

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:37:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124881.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_SRR3124881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124881_1.fastq.gz SRR3124881_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:37:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,178,716
Mapped reads	5,084,670 / 98.18%
Unmapped reads	94,046 / 1.82%
Mapped paired reads	5,084,670 / 98.18%
Mapped reads, first in pair	2,543,864 / 49.12%
Mapped reads, second in pair	2,540,806 / 49.06%
Mapped reads, both in pair	5,066,276 / 97.83%
Mapped reads, singletons	18,394 / 0.36%
Secondary alignments	0
Supplementary alignments	23,158 / 0.45%
Read min/max/mean length	30 / 101 / 101.18
Duplicated reads (estimated)	278,233 / 5.37%
Duplication rate	3.04%
Clipped reads	3,085,011 / 59.57%

2.2. ACGT Content

Number/percentage of A's	132,058,068 / 28.41%
Number/percentage of C's	94,141,557 / 20.25%
Number/percentage of T's	136,134,053 / 29.29%
Number/percentage of G's	102,472,169 / 22.05%
Number/percentage of N's	7,974 / 0%

GC Percentage	42.3%
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2.3. Coverage

Mean	0.1502
Standard Deviation	1.5045

2.4. Mapping Quality

Mean Mapping Quality	52.69
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2.5. Insert size

Mean	73,380.39
Standard Deviation	2,589,056.55
P25/Median/P75	138 / 172 / 218

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	3,526,131
Insertions	65,774
Mapped reads with at least one insertion	1.26%
Deletions	153,502
Mapped reads with at least one deletion	2.96%
Homopolymer indels	47.33%

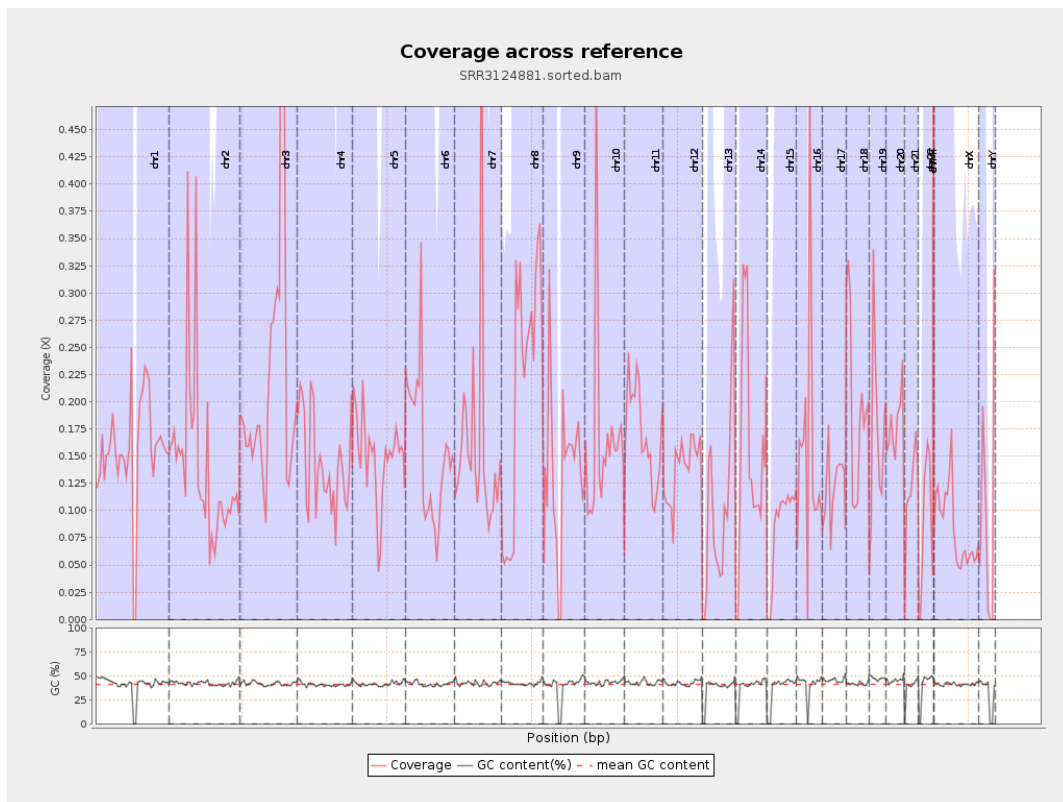
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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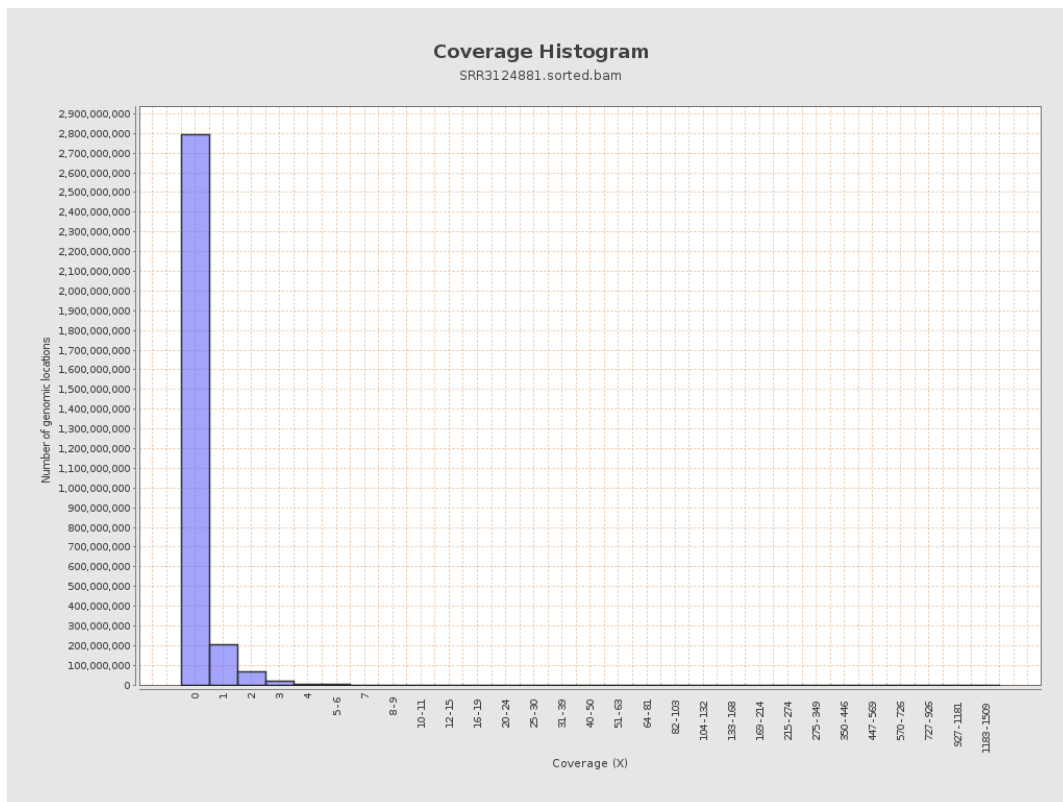
		bases	coverage	deviation
chr1	249250621	38784866	0.1556	1.5965
chr2	243199373	34581423	0.1422	1.7651
chr3	198022430	44555841	0.225	0.7168
chr4	191154276	27199781	0.1423	0.9031
chr5	180915260	27023001	0.1494	0.5172
chr6	171115067	26441532	0.1545	1.7938
chr7	159138663	26031911	0.1636	2.0612
chr8	146364022	31421098	0.2147	0.7705
chr9	141213431	19694879	0.1395	2.0978
chr10	135534747	22103403	0.1631	3.2568
chr11	135006516	22768662	0.1686	1.3963
chr12	133851895	18486518	0.1381	0.4915
chr13	115169878	11897641	0.1033	0.4331
chr14	107349540	16089505	0.1499	0.5814
chr15	102531392	8668846	0.0845	0.3786
chr16	90354753	13632987	0.1509	2.4924
chr17	81195210	9805601	0.1208	1.3281
chr18	78077248	15221280	0.195	2.3432
chr19	59128983	10392960	0.1758	1.0891
chr20	63025520	11222147	0.1781	0.607
chr21	48129895	5687471	0.1182	0.5646
chr22	51304566	4472404	0.0872	0.4172
chrMT	16571	112849	6.81	4.0965
chrX	155270560	13077814	0.0842	0.7034

chrY	59373566	5701616	0.096	1.9886
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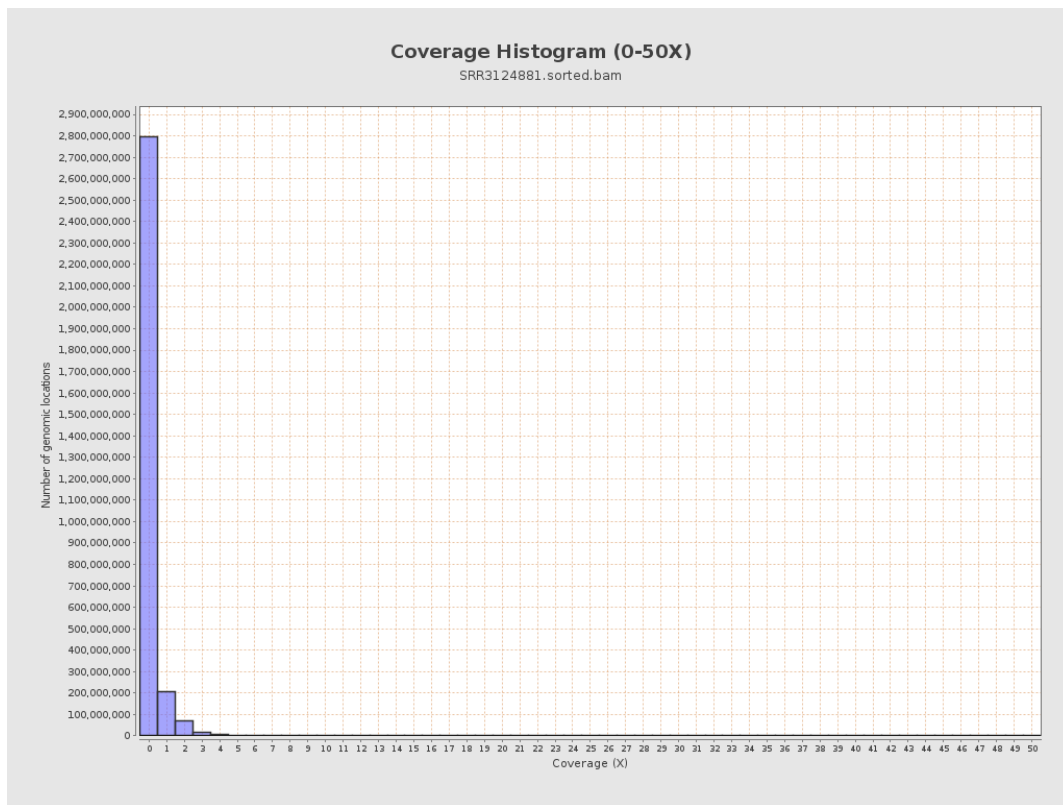
3. Results : Coverage across reference



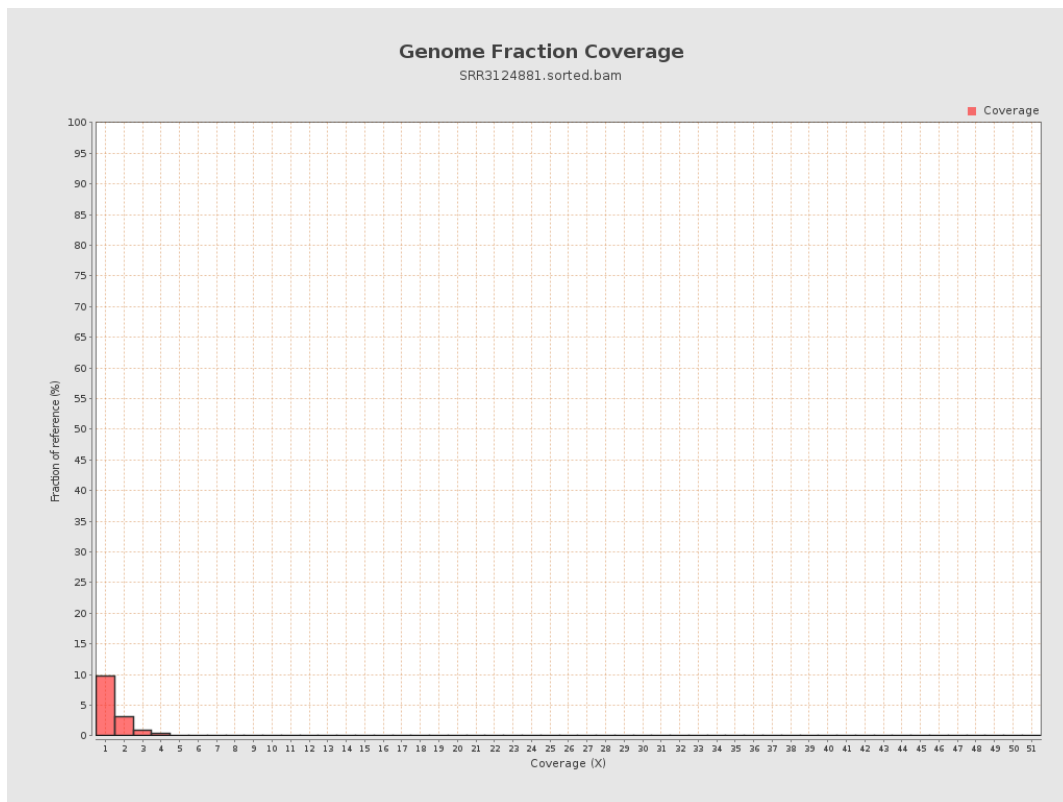
4. Results : Coverage Histogram



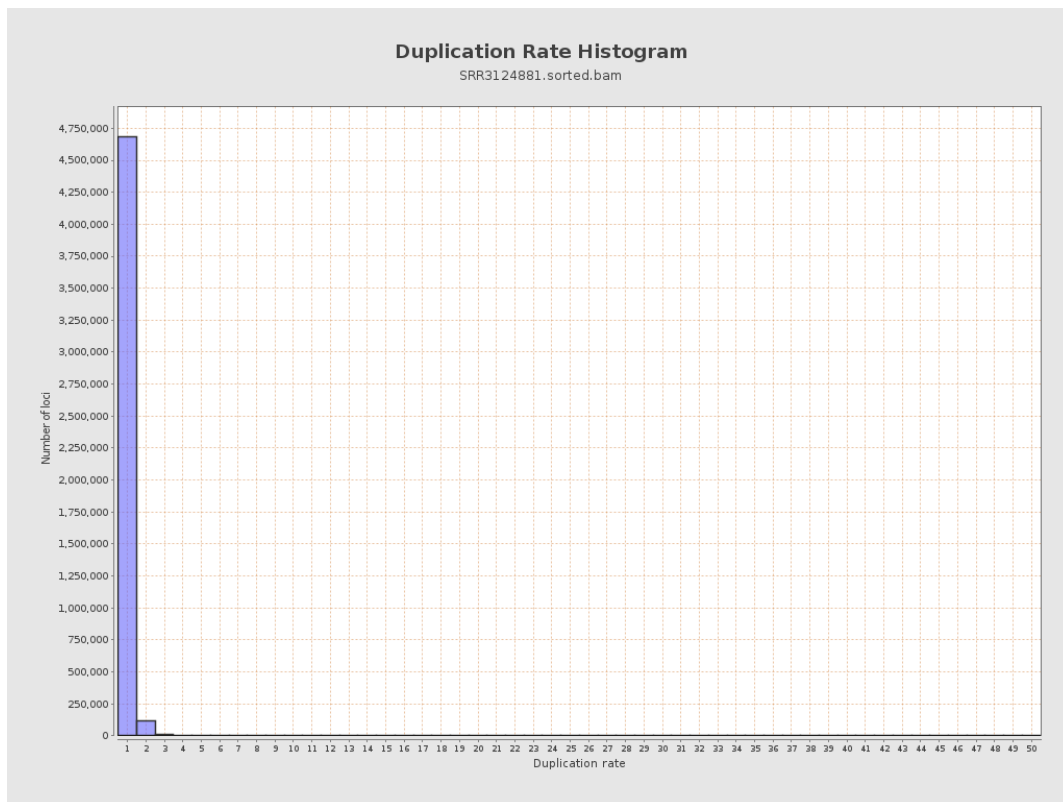
5. Results : Coverage Histogram (0-50X)



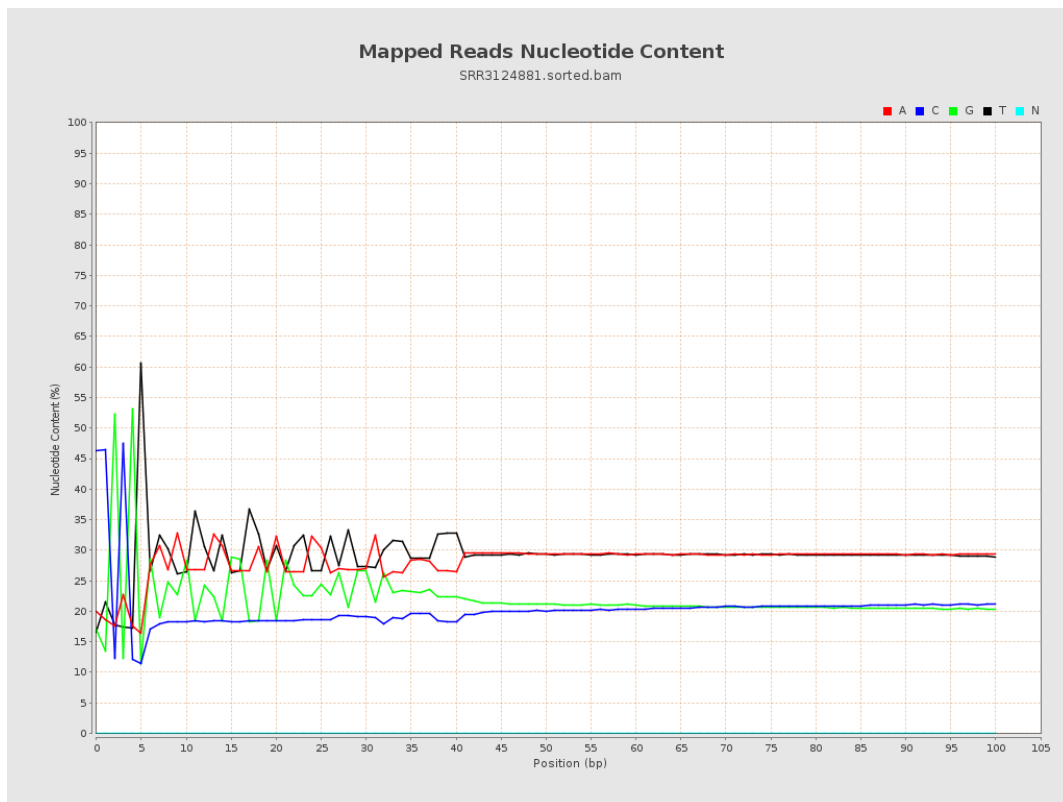
6. Results : Genome Fraction Coverage



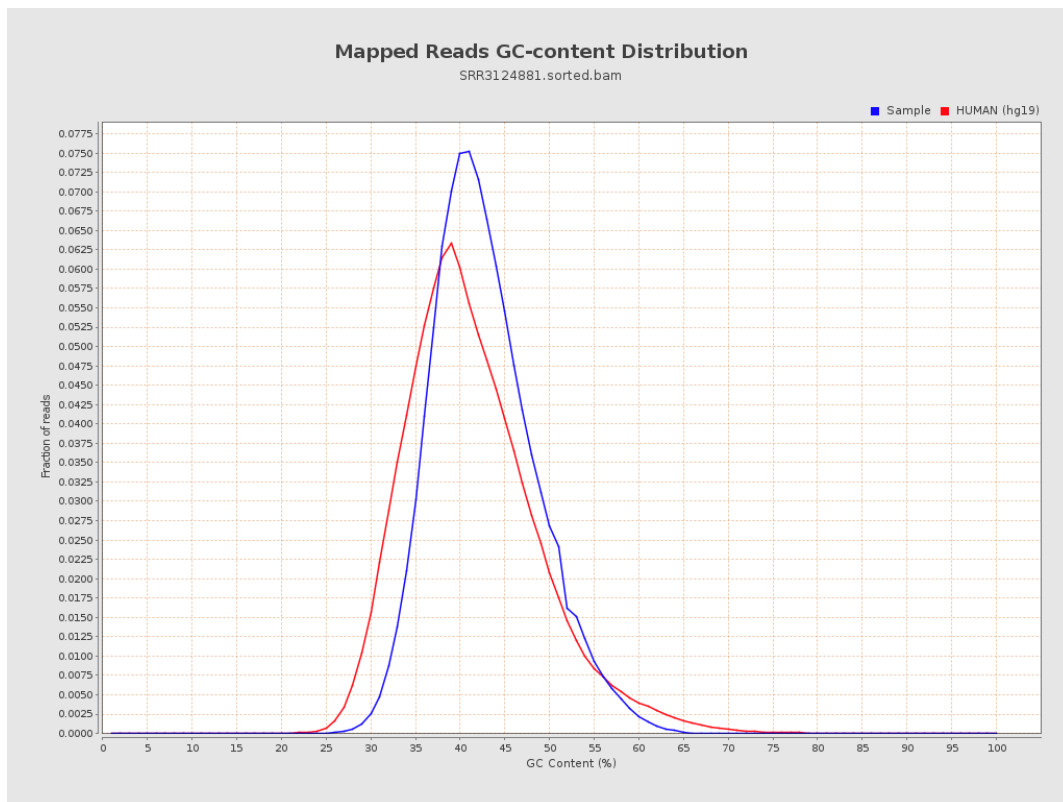
7. Results : Duplication Rate Histogram



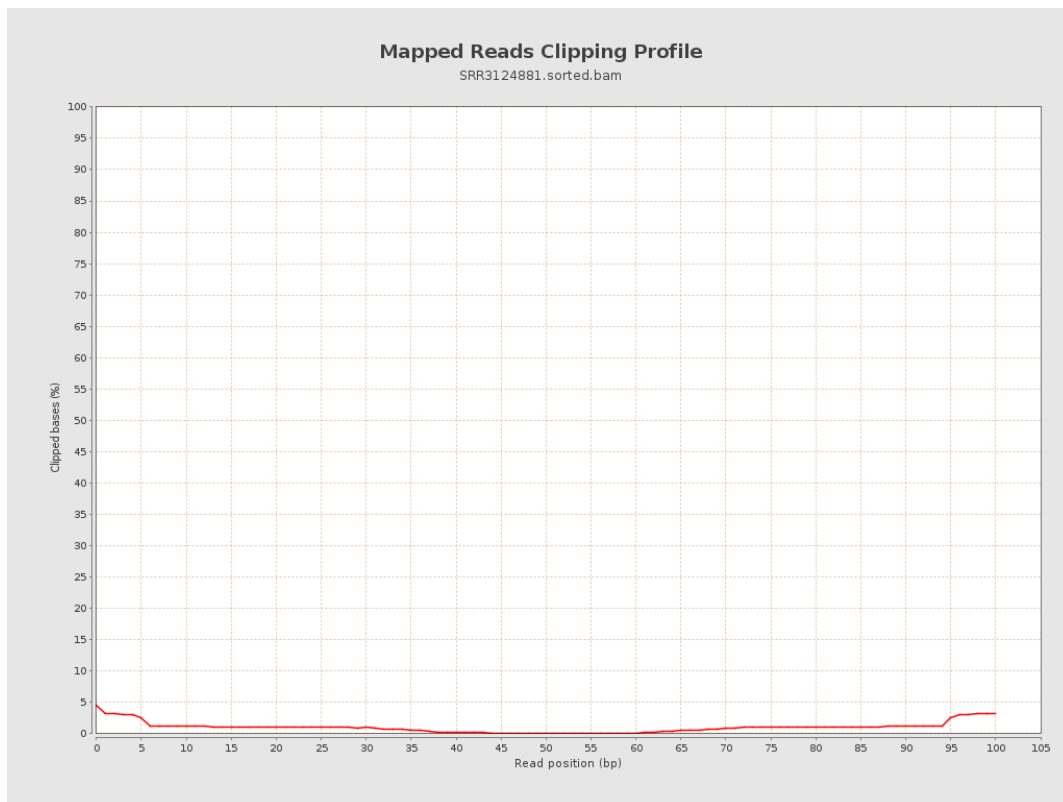
8. Results : Mapped Reads Nucleotide Content



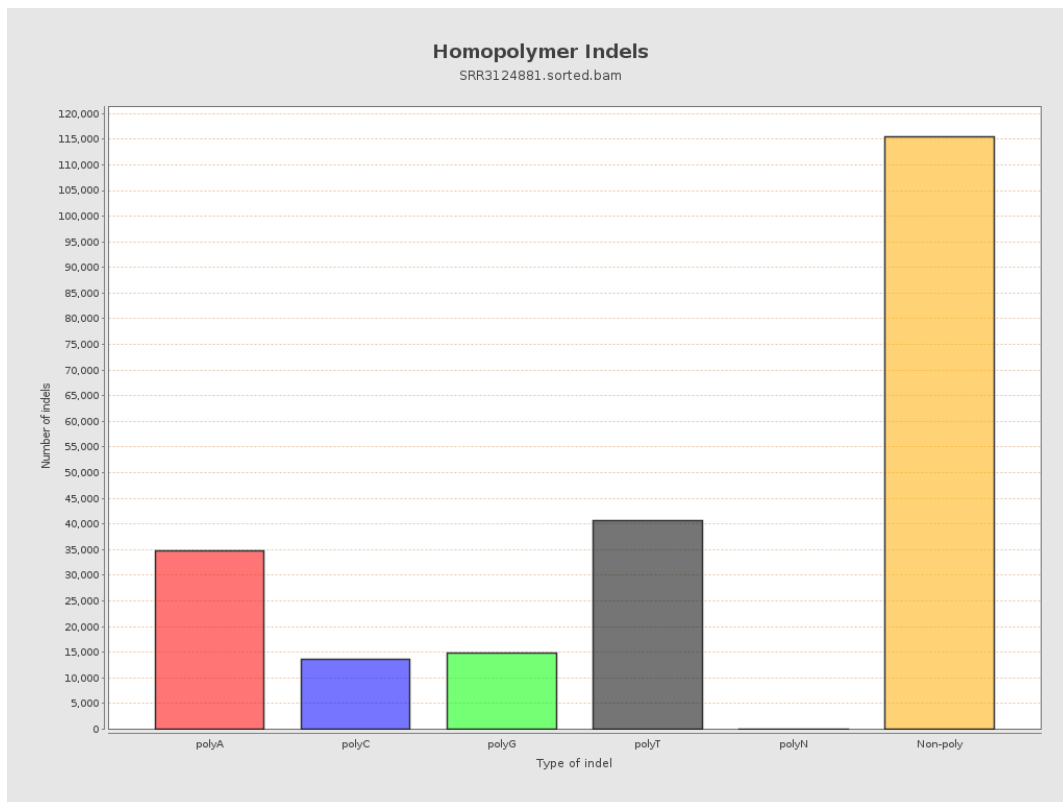
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



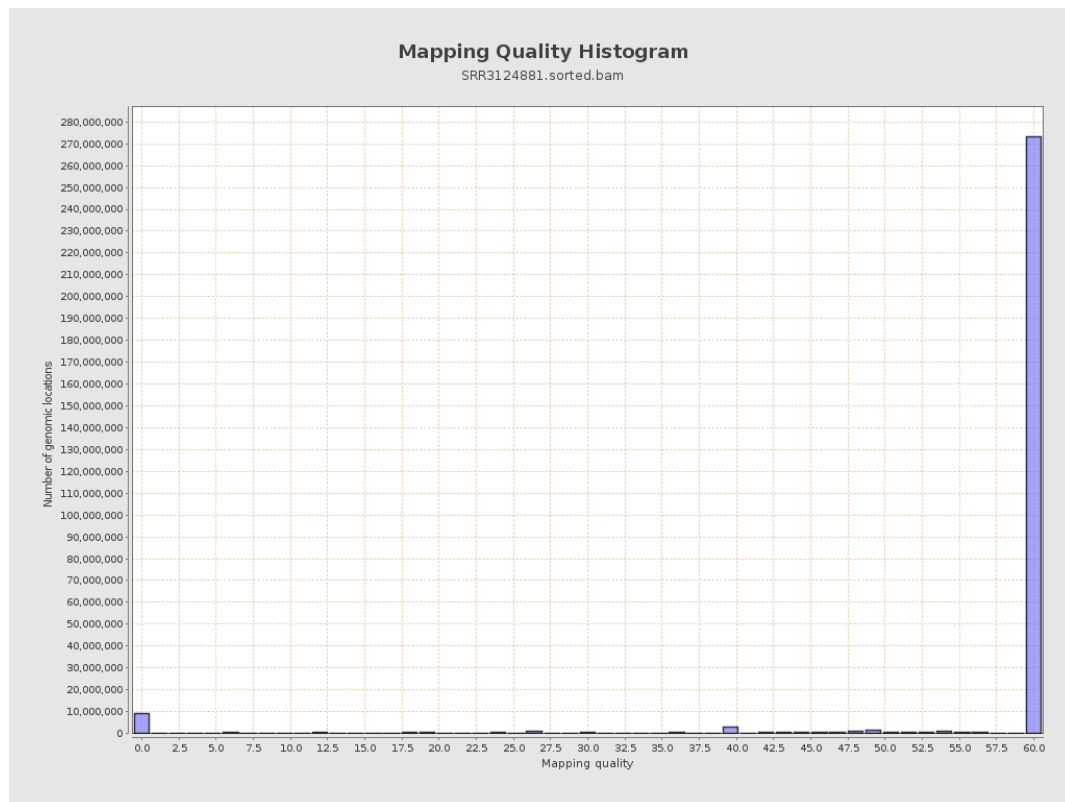
11. Results : Homopolymer Indels



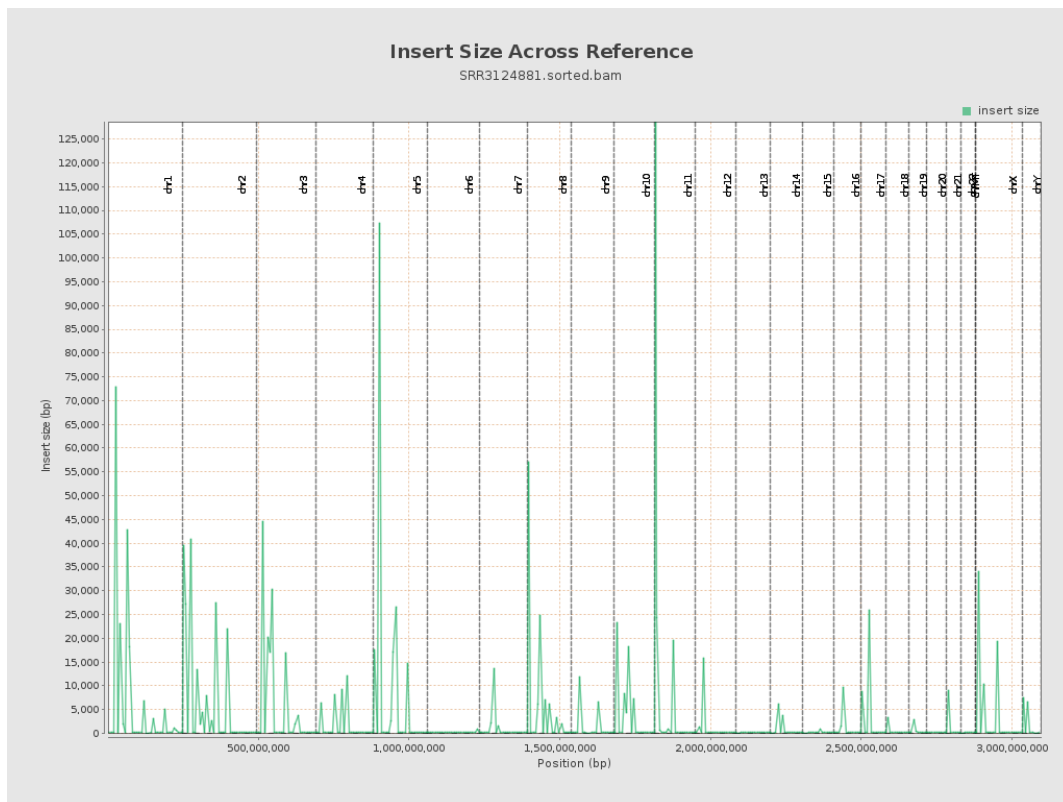
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

