Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 10:02:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472569.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_SRR3472569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472569_1.fastq.gz SRR3472569_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 10:02:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	422,354,902
Mapped reads	415,525,690 / 98.38%
Unmapped reads	6,829,212 / 1.62%
Mapped paired reads	415,525,690 / 98.38%
Mapped reads, first in pair	208,563,107 / 49.38%
Mapped reads, second in pair	206,962,583 / 49%
Mapped reads, both in pair	413,215,876 / 97.84%
Mapped reads, singletons	2,309,814 / 0.55%
Secondary alignments	0
Supplementary alignments	325,809 / 0.08%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	281,651,938 / 66.69%
Duplication rate	54.8%
Clipped reads	101,306,618 / 23.99%

2.2. ACGT Content

Number/percentage of A's	9,886,673,487 / 25.27%
Number/percentage of C's	9,696,741,368 / 24.78%
Number/percentage of T's	10,025,410,449 / 25.62%
Number/percentage of G's	9,513,513,674 / 24.31%
Number/percentage of N's	7,794,938 / 0.02%

GC Percentage	49.09%

2.3. Coverage

Mean	12.6425
Standard Deviation	127.7216

2.4. Mapping Quality

Mean Mapping Quality	51.87

2.5. Insert size

Mean	9,077.83
Standard Deviation	872,826.72
P25/Median/P75	104 / 155 / 235

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	386,981,543
Insertions	2,978,315
Mapped reads with at least one insertion	0.7%
Deletions	3,150,875
Mapped reads with at least one deletion	0.74%
Homopolymer indels	39.47%

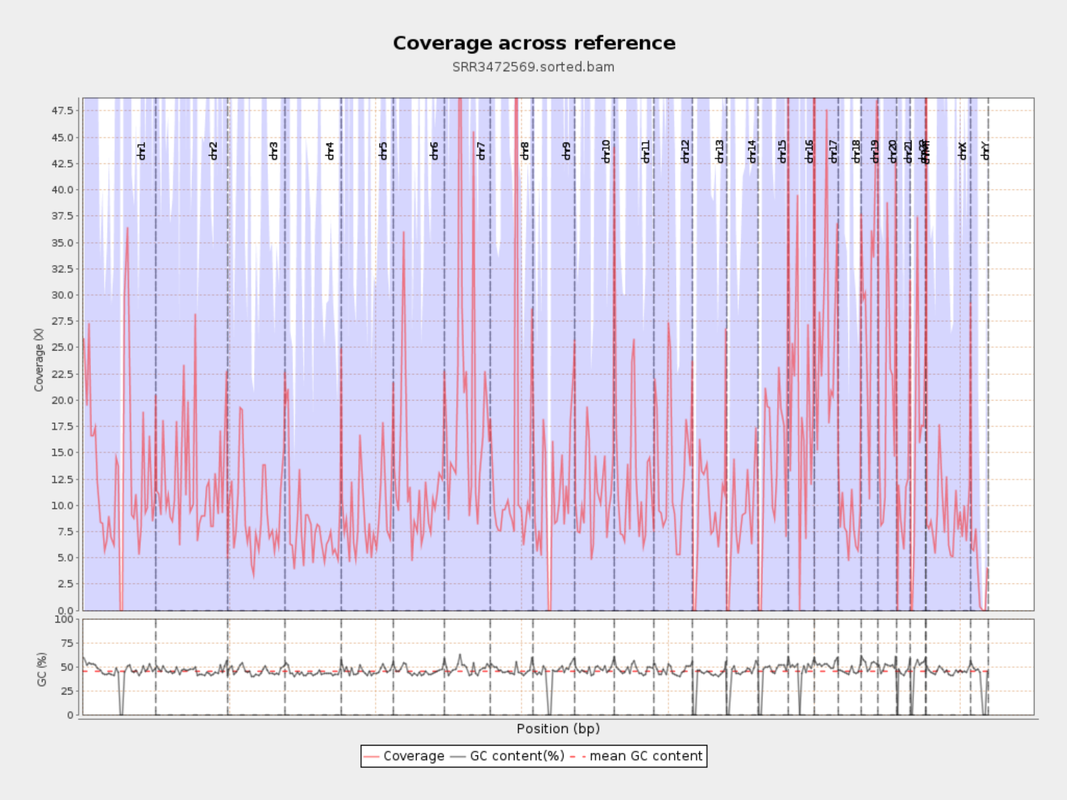
2.7. Chromosome stats

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

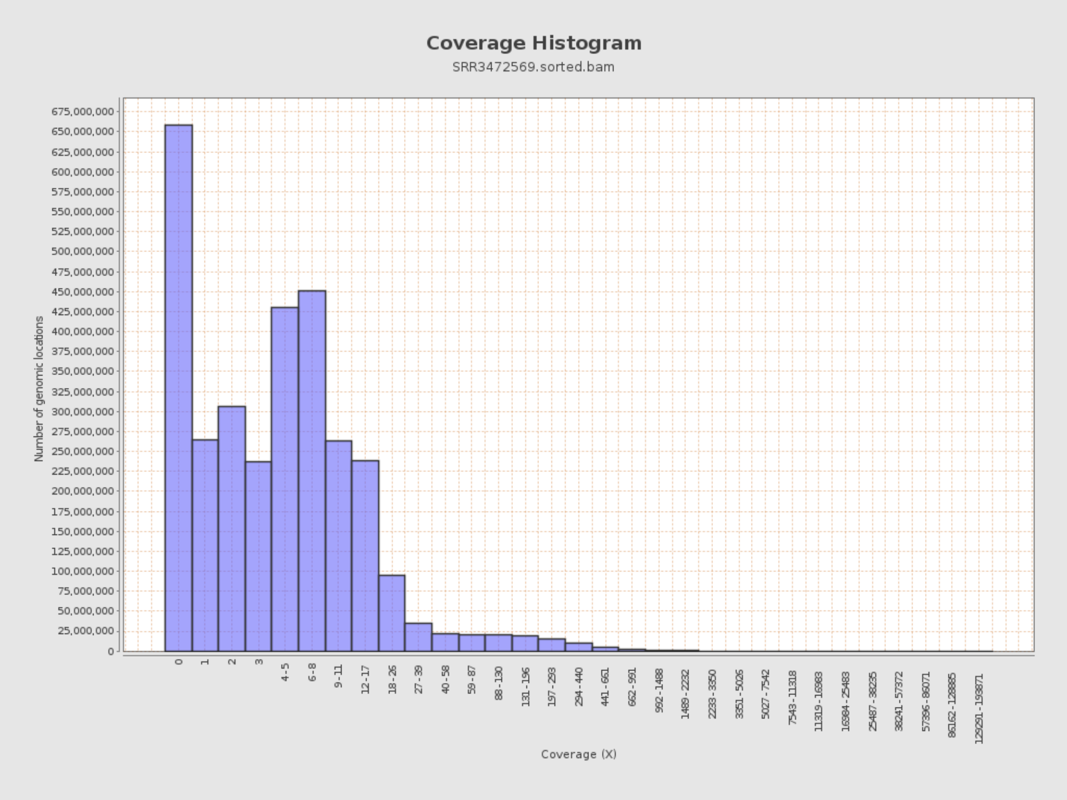
		bases	coverage	deviation
chr1	249250621	3284589943	13.1779	104.0918
chr2	243199373	3014814870	12.3965	91.9556
chr3	198022430	1865989283	9.4231	48.5916
chr4	191154276	1533596597	8.0228	59.228
chr5	180915260	1700197143	9.3978	64.0187
chr6	171115067	2041795111	11.9323	55.8169
chr7	159138663	3229751662	20.2952	432.6518
chr8	146364022	1979550501	13.5248	196.1119
chr9	141213431	1503027057	10.6437	55.975
chr10	135534747	1464137068	10.8027	75.4199
chr11	135006516	1685948086	12.4879	53.9183
chr12	133851895	1836546369	13.7207	52.4838
chr13	115169878	1099279947	9.5449	40.527
chr14	107349540	936408012	8.723	38.5901
chr15	102531392	1360054830	13.2648	66.2472
chr16	90354753	1824679640	20.1946	96.3719
chr17	81195210	2139983845	26.356	128.1846
chr18	78077248	641175861	8.2121	65.0894
chr19	59128983	1828509639	30.9241	116.585
chr20	63025520	1205965468	19.1346	84.1491
chr21	48129895	547227455	11.3698	75.6537
chr22	51304566	792527831	15.4475	78.0923
chrMT	16571	5562176	335.6572	99.8406
chrX	155270560	1417199482	9.1273	40.001

chrY	59373566	198918566	3.3503	89.1513

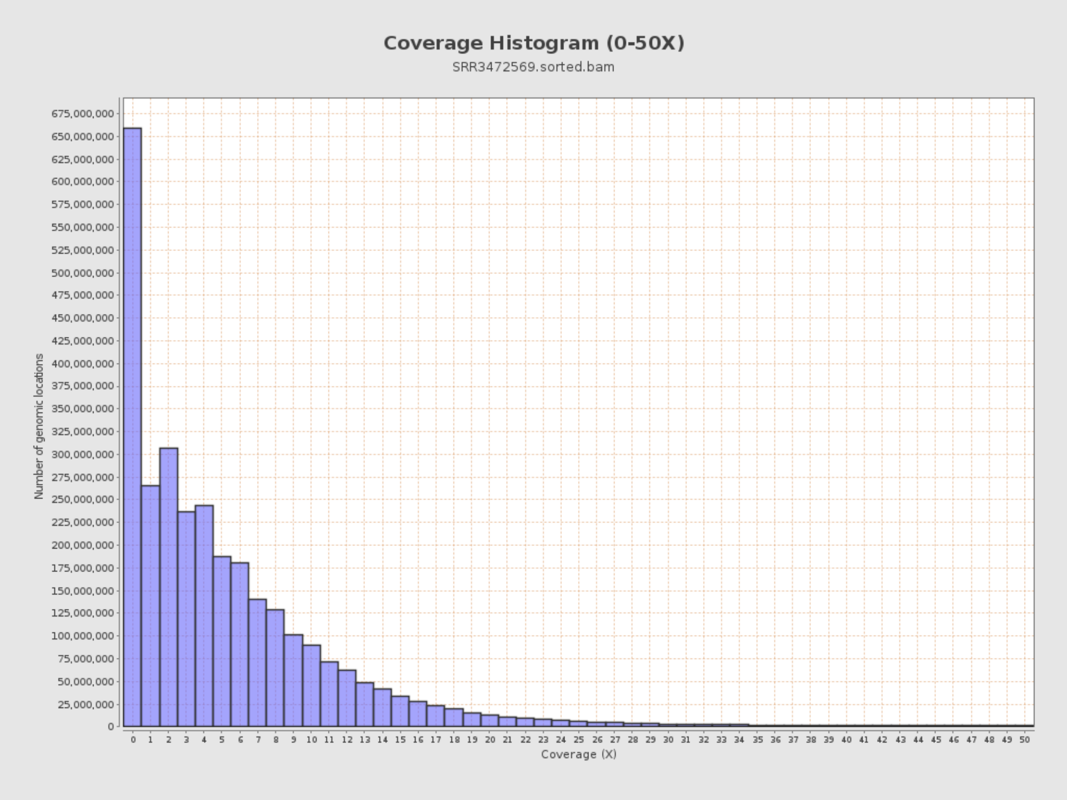
3. Results : Coverage across reference



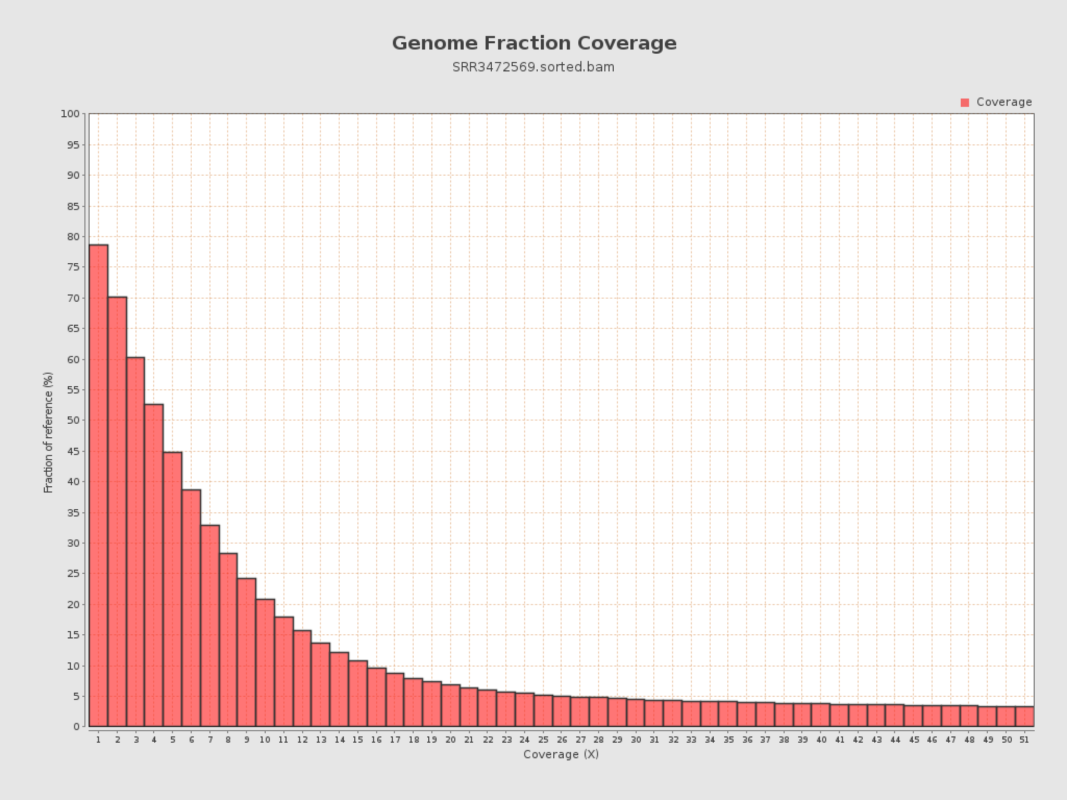
4. Results : Coverage Histogram



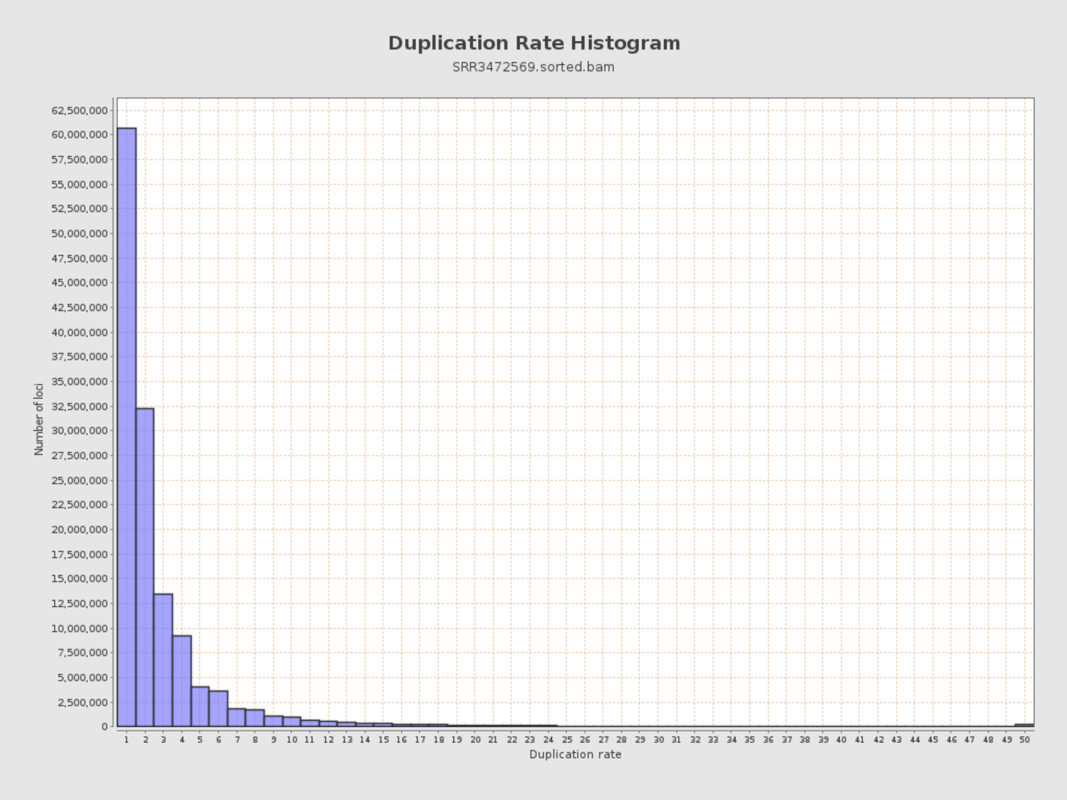
5. Results : Coverage Histogram (0-50X)



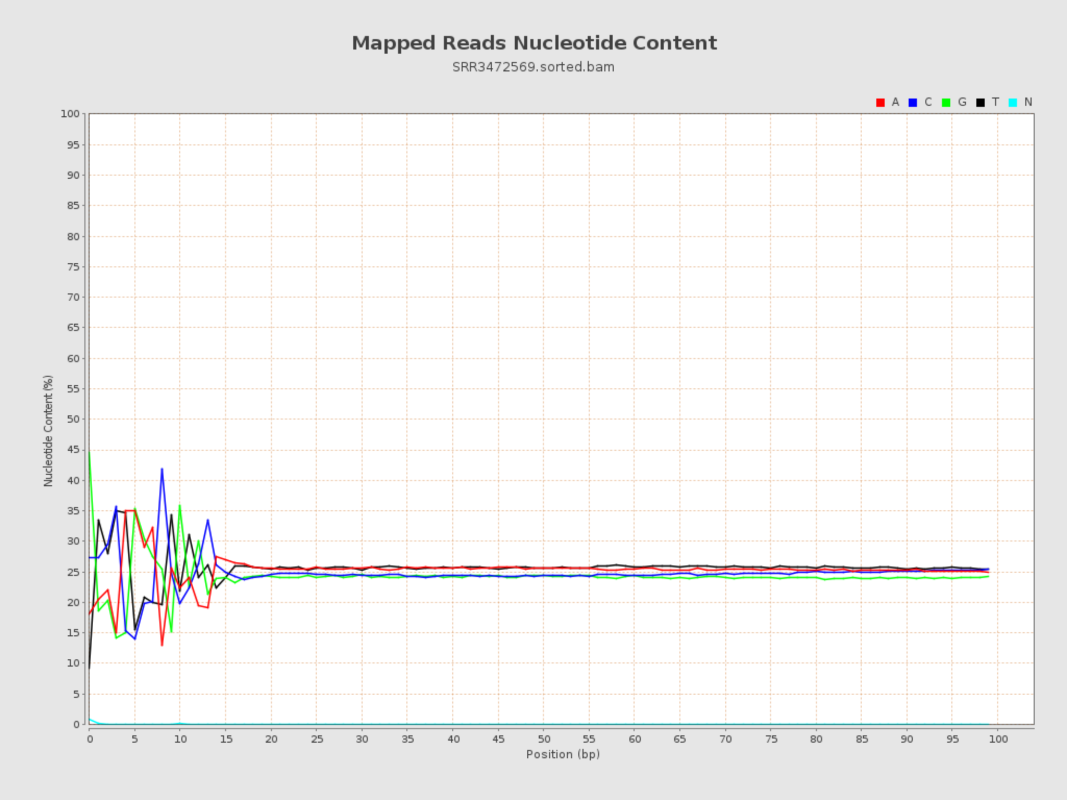
6. Results : Genome Fraction Coverage



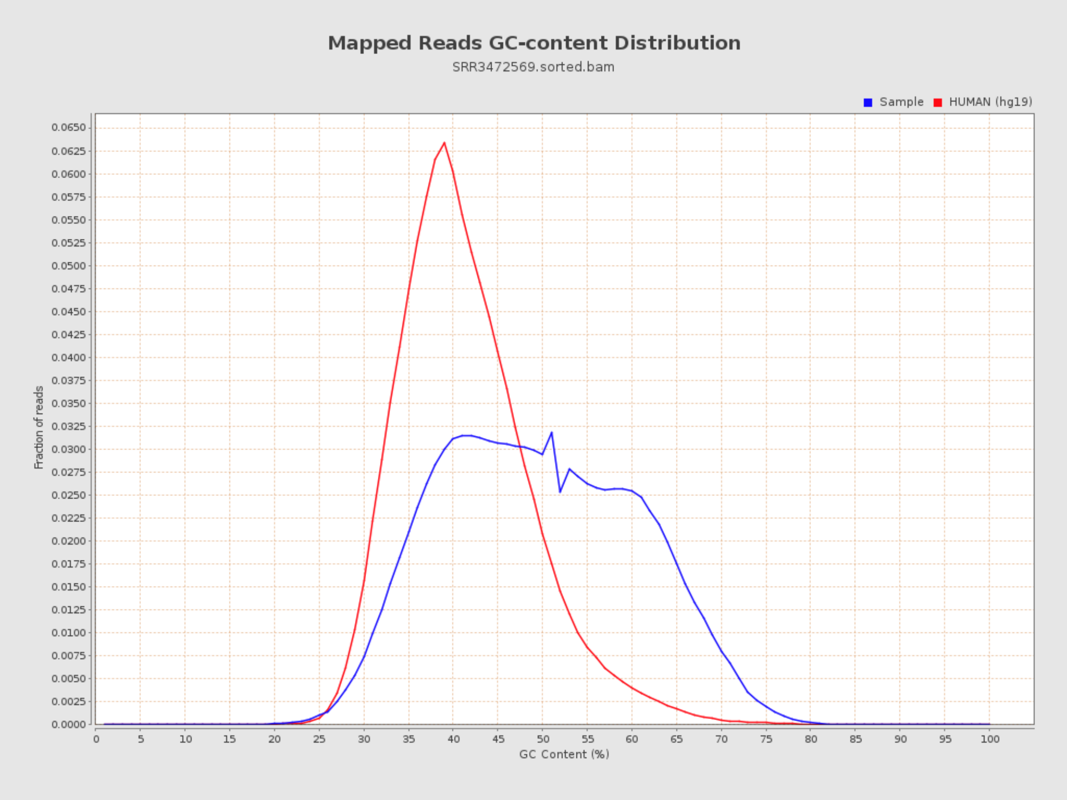
7. Results : Duplication Rate Histogram



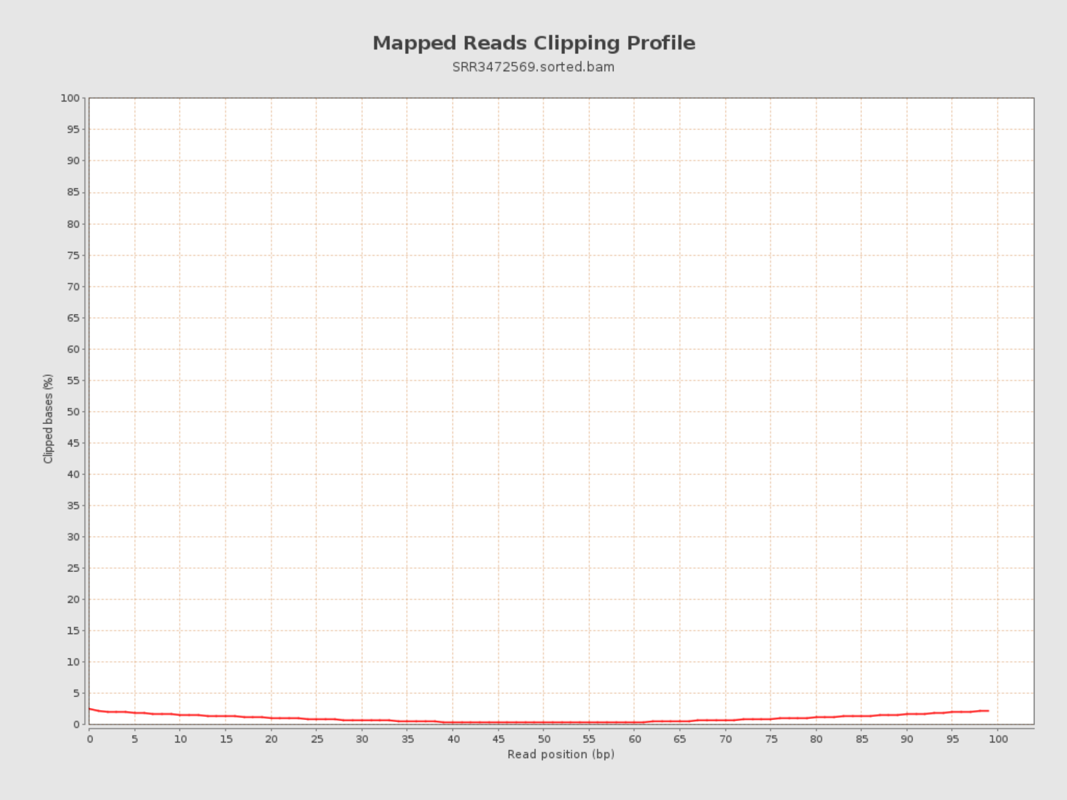
8. Results : Mapped Reads Nucleotide Content



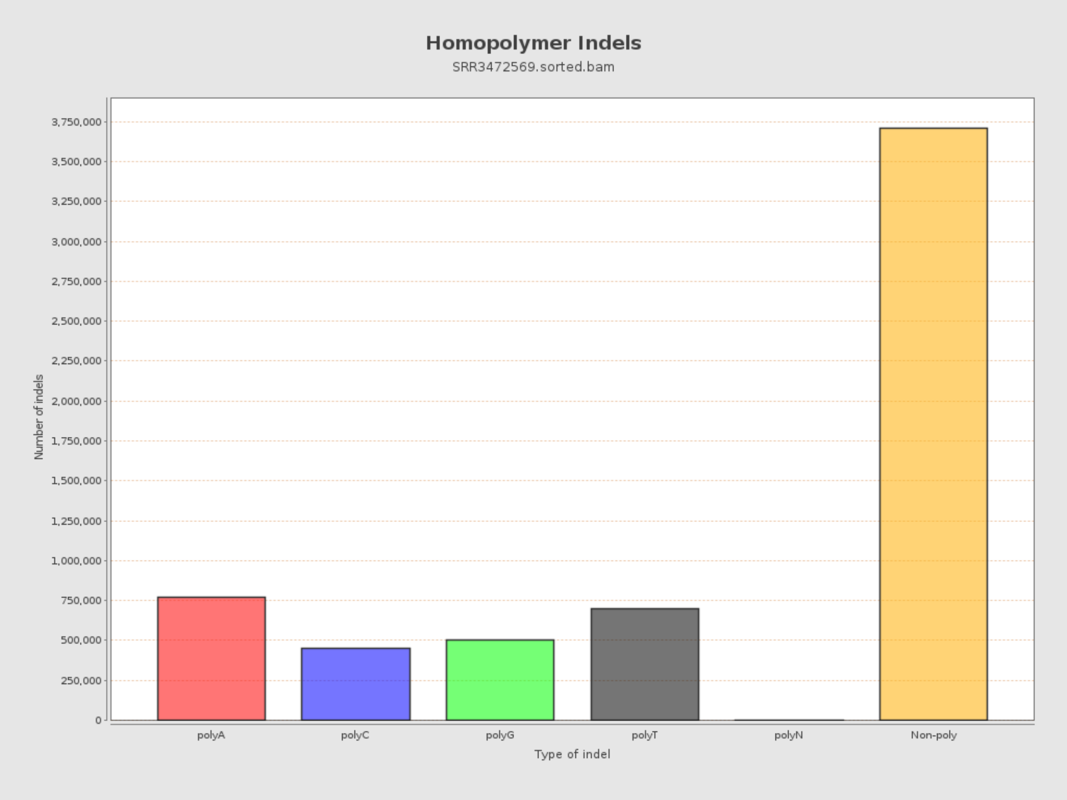
9. Results : Mapped Reads GC-content Distribution



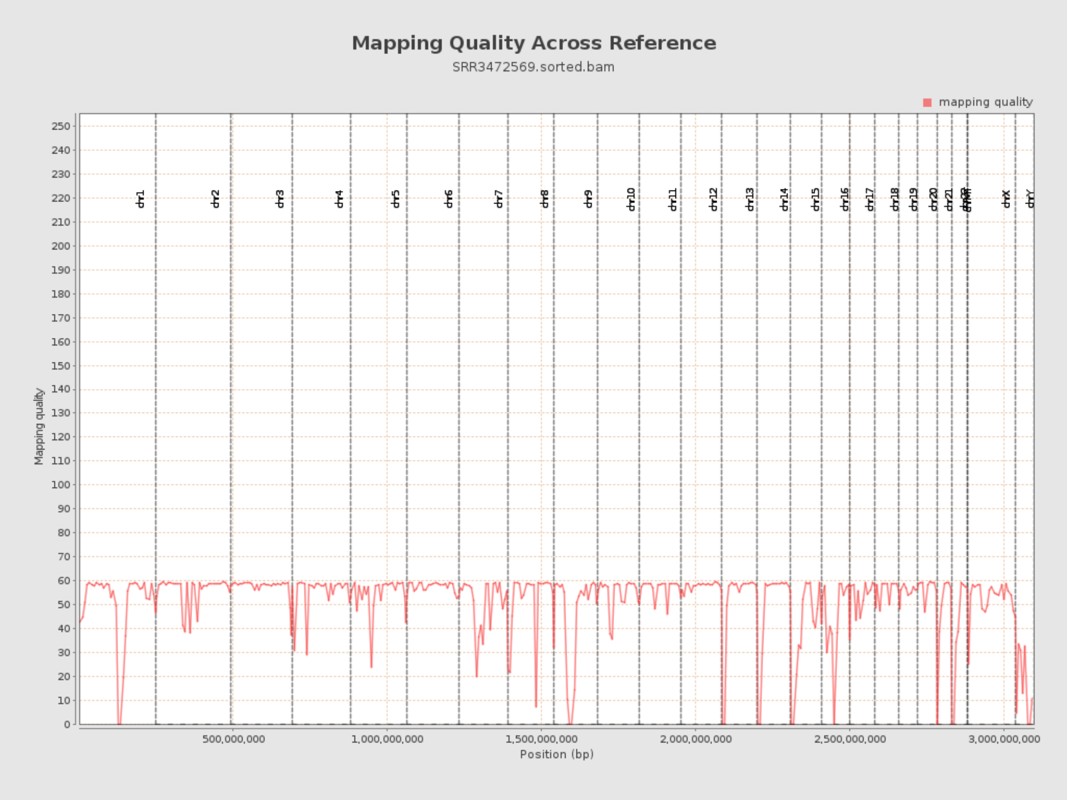
10. Results : Mapped Reads Clipping Profile



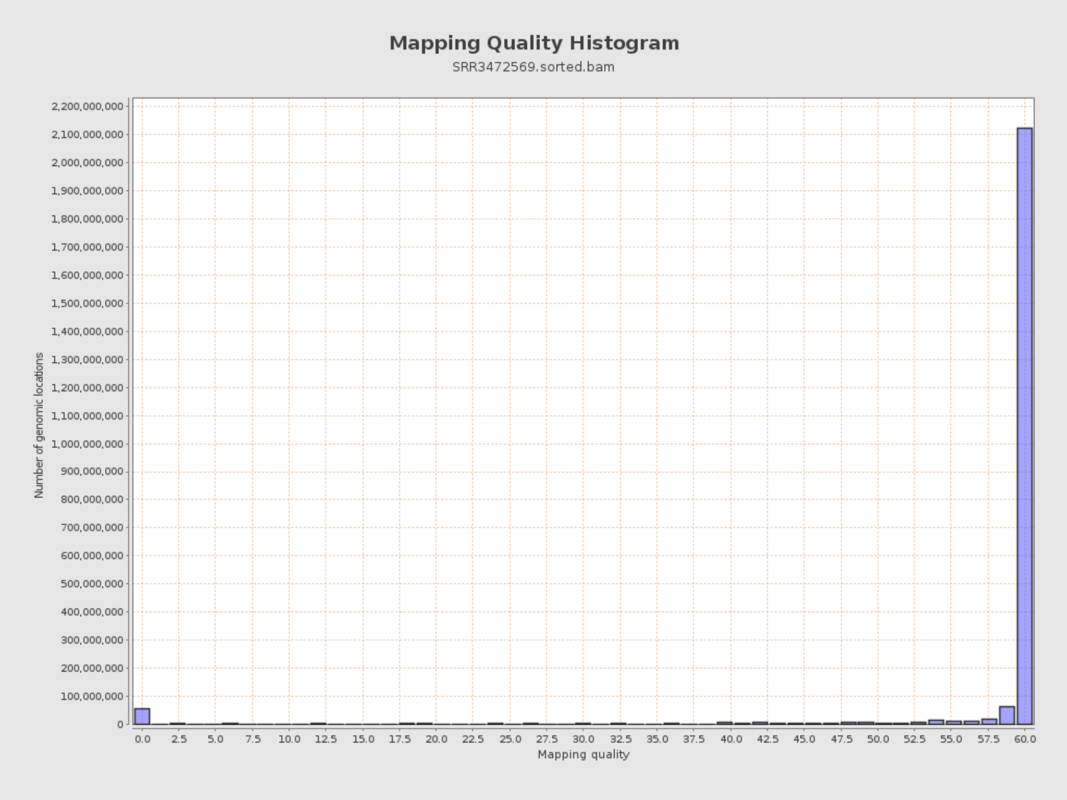
11. Results : Homopolymer Indels



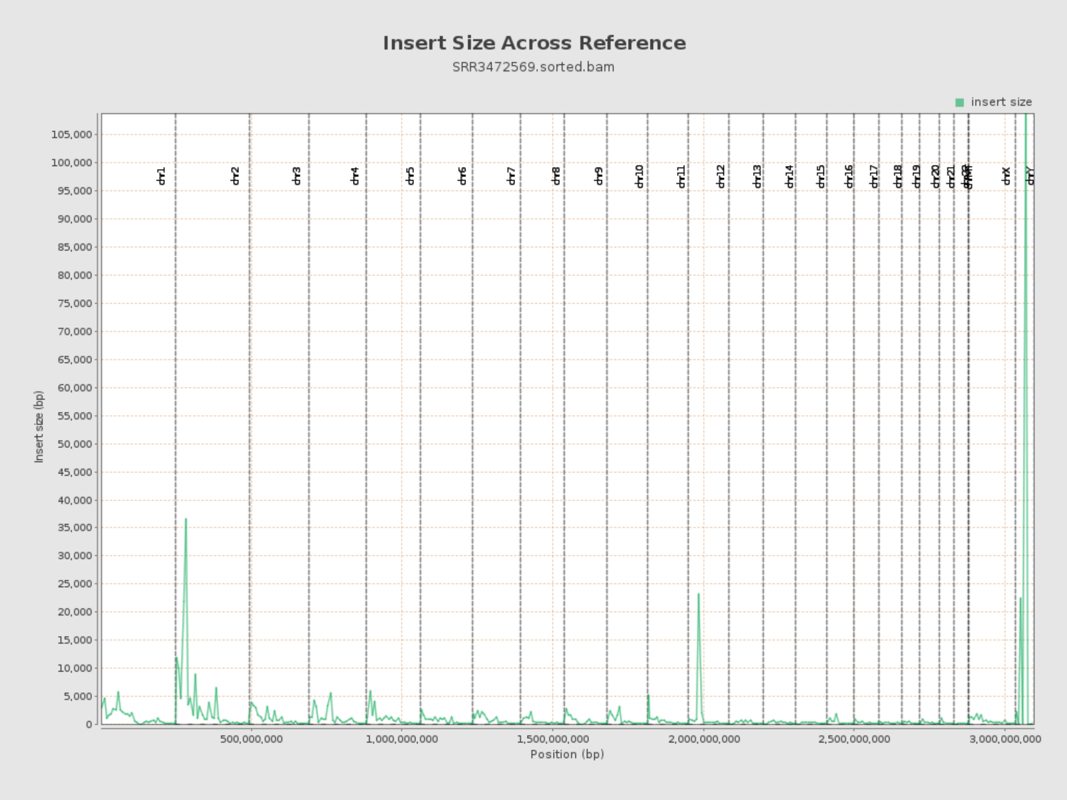
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram