

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:11:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173843.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_SRR10173843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173843_1.fastq.gz SRR10173843_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:11:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,515,036
Mapped reads	4,389,781 / 97.23%
Unmapped reads	125,255 / 2.77%
Mapped paired reads	4,389,781 / 97.23%
Mapped reads, first in pair	2,198,420 / 48.69%
Mapped reads, second in pair	2,191,361 / 48.53%
Mapped reads, both in pair	4,307,690 / 95.41%
Mapped reads, singletons	82,091 / 1.82%
Secondary alignments	0
Supplementary alignments	433,252 / 9.6%
Read min/max/mean length	30 / 133 / 127.86
Duplicated reads (estimated)	3,405,070 / 75.42%
Duplication rate	64.82%
Clipped reads	1,780,354 / 39.43%

2.2. ACGT Content

Number/percentage of A's	155,700,012 / 30.11%
Number/percentage of C's	101,411,042 / 19.61%
Number/percentage of T's	155,178,262 / 30.01%
Number/percentage of G's	104,826,164 / 20.27%
Number/percentage of N's	5,628 / 0%

GC Percentage	39.88%
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2.3. Coverage

Mean	0.1671
Standard Deviation	2.5126

2.4. Mapping Quality

Mean Mapping Quality	52.76
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2.5. Insert size

Mean	770,706.15
Standard Deviation	7,939,024.97
P25/Median/P75	143 / 201 / 289

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	5,377,306
Insertions	52,768
Mapped reads with at least one insertion	1.16%
Deletions	115,462
Mapped reads with at least one deletion	2.56%
Homopolymer indels	42.84%

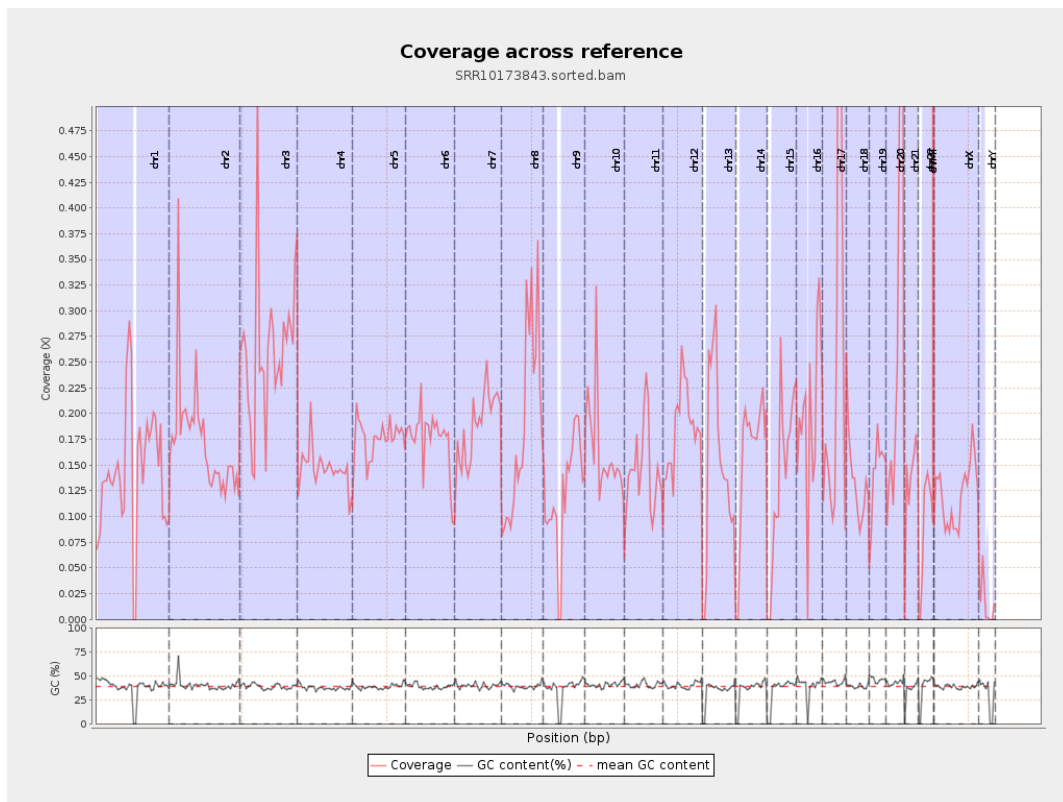
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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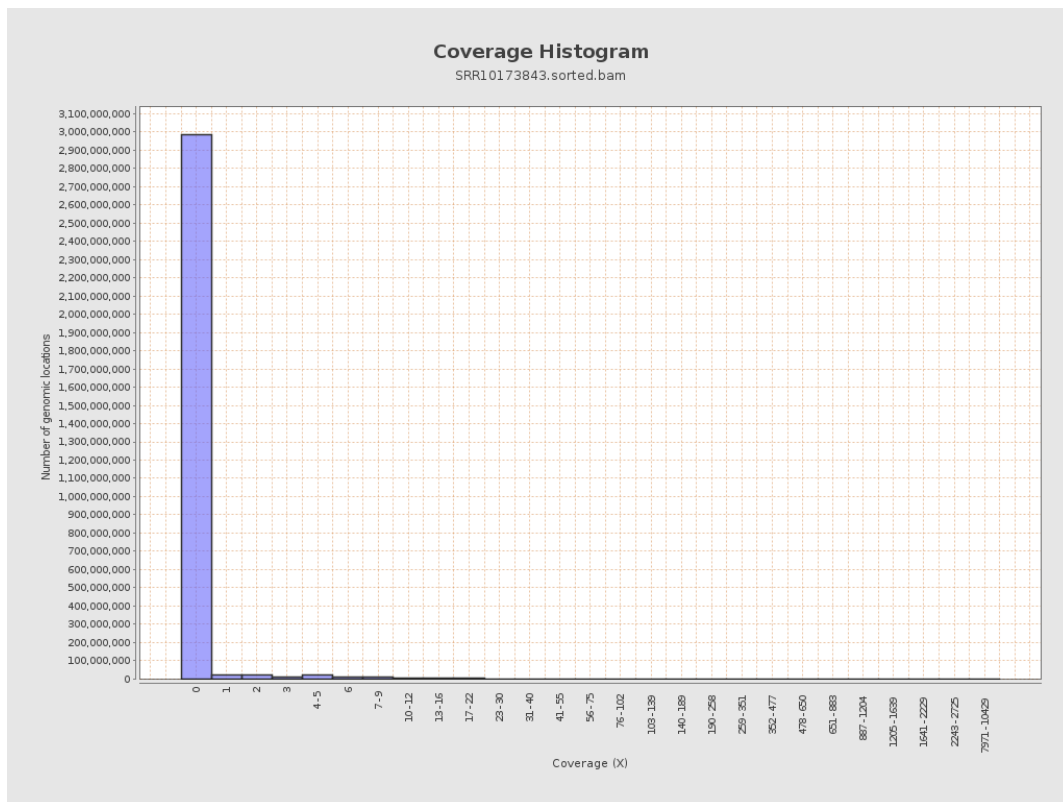
		bases	coverage	deviation
chr1	249250621	36004086	0.1444	2.155
chr2	243199373	41861722	0.1721	7.3269
chr3	198022430	51114569	0.2581	1.4874
chr4	191154276	27883047	0.1459	1.261
chr5	180915260	31898092	0.1763	1.2154
chr6	171115067	29977285	0.1752	1.3802
chr7	159138663	30123792	0.1893	1.7662
chr8	146364022	27427766	0.1874	1.7871
chr9	141213431	17200141	0.1218	1.2218
chr10	135534747	22254347	0.1642	2.1453
chr11	135006516	19561897	0.1449	1.1474
chr12	133851895	24794063	0.1852	1.2461
chr13	115169878	17032846	0.1479	1.1171
chr14	107349540	17017055	0.1585	1.1469
chr15	102531392	14135303	0.1379	1.0634
chr16	90354753	18067783	0.2	1.6331
chr17	81195210	20637173	0.2542	1.5535
chr18	78077248	10433615	0.1336	2.0373
chr19	59128983	8553995	0.1447	1.5483
chr20	63025520	20052875	0.3182	1.7458
chr21	48129895	6475996	0.1346	1.0744
chr22	51304566	4536186	0.0884	0.822
chrMT	16571	647669	39.0845	31.7747
chrX	155270560	18825986	0.1212	1.0047

chrY	59373566	888234	0.015	0.5755
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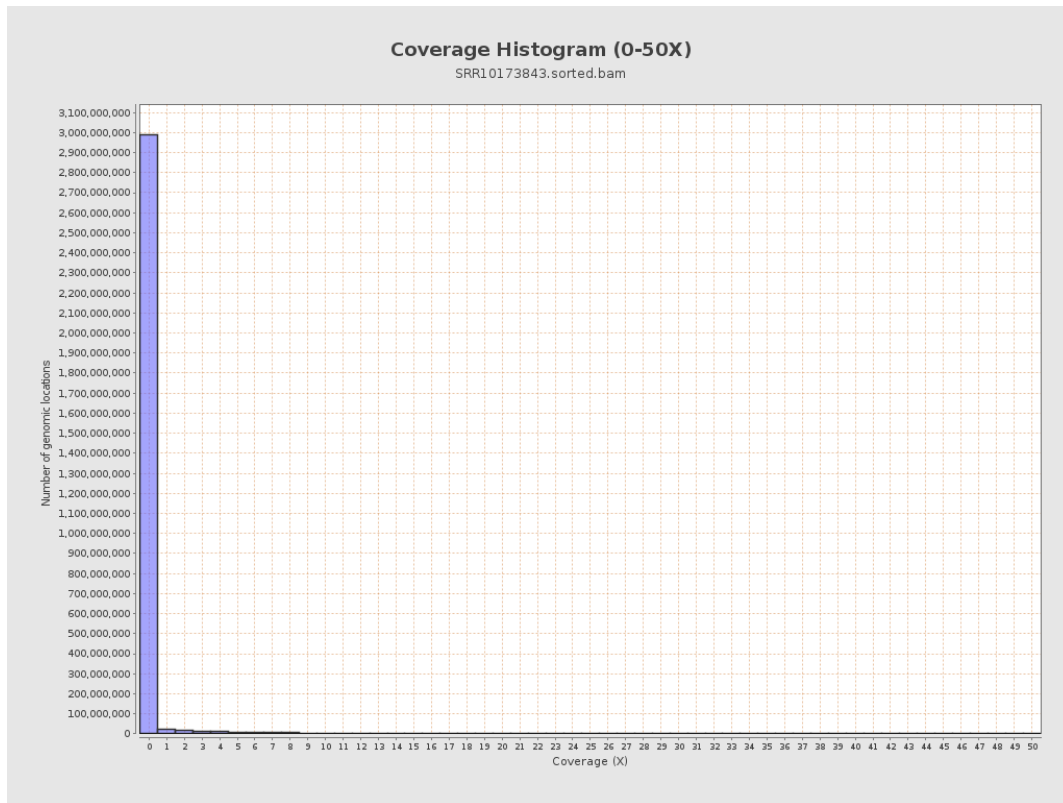
3. Results : Coverage across reference



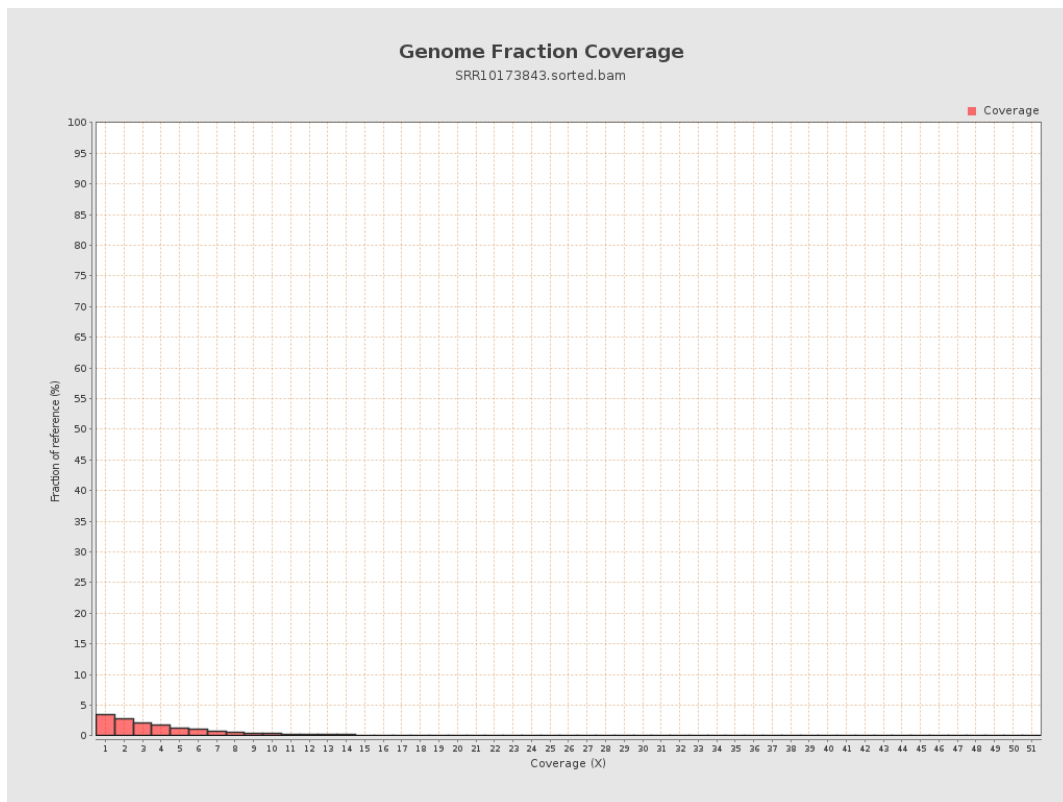
4. Results : Coverage Histogram



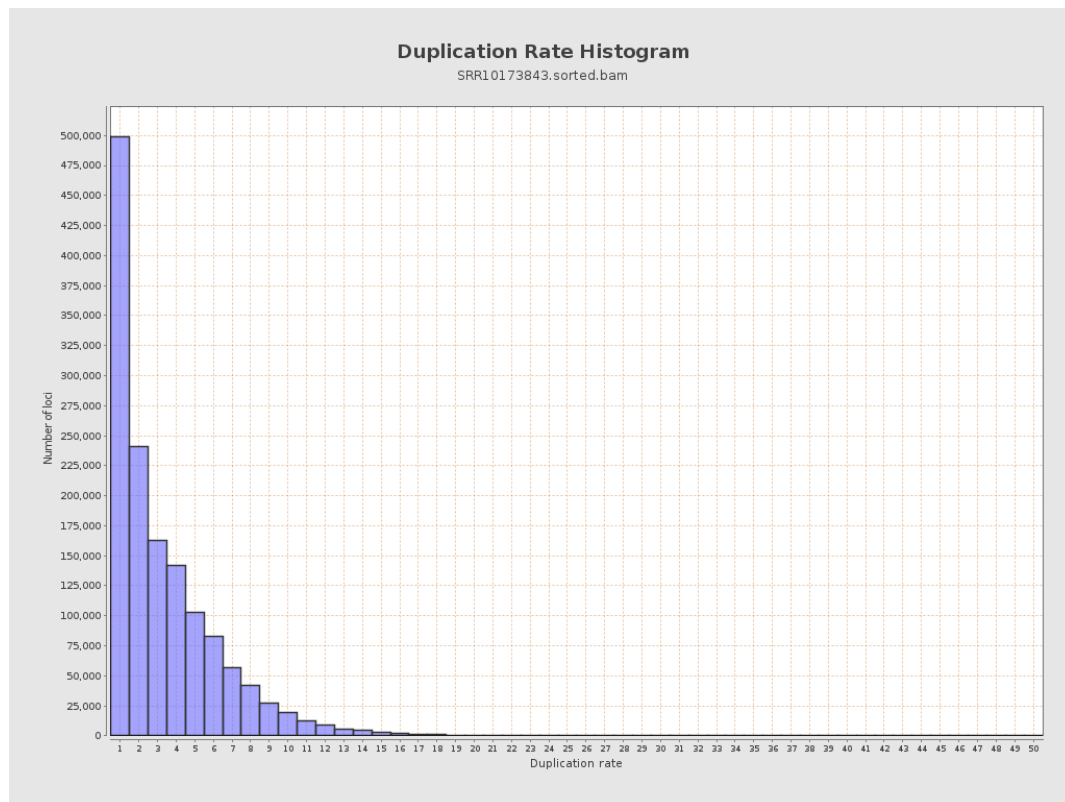
5. Results : Coverage Histogram (0-50X)



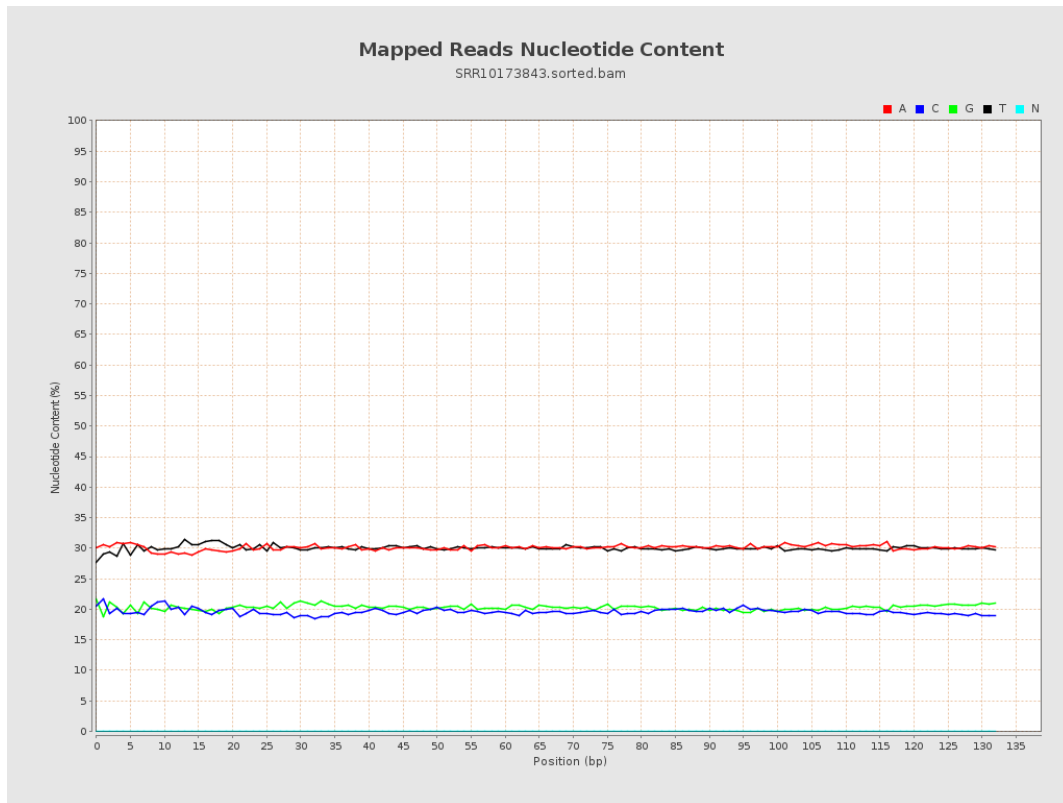
6. Results : Genome Fraction Coverage



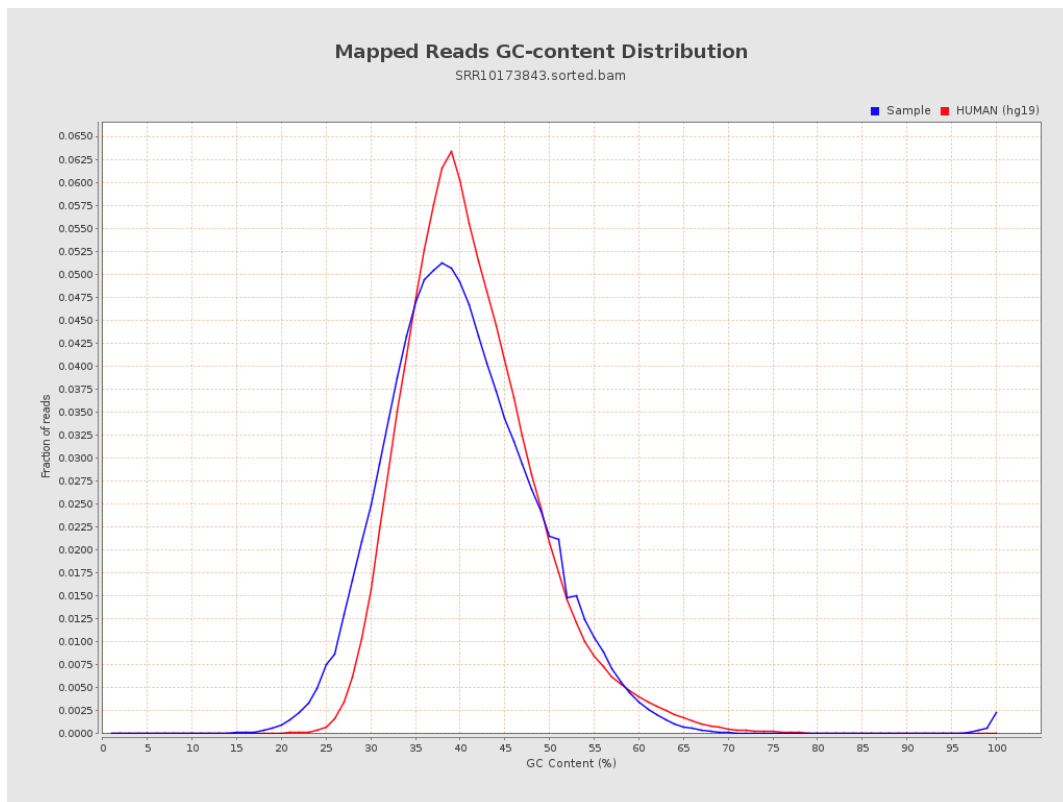
7. Results : Duplication Rate Histogram



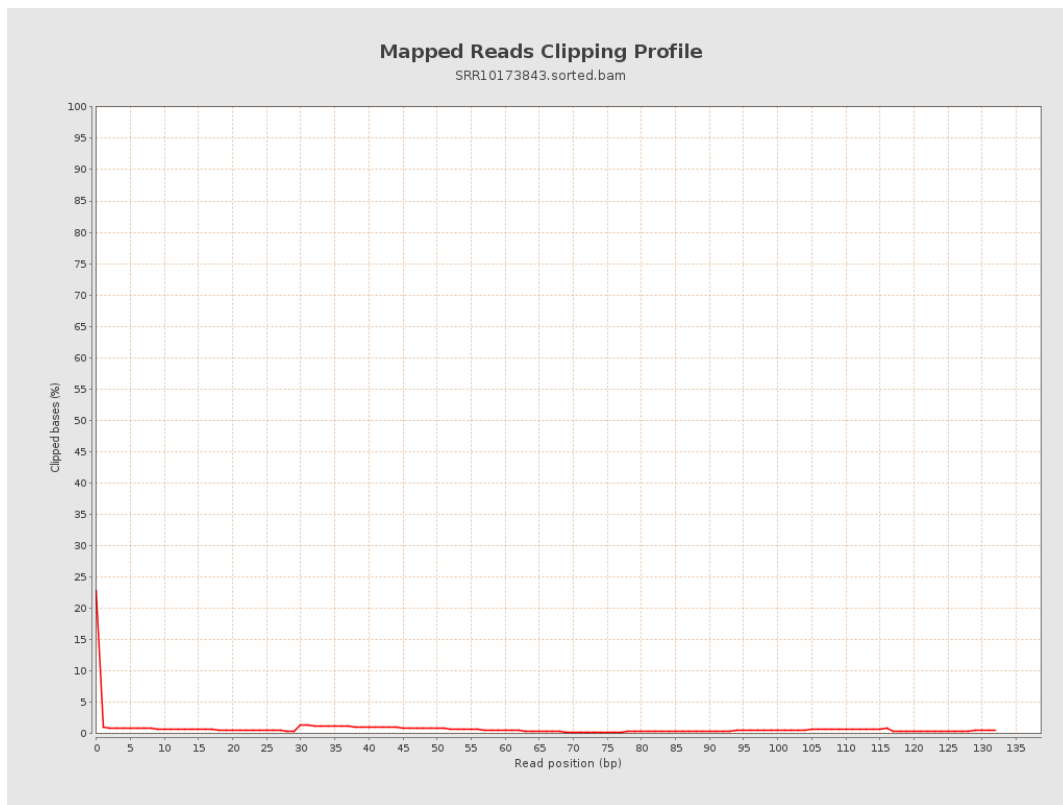
8. Results : Mapped Reads Nucleotide Content



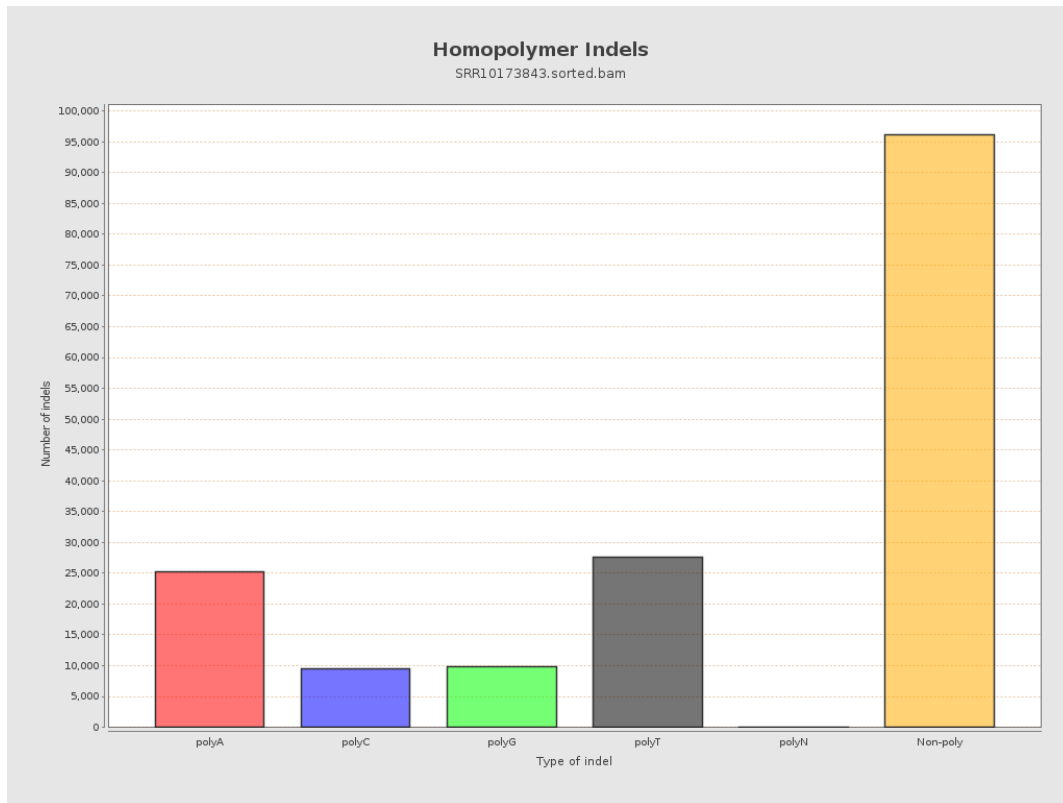
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



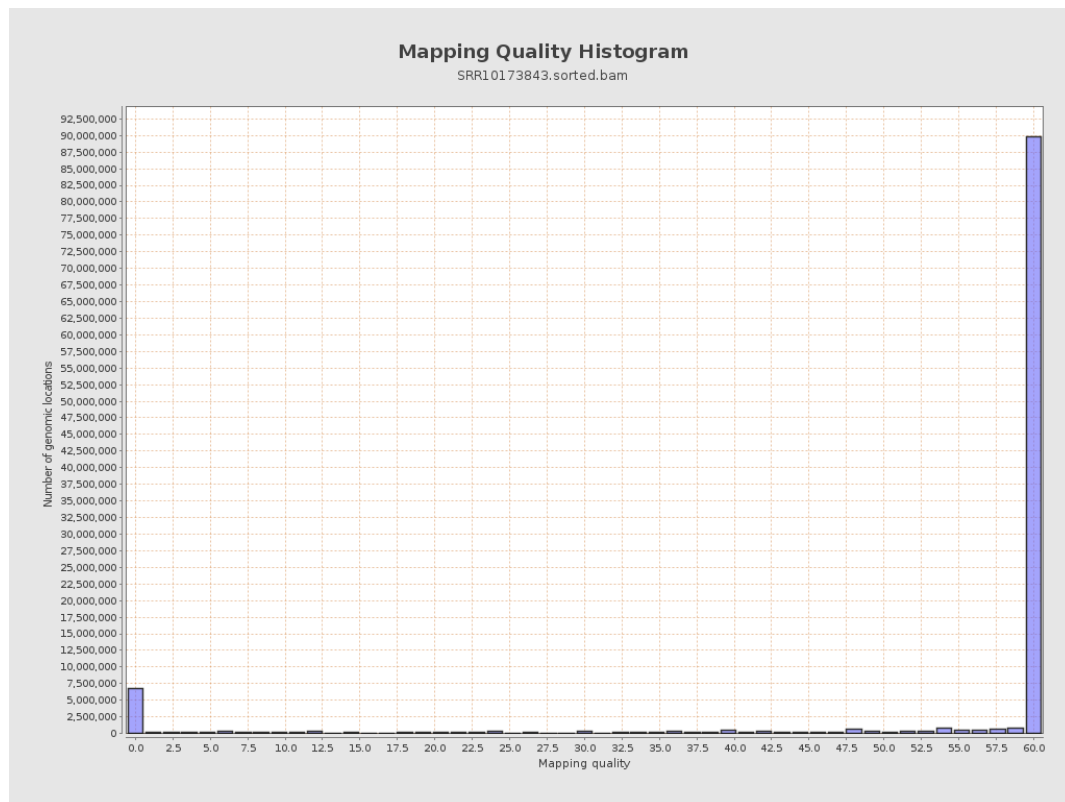
11. Results : Homopolymer Indels



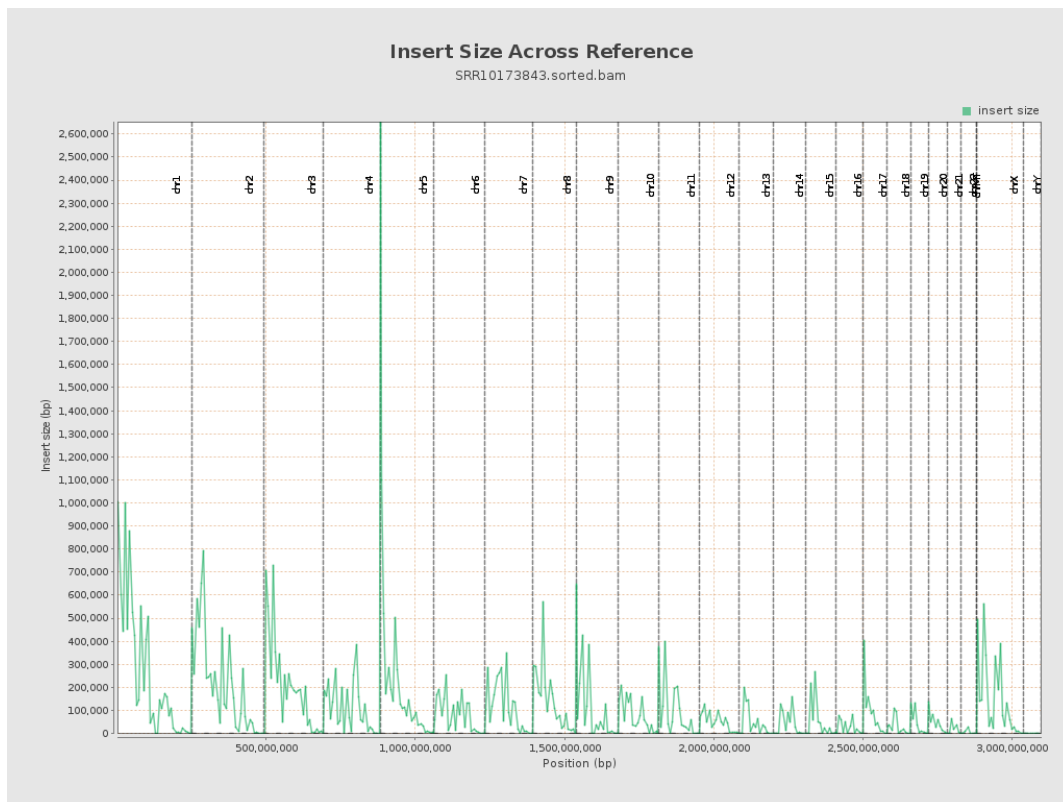
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

