

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 06:23:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472680.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_SRR3472680 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472680_1.fastq.gz SRR3472680_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 06:23:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472680.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,325,896
Mapped reads	18,164,847 / 99.12%
Unmapped reads	161,049 / 0.88%
Mapped paired reads	18,164,847 / 99.12%
Mapped reads, first in pair	9,106,282 / 49.69%
Mapped reads, second in pair	9,058,565 / 49.43%
Mapped reads, both in pair	18,054,940 / 98.52%
Mapped reads, singletons	109,907 / 0.6%
Secondary alignments	0
Supplementary alignments	110,584 / 0.6%
Read min/max/mean length	30 / 101 / 99.81
Duplicated reads (estimated)	12,538,105 / 68.42%
Duplication rate	49.56%
Clipped reads	1,377,905 / 7.52%

2.2. ACGT Content

Number/percentage of A's	483,159,543 / 27.05%
Number/percentage of C's	412,864,170 / 23.11%
Number/percentage of T's	482,110,135 / 26.99%
Number/percentage of G's	407,681,851 / 22.82%
Number/percentage of N's	333,360 / 0.02%

GC Percentage	45.94%
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2.3. Coverage

Mean	0.5771
Standard Deviation	25.7221

2.4. Mapping Quality

Mean Mapping Quality	54.88
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2.5. Insert size

Mean	26,113.25
Standard Deviation	1,626,441.77
P25/Median/P75	163 / 228 / 303

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	11,841,769
Insertions	119,961
Mapped reads with at least one insertion	0.65%
Deletions	105,192
Mapped reads with at least one deletion	0.56%
Homopolymer indels	46.61%

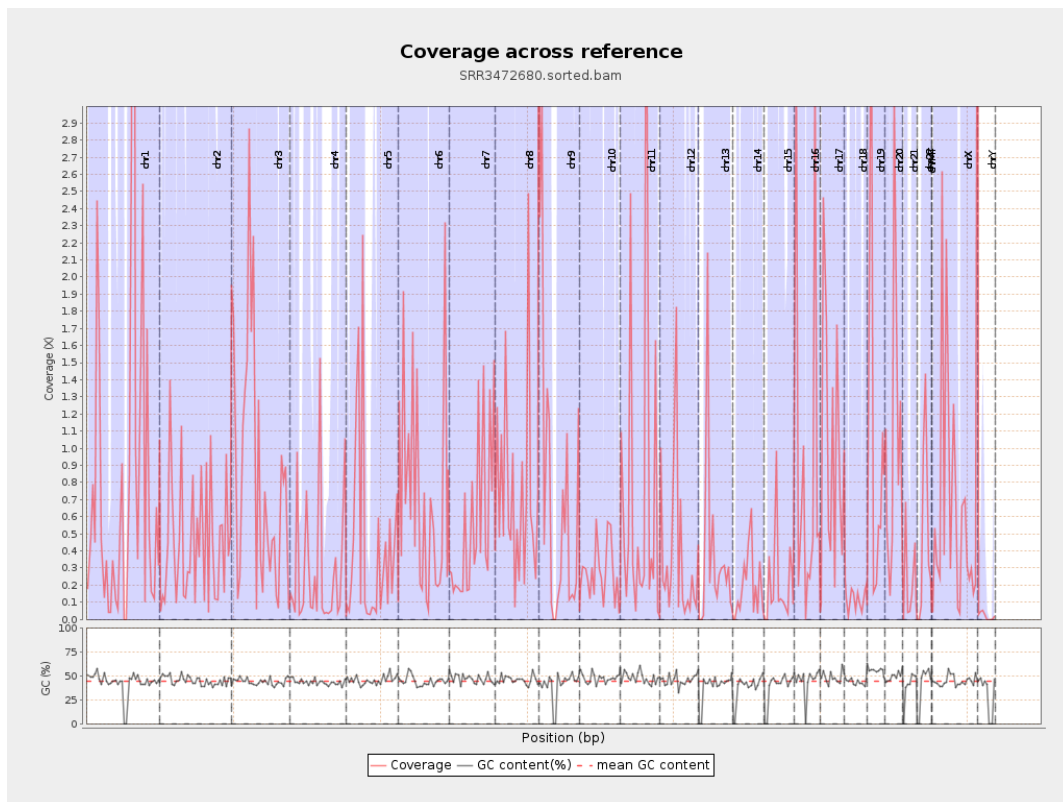
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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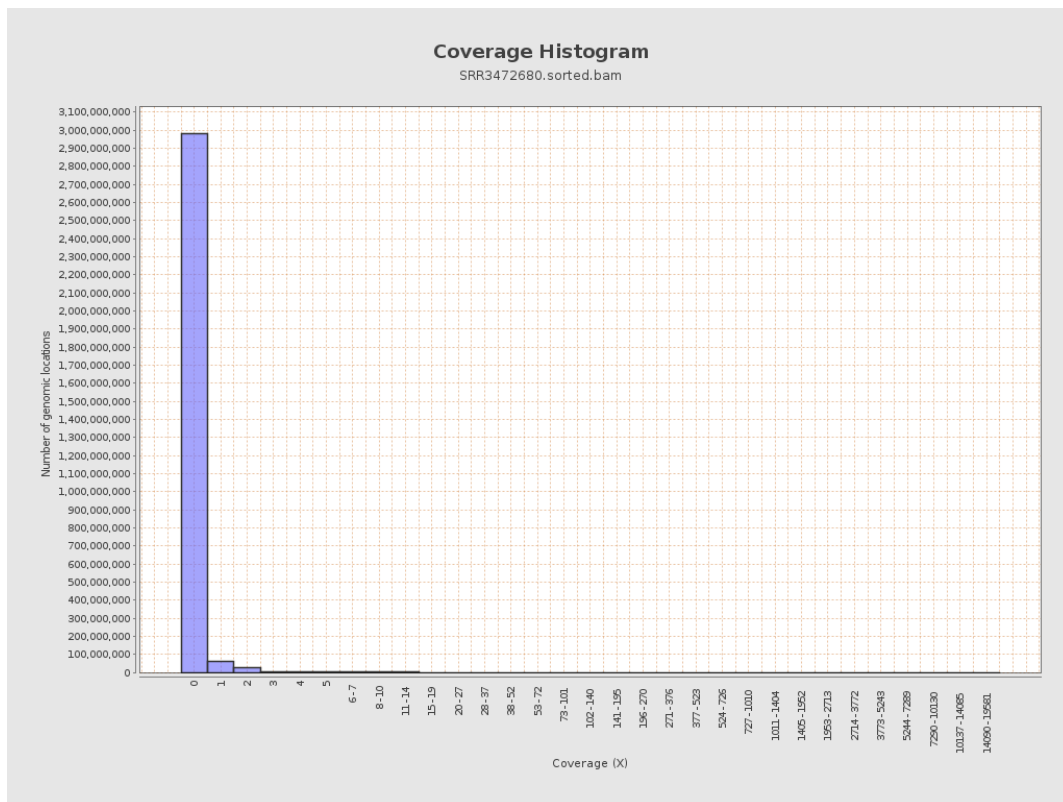
		bases	coverage	deviation
chr1	249250621	220377015	0.8842	39.9075
chr2	243199373	110689151	0.4551	18.014
chr3	198022430	171237631	0.8647	25.2853
chr4	191154276	52671032	0.2755	18.6111
chr5	180915260	77579146	0.4288	17.7159
chr6	171115067	120045083	0.7015	22.0307
chr7	159138663	88454927	0.5558	20.6243
chr8	146364022	109133124	0.7456	28.3129
chr9	141213431	106391544	0.7534	20.4291
chr10	135534747	37059599	0.2734	11.2986
chr11	135006516	99097328	0.734	54.4148
chr12	133851895	51759577	0.3867	15.4126
chr13	115169878	43355147	0.3764	14.7645
chr14	107349540	20567343	0.1916	10.26
chr15	102531392	21313537	0.2079	9.3452
chr16	90354753	85725403	0.9488	28.6529
chr17	81195210	78243638	0.9636	48.6944
chr18	78077248	9508212	0.1218	5.1529
chr19	59128983	66281085	1.121	32.516
chr20	63025520	70163311	1.1133	26.2182
chr21	48129895	11009055	0.2287	14.9197
chr22	51304566	24074943	0.4693	17.7001
chrMT	16571	3699	0.2232	0.5837
chrX	155270560	110459839	0.7114	25.3565

chrY	59373566	1283881	0.0216	0.6777
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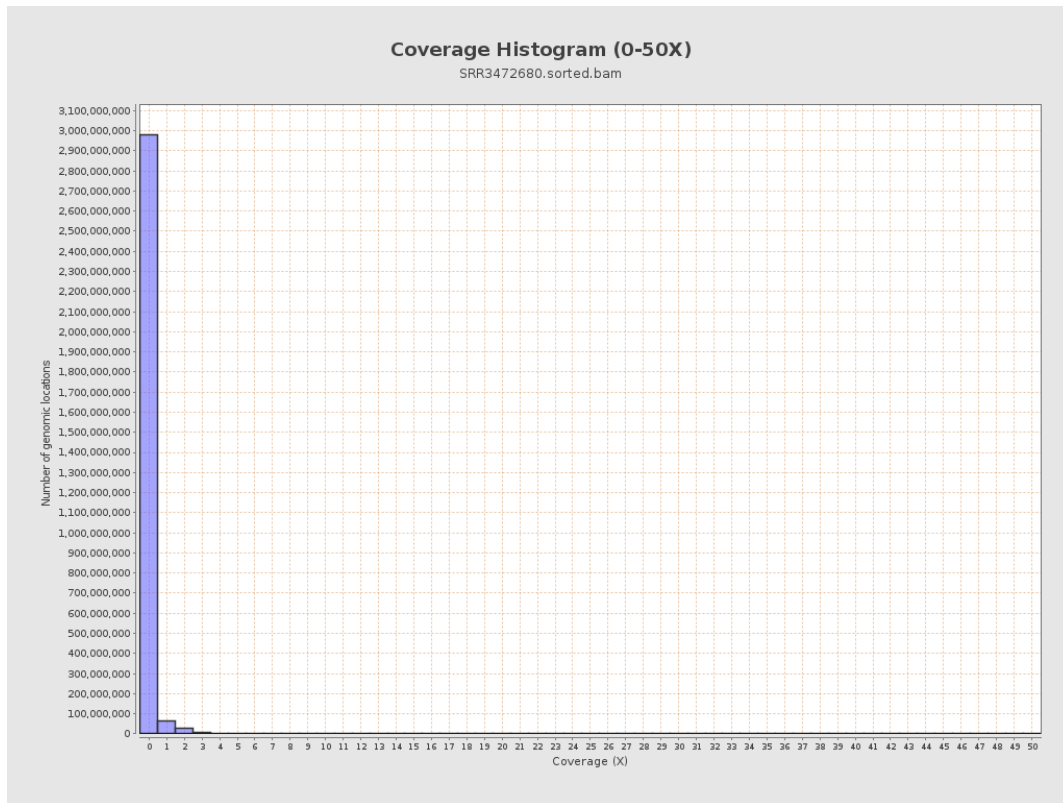
3. Results : Coverage across reference



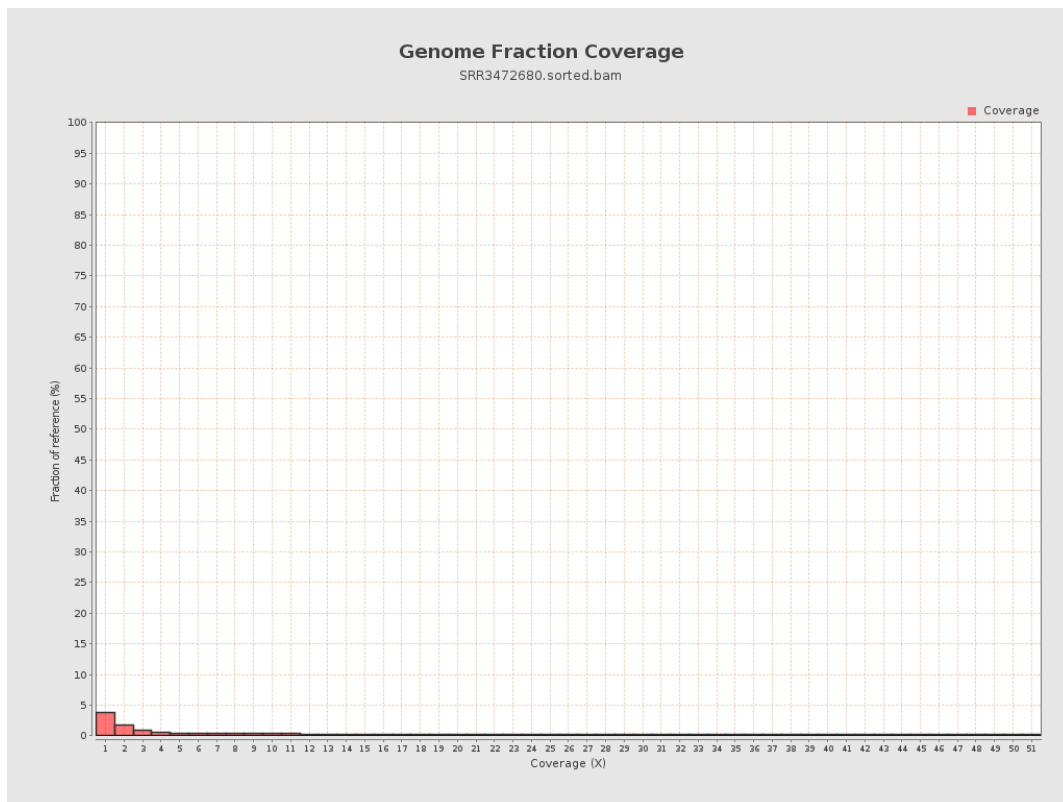
4. Results : Coverage Histogram



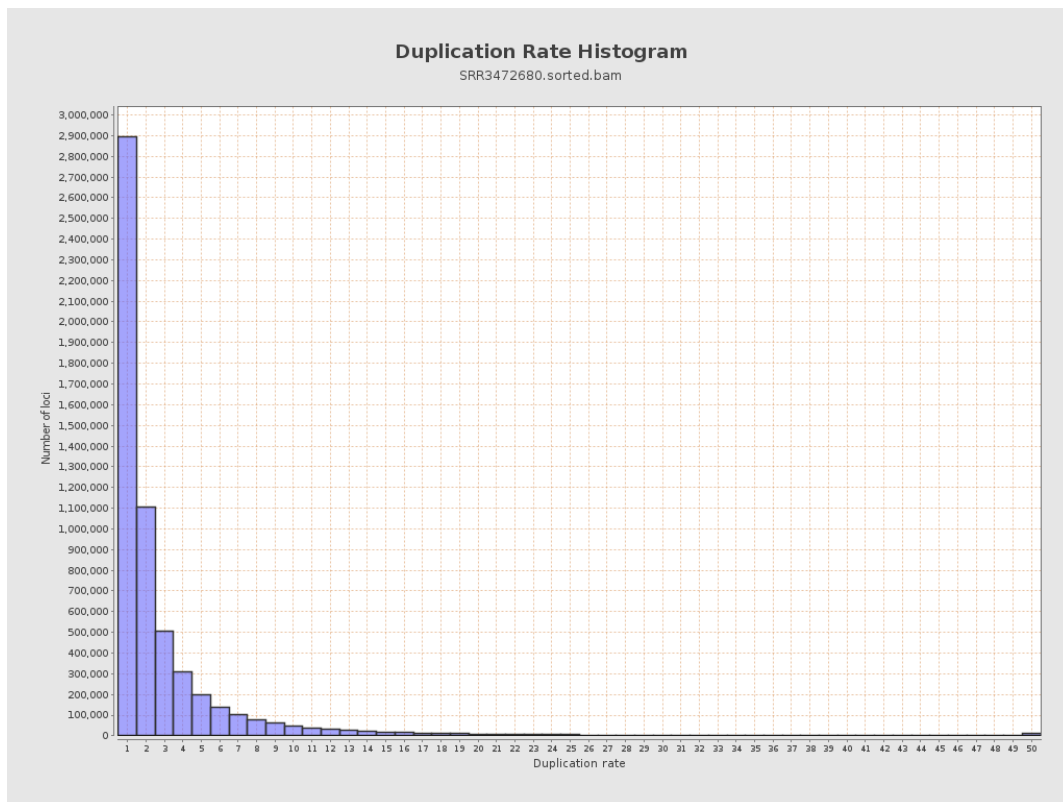
5. Results : Coverage Histogram (0-50X)



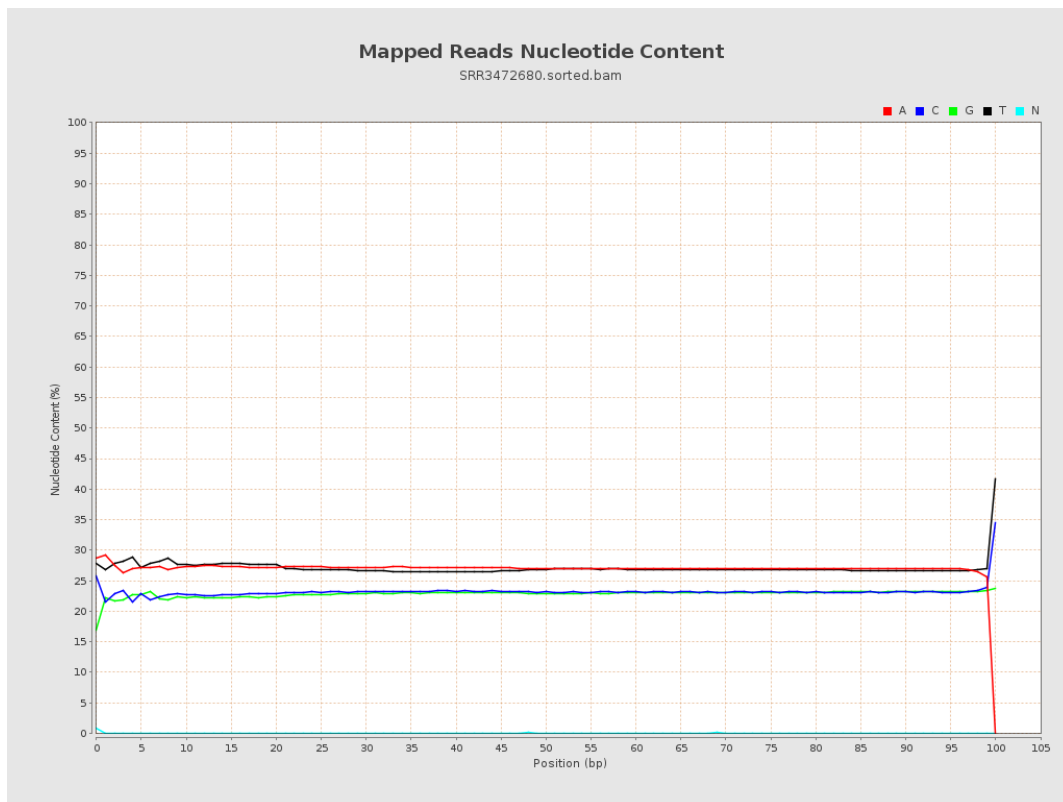
6. Results : Genome Fraction Coverage



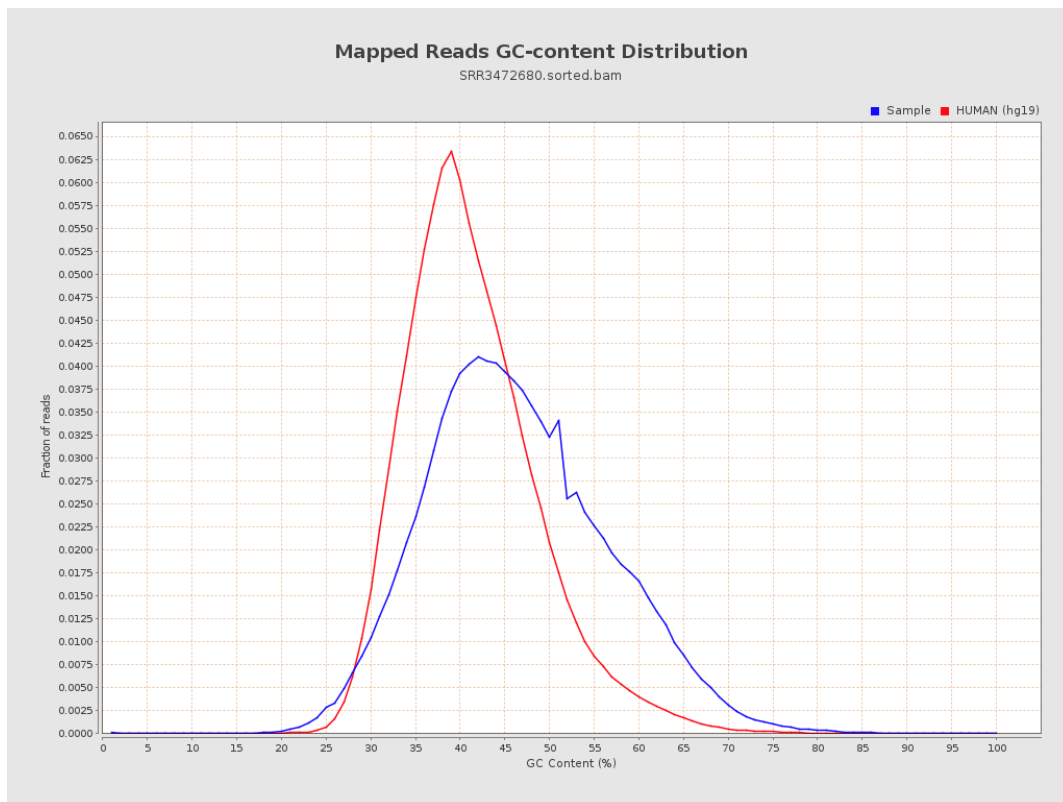
7. Results : Duplication Rate Histogram



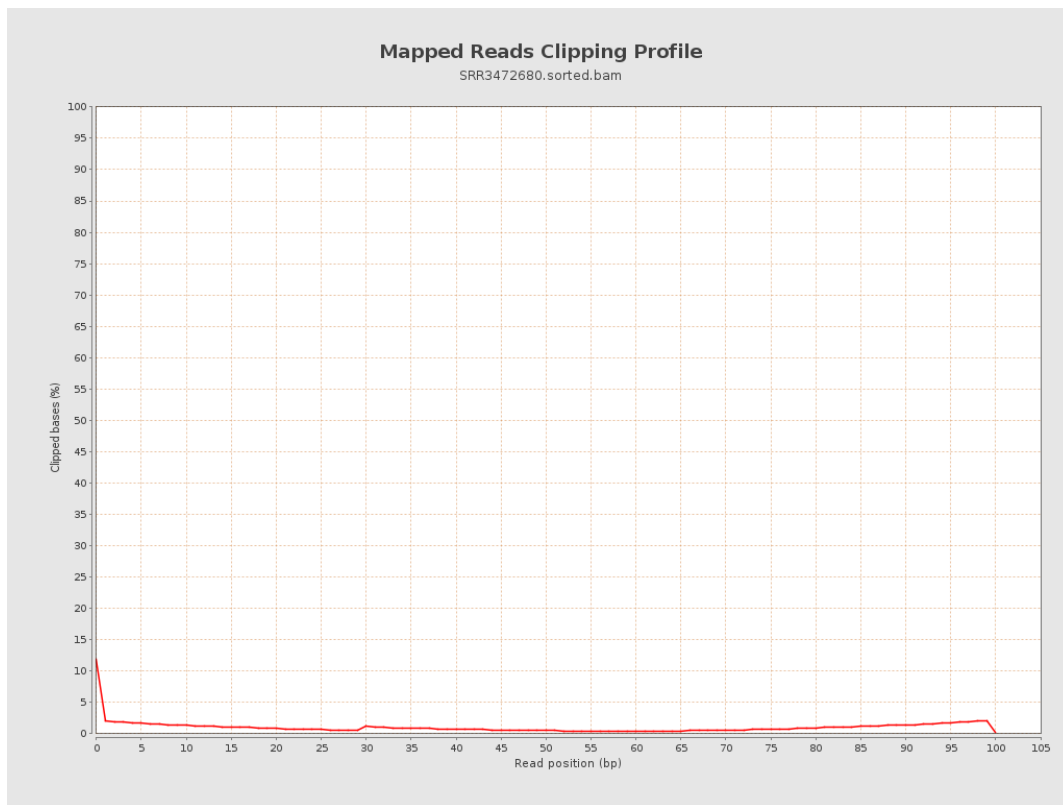
8. Results : Mapped Reads Nucleotide Content



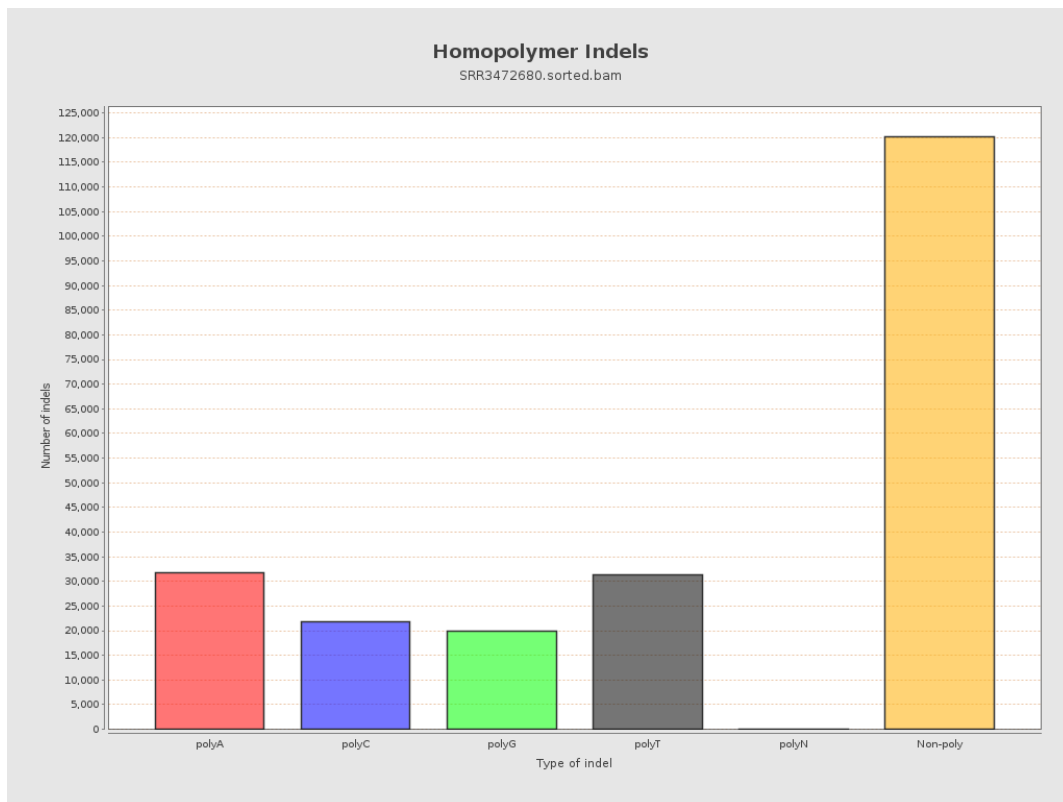
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



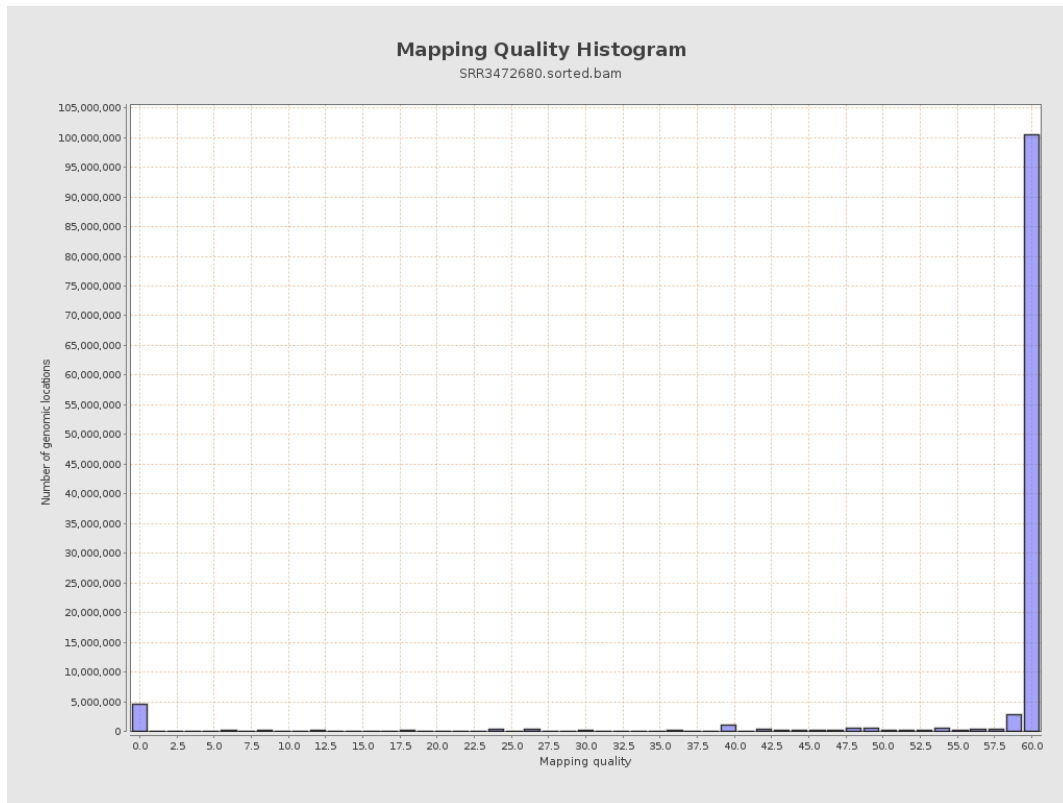
11. Results : Homopolymer Indels



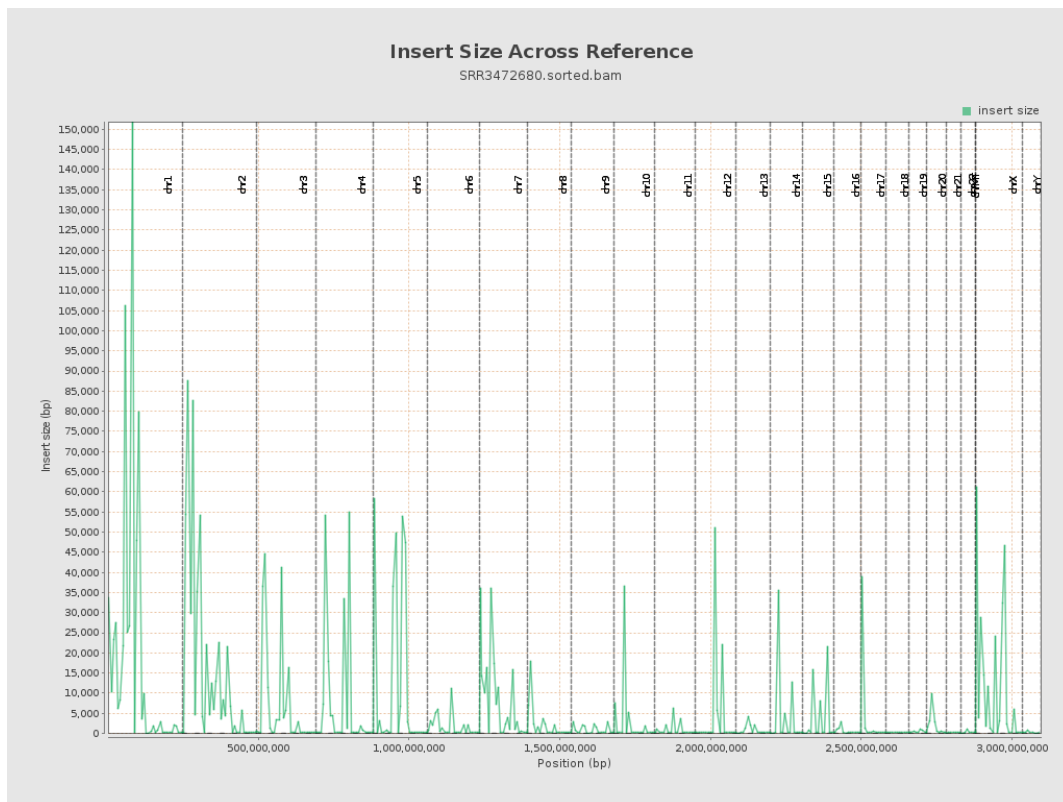
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

