Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:18:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124777.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_SRR3124777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:18:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	654,711
Mapped reads	654,094 / 99.91%
Unmapped reads	617 / 0.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	289,232 / 44.18%
Read min/max/mean length	30 / 151 / 180.85
Duplicated reads (estimated)	940,753 / 143.69%
Duplication rate	30.66%
Clipped reads	619,759 / 94.66%

2.2. ACGT Content

Number/percentage of A's	27,524,643 / 28.04%
Number/percentage of C's	18,176,262 / 18.51%
Number/percentage of T's	31,913,200 / 32.51%
Number/percentage of G's	20,559,843 / 20.94%
Number/percentage of N's	1 / 0%
GC Percentage	39.46%

2.3. Coverage

Mean	0.0317

Standard Deviation	57.638

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

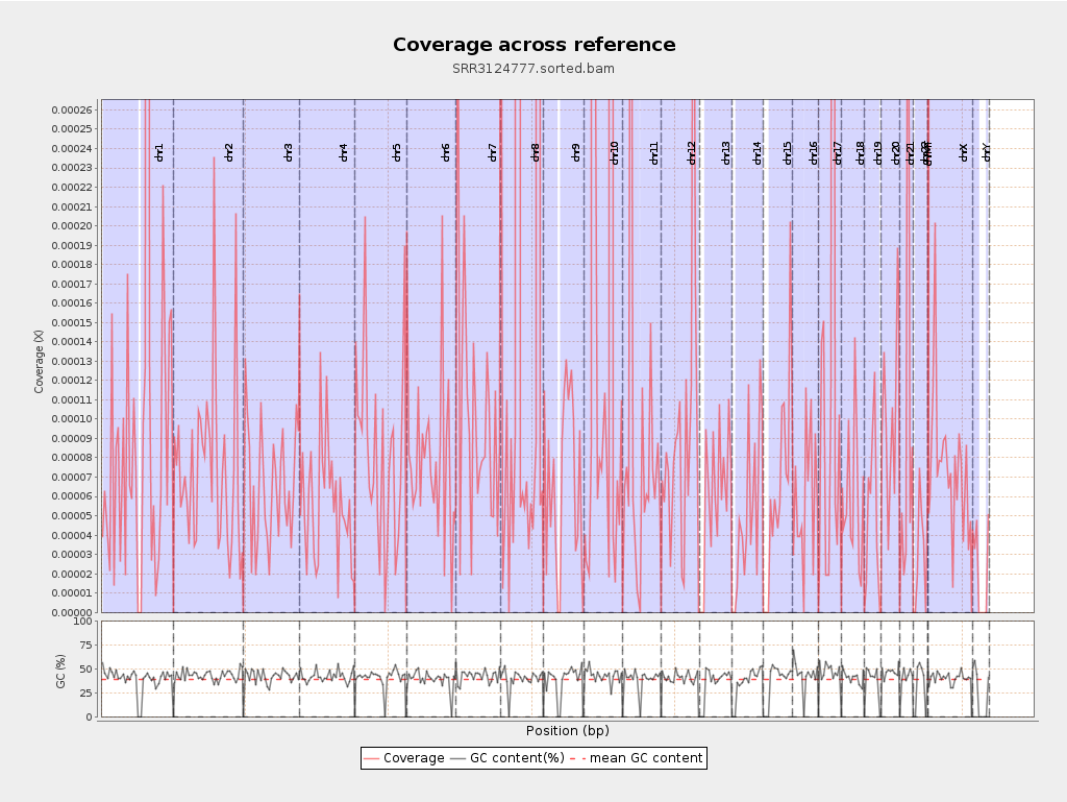
General error rate	0.76%
Mismatches	728,465
Insertions	13,908
Mapped reads with at least one insertion	2.11%
Deletions	53,842
Mapped reads with at least one deletion	7.99%
Homopolymer indels	78.31%

2.6. Chromosome stats

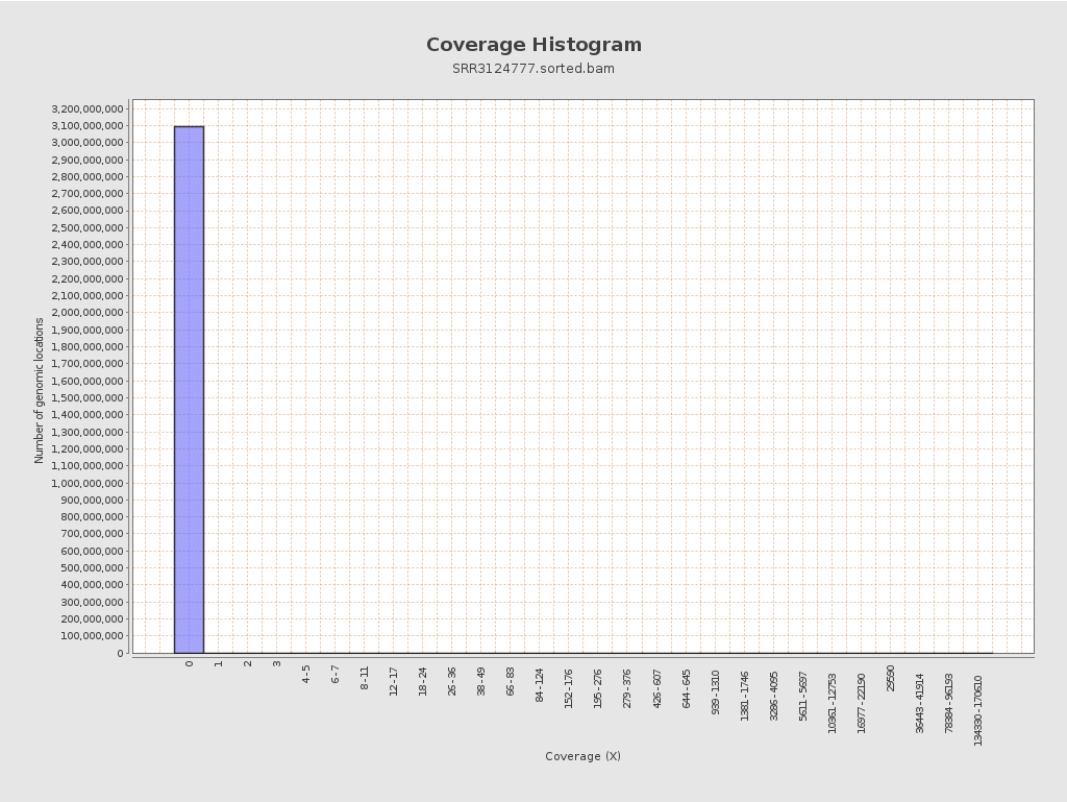
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	143215	0.0006	0.4637
chr2	243199373	18259	0.0001	0.0189
chr3	198022430	12996	0.0001	0.0082
chr4	191154276	10654	0.0001	0.0084
chr5	180915260	14954	0.0001	0.0112
chr6	171115067	13838	0.0001	0.0222
chr7	159138663	16232	0.0001	0.0374

chr8	146364022	85587214	0.5848	258.5855
chr9	141213431	9556	0.0001	0.0082
chr10	135534747	12311460	0.0908	60.5792
chr11	135006516	11995	0.0001	0.0242
chr12	133851895	12937	0.0001	0.0229
chr13	115169878	6680	0.0001	0.0089
chr14	107349540	5478	0.0001	0.008
chr15	102531392	6570	0.0001	0.0108
chr16	90354753	5254	0.0001	0.0076
chr17	81195210	14760	0.0002	0.0878
chr18	78077248	4694	0.0001	0.0087
chr19	59128983	3100	0.0001	0.0083
chr20	63025520	6426	0.0001	0.0108
chr21	48129895	5125	0.0001	0.0334
chr22	51304566	1560	0	0.0055
chrMT	16571	151	0.0091	0.095
chrX	155270560	11478	0.0001	0.0151
chrY	59373566	1238	0	0.0045

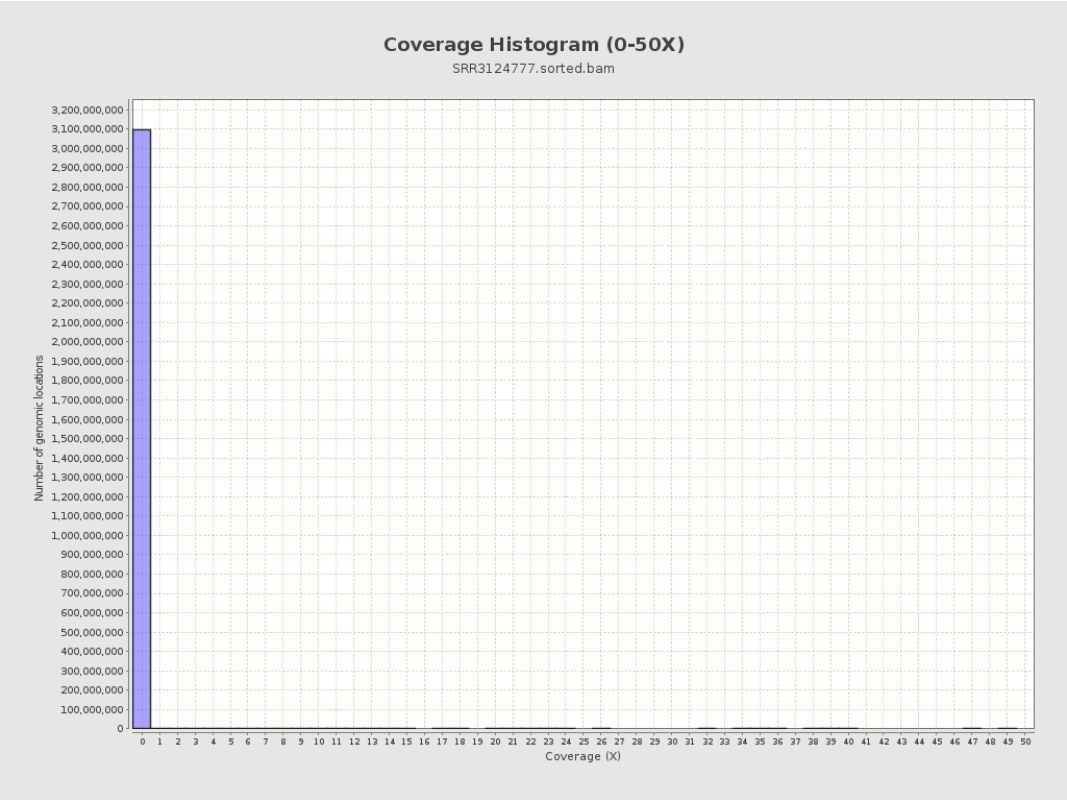
3. Results : Coverage across reference



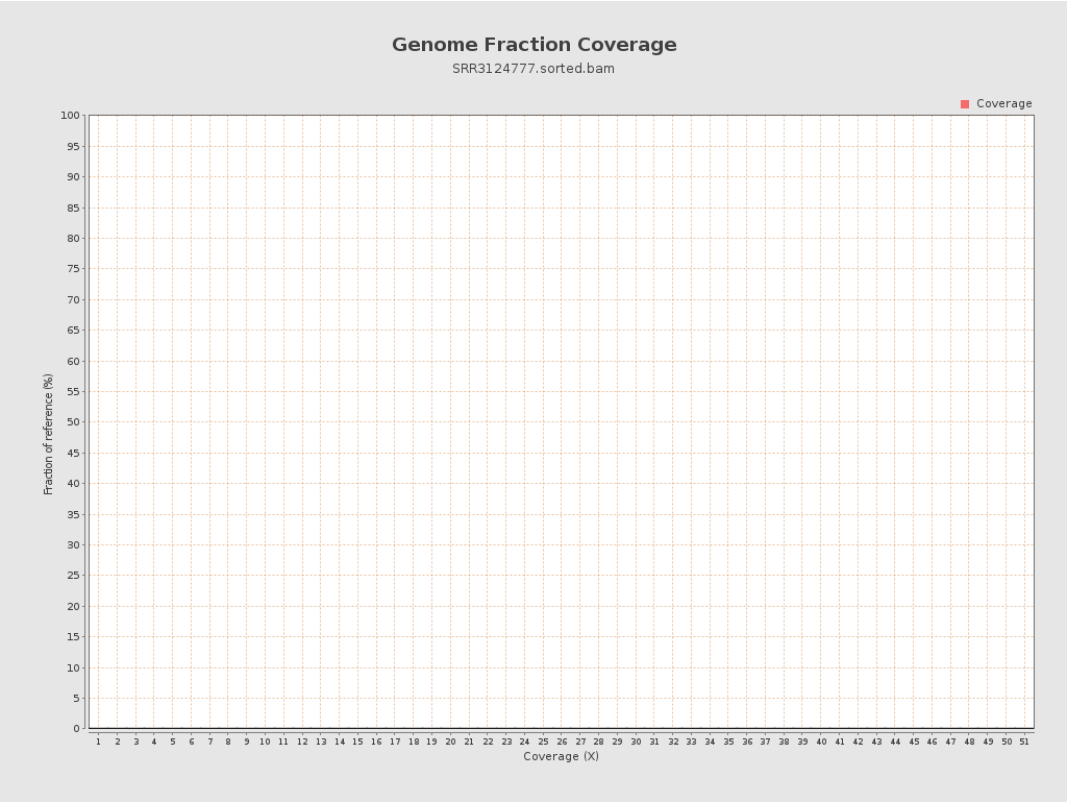
4. Results : Coverage Histogram



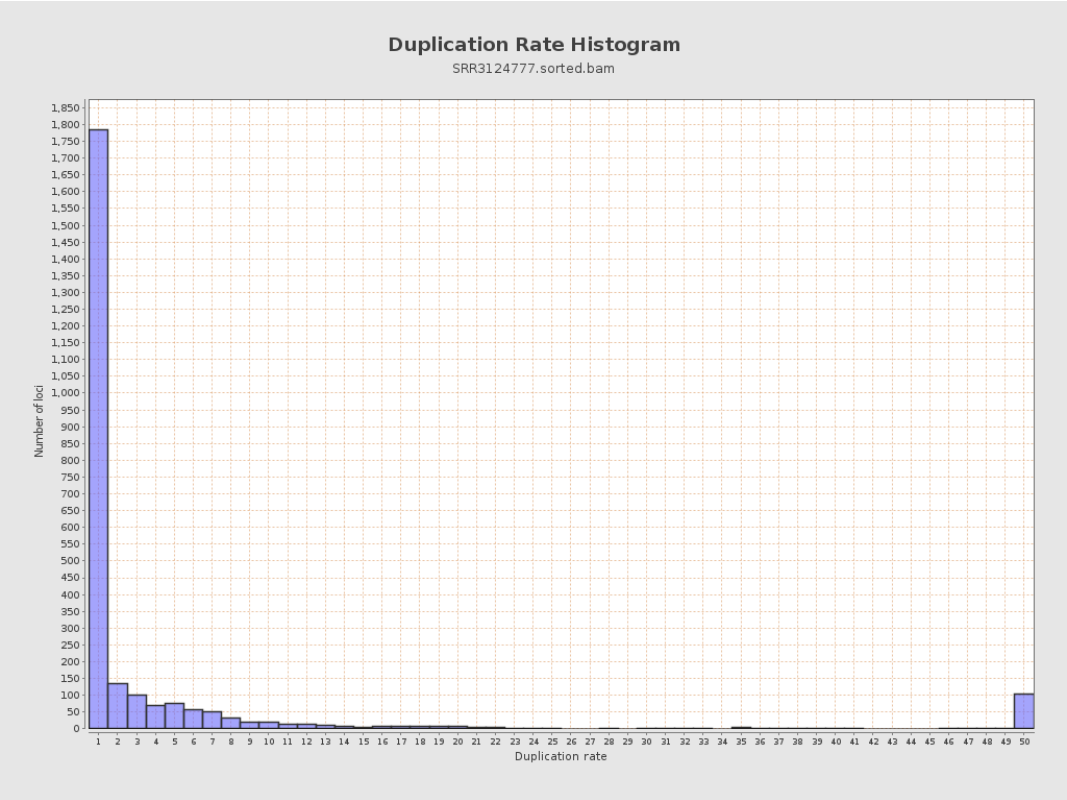
5. Results : Coverage Histogram (0-50X)



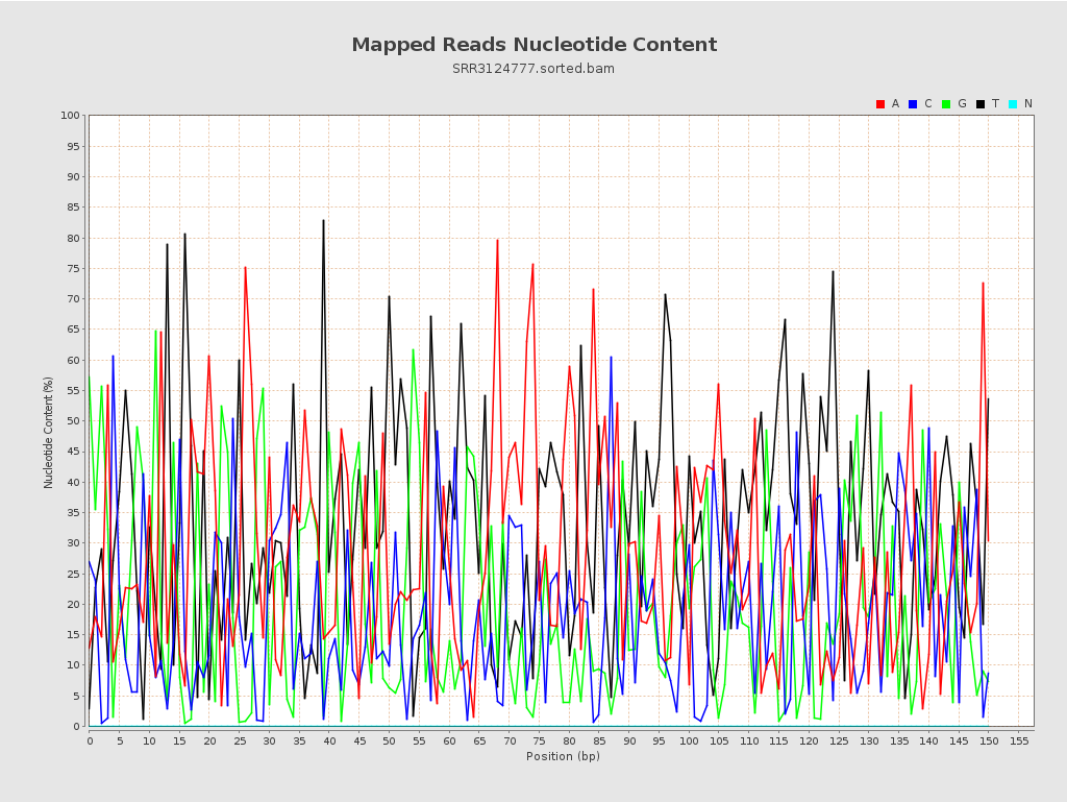
6. Results : Genome Fraction Coverage



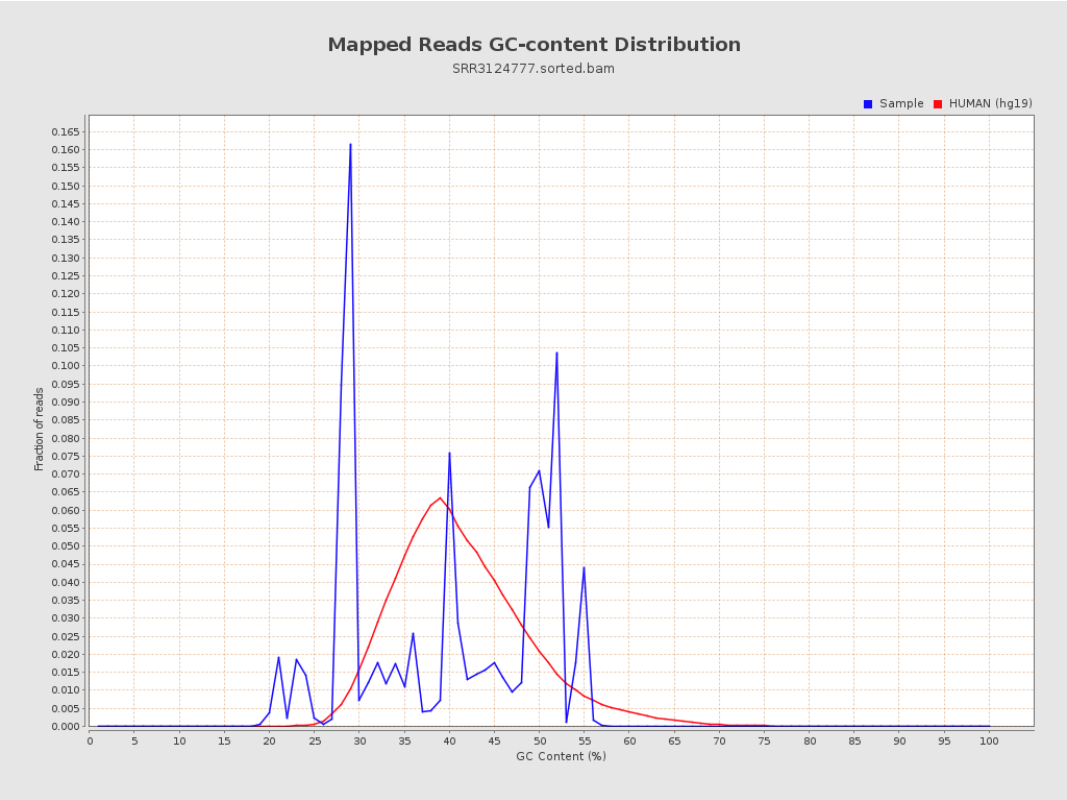
7. Results : Duplication Rate Histogram



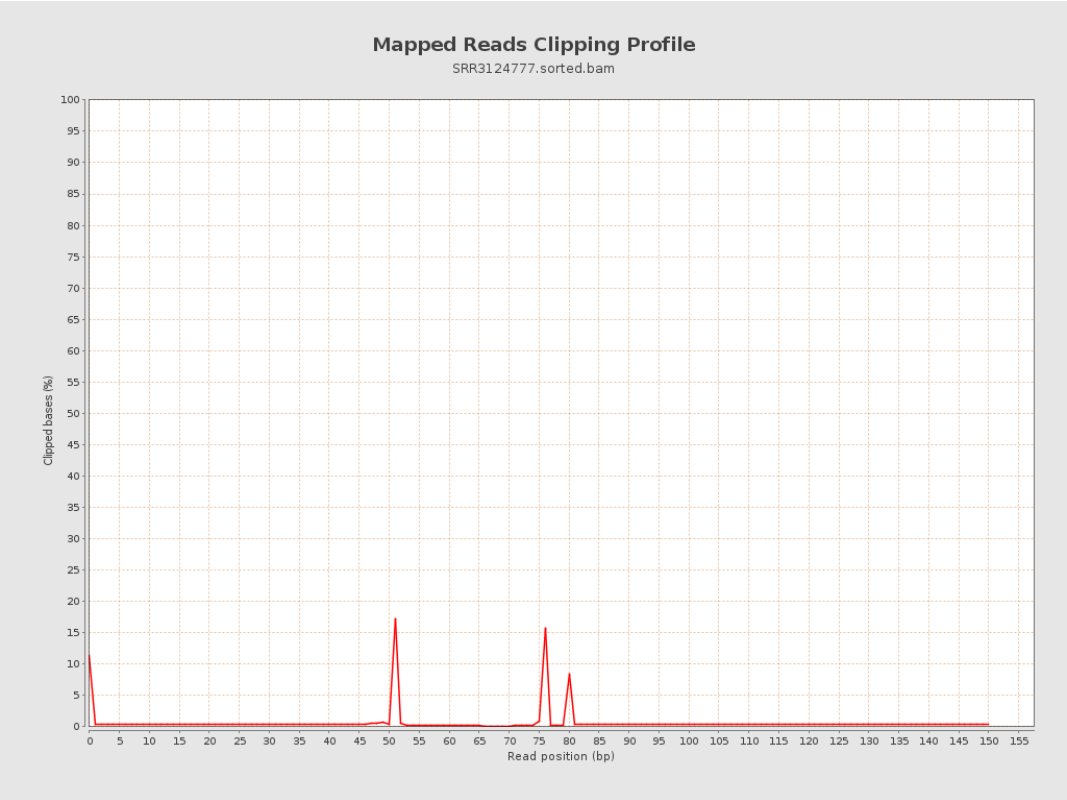
8. Results : Mapped Reads Nucleotide Content



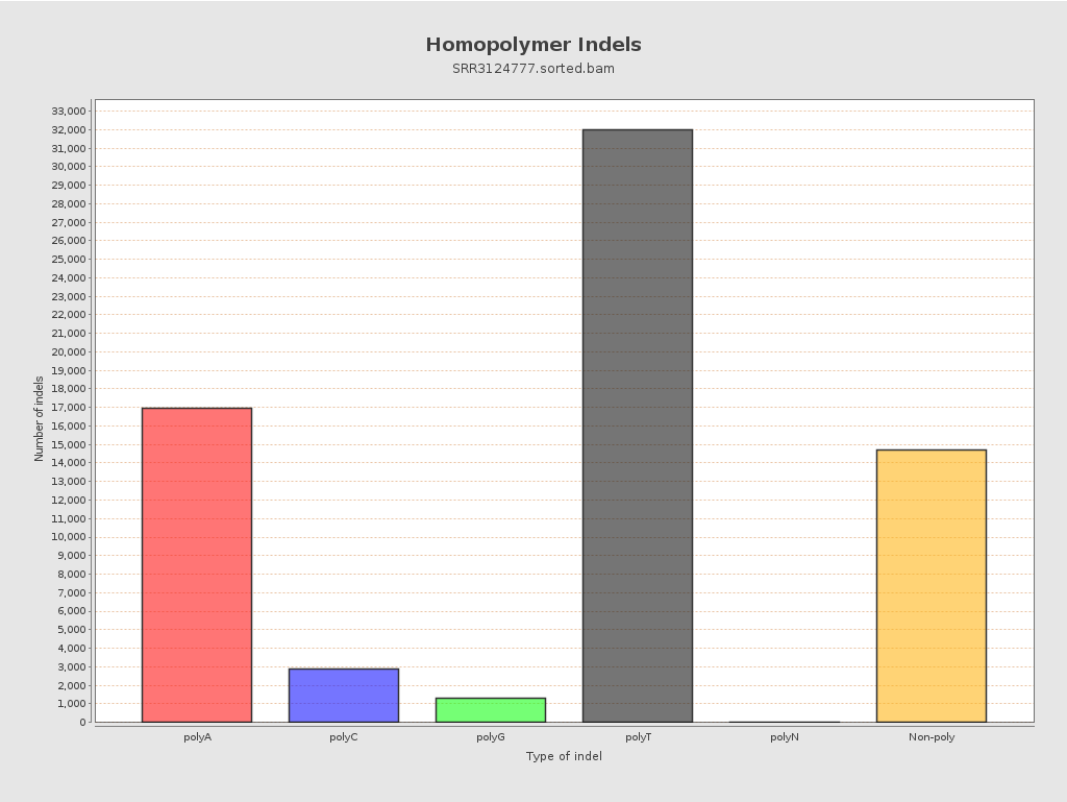
9. Results : Mapped Reads GC-content Distribution



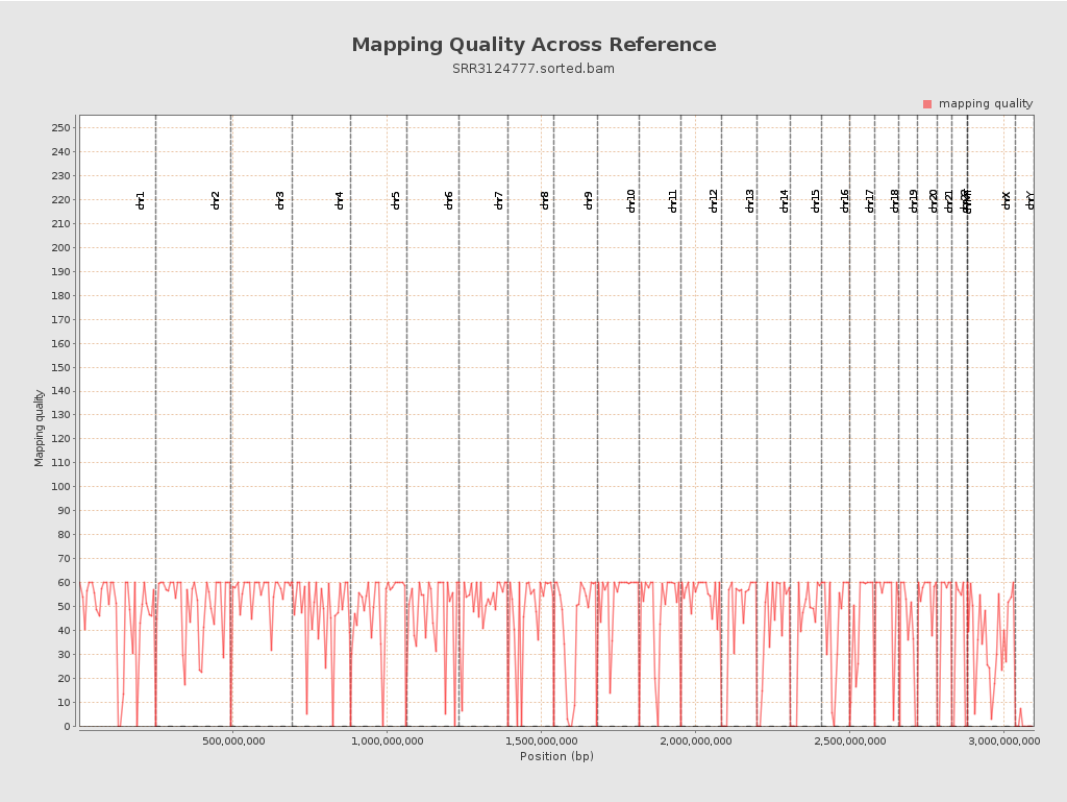
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram