

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 09:14:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695988.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695988 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695988.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 09:14:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,769,833
Mapped reads	16,340,435 / 91.96%
Unmapped reads	1,429,398 / 8.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	271,208 / 1.53%
Read min/max/mean length	8 / 358 / 145.36
Duplicated reads (estimated)	3,841,551 / 21.62%
Duplication rate	20.08%
Clipped reads	4,125,738 / 23.22%

2.2. ACGT Content

Number/percentage of A's	698,782,509 / 28.69%
Number/percentage of C's	516,125,577 / 21.19%
Number/percentage of T's	694,137,758 / 28.5%
Number/percentage of G's	526,675,316 / 21.62%
Number/percentage of N's	0 / 0%
GC Percentage	42.81%

2.3. Coverage

Mean	0.7921

Standard Deviation	2.0371
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2.4. Mapping Quality

Mean Mapping Quality	52.27
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2.5. Mismatches and indels

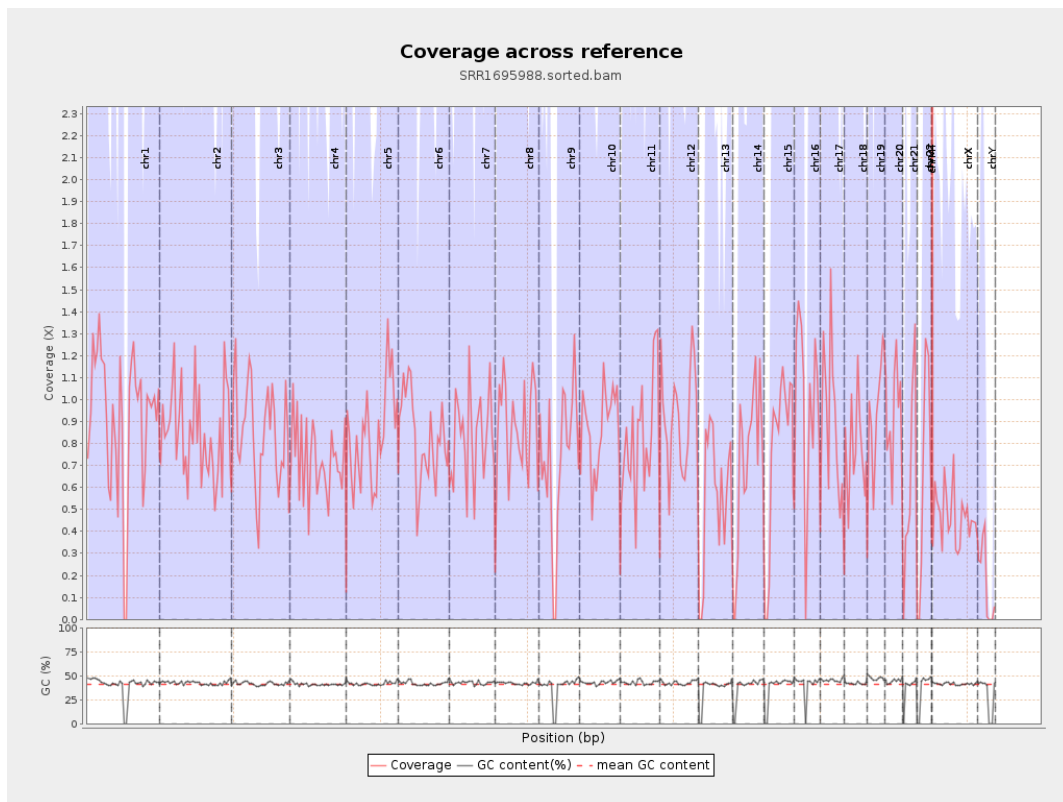
General error rate	1.63%
Mismatches	25,279,896
Insertions	13,314,267
Mapped reads with at least one insertion	46.19%
Deletions	14,836,334
Mapped reads with at least one deletion	51.88%
Homopolymer indels	37.78%

2.6. Chromosome stats

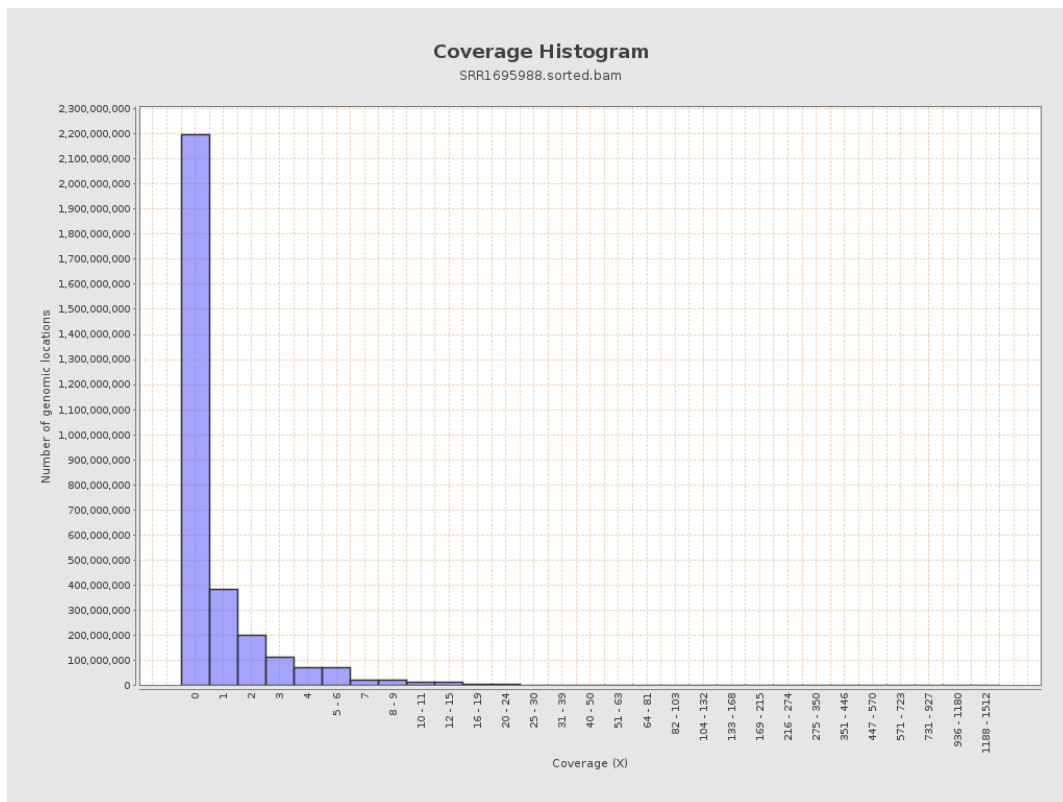
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	227750895	0.9137	2.6441
chr2	243199373	207870068	0.8547	2.0619
chr3	198022430	169564336	0.8563	1.9421
chr4	191154276	138935257	0.7268	1.7889
chr5	180915260	151699588	0.8385	1.9539
chr6	171115067	141372220	0.8262	1.9976
chr7	159138663	130994409	0.8231	1.9145

chr8	146364022	129972163	0.888	2.0094
chr9	141213431	102985584	0.7293	1.9557
chr10	135534747	117997662	0.8706	2.2403
chr11	135006516	112122165	0.8305	2.0713
chr12	133851895	122527136	0.9154	2.026
chr13	115169878	64562772	0.5606	1.5061
chr14	107349540	76730297	0.7148	1.8778
chr15	102531392	78164716	0.7623	1.8519
chr16	90354753	86285926	0.955	2.2491
chr17	81195210	71429795	0.8797	2.5091
chr18	78077248	60774515	0.7784	2.3044
chr19	59128983	55708334	0.9421	2.4593
chr20	63025520	58319152	0.9253	2.1515
chr21	48129895	30399648	0.6316	1.8574
chr22	51304566	33160825	0.6464	1.7613
chrMT	16571	409800	24.7299	14.4666
chrX	155270560	72249119	0.4653	1.3947
chrY	59373566	10263797	0.1729	1.2031

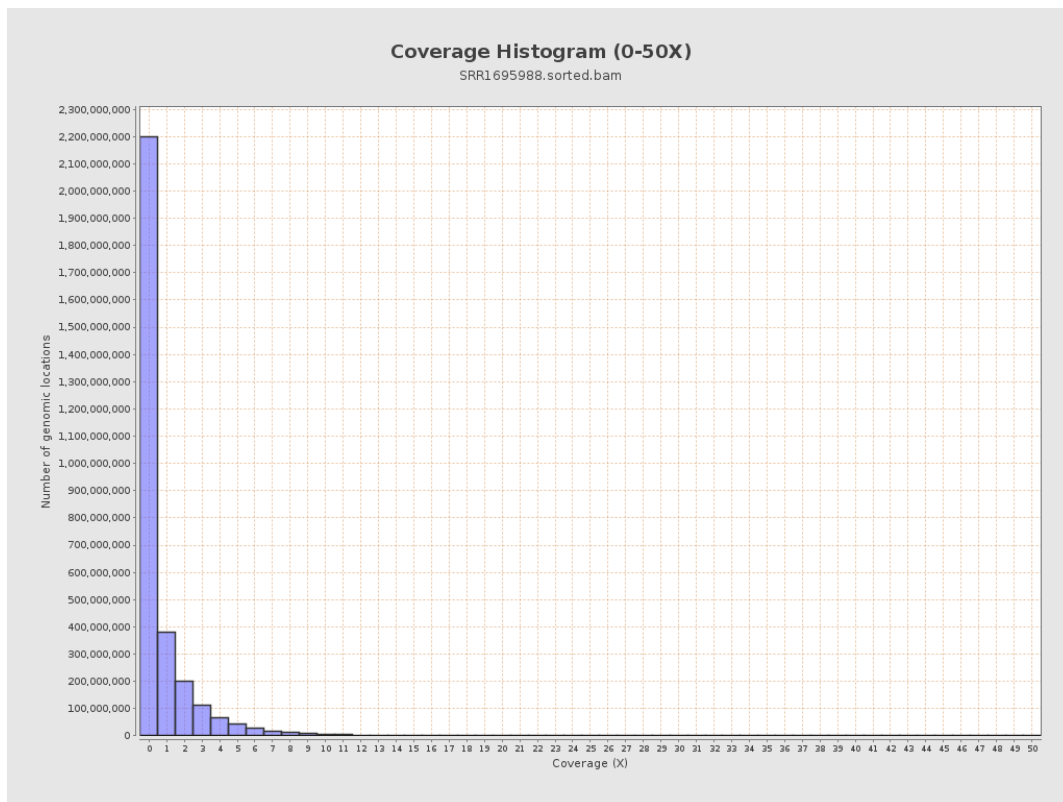
3. Results : Coverage across reference



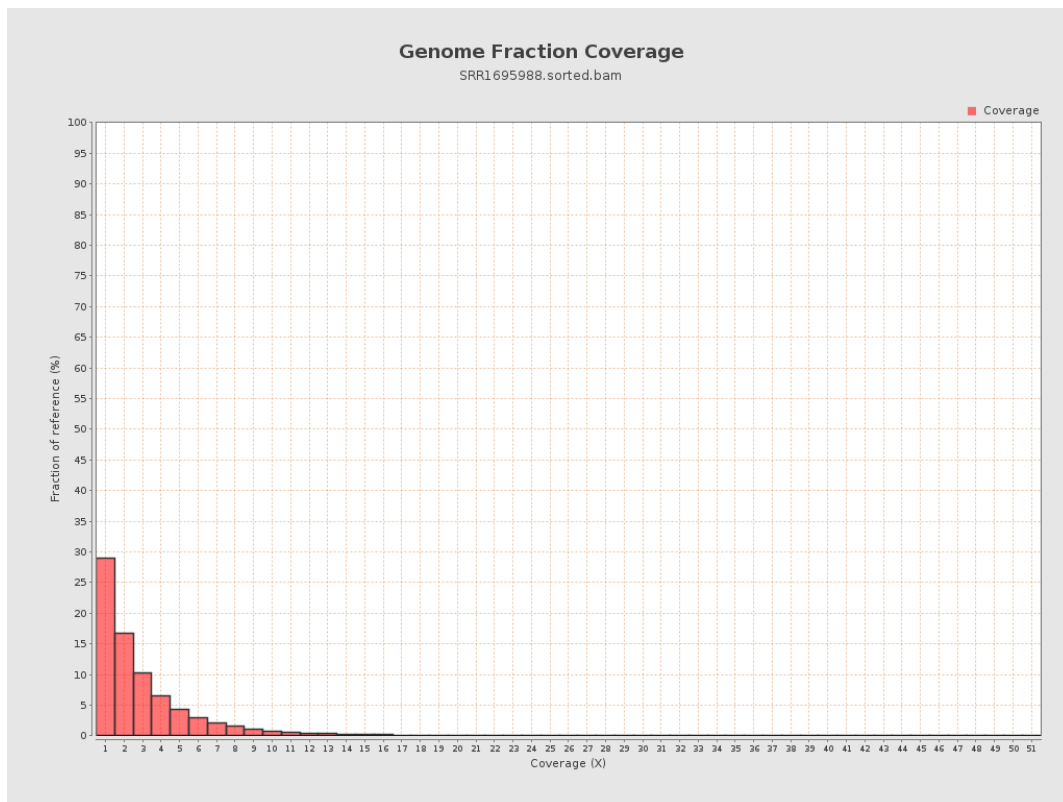
4. Results : Coverage Histogram



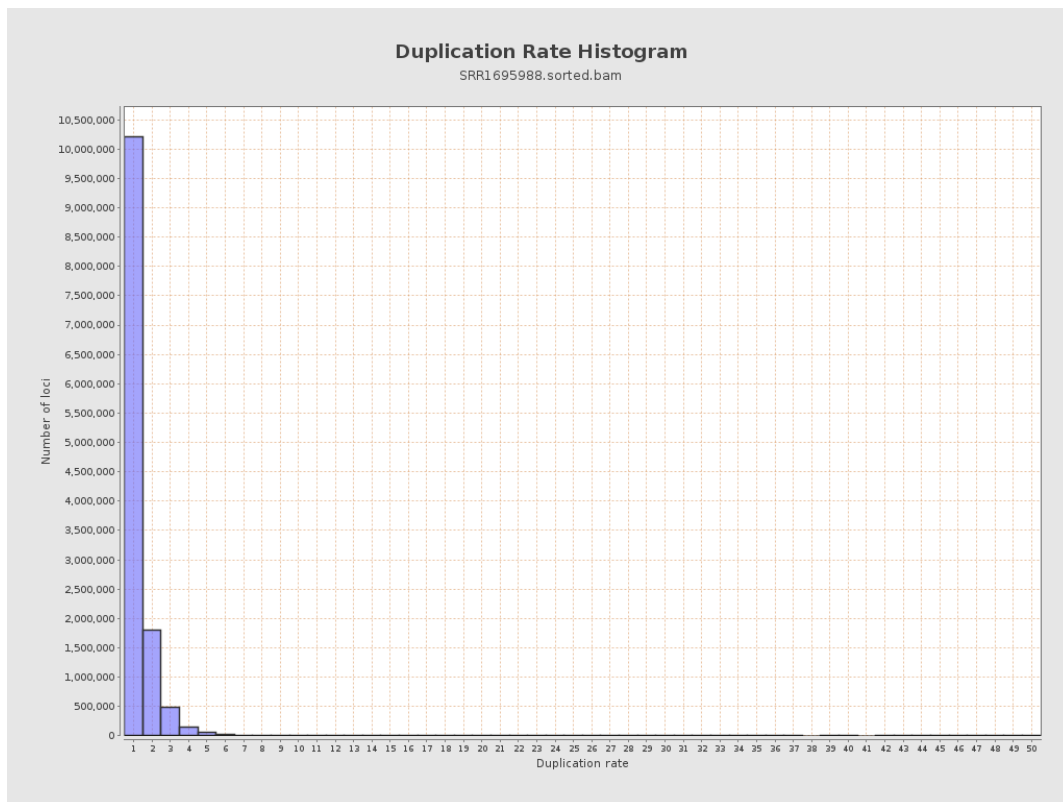
5. Results : Coverage Histogram (0-50X)



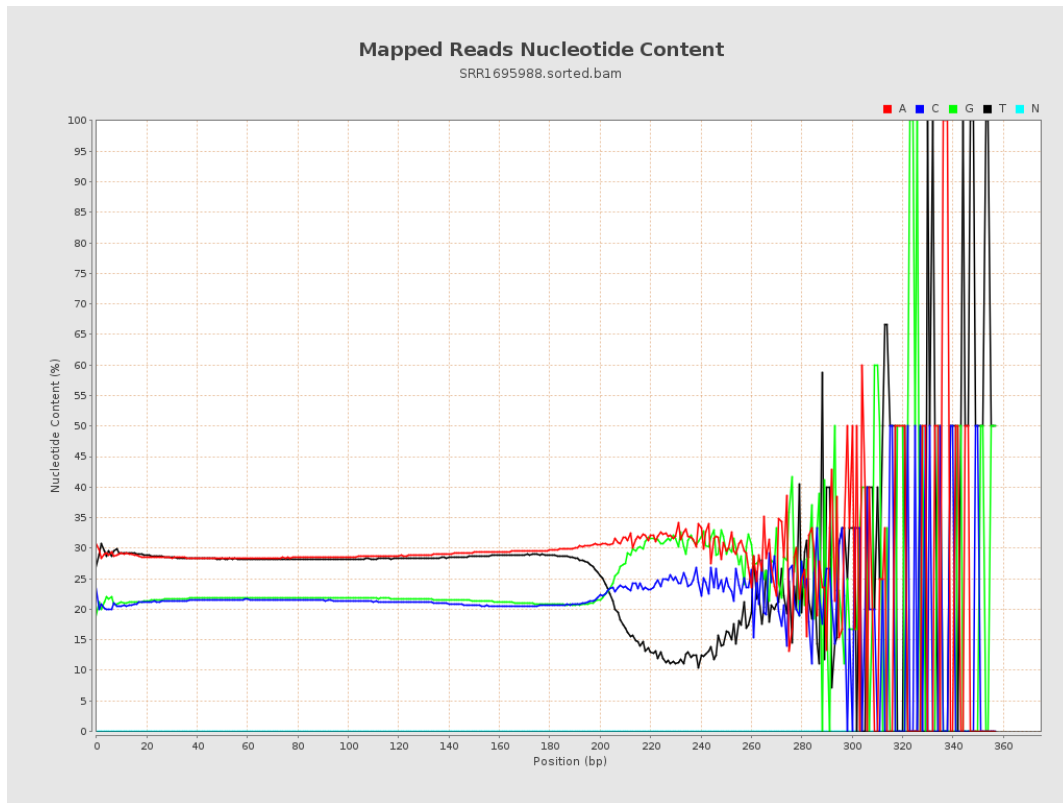
6. Results : Genome Fraction Coverage



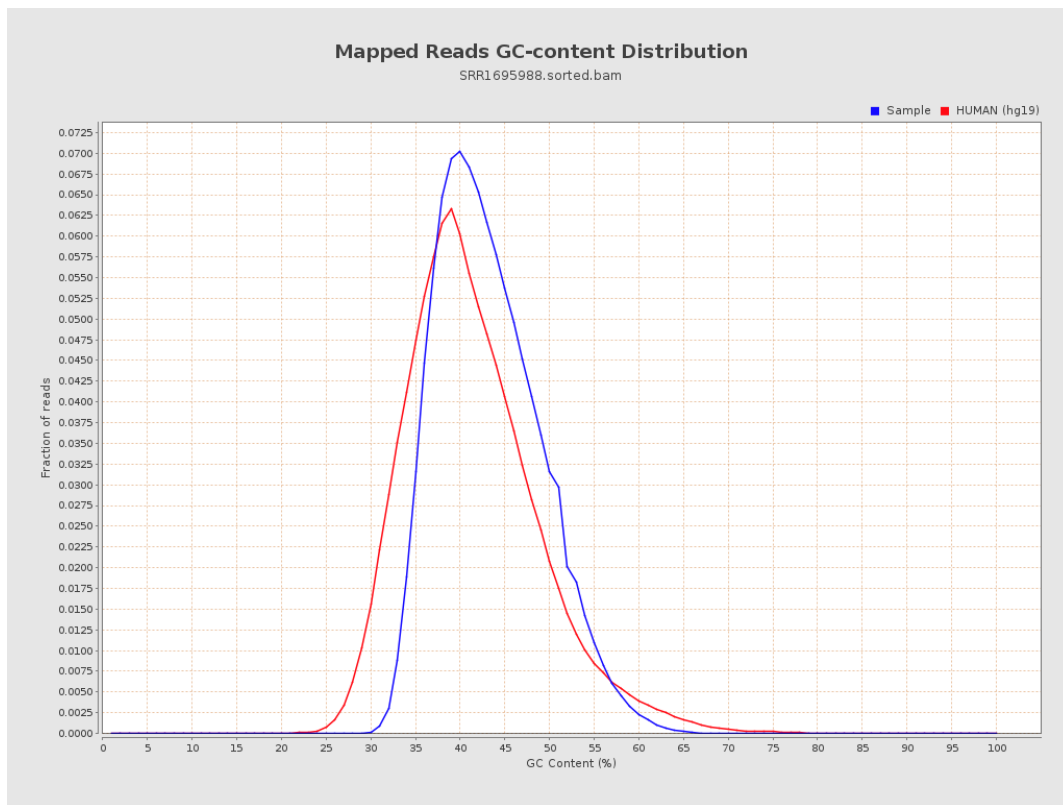
7. Results : Duplication Rate Histogram



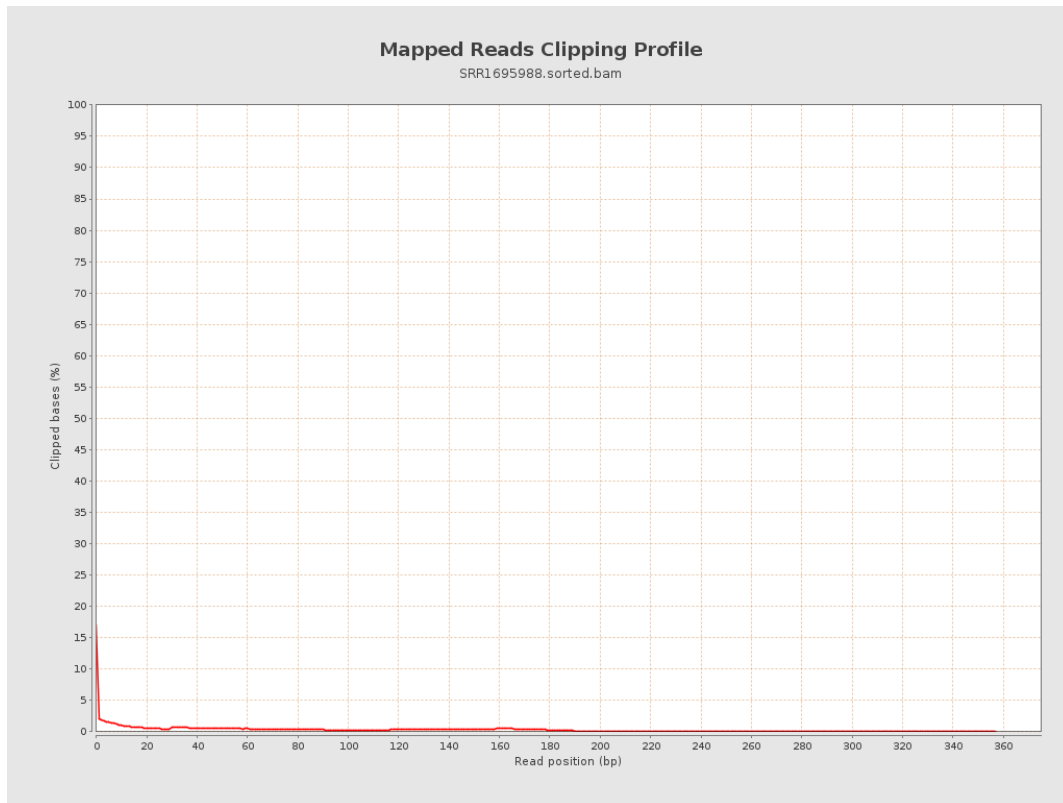
8. Results : Mapped Reads Nucleotide Content



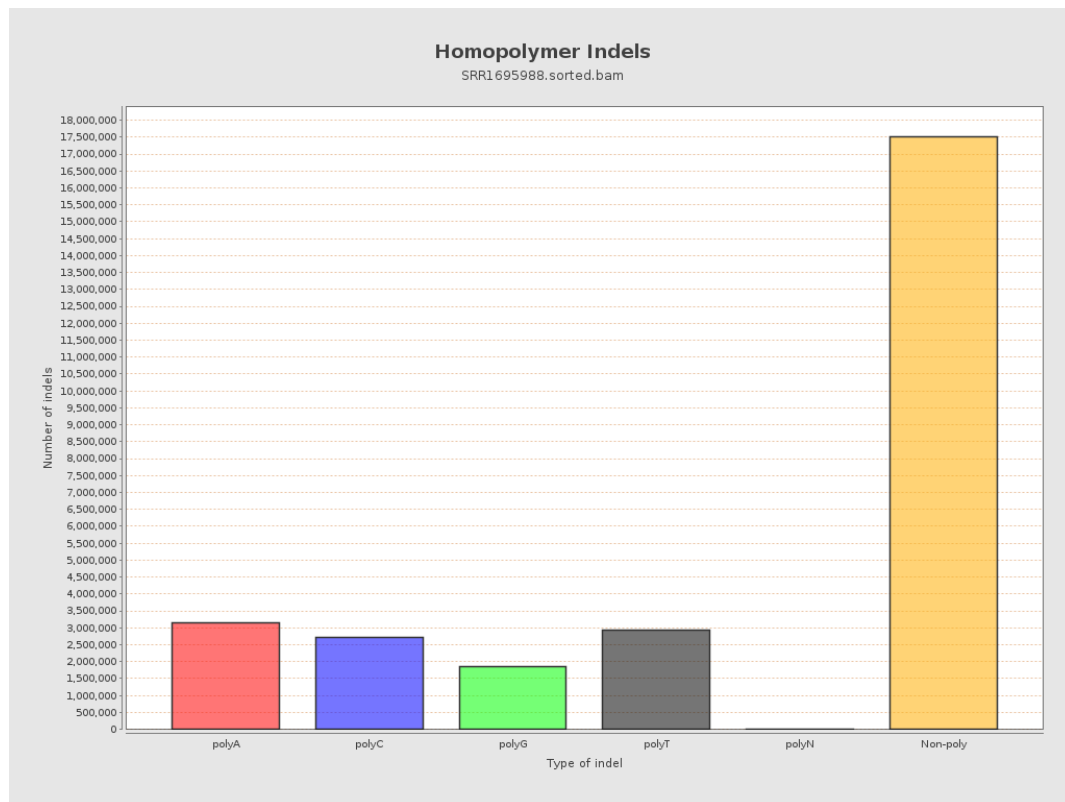
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

