

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 09:55:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472838.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_SRR3472838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472838.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 09:55:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472838.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,512,633
Mapped reads	2,208,075 / 87.88%
Unmapped reads	304,558 / 12.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,213 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	70,178 / 2.79%
Duplication rate	2.45%
Clipped reads	1,098,355 / 43.71%

2.2. ACGT Content

Number/percentage of A's	38,761,667 / 26.88%
Number/percentage of C's	28,351,951 / 19.66%
Number/percentage of T's	43,436,711 / 30.12%
Number/percentage of G's	33,654,994 / 23.34%
Number/percentage of N's	3,658 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.3334
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2.4. Mapping Quality

Mean Mapping Quality	44.85
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2.5. Mismatches and indels

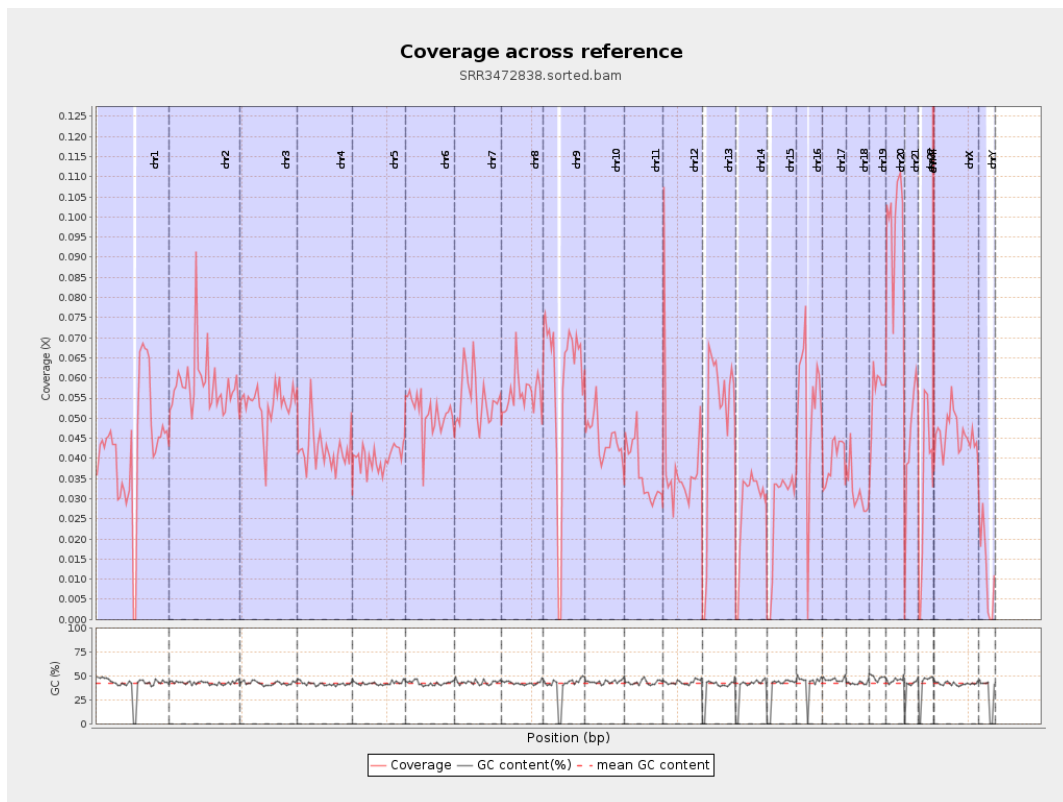
General error rate	0.85%
Mismatches	1,211,197
Insertions	11,228
Mapped reads with at least one insertion	0.5%
Deletions	33,567
Mapped reads with at least one deletion	1.5%
Homopolymer indels	46.02%

2.6. Chromosome stats

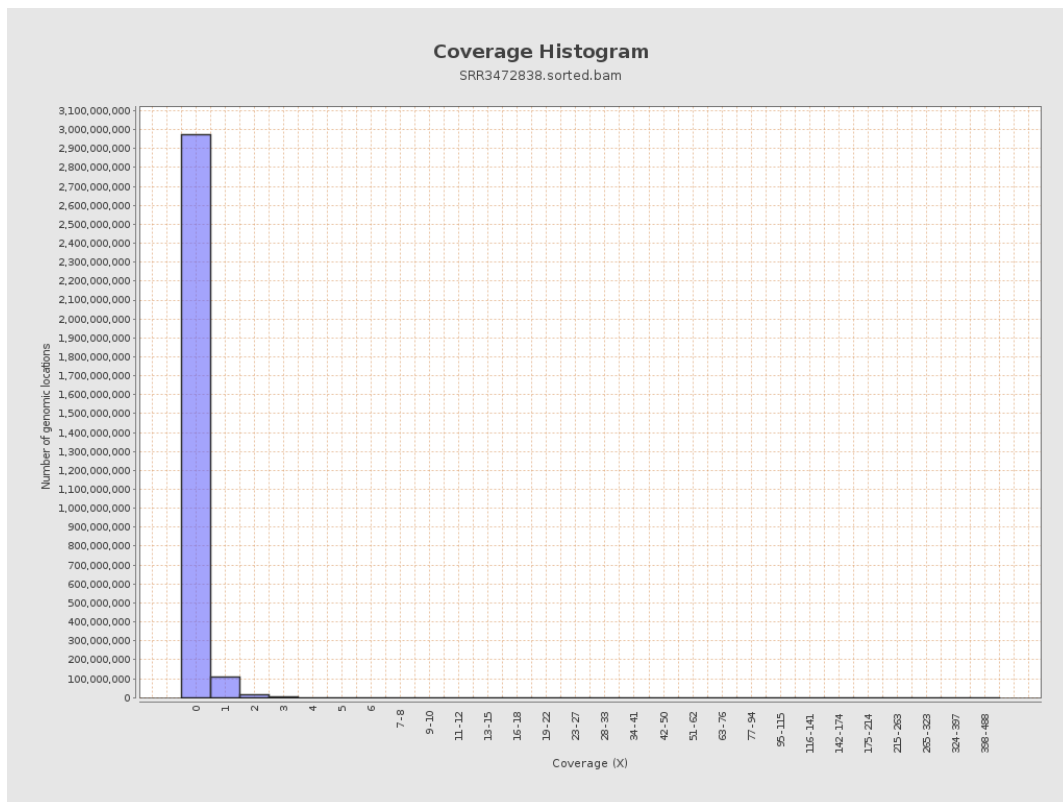
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10668592	0.0428	0.4386
chr2	243199373	14171952	0.0583	0.4714
chr3	198022430	10542462	0.0532	0.2577
chr4	191154276	8042820	0.0421	0.251
chr5	180915260	7265173	0.0402	0.2246
chr6	171115067	8751618	0.0511	0.2787
chr7	159138663	8769000	0.0551	0.4234

chr8	146364022	8228641	0.0562	0.3481
chr9	141213431	8301287	0.0588	0.3933
chr10	135534747	6093897	0.045	0.299
chr11	135006516	4890984	0.0362	0.3222
chr12	133851895	5200813	0.0389	0.2367
chr13	115169878	5678646	0.0493	0.2567
chr14	107349540	3005138	0.028	0.2161
chr15	102531392	2762385	0.0269	0.1925
chr16	90354753	4873597	0.0539	0.2847
chr17	81195210	3219005	0.0396	0.2419
chr18	78077248	2481623	0.0318	0.6048
chr19	59128983	3336144	0.0564	0.3608
chr20	63025520	6226804	0.0988	0.3736
chr21	48129895	2174576	0.0452	0.2798
chr22	51304566	1713042	0.0334	0.2189
chrMT	16571	18719	1.1296	1.3549
chrX	155270560	7146922	0.046	0.2667
chrY	59373566	704891	0.0119	0.1544

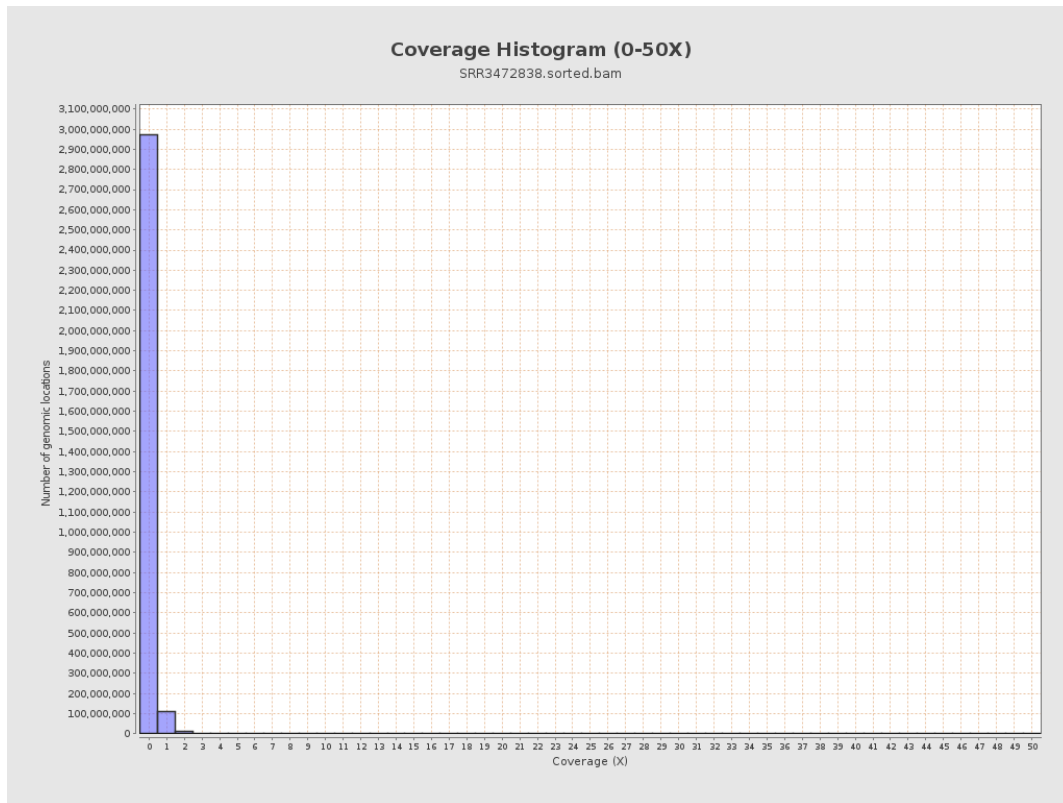
3. Results : Coverage across reference



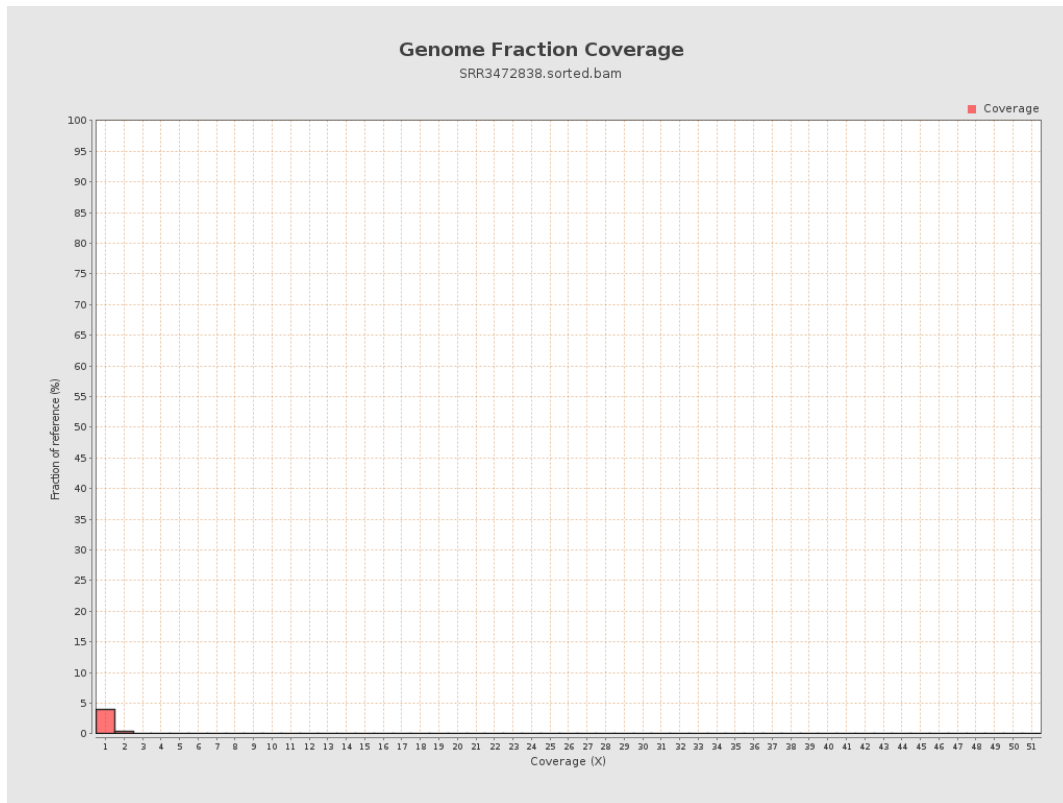
4. Results : Coverage Histogram



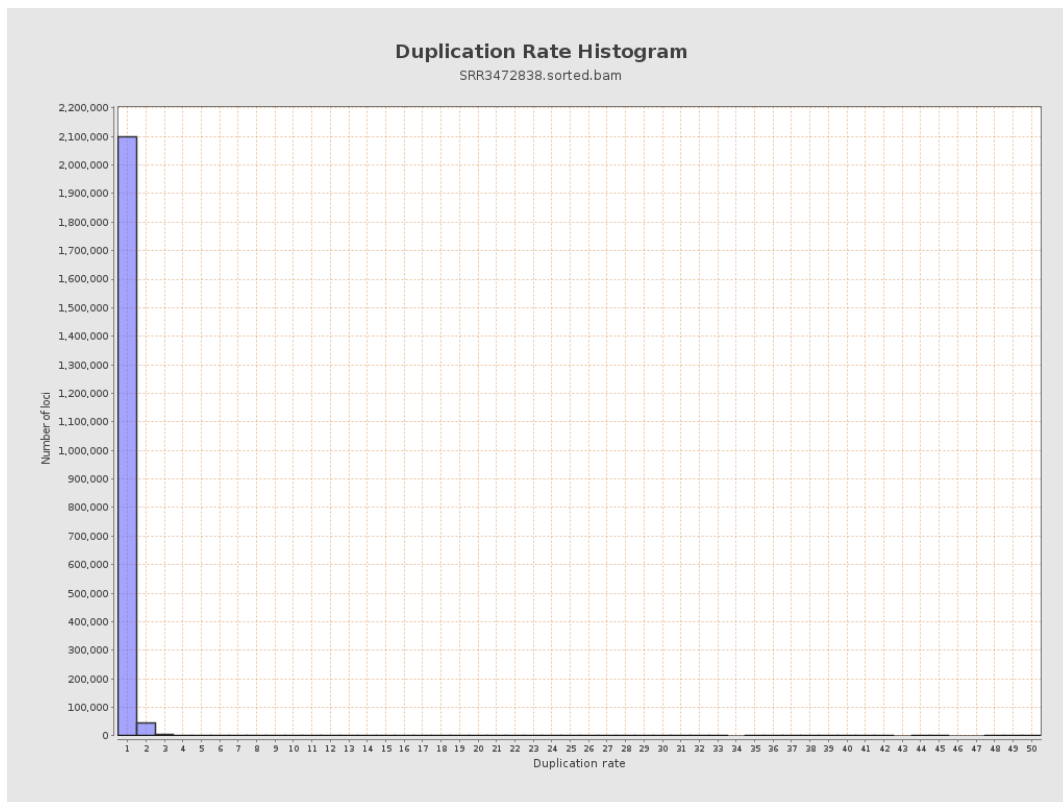
5. Results : Coverage Histogram (0-50X)



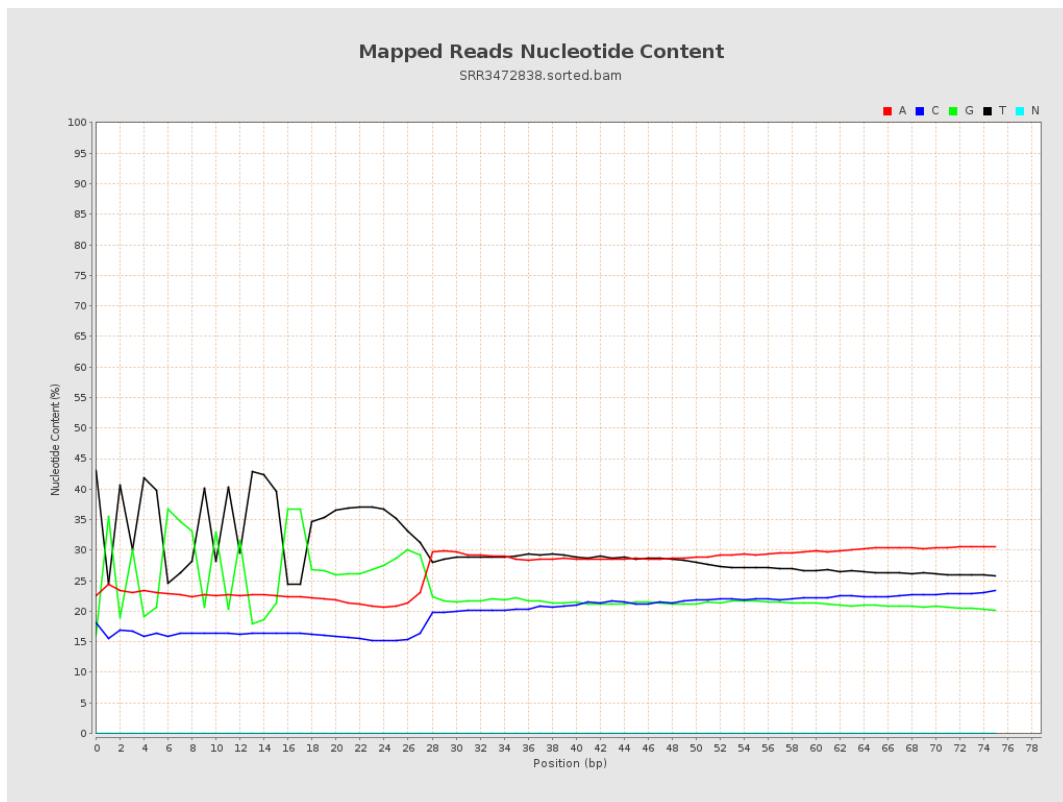
6. Results : Genome Fraction Coverage



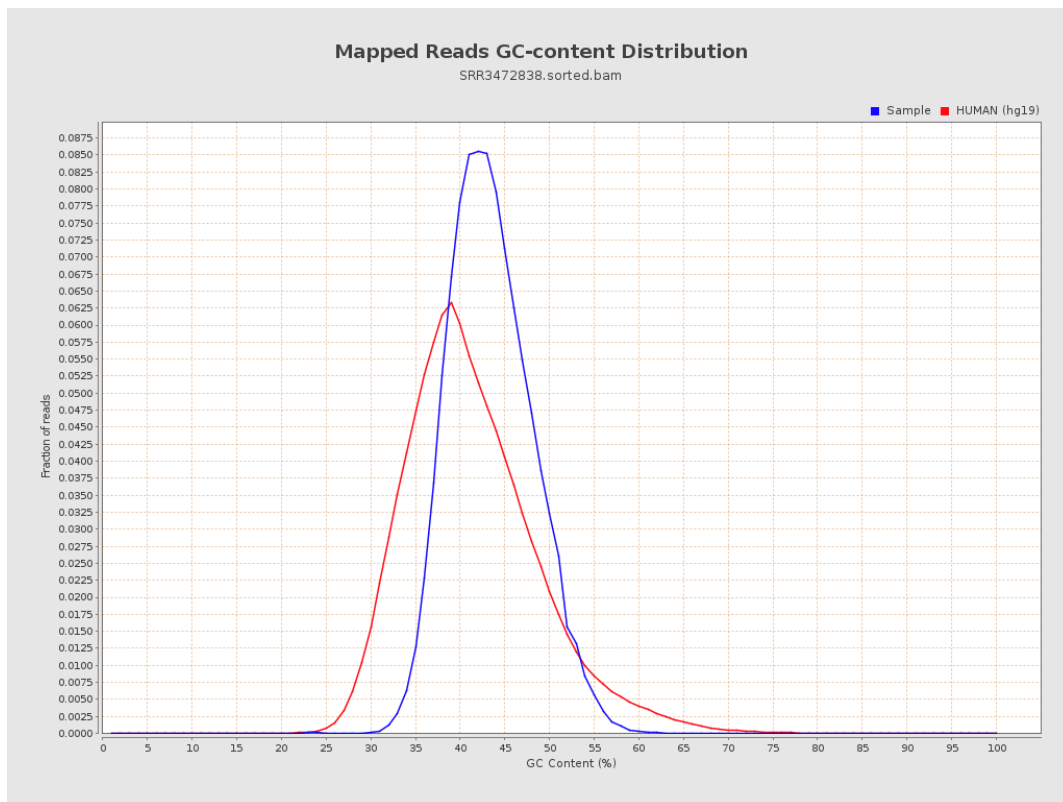
7. Results : Duplication Rate Histogram



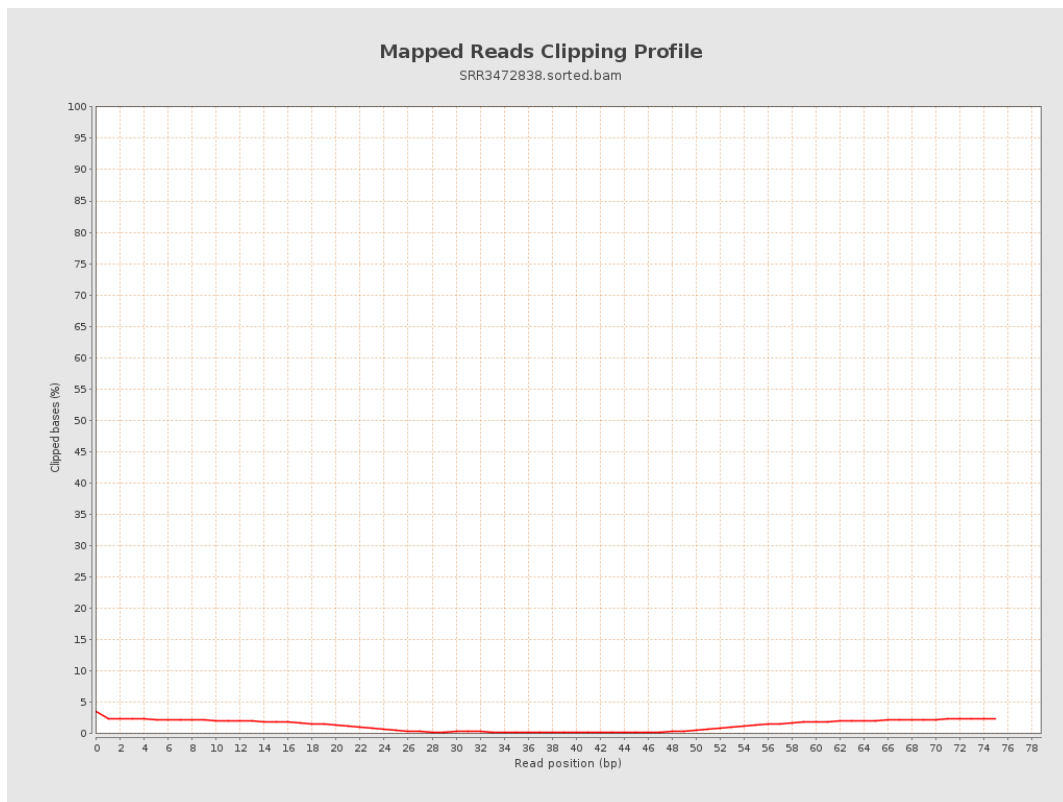
8. Results : Mapped Reads Nucleotide Content



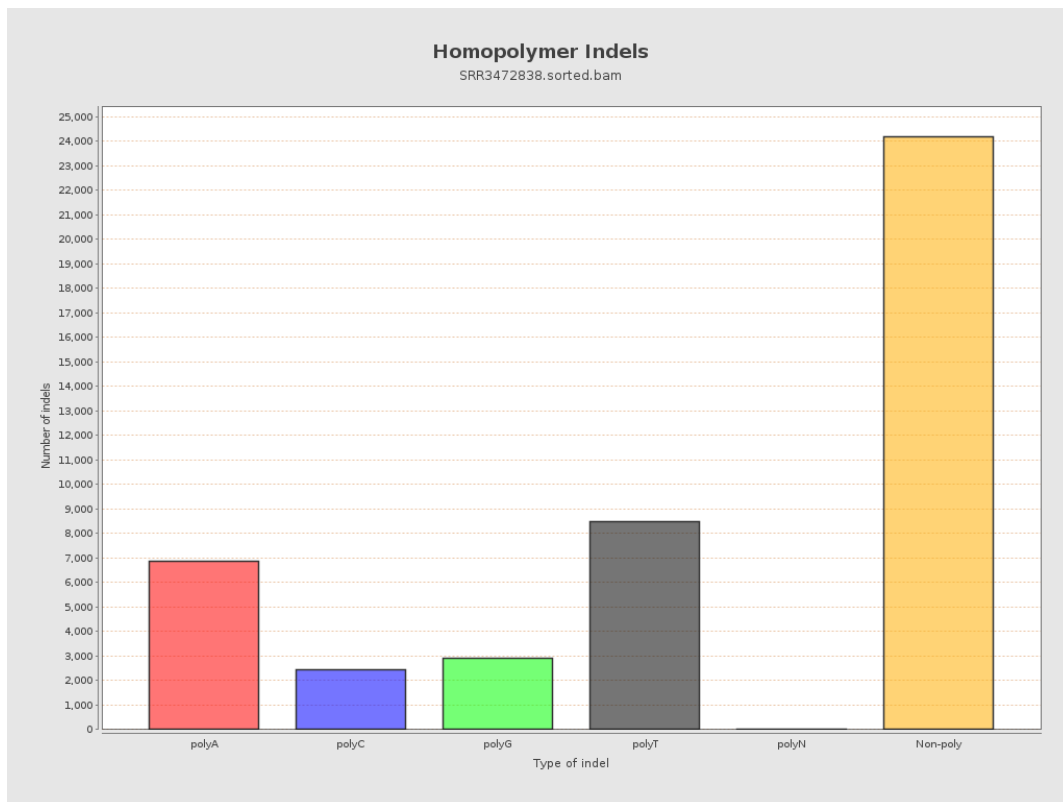
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

