Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:12:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716480.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_SRR9716480 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716480.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:12:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716480.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,335,654
Mapped reads	2,107,148 / 90.22%
Unmapped reads	228,506 / 9.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,765 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	110,833 / 4.75%
Duplication rate	4.09%
Clipped reads	2,112,260 / 90.44%

2.2. ACGT Content

Number/percentage of A's	32,065,047 / 26.29%
Number/percentage of C's	23,297,027 / 19.1%
Number/percentage of T's	36,782,253 / 30.16%
Number/percentage of G's	29,831,821 / 24.46%
Number/percentage of N's	929 / 0%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.3365

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

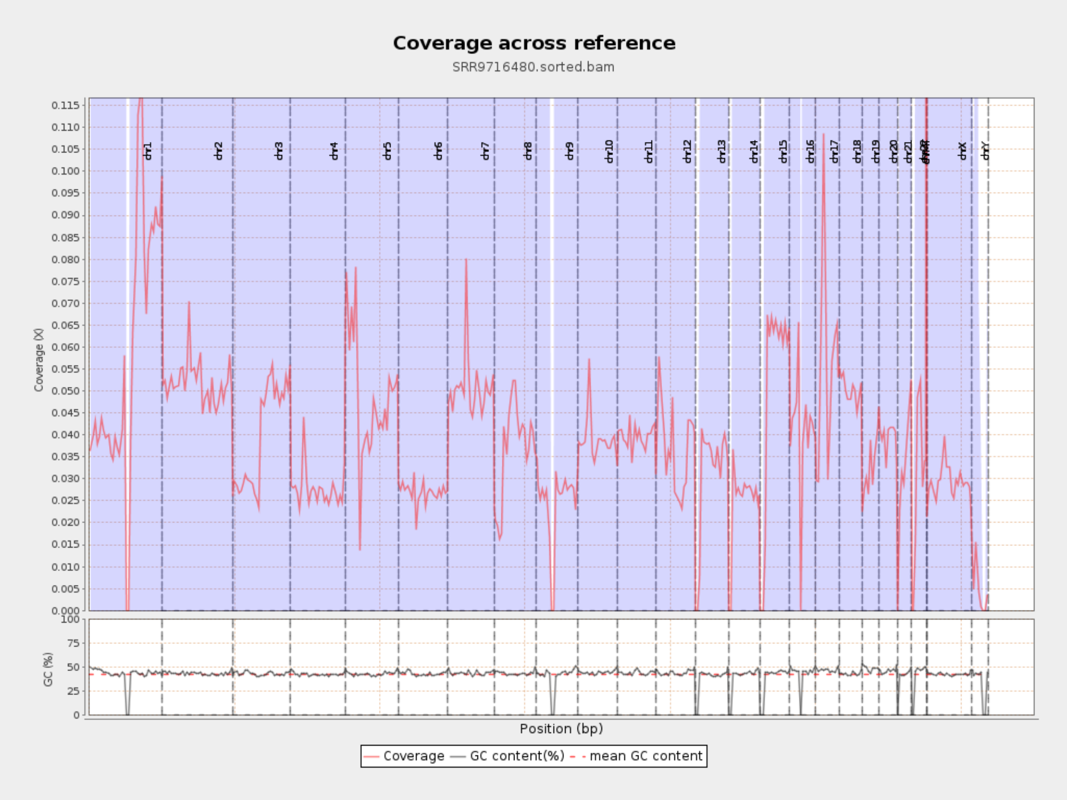
General error rate	0.51%
Mismatches	602,207
Insertions	9,903
Mapped reads with at least one insertion	0.47%
Deletions	21,726
Mapped reads with at least one deletion	1.02%
Homopolymer indels	42.23%

2.6. Chromosome stats

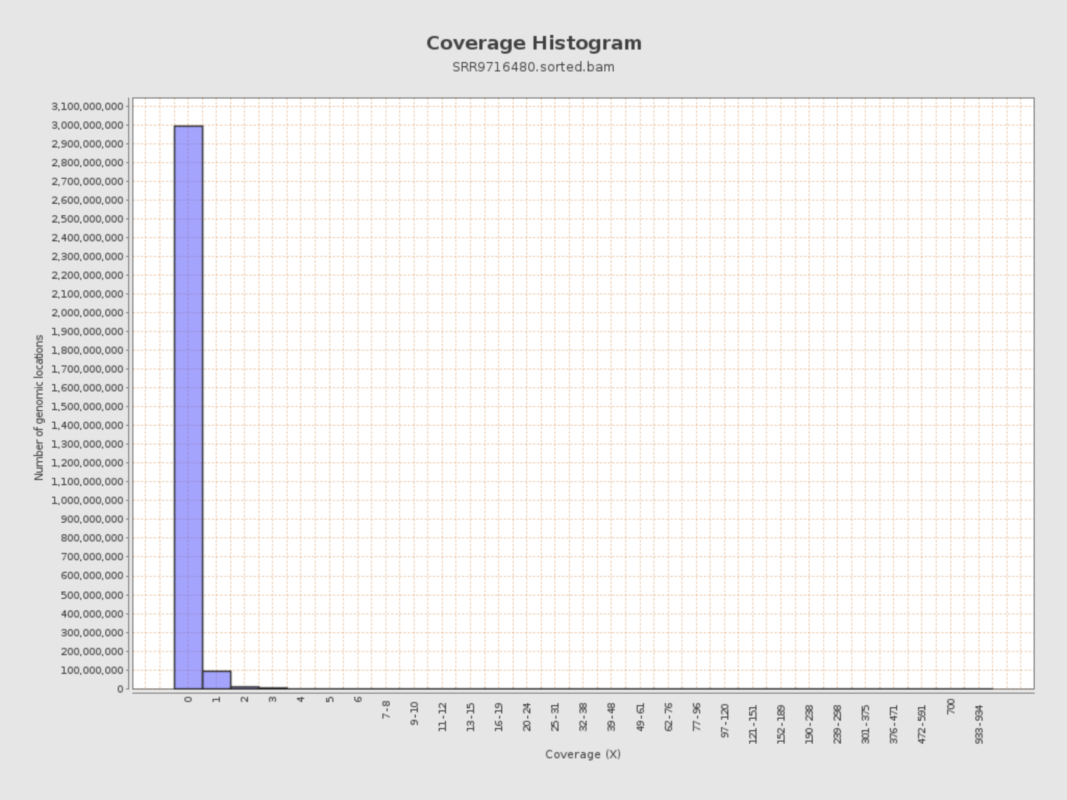
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14439978	0.0579	0.5362
chr2	243199373	12634387	0.052	0.4847
chr3	198022430	7837140	0.0396	0.2267
chr4	191154276	5262118	0.0275	0.2181
chr5	180915260	8768657	0.0485	0.2509
chr6	171115067	4610401	0.0269	0.2148
chr7	159138663	8122787	0.051	0.562

chr8	146364022	5451765	0.0372	0.296
chr9	141213431	3379829	0.0239	0.2504
chr10	135534747	5306866	0.0392	0.2885
chr11	135006516	5335131	0.0395	0.3243
chr12	133851895	4932969	0.0369	0.2209
chr13	115169878	3539310	0.0307	0.1999
chr14	107349540	2610752	0.0243	0.1883
chr15	102531392	5259739	0.0513	0.2594
chr16	90354753	3690772	0.0408	0.2448
chr17	81195210	4608373	0.0568	0.2975
chr18	78077248	3921616	0.0502	0.5663
chr19	59128983	1932156	0.0327	0.405
chr20	63025520	2489416	0.0395	0.2317
chr21	48129895	1566232	0.0325	0.2191
chr22	51304566	1451249	0.0283	0.1905
chrMT	16571	15038	0.9075	1.0843
chrX	155270560	4562712	0.0294	0.2225
chrY	59373566	281906	0.0047	0.1148

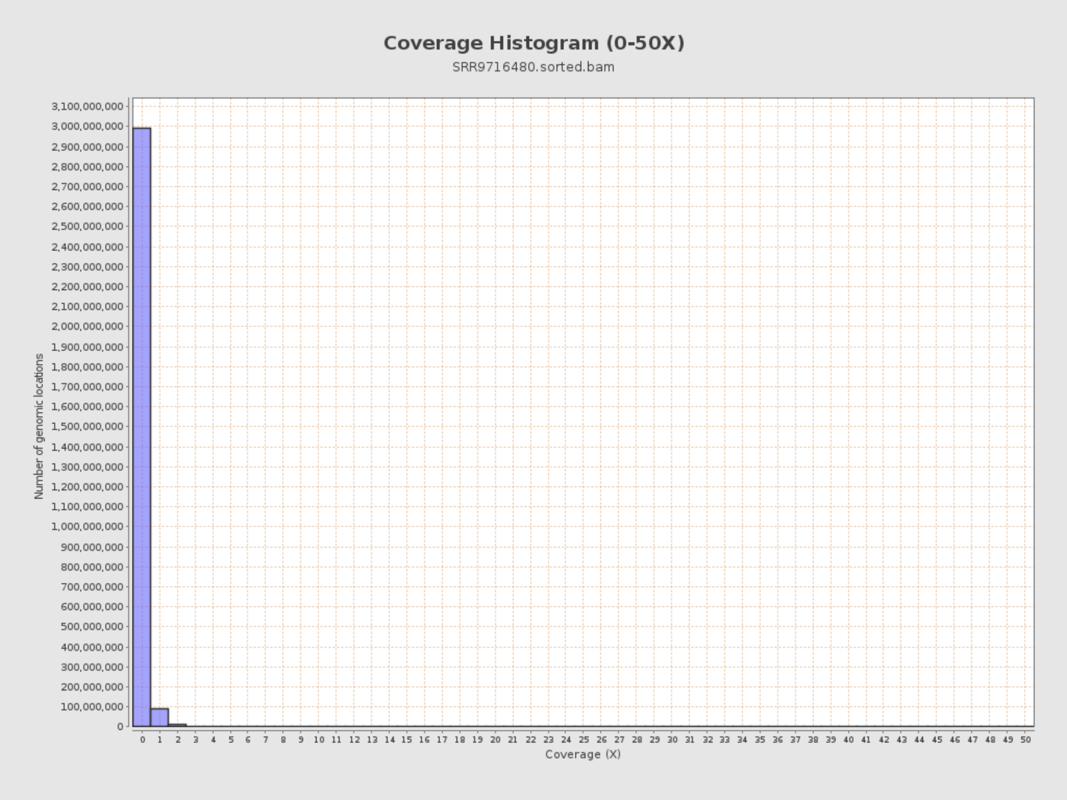
3. Results : Coverage across reference



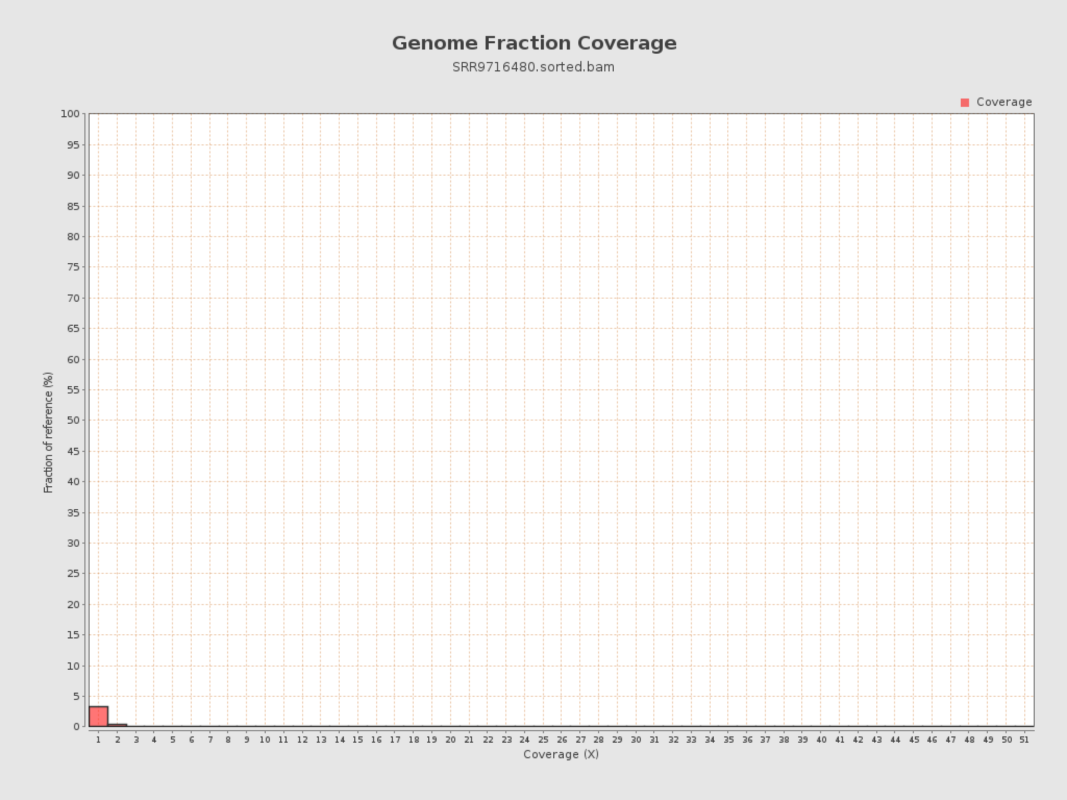
4. Results : Coverage Histogram



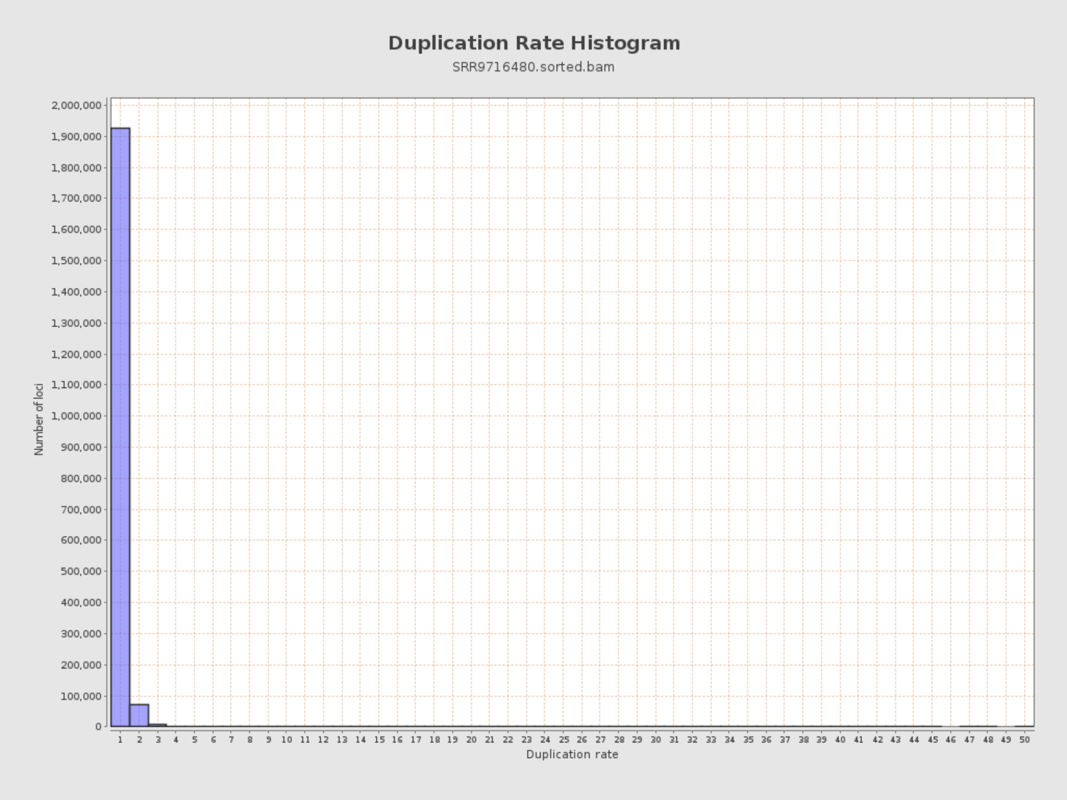
5. Results : Coverage Histogram (0-50X)



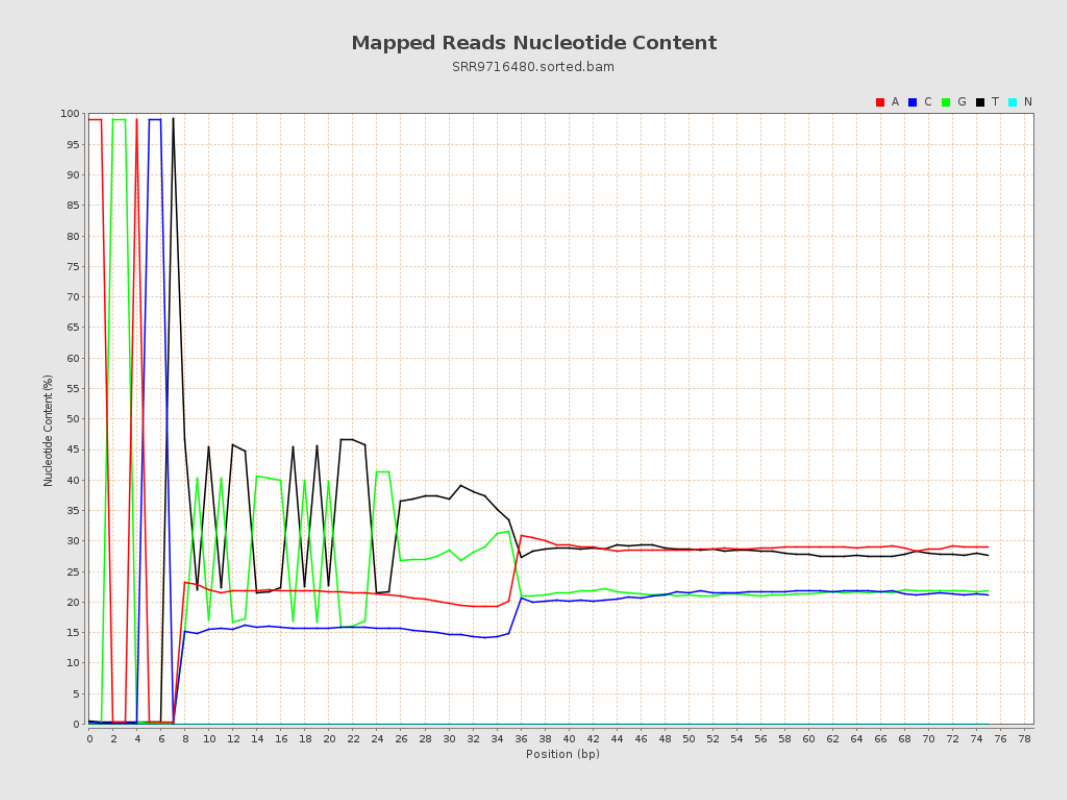
6. Results : Genome Fraction Coverage



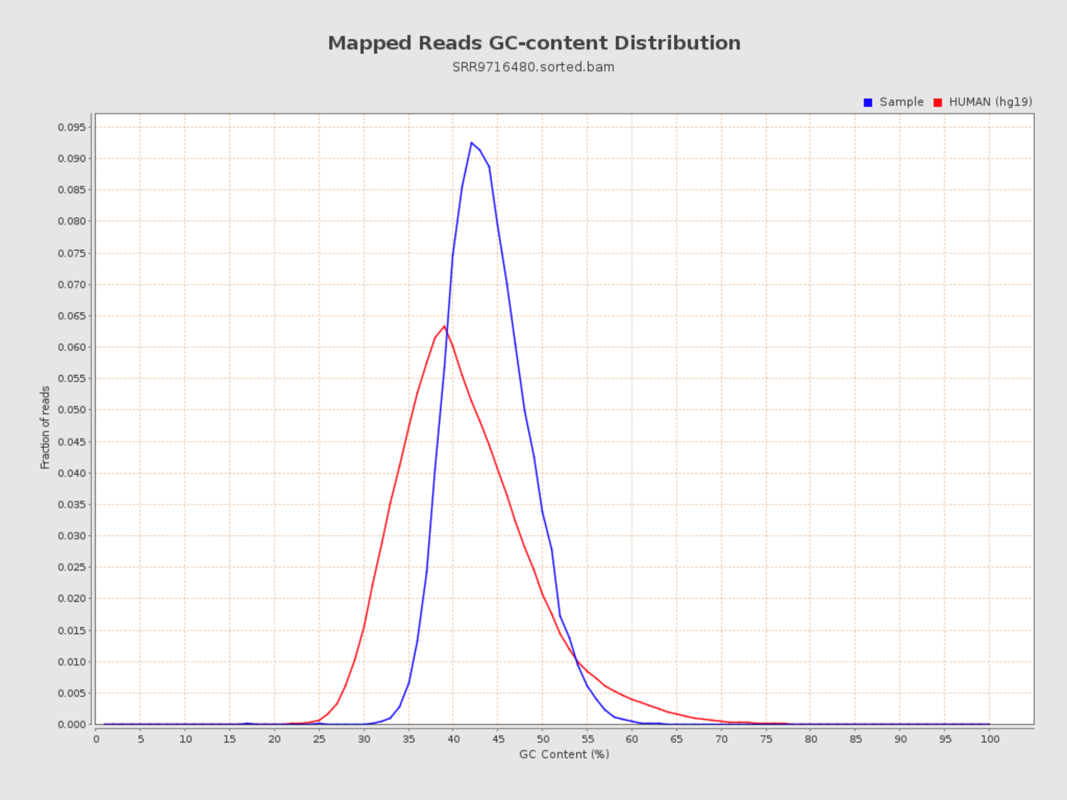
7. Results : Duplication Rate Histogram



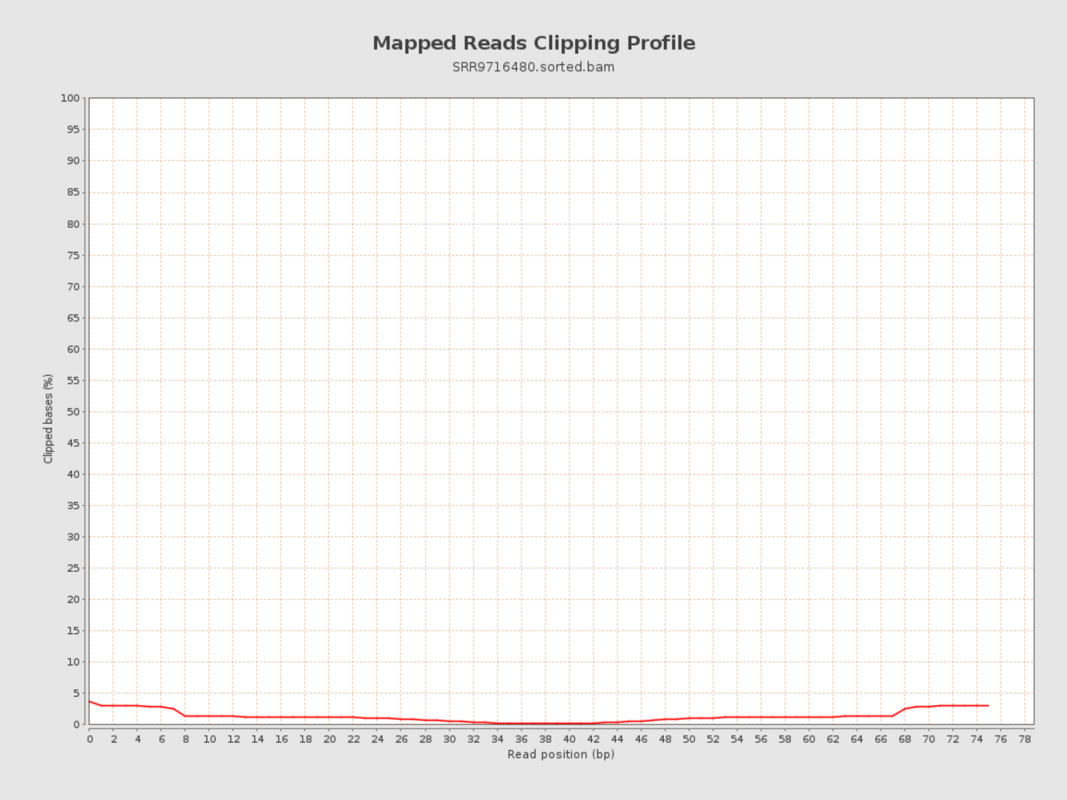
8. Results : Mapped Reads Nucleotide Content



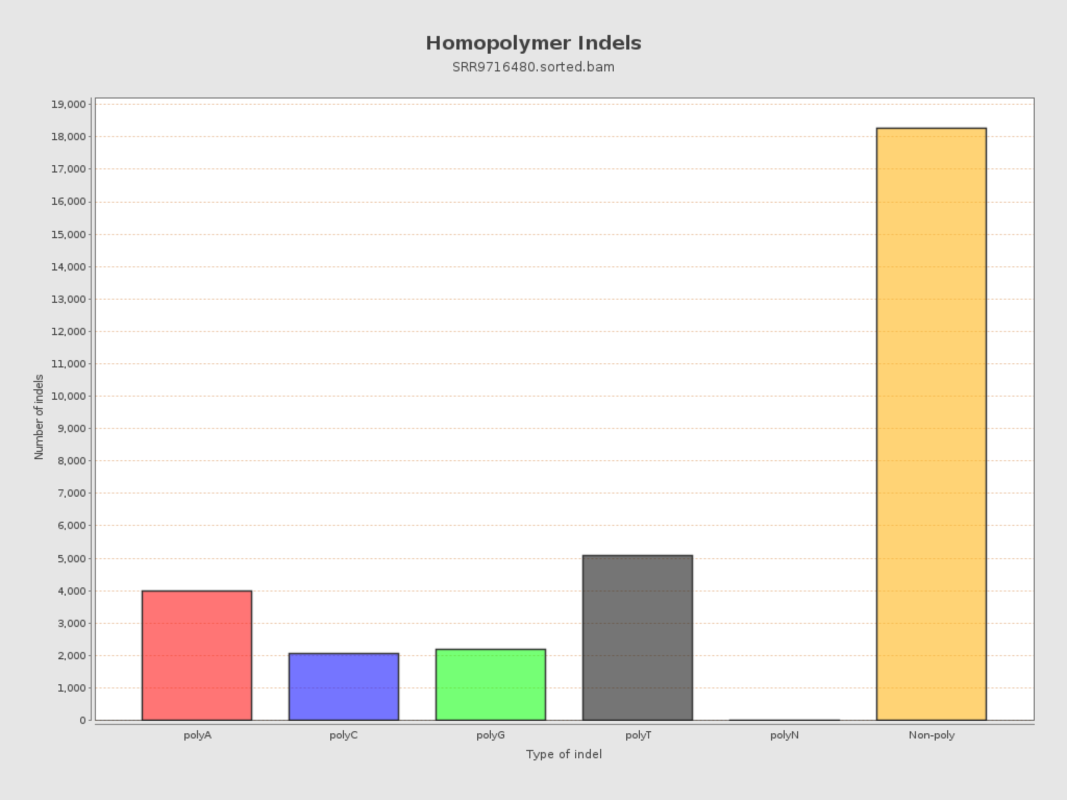
9. Results : Mapped Reads GC-content Distribution



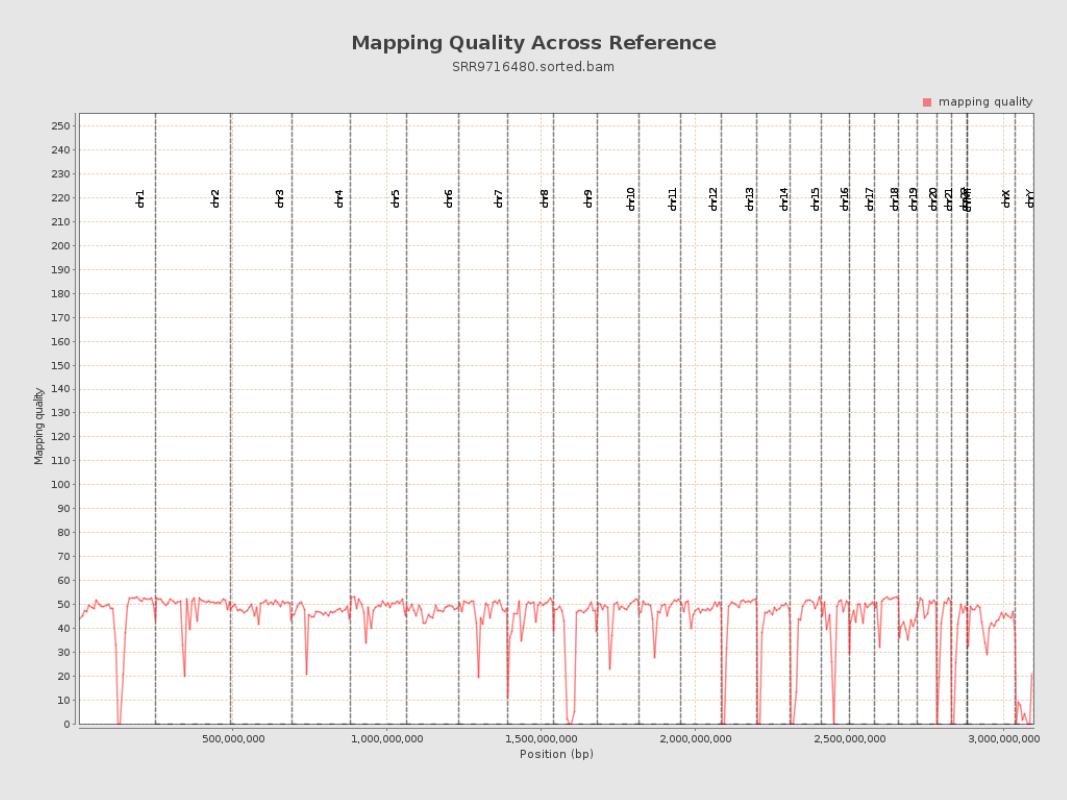
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram