

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 10:49:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251057.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_SRR10251057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251057_1.fastq.gz SRR10251057_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 10:49:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,709,622
Mapped reads	1,559,676 / 91.23%
Unmapped reads	149,946 / 8.77%
Mapped paired reads	1,559,676 / 91.23%
Mapped reads, first in pair	782,712 / 45.78%
Mapped reads, second in pair	776,964 / 45.45%
Mapped reads, both in pair	1,549,034 / 90.61%
Mapped reads, singletons	10,642 / 0.62%
Secondary alignments	0
Supplementary alignments	49,957 / 2.92%
Read min/max/mean length	30 / 127 / 128.33
Duplicated reads (estimated)	259,139 / 15.16%
Duplication rate	14.76%
Clipped reads	393,039 / 22.99%

2.2. ACGT Content

Number/percentage of A's	56,754,287 / 29.64%
Number/percentage of C's	38,688,796 / 20.21%
Number/percentage of T's	56,652,770 / 29.59%
Number/percentage of G's	39,379,353 / 20.57%
Number/percentage of N's	5,889 / 0%

GC Percentage	40.77%
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2.3. Coverage

Mean	0.0619
Standard Deviation	0.7179

2.4. Mapping Quality

Mean Mapping Quality	53.11
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2.5. Insert size

Mean	106,389.78
Standard Deviation	3,182,336.74
P25/Median/P75	152 / 193 / 261

2.6. Mismatches and indels

General error rate	0.81%
Mismatches	1,466,554
Insertions	33,030
Mapped reads with at least one insertion	1.98%
Deletions	87,446
Mapped reads with at least one deletion	5.37%
Homopolymer indels	43.86%

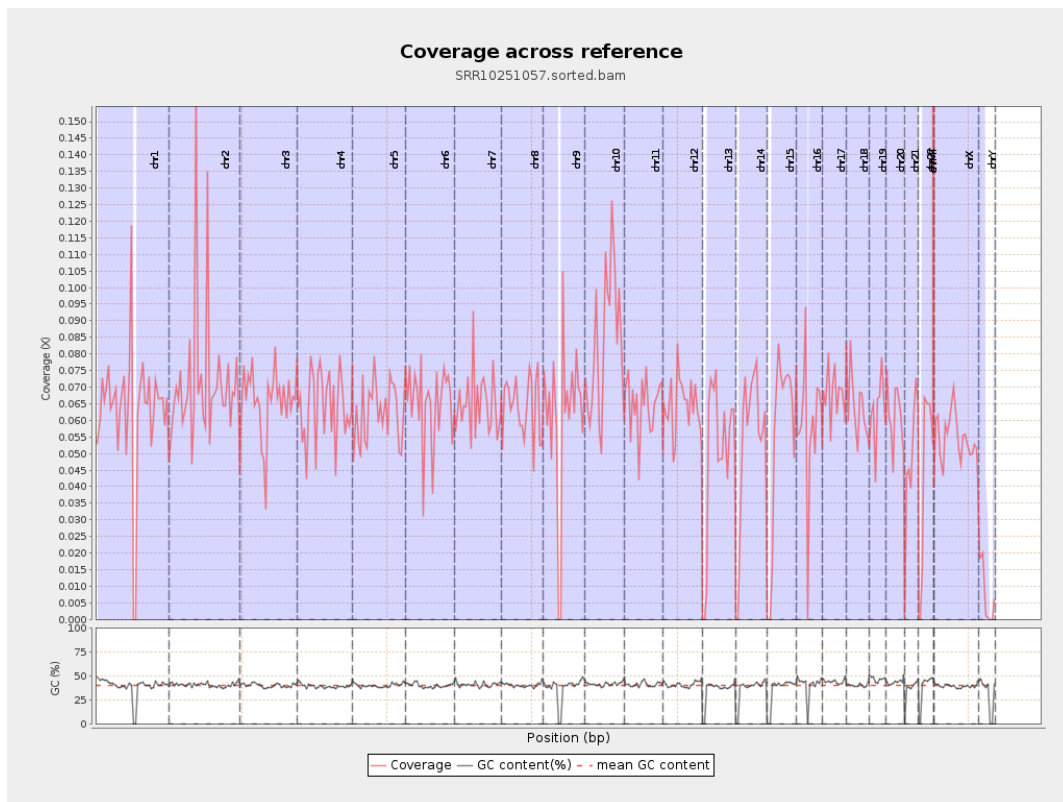
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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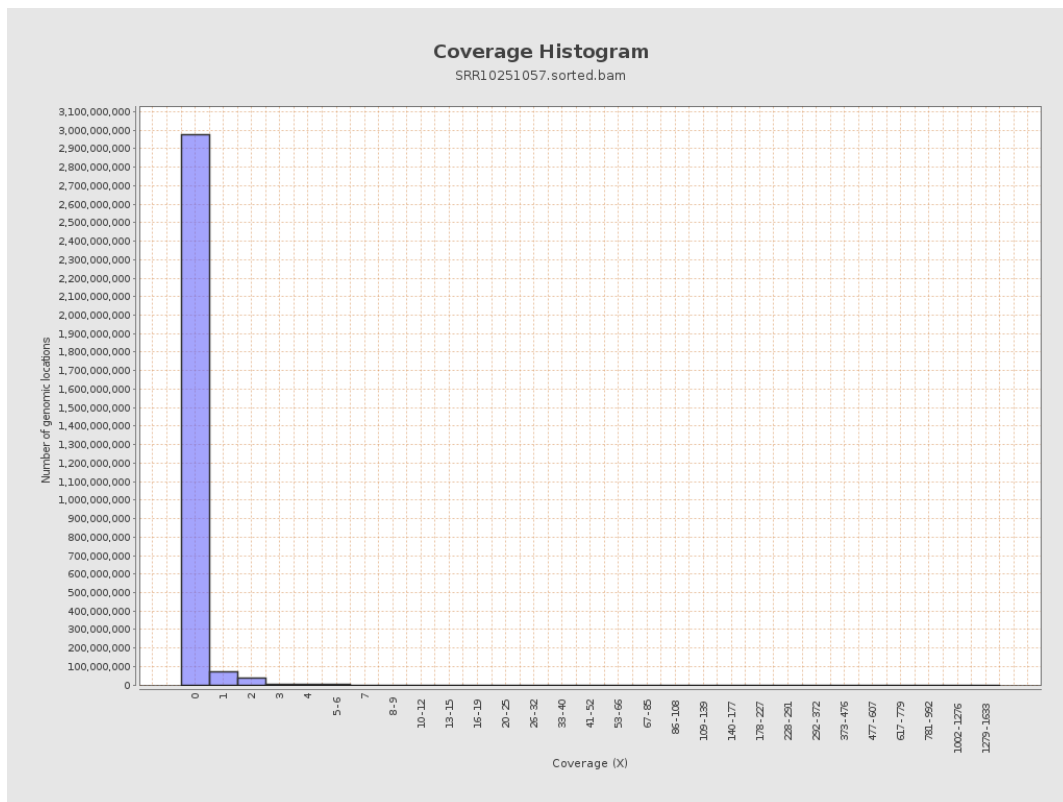
		bases	coverage	deviation
chr1	249250621	15687508	0.0629	1.4104
chr2	243199373	17376239	0.0714	1.0717
chr3	198022430	12969019	0.0655	0.3685
chr4	191154276	12169333	0.0637	0.4286
chr5	180915260	11269978	0.0623	0.3663
chr6	171115067	11094233	0.0648	0.4384
chr7	159138663	10360208	0.0651	0.8958
chr8	146364022	9321286	0.0637	0.5318
chr9	141213431	8574728	0.0607	1.0255
chr10	135534747	11298566	0.0834	0.8392
chr11	135006516	8741414	0.0647	0.5001
chr12	133851895	8629214	0.0645	0.371
chr13	115169878	5708289	0.0496	0.321
chr14	107349540	5729379	0.0534	0.3565
chr15	102531392	5684294	0.0554	0.3411
chr16	90354753	5272013	0.0583	0.6199
chr17	81195210	5485473	0.0676	0.4729
chr18	78077248	5066572	0.0649	0.8578
chr19	59128983	3691178	0.0624	0.7132
chr20	63025520	3833788	0.0608	0.3686
chr21	48129895	2361407	0.0491	0.3383
chr22	51304566	2212937	0.0431	0.3127
chrMT	16571	204206	12.3231	7.354
chrX	155270560	8469690	0.0545	0.3521

chrY	59373566	453145	0.0076	0.5229
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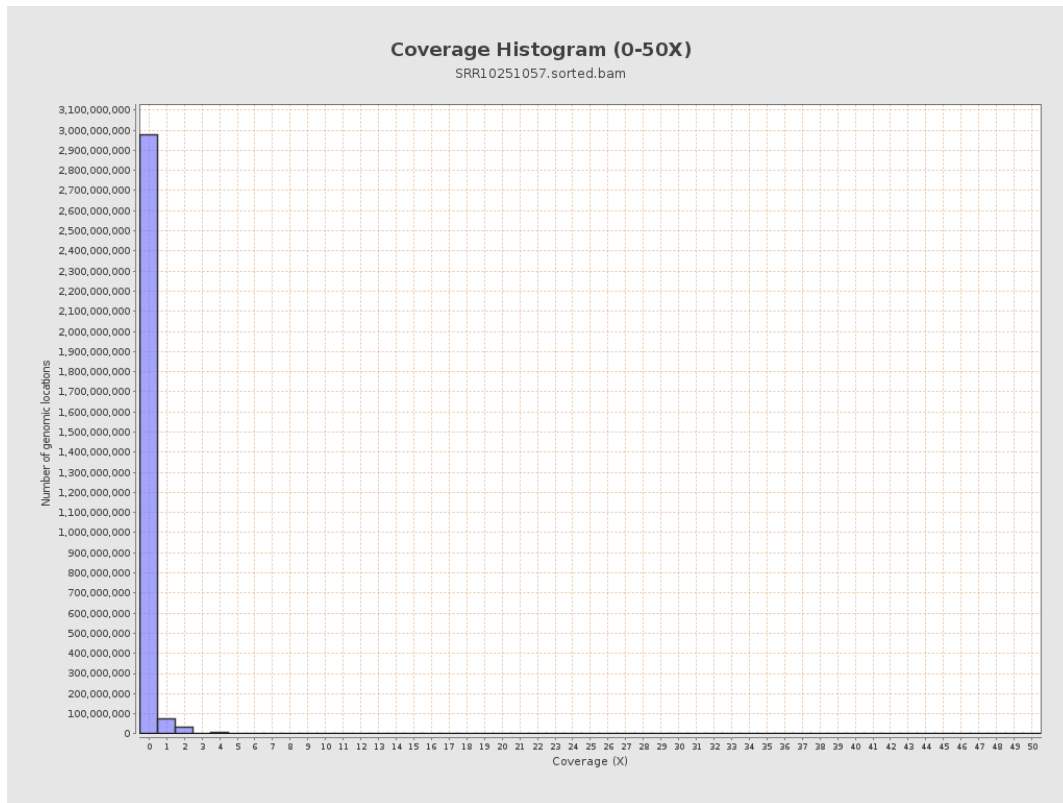
3. Results : Coverage across reference



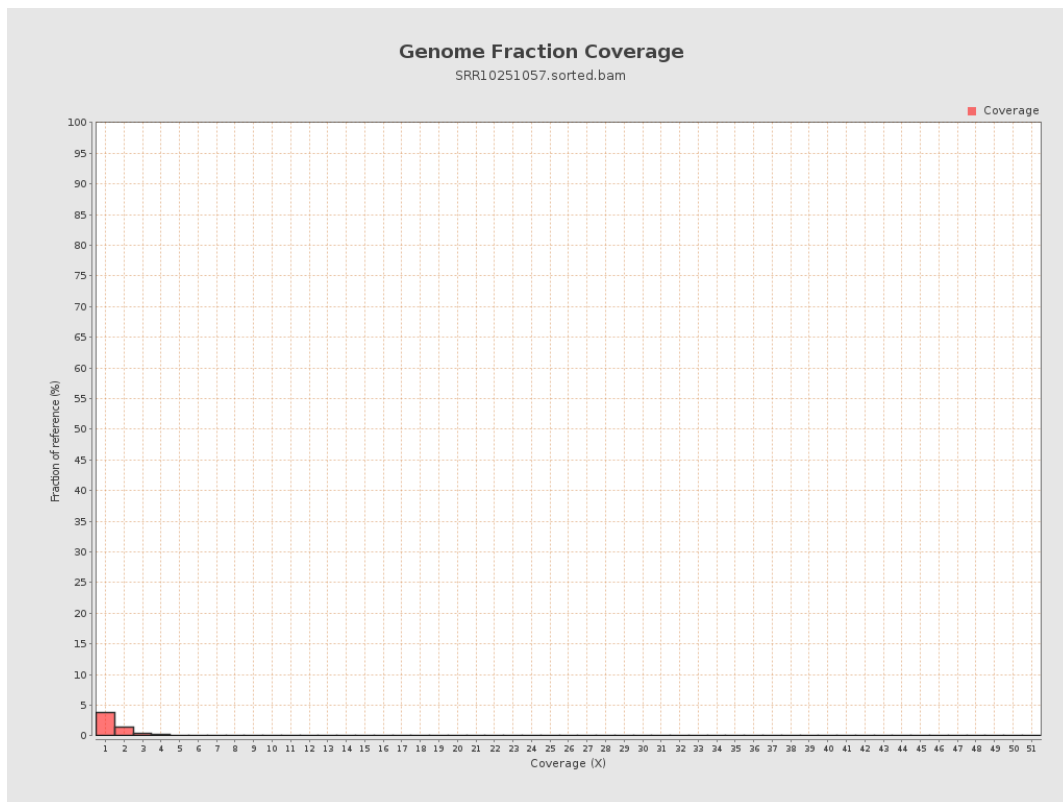
4. Results : Coverage Histogram



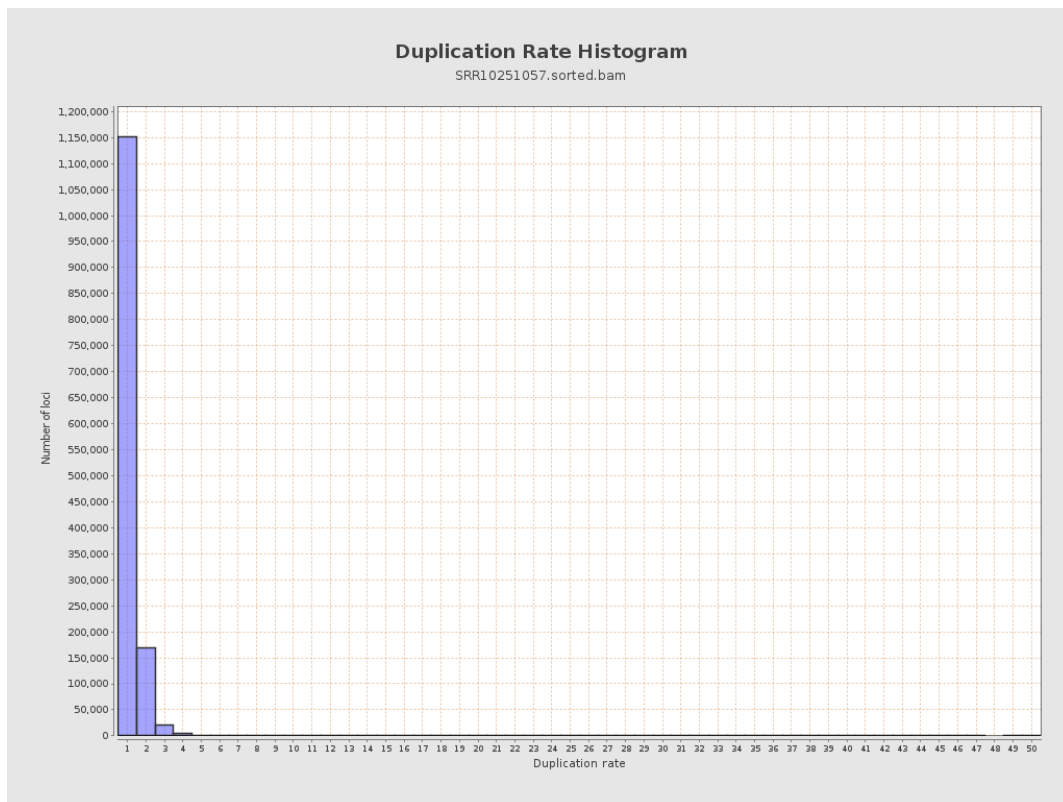
5. Results : Coverage Histogram (0-50X)



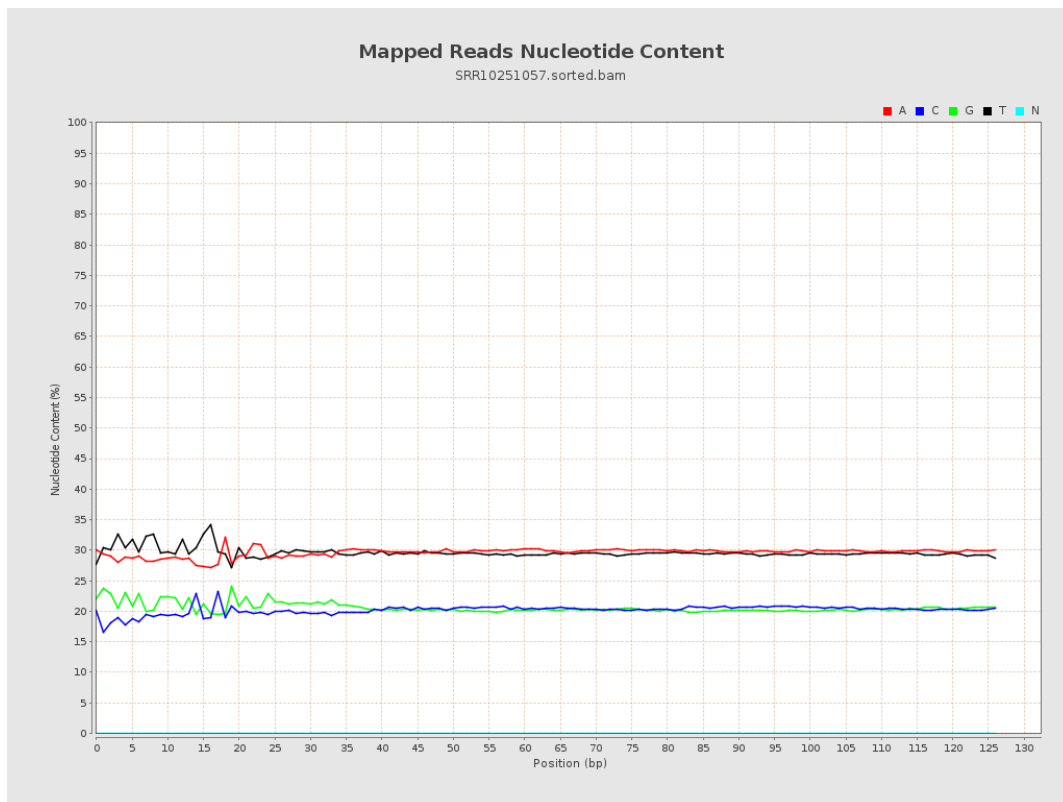
6. Results : Genome Fraction Coverage



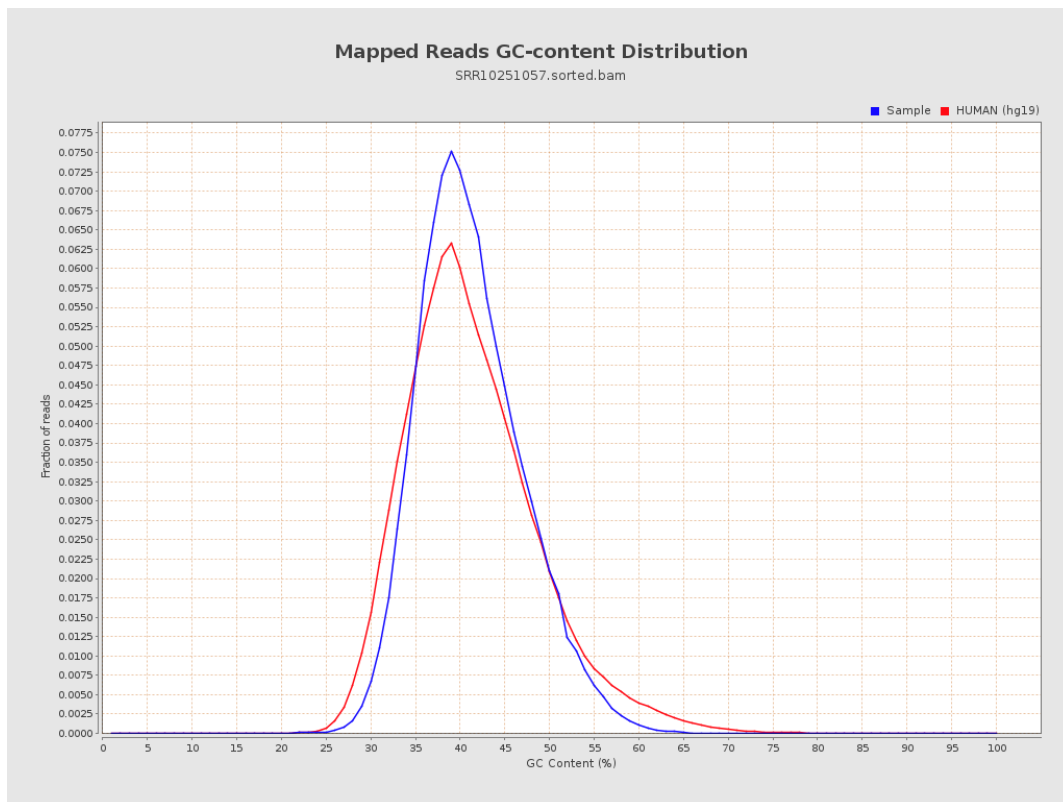
7. Results : Duplication Rate Histogram



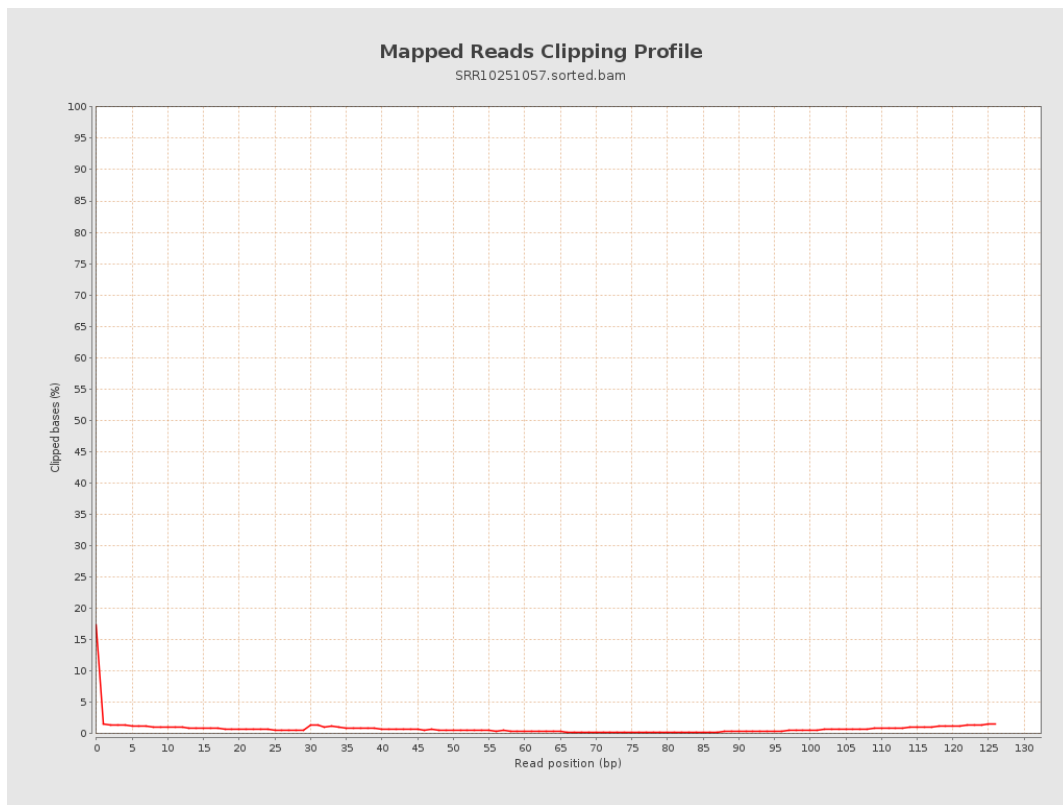
8. Results : Mapped Reads Nucleotide Content



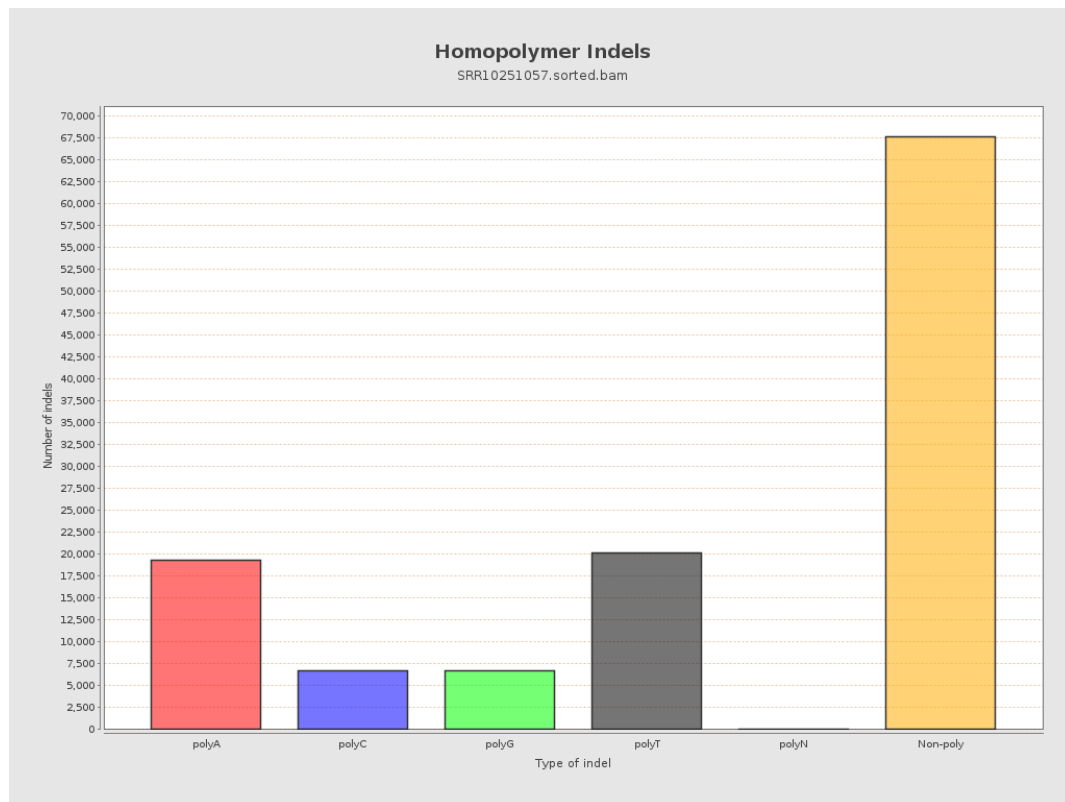
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



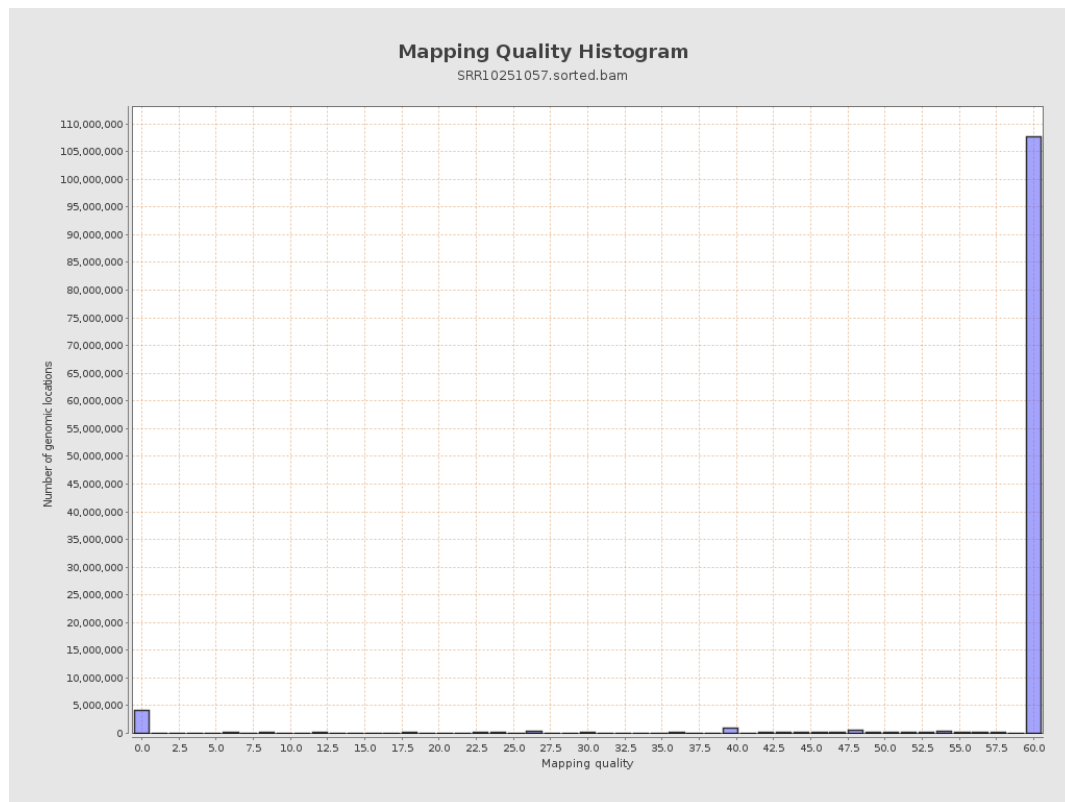
11. Results : Homopolymer Indels



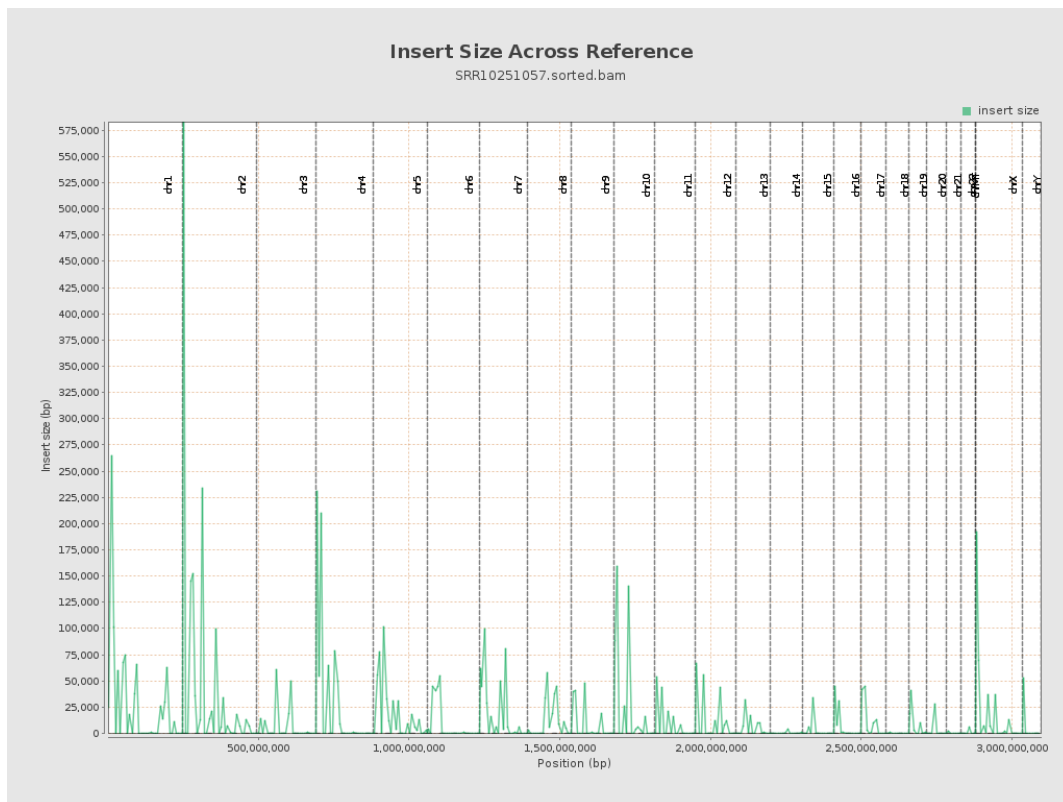
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

