Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:59:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472437.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_SRR3472437 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472437_1.fastq.gz SRR3472437_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:59:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472437.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,242,822
Mapped reads	16,102,853 / 99.14%
Unmapped reads	139,969 / 0.86%
Mapped paired reads	16,102,853 / 99.14%
Mapped reads, first in pair	8,070,654 / 49.69%
Mapped reads, second in pair	8,032,199 / 49.45%
Mapped reads, both in pair	16,030,734 / 98.69%
Mapped reads, singletons	72,119 / 0.44%
Secondary alignments	0
Supplementary alignments	53,941 / 0.33%
Read min/max/mean length	30 / 100 / 99.12
Duplicated reads (estimated)	10,305,436 / 63.45%
Duplication rate	47.92%
Clipped reads	1,163,798 / 7.16%

2.2. ACGT Content

Number/percentage of A's	418,920,574 / 26.6%
Number/percentage of C's	369,655,957 / 23.47%
Number/percentage of T's	420,152,751 / 26.68%
Number/percentage of G's	365,897,518 / 23.23%
Number/percentage of N's	197,685 / 0.01%

GC Percentage	46.71%

2.3. Coverage

Mean	0.5088
Standard Deviation	17.4684

2.4. Mapping Quality

Mean Mapping Quality	54.73

2.5. Insert size

Mean	14,734.67
Standard Deviation	1,183,101.72
P25/Median/P75	144 / 198 / 266

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	8,039,875
Insertions	84,711
Mapped reads with at least one insertion	0.52%
Deletions	75,289
Mapped reads with at least one deletion	0.46%
Homopolymer indels	45.83%

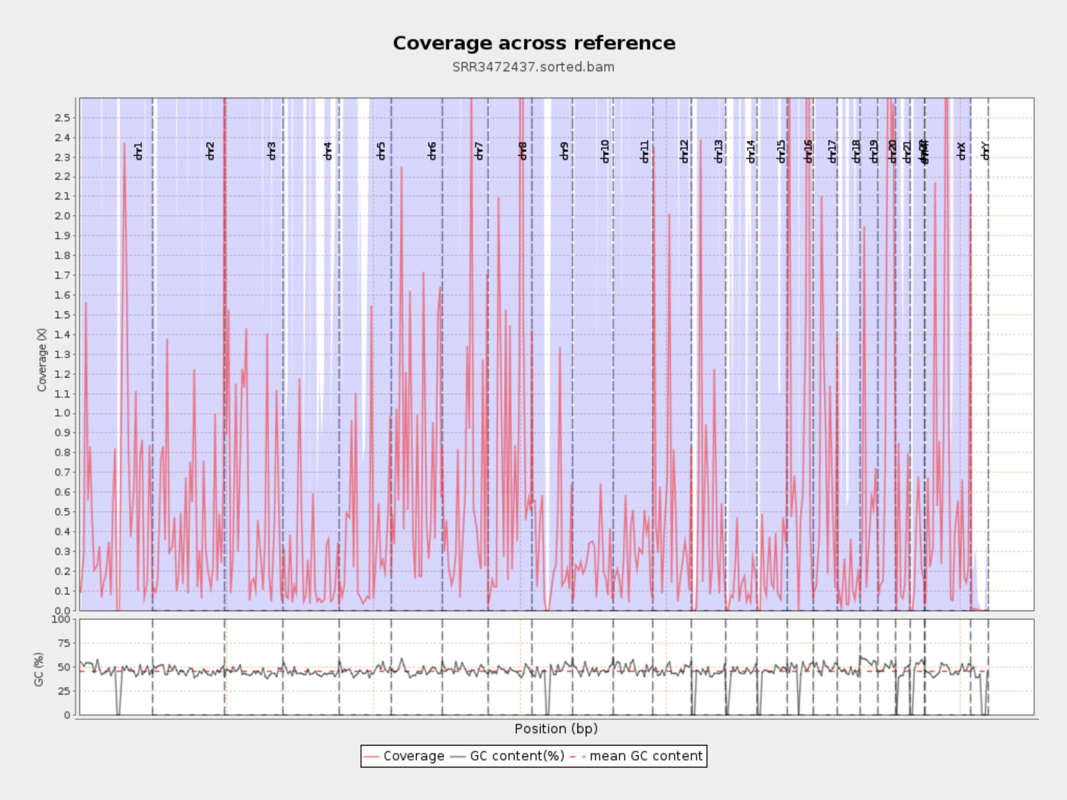
2.7. Chromosome stats

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

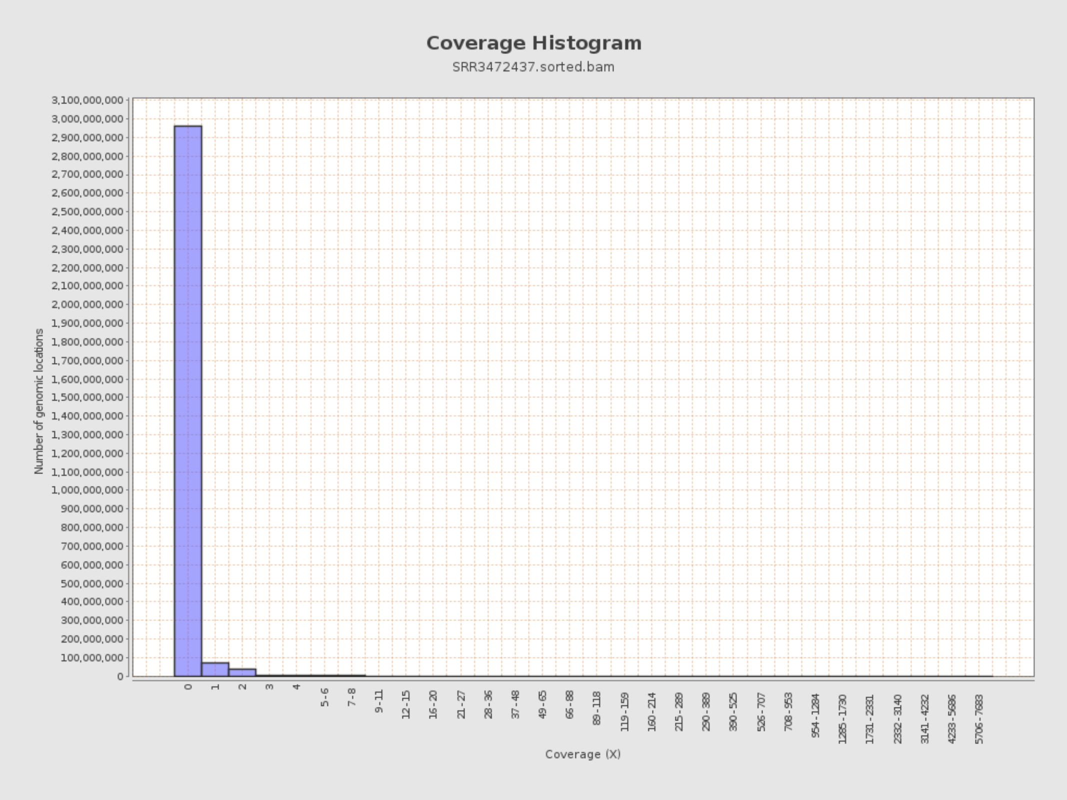
		bases	**coverage**	**deviation**
chr1	249250621	142768984	0.5728	17.4351
chr2	243199373	103569189	0.4259	13.6367
chr3	198022430	120084442	0.6064	18.606
chr4	191154276	40521775	0.212	9.4276
chr5	180915260	66990396	0.3703	12.8728
chr6	171115067	136773169	0.7993	21.7556
chr7	159138663	103730672	0.6518	18.3843
chr8	146364022	137092206	0.9367	27.6346
chr9	141213431	47253241	0.3346	11.8567
chr10	135534747	33254080	0.2454	10.1959
chr11	135006516	38847240	0.2877	8.2229
chr12	133851895	75152145	0.5615	13.7009
chr13	115169878	57912632	0.5028	19.2855
chr14	107349540	13981753	0.1302	4.3568
chr15	102531392	21941045	0.214	7.3186
chr16	90354753	103271155	1.143	36.7937
chr17	81195210	58971535	0.7263	19.5456
chr18	78077248	9700749	0.1242	5.5271
chr19	59128983	37012126	0.626	14.7881
chr20	63025520	93870888	1.4894	38.7074
chr21	48129895	15681644	0.3258	17.1389
chr22	51304566	12559726	0.2448	7.219
chrMT	16571	1651	0.0996	0.3776
chrX	155270560	103812229	0.6686	20.121

chrY	59373566	243067	0.0041	0.2088

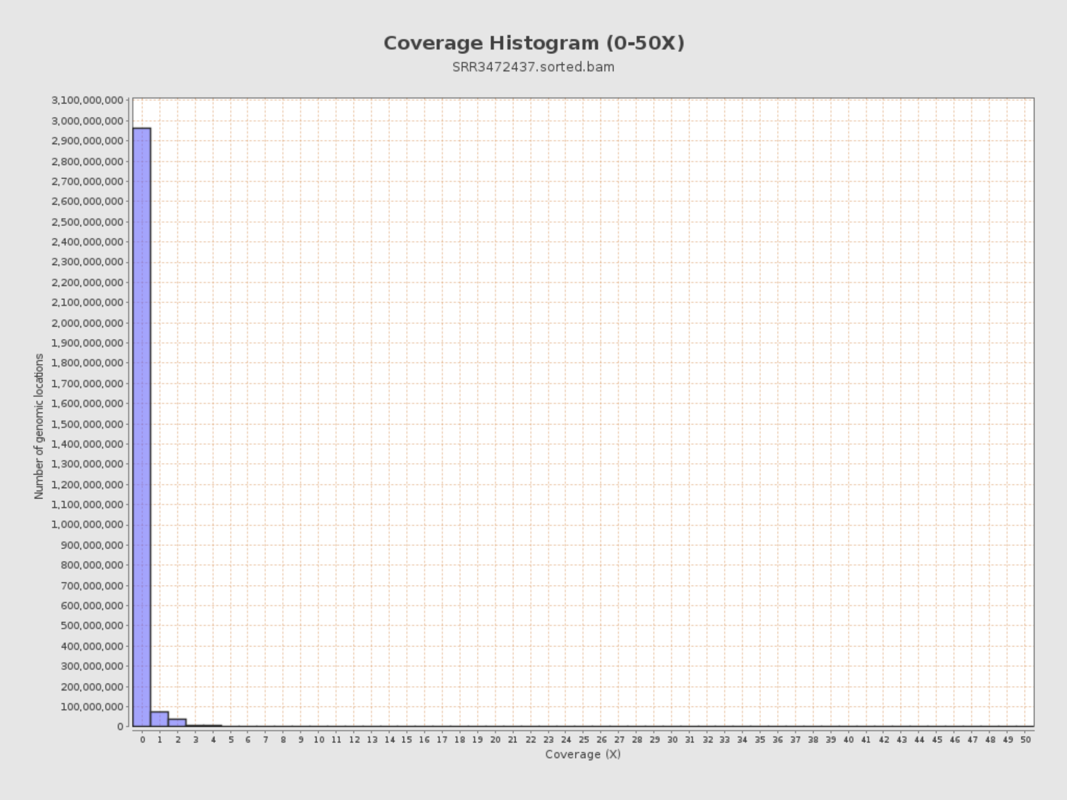
3. Results : Coverage across reference



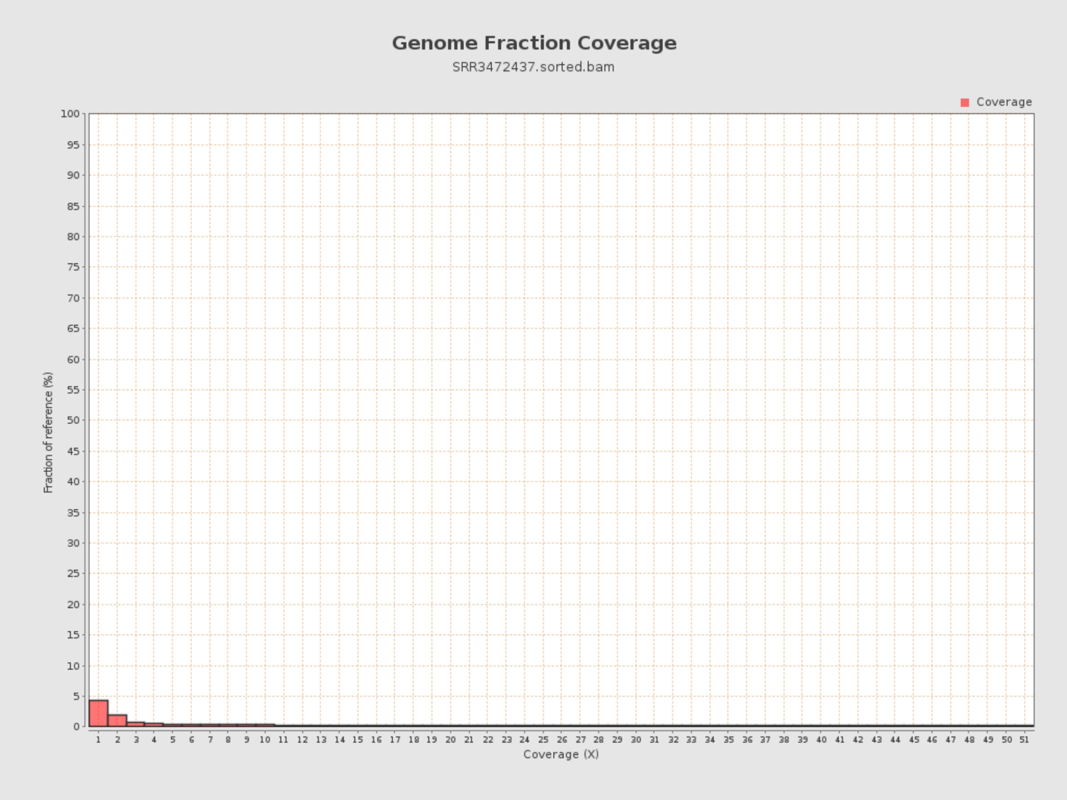
4. Results : Coverage Histogram



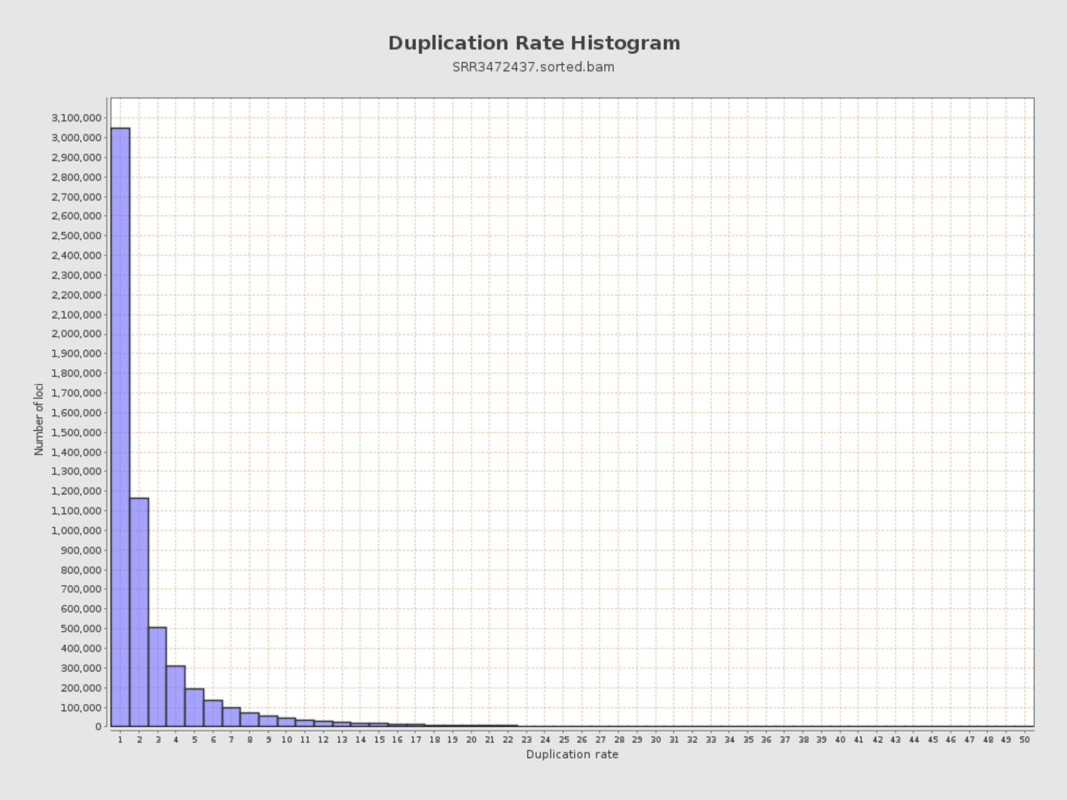
5. Results : Coverage Histogram (0-50X)



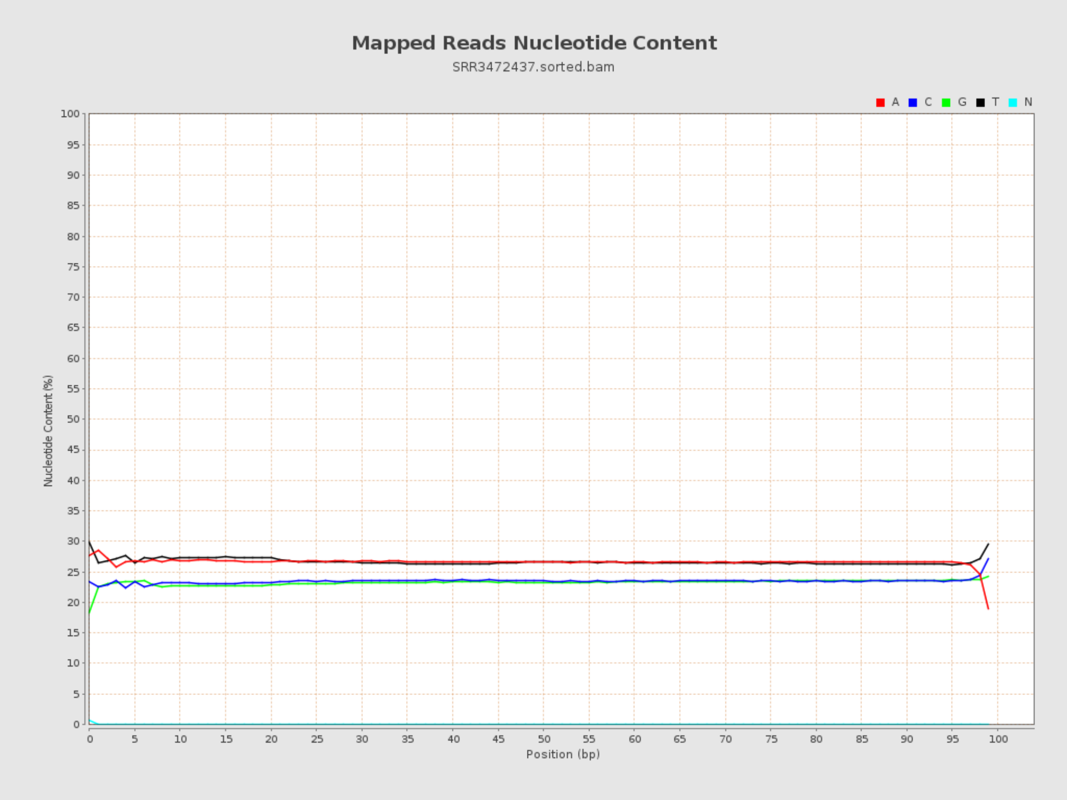
6. Results : Genome Fraction Coverage



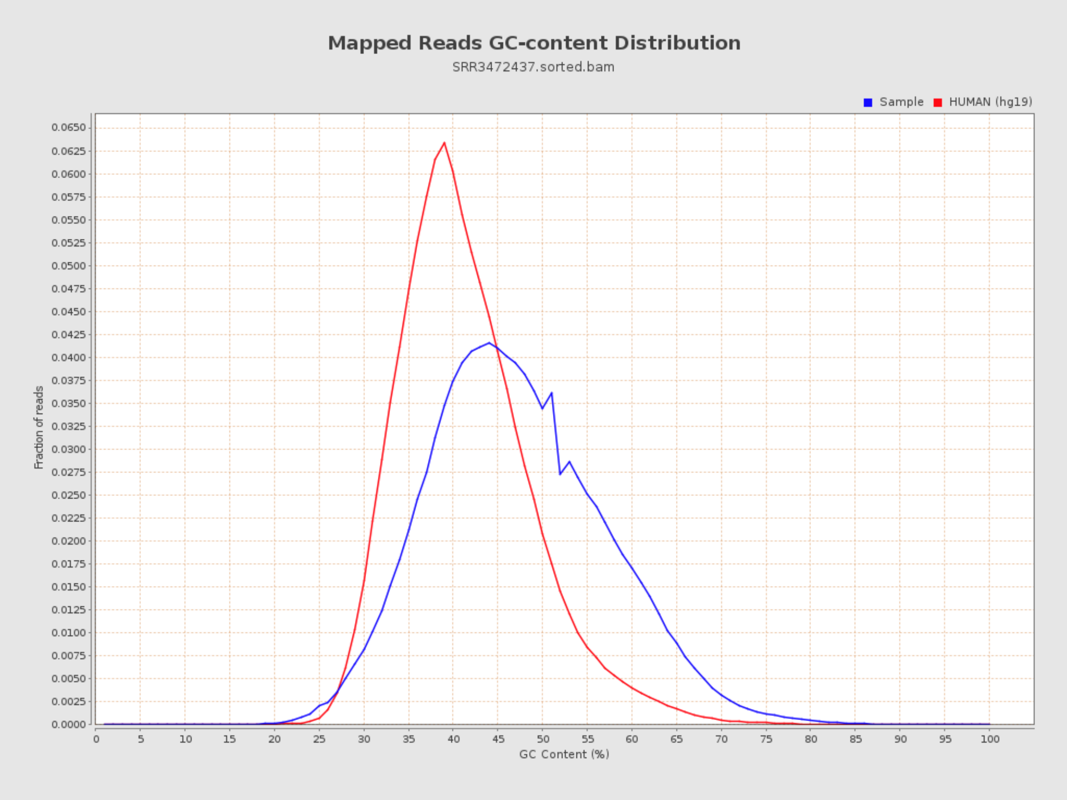
7. Results : Duplication Rate Histogram



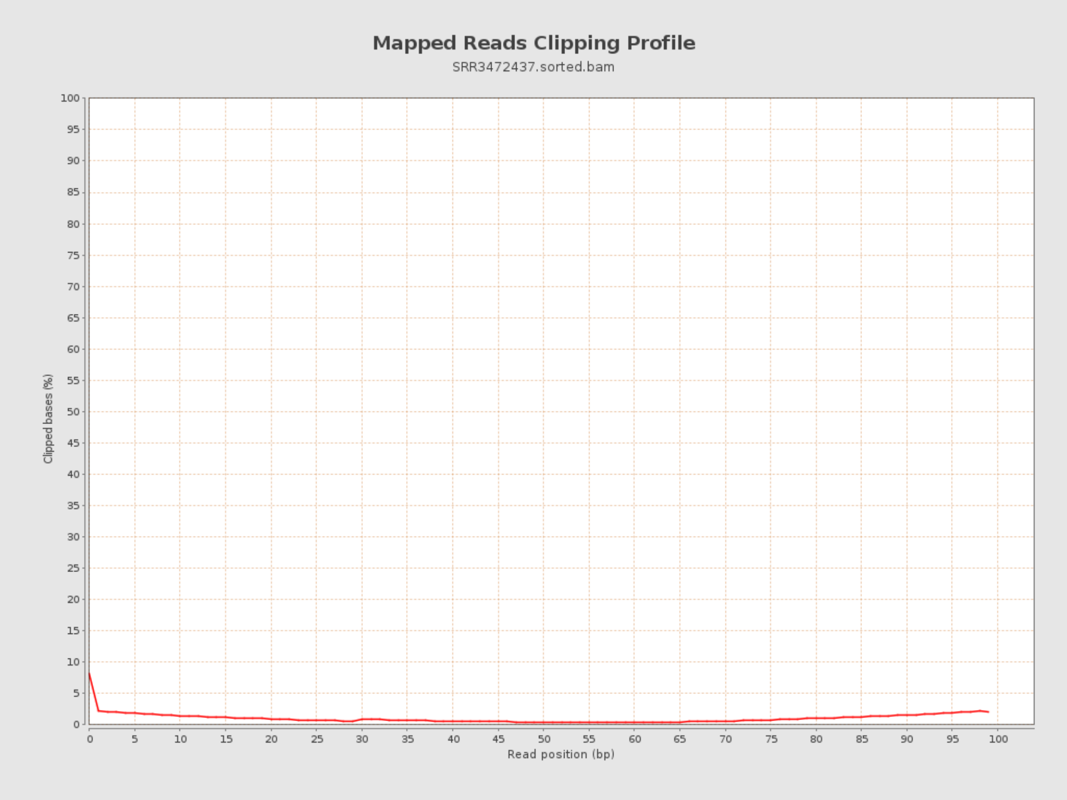
8. Results : Mapped Reads Nucleotide Content



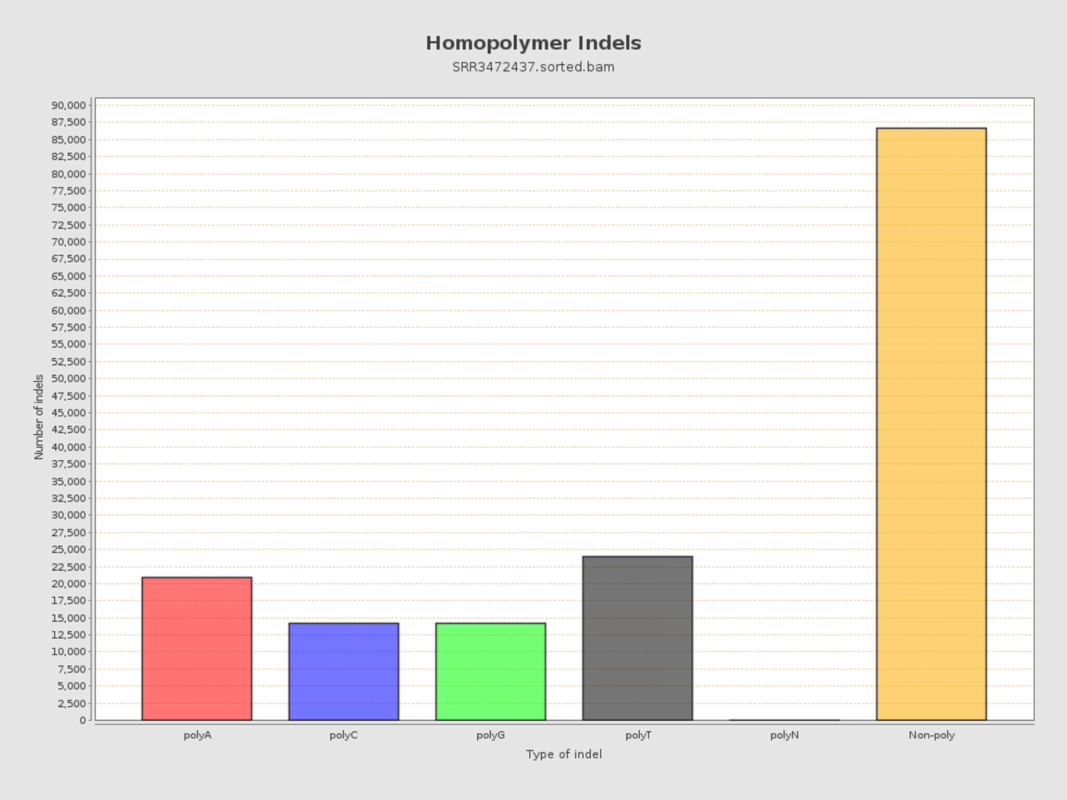
9. Results : Mapped Reads GC-content Distribution



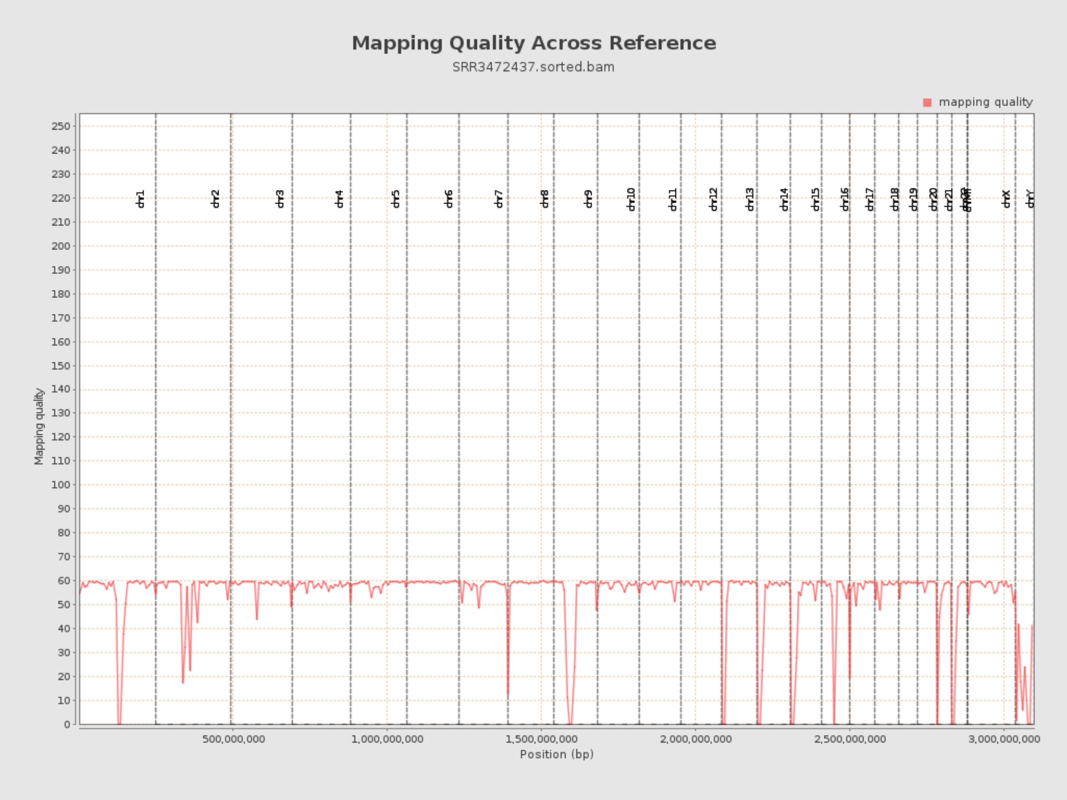
10. Results : Mapped Reads Clipping Profile



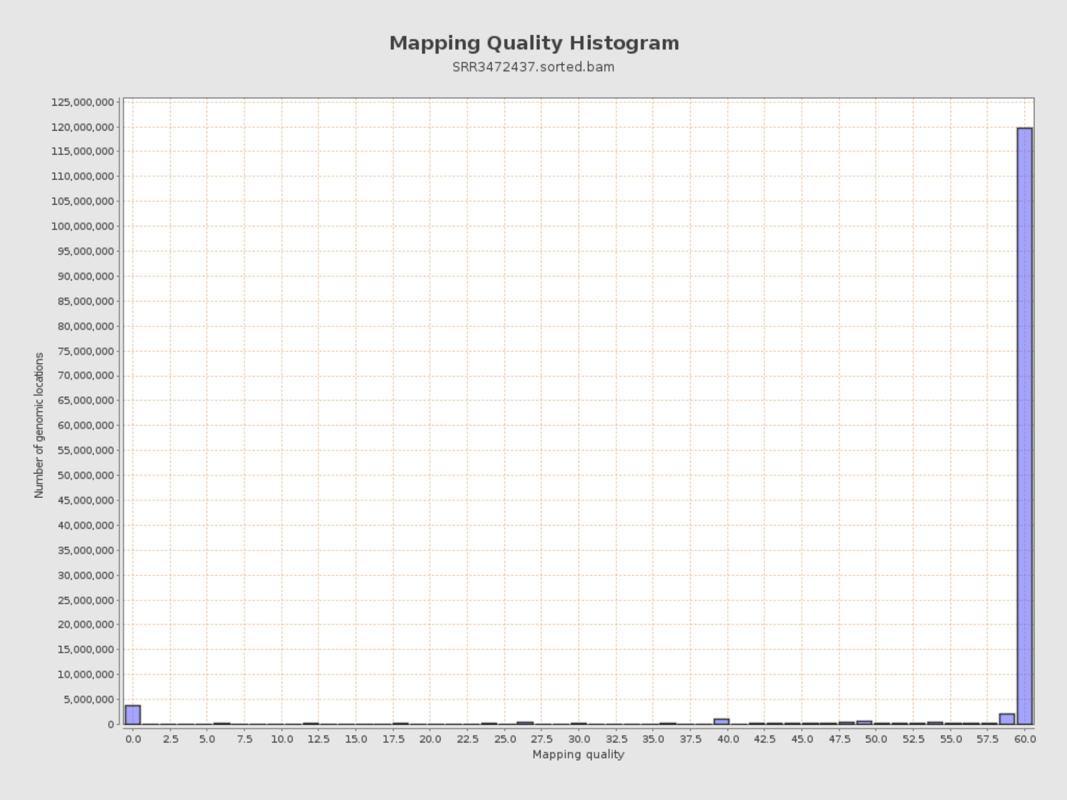
11. Results : Homopolymer Indels



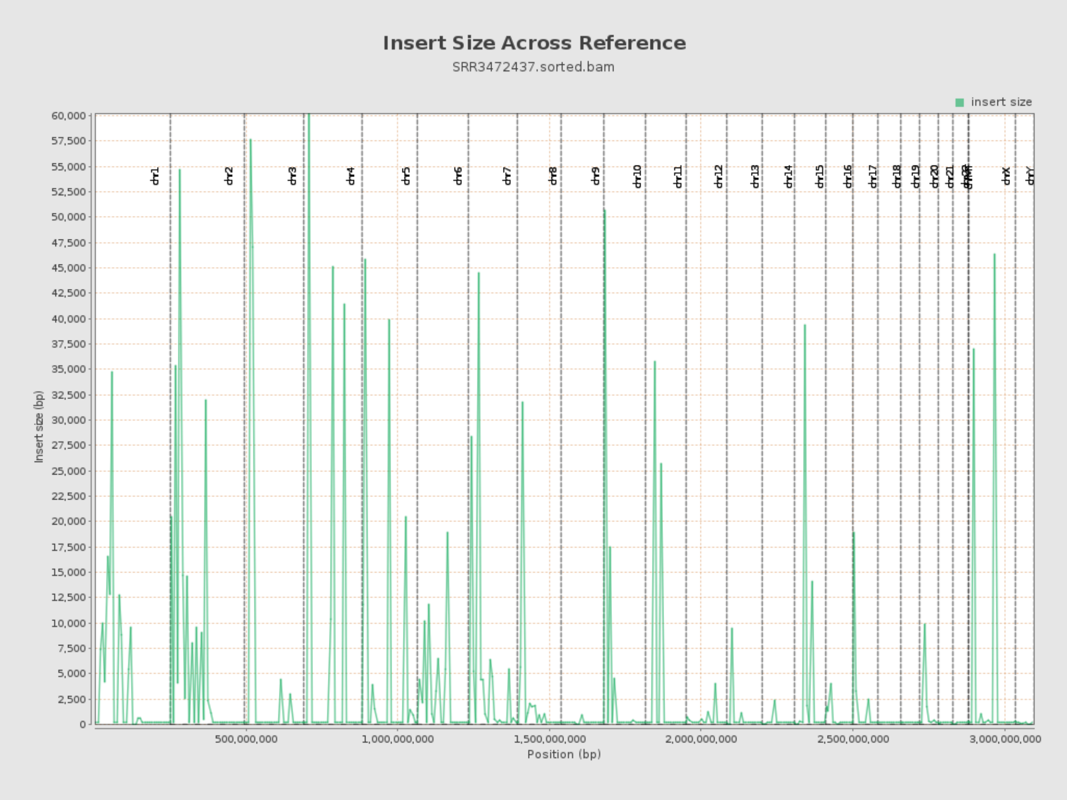
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram