Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:30:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472518.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_SRR3472518 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472518_1.fastq.gz SRR3472518_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:30:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472518.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,966,466
Mapped reads	13,787,008 / 98.72%
Unmapped reads	179,458 / 1.28%
Mapped paired reads	13,787,008 / 98.72%
Mapped reads, first in pair	6,919,781 / 49.55%
Mapped reads, second in pair	6,867,227 / 49.17%
Mapped reads, both in pair	13,694,928 / 98.06%
Mapped reads, singletons	92,080 / 0.66%
Secondary alignments	0
Supplementary alignments	60,060 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	8,290,004 / 59.36%
Duplication rate	44.93%
Clipped reads	1,182,199 / 8.46%

2.2. ACGT Content

Number/percentage of A's	378,377,800 / 27.9%
Number/percentage of C's	302,027,883 / 22.27%
Number/percentage of T's	375,977,767 / 27.72%
Number/percentage of G's	299,615,145 / 22.09%
Number/percentage of N's	209,616 / 0.02%

GC Percentage	44.36%

2.3. Coverage

Mean	0.4381
Standard Deviation	15.2459

2.4. Mapping Quality

Mean Mapping Quality	54.94

2.5. Insert size

Mean	35,595.99
Standard Deviation	1,876,085.33
P25/Median/P75	173 / 244 / 332

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	8,404,763
Insertions	76,860
Mapped reads with at least one insertion	0.55%
Deletions	69,600
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.52%

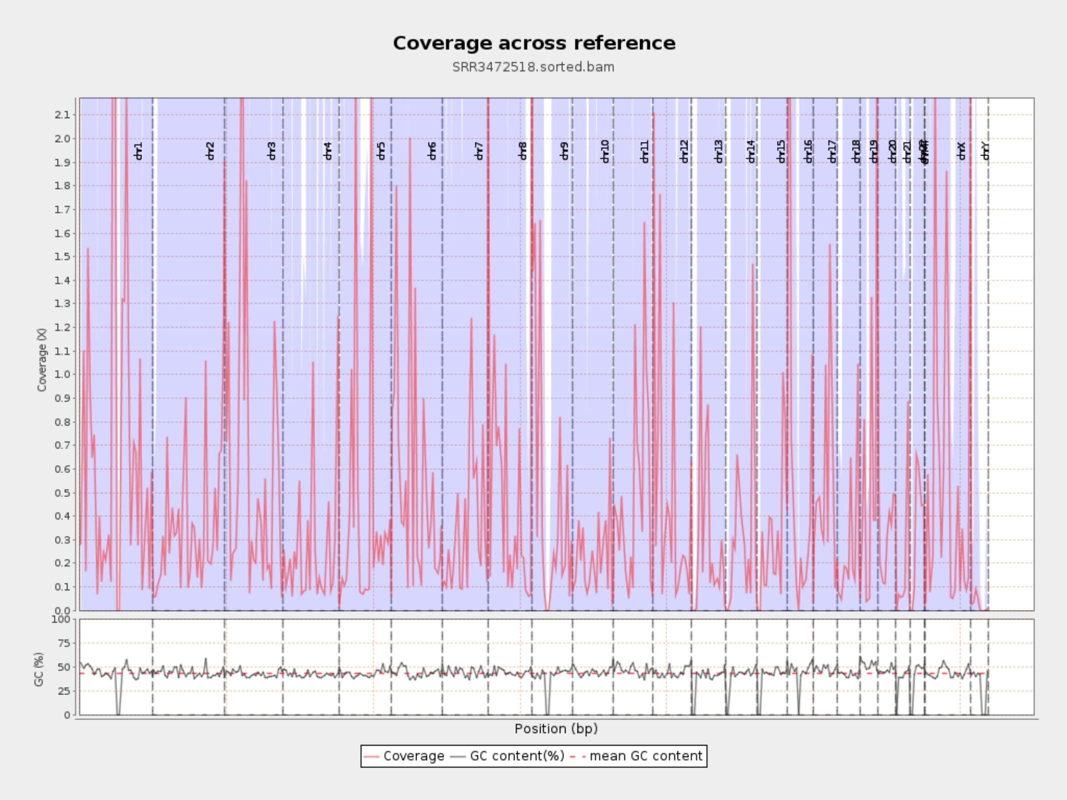
2.7. Chromosome stats

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

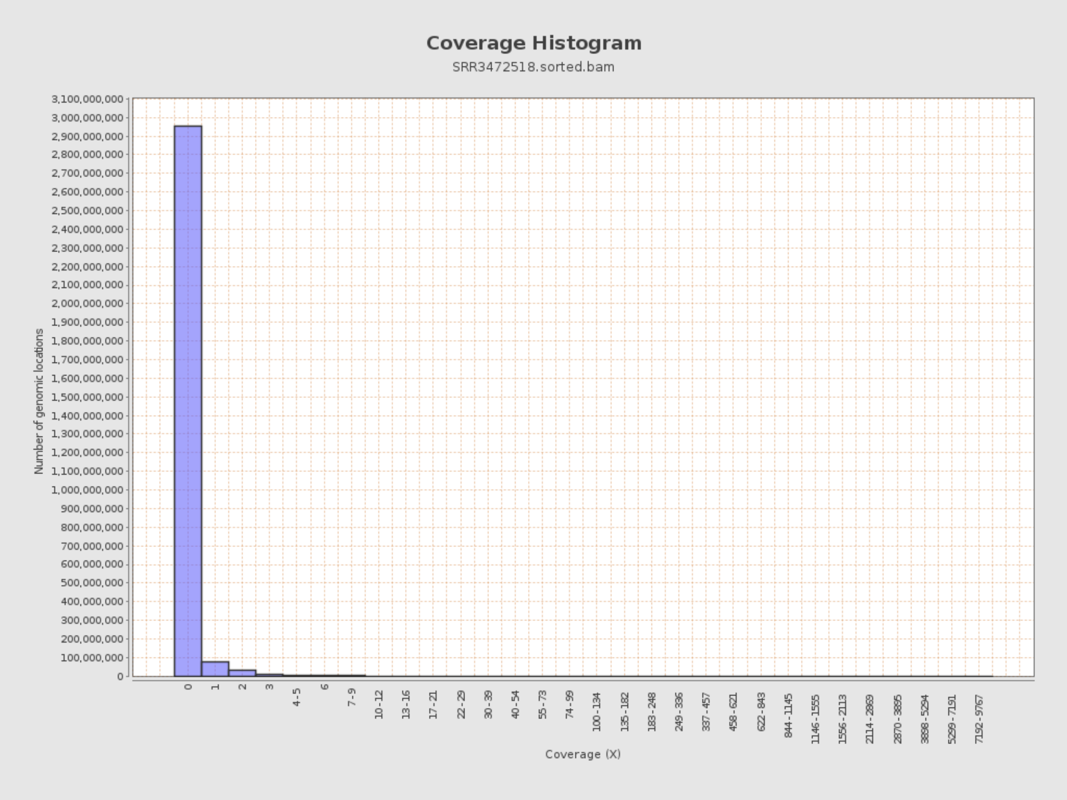
		bases	coverage	deviation
chr1	249250621	176155680	0.7067	28.3778
chr2	243199373	86289486	0.3548	12.2839
chr3	198022430	131743085	0.6653	15.2649
chr4	191154276	50158611	0.2624	11.2635
chr5	180915260	77133442	0.4264	15.7961
chr6	171115067	98462519	0.5754	18.0589
chr7	159138663	56526394	0.3552	10.7021
chr8	146364022	60942542	0.4164	11.8507
chr9	141213431	67610148	0.4788	12.1839
chr10	135534747	31666085	0.2336	8.3737
chr11	135006516	69377891	0.5139	17.5113
chr12	133851895	67423197	0.5037	15.3048
chr13	115169878	34687013	0.3012	10.4585
chr14	107349540	34683198	0.3231	11.6717
chr15	102531392	31689206	0.3091	9.4247
chr16	90354753	54682595	0.6052	18.4248
chr17	81195210	43453068	0.5352	15.0297
chr18	78077248	21517597	0.2756	8.9554
chr19	59128983	30720668	0.5196	18.3684
chr20	63025520	20129384	0.3194	7.8478
chr21	48129895	9280736	0.1928	9.2101
chr22	51304566	17616738	0.3434	10.4636
chrMT	16571	1843	0.1112	0.3933
chrX	155270560	82800214	0.5333	16.7426

chrY	59373566	1621507	0.0273	0.9783

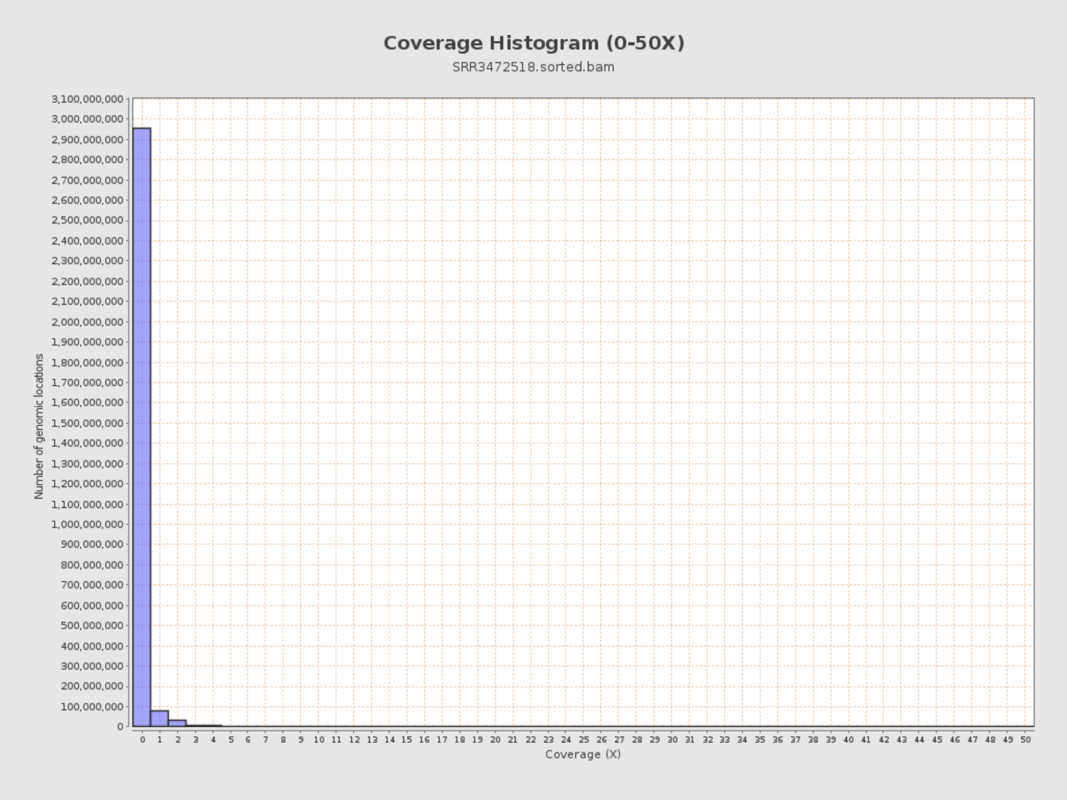
3. Results : Coverage across reference



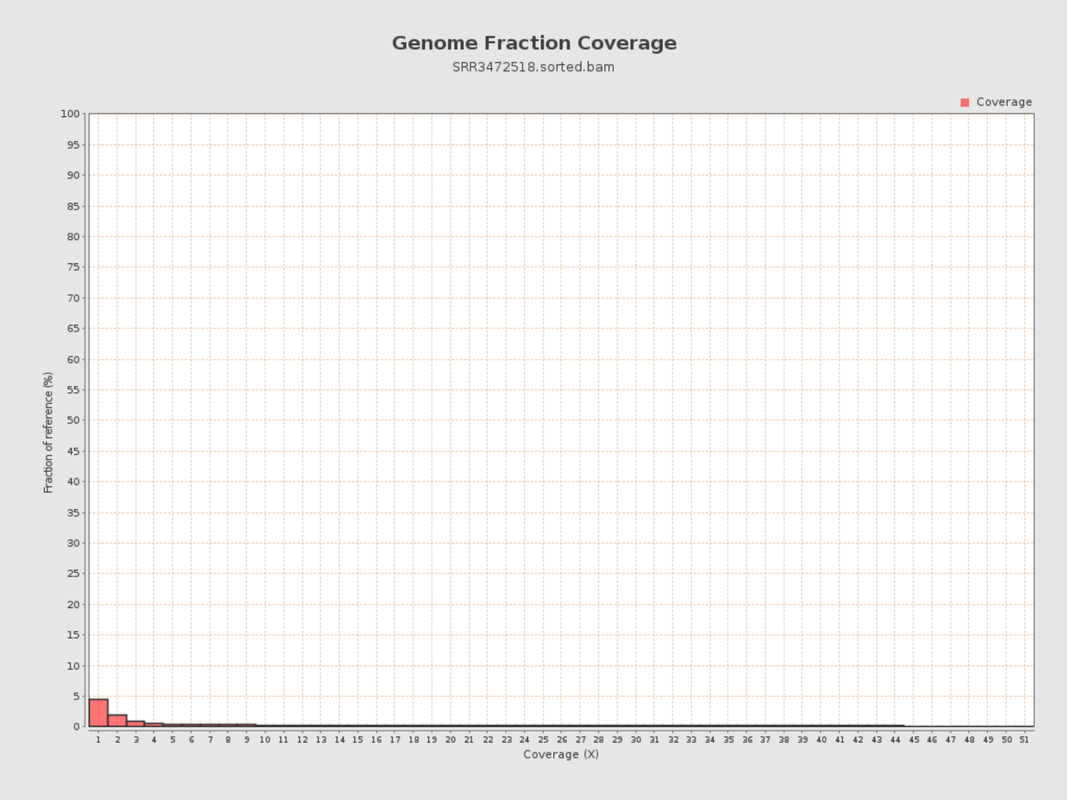
4. Results : Coverage Histogram



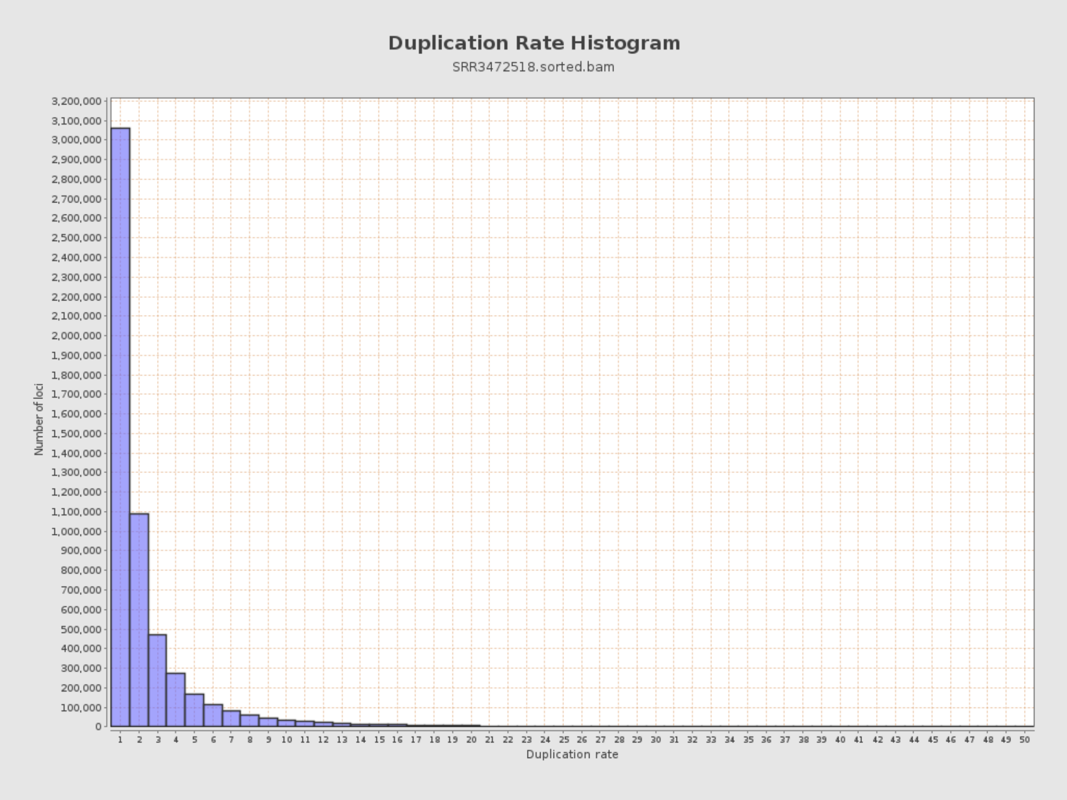
5. Results : Coverage Histogram (0-50X)



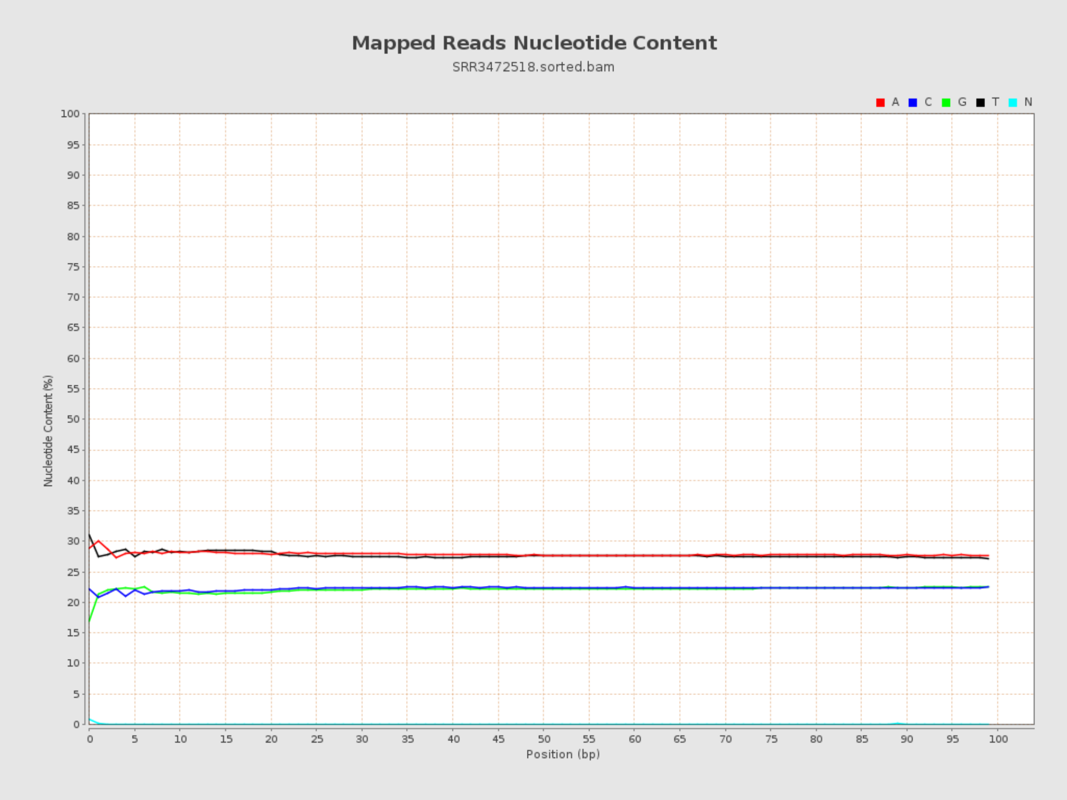
6. Results : Genome Fraction Coverage



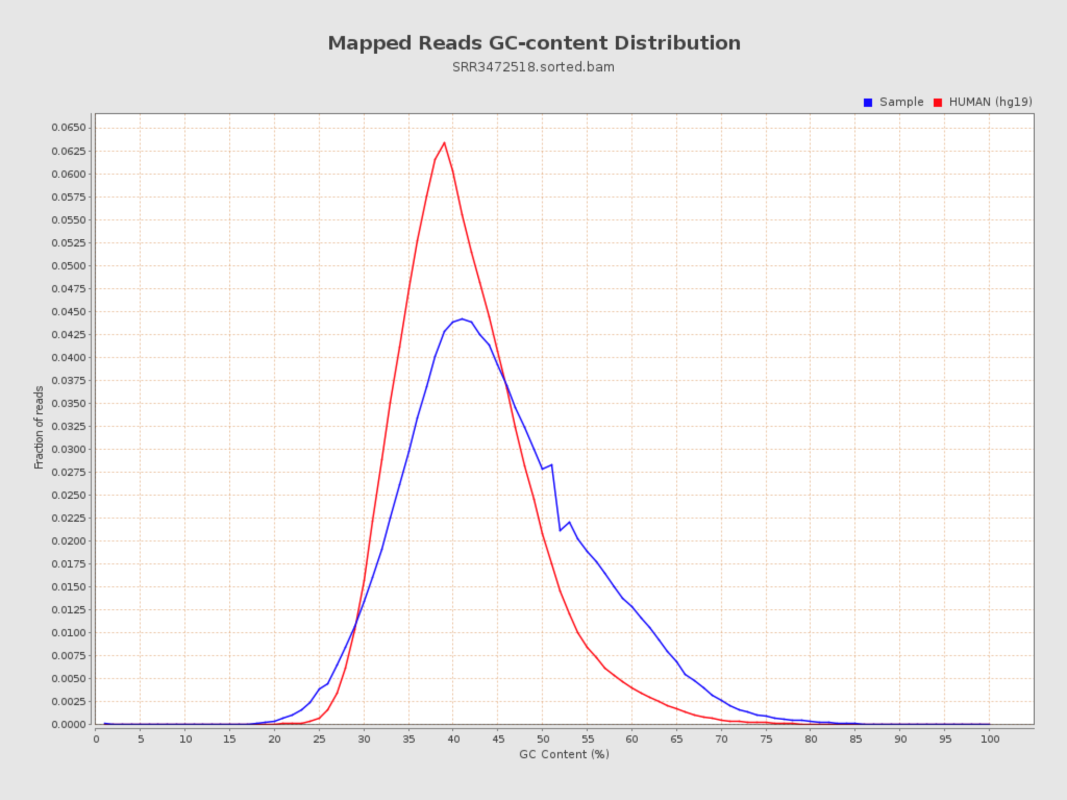
7. Results : Duplication Rate Histogram



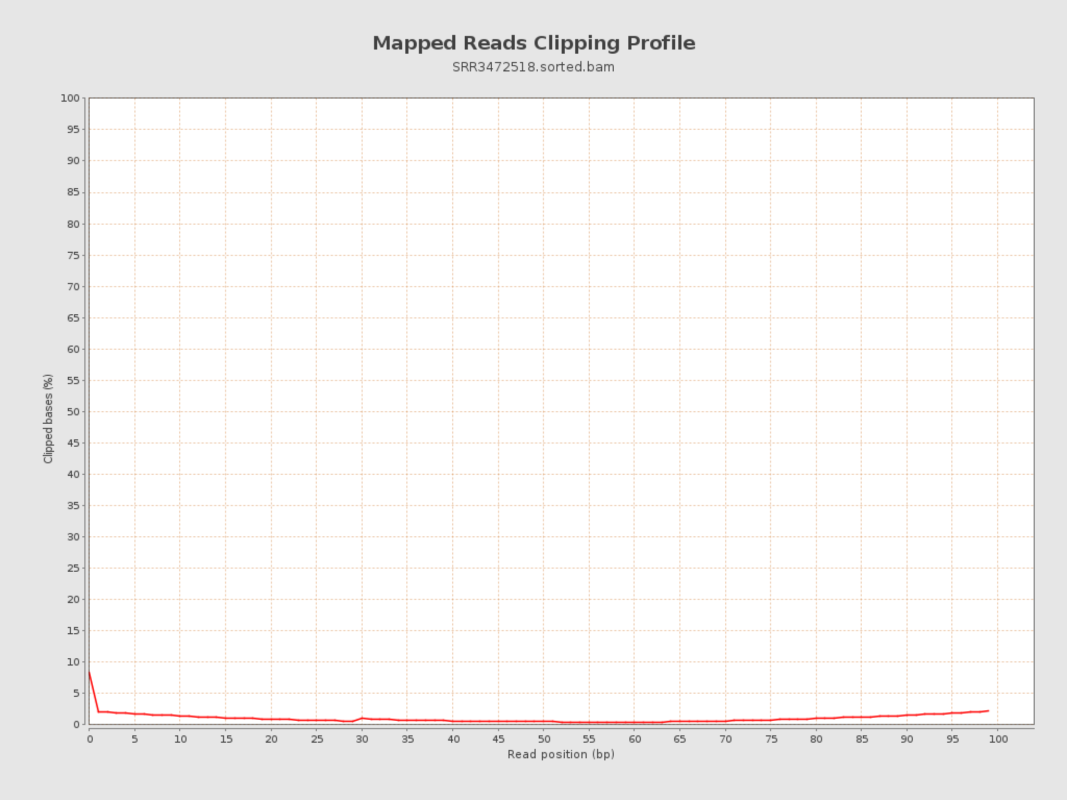
8. Results : Mapped Reads Nucleotide Content



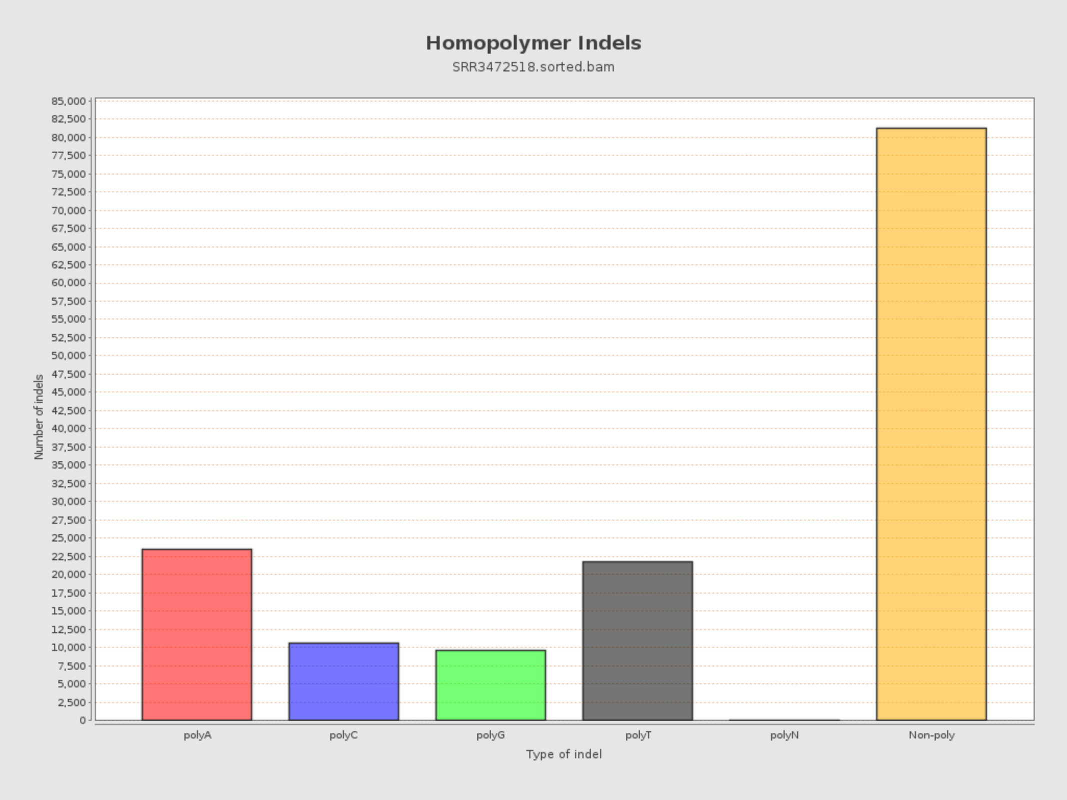
9. Results : Mapped Reads GC-content Distribution



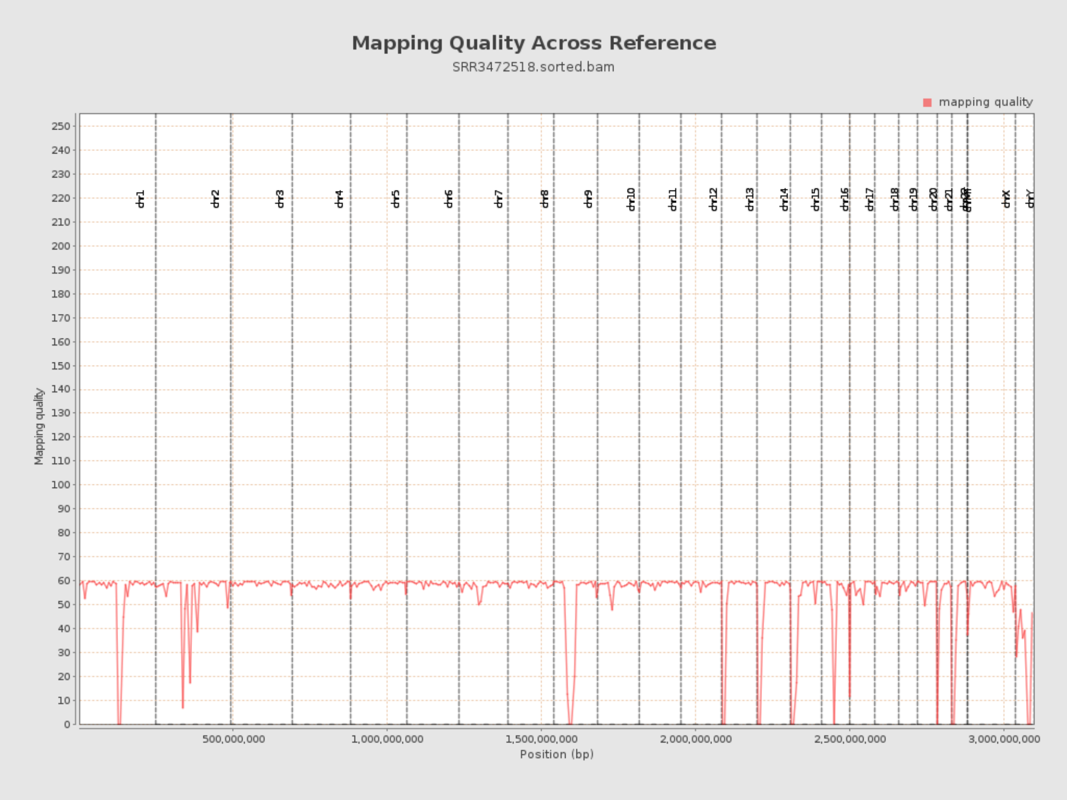
10. Results : Mapped Reads Clipping Profile



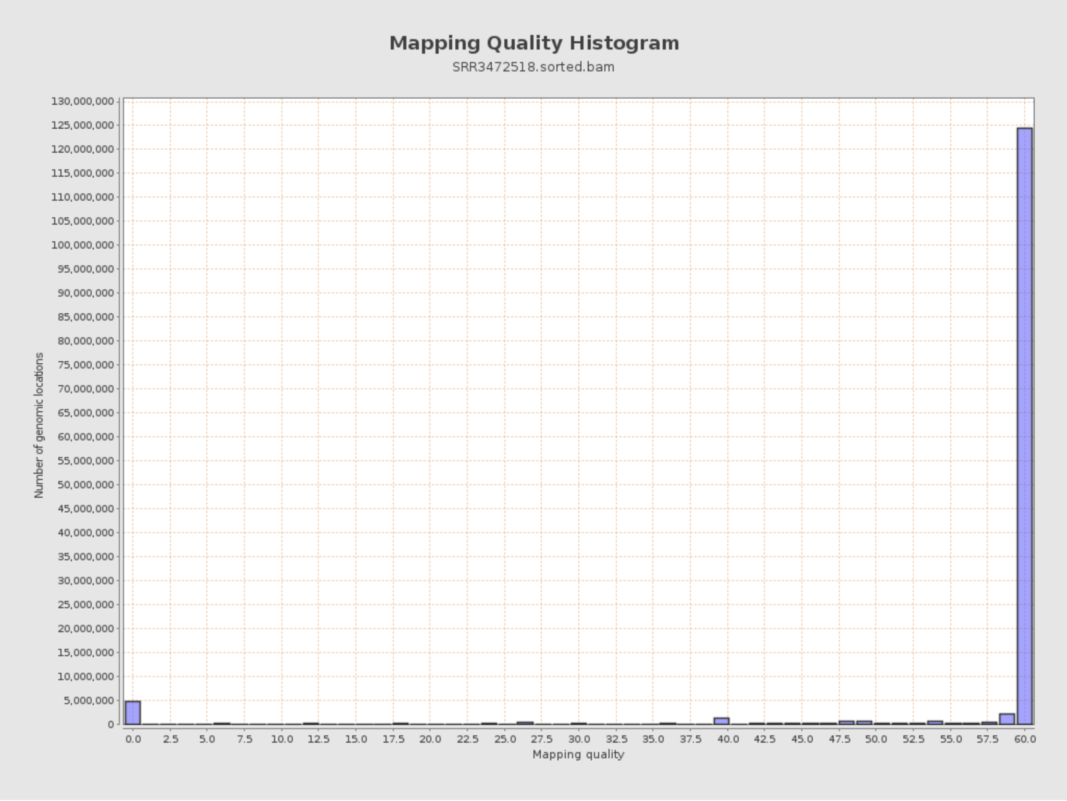
11. Results : Homopolymer Indels



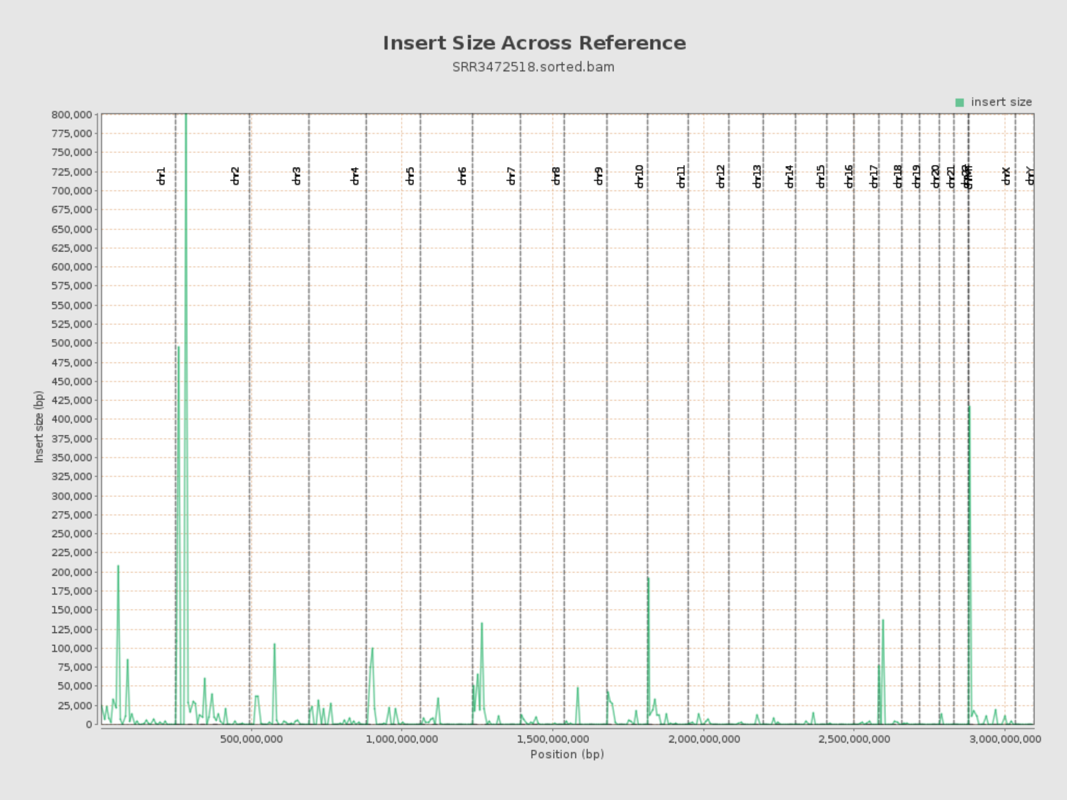
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram