

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:00:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238669.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_SRR6238669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238669.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:00:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,778,756
Mapped reads	1,686,729 / 60.7%
Unmapped reads	1,092,027 / 39.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,496 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	205,374 / 7.39%
Duplication rate	10.43%
Clipped reads	1,089,238 / 39.2%

2.2. ACGT Content

Number/percentage of A's	26,021,978 / 25.14%
Number/percentage of C's	18,231,805 / 17.61%
Number/percentage of T's	34,587,891 / 33.41%
Number/percentage of G's	24,667,448 / 23.83%
Number/percentage of N's	5,201 / 0.01%
GC Percentage	41.44%

2.3. Coverage

Mean	0.0335

Standard Deviation	0.4197
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2.4. Mapping Quality

Mean Mapping Quality	44.63
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2.5. Mismatches and indels

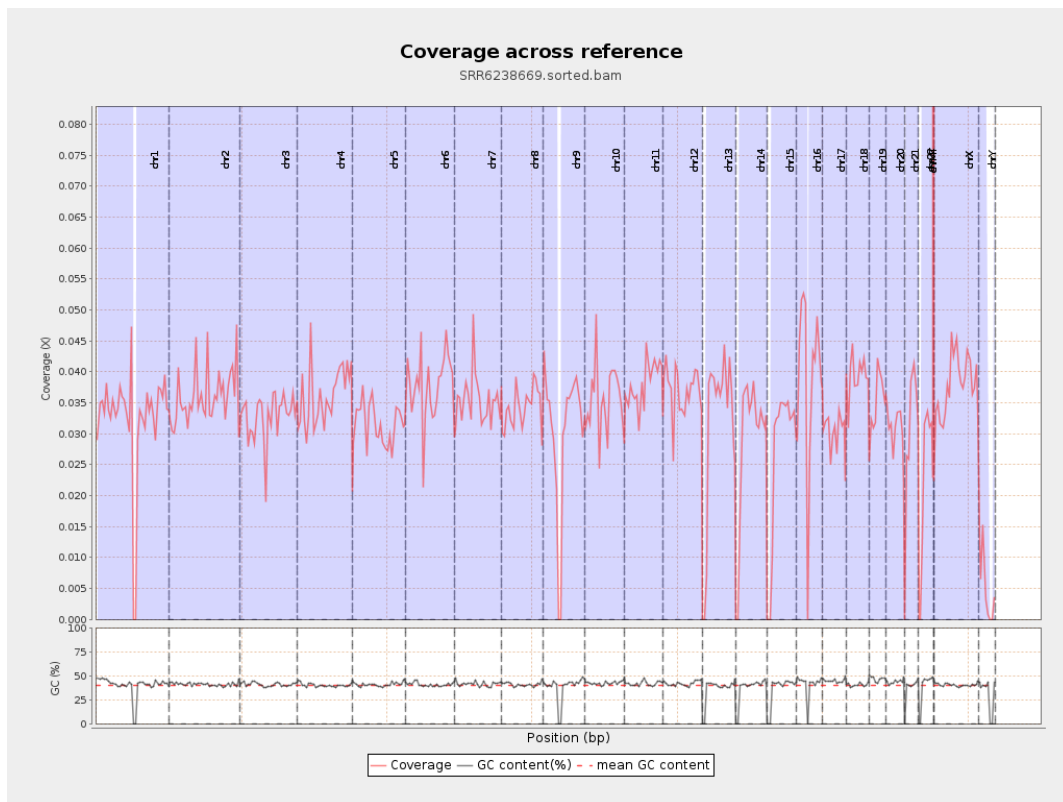
General error rate	0.68%
Mismatches	692,252
Insertions	7,206
Mapped reads with at least one insertion	0.42%
Deletions	38,899
Mapped reads with at least one deletion	2.28%
Homopolymer indels	41.6%

2.6. Chromosome stats

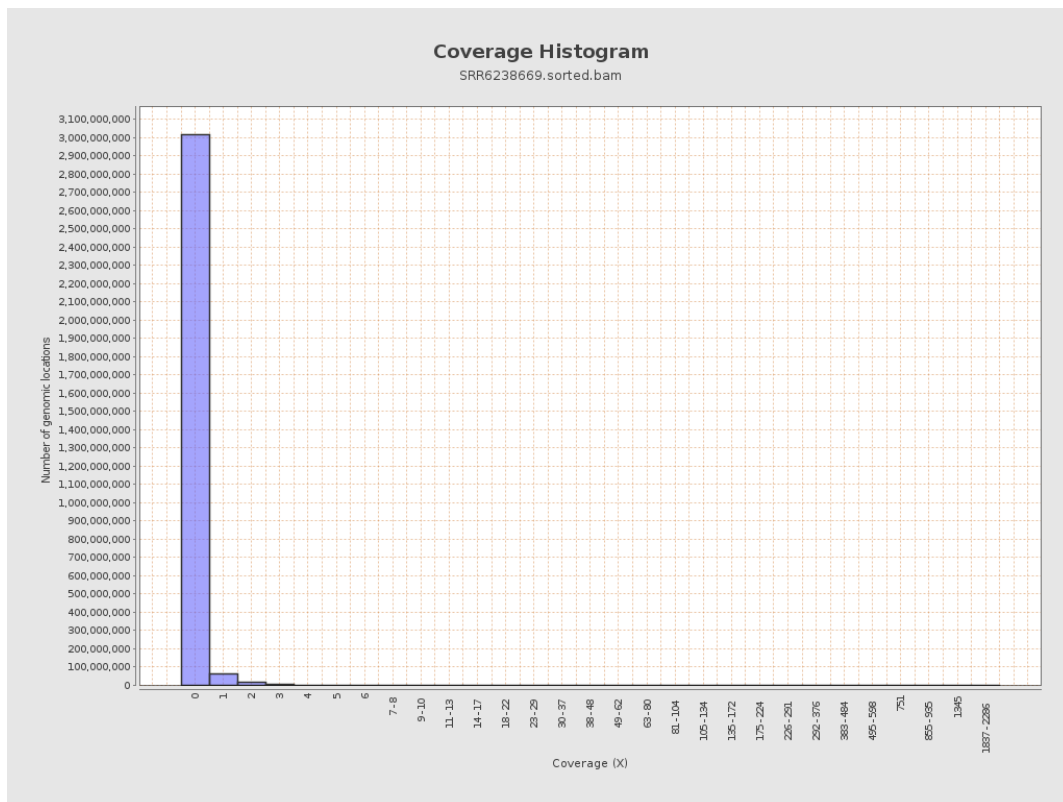
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8085020	0.0324	0.413
chr2	243199373	8779121	0.0361	1.0245
chr3	198022430	6481991	0.0327	0.2385
chr4	191154276	6892057	0.0361	0.2565
chr5	180915260	5696412	0.0315	0.2318
chr6	171115067	6448989	0.0377	0.3951
chr7	159138663	5659877	0.0356	0.35

chr8	146364022	5010934	0.0342	0.381
chr9	141213431	4258348	0.0302	0.2607
chr10	135534747	4817409	0.0355	0.3034
chr11	135006516	5132048	0.038	0.2752
chr12	133851895	4954555	0.037	0.251
chr13	115169878	3599412	0.0313	0.2865
chr14	107349540	3082155	0.0287	0.2201
chr15	102531392	2756797	0.0269	0.2823
chr16	90354753	3590515	0.0397	0.2829
chr17	81195210	2443819	0.0301	0.2287
chr18	78077248	3075751	0.0394	0.7532
chr19	59128983	2094860	0.0354	0.3398
chr20	63025520	1943327	0.0308	0.2274
chr21	48129895	1467816	0.0305	0.2347
chr22	51304566	1140643	0.0222	0.1895
chrMT	16571	15368	0.9274	1.2956
chrX	155270560	5856873	0.0377	0.26
chrY	59373566	297173	0.005	0.1756

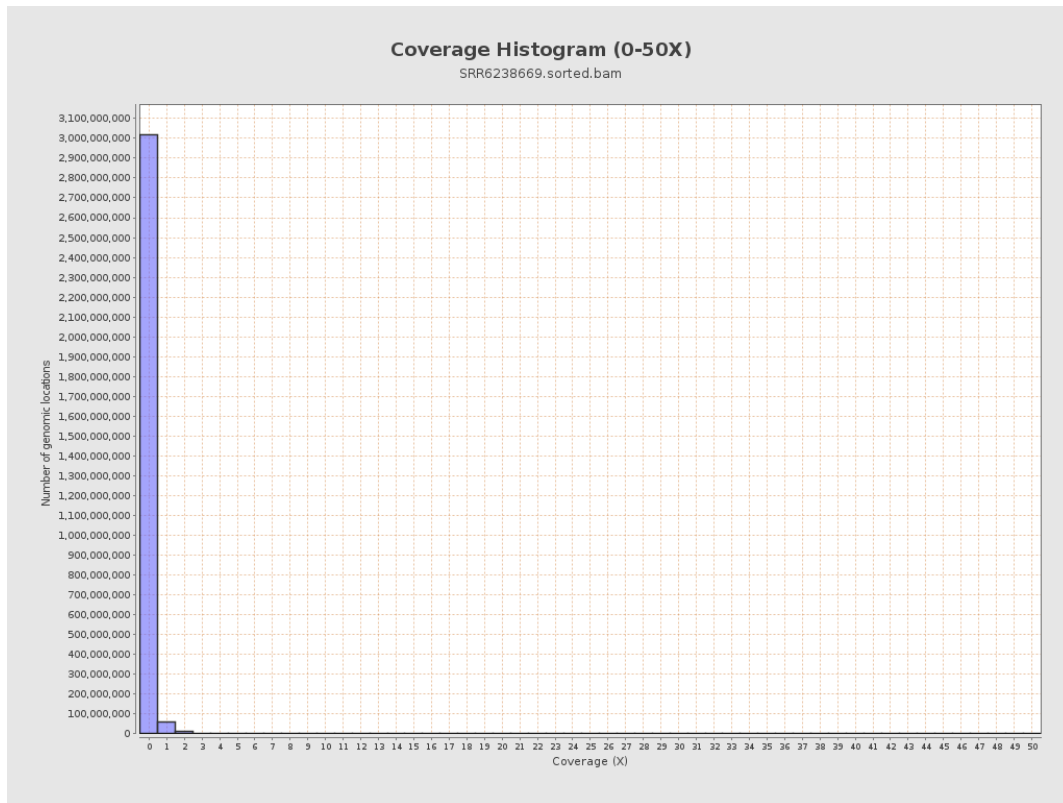
3. Results : Coverage across reference



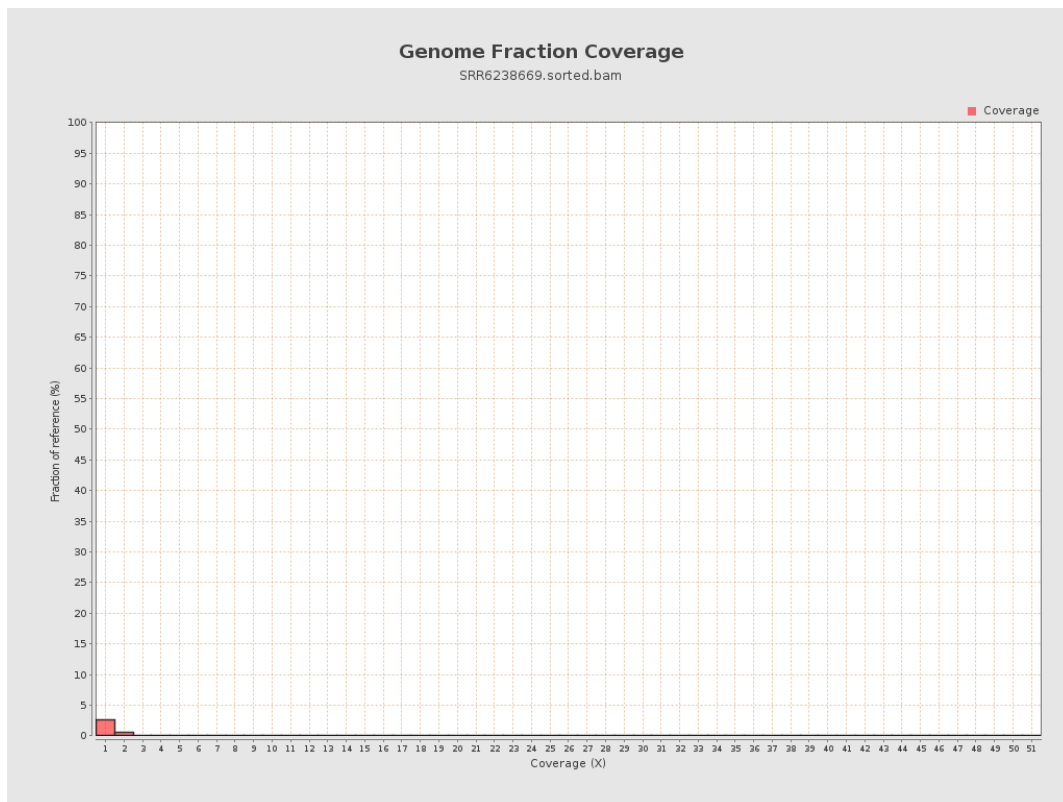
4. Results : Coverage Histogram



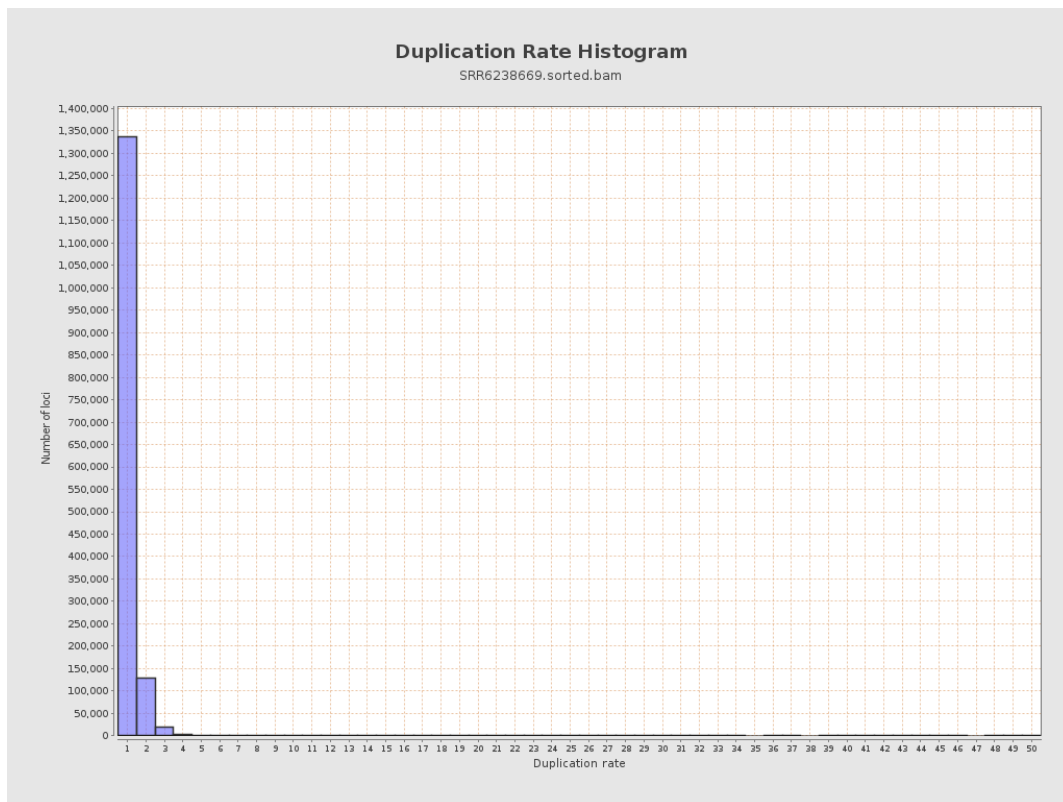
5. Results : Coverage Histogram (0-50X)



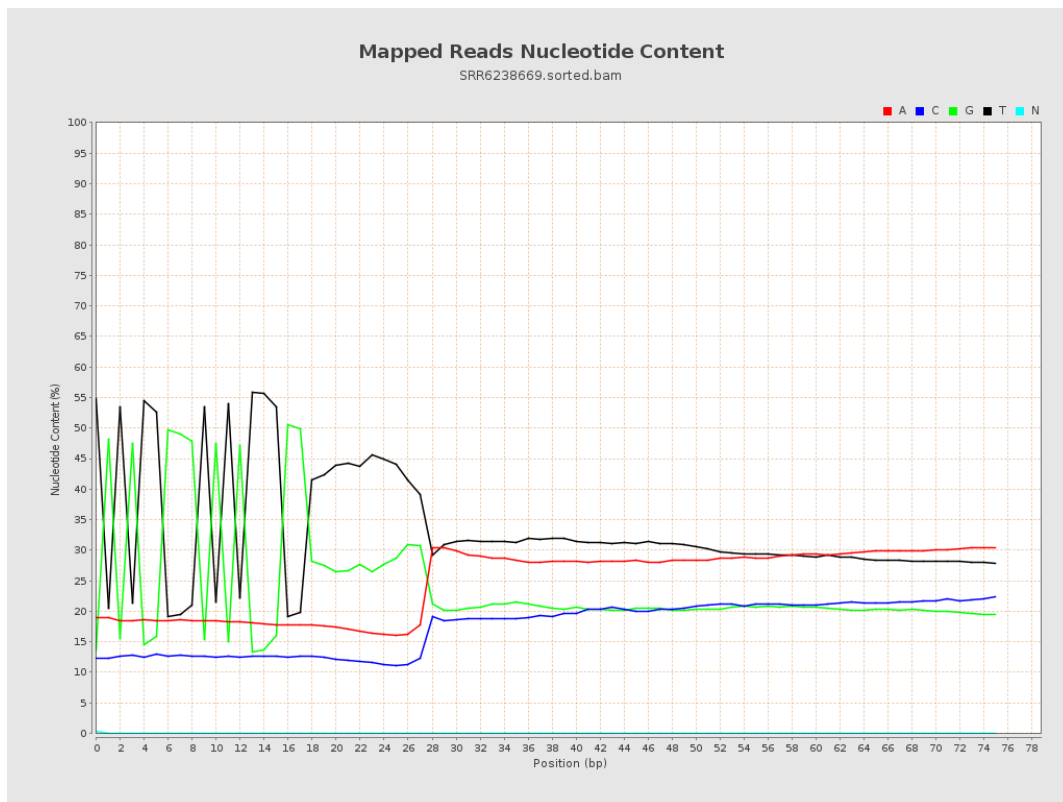
6. Results : Genome Fraction Coverage



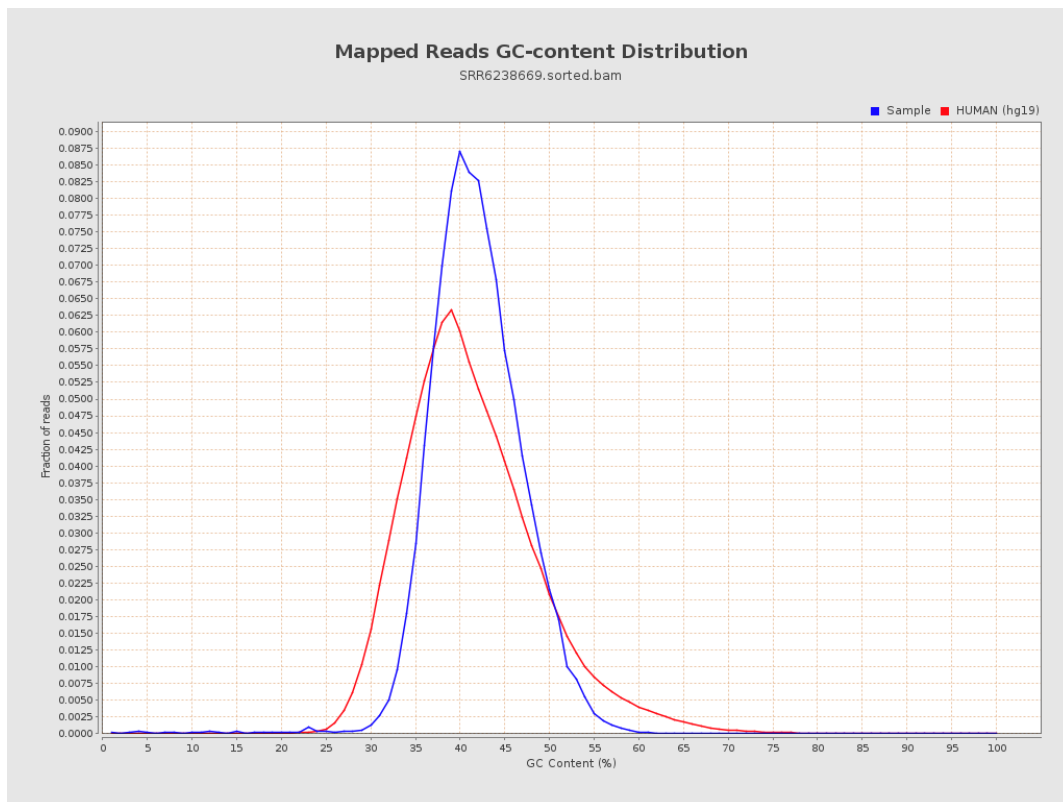
7. Results : Duplication Rate Histogram



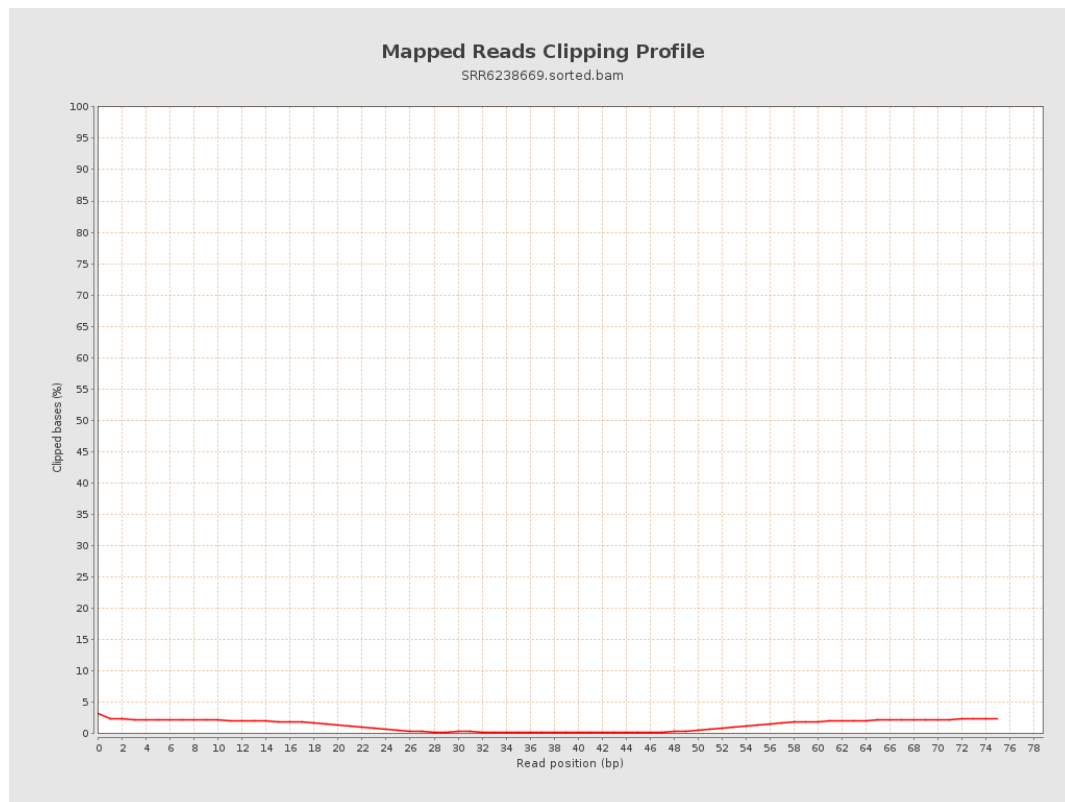
8. Results : Mapped Reads Nucleotide Content



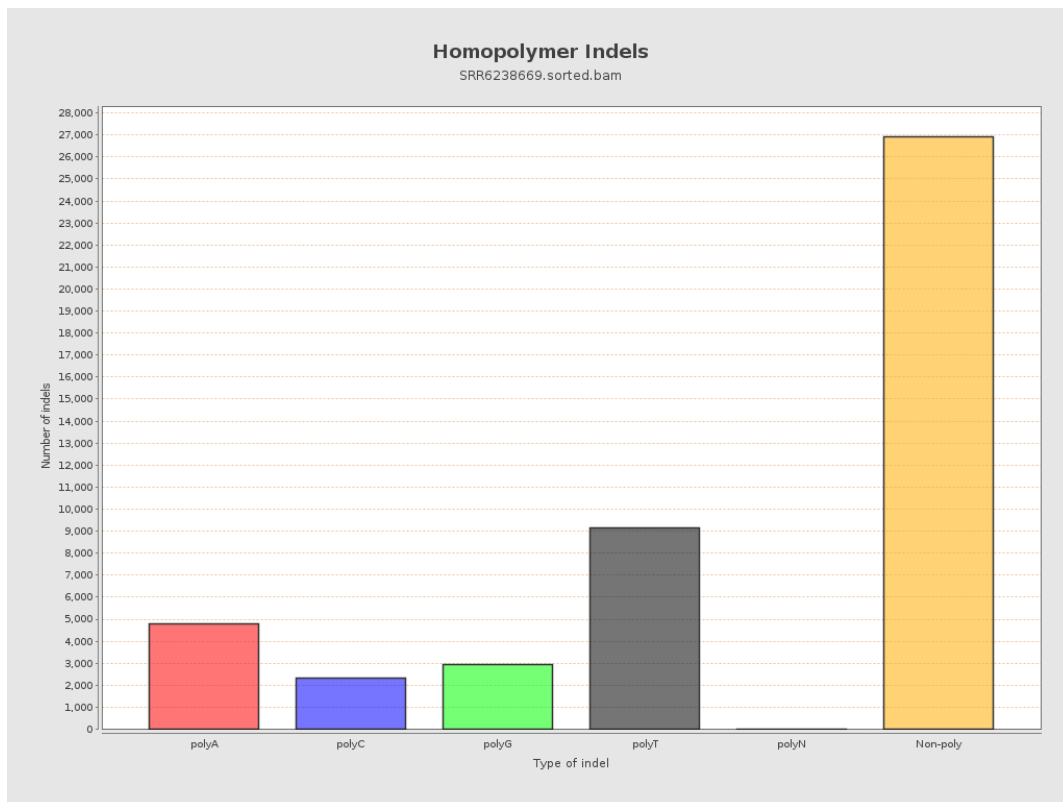
9. Results : Mapped Reads GC-content Distribution



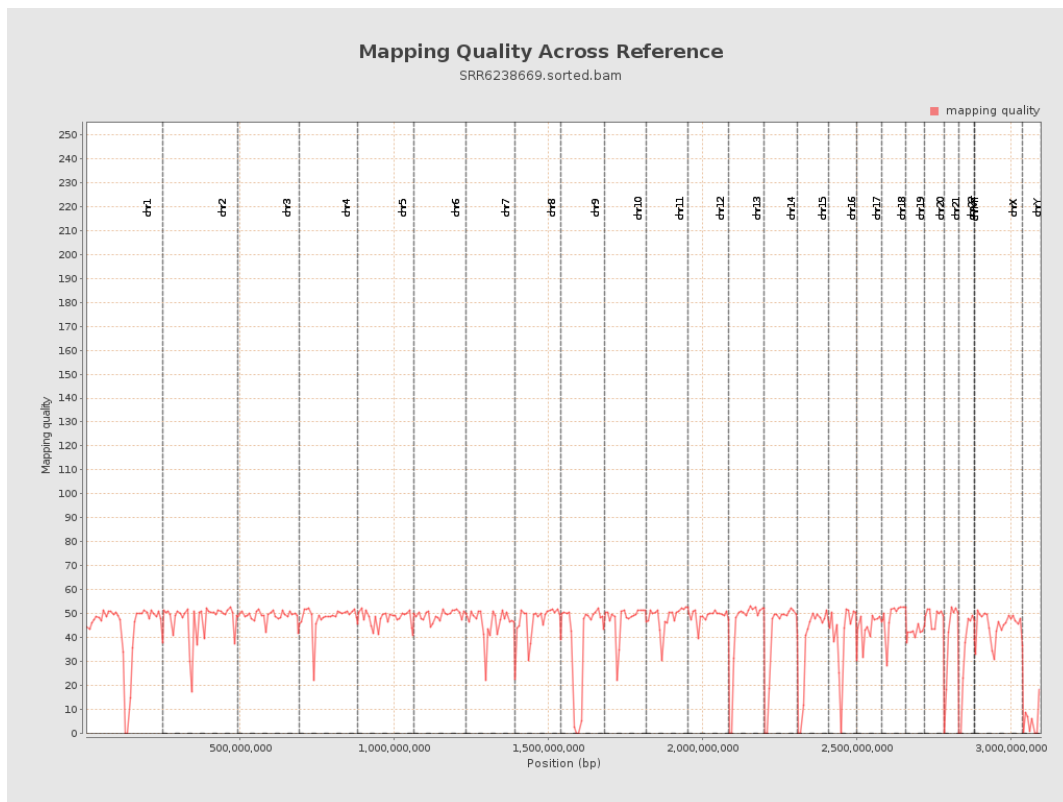
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

