

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:15:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472508.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_SRR3472508 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472508_1.fastq.gz SRR3472508_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:15:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472508.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,579,926
Mapped reads	18,290,719 / 98.44%
Unmapped reads	289,207 / 1.56%
Mapped paired reads	18,290,719 / 98.44%
Mapped reads, first in pair	9,186,718 / 49.44%
Mapped reads, second in pair	9,104,001 / 49%
Mapped reads, both in pair	18,144,360 / 97.66%
Mapped reads, singletons	146,359 / 0.79%
Secondary alignments	0
Supplementary alignments	65,954 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,962,368 / 64.38%
Duplication rate	47.05%
Clipped reads	1,497,479 / 8.06%

2.2. ACGT Content

Number/percentage of A's	500,999,619 / 27.85%
Number/percentage of C's	401,466,854 / 22.32%
Number/percentage of T's	497,537,318 / 27.66%
Number/percentage of G's	398,612,065 / 22.16%
Number/percentage of N's	278,621 / 0.02%

GC Percentage	44.48%
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2.3. Coverage

Mean	0.5812
Standard Deviation	21.5375

2.4. Mapping Quality

Mean Mapping Quality	55.03
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2.5. Insert size

Mean	26,566.55
Standard Deviation	1,579,222.43
P25/Median/P75	173 / 242 / 327

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	11,334,532
Insertions	95,812
Mapped reads with at least one insertion	0.52%
Deletions	95,811
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.95%

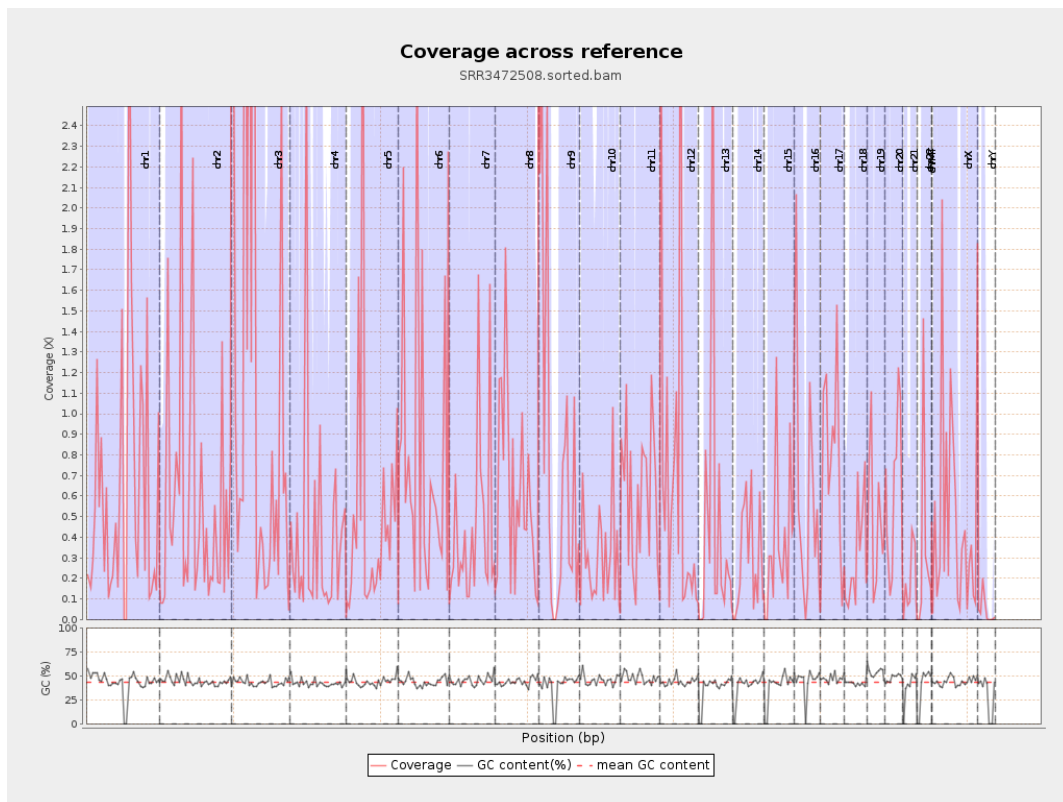
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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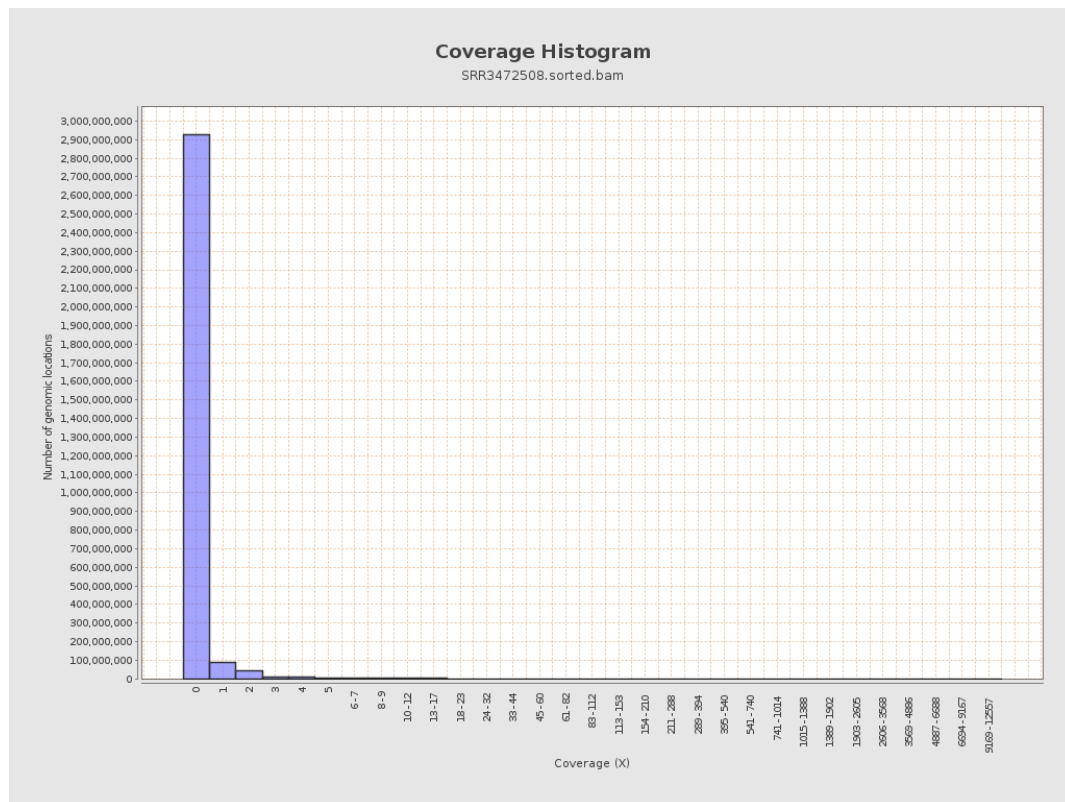
		bases	coverage	deviation
chr1	249250621	157853798	0.6333	18.0186
chr2	243199373	140613052	0.5782	20.5653
chr3	198022430	254629098	1.2859	40.5393
chr4	191154276	76056586	0.3979	16.0927
chr5	180915260	98776762	0.546	17.5499
chr6	171115067	135704337	0.7931	23.8024
chr7	159138663	71052834	0.4465	13.7077
chr8	146364022	92617159	0.6328	24.393
chr9	141213431	111497575	0.7896	23.8491
chr10	135534747	42379987	0.3127	12.0655
chr11	135006516	84640749	0.6269	25.2674
chr12	133851895	102886004	0.7687	29.3037
chr13	115169878	52386346	0.4549	29.3651
chr14	107349540	31660377	0.2949	11.9832
chr15	102531392	37561616	0.3663	12.1221
chr16	90354753	53175107	0.5885	19.3269
chr17	81195210	60187825	0.7413	22.0736
chr18	78077248	23745632	0.3041	11.4859
chr19	59128983	29466905	0.4983	12.2751
chr20	63025520	40121638	0.6366	23.1908
chr21	48129895	9249973	0.1922	9.7795
chr22	51304566	17236136	0.336	11.9092
chrMT	16571	7906	0.4771	1.1415
chrX	155270560	72754923	0.4686	15.6304

chrY	59373566	2886208	0.0486	1.8605
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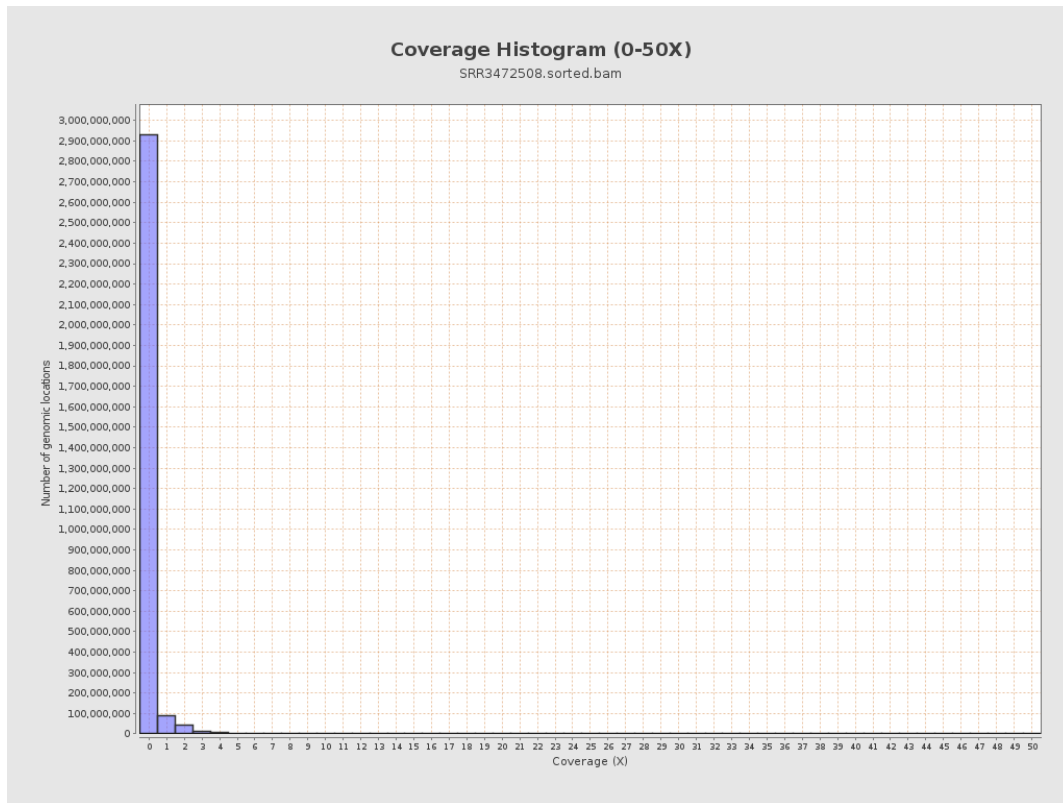
3. Results : Coverage across reference



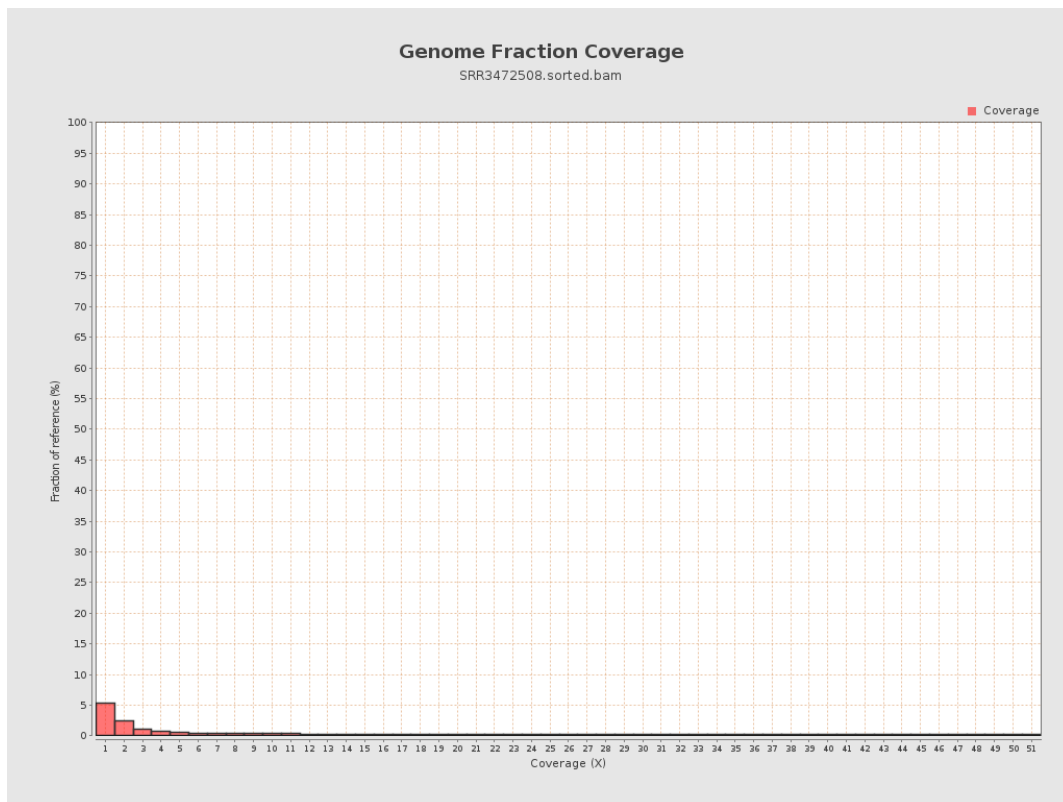
4. Results : Coverage Histogram



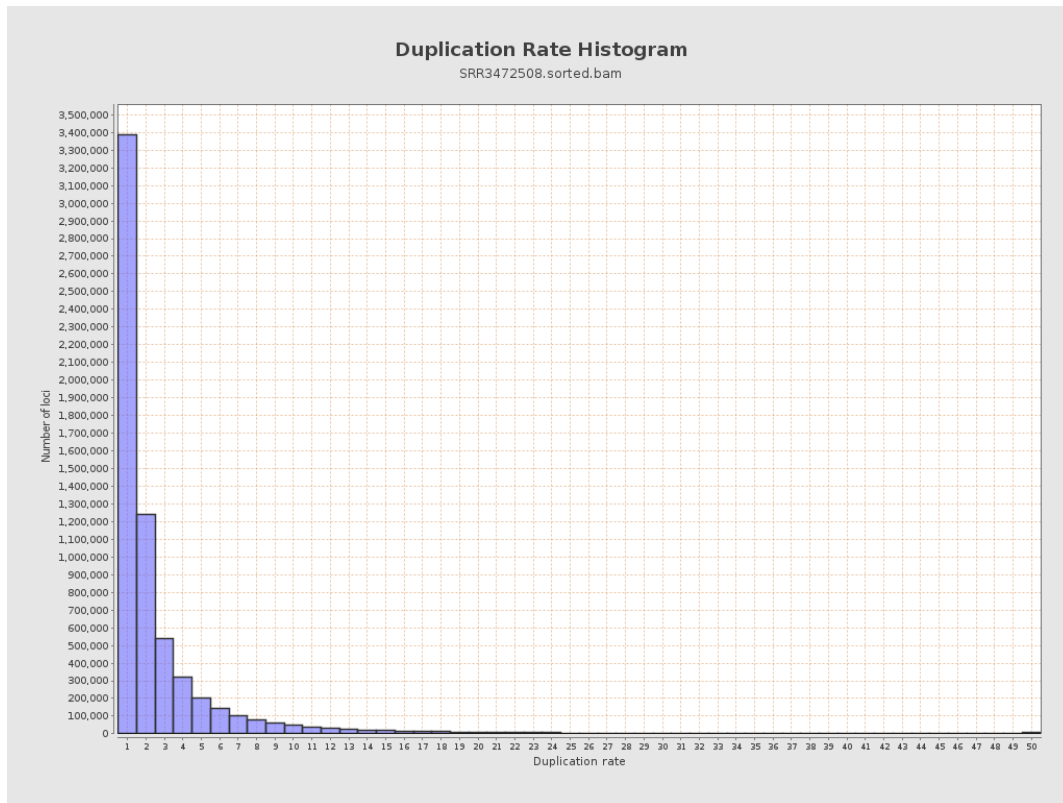
5. Results : Coverage Histogram (0-50X)



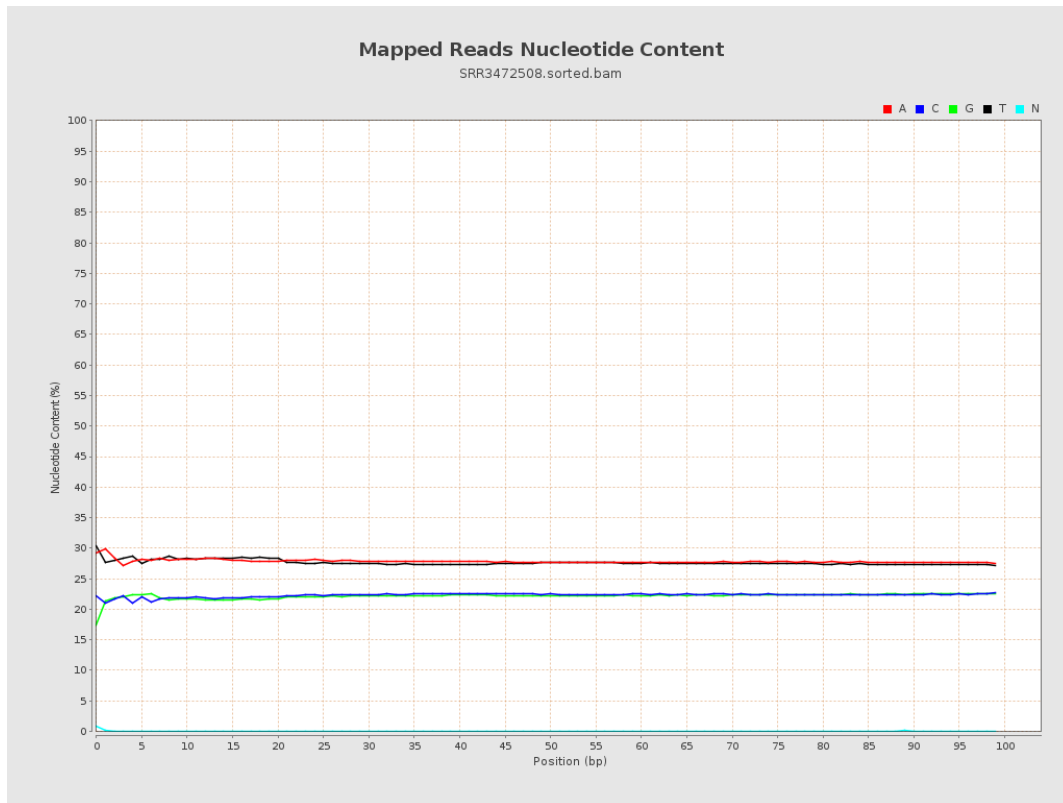
6. Results : Genome Fraction Coverage



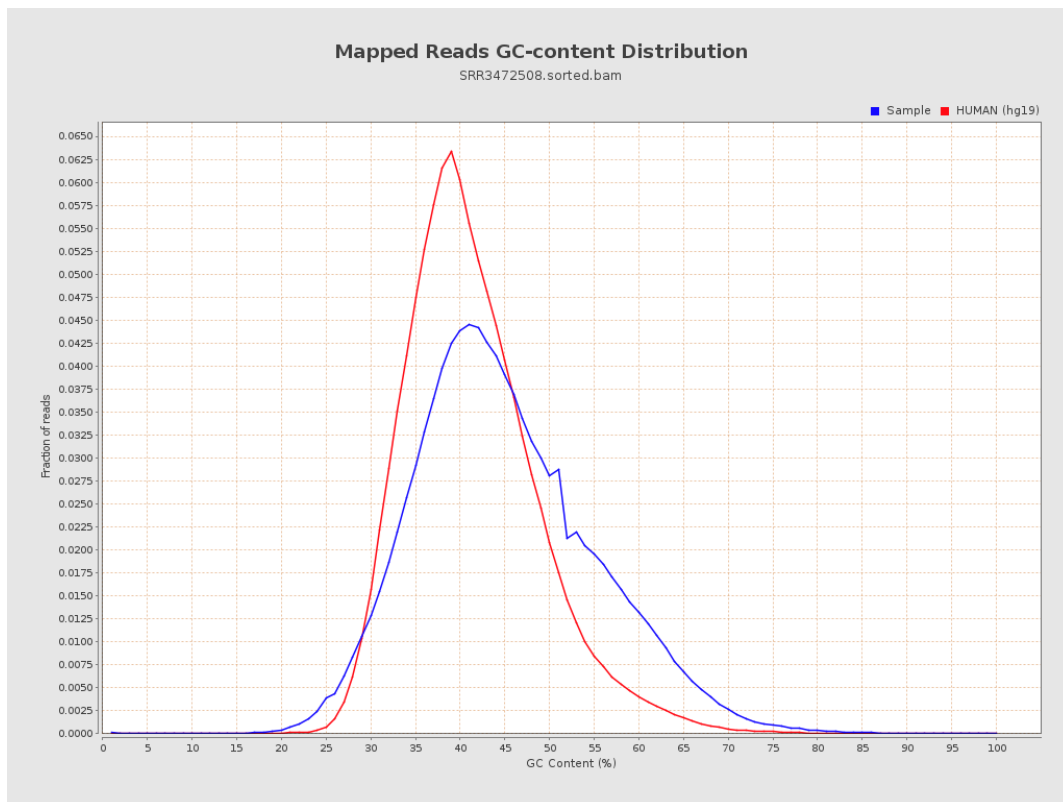
7. Results : Duplication Rate Histogram



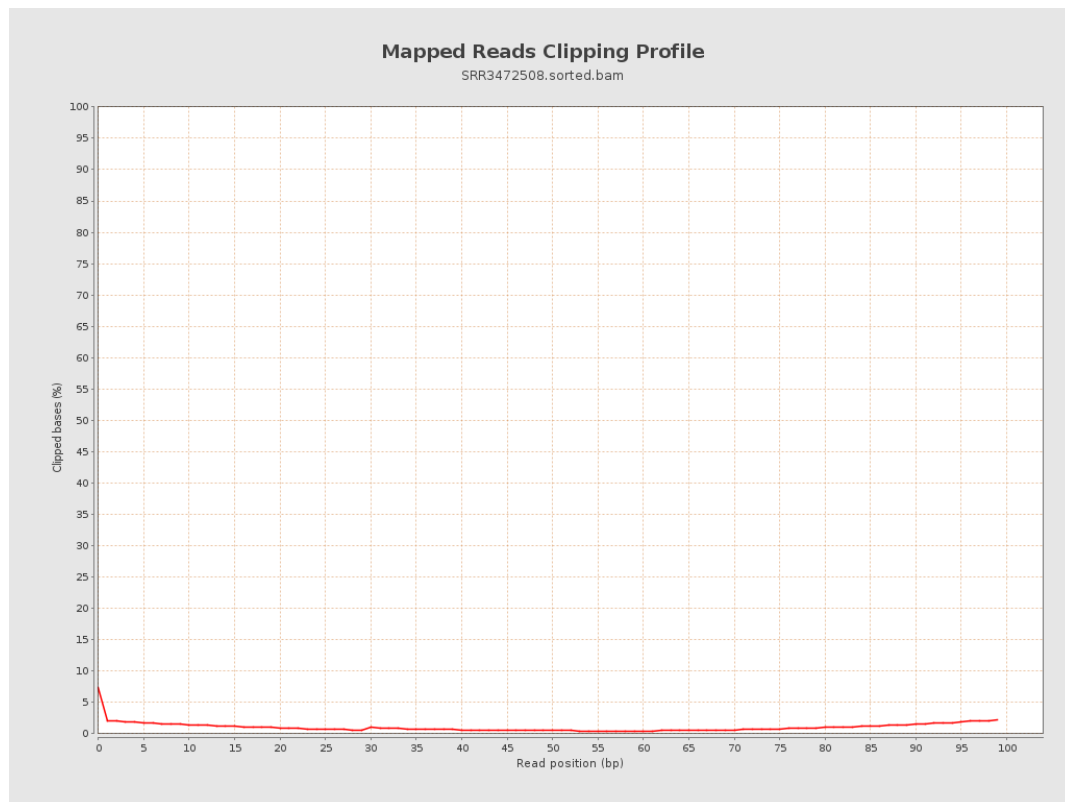
8. Results : Mapped Reads Nucleotide Content



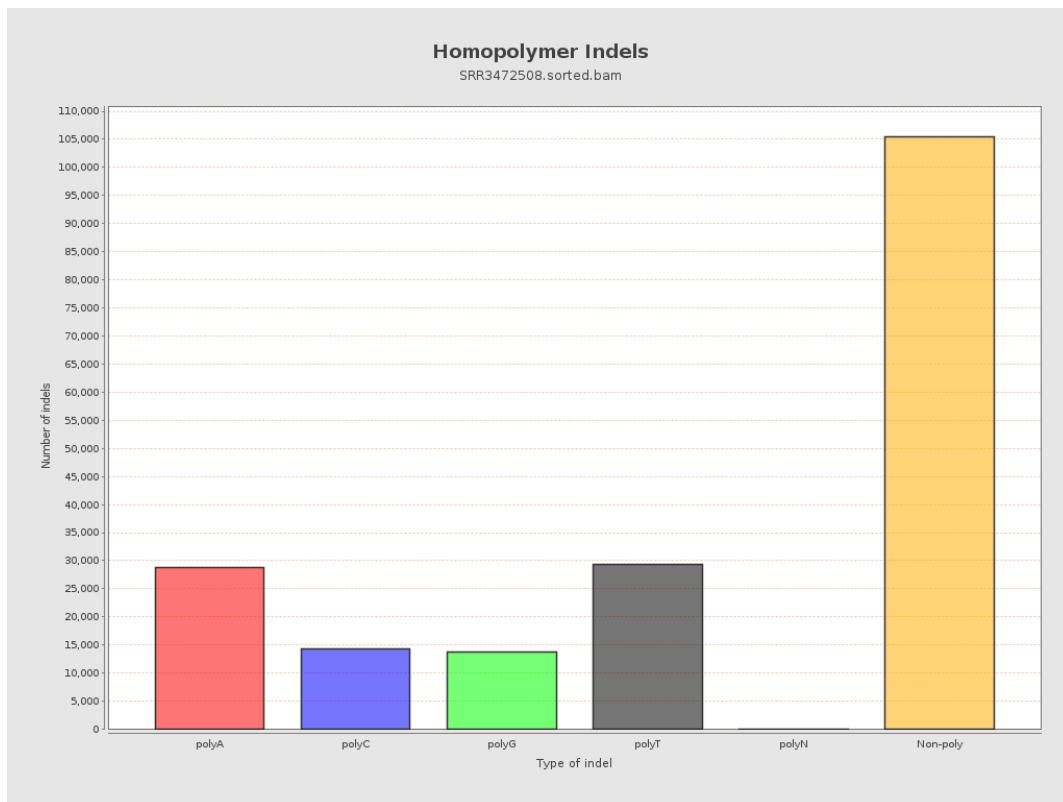
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



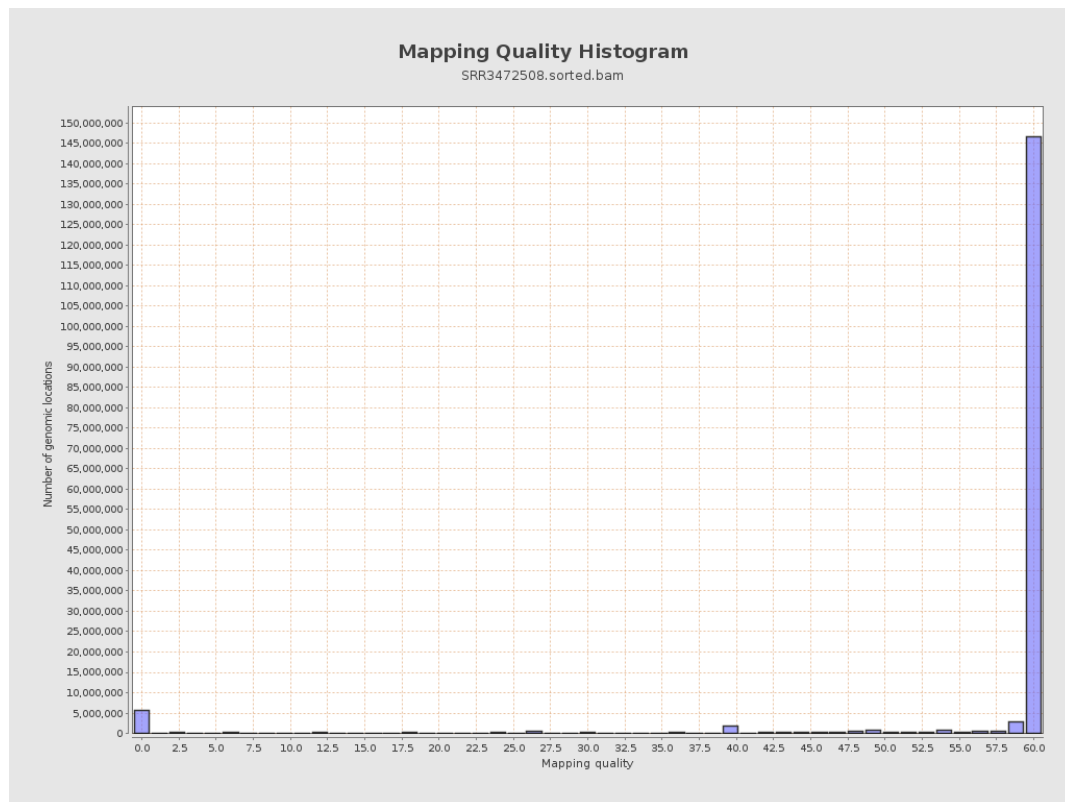
11. Results : Homopolymer Indels



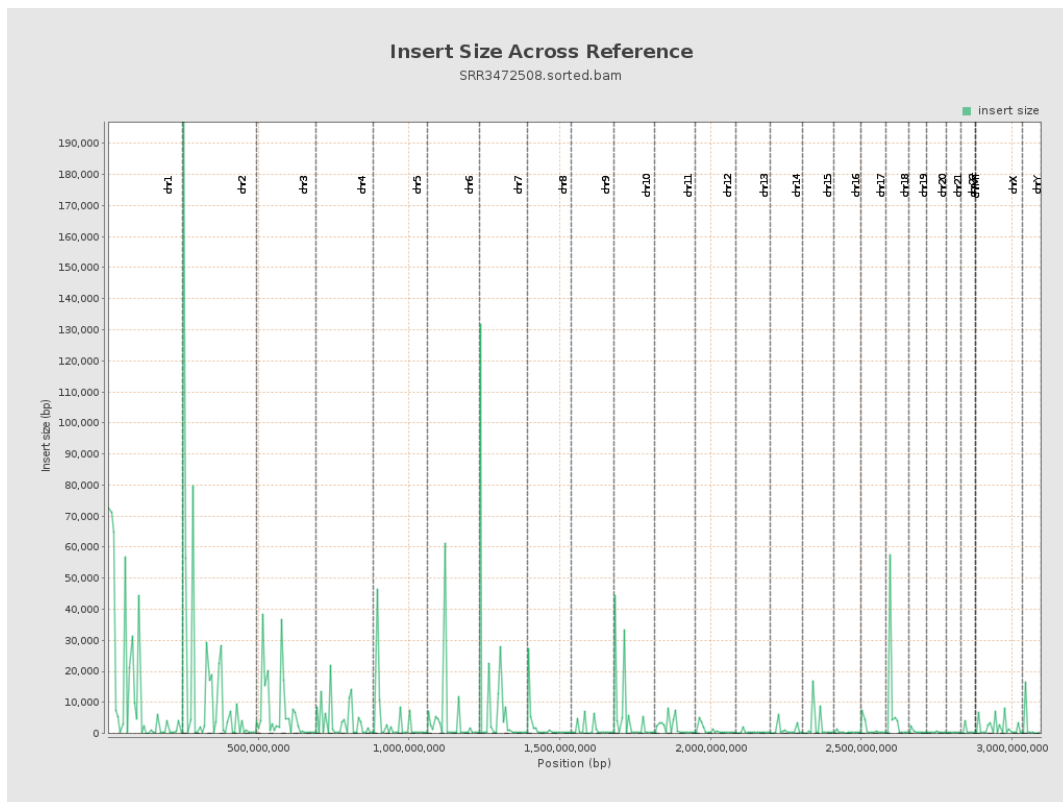
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

