Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:18:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716881.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_SRR9716881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716881.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:18:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	456,084
Mapped reads	407,892 / 89.43%
Unmapped reads	48,192 / 10.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	911 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	7,203 / 1.58%
Duplication rate	1.4%
Clipped reads	408,478 / 89.56%

2.2. ACGT Content

Number/percentage of A's	5,648,963 / 24.47%
Number/percentage of C's	4,386,829 / 19.01%
Number/percentage of T's	7,390,366 / 32.02%
Number/percentage of G's	5,654,982 / 24.5%
Number/percentage of N's	148 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.0995

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

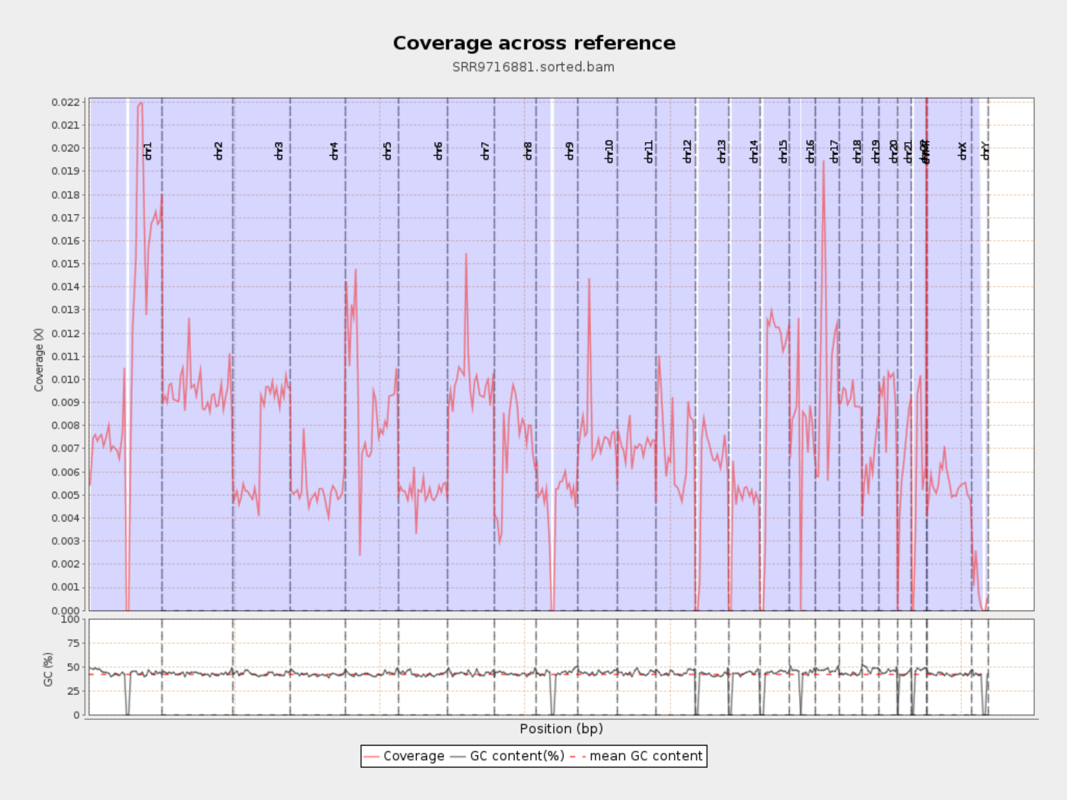
General error rate	0.51%
Mismatches	114,244
Insertions	1,365
Mapped reads with at least one insertion	0.33%
Deletions	4,193
Mapped reads with at least one deletion	1.02%
Homopolymer indels	44.19%

2.6. Chromosome stats

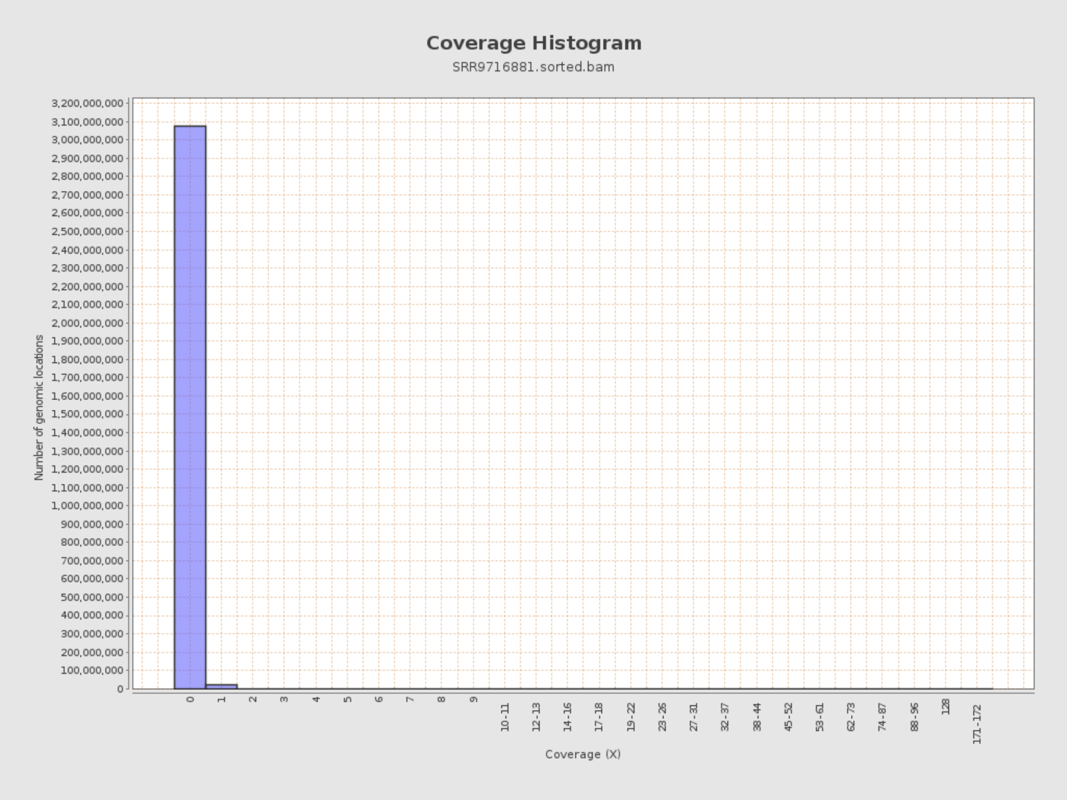
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2728079	0.0109	0.1289
chr2	243199373	2311620	0.0095	0.1269
chr3	198022430	1444691	0.0073	0.0886
chr4	191154276	980195	0.0051	0.075
chr5	180915260	1643917	0.0091	0.0982
chr6	171115067	875243	0.0051	0.0776
chr7	159138663	1589189	0.01	0.1386

chr8	146364022	1035617	0.0071	0.09
chr9	141213431	642112	0.0045	0.0759
chr10	135534747	1050239	0.0077	0.1084
chr11	135006516	962528	0.0071	0.0971
chr12	133851895	951918	0.0071	0.0869
chr13	115169878	672347	0.0058	0.079
chr14	107349540	483093	0.0045	0.0696
chr15	102531392	997151	0.0097	0.1019
chr16	90354753	700128	0.0077	0.0937
chr17	81195210	875015	0.0108	0.109
chr18	78077248	714710	0.0092	0.1279
chr19	59128983	376246	0.0064	0.0968
chr20	63025520	586057	0.0093	0.0994
chr21	48129895	299251	0.0062	0.0818
chr22	51304566	273359	0.0053	0.0751
chrMT	16571	697	0.0421	0.2007
chrX	155270560	841975	0.0054	0.0814
chrY	59373566	52614	0.0009	0.0341

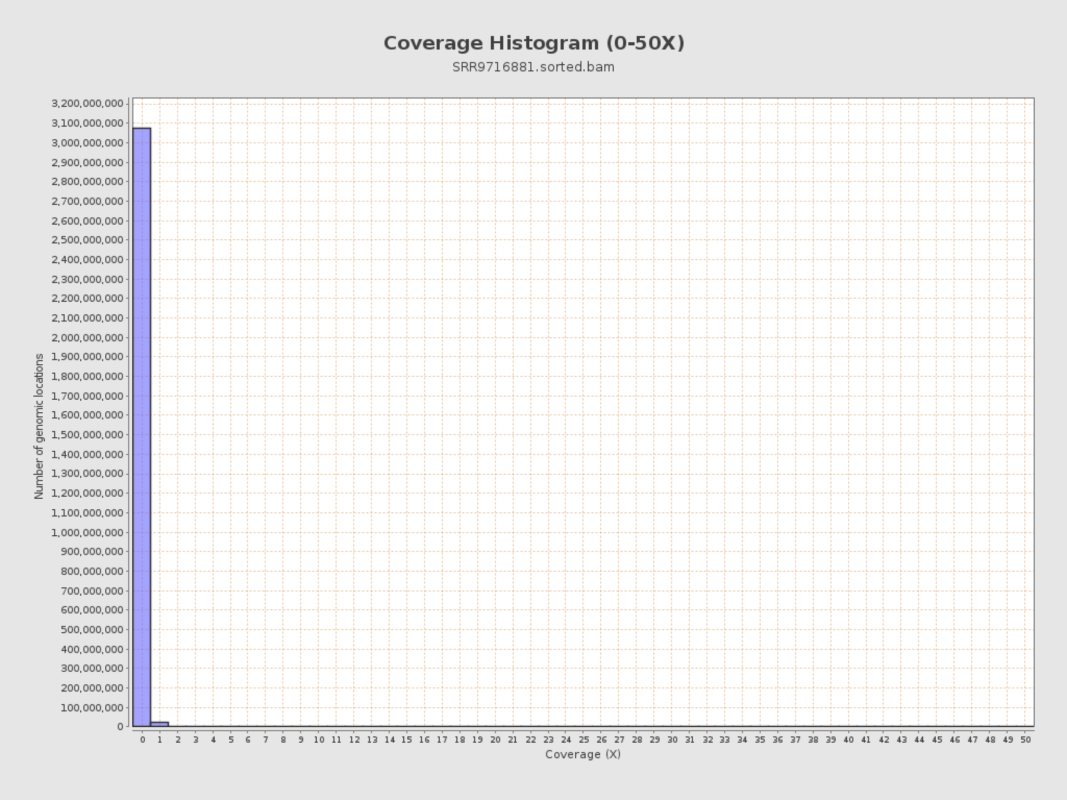
3. Results : Coverage across reference



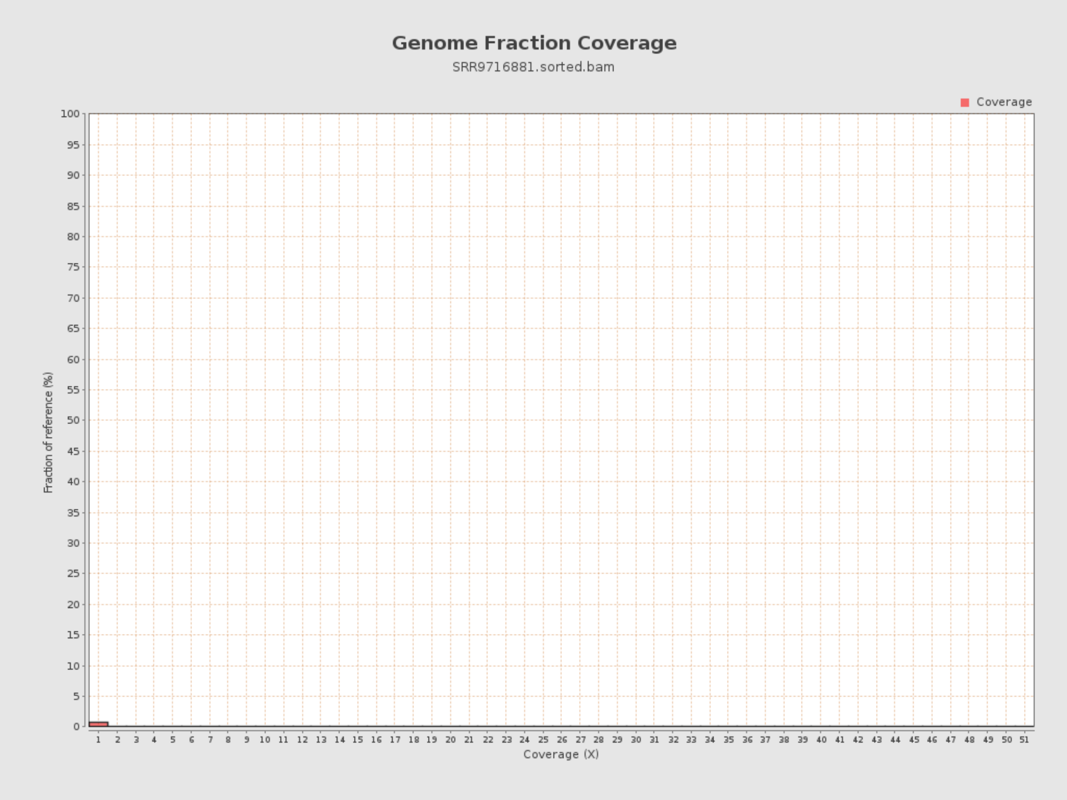
4. Results : Coverage Histogram



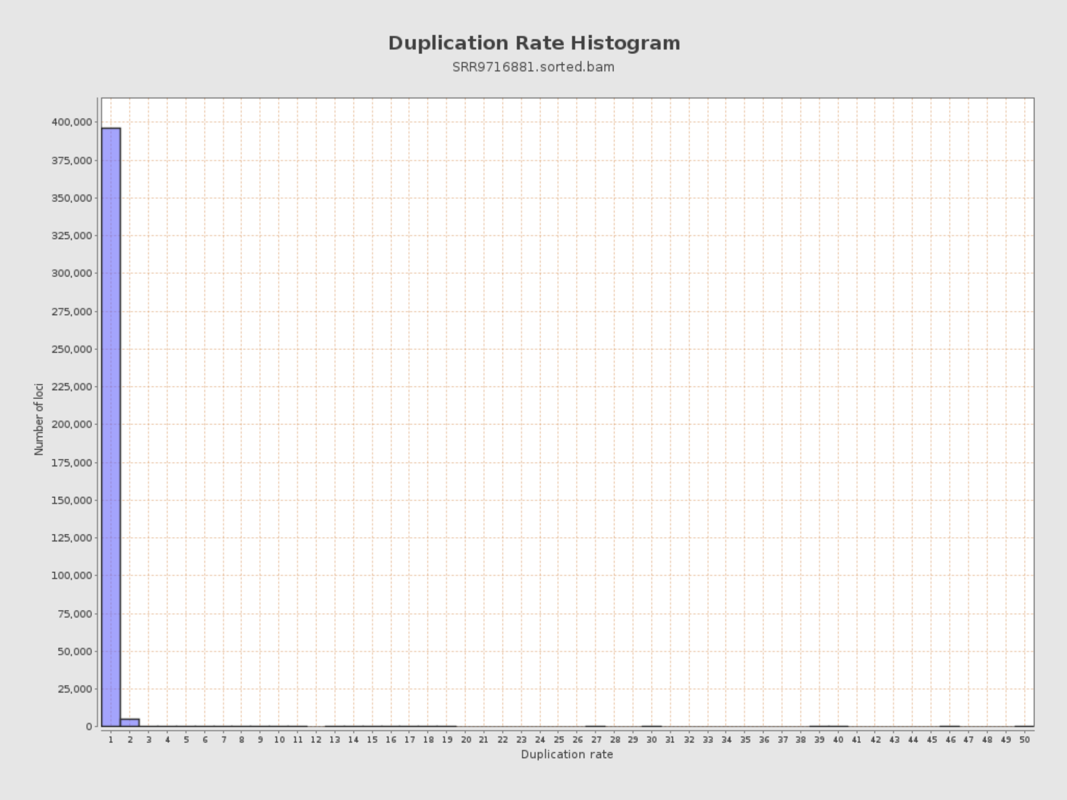
5. Results : Coverage Histogram (0-50X)



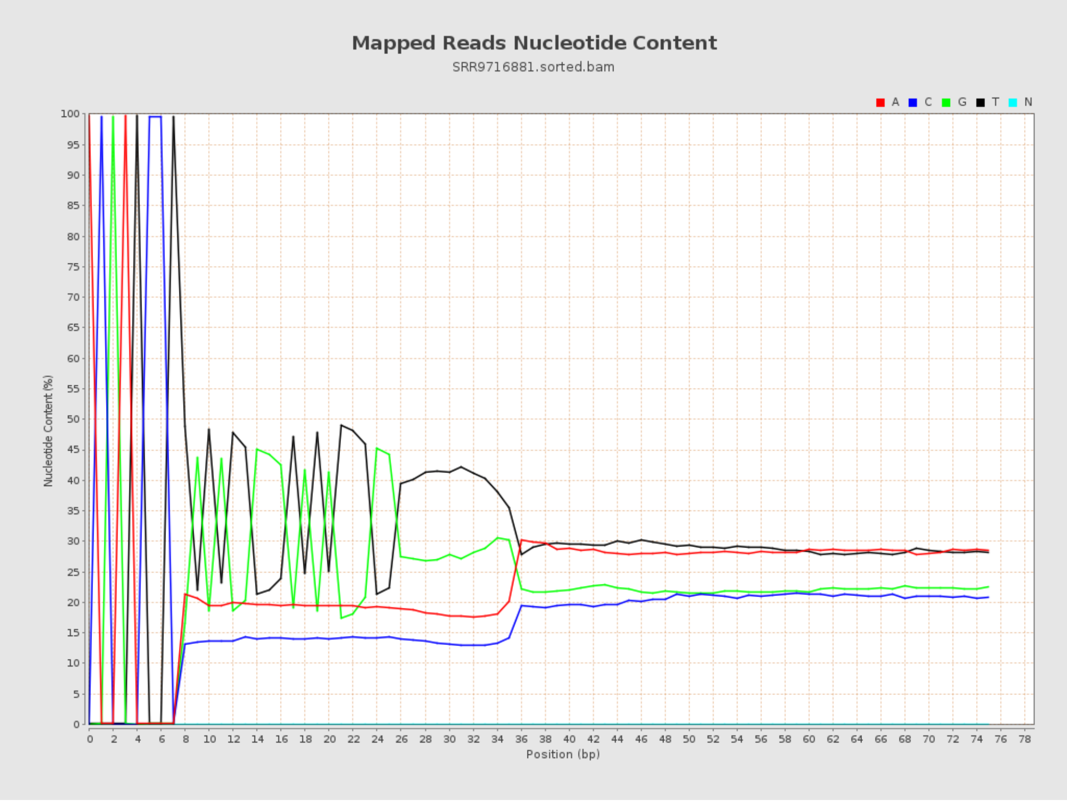
6. Results : Genome Fraction Coverage



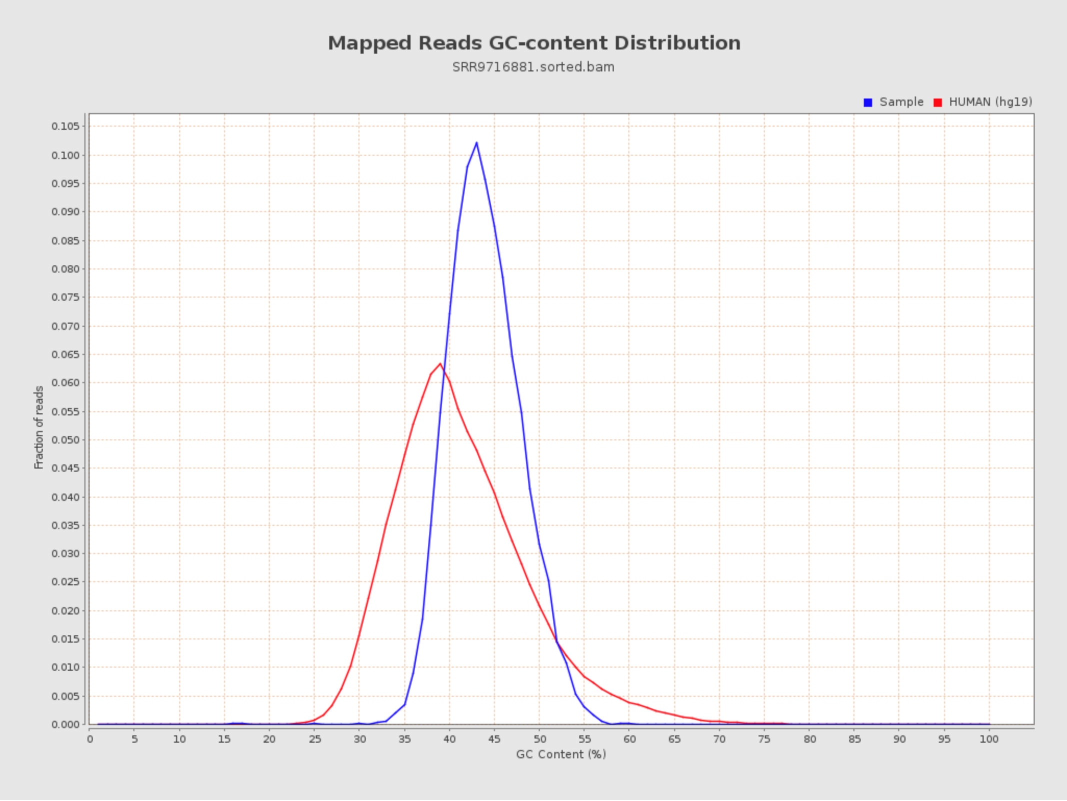
7. Results : Duplication Rate Histogram



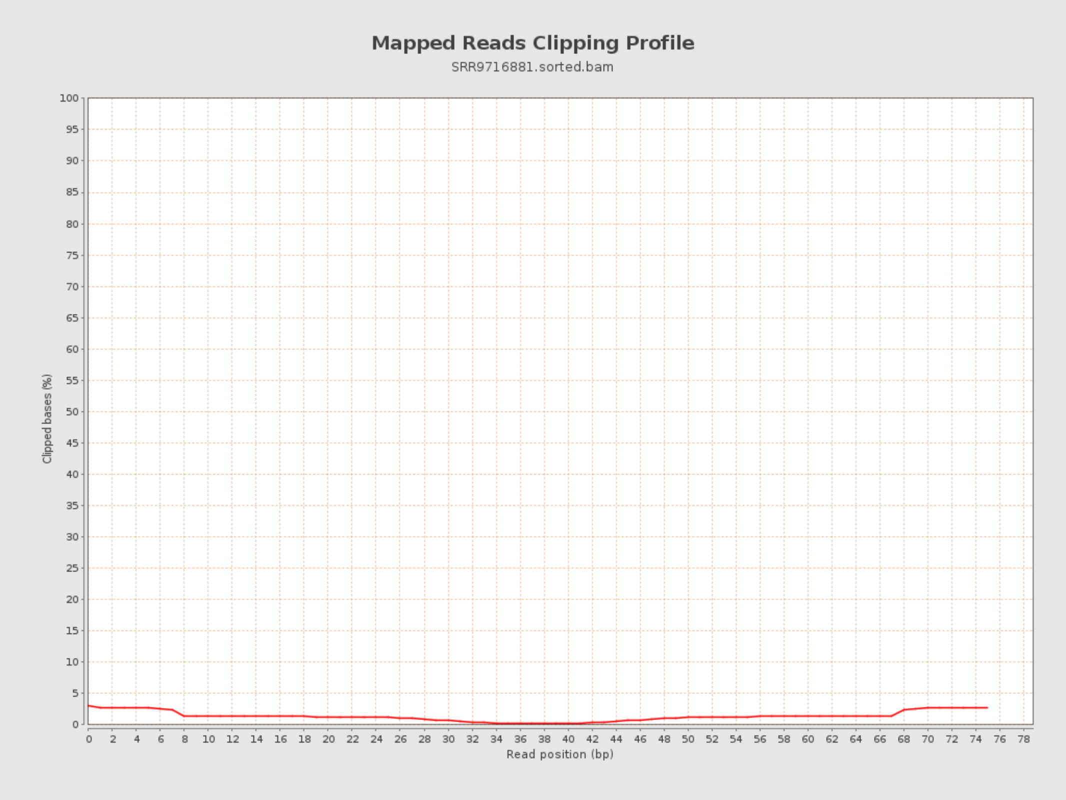
8. Results : Mapped Reads Nucleotide Content



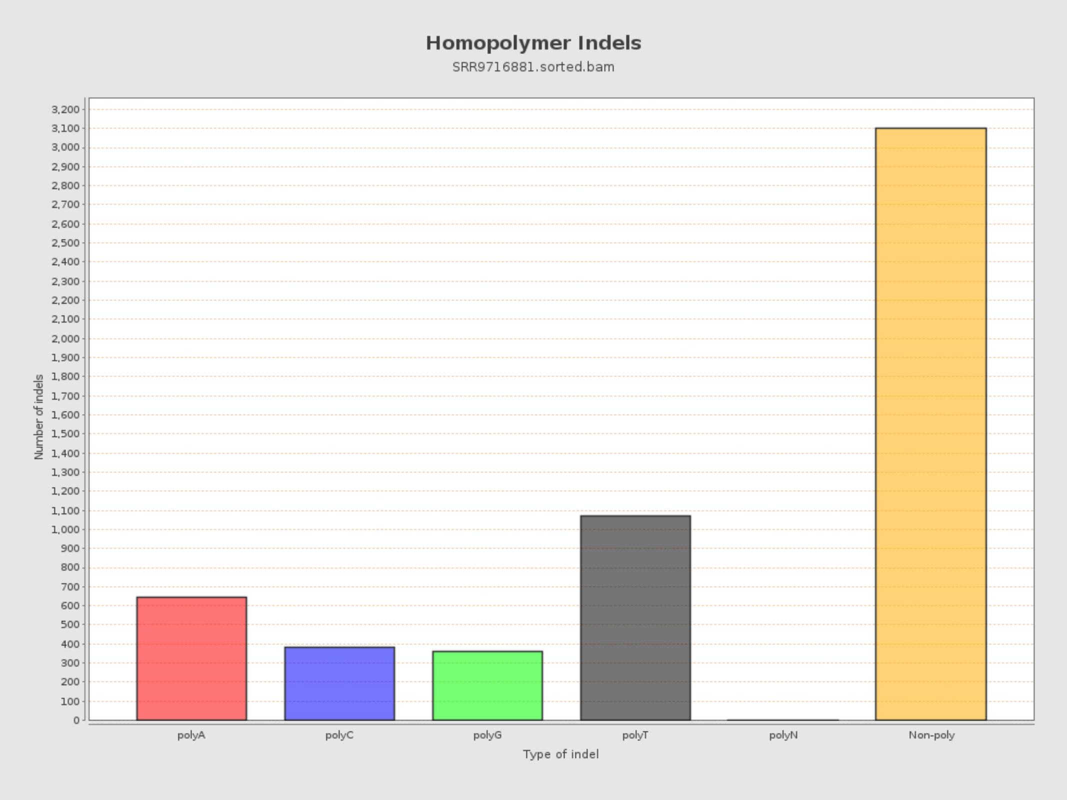
9. Results : Mapped Reads GC-content Distribution



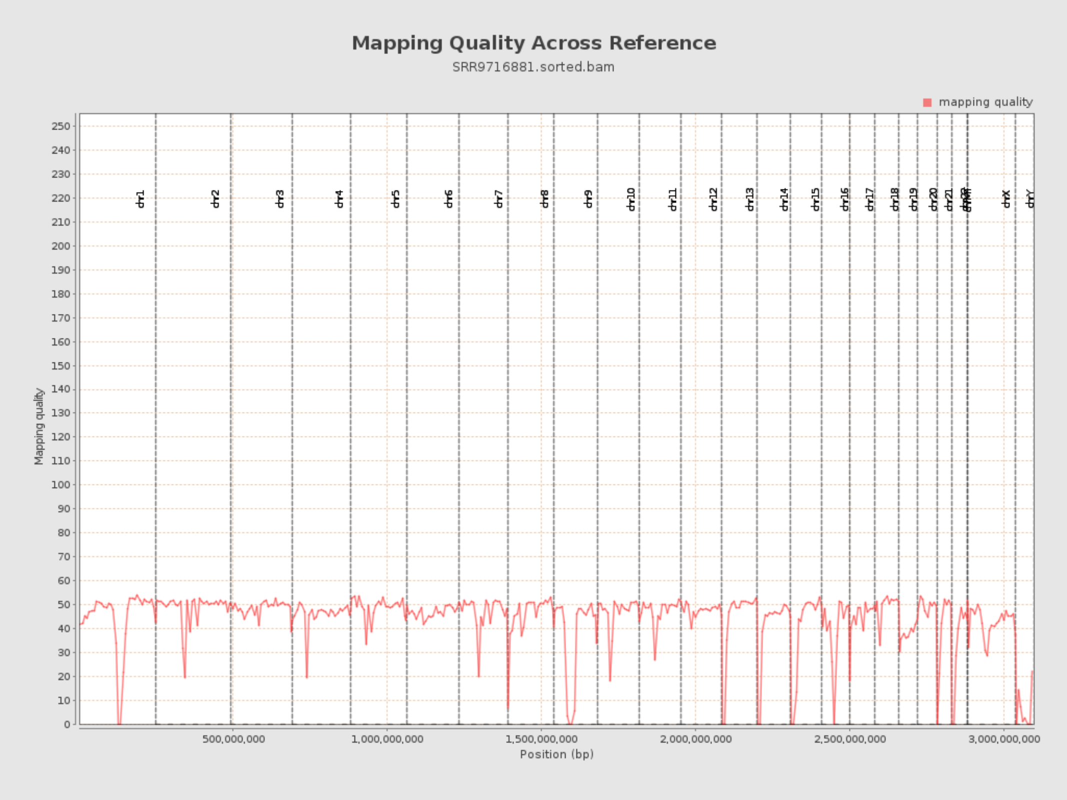
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram