Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 16:15:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617490.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_SRR617490 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617490_1.fastq.gz SRR617490_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 16:15:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617490.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,245,925 / 94.52%
Unmapped reads	1,754,075 / 5.48%
Mapped paired reads	30,245,925 / 94.52%
Mapped reads, first in pair	15,235,160 / 47.61%
Mapped reads, second in pair	15,010,765 / 46.91%
Mapped reads, both in pair	29,688,690 / 92.78%
Mapped reads, singletons	557,235 / 1.74%
Secondary alignments	0
Supplementary alignments	162,815 / 0.51%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,187,213 / 19.34%
Duplication rate	9.9%
Clipped reads	6,136,156 / 19.18%

2.2. ACGT Content

Number/percentage of A's	866,347,201 / 29.5%
Number/percentage of C's	592,732,992 / 20.18%
Number/percentage of T's	866,024,323 / 29.49%
Number/percentage of G's	607,712,189 / 20.69%
Number/percentage of N's	3,908,159 / 0.13%

GC Percentage	40.88%

2.3. Coverage

Mean	0.9492
Standard Deviation	9.5122

2.4. Mapping Quality

Mean Mapping Quality	52.66

2.5. Insert size

Mean	41,515.57
Standard Deviation	1,916,405.47
P25/Median/P75	174 / 220 / 292

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	37,080,553
Insertions	440,337
Mapped reads with at least one insertion	1.43%
Deletions	1,020,807
Mapped reads with at least one deletion	3.31%
Homopolymer indels	47.44%

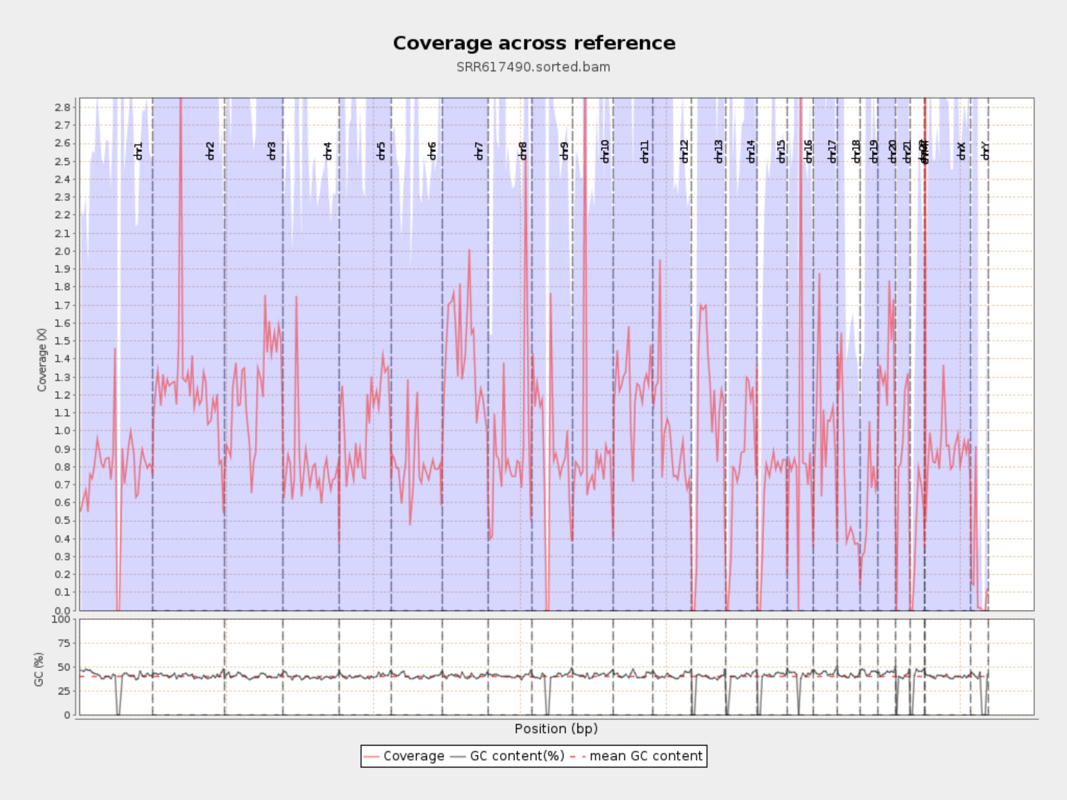
2.7. Chromosome stats

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

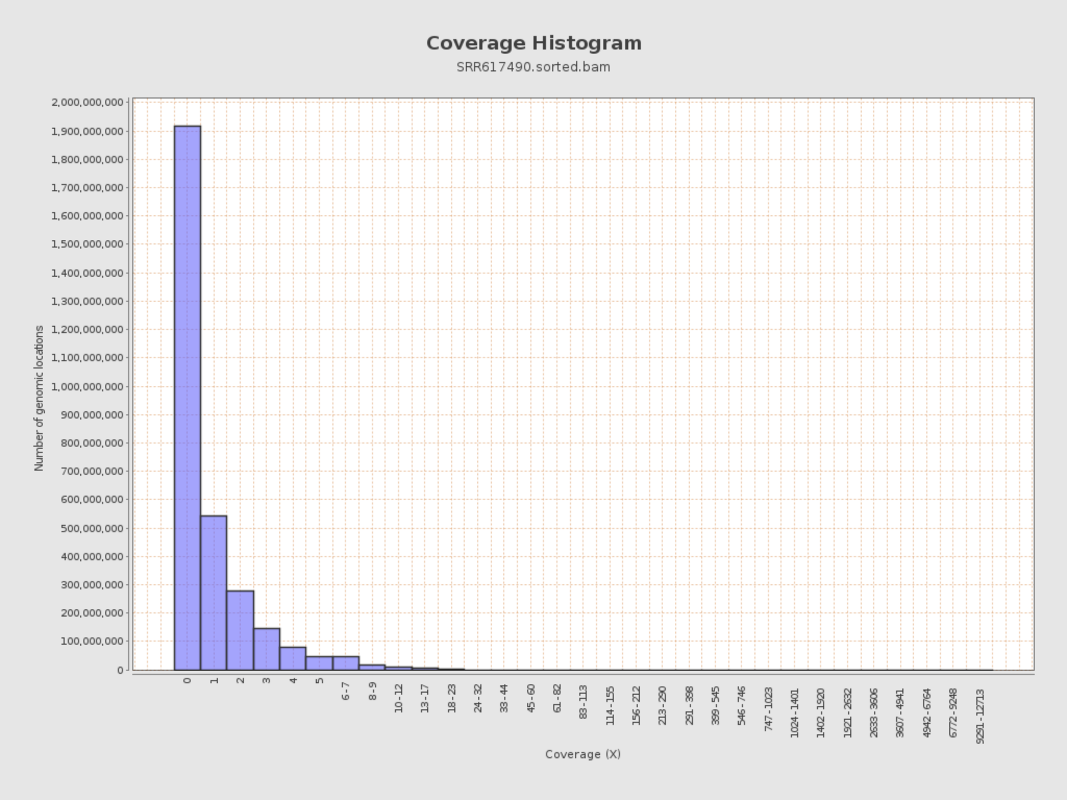
		bases	coverage	deviation
chr1	249250621	189676296	0.761	9.2984
chr2	243199373	303783444	1.2491	11.2727
chr3	198022430	242776116	1.226	2.2322
chr4	191154276	151489773	0.7925	5.9292
chr5	180915260	188075135	1.0396	2.0703
chr6	171115067	138274983	0.8081	5.3305
chr7	159138663	226582135	1.4238	12.9213
chr8	146364022	130440506	0.8912	3.7786
chr9	141213431	121841688	0.8628	17.8398
chr10	135534747	124521488	0.9187	18.2554
chr11	135006516	165671765	1.2271	12.4324
chr12	133851895	128446279	0.9596	2.0286
chr13	115169878	124842565	1.084	2.1289
chr14	107349540	85451804	0.796	2.177
chr15	102531392	66463224	0.6482	1.5584
chr16	90354753	79272542	0.8773	14.6045
chr17	81195210	82032436	1.0103	13.4221
chr18	78077248	52669922	0.6746	16.8124
chr19	59128983	34915473	0.5905	5.6021
chr20	63025520	86844087	1.3779	2.7955
chr21	48129895	42361968	0.8802	3.7343
chr22	51304566	21958450	0.428	1.2422
chrMT	16571	2062491	124.4639	93.0434
chrX	155270560	137907515	0.8882	4.083

chrY	59373566	10102616	0.1702	13.3575

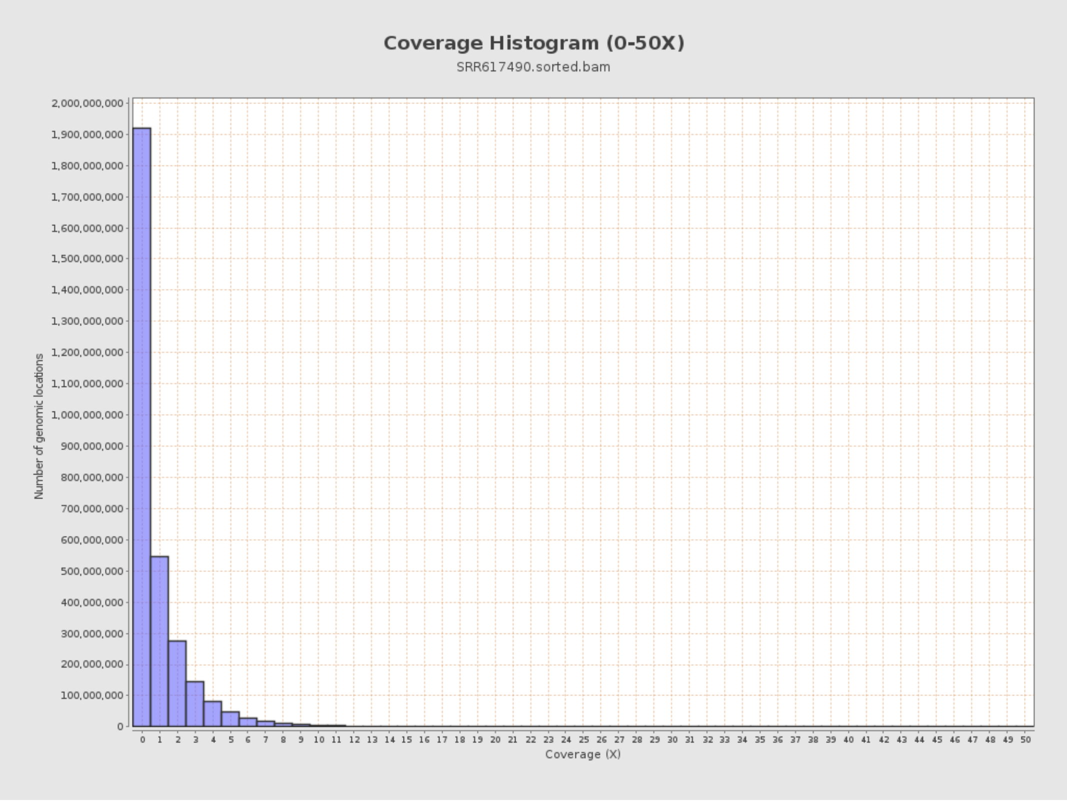
3. Results : Coverage across reference



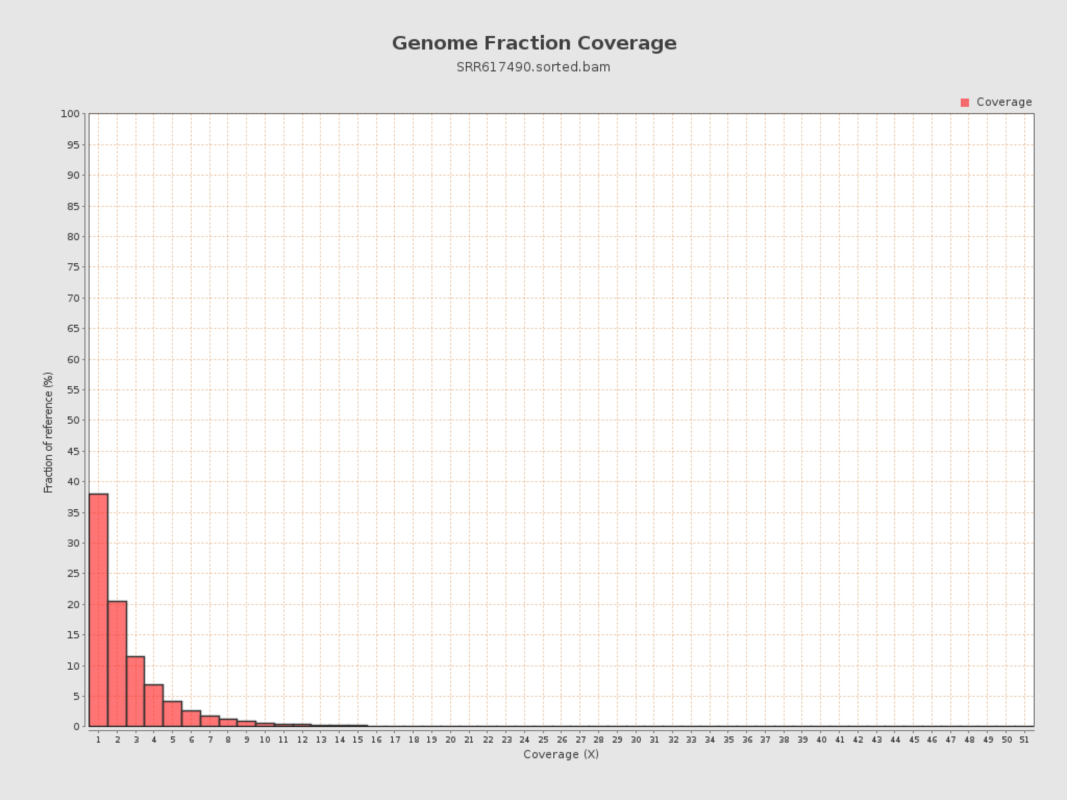
4. Results : Coverage Histogram



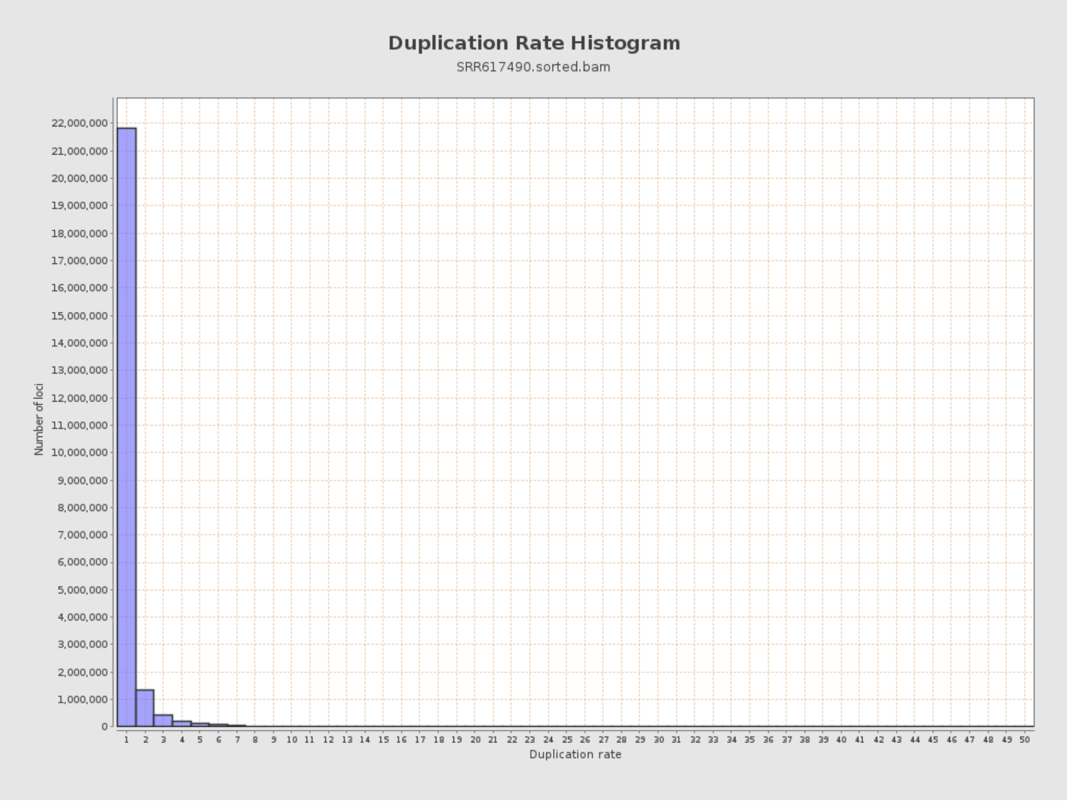
5. Results : Coverage Histogram (0-50X)



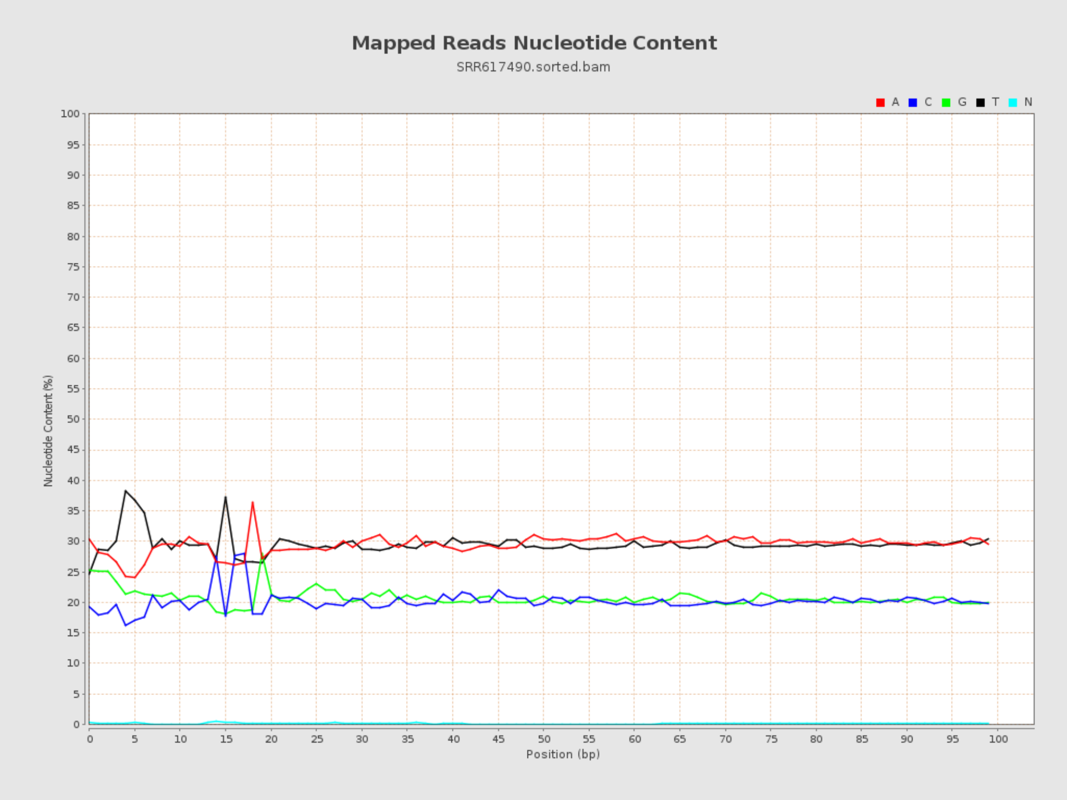
6. Results : Genome Fraction Coverage



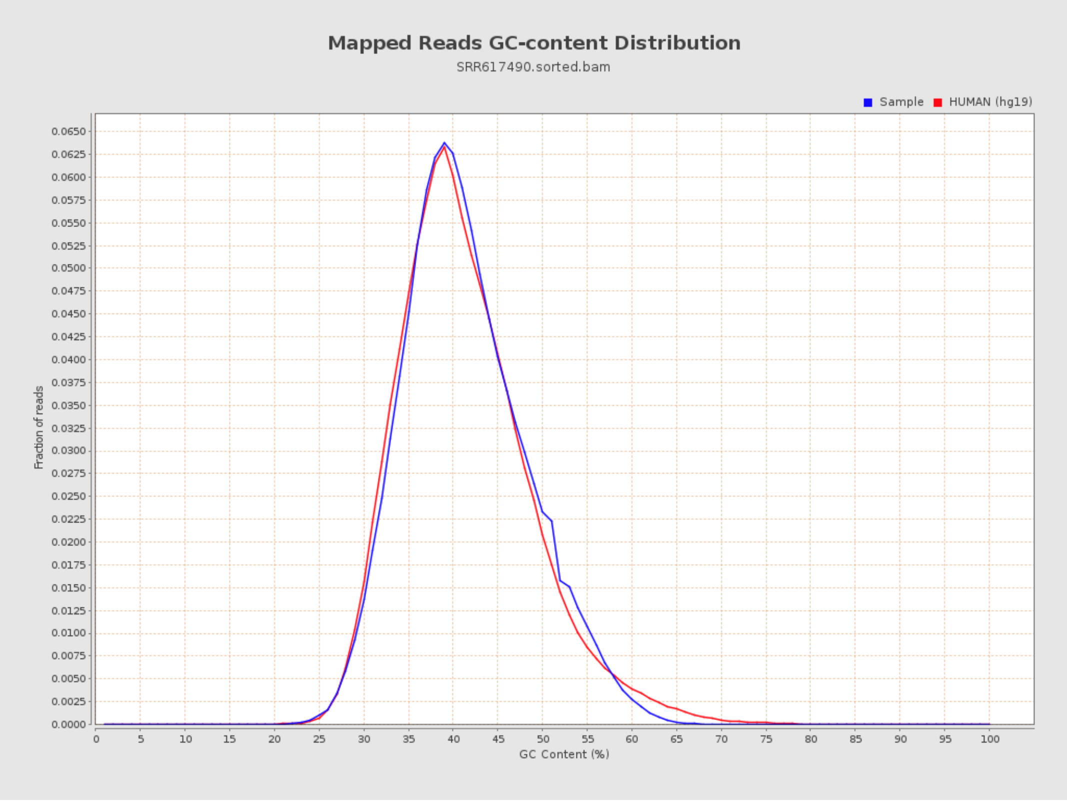
7. Results : Duplication Rate Histogram



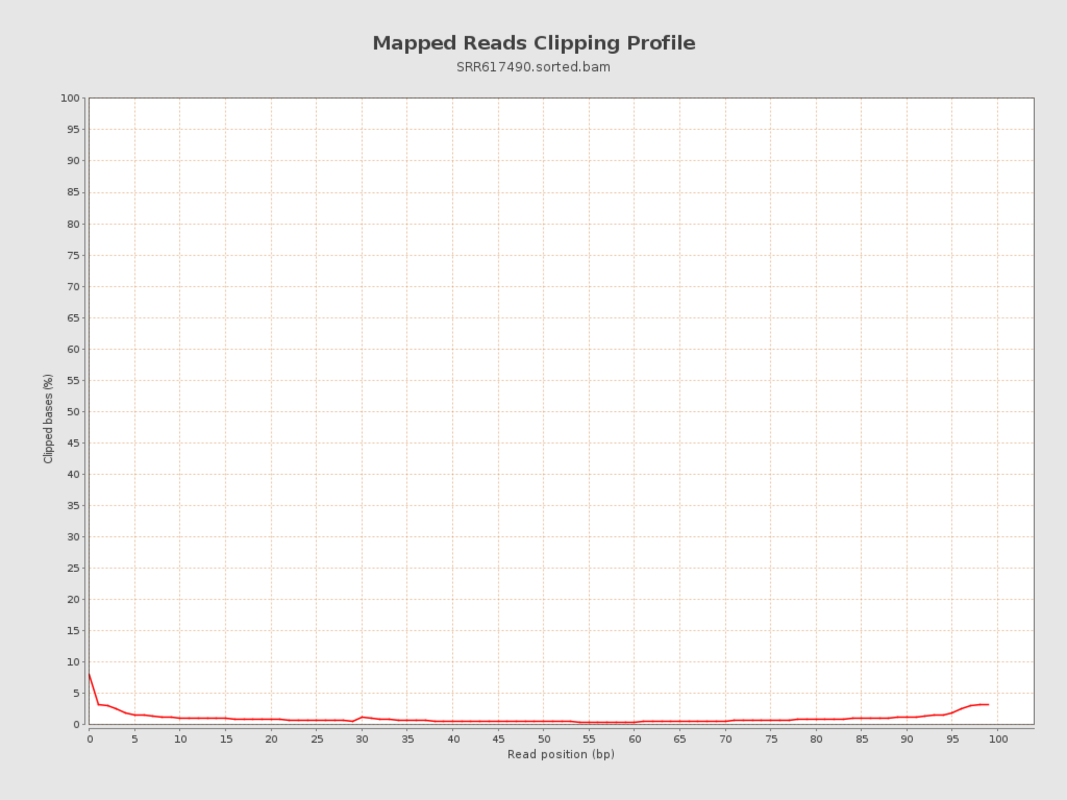
8. Results : Mapped Reads Nucleotide Content



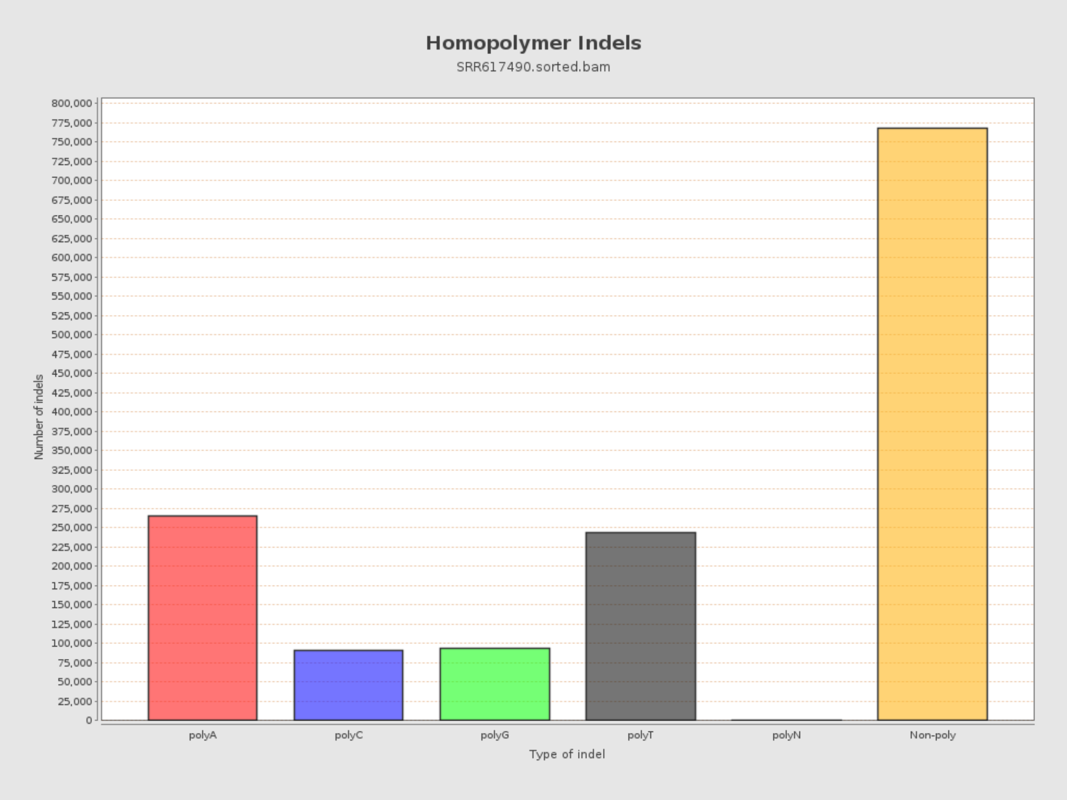
9. Results : Mapped Reads GC-content Distribution



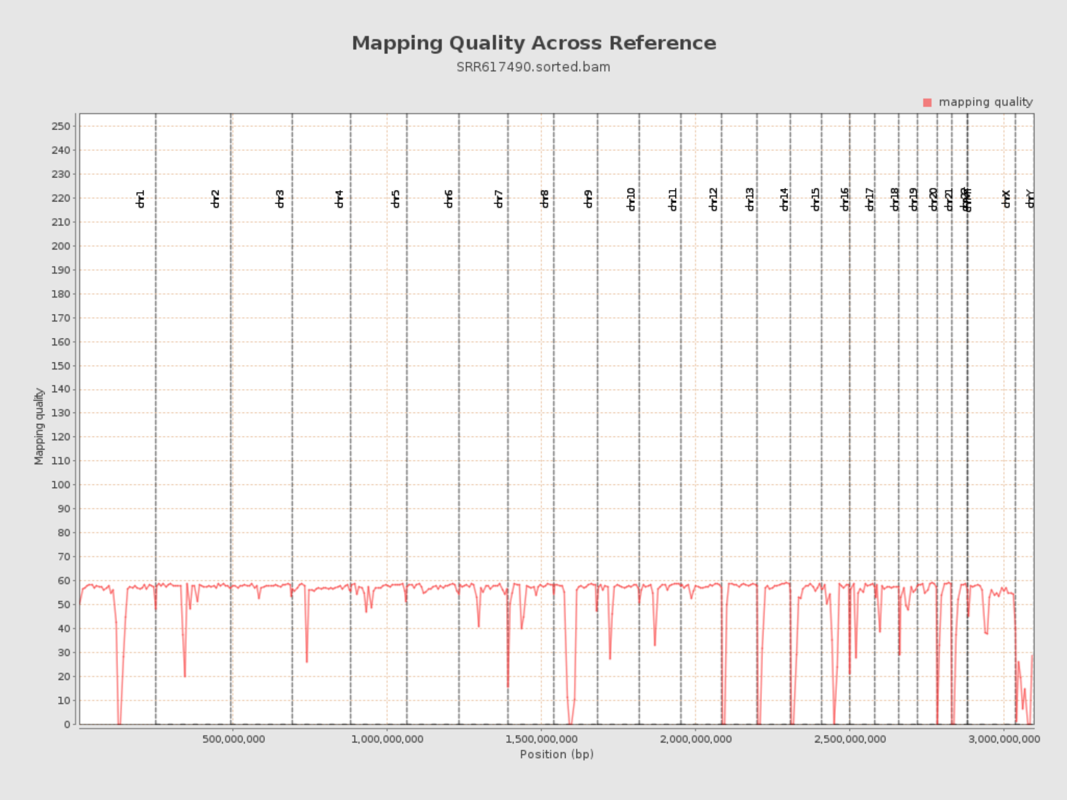
10. Results : Mapped Reads Clipping Profile



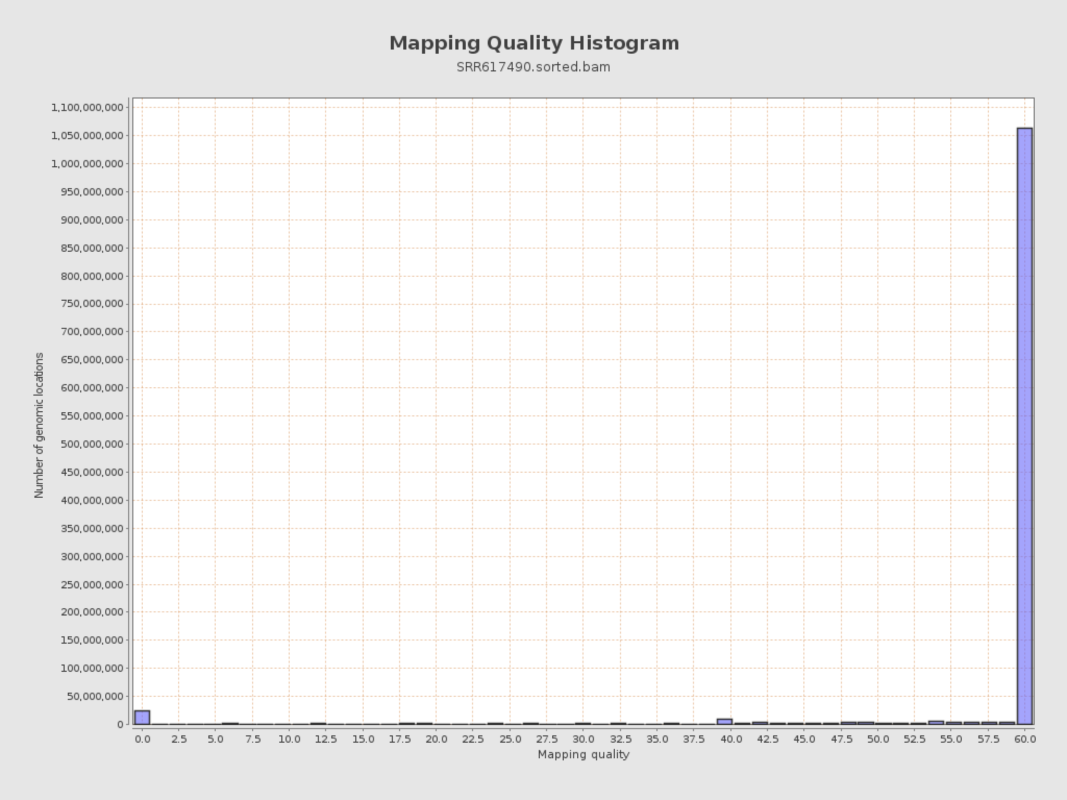
11. Results : Homopolymer Indels



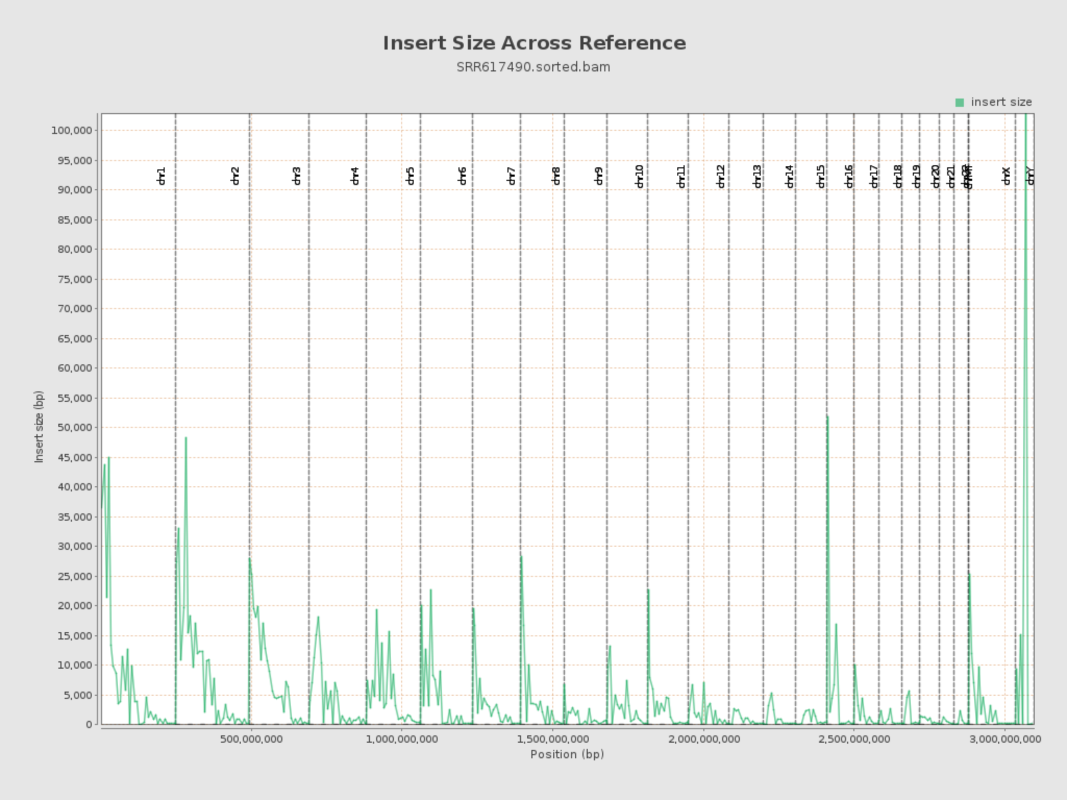
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram