Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:22:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124779.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_SRR3124779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:22:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	648,198
Mapped reads	647,655 / 99.92%
Unmapped reads	543 / 0.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	262,666 / 40.52%
Read min/max/mean length	30 / 151 / 178.08
Duplicated reads (estimated)	907,499 / 140%
Duplication rate	31.79%
Clipped reads	576,533 / 88.94%

2.2. ACGT Content

Number/percentage of A's	28,011,230 / 28.92%
Number/percentage of C's	18,014,726 / 18.6%
Number/percentage of T's	31,239,165 / 32.26%
Number/percentage of G's	19,577,302 / 20.22%
Number/percentage of N's	0 / 0%
GC Percentage	38.82%

2.3. Coverage

Mean	0.0313

Standard Deviation	49.9982

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

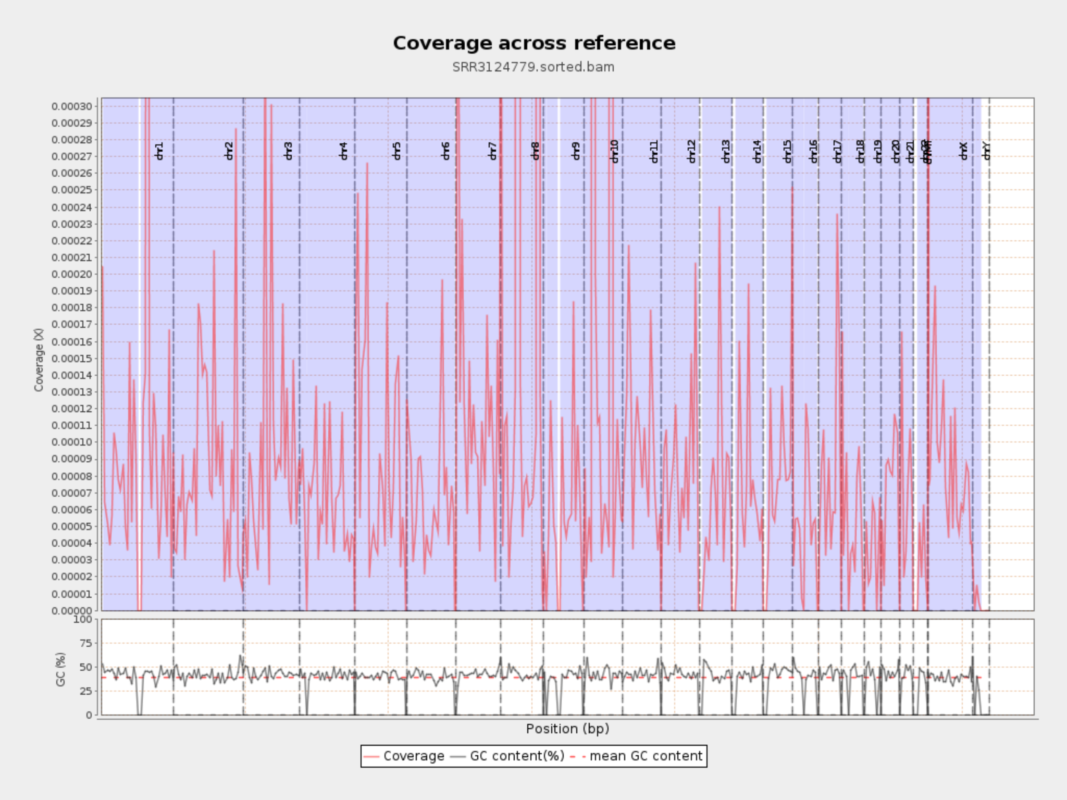
General error rate	0.76%
Mismatches	711,455
Insertions	26,981
Mapped reads with at least one insertion	4.15%
Deletions	37,040
Mapped reads with at least one deletion	5.59%
Homopolymer indels	81%

2.6. Chromosome stats

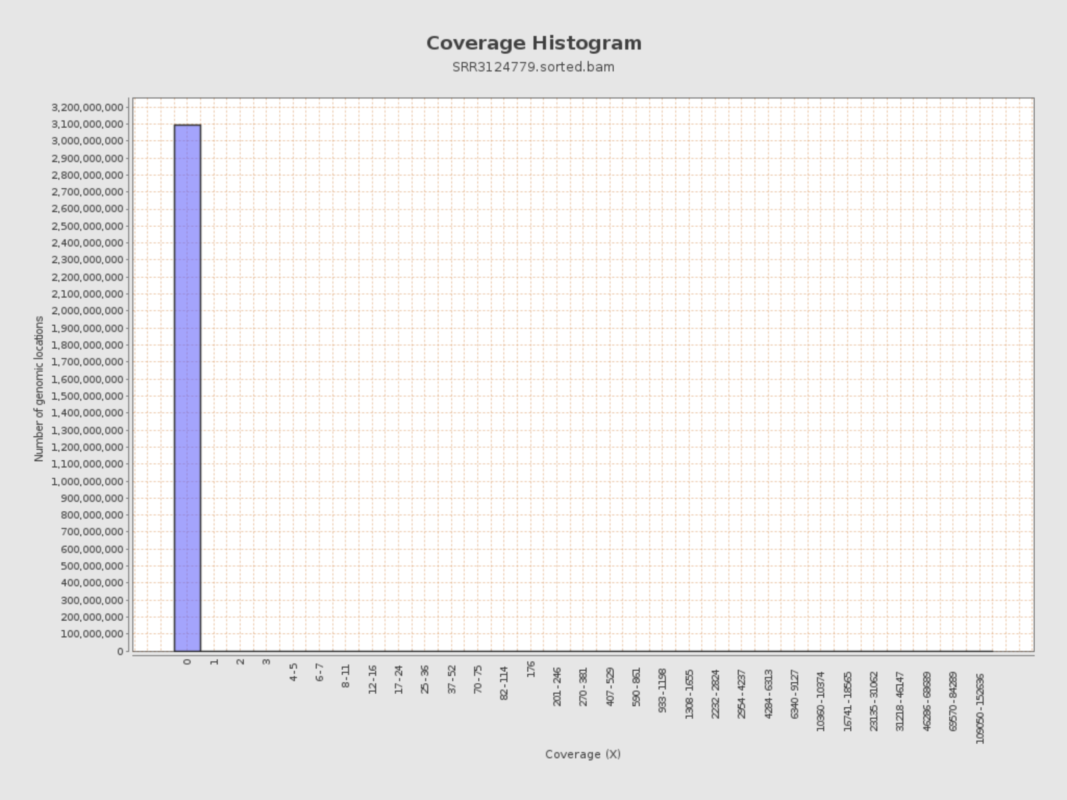
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30611	0.0001	0.0404
chr2	243199373	21316	0.0001	0.0217
chr3	198022430	19160	0.0001	0.0234
chr4	191154276	12584	0.0001	0.0116
chr5	180915260	16953	0.0001	0.0102
chr6	171115067	12070	0.0001	0.015
chr7	159138663	19908	0.0001	0.0533

chr8	146364022	81486828	0.5567	220.586
chr9	141213431	8163	0.0001	0.0082
chr10	135534747	15165069	0.1119	67.4617
chr11	135006516	13487	0.0001	0.0103
chr12	133851895	11399	0.0001	0.0152
chr13	115169878	7765	0.0001	0.0164
chr14	107349540	7078	0.0001	0.0121
chr15	102531392	7726	0.0001	0.0087
chr16	90354753	4327	0	0.0069
chr17	81195210	7017	0.0001	0.0182
chr18	78077248	4135	0.0001	0.0073
chr19	59128983	2160	0	0.0106
chr20	63025520	4908	0.0001	0.0104
chr21	48129895	3442	0.0001	0.0158
chr22	51304566	1195	0	0.0048
chrMT	16571	285	0.0172	0.13
chrX	155270560	13594	0.0001	0.0164
chrY	59373566	305	0	0.0023

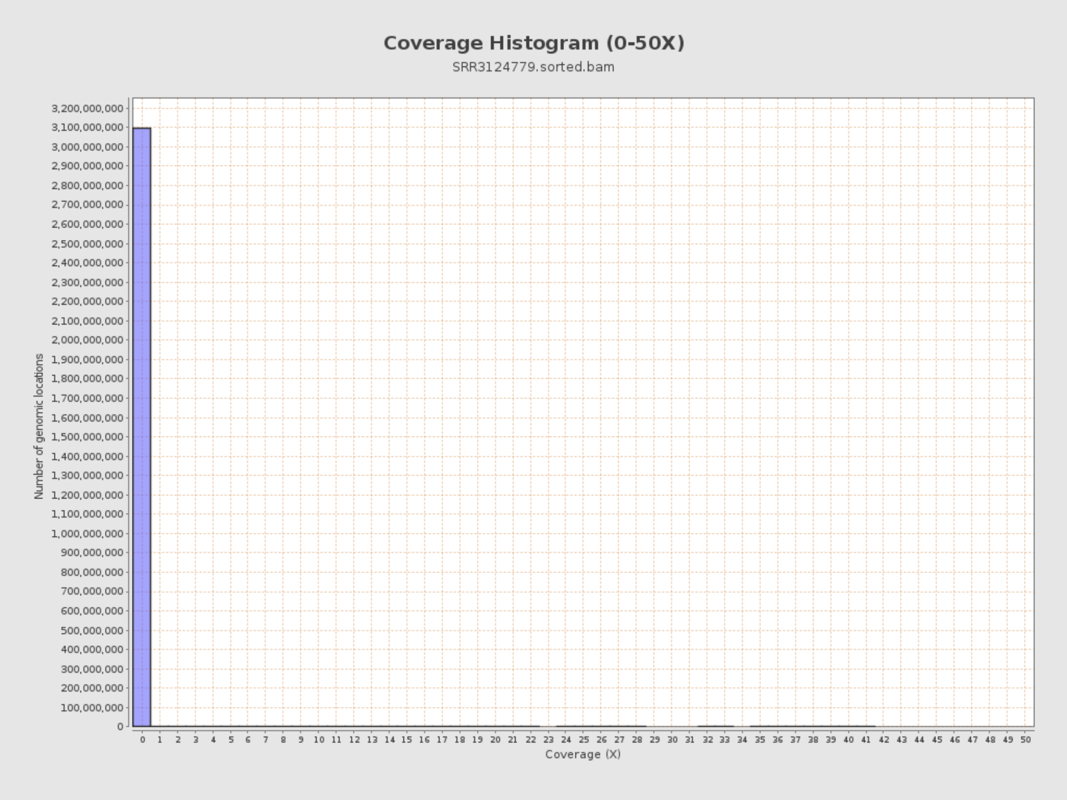
3. Results : Coverage across reference



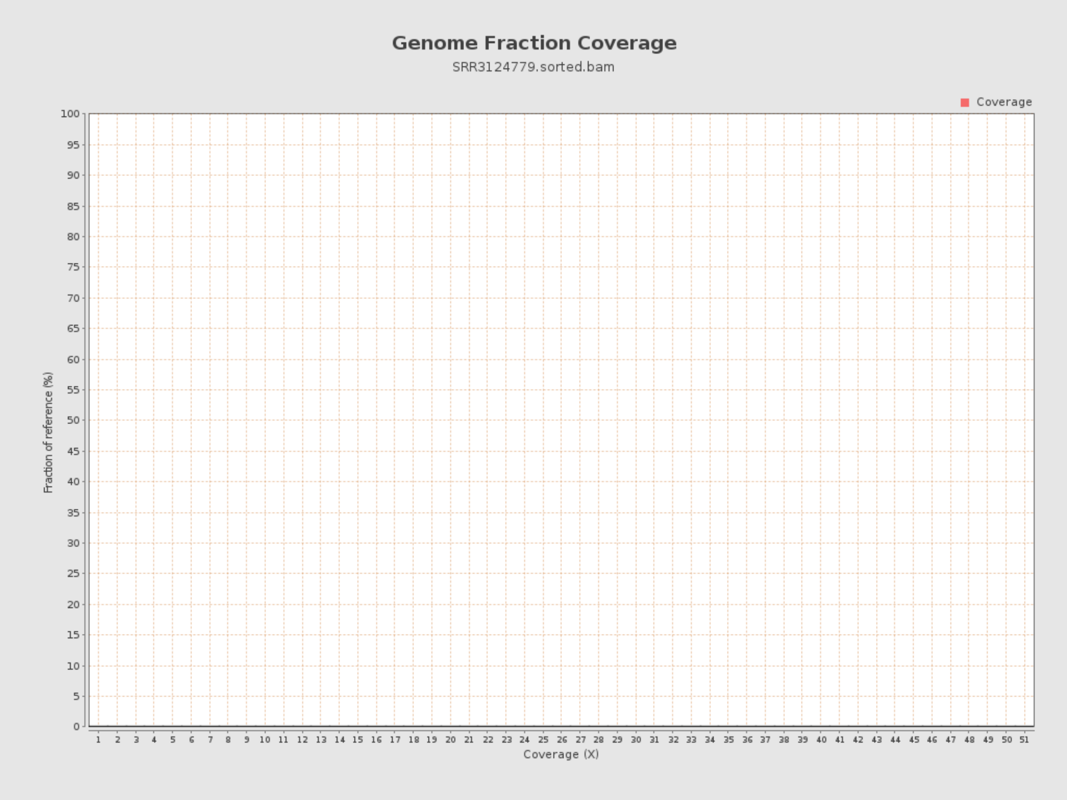
4. Results : Coverage Histogram



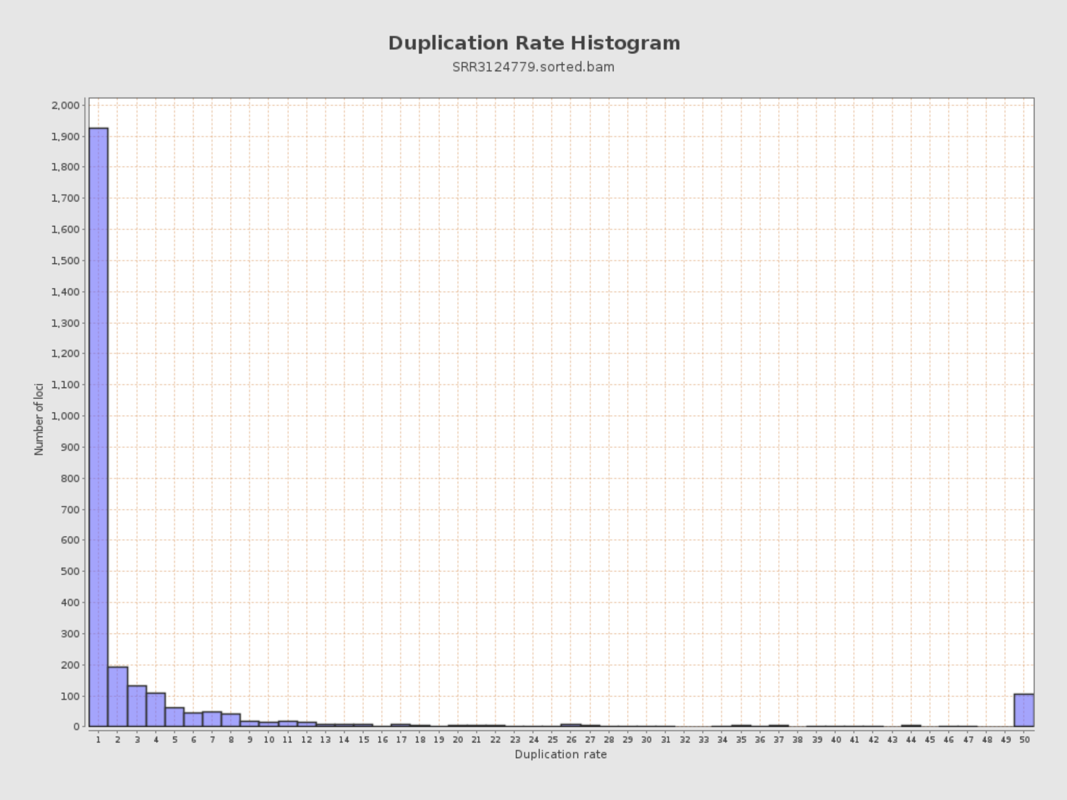
5. Results : Coverage Histogram (0-50X)



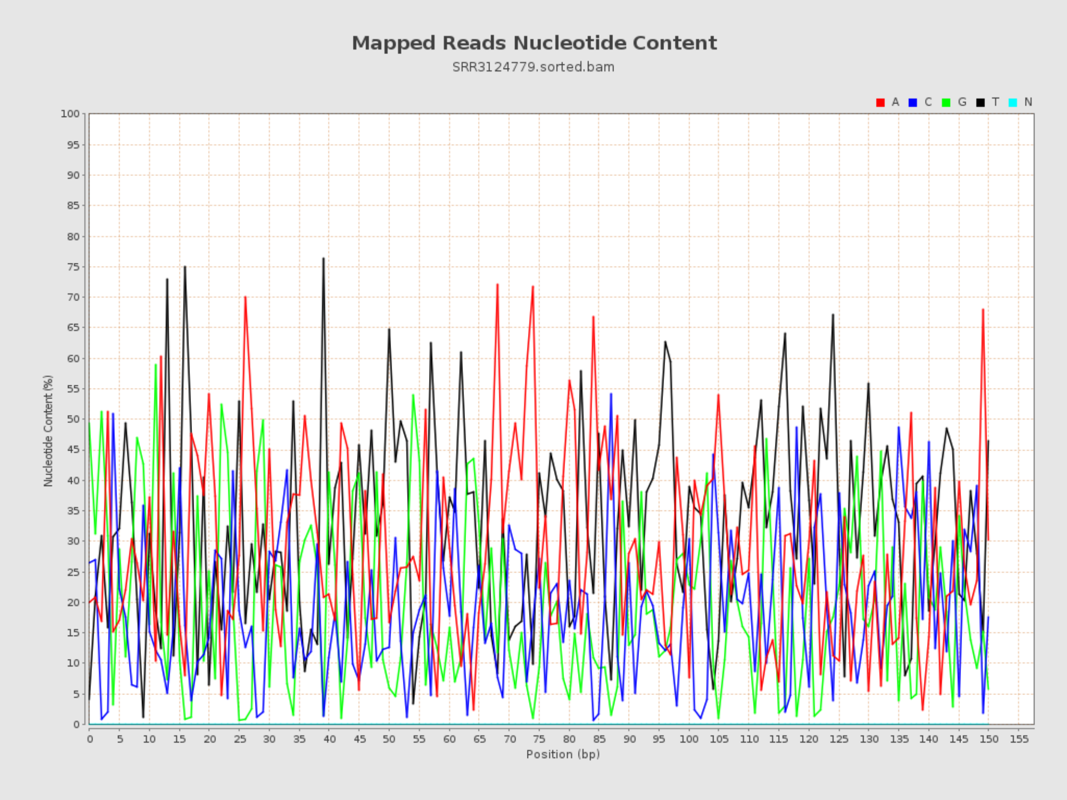
6. Results : Genome Fraction Coverage



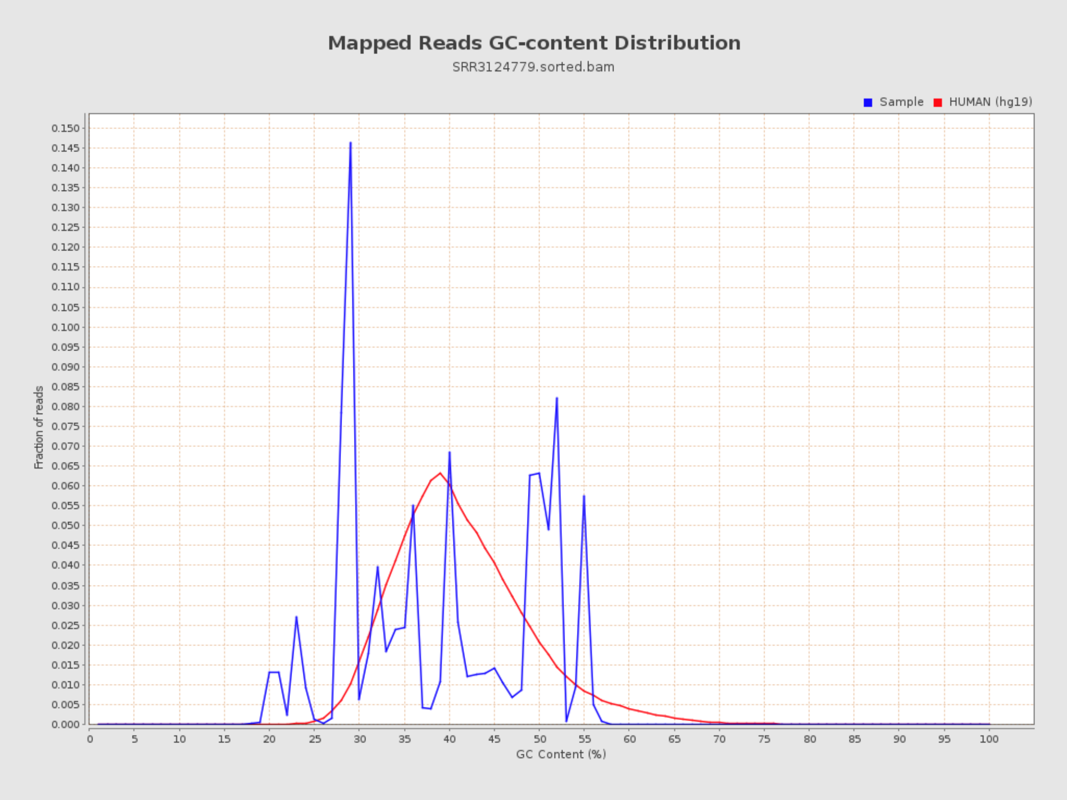
7. Results : Duplication Rate Histogram



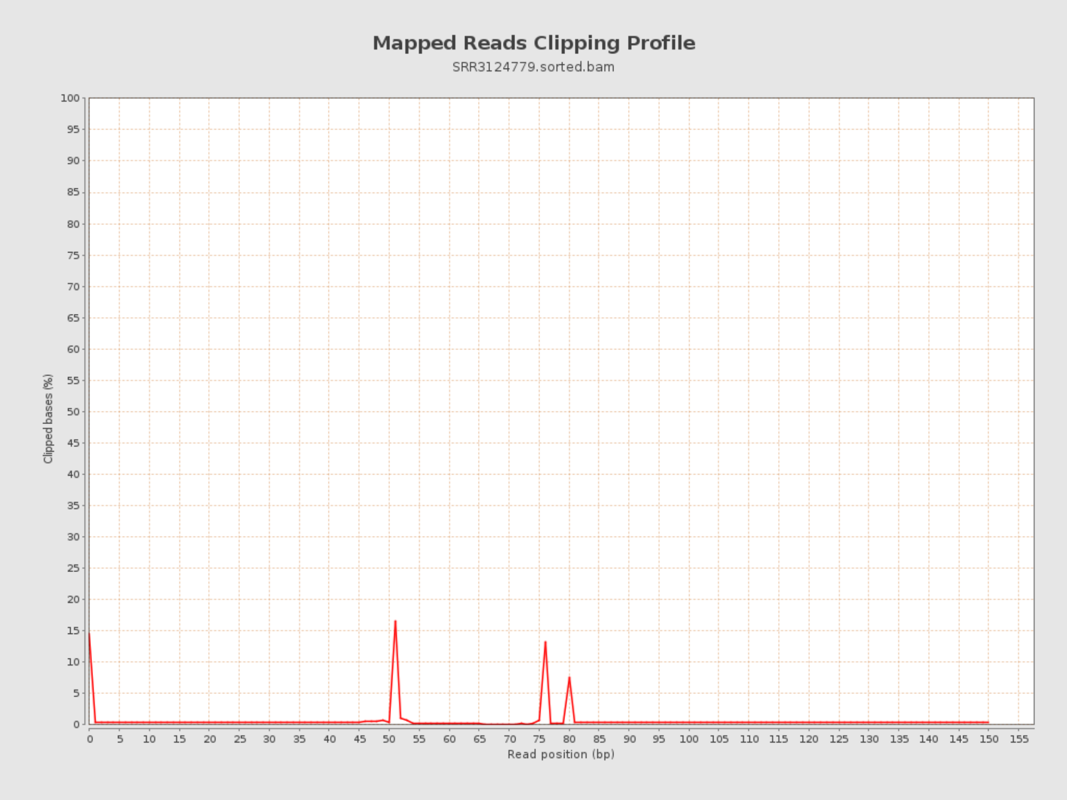
8. Results : Mapped Reads Nucleotide Content



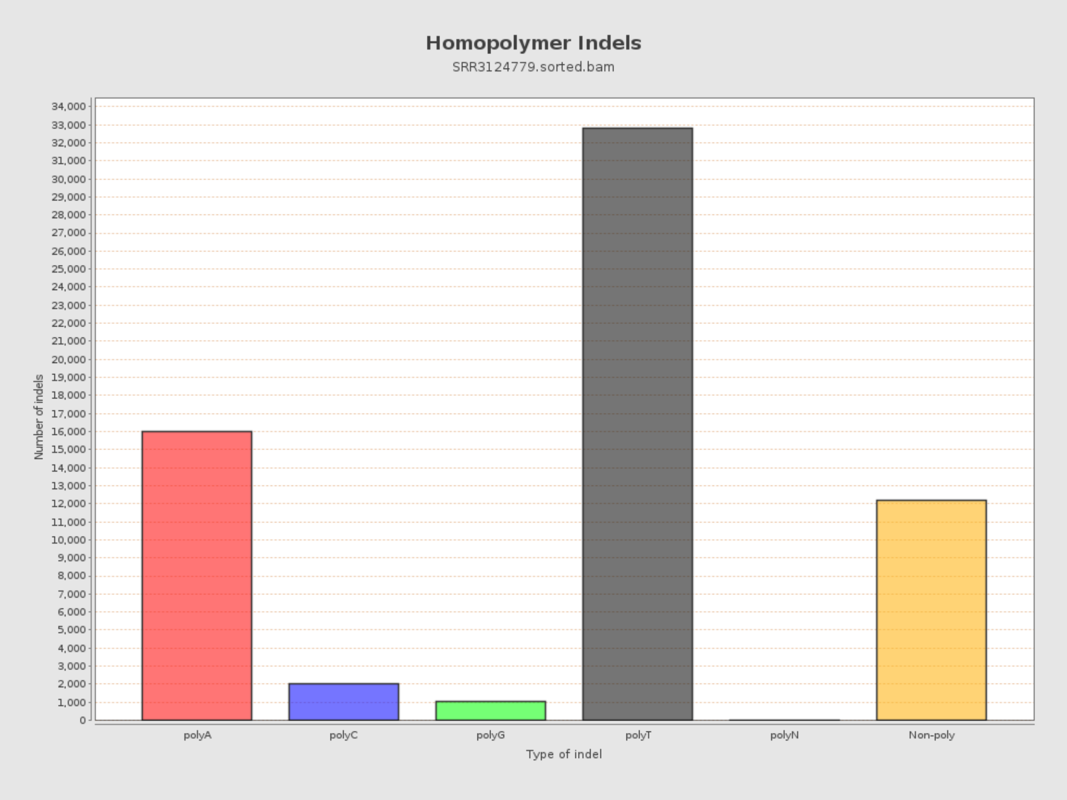
9. Results : Mapped Reads GC-content Distribution



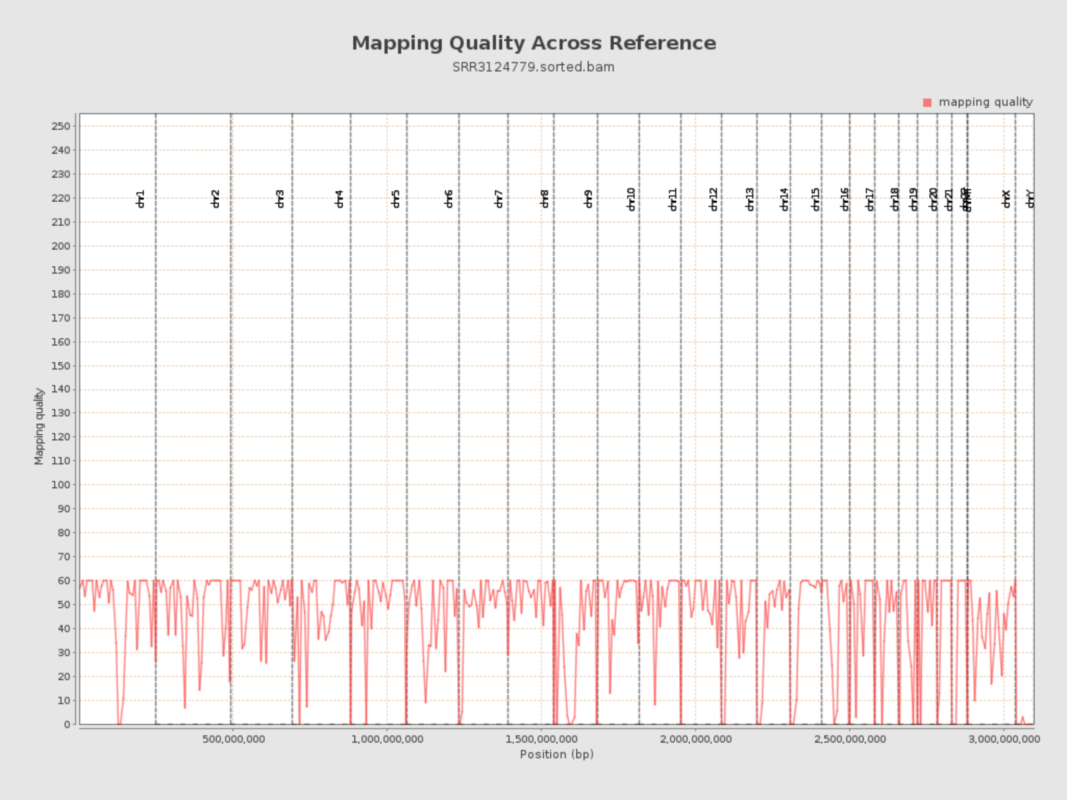
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram