

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:23:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124780.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_SRR3124780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124780.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:23:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	584,793
Mapped reads	583,855 / 99.84%
Unmapped reads	938 / 0.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	270,614 / 46.28%
Read min/max/mean length	30 / 151 / 181.64
Duplicated reads (estimated)	848,569 / 145.11%
Duplication rate	7.64%
Clipped reads	564,808 / 96.58%

2.2. ACGT Content

Number/percentage of A's	23,320,458 / 26.56%
Number/percentage of C's	17,310,054 / 19.71%
Number/percentage of T's	28,309,514 / 32.24%
Number/percentage of G's	18,869,308 / 21.49%
Number/percentage of N's	0 / 0%
GC Percentage	41.2%

2.3. Coverage

Mean	0.0284

Standard Deviation	60.1335
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2.4. Mapping Quality

Mean Mapping Quality	49.73
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2.5. Mismatches and indels

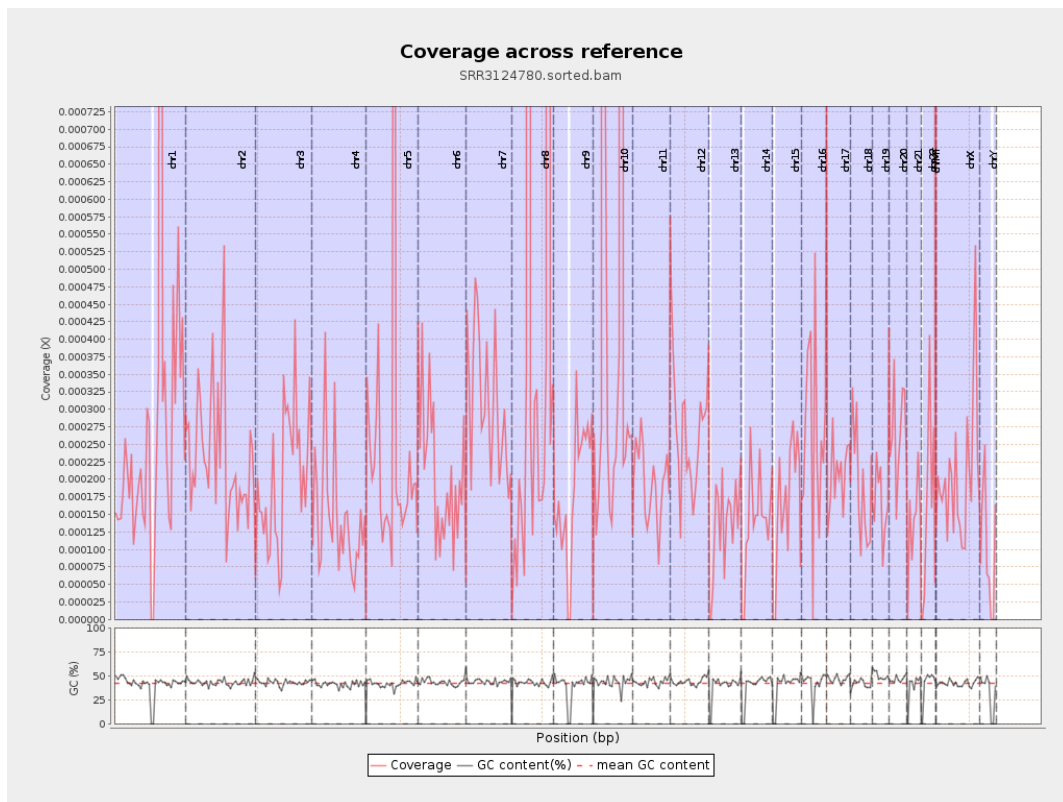
General error rate	0.85%
Mismatches	725,378
Insertions	19,330
Mapped reads with at least one insertion	3.23%
Deletions	46,135
Mapped reads with at least one deletion	7.55%
Homopolymer indels	81.72%

2.6. Chromosome stats

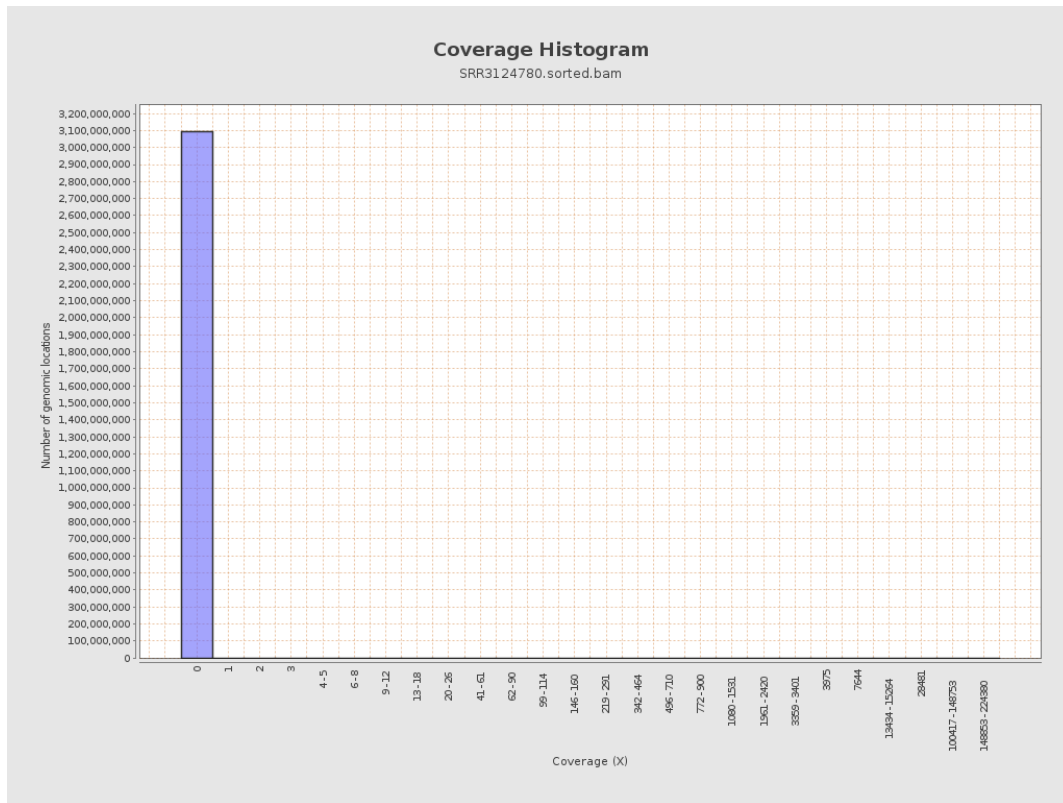
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	78398	0.0003	0.0795
chr2	243199373	56862	0.0002	0.0158
chr3	198022430	39971	0.0002	0.0143
chr4	191154276	28128	0.0001	0.0123
chr5	180915260	46423	0.0003	0.1572
chr6	171115067	35498	0.0002	0.0147
chr7	159138663	49004	0.0003	0.0176

chr8	146364022	82768230	0.5655	275.743
chr9	141213431	26143	0.0002	0.0139
chr10	135534747	4484241	0.0331	21.9681
chr11	135006516	26302	0.0002	0.014
chr12	133851895	35749	0.0003	0.0164
chr13	115169878	15224	0.0001	0.0115
chr14	107349540	14811	0.0001	0.0118
chr15	102531392	16982	0.0002	0.0129
chr16	90354753	23718	0.0003	0.0165
chr17	81195210	16700	0.0002	0.0144
chr18	78077248	14967	0.0002	0.014
chr19	59128983	10330	0.0002	0.0132
chr20	63025520	16864	0.0003	0.0164
chr21	48129895	6881	0.0001	0.0122
chr22	51304566	8482	0.0002	0.0131
chrMT	16571	1182	0.0713	0.2597
chrX	155270560	31932	0.0002	0.0207
chrY	59373566	5733	0.0001	0.0101

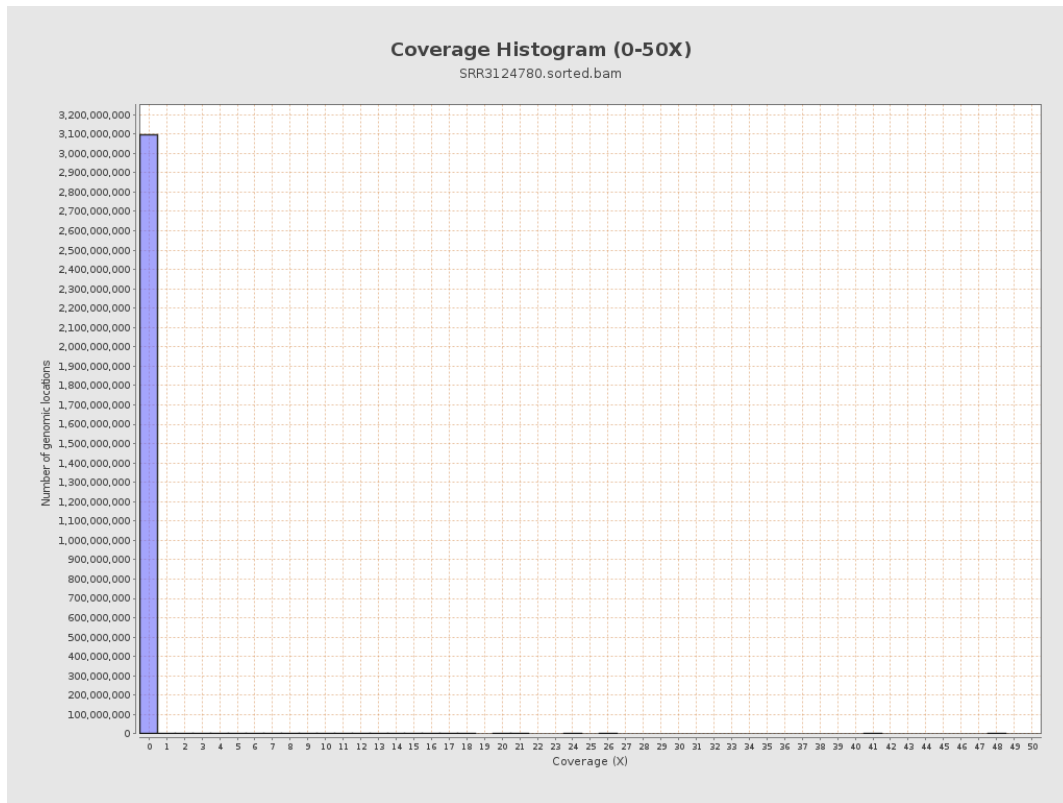
3. Results : Coverage across reference



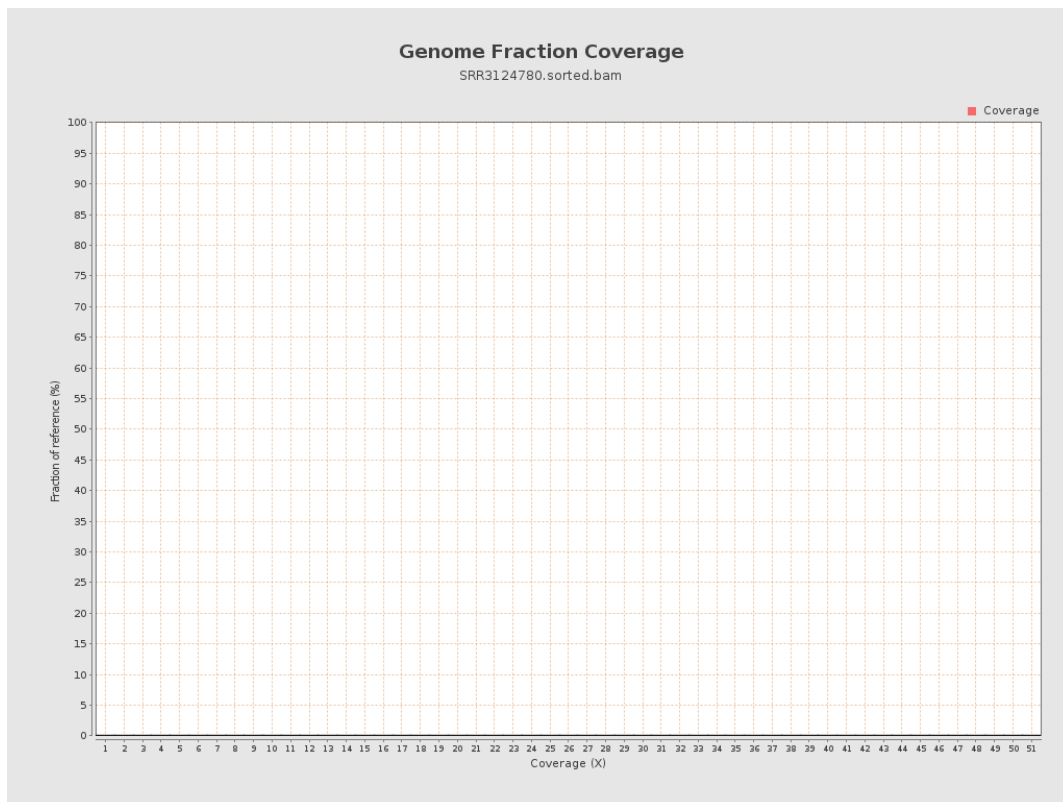
4. Results : Coverage Histogram



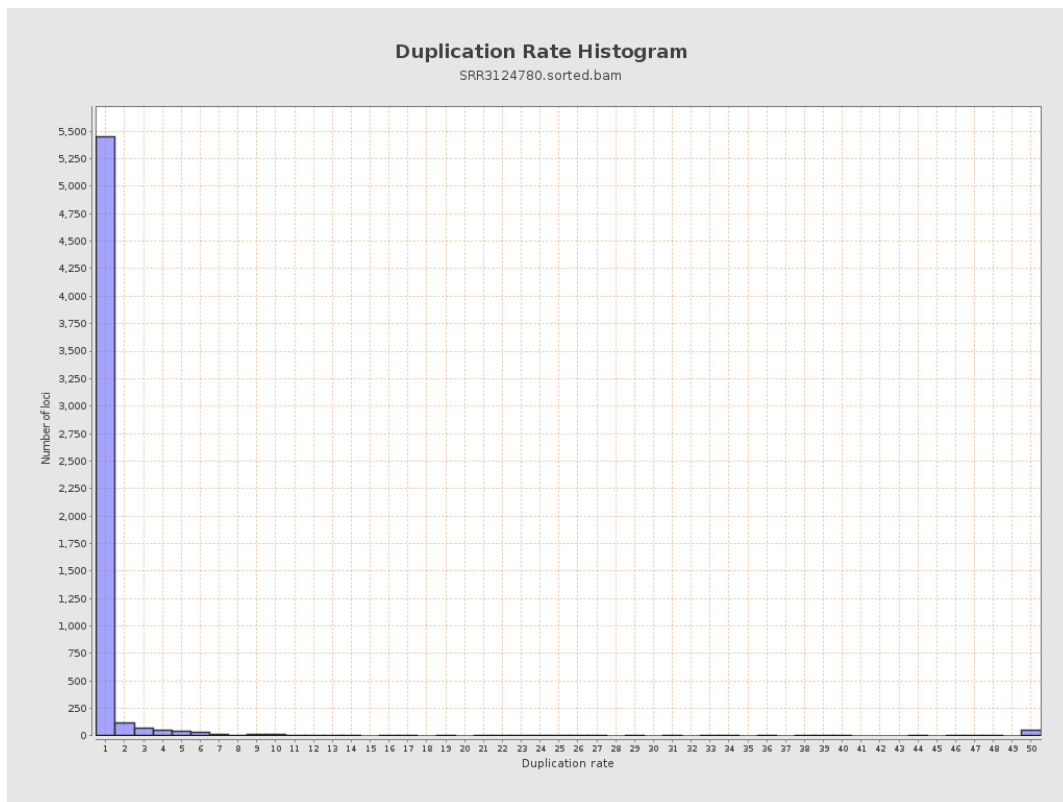
5. Results : Coverage Histogram (0-50X)



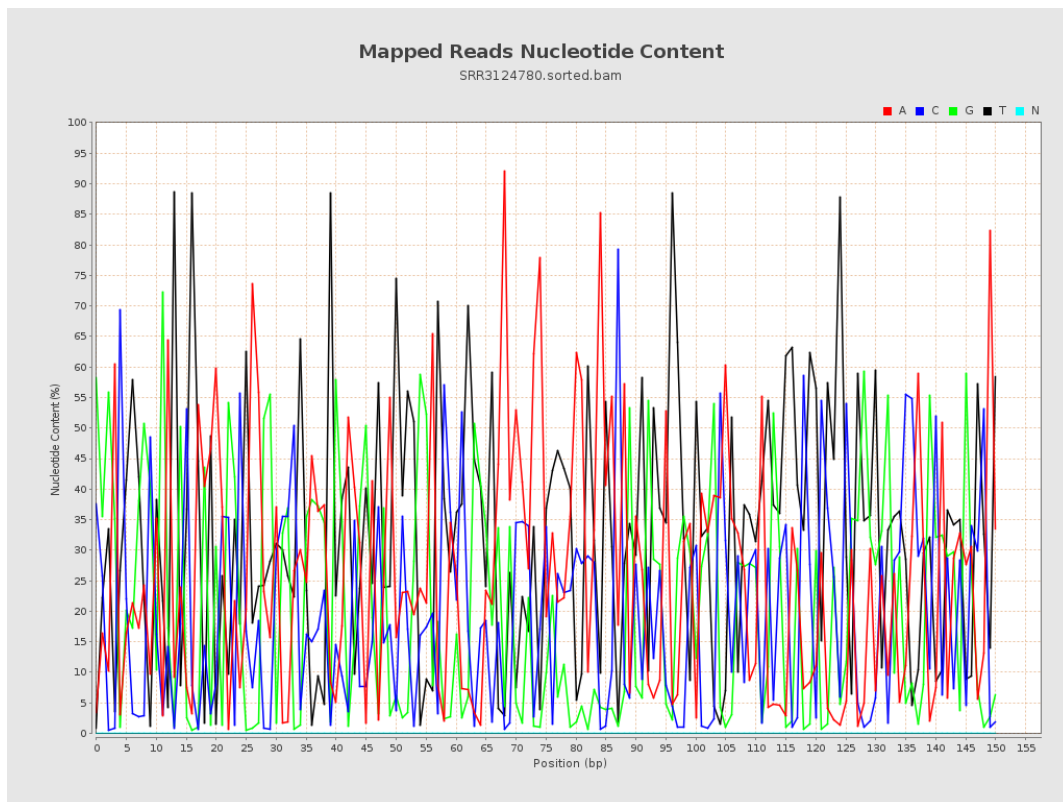
6. Results : Genome Fraction Coverage



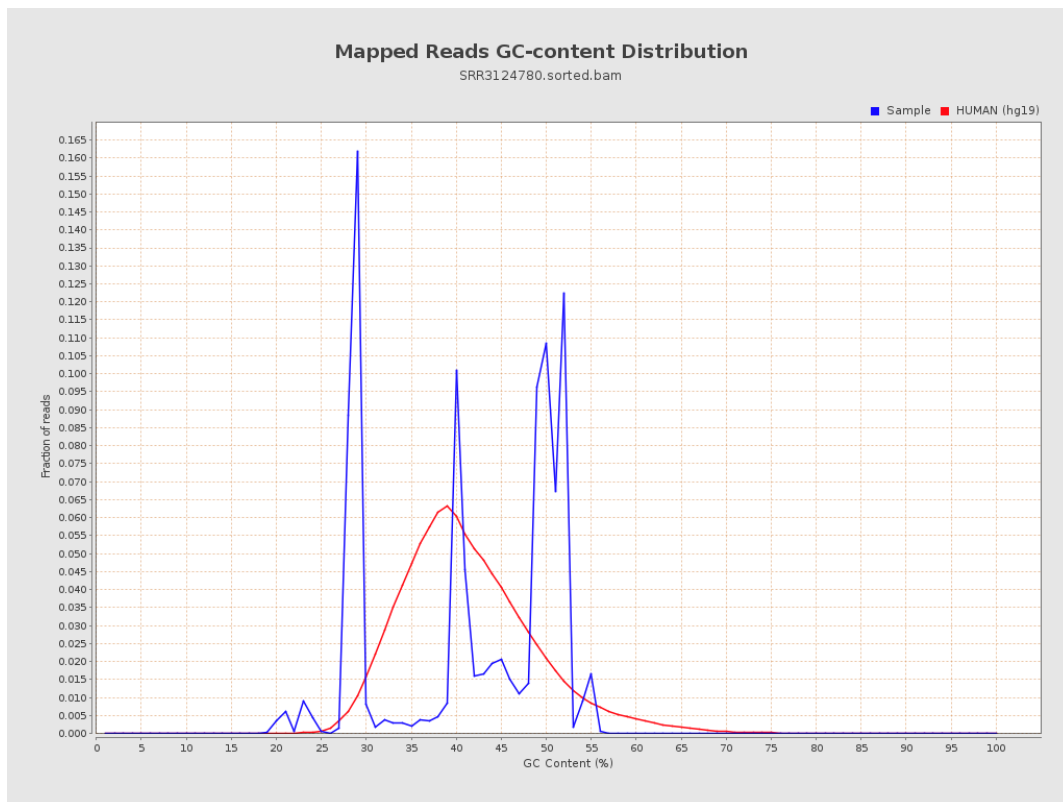
7. Results : Duplication Rate Histogram



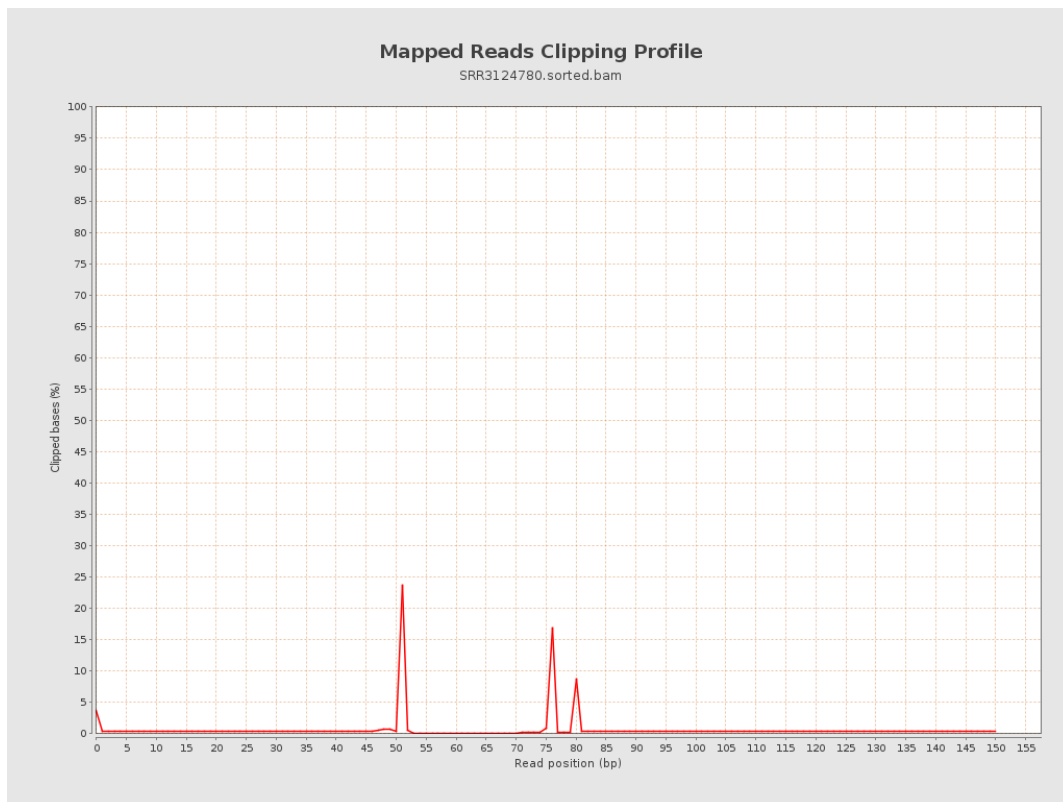
8. Results : Mapped Reads Nucleotide Content



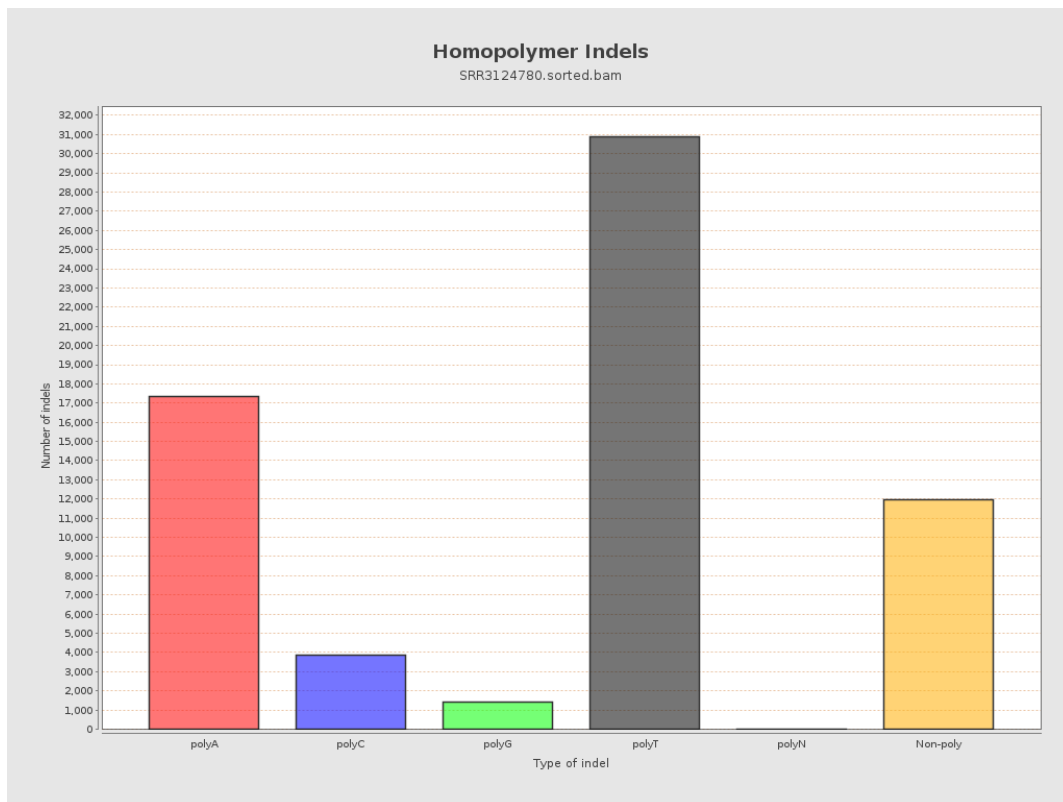
9. Results : Mapped Reads GC-content Distribution



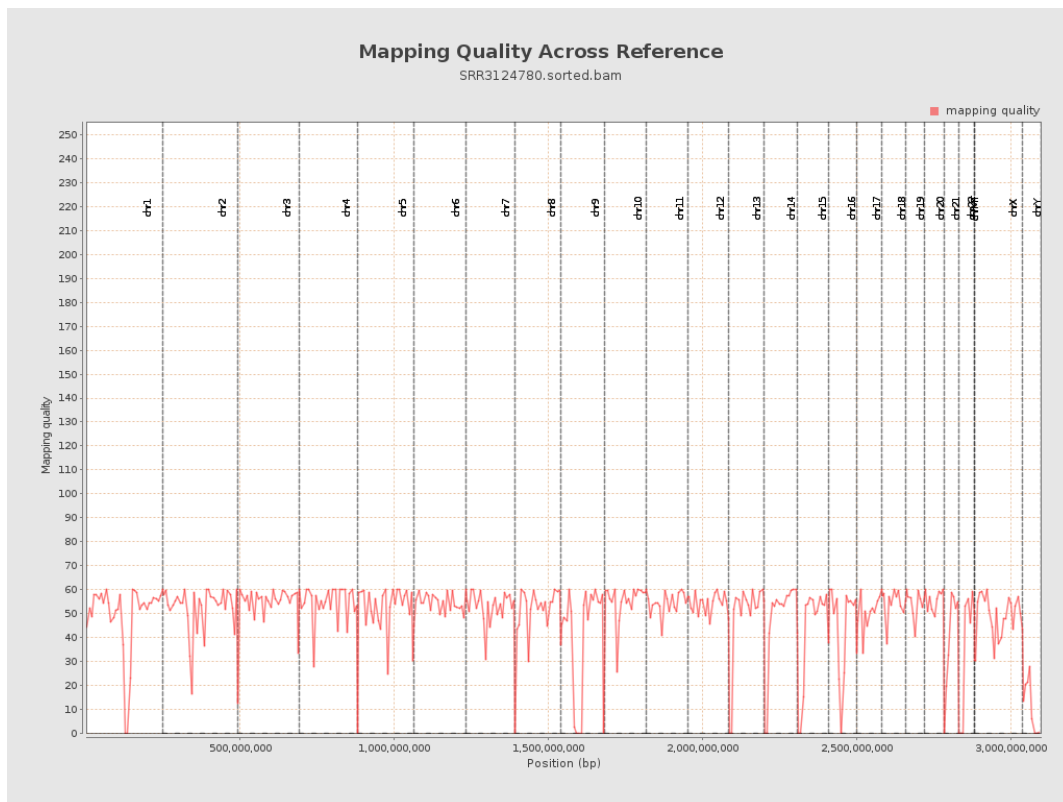
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

