Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:49:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708534.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_SRR1708534 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708534.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:49:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708534.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,194,632
Mapped reads	24,622,441 / 97.73%
Unmapped reads	572,191 / 2.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	596 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	282,820 / 1.12%
Duplication rate	1.14%
Clipped reads	294,978 / 1.17%

2.2. ACGT Content

Number/percentage of A's	379,172,801 / 30.87%
Number/percentage of C's	233,344,642 / 19%
Number/percentage of T's	379,085,872 / 30.86%
Number/percentage of G's	236,607,344 / 19.26%
Number/percentage of N's	43,079 / 0%
GC Percentage	38.26%

2.3. Coverage

Mean	0.3968

Standard Deviation	0.7361

2.4. Mapping Quality

Mean Mapping Quality	46.65

2.5. Mismatches and indels

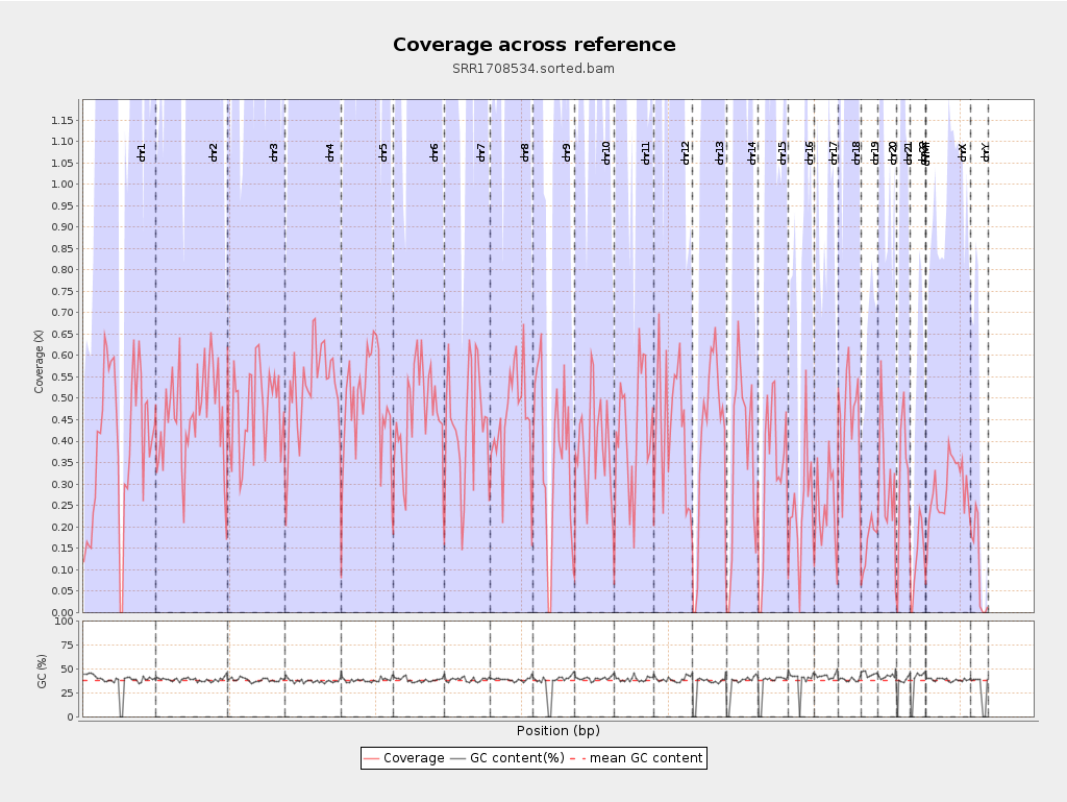
General error rate	0.2%
Mismatches	2,306,568
Insertions	70,620
Mapped reads with at least one insertion	0.29%
Deletions	64,531
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.34%

2.6. Chromosome stats

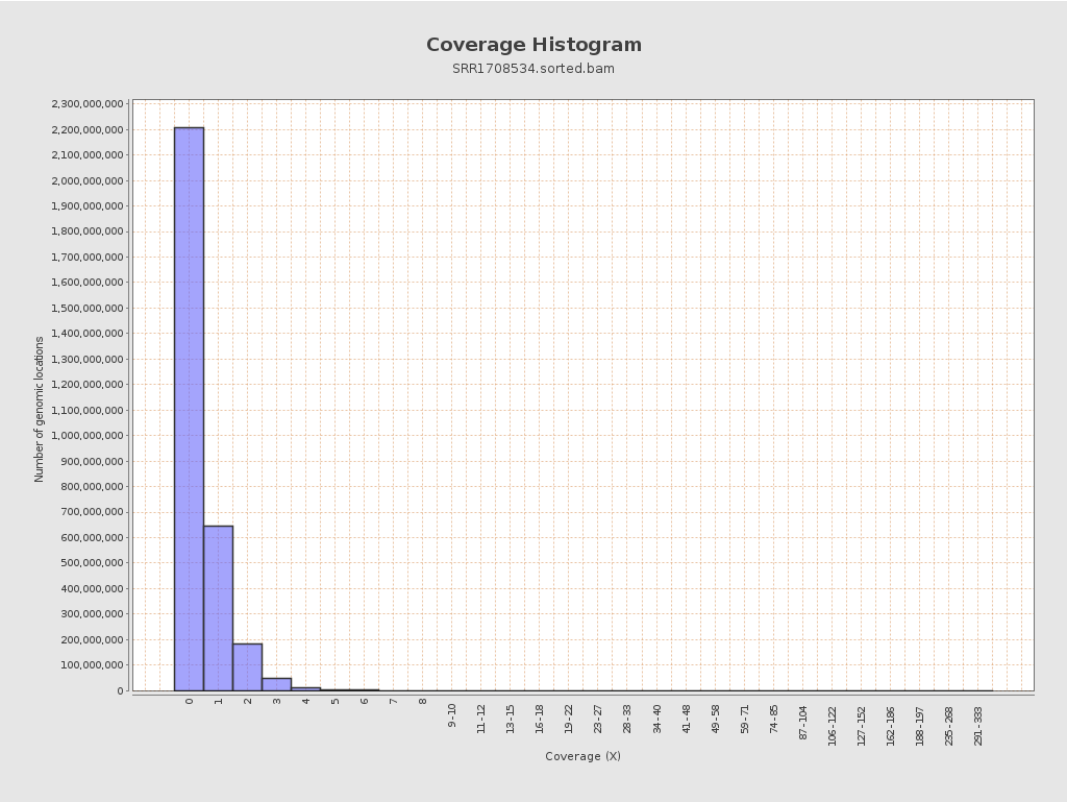
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	97760044	0.3922	0.7533
chr2	243199373	111293753	0.4576	0.7744
chr3	198022430	94245932	0.4759	0.7881
chr4	191154276	100270700	0.5246	0.8253
chr5	180915260	87782539	0.4852	0.796
chr6	171115067	80653131	0.4713	0.787
chr7	159138663	69541384	0.437	0.7693

chr8	146364022	66816995	0.4565	0.774
chr9	141213431	52126261	0.3691	0.7183
chr10	135534747	53513243	0.3948	0.717
chr11	135006516	57429414	0.4254	0.7722
chr12	133851895	57788874	0.4317	0.7663
chr13	115169878	47242301	0.4102	0.7476
chr14	107349540	39400710	0.367	0.7203
chr15	102531392	33497024	0.3267	0.686
chr16	90354753	21655469	0.2397	0.5675
chr17	81195210	20211475	0.2489	0.5799
chr18	78077248	35785067	0.4583	0.7699
chr19	59128983	9732493	0.1646	0.4581
chr20	63025520	19755605	0.3135	0.6535
chr21	48129895	14587829	0.3031	0.6711
chr22	51304566	6633122	0.1293	0.4133
chrMT	16571	1638	0.0988	0.3649
chrX	155270560	44472198	0.2864	0.5956
chrY	59373566	6164110	0.1038	0.3773

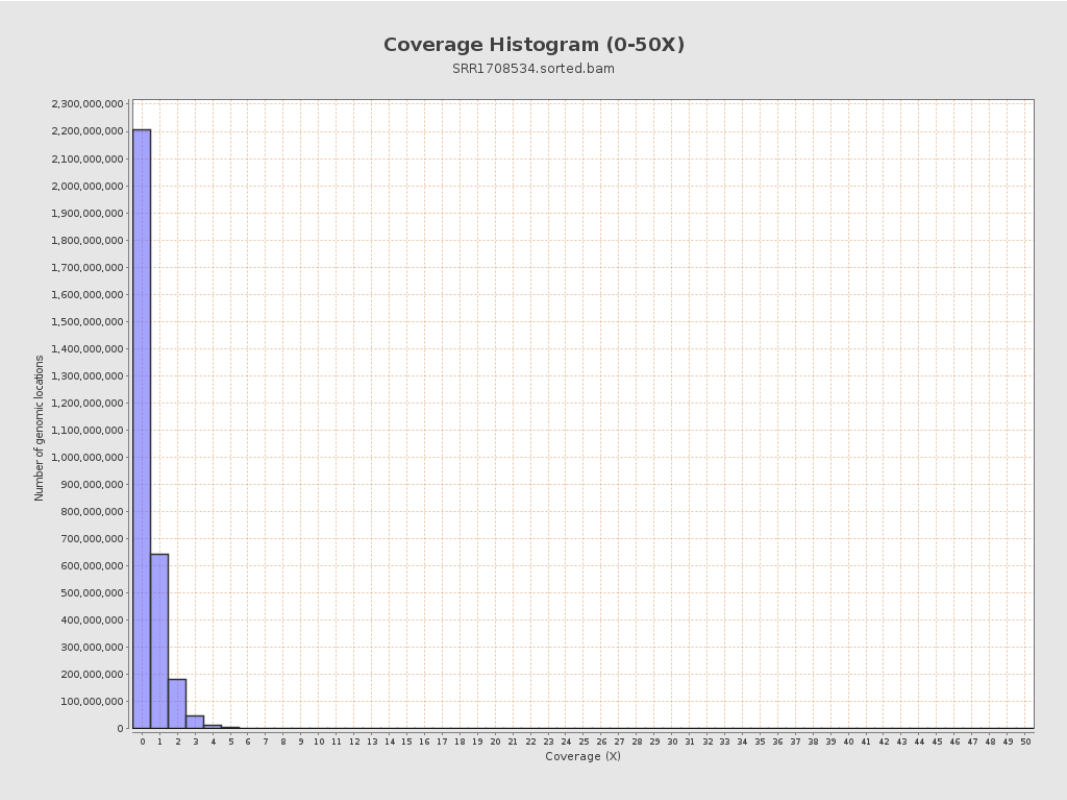
3. Results : Coverage across reference



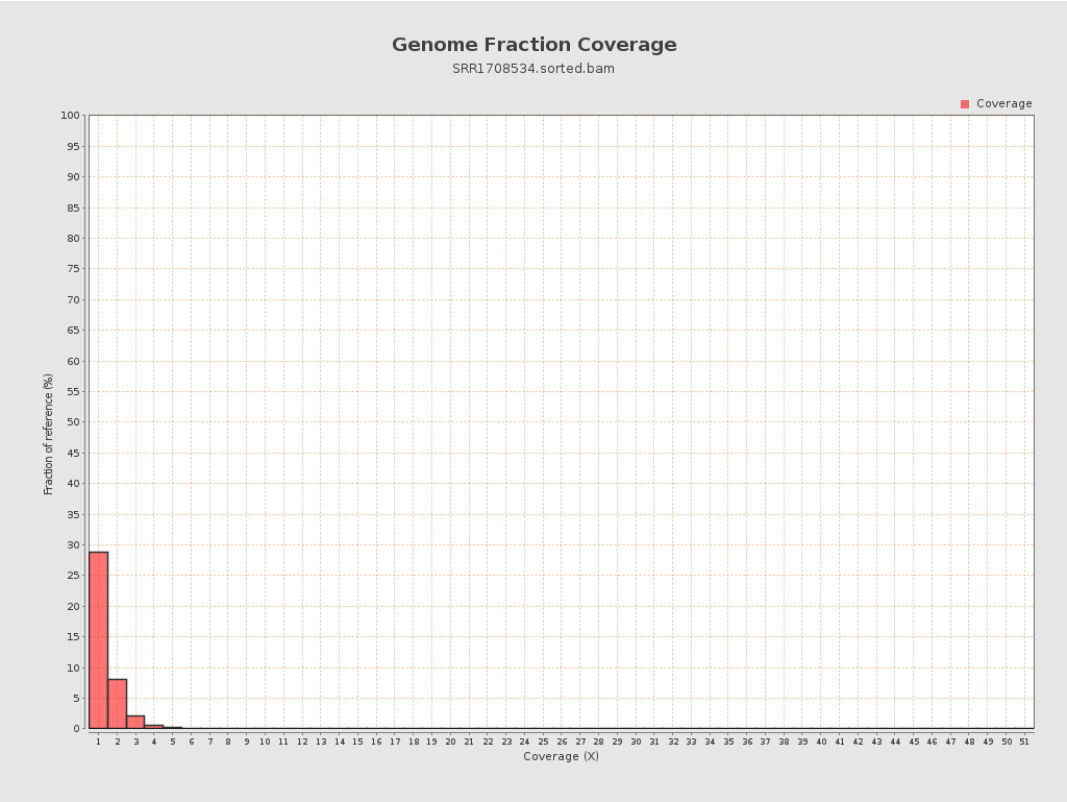
4. Results : Coverage Histogram



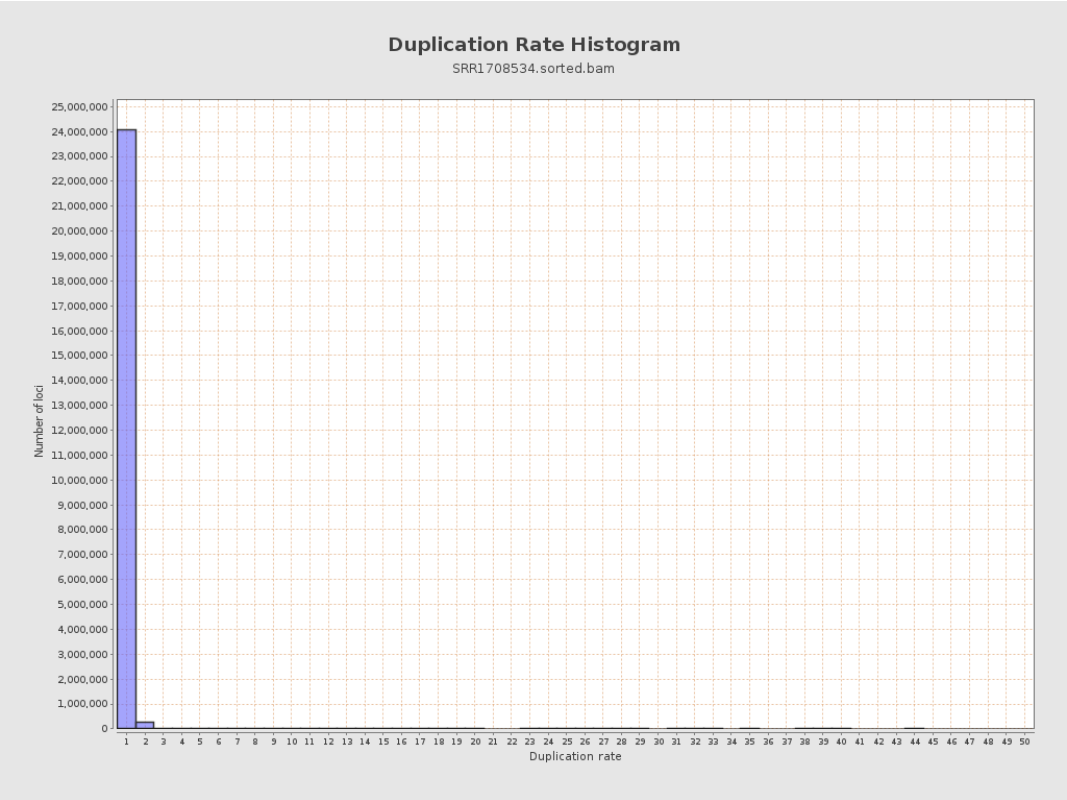
5. Results : Coverage Histogram (0-50X)



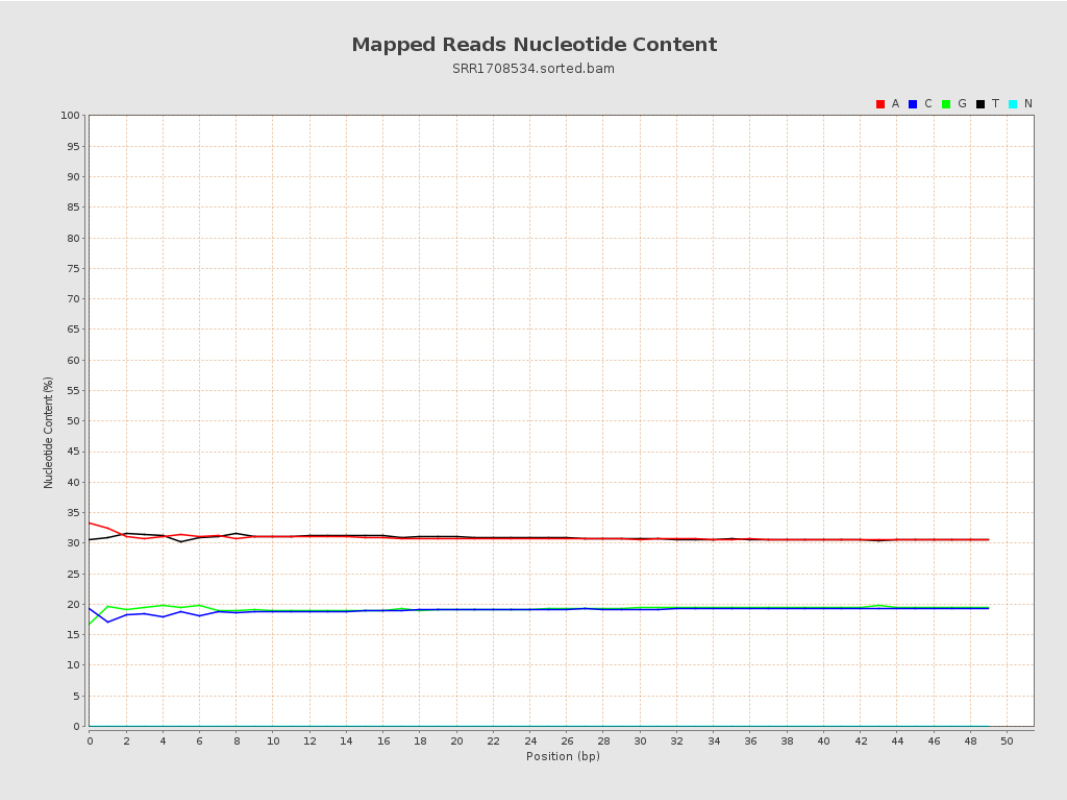
6. Results : Genome Fraction Coverage



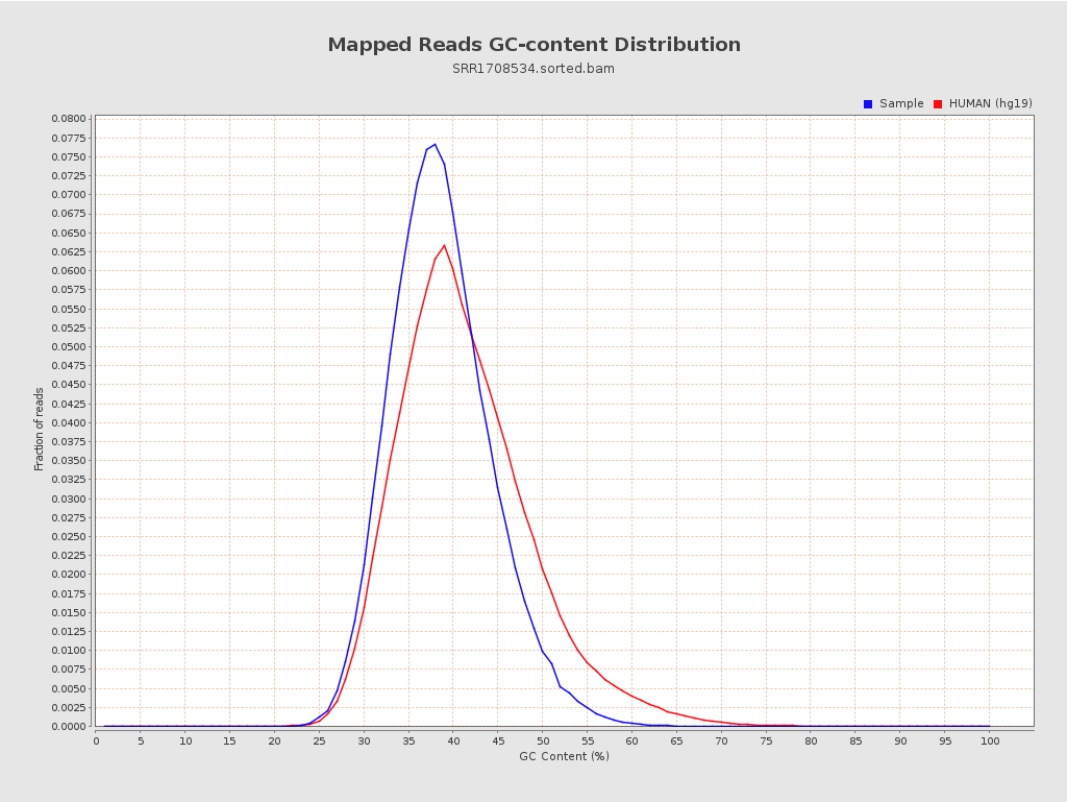
7. Results : Duplication Rate Histogram



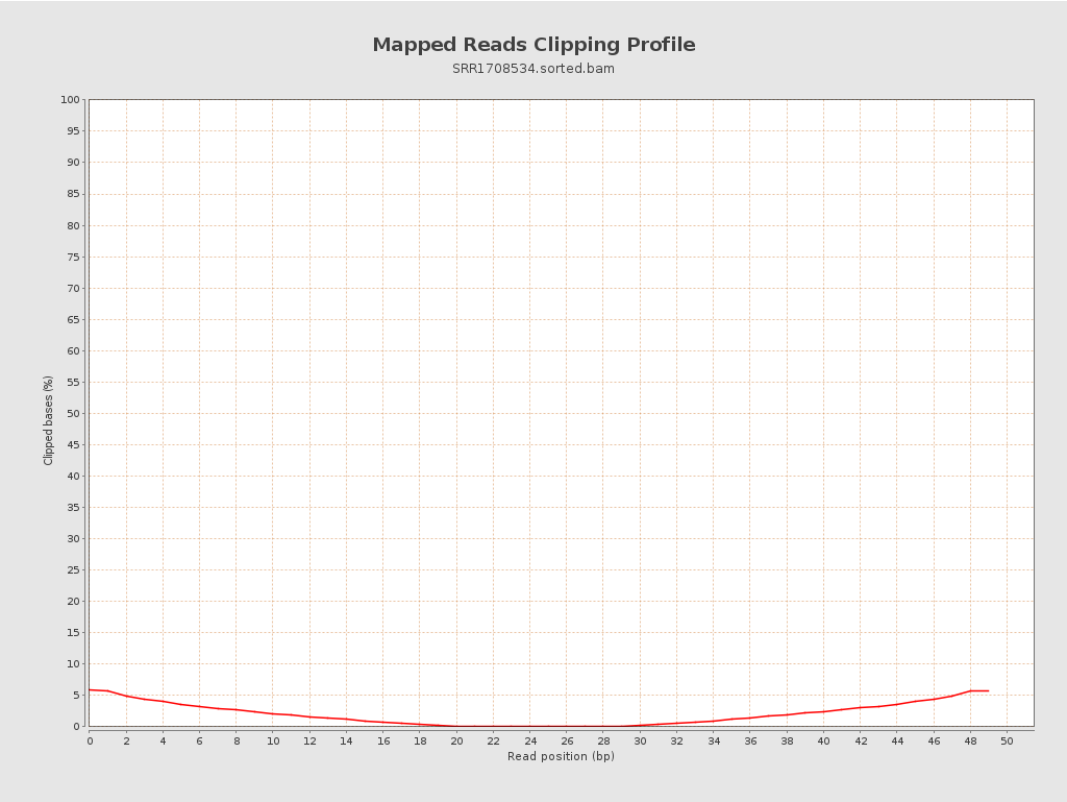
8. Results : Mapped Reads Nucleotide Content



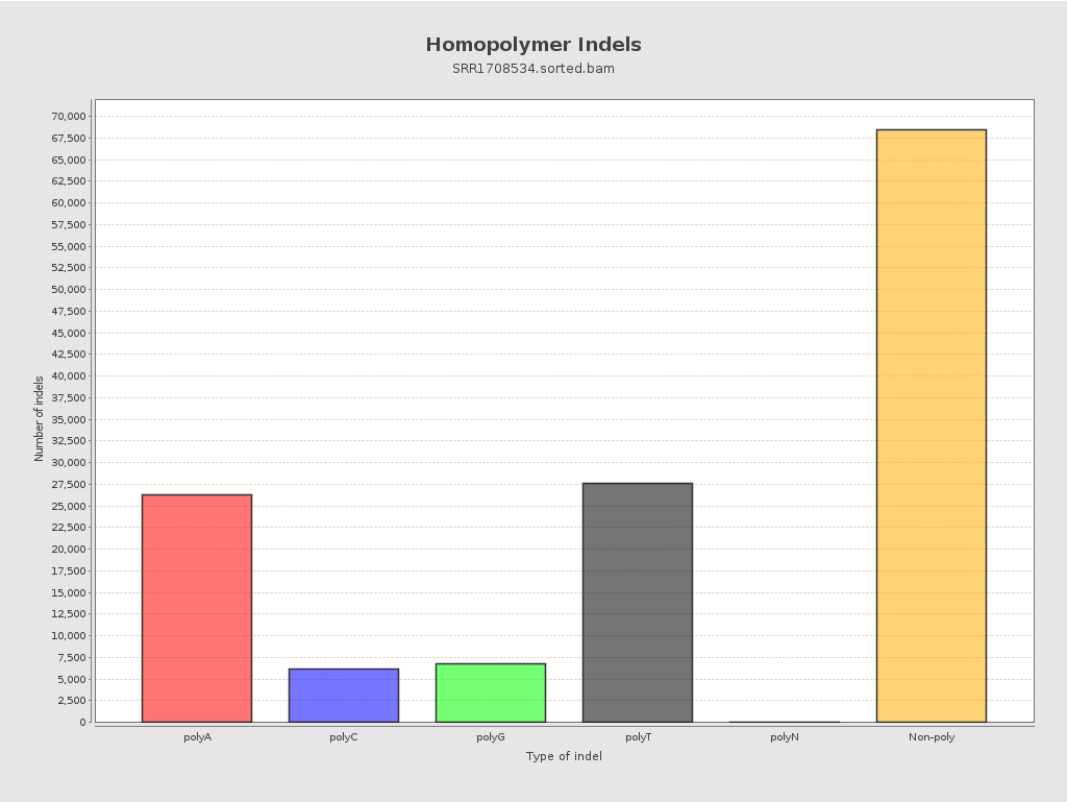
9. Results : Mapped Reads GC-content Distribution



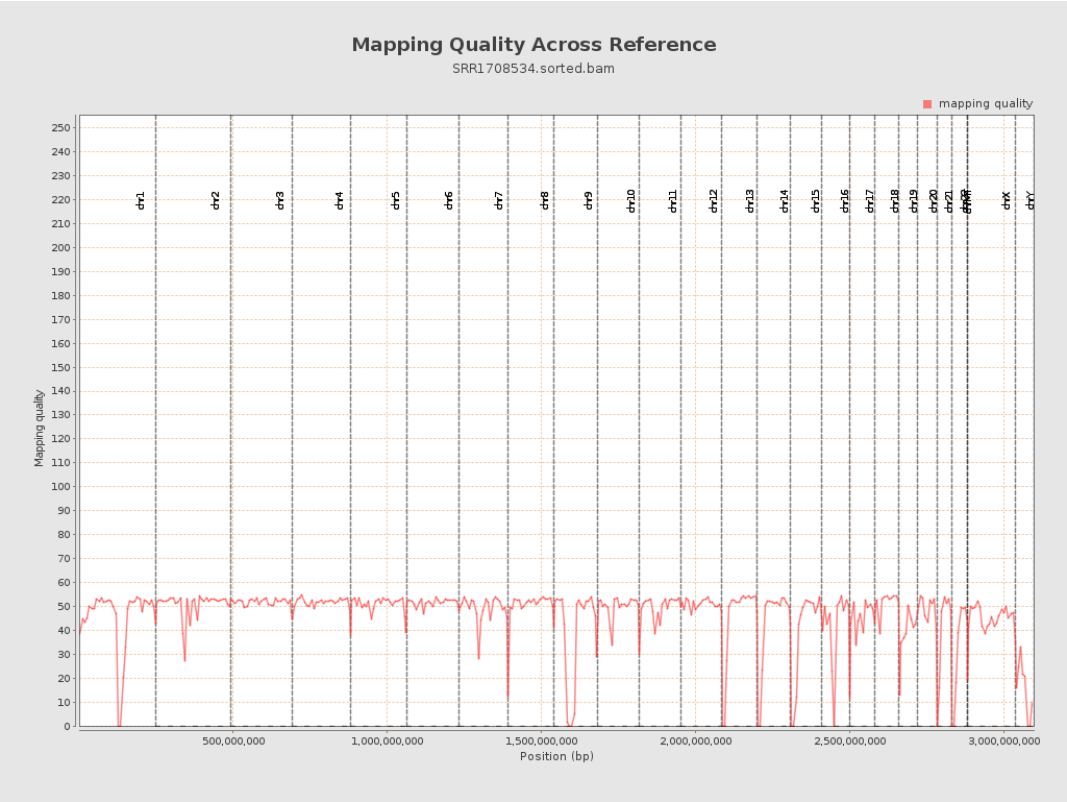
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram