

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 06:09:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438256.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_SRR8438256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438256_1.fastq.gz SRR8438256_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 06:09:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	753,173,218
Mapped reads	749,242,464 / 99.48%
Unmapped reads	3,930,754 / 0.52%
Mapped paired reads	749,242,464 / 99.48%
Mapped reads, first in pair	374,808,414 / 49.76%
Mapped reads, second in pair	374,434,050 / 49.71%
Mapped reads, both in pair	746,789,744 / 99.15%
Mapped reads, singletons	2,452,720 / 0.33%
Secondary alignments	0
Supplementary alignments	20,412,598 / 2.71%
Read min/max/mean length	30 / 149 / 143.42
Duplicated reads (estimated)	300,311,948 / 39.87%
Duplication rate	35.16%
Clipped reads	104,346,085 / 13.85%

2.2. ACGT Content

Number/percentage of A's	32,443,015,145 / 30.54%
Number/percentage of C's	20,317,460,943 / 19.13%
Number/percentage of T's	30,551,972,573 / 28.76%
Number/percentage of G's	22,907,176,415 / 21.57%
Number/percentage of N's	196,878 / 0%

GC Percentage	40.69%
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2.3. Coverage

Mean	34.3233
Standard Deviation	85.0499

2.4. Mapping Quality

Mean Mapping Quality	54.33
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2.5. Insert size

Mean	111,115.59
Standard Deviation	3,249,529.79
P25/Median/P75	373 / 445 / 562

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	570,461,494
Insertions	14,309,116
Mapped reads with at least one insertion	1.86%
Deletions	12,658,212
Mapped reads with at least one deletion	1.64%
Homopolymer indels	48.36%

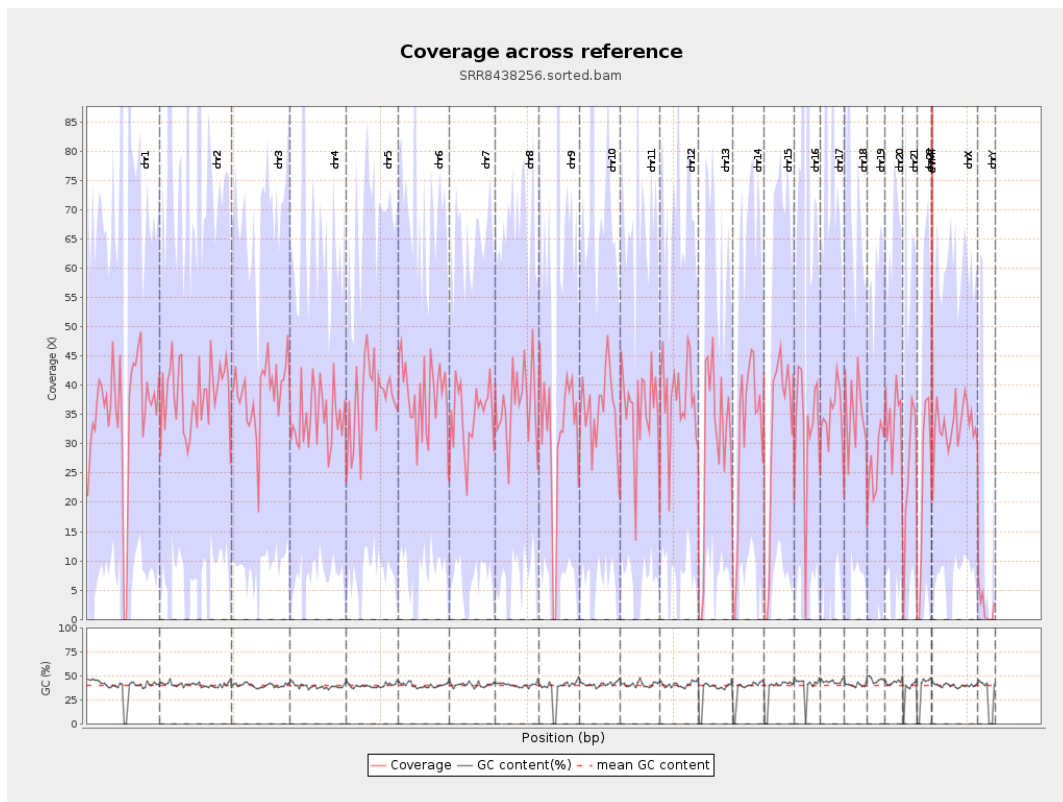
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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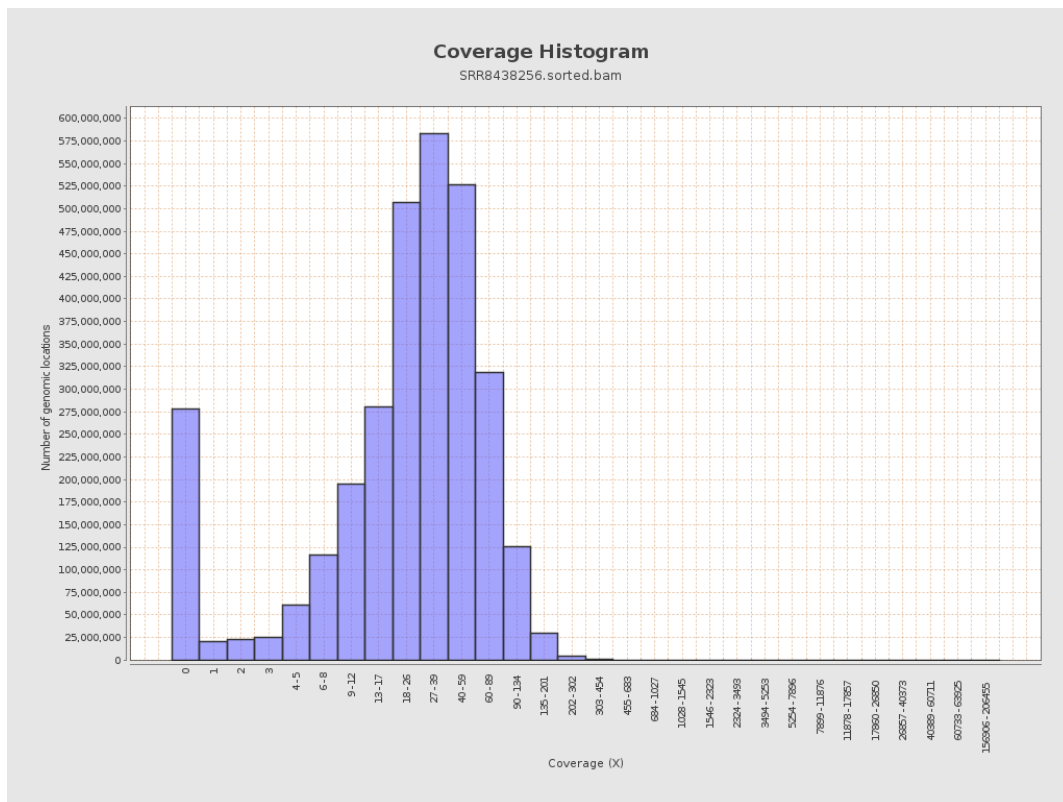
		bases	coverage	deviation
chr1	249250621	8816588872	35.3724	40.1665
chr2	243199373	9328573641	38.3577	158.5581
chr3	198022430	7679879953	38.7829	30.0012
chr4	191154276	6612652813	34.5933	33.0711
chr5	180915260	6778671958	37.4688	30.2432
chr6	171115067	6533425355	38.1815	33.369
chr7	159138663	5499239447	34.5563	29.8073
chr8	146364022	5363158835	36.6426	31.5546
chr9	141213431	4411564659	31.2404	44.453
chr10	135534747	4871263755	35.9411	65.9191
chr11	135006516	4899956781	36.2942	33.0319
chr12	133851895	5074115089	37.9084	32.2512
chr13	115169878	3456571206	30.0128	29.5363
chr14	107349540	3374594513	31.4356	31.7891
chr15	102531392	3211632022	31.3234	31.7374
chr16	90354753	2907570184	32.1795	73.3896
chr17	81195210	2807486437	34.577	46.371
chr18	78077248	2769838265	35.4756	53.1644
chr19	59128983	1601013617	27.0766	31.7841
chr20	63025520	2145311317	34.0388	32.1177
chr21	48129895	1268030273	26.346	38.4577
chr22	51304566	1176447293	22.9307	30.4883
chrMT	16571	417950155	25,221.7823	9,443.6739
chrX	155270560	5130215947	33.0405	26.6559

chrY	59373566	118563293	1.9969	31.3073
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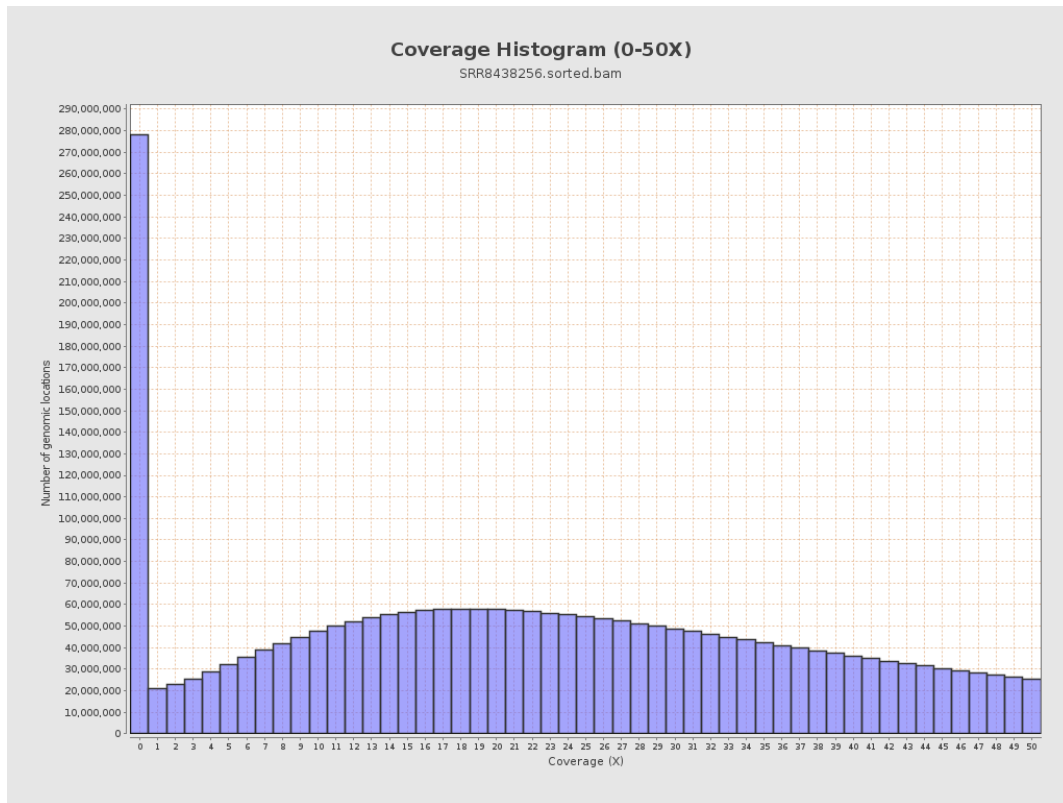
3. Results : Coverage across reference



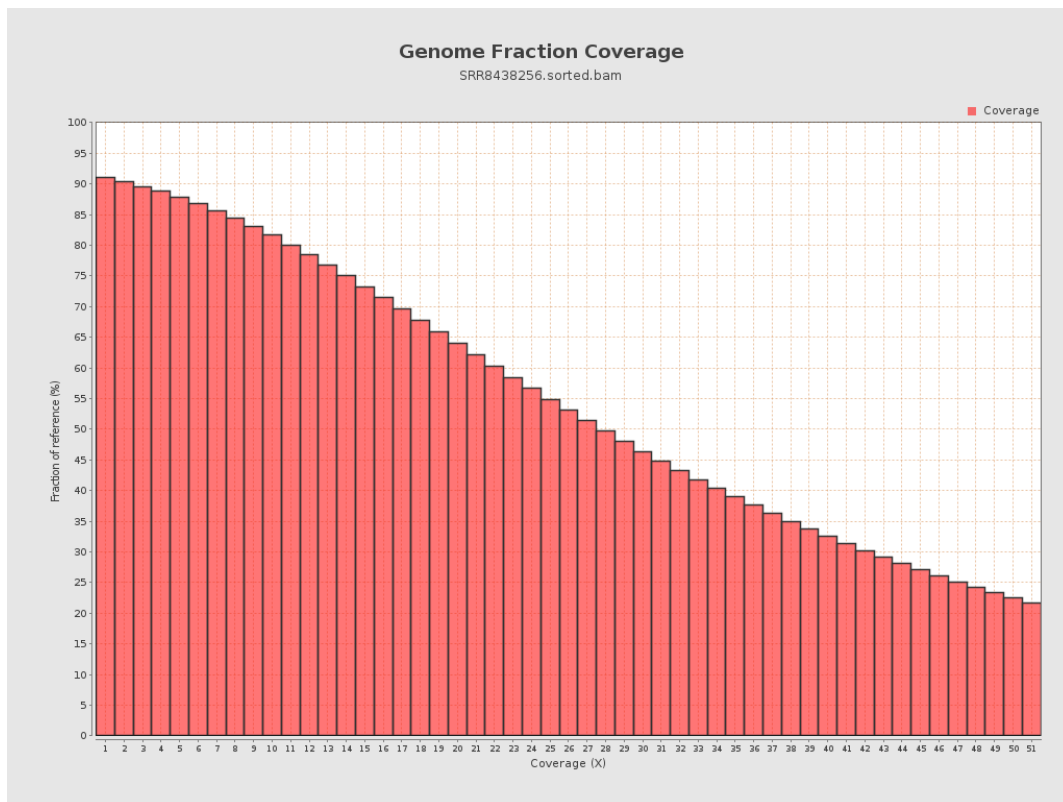
4. Results : Coverage Histogram



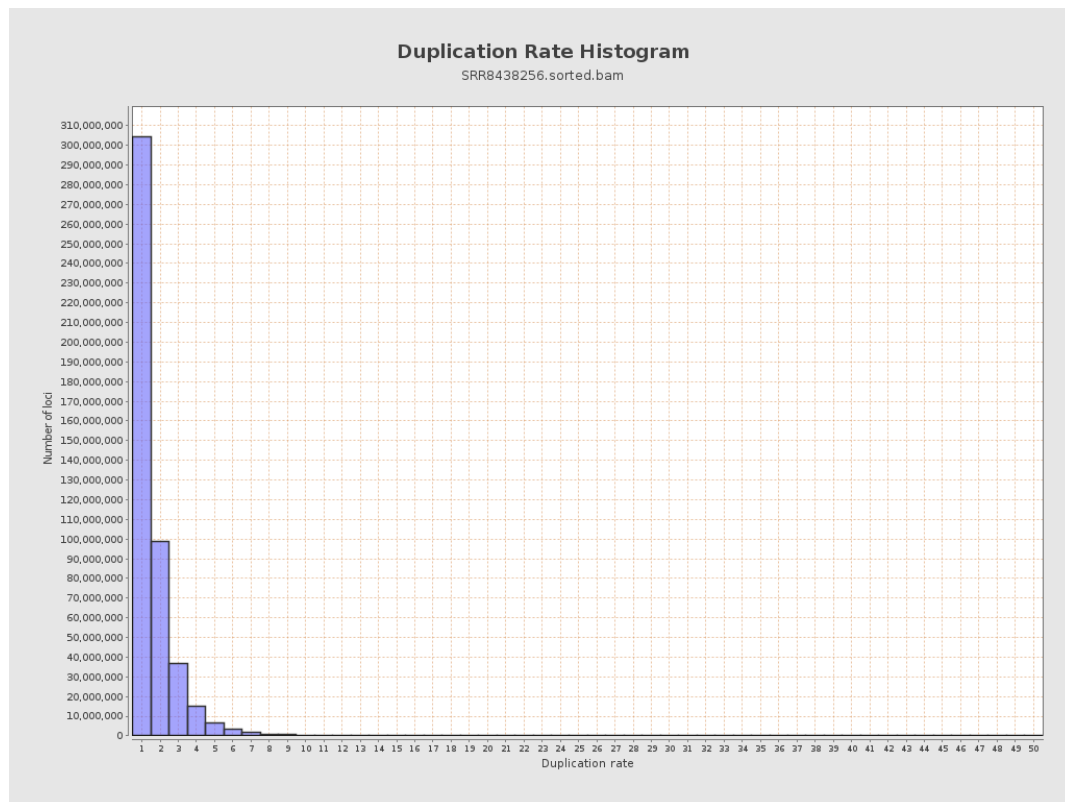
5. Results : Coverage Histogram (0-50X)



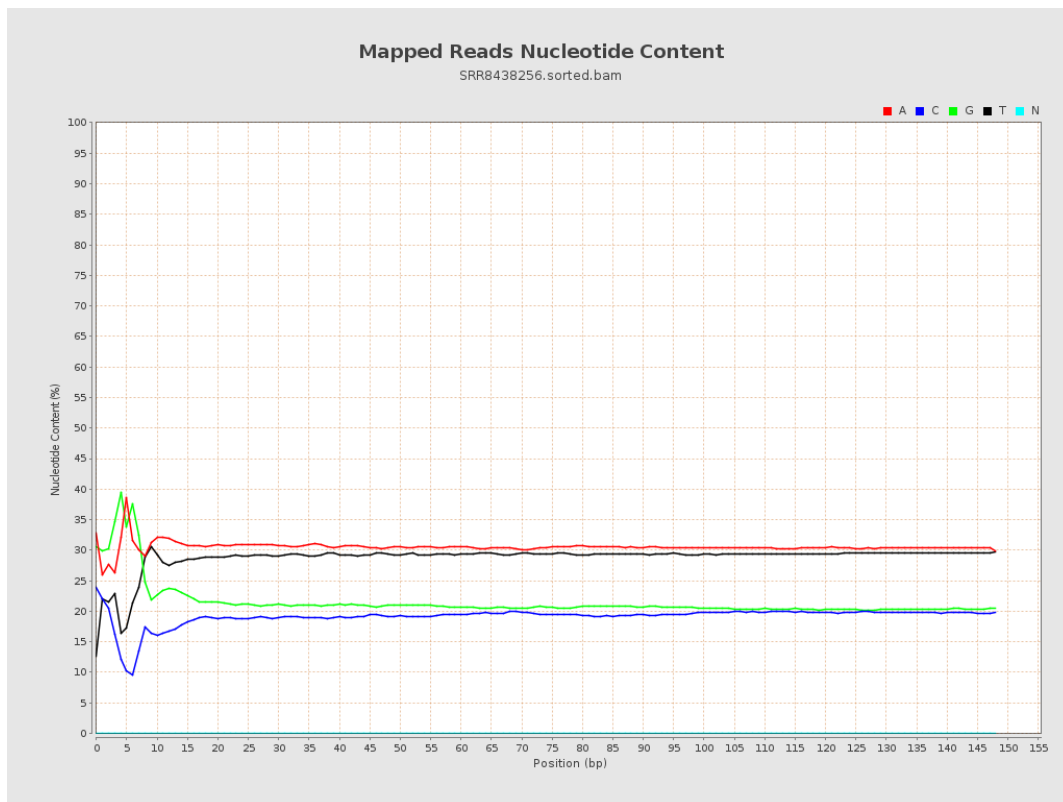
6. Results : Genome Fraction Coverage



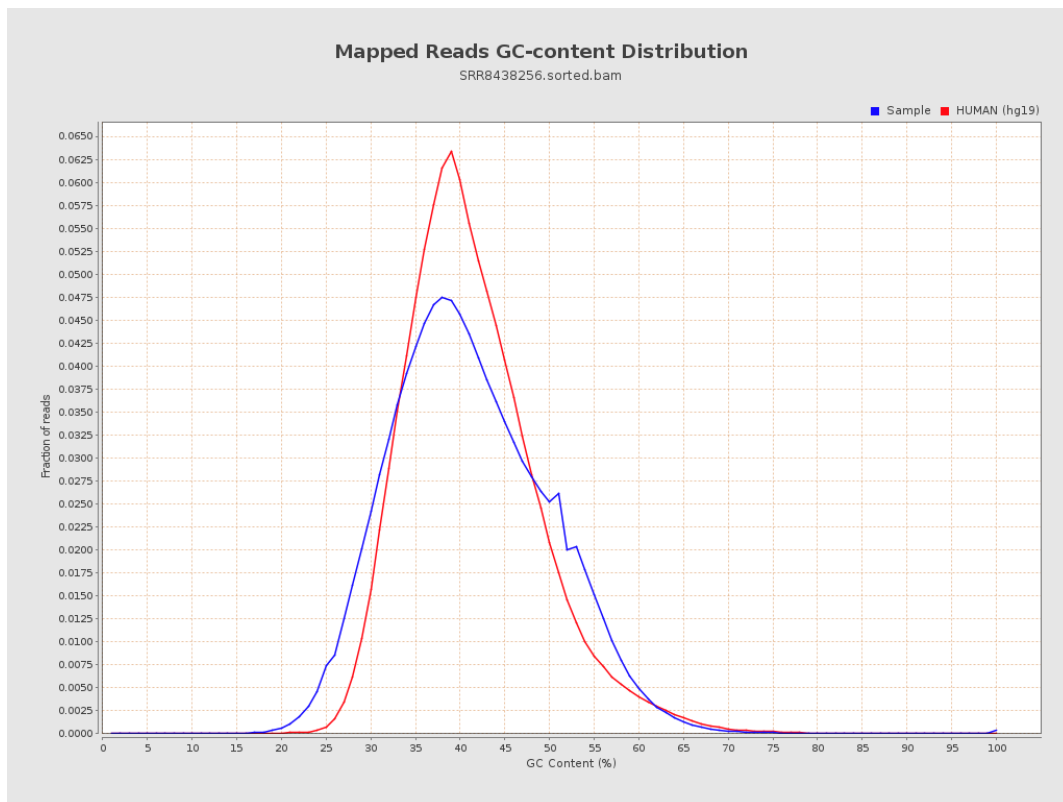
7. Results : Duplication Rate Histogram



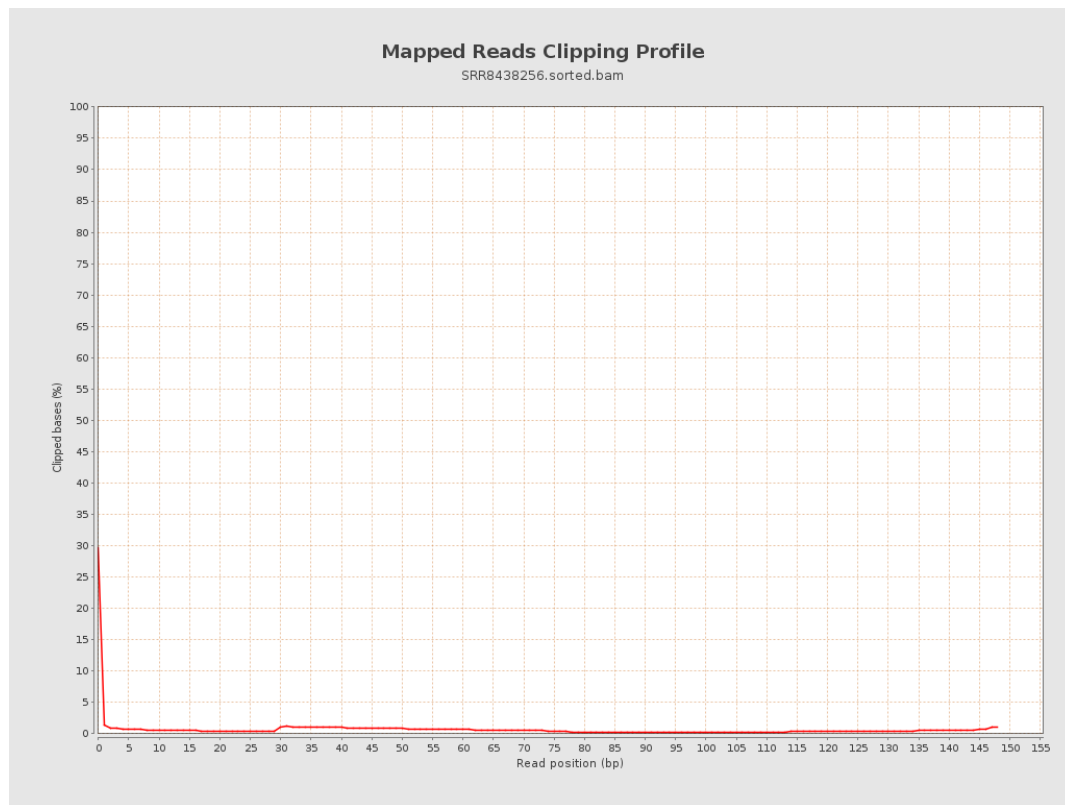
8. Results : Mapped Reads Nucleotide Content



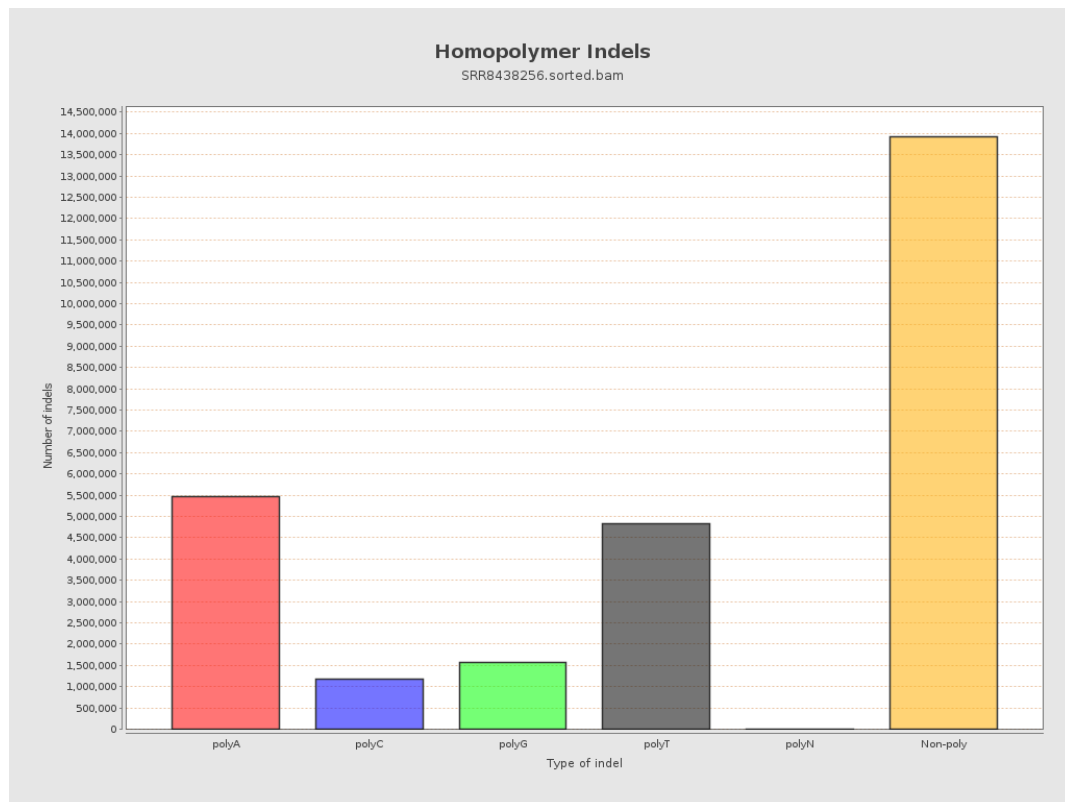
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



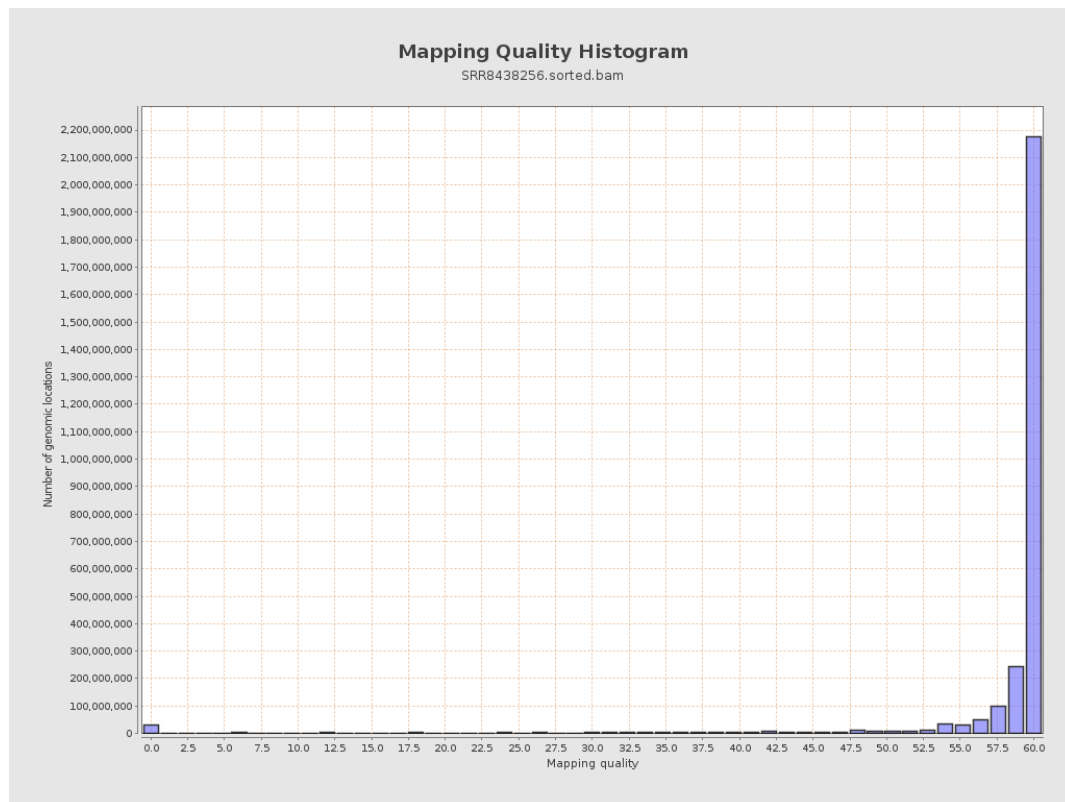
11. Results : Homopolymer Indels



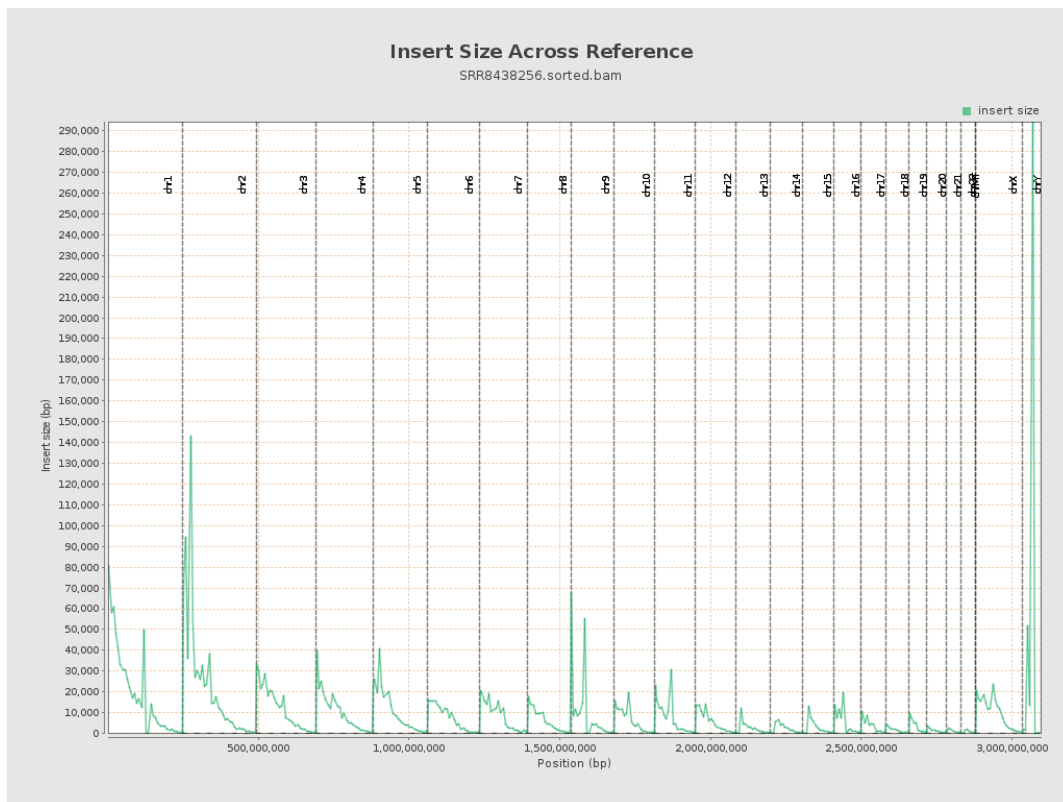
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

