Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:22:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971311.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_SRR2971311 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971311.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:22:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971311.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,287,431
Mapped reads	8,641,374 / 93.04%
Unmapped reads	646,057 / 6.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,353 / 0.01%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	702,201 / 7.56%
Duplication rate	6.48%
Clipped reads	1,907,482 / 20.54%

2.2. ACGT Content

Number/percentage of A's	115,617,792 / 27.93%
Number/percentage of C's	88,693,388 / 21.42%
Number/percentage of T's	117,606,785 / 28.41%
Number/percentage of G's	92,075,558 / 22.24%
Number/percentage of N's	21,023 / 0.01%
GC Percentage	43.66%

2.3. Coverage

Mean	0.1338

Standard Deviation	1.0456

2.4. Mapping Quality

Mean Mapping Quality	34.97

2.5. Mismatches and indels

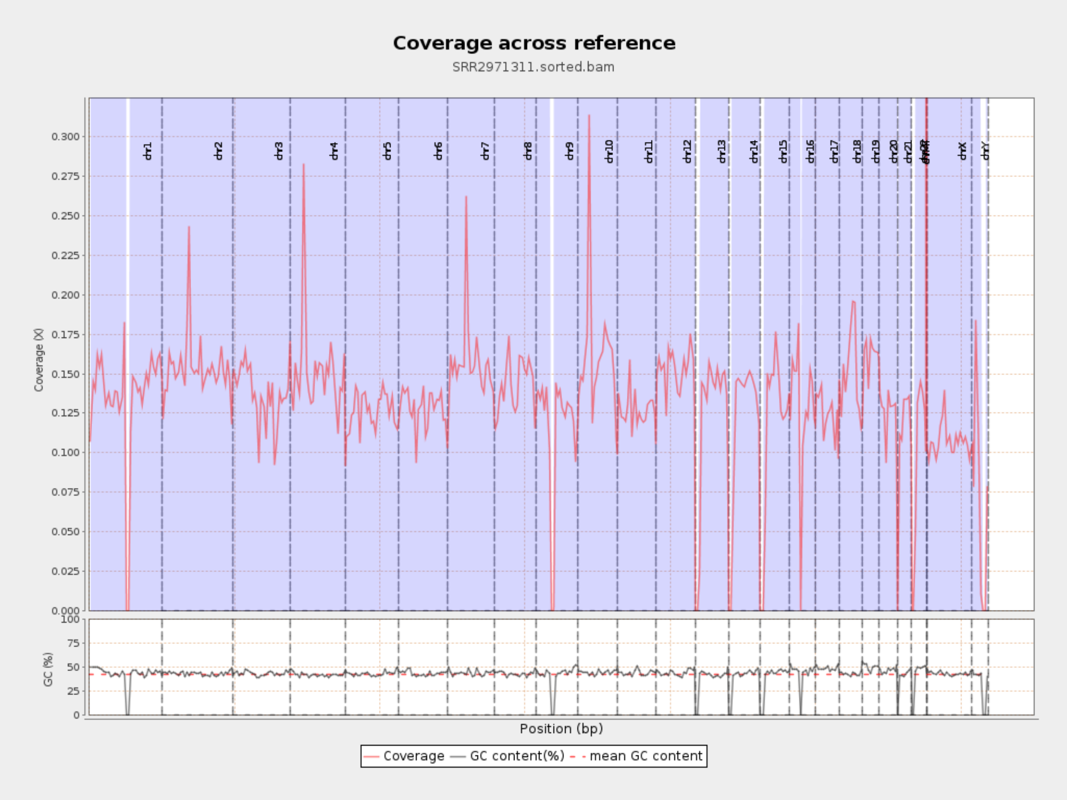
General error rate	0.53%
Mismatches	2,158,654
Insertions	28,692
Mapped reads with at least one insertion	0.33%
Deletions	62,077
Mapped reads with at least one deletion	0.72%
Homopolymer indels	40%

2.6. Chromosome stats

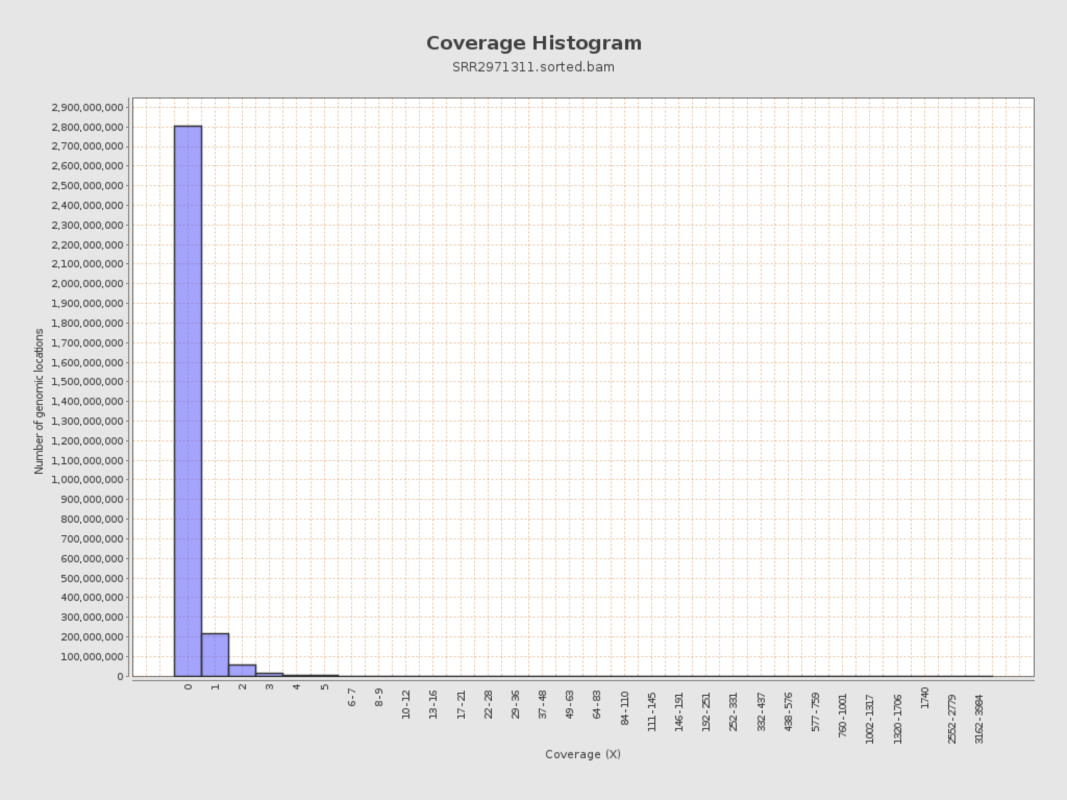
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33568899	0.1347	1.4977
chr2	243199373	37468462	0.1541	1.0861
chr3	198022430	26966829	0.1362	0.4985
chr4	191154276	28936301	0.1514	0.8456
chr5	180915260	22911969	0.1266	0.4852
chr6	171115067	21899931	0.128	0.5057
chr7	159138663	25185326	0.1583	1.6412

chr8	146364022	20915763	0.1429	2.0864
chr9	141213431	16193708	0.1147	0.9523
chr10	135534747	22090750	0.163	1.3895
chr11	135006516	17123903	0.1268	0.7788
chr12	133851895	20480976	0.153	0.5488
chr13	115169878	13898299	0.1207	0.4642
chr14	107349540	12788395	0.1191	0.652
chr15	102531392	11801369	0.1151	0.4676
chr16	90354753	11592275	0.1283	0.6345
chr17	81195210	10060699	0.1239	0.5746
chr18	78077248	11942200	0.153	1.8891
chr19	59128983	9528412	0.1611	1.3497
chr20	63025520	7885880	0.1251	0.5576
chr21	48129895	5333793	0.1108	0.8051
chr22	51304566	4759504	0.0928	0.513
chrMT	16571	26690	1.6106	1.7789
chrX	155270560	16718647	0.1077	0.5497
chrY	59373566	4025151	0.0678	0.7495

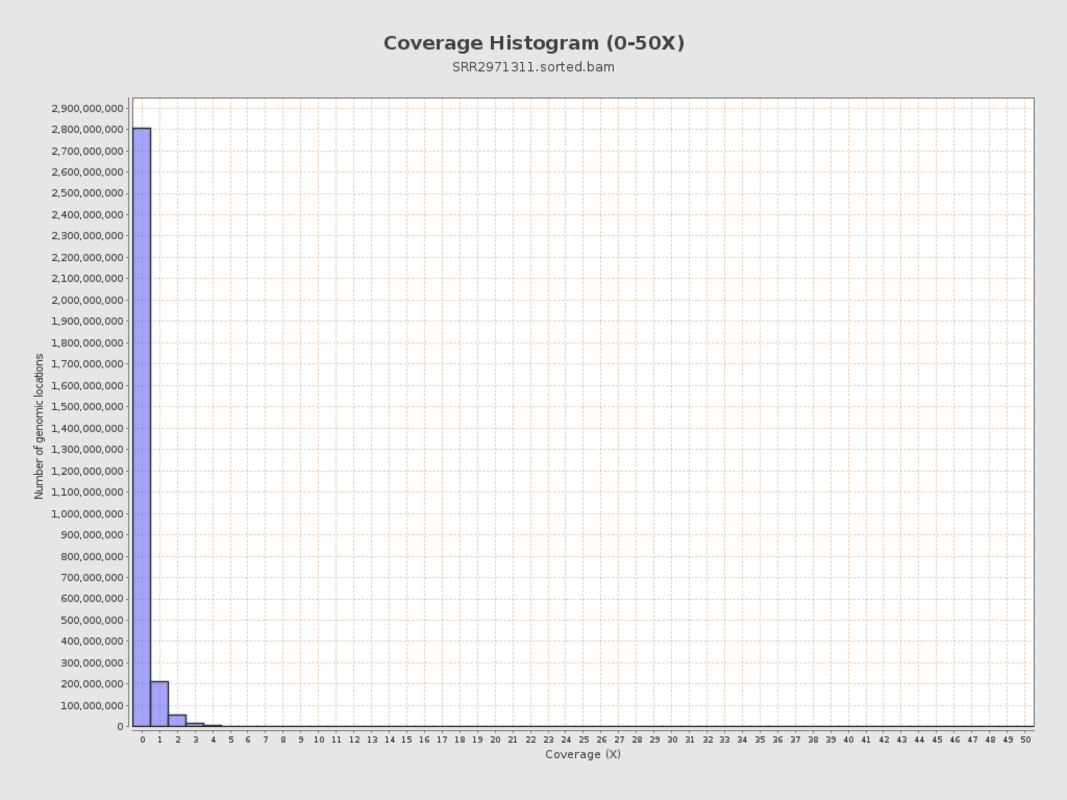
3. Results : Coverage across reference



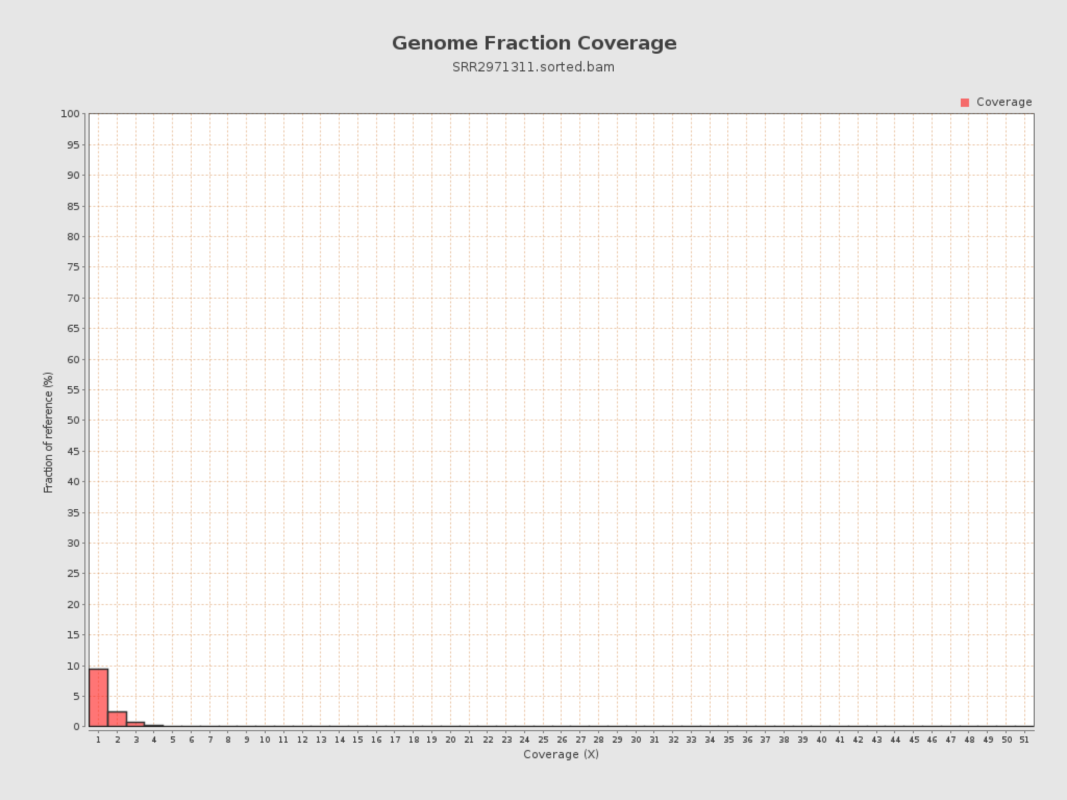
4. Results : Coverage Histogram



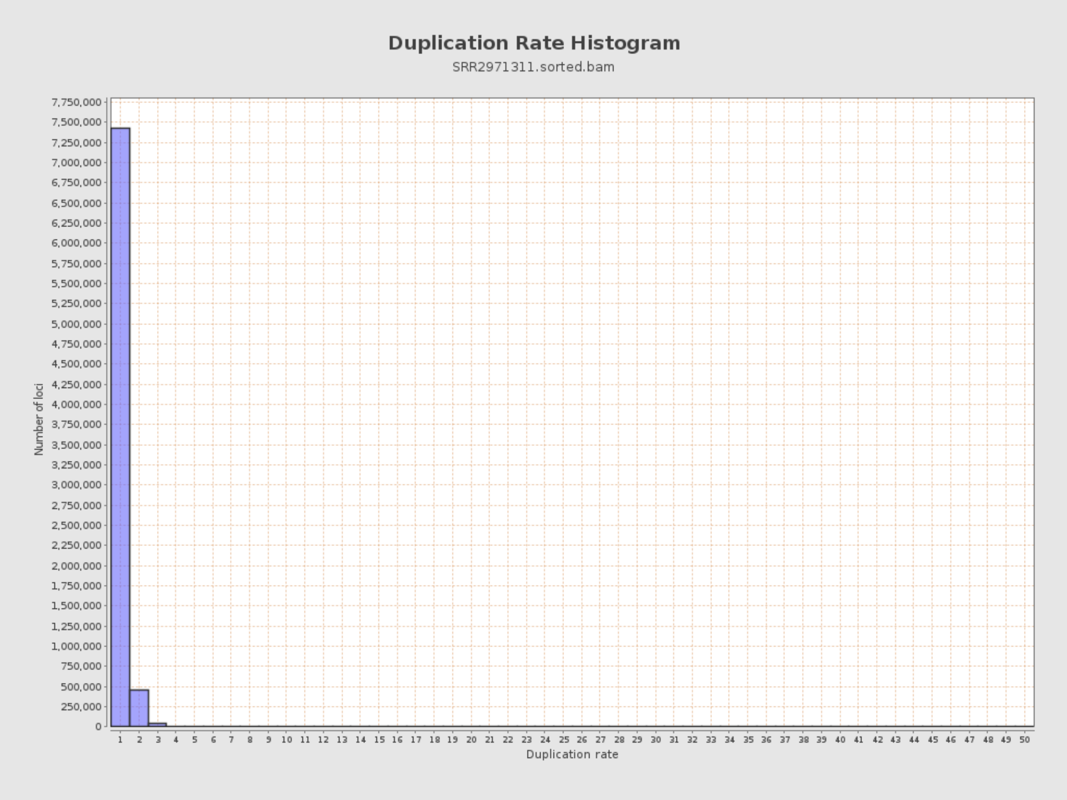
5. Results : Coverage Histogram (0-50X)



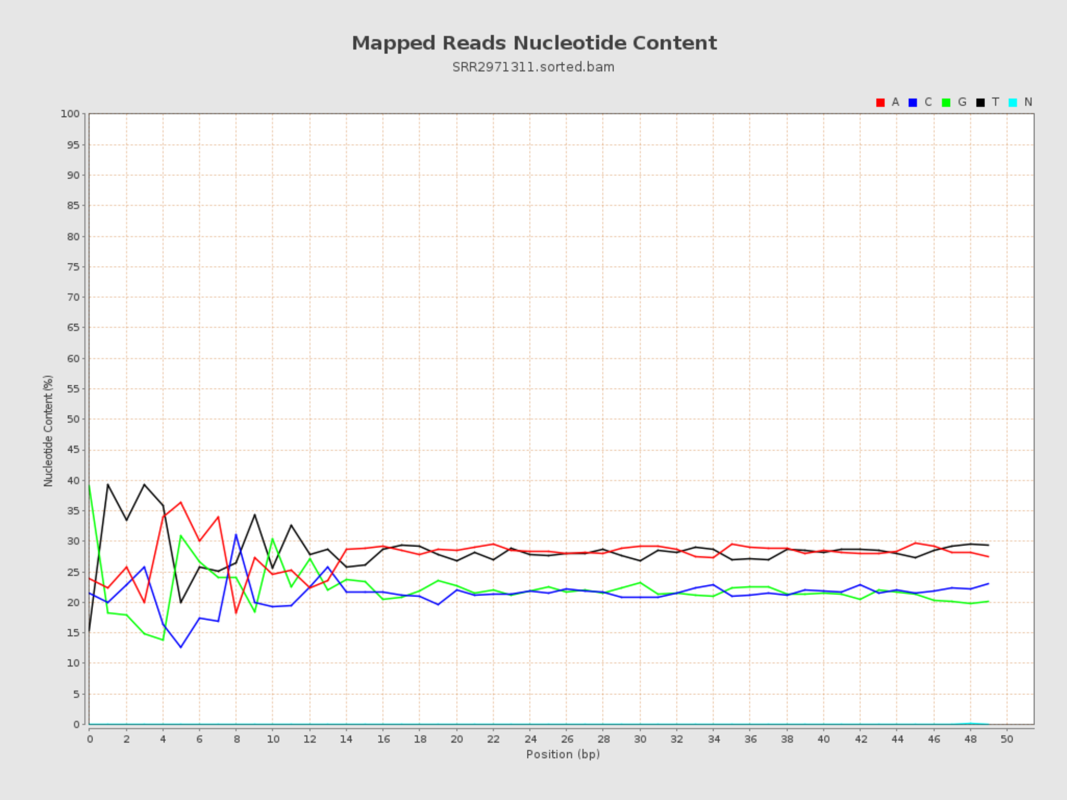
6. Results : Genome Fraction Coverage



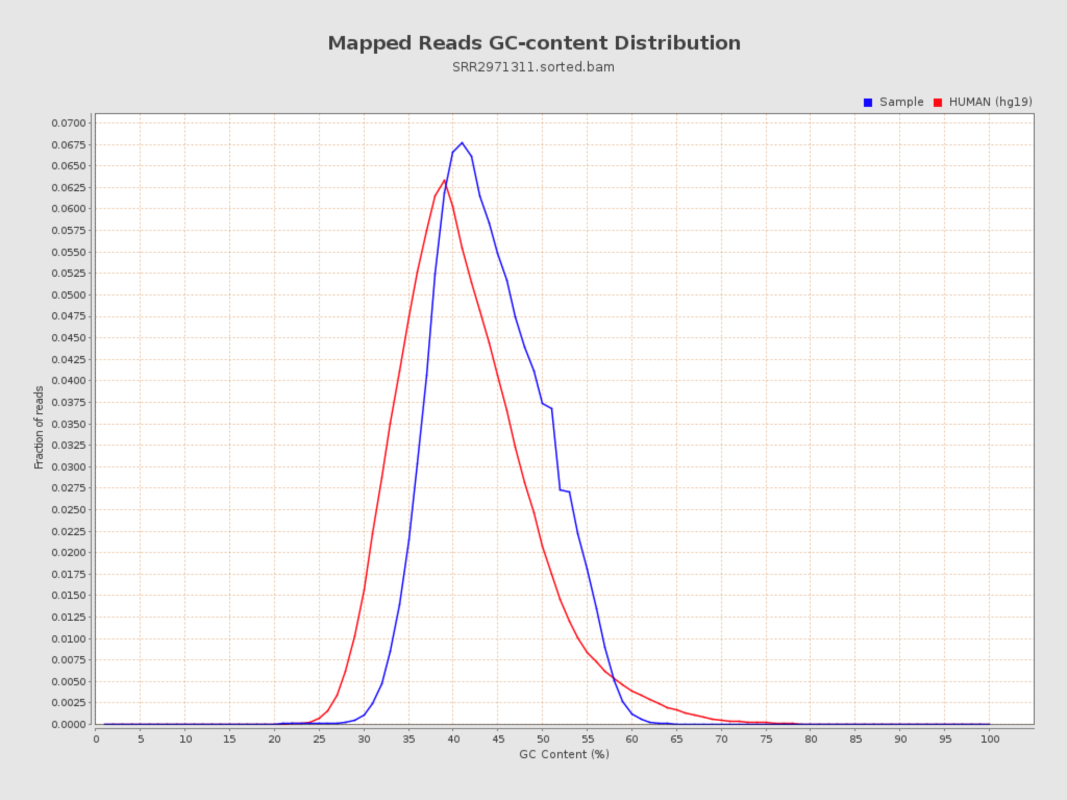
7. Results : Duplication Rate Histogram



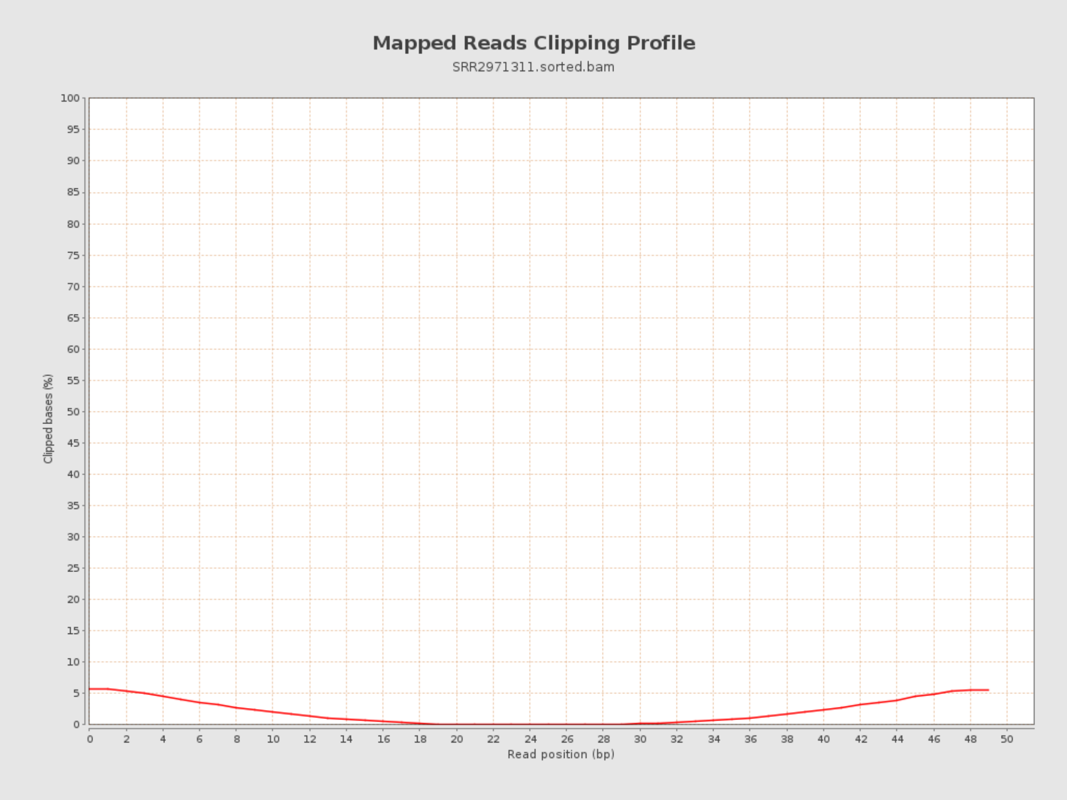
8. Results : Mapped Reads Nucleotide Content



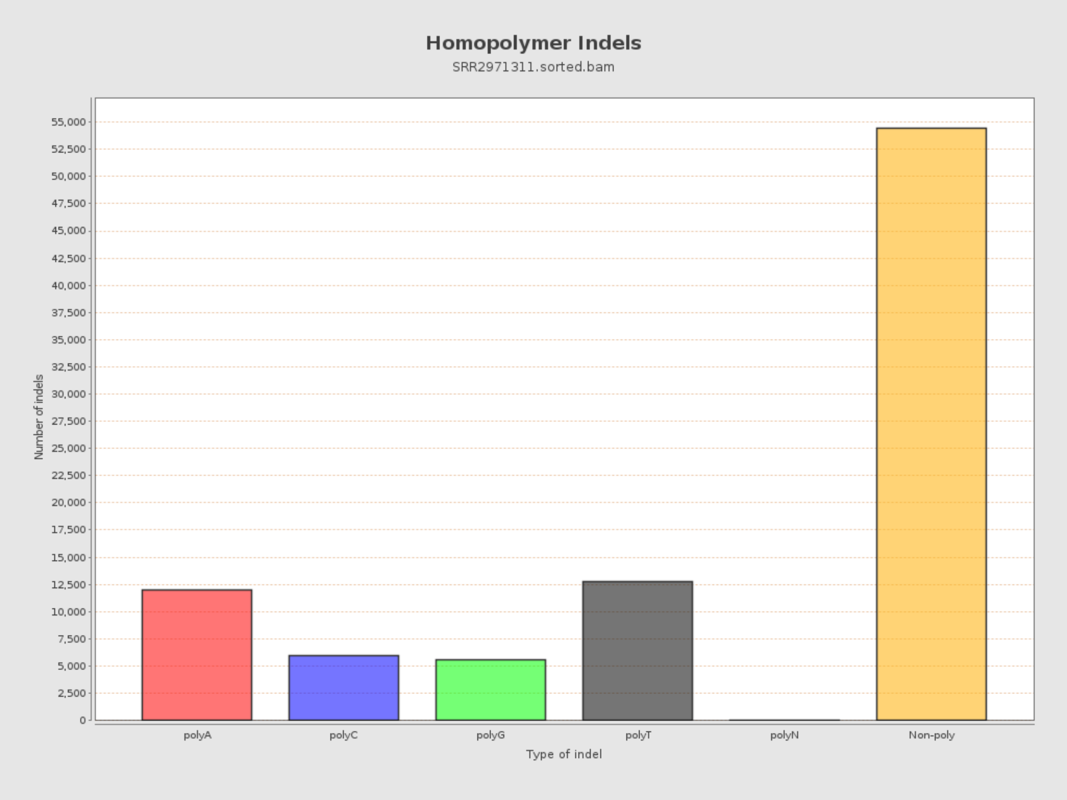
9. Results : Mapped Reads GC-content Distribution



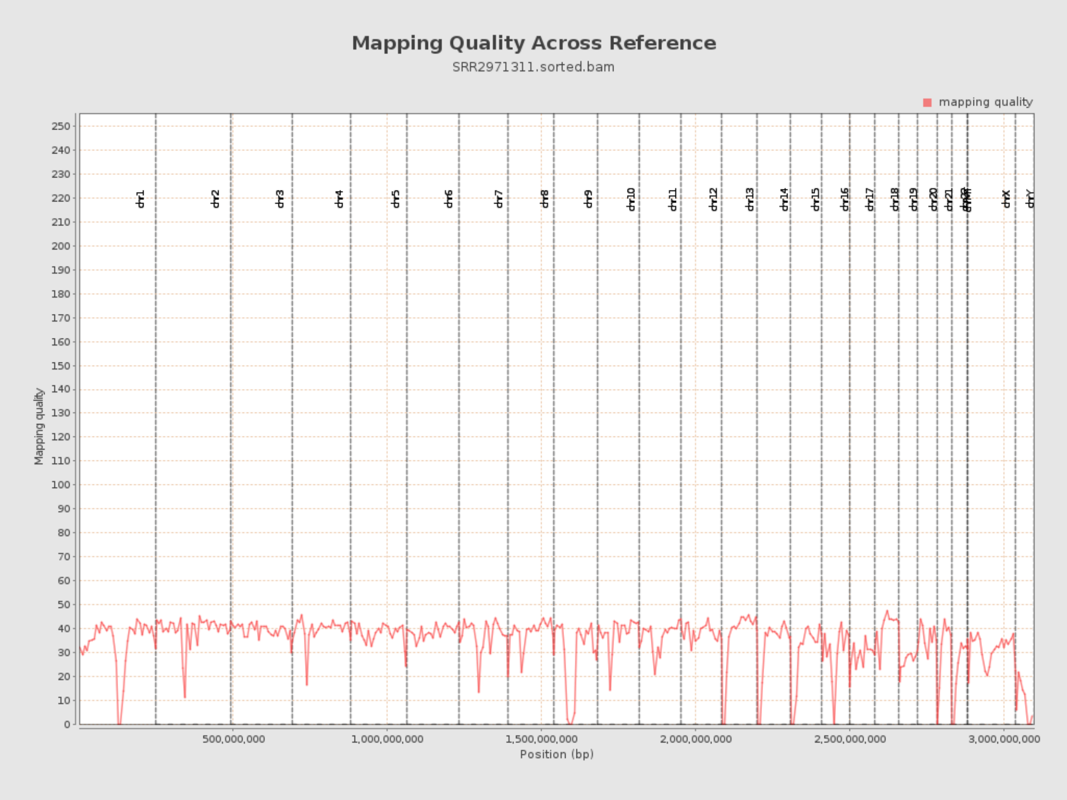
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram