

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 23:27:23

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam SRR10174033.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_SRR10174033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174033_1.fastq.gz SRR10174033_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 23:27:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,245,416
Mapped reads	3,160,113 / 97.37%
Unmapped reads	85,303 / 2.63%
Mapped paired reads	3,160,113 / 97.37%
Mapped reads, first in pair	1,580,479 / 48.7%
Mapped reads, second in pair	1,579,634 / 48.67%
Mapped reads, both in pair	3,101,586 / 95.57%
Mapped reads, singletons	58,527 / 1.8%
Secondary alignments	0
Supplementary alignments	292,366 / 9.01%
Read min/max/mean length	30 / 133 / 127.83
Duplicated reads (estimated)	2,402,599 / 74.03%
Duplication rate	64.12%
Clipped reads	1,236,786 / 38.11%

2.2. ACGT Content

Number/percentage of A's	112,744,276 / 30.21%
Number/percentage of C's	72,896,785 / 19.53%
Number/percentage of T's	112,478,344 / 30.14%
Number/percentage of G's	75,083,041 / 20.12%
Number/percentage of N's	4,530 / 0%

GC Percentage	39.65%
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2.3. Coverage

Mean	0.1206
Standard Deviation	1.9631

2.4. Mapping Quality

Mean Mapping Quality	52.81
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2.5. Insert size

Mean	939,449.8
Standard Deviation	9,103,399.08
P25/Median/P75	144 / 200 / 284

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	3,929,594
Insertions	38,930
Mapped reads with at least one insertion	1.19%
Deletions	78,546
Mapped reads with at least one deletion	2.43%
Homopolymer indels	43.61%

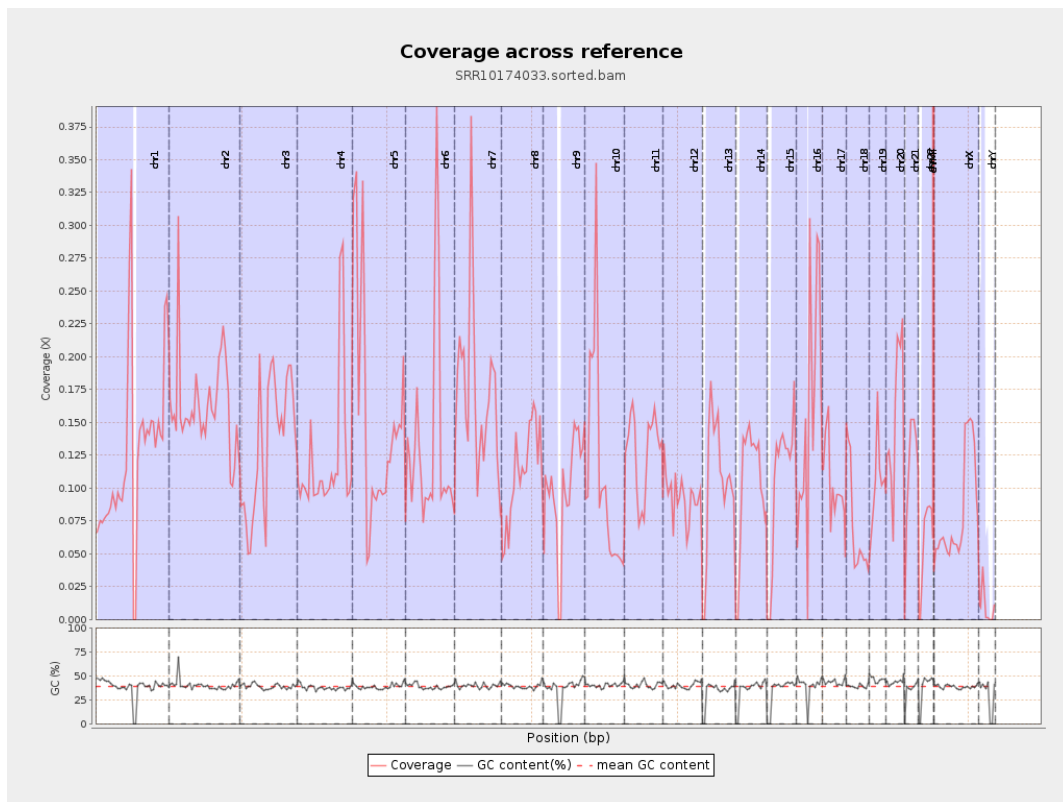
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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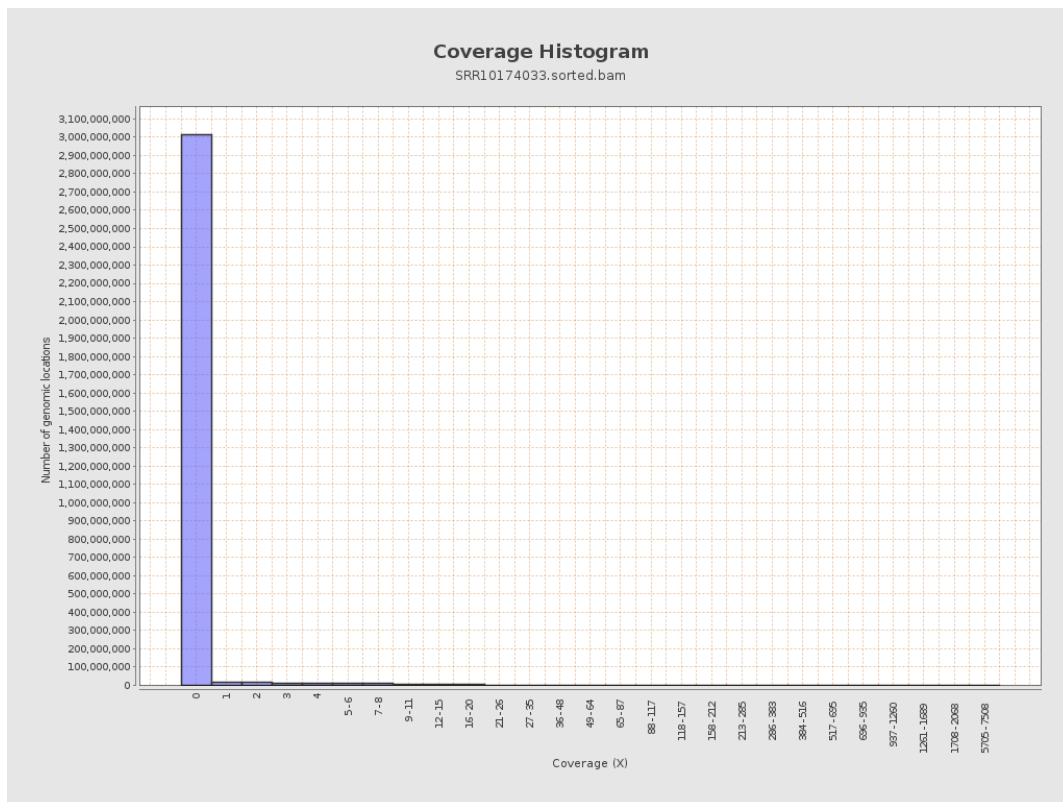
		bases	coverage	deviation
chr1	249250621	31401042	0.126	1.7386
chr2	243199373	39634740	0.163	5.3169
chr3	198022430	26374814	0.1332	1.0333
chr4	191154276	22734704	0.1189	1.1286
chr5	180915260	27674575	0.153	1.1034
chr6	171115067	22830625	0.1334	1.0559
chr7	159138663	27684294	0.174	2.4456
chr8	146364022	16351065	0.1117	1.1207
chr9	141213431	14064263	0.0996	1.0838
chr10	135534747	14736183	0.1087	2.1266
chr11	135006516	17206058	0.1274	1.0179
chr12	133851895	12383425	0.0925	0.863
chr13	115169878	11984391	0.1041	0.9184
chr14	107349540	11018796	0.1026	0.9063
chr15	102531392	10913748	0.1064	0.9074
chr16	90354753	14279669	0.158	1.5615
chr17	81195210	8172964	0.1007	1.0531
chr18	78077248	5481825	0.0702	1.3748
chr19	59128983	6133434	0.1037	1.8026
chr20	63025520	9744648	0.1546	1.1058
chr21	48129895	5467868	0.1136	0.965
chr22	51304566	2976390	0.058	0.6477
chrMT	16571	1011652	61.0495	49.9381
chrX	155270560	12599760	0.0811	0.8026

chrY	59373566	540320	0.0091	0.4603
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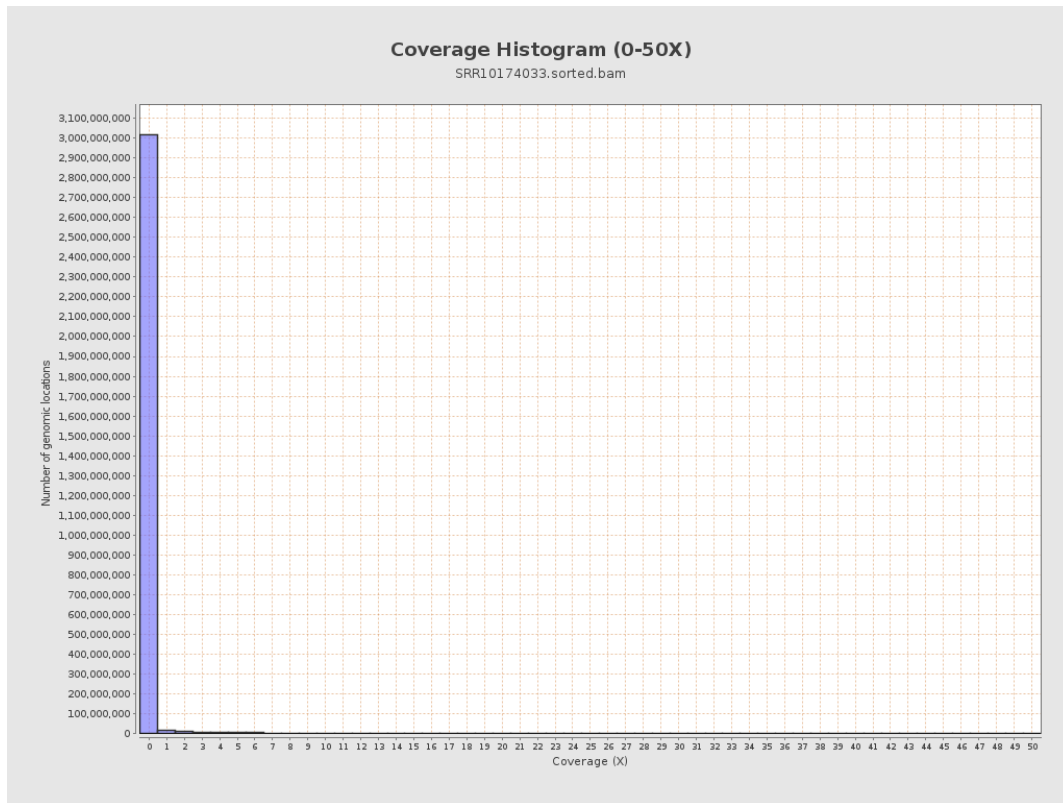
3. Results : Coverage across reference



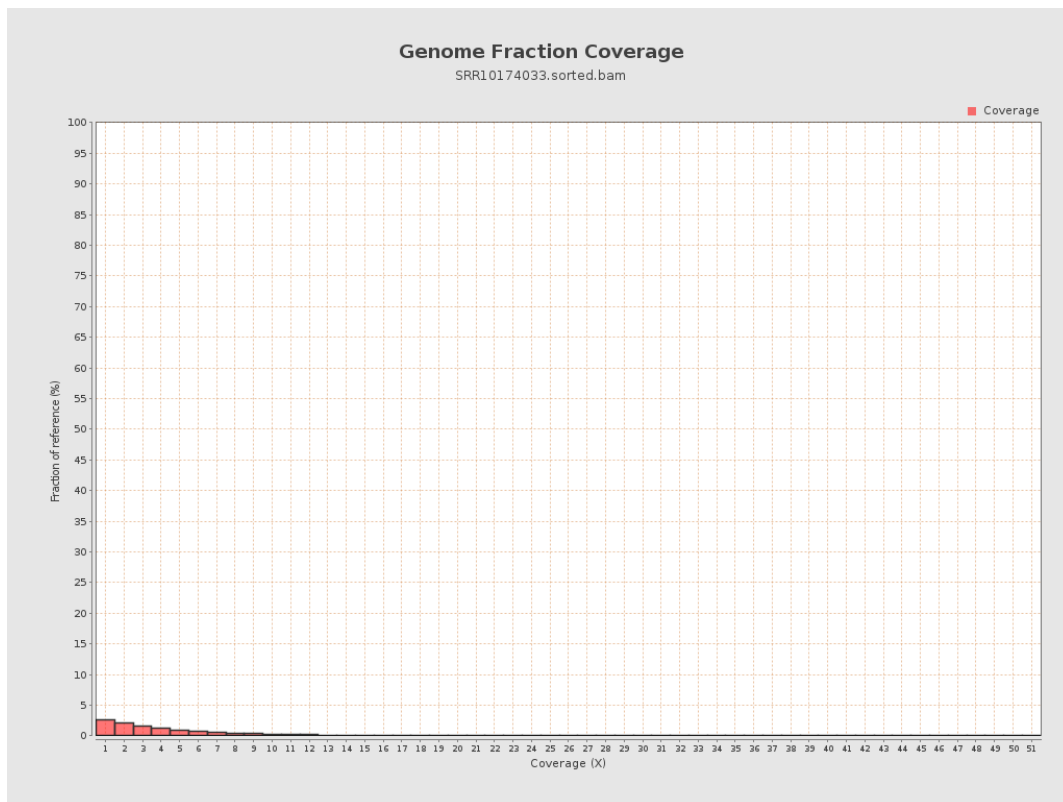
4. Results : Coverage Histogram



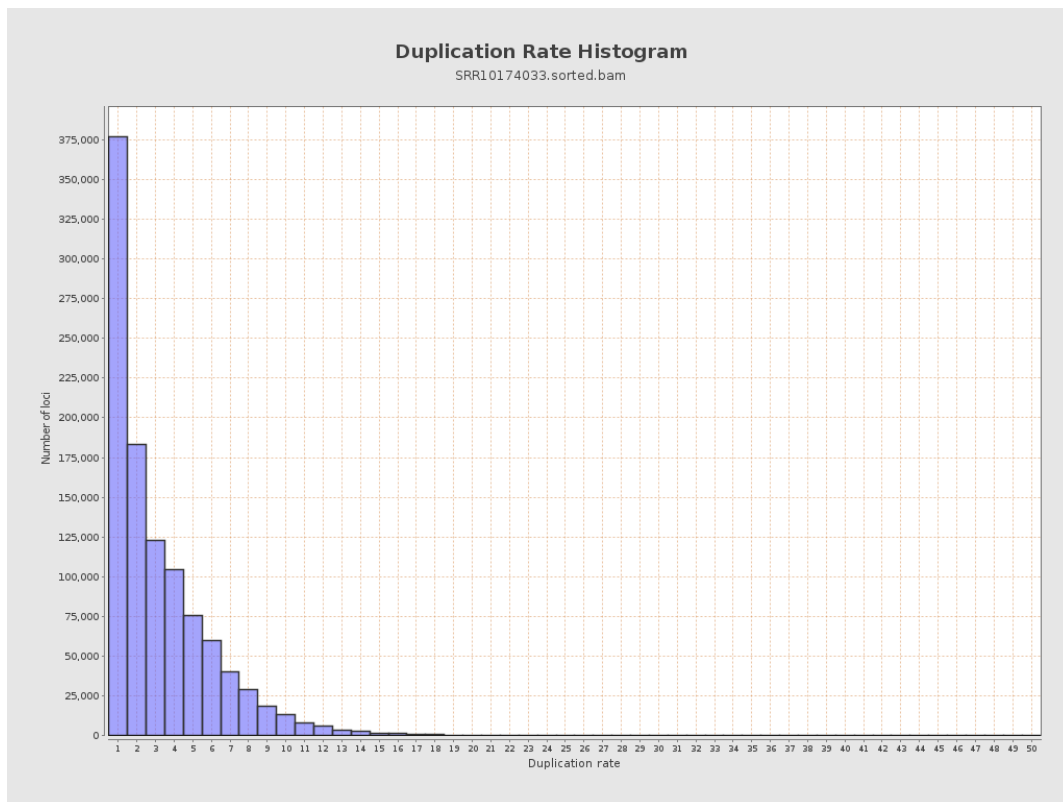
5. Results : Coverage Histogram (0-50X)



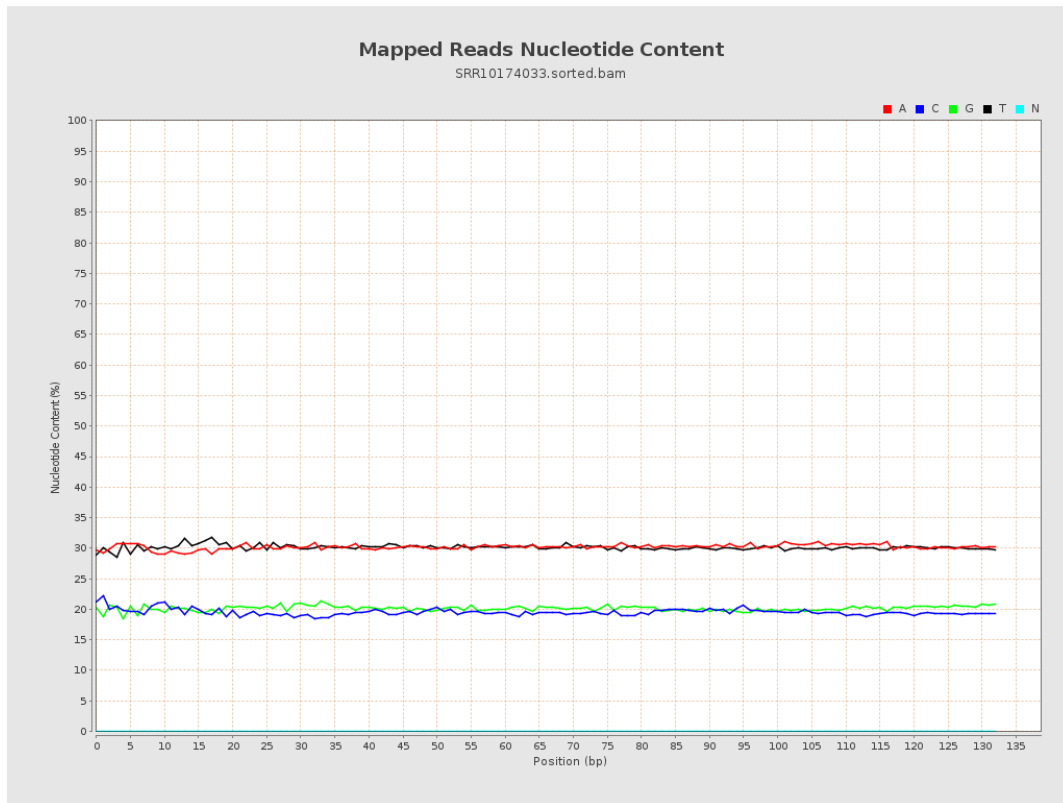
6. Results : Genome Fraction Coverage



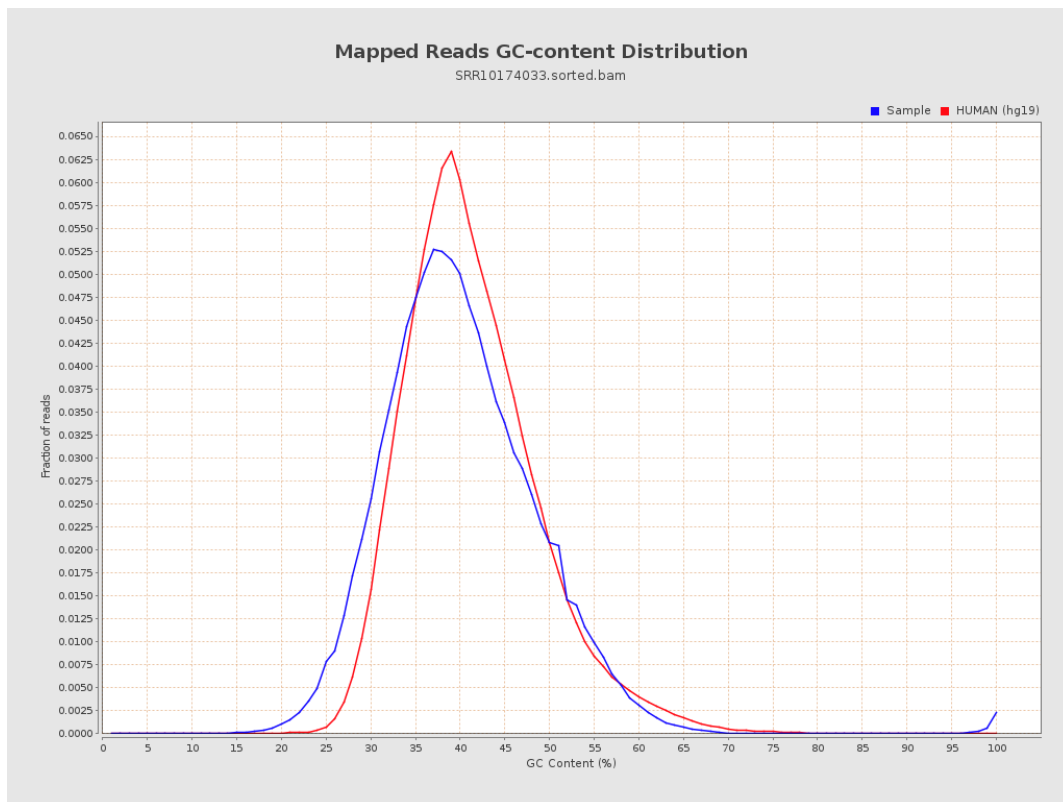
7. Results : Duplication Rate Histogram



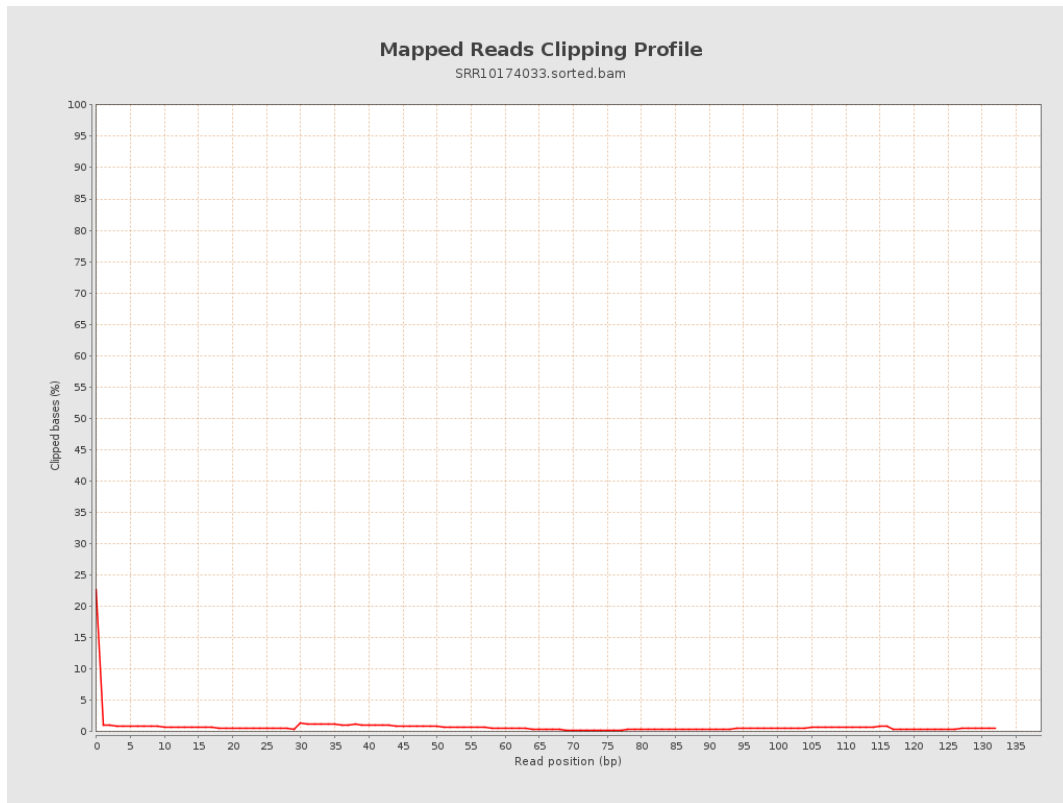
8. Results : Mapped Reads Nucleotide Content



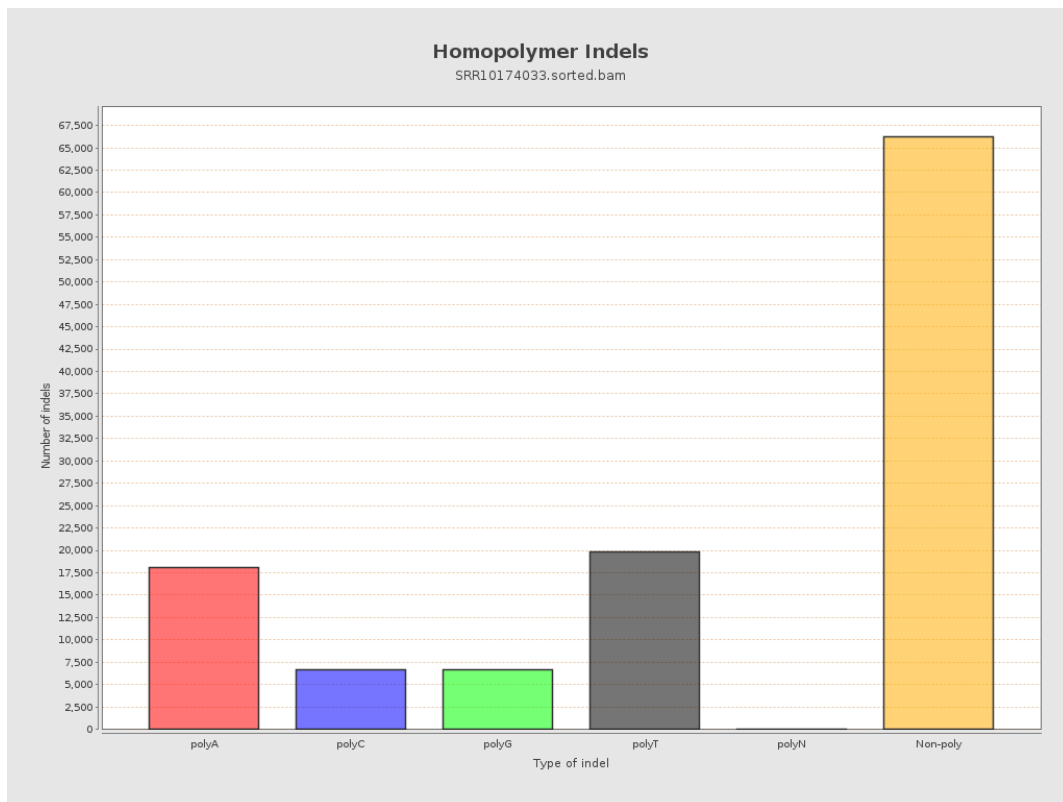
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



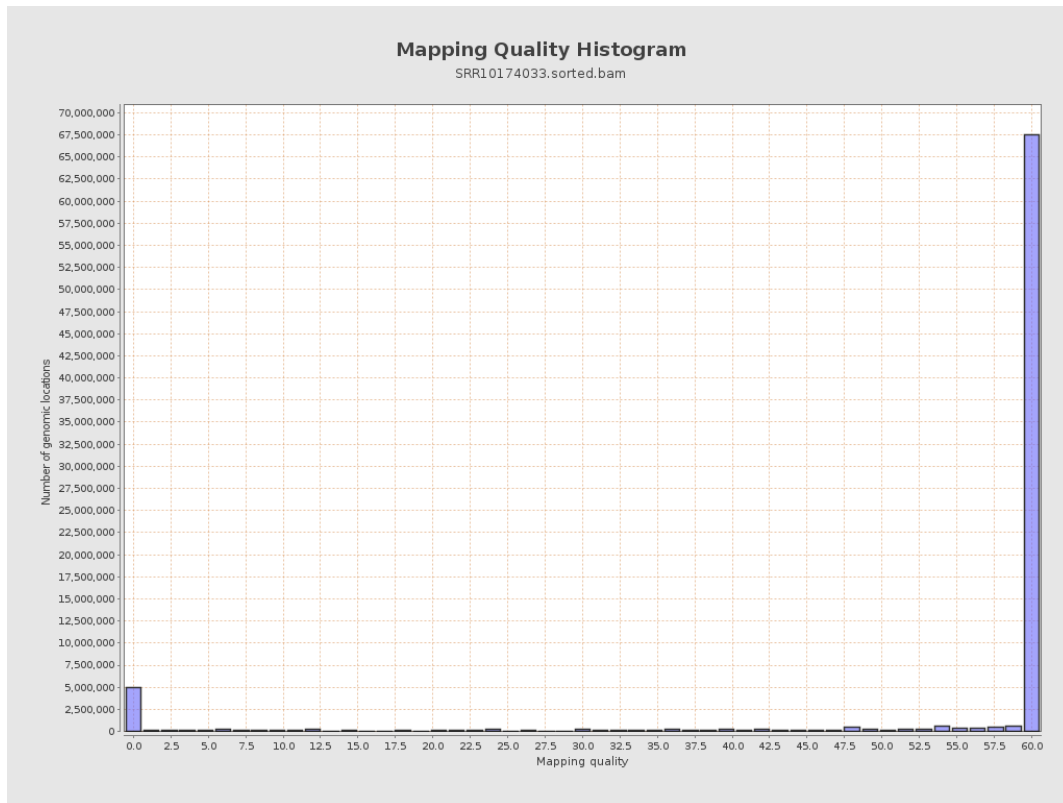
11. Results : Homopolymer Indels



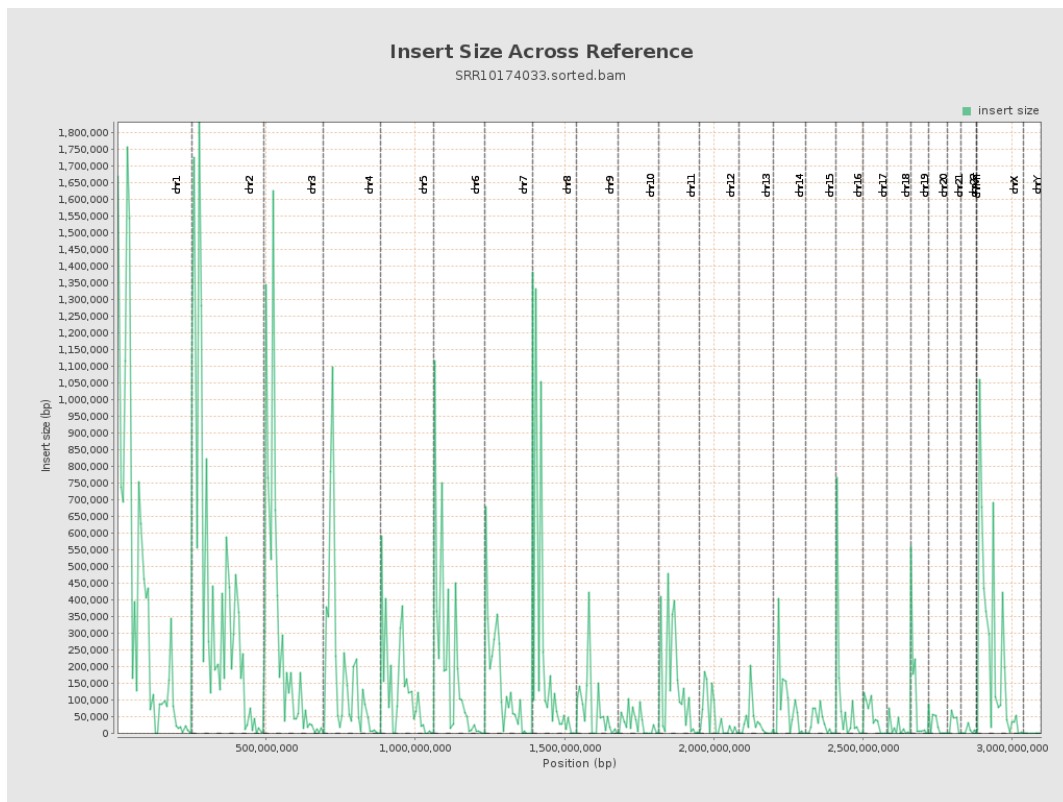
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

