

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:02:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124803.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_SRR3124803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:02:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	485,728
Mapped reads	478,596 / 98.53%
Unmapped reads	7,132 / 1.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	152,389 / 31.37%
Read min/max/mean length	30 / 151 / 174.77
Duplicated reads (estimated)	542,729 / 111.74%
Duplication rate	1.57%
Clipped reads	448,179 / 92.27%

2.2. ACGT Content

Number/percentage of A's	20,337,011 / 29.15%
Number/percentage of C's	11,453,471 / 16.42%
Number/percentage of T's	21,695,878 / 31.1%
Number/percentage of G's	16,280,698 / 23.34%
Number/percentage of N's	0 / 0%
GC Percentage	39.75%

2.3. Coverage

Mean	0.0226

Standard Deviation	45.6007
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2.4. Mapping Quality

Mean Mapping Quality	50.54
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2.5. Mismatches and indels

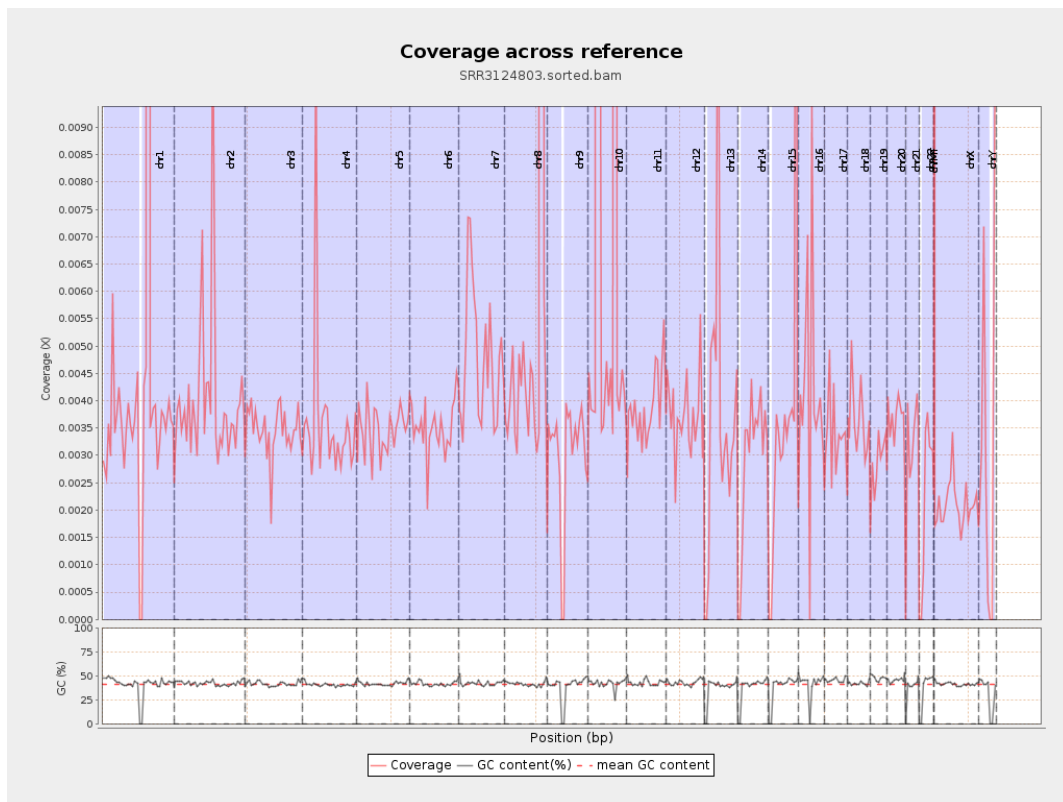
General error rate	1.24%
Mismatches	839,568
Insertions	17,497
Mapped reads with at least one insertion	3.6%
Deletions	41,390
Mapped reads with at least one deletion	8.42%
Homopolymer indels	83.5%

2.6. Chromosome stats

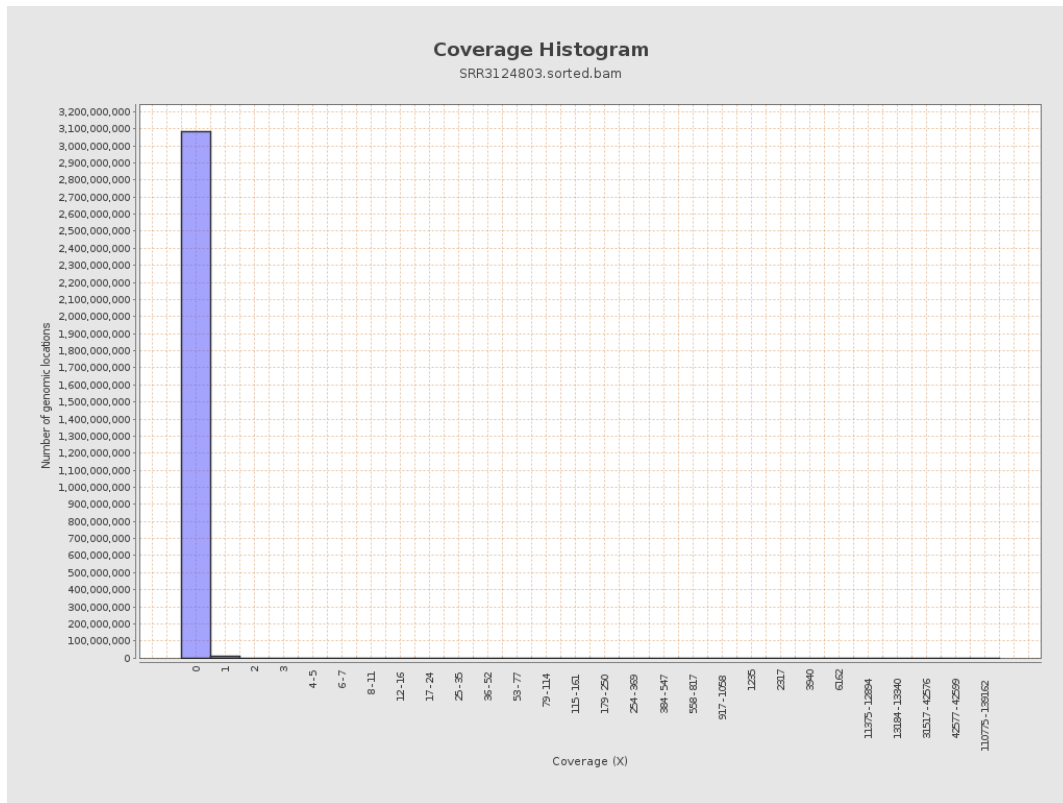
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12997777	0.0521	45.4216
chr2	243199373	980135	0.004	0.1244
chr3	198022430	684944	0.0035	0.0658
chr4	191154276	685987	0.0036	0.072
chr5	180915260	630632	0.0035	0.0626
chr6	171115067	602013	0.0035	0.0623
chr7	159138663	774855	0.0049	0.0775

chr8	146364022	43148842	0.2948	200.3183
chr9	141213431	427460	0.003	0.0689
chr10	135534747	4550500	0.0336	19.1464
chr11	135006516	525651	0.0039	0.0672
chr12	133851895	498975	0.0037	0.1082
chr13	115169878	437278	0.0038	0.4642
chr14	107349540	315036	0.0029	0.065
chr15	102531392	429410	0.0042	0.885
chr16	90354753	373168	0.0041	0.1032
chr17	81195210	274063	0.0034	0.0649
chr18	78077248	284301	0.0036	0.08
chr19	59128983	169268	0.0029	0.0622
chr20	63025520	231622	0.0037	0.0766
chr21	48129895	149521	0.0031	0.0652
chr22	51304566	115569	0.0023	0.0497
chrMT	16571	3290	0.1985	0.4382
chrX	155270560	328371	0.0021	0.0485
chrY	59373566	198588	0.0033	0.1141

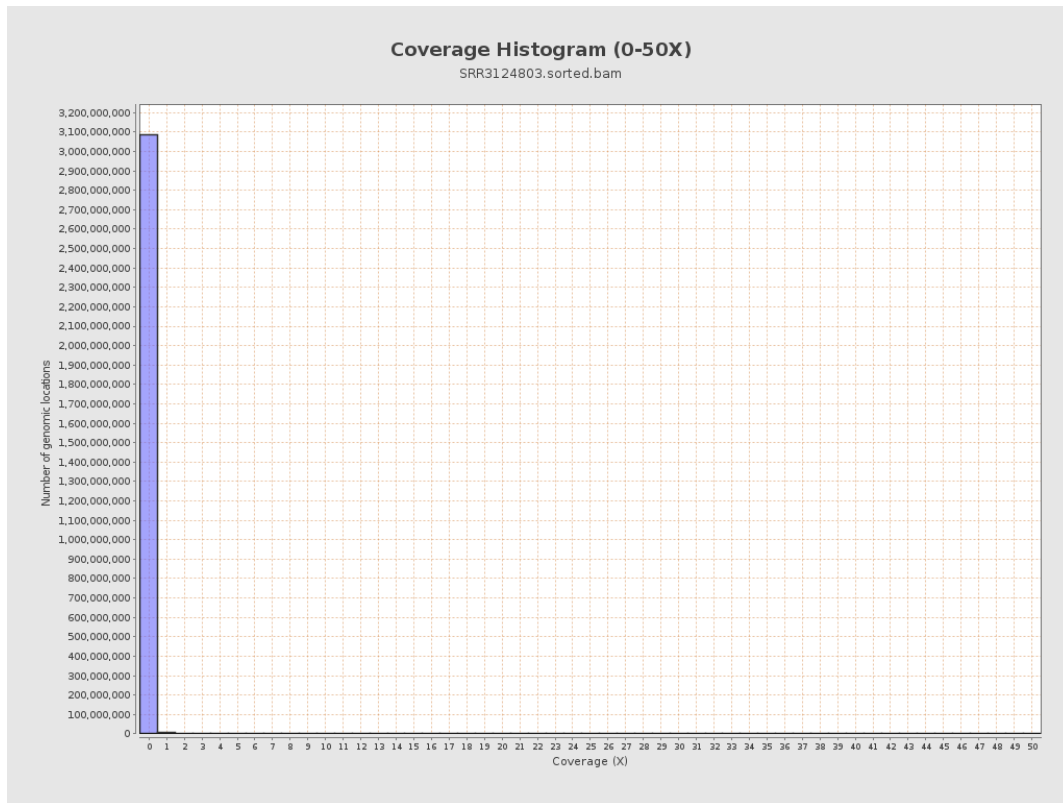
3. Results : Coverage across reference



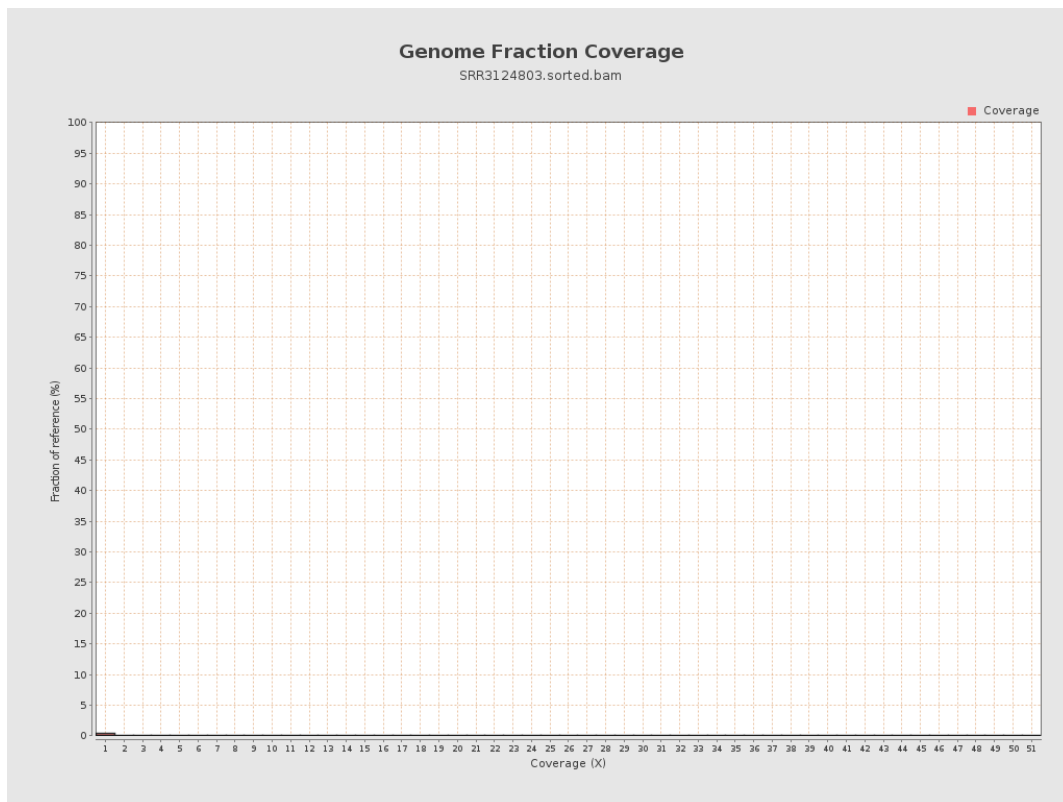
4. Results : Coverage Histogram



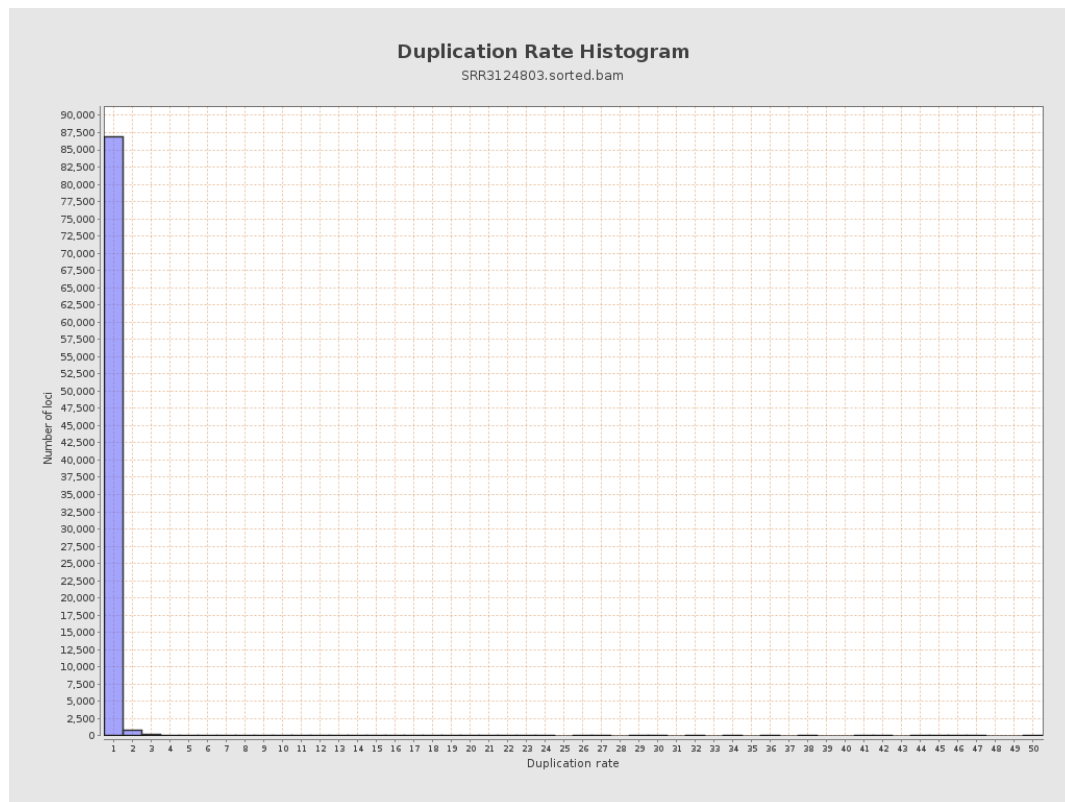
5. Results : Coverage Histogram (0-50X)



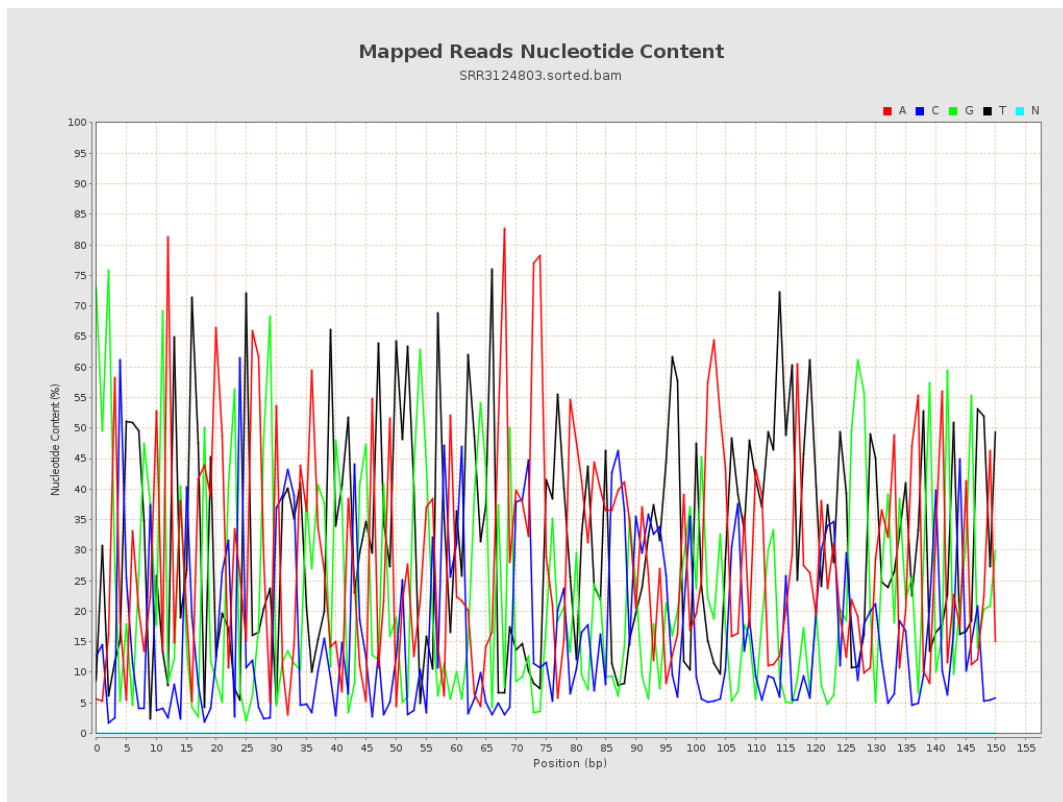
6. Results : Genome Fraction Coverage



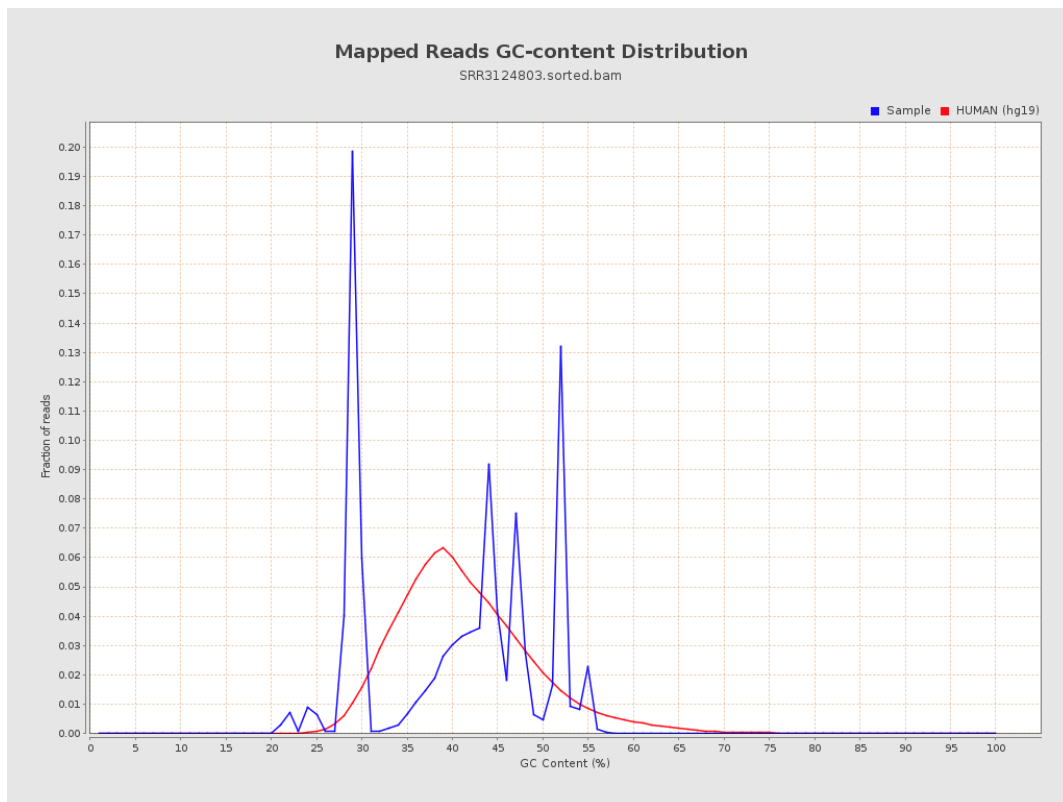
7. Results : Duplication Rate Histogram



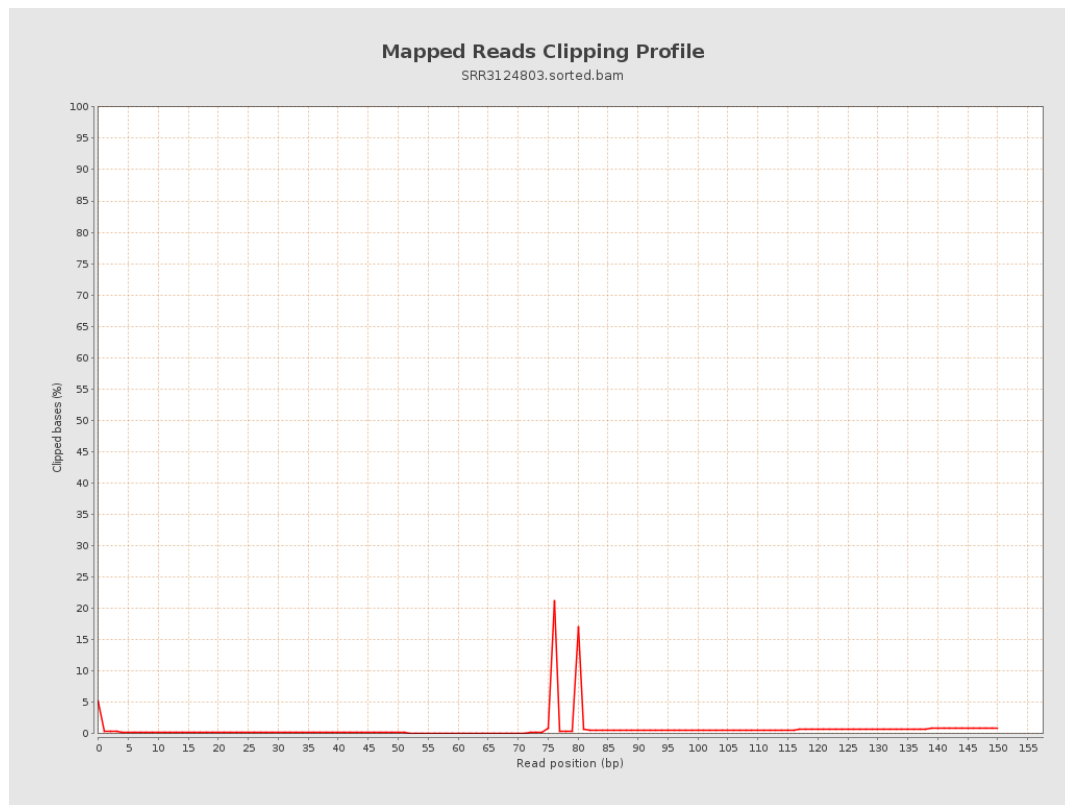
8. Results : Mapped Reads Nucleotide Content



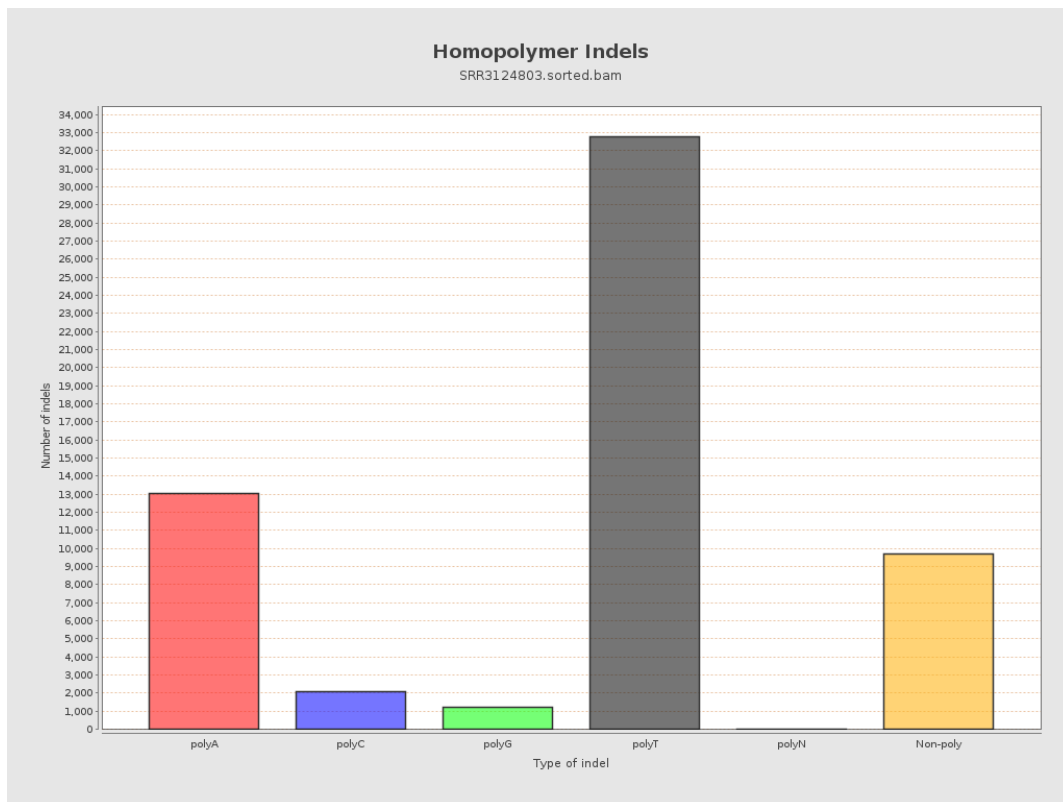
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

