Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 23:15:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617409.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_SRR617409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617409_1.fastq.gz SRR617409_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 23:15:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,762,935 / 93.01%
Unmapped reads	2,237,065 / 6.99%
Mapped paired reads	29,762,935 / 93.01%
Mapped reads, first in pair	15,002,900 / 46.88%
Mapped reads, second in pair	14,760,035 / 46.13%
Mapped reads, both in pair	29,219,894 / 91.31%
Mapped reads, singletons	543,041 / 1.7%
Secondary alignments	0
Supplementary alignments	447,149 / 1.4%
Read min/max/mean length	30 / 100 / 100.58
Duplicated reads (estimated)	1,347,977 / 4.21%
Duplication rate	4.13%
Clipped reads	3,357,371 / 10.49%

2.2. ACGT Content

Number/percentage of A's	874,213,825 / 29.88%
Number/percentage of C's	586,921,361 / 20.06%
Number/percentage of T's	864,165,052 / 29.53%
Number/percentage of G's	598,386,755 / 20.45%
Number/percentage of N's	2,463,254 / 0.08%

GC Percentage	40.51%

2.3. Coverage

Mean	0.9454
Standard Deviation	2.8868

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	47,711.54
Standard Deviation	2,073,353.64
P25/Median/P75	170 / 208 / 268

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	33,089,007
Insertions	235,271
Mapped reads with at least one insertion	0.78%
Deletions	282,423
Mapped reads with at least one deletion	0.93%
Homopolymer indels	44.71%

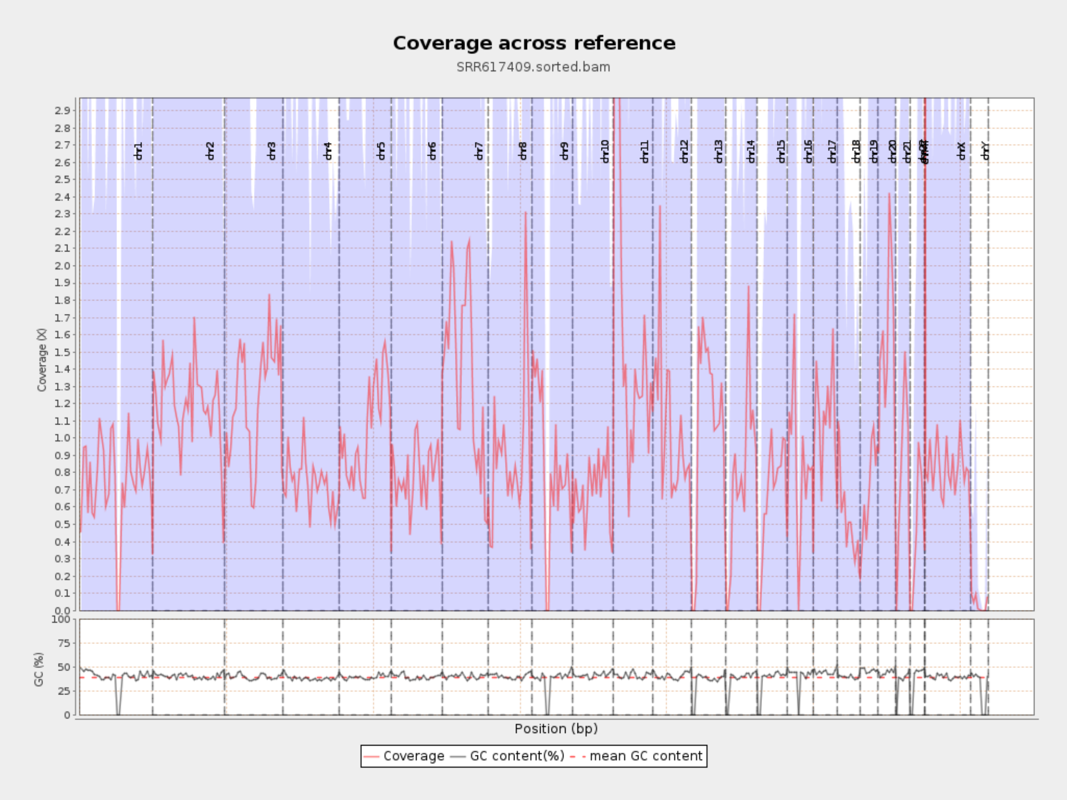
2.7. Chromosome stats

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

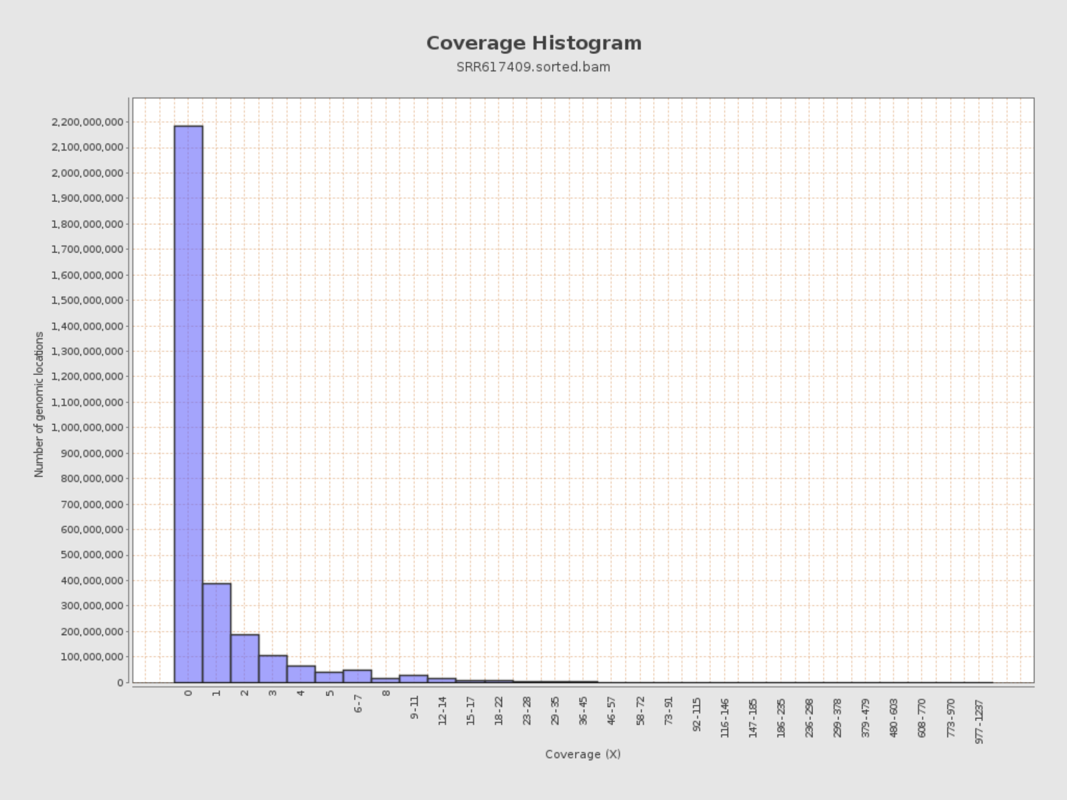
		bases	coverage	deviation
chr1	249250621	188160087	0.7549	2.7143
chr2	243199373	292305335	1.2019	3.0401
chr3	198022430	247446966	1.2496	3.3764
chr4	191154276	141150528	0.7384	2.2575
chr5	180915260	187630763	1.0371	2.8406
chr6	171115067	134197810	0.7843	2.5715
chr7	159138663	219403528	1.3787	3.2034
chr8	146364022	129522281	0.8849	3.2114
chr9	141213431	117340148	0.8309	2.584
chr10	135534747	93779318	0.6919	2.3708
chr11	135006516	217063697	1.6078	3.7871
chr12	133851895	139319292	1.0408	2.7455
chr13	115169878	126969989	1.1025	2.7397
chr14	107349540	84712140	0.7891	2.8532
chr15	102531392	67056671	0.654	2.3315
chr16	90354753	73376058	0.8121	3.2577
chr17	81195210	89825902	1.1063	3.604
chr18	78077248	41891400	0.5365	1.9749
chr19	59128983	41465591	0.7013	2.2846
chr20	63025520	99445895	1.5779	4.6509
chr21	48129895	40150456	0.8342	2.4932
chr22	51304566	23444303	0.457	2.0487
chrMT	16571	179060	10.8056	5.2515
chrX	155270560	128627281	0.8284	2.5322

chrY	59373566	2316635	0.039	0.5553

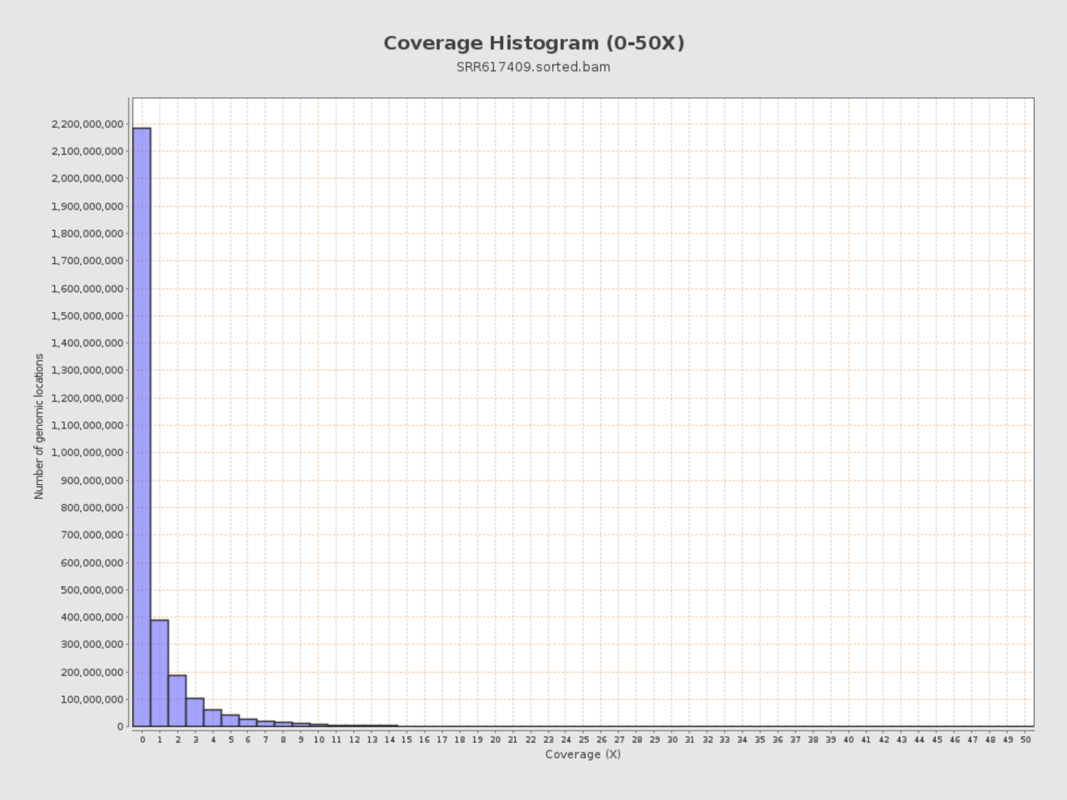
3. Results : Coverage across reference



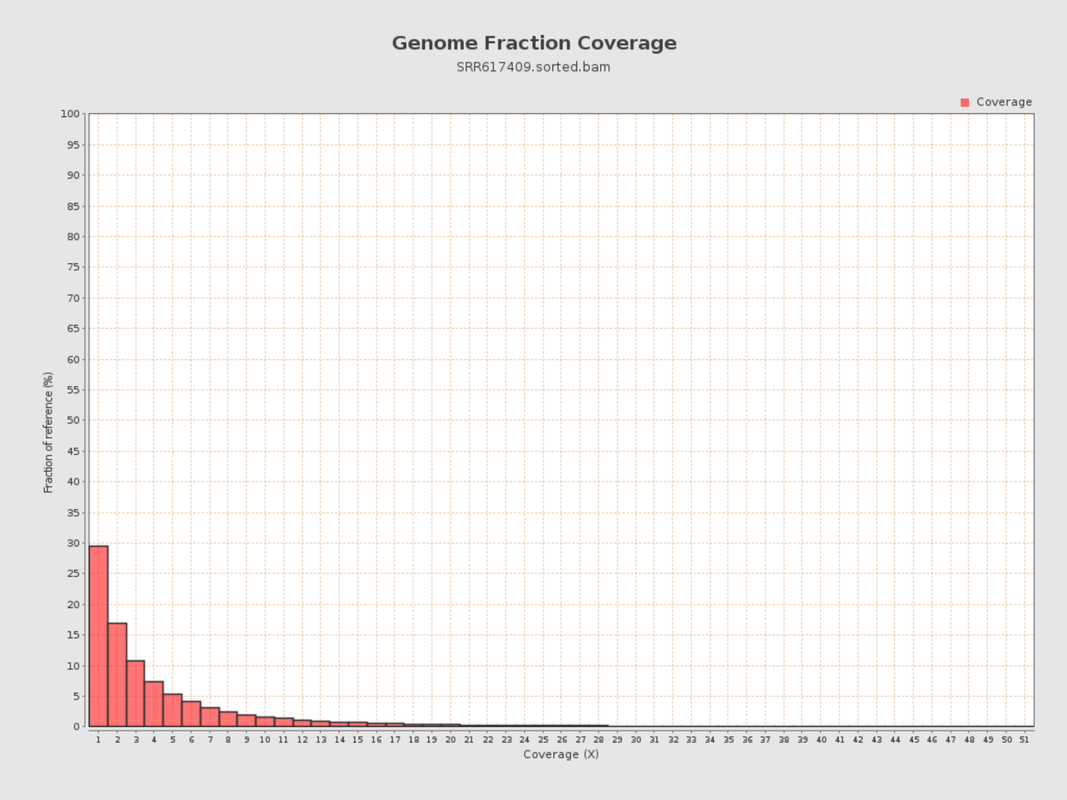
4. Results : Coverage Histogram



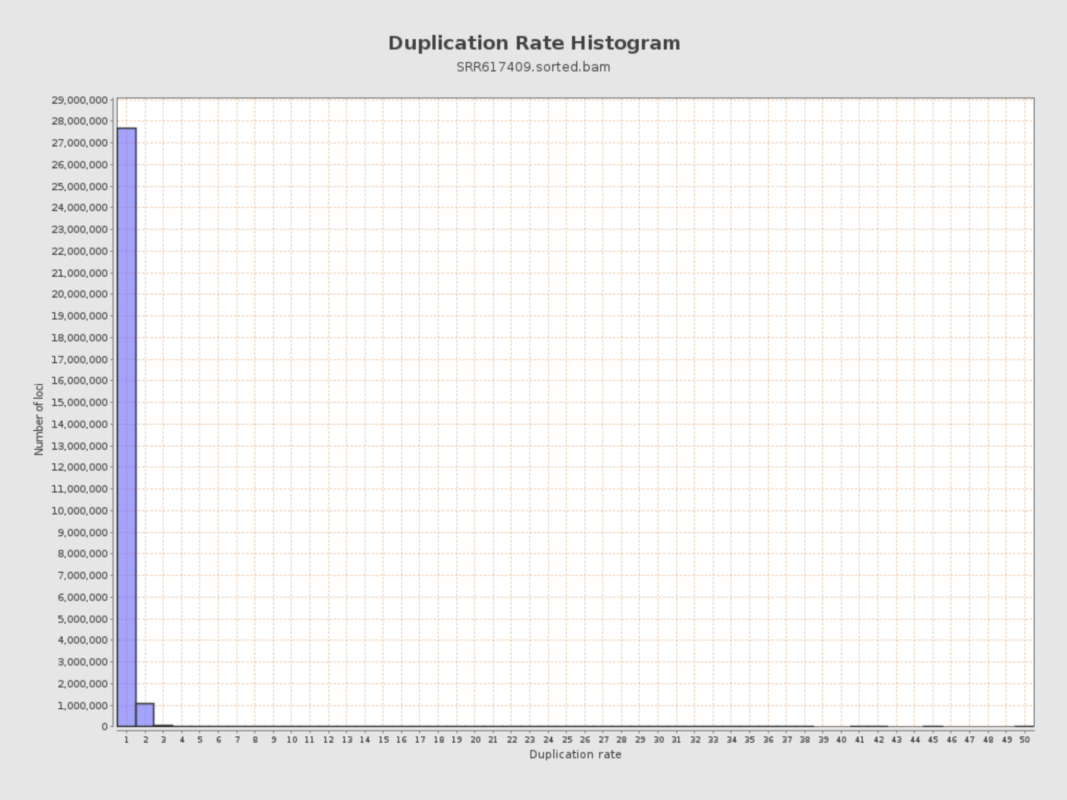
5. Results : Coverage Histogram (0-50X)



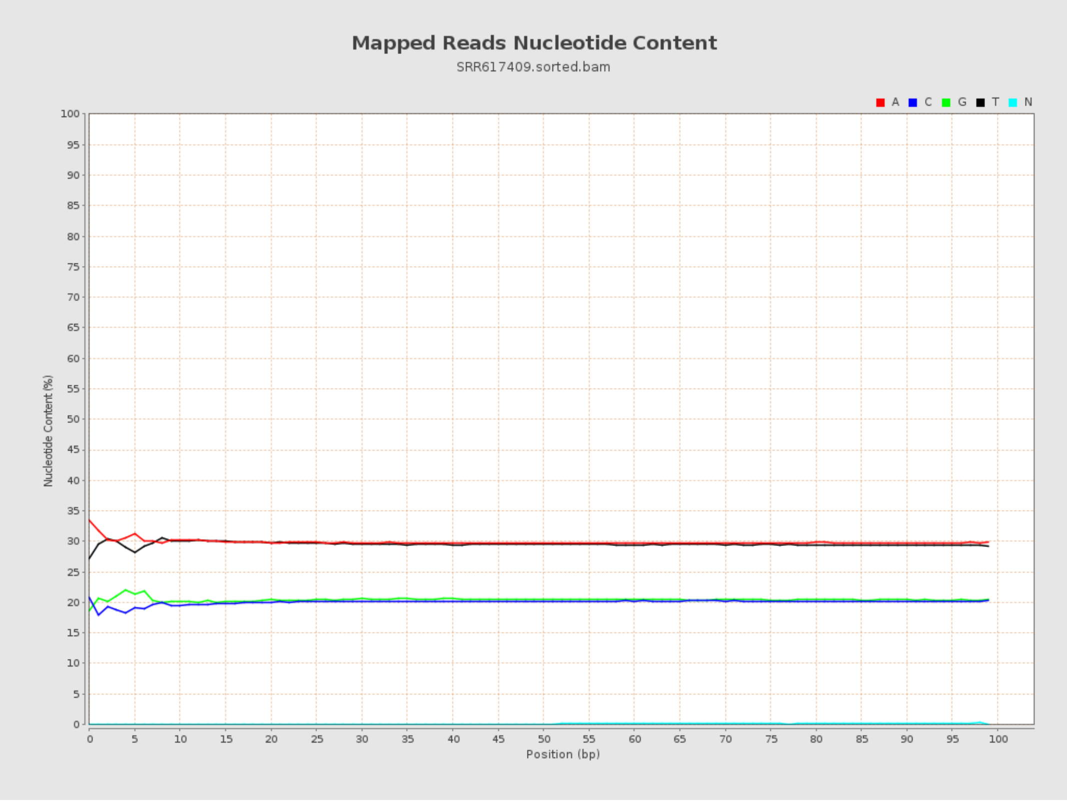
6. Results : Genome Fraction Coverage



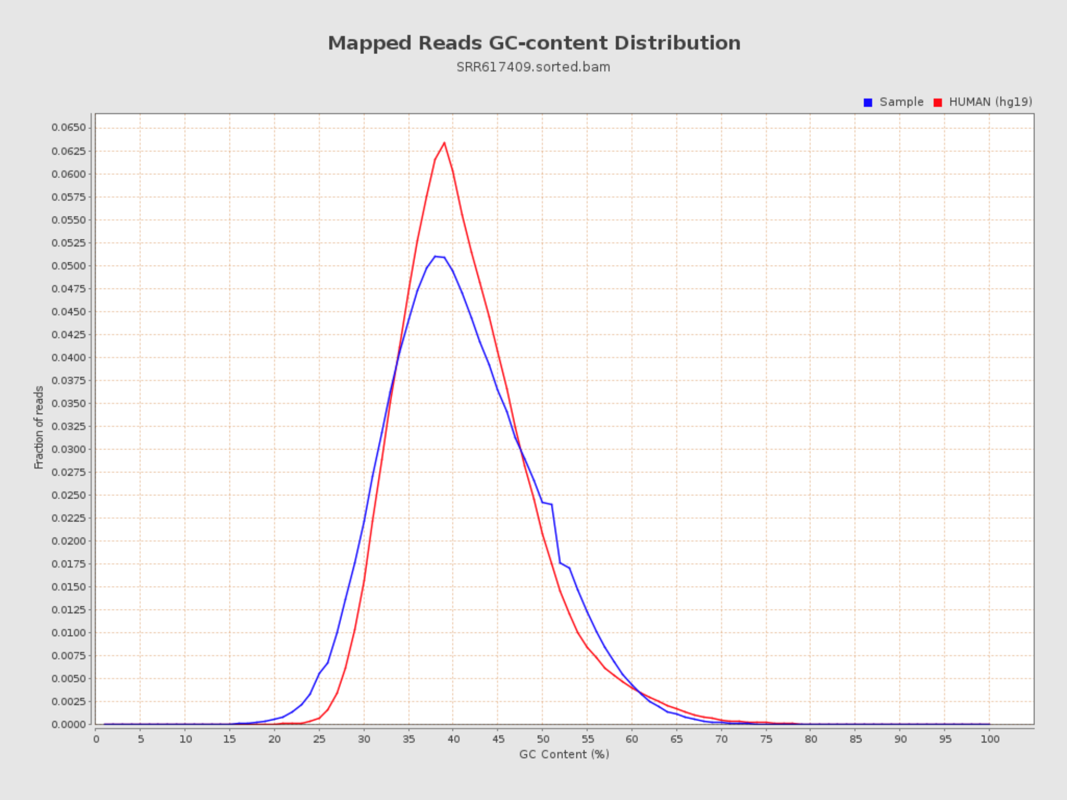
7. Results : Duplication Rate Histogram



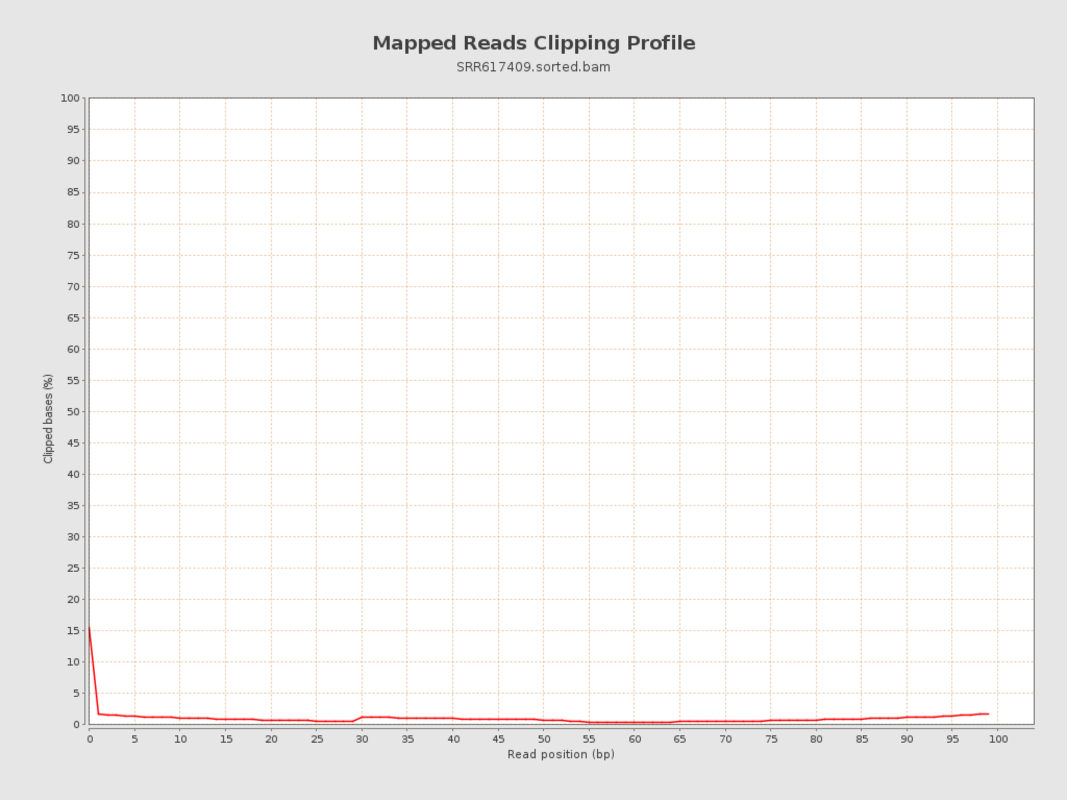
8. Results : Mapped Reads Nucleotide Content



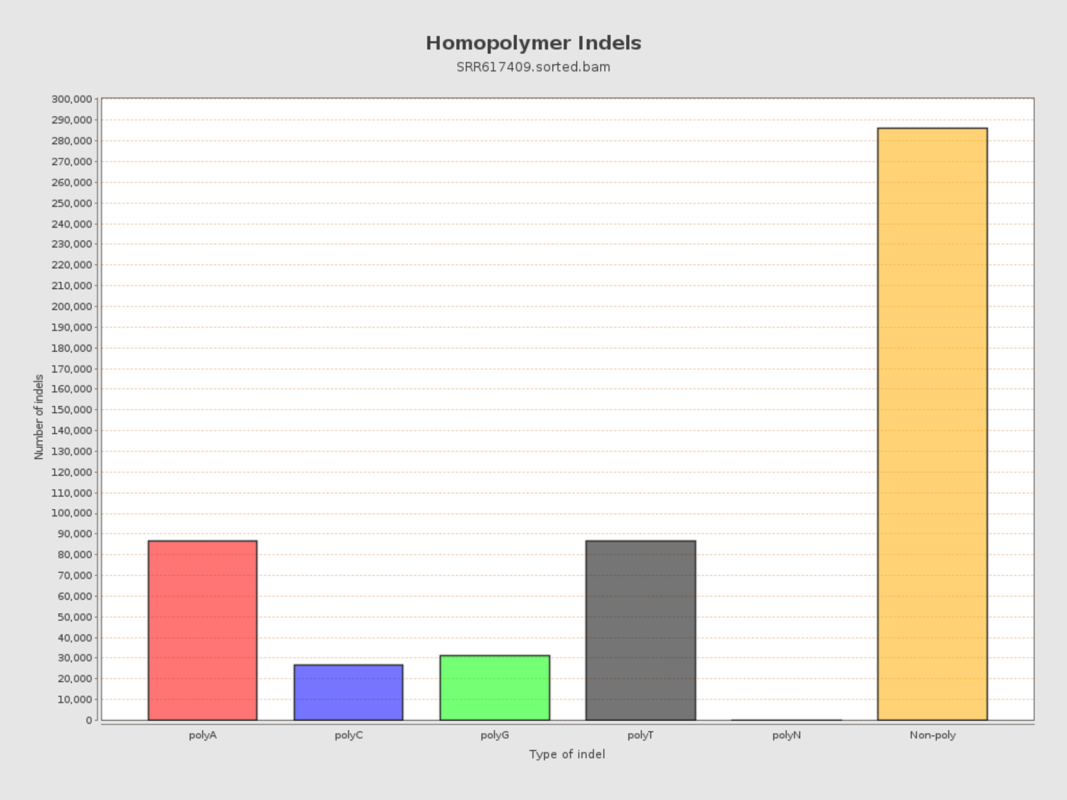
9. Results : Mapped Reads GC-content Distribution



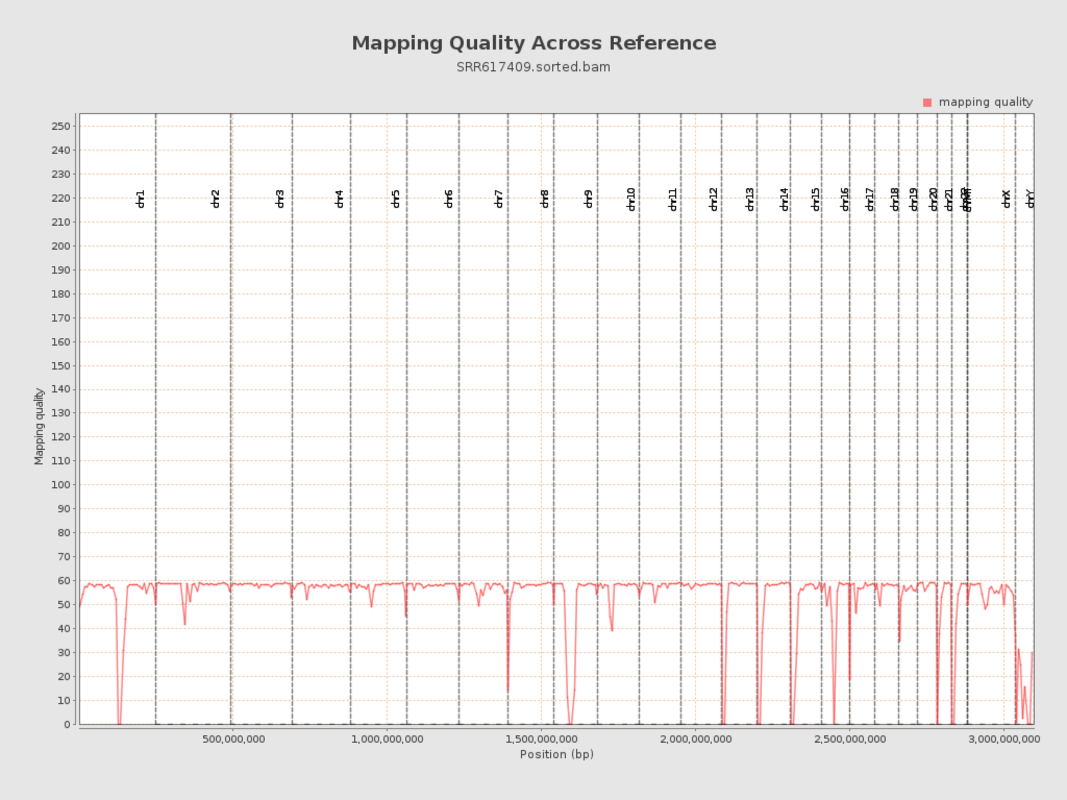
10. Results : Mapped Reads Clipping Profile



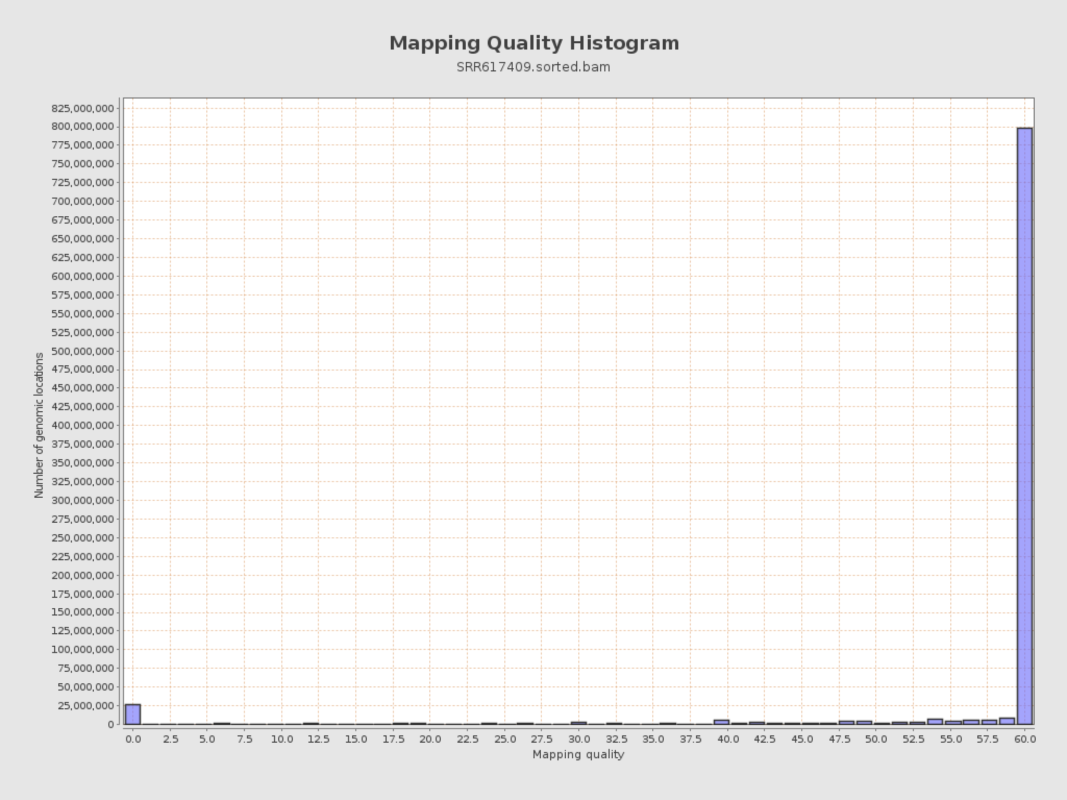
11. Results : Homopolymer Indels



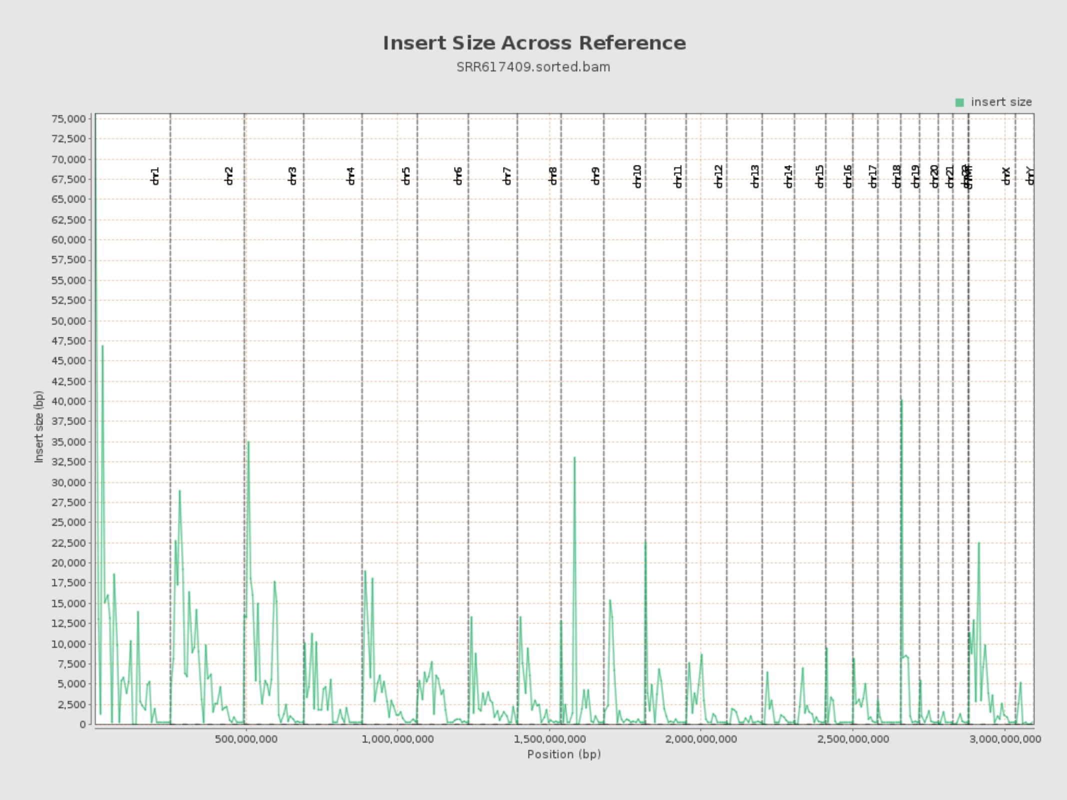
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram