

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 04:15:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618643.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_SRR618643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618643_1.fastq.gz SRR618643_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 04:15:12 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,261,122
Mapped reads	45,740,408 / 89.23%
Unmapped reads	5,520,714 / 10.77%
Mapped paired reads	45,740,408 / 89.23%
Mapped reads, first in pair	24,637,073 / 48.06%
Mapped reads, second in pair	21,103,335 / 41.17%
Mapped reads, both in pair	41,668,568 / 81.29%
Mapped reads, singletons	4,071,840 / 7.94%
Secondary alignments	0
Supplementary alignments	208,548 / 0.41%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	9,755,362 / 19.03%
Duplication rate	18.17%
Clipped reads	12,886,054 / 25.14%

2.2. ACGT Content

Number/percentage of A's	1,133,440,360 / 26.81%
Number/percentage of C's	933,580,562 / 22.09%
Number/percentage of T's	1,164,975,563 / 27.56%
Number/percentage of G's	994,678,216 / 23.53%
Number/percentage of N's	243,593 / 0.01%

GC Percentage	45.62%
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2.3. Coverage

Mean	1.3664
Standard Deviation	5.4586

2.4. Mapping Quality

Mean Mapping Quality	53.26
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2.5. Insert size

Mean	141,683.09
Standard Deviation	3,761,273.18
P25/Median/P75	187 / 218 / 257

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	61,492,823
Insertions	777,101
Mapped reads with at least one insertion	1.67%
Deletions	2,132,867
Mapped reads with at least one deletion	4.55%
Homopolymer indels	52.48%

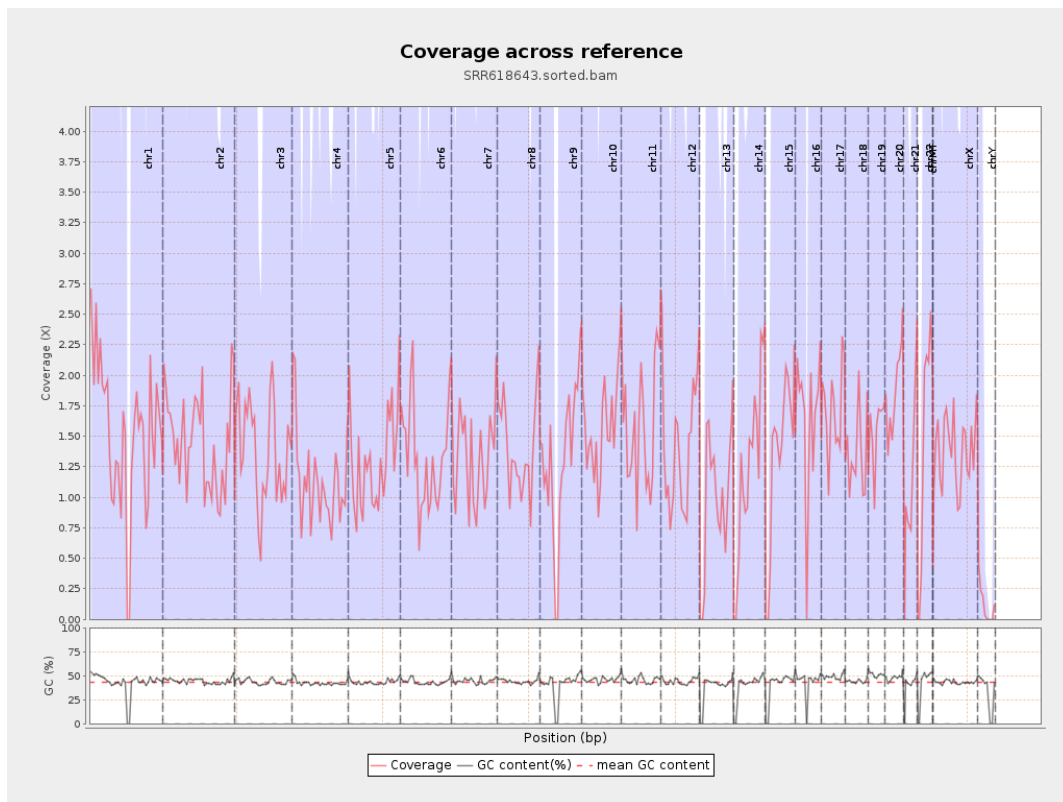
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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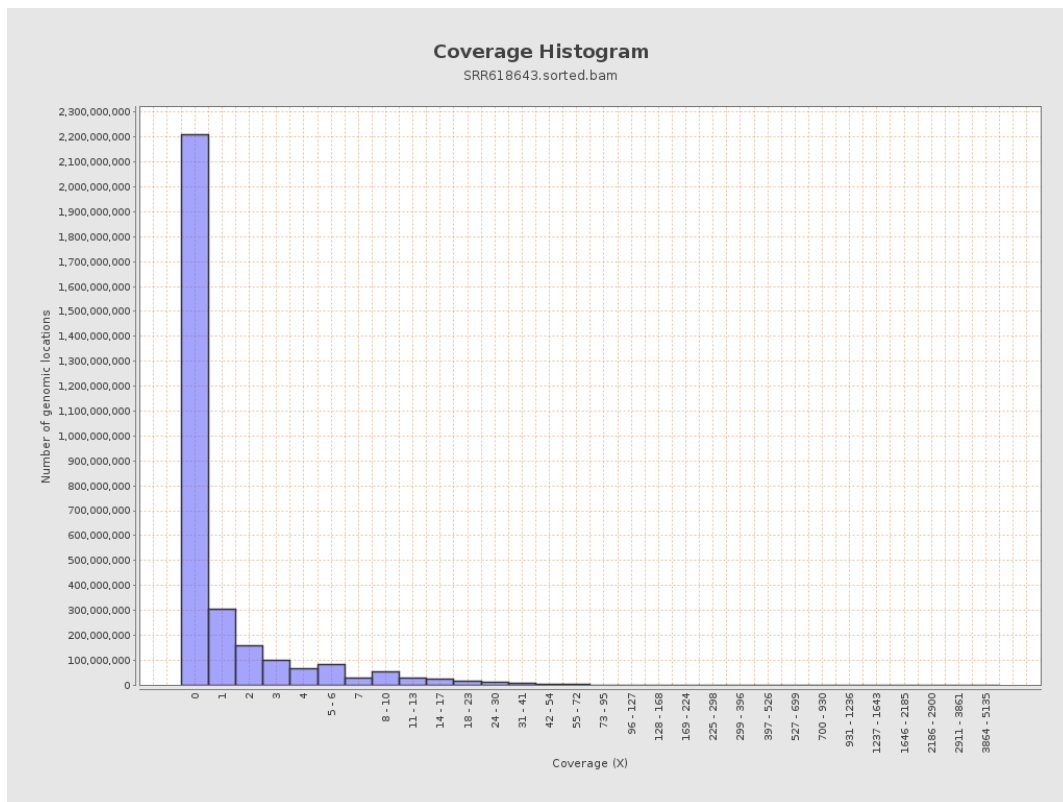
		bases	coverage	deviation
chr1	249250621	375875371	1.508	6.4183
chr2	243199373	352491143	1.4494	6.8515
chr3	198022430	272202773	1.3746	4.6211
chr4	191154276	215752536	1.1287	4.285
chr5	180915260	237882630	1.3149	4.5413
chr6	171115067	226513388	1.3237	4.6091
chr7	159138663	213197469	1.3397	4.6899
chr8	146364022	205939230	1.407	4.9577
chr9	141213431	183233127	1.2976	5.4733
chr10	135534747	211148384	1.5579	5.4339
chr11	135006516	211904840	1.5696	5.9701
chr12	133851895	189583268	1.4164	5.2717
chr13	115169878	113396952	0.9846	3.9266
chr14	107349540	132966151	1.2386	4.6855
chr15	102531392	136100370	1.3274	5.2193
chr16	90354753	147317859	1.6304	9.3666
chr17	81195210	138809666	1.7096	5.8319
chr18	78077248	104454123	1.3378	5.0844
chr19	59128983	90822660	1.536	5.8955
chr20	63025520	116677665	1.8513	6.0735
chr21	48129895	56611086	1.1762	6.7071
chr22	51304566	75412871	1.4699	5.6037
chrMT	16571	7102	0.4286	1.3204
chrX	155270560	214666046	1.3825	4.3626

chrY	59373566	6893956	0.1161	3.3554
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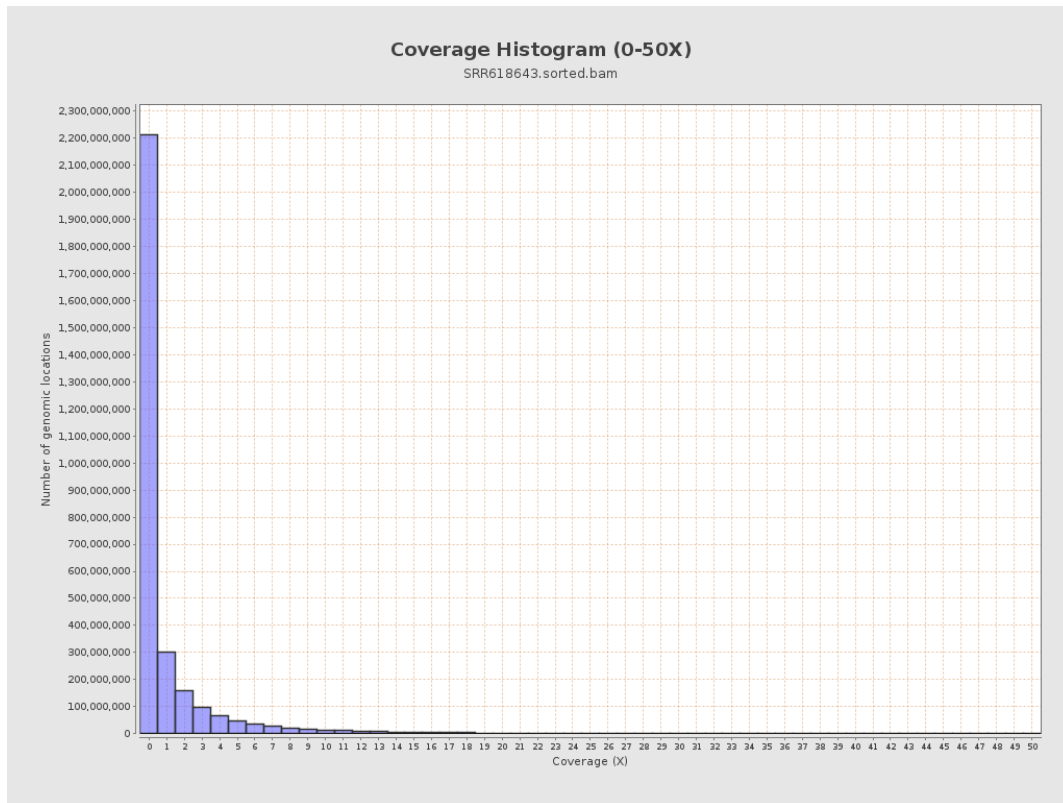
3. Results : Coverage across reference



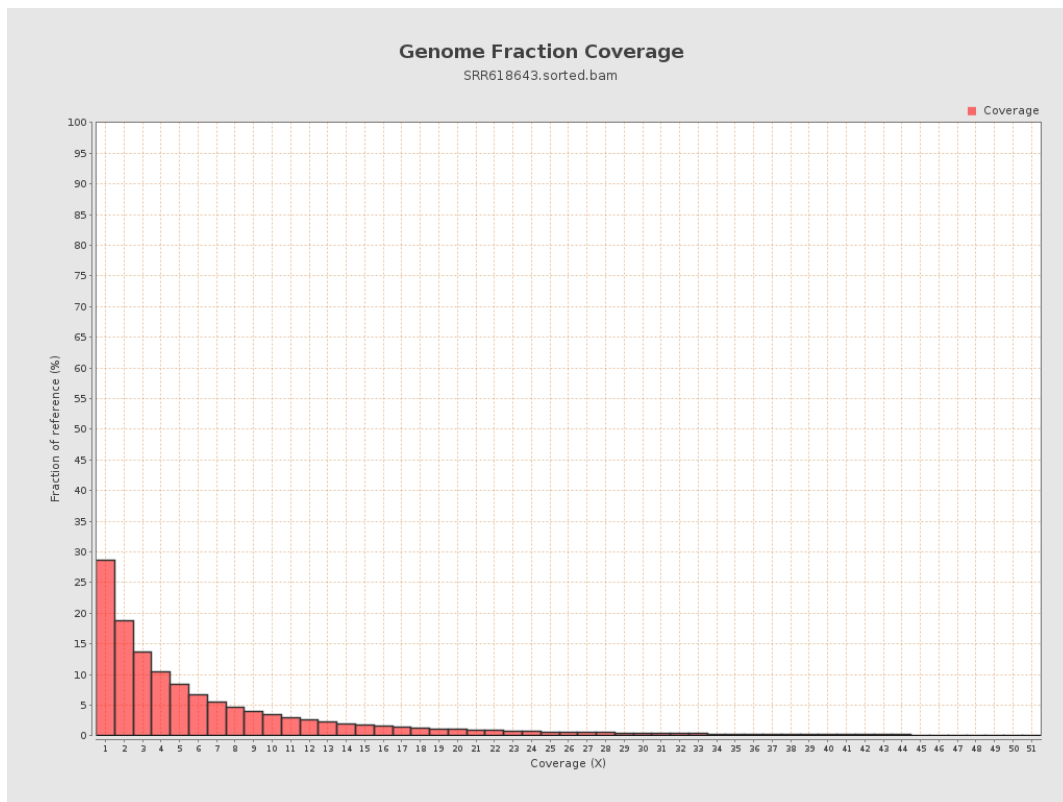
4. Results : Coverage Histogram



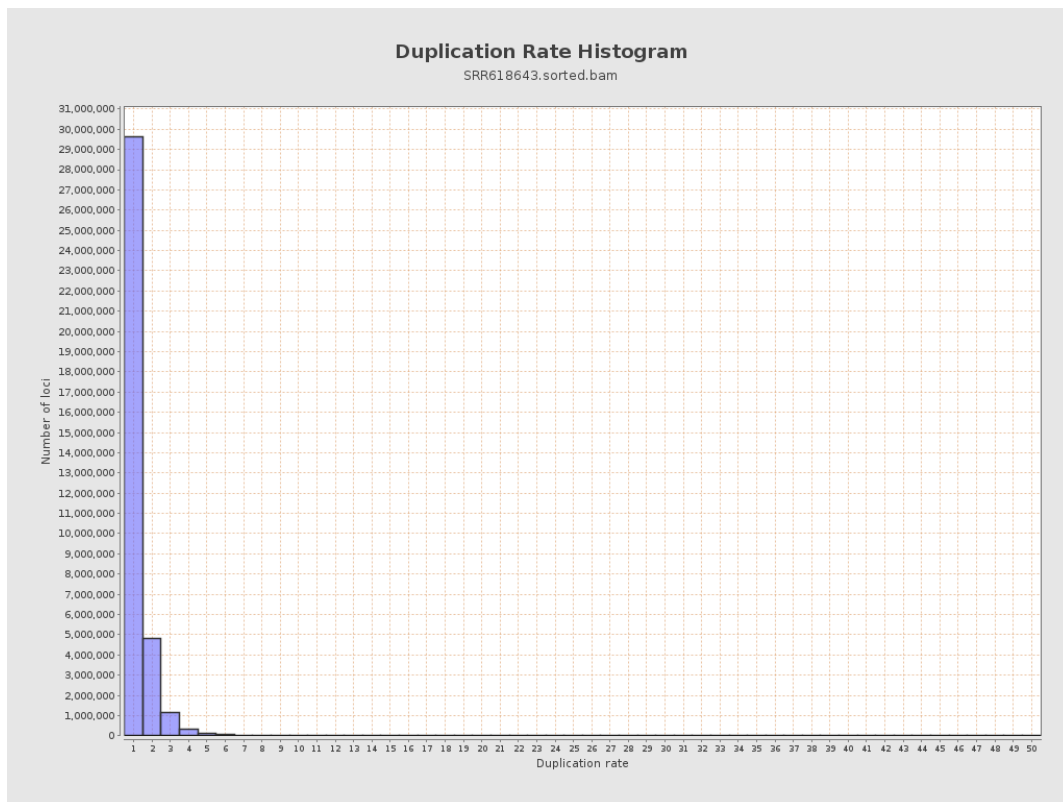
5. Results : Coverage Histogram (0-50X)



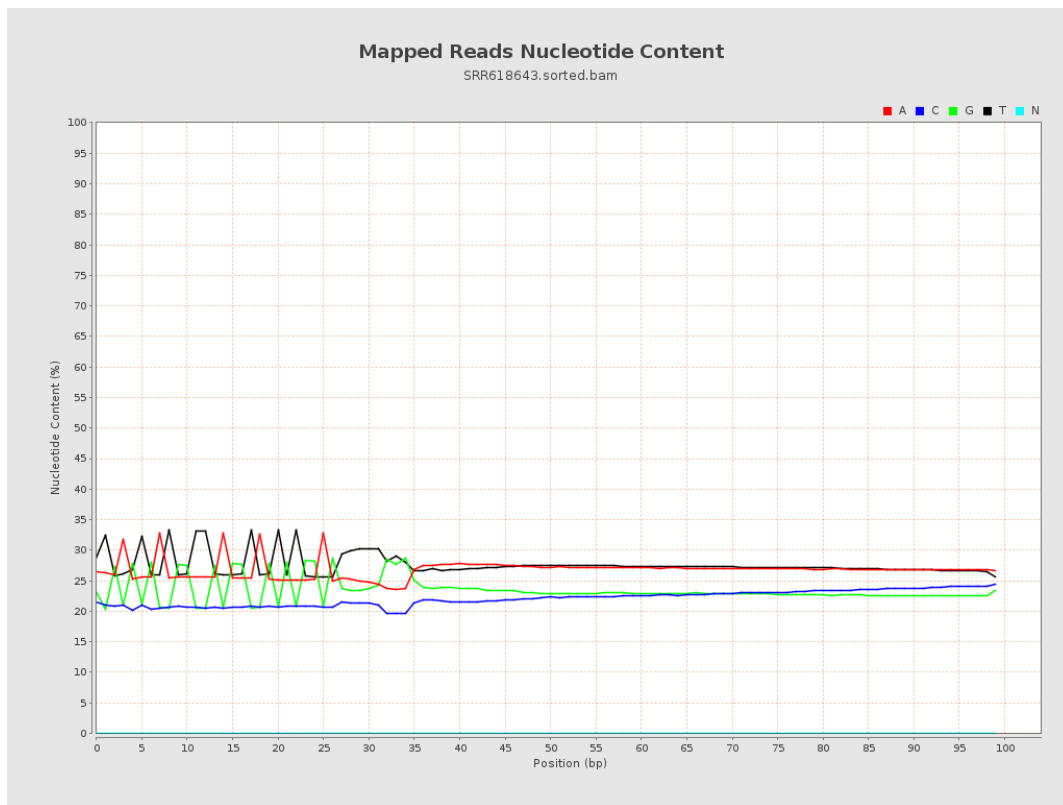
6. Results : Genome Fraction Coverage



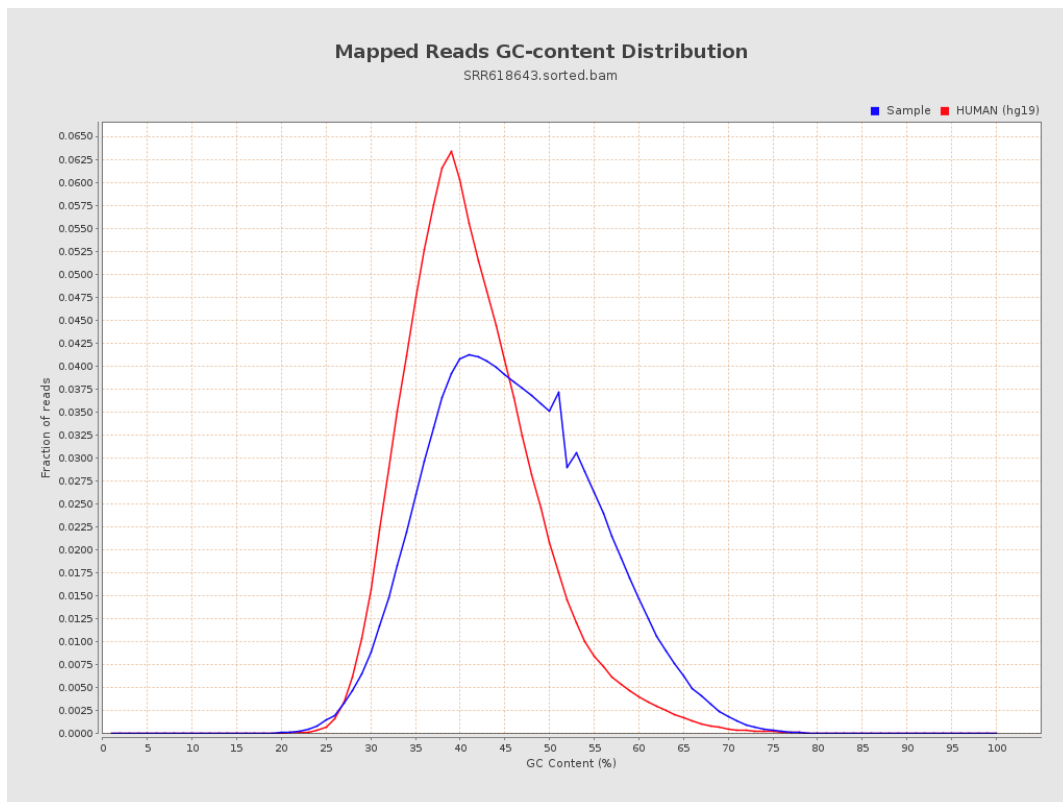
7. Results : Duplication Rate Histogram



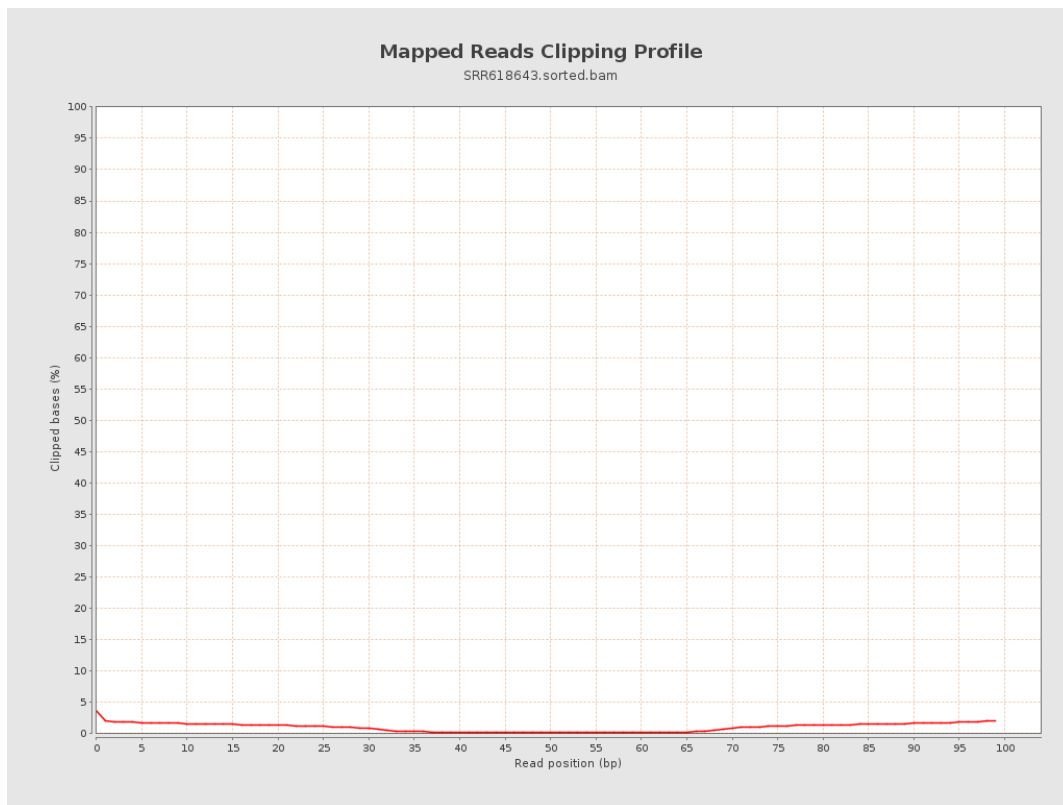
8. Results : Mapped Reads Nucleotide Content



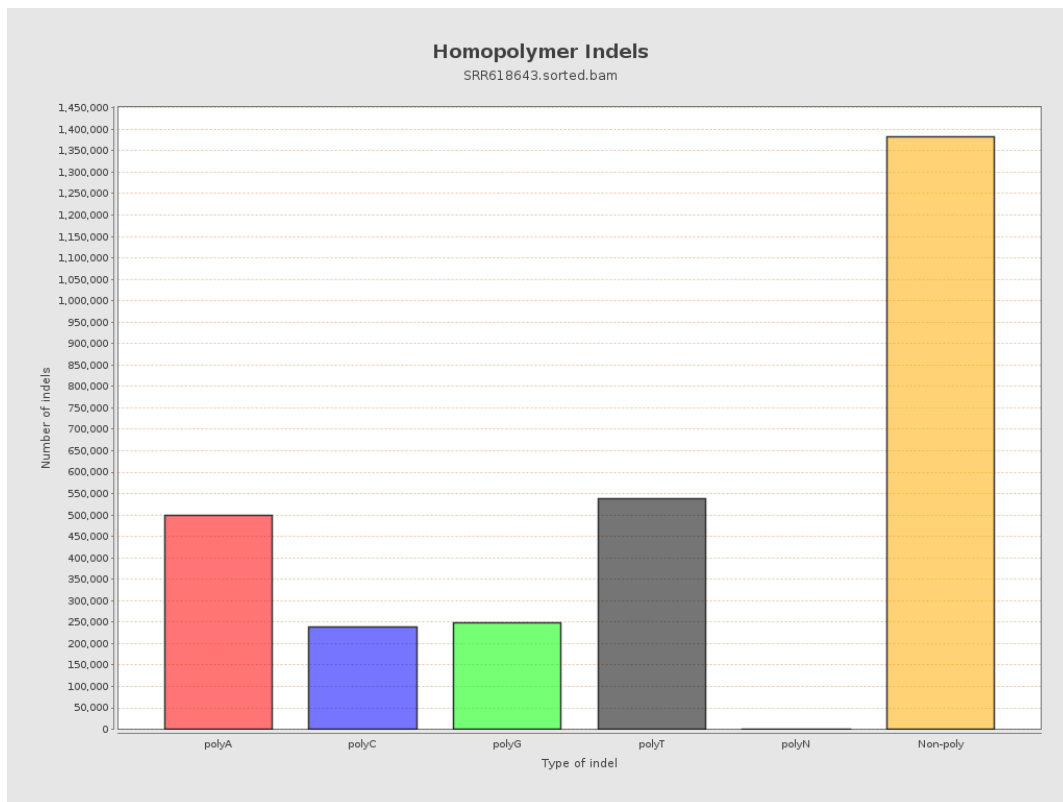
9. Results : Mapped Reads GC-content Distribution



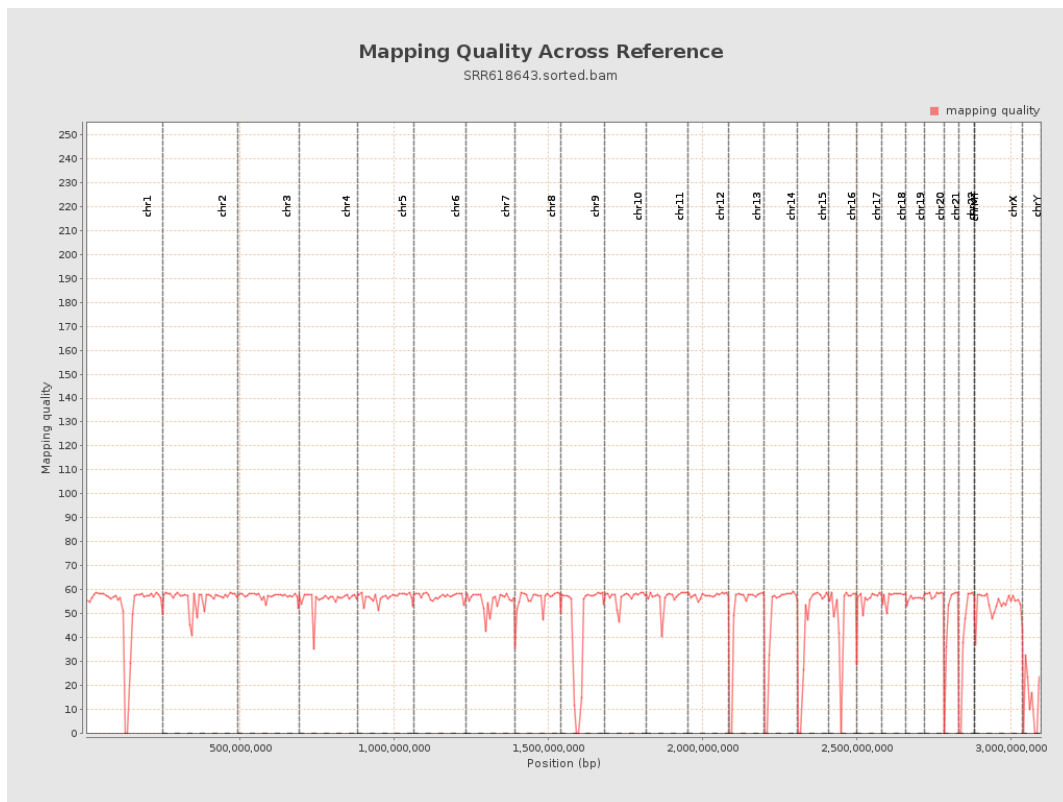
10. Results : Mapped Reads Clipping Profile



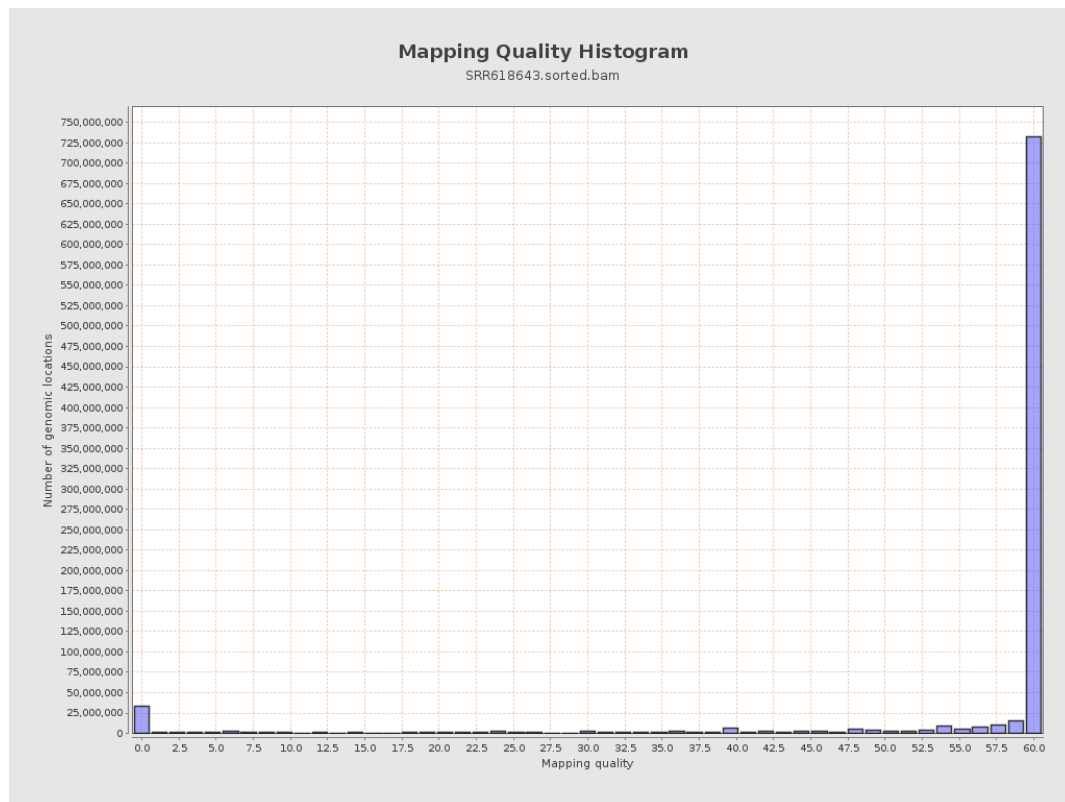
11. Results : Homopolymer Indels



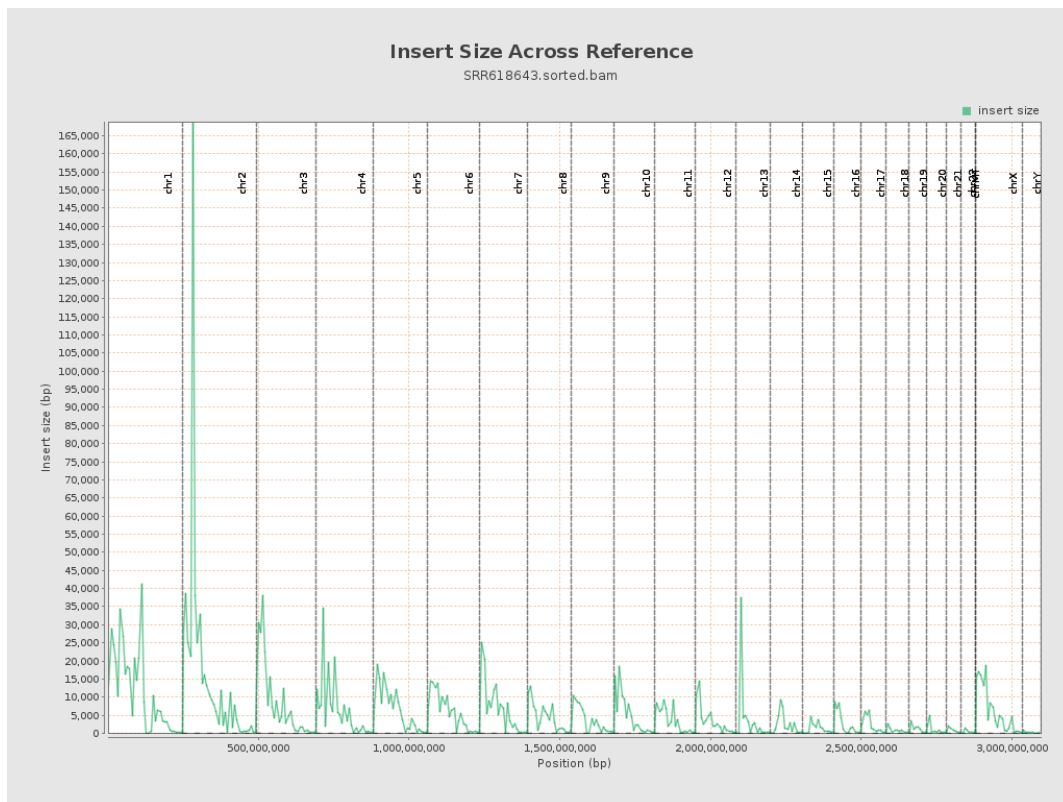
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

