Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 23:14:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617656.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_SRR617656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617656_1.fastq.gz SRR617656_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 23:13:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617656.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,599,331 / 95.62%
Unmapped reads	1,400,669 / 4.38%
Mapped paired reads	30,599,331 / 95.62%
Mapped reads, first in pair	15,471,189 / 48.35%
Mapped reads, second in pair	15,128,142 / 47.28%
Mapped reads, both in pair	29,931,930 / 93.54%
Mapped reads, singletons	667,401 / 2.09%
Secondary alignments	0
Supplementary alignments	165,956 / 0.52%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	7,158,830 / 22.37%
Duplication rate	10.95%
Clipped reads	6,450,902 / 20.16%

2.2. ACGT Content

Number/percentage of A's	879,593,161 / 29.67%
Number/percentage of C's	591,154,336 / 19.94%
Number/percentage of T's	881,157,648 / 29.72%
Number/percentage of G's	608,902,083 / 20.54%
Number/percentage of N's	3,597,690 / 0.12%

GC Percentage	40.48%

2.3. Coverage

Mean	0.9582
Standard Deviation	10.5611

2.4. Mapping Quality

Mean Mapping Quality	52.63

2.5. Insert size

Mean	42,659.02
Standard Deviation	1,918,265.97
P25/Median/P75	181 / 227 / 297

2.6. Mismatches and indels

General error rate	1.47%
Mismatches	42,703,685
Insertions	467,303
Mapped reads with at least one insertion	1.5%
Deletions	1,094,032
Mapped reads with at least one deletion	3.5%
Homopolymer indels	47.46%

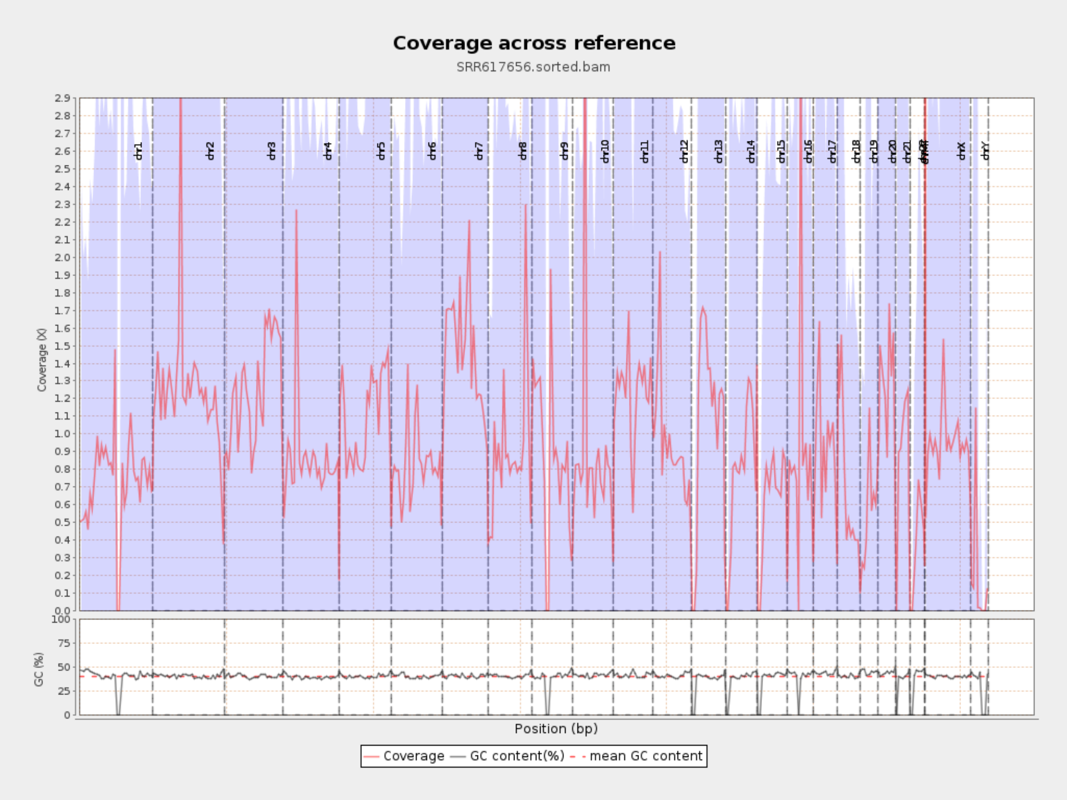
2.7. Chromosome stats

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

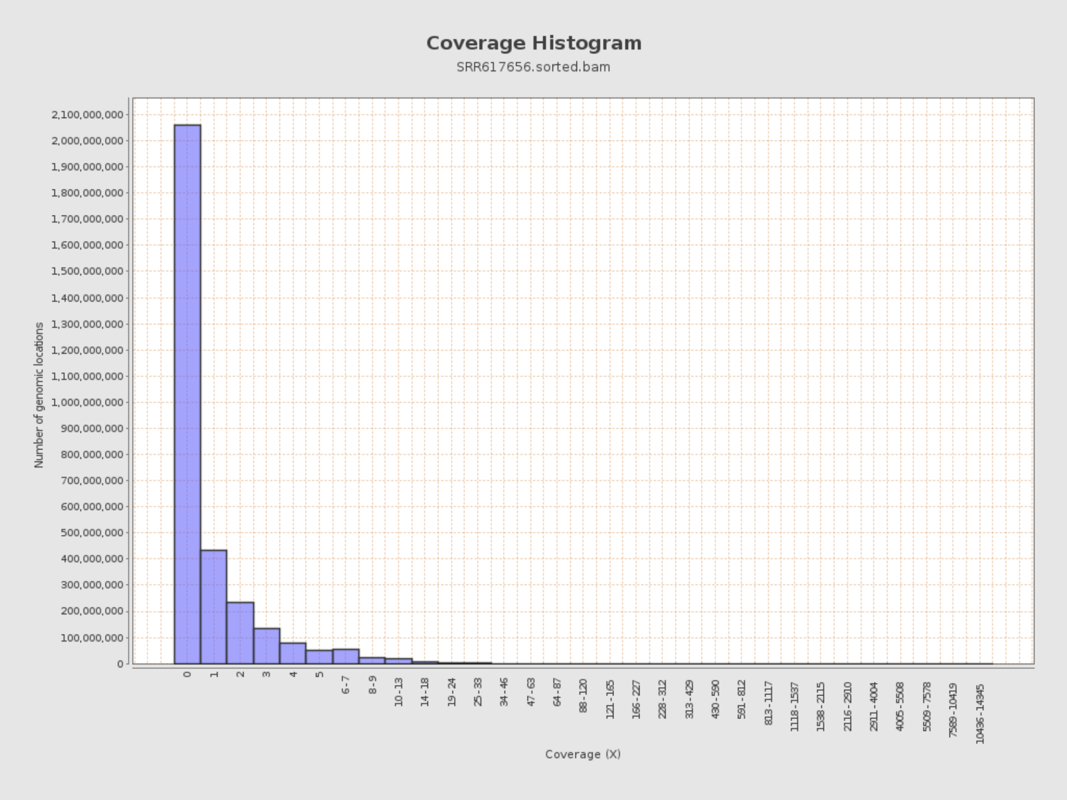
		bases	coverage	deviation
chr1	249250621	182378563	0.7317	10.2901
chr2	243199373	306504452	1.2603	12.1852
chr3	198022430	248073613	1.2528	2.4999
chr4	191154276	165166013	0.864	8.3254
chr5	180915260	196178927	1.0844	2.3507
chr6	171115067	143775817	0.8402	5.8272
chr7	159138663	232178925	1.459	13.538
chr8	146364022	131986394	0.9018	4.1049
chr9	141213431	121533350	0.8606	20.1229
chr10	135534747	125595454	0.9267	21.2865
chr11	135006516	163163277	1.2086	11.8707
chr12	133851895	126785148	0.9472	2.1838
chr13	115169878	127228640	1.1047	2.3191
chr14	107349540	84902801	0.7909	2.5144
chr15	102531392	63495359	0.6193	1.6849
chr16	90354753	82187244	0.9096	16.6849
chr17	81195210	73387952	0.9038	12.7884
chr18	78077248	54534591	0.6985	18.2265
chr19	59128983	31906526	0.5396	6.1618
chr20	63025520	80581523	1.2786	3.0725
chr21	48129895	43288974	0.8994	4.4172
chr22	51304566	19333209	0.3768	1.2984
chrMT	16571	3120041	188.2832	130.1542
chrX	155270560	147084595	0.9473	4.4065

chrY	59373566	11855903	0.1997	17.2616

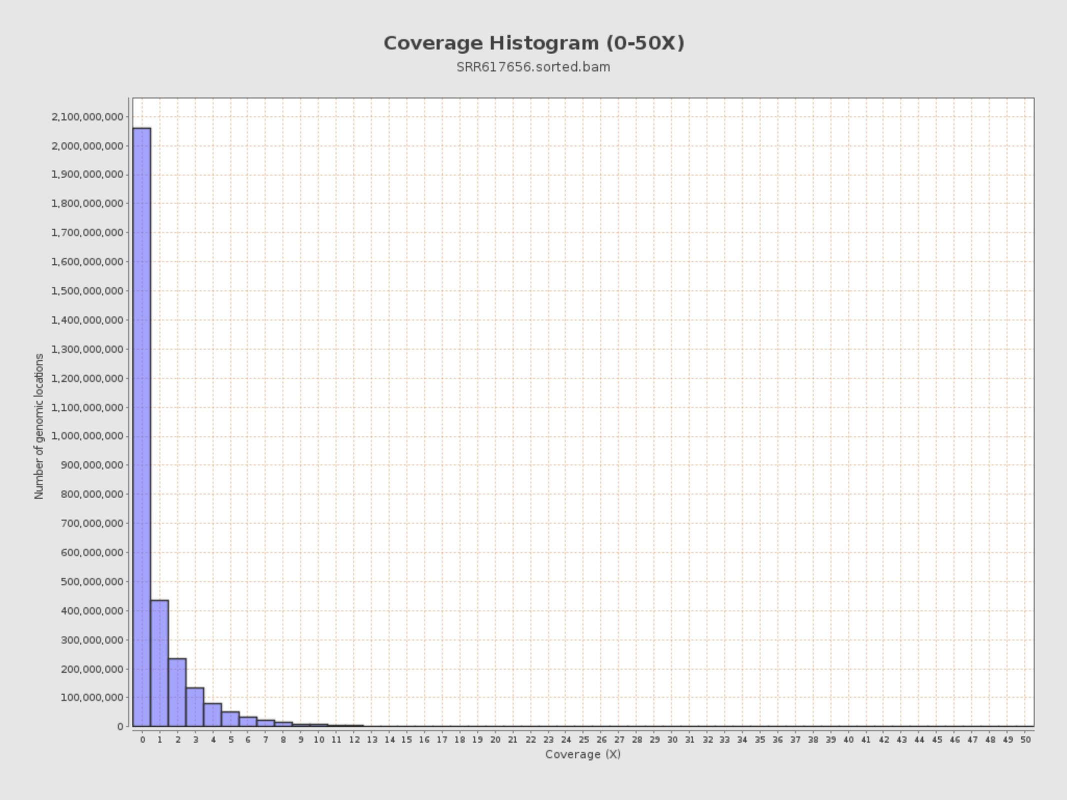
3. Results : Coverage across reference



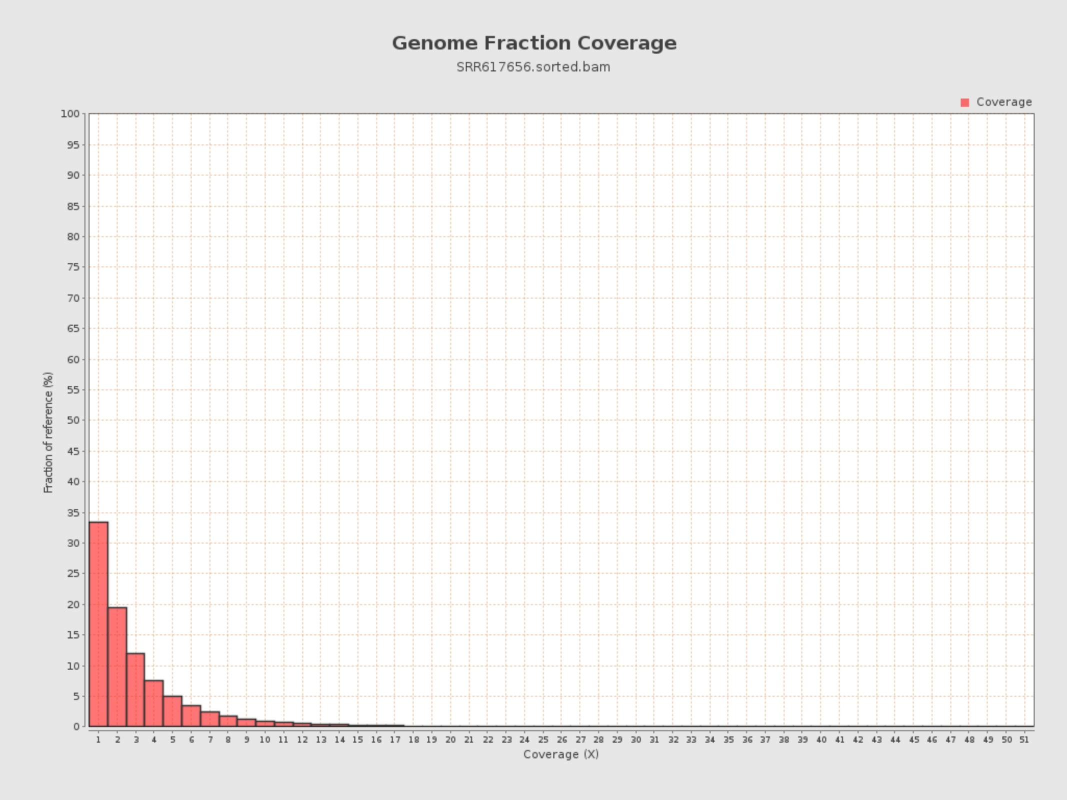
4. Results : Coverage Histogram



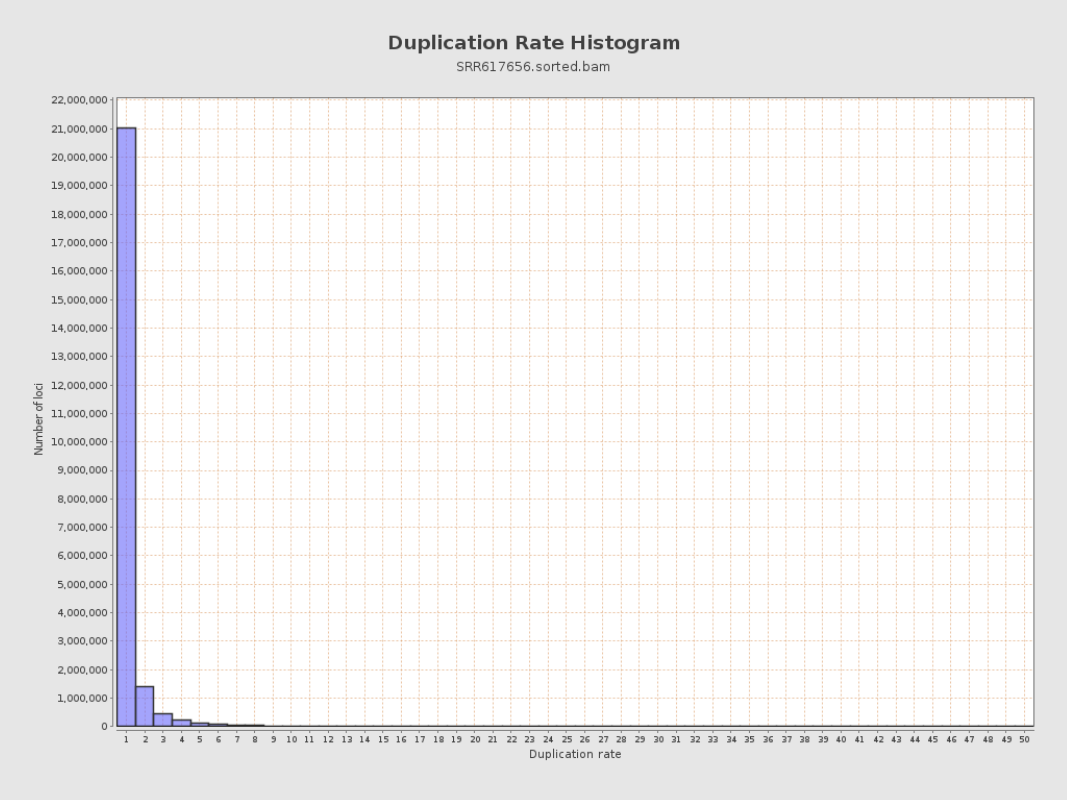
5. Results : Coverage Histogram (0-50X)



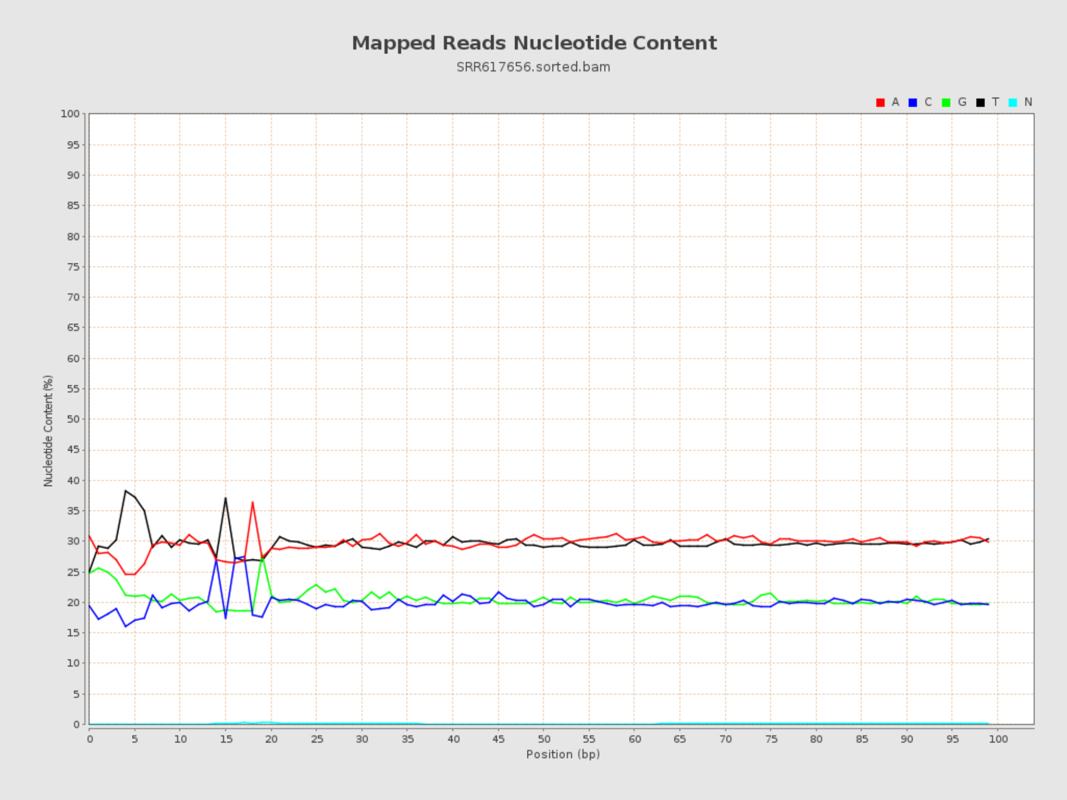
6. Results : Genome Fraction Coverage



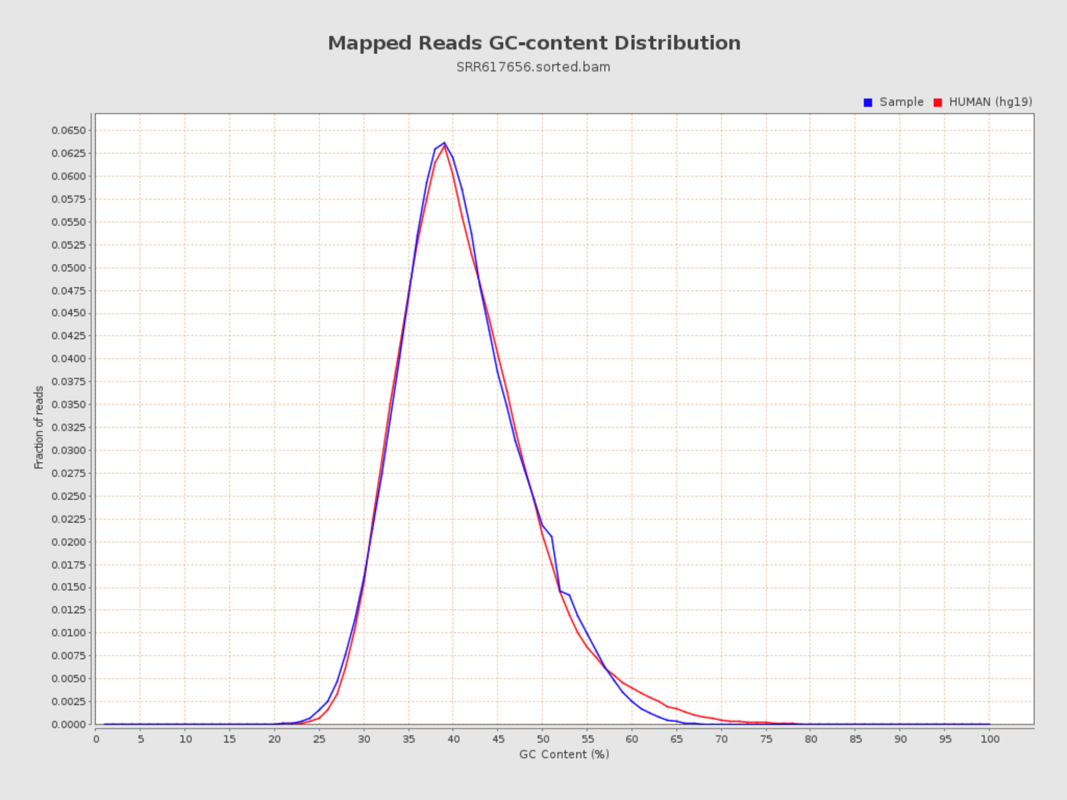
7. Results : Duplication Rate Histogram



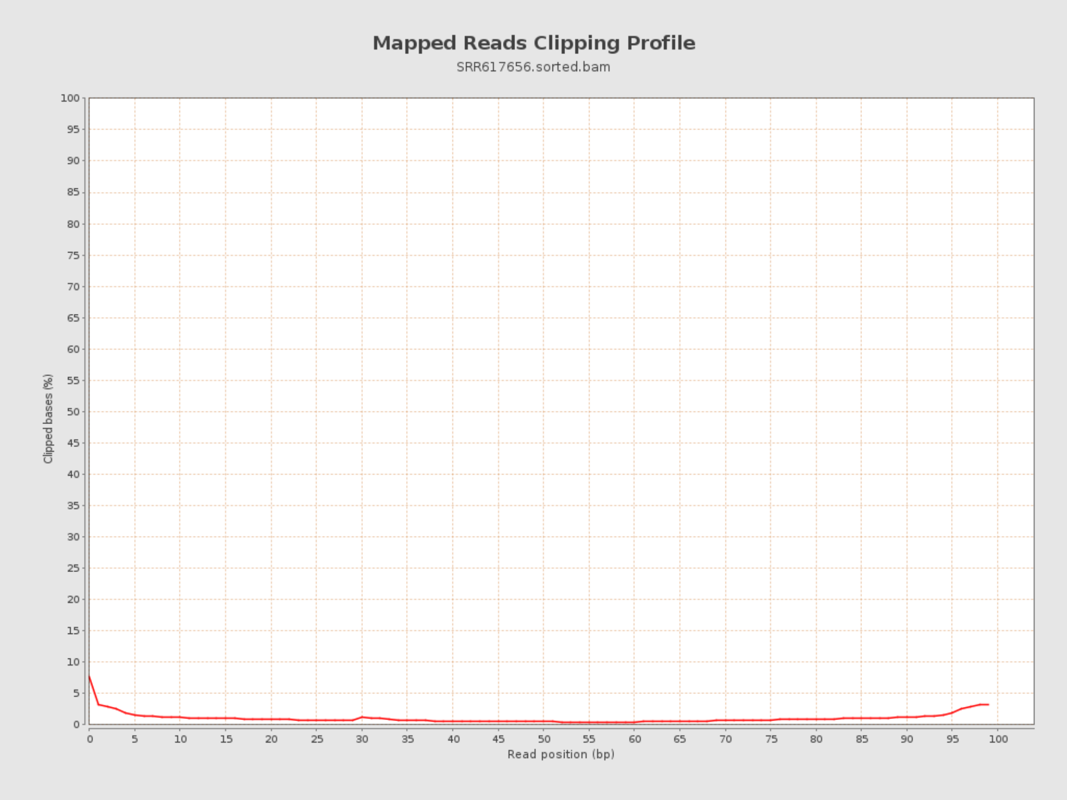
8. Results : Mapped Reads Nucleotide Content



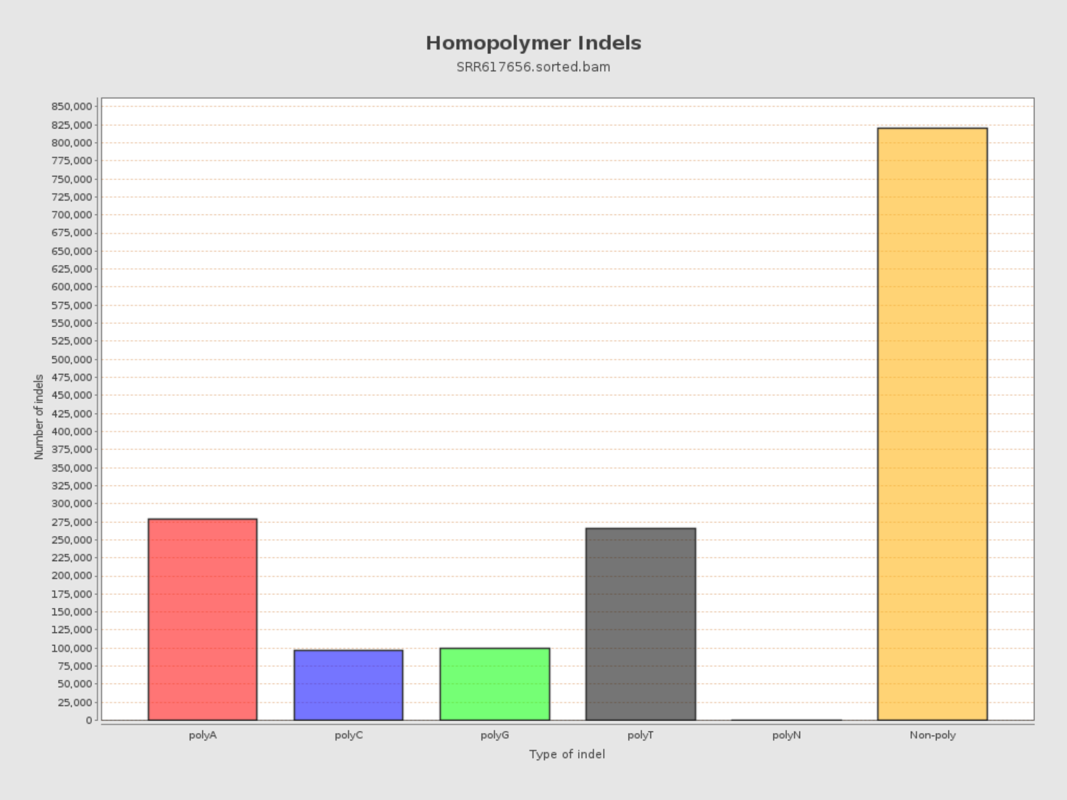
9. Results : Mapped Reads GC-content Distribution



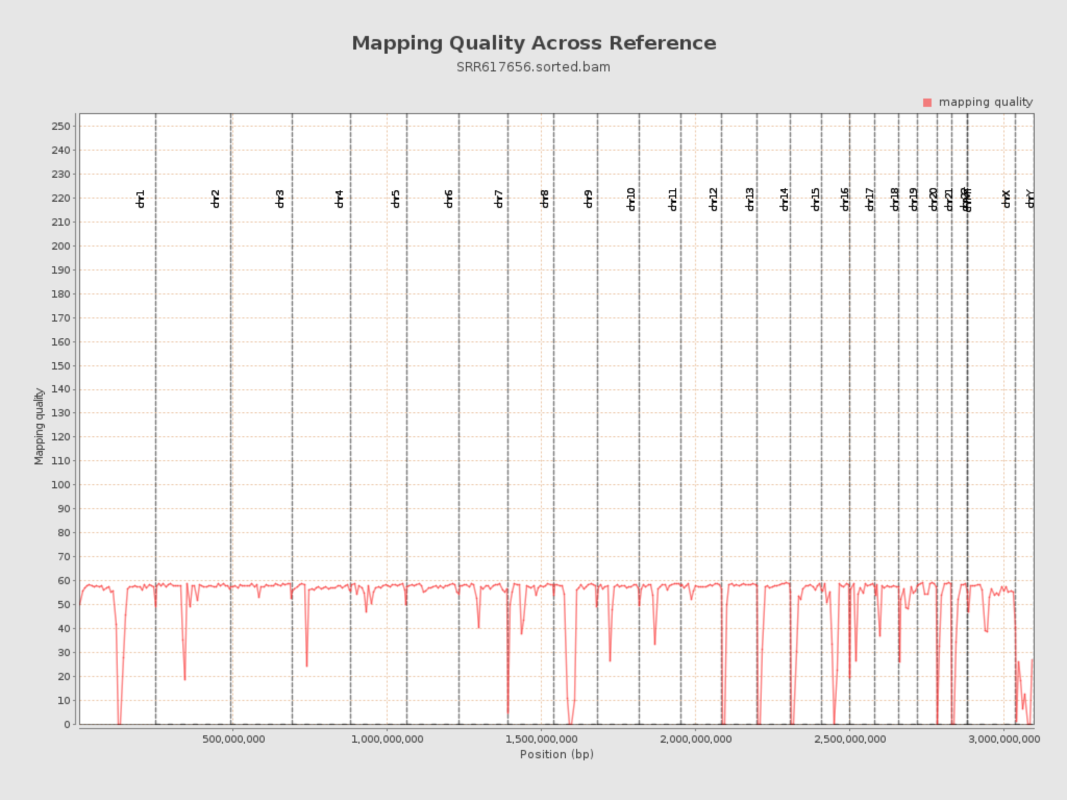
10. Results : Mapped Reads Clipping Profile



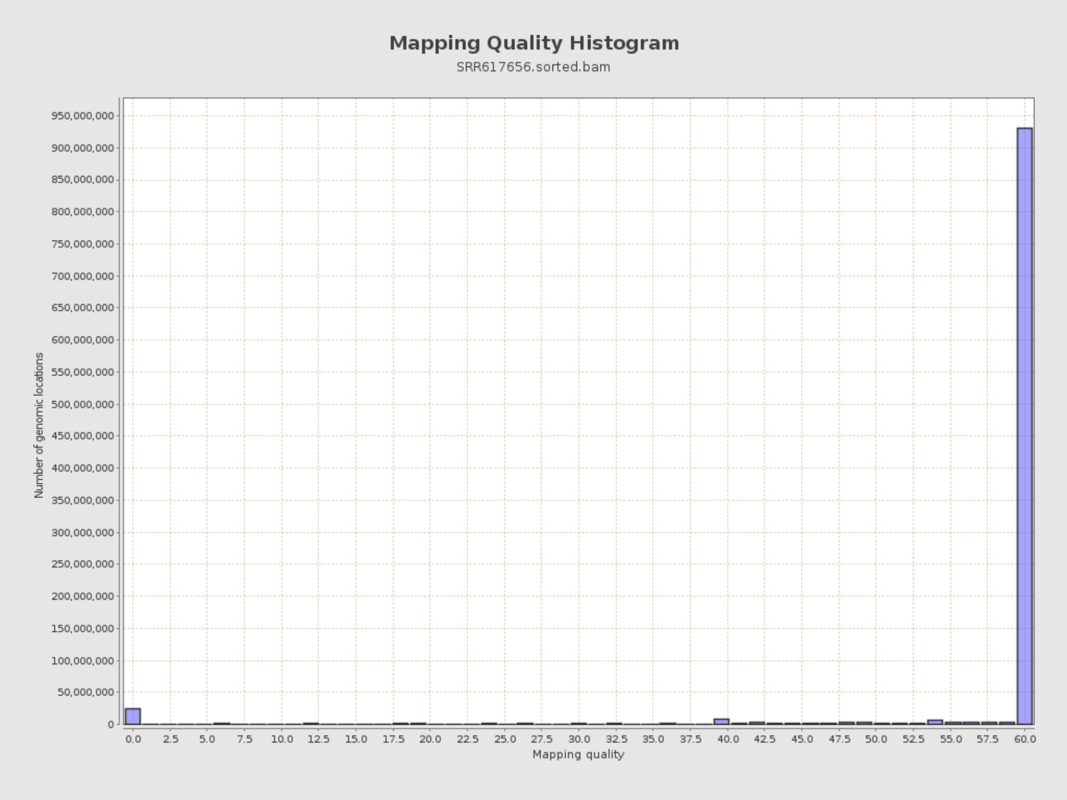
11. Results : Homopolymer Indels



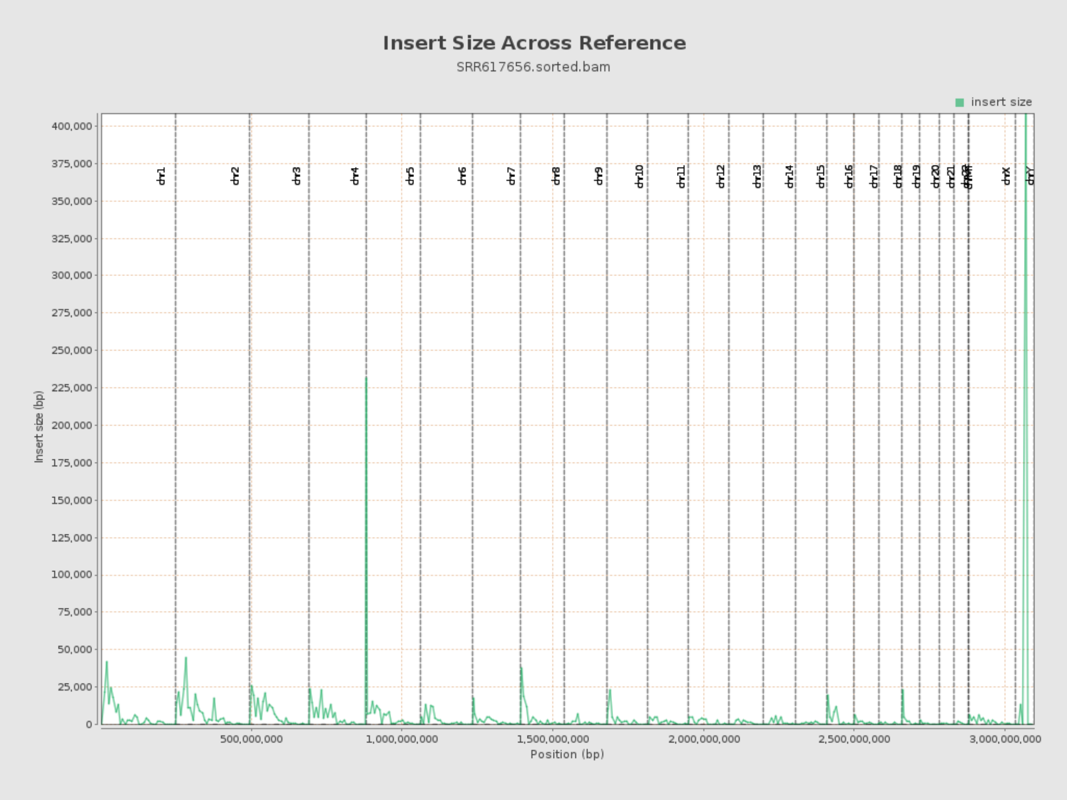
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram