Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 21:25:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617496.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_SRR617496 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617496_1.fastq.gz SRR617496_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 21:25:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617496.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,280,258 / 94.63%
Unmapped reads	1,719,742 / 5.37%
Mapped paired reads	30,280,258 / 94.63%
Mapped reads, first in pair	15,211,589 / 47.54%
Mapped reads, second in pair	15,068,669 / 47.09%
Mapped reads, both in pair	29,759,770 / 93%
Mapped reads, singletons	520,488 / 1.63%
Secondary alignments	0
Supplementary alignments	140,356 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	6,139,429 / 19.19%
Duplication rate	9.79%
Clipped reads	6,075,734 / 18.99%

2.2. ACGT Content

Number/percentage of A's	871,050,564 / 29.55%
Number/percentage of C's	595,134,887 / 20.19%
Number/percentage of T's	869,225,767 / 29.49%
Number/percentage of G's	609,859,821 / 20.69%
Number/percentage of N's	1,964,236 / 0.07%

GC Percentage	40.89%

2.3. Coverage

Mean	0.9526
Standard Deviation	9.6469

2.4. Mapping Quality

Mean Mapping Quality	52.73

2.5. Insert size

Mean	30,818.09
Standard Deviation	1,634,530.67
P25/Median/P75	173 / 217 / 286

2.6. Mismatches and indels

General error rate	1.36%
Mismatches	39,304,680
Insertions	433,749
Mapped reads with at least one insertion	1.4%
Deletions	1,017,101
Mapped reads with at least one deletion	3.29%
Homopolymer indels	47.4%

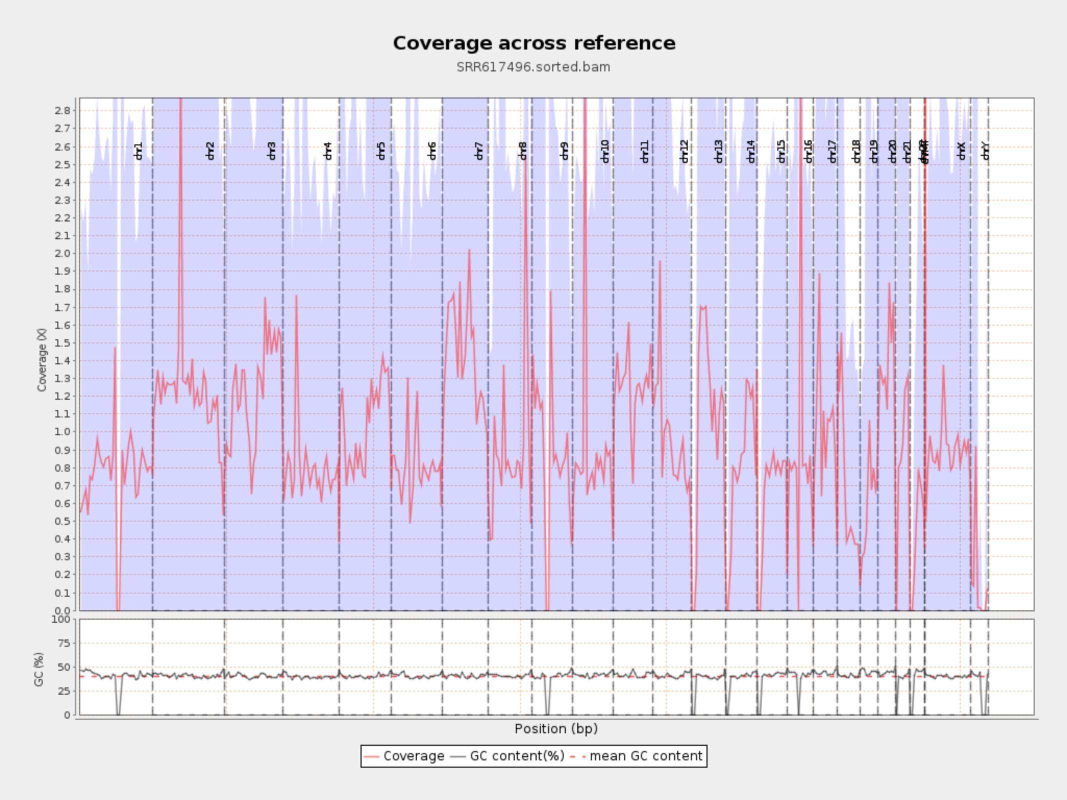
2.7. Chromosome stats

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

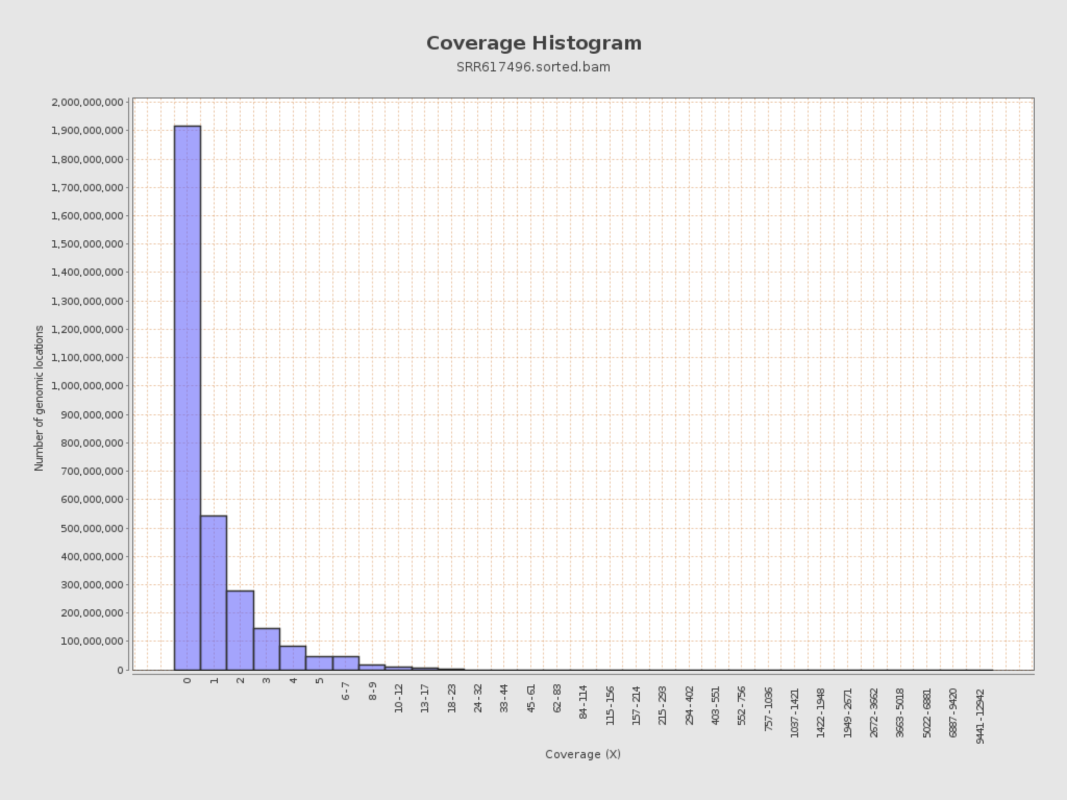
		bases	coverage	deviation
chr1	249250621	189942242	0.7621	9.379
chr2	243199373	304587147	1.2524	11.2267
chr3	198022430	243604339	1.2302	2.2198
chr4	191154276	152555098	0.7981	5.9606
chr5	180915260	189042934	1.0449	2.0711
chr6	171115067	138991262	0.8123	5.3921
chr7	159138663	227750992	1.4311	13.1501
chr8	146364022	130793286	0.8936	3.8237
chr9	141213431	122105329	0.8647	18.165
chr10	135534747	125032595	0.9225	18.6414
chr11	135006516	166298337	1.2318	12.7899
chr12	133851895	129041870	0.9641	1.9676
chr13	115169878	125435083	1.0891	2.1055
chr14	107349540	85754035	0.7988	2.1795
chr15	102531392	66412096	0.6477	1.4388
chr16	90354753	79532131	0.8802	15.0017
chr17	81195210	82071743	1.0108	13.6114
chr18	78077248	53003556	0.6789	16.7482
chr19	59128983	34905231	0.5903	5.7957
chr20	63025520	86745992	1.3764	2.7564
chr21	48129895	42518731	0.8834	3.7179
chr22	51304566	21840241	0.4257	1.234
chrMT	16571	2103299	126.9265	92.8328
chrX	155270560	138732455	0.8935	4.1154

chrY	59373566	10158016	0.1711	13.6675

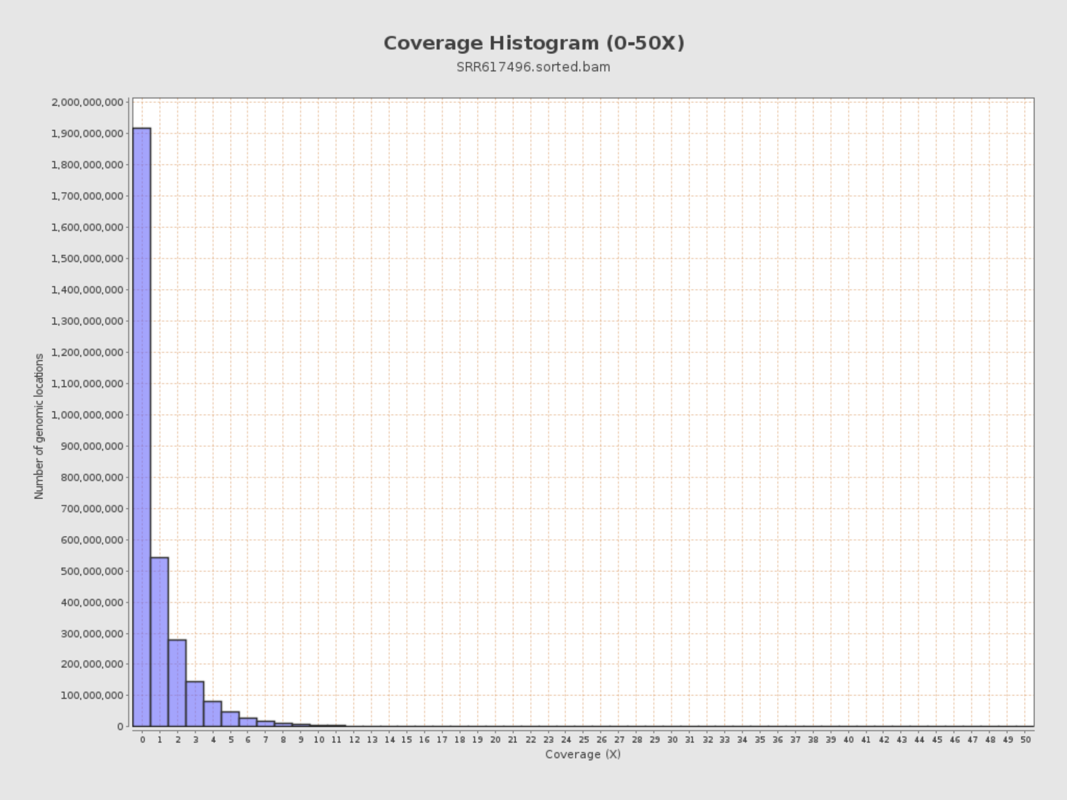
3. Results : Coverage across reference



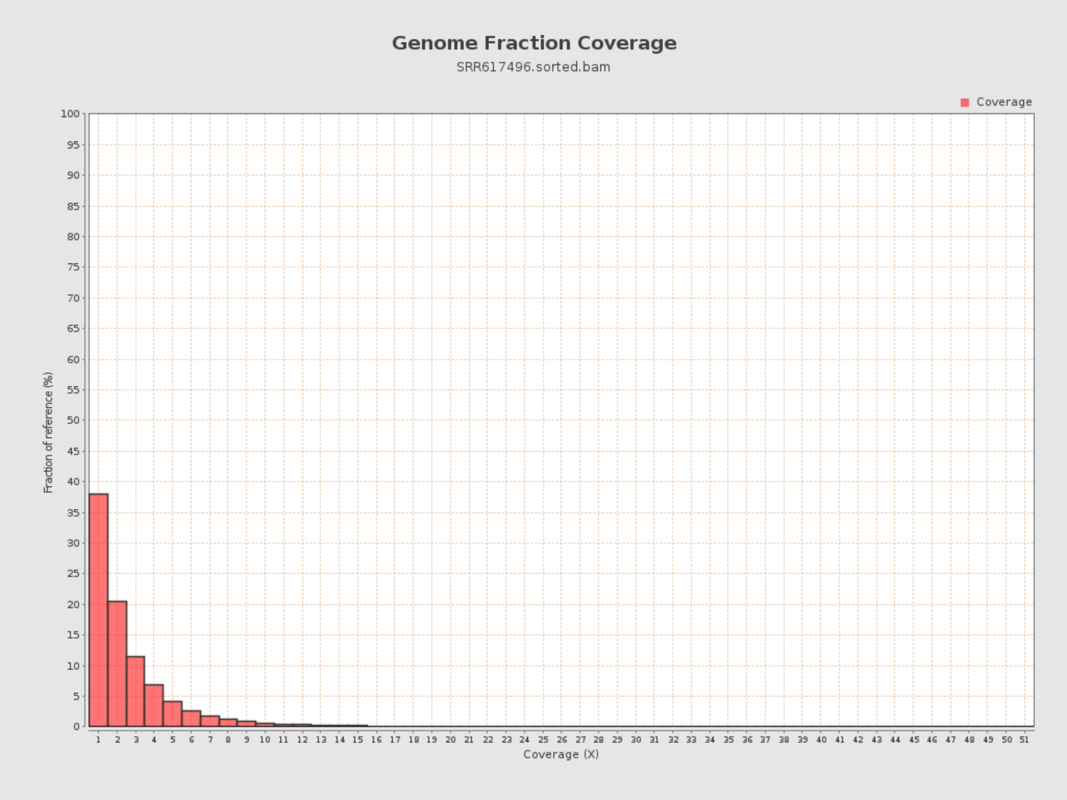
4. Results : Coverage Histogram



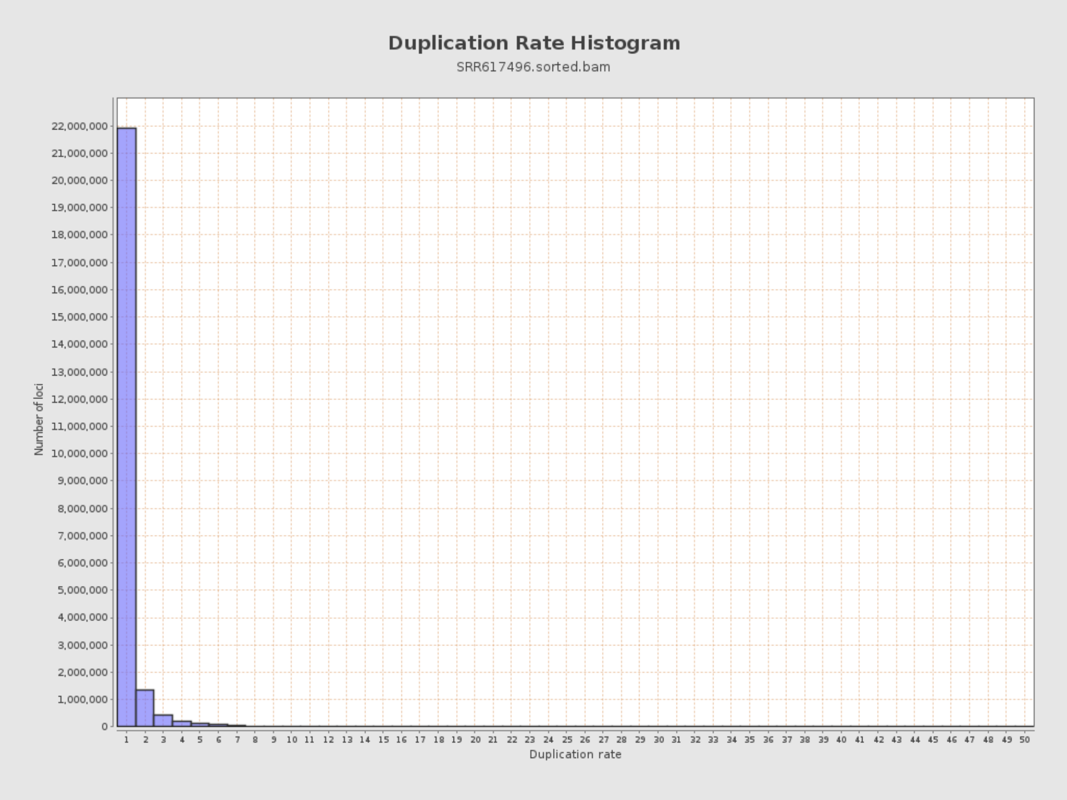
5. Results : Coverage Histogram (0-50X)



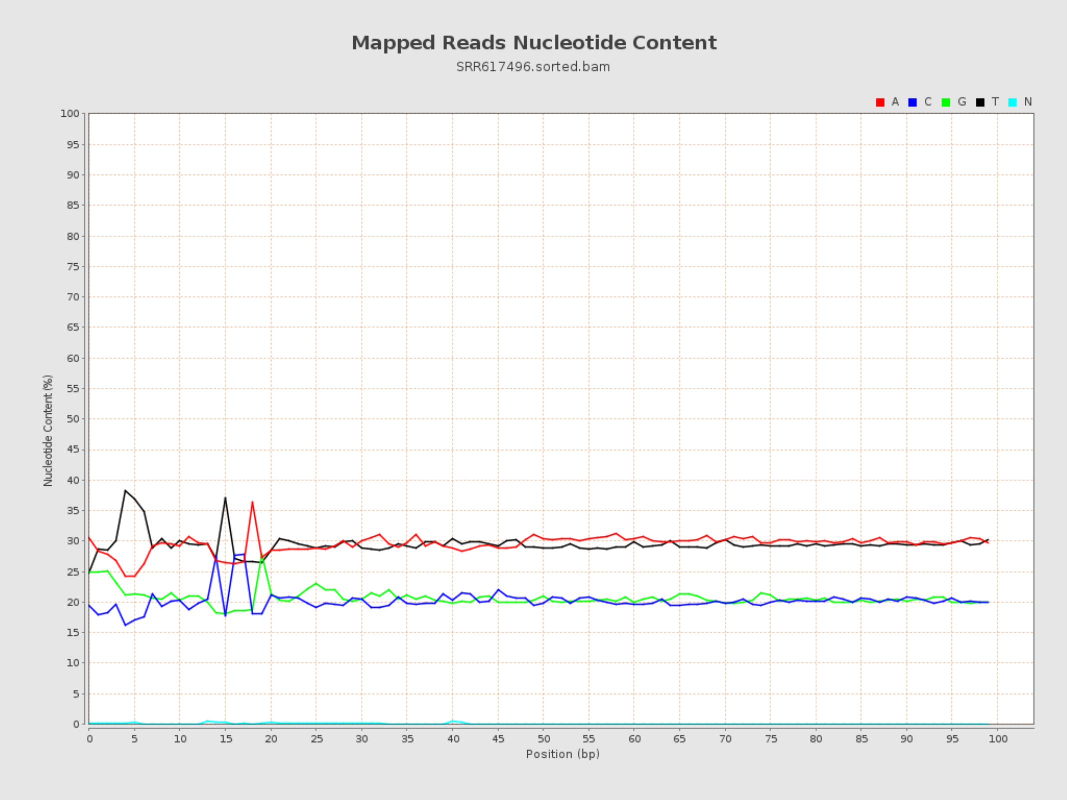
6. Results : Genome Fraction Coverage



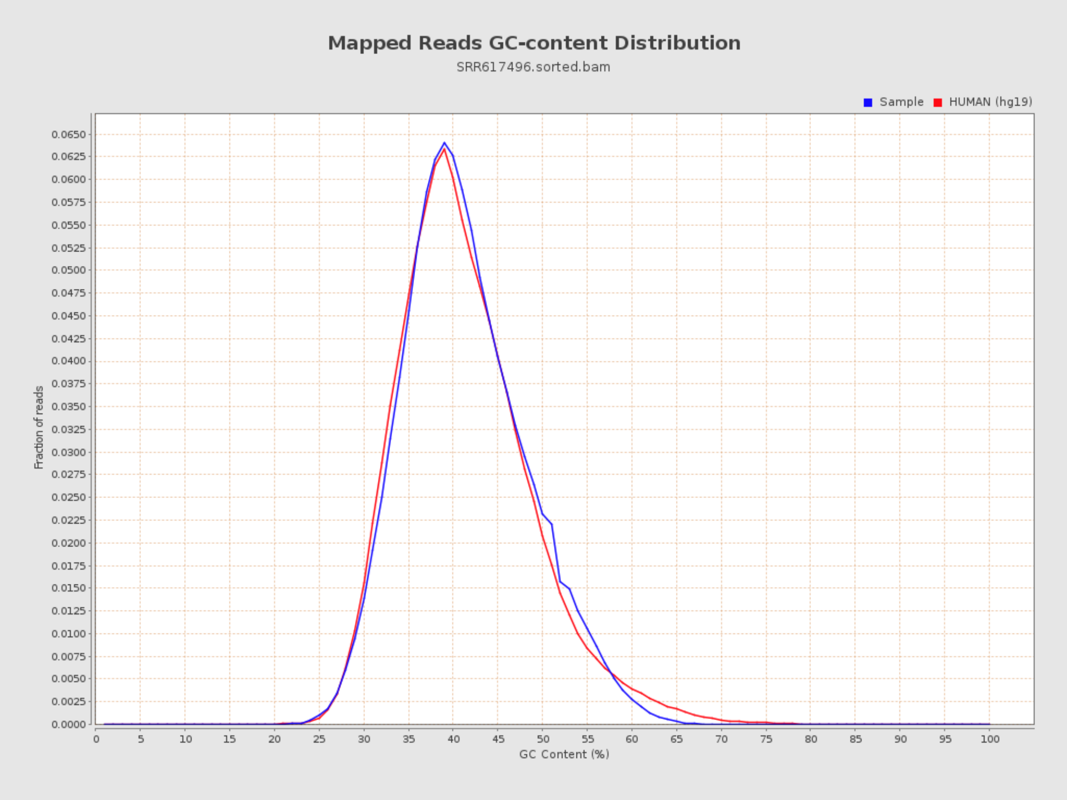
7. Results : Duplication Rate Histogram



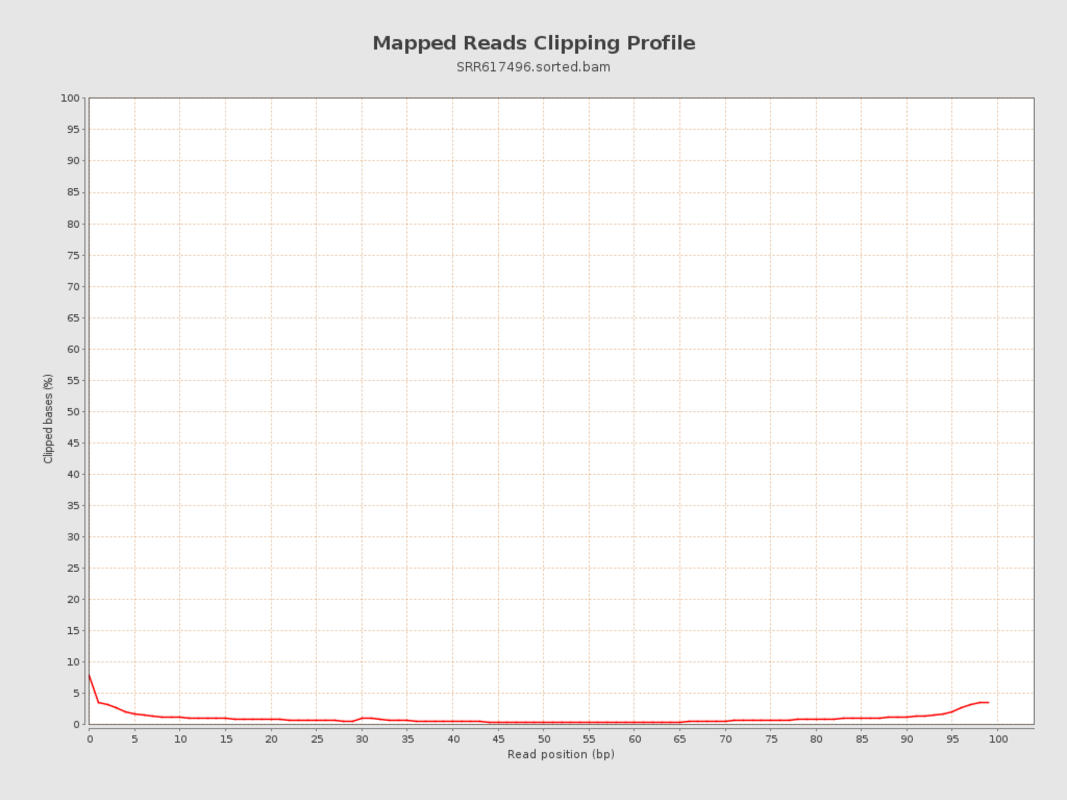
8. Results : Mapped Reads Nucleotide Content



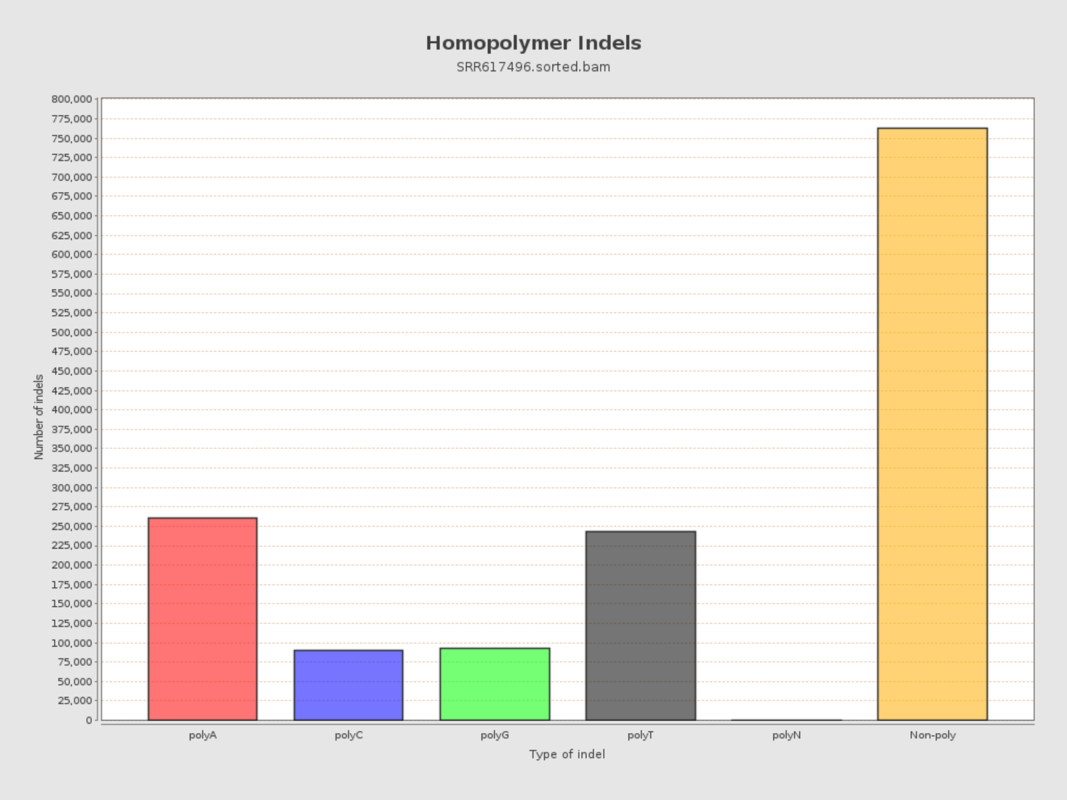
9. Results : Mapped Reads GC-content Distribution



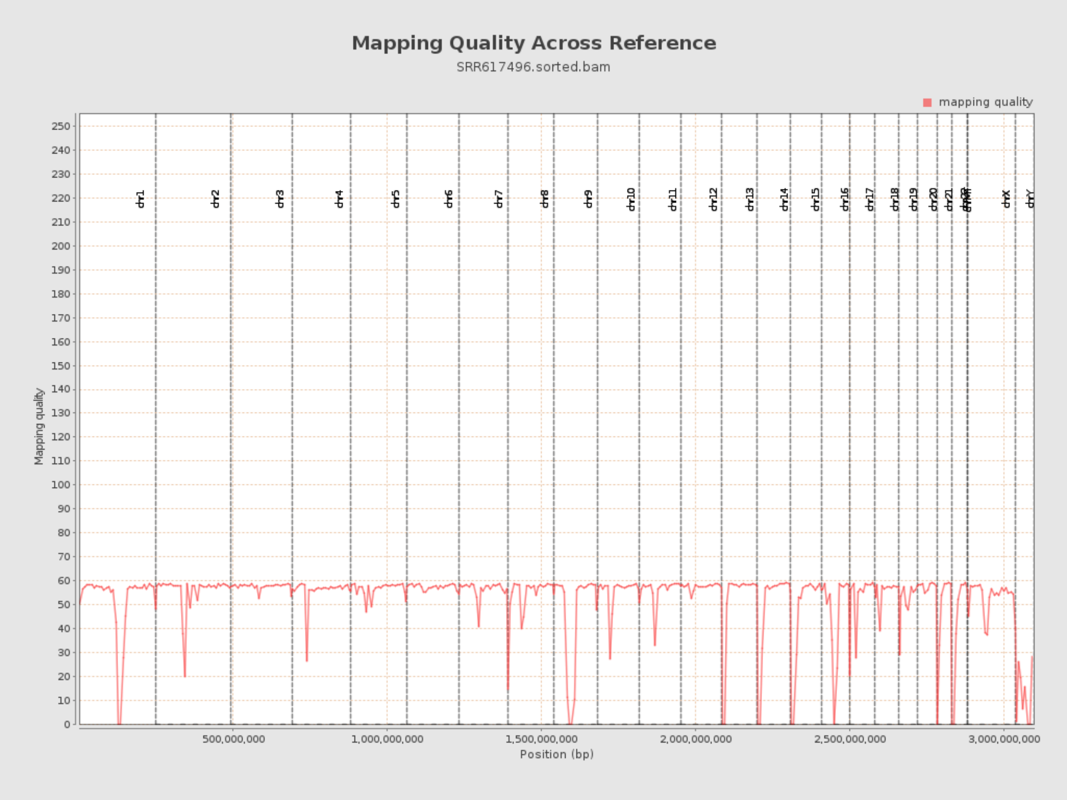
10. Results : Mapped Reads Clipping Profile



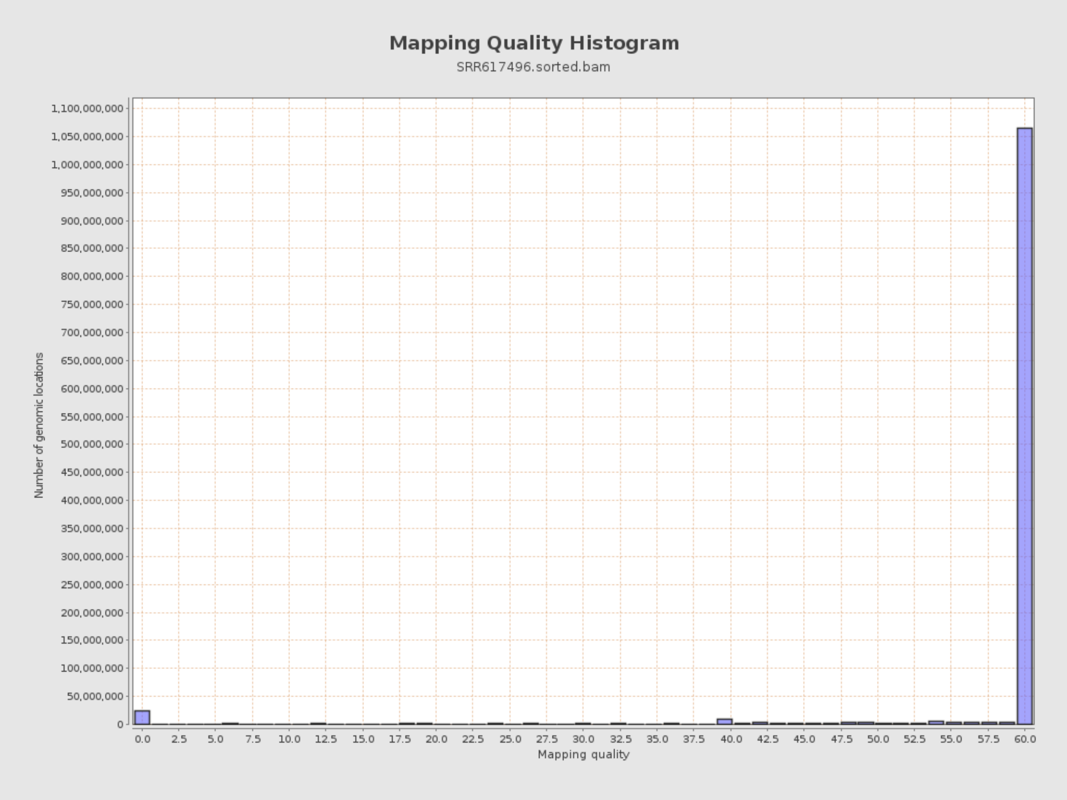
11. Results : Homopolymer Indels



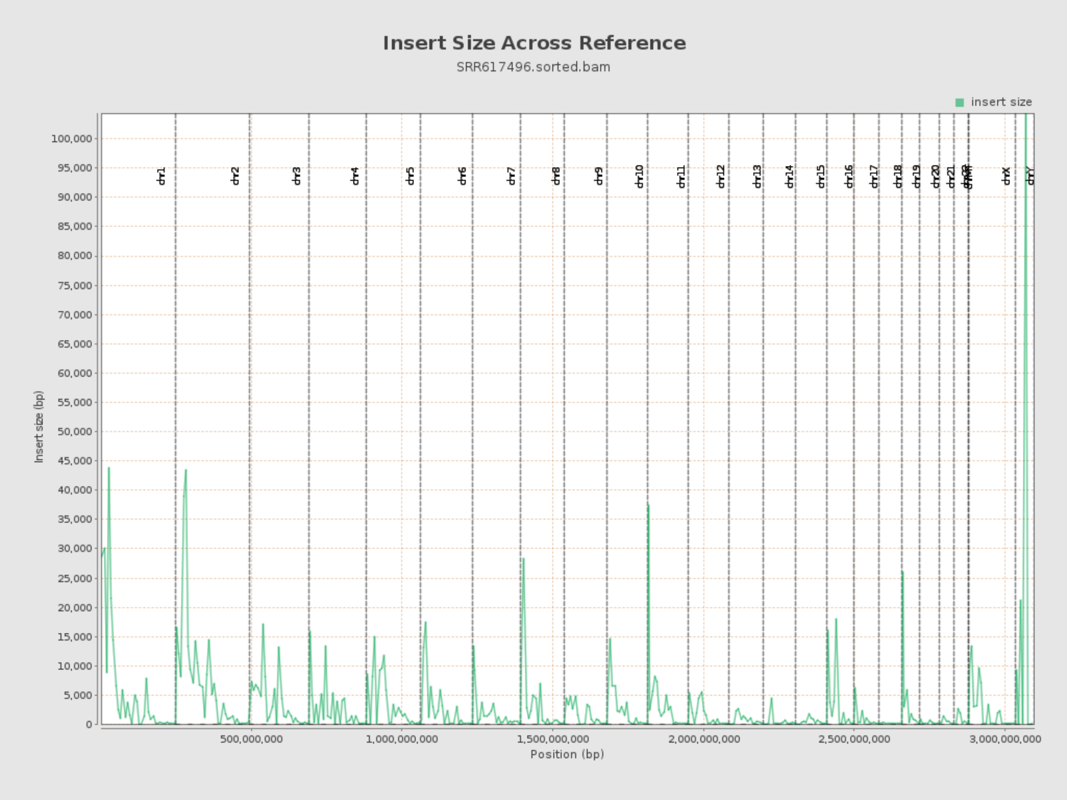
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram