

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 05:17:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124828.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_SRR3124828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124828_1.fastq.gz SRR3124828_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 05:17:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,536,072
Mapped reads	23,116,279 / 98.22%
Unmapped reads	419,793 / 1.78%
Mapped paired reads	23,116,279 / 98.22%
Mapped reads, first in pair	11,582,064 / 49.21%
Mapped reads, second in pair	11,534,215 / 49.01%
Mapped reads, both in pair	23,027,334 / 97.84%
Mapped reads, singletons	88,945 / 0.38%
Secondary alignments	0
Supplementary alignments	89,906 / 0.38%
Read min/max/mean length	30 / 101 / 101.15
Duplicated reads (estimated)	4,350,791 / 18.49%
Duplication rate	12.51%
Clipped reads	11,339,201 / 48.18%

2.2. ACGT Content

Number/percentage of A's	558,096,112 / 27.89%
Number/percentage of C's	375,704,490 / 18.78%
Number/percentage of T's	588,576,178 / 29.42%
Number/percentage of G's	478,420,921 / 23.91%
Number/percentage of N's	18,898 / 0%

GC Percentage	42.69%
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2.3. Coverage

Mean	0.6467
Standard Deviation	4.6299

2.4. Mapping Quality

Mean Mapping Quality	52.87
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2.5. Insert size

Mean	33,484.45
Standard Deviation	1,717,006.84
P25/Median/P75	148 / 201 / 282

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	14,914,761
Insertions	271,266
Mapped reads with at least one insertion	1.14%
Deletions	673,933
Mapped reads with at least one deletion	2.86%
Homopolymer indels	47.52%

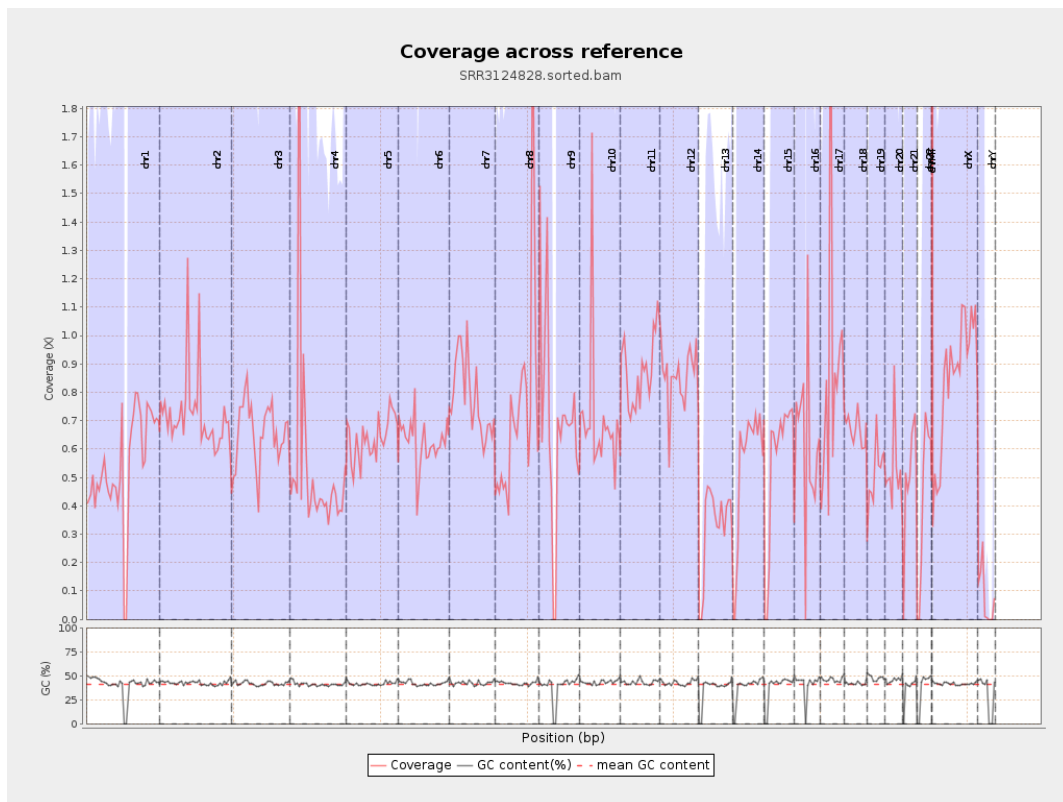
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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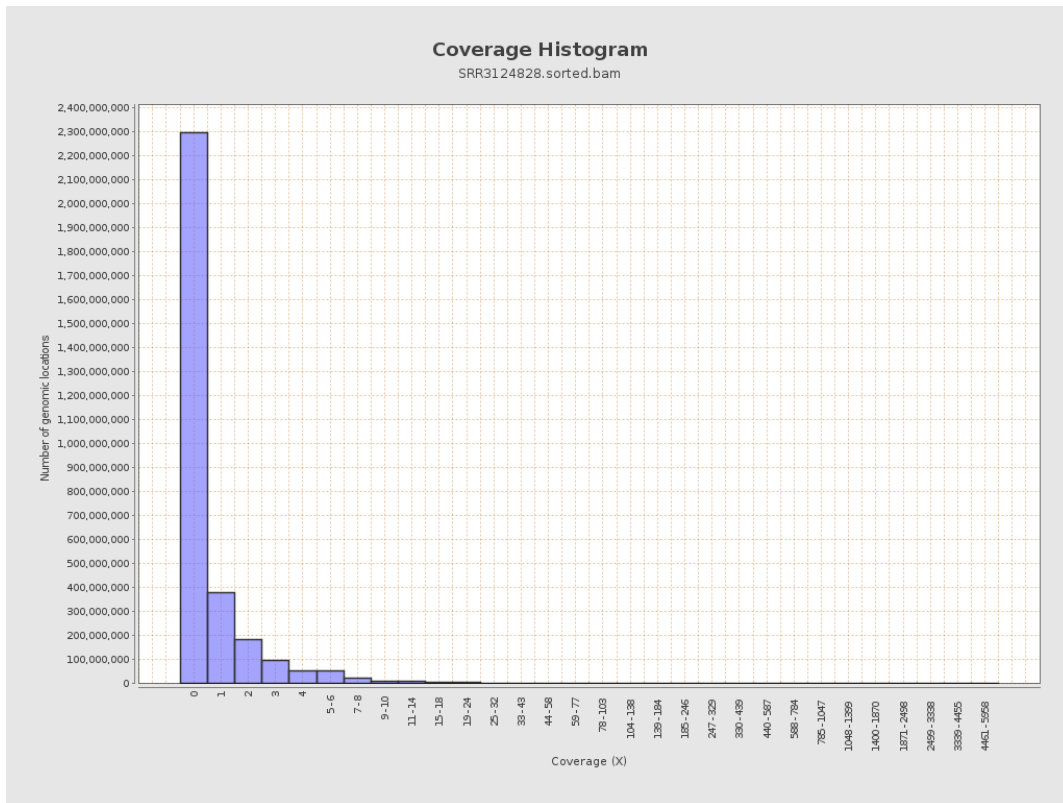
		bases	coverage	deviation
chr1	249250621	136052140	0.5458	4.8518
chr2	243199373	175443863	0.7214	6.1433
chr3	198022430	130292723	0.658	1.5834
chr4	191154276	102638418	0.5369	4.377
chr5	180915260	115452909	0.6382	1.6464
chr6	171115067	107337195	0.6273	2.7055
chr7	159138663	124428478	0.7819	7.4486
chr8	146364022	107059545	0.7315	3.3884
chr9	141213431	96074403	0.6803	5.6519
chr10	135534747	95486808	0.7045	9.1729
chr11	135006516	117325431	0.869	4.067
chr12	133851895	114558917	0.8559	1.9162
chr13	115169878	37983084	0.3298	1.048
chr14	107349540	58204695	0.5422	1.7548
chr15	102531392	56163485	0.5478	1.4708
chr16	90354753	55754268	0.6171	6.8205
chr17	81195210	71873401	0.8852	7.8116
chr18	78077248	52313035	0.67	5.9285
chr19	59128983	30593353	0.5174	2.79
chr20	63025520	33067956	0.5247	1.7693
chr21	48129895	24734187	0.5139	2.224
chr22	51304566	22331017	0.4353	1.4721
chrMT	16571	224965	13.5758	8.0415
chrX	155270560	131783397	0.8487	2.7276

chrY	59373566	4776539	0.0804	4.933
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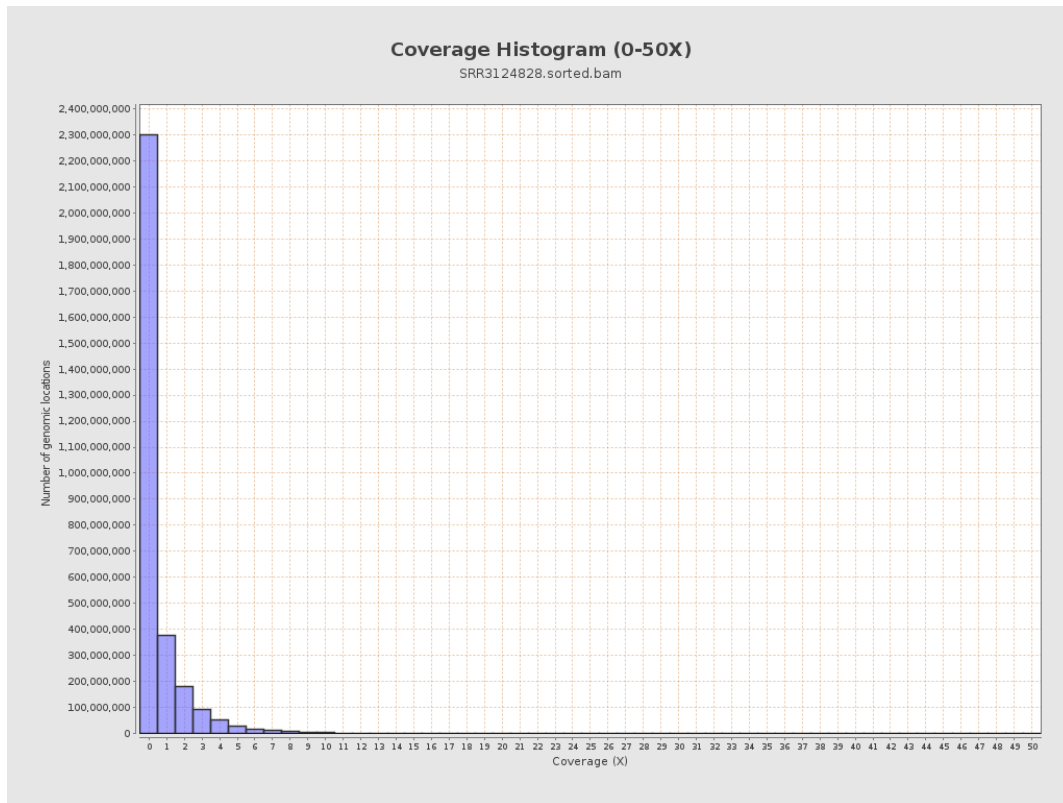
3. Results : Coverage across reference



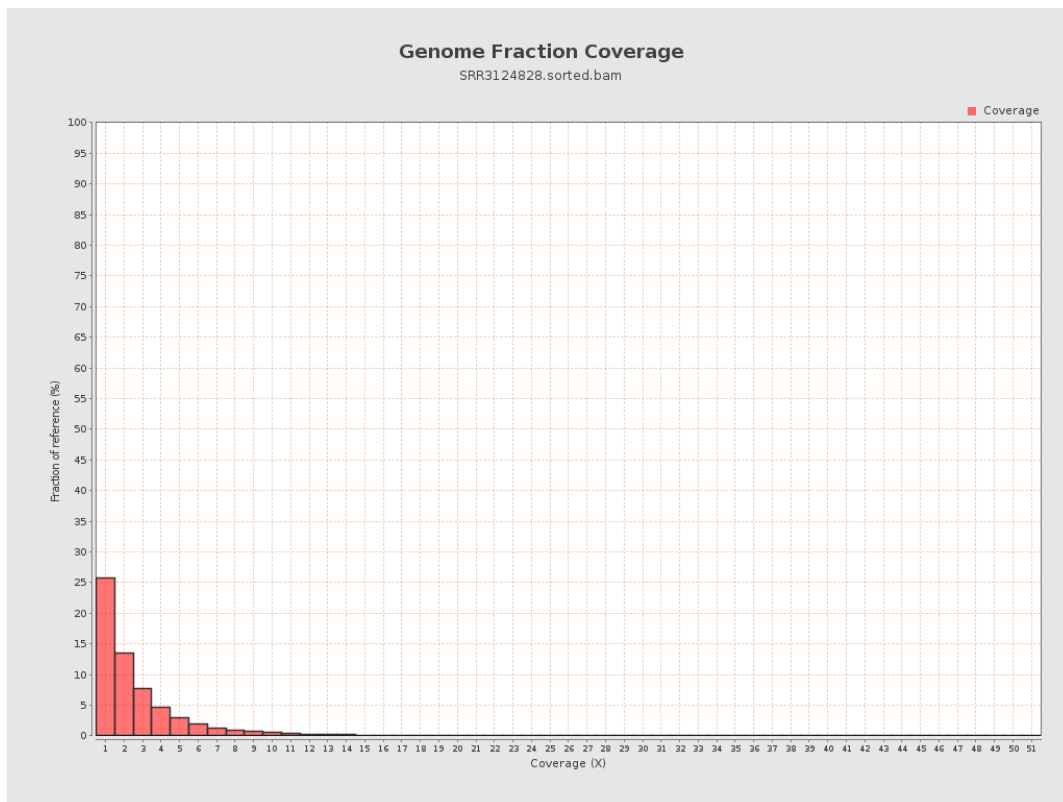
4. Results : Coverage Histogram



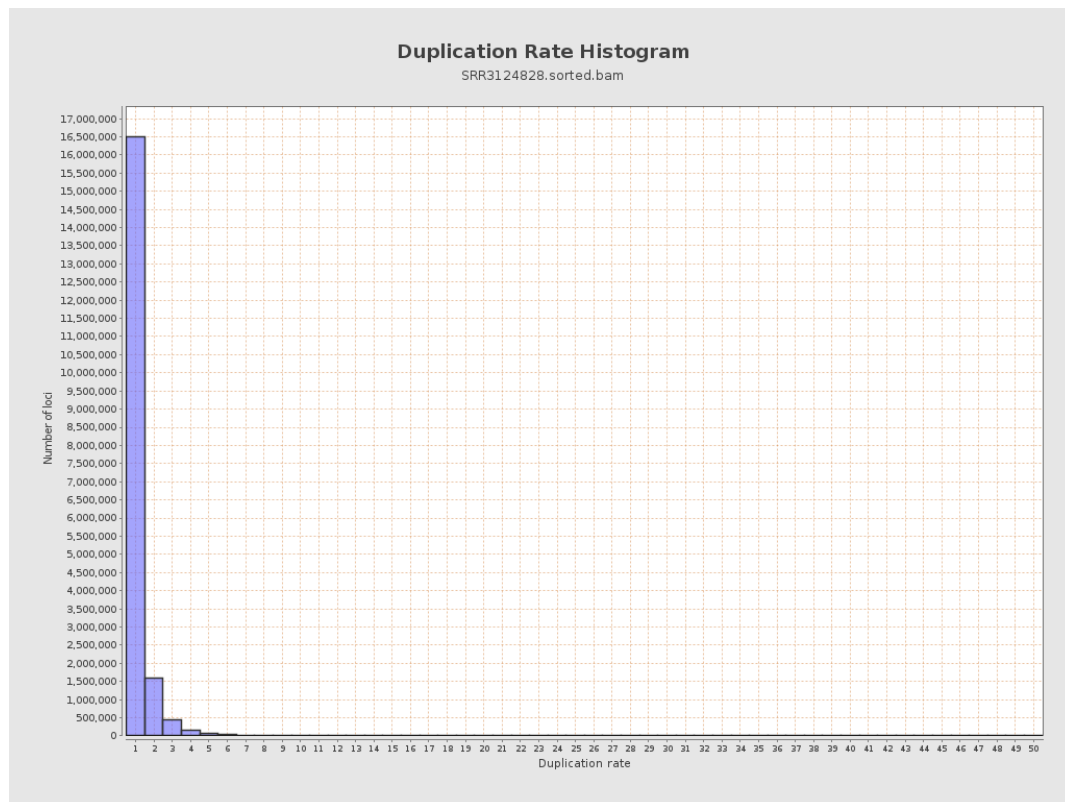
5. Results : Coverage Histogram (0-50X)



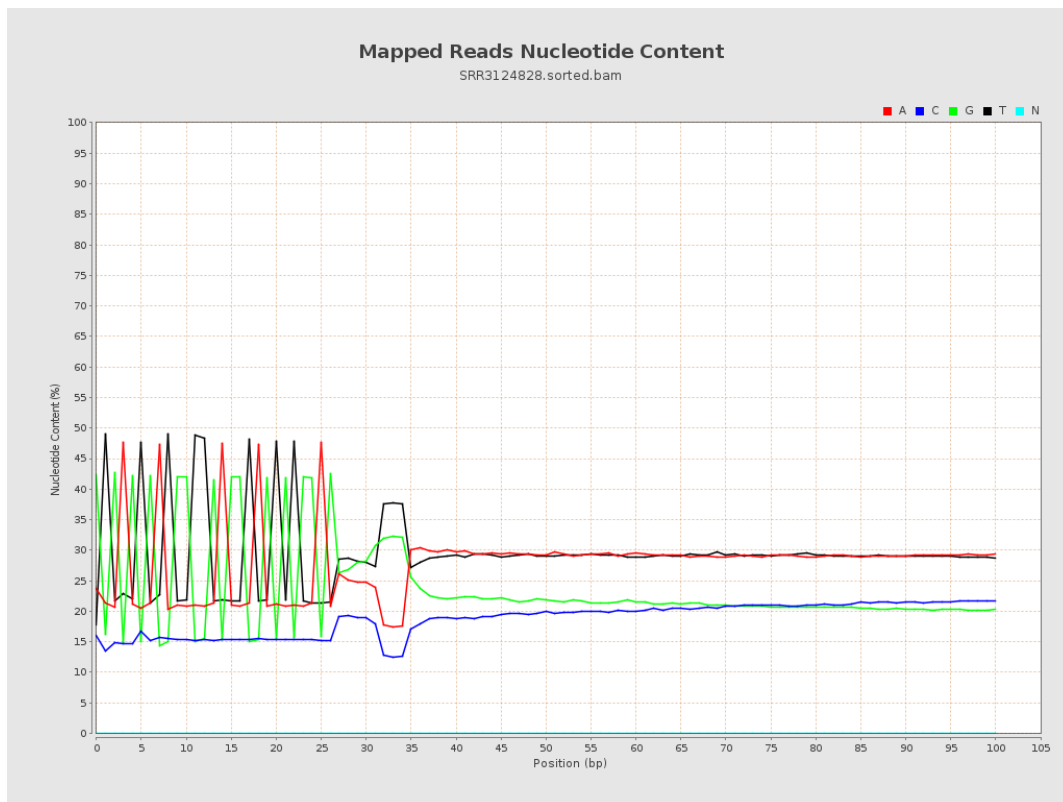
6. Results : Genome Fraction Coverage



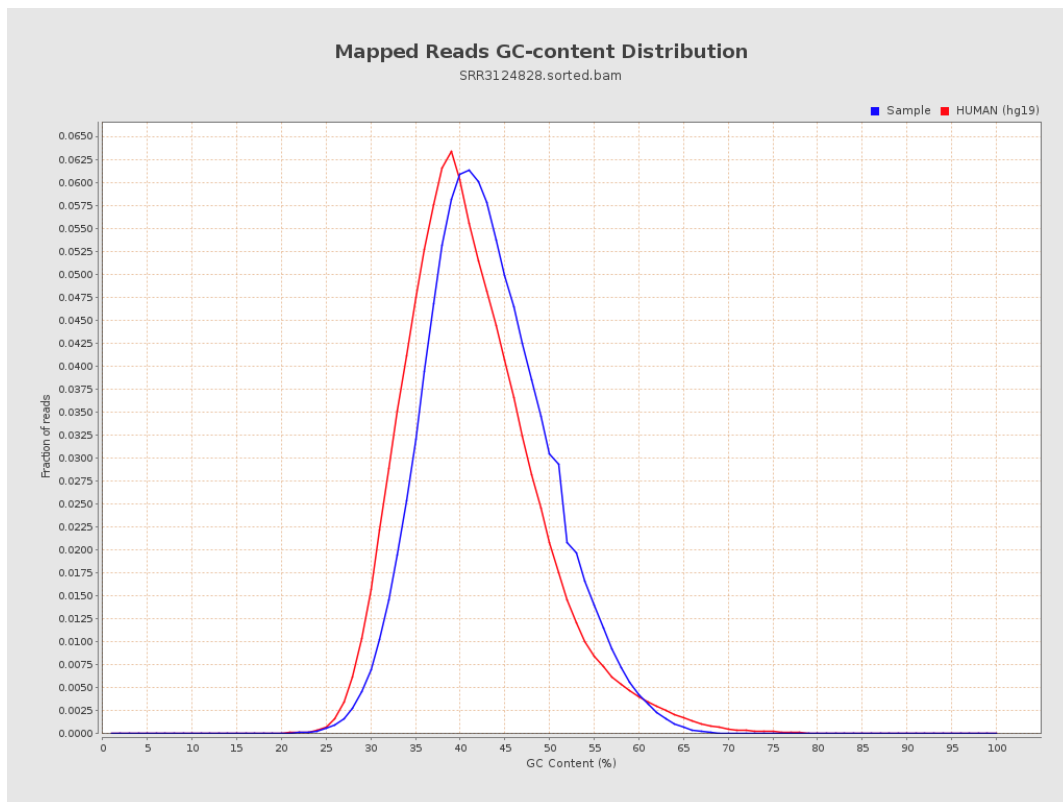
7. Results : Duplication Rate Histogram



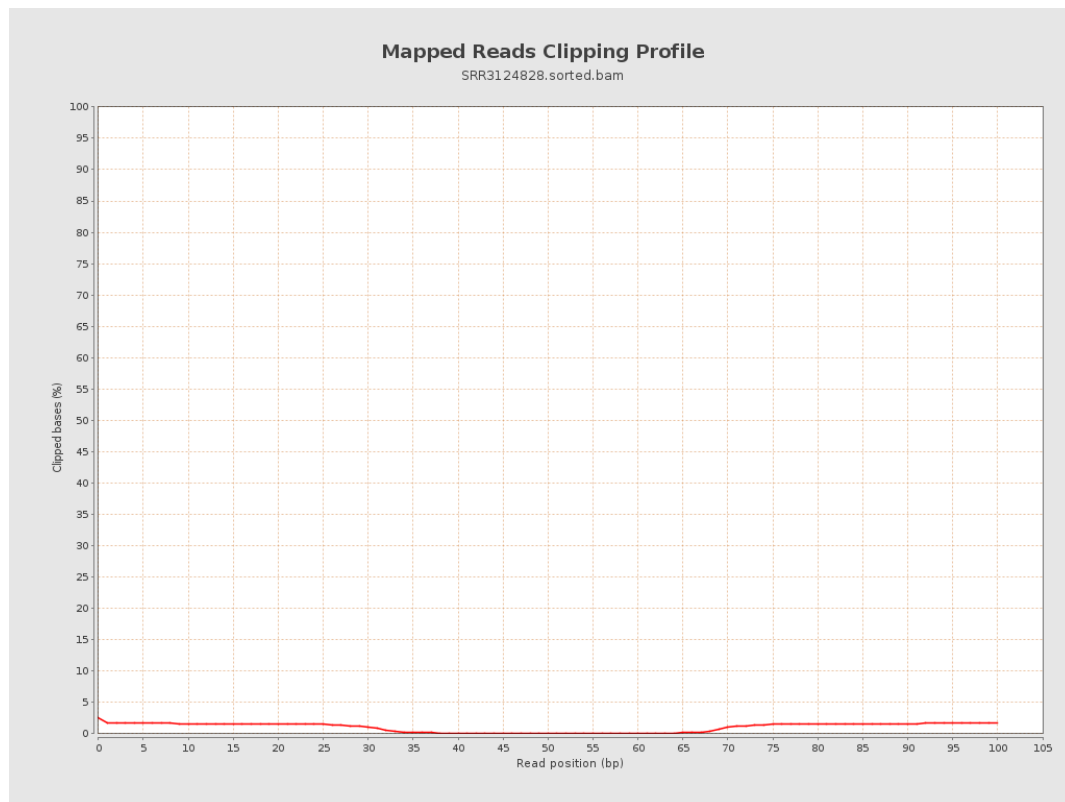
8. Results : Mapped Reads Nucleotide Content



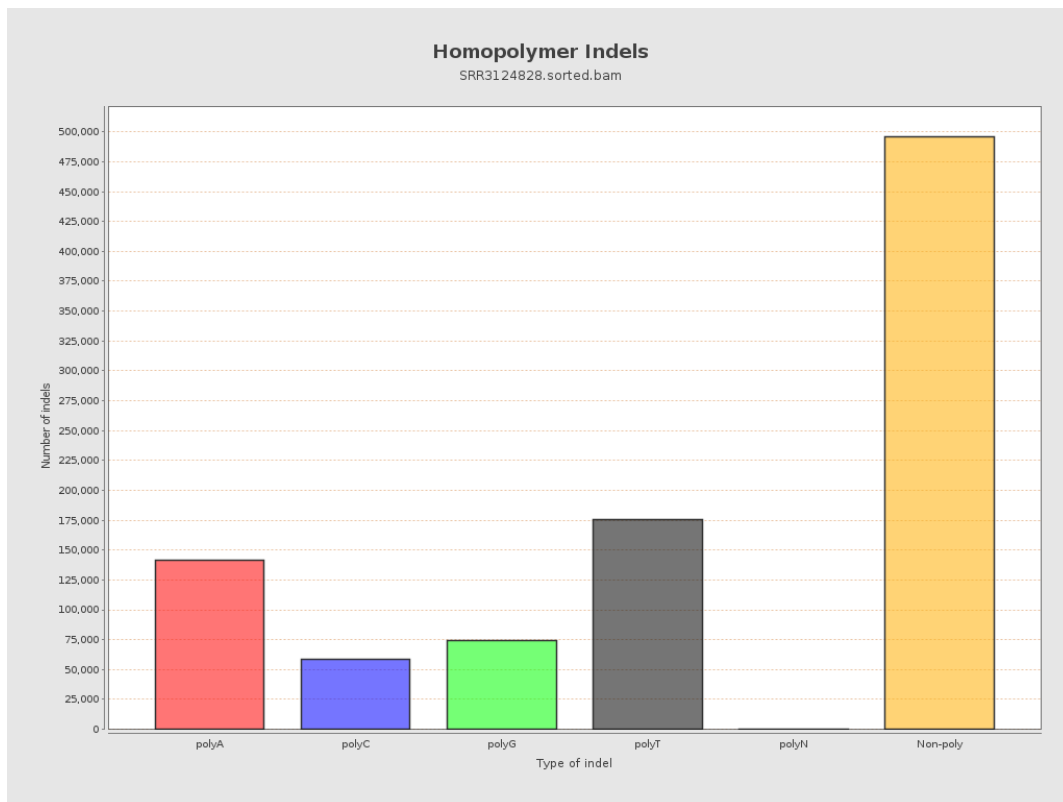
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



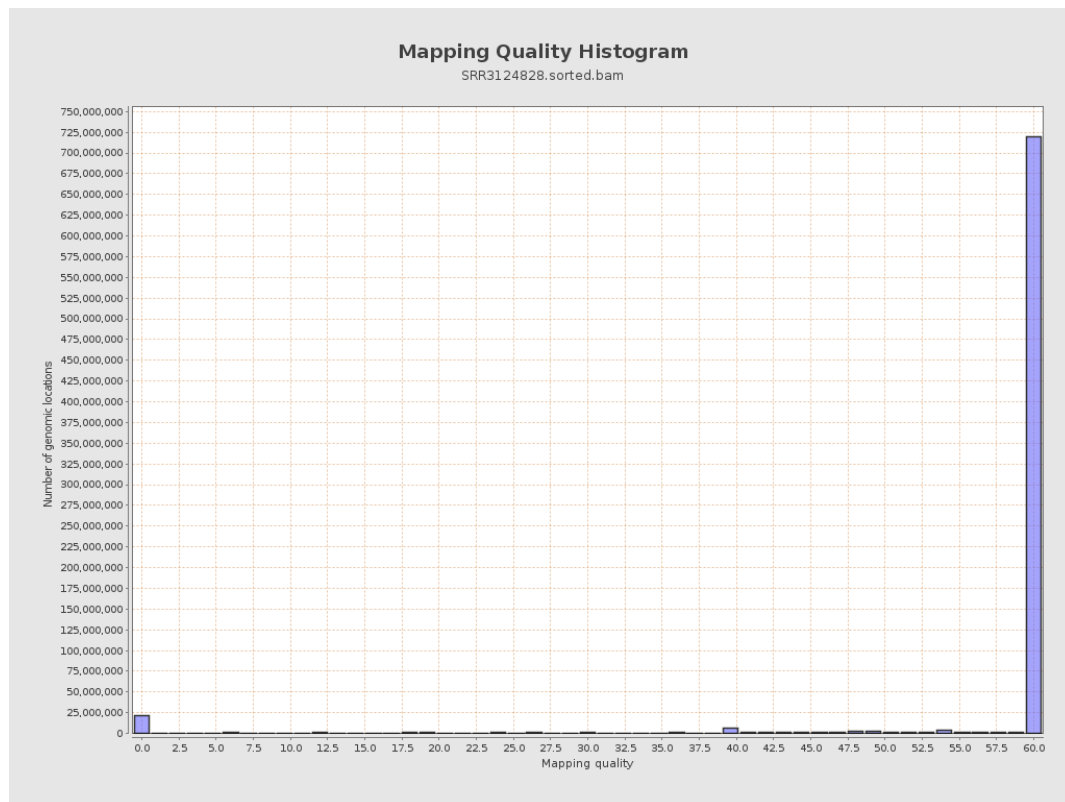
11. Results : Homopolymer Indels



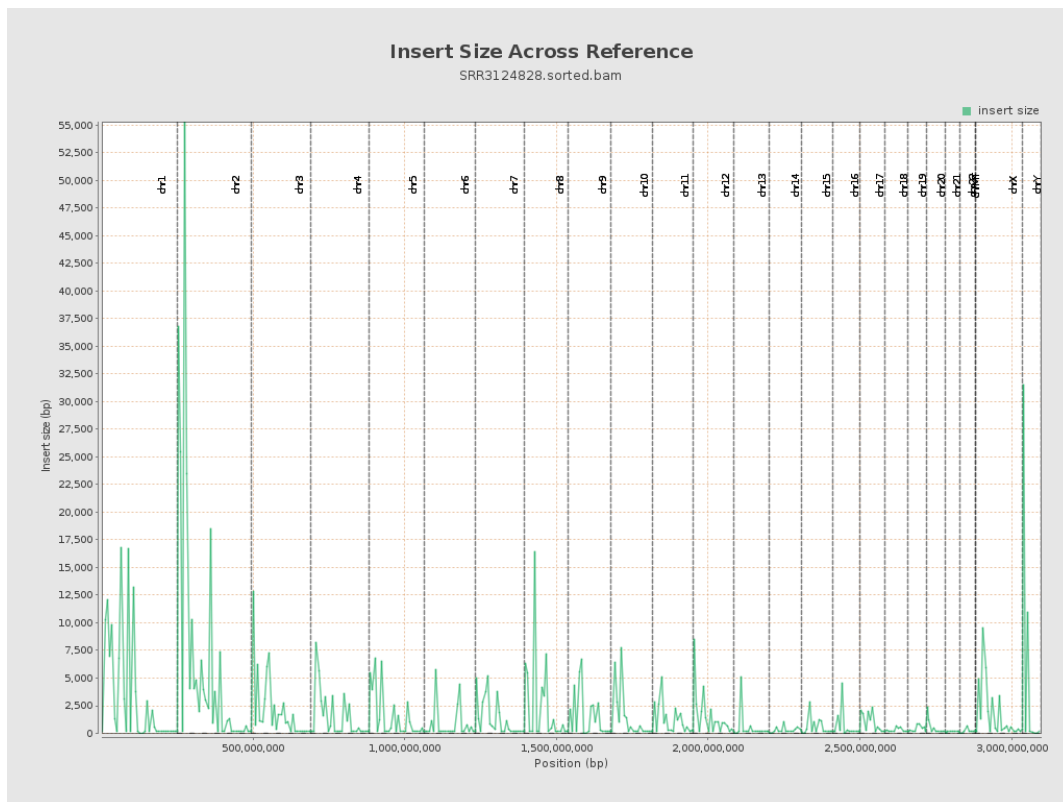
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

