

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:23:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472558.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_SRR3472558 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472558_1.fastq.gz SRR3472558_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:23:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472558.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,104,146
Mapped reads	9,909,638 / 98.07%
Unmapped reads	194,508 / 1.93%
Mapped paired reads	9,909,638 / 98.07%
Mapped reads, first in pair	4,974,341 / 49.23%
Mapped reads, second in pair	4,935,297 / 48.84%
Mapped reads, both in pair	9,819,640 / 97.18%
Mapped reads, singletons	89,998 / 0.89%
Secondary alignments	0
Supplementary alignments	43,424 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	5,362,377 / 53.07%
Duplication rate	42.77%
Clipped reads	982,750 / 9.73%

2.2. ACGT Content

Number/percentage of A's	273,709,583 / 28.22%
Number/percentage of C's	213,302,033 / 21.99%
Number/percentage of T's	271,010,840 / 27.94%
Number/percentage of G's	211,740,661 / 21.83%
Number/percentage of N's	149,623 / 0.02%

GC Percentage	43.82%
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2.3. Coverage

Mean	0.3134
Standard Deviation	10.2151

2.4. Mapping Quality

Mean Mapping Quality	54.94
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2.5. Insert size

Mean	37,306.95
Standard Deviation	1,882,786.1
P25/Median/P75	167 / 240 / 329

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	6,169,426
Insertions	54,863
Mapped reads with at least one insertion	0.55%
Deletions	52,996
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.6%

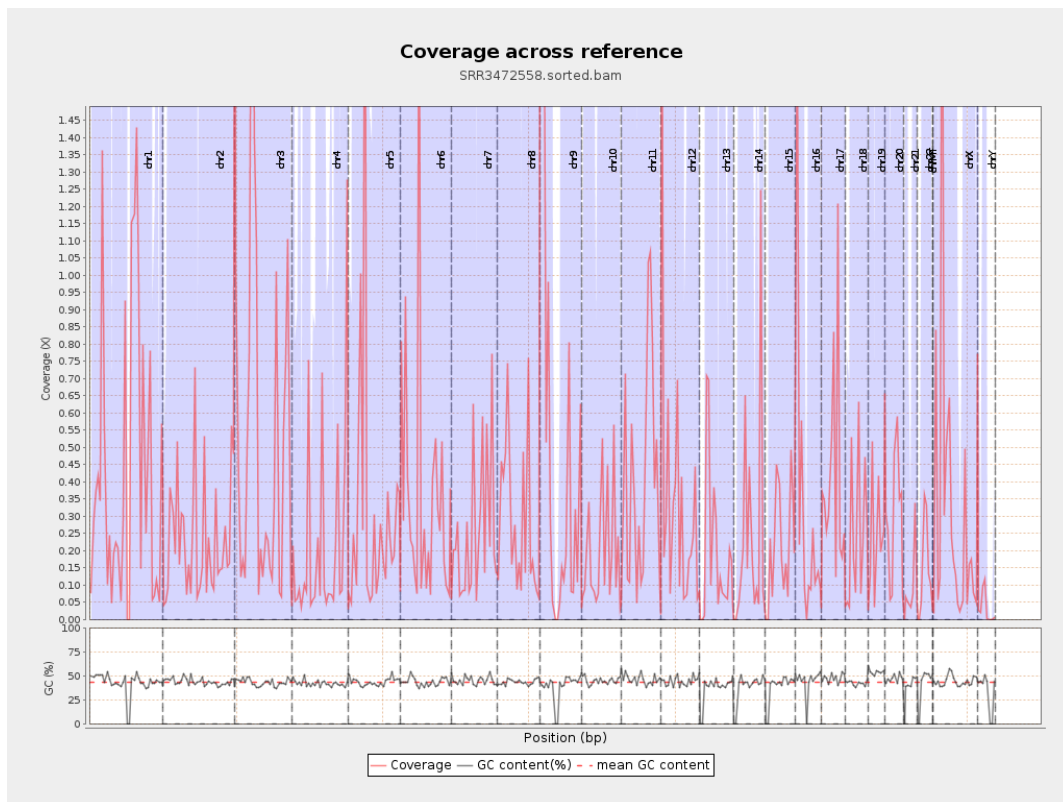
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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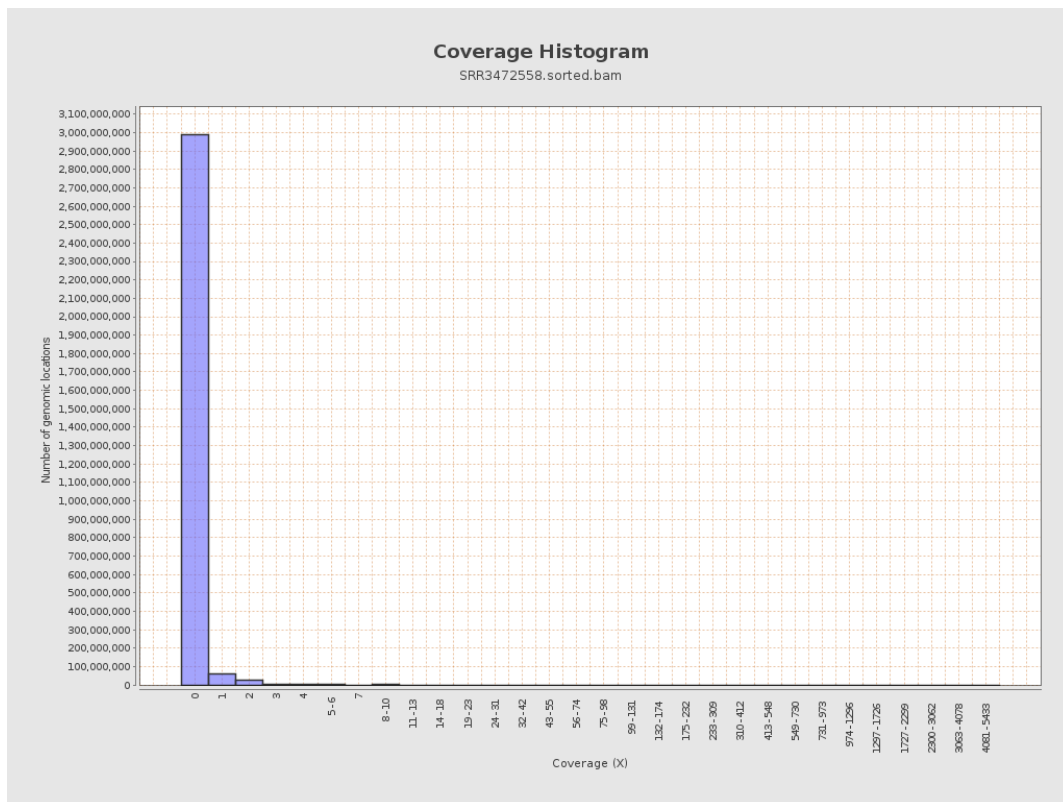
		bases	coverage	deviation
chr1	249250621	107493864	0.4313	14.771
chr2	243199373	56495243	0.2323	8.2323
chr3	198022430	110362743	0.5573	16.8525
chr4	191154276	42429247	0.222	8.0851
chr5	180915260	58986293	0.326	10.4445
chr6	171115067	63196291	0.3693	10.0681
chr7	159138663	40575471	0.255	7.9235
chr8	146364022	41677629	0.2848	8.5609
chr9	141213431	62933920	0.4457	11.2684
chr10	135534747	27641128	0.2039	7.0529
chr11	135006516	56251640	0.4167	13.6952
chr12	133851895	48591532	0.363	9.8243
chr13	115169878	22853228	0.1984	6.7434
chr14	107349540	25466821	0.2372	8.1012
chr15	102531392	21421469	0.2089	7.051
chr16	90354753	29691352	0.3286	8.6612
chr17	81195210	34609216	0.4262	8.5303
chr18	78077248	19037381	0.2438	9.0635
chr19	59128983	15021429	0.254	6.0221
chr20	63025520	18822333	0.2986	8.2613
chr21	48129895	4601683	0.0956	3.2727
chr22	51304566	7624483	0.1486	3.3712
chrMT	16571	1383	0.0835	0.3117
chrX	155270560	52231763	0.3364	10.9122

chrY	59373566	2025996	0.0341	1.6634
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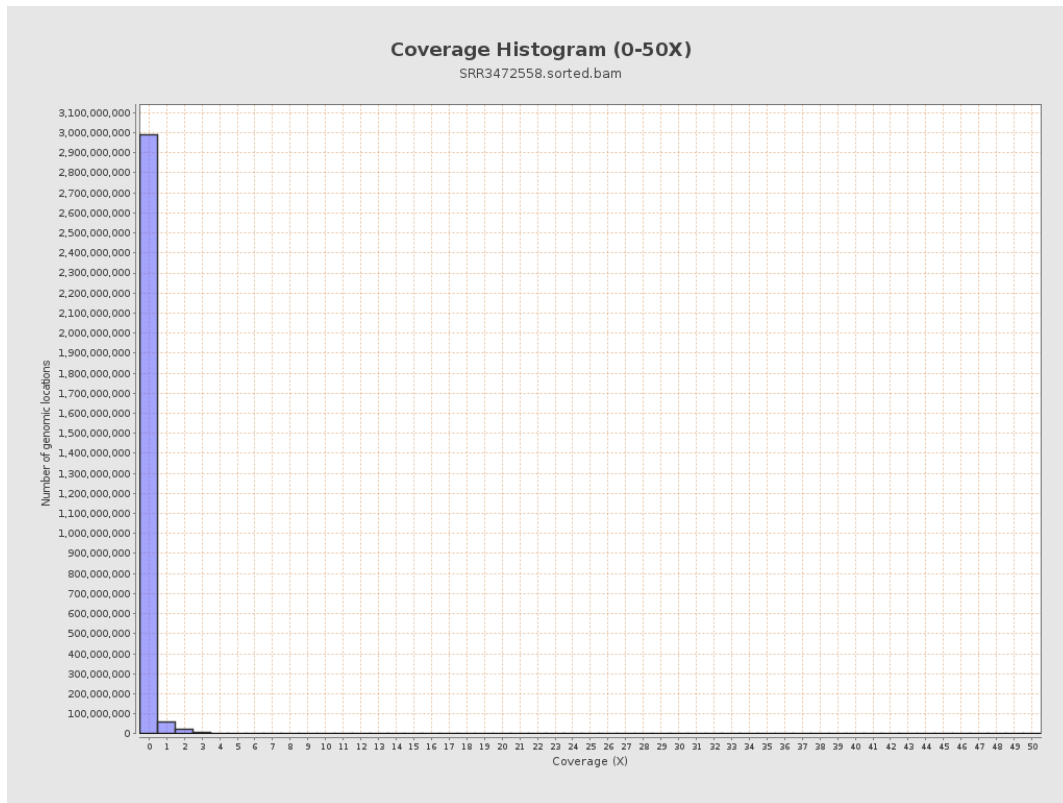
3. Results : Coverage across reference



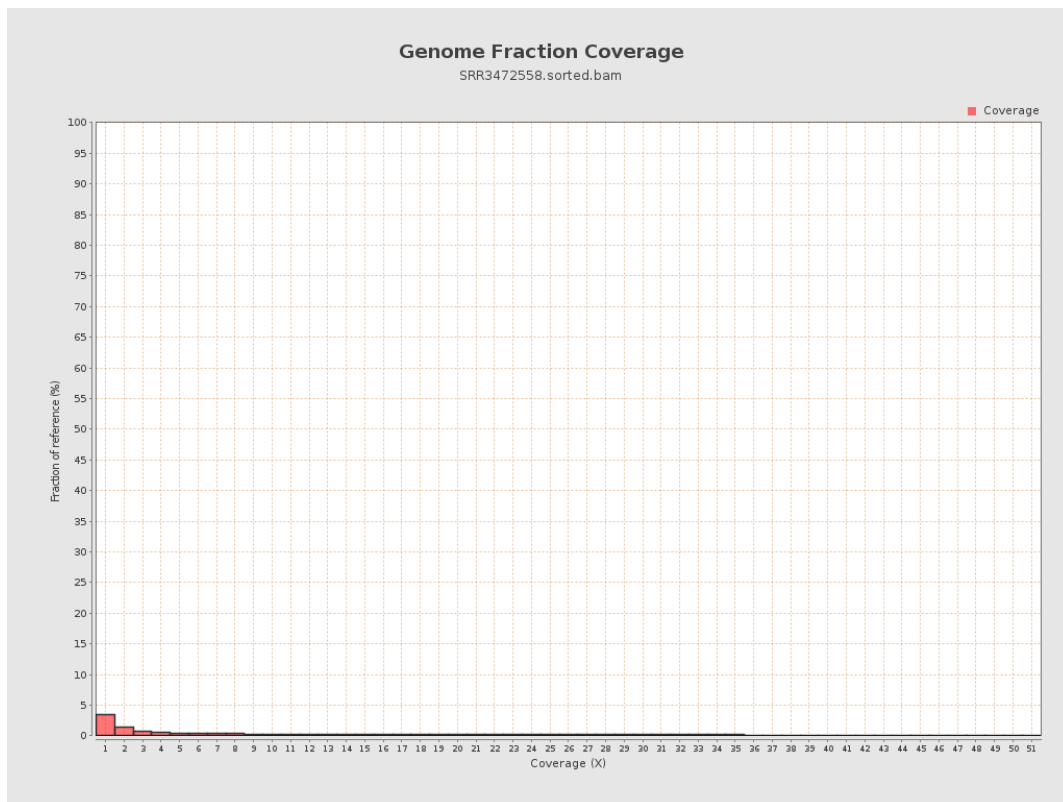
4. Results : Coverage Histogram



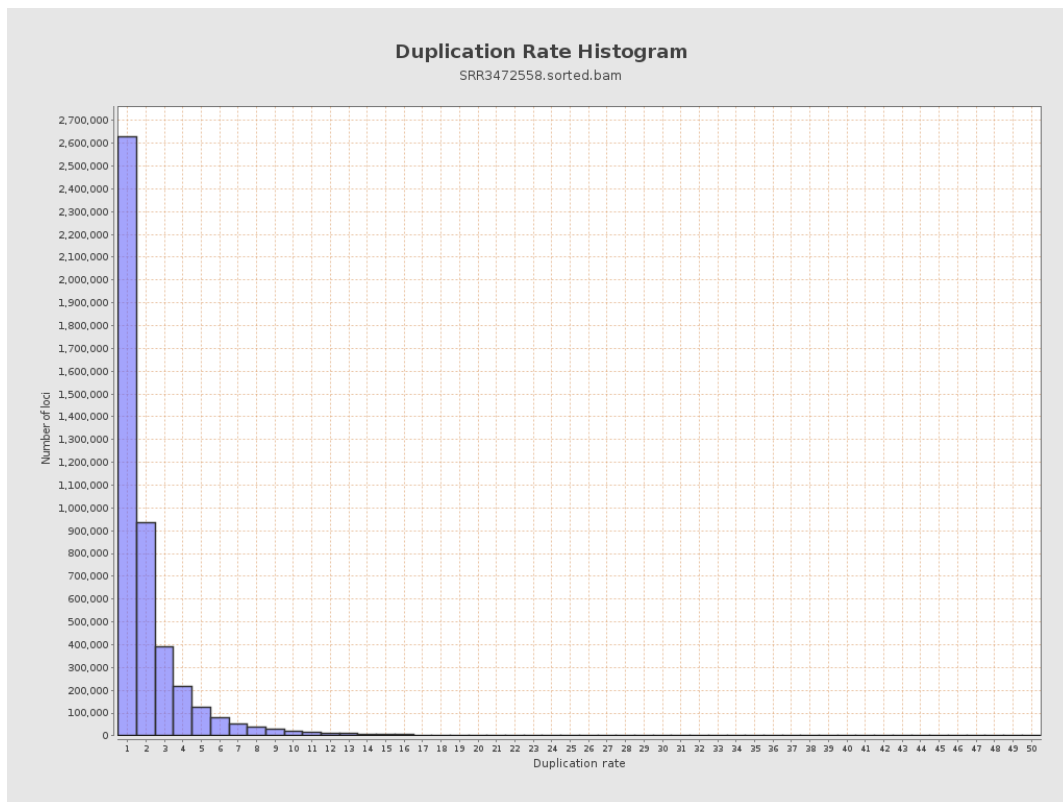
5. Results : Coverage Histogram (0-50X)



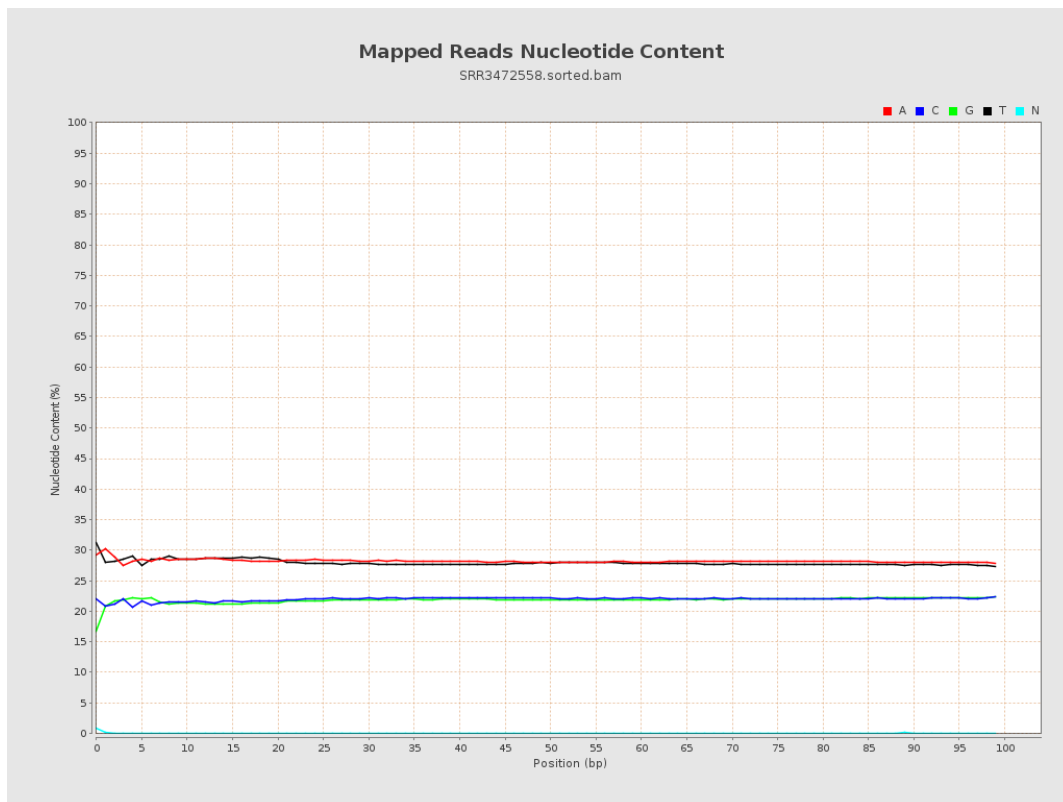
6. Results : Genome Fraction Coverage



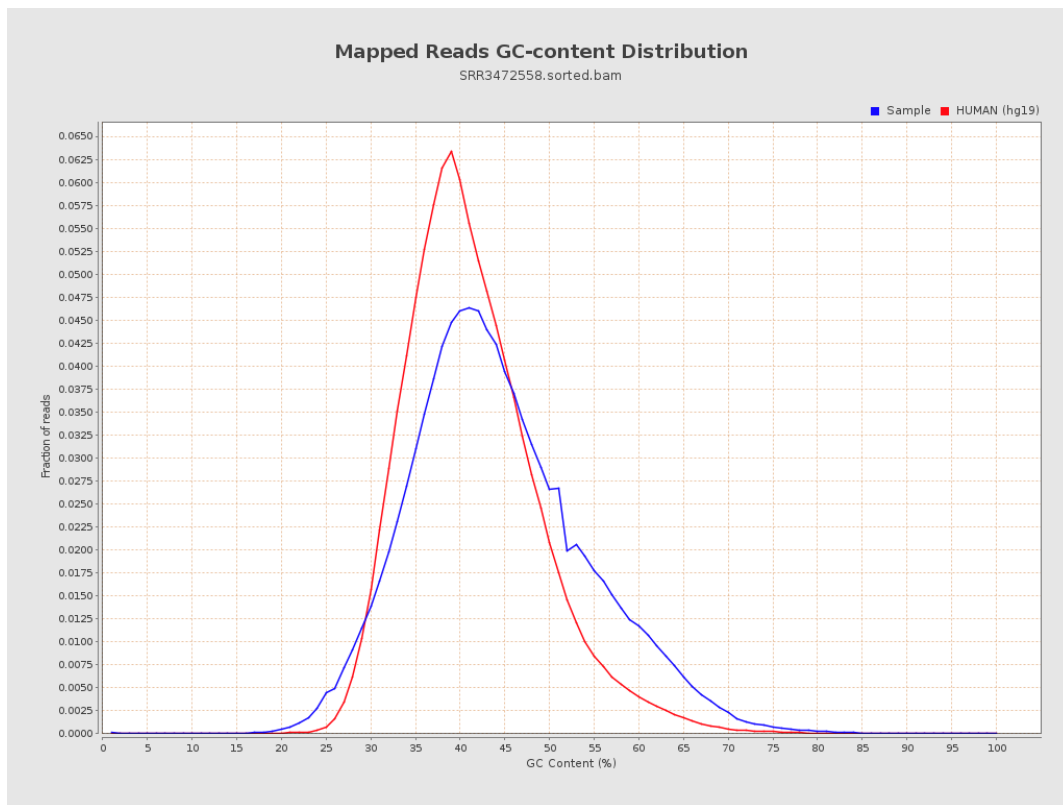
7. Results : Duplication Rate Histogram



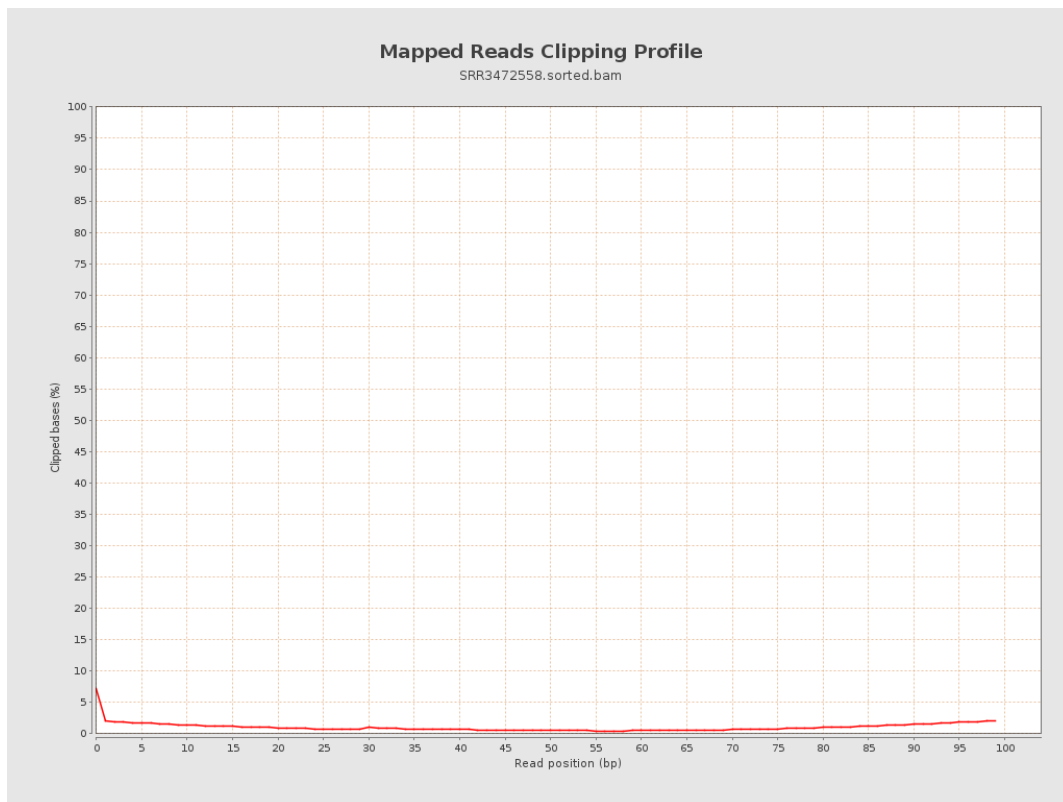
8. Results : Mapped Reads Nucleotide Content



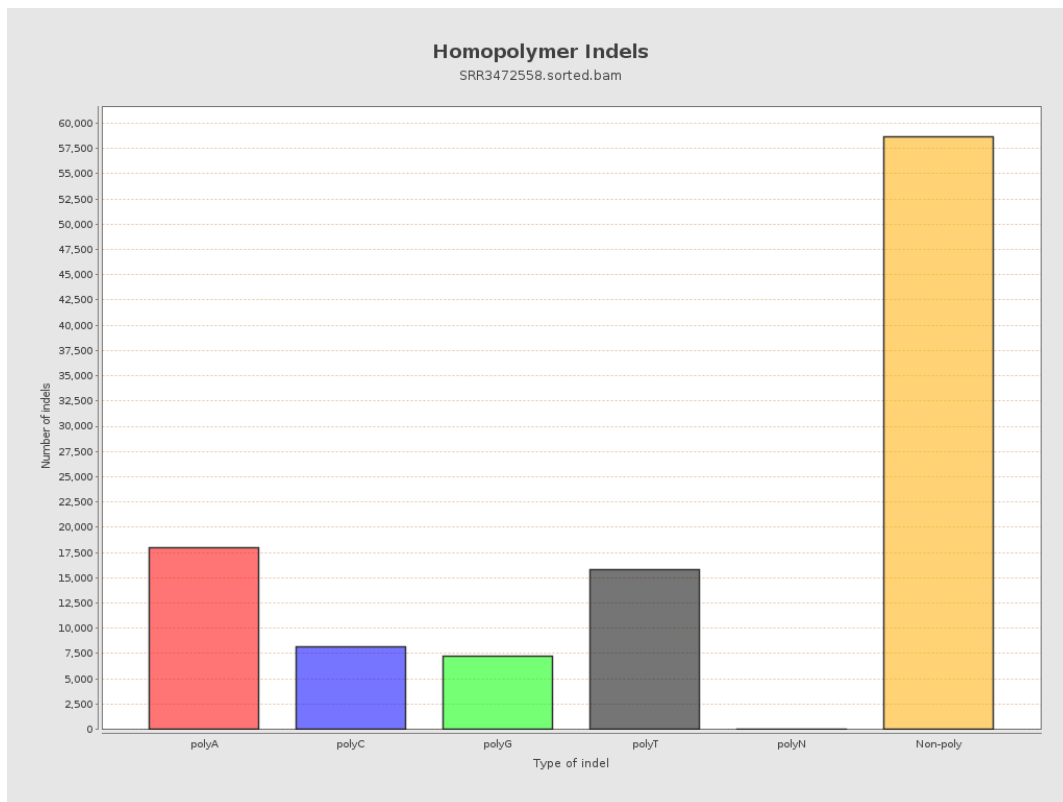
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



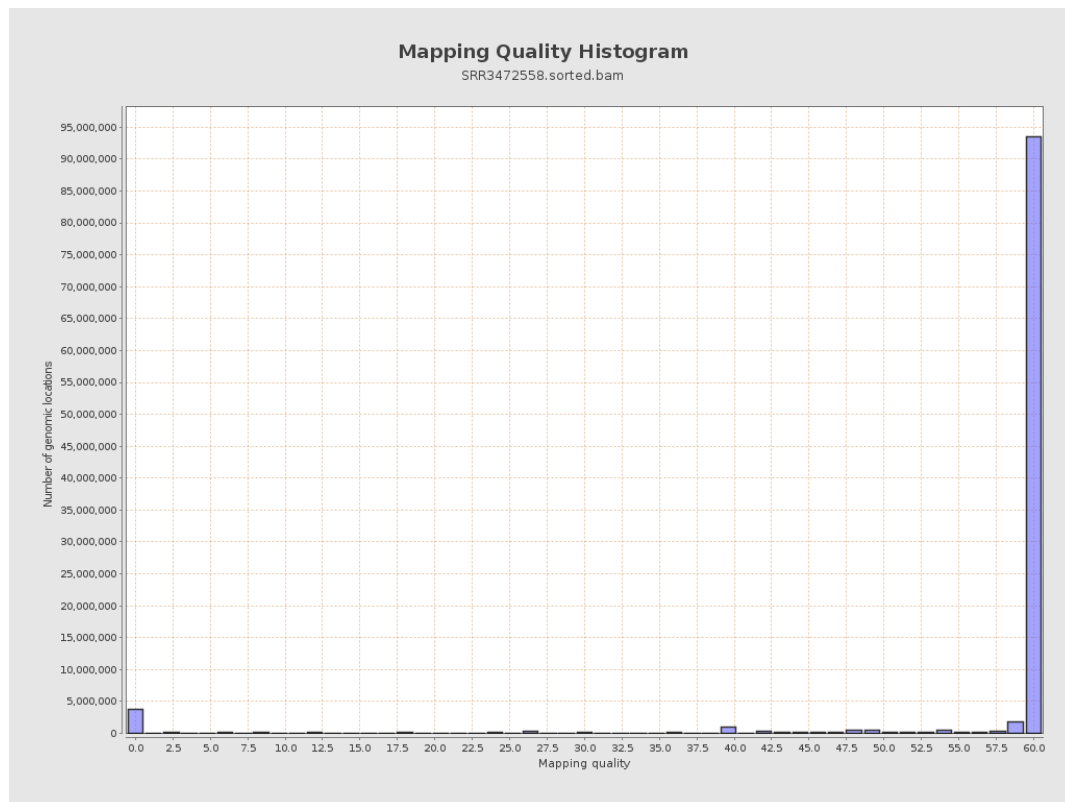
11. Results : Homopolymer Indels



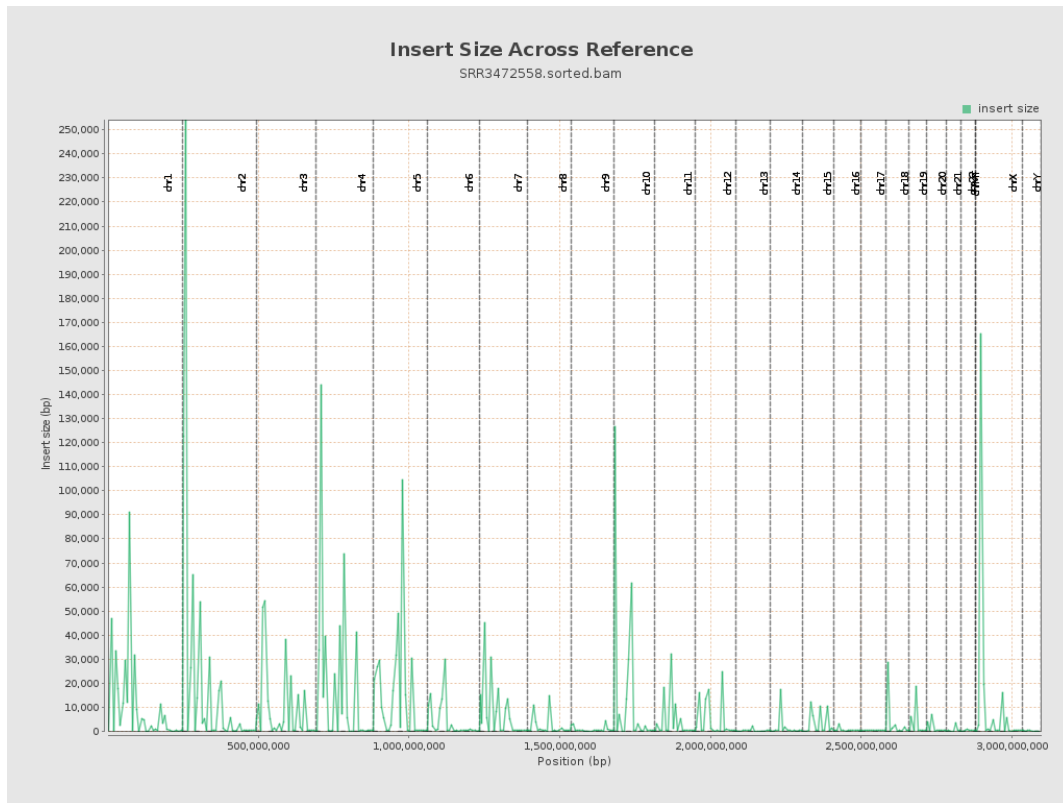
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

