

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 01:54:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617659.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_SRR617659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617659_1.fastq.gz SRR617659_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 01:54:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,126,397 / 94.14%
Unmapped reads	1,873,603 / 5.86%
Mapped paired reads	30,126,397 / 94.14%
Mapped reads, first in pair	15,283,873 / 47.76%
Mapped reads, second in pair	14,842,524 / 46.38%
Mapped reads, both in pair	29,312,920 / 91.6%
Mapped reads, singletons	813,477 / 2.54%
Secondary alignments	0
Supplementary alignments	184,479 / 0.58%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	6,946,659 / 21.71%
Duplication rate	10.76%
Clipped reads	6,654,807 / 20.8%

2.2. ACGT Content

Number/percentage of A's	865,728,673 / 29.79%
Number/percentage of C's	577,965,723 / 19.89%
Number/percentage of T's	864,660,351 / 29.76%
Number/percentage of G's	594,312,710 / 20.45%
Number/percentage of N's	3,096,862 / 0.11%

GC Percentage	40.34%
---------------	--------

2.3. Coverage

Mean	0.9392
Standard Deviation	10.5454

2.4. Mapping Quality

Mean Mapping Quality	52.51
----------------------	-------

2.5. Insert size

Mean	51,013.78
Standard Deviation	2,128,170.38
P25/Median/P75	179 / 223 / 291

2.6. Mismatches and indels

General error rate	1.41%
Mismatches	40,167,194
Insertions	458,140
Mapped reads with at least one insertion	1.49%
Deletions	1,065,604
Mapped reads with at least one deletion	3.46%
Homopolymer indels	47.57%

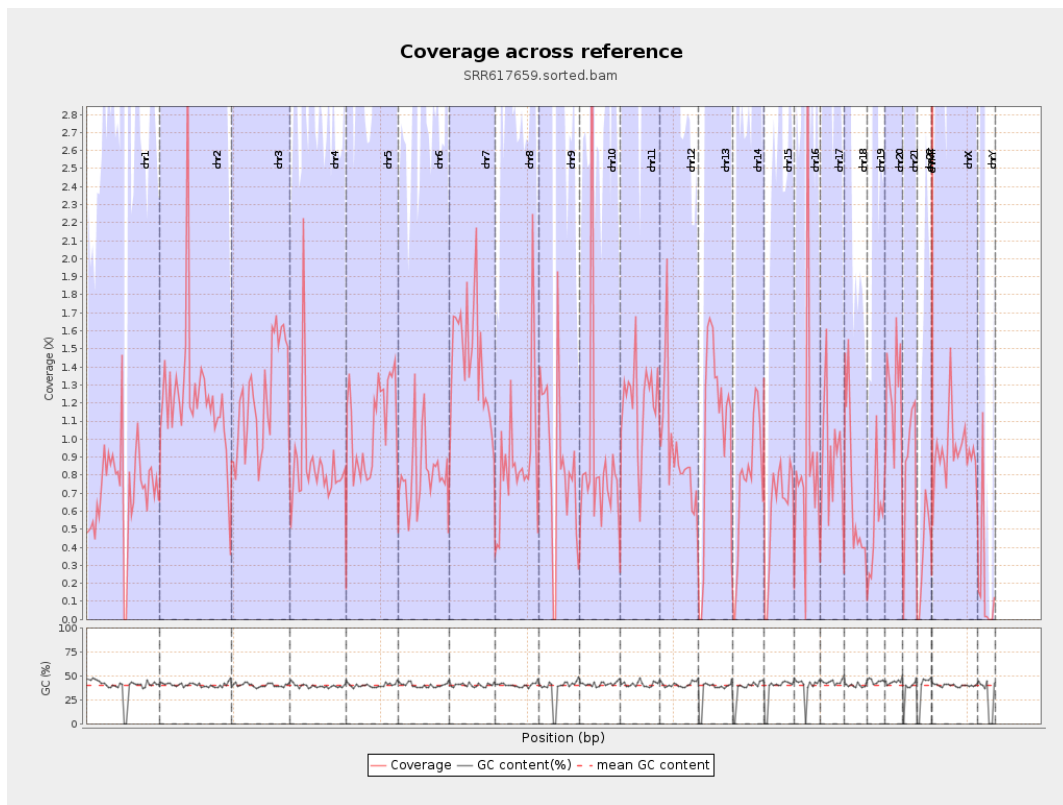
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

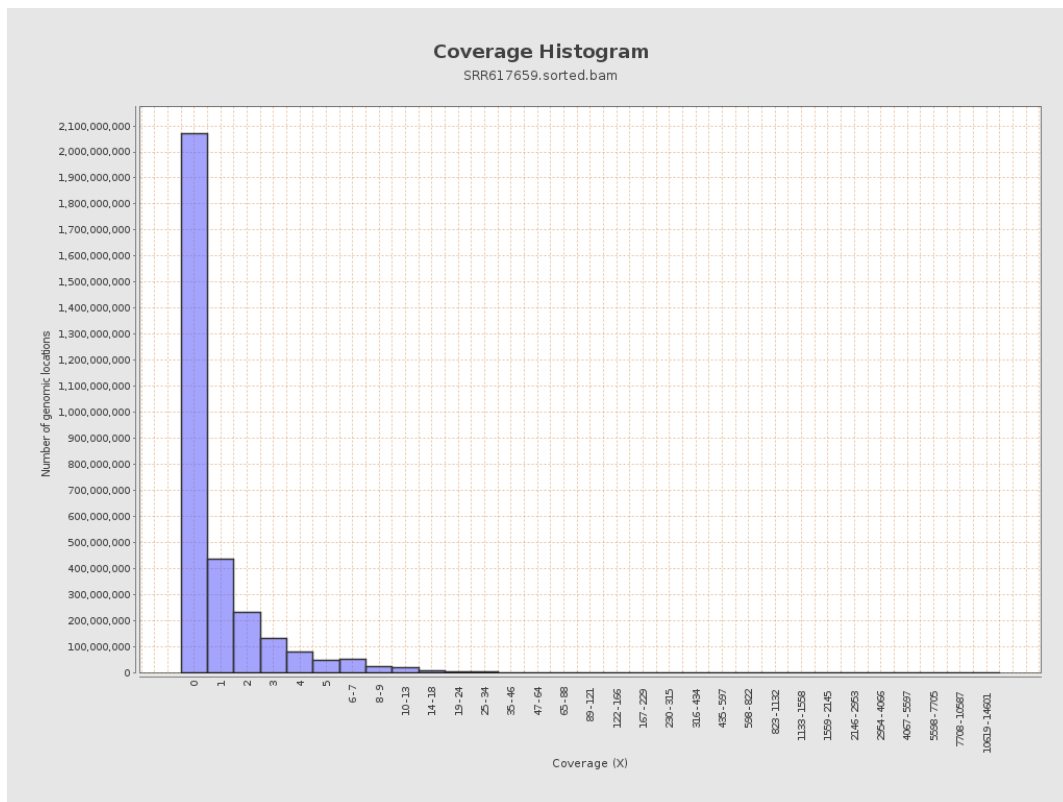
		bases	coverage	deviation
chr1	249250621	178170109	0.7148	10.1596
chr2	243199373	300807832	1.2369	12.1384
chr3	198022430	243292808	1.2286	2.4821
chr4	191154276	162808608	0.8517	8.2592
chr5	180915260	192416166	1.0636	2.3251
chr6	171115067	140877158	0.8233	5.7106
chr7	159138663	227503846	1.4296	13.2169
chr8	146364022	129107435	0.8821	4.0683
chr9	141213431	119324630	0.845	20.4111
chr10	135534747	123028992	0.9077	21.3149
chr11	135006516	159790122	1.1836	11.9685
chr12	133851895	124171260	0.9277	2.2115
chr13	115169878	124652746	1.0823	2.3258
chr14	107349540	83180386	0.7749	2.4499
chr15	102531392	62257829	0.6072	1.7808
chr16	90354753	80553583	0.8915	16.5903
chr17	81195210	71781075	0.8841	12.6641
chr18	78077248	53710798	0.6879	18.2464
chr19	59128983	30888278	0.5224	6.1892
chr20	63025520	78542056	1.2462	3.028
chr21	48129895	42436772	0.8817	4.3213
chr22	51304566	18730451	0.3651	1.2769
chrMT	16571	3081439	185.9537	131.5265
chrX	155270560	144601137	0.9313	4.3724

chrY	59373566	11820061	0.1991	17.3827
------	----------	----------	--------	---------

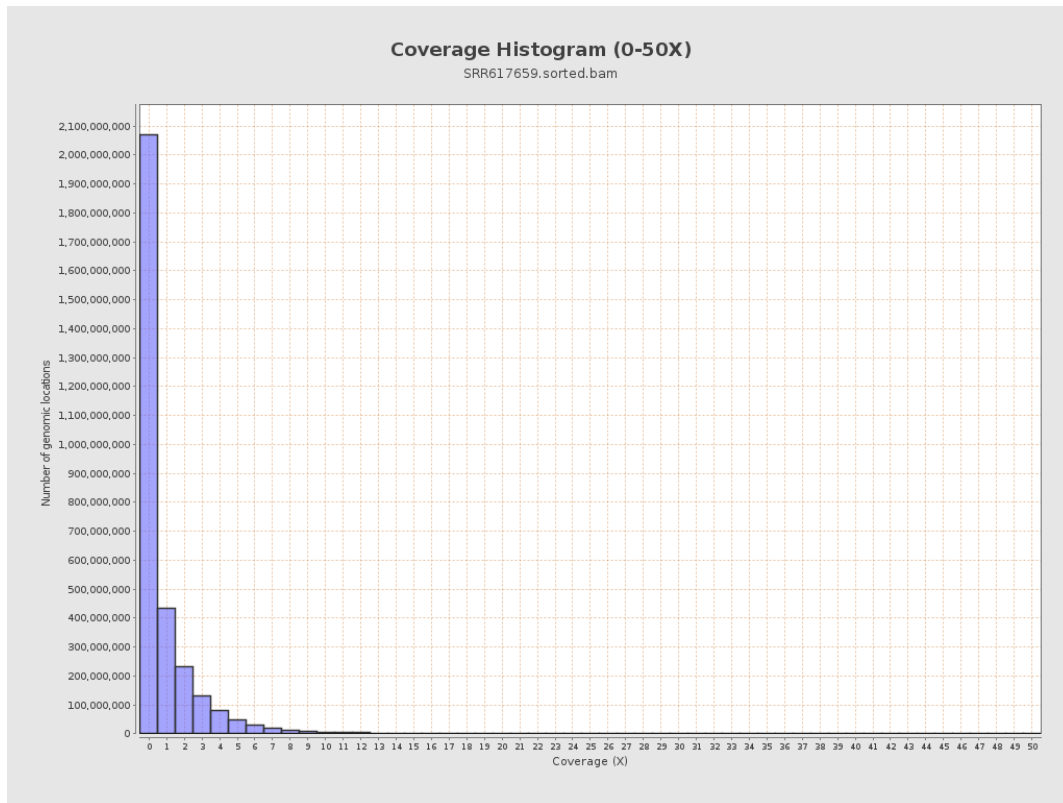
3. Results : Coverage across reference



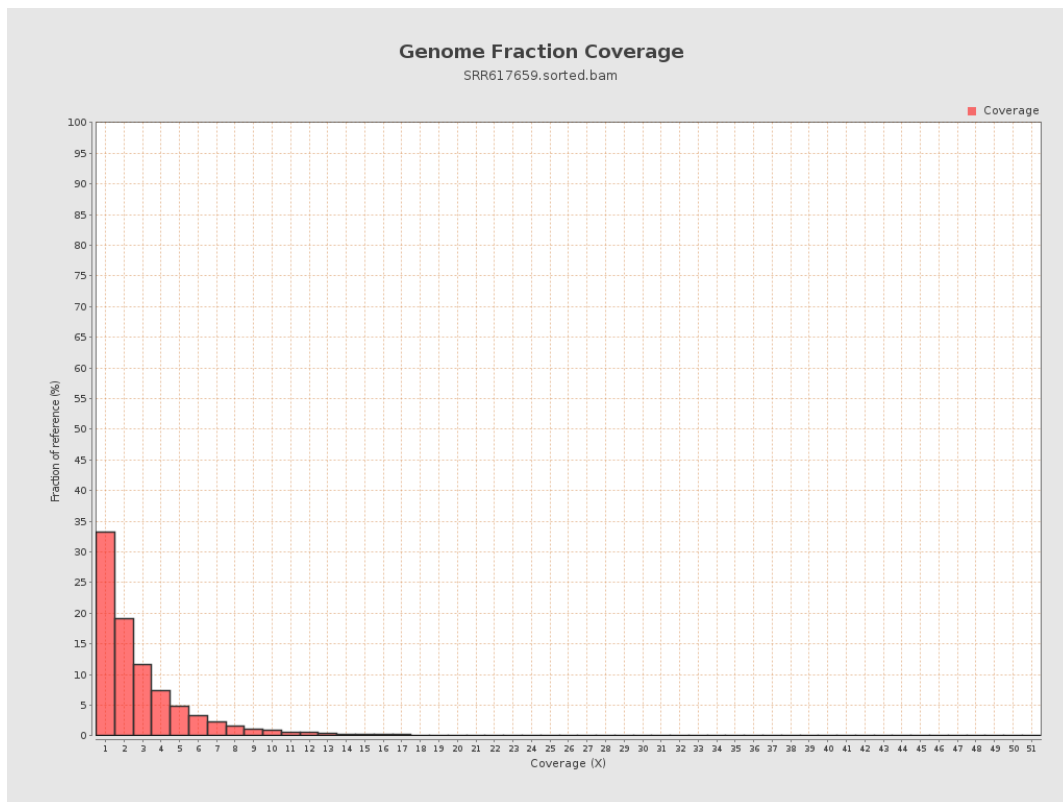
4. Results : Coverage Histogram



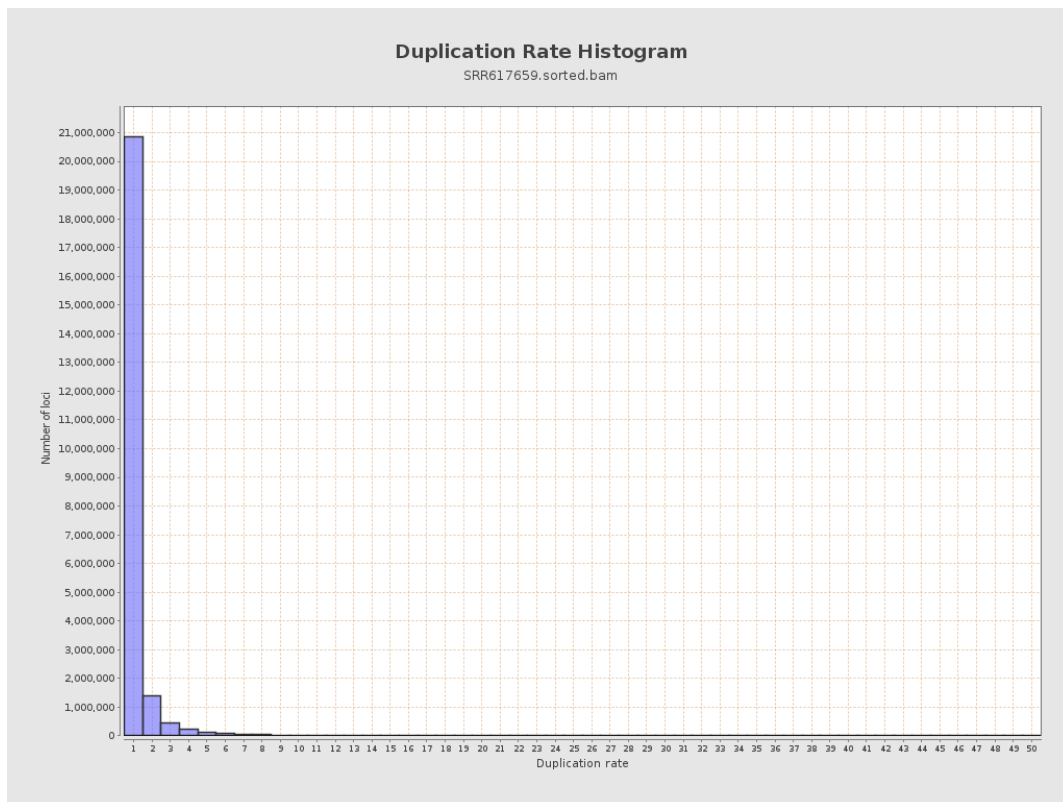
5. Results : Coverage Histogram (0-50X)



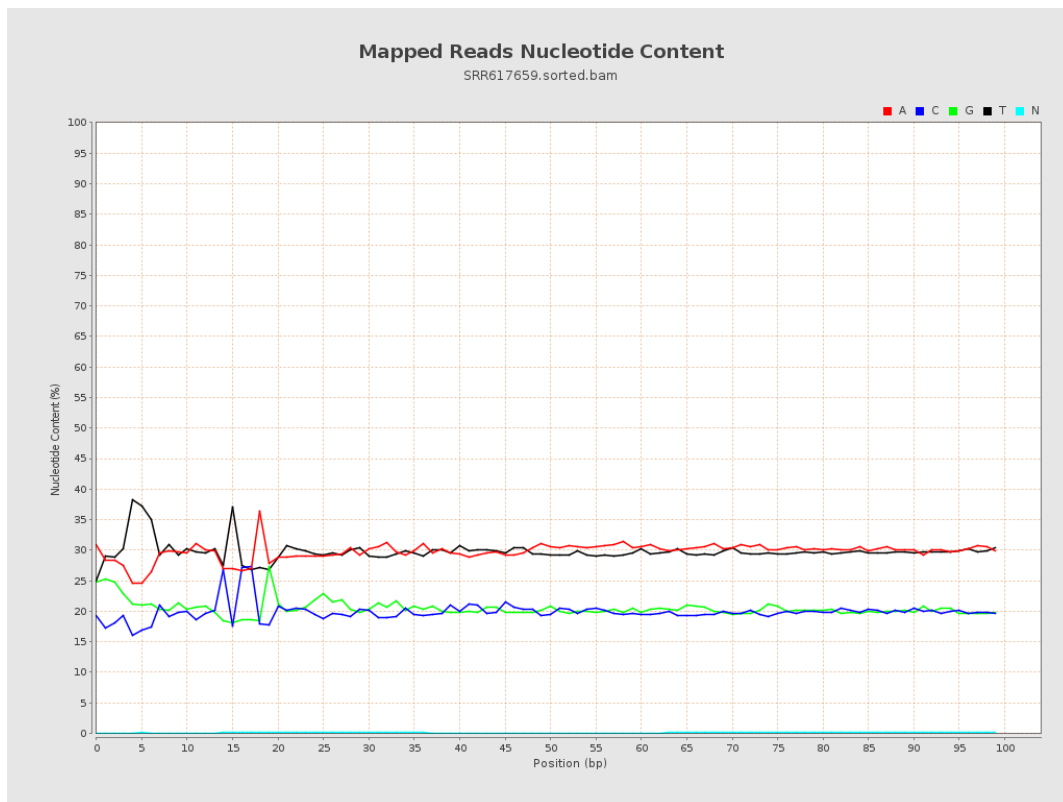
6. Results : Genome Fraction Coverage



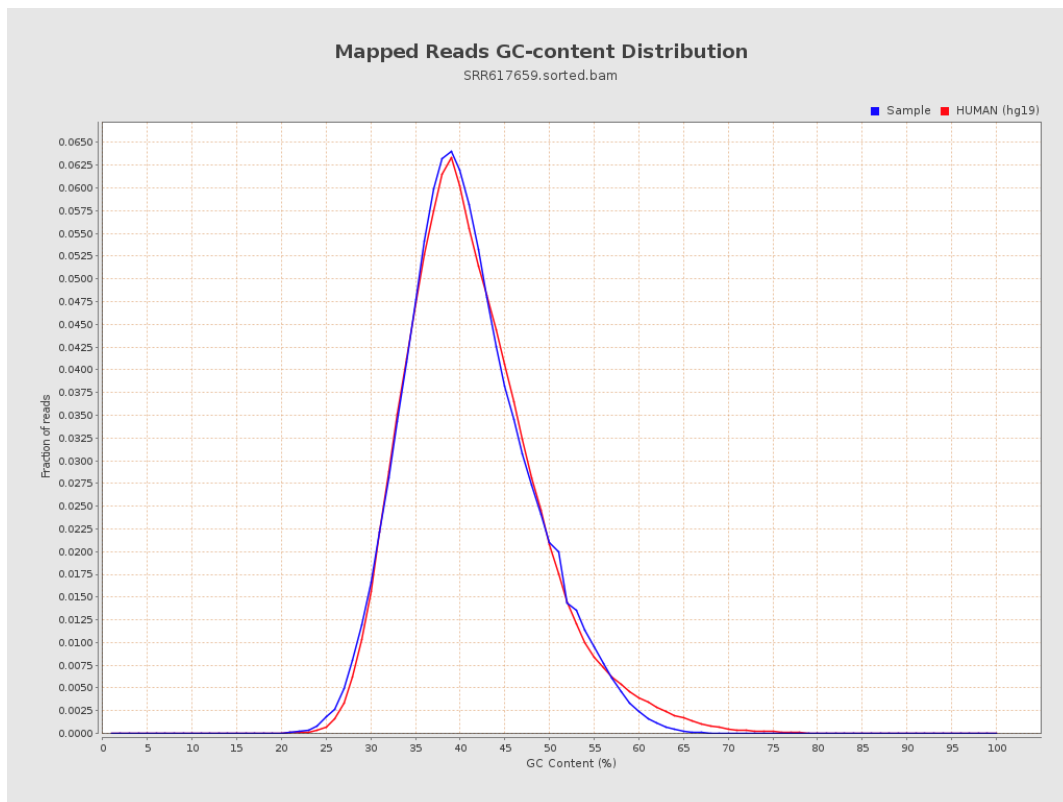
7. Results : Duplication Rate Histogram



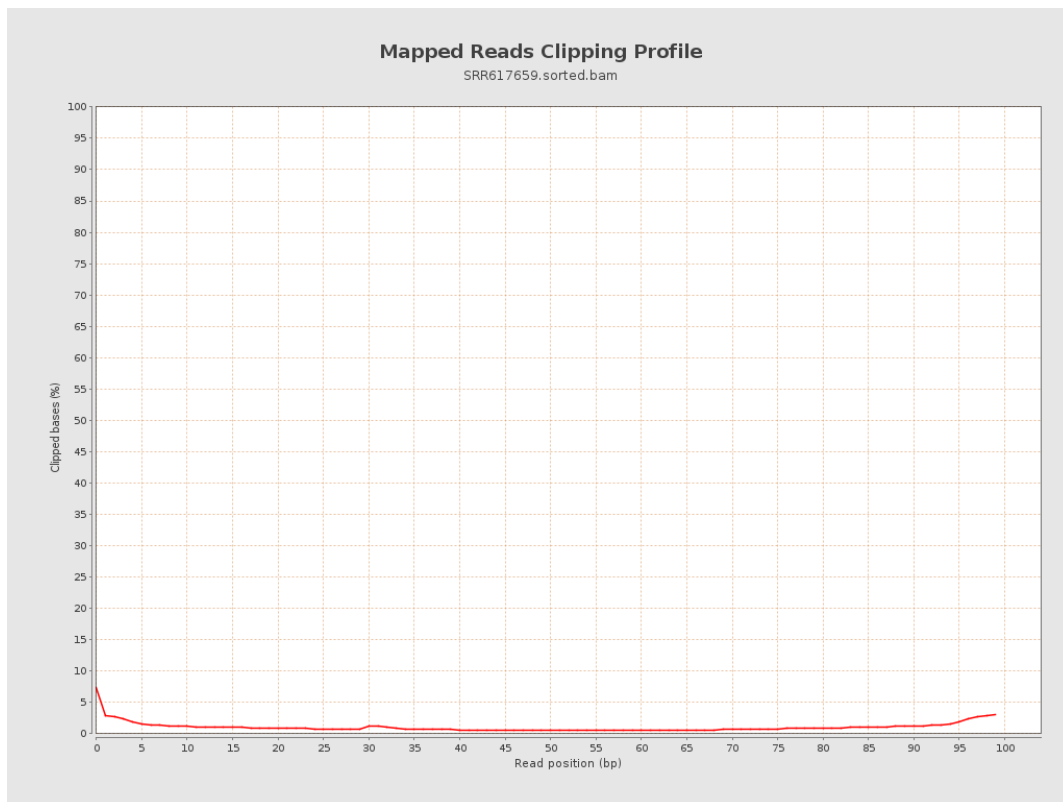
8. Results : Mapped Reads Nucleotide Content



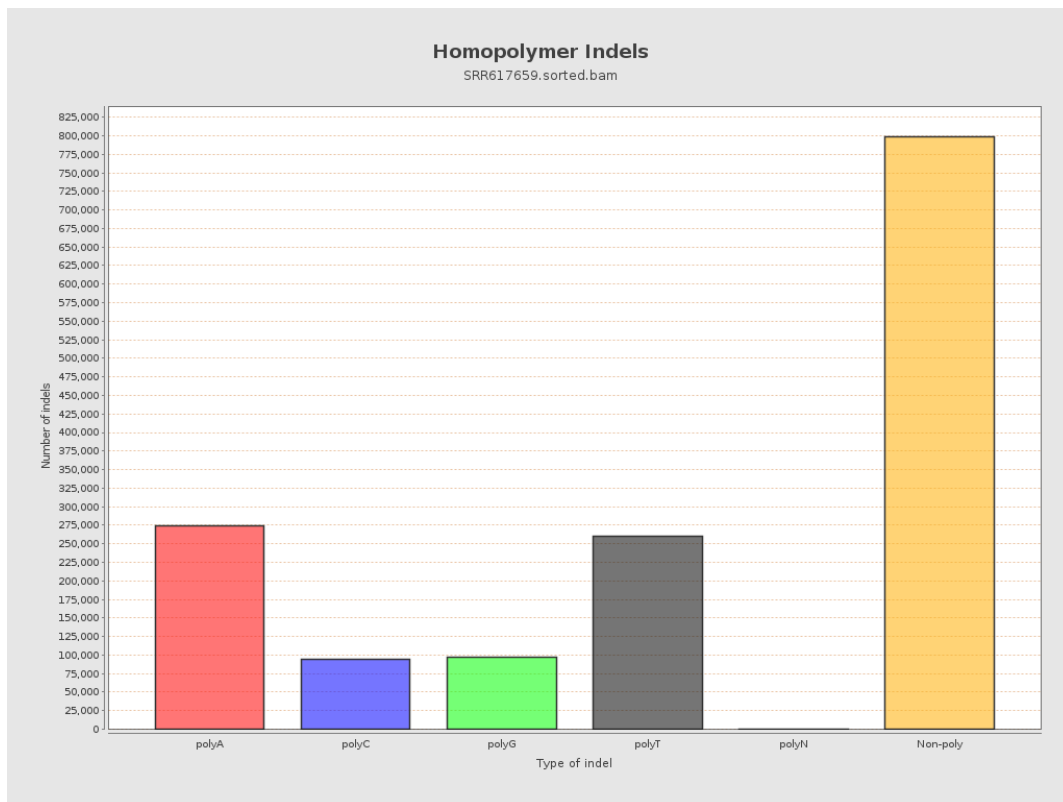
9. Results : Mapped Reads GC-content Distribution



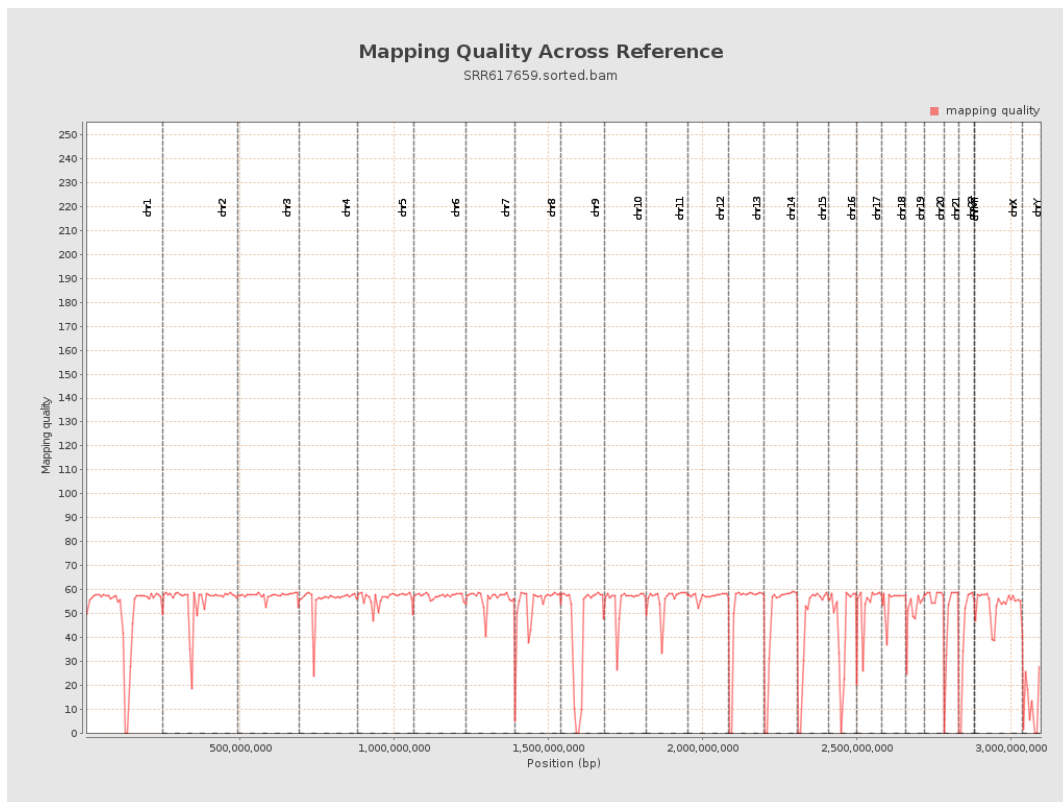
10. Results : Mapped Reads Clipping Profile



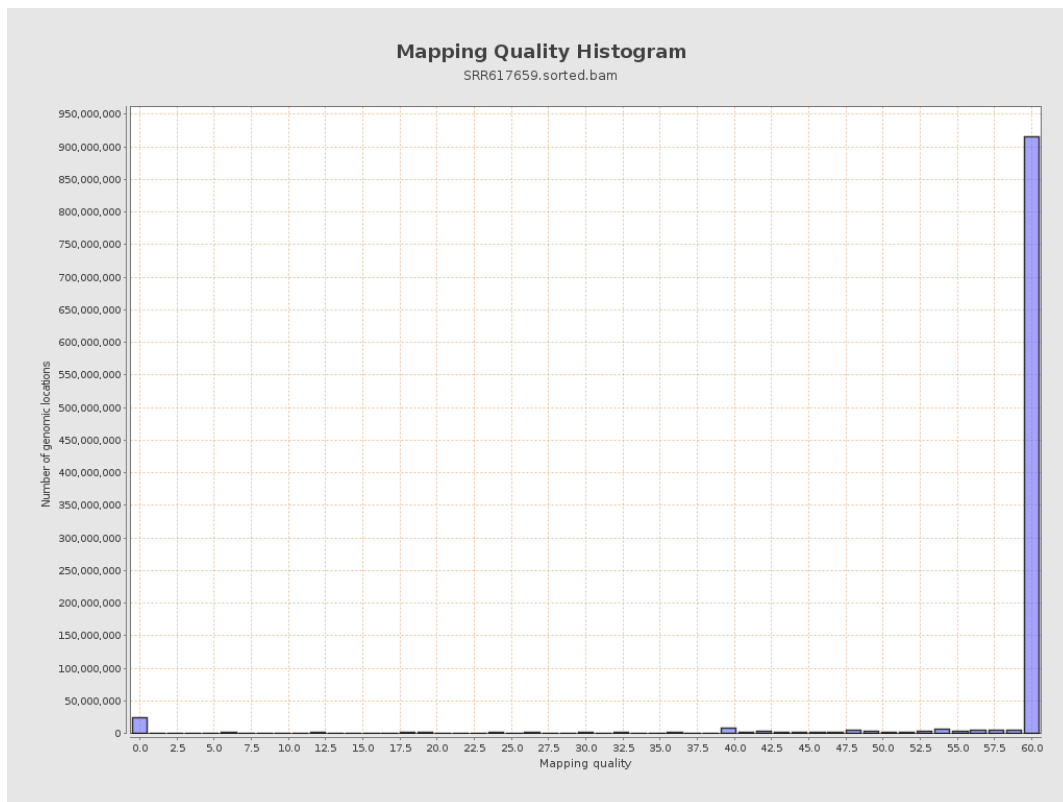
11. Results : Homopolymer Indels



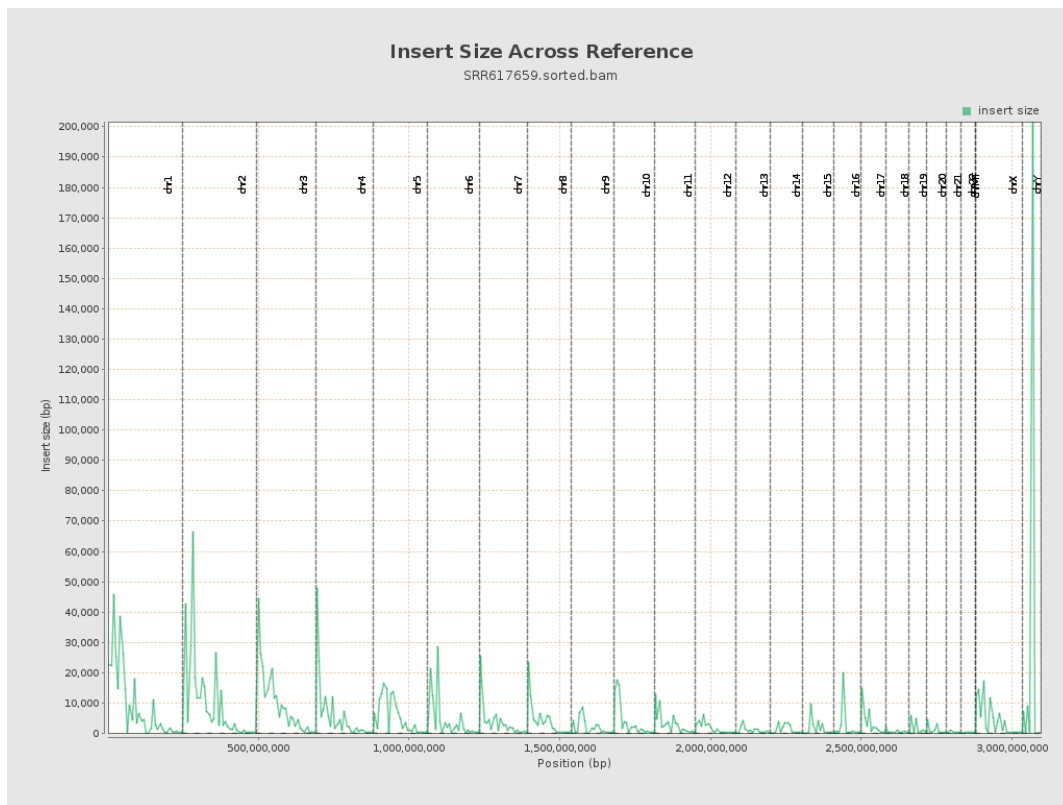
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

