Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:40:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472442.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_SRR3472442 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472442_1.fastq.gz SRR3472442_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:40:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472442.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,481,310
Mapped reads	12,925,195 / 95.87%
Unmapped reads	556,115 / 4.13%
Mapped paired reads	12,925,195 / 95.87%
Mapped reads, first in pair	6,272,455 / 46.53%
Mapped reads, second in pair	6,652,740 / 49.35%
Mapped reads, both in pair	12,431,704 / 92.21%
Mapped reads, singletons	493,491 / 3.66%
Secondary alignments	0
Supplementary alignments	51,203 / 0.38%
Read min/max/mean length	30 / 100 / 99.35
Duplicated reads (estimated)	7,566,687 / 56.13%
Duplication rate	44.18%
Clipped reads	1,187,850 / 8.81%

2.2. ACGT Content

Number/percentage of A's	346,420,611 / 27.61%
Number/percentage of C's	289,217,960 / 23.05%
Number/percentage of T's	333,037,965 / 26.54%
Number/percentage of G's	285,795,581 / 22.78%
Number/percentage of N's	157,838 / 0.01%

GC Percentage	45.83%

2.3. Coverage

Mean	0.4053
Standard Deviation	13.4673

2.4. Mapping Quality

Mean Mapping Quality	54.34

2.5. Insert size

Mean	21,460.04
Standard Deviation	1,414,686.67
P25/Median/P75	149 / 206 / 277

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	11,946,715
Insertions	77,843
Mapped reads with at least one insertion	0.6%
Deletions	60,614
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.29%

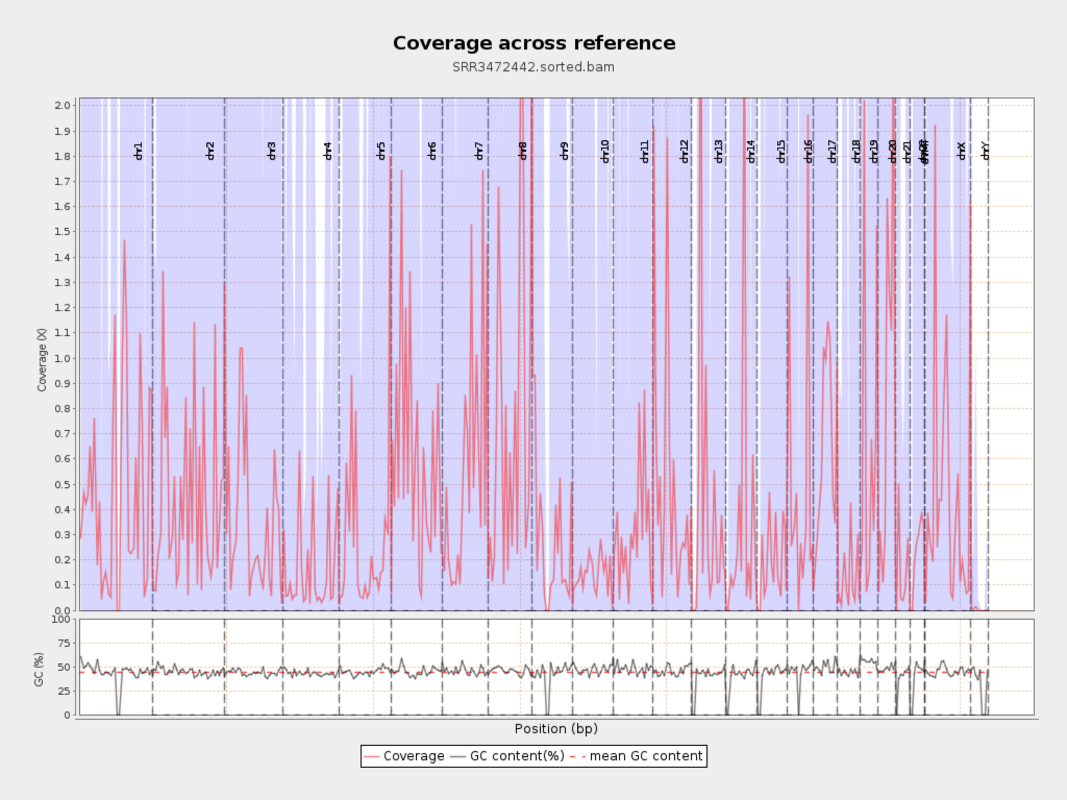
2.7. Chromosome stats

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

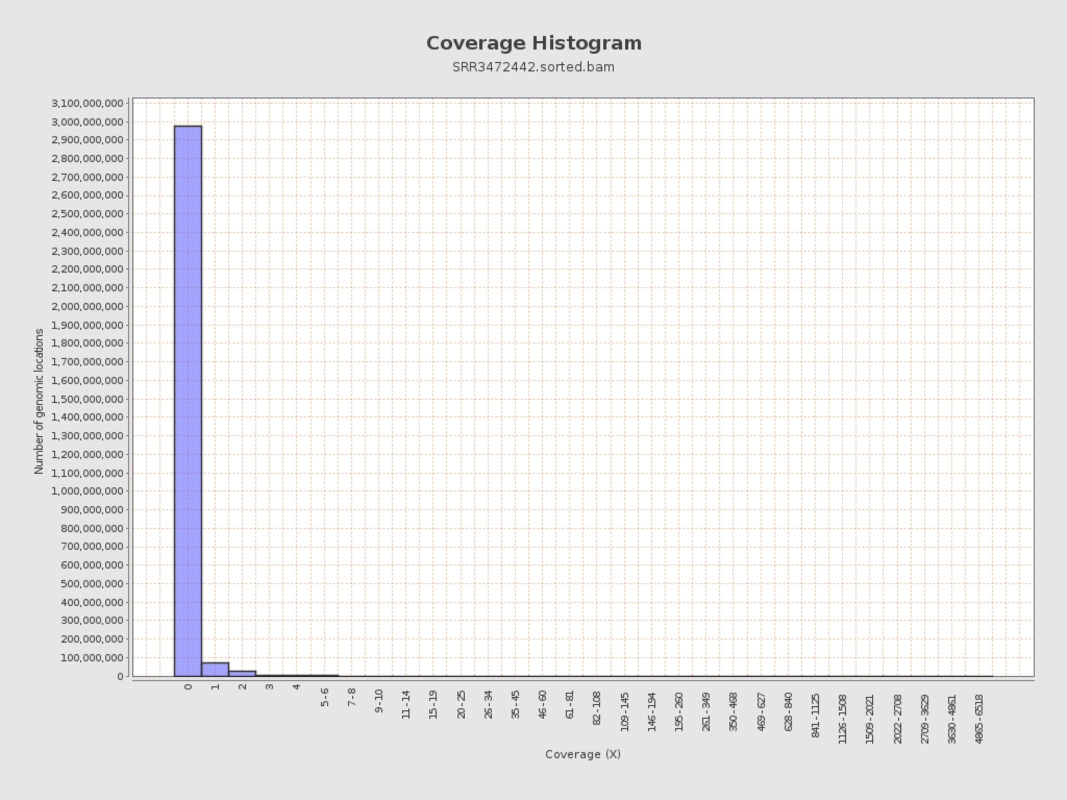
		bases	coverage	deviation
chr1	249250621	119178912	0.4781	13.747
chr2	243199373	107356335	0.4414	15.0121
chr3	198022430	72741080	0.3673	8.7762
chr4	191154276	31359936	0.1641	6.4295
chr5	180915260	53292049	0.2946	14.4814
chr6	171115067	103442013	0.6045	15.9446
chr7	159138663	88518218	0.5562	15.7746
chr8	146364022	114007847	0.7789	23.7293
chr9	141213431	42306297	0.2996	7.7316
chr10	135534747	19754145	0.1457	5.0536
chr11	135006516	42040182	0.3114	11.1535
chr12	133851895	68909566	0.5148	14.924
chr13	115169878	49489188	0.4297	17.1135
chr14	107349540	36349376	0.3386	12.9777
chr15	102531392	19925594	0.1943	6.7906
chr16	90354753	45302237	0.5014	13.1573
chr17	81195210	53432368	0.6581	14.5738
chr18	78077248	10029652	0.1285	5.5366
chr19	59128983	36038571	0.6095	14.8599
chr20	63025520	55276490	0.877	23.7751
chr21	48129895	8063358	0.1675	7.9237
chr22	51304566	11458816	0.2233	8.8808
chrMT	16571	2104	0.127	0.3986
chrX	155270560	66225755	0.4265	13.1231

chrY	59373566	271535	0.0046	0.4183

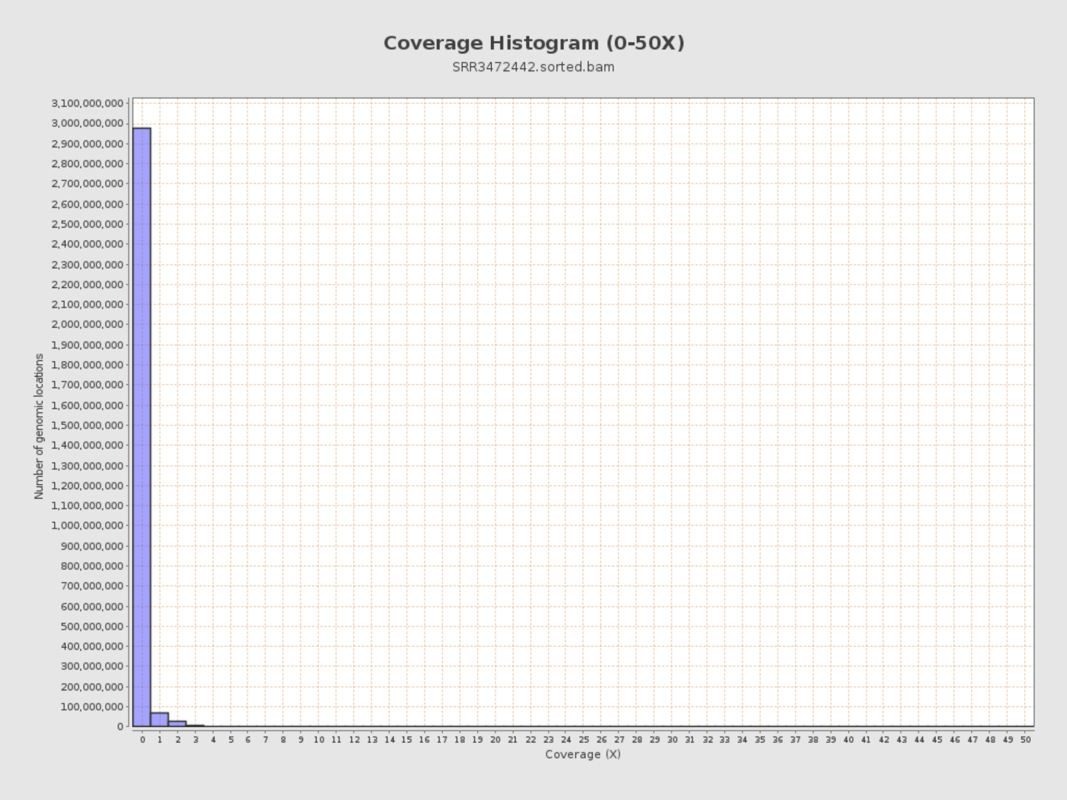
3. Results : Coverage across reference



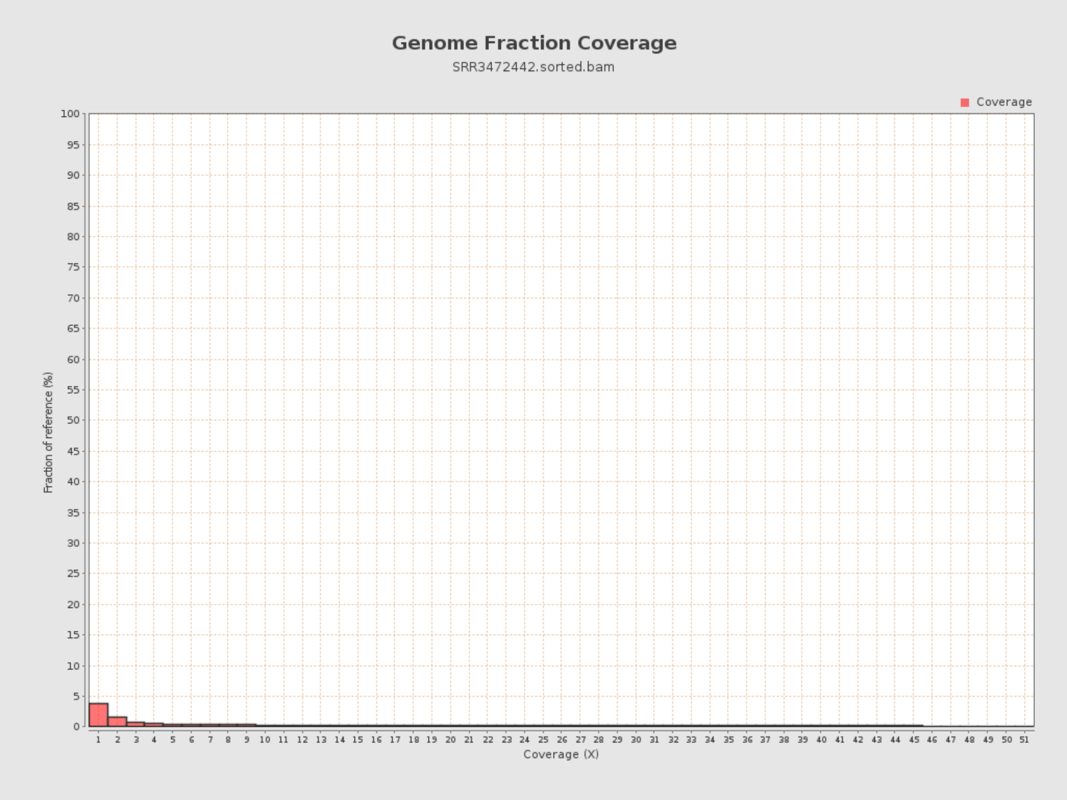
4. Results : Coverage Histogram



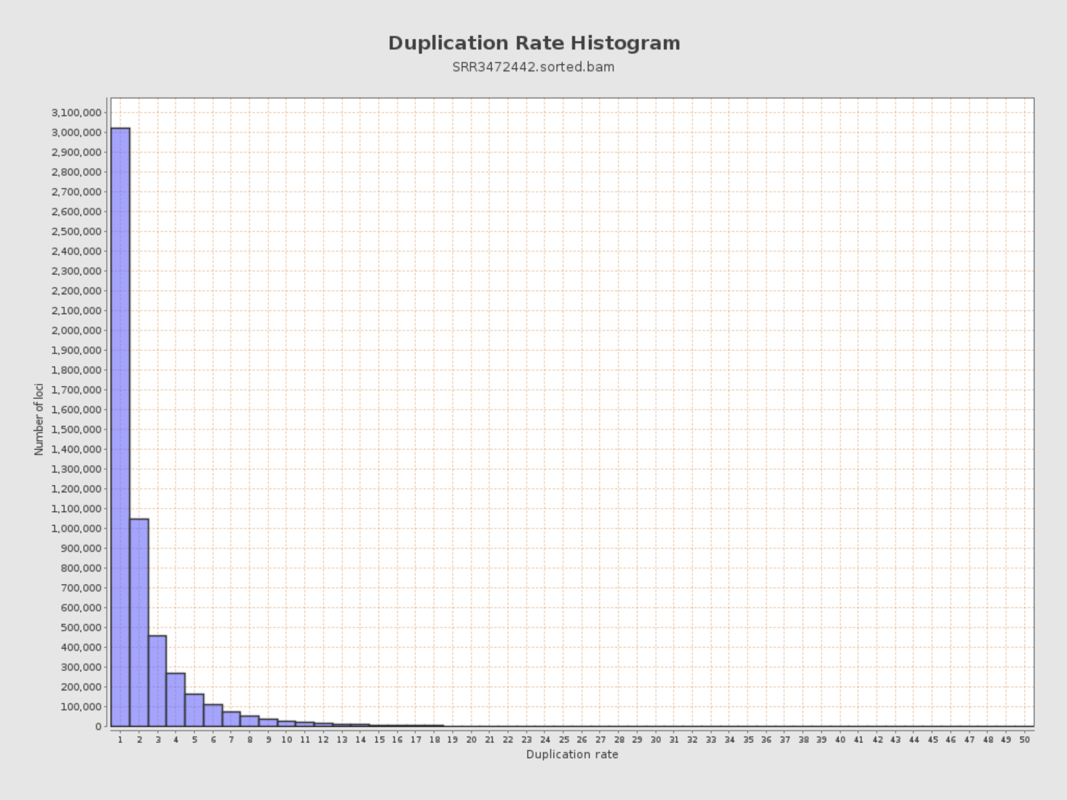
5. Results : Coverage Histogram (0-50X)



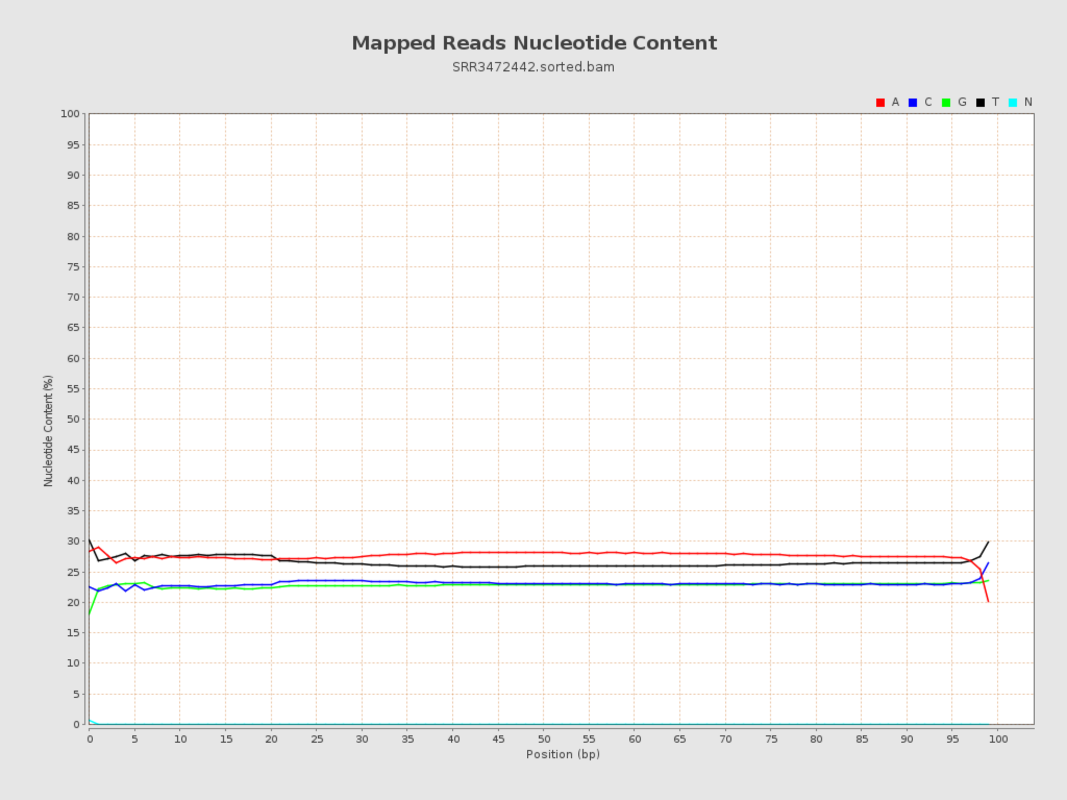
6. Results : Genome Fraction Coverage



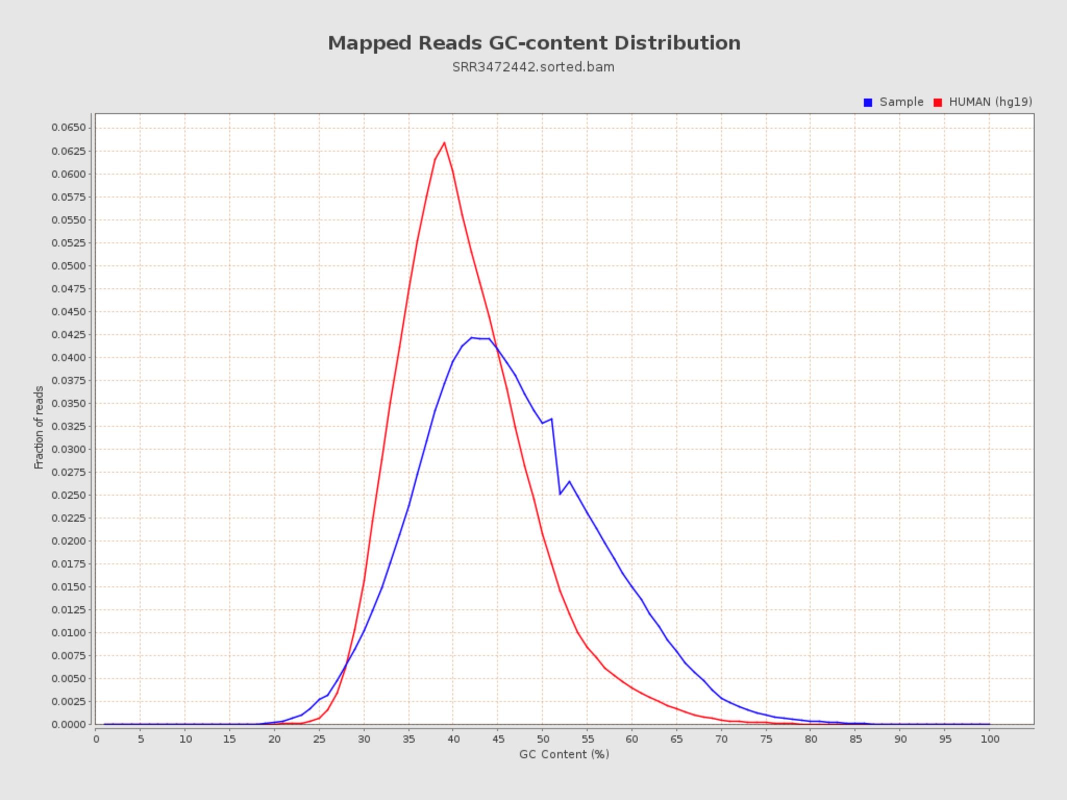
7. Results : Duplication Rate Histogram



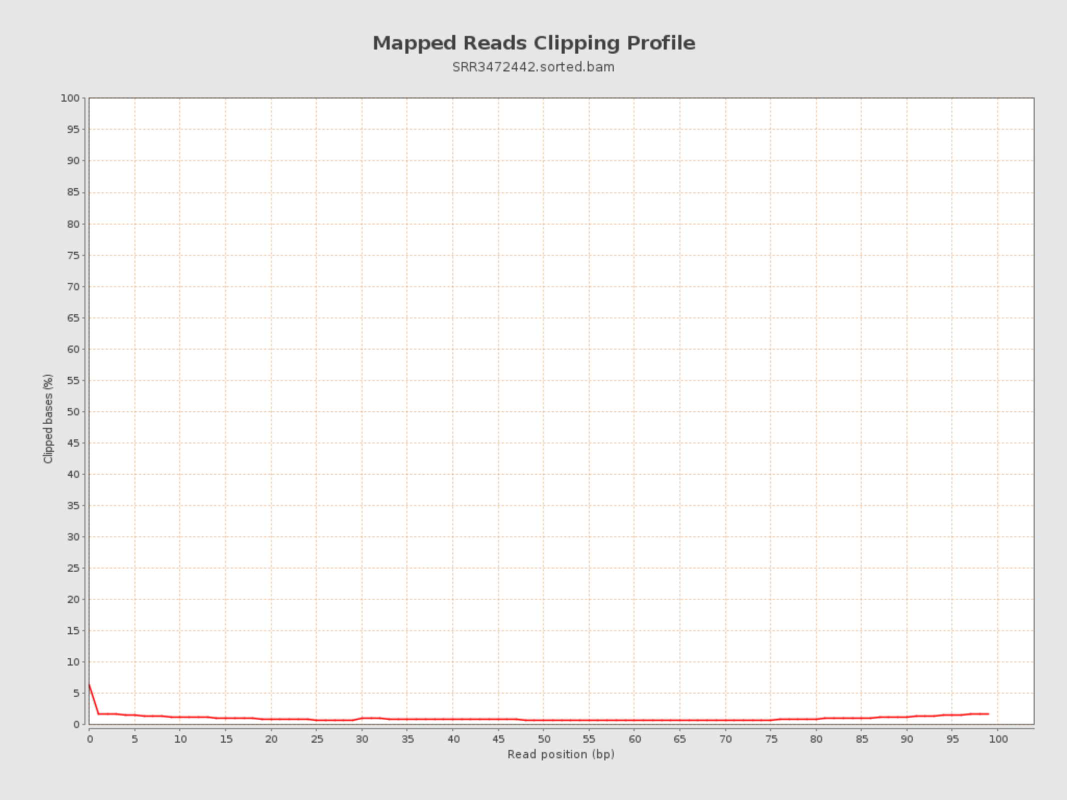
8. Results : Mapped Reads Nucleotide Content



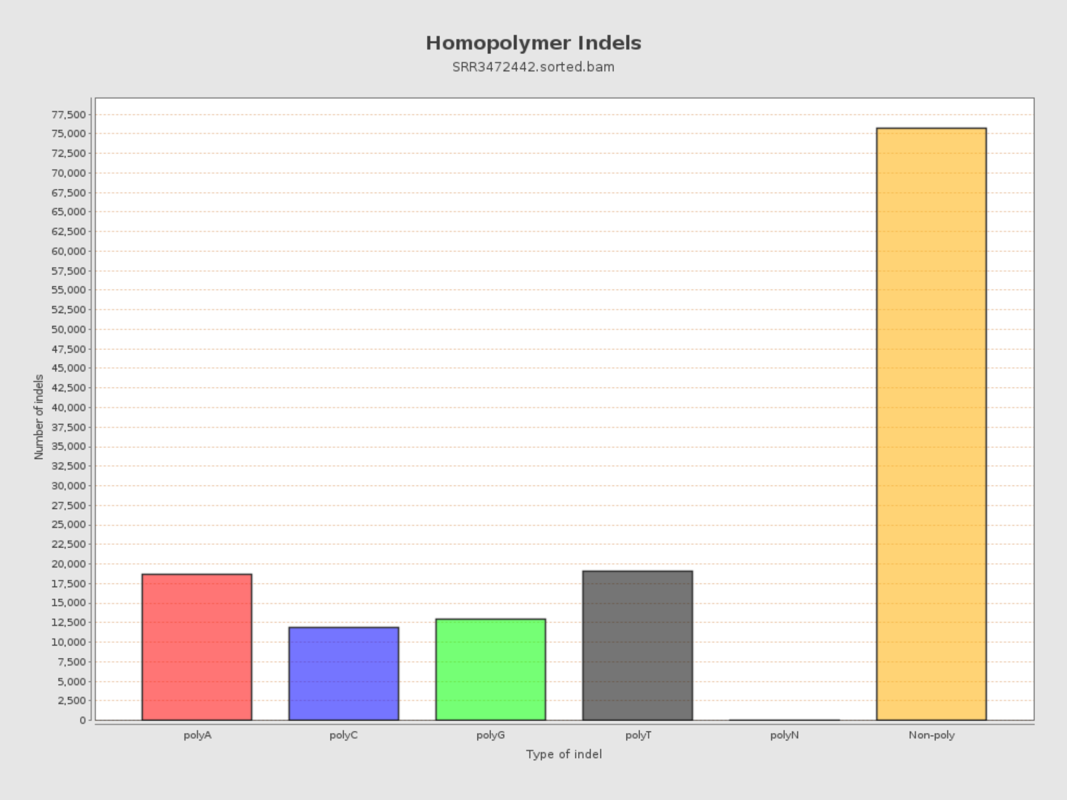
9. Results : Mapped Reads GC-content Distribution



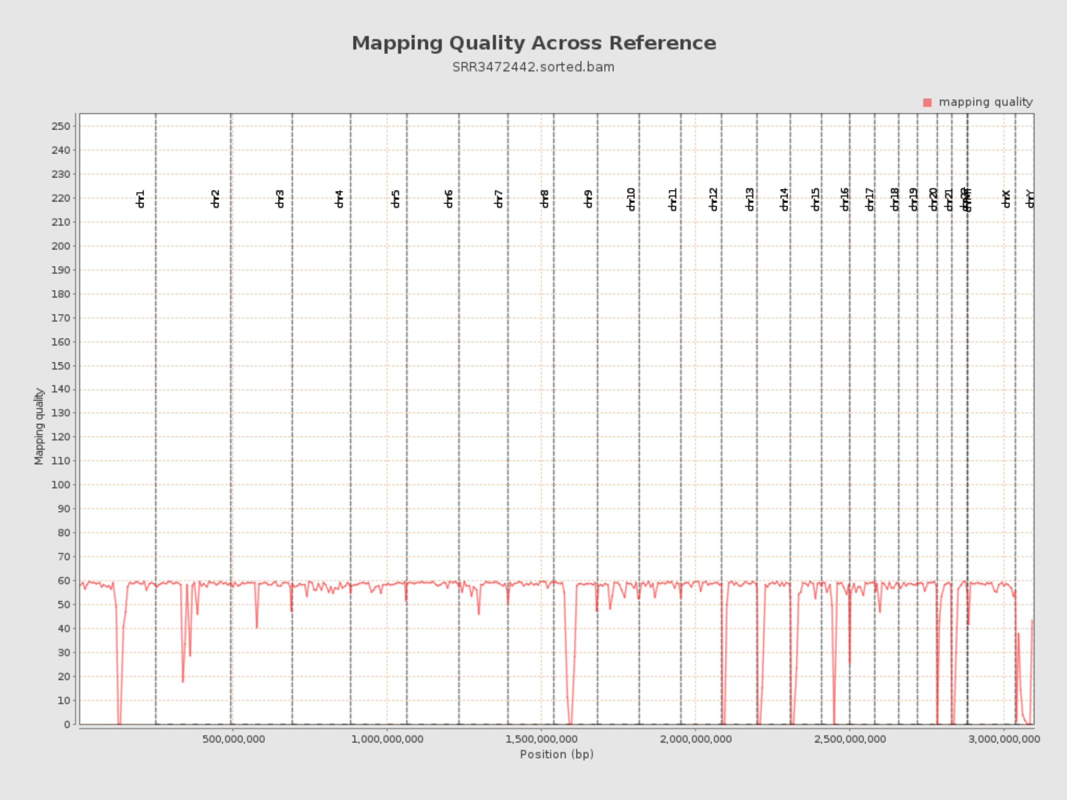
10. Results : Mapped Reads Clipping Profile



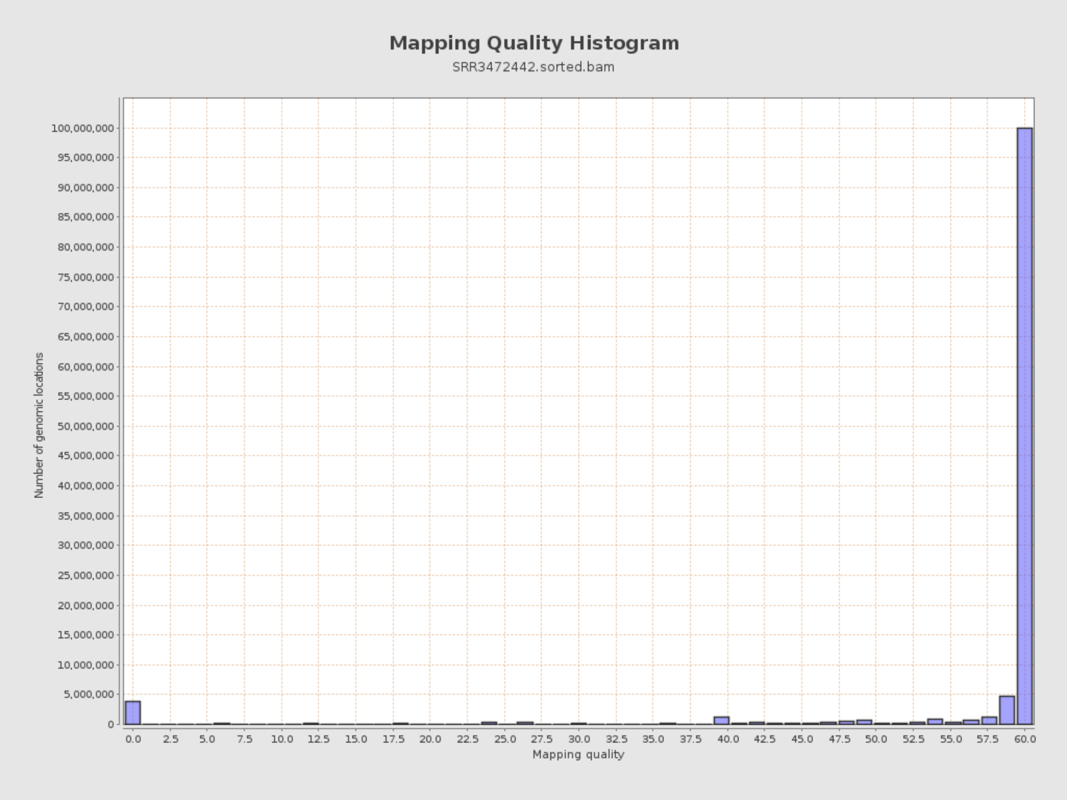
11. Results : Homopolymer Indels



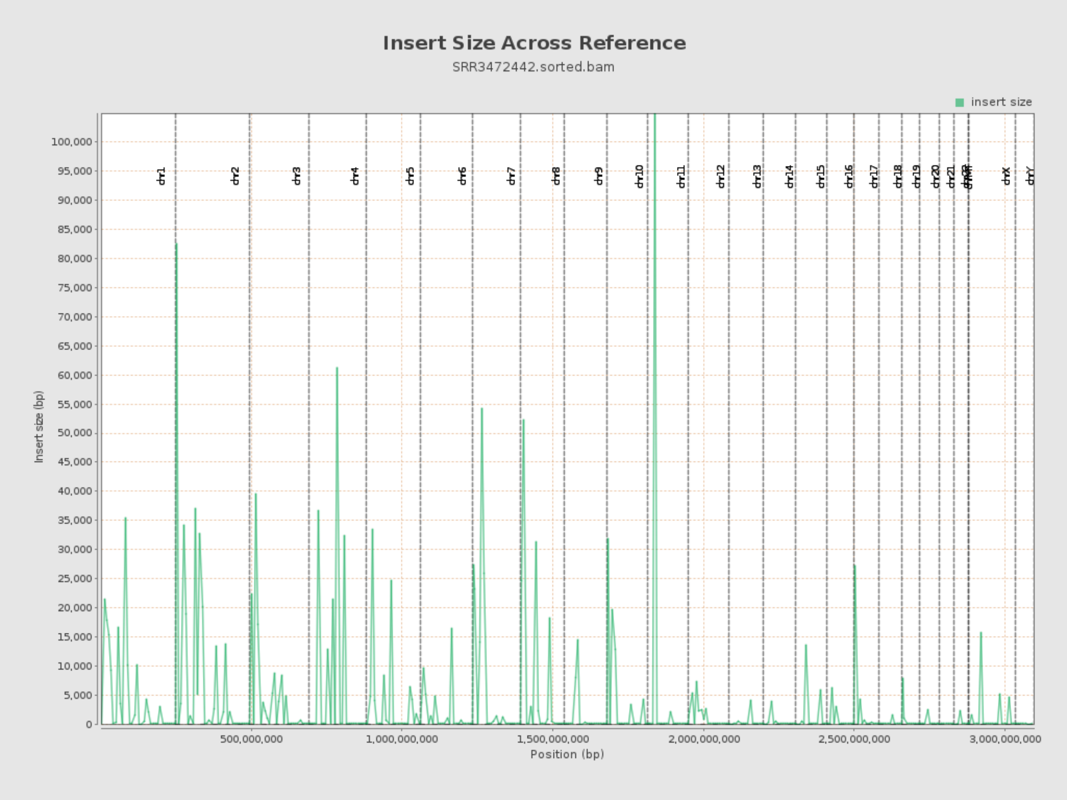
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram