

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 02:14:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695972.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_SRR1695972 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695972_1.fastq.gz SRR1695972_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 02:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	60,544,978
Mapped reads	60,188,225 / 99.41%
Unmapped reads	356,753 / 0.59%
Mapped paired reads	60,188,225 / 99.41%
Mapped reads, first in pair	30,186,623 / 49.86%
Mapped reads, second in pair	30,001,602 / 49.55%
Mapped reads, both in pair	59,934,144 / 98.99%
Mapped reads, singletons	254,081 / 0.42%
Secondary alignments	0
Supplementary alignments	597,319 / 0.99%
Read min/max/mean length	30 / 100 / 100.41
Duplicated reads (estimated)	1,822,551 / 3.01%
Duplication rate	2.62%
Clipped reads	4,206,752 / 6.95%

2.2. ACGT Content

Number/percentage of A's	1,768,689,955 / 29.62%
Number/percentage of C's	1,200,903,330 / 20.11%
Number/percentage of T's	1,759,312,004 / 29.46%
Number/percentage of G's	1,235,838,911 / 20.7%
Number/percentage of N's	6,488,499 / 0.11%

GC Percentage	40.81%
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2.3. Coverage

Mean	1.9293
Standard Deviation	2.7925

2.4. Mapping Quality

Mean Mapping Quality	53.91
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2.5. Insert size

Mean	73,018.73
Standard Deviation	2,597,404.02
P25/Median/P75	315 / 325 / 334

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	38,551,101
Insertions	557,293
Mapped reads with at least one insertion	0.91%
Deletions	563,416
Mapped reads with at least one deletion	0.92%
Homopolymer indels	45.69%

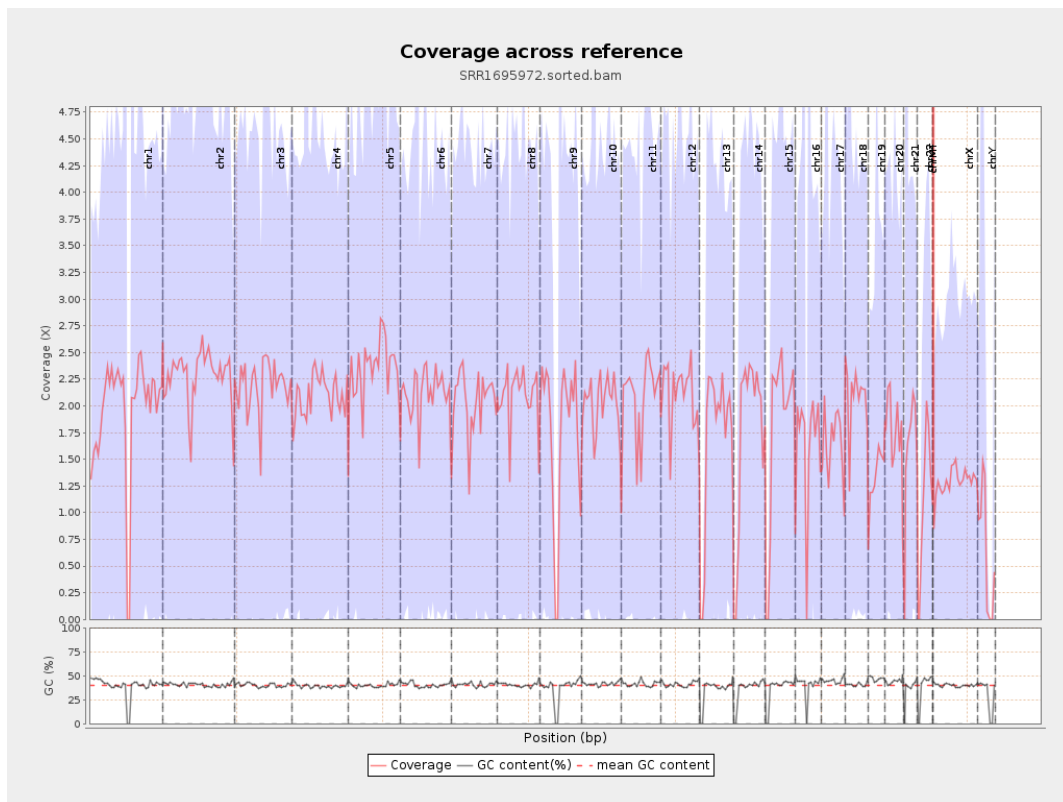
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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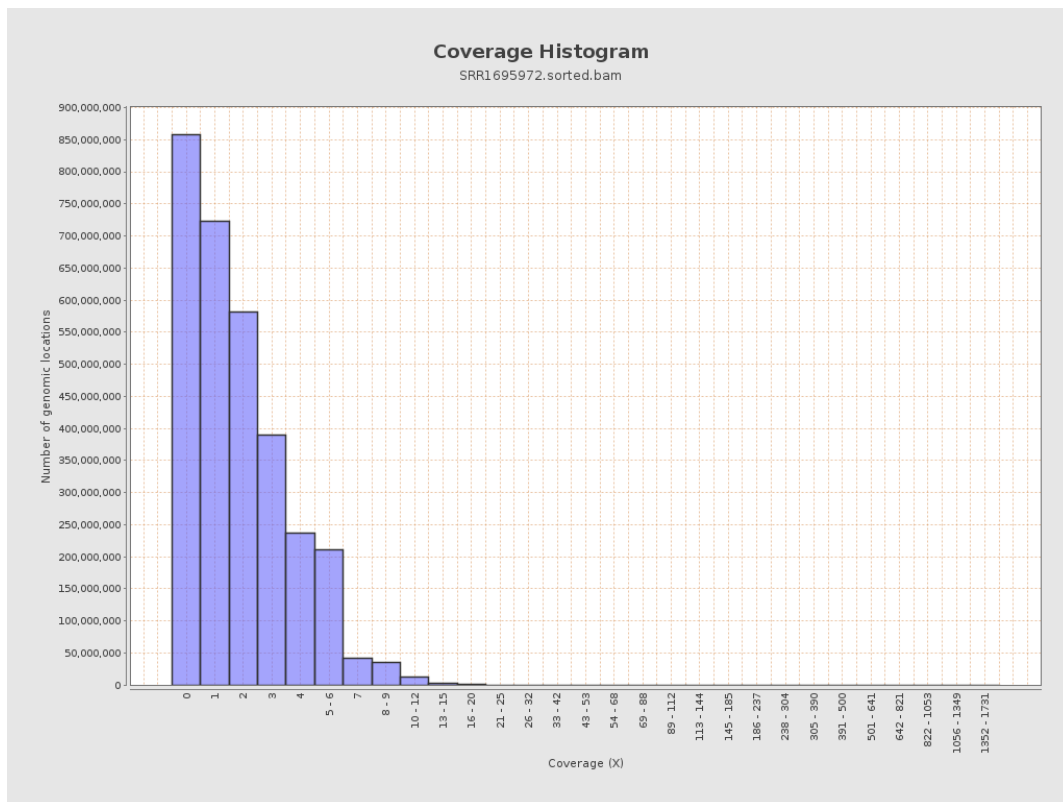
		bases	coverage	deviation
chr1	249250621	486609946	1.9523	2.9008
chr2	243199373	553904145	2.2776	2.6952
chr3	198022430	433487028	2.1891	2.0288
chr4	191154276	401903505	2.1025	2.5109
chr5	180915260	424121172	2.3443	2.1281
chr6	171115067	363408876	2.1238	2.3447
chr7	159138663	323497400	2.0328	2.1044
chr8	146364022	306306317	2.0928	2.0556
chr9	141213431	248470376	1.7595	2.3442
chr10	135534747	275876184	2.0355	3.0802
chr11	135006516	282305540	2.0911	2.1219
chr12	133851895	283642526	2.1191	2.1121
chr13	115169878	194091207	1.6853	1.9283
chr14	107349540	191889689	1.7875	2.0396
chr15	102531392	183559560	1.7903	2.1214
chr16	90354753	144945015	1.6042	2.6637
chr17	81195210	135289352	1.6662	2.3483
chr18	78077248	161865320	2.0731	2.9853
chr19	59128983	80946081	1.369	2.0905
chr20	63025520	111897372	1.7754	2.0941
chr21	48129895	77222456	1.6045	3.2842
chr22	51304566	58589572	1.142	1.7767
chrMT	16571	10041051	605.9412	164.1496
chrX	155270560	200512797	1.2914	1.4933

chrY	59373566	38141251	0.6424	2.5297
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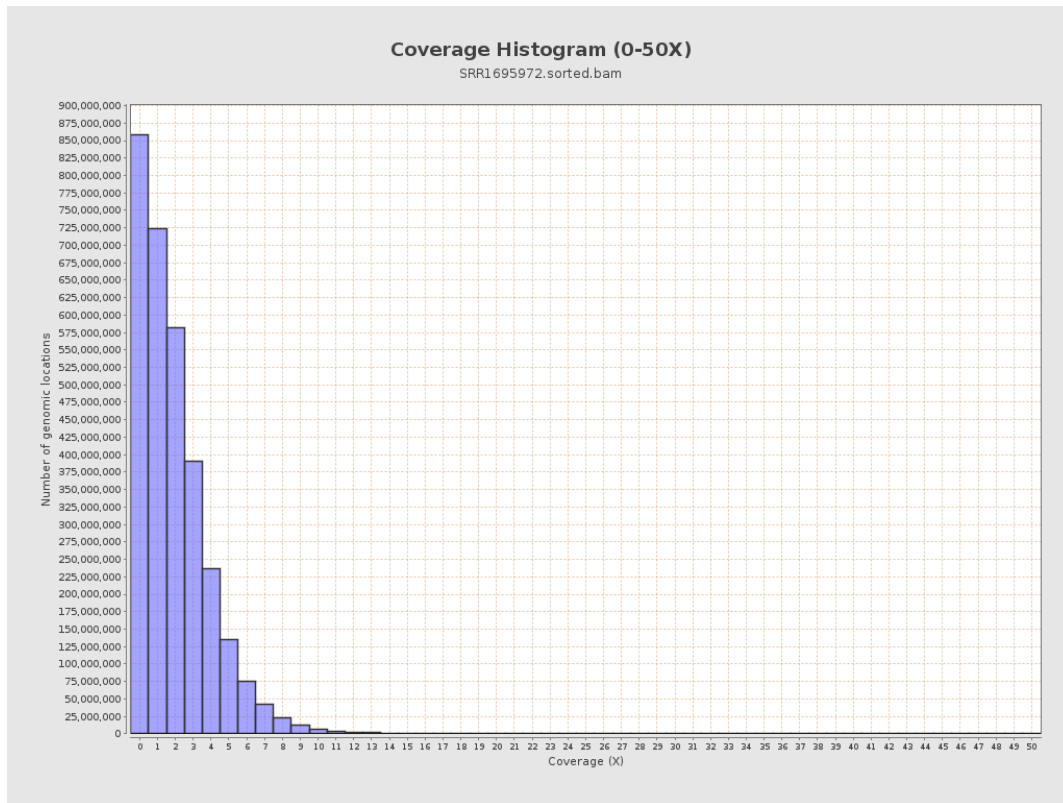
3. Results : Coverage across reference



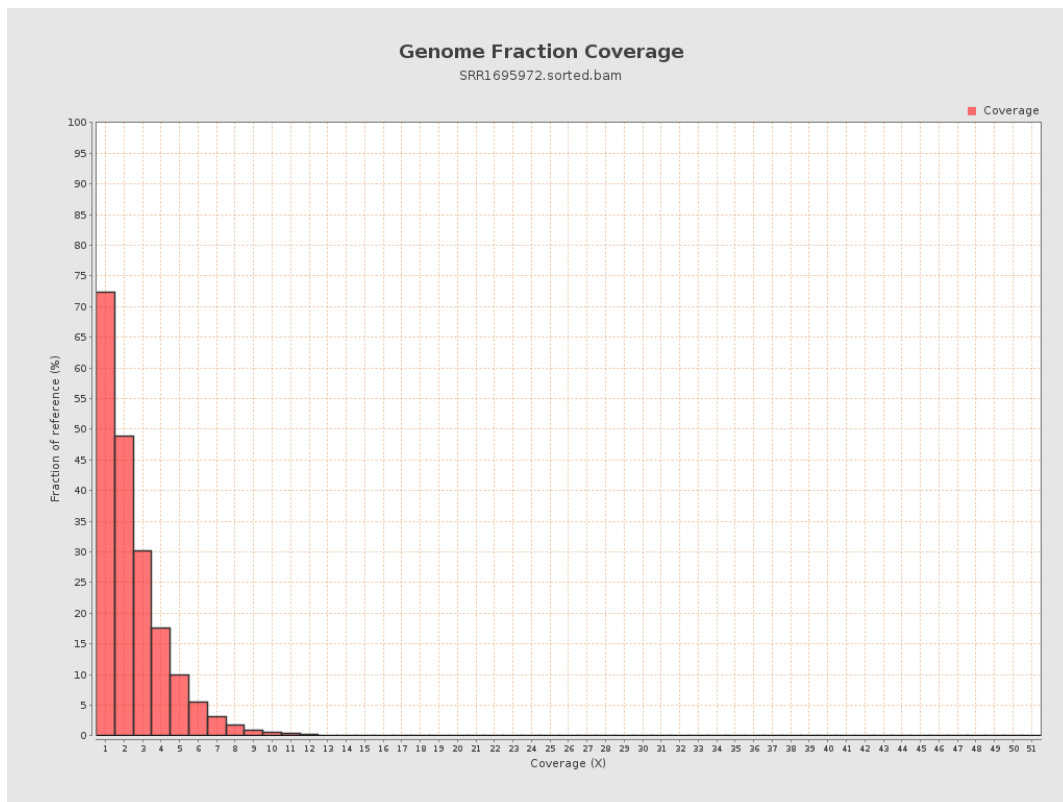
4. Results : Coverage Histogram



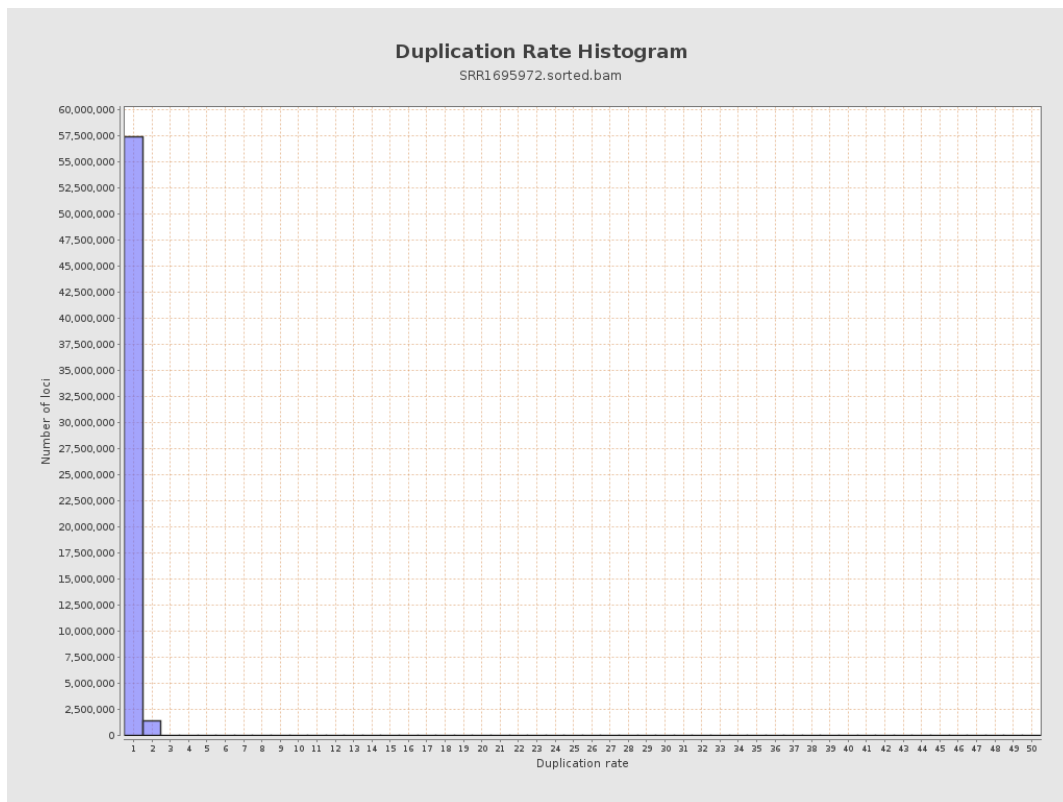
5. Results : Coverage Histogram (0-50X)



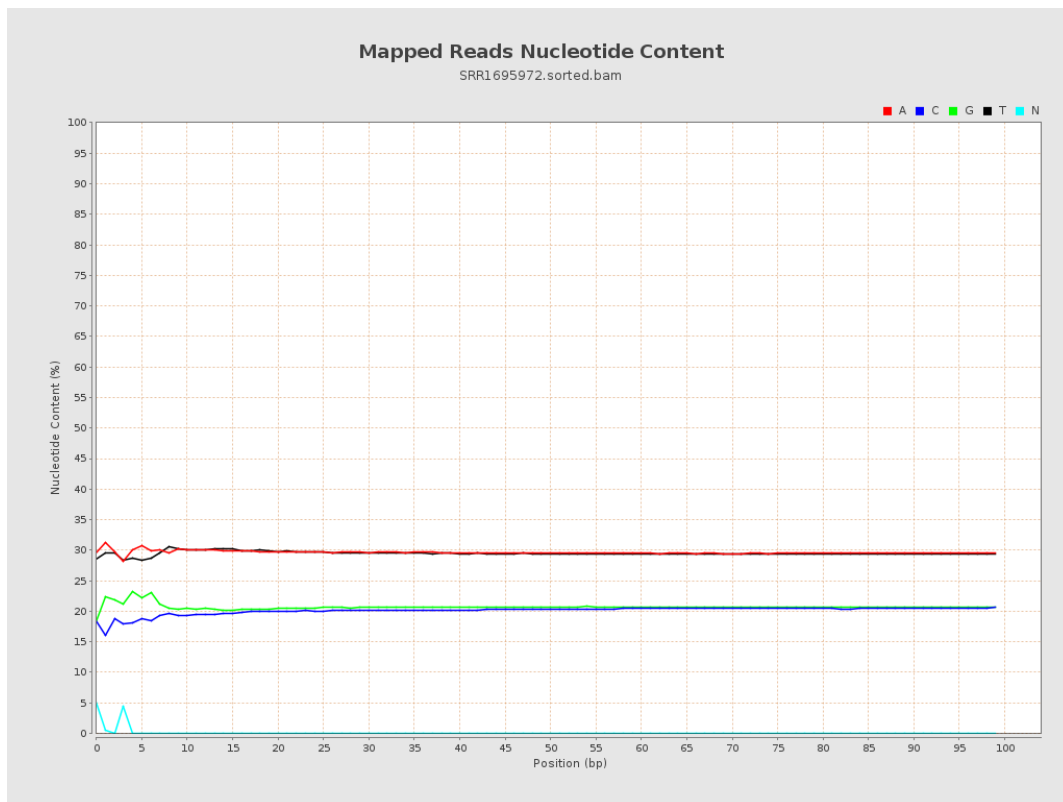
6. Results : Genome Fraction Coverage



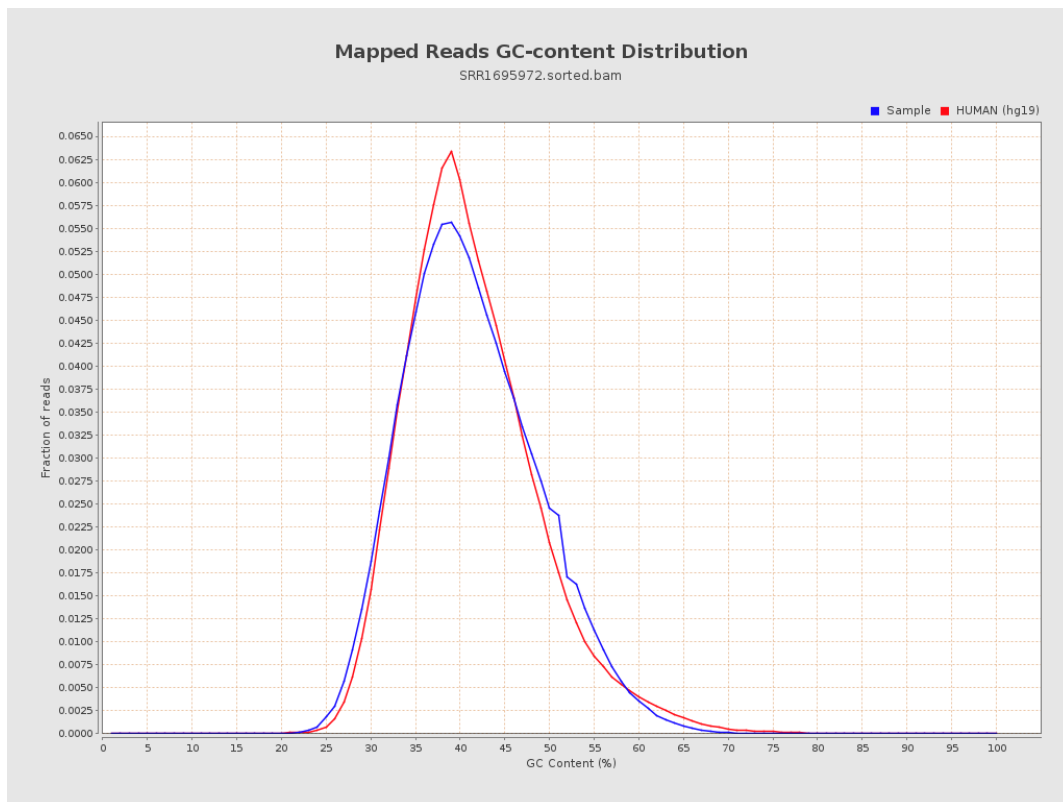
7. Results : Duplication Rate Histogram



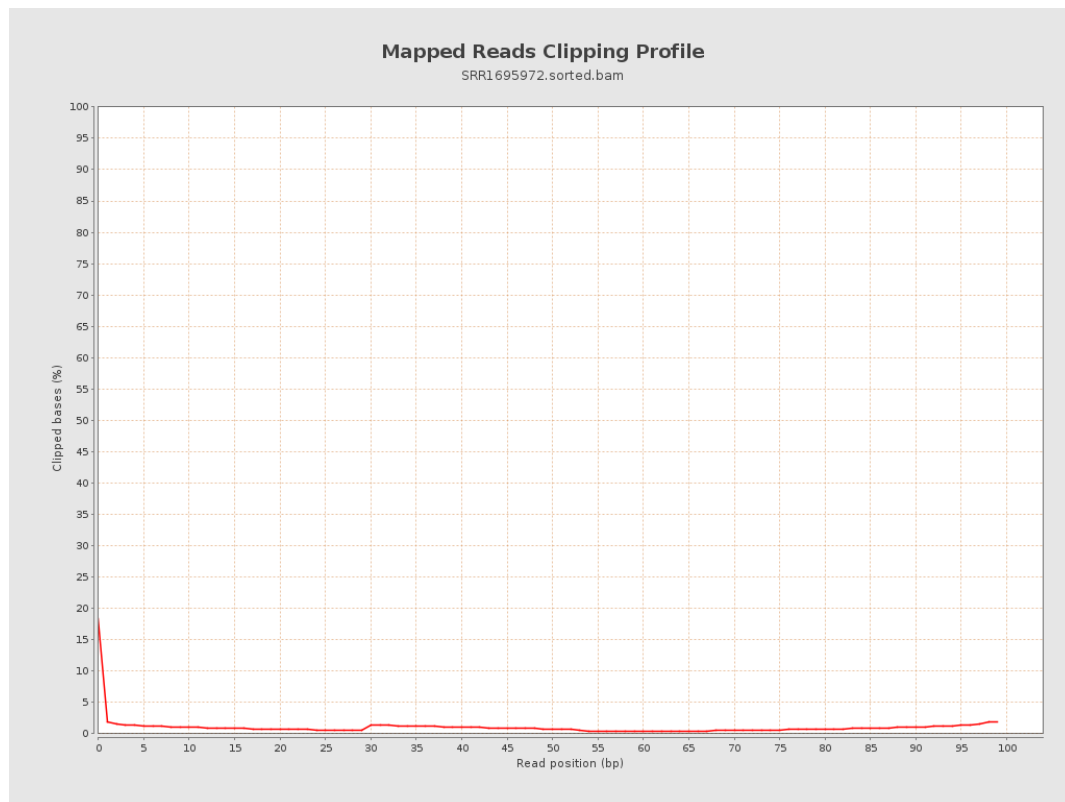
8. Results : Mapped Reads Nucleotide Content



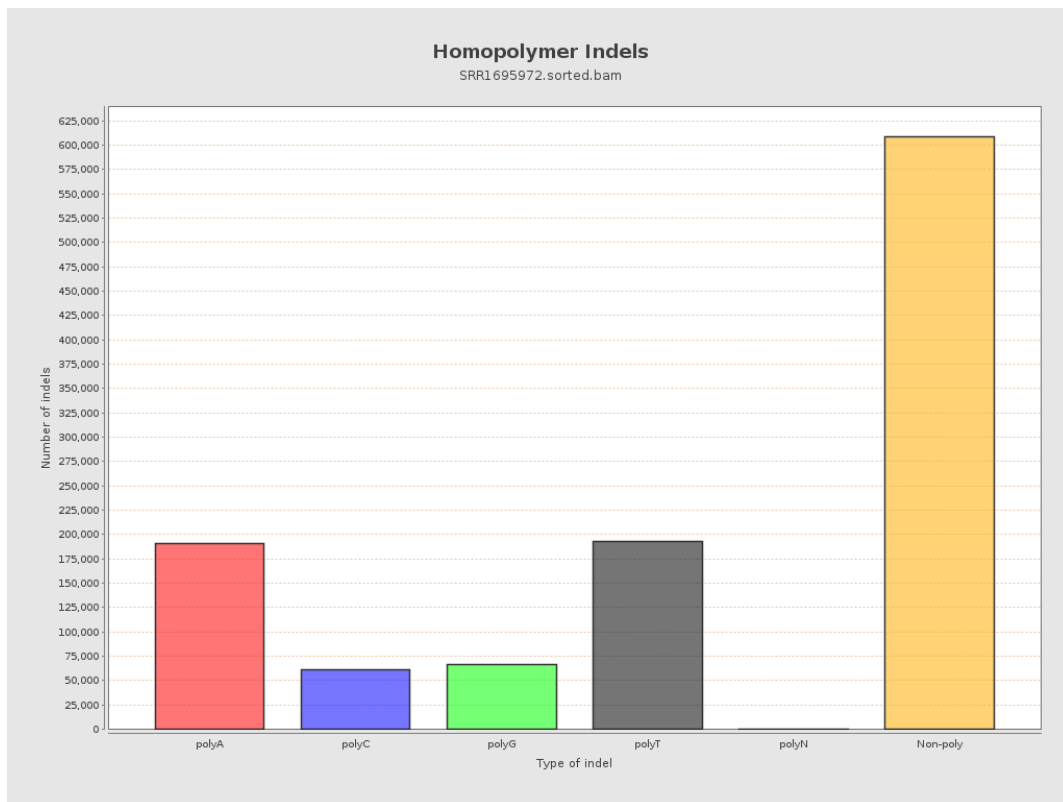
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



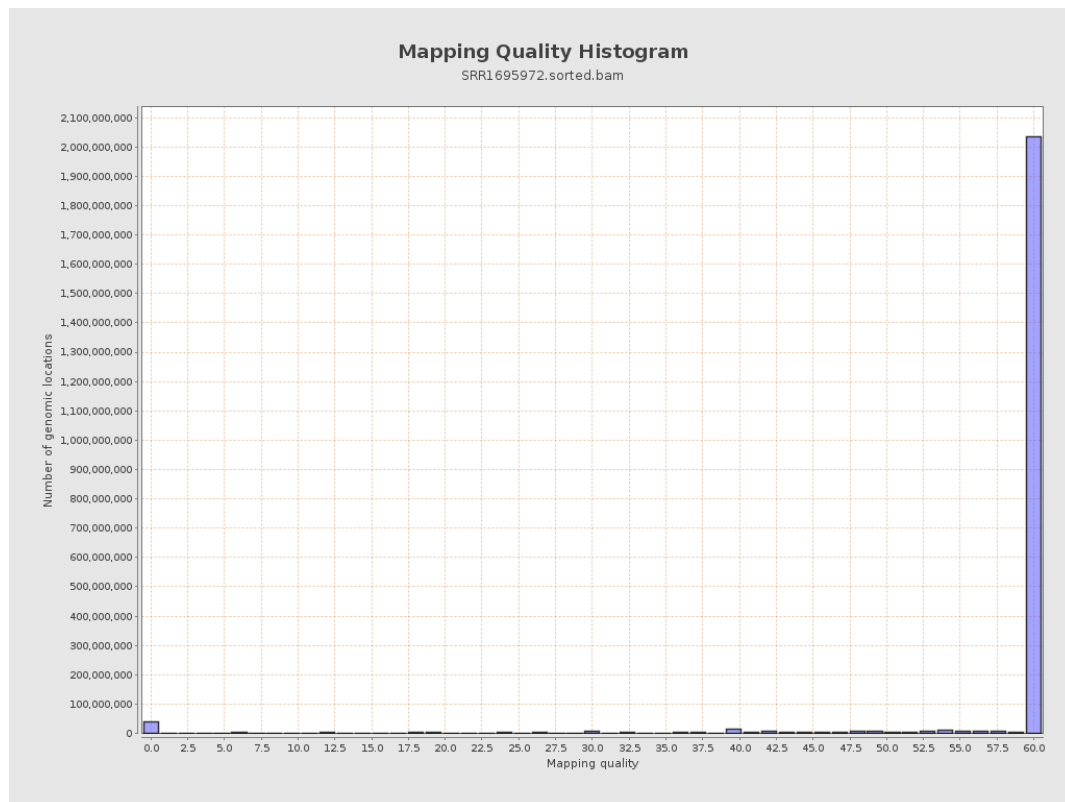
11. Results : Homopolymer Indels



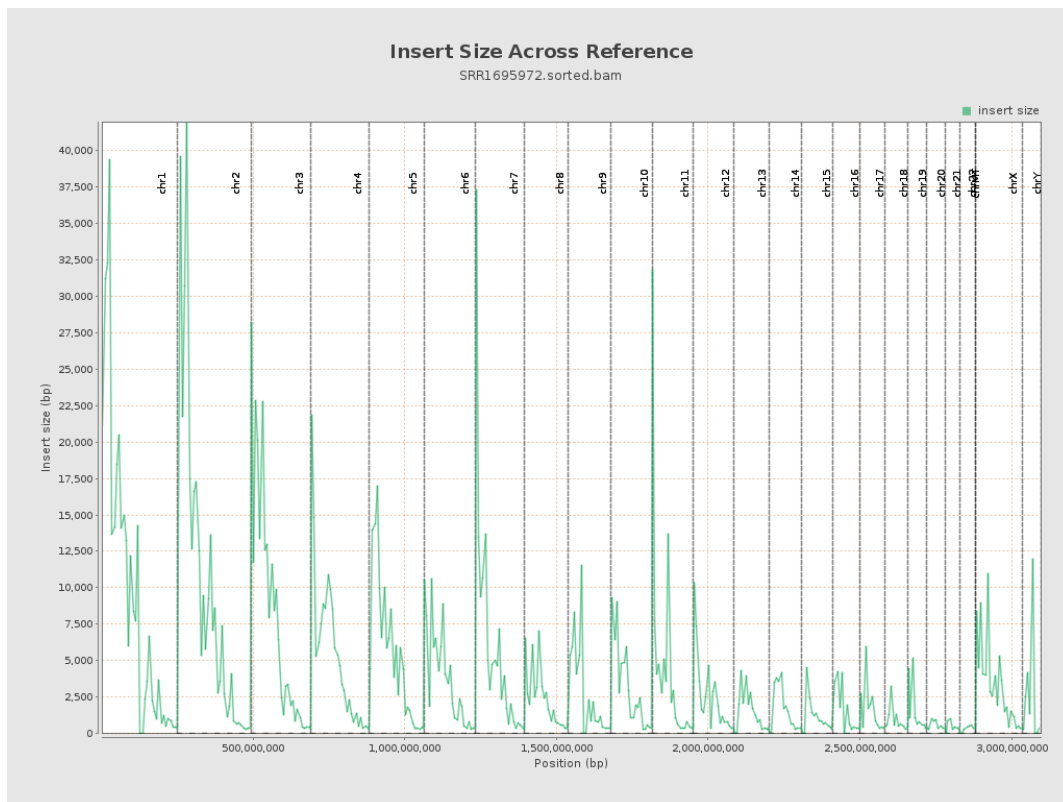
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

