Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:59:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971298.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_SRR2971298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971298.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:59:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,008,842
Mapped reads	8,481,521 / 84.74%
Unmapped reads	1,527,321 / 15.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	588,737 / 5.88%
Duplication rate	5.41%
Clipped reads	829,148 / 8.28%

2.2. ACGT Content

Number/percentage of A's	96,783,062 / 28.95%
Number/percentage of C's	67,690,465 / 20.25%
Number/percentage of T's	99,886,168 / 29.88%
Number/percentage of G's	69,918,439 / 20.92%
Number/percentage of N's	2,516 / 0%
GC Percentage	41.17%

2.3. Coverage

Mean	0.108
Standard Deviation	0.9539

2.4. Mapping Quality

Mean Mapping Quality	38.33

2.5. Mismatches and indels

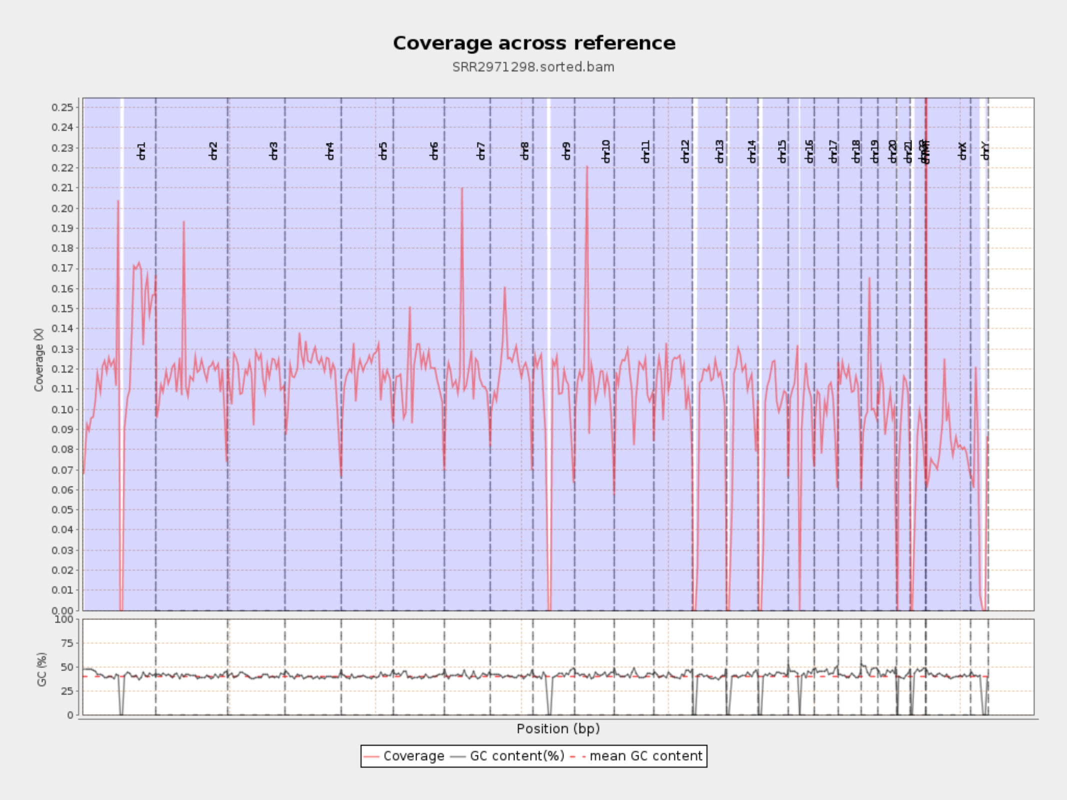
General error rate	0.31%
Mismatches	1,031,800
Insertions	12,015
Mapped reads with at least one insertion	0.14%
Deletions	26,570
Mapped reads with at least one deletion	0.31%
Homopolymer indels	40.24%

2.6. Chromosome stats

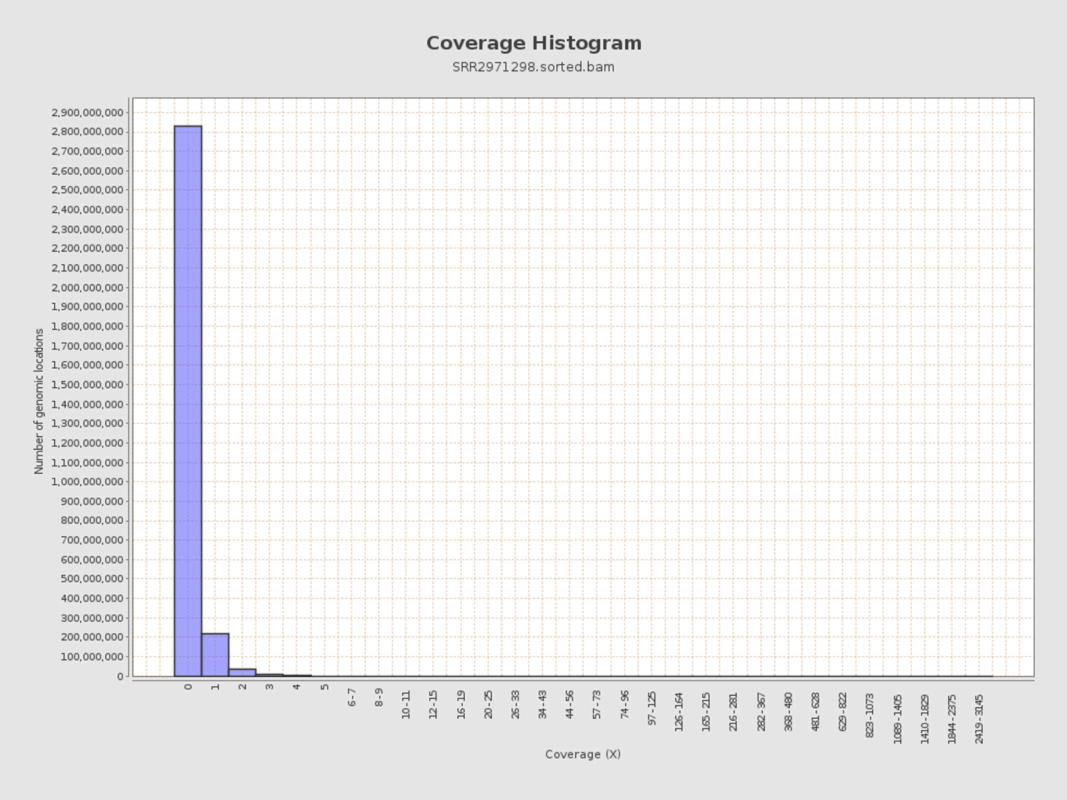
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30211575	0.1212	2.1275
chr2	243199373	28448339	0.117	0.773
chr3	198022430	23266113	0.1175	0.4223
chr4	191154276	22708271	0.1188	0.4545
chr5	180915260	21234270	0.1174	0.4422
chr6	171115067	20063691	0.1173	0.5338
chr7	159138663	18747970	0.1178	1.155
chr8	146364022	17462980	0.1193	1.4852

chr9	141213431	14007273	0.0992	0.7608
chr10	135534747	15780854	0.1164	0.9417
chr11	135006516	15357013	0.1138	0.706
chr12	133851895	15335927	0.1146	0.4455
chr13	115169878	11054130	0.096	0.3649
chr14	107349540	10224115	0.0952	0.487
chr15	102531392	9044289	0.0882	0.3543
chr16	90354753	8680264	0.0961	0.4731
chr17	81195210	8037508	0.099	0.428
chr18	78077248	8904100	0.114	1.5025
chr19	59128983	6161582	0.1042	1.8802
chr20	63025520	6319204	0.1003	0.4253
chr21	48129895	4238768	0.0881	0.4561
chr22	51304566	3166637	0.0617	0.349
chrMT	16571	35301	2.1303	2.4196
chrX	155270560	12655478	0.0815	0.4898
chrY	59373566	3168162	0.0534	0.4774

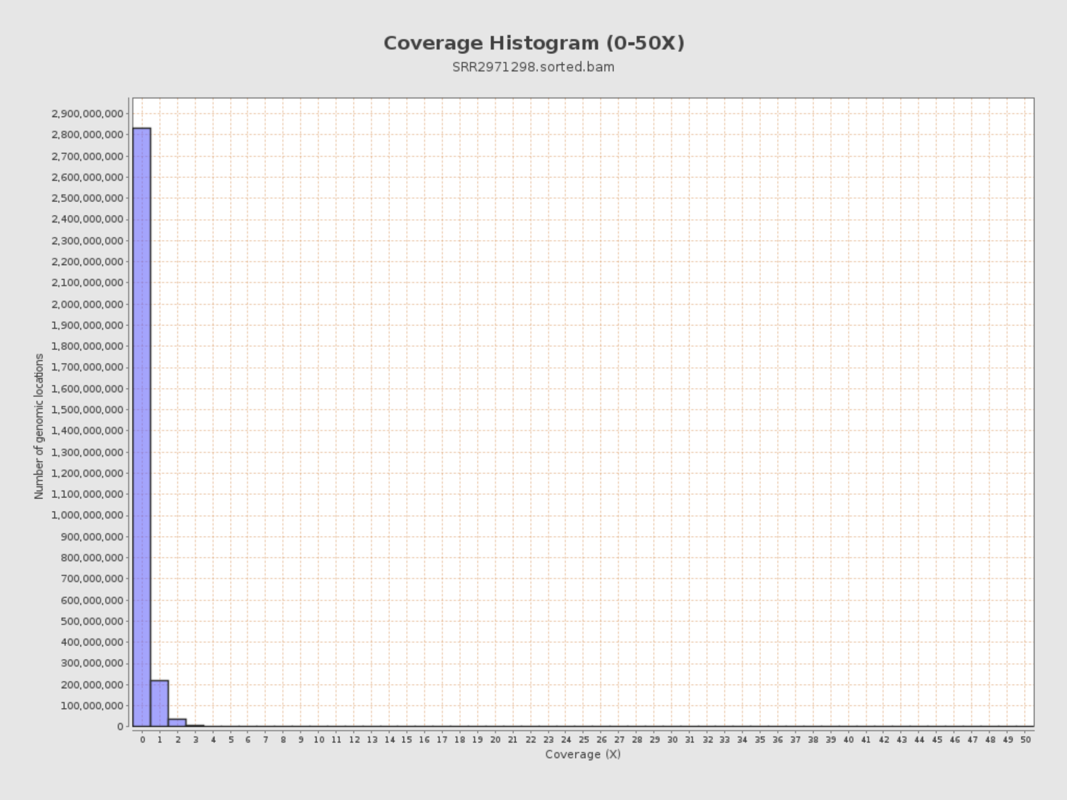
3. Results : Coverage across reference



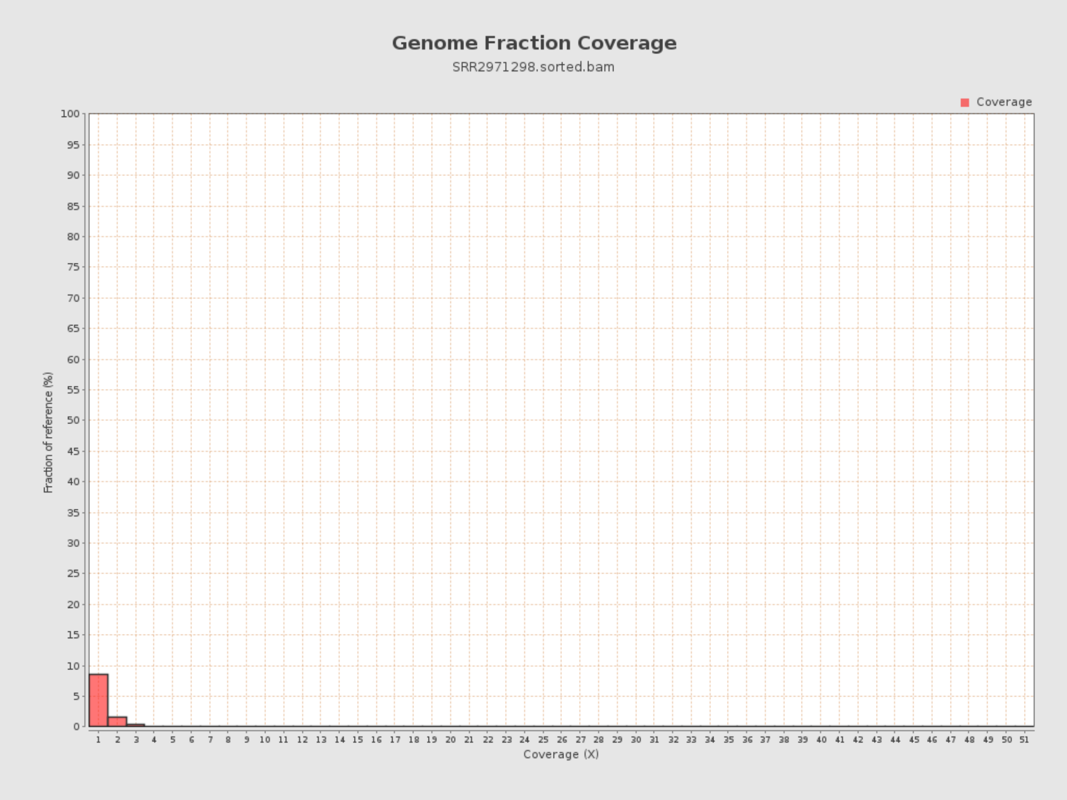
4. Results : Coverage Histogram



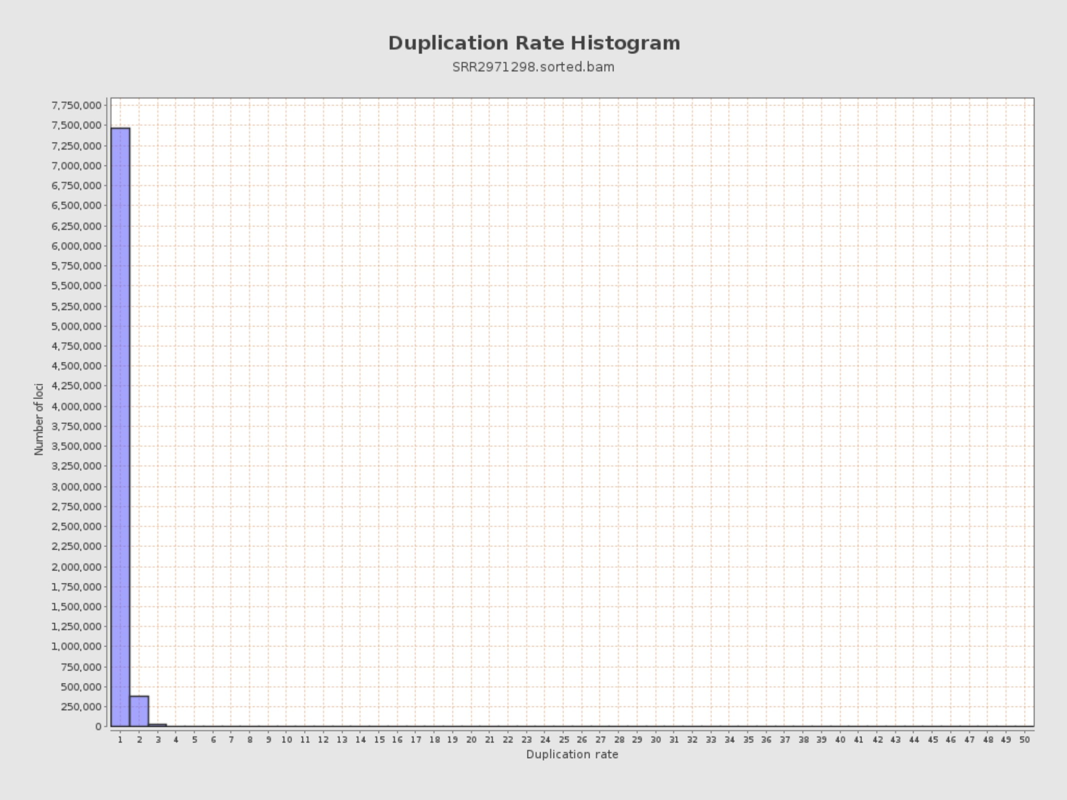
5. Results : Coverage Histogram (0-50X)



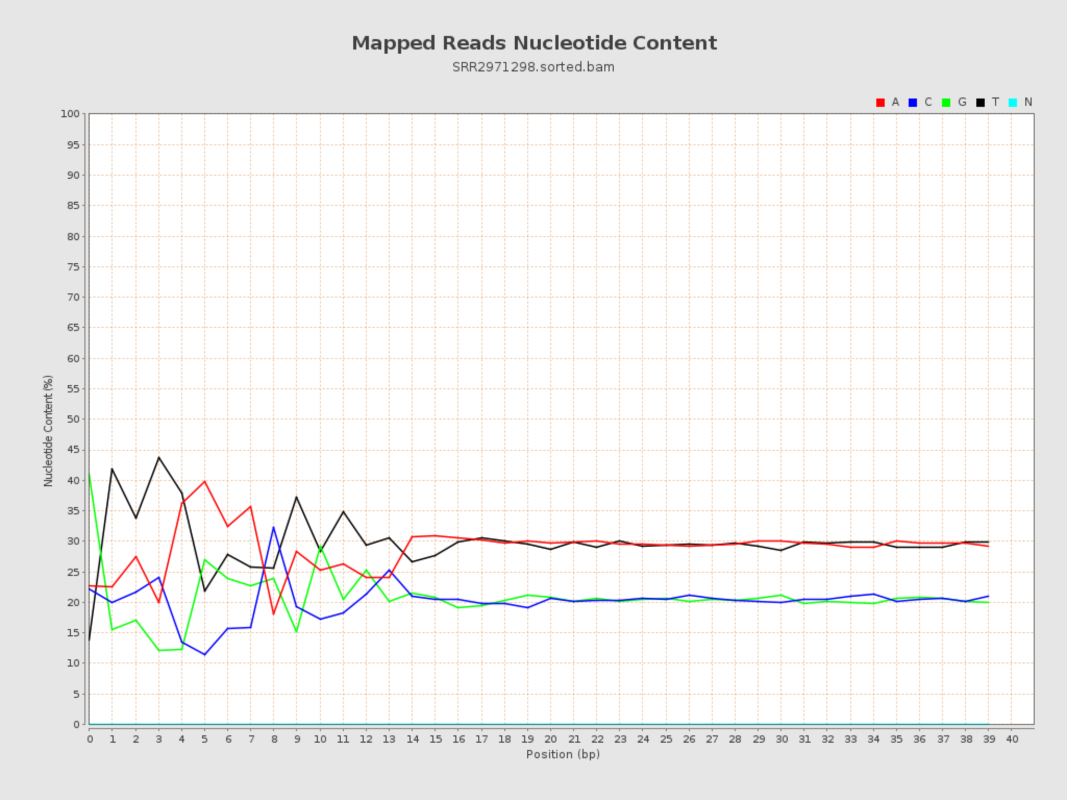
6. Results : Genome Fraction Coverage



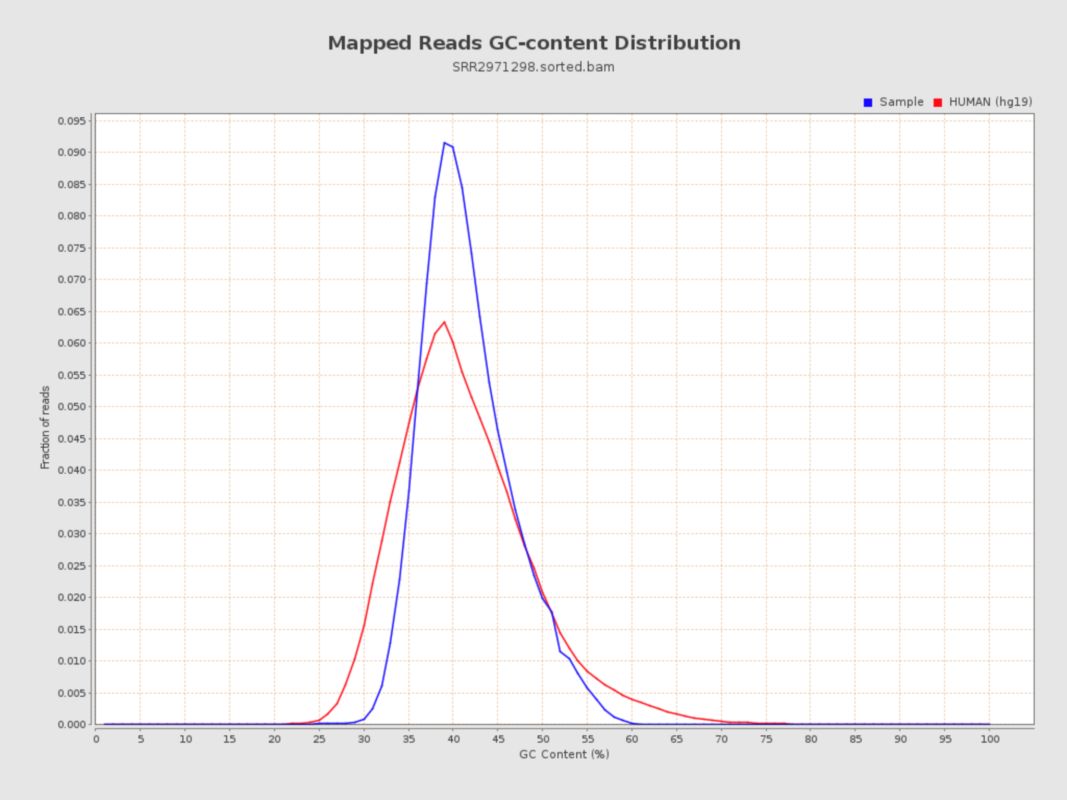
7. Results : Duplication Rate Histogram



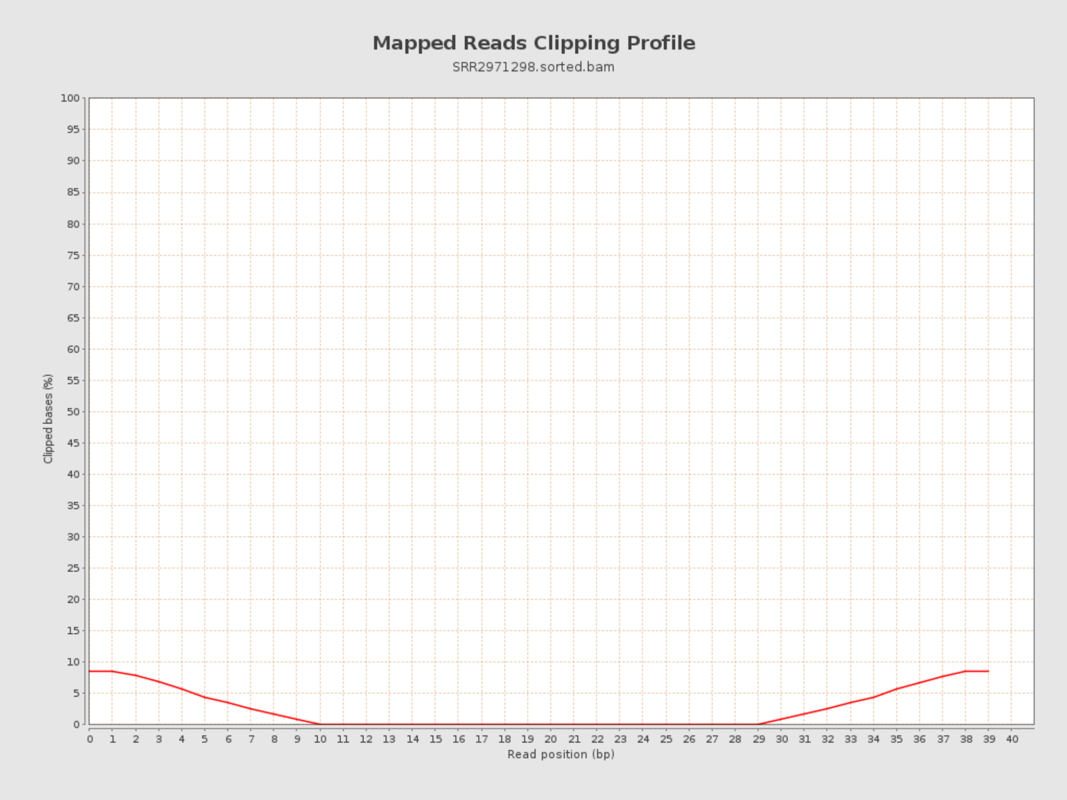
8. Results : Mapped Reads Nucleotide Content



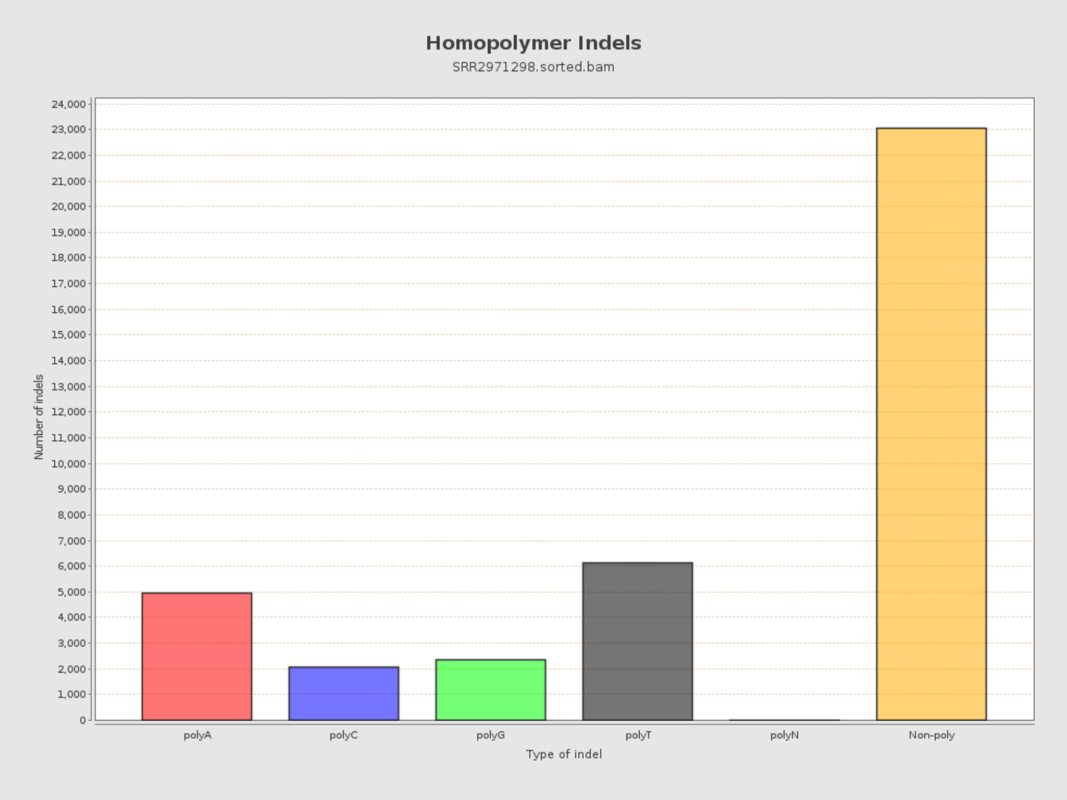
9. Results : Mapped Reads GC-content Distribution



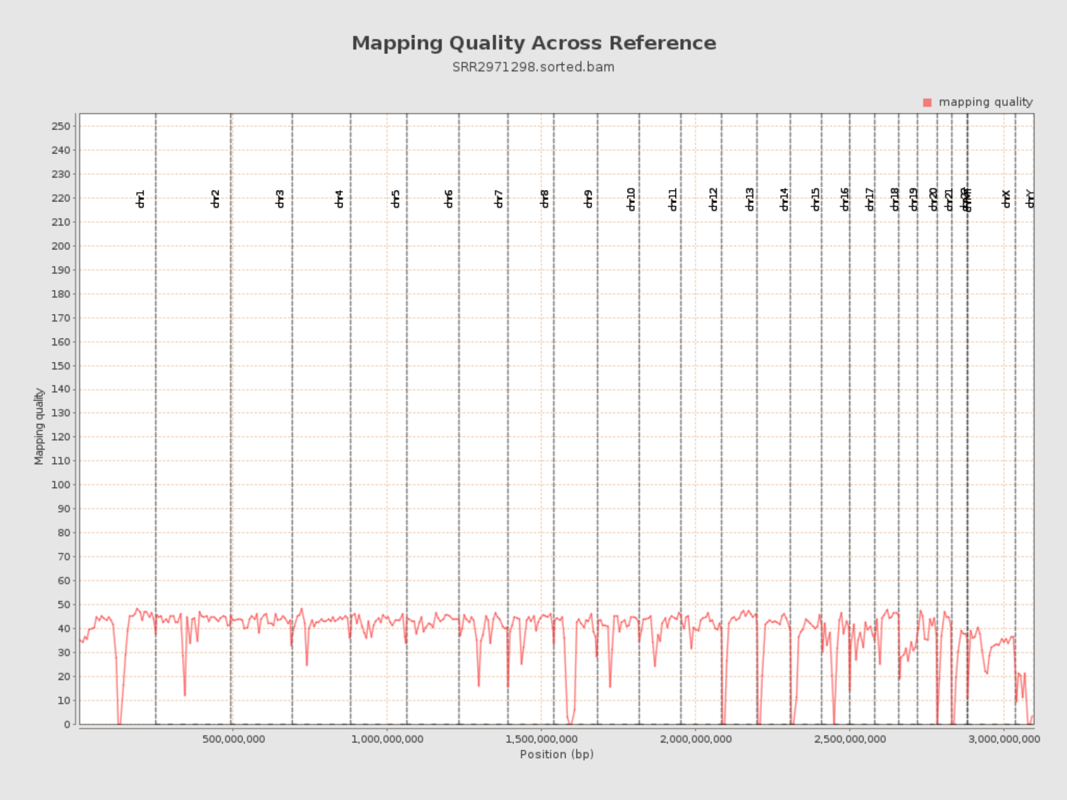
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram