Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 05:19:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472749.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_SRR3472749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472749_1.fastq.gz SRR3472749_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 05:19:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,700,538
Mapped reads	12,569,921 / 98.97%
Unmapped reads	130,617 / 1.03%
Mapped paired reads	12,569,921 / 98.97%
Mapped reads, first in pair	6,312,678 / 49.7%
Mapped reads, second in pair	6,257,243 / 49.27%
Mapped reads, both in pair	12,487,570 / 98.32%
Mapped reads, singletons	82,351 / 0.65%
Secondary alignments	0
Supplementary alignments	45,210 / 0.36%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	7,374,601 / 58.07%
Duplication rate	45.62%
Clipped reads	1,006,913 / 7.93%

2.2. ACGT Content

Number/percentage of A's	348,218,983 / 28.12%
Number/percentage of C's	272,386,617 / 22%
Number/percentage of T's	346,361,371 / 27.97%
Number/percentage of G's	271,083,121 / 21.89%
Number/percentage of N's	235,848 / 0.02%

GC Percentage	43.89%

2.3. Coverage

Mean	0.4001
Standard Deviation	13.2339

2.4. Mapping Quality

Mean Mapping Quality	55.21

2.5. Insert size

Mean	23,845.52
Standard Deviation	1,523,470.49
P25/Median/P75	176 / 249 / 338

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	8,110,764
Insertions	73,927
Mapped reads with at least one insertion	0.58%
Deletions	71,782
Mapped reads with at least one deletion	0.56%
Homopolymer indels	45.86%

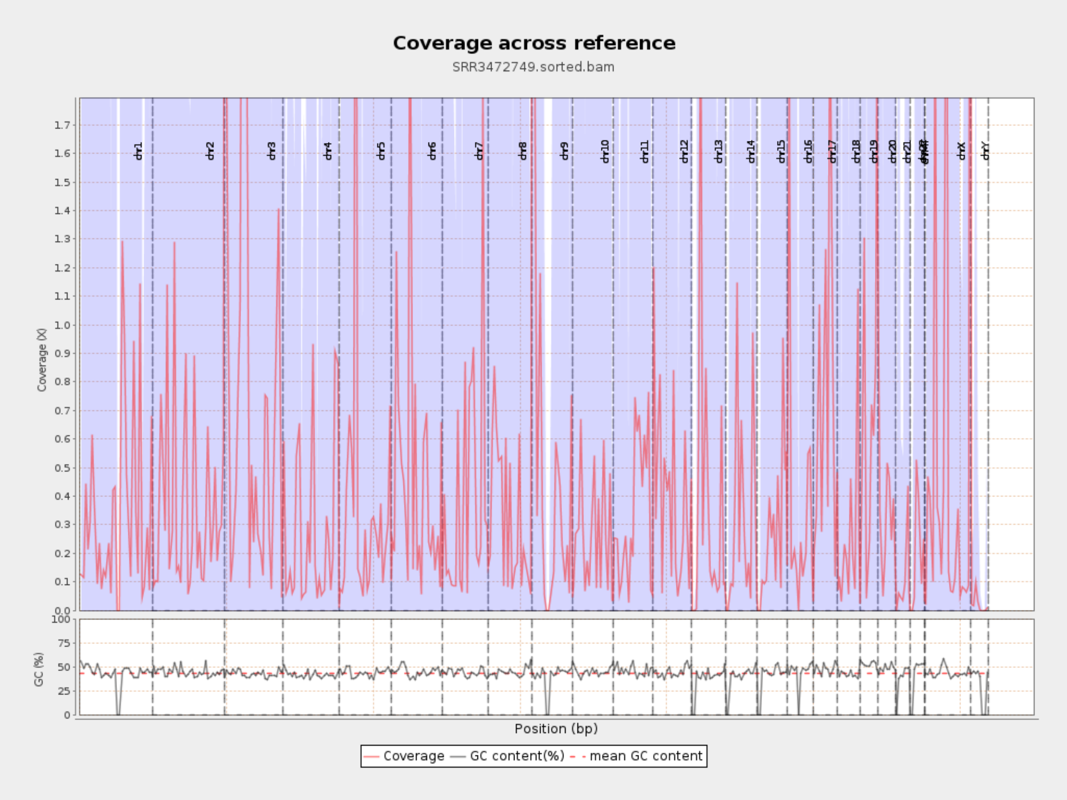
2.7. Chromosome stats

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

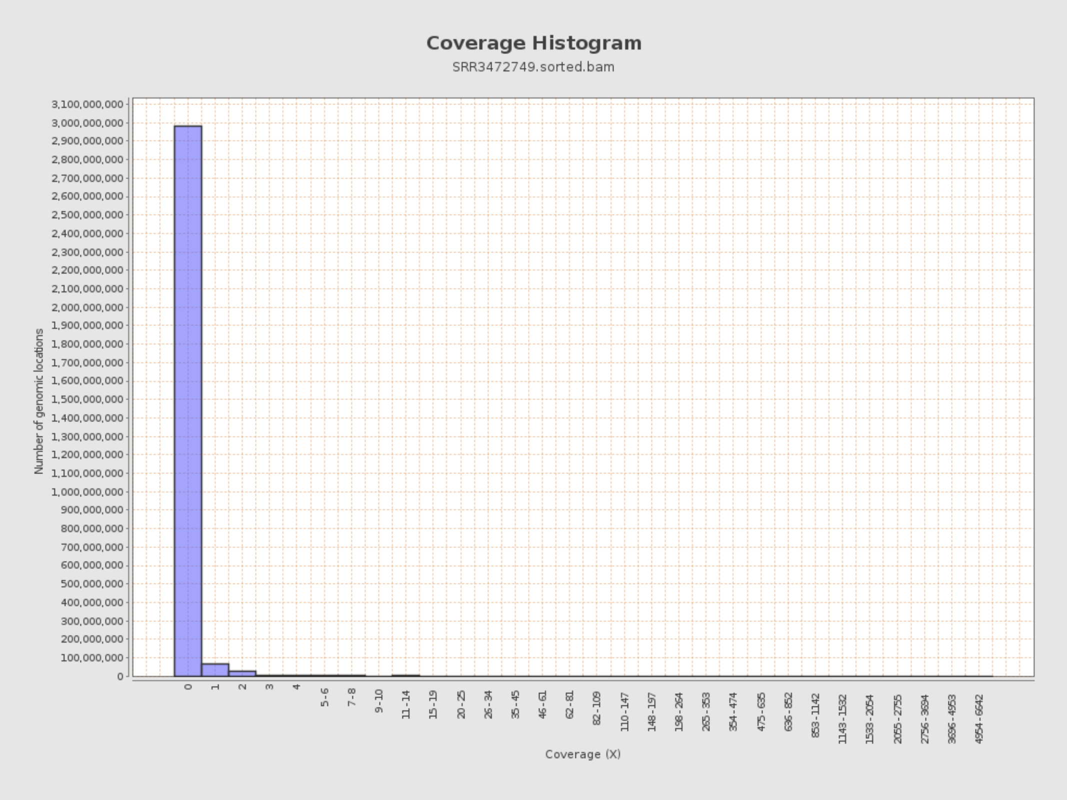
		bases	coverage	deviation
chr1	249250621	84966247	0.3409	9.6643
chr2	243199373	87540668	0.36	11.6919
chr3	198022430	169633139	0.8566	19.0174
chr4	191154276	51327165	0.2685	9.8611
chr5	180915260	71453869	0.395	13.5784
chr6	171115067	79555635	0.4649	12.4233
chr7	159138663	64442868	0.4049	17.5886
chr8	146364022	48807544	0.3335	11.4865
chr9	141213431	69587133	0.4928	16.3794
chr10	135534747	37034836	0.2732	11.039
chr11	135006516	46752574	0.3463	9.7308
chr12	133851895	54895313	0.4101	11.5657
chr13	115169878	44260468	0.3843	19.3646
chr14	107349540	33867010	0.3155	10.0873
chr15	102531392	27893704	0.2721	8.4974
chr16	90354753	33493126	0.3707	9.2813
chr17	81195210	59568073	0.7336	16.1063
chr18	78077248	20597812	0.2638	9.2082
chr19	59128983	37435985	0.6331	16.1243
chr20	63025520	22099334	0.3506	11.576
chr21	48129895	5513430	0.1146	4.8882
chr22	51304566	10294274	0.2007	5.5146
chrMT	16571	1366	0.0824	0.3359
chrX	155270560	76128192	0.4903	19.3959

chrY	59373566	1306746	0.022	0.7824

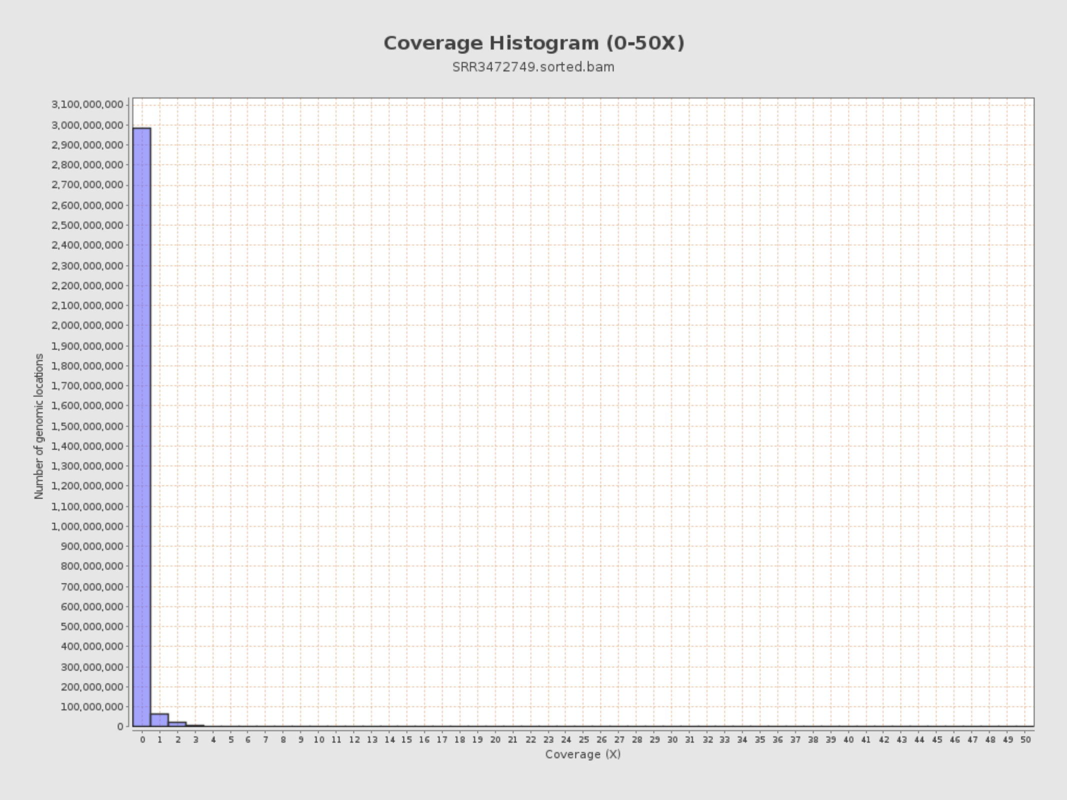
3. Results : Coverage across reference



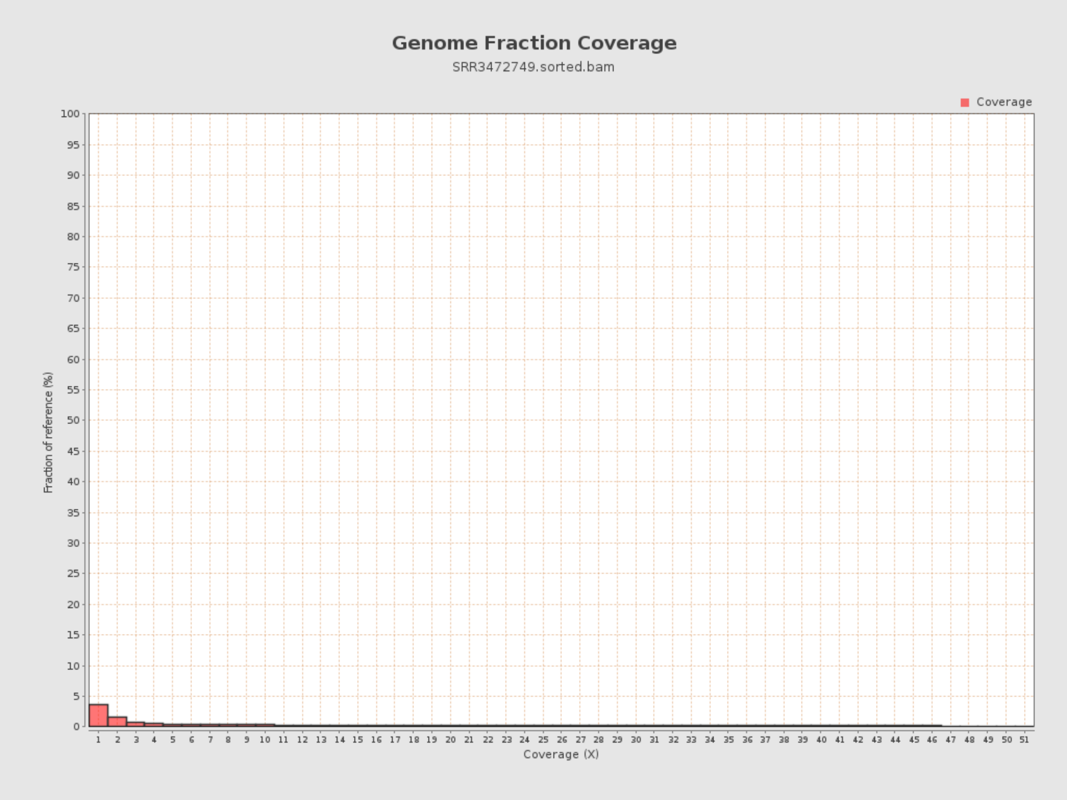
4. Results : Coverage Histogram



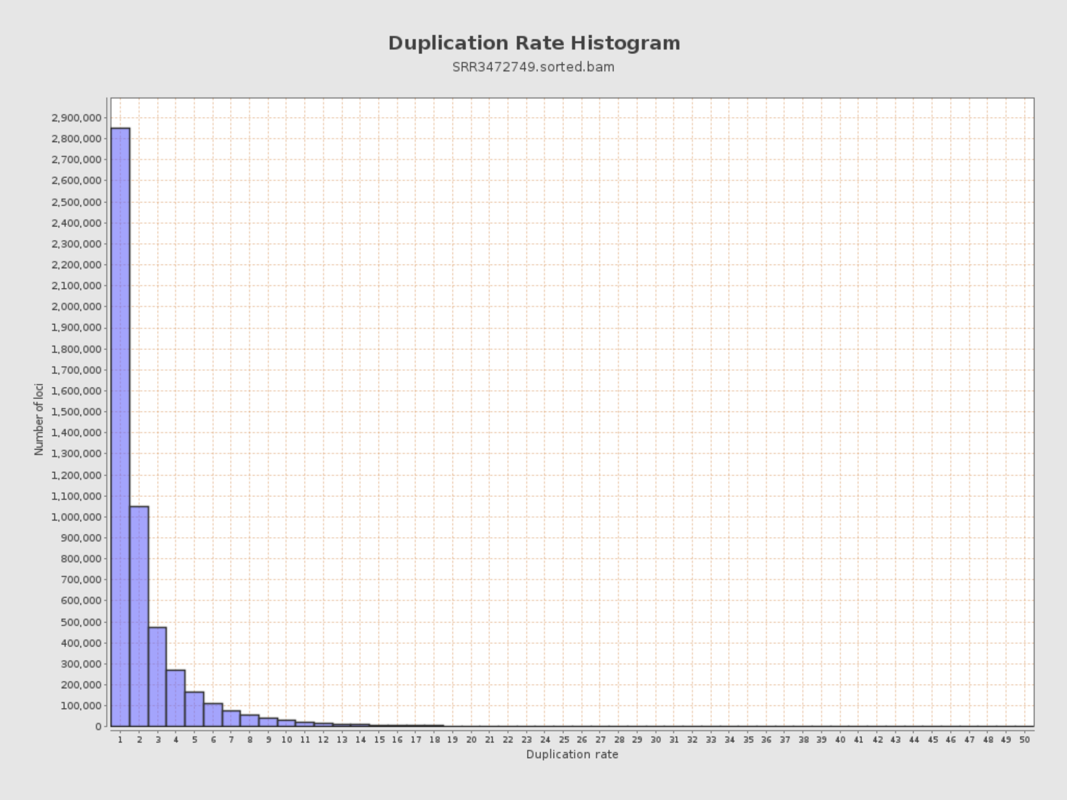
5. Results : Coverage Histogram (0-50X)



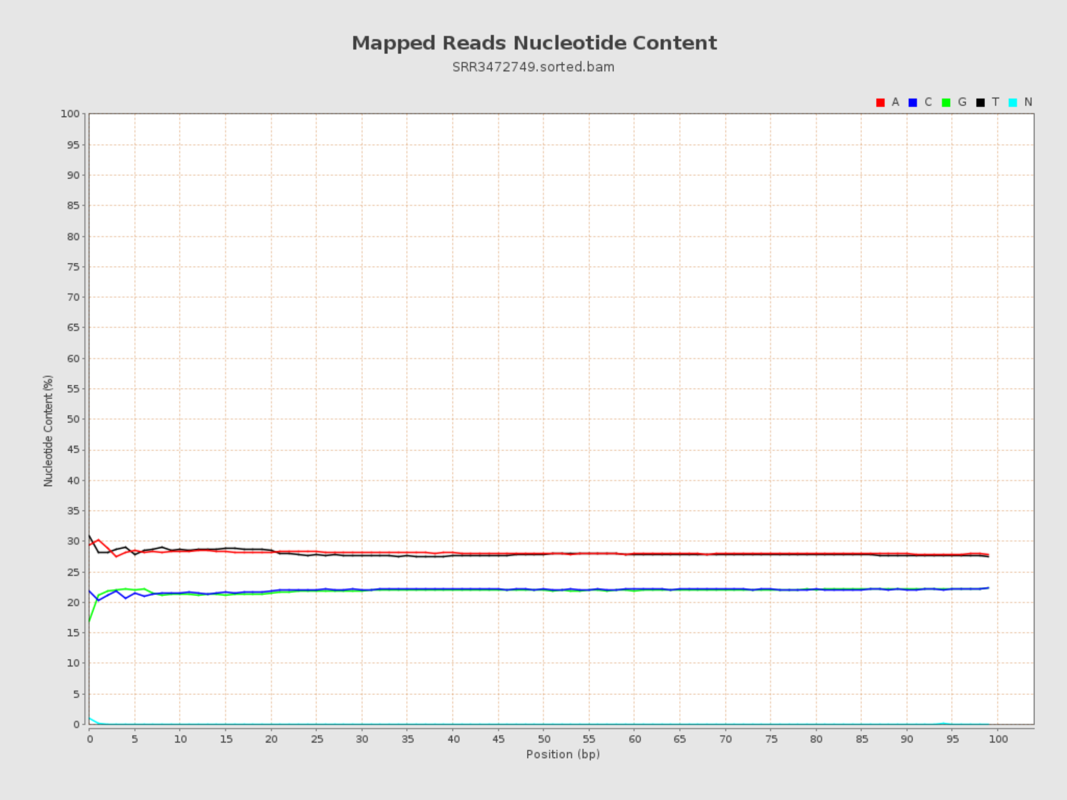
6. Results : Genome Fraction Coverage



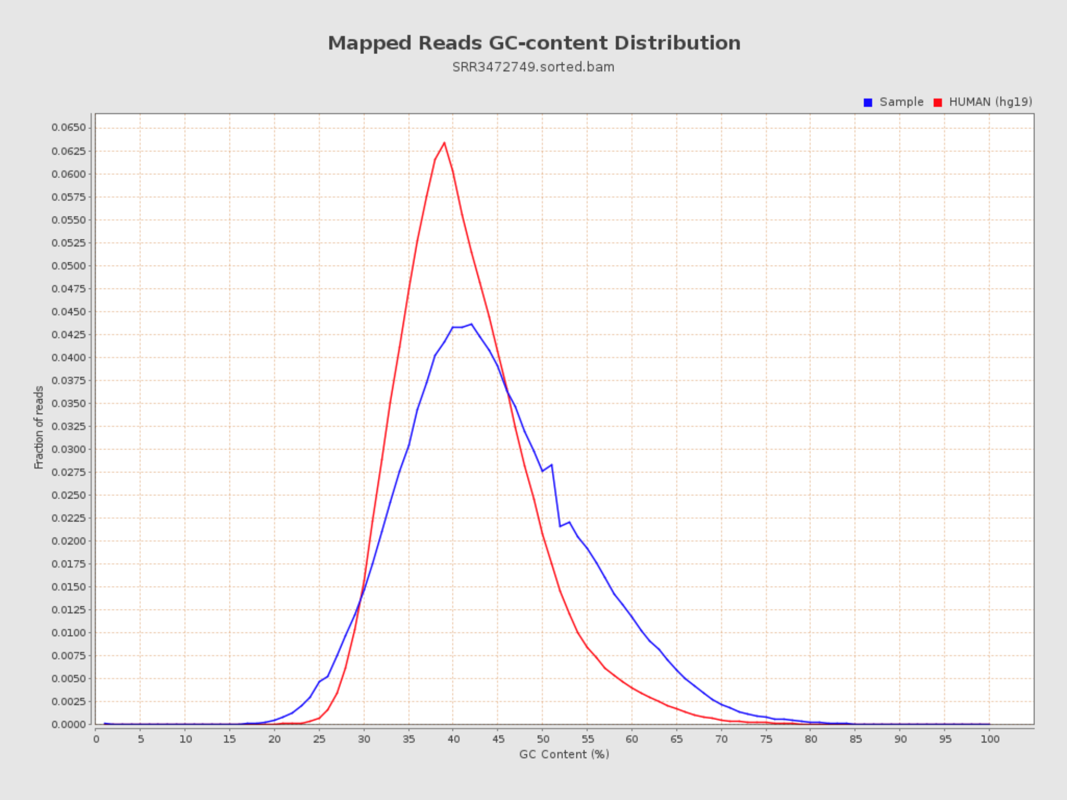
7. Results : Duplication Rate Histogram



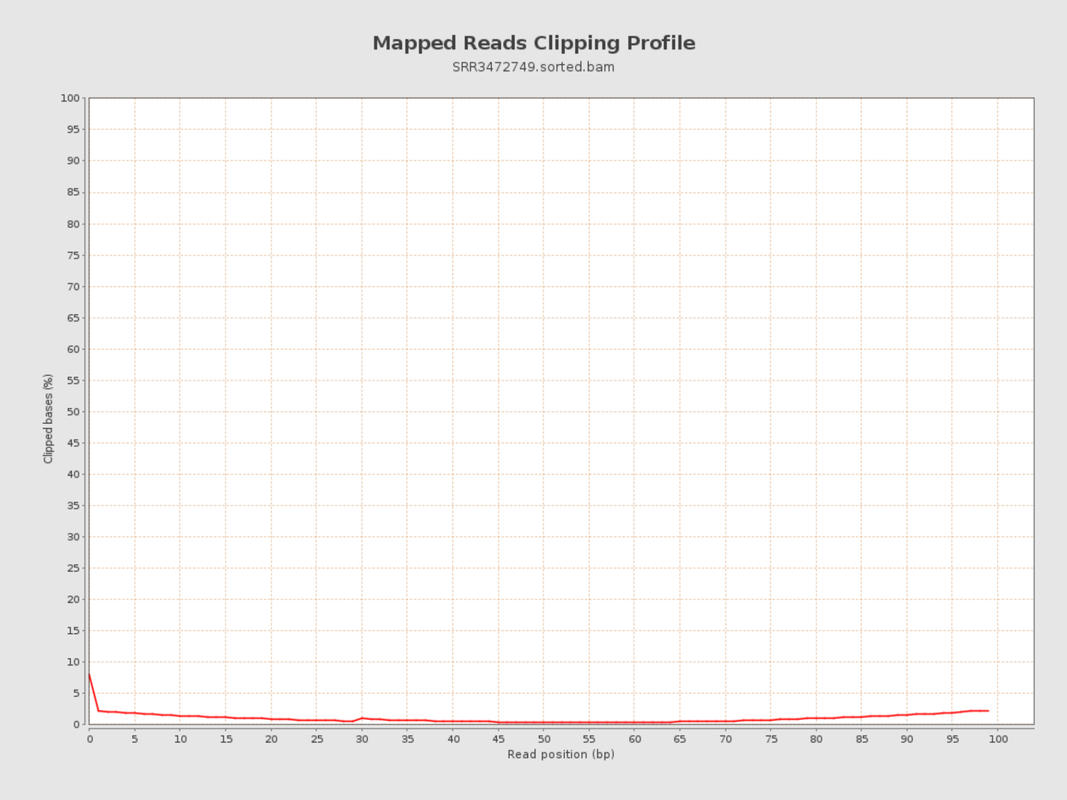
8. Results : Mapped Reads Nucleotide Content



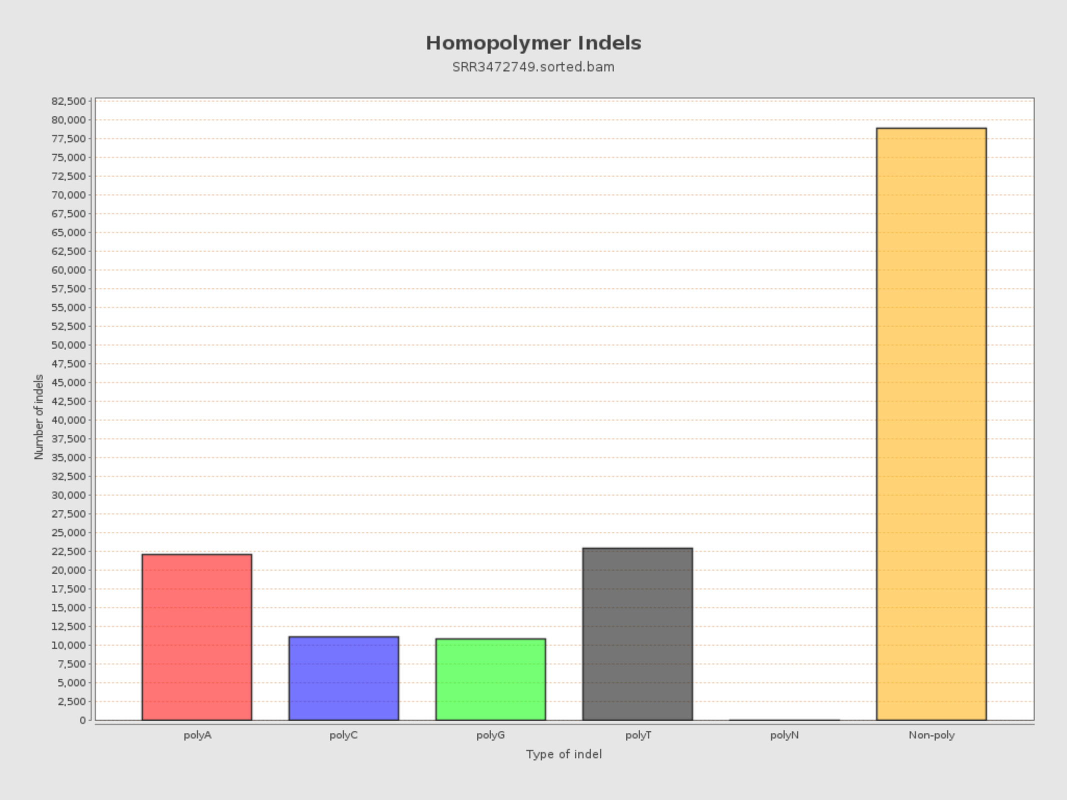
9. Results : Mapped Reads GC-content Distribution



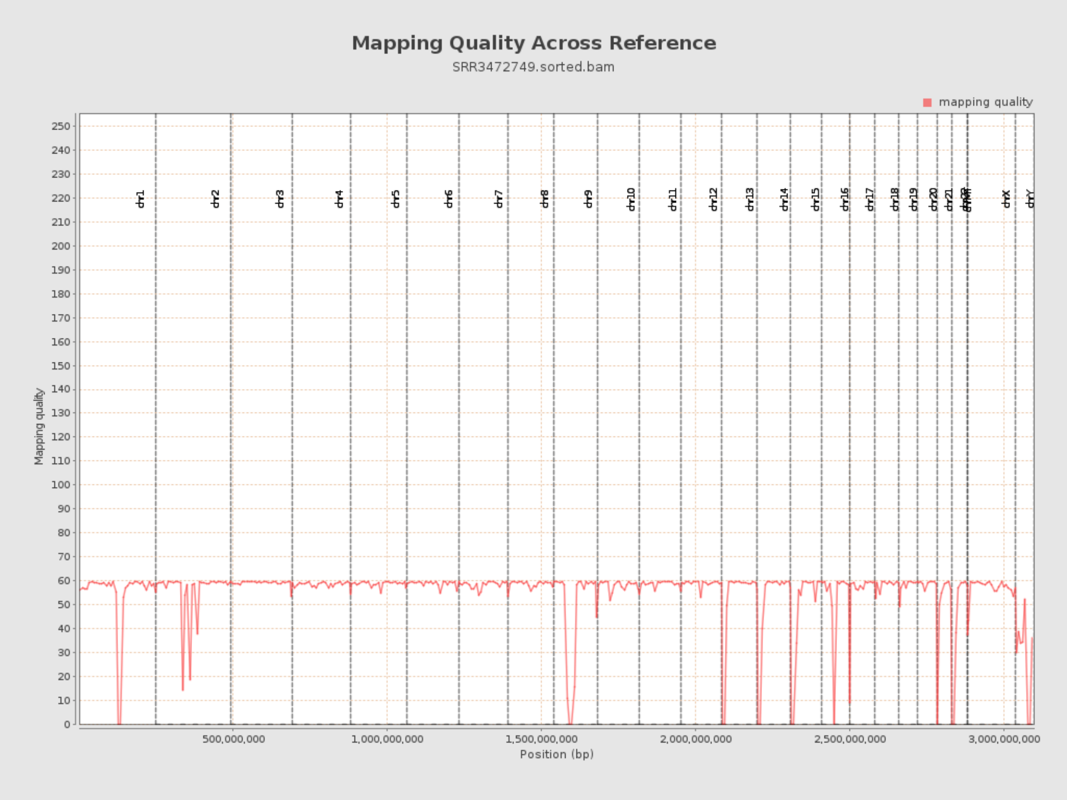
10. Results : Mapped Reads Clipping Profile



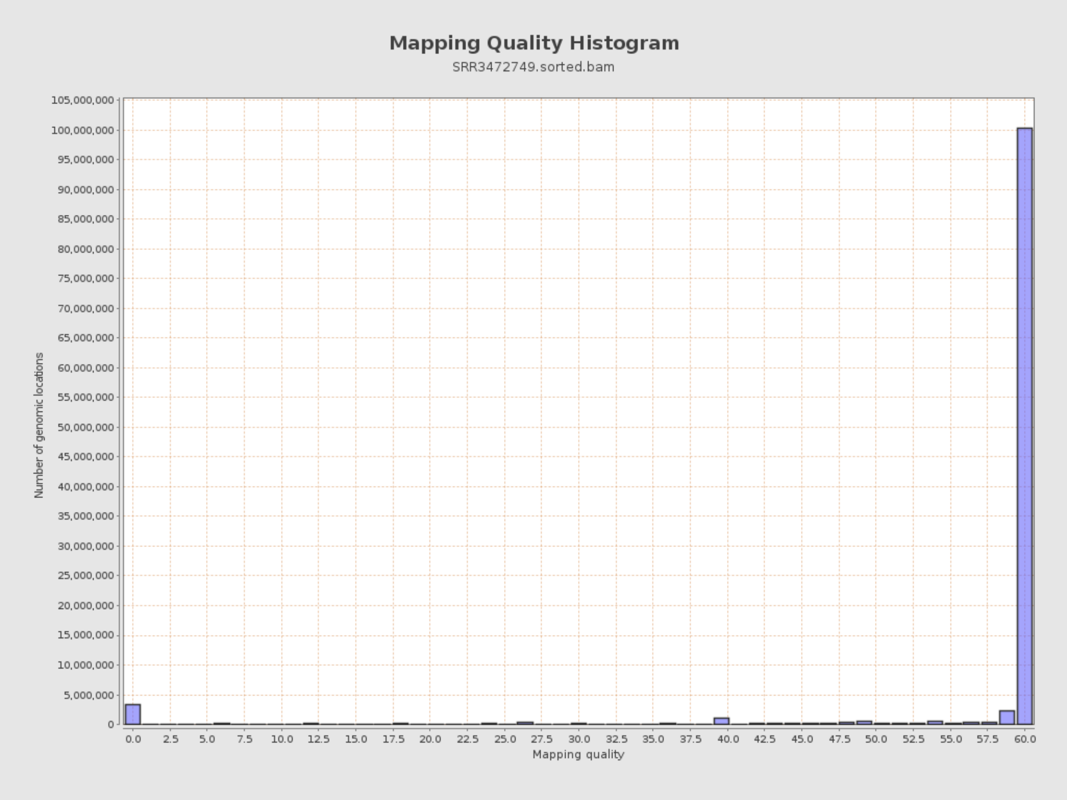
11. Results : Homopolymer Indels



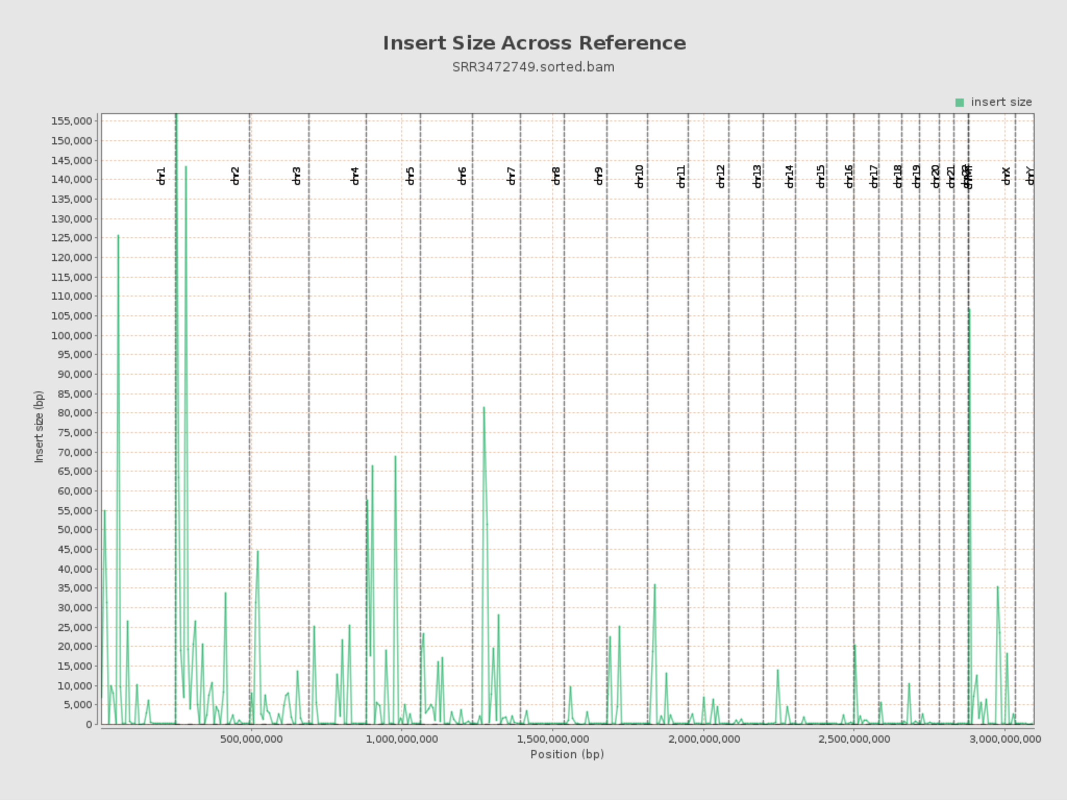
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram