

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:07:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472448.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_SRR3472448 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472448_1.fastq.gz SRR3472448_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:07:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472448.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,734,958
Mapped reads	17,567,064 / 99.05%
Unmapped reads	167,894 / 0.95%
Mapped paired reads	17,567,064 / 99.05%
Mapped reads, first in pair	8,811,654 / 49.69%
Mapped reads, second in pair	8,755,410 / 49.37%
Mapped reads, both in pair	17,467,584 / 98.49%
Mapped reads, singletons	99,480 / 0.56%
Secondary alignments	0
Supplementary alignments	71,175 / 0.4%
Read min/max/mean length	30 / 100 / 99.4
Duplicated reads (estimated)	11,048,226 / 62.3%
Duplication rate	47.12%
Clipped reads	1,137,709 / 6.42%

2.2. ACGT Content

Number/percentage of A's	473,568,714 / 27.45%
Number/percentage of C's	390,036,722 / 22.61%
Number/percentage of T's	475,005,324 / 27.53%
Number/percentage of G's	386,543,532 / 22.4%
Number/percentage of N's	210,493 / 0.01%

GC Percentage	45.01%
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2.3. Coverage

Mean	0.5574
Standard Deviation	17.4016

2.4. Mapping Quality

Mean Mapping Quality	54.77
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2.5. Insert size

Mean	18,392.6
Standard Deviation	1,313,691.42
P25/Median/P75	162 / 226 / 304

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	9,591,093
Insertions	111,624
Mapped reads with at least one insertion	0.63%
Deletions	87,658
Mapped reads with at least one deletion	0.49%
Homopolymer indels	46.16%

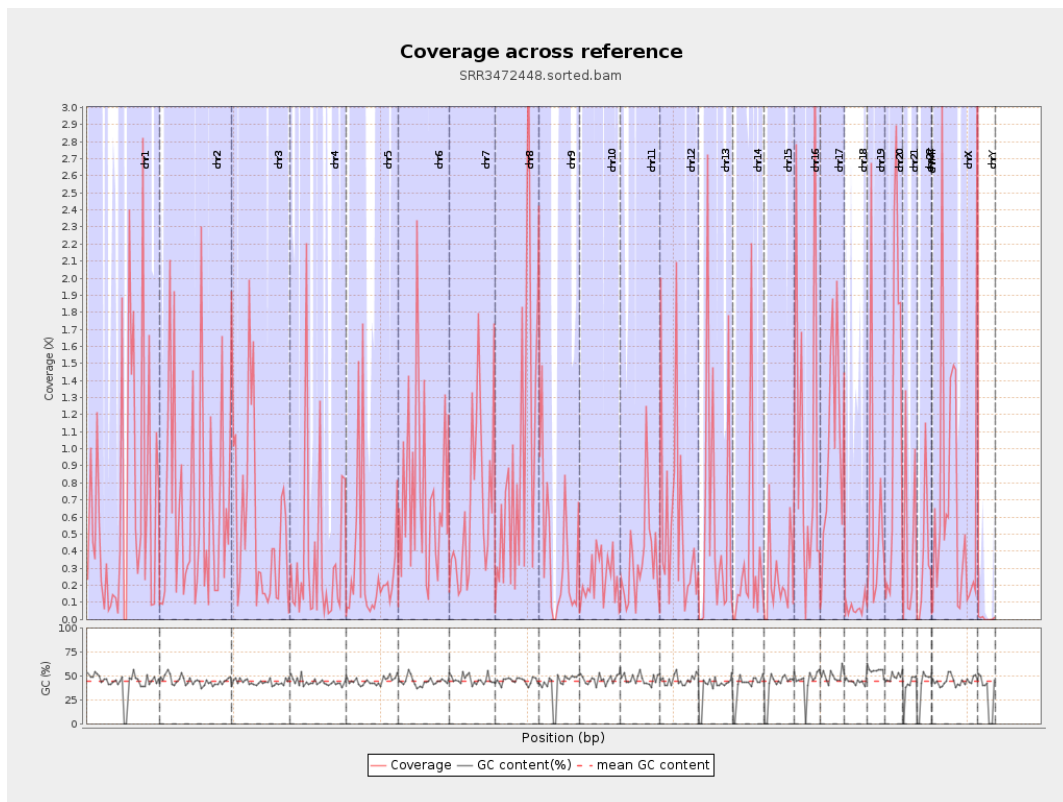
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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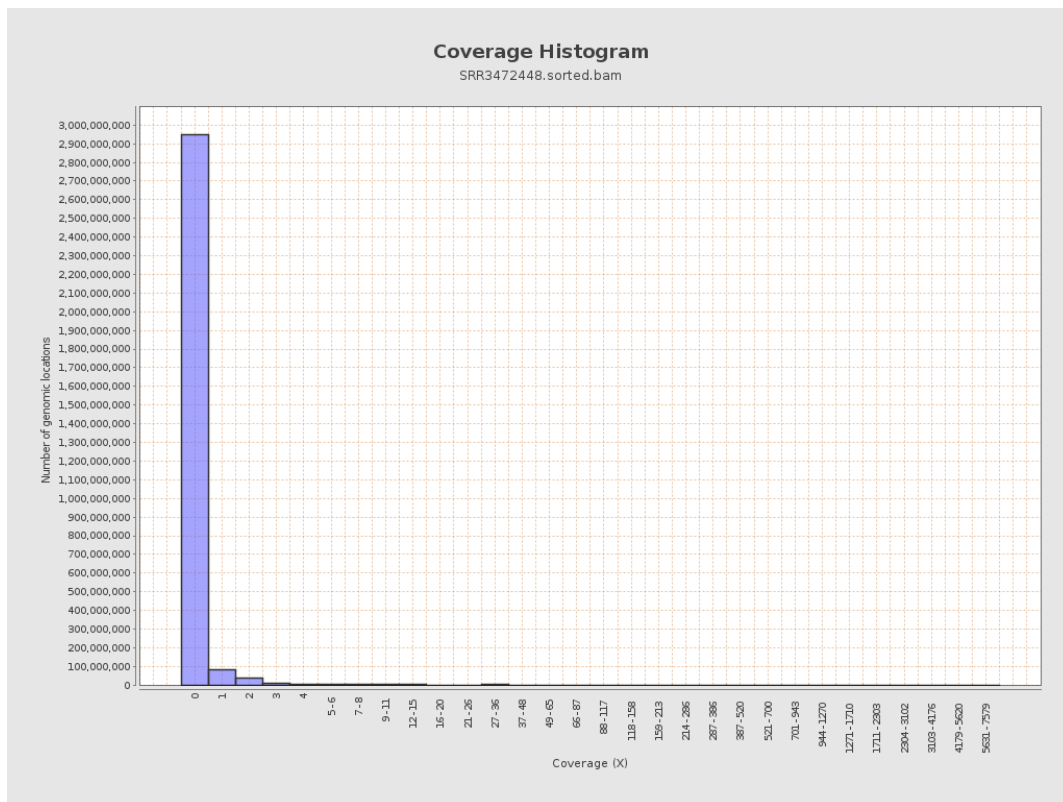
		bases	coverage	deviation
chr1	249250621	167457106	0.6718	20.8383
chr2	243199373	161901205	0.6657	21.018
chr3	198022430	112449172	0.5679	12.4487
chr4	191154276	65226579	0.3412	14.7446
chr5	180915260	58476107	0.3232	11.6352
chr6	171115067	124284106	0.7263	15.3167
chr7	159138663	106446277	0.6689	20.2131
chr8	146364022	141802419	0.9688	28.4616
chr9	141213431	57386198	0.4064	10.7798
chr10	135534747	32882396	0.2426	8.6128
chr11	135006516	46283832	0.3428	10.824
chr12	133851895	77617752	0.5799	14.4256
chr13	115169878	67896362	0.5895	20.7276
chr14	107349540	33225499	0.3095	11.0261
chr15	102531392	25402324	0.2478	7.9328
chr16	90354753	92955307	1.0288	24.6382
chr17	81195210	85697869	1.0555	24.161
chr18	78077248	5442309	0.0697	1.8925
chr19	59128983	40770374	0.6895	15.3369
chr20	63025520	77531263	1.2302	29.8087
chr21	48129895	22137287	0.4599	21.7789
chr22	51304566	17700805	0.345	12.1695
chrMT	16571	1652	0.0997	0.533
chrX	155270560	104276469	0.6716	19.5093

chrY	59373566	317863	0.0054	0.3612
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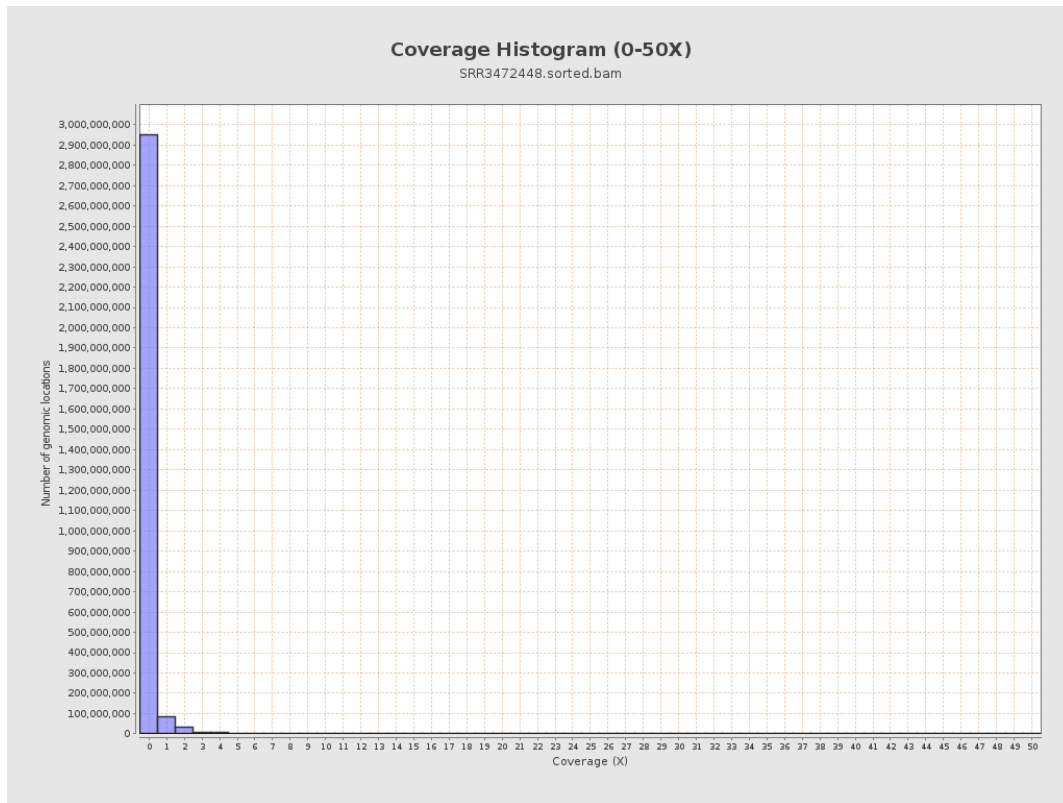
3. Results : Coverage across reference



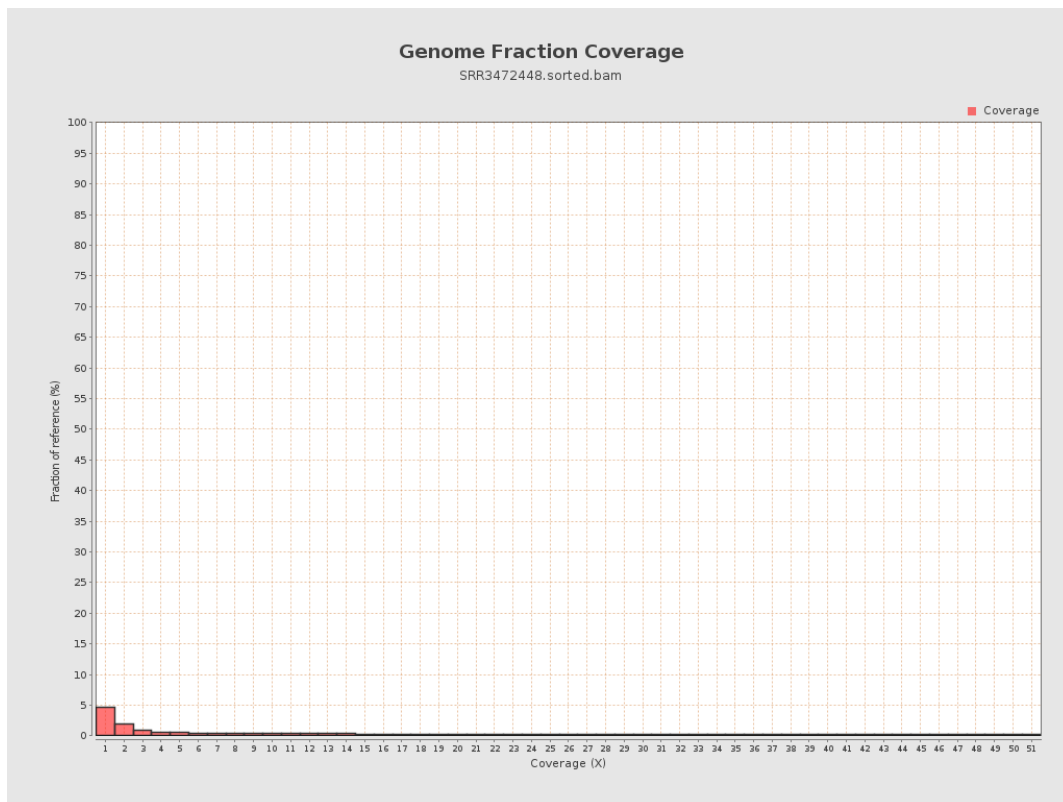
4. Results : Coverage Histogram



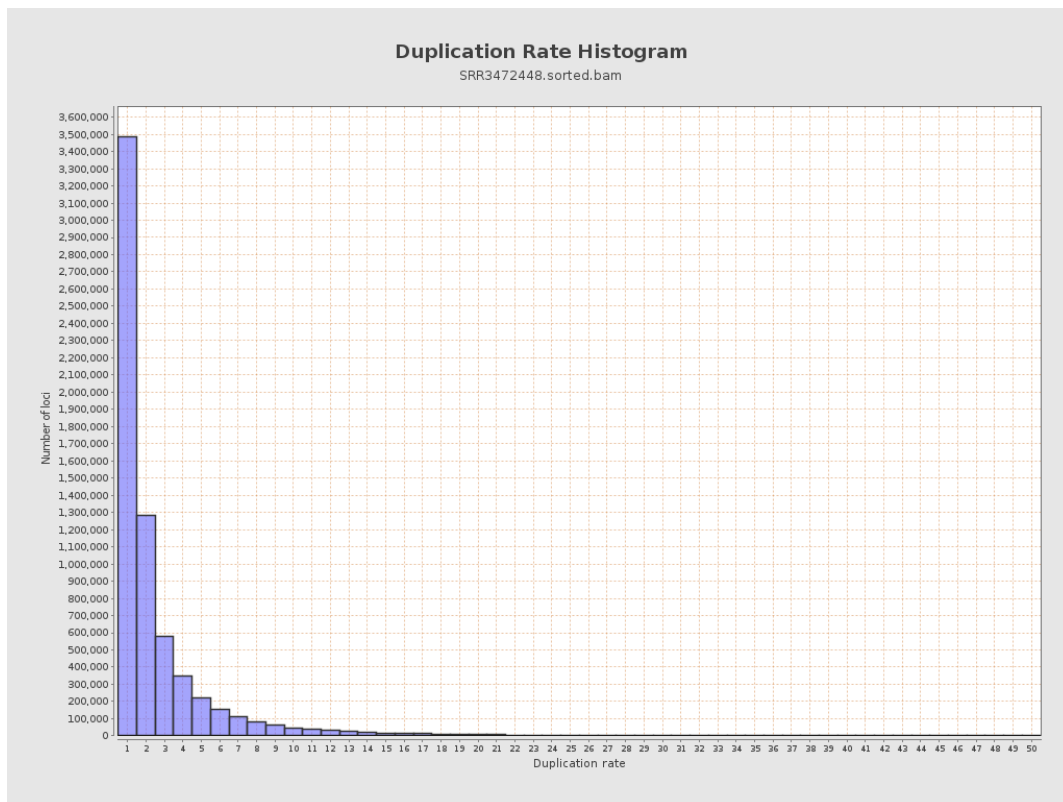
5. Results : Coverage Histogram (0-50X)



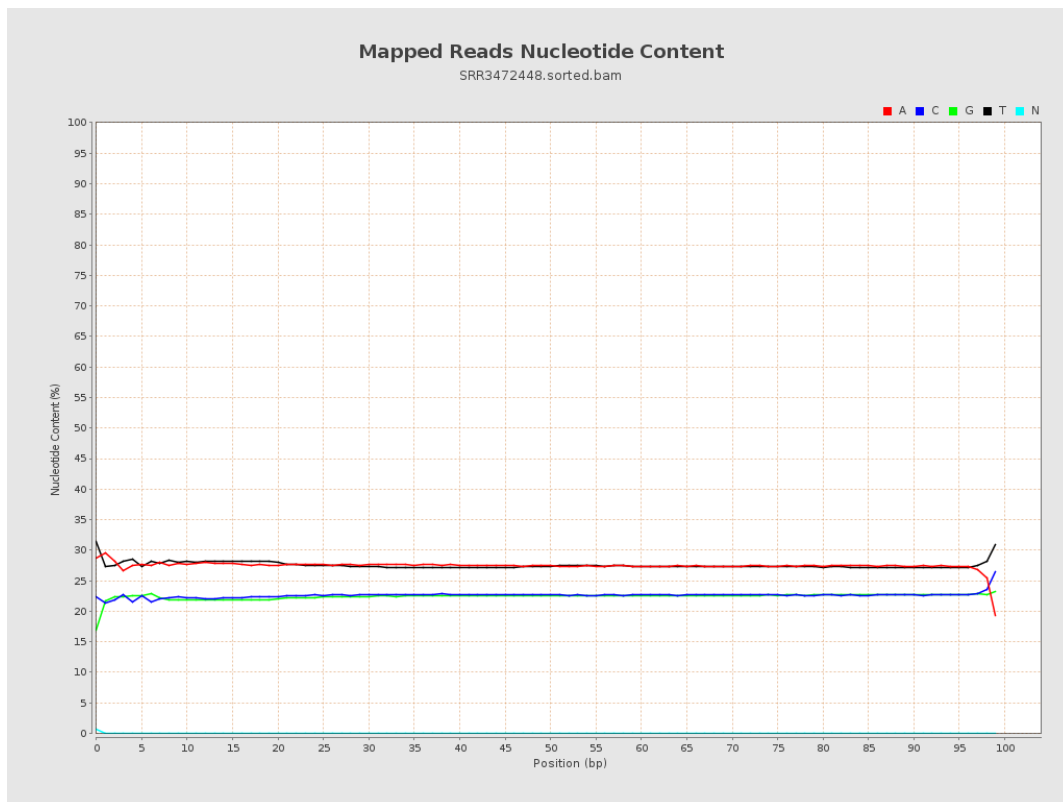
6. Results : Genome Fraction Coverage



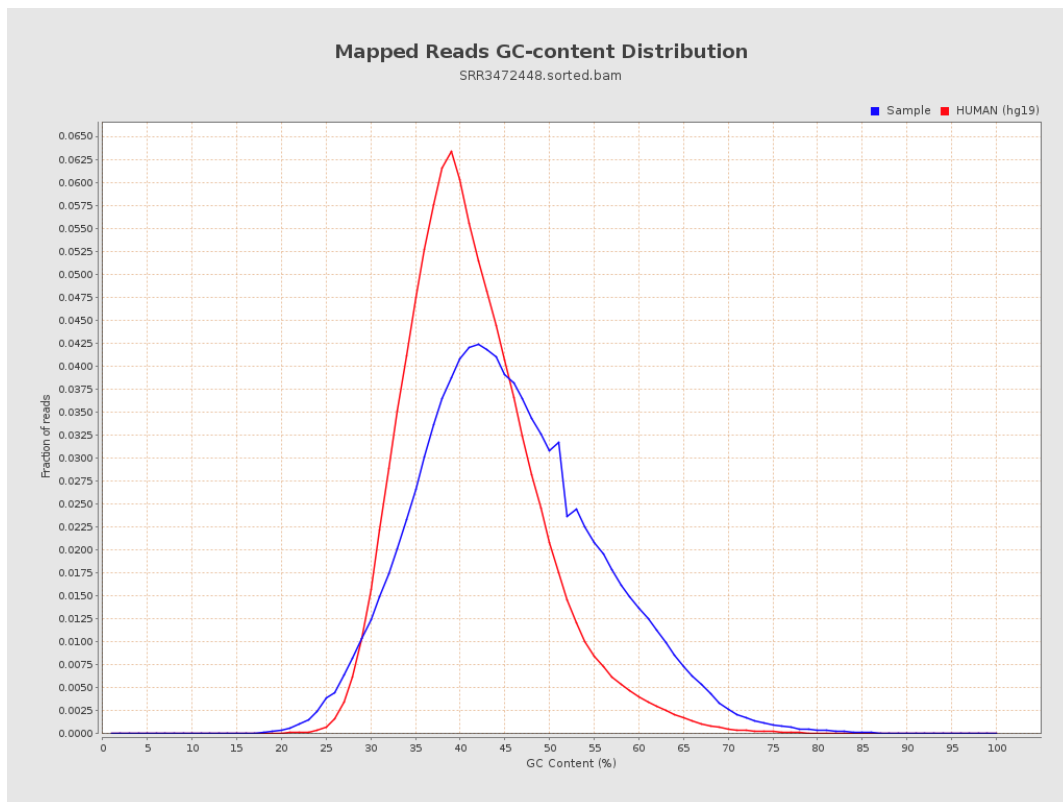
7. Results : Duplication Rate Histogram



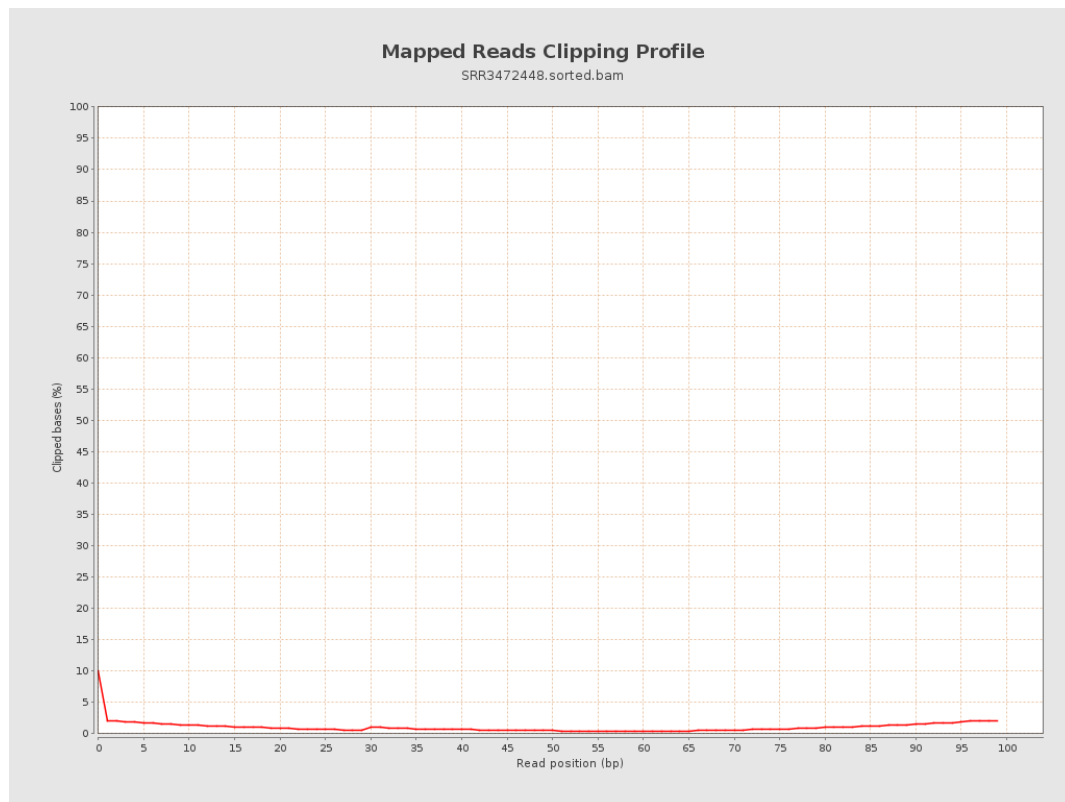
8. Results : Mapped Reads Nucleotide Content



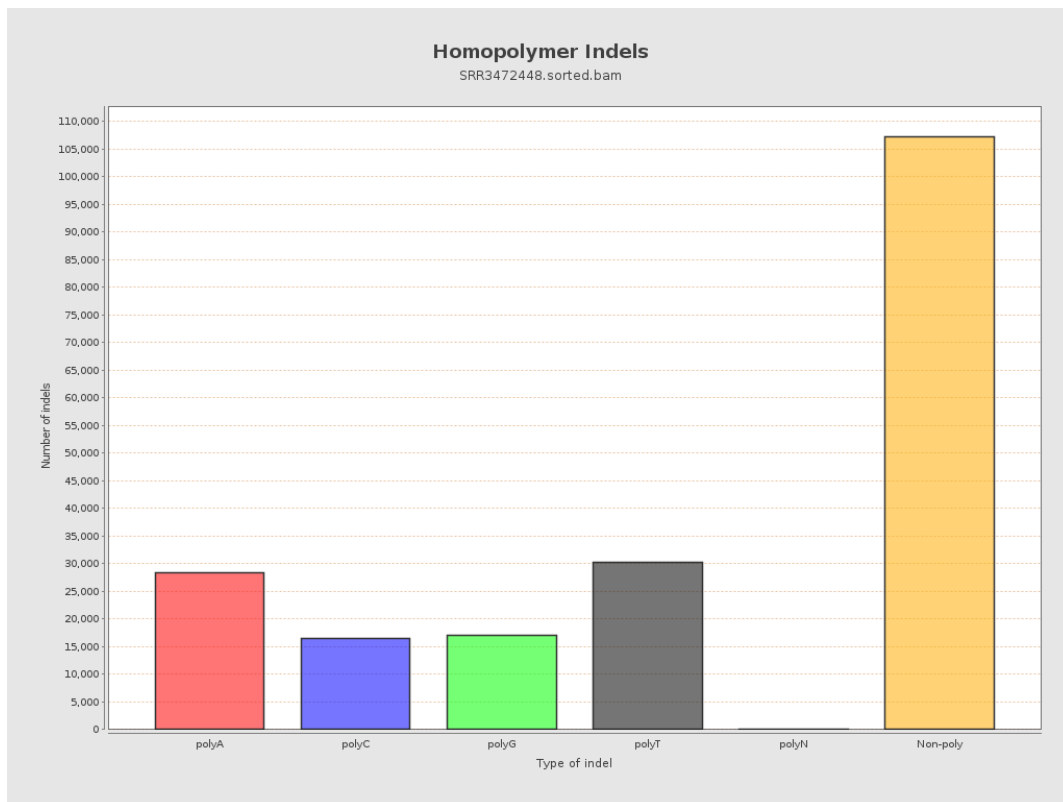
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



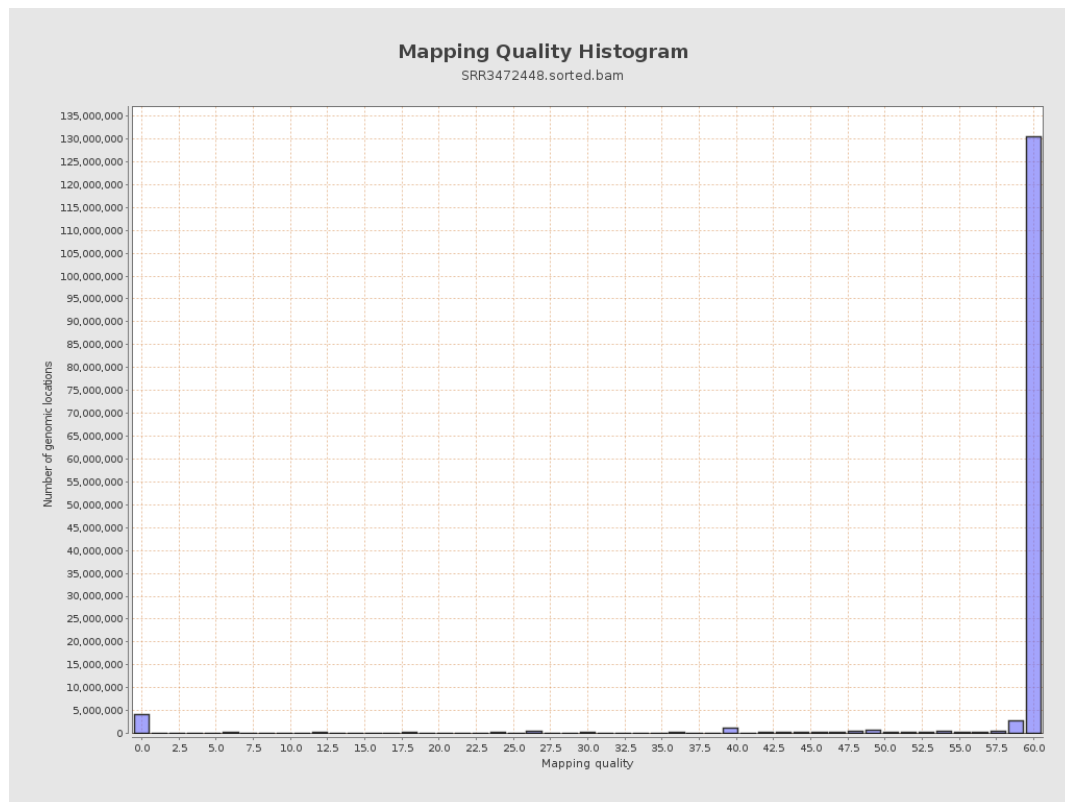
11. Results : Homopolymer Indels



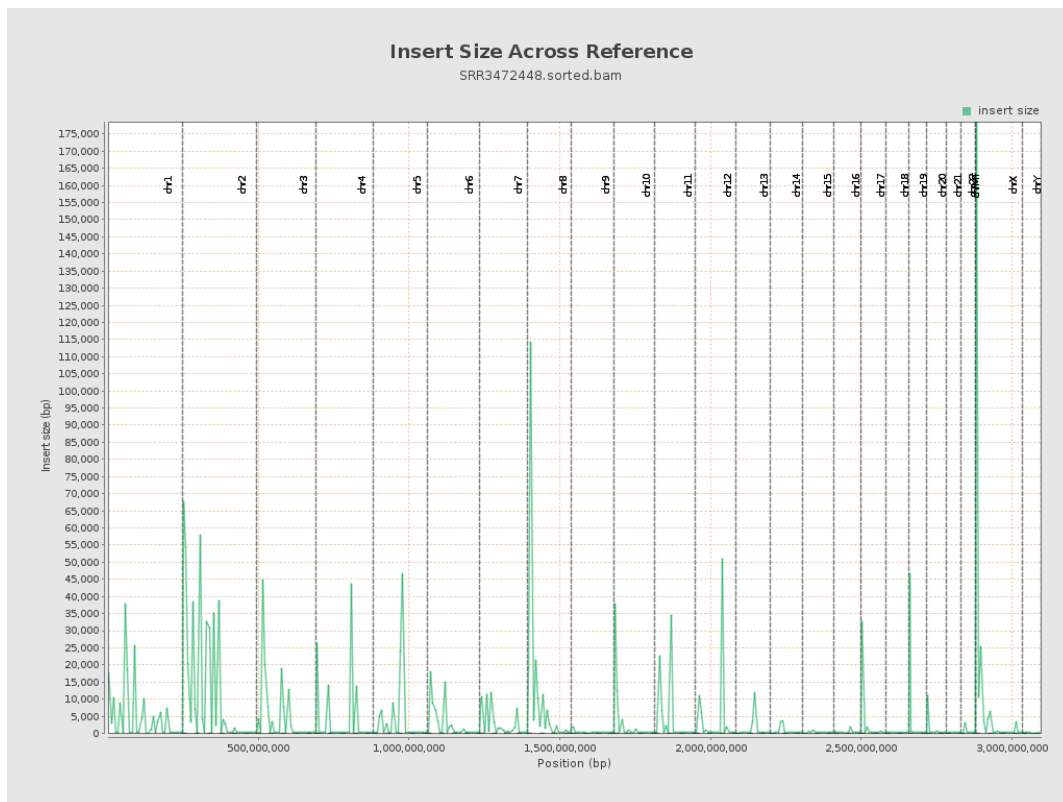
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

