Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 05:48:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472549.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_SRR3472549 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472549_1.fastq.gz SRR3472549_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 05:48:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472549.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,109,412
Mapped reads	14,944,439 / 98.91%
Unmapped reads	164,973 / 1.09%
Mapped paired reads	14,944,439 / 98.91%
Mapped reads, first in pair	7,500,450 / 49.64%
Mapped reads, second in pair	7,443,989 / 49.27%
Mapped reads, both in pair	14,849,974 / 98.28%
Mapped reads, singletons	94,465 / 0.63%
Secondary alignments	0
Supplementary alignments	56,316 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	9,503,081 / 62.9%
Duplication rate	45%
Clipped reads	1,073,732 / 7.11%

2.2. ACGT Content

Number/percentage of A's	418,128,321 / 28.36%
Number/percentage of C's	321,189,030 / 21.79%
Number/percentage of T's	416,562,383 / 28.25%
Number/percentage of G's	318,228,509 / 21.58%
Number/percentage of N's	227,134 / 0.02%

GC Percentage	43.37%

2.3. Coverage

Mean	0.4763
Standard Deviation	18.9832

2.4. Mapping Quality

Mean Mapping Quality	54.83

2.5. Insert size

Mean	27,576.5
Standard Deviation	1,597,172.07
P25/Median/P75	181 / 252 / 338

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	9,261,149
Insertions	88,774
Mapped reads with at least one insertion	0.59%
Deletions	80,514
Mapped reads with at least one deletion	0.53%
Homopolymer indels	44.24%

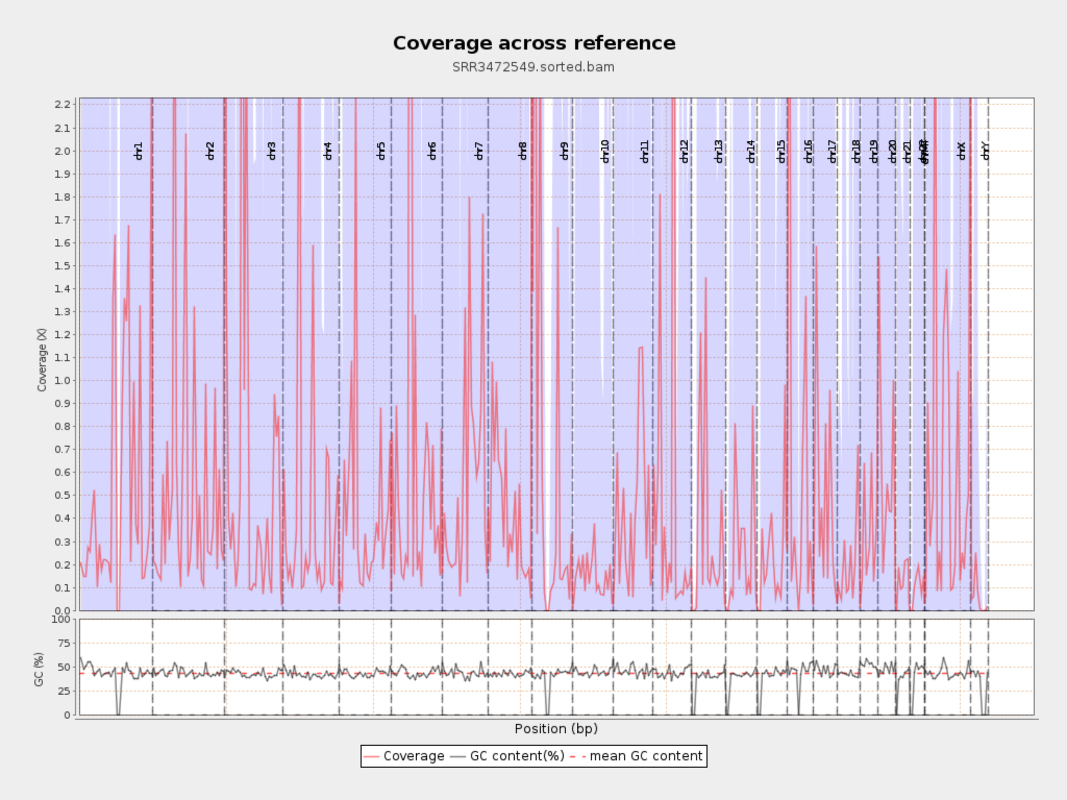
2.7. Chromosome stats

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

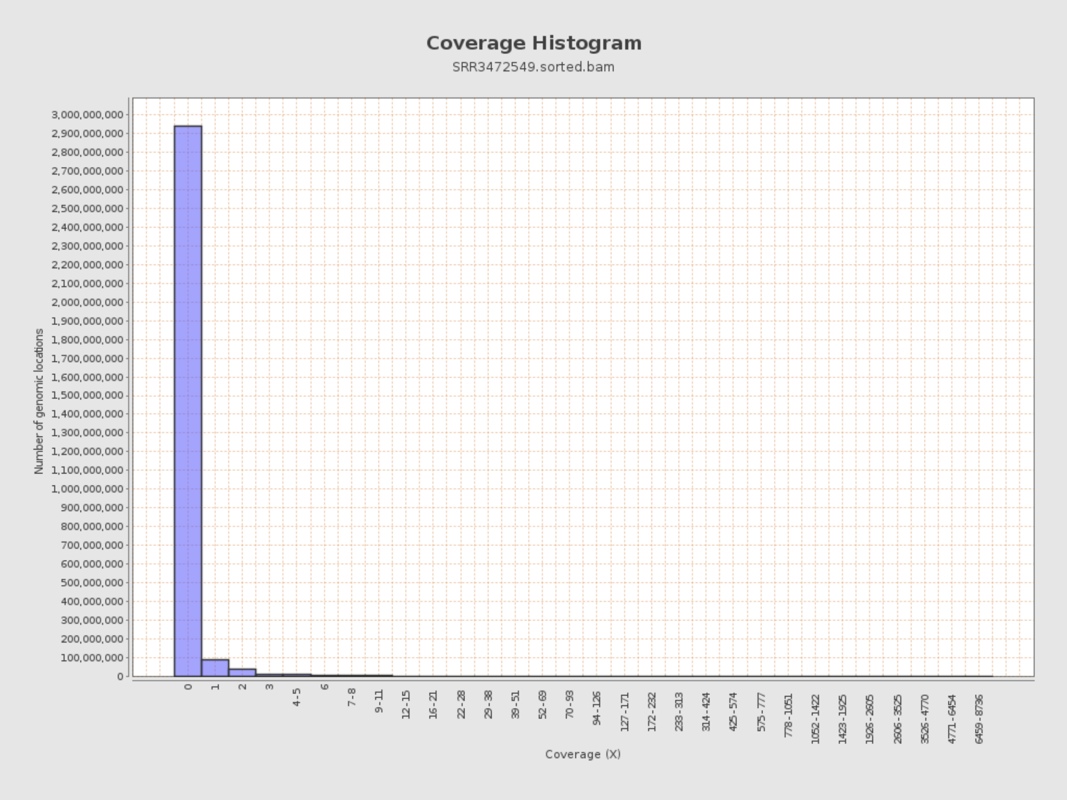
		bases	coverage	deviation
chr1	249250621	140695137	0.5645	22.1894
chr2	243199373	134147004	0.5516	22.3786
chr3	198022430	135811527	0.6858	19.18
chr4	191154276	80146870	0.4193	17.7073
chr5	180915260	80180320	0.4432	14.8962
chr6	171115067	118173358	0.6906	22.3415
chr7	159138663	90688342	0.5699	18.856
chr8	146364022	61598037	0.4209	12.6071
chr9	141213431	98680427	0.6988	19.5226
chr10	135534747	20708906	0.1528	5.2973
chr11	135006516	57484683	0.4258	16.6712
chr12	133851895	75786219	0.5662	36.0492
chr13	115169878	40188500	0.3489	12.534
chr14	107349540	27477619	0.256	9.0297
chr15	102531392	25054995	0.2444	9.6368
chr16	90354753	58064801	0.6426	26.1147
chr17	81195210	38209368	0.4706	19.1677
chr18	78077248	16674275	0.2136	7.5965
chr19	59128983	18869050	0.3191	10.1254
chr20	63025520	40632999	0.6447	24.5789
chr21	48129895	6549246	0.1361	5.3951
chr22	51304566	5165544	0.1007	4.2724
chrMT	16571	2849	0.1719	0.4453
chrX	155270560	100051698	0.6444	23.336

chrY	59373566	3488147	0.0587	2.3365

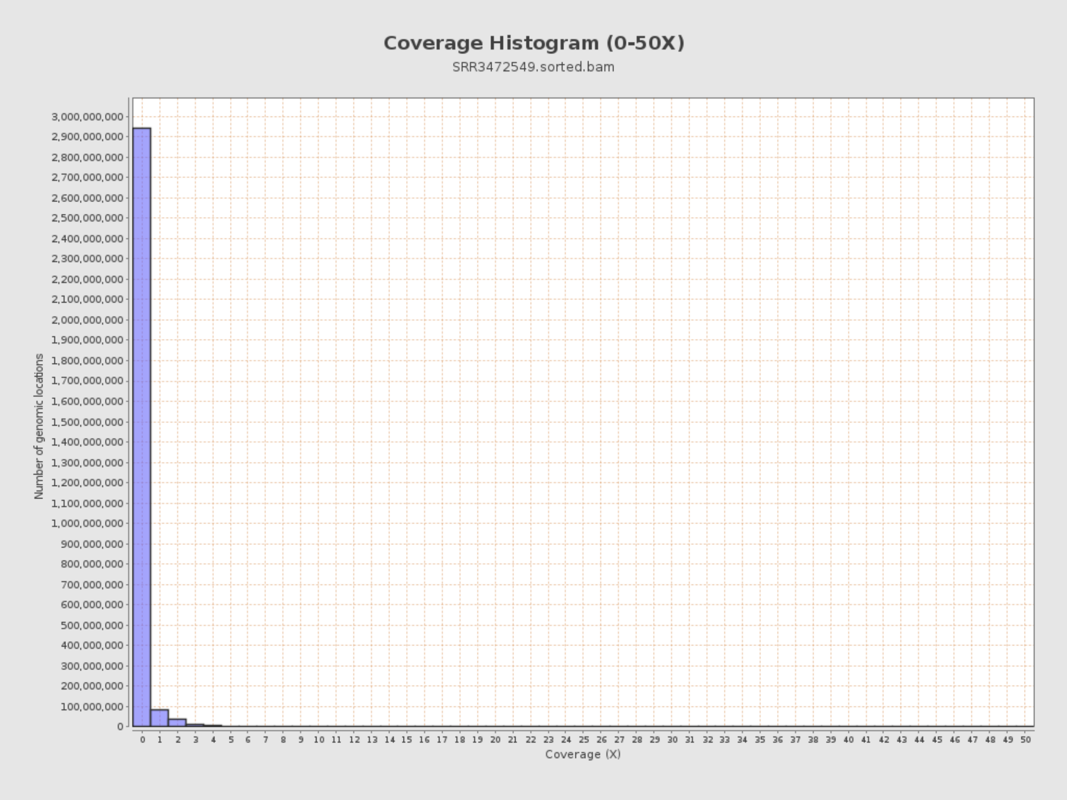
3. Results : Coverage across reference



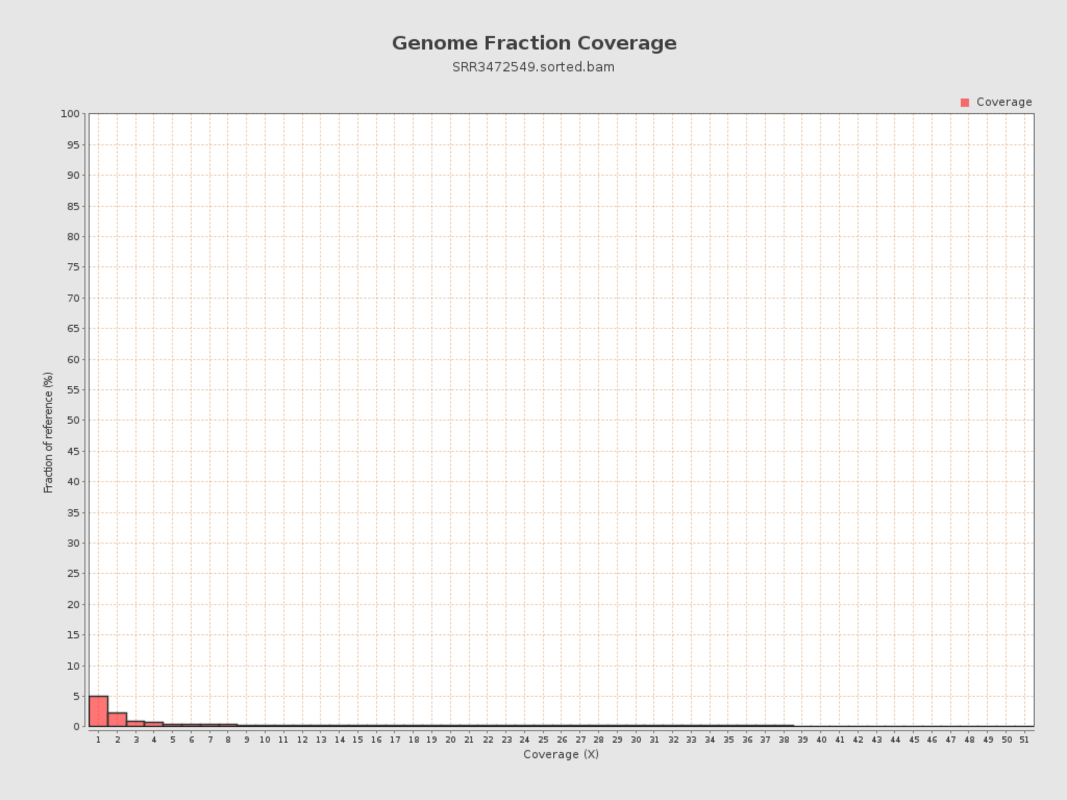
4. Results : Coverage Histogram



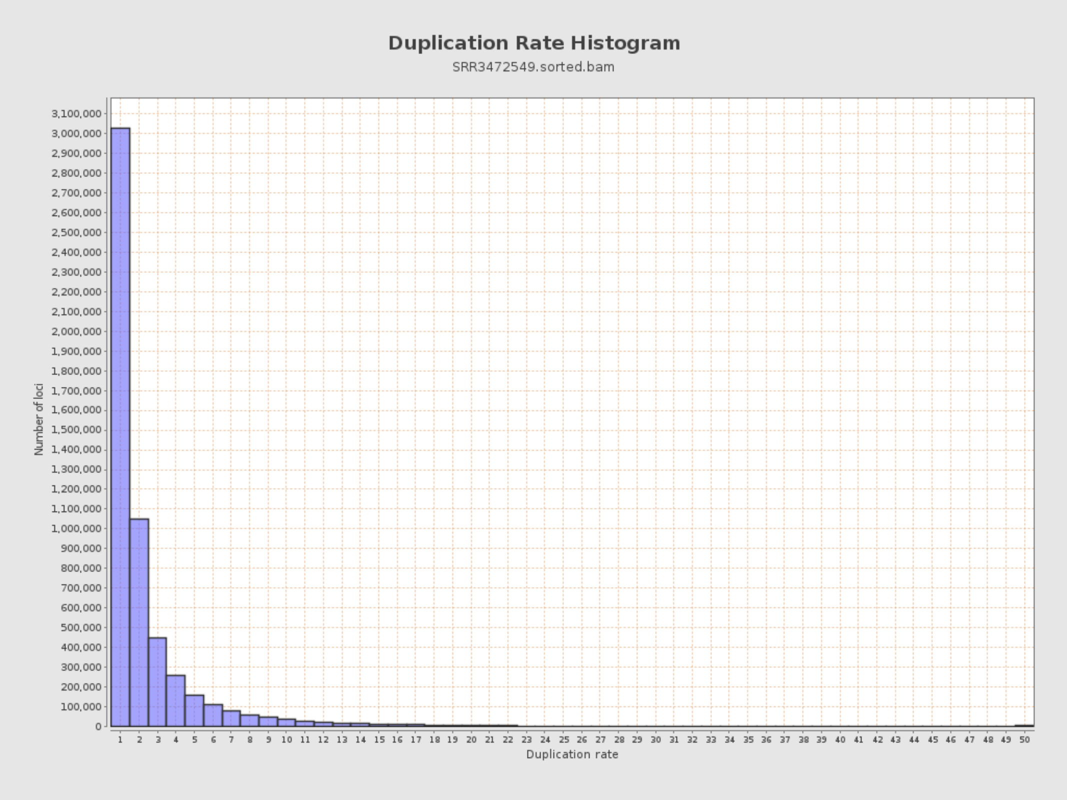
5. Results : Coverage Histogram (0-50X)



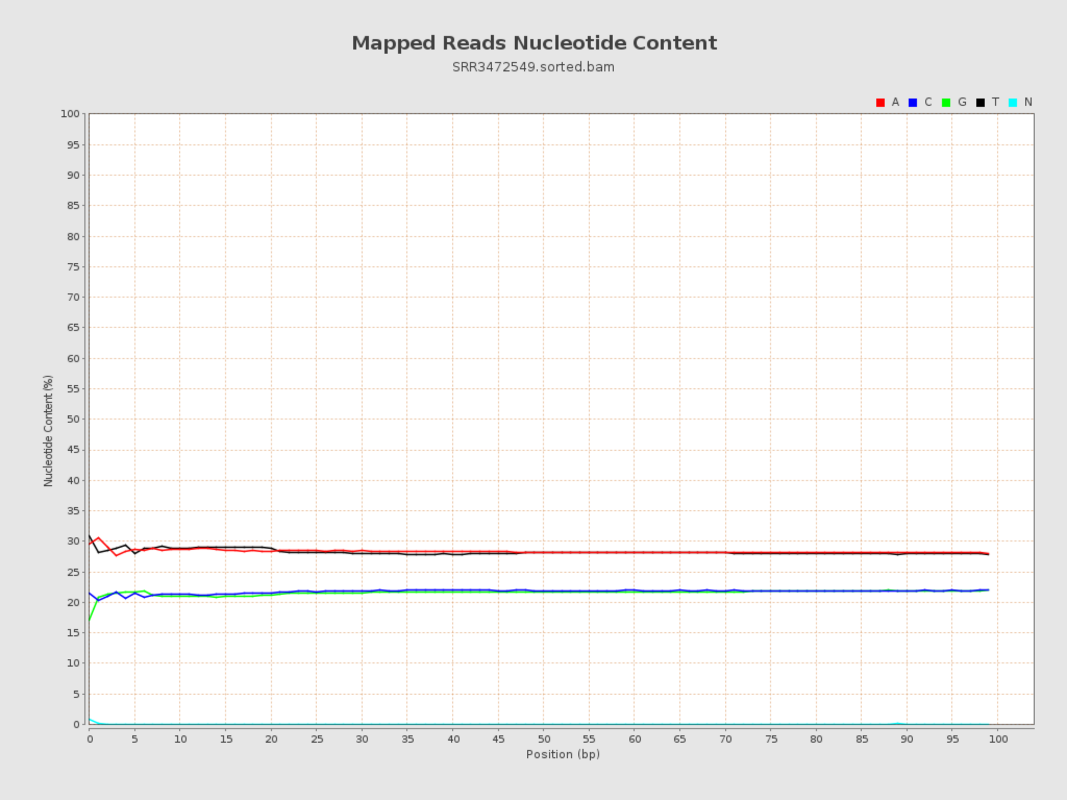
6. Results : Genome Fraction Coverage



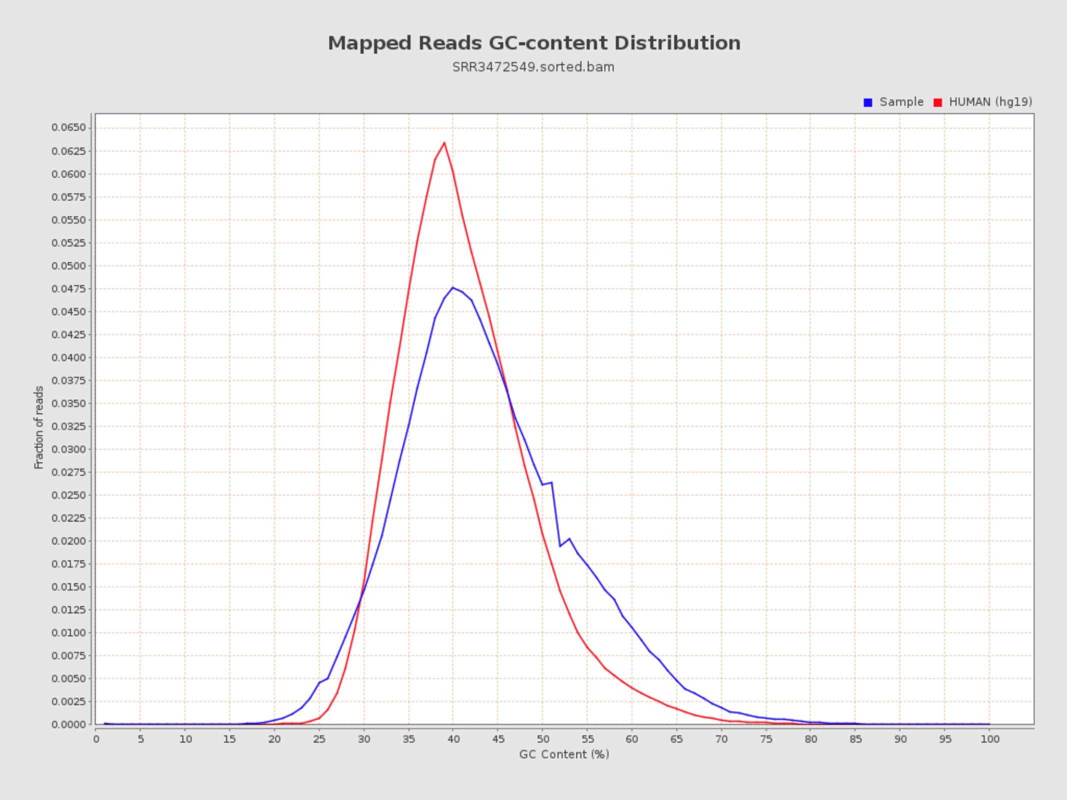
7. Results : Duplication Rate Histogram



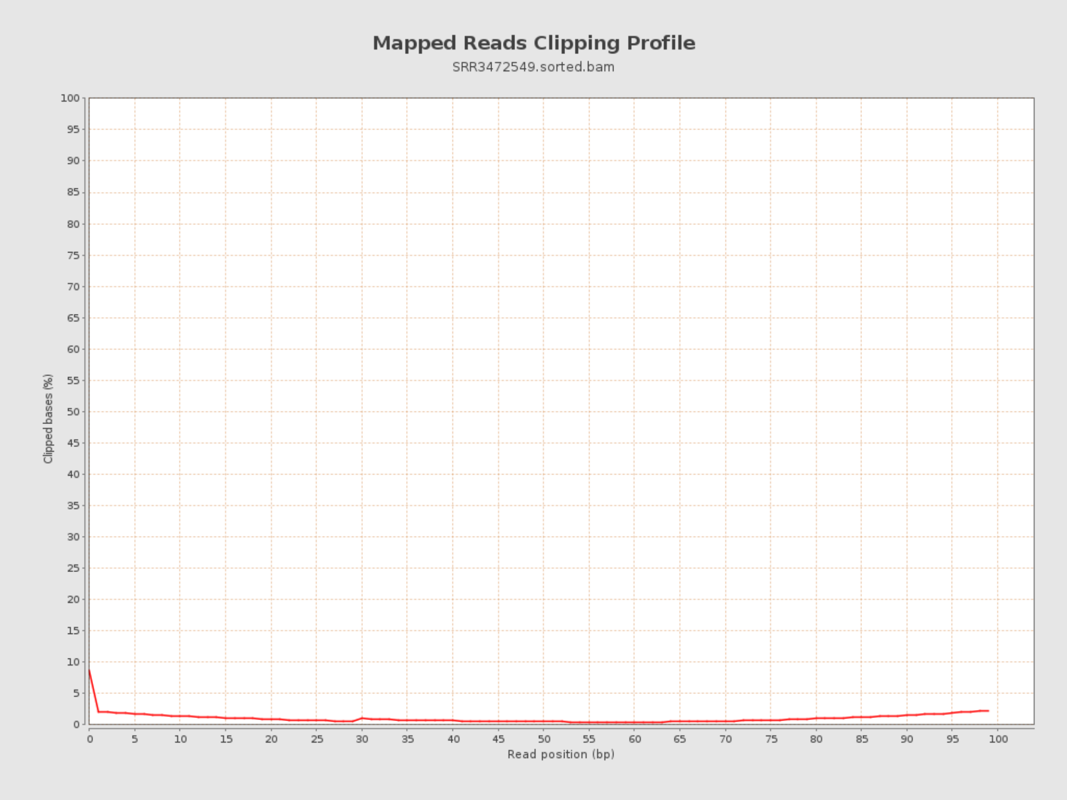
8. Results : Mapped Reads Nucleotide Content



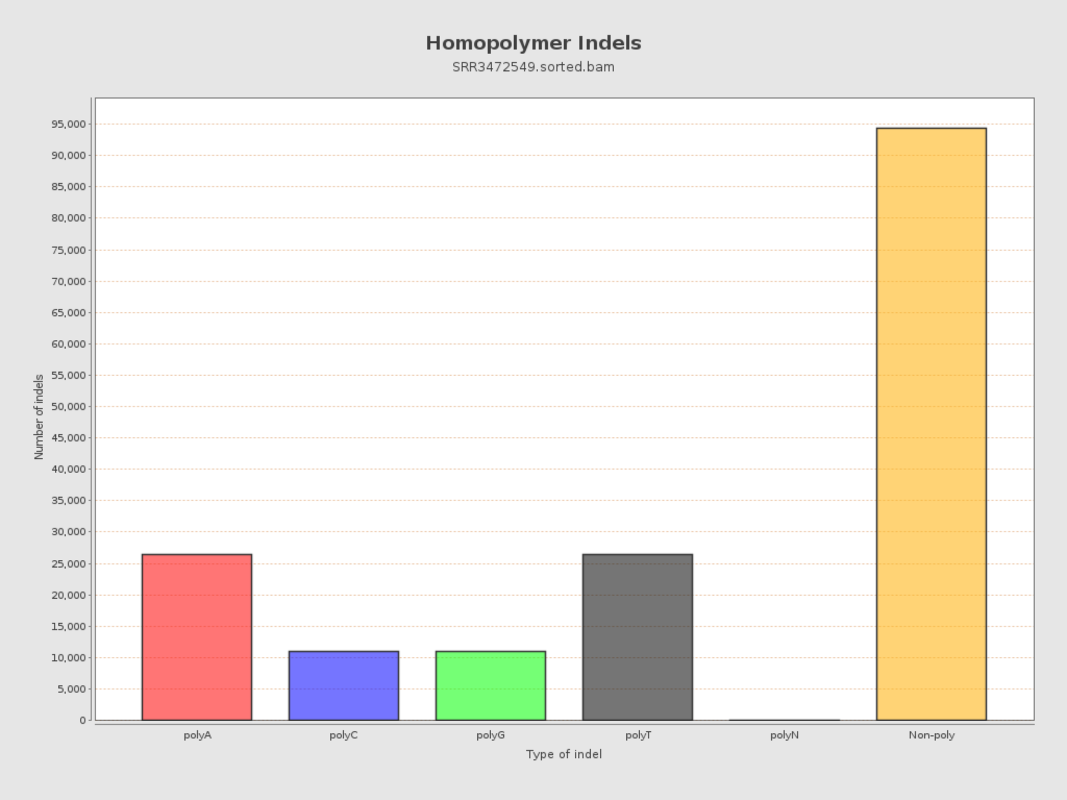
9. Results : Mapped Reads GC-content Distribution



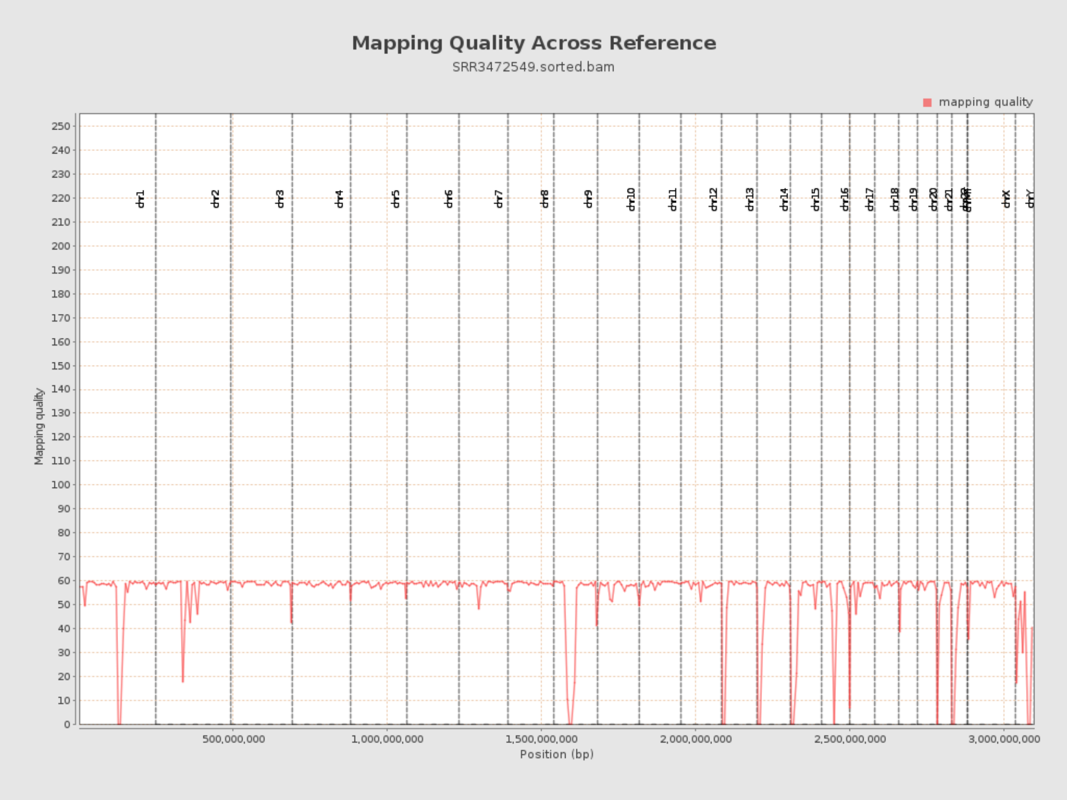
10. Results : Mapped Reads Clipping Profile



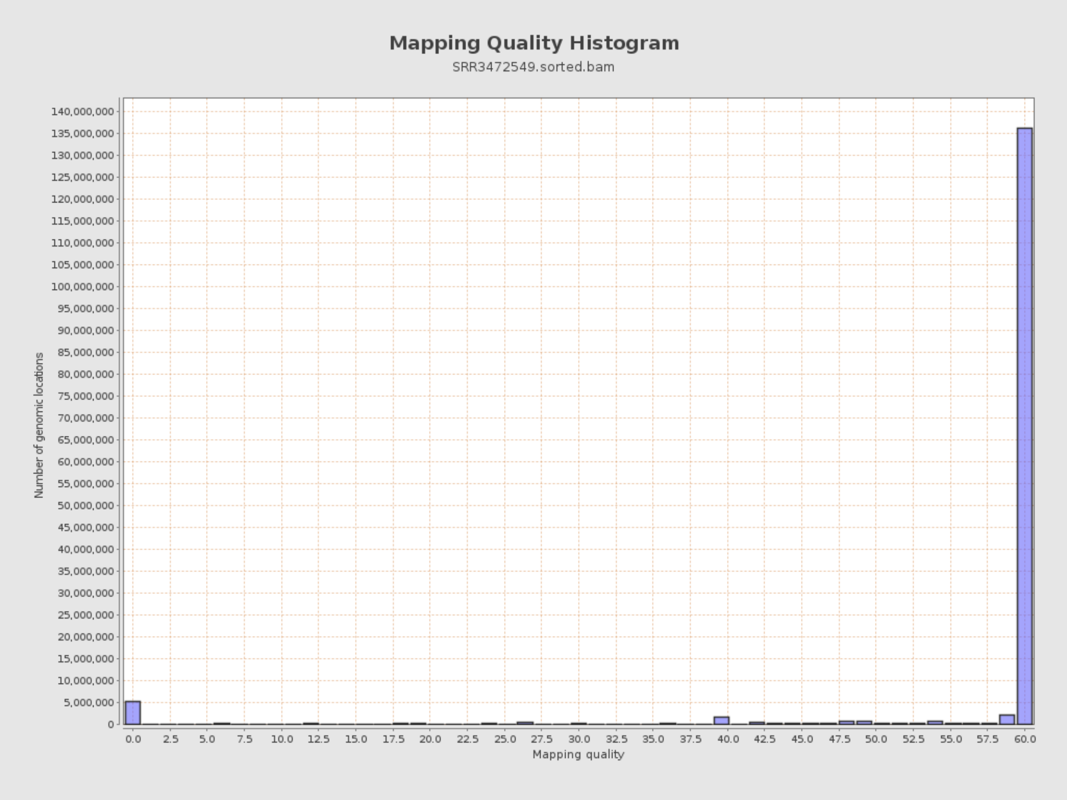
11. Results : Homopolymer Indels



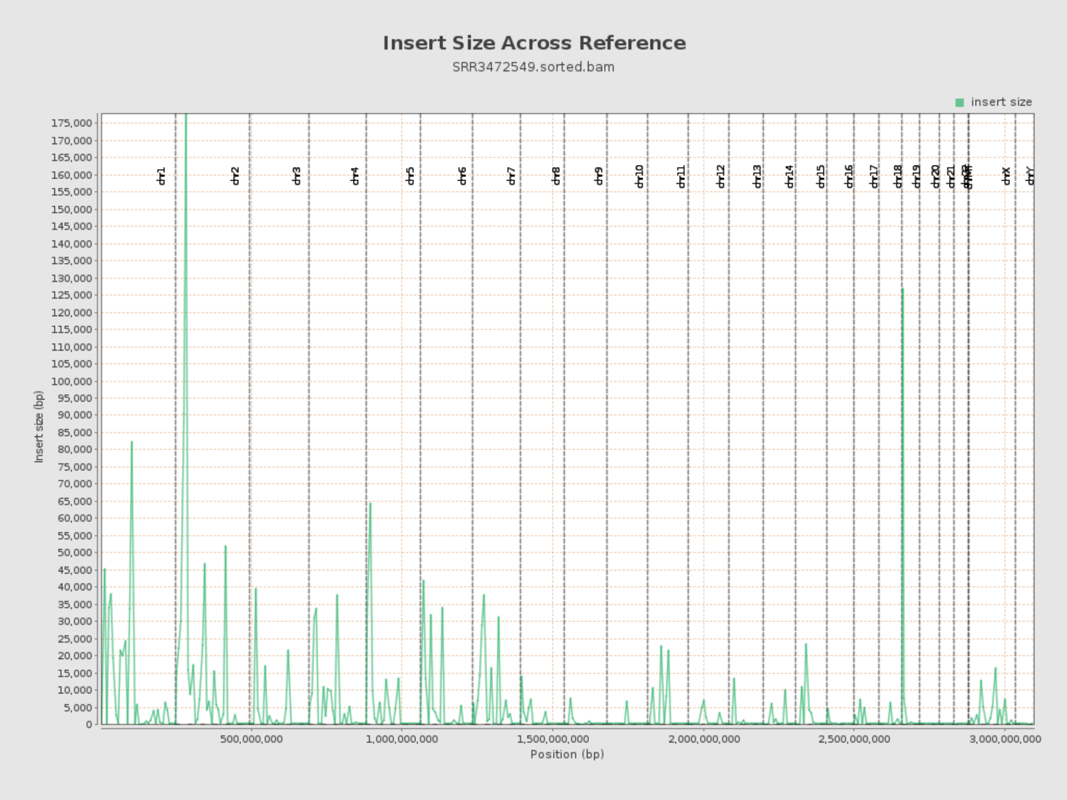
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram