Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:47:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124794.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_SRR3124794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124794.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:47:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124794.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	494,893
Mapped reads	494,132 / 99.85%
Unmapped reads	761 / 0.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	217,614 / 43.97%
Read min/max/mean length	30 / 151 / 177.83
Duplicated reads (estimated)	708,706 / 143.2%
Duplication rate	13.12%
Clipped reads	453,233 / 91.58%

2.2. ACGT Content

Number/percentage of A's	22,287,923 / 30.23%
Number/percentage of C's	14,066,096 / 19.08%
Number/percentage of T's	23,000,281 / 31.2%
Number/percentage of G's	14,373,780 / 19.5%
Number/percentage of N's	0 / 0%
GC Percentage	38.57%

2.3. Coverage

Mean	0.0238

Standard Deviation	55.2851

2.4. Mapping Quality

Mean Mapping Quality	47.3

2.5. Mismatches and indels

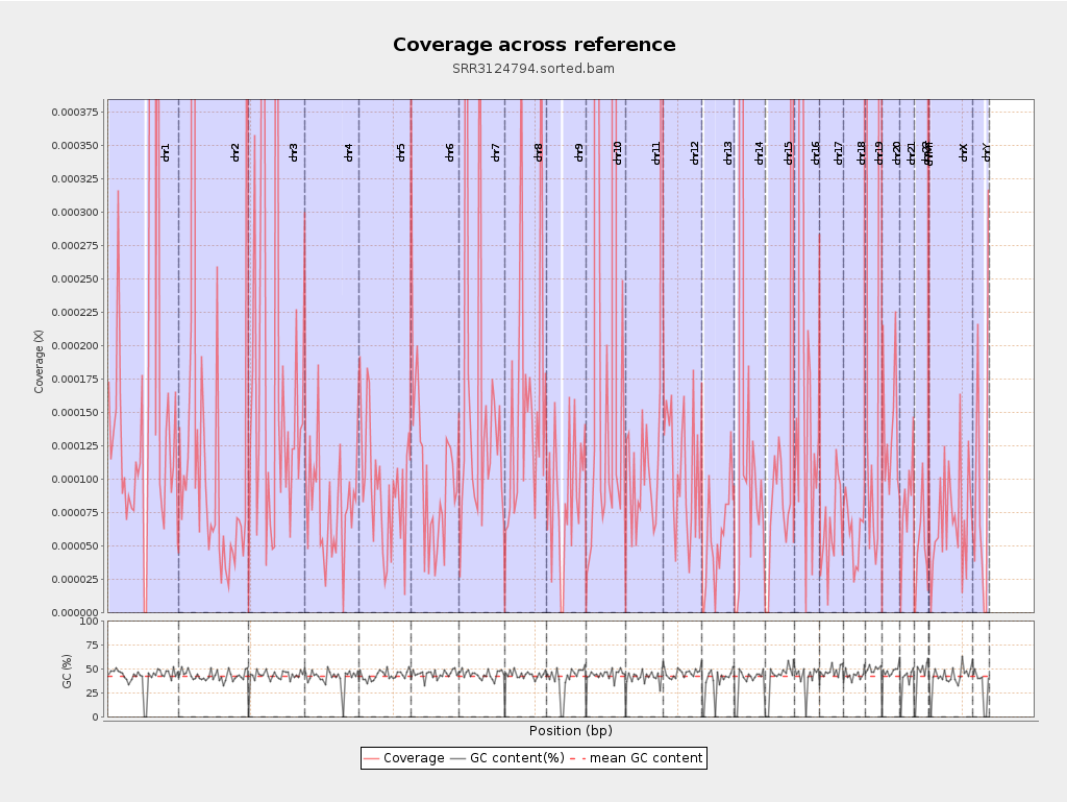
General error rate	0.72%
Mismatches	525,346
Insertions	2,948
Mapped reads with at least one insertion	0.59%
Deletions	19,133
Mapped reads with at least one deletion	3.83%
Homopolymer indels	60.47%

2.6. Chromosome stats

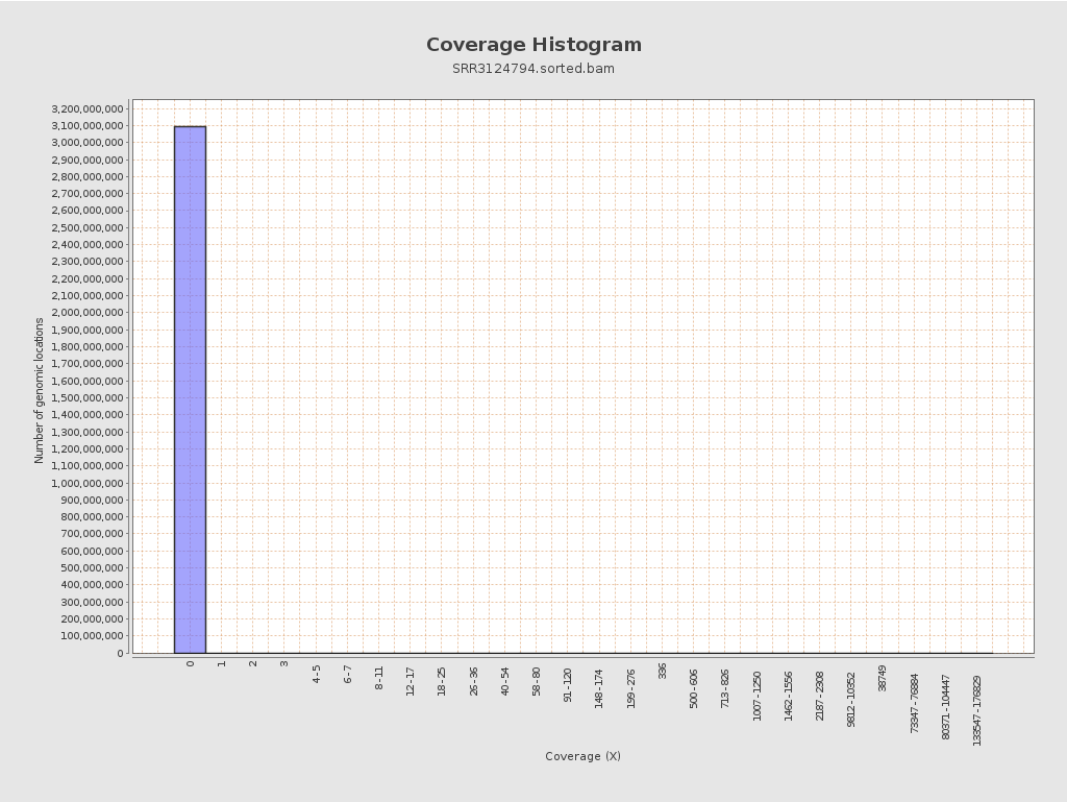
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	471044	0.0019	1.6183
chr2	243199373	37551	0.0002	0.0725
chr3	198022430	38169	0.0002	0.0848
chr4	191154276	15430	0.0001	0.0091
chr5	180915260	16975	0.0001	0.0097
chr6	171115067	18207	0.0001	0.0158
chr7	159138663	26799	0.0002	0.066

chr8	146364022	23894	0.0002	0.0222
chr9	141213431	12322	0.0001	0.0094
chr10	135534747	72913292	0.538	264.2075
chr11	135006516	19709	0.0001	0.0579
chr12	133851895	14376	0.0001	0.0105
chr13	115169878	6399	0.0001	0.0074
chr14	107349540	33873	0.0003	0.3796
chr15	102531392	19010	0.0002	0.0732
chr16	90354753	22377	0.0002	0.1647
chr17	81195210	5227	0.0001	0.0081
chr18	78077248	4775	0.0001	0.0083
chr19	59128983	16675	0.0003	0.0789
chr20	63025520	8586	0.0001	0.0122
chr21	48129895	3953	0.0001	0.0091
chr22	51304566	2415	0	0.0069
chrMT	16571	129	0.0078	0.0879
chrX	155270560	11160	0.0001	0.0094
chrY	59373566	5488	0.0001	0.0097

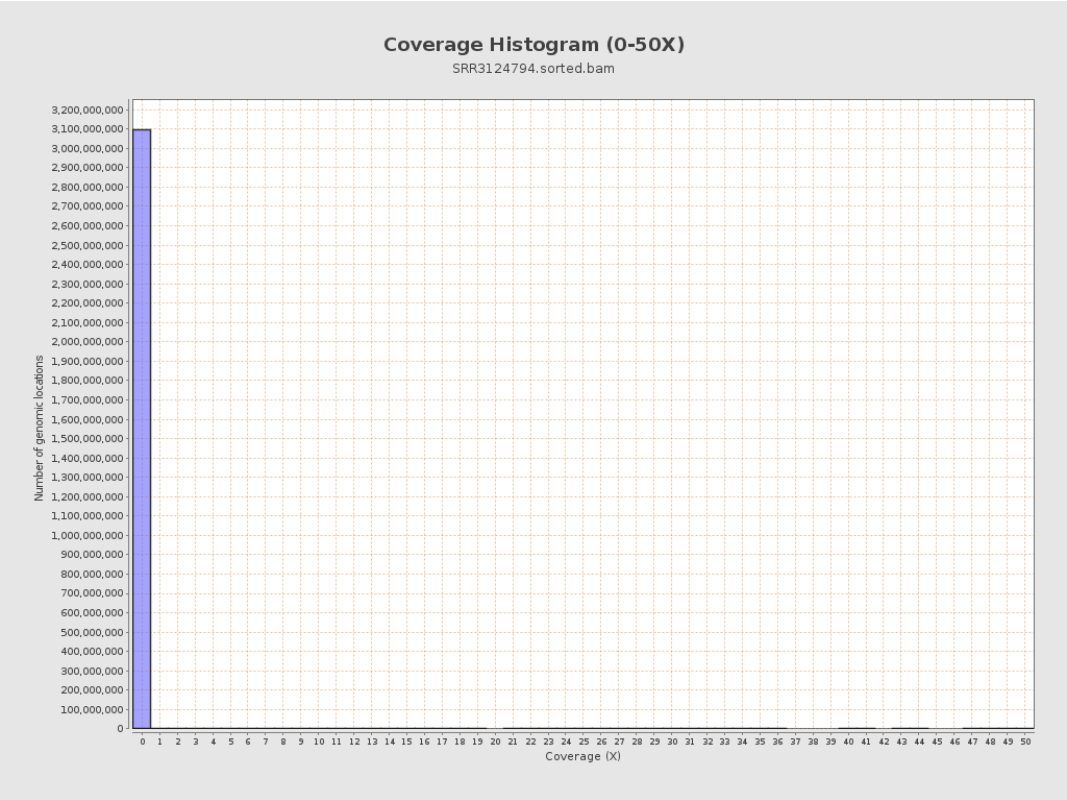
3. Results : Coverage across reference



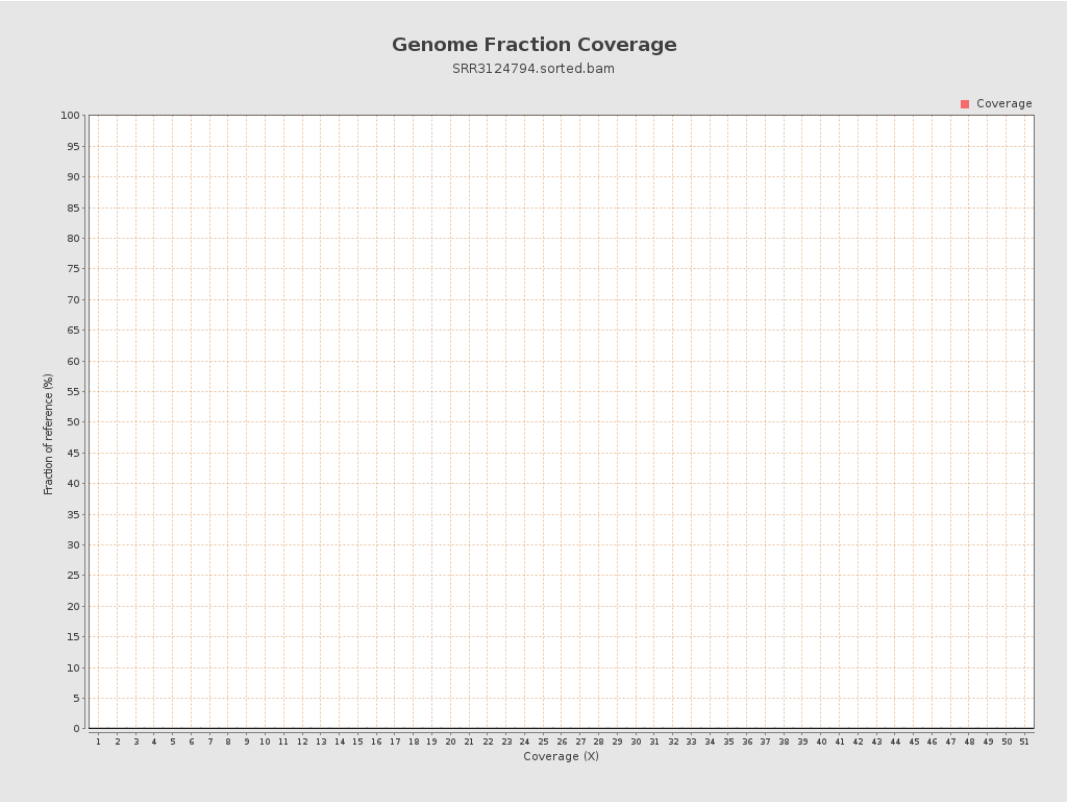
4. Results : Coverage Histogram



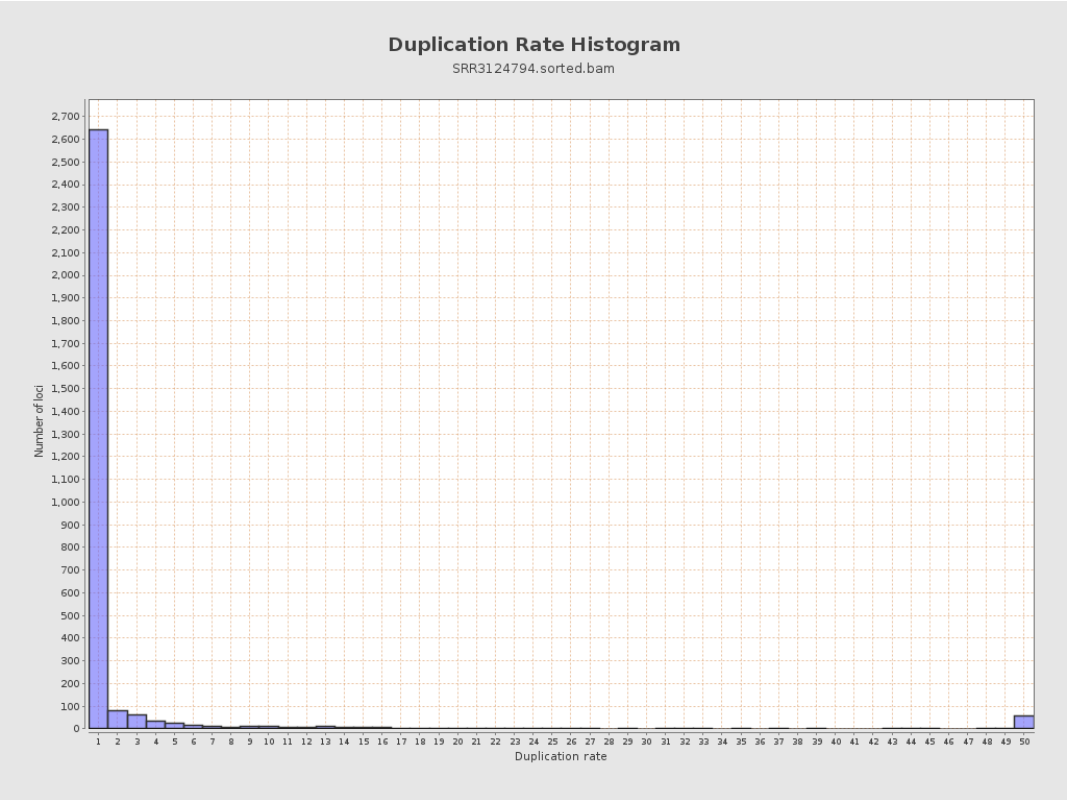
5. Results : Coverage Histogram (0-50X)



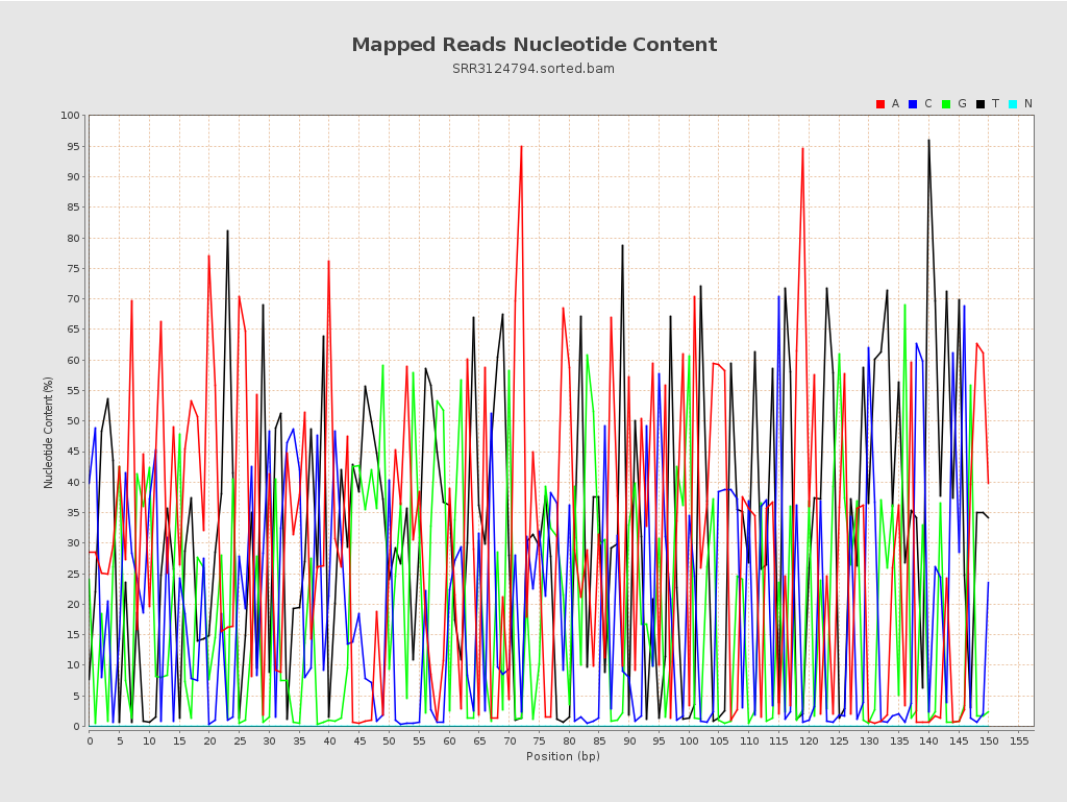
6. Results : Genome Fraction Coverage



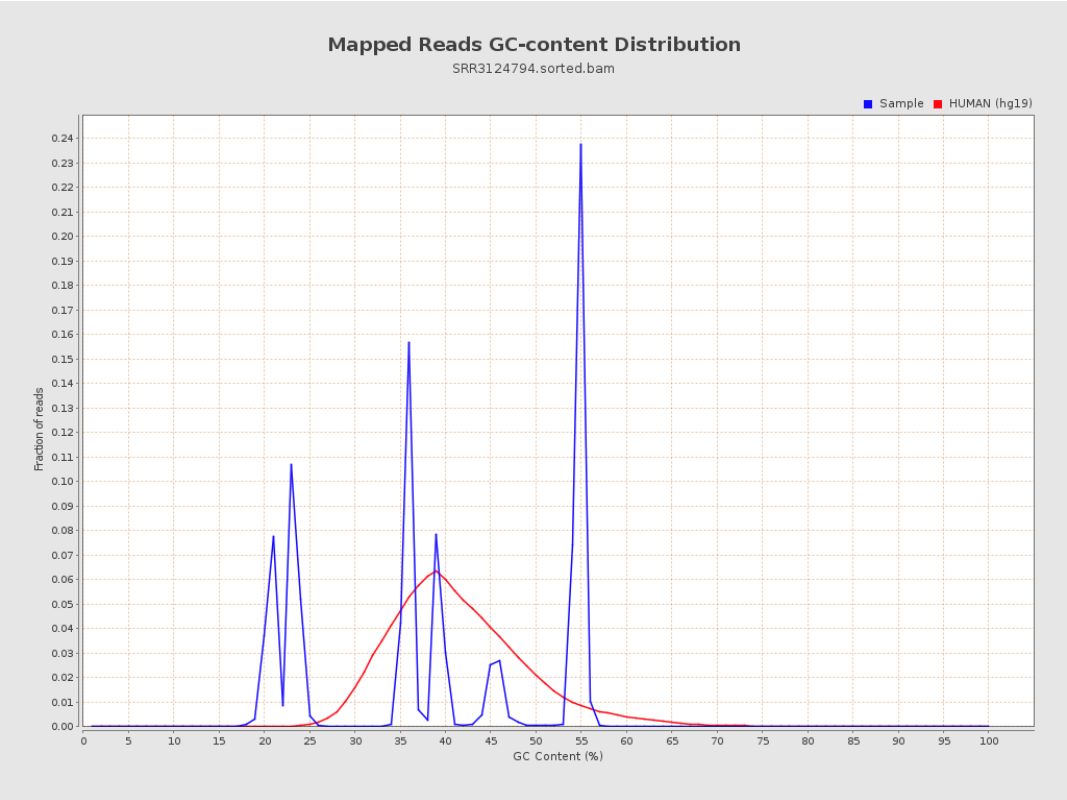
7. Results : Duplication Rate Histogram



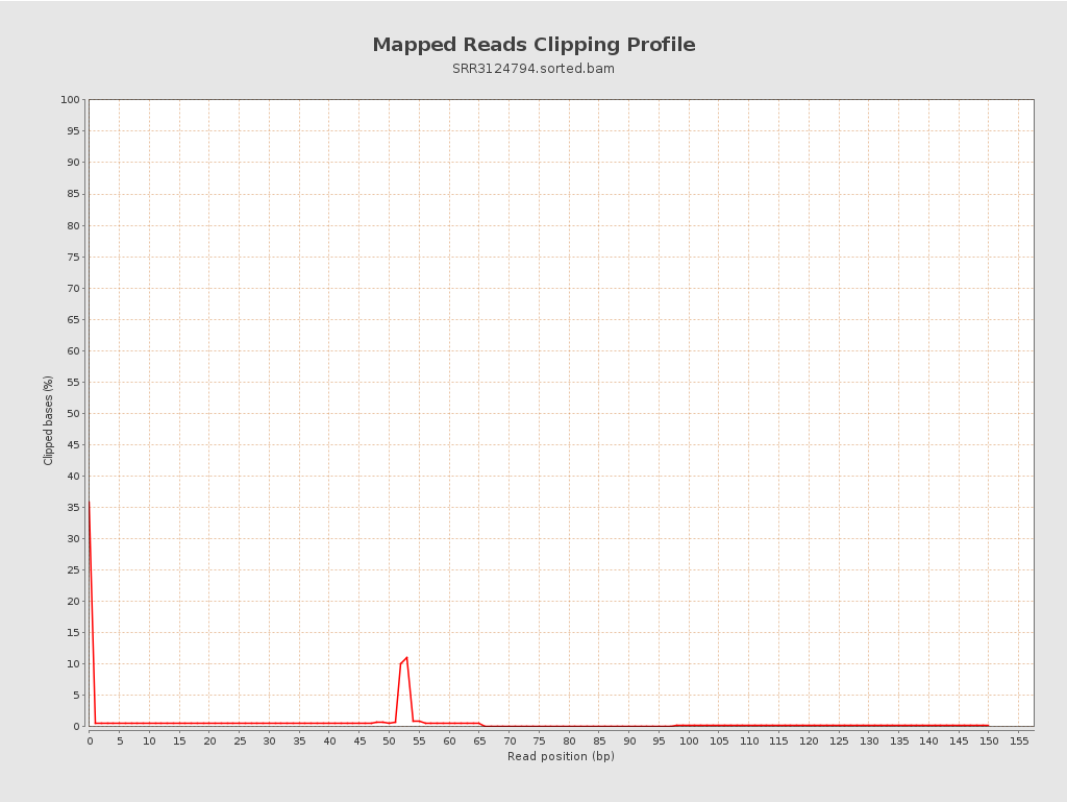
8. Results : Mapped Reads Nucleotide Content



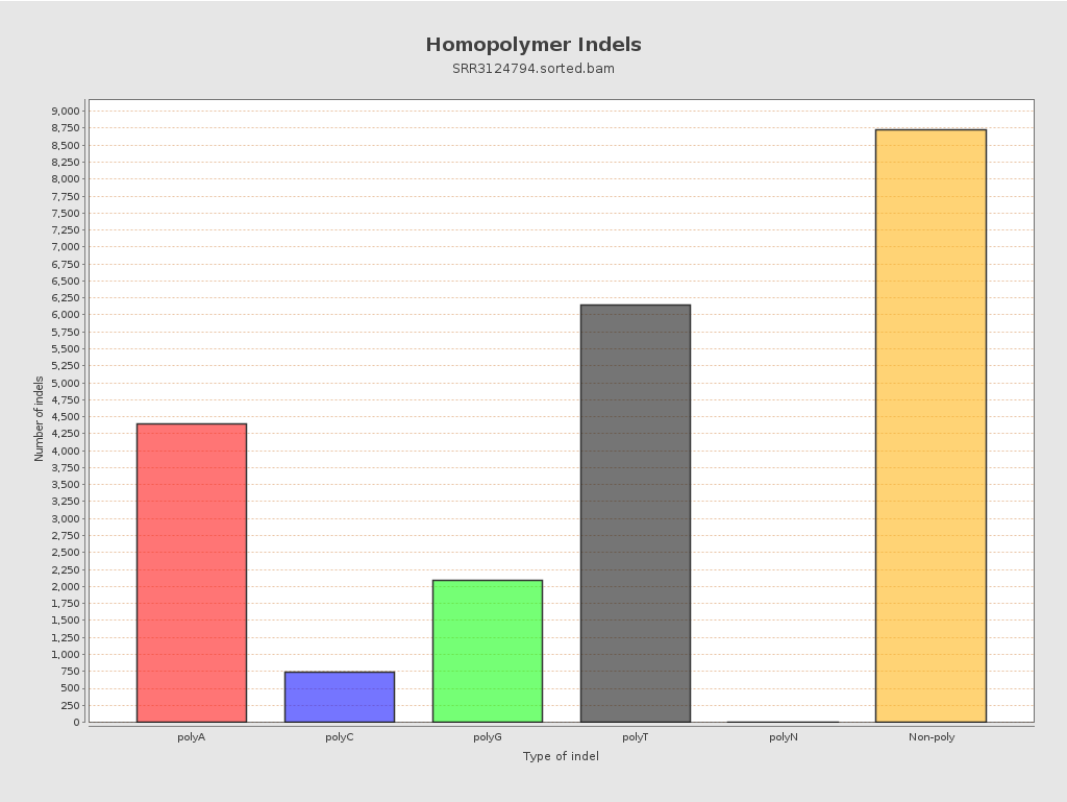
9. Results : Mapped Reads GC-content Distribution



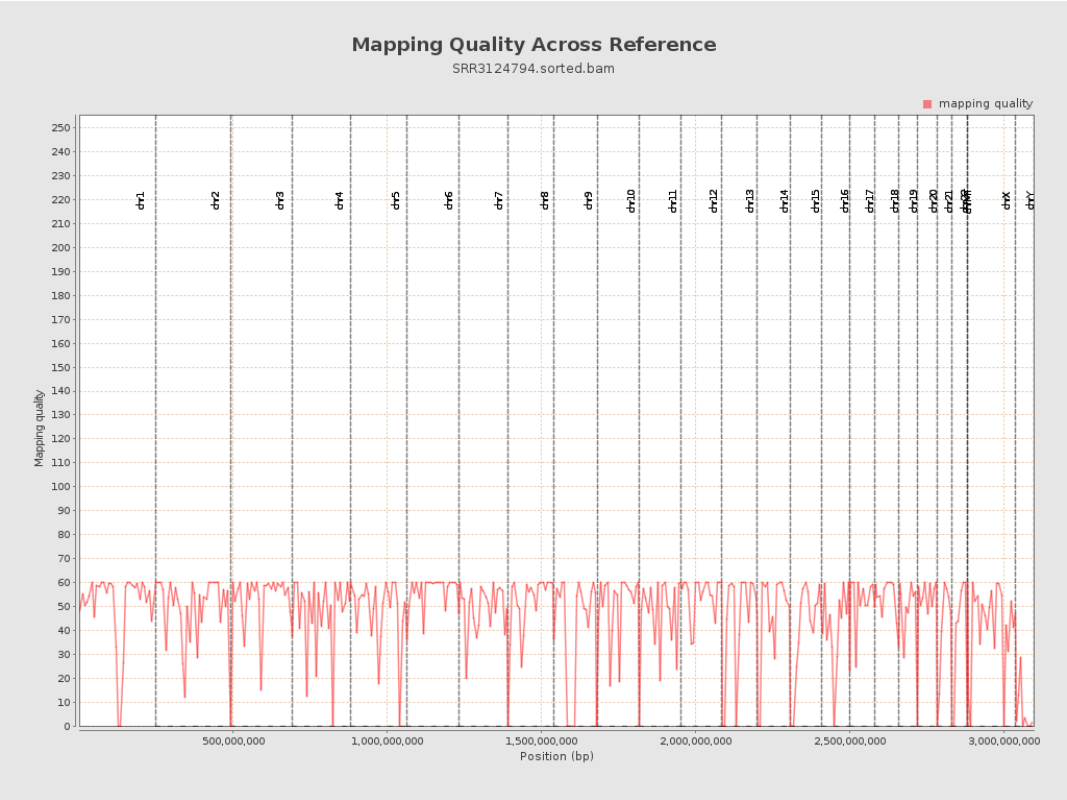
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram