Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 09:47:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617676.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_SRR8617676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617676_1.fastq.gz SRR8617676_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 09:47:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,309,872
Mapped reads	5,265,383 / 99.16%
Unmapped reads	44,489 / 0.84%
Mapped paired reads	5,265,383 / 99.16%
Mapped reads, first in pair	2,632,396 / 49.58%
Mapped reads, second in pair	2,632,987 / 49.59%
Mapped reads, both in pair	5,252,402 / 98.92%
Mapped reads, singletons	12,981 / 0.24%
Secondary alignments	0
Supplementary alignments	89,524 / 1.69%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	196,398 / 3.7%
Duplication rate	1.85%
Clipped reads	2,863,502 / 53.93%

2.2. ACGT Content

Number/percentage of A's	149,271,211 / 29.18%
Number/percentage of C's	105,197,690 / 20.56%
Number/percentage of T's	151,836,266 / 29.68%
Number/percentage of G's	105,267,188 / 20.58%
Number/percentage of N's	13,708 / 0%

GC Percentage	41.14%

2.3. Coverage

Mean	0.1653
Standard Deviation	1.8717

2.4. Mapping Quality

Mean Mapping Quality	53.45

2.5. Insert size

Mean	190,999.25
Standard Deviation	4,128,444.88
P25/Median/P75	141 / 176 / 227

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	2,515,331
Insertions	71,585
Mapped reads with at least one insertion	1.33%
Deletions	69,055
Mapped reads with at least one deletion	1.28%
Homopolymer indels	38.49%

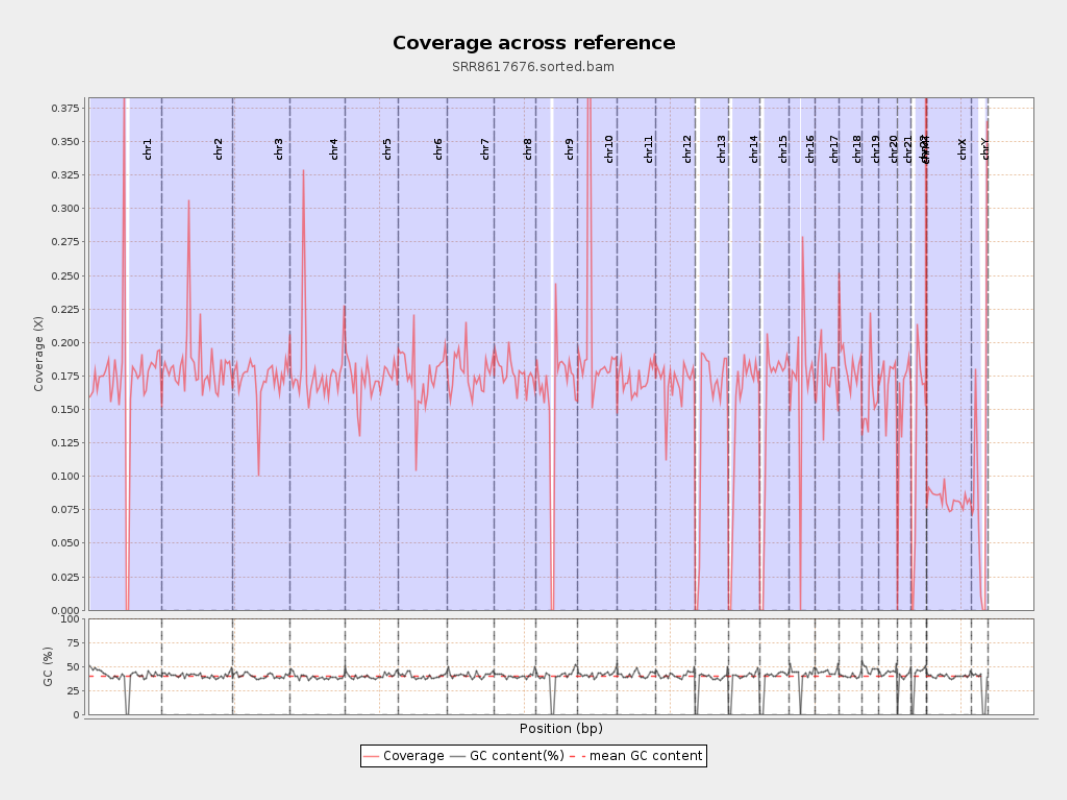
2.7. Chromosome stats

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

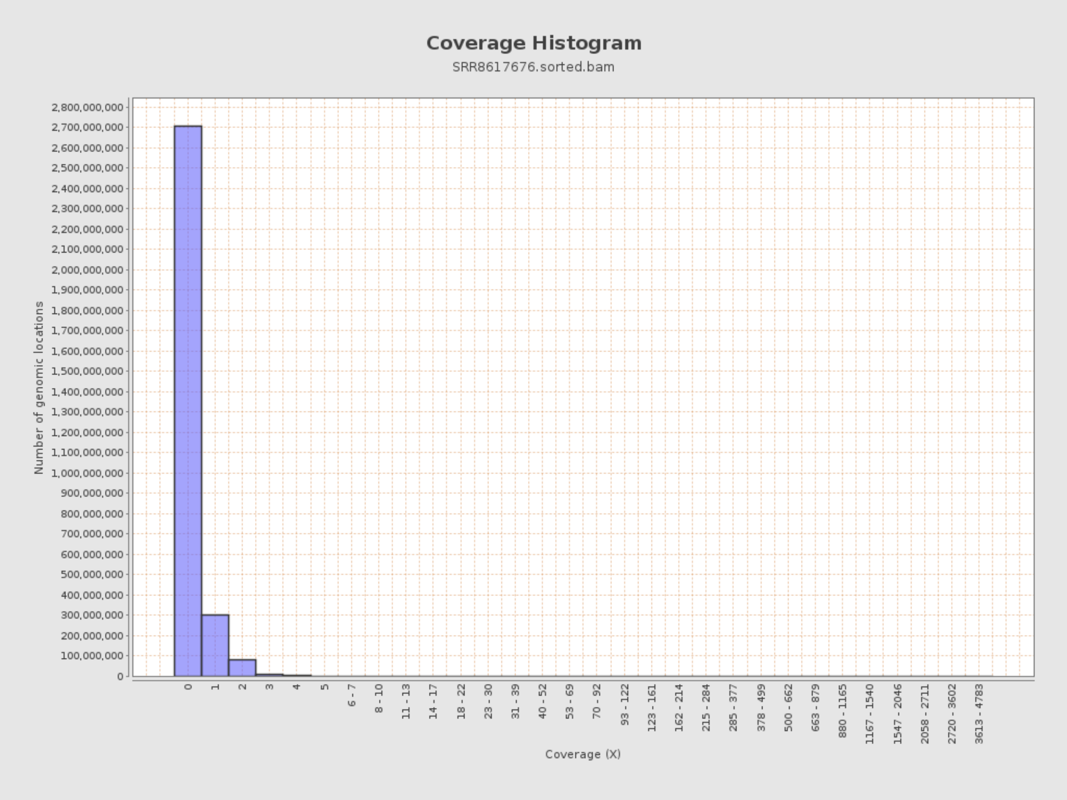
		bases	coverage	deviation
chr1	249250621	42582698	0.1708	4.8612
chr2	243199373	44599759	0.1834	1.1078
chr3	198022430	34181520	0.1726	0.5381
chr4	191154276	34211275	0.179	1.3656
chr5	180915260	31182172	0.1724	0.4818
chr6	171115067	30015628	0.1754	0.7404
chr7	159138663	28171855	0.177	1.395
chr8	146364022	25932116	0.1772	1.4448
chr9	141213431	22248930	0.1576	1.661
chr10	135534747	27688836	0.2043	3.5522
chr11	135006516	23202093	0.1719	1.0489
chr12	133851895	22786771	0.1702	0.4848
chr13	115169878	17055932	0.1481	0.4445
chr14	107349540	15575216	0.1451	0.4559
chr15	102531392	15522319	0.1514	0.4517
chr16	90354753	15433547	0.1708	1.0472
chr17	81195210	13940336	0.1717	0.7077
chr18	78077248	14449223	0.1851	1.6977
chr19	59128983	9372379	0.1585	2.3555
chr20	63025520	10807864	0.1715	0.5622
chr21	48129895	7313860	0.152	1.1834
chr22	51304566	6371917	0.1242	1.3675
chrMT	16571	456234	27.5321	9.1963
chrX	155270560	12913194	0.0832	0.5483

chrY	59373566	5731291	0.0965	1.8696

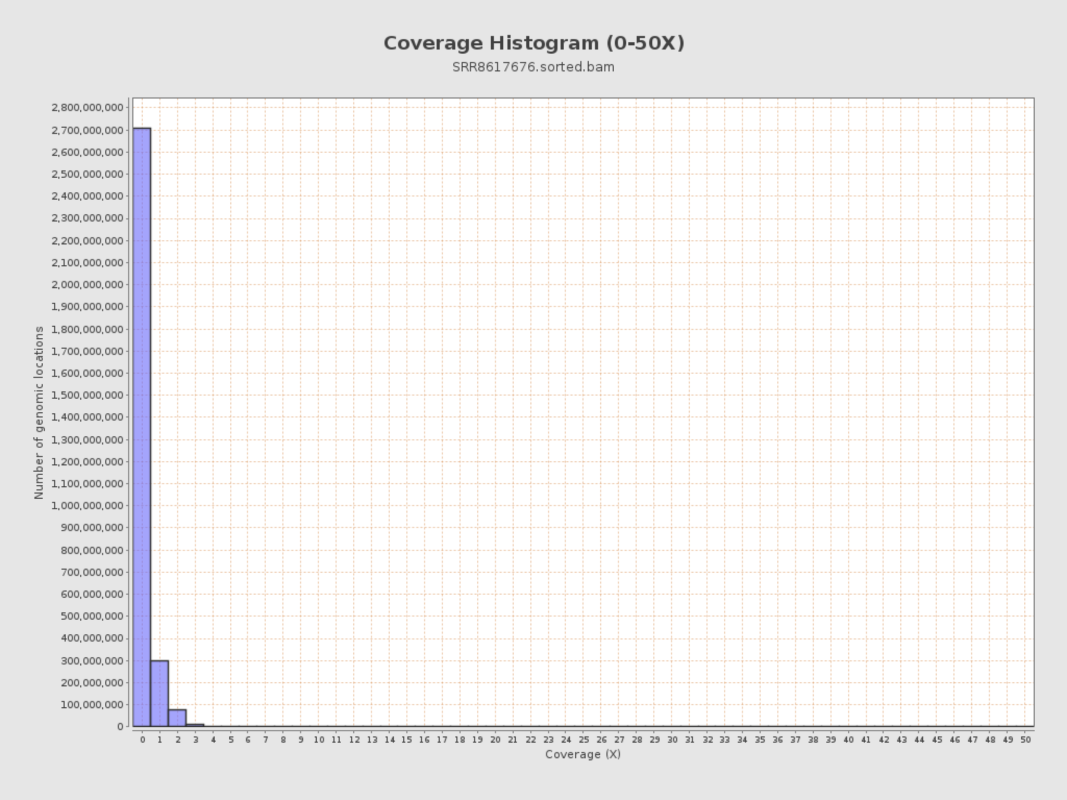
3. Results : Coverage across reference



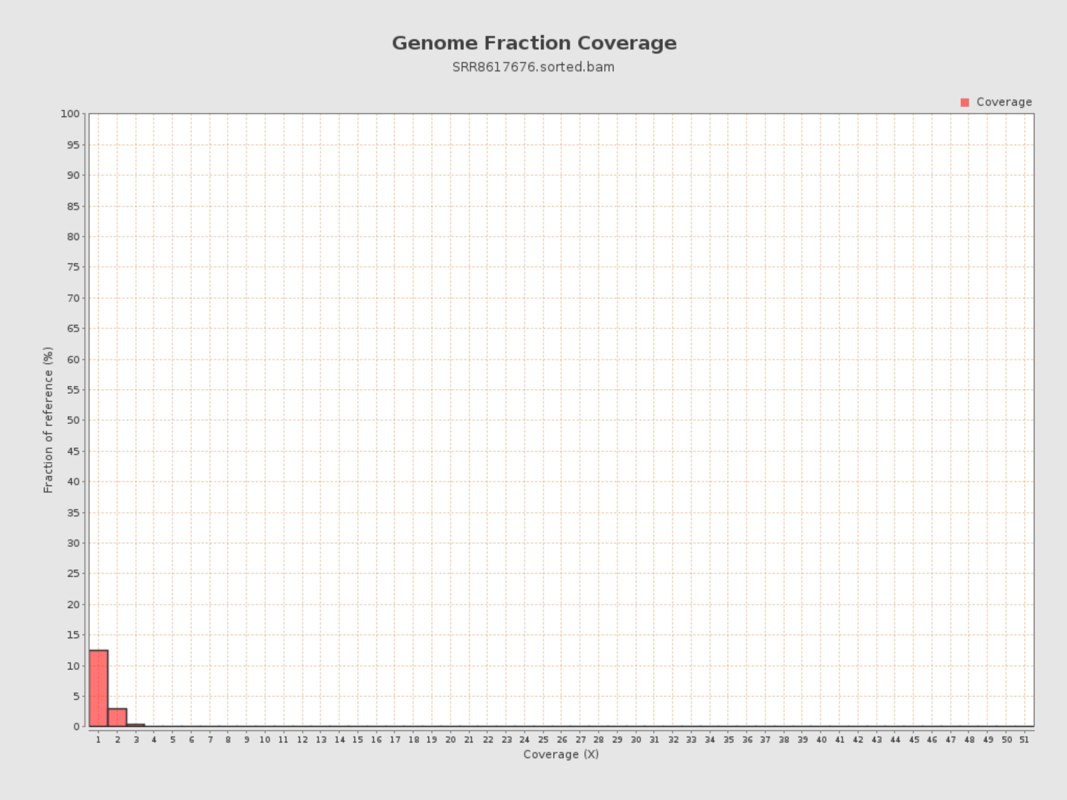
4. Results : Coverage Histogram



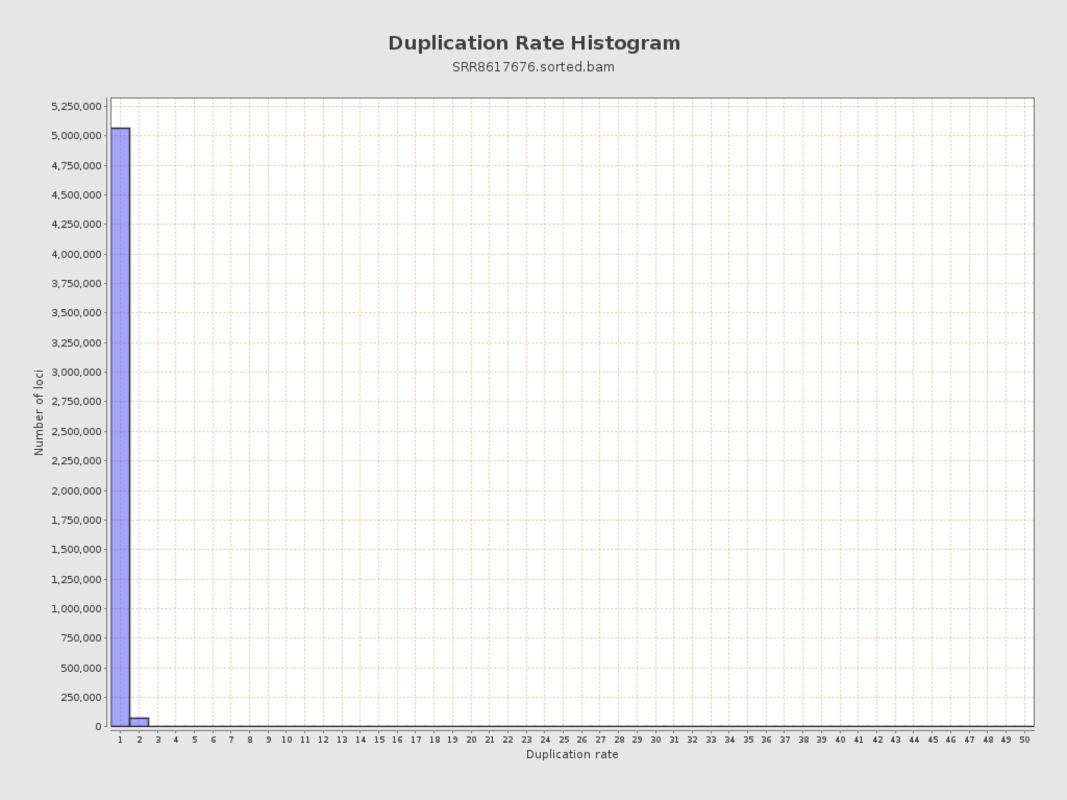
5. Results : Coverage Histogram (0-50X)



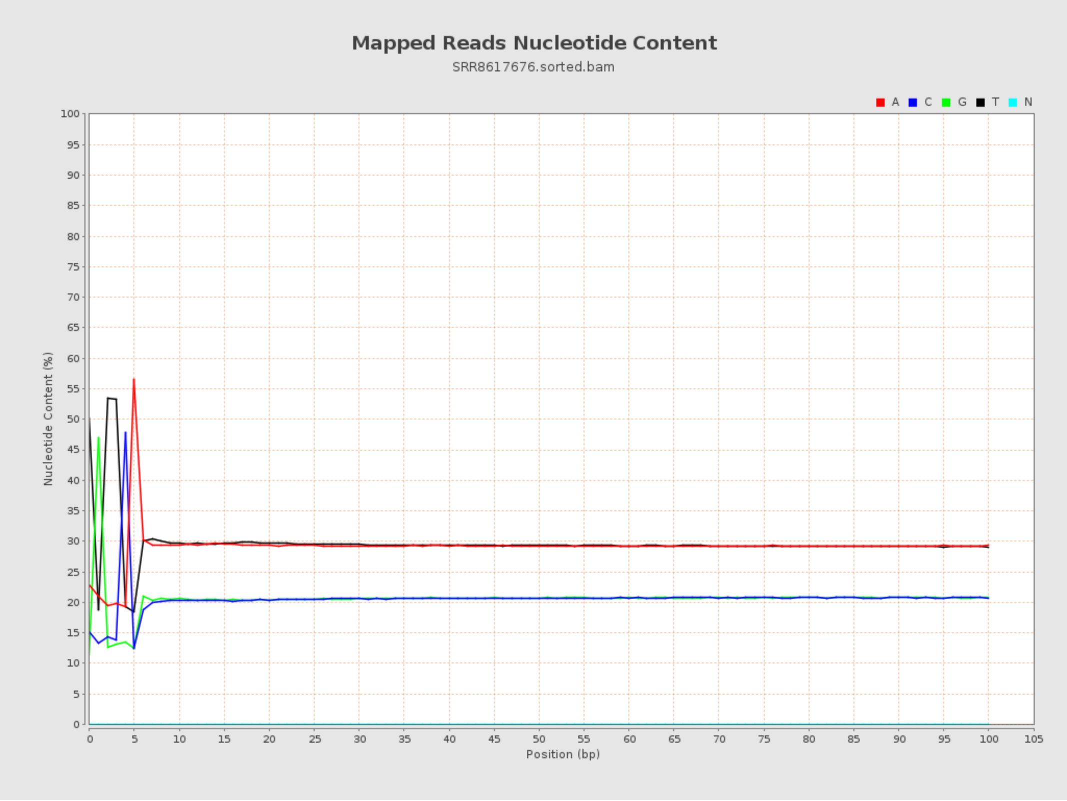
6. Results : Genome Fraction Coverage



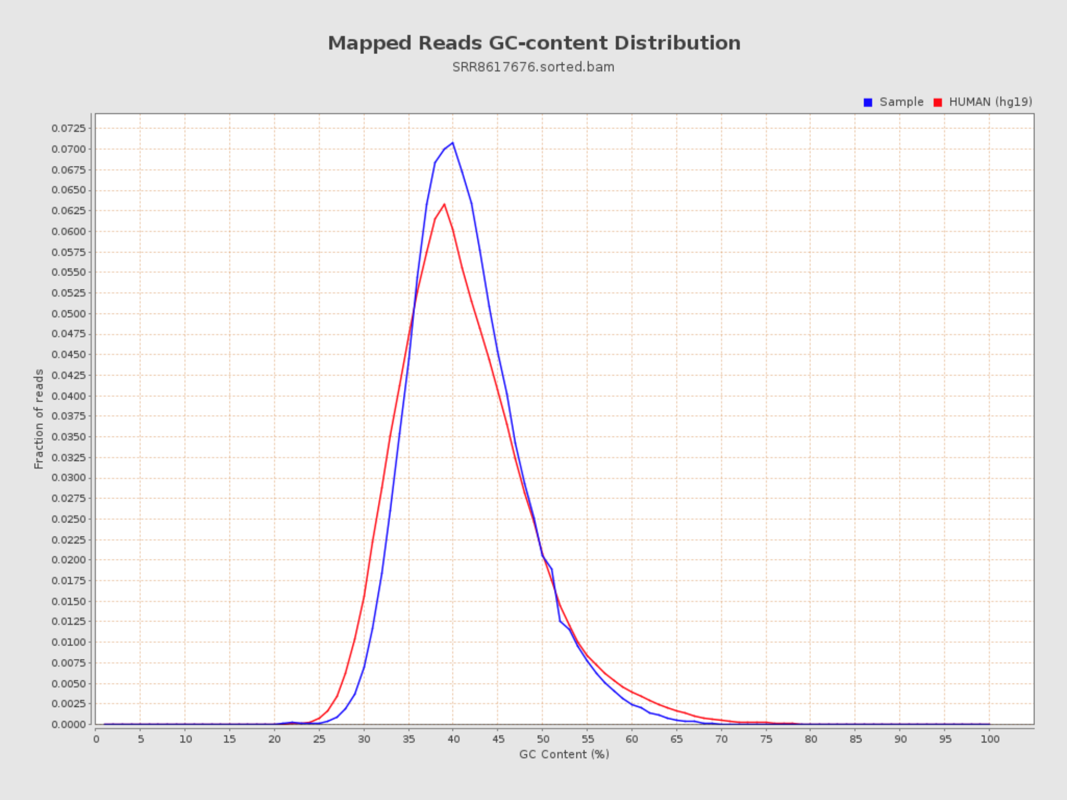
7. Results : Duplication Rate Histogram



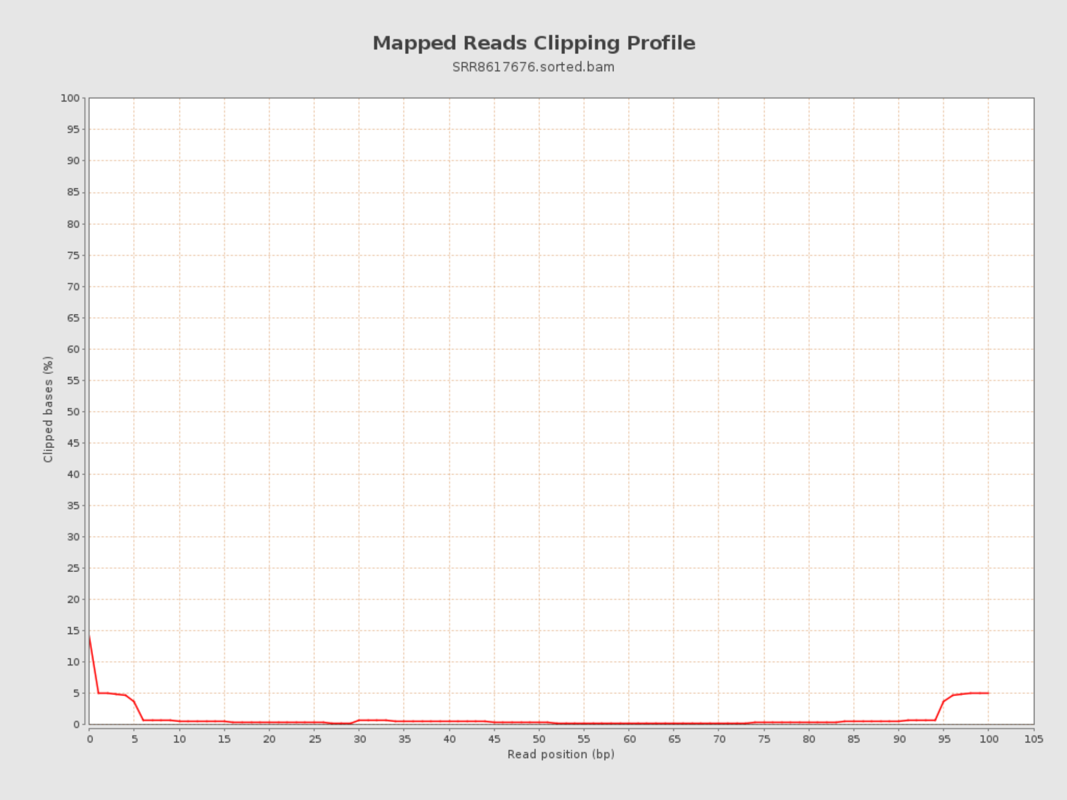
8. Results : Mapped Reads Nucleotide Content



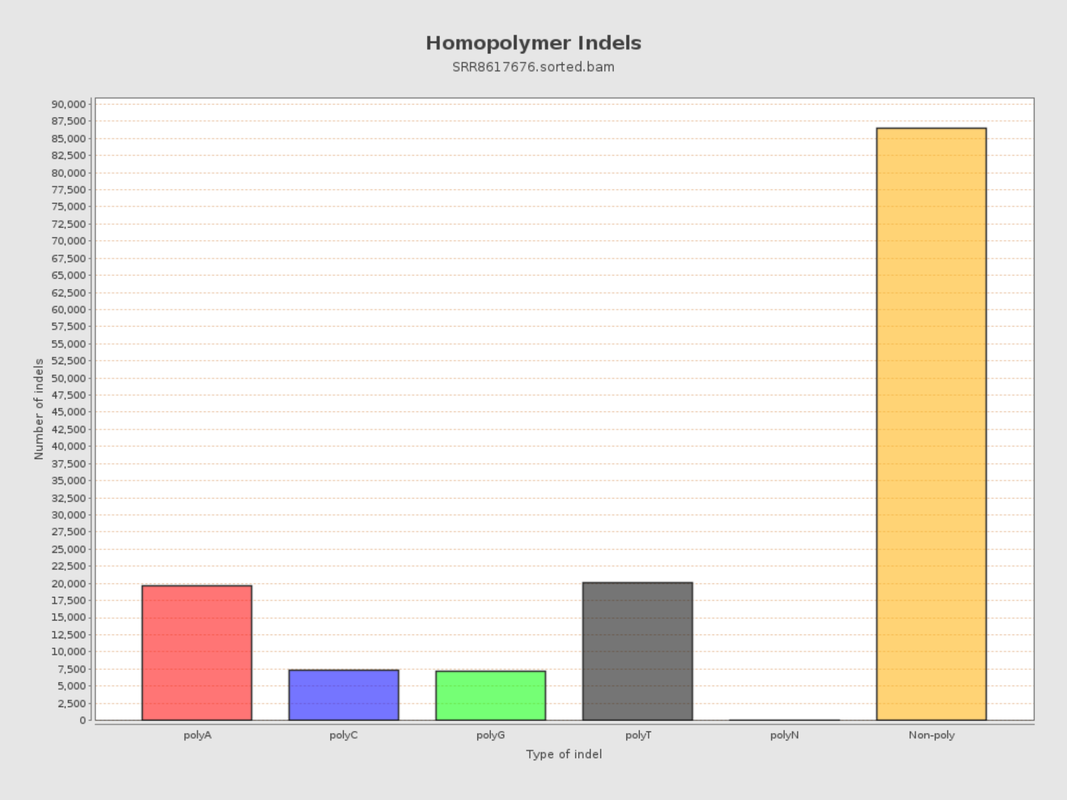
9. Results : Mapped Reads GC-content Distribution



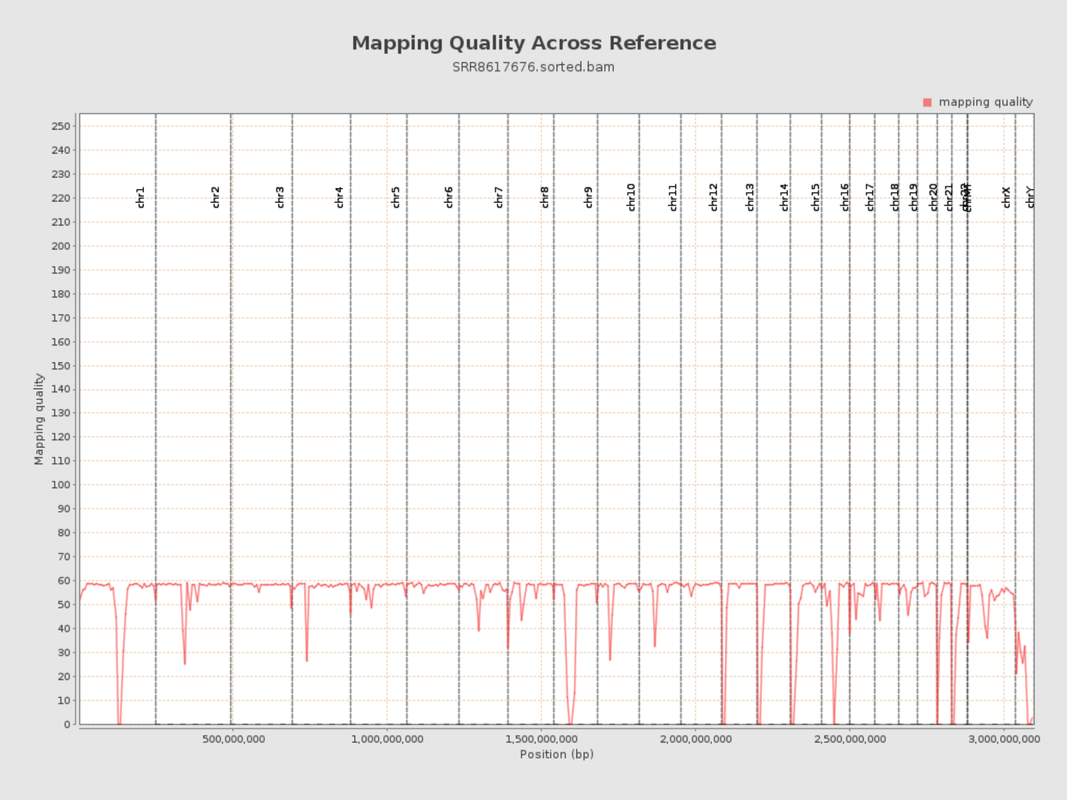
10. Results : Mapped Reads Clipping Profile



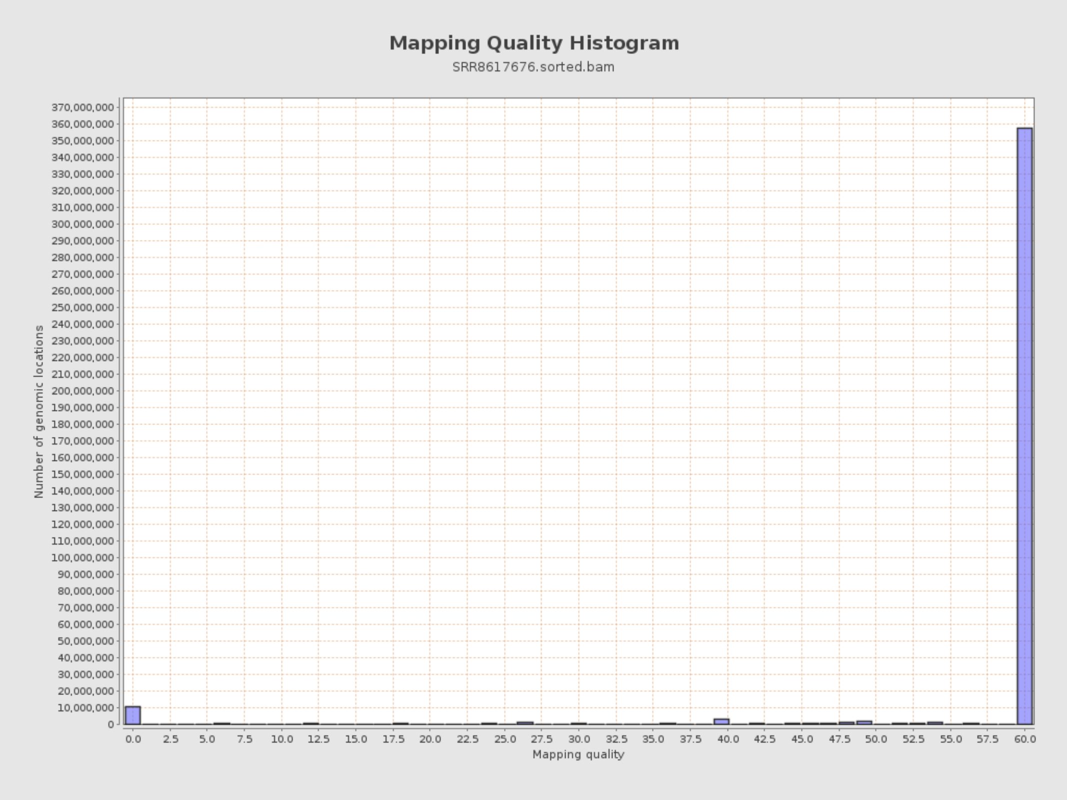
11. Results : Homopolymer Indels



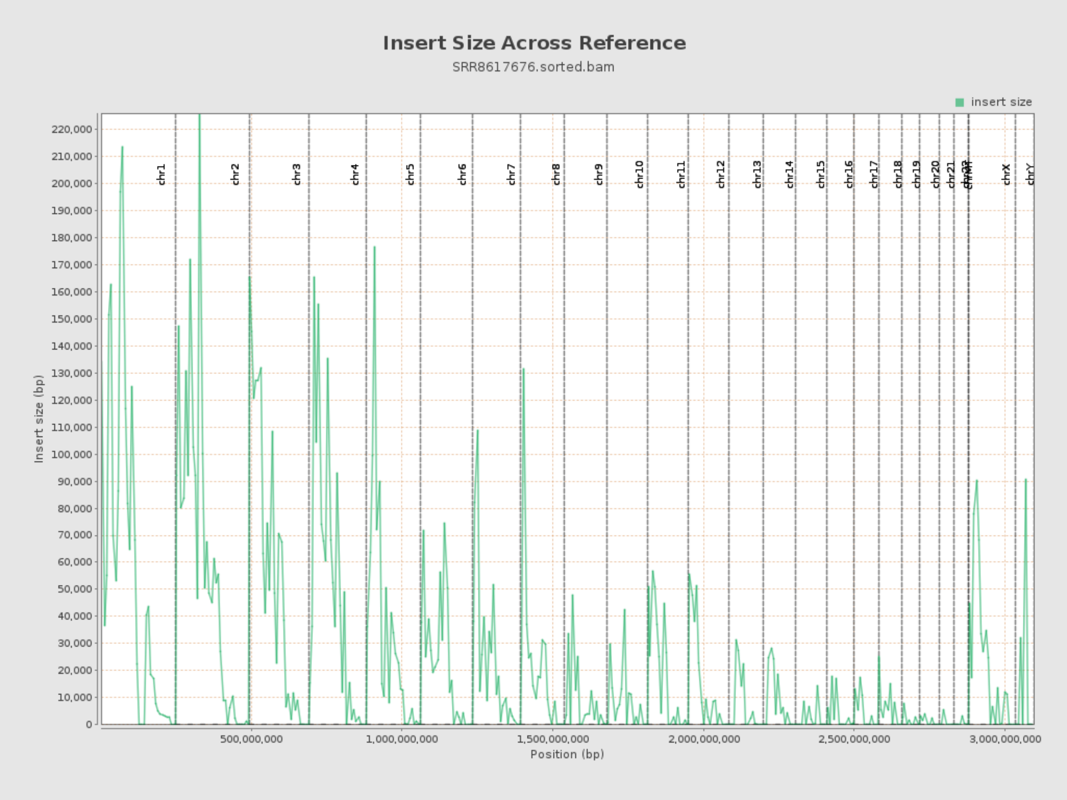
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram