Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:10:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716261.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_SRR9716261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716261.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:10:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,587,456
Mapped reads	1,458,990 / 91.91%
Unmapped reads	128,466 / 8.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,151 / 0.64%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	58,309 / 3.67%
Duplication rate	3%
Clipped reads	1,464,731 / 92.27%

2.2. ACGT Content

Number/percentage of A's	22,572,554 / 26.03%
Number/percentage of C's	15,749,258 / 18.16%
Number/percentage of T's	26,867,857 / 30.98%
Number/percentage of G's	21,532,374 / 24.83%
Number/percentage of N's	1,169 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.028

Standard Deviation	0.2631

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

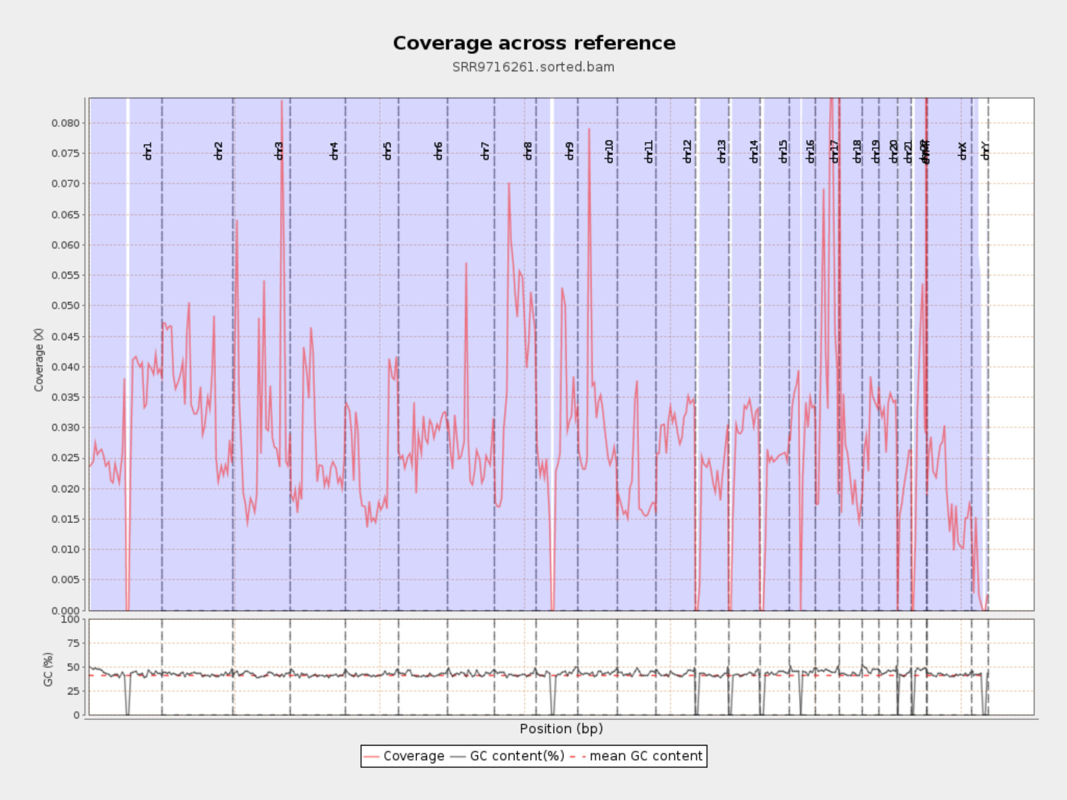
General error rate	0.51%
Mismatches	429,947
Insertions	6,512
Mapped reads with at least one insertion	0.44%
Deletions	16,763
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.16%

2.6. Chromosome stats

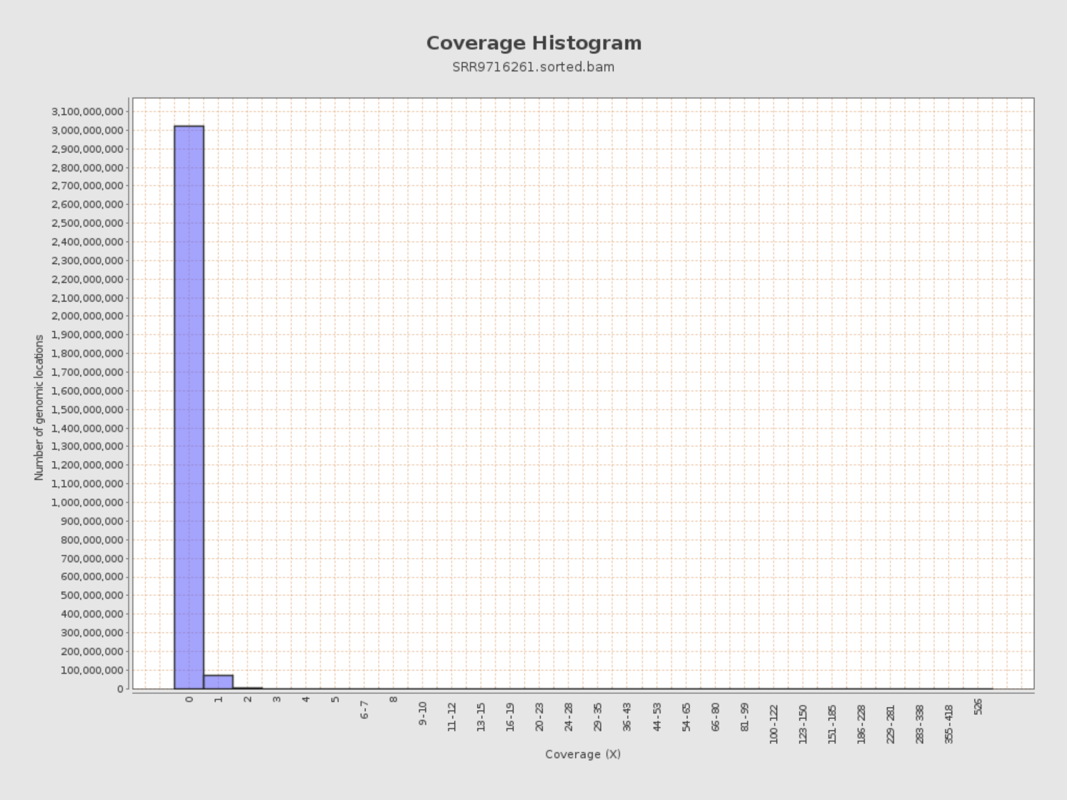
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7311791	0.0293	0.3549
chr2	243199373	8596503	0.0353	0.3315
chr3	198022430	6363399	0.0321	0.206
chr4	191154276	4888208	0.0256	0.2195
chr5	180915260	4406465	0.0244	0.1722
chr6	171115067	4809454	0.0281	0.1935
chr7	159138663	4284152	0.0269	0.4344

chr8	146364022	6251086	0.0427	0.3404
chr9	141213431	3710125	0.0263	0.2019
chr10	135534747	4273537	0.0315	0.3974
chr11	135006516	2605482	0.0193	0.1789
chr12	133851895	4092426	0.0306	0.2101
chr13	115169878	2252571	0.0196	0.1536
chr14	107349540	2844567	0.0265	0.1832
chr15	102531392	2115050	0.0206	0.1601
chr16	90354753	2738532	0.0303	0.1998
chr17	81195210	3797753	0.0468	0.2512
chr18	78077248	1951582	0.025	0.2983
chr19	59128983	1828196	0.0309	0.3158
chr20	63025520	2055545	0.0326	0.2079
chr21	48129895	929555	0.0193	0.1805
chr22	51304566	1412905	0.0275	0.184
chrMT	16571	10716	0.6467	0.9339
chrX	155270560	2985585	0.0192	0.1661
chrY	59373566	235072	0.004	0.153

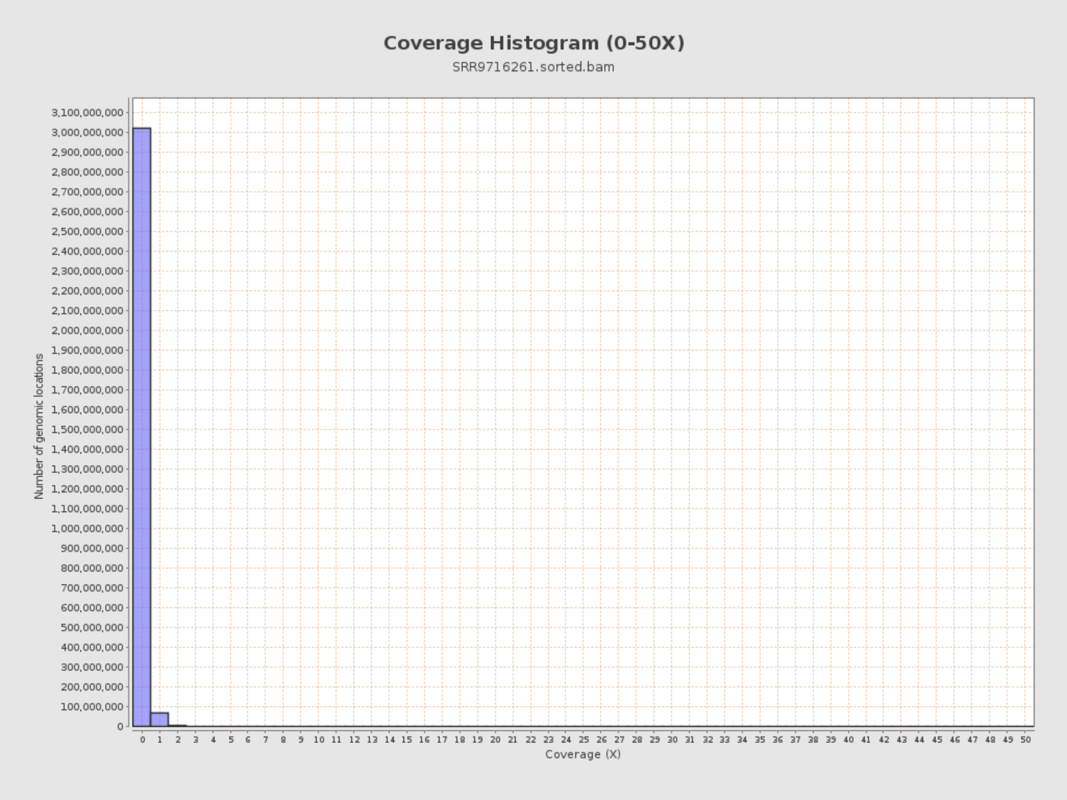
3. Results : Coverage across reference



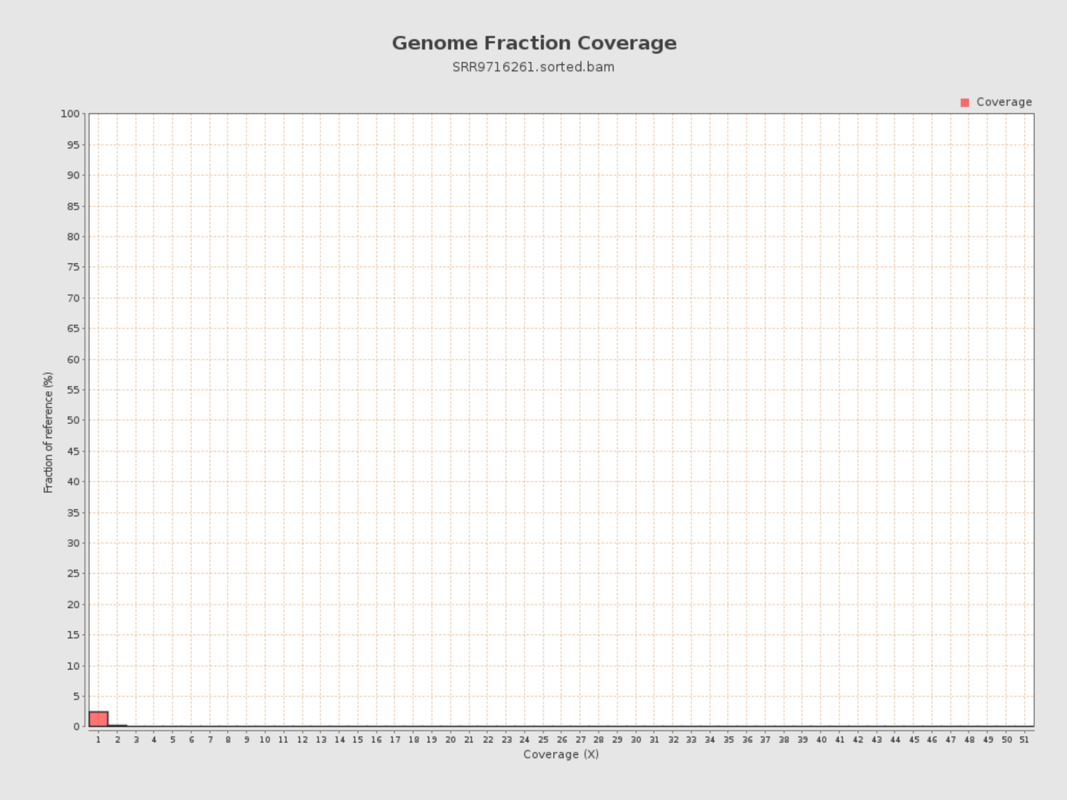
4. Results : Coverage Histogram



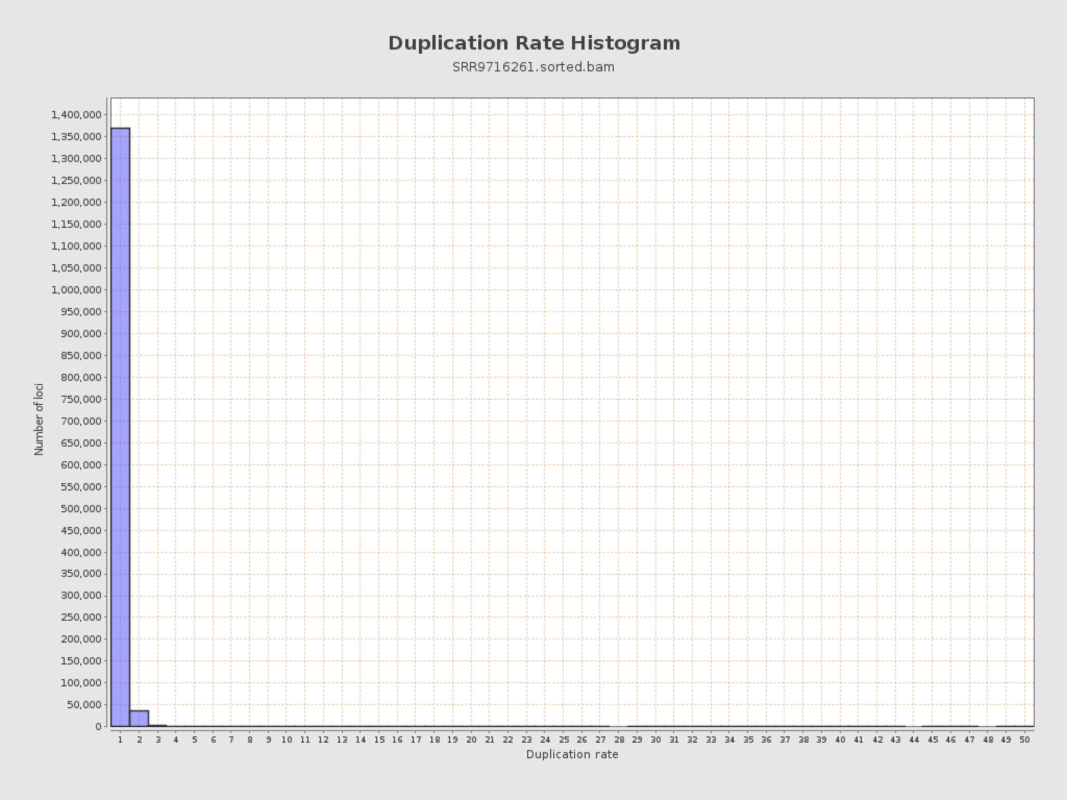
5. Results : Coverage Histogram (0-50X)



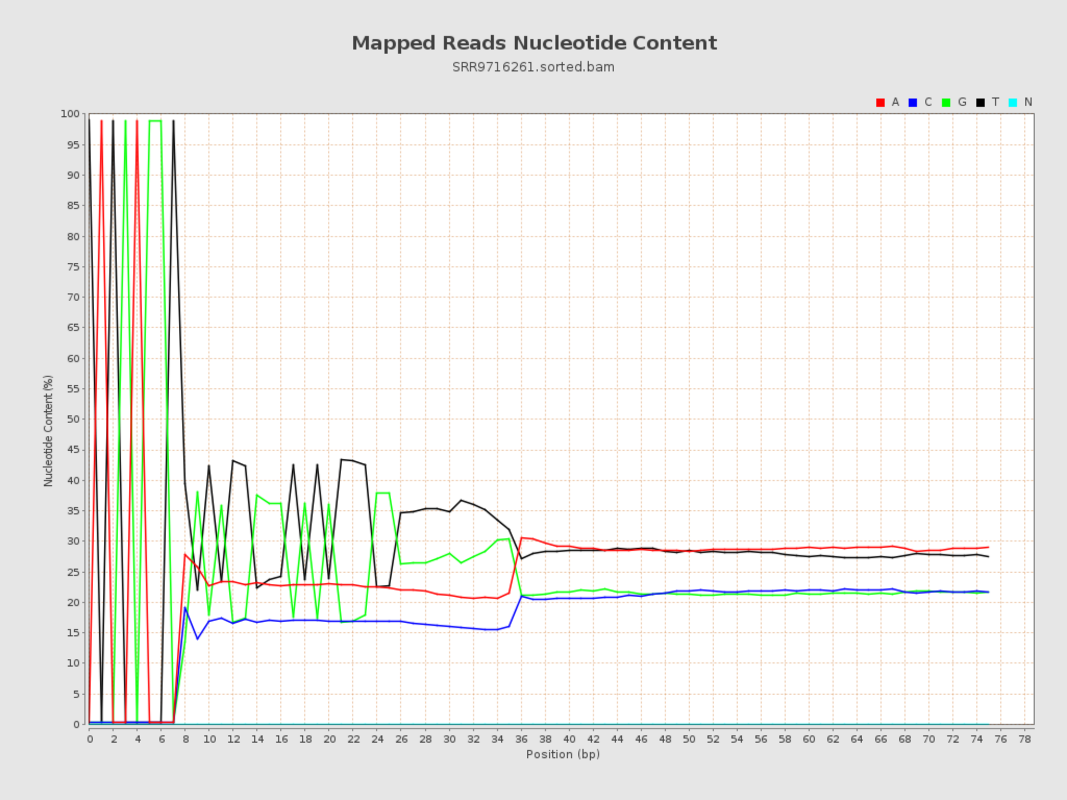
6. Results : Genome Fraction Coverage



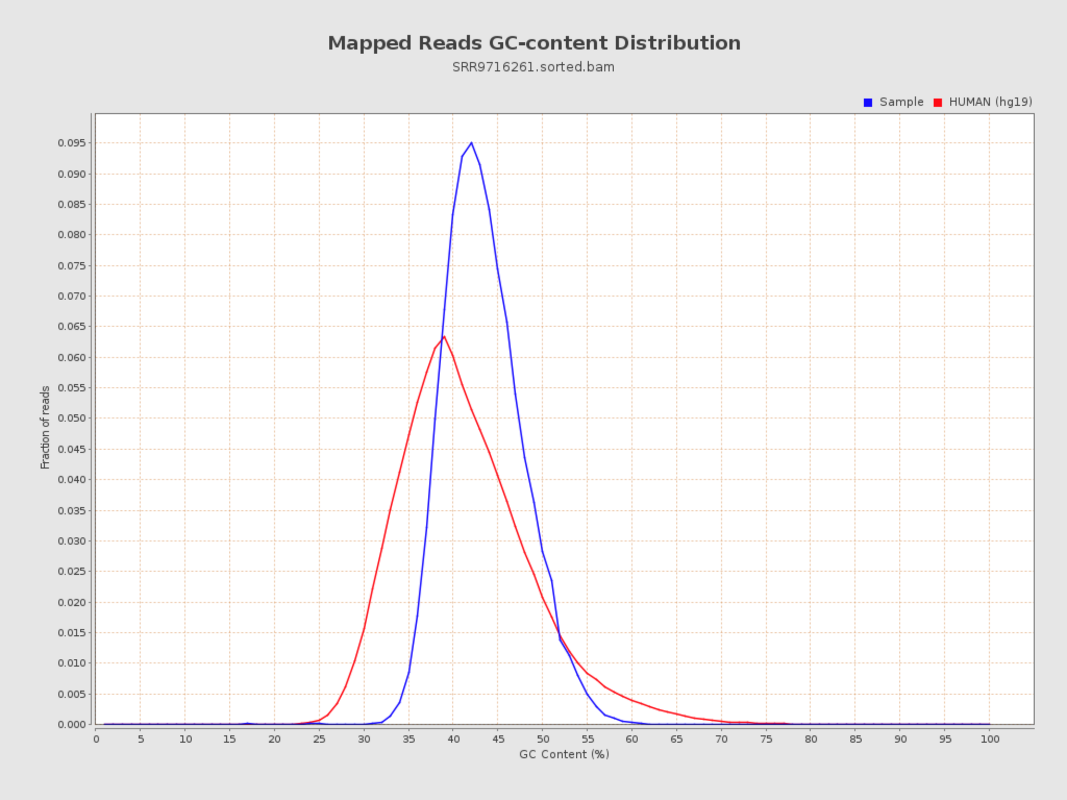
7. Results : Duplication Rate Histogram



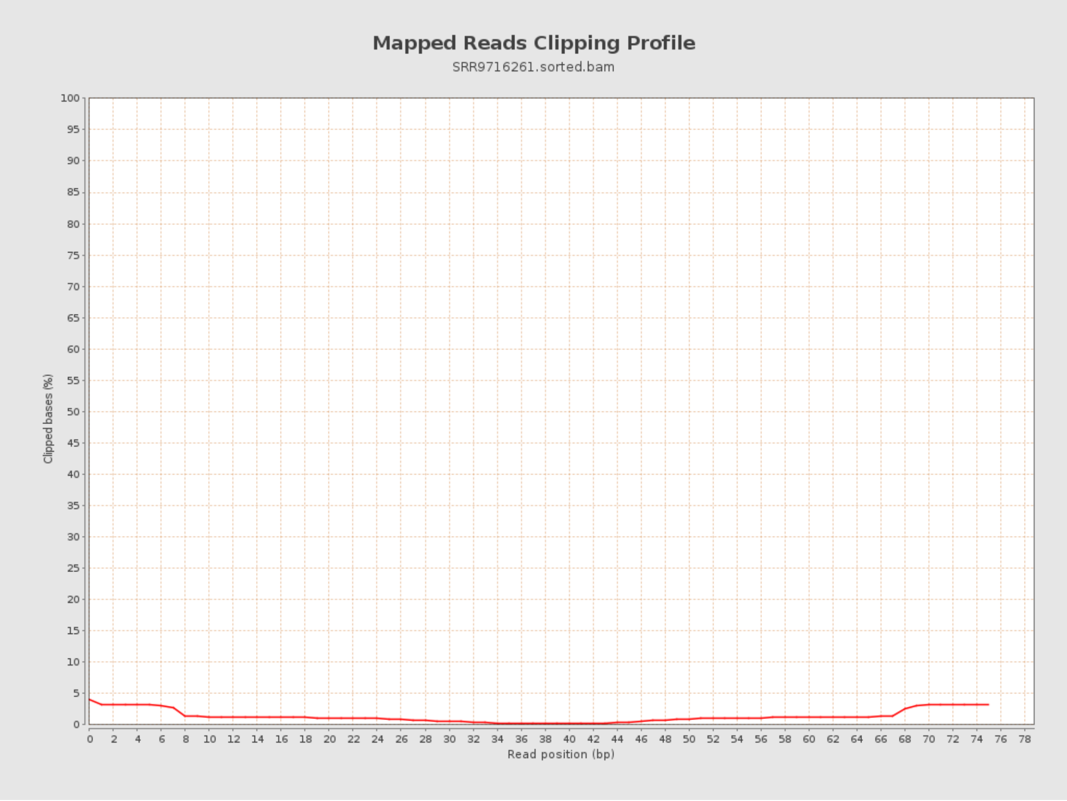
8. Results : Mapped Reads Nucleotide Content



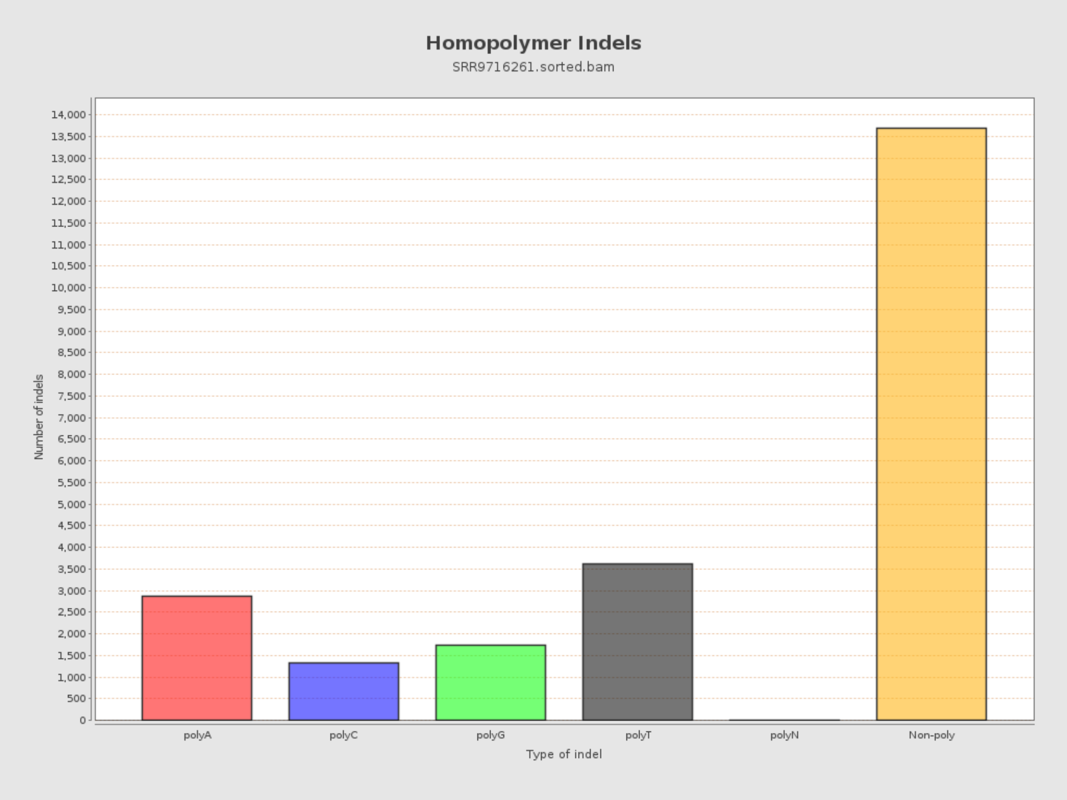
9. Results : Mapped Reads GC-content Distribution



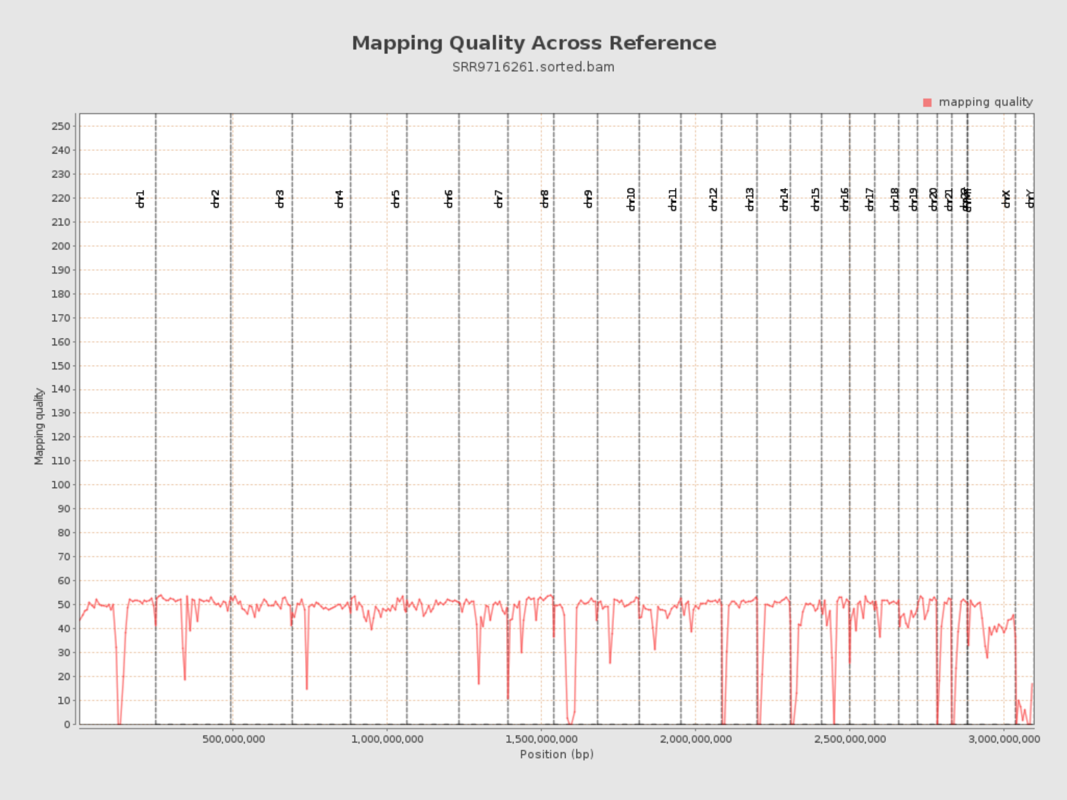
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram