

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:25:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10156427.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_SRR10156427 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10156427_1.fastq.gz SRR10156427_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:25:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10156427.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,198,590
Mapped reads	3,131,273 / 97.9%
Unmapped reads	67,317 / 2.1%
Mapped paired reads	3,131,273 / 97.9%
Mapped reads, first in pair	1,568,020 / 49.02%
Mapped reads, second in pair	1,563,253 / 48.87%
Mapped reads, both in pair	3,088,164 / 96.55%
Mapped reads, singletons	43,109 / 1.35%
Secondary alignments	0
Supplementary alignments	391,885 / 12.25%
Read min/max/mean length	30 / 133 / 125.12
Duplicated reads (estimated)	2,567,254 / 80.26%
Duplication rate	67%
Clipped reads	1,499,694 / 46.89%

2.2. ACGT Content

Number/percentage of A's	106,532,011 / 29.95%
Number/percentage of C's	70,430,672 / 19.8%
Number/percentage of T's	105,654,317 / 29.7%
Number/percentage of G's	73,119,712 / 20.55%
Number/percentage of N's	2,826 / 0%

GC Percentage	40.35%
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2.3. Coverage

Mean	0.115
Standard Deviation	2.2486

2.4. Mapping Quality

Mean Mapping Quality	52.56
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2.5. Insert size

Mean	922,605.12
Standard Deviation	9,198,944.76
P25/Median/P75	107 / 155 / 234

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	3,105,877
Insertions	41,092
Mapped reads with at least one insertion	1.26%
Deletions	103,263
Mapped reads with at least one deletion	3.21%
Homopolymer indels	40.91%

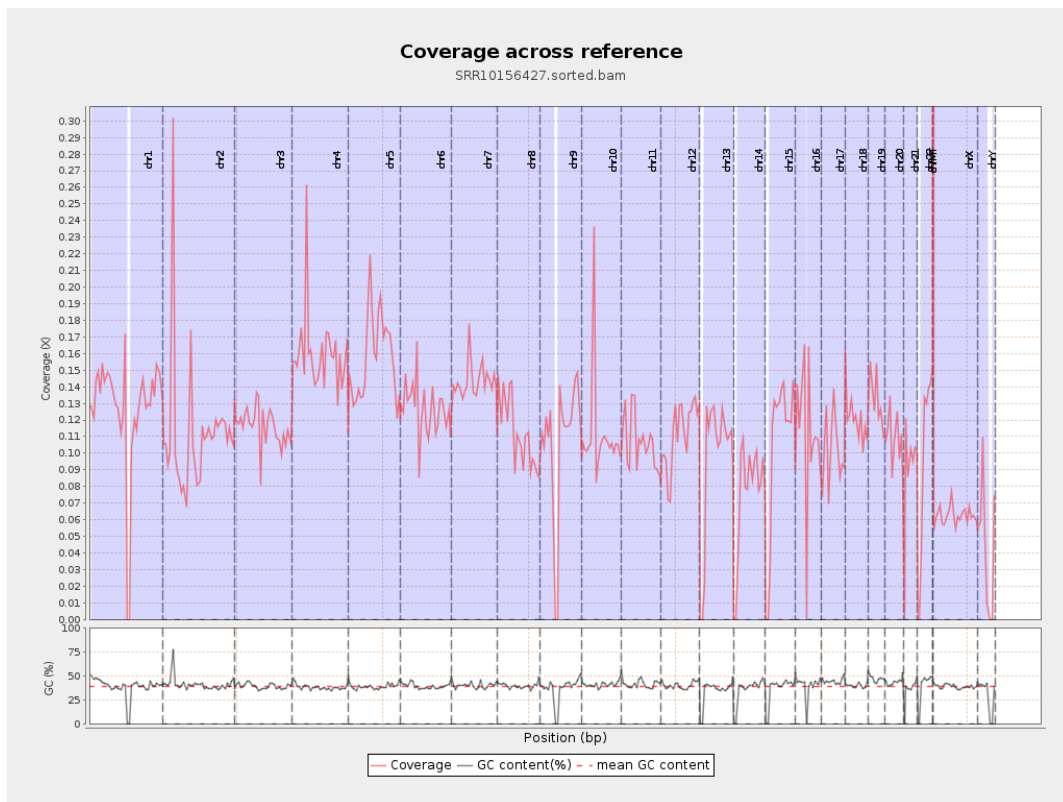
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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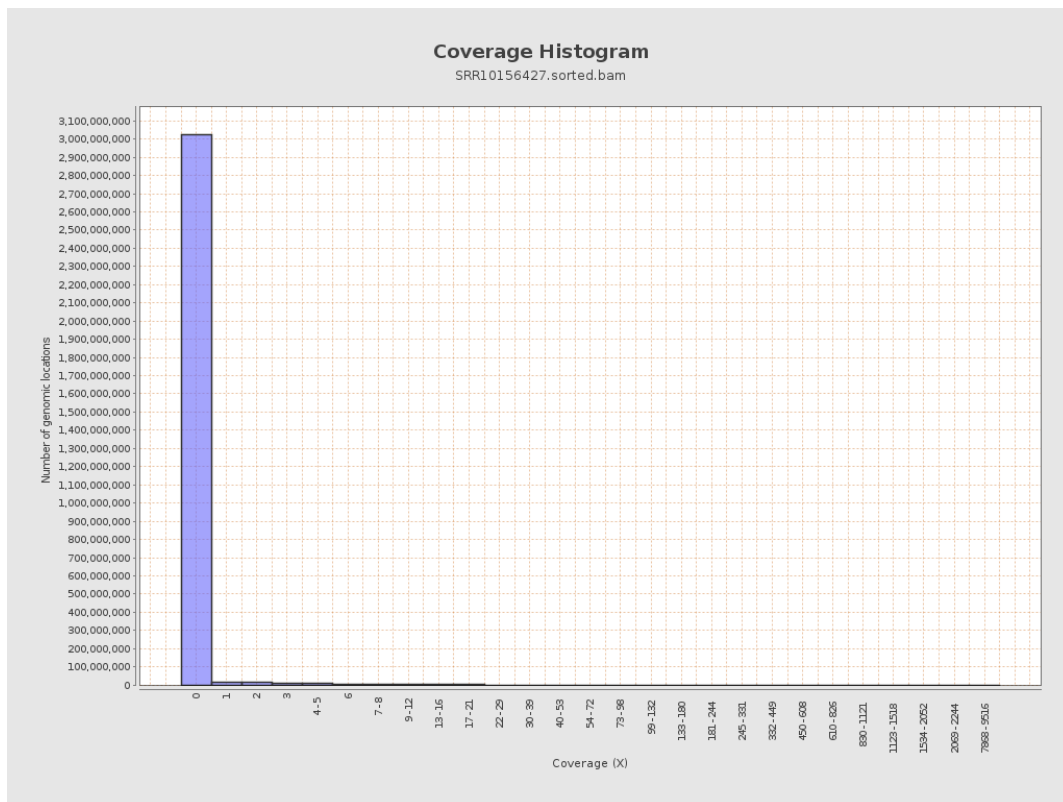
		bases	coverage	deviation
chr1	249250621	31653252	0.127	1.5956
chr2	243199373	26997236	0.111	6.7444
chr3	198022430	23061945	0.1165	1.0749
chr4	191154276	30663678	0.1604	1.5002
chr5	180915260	28445265	0.1572	1.2421
chr6	171115067	21672294	0.1267	1.2632
chr7	159138663	22870432	0.1437	1.5055
chr8	146364022	16350721	0.1117	1.5595
chr9	141213431	15170715	0.1074	1.3235
chr10	135534747	14973985	0.1105	1.5277
chr11	135006516	14358374	0.1064	1.0637
chr12	133851895	15032459	0.1123	1.0649
chr13	115169878	11149392	0.0968	0.9742
chr14	107349540	8262538	0.077	0.8794
chr15	102531392	10651080	0.1039	1.011
chr16	90354753	9994027	0.1106	1.2084
chr17	81195210	8329446	0.1026	1.0521
chr18	78077248	9370486	0.12	1.4805
chr19	59128983	7816967	0.1322	1.2752
chr20	63025520	6894549	0.1094	1.0658
chr21	48129895	4428559	0.092	1.0688
chr22	51304566	4828249	0.0941	0.958
chrMT	16571	675721	40.7773	36.7185
chrX	155270560	9689793	0.0624	0.7794

chrY	59373566	2637990	0.0444	0.9484
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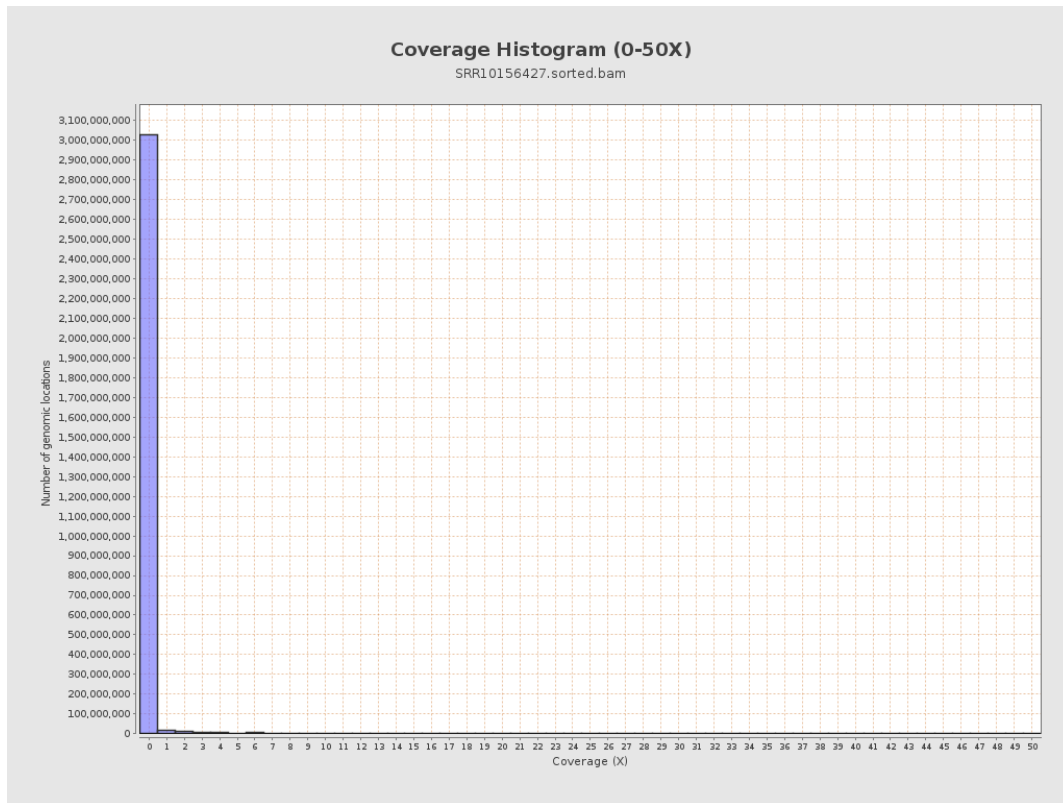
3. Results : Coverage across reference



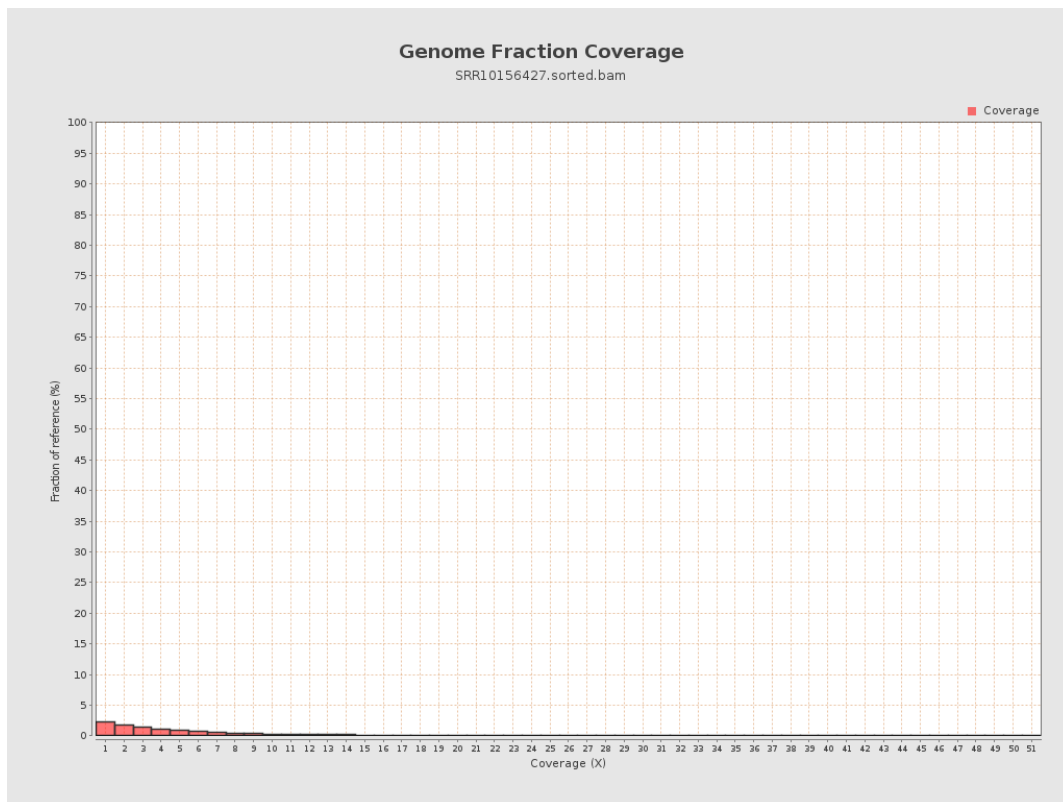
4. Results : Coverage Histogram



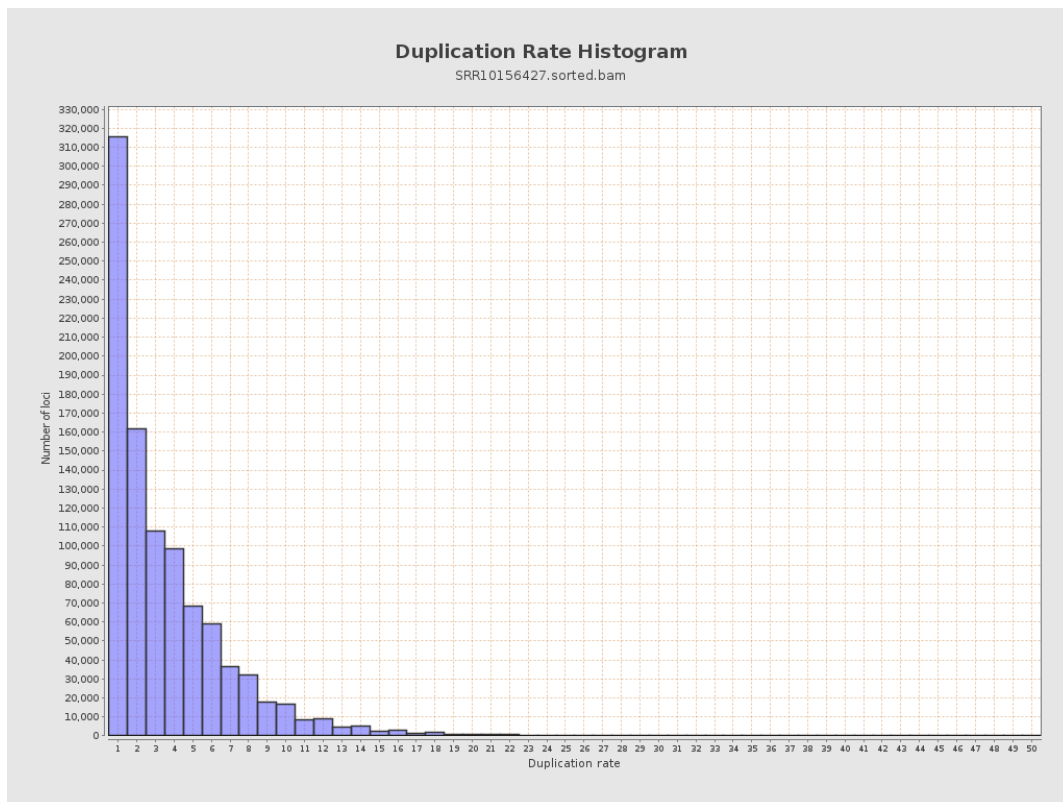
5. Results : Coverage Histogram (0-50X)



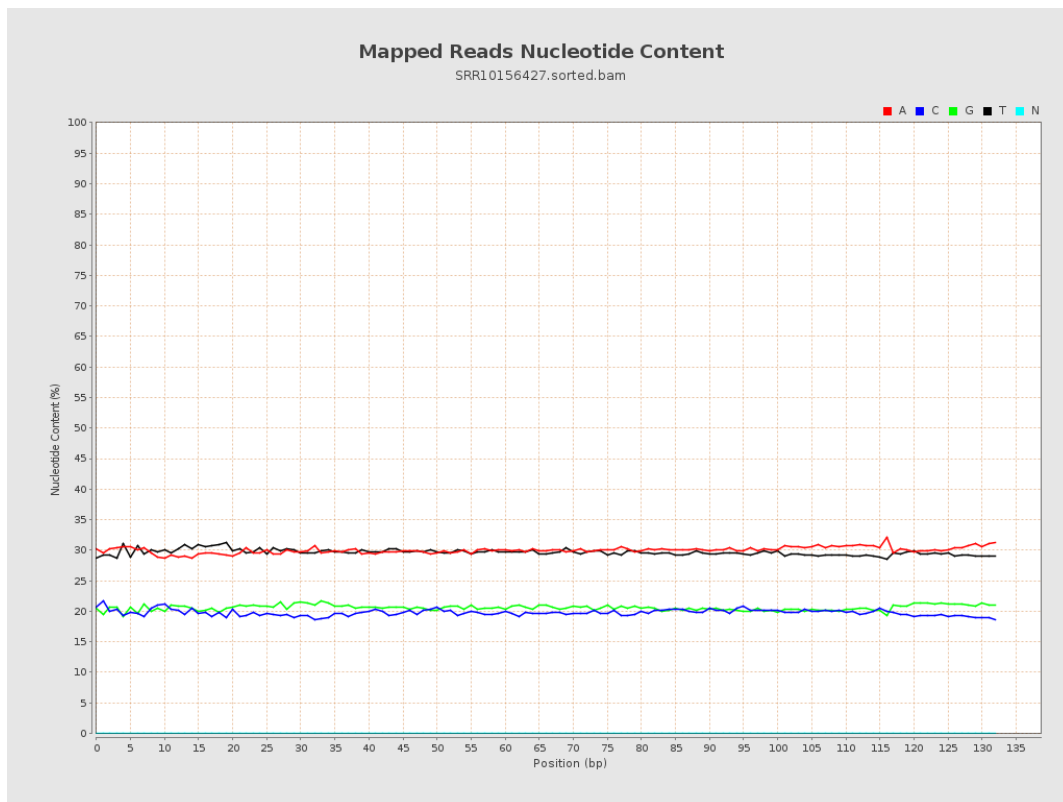
6. Results : Genome Fraction Coverage



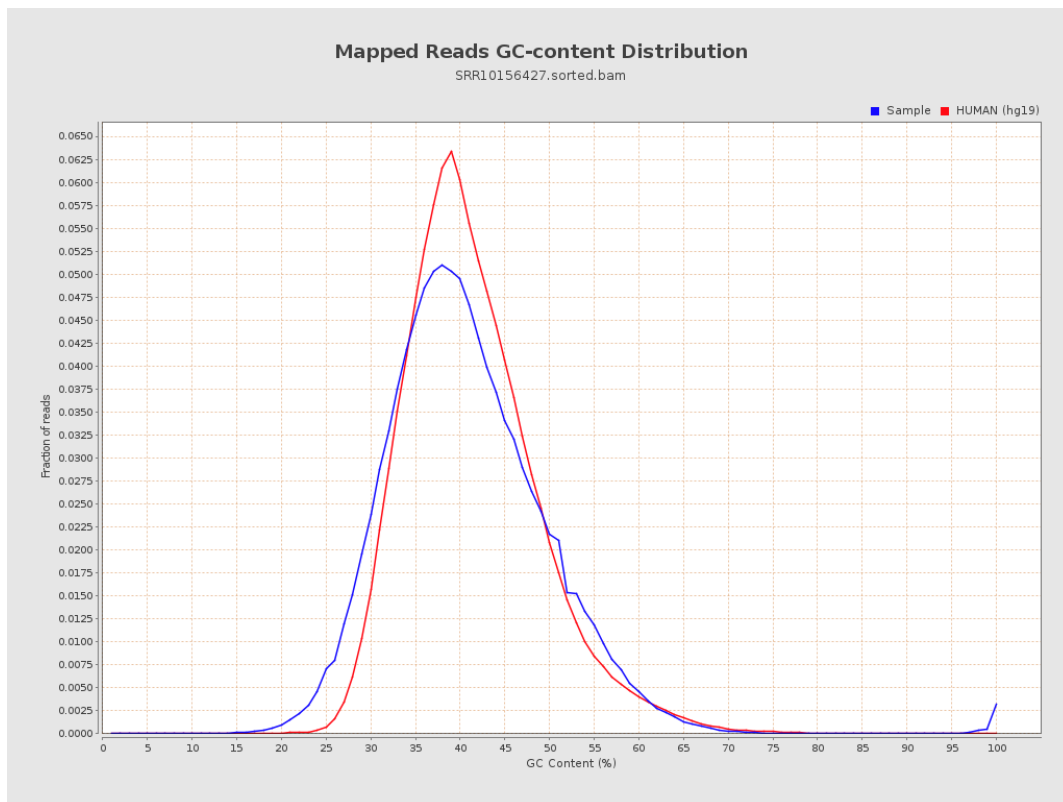
7. Results : Duplication Rate Histogram



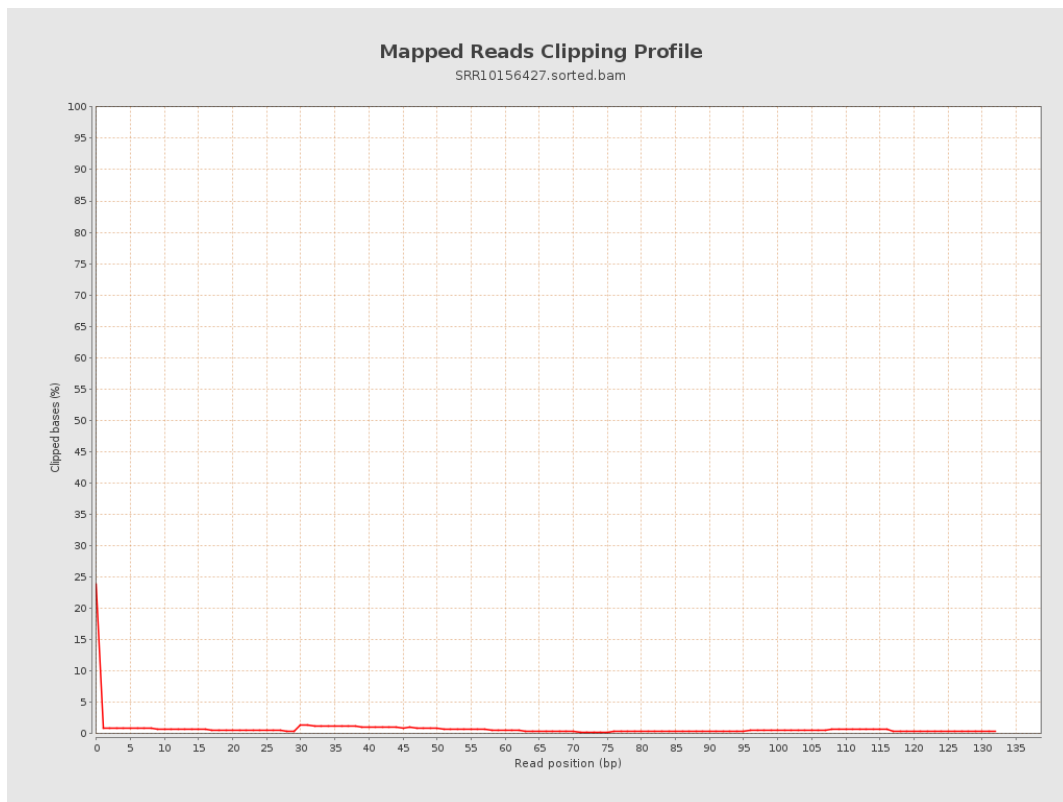
8. Results : Mapped Reads Nucleotide Content



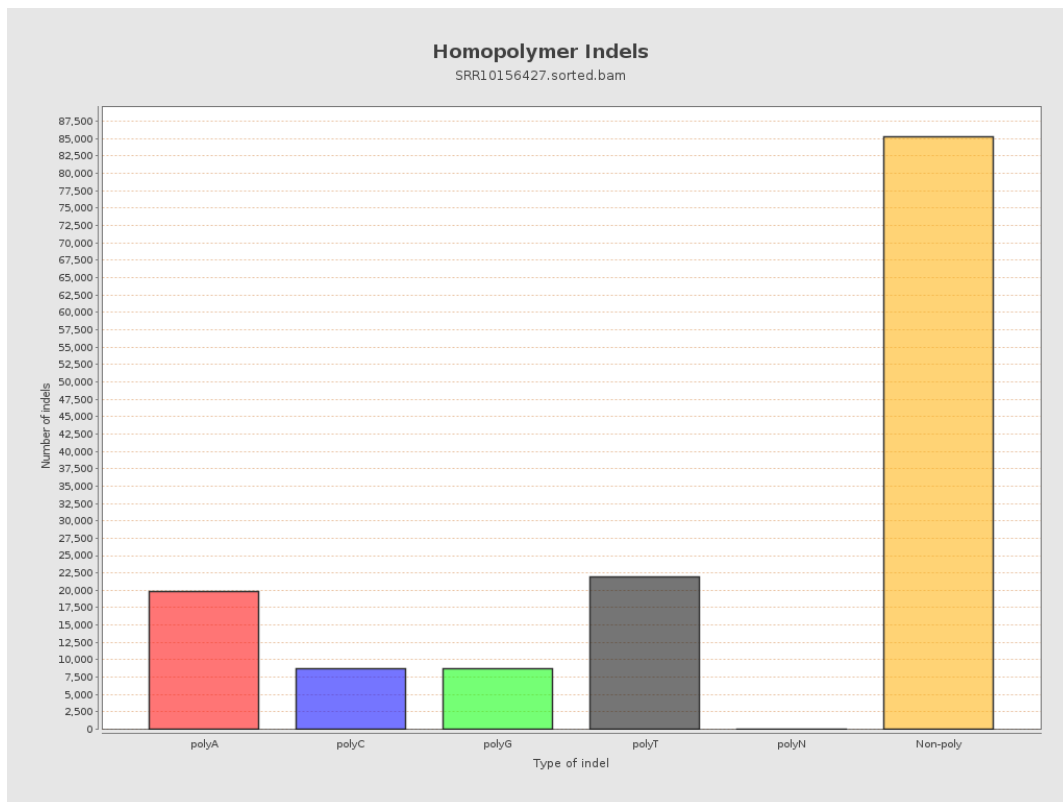
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



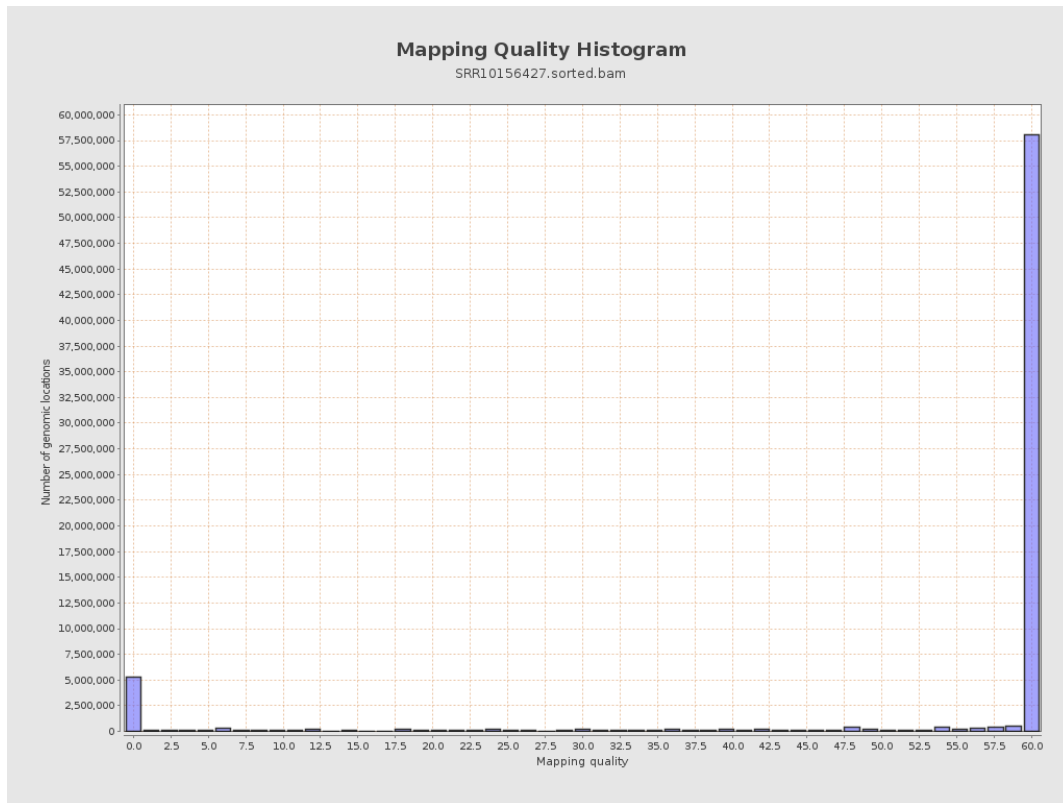
11. Results : Homopolymer Indels



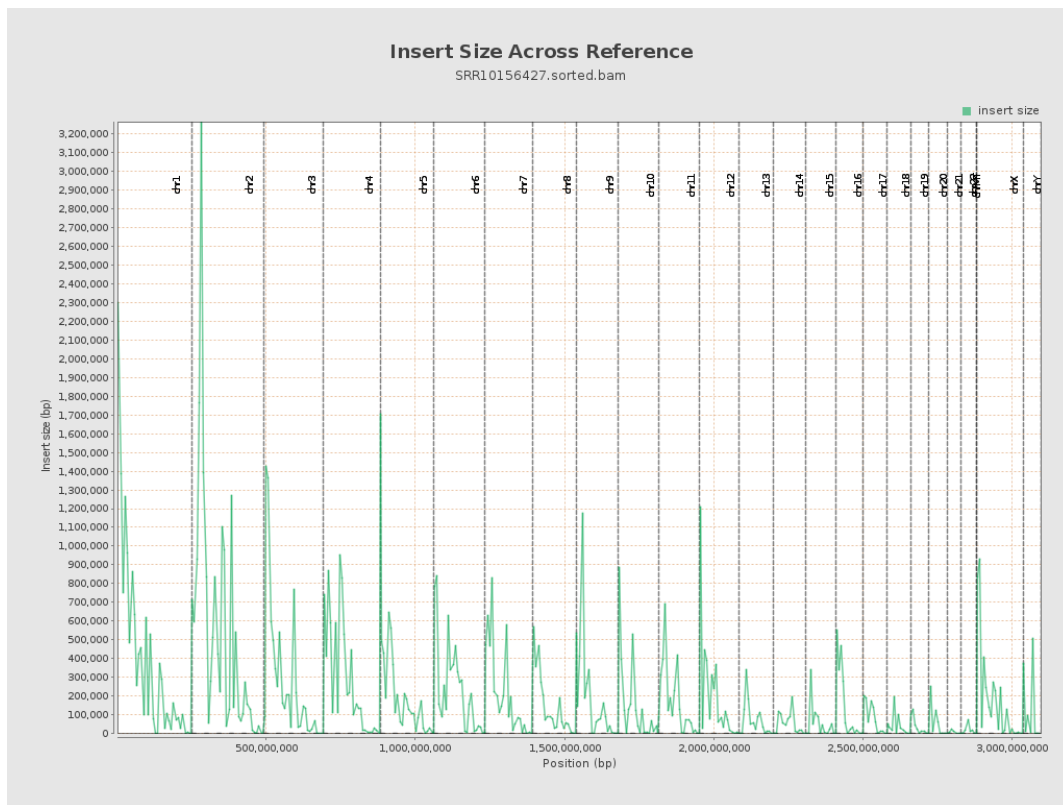
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

