

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:51:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472536.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_SRR3472536 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472536_1.fastq.gz SRR3472536_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:51:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472536.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,741,172
Mapped reads	18,491,038 / 98.67%
Unmapped reads	250,134 / 1.33%
Mapped paired reads	18,491,038 / 98.67%
Mapped reads, first in pair	9,273,791 / 49.48%
Mapped reads, second in pair	9,217,247 / 49.18%
Mapped reads, both in pair	18,366,748 / 98%
Mapped reads, singletons	124,290 / 0.66%
Secondary alignments	0
Supplementary alignments	66,834 / 0.36%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	12,098,015 / 64.55%
Duplication rate	45.53%
Clipped reads	1,437,976 / 7.67%

2.2. ACGT Content

Number/percentage of A's	509,115,410 / 27.97%
Number/percentage of C's	404,032,488 / 22.19%
Number/percentage of T's	506,116,102 / 27.8%
Number/percentage of G's	400,881,364 / 22.02%
Number/percentage of N's	280,030 / 0.02%

GC Percentage	44.22%
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2.3. Coverage

Mean	0.5881
Standard Deviation	22.8472

2.4. Mapping Quality

Mean Mapping Quality	54.77
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2.5. Insert size

Mean	23,800.54
Standard Deviation	1,490,673.19
P25/Median/P75	175 / 243 / 326

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	10,992,276
Insertions	95,472
Mapped reads with at least one insertion	0.51%
Deletions	90,634
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.52%

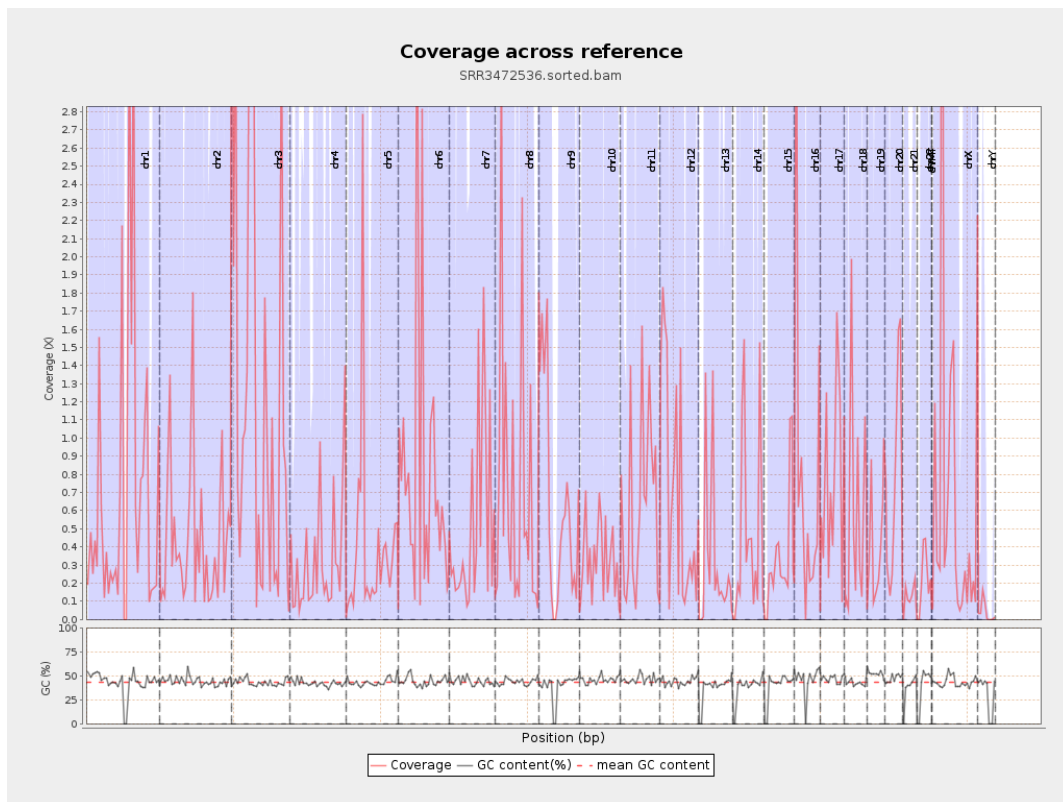
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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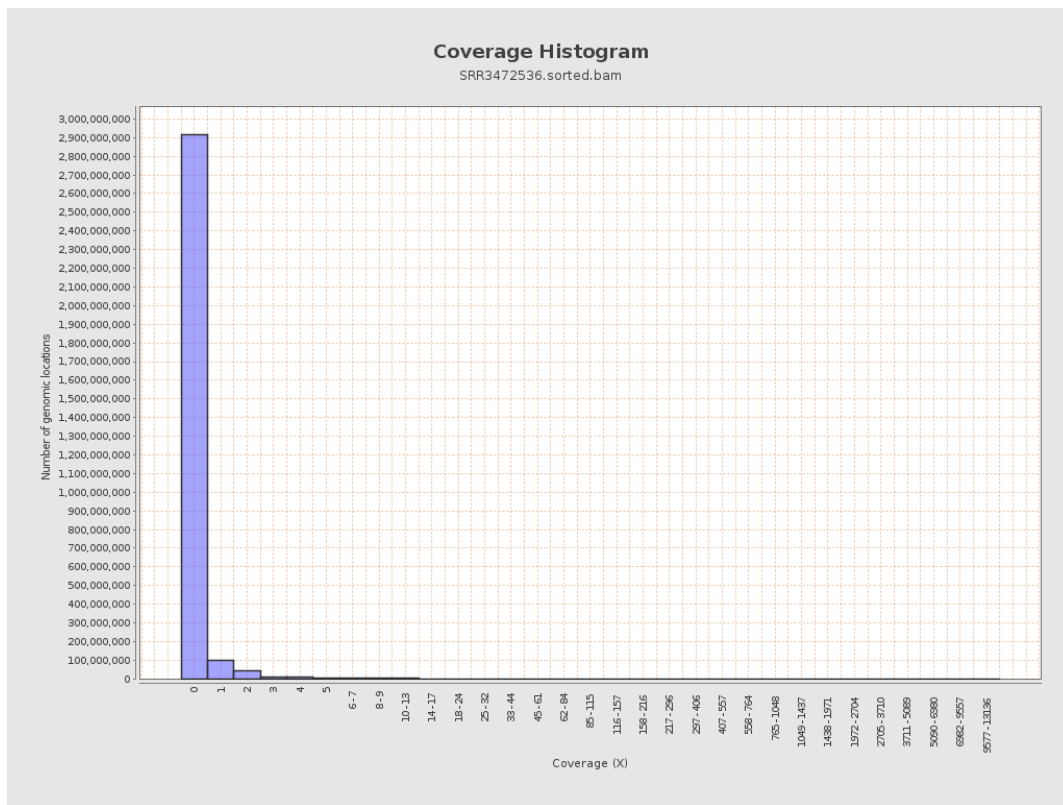
		bases	coverage	deviation
chr1	249250621	180635723	0.7247	24.7927
chr2	243199373	106332252	0.4372	18.5899
chr3	198022430	258811912	1.307	39.0688
chr4	191154276	60754492	0.3178	11.2998
chr5	180915260	71921157	0.3975	13.3043
chr6	171115067	139507603	0.8153	28.0327
chr7	159138663	82174077	0.5164	21.4616
chr8	146364022	106064467	0.7247	36.218
chr9	141213431	87061249	0.6165	16.8384
chr10	135534747	44995920	0.332	14.1978
chr11	135006516	86849805	0.6433	22.1336
chr12	133851895	96243658	0.719	28.9333
chr13	115169878	36347844	0.3156	12.6519
chr14	107349540	49310364	0.4593	17.6803
chr15	102531392	36685522	0.3578	11.7544
chr16	90354753	71151010	0.7875	24.1834
chr17	81195210	61693888	0.7598	24.3858
chr18	78077248	45449383	0.5821	30.8872
chr19	59128983	23154664	0.3916	8.972
chr20	63025520	47925793	0.7604	25.5286
chr21	48129895	6108758	0.1269	5.197
chr22	51304566	11162424	0.2176	5.3526
chrMT	16571	3620	0.2185	0.6307
chrX	155270560	107722252	0.6938	23.2599

chrY	59373566	2585362	0.0435	1.1983
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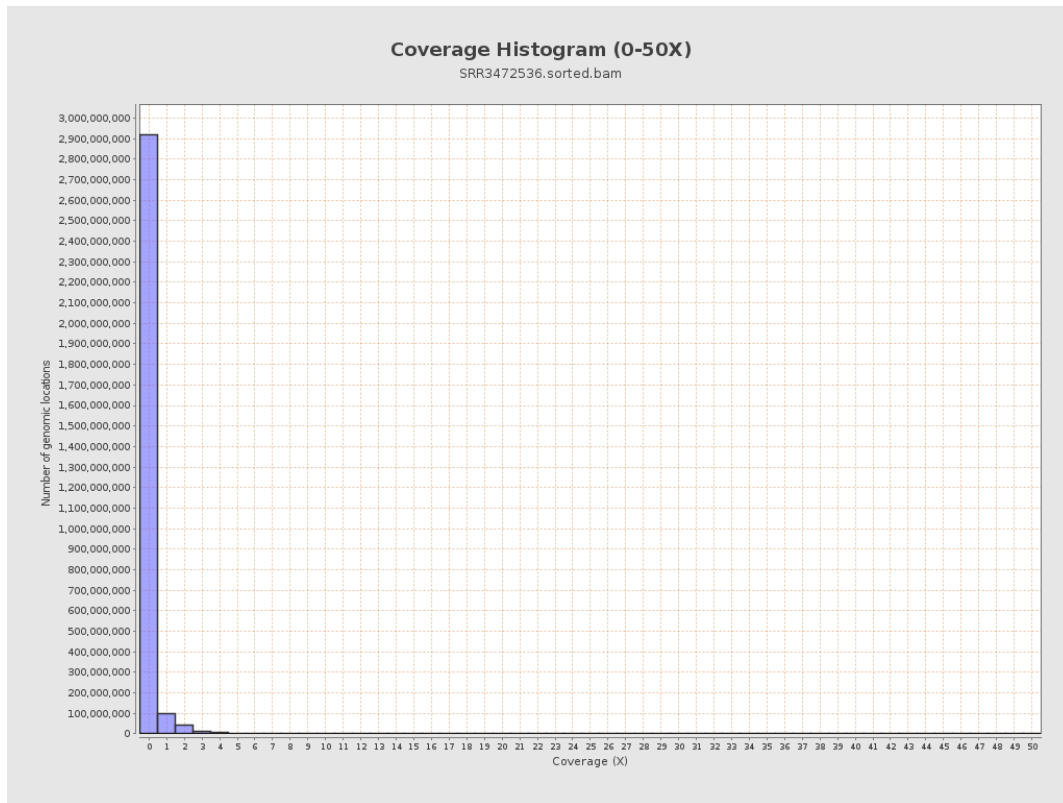
3. Results : Coverage across reference



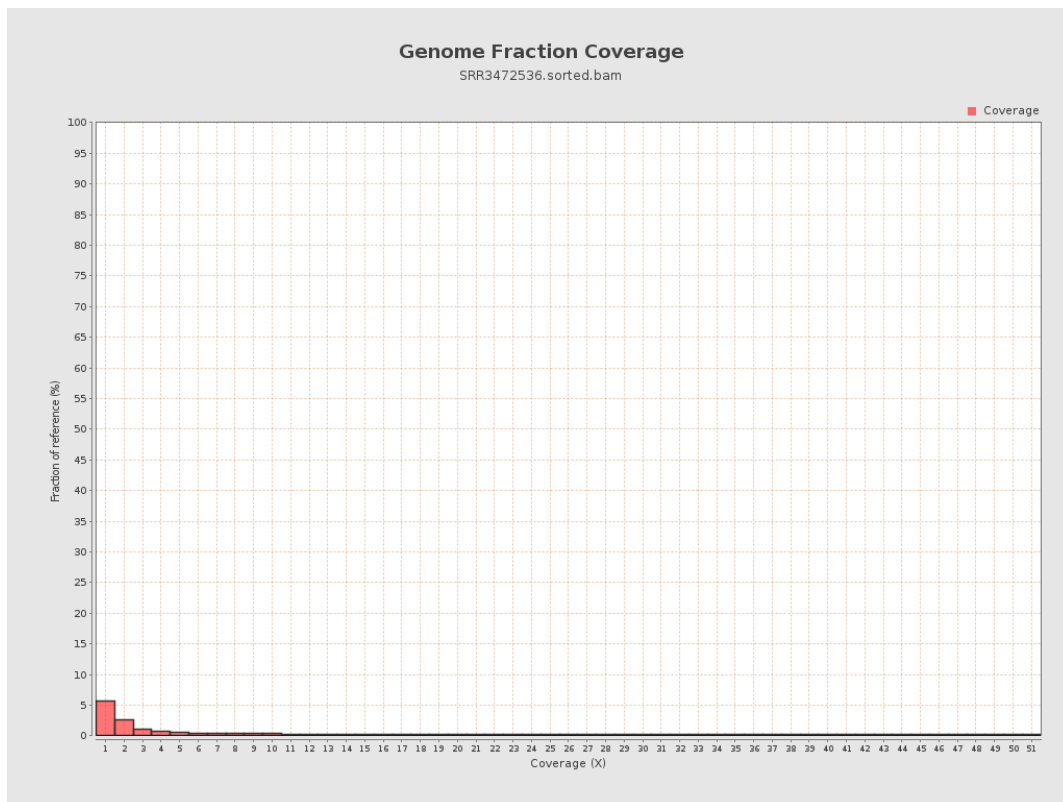
4. Results : Coverage Histogram



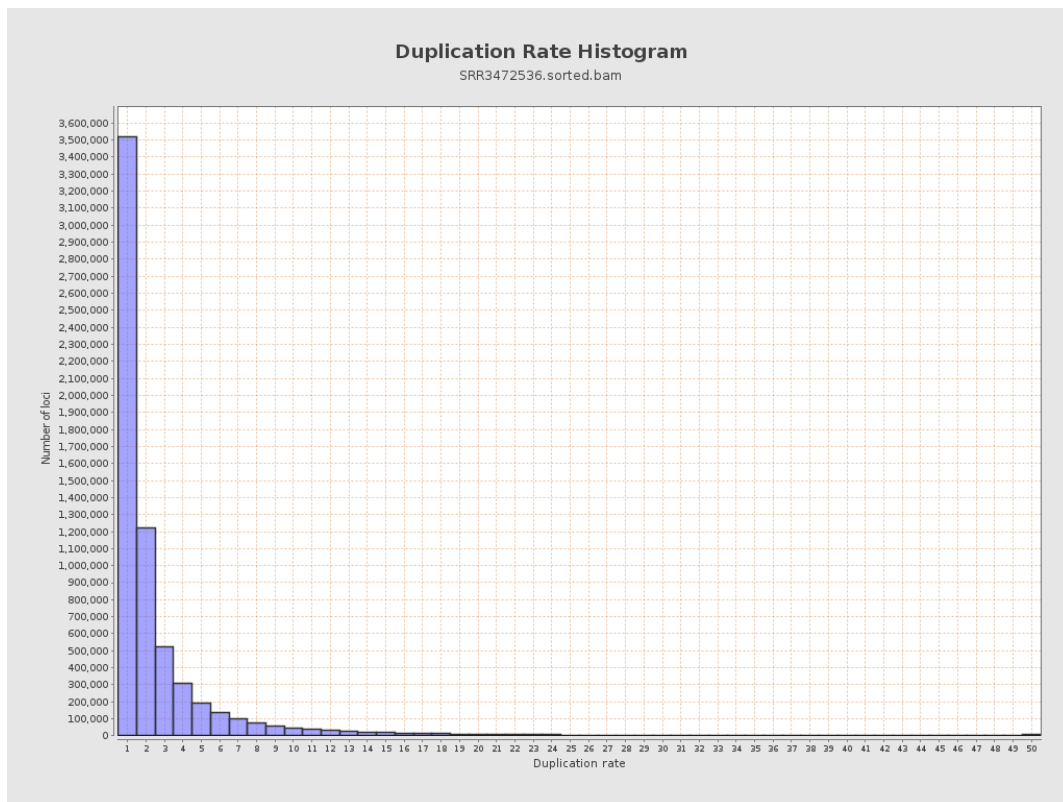
5. Results : Coverage Histogram (0-50X)



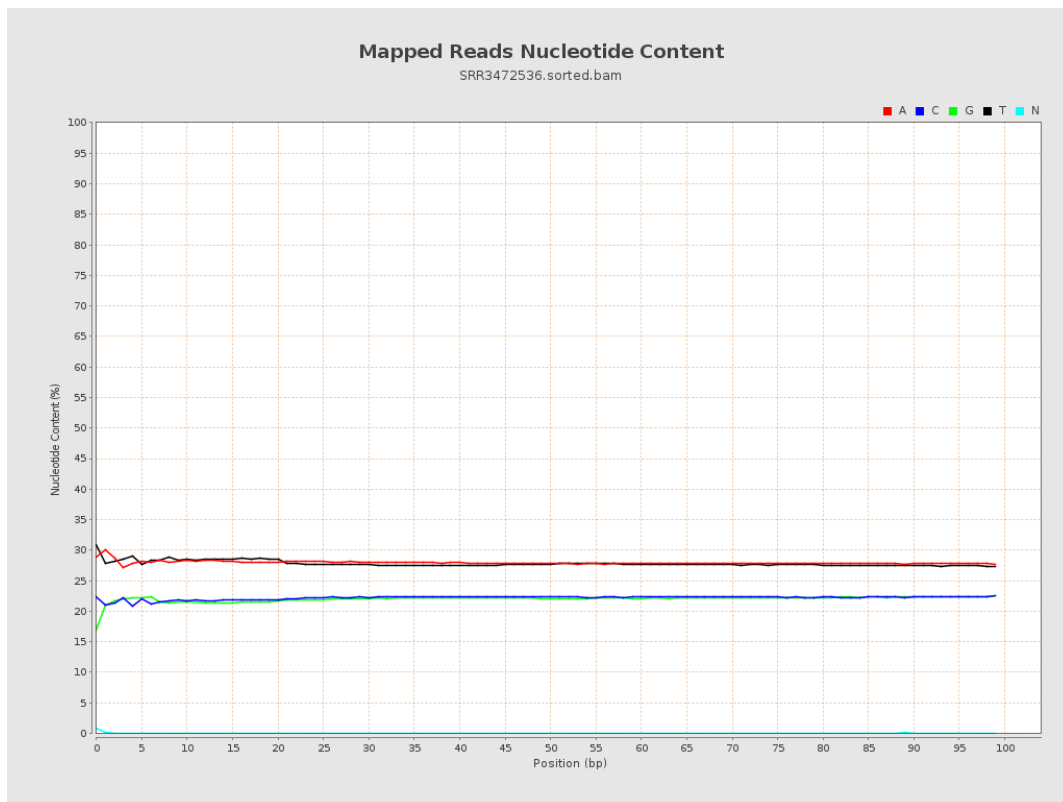
6. Results : Genome Fraction Coverage



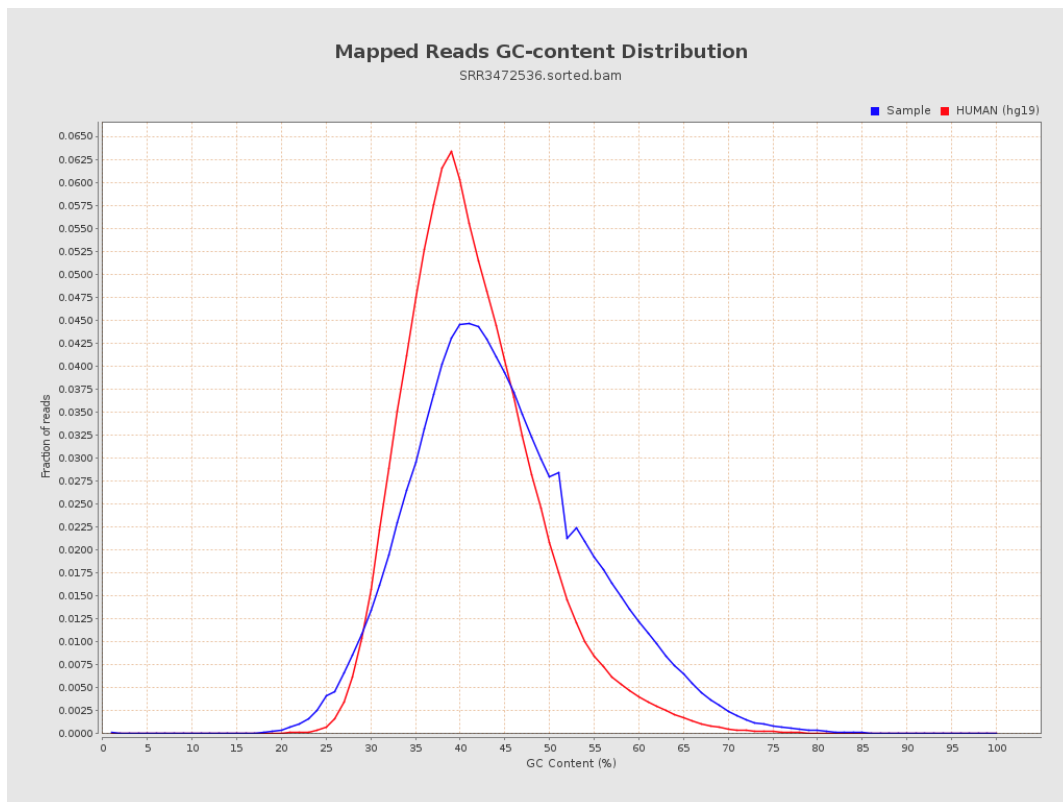
7. Results : Duplication Rate Histogram



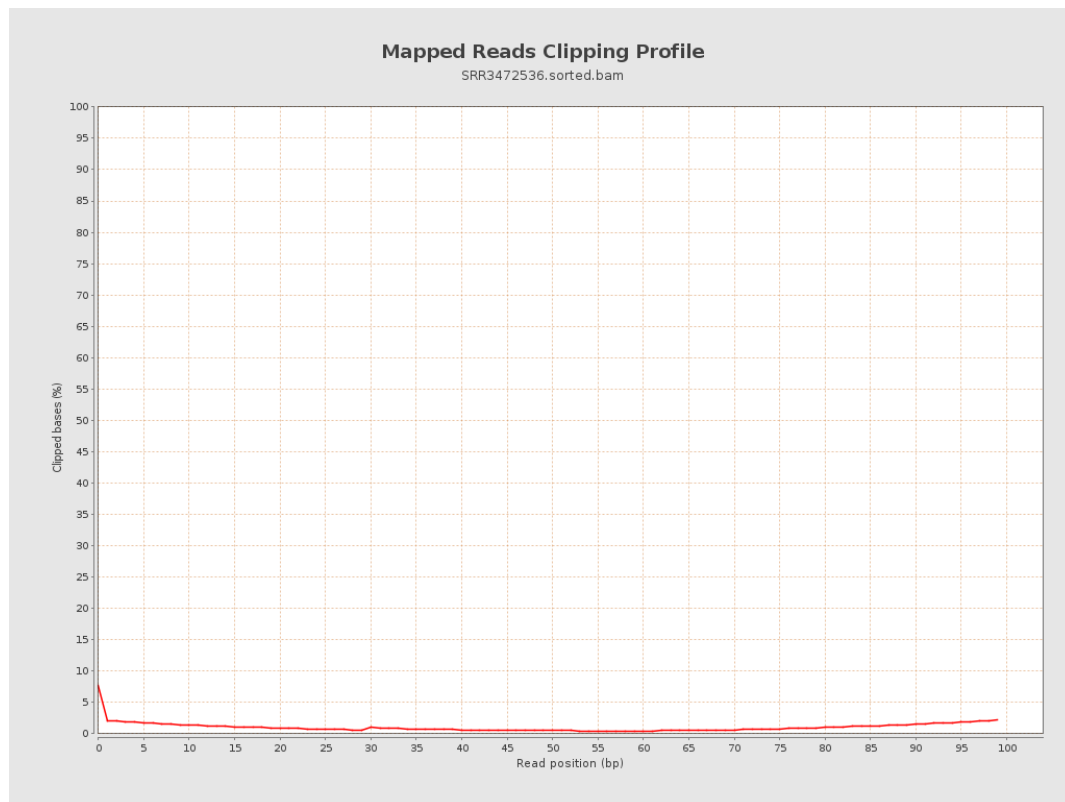
8. Results : Mapped Reads Nucleotide Content



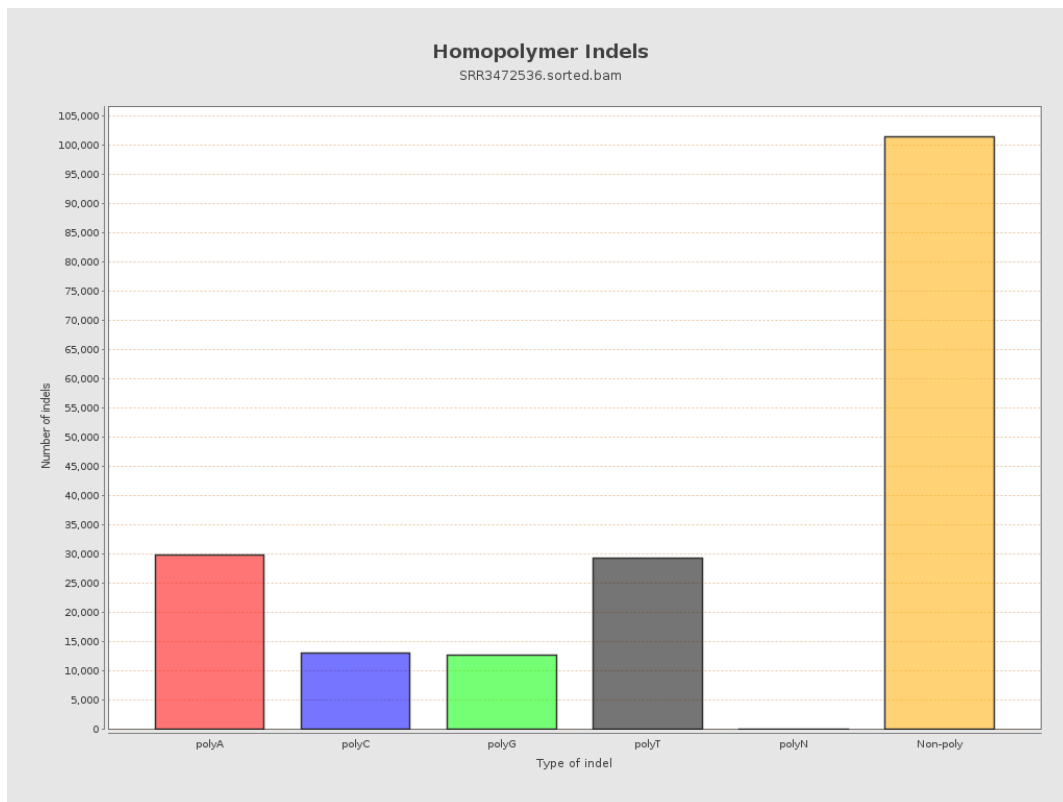
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



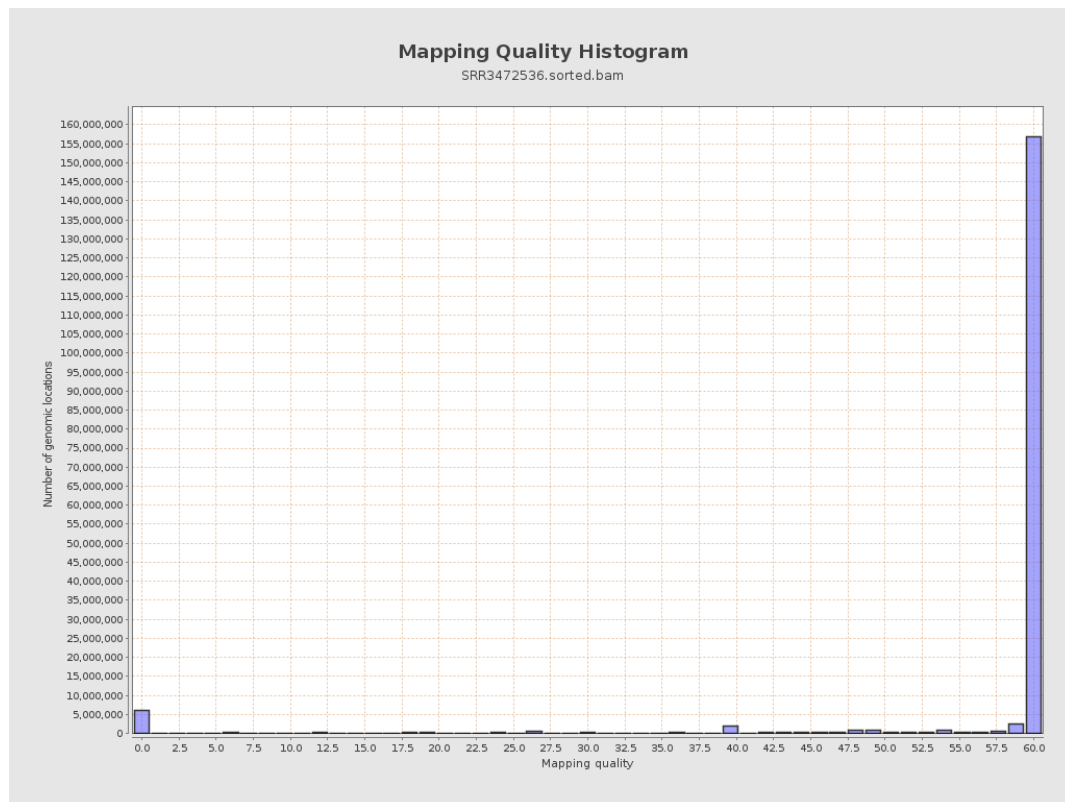
11. Results : Homopolymer Indels



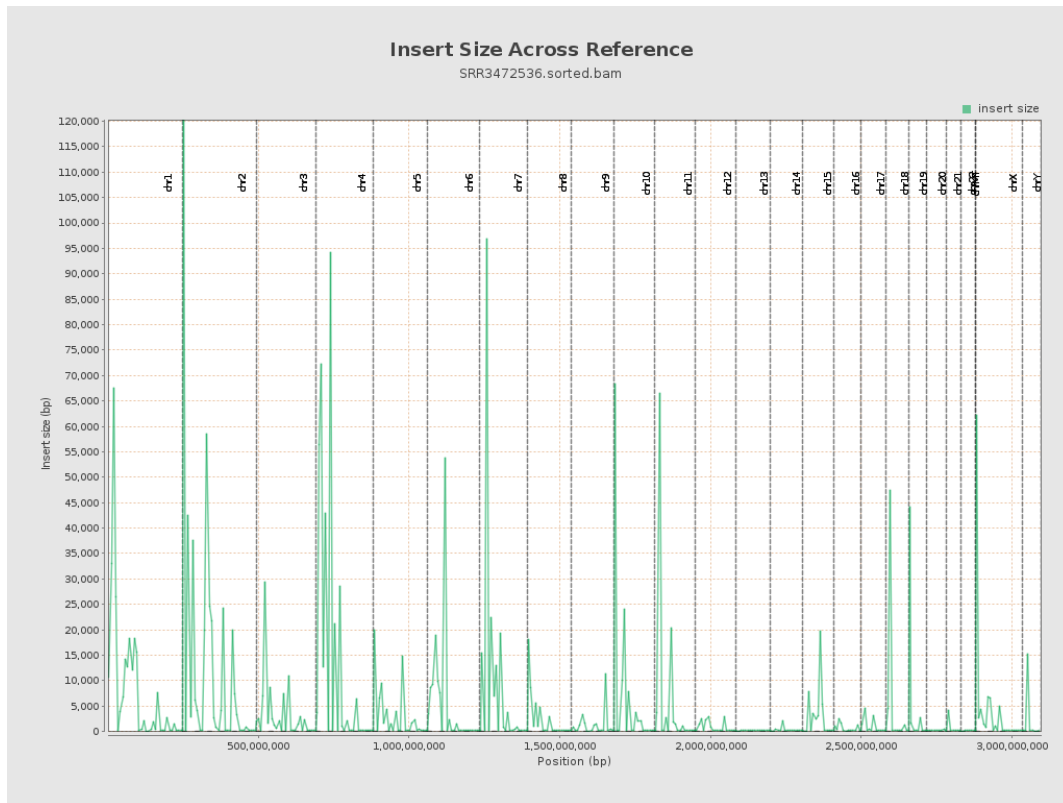
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

