

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 22:19:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618599.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_SRR618599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618599_1.fastq.gz SRR618599_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 22:19:22 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618599.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,663,890
Mapped reads	41,124,949 / 96.39%
Unmapped reads	1,538,941 / 3.61%
Mapped paired reads	41,124,949 / 96.39%
Mapped reads, first in pair	20,773,789 / 48.69%
Mapped reads, second in pair	20,351,160 / 47.7%
Mapped reads, both in pair	40,463,108 / 94.84%
Mapped reads, singletons	661,841 / 1.55%
Secondary alignments	0
Supplementary alignments	59,521 / 0.14%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	9,184,416 / 21.53%
Duplication rate	19.75%
Clipped reads	6,615,576 / 15.51%

2.2. ACGT Content

Number/percentage of A's	1,069,140,390 / 27.1%
Number/percentage of C's	877,044,150 / 22.23%
Number/percentage of T's	1,076,390,972 / 27.28%
Number/percentage of G's	922,216,368 / 23.38%
Number/percentage of N's	221,348 / 0.01%

GC Percentage	45.61%
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2.3. Coverage

Mean	1.2752
Standard Deviation	5.4885

2.4. Mapping Quality

Mean Mapping Quality	52.44
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2.5. Insert size

Mean	28,878.01
Standard Deviation	1,686,153.44
P25/Median/P75	174 / 206 / 246

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	45,348,282
Insertions	691,966
Mapped reads with at least one insertion	1.65%
Deletions	1,898,473
Mapped reads with at least one deletion	4.51%
Homopolymer indels	52.91%

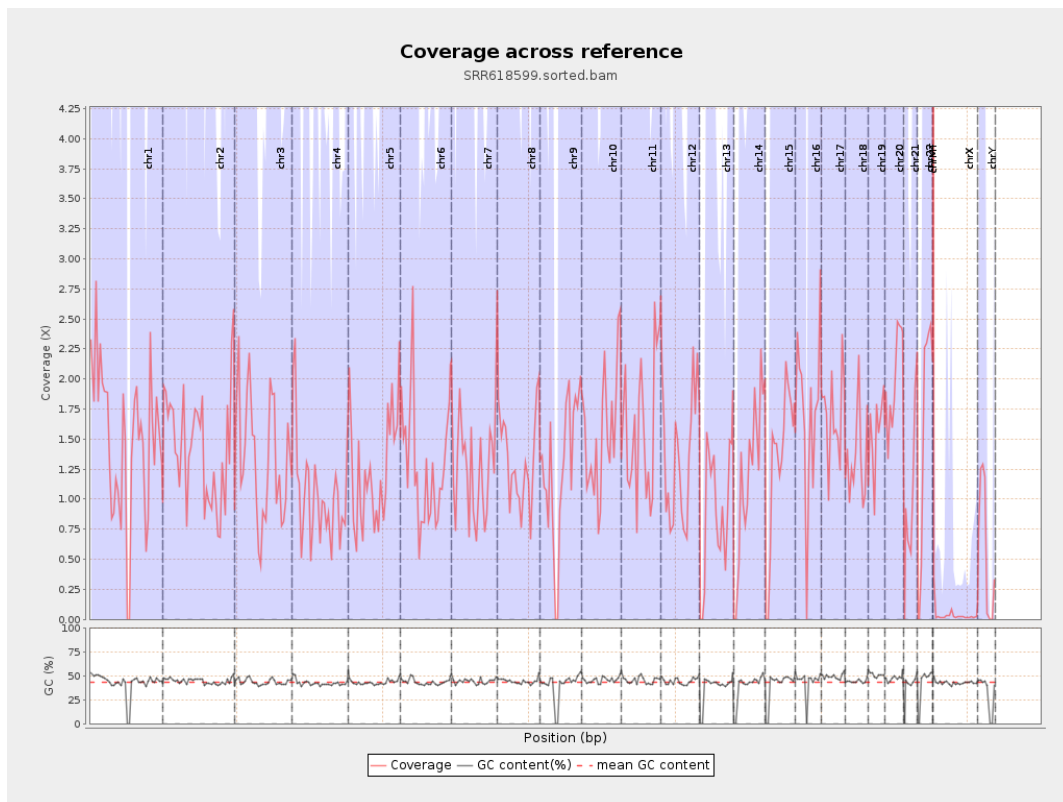
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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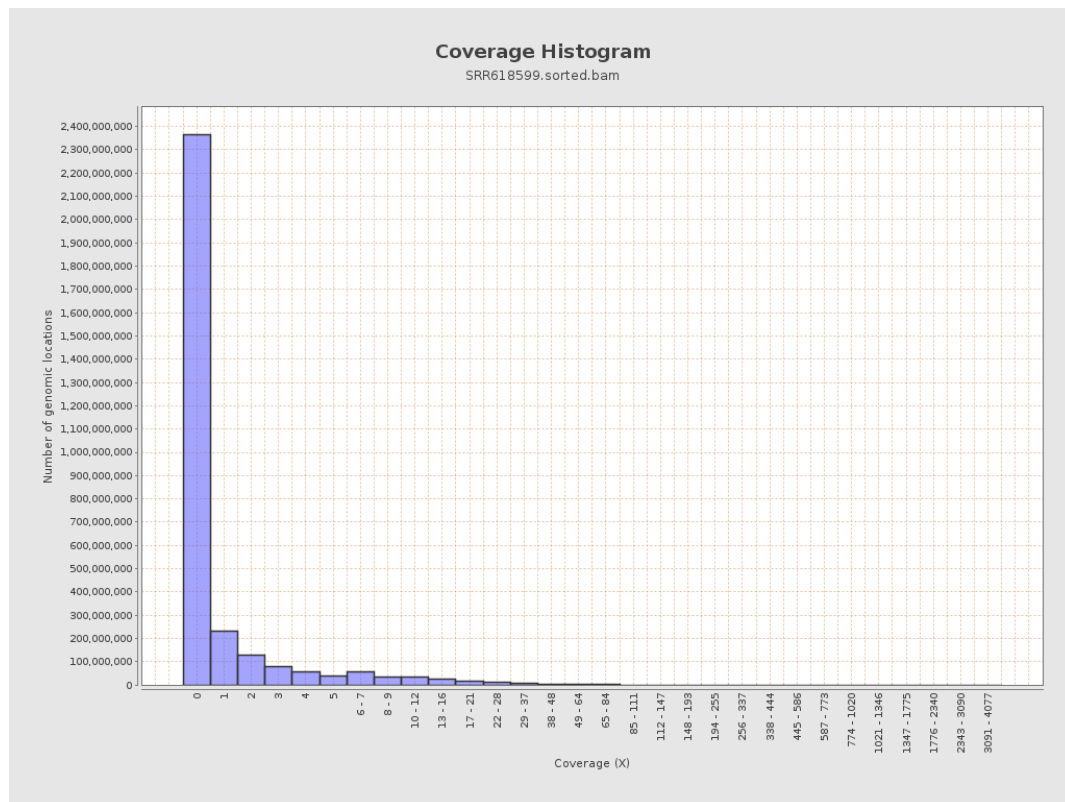
		bases	coverage	deviation
chr1	249250621	367212537	1.4733	6.785
chr2	243199373	345441008	1.4204	6.0673
chr3	198022430	262501769	1.3256	4.6876
chr4	191154276	198187939	1.0368	5.0264
chr5	180915260	227207201	1.2559	4.4836
chr6	171115067	219526908	1.2829	4.6682
chr7	159138663	201426440	1.2657	4.6625
chr8	146364022	192652700	1.3163	4.7573
chr9	141213431	176741019	1.2516	5.4906
chr10	135534747	208530253	1.5386	5.6179
chr11	135006516	214705134	1.5903	5.7606
chr12	133851895	183014833	1.3673	5.0359
chr13	115169878	104478429	0.9072	3.4946
chr14	107349540	127469624	1.1874	4.6852
chr15	102531392	133743063	1.3044	5.0095
chr16	90354753	153863195	1.7029	9.26
chr17	81195210	136759404	1.6843	6.0854
chr18	78077248	103145168	1.3211	5.4227
chr19	59128983	91403638	1.5458	6.2721
chr20	63025520	125888190	1.9974	6.6034
chr21	48129895	51381808	1.0676	10.1175
chr22	51304566	80599870	1.571	6.276
chrMT	16571	289064	17.444	24.1781
chrX	155270560	5846718	0.0377	1.111

chrY	59373566	35610474	0.5998	4.261
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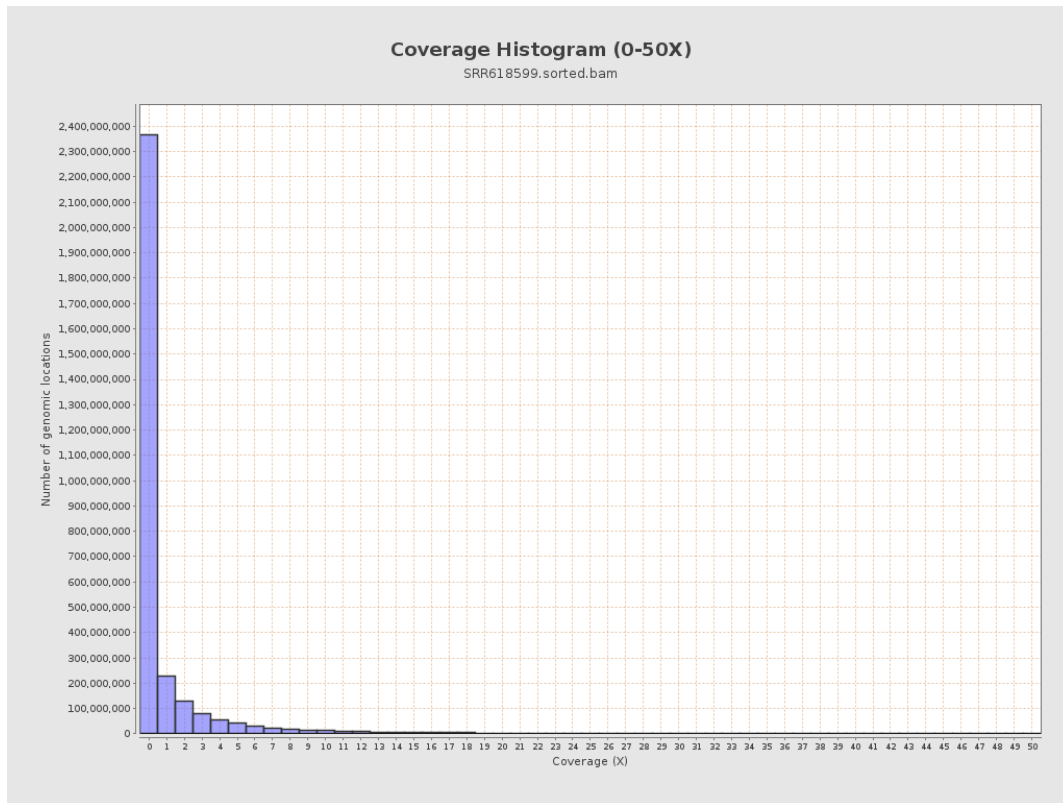
3. Results : Coverage across reference



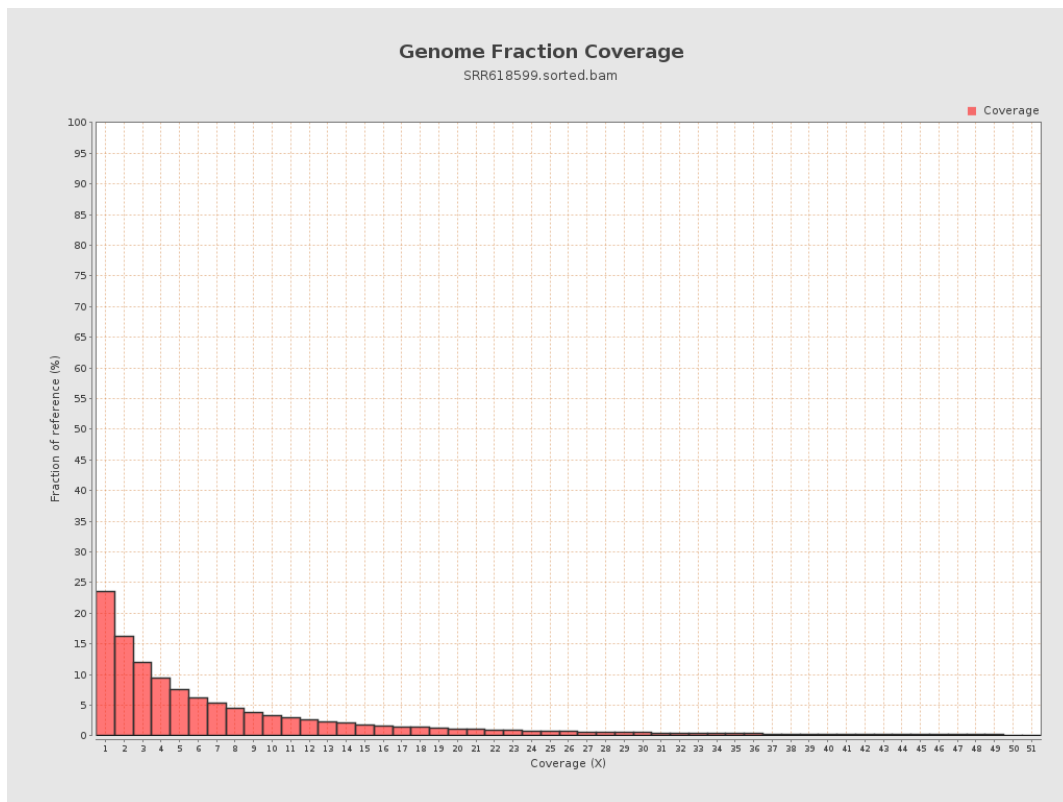
4. Results : Coverage Histogram



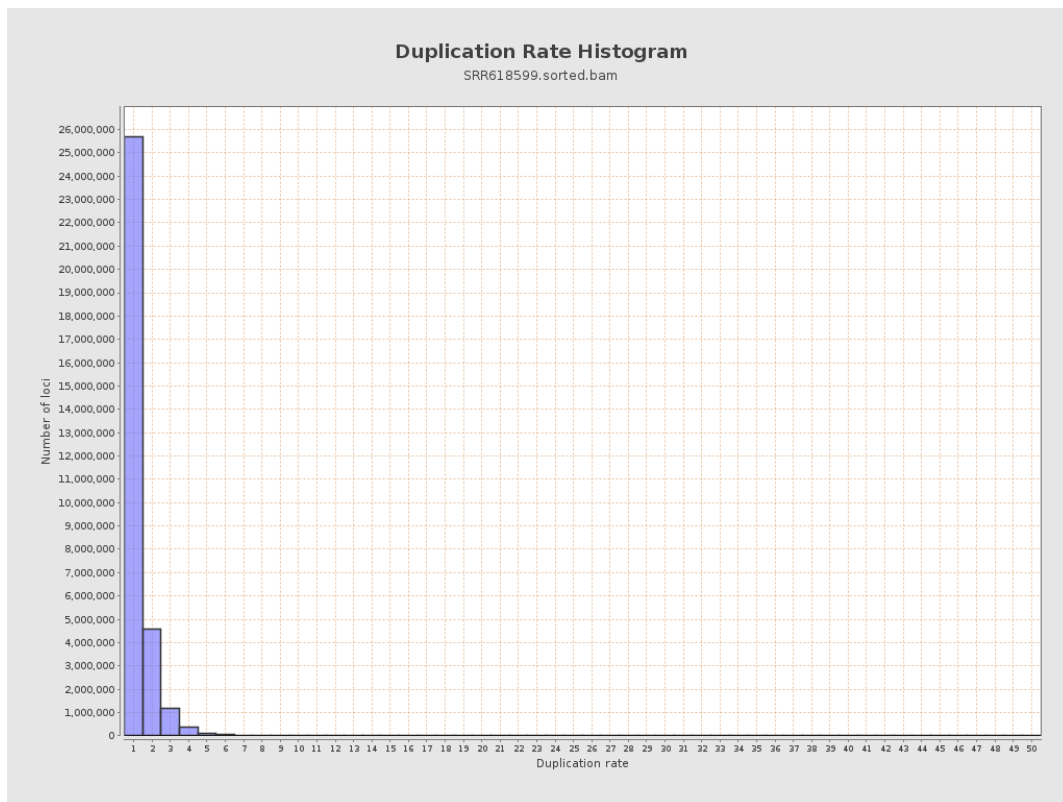
5. Results : Coverage Histogram (0-50X)



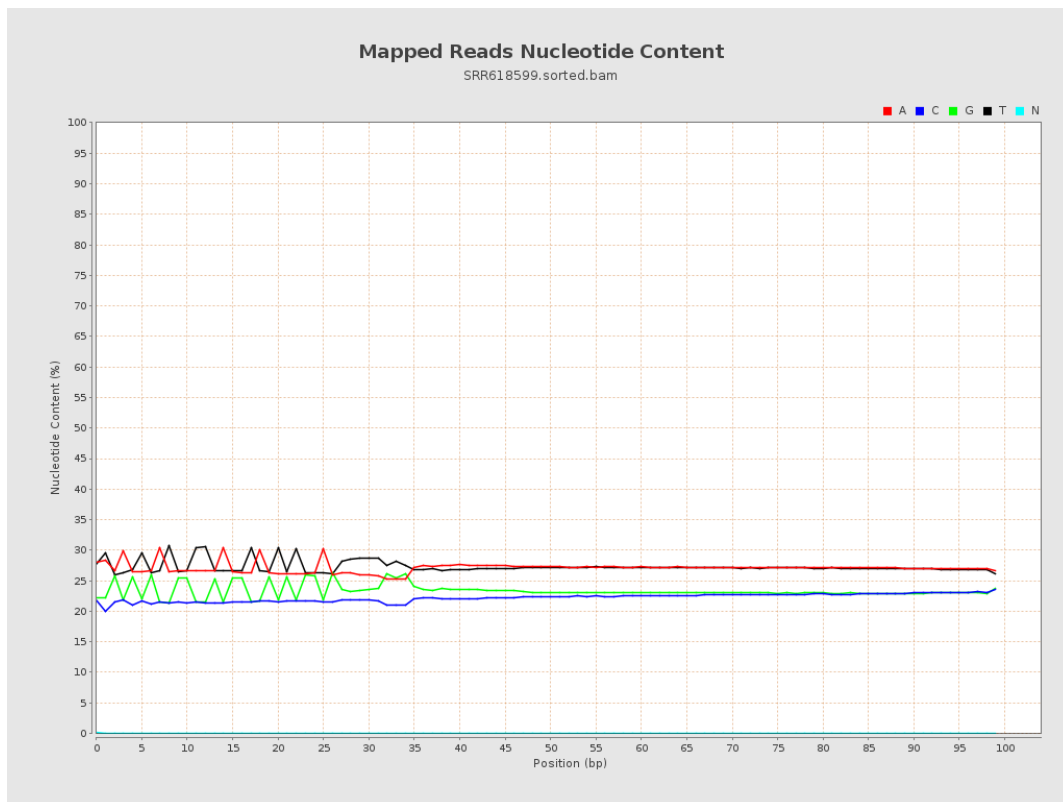
6. Results : Genome Fraction Coverage



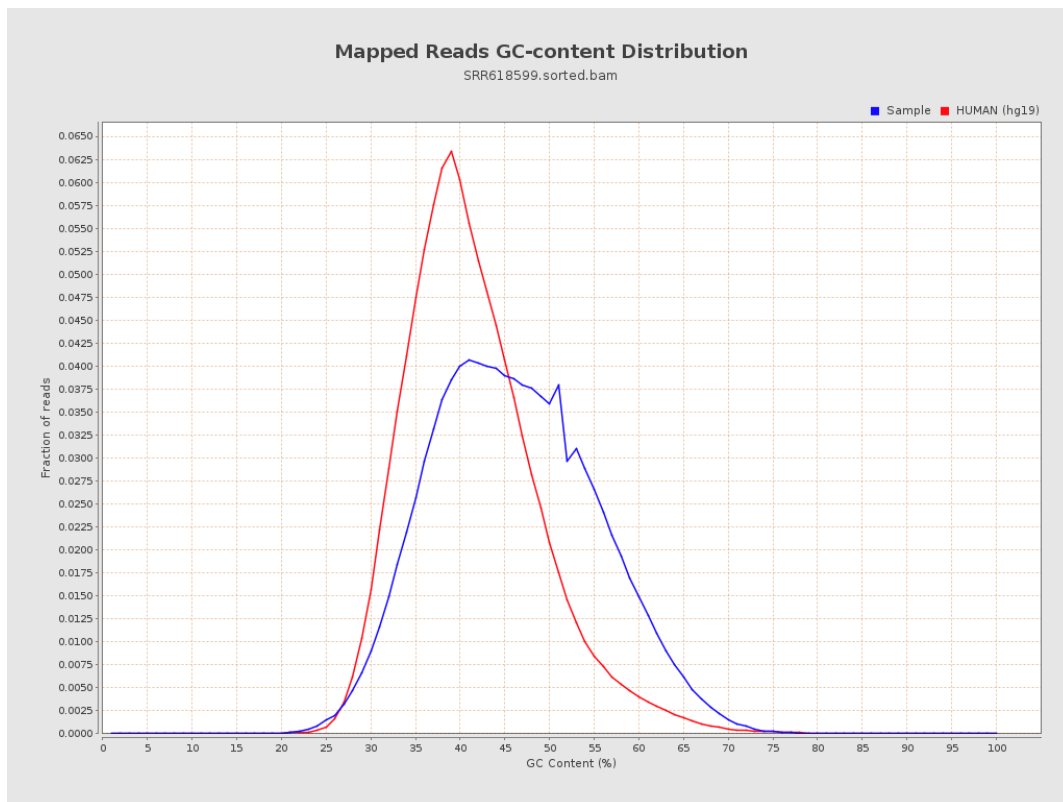
7. Results : Duplication Rate Histogram



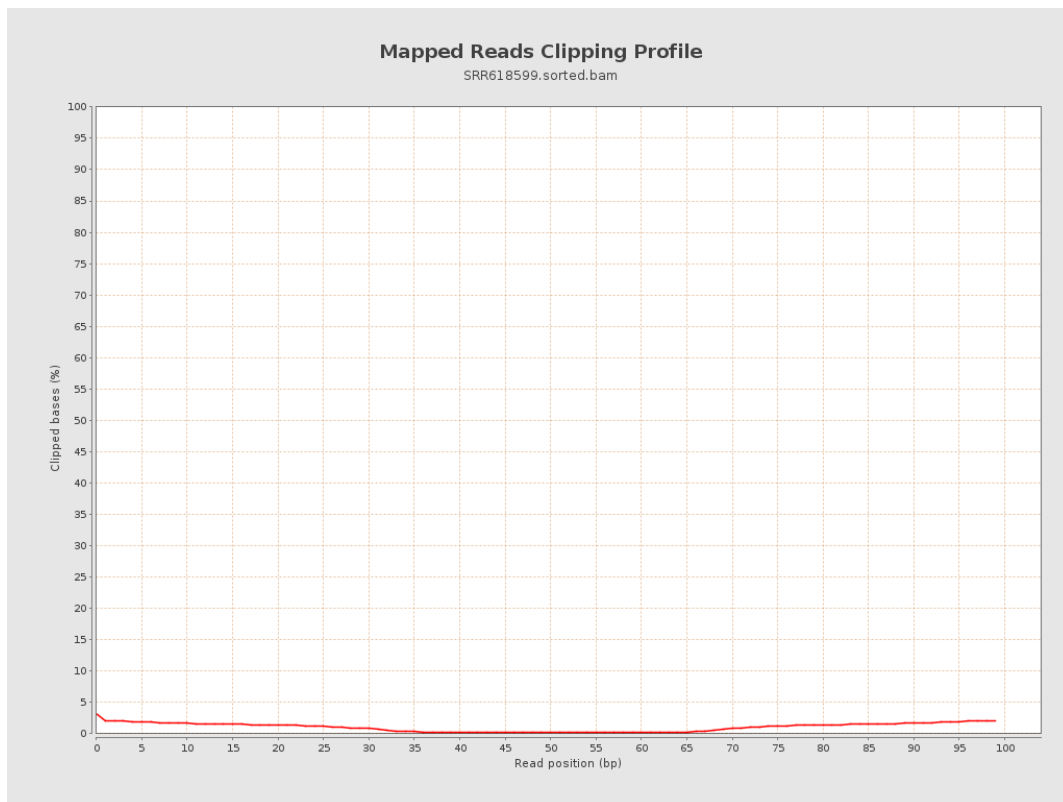
8. Results : Mapped Reads Nucleotide Content



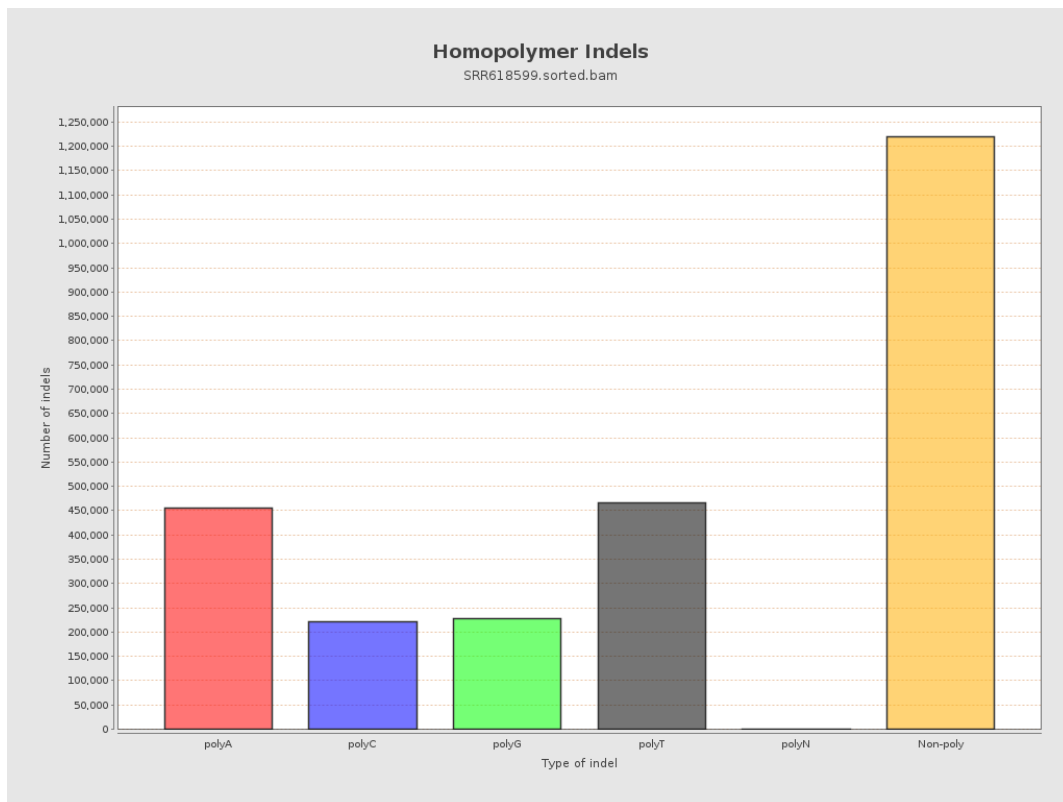
9. Results : Mapped Reads GC-content Distribution



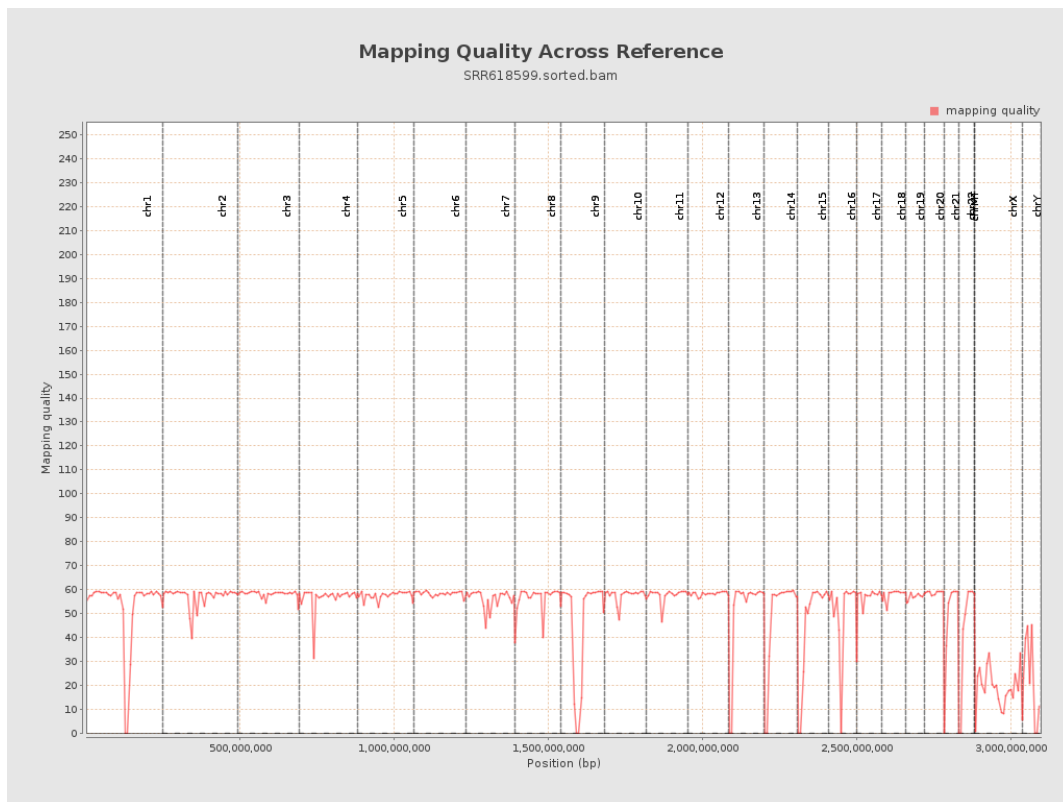
10. Results : Mapped Reads Clipping Profile



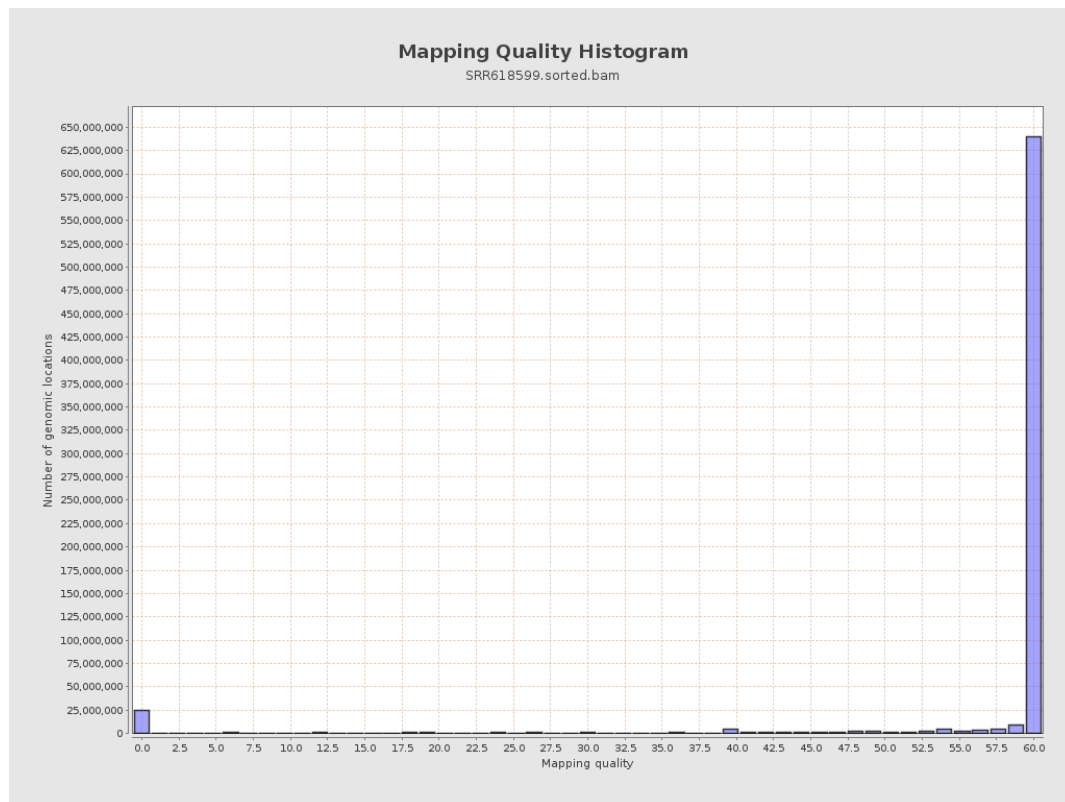
11. Results : Homopolymer Indels



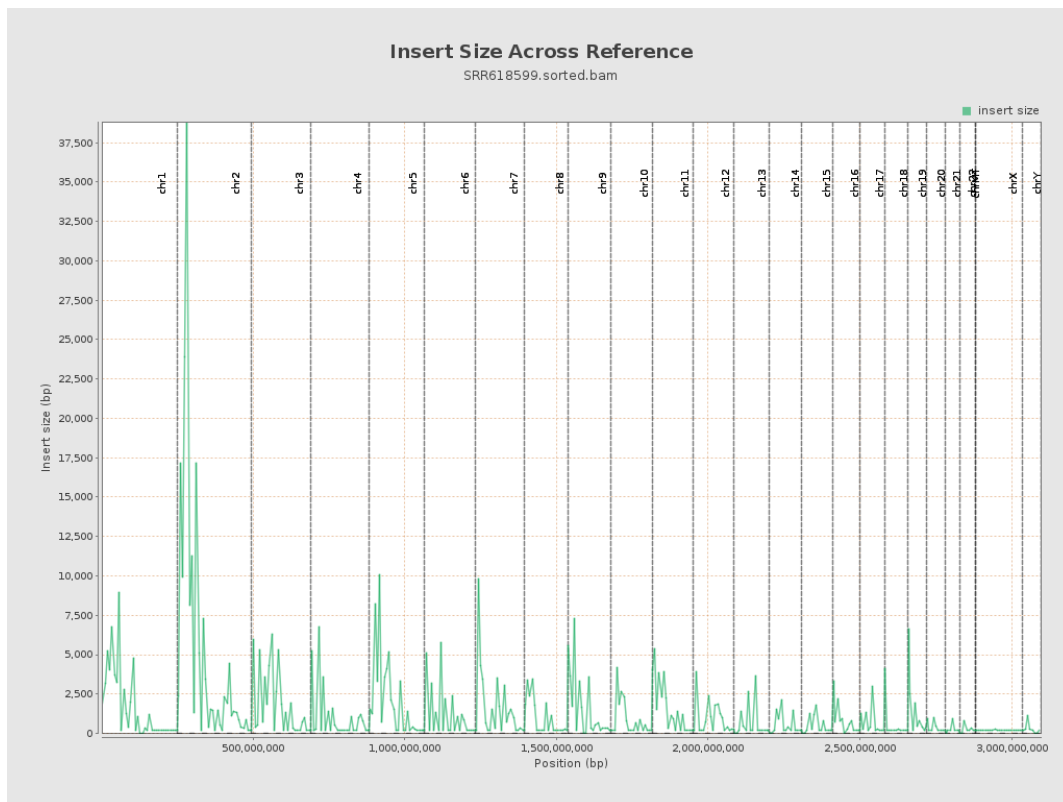
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

