Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:05:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124805.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_SRR3124805 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124805.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:05:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124805.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	589,044
Mapped reads	588,173 / 99.85%
Unmapped reads	871 / 0.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	268,155 / 45.52%
Read min/max/mean length	30 / 151 / 182.7
Duplicated reads (estimated)	855,088 / 145.17%
Duplication rate	30.32%
Clipped reads	555,383 / 94.29%

2.2. ACGT Content

Number/percentage of A's	27,120,031 / 30.58%
Number/percentage of C's	15,190,818 / 17.13%
Number/percentage of T's	28,119,610 / 31.7%
Number/percentage of G's	18,267,893 / 20.6%
Number/percentage of N's	0 / 0%
GC Percentage	37.72%

2.3. Coverage

Mean	0.0287

Standard Deviation	68.0972

2.4. Mapping Quality

Mean Mapping Quality	39.76

2.5. Mismatches and indels

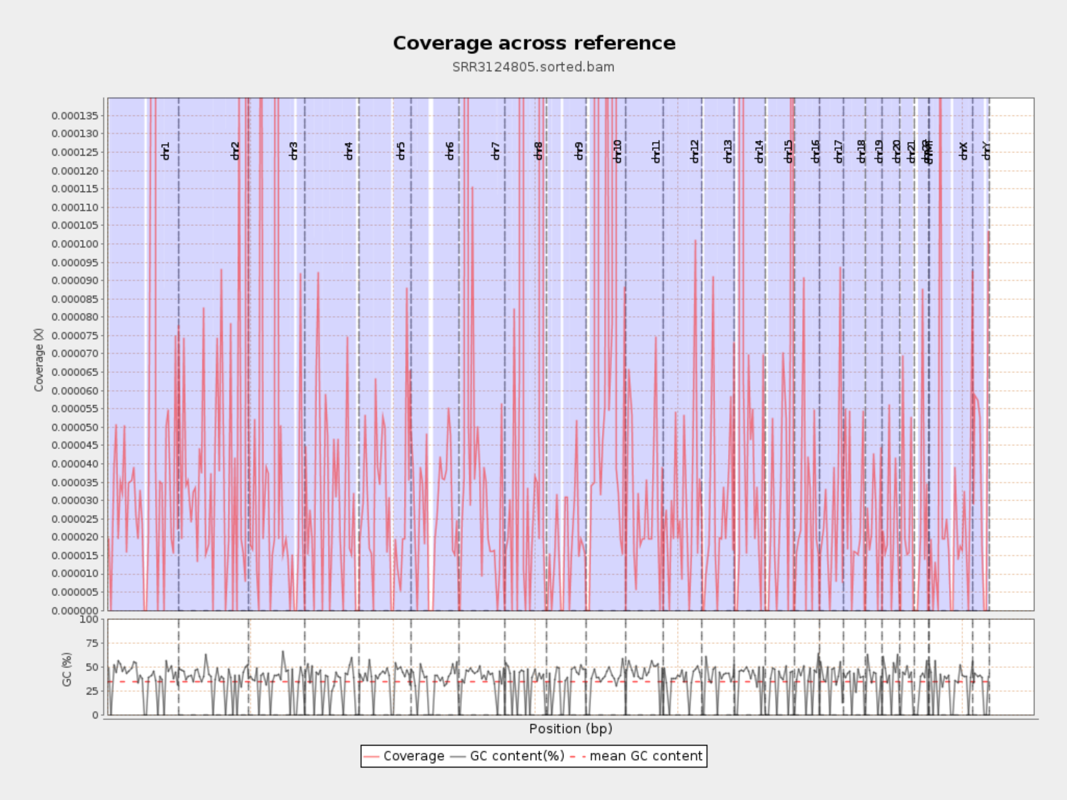
General error rate	1.06%
Mismatches	913,996
Insertions	20,936
Mapped reads with at least one insertion	3.52%
Deletions	40,484
Mapped reads with at least one deletion	6.71%
Homopolymer indels	86.49%

2.6. Chromosome stats

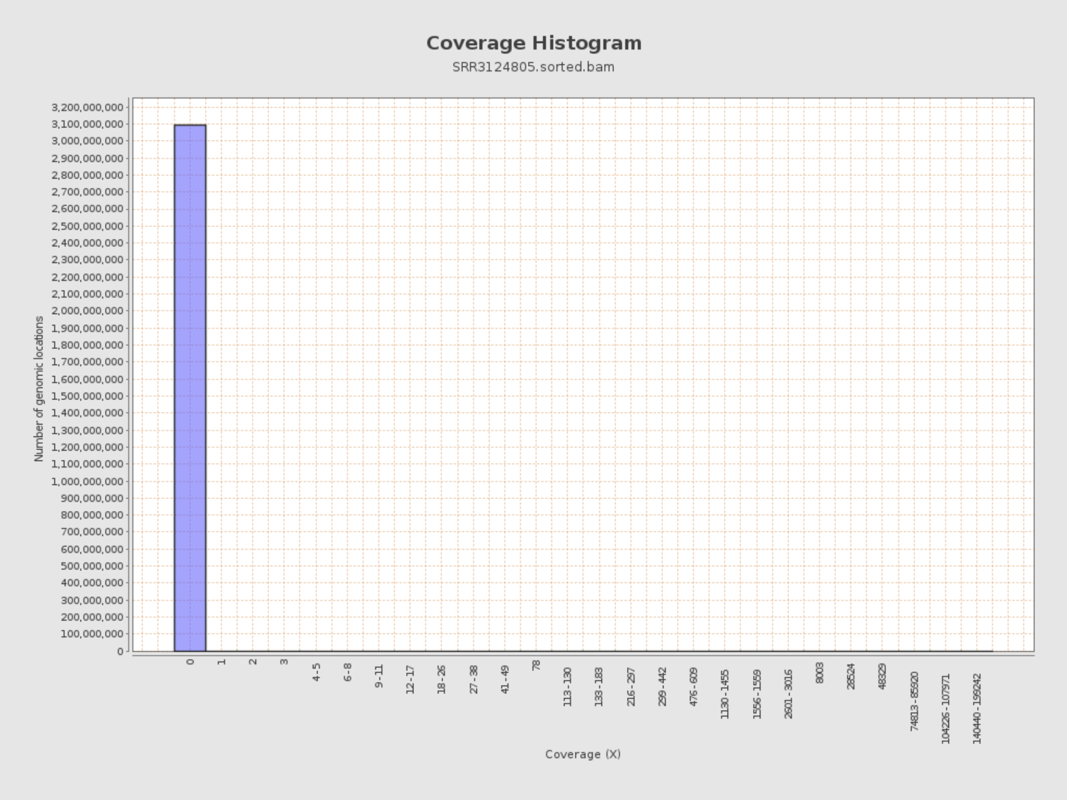
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	120994	0.0005	0.4208
chr2	243199373	13303	0.0001	0.0468
chr3	198022430	12372	0.0001	0.0695
chr4	191154276	5706	0	0.0056
chr5	180915260	5197	0	0.0054
chr6	171115067	4561	0	0.0052
chr7	159138663	11351	0.0001	0.0741

chr8	146364022	60059592	0.4103	281.0722
chr9	141213431	2366	0	0.0041
chr10	135534747	28448832	0.2099	143.5359
chr11	135006516	3946	0	0.0056
chr12	133851895	4030	0	0.0055
chr13	115169878	3175	0	0.0053
chr14	107349540	21994	0.0002	0.2765
chr15	102531392	5373	0.0001	0.0166
chr16	90354753	2422	0	0.0053
chr17	81195210	2199	0	0.0052
chr18	78077248	2049	0	0.0051
chr19	59128983	1412	0	0.0049
chr20	63025520	1427	0	0.0048
chr21	48129895	1338	0	0.0053
chr22	51304566	1205	0	0.0048
chrMT	16571	0	0	0
chrX	155270560	3899	0	0.0154
chrY	59373566	2389	0	0.0065

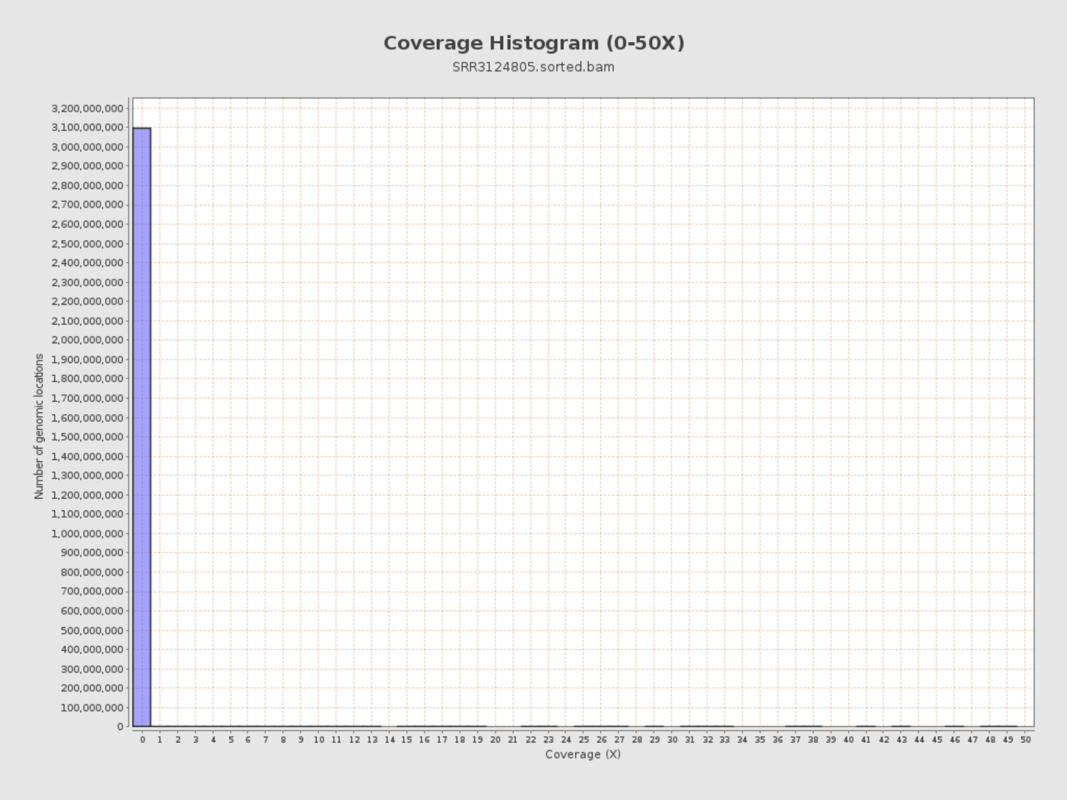
3. Results : Coverage across reference



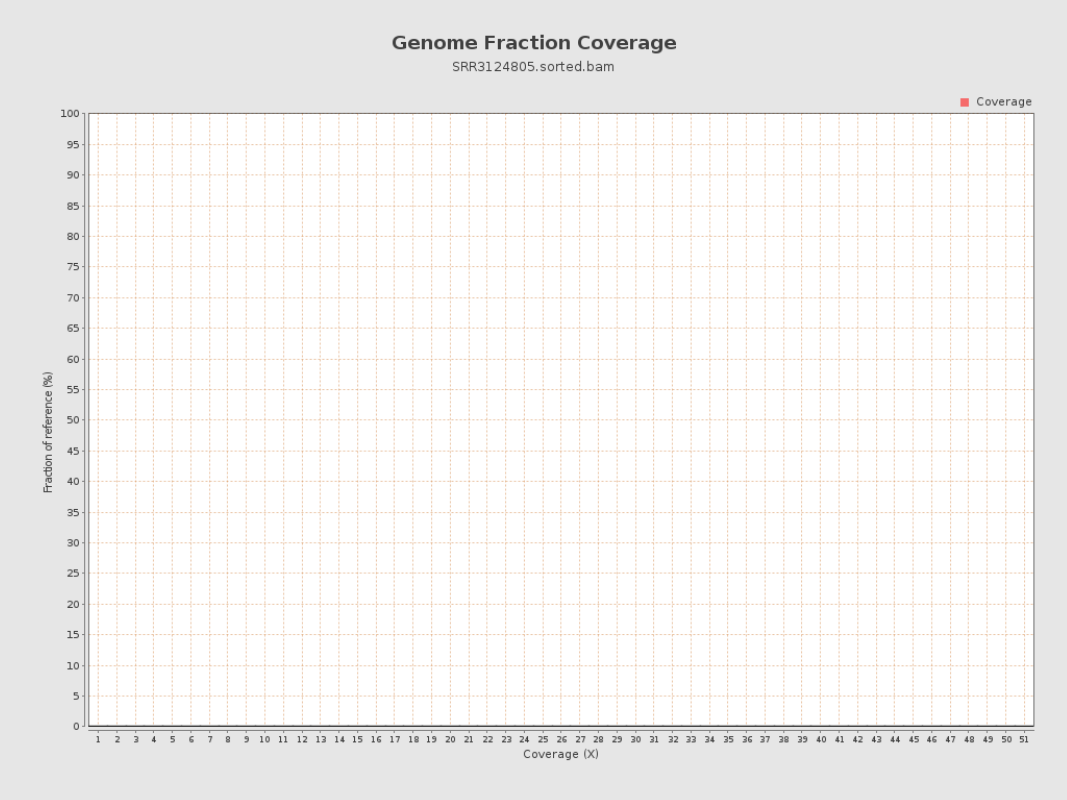
4. Results : Coverage Histogram



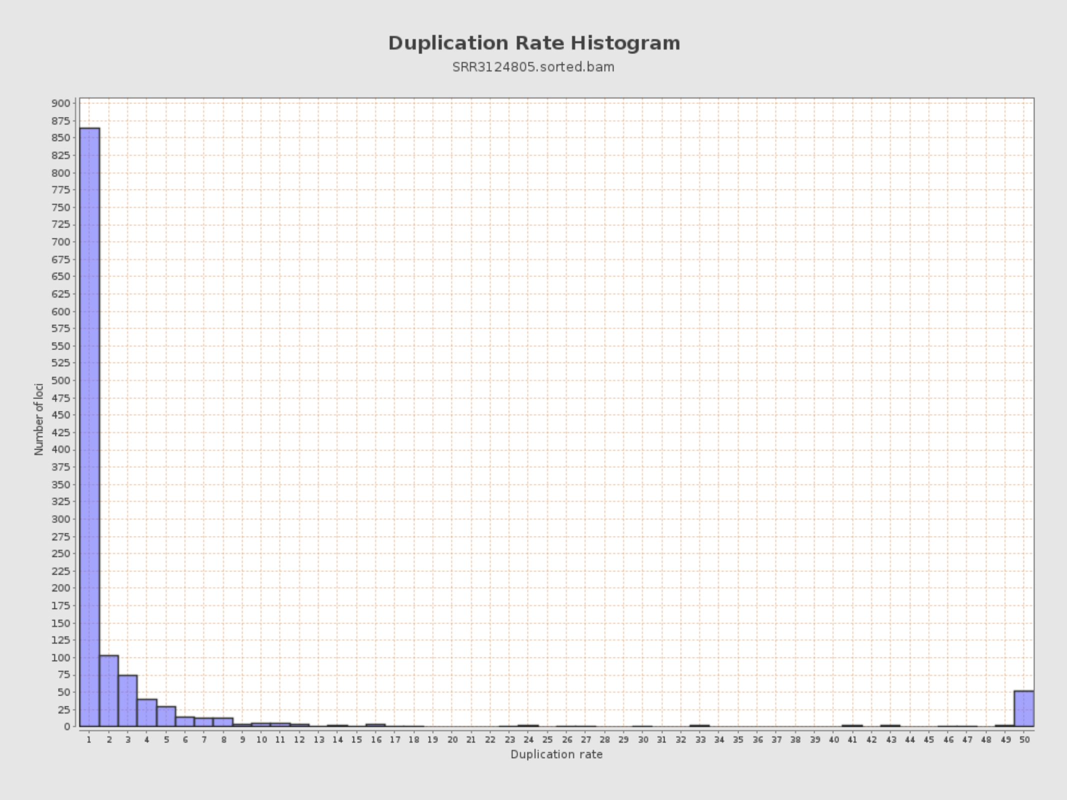
5. Results : Coverage Histogram (0-50X)



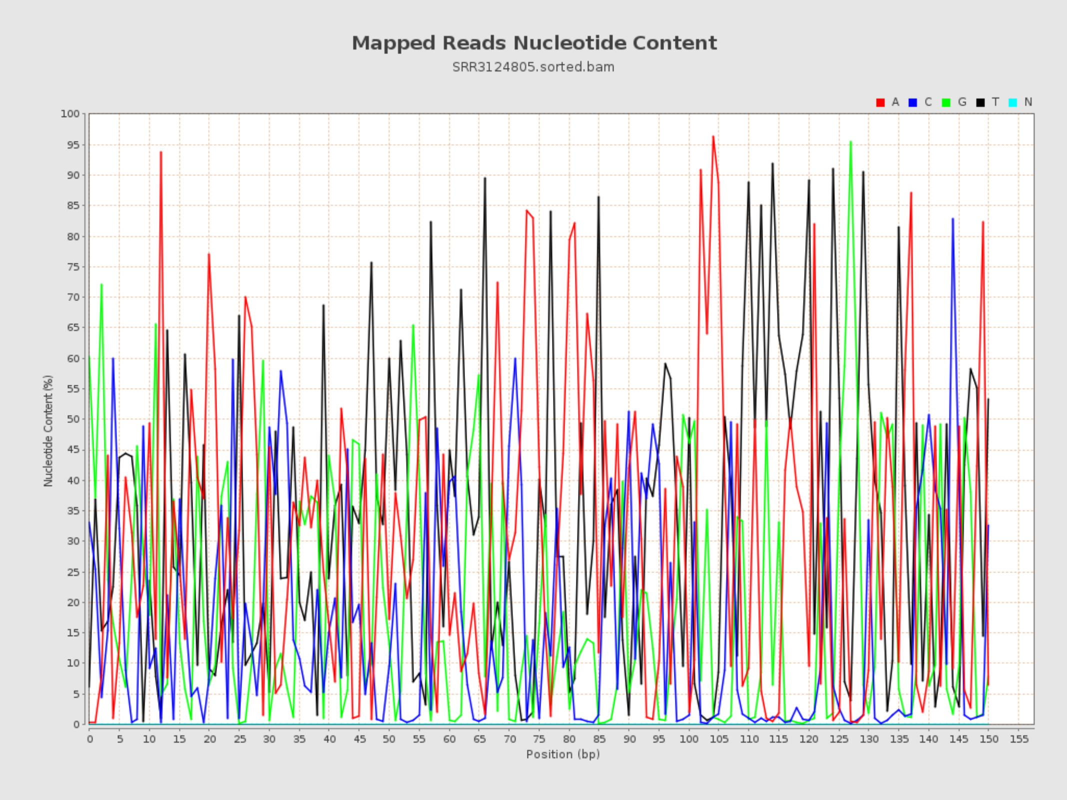
6. Results : Genome Fraction Coverage



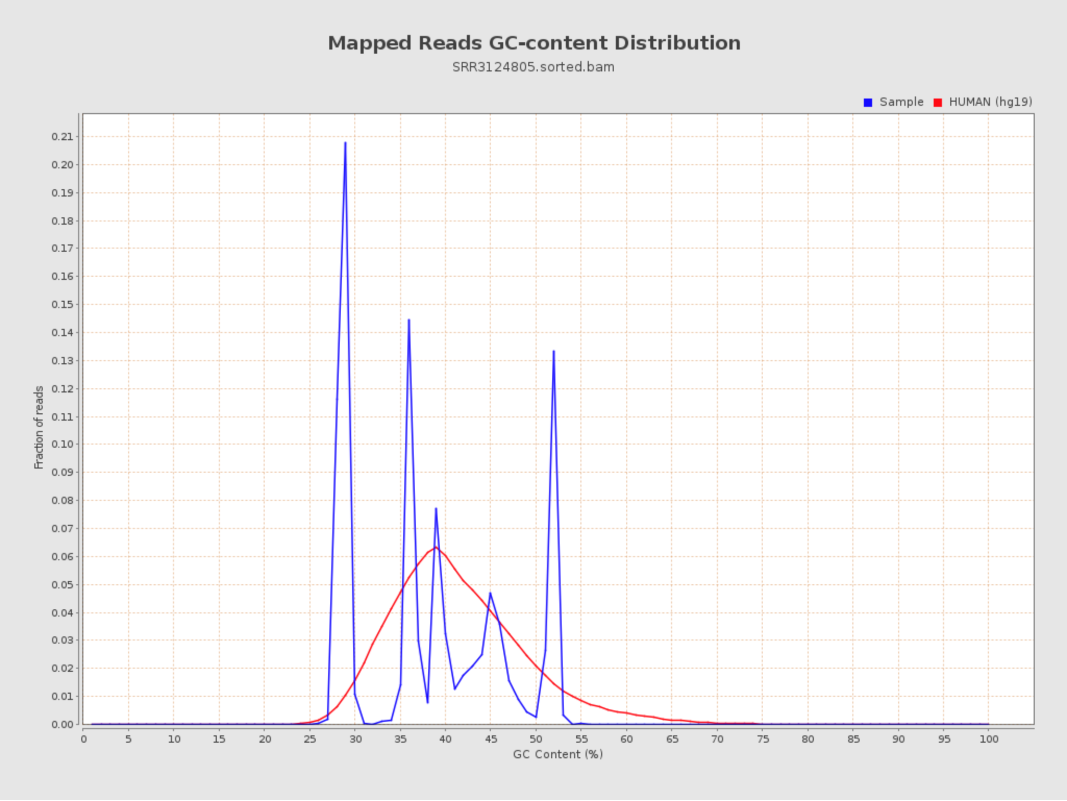
7. Results : Duplication Rate Histogram



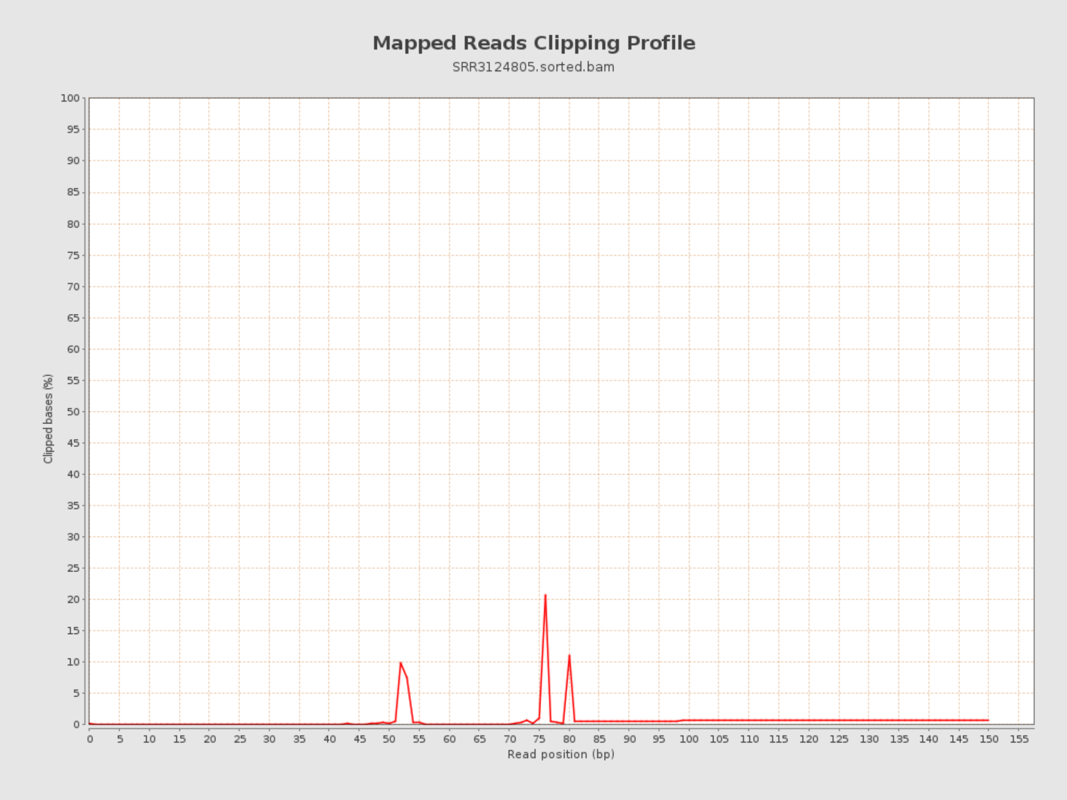
8. Results : Mapped Reads Nucleotide Content



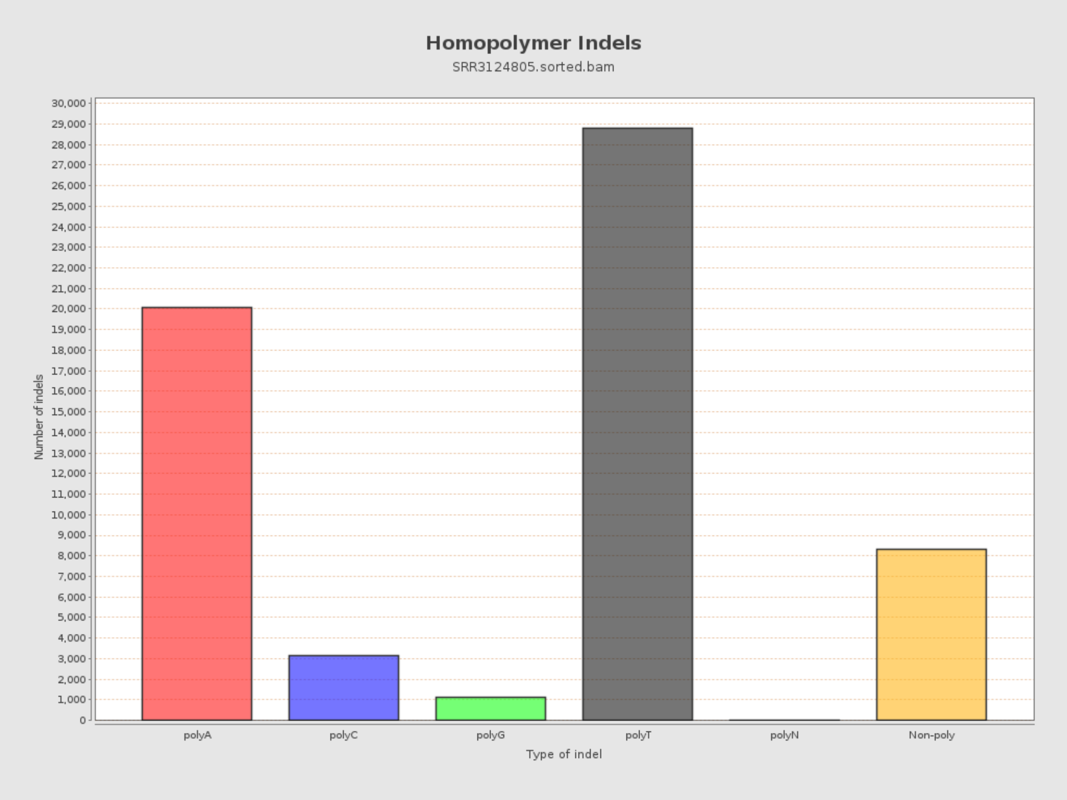
9. Results : Mapped Reads GC-content Distribution



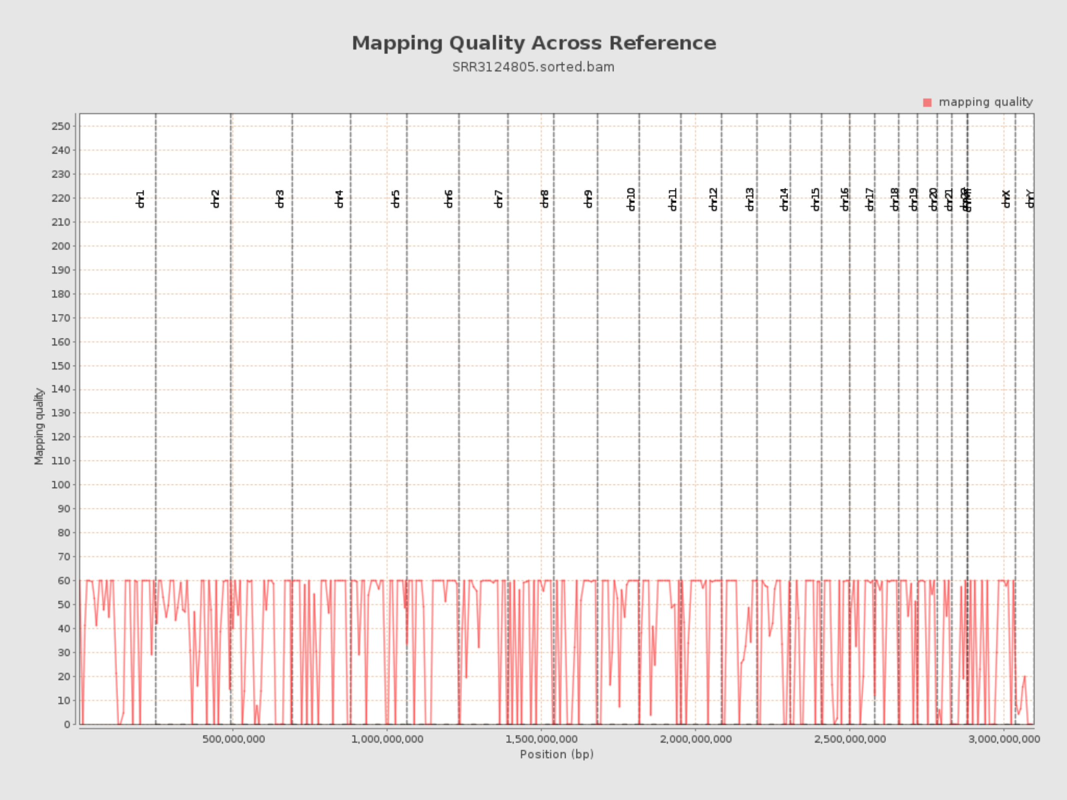
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram