Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:54:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124798.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_SRR3124798 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124798.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:54:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124798.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	763,555
Mapped reads	762,283 / 99.83%
Unmapped reads	1,272 / 0.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	295,337 / 38.68%
Read min/max/mean length	30 / 151 / 171.86
Duplicated reads (estimated)	1,052,079 / 137.79%
Duplication rate	7.47%
Clipped reads	626,896 / 82.1%

2.2. ACGT Content

Number/percentage of A's	38,735,661 / 34.2%
Number/percentage of C's	24,502,611 / 21.64%
Number/percentage of T's	31,523,799 / 27.83%
Number/percentage of G's	18,491,361 / 16.33%
Number/percentage of N's	0 / 0%
GC Percentage	37.96%

2.3. Coverage

Mean	0.0366

Standard Deviation	109.2113

2.4. Mapping Quality

Mean Mapping Quality	48.83

2.5. Mismatches and indels

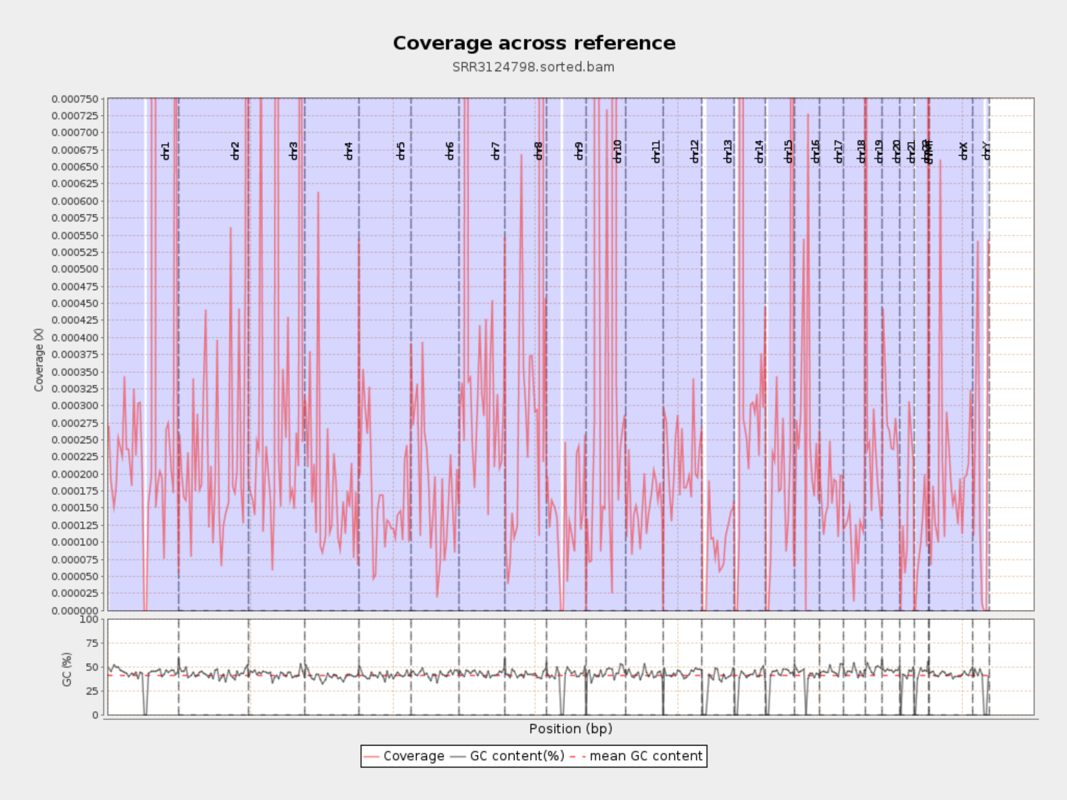
General error rate	0.97%
Mismatches	1,096,880
Insertions	5,483
Mapped reads with at least one insertion	0.72%
Deletions	28,175
Mapped reads with at least one deletion	3.67%
Homopolymer indels	57.04%

2.6. Chromosome stats

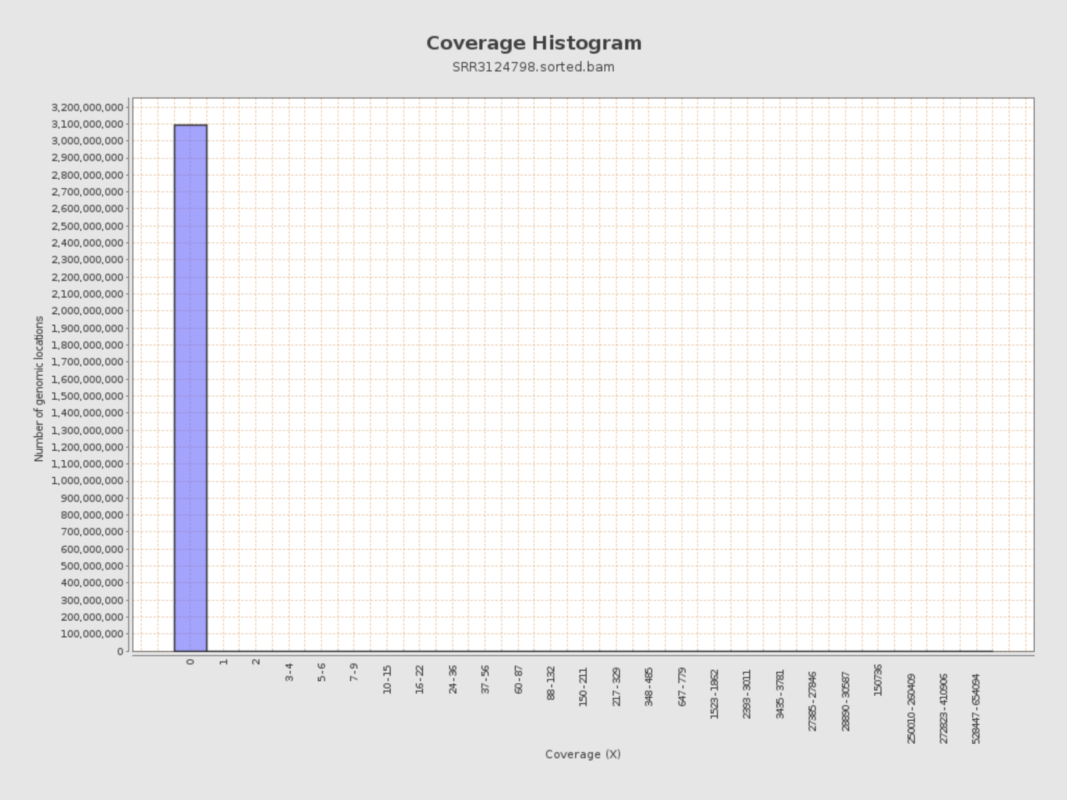
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	265653	0.0011	0.7786
chr2	243199373	67489	0.0003	0.1394
chr3	198022430	72485	0.0004	0.1897
chr4	191154276	34566	0.0002	0.0165
chr5	180915260	30583	0.0002	0.013
chr6	171115067	32119	0.0002	0.0139
chr7	159138663	66745	0.0004	0.2459

chr8	146364022	1164587	0.008	5.311
chr9	141213431	19097	0.0001	0.0117
chr10	135534747	111232544	0.8207	521.9095
chr11	135006516	20620	0.0002	0.0125
chr12	133851895	29570	0.0002	0.016
chr13	115169878	10414	0.0001	0.0095
chr14	107349540	58544	0.0005	0.4846
chr15	102531392	41241	0.0004	0.1571
chr16	90354753	24260	0.0003	0.0175
chr17	81195210	13779	0.0002	0.0139
chr18	78077248	8431	0.0001	0.0104
chr19	59128983	15796	0.0003	0.0315
chr20	63025520	17509	0.0003	0.0185
chr21	48129895	7535	0.0002	0.0125
chr22	51304566	4921	0.0001	0.0098
chrMT	16571	991	0.0598	0.2777
chrX	155270560	31383	0.0002	0.0571
chrY	59373566	11602	0.0002	0.0156

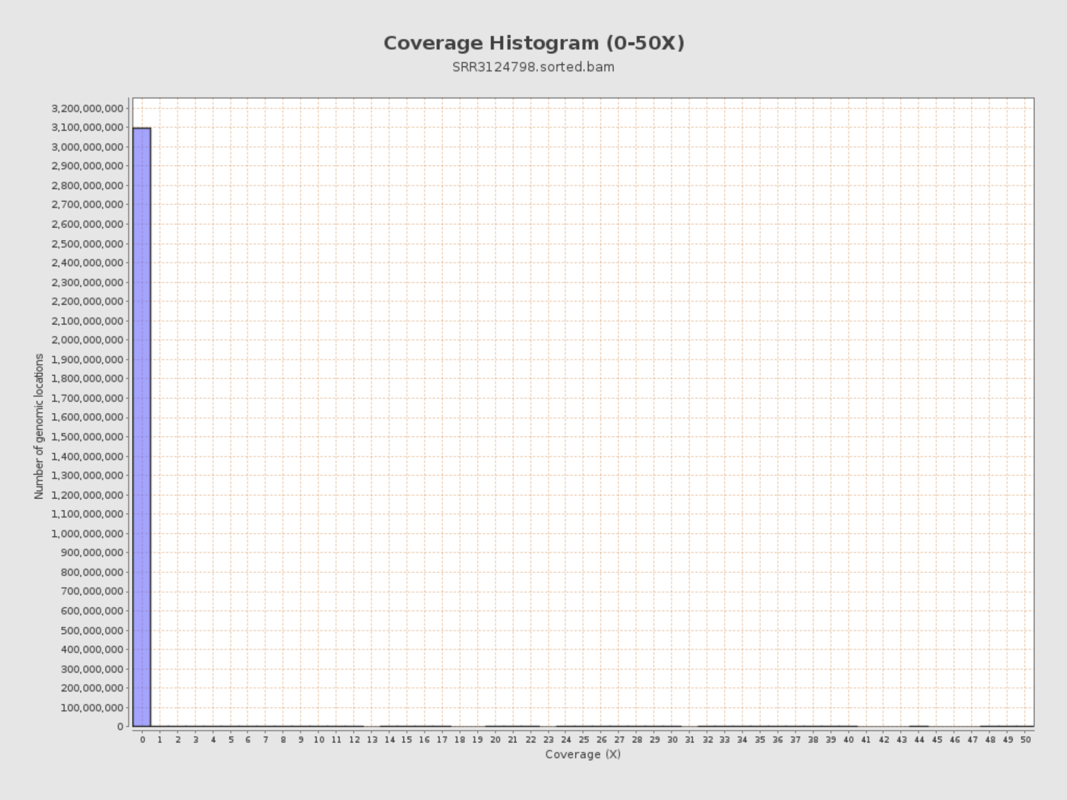
3. Results : Coverage across reference



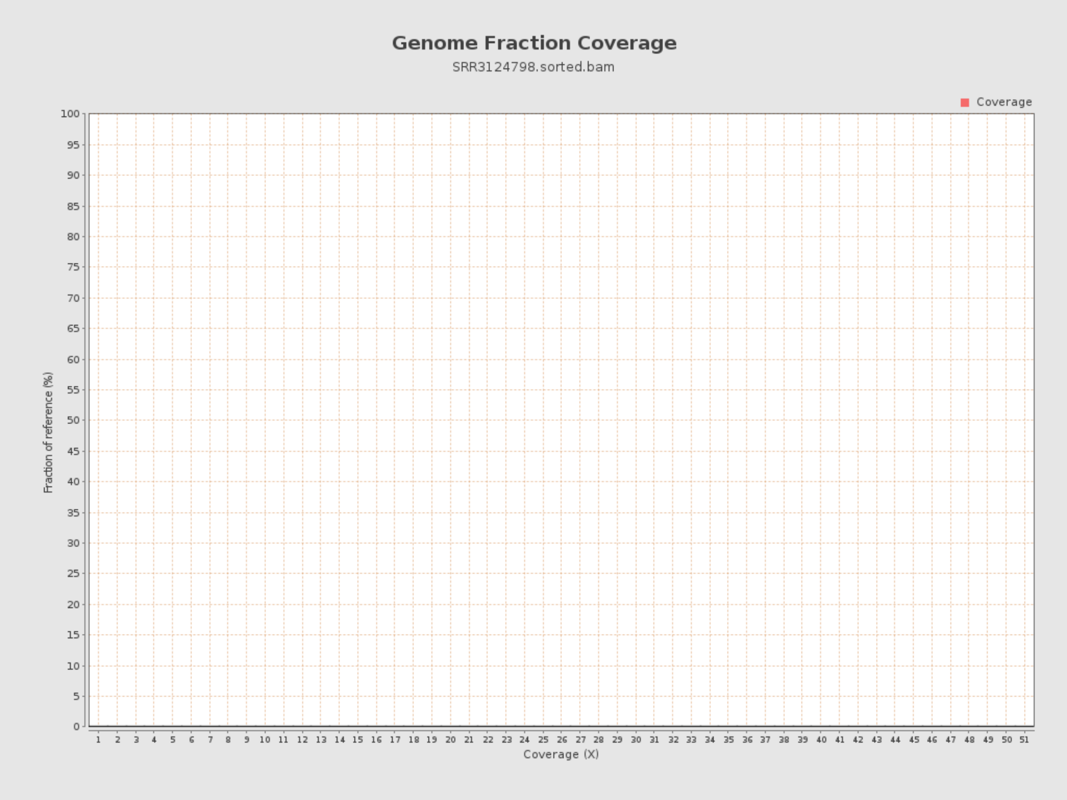
4. Results : Coverage Histogram



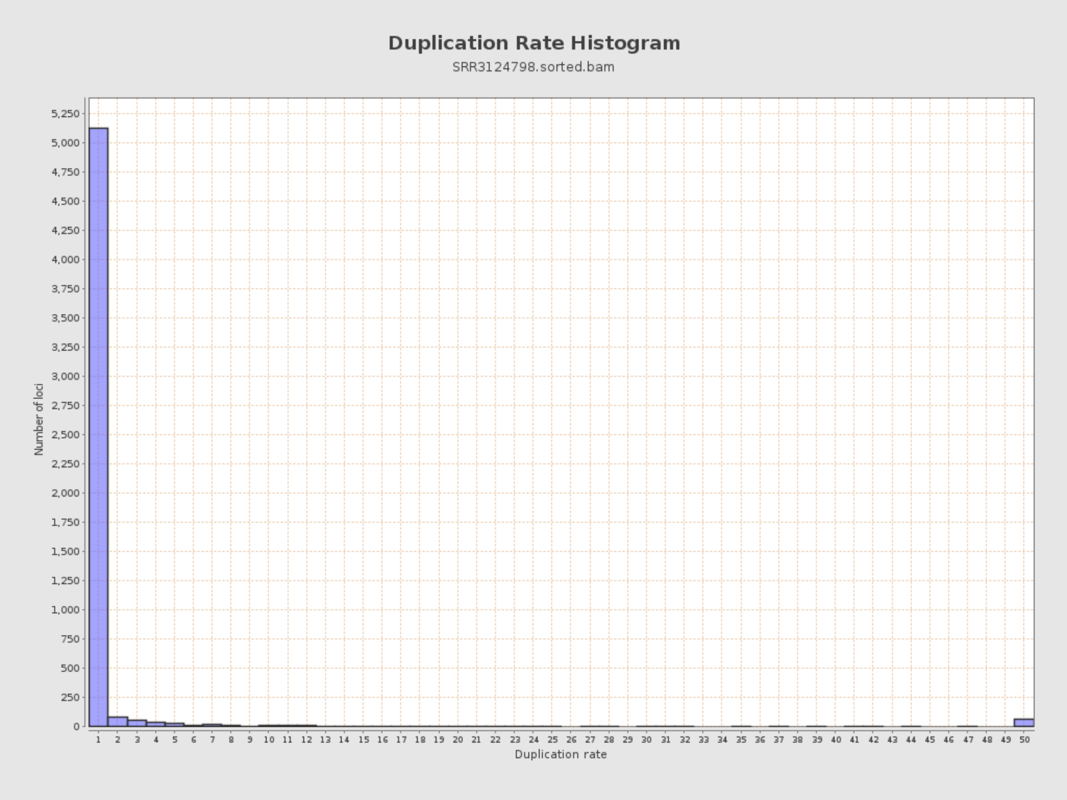
5. Results : Coverage Histogram (0-50X)



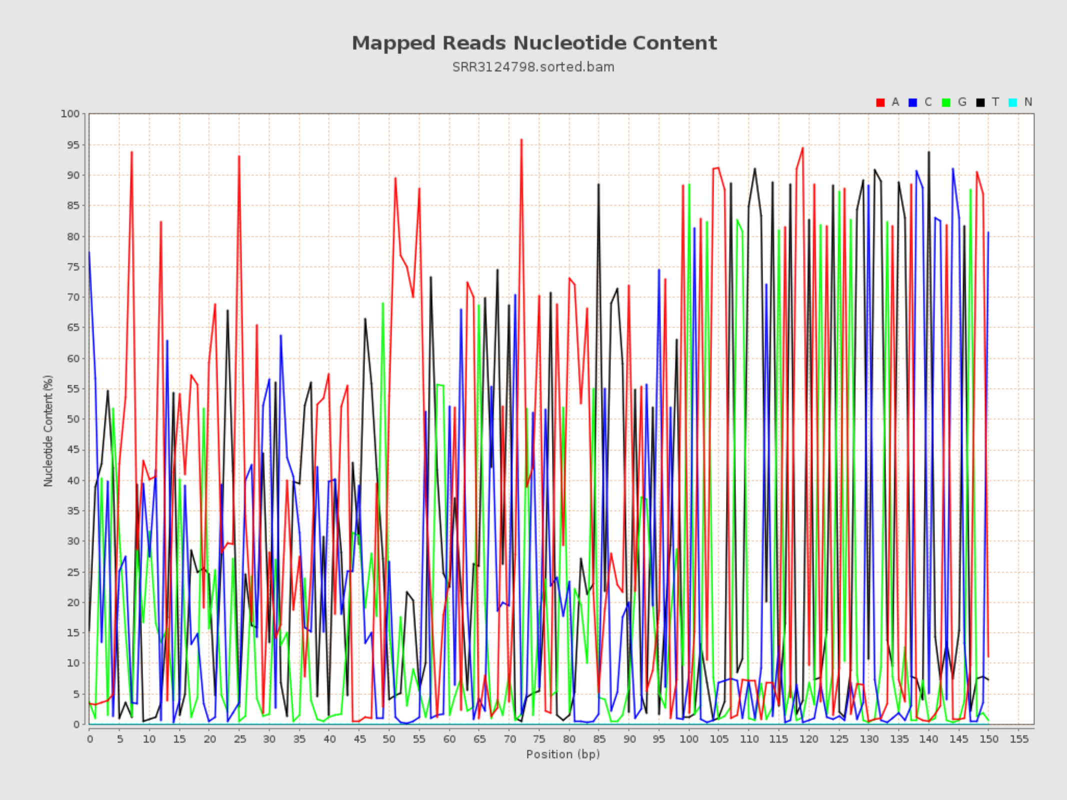
6. Results : Genome Fraction Coverage



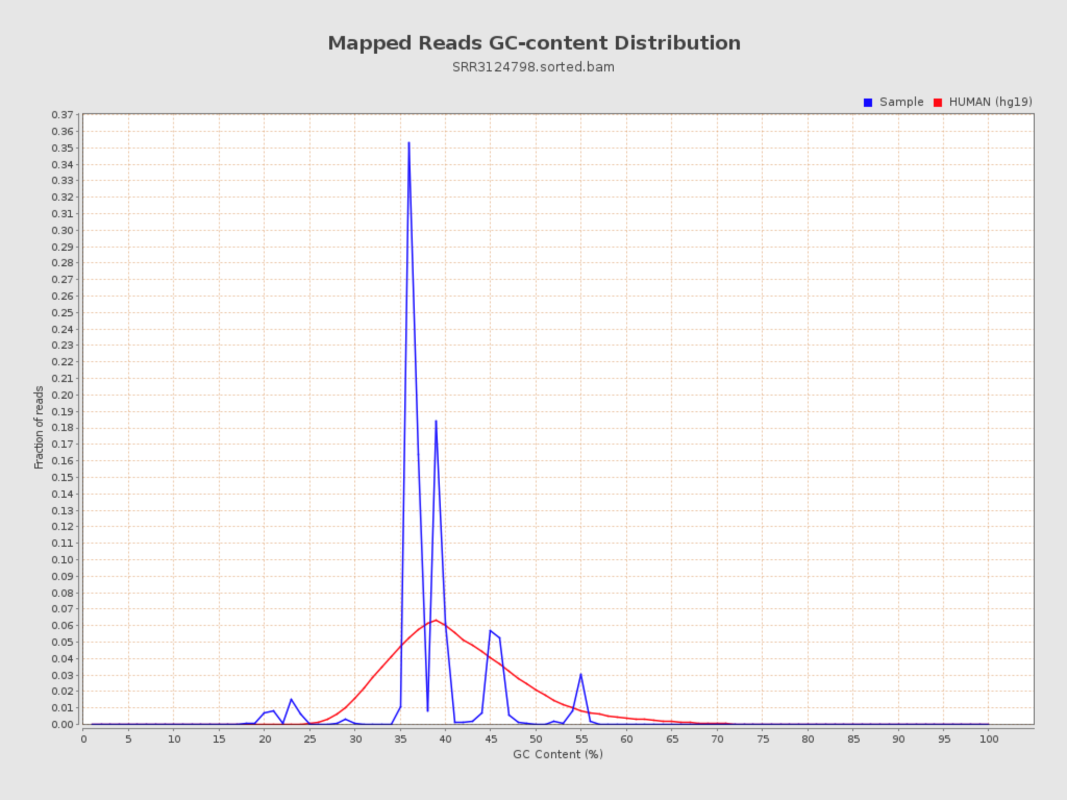
7. Results : Duplication Rate Histogram



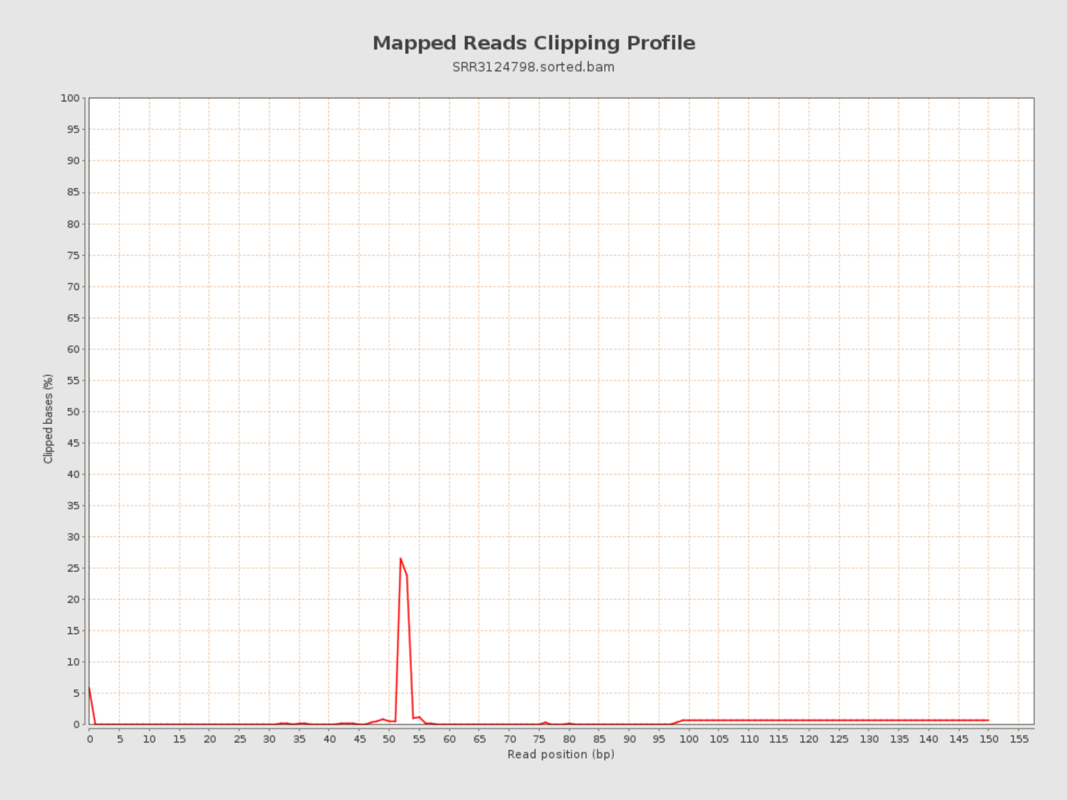
8. Results : Mapped Reads Nucleotide Content



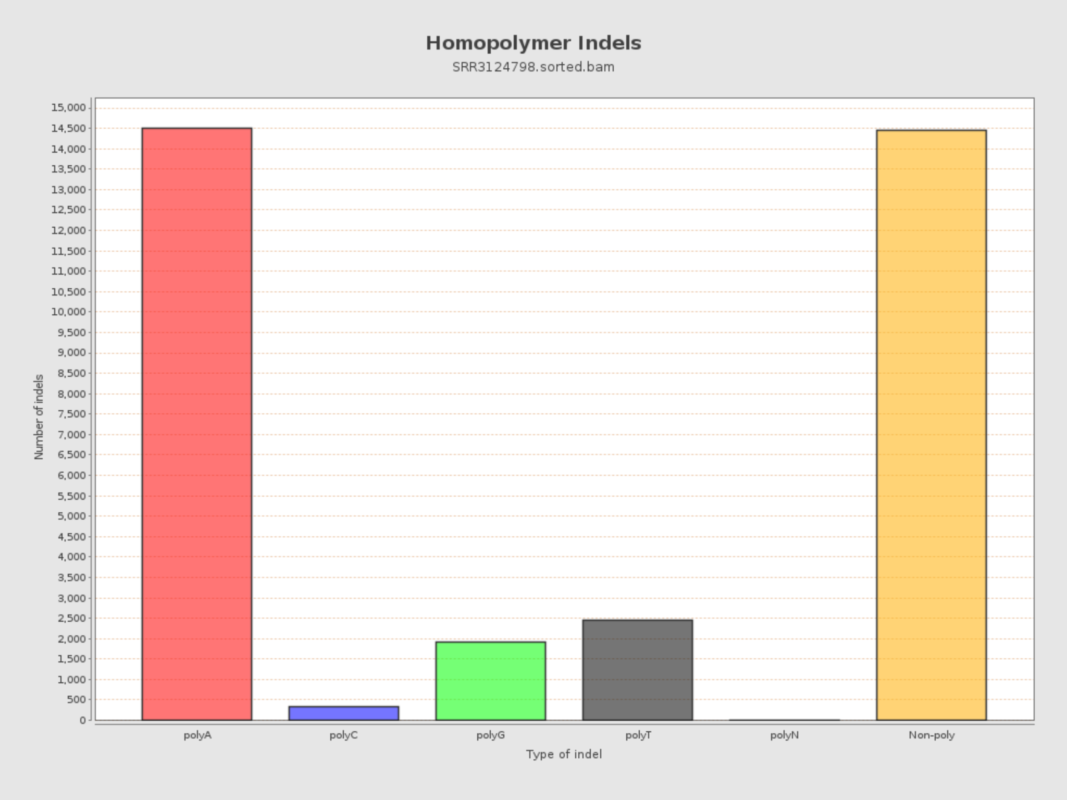
9. Results : Mapped Reads GC-content Distribution



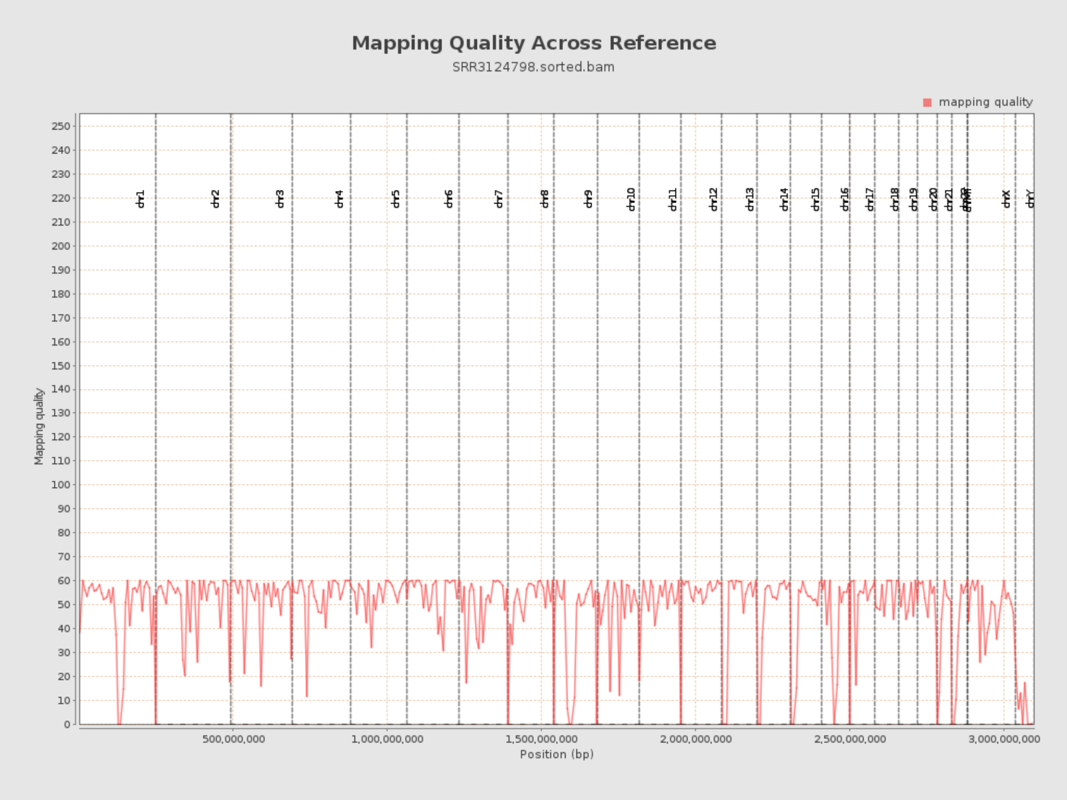
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram