Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 14:09:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617370.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_SRR617370 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617370_1.fastq.gz SRR617370_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 14:09:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617370.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,882,296 / 93.38%
Unmapped reads	2,117,704 / 6.62%
Mapped paired reads	29,882,296 / 93.38%
Mapped reads, first in pair	15,100,538 / 47.19%
Mapped reads, second in pair	14,781,758 / 46.19%
Mapped reads, both in pair	29,174,518 / 91.17%
Mapped reads, singletons	707,778 / 2.21%
Secondary alignments	0
Supplementary alignments	88,261 / 0.28%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	1,554,836 / 4.86%
Duplication rate	1.56%
Clipped reads	2,685,775 / 8.39%

2.2. ACGT Content

Number/percentage of A's	883,396,117 / 30.22%
Number/percentage of C's	579,594,617 / 19.83%
Number/percentage of T's	872,957,192 / 29.87%
Number/percentage of G's	586,007,446 / 20.05%
Number/percentage of N's	905,916 / 0.03%

GC Percentage	39.88%

2.3. Coverage

Mean	0.9444
Standard Deviation	9.375

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	65,912.45
Standard Deviation	2,455,918.96
P25/Median/P75	172 / 213 / 278

2.6. Mismatches and indels

General error rate	1.35%
Mismatches	38,570,886
Insertions	301,771
Mapped reads with at least one insertion	0.98%
Deletions	358,908
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.11%

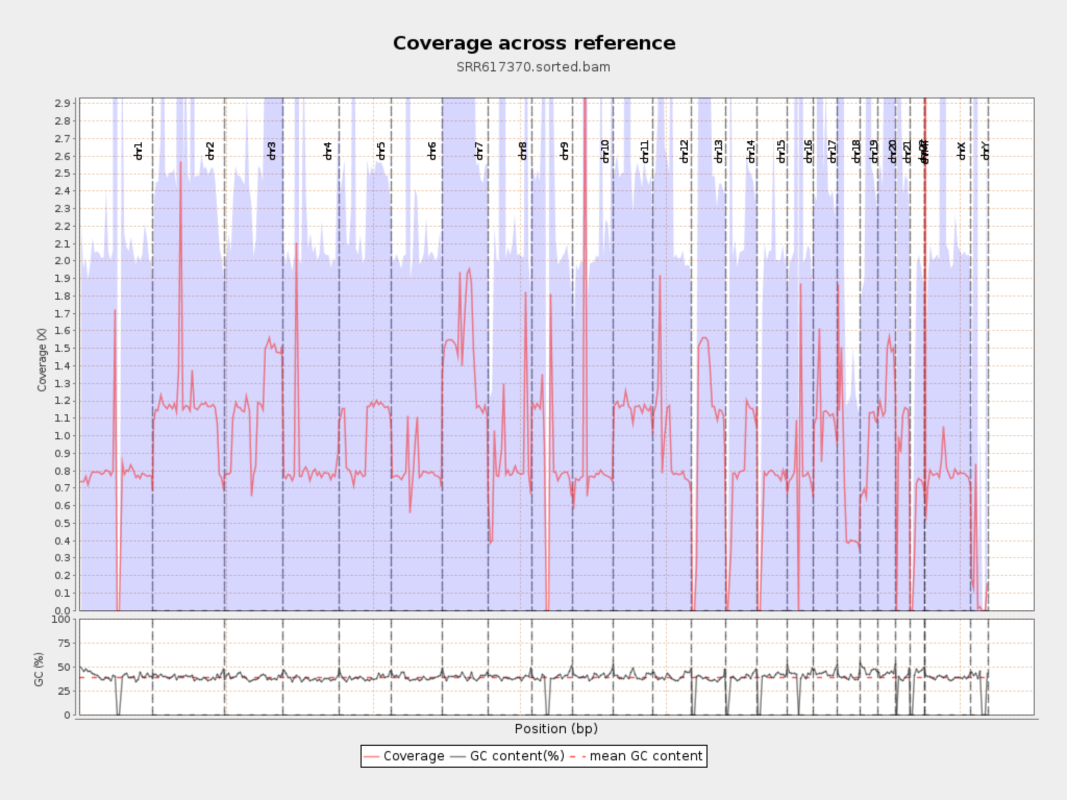
2.7. Chromosome stats

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

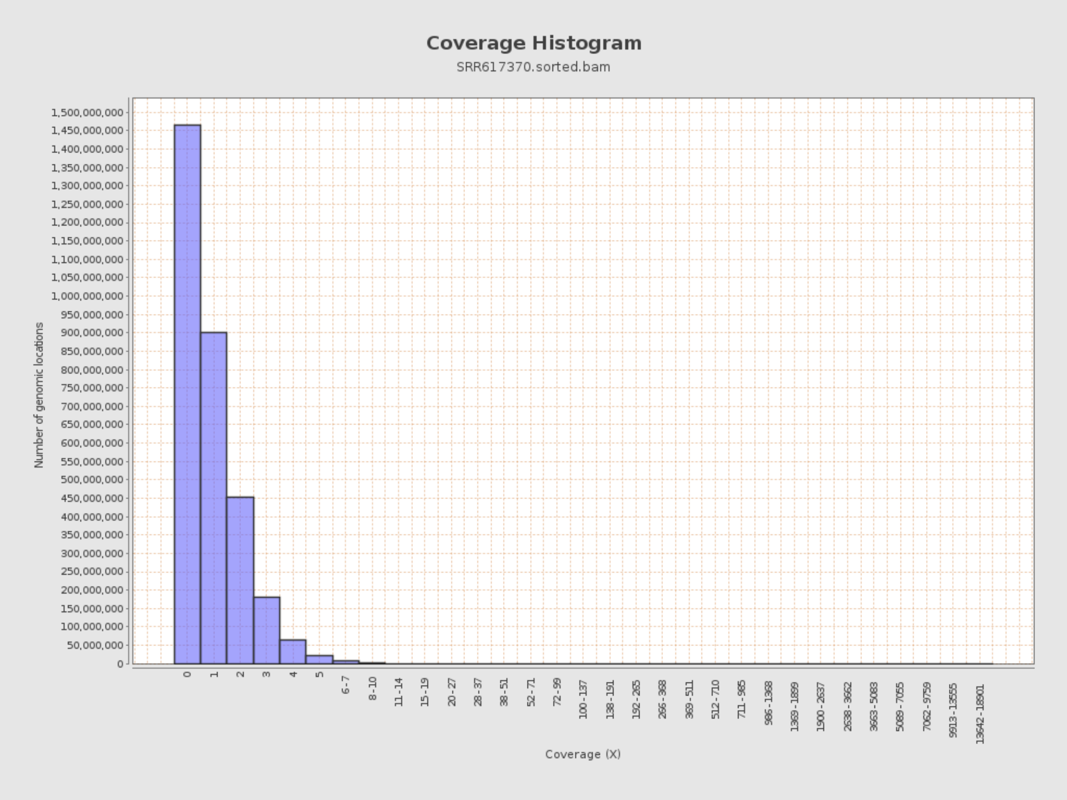
		bases	coverage	deviation
chr1	249250621	189733816	0.7612	19.2471
chr2	243199373	288447851	1.1861	8.4705
chr3	198022430	232644235	1.1748	1.4608
chr4	191154276	159826420	0.8361	8.6845
chr5	180915260	183506918	1.0143	1.4566
chr6	171115067	137333287	0.8026	3.6247
chr7	159138663	237342602	1.4914	10.7061
chr8	146364022	123002667	0.8404	7.1189
chr9	141213431	123047315	0.8714	13.9087
chr10	135534747	122685228	0.9052	19.2784
chr11	135006516	156705757	1.1607	5.2705
chr12	133851895	129352109	0.9664	1.4838
chr13	115169878	127124892	1.1038	1.3022
chr14	107349540	84821029	0.7901	1.3665
chr15	102531392	65995135	0.6437	1.0596
chr16	90354753	73539495	0.8139	7.6937
chr17	81195210	91340234	1.1249	6.7006
chr18	78077248	52724666	0.6753	14.6434
chr19	59128983	54354911	0.9193	9.1724
chr20	63025520	84045064	1.3335	2.3772
chr21	48129895	46401859	0.9641	3.1877
chr22	51304566	26097582	0.5087	0.9103
chrMT	16571	1987941	119.9651	19.8519
chrX	155270560	121811670	0.7845	2.8823

chrY	59373566	9853025	0.1659	7.8005

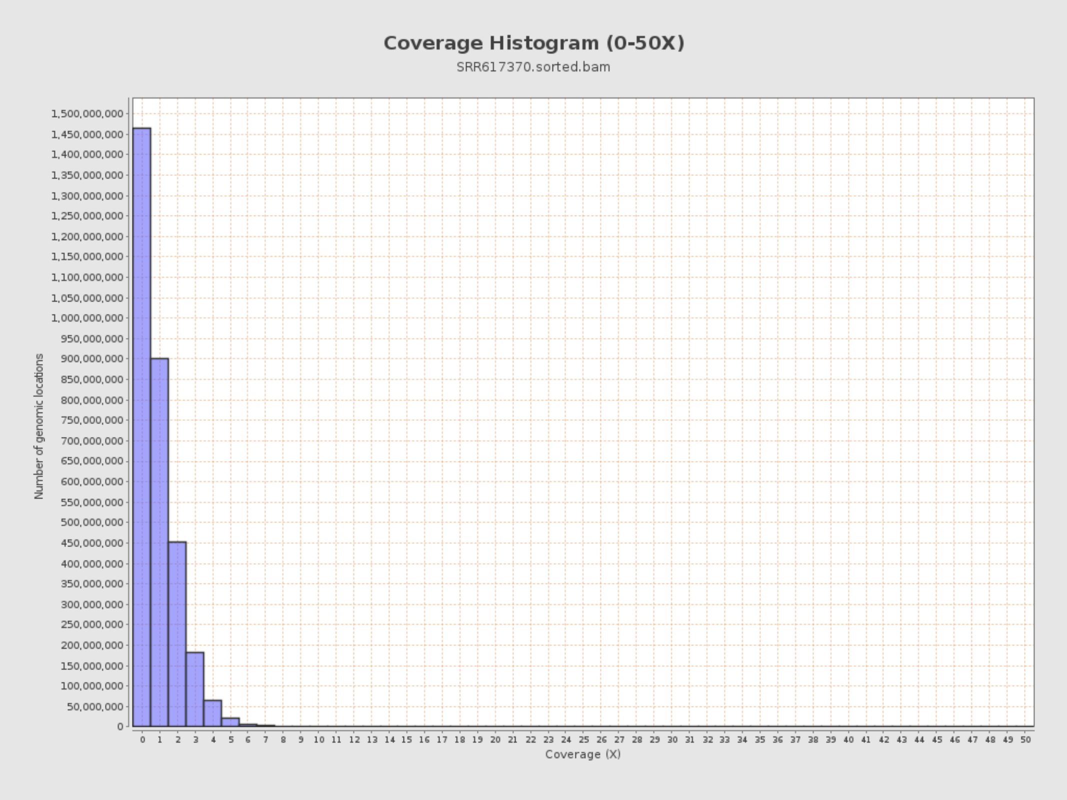
3. Results : Coverage across reference



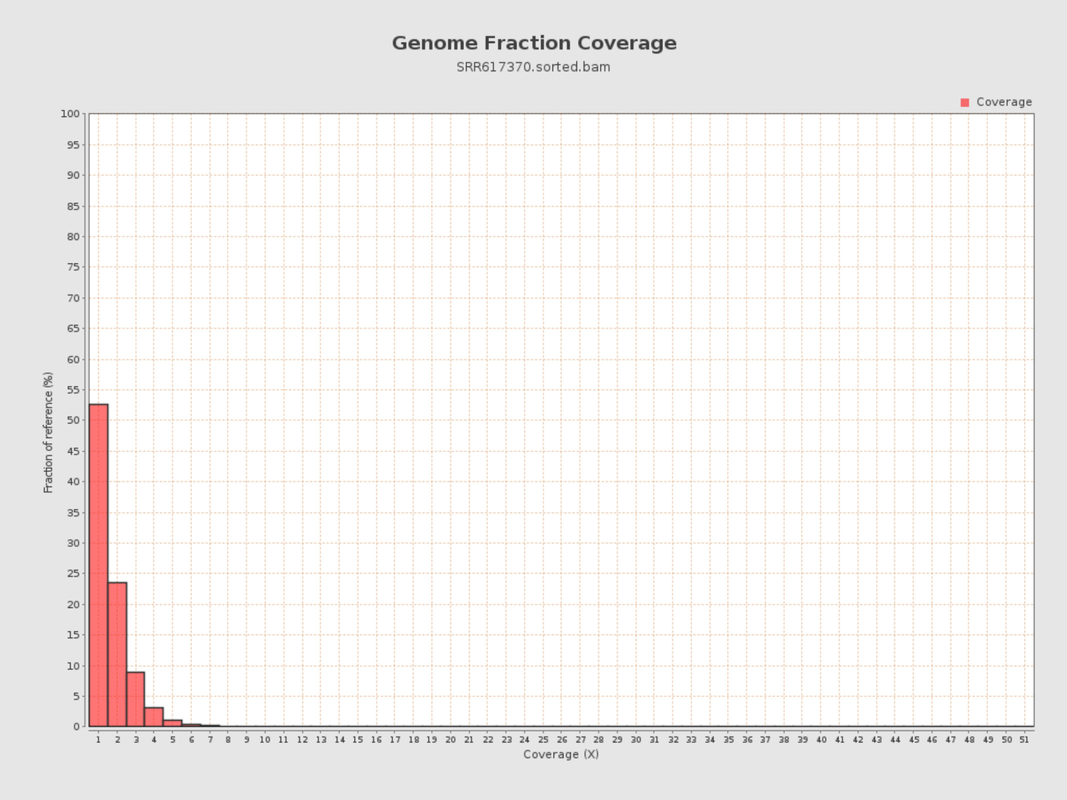
4. Results : Coverage Histogram



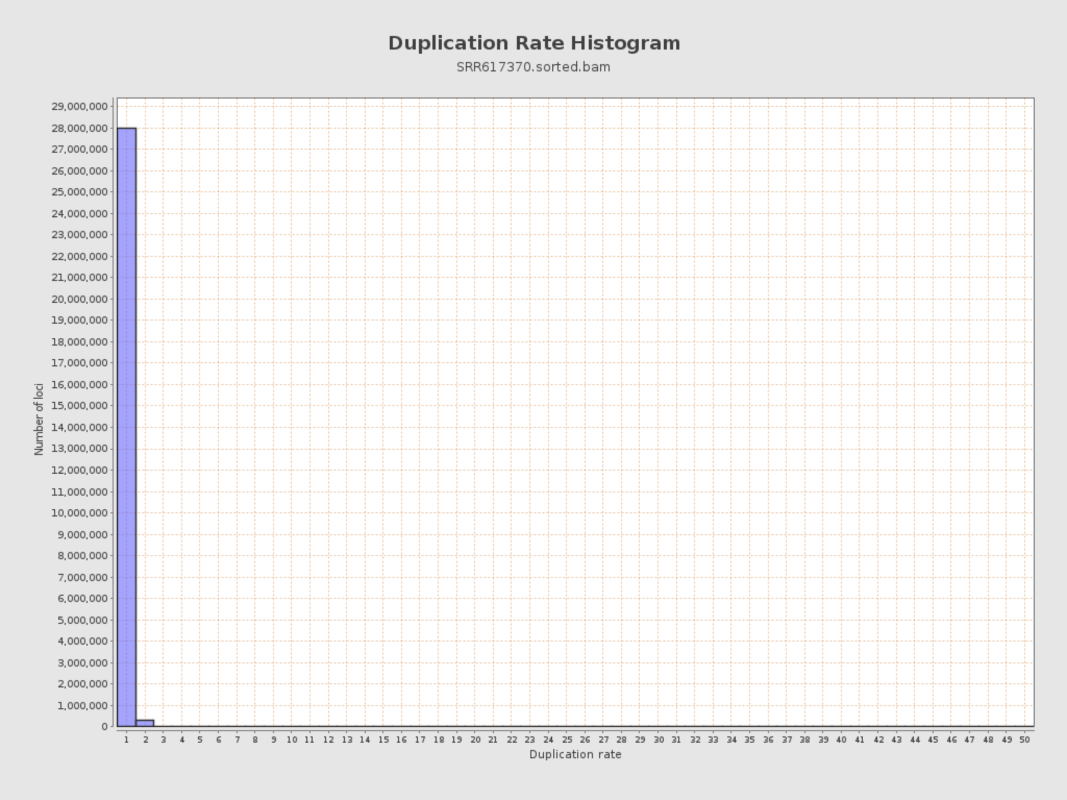
5. Results : Coverage Histogram (0-50X)



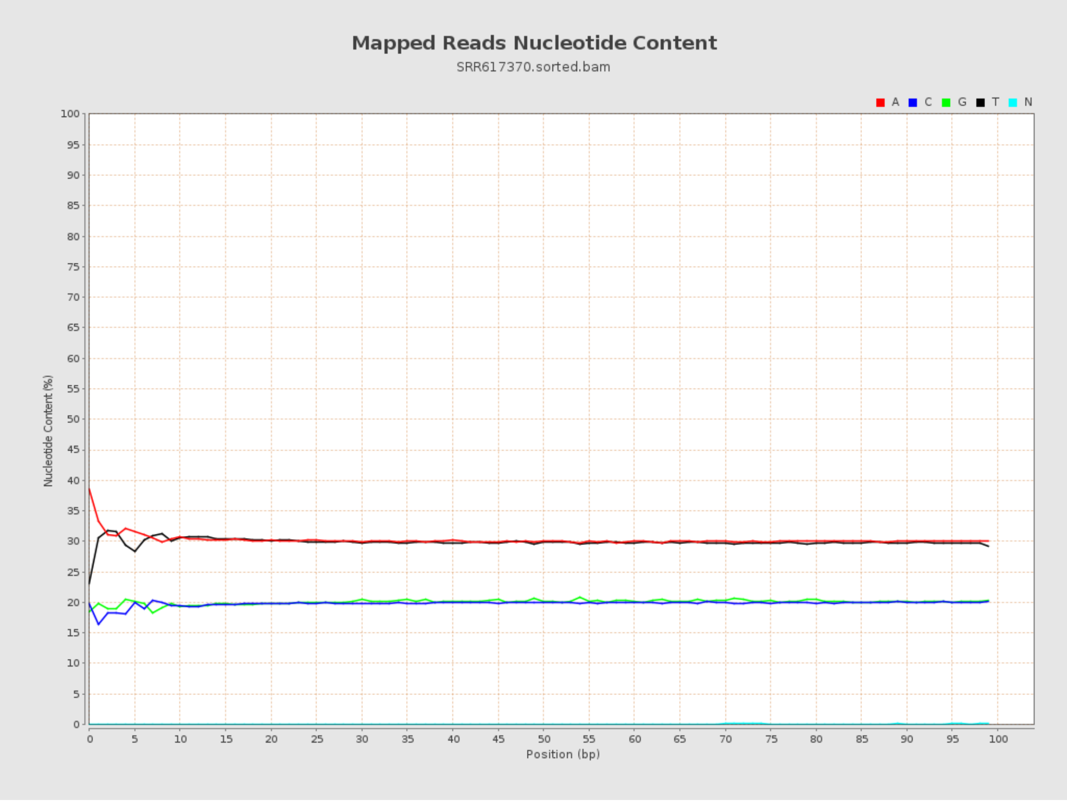
6. Results : Genome Fraction Coverage



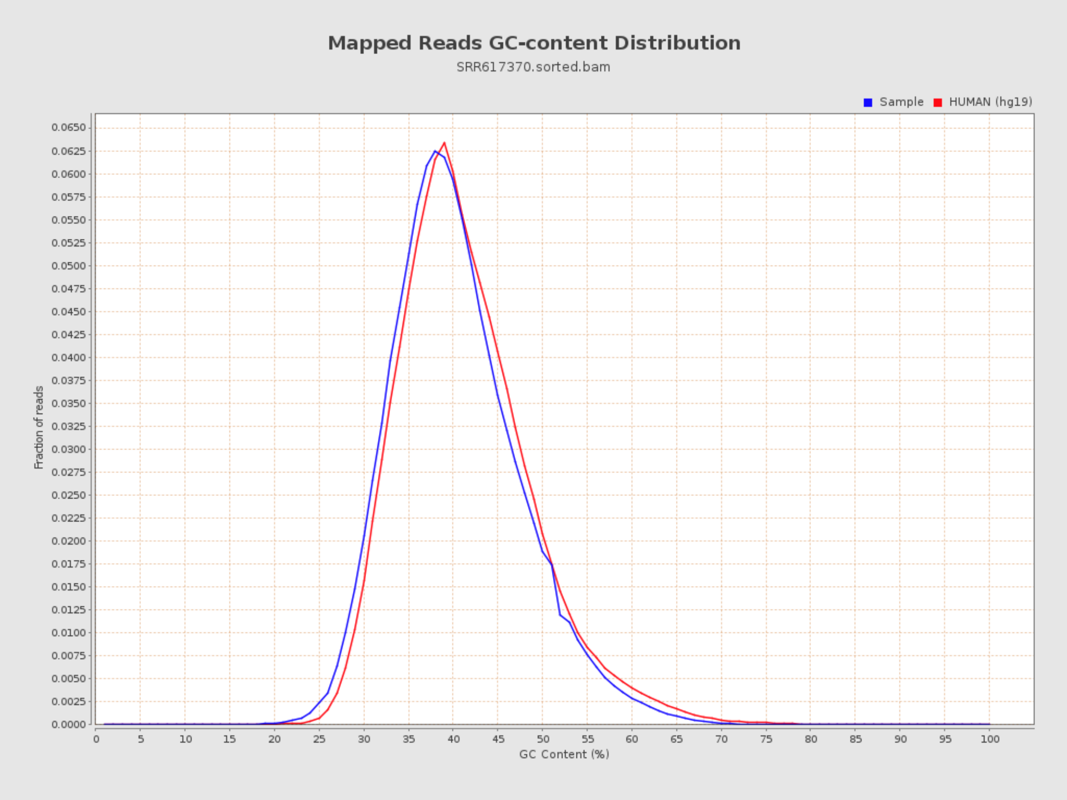
7. Results : Duplication Rate Histogram



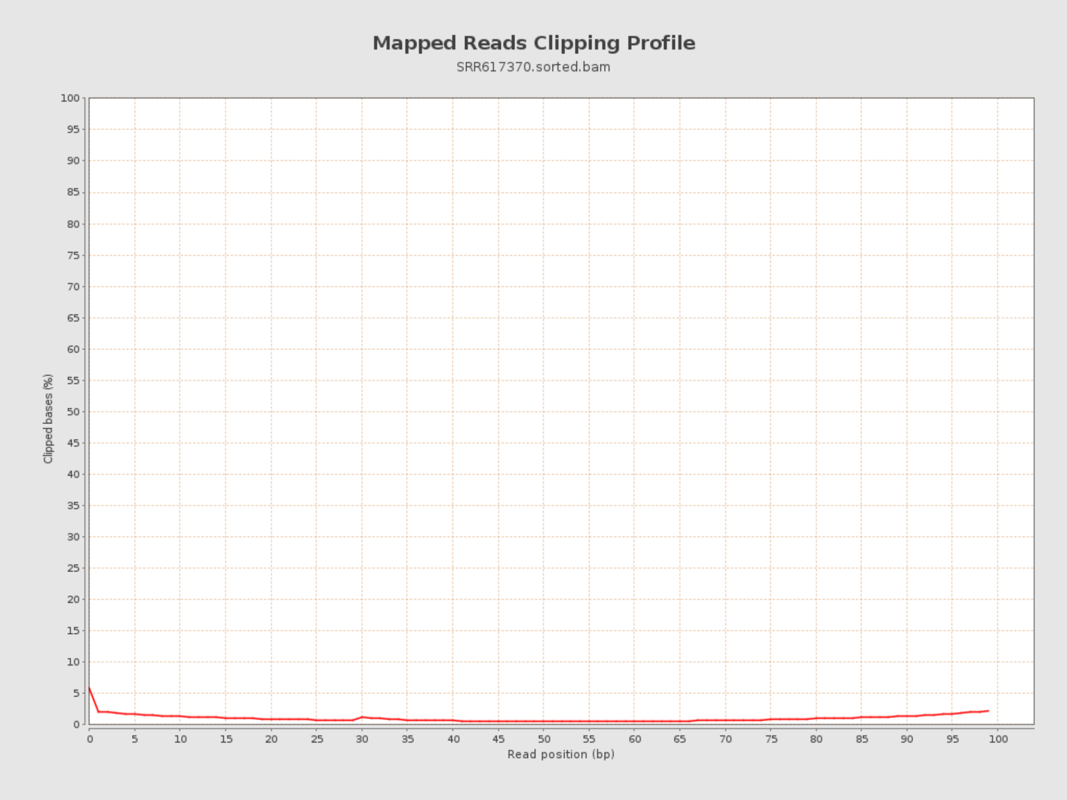
8. Results : Mapped Reads Nucleotide Content



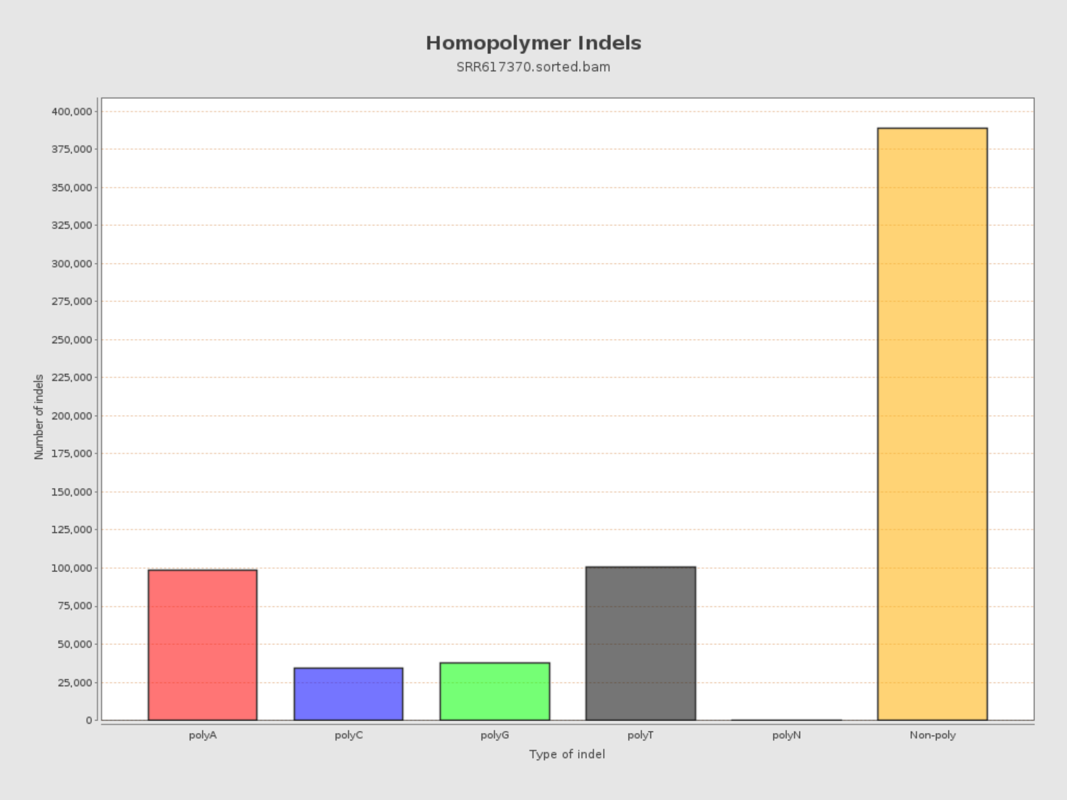
9. Results : Mapped Reads GC-content Distribution



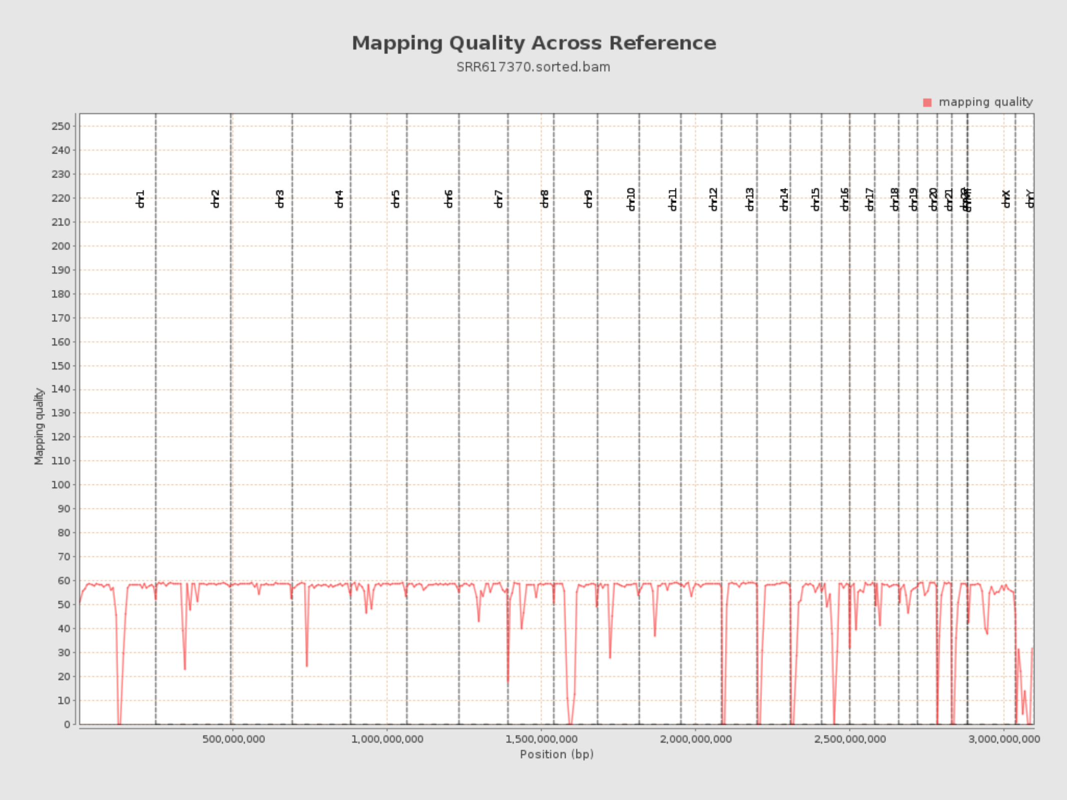
10. Results : Mapped Reads Clipping Profile



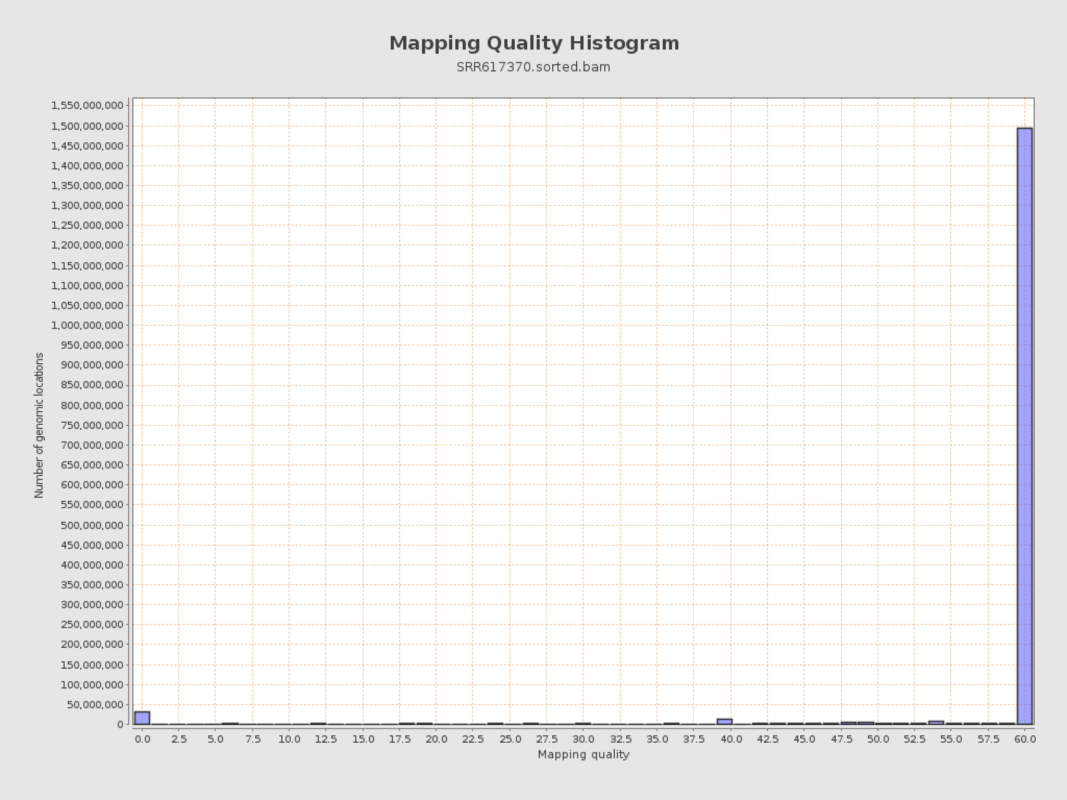
11. Results : Homopolymer Indels



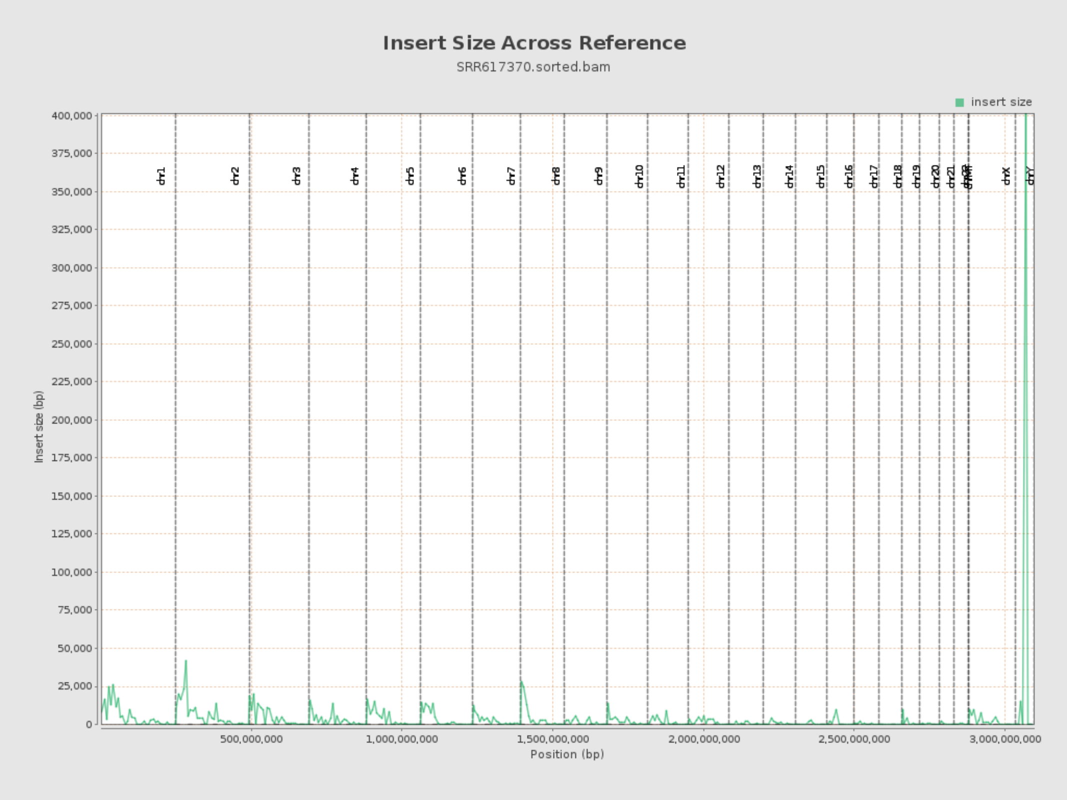
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram