

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/21 12:11:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618669.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_SRR618669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618669_1.fastq.gz SRR618669_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 21 12:11:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	590,513,222
Mapped reads	514,933,663 / 87.2%
Unmapped reads	75,579,559 / 12.8%
Mapped paired reads	514,933,663 / 87.2%
Mapped reads, first in pair	268,422,538 / 45.46%
Mapped reads, second in pair	246,511,125 / 41.75%
Mapped reads, both in pair	487,783,156 / 82.6%
Mapped reads, singletons	27,150,507 / 4.6%
Secondary alignments	0
Supplementary alignments	1,492,832 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	83,431,124 / 14.13%
Duplication rate	11.73%
Clipped reads	58,663,242 / 9.93%

2.2. ACGT Content

Number/percentage of A's	14,696,788,973 / 29.37%
Number/percentage of C's	10,325,644,352 / 20.63%
Number/percentage of T's	14,527,172,327 / 29.03%
Number/percentage of G's	10,415,021,376 / 20.81%
Number/percentage of N's	82,047,649 / 0.16%

GC Percentage	41.44%
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2.3. Coverage

Mean	16.1709
Standard Deviation	168.696

2.4. Mapping Quality

Mean Mapping Quality	53.33
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2.5. Insert size

Mean	44,951.4
Standard Deviation	2,034,860.79
P25/Median/P75	165 / 173 / 181

2.6. Mismatches and indels

General error rate	1.64%
Mismatches	796,783,430
Insertions	17,105,125
Mapped reads with at least one insertion	3.27%
Deletions	5,735,846
Mapped reads with at least one deletion	1.08%
Homopolymer indels	35.08%

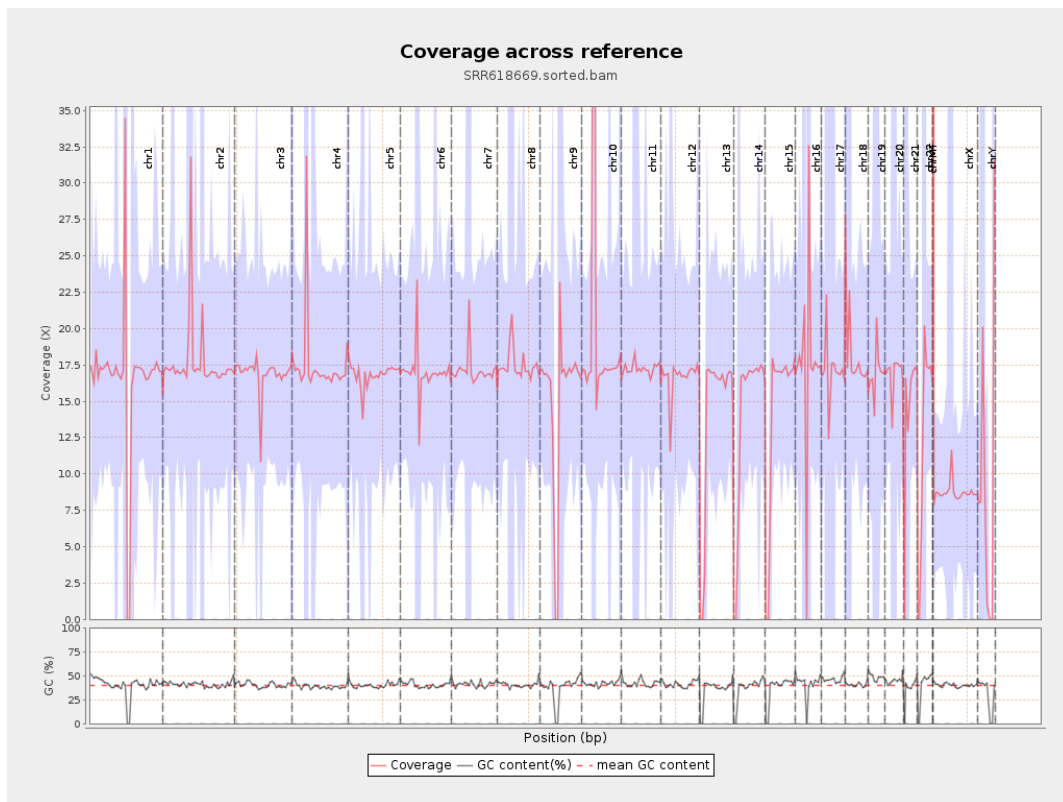
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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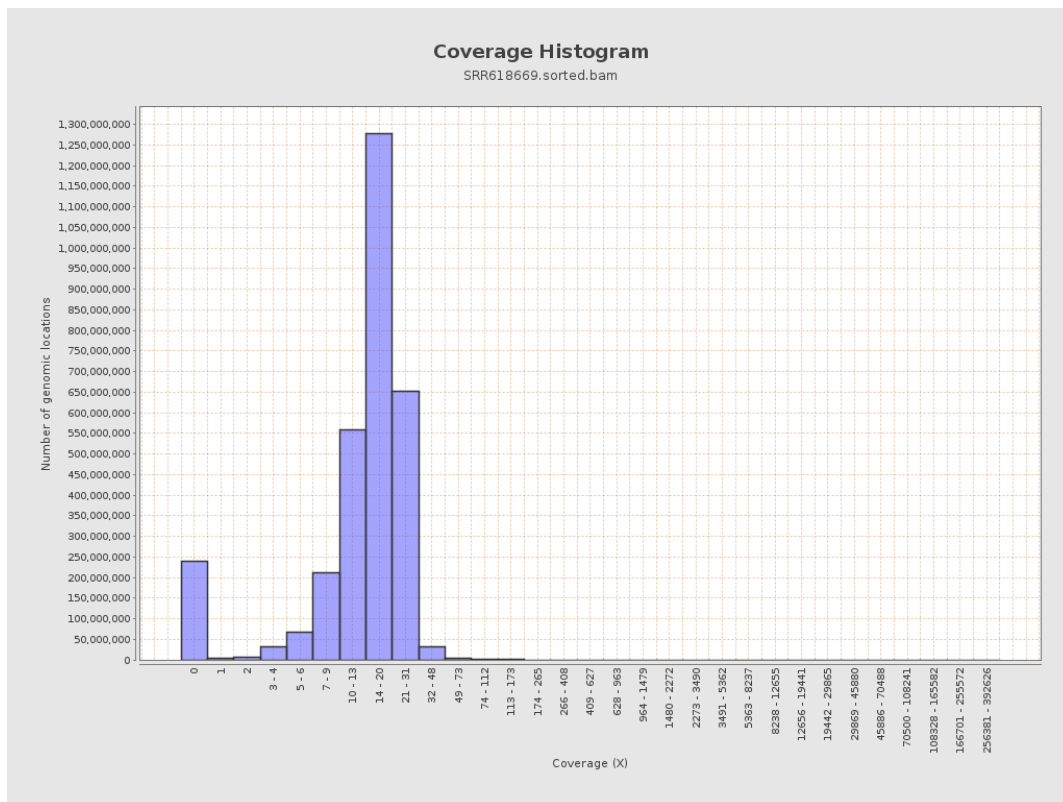
		bases	coverage	deviation
chr1	249250621	4127023552	16.5577	402.7535
chr2	243199373	4311571302	17.7285	106.4949
chr3	198022430	3338971293	16.8616	16.1351
chr4	191154276	3347922151	17.5142	83.1479
chr5	180915260	3040599835	16.8068	13.9464
chr6	171115067	2905887695	16.9821	77.1955
chr7	159138663	2730073232	17.1553	125.1043
chr8	146364022	2555993321	17.4633	168.6374
chr9	141213431	2153697990	15.2514	168.2527
chr10	135534747	2645940677	19.5222	388.971
chr11	135006516	2325085442	17.222	89.1138
chr12	133851895	2233061452	16.6831	12.6755
chr13	115169878	1612889904	14.0044	9.3517
chr14	107349540	1529040704	14.2436	15.954
chr15	102531392	1442530262	14.0692	9.9707
chr16	90354753	1587985153	17.575	126.839
chr17	81195210	1392373296	17.1485	76.5948
chr18	78077248	1411418203	18.0772	215.8369
chr19	59128983	1003801790	16.9765	177.4696
chr20	63025520	1059902326	16.817	43.7686
chr21	48129895	705213911	14.6523	77.0855
chr22	51304566	638291856	12.4412	70.8092
chrMT	16571	23391018	1,411.5635	255.6901
chrX	155270560	1358452161	8.7489	37.5371

chrY	59373566	578919441	9.7505	175.0844
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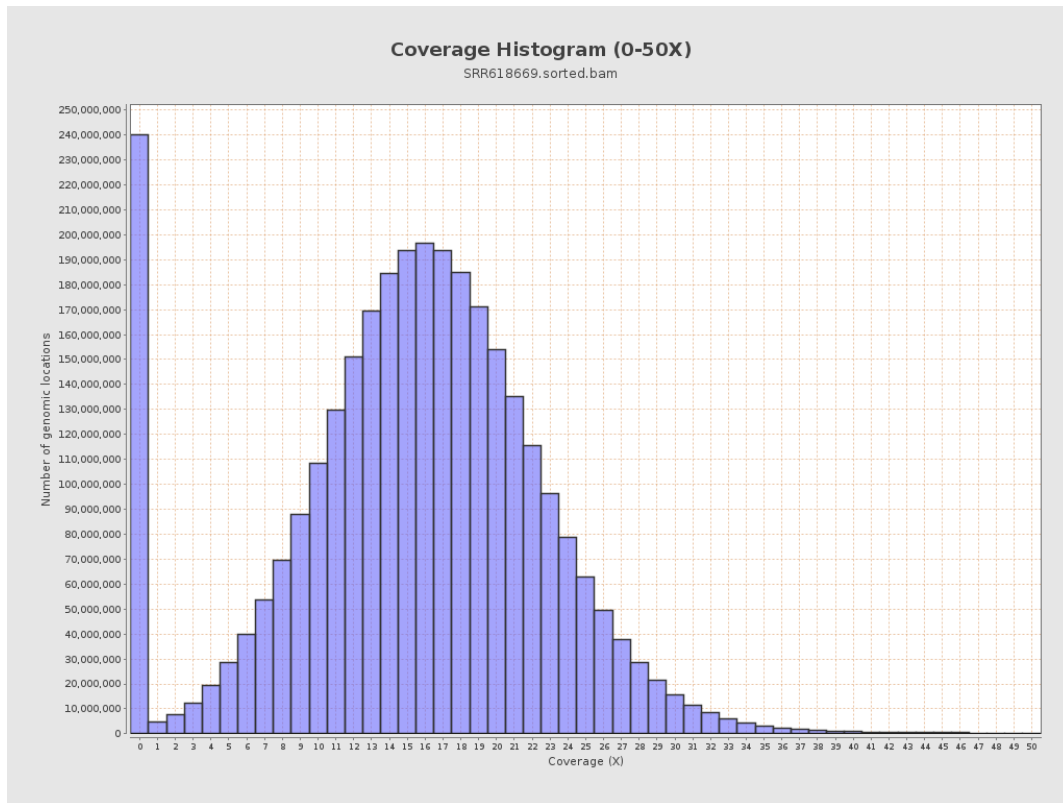
3. Results : Coverage across reference



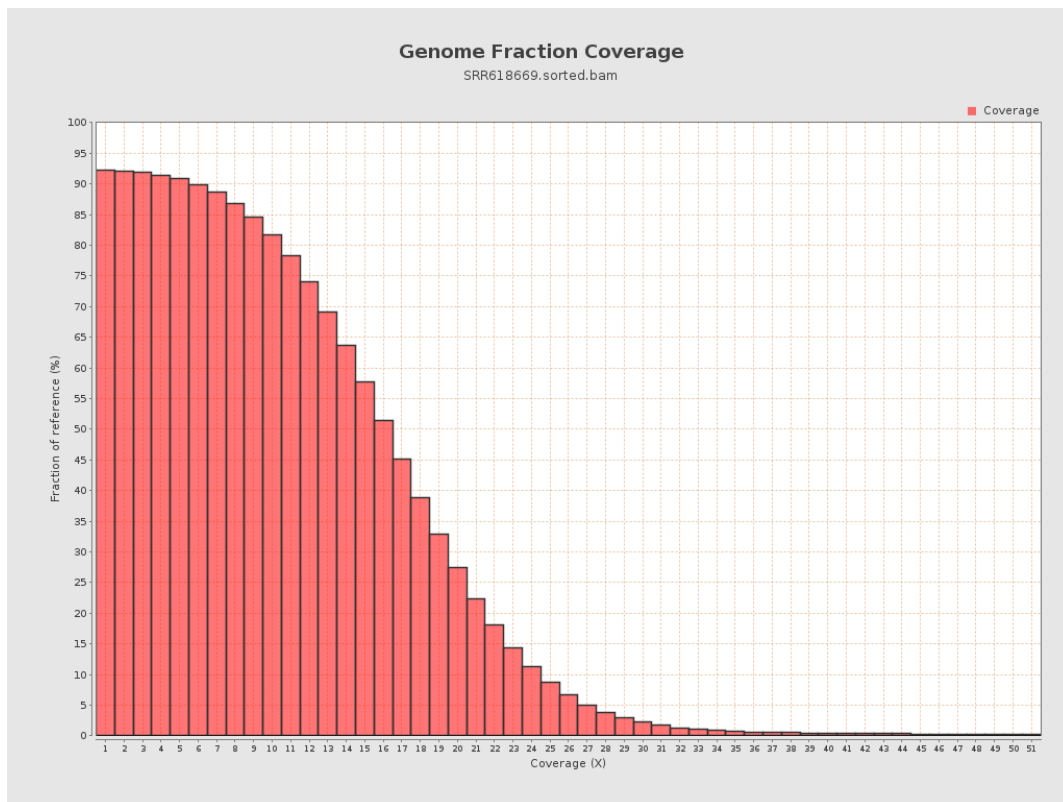
4. Results : Coverage Histogram



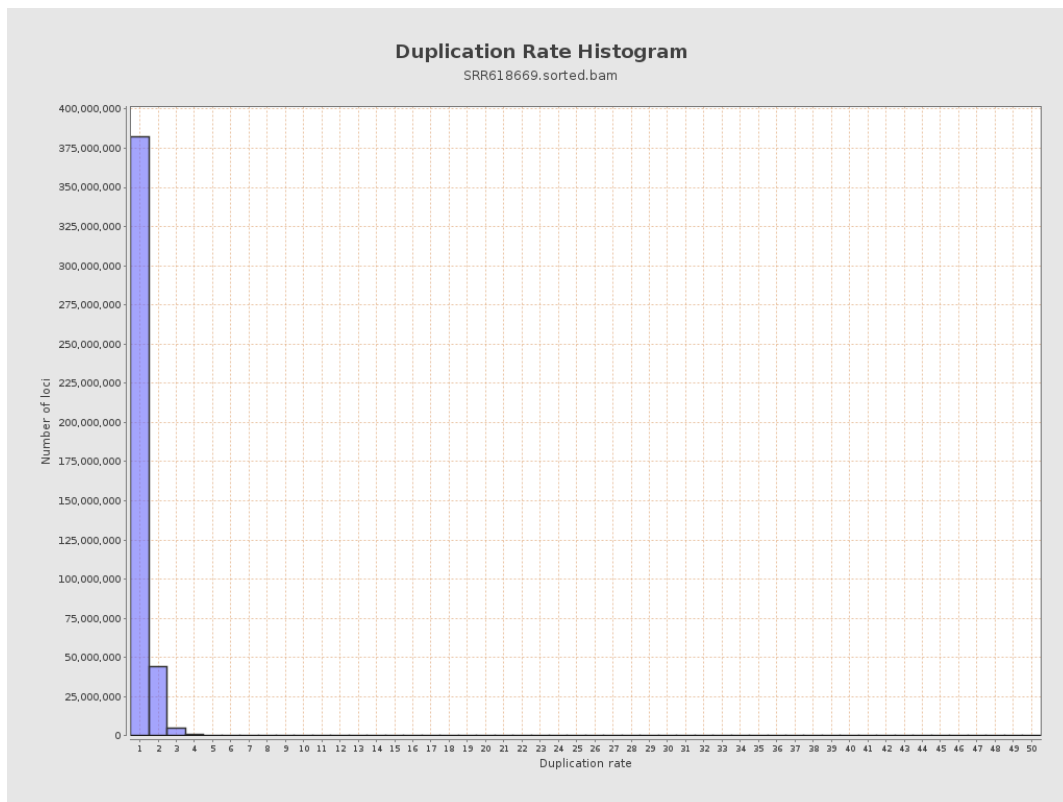
5. Results : Coverage Histogram (0-50X)



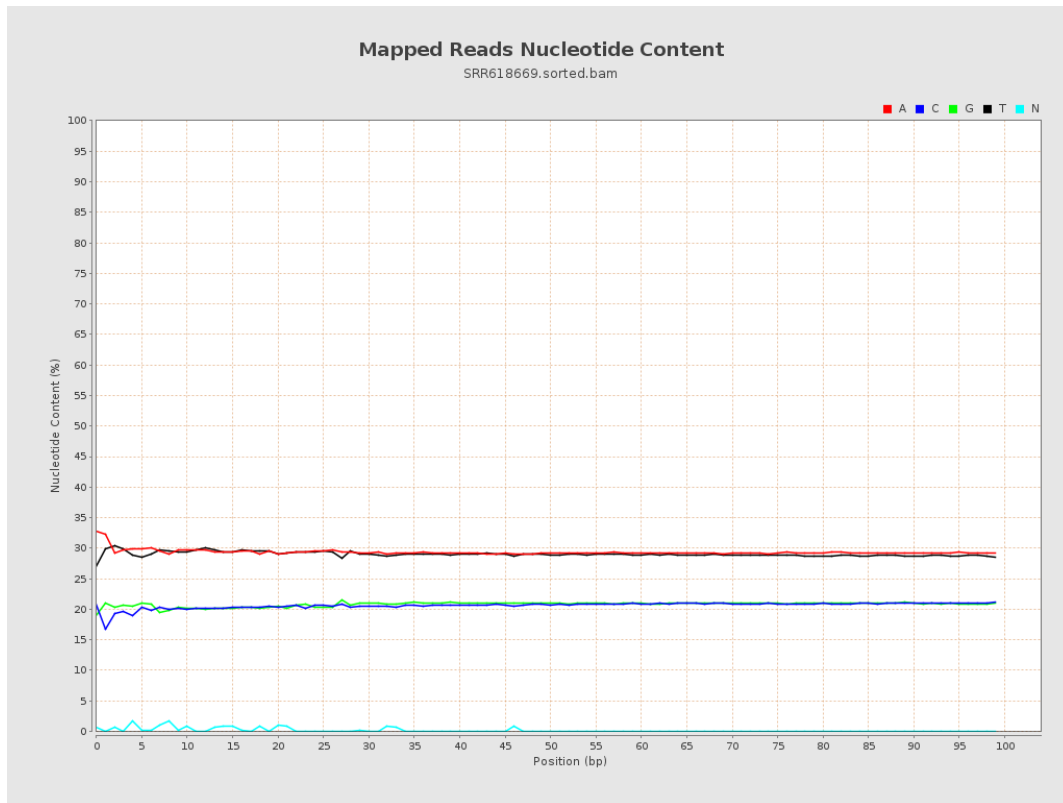
6. Results : Genome Fraction Coverage



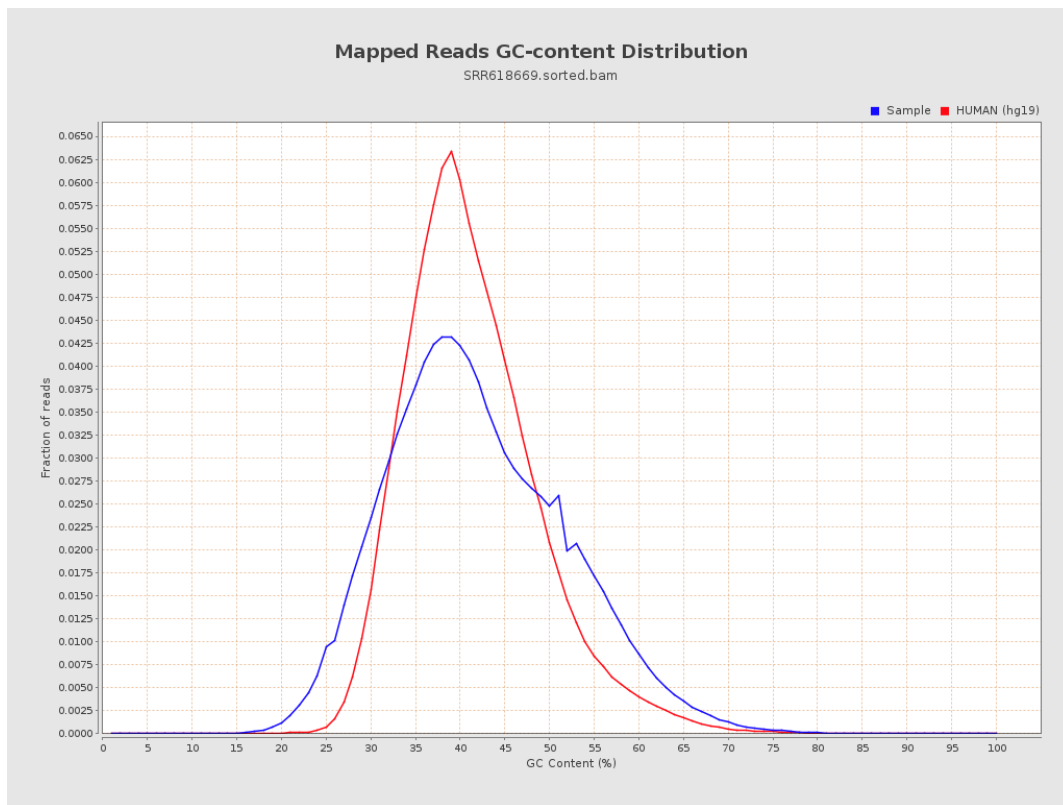
7. Results : Duplication Rate Histogram



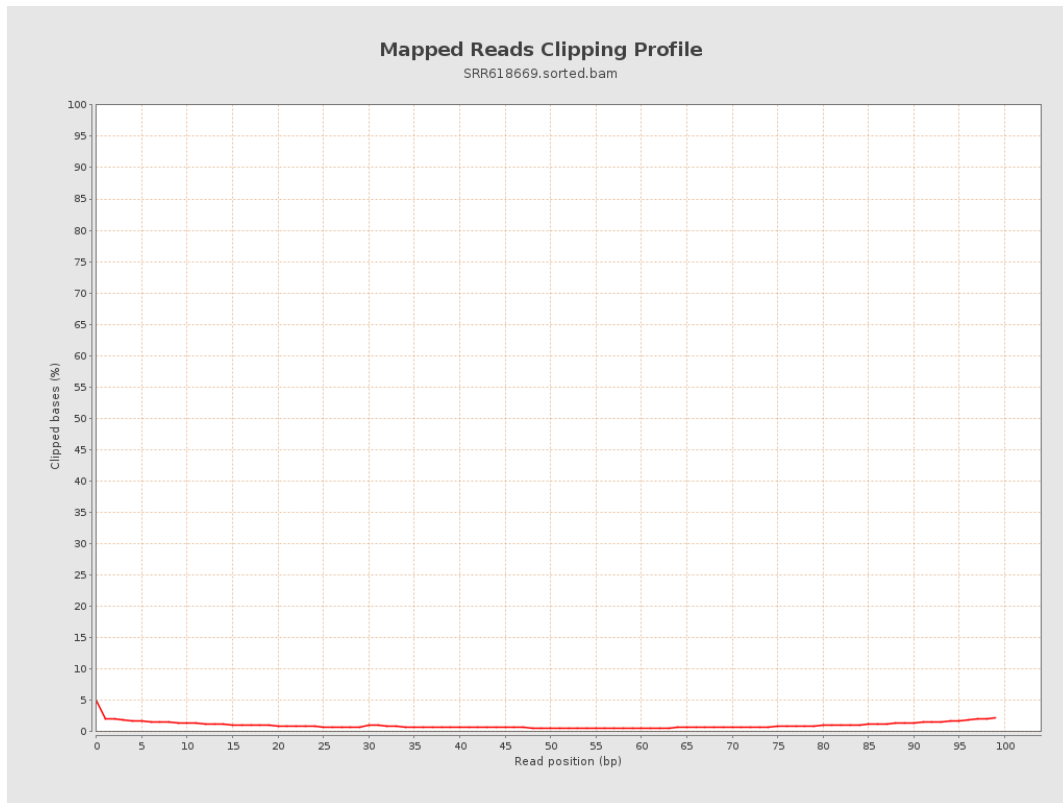
8. Results : Mapped Reads Nucleotide Content



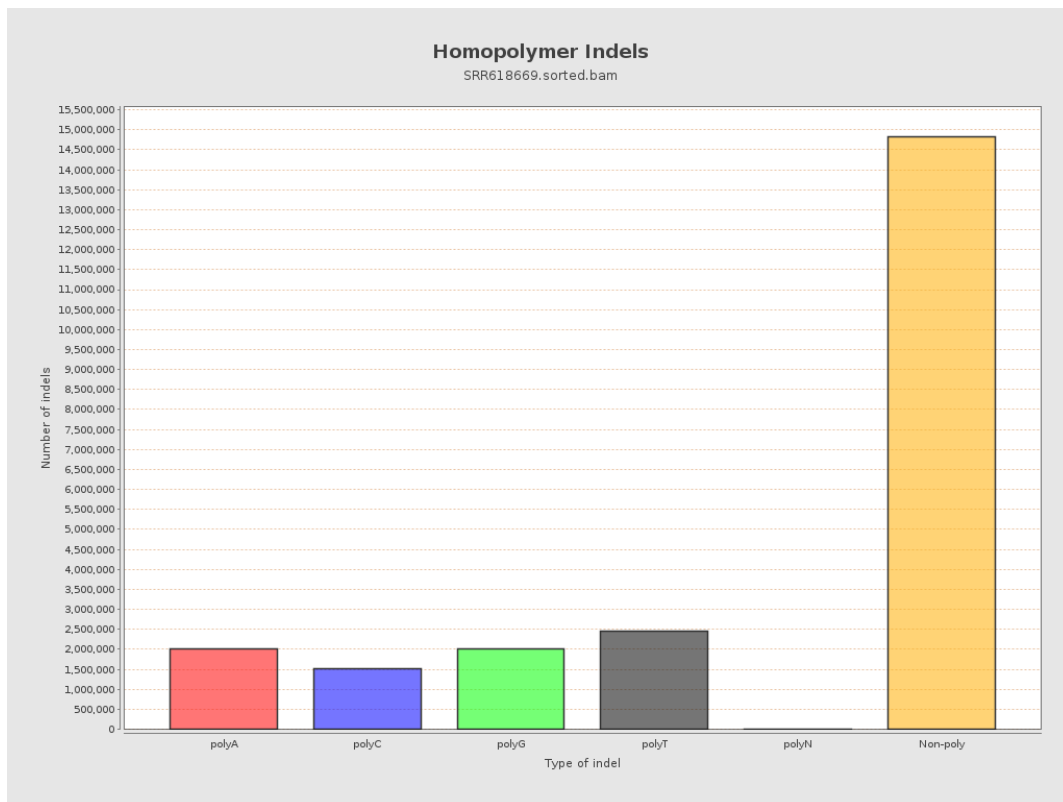
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



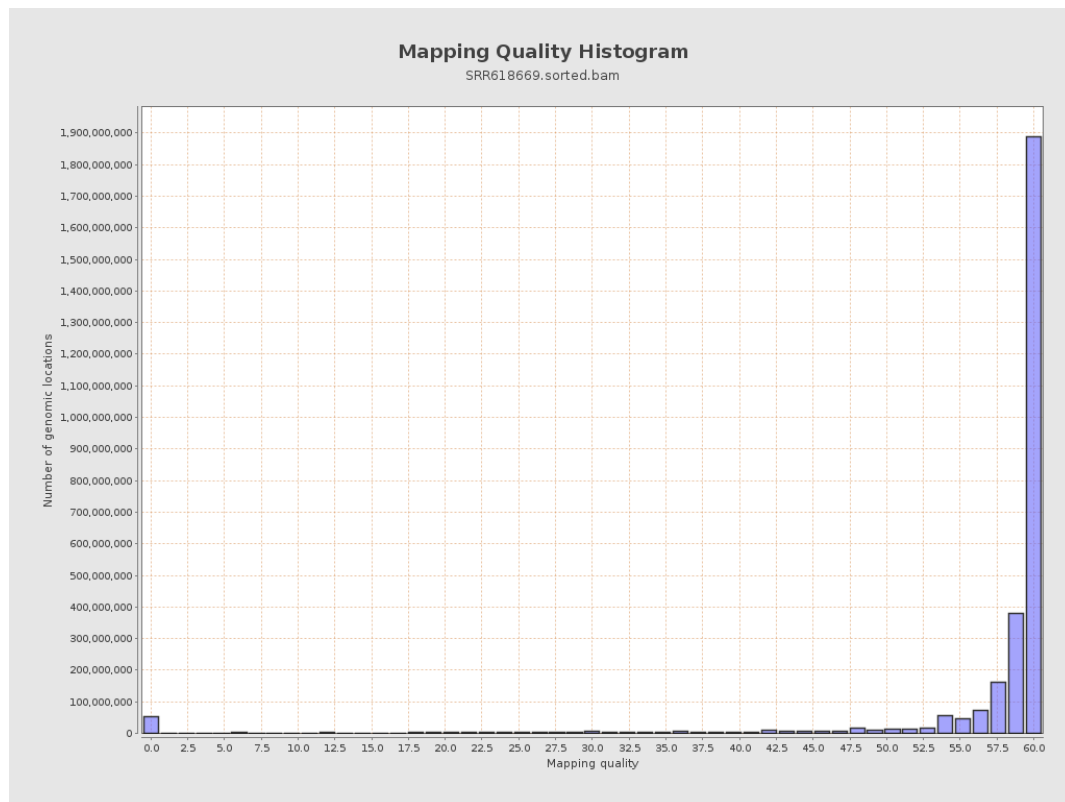
11. Results : Homopolymer Indels



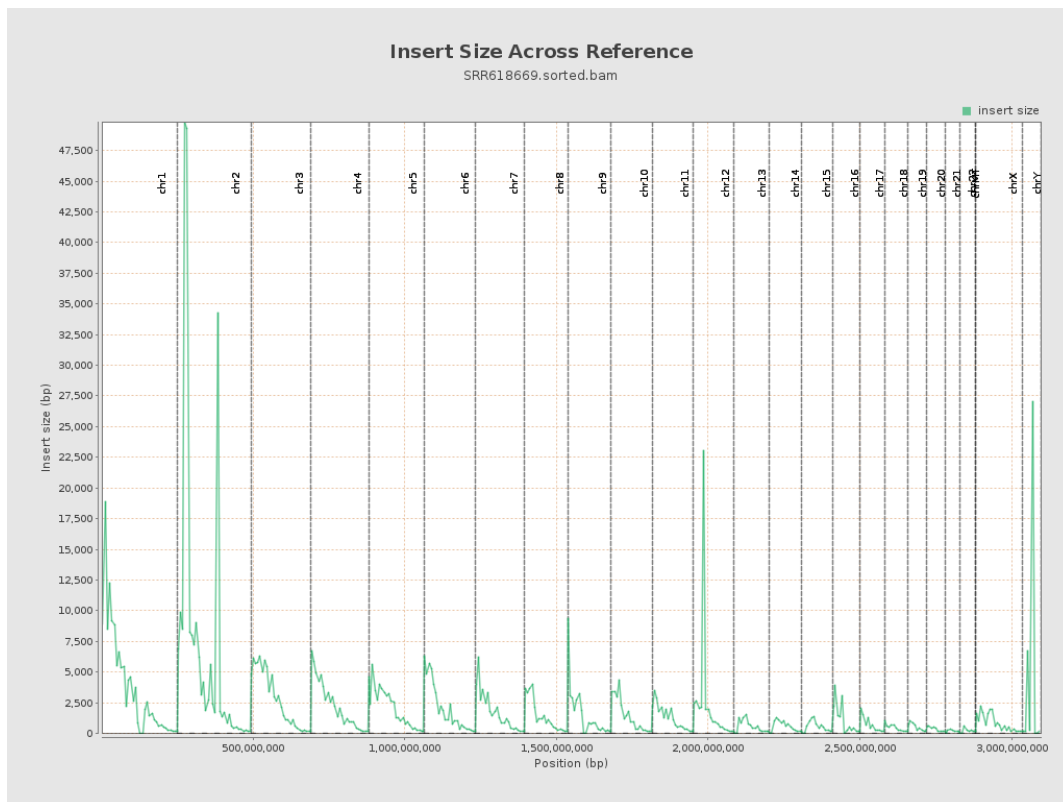
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

