

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:04:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173842.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_SRR10173842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173842_1.fastq.gz SRR10173842_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:04:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,343,812
Mapped reads	4,234,716 / 97.49%
Unmapped reads	109,096 / 2.51%
Mapped paired reads	4,234,716 / 97.49%
Mapped reads, first in pair	2,117,479 / 48.75%
Mapped reads, second in pair	2,117,237 / 48.74%
Mapped reads, both in pair	4,162,046 / 95.82%
Mapped reads, singletons	72,670 / 1.67%
Secondary alignments	0
Supplementary alignments	428,694 / 9.87%
Read min/max/mean length	30 / 133 / 128
Duplicated reads (estimated)	3,276,628 / 75.43%
Duplication rate	64.73%
Clipped reads	1,695,731 / 39.04%

2.2. ACGT Content

Number/percentage of A's	150,506,558 / 30.09%
Number/percentage of C's	98,240,725 / 19.64%
Number/percentage of T's	149,981,179 / 29.98%
Number/percentage of G's	101,486,839 / 20.29%
Number/percentage of N's	5,960 / 0%

GC Percentage	39.93%
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2.3. Coverage

Mean	0.1617
Standard Deviation	2.3977

2.4. Mapping Quality

Mean Mapping Quality	52.69
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2.5. Insert size

Mean	860,150.7
Standard Deviation	8,380,562.32
P25/Median/P75	143 / 200 / 288

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	5,101,973
Insertions	50,938
Mapped reads with at least one insertion	1.17%
Deletions	114,512
Mapped reads with at least one deletion	2.64%
Homopolymer indels	43.72%

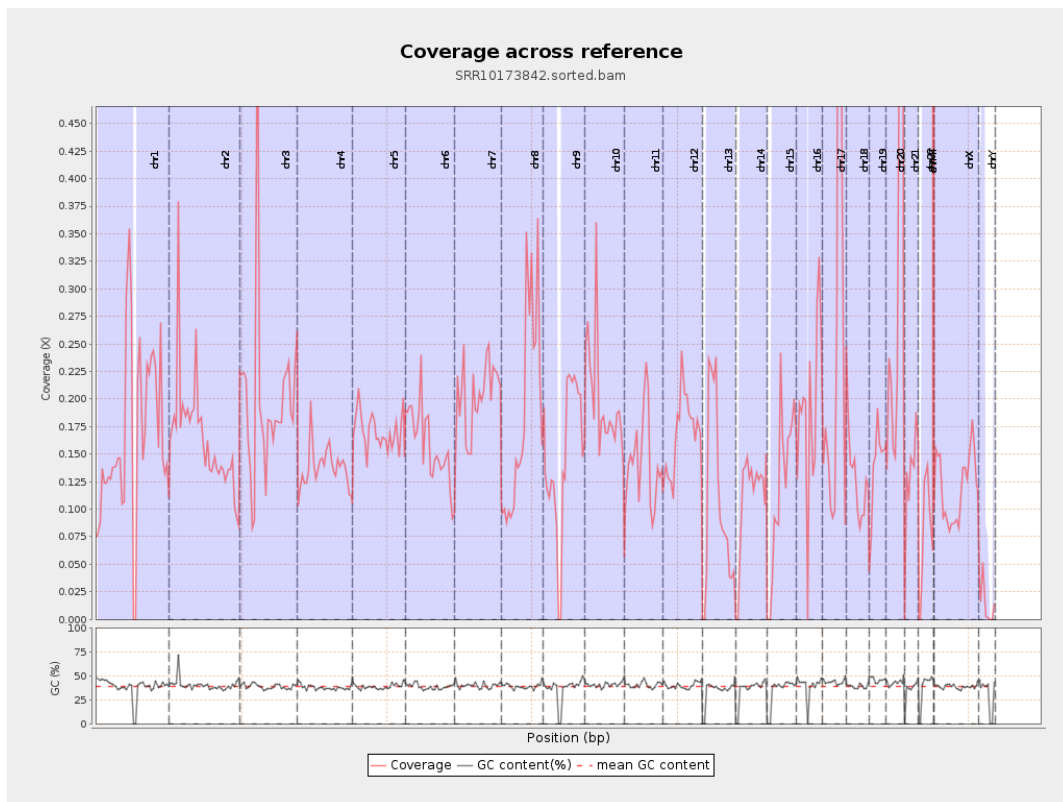
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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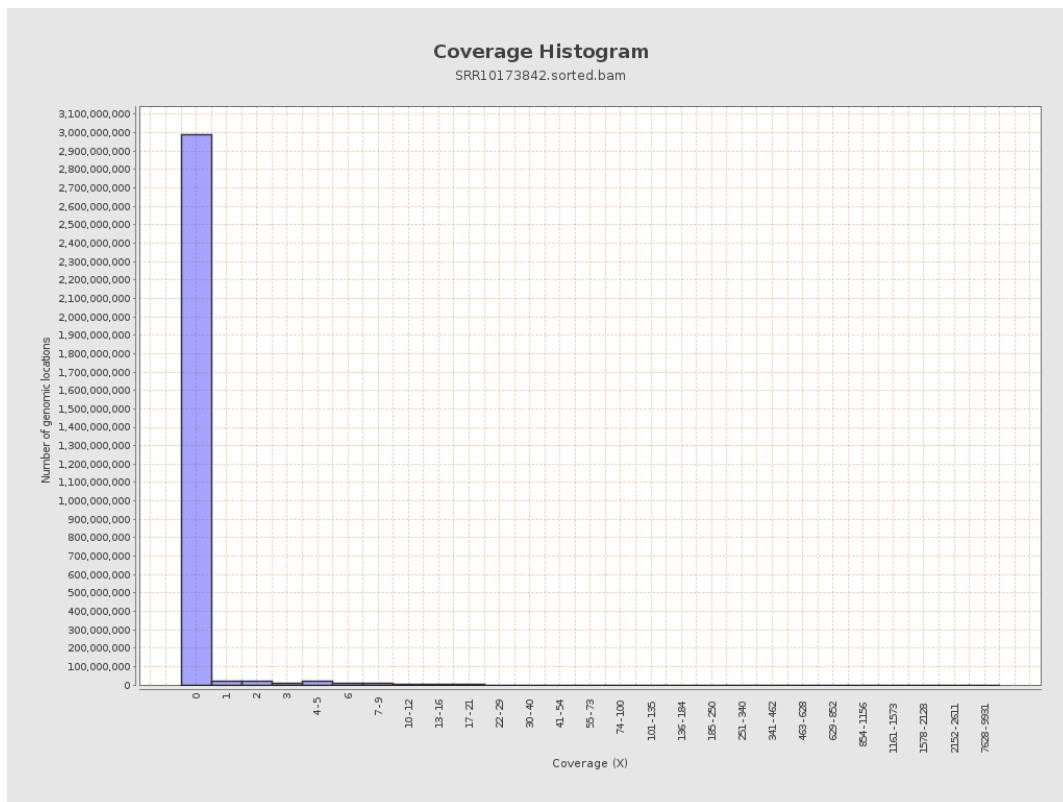
		bases	coverage	deviation
chr1	249250621	41345578	0.1659	1.8204
chr2	243199373	40110719	0.1649	6.9913
chr3	198022430	38953527	0.1967	1.3007
chr4	191154276	26215869	0.1371	1.2226
chr5	180915260	30850870	0.1705	1.1812
chr6	171115067	27079576	0.1583	1.3564
chr7	159138663	32462507	0.204	1.843
chr8	146364022	27109222	0.1852	1.5761
chr9	141213431	20512494	0.1453	1.2784
chr10	135534747	26967869	0.199	2.282
chr11	135006516	19337410	0.1432	1.1075
chr12	133851895	22544304	0.1684	1.1824
chr13	115169878	11907910	0.1034	0.9237
chr14	107349540	11647192	0.1085	0.9452
chr15	102531392	12365934	0.1206	0.9858
chr16	90354753	17440198	0.193	1.5523
chr17	81195210	21332278	0.2627	1.5737
chr18	78077248	10014585	0.1283	1.7112
chr19	59128983	8353840	0.1413	1.5067
chr20	63025520	23057420	0.3658	1.8731
chr21	48129895	6341753	0.1318	1.0824
chr22	51304566	3926318	0.0765	0.7508
chrMT	16571	1210891	73.0729	59.636
chrX	155270560	18604001	0.1198	0.9848

chrY	59373566	816461	0.0138	0.5189
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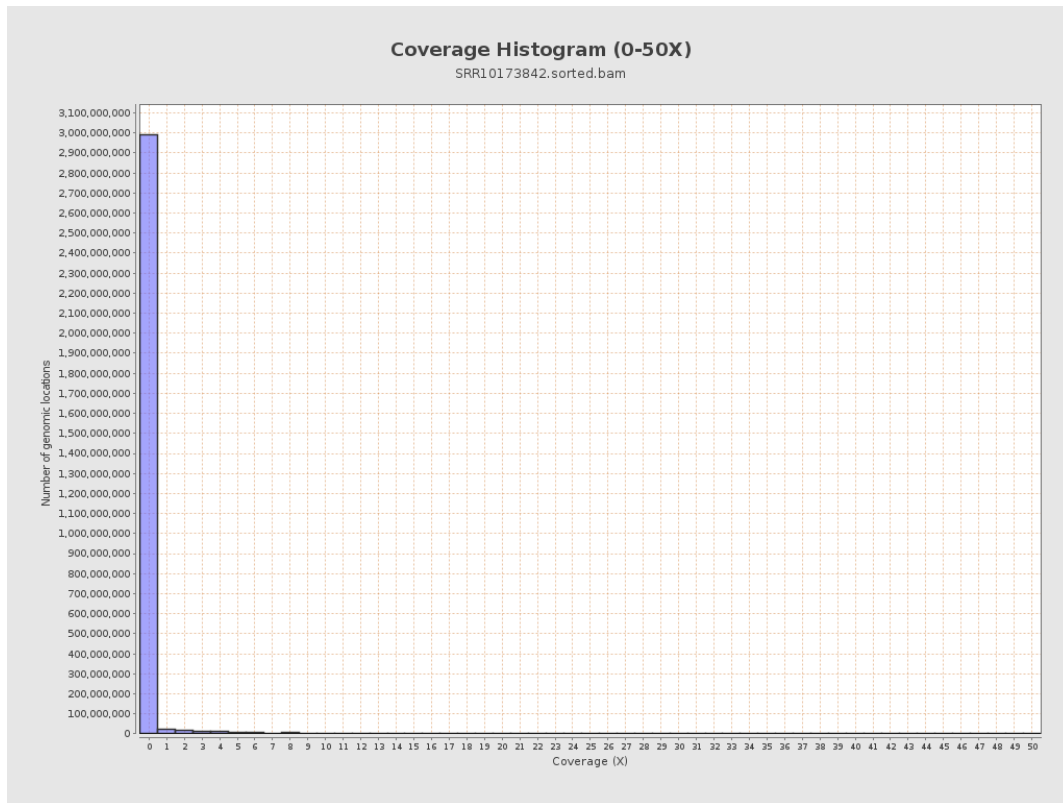
3. Results : Coverage across reference



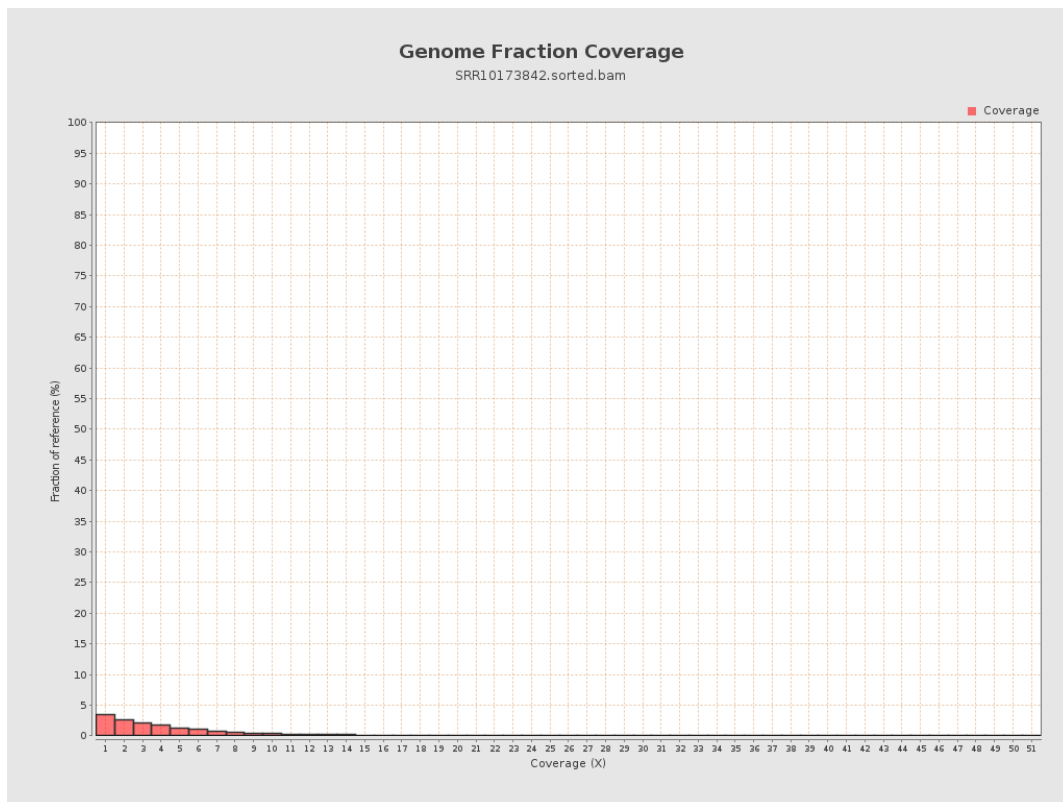
4. Results : Coverage Histogram



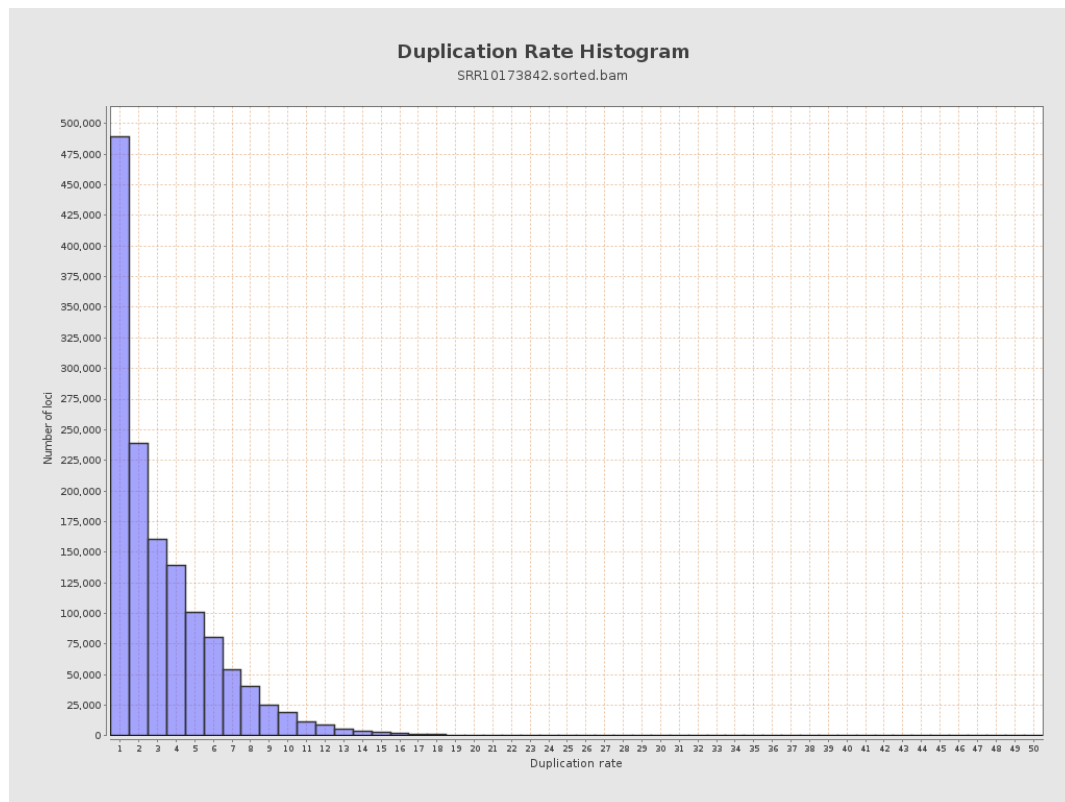
5. Results : Coverage Histogram (0-50X)



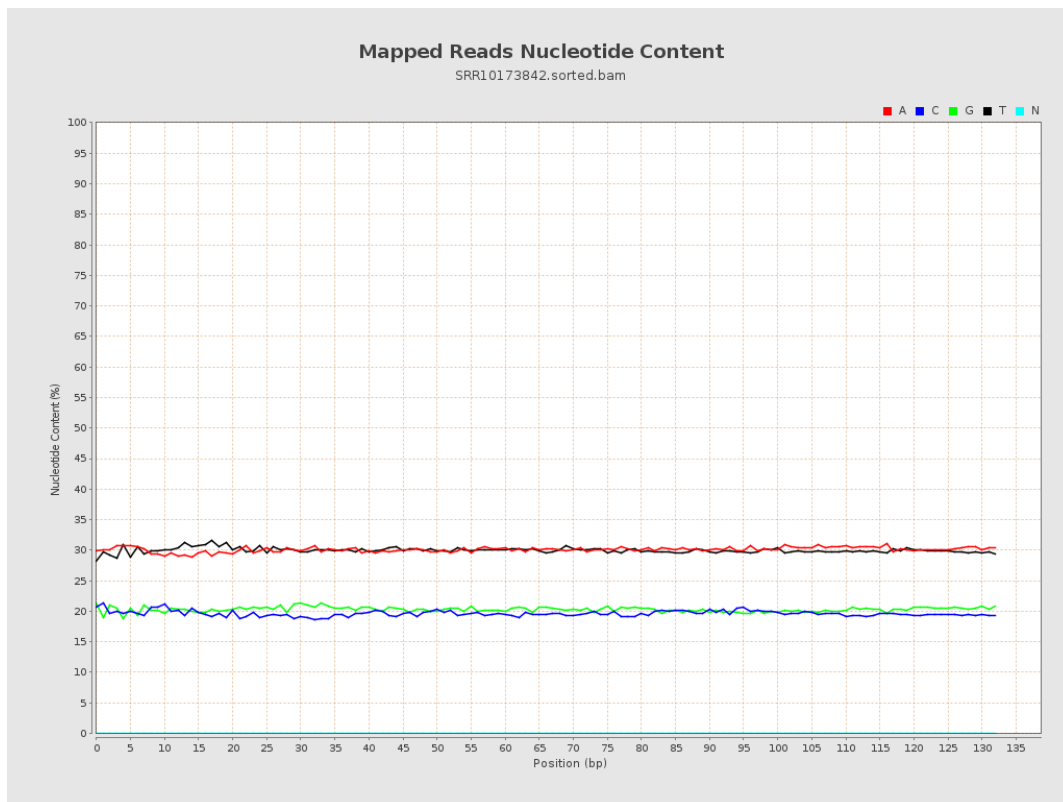
6. Results : Genome Fraction Coverage



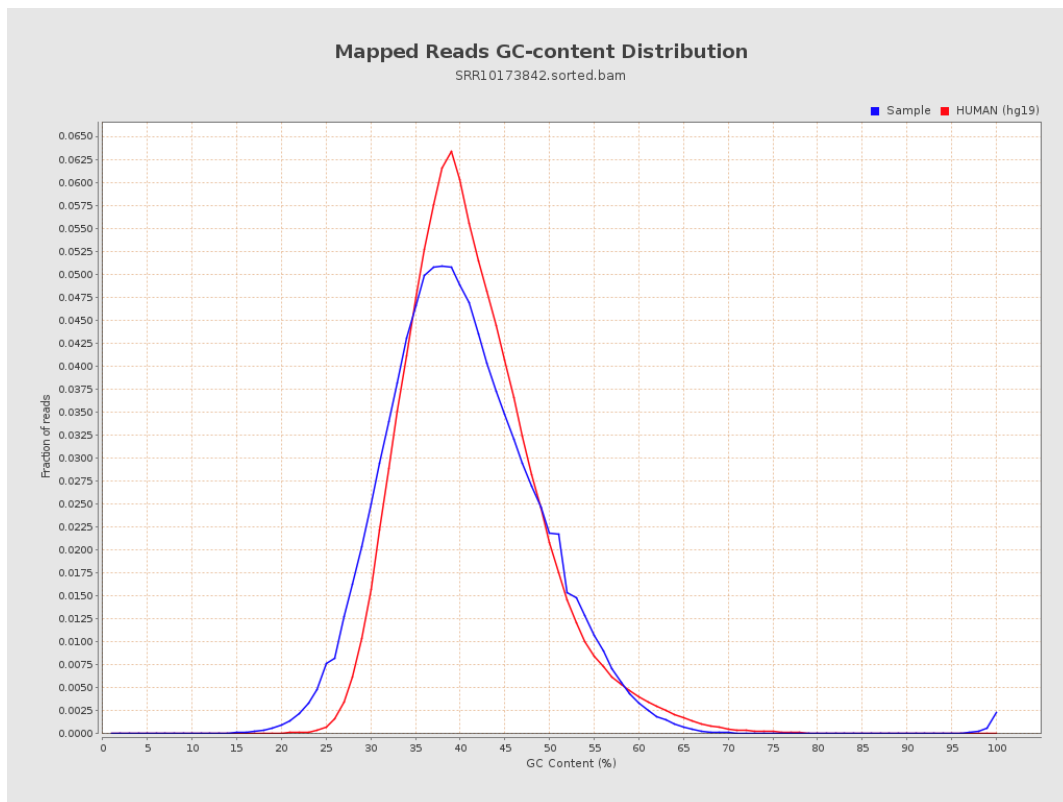
7. Results : Duplication Rate Histogram



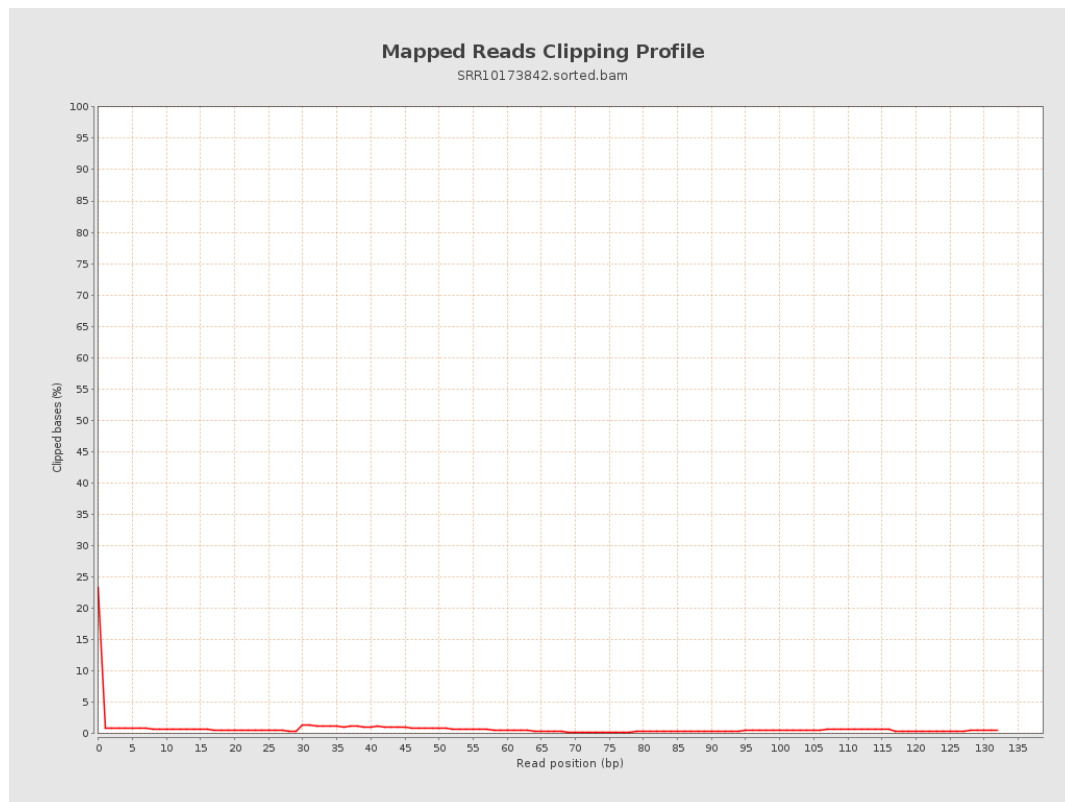
8. Results : Mapped Reads Nucleotide Content



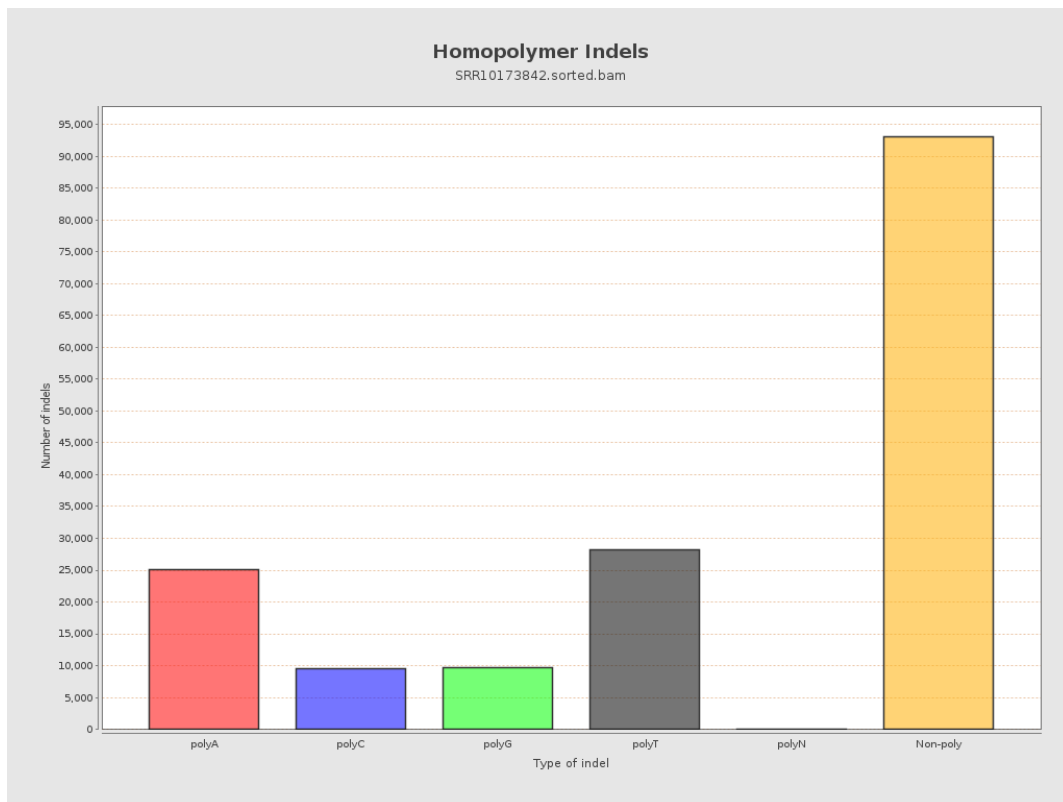
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



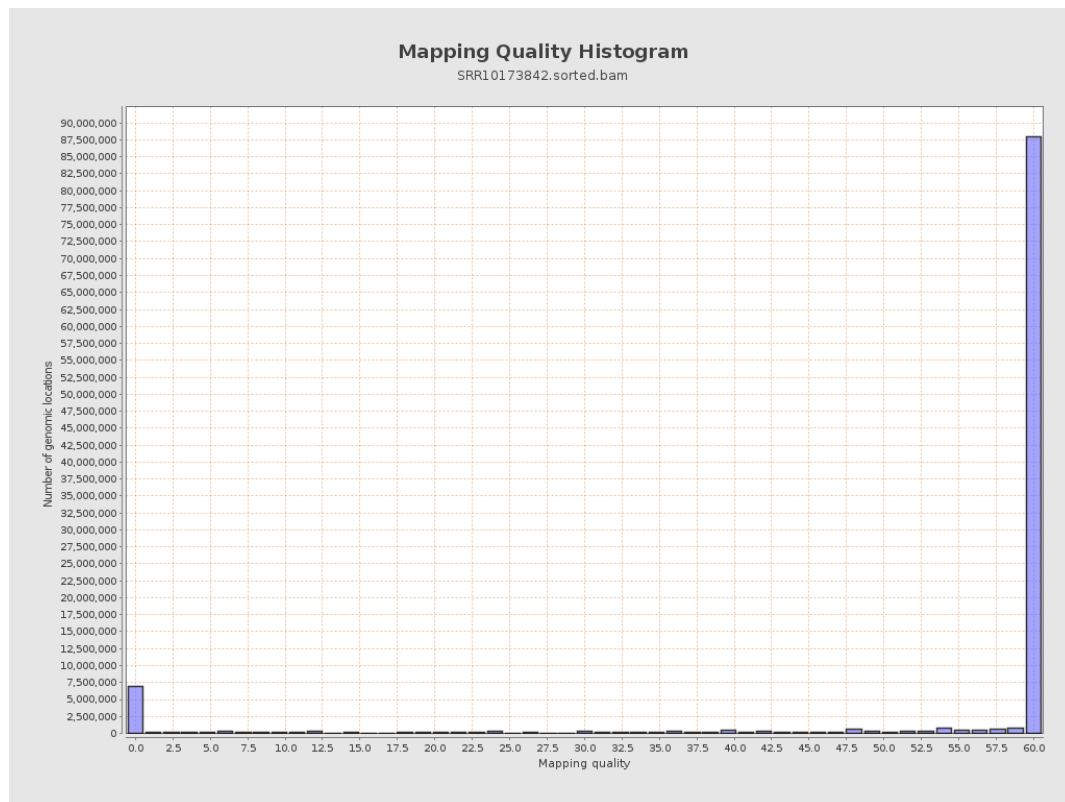
11. Results : Homopolymer Indels



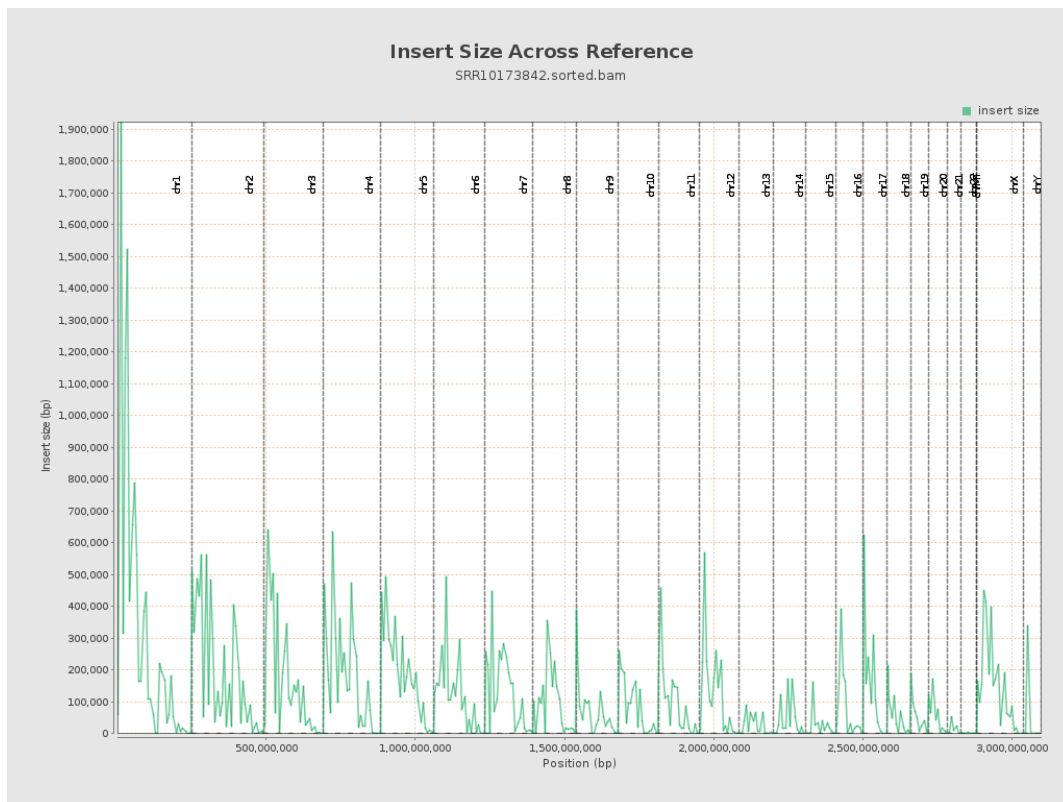
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

