Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 22:29:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472654.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_SRR3472654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472654_1.fastq.gz SRR3472654_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 22:29:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,115,734
Mapped reads	15,936,240 / 98.89%
Unmapped reads	179,494 / 1.11%
Mapped paired reads	15,936,240 / 98.89%
Mapped reads, first in pair	7,994,396 / 49.61%
Mapped reads, second in pair	7,941,844 / 49.28%
Mapped reads, both in pair	15,818,548 / 98.16%
Mapped reads, singletons	117,692 / 0.73%
Secondary alignments	0
Supplementary alignments	107,337 / 0.67%
Read min/max/mean length	30 / 101 / 99.97
Duplicated reads (estimated)	10,786,308 / 66.93%
Duplication rate	47.73%
Clipped reads	1,108,203 / 6.88%

2.2. ACGT Content

Number/percentage of A's	432,360,578 / 27.51%
Number/percentage of C's	355,391,371 / 22.61%
Number/percentage of T's	433,284,584 / 27.57%
Number/percentage of G's	350,455,727 / 22.3%
Number/percentage of N's	296,176 / 0.02%

GC Percentage	44.91%

2.3. Coverage

Mean	0.5078
Standard Deviation	21.9263

2.4. Mapping Quality

Mean Mapping Quality	54.76

2.5. Insert size

Mean	23,257.69
Standard Deviation	1,475,169.2
P25/Median/P75	180 / 246 / 324

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	10,692,925
Insertions	110,853
Mapped reads with at least one insertion	0.69%
Deletions	83,839
Mapped reads with at least one deletion	0.52%
Homopolymer indels	48.51%

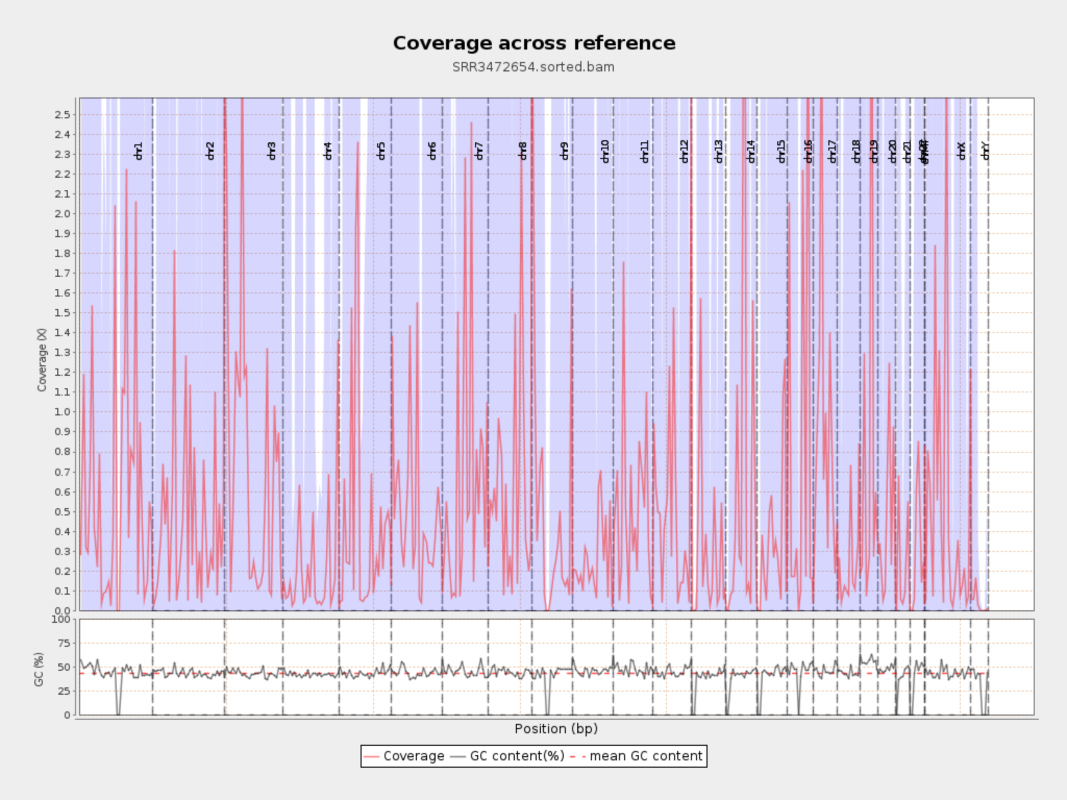
2.7. Chromosome stats

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

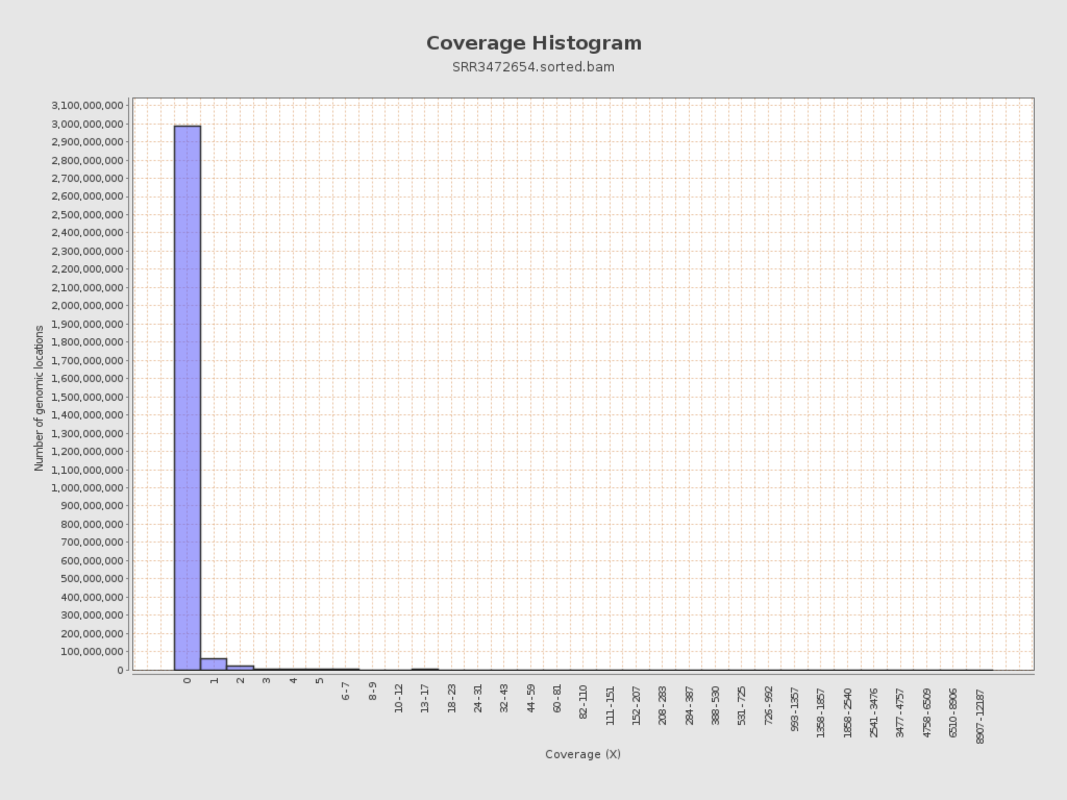
		bases	coverage	deviation
chr1	249250621	152102114	0.6102	20.4098
chr2	243199373	107127009	0.4405	18.9472
chr3	198022430	154923183	0.7824	22.5481
chr4	191154276	39267199	0.2054	13.3215
chr5	180915260	84021650	0.4644	26.0577
chr6	171115067	86417746	0.505	14.176
chr7	159138663	104602715	0.6573	28.3975
chr8	146364022	91118081	0.6225	20.9749
chr9	141213431	74545440	0.5279	17.3382
chr10	135534747	36033276	0.2659	11.7866
chr11	135006516	69168376	0.5123	19.0726
chr12	133851895	70377410	0.5258	17.5892
chr13	115169878	34059607	0.2957	14.8465
chr14	107349540	67056008	0.6247	29.5947
chr15	102531392	38766868	0.3781	16.5695
chr16	90354753	73711503	0.8158	36.3485
chr17	81195210	76872343	0.9468	33.1428
chr18	78077248	19274578	0.2469	11.0693
chr19	59128983	53414009	0.9033	56.2518
chr20	63025520	29332579	0.4654	15.1867
chr21	48129895	11639063	0.2418	15.1197
chr22	51304566	14803084	0.2885	11.7003
chrMT	16571	13794	0.8324	1.203
chrX	155270560	81012703	0.5218	21.9649

chrY	59373566	2322037	0.0391	2.6792

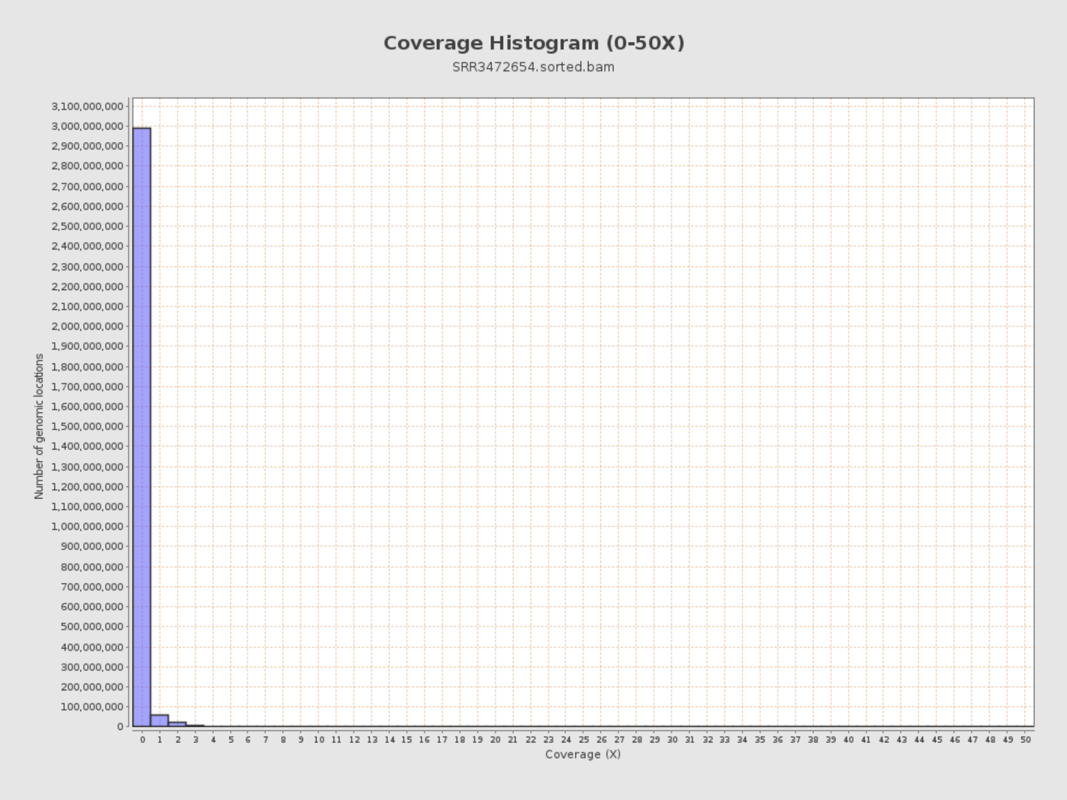
3. Results : Coverage across reference



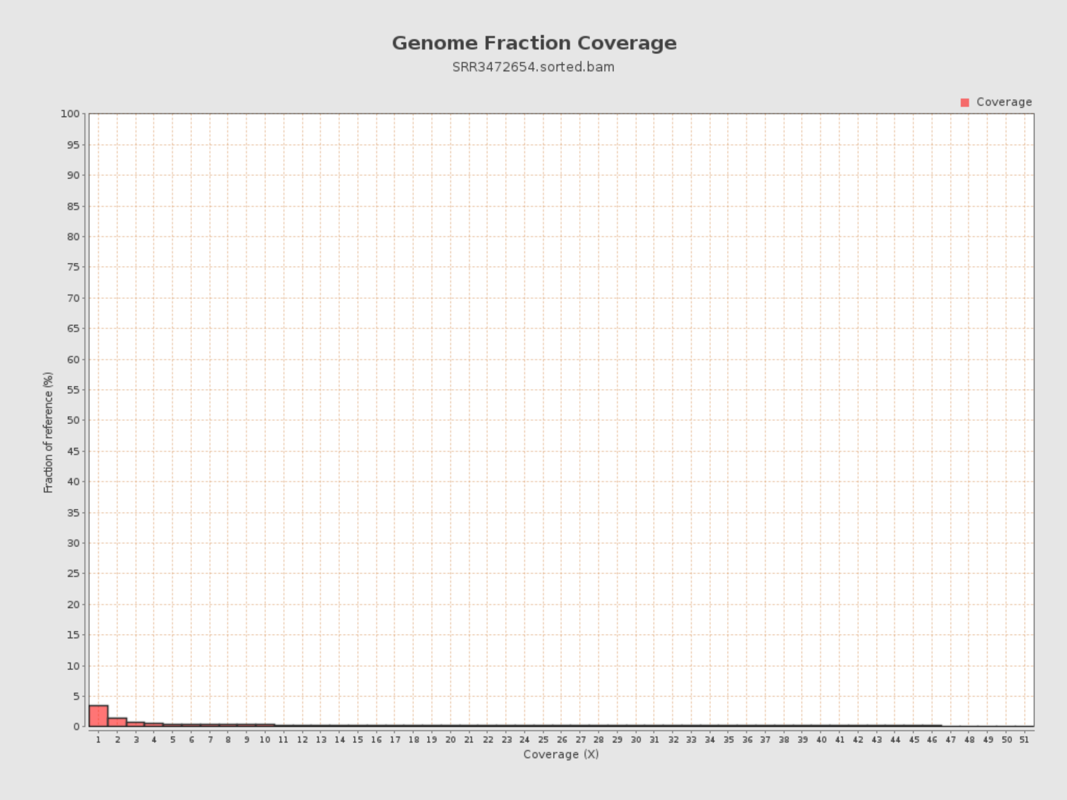
4. Results : Coverage Histogram



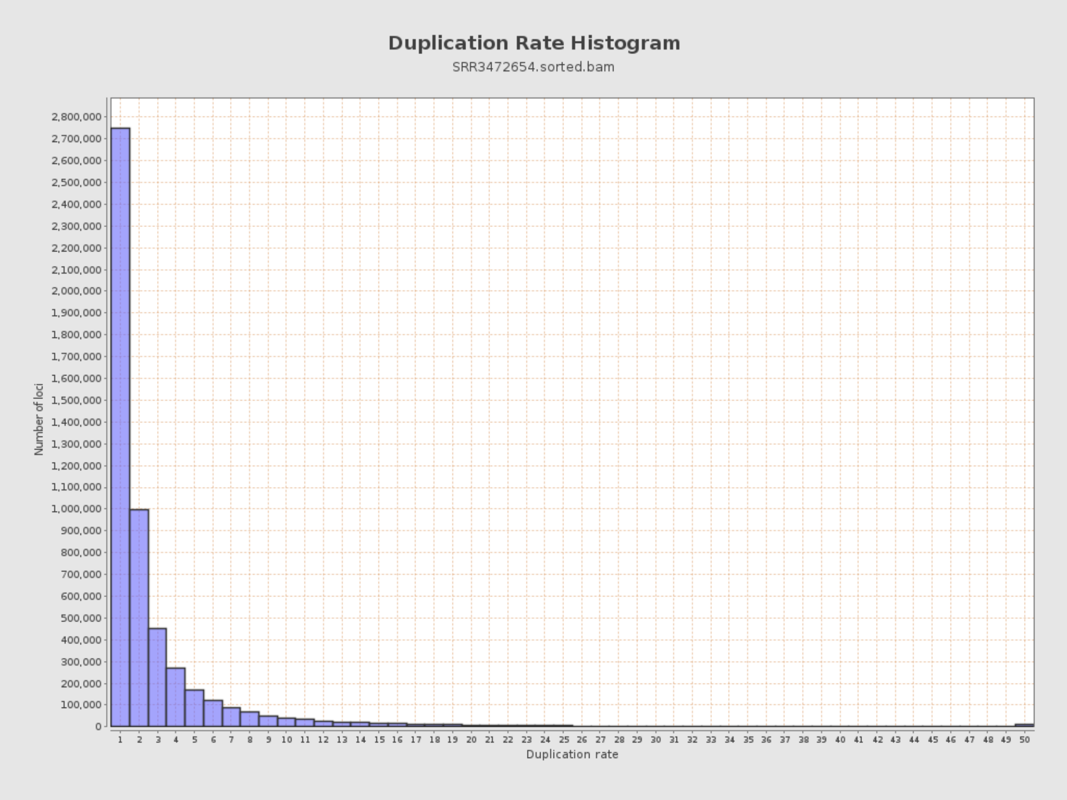
5. Results : Coverage Histogram (0-50X)



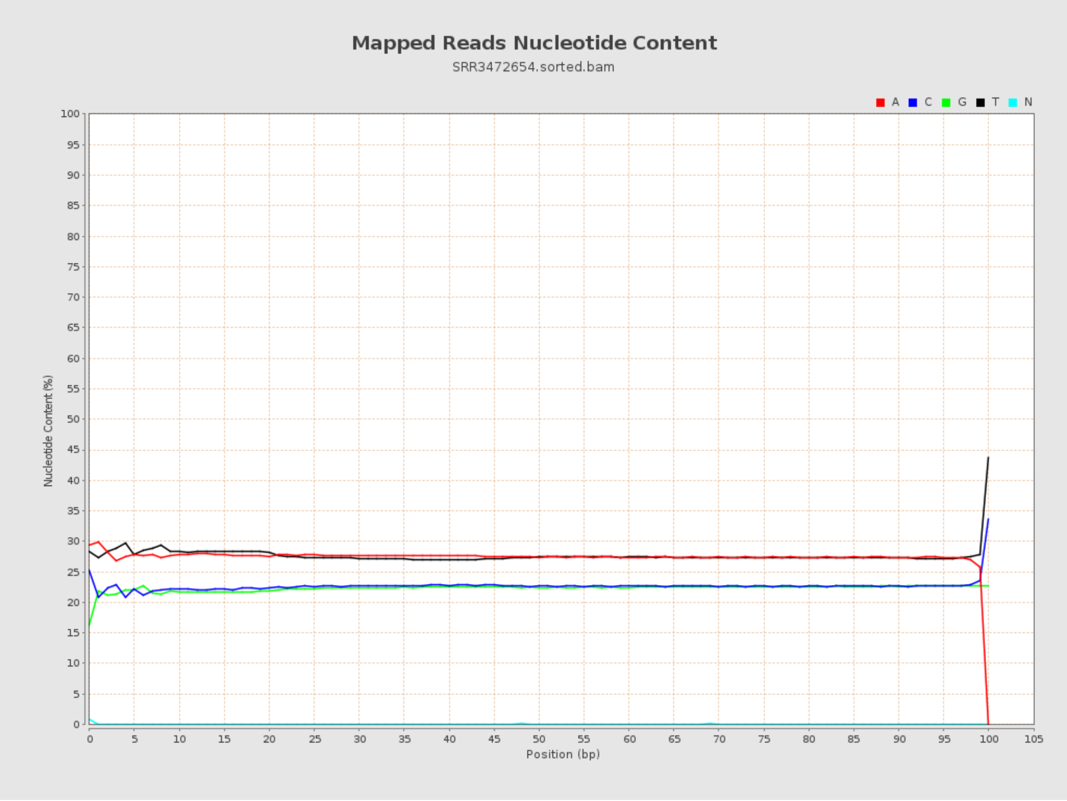
6. Results : Genome Fraction Coverage



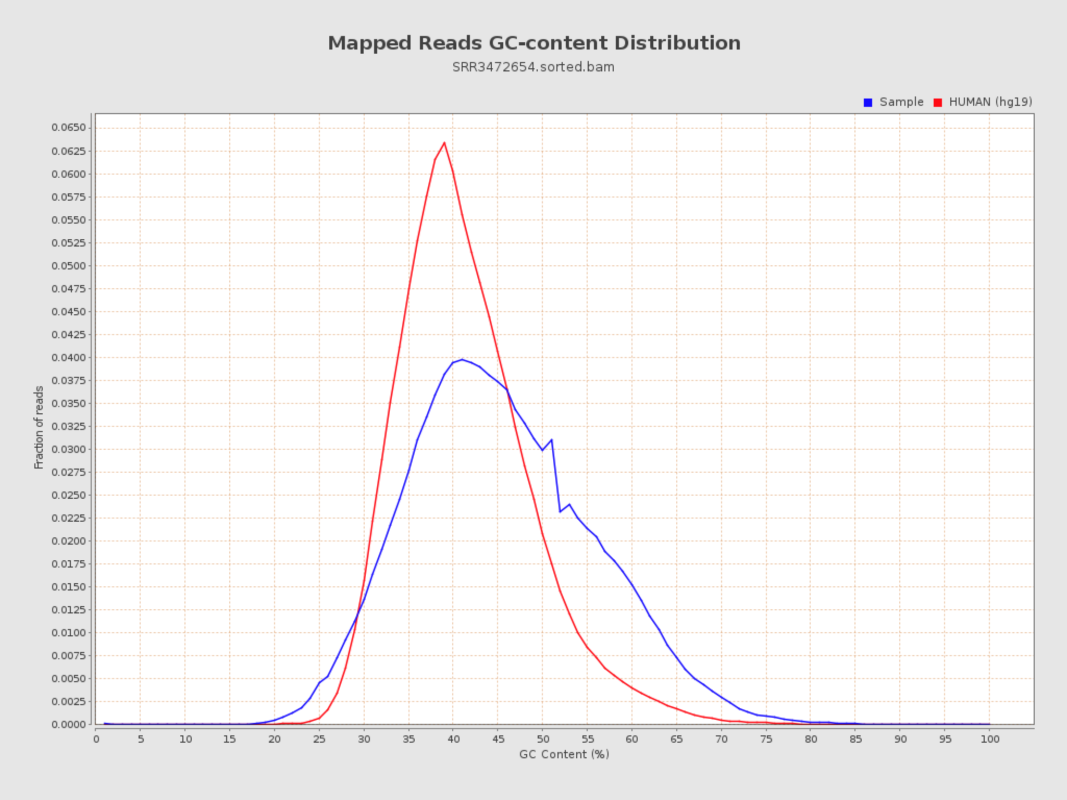
7. Results : Duplication Rate Histogram



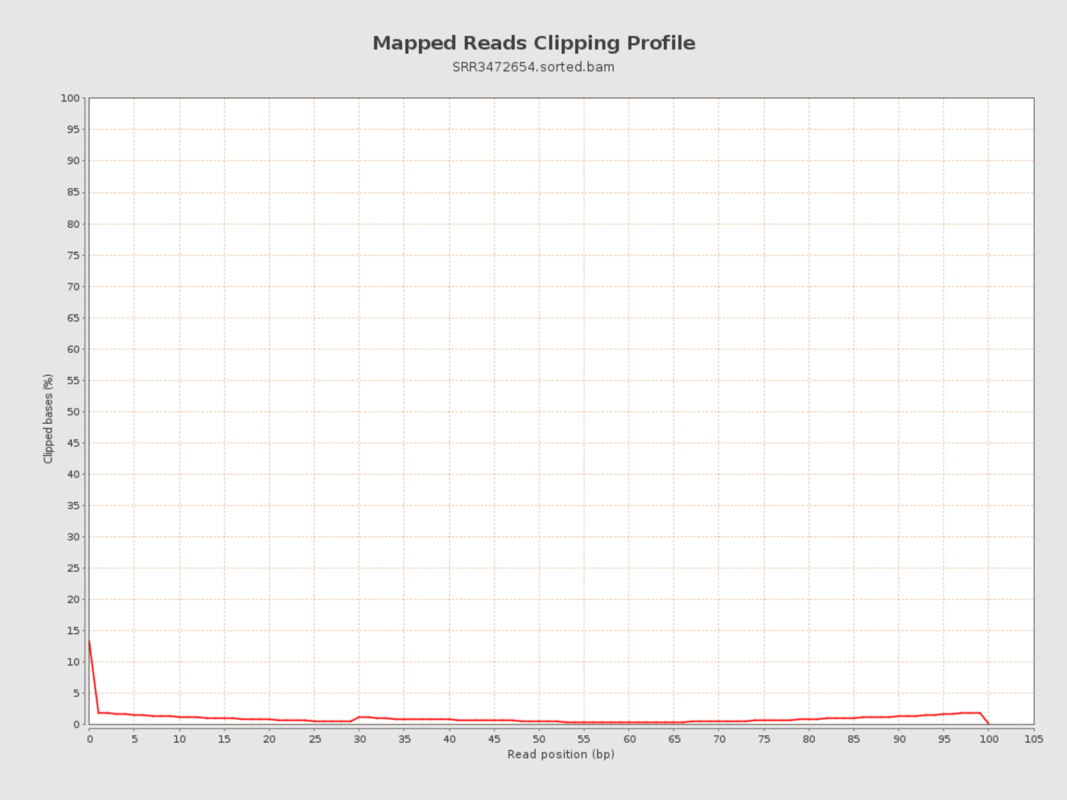
8. Results : Mapped Reads Nucleotide Content



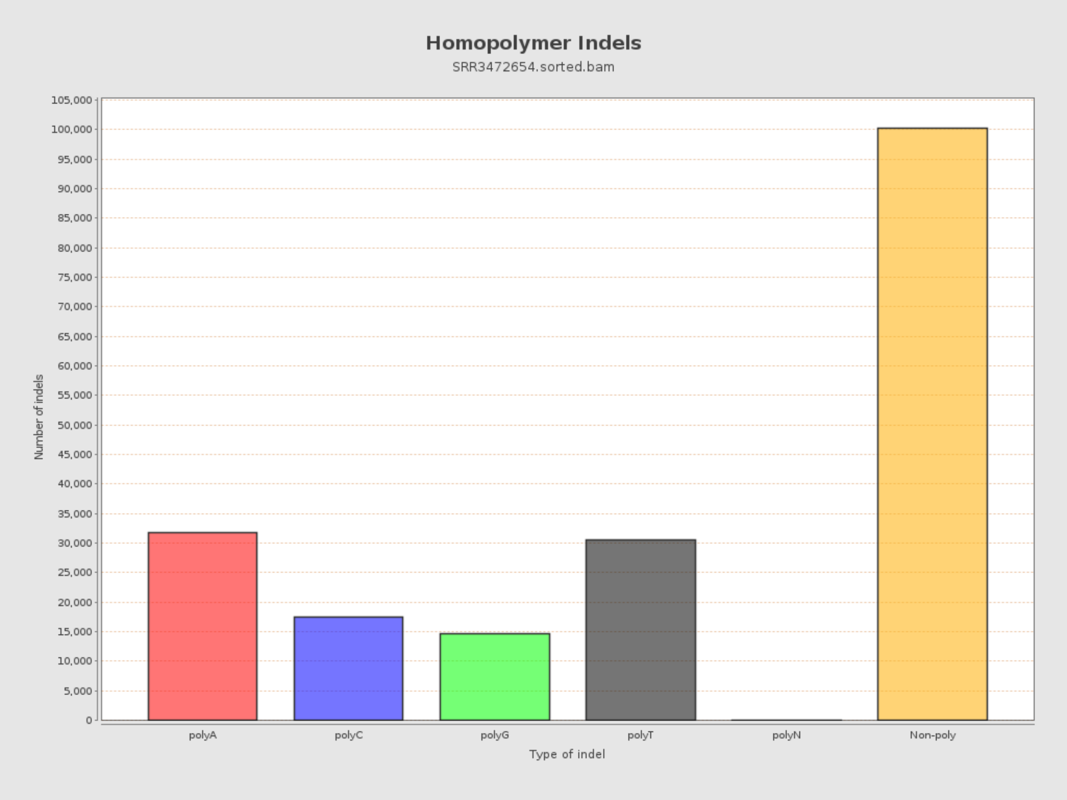
9. Results : Mapped Reads GC-content Distribution



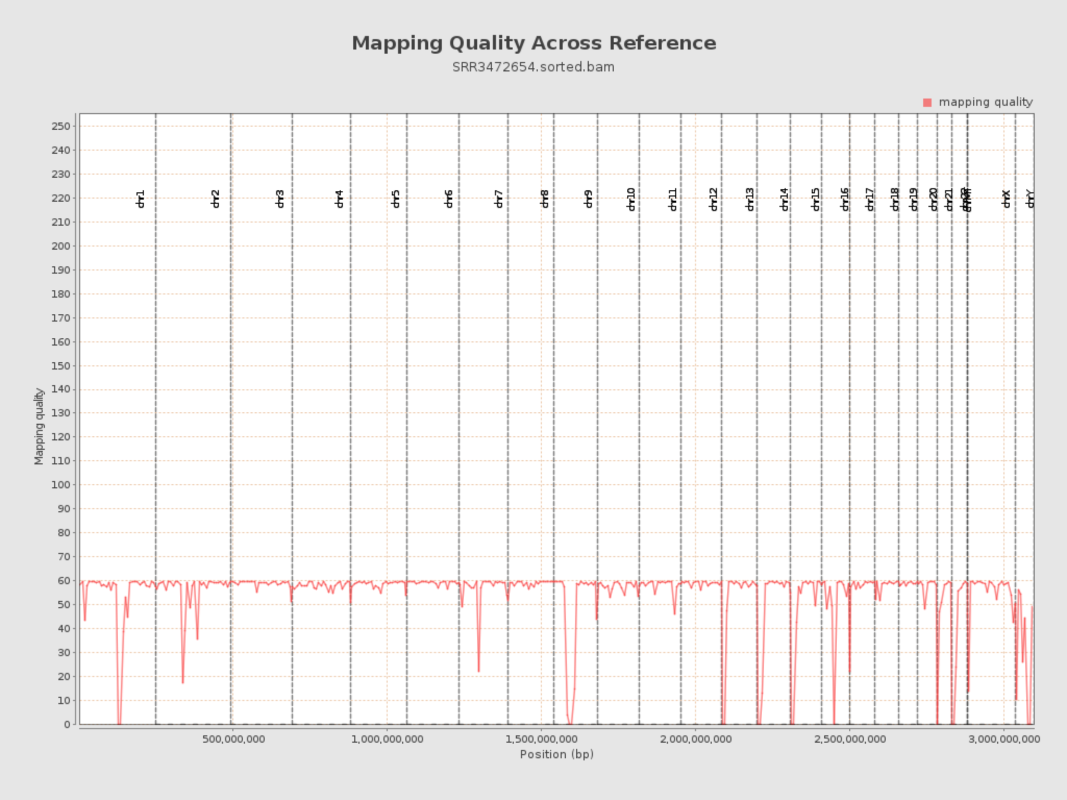
10. Results : Mapped Reads Clipping Profile



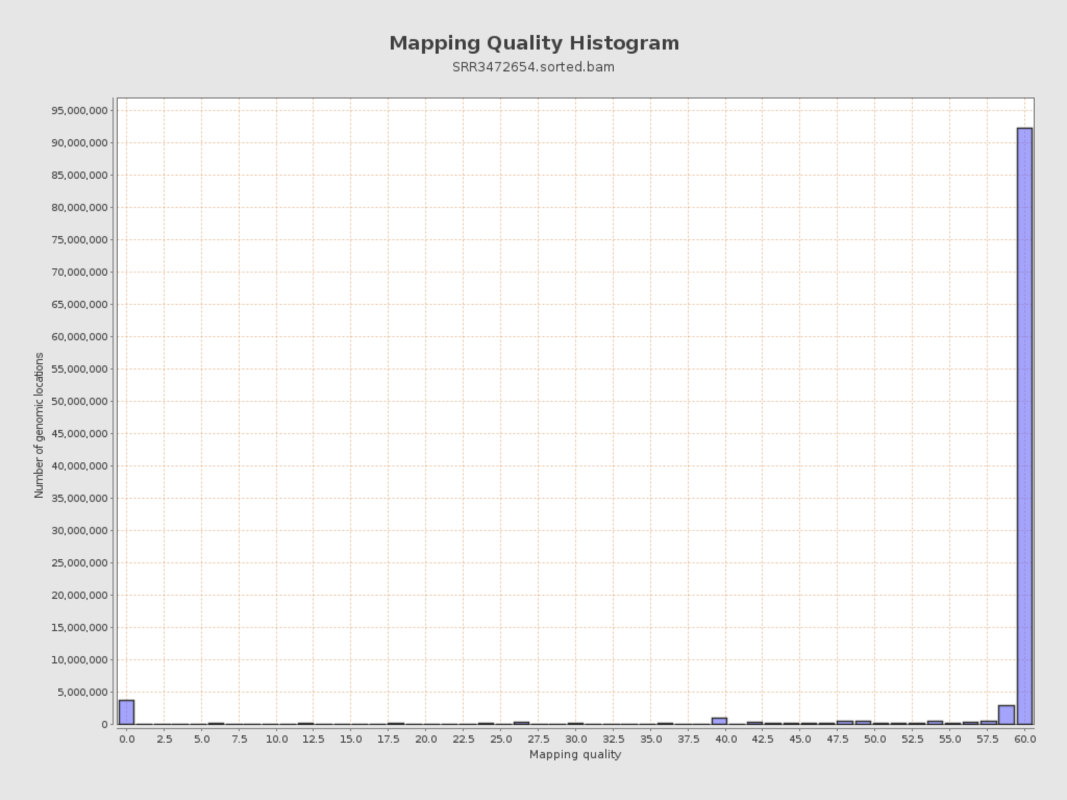
11. Results : Homopolymer Indels



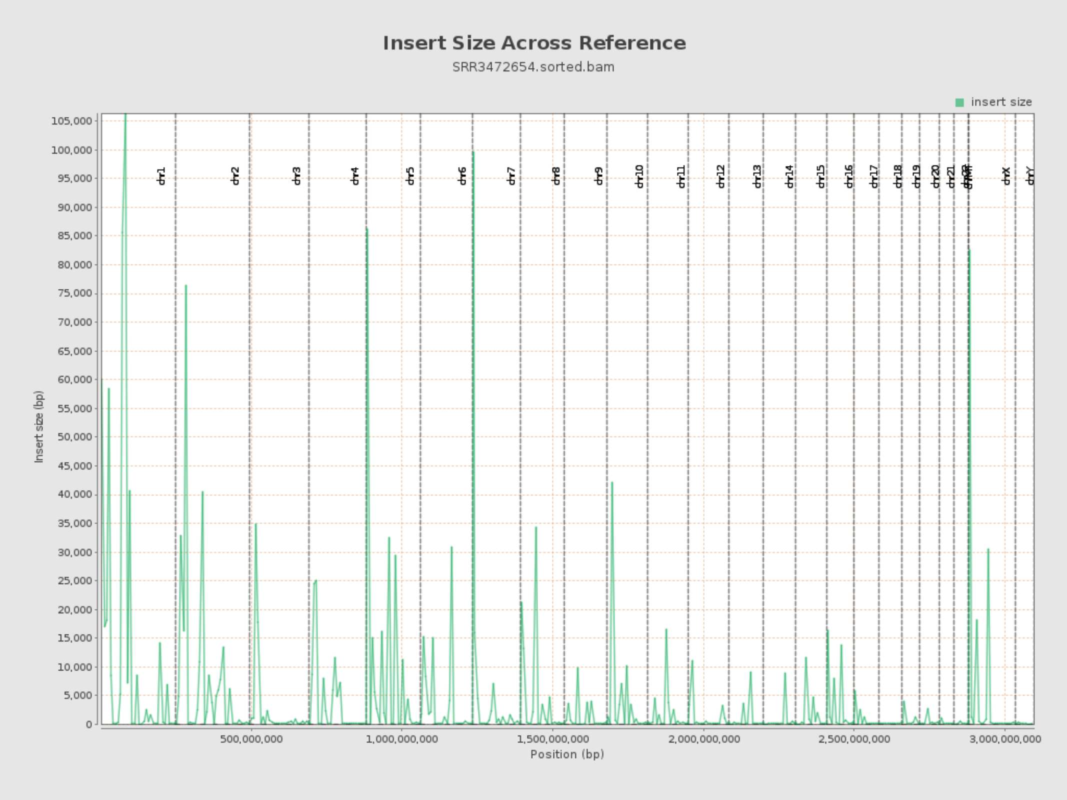
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram