Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:03:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472547.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_SRR3472547 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472547_1.fastq.gz SRR3472547_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:03:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472547.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,932,376
Mapped reads	11,783,081 / 98.75%
Unmapped reads	149,295 / 1.25%
Mapped paired reads	11,783,081 / 98.75%
Mapped reads, first in pair	5,907,350 / 49.51%
Mapped reads, second in pair	5,875,731 / 49.24%
Mapped reads, both in pair	11,712,784 / 98.16%
Mapped reads, singletons	70,297 / 0.59%
Secondary alignments	0
Supplementary alignments	54,984 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	9,443,982 / 79.15%
Duplication rate	35.76%
Clipped reads	1,177,599 / 9.87%

2.2. ACGT Content

Number/percentage of A's	326,476,683 / 28.26%
Number/percentage of C's	251,945,608 / 21.81%
Number/percentage of T's	323,193,535 / 27.97%
Number/percentage of G's	253,561,999 / 21.95%
Number/percentage of N's	181,468 / 0.02%

GC Percentage	43.75%

2.3. Coverage

Mean	0.3733
Standard Deviation	70.2926

2.4. Mapping Quality

Mean Mapping Quality	49.53

2.5. Insert size

Mean	26,783.89
Standard Deviation	1,520,492.05
P25/Median/P75	153 / 211 / 284

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	6,746,001
Insertions	49,738
Mapped reads with at least one insertion	0.42%
Deletions	56,731
Mapped reads with at least one deletion	0.48%
Homopolymer indels	49.25%

2.7. Chromosome stats

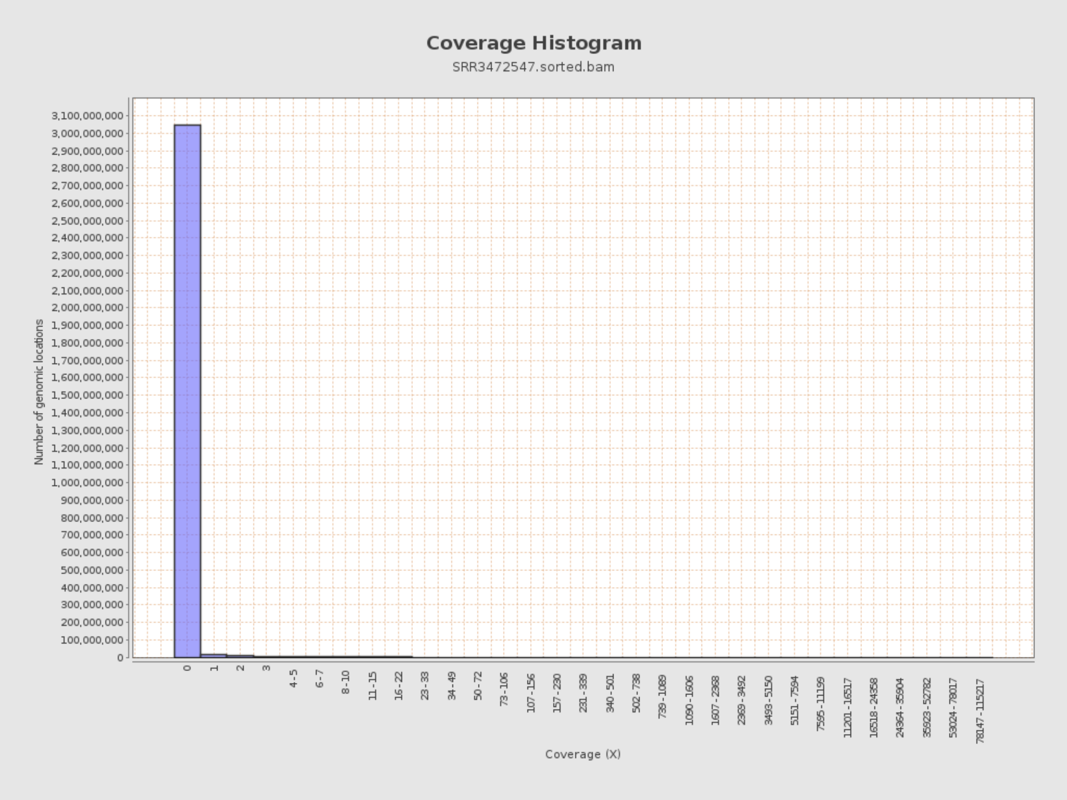
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	39797520	0.1597	25.4026
chr2	243199373	182015739	0.7484	121.8139
chr3	198022430	18415788	0.093	14.0515
chr4	191154276	16073650	0.0841	3.3812
chr5	180915260	67336031	0.3722	59.2286
chr6	171115067	92795410	0.5423	57.3315
chr7	159138663	20113428	0.1264	17.5147
chr8	146364022	63174947	0.4316	60.7405
chr9	141213431	113348670	0.8027	98.8271
chr10	135534747	7855996	0.058	3.5111
chr11	135006516	26673168	0.1976	8.5795
chr12	133851895	60993806	0.4557	66.3581
chr13	115169878	48713790	0.423	44.5576
chr14	107349540	60465234	0.5633	49.4538
chr15	102531392	2220566	0.0217	1.2749
chr16	90354753	6012327	0.0665	1.3927
chr17	81195210	60438199	0.7444	75.1328
chr18	78077248	18918241	0.2423	24.917
chr19	59128983	11284342	0.1908	10.5138
chr20	63025520	1614447	0.0256	0.4763
chr21	48129895	4959419	0.103	1.7941
chr22	51304566	894911	0.0174	1.5188
chrMT	16571	2608	0.1574	0.7916
chrX	155270560	222108274	1.4305	207.2992

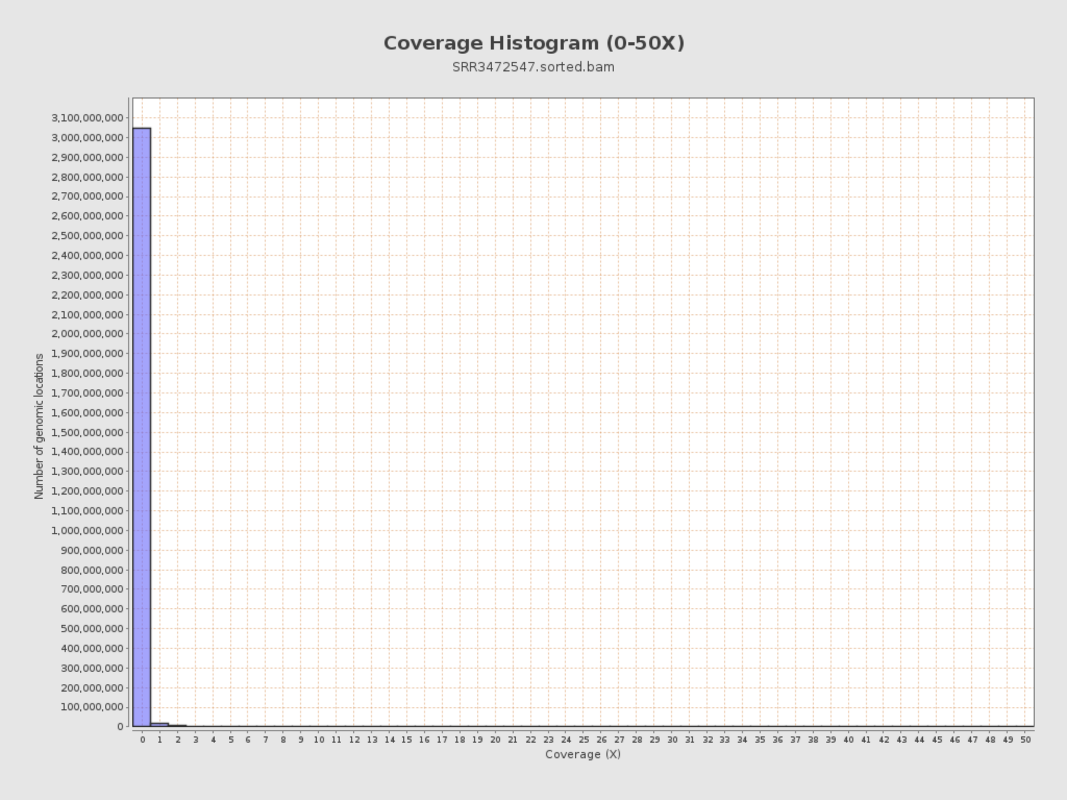
chrY	59373566	9331557	0.1572	26.2827

3. Results : Coverage across reference

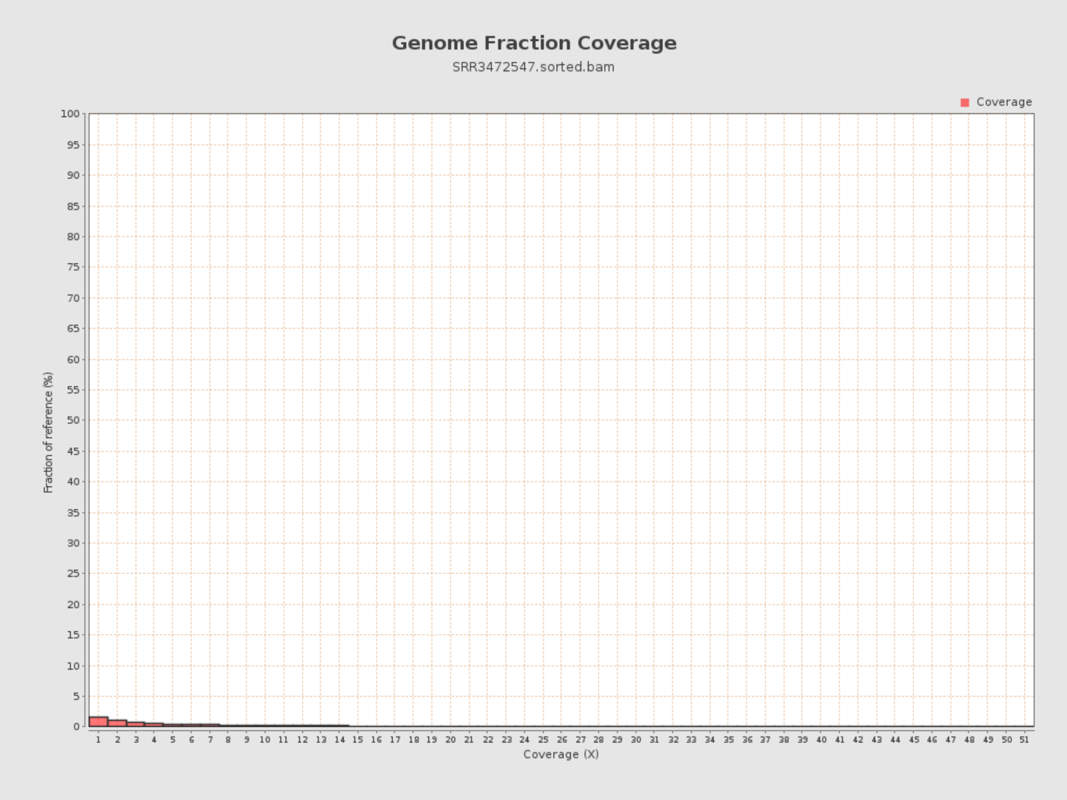
4. Results : Coverage Histogram



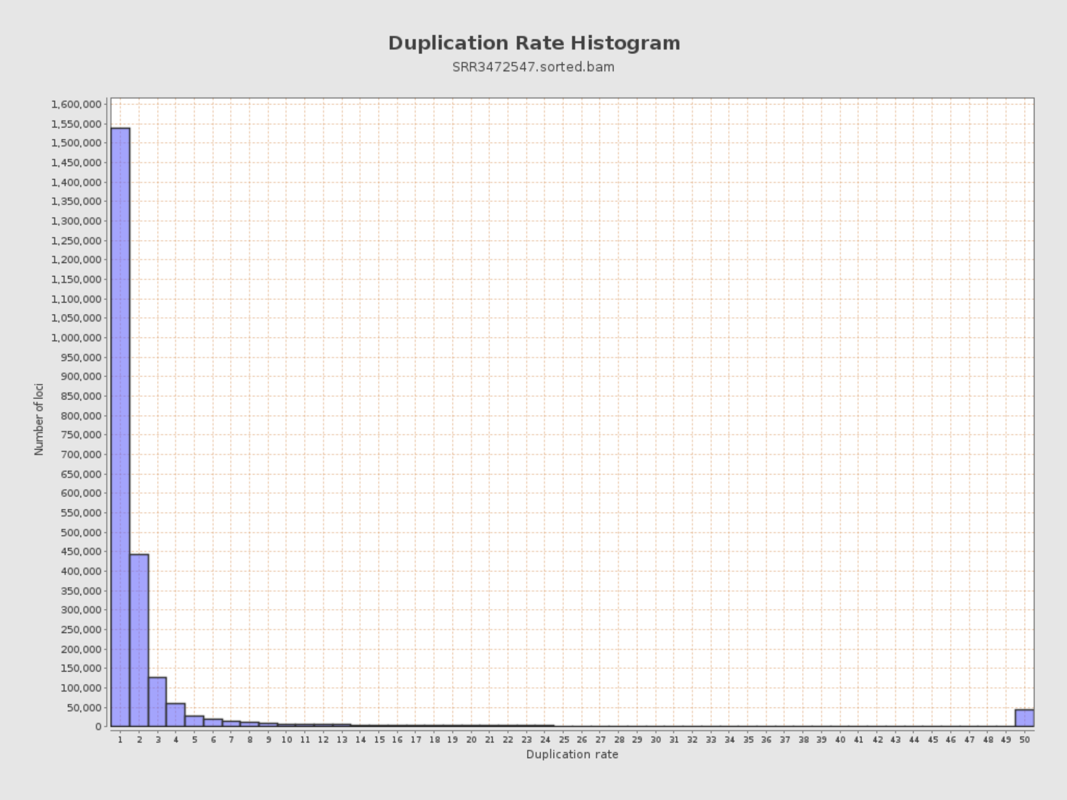
5. Results : Coverage Histogram (0-50X)



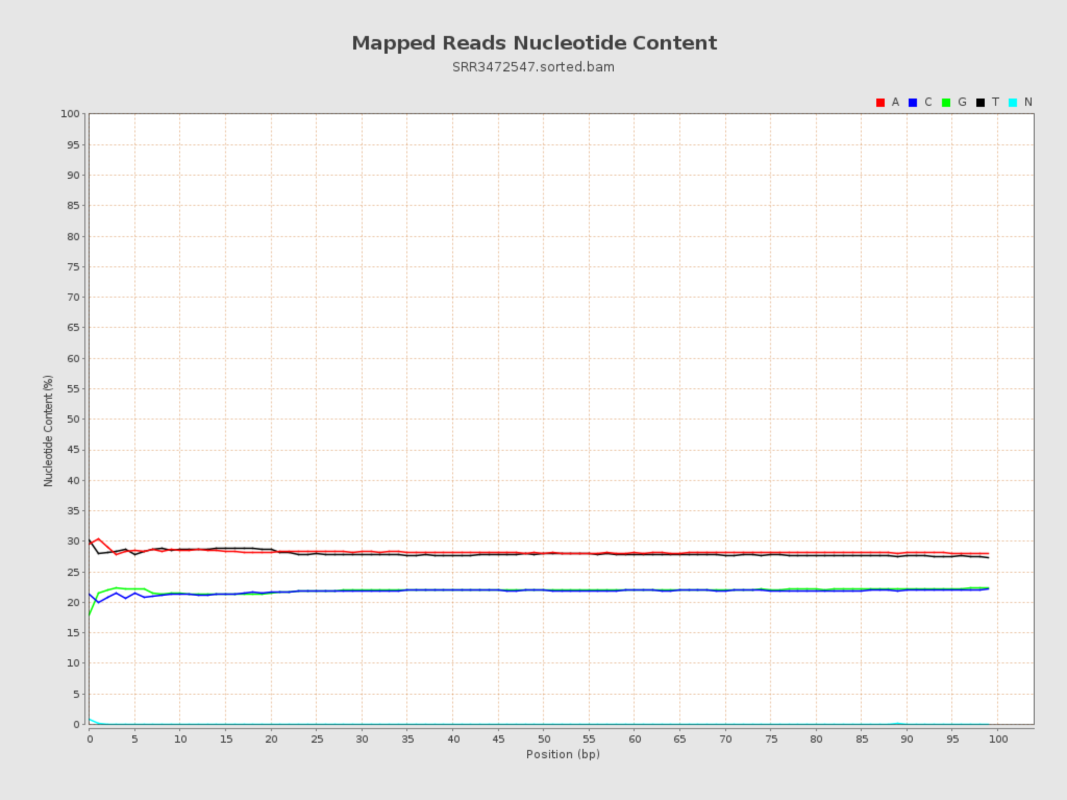
6. Results : Genome Fraction Coverage



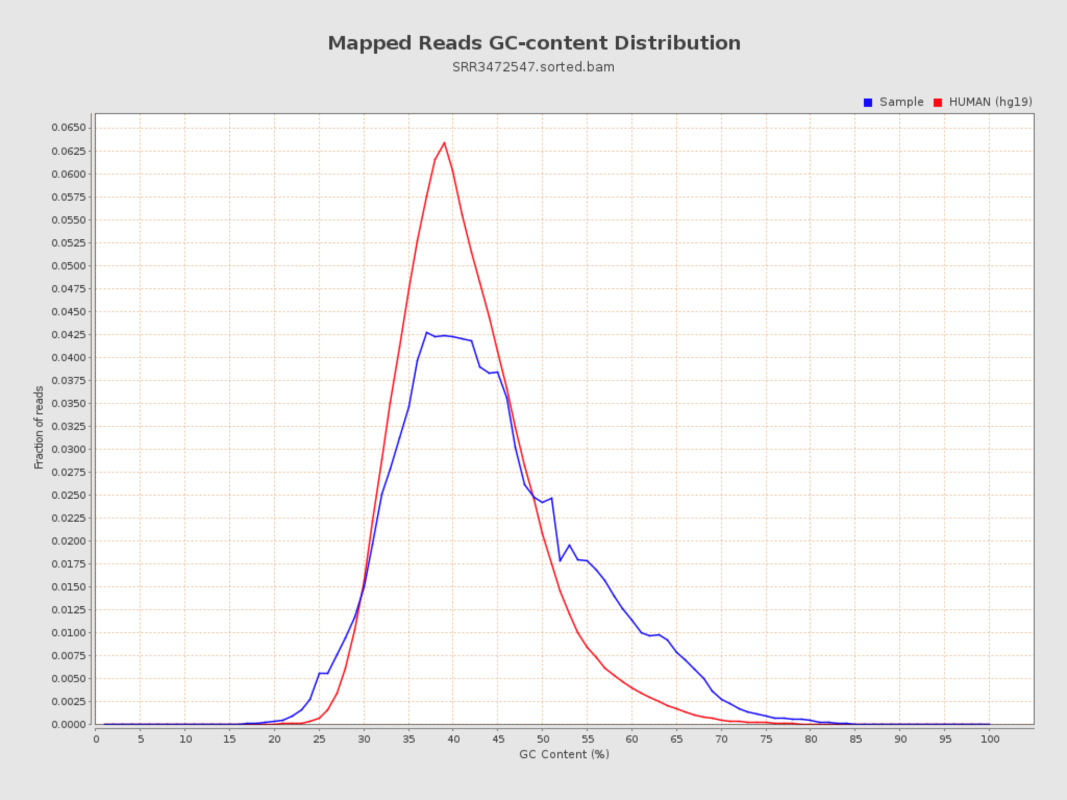
7. Results : Duplication Rate Histogram



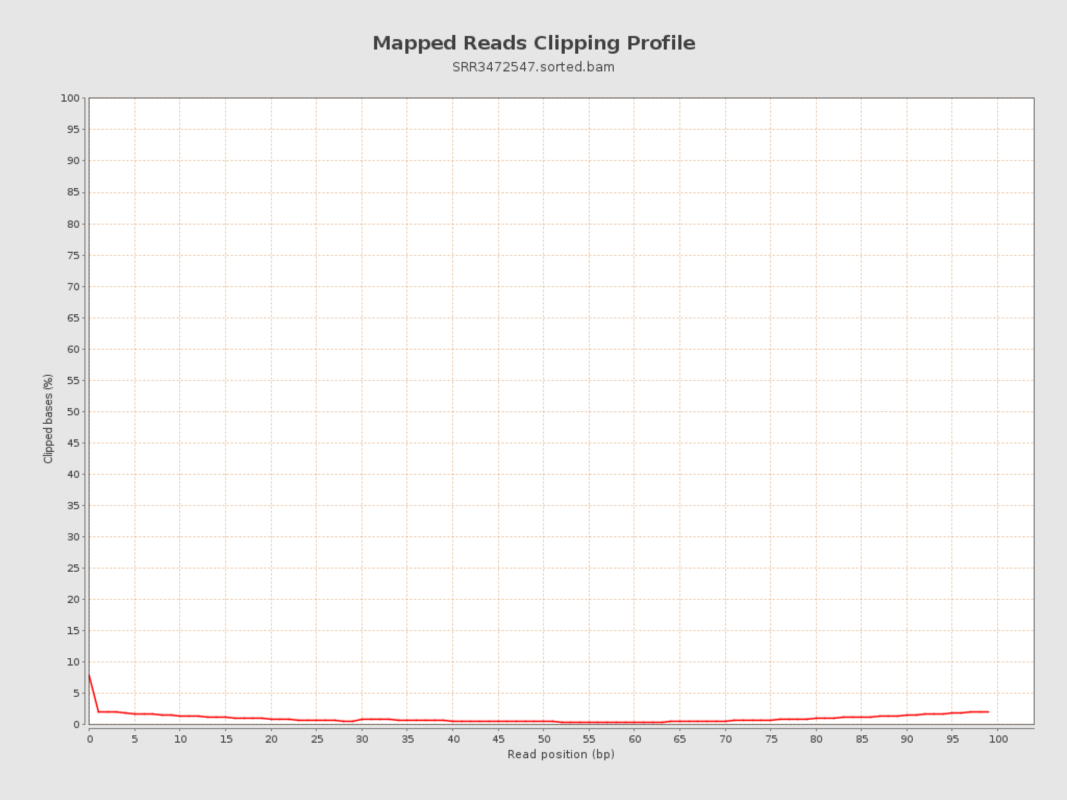
8. Results : Mapped Reads Nucleotide Content



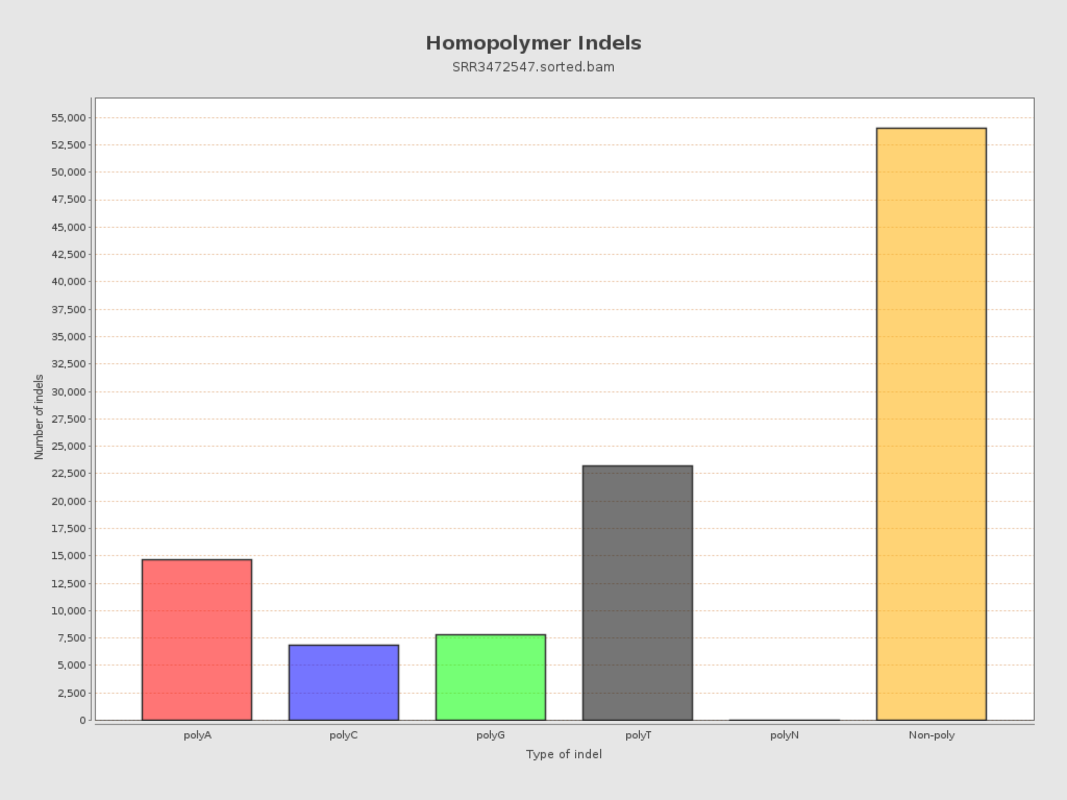
9. Results : Mapped Reads GC-content Distribution



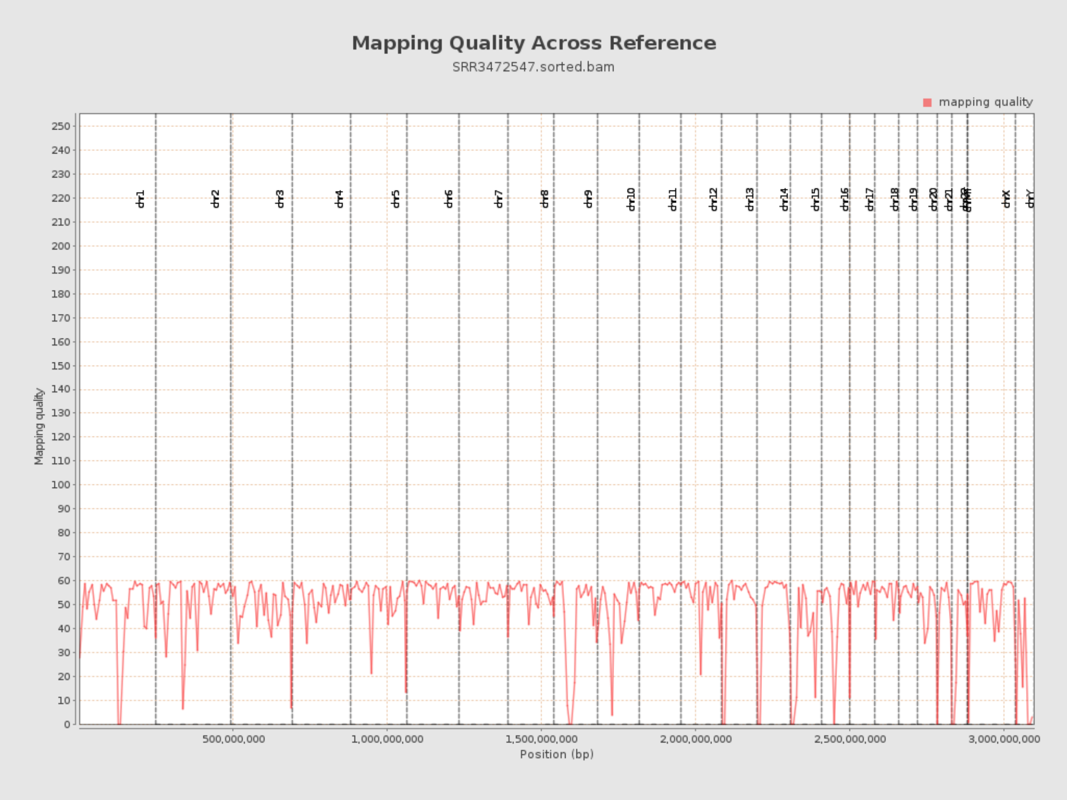
10. Results : Mapped Reads Clipping Profile



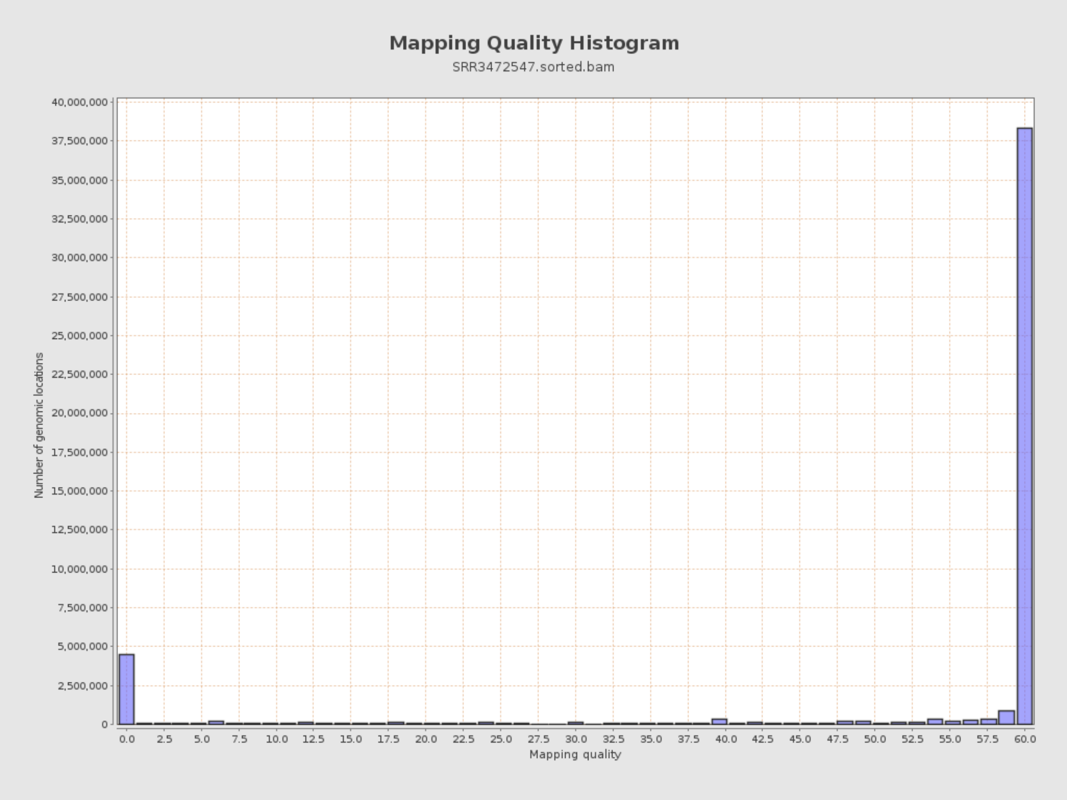
11. Results : Homopolymer Indels



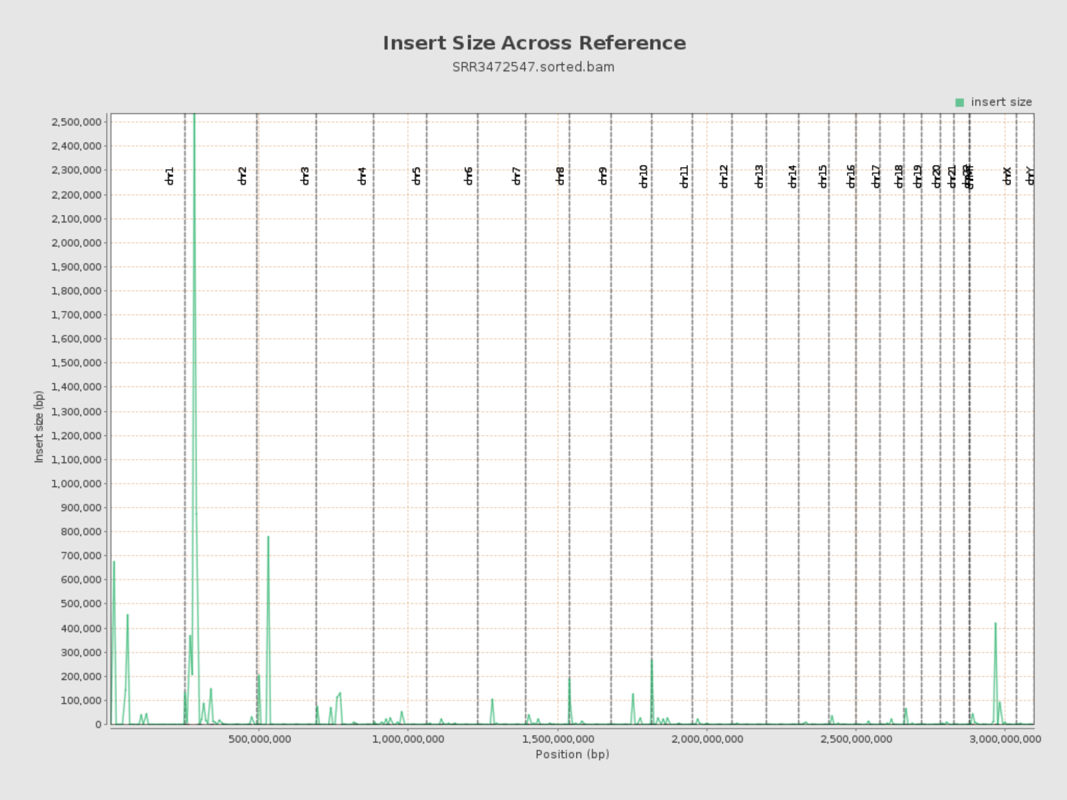
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram