

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 21:20:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472726.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_SRR3472726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472726_1.fastq.gz SRR3472726_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 21:20:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,630,146
Mapped reads	17,481,087 / 99.15%
Unmapped reads	149,059 / 0.85%
Mapped paired reads	17,481,087 / 99.15%
Mapped reads, first in pair	8,766,122 / 49.72%
Mapped reads, second in pair	8,714,965 / 49.43%
Mapped reads, both in pair	17,392,572 / 98.65%
Mapped reads, singletons	88,515 / 0.5%
Secondary alignments	0
Supplementary alignments	58,107 / 0.33%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	11,179,862 / 63.41%
Duplication rate	47.29%
Clipped reads	1,515,821 / 8.6%

2.2. ACGT Content

Number/percentage of A's	466,710,310 / 27.15%
Number/percentage of C's	395,689,926 / 23.02%
Number/percentage of T's	463,215,825 / 26.94%
Number/percentage of G's	393,267,636 / 22.87%
Number/percentage of N's	335,288 / 0.02%

GC Percentage	45.89%
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2.3. Coverage

Mean	0.5554
Standard Deviation	19.3301

2.4. Mapping Quality

Mean Mapping Quality	55.14
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2.5. Insert size

Mean	20,000.52
Standard Deviation	1,394,444.2
P25/Median/P75	162 / 228 / 309

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	9,934,421
Insertions	96,271
Mapped reads with at least one insertion	0.55%
Deletions	91,695
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.5%

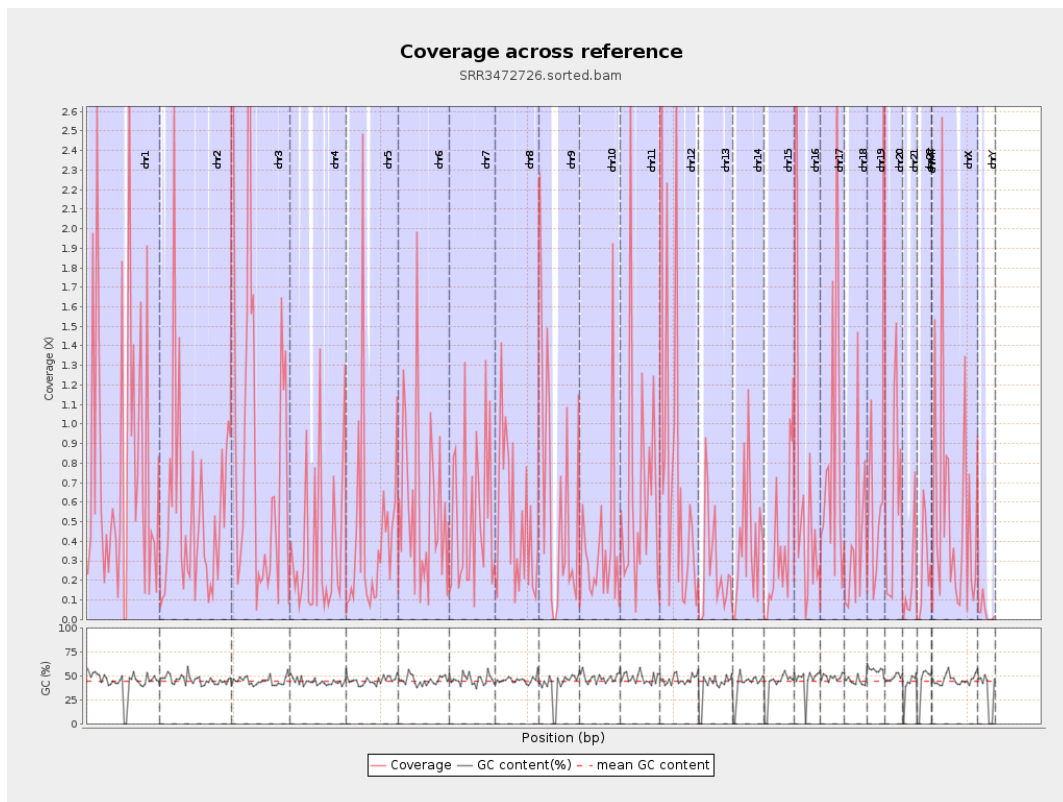
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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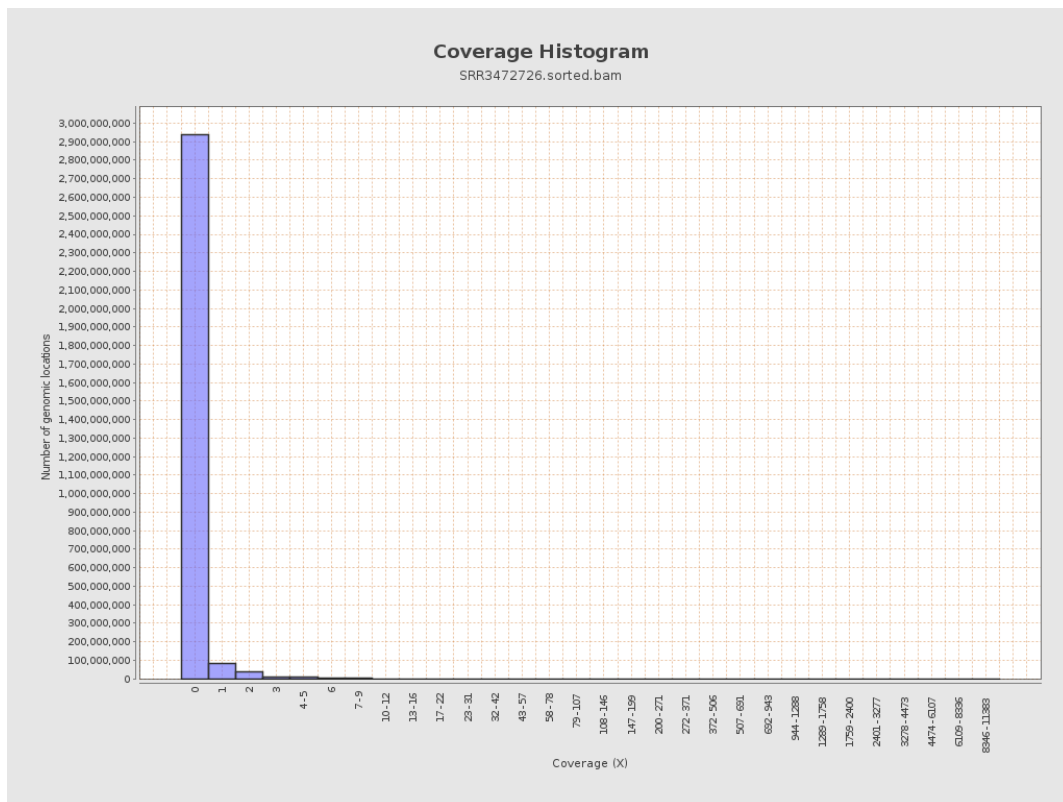
		bases	coverage	deviation
chr1	249250621	194355630	0.7798	27.8749
chr2	243199373	130134798	0.5351	19.2657
chr3	198022430	180284340	0.9104	21.0095
chr4	191154276	68322775	0.3574	12.6089
chr5	180915260	79227202	0.4379	13.3531
chr6	171115067	96292641	0.5627	15.4396
chr7	159138663	84855355	0.5332	19.0911
chr8	146364022	74728480	0.5106	15.3578
chr9	141213431	87490899	0.6196	17.2718
chr10	135534747	49180894	0.3629	13.9891
chr11	135006516	89846638	0.6655	28.9985
chr12	133851895	130803824	0.9772	34.6992
chr13	115169878	31121378	0.2702	9.5682
chr14	107349540	41016154	0.3821	15.4542
chr15	102531392	36814172	0.3591	10.1651
chr16	90354753	60835209	0.6733	18.5386
chr17	81195210	66302332	0.8166	22.6845
chr18	78077248	31880678	0.4083	18.4697
chr19	59128983	39626984	0.6702	21.8615
chr20	63025520	36999835	0.5871	17.5944
chr21	48129895	9336439	0.194	7.7283
chr22	51304566	13594082	0.265	6.6897
chrMT	16571	978	0.059	0.2694
chrX	155270560	84127756	0.5418	17.3305

chrY	59373566	2266555	0.0382	1.4051
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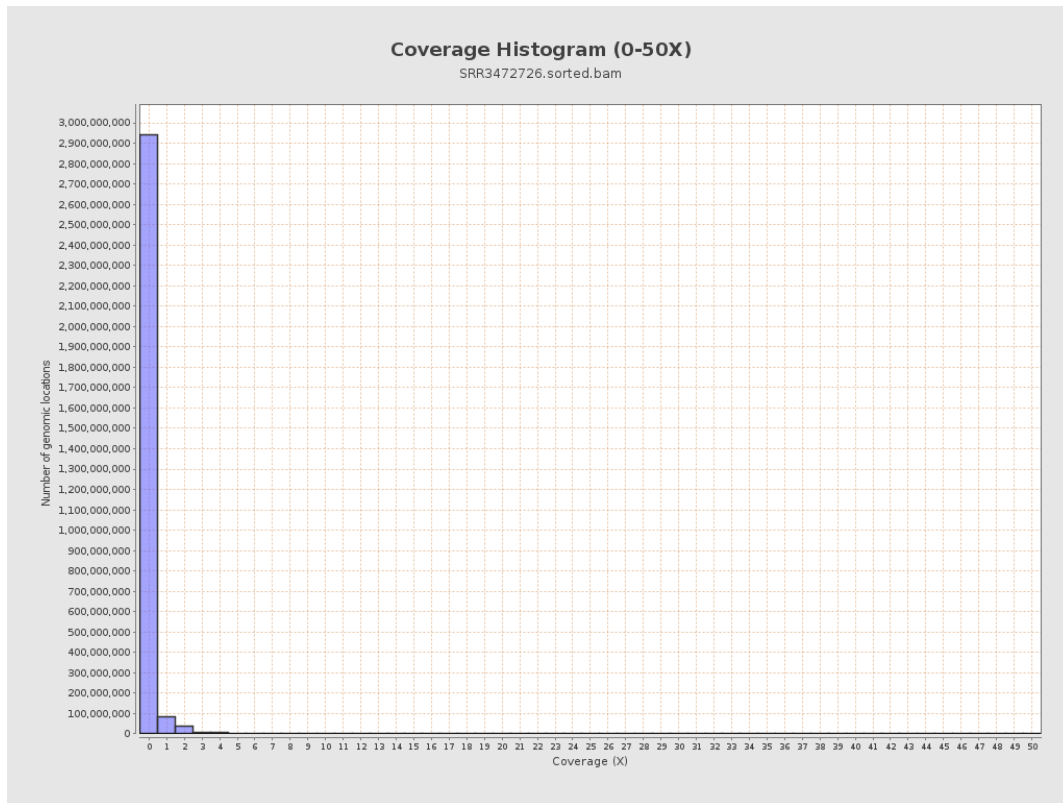
3. Results : Coverage across reference



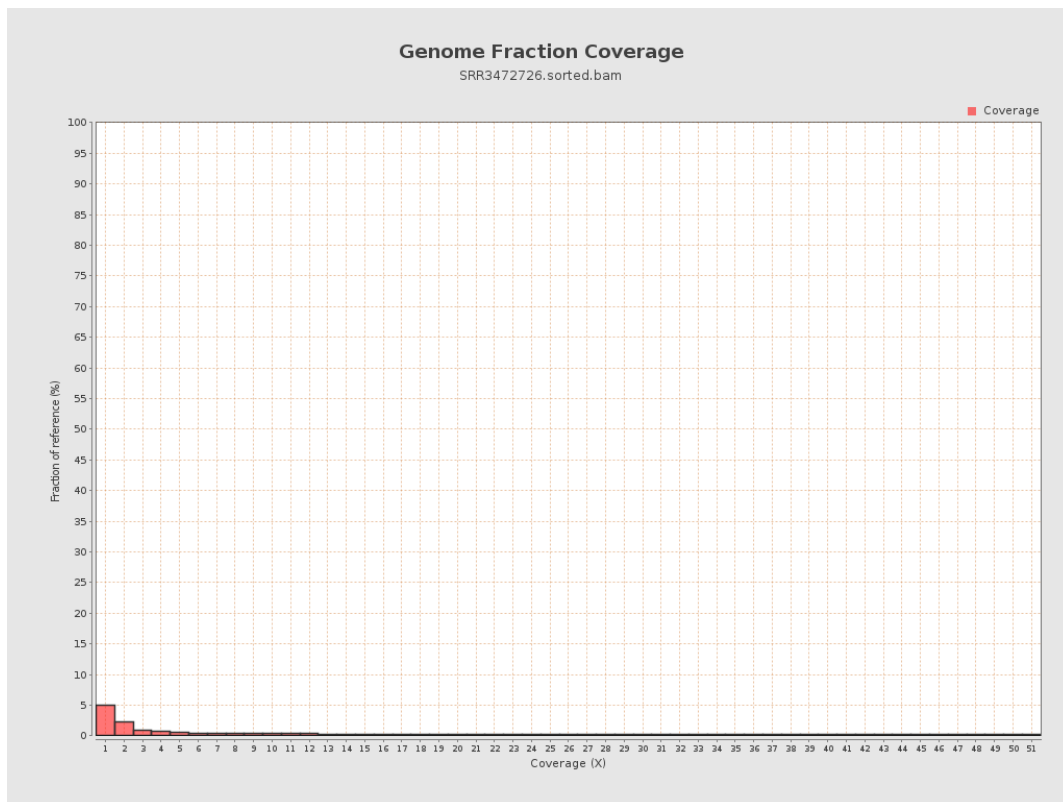
4. Results : Coverage Histogram



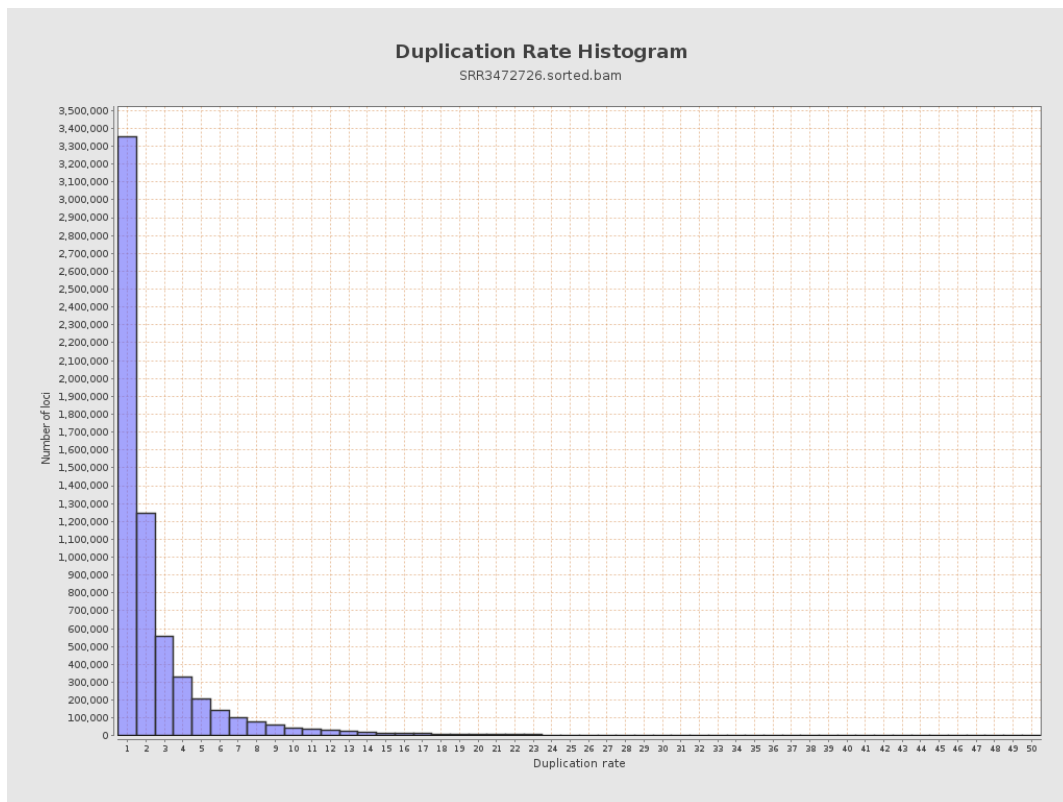
5. Results : Coverage Histogram (0-50X)



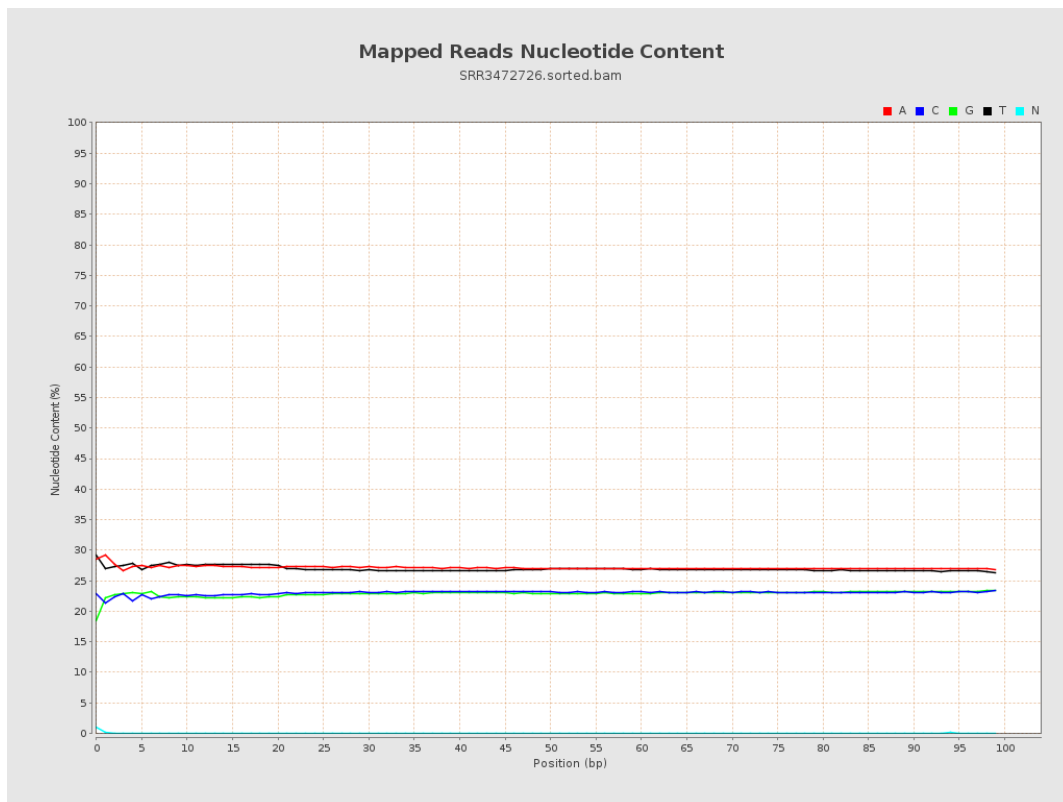
6. Results : Genome Fraction Coverage



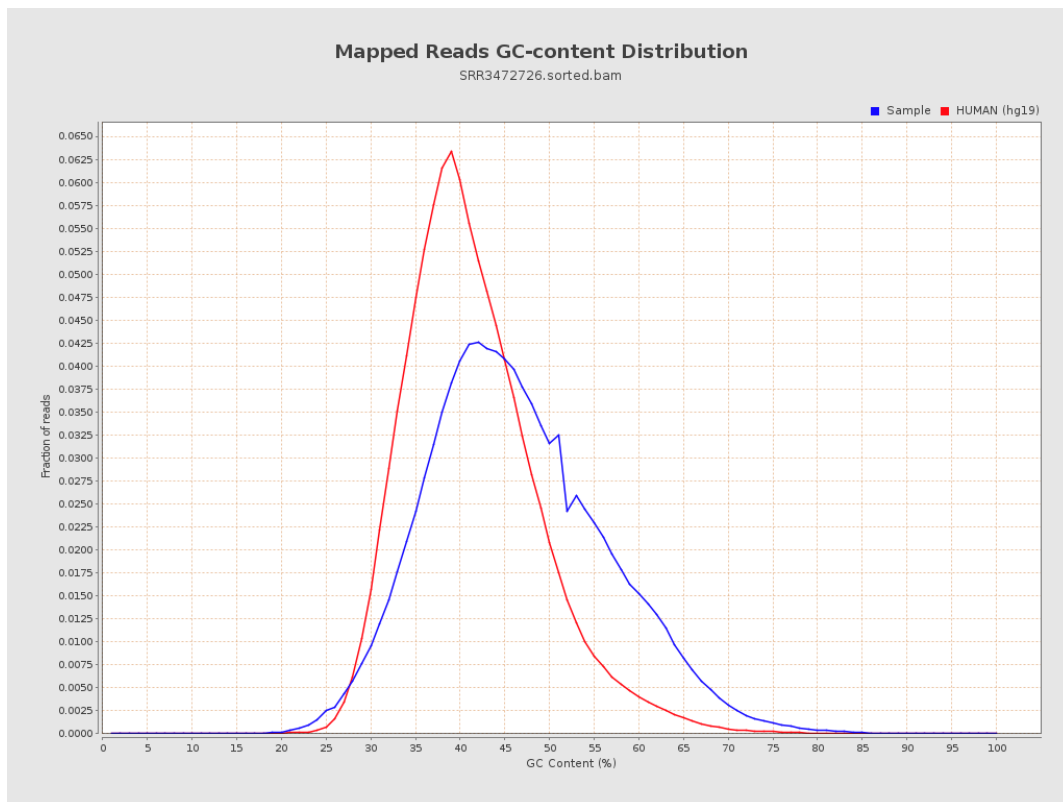
7. Results : Duplication Rate Histogram



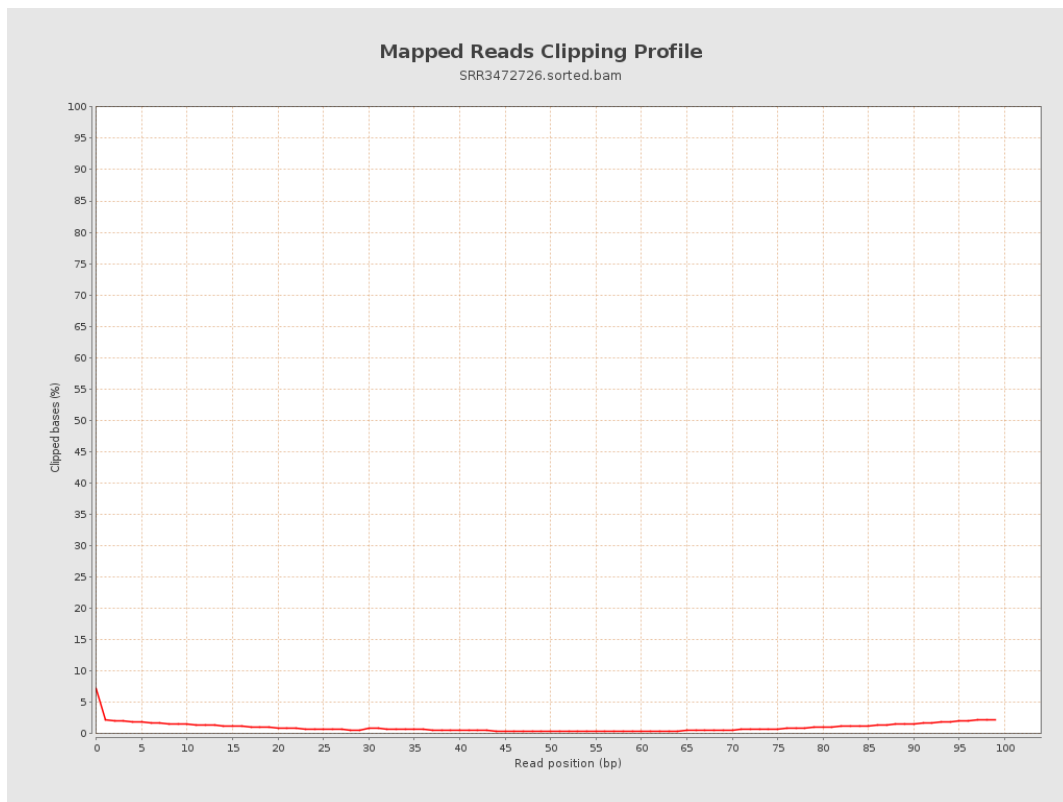
8. Results : Mapped Reads Nucleotide Content



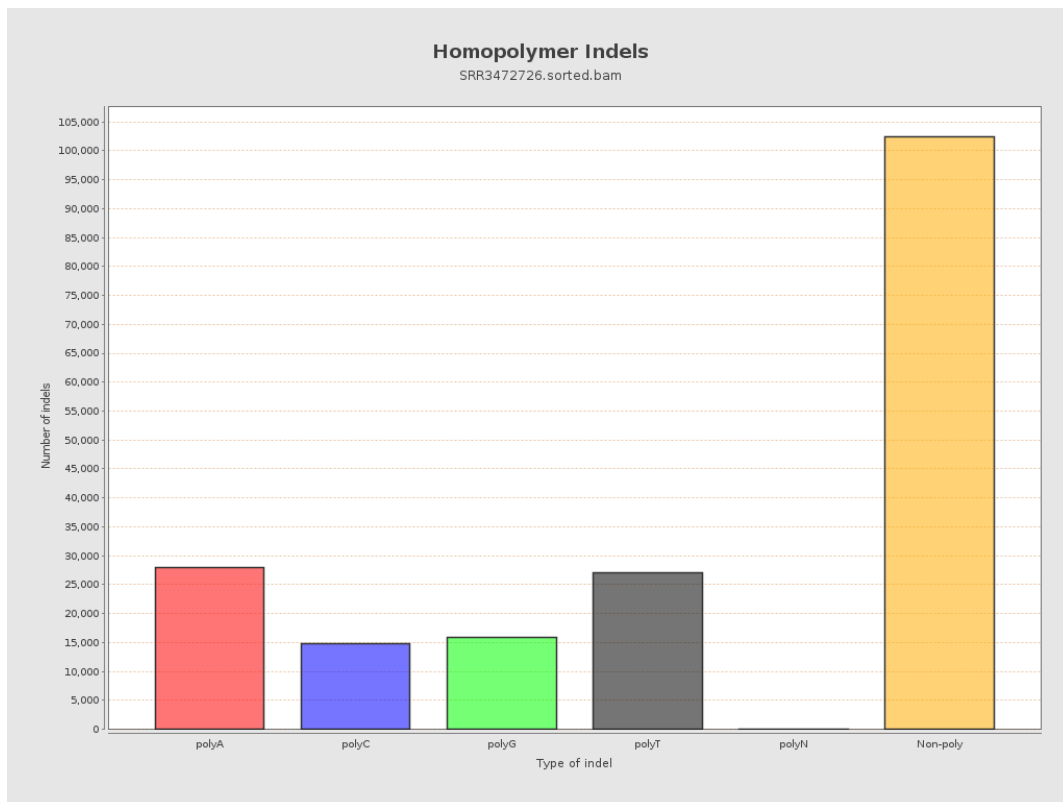
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



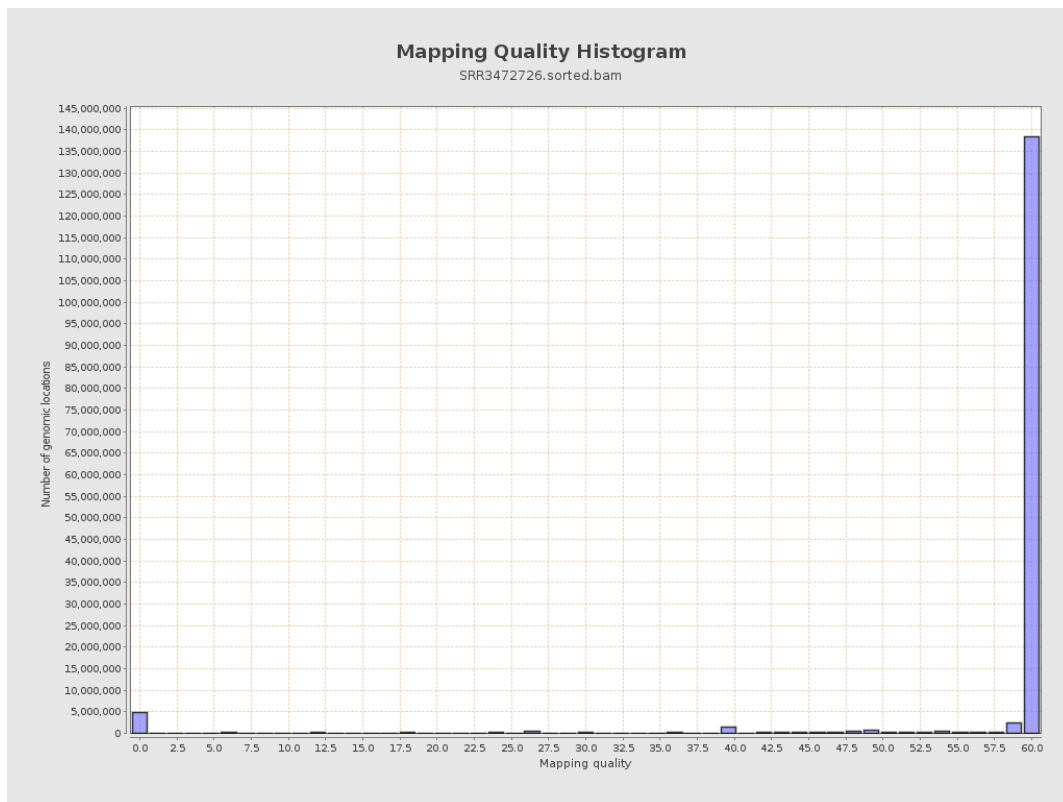
11. Results : Homopolymer Indels



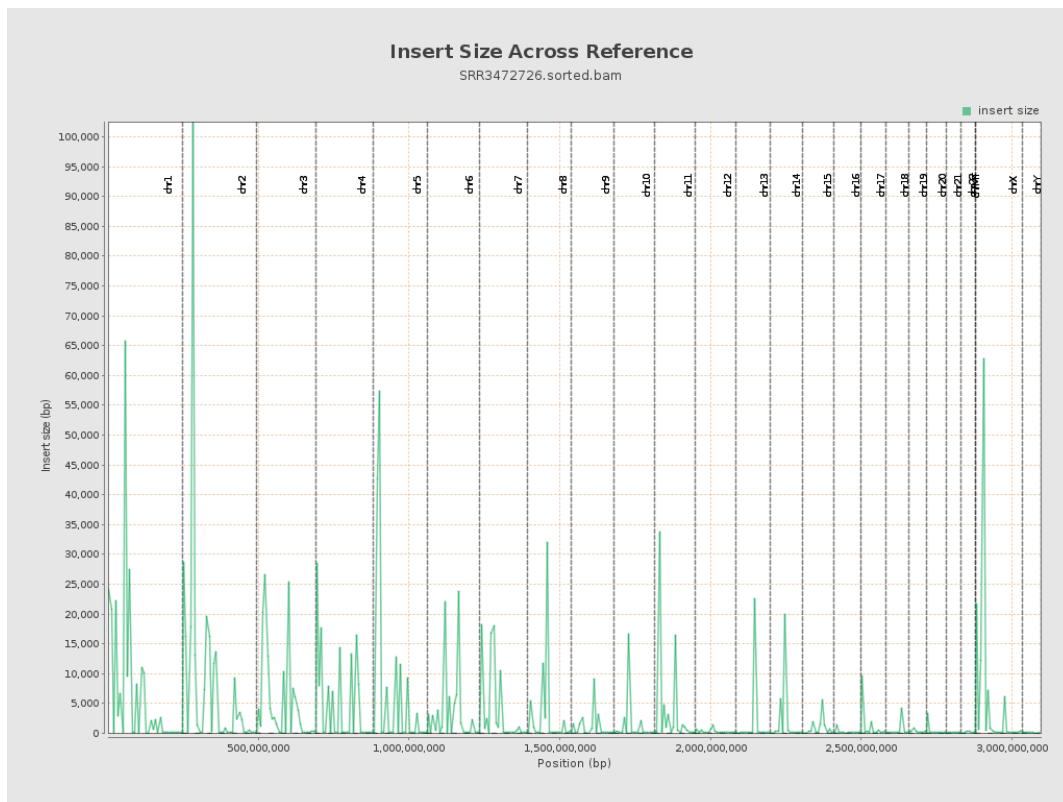
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

