

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:09:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472386.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_SRR3472386 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472386_1.fastq.gz SRR3472386_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:09:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472386.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,483,750
Mapped reads	20,268,067 / 98.95%
Unmapped reads	215,683 / 1.05%
Mapped paired reads	20,268,067 / 98.95%
Mapped reads, first in pair	10,189,589 / 49.74%
Mapped reads, second in pair	10,078,478 / 49.2%
Mapped reads, both in pair	20,113,808 / 98.19%
Mapped reads, singletons	154,259 / 0.75%
Secondary alignments	0
Supplementary alignments	77,022 / 0.38%
Read min/max/mean length	30 / 100 / 99.52
Duplicated reads (estimated)	12,909,999 / 63.03%
Duplication rate	48.1%
Clipped reads	1,337,036 / 6.53%

2.2. ACGT Content

Number/percentage of A's	536,689,364 / 26.95%
Number/percentage of C's	460,327,335 / 23.12%
Number/percentage of T's	537,230,957 / 26.98%
Number/percentage of G's	456,874,897 / 22.94%
Number/percentage of N's	249,825 / 0.01%

GC Percentage	46.06%
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2.3. Coverage

Mean	0.6434
Standard Deviation	19.5071

2.4. Mapping Quality

Mean Mapping Quality	54.93
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2.5. Insert size

Mean	20,125.34
Standard Deviation	1,420,066.7
P25/Median/P75	164 / 228 / 306

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	11,295,503
Insertions	119,221
Mapped reads with at least one insertion	0.58%
Deletions	100,216
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.8%

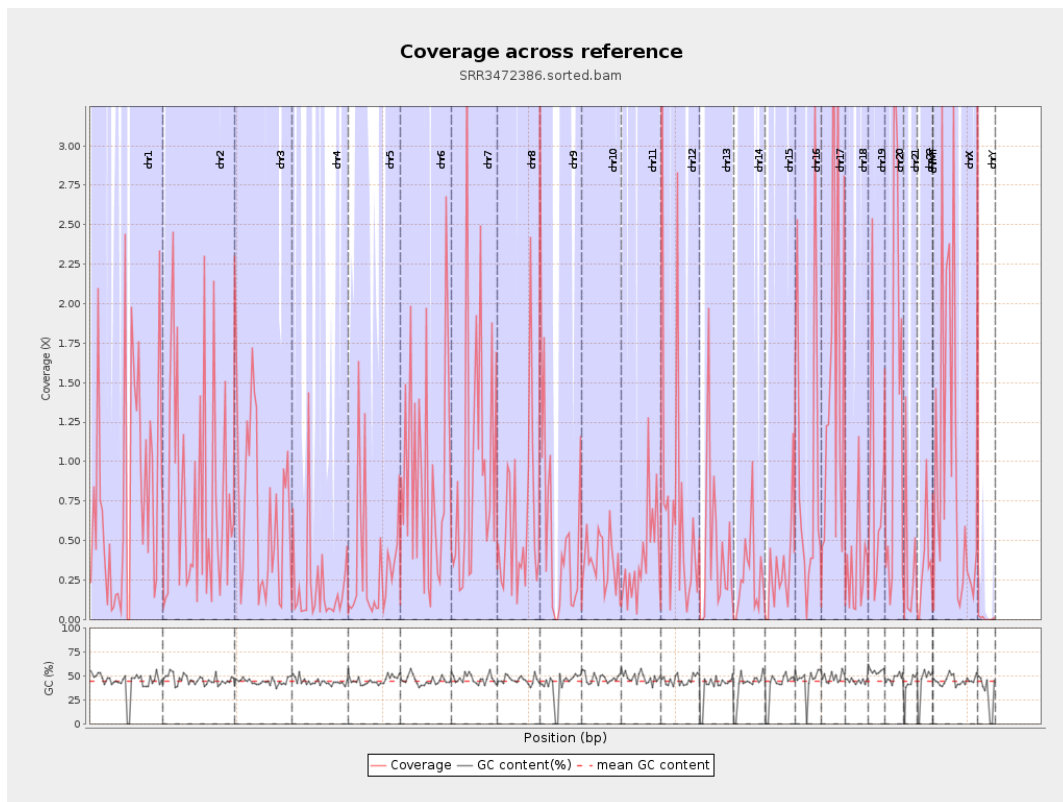
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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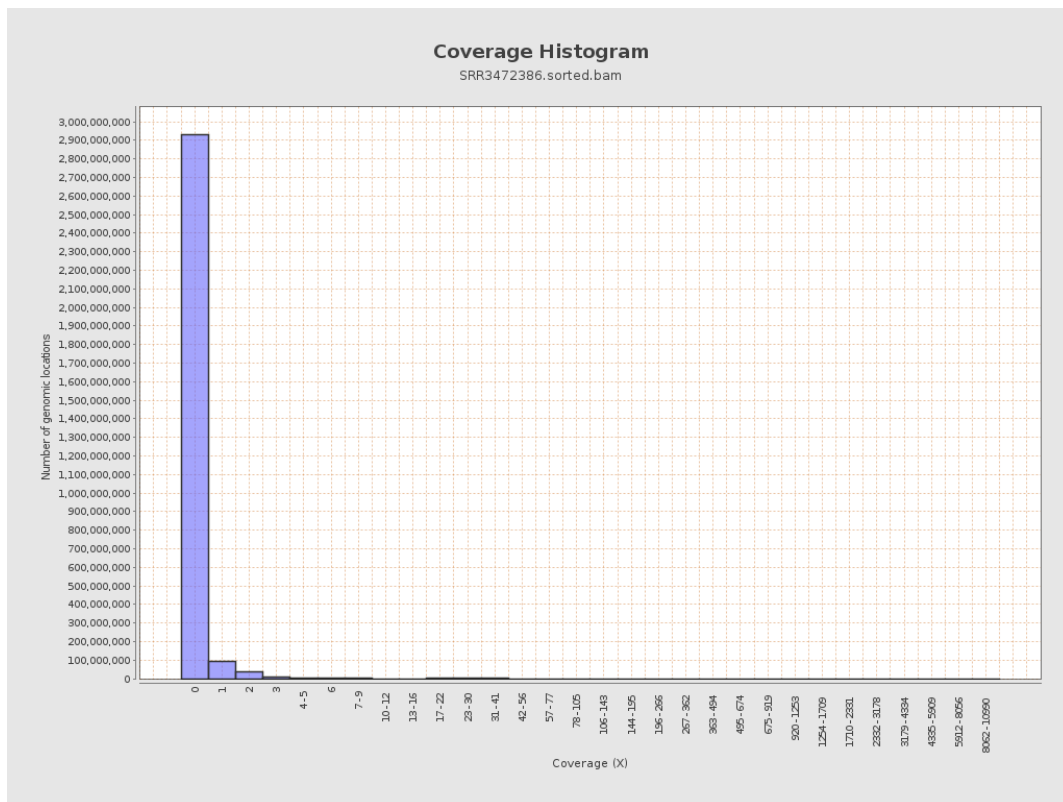
		bases	coverage	deviation
chr1	249250621	194258806	0.7794	23.0236
chr2	243199373	184183941	0.7573	25.0838
chr3	198022430	141568956	0.7149	15.2092
chr4	191154276	40576217	0.2123	7.2073
chr5	180915260	63862910	0.353	10.3235
chr6	171115067	153289087	0.8958	19.2813
chr7	159138663	161274350	1.0134	33.0945
chr8	146364022	88870200	0.6072	16.3705
chr9	141213431	70258824	0.4975	12.07
chr10	135534747	51588593	0.3806	10.598
chr11	135006516	52857647	0.3915	13.1859
chr12	133851895	106794239	0.7979	23.0784
chr13	115169878	52472075	0.4556	12.8665
chr14	107349540	29204470	0.2721	6.8002
chr15	102531392	32655860	0.3185	10.9276
chr16	90354753	82722089	0.9155	21.6257
chr17	81195210	129461472	1.5944	34.5471
chr18	78077248	25661135	0.3287	11.791
chr19	59128983	50713478	0.8577	17.7088
chr20	63025520	85804664	1.3614	34.3065
chr21	48129895	17942904	0.3728	22.8577
chr22	51304566	18381314	0.3583	9.9196
chrMT	16571	13197	0.7964	1.2575
chrX	155270560	156824535	1.01	25.4539

chrY	59373566	374733	0.0063	0.4037
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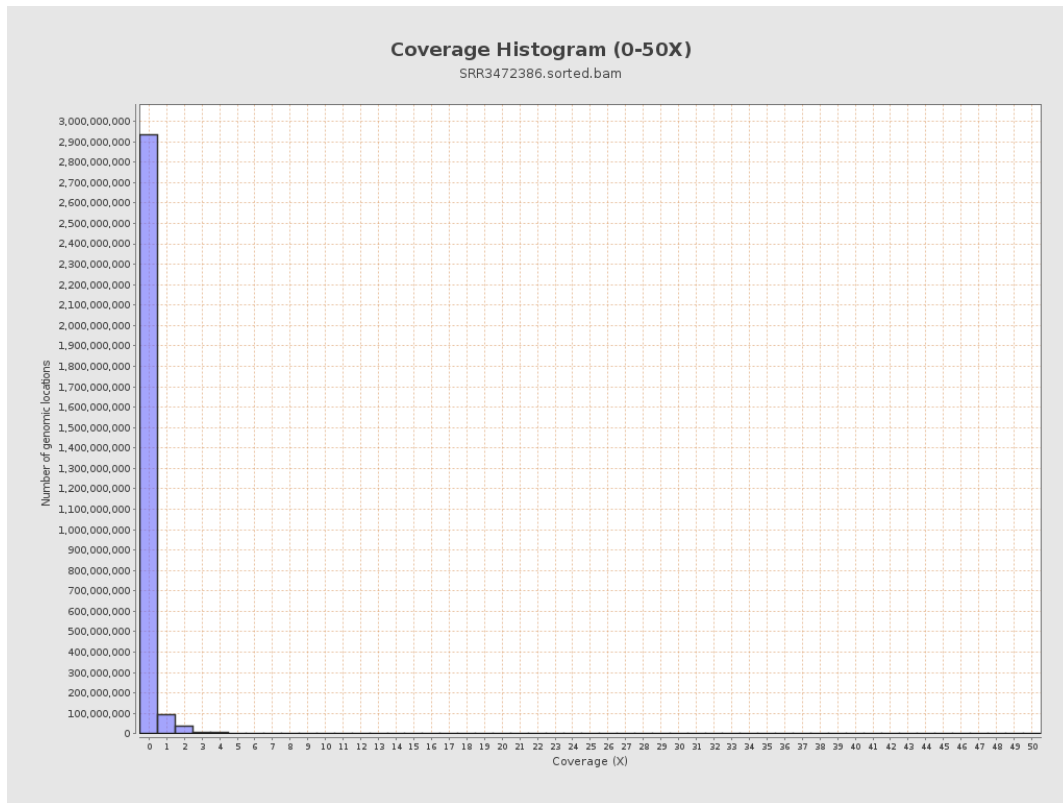
3. Results : Coverage across reference



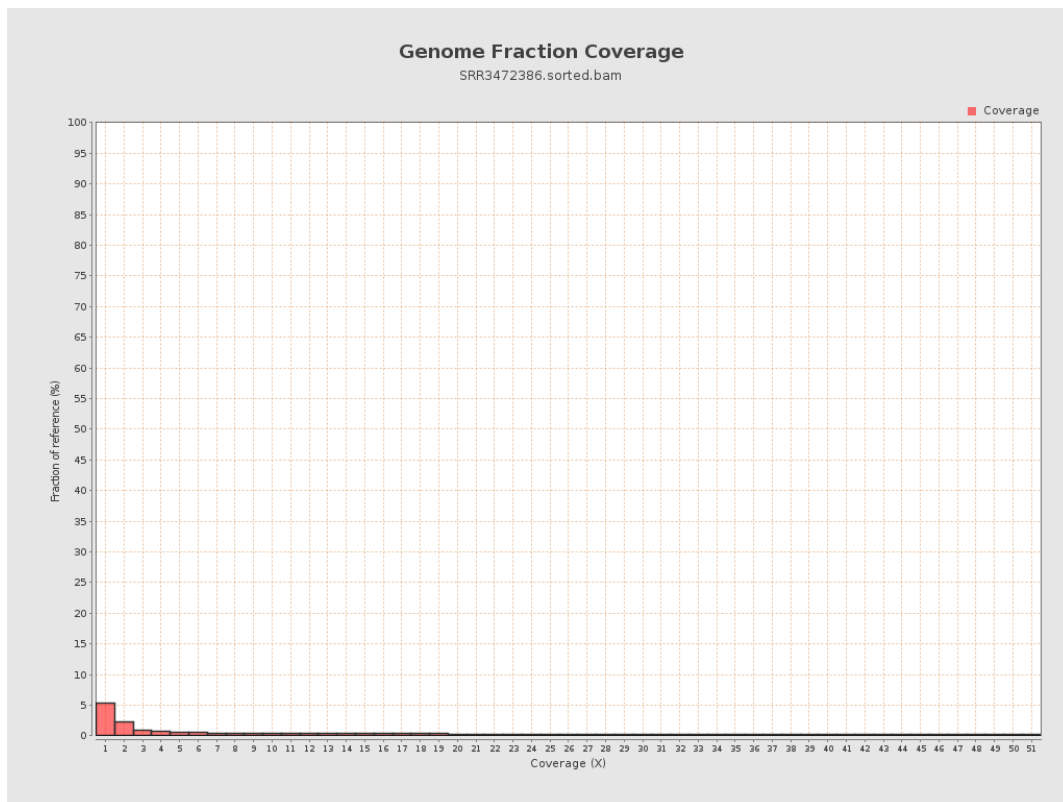
4. Results : Coverage Histogram



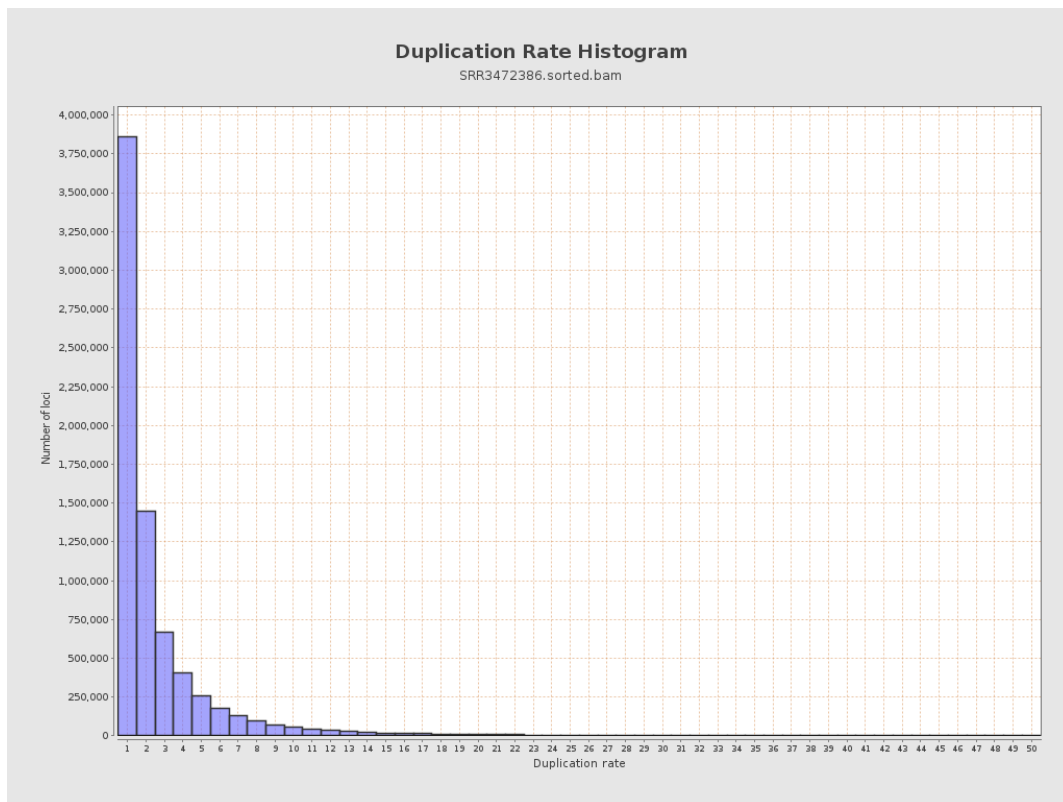
5. Results : Coverage Histogram (0-50X)



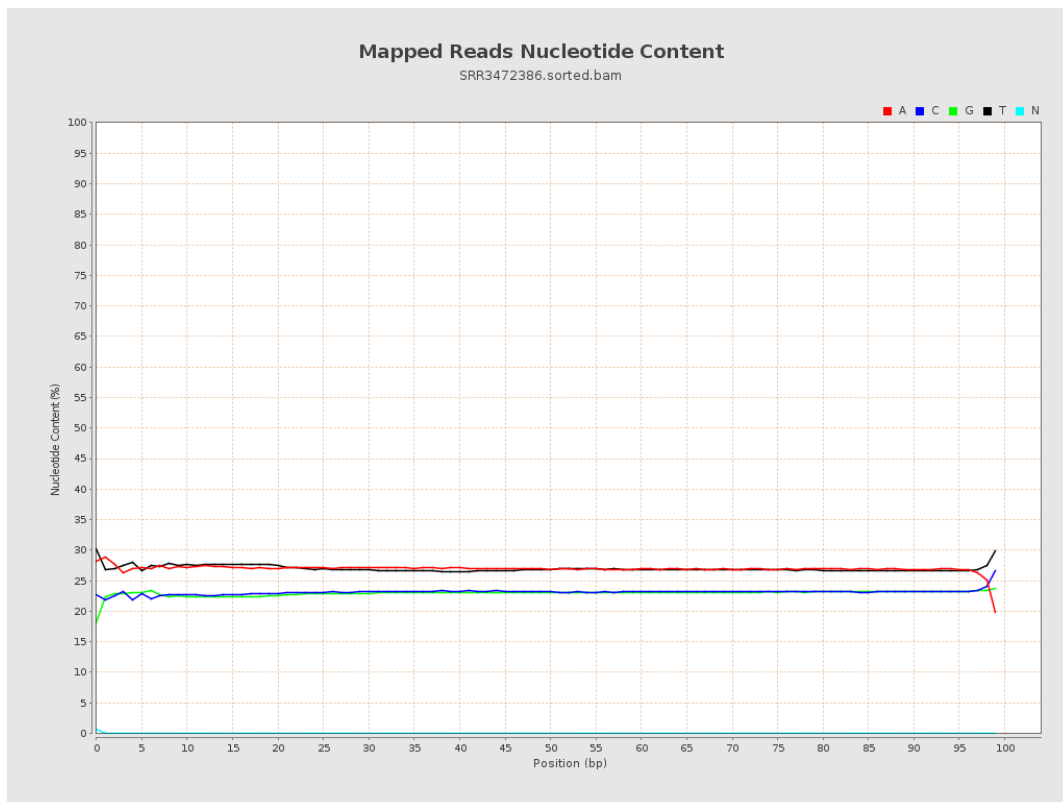
6. Results : Genome Fraction Coverage



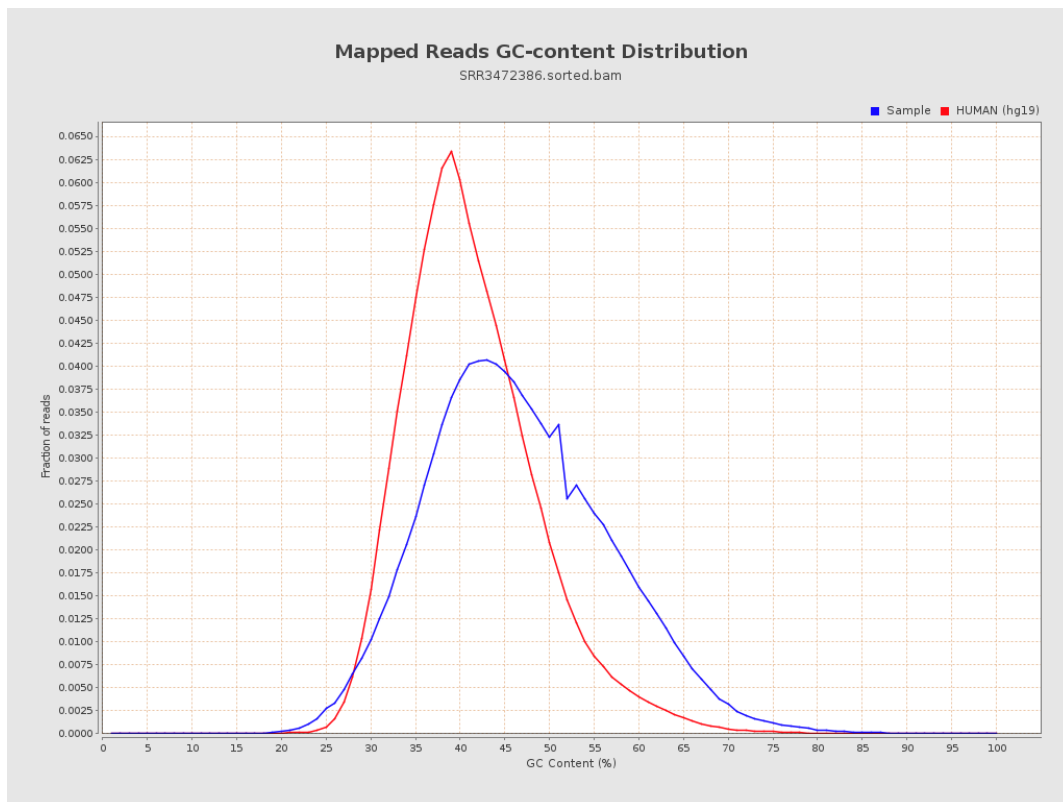
7. Results : Duplication Rate Histogram



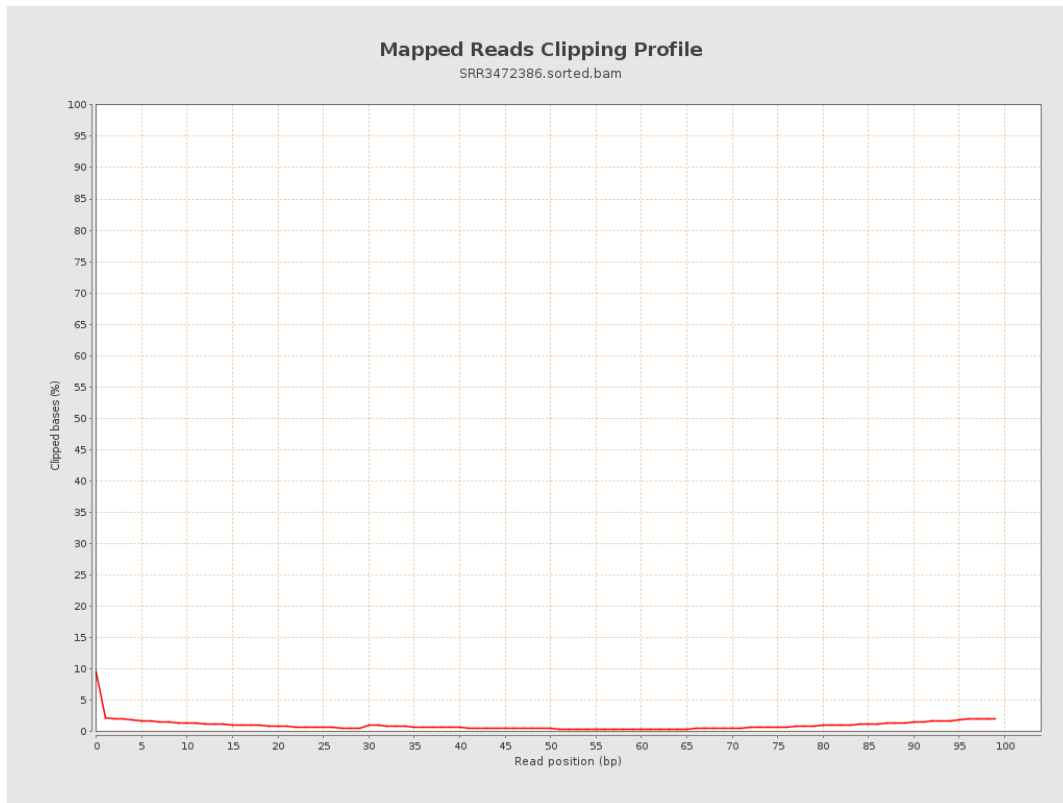
8. Results : Mapped Reads Nucleotide Content



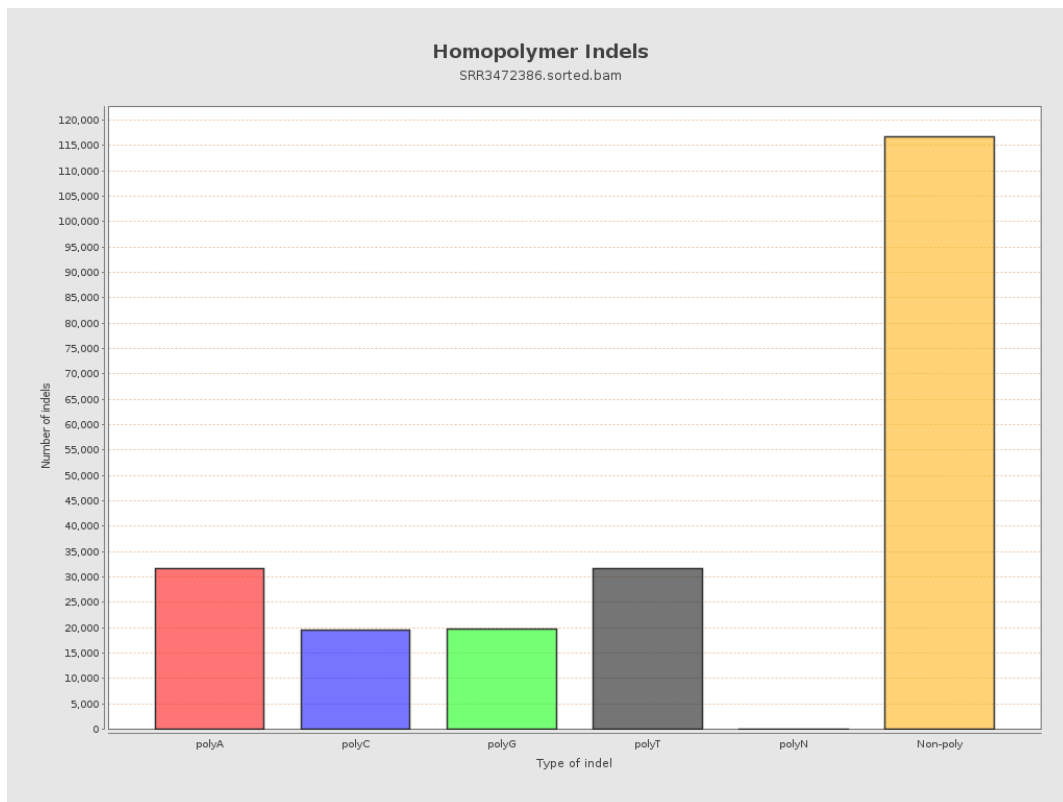
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



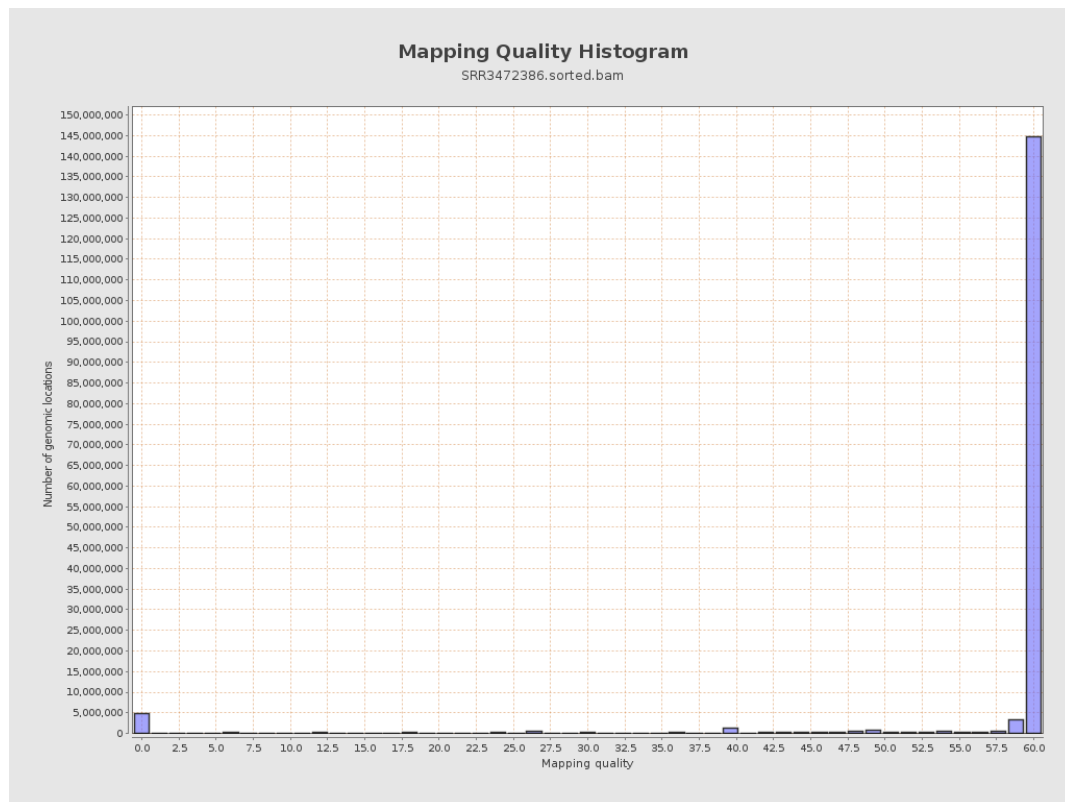
11. Results : Homopolymer Indels



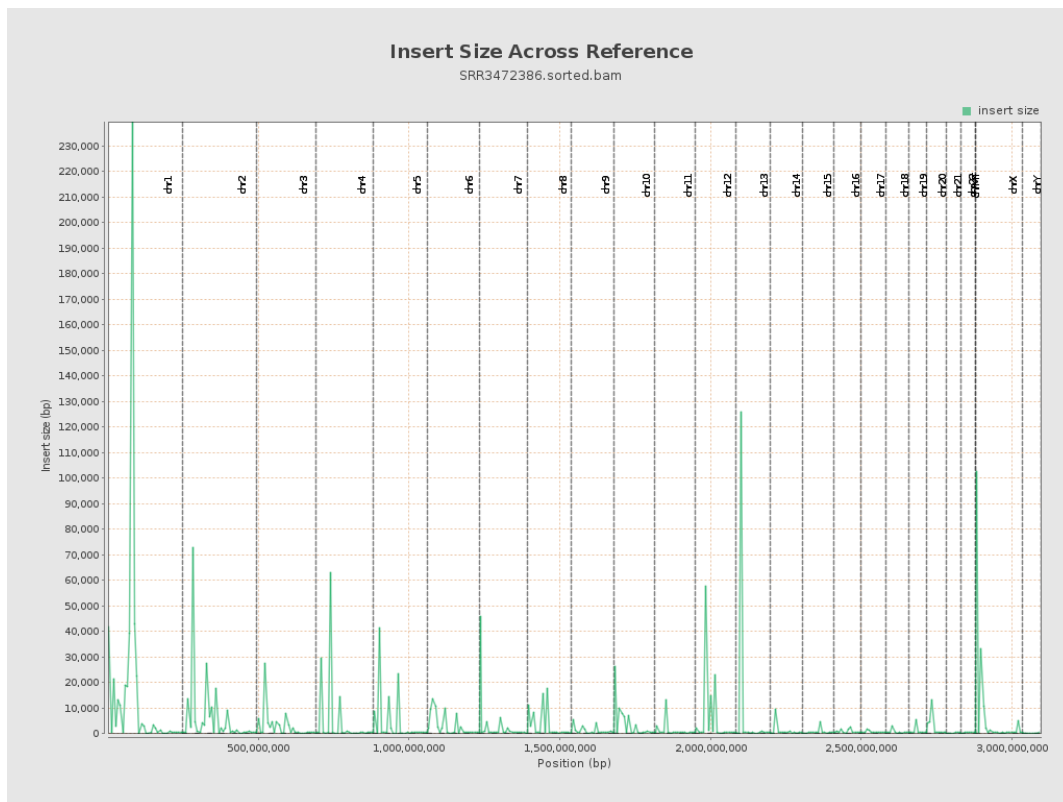
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

