Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 00:48:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472737.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_SRR3472737 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472737_1.fastq.gz SRR3472737_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 00:48:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472737.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,990,156
Mapped reads	18,776,229 / 98.87%
Unmapped reads	213,927 / 1.13%
Mapped paired reads	18,776,229 / 98.87%
Mapped reads, first in pair	9,431,074 / 49.66%
Mapped reads, second in pair	9,345,155 / 49.21%
Mapped reads, both in pair	18,648,714 / 98.2%
Mapped reads, singletons	127,515 / 0.67%
Secondary alignments	0
Supplementary alignments	65,225 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,802,592 / 62.15%
Duplication rate	47.43%
Clipped reads	1,391,876 / 7.33%

2.2. ACGT Content

Number/percentage of A's	512,282,214 / 27.67%
Number/percentage of C's	416,139,000 / 22.47%
Number/percentage of T's	508,901,890 / 27.48%
Number/percentage of G's	413,931,801 / 22.36%
Number/percentage of N's	351,212 / 0.02%

GC Percentage	44.83%

2.3. Coverage

Mean	0.5982
Standard Deviation	18.8701

2.4. Mapping Quality

Mean Mapping Quality	55.19

2.5. Insert size

Mean	21,715.55
Standard Deviation	1,442,669.63
P25/Median/P75	185 / 259 / 349

2.6. Mismatches and indels

General error rate	0.68%
Mismatches	12,402,563
Insertions	112,535
Mapped reads with at least one insertion	0.59%
Deletions	102,051
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.04%

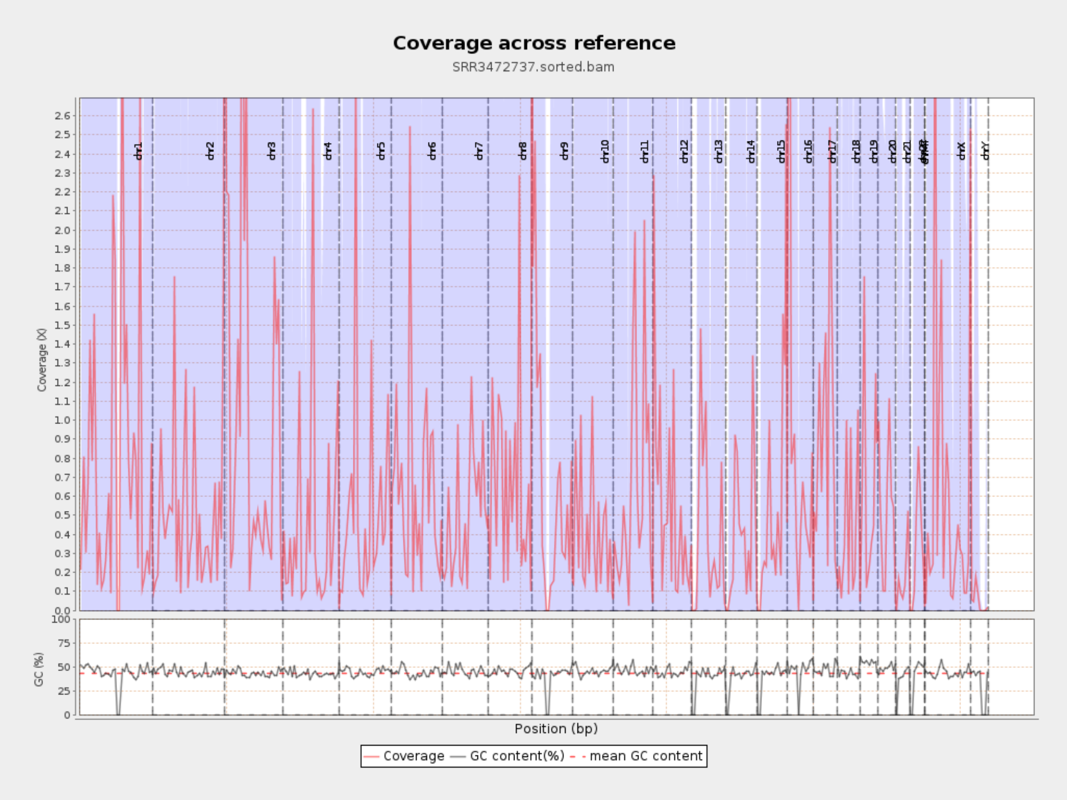
2.7. Chromosome stats

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

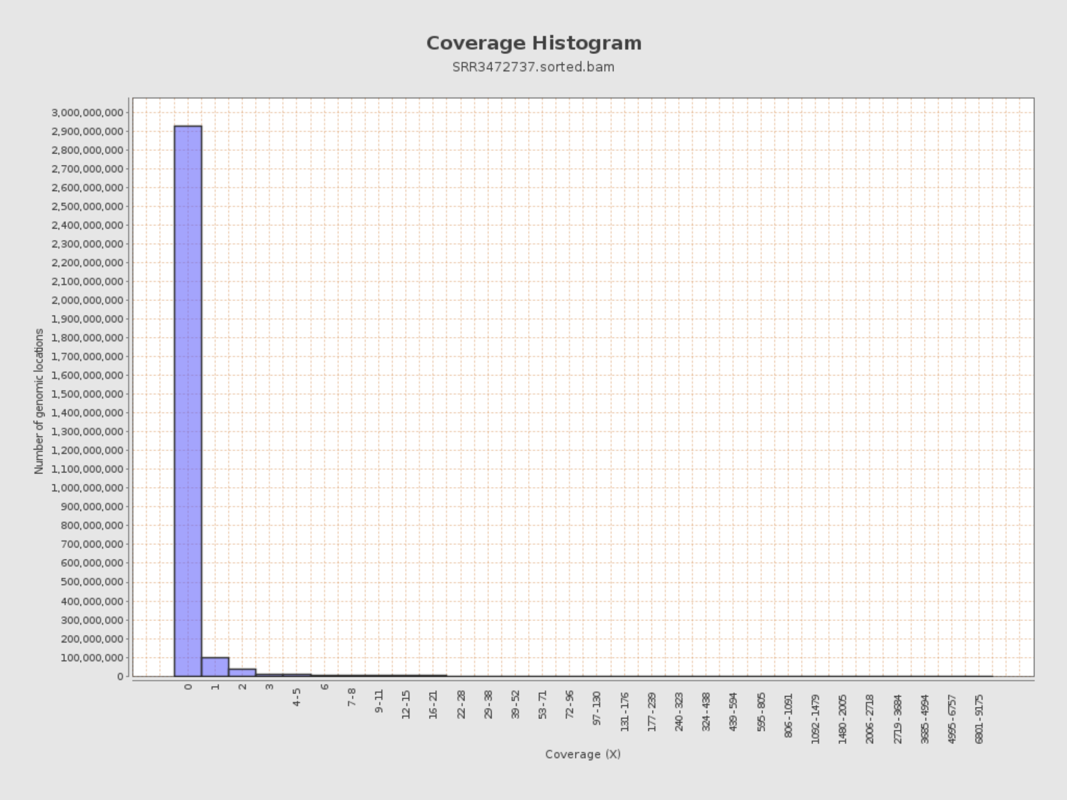
		bases	coverage	deviation
chr1	249250621	195040499	0.7825	23.8655
chr2	243199373	119649918	0.492	14.0384
chr3	198022430	222103605	1.1216	26.5846
chr4	191154276	83702742	0.4379	19.7099
chr5	180915260	97153784	0.537	14.6766
chr6	171115067	108478646	0.634	15.4558
chr7	159138663	80134658	0.5036	14.6763
chr8	146364022	97014556	0.6628	24.8803
chr9	141213431	94265230	0.6675	15.7976
chr10	135534747	55229048	0.4075	16.2228
chr11	135006516	91219381	0.6757	26.5984
chr12	133851895	76884719	0.5744	16.5013
chr13	115169878	46237876	0.4015	17.3634
chr14	107349540	43193147	0.4024	12.0229
chr15	102531392	54171741	0.5283	18.8565
chr16	90354753	80915759	0.8955	21.963
chr17	81195210	74604441	0.9188	20.7442
chr18	78077248	34170008	0.4376	16.4787
chr19	59128983	39165132	0.6624	17.0698
chr20	63025520	34860713	0.5531	17.3382
chr21	48129895	8803483	0.1829	7.4664
chr22	51304566	16380794	0.3193	10.4604
chrMT	16571	4959	0.2993	0.8964
chrX	155270560	95535022	0.6153	19.5662

chrY	59373566	2952139	0.0497	1.5516

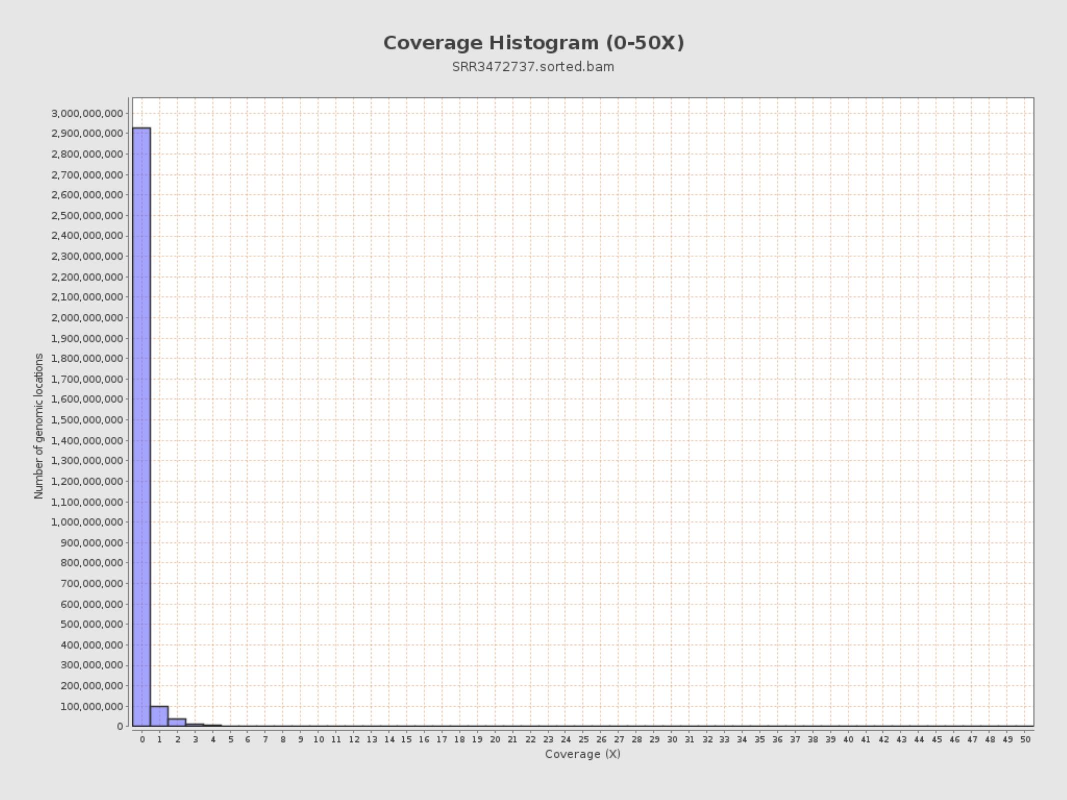
3. Results : Coverage across reference



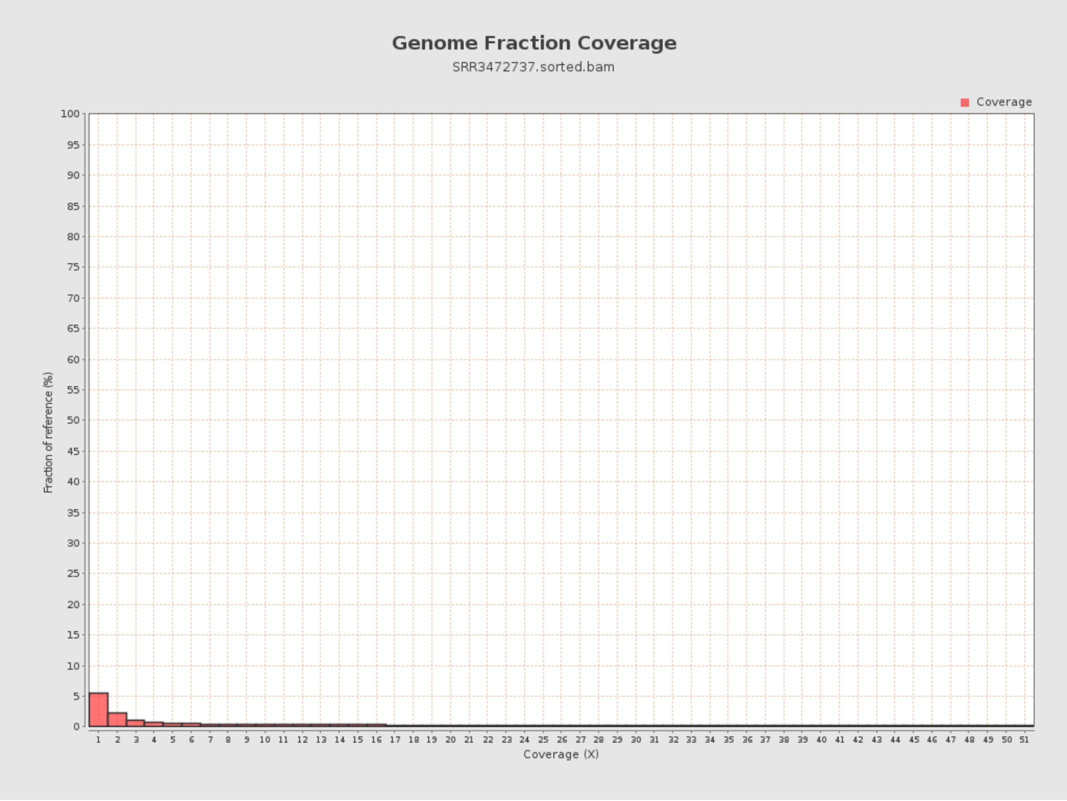
4. Results : Coverage Histogram



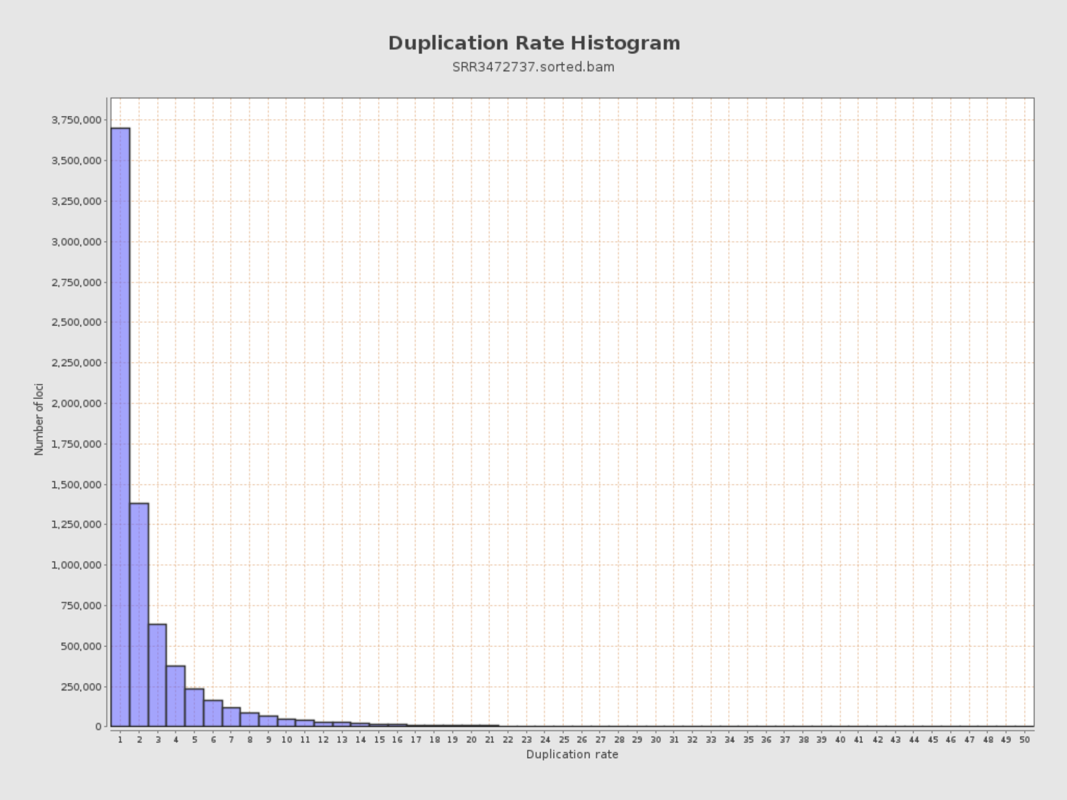
5. Results : Coverage Histogram (0-50X)



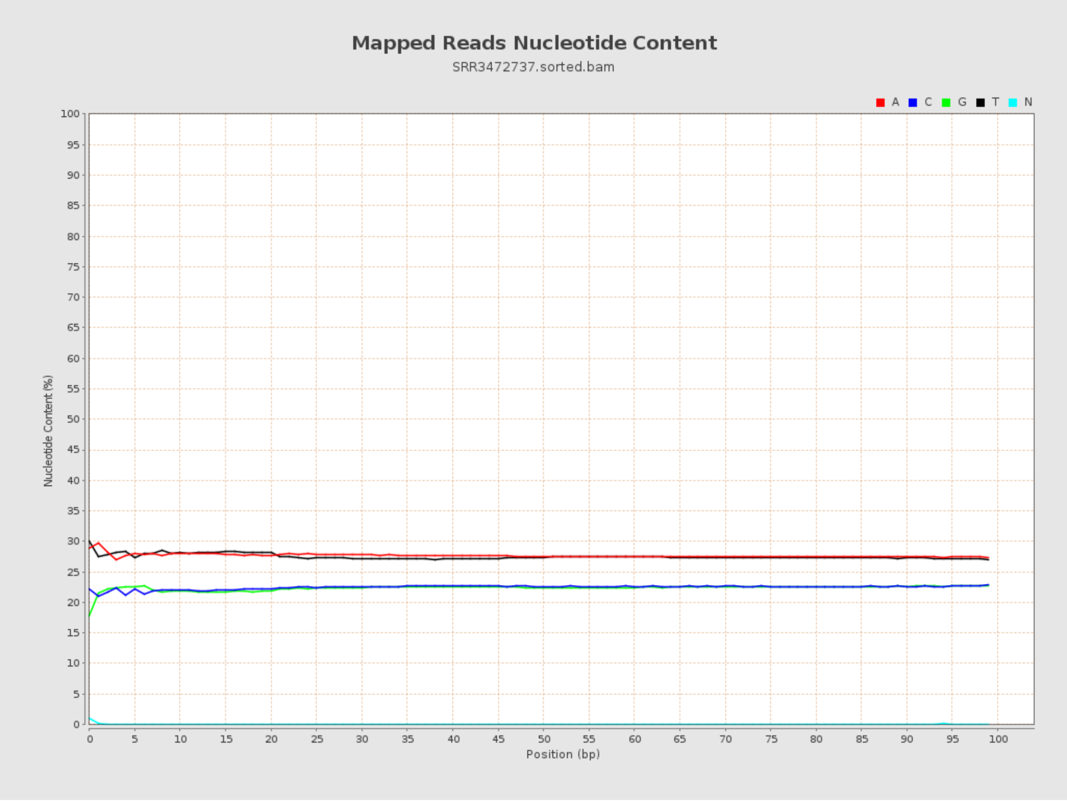
6. Results : Genome Fraction Coverage



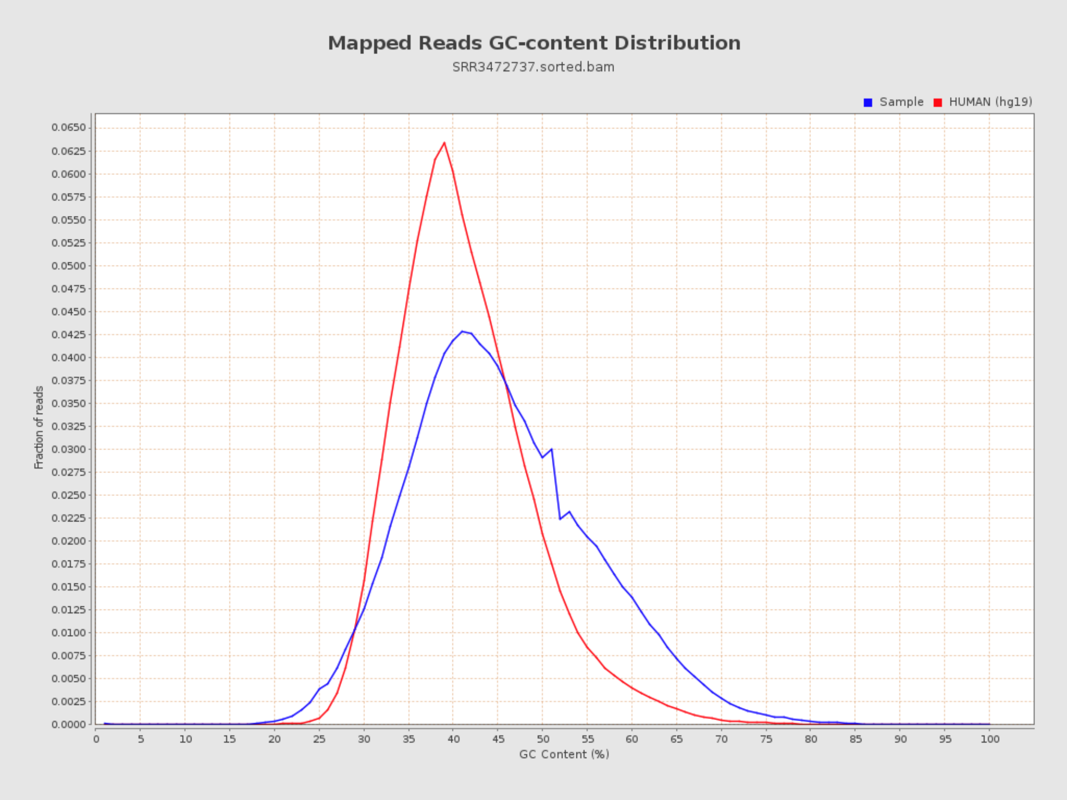
7. Results : Duplication Rate Histogram



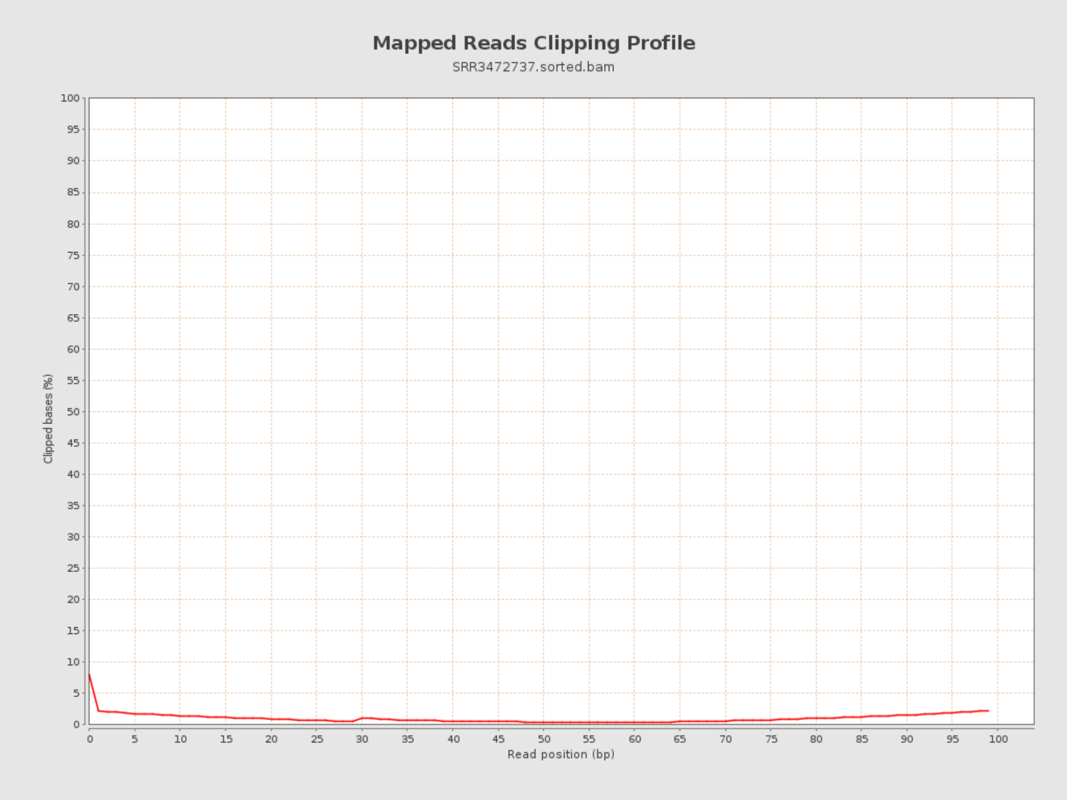
8. Results : Mapped Reads Nucleotide Content



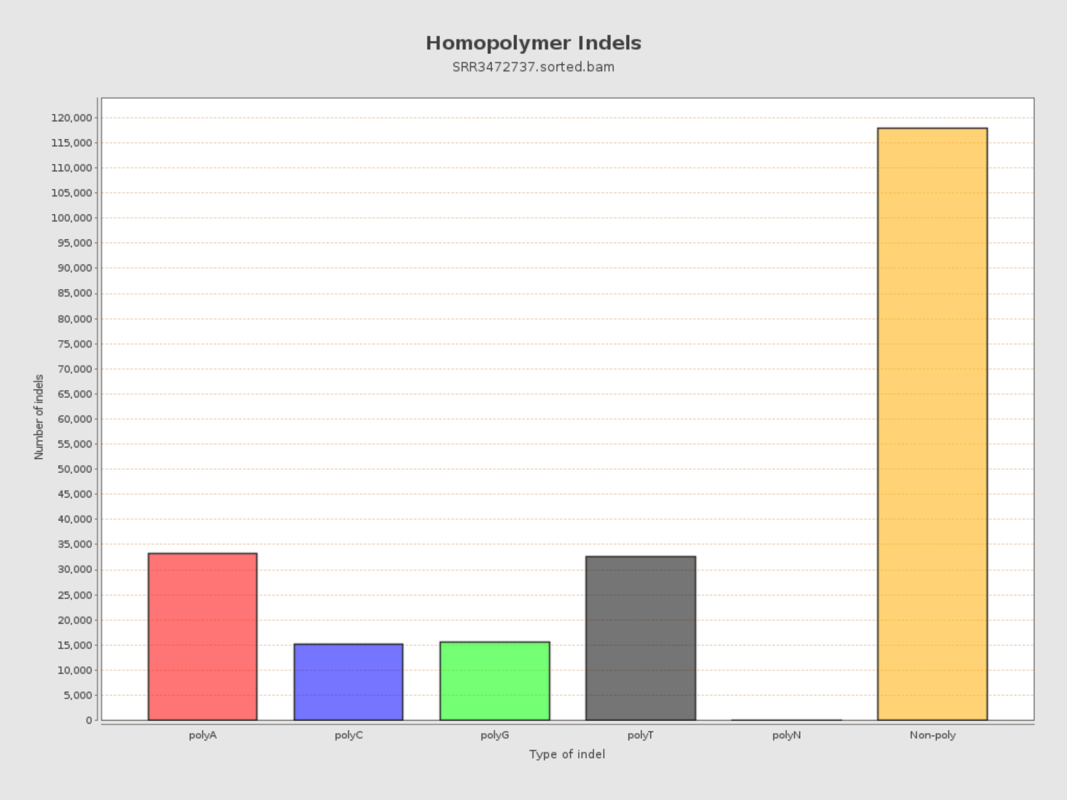
9. Results : Mapped Reads GC-content Distribution



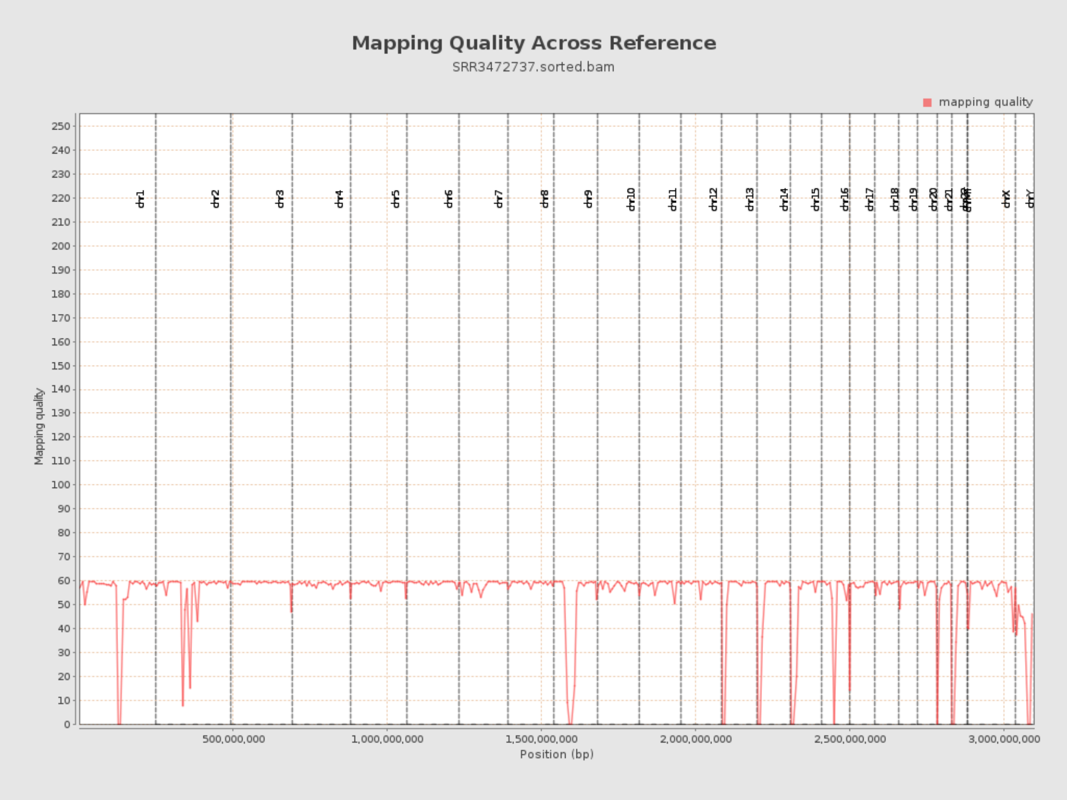
10. Results : Mapped Reads Clipping Profile



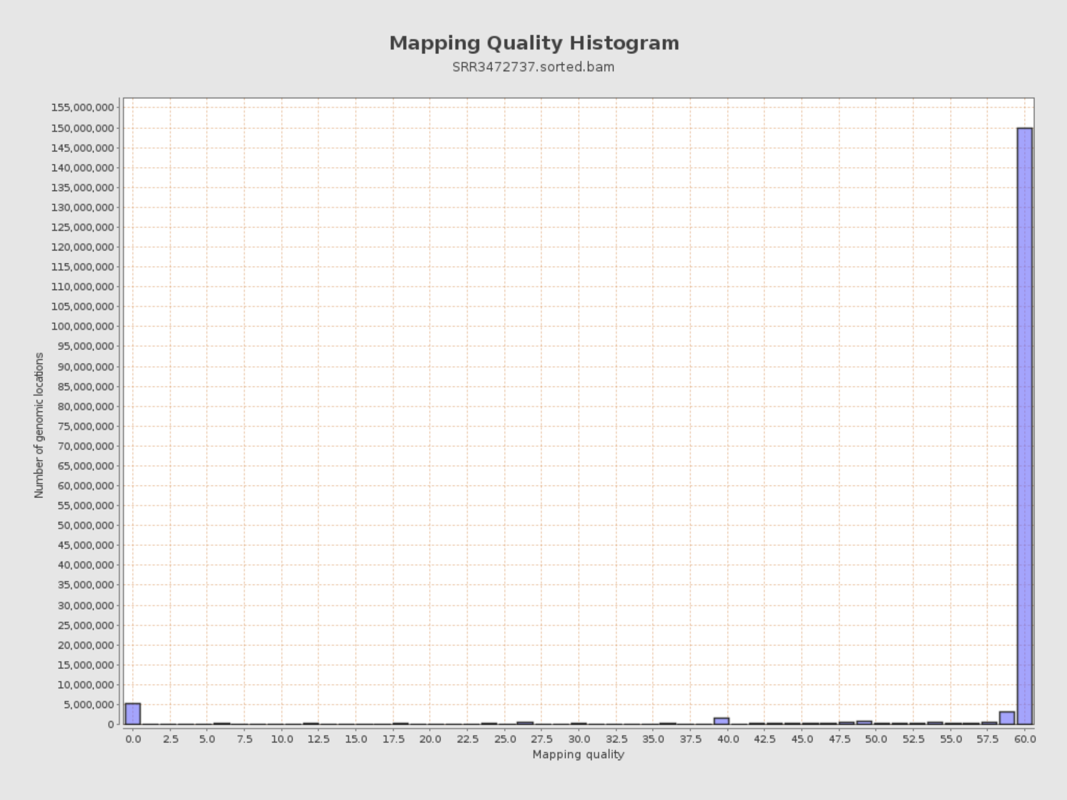
11. Results : Homopolymer Indels



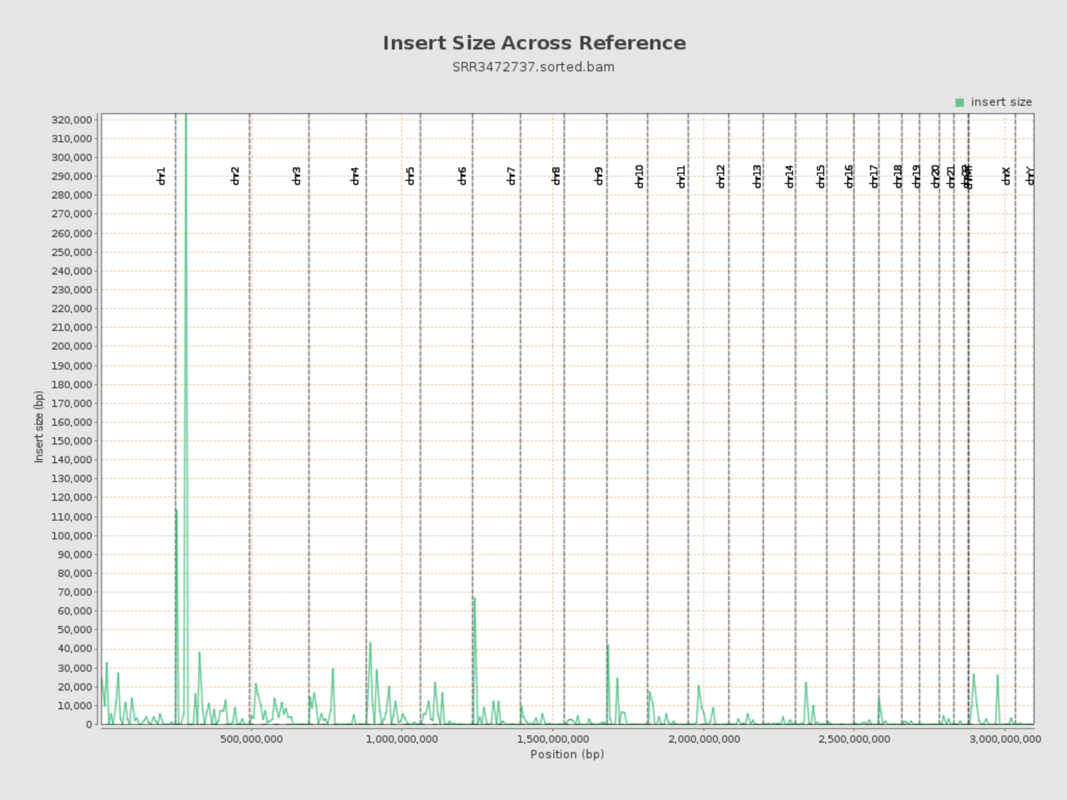
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram