Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 10:22:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867846.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_SRR9867846 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867846.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 10:22:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9867846.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,380,174
Mapped reads	2,190,684 / 92.04%
Unmapped reads	189,490 / 7.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,756 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	119,266 / 5.01%
Duplication rate	4.03%
Clipped reads	2,193,118 / 92.14%

2.2. ACGT Content

Number/percentage of A's	33,536,470 / 25.99%
Number/percentage of C's	24,026,678 / 18.62%
Number/percentage of T's	41,479,125 / 32.14%
Number/percentage of G's	29,983,101 / 23.24%
Number/percentage of N's	16,862 / 0.01%
GC Percentage	41.85%

2.3. Coverage

Mean	0.0417

Standard Deviation	0.3879

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

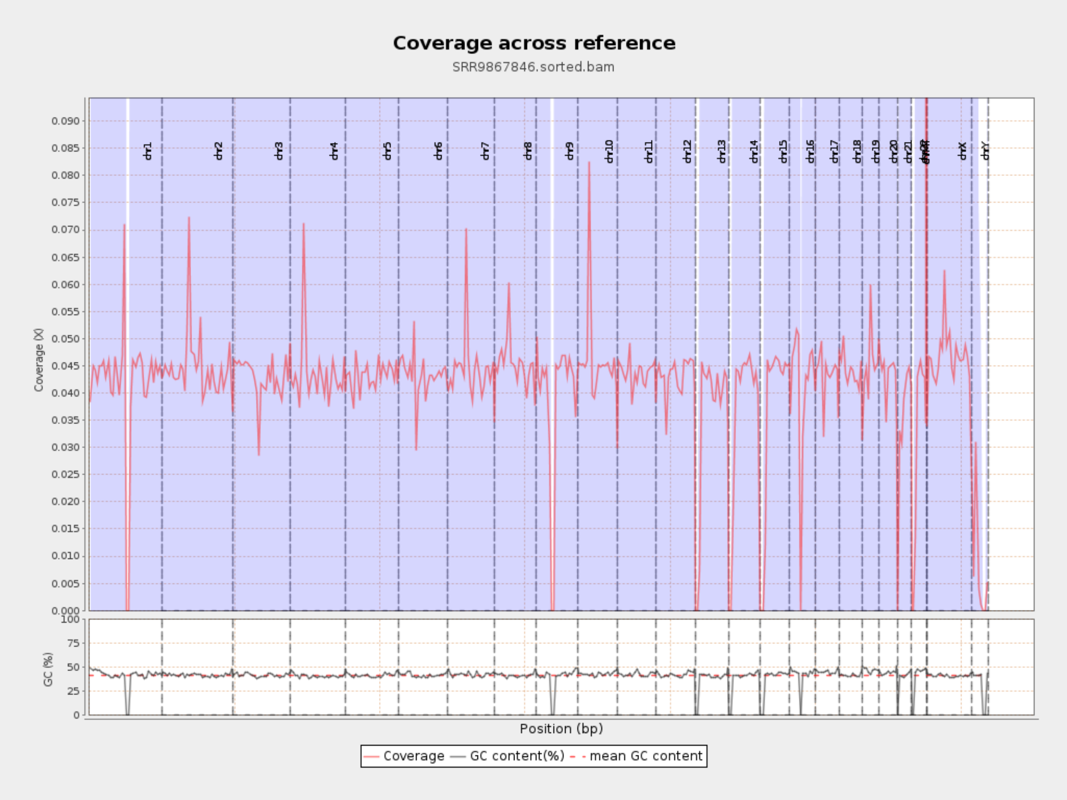
General error rate	0.52%
Mismatches	652,339
Insertions	10,629
Mapped reads with at least one insertion	0.48%
Deletions	24,724
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.38%

2.6. Chromosome stats

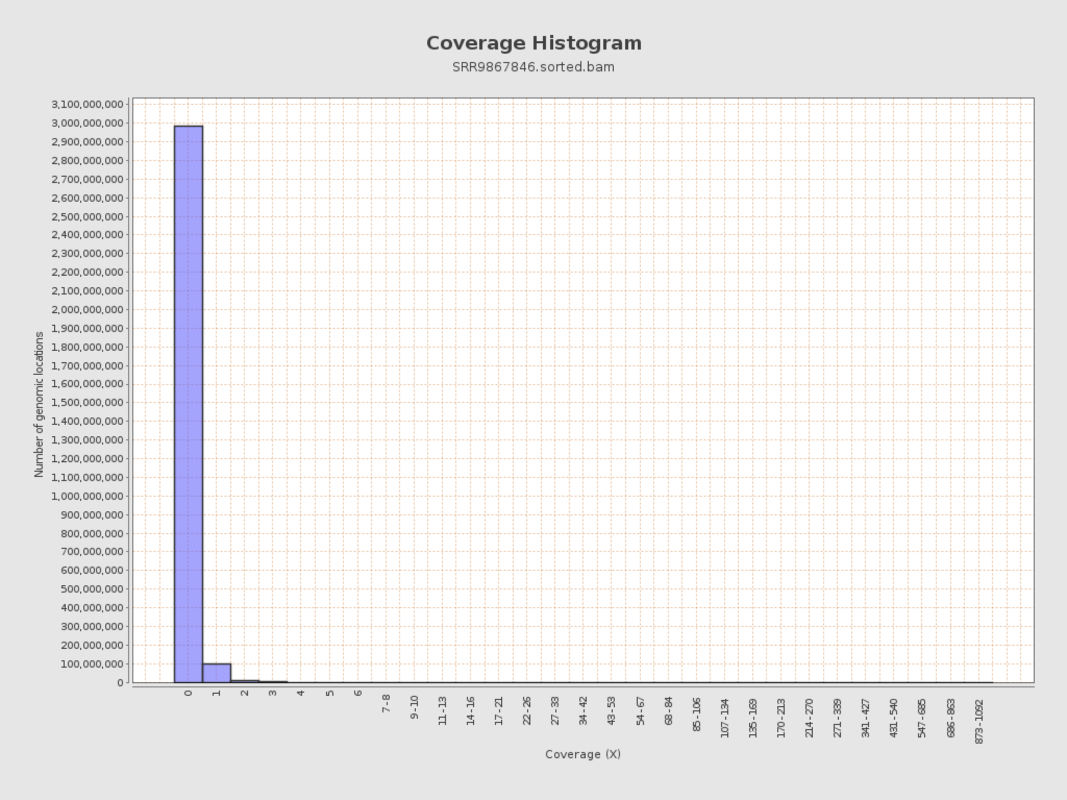
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10385720	0.0417	0.7208
chr2	243199373	10918193	0.0449	0.5402
chr3	198022430	8477361	0.0428	0.2311
chr4	191154276	8309267	0.0435	0.2817
chr5	180915260	7808411	0.0432	0.2353
chr6	171115067	7407584	0.0433	0.2723
chr7	159138663	7116606	0.0447	0.4666

chr8	146364022	6647217	0.0454	0.4488
chr9	141213431	5411434	0.0383	0.3079
chr10	135534747	6266756	0.0462	0.4023
chr11	135006516	5877675	0.0435	0.3163
chr12	133851895	5783543	0.0432	0.2366
chr13	115169878	4042892	0.0351	0.2168
chr14	107349540	3890818	0.0362	0.2225
chr15	102531392	3715437	0.0362	0.2158
chr16	90354753	3705220	0.041	0.2521
chr17	81195210	3507891	0.0432	0.2578
chr18	78077248	3456746	0.0443	0.5811
chr19	59128983	2690855	0.0455	0.5317
chr20	63025520	2730234	0.0433	0.242
chr21	48129895	1682694	0.035	0.2553
chr22	51304566	1529651	0.0298	0.1936
chrMT	16571	47717	2.8795	2.3341
chrX	155270560	7212251	0.0464	0.2731
chrY	59373566	459266	0.0077	0.321

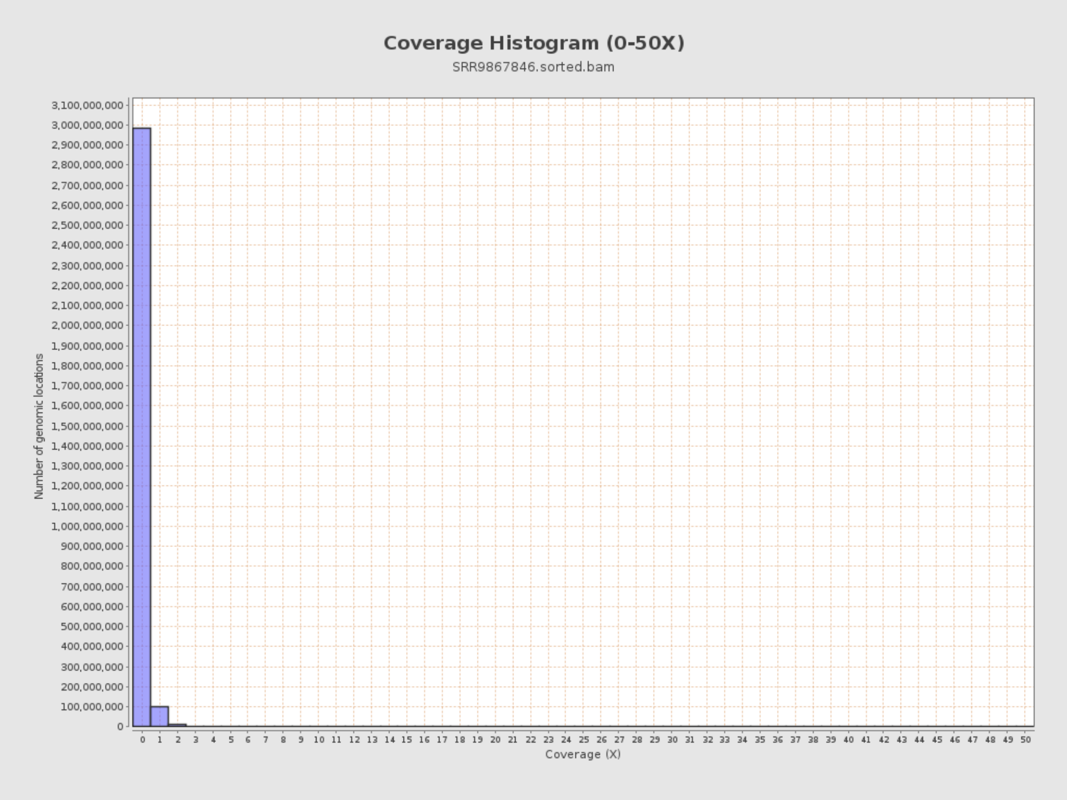
3. Results : Coverage across reference



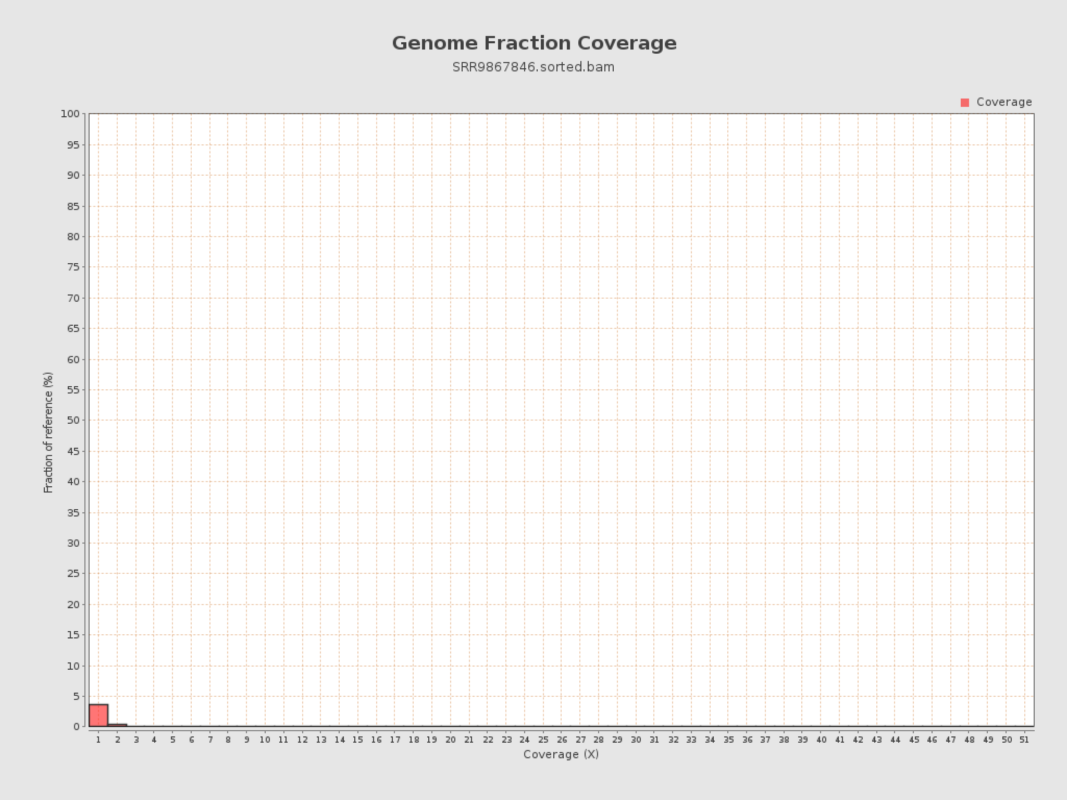
4. Results : Coverage Histogram



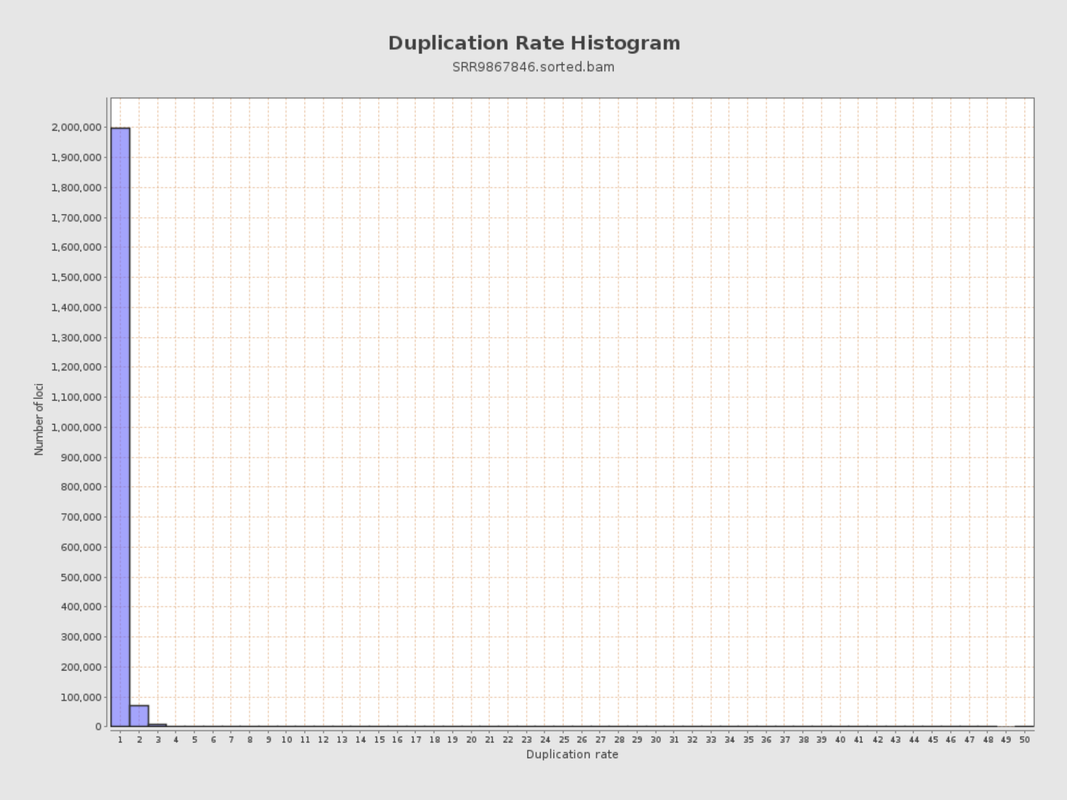
5. Results : Coverage Histogram (0-50X)



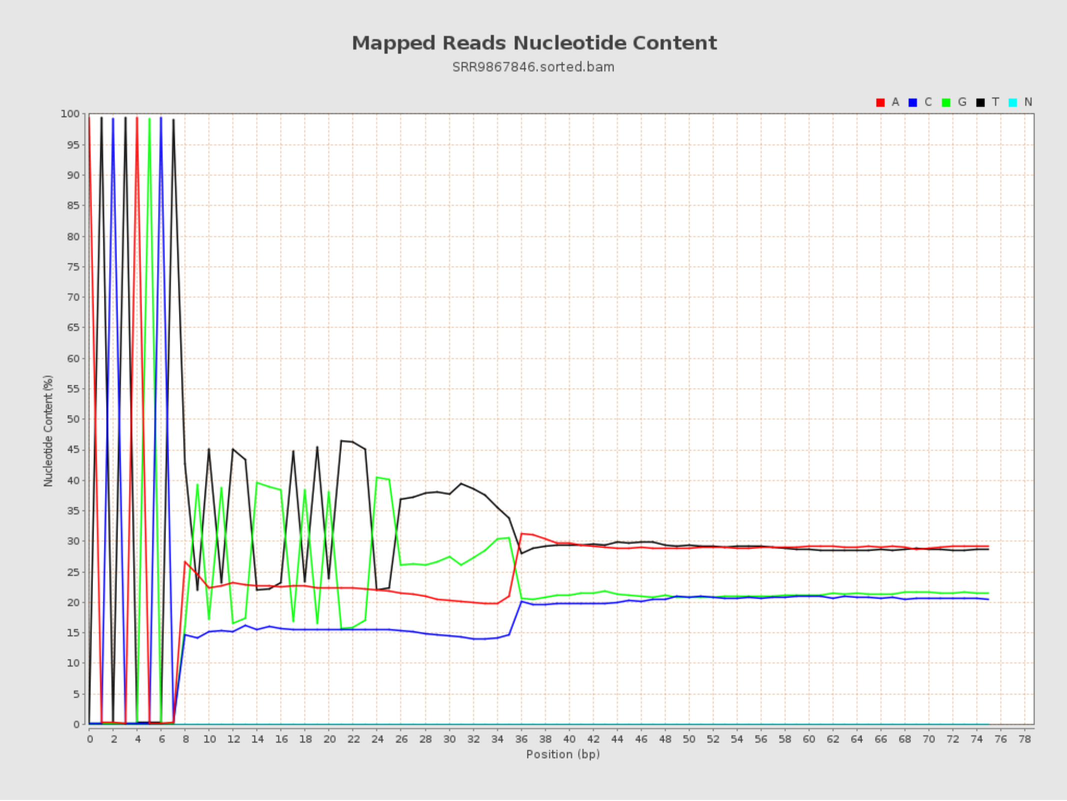
6. Results : Genome Fraction Coverage



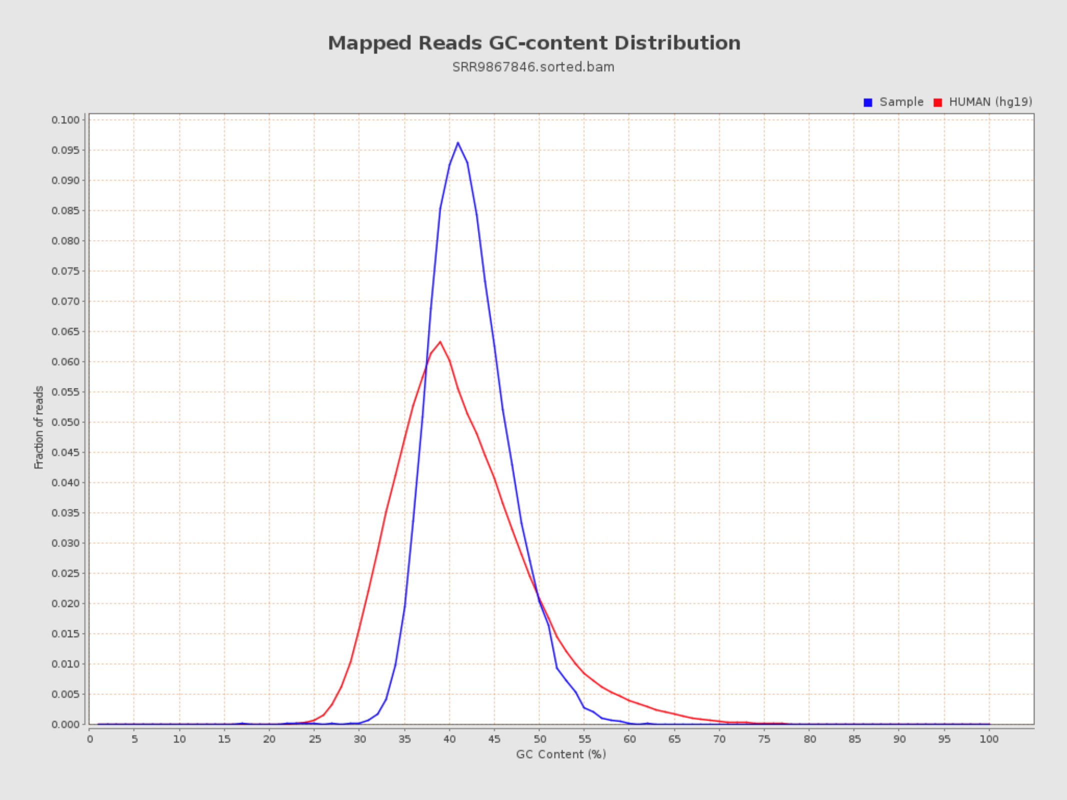
7. Results : Duplication Rate Histogram



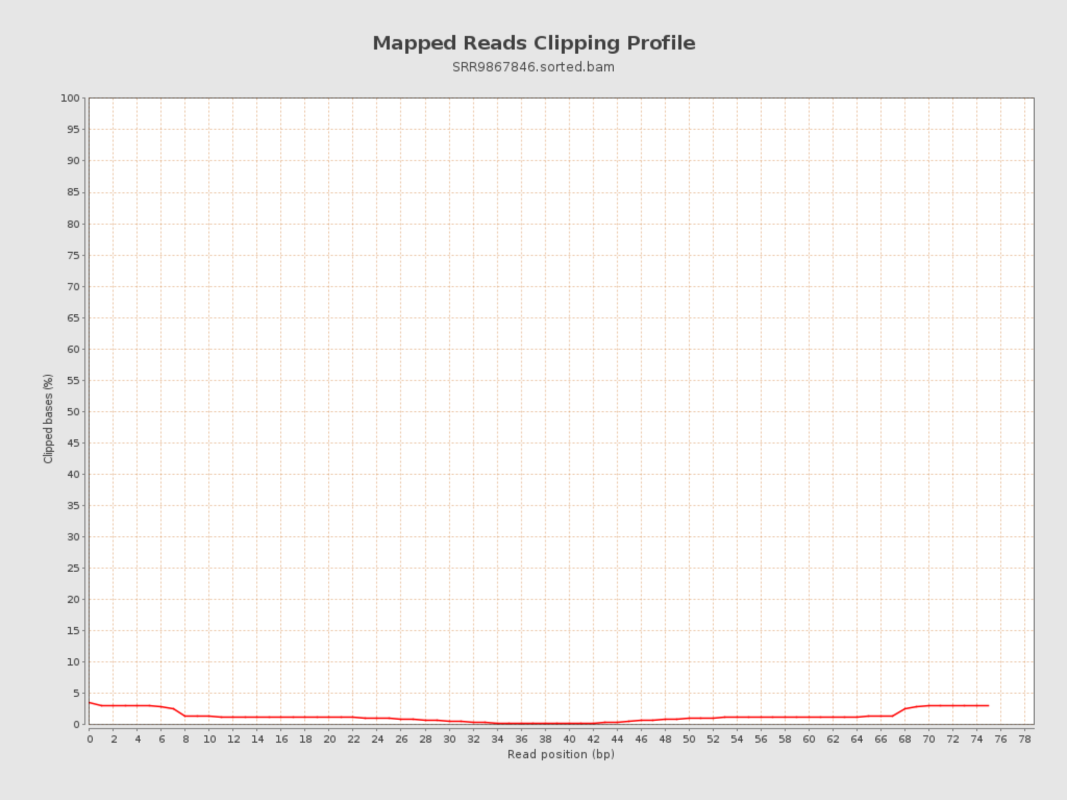
8. Results : Mapped Reads Nucleotide Content



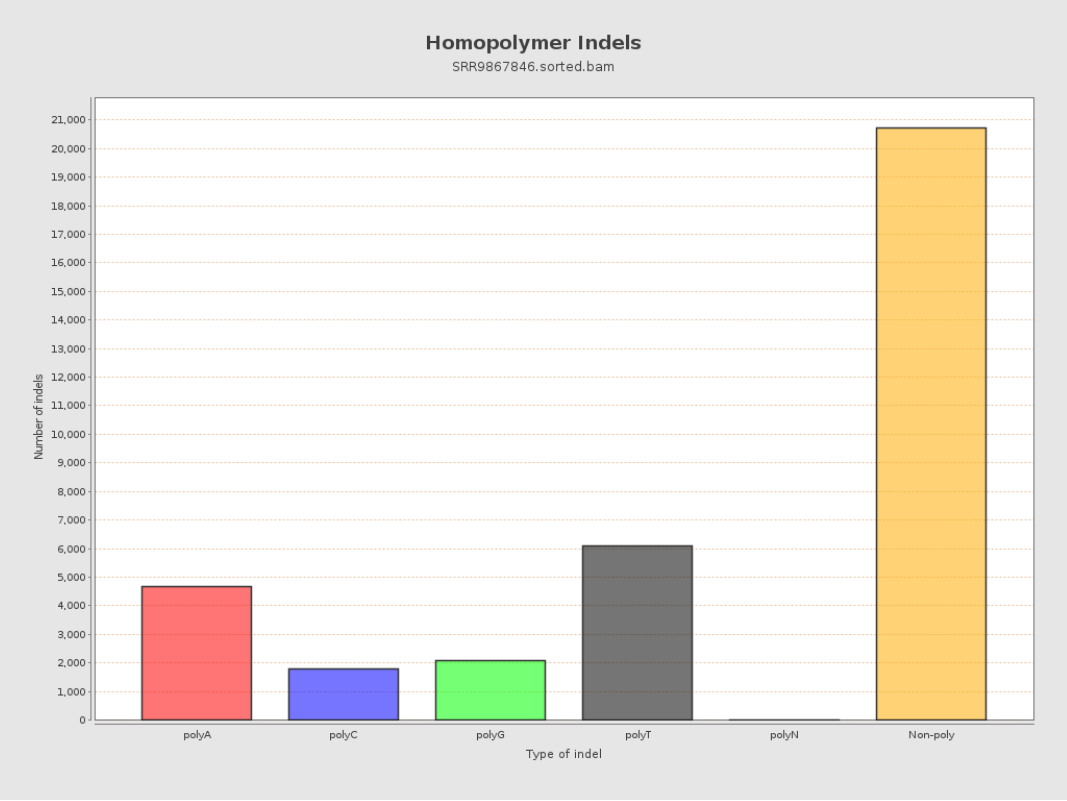
9. Results : Mapped Reads GC-content Distribution



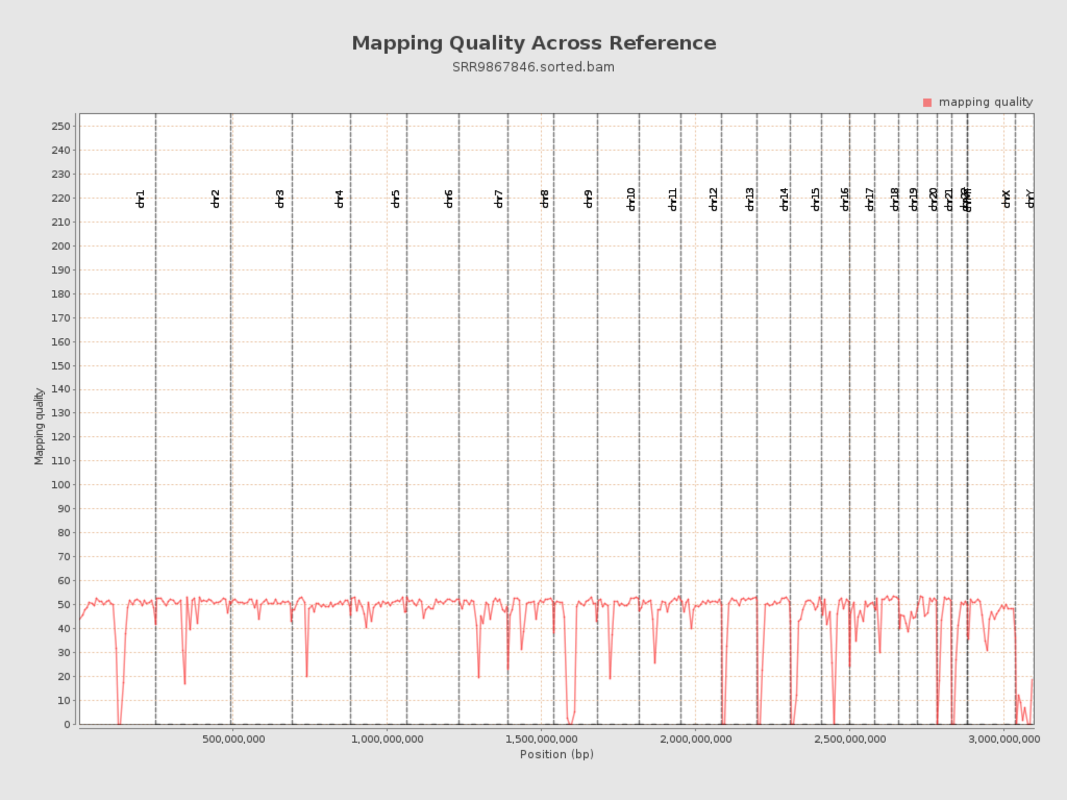
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram