

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:36:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173967.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_SRR10173967 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173967_1.fastq.gz SRR10173967_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:36:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173967.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,706,514
Mapped reads	5,563,247 / 97.49%
Unmapped reads	143,267 / 2.51%
Mapped paired reads	5,563,247 / 97.49%
Mapped reads, first in pair	2,785,312 / 48.81%
Mapped reads, second in pair	2,777,935 / 48.68%
Mapped reads, both in pair	5,473,448 / 95.92%
Mapped reads, singletons	89,799 / 1.57%
Secondary alignments	0
Supplementary alignments	695,857 / 12.19%
Read min/max/mean length	30 / 133 / 125.13
Duplicated reads (estimated)	4,259,408 / 74.64%
Duplication rate	63.13%
Clipped reads	2,901,741 / 50.85%

2.2. ACGT Content

Number/percentage of A's	186,745,283 / 29.85%
Number/percentage of C's	124,407,660 / 19.89%
Number/percentage of T's	184,937,924 / 29.56%
Number/percentage of G's	129,530,134 / 20.7%
Number/percentage of N's	4,514 / 0%

GC Percentage	40.59%
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2.3. Coverage

Mean	0.2022
Standard Deviation	3.8592

2.4. Mapping Quality

Mean Mapping Quality	52.46
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2.5. Insert size

Mean	999,879.19
Standard Deviation	9,323,527.37
P25/Median/P75	105 / 156 / 245

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	5,832,858
Insertions	92,826
Mapped reads with at least one insertion	1.58%
Deletions	181,739
Mapped reads with at least one deletion	3.17%
Homopolymer indels	40.05%

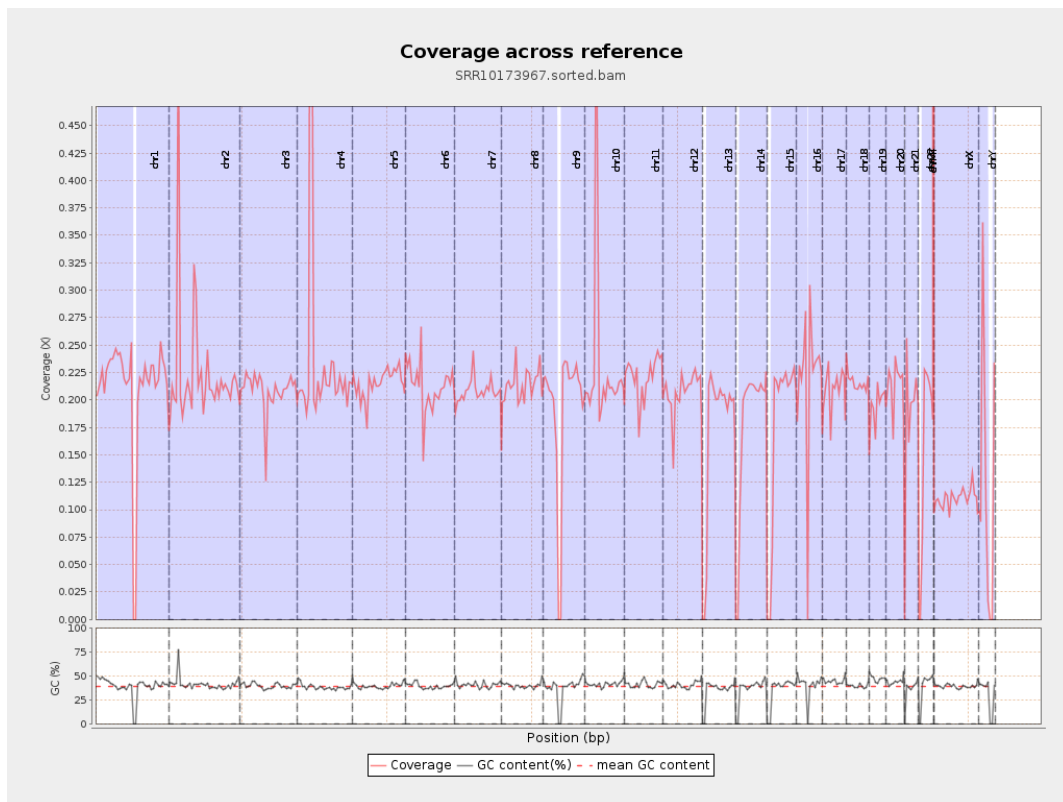
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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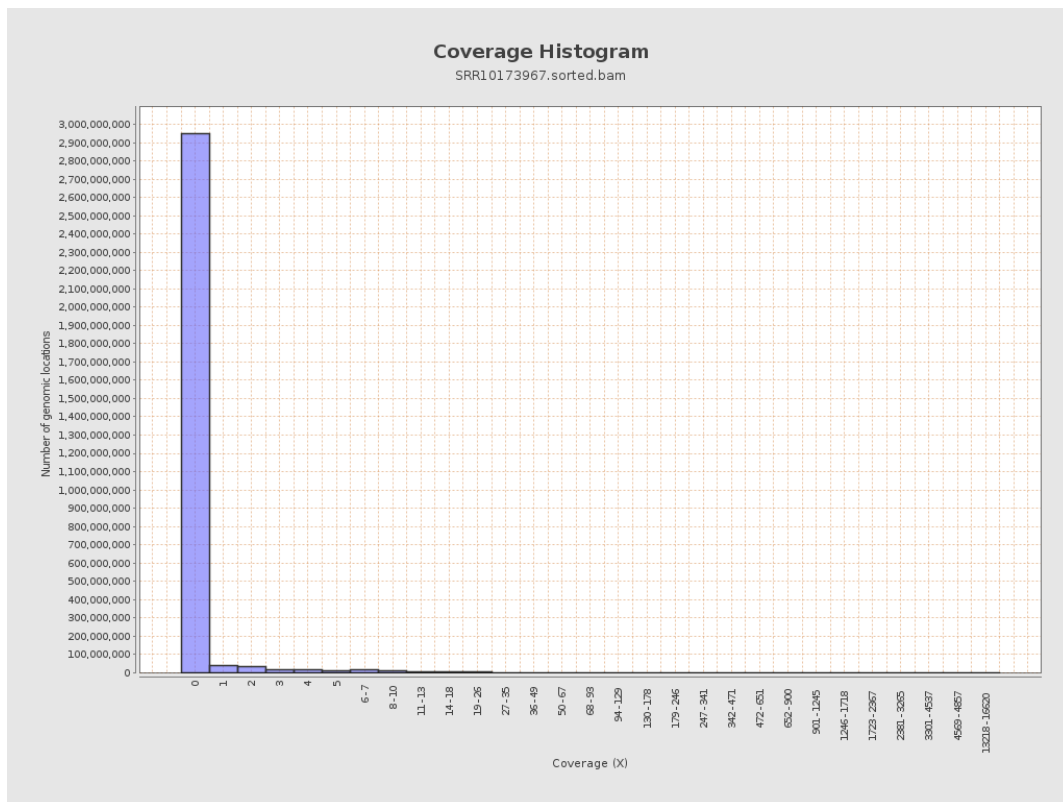
		bases	coverage	deviation
chr1	249250621	52809962	0.2119	1.8961
chr2	243199373	54889646	0.2257	11.7275
chr3	198022430	41284757	0.2085	1.2884
chr4	191154276	45493932	0.238	4.5637
chr5	180915260	38958376	0.2153	1.3116
chr6	171115067	36345047	0.2124	1.5058
chr7	159138663	33203257	0.2086	1.7805
chr8	146364022	31303327	0.2139	2.2939
chr9	141213431	26937853	0.1908	1.7063
chr10	135534747	31031120	0.229	3.0765
chr11	135006516	29840114	0.221	1.392
chr12	133851895	27710209	0.207	1.3153
chr13	115169878	19683410	0.1709	1.1563
chr14	107349540	18906001	0.1761	1.1957
chr15	102531392	18025035	0.1758	1.2038
chr16	90354753	19790771	0.219	1.7213
chr17	81195210	16957622	0.2089	1.4649
chr18	78077248	16870706	0.2161	2.321
chr19	59128983	11514153	0.1947	1.5801
chr20	63025520	13474350	0.2138	2.1196
chr21	48129895	8977688	0.1865	3.0055
chr22	51304566	7638723	0.1489	1.3128
chrMT	16571	477143	28.7939	22.976
chrX	155270560	17200410	0.1108	0.9586

chrY	59373566	6771868	0.1141	3.7806
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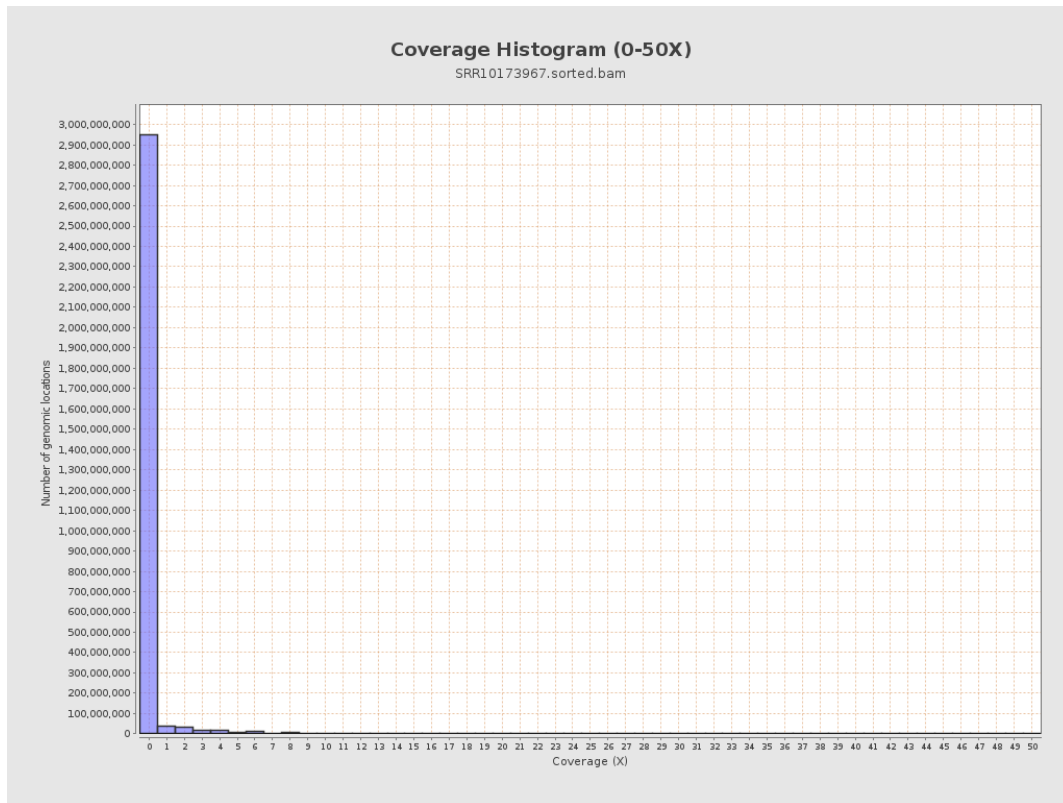
3. Results : Coverage across reference



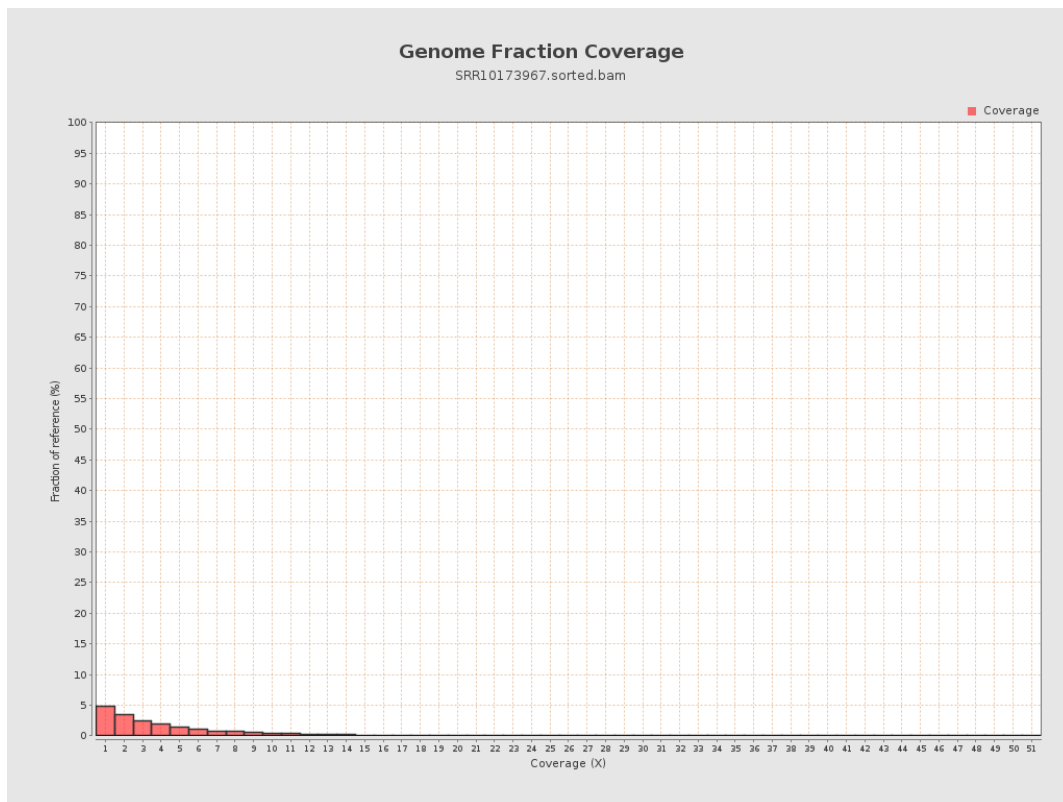
4. Results : Coverage Histogram



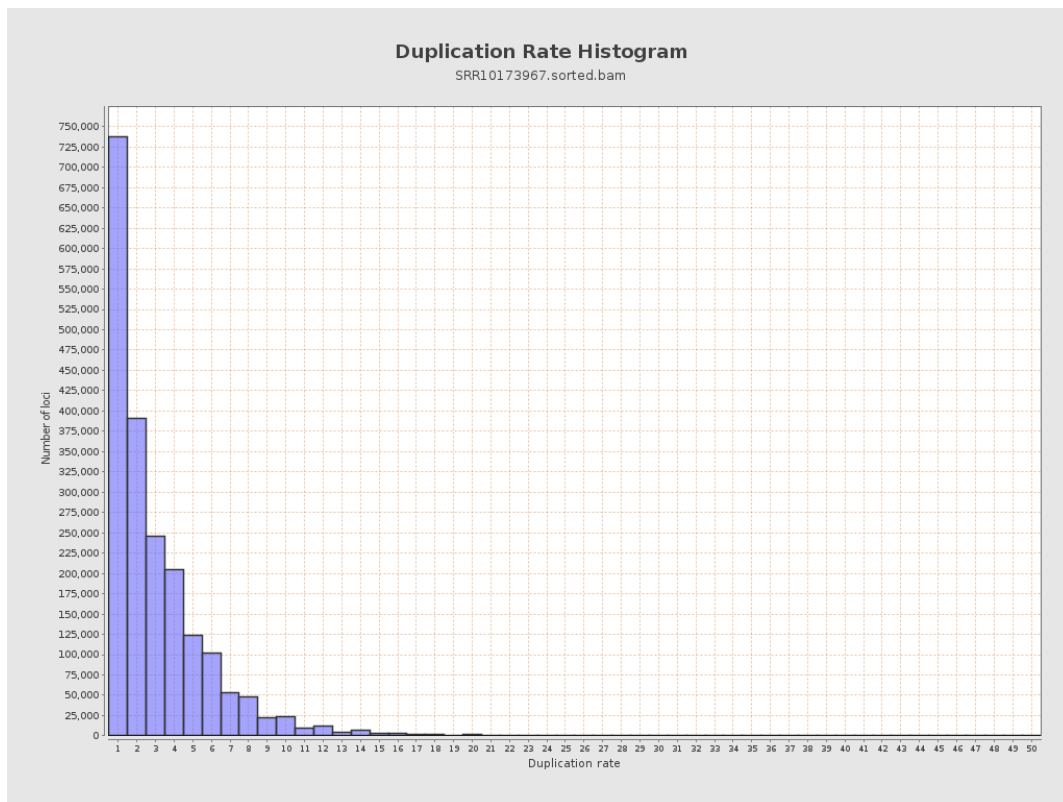
5. Results : Coverage Histogram (0-50X)



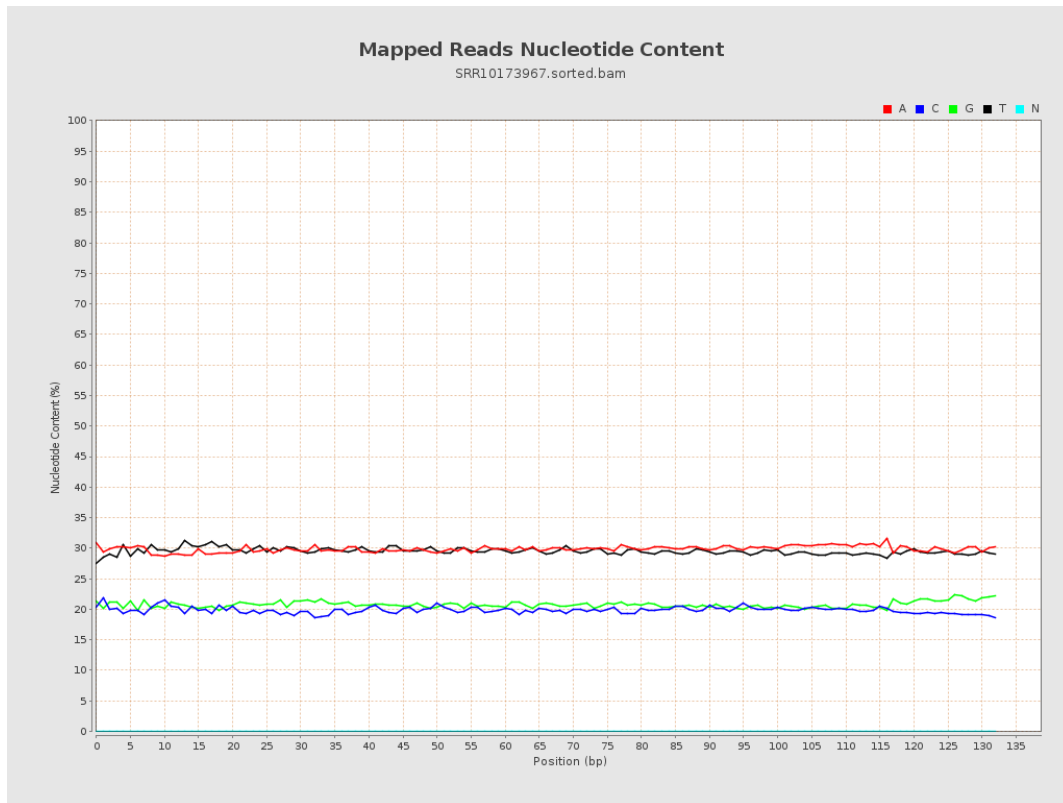
6. Results : Genome Fraction Coverage



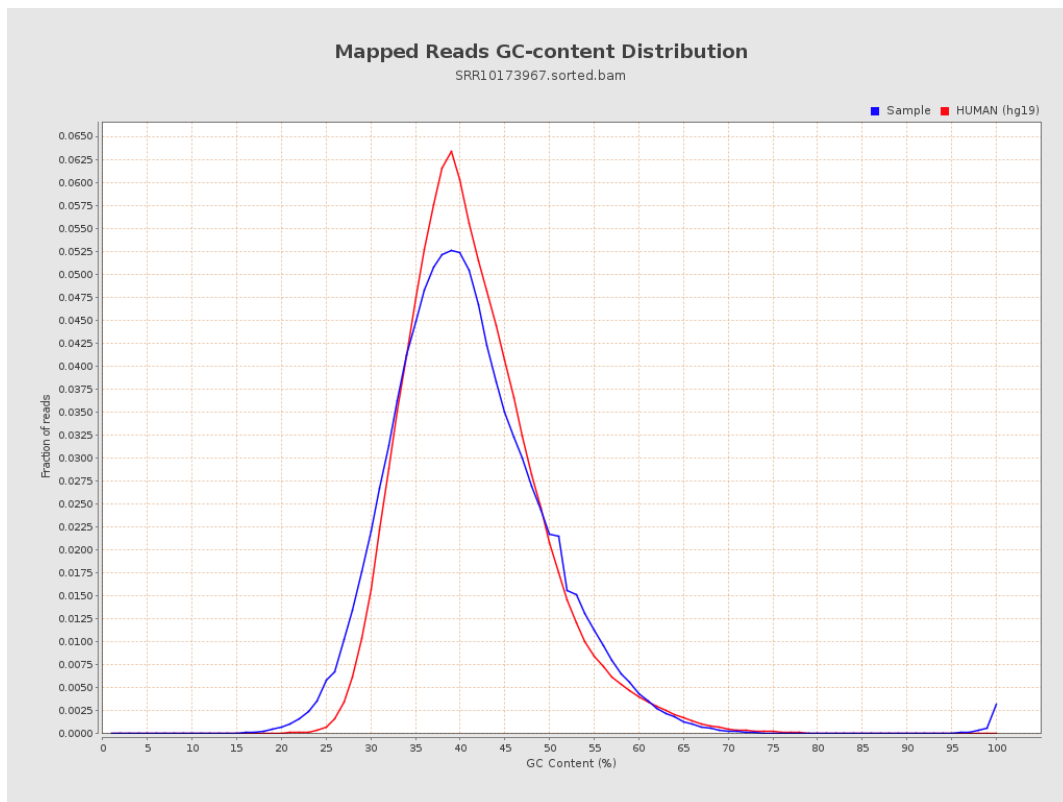
7. Results : Duplication Rate Histogram



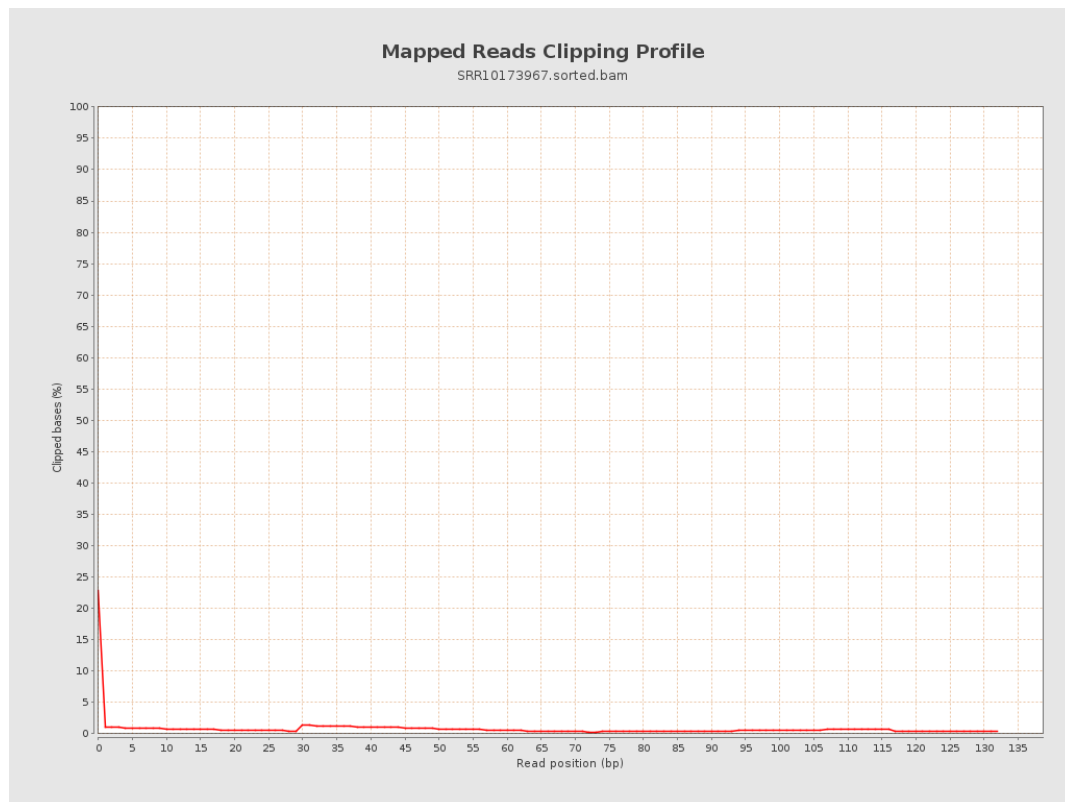
8. Results : Mapped Reads Nucleotide Content



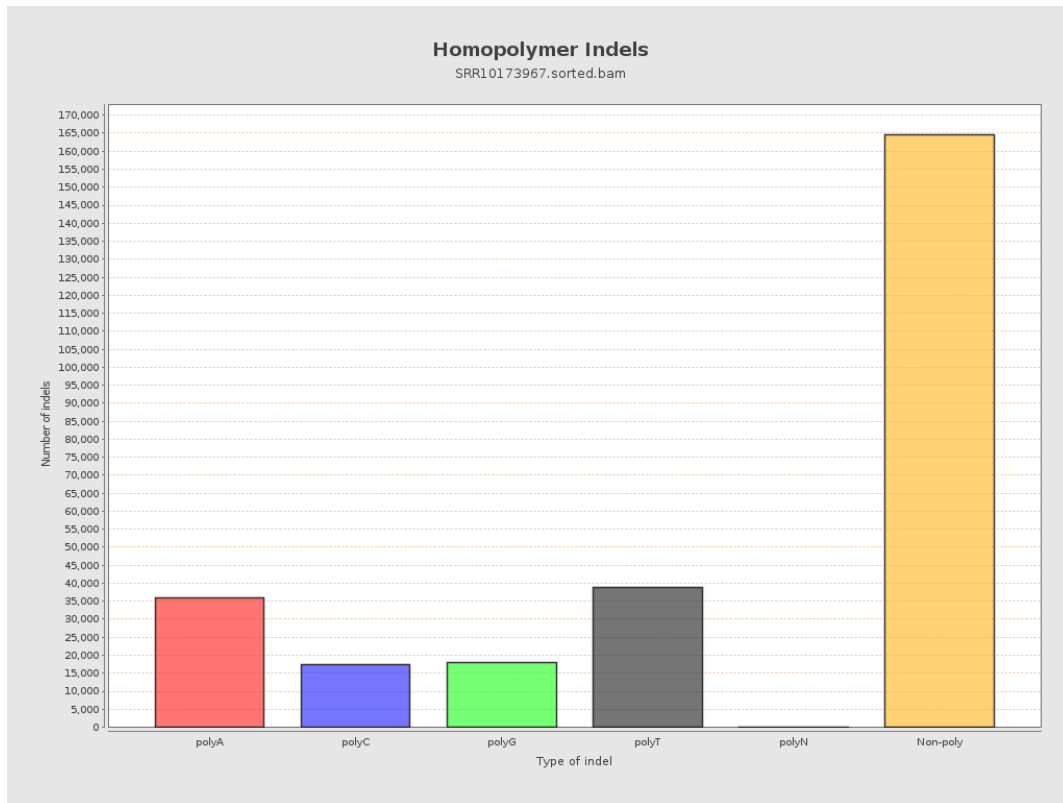
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



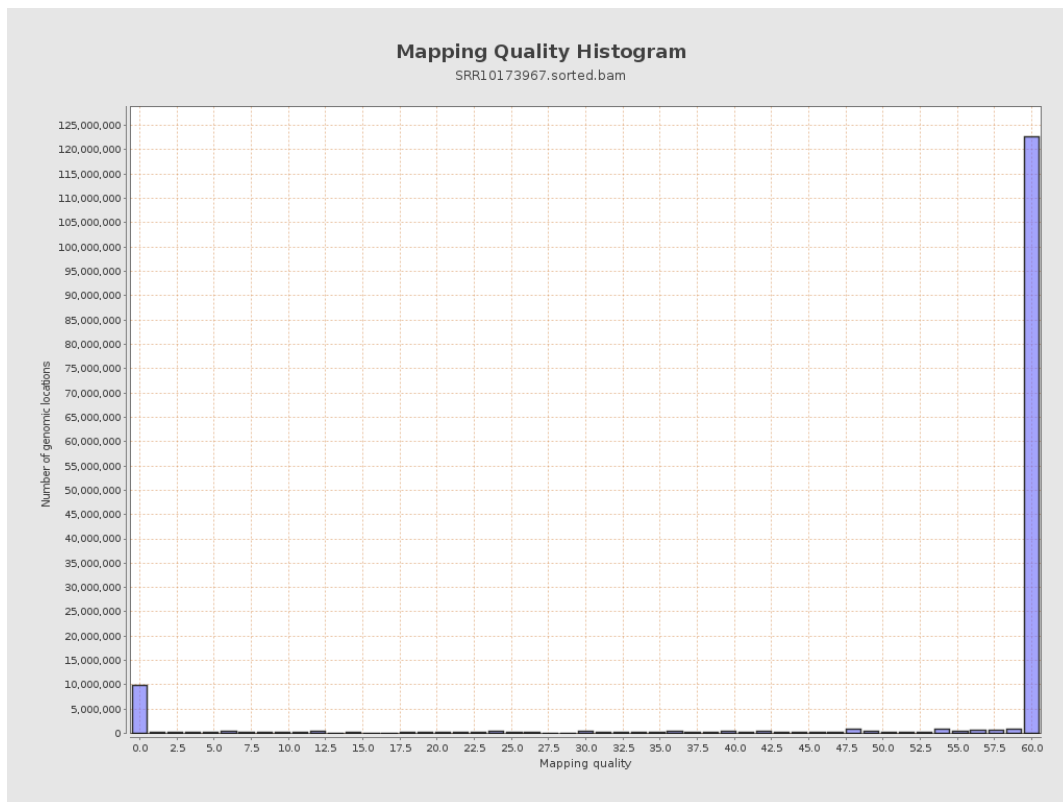
11. Results : Homopolymer Indels



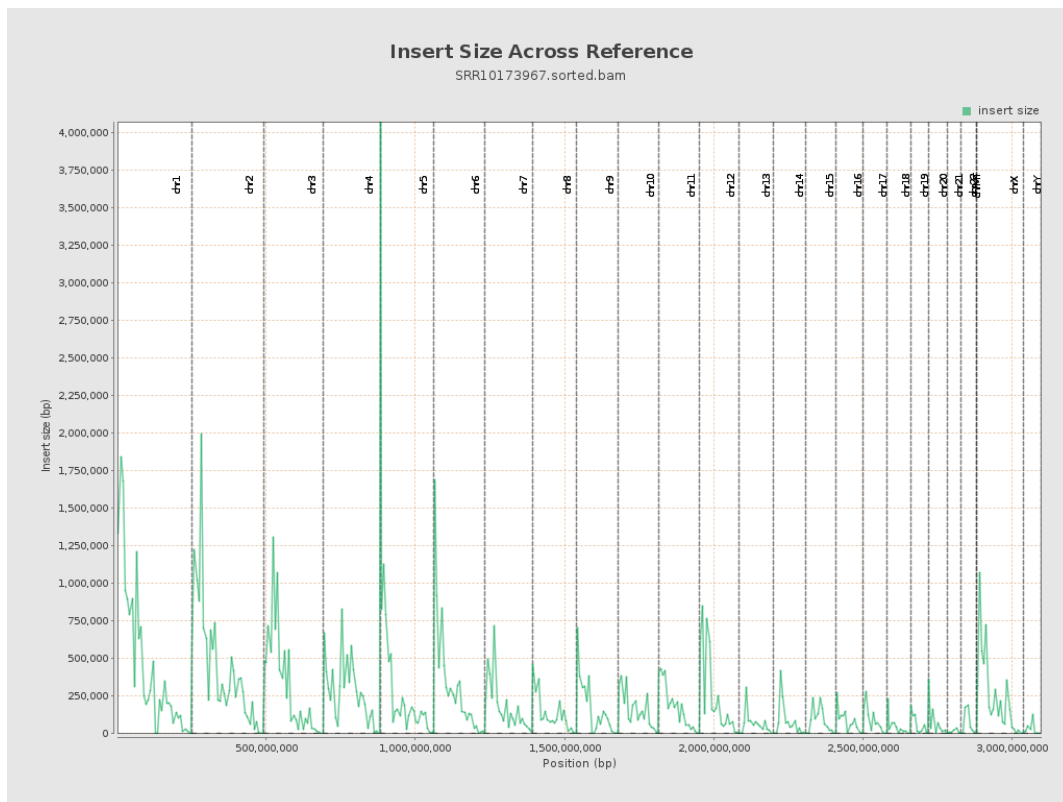
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

