

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:39:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472506.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_SRR3472506 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472506_1.fastq.gz SRR3472506_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:39:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472506.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,382,590
Mapped reads	17,120,833 / 98.49%
Unmapped reads	261,757 / 1.51%
Mapped paired reads	17,120,833 / 98.49%
Mapped reads, first in pair	8,605,884 / 49.51%
Mapped reads, second in pair	8,514,949 / 48.99%
Mapped reads, both in pair	16,977,146 / 97.67%
Mapped reads, singletons	143,687 / 0.83%
Secondary alignments	0
Supplementary alignments	69,295 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	10,760,582 / 61.9%
Duplication rate	45.57%
Clipped reads	1,355,224 / 7.8%

2.2. ACGT Content

Number/percentage of A's	469,582,077 / 27.84%
Number/percentage of C's	376,326,825 / 22.31%
Number/percentage of T's	466,217,894 / 27.64%
Number/percentage of G's	374,063,065 / 22.18%
Number/percentage of N's	258,828 / 0.02%

GC Percentage	44.5%
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2.3. Coverage

Mean	0.5448
Standard Deviation	18.9698

2.4. Mapping Quality

Mean Mapping Quality	54.98
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2.5. Insert size

Mean	30,396.6
Standard Deviation	1,670,269.71
P25/Median/P75	176 / 246 / 334

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	11,129,284
Insertions	91,815
Mapped reads with at least one insertion	0.53%
Deletions	89,957
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.59%

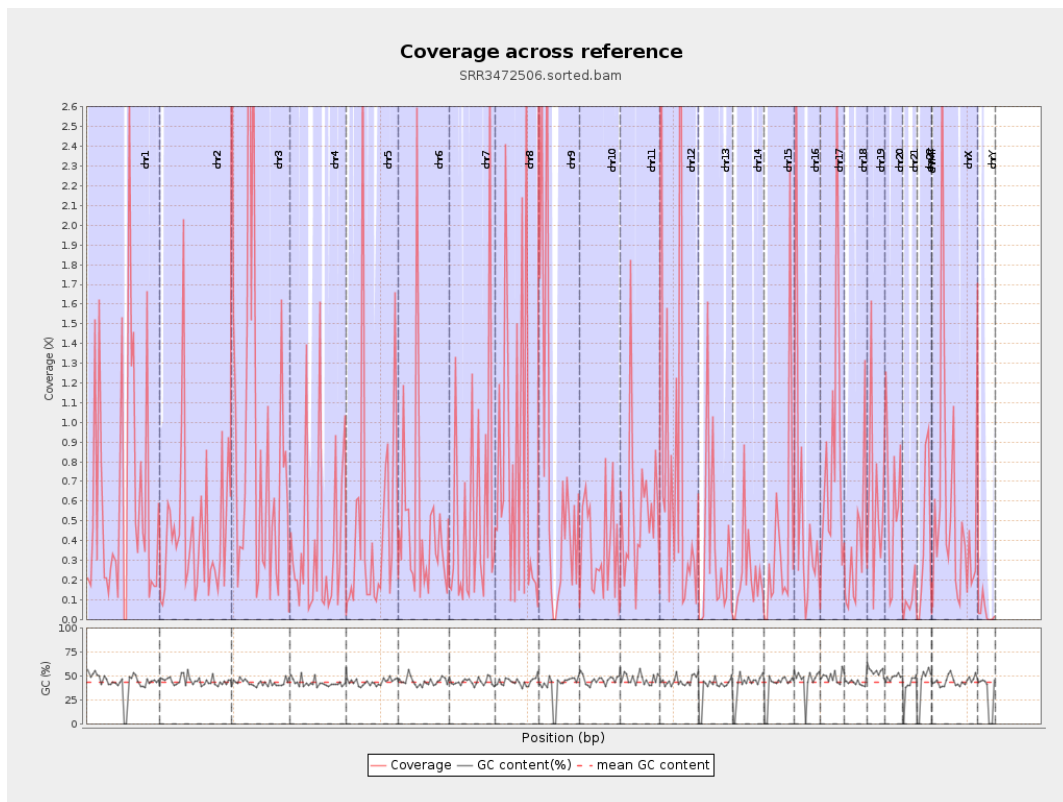
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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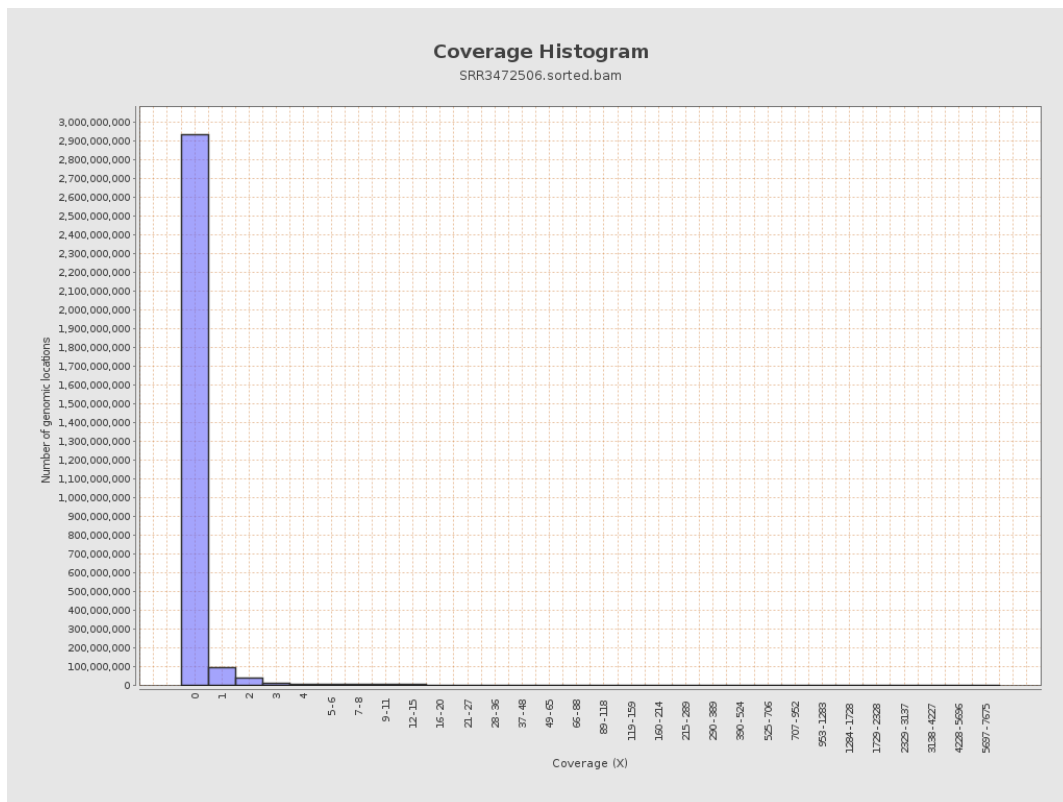
		bases	coverage	deviation
chr1	249250621	153113947	0.6143	18.3405
chr2	243199373	108749303	0.4472	17.9288
chr3	198022430	184609368	0.9323	20.225
chr4	191154276	71729715	0.3752	13.5369
chr5	180915260	89200137	0.493	18.0126
chr6	171115067	80606947	0.4711	13.3915
chr7	159138663	86303896	0.5423	23.4089
chr8	146364022	115138455	0.7867	31.6468
chr9	141213431	106558879	0.7546	21.7957
chr10	135534747	50667725	0.3738	13.4043
chr11	135006516	76409426	0.566	18.0003
chr12	133851895	122624014	0.9161	32.1489
chr13	115169878	41412515	0.3596	14.5218
chr14	107349540	23793527	0.2216	7.1275
chr15	102531392	43309132	0.4224	14.5696
chr16	90354753	49815275	0.5513	18.2674
chr17	81195210	66126761	0.8144	17.7498
chr18	78077248	27884292	0.3571	13.3862
chr19	59128983	36765768	0.6218	17.8215
chr20	63025520	38474999	0.6105	26.049
chr21	48129895	4983422	0.1035	3.5082
chr22	51304566	19423689	0.3786	12.1287
chrMT	16571	3136	0.1892	0.7241
chrX	155270560	86733837	0.5586	17.5989

chrY	59373566	2235312	0.0376	1.4105
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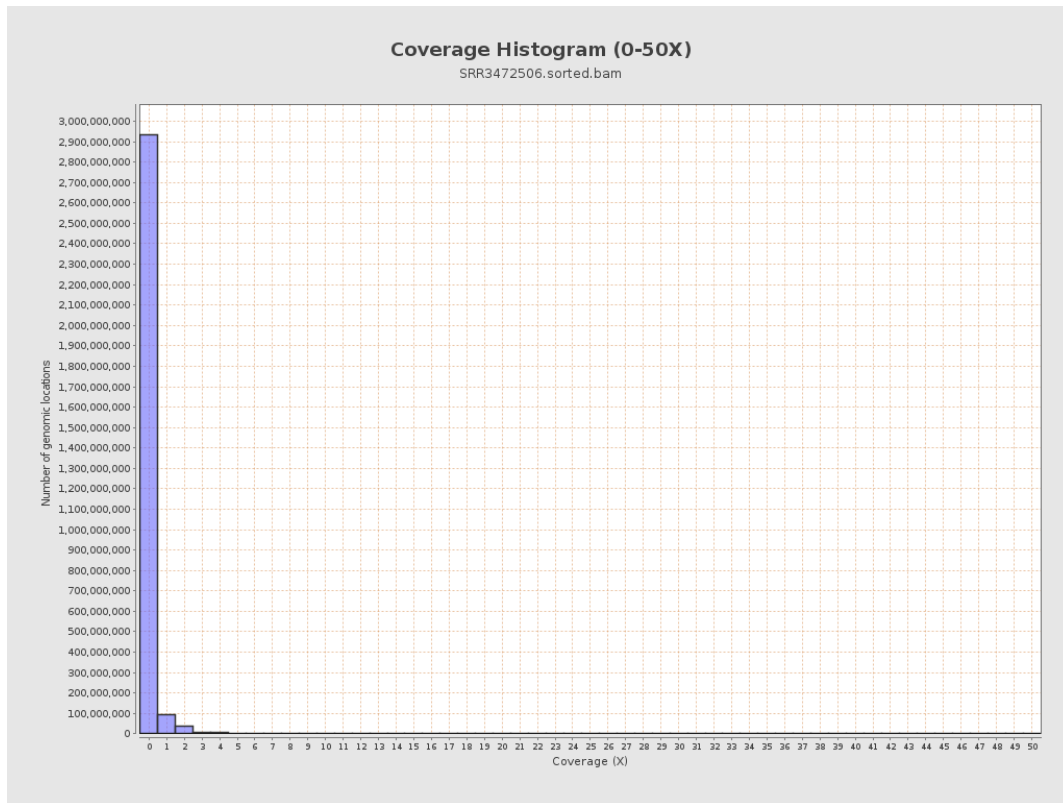
3. Results : Coverage across reference



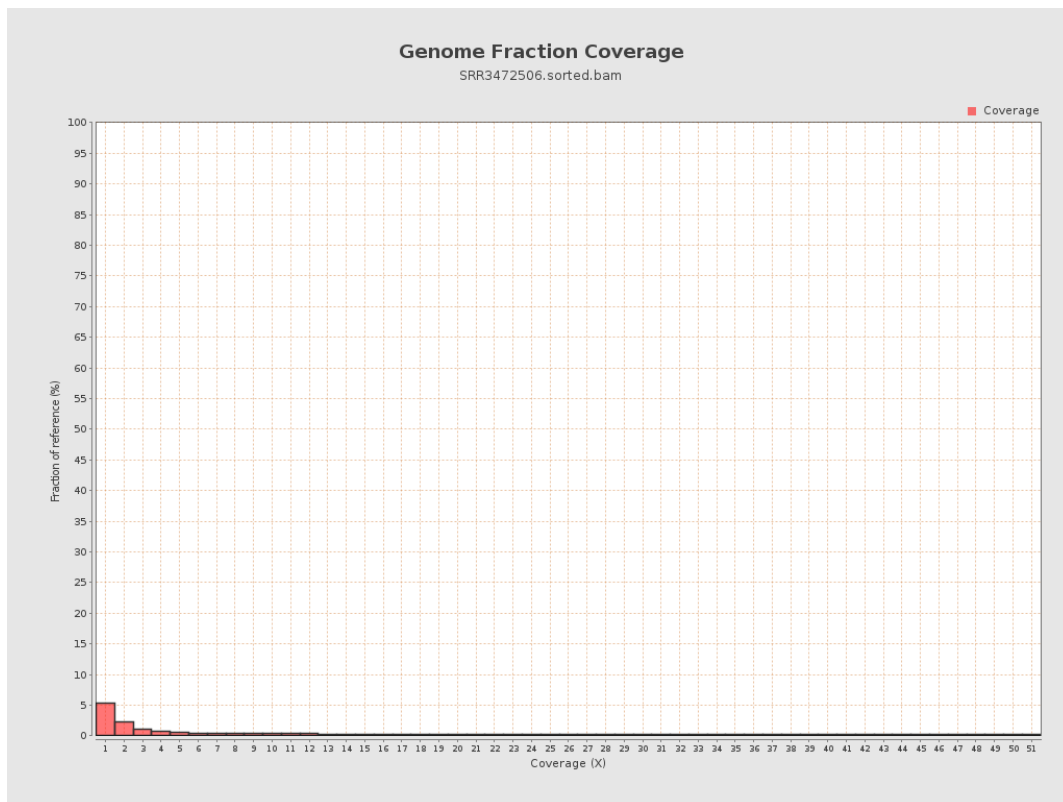
4. Results : Coverage Histogram



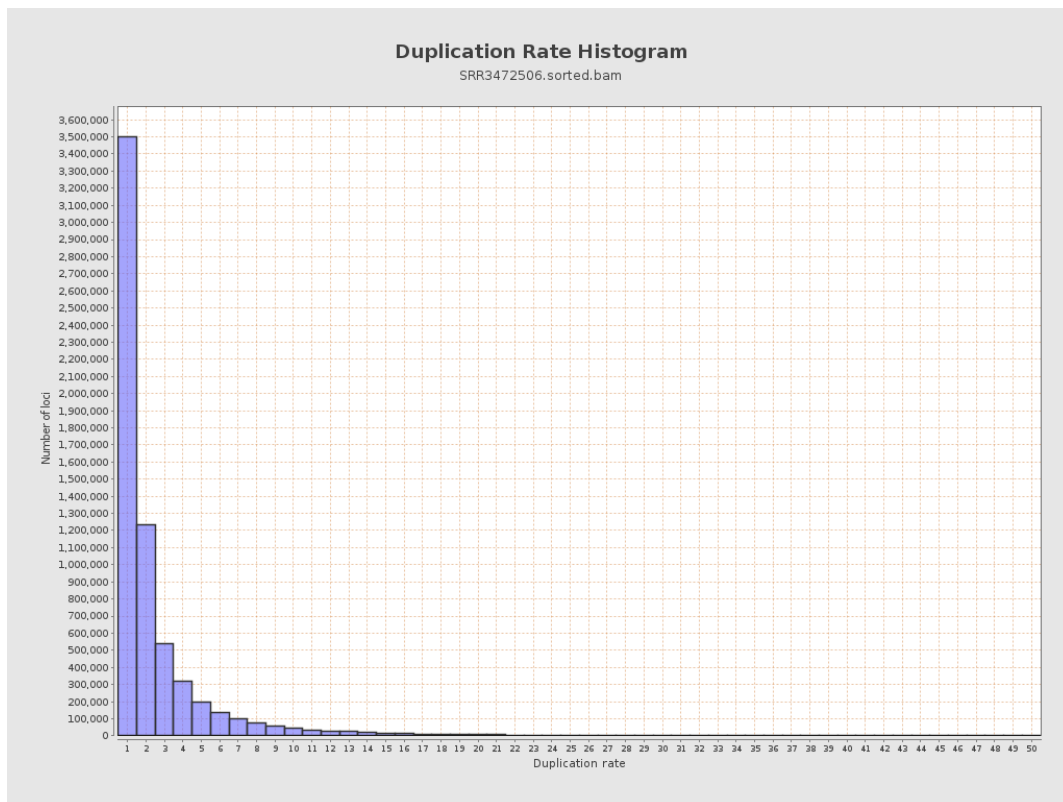
5. Results : Coverage Histogram (0-50X)



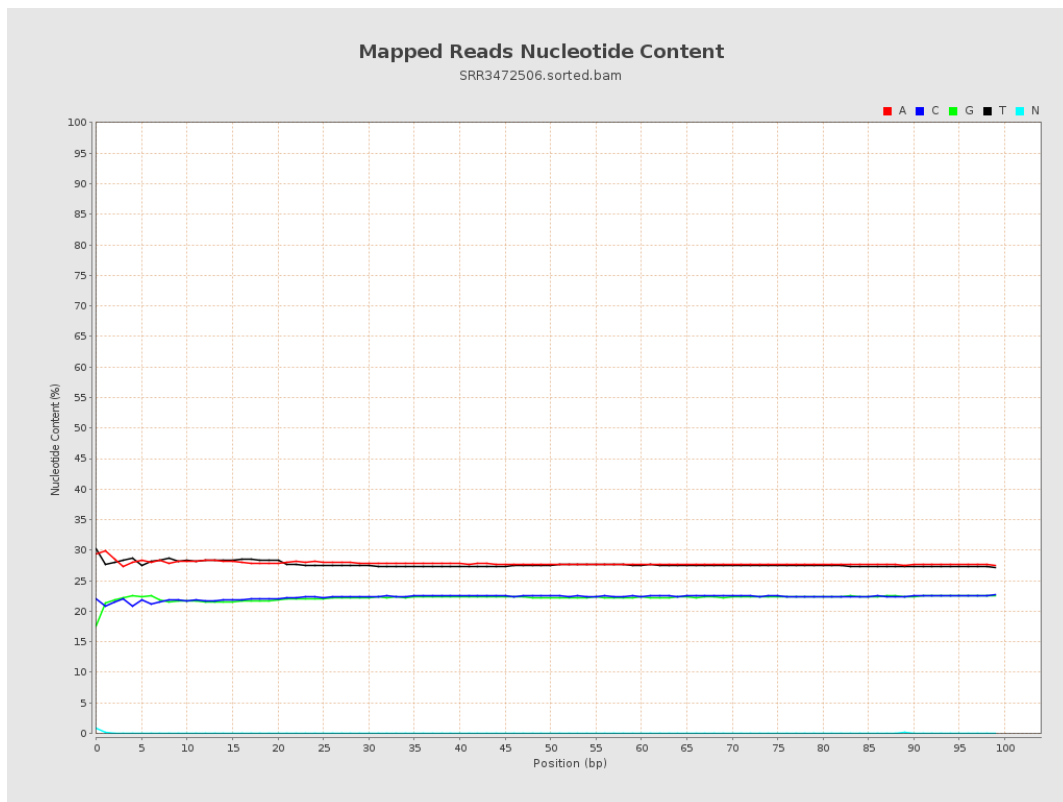
6. Results : Genome Fraction Coverage



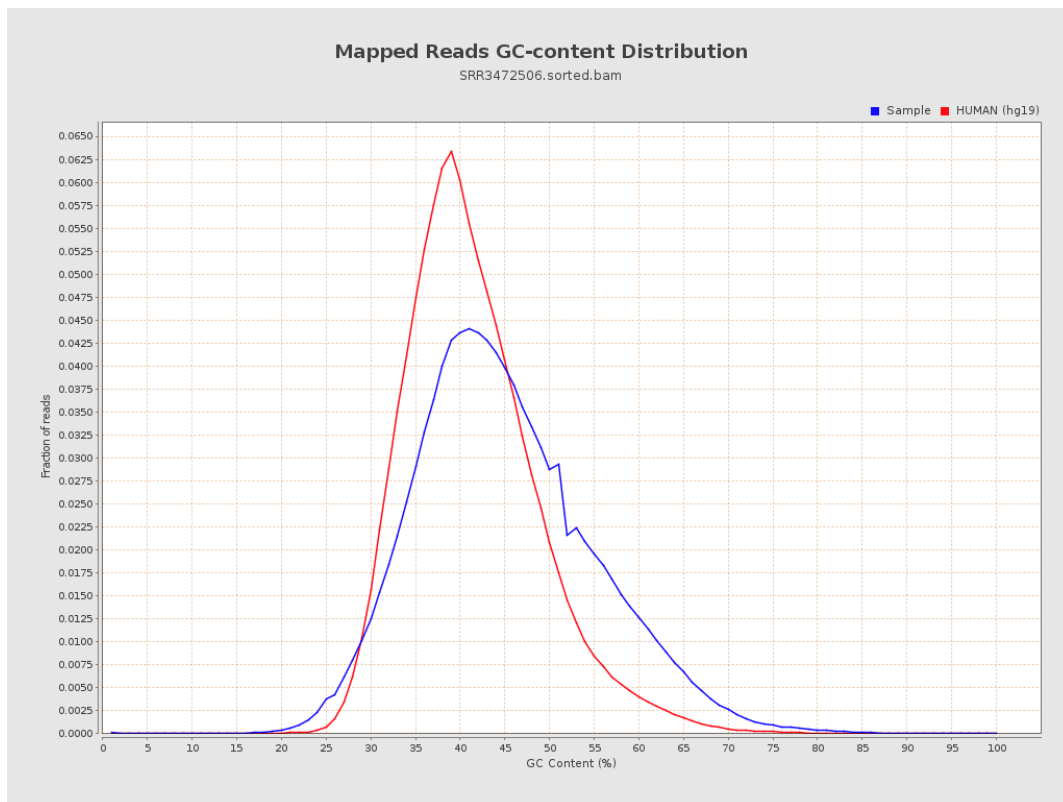
7. Results : Duplication Rate Histogram



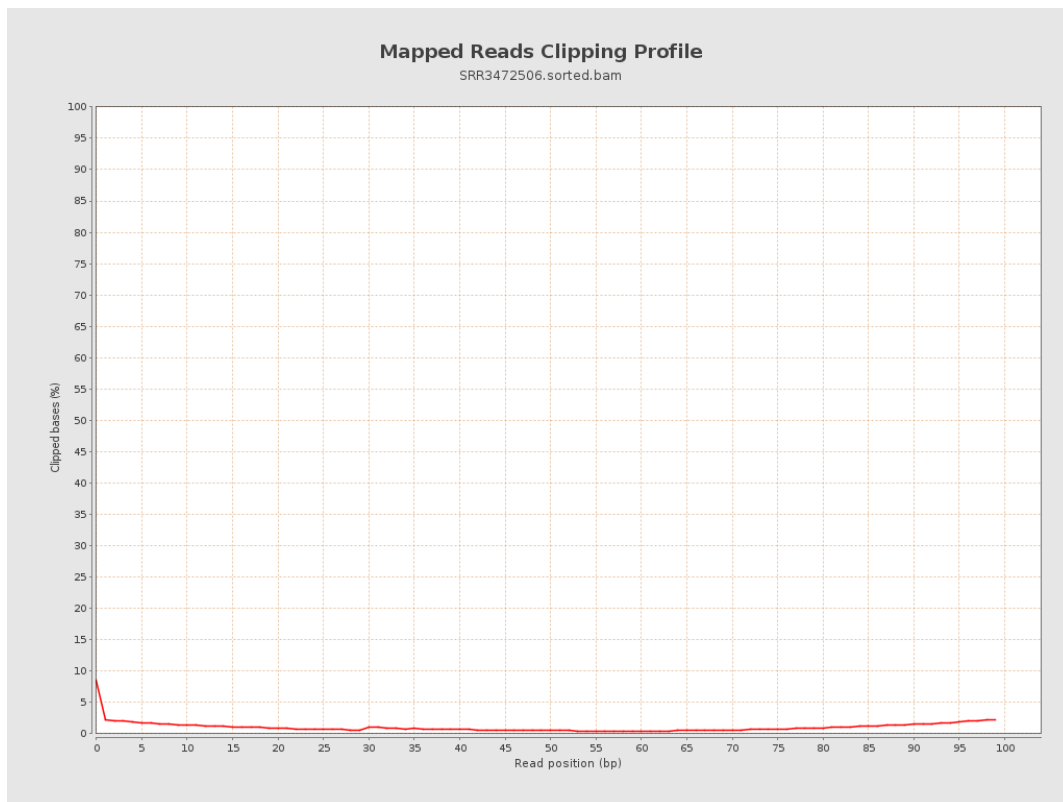
8. Results : Mapped Reads Nucleotide Content



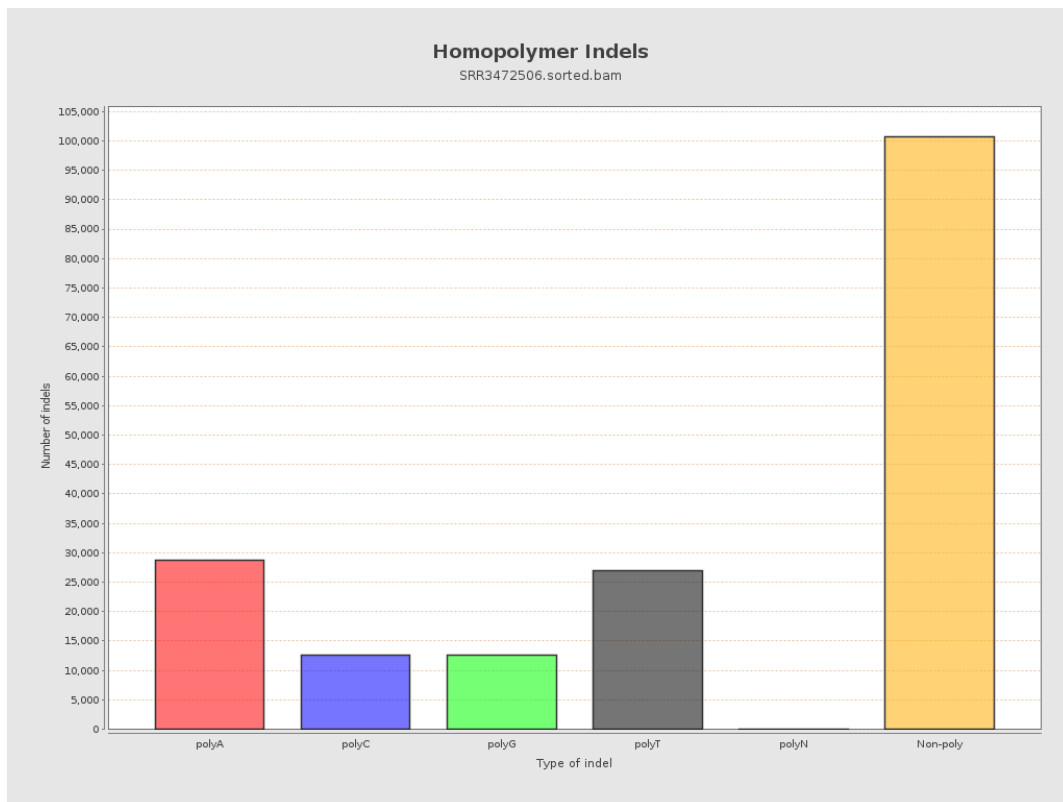
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



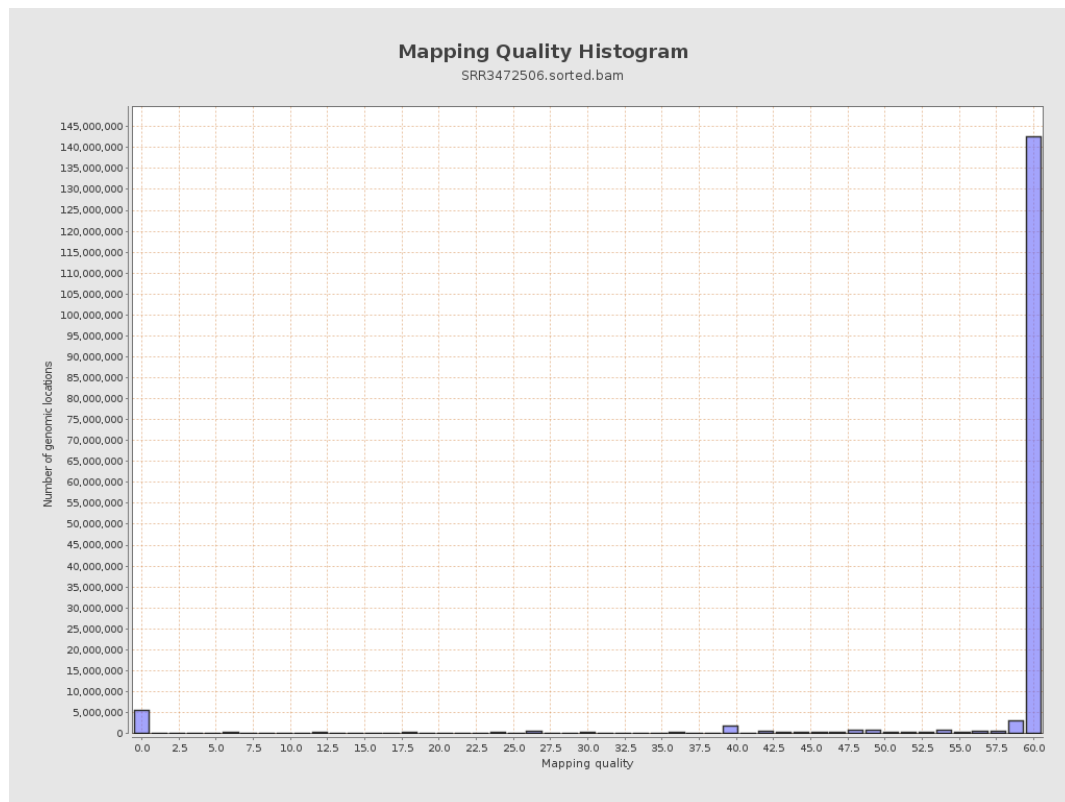
11. Results : Homopolymer Indels



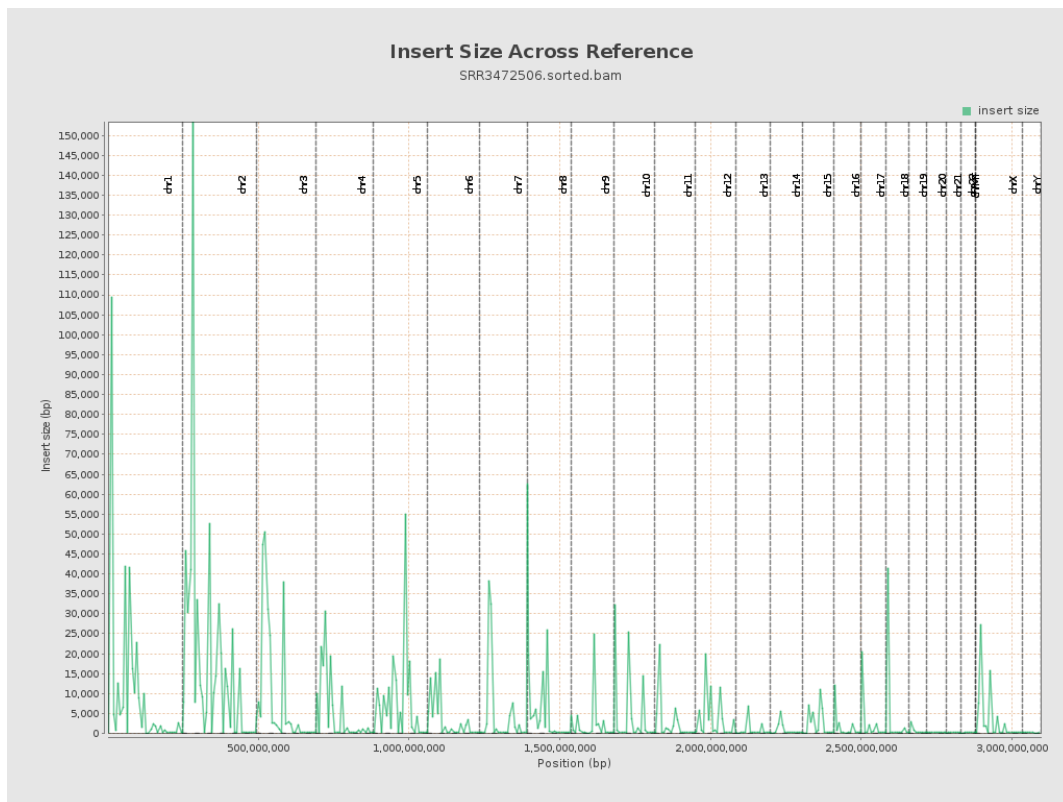
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

