

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:27:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971284.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_SRR2971284 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971284.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:27:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971284.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,730,370
Mapped reads	10,732,059 / 84.3%
Unmapped reads	1,998,311 / 15.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	943,120 / 7.41%
Duplication rate	6.93%
Clipped reads	1,137,327 / 8.93%

2.2. ACGT Content

Number/percentage of A's	121,567,841 / 28.78%
Number/percentage of C's	86,418,118 / 20.46%
Number/percentage of T's	125,546,148 / 29.72%
Number/percentage of G's	88,915,928 / 21.05%
Number/percentage of N's	3,166 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.1365
Standard Deviation	1.4769

2.4. Mapping Quality

Mean Mapping Quality	37.21
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2.5. Mismatches and indels

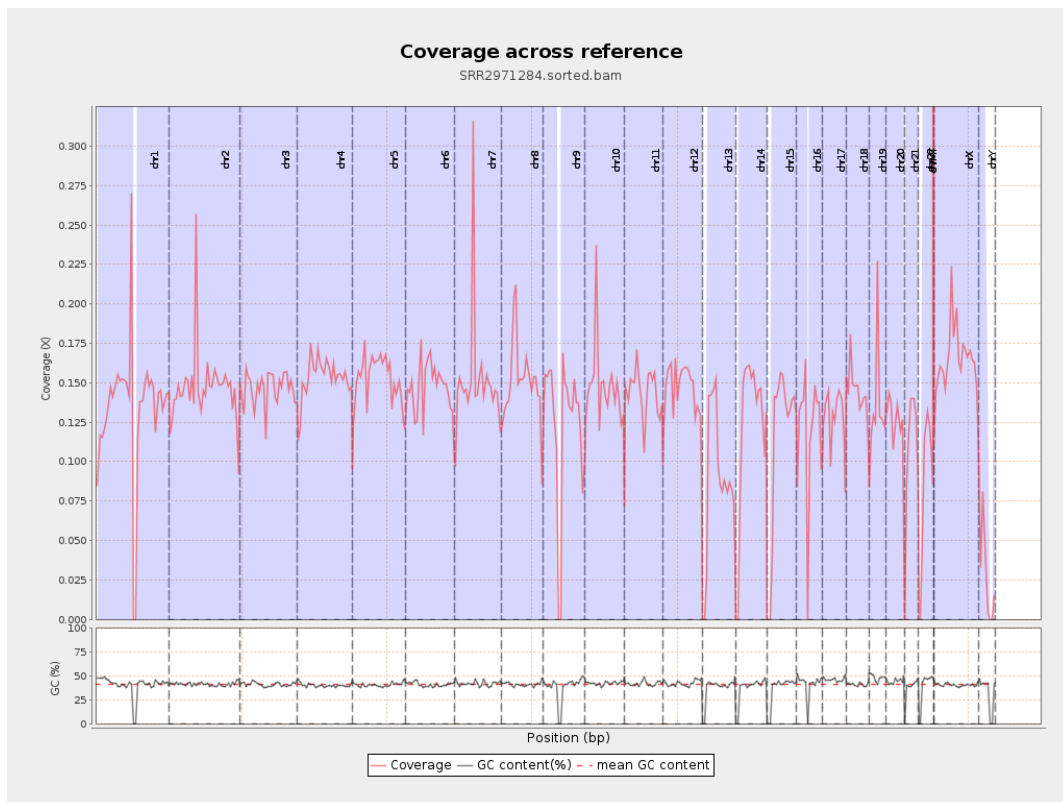
General error rate	0.33%
Mismatches	1,379,811
Insertions	15,879
Mapped reads with at least one insertion	0.15%
Deletions	35,011
Mapped reads with at least one deletion	0.33%
Homopolymer indels	38.73%

2.6. Chromosome stats

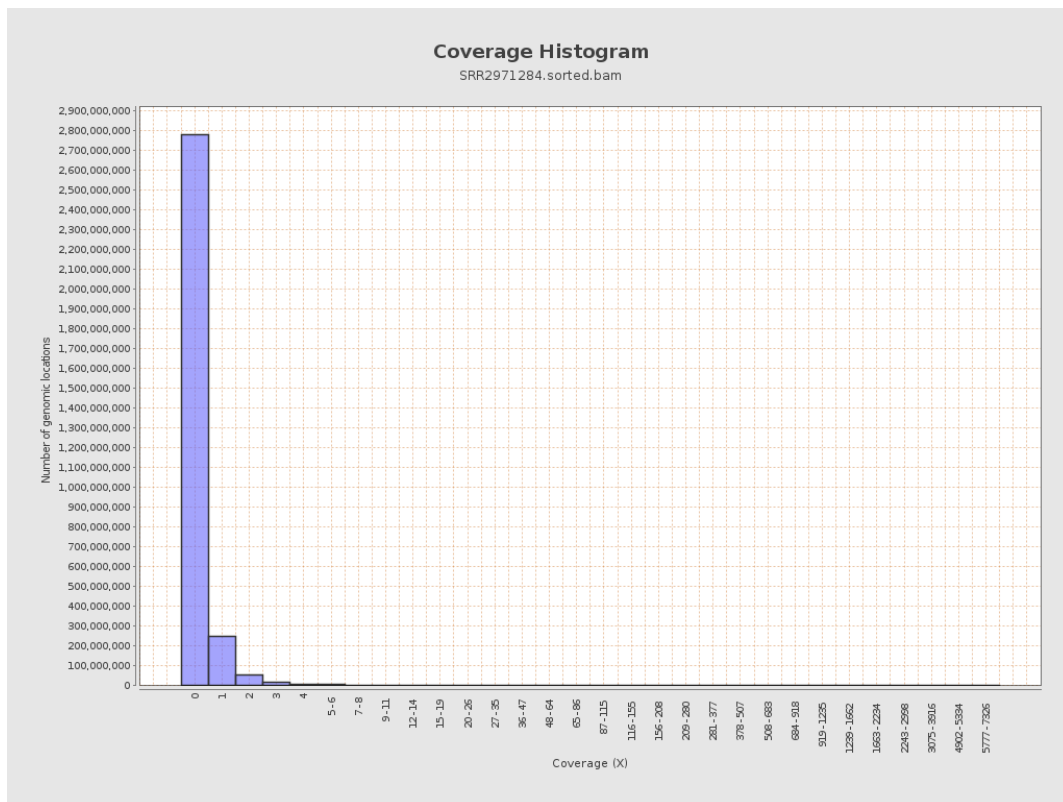
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	33358198	0.1338	2.871
chr2	243199373	35764392	0.1471	1.0743
chr3	198022430	29001784	0.1465	0.4942
chr4	191154276	29287771	0.1532	0.5388
chr5	180915260	27680561	0.153	0.5458
chr6	171115067	25107709	0.1467	0.5758
chr7	159138663	24264483	0.1525	1.9602
chr8	146364022	21976697	0.1502	3.5922

chr9	141213431	17454768	0.1236	1.0742
chr10	135534747	19973891	0.1474	1.0582
chr11	135006516	19241708	0.1425	0.8986
chr12	133851895	19597699	0.1464	0.5702
chr13	115169878	10049181	0.0873	0.3607
chr14	107349540	13076656	0.1218	0.7487
chr15	102531392	11686950	0.114	0.4232
chr16	90354753	10750926	0.119	0.5779
chr17	81195210	10318222	0.1271	0.567
chr18	78077248	11331272	0.1451	2.4846
chr19	59128983	8094183	0.1369	2.766
chr20	63025520	7874191	0.1249	0.5355
chr21	48129895	5173897	0.1075	0.5693
chr22	51304566	4211320	0.0821	0.3614
chrMT	16571	26341	1.5896	1.8825
chrX	155270560	25532232	0.1644	0.814
chrY	59373566	1659823	0.028	0.3318

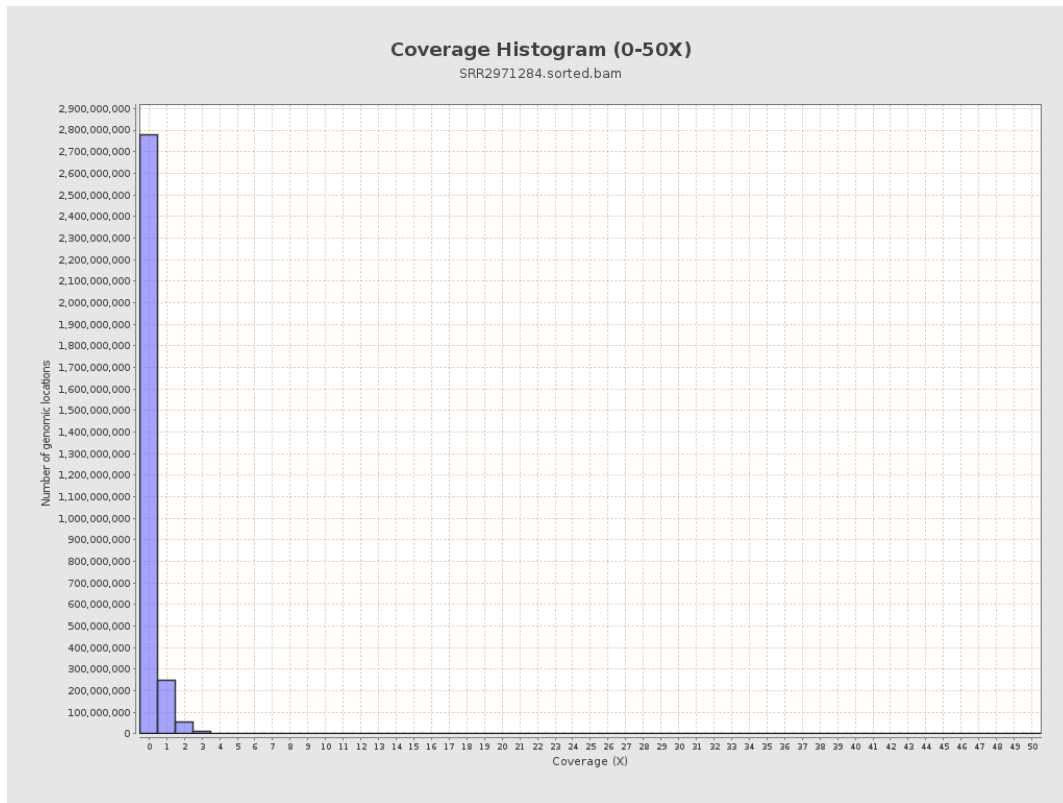
3. Results : Coverage across reference



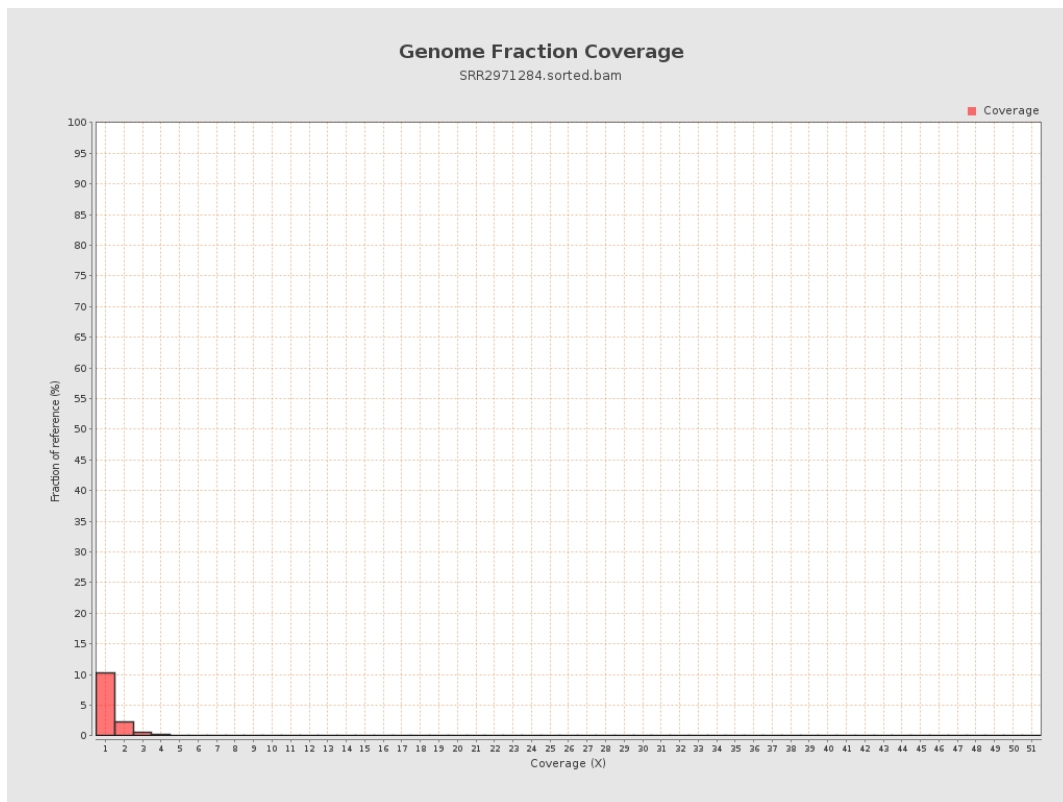
4. Results : Coverage Histogram



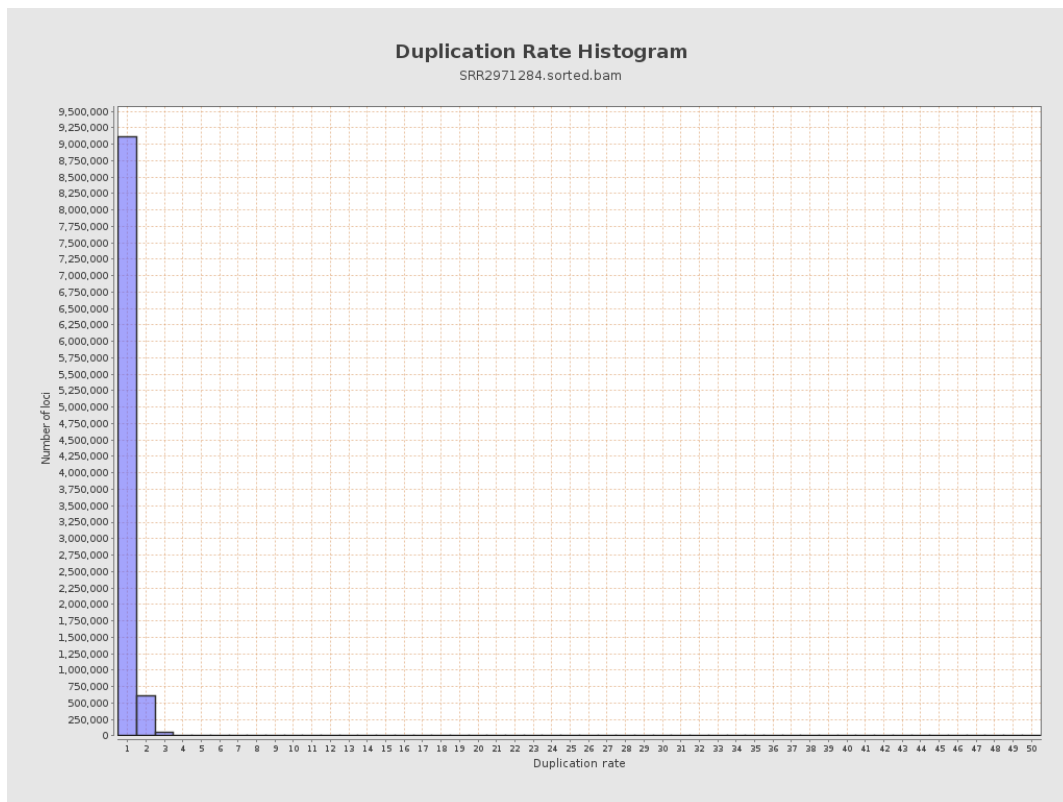
5. Results : Coverage Histogram (0-50X)



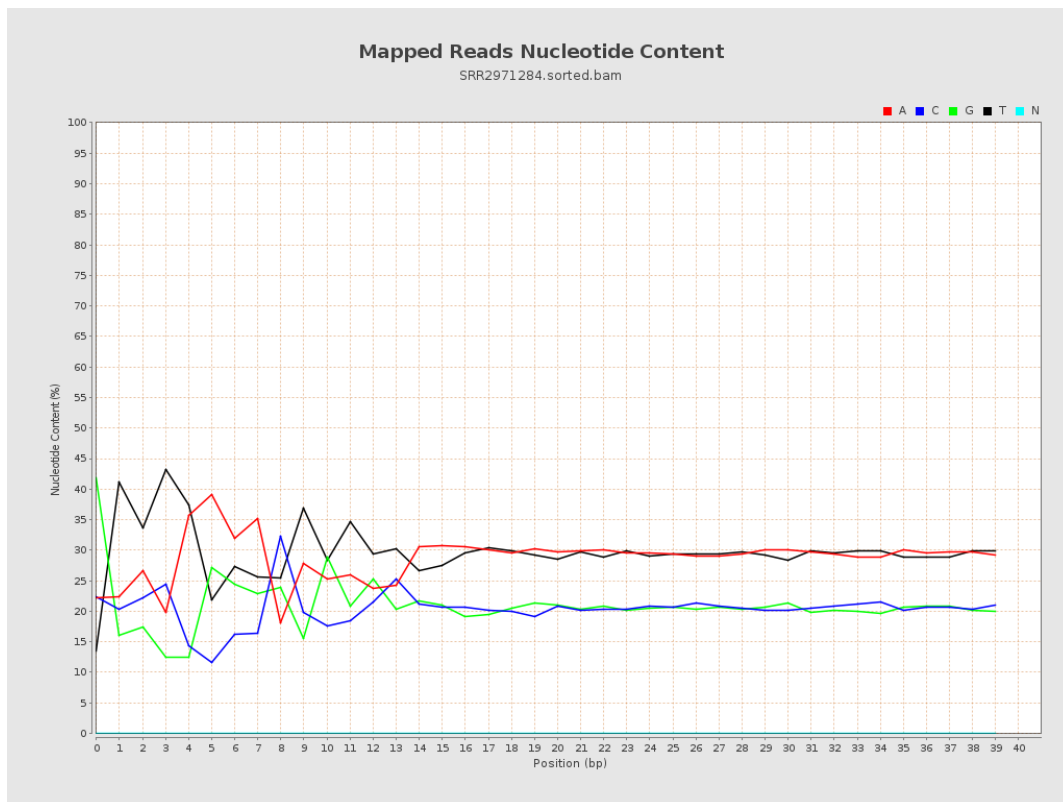
6. Results : Genome Fraction Coverage



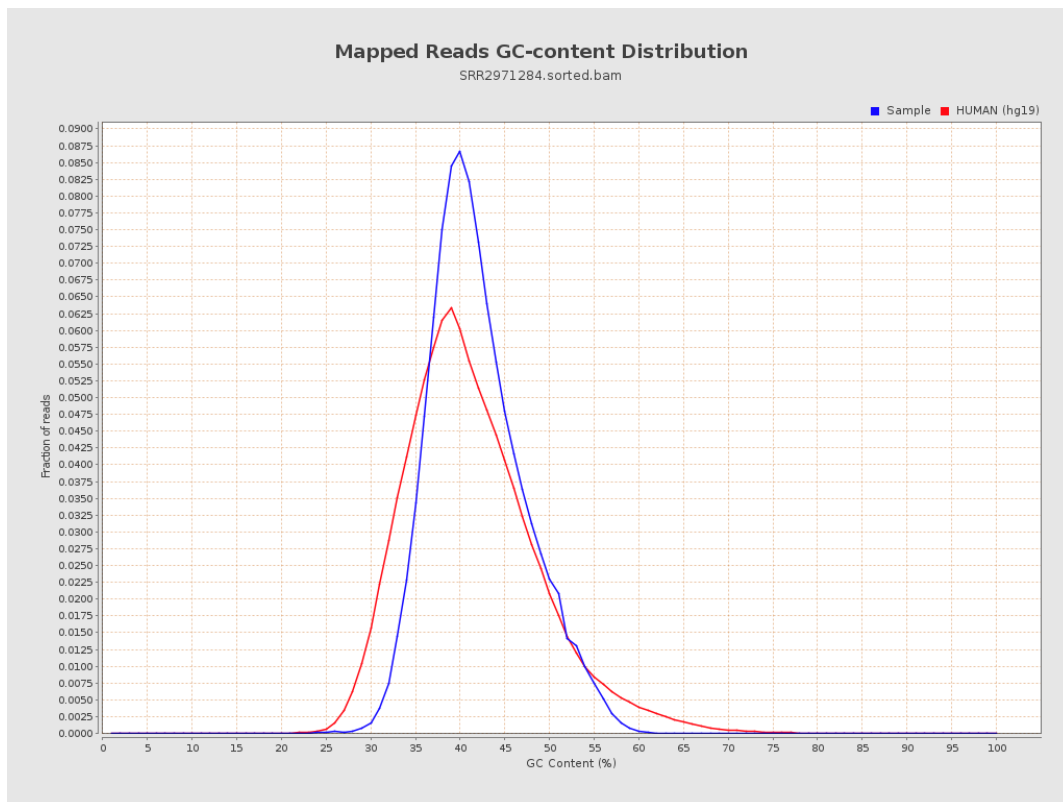
7. Results : Duplication Rate Histogram



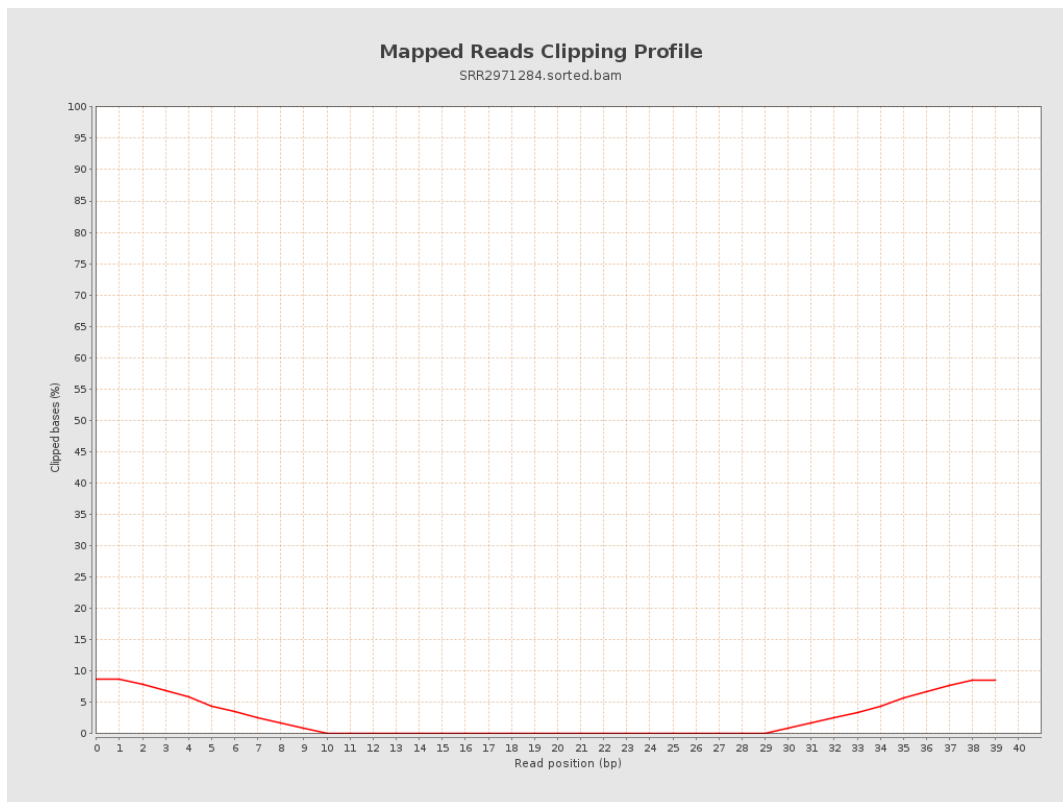
8. Results : Mapped Reads Nucleotide Content



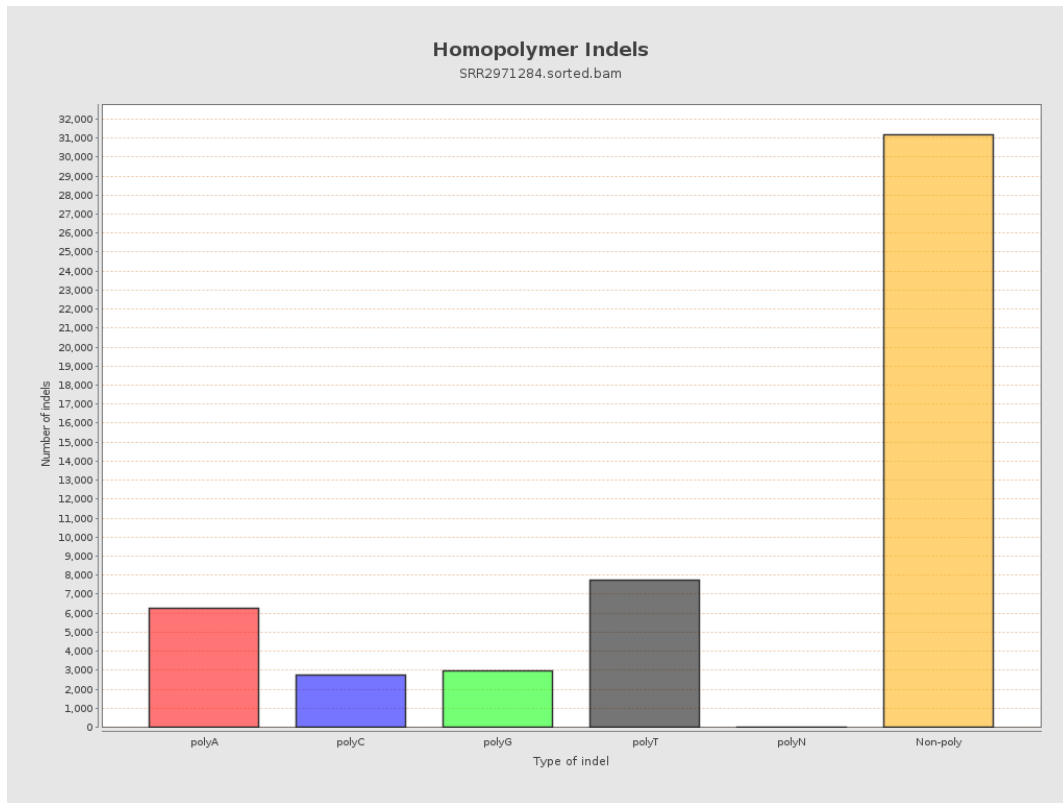
9. Results : Mapped Reads GC-content Distribution



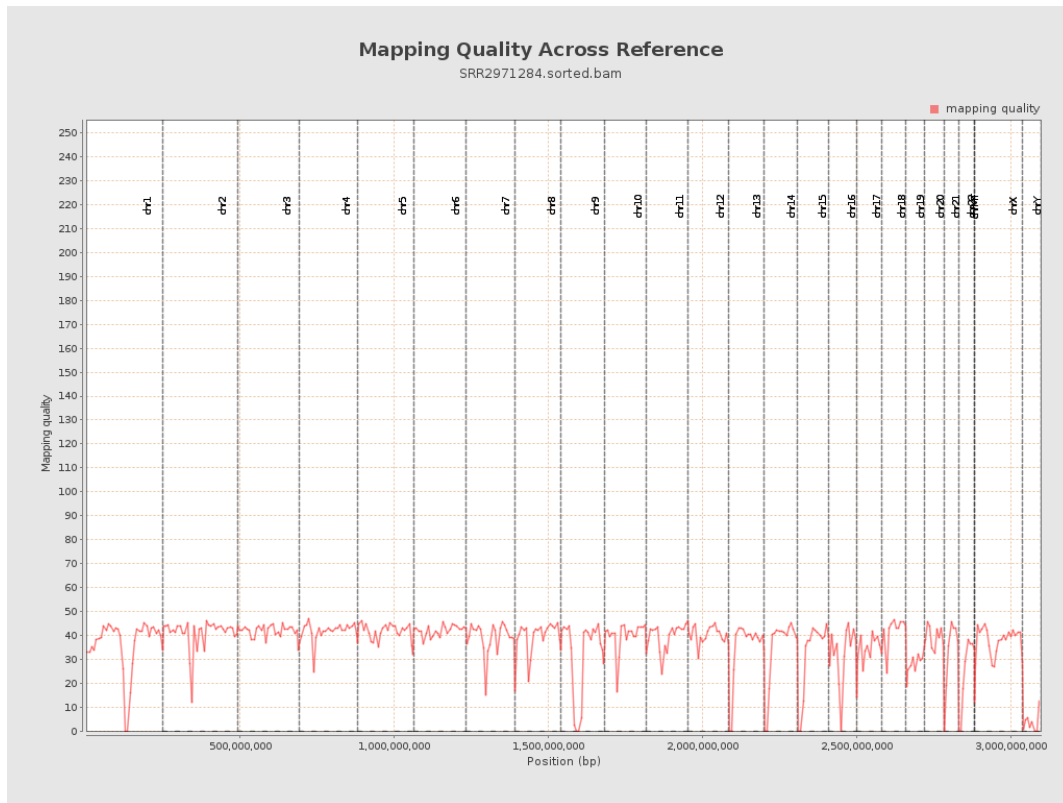
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

