Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:25:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716940.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_SRR9716940 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716940.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:25:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716940.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	579,862
Mapped reads	450,945 / 77.77%
Unmapped reads	128,917 / 22.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	623 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	23,122 / 3.99%
Duplication rate	4.46%
Clipped reads	451,410 / 77.85%

2.2. ACGT Content

Number/percentage of A's	5,337,727 / 21.94%
Number/percentage of C's	4,684,463 / 19.25%
Number/percentage of T's	7,671,944 / 31.53%
Number/percentage of G's	6,639,645 / 27.29%
Number/percentage of N's	453 / 0%
GC Percentage	46.54%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1036

2.4. Mapping Quality

Mean Mapping Quality	43.79

2.5. Mismatches and indels

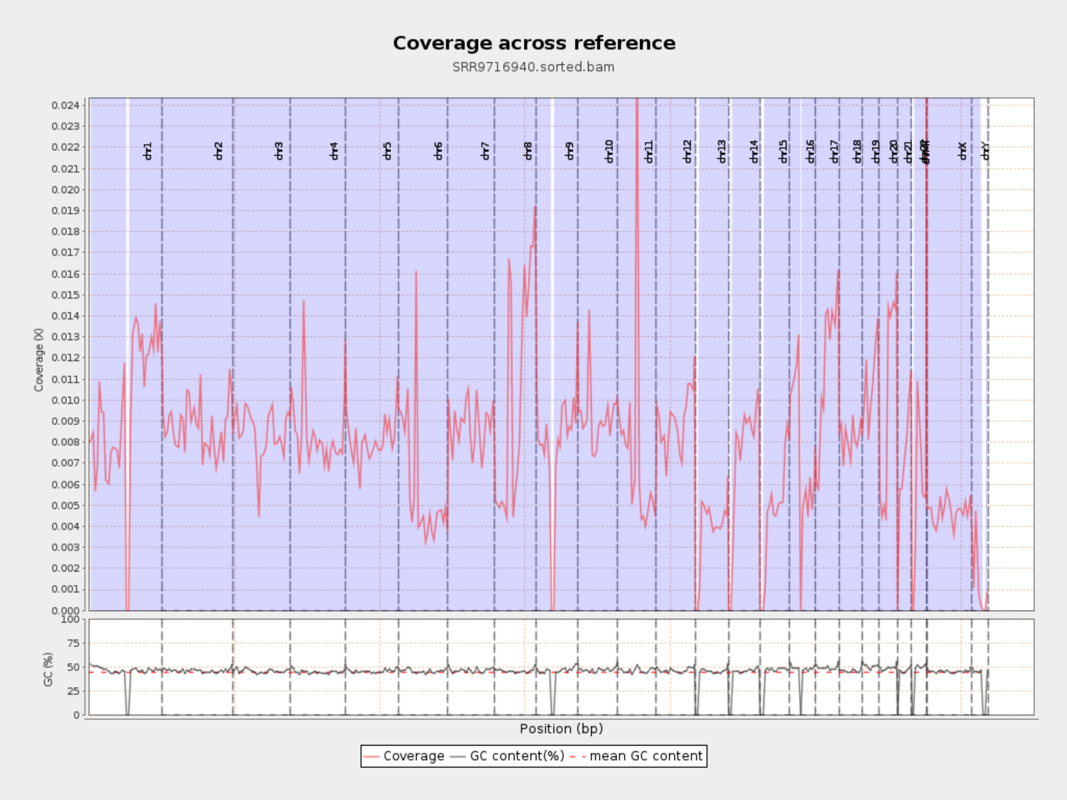
General error rate	0.66%
Mismatches	158,772
Insertions	1,315
Mapped reads with at least one insertion	0.29%
Deletions	3,844
Mapped reads with at least one deletion	0.85%
Homopolymer indels	40.36%

2.6. Chromosome stats

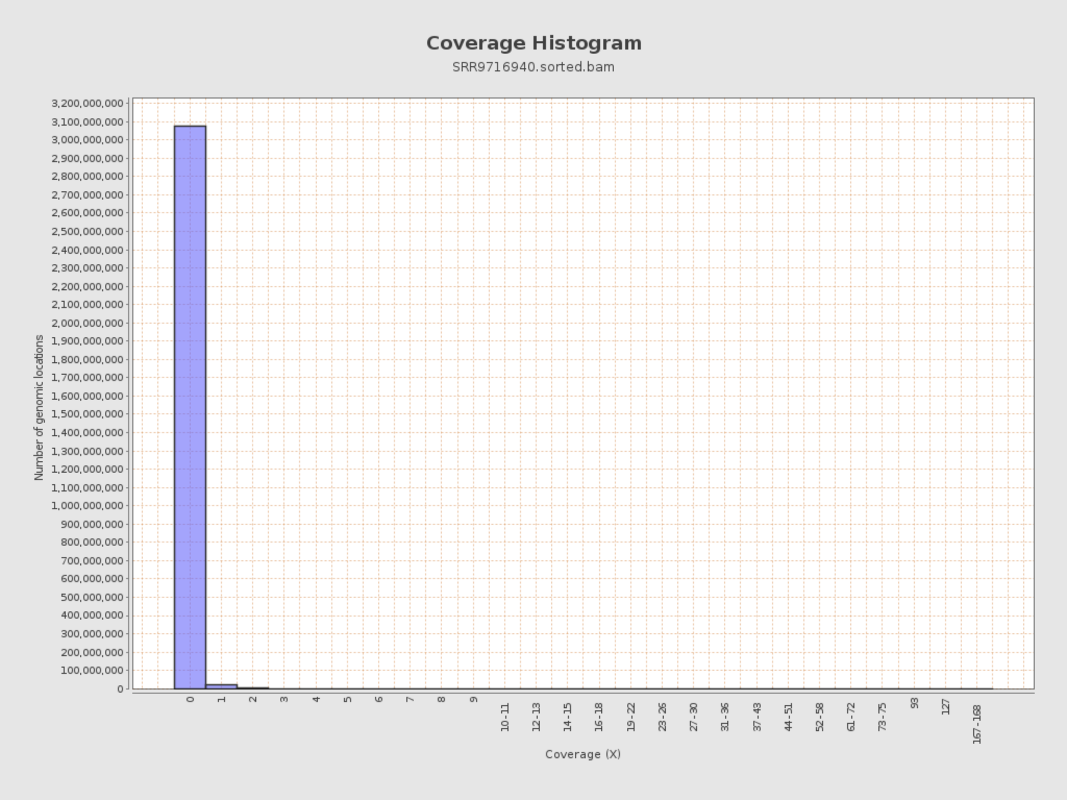
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2390315	0.0096	0.1184
chr2	243199373	2121694	0.0087	0.1268
chr3	198022430	1668786	0.0084	0.1006
chr4	191154276	1579433	0.0083	0.1024
chr5	180915260	1457361	0.0081	0.098
chr6	171115067	1016393	0.0059	0.0889
chr7	159138663	1393553	0.0088	0.1094

chr8	146364022	1534132	0.0105	0.117
chr9	141213431	1061360	0.0075	0.0972
chr10	135534747	1235343	0.0091	0.117
chr11	135006516	1051762	0.0078	0.1025
chr12	133851895	1202939	0.009	0.1051
chr13	115169878	430616	0.0037	0.0667
chr14	107349540	777557	0.0072	0.0934
chr15	102531392	470494	0.0046	0.0737
chr16	90354753	662011	0.0073	0.0992
chr17	81195210	963813	0.0119	0.1229
chr18	78077248	640368	0.0082	0.1067
chr19	59128983	635647	0.0108	0.1359
chr20	63025520	633203	0.01	0.1138
chr21	48129895	341593	0.0071	0.0958
chr22	51304566	263570	0.0051	0.0816
chrMT	16571	849	0.0512	0.2629
chrX	155270560	733783	0.0047	0.0758
chrY	59373566	74423	0.0013	0.0498

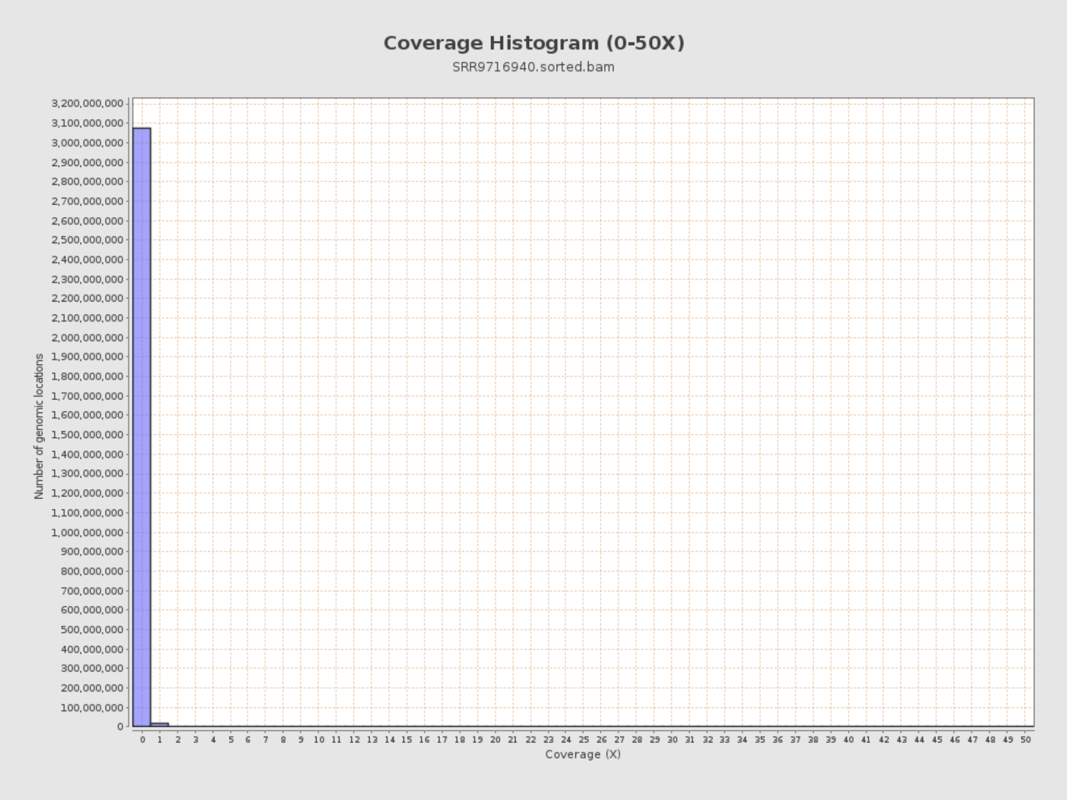
3. Results : Coverage across reference



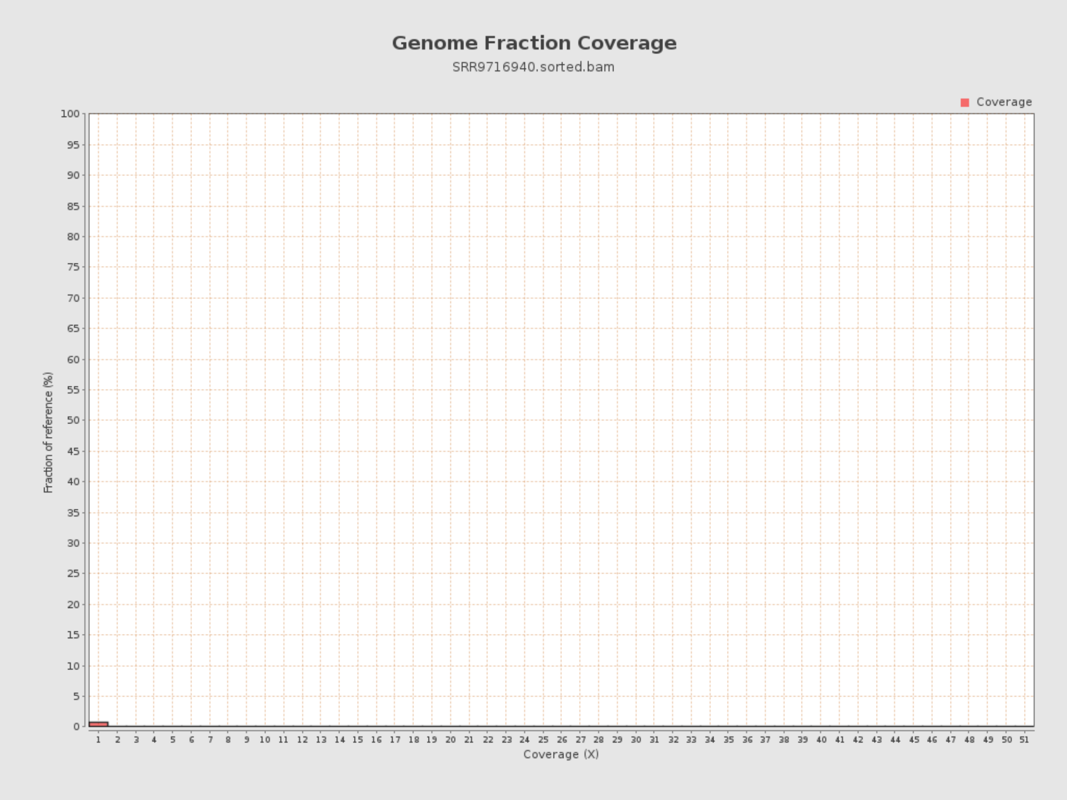
4. Results : Coverage Histogram



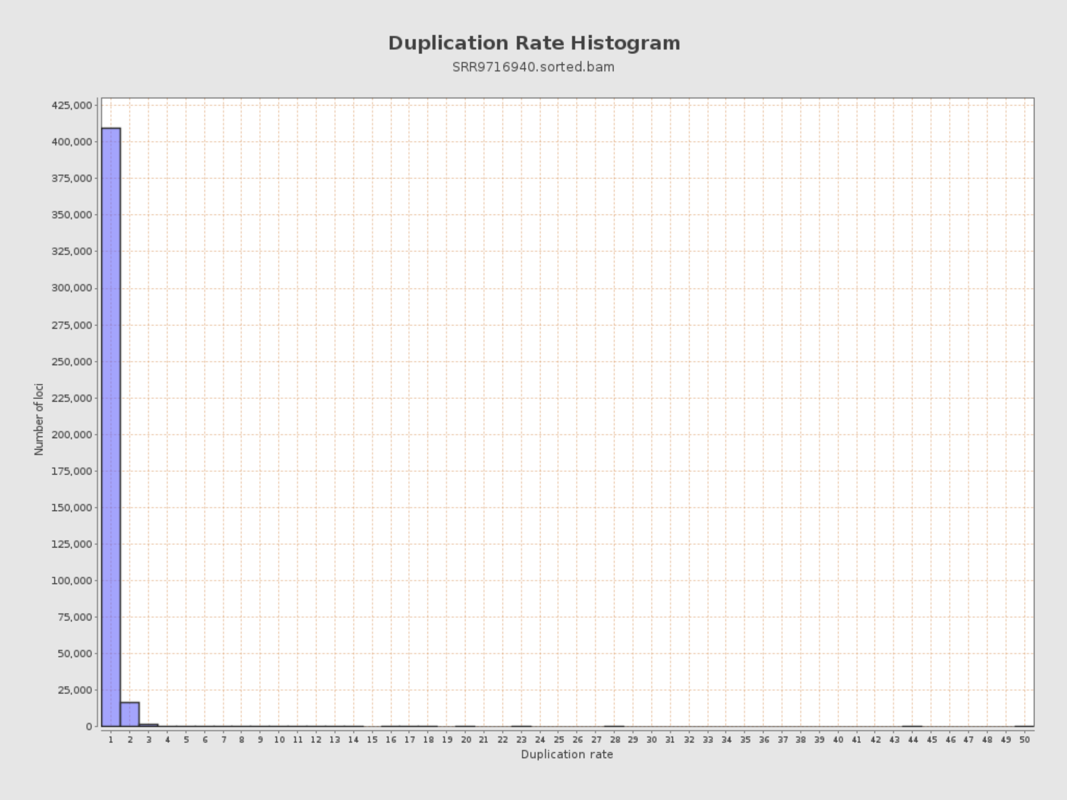
5. Results : Coverage Histogram (0-50X)



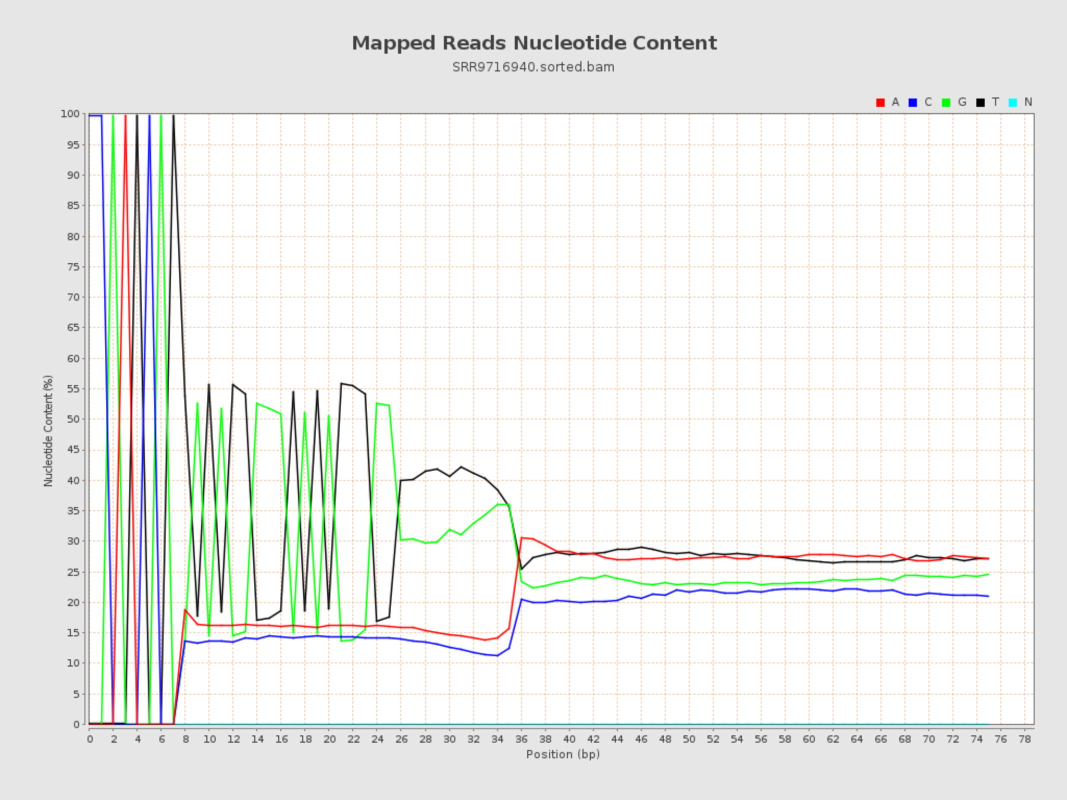
6. Results : Genome Fraction Coverage



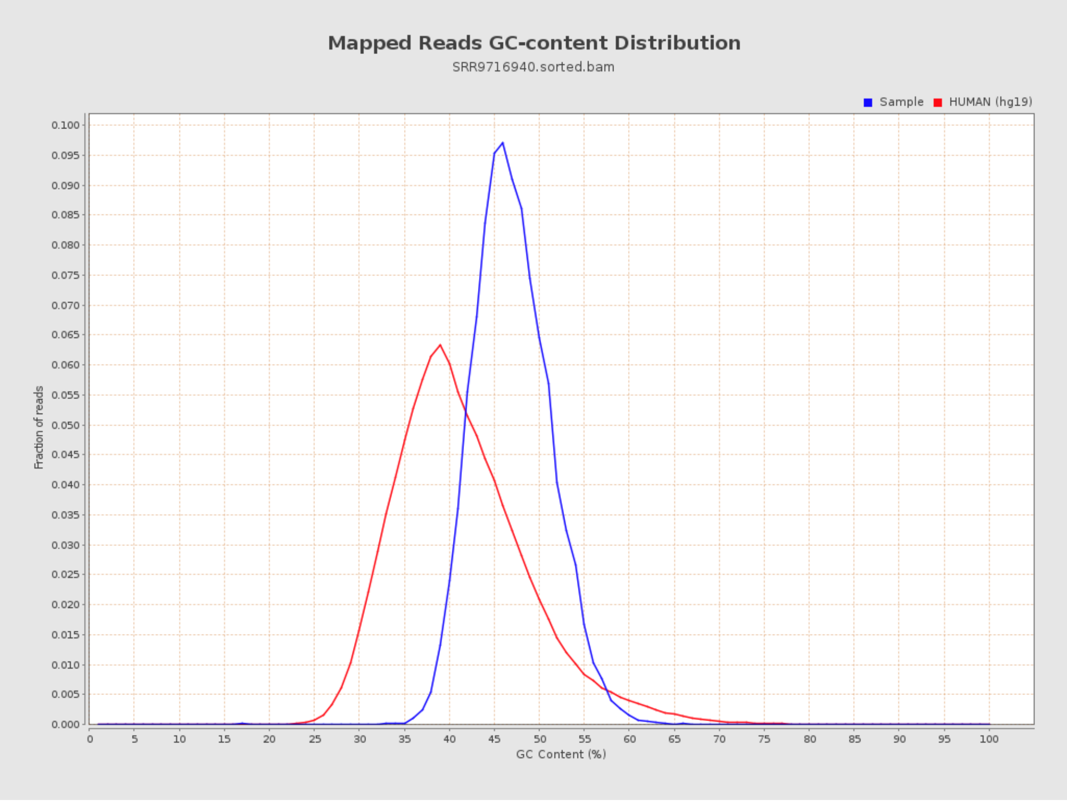
7. Results : Duplication Rate Histogram



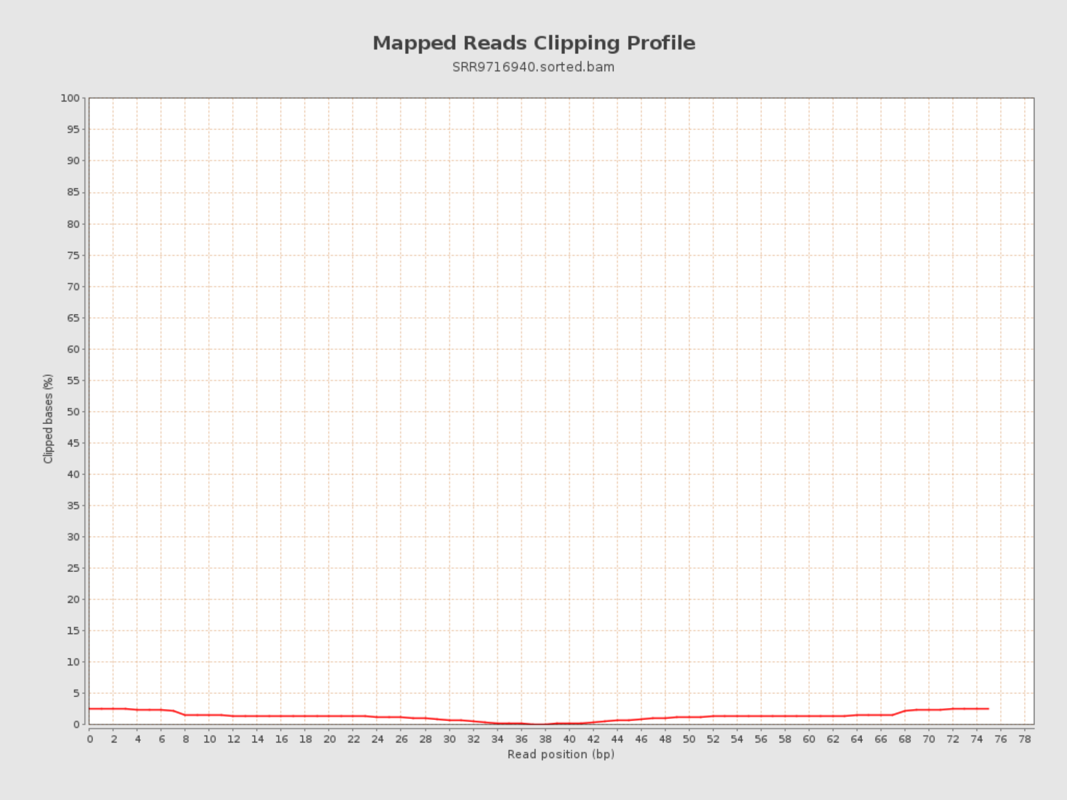
8. Results : Mapped Reads Nucleotide Content



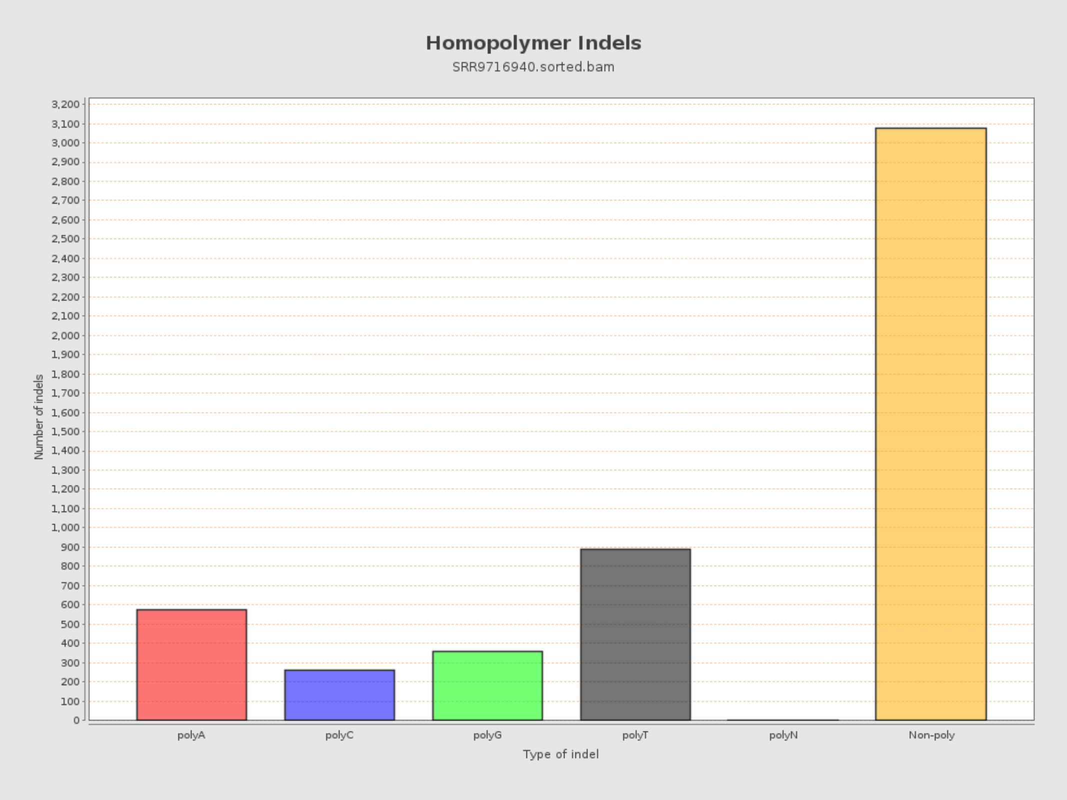
9. Results : Mapped Reads GC-content Distribution



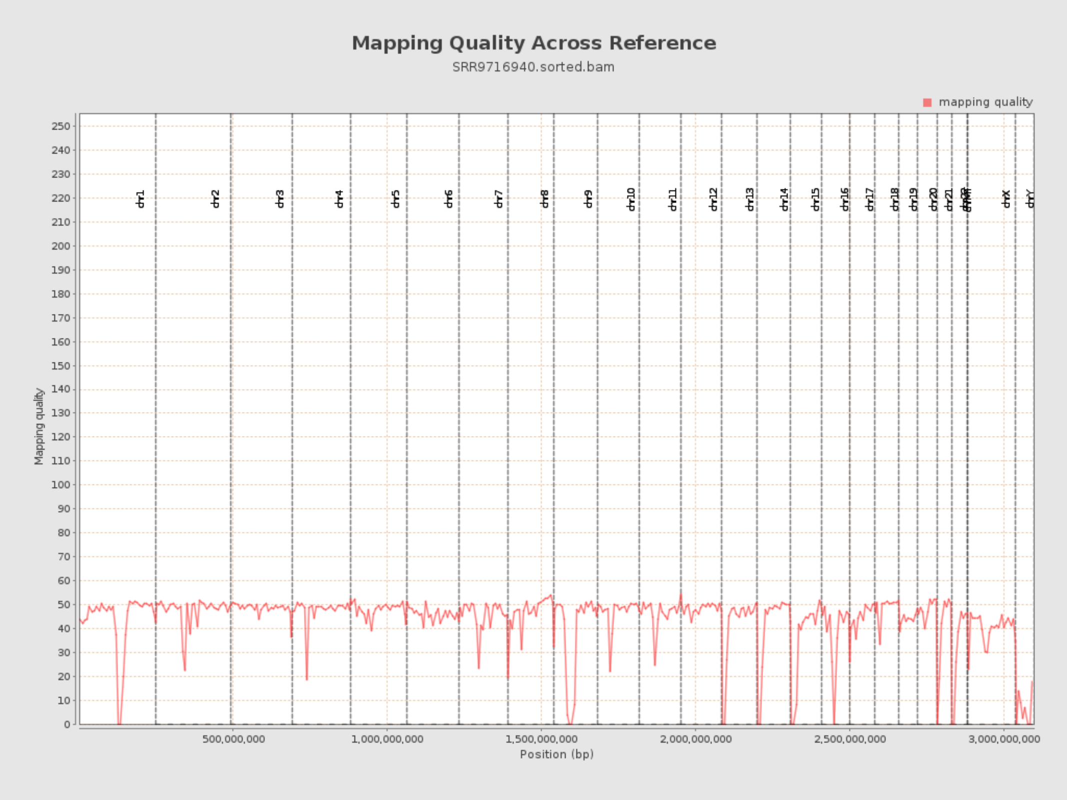
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram