

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 17:01:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173985.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_SRR10173985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173985_1.fastq.gz SRR10173985_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 17:01:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,844,084
Mapped reads	2,760,564 / 97.06%
Unmapped reads	83,520 / 2.94%
Mapped paired reads	2,760,564 / 97.06%
Mapped reads, first in pair	1,383,396 / 48.64%
Mapped reads, second in pair	1,377,168 / 48.42%
Mapped reads, both in pair	2,706,166 / 95.15%
Mapped reads, singletons	54,398 / 1.91%
Secondary alignments	0
Supplementary alignments	274,576 / 9.65%
Read min/max/mean length	30 / 133 / 128.25
Duplicated reads (estimated)	2,151,537 / 75.65%
Duplication rate	64.29%
Clipped reads	1,161,184 / 40.83%

2.2. ACGT Content

Number/percentage of A's	97,589,944 / 30%
Number/percentage of C's	64,036,512 / 19.69%
Number/percentage of T's	97,325,007 / 29.92%
Number/percentage of G's	66,324,720 / 20.39%
Number/percentage of N's	3,749 / 0%

GC Percentage	40.08%
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2.3. Coverage

Mean	0.1051
Standard Deviation	1.6794

2.4. Mapping Quality

Mean Mapping Quality	52.7
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2.5. Insert size

Mean	962,796.5
Standard Deviation	9,229,434.56
P25/Median/P75	146 / 204 / 292

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	3,458,685
Insertions	34,061
Mapped reads with at least one insertion	1.2%
Deletions	76,351
Mapped reads with at least one deletion	2.7%
Homopolymer indels	42.58%

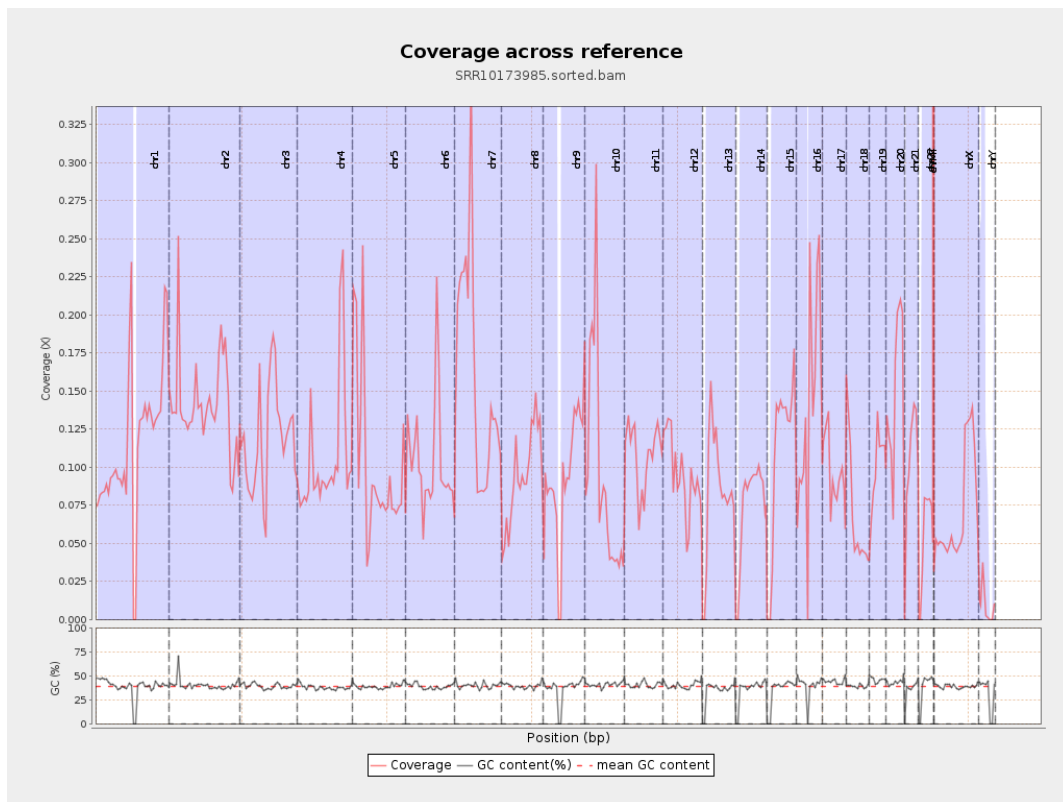
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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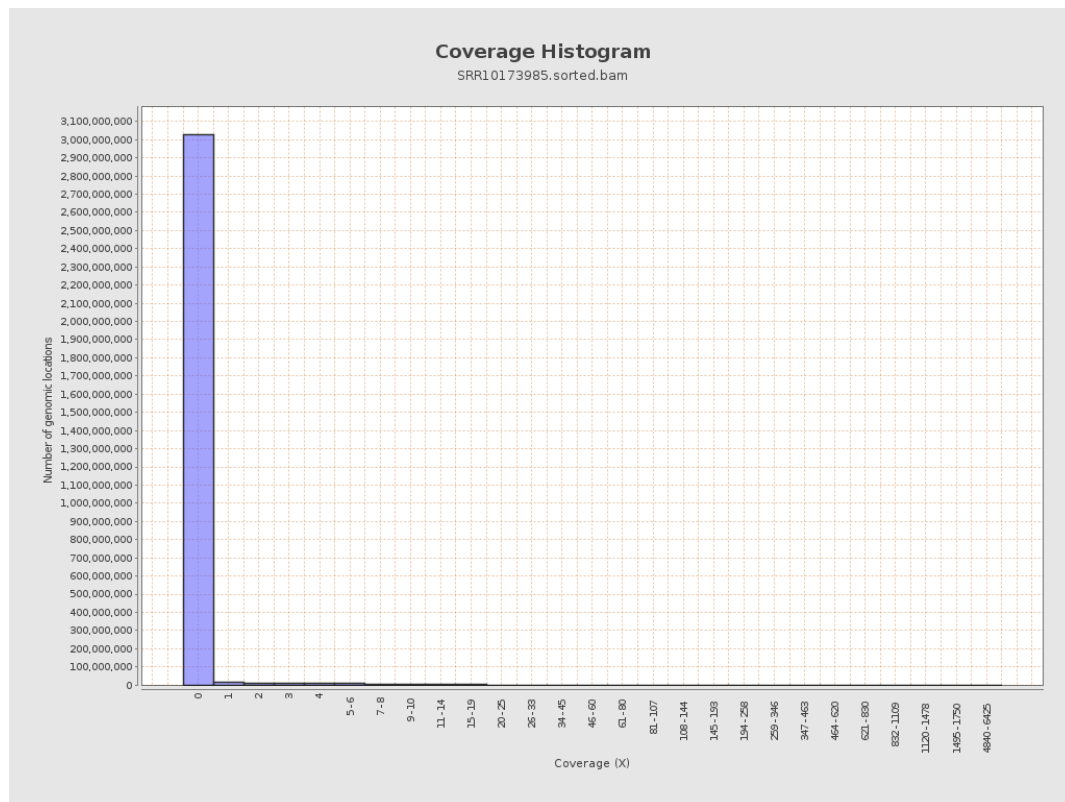
		bases	coverage	deviation
chr1	249250621	28943814	0.1161	1.3078
chr2	243199373	34280853	0.141	4.5754
chr3	198022430	23540111	0.1189	1.0099
chr4	191154276	19889037	0.104	1.0745
chr5	180915260	18379933	0.1016	0.9228
chr6	171115067	17903281	0.1046	0.9589
chr7	159138663	25391469	0.1596	1.6305
chr8	146364022	13839932	0.0946	1.1086
chr9	141213431	13174650	0.0933	1.001
chr10	135534747	12786028	0.0943	1.7062
chr11	135006516	14494491	0.1074	0.96
chr12	133851895	12605539	0.0942	0.8888
chr13	115169878	9515424	0.0826	0.8366
chr14	107349540	7971471	0.0743	0.786
chr15	102531392	11281798	0.11	0.9541
chr16	90354753	12646635	0.14	1.3849
chr17	81195210	7728127	0.0952	0.9461
chr18	78077248	5296748	0.0678	1.2029
chr19	59128983	5897959	0.0997	1.3634
chr20	63025520	9456188	0.15	1.1218
chr21	48129895	4964067	0.1031	0.9415
chr22	51304566	2773216	0.0541	0.6357
chrMT	16571	1243400	75.0347	60.0553
chrX	155270560	10938566	0.0704	0.7709

chrY	59373566	534677	0.009	0.433
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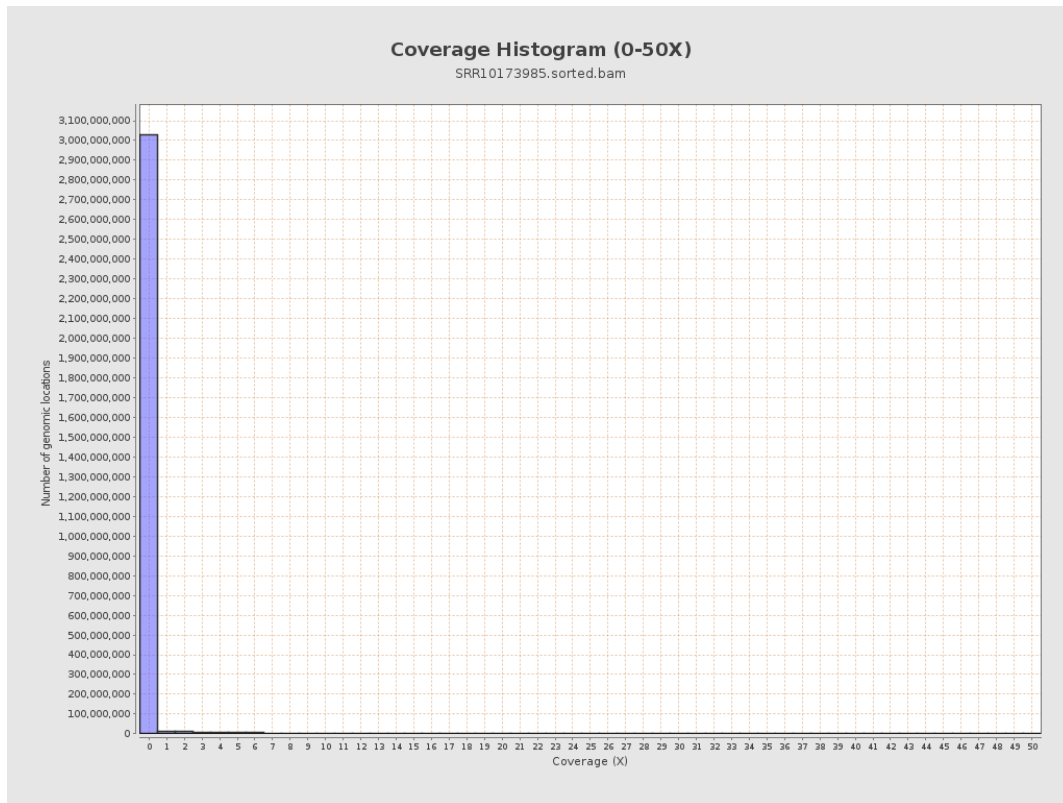
3. Results : Coverage across reference



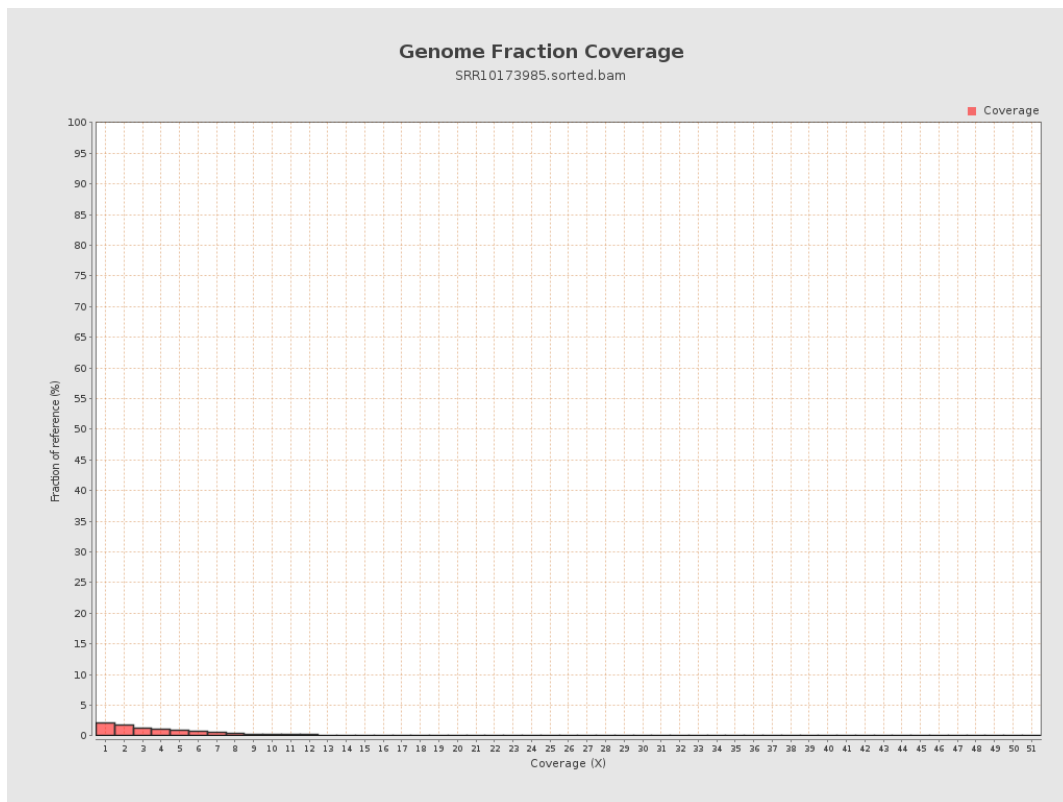
4. Results : Coverage Histogram



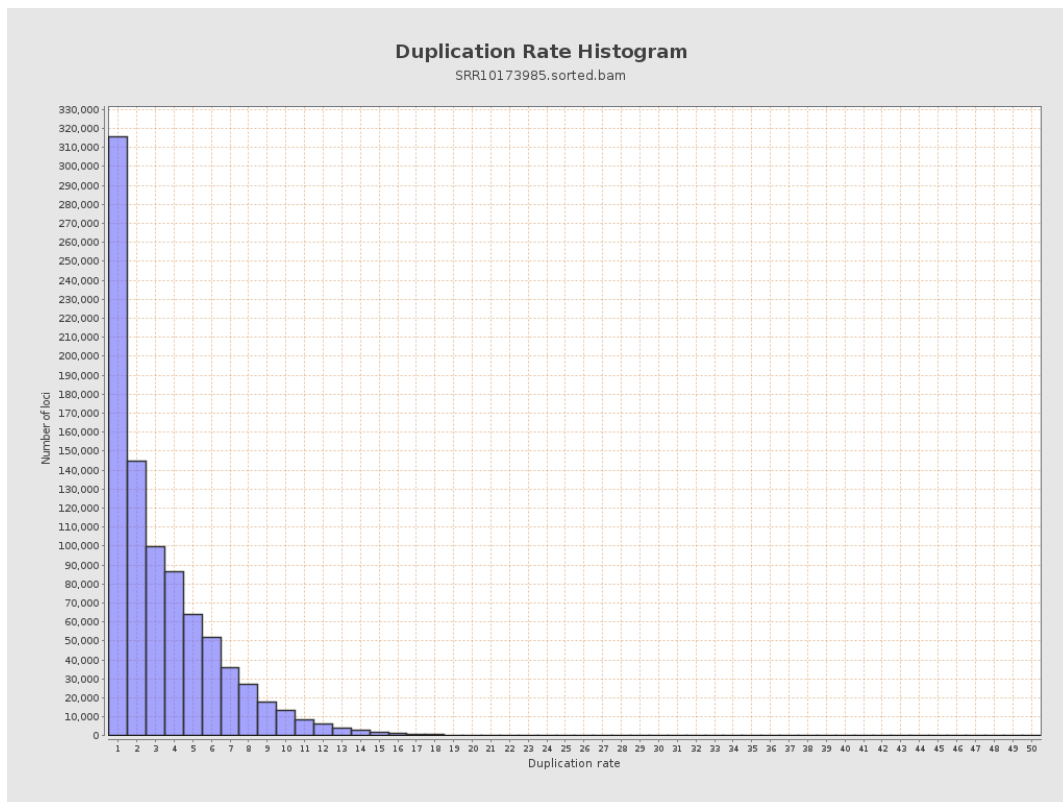
5. Results : Coverage Histogram (0-50X)



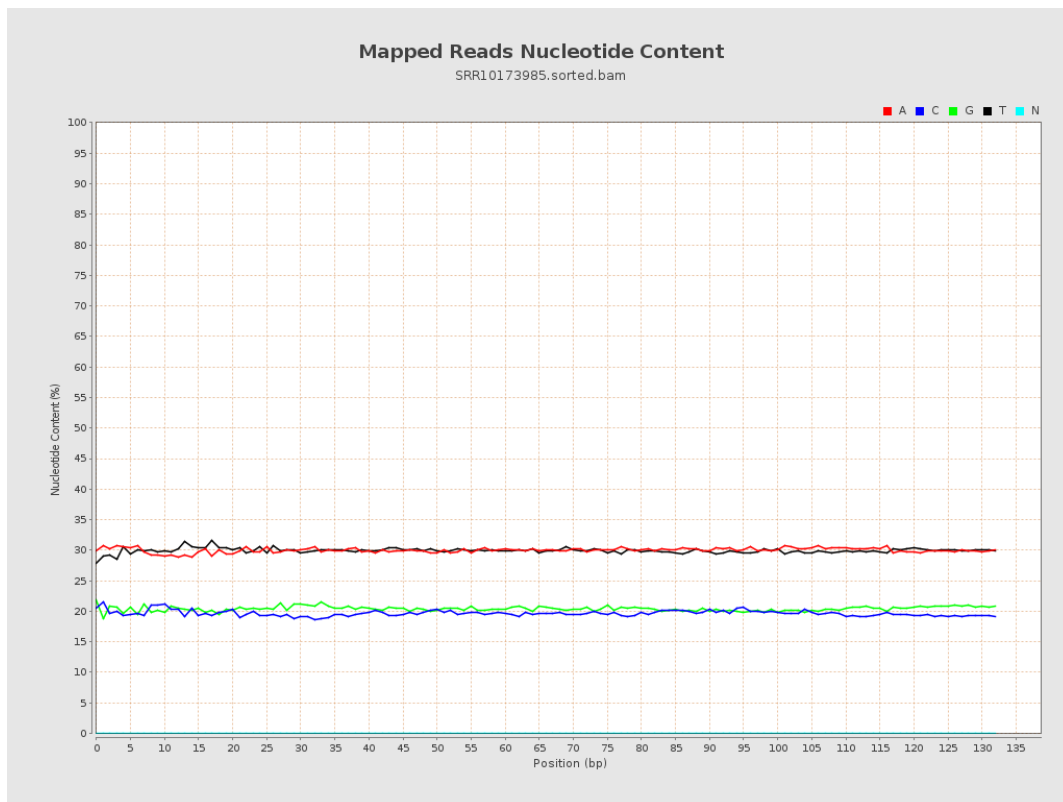
6. Results : Genome Fraction Coverage



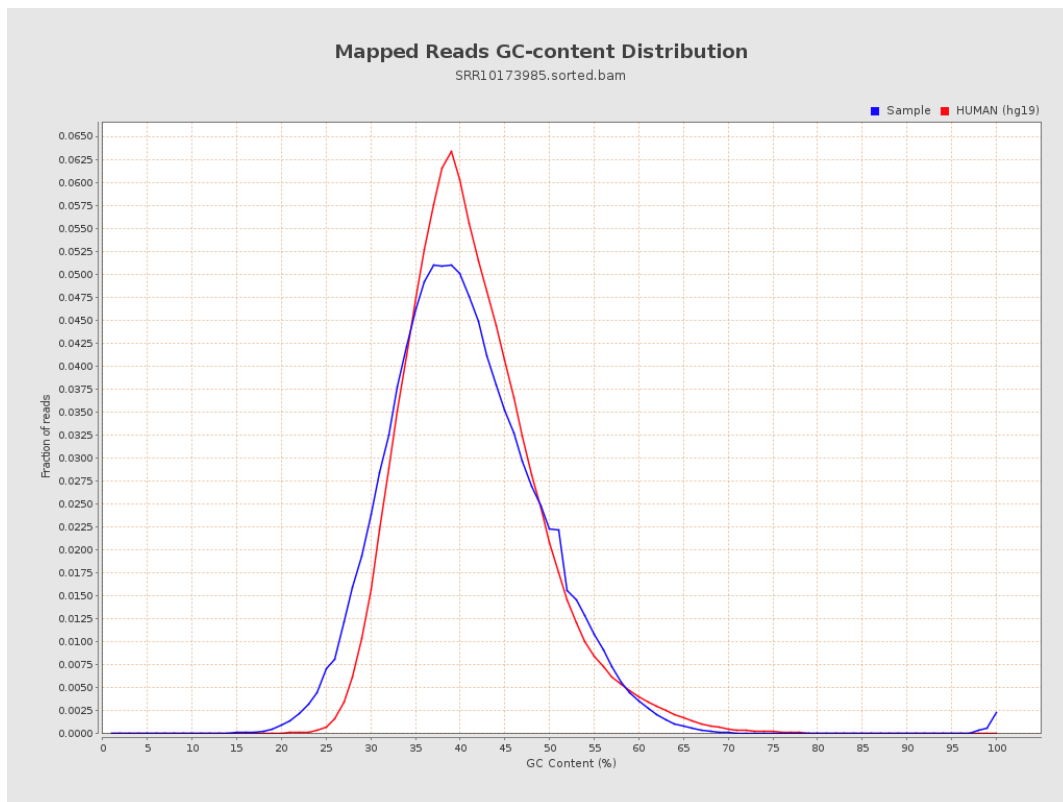
7. Results : Duplication Rate Histogram



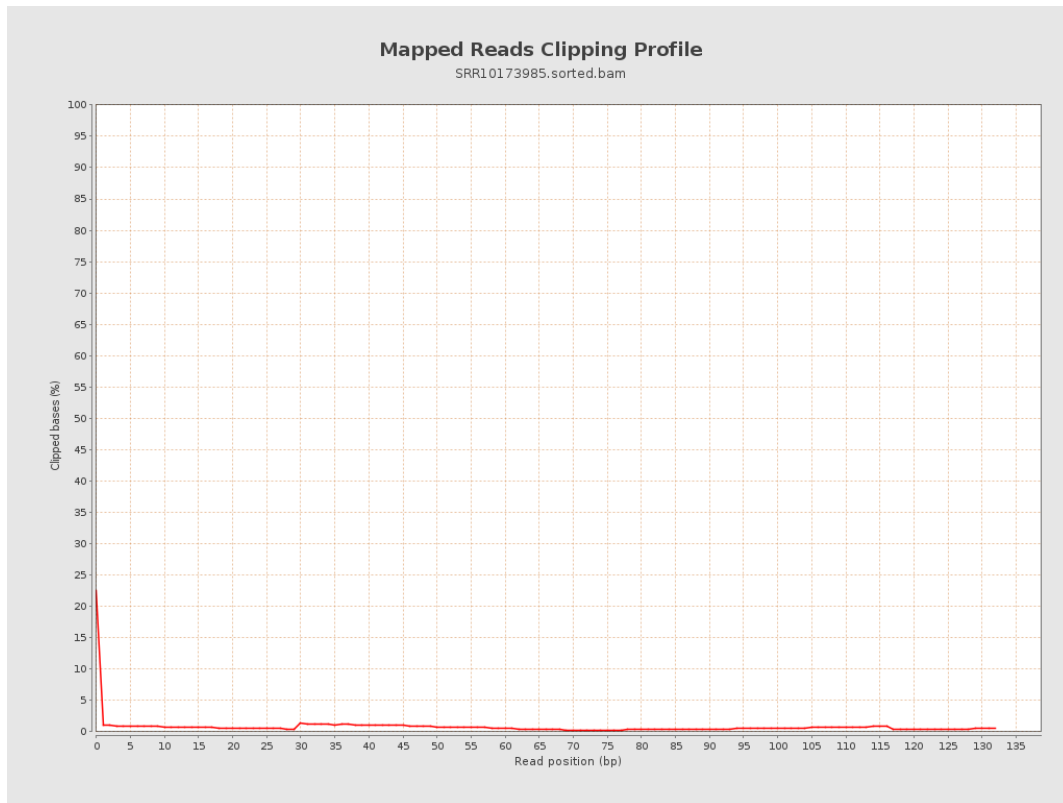
8. Results : Mapped Reads Nucleotide Content



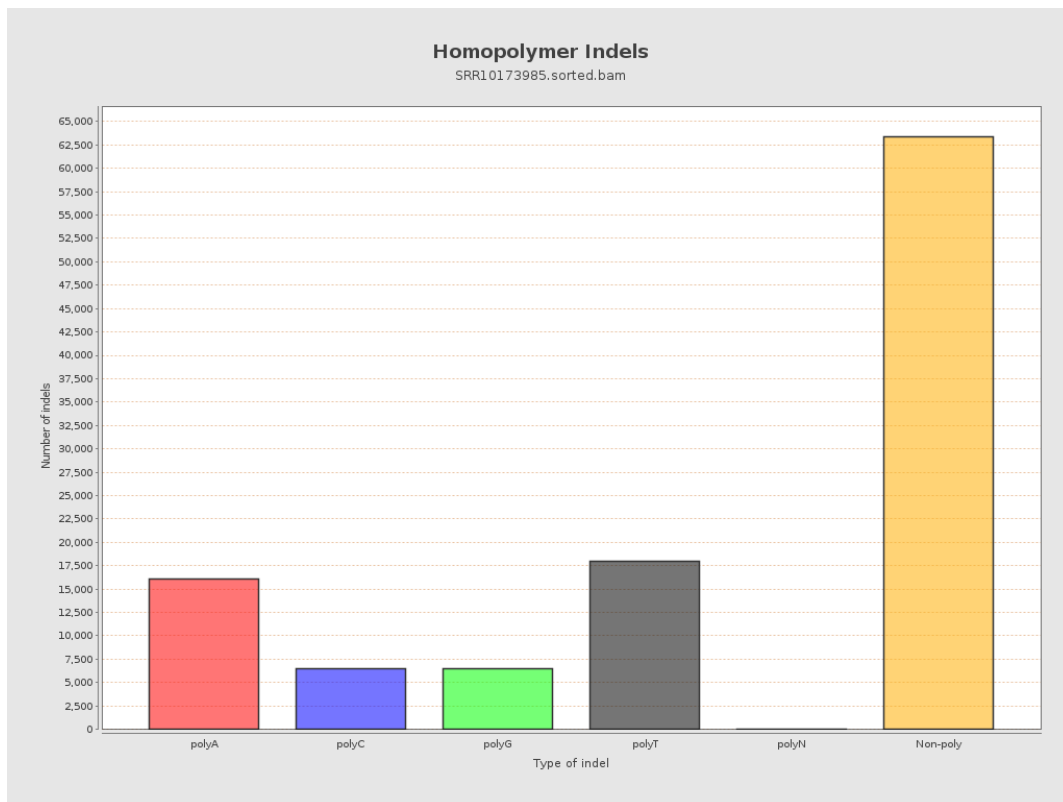
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



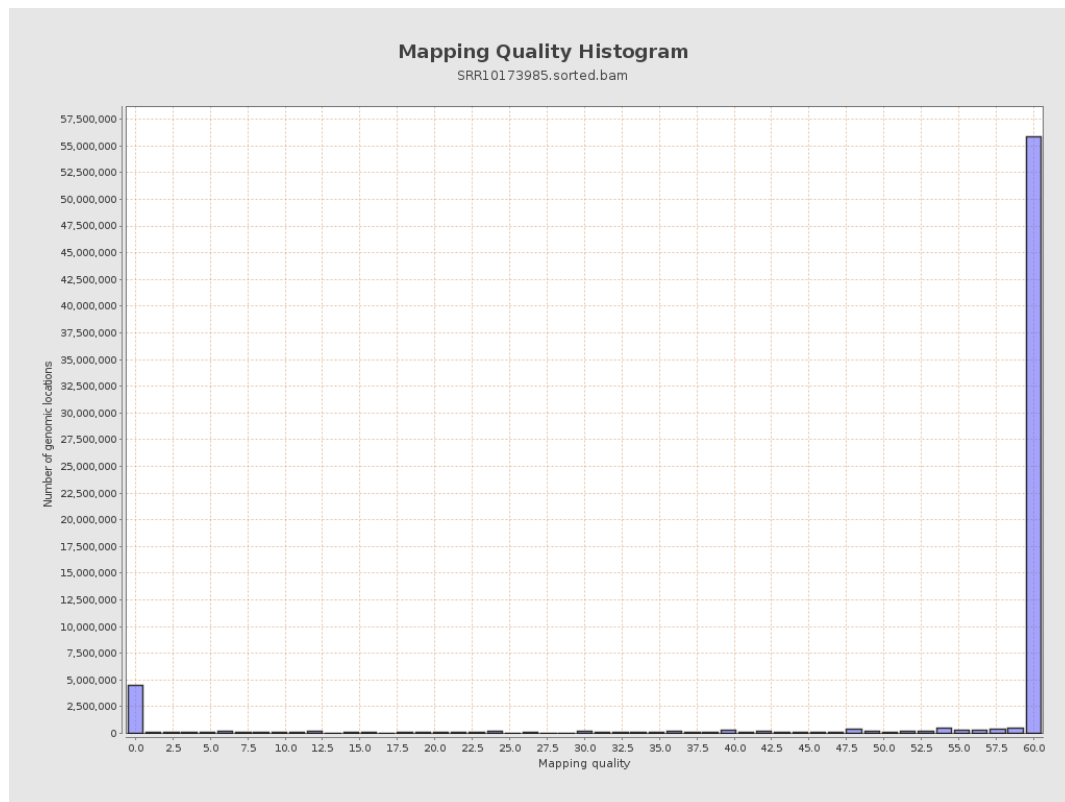
11. Results : Homopolymer Indels



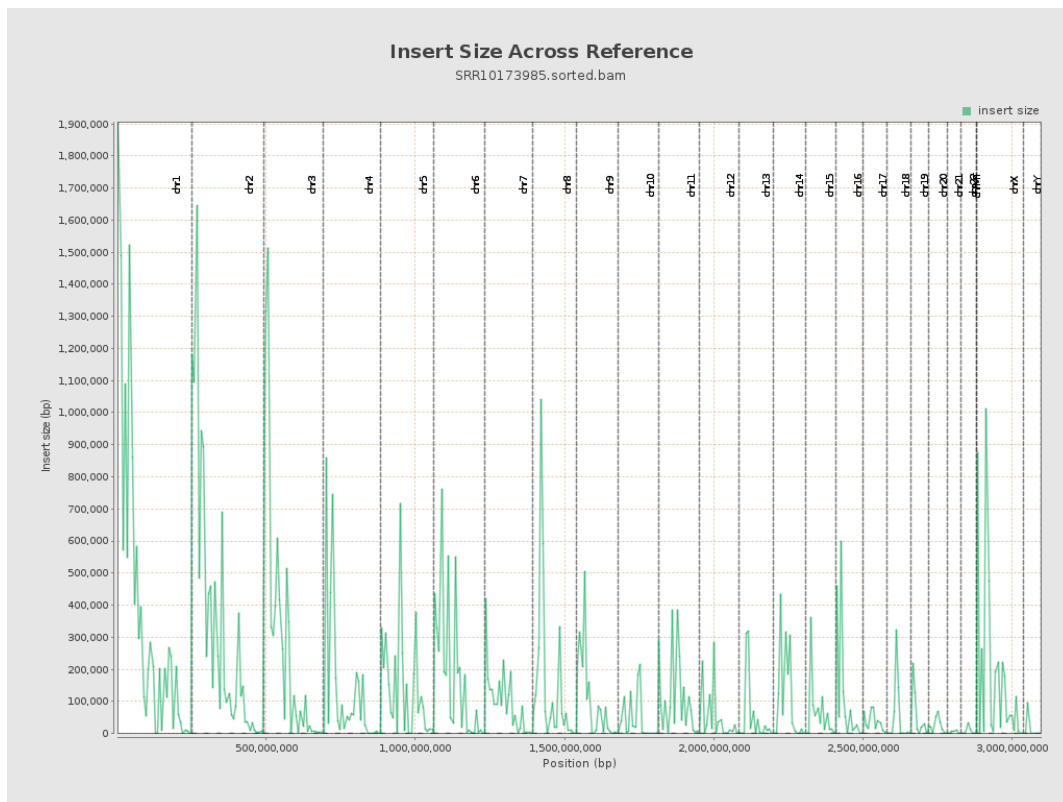
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

