

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 23:52:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472734.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_SRR3472734 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472734_1.fastq.gz SRR3472734_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 23:52:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472734.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,513,370
Mapped reads	14,313,242 / 98.62%
Unmapped reads	200,128 / 1.38%
Mapped paired reads	14,313,242 / 98.62%
Mapped reads, first in pair	7,201,493 / 49.62%
Mapped reads, second in pair	7,111,749 / 49%
Mapped reads, both in pair	14,190,530 / 97.78%
Mapped reads, singletons	122,712 / 0.85%
Secondary alignments	0
Supplementary alignments	49,149 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	8,412,716 / 57.97%
Duplication rate	45.84%
Clipped reads	1,140,287 / 7.86%

2.2. ACGT Content

Number/percentage of A's	394,736,750 / 28%
Number/percentage of C's	313,649,278 / 22.24%
Number/percentage of T's	390,613,147 / 27.7%
Number/percentage of G's	310,735,492 / 22.04%
Number/percentage of N's	257,886 / 0.02%

GC Percentage	44.28%
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2.3. Coverage

Mean	0.4555
Standard Deviation	13.9229

2.4. Mapping Quality

Mean Mapping Quality	55.35
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2.5. Insert size

Mean	22,824.17
Standard Deviation	1,494,418.87
P25/Median/P75	181 / 254 / 342

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	11,142,002
Insertions	84,401
Mapped reads with at least one insertion	0.58%
Deletions	82,934
Mapped reads with at least one deletion	0.57%
Homopolymer indels	45.39%

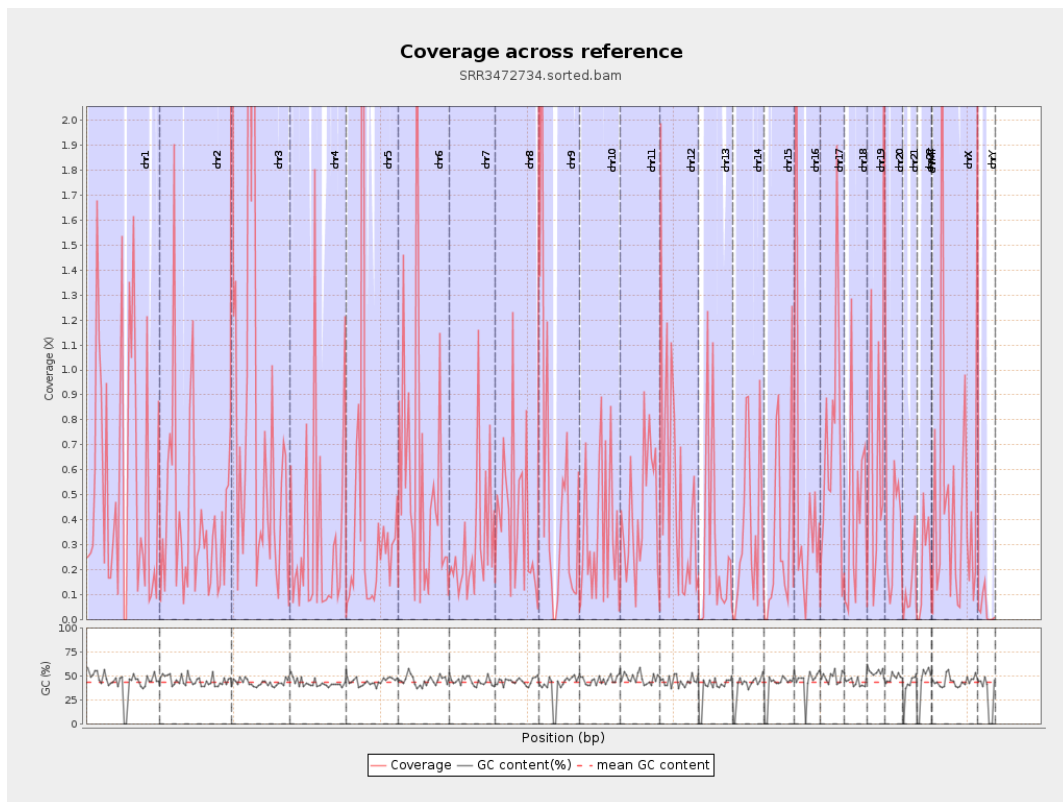
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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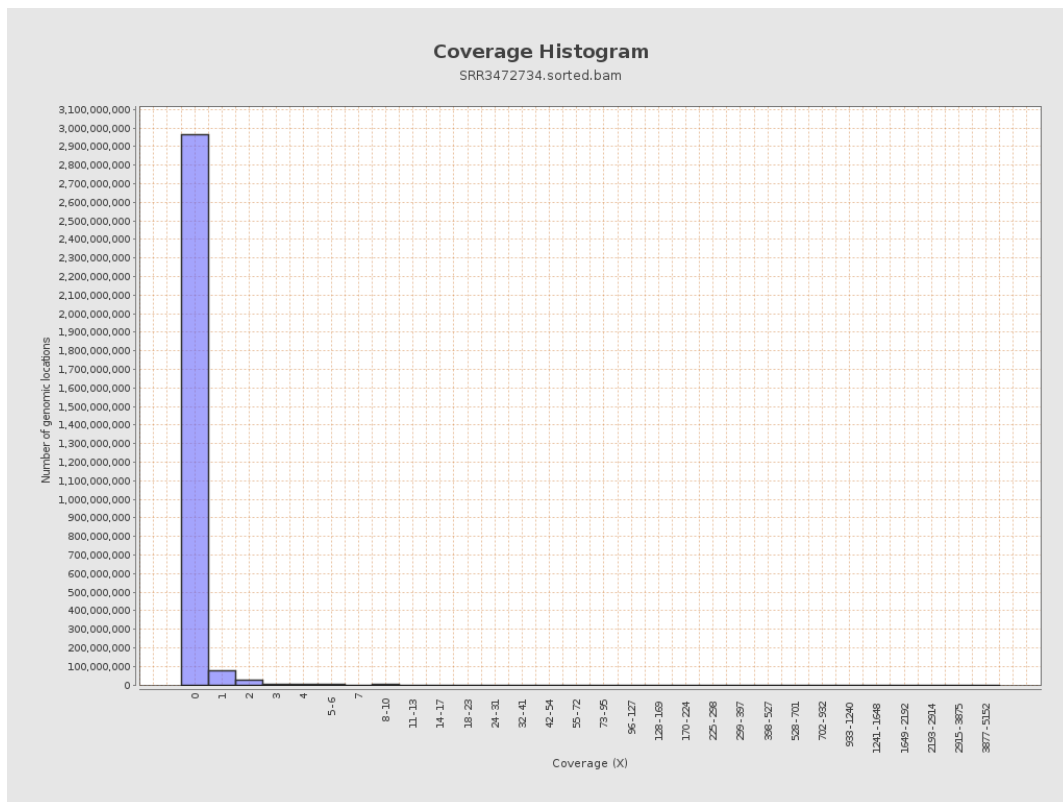
		bases	coverage	deviation
chr1	249250621	141242478	0.5667	16.496
chr2	243199373	99100692	0.4075	14.7128
chr3	198022430	173893009	0.8781	18.7328
chr4	191154276	59720854	0.3124	13.3861
chr5	180915260	79268481	0.4382	14.25
chr6	171115067	96268747	0.5626	17.2502
chr7	159138663	49887822	0.3135	9.2082
chr8	146364022	59217957	0.4046	13.2876
chr9	141213431	76170665	0.5394	11.9796
chr10	135534747	47089822	0.3474	12.645
chr11	135006516	58801621	0.4355	12.1839
chr12	133851895	70472595	0.5265	14.5922
chr13	115169878	33565867	0.2914	10.7478
chr14	107349540	36819051	0.343	11.0935
chr15	102531392	35041288	0.3418	11.7754
chr16	90354753	45352580	0.5019	12.3802
chr17	81195210	54600346	0.6725	14.029
chr18	78077248	32537517	0.4167	18.8224
chr19	59128983	39725469	0.6718	17.364
chr20	63025520	25764321	0.4088	10.6726
chr21	48129895	6400996	0.133	6.0345
chr22	51304566	11349751	0.2212	6.1471
chrMT	16571	3337	0.2014	0.5533
chrX	155270560	75335665	0.4852	14.1732

chrY	59373566	2562733	0.0432	1.8977
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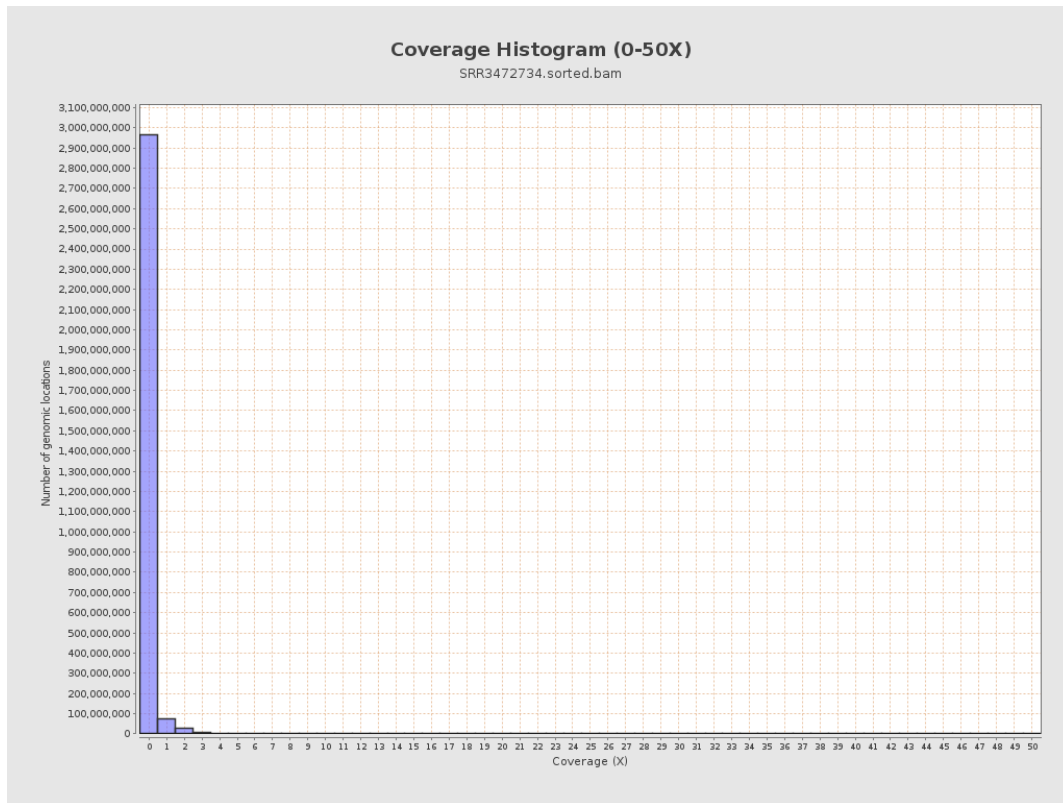
3. Results : Coverage across reference



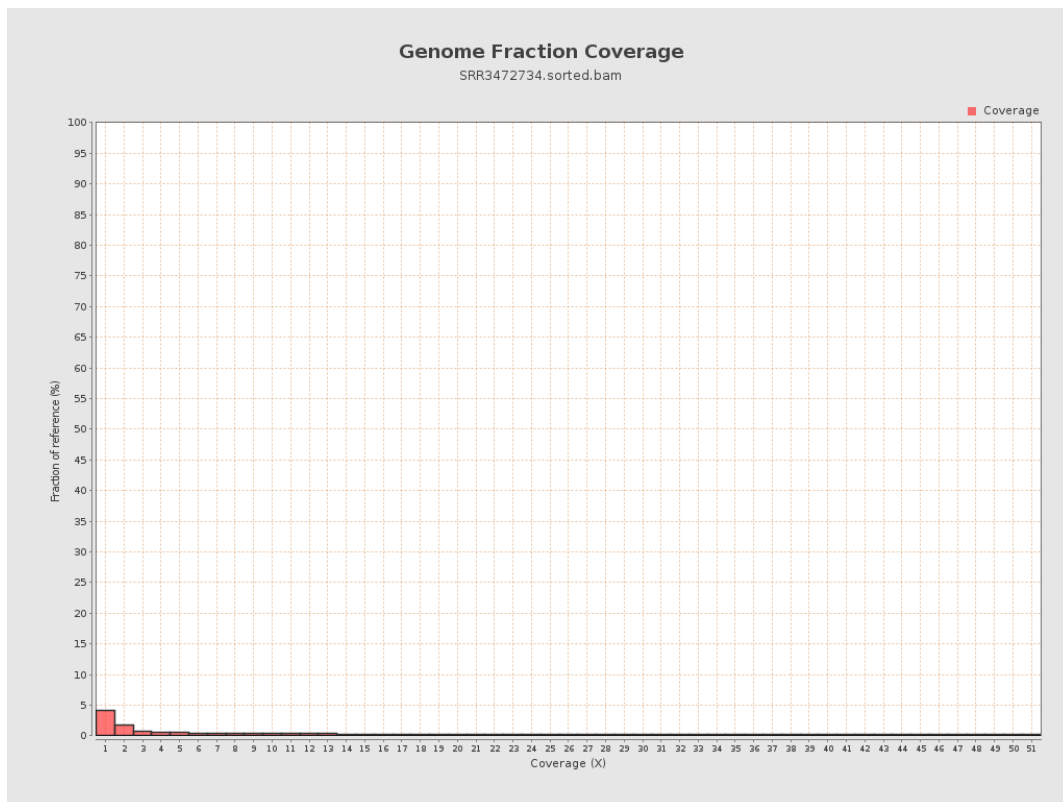
4. Results : Coverage Histogram



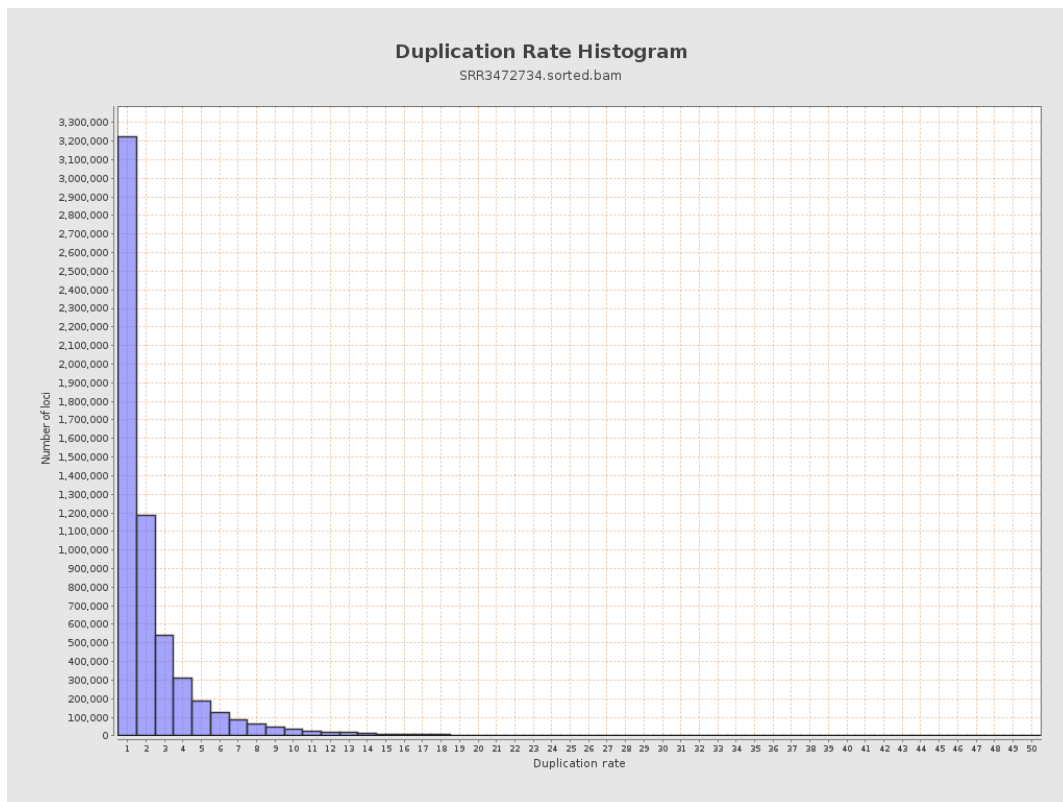
5. Results : Coverage Histogram (0-50X)



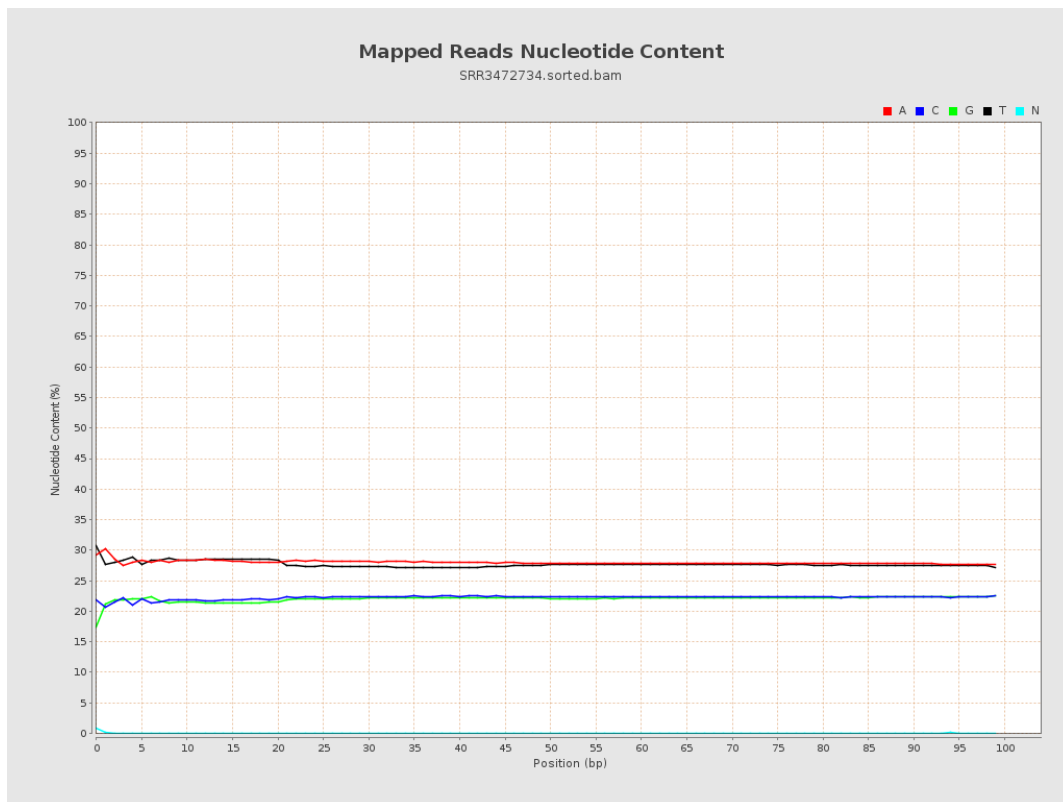
6. Results : Genome Fraction Coverage



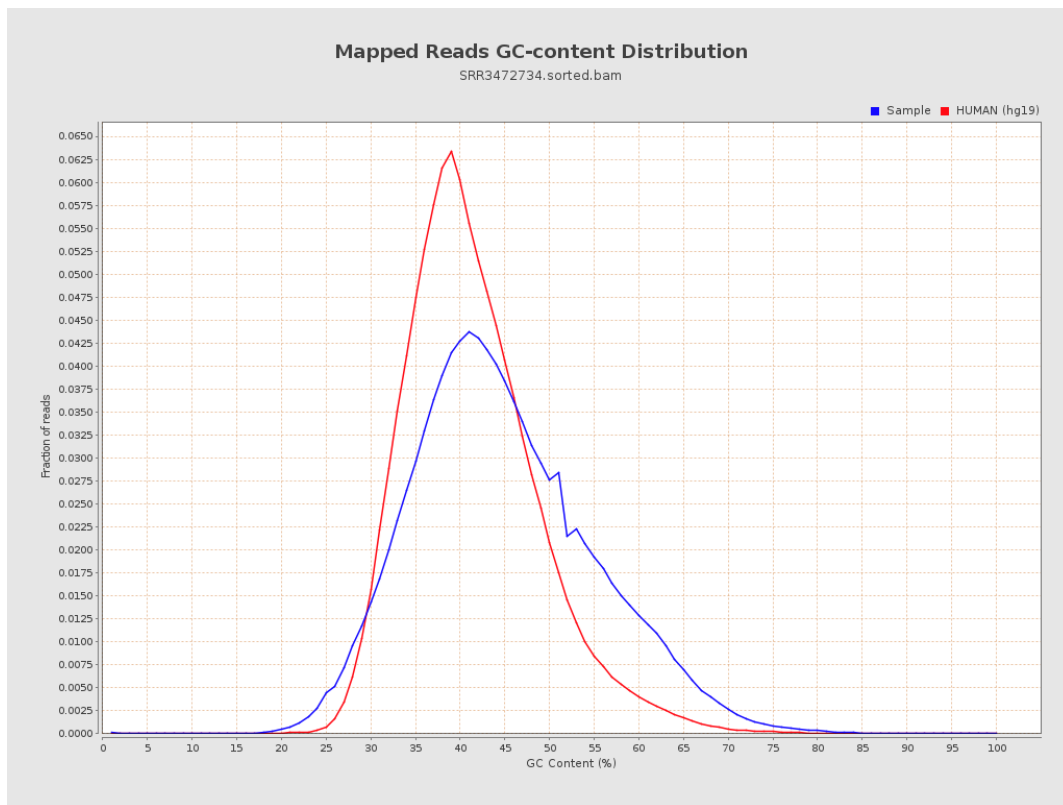
7. Results : Duplication Rate Histogram



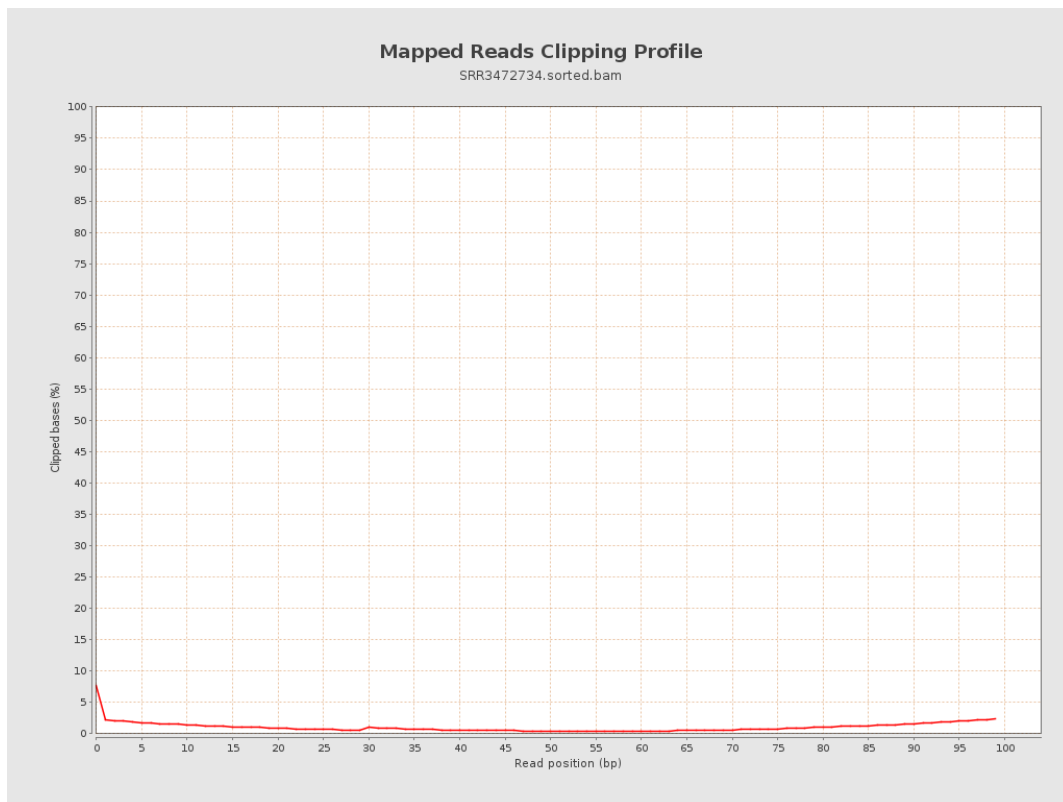
8. Results : Mapped Reads Nucleotide Content



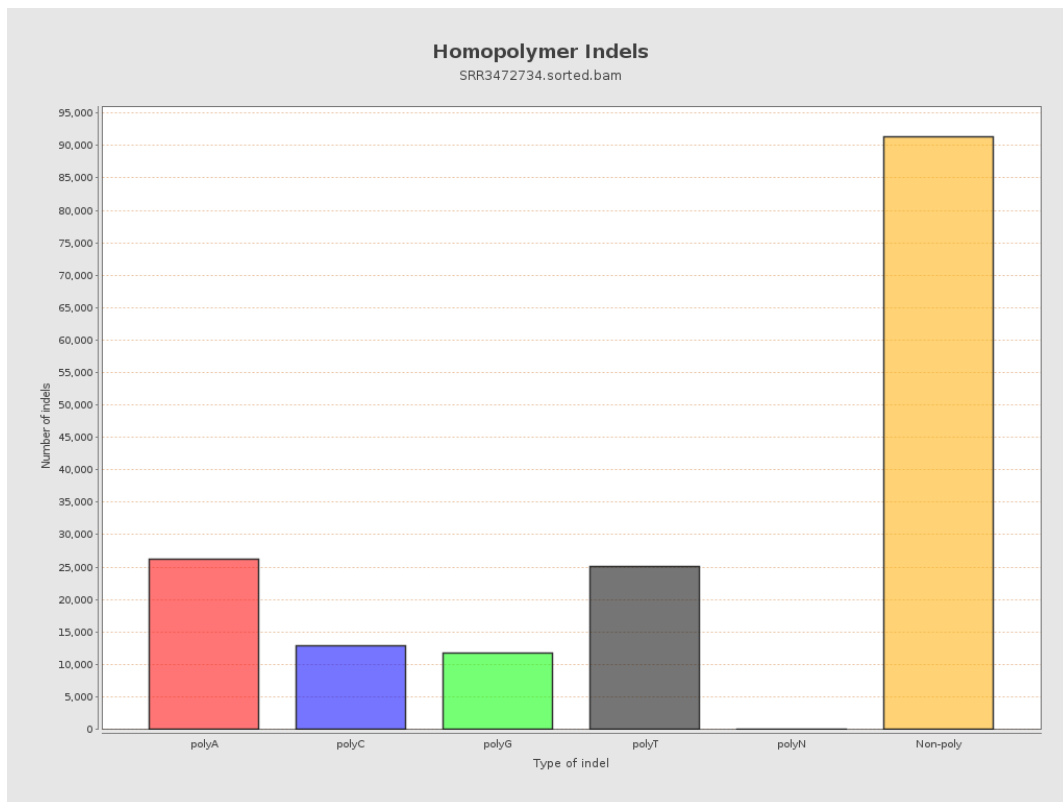
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



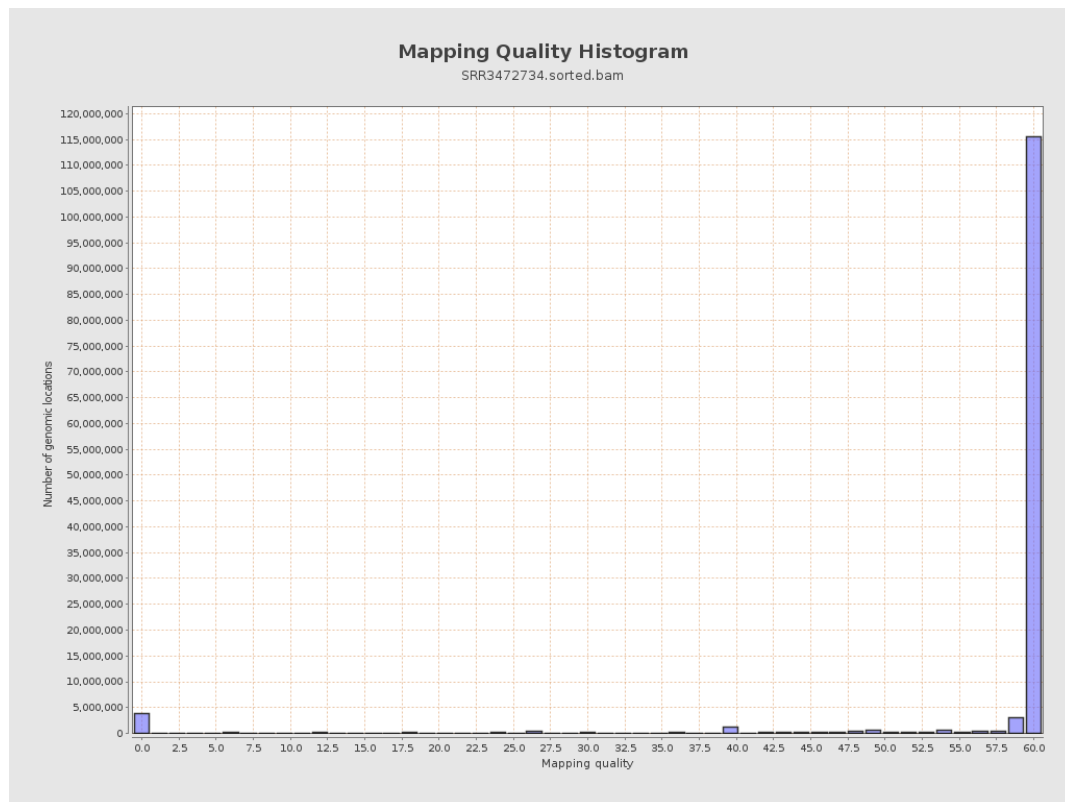
11. Results : Homopolymer Indels



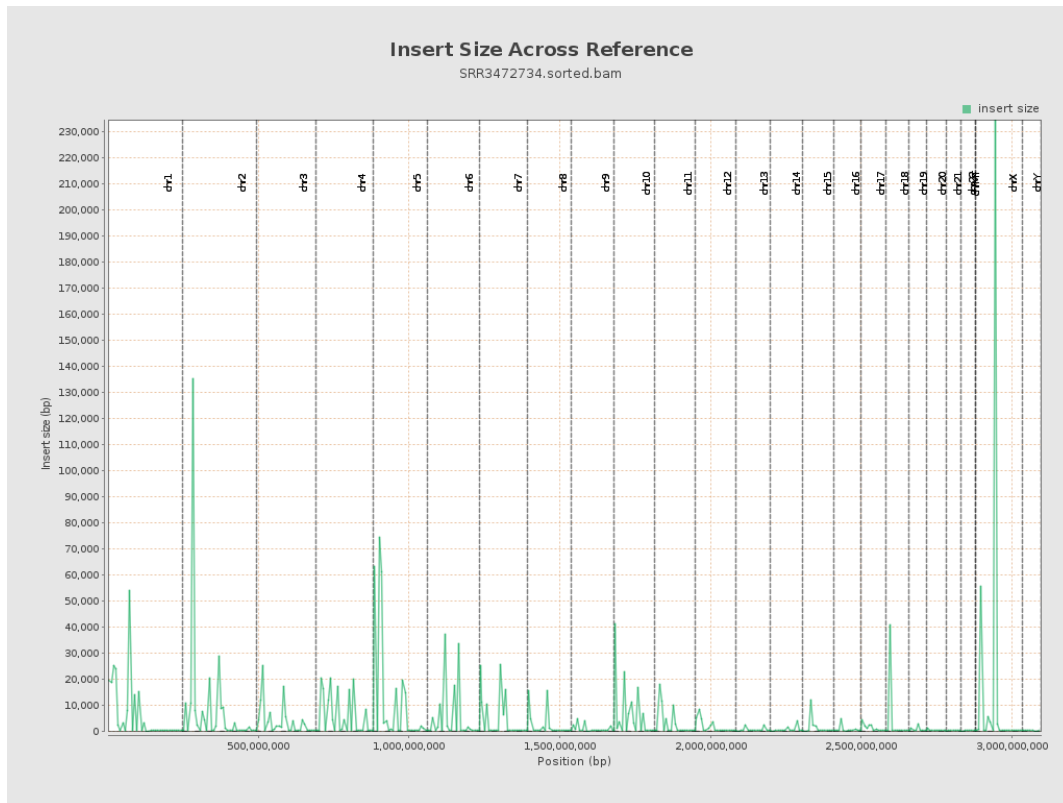
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

