Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:25:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472455.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_SRR3472455 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472455_1.fastq.gz SRR3472455_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:25:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472455.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,547,244
Mapped reads	12,436,500 / 99.12%
Unmapped reads	110,744 / 0.88%
Mapped paired reads	12,436,500 / 99.12%
Mapped reads, first in pair	6,238,602 / 49.72%
Mapped reads, second in pair	6,197,898 / 49.4%
Mapped reads, both in pair	12,378,564 / 98.66%
Mapped reads, singletons	57,936 / 0.46%
Secondary alignments	0
Supplementary alignments	38,437 / 0.31%
Read min/max/mean length	30 / 100 / 98.94
Duplicated reads (estimated)	6,555,100 / 52.24%
Duplication rate	44.29%
Clipped reads	880,767 / 7.02%

2.2. ACGT Content

Number/percentage of A's	335,028,860 / 27.59%
Number/percentage of C's	272,243,016 / 22.42%
Number/percentage of T's	337,239,659 / 27.77%
Number/percentage of G's	269,619,670 / 22.2%
Number/percentage of N's	164,208 / 0.01%

GC Percentage	44.62%

2.3. Coverage

Mean	0.3923
Standard Deviation	9.647

2.4. Mapping Quality

Mean Mapping Quality	55.13

2.5. Insert size

Mean	17,388.45
Standard Deviation	1,287,274.14
P25/Median/P75	145 / 203 / 273

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	5,433,590
Insertions	77,886
Mapped reads with at least one insertion	0.62%
Deletions	60,362
Mapped reads with at least one deletion	0.48%
Homopolymer indels	46.54%

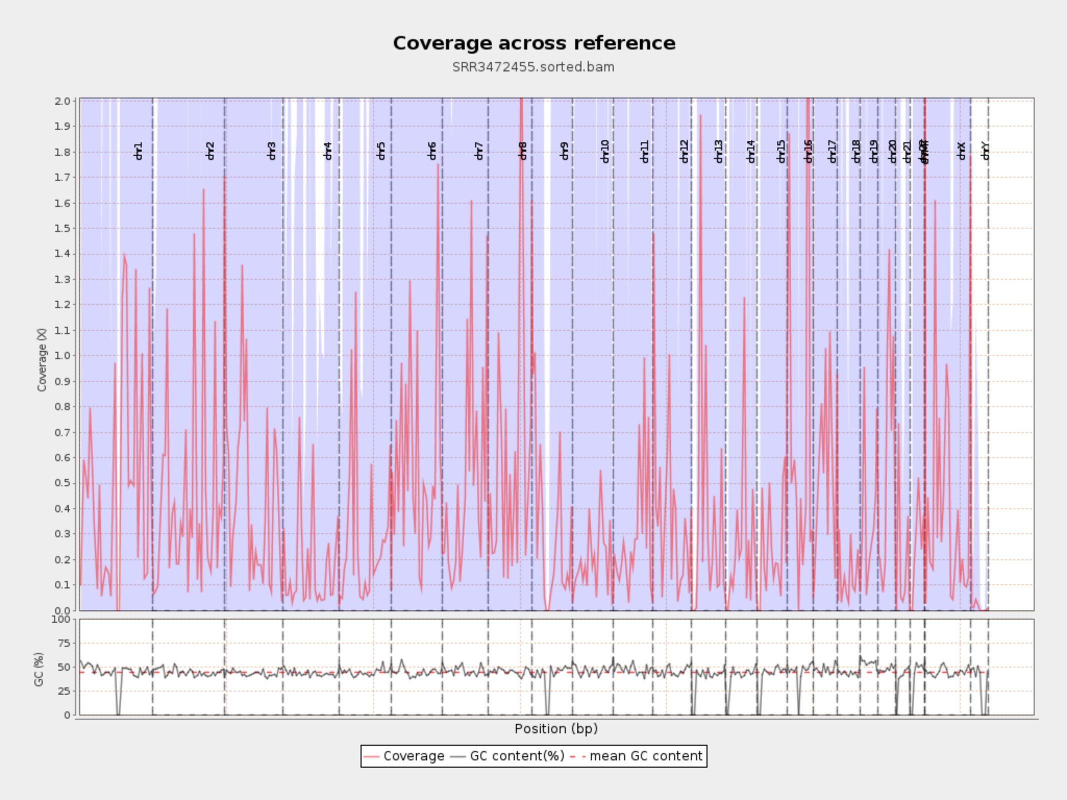
2.7. Chromosome stats

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

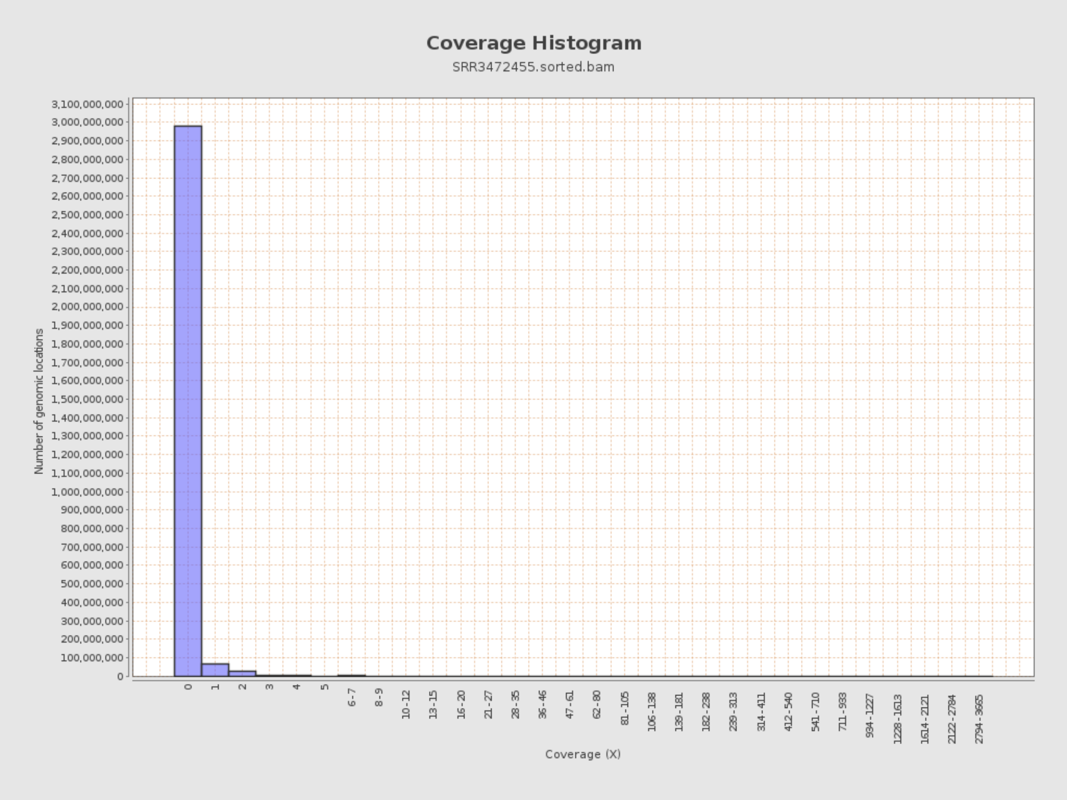
		bases	coverage	deviation
chr1	249250621	128558916	0.5158	11.418
chr2	243199373	106909840	0.4396	11.4186
chr3	198022430	91060430	0.4598	8.2368
chr4	191154276	32301821	0.169	5.2754
chr5	180915260	52874394	0.2923	7.1766
chr6	171115067	98313548	0.5745	10.8176
chr7	159138663	81812475	0.5141	12.9072
chr8	146364022	91999254	0.6286	14.082
chr9	141213431	45738342	0.3239	6.4256
chr10	135534747	27455561	0.2026	5.9694
chr11	135006516	40789265	0.3021	7.634
chr12	133851895	52333365	0.391	7.5303
chr13	115169878	43251213	0.3755	11.3484
chr14	107349540	26720454	0.2489	6.3975
chr15	102531392	24966271	0.2435	6.1624
chr16	90354753	68579747	0.759	17.4247
chr17	81195210	45869015	0.5649	10.0066
chr18	78077248	10784388	0.1381	3.582
chr19	59128983	21535247	0.3642	6.2975
chr20	63025520	37765753	0.5992	13.9348
chr21	48129895	10112765	0.2101	11.617
chr22	51304566	12924094	0.2519	6.1007
chrMT	16571	95112	5.7397	3.6588
chrX	155270560	60966897	0.3926	8.5608

chrY	59373566	719743	0.0121	0.517

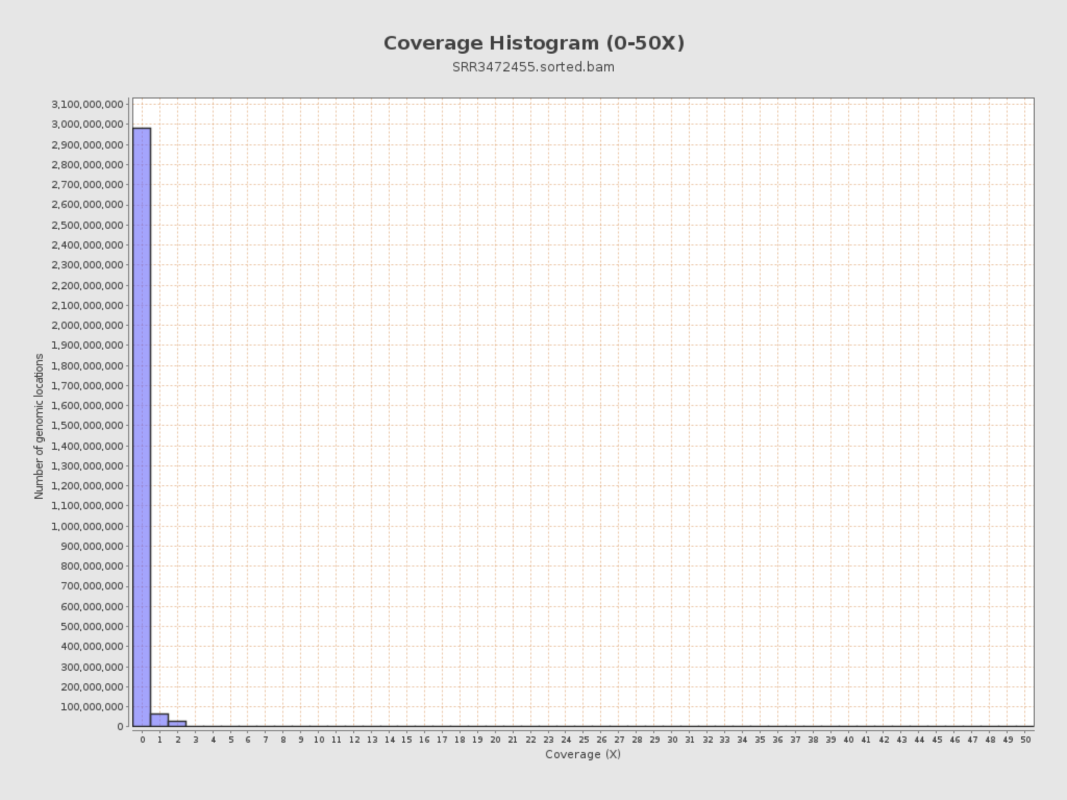
3. Results : Coverage across reference



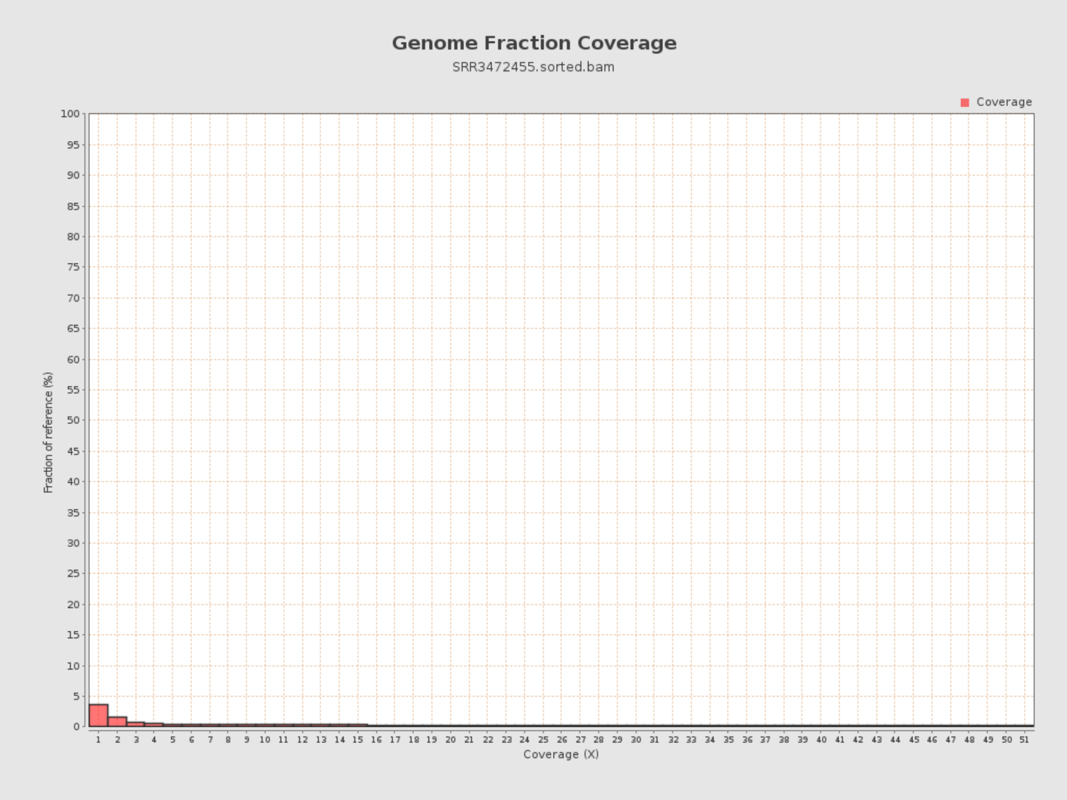
4. Results : Coverage Histogram



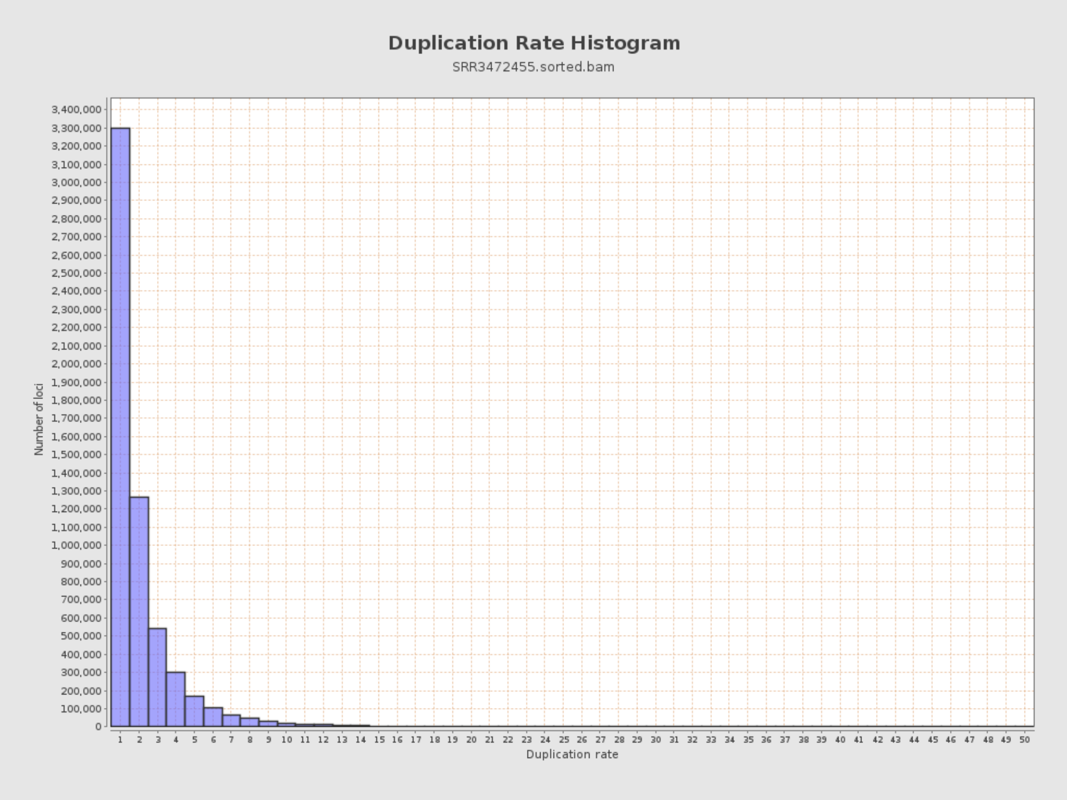
5. Results : Coverage Histogram (0-50X)



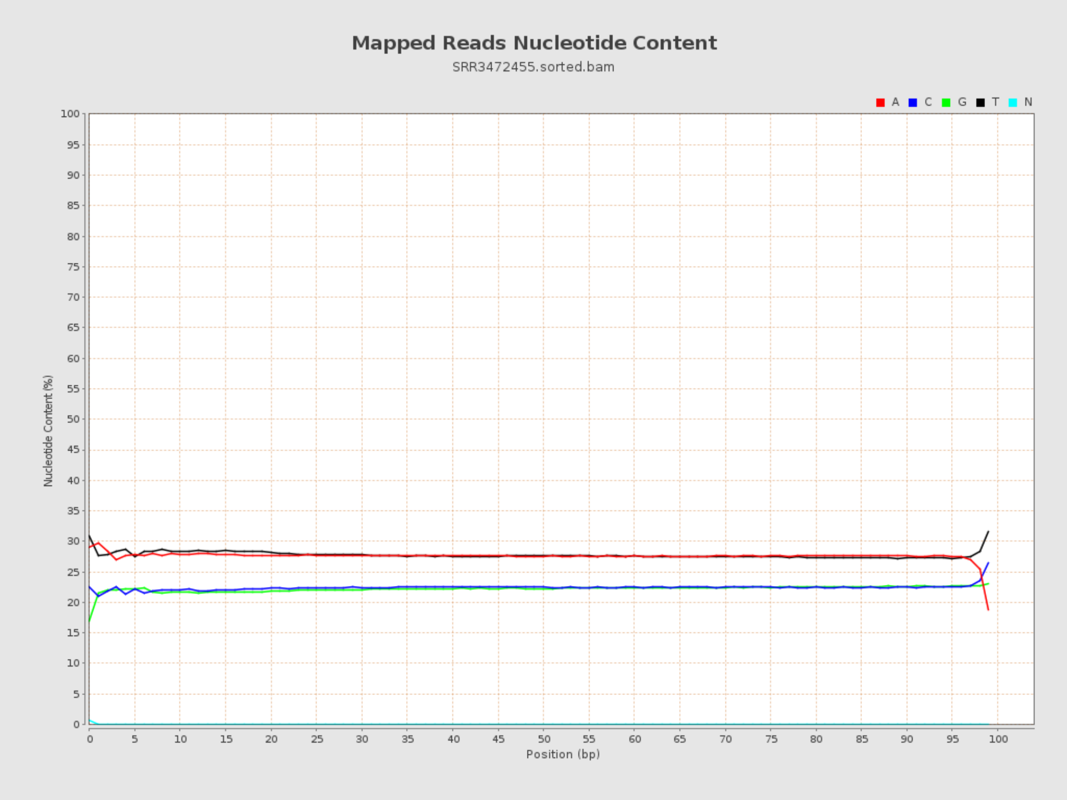
6. Results : Genome Fraction Coverage



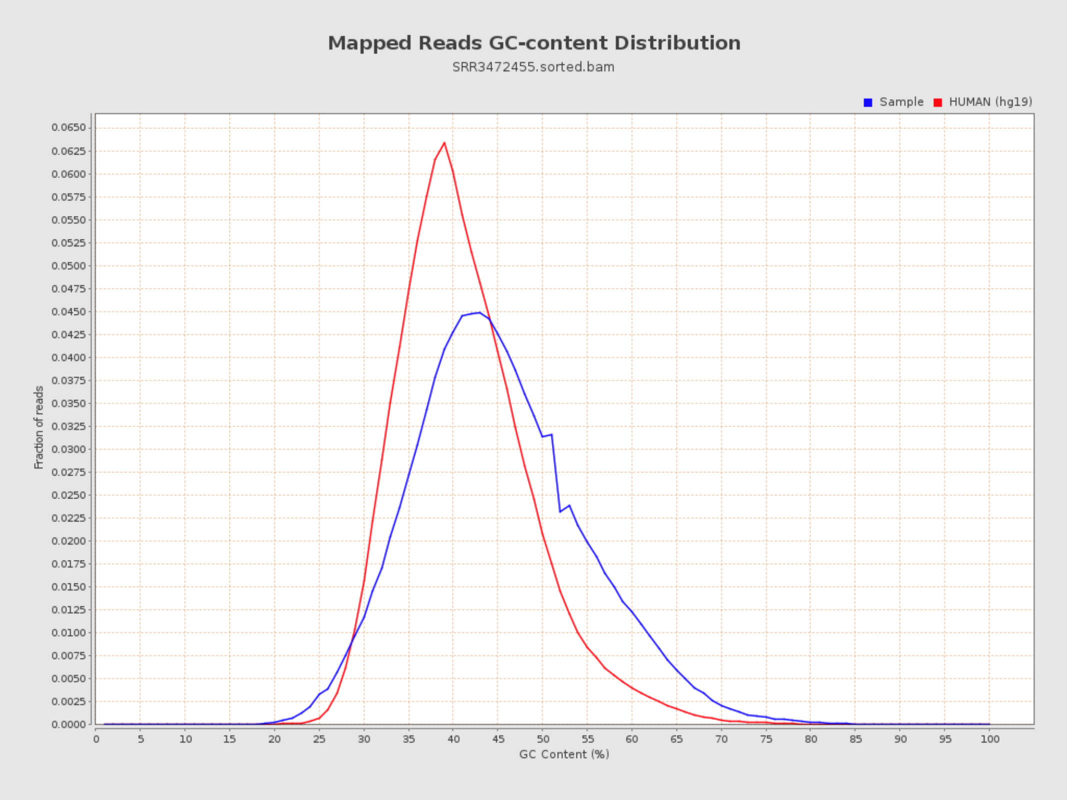
7. Results : Duplication Rate Histogram



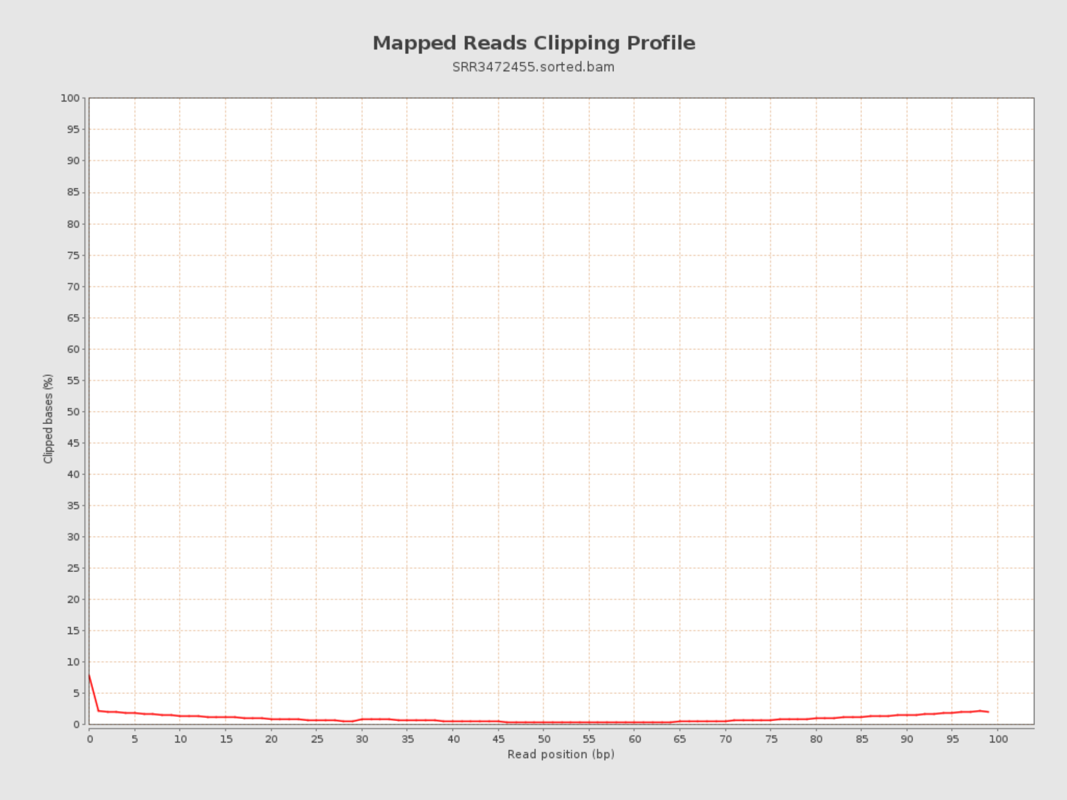
8. Results : Mapped Reads Nucleotide Content



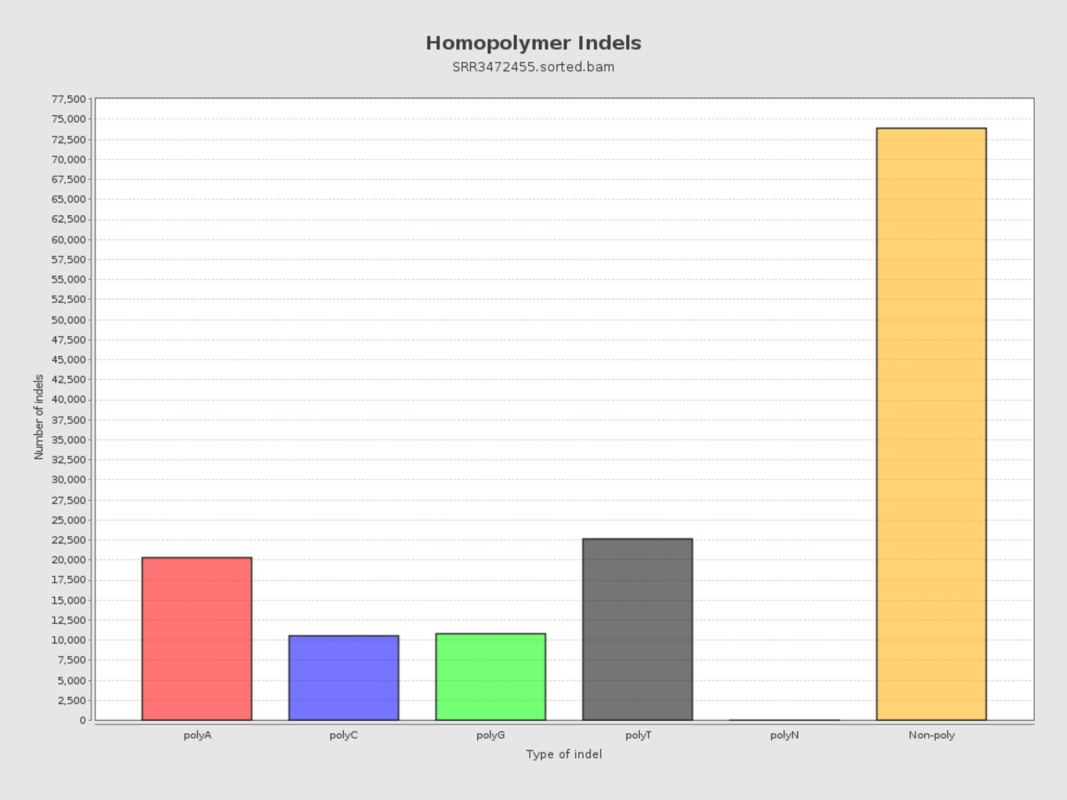
9. Results : Mapped Reads GC-content Distribution



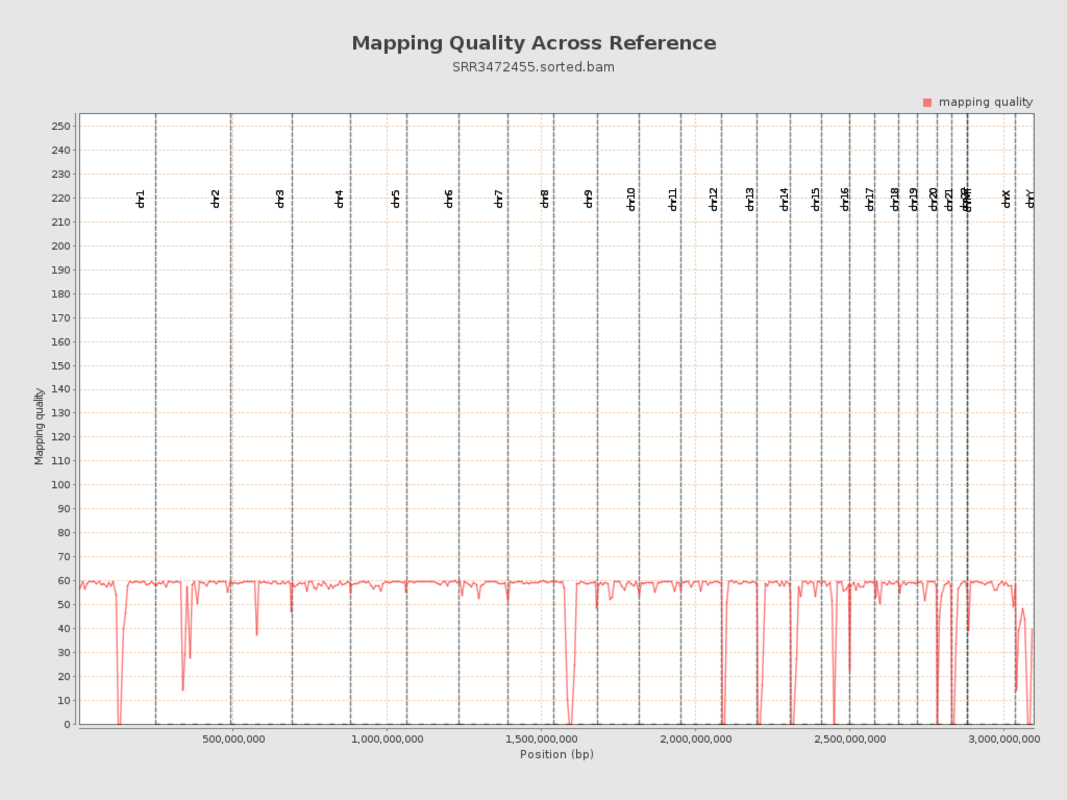
10. Results : Mapped Reads Clipping Profile



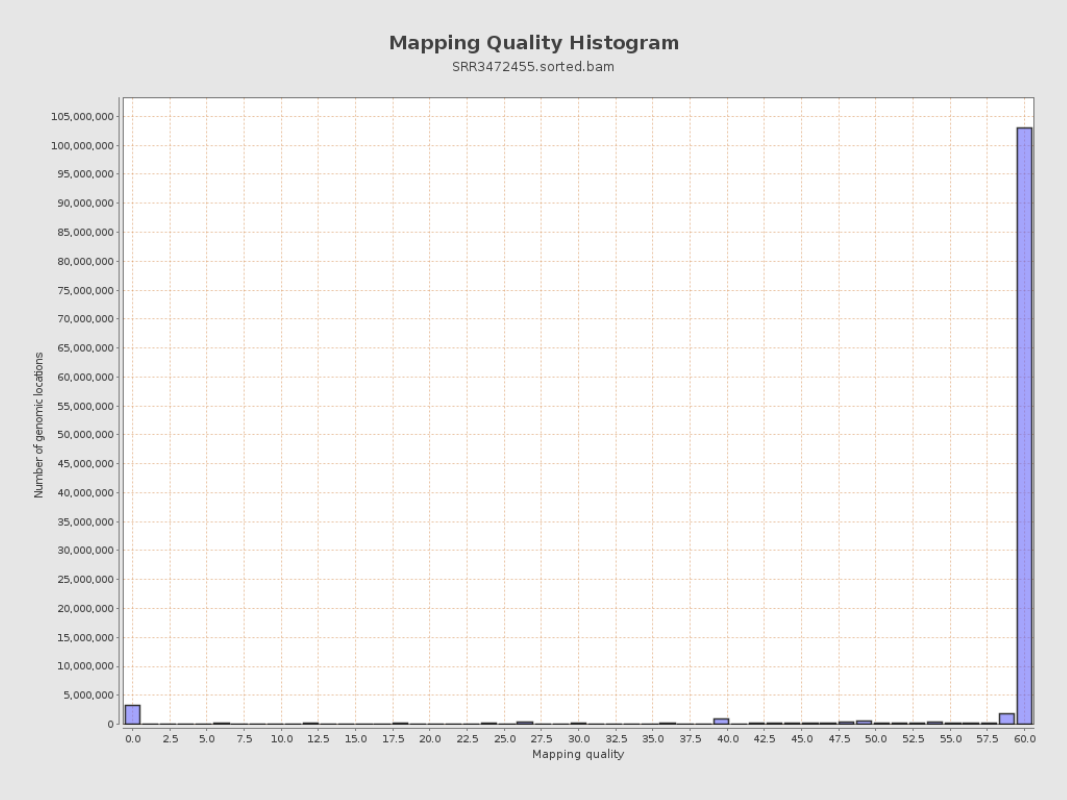
11. Results : Homopolymer Indels



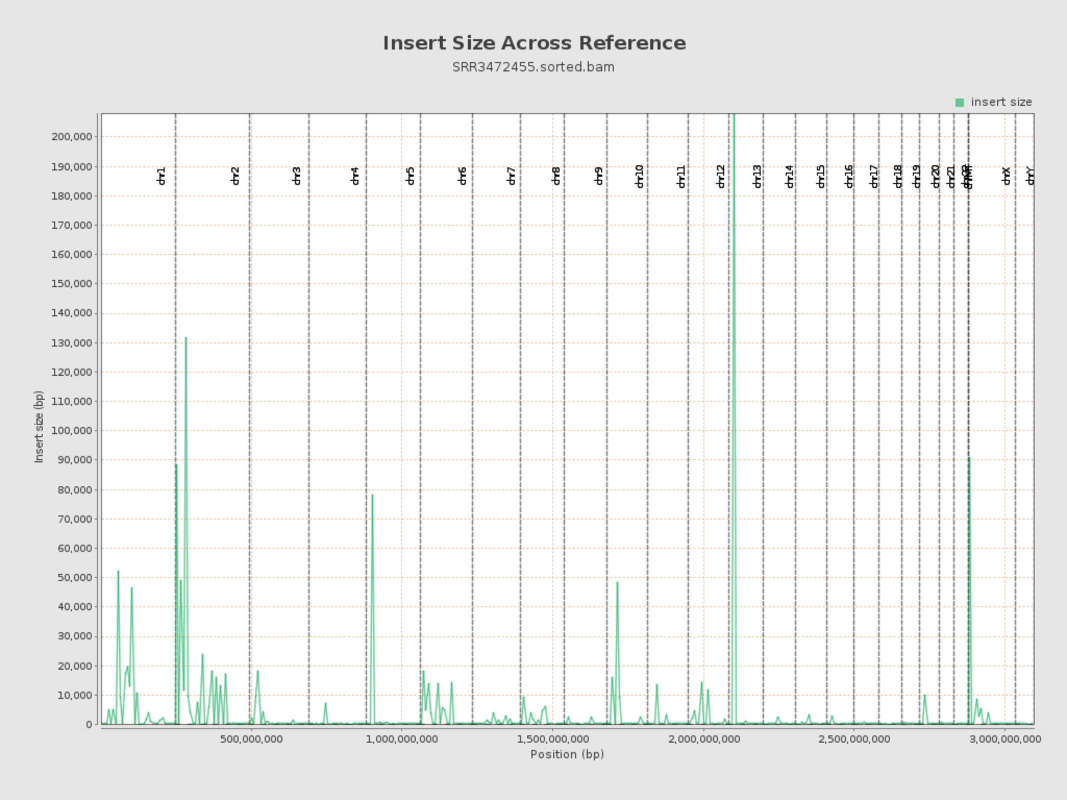
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram