Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 20:18:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617676.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_SRR617676 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617676_1.fastq.gz SRR617676_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 20:18:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617676.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	428,796,288
Mapped reads	425,599,389 / 99.25%
Unmapped reads	3,196,899 / 0.75%
Mapped paired reads	425,599,389 / 99.25%
Mapped reads, first in pair	212,870,124 / 49.64%
Mapped reads, second in pair	212,729,265 / 49.61%
Mapped reads, both in pair	423,767,070 / 98.83%
Mapped reads, singletons	1,832,319 / 0.43%
Secondary alignments	0
Supplementary alignments	2,038,134 / 0.48%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	206,302,589 / 48.11%
Duplication rate	21.65%
Clipped reads	78,507,323 / 18.31%

2.2. ACGT Content

Number/percentage of A's	12,399,298,489 / 29.77%
Number/percentage of C's	8,312,179,962 / 19.95%
Number/percentage of T's	12,433,485,150 / 29.85%
Number/percentage of G's	8,505,153,738 / 20.42%
Number/percentage of N's	4,882,820 / 0.01%

GC Percentage	40.37%

2.3. Coverage

Mean	13.4643
Standard Deviation	156.3015

2.4. Mapping Quality

Mean Mapping Quality	52.9

2.5. Insert size

Mean	25,032.72
Standard Deviation	1,413,187.47
P25/Median/P75	180 / 224 / 292

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	431,983,396
Insertions	6,606,518
Mapped reads with at least one insertion	1.52%
Deletions	15,594,806
Mapped reads with at least one deletion	3.59%
Homopolymer indels	47.91%

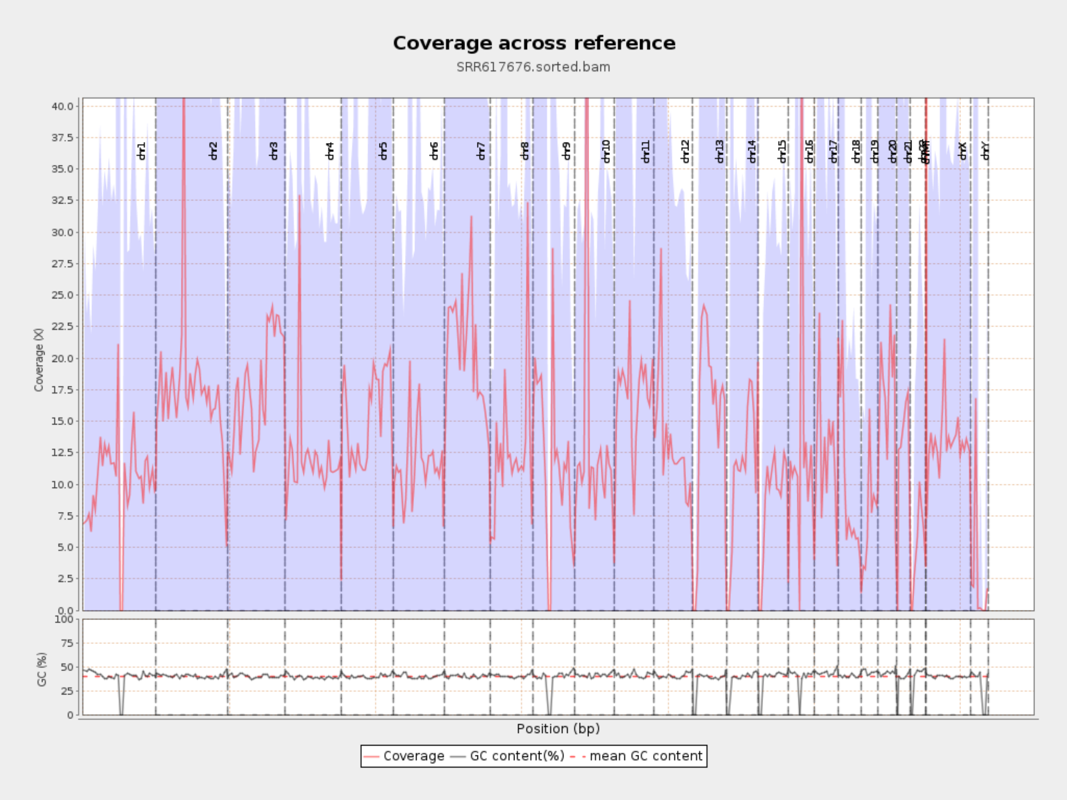
2.7. Chromosome stats

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

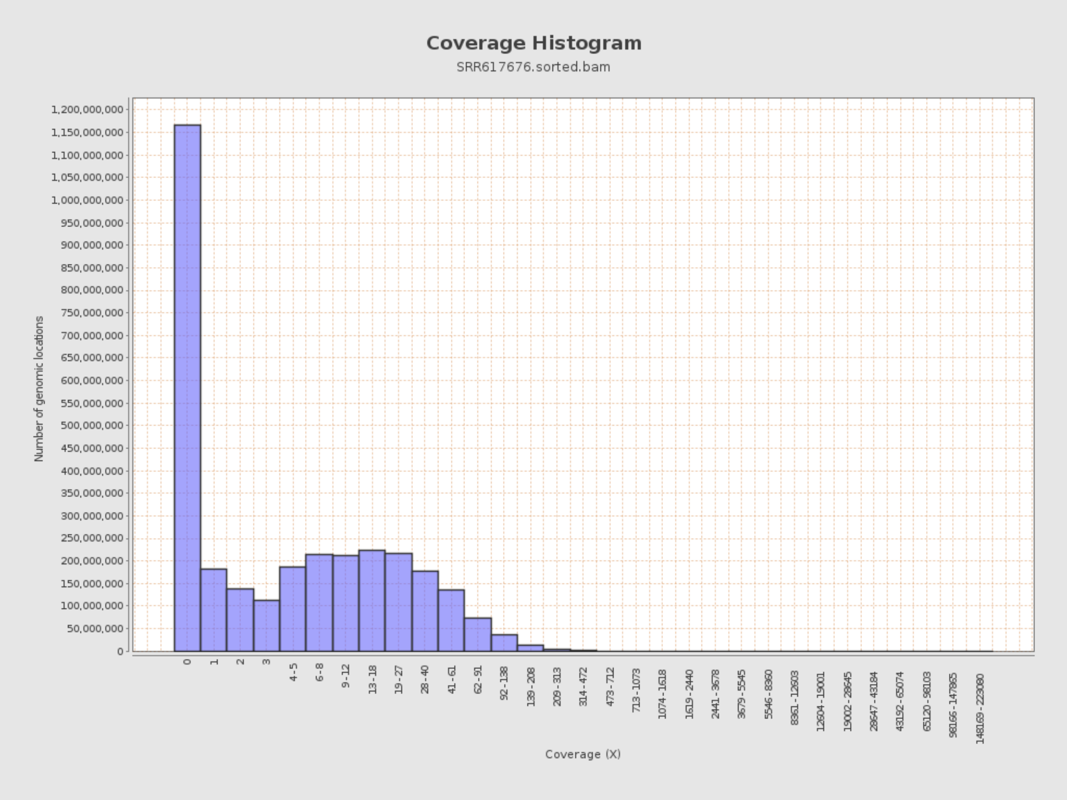
		bases	coverage	deviation
chr1	249250621	2551761152	10.2377	148.5407
chr2	243199373	4311327687	17.7275	179.8233
chr3	198022430	3488630669	17.6174	31.2568
chr4	191154276	2335138231	12.216	126.4881
chr5	180915260	2755998153	15.2336	29.6365
chr6	171115067	2018988937	11.799	81.8031
chr7	159138663	3259624677	20.4829	192.1702
chr8	146364022	1851820580	12.6522	57.5244
chr9	141213431	1718718294	12.1711	312.7013
chr10	135534747	1770367240	13.0621	313.6401
chr11	135006516	2294393726	16.9947	179.0358
chr12	133851895	1776482873	13.272	27.1475
chr13	115169878	1791433009	15.5547	28.8123
chr14	107349540	1188770806	11.0738	32.4895
chr15	102531392	887696556	8.6578	19.2688
chr16	90354753	1152673832	12.7572	238.7306
chr17	81195210	1027721731	12.6574	189.19
chr18	78077248	775727762	9.9354	273.3019
chr19	59128983	439186277	7.4276	88.1422
chr20	63025520	1124281870	17.8385	40.5892
chr21	48129895	608876271	12.6507	62.3956
chr22	51304566	265874383	5.1823	15.6398
chrMT	16571	43943834	2,651.8517	1,834.0171
chrX	155270560	2070057406	13.3319	61.9866

chrY	59373566	171744853	2.8926	261.9985

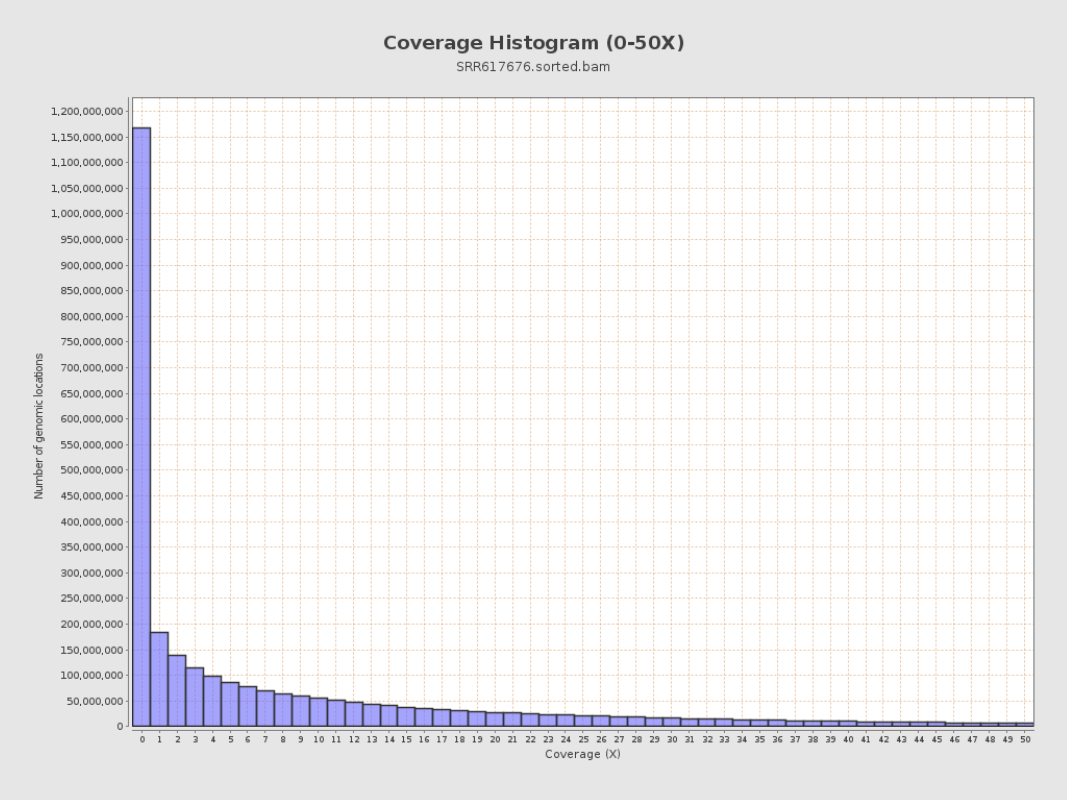
3. Results : Coverage across reference



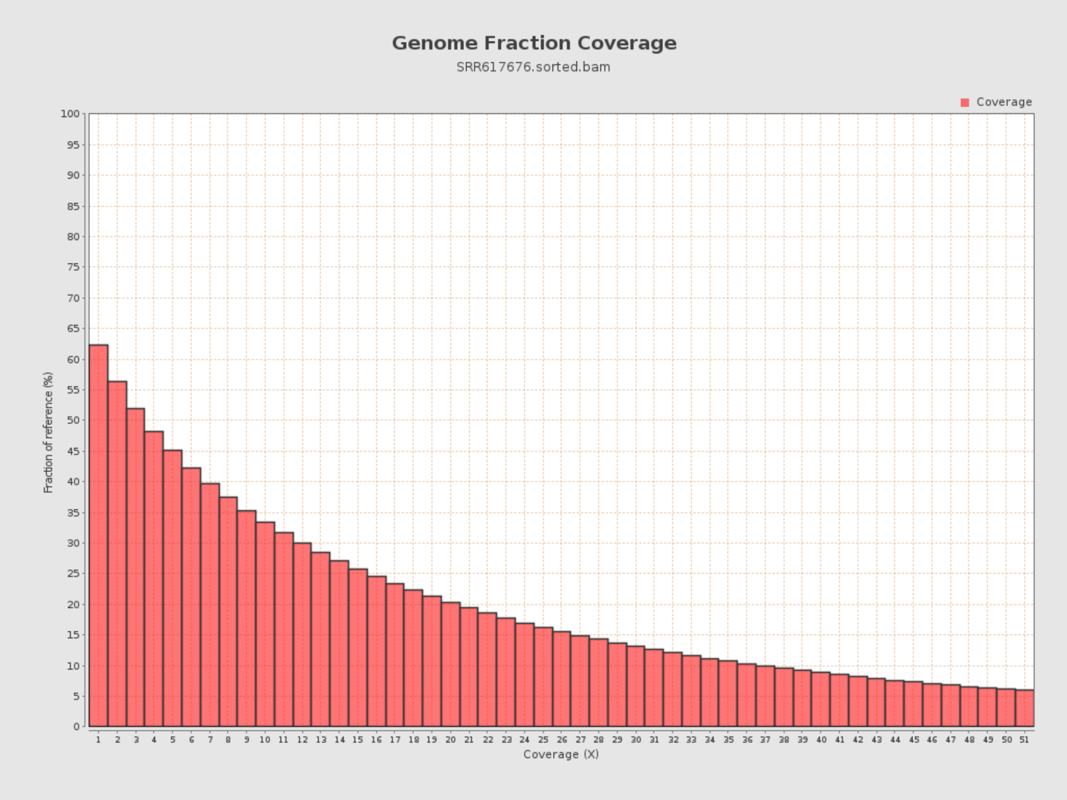
4. Results : Coverage Histogram



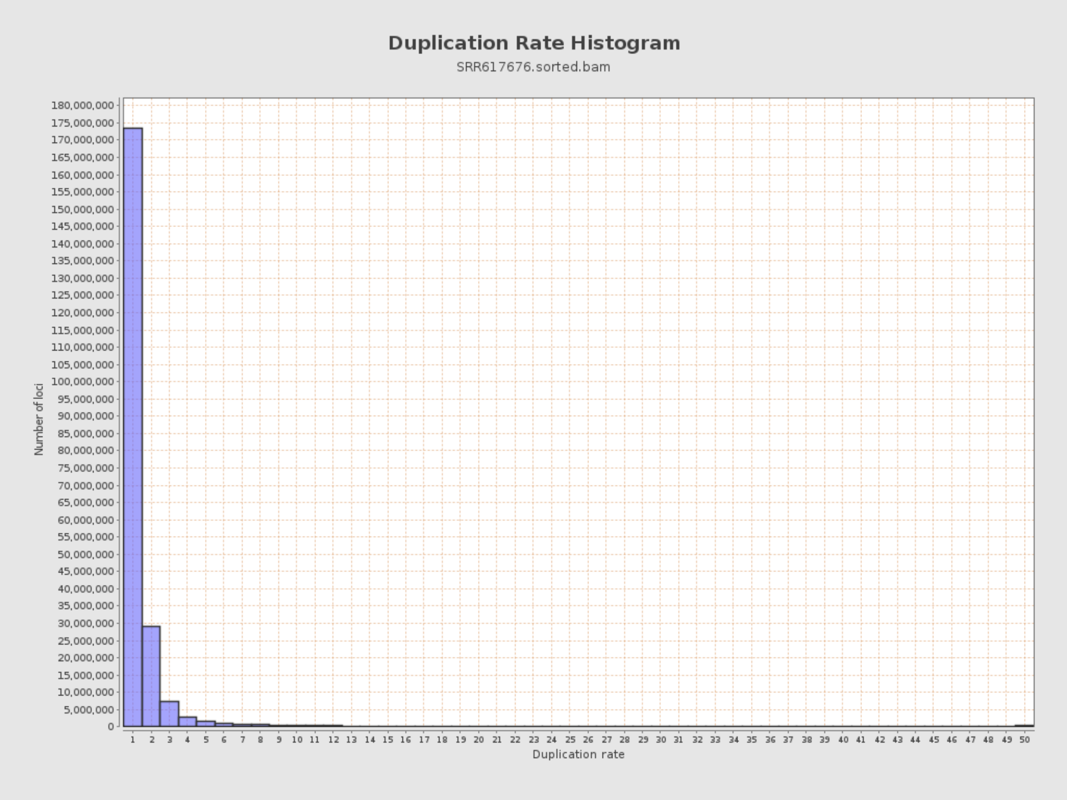
5. Results : Coverage Histogram (0-50X)



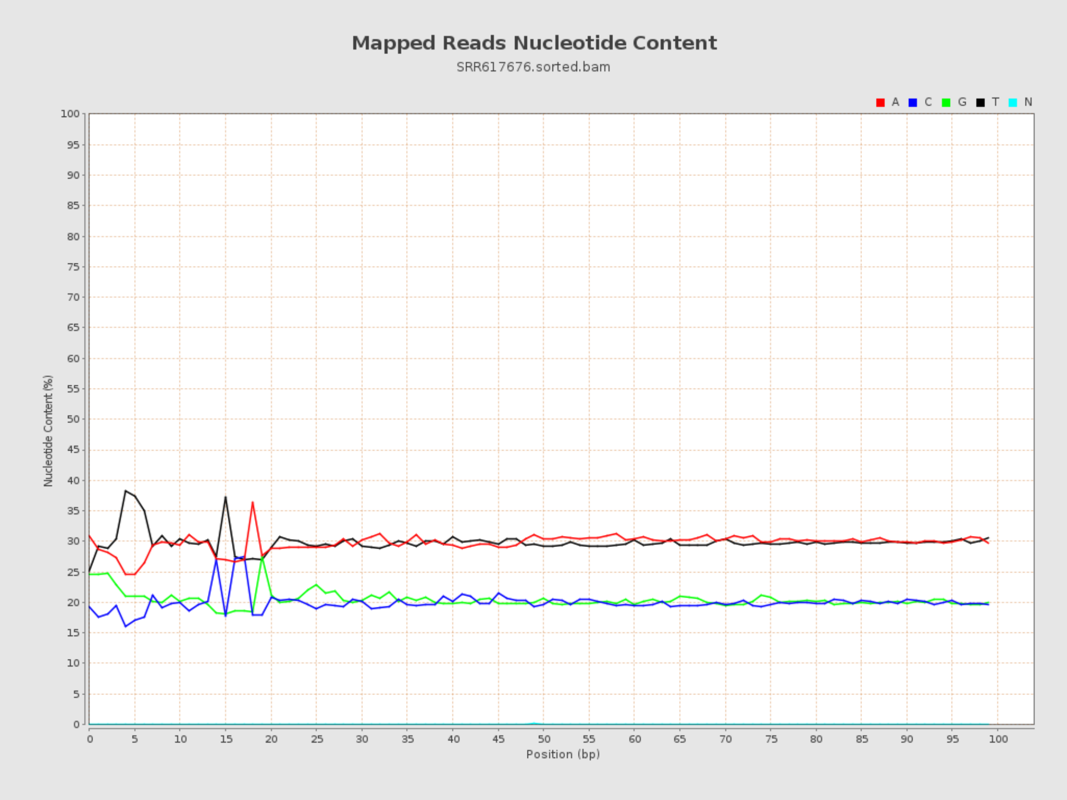
6. Results : Genome Fraction Coverage



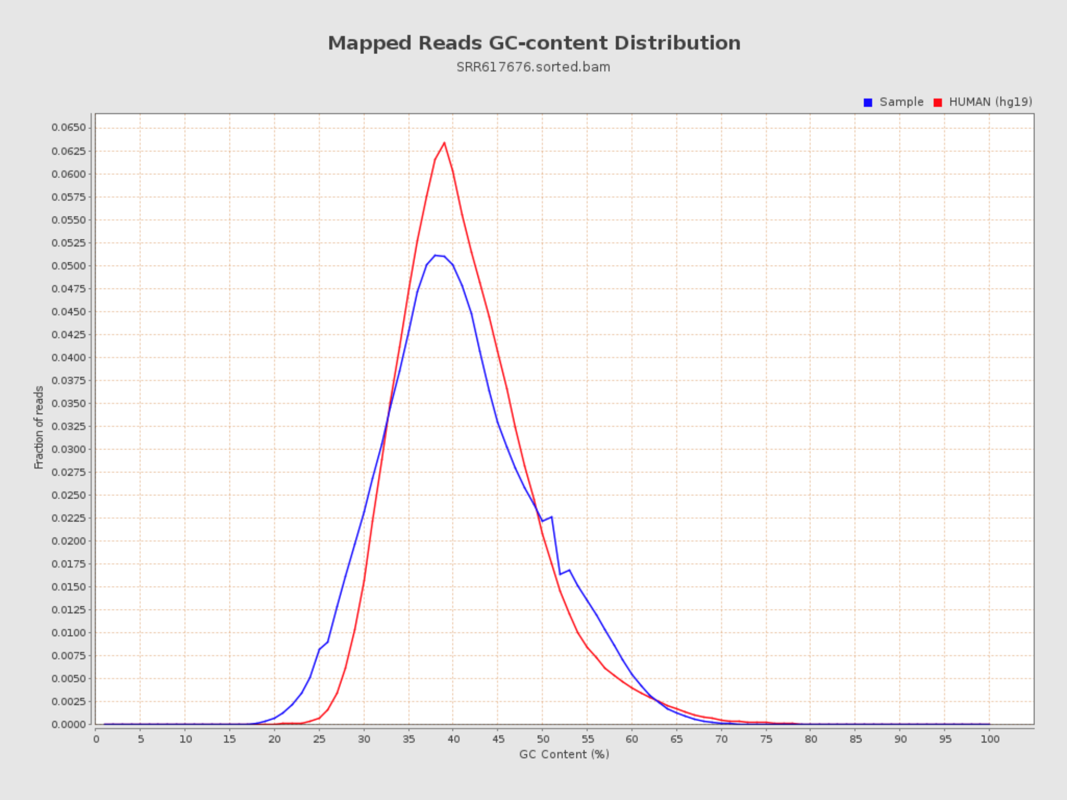
7. Results : Duplication Rate Histogram



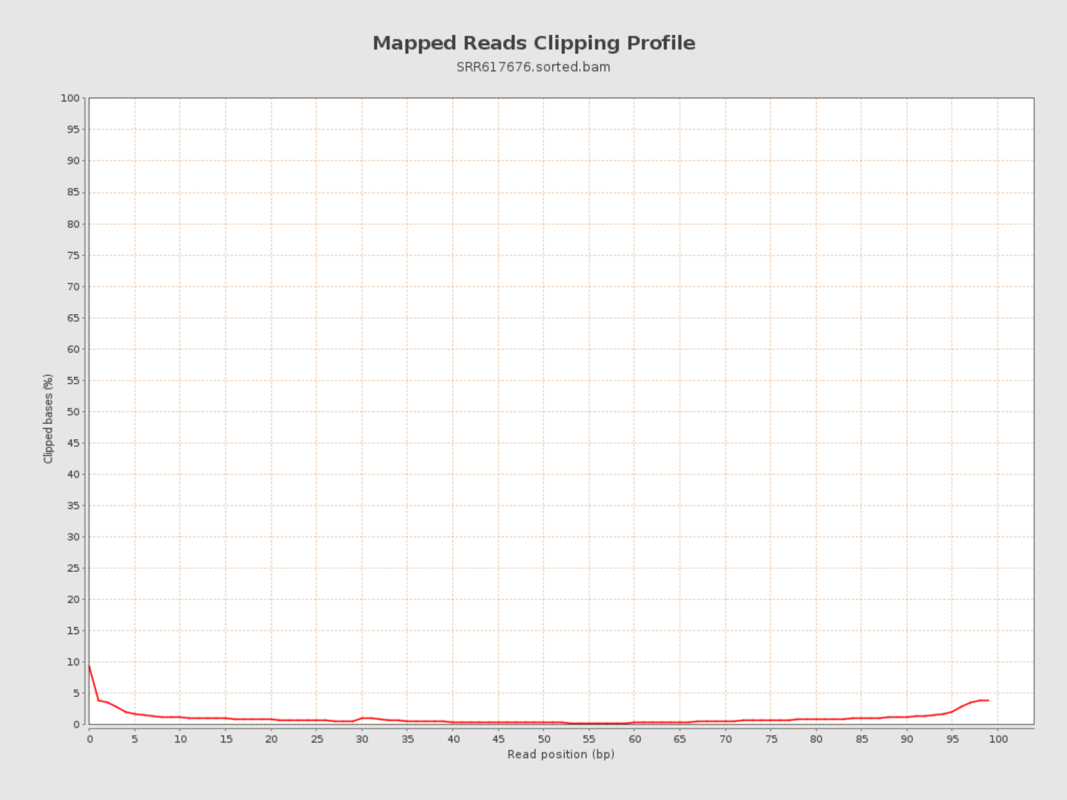
8. Results : Mapped Reads Nucleotide Content



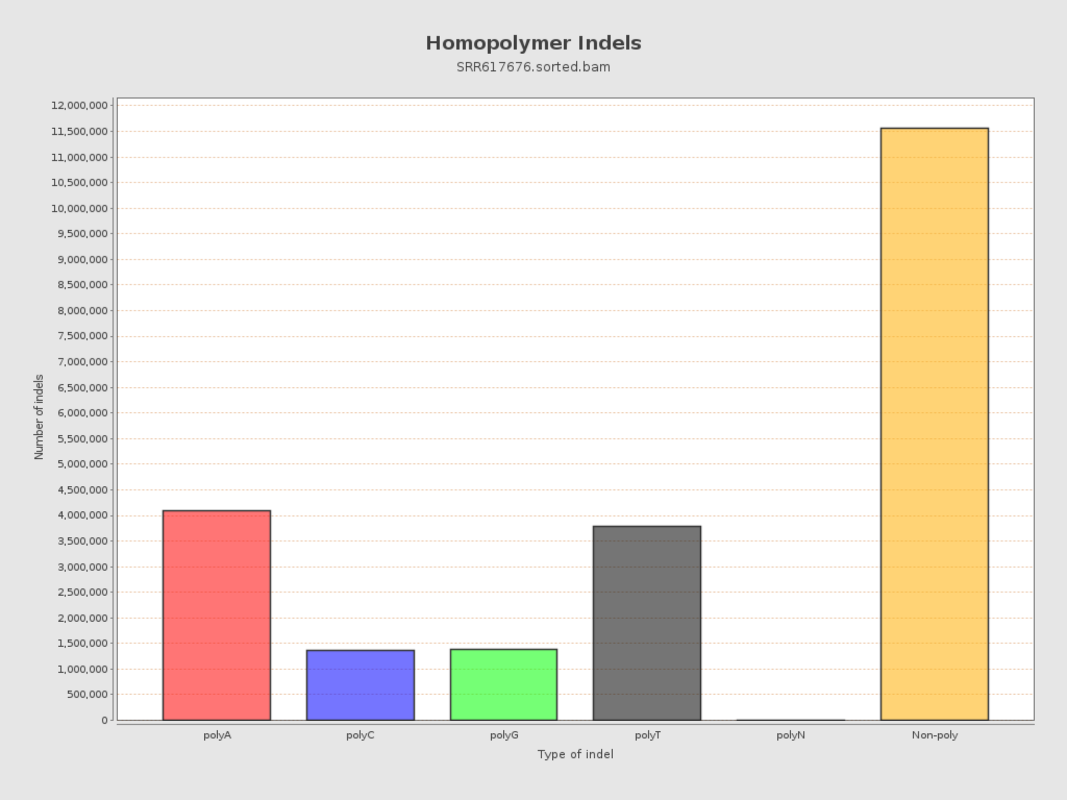
9. Results : Mapped Reads GC-content Distribution



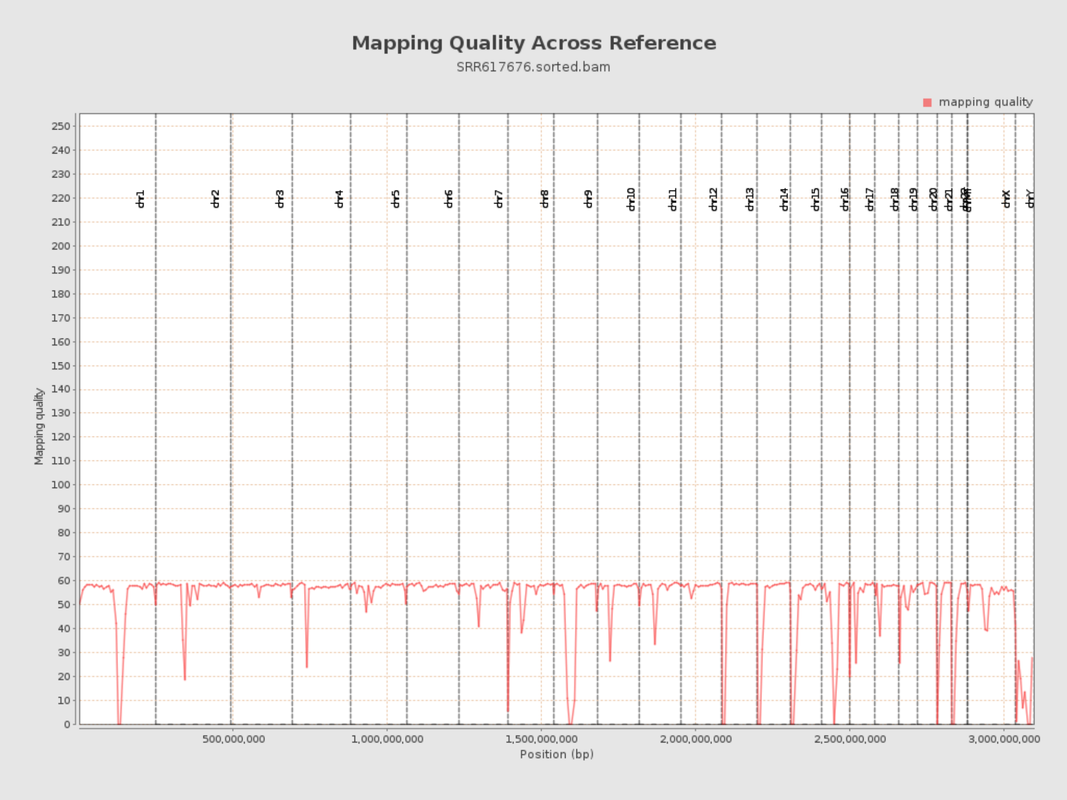
10. Results : Mapped Reads Clipping Profile



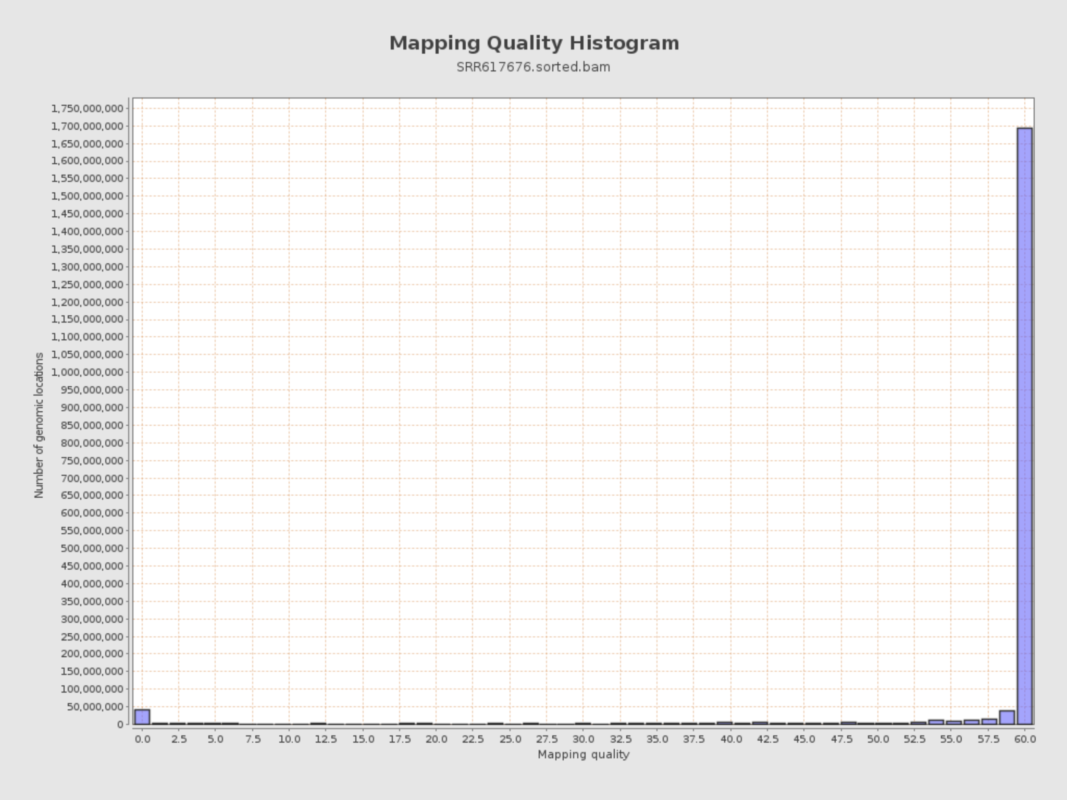
11. Results : Homopolymer Indels



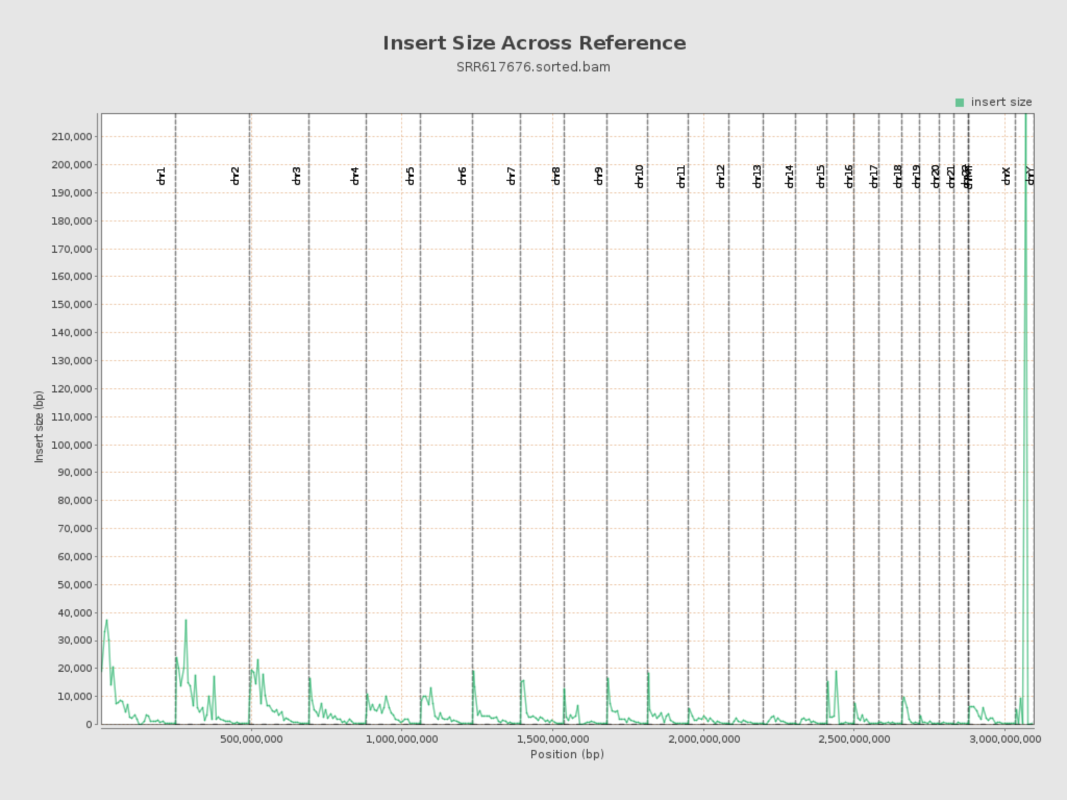
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram