

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 14:25:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618673.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_SRR618673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618673_1.fastq.gz SRR618673_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 14:25:51 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	209,057,054
Mapped reads	202,780,800 / 97%
Unmapped reads	6,276,254 / 3%
Mapped paired reads	202,780,800 / 97%
Mapped reads, first in pair	101,345,773 / 48.48%
Mapped reads, second in pair	101,435,027 / 48.52%
Mapped reads, both in pair	200,093,534 / 95.71%
Mapped reads, singletons	2,687,266 / 1.29%
Secondary alignments	0
Supplementary alignments	514,751 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	29,198,206 / 13.97%
Duplication rate	10.46%
Clipped reads	28,335,309 / 13.55%

2.2. ACGT Content

Number/percentage of A's	5,741,177,879 / 29.23%
Number/percentage of C's	4,102,007,878 / 20.89%
Number/percentage of T's	5,713,993,643 / 29.1%
Number/percentage of G's	4,080,641,452 / 20.78%
Number/percentage of N's	806,767 / 0%

GC Percentage	41.67%
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2.3. Coverage

Mean	6.3456
Standard Deviation	60.0629

2.4. Mapping Quality

Mean Mapping Quality	53.61
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2.5. Insert size

Mean	37,986.1
Standard Deviation	1,866,846.05
P25/Median/P75	212 / 239 / 276

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	208,936,383
Insertions	2,221,269
Mapped reads with at least one insertion	1.07%
Deletions	2,457,685
Mapped reads with at least one deletion	1.18%
Homopolymer indels	41.22%

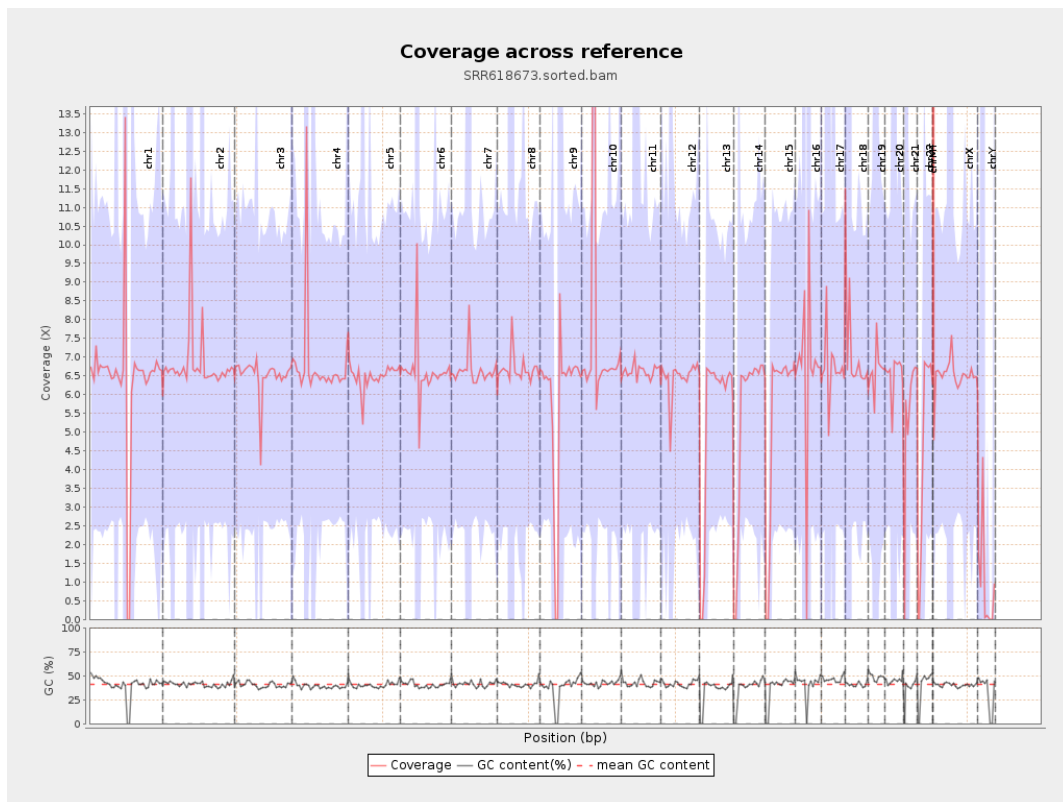
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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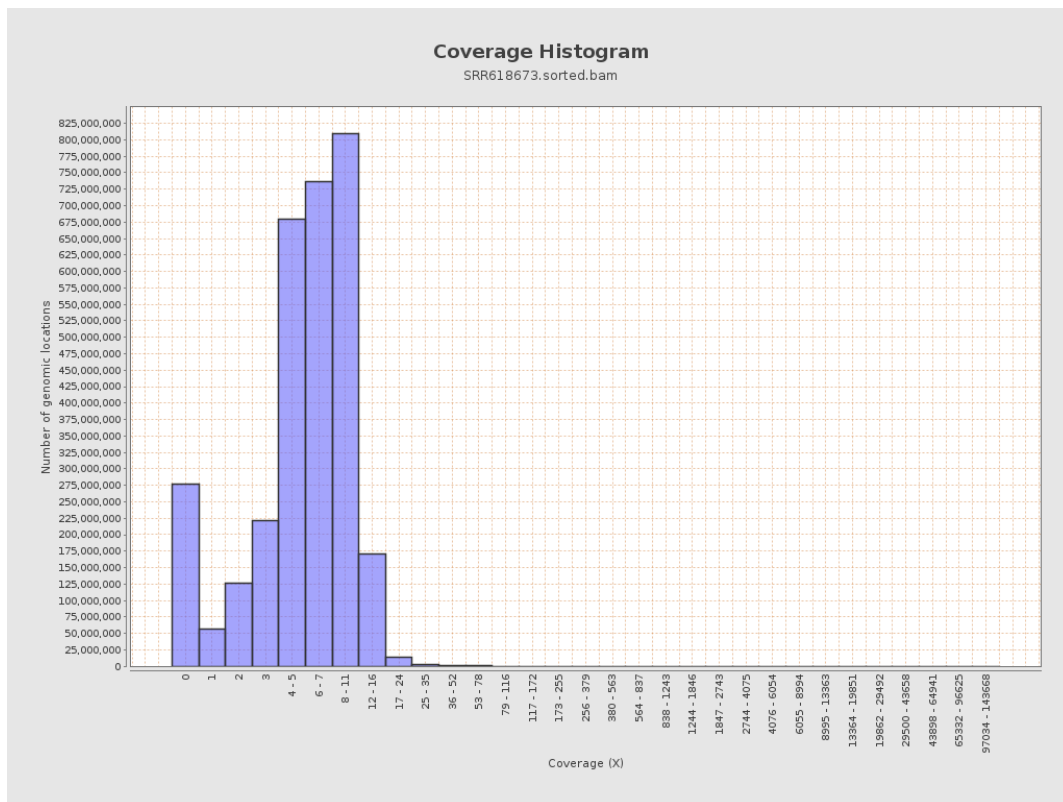
		bases	coverage	deviation
chr1	249250621	1598141970	6.4118	150.1017
chr2	243199373	1660885307	6.8293	35.172
chr3	198022430	1289075460	6.5097	4.3746
chr4	191154276	1299755984	6.7995	51.1439
chr5	180915260	1173289792	6.4853	5.0843
chr6	171115067	1130850896	6.6087	40.3172
chr7	159138663	1057802962	6.6471	45.6276
chr8	146364022	976416104	6.6711	36.5722
chr9	141213431	831208635	5.8862	60.478
chr10	135534747	1013271667	7.4761	124.1915
chr11	135006516	893149604	6.6156	27.8017
chr12	133851895	865350308	6.465	5.3957
chr13	115169878	622867299	5.4082	4.0755
chr14	107349540	588582037	5.4829	5.4194
chr15	102531392	553403044	5.3974	4.0881
chr16	90354753	606394784	6.7113	37.5588
chr17	81195210	547123336	6.7384	30.7889
chr18	78077248	549211834	7.0342	87.599
chr19	59128983	394201200	6.6668	62.1893
chr20	63025520	410707761	6.5165	15.7575
chr21	48129895	268410549	5.5768	18.3458
chr22	51304566	240182501	4.6815	4.8834
chrMT	16571	5792536	349.5586	44.029
chrX	155270560	1010493926	6.508	16.3021

chrY	59373566	57620610	0.9705	41.9468
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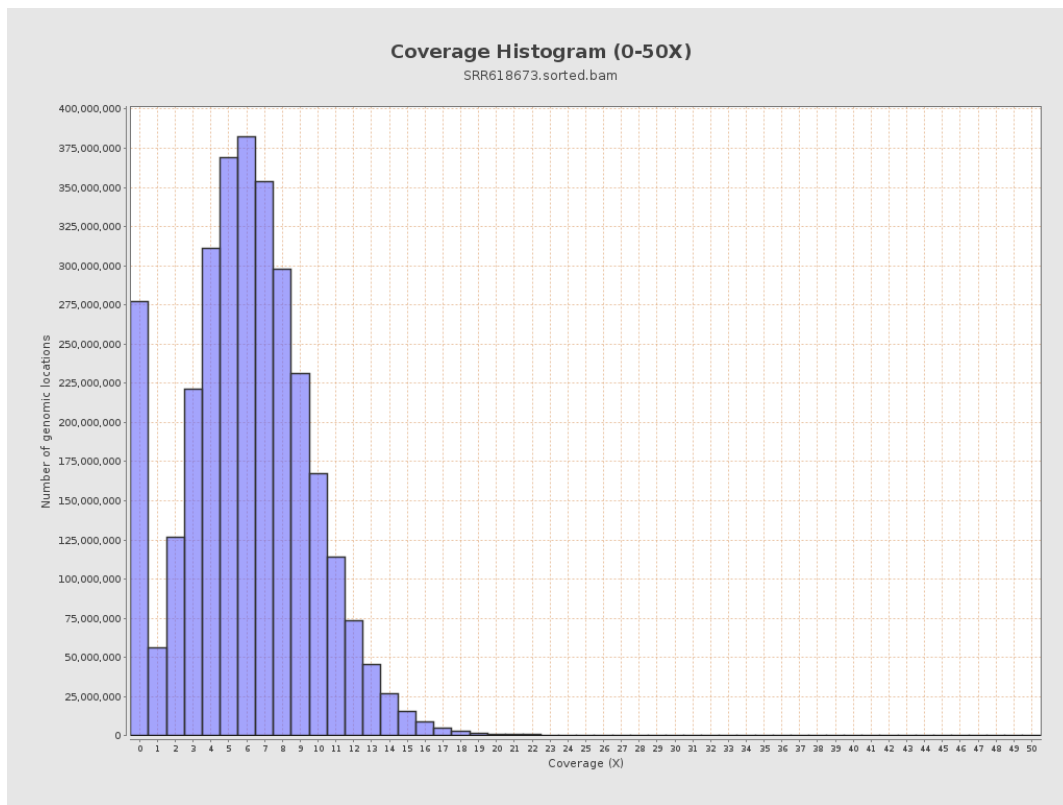
3. Results : Coverage across reference



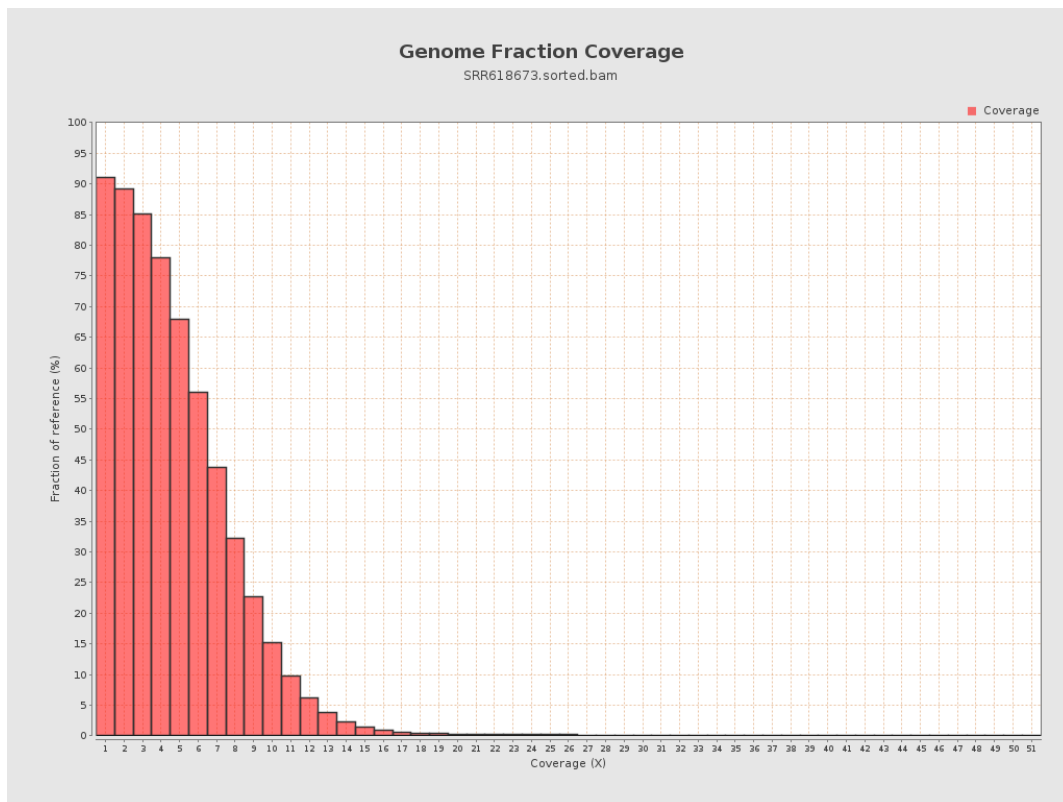
4. Results : Coverage Histogram



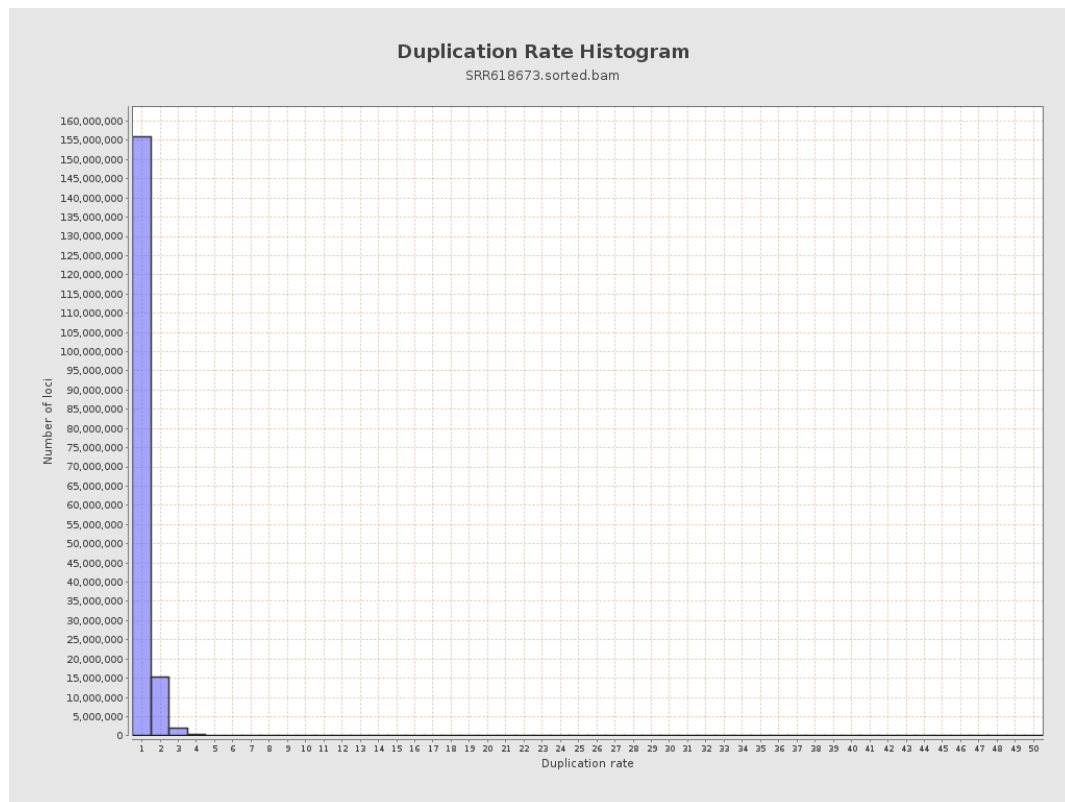
5. Results : Coverage Histogram (0-50X)



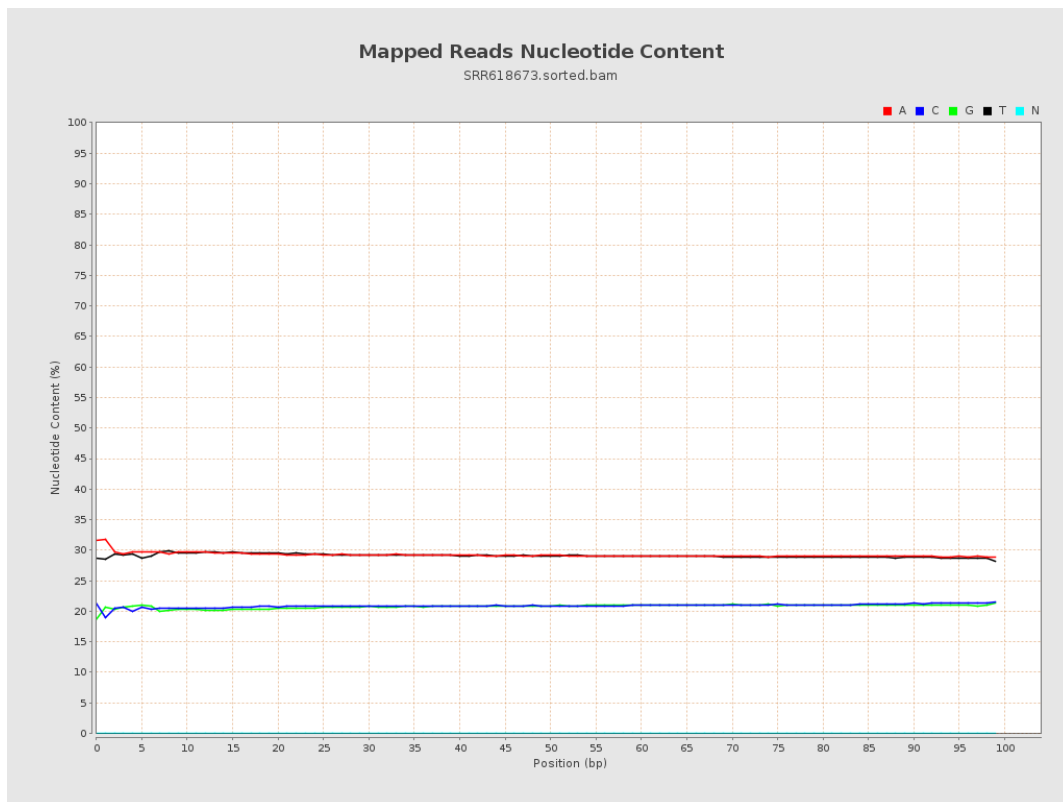
6. Results : Genome Fraction Coverage



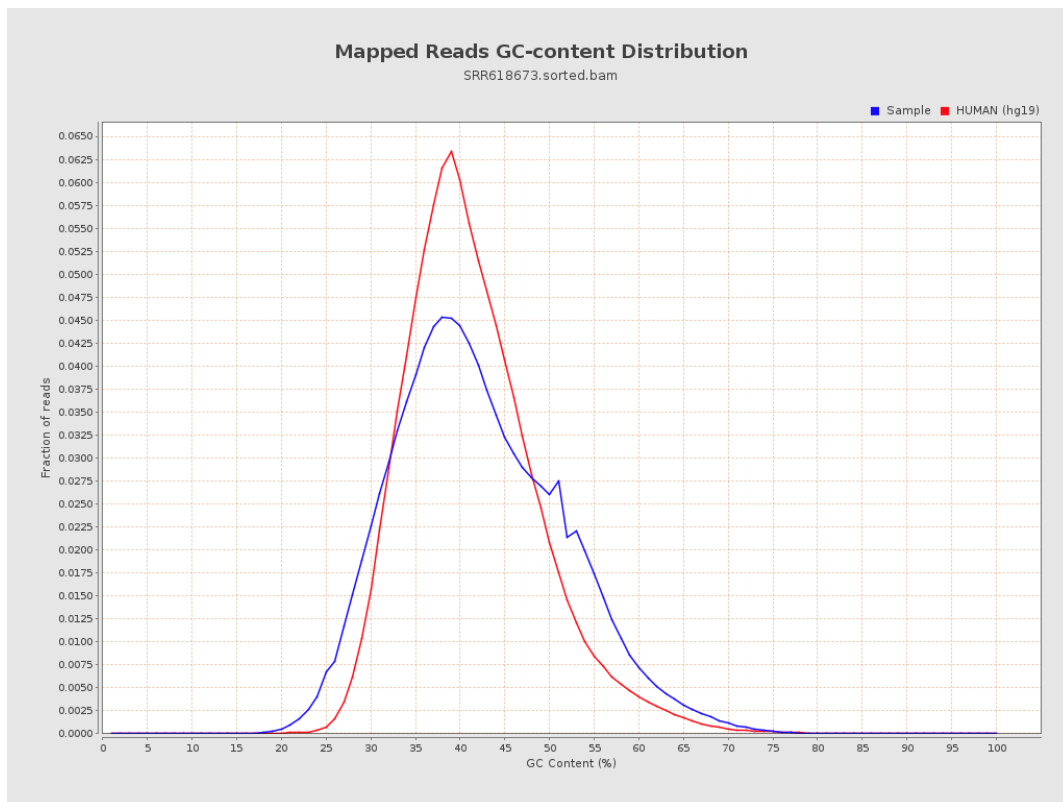
7. Results : Duplication Rate Histogram



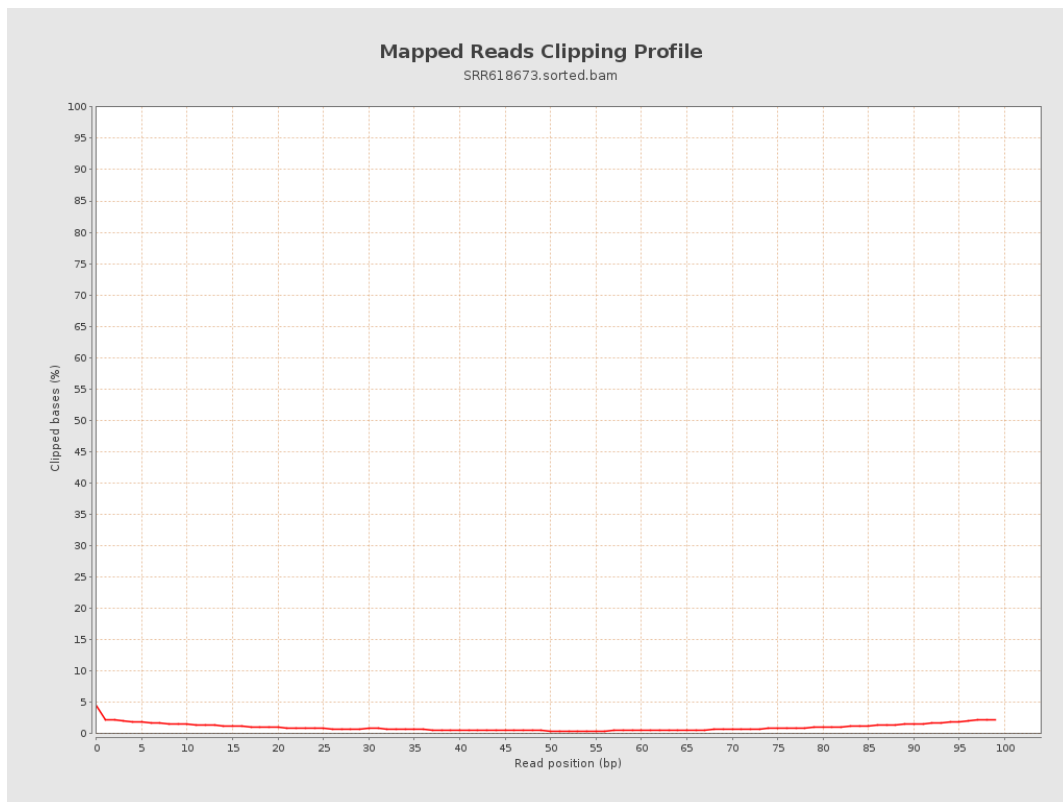
8. Results : Mapped Reads Nucleotide Content



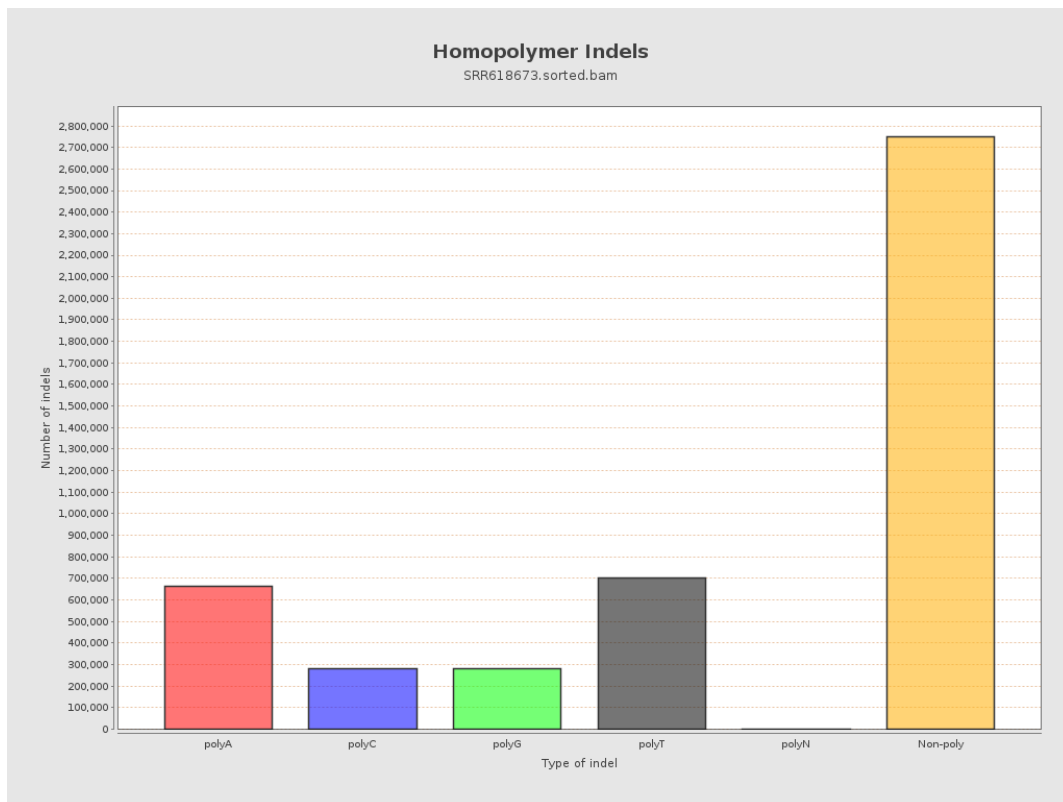
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



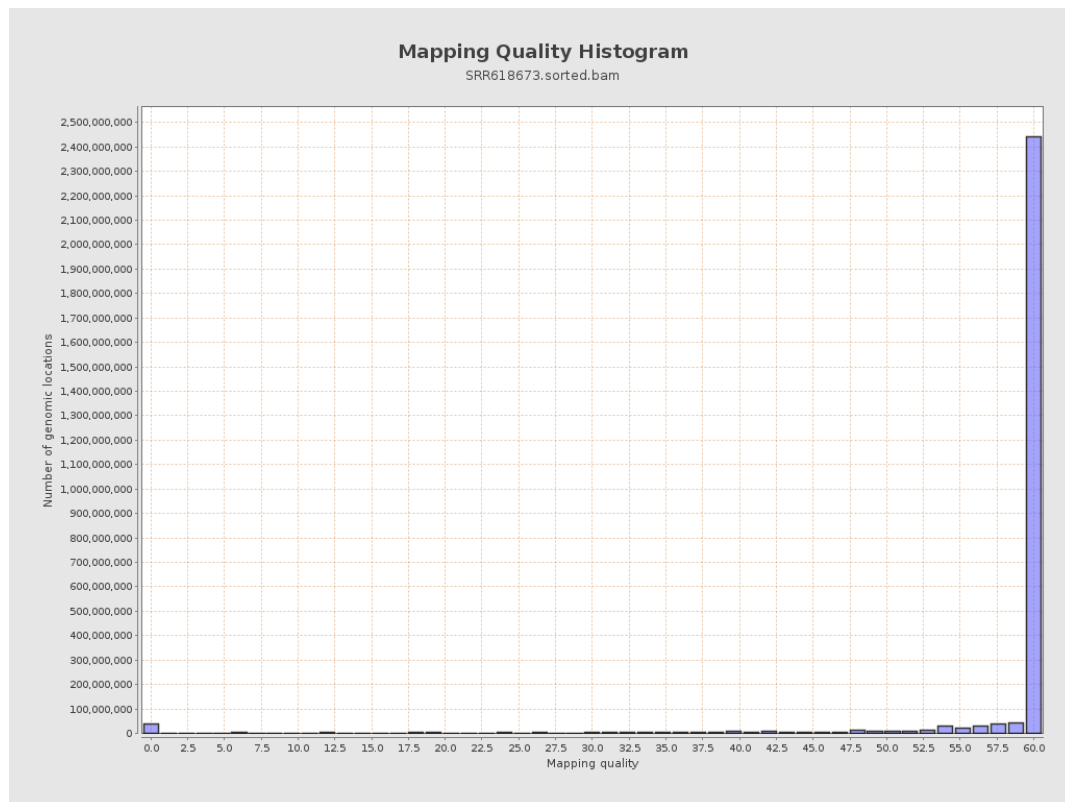
11. Results : Homopolymer Indels



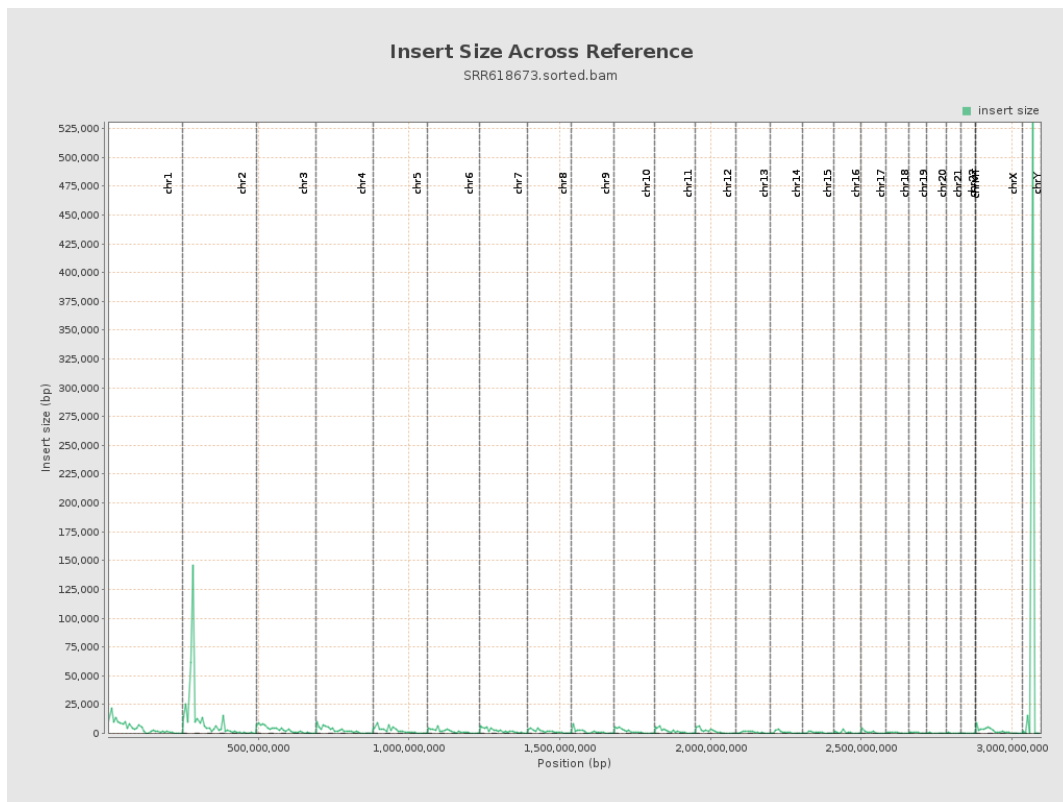
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

