Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 15:10:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617646.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_SRR617646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617646_1.fastq.gz SRR617646_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 15:10:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,703,397 / 95.95%
Unmapped reads	1,296,603 / 4.05%
Mapped paired reads	30,703,397 / 95.95%
Mapped reads, first in pair	15,360,811 / 48%
Mapped reads, second in pair	15,342,586 / 47.95%
Mapped reads, both in pair	30,270,672 / 94.6%
Mapped reads, singletons	432,725 / 1.35%
Secondary alignments	0
Supplementary alignments	141,864 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,204,308 / 22.51%
Duplication rate	10.95%
Clipped reads	6,146,457 / 19.21%

2.2. ACGT Content

Number/percentage of A's	888,790,605 / 29.71%
Number/percentage of C's	597,757,610 / 19.98%
Number/percentage of T's	888,458,227 / 29.7%
Number/percentage of G's	614,156,730 / 20.53%
Number/percentage of N's	2,148,594 / 0.07%

GC Percentage	40.51%

2.3. Coverage

Mean	0.9669
Standard Deviation	10.8793

2.4. Mapping Quality

Mean Mapping Quality	52.75

2.5. Insert size

Mean	30,907.79
Standard Deviation	1,606,343.68
P25/Median/P75	181 / 227 / 297

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	40,524,515
Insertions	467,401
Mapped reads with at least one insertion	1.49%
Deletions	1,101,813
Mapped reads with at least one deletion	3.51%
Homopolymer indels	47.72%

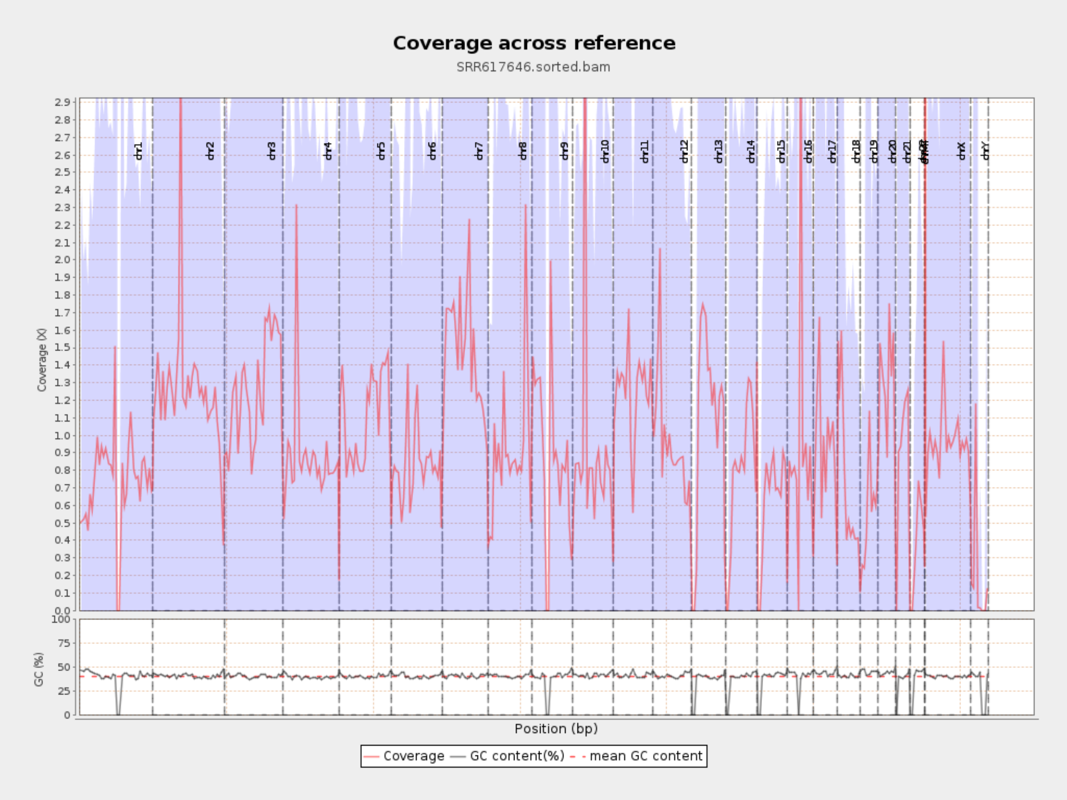
2.7. Chromosome stats

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

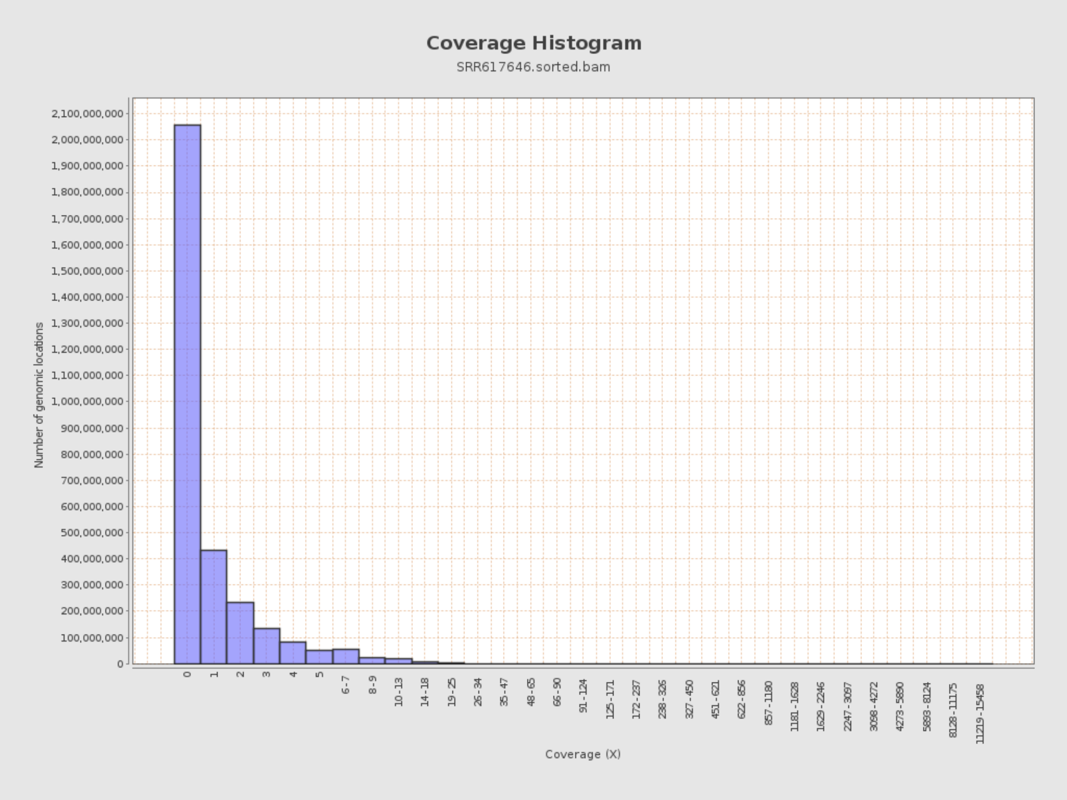
		bases	coverage	deviation
chr1	249250621	183572662	0.7365	10.5063
chr2	243199373	309029098	1.2707	12.4461
chr3	198022430	250582978	1.2654	2.5088
chr4	191154276	167208172	0.8747	8.7346
chr5	180915260	198023581	1.0946	2.3685
chr6	171115067	144740917	0.8459	5.802
chr7	159138663	233895256	1.4698	13.6293
chr8	146364022	132860338	0.9077	4.1367
chr9	141213431	123151307	0.8721	21.4078
chr10	135534747	126923891	0.9365	21.8146
chr11	135006516	164924428	1.2216	12.2632
chr12	133851895	127915944	0.9557	2.1728
chr13	115169878	128405320	1.1149	2.3246
chr14	107349540	85607193	0.7975	2.4994
chr15	102531392	64035463	0.6245	1.6002
chr16	90354753	82686348	0.9151	16.875
chr17	81195210	74241726	0.9144	13.2304
chr18	78077248	55137699	0.7062	18.7623
chr19	59128983	31826877	0.5383	6.1997
chr20	63025520	81317952	1.2902	3.098
chr21	48129895	43801415	0.9101	4.5323
chr22	51304566	19372855	0.3776	1.2899
chrMT	16571	3174287	191.5568	133.8337
chrX	155270560	148577034	0.9569	4.4288

chrY	59373566	12130342	0.2043	18.0354

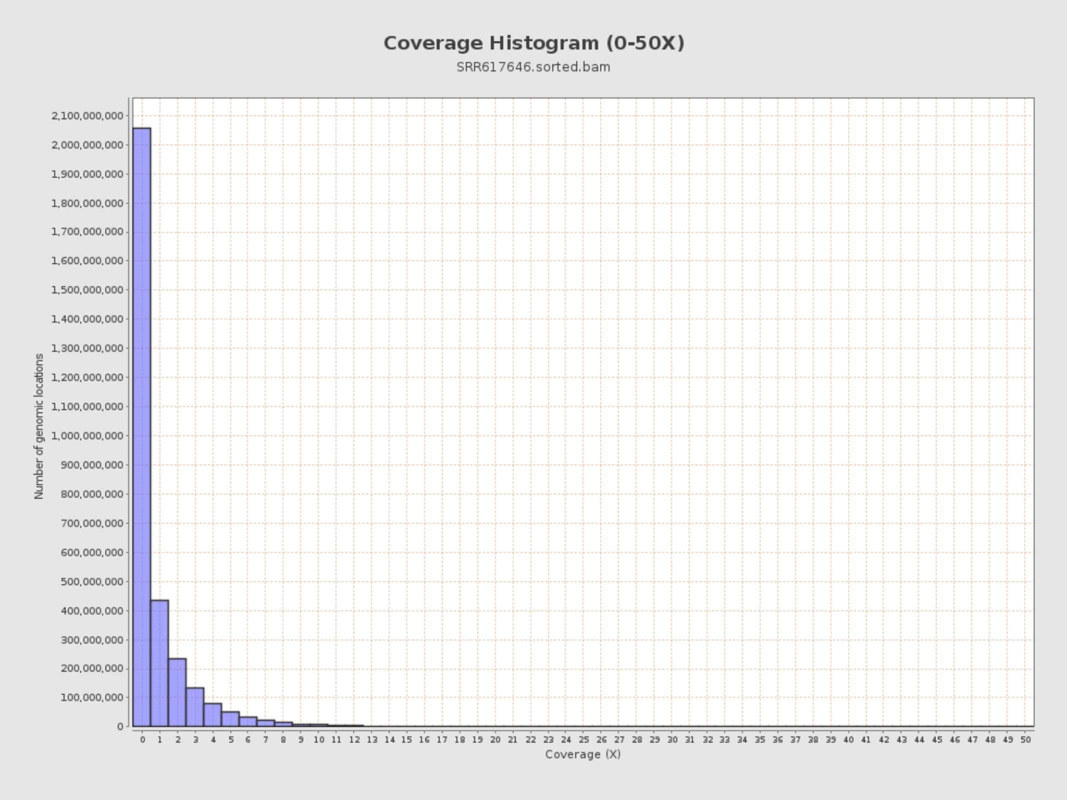
3. Results : Coverage across reference



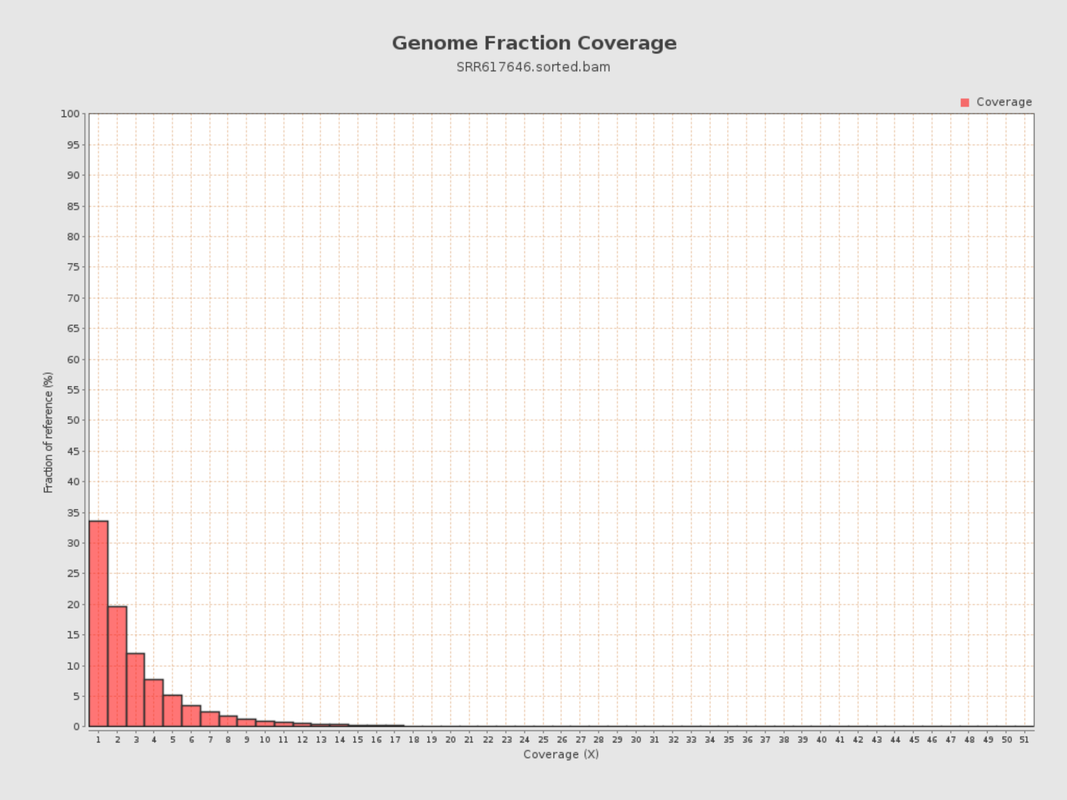
4. Results : Coverage Histogram



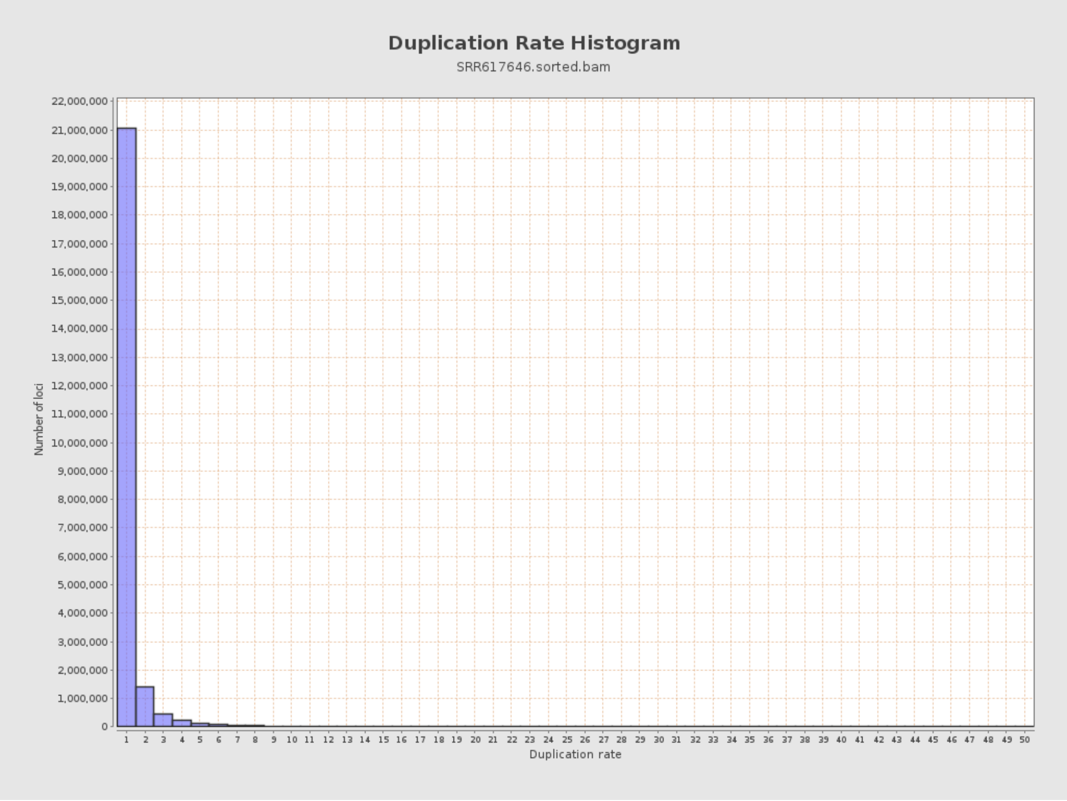
5. Results : Coverage Histogram (0-50X)



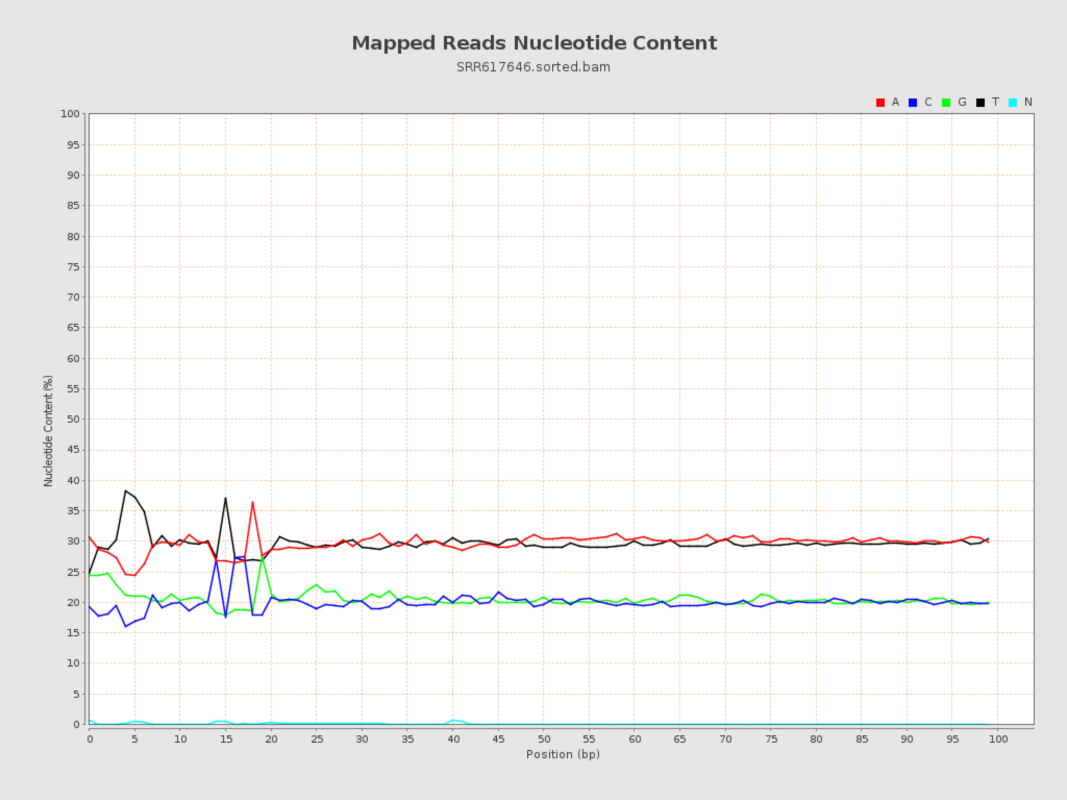
6. Results : Genome Fraction Coverage



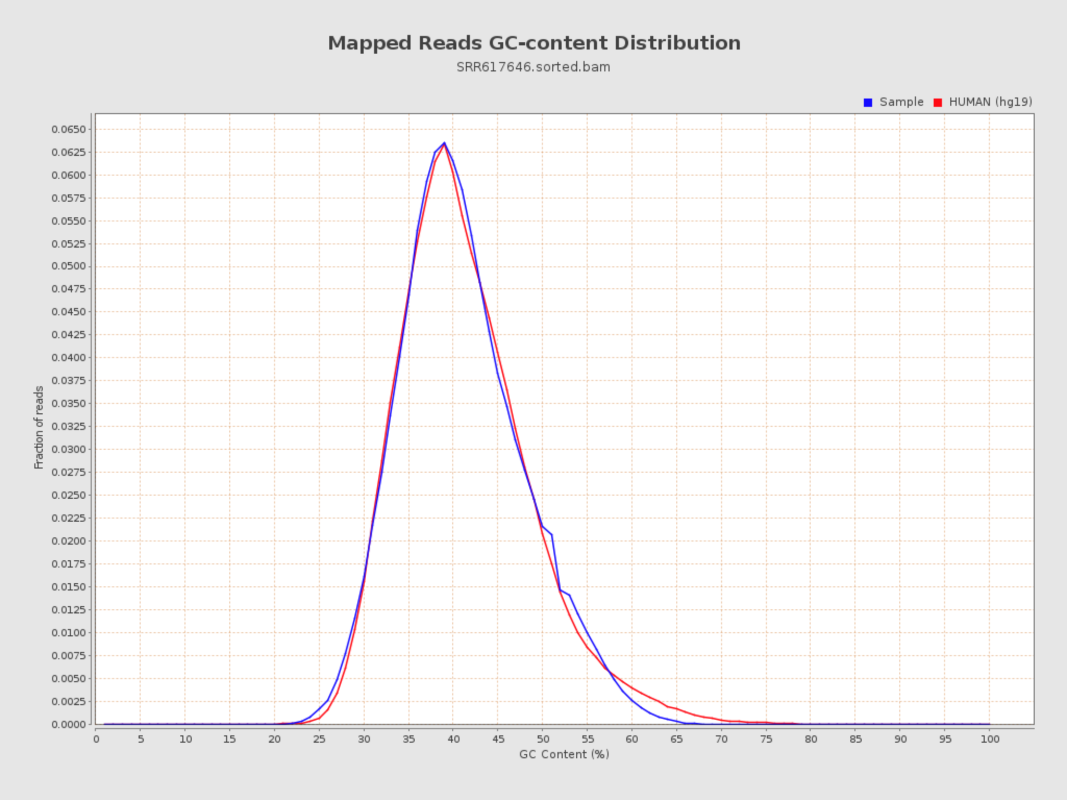
7. Results : Duplication Rate Histogram



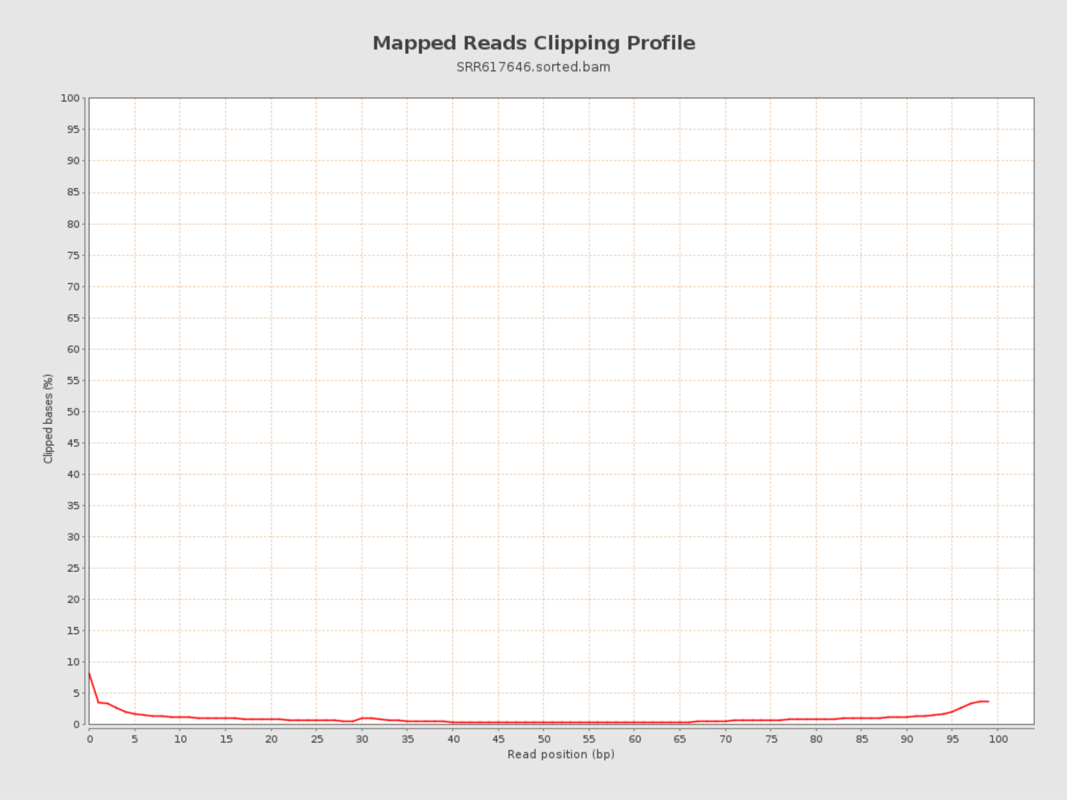
8. Results : Mapped Reads Nucleotide Content



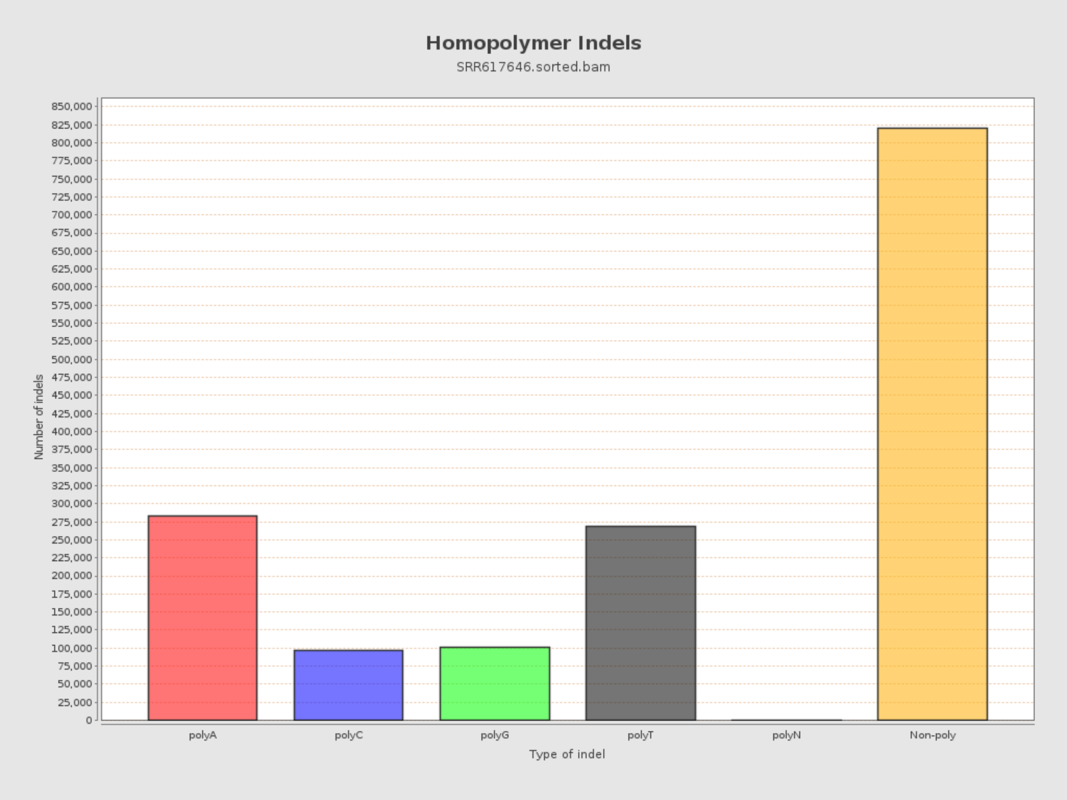
9. Results : Mapped Reads GC-content Distribution



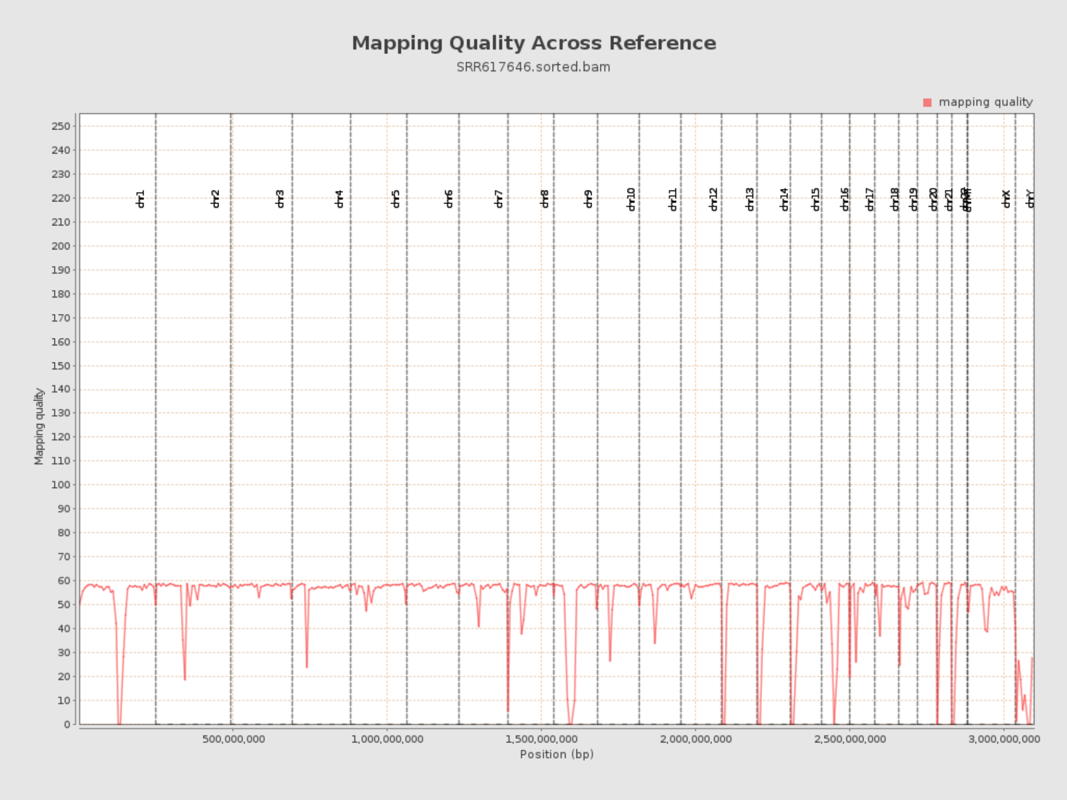
10. Results : Mapped Reads Clipping Profile



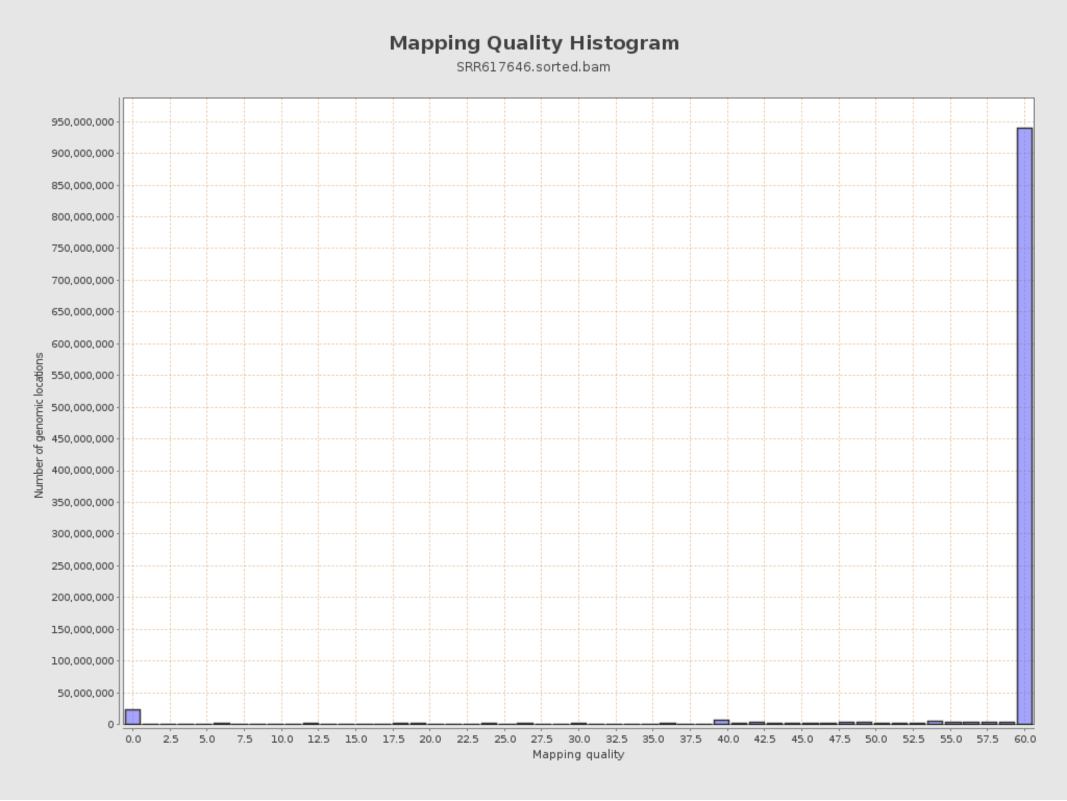
11. Results : Homopolymer Indels



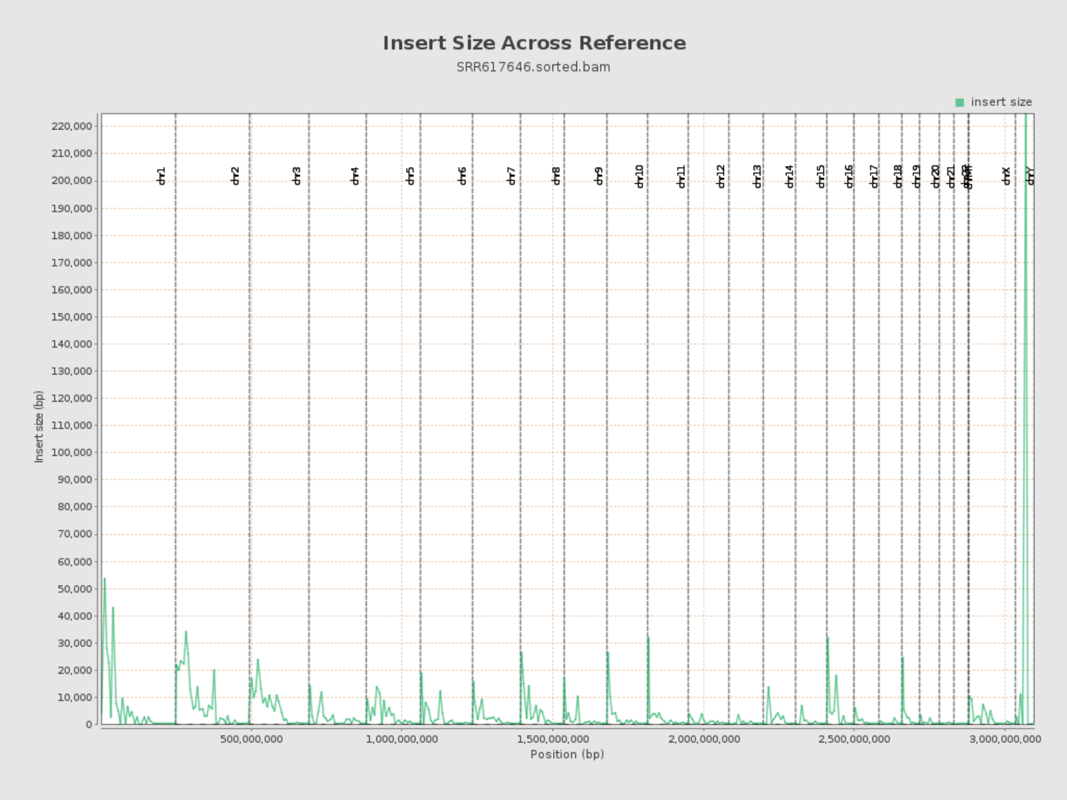
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram