

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 22:14:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472729.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_SRR3472729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472729_1.fastq.gz SRR3472729_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 22:14:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,898,008
Mapped reads	15,761,149 / 99.14%
Unmapped reads	136,859 / 0.86%
Mapped paired reads	15,761,149 / 99.14%
Mapped reads, first in pair	7,903,656 / 49.71%
Mapped reads, second in pair	7,857,493 / 49.42%
Mapped reads, both in pair	15,681,100 / 98.64%
Mapped reads, singletons	80,049 / 0.5%
Secondary alignments	0
Supplementary alignments	61,141 / 0.38%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	9,867,475 / 62.07%
Duplication rate	47.52%
Clipped reads	1,221,125 / 7.68%

2.2. ACGT Content

Number/percentage of A's	420,706,389 / 27.07%
Number/percentage of C's	358,412,988 / 23.06%
Number/percentage of T's	419,174,086 / 26.97%
Number/percentage of G's	355,593,002 / 22.88%
Number/percentage of N's	301,834 / 0.02%

GC Percentage	45.94%
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2.3. Coverage

Mean	0.5021
Standard Deviation	17.4841

2.4. Mapping Quality

Mean Mapping Quality	55.31
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2.5. Insert size

Mean	23,050.61
Standard Deviation	1,477,391.22
P25/Median/P75	165 / 227 / 305

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	9,015,606
Insertions	90,283
Mapped reads with at least one insertion	0.57%
Deletions	81,727
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.92%

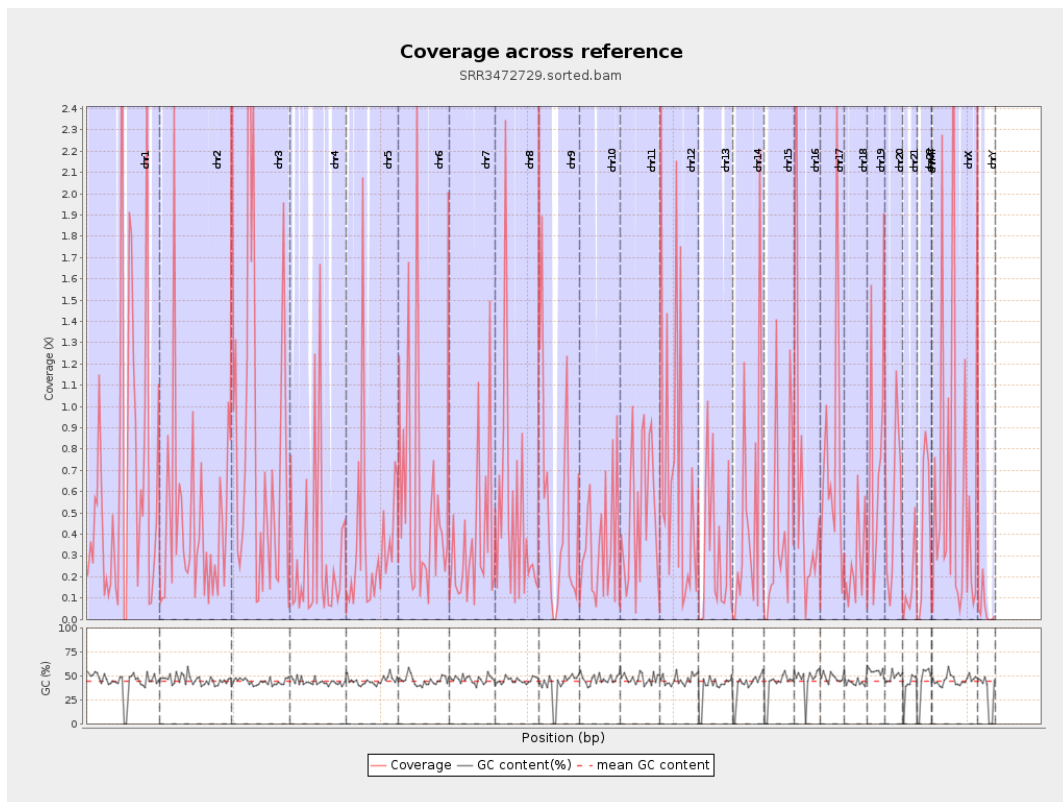
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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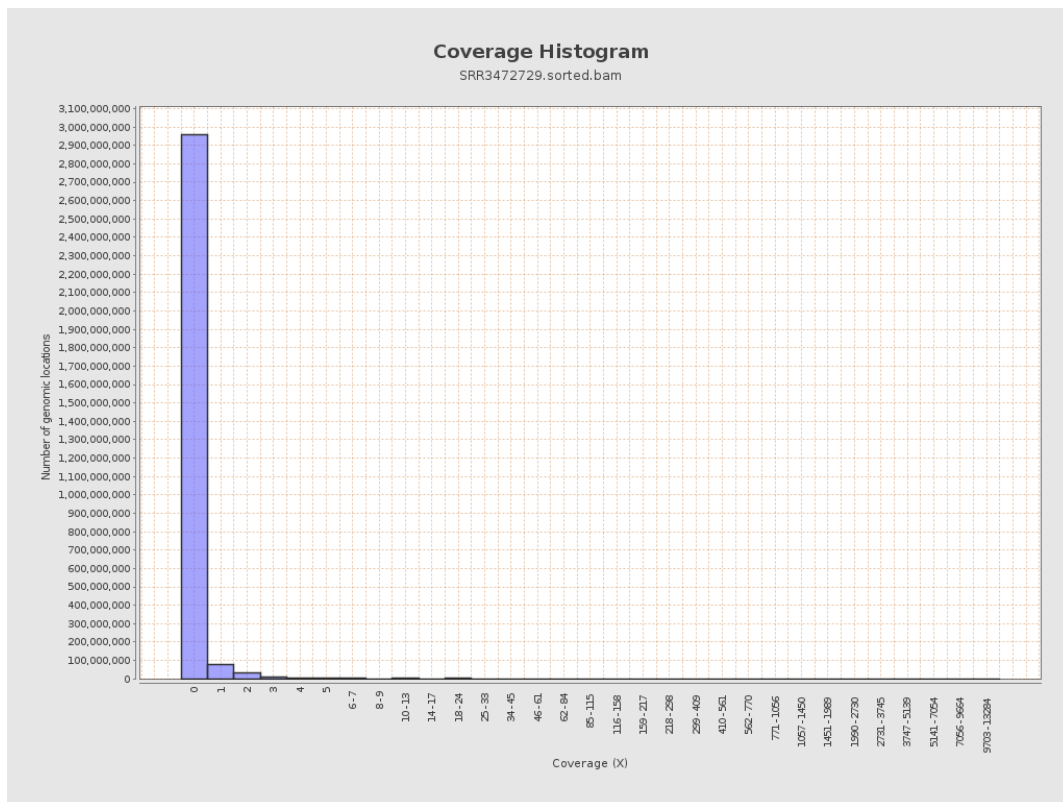
		bases	coverage	deviation
chr1	249250621	171057578	0.6863	21.6623
chr2	243199373	108080186	0.4444	20.7539
chr3	198022430	175642095	0.887	22.039
chr4	191154276	56021802	0.2931	13.238
chr5	180915260	66309624	0.3665	11.1607
chr6	171115067	96493985	0.5639	16.2752
chr7	159138663	58139404	0.3653	12.7364
chr8	146364022	69046410	0.4717	18.7772
chr9	141213431	72177702	0.5111	12.2851
chr10	135534747	48242811	0.3559	12.2728
chr11	135006516	67818042	0.5023	15.8118
chr12	133851895	98318863	0.7345	22.202
chr13	115169878	36907336	0.3205	12.6011
chr14	107349540	49279997	0.4591	31.7468
chr15	102531392	42777776	0.4172	13.0093
chr16	90354753	55754076	0.6171	17.0578
chr17	81195210	57485329	0.708	17.7493
chr18	78077248	21441988	0.2746	9.1653
chr19	59128983	41805304	0.707	17.9257
chr20	63025520	33809340	0.5364	15.892
chr21	48129895	8120118	0.1687	8.1473
chr22	51304566	21088908	0.4111	11.1557
chrMT	16571	1699	0.1025	0.3569
chrX	155270560	95669648	0.6161	19.8223

chrY	59373566	2899326	0.0488	2.348
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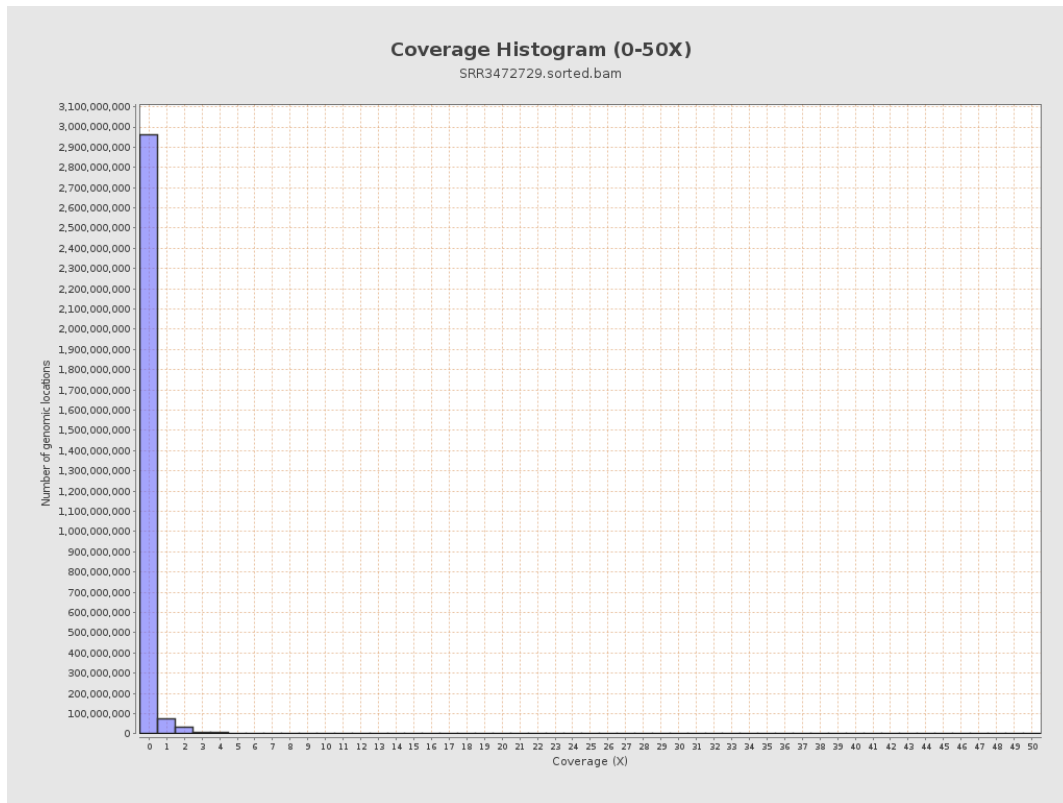
3. Results : Coverage across reference



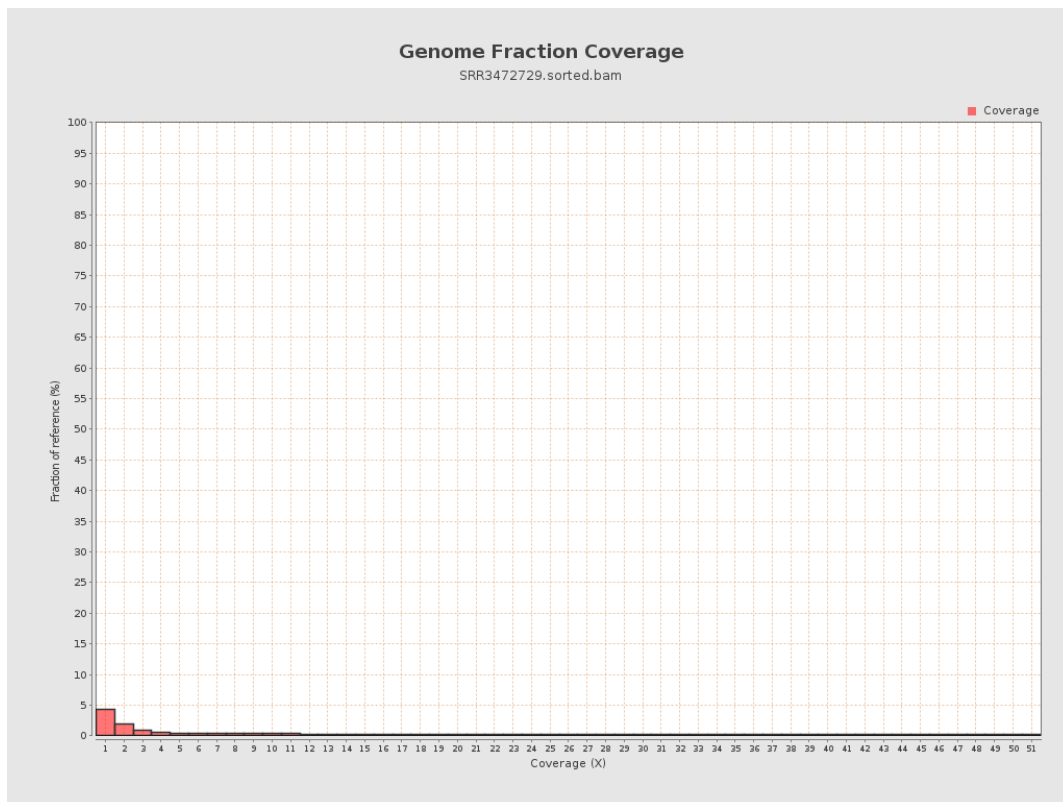
4. Results : Coverage Histogram



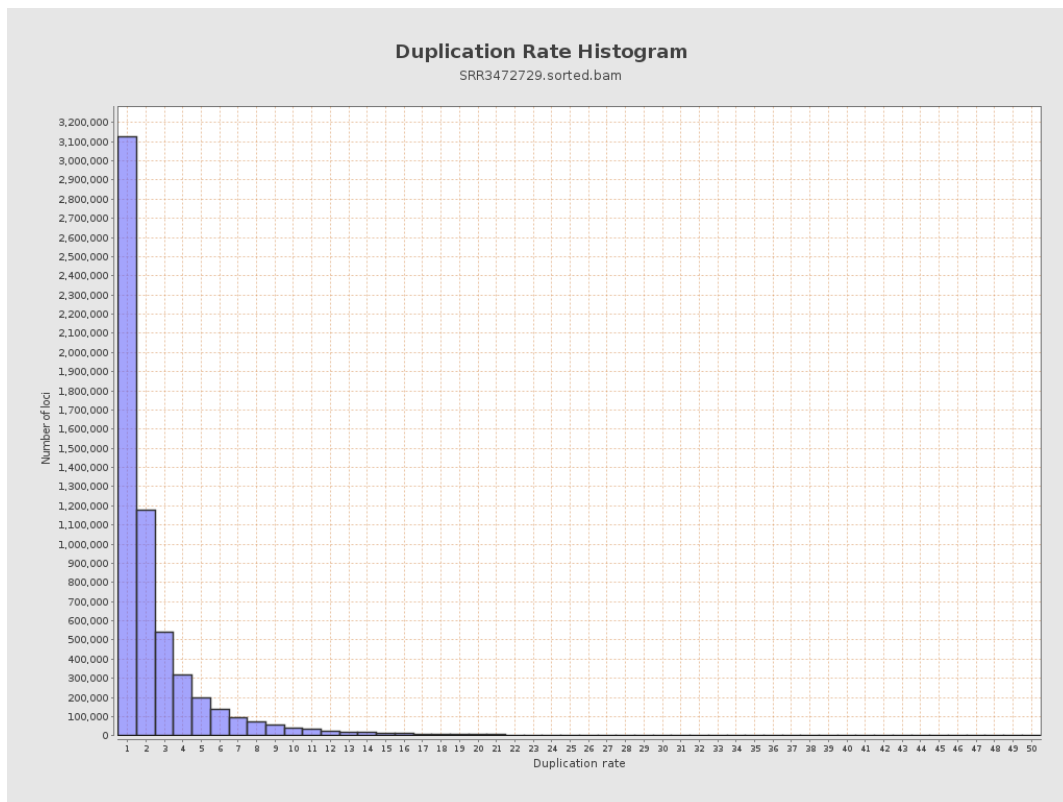
5. Results : Coverage Histogram (0-50X)



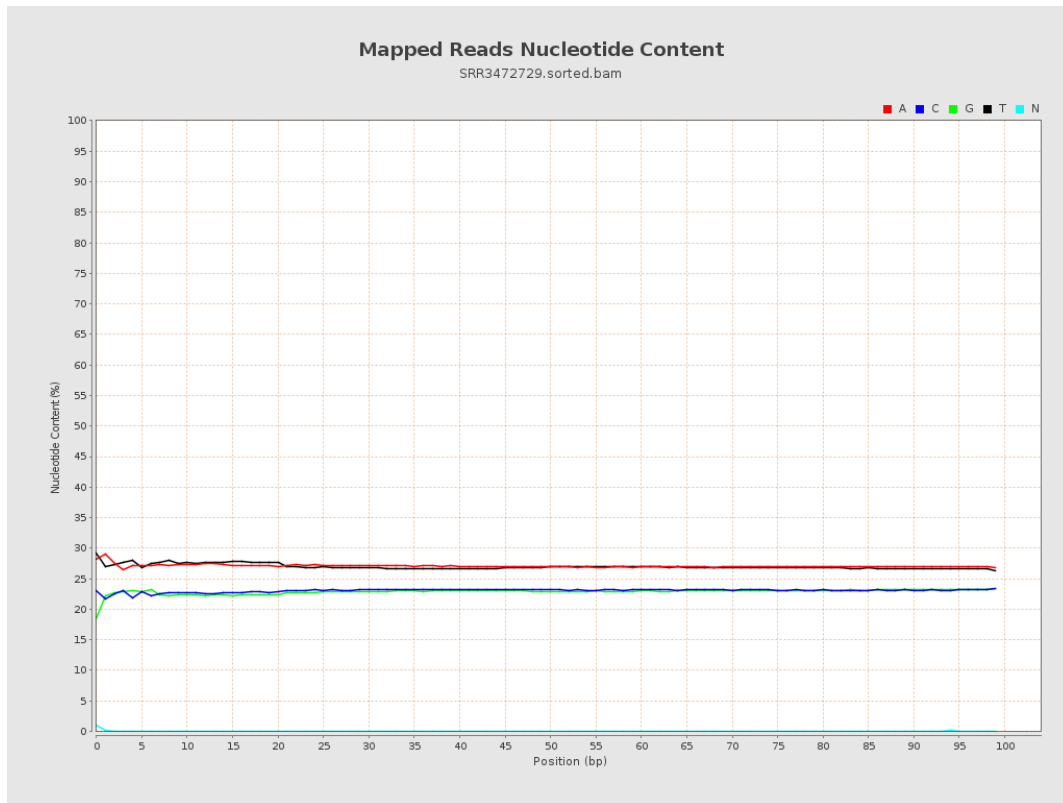
6. Results : Genome Fraction Coverage



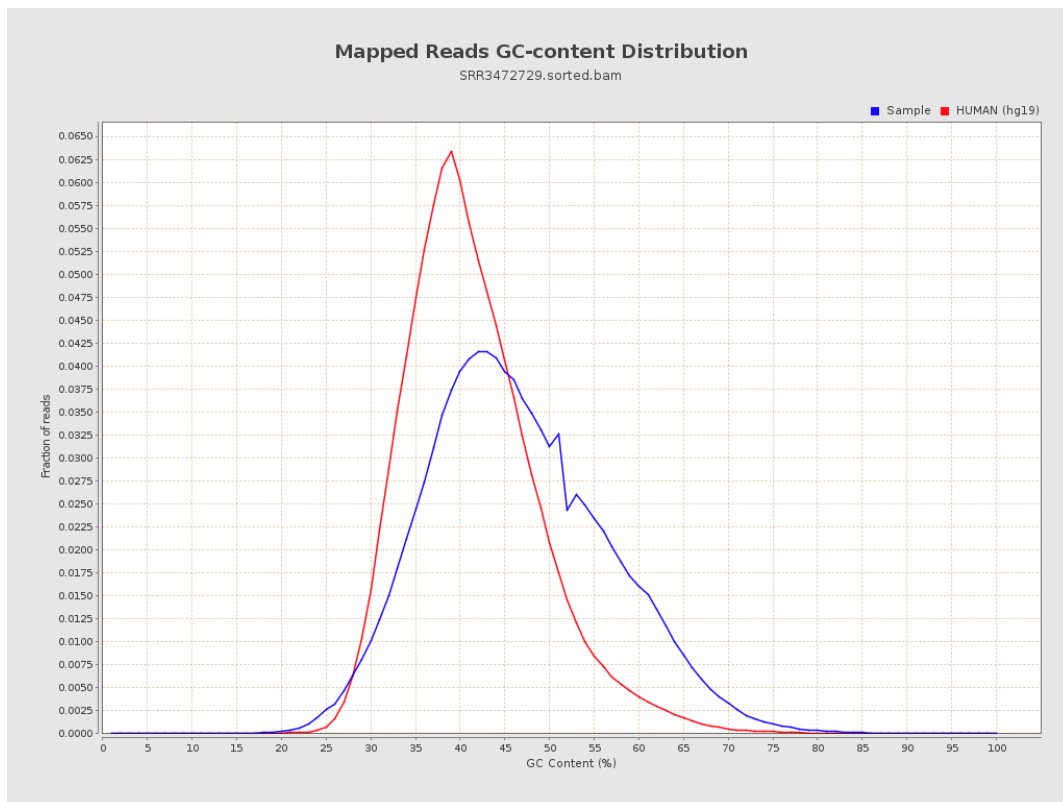
7. Results : Duplication Rate Histogram



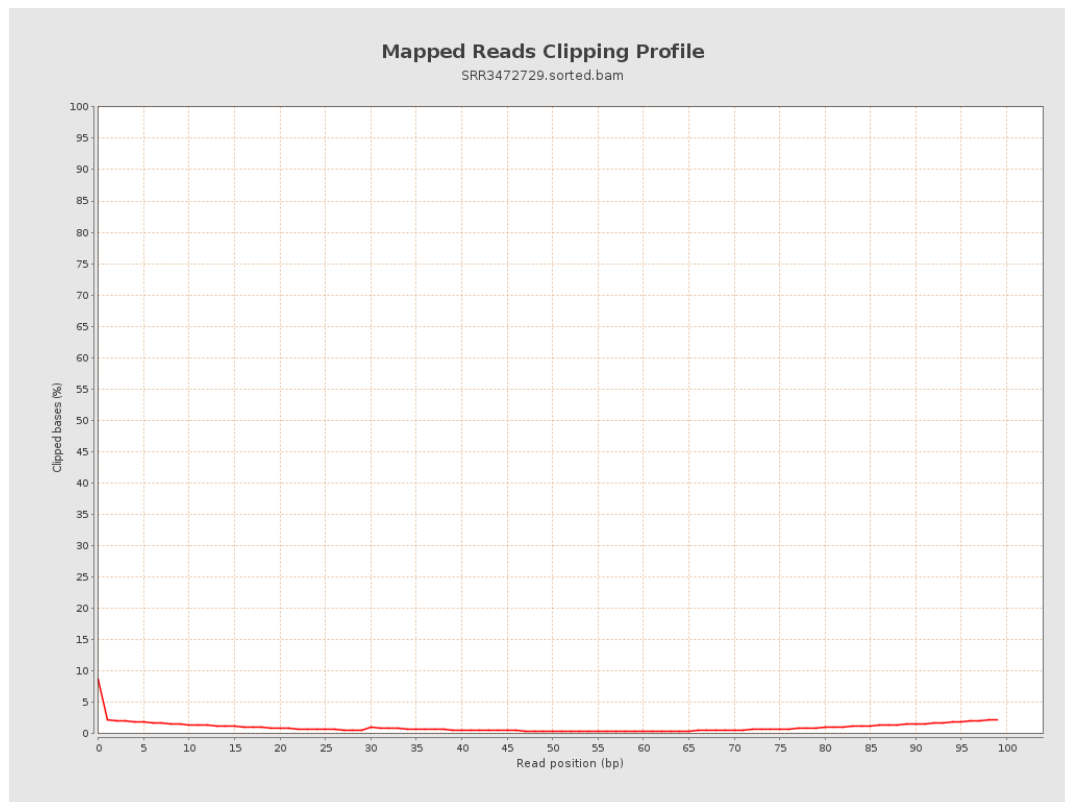
8. Results : Mapped Reads Nucleotide Content



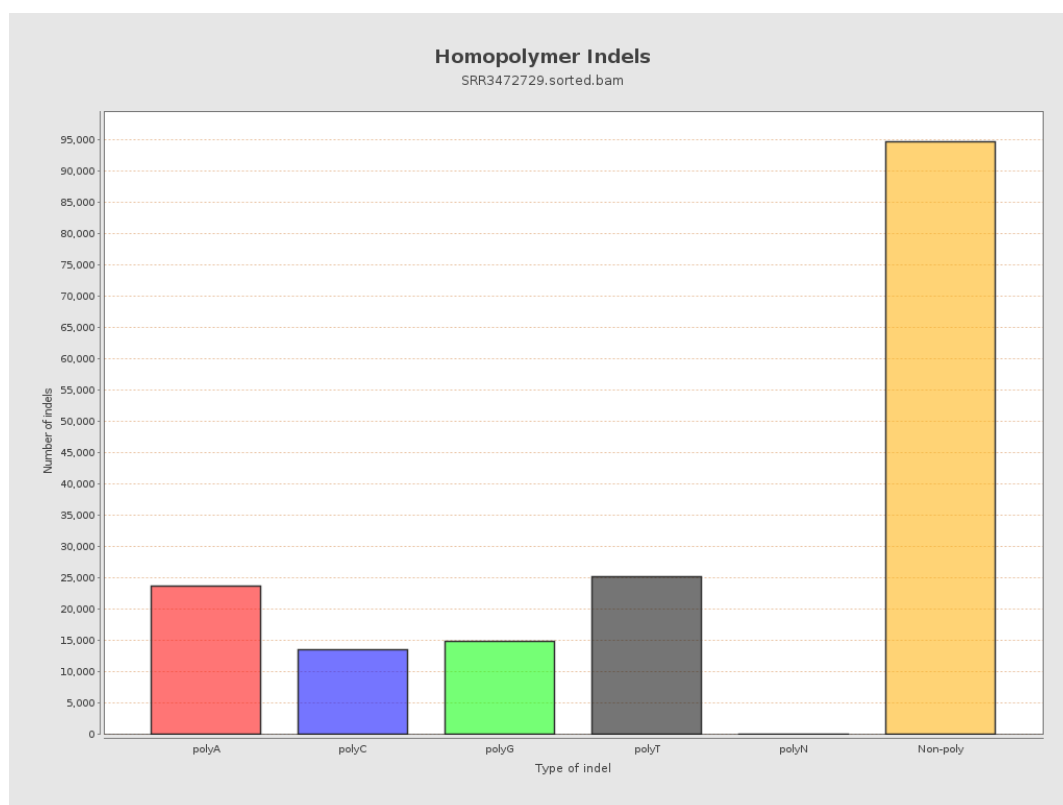
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



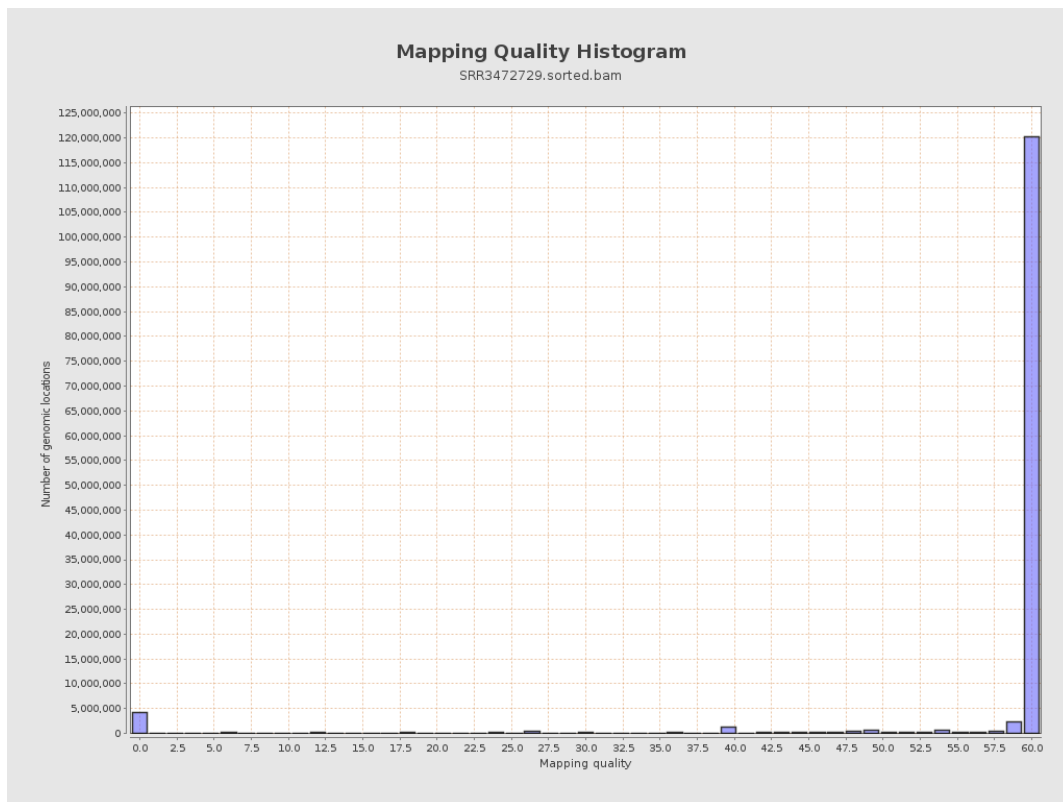
11. Results : Homopolymer Indels



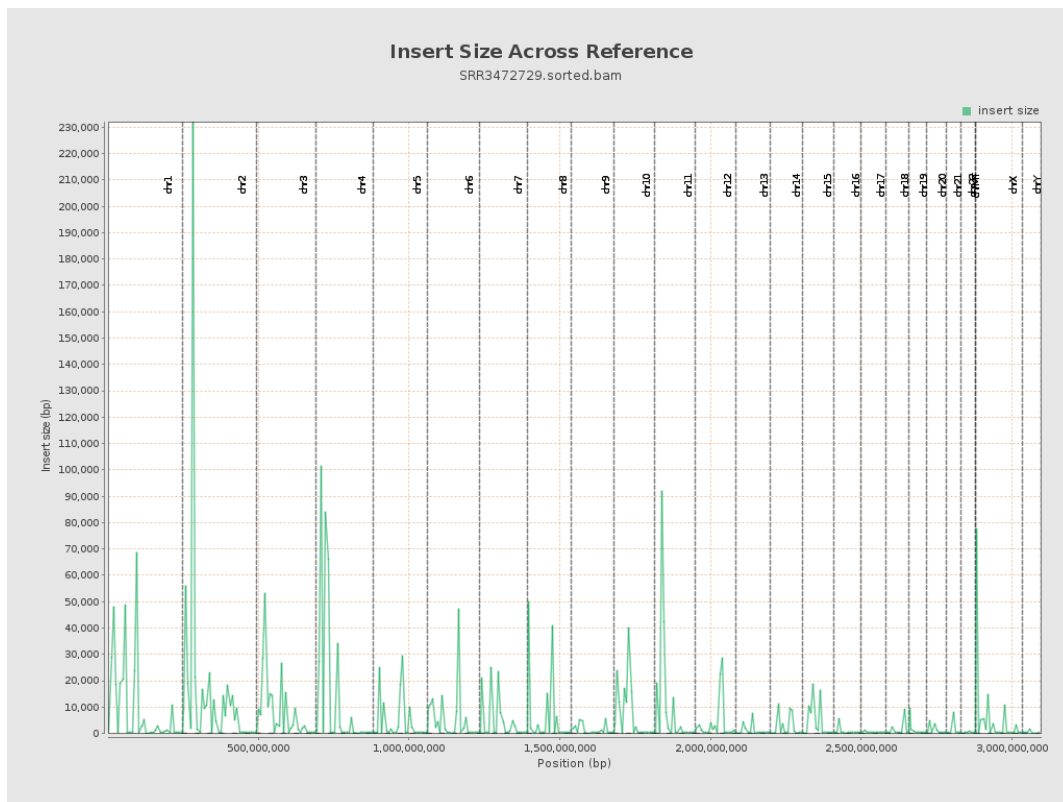
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

