Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 17:51:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472634.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_SRR3472634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472634_1.fastq.gz SRR3472634_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 17:51:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,321,258
Mapped reads	16,179,238 / 99.13%
Unmapped reads	142,020 / 0.87%
Mapped paired reads	16,179,238 / 99.13%
Mapped reads, first in pair	8,107,152 / 49.67%
Mapped reads, second in pair	8,072,086 / 49.46%
Mapped reads, both in pair	16,087,152 / 98.57%
Mapped reads, singletons	92,086 / 0.56%
Secondary alignments	0
Supplementary alignments	71,366 / 0.44%
Read min/max/mean length	30 / 101 / 99.68
Duplicated reads (estimated)	10,825,863 / 66.33%
Duplication rate	49.65%
Clipped reads	1,157,042 / 7.09%

2.2. ACGT Content

Number/percentage of A's	419,597,427 / 26.39%
Number/percentage of C's	377,368,644 / 23.74%
Number/percentage of T's	419,650,220 / 26.4%
Number/percentage of G's	372,946,651 / 23.46%
Number/percentage of N's	295,544 / 0.02%

GC Percentage	47.19%

2.3. Coverage

Mean	0.5136
Standard Deviation	20.323

2.4. Mapping Quality

Mean Mapping Quality	54.84

2.5. Insert size

Mean	20,860.7
Standard Deviation	1,472,838
P25/Median/P75	156 / 214 / 283

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	10,110,156
Insertions	106,214
Mapped reads with at least one insertion	0.65%
Deletions	84,138
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.63%

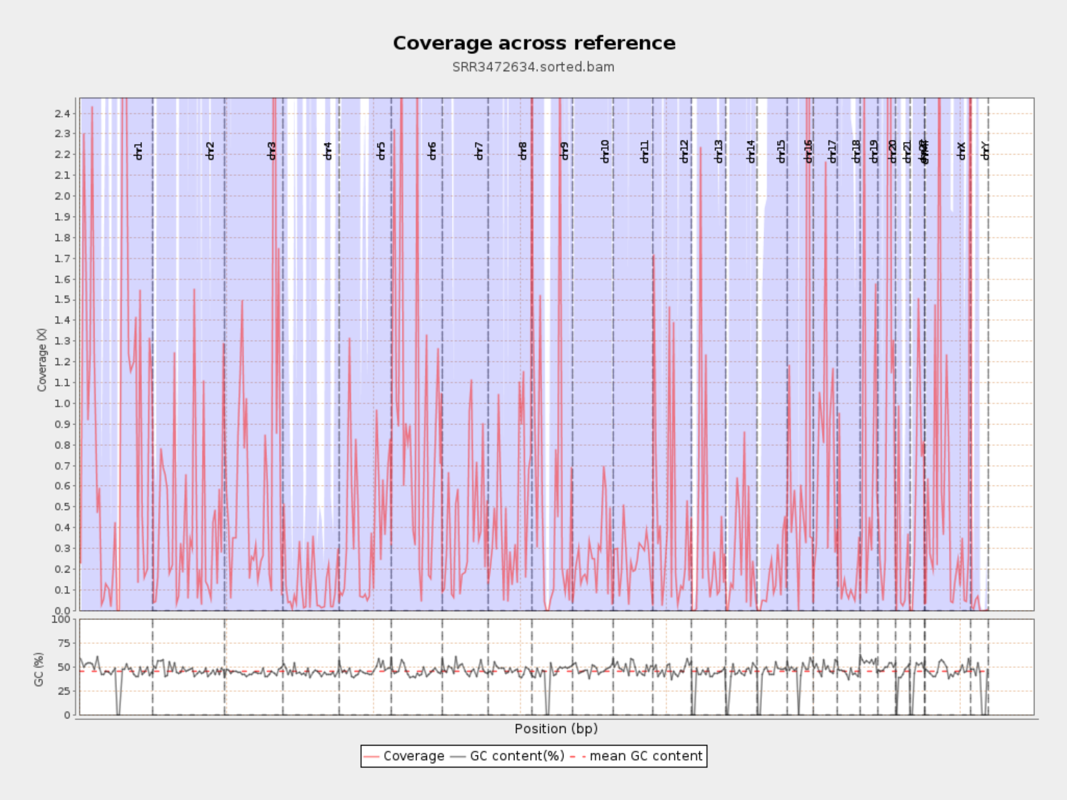
2.7. Chromosome stats

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

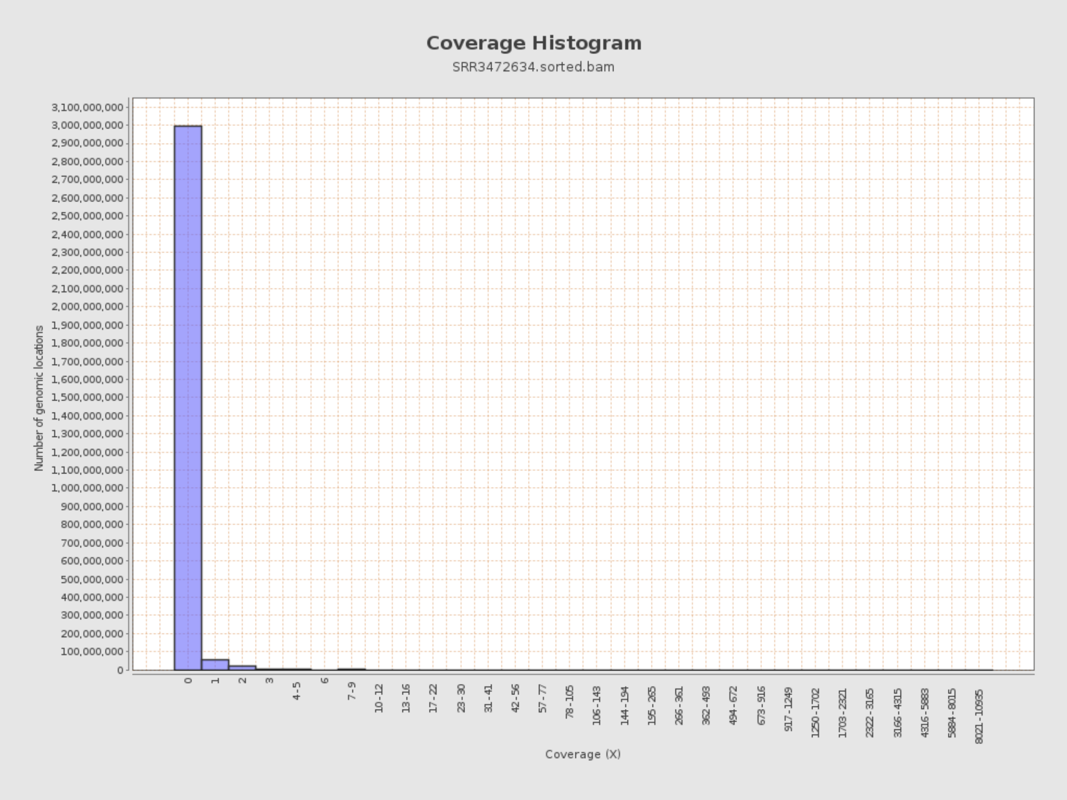
		bases	coverage	deviation
chr1	249250621	239881310	0.9624	28.2417
chr2	243199373	97283909	0.4	14.515
chr3	198022430	136212470	0.6879	24.6507
chr4	191154276	22787398	0.1192	5.2063
chr5	180915260	73161119	0.4044	17.4905
chr6	171115067	158994722	0.9292	30.3115
chr7	159138663	65636648	0.4124	13.7649
chr8	146364022	68503669	0.468	13.9517
chr9	141213431	81134369	0.5746	22.159
chr10	135534747	35404955	0.2612	9.9446
chr11	135006516	33751025	0.25	8.3913
chr12	133851895	62110328	0.464	18.2654
chr13	115169878	44577015	0.3871	13.4521
chr14	107349540	28666420	0.267	13.0891
chr15	102531392	15878683	0.1549	6.292
chr16	90354753	79984746	0.8852	33.8313
chr17	81195210	64792195	0.798	18.7326
chr18	78077248	15839439	0.2029	10.9243
chr19	59128983	49563693	0.8382	22.799
chr20	63025520	80810704	1.2822	46.9061
chr21	48129895	11738112	0.2439	17.8403
chr22	51304566	31391465	0.6119	18.3778
chrMT	16571	3384	0.2042	0.5641
chrX	155270560	90777068	0.5846	26.3721

chrY	59373566	1175949	0.0198	1.4644

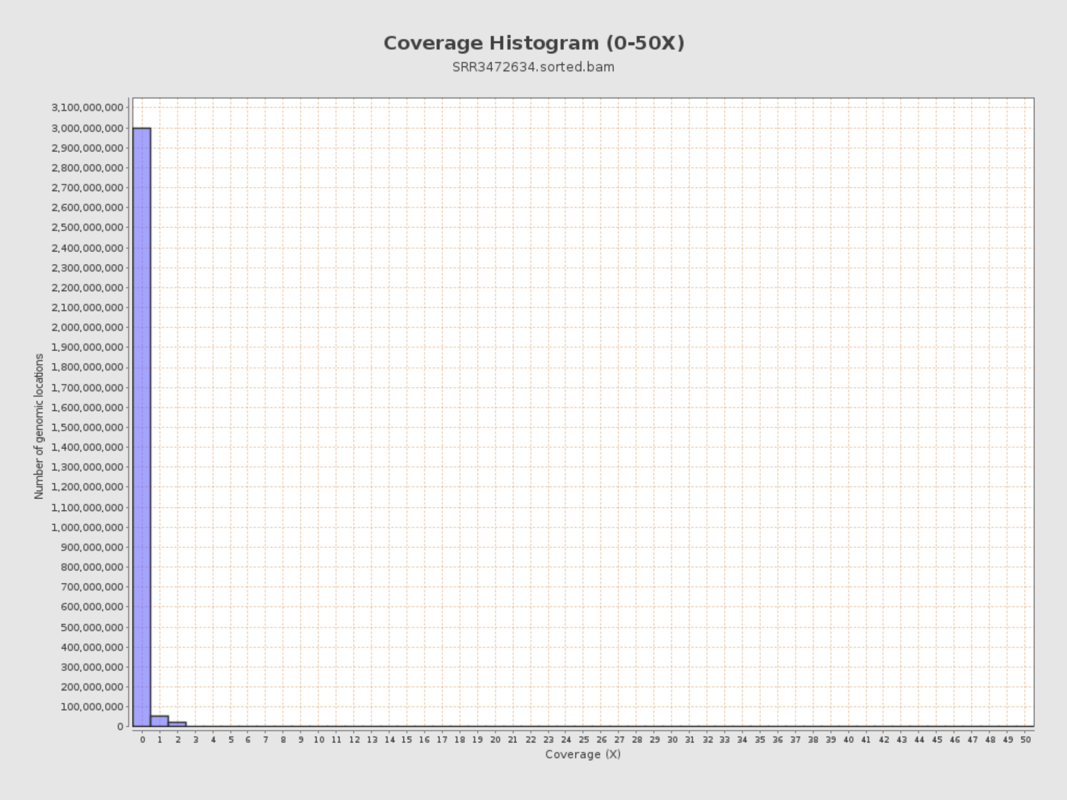
3. Results : Coverage across reference



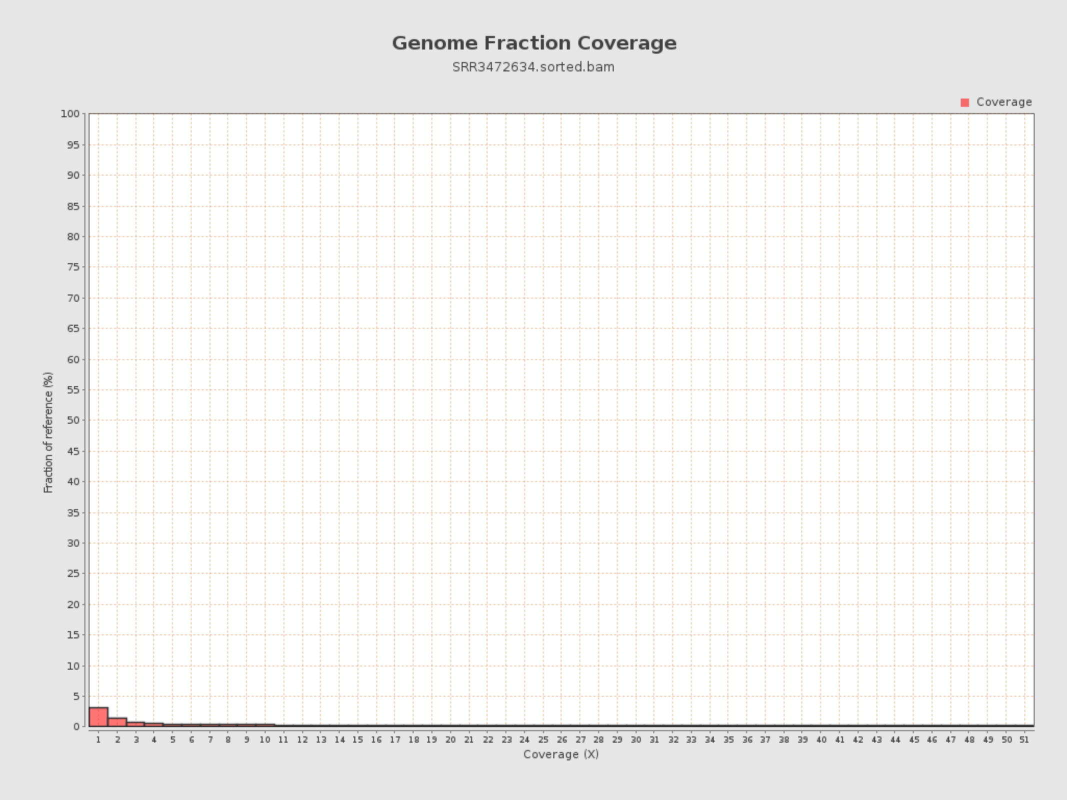
4. Results : Coverage Histogram



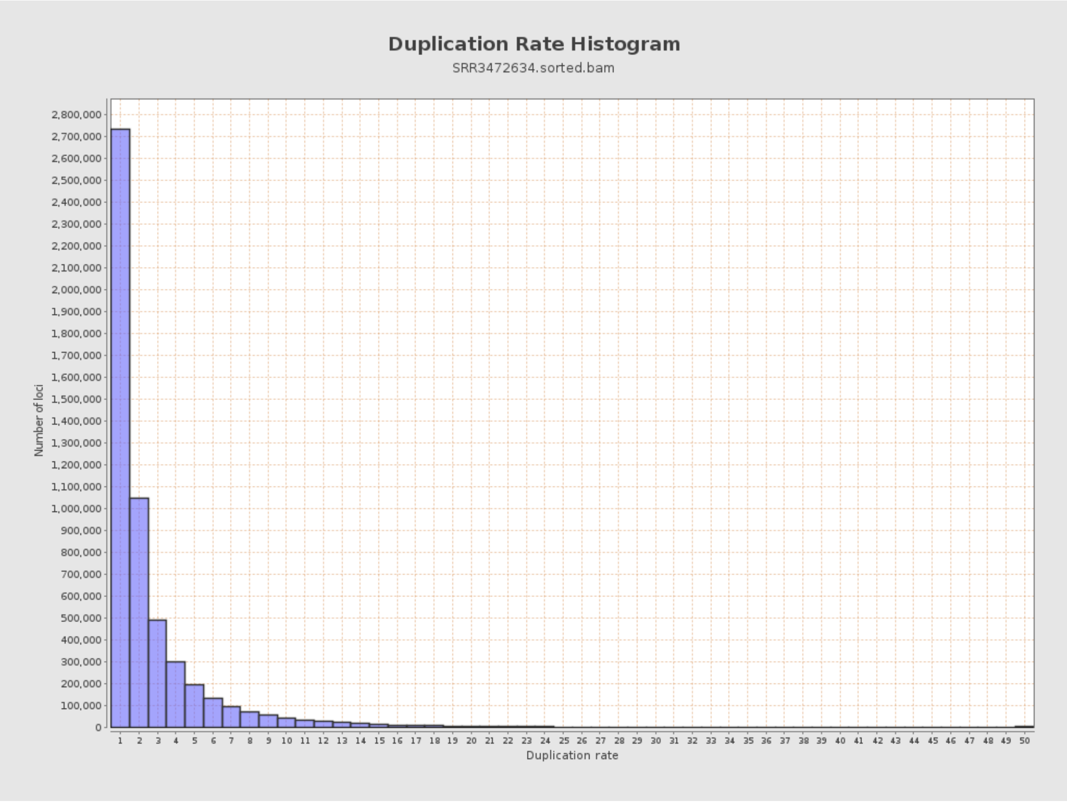
5. Results : Coverage Histogram (0-50X)



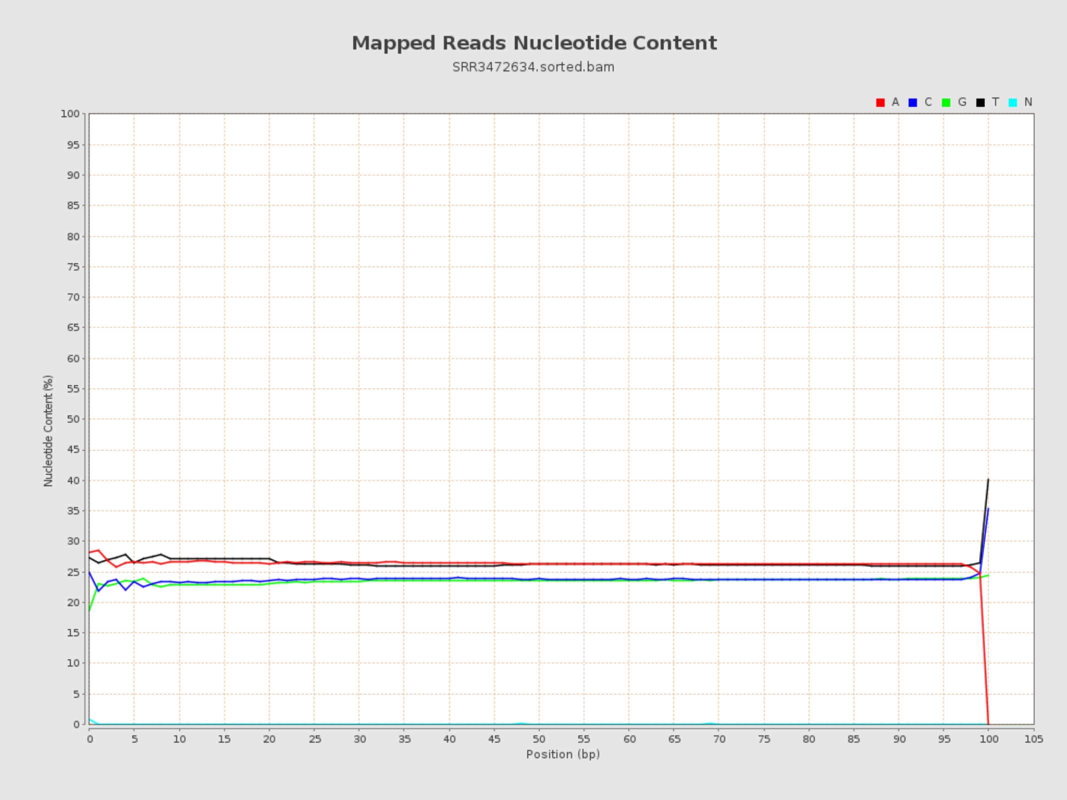
6. Results : Genome Fraction Coverage



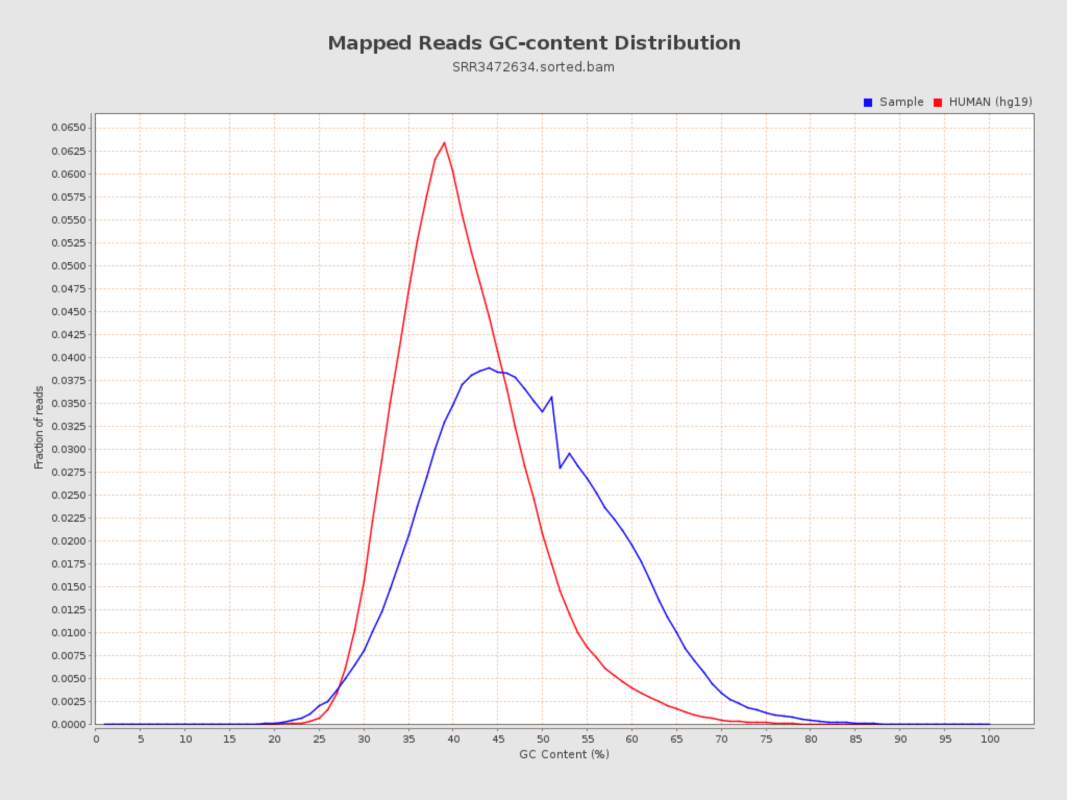
7. Results : Duplication Rate Histogram



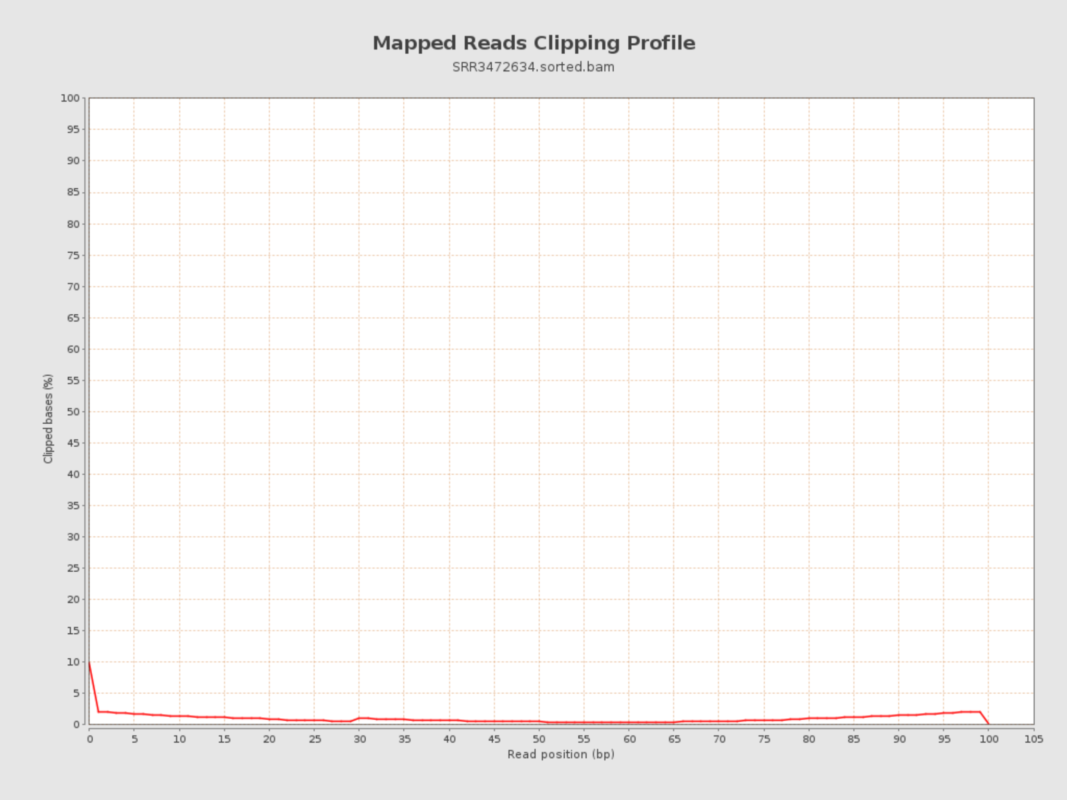
8. Results : Mapped Reads Nucleotide Content



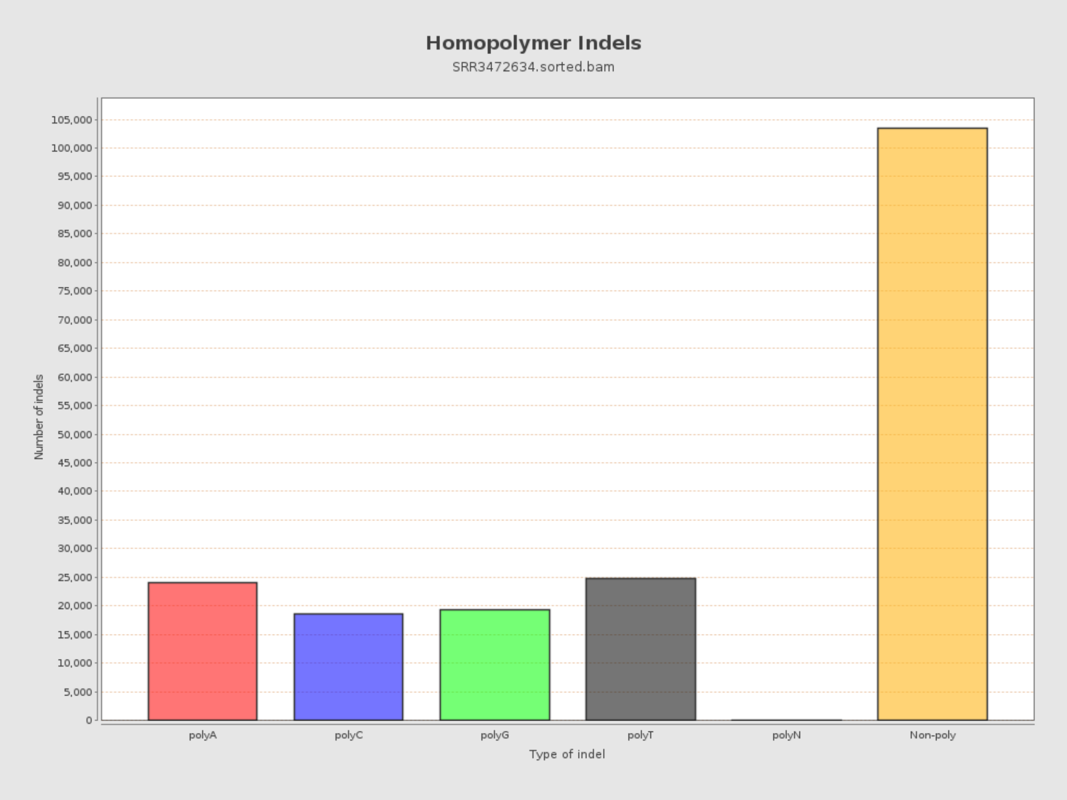
9. Results : Mapped Reads GC-content Distribution



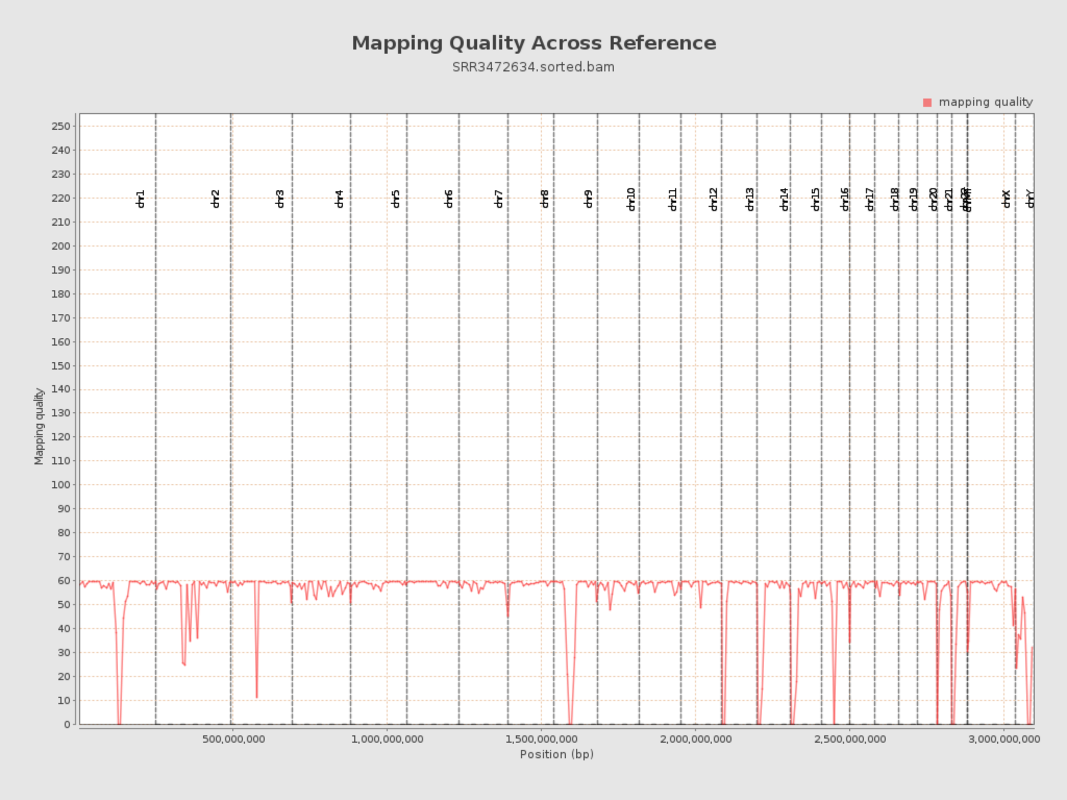
10. Results : Mapped Reads Clipping Profile



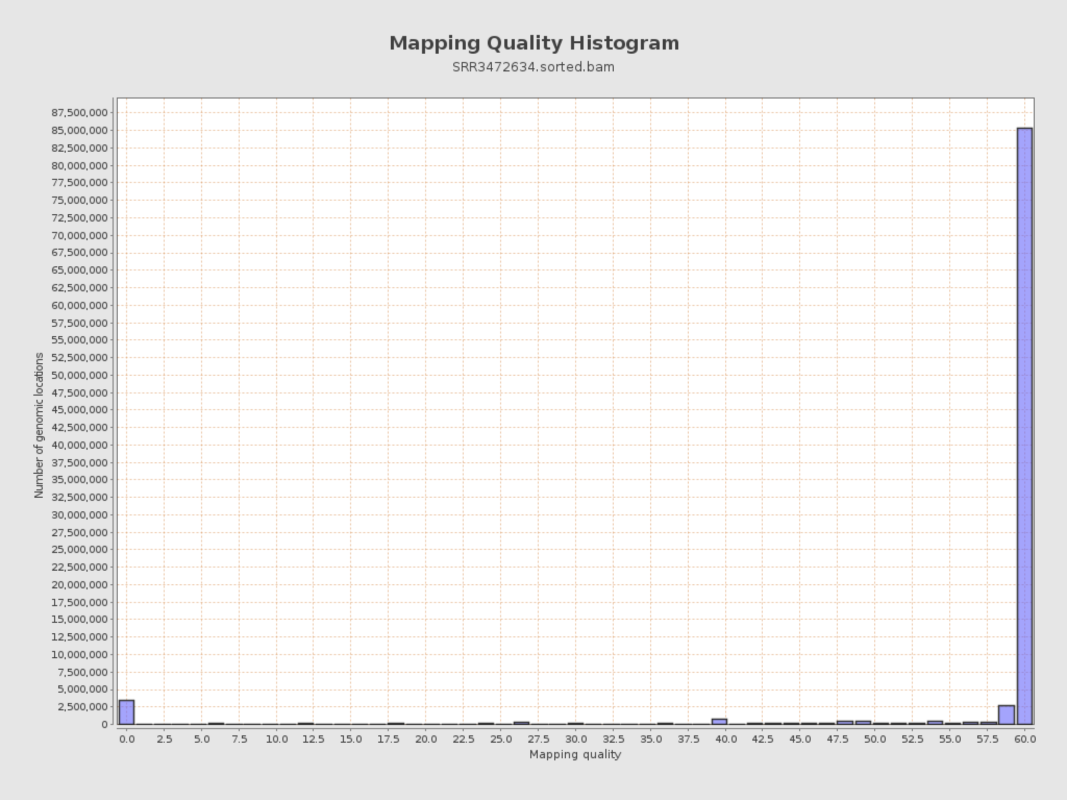
11. Results : Homopolymer Indels



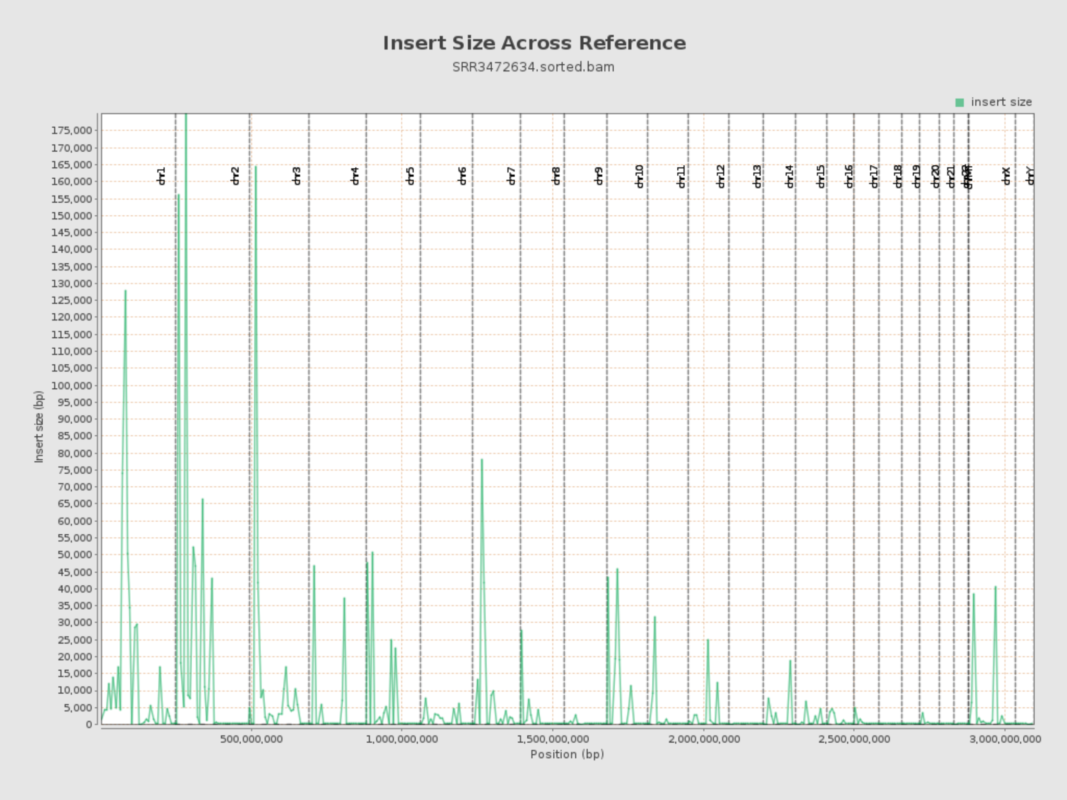
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram