

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 08:00:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173927.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_SRR10173927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173927_1.fastq.gz SRR10173927_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 08:00:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,496,860
Mapped reads	10,269,908 / 97.84%
Unmapped reads	226,952 / 2.16%
Mapped paired reads	10,269,908 / 97.84%
Mapped reads, first in pair	5,138,776 / 48.96%
Mapped reads, second in pair	5,131,132 / 48.88%
Mapped reads, both in pair	10,128,322 / 96.49%
Mapped reads, singletons	141,586 / 1.35%
Secondary alignments	0
Supplementary alignments	1,427,944 / 13.6%
Read min/max/mean length	30 / 133 / 125.49
Duplicated reads (estimated)	8,504,710 / 81.02%
Duplication rate	66.96%
Clipped reads	5,362,451 / 51.09%

2.2. ACGT Content

Number/percentage of A's	345,013,150 / 29.7%
Number/percentage of C's	231,907,217 / 19.96%
Number/percentage of T's	342,988,389 / 29.53%
Number/percentage of G's	241,663,236 / 20.8%
Number/percentage of N's	9,156 / 0%

GC Percentage	40.77%
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2.3. Coverage

Mean	0.3755
Standard Deviation	6.6499

2.4. Mapping Quality

Mean Mapping Quality	52.48
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2.5. Insert size

Mean	1,091,793
Standard Deviation	9,867,821.18
P25/Median/P75	104 / 152 / 231

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	10,076,795
Insertions	131,148
Mapped reads with at least one insertion	1.23%
Deletions	408,506
Mapped reads with at least one deletion	3.88%
Homopolymer indels	40.03%

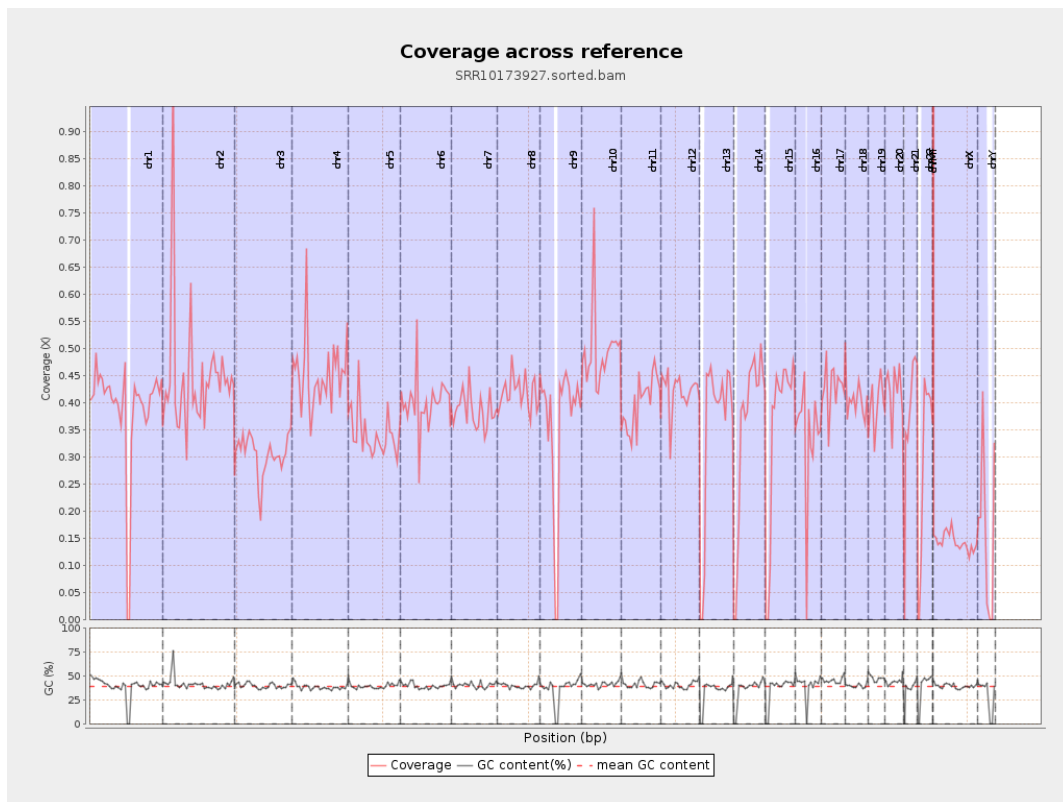
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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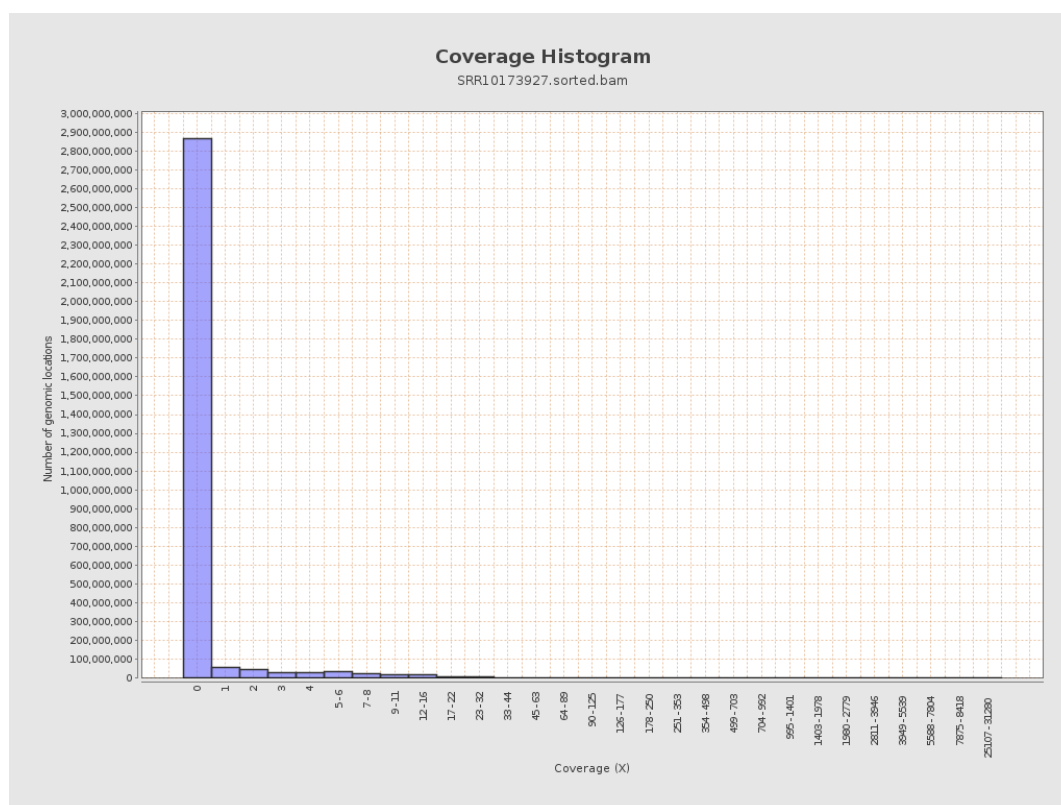
		bases	coverage	deviation
chr1	249250621	97126985	0.3897	3.1212
chr2	243199373	108516098	0.4462	21.8595
chr3	198022430	60275114	0.3044	1.7344
chr4	191154276	86663863	0.4534	2.8399
chr5	180915260	62249717	0.3441	1.8393
chr6	171115067	68291233	0.3991	2.7361
chr7	159138663	61340568	0.3855	3.234
chr8	146364022	61224472	0.4183	4.1053
chr9	141213431	50919819	0.3606	3.0981
chr10	135534747	66992966	0.4943	3.964
chr11	135006516	54031303	0.4002	2.2688
chr12	133851895	56636687	0.4231	2.1754
chr13	115169878	40976003	0.3558	1.8768
chr14	107349540	38833744	0.3618	1.9407
chr15	102531392	35662526	0.3478	1.9356
chr16	90354753	30401532	0.3365	2.2472
chr17	81195210	34782304	0.4284	2.3724
chr18	78077248	31481916	0.4032	3.8609
chr19	59128983	23373716	0.3953	2.5227
chr20	63025520	26594813	0.422	2.1515
chr21	48129895	18145989	0.377	2.6953
chr22	51304566	14726976	0.2871	2.1591
chrMT	16571	839959	50.6885	40.0639
chrX	155270560	22295850	0.1436	1.2366

chrY	59373566	10110420	0.1703	2.6973
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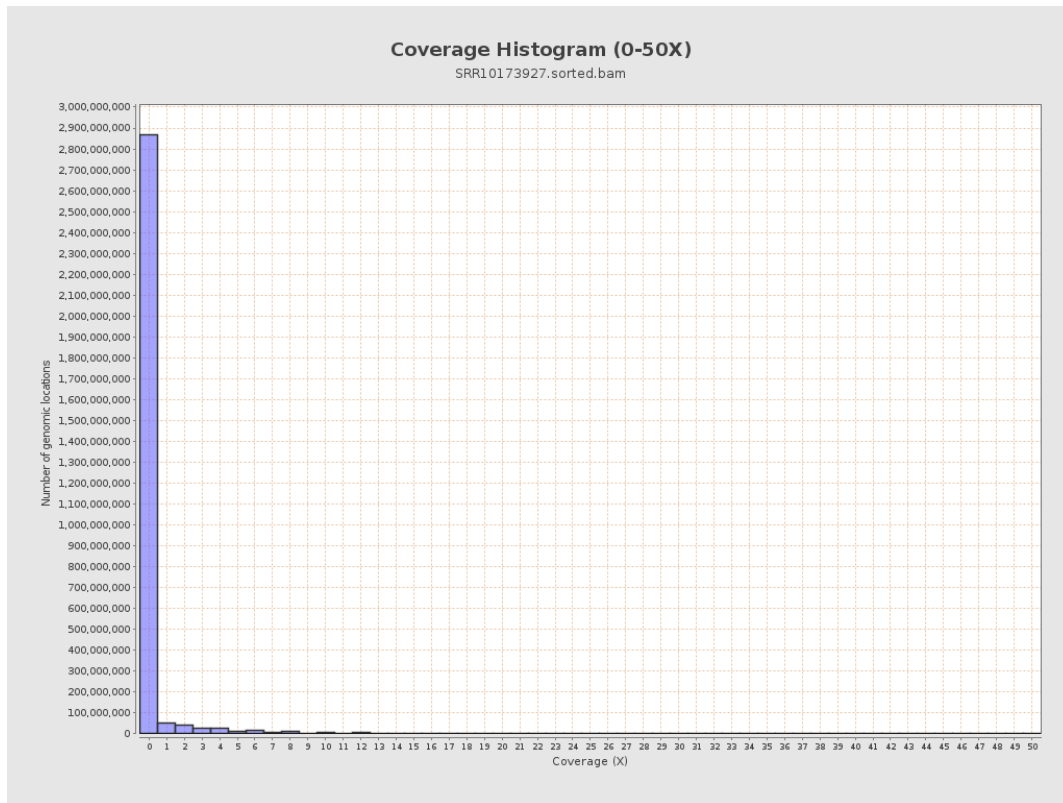
3. Results : Coverage across reference



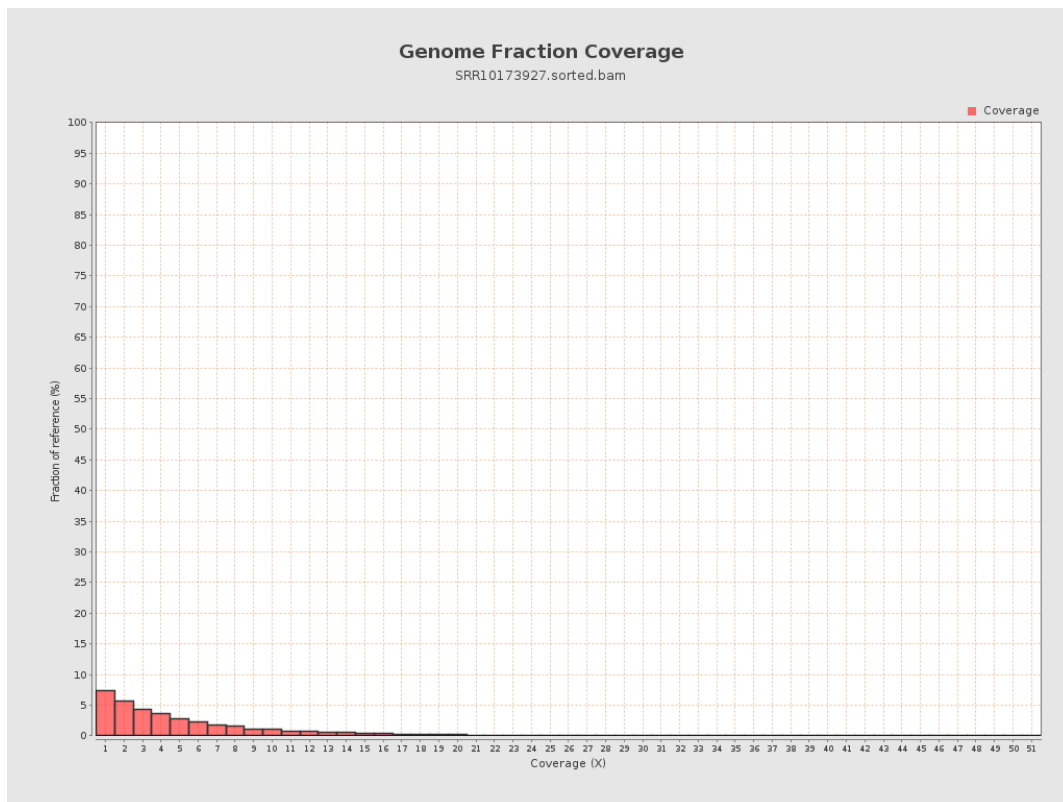
4. Results : Coverage Histogram



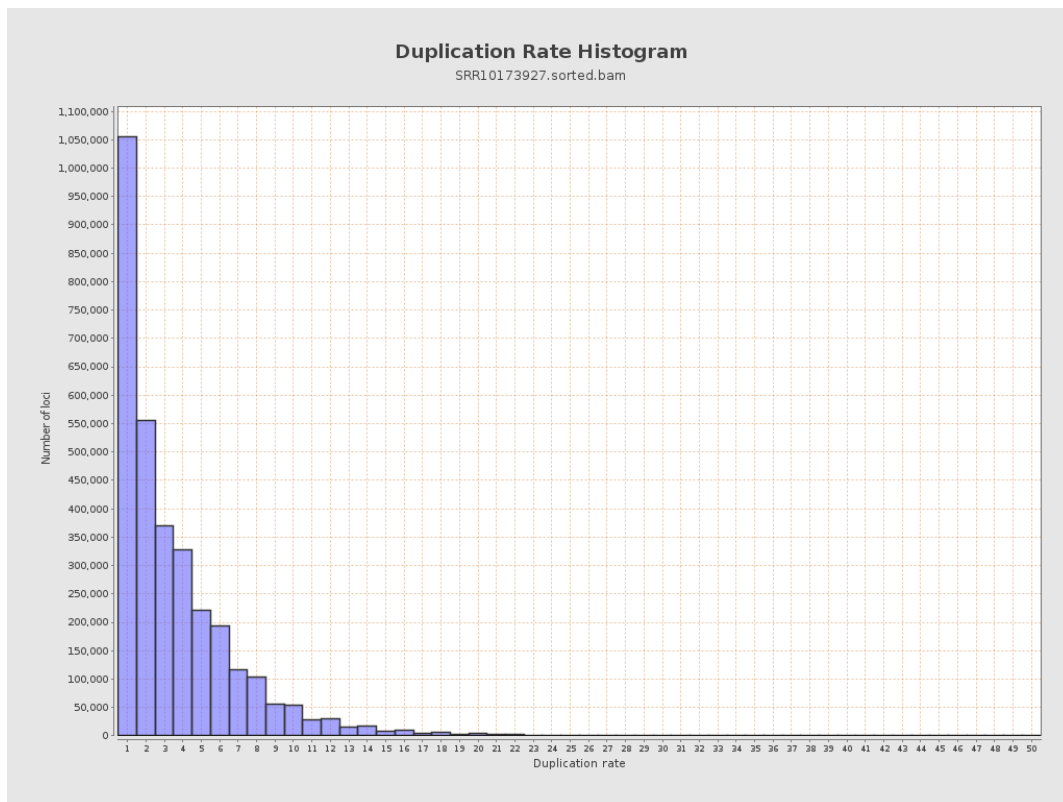
5. Results : Coverage Histogram (0-50X)



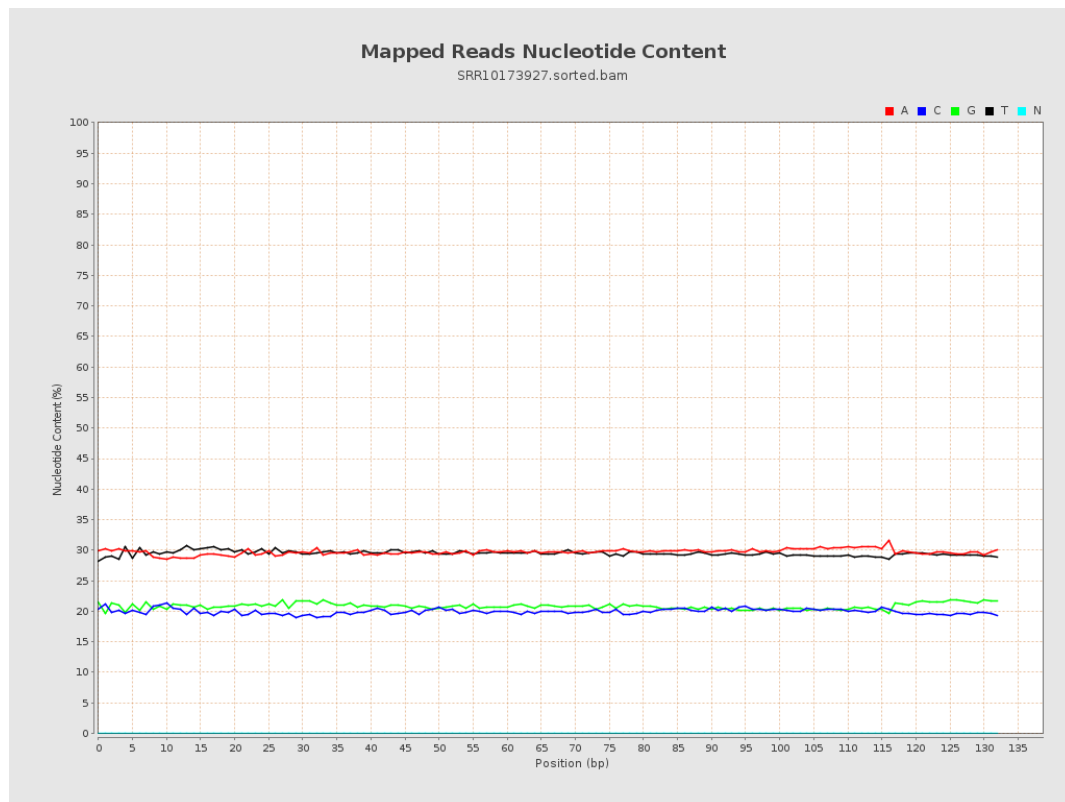
6. Results : Genome Fraction Coverage



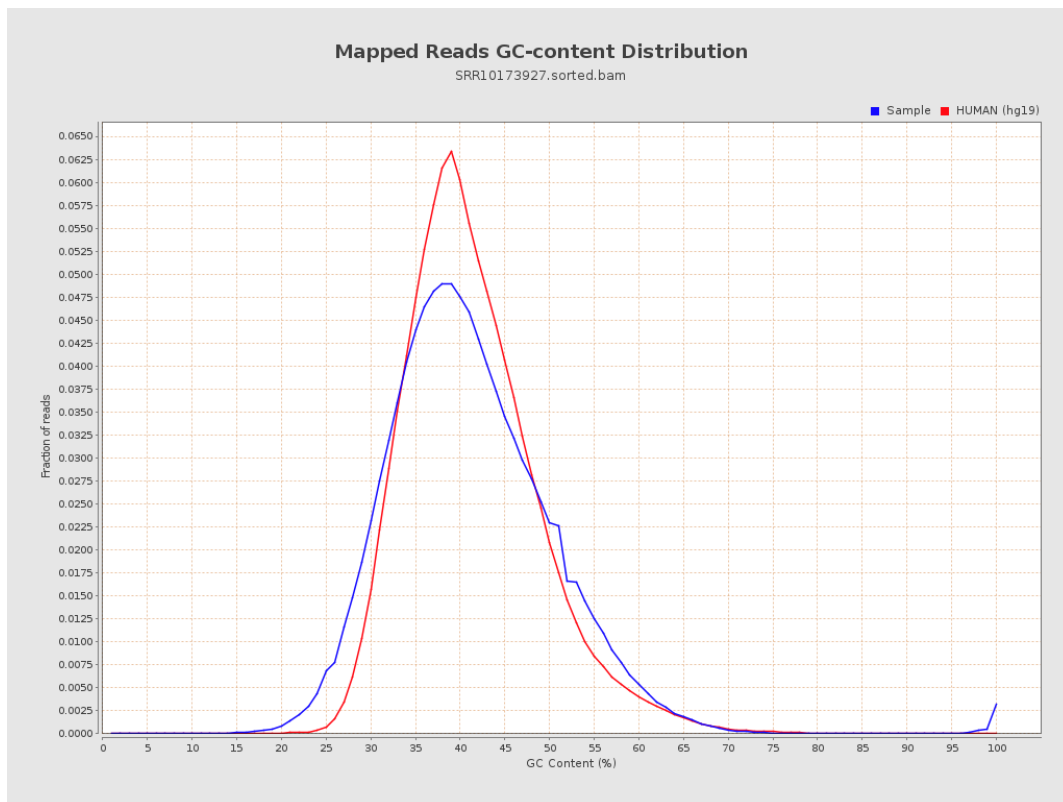
7. Results : Duplication Rate Histogram



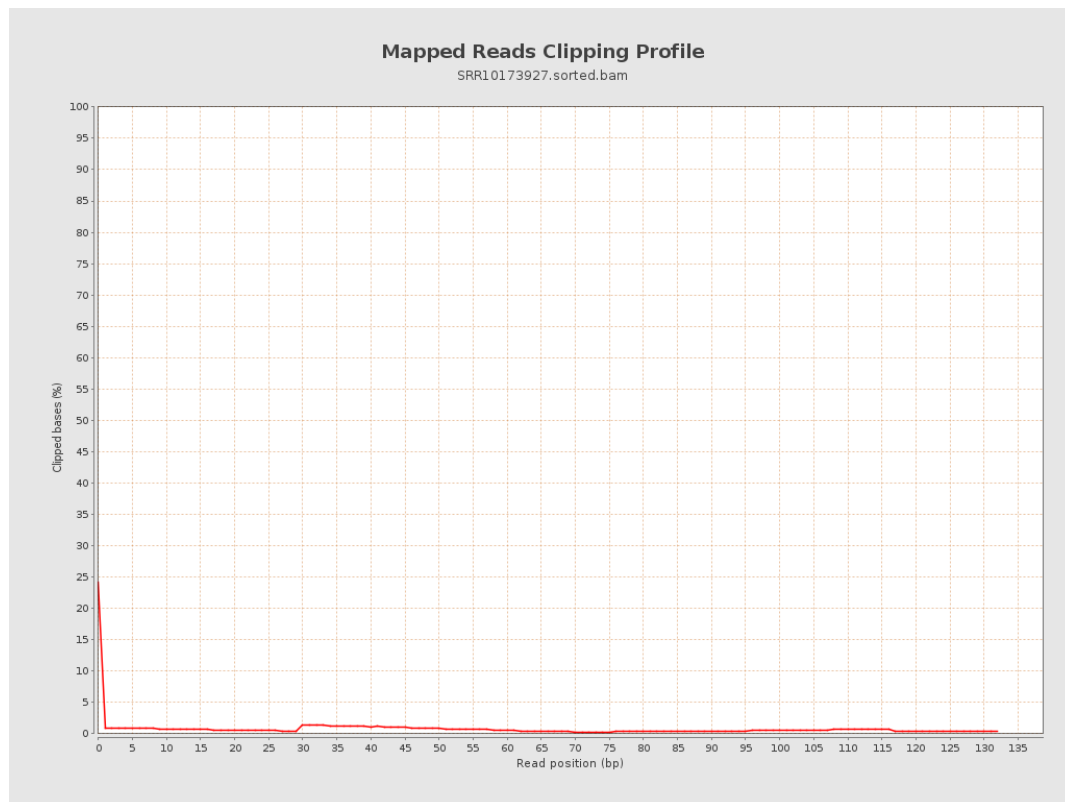
8. Results : Mapped Reads Nucleotide Content



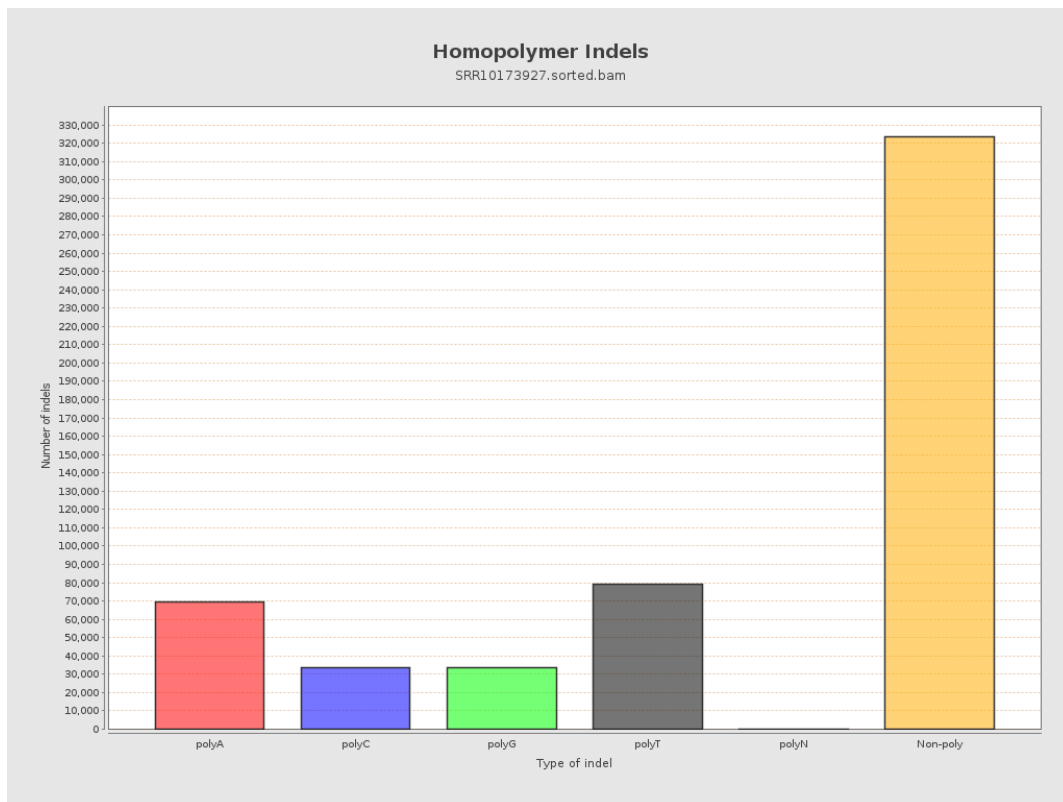
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



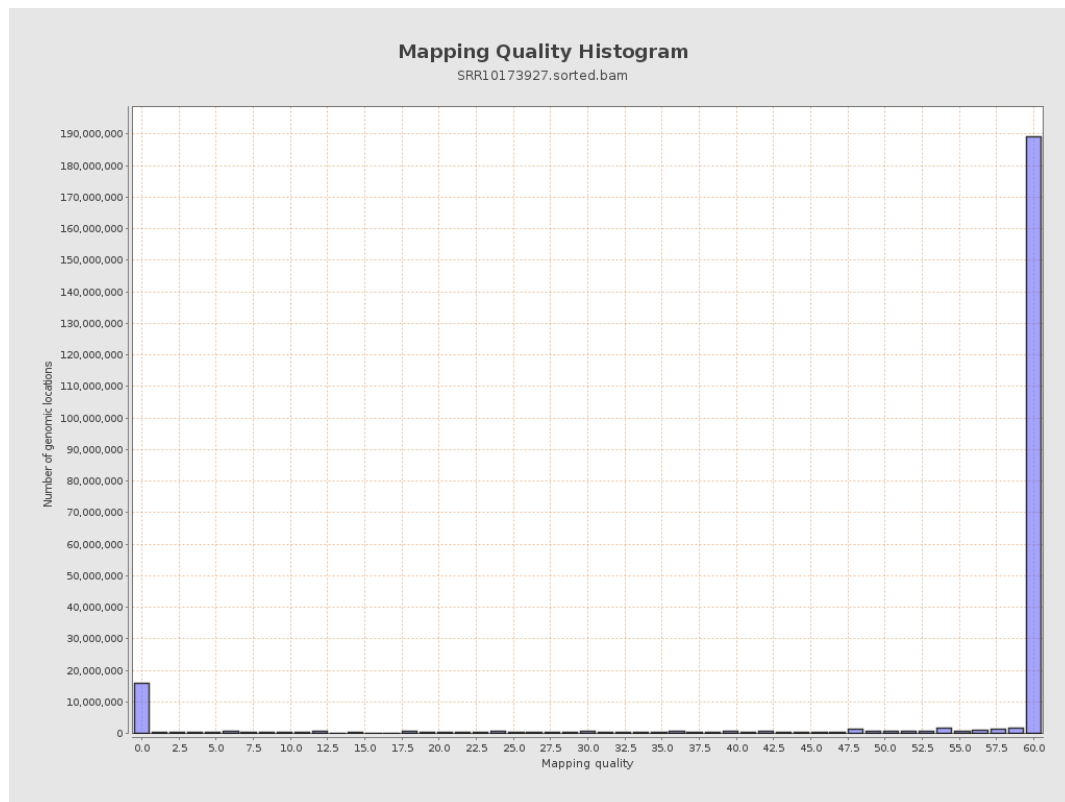
11. Results : Homopolymer Indels



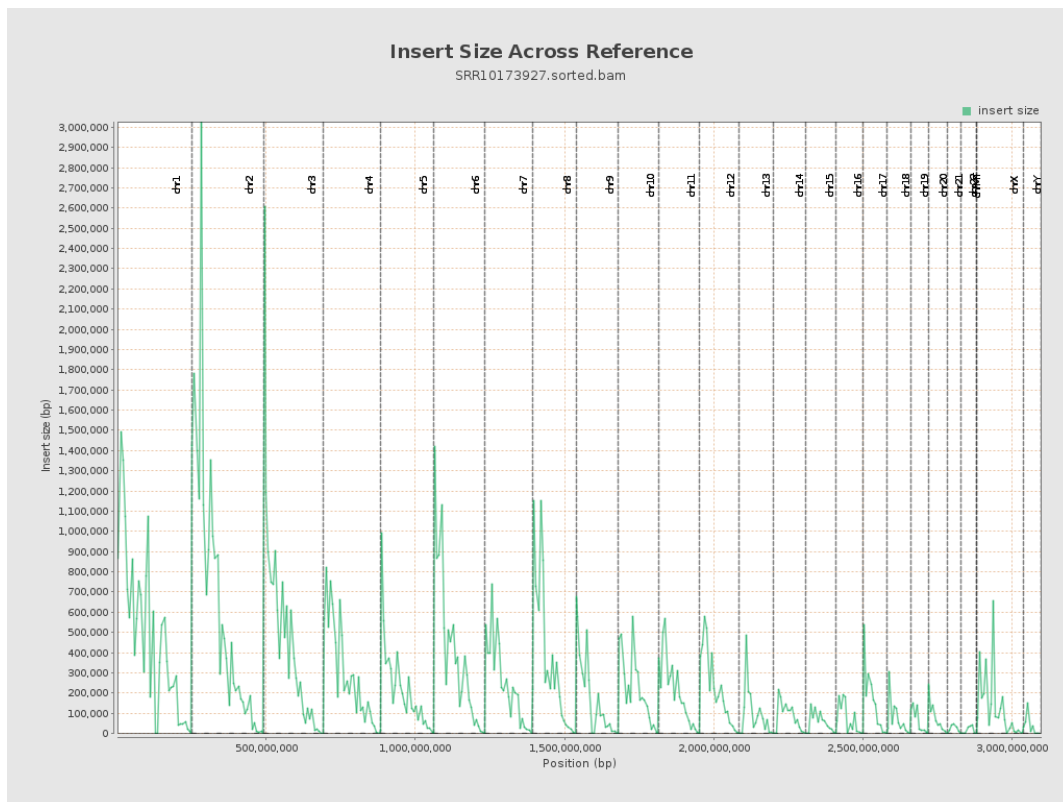
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

