

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:40:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708574.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_SRR1708574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708574.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:40:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,236,376
Mapped reads	3,493,503 / 82.46%
Unmapped reads	742,873 / 17.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	72 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	16,717 / 0.39%
Duplication rate	0.48%
Clipped reads	47,811 / 1.13%

2.2. ACGT Content

Number/percentage of A's	54,026,322 / 31.01%
Number/percentage of C's	33,052,284 / 18.97%
Number/percentage of T's	53,752,560 / 30.86%
Number/percentage of G's	33,358,898 / 19.15%
Number/percentage of N's	8,404 / 0%
GC Percentage	38.12%

2.3. Coverage

Mean	0.0563

Standard Deviation	0.2444
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2.4. Mapping Quality

Mean Mapping Quality	46.61
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2.5. Mismatches and indels

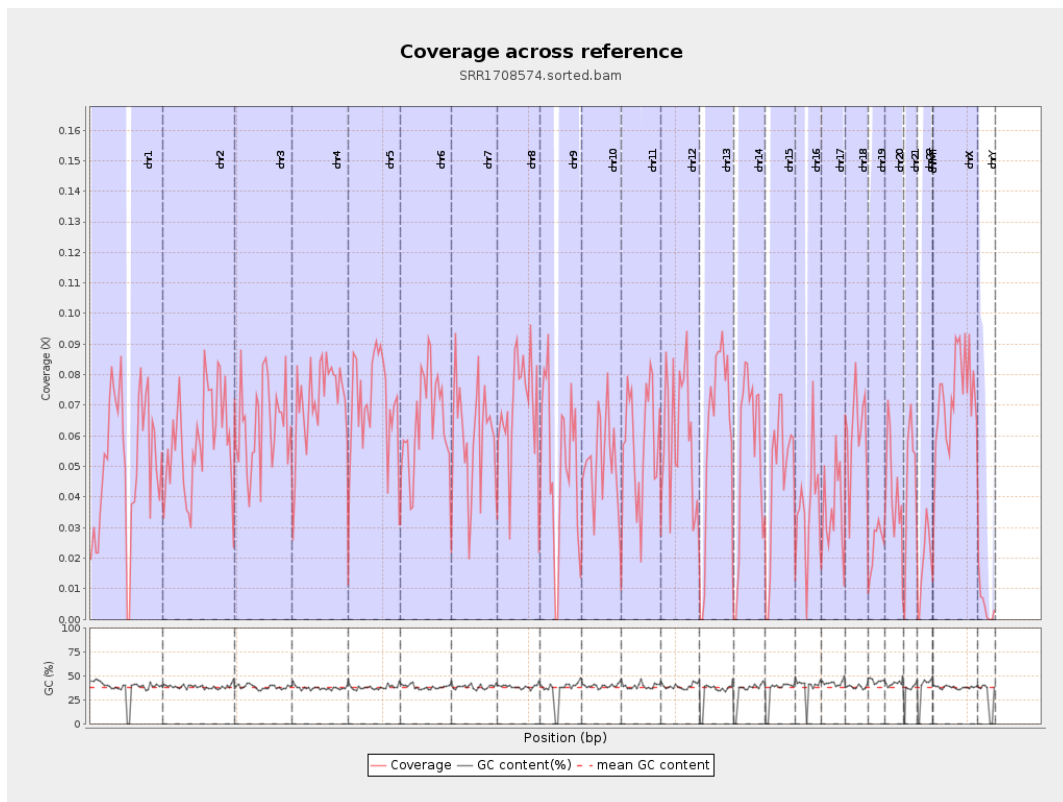
General error rate	0.17%
Mismatches	276,254
Insertions	11,604
Mapped reads with at least one insertion	0.33%
Deletions	9,361
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.34%

2.6. Chromosome stats

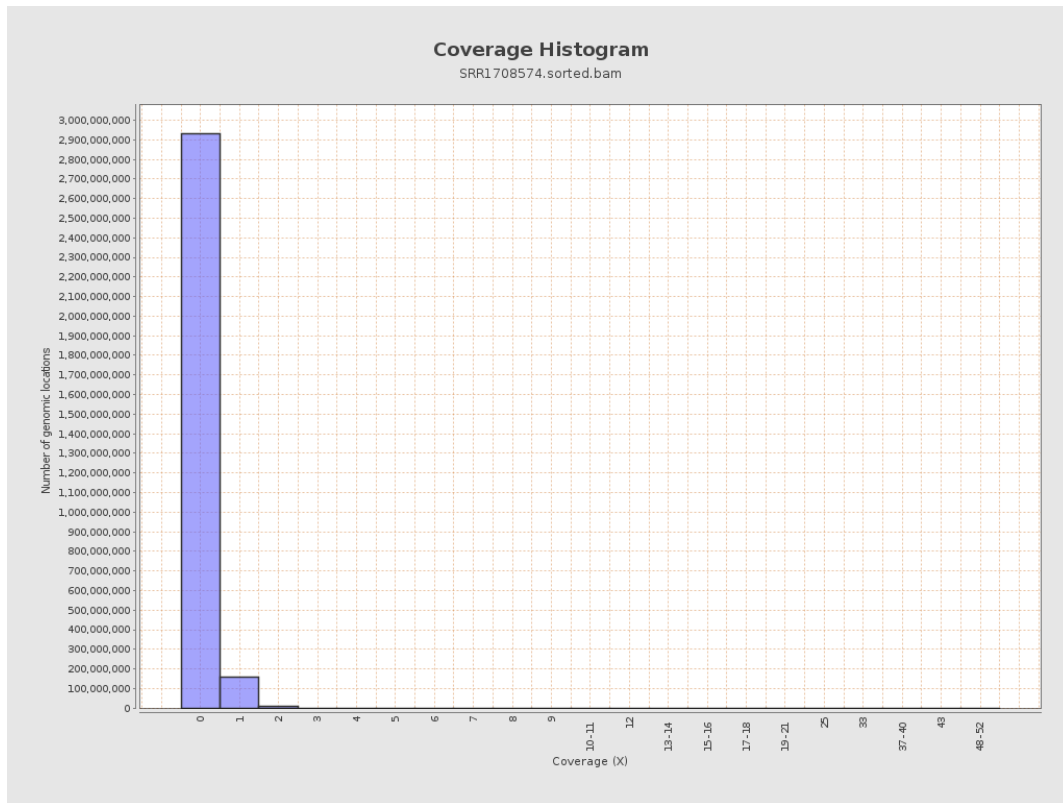
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12754148	0.0512	0.2338
chr2	243199373	14270237	0.0587	0.2488
chr3	198022430	12641761	0.0638	0.2589
chr4	191154276	13716138	0.0718	0.2746
chr5	180915260	12637449	0.0699	0.2715
chr6	171115067	11091885	0.0648	0.2616
chr7	159138663	9453066	0.0594	0.251

chr8	146364022	10101174	0.069	0.2699
chr9	141213431	7197748	0.051	0.2331
chr10	135534747	7014882	0.0518	0.2331
chr11	135006516	7867611	0.0583	0.2487
chr12	133851895	7983792	0.0596	0.2517
chr13	115169878	7097375	0.0616	0.256
chr14	107349540	5821218	0.0542	0.2404
chr15	102531392	4744546	0.0463	0.2221
chr16	90354753	3234586	0.0358	0.1945
chr17	81195210	2944341	0.0363	0.1956
chr18	78077248	4784780	0.0613	0.2537
chr19	59128983	1462299	0.0247	0.1612
chr20	63025520	2697937	0.0428	0.213
chr21	48129895	2118611	0.044	0.2181
chr22	51304566	988262	0.0193	0.1421
chrMT	16571	200	0.0121	0.1092
chrX	155270560	11320669	0.0729	0.278
chrY	59373566	269790	0.0045	0.0702

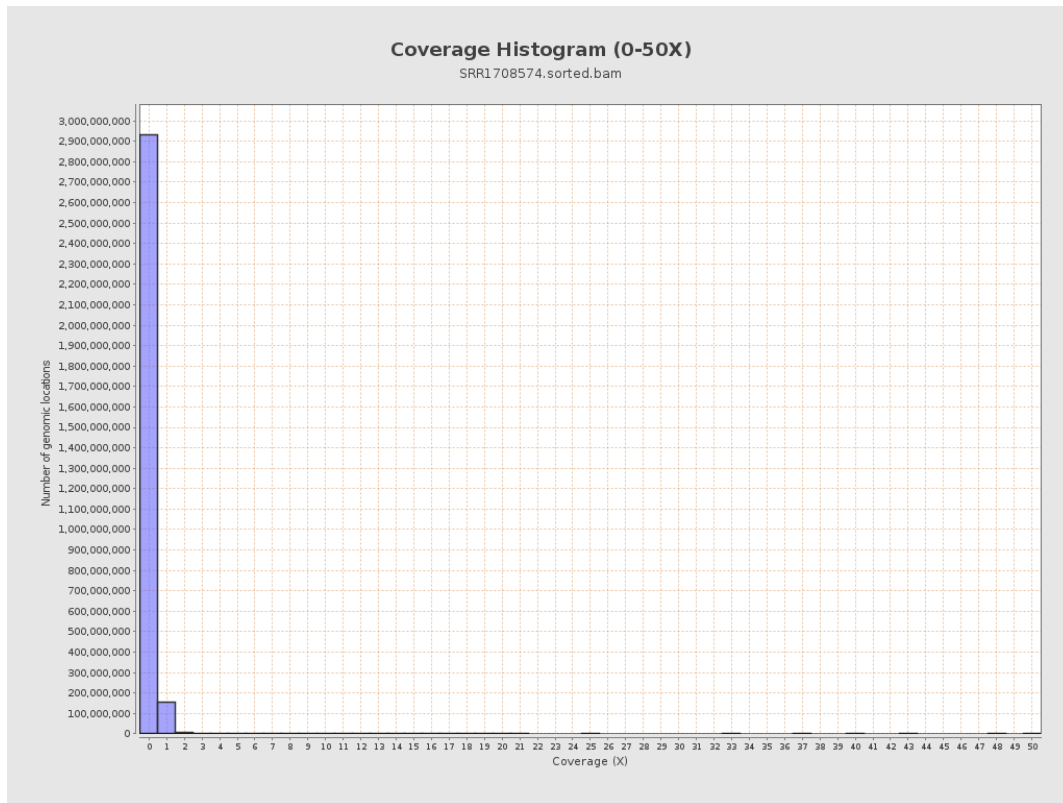
3. Results : Coverage across reference



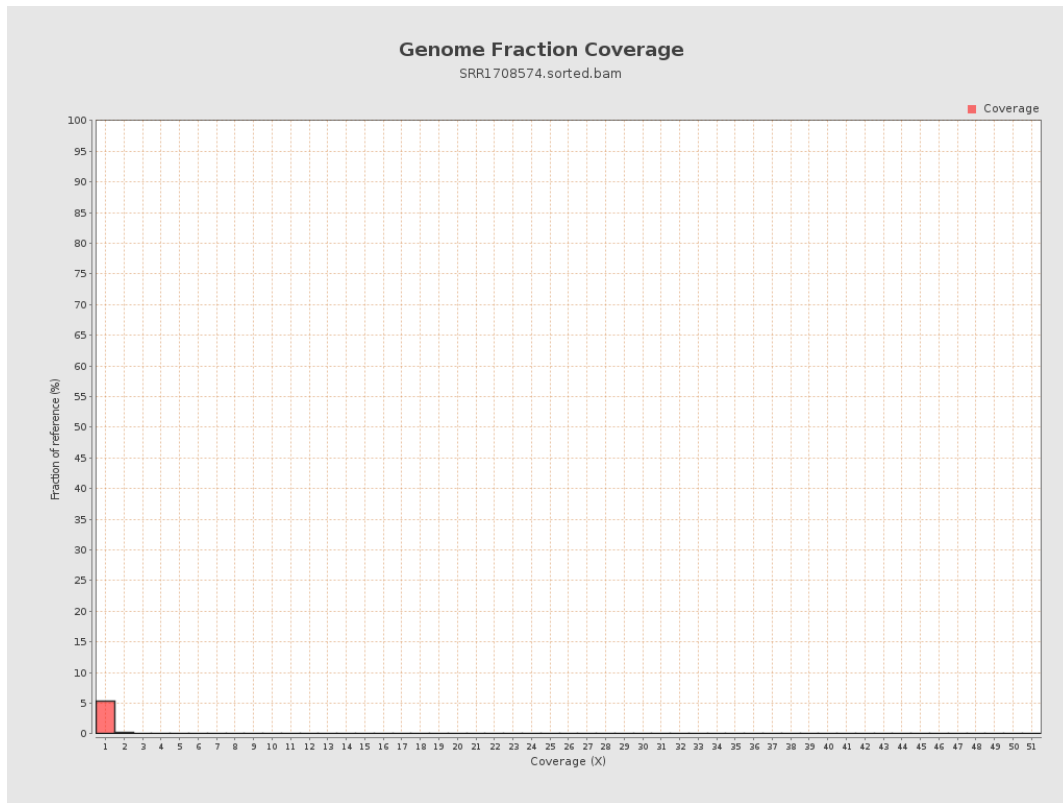
4. Results : Coverage Histogram



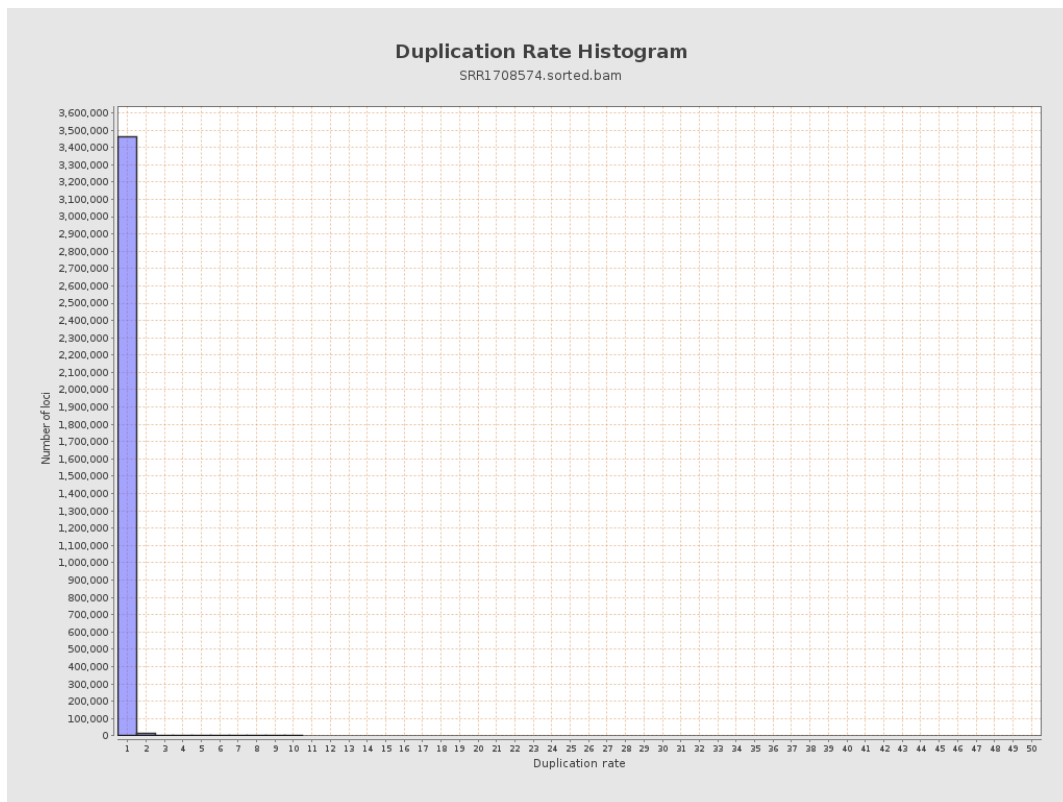
5. Results : Coverage Histogram (0-50X)



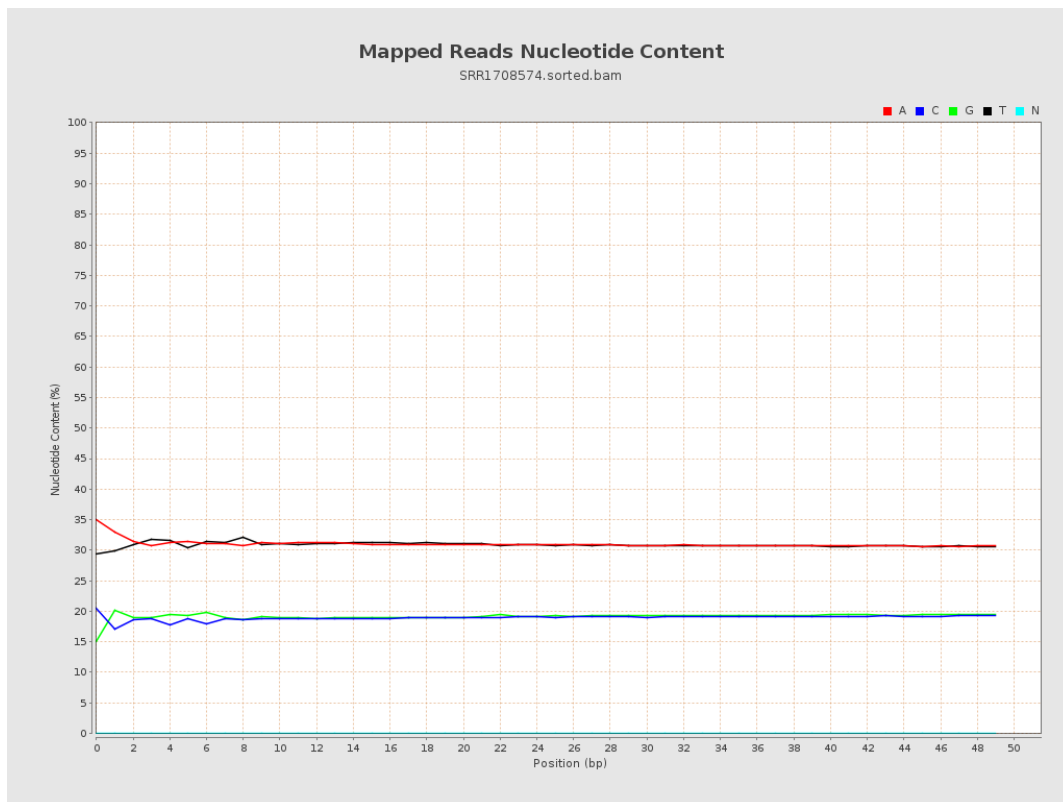
6. Results : Genome Fraction Coverage



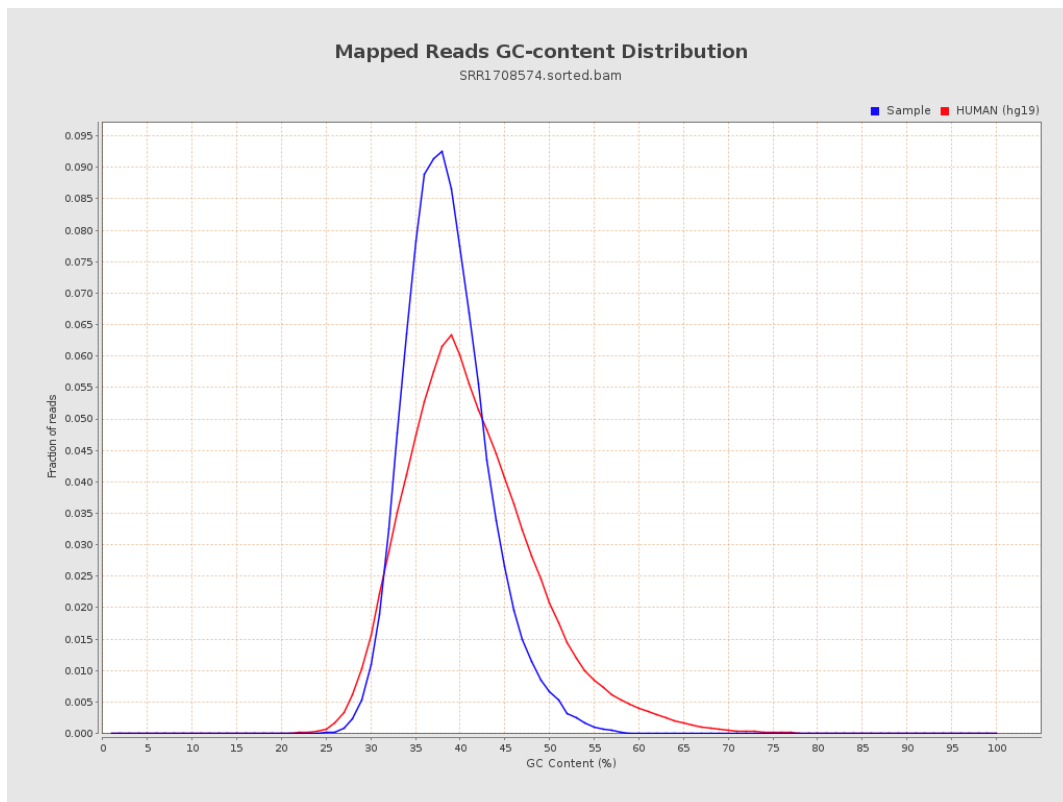
7. Results : Duplication Rate Histogram



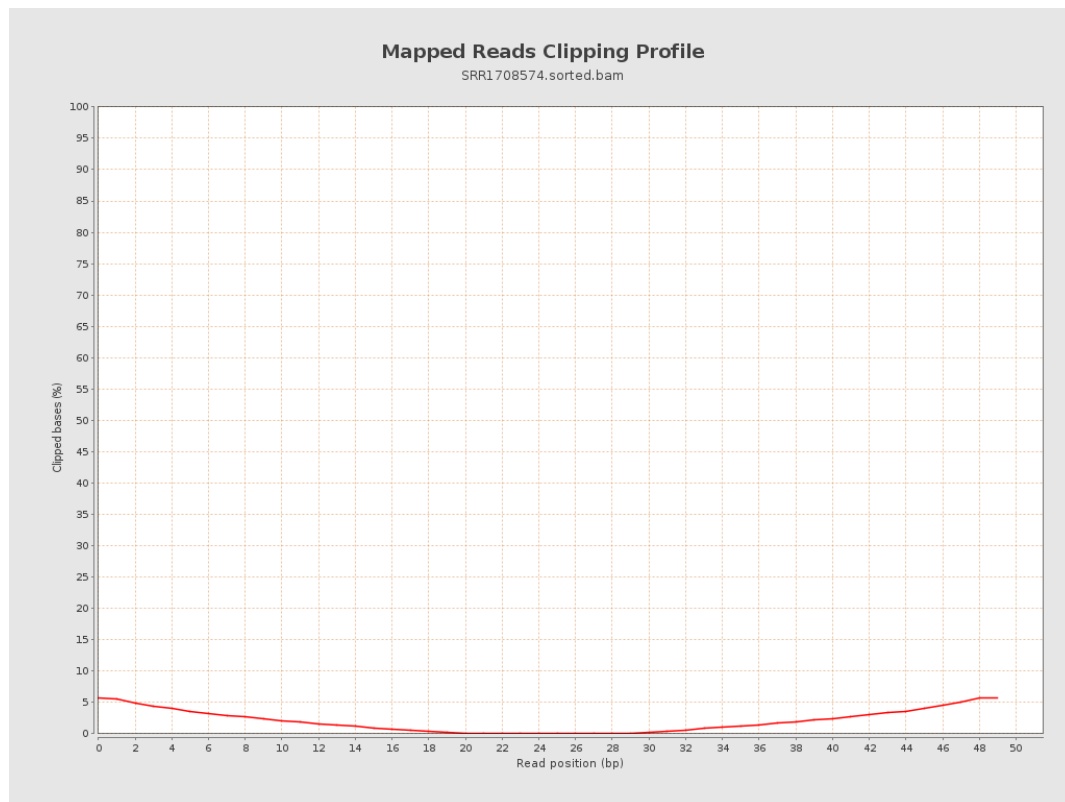
8. Results : Mapped Reads Nucleotide Content



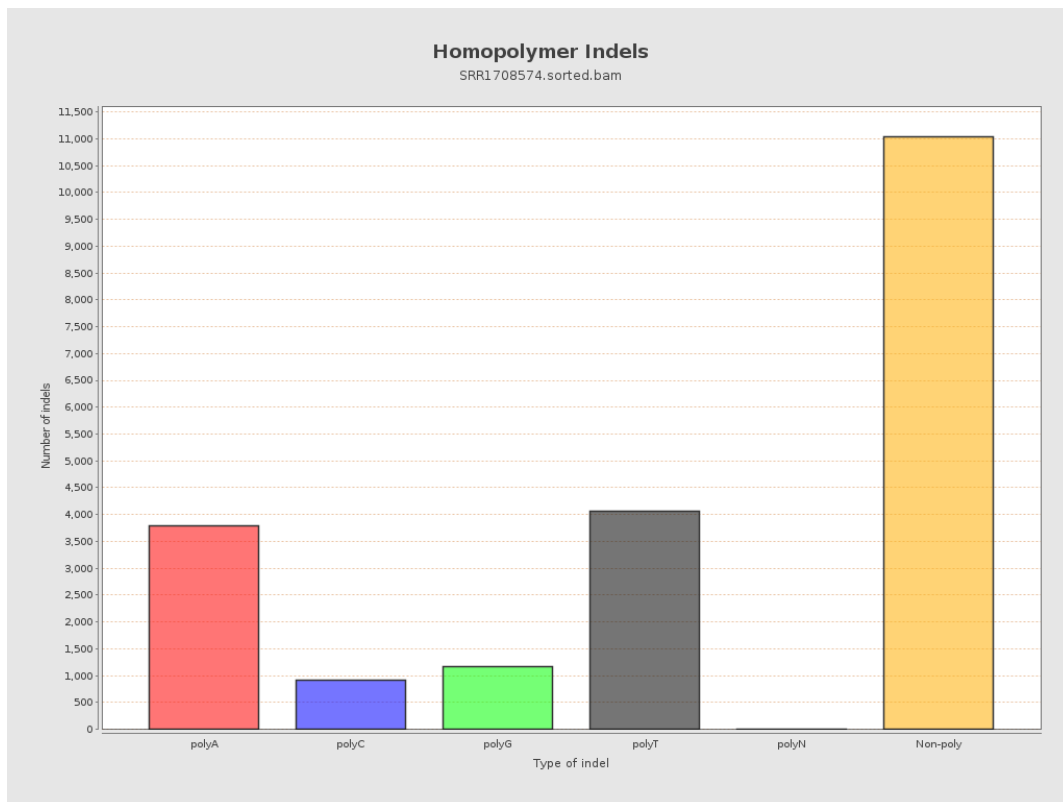
9. Results : Mapped Reads GC-content Distribution



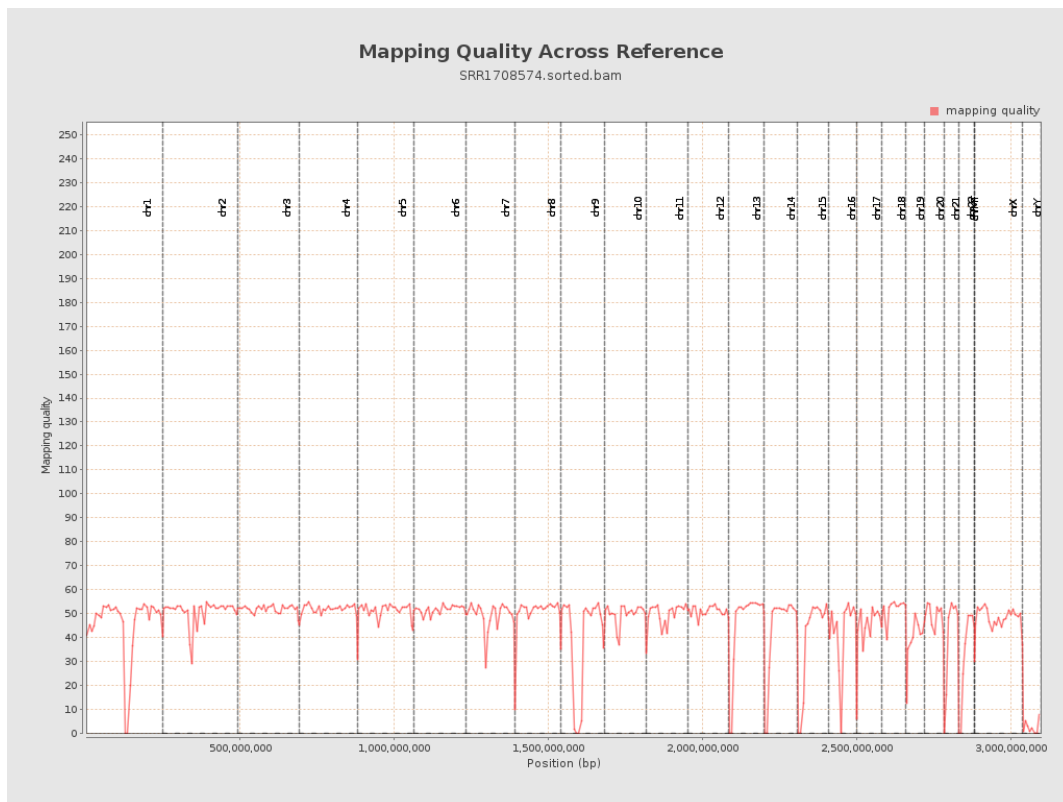
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

