

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 03:37:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472586.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_SRR3472586 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472586_1.fastq.gz SRR3472586_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 03:37:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472586.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,044,008
Mapped reads	7,196,117 / 89.46%
Unmapped reads	847,891 / 10.54%
Mapped paired reads	7,196,117 / 89.46%
Mapped reads, first in pair	3,637,885 / 45.22%
Mapped reads, second in pair	3,558,232 / 44.23%
Mapped reads, both in pair	6,995,350 / 86.96%
Mapped reads, singletons	200,767 / 2.5%
Secondary alignments	0
Supplementary alignments	240,776 / 2.99%
Read min/max/mean length	30 / 100 / 101.17
Duplicated reads (estimated)	1,079,827 / 13.42%
Duplication rate	13.3%
Clipped reads	5,702,561 / 70.89%

2.2. ACGT Content

Number/percentage of A's	148,689,179 / 25.69%
Number/percentage of C's	115,916,391 / 20.03%
Number/percentage of T's	172,121,307 / 29.74%
Number/percentage of G's	141,678,279 / 24.48%
Number/percentage of N's	354,112 / 0.06%

GC Percentage	44.51%
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2.3. Coverage

Mean	0.187
Standard Deviation	1.7709

2.4. Mapping Quality

Mean Mapping Quality	50.06
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2.5. Insert size

Mean	251,401.26
Standard Deviation	4,882,239.52
P25/Median/P75	87 / 123 / 171

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	7,089,533
Insertions	57,839
Mapped reads with at least one insertion	0.79%
Deletions	132,630
Mapped reads with at least one deletion	1.8%
Homopolymer indels	42.2%

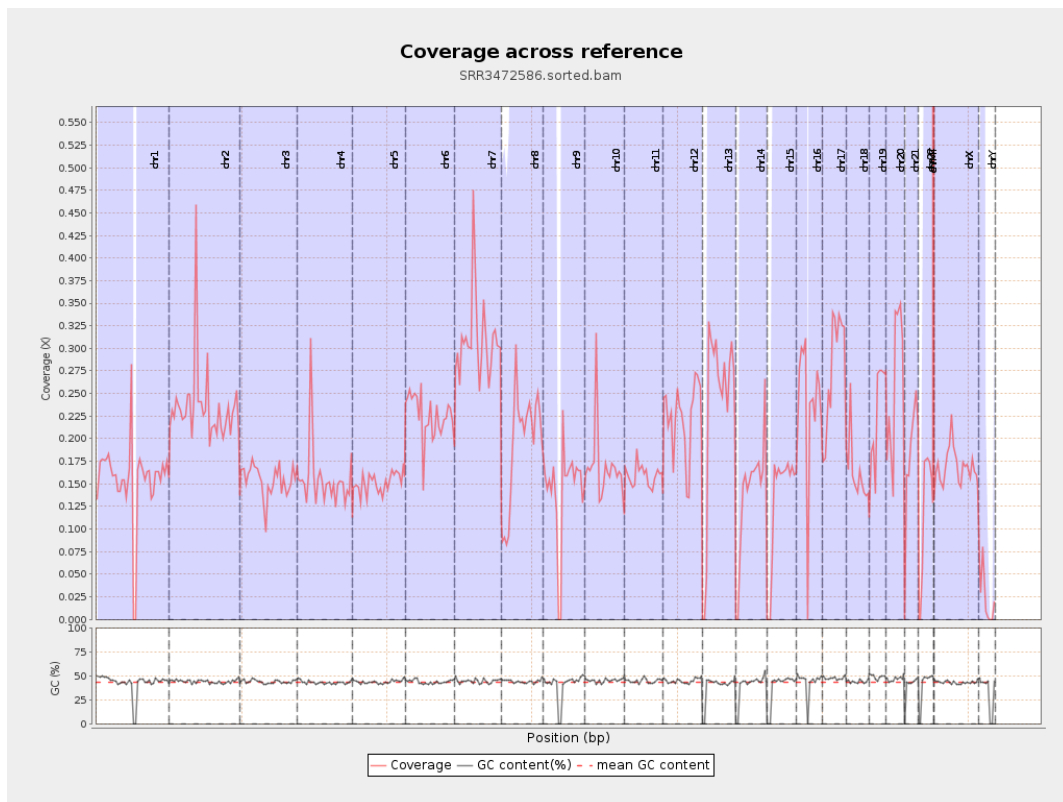
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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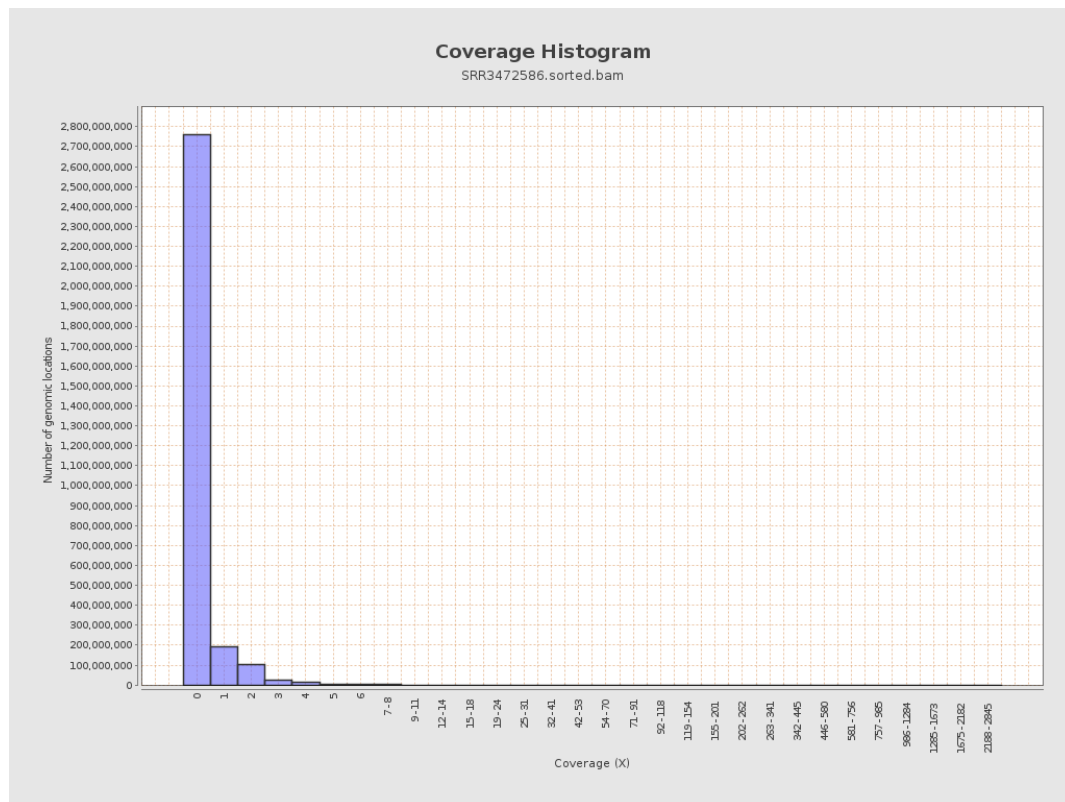
		bases	coverage	deviation
chr1	249250621	38486811	0.1544	2.3556
chr2	243199373	57281366	0.2355	1.9927
chr3	198022430	30481647	0.1539	0.5657
chr4	191154276	29554366	0.1546	1.0389
chr5	180915260	27386259	0.1514	0.5894
chr6	171115067	38523128	0.2251	1.0397
chr7	159138663	49431110	0.3106	3.3396
chr8	146364022	28412062	0.1941	1.4551
chr9	141213431	20085681	0.1422	1.6339
chr10	135534747	22800569	0.1682	1.6671
chr11	135006516	21344602	0.1581	1.2746
chr12	133851895	29798774	0.2226	0.7099
chr13	115169878	27126595	0.2355	0.7367
chr14	107349540	15082166	0.1405	4.5167
chr15	102531392	13771906	0.1343	0.5385
chr16	90354753	21498762	0.2379	1.0793
chr17	81195210	22735100	0.28	1.478
chr18	78077248	12747473	0.1633	3.0179
chr19	59128983	13389671	0.2264	1.6695
chr20	63025520	16280409	0.2583	0.9875
chr21	48129895	8789504	0.1826	0.7778
chr22	51304566	5984480	0.1166	0.4995
chrMT	16571	395271	23.8532	13.8489
chrX	155270560	26221225	0.1689	0.8425

chrY	59373566	1401576	0.0236	0.8375
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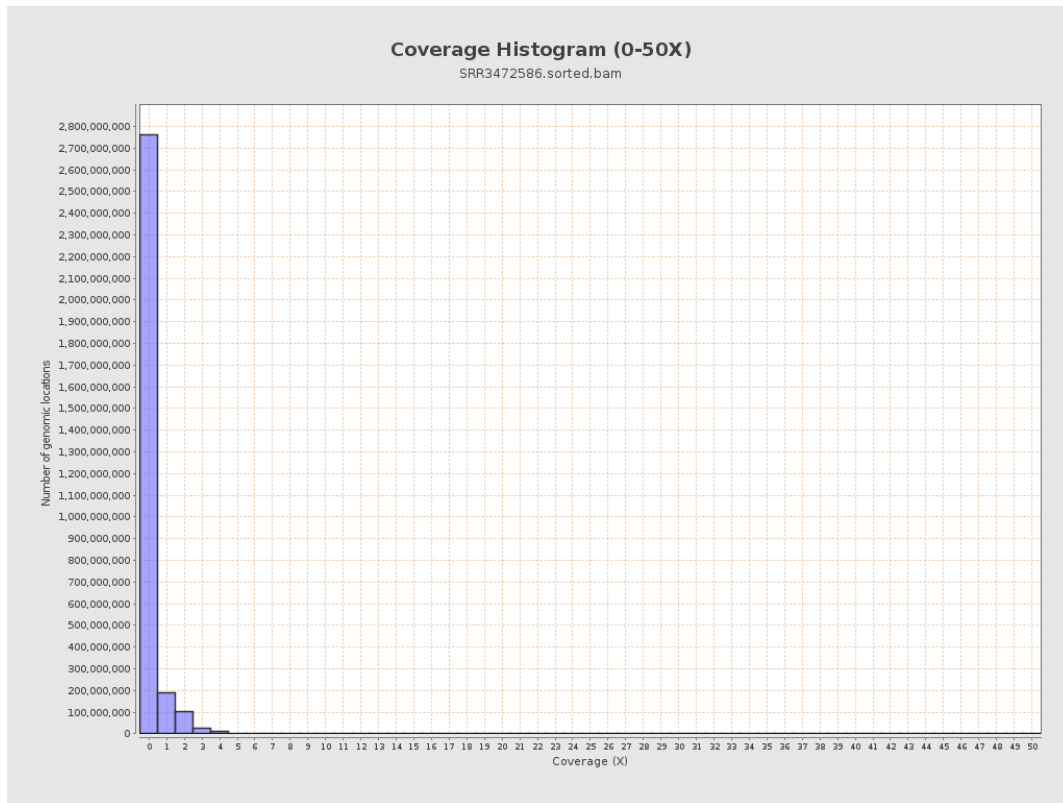
3. Results : Coverage across reference



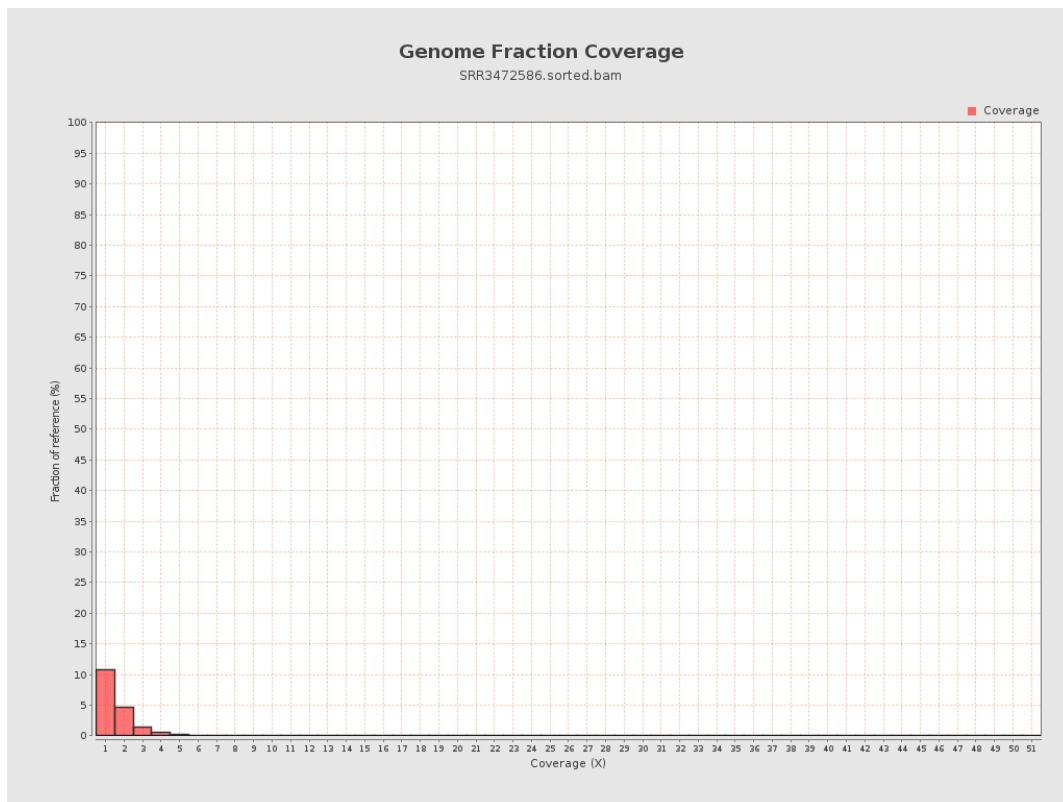
4. Results : Coverage Histogram



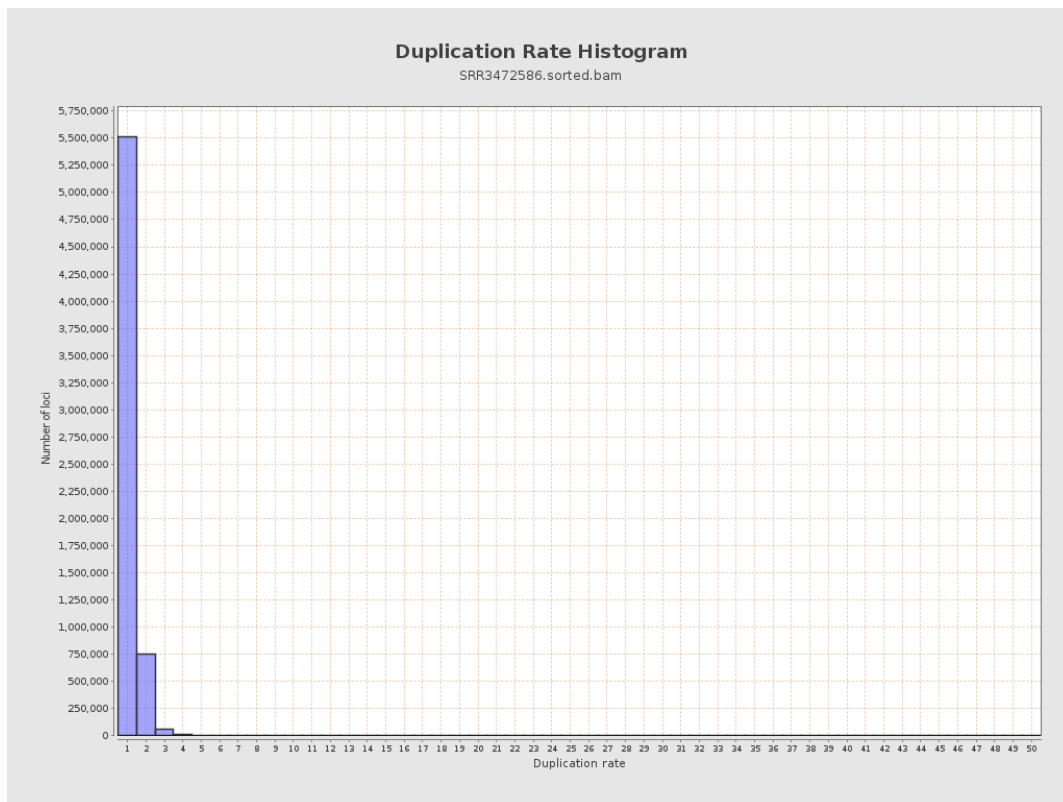
5. Results : Coverage Histogram (0-50X)



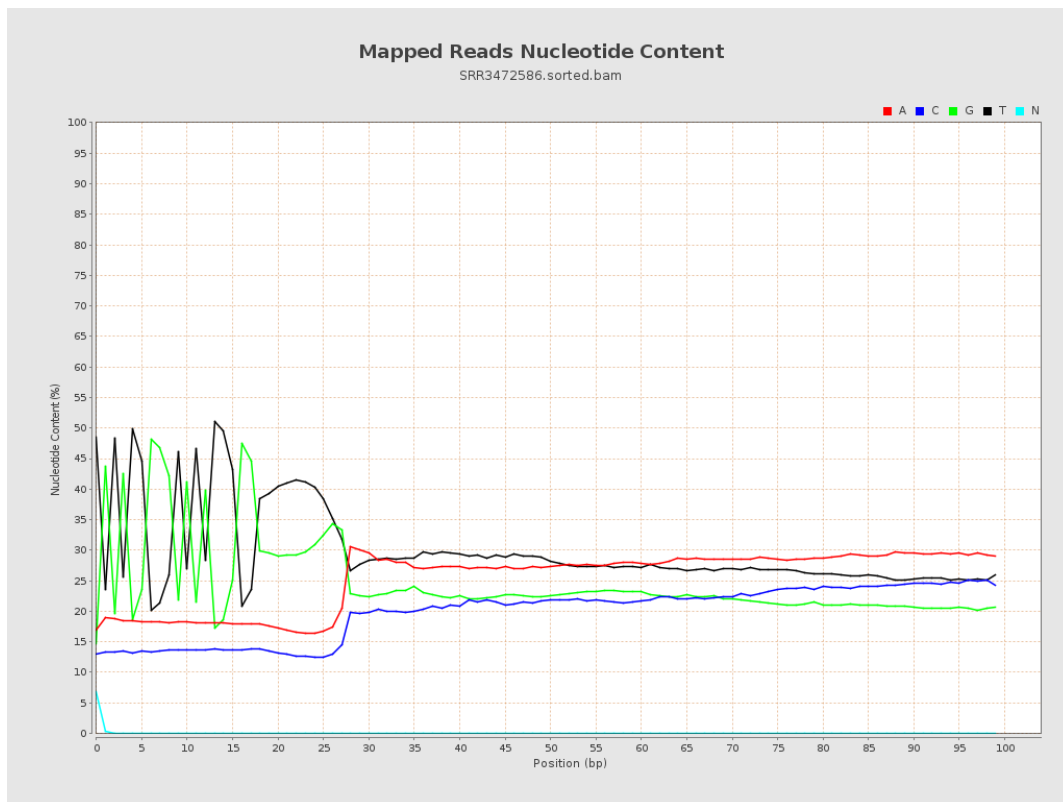
6. Results : Genome Fraction Coverage



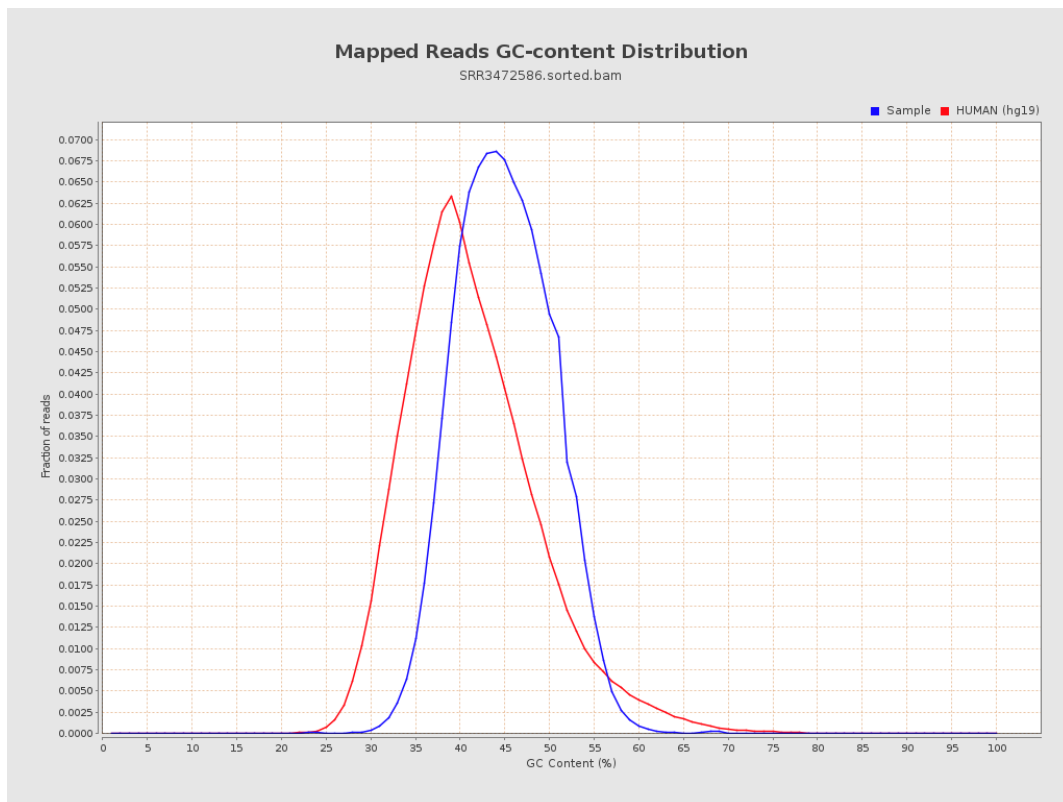
7. Results : Duplication Rate Histogram



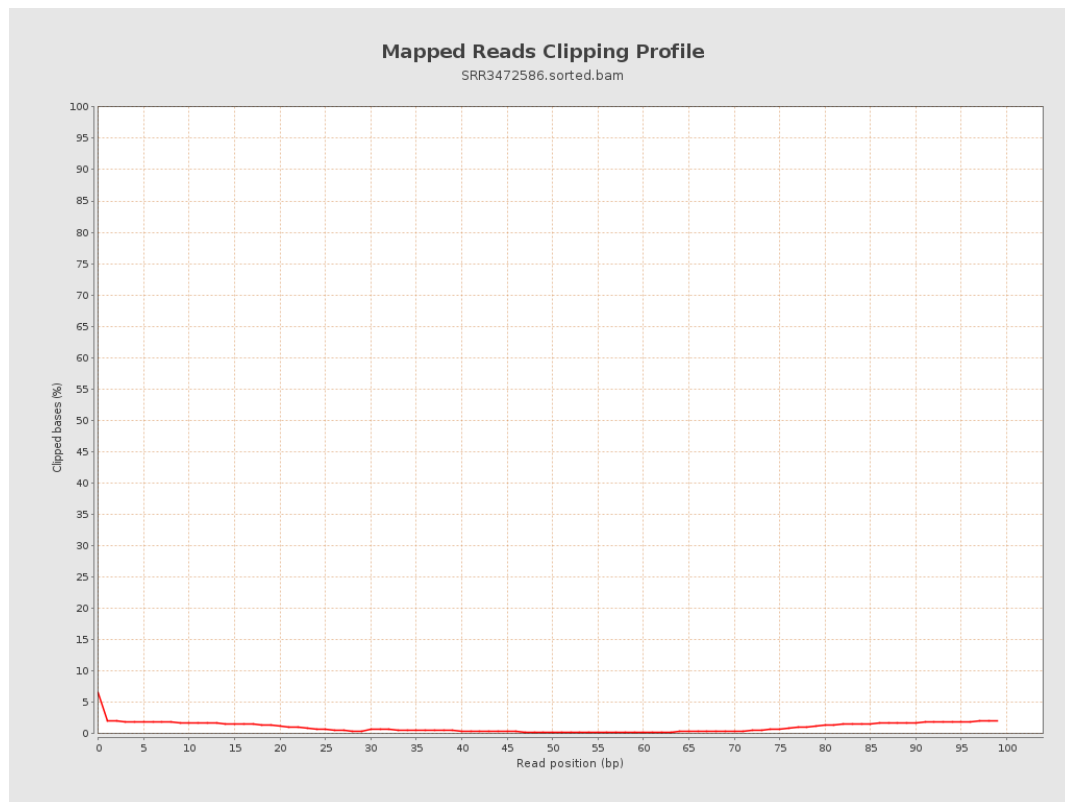
8. Results : Mapped Reads Nucleotide Content



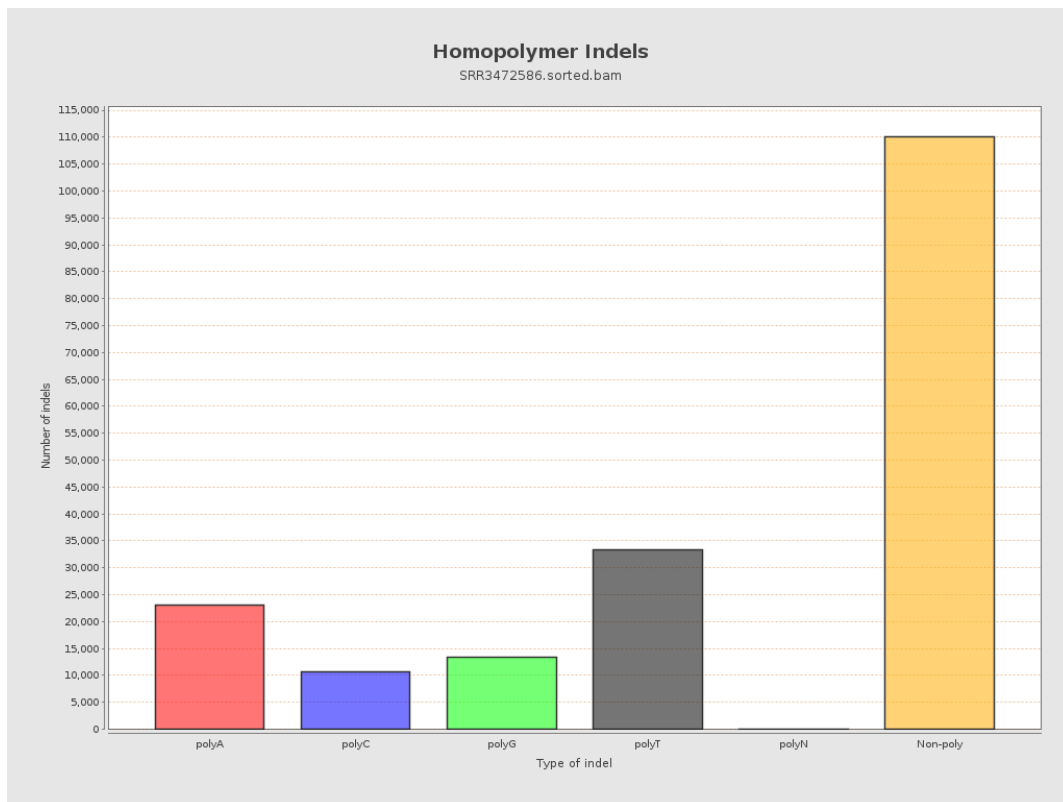
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



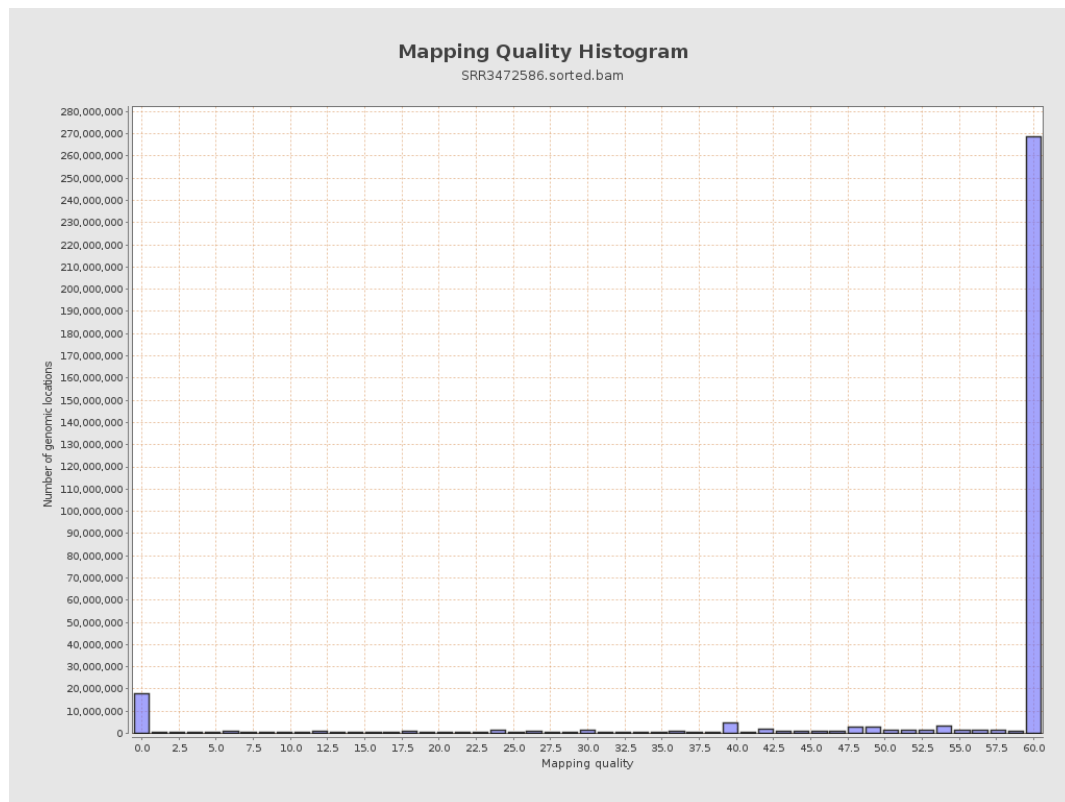
11. Results : Homopolymer Indels



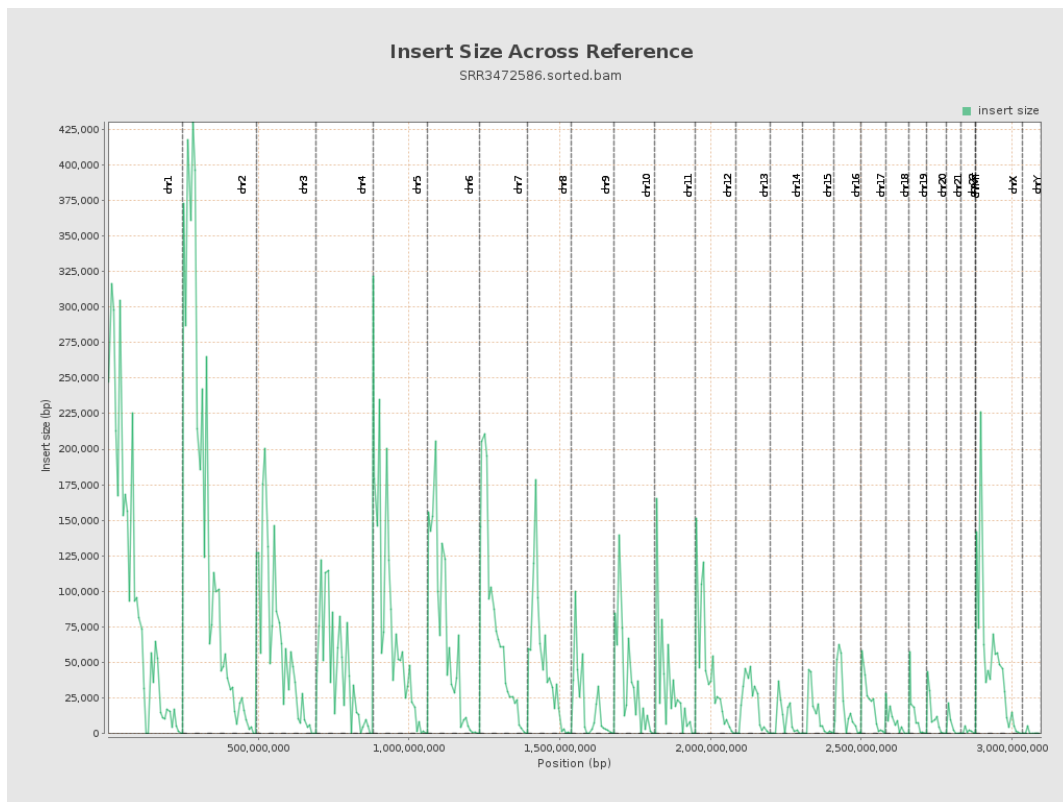
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

