Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 15:28:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617489.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_SRR617489 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617489_1.fastq.gz SRR617489_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 15:28:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617489.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,523,432 / 95.39%
Unmapped reads	1,476,568 / 4.61%
Mapped paired reads	30,523,432 / 95.39%
Mapped reads, first in pair	15,360,029 / 48%
Mapped reads, second in pair	15,163,403 / 47.39%
Mapped reads, both in pair	30,008,714 / 93.78%
Mapped reads, singletons	514,718 / 1.61%
Secondary alignments	0
Supplementary alignments	174,870 / 0.55%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,290,976 / 19.66%
Duplication rate	9.98%
Clipped reads	6,215,834 / 19.42%

2.2. ACGT Content

Number/percentage of A's	873,660,686 / 29.48%
Number/percentage of C's	597,674,378 / 20.17%
Number/percentage of T's	873,844,749 / 29.49%
Number/percentage of G's	613,659,311 / 20.71%
Number/percentage of N's	4,780,323 / 0.16%

GC Percentage	40.87%

2.3. Coverage

Mean	0.9579
Standard Deviation	9.5206

2.4. Mapping Quality

Mean Mapping Quality	52.67

2.5. Insert size

Mean	48,033.18
Standard Deviation	2,084,642.18
P25/Median/P75	175 / 221 / 293

2.6. Mismatches and indels

General error rate	1.34%
Mismatches	38,909,249
Insertions	444,093
Mapped reads with at least one insertion	1.43%
Deletions	1,030,350
Mapped reads with at least one deletion	3.3%
Homopolymer indels	47.28%

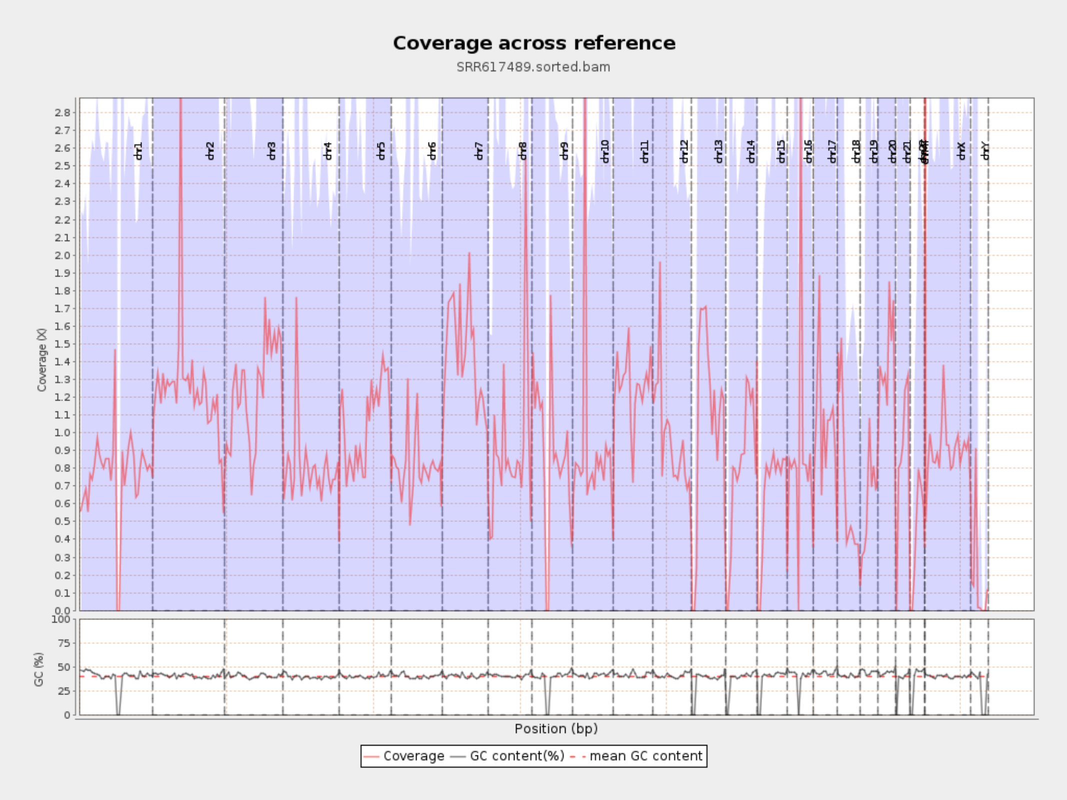
2.7. Chromosome stats

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

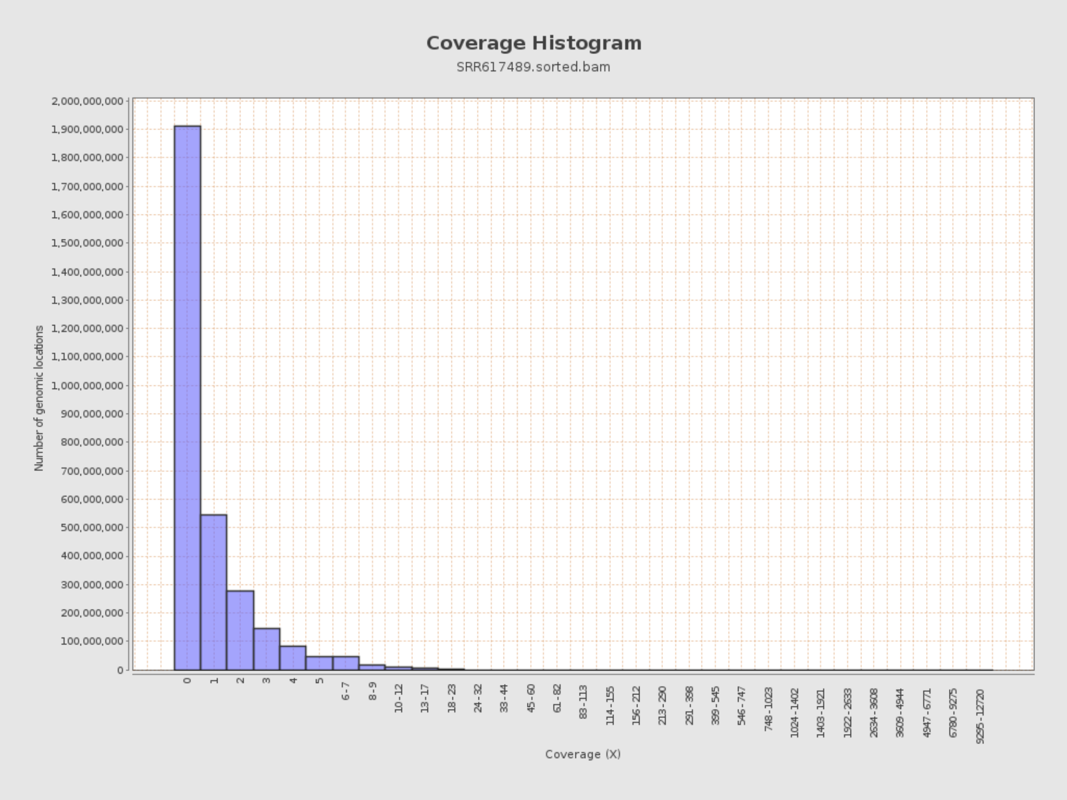
		bases	coverage	deviation
chr1	249250621	190690234	0.7651	9.2666
chr2	243199373	306554818	1.2605	11.235
chr3	198022430	244799798	1.2362	2.2424
chr4	191154276	153138583	0.8011	5.9862
chr5	180915260	189816419	1.0492	2.0906
chr6	171115067	139790843	0.8169	5.3831
chr7	159138663	228889084	1.4383	13.0708
chr8	146364022	131726879	0.9	3.8115
chr9	141213431	122946233	0.8706	17.8685
chr10	135534747	125438895	0.9255	18.3894
chr11	135006516	167141958	1.238	12.3107
chr12	133851895	129901842	0.9705	2.0528
chr13	115169878	125737227	1.0918	2.1675
chr14	107349540	86133299	0.8024	2.2368
chr15	102531392	67114208	0.6546	1.6381
chr16	90354753	80154185	0.8871	14.7117
chr17	81195210	82840879	1.0203	13.3858
chr18	78077248	52935810	0.678	16.5808
chr19	59128983	35531420	0.6009	5.7115
chr20	63025520	87571528	1.3895	2.7907
chr21	48129895	42667594	0.8865	3.7134
chr22	51304566	22187670	0.4325	1.264
chrMT	16571	2116521	127.7244	92.1639
chrX	155270560	139411951	0.8979	4.1141

chrY	59373566	10139099	0.1708	13.1867

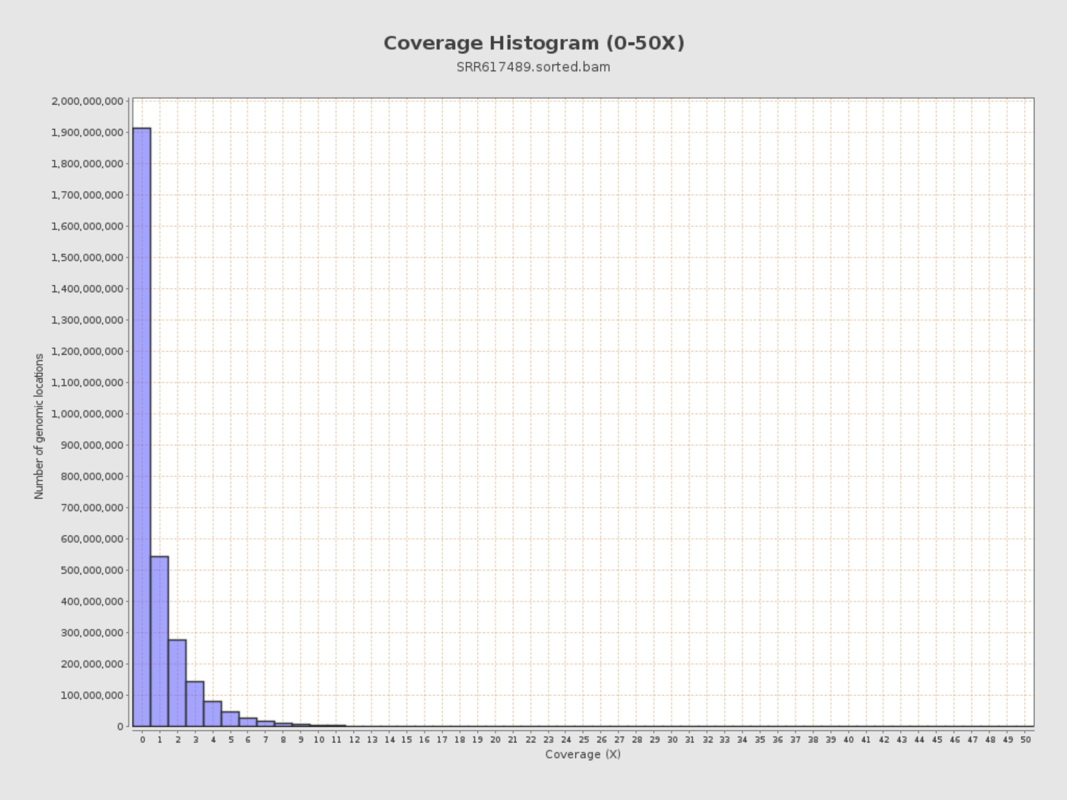
3. Results : Coverage across reference



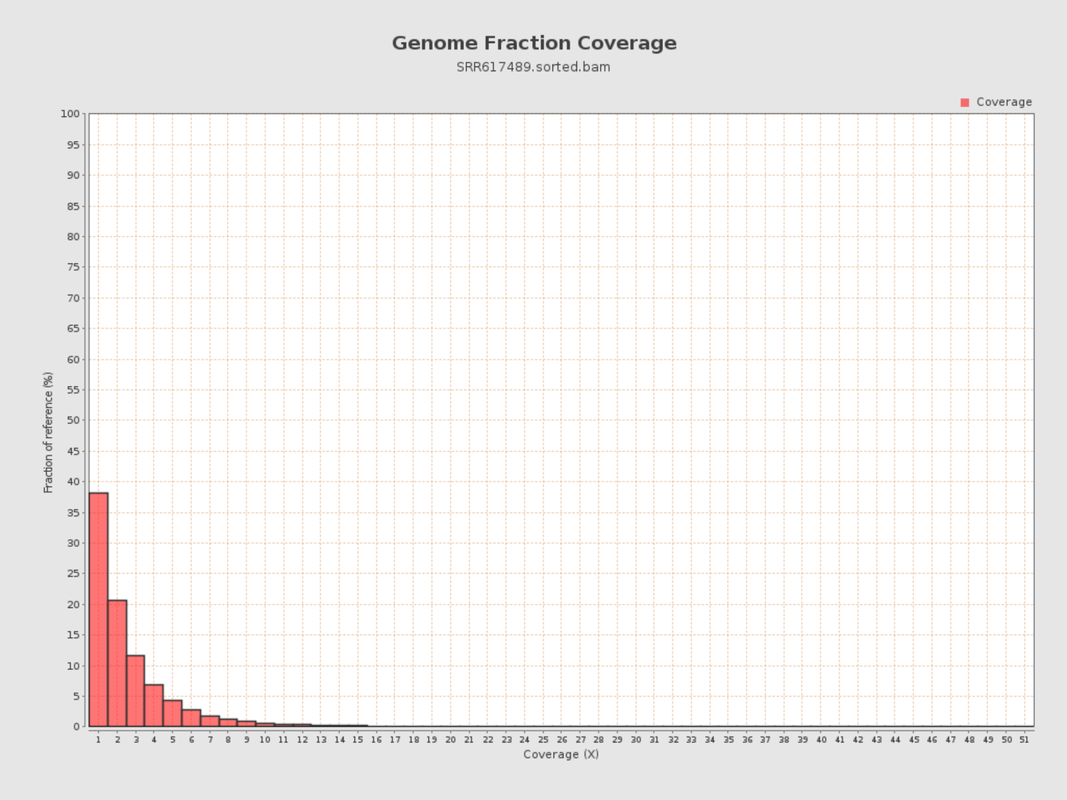
4. Results : Coverage Histogram



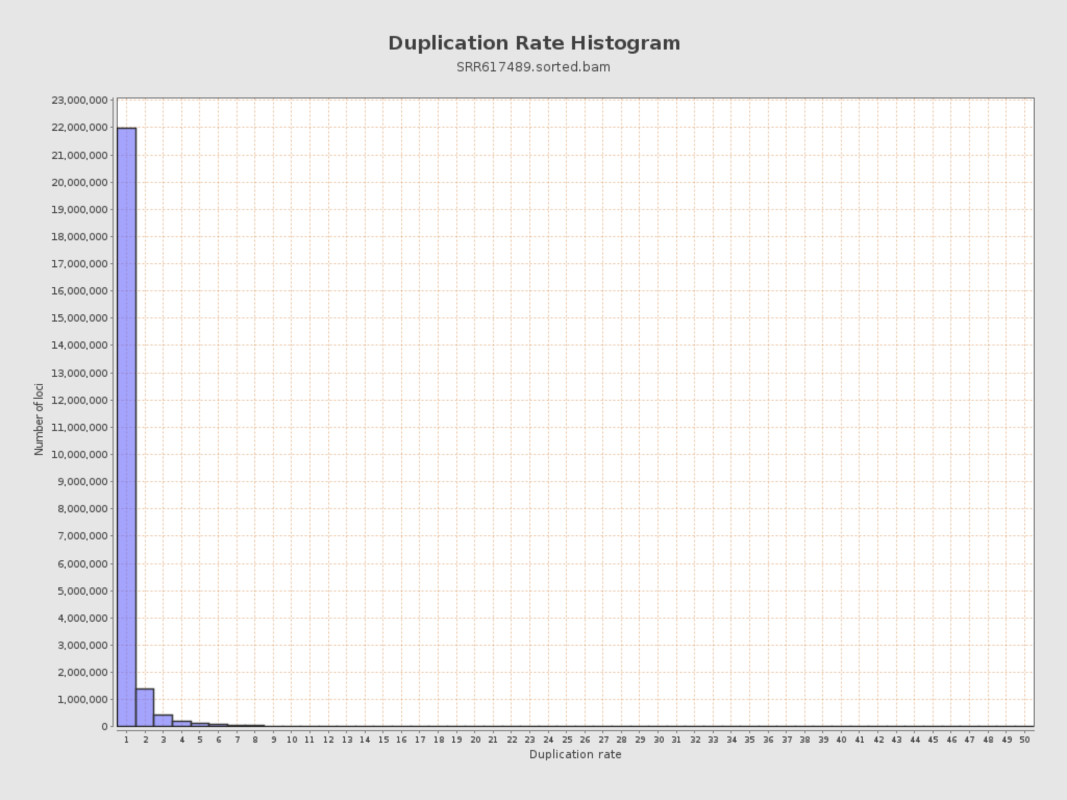
5. Results : Coverage Histogram (0-50X)



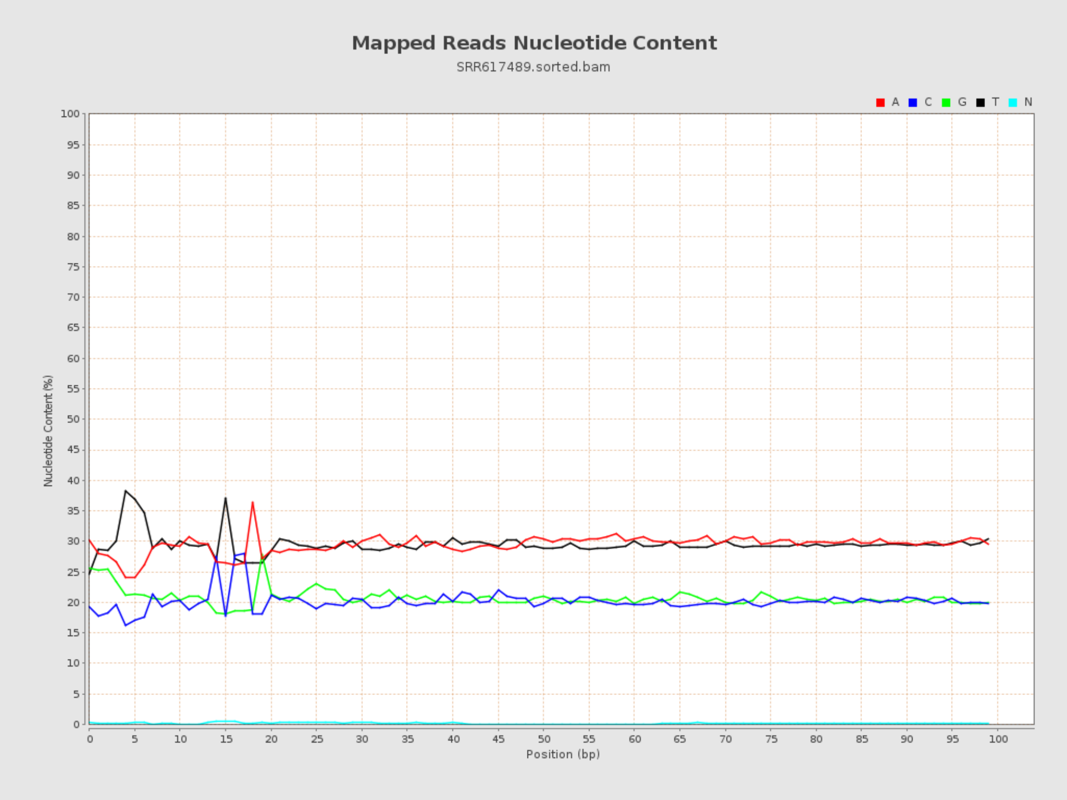
6. Results : Genome Fraction Coverage



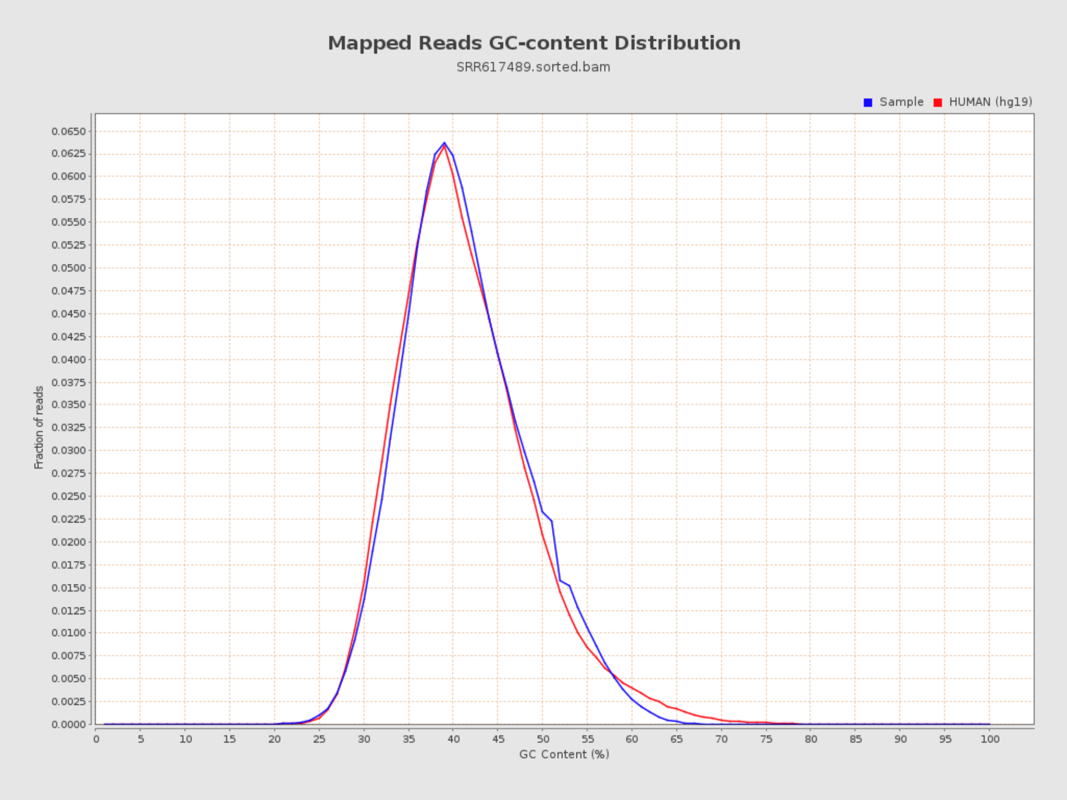
7. Results : Duplication Rate Histogram



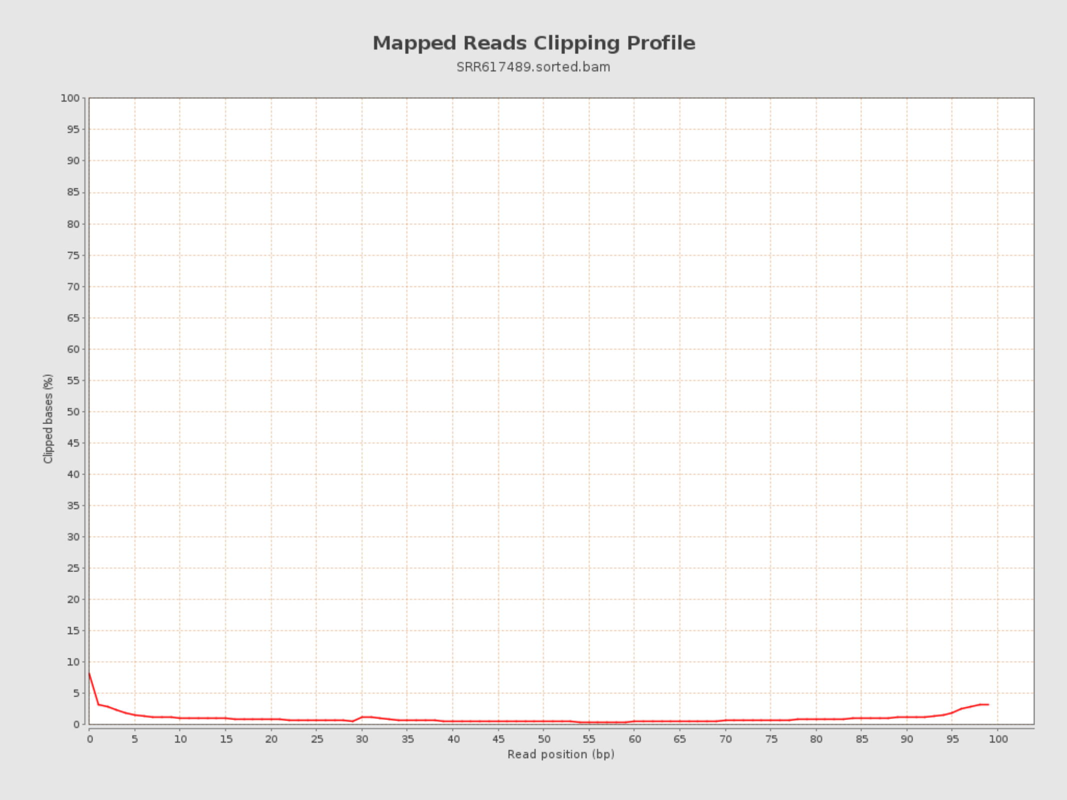
8. Results : Mapped Reads Nucleotide Content



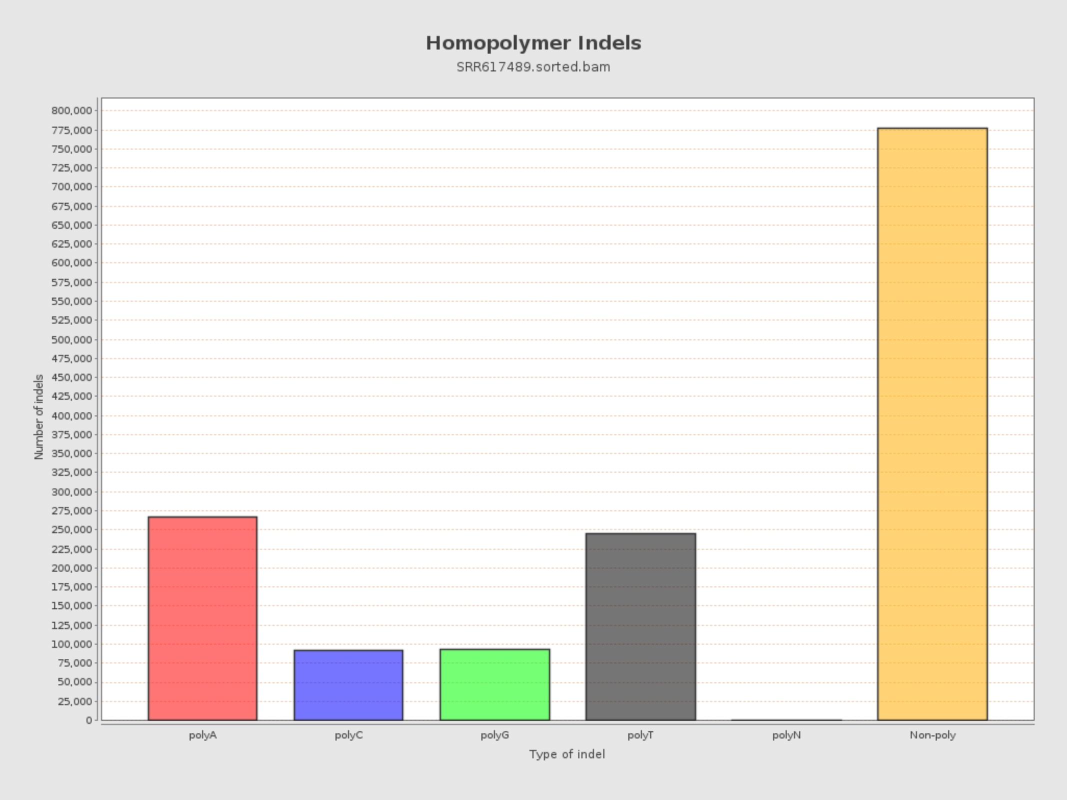
9. Results : Mapped Reads GC-content Distribution



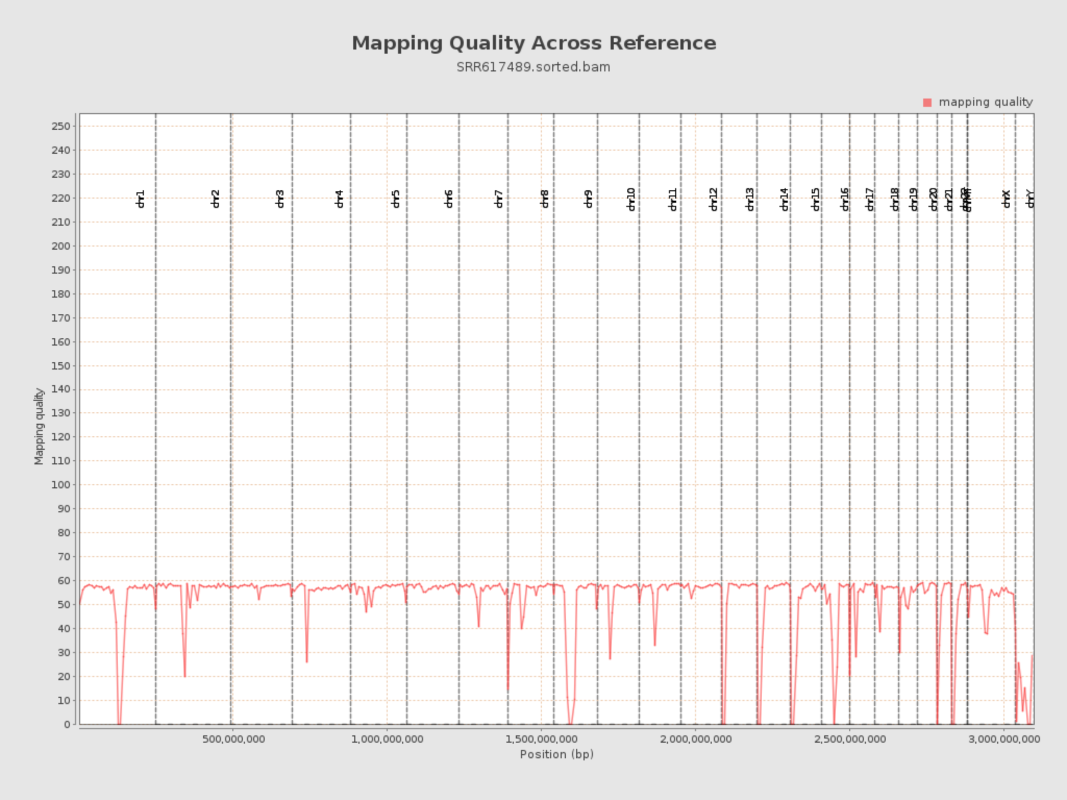
10. Results : Mapped Reads Clipping Profile



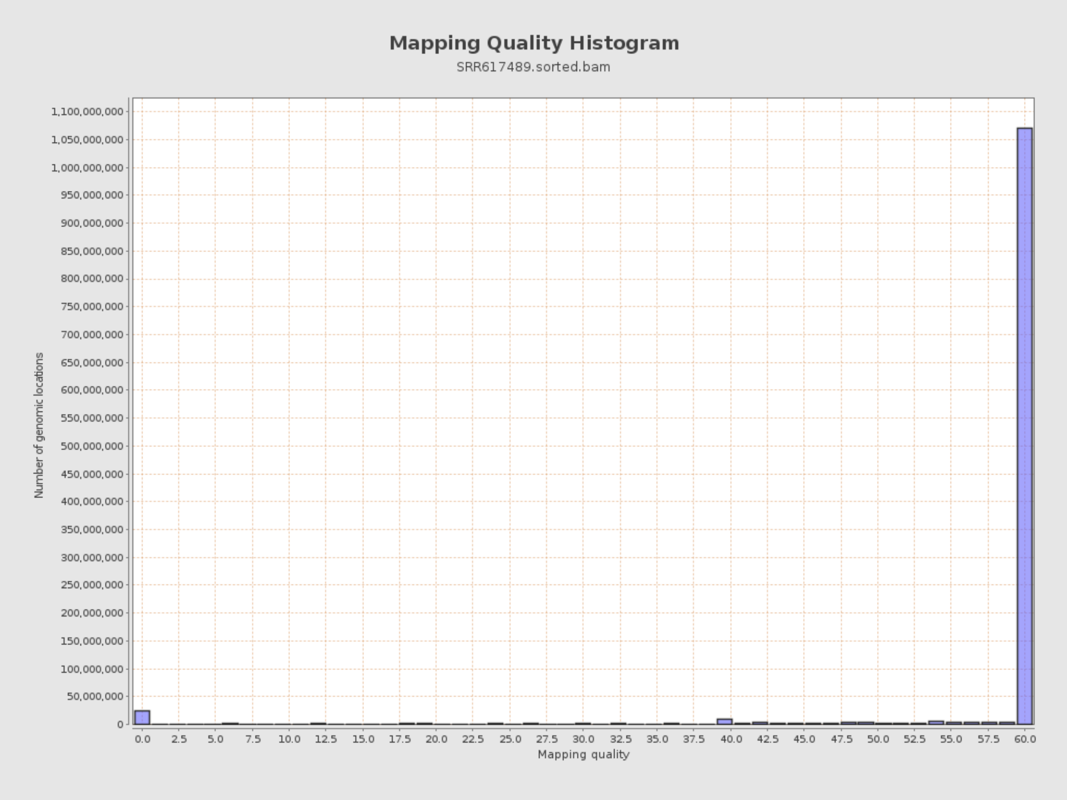
11. Results : Homopolymer Indels



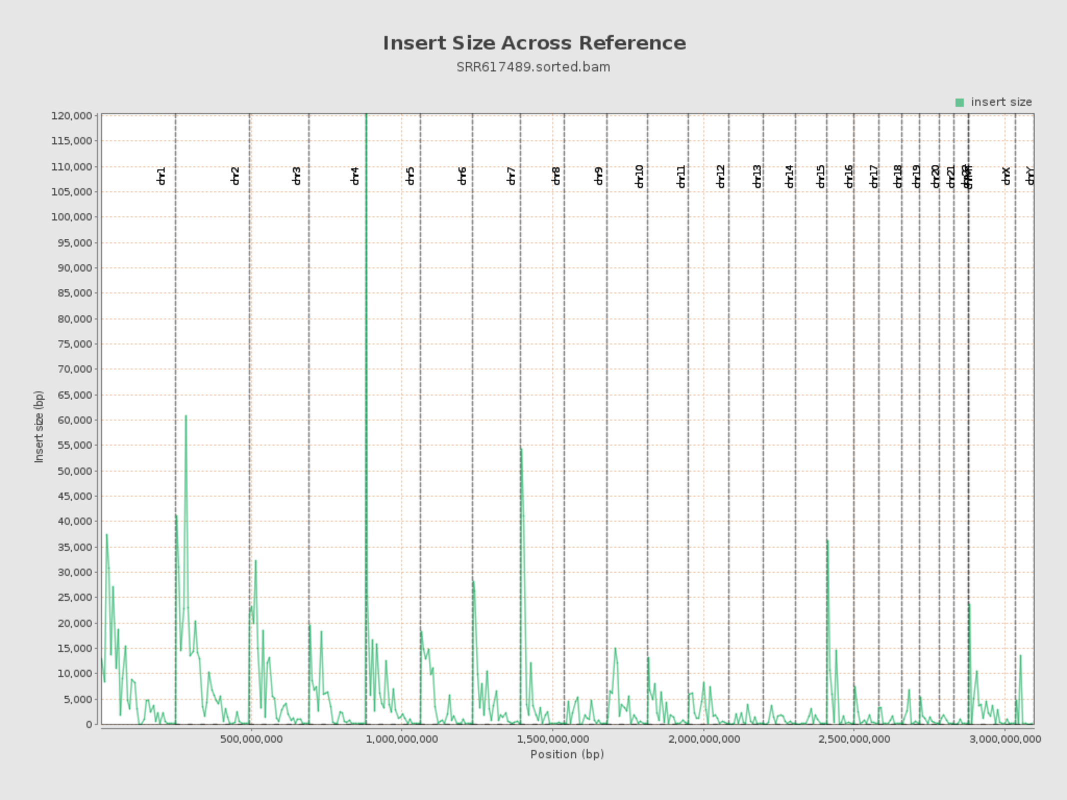
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram