

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:11:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708571.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_SRR1708571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708571.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:11:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708571.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,016,816
Mapped reads	3,286,957 / 81.83%
Unmapped reads	729,859 / 18.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	82 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	15,654 / 0.39%
Duplication rate	0.47%
Clipped reads	44,753 / 1.11%

2.2. ACGT Content

Number/percentage of A's	50,729,360 / 30.95%
Number/percentage of C's	31,154,468 / 19.01%
Number/percentage of T's	50,599,956 / 30.87%
Number/percentage of G's	31,411,484 / 19.17%
Number/percentage of N's	4,115 / 0%
GC Percentage	38.17%

2.3. Coverage

Mean	0.0529

Standard Deviation	0.239
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2.4. Mapping Quality

Mean Mapping Quality	44.86
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2.5. Mismatches and indels

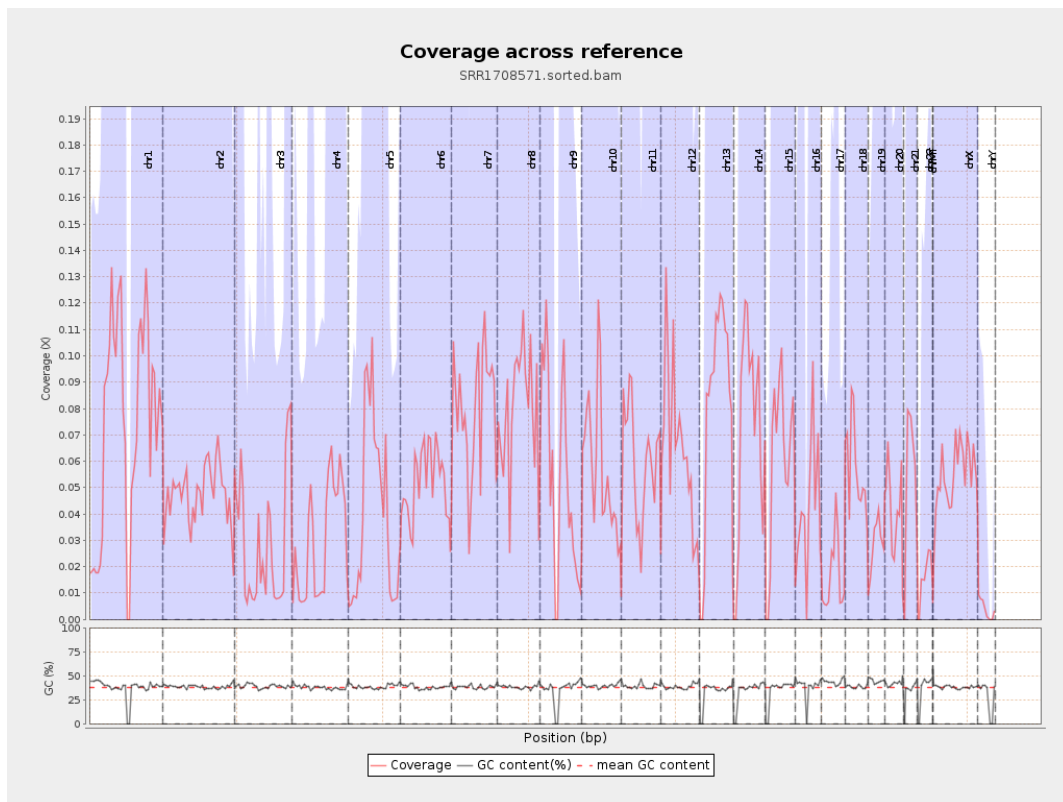
General error rate	0.17%
Mismatches	259,237
Insertions	11,192
Mapped reads with at least one insertion	0.34%
Deletions	8,750
Mapped reads with at least one deletion	0.27%
Homopolymer indels	47.36%

2.6. Chromosome stats

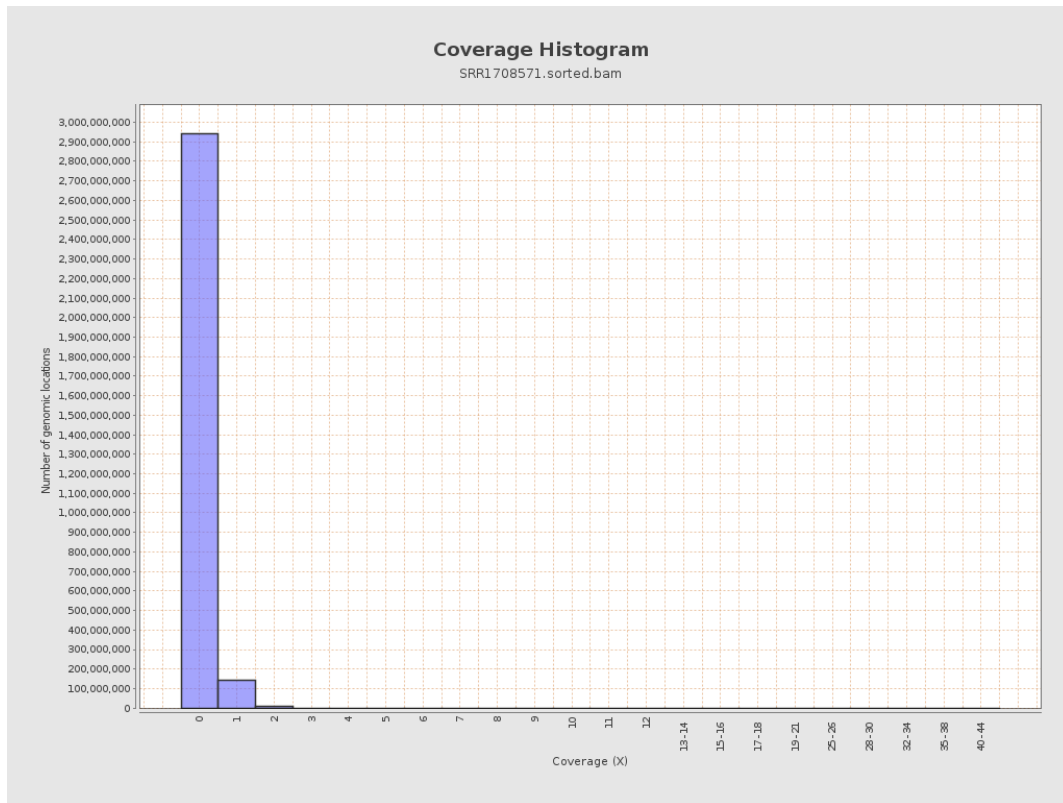
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18435035	0.074	0.2842
chr2	243199373	11567628	0.0476	0.2235
chr3	198022430	5750434	0.029	0.1768
chr4	191154276	5759331	0.0301	0.1791
chr5	180915260	7243145	0.04	0.2075
chr6	171115067	8912791	0.0521	0.2338
chr7	159138663	12534236	0.0788	0.291

chr8	146364022	11680409	0.0798	0.2919
chr9	141213431	7708317	0.0546	0.244
chr10	135534747	7911505	0.0584	0.2492
chr11	135006516	8013322	0.0594	0.2523
chr12	133851895	8621729	0.0644	0.2627
chr13	115169878	9537158	0.0828	0.2988
chr14	107349540	7858238	0.0732	0.2818
chr15	102531392	6190967	0.0604	0.2557
chr16	90354753	3784106	0.0419	0.2123
chr17	81195210	1351430	0.0166	0.1331
chr18	78077248	4510246	0.0578	0.2468
chr19	59128983	1758180	0.0297	0.1767
chr20	63025520	2675738	0.0425	0.2129
chr21	48129895	2554489	0.0531	0.2404
chr22	51304566	825984	0.0161	0.1309
chrMT	16571	100	0.006	0.0774
chrX	155270560	8501970	0.0548	0.2402
chrY	59373566	227865	0.0038	0.0652

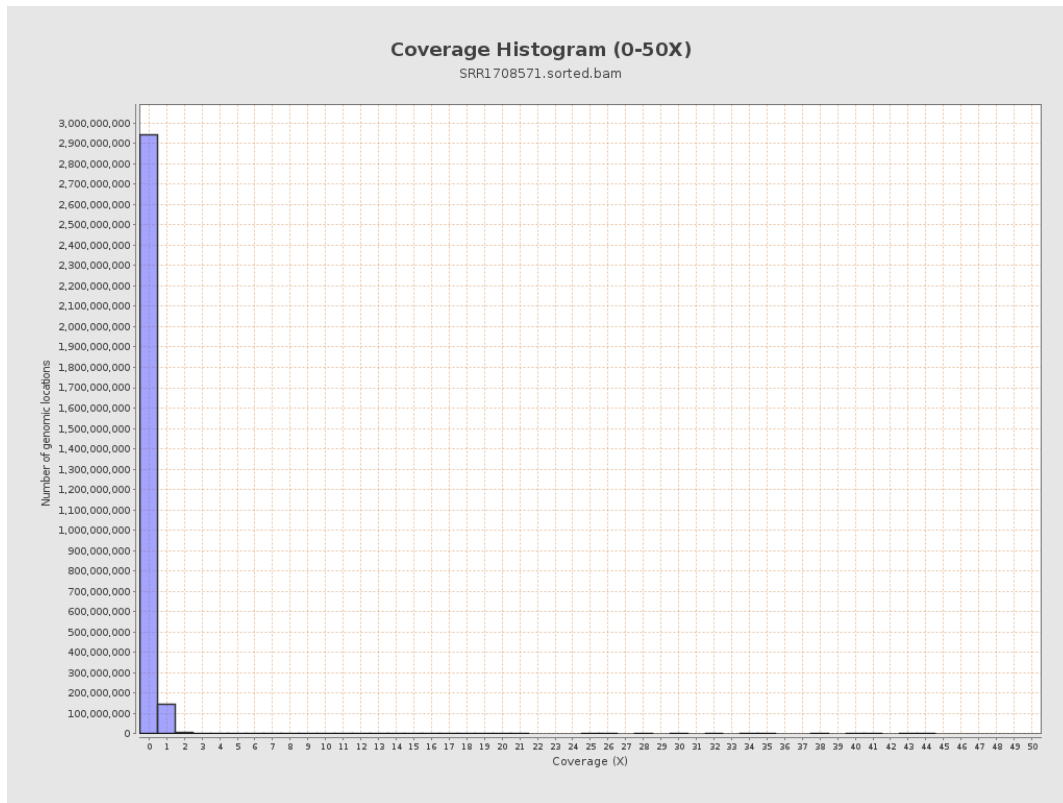
3. Results : Coverage across reference



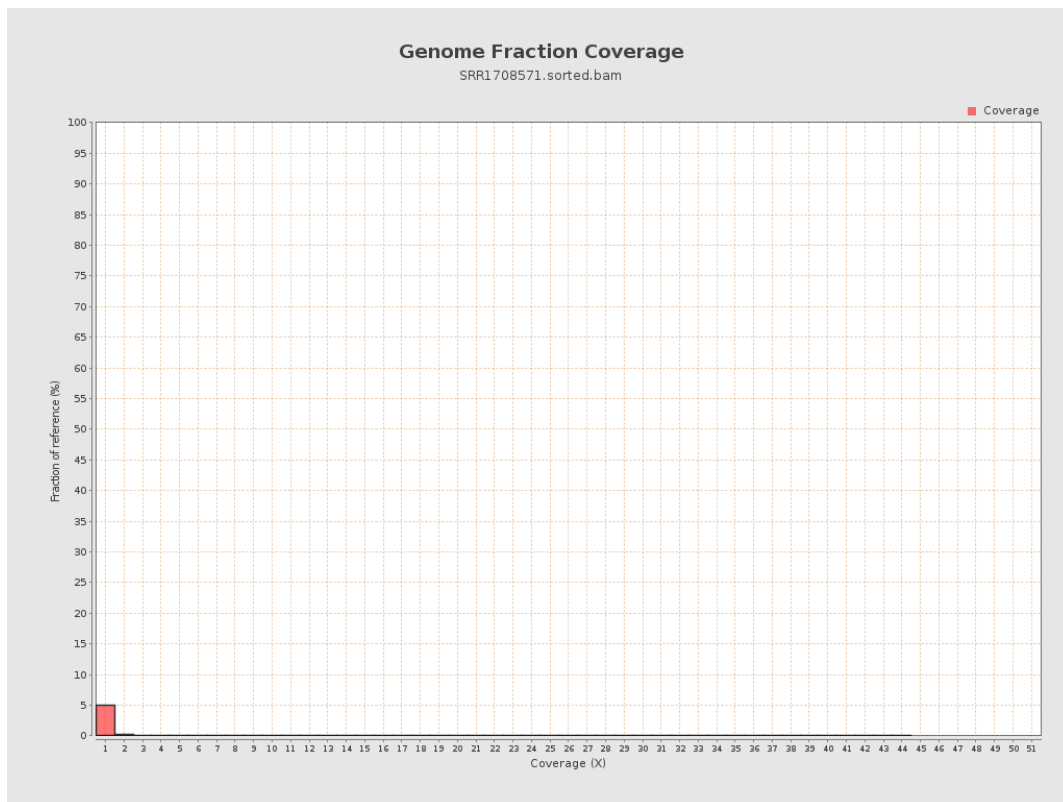
4. Results : Coverage Histogram



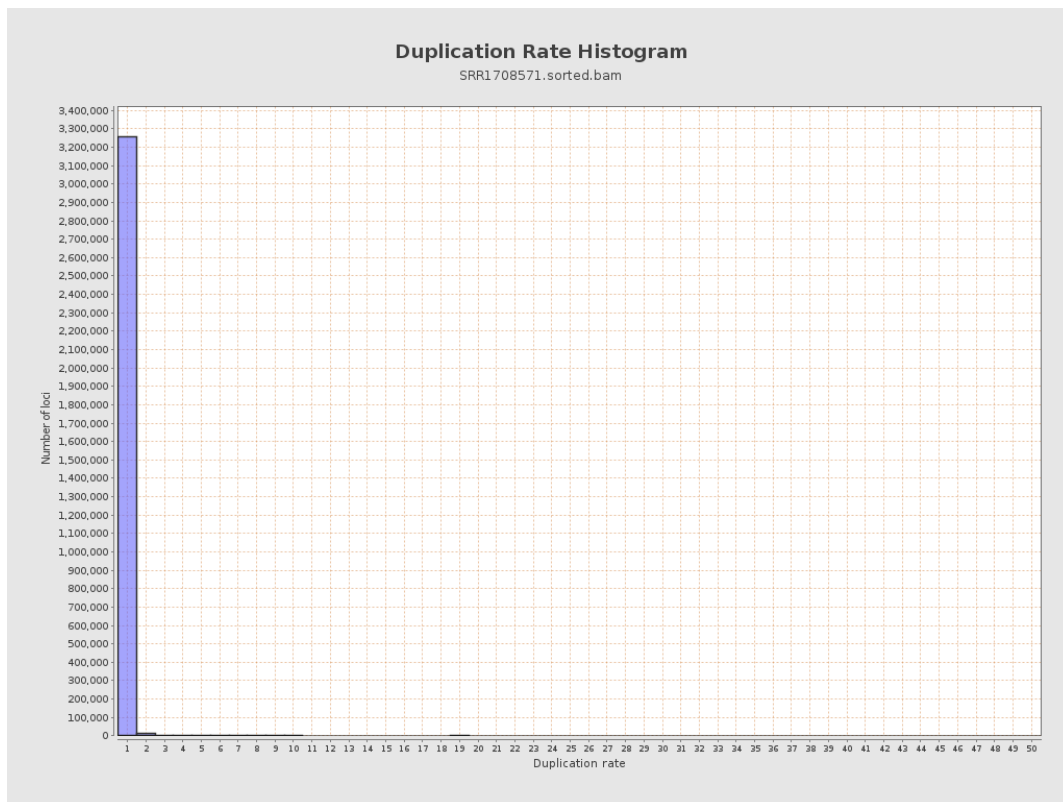
5. Results : Coverage Histogram (0-50X)



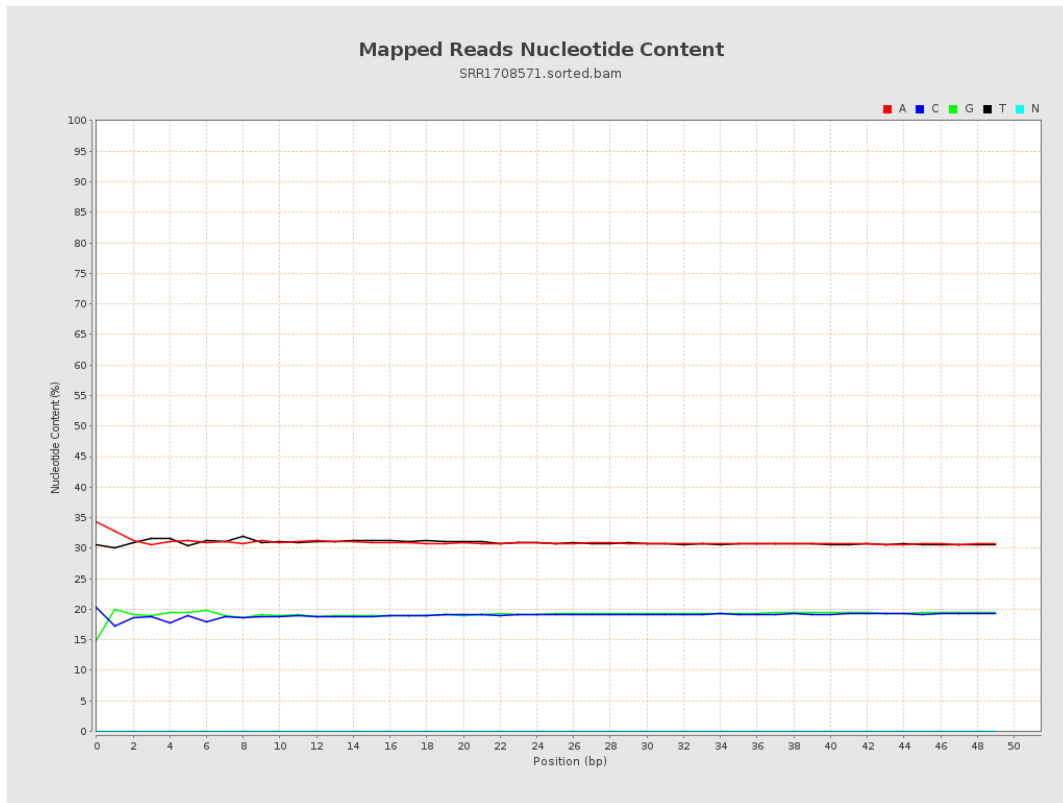
6. Results : Genome Fraction Coverage



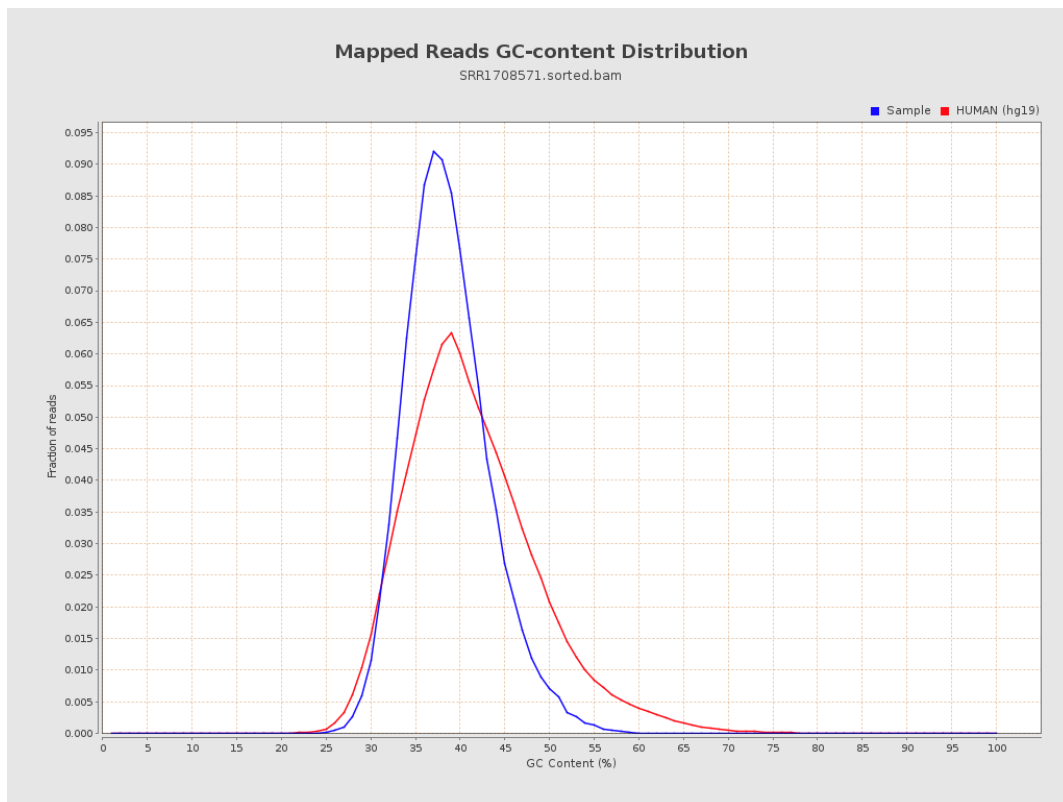
7. Results : Duplication Rate Histogram



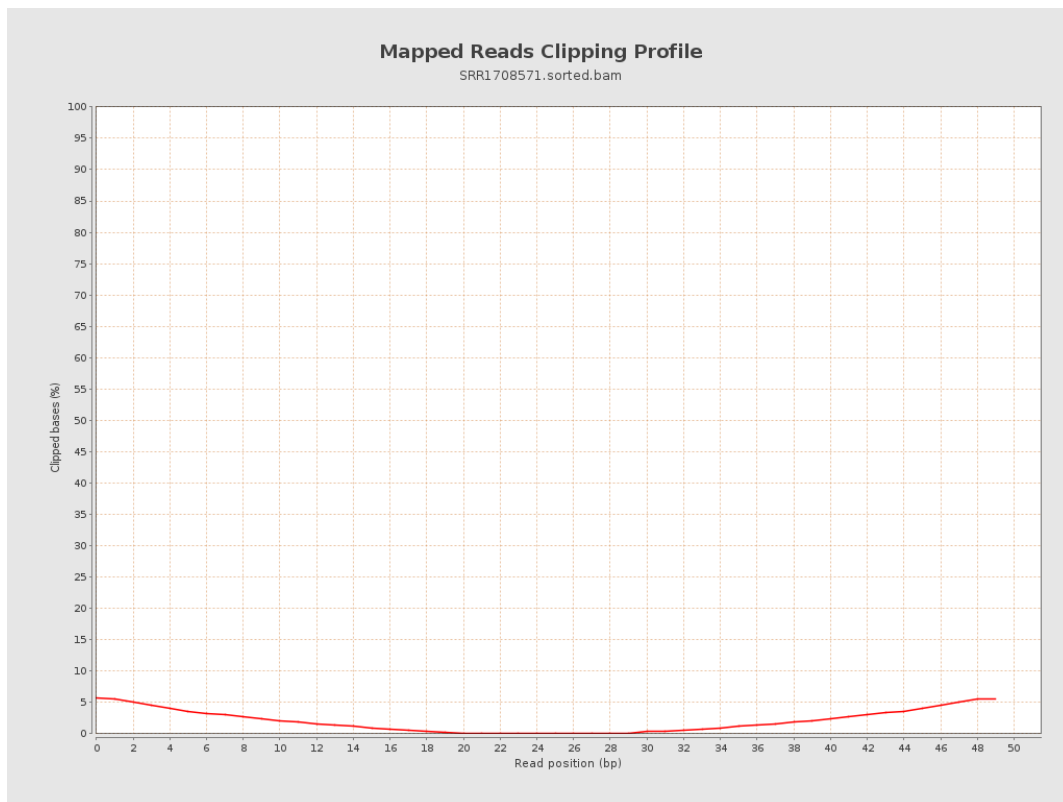
8. Results : Mapped Reads Nucleotide Content



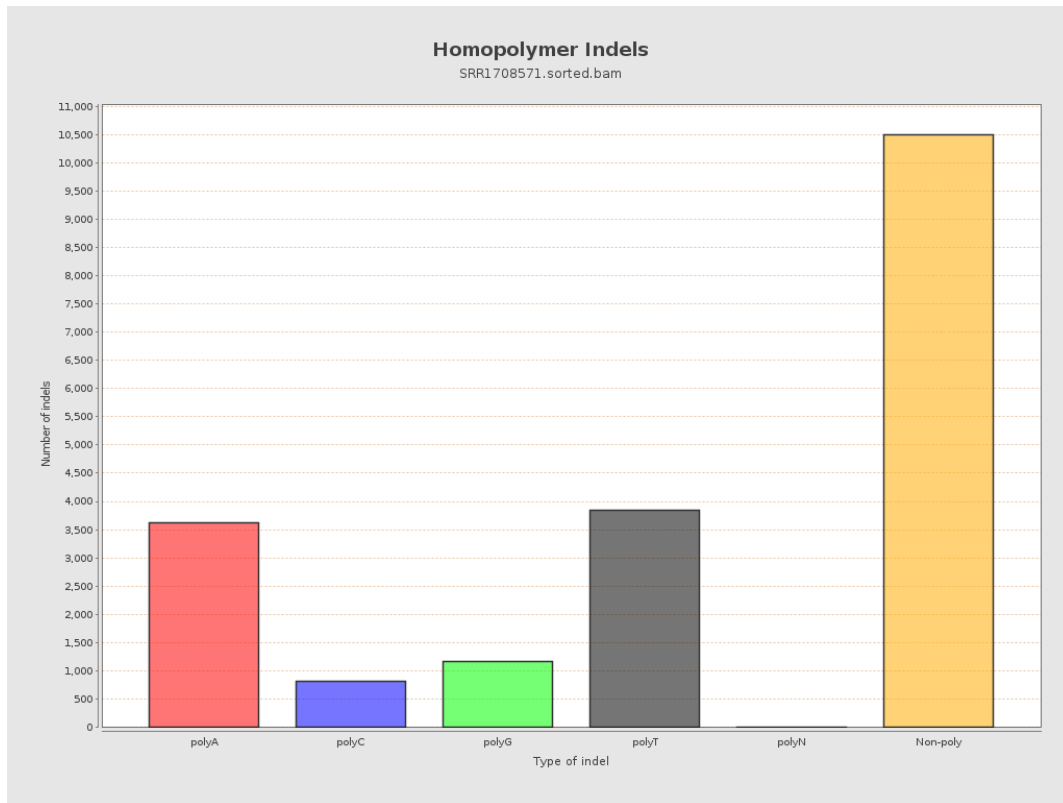
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

