Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 01:03:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617658.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_SRR617658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617658_1.fastq.gz SRR617658_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 01:03:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,199,824 / 94.37%
Unmapped reads	1,800,176 / 5.63%
Mapped paired reads	30,199,824 / 94.37%
Mapped reads, first in pair	15,299,281 / 47.81%
Mapped reads, second in pair	14,900,543 / 46.56%
Mapped reads, both in pair	29,439,552 / 92%
Mapped reads, singletons	760,272 / 2.38%
Secondary alignments	0
Supplementary alignments	171,676 / 0.54%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	6,970,407 / 21.78%
Duplication rate	10.78%
Clipped reads	6,584,554 / 20.58%

2.2. ACGT Content

Number/percentage of A's	868,054,362 / 29.76%
Number/percentage of C's	580,792,037 / 19.91%
Number/percentage of T's	867,841,260 / 29.75%
Number/percentage of G's	597,337,784 / 20.48%
Number/percentage of N's	3,270,268 / 0.11%

GC Percentage	40.38%

2.3. Coverage

Mean	0.9429
Standard Deviation	10.5235

2.4. Mapping Quality

Mean Mapping Quality	52.56

2.5. Insert size

Mean	45,481.15
Standard Deviation	2,004,612.58
P25/Median/P75	180 / 225 / 294

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	40,334,490
Insertions	459,227
Mapped reads with at least one insertion	1.49%
Deletions	1,074,070
Mapped reads with at least one deletion	3.48%
Homopolymer indels	47.6%

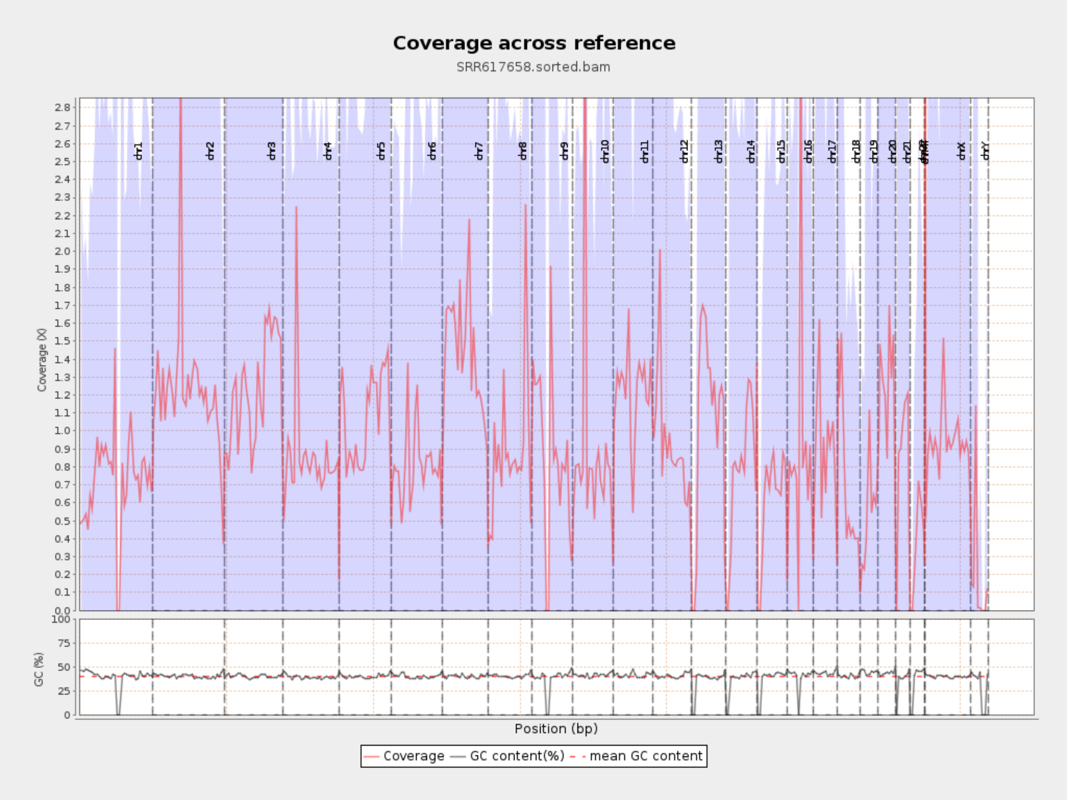
2.7. Chromosome stats

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

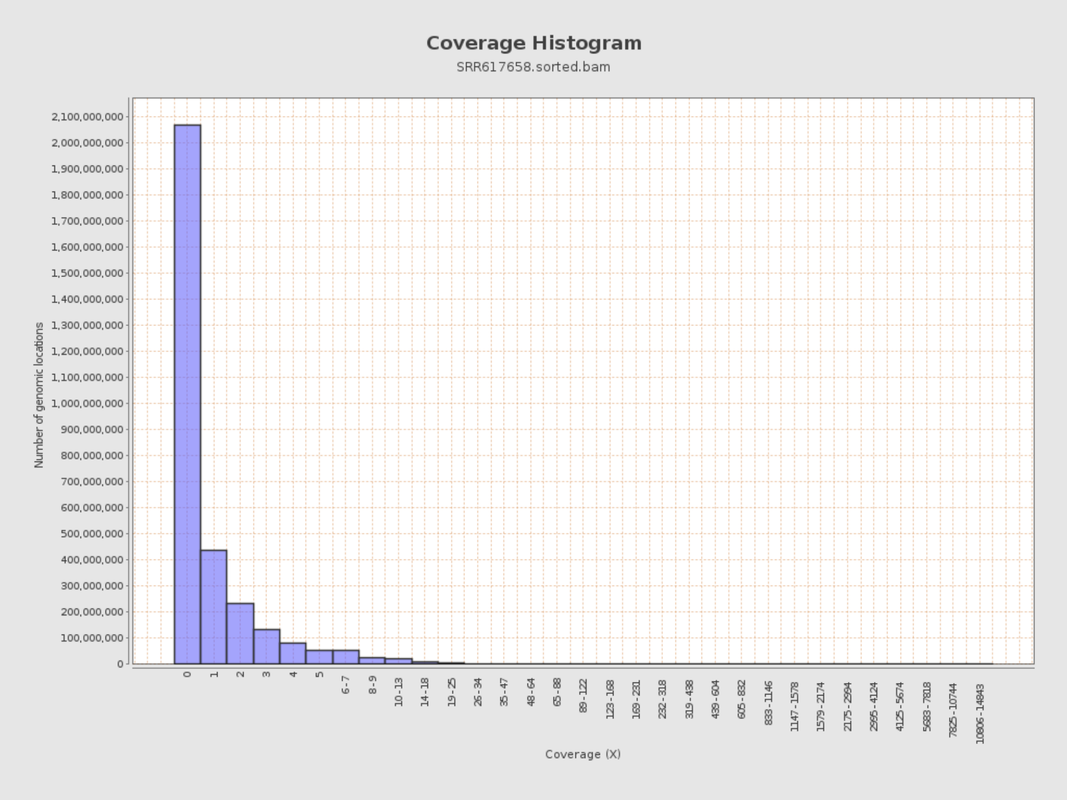
		bases	coverage	deviation
chr1	249250621	179489882	0.7201	10.1575
chr2	243199373	301736056	1.2407	12.1223
chr3	198022430	244391617	1.2342	2.4692
chr4	191154276	163135432	0.8534	8.4266
chr5	180915260	192844512	1.0659	2.3129
chr6	171115067	141404934	0.8264	5.6677
chr7	159138663	227933265	1.4323	13.1291
chr8	146364022	129655104	0.8858	4.0615
chr9	141213431	119723211	0.8478	20.3924
chr10	135534747	123713728	0.9128	21.3489
chr11	135006516	160697058	1.1903	11.8492
chr12	133851895	124671055	0.9314	2.2487
chr13	115169878	125446798	1.0892	2.312
chr14	107349540	83532900	0.7781	2.4371
chr15	102531392	62498760	0.6096	1.7007
chr16	90354753	80899567	0.8954	16.5476
chr17	81195210	72092277	0.8879	12.5933
chr18	78077248	54120748	0.6932	18.1685
chr19	59128983	30942775	0.5233	6.0041
chr20	63025520	78872091	1.2514	3.0683
chr21	48129895	42378877	0.8805	4.3252
chr22	51304566	18910331	0.3686	1.2836
chrMT	16571	3135509	189.2166	134.4532
chrX	155270560	145075432	0.9343	4.3493

chrY	59373566	11777463	0.1984	17.1622

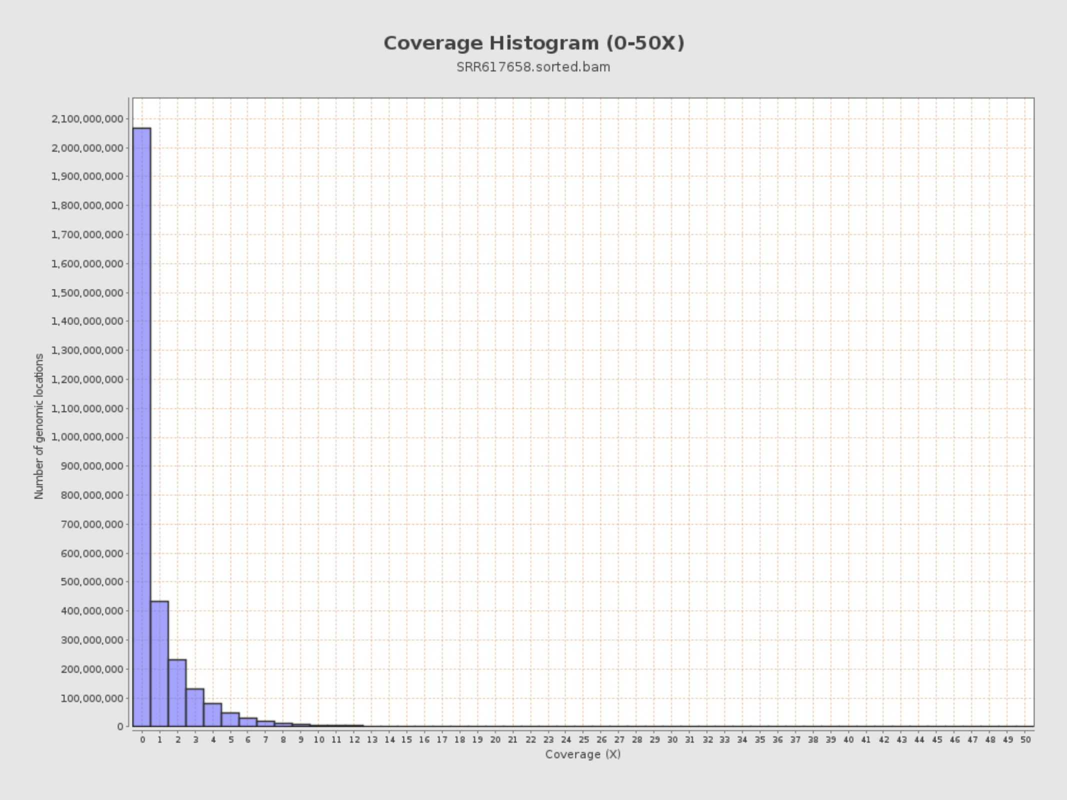
3. Results : Coverage across reference



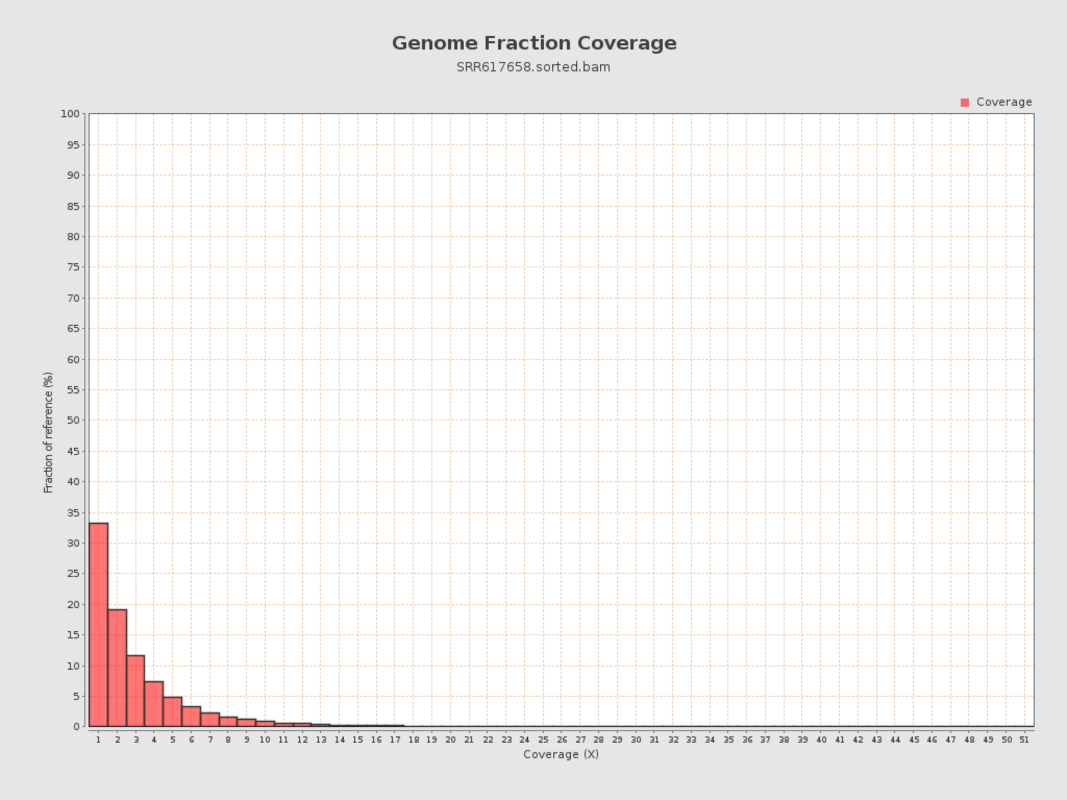
4. Results : Coverage Histogram



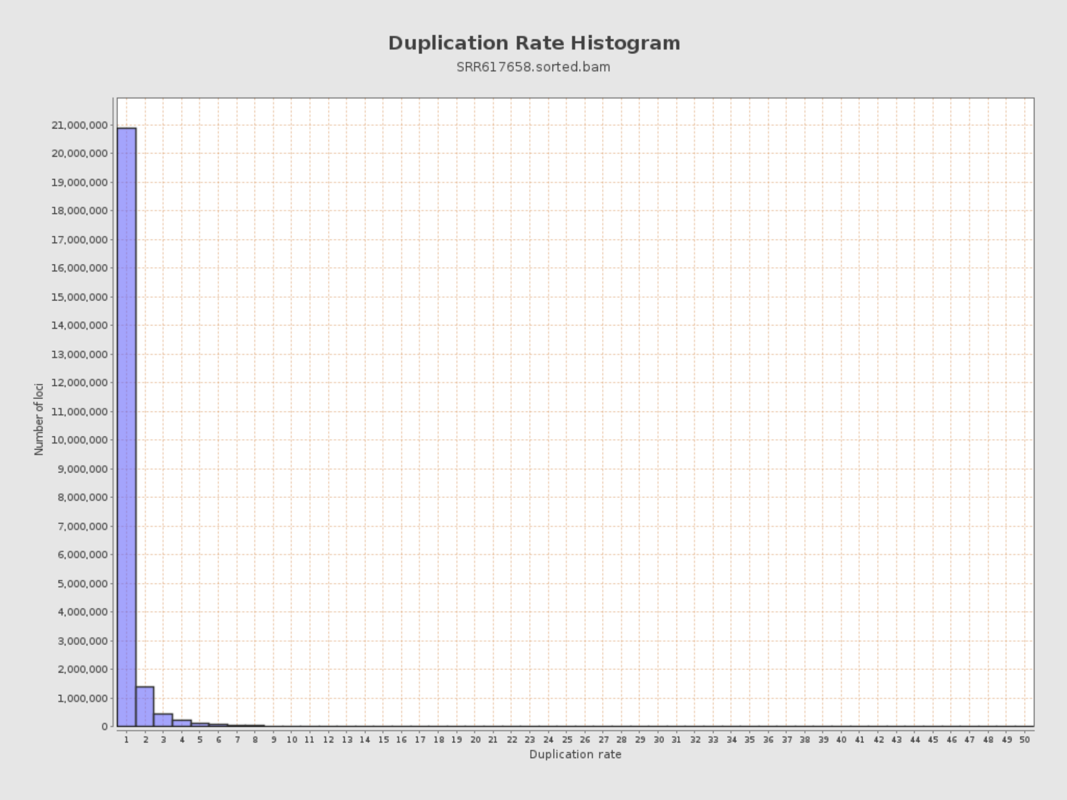
5. Results : Coverage Histogram (0-50X)



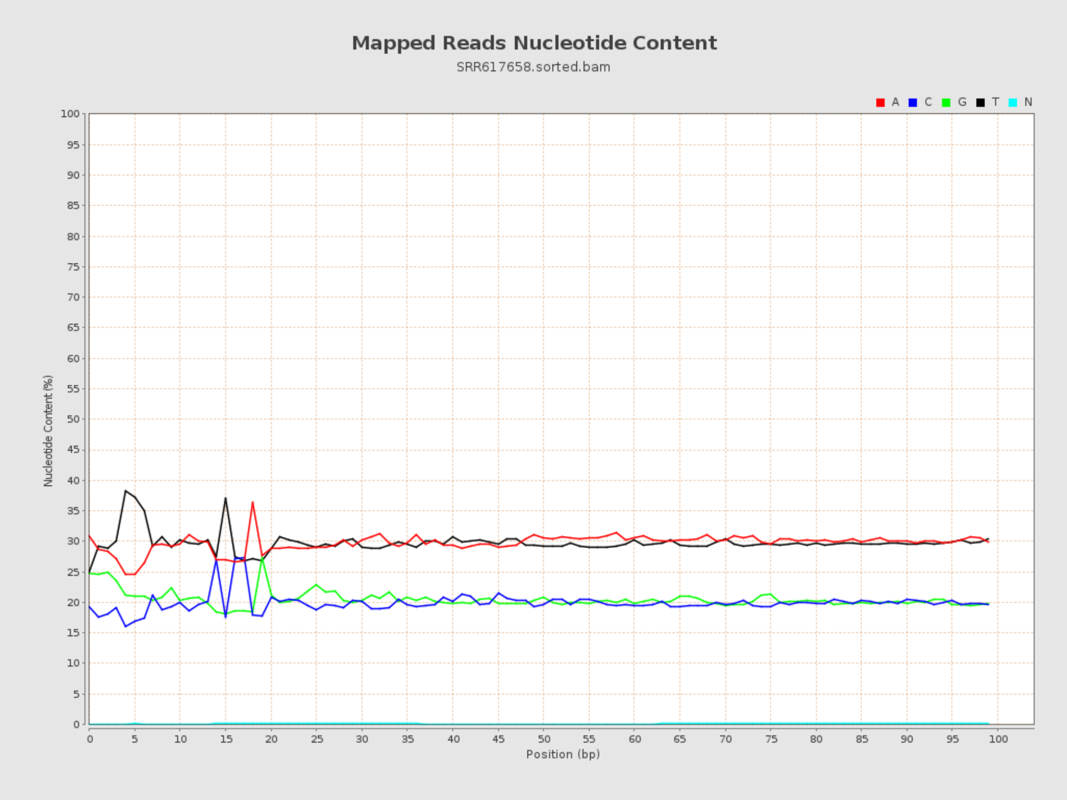
6. Results : Genome Fraction Coverage



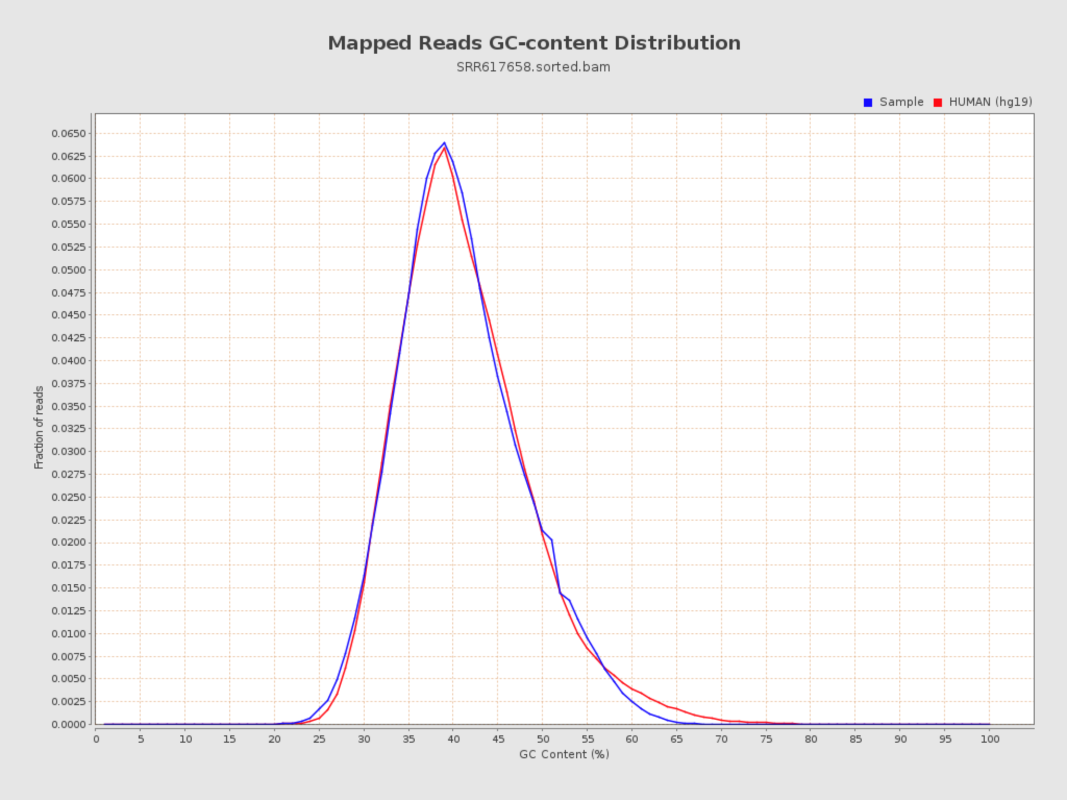
7. Results : Duplication Rate Histogram



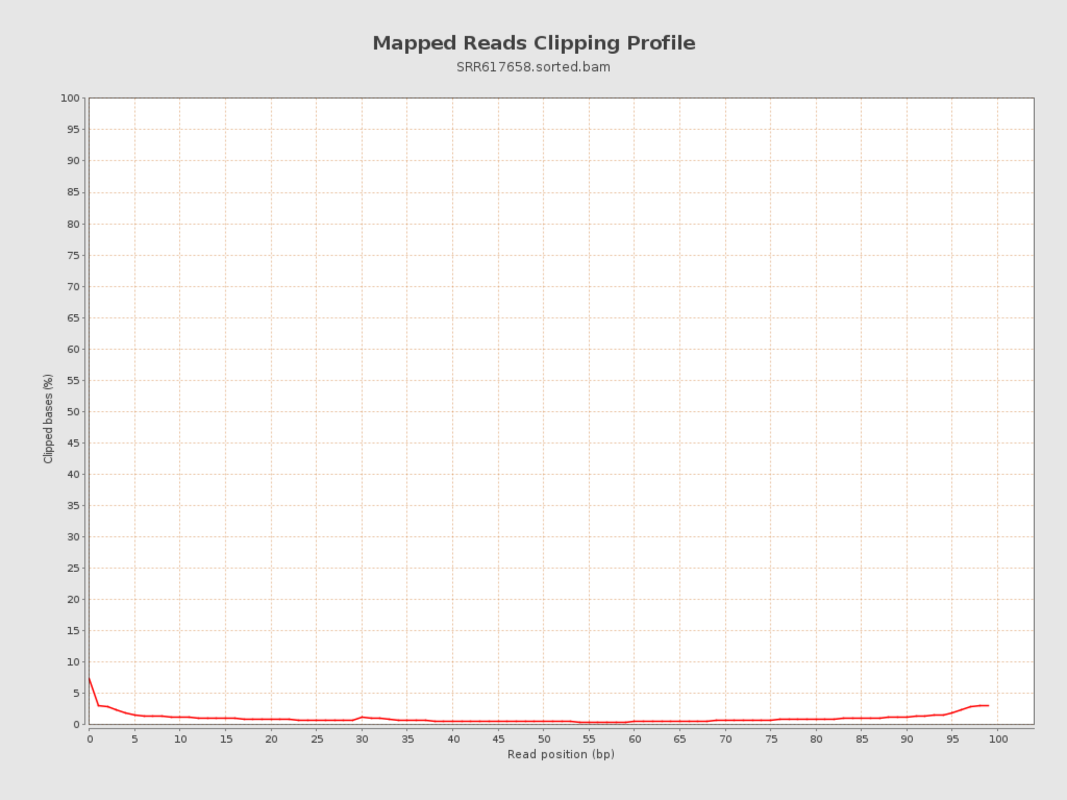
8. Results : Mapped Reads Nucleotide Content



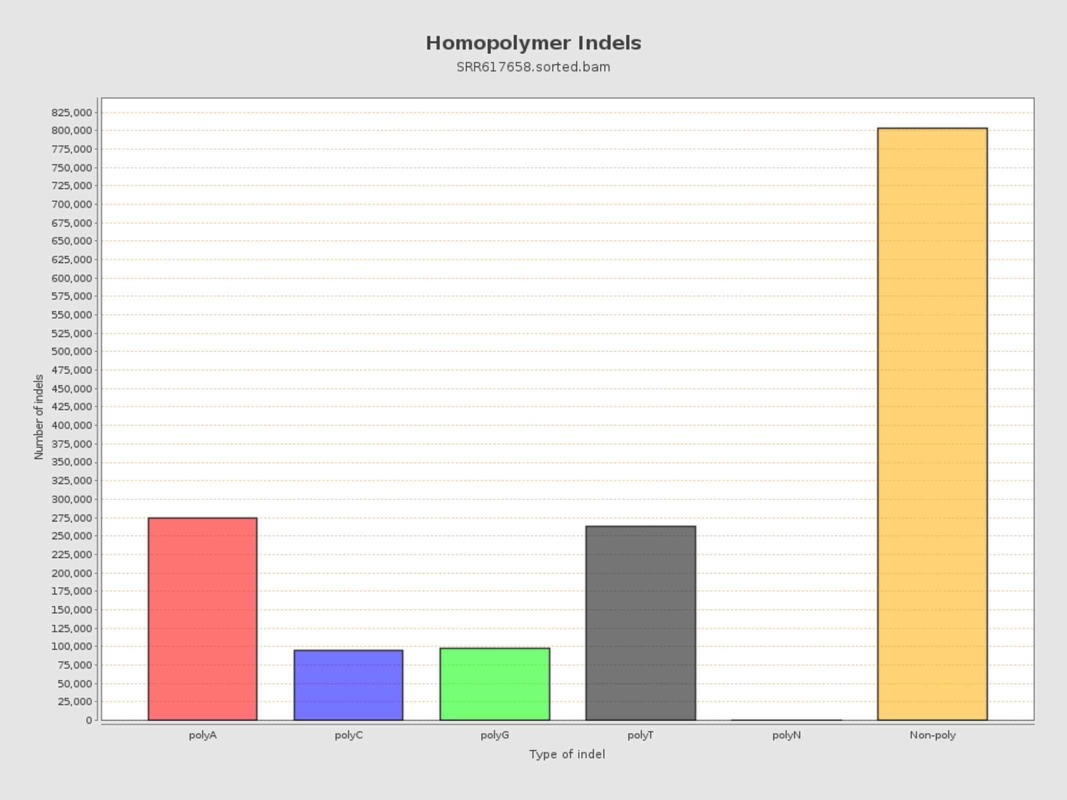
9. Results : Mapped Reads GC-content Distribution



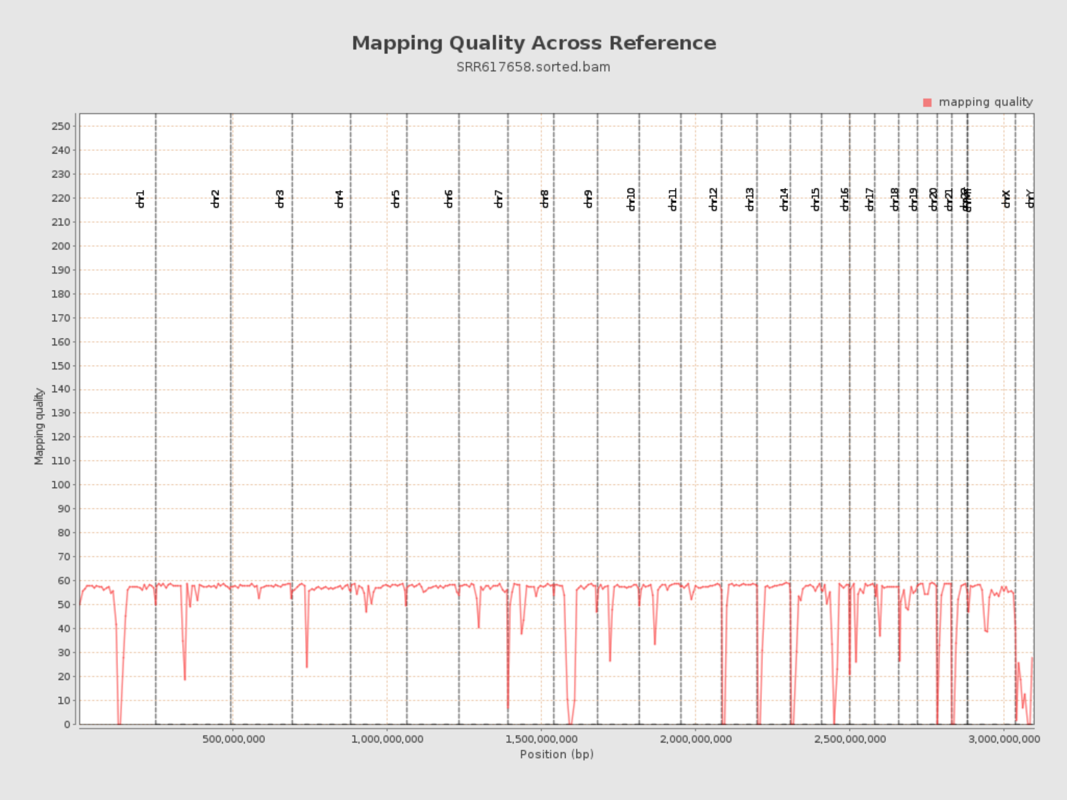
10. Results : Mapped Reads Clipping Profile



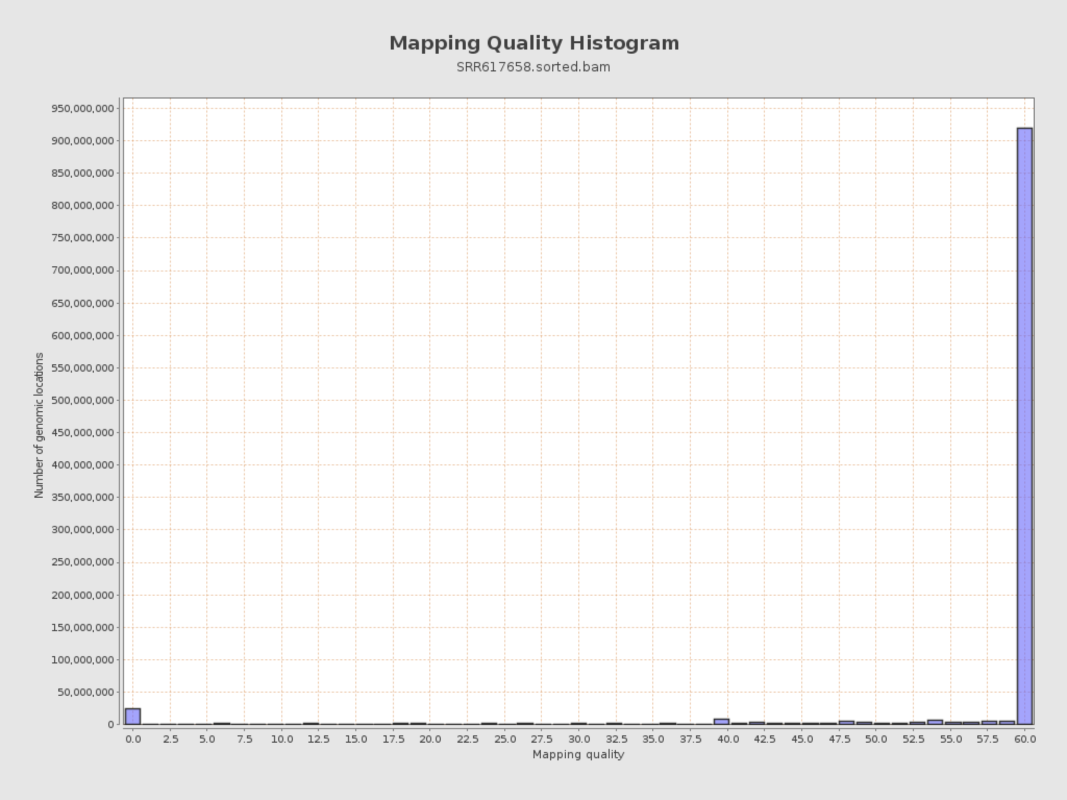
11. Results : Homopolymer Indels



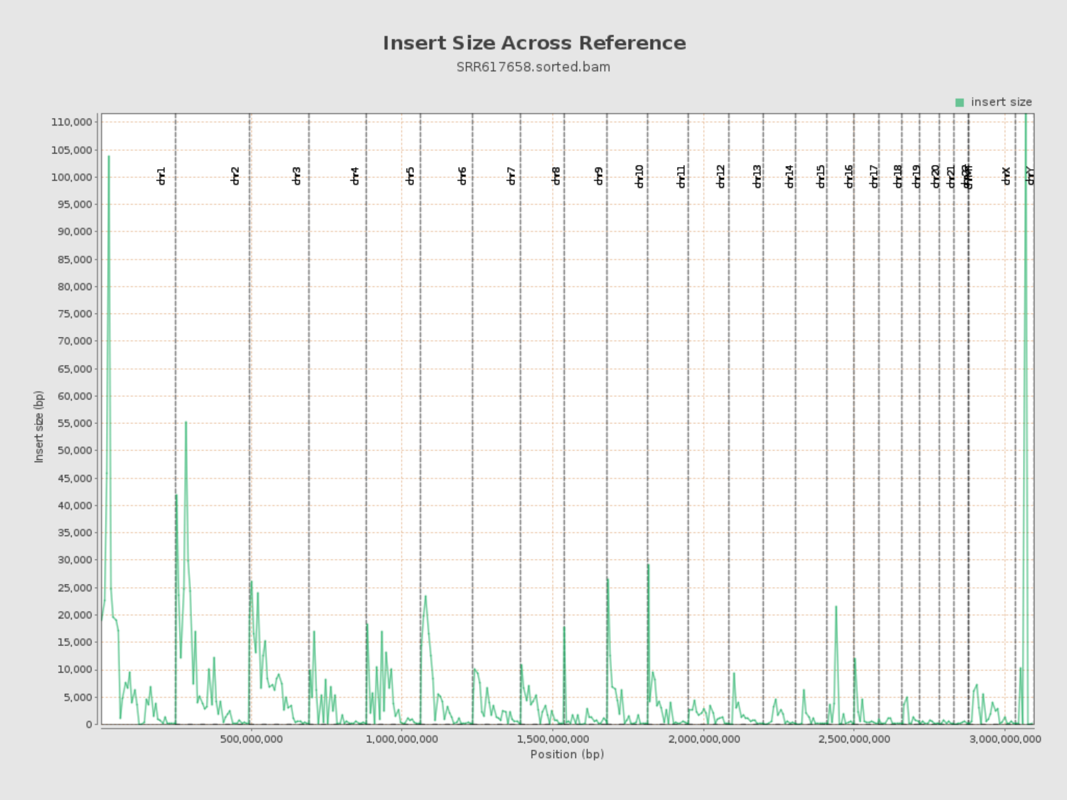
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram