Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:57:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124800.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_SRR3124800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:57:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	598,057
Mapped reads	597,214 / 99.86%
Unmapped reads	843 / 0.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	285,541 / 47.74%
Read min/max/mean length	30 / 151 / 187.85
Duplicated reads (estimated)	880,494 / 147.23%
Duplication rate	14.06%
Clipped reads	589,036 / 98.49%

2.2. ACGT Content

Number/percentage of A's	26,133,536 / 28.82%
Number/percentage of C's	13,367,912 / 14.74%
Number/percentage of T's	30,473,704 / 33.6%
Number/percentage of G's	20,707,542 / 22.84%
Number/percentage of N's	0 / 0%
GC Percentage	37.58%

2.3. Coverage

Mean	0.0293

Standard Deviation	92.338

2.4. Mapping Quality

Mean Mapping Quality	48.94

2.5. Mismatches and indels

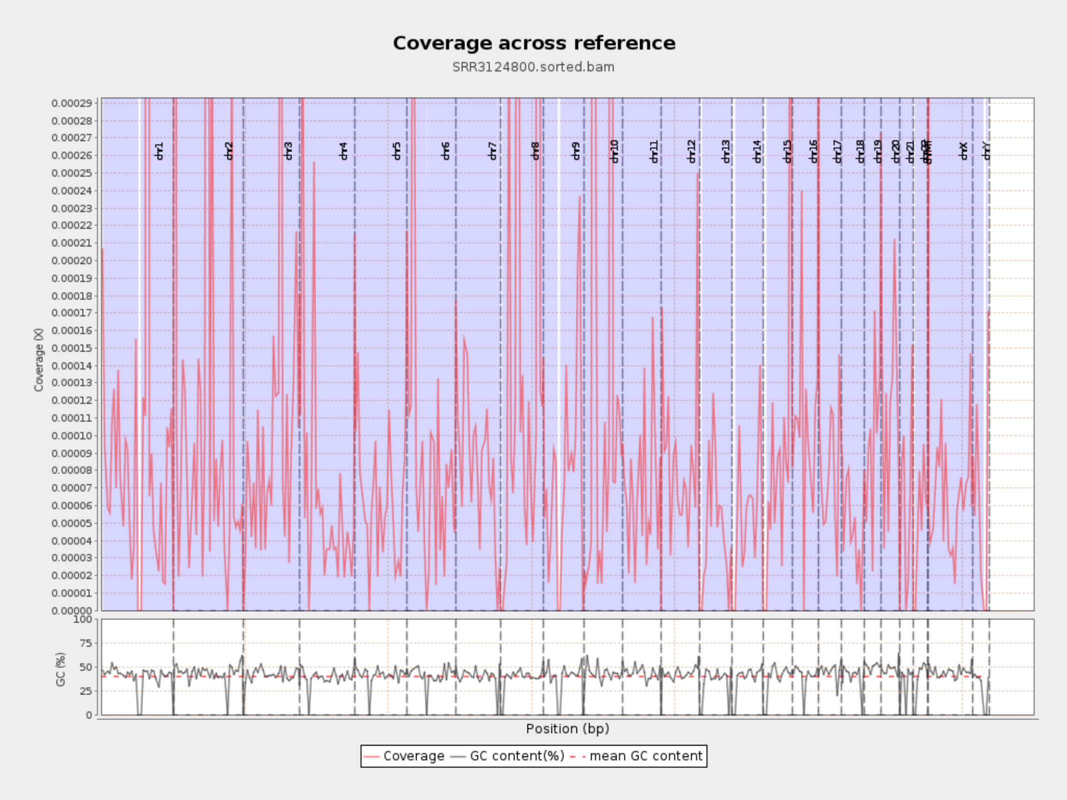
General error rate	0.88%
Mismatches	778,129
Insertions	22,290
Mapped reads with at least one insertion	3.7%
Deletions	52,480
Mapped reads with at least one deletion	8.52%
Homopolymer indels	86.53%

2.6. Chromosome stats

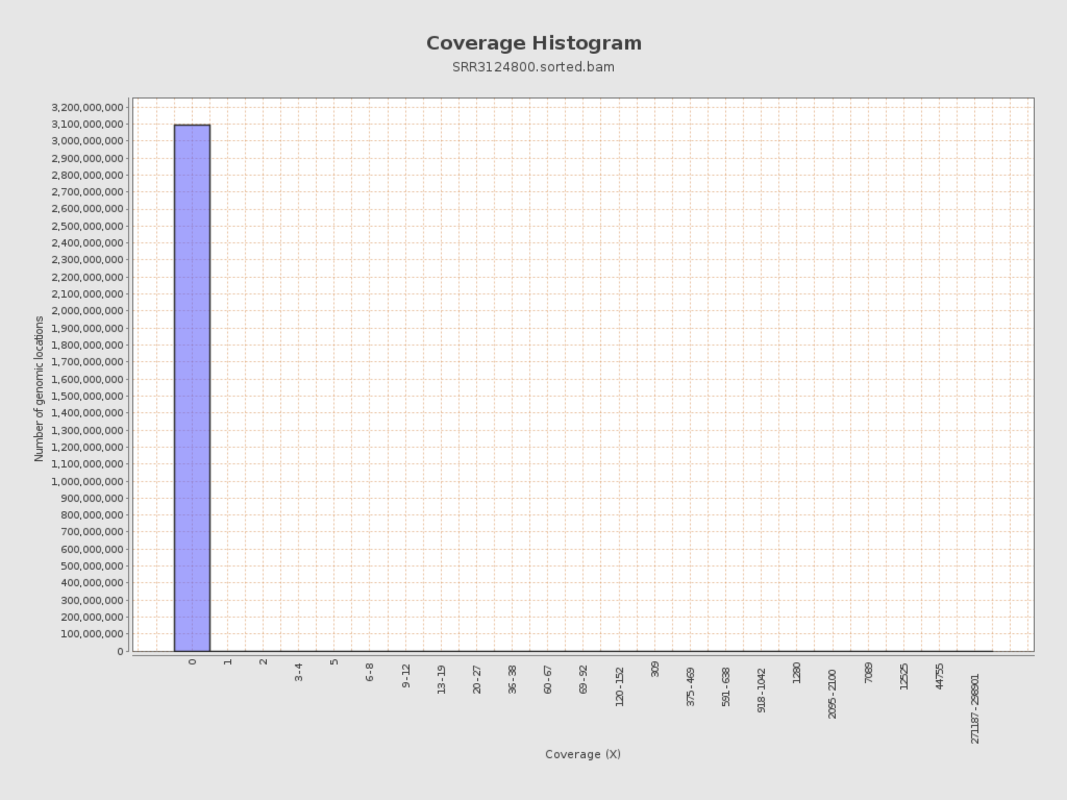
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	314352	0.0013	1.1042
chr2	243199373	39200	0.0002	0.0496
chr3	198022430	20906	0.0001	0.0239
chr4	191154276	13023	0.0001	0.0092
chr5	180915260	11425	0.0001	0.0079
chr6	171115067	15445	0.0001	0.0201
chr7	159138663	13303	0.0001	0.0091

chr8	146364022	90169374	0.6161	424.6581
chr9	141213431	11332	0.0001	0.0092
chr10	135534747	36962	0.0003	0.1214
chr11	135006516	9406	0.0001	0.0088
chr12	133851895	11864	0.0001	0.0094
chr13	115169878	5263	0	0.0068
chr14	107349540	5784	0.0001	0.0073
chr15	102531392	9589	0.0001	0.0188
chr16	90354753	9584	0.0001	0.0104
chr17	81195210	6568	0.0001	0.009
chr18	78077248	3487	0	0.0067
chr19	59128983	6050	0.0001	0.0107
chr20	63025520	7173	0.0001	0.0119
chr21	48129895	2786	0.0001	0.0077
chr22	51304566	2616	0.0001	0.0071
chrMT	16571	459	0.0277	0.1641
chrX	155270560	10179	0.0001	0.0081
chrY	59373566	3820	0.0001	0.008

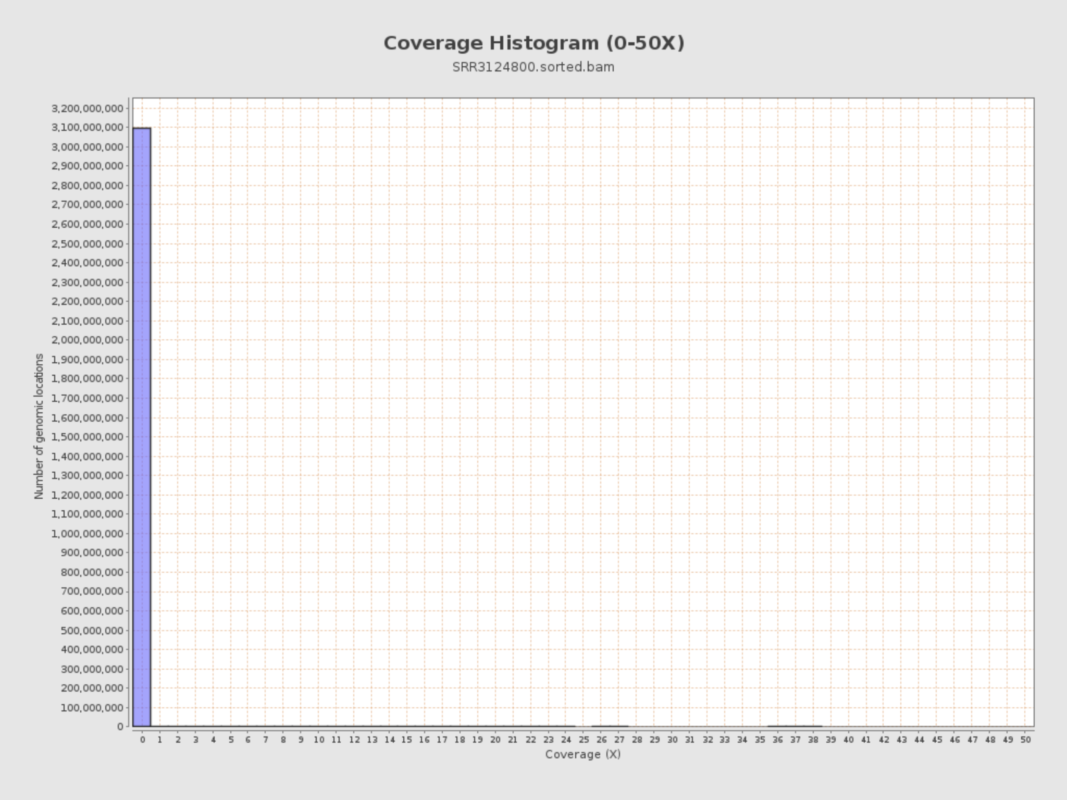
3. Results : Coverage across reference



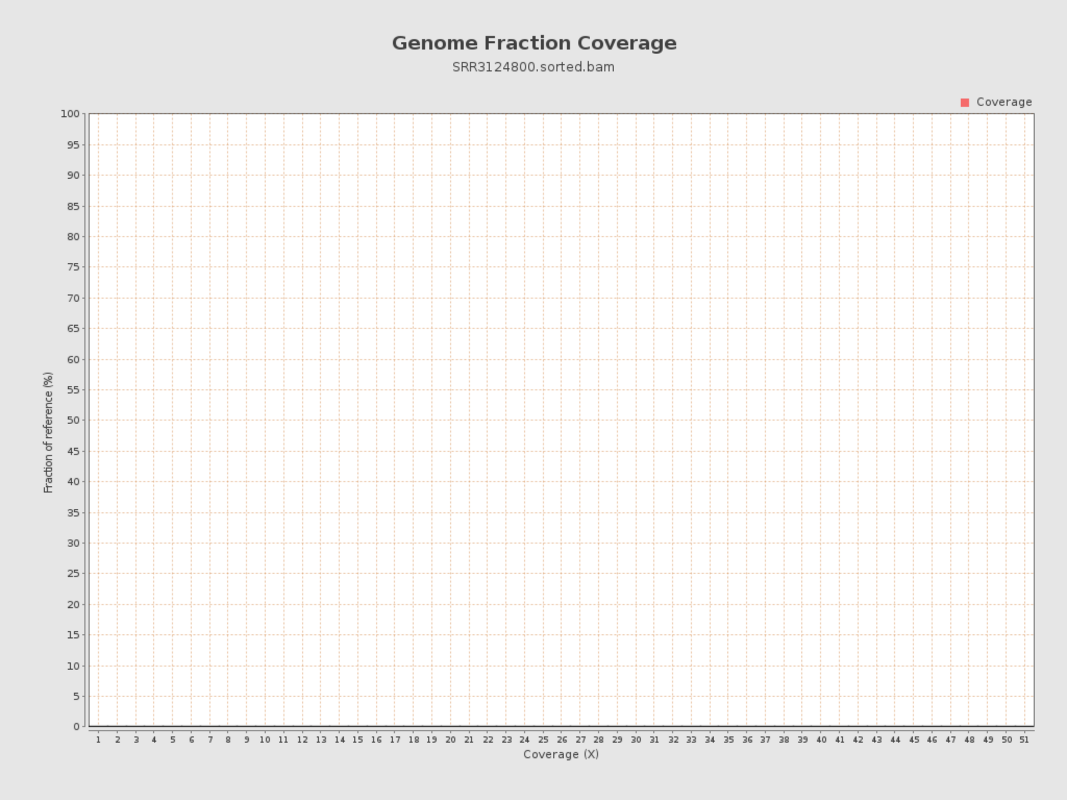
4. Results : Coverage Histogram



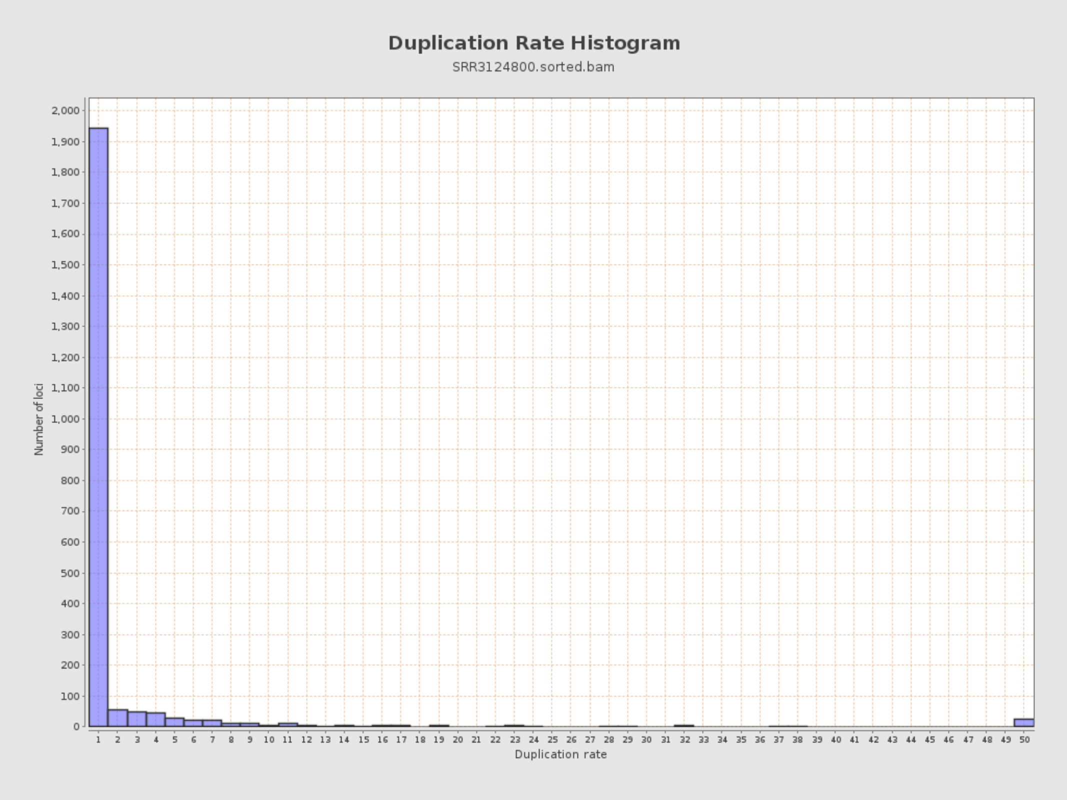
5. Results : Coverage Histogram (0-50X)



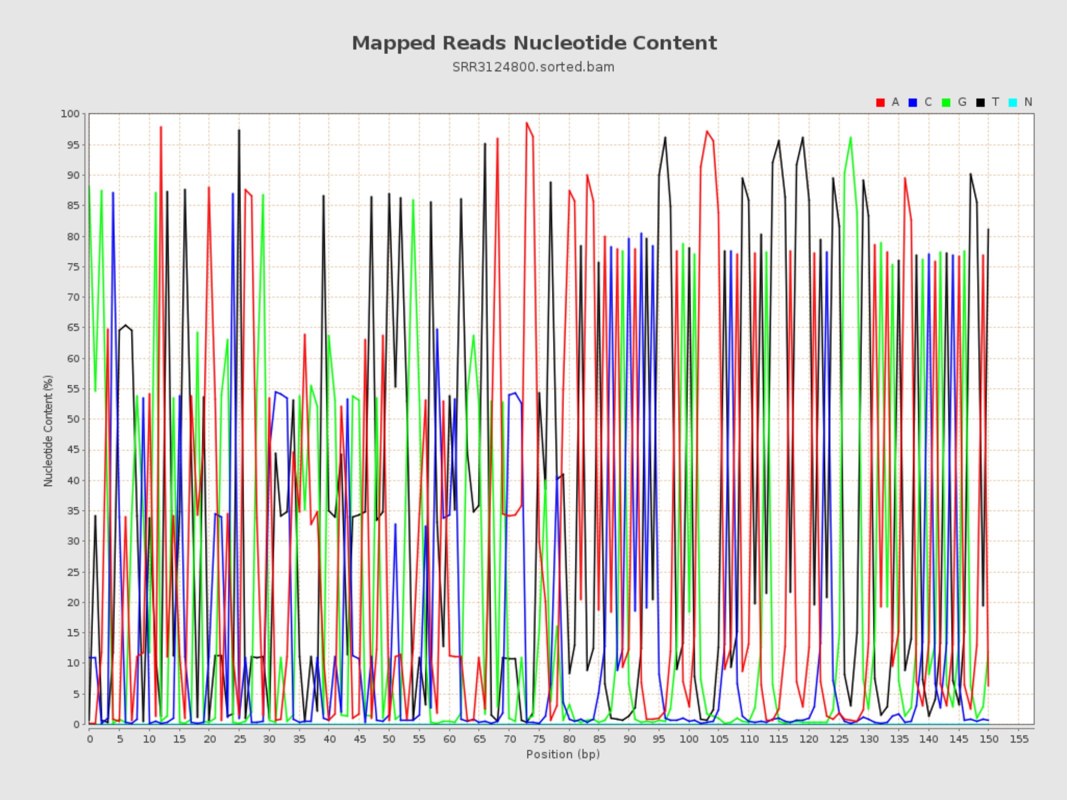
6. Results : Genome Fraction Coverage



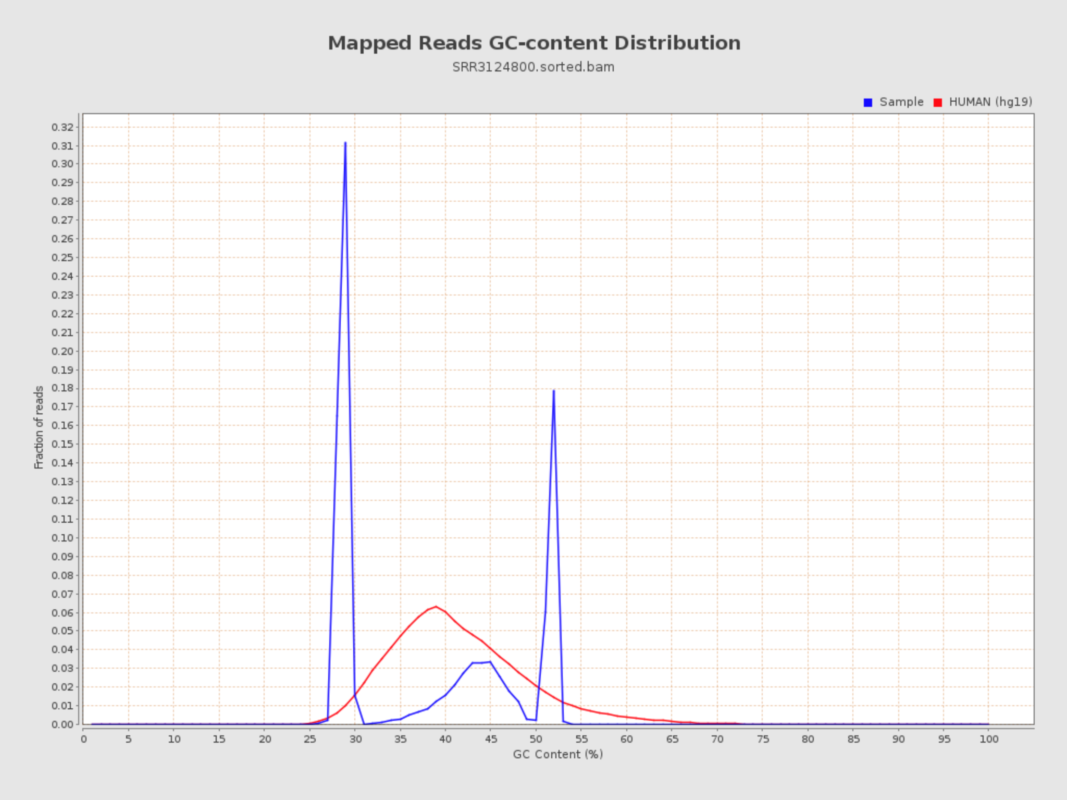
7. Results : Duplication Rate Histogram



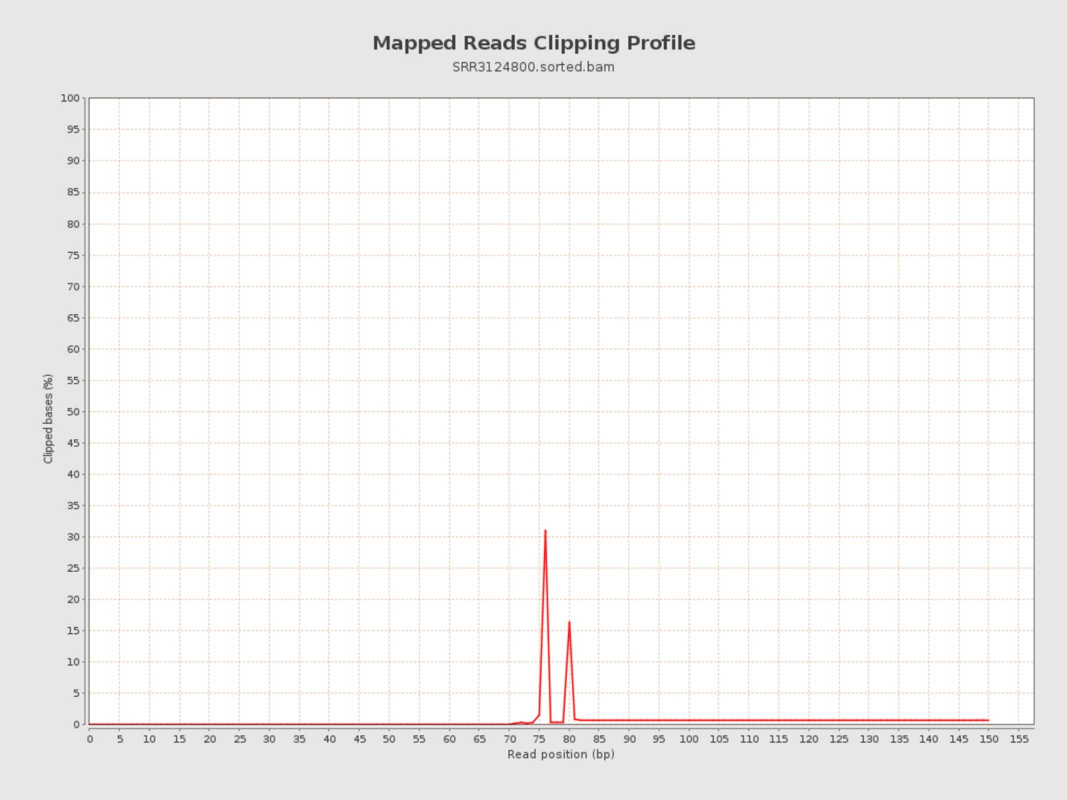
8. Results : Mapped Reads Nucleotide Content



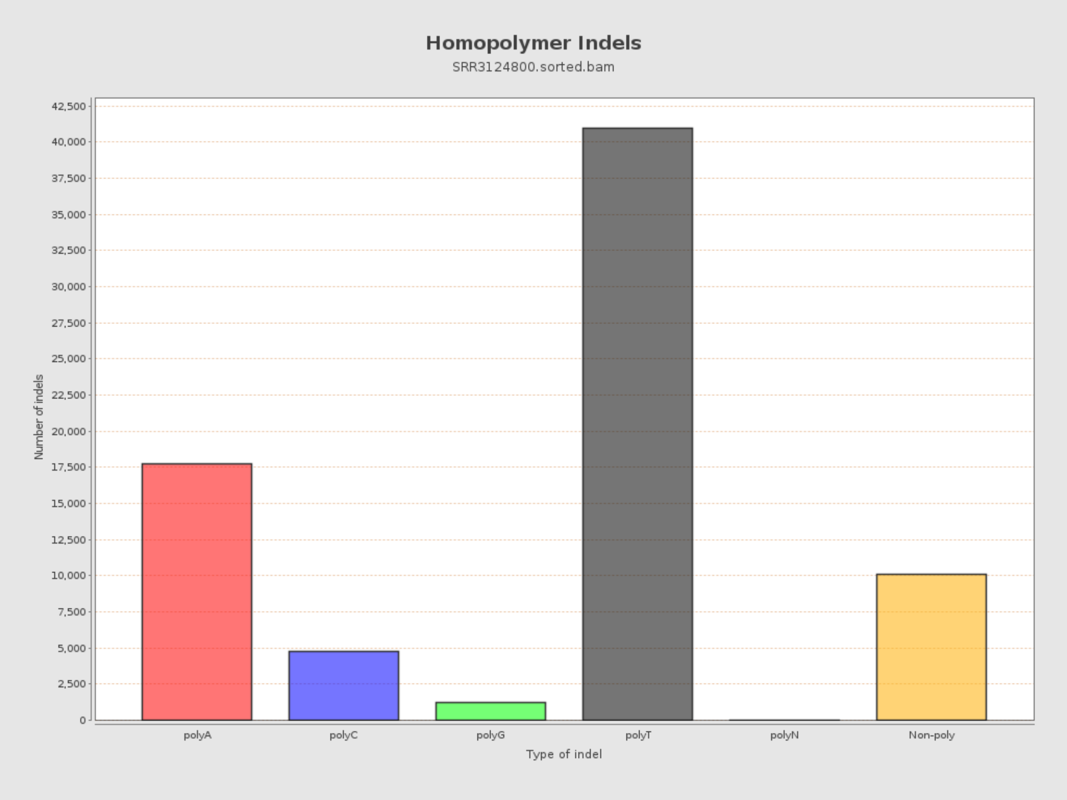
9. Results : Mapped Reads GC-content Distribution



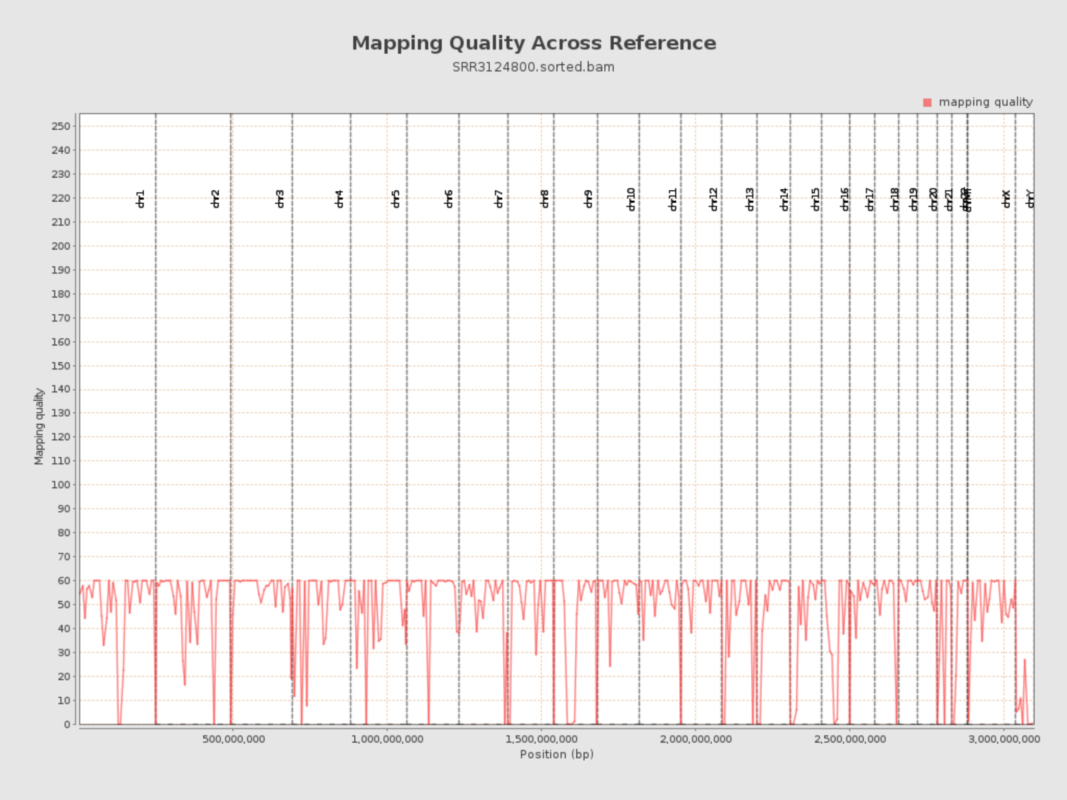
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram