Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 17:36:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617491.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_SRR617491 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617491_1.fastq.gz SRR617491_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 17:36:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617491.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,603,200 / 95.64%
Unmapped reads	1,396,800 / 4.36%
Mapped paired reads	30,603,200 / 95.64%
Mapped reads, first in pair	15,416,224 / 48.18%
Mapped reads, second in pair	15,186,976 / 47.46%
Mapped reads, both in pair	30,091,210 / 94.04%
Mapped reads, singletons	511,990 / 1.6%
Secondary alignments	0
Supplementary alignments	158,418 / 0.5%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,322,665 / 19.76%
Duplication rate	9.99%
Clipped reads	5,956,452 / 18.61%

2.2. ACGT Content

Number/percentage of A's	878,120,378 / 29.47%
Number/percentage of C's	602,286,466 / 20.21%
Number/percentage of T's	878,470,983 / 29.48%
Number/percentage of G's	617,659,783 / 20.73%
Number/percentage of N's	3,080,532 / 0.1%

GC Percentage	40.94%

2.3. Coverage

Mean	0.9631
Standard Deviation	9.6643

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	37,622.94
Standard Deviation	1,796,888.81
P25/Median/P75	174 / 220 / 291

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	35,566,700
Insertions	445,520
Mapped reads with at least one insertion	1.43%
Deletions	1,039,587
Mapped reads with at least one deletion	3.33%
Homopolymer indels	47.46%

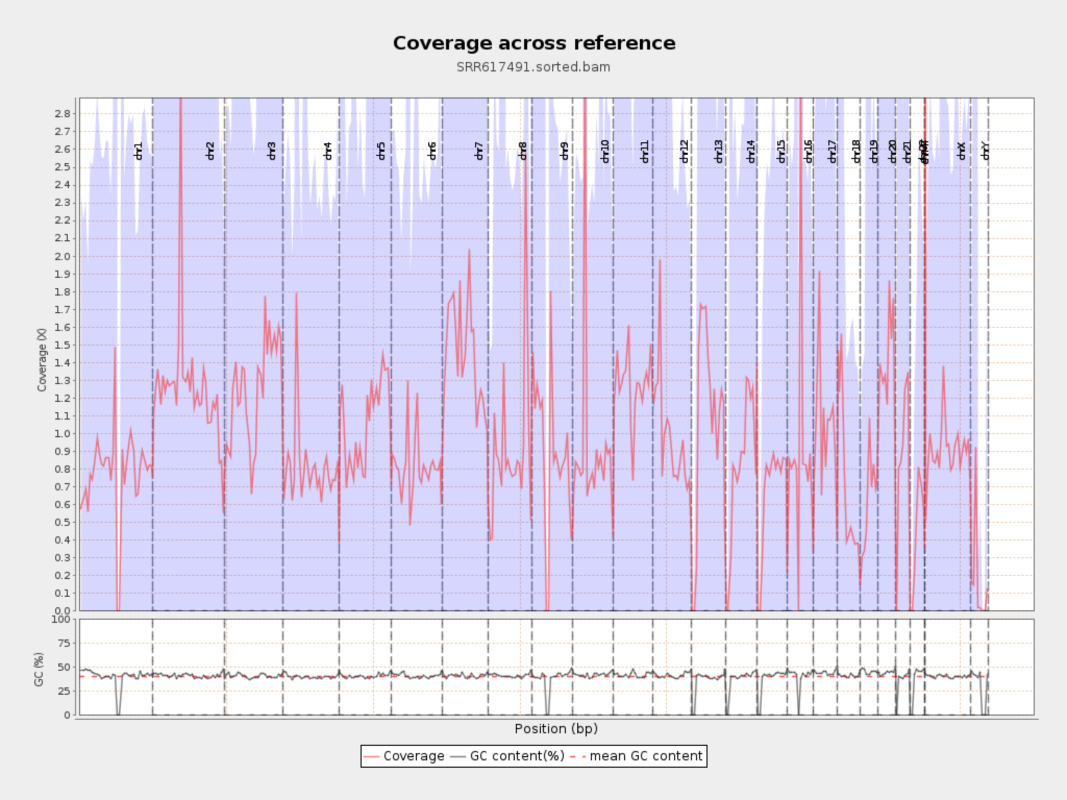
2.7. Chromosome stats

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

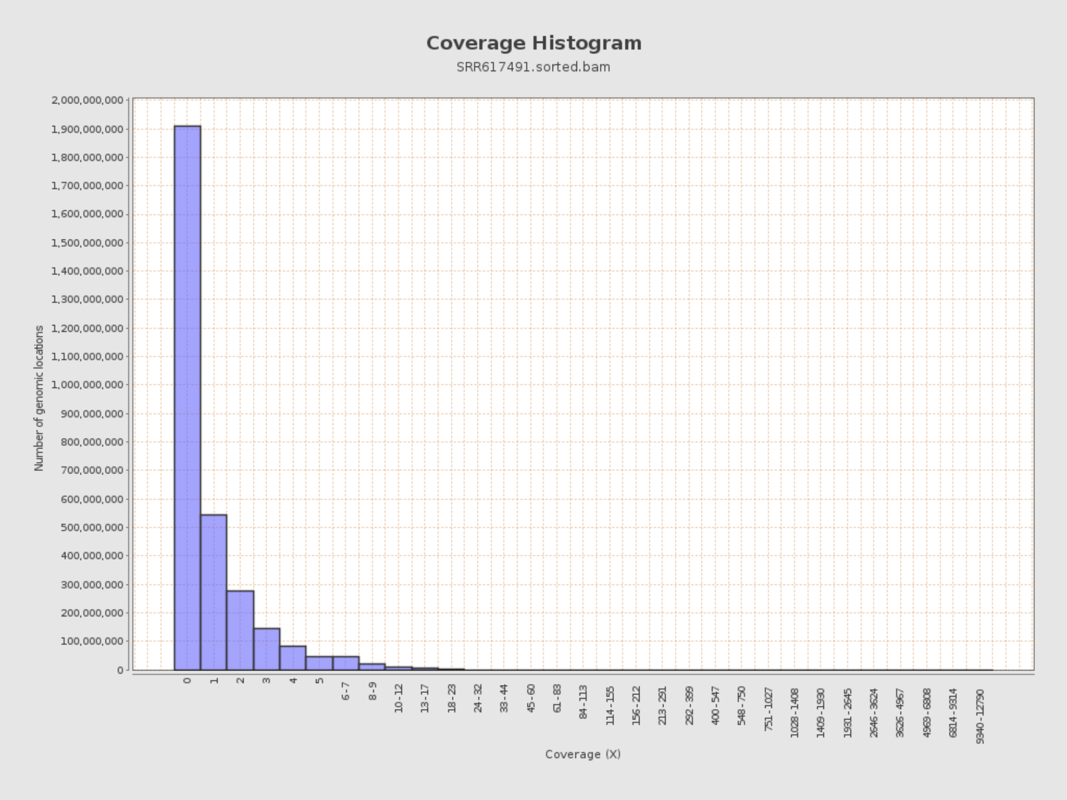
		bases	coverage	deviation
chr1	249250621	192305435	0.7715	9.4496
chr2	243199373	308053950	1.2667	11.4261
chr3	198022430	245896090	1.2418	2.2425
chr4	191154276	153755224	0.8044	6.0681
chr5	180915260	190903444	1.0552	2.0957
chr6	171115067	140415143	0.8206	5.4121
chr7	159138663	229989074	1.4452	13.1904
chr8	146364022	132355719	0.9043	3.8773
chr9	141213431	123352865	0.8735	18.203
chr10	135534747	126229569	0.9313	18.5933
chr11	135006516	168424982	1.2475	12.6696
chr12	133851895	130269445	0.9732	1.9974
chr13	115169878	126516630	1.0985	2.1297
chr14	107349540	86763932	0.8082	2.2377
chr15	102531392	67524242	0.6586	1.4958
chr16	90354753	80385092	0.8897	14.6964
chr17	81195210	83435998	1.0276	13.5074
chr18	78077248	53198172	0.6814	16.9887
chr19	59128983	35806356	0.6056	5.8135
chr20	63025520	88304868	1.4011	2.83
chr21	48129895	42986750	0.8931	3.8021
chr22	51304566	22323157	0.4351	1.2499
chrMT	16571	2137173	128.9707	97.568
chrX	155270560	139834411	0.9006	4.1007

chrY	59373566	10226707	0.1722	13.5332

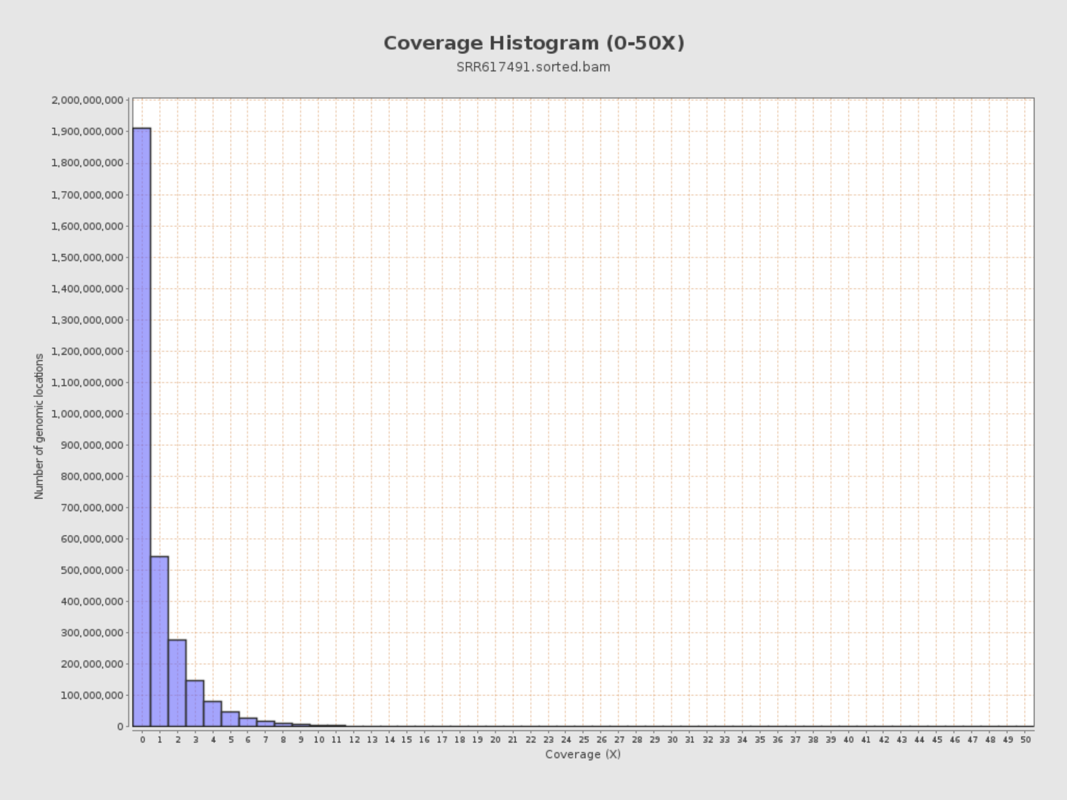
3. Results : Coverage across reference



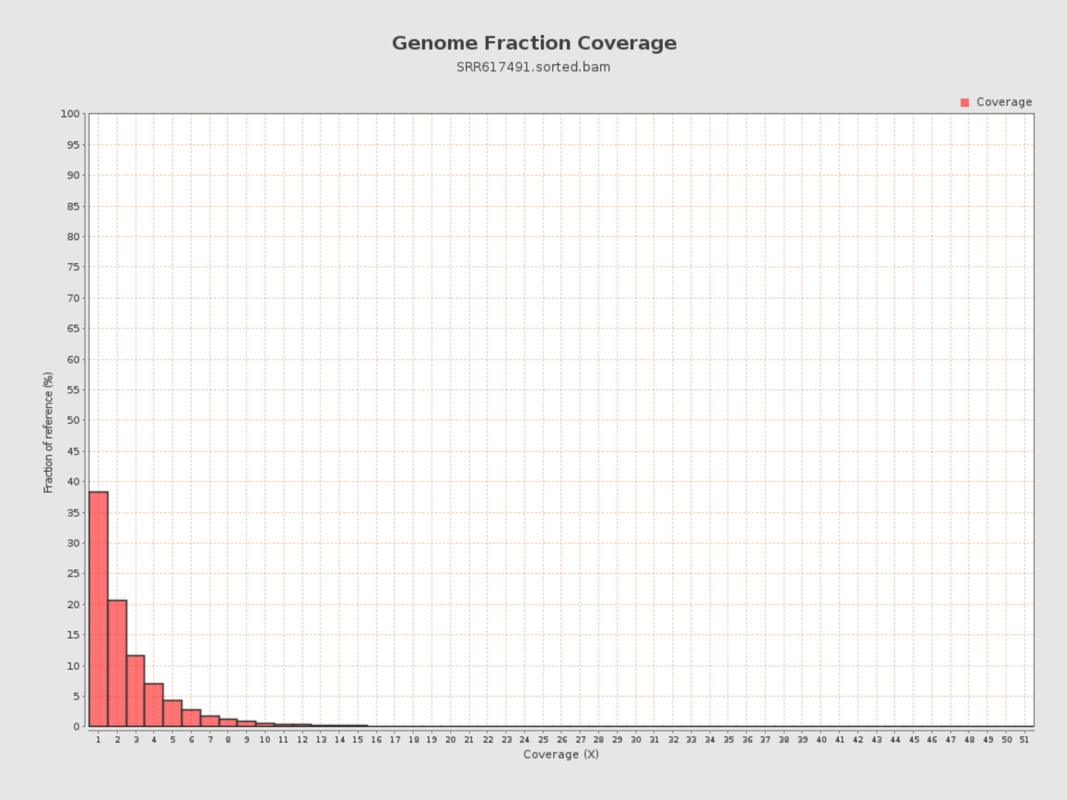
4. Results : Coverage Histogram



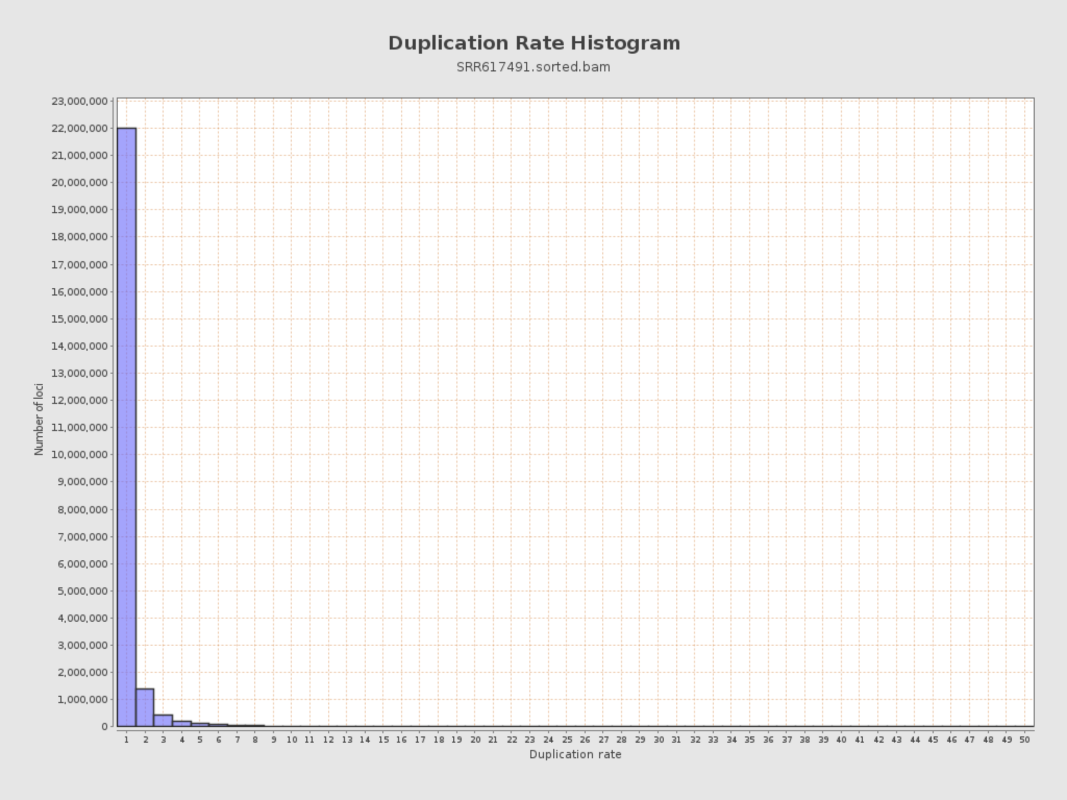
5. Results : Coverage Histogram (0-50X)



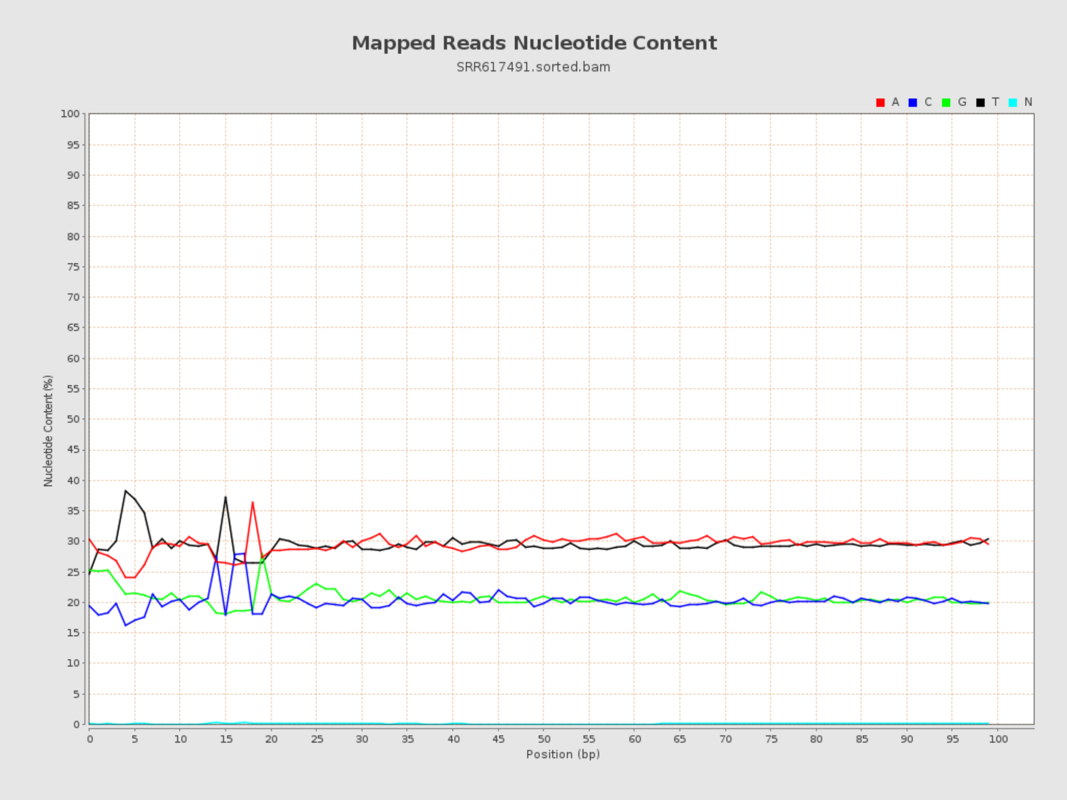
6. Results : Genome Fraction Coverage



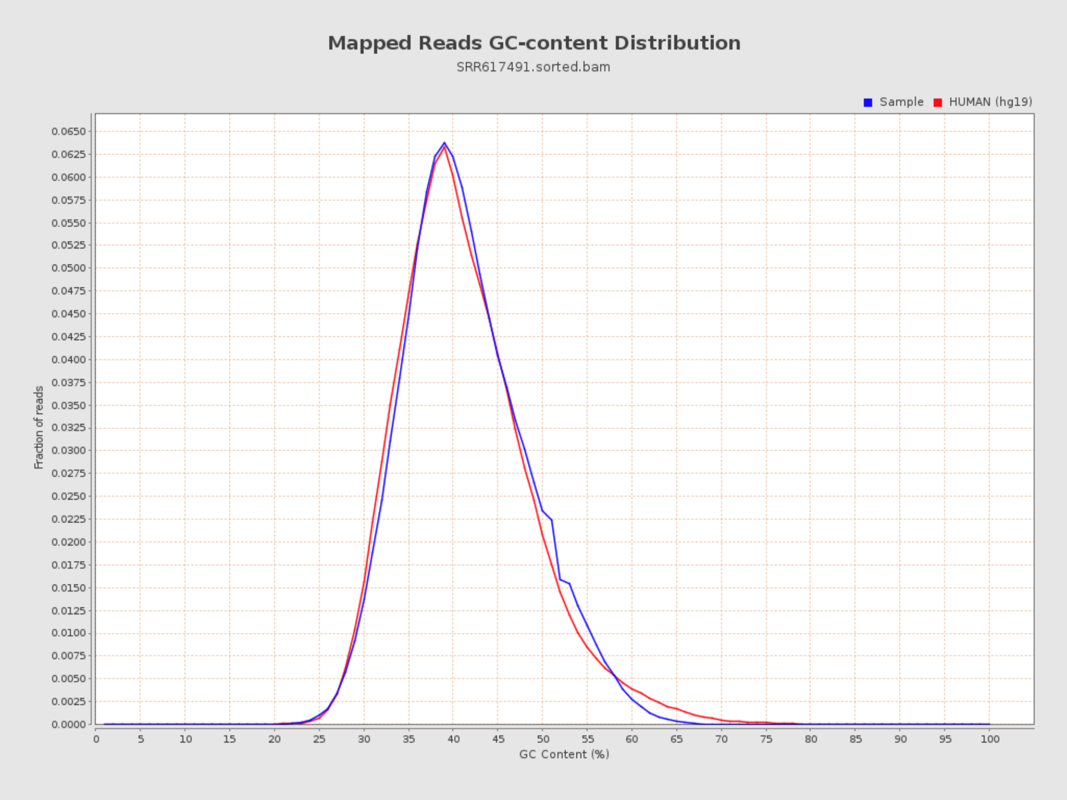
7. Results : Duplication Rate Histogram



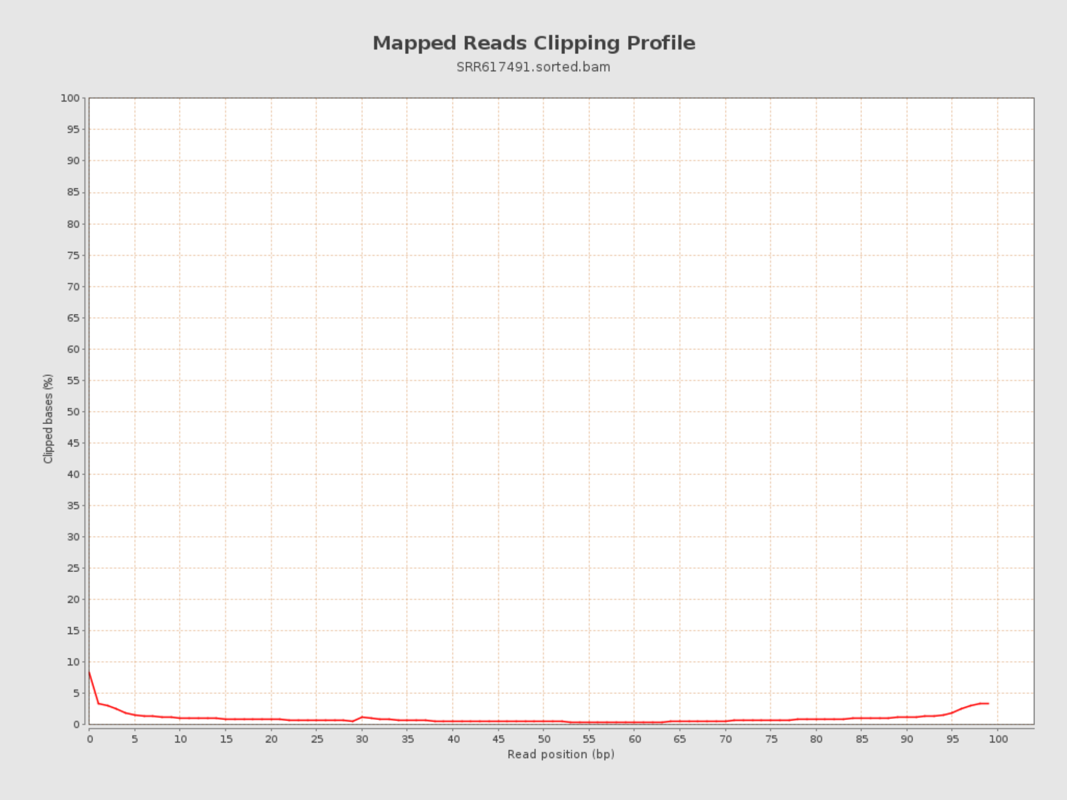
8. Results : Mapped Reads Nucleotide Content



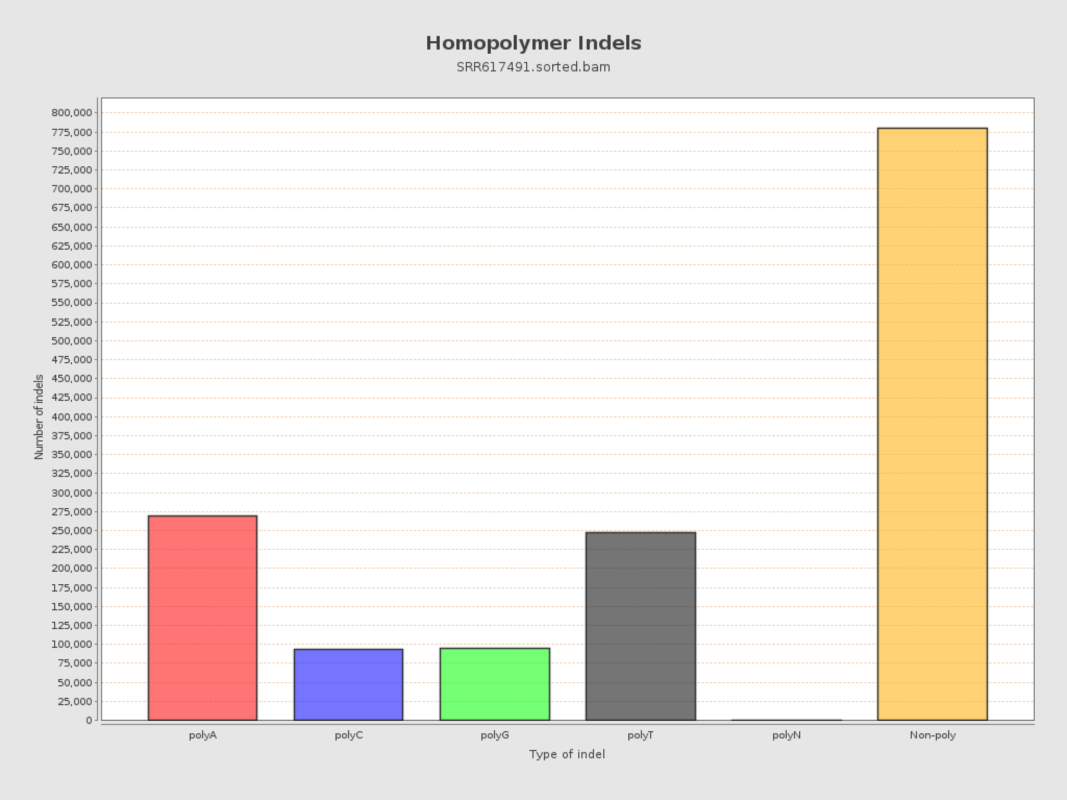
9. Results : Mapped Reads GC-content Distribution



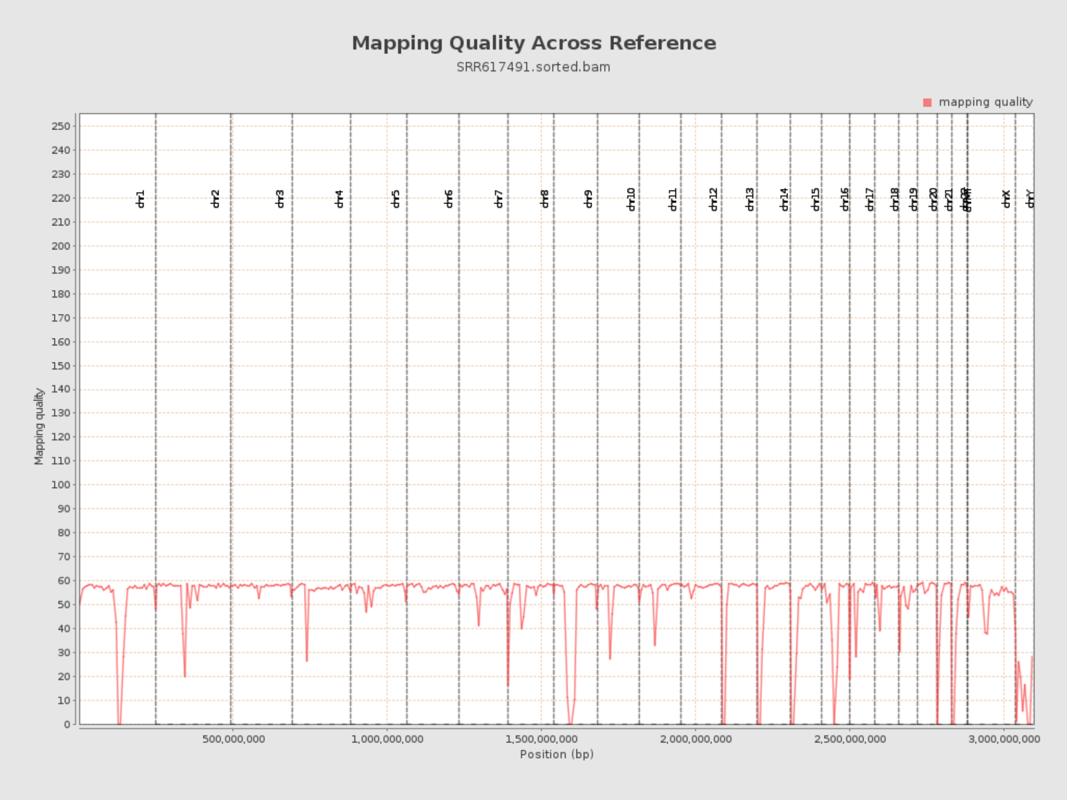
10. Results : Mapped Reads Clipping Profile



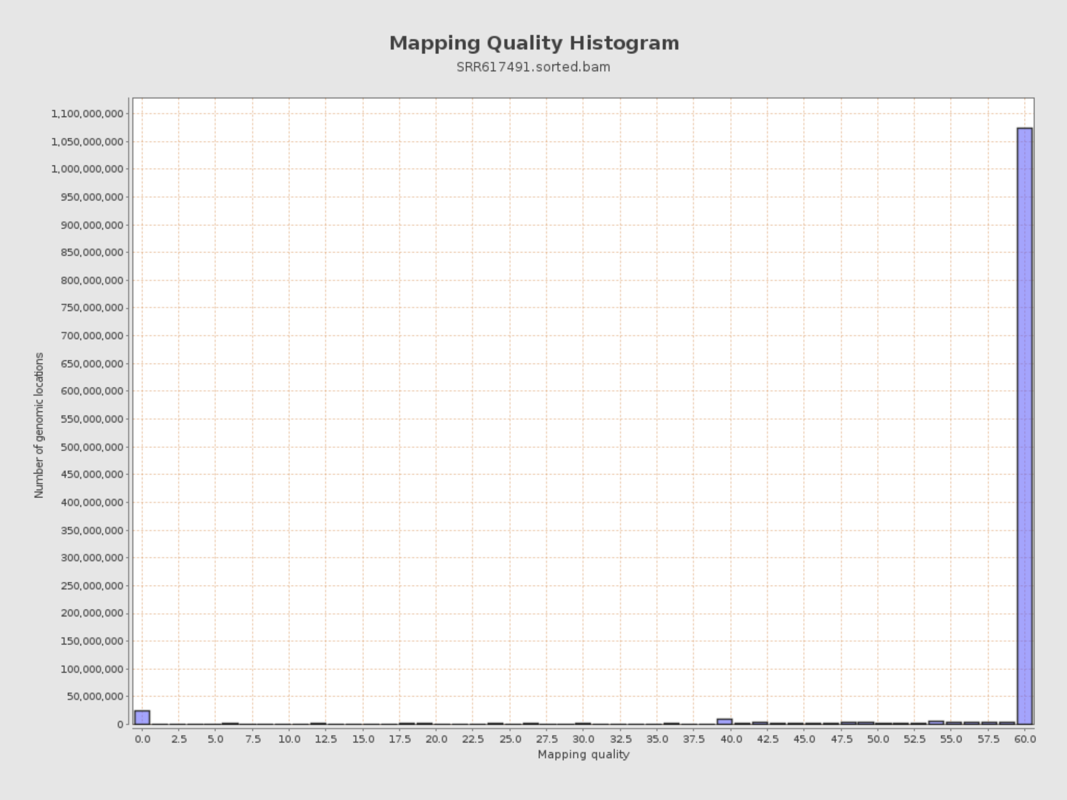
11. Results : Homopolymer Indels



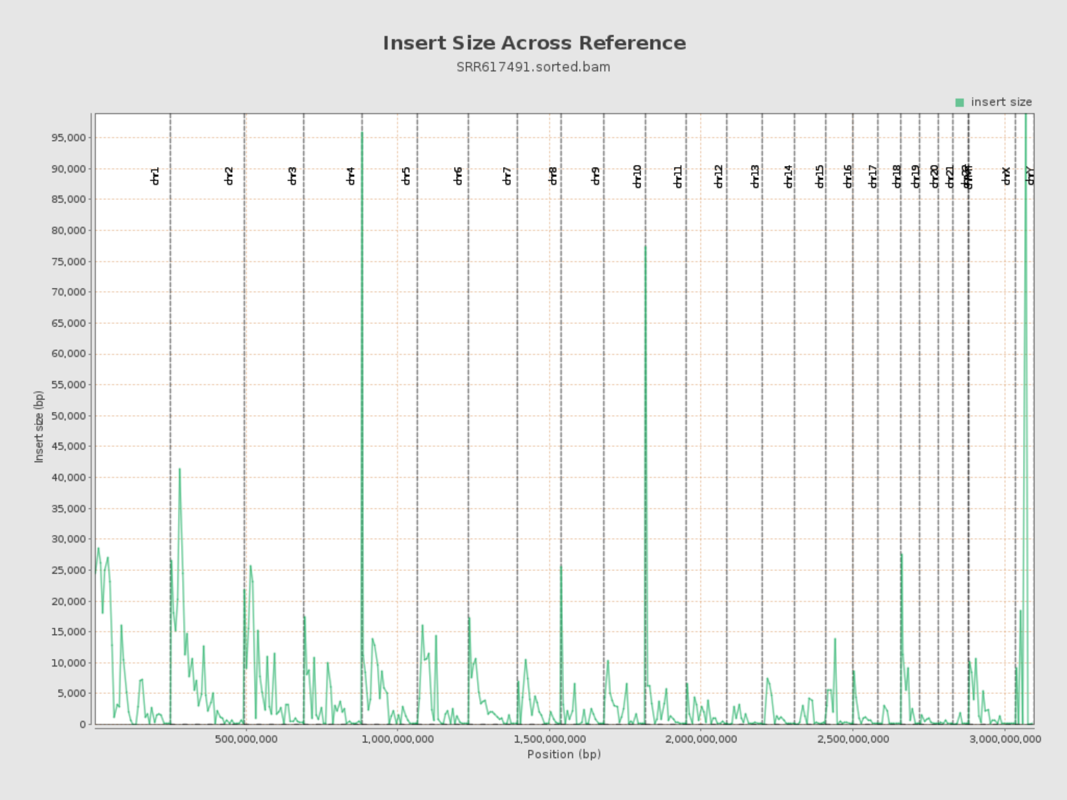
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram