

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/30 03:20:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432726.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_SRR6432726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432726_1.fastq.gz SRR6432726_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 30 03:20:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	375,478,790
Mapped reads	375,346,486 / 99.96%
Unmapped reads	132,304 / 0.04%
Mapped paired reads	375,346,486 / 99.96%
Mapped reads, first in pair	187,676,278 / 49.98%
Mapped reads, second in pair	187,670,208 / 49.98%
Mapped reads, both in pair	375,294,720 / 99.95%
Mapped reads, singletons	51,766 / 0.01%
Secondary alignments	0
Supplementary alignments	5,089,653 / 1.36%
Read min/max/mean length	30 / 150 / 139.67
Duplicated reads (estimated)	182,205,469 / 48.53%
Duplication rate	31.46%
Clipped reads	110,197,467 / 29.35%

2.2. ACGT Content

Number/percentage of A's	14,304,964,644 / 27.88%
Number/percentage of C's	10,770,920,174 / 20.99%
Number/percentage of T's	14,140,945,834 / 27.56%
Number/percentage of G's	12,077,224,401 / 23.54%
Number/percentage of N's	12,727,418 / 0.02%

GC Percentage	44.53%
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2.3. Coverage

Mean	16.5903
Standard Deviation	43.9139

2.4. Mapping Quality

Mean Mapping Quality	57.39
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2.5. Insert size

Mean	81,711.5
Standard Deviation	2,903,575.4
P25/Median/P75	289 / 306 / 324

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	411,864,371
Insertions	11,331,468
Mapped reads with at least one insertion	2.96%
Deletions	35,369,327
Mapped reads with at least one deletion	8.99%
Homopolymer indels	52.33%

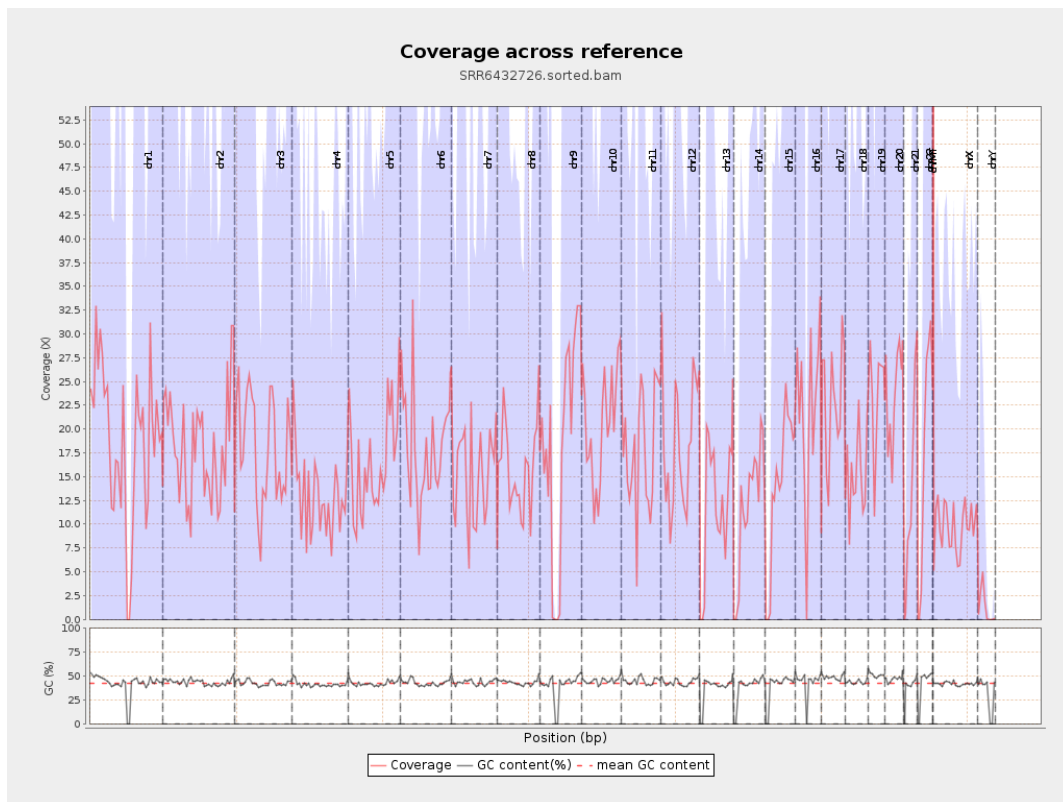
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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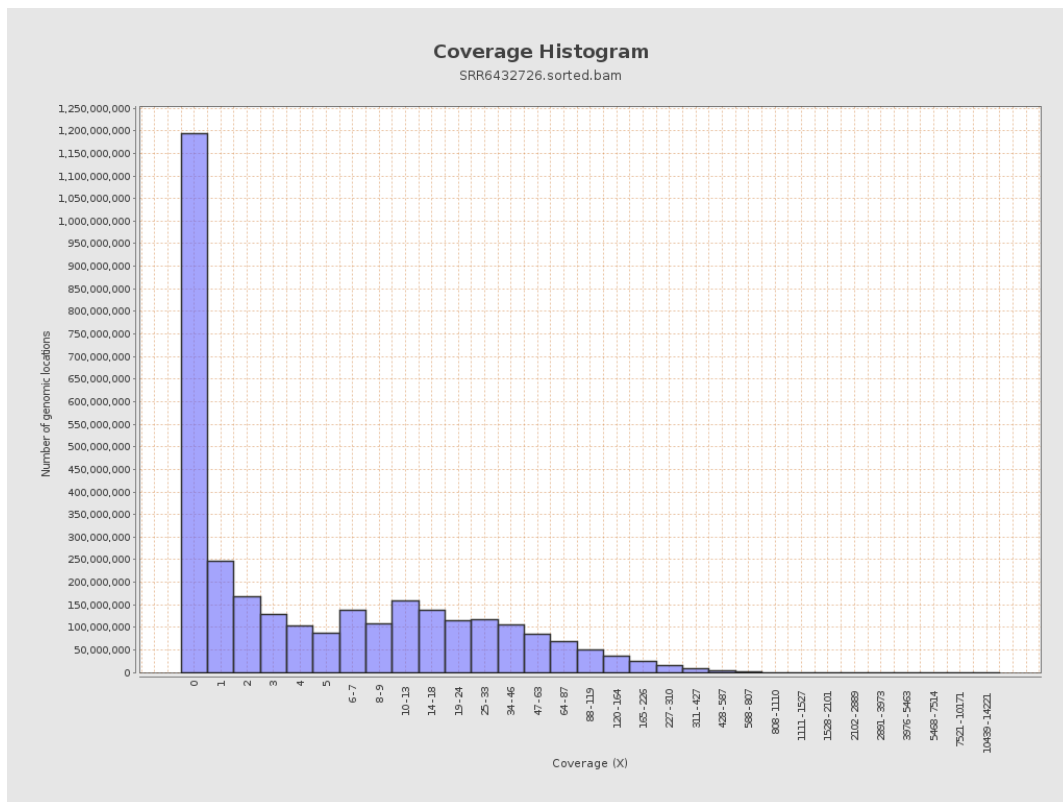
		bases	coverage	deviation
chr1	249250621	4665642656	18.7187	47.8526
chr2	243199373	4377190189	17.9984	48.3709
chr3	198022430	3546714872	17.9107	43.8199
chr4	191154276	2469621014	12.9195	34.653
chr5	180915260	3029537339	16.7456	42.4232
chr6	171115067	3092802915	18.0744	45.5797
chr7	159138663	2466033031	15.4961	40.0576
chr8	146364022	2344848006	16.0207	40.3992
chr9	141213431	2600623506	18.4163	49.643
chr10	135534747	2759120147	20.3573	48.8145
chr11	135006516	2406907105	17.8281	44.1728
chr12	133851895	2490784240	18.6085	46.4612
chr13	115169878	1380471852	11.9864	34.6339
chr14	107349540	1282377954	11.9458	32.8343
chr15	102531392	1423198085	13.8806	38.7793
chr16	90354753	1981522086	21.9305	57.3595
chr17	81195210	1869979832	23.0307	54.8824
chr18	78077248	1166918660	14.9457	38.9263
chr19	59128983	1380075167	23.3401	58.1437
chr20	63025520	1473436736	23.3784	53.1592
chr21	48129895	647882884	13.4611	39.9014
chr22	51304566	903323731	17.6071	48.651
chrMT	16571	5280537	318.6613	469.5937
chrX	155270560	1512623651	9.7419	26.9551

chrY	59373566	81469639	1.3722	14.4105
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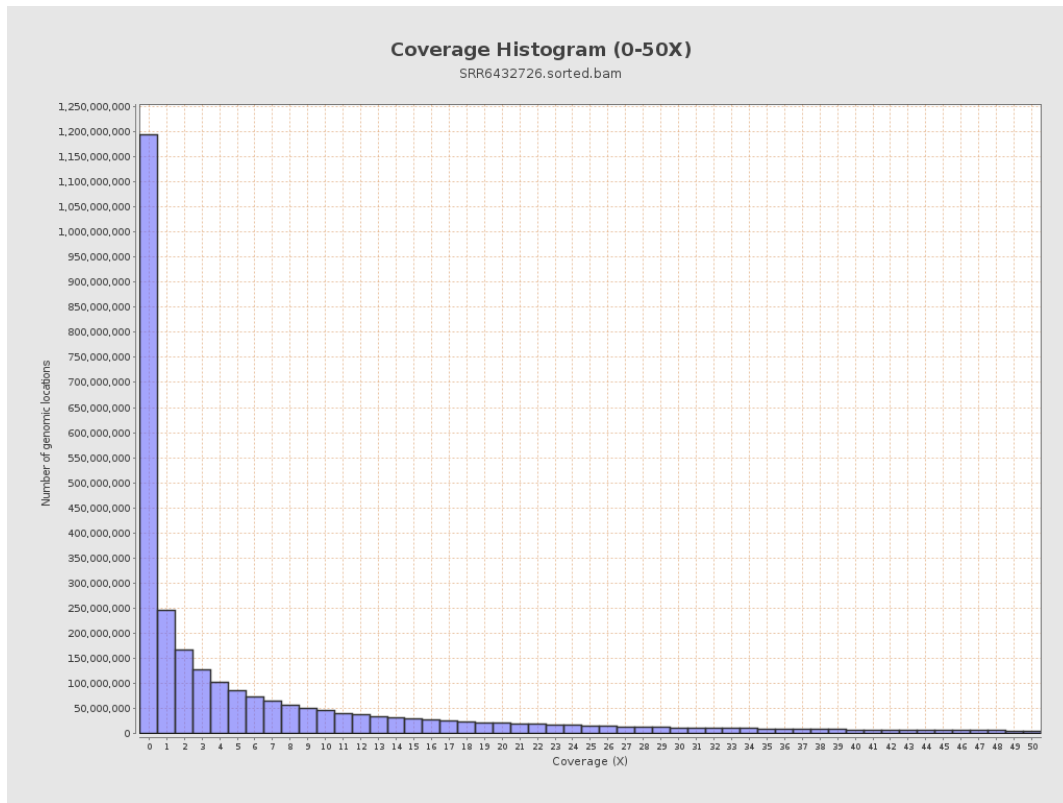
3. Results : Coverage across reference



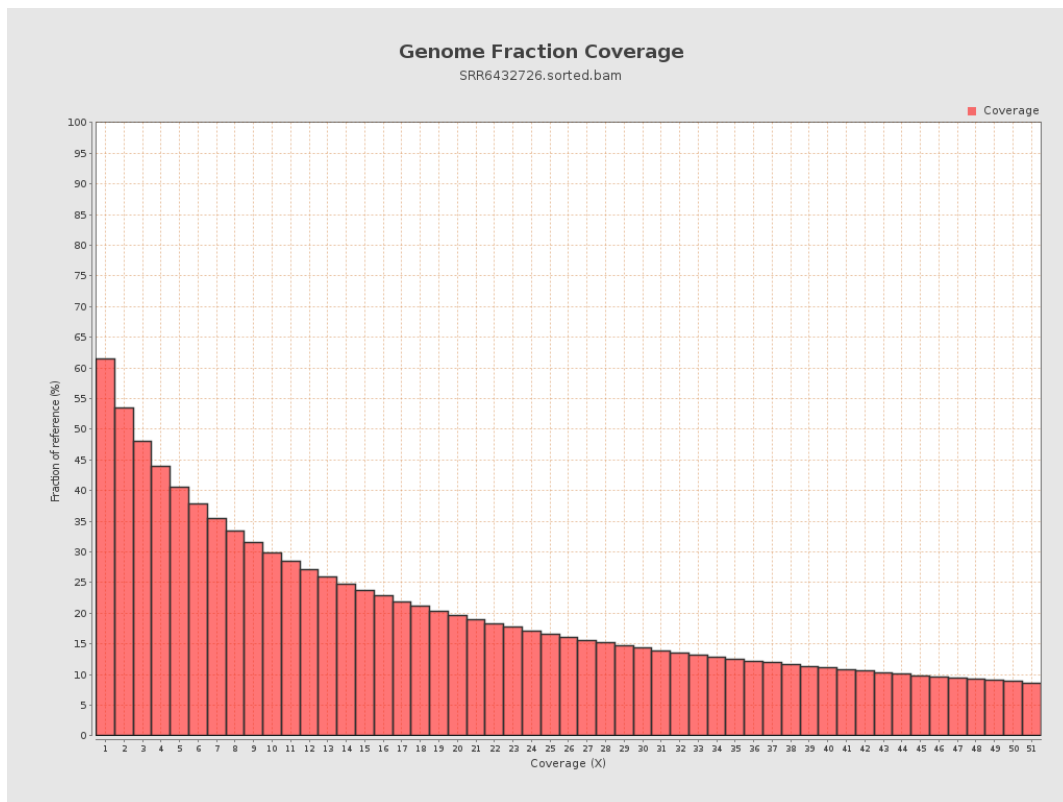
4. Results : Coverage Histogram



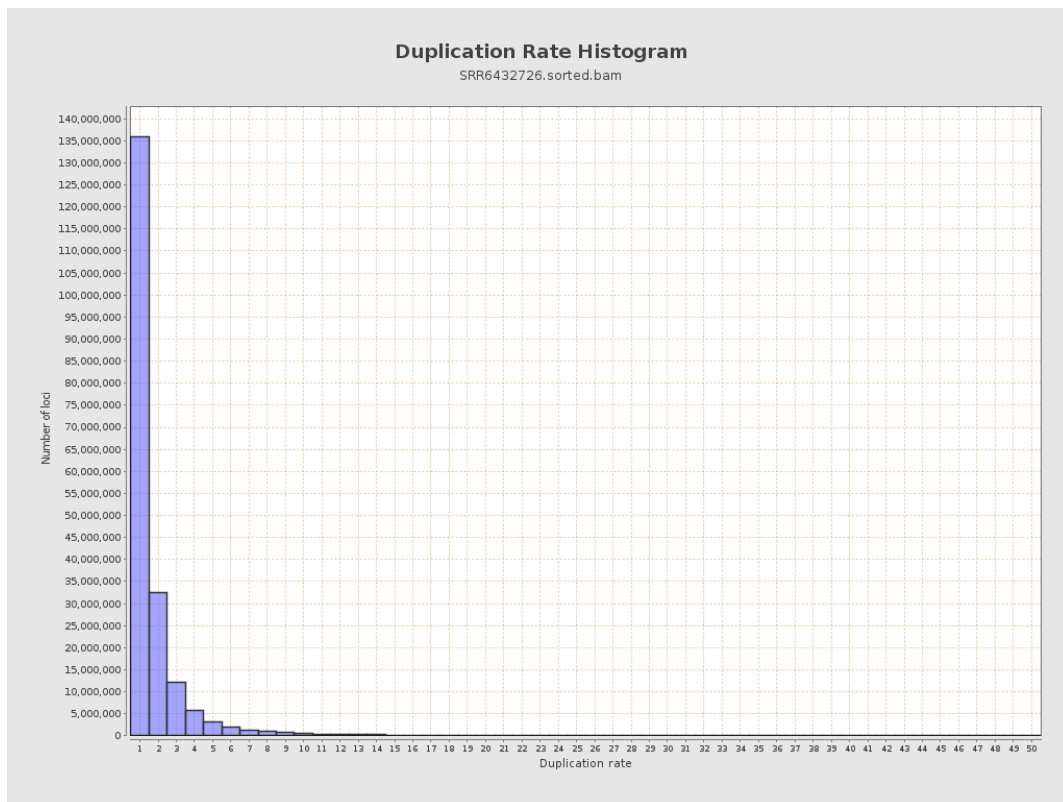
5. Results : Coverage Histogram (0-50X)



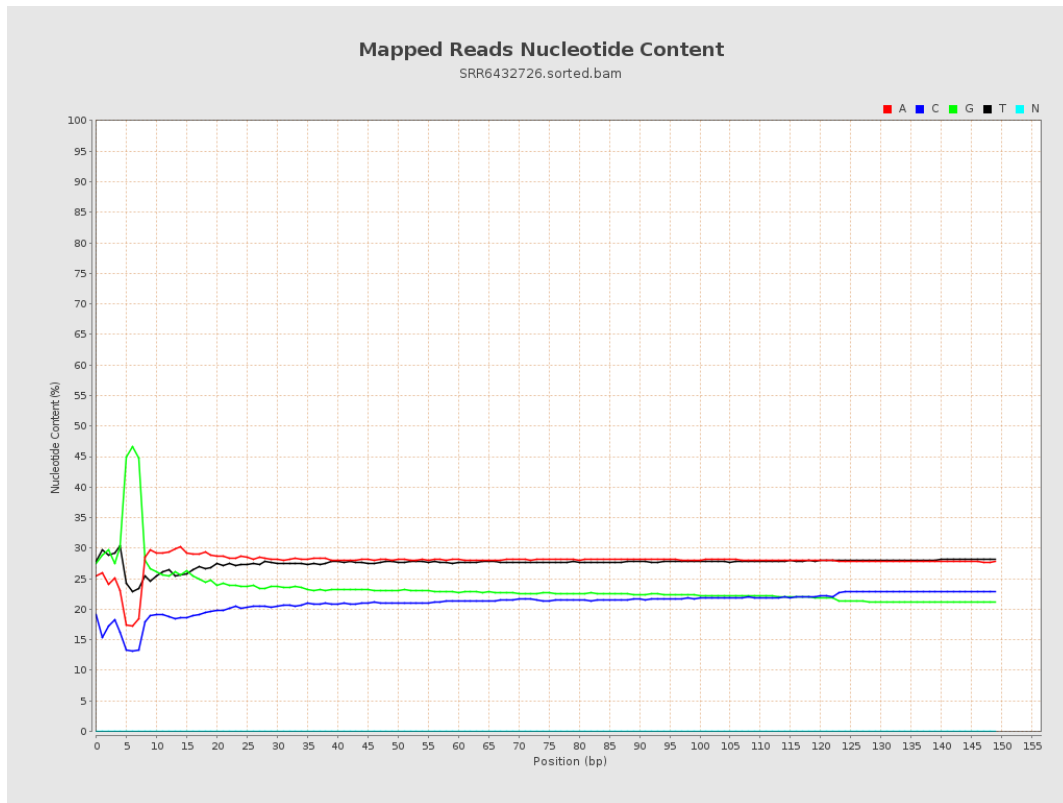
6. Results : Genome Fraction Coverage



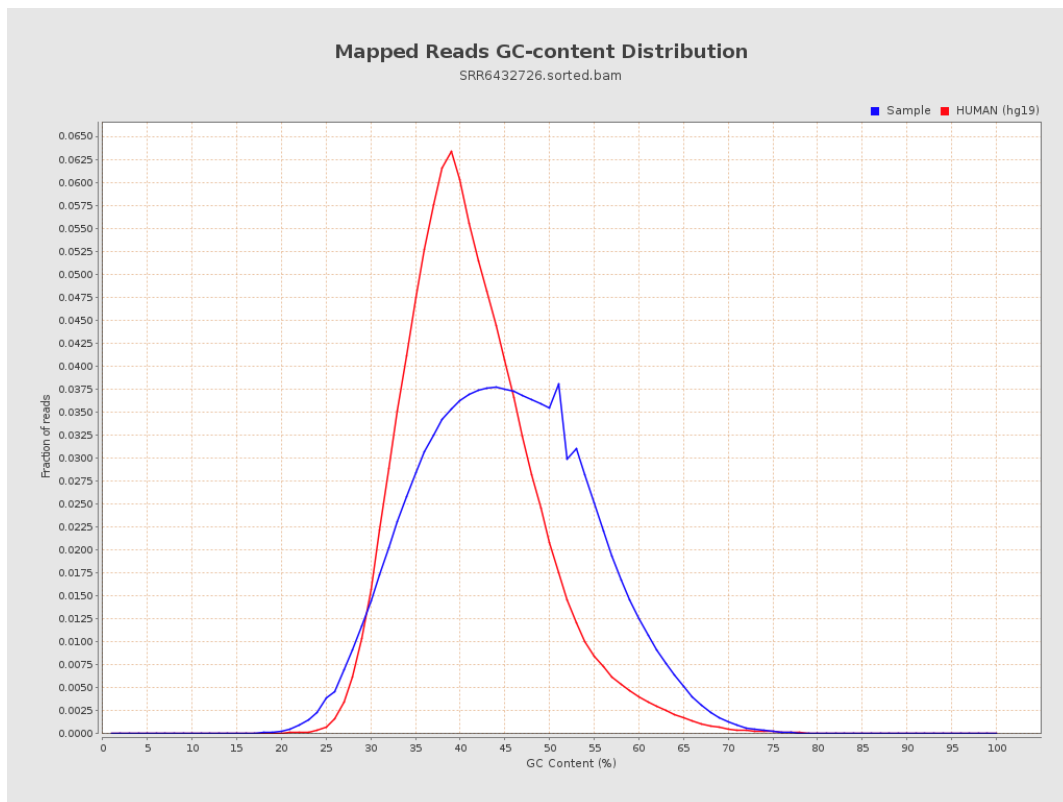
7. Results : Duplication Rate Histogram



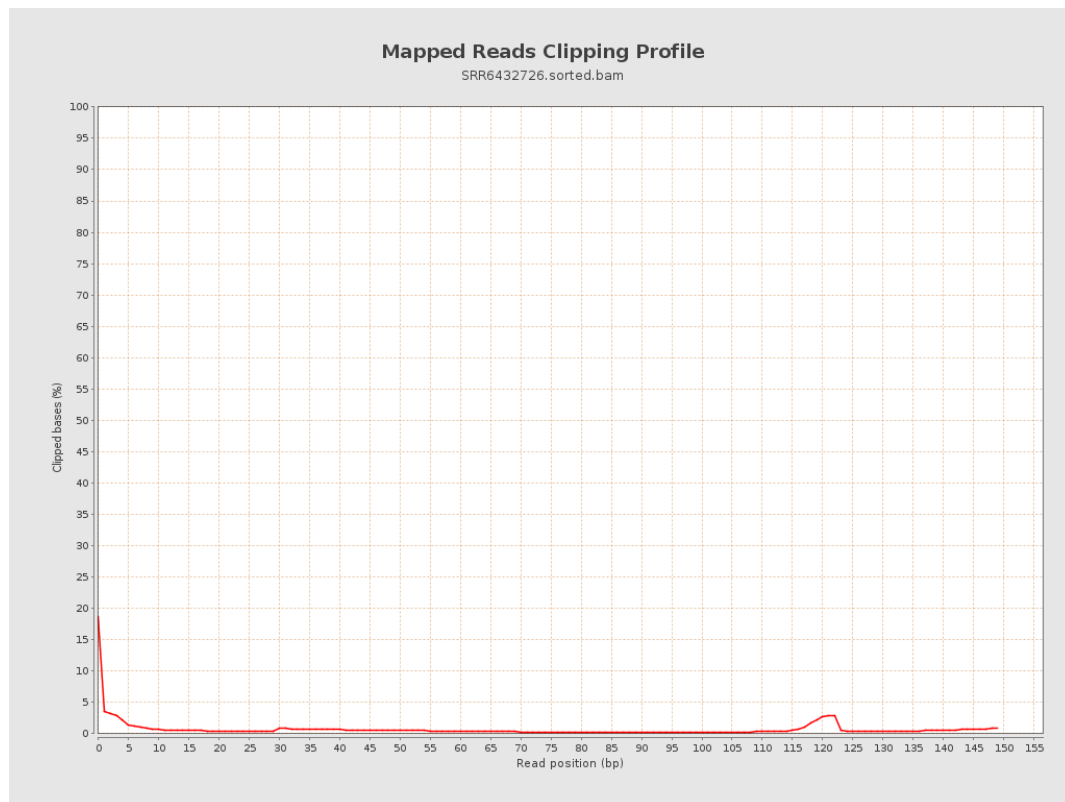
8. Results : Mapped Reads Nucleotide Content



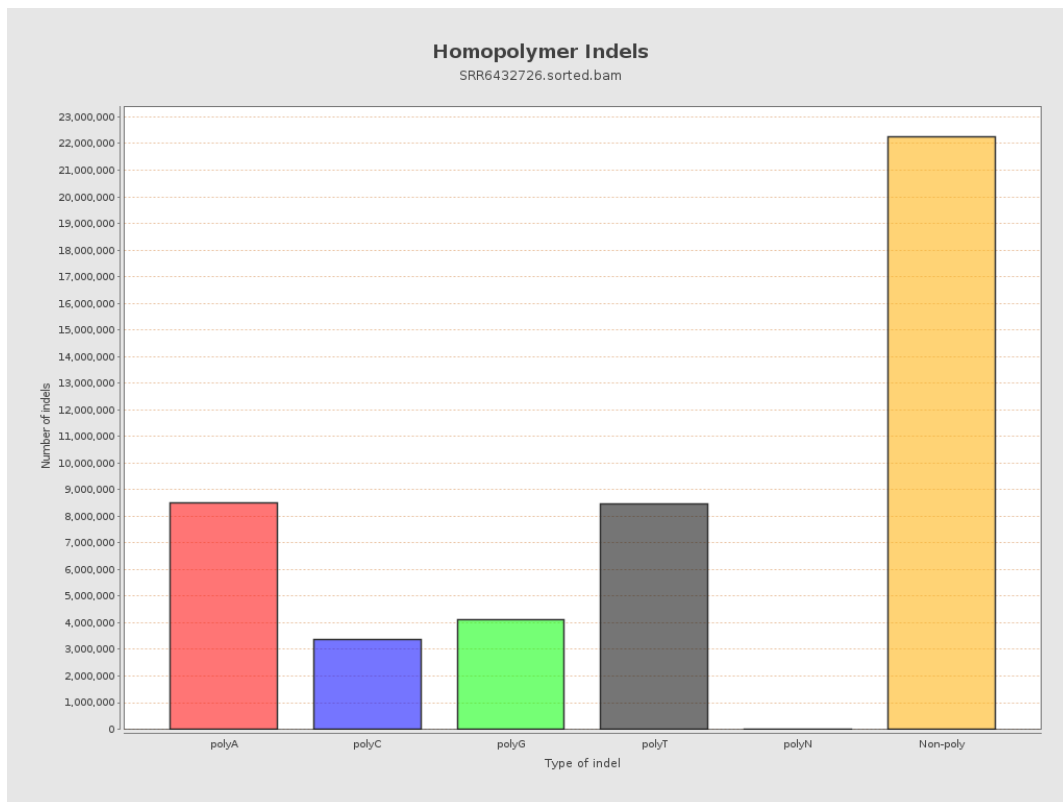
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



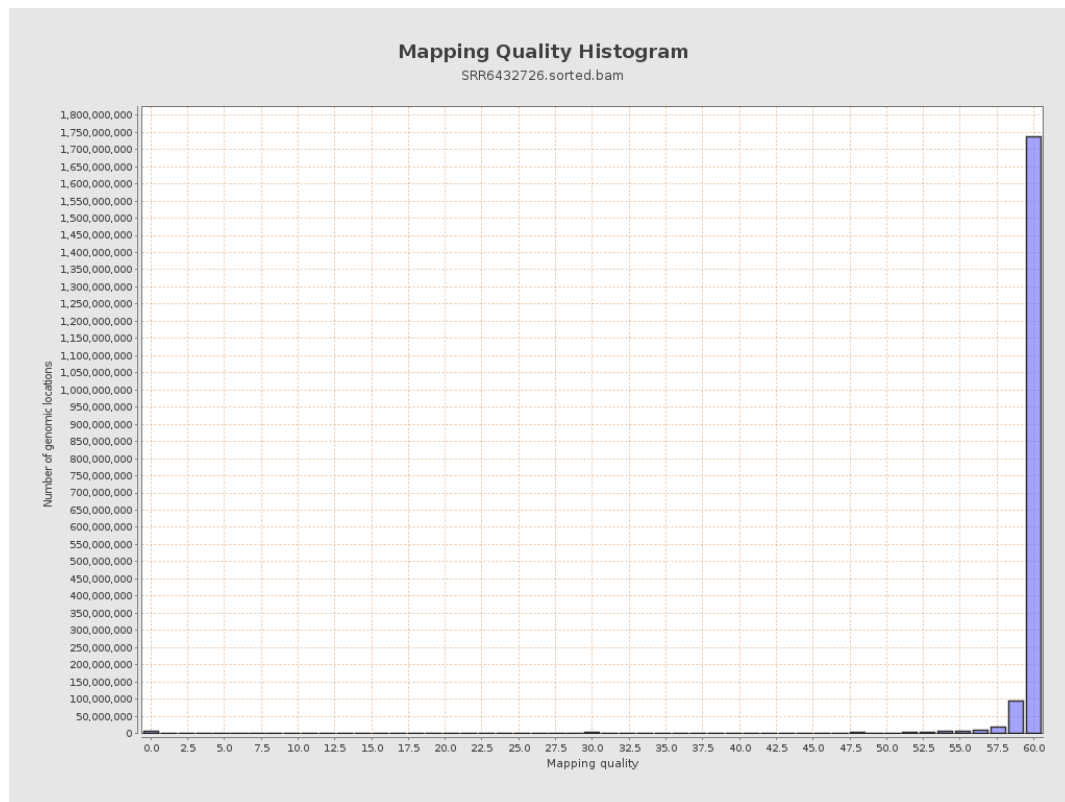
11. Results : Homopolymer Indels



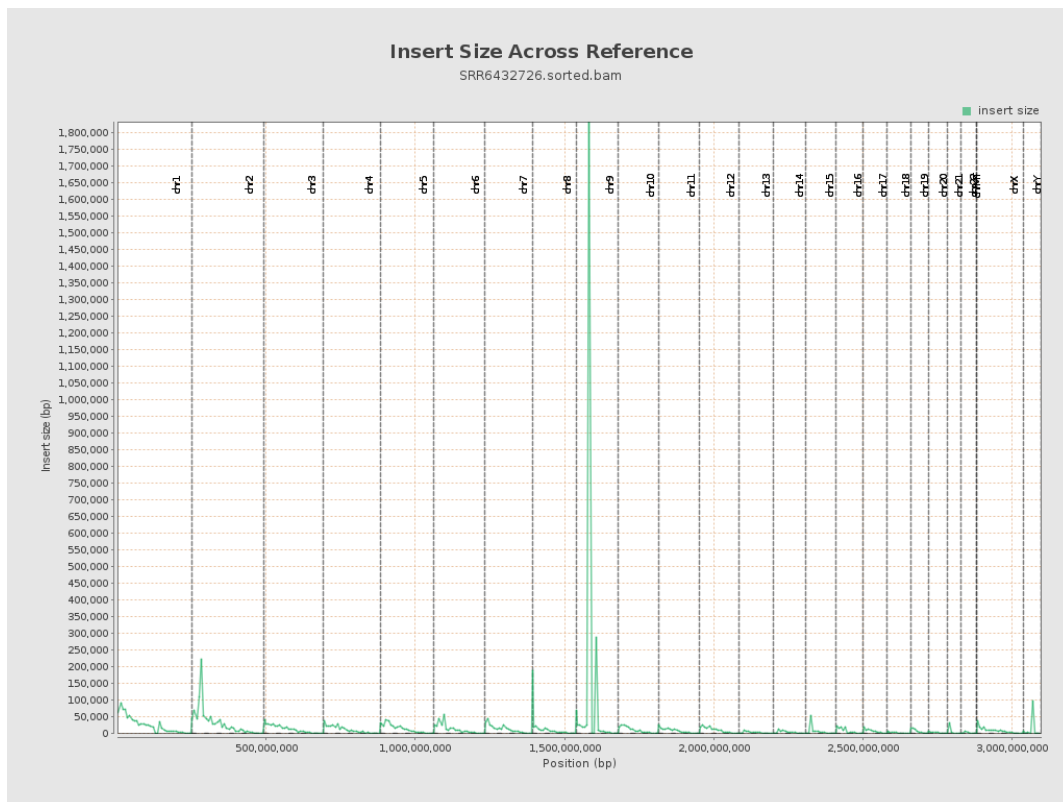
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

