

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 18:22:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006084.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_SRR1006084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006084_1.fastq.gz SRR1006084_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 18:22:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,288,266
Mapped reads	7,919,152 / 85.26%
Unmapped reads	1,369,114 / 14.74%
Mapped paired reads	7,919,152 / 85.26%
Mapped reads, first in pair	4,009,928 / 43.17%
Mapped reads, second in pair	3,909,224 / 42.09%
Mapped reads, both in pair	7,131,254 / 76.78%
Mapped reads, singletons	787,898 / 8.48%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,201,363 / 12.93%
Duplication rate	13.68%
Clipped reads	838,168 / 9.02%

2.2. ACGT Content

Number/percentage of A's	79,779,297 / 26.19%
Number/percentage of C's	68,180,113 / 22.38%
Number/percentage of T's	83,486,258 / 27.4%
Number/percentage of G's	73,189,829 / 24.02%
Number/percentage of N's	12,327 / 0%
GC Percentage	46.4%

2.3. Coverage

Mean	0.0984
Standard Deviation	0.7648

2.4. Mapping Quality

Mean Mapping Quality	45.56
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2.5. Insert size

Mean	89,811.45
Standard Deviation	2,975,573.69
P25/Median/P75	66 / 94 / 125

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	1,629,806
Insertions	11,400
Mapped reads with at least one insertion	0.14%
Deletions	26,759
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.68%

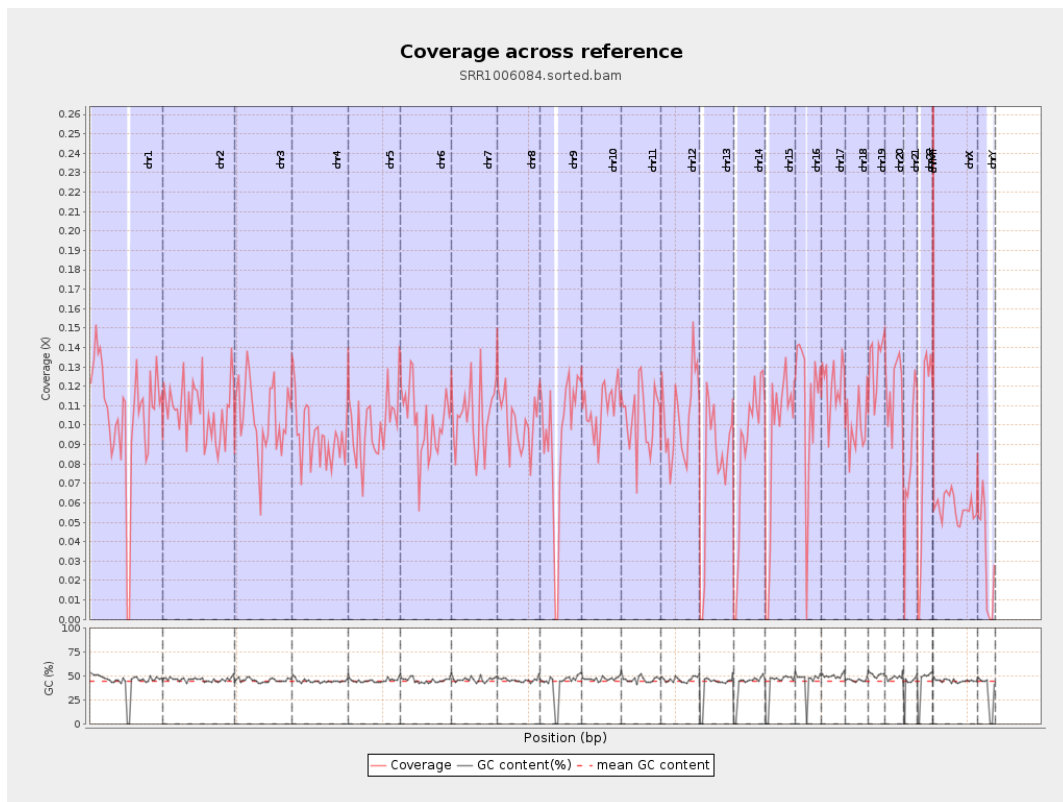
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

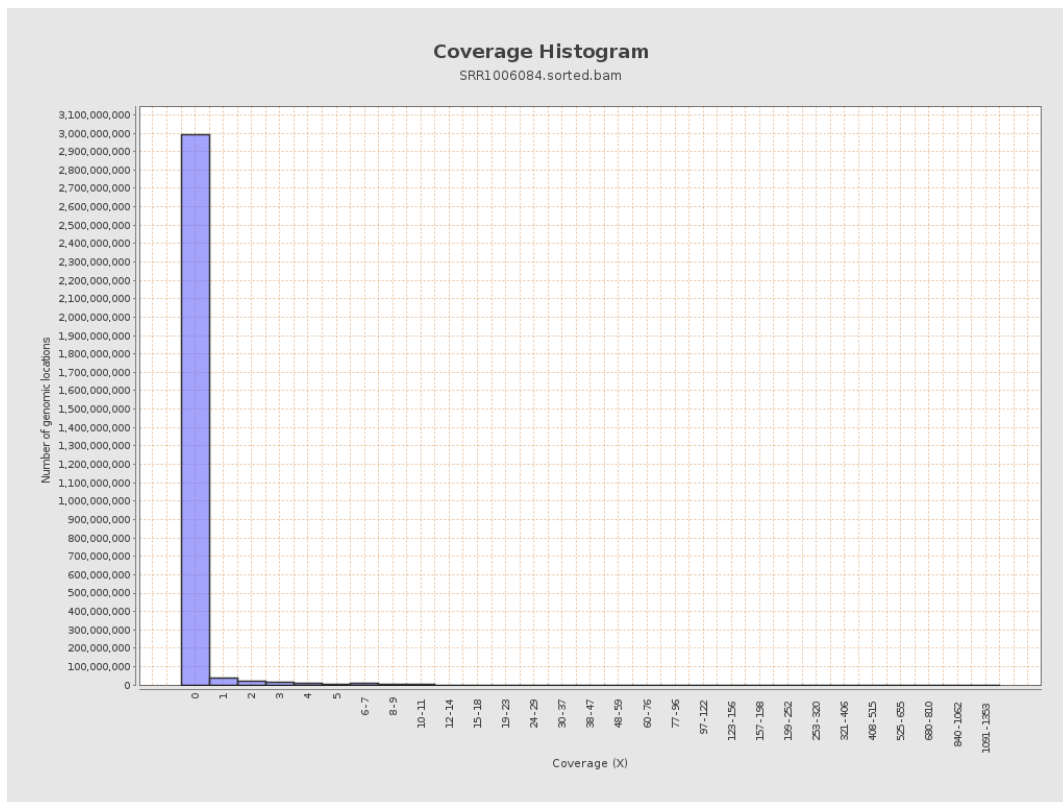
chr1	249250621	26204013	0.1051	0.8823
chr2	243199373	26184709	0.1077	0.7947
chr3	198022430	20608426	0.1041	0.7257
chr4	191154276	17988940	0.0941	0.7101
chr5	180915260	18126795	0.1002	0.713
chr6	171115067	17350457	0.1014	0.7801
chr7	159138663	16749645	0.1053	0.8516
chr8	146364022	14829227	0.1013	0.7858
chr9	141213431	13201424	0.0935	0.7036
chr10	135534747	14732617	0.1087	0.7666
chr11	135006516	14034972	0.104	1.0173
chr12	133851895	14094958	0.1053	0.7386
chr13	115169878	9036626	0.0785	0.635
chr14	107349540	9481733	0.0883	0.676
chr15	102531392	9445394	0.0921	0.692
chr16	90354753	10119129	0.112	0.7713
chr17	81195210	9863371	0.1215	0.8297
chr18	78077248	7691678	0.0985	0.772
chr19	59128983	7823149	0.1323	0.9568
chr20	63025520	7478117	0.1187	0.7989
chr21	48129895	4045229	0.084	0.6922
chr22	51304566	4627922	0.0902	0.7058
chrMT	16571	20232	1.2209	2.8277
chrX	155270560	9015036	0.0581	0.5364

chrY	59373566	1927783	0.0325	0.3848
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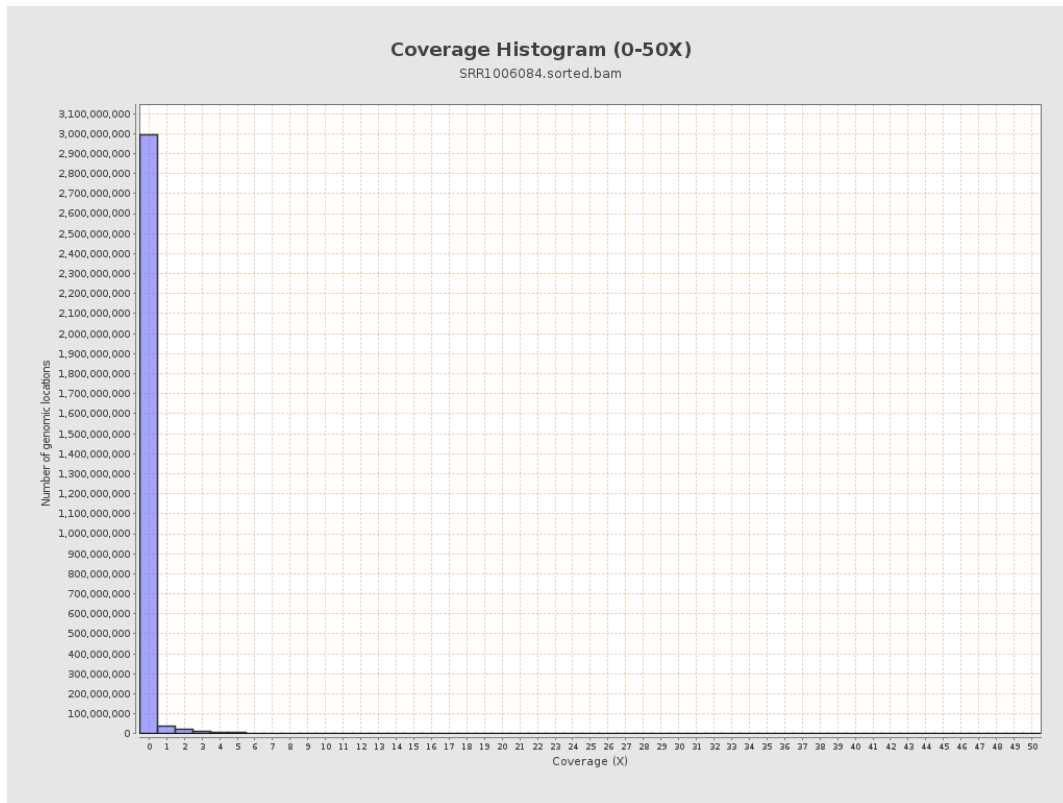
3. Results : Coverage across reference



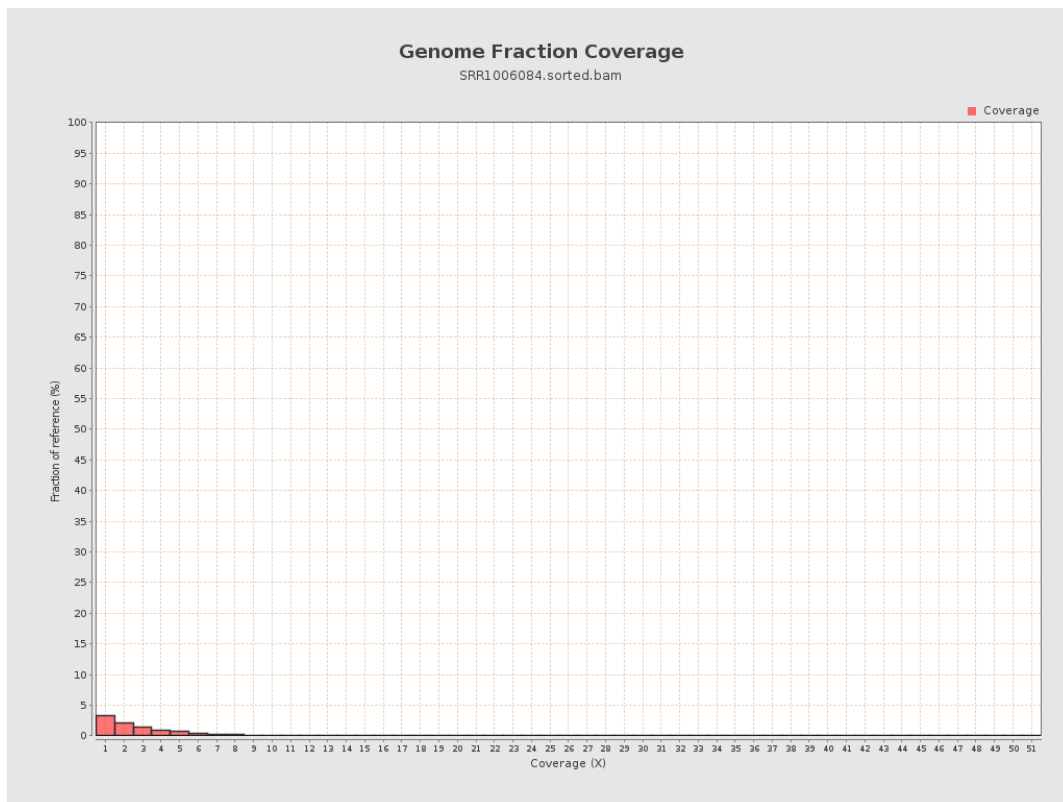
4. Results : Coverage Histogram



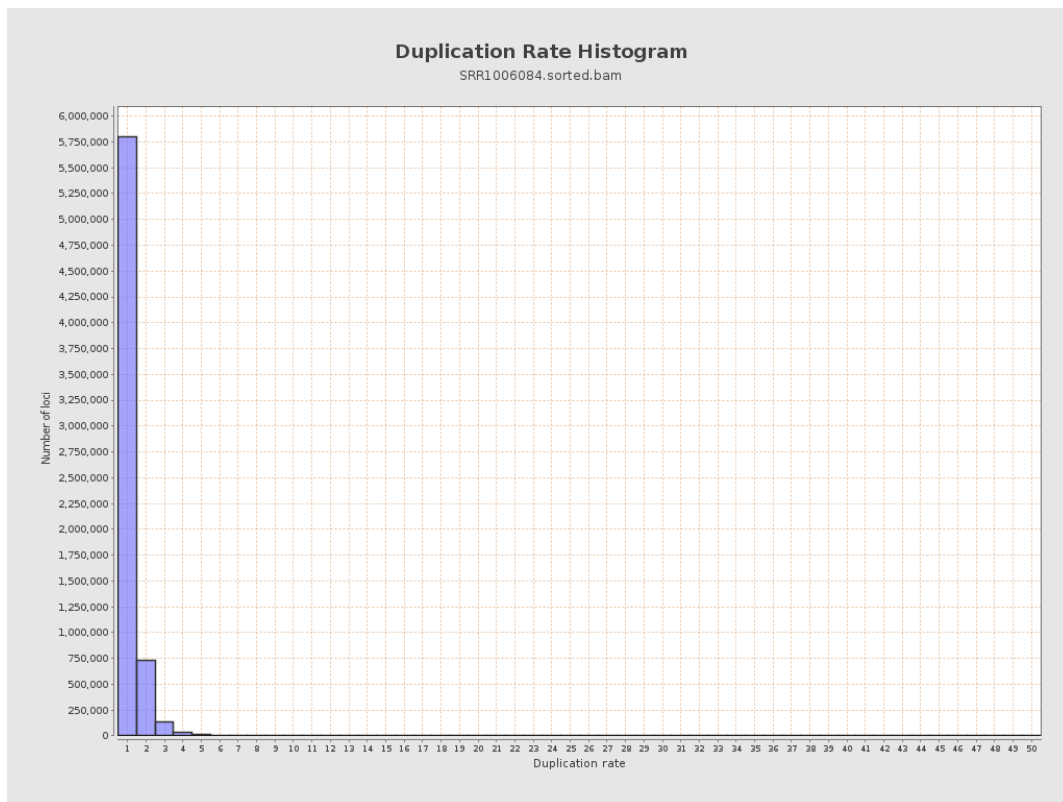
5. Results : Coverage Histogram (0-50X)



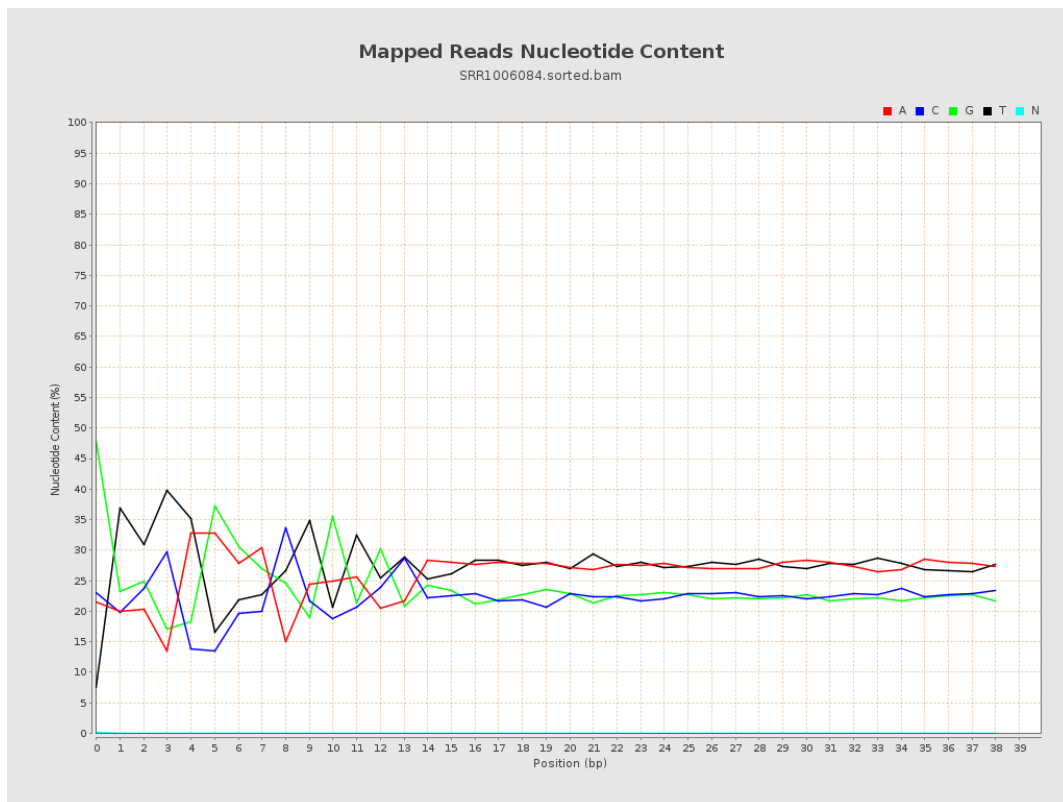
6. Results : Genome Fraction Coverage



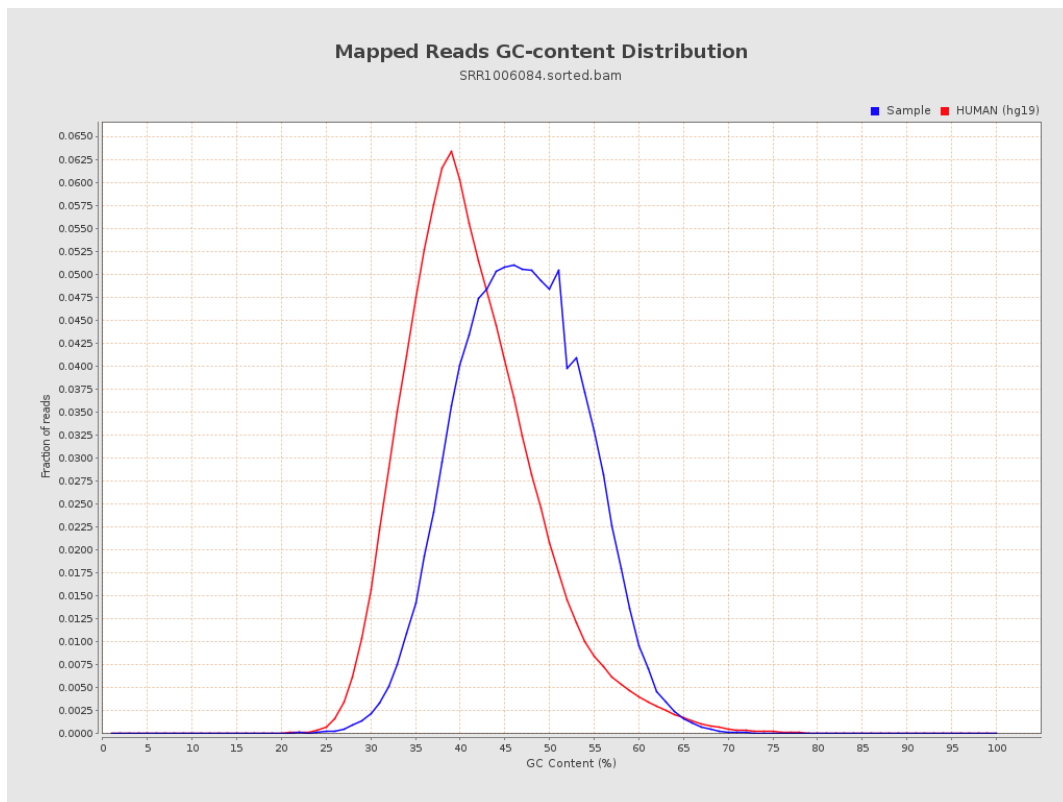
7. Results : Duplication Rate Histogram



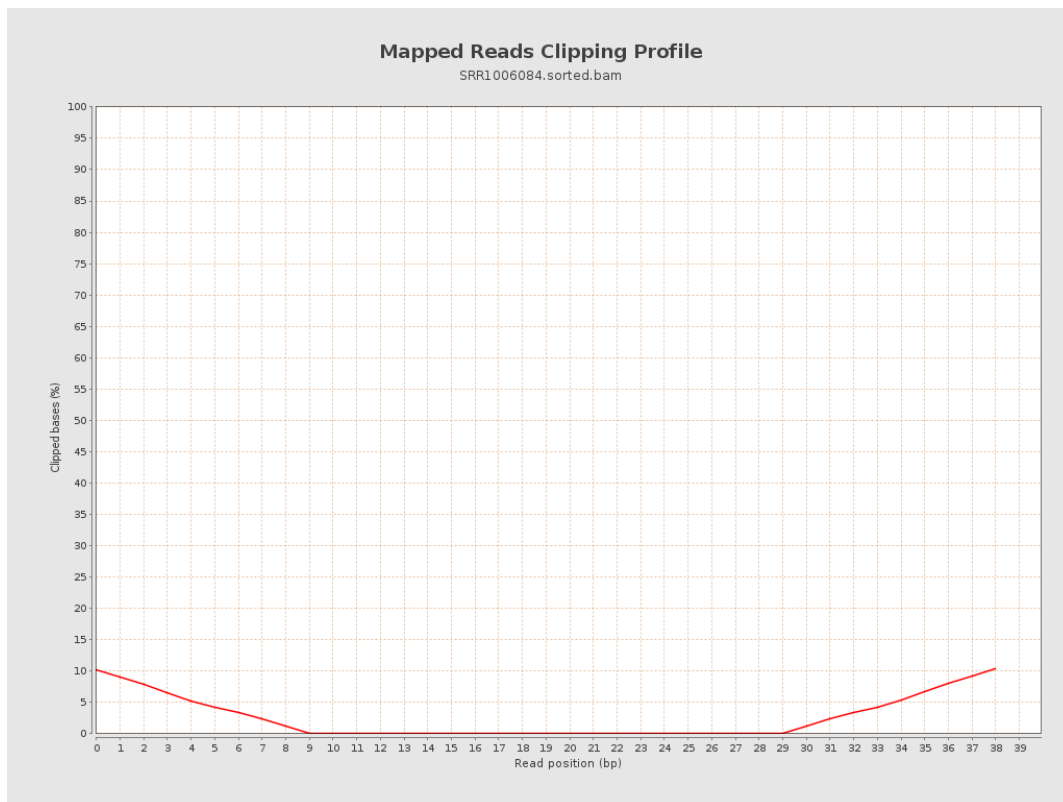
8. Results : Mapped Reads Nucleotide Content



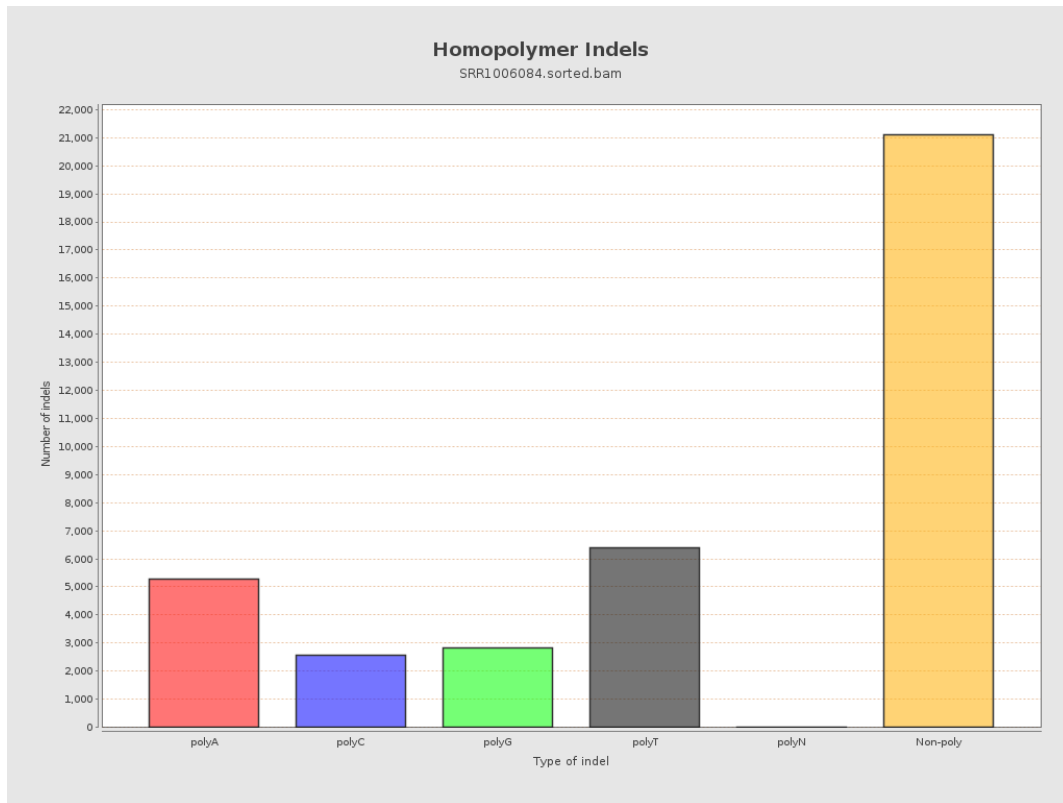
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



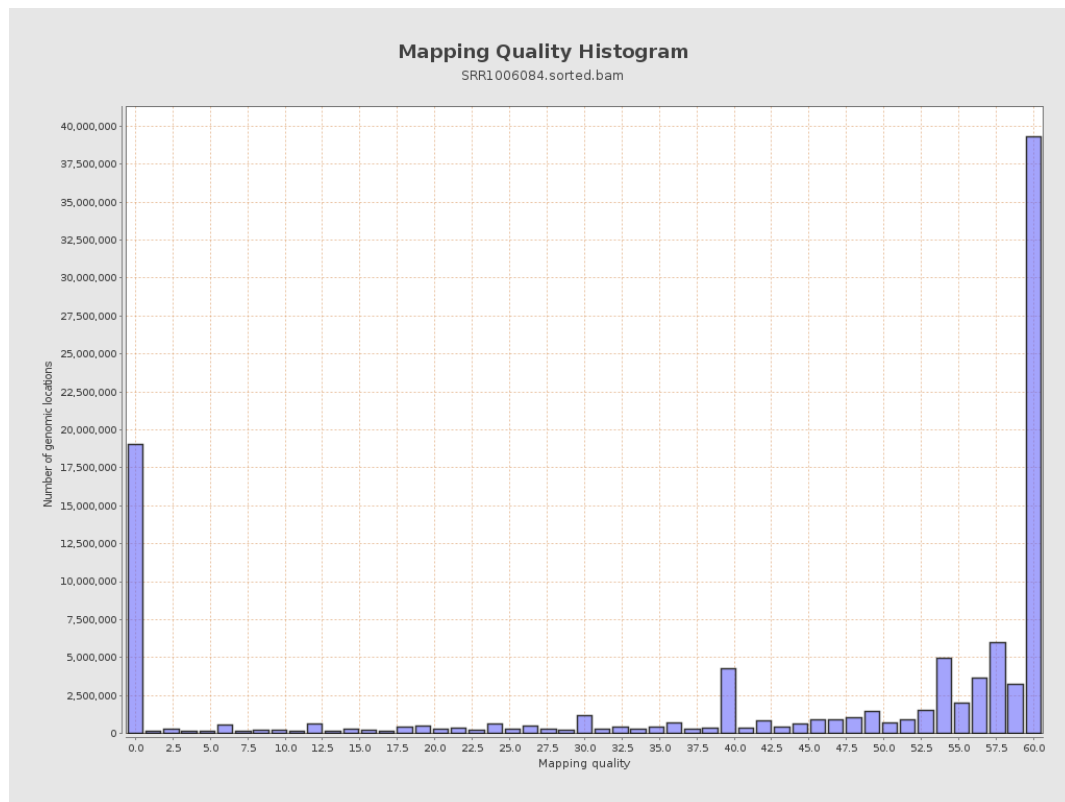
11. Results : Homopolymer Indels



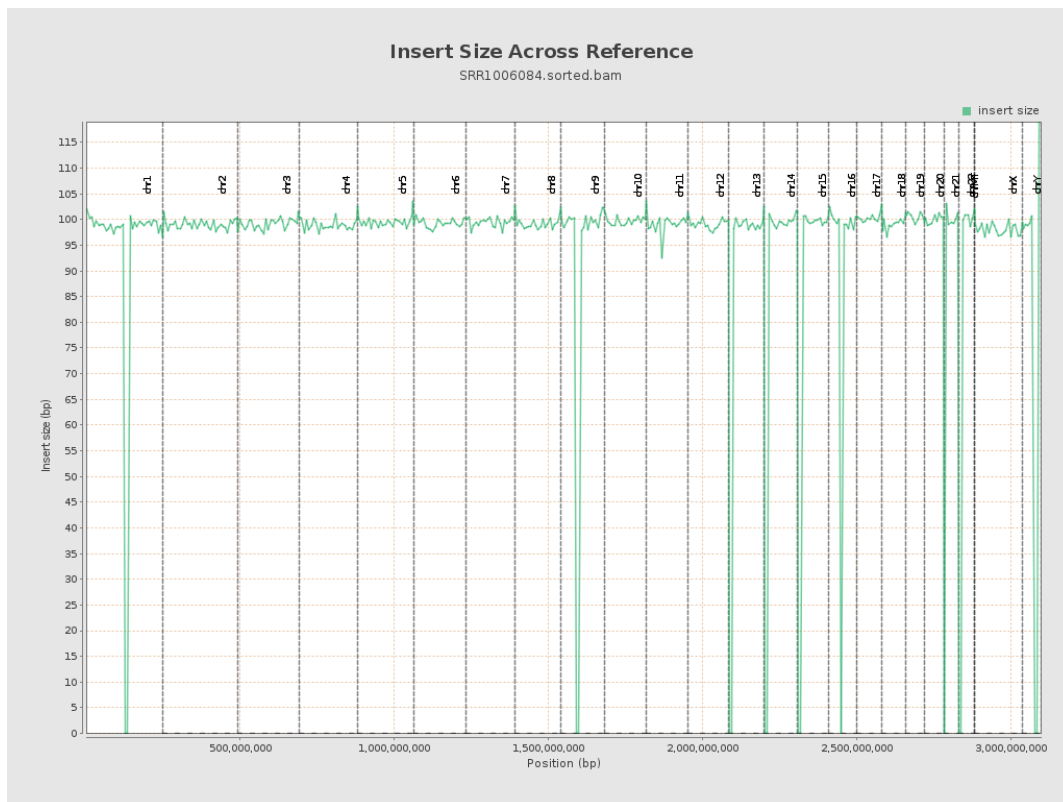
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

