Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:58:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716951.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_SRR9716951 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716951.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:58:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716951.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,196,325
Mapped reads	1,063,241 / 88.88%
Unmapped reads	133,084 / 11.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,746 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	31,135 / 2.6%
Duplication rate	2.26%
Clipped reads	1,065,911 / 89.1%

2.2. ACGT Content

Number/percentage of A's	14,759,029 / 23.91%
Number/percentage of C's	12,428,564 / 20.13%
Number/percentage of T's	19,891,431 / 32.22%
Number/percentage of G's	14,651,744 / 23.73%
Number/percentage of N's	850 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.1909

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

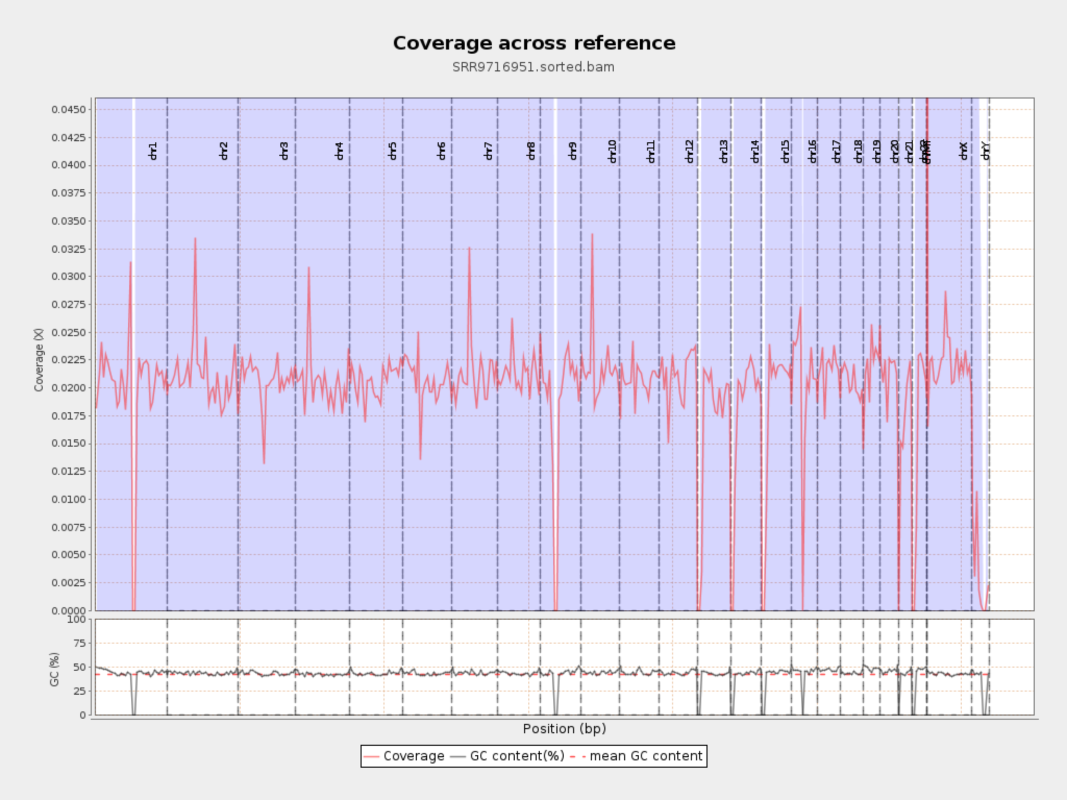
General error rate	0.52%
Mismatches	312,686
Insertions	4,778
Mapped reads with at least one insertion	0.45%
Deletions	11,422
Mapped reads with at least one deletion	1.07%
Homopolymer indels	39.39%

2.6. Chromosome stats

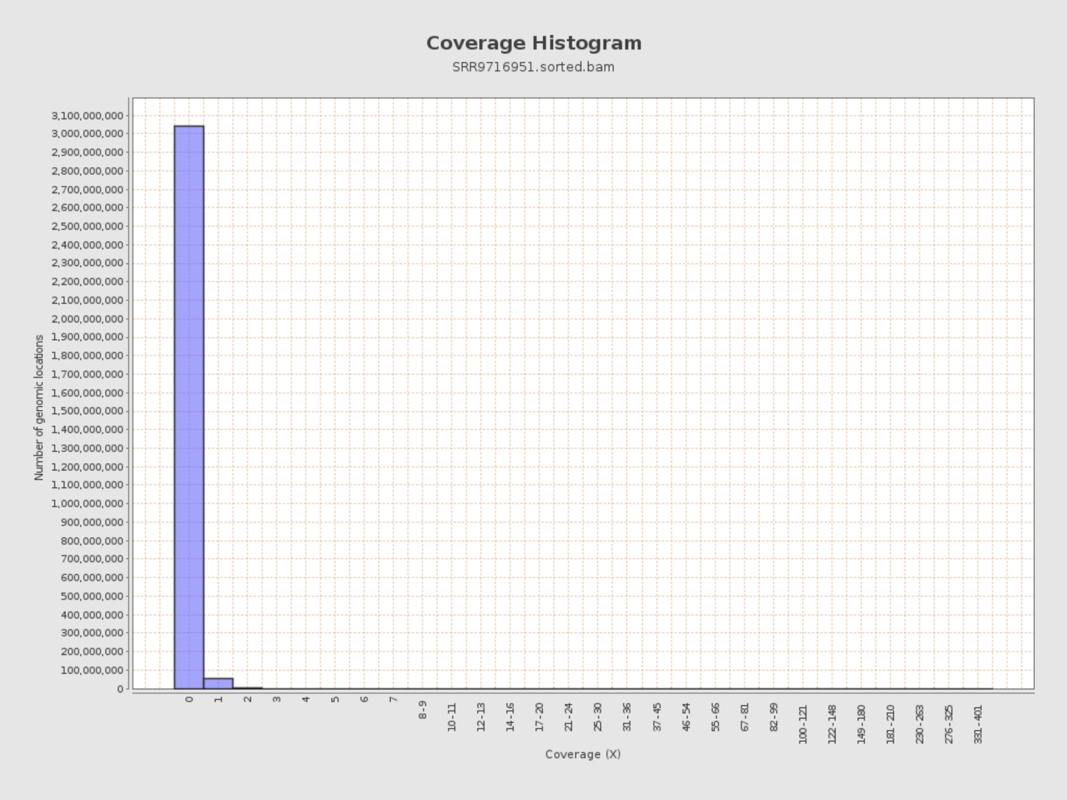
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4944833	0.0198	0.2849
chr2	243199373	5150832	0.0212	0.2398
chr3	198022430	4088323	0.0206	0.1537
chr4	191154276	3939394	0.0206	0.1654
chr5	180915260	3744814	0.0207	0.1537
chr6	171115067	3532633	0.0206	0.1629
chr7	159138663	3405206	0.0214	0.25

chr8	146364022	3118705	0.0213	0.1894
chr9	141213431	2588495	0.0183	0.1652
chr10	135534747	2958402	0.0218	0.1952
chr11	135006516	2810854	0.0208	0.1826
chr12	133851895	2827051	0.0211	0.1562
chr13	115169878	1894597	0.0165	0.137
chr14	107349540	1879003	0.0175	0.1456
chr15	102531392	1822425	0.0178	0.1431
chr16	90354753	1810407	0.02	0.1568
chr17	81195210	1757686	0.0216	0.168
chr18	78077248	1605488	0.0206	0.2525
chr19	59128983	1310475	0.0222	0.2371
chr20	63025520	1330124	0.0211	0.1583
chr21	48129895	795517	0.0165	0.1468
chr22	51304566	786401	0.0153	0.1327
chrMT	16571	17249	1.0409	1.1502
chrX	155270560	3442755	0.0222	0.1687
chrY	59373566	188018	0.0032	0.0951

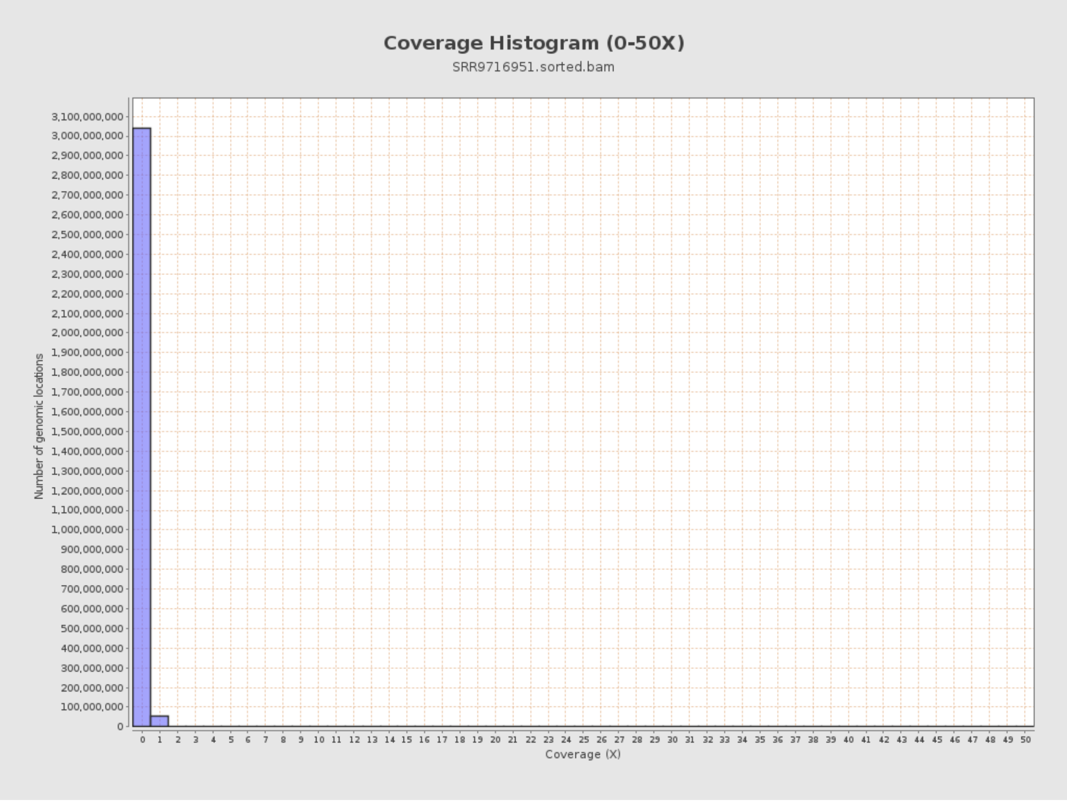
3. Results : Coverage across reference



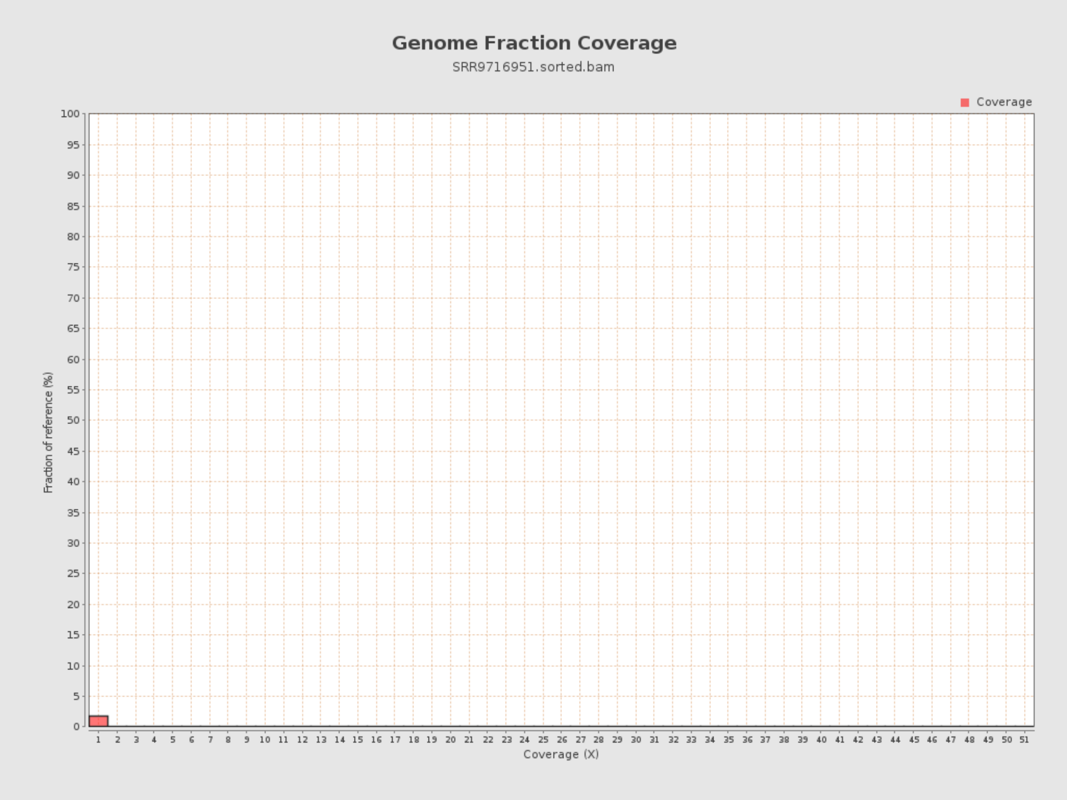
4. Results : Coverage Histogram



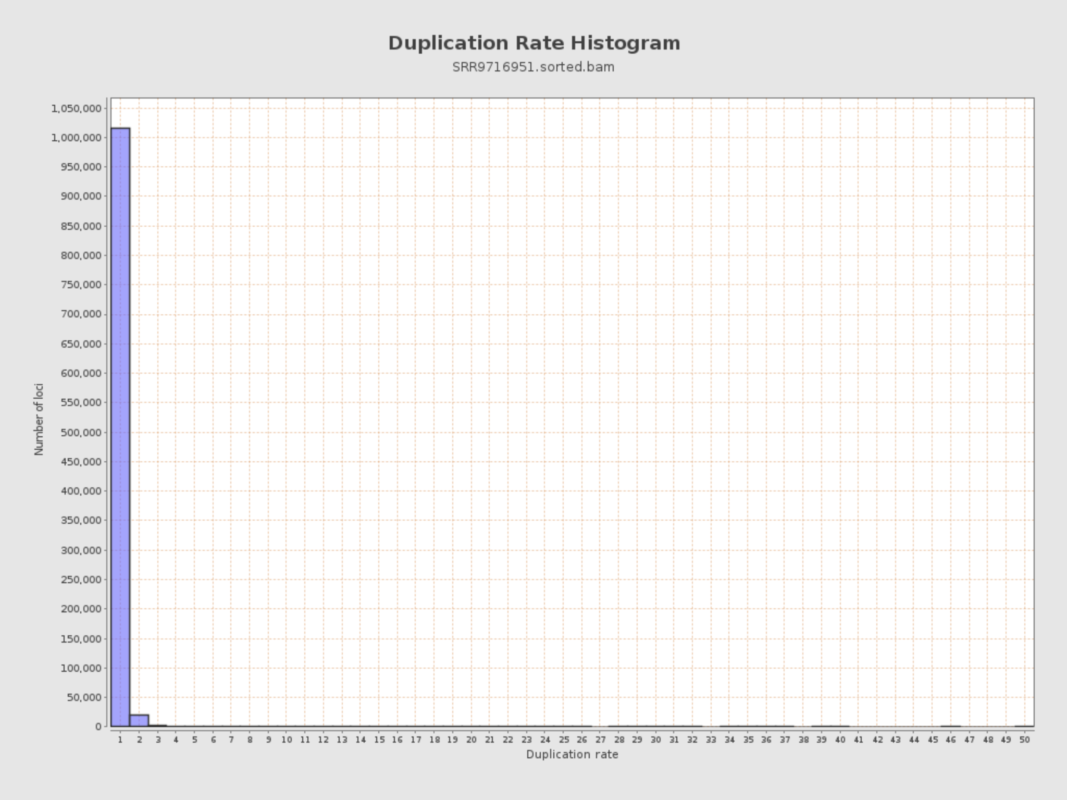
5. Results : Coverage Histogram (0-50X)



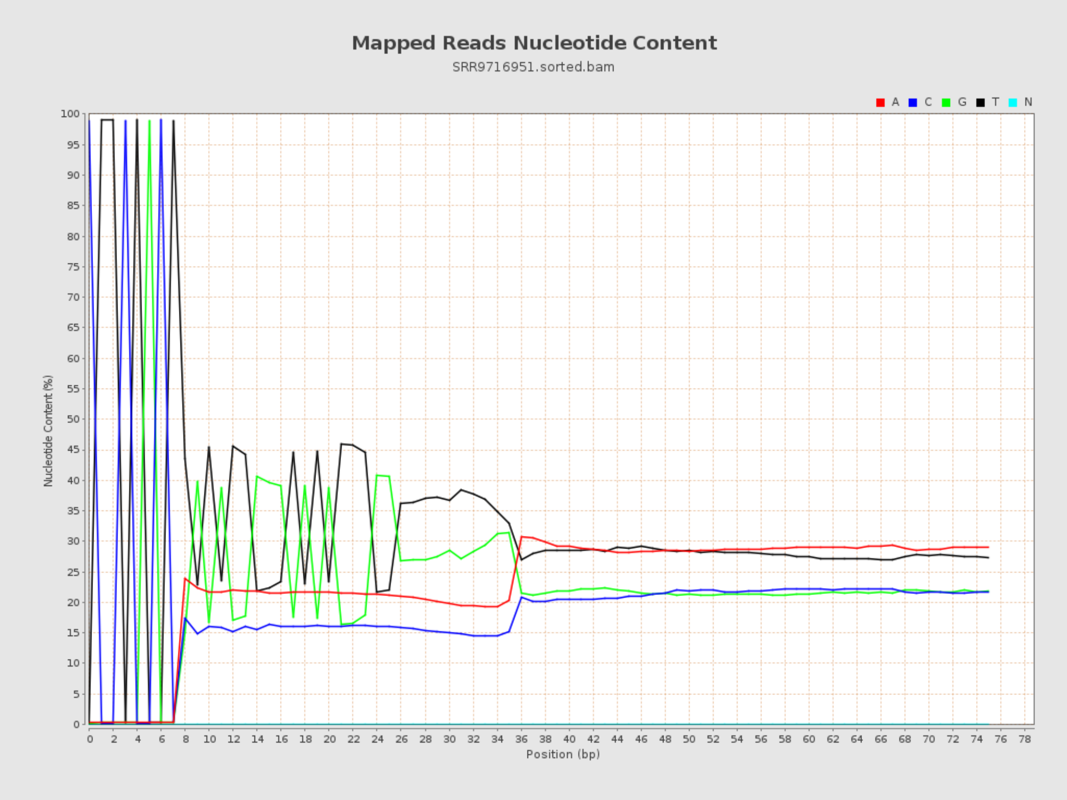
6. Results : Genome Fraction Coverage



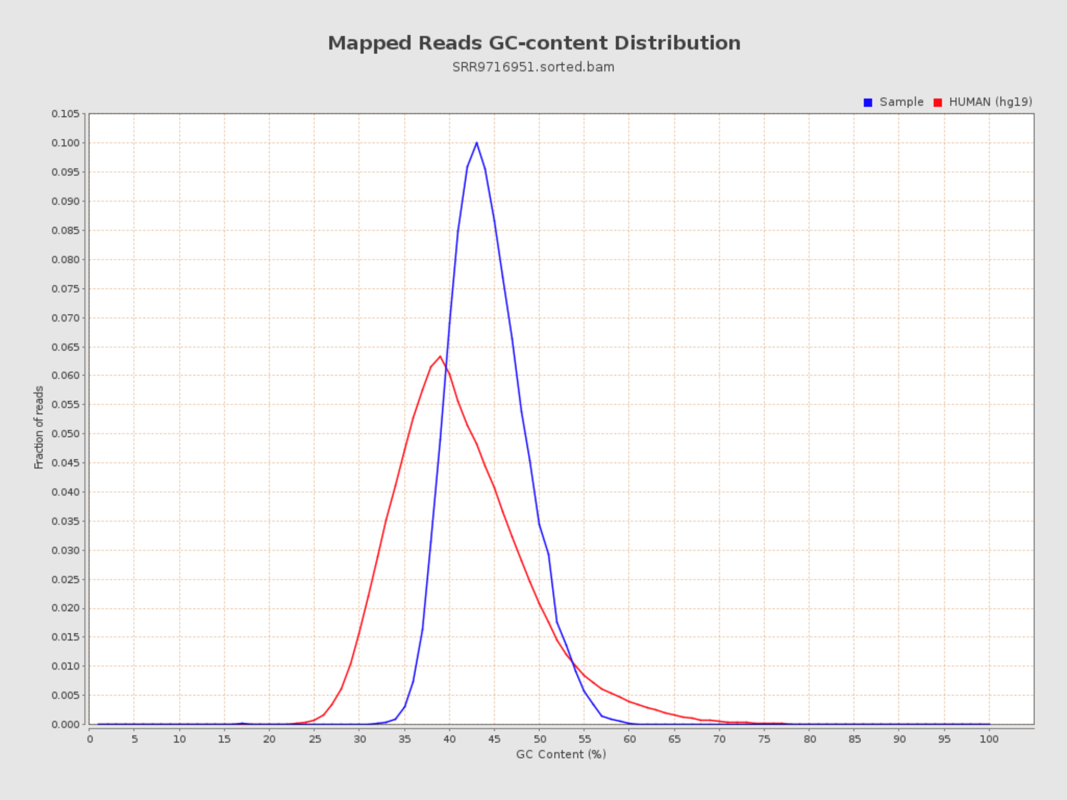
7. Results : Duplication Rate Histogram



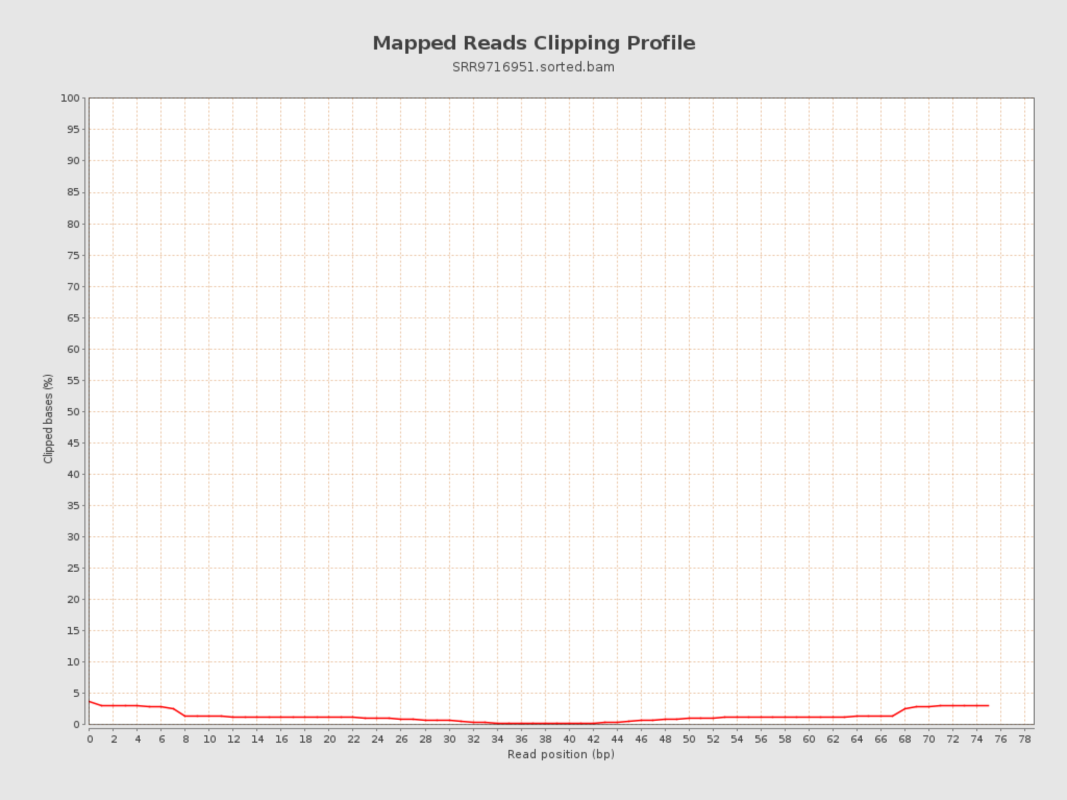
8. Results : Mapped Reads Nucleotide Content



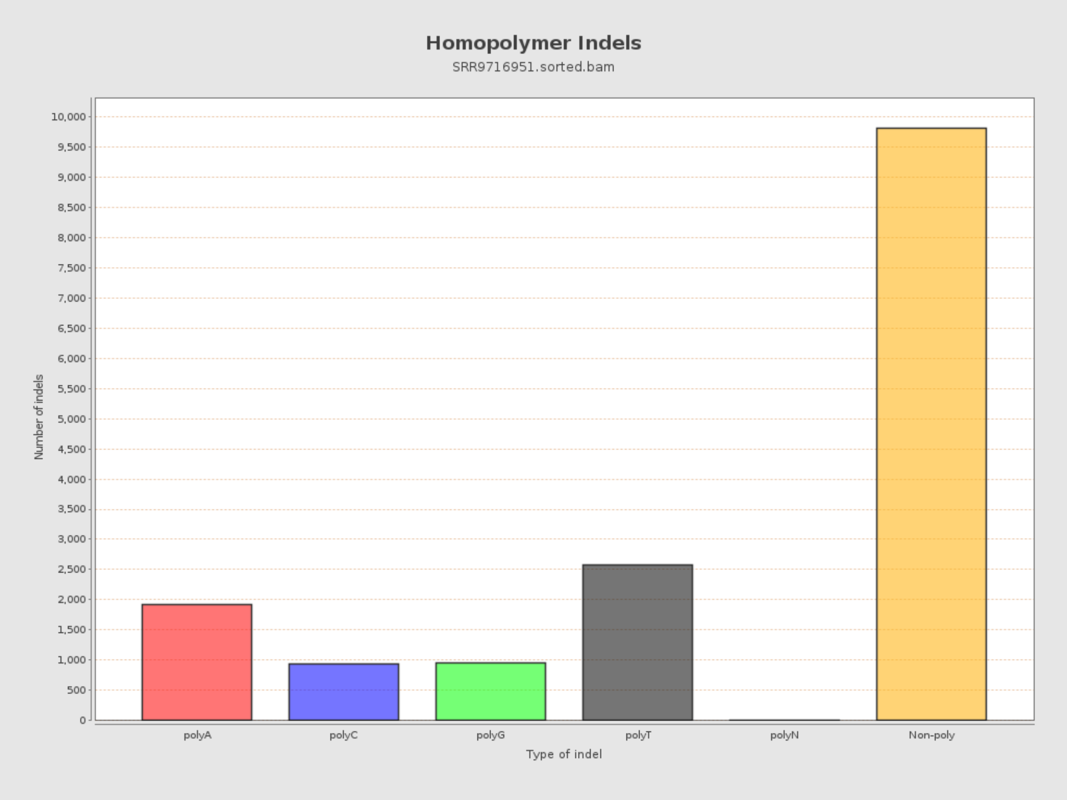
9. Results : Mapped Reads GC-content Distribution



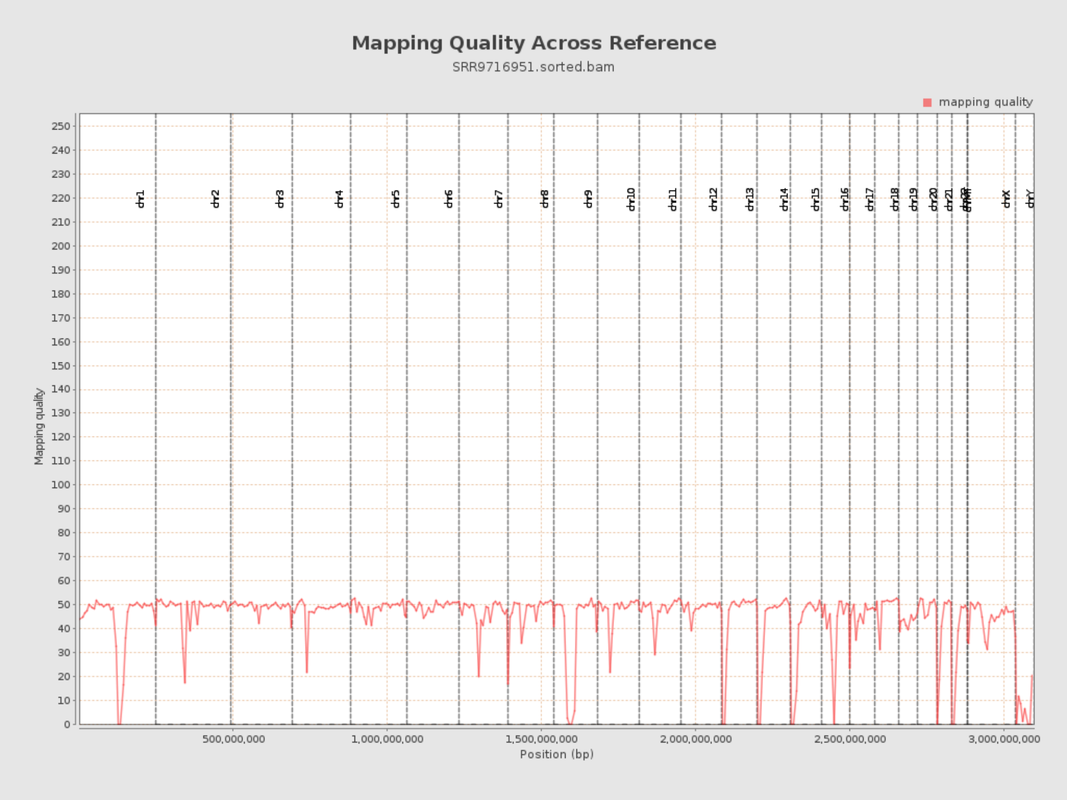
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram