Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:20:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240181.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_SRR6240181 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240181.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:20:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240181.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,868,747
Mapped reads	1,484,227 / 79.42%
Unmapped reads	384,520 / 20.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,185 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	174,052 / 9.31%
Duplication rate	8.91%
Clipped reads	653,333 / 34.96%

2.2. ACGT Content

Number/percentage of A's	28,584,731 / 28.67%
Number/percentage of C's	18,756,801 / 18.81%
Number/percentage of T's	31,282,671 / 31.38%
Number/percentage of G's	21,002,421 / 21.07%
Number/percentage of N's	75,886 / 0.08%
GC Percentage	39.88%

2.3. Coverage

Mean	0.0322

Standard Deviation	0.4053

2.4. Mapping Quality

Mean Mapping Quality	47.3

2.5. Mismatches and indels

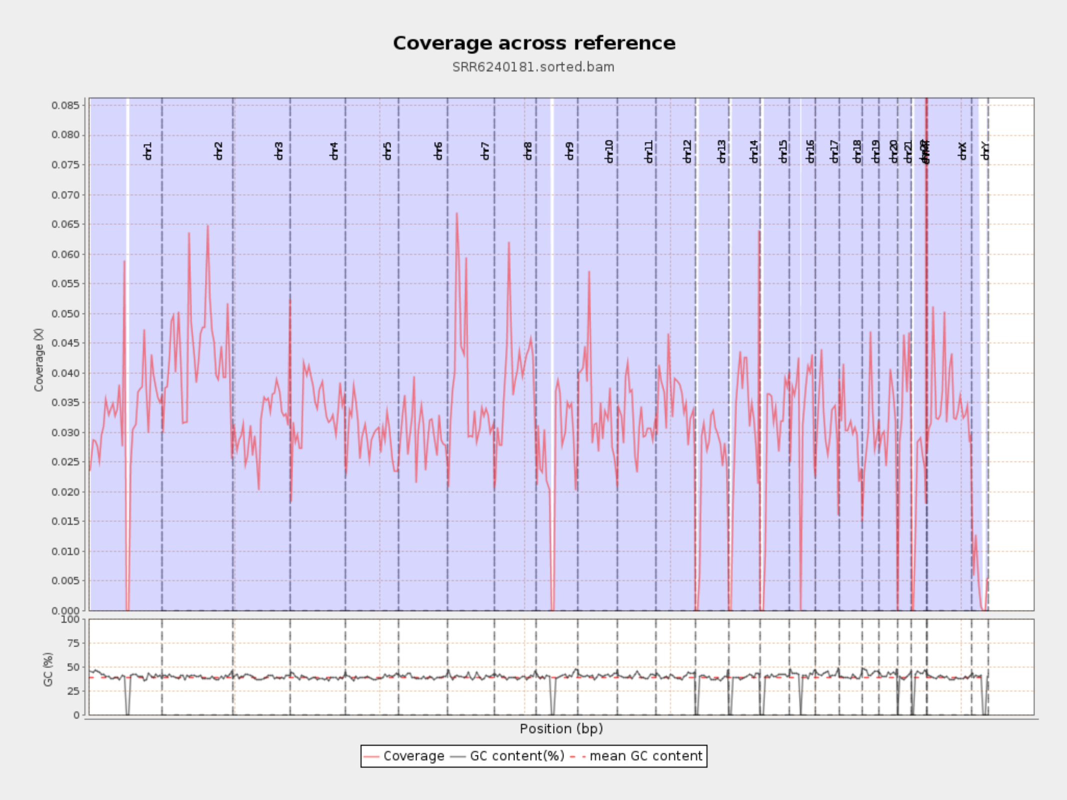
General error rate	0.89%
Mismatches	878,315
Insertions	7,151
Mapped reads with at least one insertion	0.48%
Deletions	26,644
Mapped reads with at least one deletion	1.77%
Homopolymer indels	48.5%

2.6. Chromosome stats

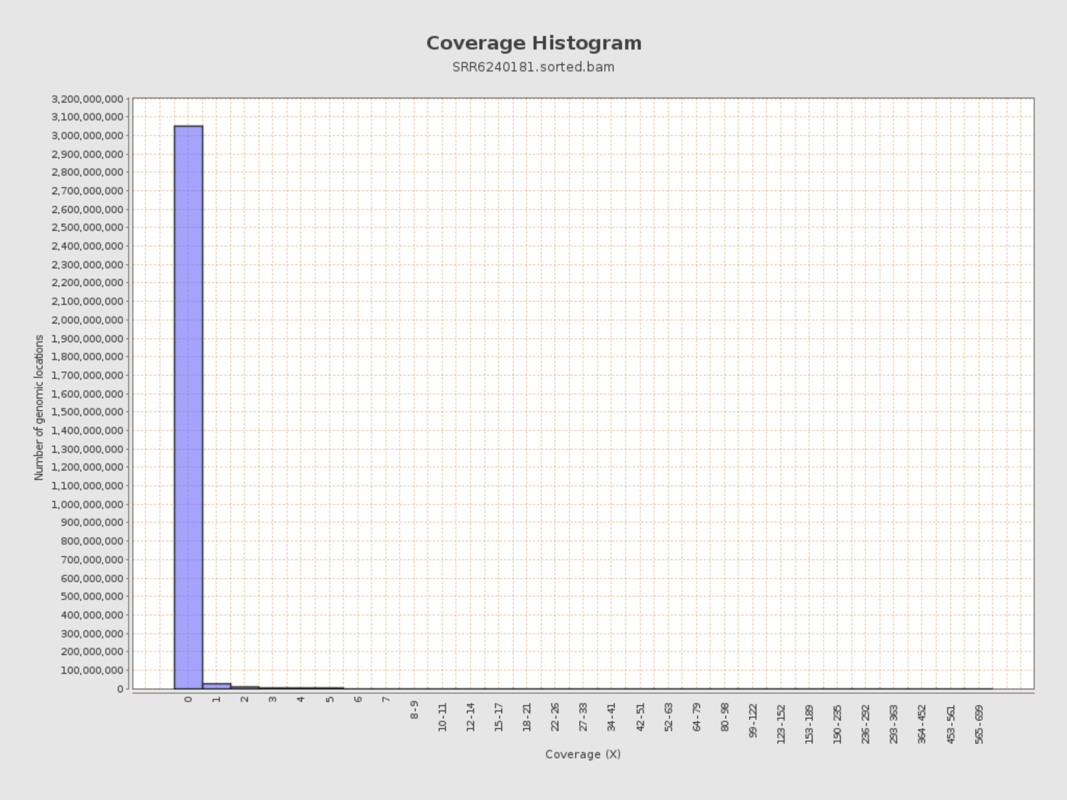
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8003886	0.0321	0.6516
chr2	243199373	10554402	0.0434	0.4413
chr3	198022430	6222755	0.0314	0.3225
chr4	191154276	6471333	0.0339	0.3407
chr5	180915260	5315236	0.0294	0.3167
chr6	171115067	5115197	0.0299	0.3314
chr7	159138663	5951717	0.0374	0.5156

chr8	146364022	5738840	0.0392	0.4794
chr9	141213431	3716317	0.0263	0.3626
chr10	135534747	4715039	0.0348	0.4047
chr11	135006516	4295677	0.0318	0.386
chr12	133851895	4775043	0.0357	0.3493
chr13	115169878	2773577	0.0241	0.2866
chr14	107349540	3209570	0.0299	0.3186
chr15	102531392	2838093	0.0277	0.3014
chr16	90354753	3010898	0.0333	0.3414
chr17	81195210	2530993	0.0312	0.3363
chr18	78077248	2402396	0.0308	0.5568
chr19	59128983	1804460	0.0305	0.4535
chr20	63025520	1949793	0.0309	0.3258
chr21	48129895	1632049	0.0339	0.3365
chr22	51304566	959068	0.0187	0.2432
chrMT	16571	12735	0.7685	1.4053
chrX	155270560	5463201	0.0352	0.363
chrY	59373566	287215	0.0048	0.1193

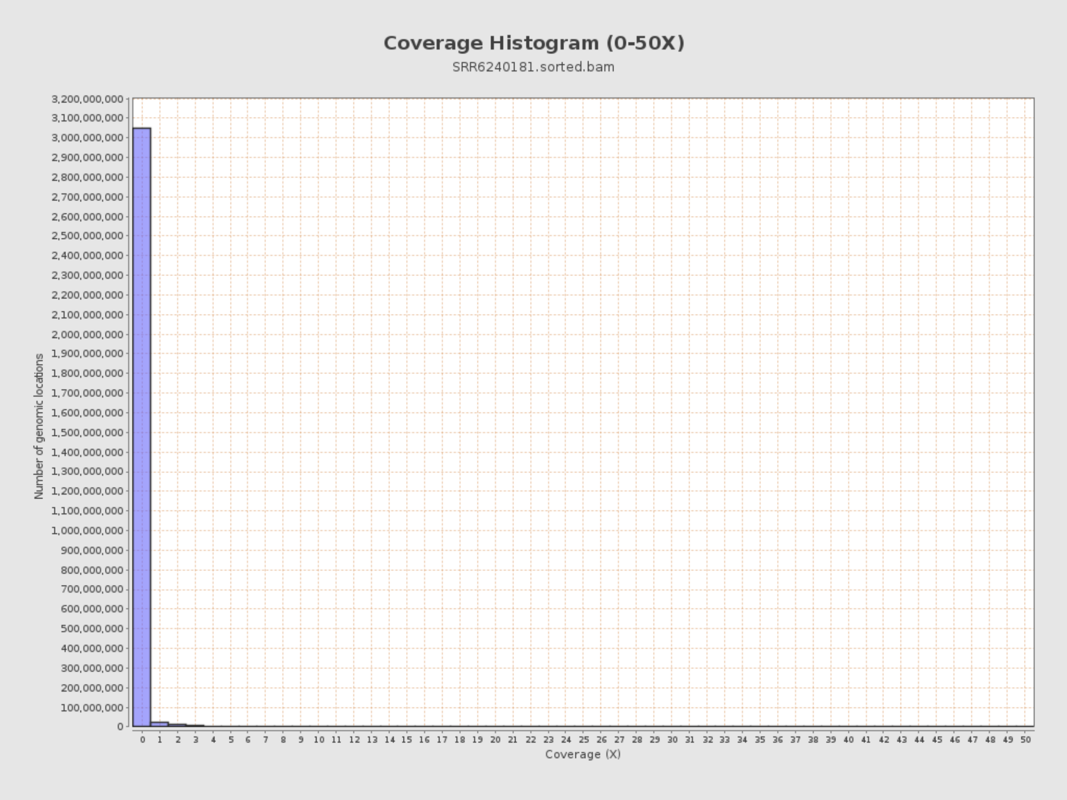
3. Results : Coverage across reference



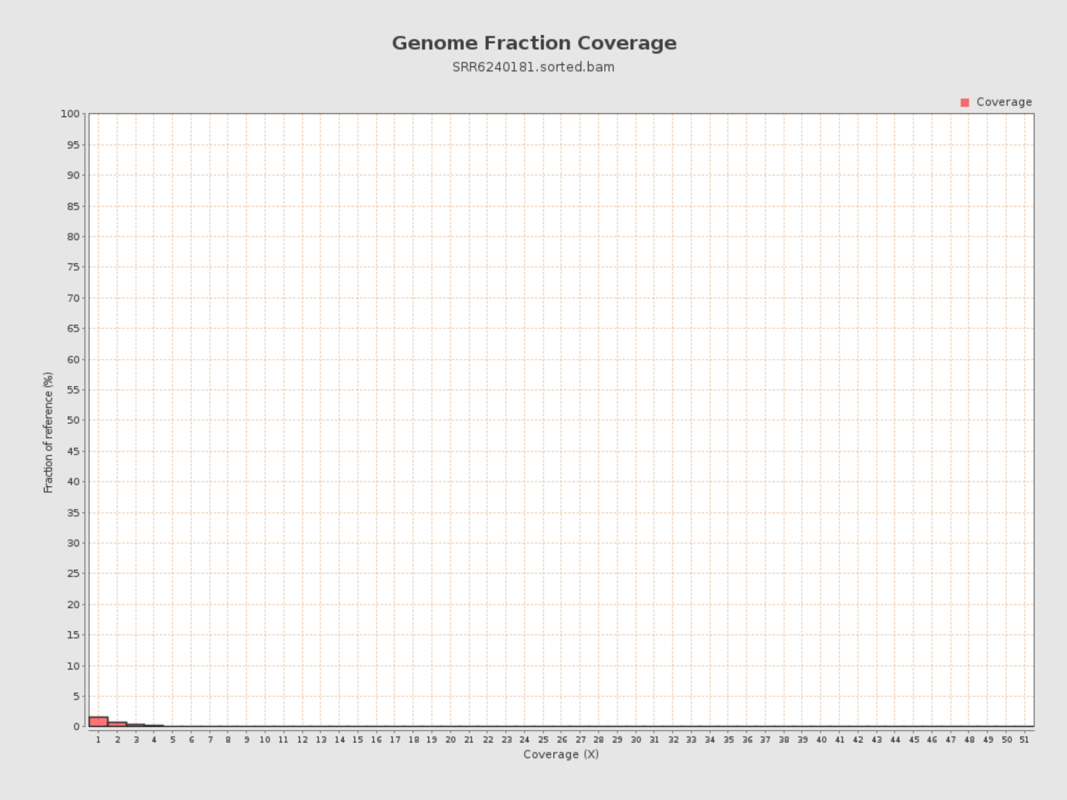
4. Results : Coverage Histogram



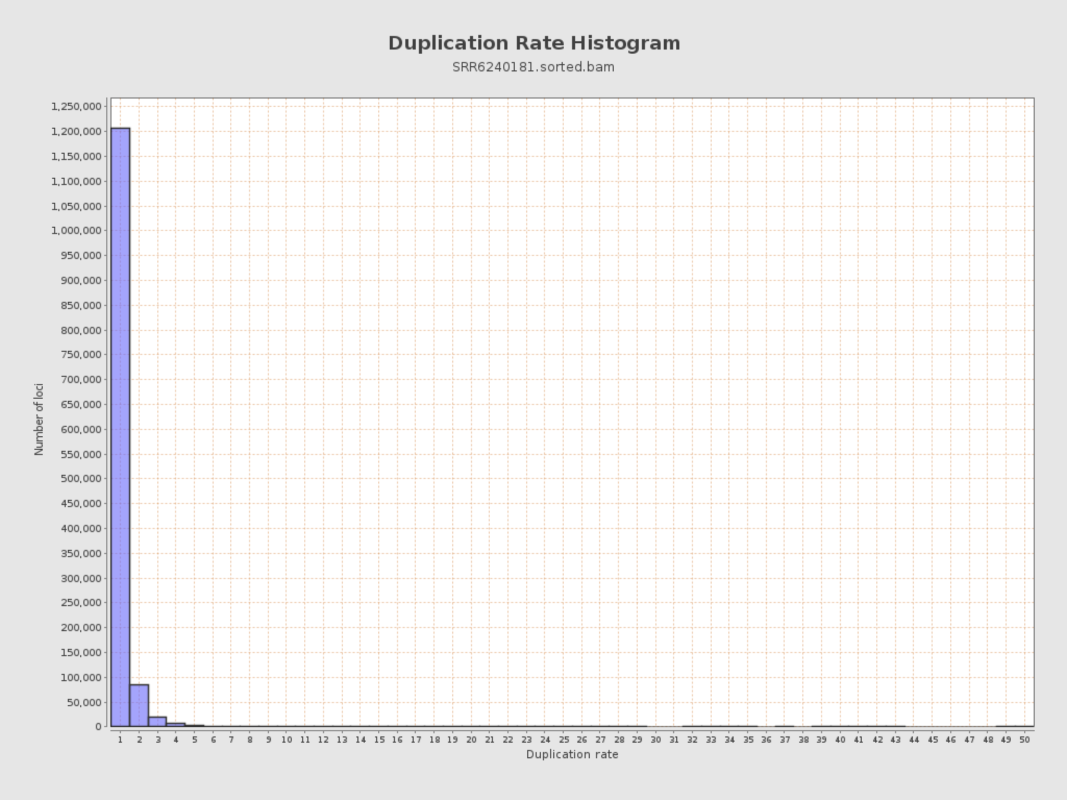
5. Results : Coverage Histogram (0-50X)



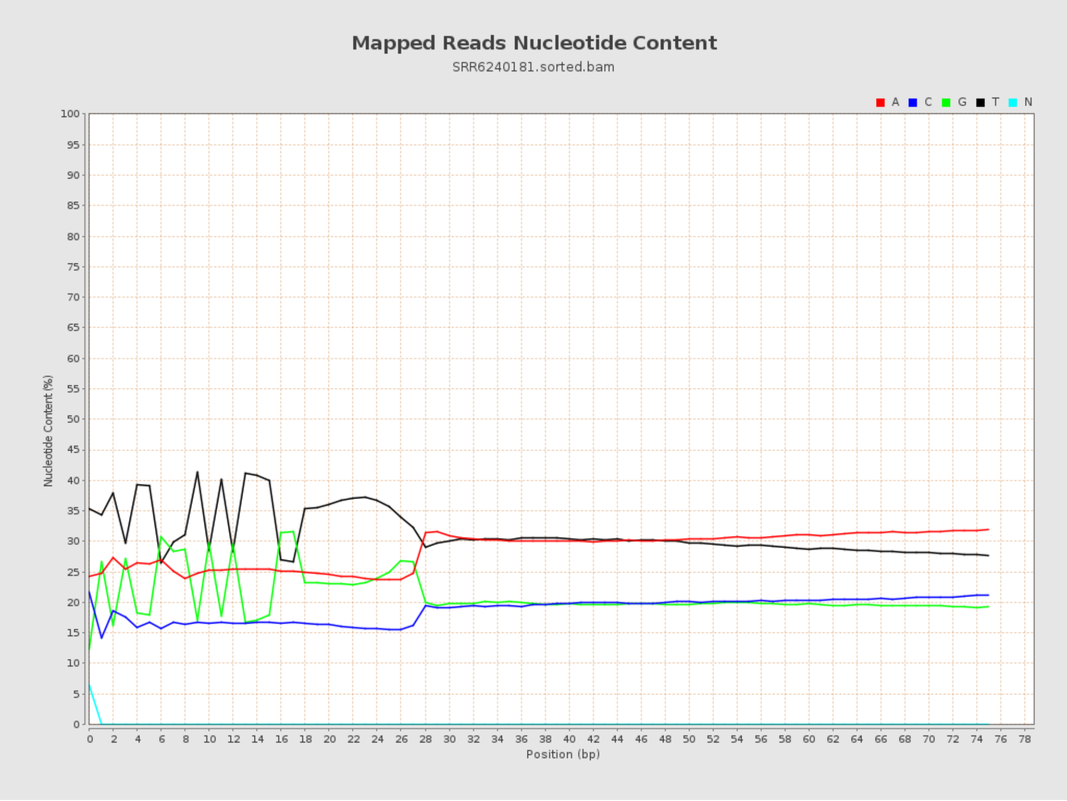
6. Results : Genome Fraction Coverage



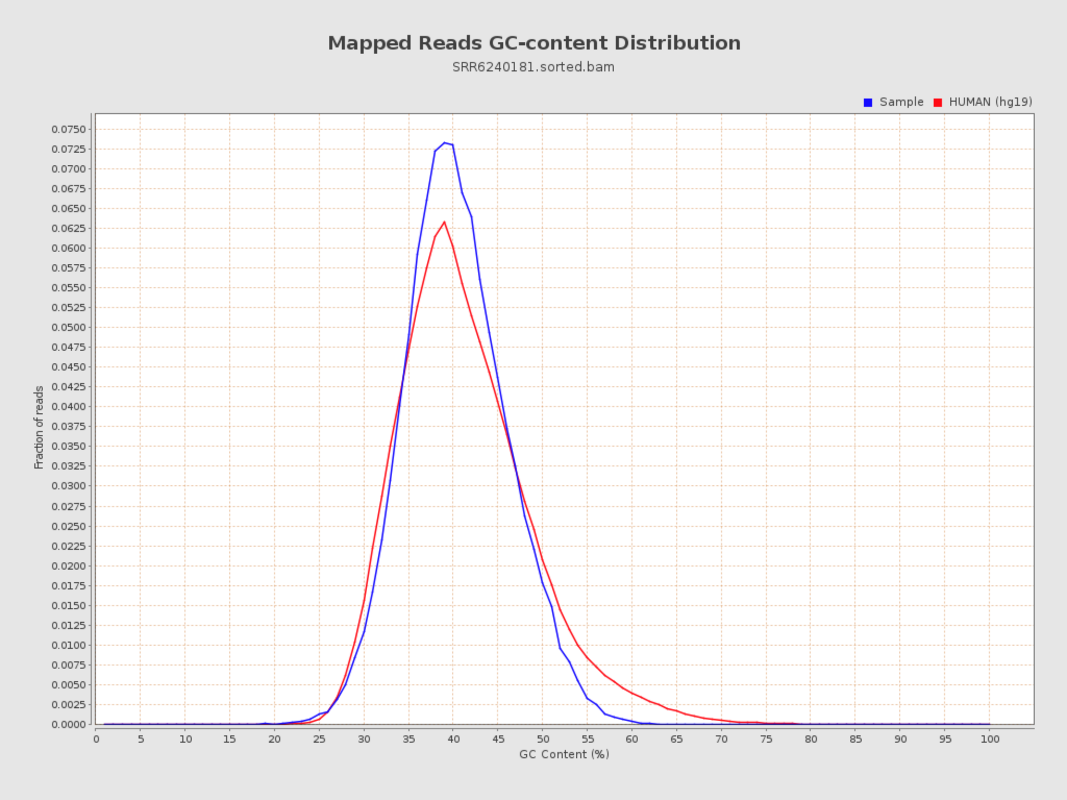
7. Results : Duplication Rate Histogram



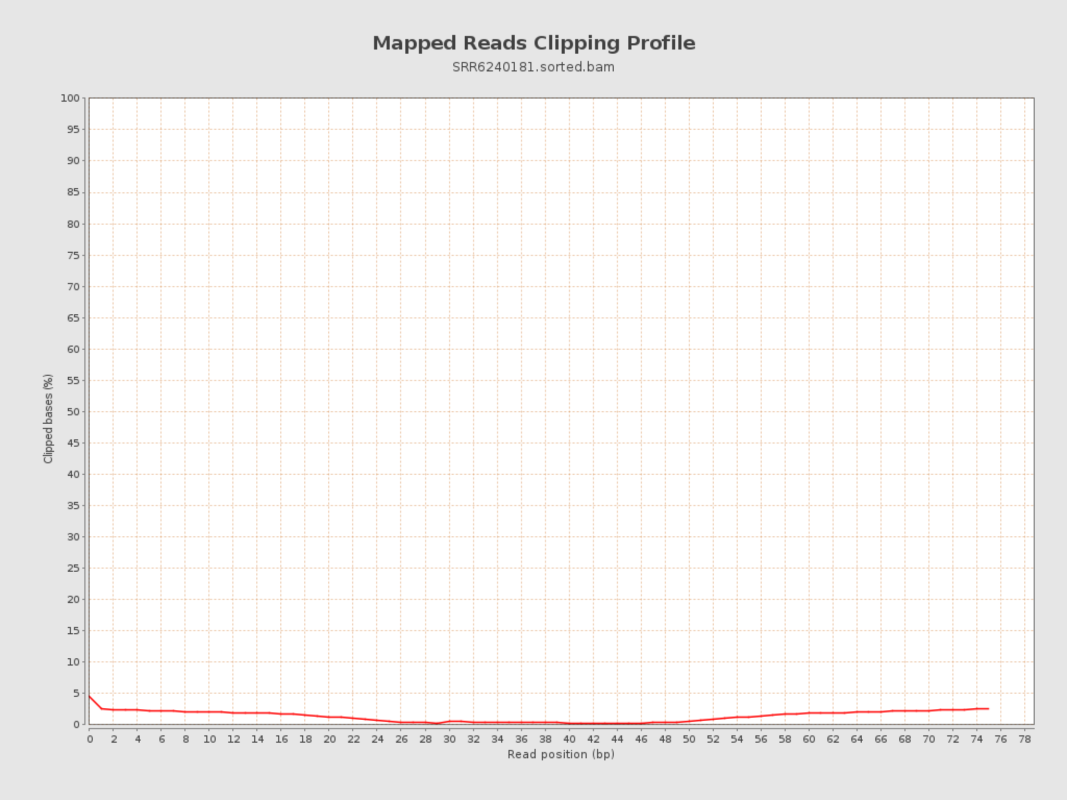
8. Results : Mapped Reads Nucleotide Content



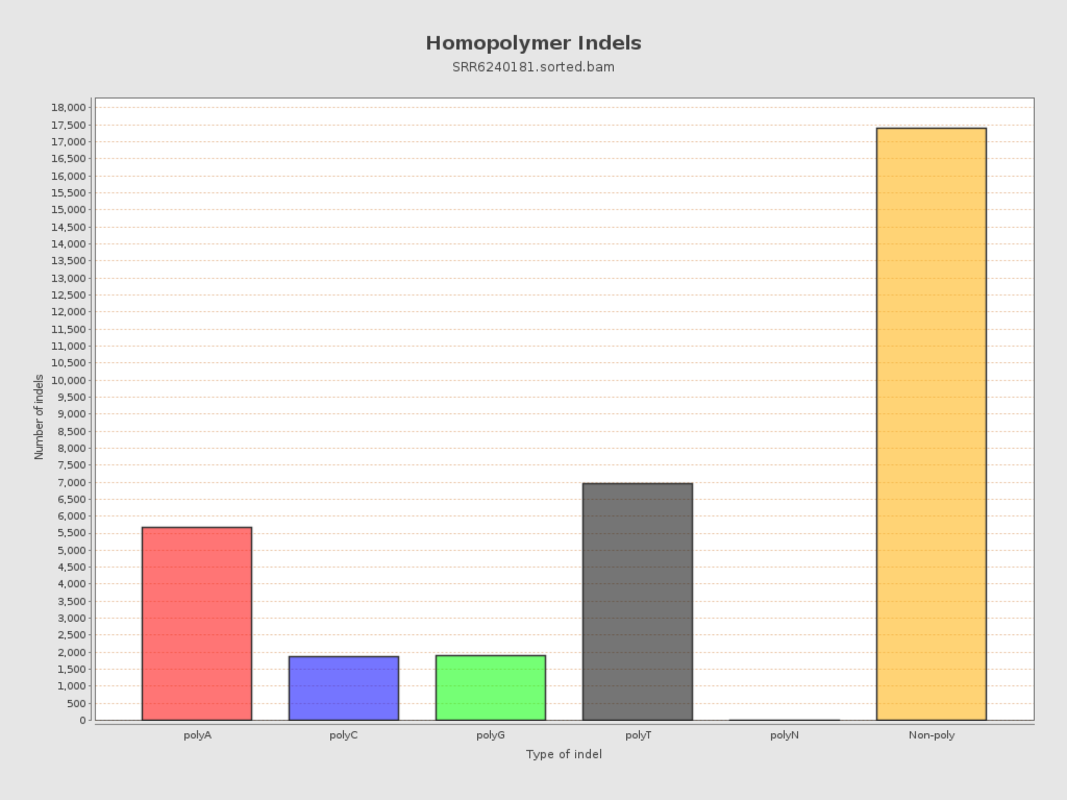
9. Results : Mapped Reads GC-content Distribution



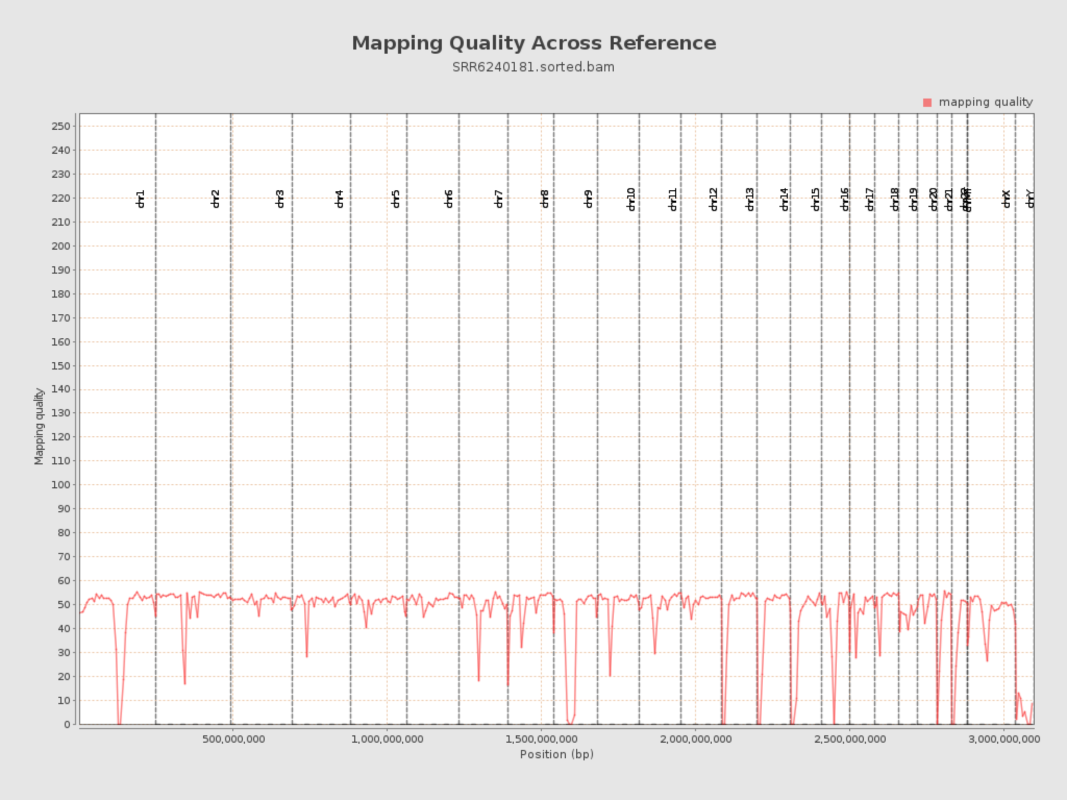
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram