Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:00:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716644.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_SRR9716644 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716644.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:00:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716644.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,680,994
Mapped reads	2,283,466 / 85.17%
Unmapped reads	397,528 / 14.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,345 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	88,799 / 3.31%
Duplication rate	2.92%
Clipped reads	2,284,045 / 85.19%

2.2. ACGT Content

Number/percentage of A's	35,270,022 / 26.67%
Number/percentage of C's	25,362,030 / 19.18%
Number/percentage of T's	39,853,518 / 30.13%
Number/percentage of G's	31,778,002 / 24.03%
Number/percentage of N's	1,940 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0427

Standard Deviation	0.3276

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

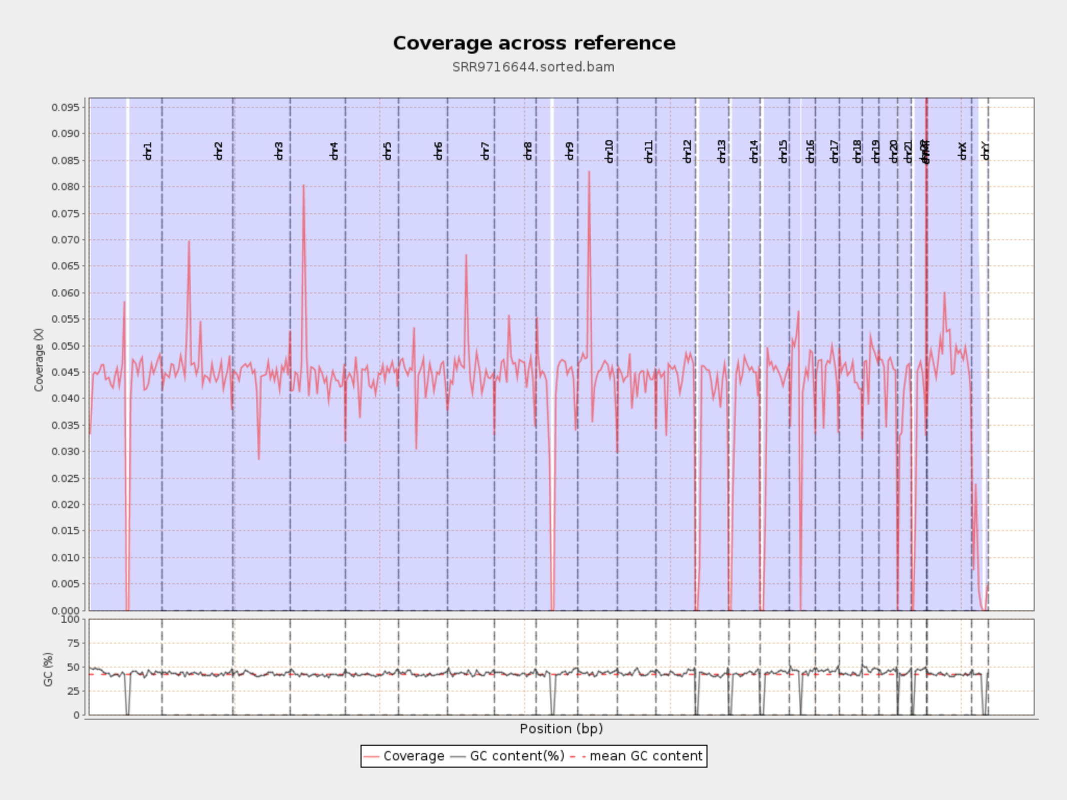
General error rate	0.52%
Mismatches	669,038
Insertions	10,935
Mapped reads with at least one insertion	0.48%
Deletions	25,398
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.95%

2.6. Chromosome stats

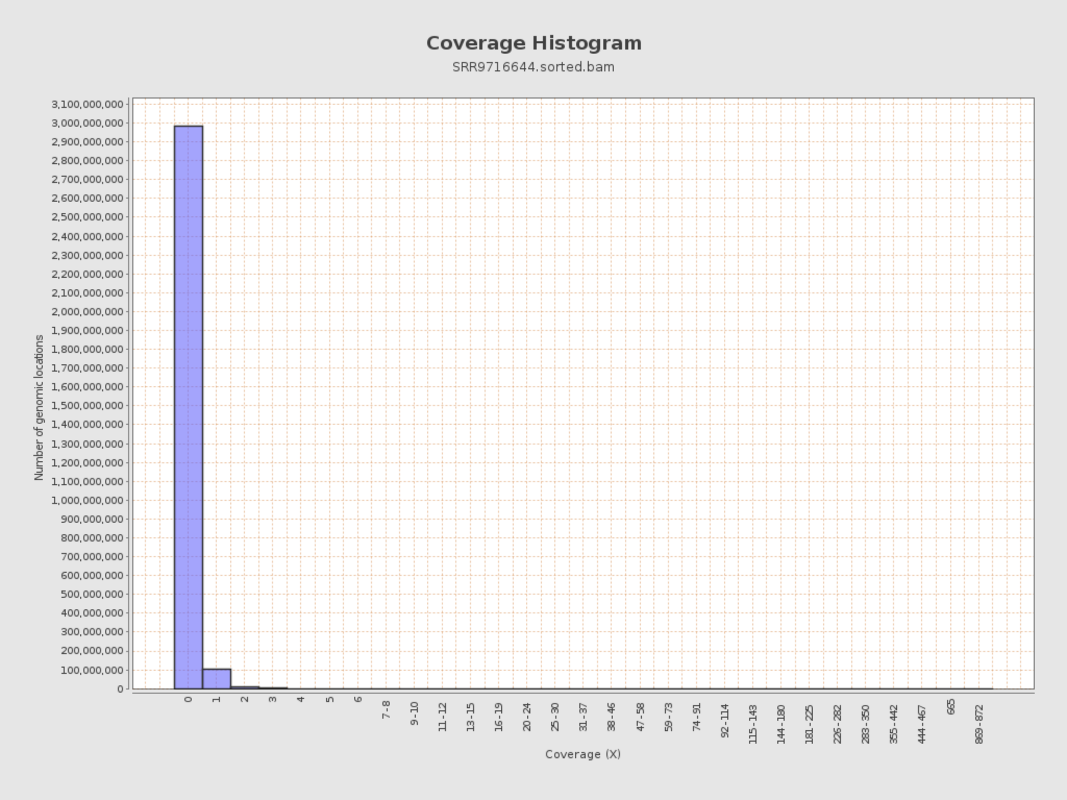
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10509459	0.0422	0.4493
chr2	243199373	11243668	0.0462	0.4803
chr3	198022430	8792338	0.0444	0.2408
chr4	191154276	8653631	0.0453	0.2877
chr5	180915260	7982408	0.0441	0.2369
chr6	171115067	7642754	0.0447	0.2757
chr7	159138663	7308649	0.0459	0.4568

chr8	146364022	6669845	0.0456	0.3133
chr9	141213431	5485344	0.0388	0.278
chr10	135534747	6381579	0.0471	0.39
chr11	135006516	5895155	0.0437	0.3007
chr12	133851895	5969355	0.0446	0.2412
chr13	115169878	4182412	0.0363	0.2165
chr14	107349540	4061126	0.0378	0.2308
chr15	102531392	3793723	0.037	0.2199
chr16	90354753	3880875	0.043	0.2701
chr17	81195210	3622743	0.0446	0.259
chr18	78077248	3495768	0.0448	0.4616
chr19	59128983	2750156	0.0465	0.3795
chr20	63025520	2788963	0.0443	0.2483
chr21	48129895	1741271	0.0362	0.253
chr22	51304566	1562436	0.0305	0.1979
chrMT	16571	4718	0.2847	0.6521
chrX	155270560	7476940	0.0482	0.2729
chrY	59373566	411070	0.0069	0.1939

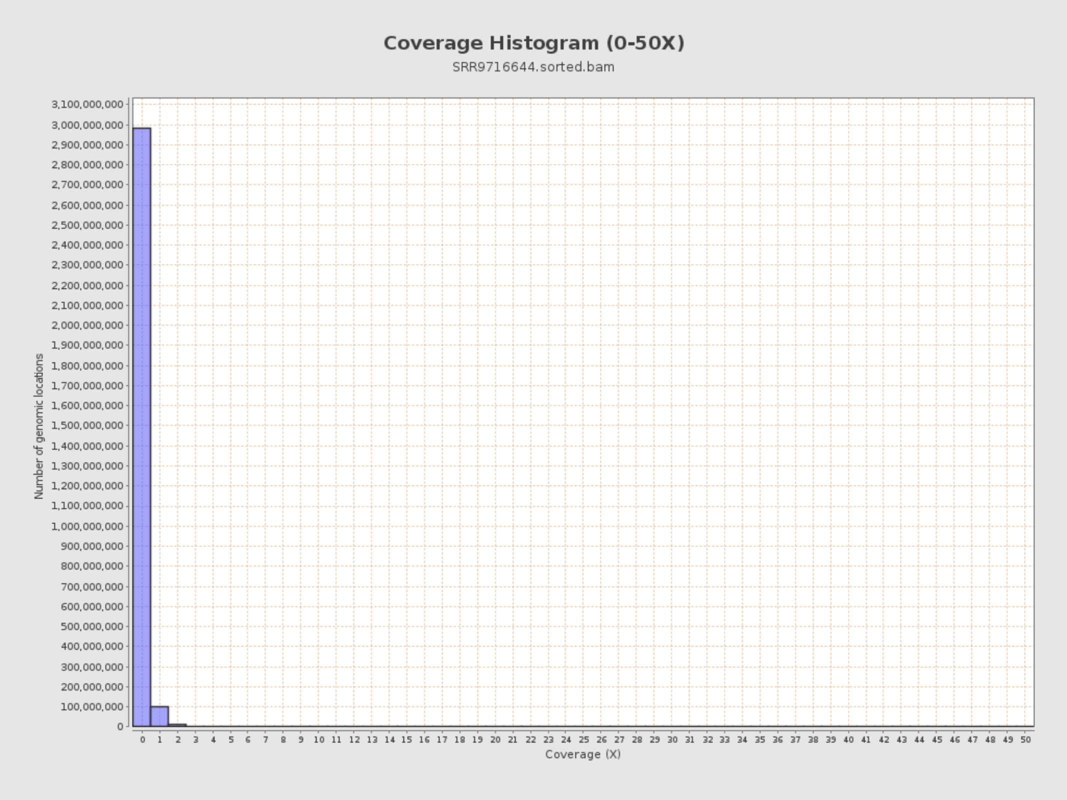
3. Results : Coverage across reference



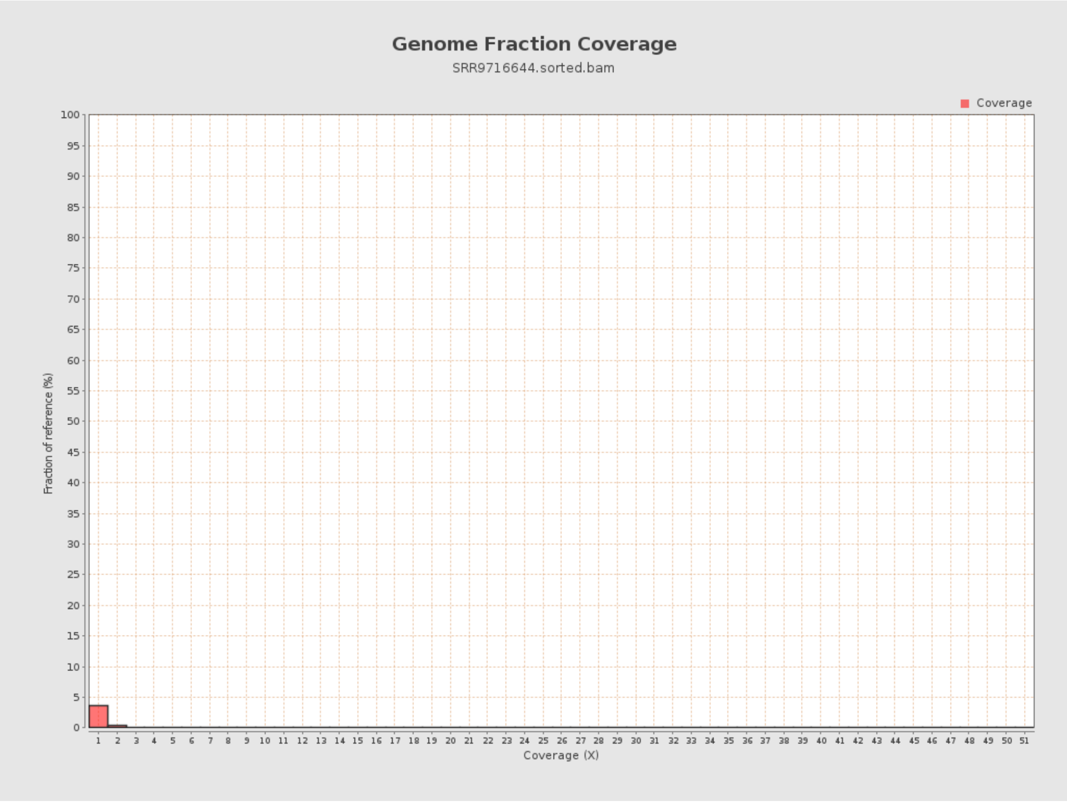
4. Results : Coverage Histogram



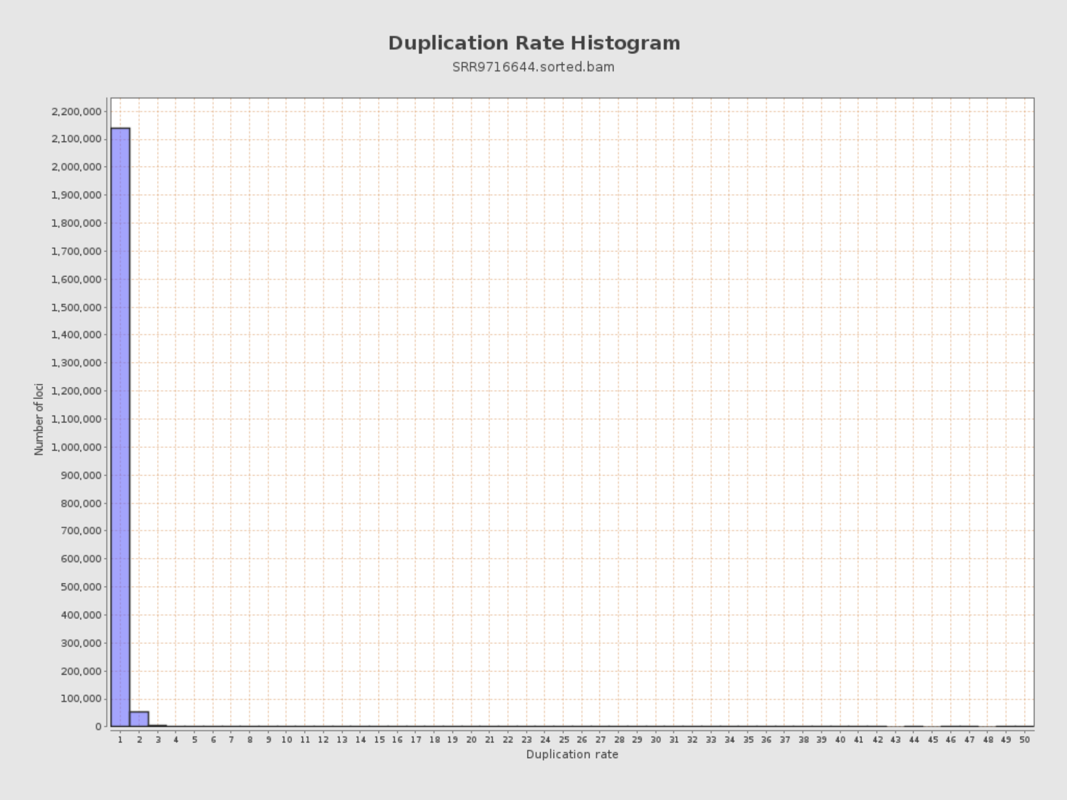
5. Results : Coverage Histogram (0-50X)



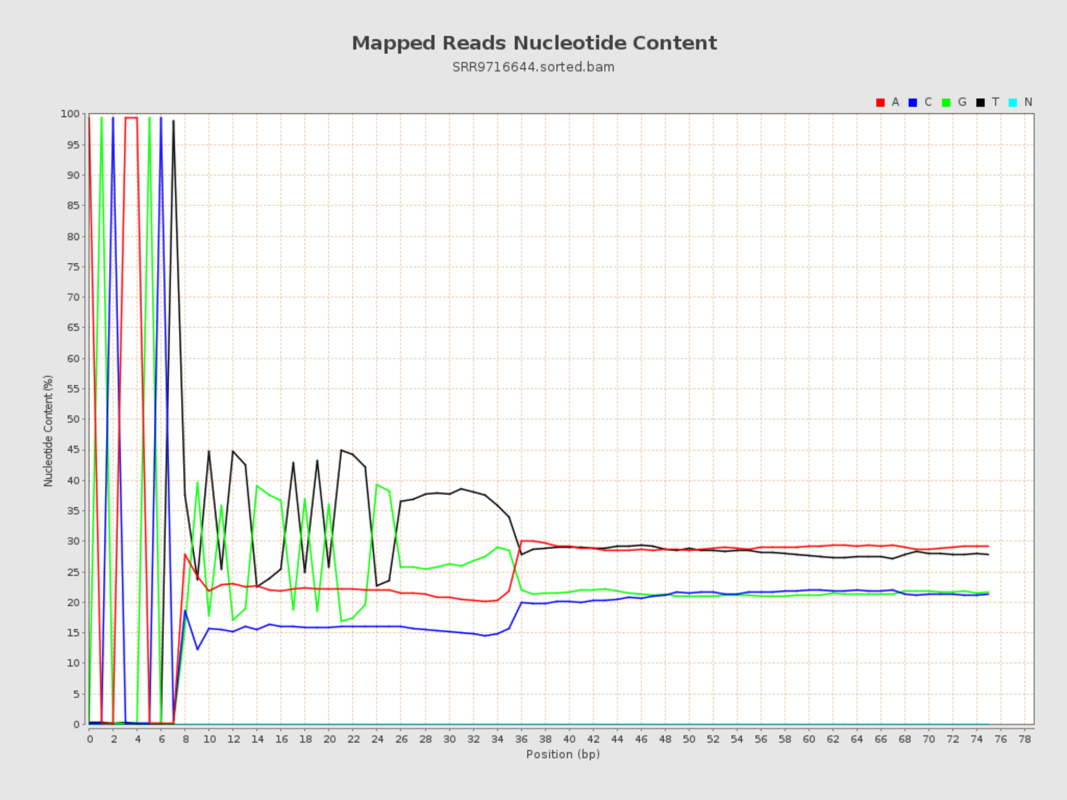
6. Results : Genome Fraction Coverage



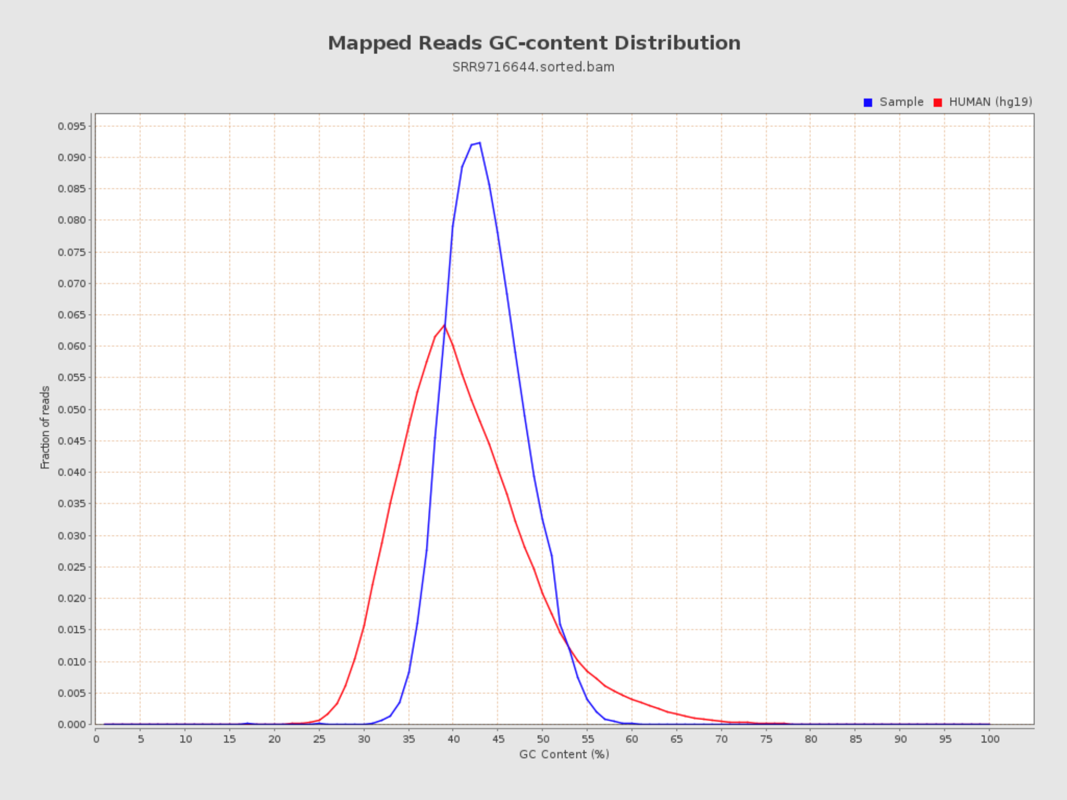
7. Results : Duplication Rate Histogram



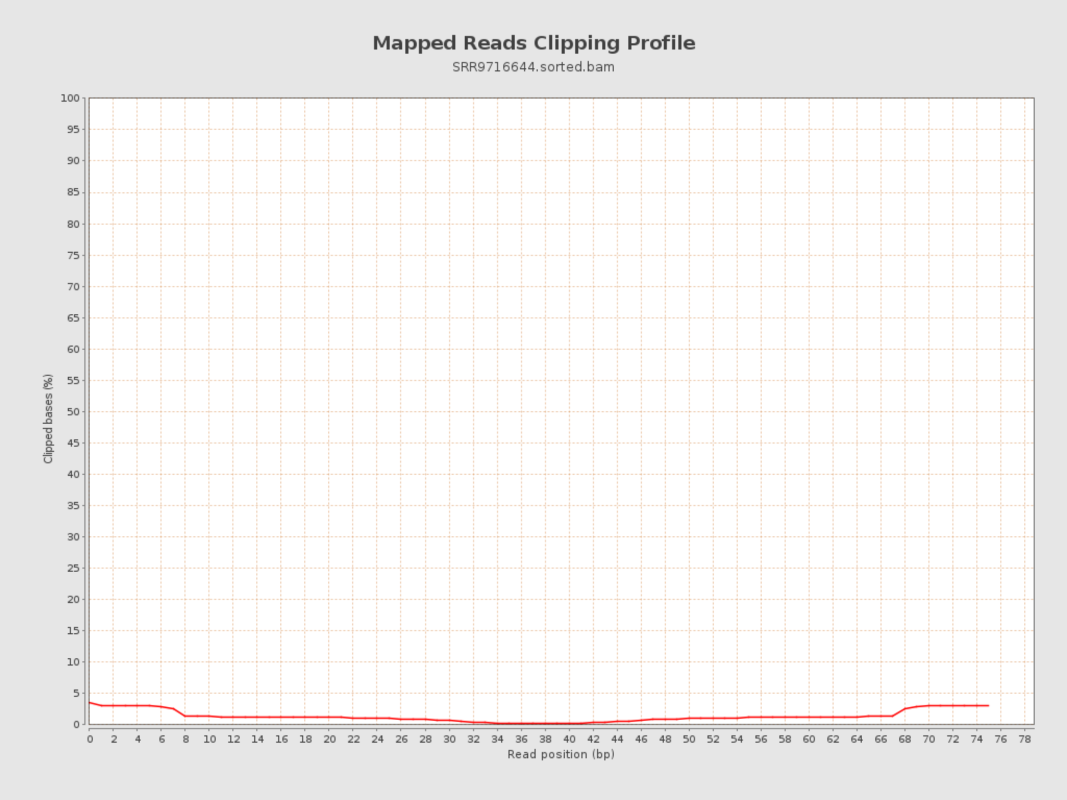
8. Results : Mapped Reads Nucleotide Content



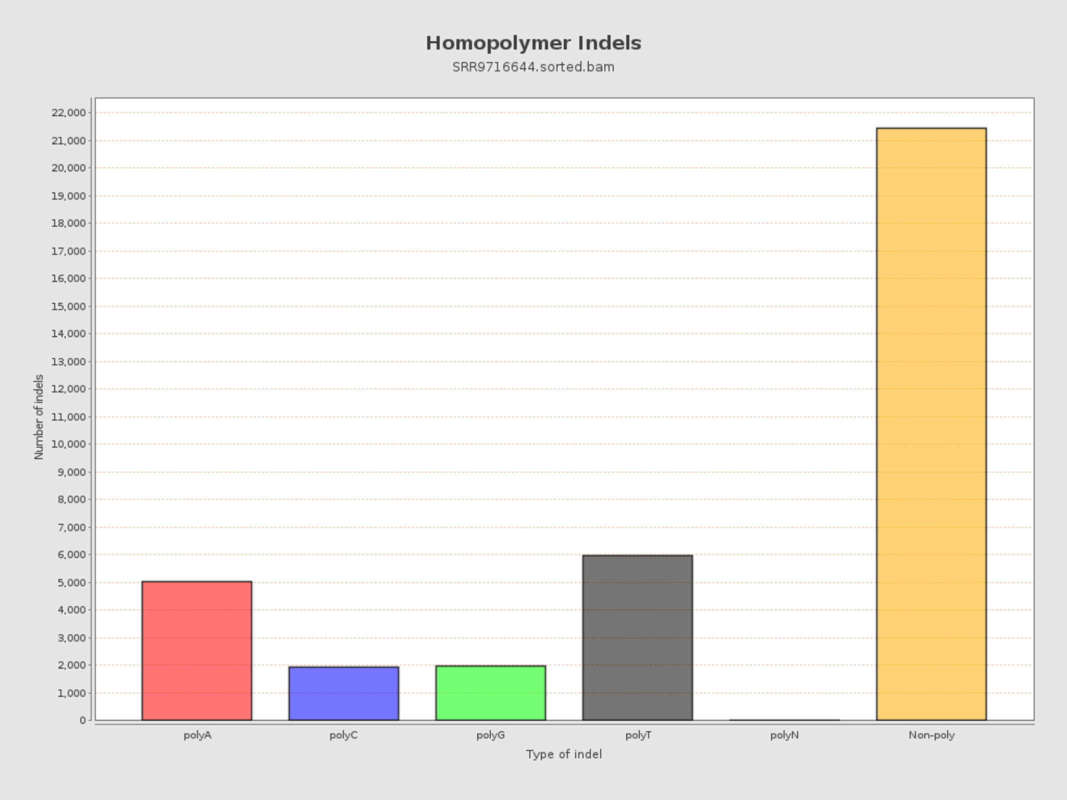
9. Results : Mapped Reads GC-content Distribution



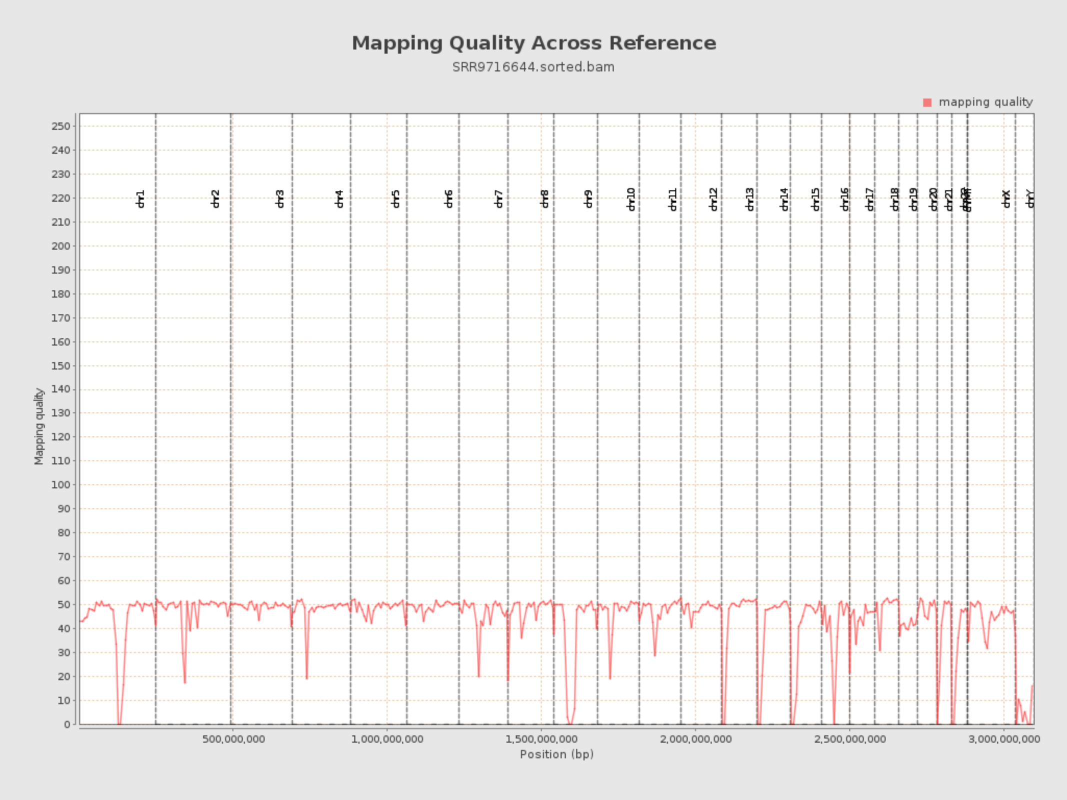
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram