

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:25:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971295.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_SRR2971295 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971295.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:25:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971295.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,030,380
Mapped reads	13,814,785 / 86.18%
Unmapped reads	2,215,595 / 13.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	1,206,370 / 7.53%
Duplication rate	7.43%
Clipped reads	1,001,736 / 6.25%

2.2. ACGT Content

Number/percentage of A's	159,399,271 / 29.17%
Number/percentage of C's	110,996,493 / 20.31%
Number/percentage of T's	162,002,602 / 29.64%
Number/percentage of G's	114,072,915 / 20.87%
Number/percentage of N's	9,520 / 0%
GC Percentage	41.19%

2.3. Coverage

Mean	0.1765
Standard Deviation	1.2738

2.4. Mapping Quality

Mean Mapping Quality	42.85
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2.5. Mismatches and indels

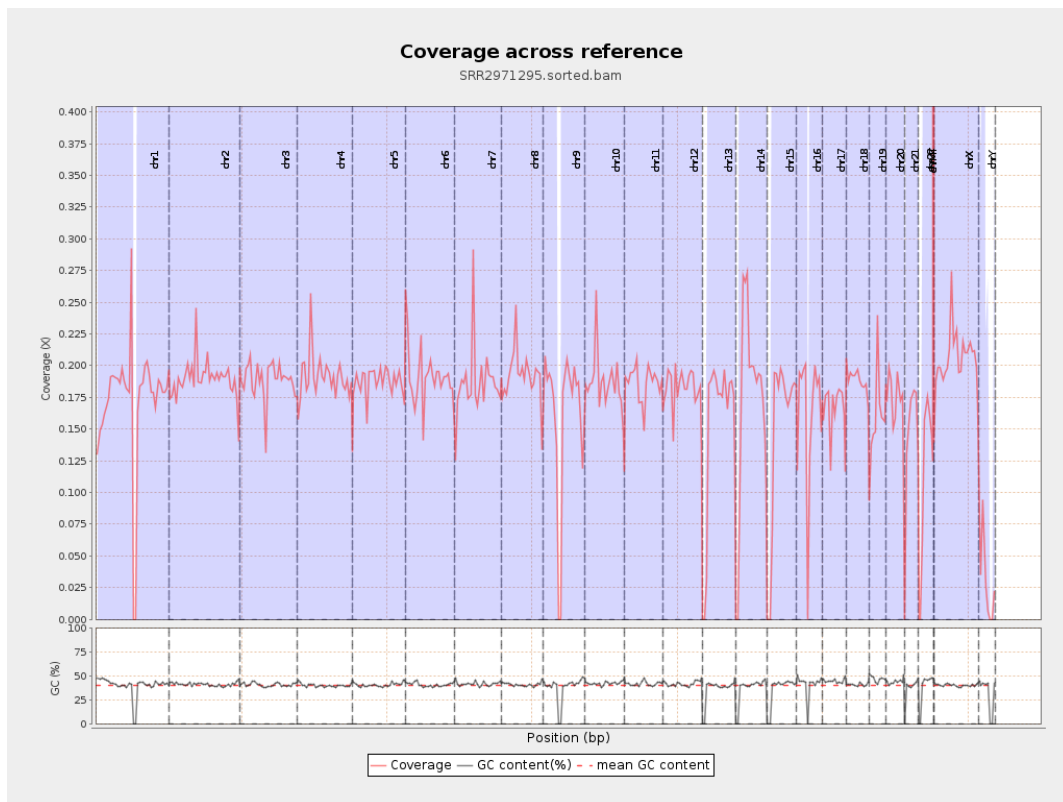
General error rate	0.25%
Mismatches	1,349,601
Insertions	14,718
Mapped reads with at least one insertion	0.11%
Deletions	36,306
Mapped reads with at least one deletion	0.26%
Homopolymer indels	41.55%

2.6. Chromosome stats

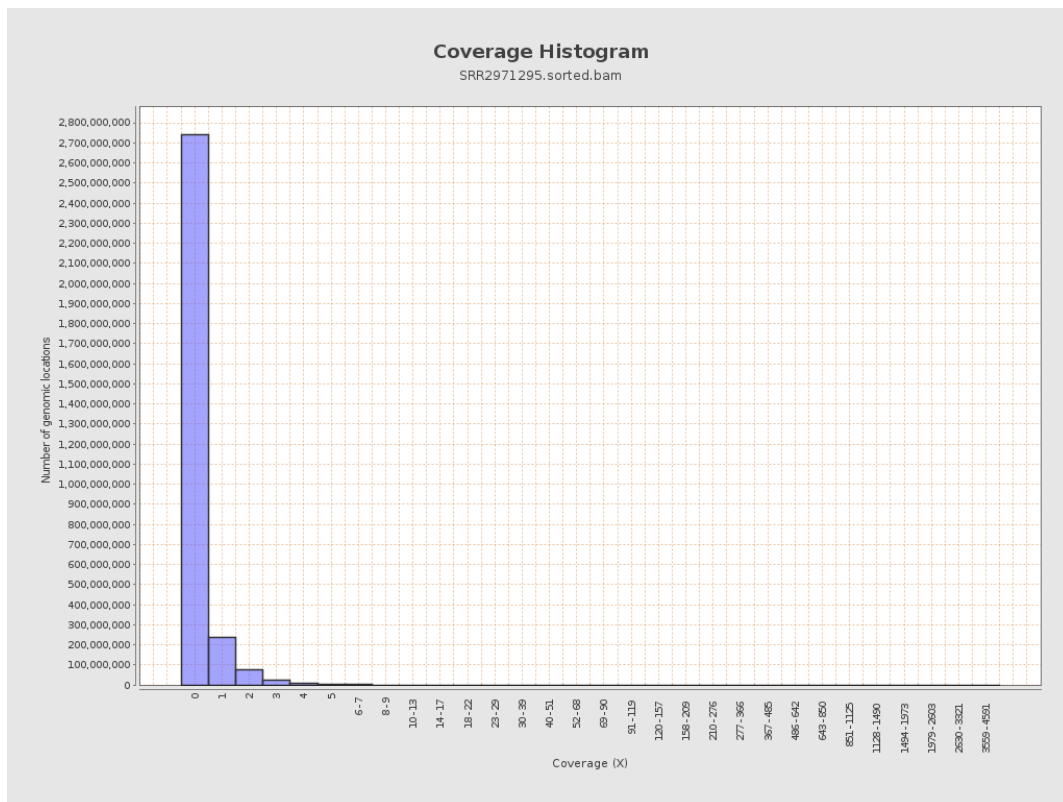
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	42861276	0.172	2.6325
chr2	243199373	46139594	0.1897	0.9749
chr3	198022430	37430456	0.189	0.6263
chr4	191154276	36476275	0.1908	0.7345
chr5	180915260	33879474	0.1873	0.6359
chr6	171115067	32782607	0.1916	0.774
chr7	159138663	29832660	0.1875	1.594
chr8	146364022	28124159	0.1922	2.335

chr9	141213431	22704384	0.1608	0.9177
chr10	135534747	25362032	0.1871	1.0442
chr11	135006516	25045857	0.1855	1.0054
chr12	133851895	24409179	0.1824	0.6401
chr13	115169878	17556093	0.1524	0.5465
chr14	107349540	18735962	0.1745	0.7433
chr15	102531392	15395083	0.1501	0.551
chr16	90354753	14687859	0.1626	0.6742
chr17	81195210	13340889	0.1643	0.6903
chr18	78077248	14728505	0.1886	2.1935
chr19	59128983	9614420	0.1626	2.2095
chr20	63025520	10916901	0.1732	0.6385
chr21	48129895	6968409	0.1448	0.6974
chr22	51304566	5682395	0.1108	0.4623
chrMT	16571	82536	4.9807	5.5364
chrX	155270560	31954610	0.2058	0.8069
chrY	59373566	1817850	0.0306	0.4966

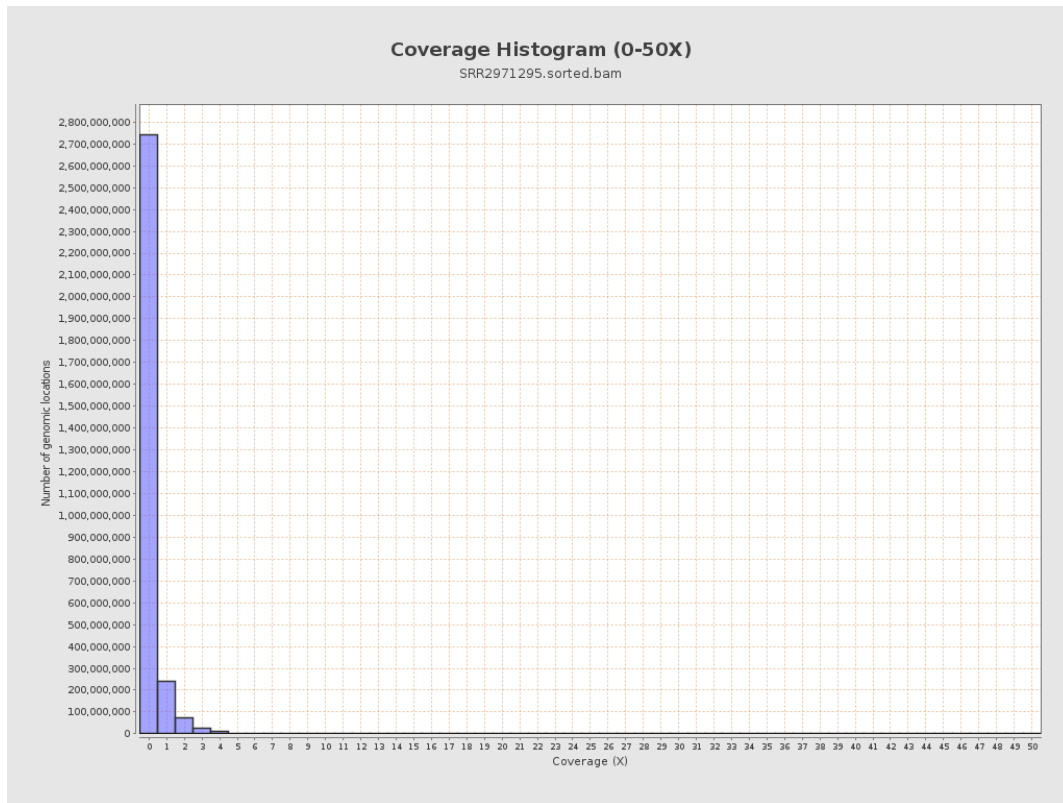
3. Results : Coverage across reference



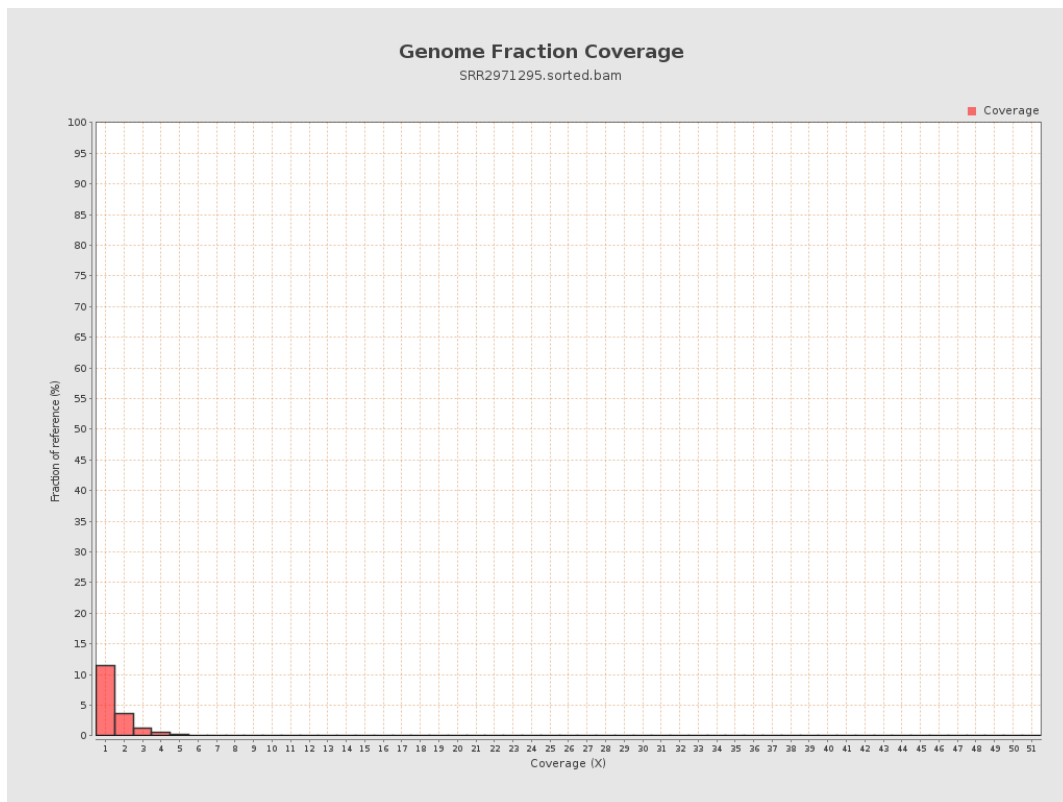
4. Results : Coverage Histogram



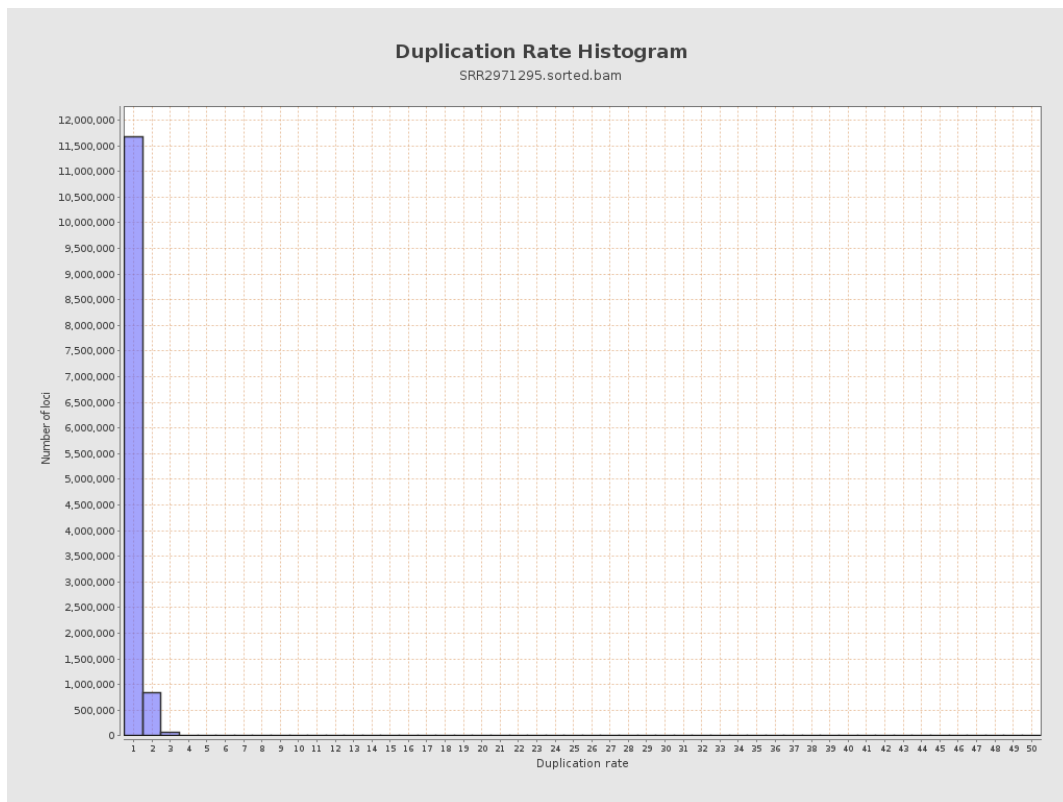
5. Results : Coverage Histogram (0-50X)



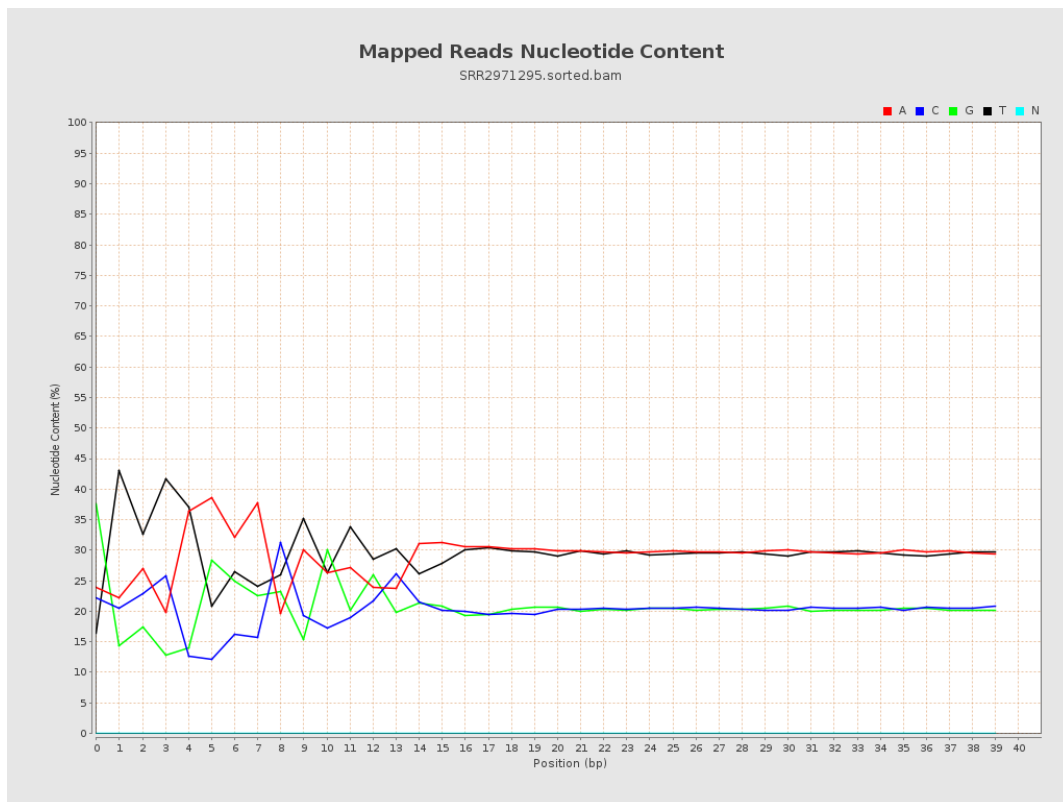
6. Results : Genome Fraction Coverage



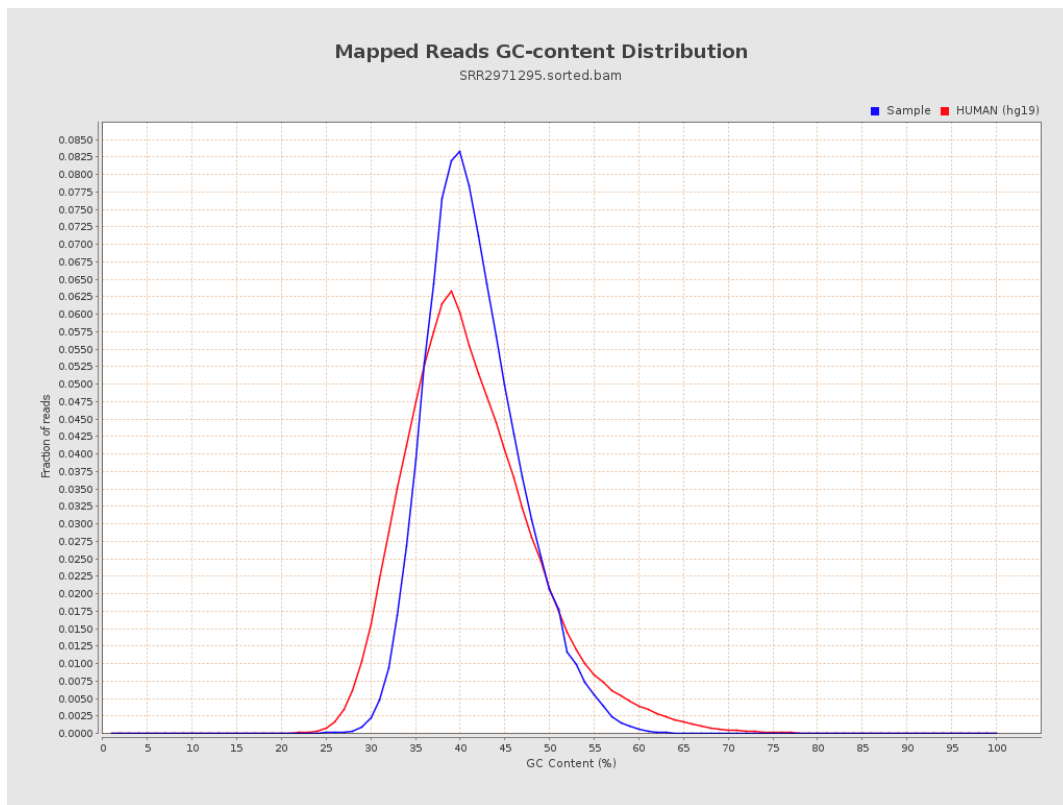
7. Results : Duplication Rate Histogram



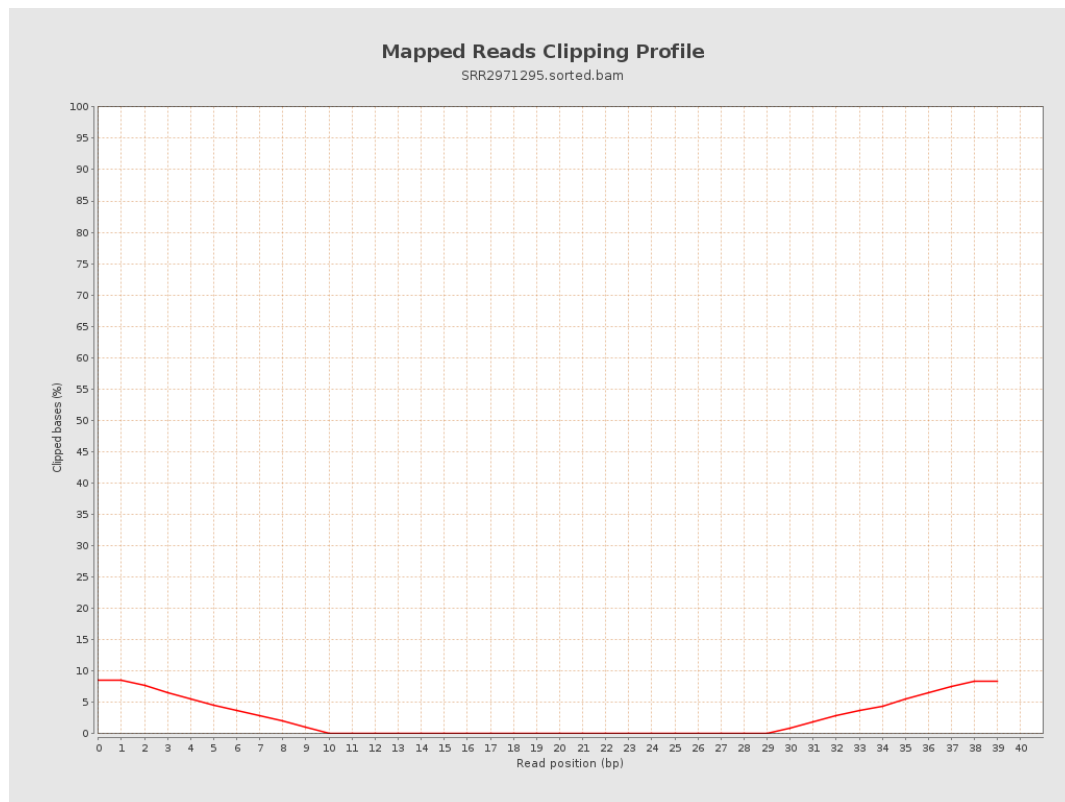
8. Results : Mapped Reads Nucleotide Content



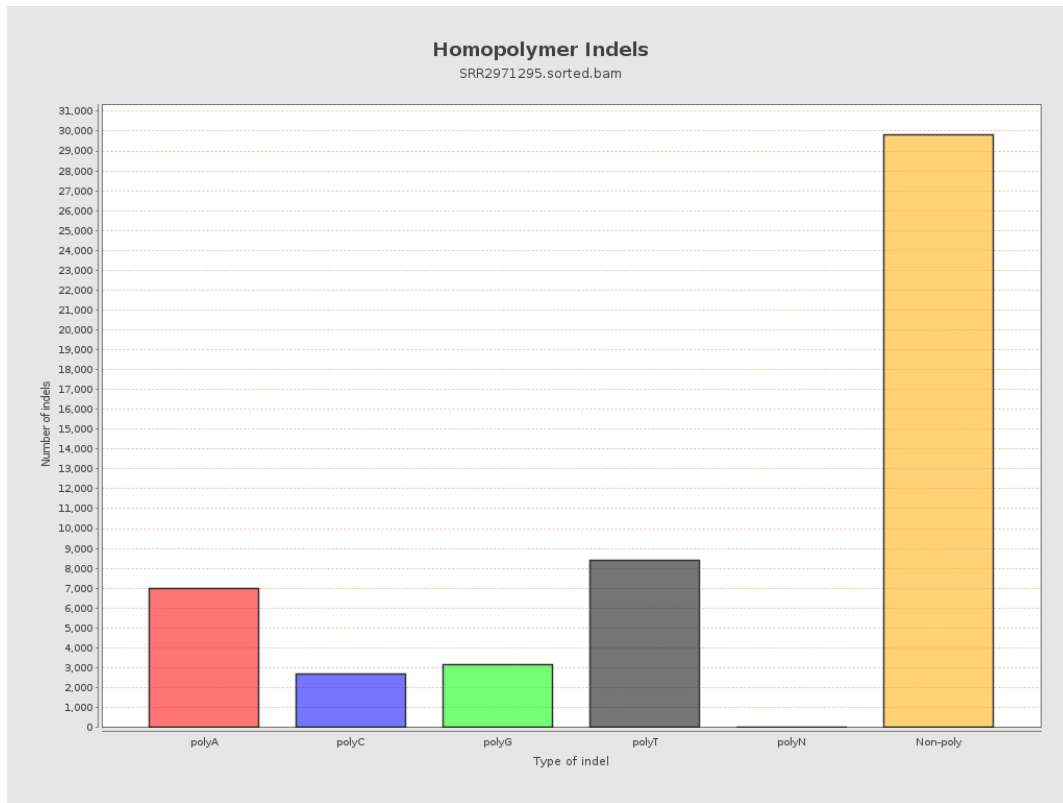
9. Results : Mapped Reads GC-content Distribution



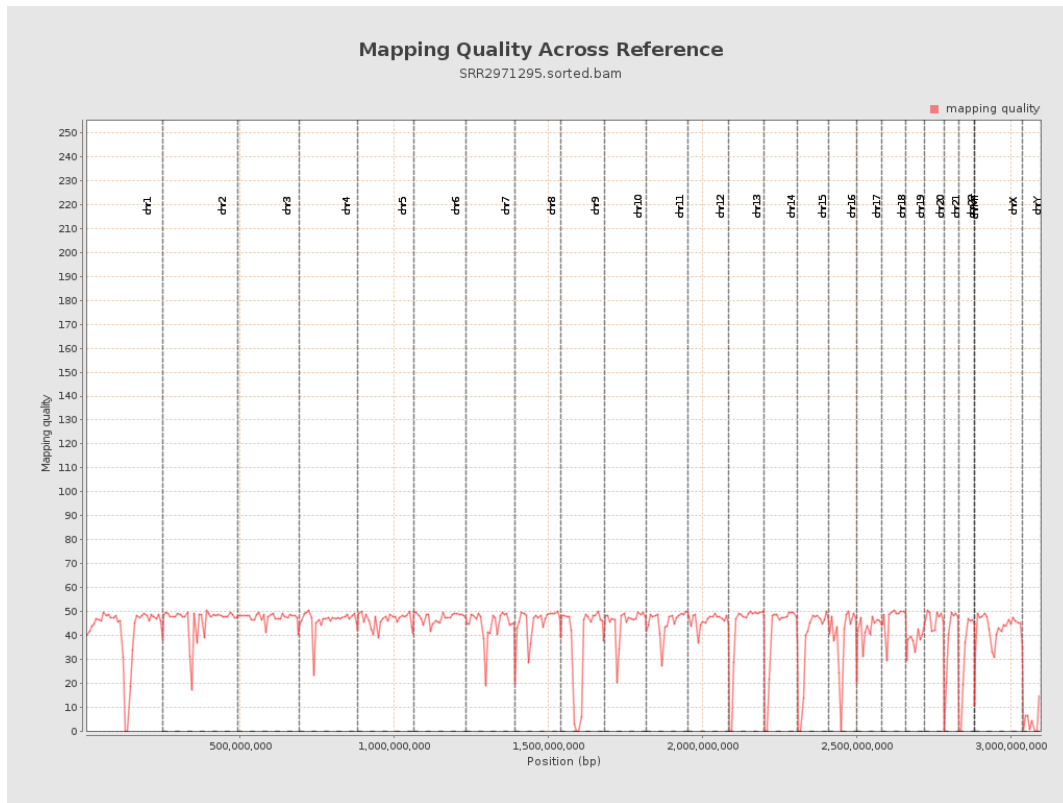
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

