Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 17:02:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617400.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_SRR617400 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617400_1.fastq.gz SRR617400_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 17:02:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617400.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,964,957 / 93.64%
Unmapped reads	2,035,043 / 6.36%
Mapped paired reads	29,964,957 / 93.64%
Mapped reads, first in pair	15,087,098 / 47.15%
Mapped reads, second in pair	14,877,859 / 46.49%
Mapped reads, both in pair	29,399,726 / 91.87%
Mapped reads, singletons	565,231 / 1.77%
Secondary alignments	0
Supplementary alignments	488,661 / 1.53%
Read min/max/mean length	30 / 100 / 100.63
Duplicated reads (estimated)	1,405,173 / 4.39%
Duplication rate	4.2%
Clipped reads	3,225,613 / 10.08%

2.2. ACGT Content

Number/percentage of A's	880,319,525 / 29.85%
Number/percentage of C's	592,897,703 / 20.1%
Number/percentage of T's	871,813,092 / 29.56%
Number/percentage of G's	603,683,266 / 20.47%
Number/percentage of N's	320,807 / 0.01%

GC Percentage	40.58%

2.3. Coverage

Mean	0.9528
Standard Deviation	2.9296

2.4. Mapping Quality

Mean Mapping Quality	53.89

2.5. Insert size

Mean	58,247.99
Standard Deviation	2,307,932.36
P25/Median/P75	171 / 210 / 272

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	26,151,525
Insertions	421,085
Mapped reads with at least one insertion	1.39%
Deletions	292,005
Mapped reads with at least one deletion	0.95%
Homopolymer indels	37.45%

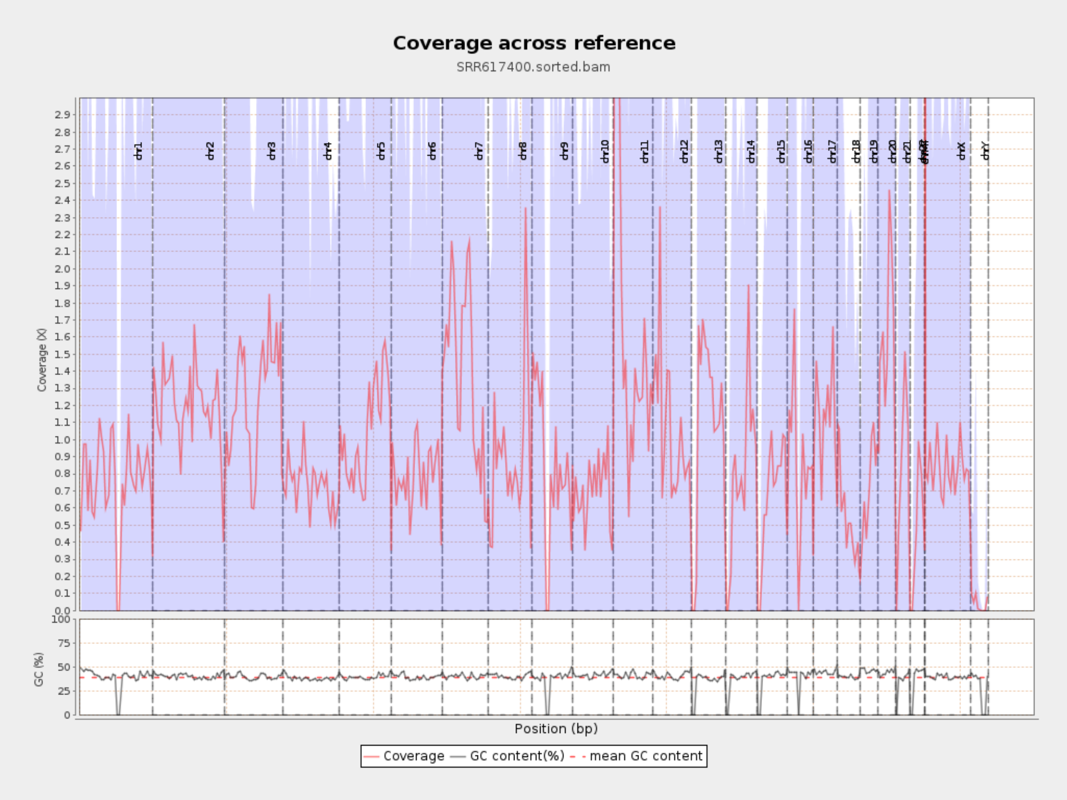
2.7. Chromosome stats

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

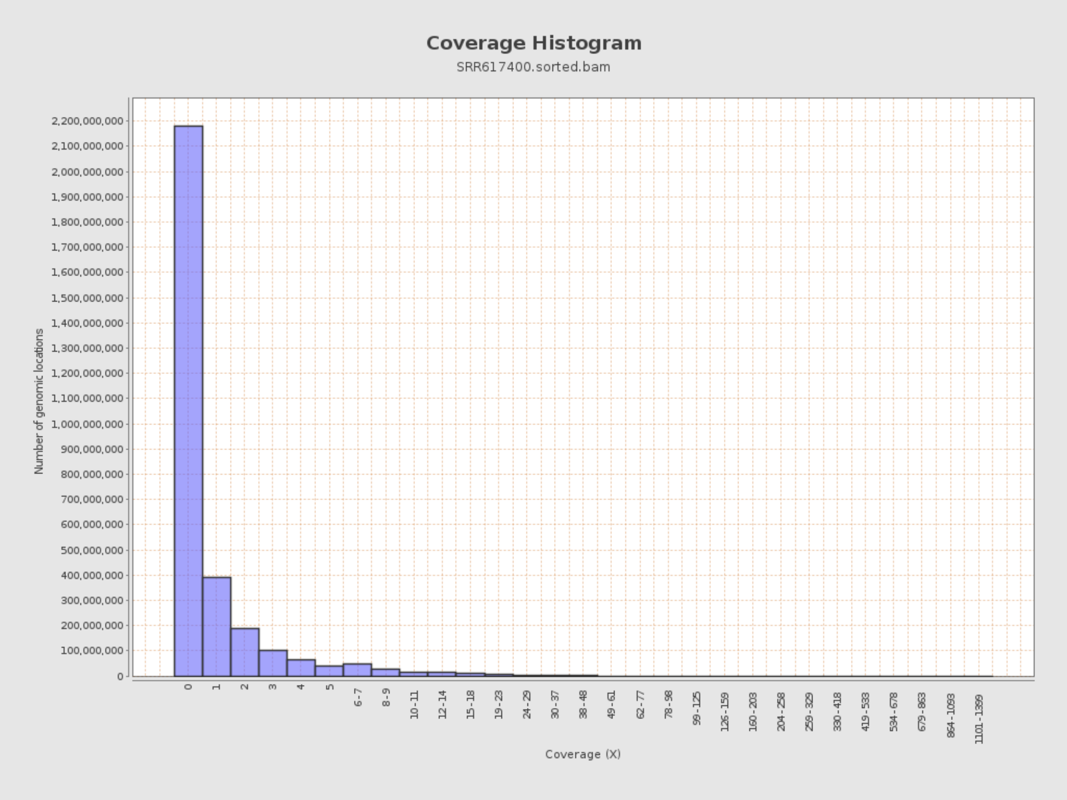
		bases	coverage	deviation
chr1	249250621	190028468	0.7624	2.7493
chr2	243199373	293841969	1.2082	3.1093
chr3	198022430	249066641	1.2578	3.4148
chr4	191154276	141392776	0.7397	2.2696
chr5	180915260	188434875	1.0416	2.861
chr6	171115067	135132873	0.7897	2.5964
chr7	159138663	220882946	1.388	3.2409
chr8	146364022	130630252	0.8925	3.2512
chr9	141213431	117898966	0.8349	2.6017
chr10	135534747	94664852	0.6985	2.4146
chr11	135006516	218830859	1.6209	3.8232
chr12	133851895	140455544	1.0493	2.8062
chr13	115169878	127650726	1.1084	2.7644
chr14	107349540	85654594	0.7979	2.8964
chr15	102531392	67864403	0.6619	2.3788
chr16	90354753	74685584	0.8266	3.3397
chr17	81195210	91494981	1.1269	3.7264
chr18	78077248	42039722	0.5384	1.9842
chr19	59128983	42380679	0.7167	2.3503
chr20	63025520	101003015	1.6026	4.7663
chr21	48129895	40397040	0.8393	2.5183
chr22	51304566	23773346	0.4634	2.0713
chrMT	16571	181491	10.9523	4.7437
chrX	155270560	128921222	0.8303	2.5575

chrY	59373566	2383630	0.0401	0.6188

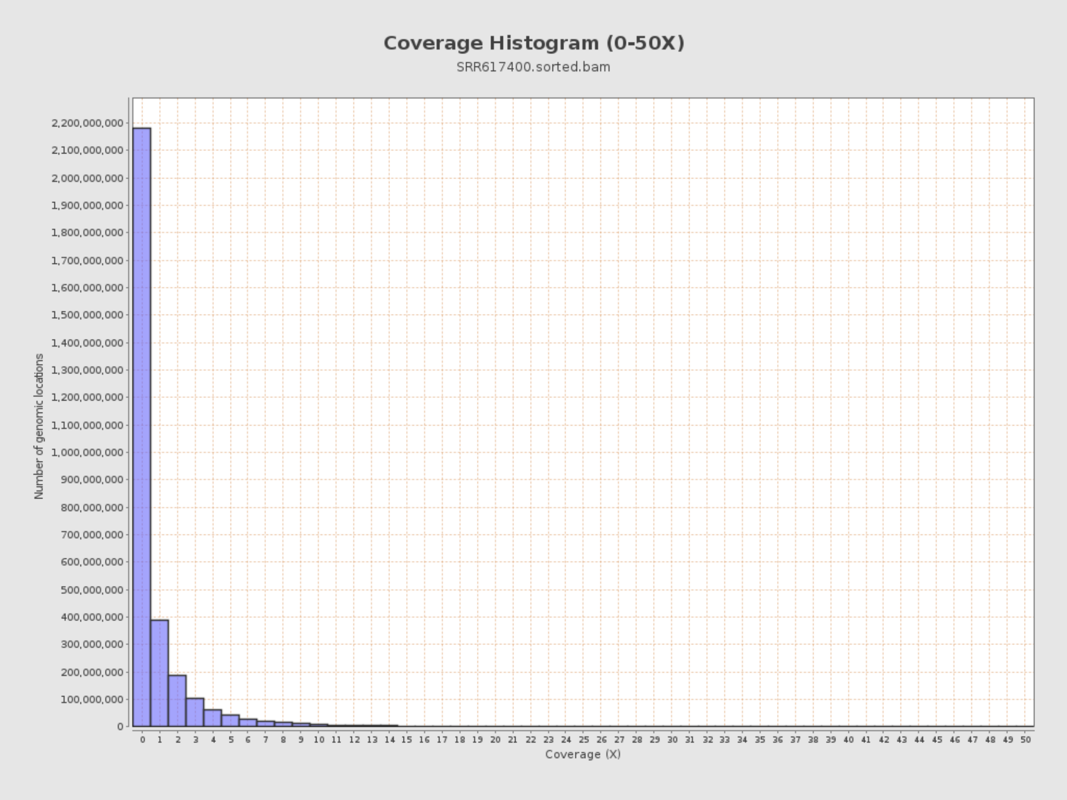
3. Results : Coverage across reference



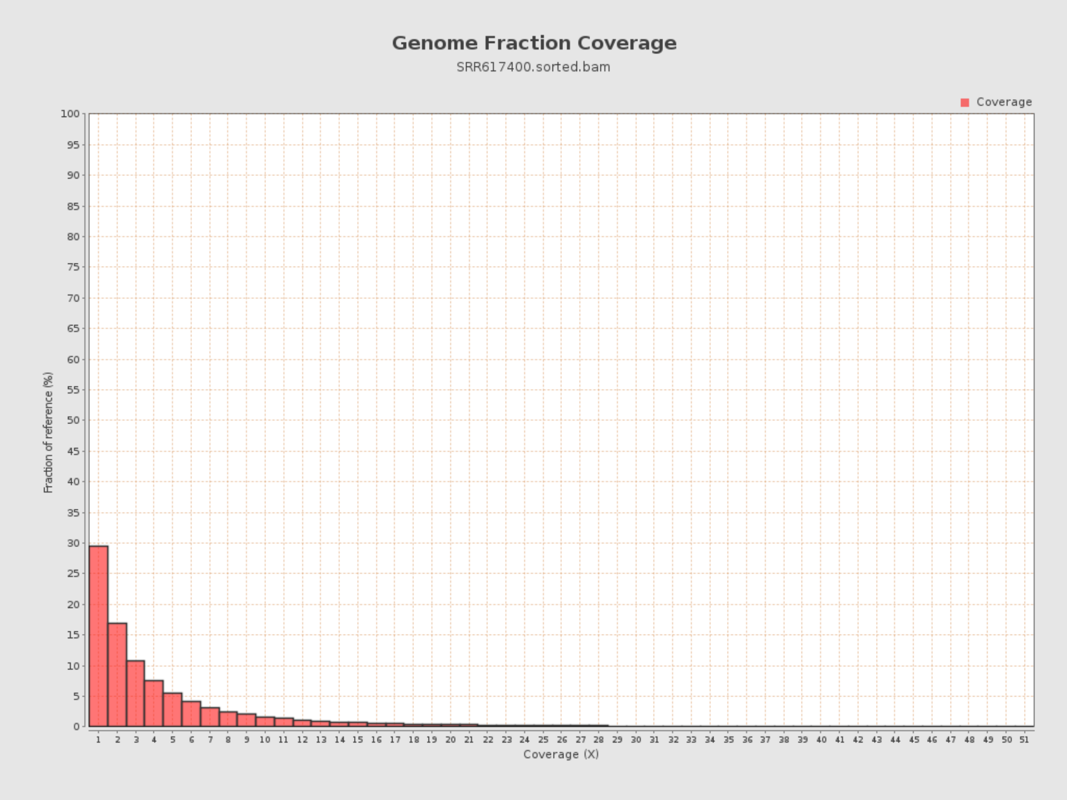
4. Results : Coverage Histogram



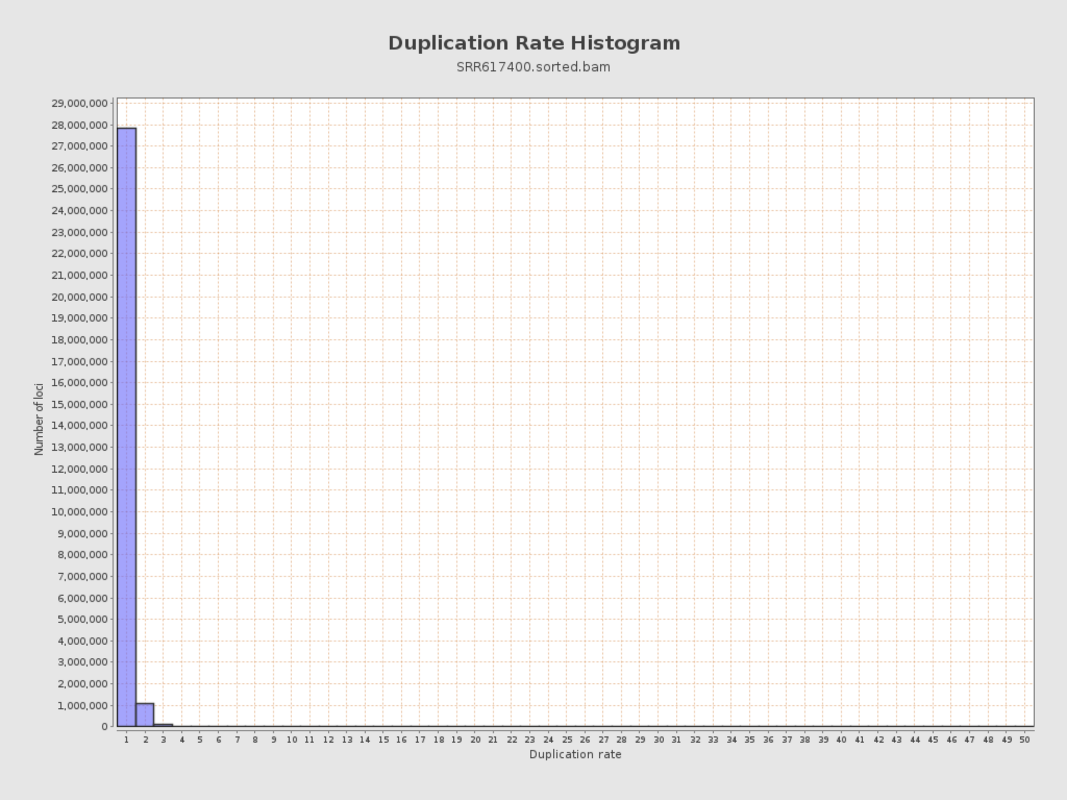
5. Results : Coverage Histogram (0-50X)



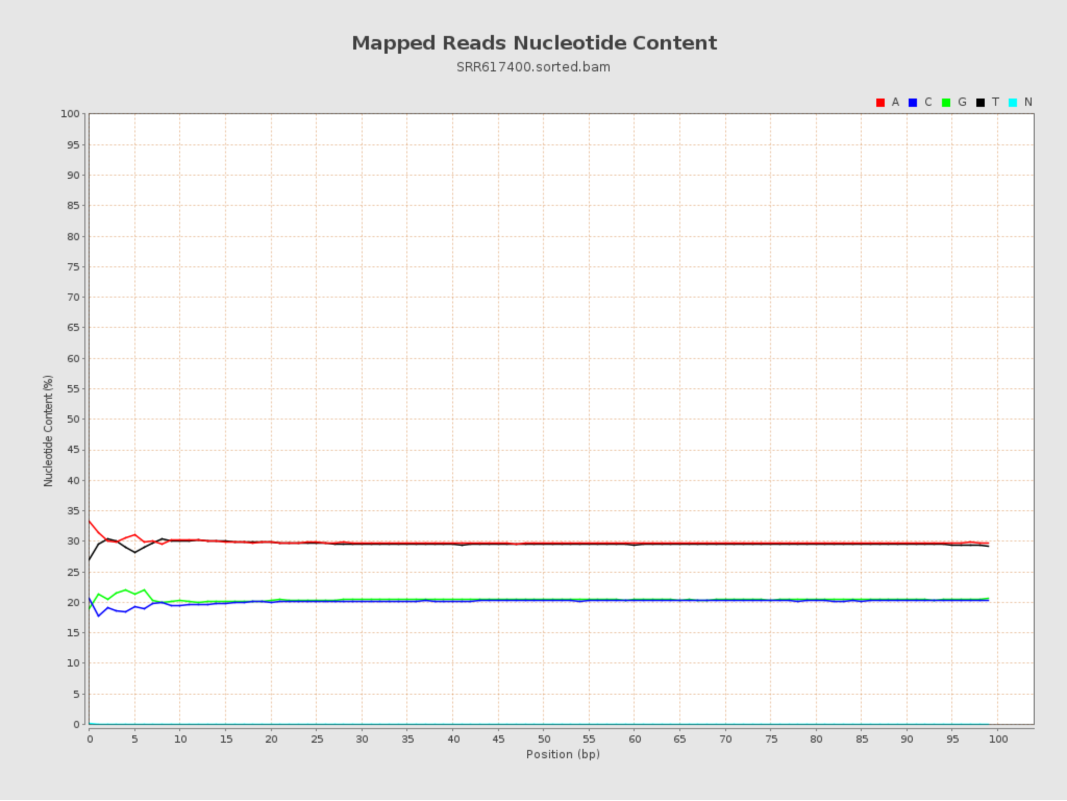
6. Results : Genome Fraction Coverage



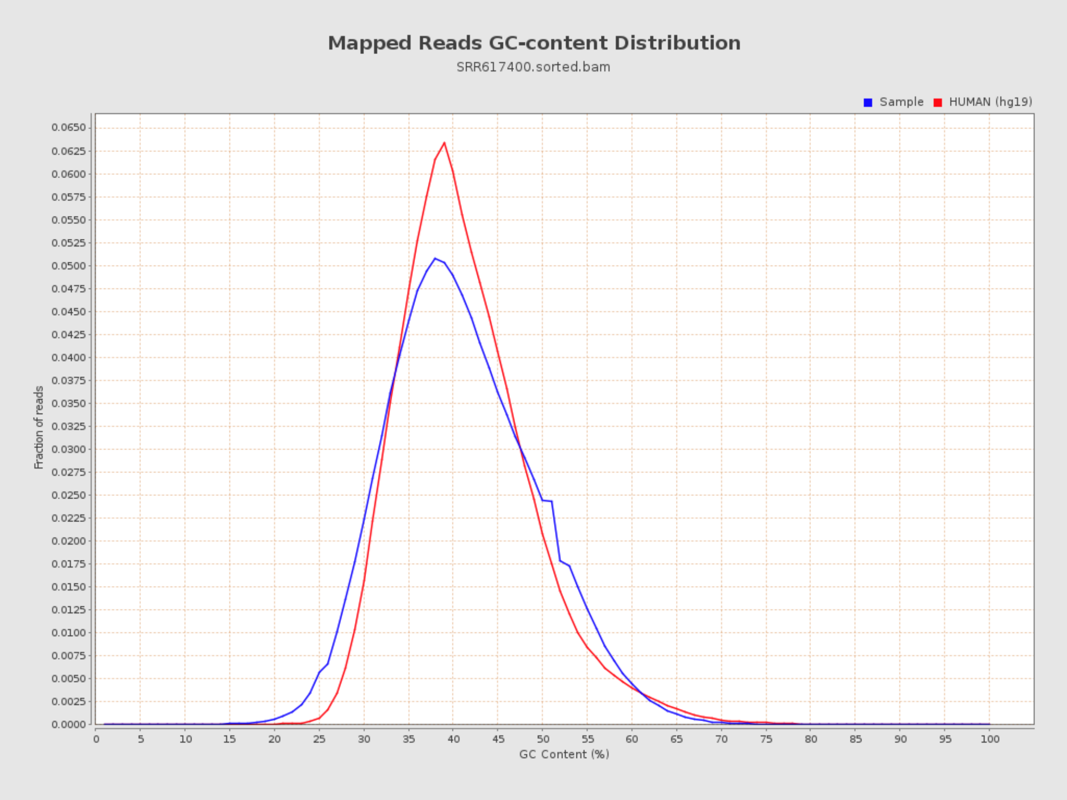
7. Results : Duplication Rate Histogram



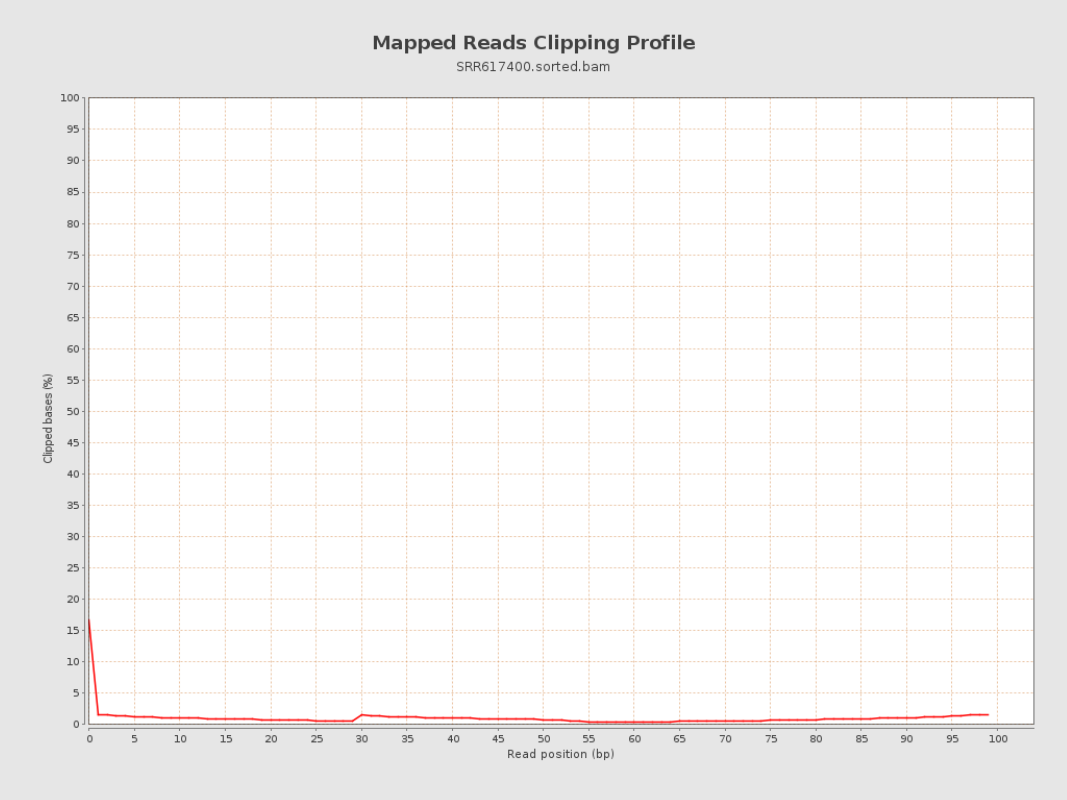
8. Results : Mapped Reads Nucleotide Content



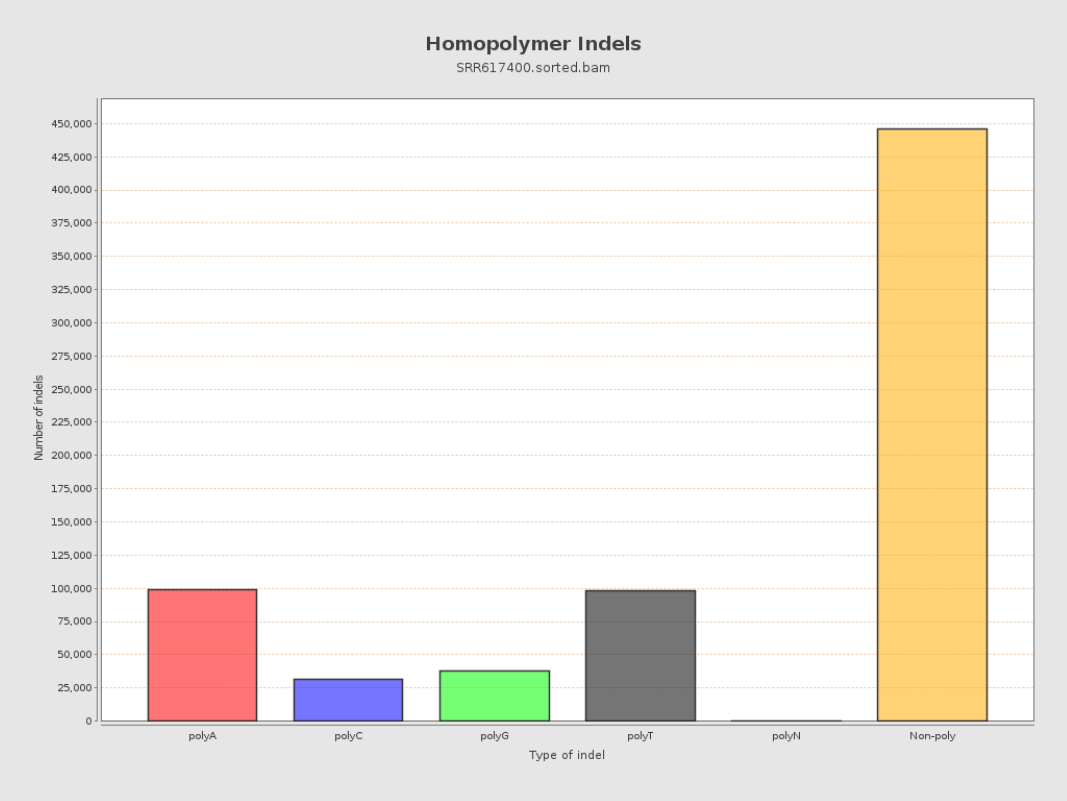
9. Results : Mapped Reads GC-content Distribution



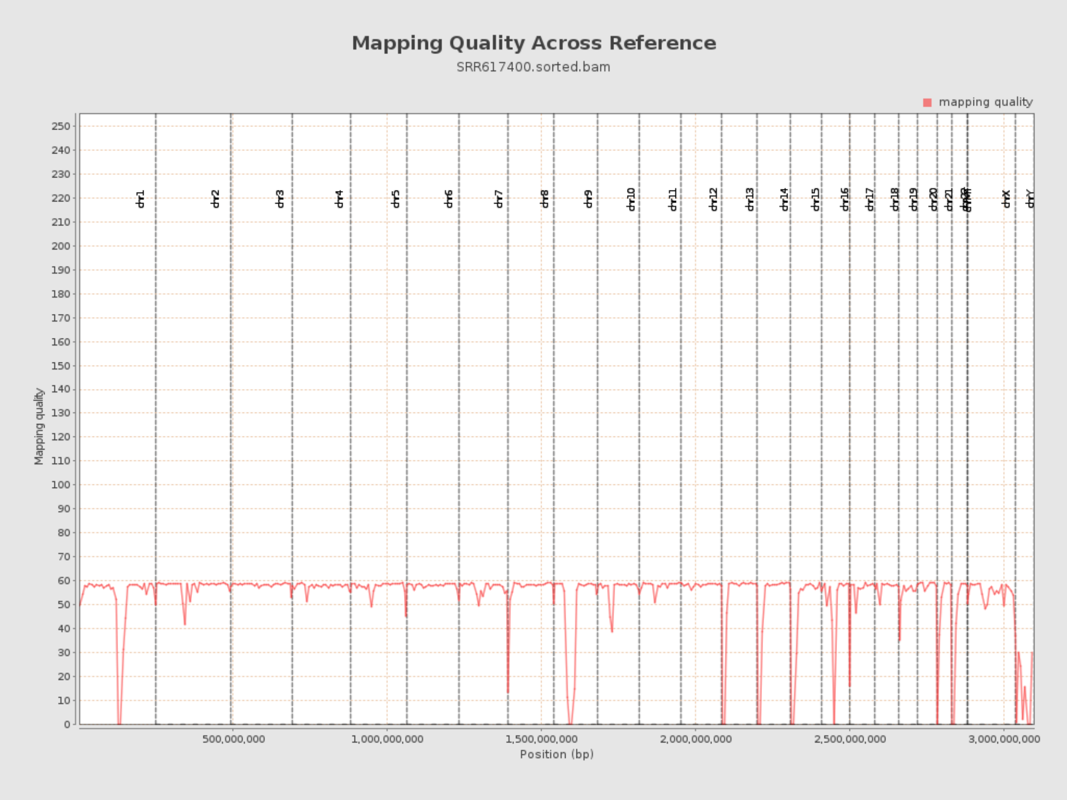
10. Results : Mapped Reads Clipping Profile



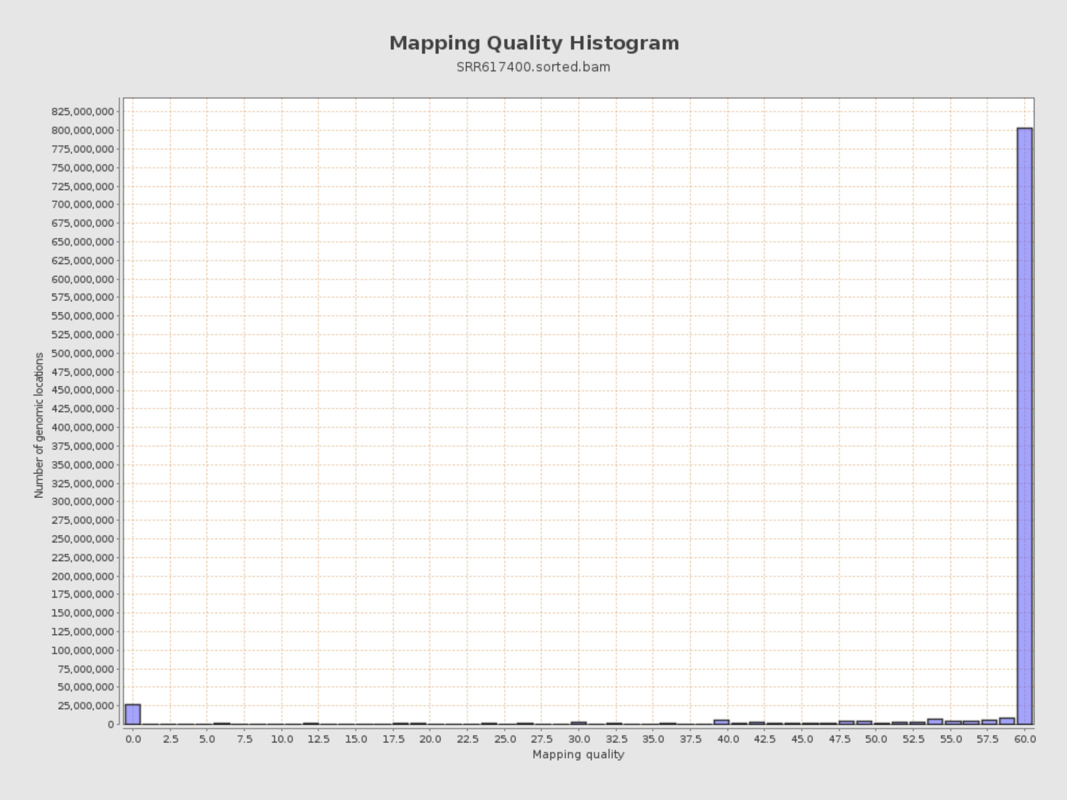
11. Results : Homopolymer Indels



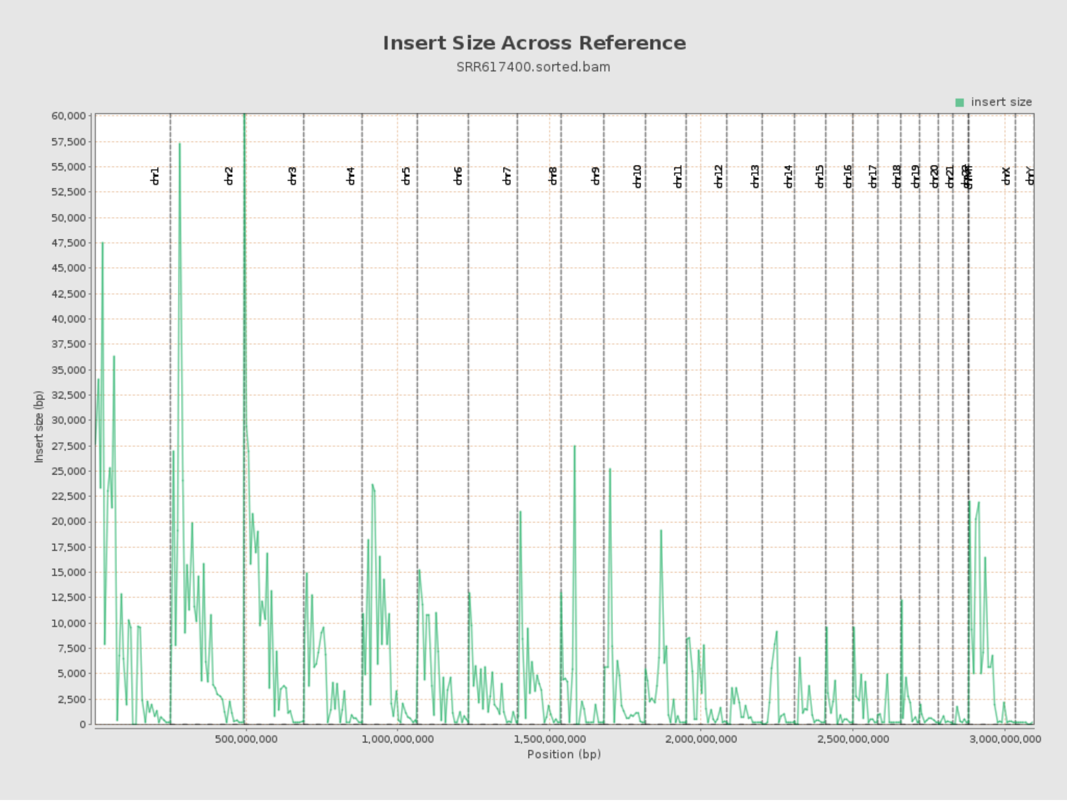
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram