Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:12:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124809.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_SRR3124809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:12:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	767,471
Mapped reads	766,436 / 99.87%
Unmapped reads	1,035 / 0.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	288,010 / 37.53%
Read min/max/mean length	30 / 151 / 176.16
Duplicated reads (estimated)	1,052,543 / 137.14%
Duplication rate	32.37%
Clipped reads	668,911 / 87.16%

2.2. ACGT Content

Number/percentage of A's	32,817,015 / 28.83%
Number/percentage of C's	21,210,023 / 18.63%
Number/percentage of T's	36,358,517 / 31.94%
Number/percentage of G's	23,438,801 / 20.59%
Number/percentage of N's	0 / 0%
GC Percentage	39.23%

2.3. Coverage

Mean	0.0368

Standard Deviation	67.2773

2.4. Mapping Quality

Mean Mapping Quality	41.42

2.5. Mismatches and indels

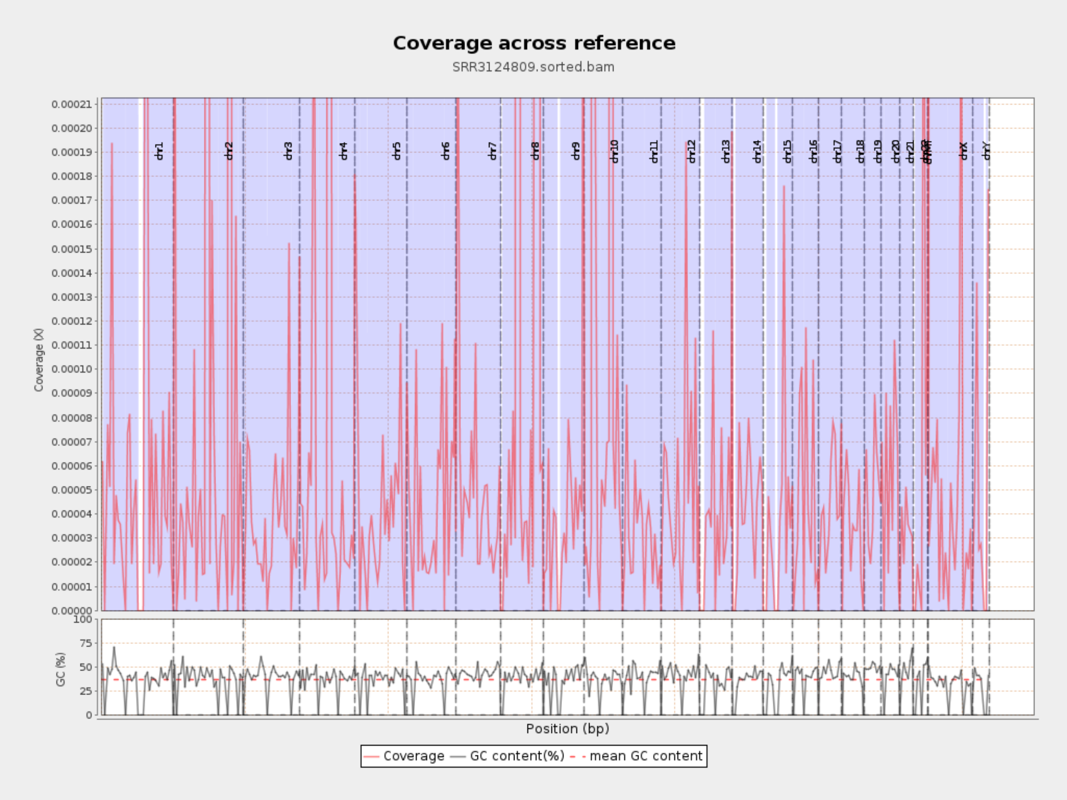
General error rate	0.87%
Mismatches	971,085
Insertions	16,914
Mapped reads with at least one insertion	2.18%
Deletions	63,735
Mapped reads with at least one deletion	7.86%
Homopolymer indels	79.22%

2.6. Chromosome stats

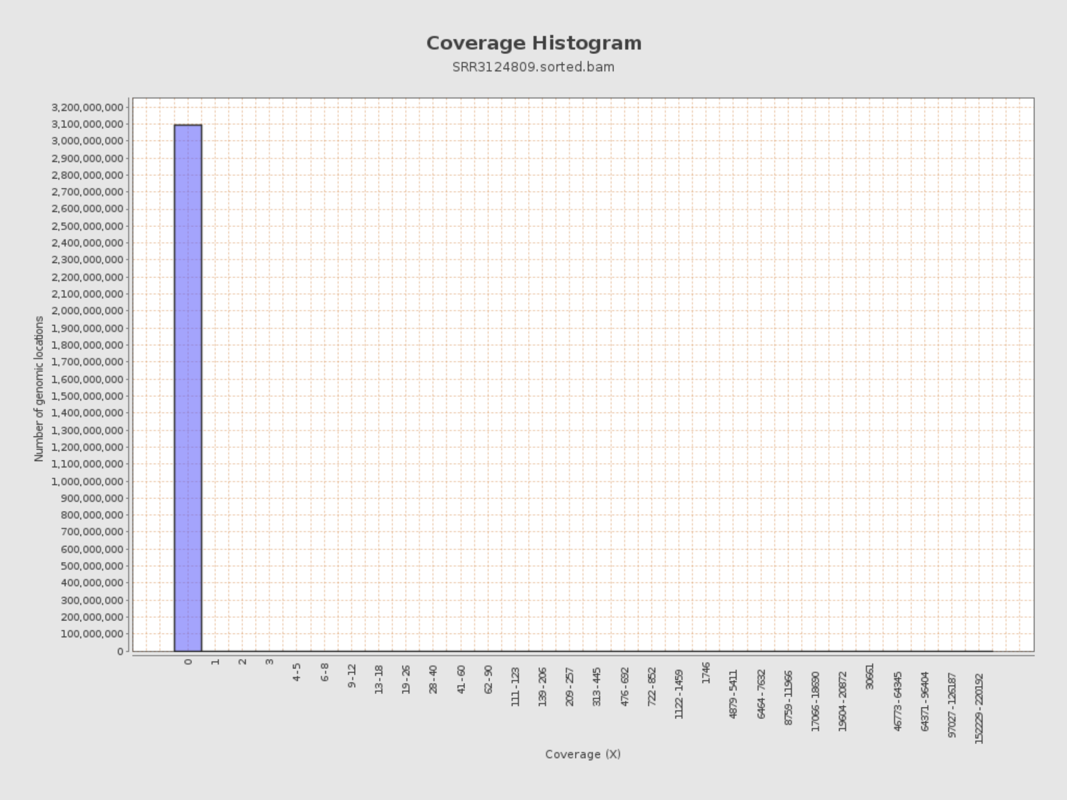
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14425	0.0001	0.0136
chr2	243199373	48819	0.0002	0.1583
chr3	198022430	7764	0	0.0074
chr4	191154276	23709	0.0001	0.2204
chr5	180915260	7721	0	0.0089
chr6	171115067	7748	0	0.0121
chr7	159138663	8528	0.0001	0.0243

chr8	146364022	110634670	0.7559	309.1091
chr9	141213431	4870	0	0.006
chr10	135534747	3077985	0.0227	14.0865
chr11	135006516	4231	0	0.0057
chr12	133851895	7016	0.0001	0.0221
chr13	115169878	4411	0	0.0098
chr14	107349540	4392	0	0.008
chr15	102531392	3783	0	0.0093
chr16	90354753	4220	0	0.0069
chr17	81195210	3686	0	0.0069
chr18	78077248	2696	0	0.0059
chr19	59128983	2920	0	0.0071
chr20	63025520	3542	0.0001	0.0076
chr21	48129895	1566	0	0.0065
chr22	51304566	3526	0.0001	0.0264
chrMT	16571	234	0.0141	0.118
chrX	155270560	7044	0	0.0189
chrY	59373566	3245	0.0001	0.0077

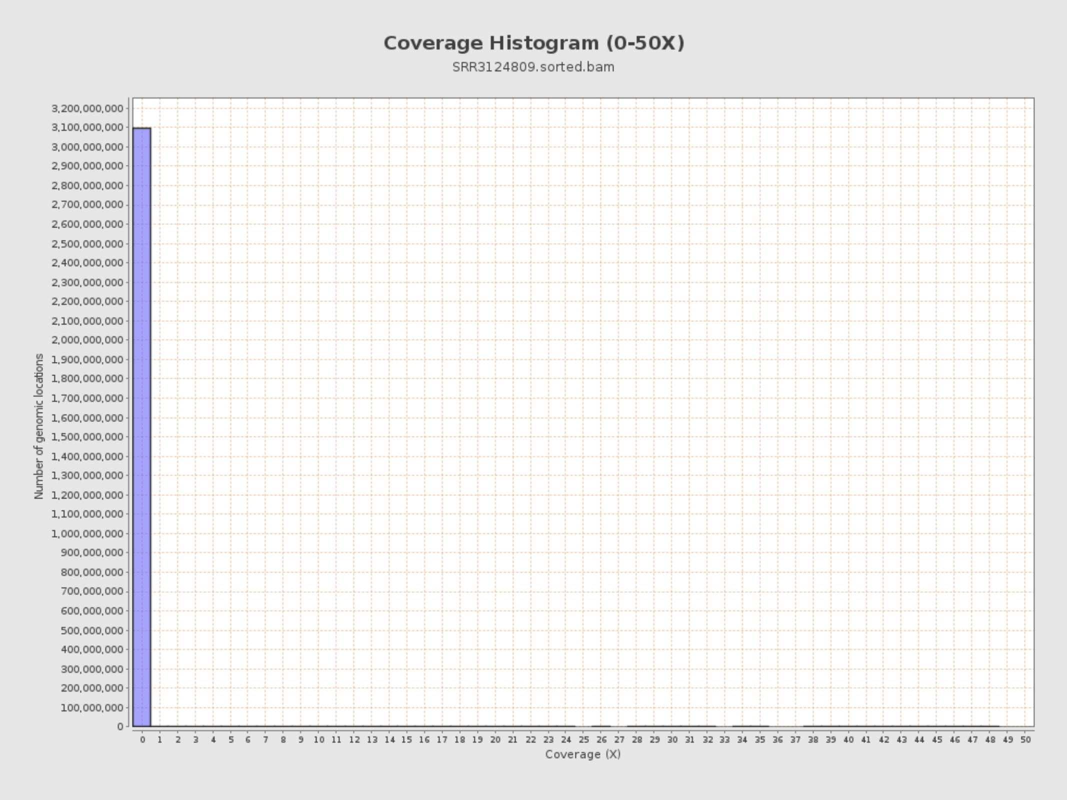
3. Results : Coverage across reference



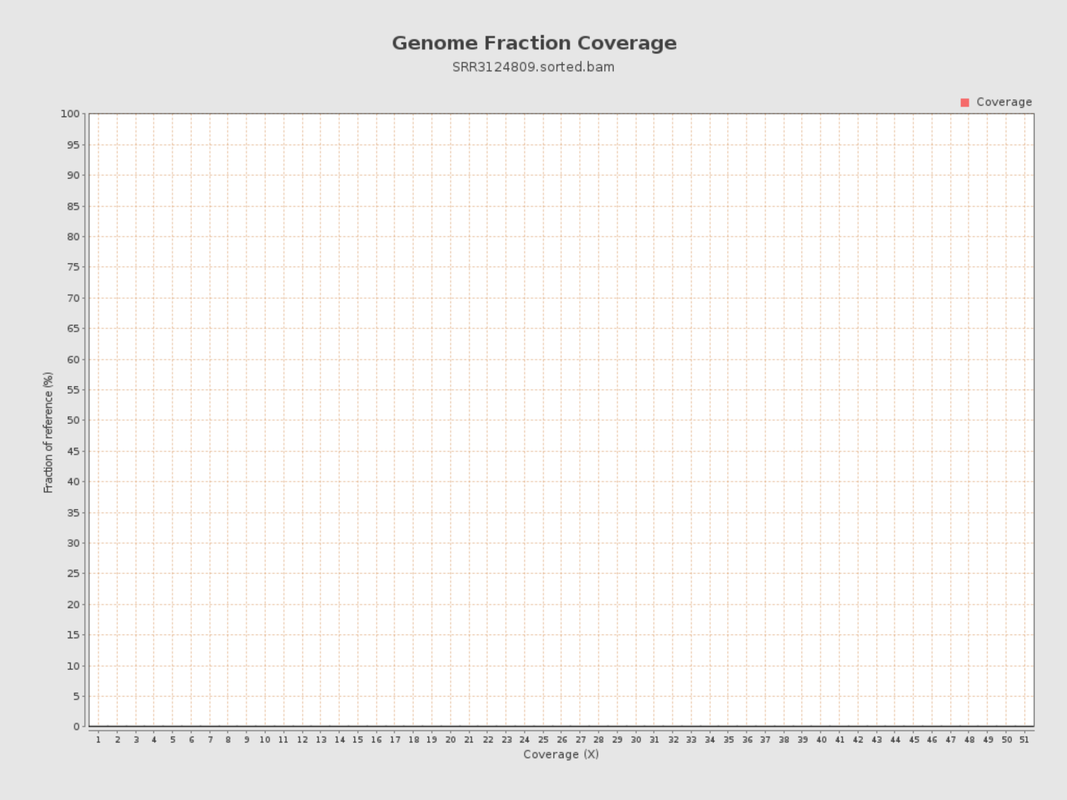
4. Results : Coverage Histogram



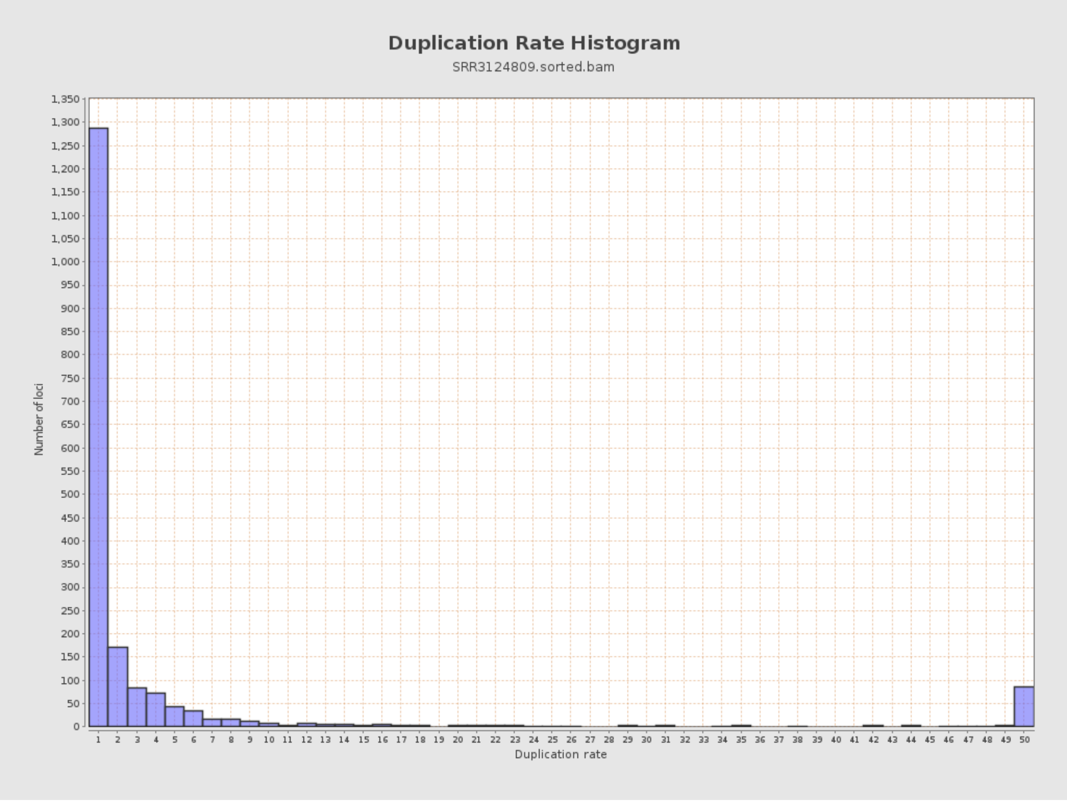
5. Results : Coverage Histogram (0-50X)



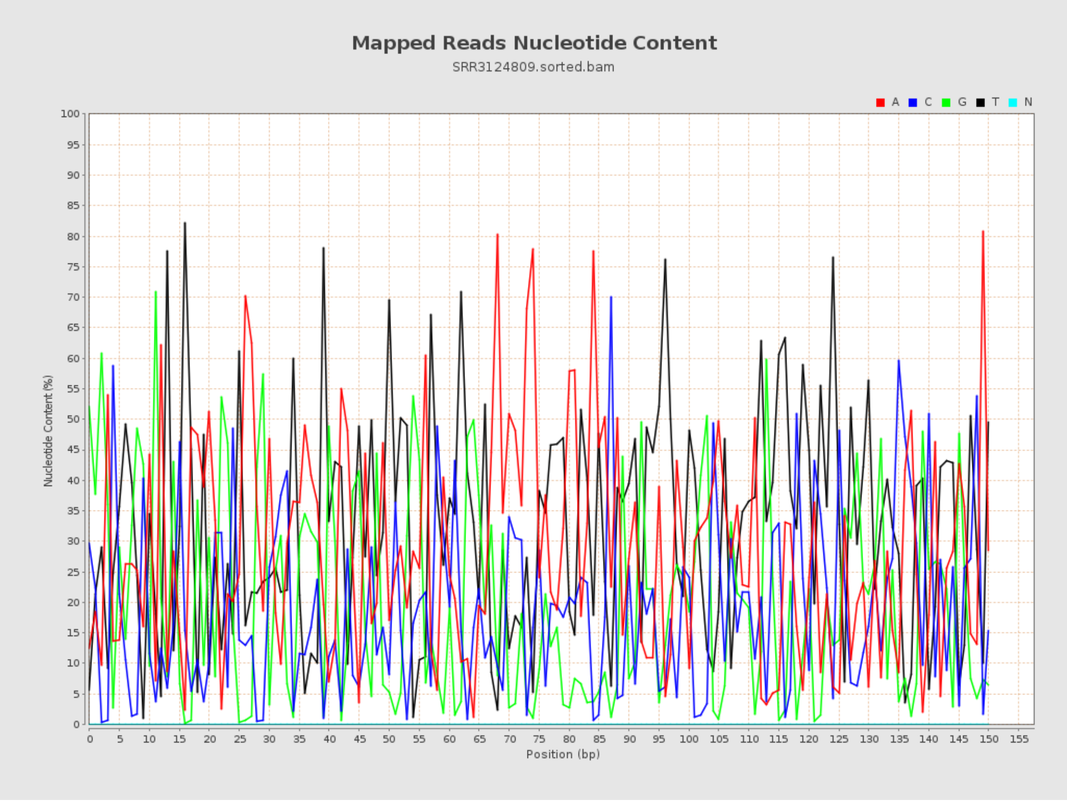
6. Results : Genome Fraction Coverage



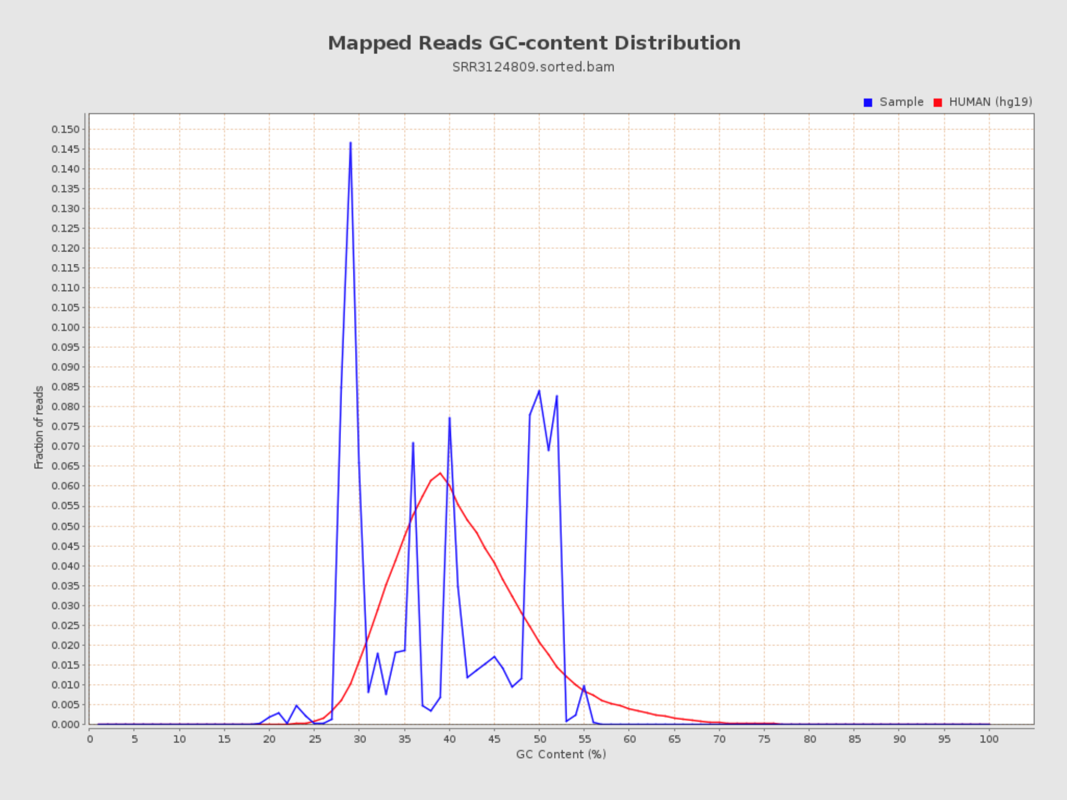
7. Results : Duplication Rate Histogram



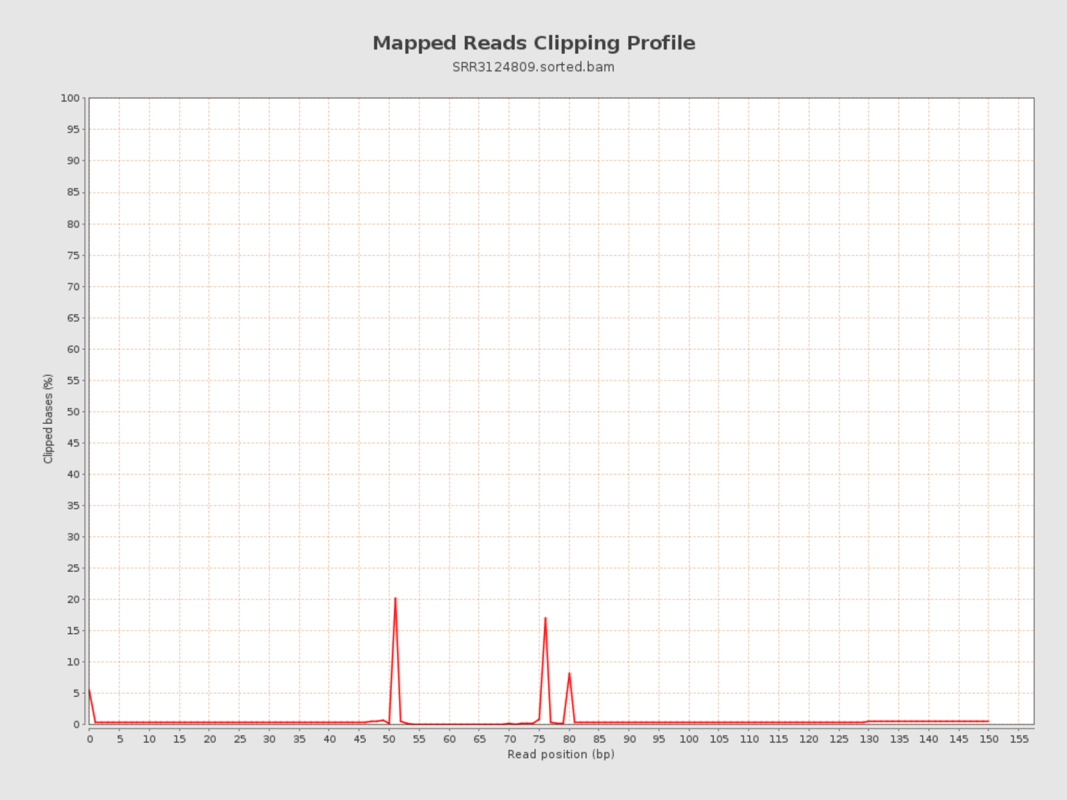
8. Results : Mapped Reads Nucleotide Content



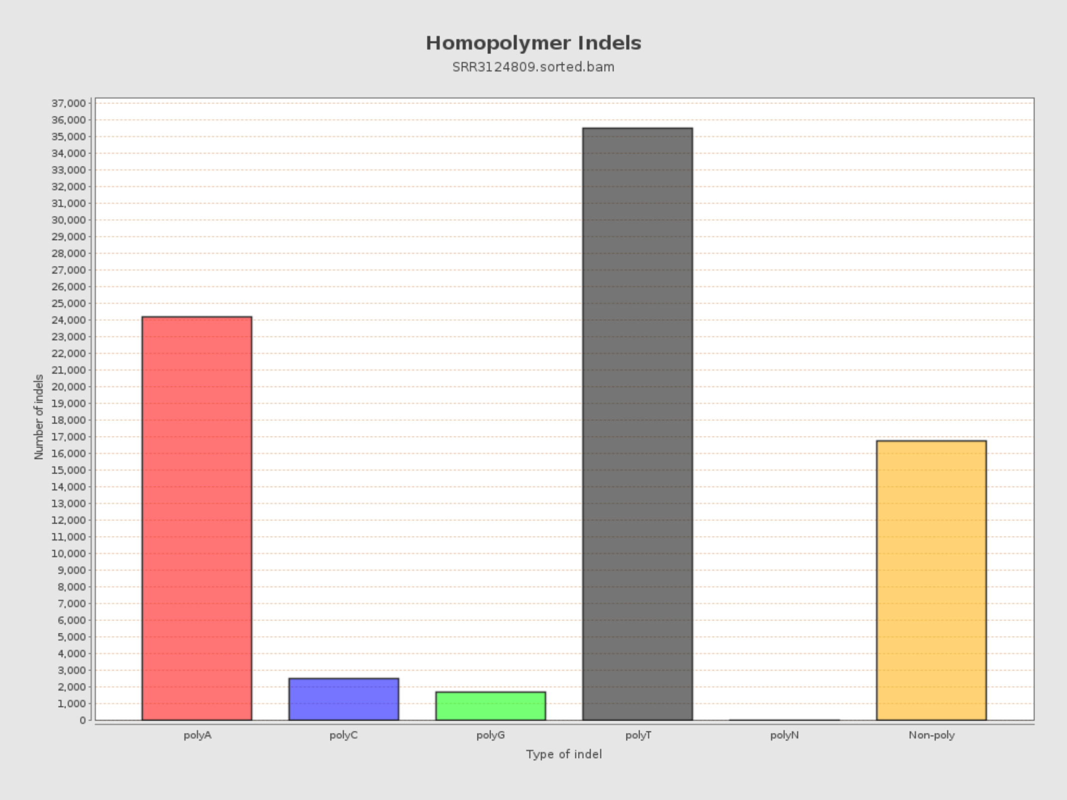
9. Results : Mapped Reads GC-content Distribution



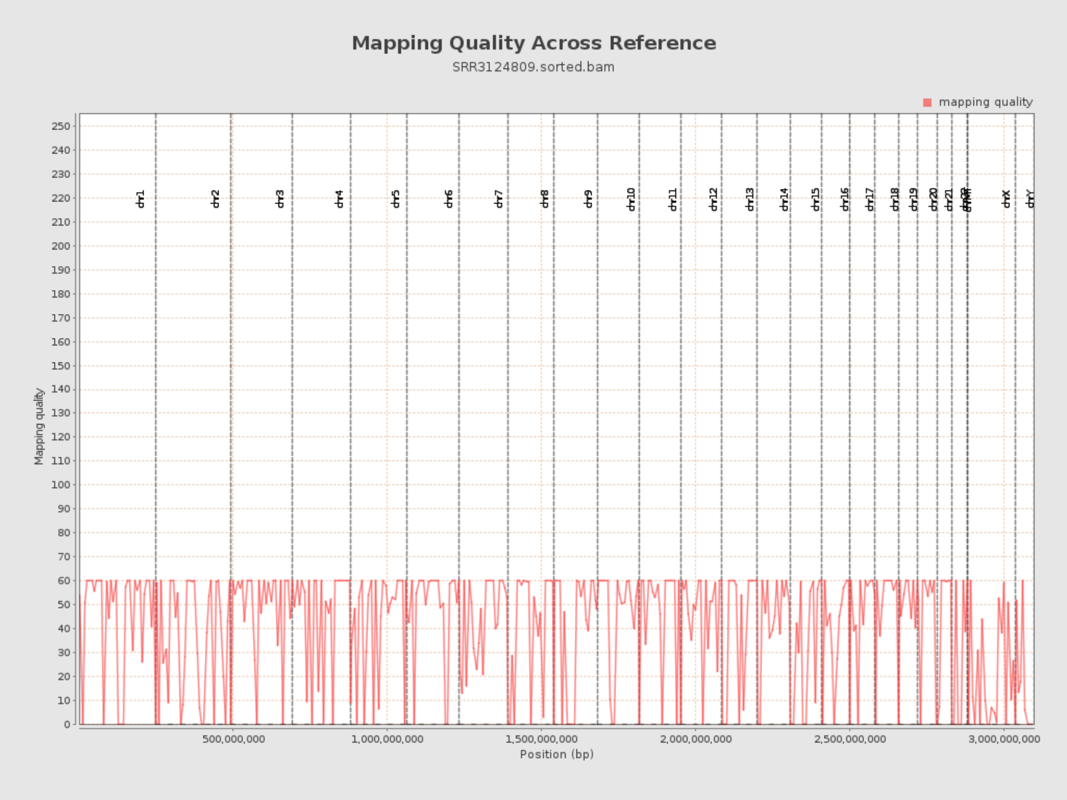
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram