Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 23:19:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163161.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_SRR1163161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 23:19:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	110,077,812
Mapped reads	108,489,691 / 98.56%
Unmapped reads	1,588,121 / 1.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,299,649 / 1.18%
Read min/max/mean length	30 / 100 / 100.49
Duplicated reads (estimated)	72,407,191 / 65.78%
Duplication rate	54.08%
Clipped reads	6,544,550 / 5.95%

2.2. ACGT Content

Number/percentage of A's	2,807,900,560 / 26.02%
Number/percentage of C's	2,583,555,560 / 23.94%
Number/percentage of T's	2,840,652,588 / 26.33%
Number/percentage of G's	2,549,643,195 / 23.63%
Number/percentage of N's	8,105,232 / 0.08%
GC Percentage	47.57%

2.3. Coverage

Mean	3.486

Standard Deviation	48.7711

2.4. Mapping Quality

Mean Mapping Quality	49.83

2.5. Mismatches and indels

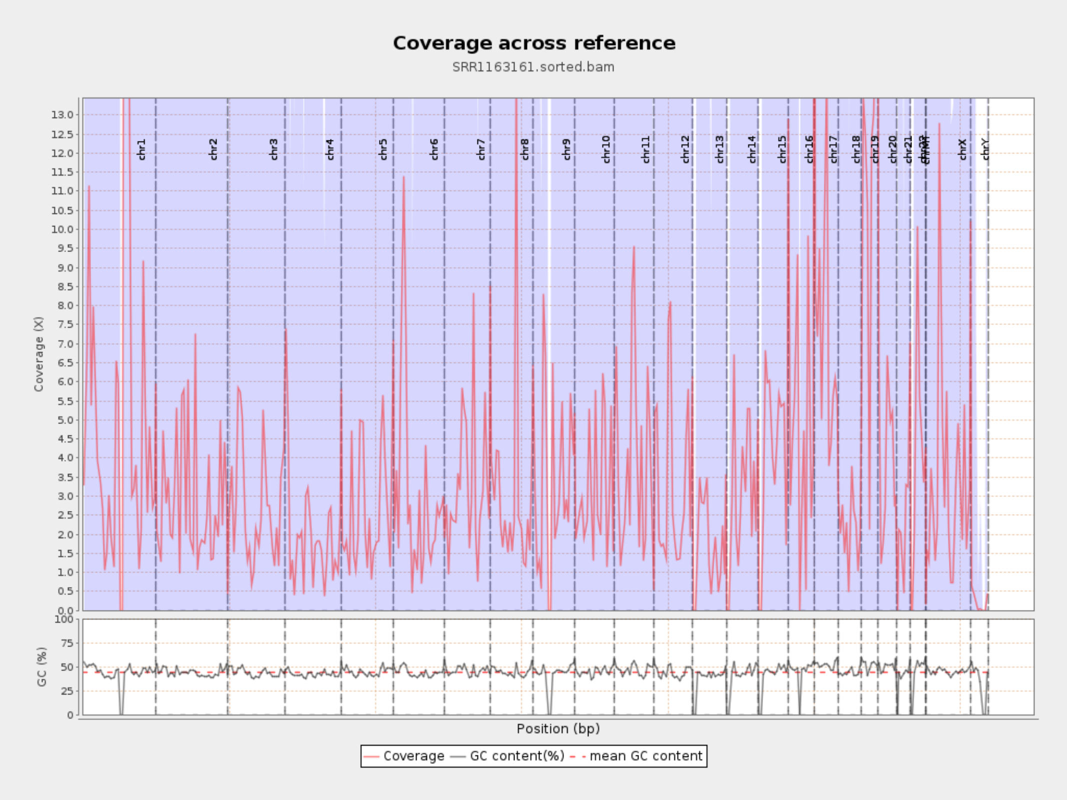
General error rate	0.68%
Mismatches	71,747,842
Insertions	827,612
Mapped reads with at least one insertion	0.75%
Deletions	807,587
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.45%

2.6. Chromosome stats

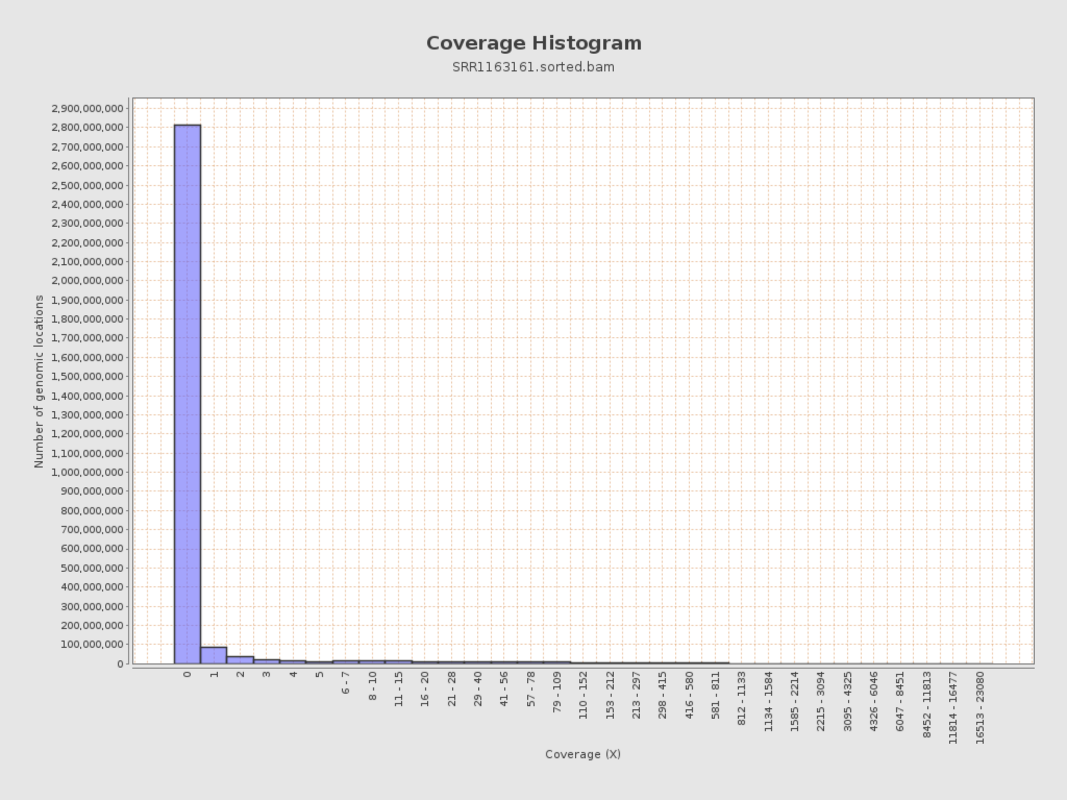
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1397191084	5.6056	77.002
chr2	243199373	718718703	2.9553	39.6132
chr3	198022430	543506115	2.7447	37.965
chr4	191154276	369760319	1.9344	33.0458
chr5	180915260	482118509	2.6649	40.3904
chr6	171115067	506895189	2.9623	40.9936
chr7	159138663	522835233	3.2854	40.4066

chr8	146364022	452932791	3.0946	51.0952
chr9	141213431	454399709	3.2178	37.9806
chr10	135534747	427244698	3.1523	47.094
chr11	135006516	537717379	3.9829	52.326
chr12	133851895	455821083	3.4054	40.4216
chr13	115169878	191256671	1.6606	28.5511
chr14	107349540	323245623	3.0112	53.6085
chr15	102531392	407977009	3.979	43.5905
chr16	90354753	432337318	4.7849	55.3902
chr17	81195210	598974993	7.377	69.3653
chr18	78077248	166040017	2.1266	29.8155
chr19	59128983	684845019	11.5822	92.9521
chr20	63025520	241503618	3.8318	50.2877
chr21	48129895	121136922	2.5169	35.7923
chr22	51304566	207312380	4.0408	45.2434
chrMT	16571	2500	0.1509	0.5439
chrX	155270560	535271014	3.4473	56.1077
chrY	59373566	12530044	0.211	19.9819

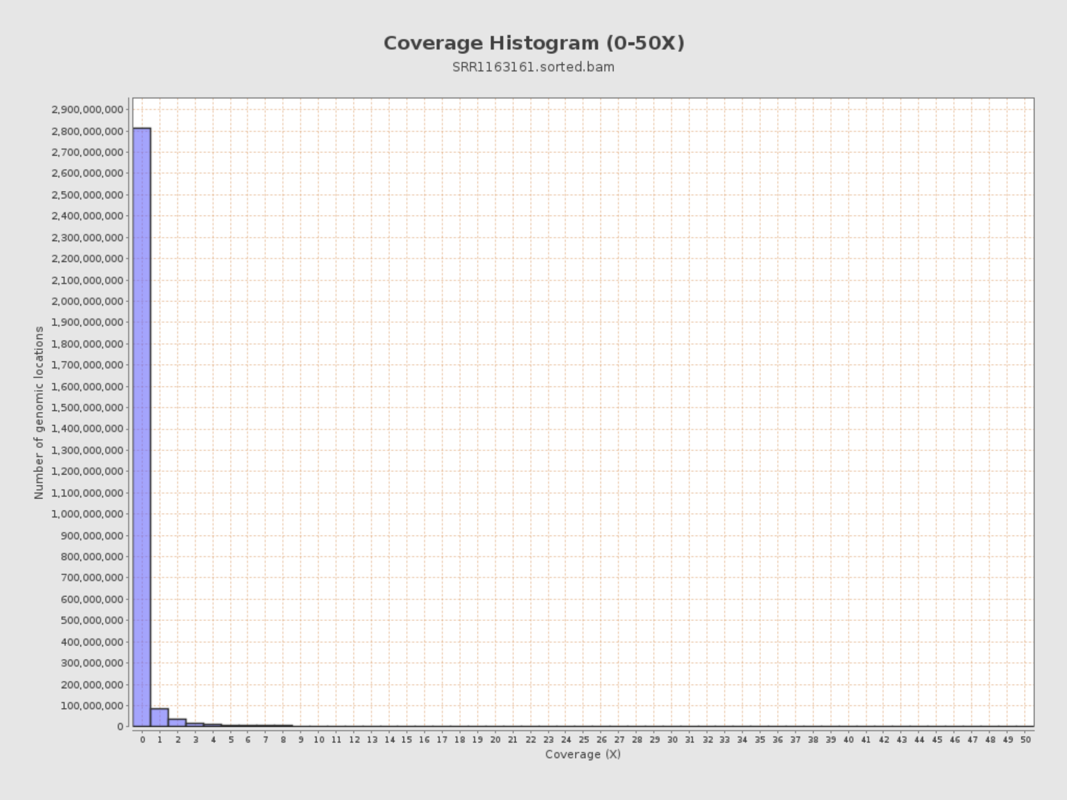
3. Results : Coverage across reference



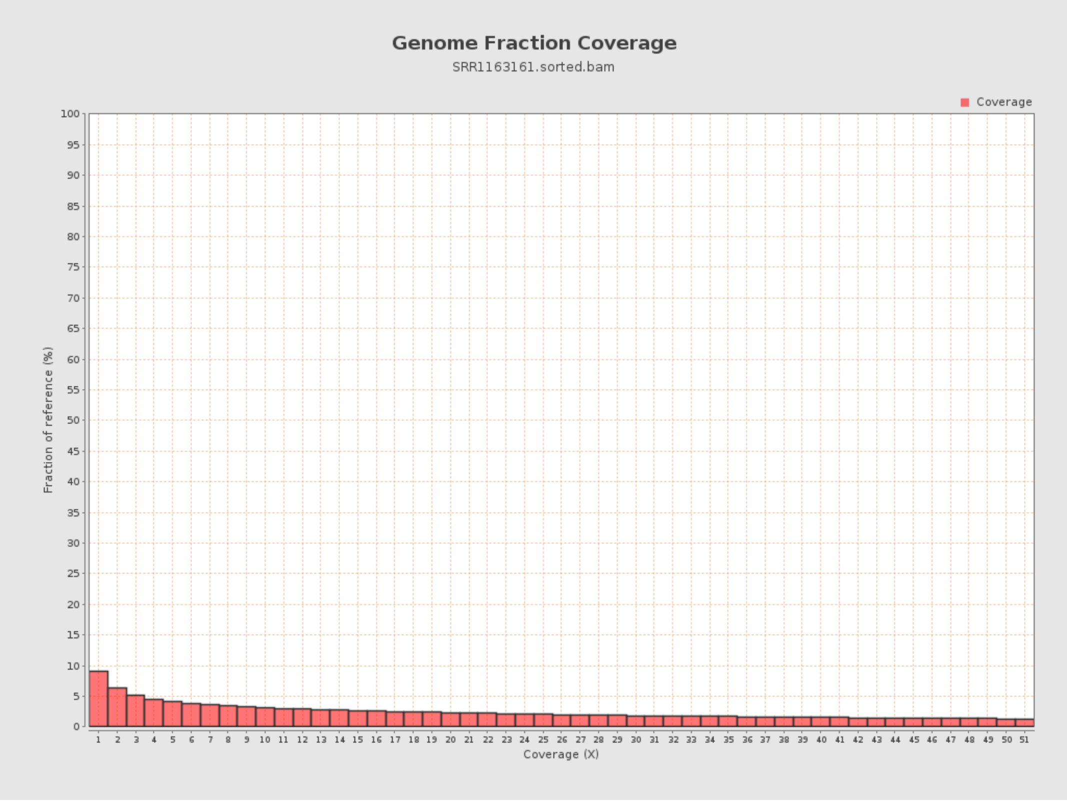
4. Results : Coverage Histogram



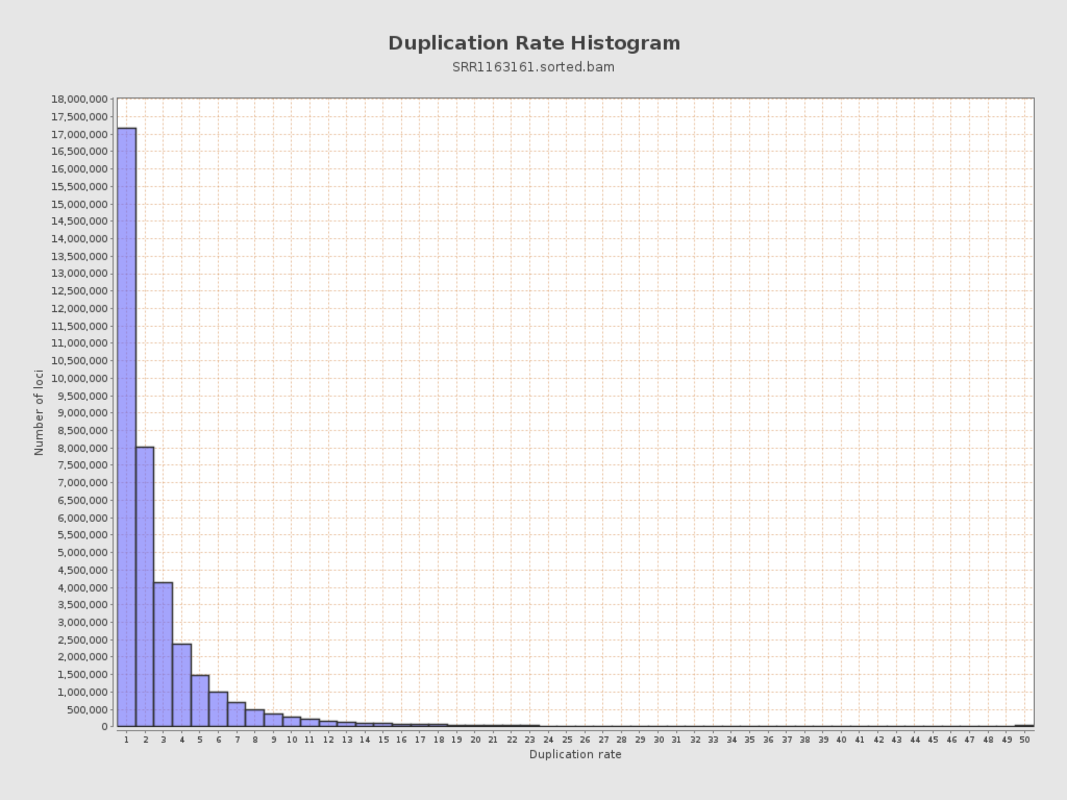
5. Results : Coverage Histogram (0-50X)



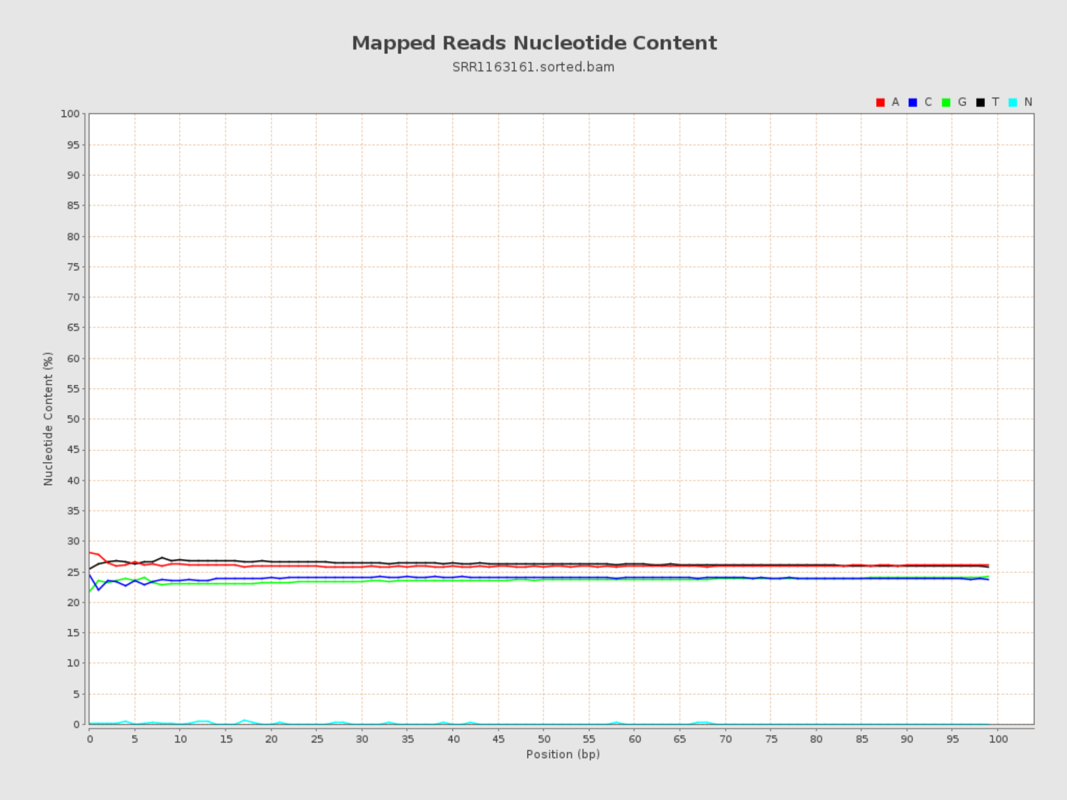
6. Results : Genome Fraction Coverage



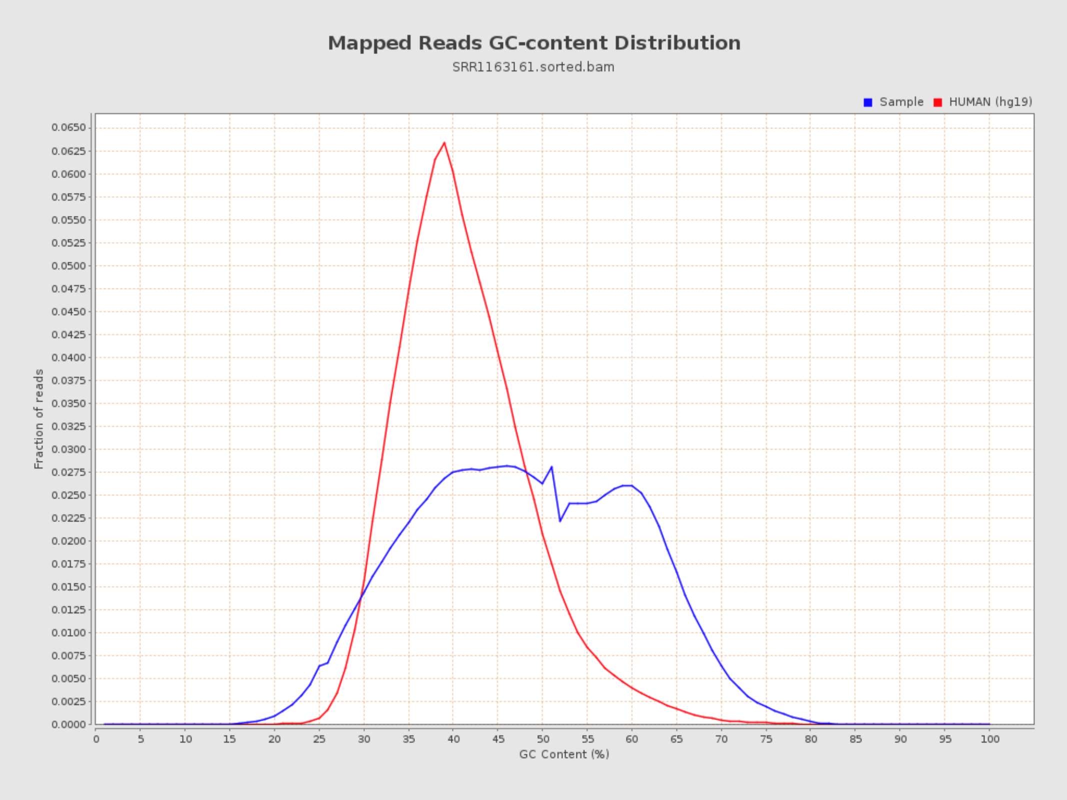
7. Results : Duplication Rate Histogram



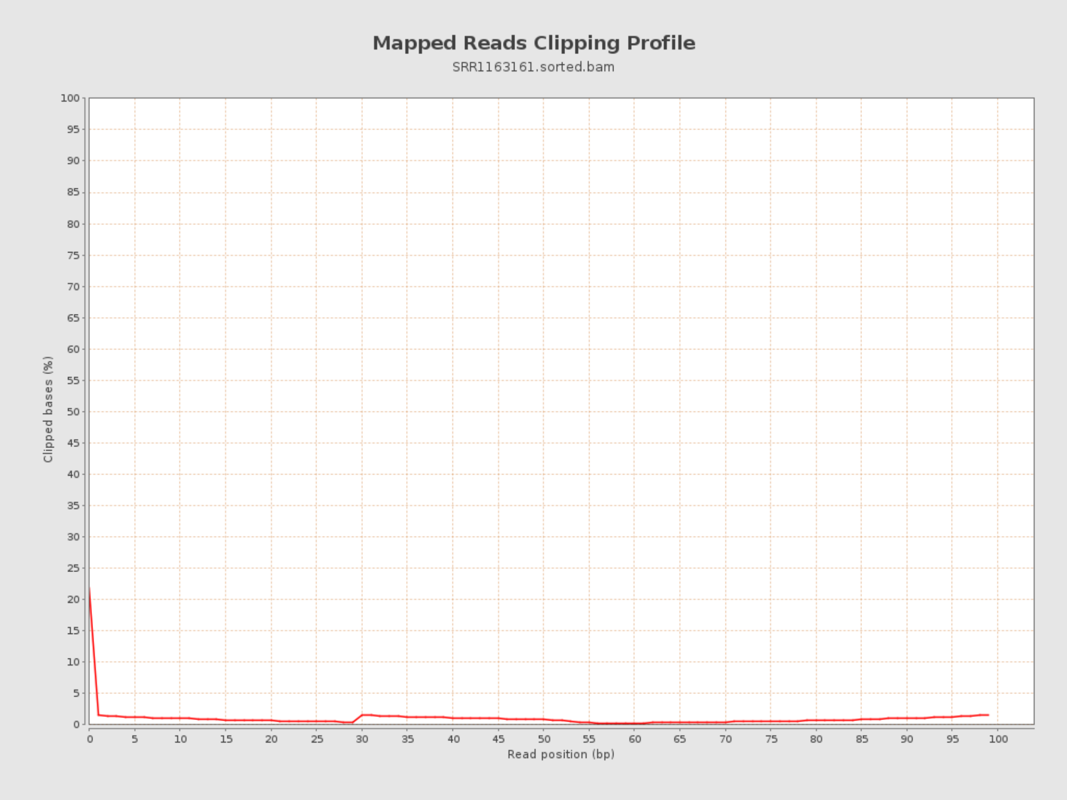
8. Results : Mapped Reads Nucleotide Content



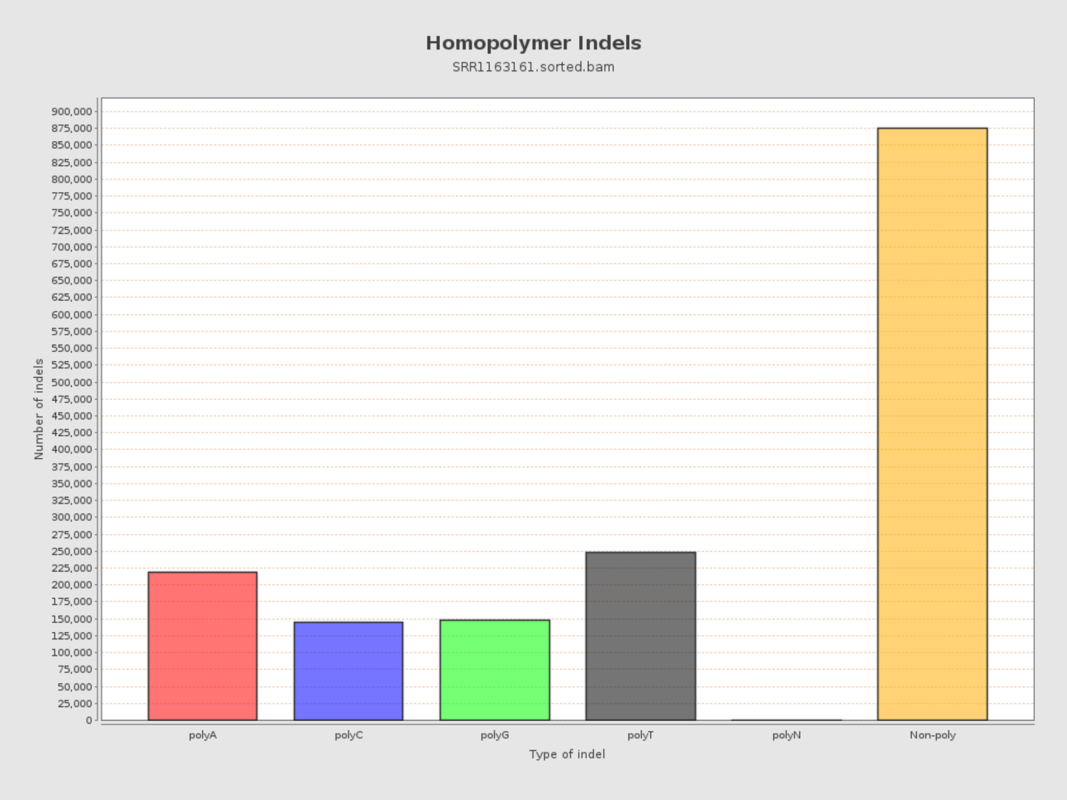
9. Results : Mapped Reads GC-content Distribution



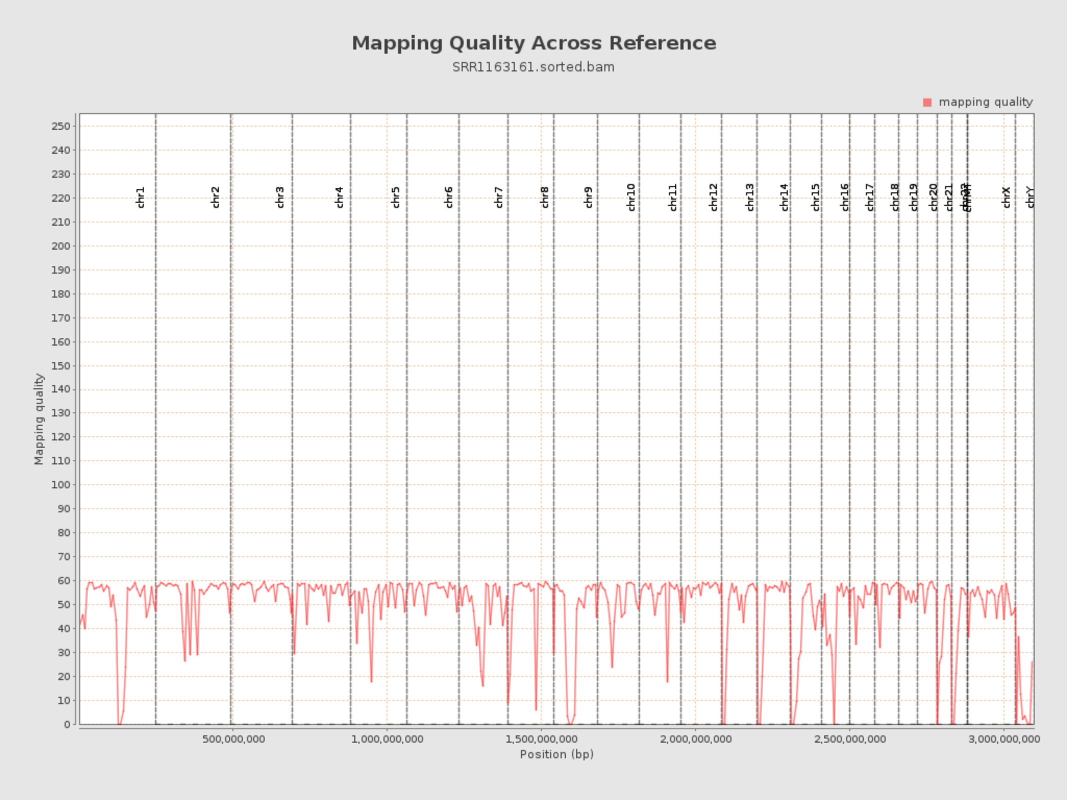
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram