

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:45:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971306.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_SRR2971306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:45:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,237,735
Mapped reads	6,170,217 / 85.25%
Unmapped reads	1,067,518 / 14.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	346,737 / 4.79%
Duplication rate	4.21%
Clipped reads	737,677 / 10.19%

2.2. ACGT Content

Number/percentage of A's	68,739,483 / 28.34%
Number/percentage of C's	50,865,257 / 20.97%
Number/percentage of T's	70,749,005 / 29.17%
Number/percentage of G's	52,159,627 / 21.51%
Number/percentage of N's	13,577 / 0.01%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0784
Standard Deviation	0.666

2.4. Mapping Quality

Mean Mapping Quality	35.44
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2.5. Mismatches and indels

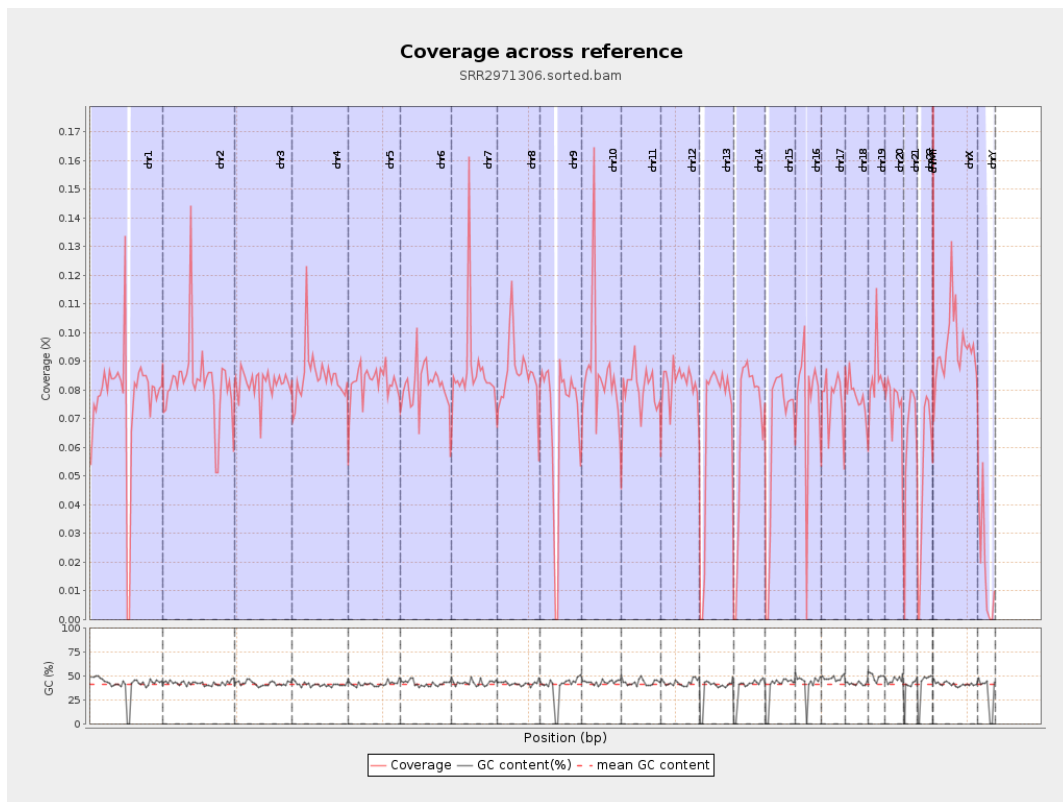
General error rate	0.35%
Mismatches	848,520
Insertions	10,043
Mapped reads with at least one insertion	0.16%
Deletions	19,936
Mapped reads with at least one deletion	0.32%
Homopolymer indels	37.27%

2.6. Chromosome stats

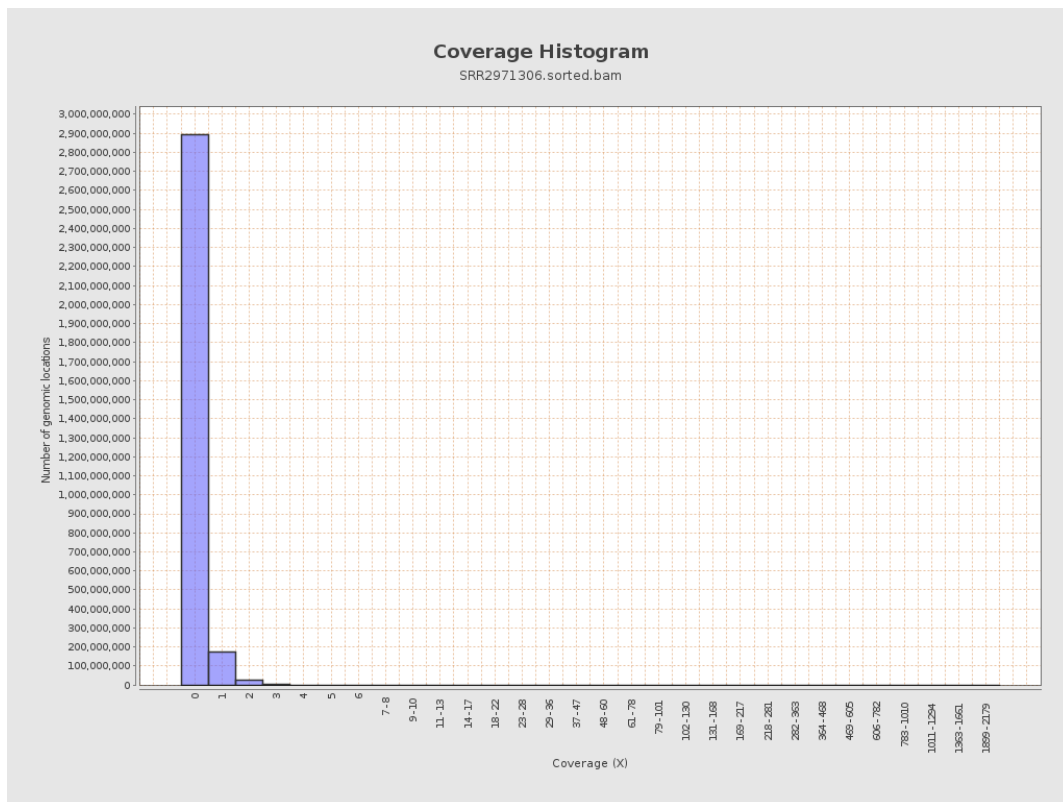
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19143894	0.0768	1.2075
chr2	243199373	20001211	0.0822	0.6258
chr3	198022430	16305863	0.0823	0.3357
chr4	191154276	16236826	0.0849	0.3949
chr5	180915260	14963119	0.0827	0.3434
chr6	171115067	13959993	0.0816	0.4011
chr7	159138663	13800464	0.0867	0.9479
chr8	146364022	12536822	0.0857	1.1606

chr9	141213431	9948781	0.0705	0.6202
chr10	135534747	11623836	0.0858	0.7062
chr11	135006516	10855835	0.0804	0.5036
chr12	133851895	11051426	0.0826	0.354
chr13	115169878	7862205	0.0683	0.2967
chr14	107349540	7336415	0.0683	0.4152
chr15	102531392	6589010	0.0643	0.2934
chr16	90354753	6753715	0.0747	0.4196
chr17	81195210	6305485	0.0777	0.3692
chr18	78077248	6107805	0.0782	1.1252
chr19	59128983	5027239	0.085	1.1738
chr20	63025520	4736647	0.0752	0.3391
chr21	48129895	3017262	0.0627	0.3855
chr22	51304566	2614331	0.051	0.2675
chrMT	16571	5588	0.3372	0.6444
chrX	155270560	14700380	0.0947	0.4607
chrY	59373566	1067038	0.018	0.2703

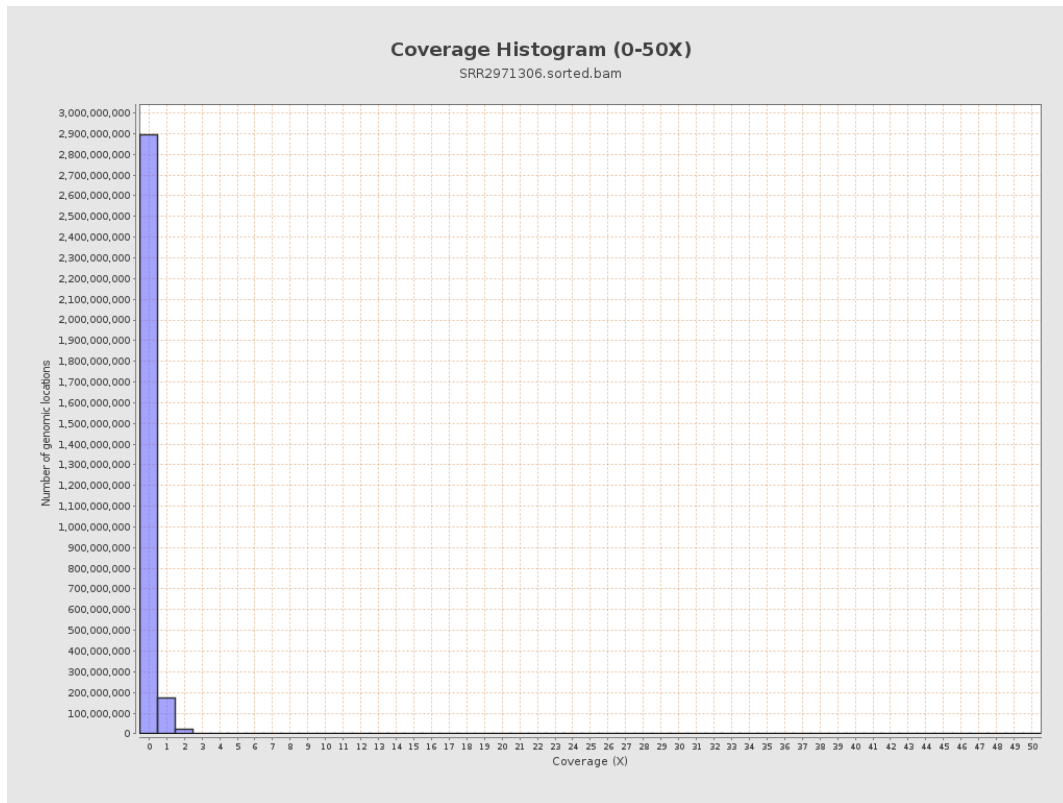
3. Results : Coverage across reference



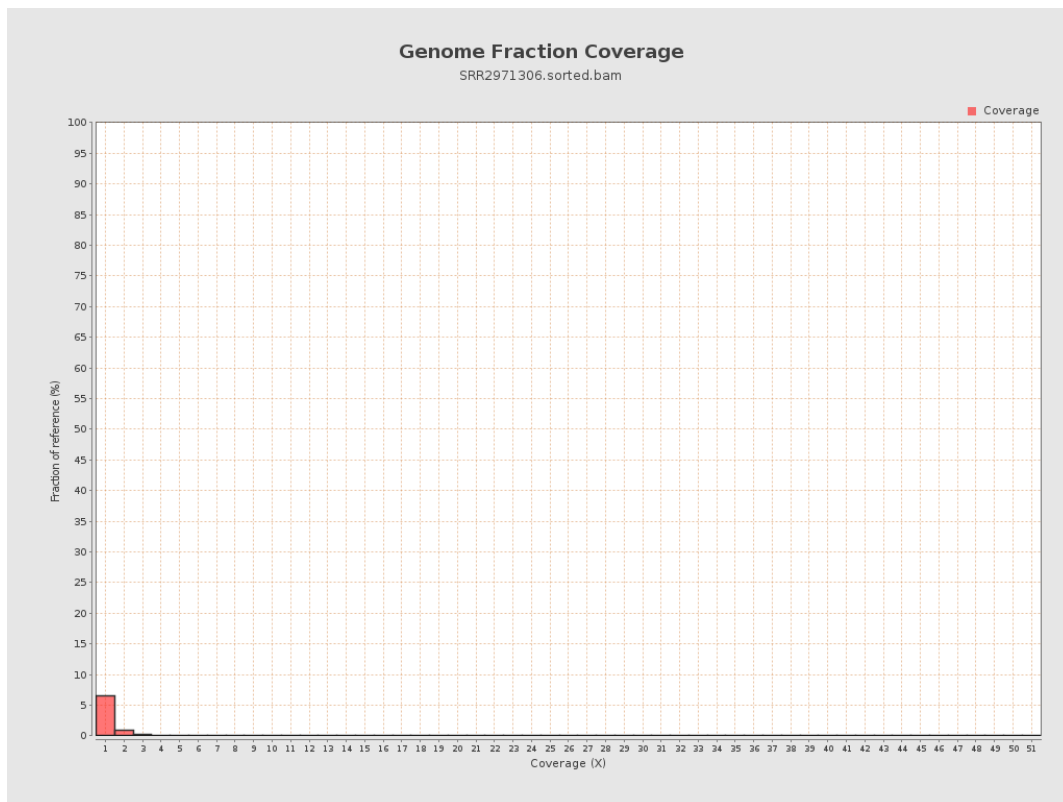
4. Results : Coverage Histogram



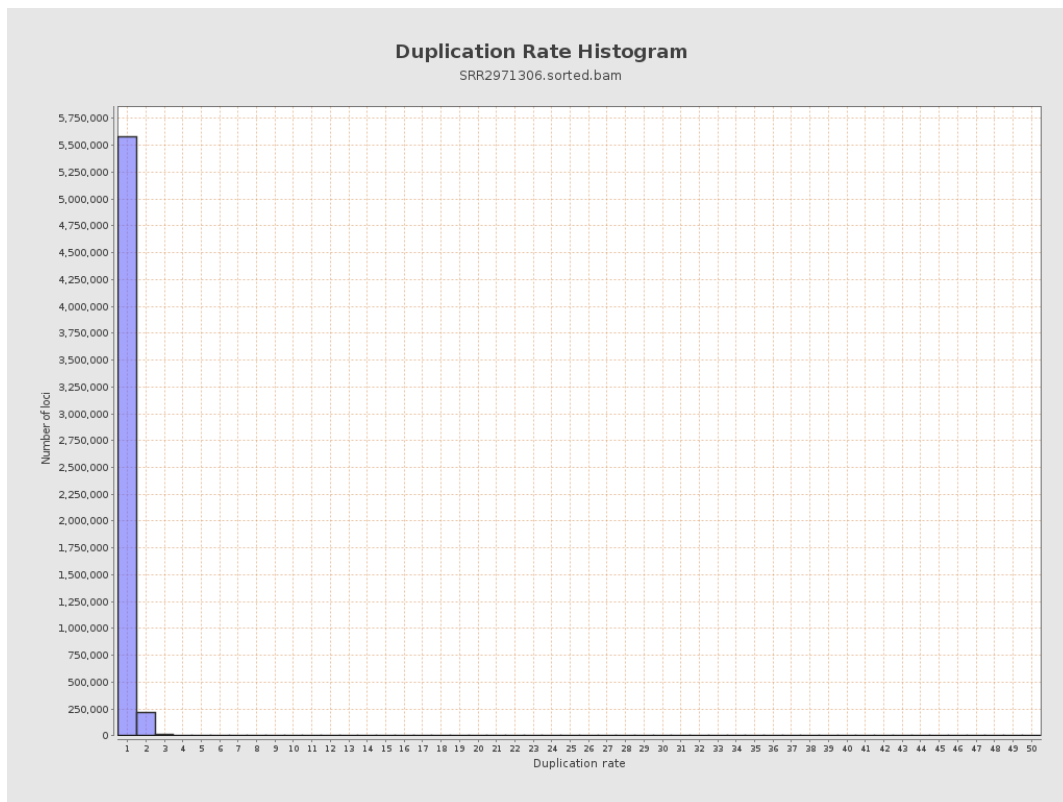
5. Results : Coverage Histogram (0-50X)



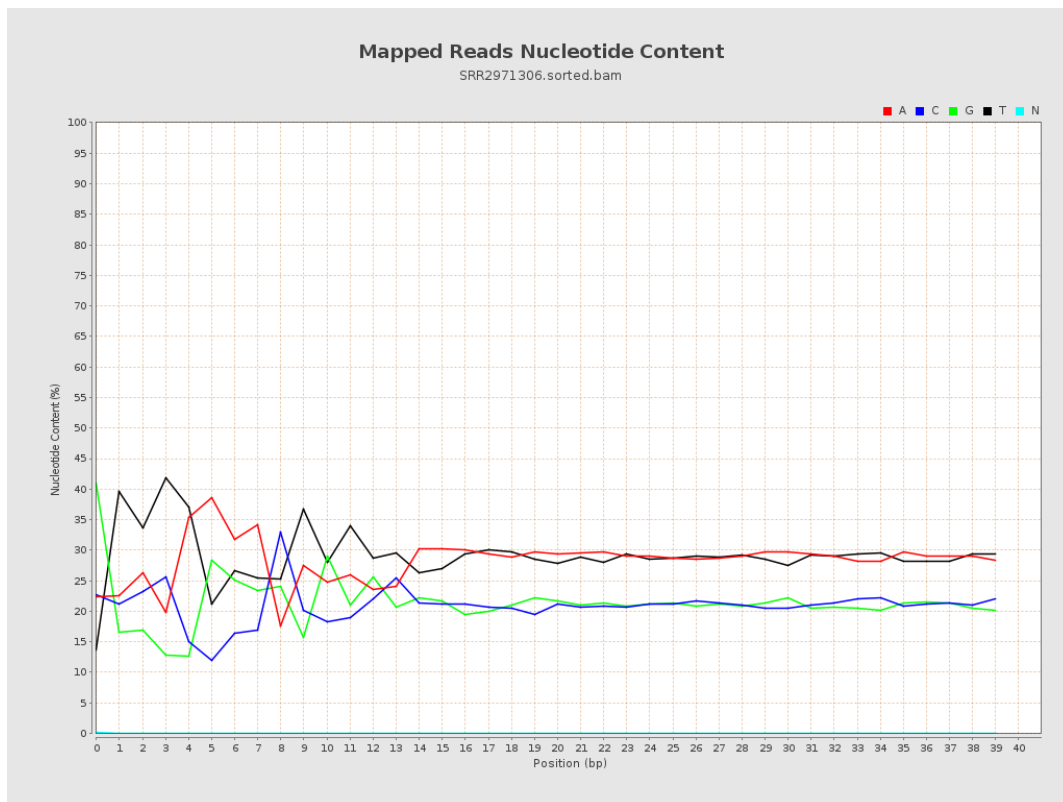
6. Results : Genome Fraction Coverage



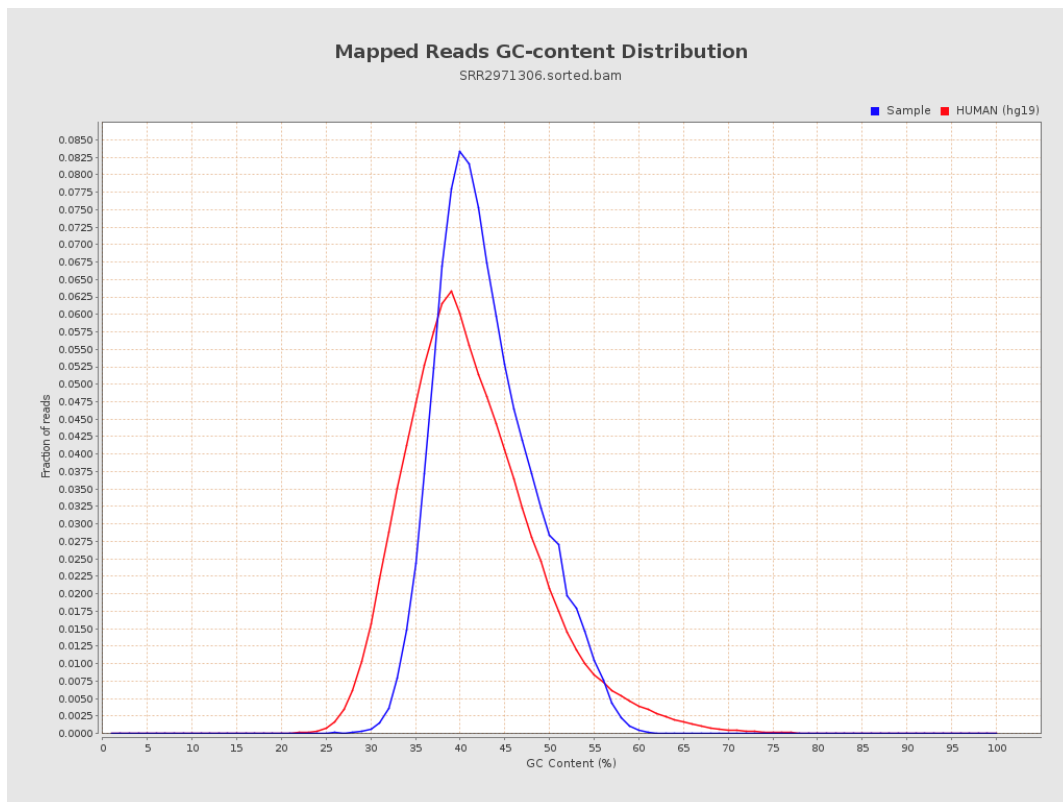
7. Results : Duplication Rate Histogram



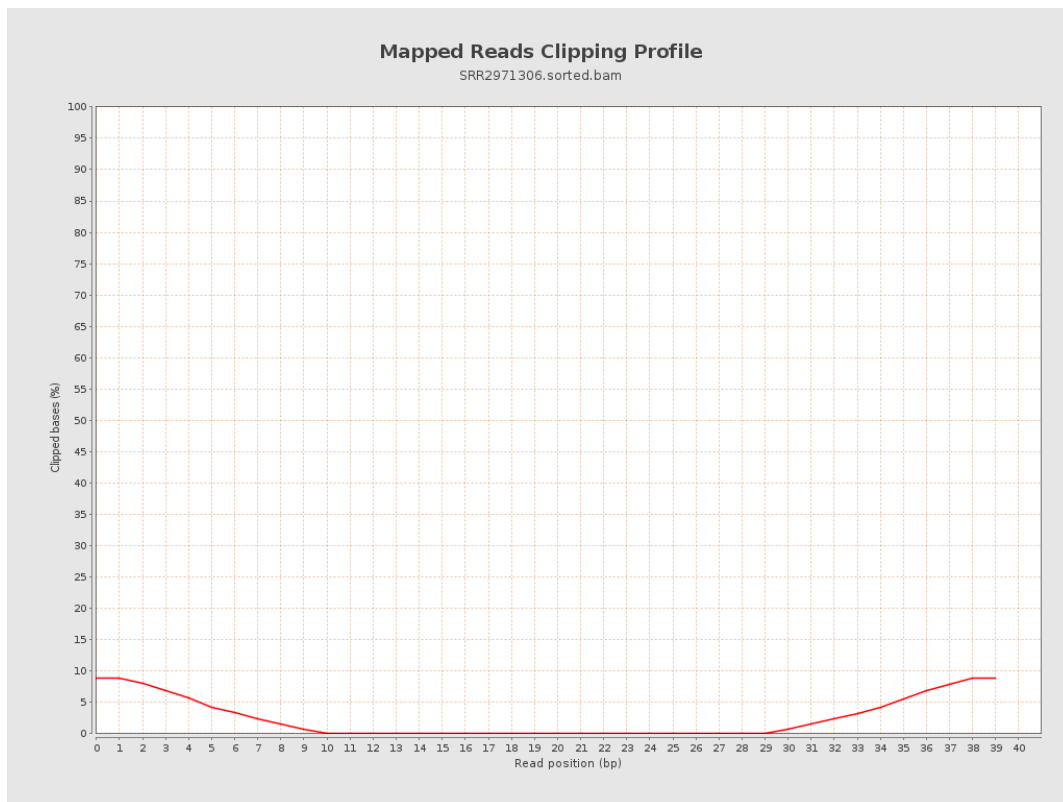
8. Results : Mapped Reads Nucleotide Content



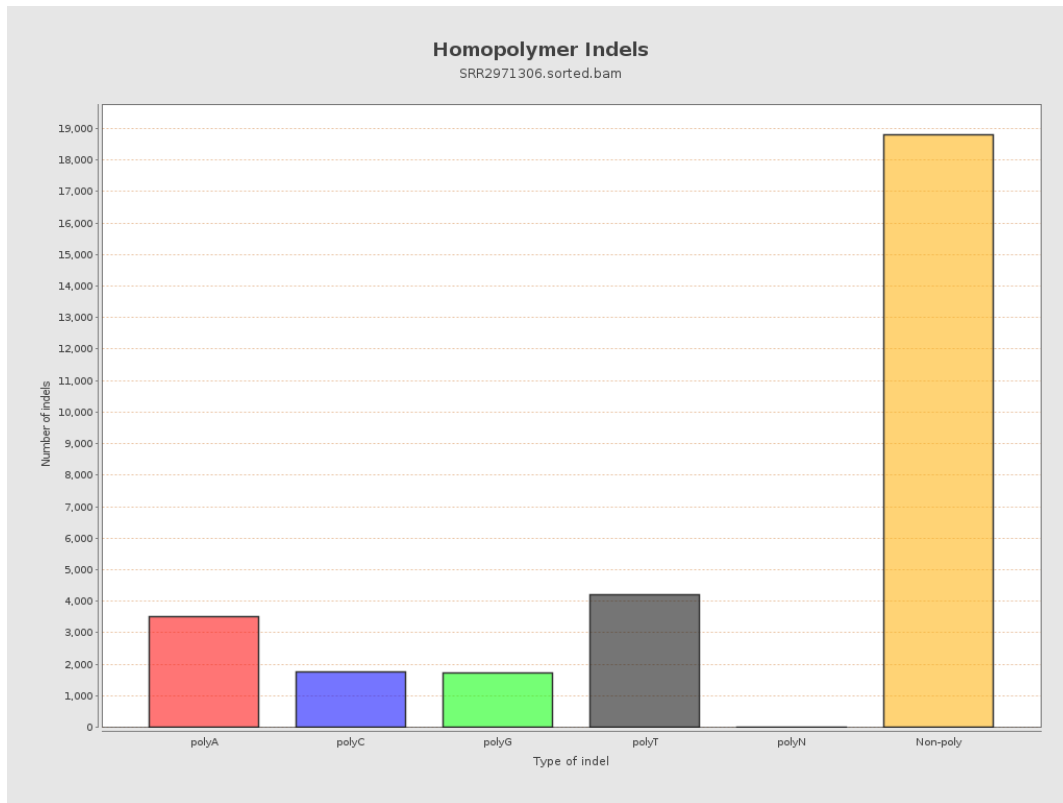
9. Results : Mapped Reads GC-content Distribution



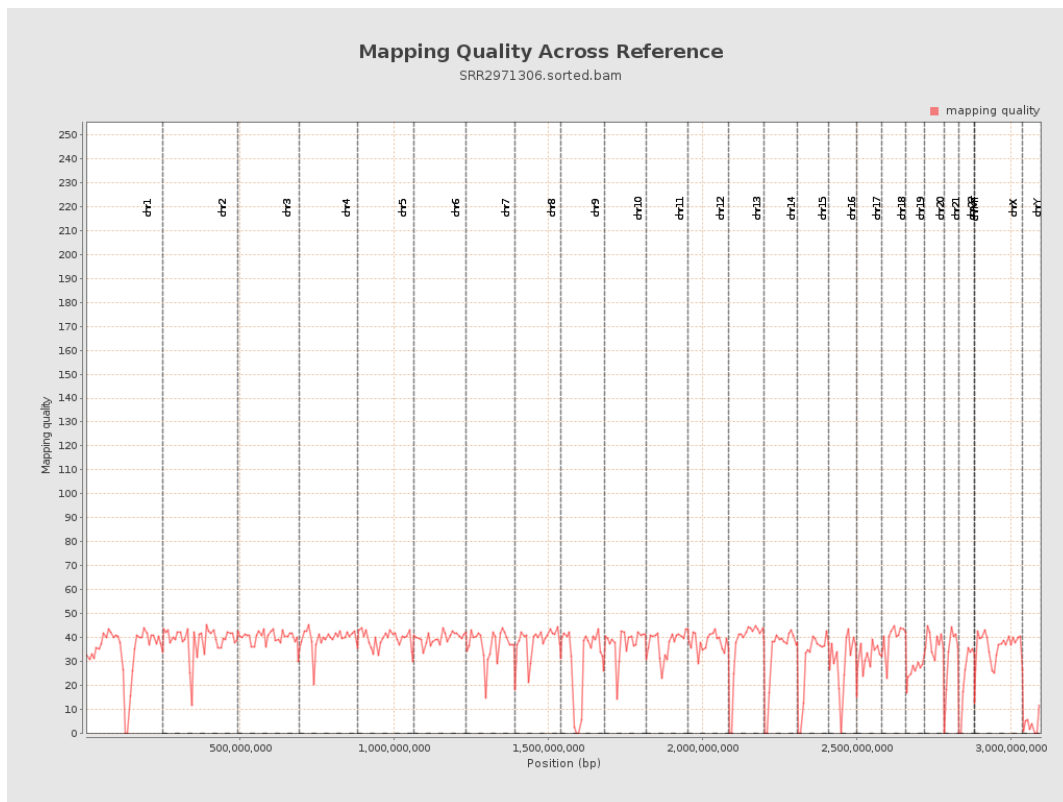
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

