Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:40:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971279.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_SRR2971279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971279.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:40:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,524,774
Mapped reads	7,610,356 / 72.31%
Unmapped reads	2,914,418 / 27.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	880,092 / 8.36%
Duplication rate	10.12%
Clipped reads	626,914 / 5.96%

2.2. ACGT Content

Number/percentage of A's	87,264,832 / 29.04%
Number/percentage of C's	61,529,410 / 20.47%
Number/percentage of T's	88,425,472 / 29.42%
Number/percentage of G's	63,307,939 / 21.07%
Number/percentage of N's	2,475 / 0%
GC Percentage	41.54%

2.3. Coverage

Mean	0.0971
Standard Deviation	1.4228

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Mismatches and indels

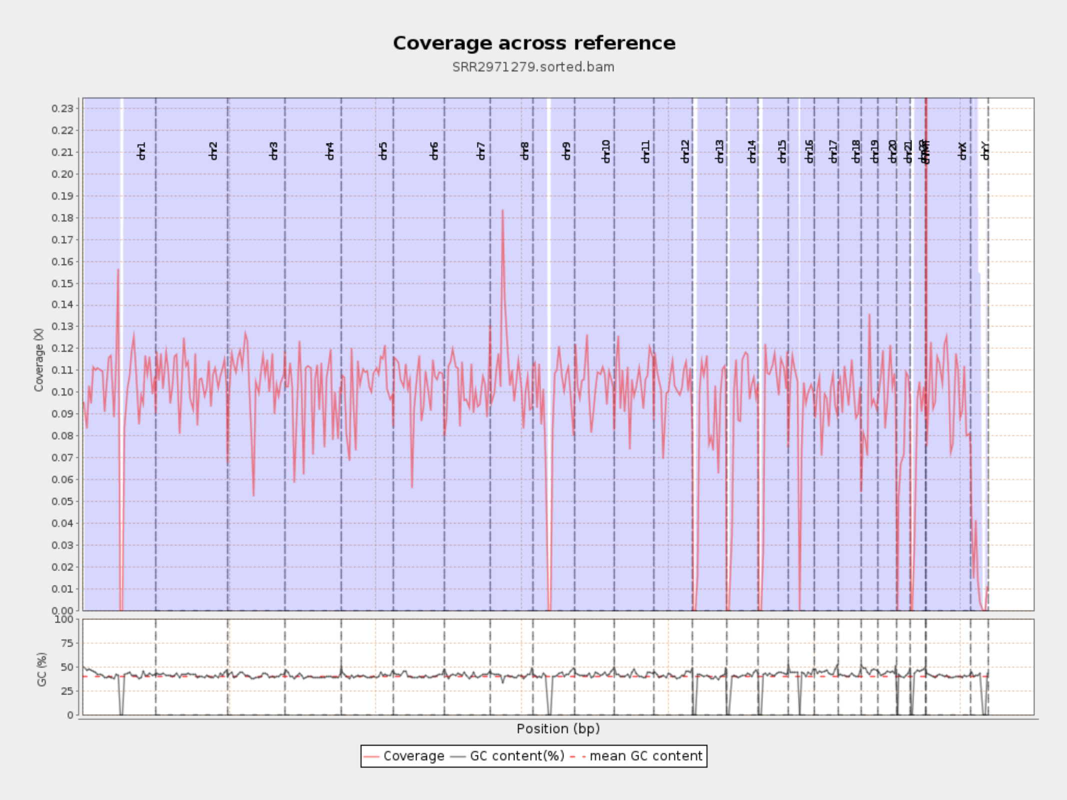
General error rate	0.27%
Mismatches	797,558
Insertions	9,414
Mapped reads with at least one insertion	0.12%
Deletions	22,794
Mapped reads with at least one deletion	0.3%
Homopolymer indels	40.21%

2.6. Chromosome stats

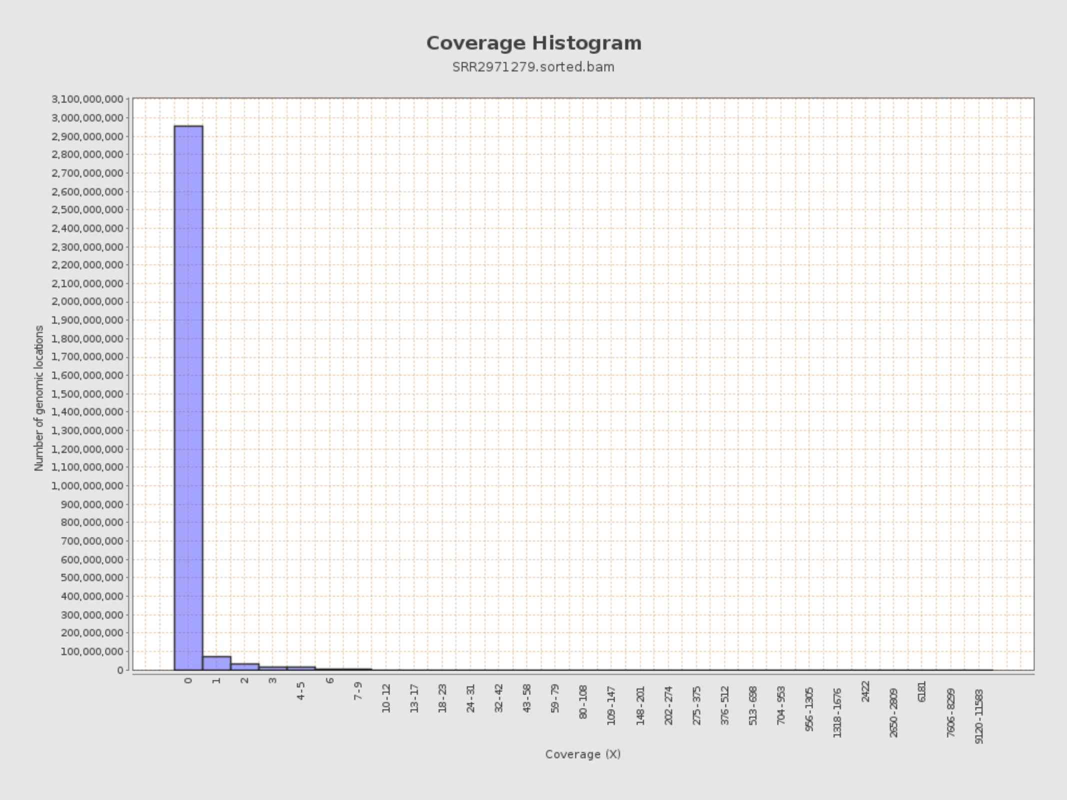
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24857421	0.0997	1.4585
chr2	243199373	25890955	0.1065	0.6819
chr3	198022430	20822948	0.1052	0.6
chr4	191154276	18863872	0.0987	0.6087
chr5	180915260	18662758	0.1032	0.6024
chr6	171115067	17662249	0.1032	0.6045
chr7	159138663	16165804	0.1016	0.8339
chr8	146364022	16012147	0.1094	5.5823

chr9	141213431	12652510	0.0896	0.6337
chr10	135534747	14139302	0.1043	0.7281
chr11	135006516	14075588	0.1043	0.6505
chr12	133851895	13853301	0.1035	0.617
chr13	115169878	9283780	0.0806	0.5278
chr14	107349540	9239738	0.0861	0.5879
chr15	102531392	9089940	0.0887	0.5537
chr16	90354753	8251510	0.0913	0.5782
chr17	81195210	7718245	0.0951	0.5939
chr18	78077248	7828530	0.1003	0.9221
chr19	59128983	5382583	0.091	1.2904
chr20	63025520	6585079	0.1045	0.6223
chr21	48129895	3624005	0.0753	0.5604
chr22	51304566	3449762	0.0672	0.5132
chrMT	16571	34322	2.0712	3.3317
chrX	155270560	15538197	0.1001	0.6373
chrY	59373566	875100	0.0147	0.2577

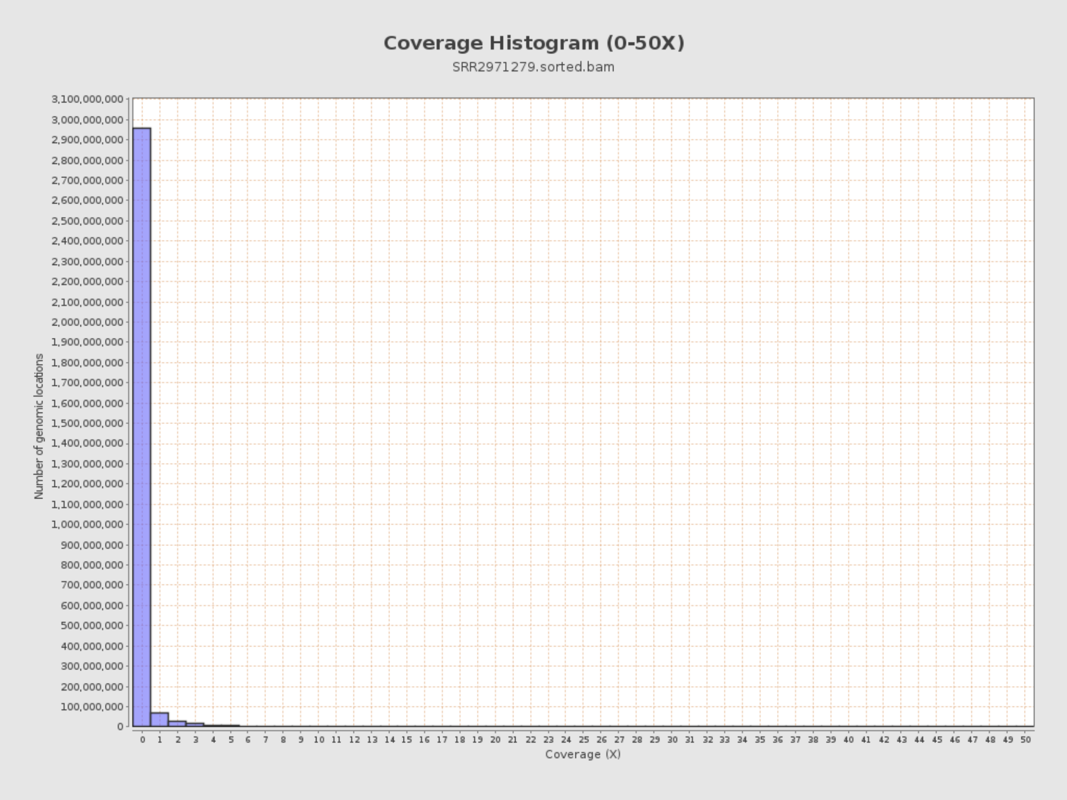
3. Results : Coverage across reference



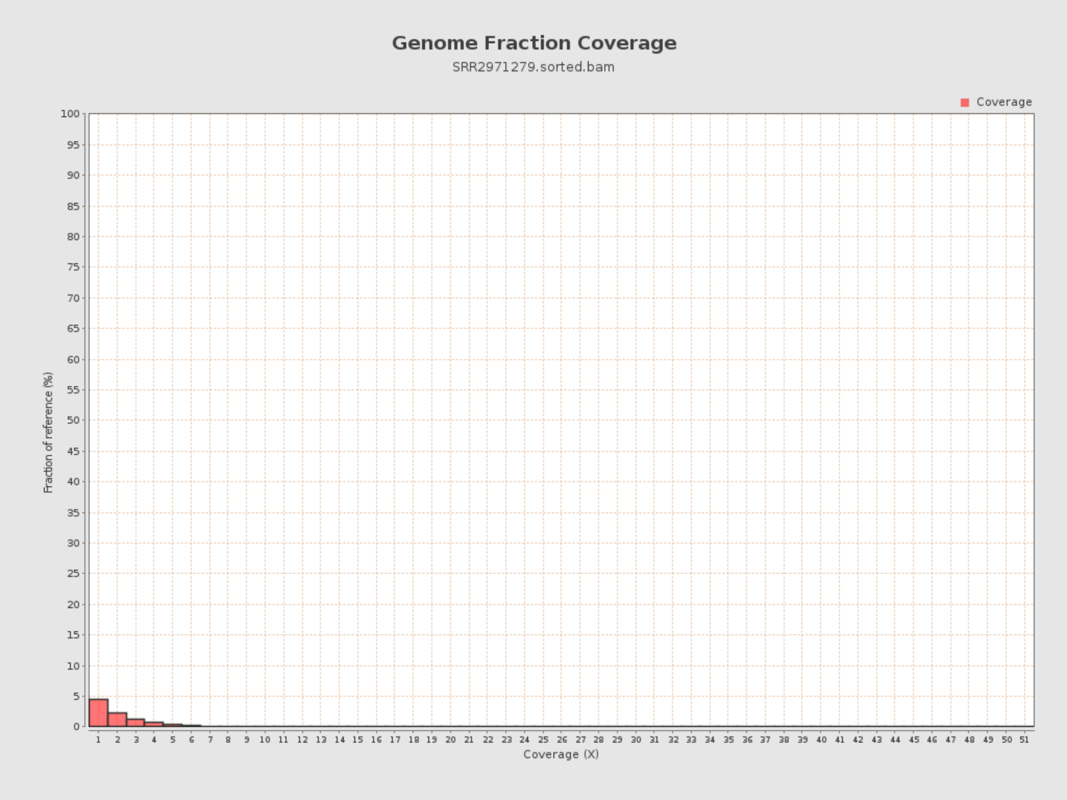
4. Results : Coverage Histogram



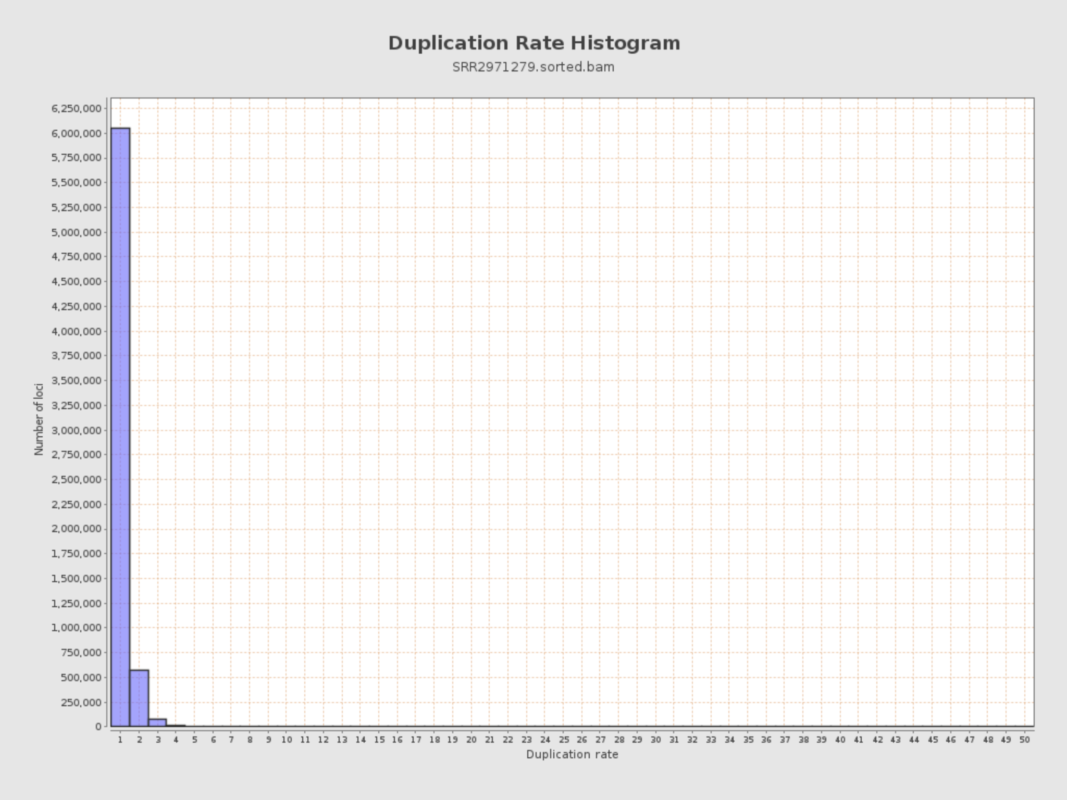
5. Results : Coverage Histogram (0-50X)



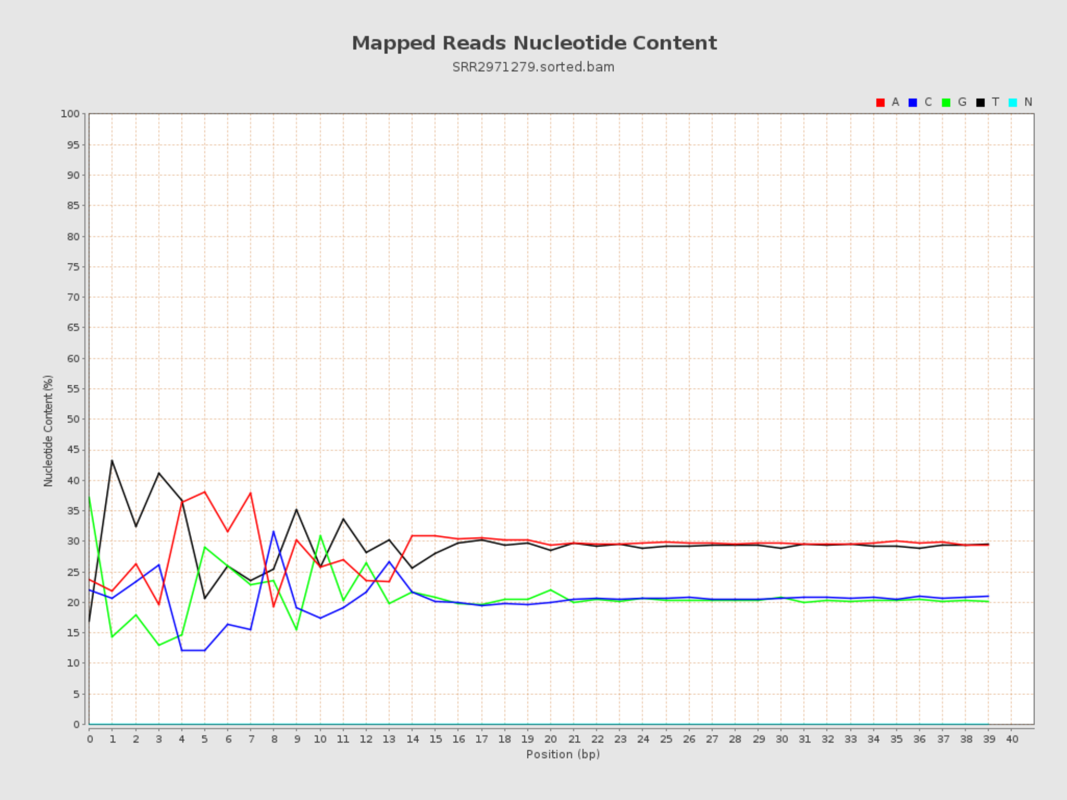
6. Results : Genome Fraction Coverage



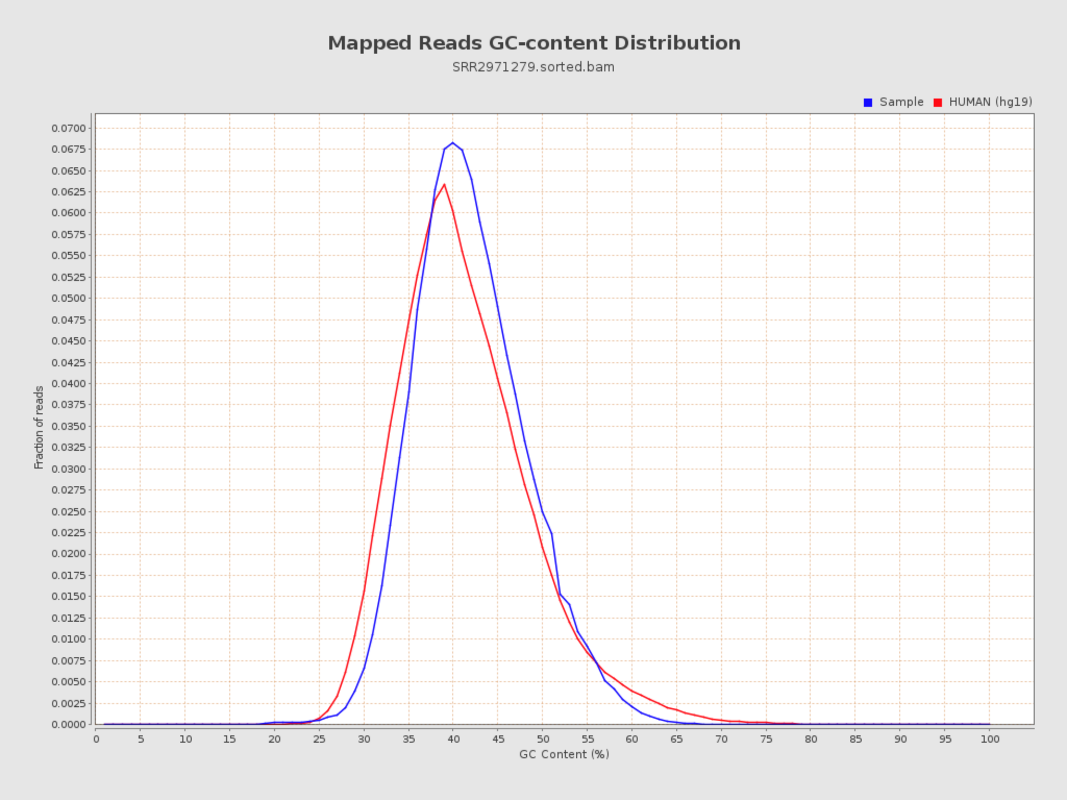
7. Results : Duplication Rate Histogram



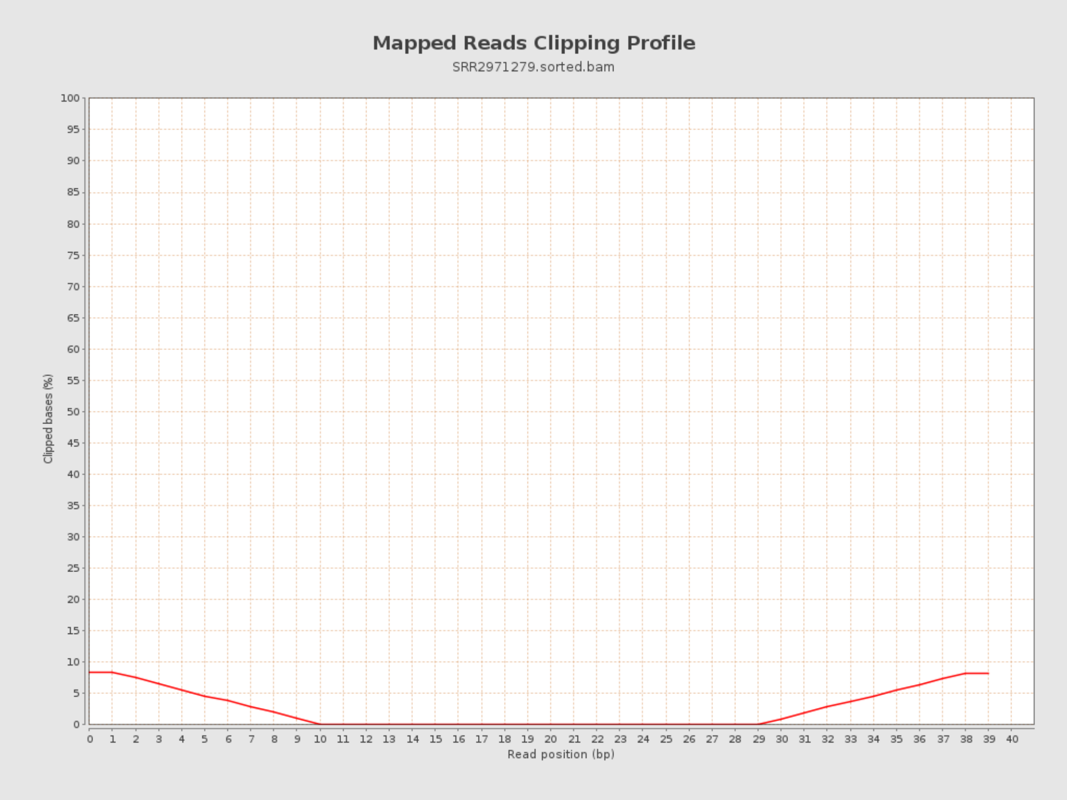
8. Results : Mapped Reads Nucleotide Content



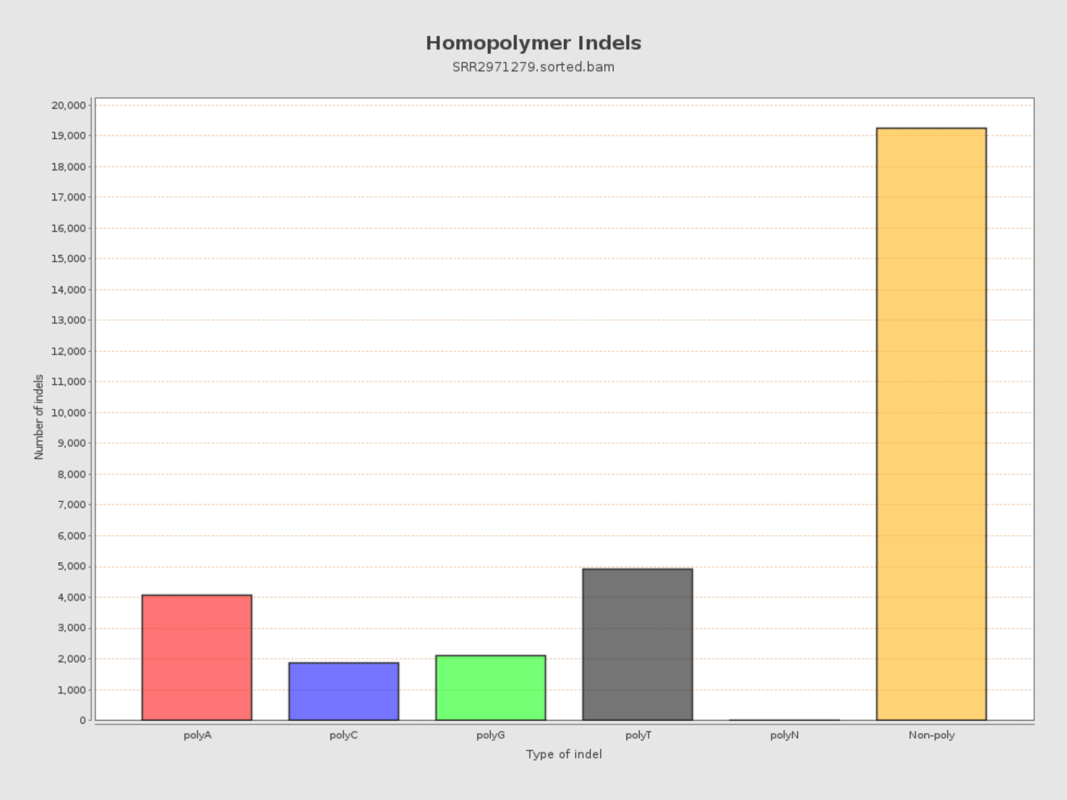
9. Results : Mapped Reads GC-content Distribution



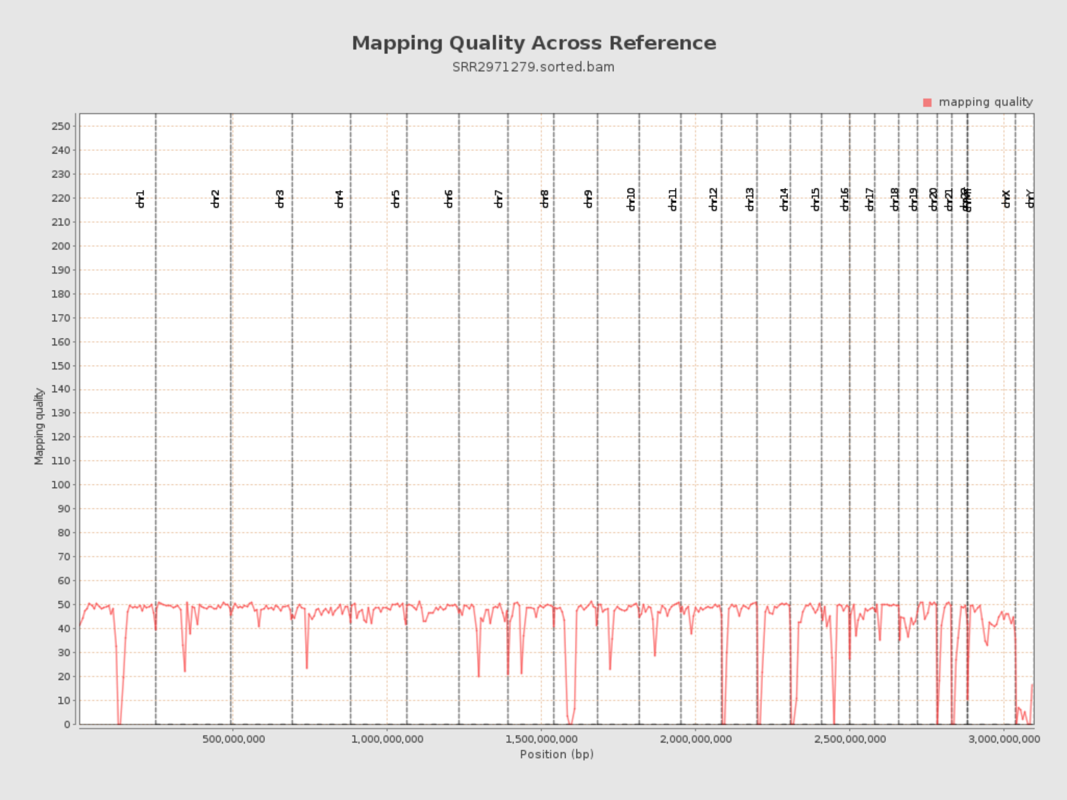
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram