

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:13:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472528.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_SRR3472528 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472528_1.fastq.gz SRR3472528_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:13:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472528.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,163,478
Mapped reads	18,956,854 / 98.92%
Unmapped reads	206,624 / 1.08%
Mapped paired reads	18,956,854 / 98.92%
Mapped reads, first in pair	9,504,625 / 49.6%
Mapped reads, second in pair	9,452,229 / 49.32%
Mapped reads, both in pair	18,848,676 / 98.36%
Mapped reads, singletons	108,178 / 0.56%
Secondary alignments	0
Supplementary alignments	75,658 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	12,305,081 / 64.21%
Duplication rate	45.88%
Clipped reads	1,435,900 / 7.49%

2.2. ACGT Content

Number/percentage of A's	506,388,570 / 27.09%
Number/percentage of C's	430,326,450 / 23.02%
Number/percentage of T's	504,083,192 / 26.97%
Number/percentage of G's	427,886,078 / 22.89%
Number/percentage of N's	290,270 / 0.02%

GC Percentage	45.92%
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2.3. Coverage

Mean	0.6038
Standard Deviation	22.6275

2.4. Mapping Quality

Mean Mapping Quality	54.82
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2.5. Insert size

Mean	29,493.99
Standard Deviation	1,642,929.59
P25/Median/P75	172 / 234 / 311

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	10,920,136
Insertions	103,838
Mapped reads with at least one insertion	0.54%
Deletions	94,340
Mapped reads with at least one deletion	0.49%
Homopolymer indels	44.64%

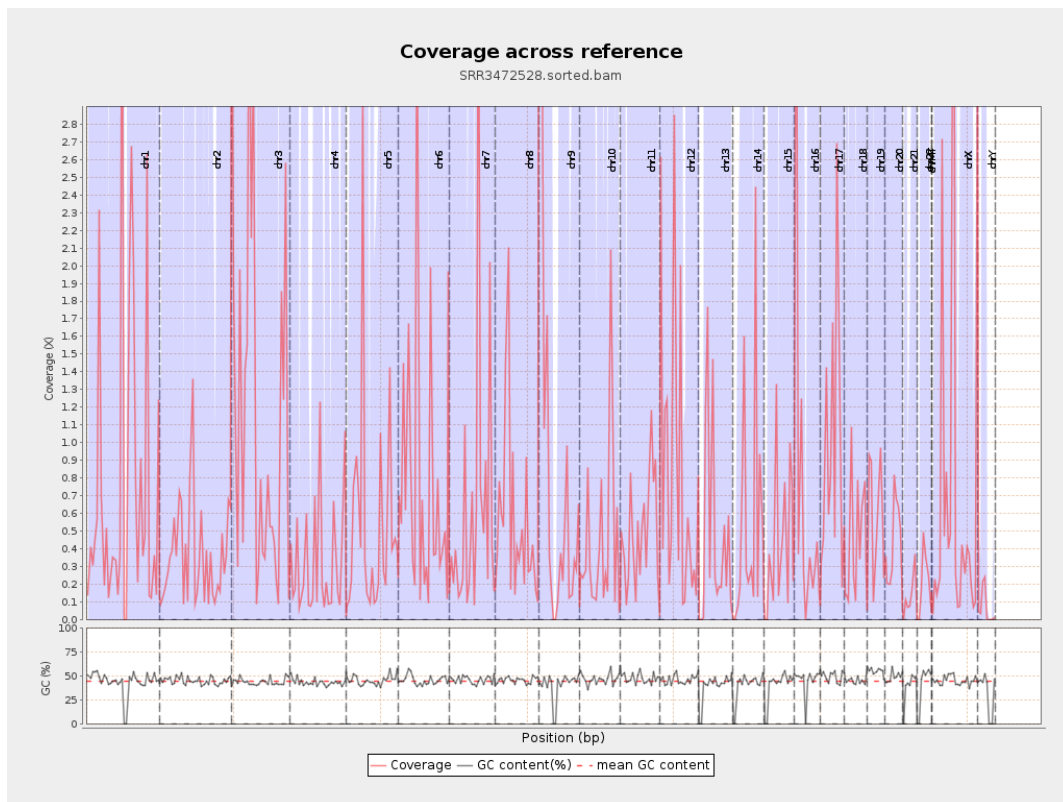
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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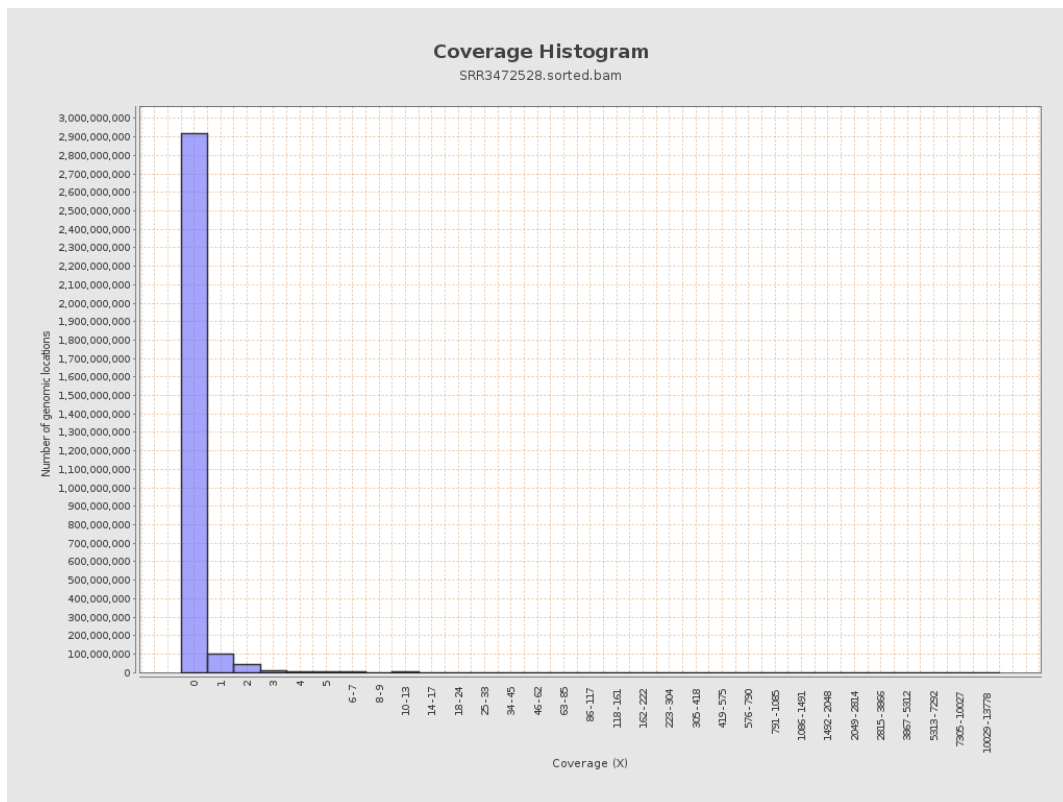
		bases	coverage	deviation
chr1	249250621	197664145	0.793	31.5898
chr2	243199373	87879533	0.3613	13.3225
chr3	198022430	234347604	1.1834	31.2858
chr4	191154276	60558452	0.3168	13.7032
chr5	180915260	96634916	0.5341	17.3828
chr6	171115067	130728225	0.764	22.5283
chr7	159138663	102661975	0.6451	22.8287
chr8	146364022	82469997	0.5635	17.9354
chr9	141213431	113308083	0.8024	32.3578
chr10	135534747	61507197	0.4538	23.2259
chr11	135006516	68516189	0.5075	16.9832
chr12	133851895	110128850	0.8228	22.6623
chr13	115169878	53264383	0.4625	18.8501
chr14	107349540	58161953	0.5418	34.2844
chr15	102531392	43856914	0.4277	12.7164
chr16	90354753	64201142	0.7105	24.2672
chr17	81195210	77967799	0.9603	25.2423
chr18	78077248	34614403	0.4433	19.1176
chr19	59128983	36352079	0.6148	17.2167
chr20	63025520	28020395	0.4446	12.5224
chr21	48129895	7005510	0.1456	4.7678
chr22	51304566	10619870	0.207	5.8996
chrMT	16571	2637	0.1591	0.5032
chrX	155270560	104602293	0.6737	27.1823

chrY	59373566	4125662	0.0695	3.7804
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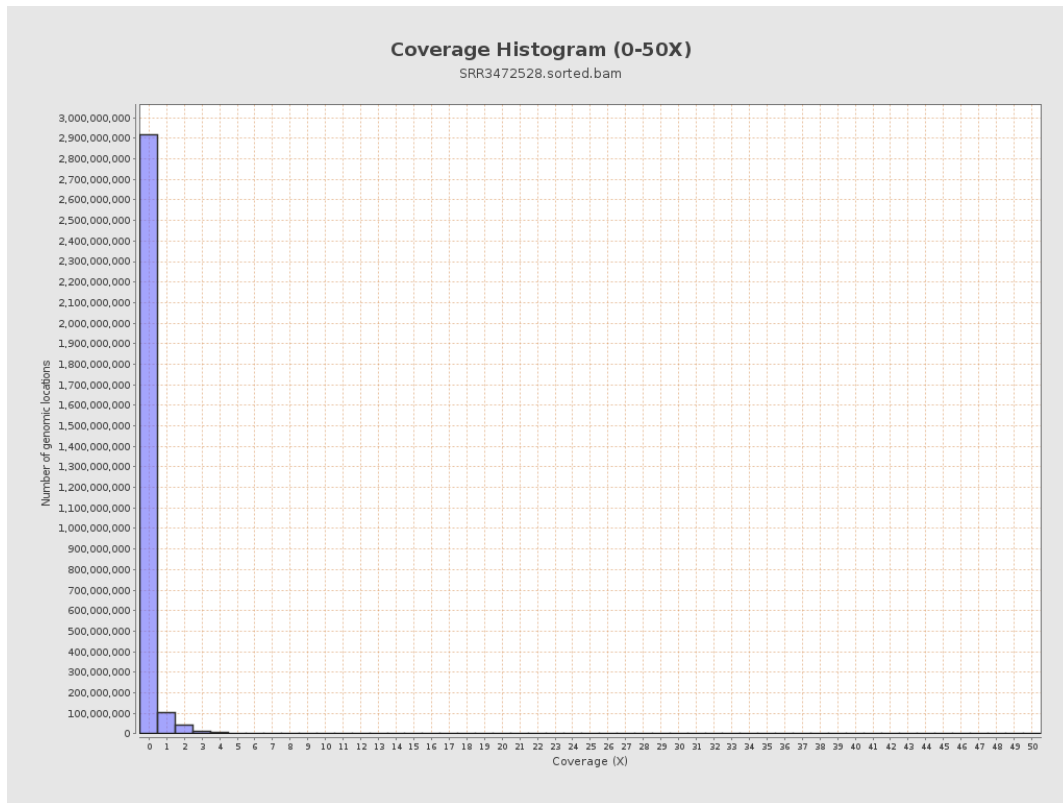
3. Results : Coverage across reference



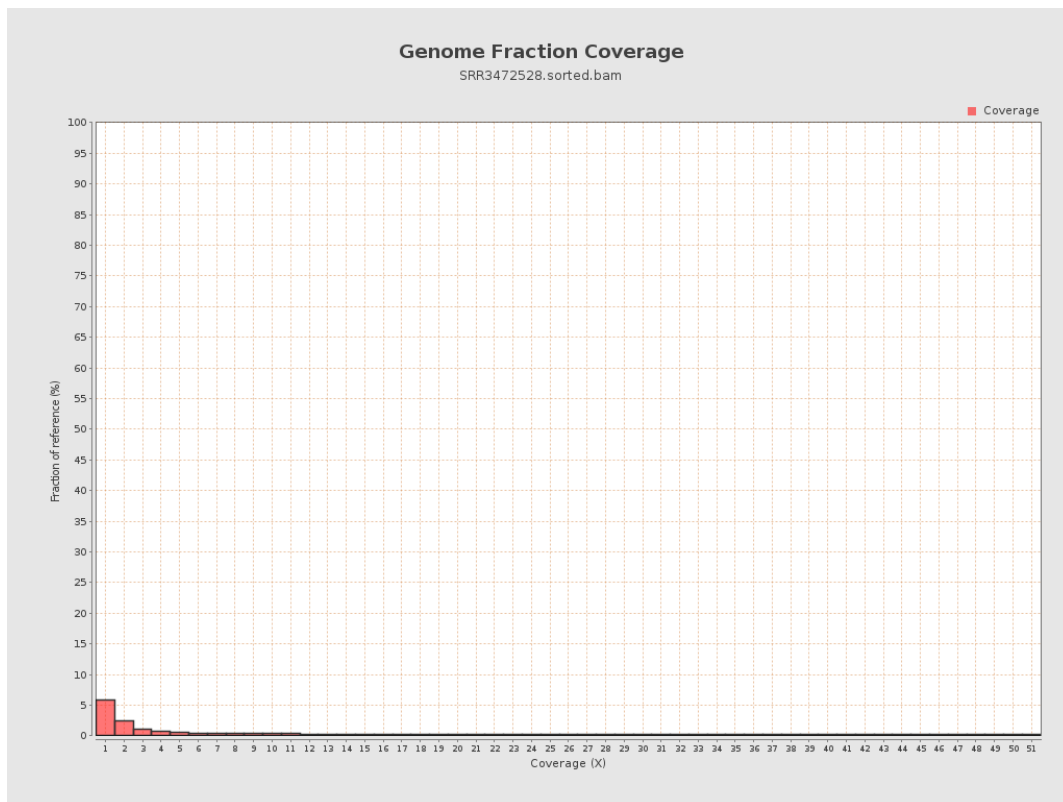
4. Results : Coverage Histogram



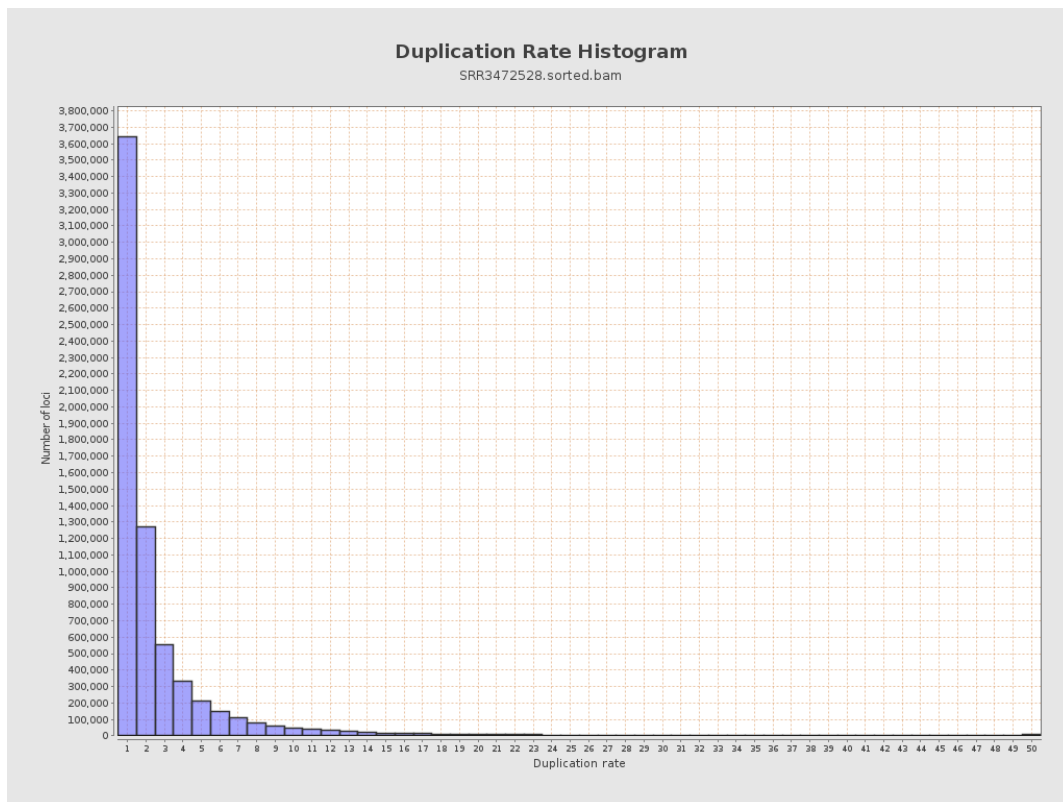
5. Results : Coverage Histogram (0-50X)



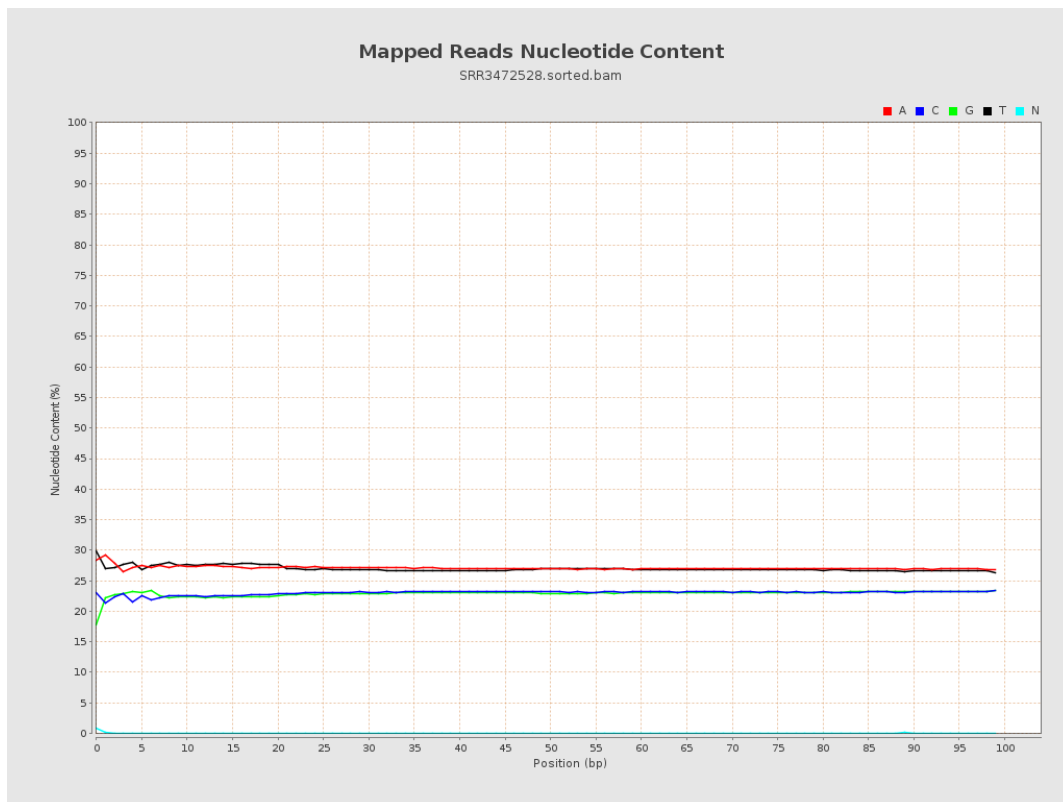
6. Results : Genome Fraction Coverage



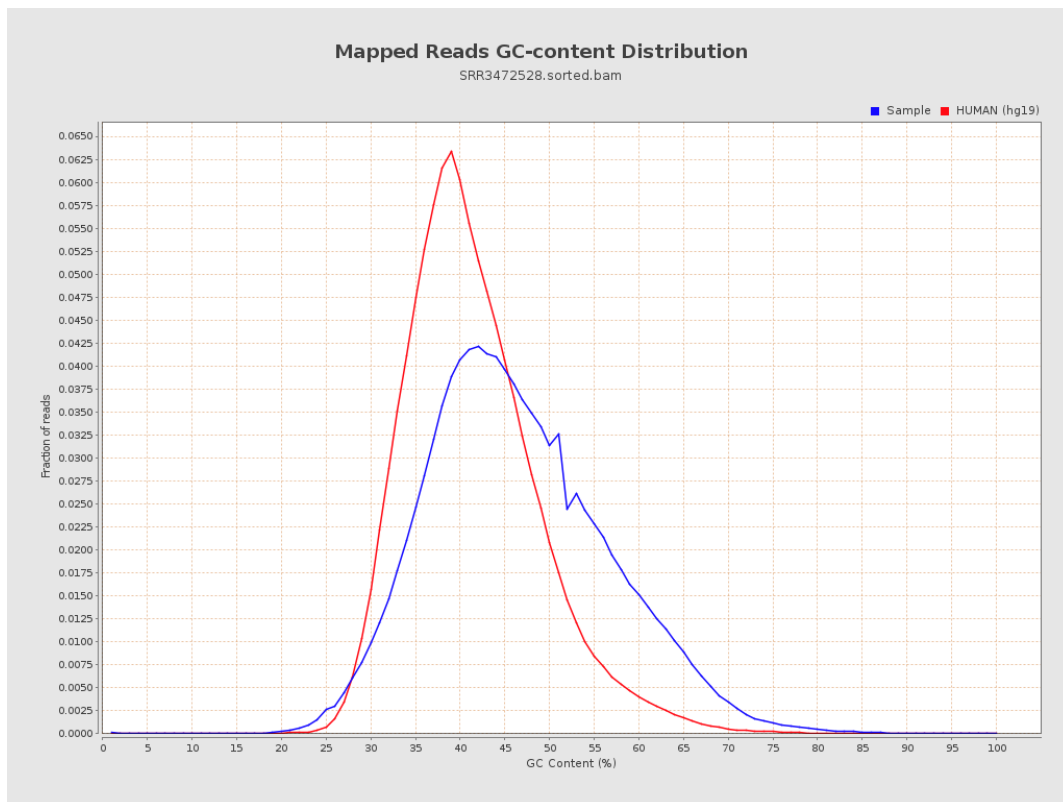
7. Results : Duplication Rate Histogram



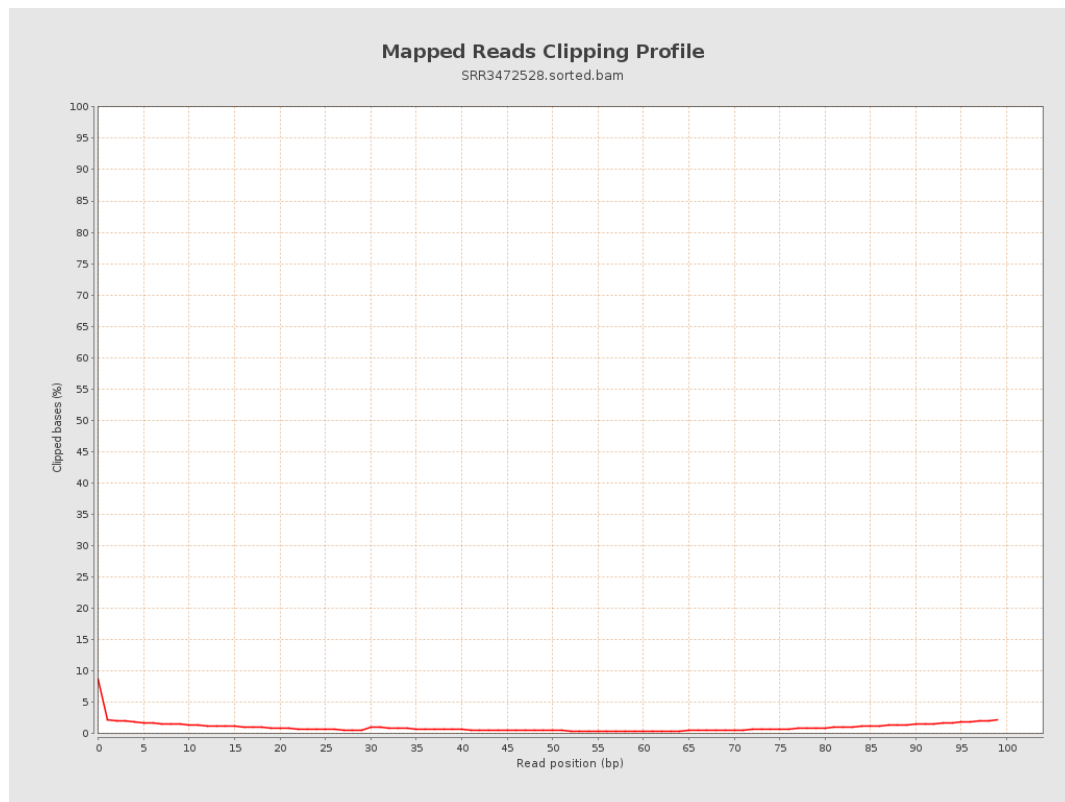
8. Results : Mapped Reads Nucleotide Content



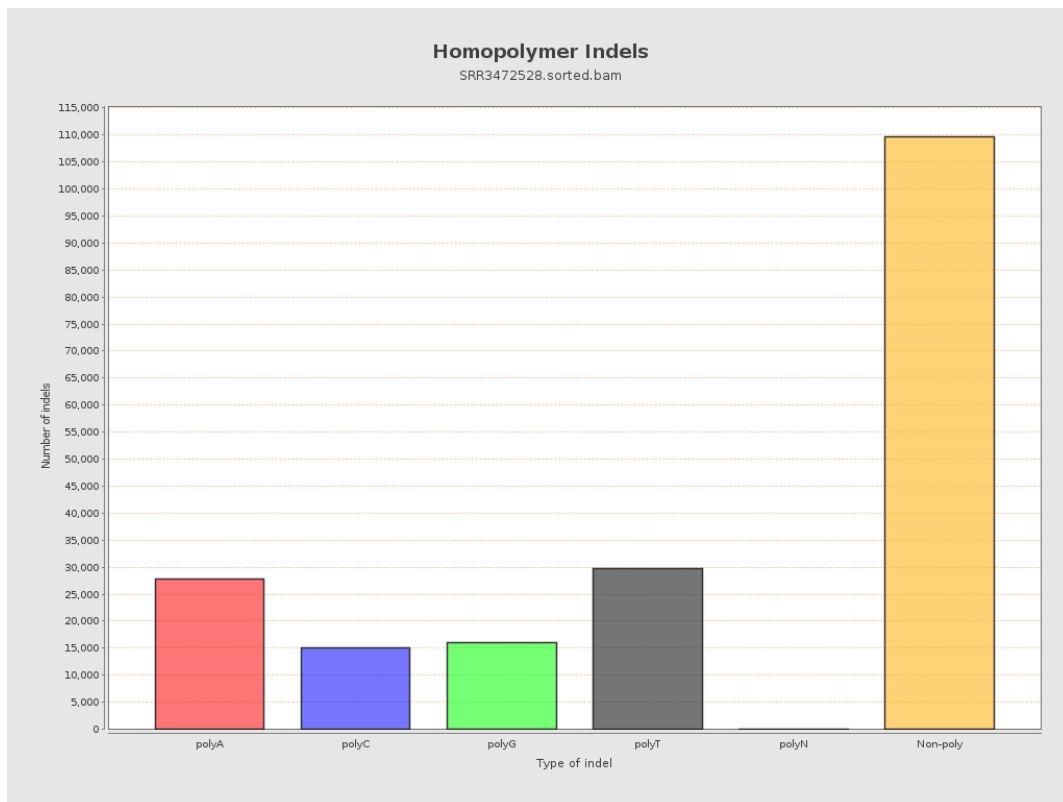
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



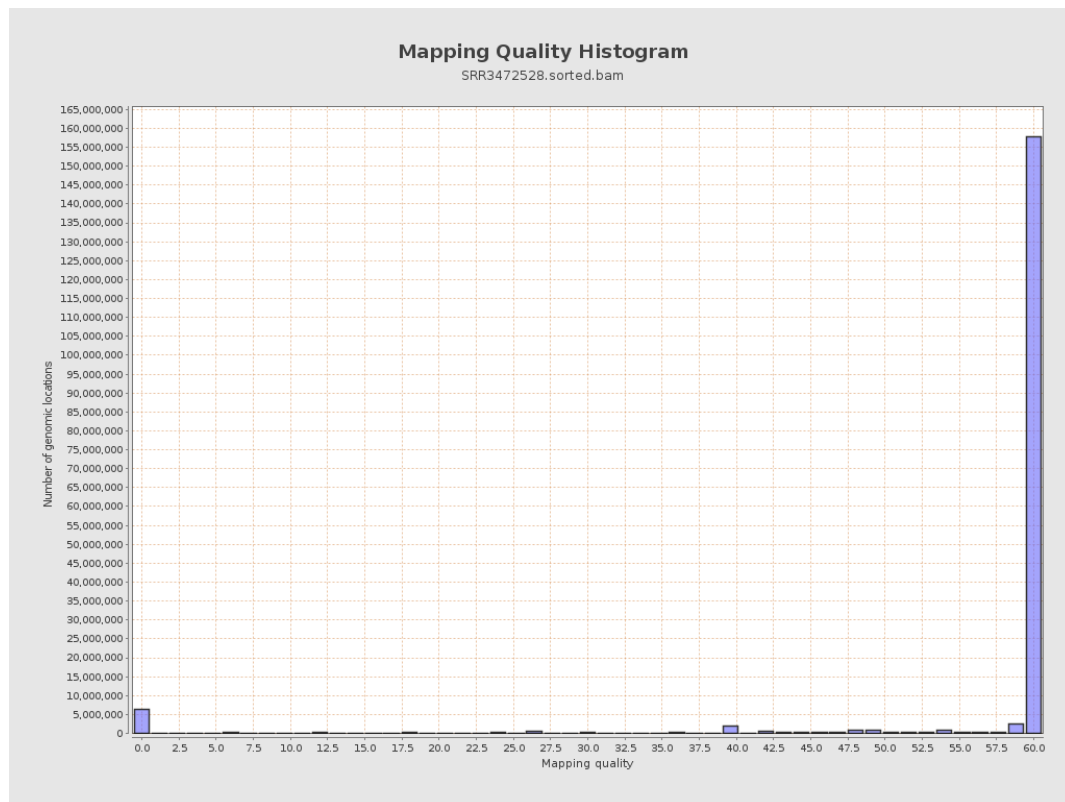
11. Results : Homopolymer Indels



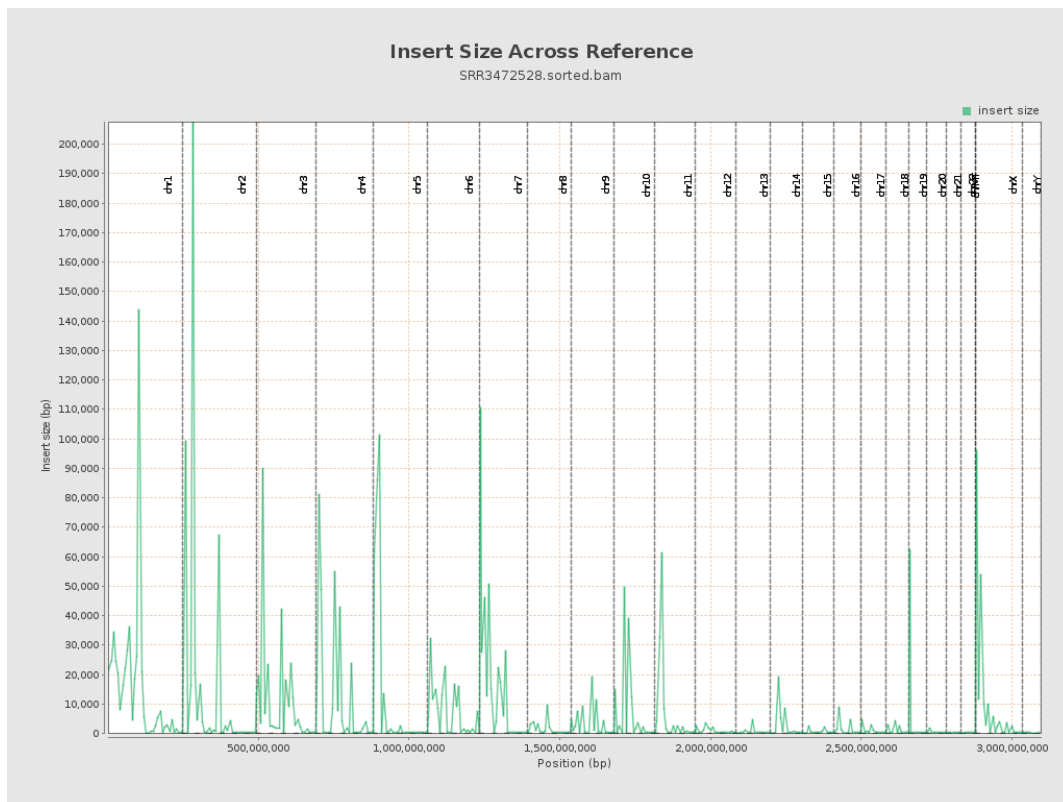
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

