

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:31:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173908.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_SRR10173908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173908_1.fastq.gz SRR10173908_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:31:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,438,210
Mapped reads	4,340,396 / 97.8%
Unmapped reads	97,814 / 2.2%
Mapped paired reads	4,340,396 / 97.8%
Mapped reads, first in pair	2,168,771 / 48.87%
Mapped reads, second in pair	2,171,625 / 48.93%
Mapped reads, both in pair	4,270,374 / 96.22%
Mapped reads, singletons	70,022 / 1.58%
Secondary alignments	0
Supplementary alignments	451,010 / 10.16%
Read min/max/mean length	30 / 133 / 128.39
Duplicated reads (estimated)	3,294,126 / 74.22%
Duplication rate	64.33%
Clipped reads	1,718,558 / 38.72%

2.2. ACGT Content

Number/percentage of A's	153,063,537 / 29.72%
Number/percentage of C's	102,635,644 / 19.93%
Number/percentage of T's	152,959,311 / 29.7%
Number/percentage of G's	106,412,924 / 20.66%
Number/percentage of N's	6,295 / 0%

GC Percentage	40.59%
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2.3. Coverage

Mean	0.1665
Standard Deviation	2.348

2.4. Mapping Quality

Mean Mapping Quality	52.66
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2.5. Insert size

Mean	1,055,249.83
Standard Deviation	9,525,501.5
P25/Median/P75	145 / 201 / 287

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	4,978,738
Insertions	49,713
Mapped reads with at least one insertion	1.11%
Deletions	121,347
Mapped reads with at least one deletion	2.73%
Homopolymer indels	43.11%

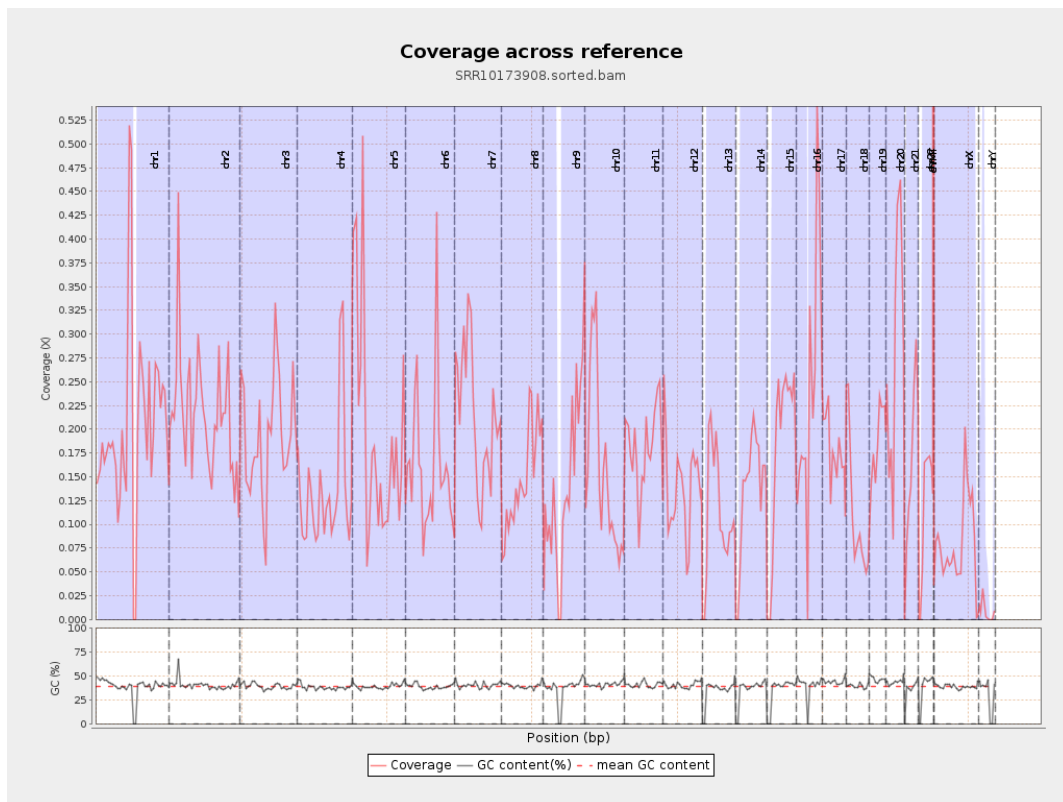
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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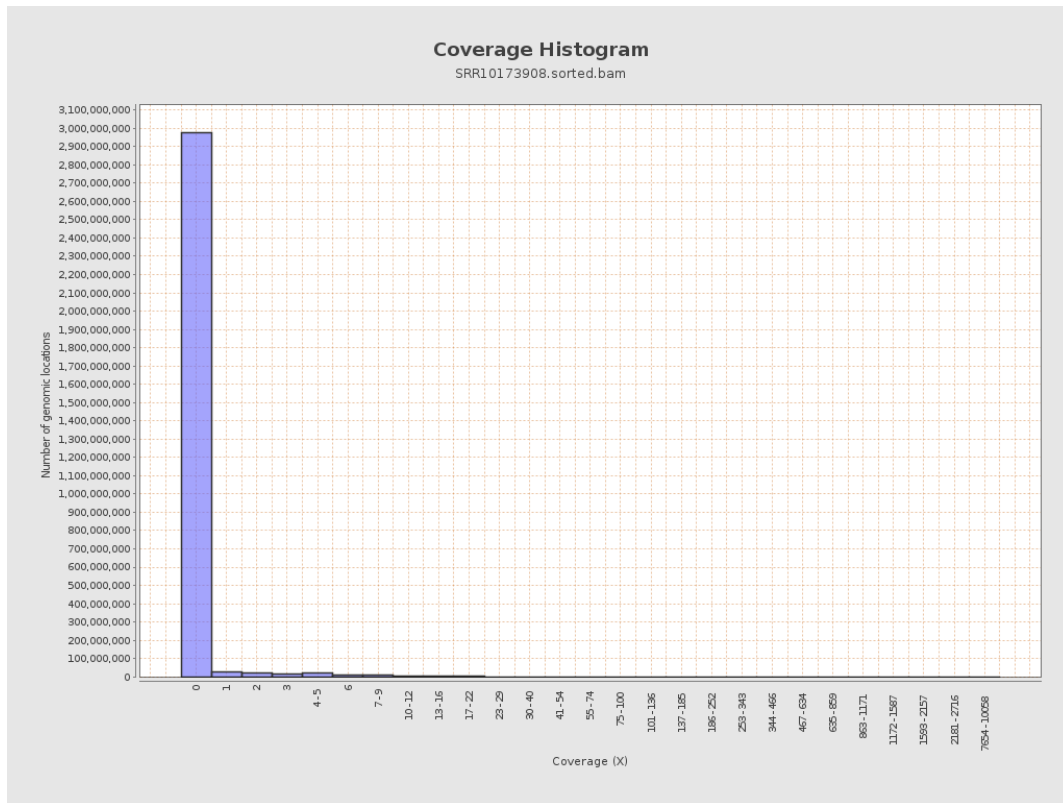
		bases	coverage	deviation
chr1	249250621	50132045	0.2011	1.7359
chr2	243199373	52565574	0.2161	7.0661
chr3	198022430	38142952	0.1926	1.2302
chr4	191154276	25144688	0.1315	1.0906
chr5	180915260	35362311	0.1955	1.2395
chr6	171115067	27829544	0.1626	1.1545
chr7	159138663	33784229	0.2123	1.74
chr8	146364022	21626737	0.1478	1.1663
chr9	141213431	19344927	0.137	1.1152
chr10	135534747	21369736	0.1577	1.8093
chr11	135006516	24585889	0.1821	1.1875
chr12	133851895	18741267	0.14	1.0338
chr13	115169878	12651539	0.1099	0.9251
chr14	107349540	14587598	0.1359	1.0247
chr15	102531392	18401054	0.1795	1.168
chr16	90354753	22252333	0.2463	1.651
chr17	81195210	14164600	0.1745	1.1781
chr18	78077248	8417118	0.1078	1.3773
chr19	59128983	10927230	0.1848	1.7291
chr20	63025520	17762137	0.2818	1.4672
chr21	48129895	7883845	0.1638	1.122
chr22	51304566	5821760	0.1135	0.8883
chrMT	16571	1137401	68.638	55.7574
chrX	155270560	12258667	0.079	0.7717

chrY	59373566	471370	0.0079	0.3066
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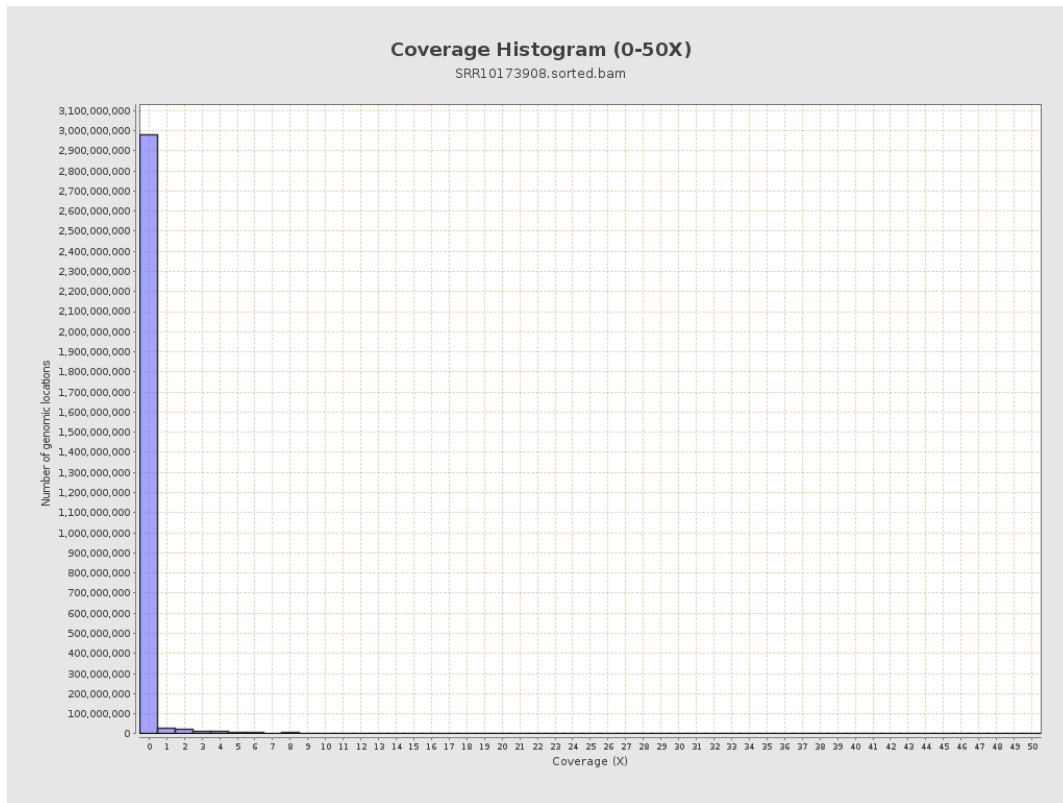
3. Results : Coverage across reference



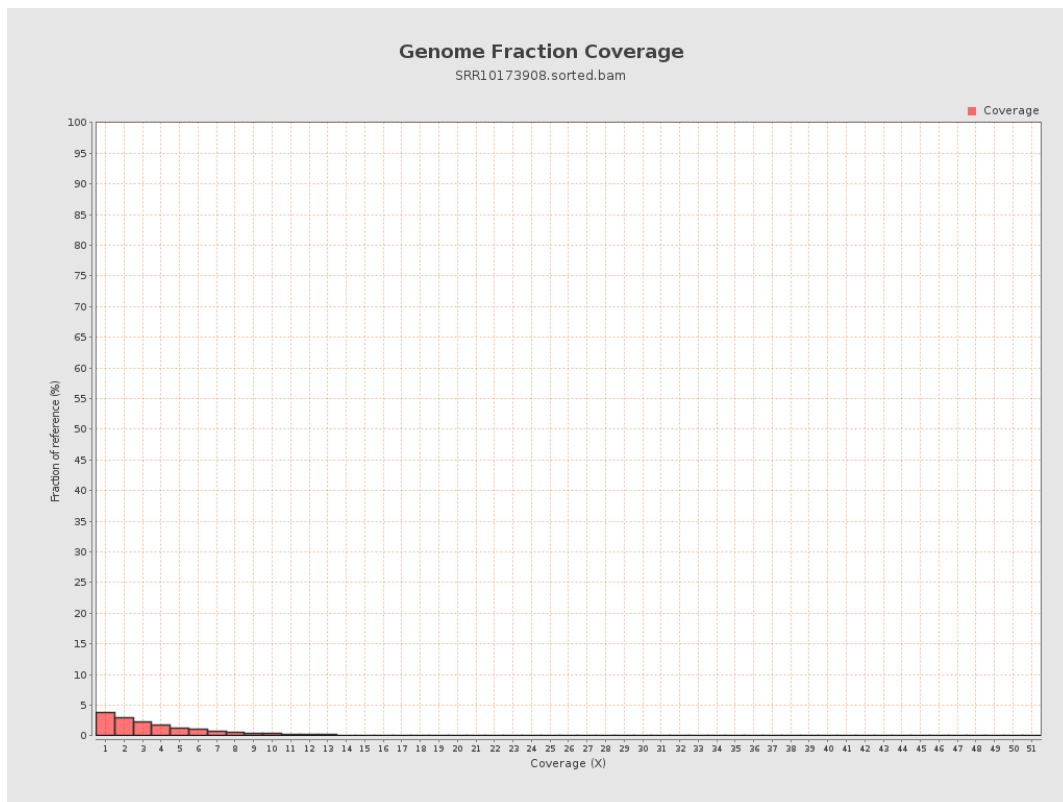
4. Results : Coverage Histogram



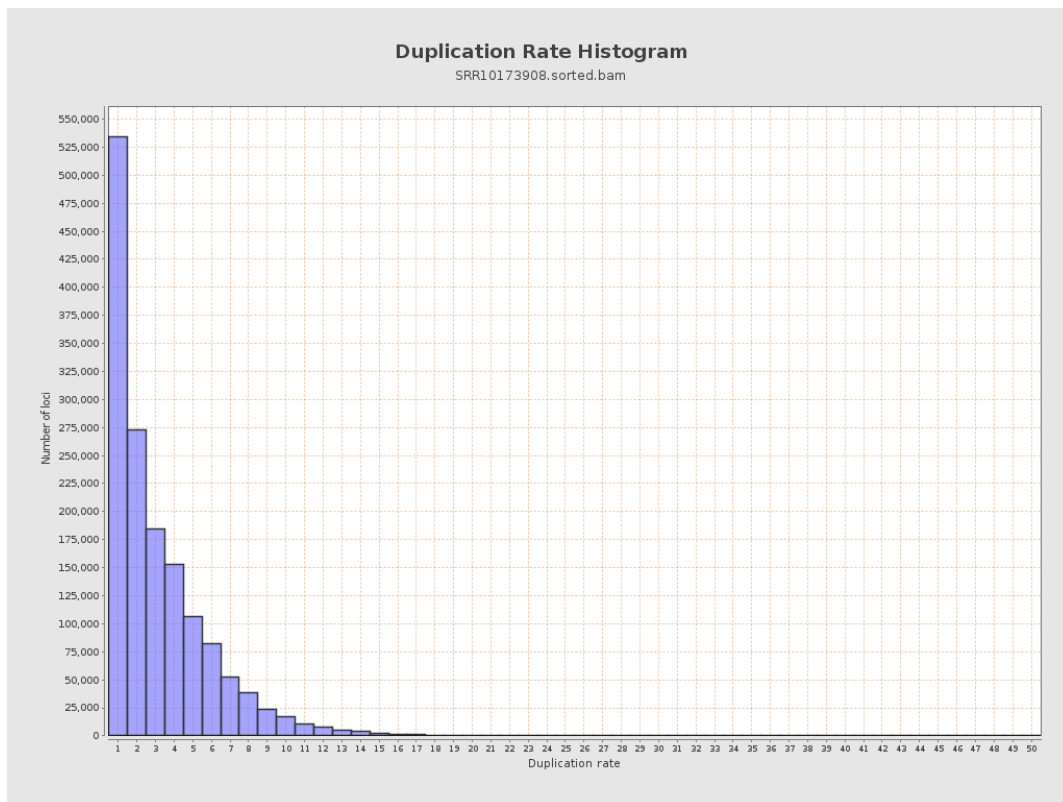
5. Results : Coverage Histogram (0-50X)



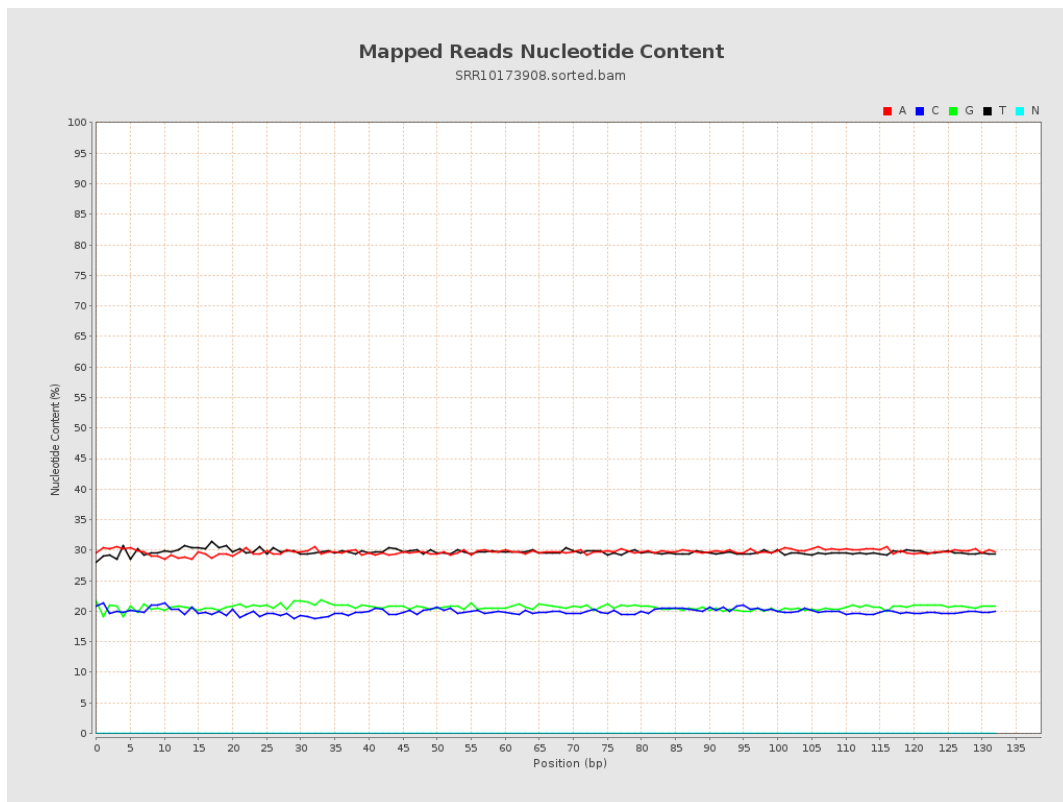
6. Results : Genome Fraction Coverage



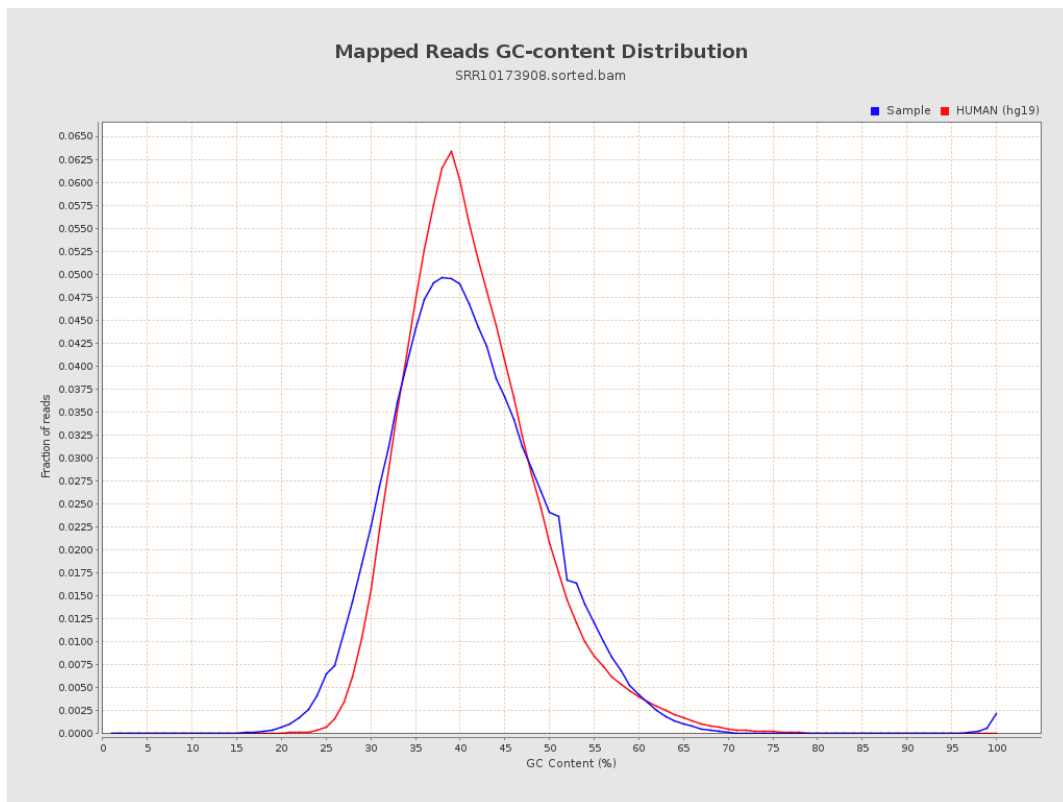
7. Results : Duplication Rate Histogram



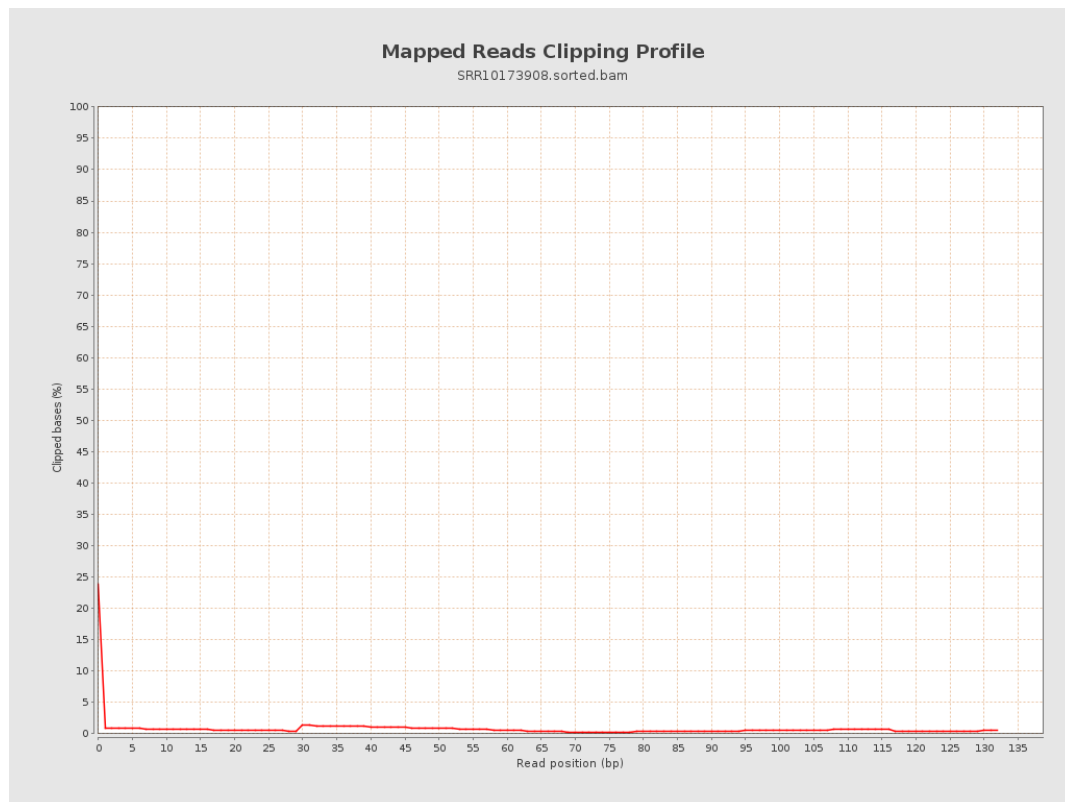
8. Results : Mapped Reads Nucleotide Content



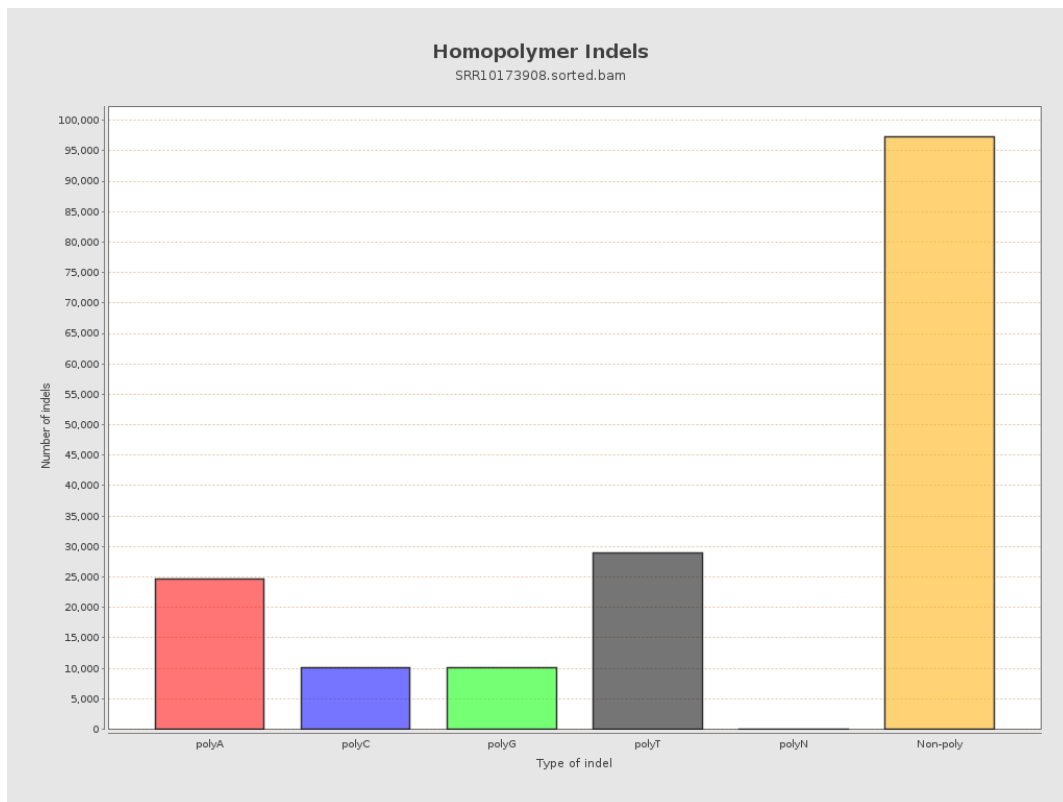
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



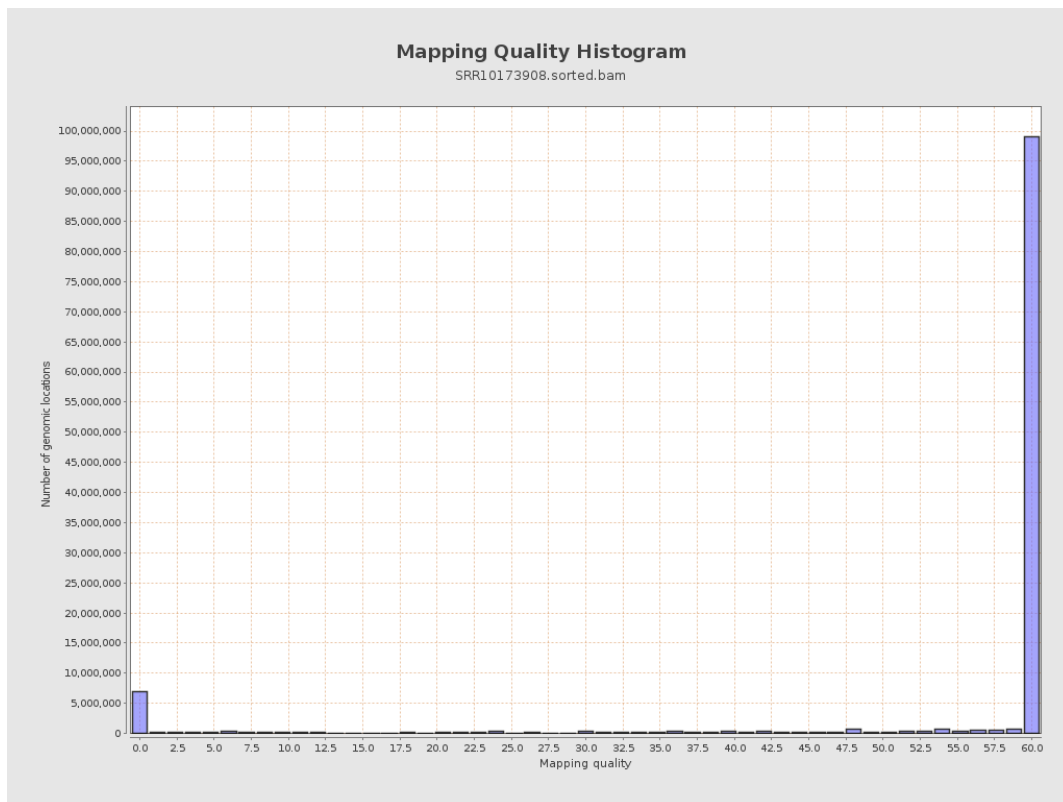
11. Results : Homopolymer Indels



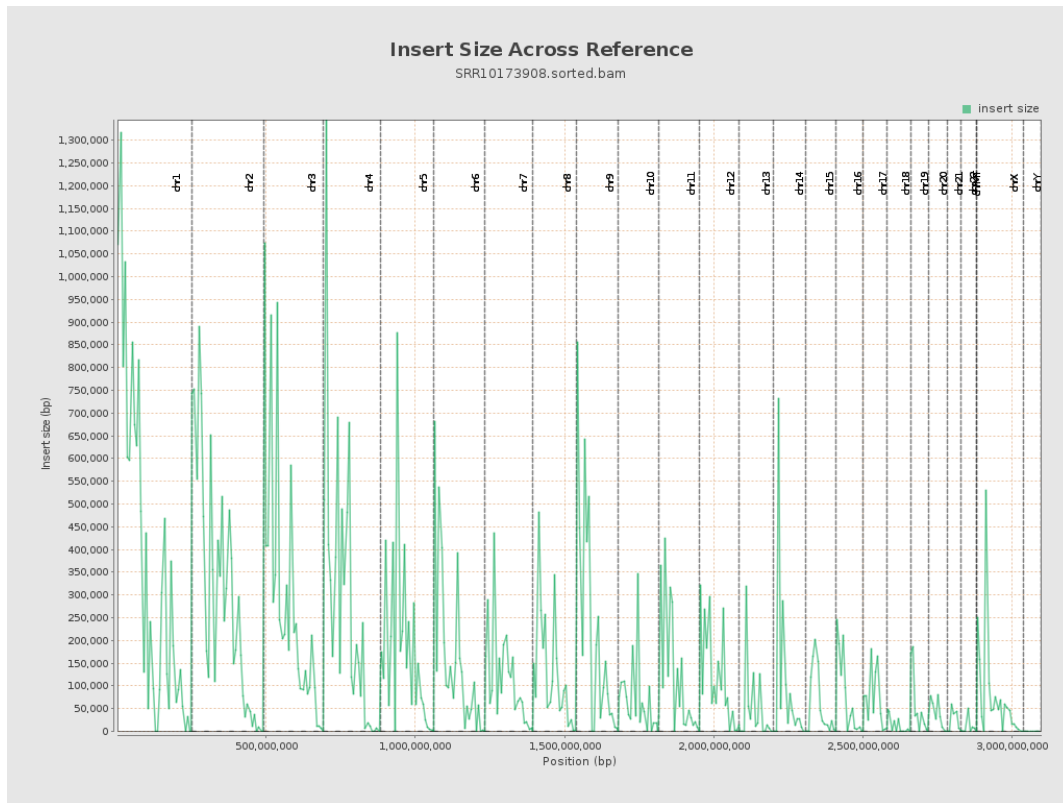
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

