

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:14:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472494.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_SRR3472494 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472494_1.fastq.gz SRR3472494_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:14:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472494.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,839,234
Mapped reads	18,568,693 / 98.56%
Unmapped reads	270,541 / 1.44%
Mapped paired reads	18,568,693 / 98.56%
Mapped reads, first in pair	9,322,213 / 49.48%
Mapped reads, second in pair	9,246,480 / 49.08%
Mapped reads, both in pair	18,430,432 / 97.83%
Mapped reads, singletons	138,261 / 0.73%
Secondary alignments	0
Supplementary alignments	66,269 / 0.35%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	11,534,104 / 61.22%
Duplication rate	46.64%
Clipped reads	1,555,551 / 8.26%

2.2. ACGT Content

Number/percentage of A's	506,651,104 / 27.76%
Number/percentage of C's	409,171,825 / 22.42%
Number/percentage of T's	503,138,183 / 27.56%
Number/percentage of G's	406,073,309 / 22.25%
Number/percentage of N's	278,965 / 0.02%

GC Percentage	44.66%
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2.3. Coverage

Mean	0.5897
Standard Deviation	17.805

2.4. Mapping Quality

Mean Mapping Quality	55.05
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2.5. Insert size

Mean	28,019.4
Standard Deviation	1,675,976.82
P25/Median/P75	176 / 248 / 336

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	11,797,475
Insertions	103,862
Mapped reads with at least one insertion	0.55%
Deletions	98,478
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.81%

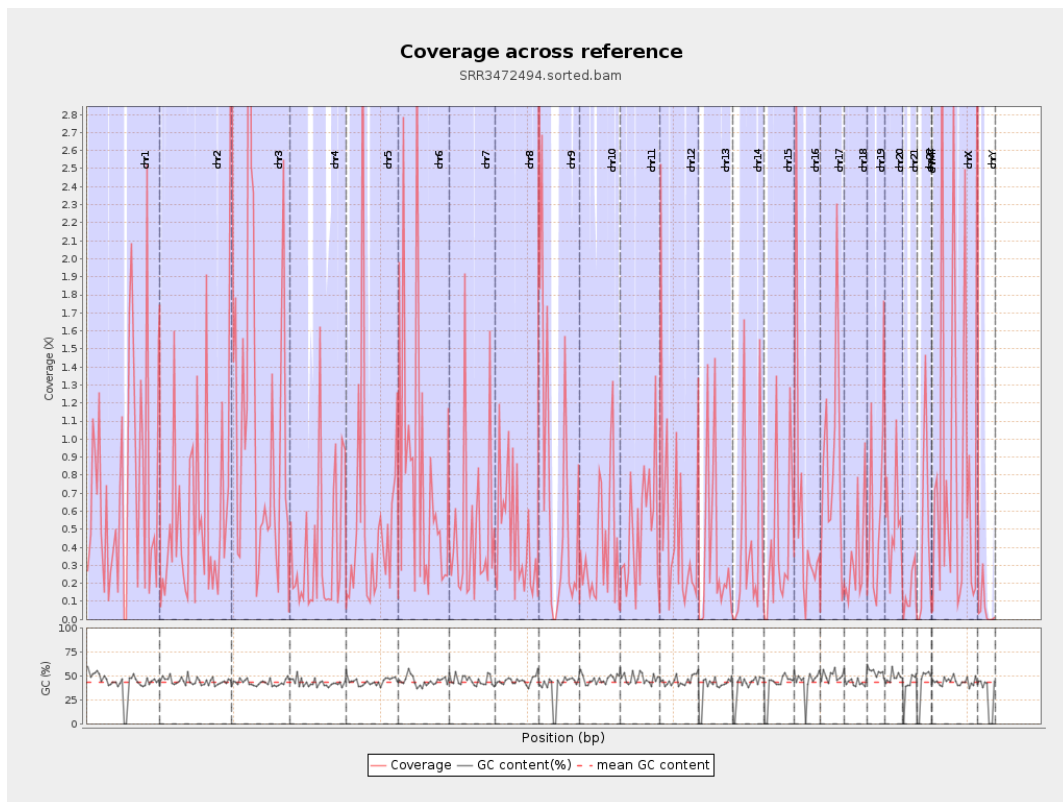
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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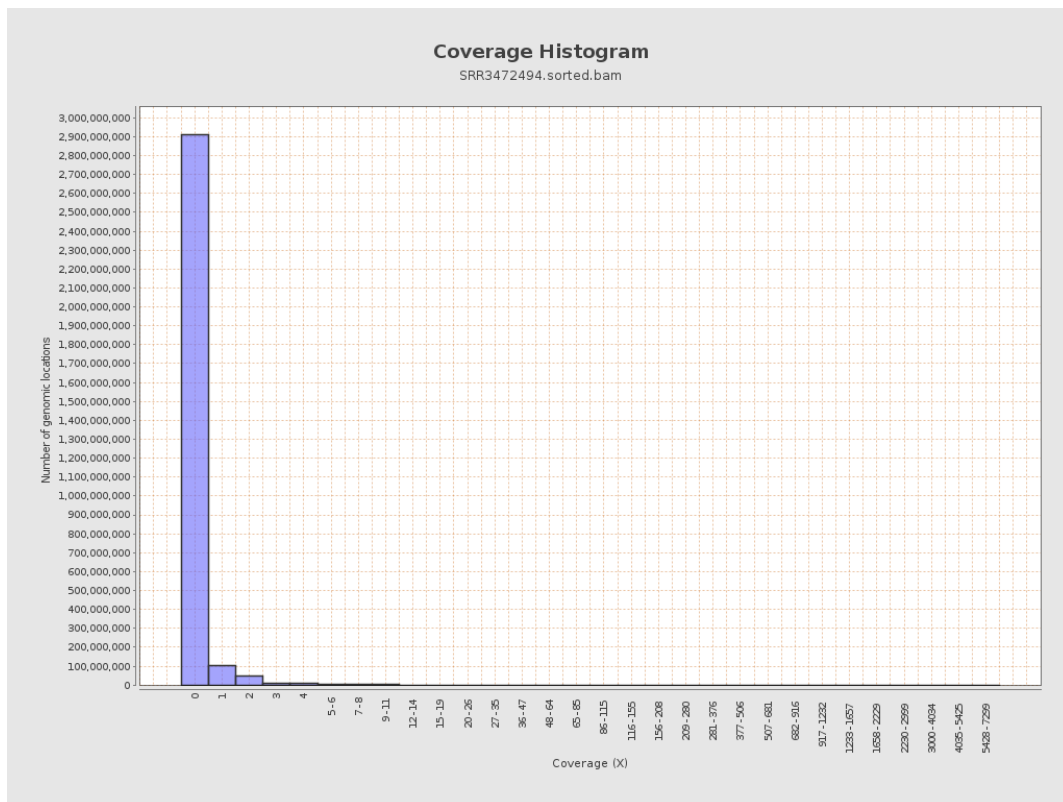
		bases	coverage	deviation
chr1	249250621	184132175	0.7387	18.5897
chr2	243199373	139401451	0.5732	21.8254
chr3	198022430	236495651	1.1943	25.5912
chr4	191154276	70553880	0.3691	14.0883
chr5	180915260	101626856	0.5617	16.5439
chr6	171115067	137894588	0.8059	20.9651
chr7	159138663	76714629	0.4821	15.8758
chr8	146364022	67897995	0.4639	13.474
chr9	141213431	99971002	0.7079	16.2396
chr10	135534747	54356921	0.4011	15.6232
chr11	135006516	68740334	0.5092	13.4354
chr12	133851895	71090925	0.5311	14.7482
chr13	115169878	44055669	0.3825	14.9283
chr14	107349540	43293950	0.4033	19.5032
chr15	102531392	42865537	0.4181	16.4638
chr16	90354753	51119964	0.5658	13.7641
chr17	81195210	66869518	0.8236	18.8585
chr18	78077248	28170315	0.3608	10.5694
chr19	59128983	34685974	0.5866	15.5115
chr20	63025520	34320631	0.5446	14.2408
chr21	48129895	7278101	0.1512	5.6939
chr22	51304566	23064479	0.4496	13.9419
chrMT	16571	2161	0.1304	0.5129
chrX	155270560	137379139	0.8848	26.4397

chrY	59373566	3580551	0.0603	2.2557
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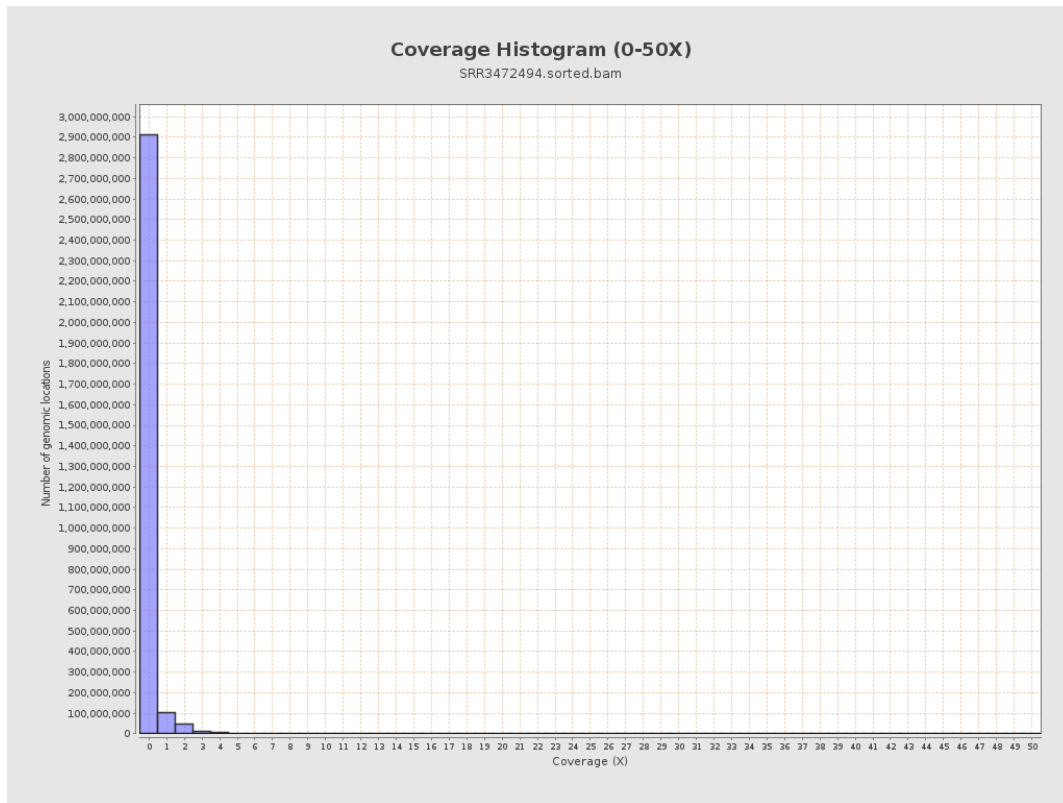
3. Results : Coverage across reference



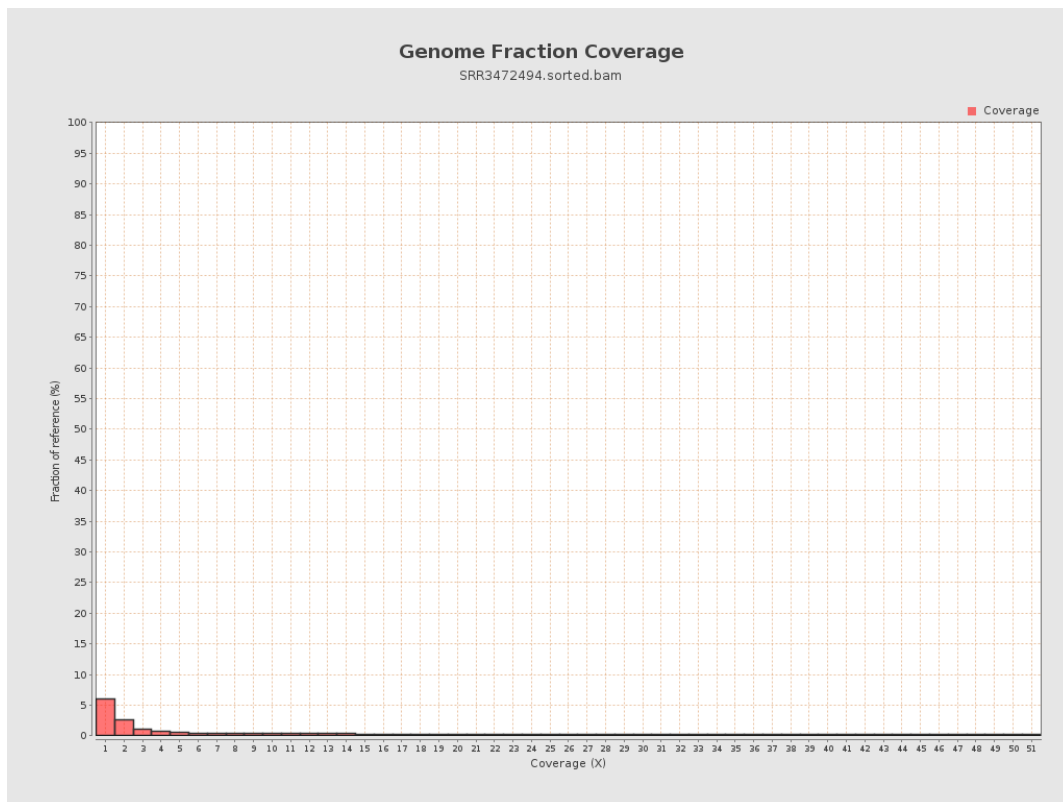
4. Results : Coverage Histogram



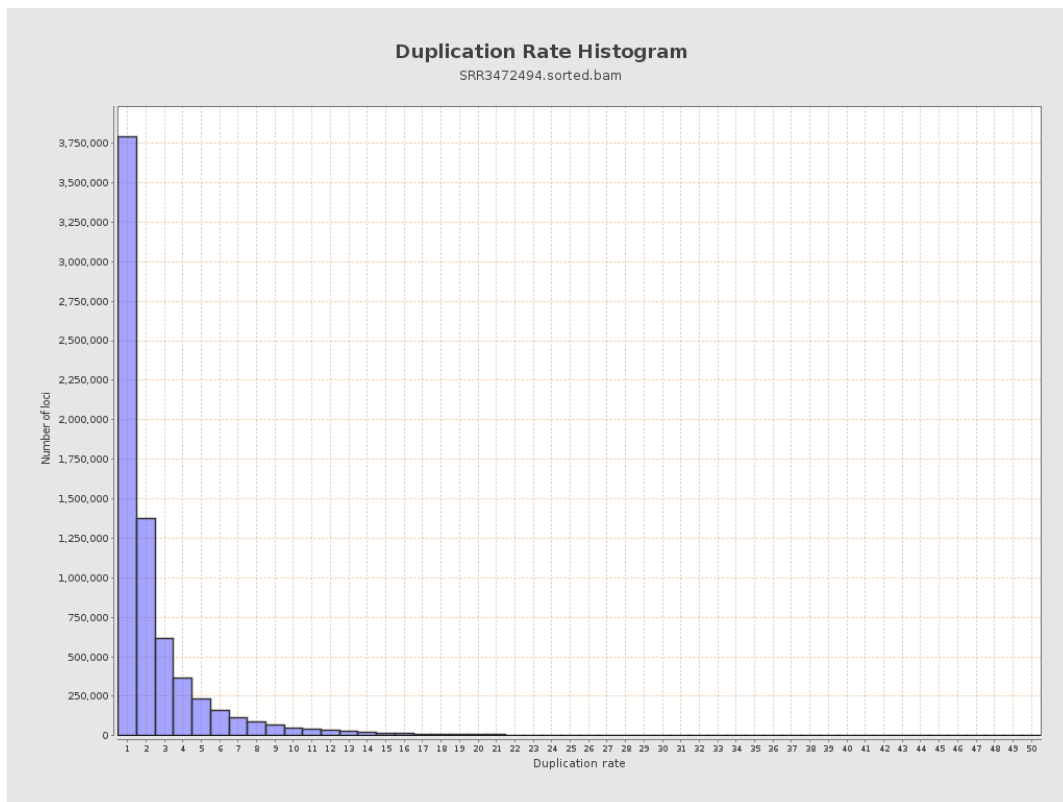
5. Results : Coverage Histogram (0-50X)



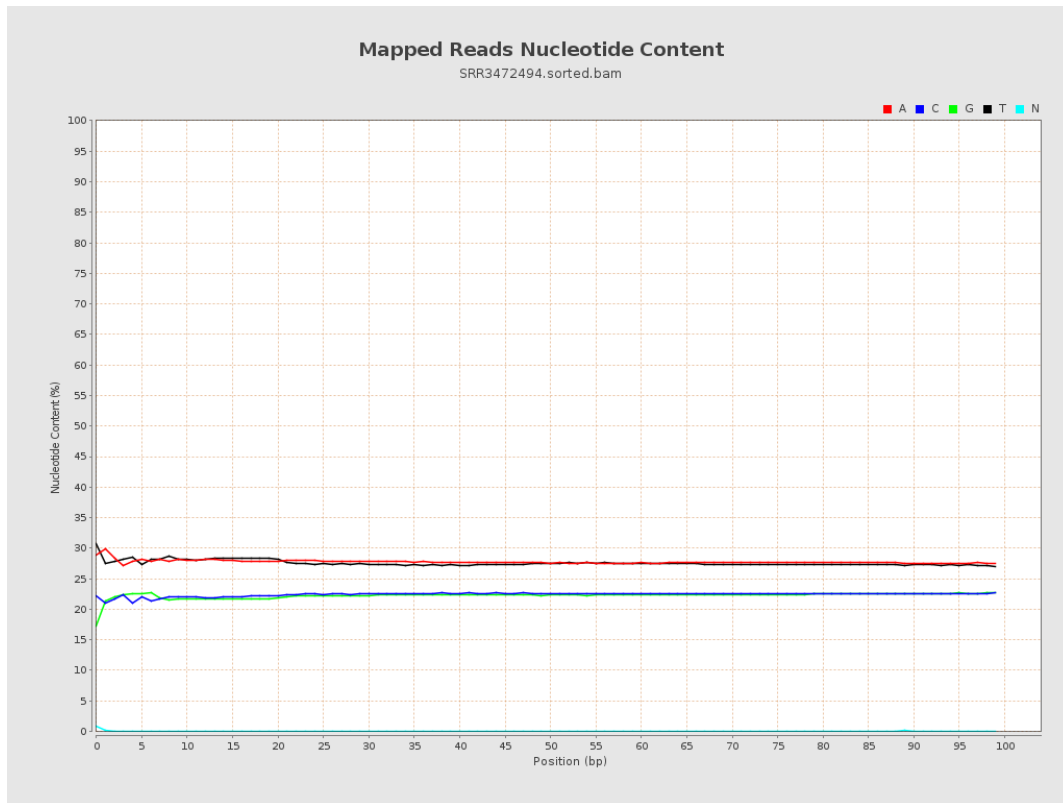
6. Results : Genome Fraction Coverage



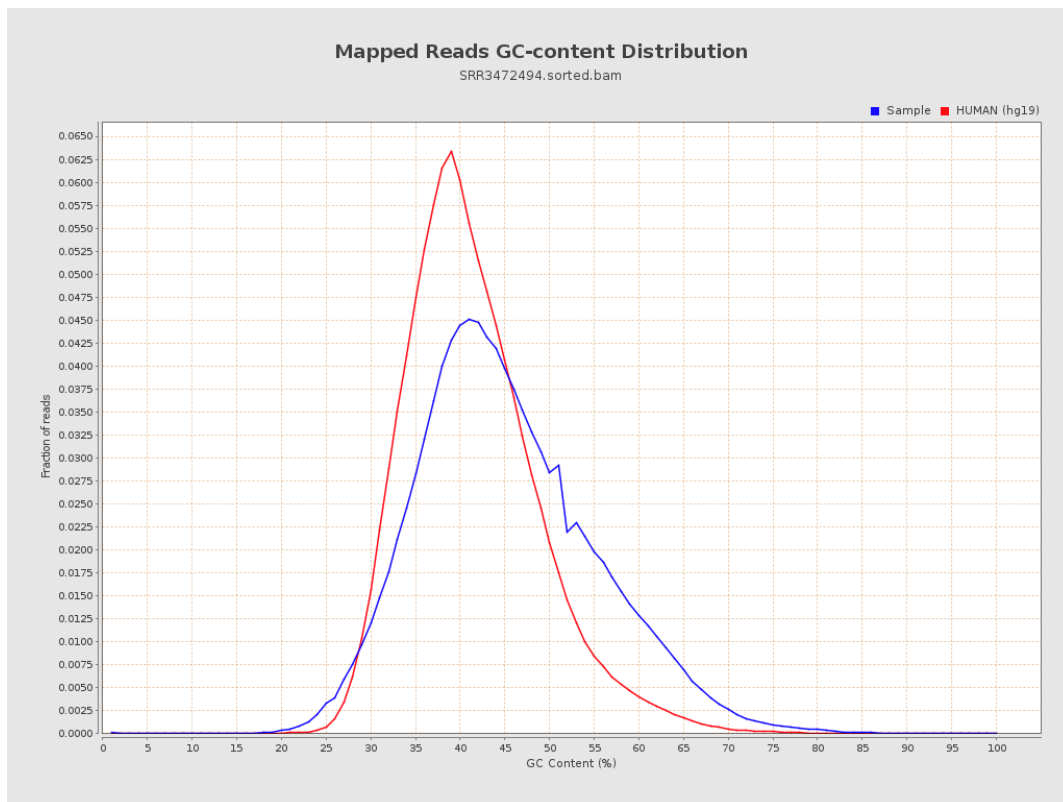
7. Results : Duplication Rate Histogram



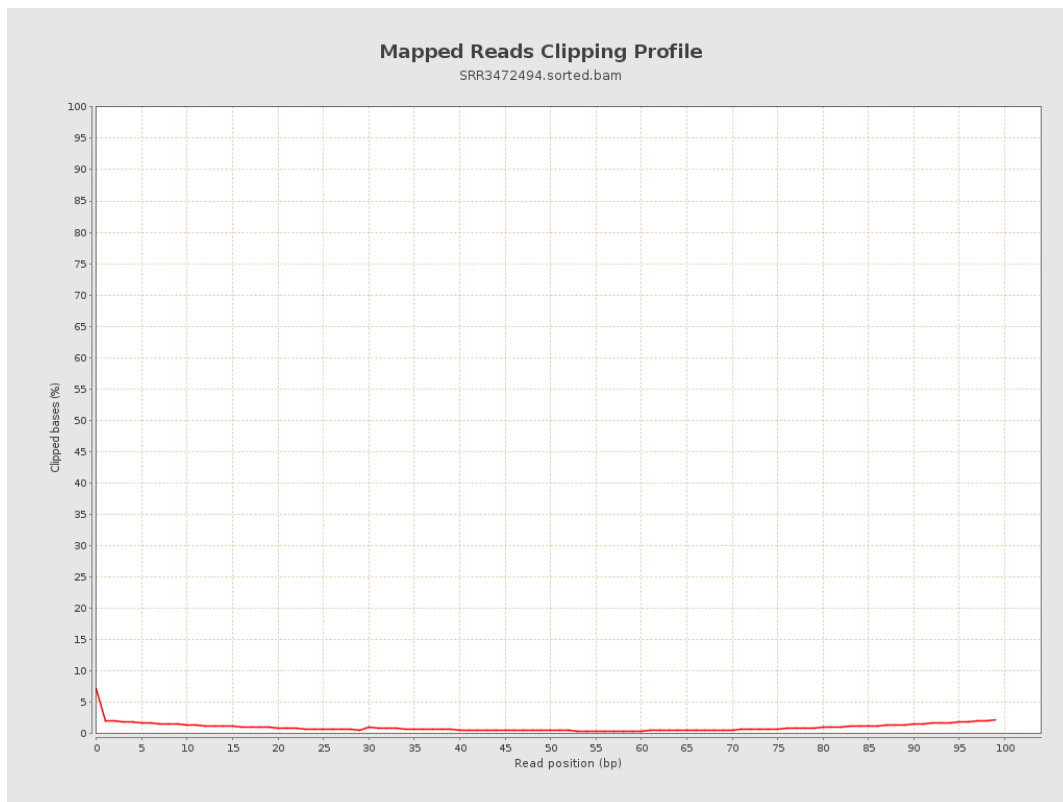
8. Results : Mapped Reads Nucleotide Content



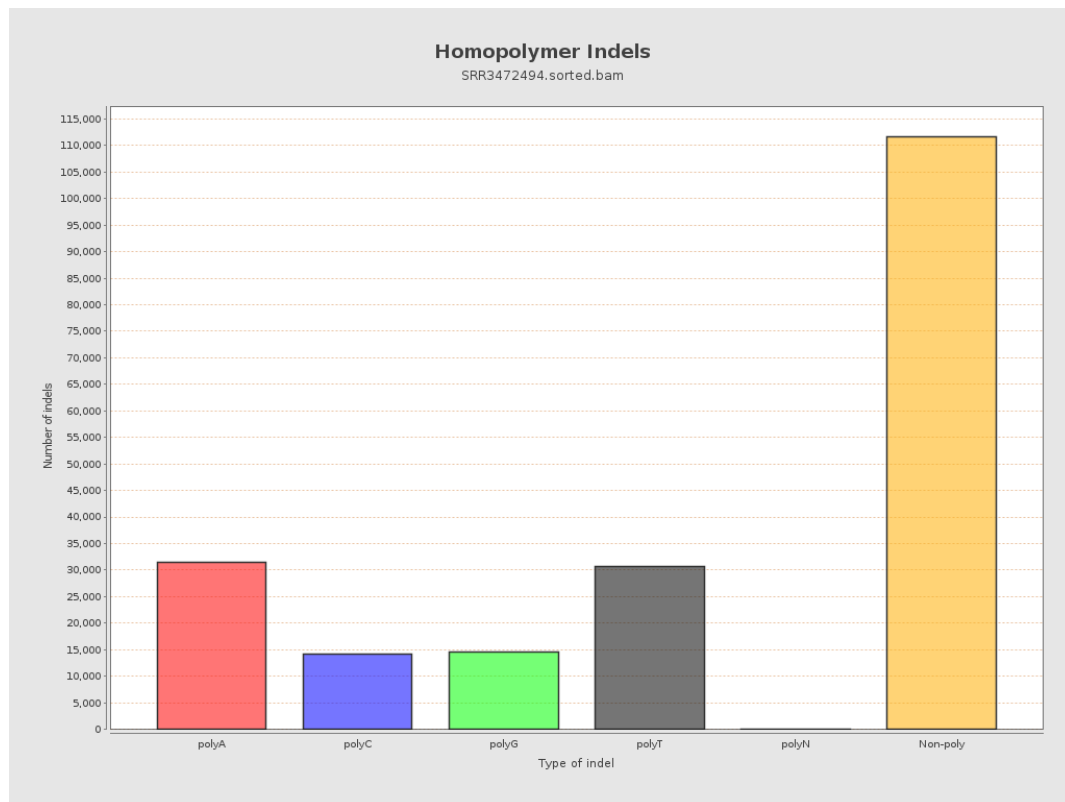
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



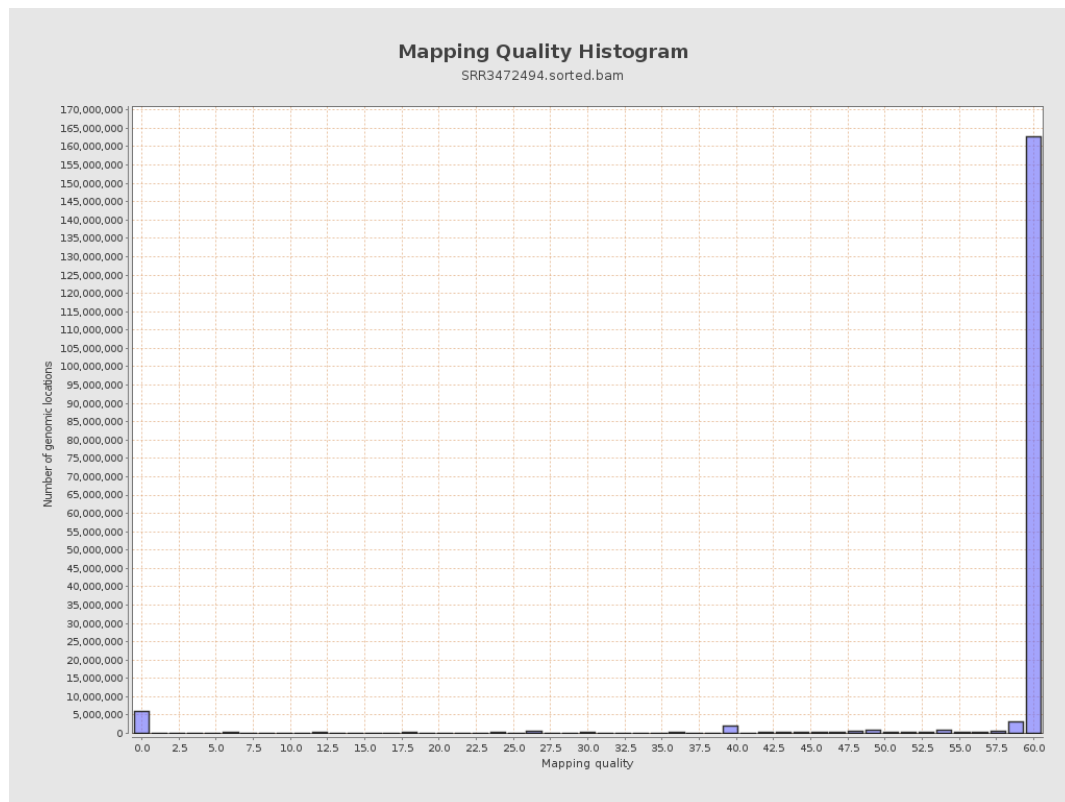
11. Results : Homopolymer Indels



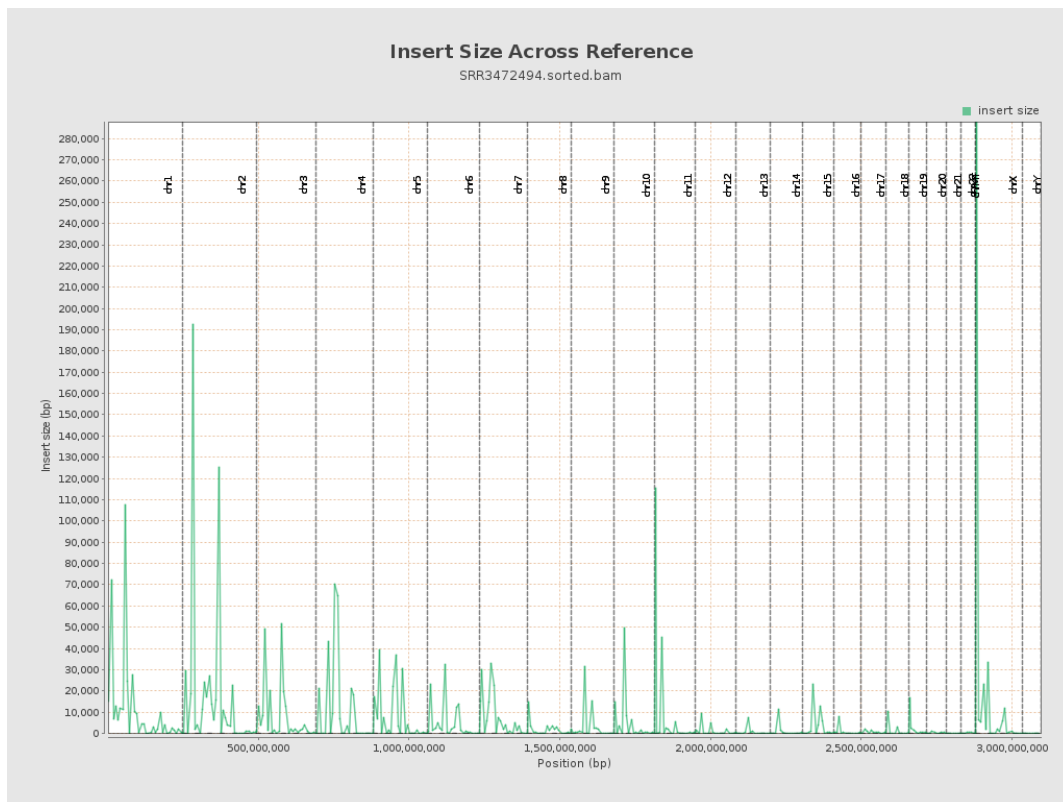
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

