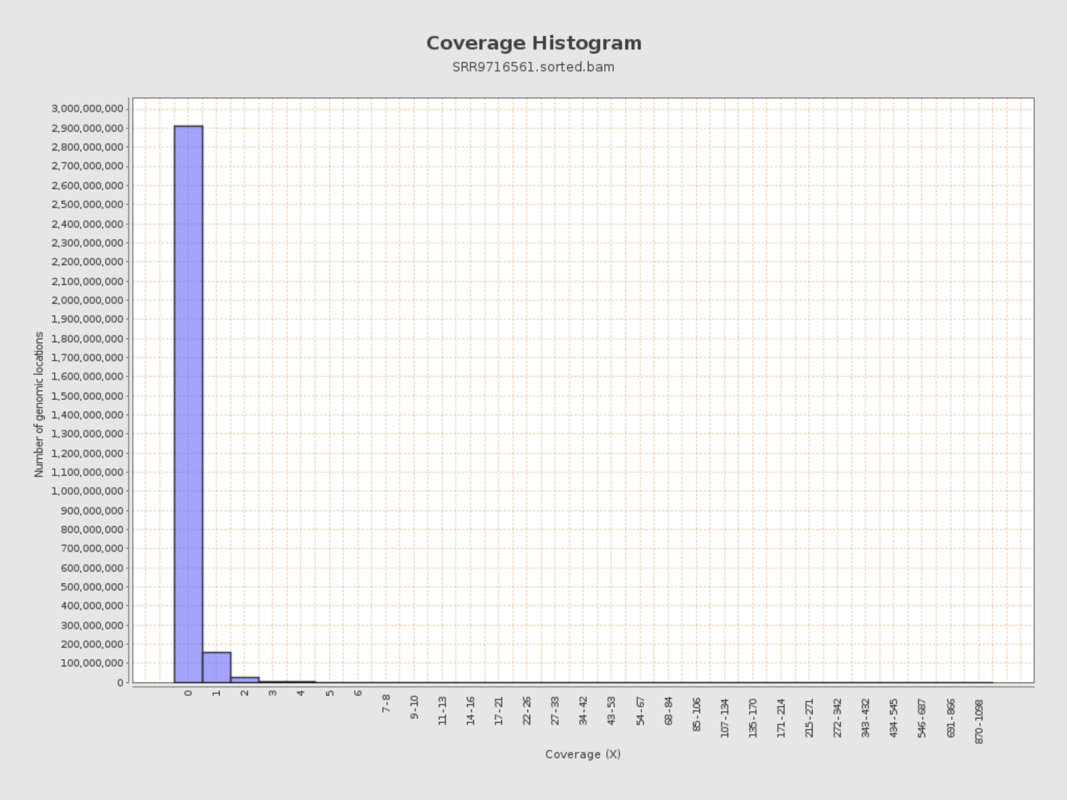
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18658255	0.0749	0.8663
chr2	243199373	19607128	0.0806	0.5933
chr3	198022430	15096157	0.0762	0.3358
chr4	191154276	14816775	0.0775	0.3905
chr5	180915260	13803747	0.0763	0.3416
chr6	171115067	13298550	0.0777	0.3723
chr7	159138663	12632473	0.0794	0.4904

chr8	146364022	11649878	0.0796	0.4456
chr9	141213431	9803666	0.0694	0.5133
chr10	135534747	11118735	0.082	0.4894
chr11	135006516	10603449	0.0785	0.4936
chr12	133851895	10632303	0.0794	0.3485
chr13	115169878	7239408	0.0629	0.3007
chr14	107349540	7076686	0.0659	0.3521
chr15	102531392	6792722	0.0663	0.3162
chr16	90354753	6818247	0.0755	0.385
chr17	81195210	6491207	0.0799	0.3657
chr18	78077248	6124968	0.0784	1.0261
chr19	59128983	4882585	0.0826	0.6116
chr20	63025520	5057911	0.0803	0.3643
chr21	48129895	3041192	0.0632	0.3716
chr22	51304566	2768636	0.054	0.2808
chrMT	16571	203941	12.3071	7.4166
chrX	155270560	12726596	0.082	0.4263
chrY	59373566	662732	0.0112	0.2279

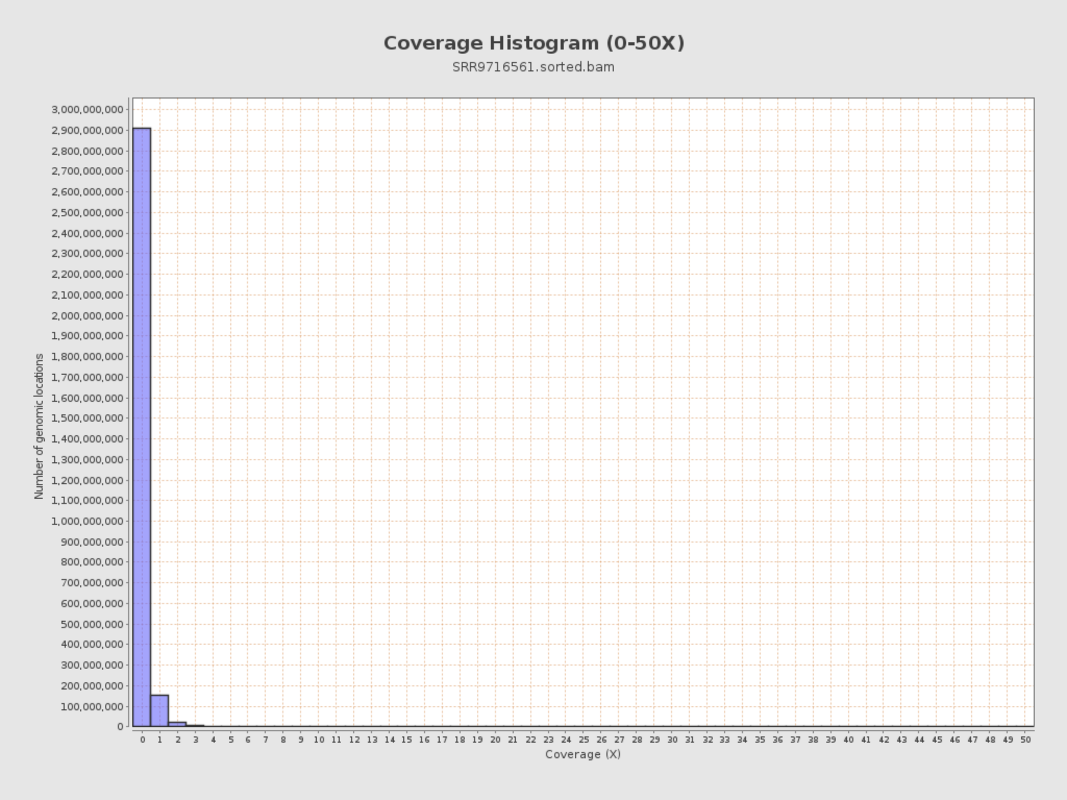
3. Results : Coverage across reference



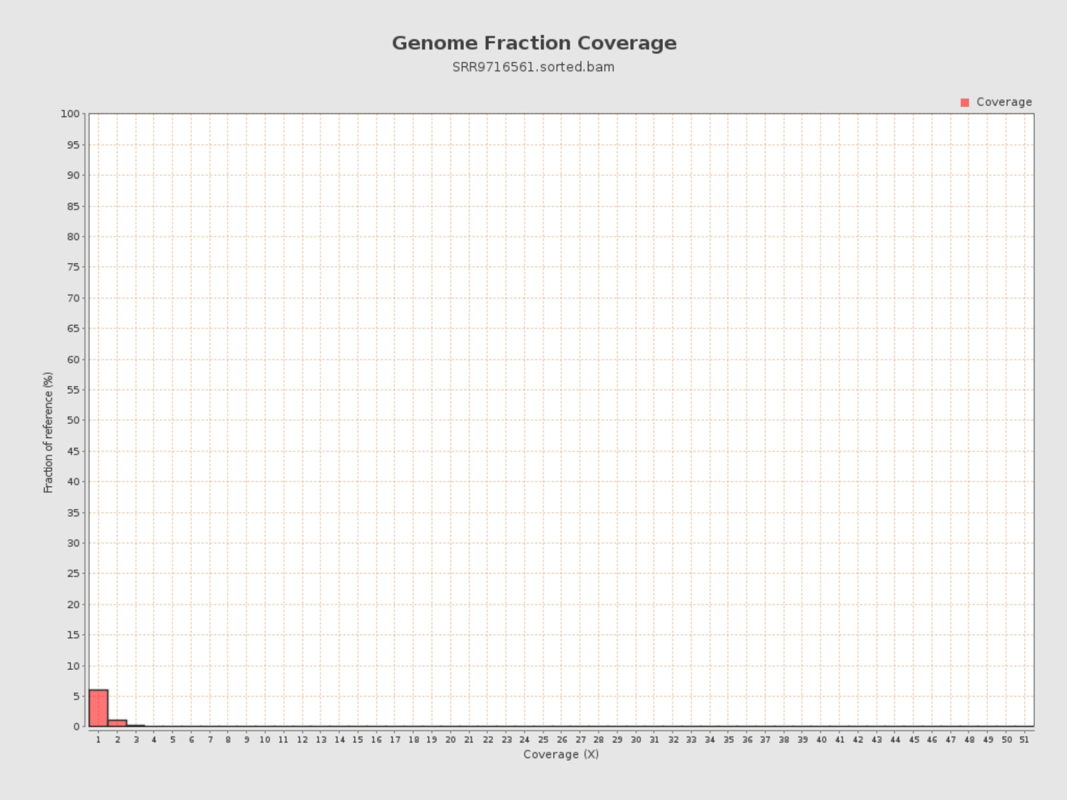
4. Results : Coverage Histogram



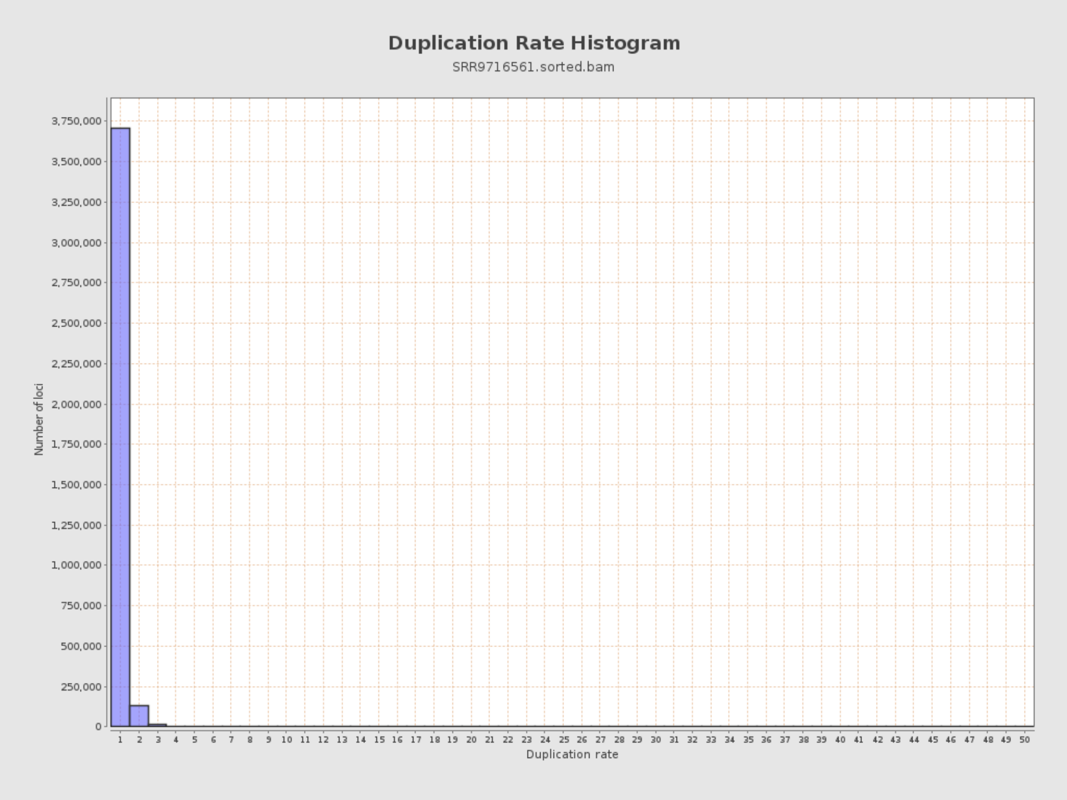
5. Results : Coverage Histogram (0-50X)



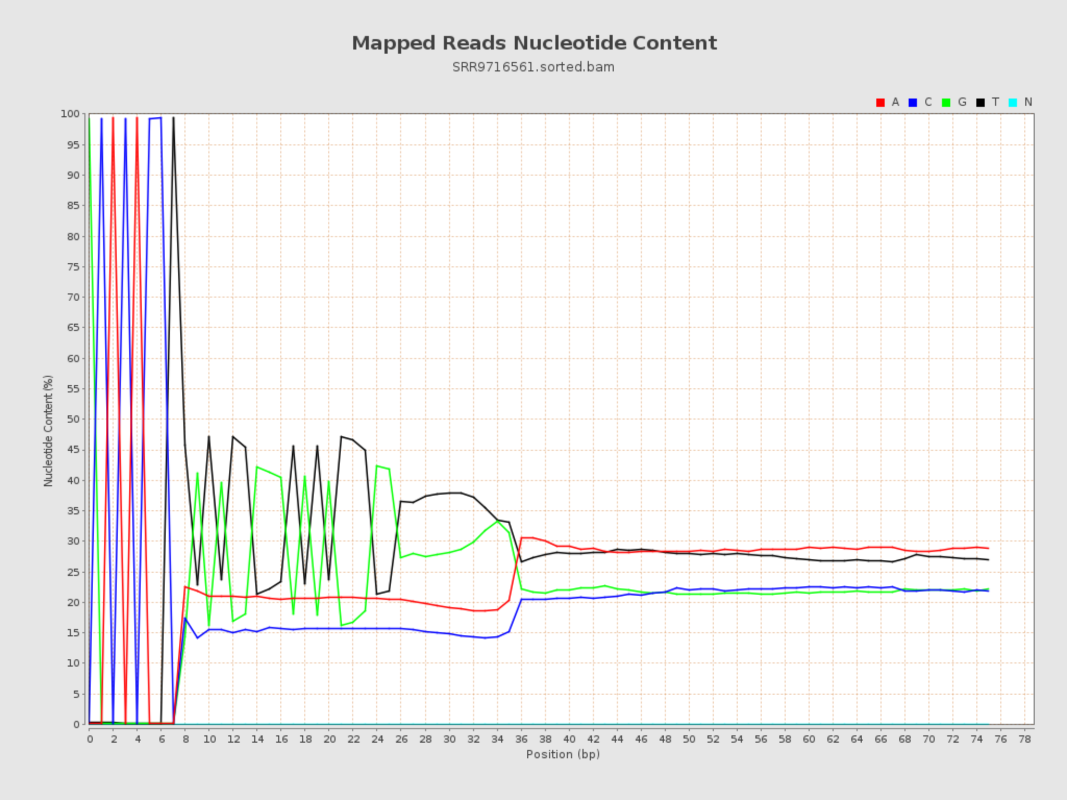
6. Results : Genome Fraction Coverage



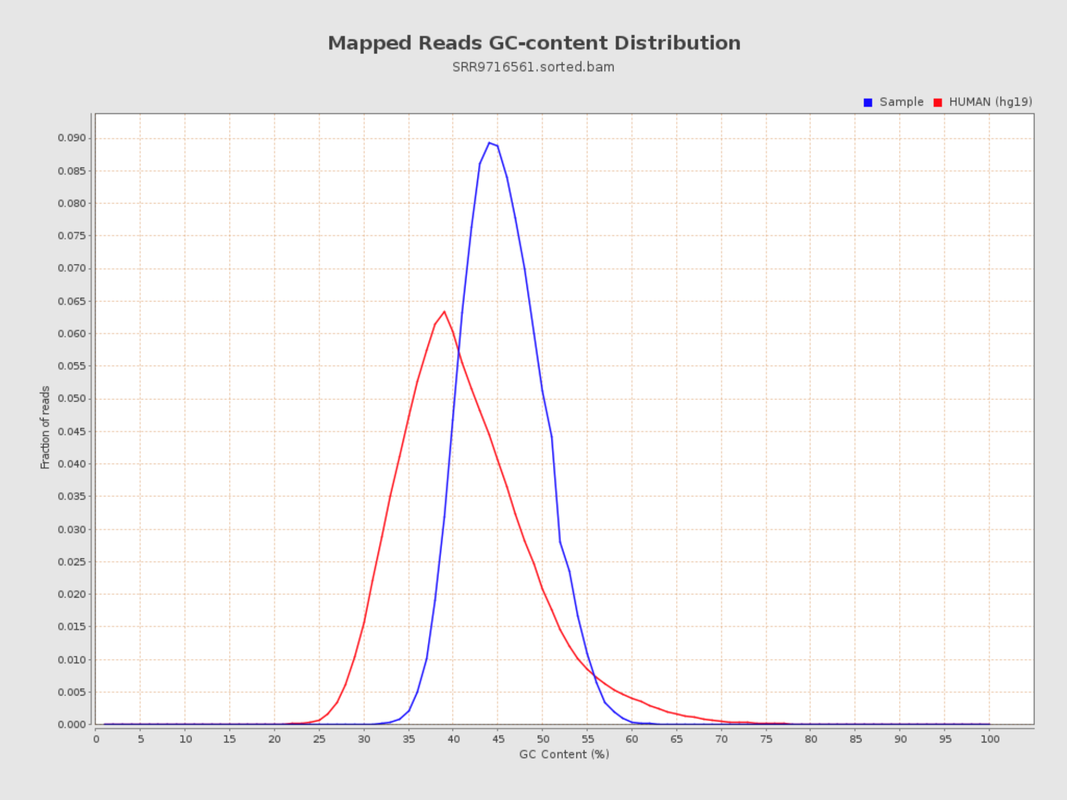
7. Results : Duplication Rate Histogram



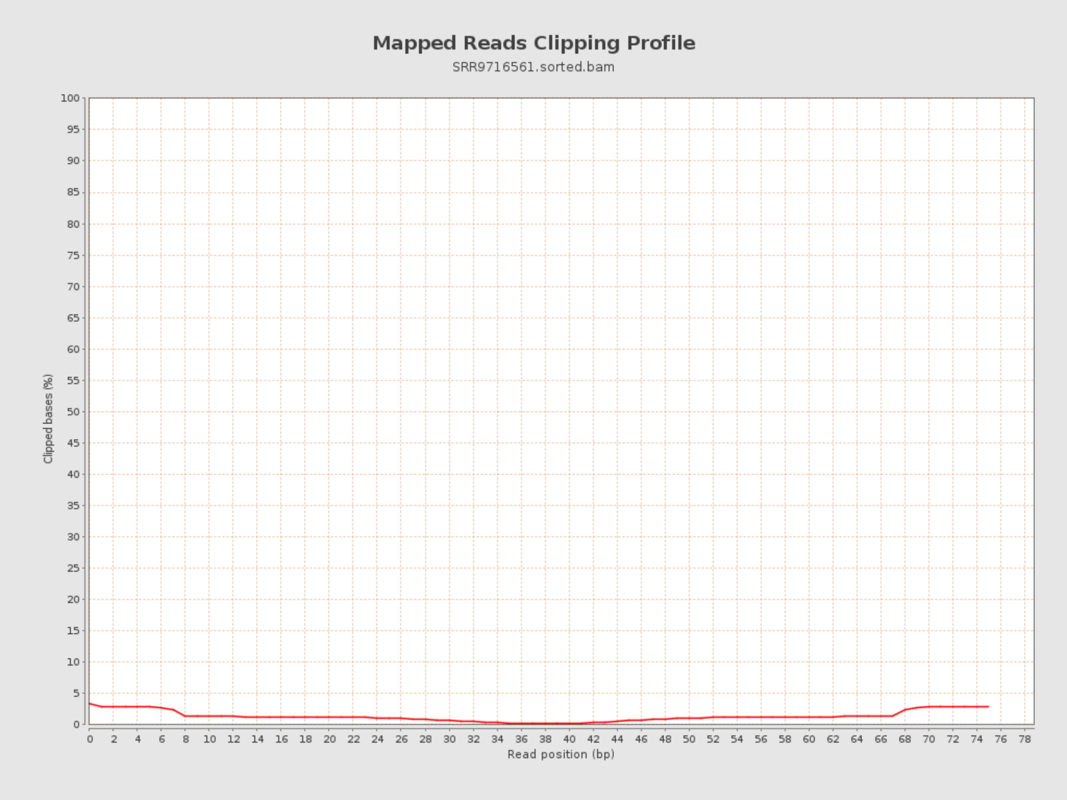
8. Results : Mapped Reads Nucleotide Content



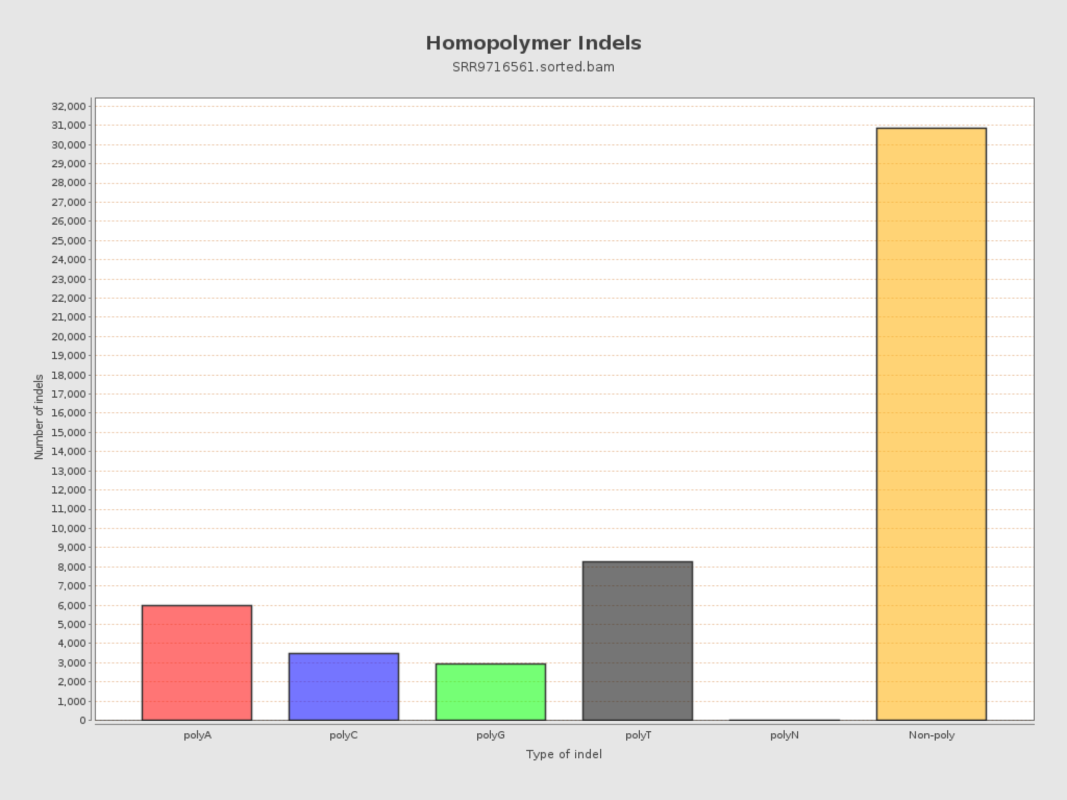
9. Results : Mapped Reads GC-content Distribution



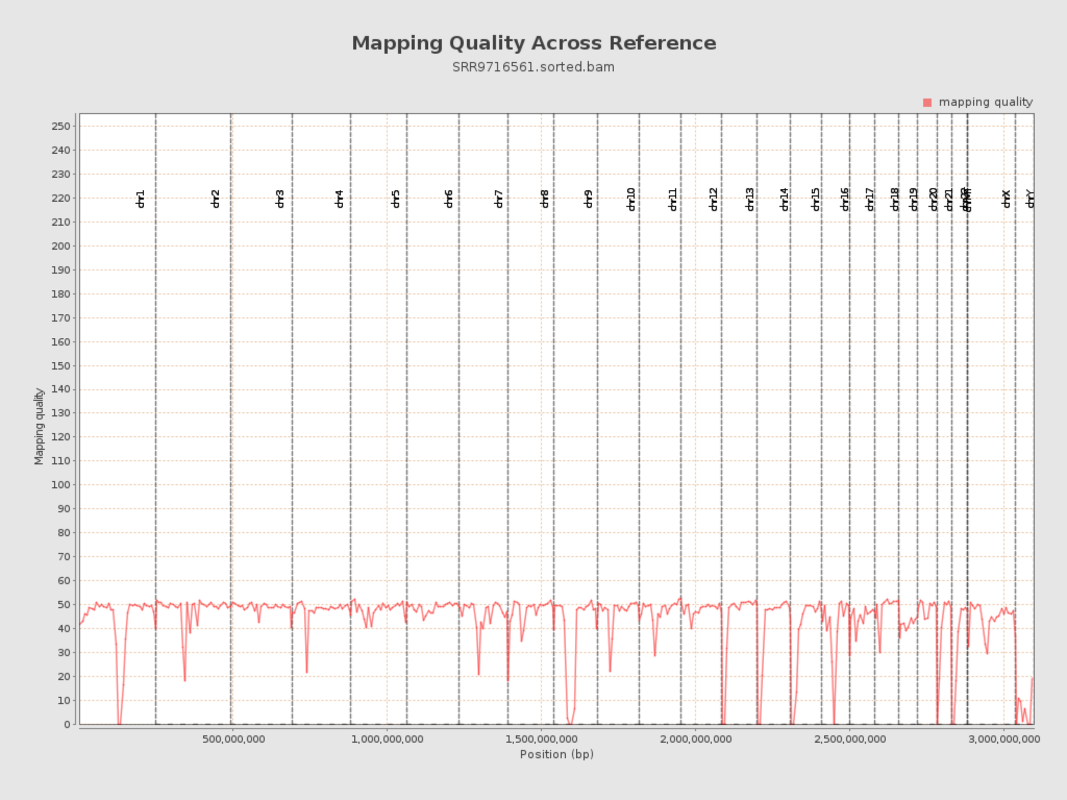
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram