Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 23:53:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617499.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_SRR617499 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617499_1.fastq.gz SRR617499_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 23:53:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617499.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,678,712 / 95.87%
Unmapped reads	1,321,288 / 4.13%
Mapped paired reads	30,678,712 / 95.87%
Mapped reads, first in pair	15,409,182 / 48.15%
Mapped reads, second in pair	15,269,530 / 47.72%
Mapped reads, both in pair	30,213,984 / 94.42%
Mapped reads, singletons	464,728 / 1.45%
Secondary alignments	0
Supplementary alignments	139,852 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,350,220 / 19.84%
Duplication rate	9.99%
Clipped reads	5,794,758 / 18.11%

2.2. ACGT Content

Number/percentage of A's	883,739,787 / 29.48%
Number/percentage of C's	606,410,607 / 20.23%
Number/percentage of T's	883,359,474 / 29.47%
Number/percentage of G's	621,750,527 / 20.74%
Number/percentage of N's	2,112,147 / 0.07%

GC Percentage	40.97%

2.3. Coverage

Mean	0.9688
Standard Deviation	9.8008

2.4. Mapping Quality

Mean Mapping Quality	52.81

2.5. Insert size

Mean	30,450.65
Standard Deviation	1,615,580.88
P25/Median/P75	174 / 220 / 292

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	35,648,600
Insertions	445,903
Mapped reads with at least one insertion	1.43%
Deletions	1,047,583
Mapped reads with at least one deletion	3.34%
Homopolymer indels	47.46%

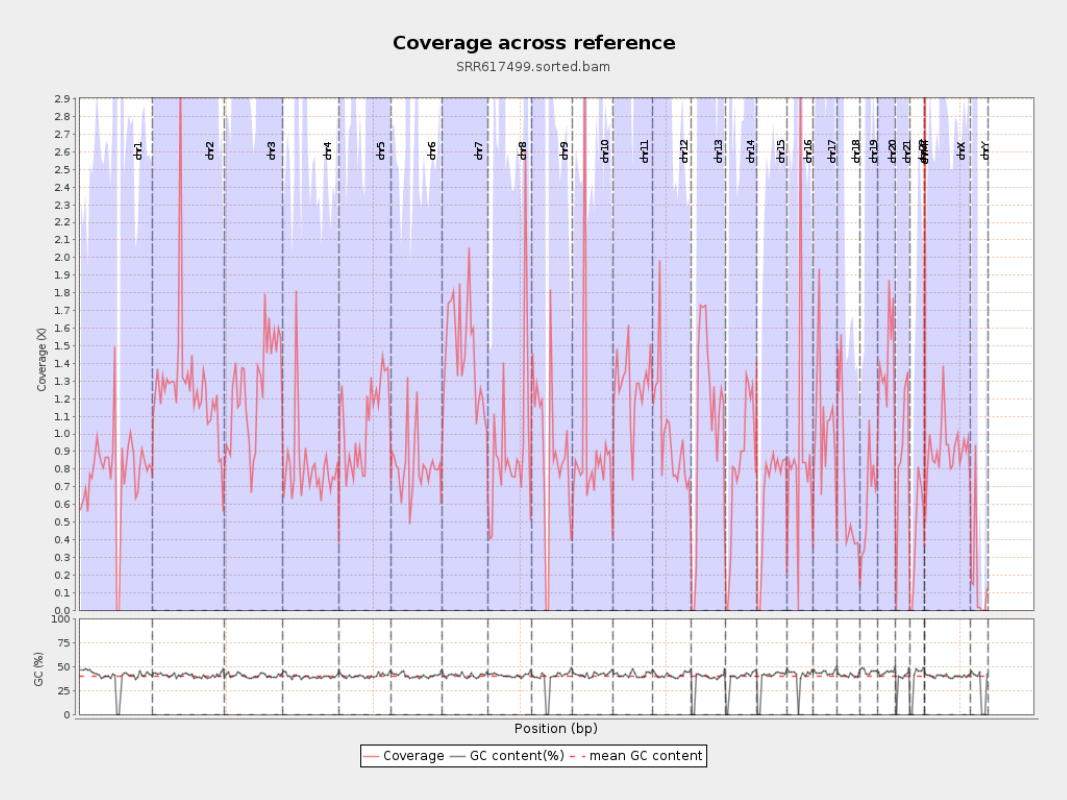
2.7. Chromosome stats

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

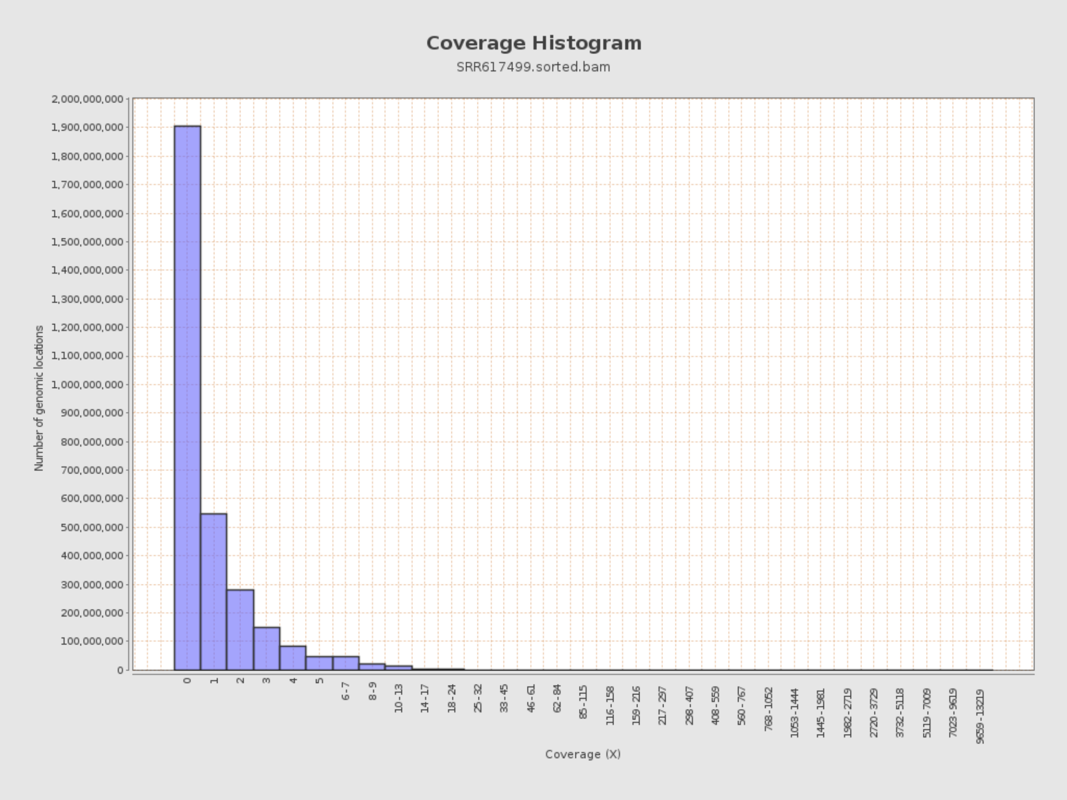
		bases	coverage	deviation
chr1	249250621	193183857	0.7751	9.5241
chr2	243199373	309858982	1.2741	11.5875
chr3	198022430	247832924	1.2515	2.2626
chr4	191154276	155142065	0.8116	6.2661
chr5	180915260	191883764	1.0606	2.0915
chr6	171115067	141397542	0.8263	5.4728
chr7	159138663	231309561	1.4535	13.2404
chr8	146364022	133194499	0.91	3.8626
chr9	141213431	124369345	0.8807	18.6289
chr10	135534747	126796608	0.9355	18.7281
chr11	135006516	169089404	1.2525	12.8256
chr12	133851895	130926752	0.9781	1.9892
chr13	115169878	127431260	1.1065	2.1378
chr14	107349540	87450160	0.8146	2.2313
chr15	102531392	67711973	0.6604	1.4505
chr16	90354753	80826135	0.8945	14.9915
chr17	81195210	83825116	1.0324	13.9137
chr18	78077248	53610297	0.6866	17.0711
chr19	59128983	35861685	0.6065	5.8948
chr20	63025520	88561305	1.4052	2.8099
chr21	48129895	43239730	0.8984	3.8279
chr22	51304566	22429005	0.4372	1.2612
chrMT	16571	2127844	128.4077	93.9148
chrX	155270560	140735031	0.9064	4.1338

chrY	59373566	10359716	0.1745	13.9974

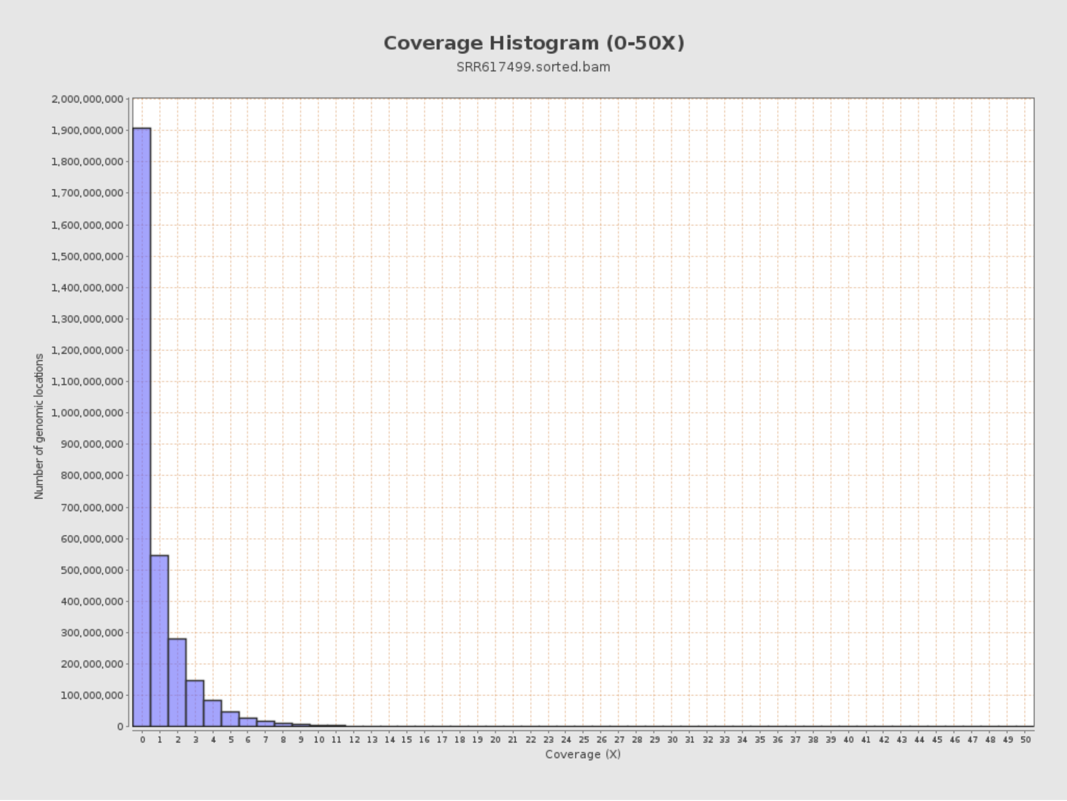
3. Results : Coverage across reference



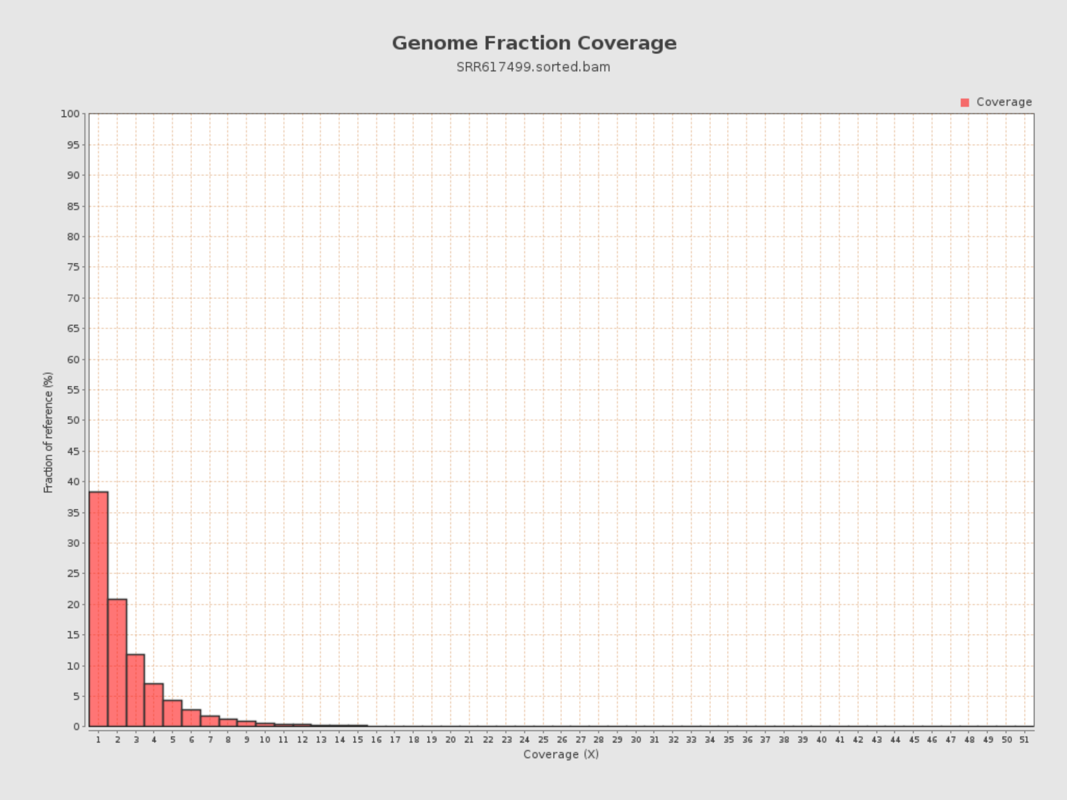
4. Results : Coverage Histogram



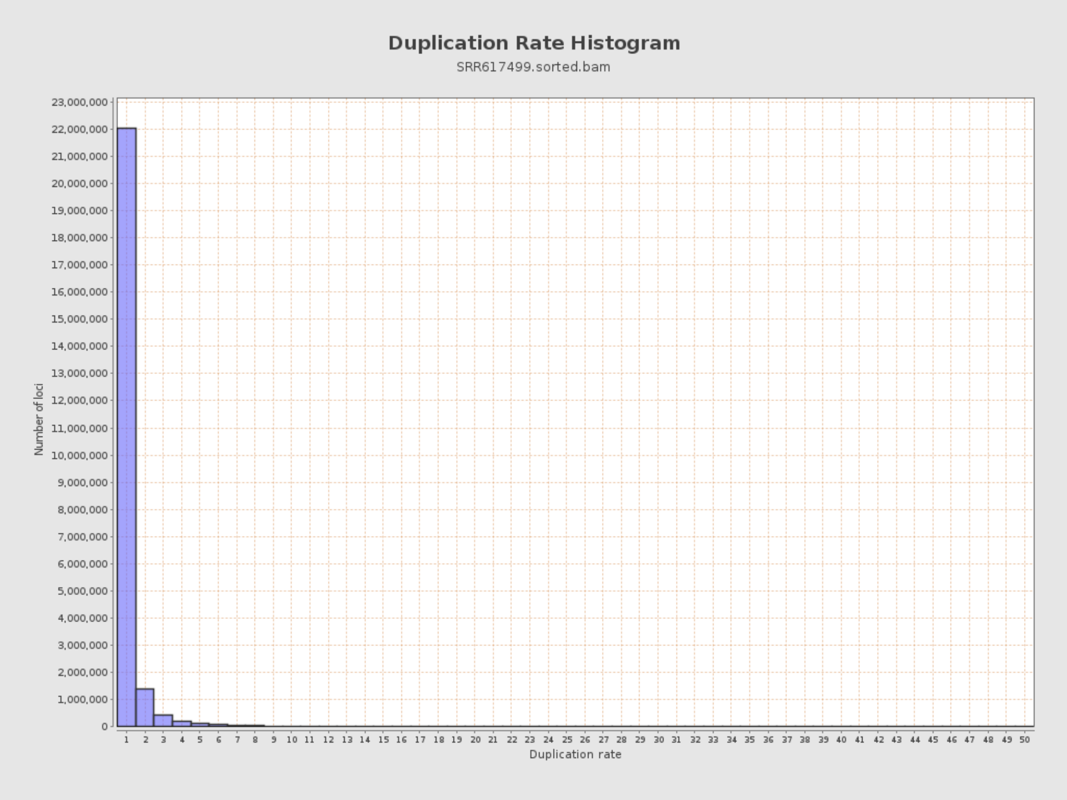
5. Results : Coverage Histogram (0-50X)



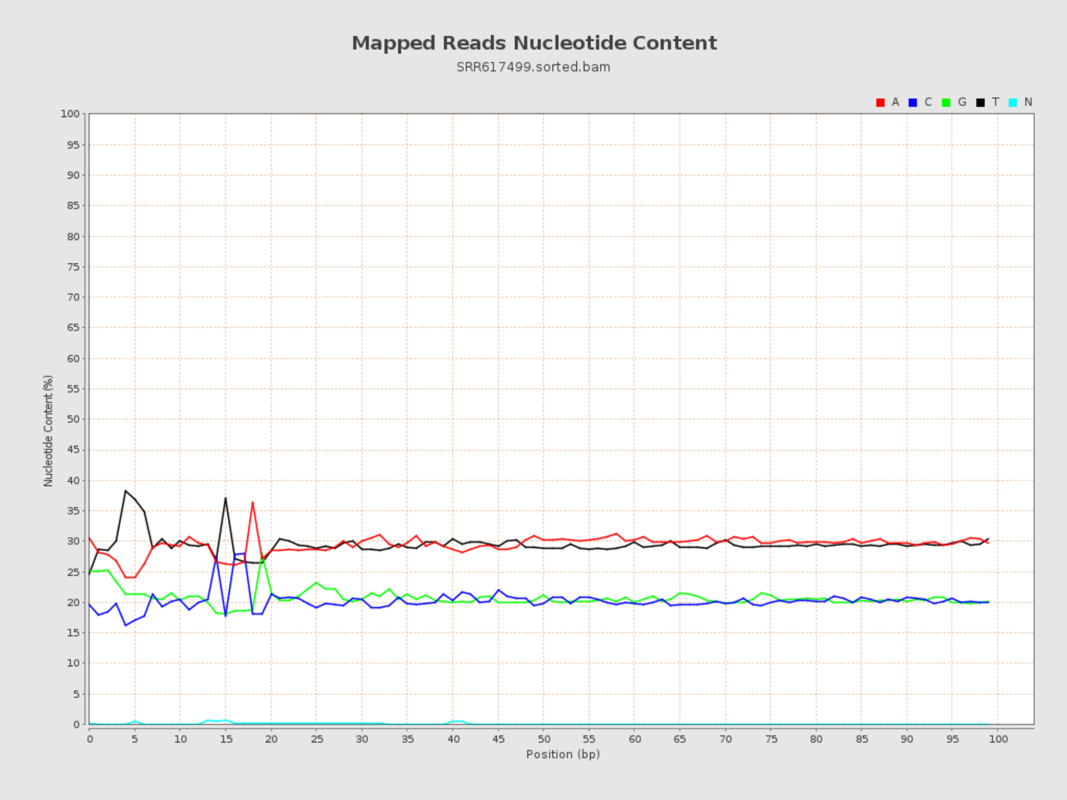
6. Results : Genome Fraction Coverage



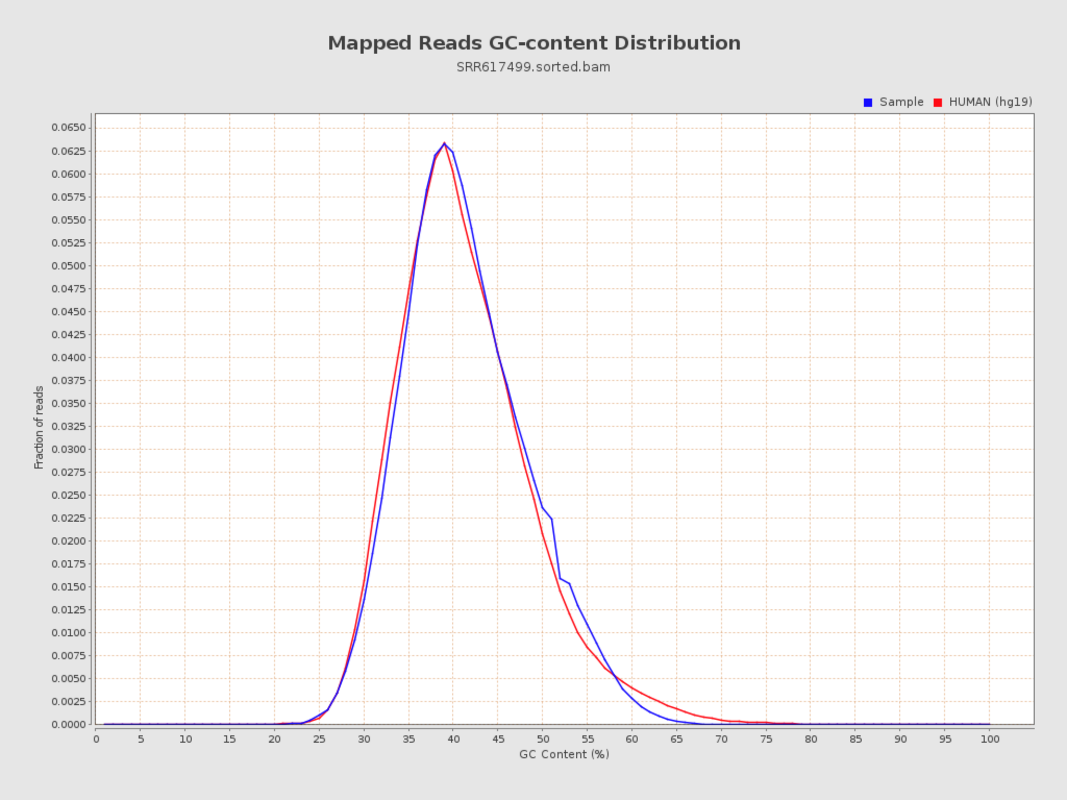
7. Results : Duplication Rate Histogram



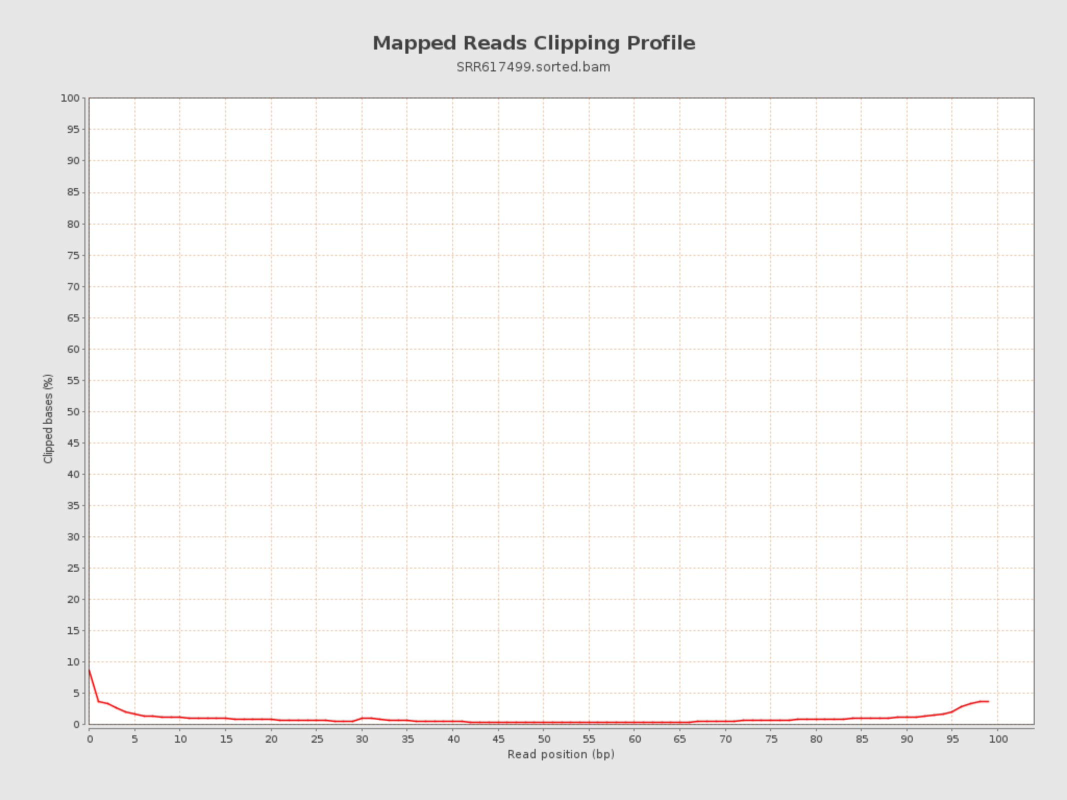
8. Results : Mapped Reads Nucleotide Content



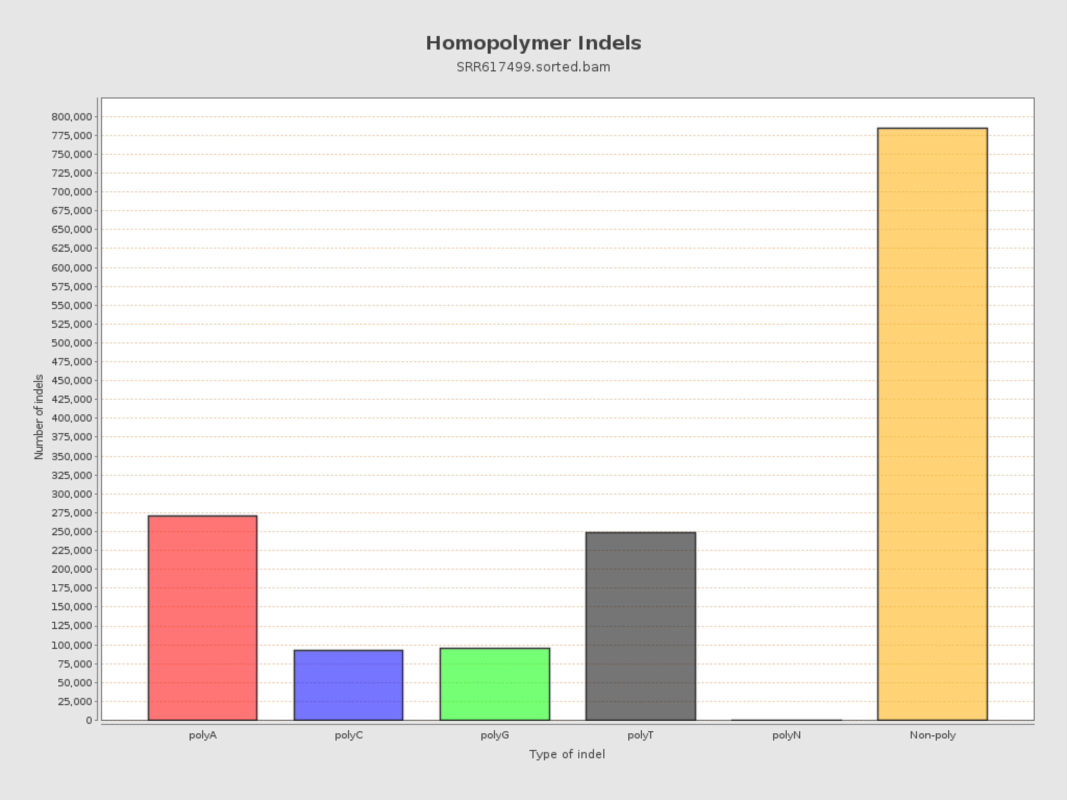
9. Results : Mapped Reads GC-content Distribution



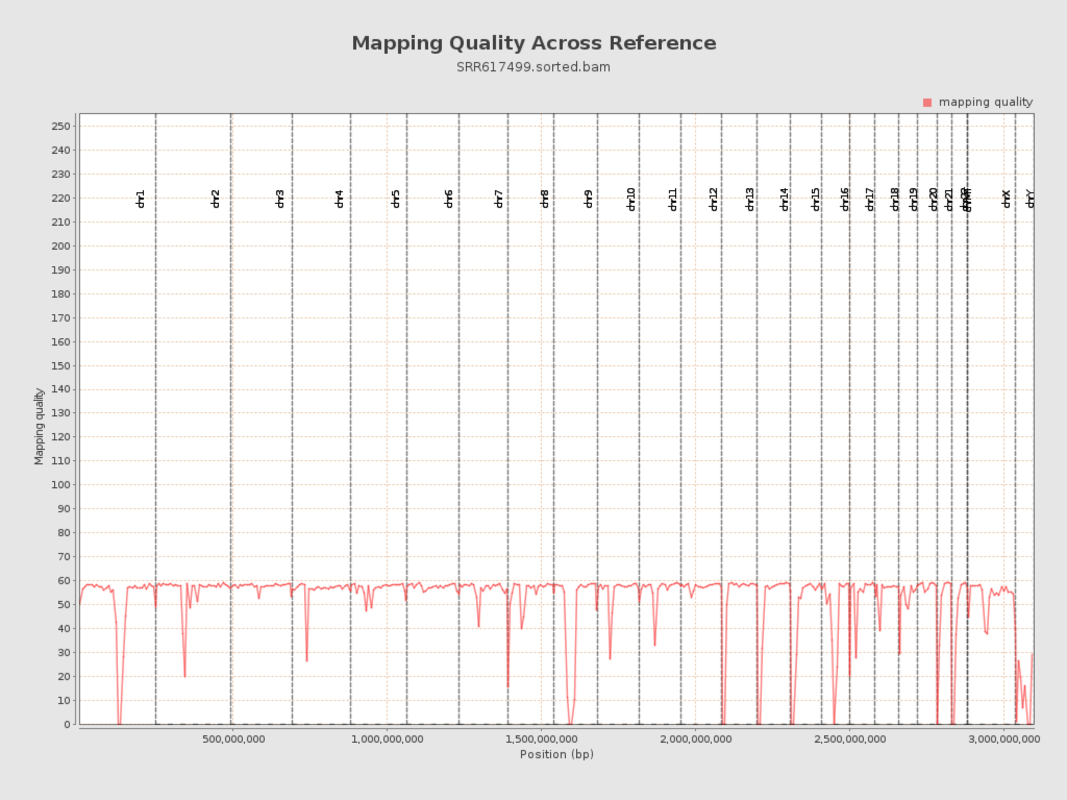
10. Results : Mapped Reads Clipping Profile



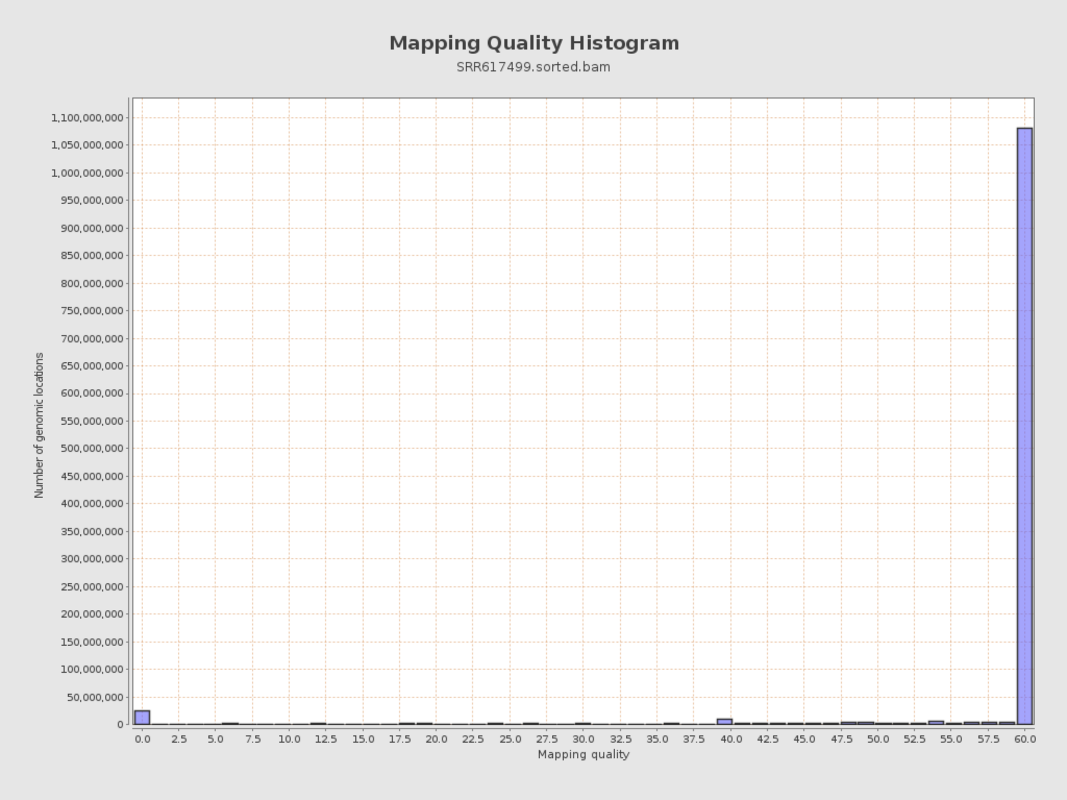
11. Results : Homopolymer Indels



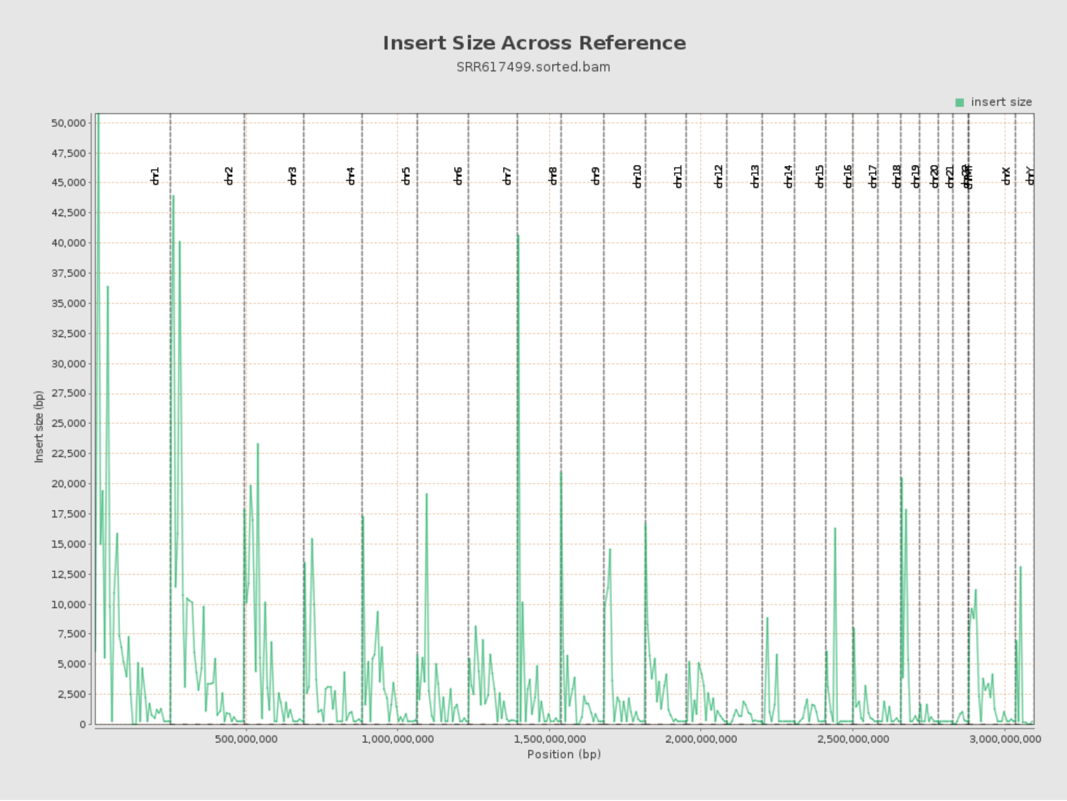
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram