Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:54:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240195.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_SRR6240195 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240195.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:54:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240195.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,886,971
Mapped reads	1,538,451 / 81.53%
Unmapped reads	348,520 / 18.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,539 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	123,902 / 6.57%
Duplication rate	6.79%
Clipped reads	974,918 / 51.67%

2.2. ACGT Content

Number/percentage of A's	26,553,750 / 27.74%
Number/percentage of C's	16,989,660 / 17.75%
Number/percentage of T's	30,742,234 / 32.12%
Number/percentage of G's	21,402,565 / 22.36%
Number/percentage of N's	25,260 / 0.03%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2969

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

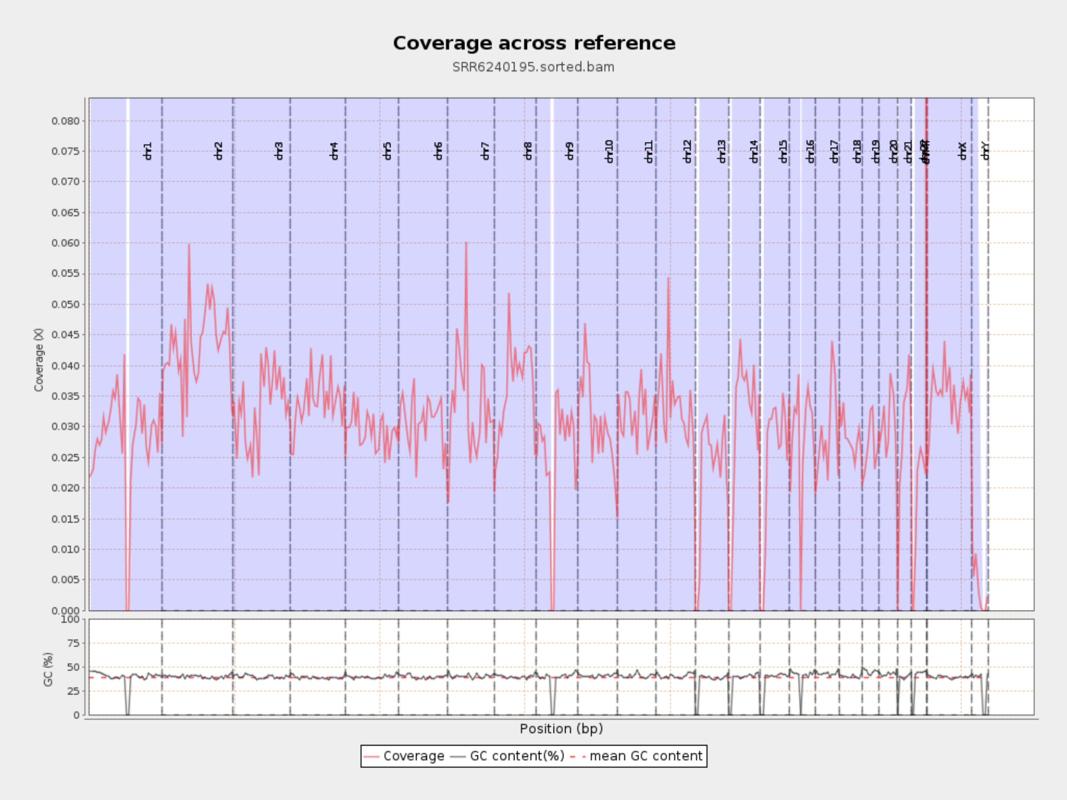
General error rate	0.91%
Mismatches	859,553
Insertions	6,613
Mapped reads with at least one insertion	0.43%
Deletions	28,198
Mapped reads with at least one deletion	1.81%
Homopolymer indels	49.14%

2.6. Chromosome stats

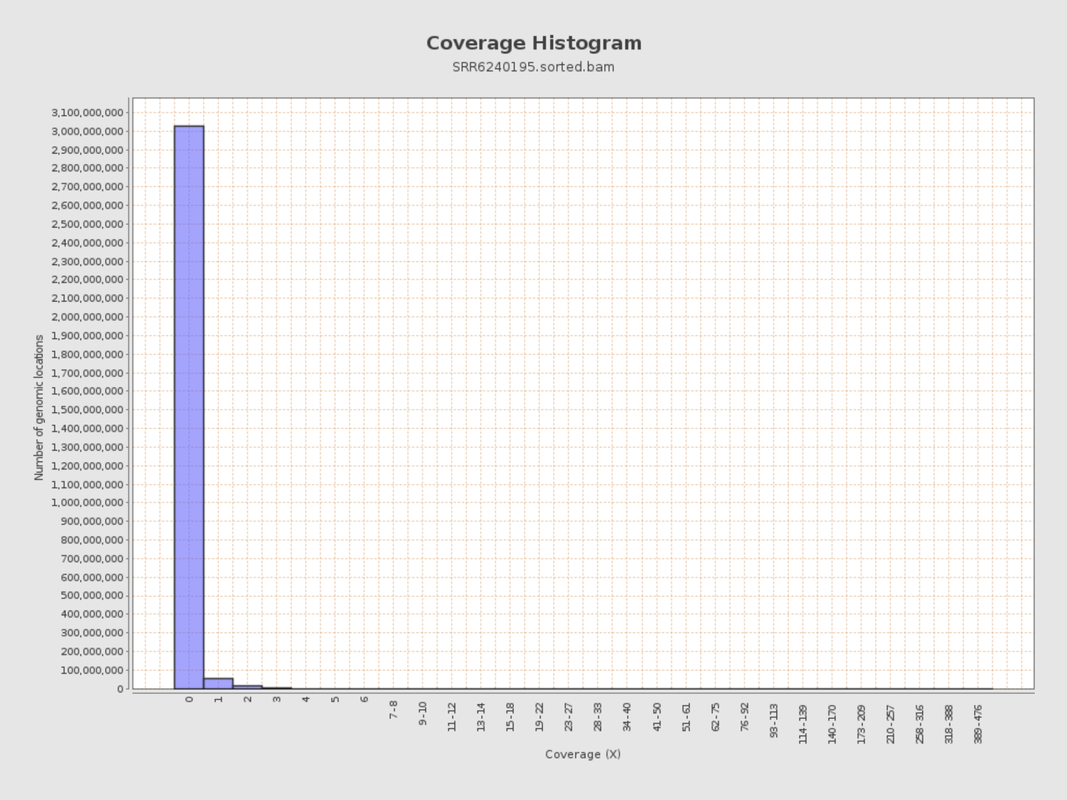
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7025519	0.0282	0.4356
chr2	243199373	10623691	0.0437	0.3589
chr3	198022430	6624425	0.0335	0.2365
chr4	191154276	6539985	0.0342	0.2451
chr5	180915260	5344052	0.0295	0.2216
chr6	171115067	5279670	0.0309	0.2526
chr7	159138663	5445391	0.0342	0.478

chr8	146364022	5390134	0.0368	0.372
chr9	141213431	3646745	0.0258	0.2591
chr10	135534747	4247442	0.0313	0.2633
chr11	135006516	4319471	0.032	0.2677
chr12	133851895	4494086	0.0336	0.2354
chr13	115169878	2578155	0.0224	0.1923
chr14	107349540	3215488	0.03	0.2278
chr15	102531392	2517162	0.0246	0.2099
chr16	90354753	2555215	0.0283	0.2208
chr17	81195210	2330744	0.0287	0.2245
chr18	78077248	2215590	0.0284	0.3994
chr19	59128983	1593619	0.027	0.3149
chr20	63025520	1909486	0.0303	0.2278
chr21	48129895	1368215	0.0284	0.221
chr22	51304566	871658	0.017	0.1625
chrMT	16571	49252	2.9722	3.6486
chrX	155270560	5367991	0.0346	0.2582
chrY	59373566	208719	0.0035	0.0825

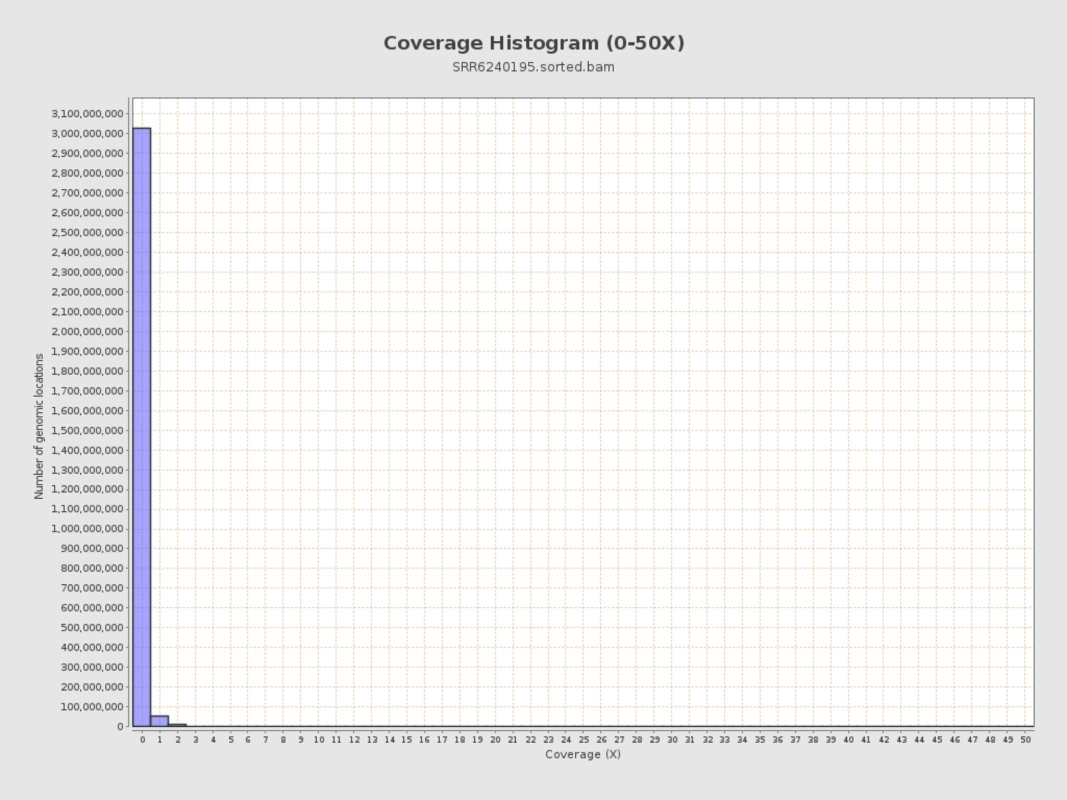
3. Results : Coverage across reference



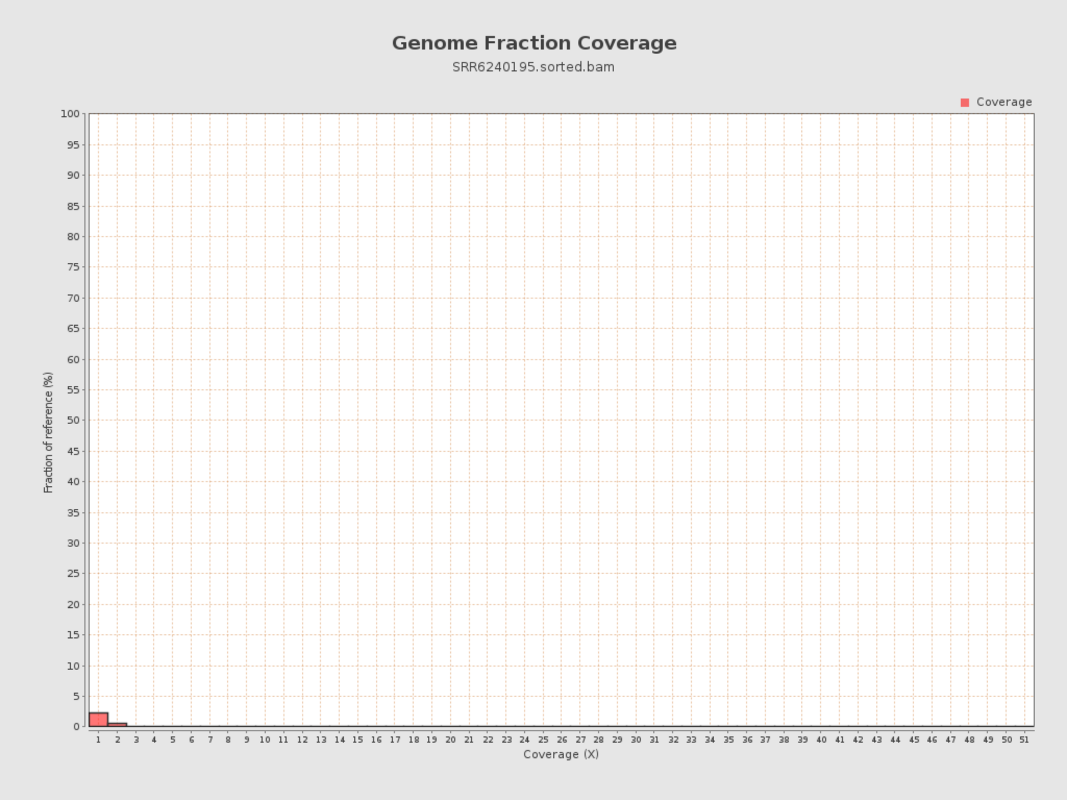
4. Results : Coverage Histogram



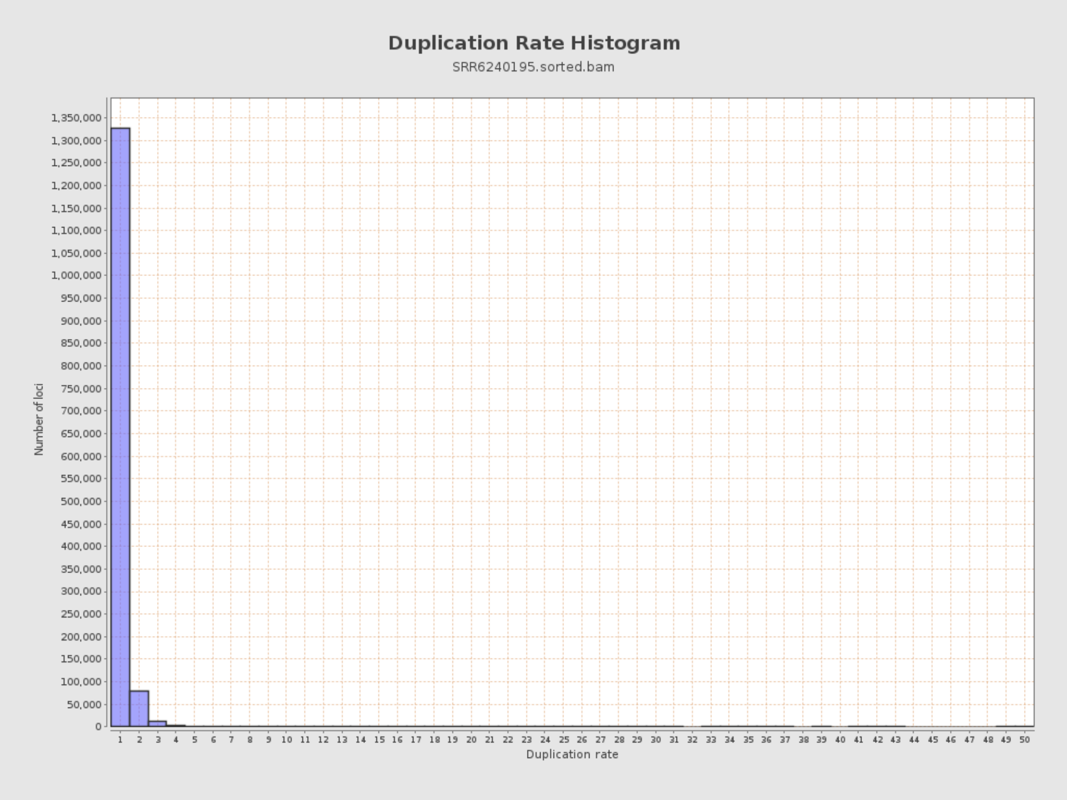
5. Results : Coverage Histogram (0-50X)



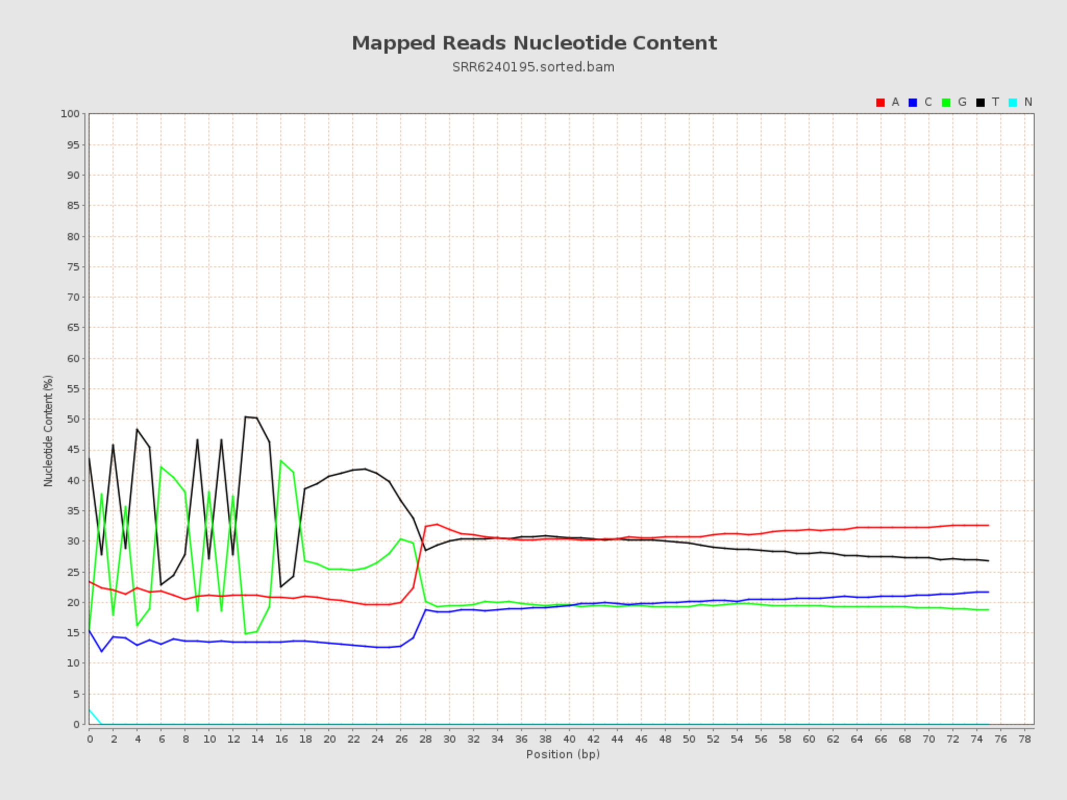
6. Results : Genome Fraction Coverage



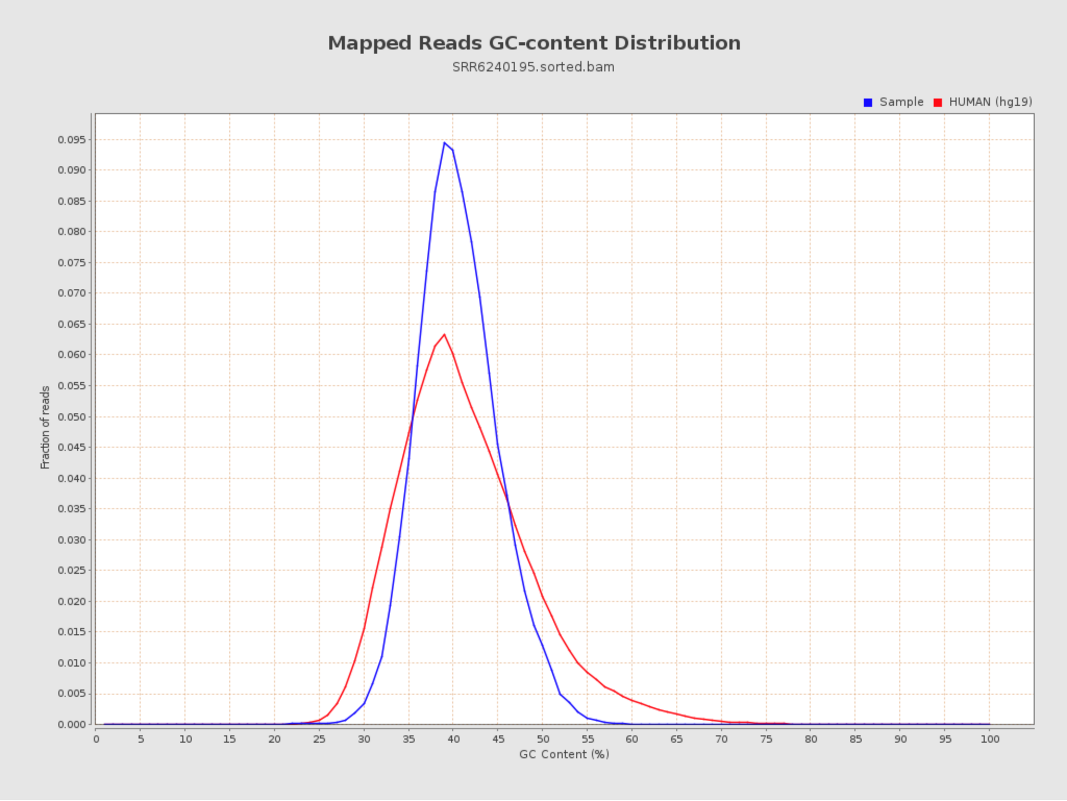
7. Results : Duplication Rate Histogram



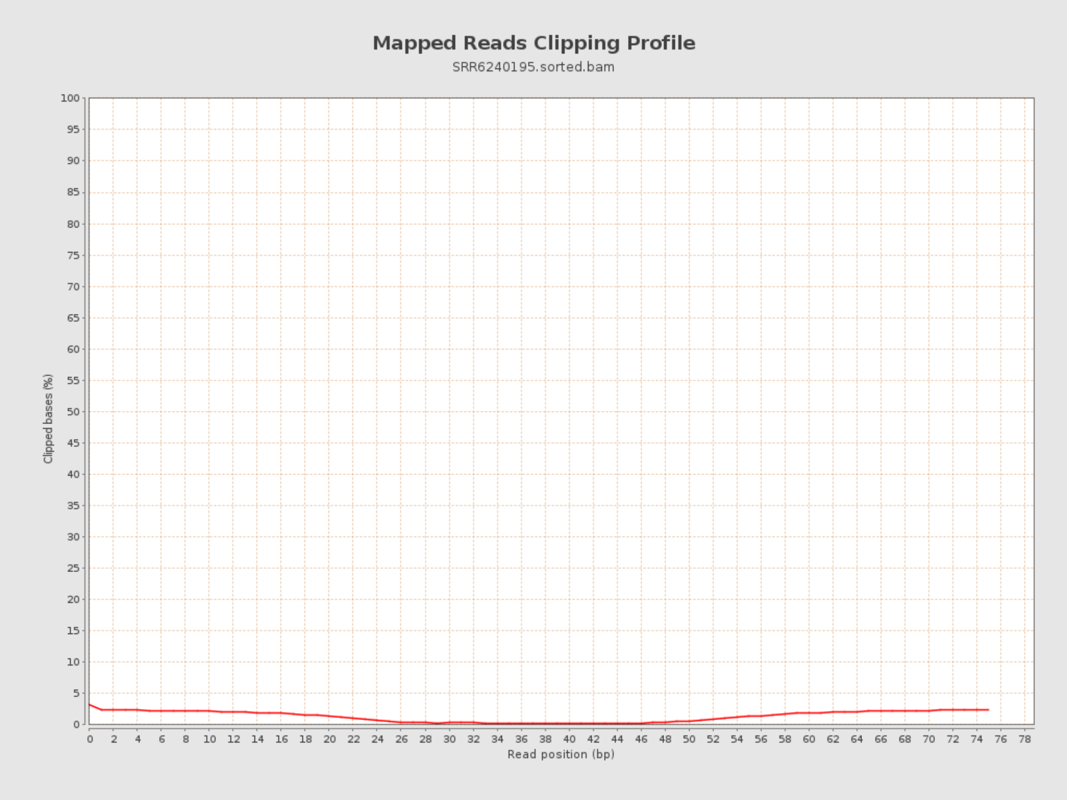
8. Results : Mapped Reads Nucleotide Content



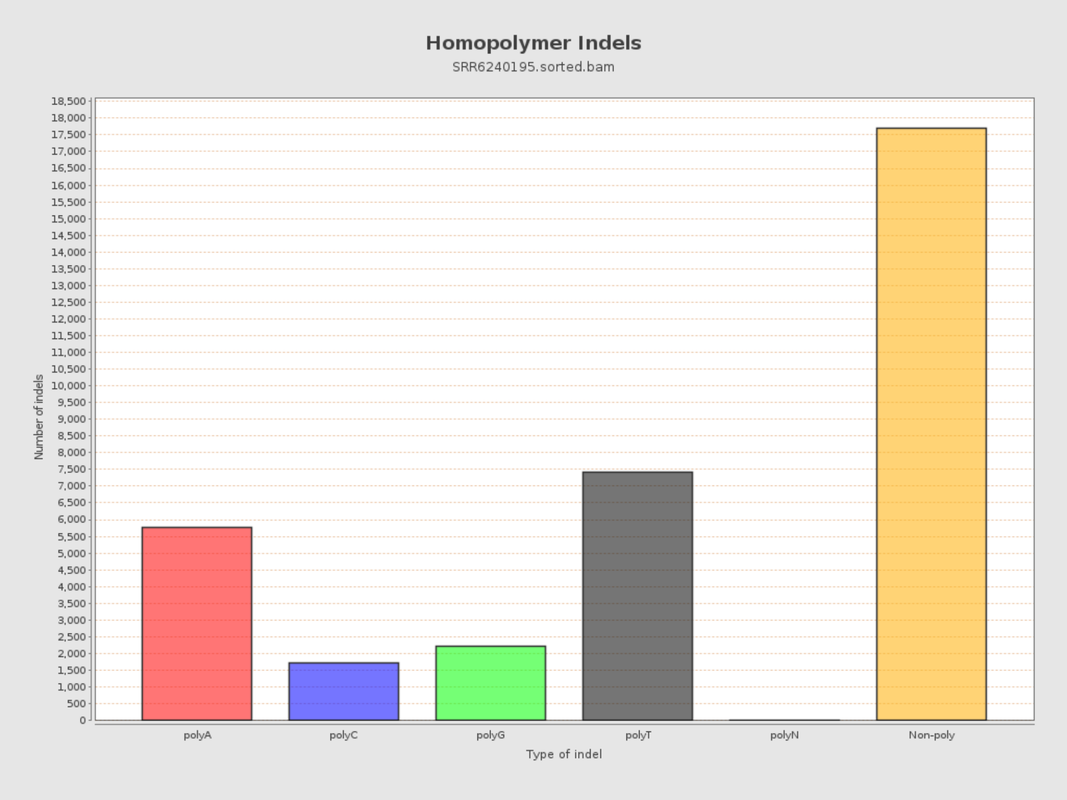
9. Results : Mapped Reads GC-content Distribution



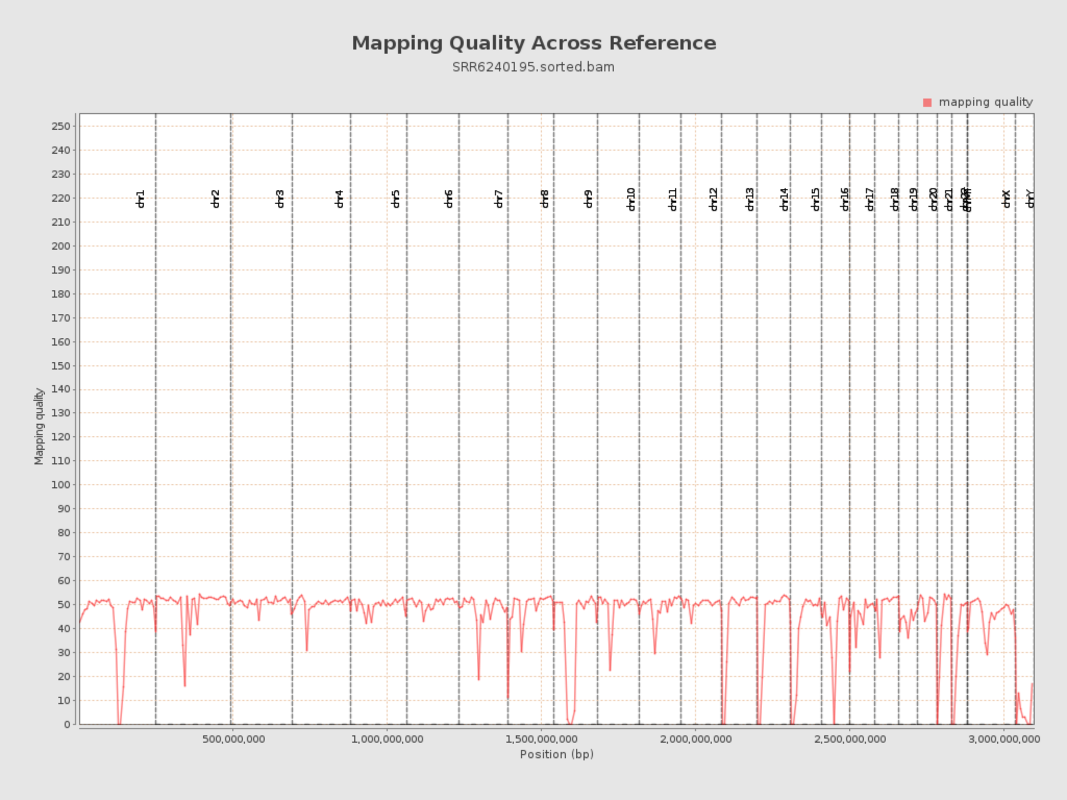
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram