Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:30:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124784.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_SRR3124784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124784.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:30:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124784.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	773,471
Mapped reads	772,461 / 99.87%
Unmapped reads	1,010 / 0.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	360,445 / 46.6%
Read min/max/mean length	30 / 151 / 182.5
Duplicated reads (estimated)	1,130,827 / 146.2%
Duplication rate	28.76%
Clipped reads	746,072 / 96.46%

2.2. ACGT Content

Number/percentage of A's	32,426,830 / 27.88%
Number/percentage of C's	21,403,097 / 18.4%
Number/percentage of T's	37,656,116 / 32.37%
Number/percentage of G's	24,827,805 / 21.35%
Number/percentage of N's	0 / 0%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0376

Standard Deviation	70.562

2.4. Mapping Quality

Mean Mapping Quality	43.11

2.5. Mismatches and indels

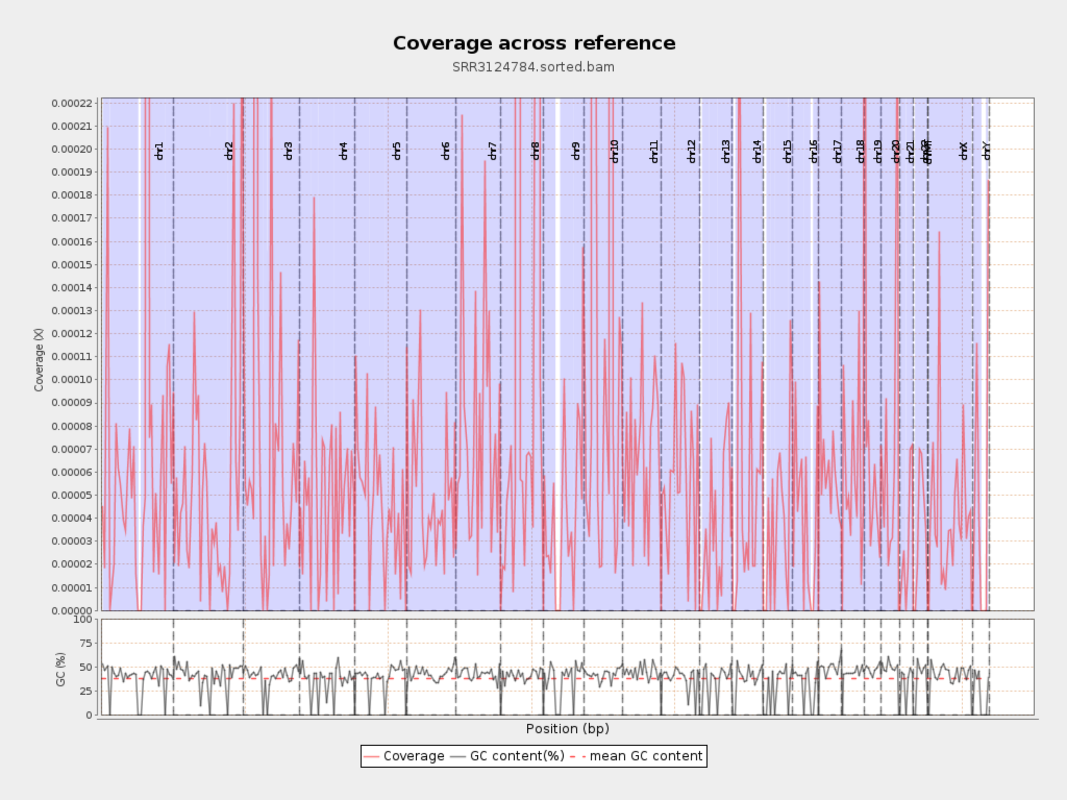
General error rate	0.78%
Mismatches	890,194
Insertions	16,518
Mapped reads with at least one insertion	2.12%
Deletions	51,793
Mapped reads with at least one deletion	6.46%
Homopolymer indels	80.17%

2.6. Chromosome stats

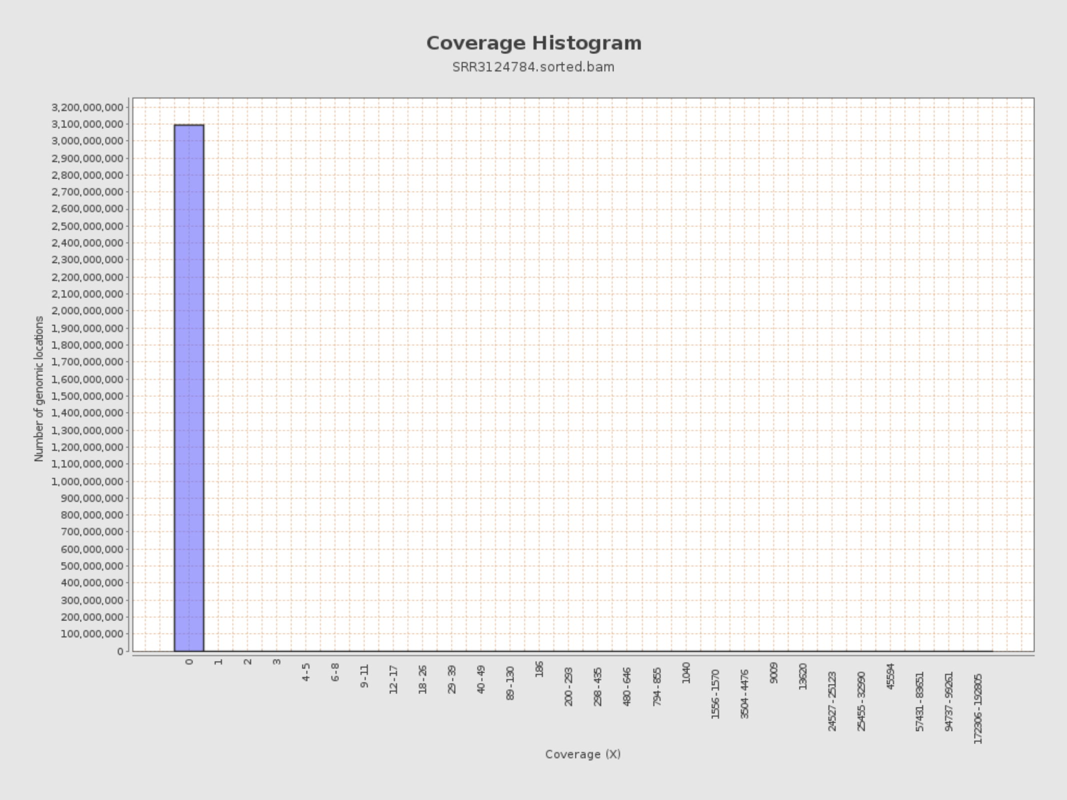
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	110513	0.0004	0.3637
chr2	243199373	13502	0.0001	0.0182
chr3	198022430	22450	0.0001	0.111
chr4	191154276	9737	0.0001	0.0072
chr5	180915260	8552	0	0.0069
chr6	171115067	8529	0	0.01
chr7	159138663	12540	0.0001	0.0192

chr8	146364022	86174680	0.5888	305.7611
chr9	141213431	5526	0	0.0063
chr10	135534747	29935228	0.2209	112.9727
chr11	135006516	9103	0.0001	0.0119
chr12	133851895	7885	0.0001	0.0077
chr13	115169878	4032	0	0.0059
chr14	107349540	6295	0.0001	0.0313
chr15	102531392	3919	0	0.0092
chr16	90354753	3648	0	0.0063
chr17	81195210	5158	0.0001	0.0082
chr18	78077248	4555	0.0001	0.0076
chr19	59128983	4286	0.0001	0.0124
chr20	63025520	4643	0.0001	0.0139
chr21	48129895	1349	0	0.0053
chr22	51304566	1892	0	0.0061
chrMT	16571	0	0	0
chrX	155270560	6540	0	0.0087
chrY	59373566	3023	0.0001	0.0072

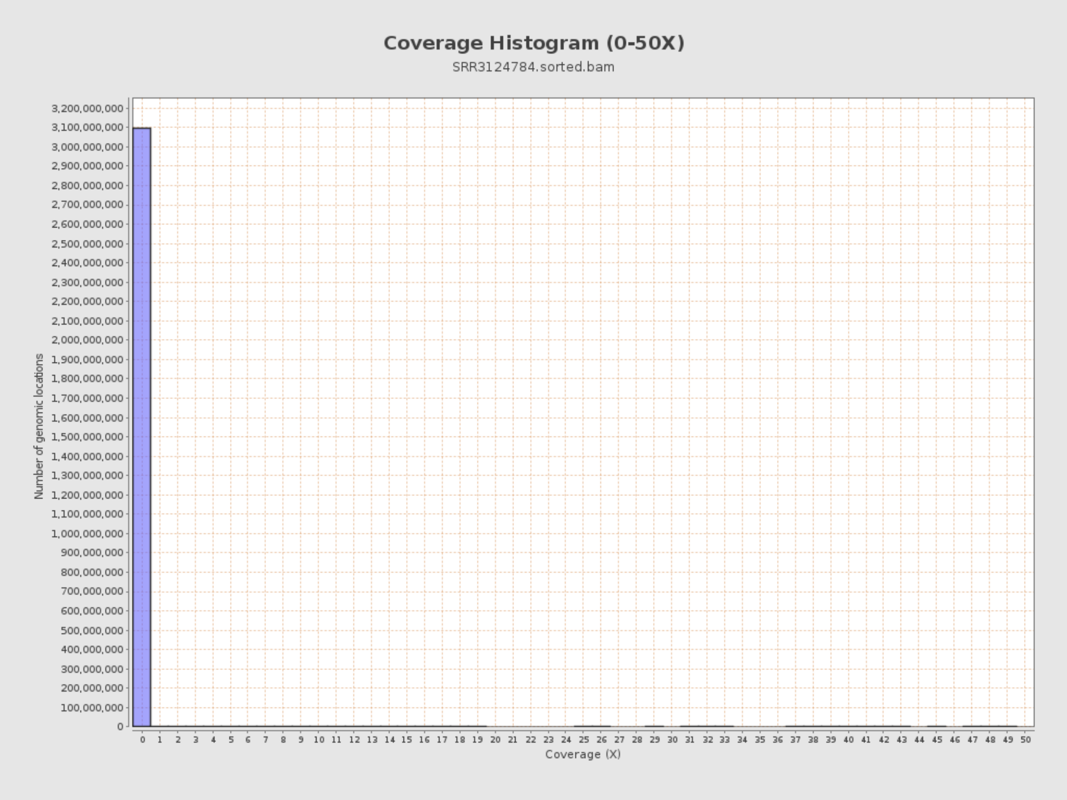
3. Results : Coverage across reference



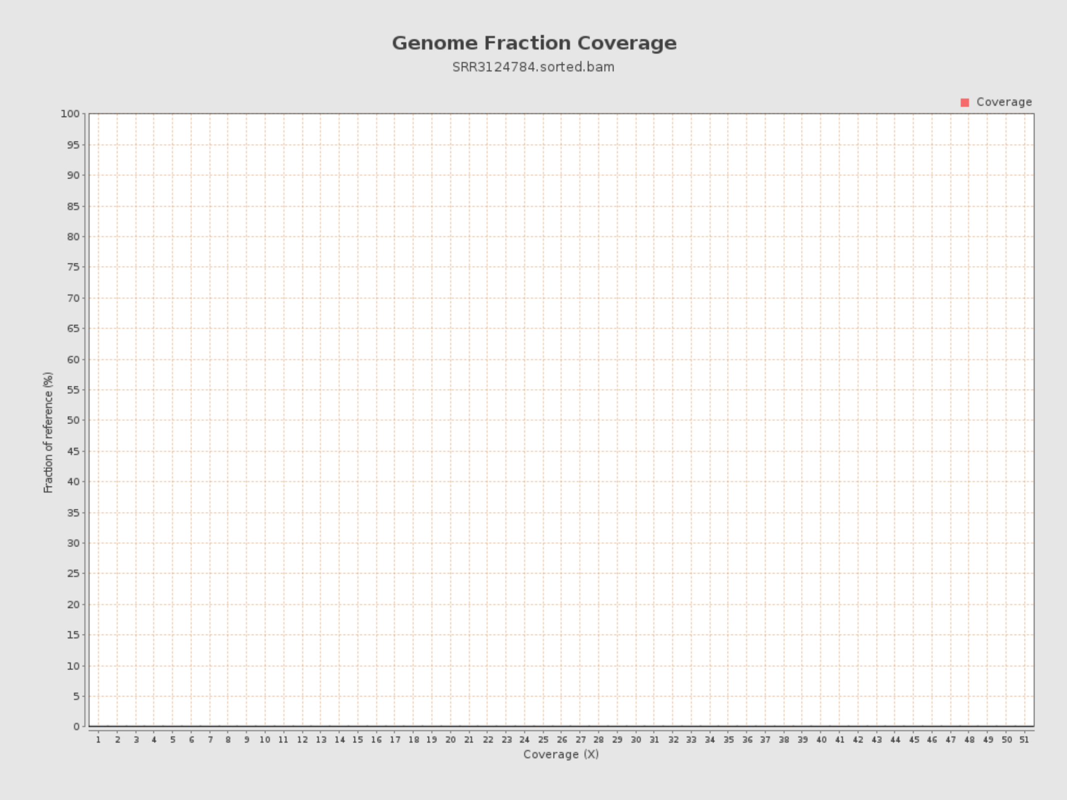
4. Results : Coverage Histogram



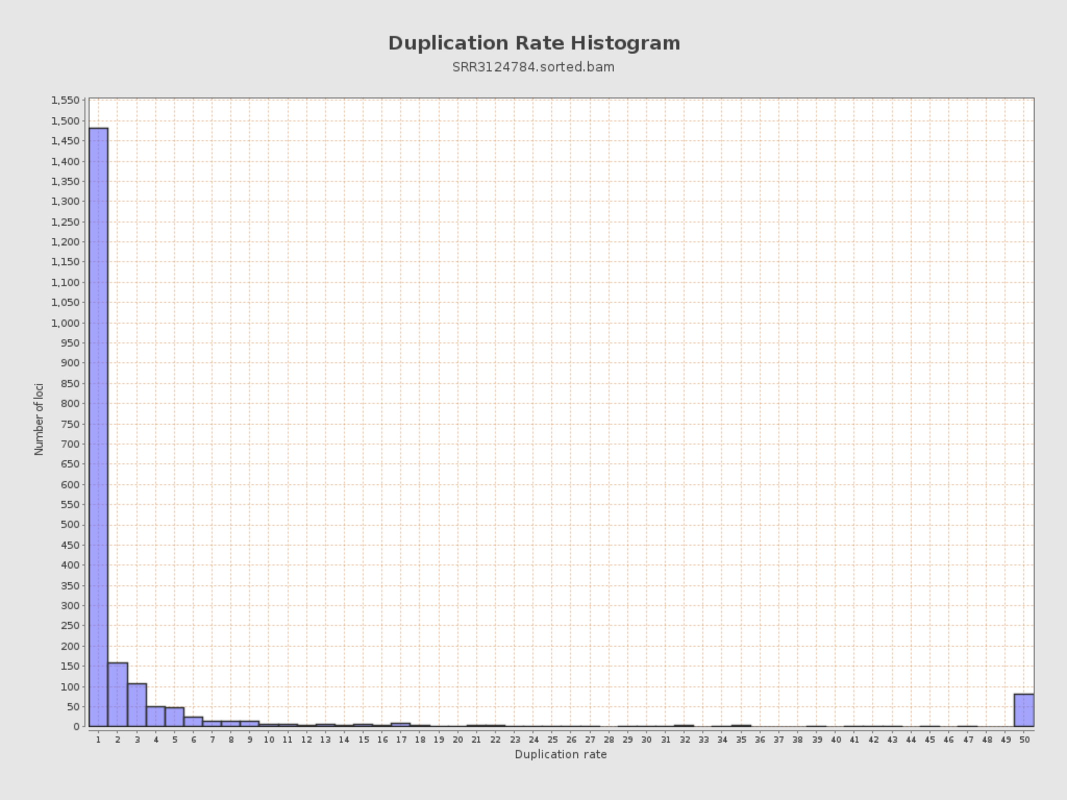
5. Results : Coverage Histogram (0-50X)



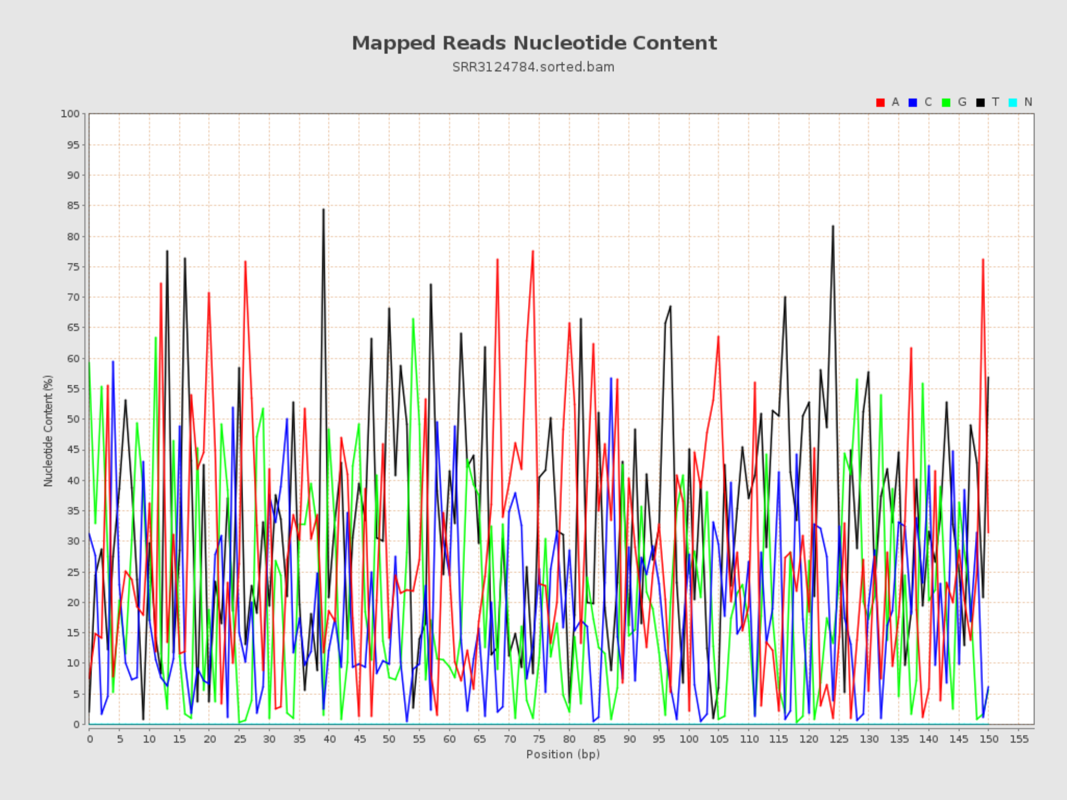
6. Results : Genome Fraction Coverage



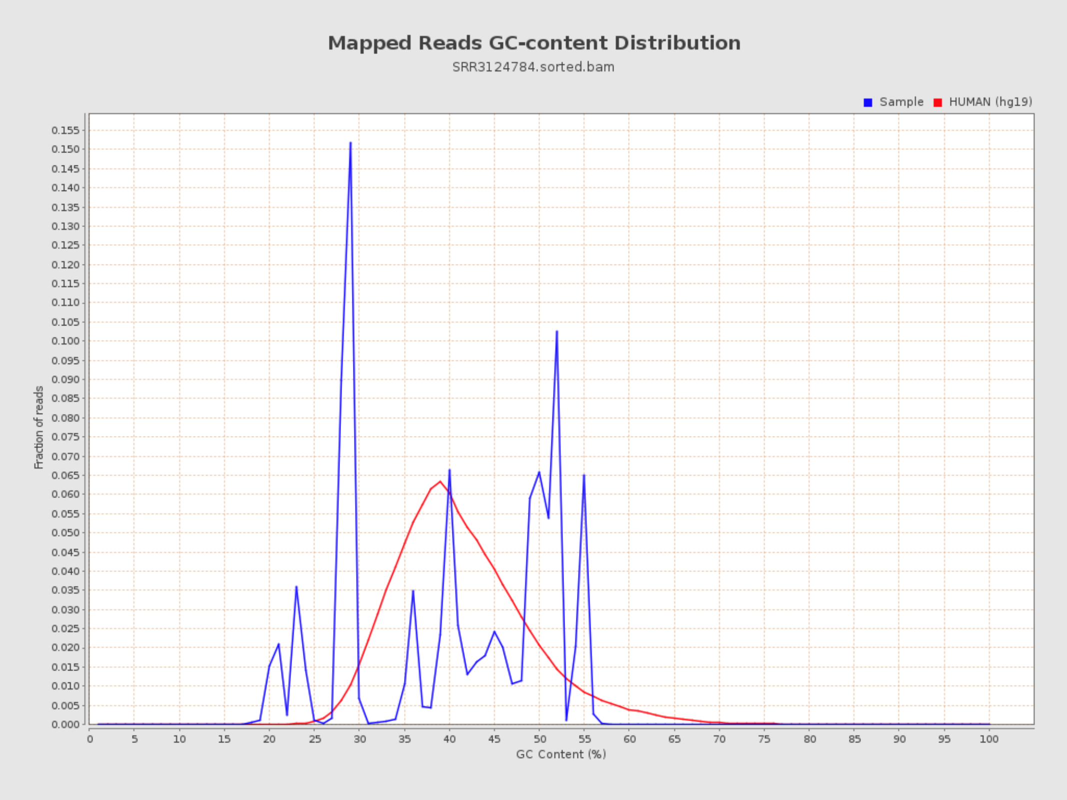
7. Results : Duplication Rate Histogram



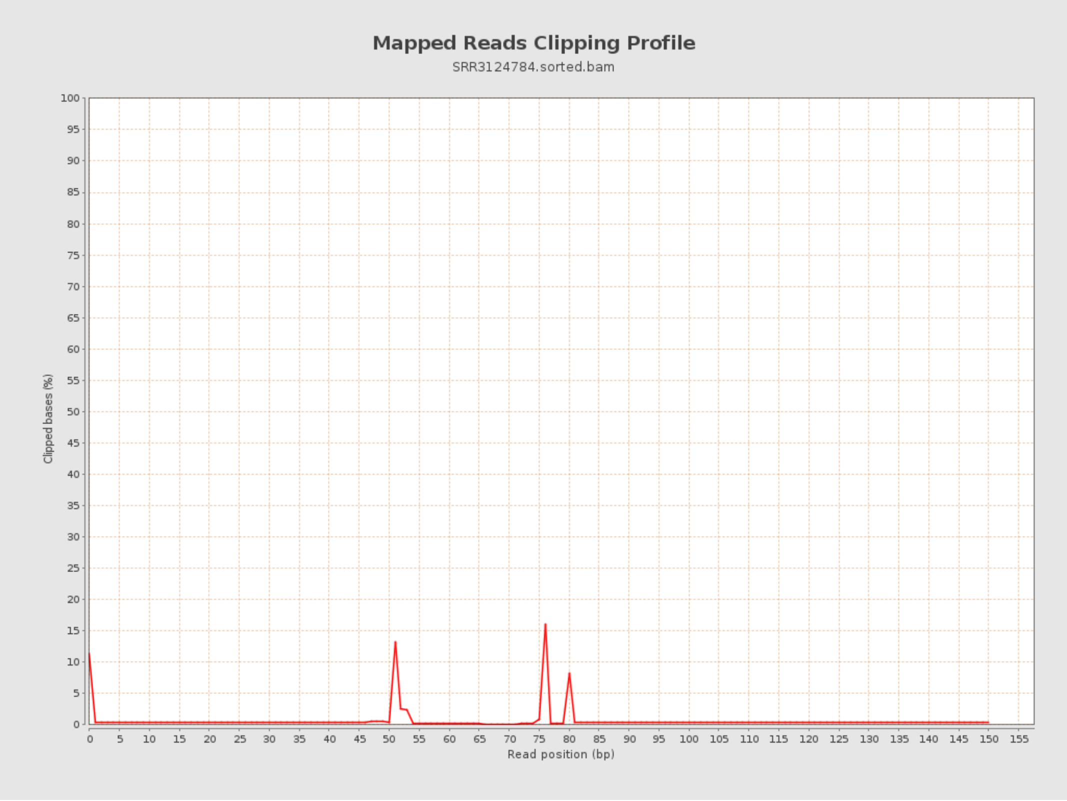
8. Results : Mapped Reads Nucleotide Content



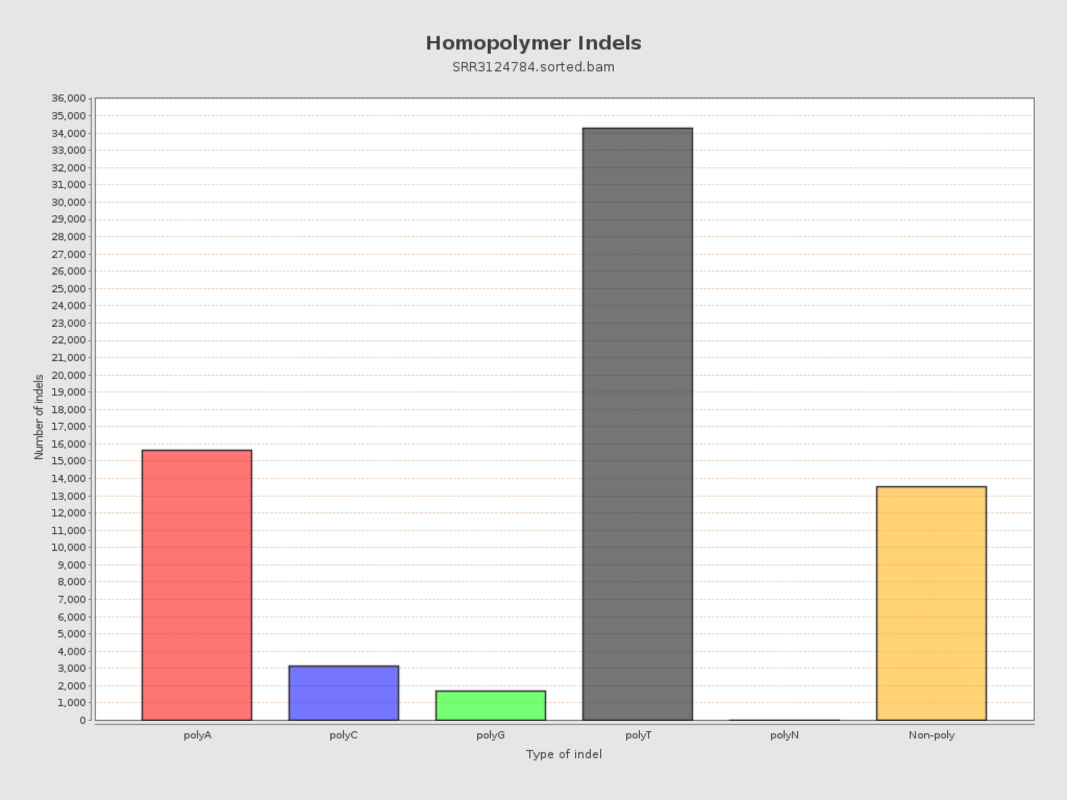
9. Results : Mapped Reads GC-content Distribution



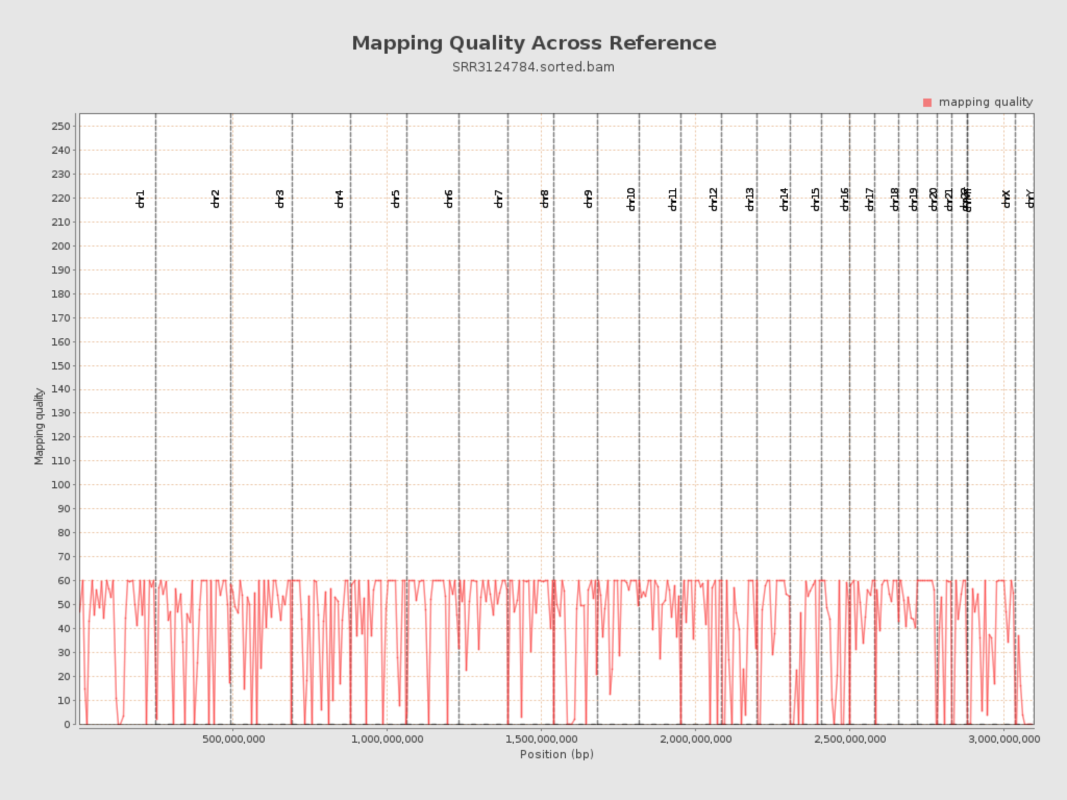
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram