Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 21:27:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617406.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_SRR617406 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617406_1.fastq.gz SRR617406_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 21:27:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617406.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,002,939 / 93.76%
Unmapped reads	1,997,061 / 6.24%
Mapped paired reads	30,002,939 / 93.76%
Mapped reads, first in pair	15,144,166 / 47.33%
Mapped reads, second in pair	14,858,773 / 46.43%
Mapped reads, both in pair	29,394,788 / 91.86%
Mapped reads, singletons	608,151 / 1.9%
Secondary alignments	0
Supplementary alignments	487,175 / 1.52%
Read min/max/mean length	30 / 100 / 100.62
Duplicated reads (estimated)	1,406,478 / 4.4%
Duplication rate	4.2%
Clipped reads	3,255,559 / 10.17%

2.2. ACGT Content

Number/percentage of A's	880,977,866 / 29.85%
Number/percentage of C's	592,830,528 / 20.09%
Number/percentage of T's	872,701,998 / 29.57%
Number/percentage of G's	603,821,152 / 20.46%
Number/percentage of N's	882,638 / 0.03%

GC Percentage	40.55%

2.3. Coverage

Mean	0.9535
Standard Deviation	2.9292

2.4. Mapping Quality

Mean Mapping Quality	53.88

2.5. Insert size

Mean	57,498.21
Standard Deviation	2,286,240.86
P25/Median/P75	170 / 209 / 270

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	27,715,072
Insertions	252,352
Mapped reads with at least one insertion	0.83%
Deletions	287,319
Mapped reads with at least one deletion	0.94%
Homopolymer indels	44.57%

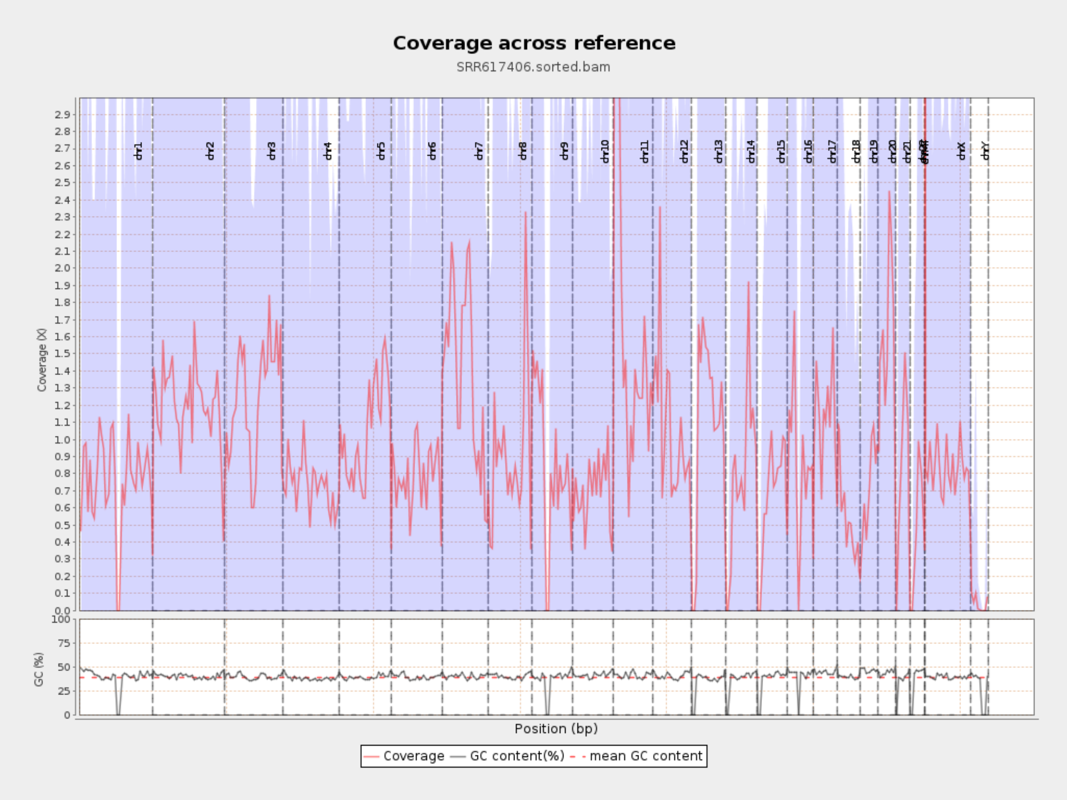
2.7. Chromosome stats

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

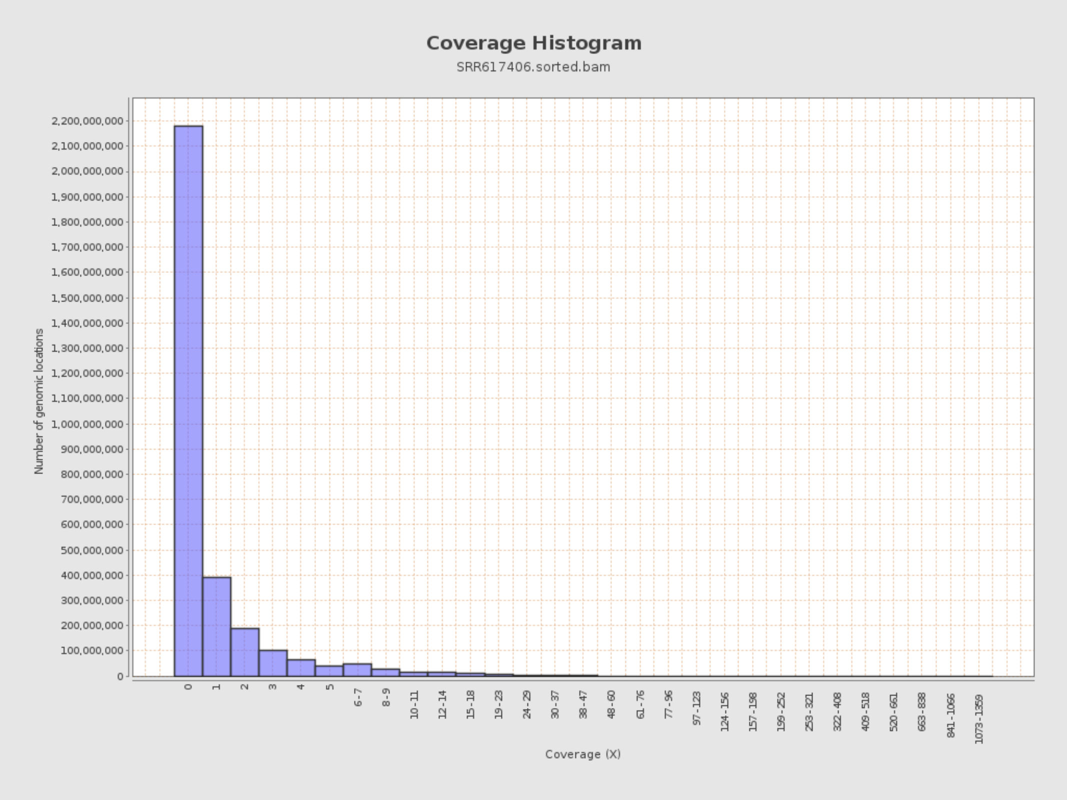
		bases	coverage	deviation
chr1	249250621	190389513	0.7638	2.7363
chr2	243199373	294594120	1.2113	3.1146
chr3	198022430	249126338	1.2581	3.4198
chr4	191154276	141618920	0.7409	2.2751
chr5	180915260	189130033	1.0454	2.8686
chr6	171115067	135000899	0.7889	2.5912
chr7	159138663	221009463	1.3888	3.2365
chr8	146364022	130531491	0.8918	3.2629
chr9	141213431	118045684	0.8359	2.6176
chr10	135534747	94636528	0.6982	2.4215
chr11	135006516	218957929	1.6218	3.8275
chr12	133851895	140491483	1.0496	2.8052
chr13	115169878	127830984	1.1099	2.7626
chr14	107349540	85886913	0.8001	2.8979
chr15	102531392	67500443	0.6583	2.3673
chr16	90354753	74446027	0.8239	3.3103
chr17	81195210	91211849	1.1234	3.7136
chr18	78077248	42094059	0.5391	1.9988
chr19	59128983	42111088	0.7122	2.3376
chr20	63025520	101018799	1.6028	4.7342
chr21	48129895	40452593	0.8405	2.5085
chr22	51304566	23834155	0.4646	2.0806
chrMT	16571	183639	11.082	5.2944
chrX	155270560	129384059	0.8333	2.5697

chrY	59373566	2376171	0.04	0.6141

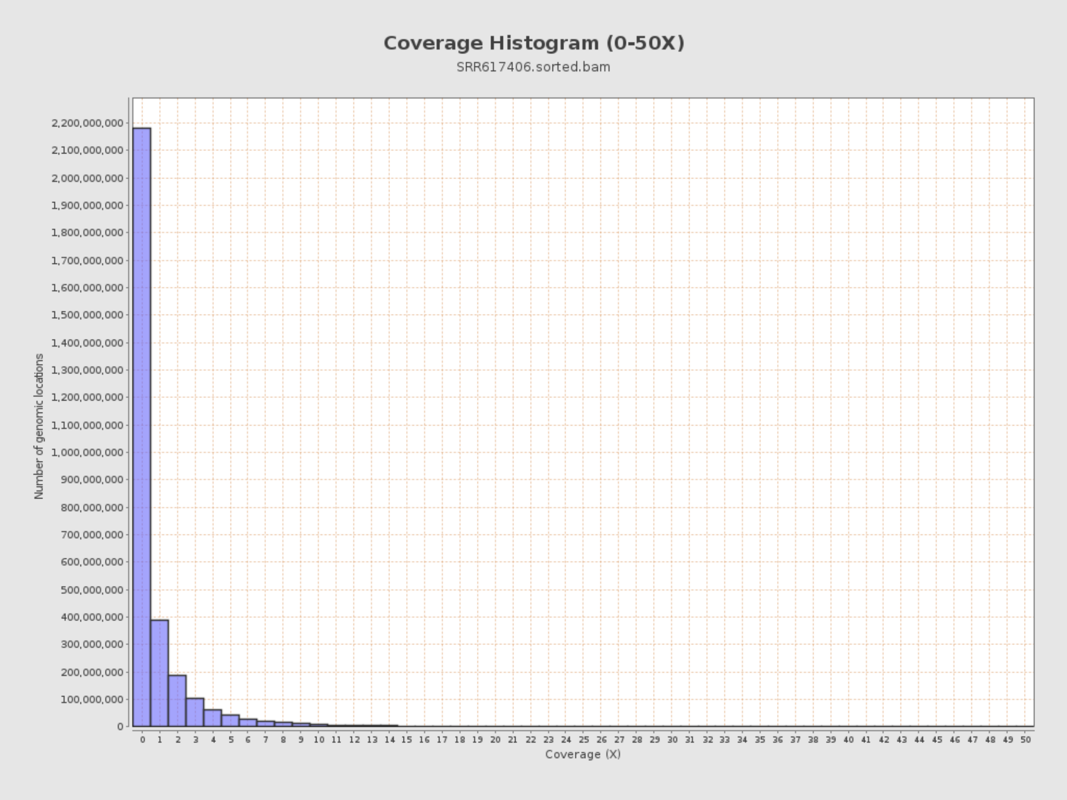
3. Results : Coverage across reference



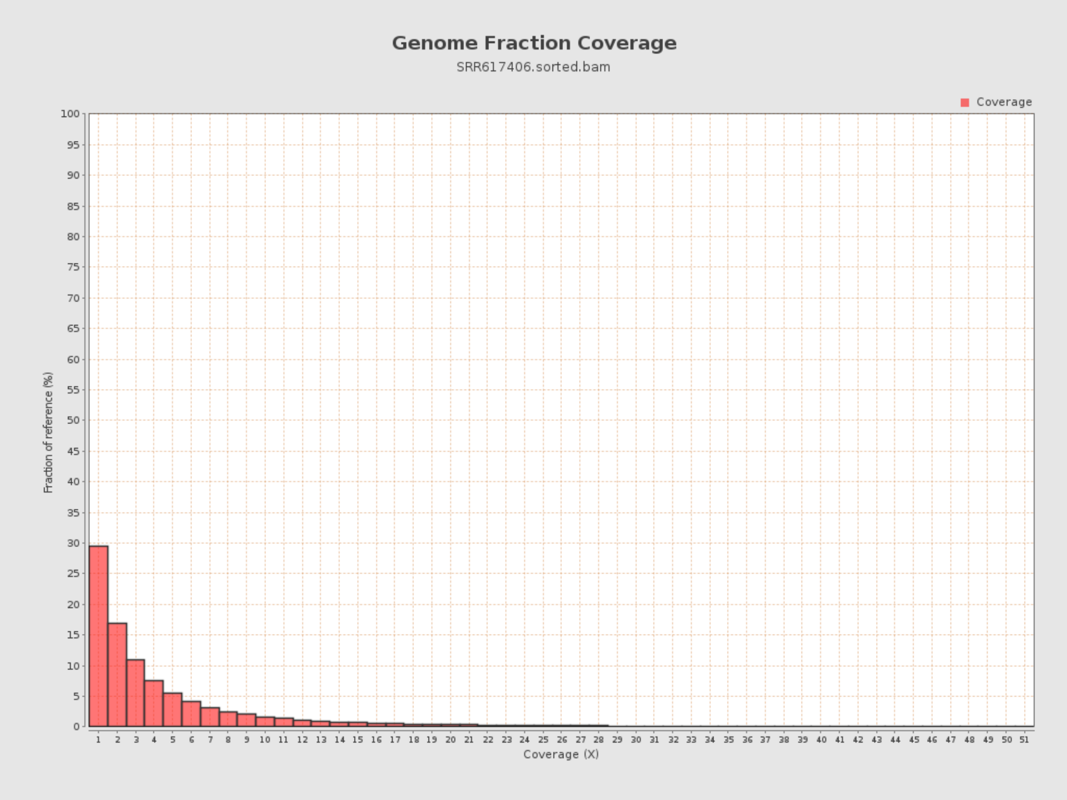
4. Results : Coverage Histogram



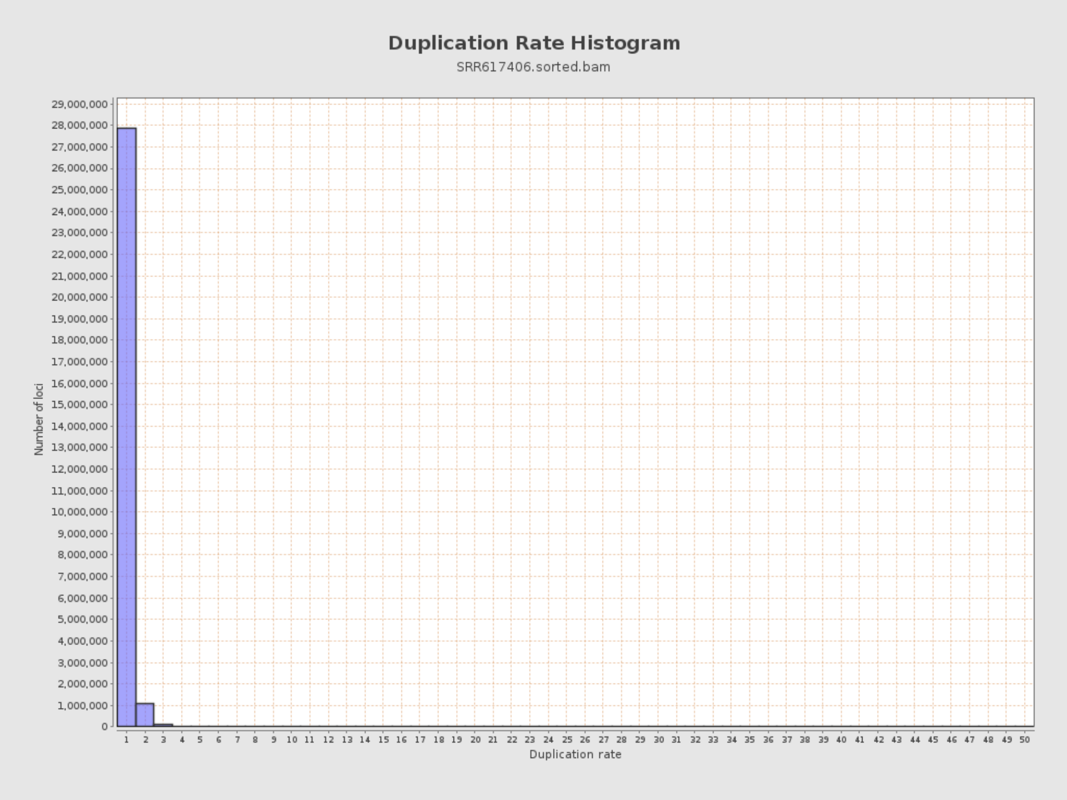
5. Results : Coverage Histogram (0-50X)



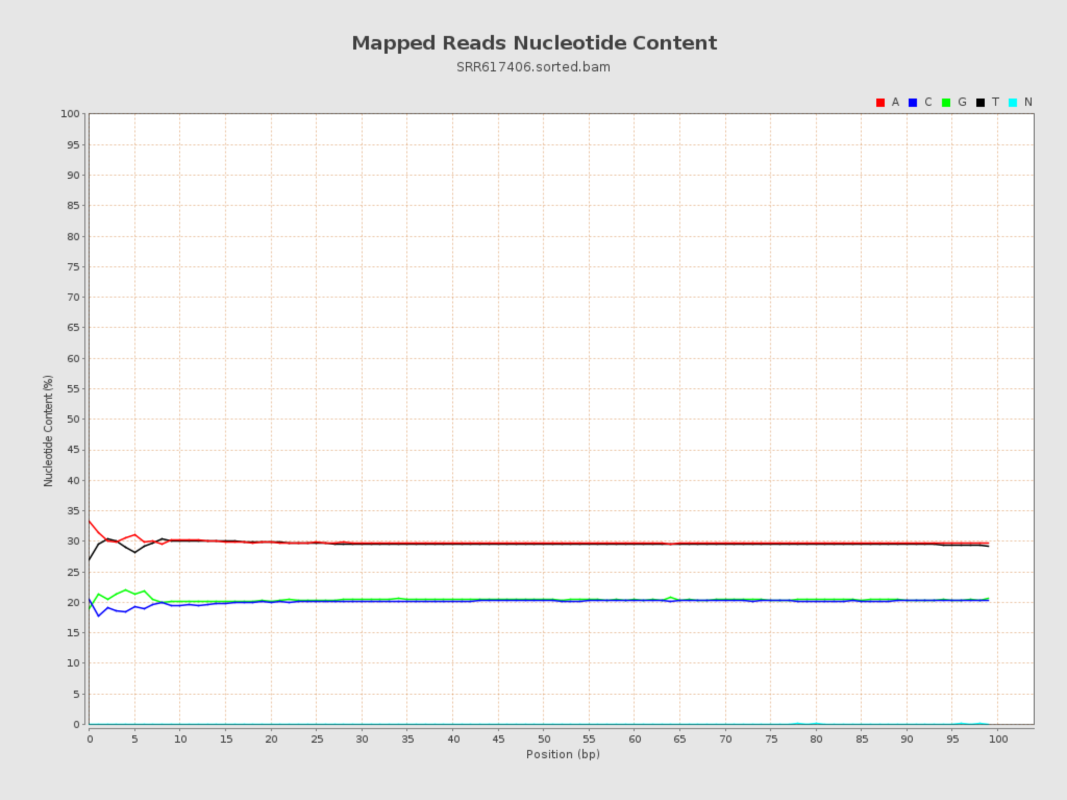
6. Results : Genome Fraction Coverage



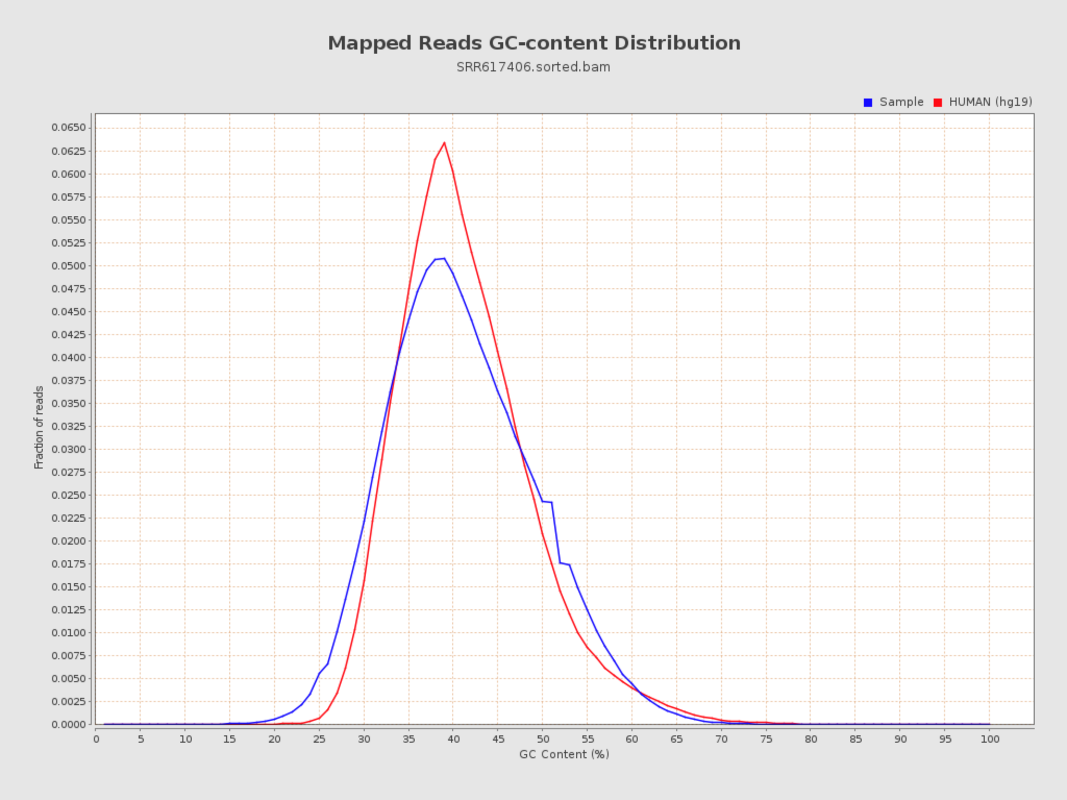
7. Results : Duplication Rate Histogram



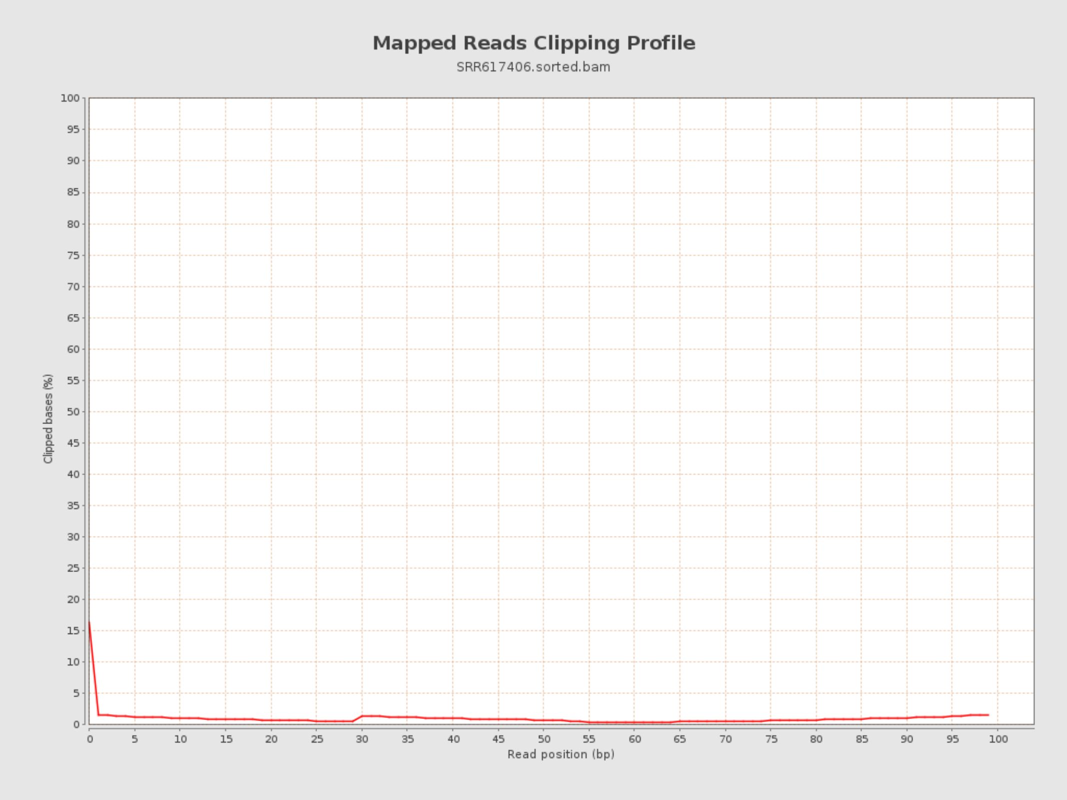
8. Results : Mapped Reads Nucleotide Content



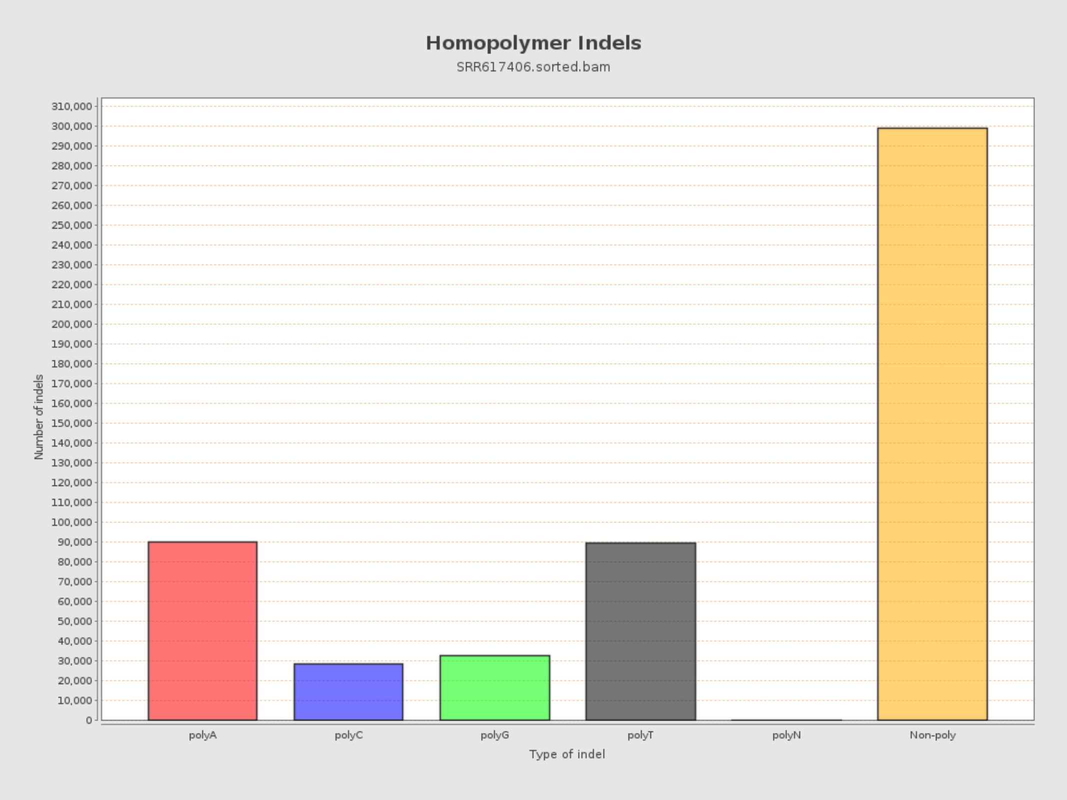
9. Results : Mapped Reads GC-content Distribution



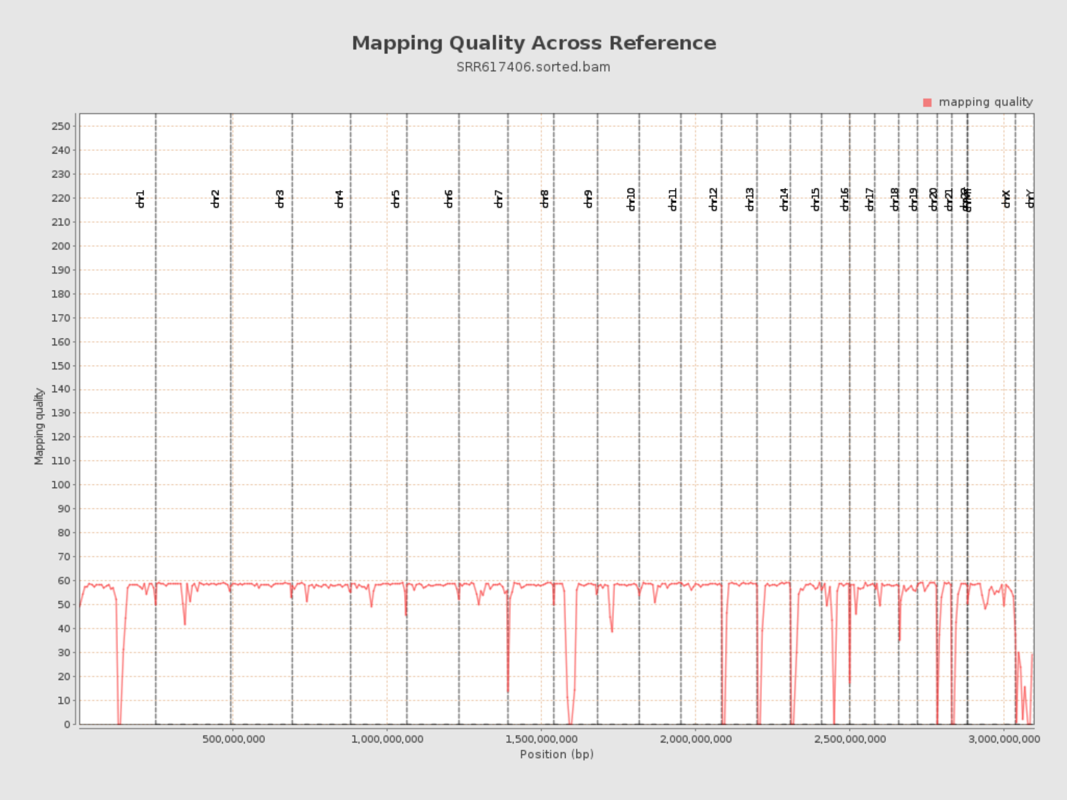
10. Results : Mapped Reads Clipping Profile



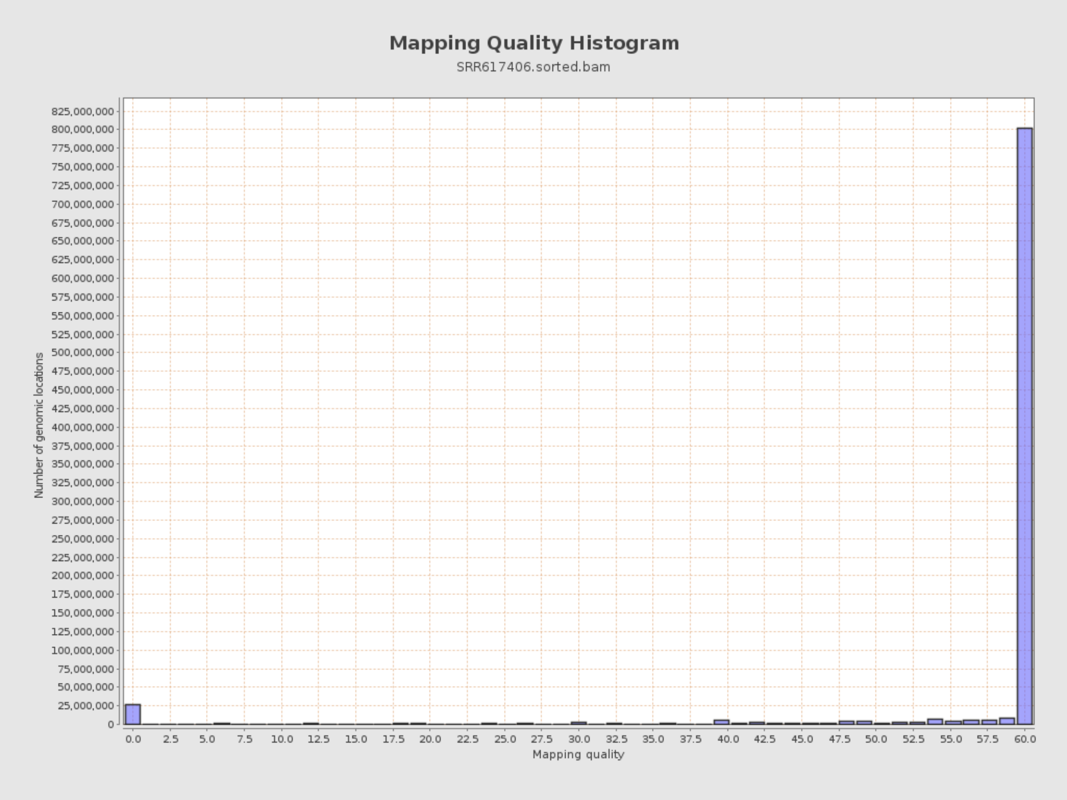
11. Results : Homopolymer Indels



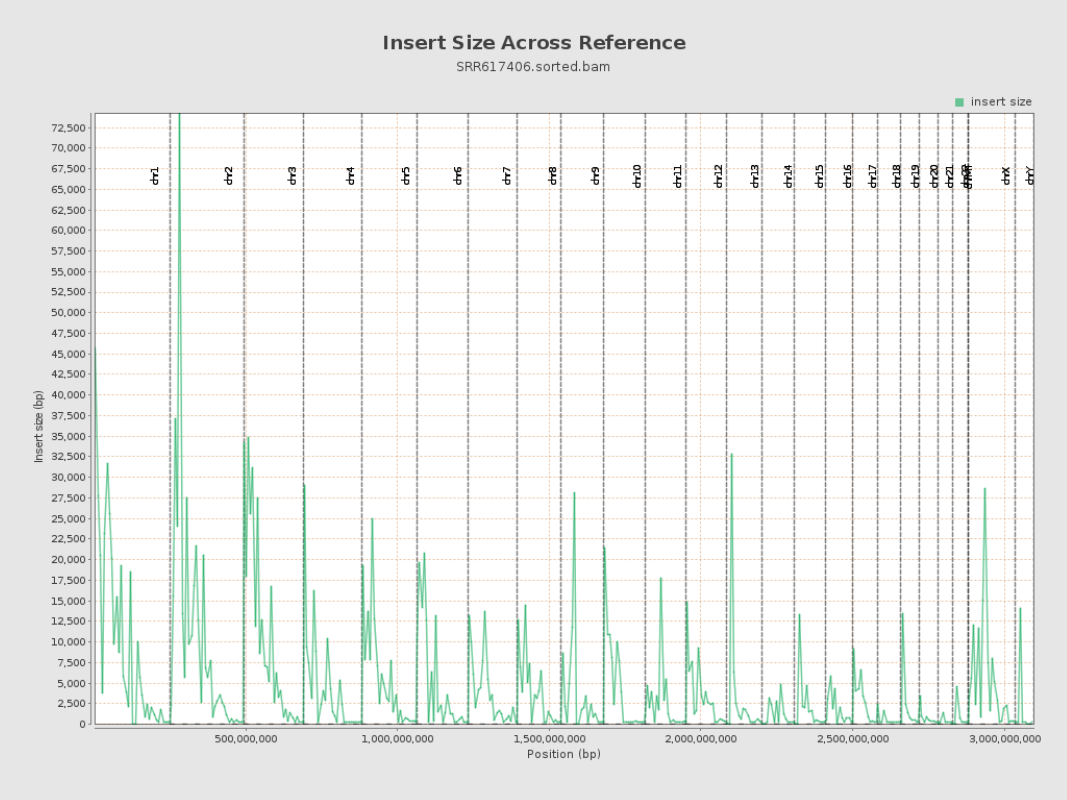
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram