

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 21:02:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046536.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_SRR2046536 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046536_1.fastq.gz SRR2046536_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 21:02:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046536.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,327,296
Mapped reads	10,135,817 / 98.15%
Unmapped reads	191,479 / 1.85%
Mapped paired reads	10,135,817 / 98.15%
Mapped reads, first in pair	5,153,649 / 49.9%
Mapped reads, second in pair	4,982,168 / 48.24%
Mapped reads, both in pair	9,956,880 / 96.41%
Mapped reads, singletons	178,937 / 1.73%
Secondary alignments	0
Supplementary alignments	47,496 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	6,649,288 / 64.39%
Duplication rate	33.25%
Clipped reads	1,077,294 / 10.43%

2.2. ACGT Content

Number/percentage of A's	290,140,562 / 29.13%
Number/percentage of C's	208,311,861 / 20.92%
Number/percentage of T's	290,786,353 / 29.2%
Number/percentage of G's	206,562,485 / 20.74%
Number/percentage of N's	94,890 / 0.01%

GC Percentage	41.66%
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2.3. Coverage

Mean	0.3218
Standard Deviation	19.4812

2.4. Mapping Quality

Mean Mapping Quality	53.73
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2.5. Insert size

Mean	29,635.84
Standard Deviation	1,732,062.25
P25/Median/P75	129 / 162 / 200

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	4,356,365
Insertions	87,440
Mapped reads with at least one insertion	0.84%
Deletions	95,677
Mapped reads with at least one deletion	0.92%
Homopolymer indels	48.49%

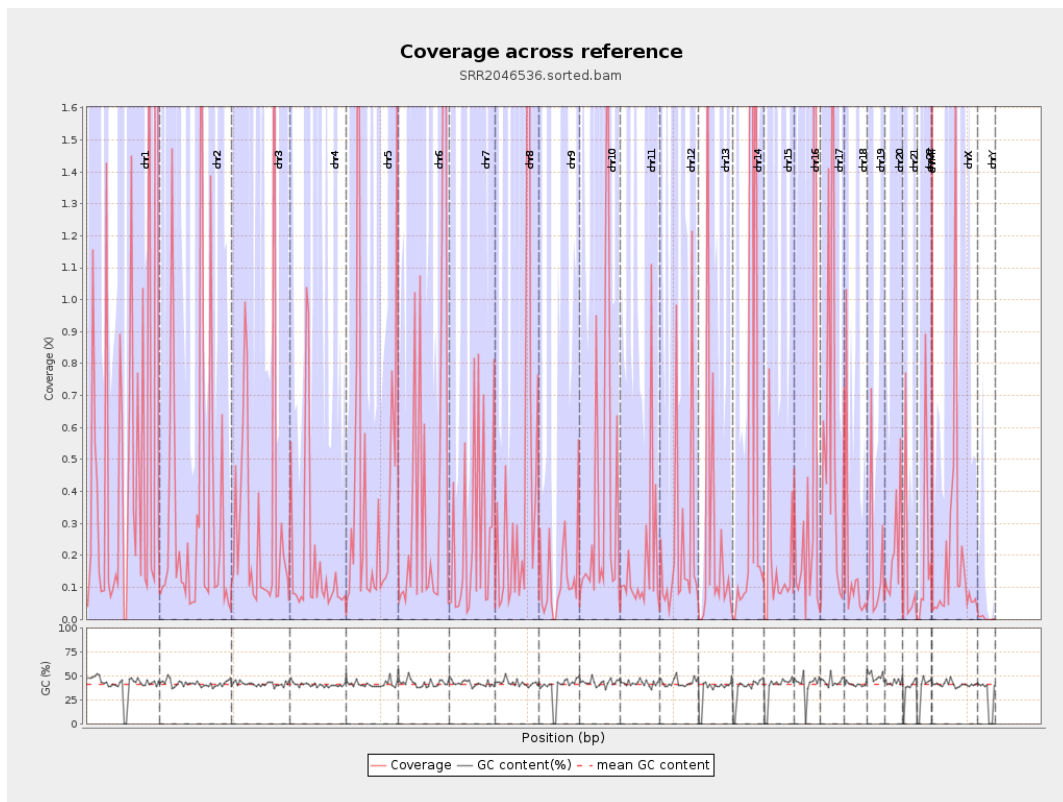
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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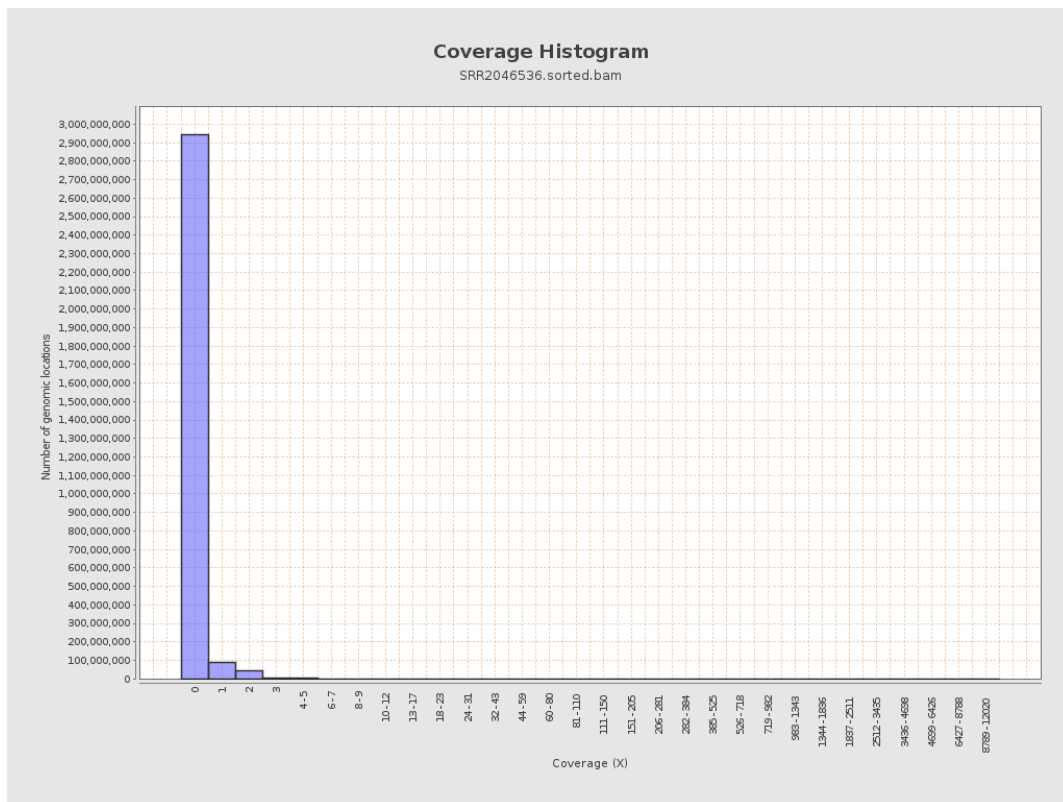
		bases	coverage	deviation
chr1	249250621	145202587	0.5826	29.8904
chr2	243199373	82426224	0.3389	15.7886
chr3	198022430	62985525	0.3181	15.4516
chr4	191154276	33939785	0.1776	8.9039
chr5	180915260	78196404	0.4322	25.4958
chr6	171115067	72501507	0.4237	19.1817
chr7	159138663	43628819	0.2742	13.983
chr8	146364022	65602767	0.4482	20.2457
chr9	141213431	19598790	0.1388	7.5436
chr10	135534747	50940703	0.3758	31.0347
chr11	135006516	24466870	0.1812	7.8595
chr12	133851895	31431719	0.2348	13.6445
chr13	115169878	29682051	0.2577	17.3347
chr14	107349540	61803338	0.5757	38.4604
chr15	102531392	16773015	0.1636	8.0484
chr16	90354753	41365495	0.4578	24.0078
chr17	81195210	49857804	0.614	25.1969
chr18	78077248	13017464	0.1667	9.2961
chr19	59128983	10786693	0.1824	8.5777
chr20	63025520	13498551	0.2142	11.1214
chr21	48129895	7308957	0.1519	15.8932
chr22	51304566	10283008	0.2004	11.7428
chrMT	16571	63429	3.8277	2.3933
chrX	155270560	30565700	0.1969	16.7854

chrY	59373566	241925	0.0041	0.3052
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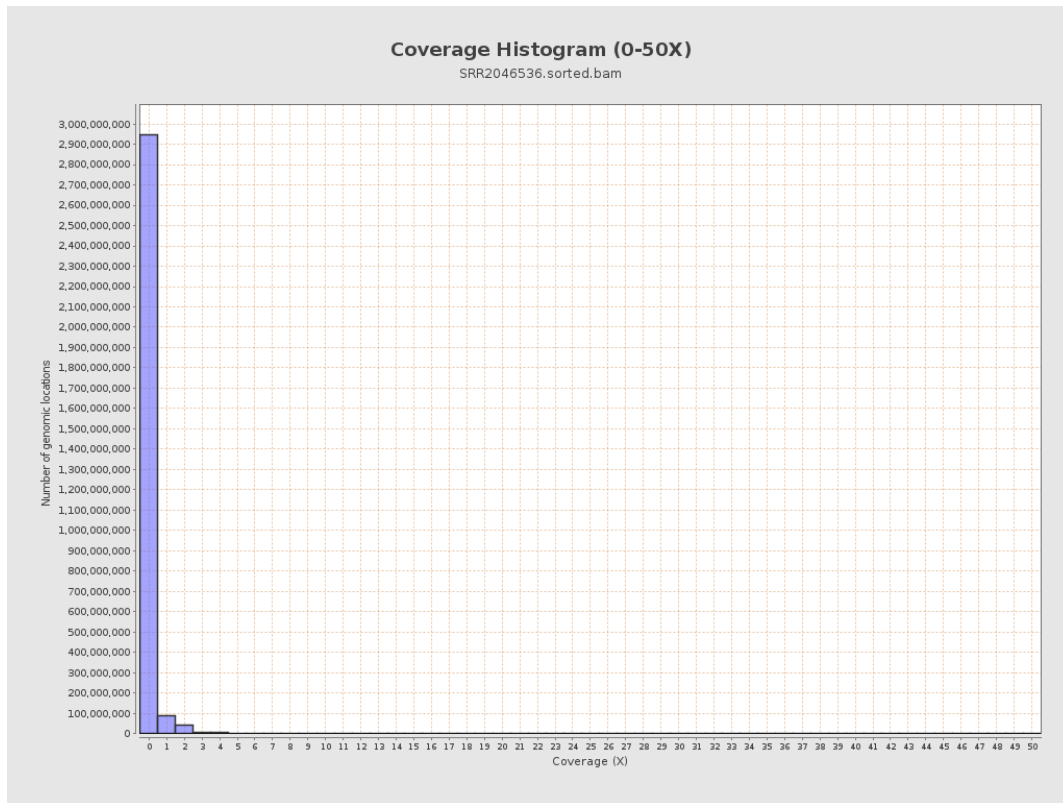
3. Results : Coverage across reference



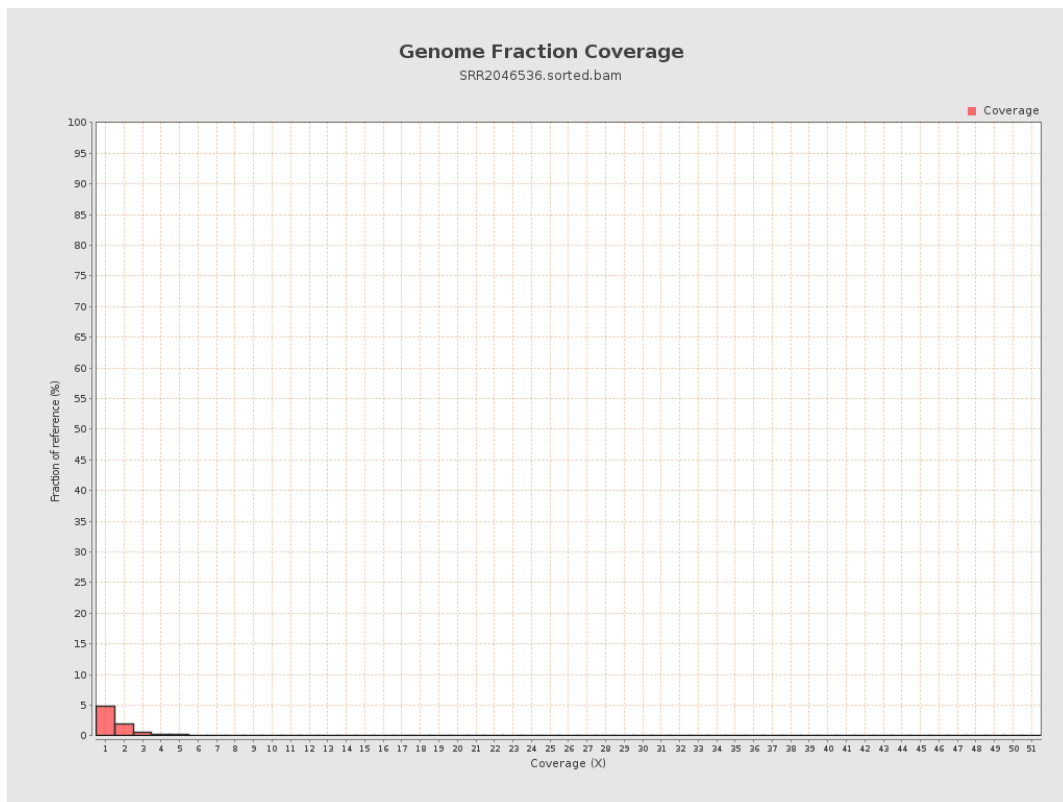
4. Results : Coverage Histogram



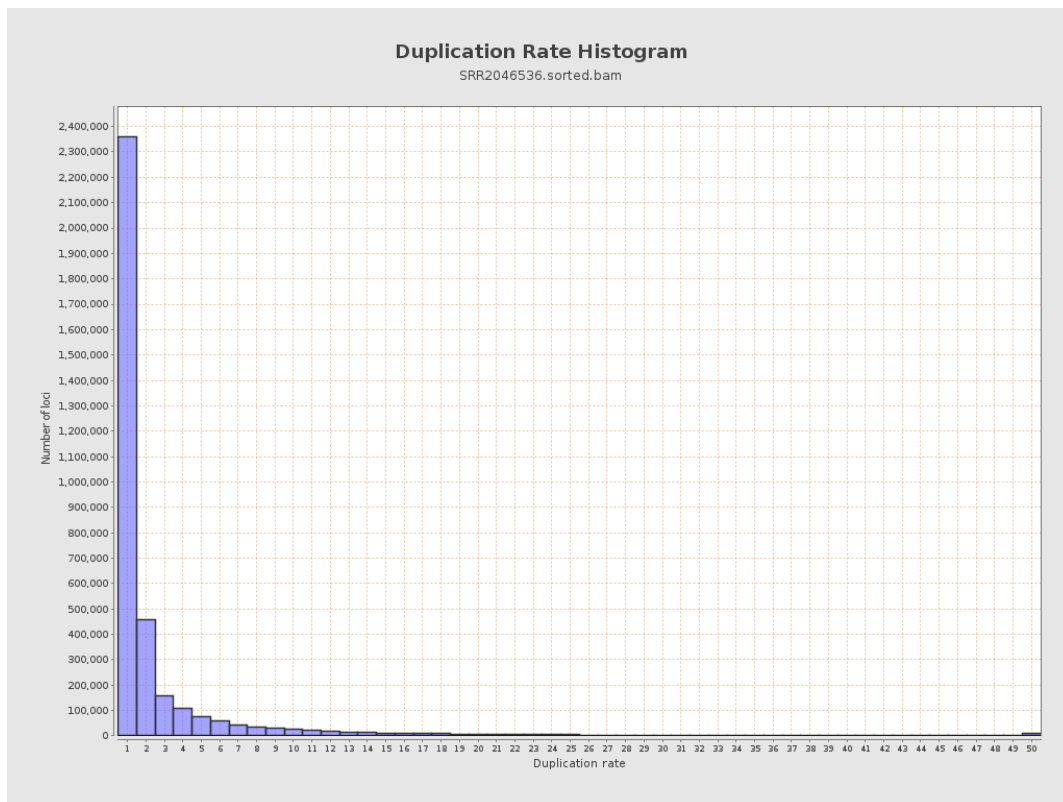
5. Results : Coverage Histogram (0-50X)



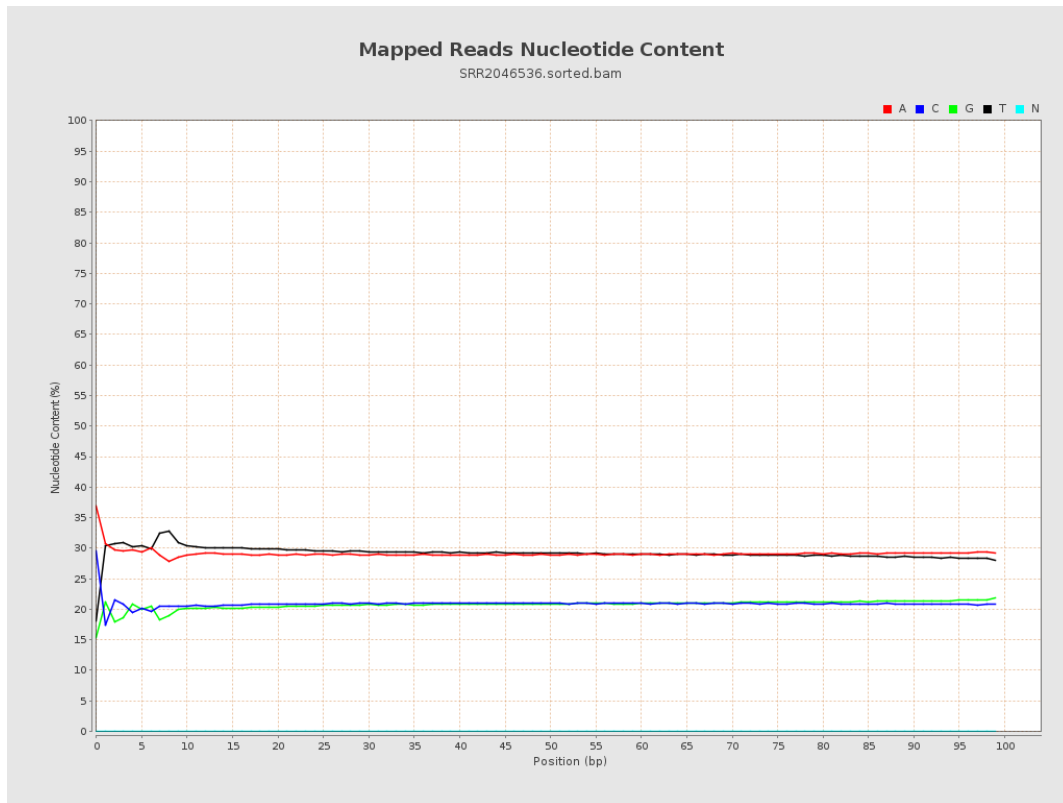
6. Results : Genome Fraction Coverage



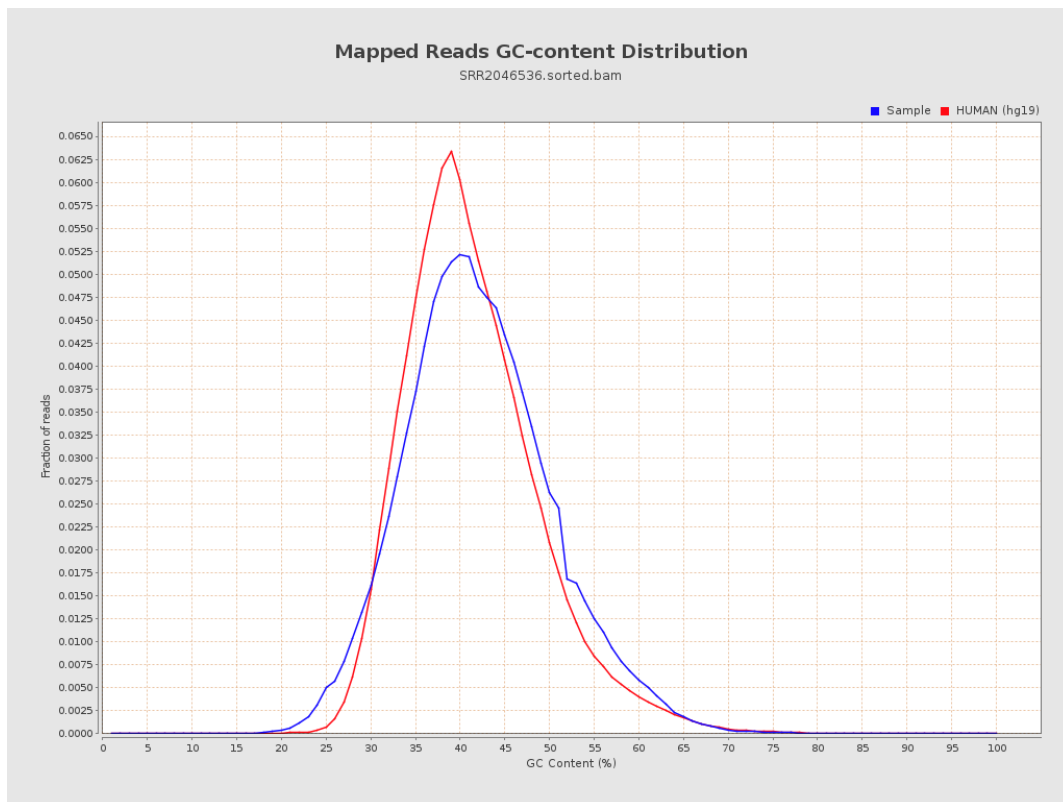
7. Results : Duplication Rate Histogram



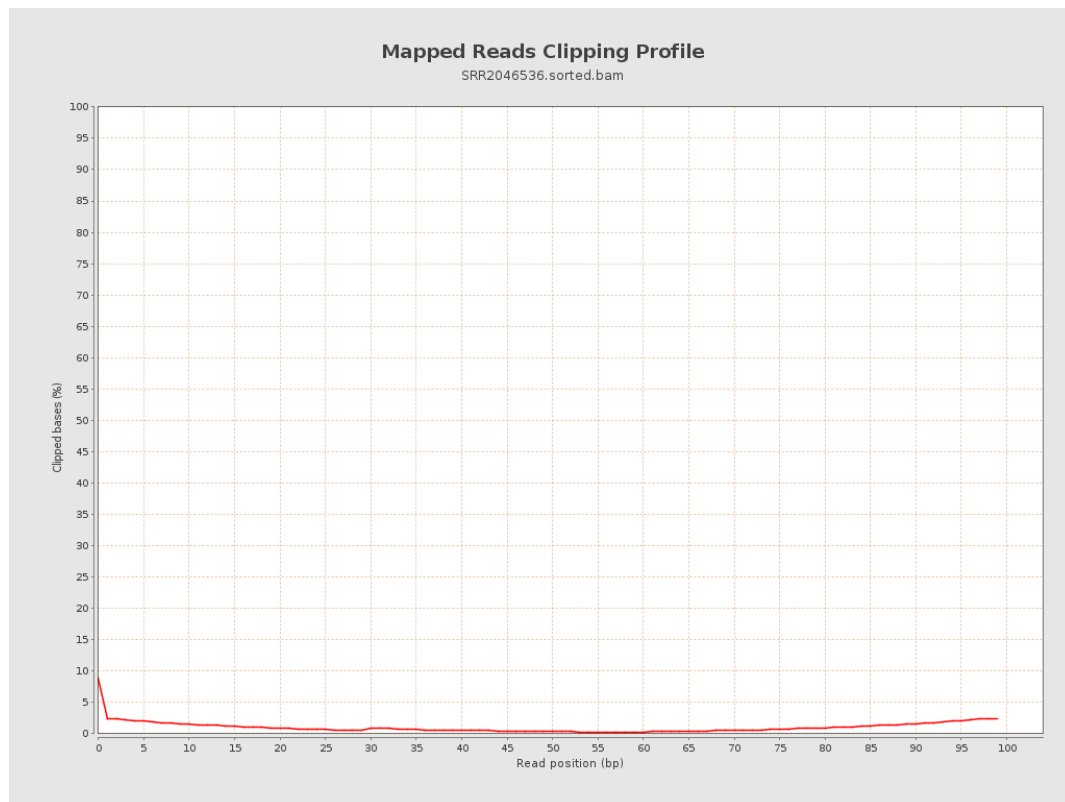
8. Results : Mapped Reads Nucleotide Content



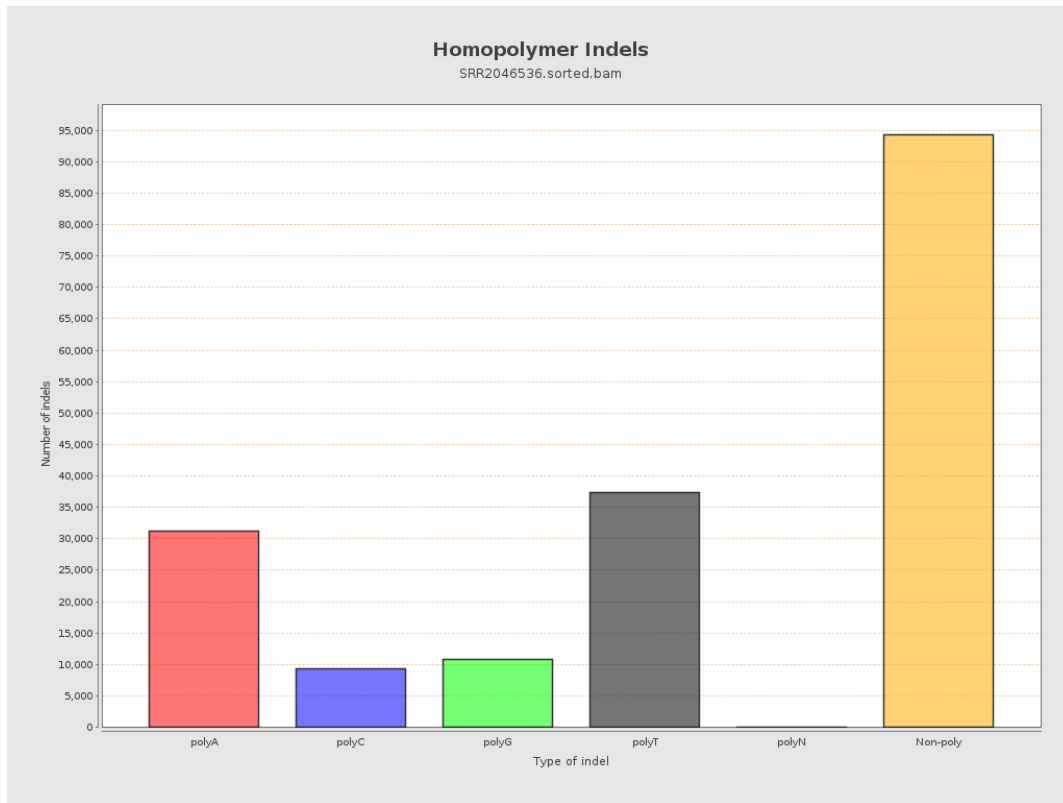
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



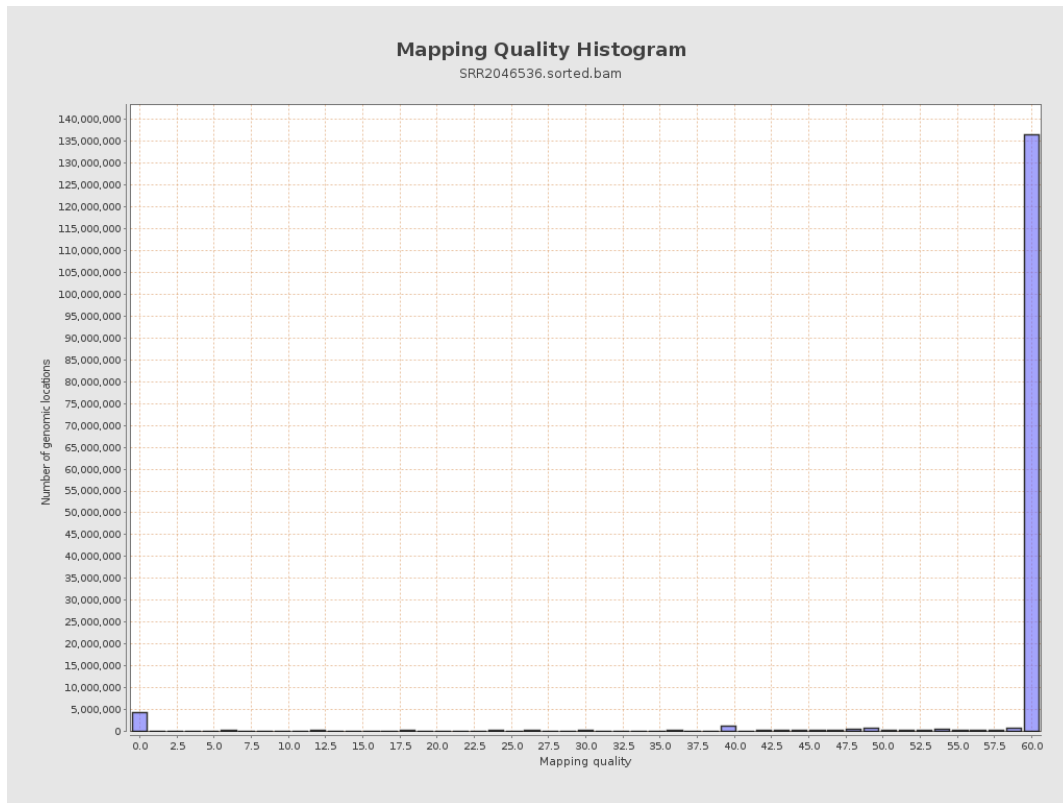
11. Results : Homopolymer Indels



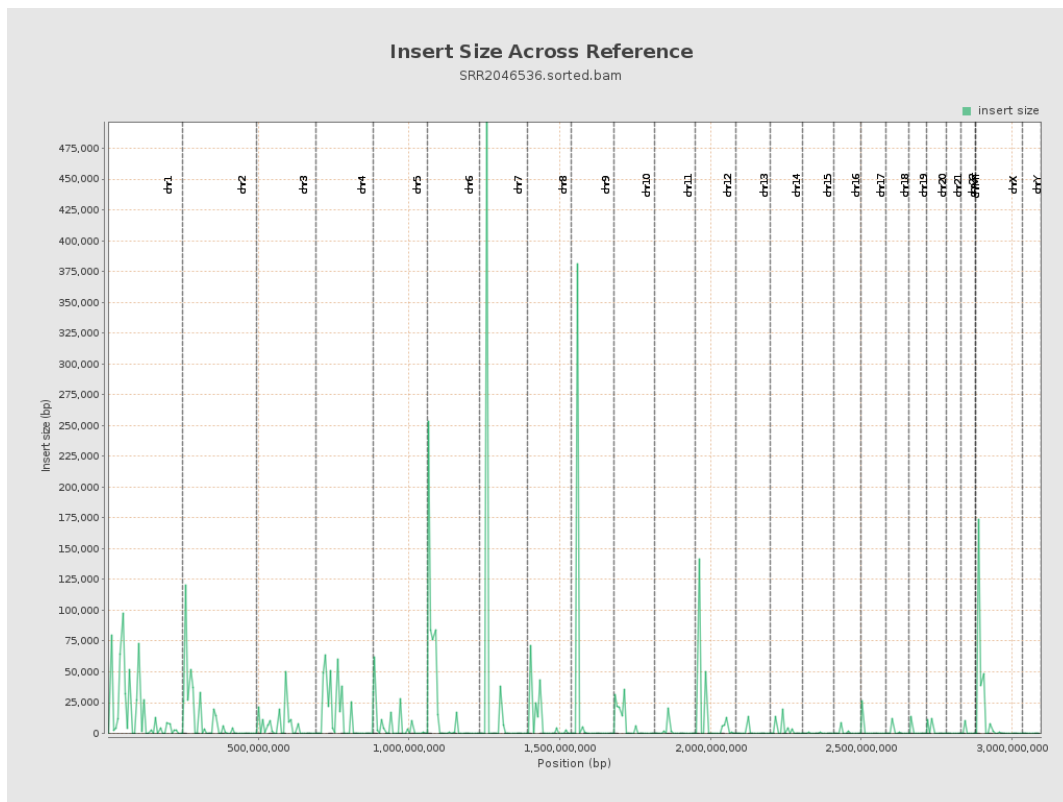
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

