Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:23:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080646.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_SRR3080646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:23:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,537,829
Mapped reads	1,362,337 / 88.59%
Unmapped reads	175,492 / 11.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,200 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	54,785 / 3.56%
Duplication rate	3.48%
Clipped reads	666,363 / 43.33%

2.2. ACGT Content

Number/percentage of A's	23,984,431 / 26.83%
Number/percentage of C's	16,564,714 / 18.53%
Number/percentage of T's	28,195,400 / 31.55%
Number/percentage of G's	20,631,192 / 23.08%
Number/percentage of N's	3,724 / 0%
GC Percentage	41.62%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2407

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

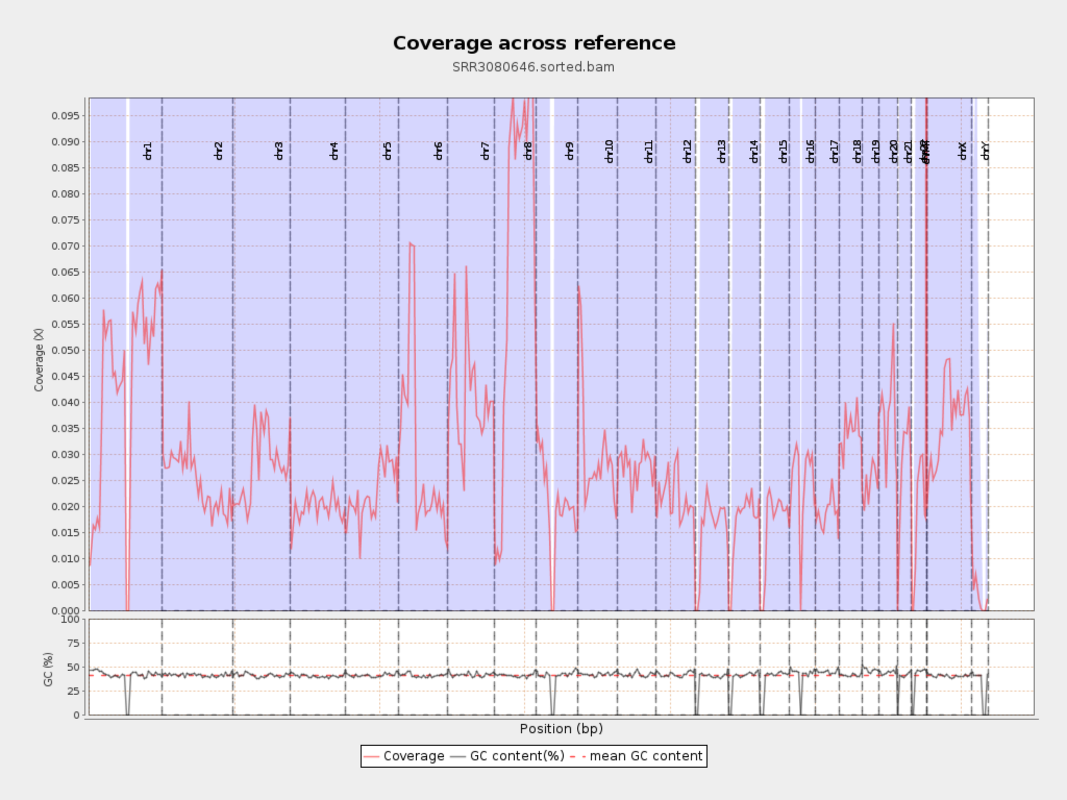
General error rate	0.7%
Mismatches	615,799
Insertions	6,530
Mapped reads with at least one insertion	0.48%
Deletions	20,534
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.29%

2.6. Chromosome stats

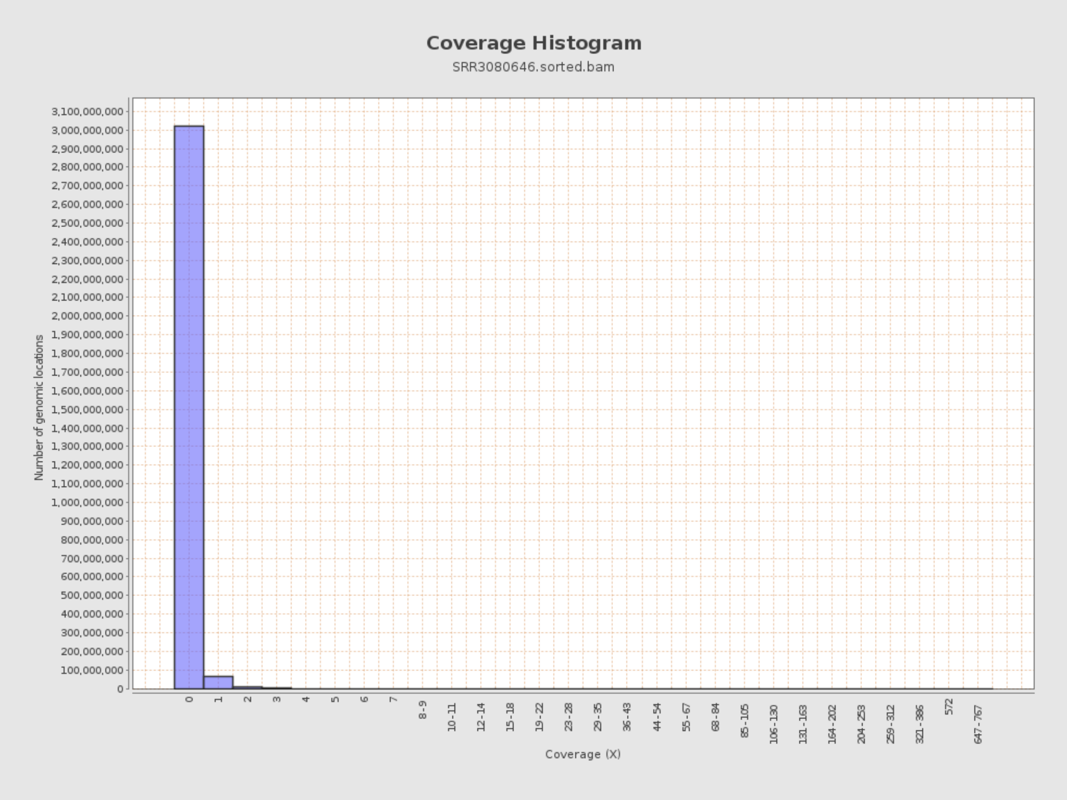
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10737932	0.0431	0.277
chr2	243199373	6033104	0.0248	0.3678
chr3	198022430	5509830	0.0278	0.1872
chr4	191154276	3751094	0.0196	0.162
chr5	180915260	4117214	0.0228	0.1703
chr6	171115067	5196040	0.0304	0.2278
chr7	159138663	6687935	0.042	0.4571

chr8	146364022	10321371	0.0705	0.321
chr9	141213431	2830810	0.02	0.1784
chr10	135534747	4166424	0.0307	0.2055
chr11	135006516	3753074	0.0278	0.2003
chr12	133851895	2876349	0.0215	0.1661
chr13	115169878	1774116	0.0154	0.1413
chr14	107349540	1762427	0.0164	0.1451
chr15	102531392	1668579	0.0163	0.1532
chr16	90354753	2234884	0.0247	0.1793
chr17	81195210	1518757	0.0187	0.1549
chr18	78077248	2698093	0.0346	0.258
chr19	59128983	1472799	0.0249	0.2006
chr20	63025520	2363752	0.0375	0.2215
chr21	48129895	1296153	0.0269	0.1889
chr22	51304566	889976	0.0173	0.1481
chrMT	16571	8629	0.5207	0.7618
chrX	155270560	5572629	0.0359	0.2203
chrY	59373566	170487	0.0029	0.0659

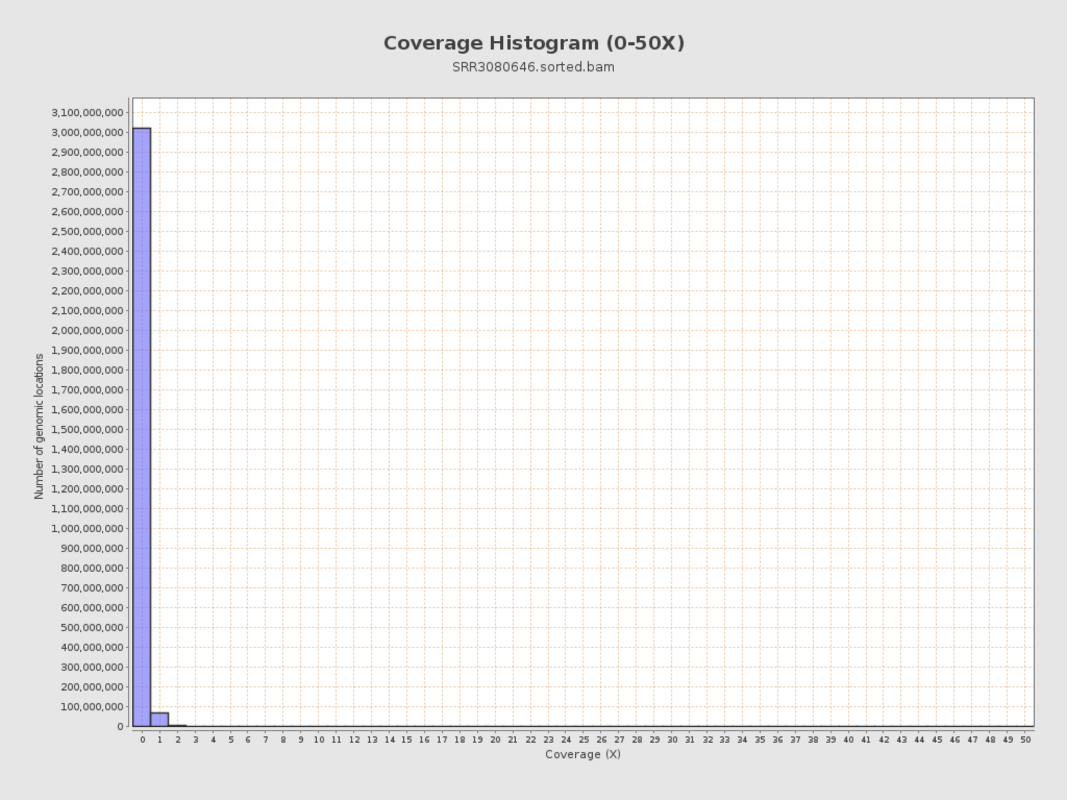
3. Results : Coverage across reference



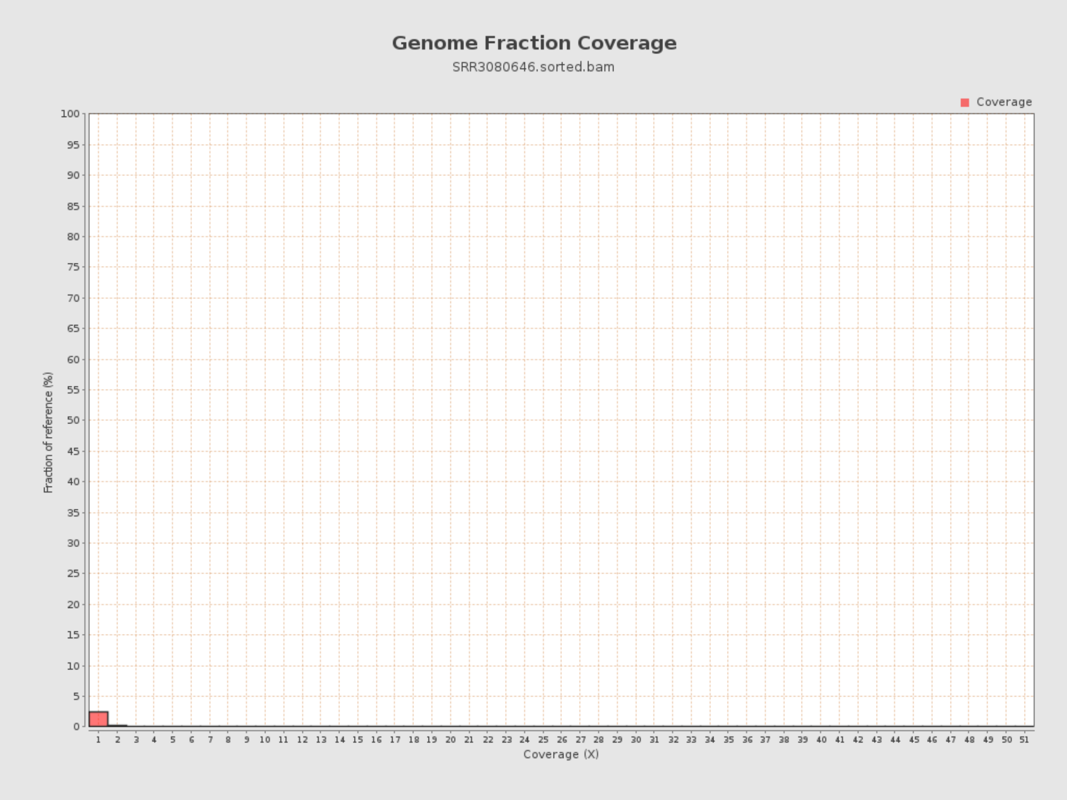
4. Results : Coverage Histogram



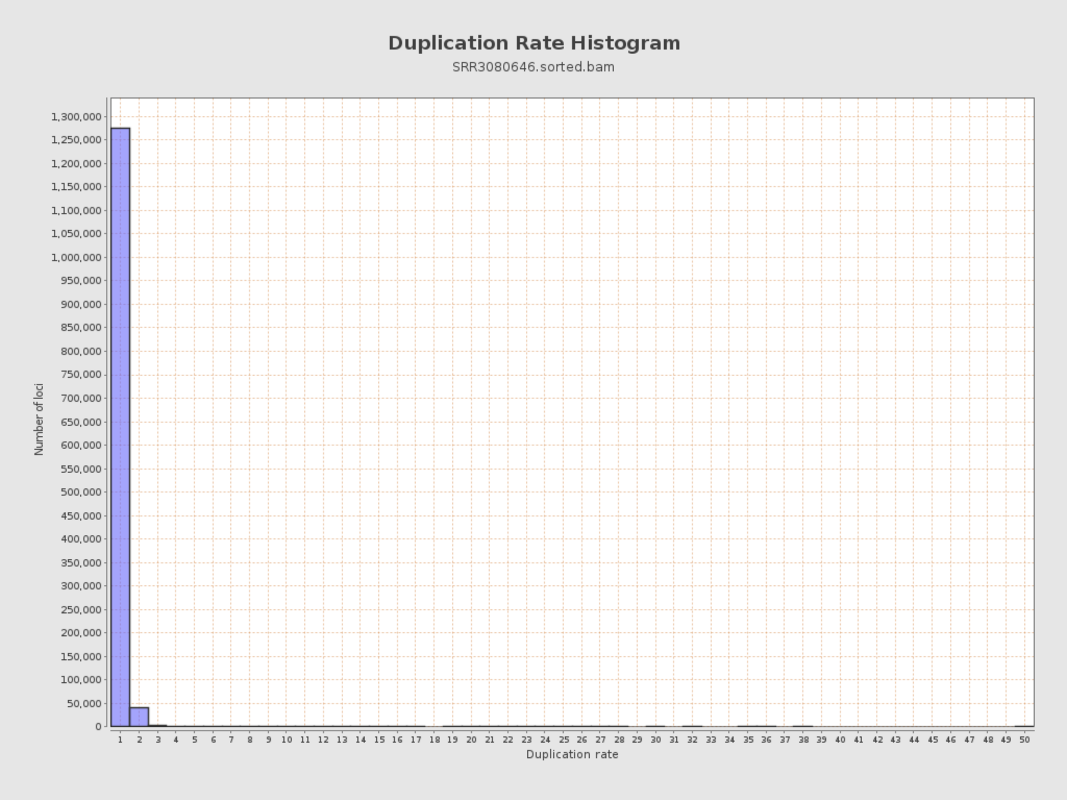
5. Results : Coverage Histogram (0-50X)



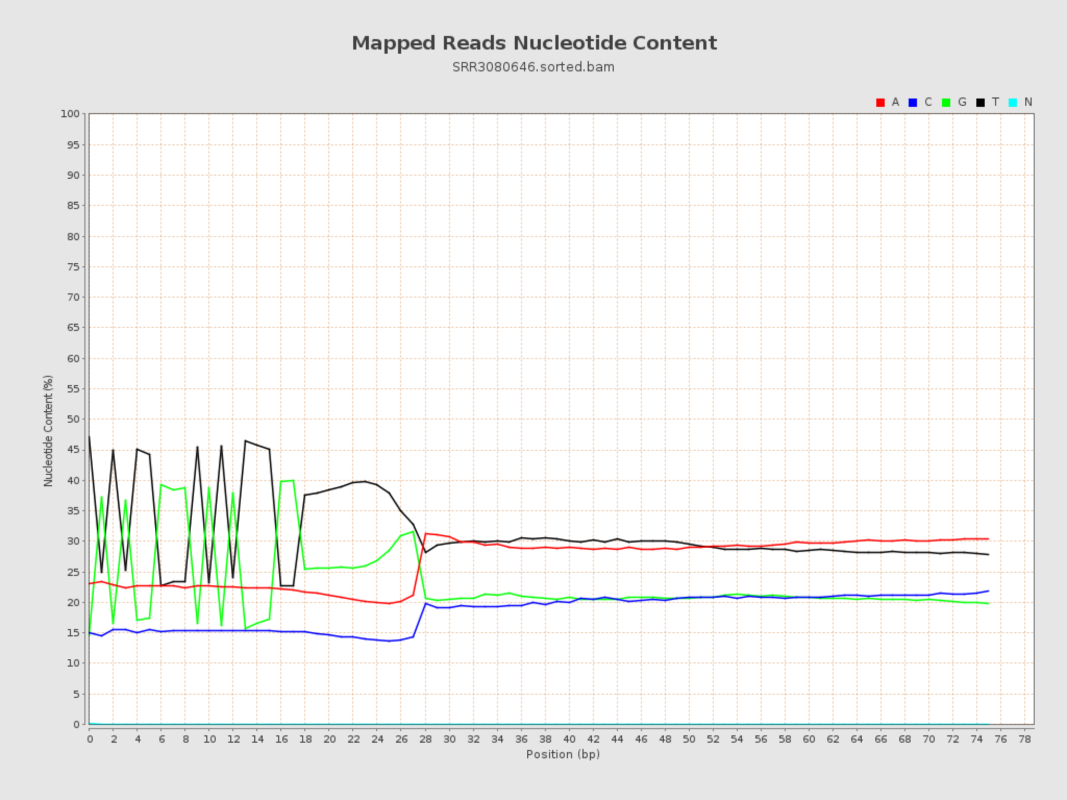
6. Results : Genome Fraction Coverage



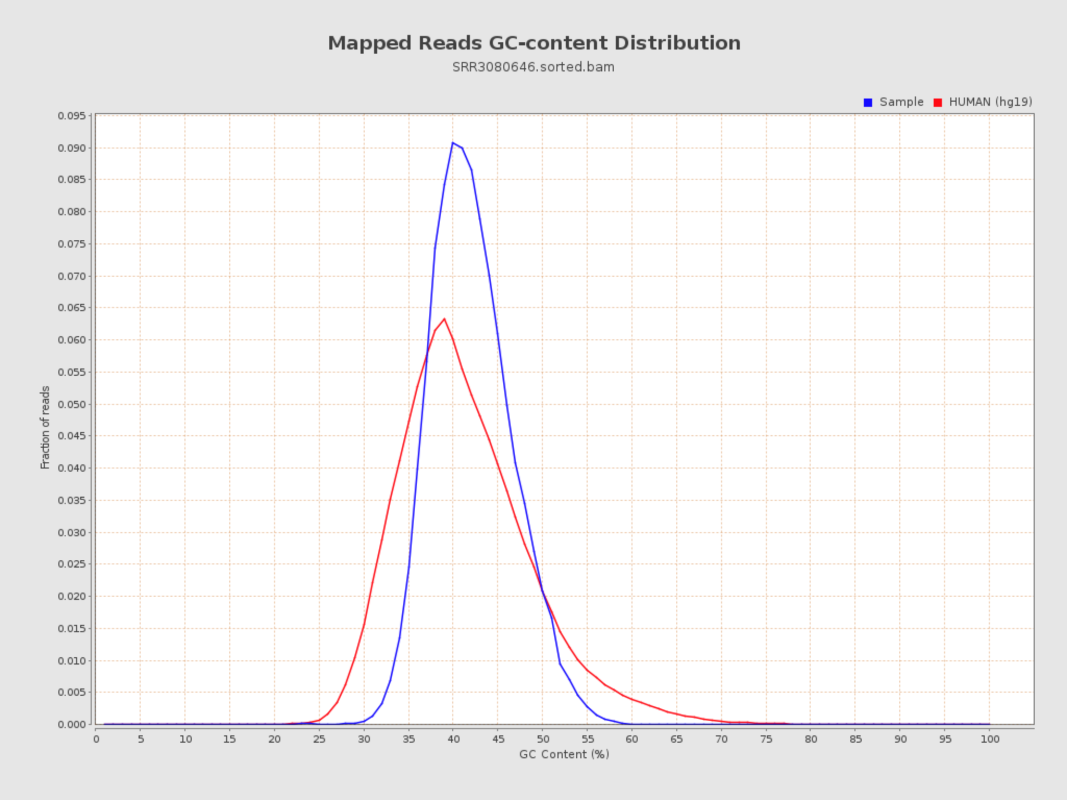
7. Results : Duplication Rate Histogram



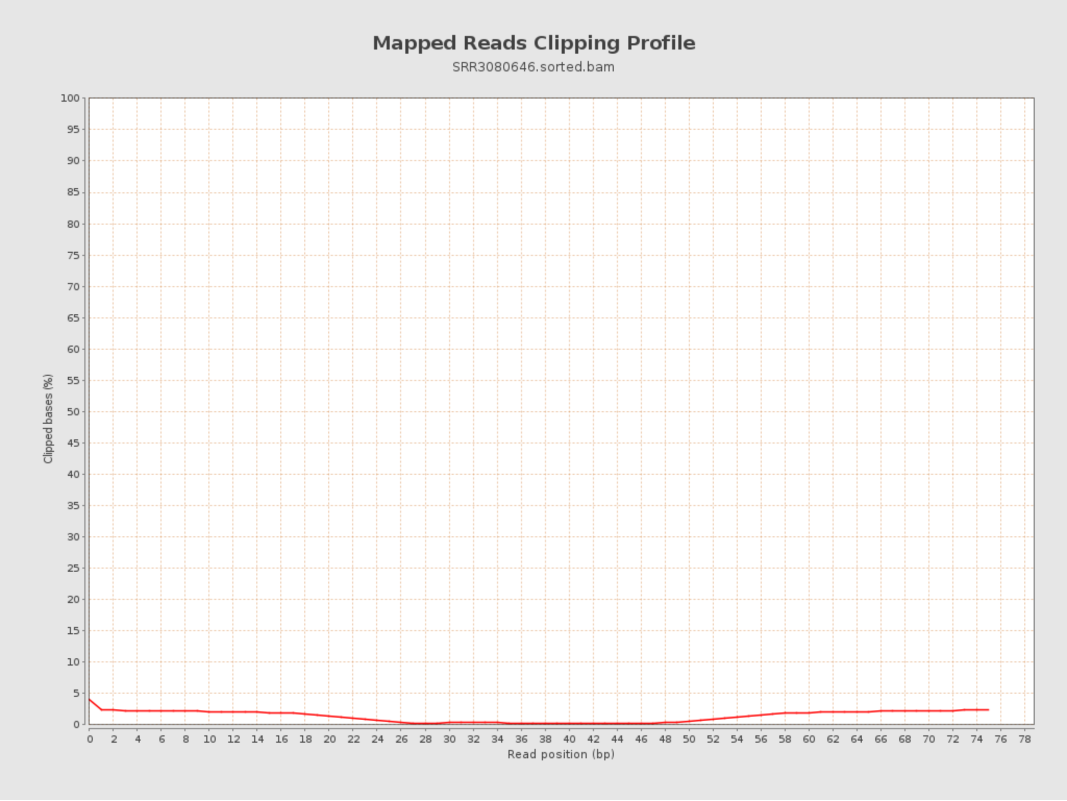
8. Results : Mapped Reads Nucleotide Content



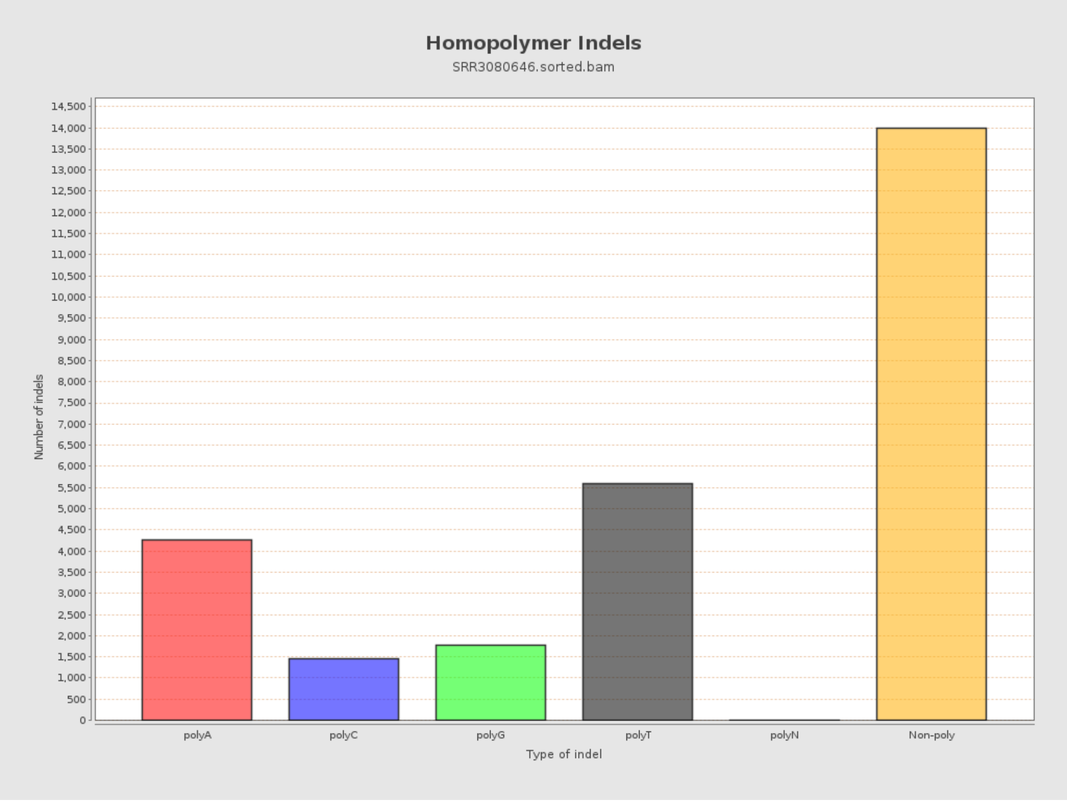
9. Results : Mapped Reads GC-content Distribution



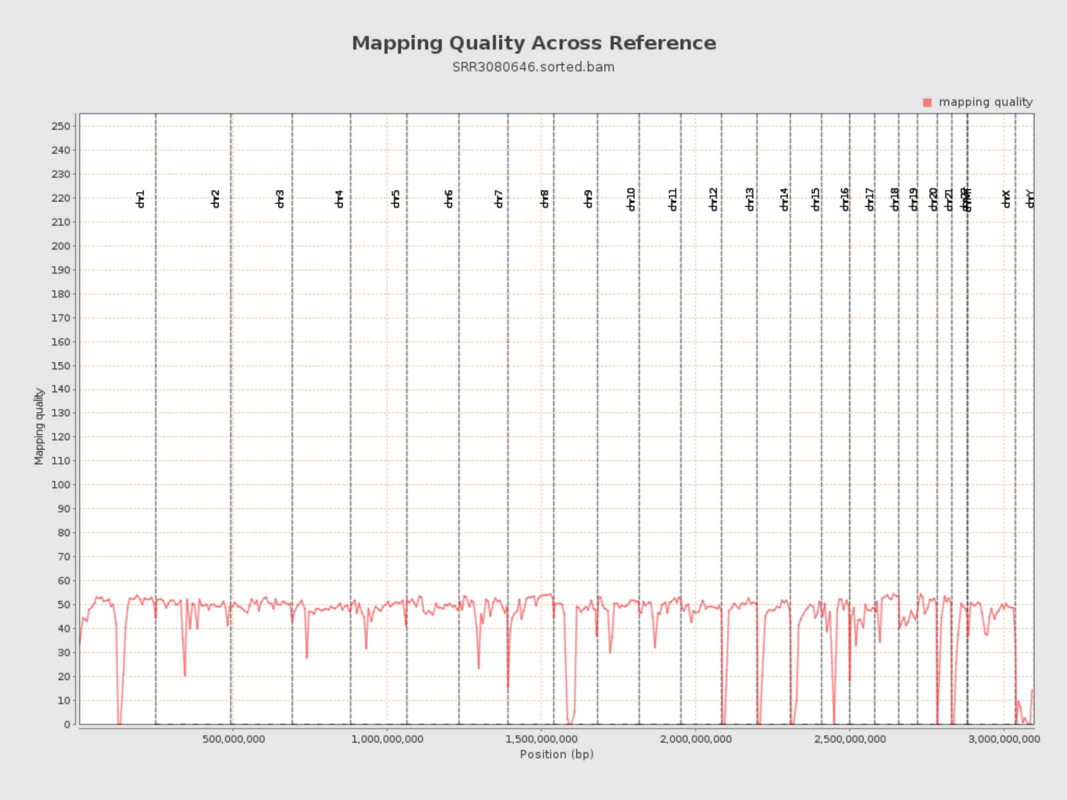
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram