

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:02:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156420.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_SRR10156420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156420_1.fastq.gz SRR10156420_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:02:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10156420.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,014,390
Mapped reads	9,807,044 / 97.93%
Unmapped reads	207,346 / 2.07%
Mapped paired reads	9,807,044 / 97.93%
Mapped reads, first in pair	4,899,967 / 48.93%
Mapped reads, second in pair	4,907,077 / 49%
Mapped reads, both in pair	9,671,492 / 96.58%
Mapped reads, singletons	135,552 / 1.35%
Secondary alignments	0
Supplementary alignments	1,389,112 / 13.87%
Read min/max/mean length	30 / 133 / 125.92
Duplicated reads (estimated)	8,050,885 / 80.39%
Duplication rate	65.82%
Clipped reads	5,111,211 / 51.04%

2.2. ACGT Content

Number/percentage of A's	331,593,101 / 29.79%
Number/percentage of C's	221,551,592 / 19.9%
Number/percentage of T's	329,271,314 / 29.58%
Number/percentage of G's	230,791,437 / 20.73%
Number/percentage of N's	8,258 / 0%

GC Percentage	40.63%
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2.3. Coverage

Mean	0.3599
Standard Deviation	6.5527

2.4. Mapping Quality

Mean Mapping Quality	52.46
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2.5. Insert size

Mean	1,131,097.97
Standard Deviation	9,752,546.05
P25/Median/P75	105 / 156 / 243

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	9,438,535
Insertions	124,177
Mapped reads with at least one insertion	1.22%
Deletions	339,021
Mapped reads with at least one deletion	3.37%
Homopolymer indels	40.93%

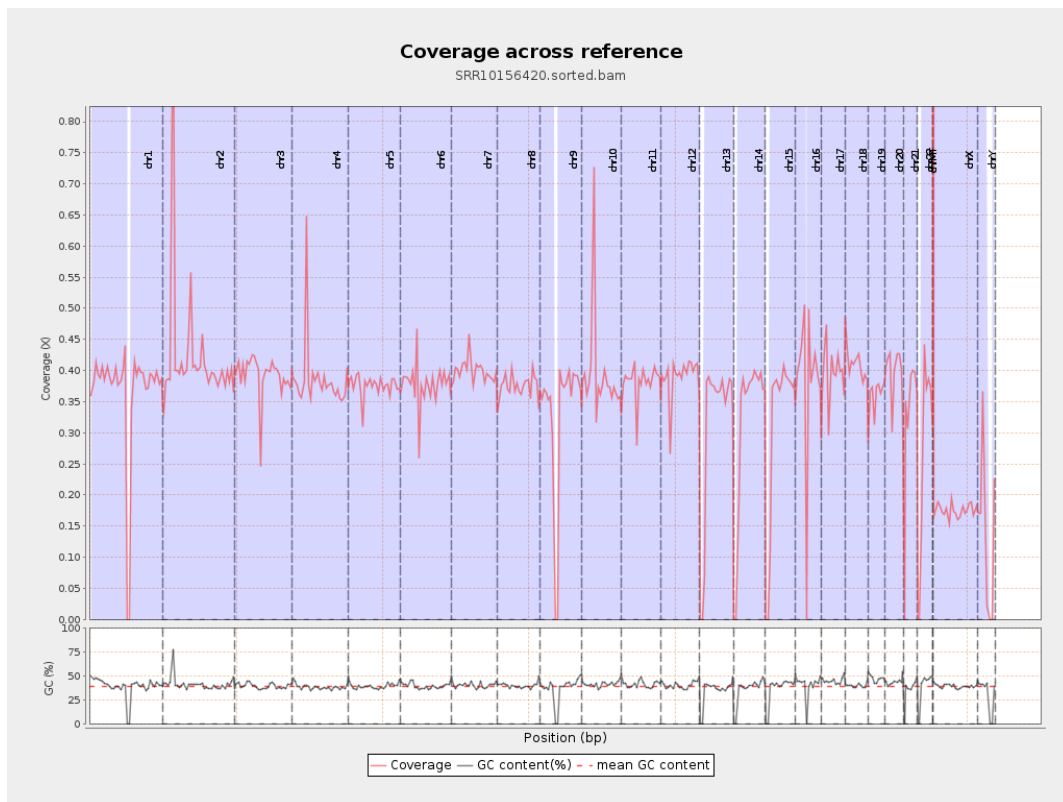
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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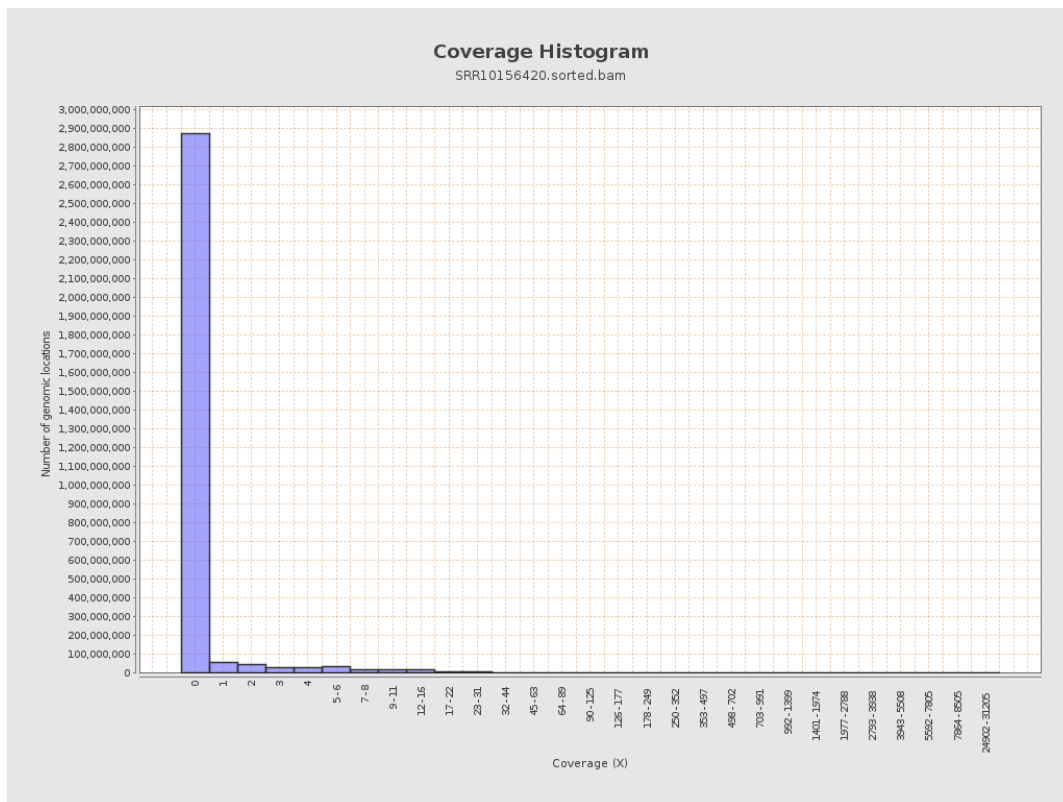
		bases	coverage	deviation
chr1	249250621	91215605	0.366	2.9179
chr2	243199373	102612838	0.4219	21.7634
chr3	198022430	77685634	0.3923	1.9329
chr4	191154276	73664963	0.3854	2.865
chr5	180915260	67917676	0.3754	1.8858
chr6	171115067	64738928	0.3783	2.2955
chr7	159138663	63620126	0.3998	2.8136
chr8	146364022	54933155	0.3753	3.1913
chr9	141213431	46635837	0.3303	2.6177
chr10	135534747	53108854	0.3918	3.8121
chr11	135006516	51544232	0.3818	1.9849
chr12	133851895	52441294	0.3918	2.0022
chr13	115169878	35987226	0.3125	1.723
chr14	107349540	34307636	0.3196	1.7753
chr15	102531392	31568207	0.3079	1.7413
chr16	90354753	34451429	0.3813	2.6372
chr17	81195210	32350388	0.3984	2.3515
chr18	78077248	32011535	0.41	3.6446
chr19	59128983	21376562	0.3615	2.3573
chr20	63025520	25082817	0.398	2.0907
chr21	48129895	16077212	0.334	2.5786
chr22	51304566	13826459	0.2695	2.2818
chrMT	16571	1203267	72.6128	60.5942
chrX	155270560	27204587	0.1752	1.2996

chrY	59373566	8451469	0.1423	2.1805
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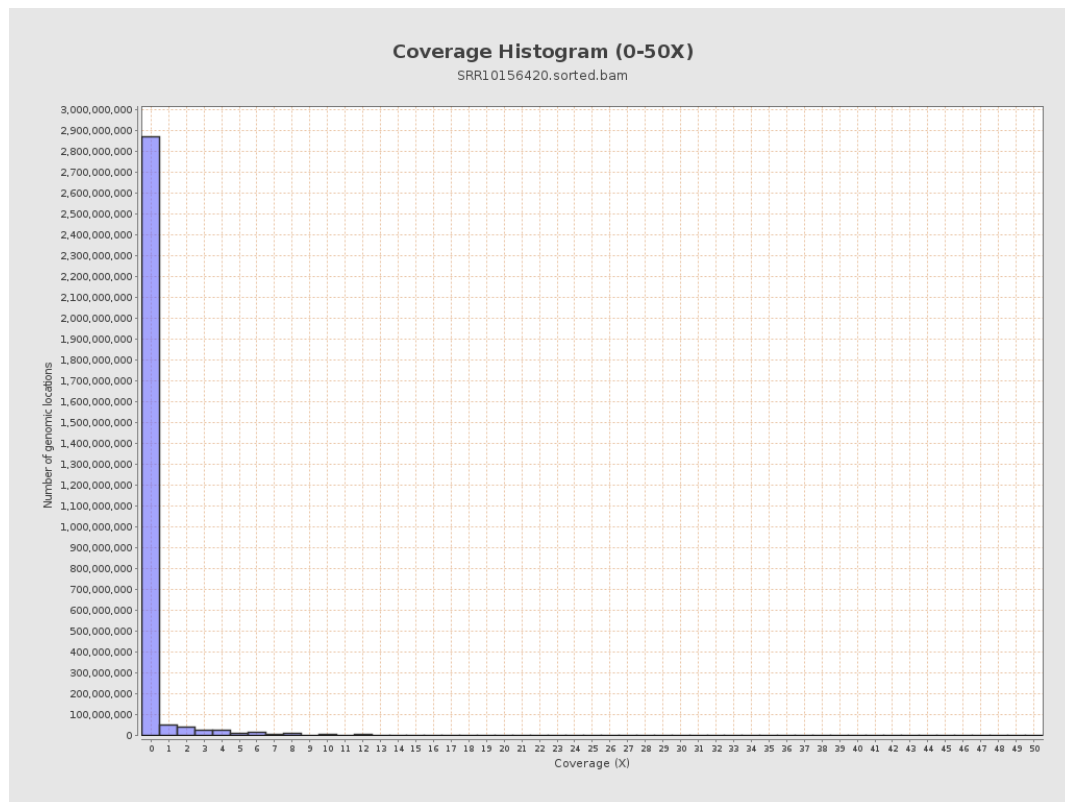
3. Results : Coverage across reference



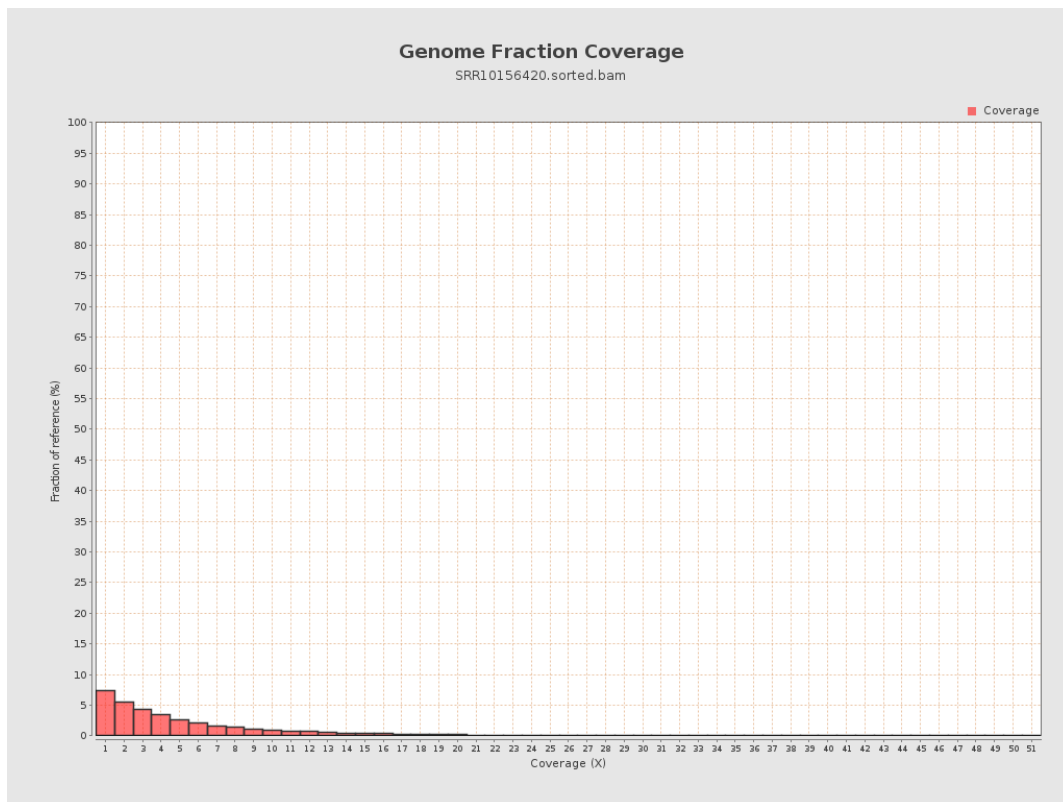
4. Results : Coverage Histogram



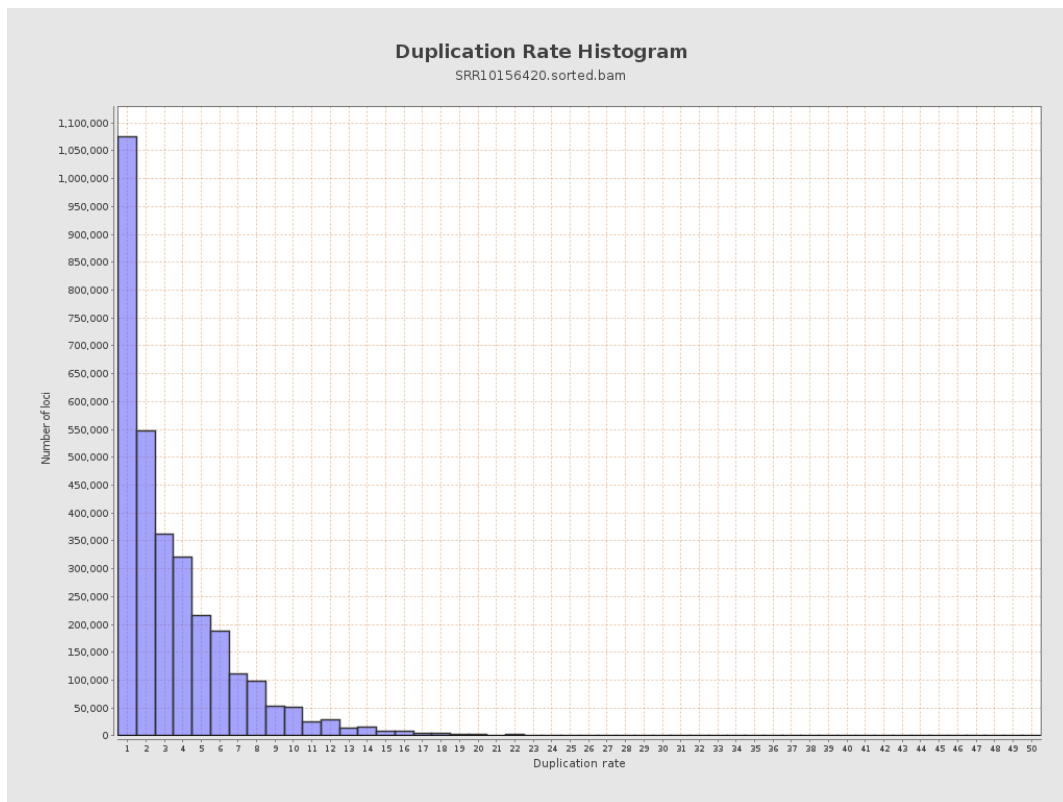
5. Results : Coverage Histogram (0-50X)



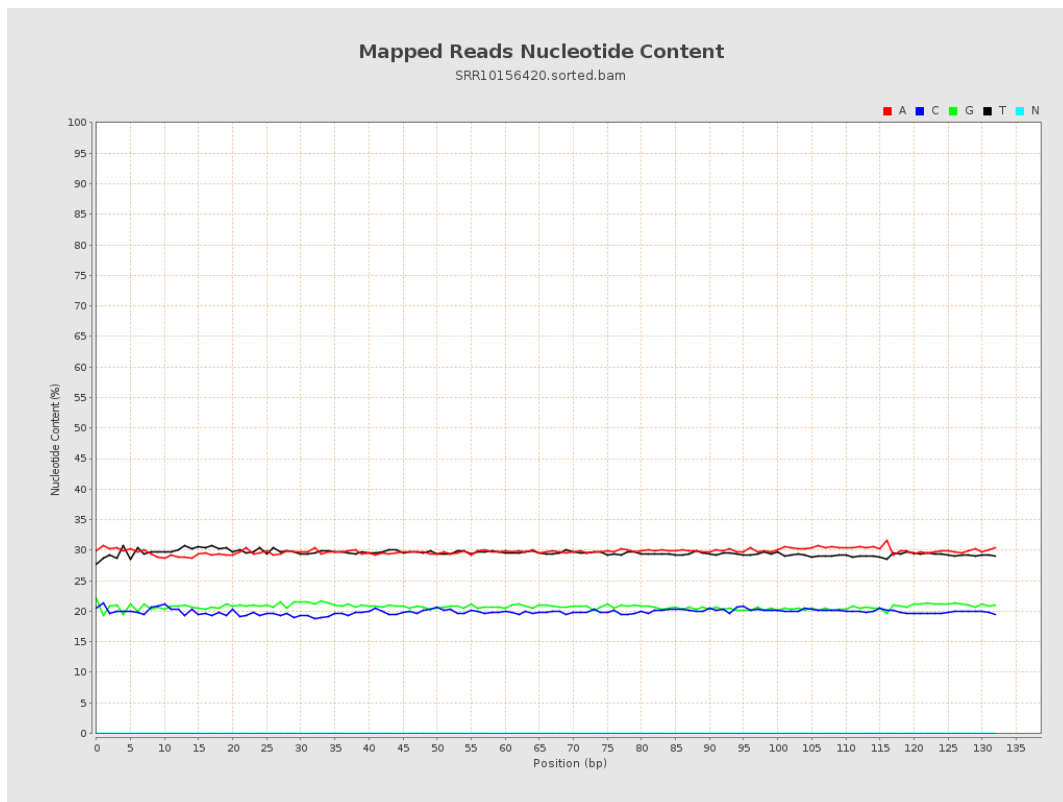
6. Results : Genome Fraction Coverage



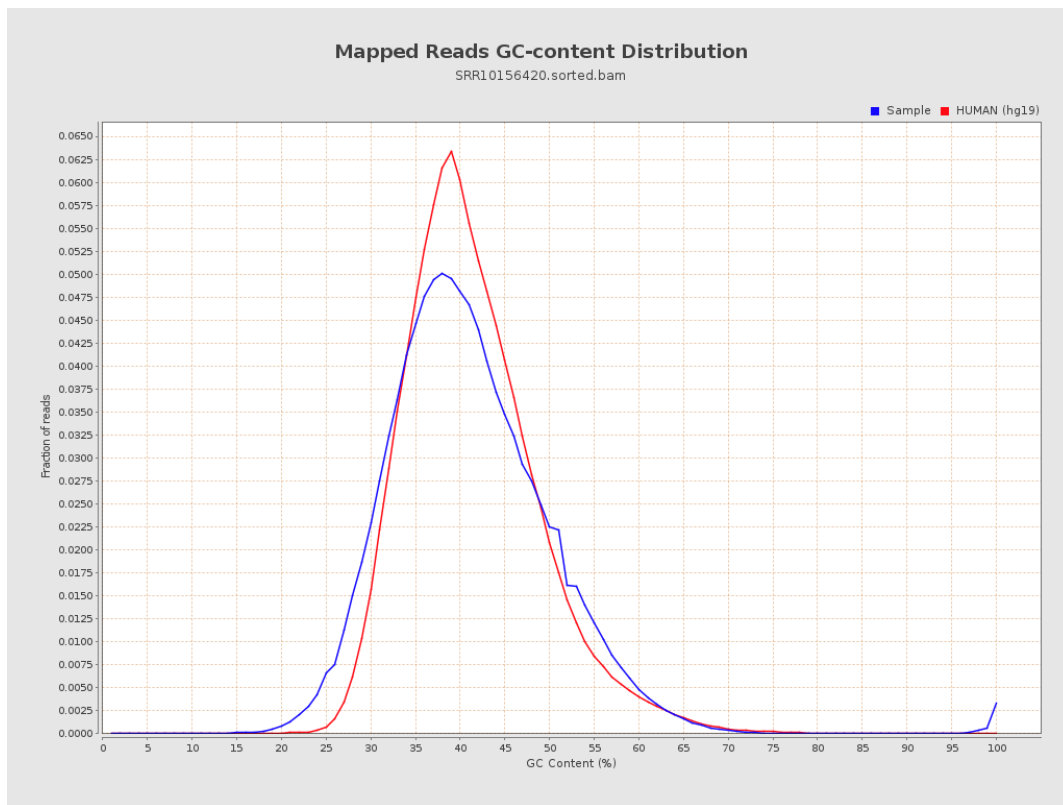
7. Results : Duplication Rate Histogram



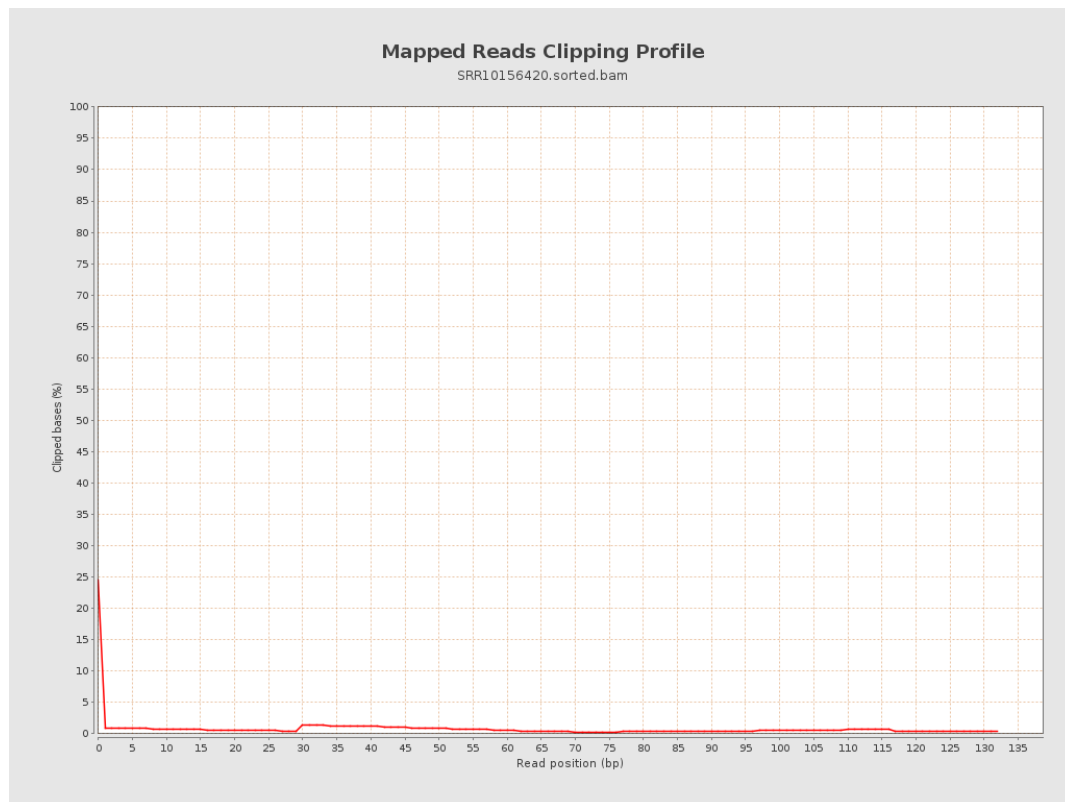
8. Results : Mapped Reads Nucleotide Content



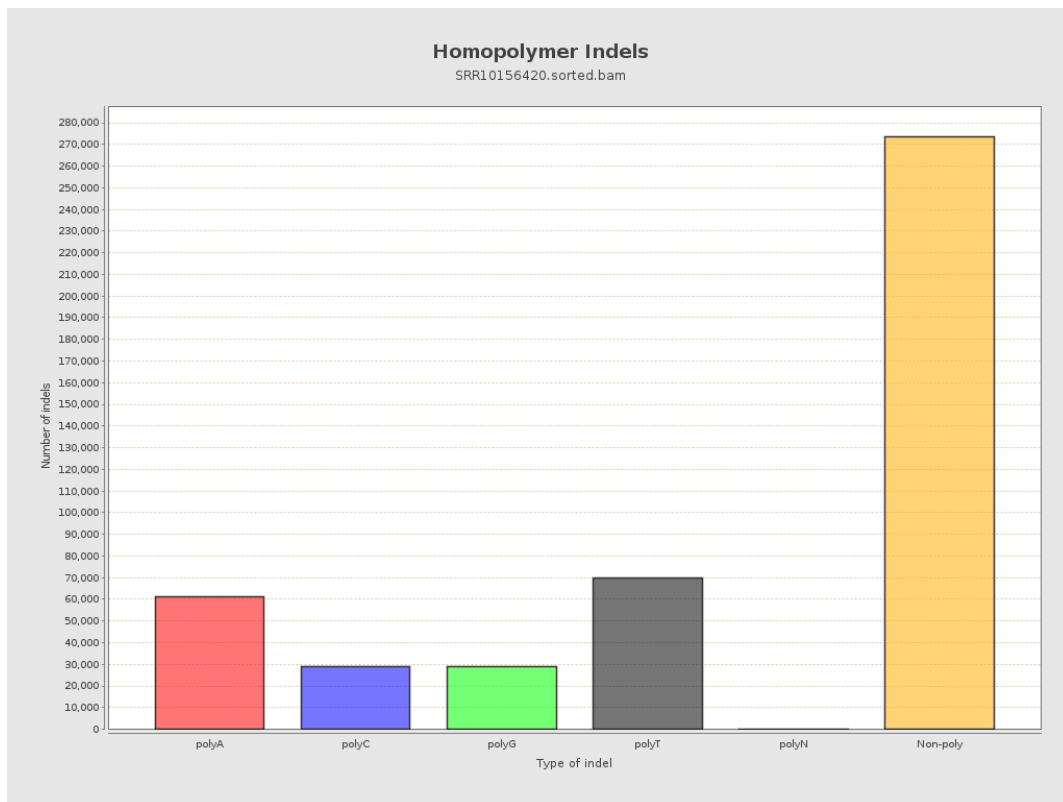
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



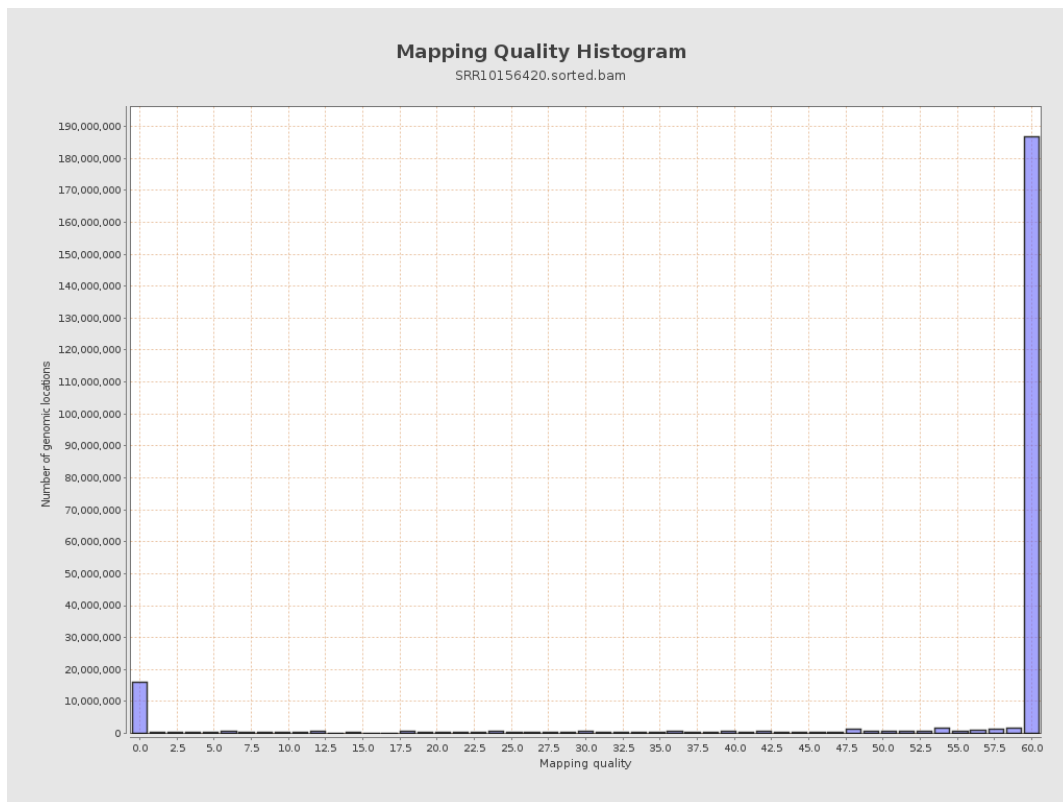
11. Results : Homopolymer Indels



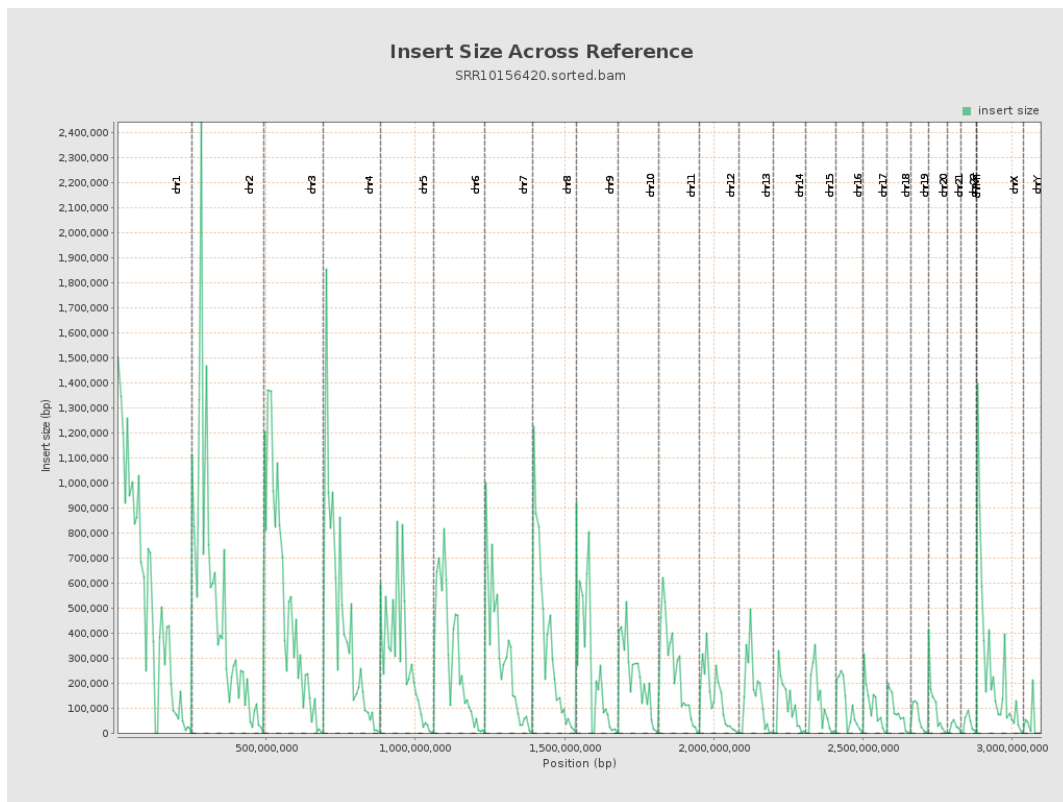
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

