Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:36:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818991.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_SRR1818991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818991.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:36:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,105,876
Mapped reads	1,982,414 / 94.14%
Unmapped reads	123,462 / 5.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,649 / 1.31%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	854,456 / 40.57%
Duplication rate	36.27%
Clipped reads	2,002,167 / 95.08%

2.2. ACGT Content

Number/percentage of A's	53,531,889 / 29.19%
Number/percentage of C's	38,453,371 / 20.97%
Number/percentage of T's	52,532,208 / 28.65%
Number/percentage of G's	38,860,963 / 21.19%
Number/percentage of N's	8,909 / 0%
GC Percentage	42.16%

2.3. Coverage

Mean	0.0593

Standard Deviation	0.6837

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

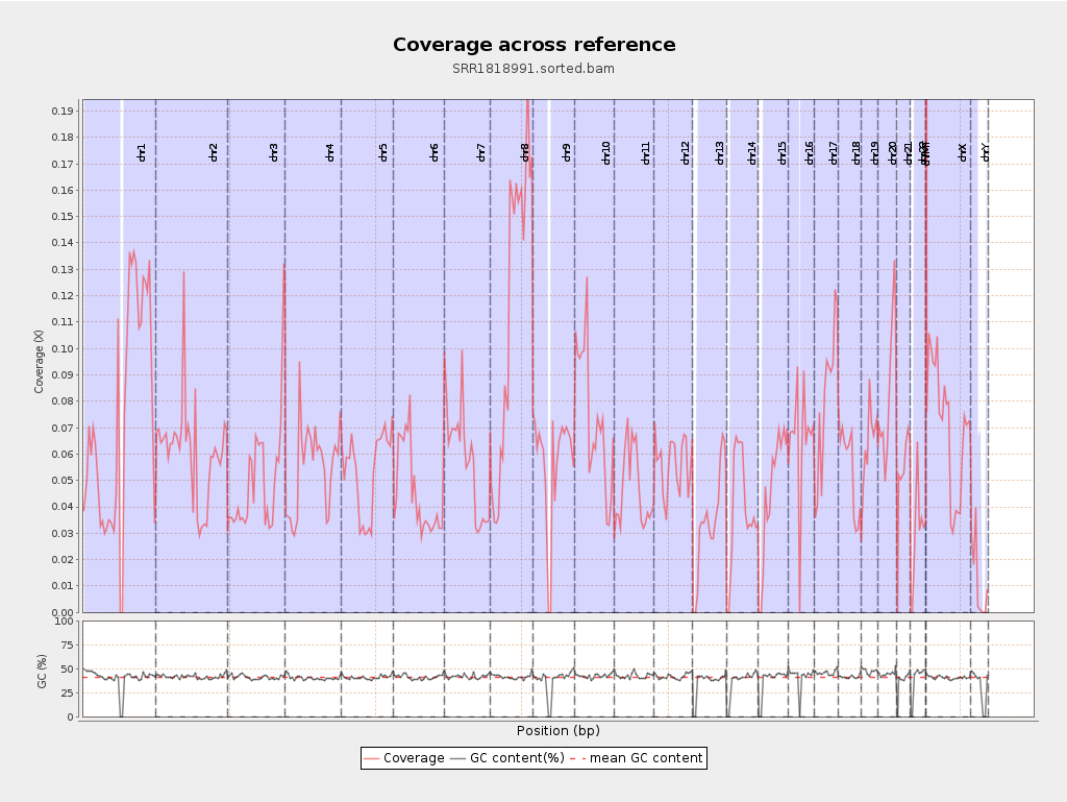
General error rate	0.66%
Mismatches	1,147,287
Insertions	27,885
Mapped reads with at least one insertion	1.37%
Deletions	58,486
Mapped reads with at least one deletion	2.89%
Homopolymer indels	41.32%

2.6. Chromosome stats

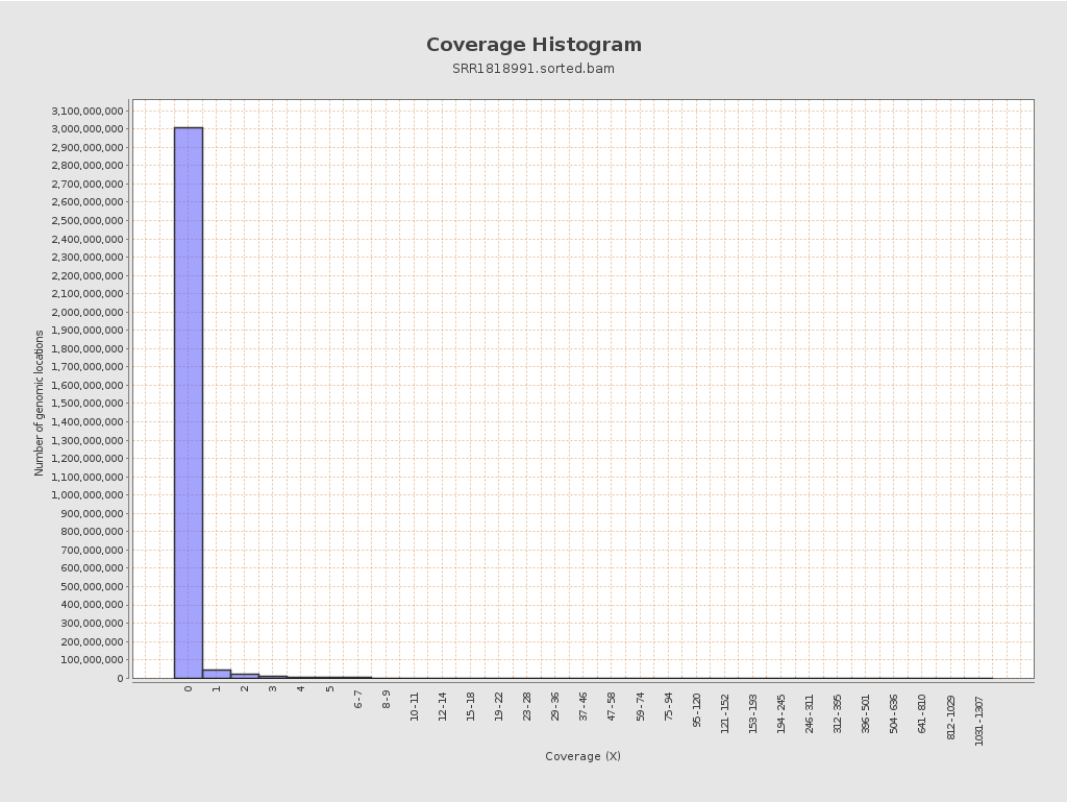
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18241841	0.0732	1.2092
chr2	243199373	14796879	0.0608	0.907
chr3	198022430	9936209	0.0502	0.4042
chr4	191154276	10472563	0.0548	0.5029
chr5	180915260	9742996	0.0539	0.4353
chr6	171115067	7799235	0.0456	0.4569
chr7	159138663	9149609	0.0575	0.8184

chr8	146364022	17142696	0.1171	0.6846
chr9	141213431	7969121	0.0564	0.6192
chr10	135534747	9826976	0.0725	0.8324
chr11	135006516	6287492	0.0466	0.4643
chr12	133851895	7603670	0.0568	0.4374
chr13	115169878	4007606	0.0348	0.3342
chr14	107349540	4286498	0.0399	0.3806
chr15	102531392	4657073	0.0454	0.386
chr16	90354753	5868276	0.0649	0.7632
chr17	81195210	6490428	0.0799	0.596
chr18	78077248	4275671	0.0548	0.7423
chr19	59128983	3815021	0.0645	1.1153
chr20	63025520	5328724	0.0845	0.5716
chr21	48129895	2560682	0.0532	0.4714
chr22	51304566	1500428	0.0292	0.3365
chrMT	16571	26605	1.6055	2.6435
chrX	155270560	11020231	0.071	0.5589
chrY	59373566	690662	0.0116	0.652

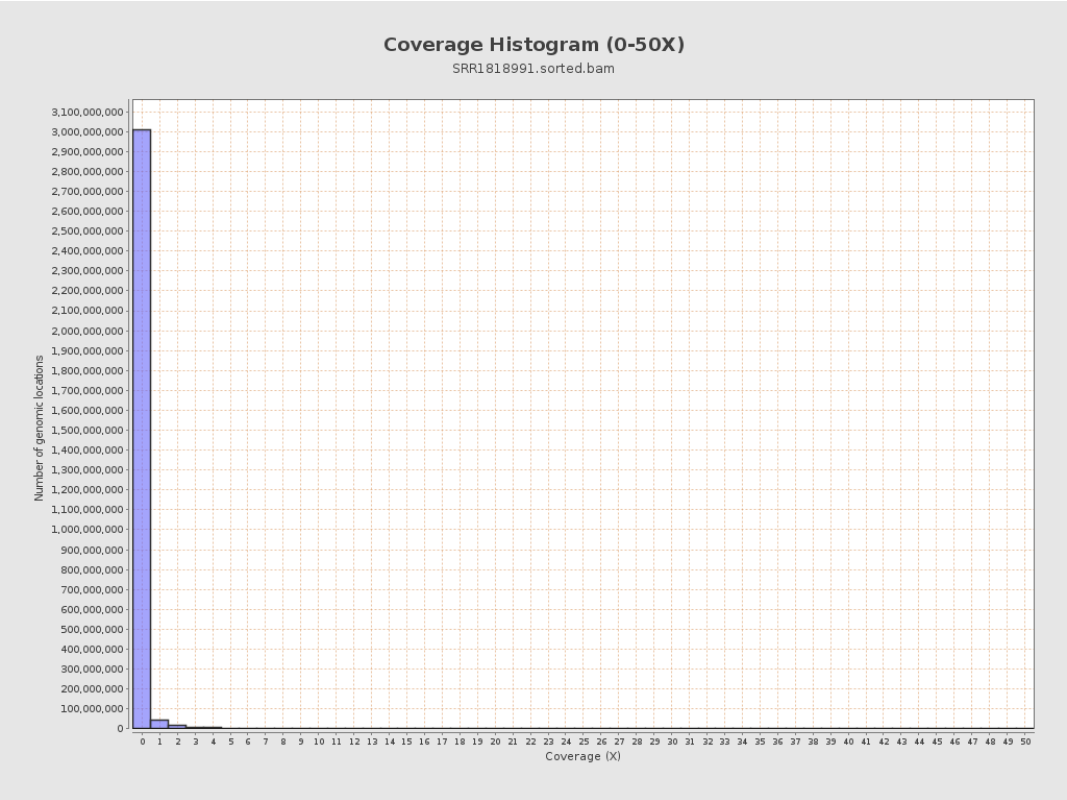
3. Results : Coverage across reference



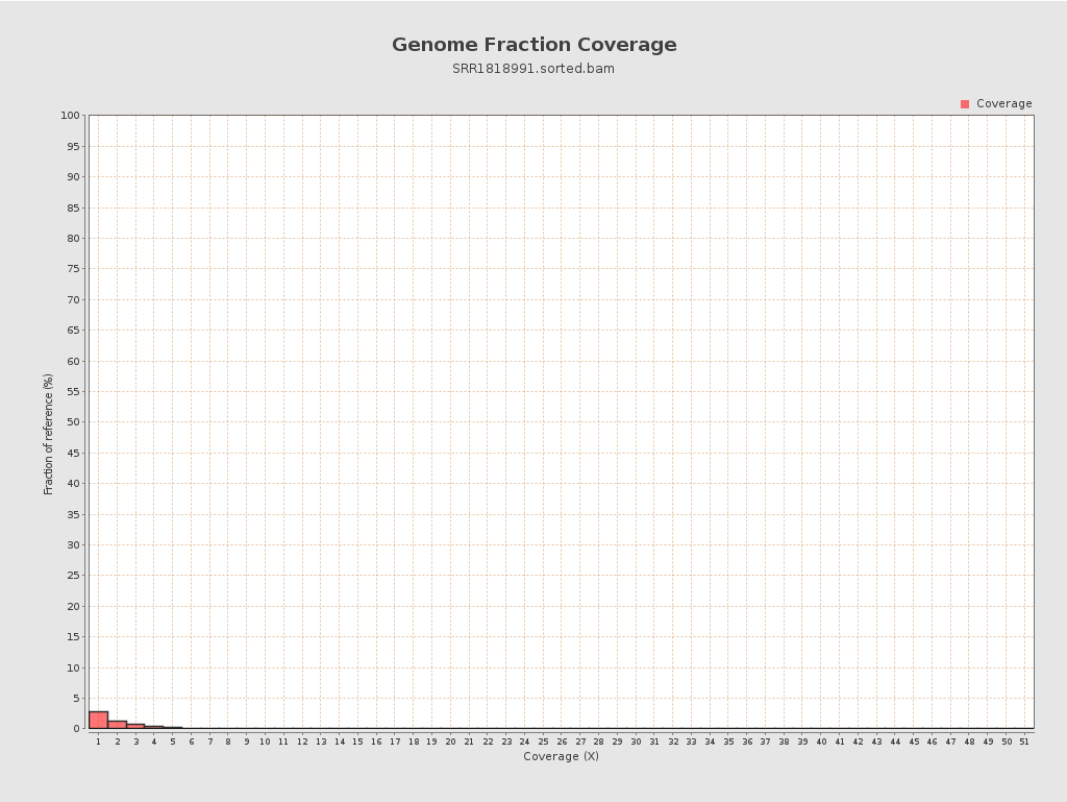
4. Results : Coverage Histogram



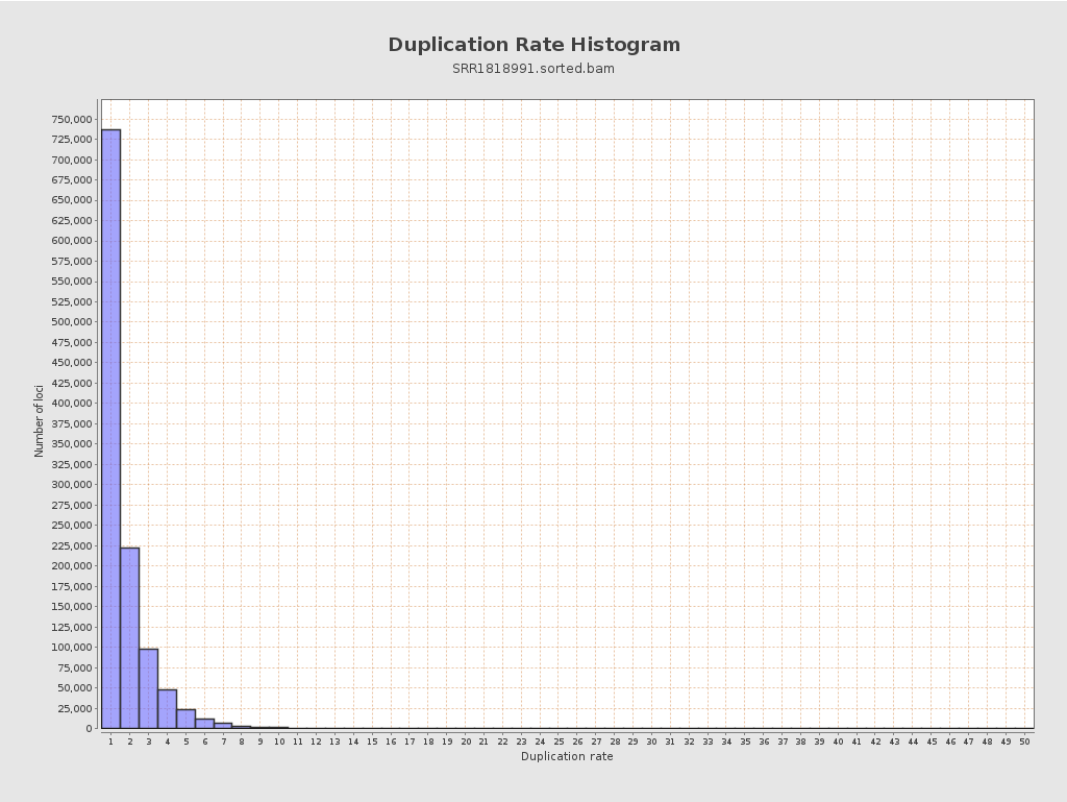
5. Results : Coverage Histogram (0-50X)



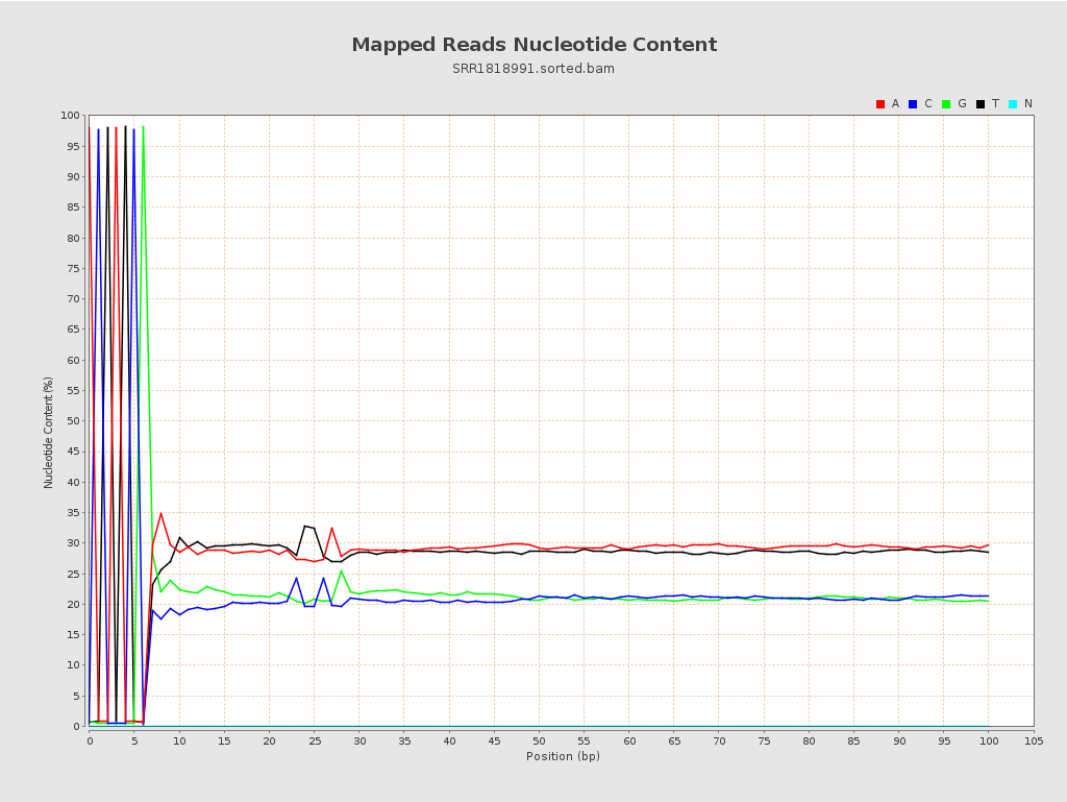
6. Results : Genome Fraction Coverage



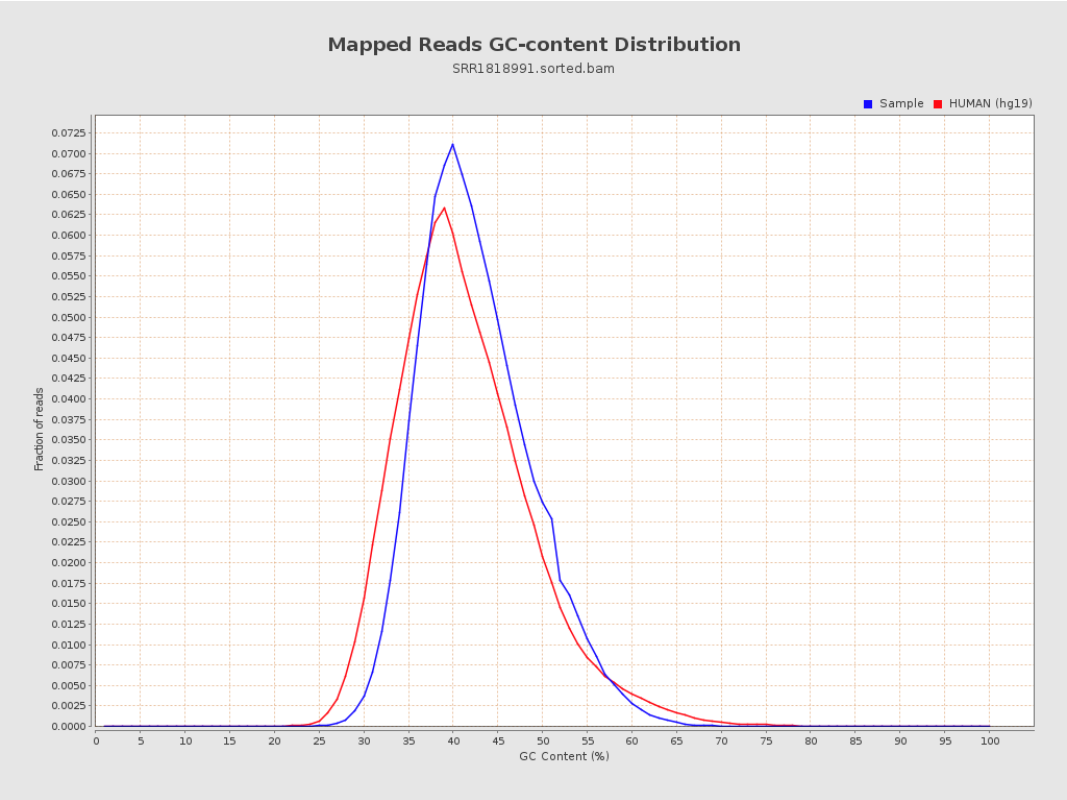
7. Results : Duplication Rate Histogram



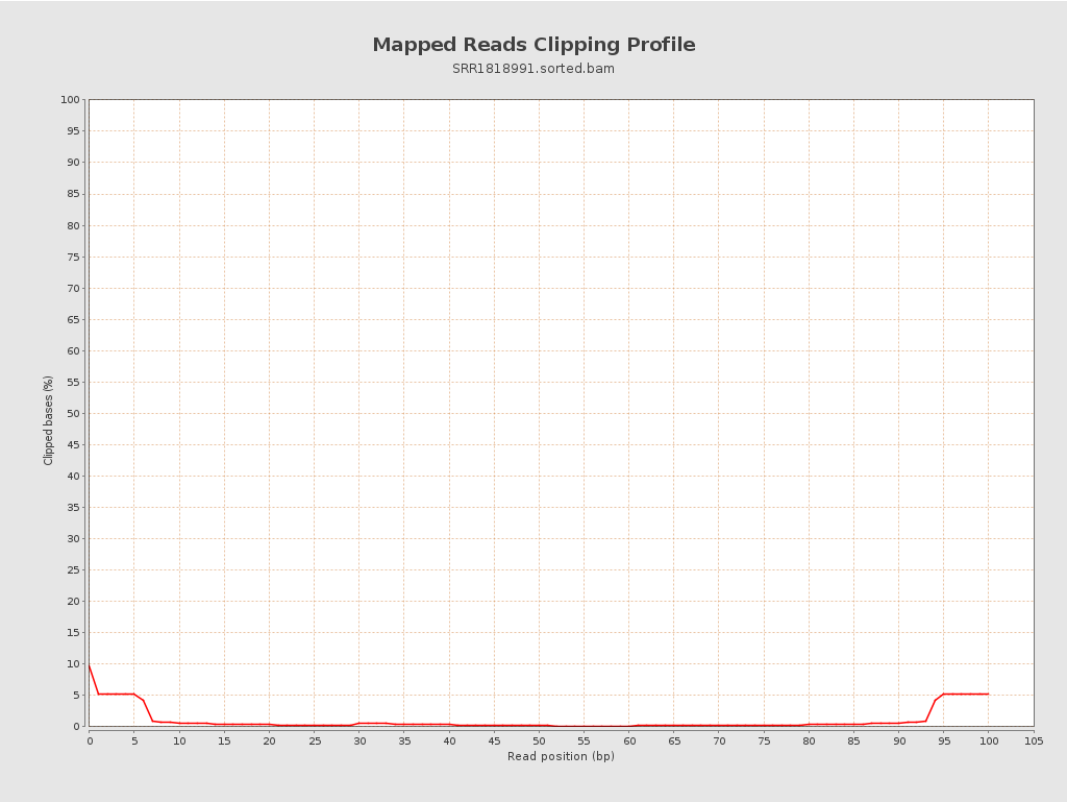
8. Results : Mapped Reads Nucleotide Content



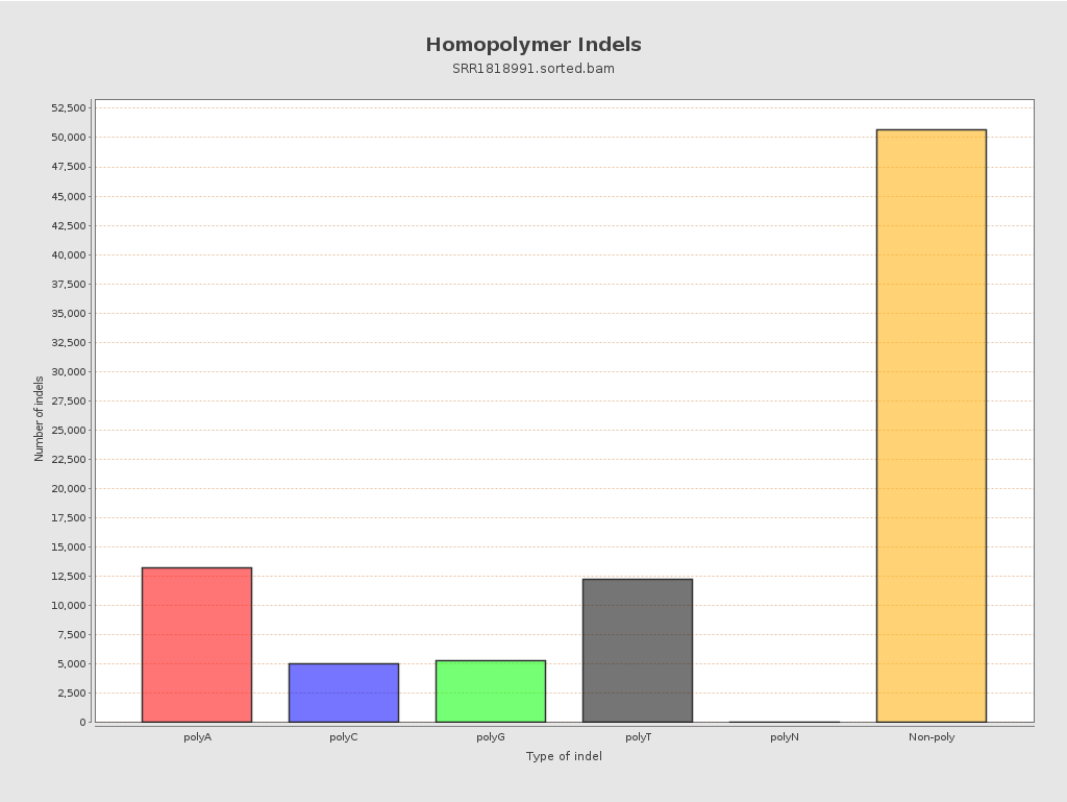
9. Results : Mapped Reads GC-content Distribution



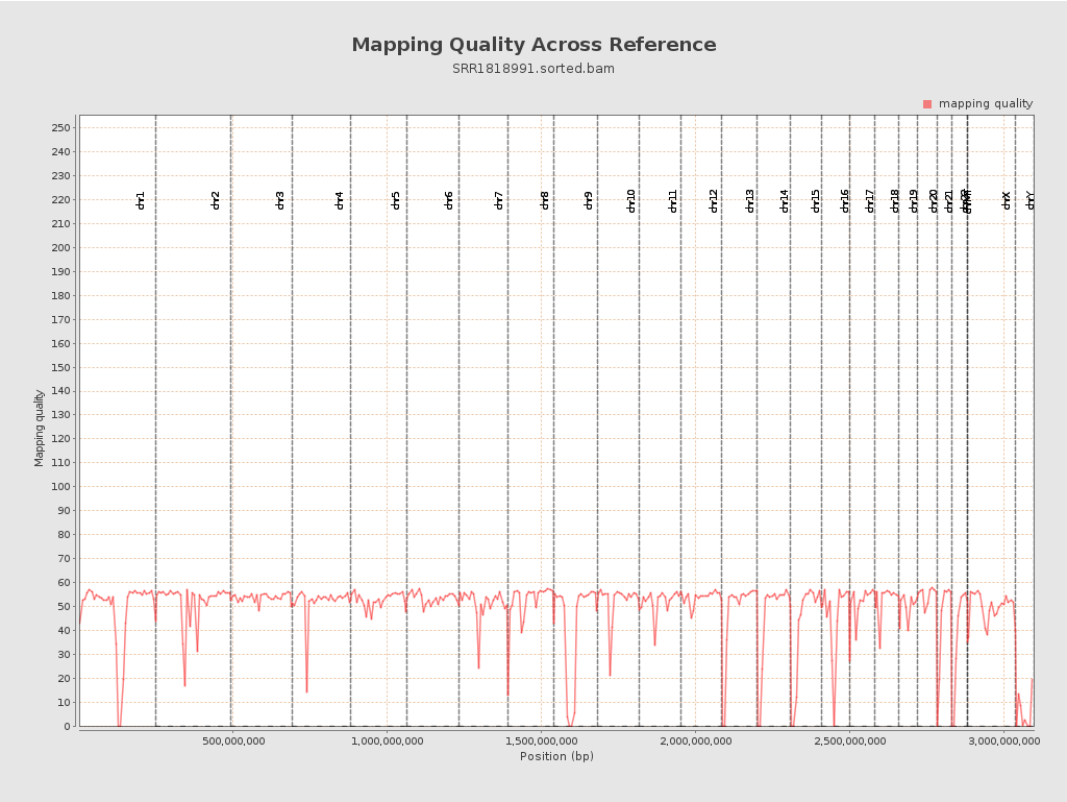
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram