

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:42:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472836.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_SRR3472836 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472836.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:42:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472836.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,684,848
Mapped reads	2,313,578 / 86.17%
Unmapped reads	371,270 / 13.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,023 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	65,862 / 2.45%
Duplication rate	2.05%
Clipped reads	1,227,635 / 45.72%

2.2. ACGT Content

Number/percentage of A's	40,541,968 / 27.11%
Number/percentage of C's	30,336,380 / 20.28%
Number/percentage of T's	43,808,483 / 29.29%
Number/percentage of G's	34,874,350 / 23.32%
Number/percentage of N's	2,912 / 0%
GC Percentage	43.6%

2.3. Coverage

Mean	0.0483

Standard Deviation	0.3514
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2.4. Mapping Quality

Mean Mapping Quality	43.75
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2.5. Mismatches and indels

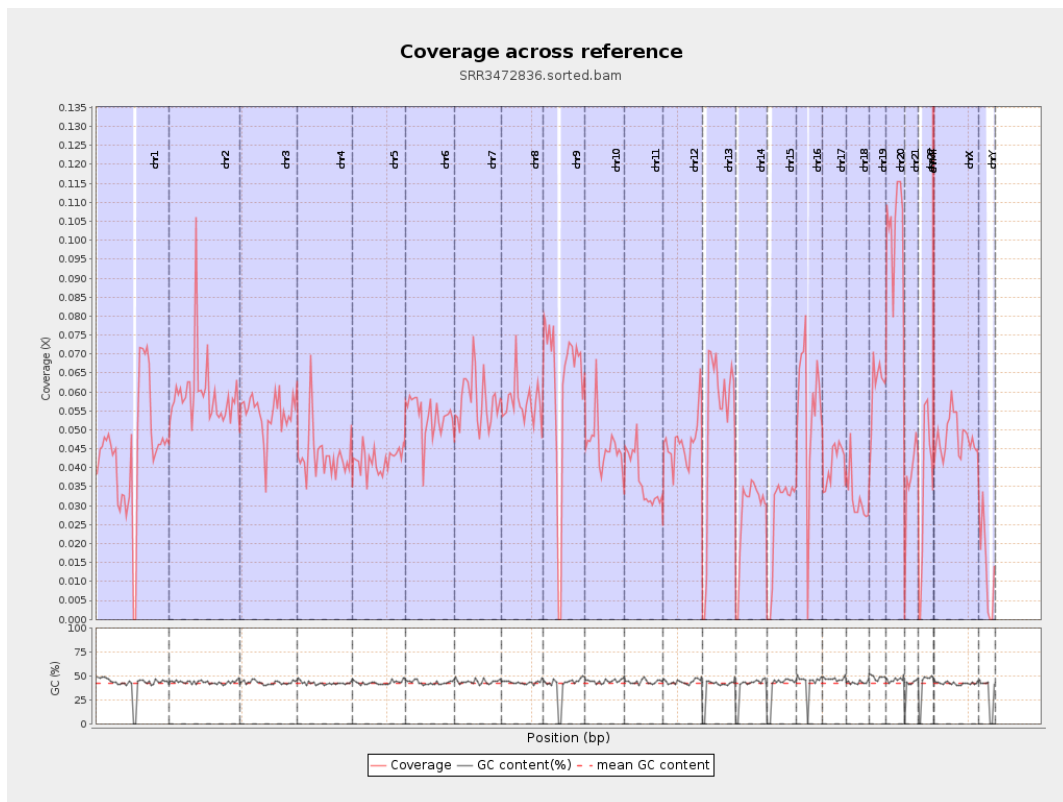
General error rate	0.86%
Mismatches	1,270,098
Insertions	11,809
Mapped reads with at least one insertion	0.51%
Deletions	33,655
Mapped reads with at least one deletion	1.44%
Homopolymer indels	43.87%

2.6. Chromosome stats

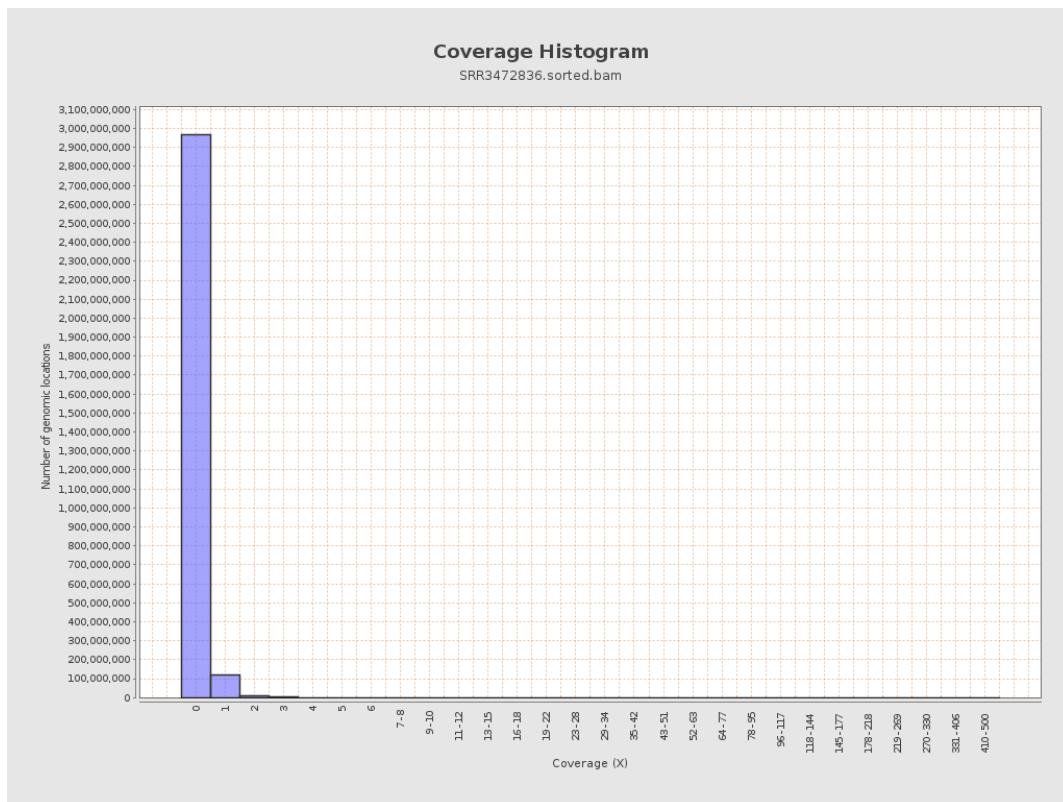
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11005679	0.0442	0.4476
chr2	243199373	14437871	0.0594	0.5298
chr3	198022430	10749065	0.0543	0.2575
chr4	191154276	8257711	0.0432	0.2592
chr5	180915260	7601086	0.042	0.2275
chr6	171115067	9159494	0.0535	0.2769
chr7	159138663	9204491	0.0578	0.4539

chr8	146364022	8351014	0.0571	0.3531
chr9	141213431	8666889	0.0614	0.4171
chr10	135534747	6208831	0.0458	0.3453
chr11	135006516	4958979	0.0367	0.3398
chr12	133851895	6255556	0.0467	0.2486
chr13	115169878	6039918	0.0524	0.2608
chr14	107349540	2997559	0.0279	0.2204
chr15	102531392	2784993	0.0272	0.1987
chr16	90354753	5118655	0.0567	0.2967
chr17	81195210	3327197	0.041	0.2453
chr18	78077248	2502180	0.032	0.6341
chr19	59128983	3637440	0.0615	0.388
chr20	63025520	6545019	0.1038	0.3771
chr21	48129895	1779607	0.037	0.2593
chr22	51304566	1772017	0.0345	0.2206
chrMT	16571	29216	1.7631	1.7248
chrX	155270560	7447861	0.048	0.2791
chrY	59373566	785646	0.0132	0.1925

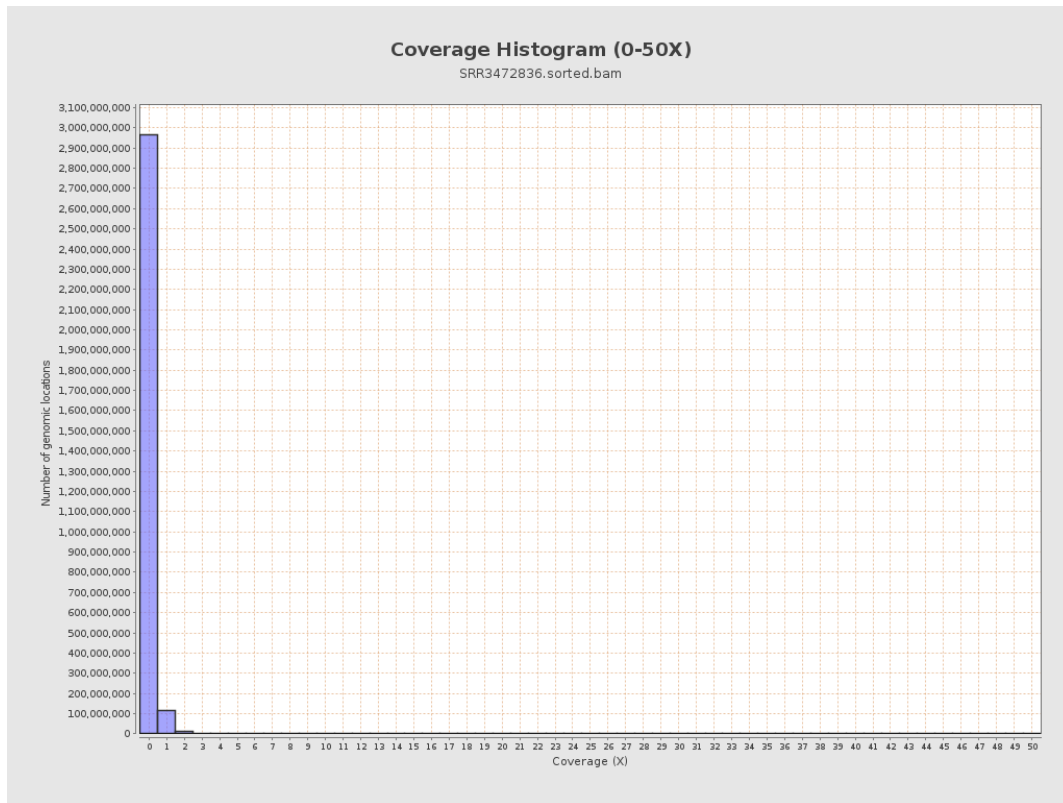
3. Results : Coverage across reference



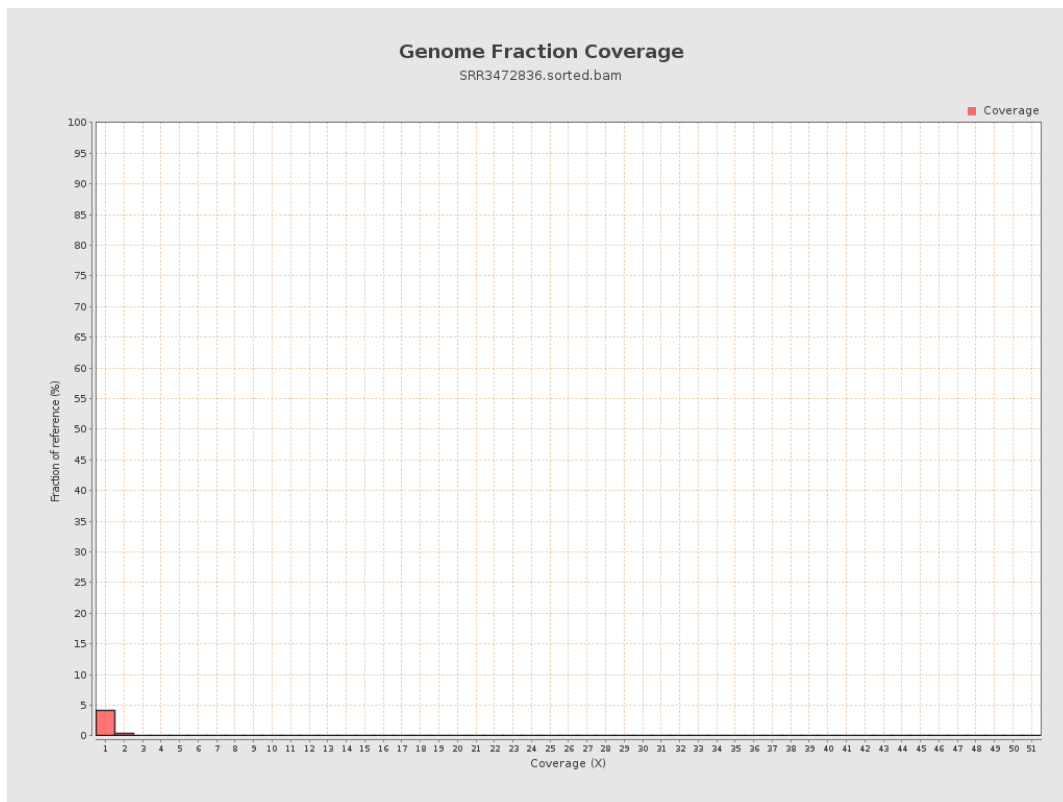
4. Results : Coverage Histogram



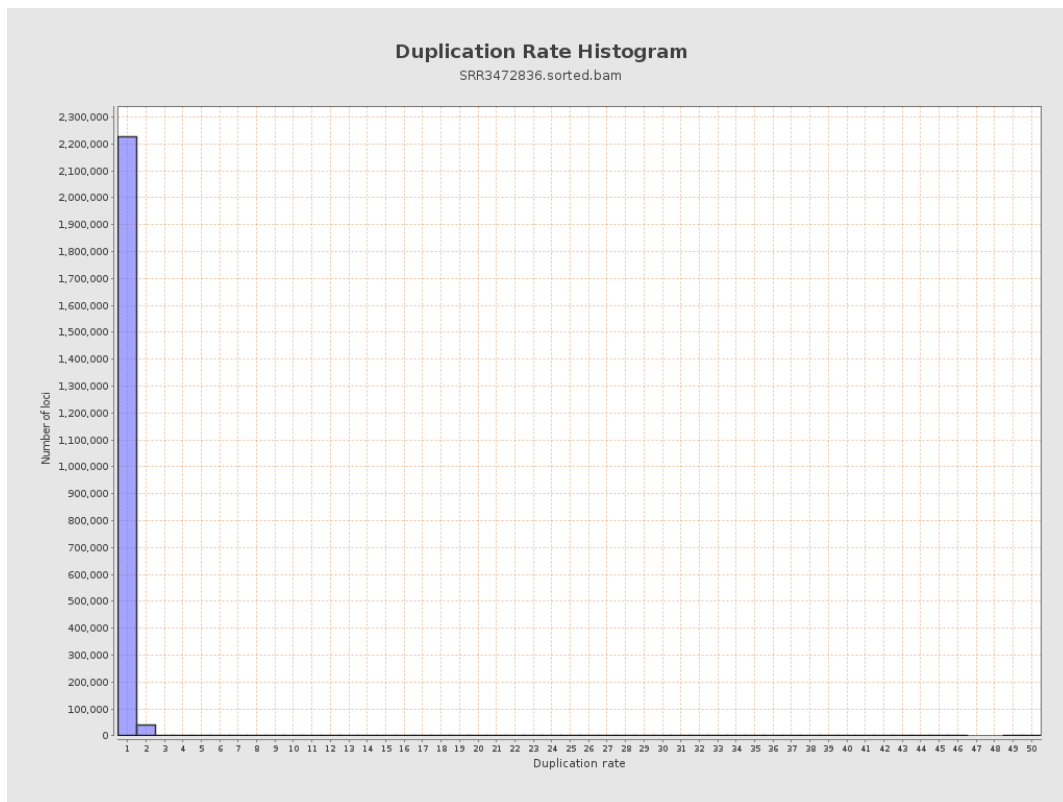
5. Results : Coverage Histogram (0-50X)



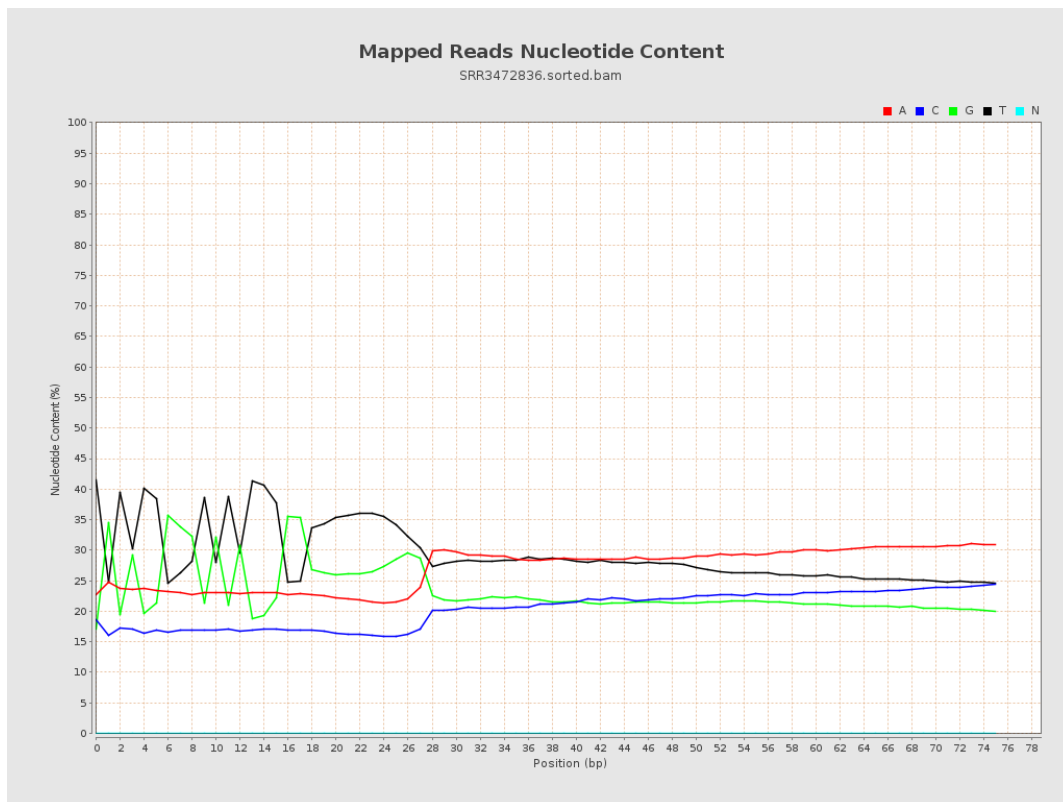
6. Results : Genome Fraction Coverage



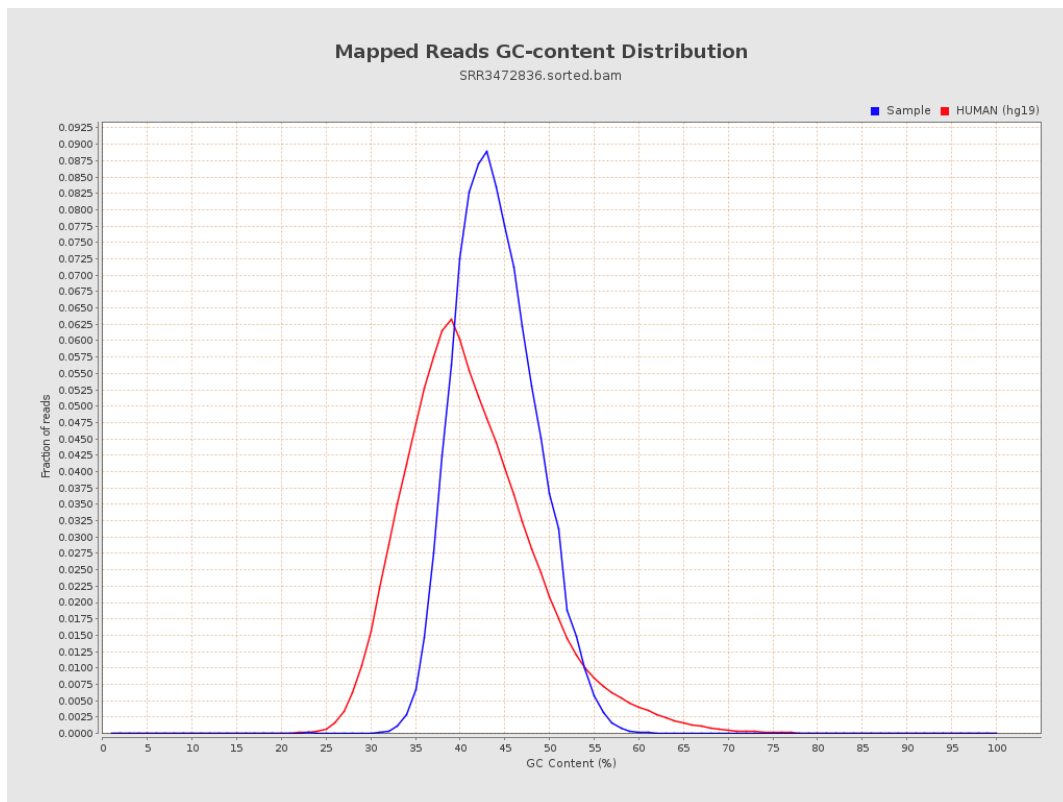
7. Results : Duplication Rate Histogram



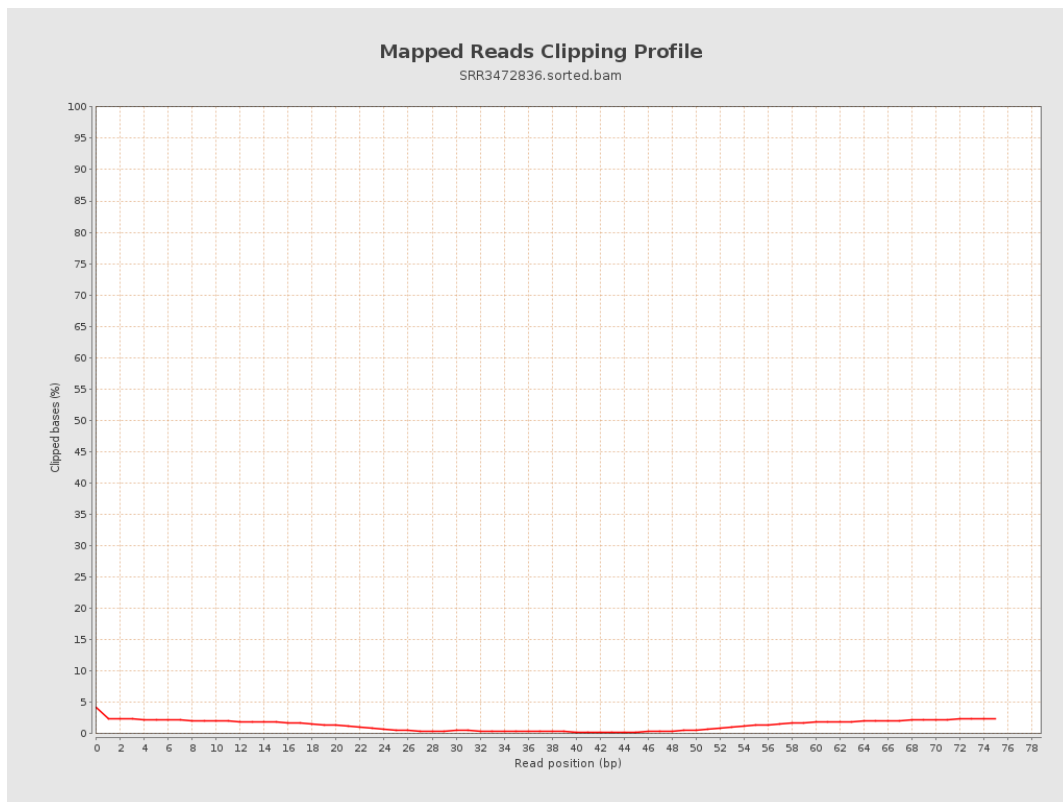
8. Results : Mapped Reads Nucleotide Content



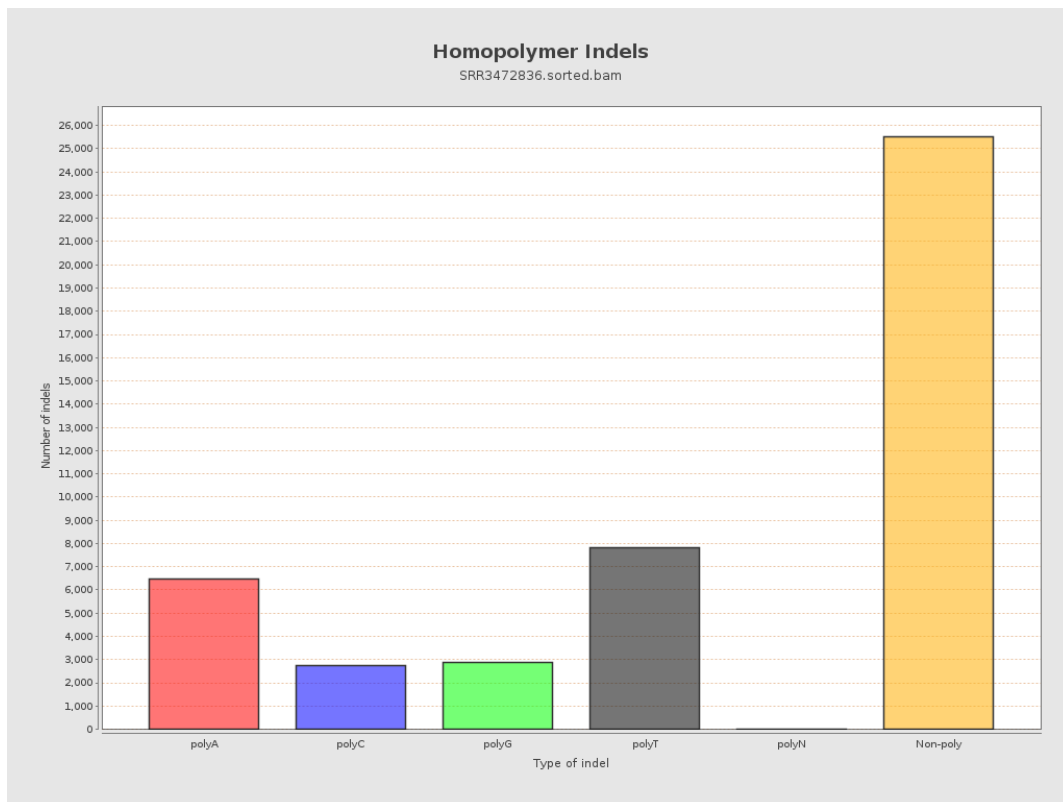
9. Results : Mapped Reads GC-content Distribution



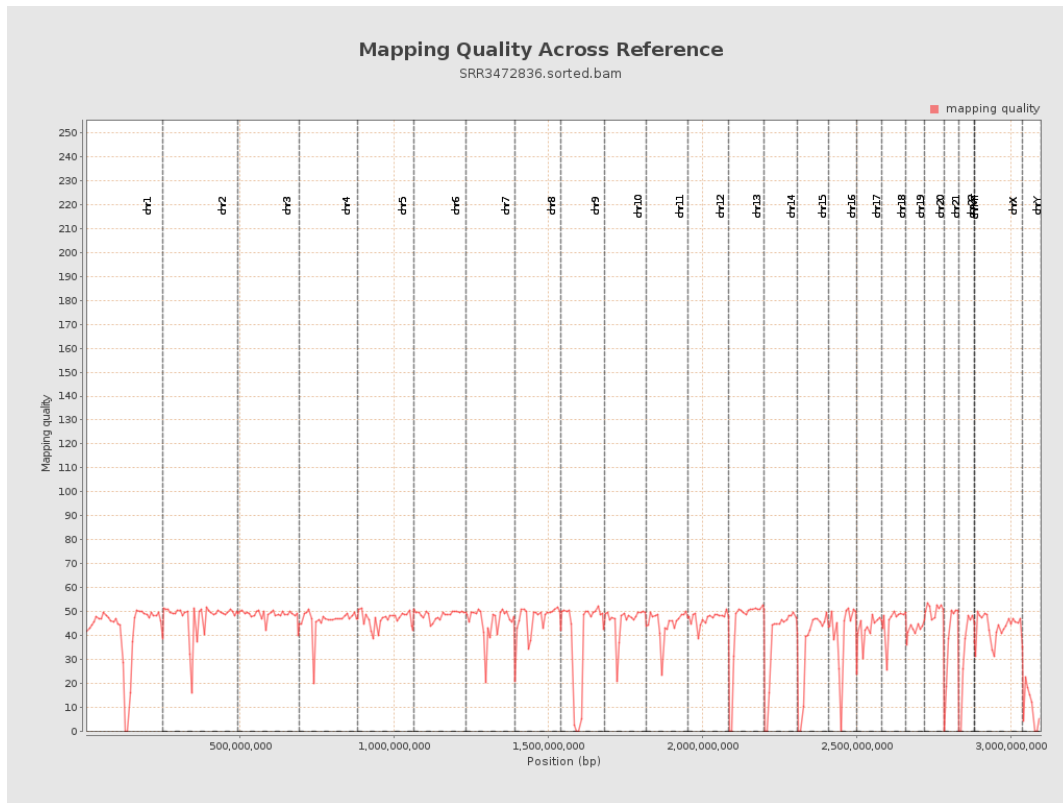
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

