Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:56:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971281.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_SRR2971281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971281.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:56:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,401,029
Mapped reads	8,947,849 / 72.15%
Unmapped reads	3,453,180 / 27.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	921,621 / 7.43%
Duplication rate	9%
Clipped reads	738,279 / 5.95%

2.2. ACGT Content

Number/percentage of A's	101,527,566 / 28.74%
Number/percentage of C's	72,693,935 / 20.58%
Number/percentage of T's	103,886,566 / 29.4%
Number/percentage of G's	75,198,829 / 21.28%
Number/percentage of N's	3,002 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.1141
Standard Deviation	1.2834

2.4. Mapping Quality

Mean Mapping Quality	43.65

2.5. Mismatches and indels

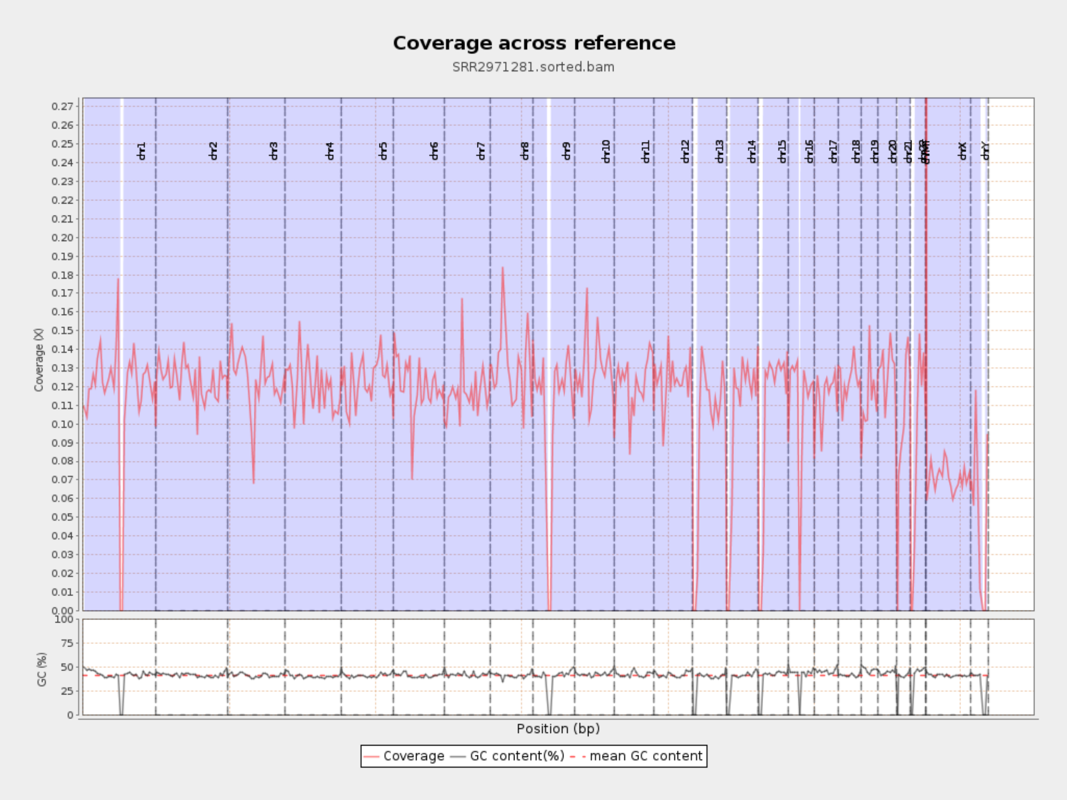
General error rate	0.27%
Mismatches	928,455
Insertions	11,120
Mapped reads with at least one insertion	0.12%
Deletions	27,775
Mapped reads with at least one deletion	0.31%
Homopolymer indels	40.84%

2.6. Chromosome stats

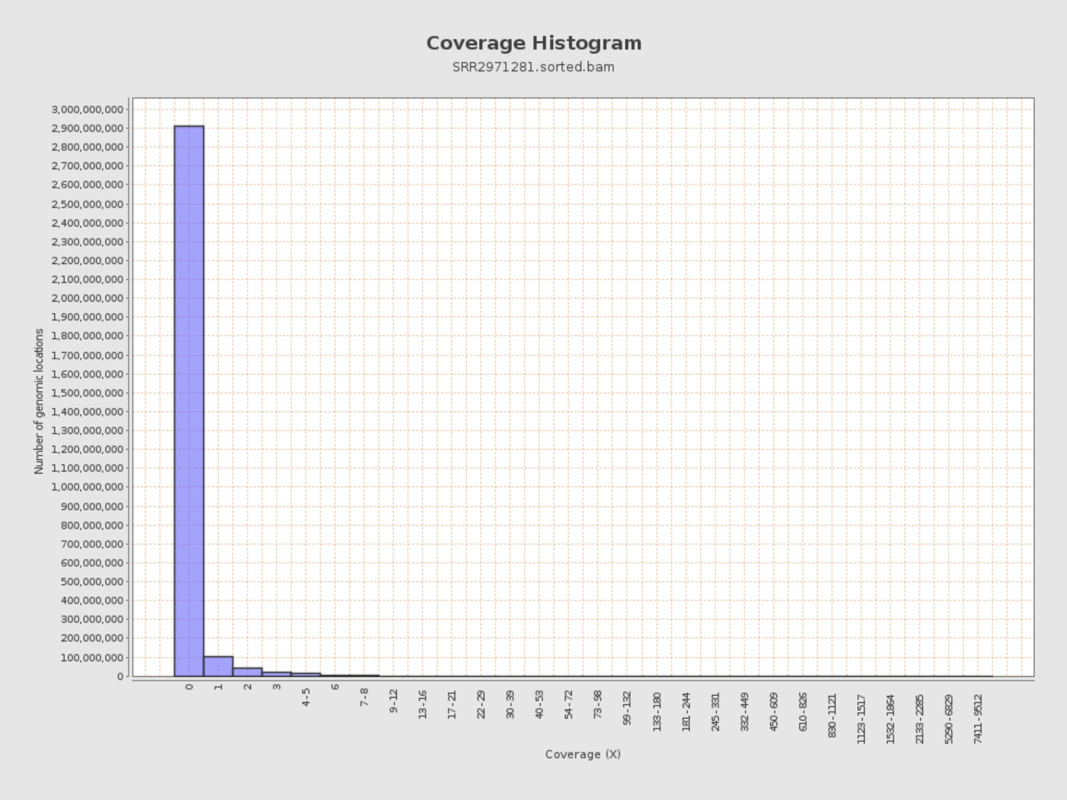
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29277921	0.1175	1.6313
chr2	243199373	30185307	0.1241	0.6946
chr3	198022430	24475234	0.1236	0.5959
chr4	191154276	23062911	0.1207	0.6378
chr5	180915260	22314872	0.1233	0.6069
chr6	171115067	20609007	0.1204	0.6101
chr7	159138663	18593447	0.1168	1.0454
chr8	146364022	19182962	0.1311	4.6449

chr9	141213431	15097580	0.1069	0.633
chr10	135534747	17516137	0.1292	0.8403
chr11	135006516	16453902	0.1219	0.6851
chr12	133851895	16606437	0.1241	0.6124
chr13	115169878	11223316	0.0975	0.5315
chr14	107349540	11030679	0.1028	0.5766
chr15	102531392	10550539	0.1029	0.5422
chr16	90354753	9845716	0.109	0.5771
chr17	81195210	9402589	0.1158	0.5907
chr18	78077248	9629479	0.1233	0.9412
chr19	59128983	6740587	0.114	1.3278
chr20	63025520	8143184	0.1292	0.635
chr21	48129895	4802896	0.0998	0.5874
chr22	51304566	4443577	0.0866	0.5187
chrMT	16571	68512	4.1345	5.3033
chrX	155270560	11049851	0.0712	0.4726
chrY	59373566	3039069	0.0512	0.5777

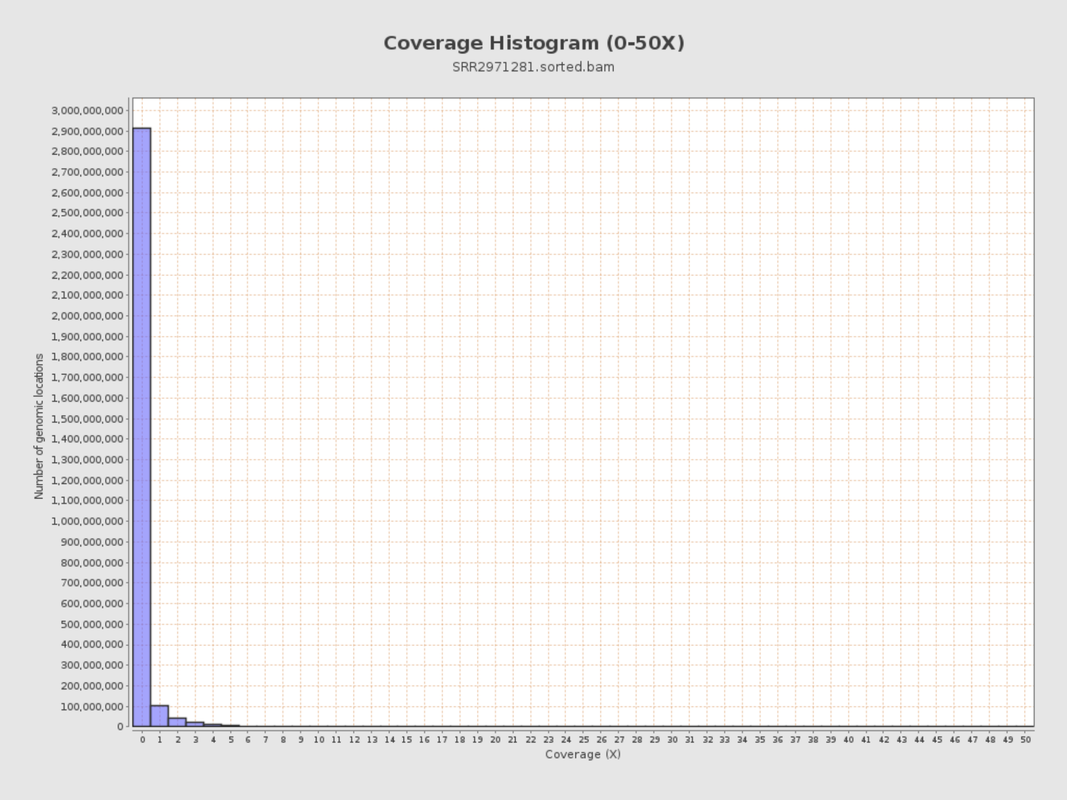
3. Results : Coverage across reference



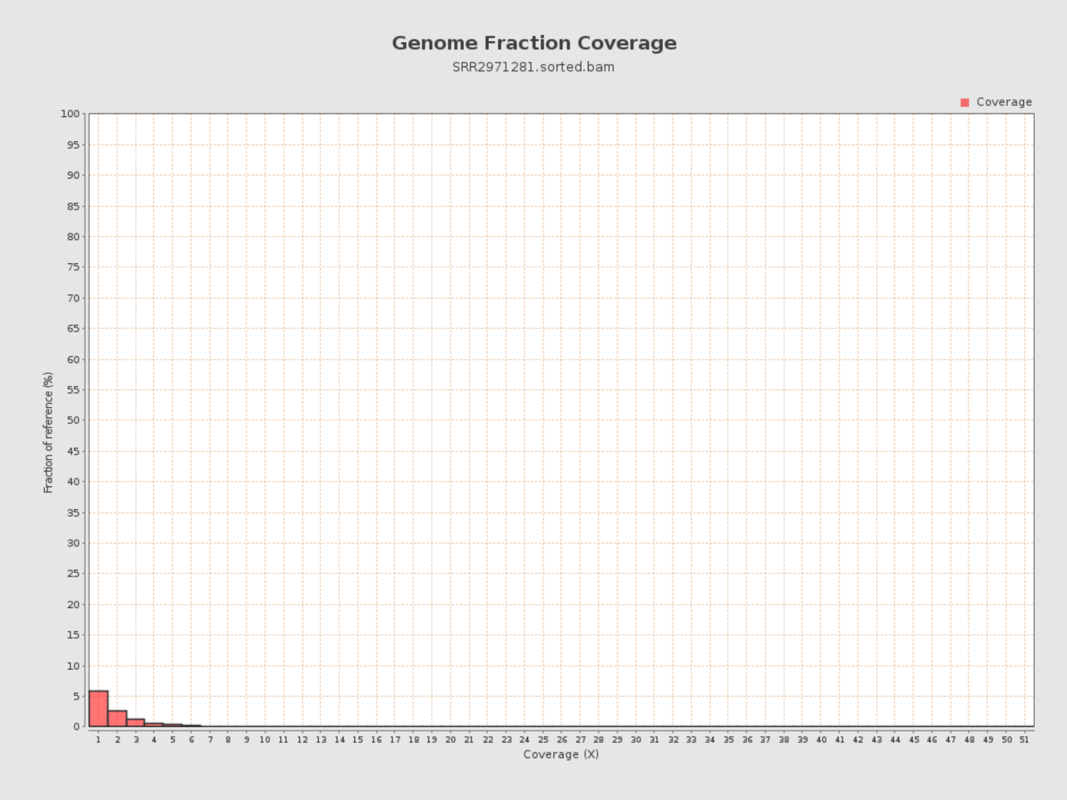
4. Results : Coverage Histogram



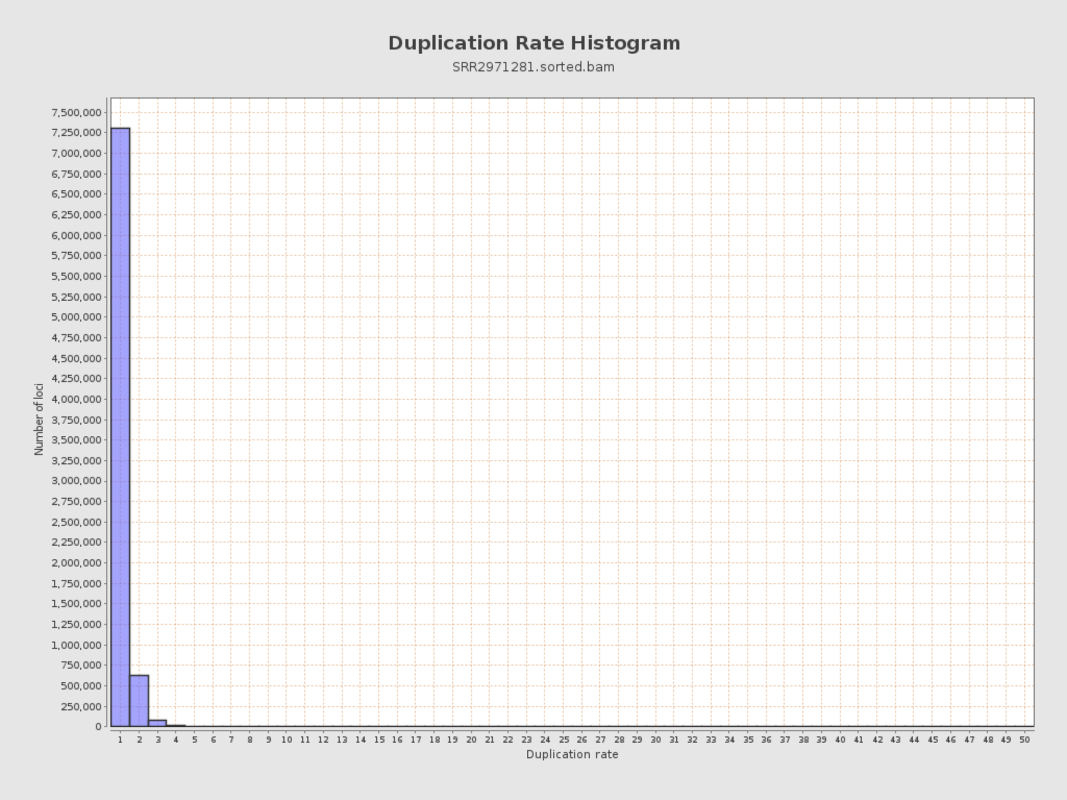
5. Results : Coverage Histogram (0-50X)



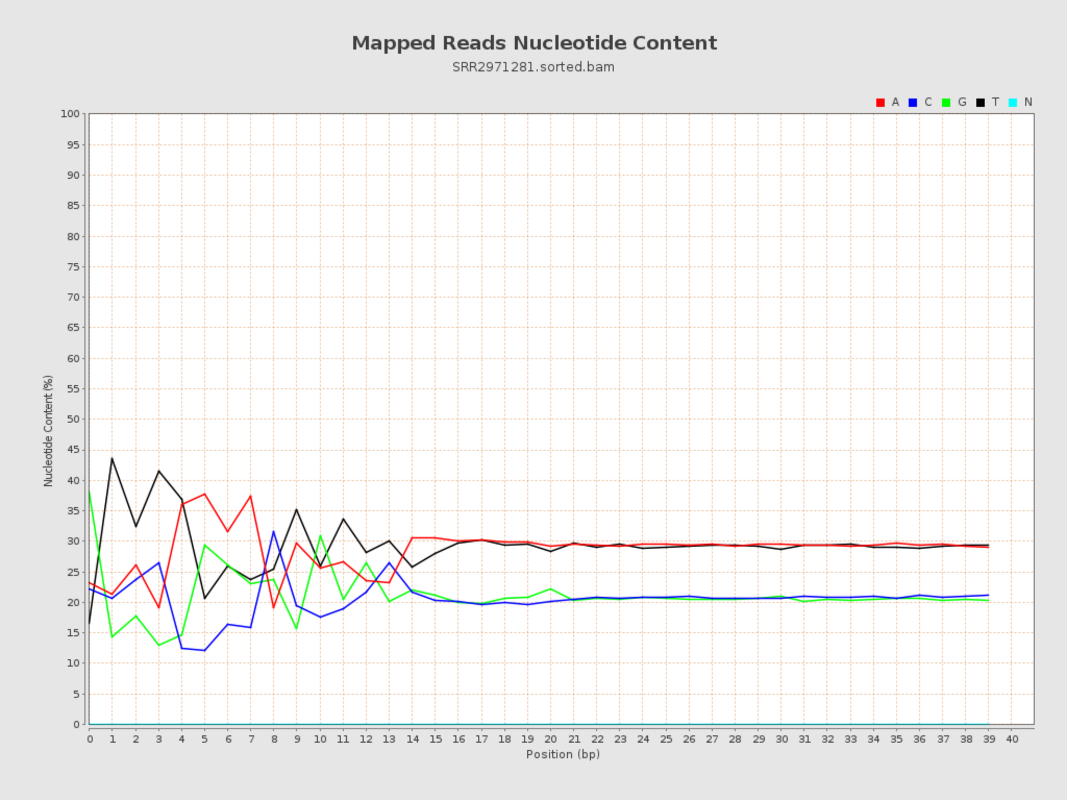
6. Results : Genome Fraction Coverage



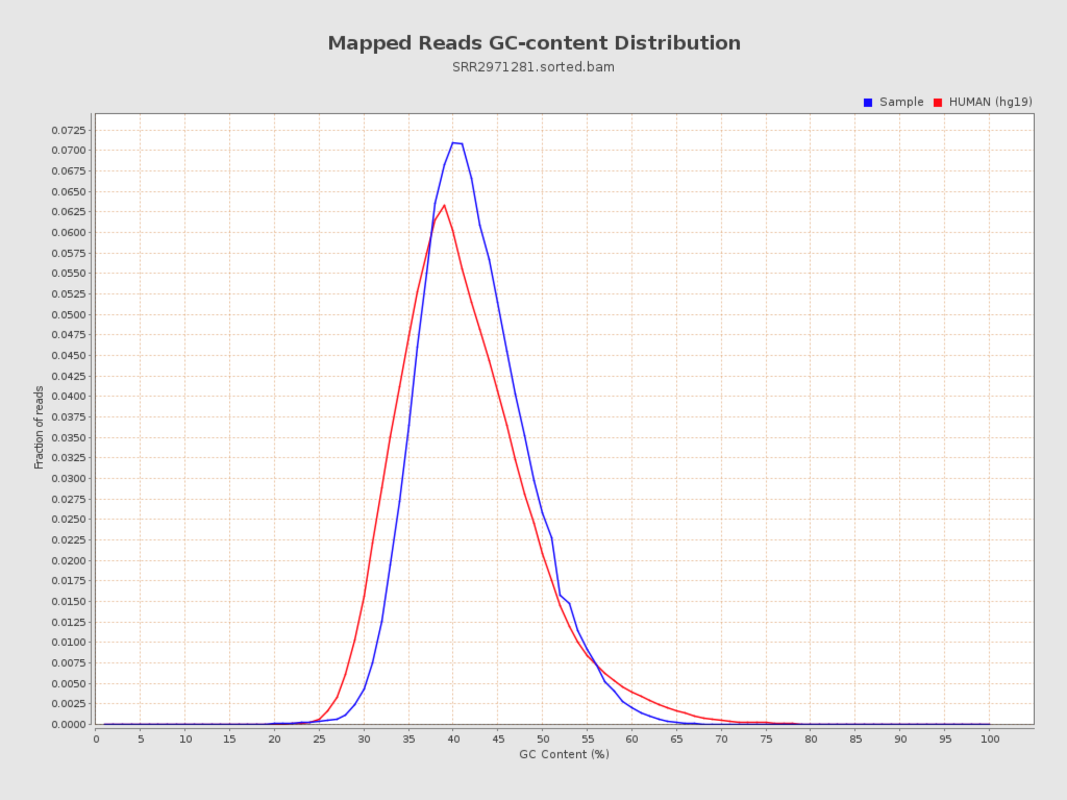
7. Results : Duplication Rate Histogram



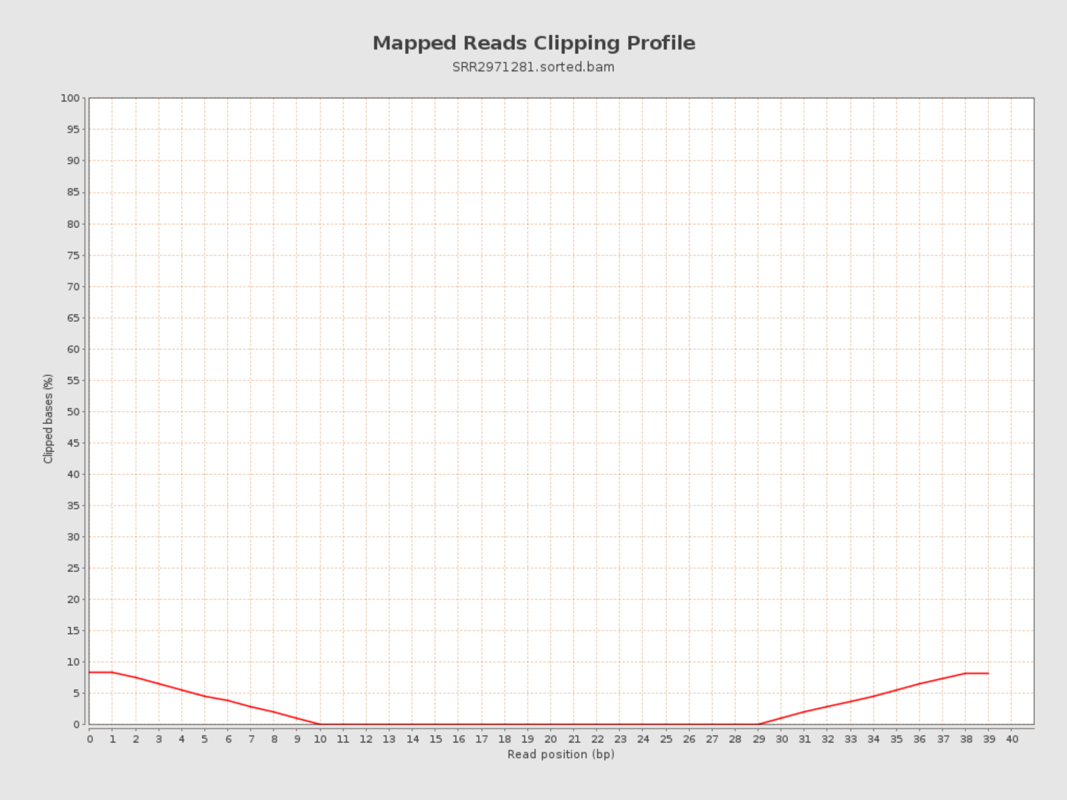
8. Results : Mapped Reads Nucleotide Content



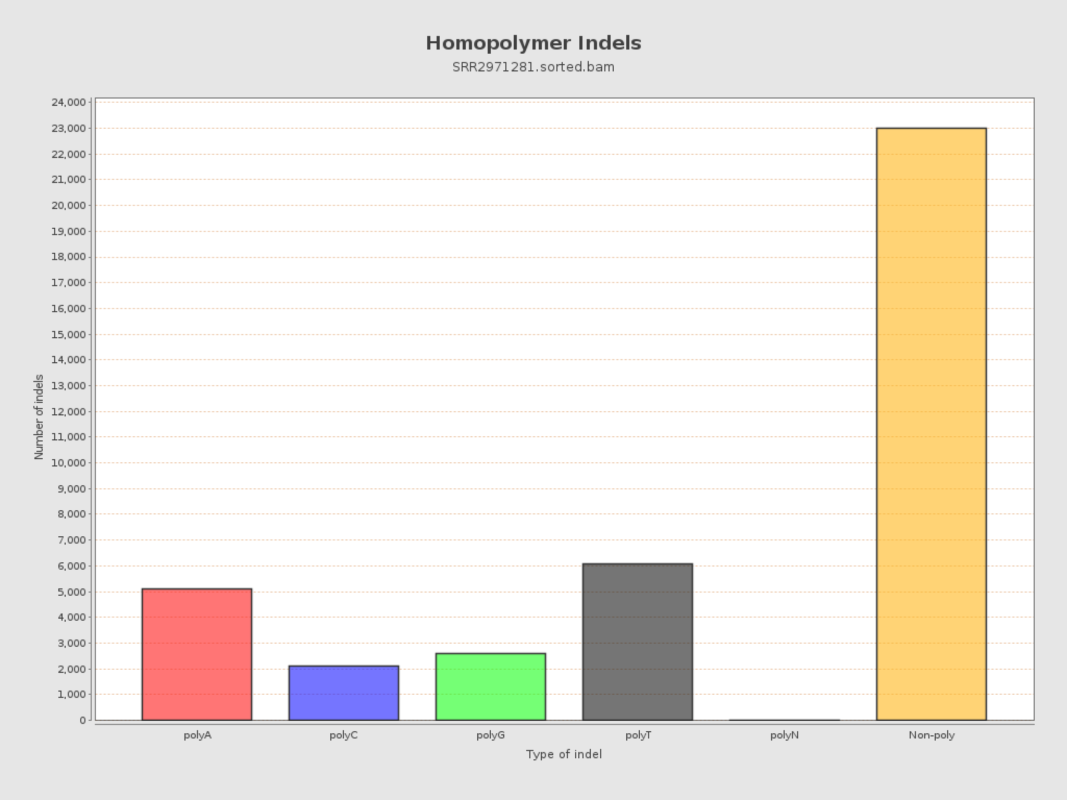
9. Results : Mapped Reads GC-content Distribution



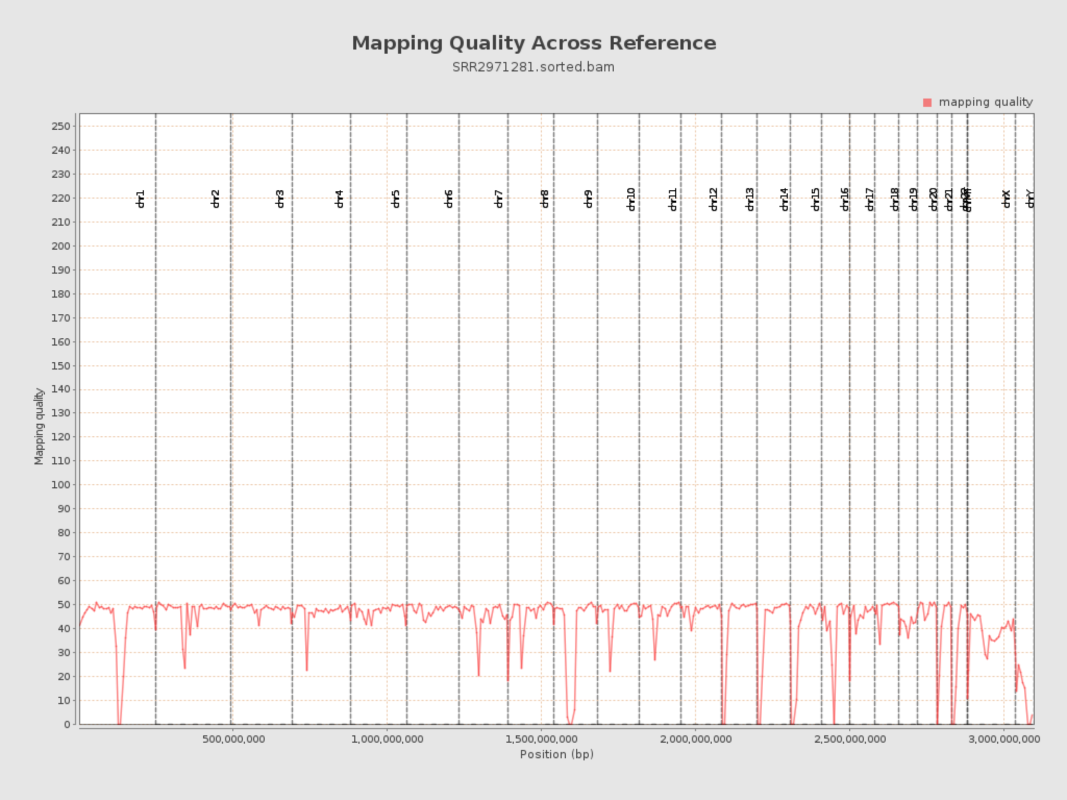
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram