Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:42:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124791.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_SRR3124791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124791.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:42:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124791.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	575,108
Mapped reads	574,415 / 99.88%
Unmapped reads	693 / 0.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	254,910 / 44.32%
Read min/max/mean length	30 / 151 / 180.96
Duplicated reads (estimated)	826,994 / 143.8%
Duplication rate	21.66%
Clipped reads	545,993 / 94.94%

2.2. ACGT Content

Number/percentage of A's	22,811,896 / 26.59%
Number/percentage of C's	16,768,161 / 19.55%
Number/percentage of T's	27,637,108 / 32.22%
Number/percentage of G's	18,569,757 / 21.65%
Number/percentage of N's	0 / 0%
GC Percentage	41.19%

2.3. Coverage

Mean	0.0277

Standard Deviation	61.6689

2.4. Mapping Quality

Mean Mapping Quality	47.62

2.5. Mismatches and indels

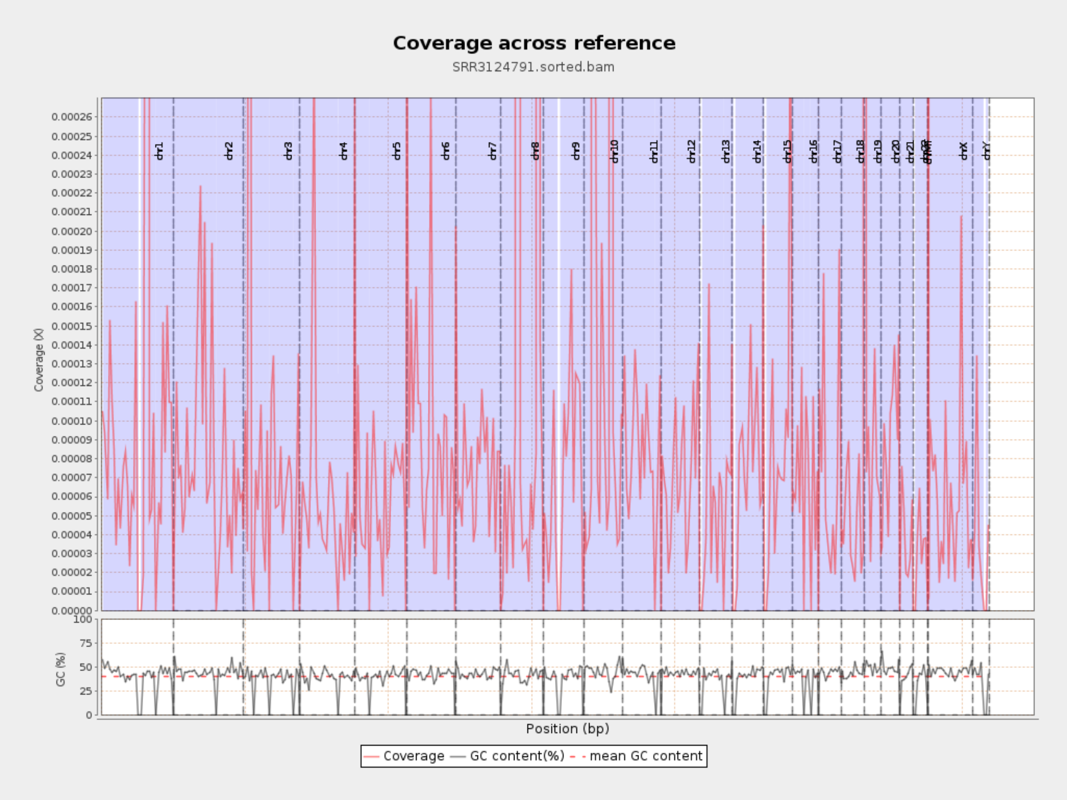
General error rate	0.82%
Mismatches	683,279
Insertions	20,091
Mapped reads with at least one insertion	3.47%
Deletions	33,289
Mapped reads with at least one deletion	5.63%
Homopolymer indels	82.63%

2.6. Chromosome stats

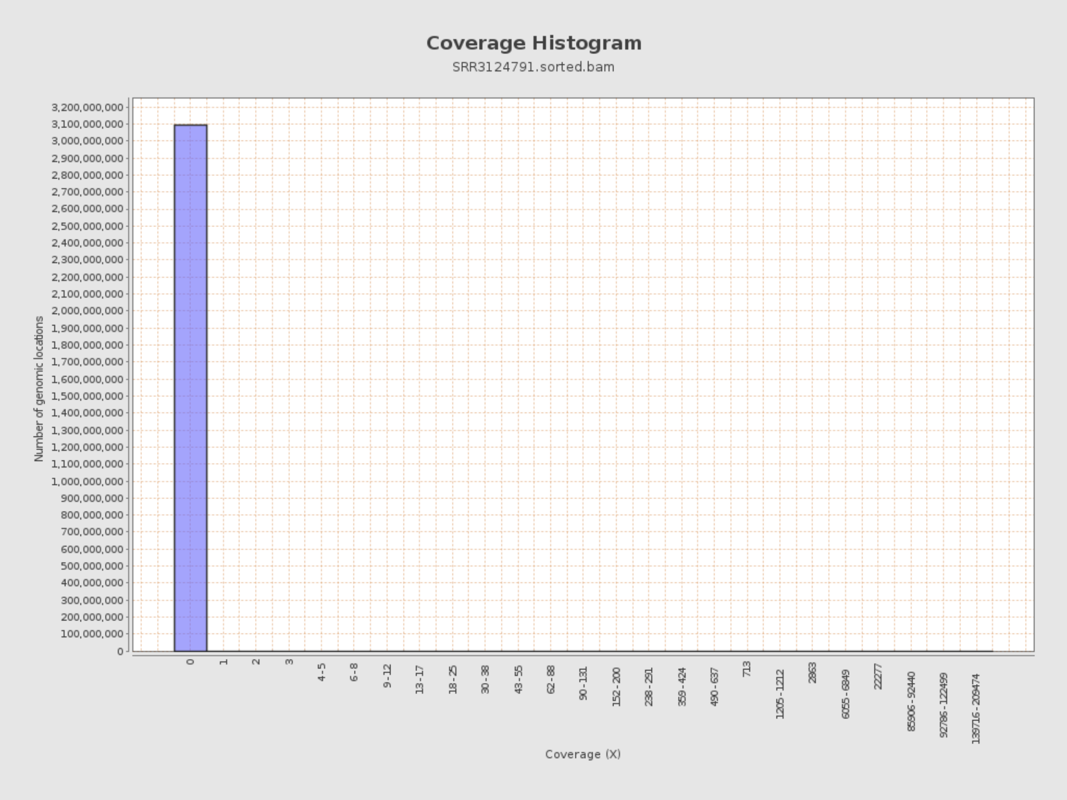
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	95269	0.0004	0.2766
chr2	243199373	19982	0.0001	0.0092
chr3	198022430	20218	0.0001	0.0464
chr4	191154276	10755	0.0001	0.0076
chr5	180915260	10884	0.0001	0.0078
chr6	171115067	16159	0.0001	0.0142
chr7	159138663	12119	0.0001	0.01

chr8	146364022	83507358	0.5705	283.4531
chr9	141213431	9970	0.0001	0.0084
chr10	135534747	2021347	0.0149	9.9059
chr11	135006516	11510	0.0001	0.0092
chr12	133851895	9834	0.0001	0.0086
chr13	115169878	6034	0.0001	0.0074
chr14	107349540	7819	0.0001	0.0095
chr15	102531392	8629	0.0001	0.0157
chr16	90354753	6159	0.0001	0.0083
chr17	81195210	6134	0.0001	0.0089
chr18	78077248	3588	0	0.0068
chr19	59128983	17320	0.0003	0.0971
chr20	63025520	5785	0.0001	0.0096
chr21	48129895	1795	0	0.0061
chr22	51304566	1576	0	0.0056
chrMT	16571	384	0.0232	0.1505
chrX	155270560	9218	0.0001	0.0077
chrY	59373566	2198	0	0.0063

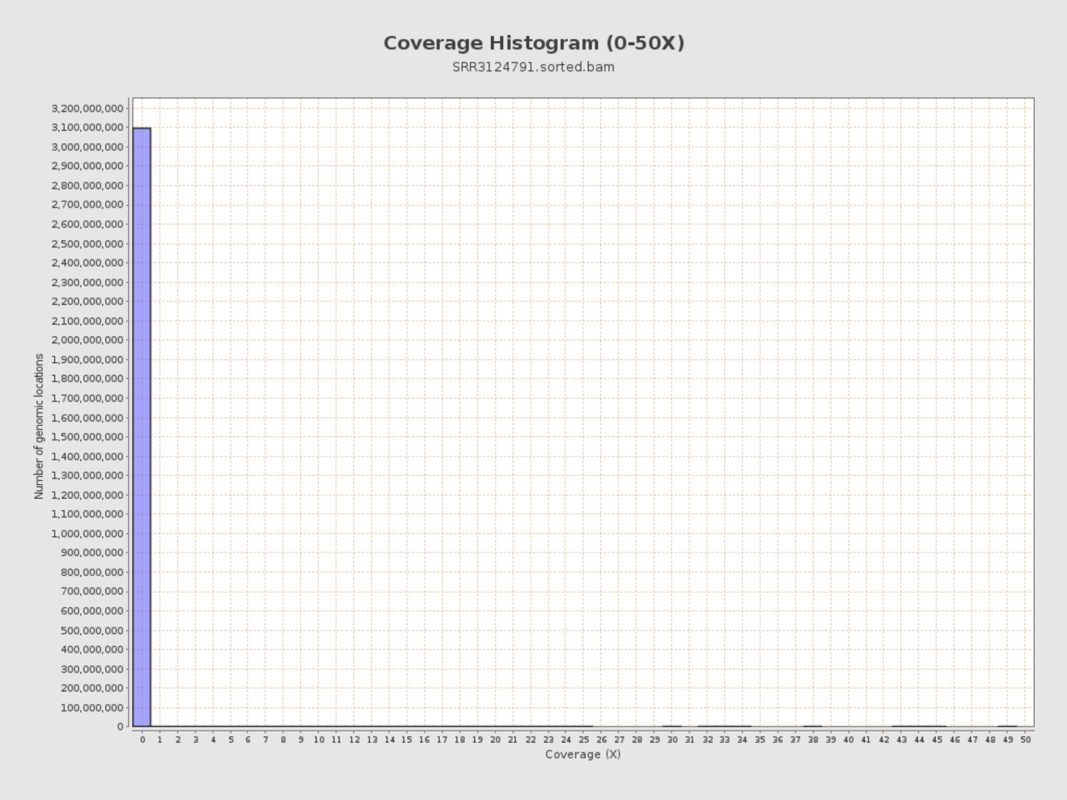
3. Results : Coverage across reference



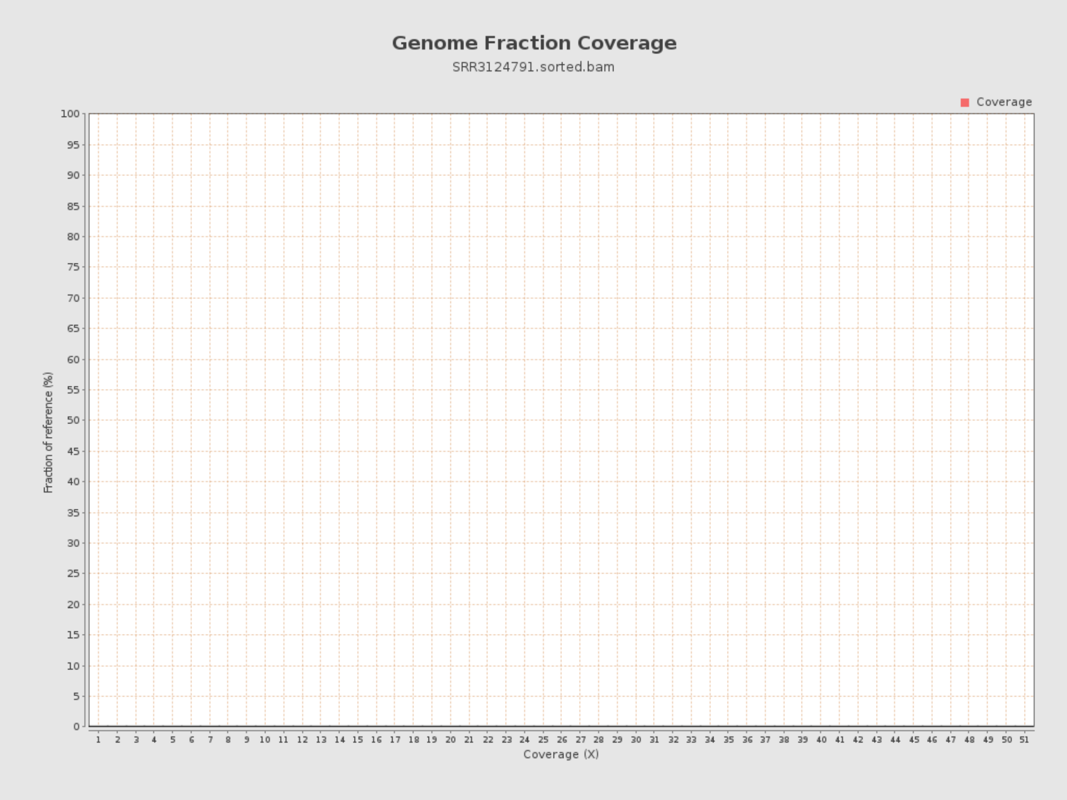
4. Results : Coverage Histogram



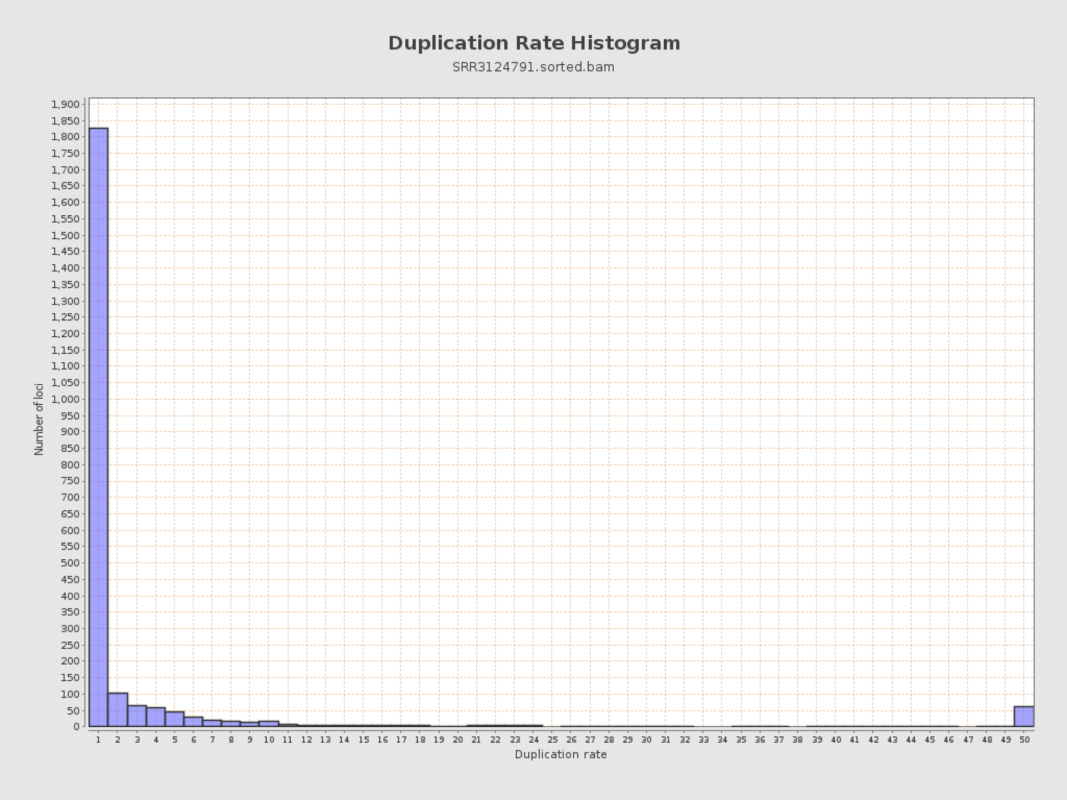
5. Results : Coverage Histogram (0-50X)



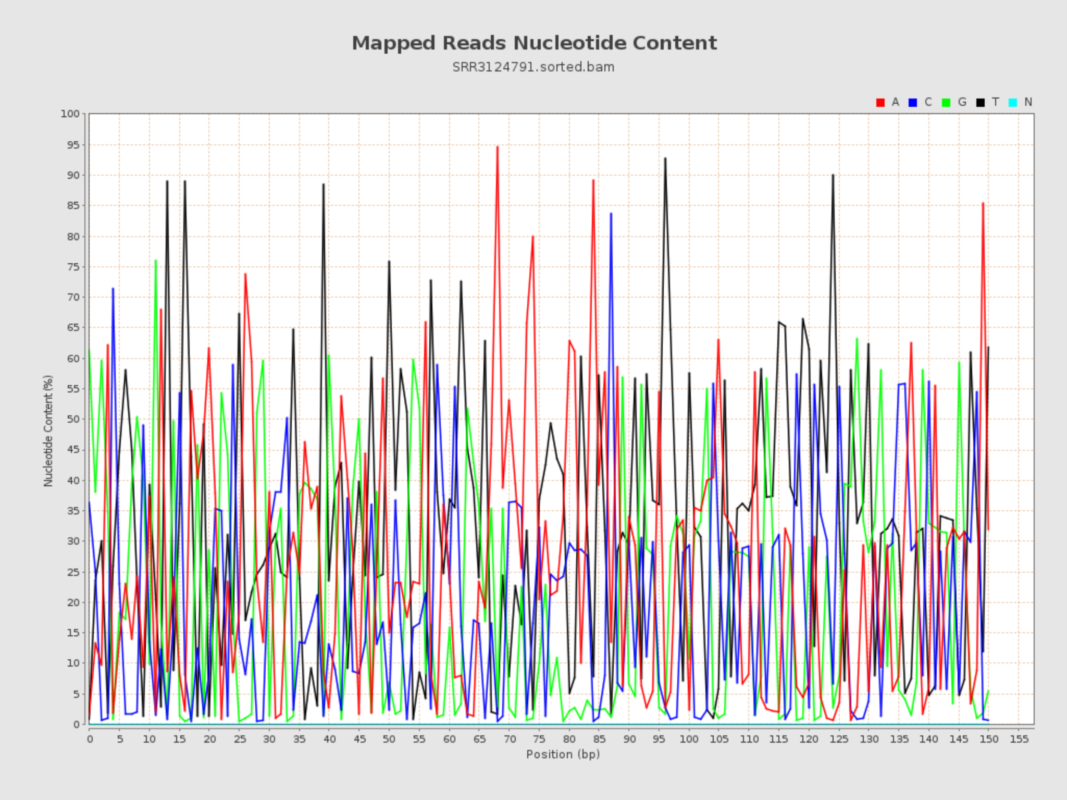
6. Results : Genome Fraction Coverage



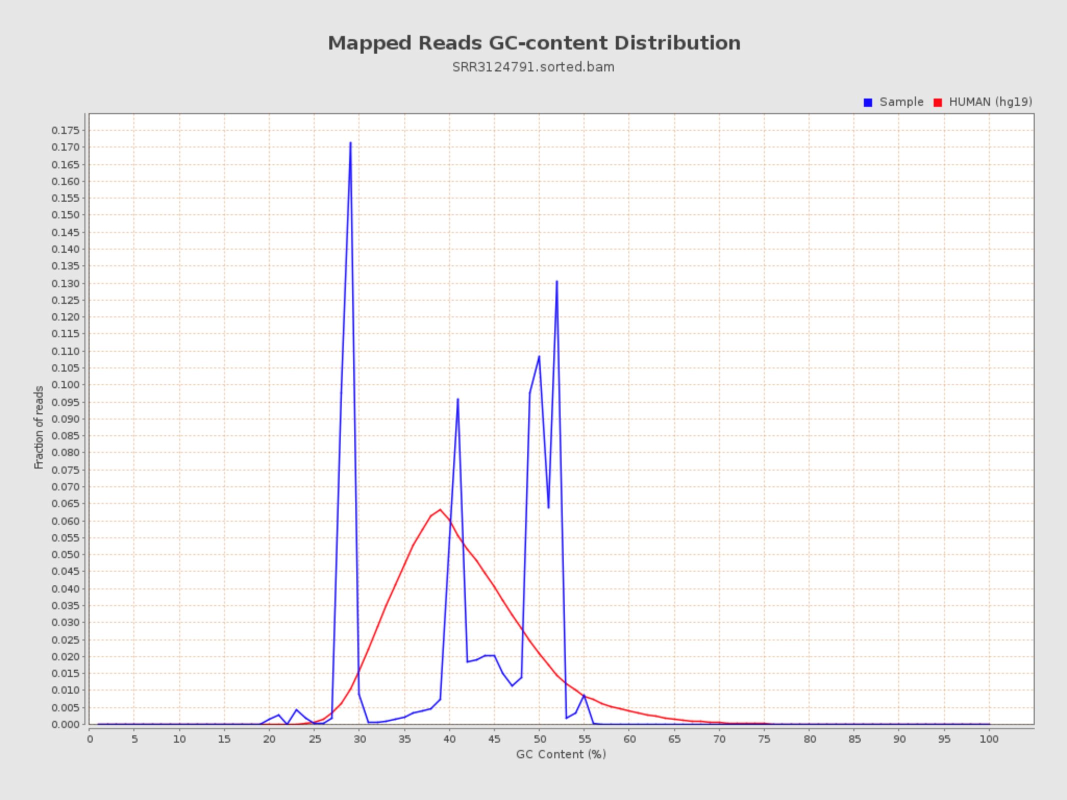
7. Results : Duplication Rate Histogram



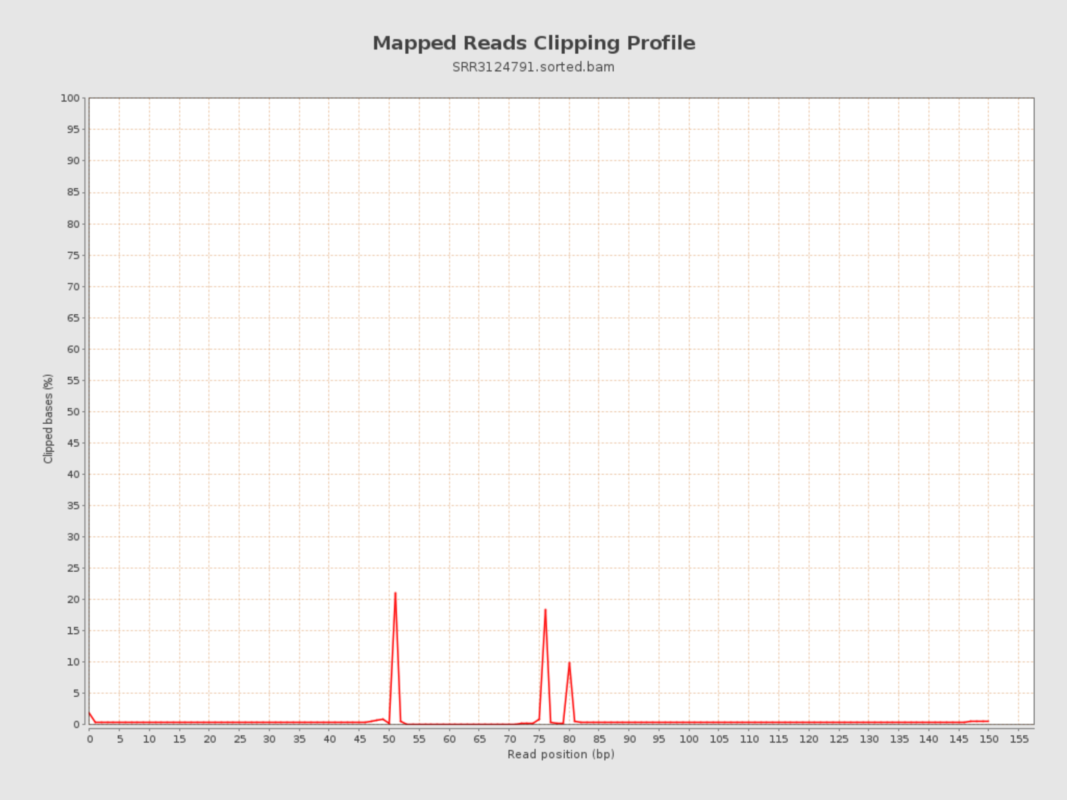
8. Results : Mapped Reads Nucleotide Content



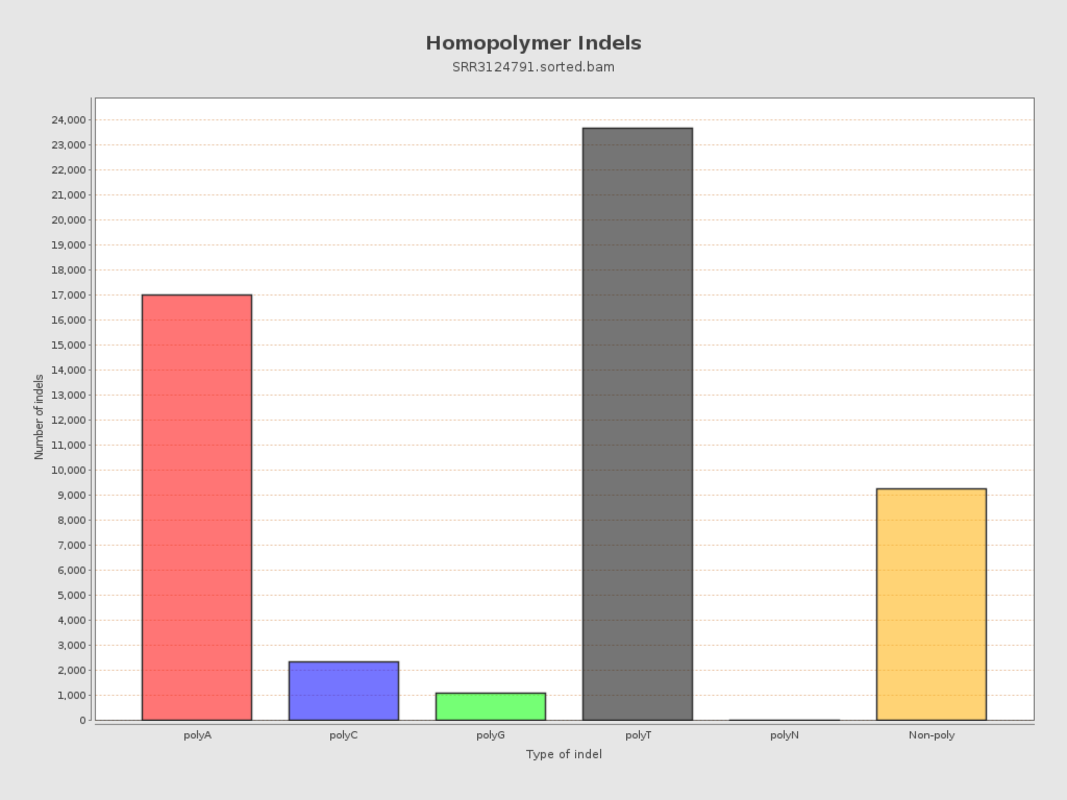
9. Results : Mapped Reads GC-content Distribution



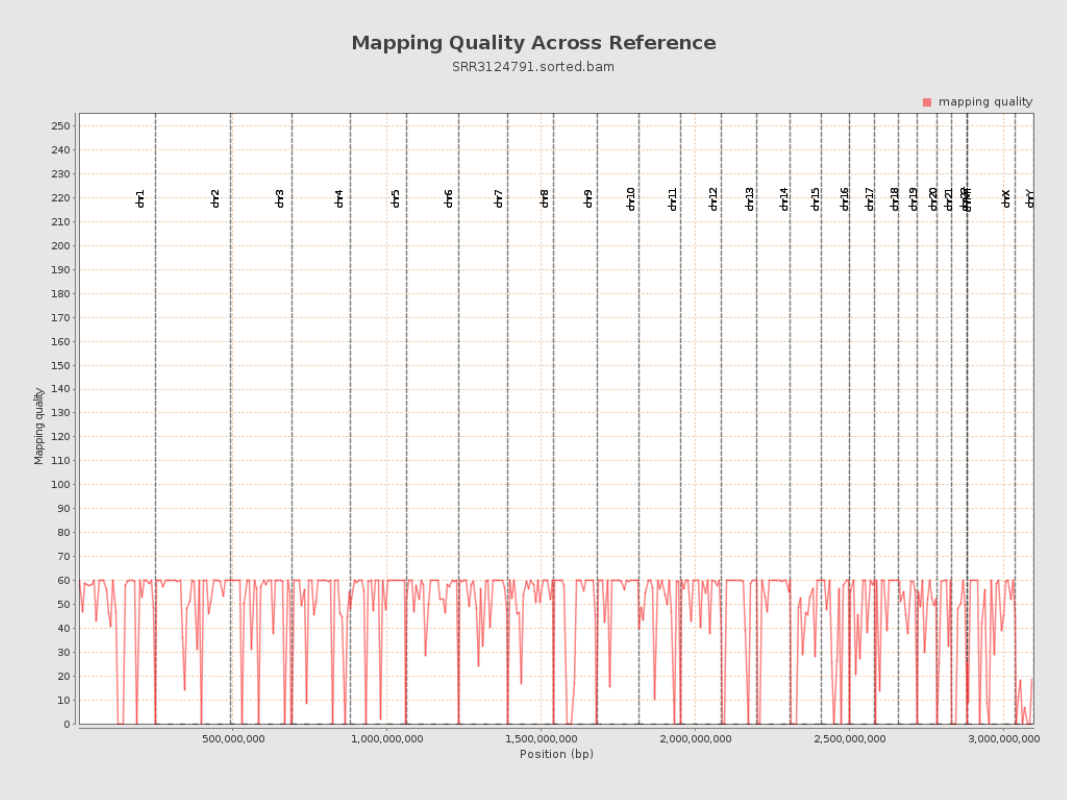
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram