Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:07:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124806.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_SRR3124806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:07:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	856,652
Mapped reads	854,933 / 99.8%
Unmapped reads	1,719 / 0.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	405,071 / 47.29%
Read min/max/mean length	30 / 151 / 181.65
Duplicated reads (estimated)	1,252,573 / 146.22%
Duplication rate	6.67%
Clipped reads	850,588 / 99.29%

2.2. ACGT Content

Number/percentage of A's	36,268,910 / 28.46%
Number/percentage of C's	22,352,115 / 17.54%
Number/percentage of T's	42,708,052 / 33.51%
Number/percentage of G's	26,127,428 / 20.5%
Number/percentage of N's	0 / 0%
GC Percentage	38.04%

2.3. Coverage

Mean	0.0412

Standard Deviation	116.0534

2.4. Mapping Quality

Mean Mapping Quality	49.25

2.5. Mismatches and indels

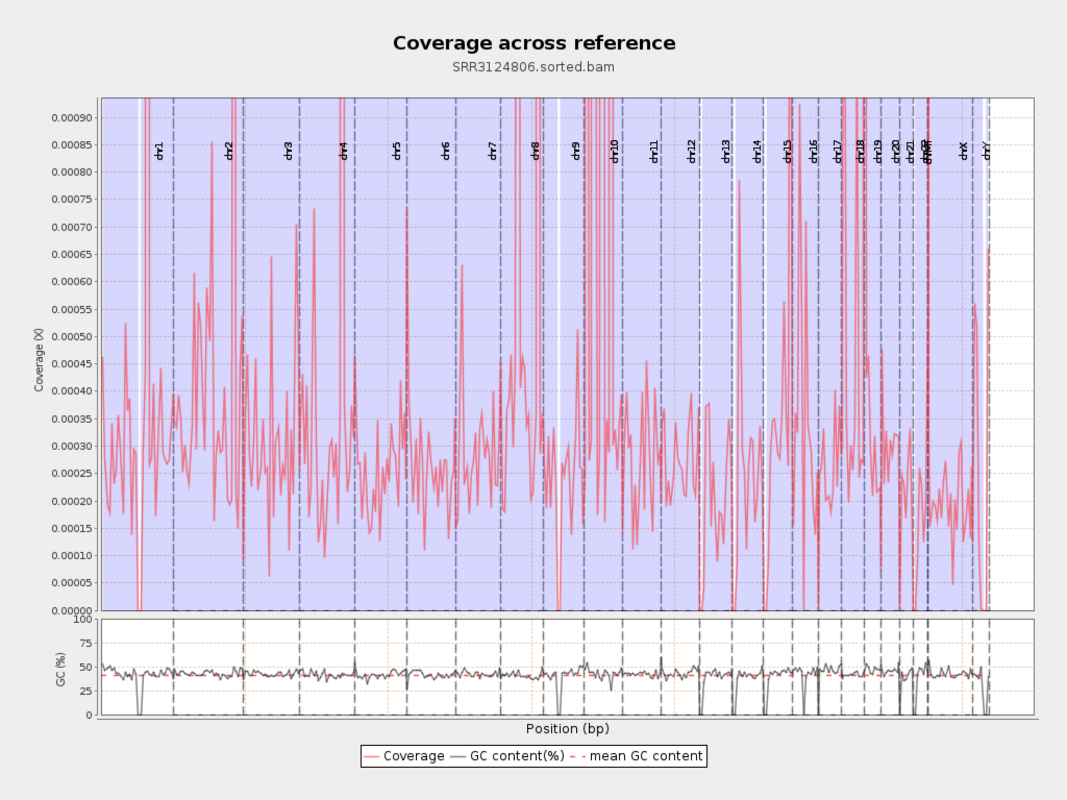
General error rate	0.81%
Mismatches	1,015,817
Insertions	12,441
Mapped reads with at least one insertion	1.45%
Deletions	32,257
Mapped reads with at least one deletion	3.72%
Homopolymer indels	54.03%

2.6. Chromosome stats

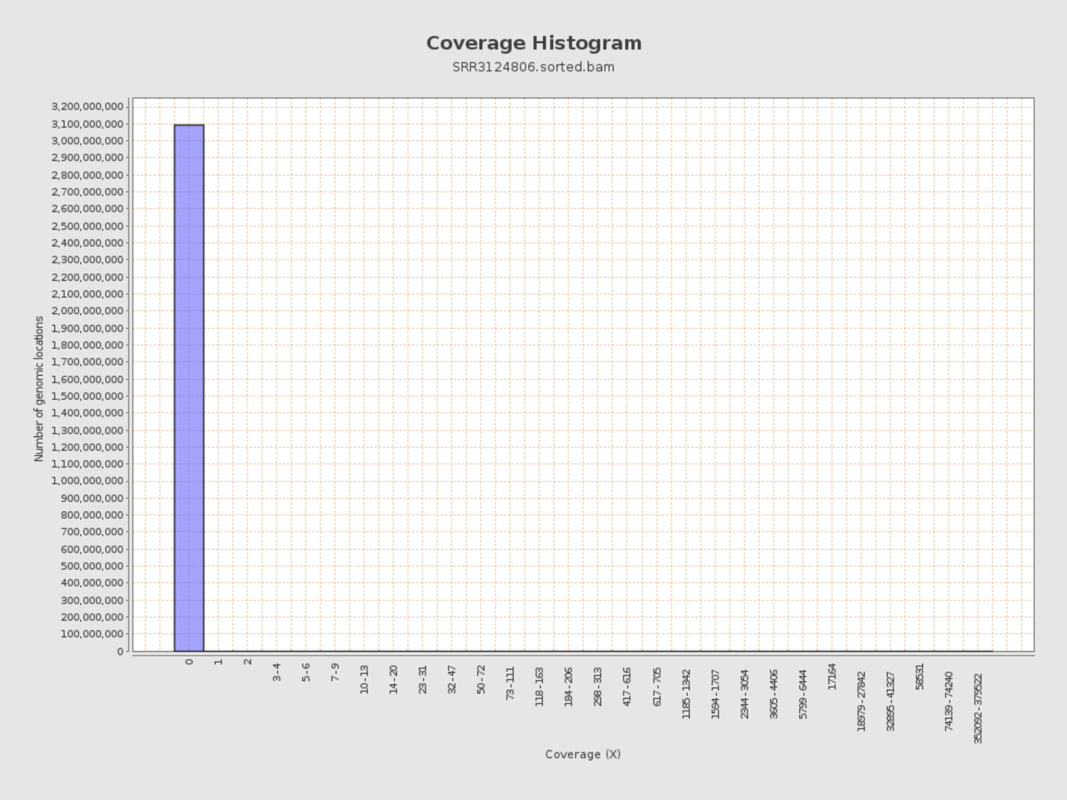
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1892465	0.0076	6.811
chr2	243199373	113809	0.0005	0.128
chr3	198022430	61931	0.0003	0.0357
chr4	191154276	221526	0.0012	0.9884
chr5	180915260	46657	0.0003	0.0162
chr6	171115067	46077	0.0003	0.0419
chr7	159138663	45973	0.0003	0.0321

chr8	146364022	1361273	0.0093	6.0536
chr9	141213431	34193	0.0002	0.0159
chr10	135534747	123266572	0.9095	554.5258
chr11	135006516	37571	0.0003	0.0245
chr12	133851895	36439	0.0003	0.017
chr13	115169878	22523	0.0002	0.0141
chr14	107349540	26050	0.0002	0.0599
chr15	102531392	38845	0.0004	0.0741
chr16	90354753	32284	0.0004	0.0451
chr17	81195210	21632	0.0003	0.0179
chr18	78077248	39180	0.0005	0.0829
chr19	59128983	60748	0.001	0.339
chr20	63025520	19434	0.0003	0.0189
chr21	48129895	10418	0.0002	0.0148
chr22	51304566	7935	0.0002	0.0126
chrMT	16571	654	0.0395	0.1947
chrX	155270560	30474	0.0002	0.0148
chrY	59373566	15113	0.0003	0.0241

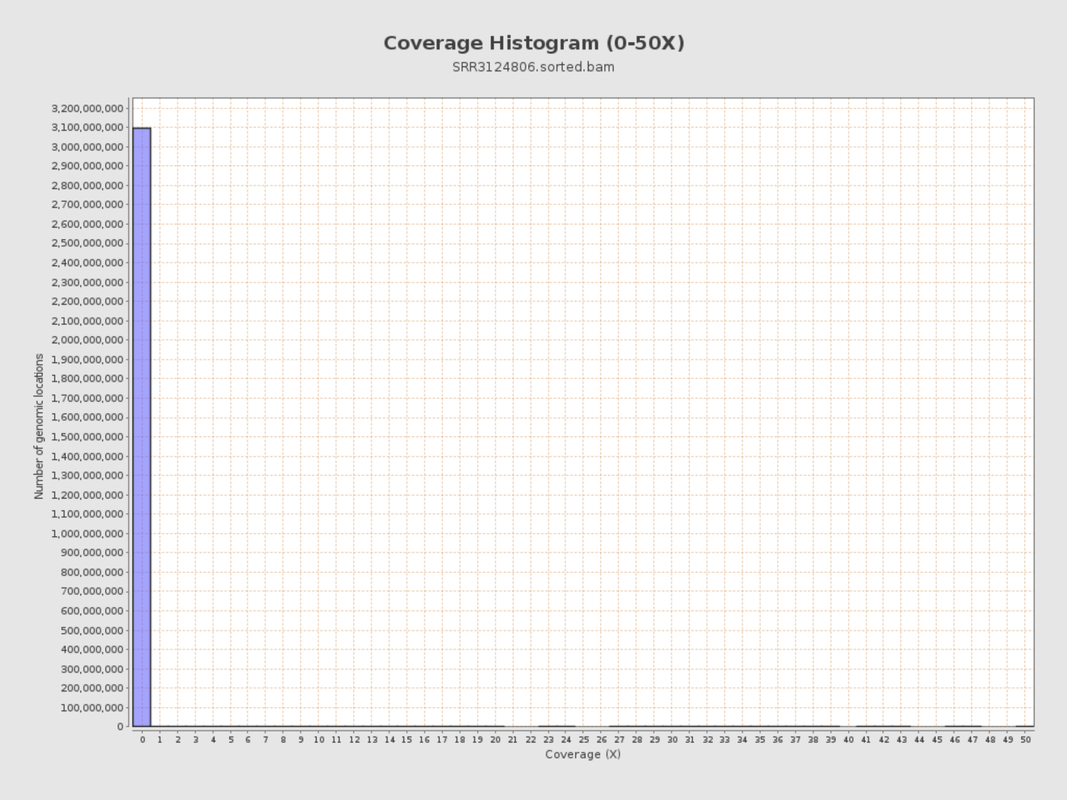
3. Results : Coverage across reference



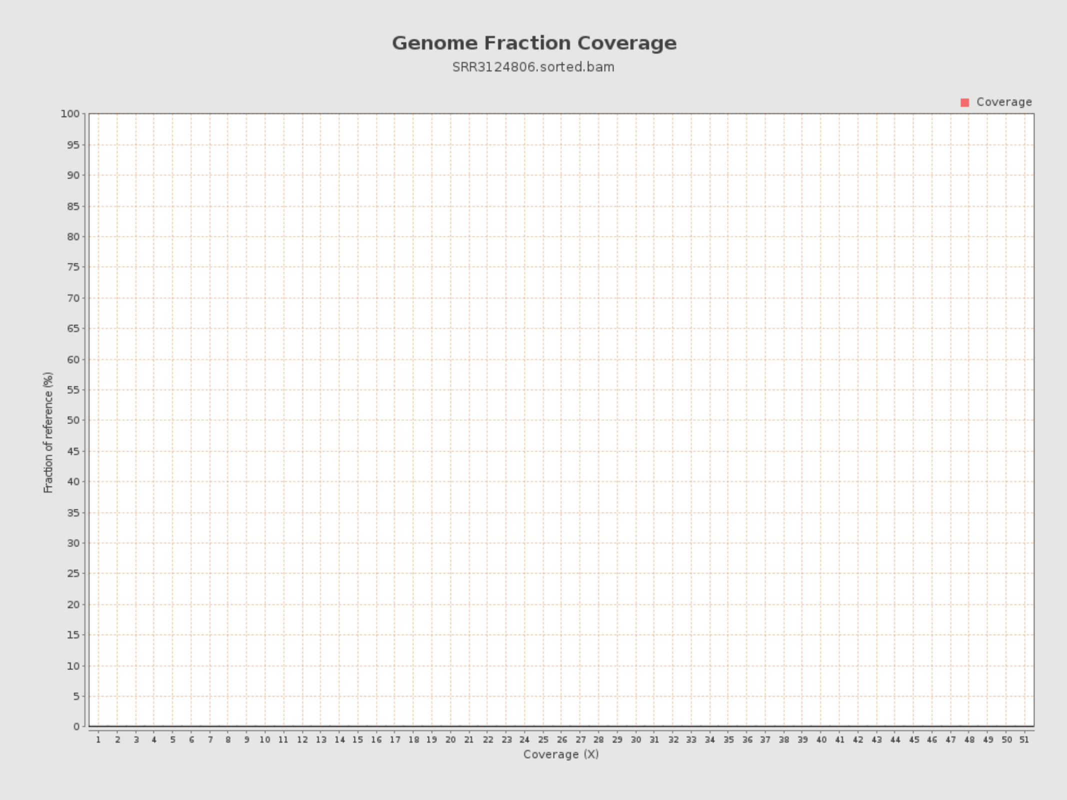
4. Results : Coverage Histogram



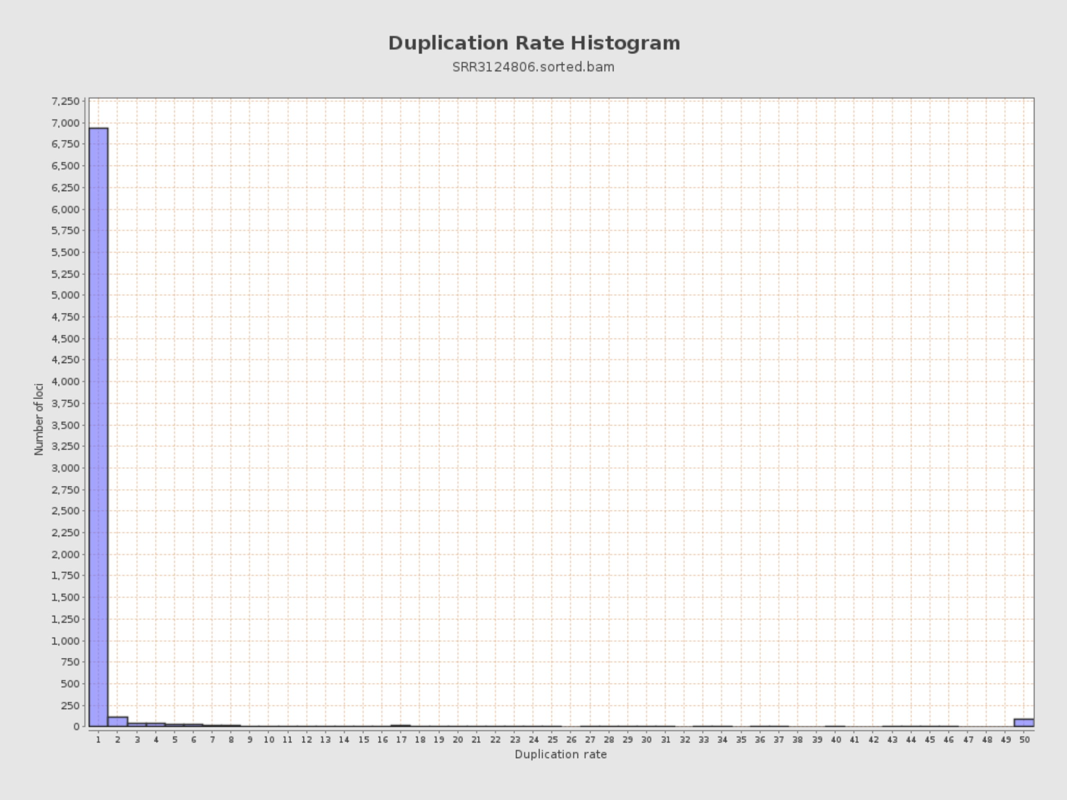
5. Results : Coverage Histogram (0-50X)



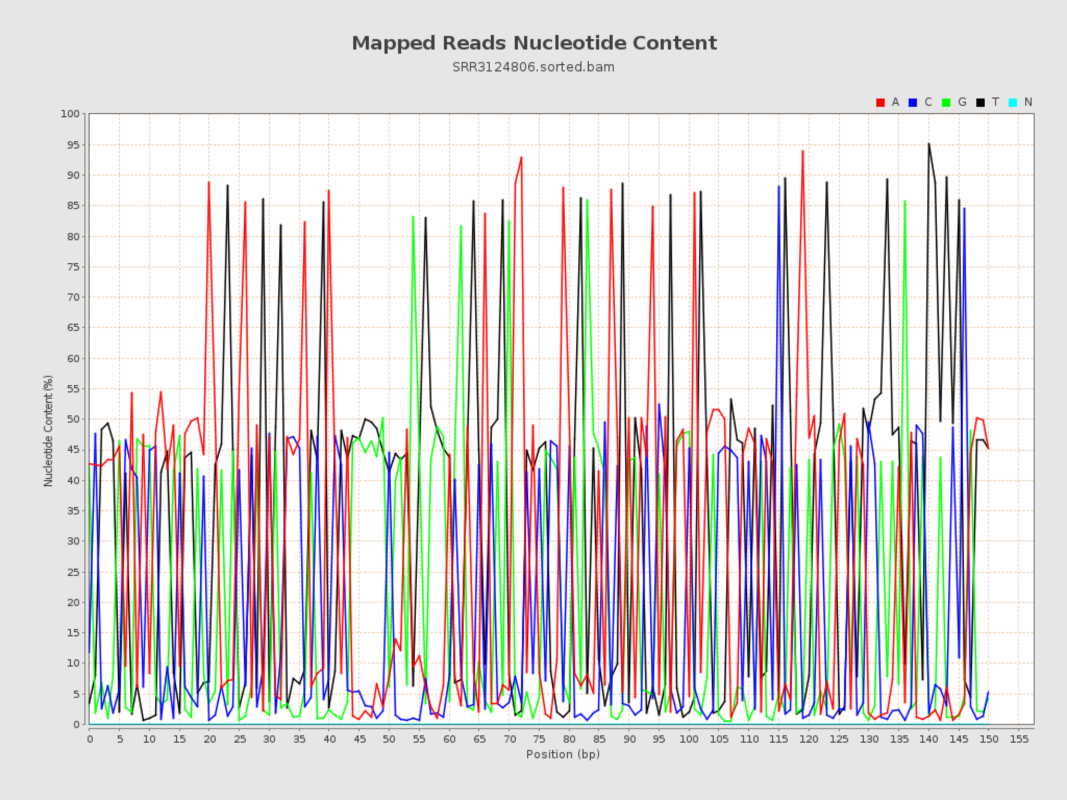
6. Results : Genome Fraction Coverage



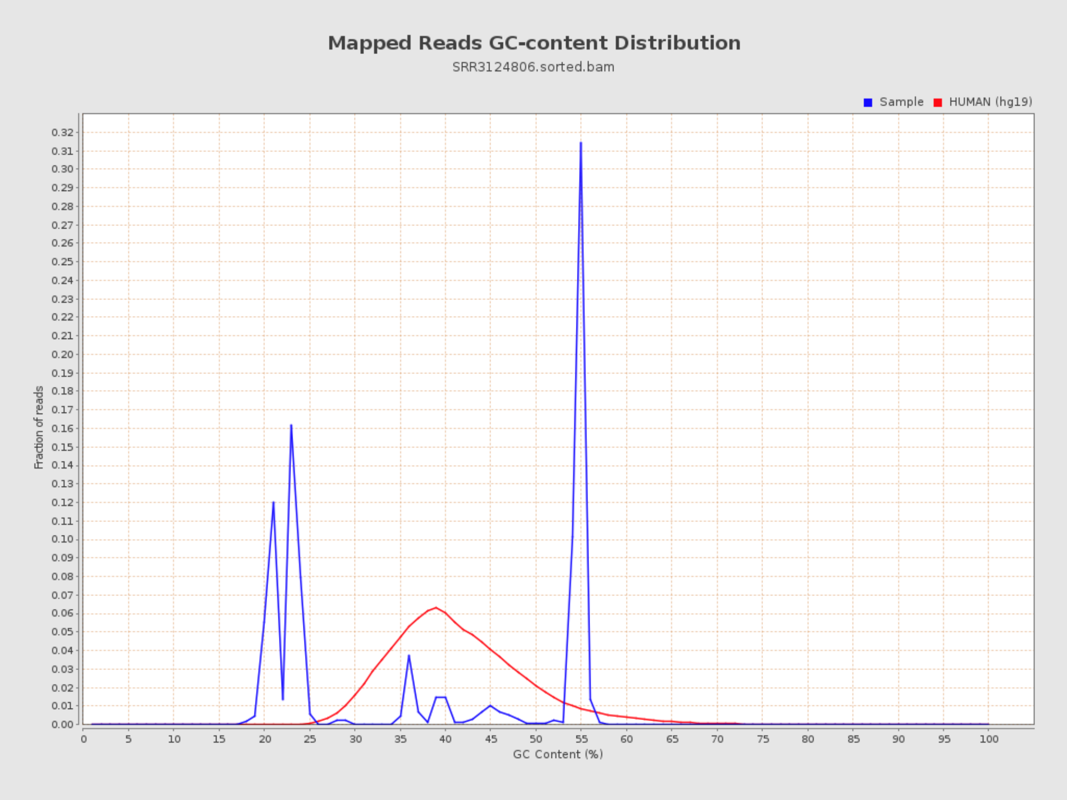
7. Results : Duplication Rate Histogram



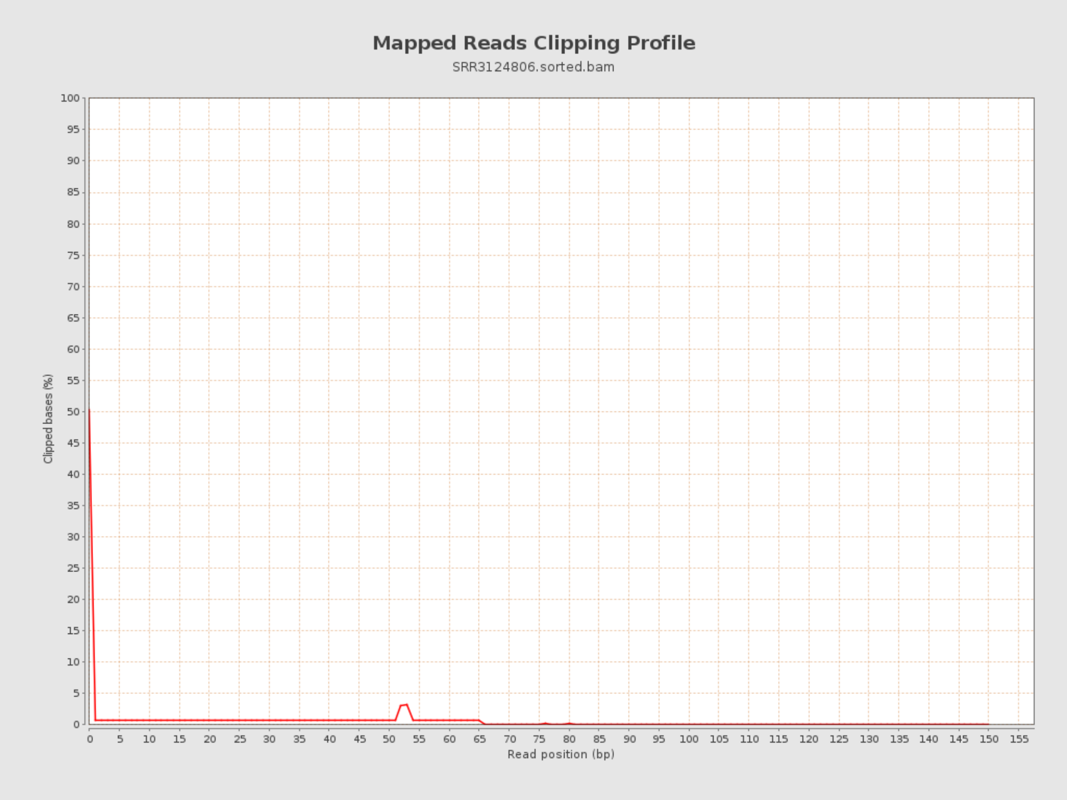
8. Results : Mapped Reads Nucleotide Content



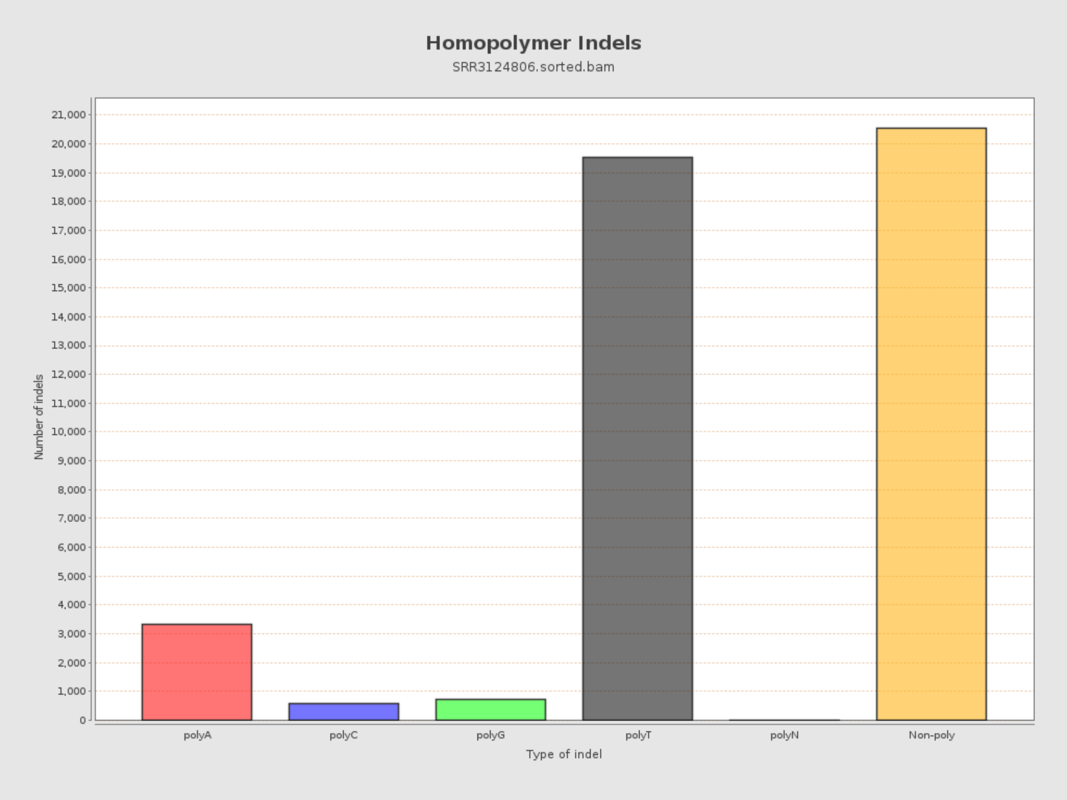
9. Results : Mapped Reads GC-content Distribution



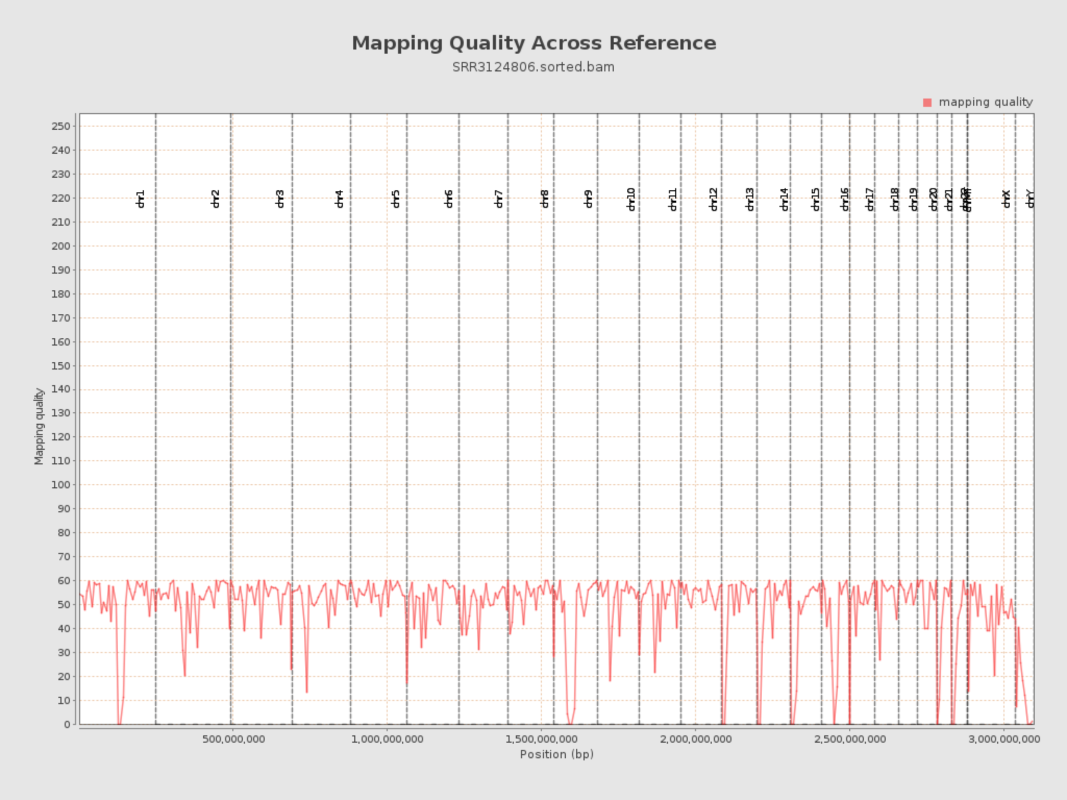
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram