Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:51:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124796.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_SRR3124796 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124796.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:51:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124796.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	593,387
Mapped reads	592,179 / 99.8%
Unmapped reads	1,208 / 0.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	233,094 / 39.28%
Read min/max/mean length	30 / 151 / 171.54
Duplicated reads (estimated)	818,204 / 137.89%
Duplication rate	5.84%
Clipped reads	510,688 / 86.06%

2.2. ACGT Content

Number/percentage of A's	30,356,719 / 34.71%
Number/percentage of C's	19,010,000 / 21.73%
Number/percentage of T's	23,940,057 / 27.37%
Number/percentage of G's	14,158,506 / 16.19%
Number/percentage of N's	0 / 0%
GC Percentage	37.92%

2.3. Coverage

Mean	0.0283

Standard Deviation	89.7759

2.4. Mapping Quality

Mean Mapping Quality	50.71

2.5. Mismatches and indels

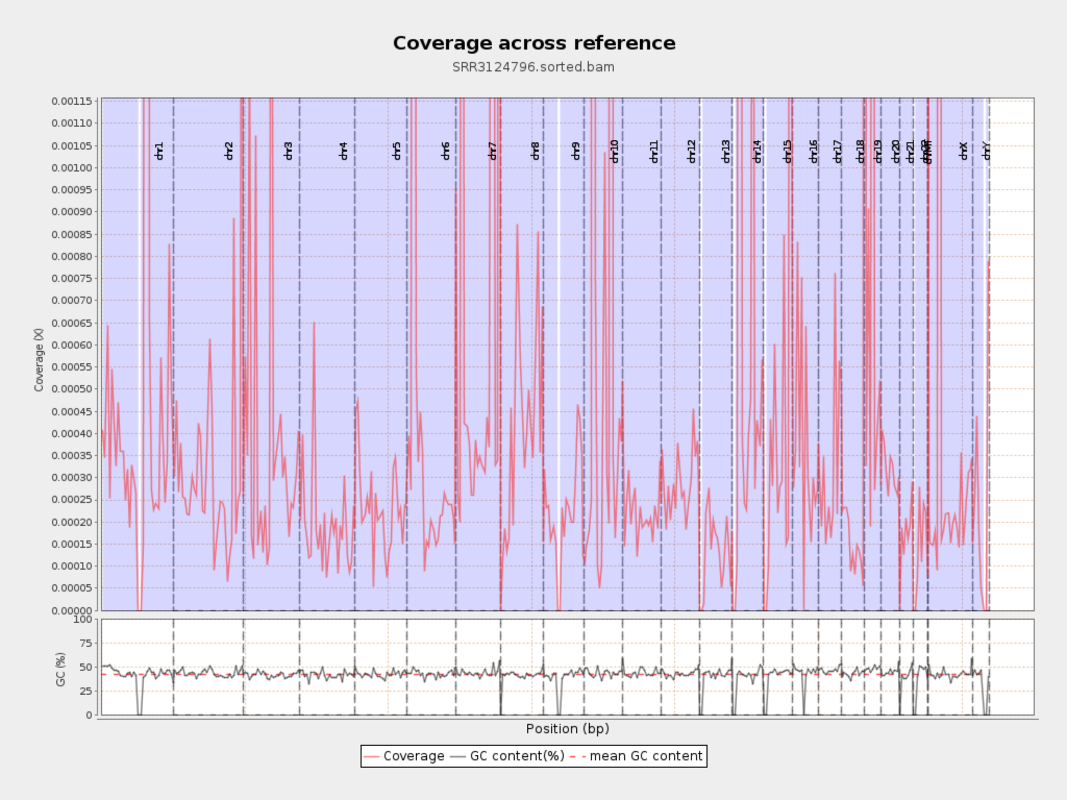
General error rate	0.73%
Mismatches	630,058
Insertions	5,721
Mapped reads with at least one insertion	0.96%
Deletions	20,725
Mapped reads with at least one deletion	3.46%
Homopolymer indels	74.2%

2.6. Chromosome stats

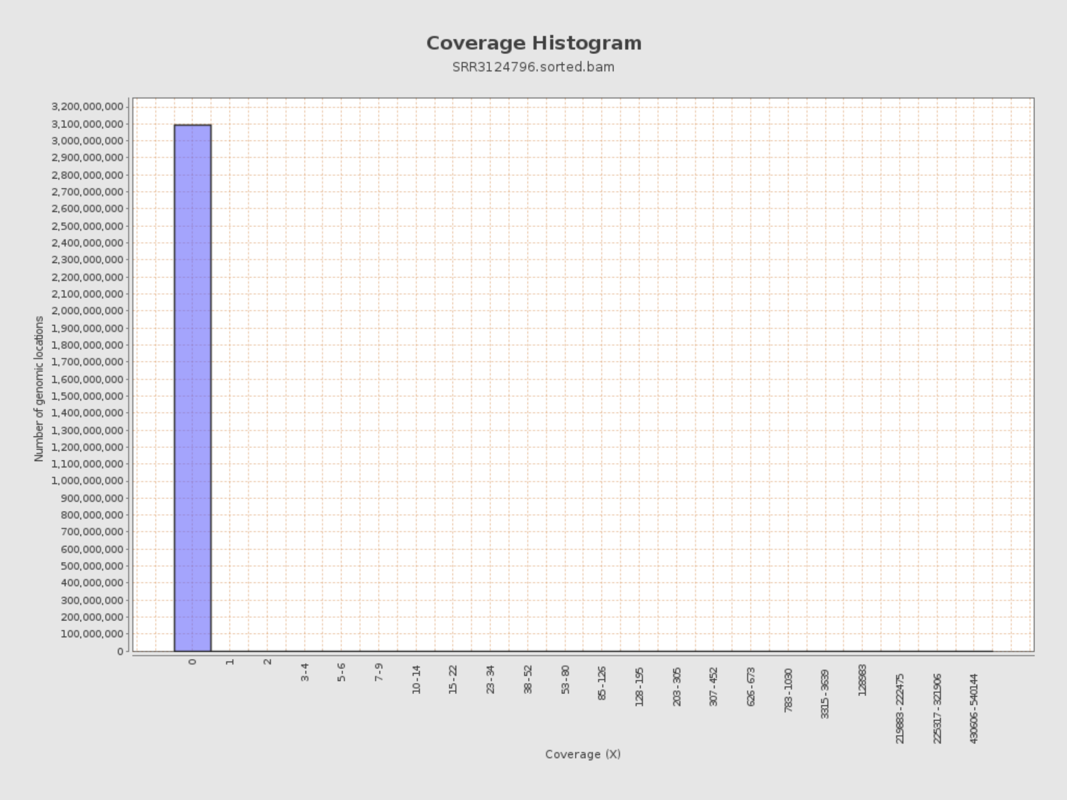
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1140370	0.0046	3.8241
chr2	243199373	81891	0.0003	0.1406
chr3	198022430	82620	0.0004	0.1841
chr4	191154276	36833	0.0002	0.0164
chr5	180915260	42216	0.0002	0.0154
chr6	171115067	85533	0.0005	0.2801
chr7	159138663	159245	0.001	0.4683

chr8	146364022	62444	0.0004	0.0228
chr9	141213431	32308	0.0002	0.0153
chr10	135534747	85238306	0.6289	429.0226
chr11	135006516	30150	0.0002	0.015
chr12	133851895	38795	0.0003	0.0183
chr13	115169878	14898	0.0001	0.0115
chr14	107349540	85694	0.0008	0.5647
chr15	102531392	53463	0.0005	0.1534
chr16	90354753	33854	0.0004	0.0301
chr17	81195210	26498	0.0003	0.0408
chr18	78077248	11601	0.0001	0.0123
chr19	59128983	84183	0.0014	0.4179
chr20	63025520	20137	0.0003	0.0194
chr21	48129895	8231	0.0002	0.0131
chr22	51304566	7318	0.0001	0.0119
chrMT	16571	120	0.0072	0.0848
chrX	155270560	96107	0.0006	0.3912
chrY	59373566	14046	0.0002	0.0164

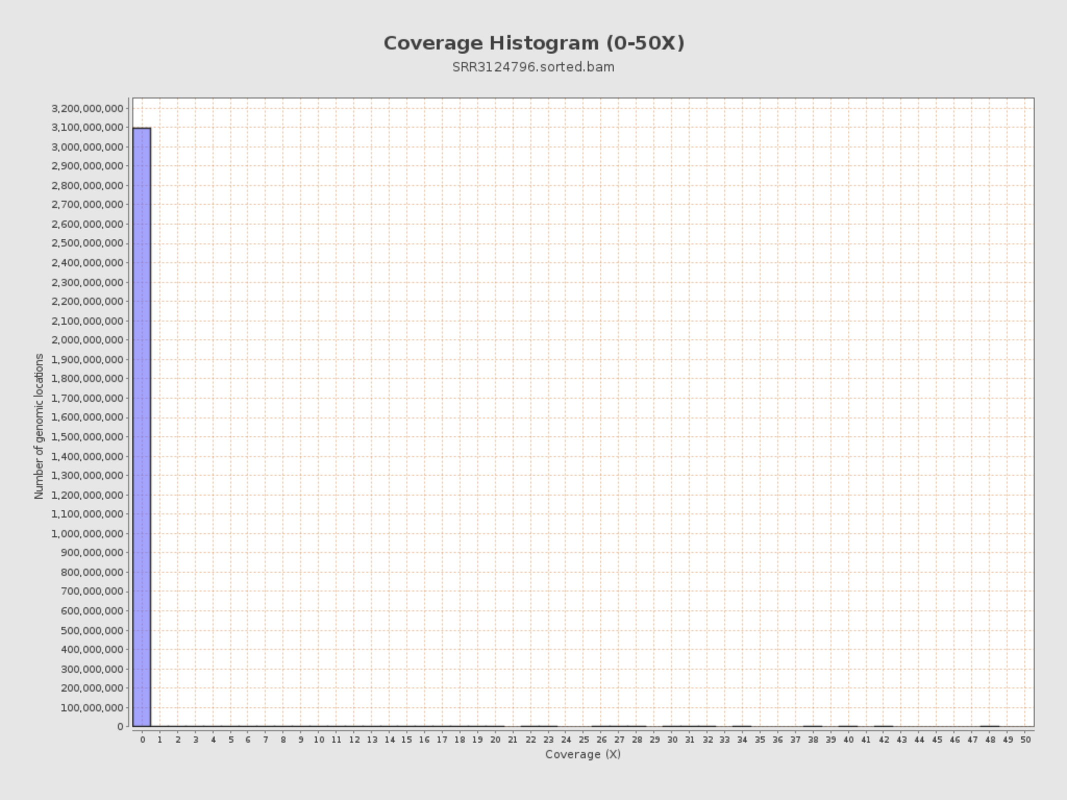
3. Results : Coverage across reference



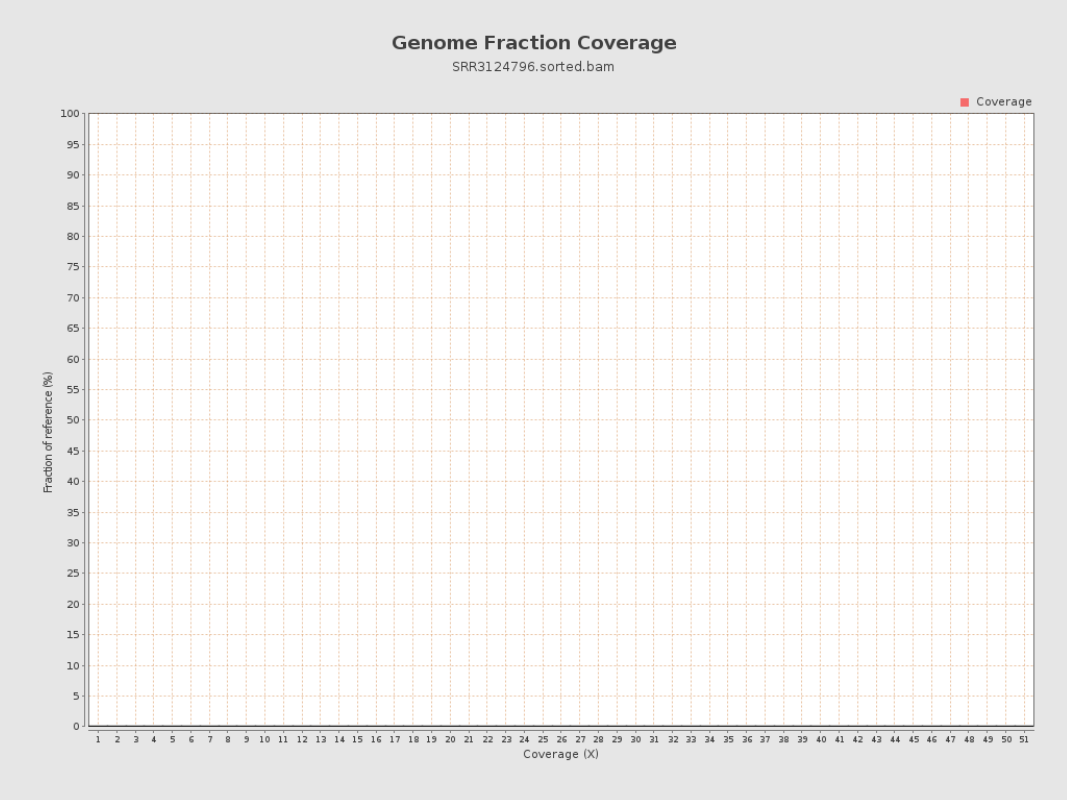
4. Results : Coverage Histogram



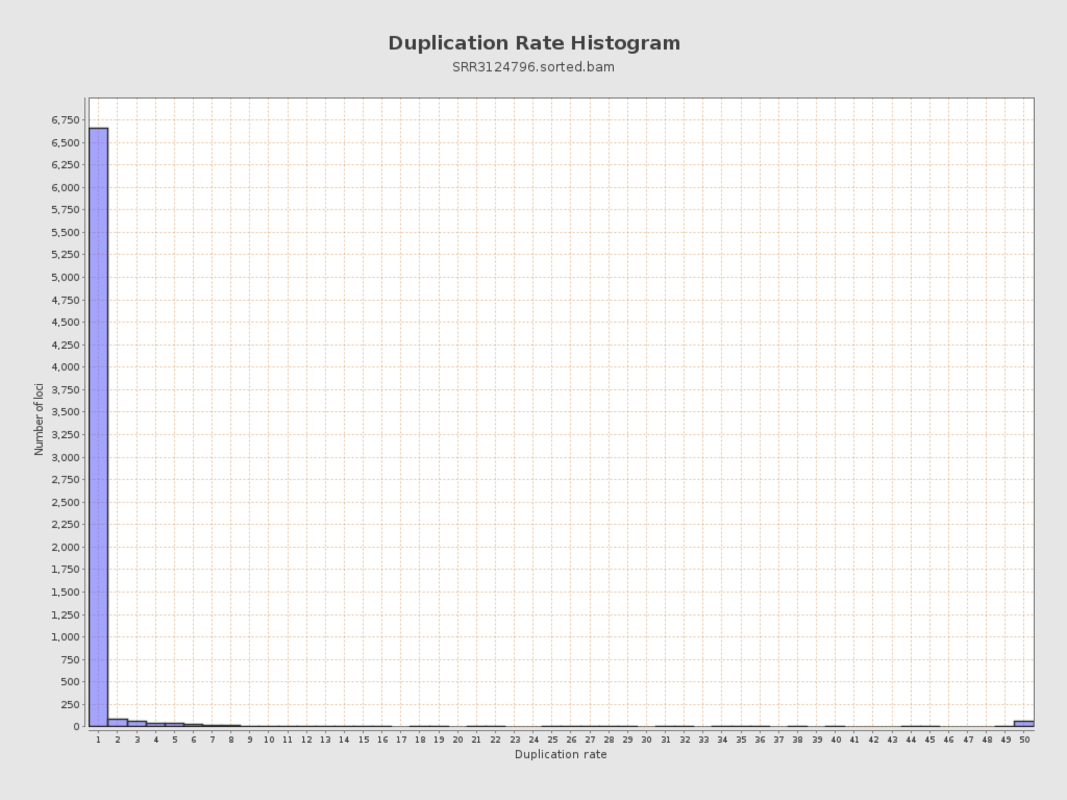
5. Results : Coverage Histogram (0-50X)



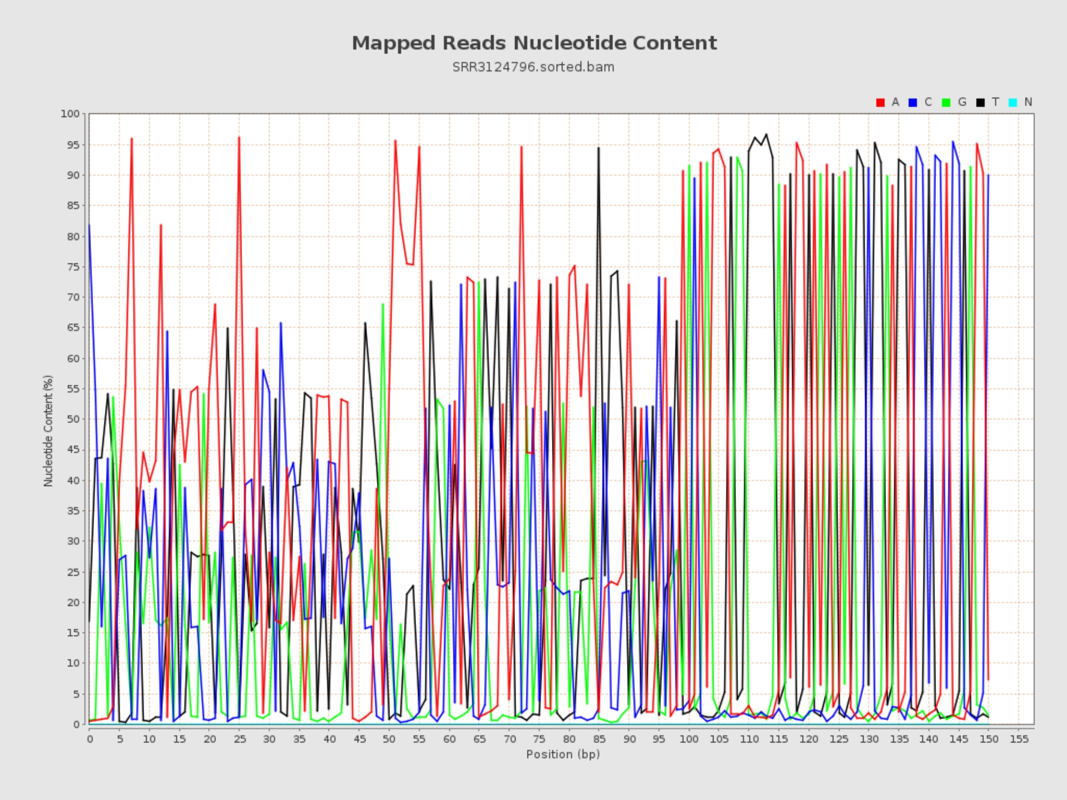
6. Results : Genome Fraction Coverage



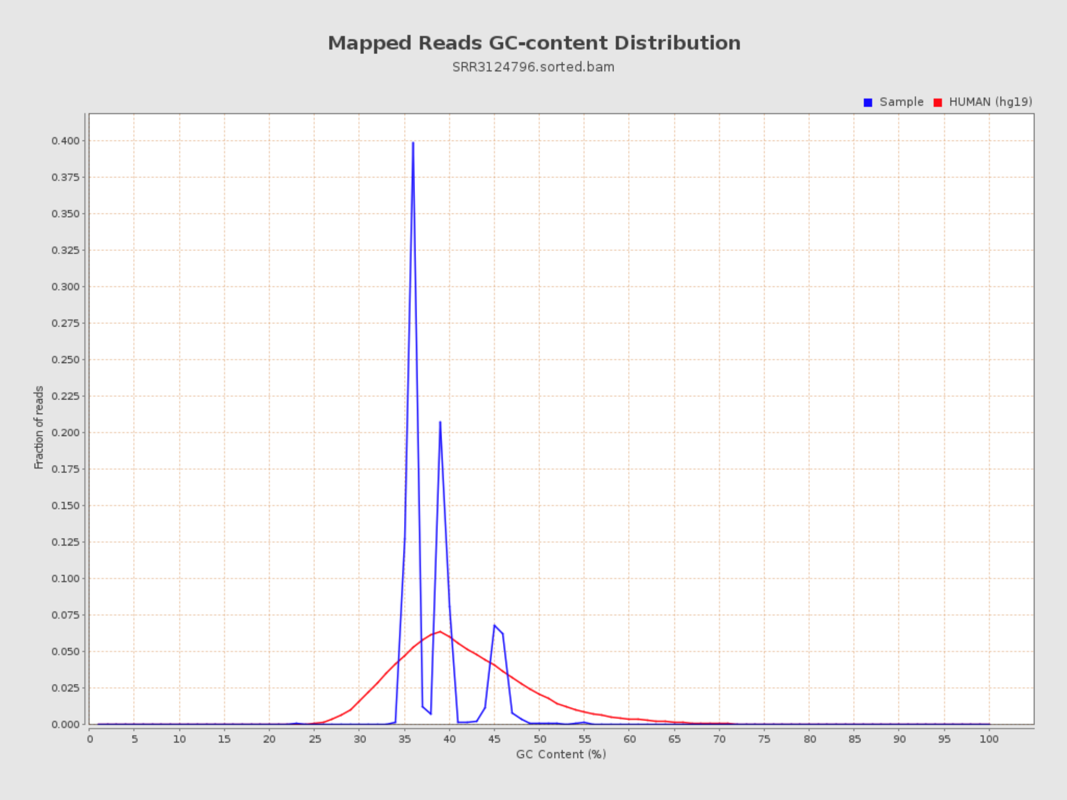
7. Results : Duplication Rate Histogram



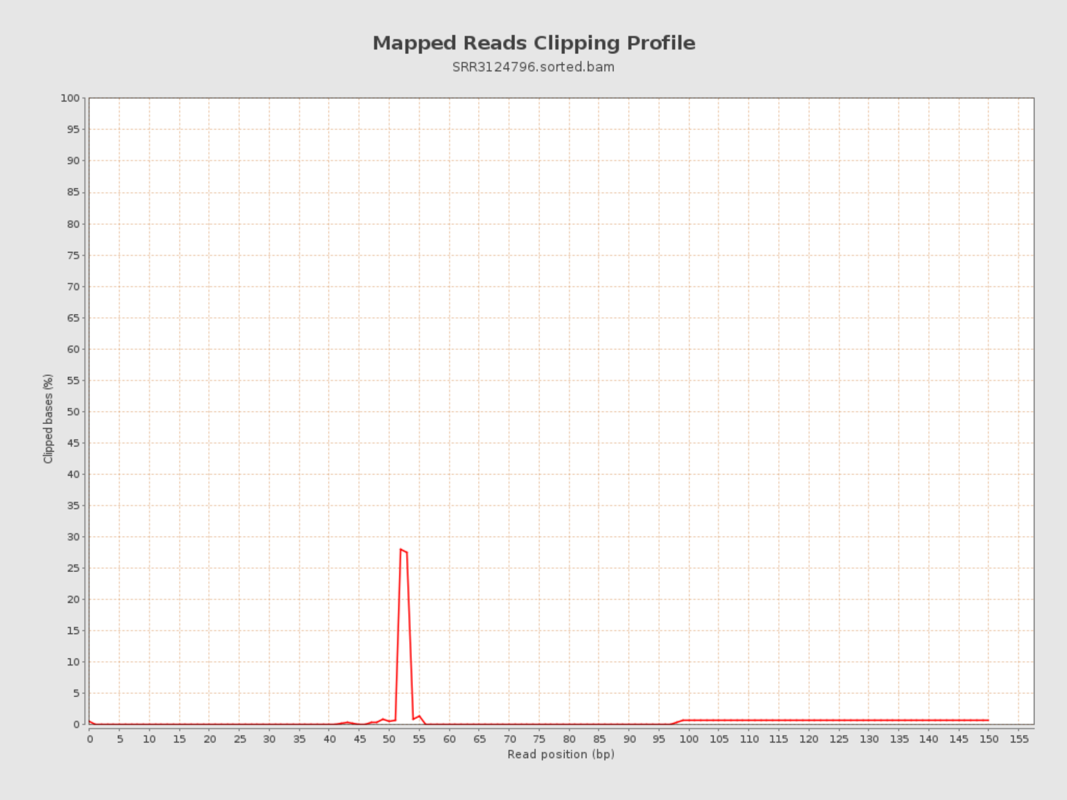
8. Results : Mapped Reads Nucleotide Content



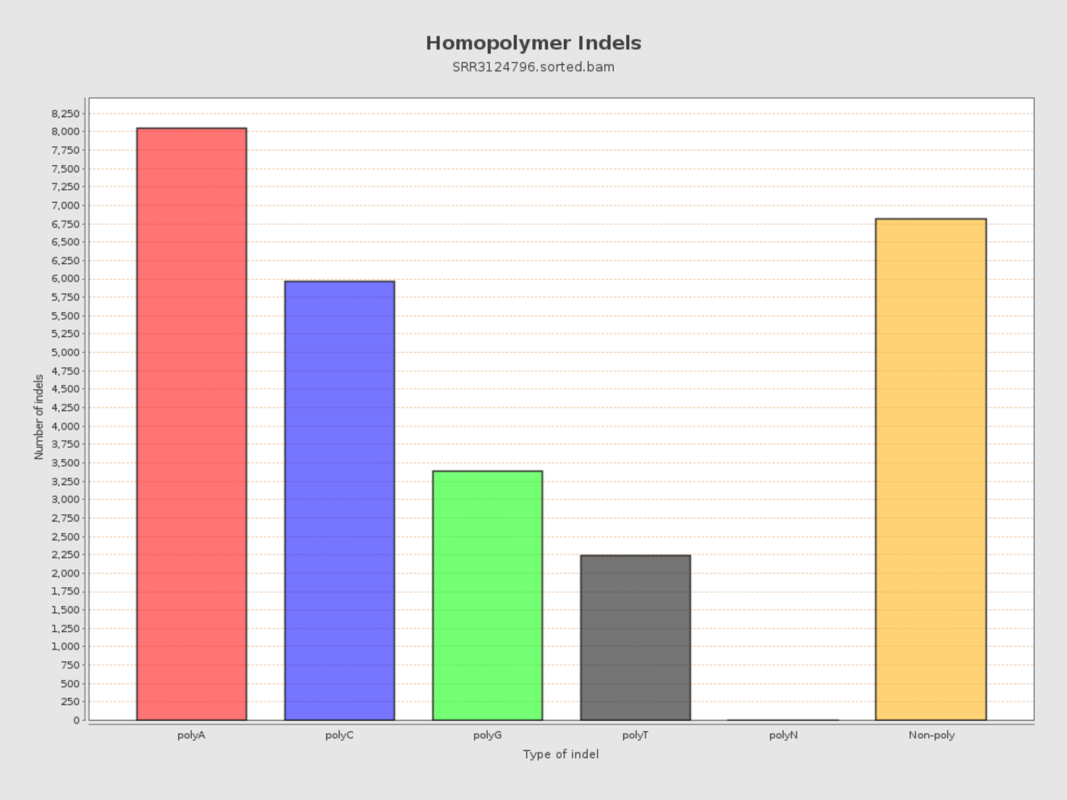
9. Results : Mapped Reads GC-content Distribution



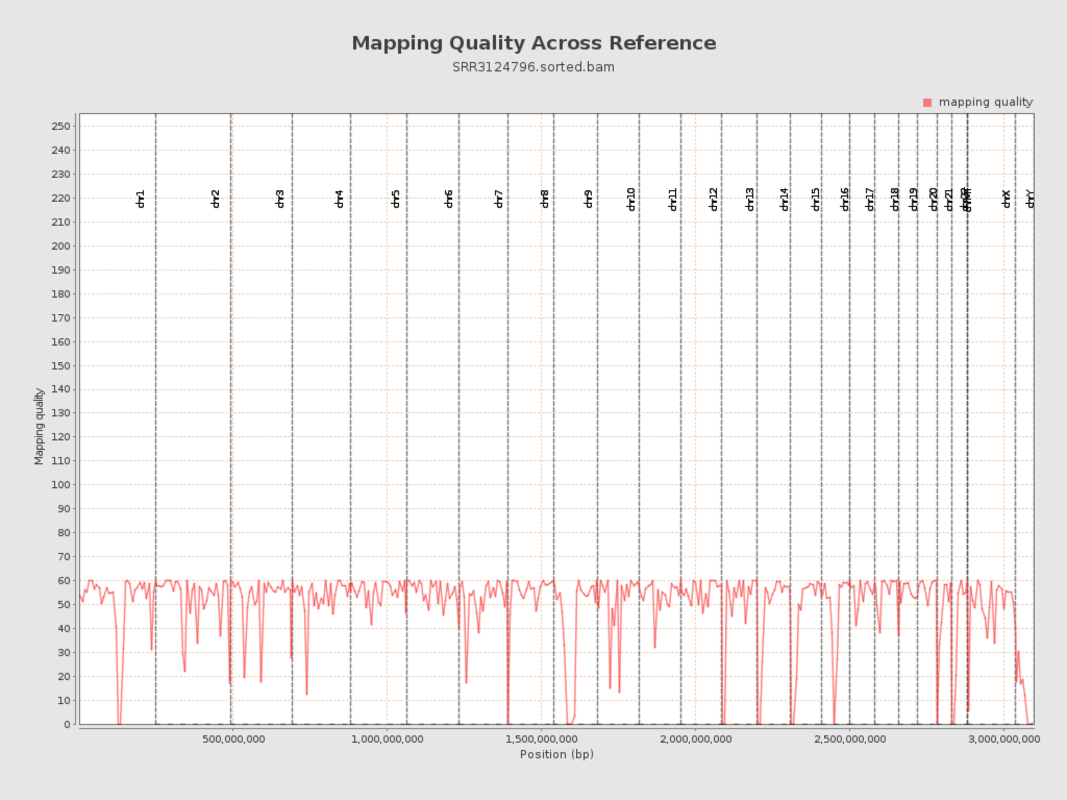
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram