

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/24 17:08:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328251.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_SRR16328251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328251_1.fastq.gz SRR16328251_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Feb 24 17:08:11 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,595,711,704
Mapped reads	1,556,279,492 / 97.53%
Unmapped reads	39,432,212 / 2.47%
Mapped paired reads	1,556,279,492 / 97.53%
Mapped reads, first in pair	779,659,371 / 48.86%
Mapped reads, second in pair	776,620,121 / 48.67%
Mapped reads, both in pair	1,545,923,410 / 96.88%
Mapped reads, singletons	10,356,082 / 0.65%
Secondary alignments	0
Supplementary alignments	69,853,797 / 4.38%
Read min/max/mean length	30 / 150 / 152.19
Duplicated reads (estimated)	706,227,464 / 44.26%
Duplication rate	39.82%
Clipped reads	1,009,633,590 / 63.27%

2.2. ACGT Content

Number/percentage of A's	62,090,361,235 / 28.72%
Number/percentage of C's	45,359,531,837 / 20.98%
Number/percentage of T's	61,384,724,415 / 28.39%
Number/percentage of G's	47,364,681,840 / 21.91%
Number/percentage of N's	4,003,189 / 0%

GC Percentage	42.89%
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2.3. Coverage

Mean	69.901
Standard Deviation	1,771.9228

2.4. Mapping Quality

Mean Mapping Quality	53.84
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2.5. Insert size

Mean	169,293.51
Standard Deviation	4,022,676.81
P25/Median/P75	196 / 265 / 374

2.6. Mismatches and indels

General error rate	0.84%
Mismatches	1,712,492,555
Insertions	39,111,450
Mapped reads with at least one insertion	2.39%
Deletions	104,714,473
Mapped reads with at least one deletion	6.46%
Homopolymer indels	44.59%

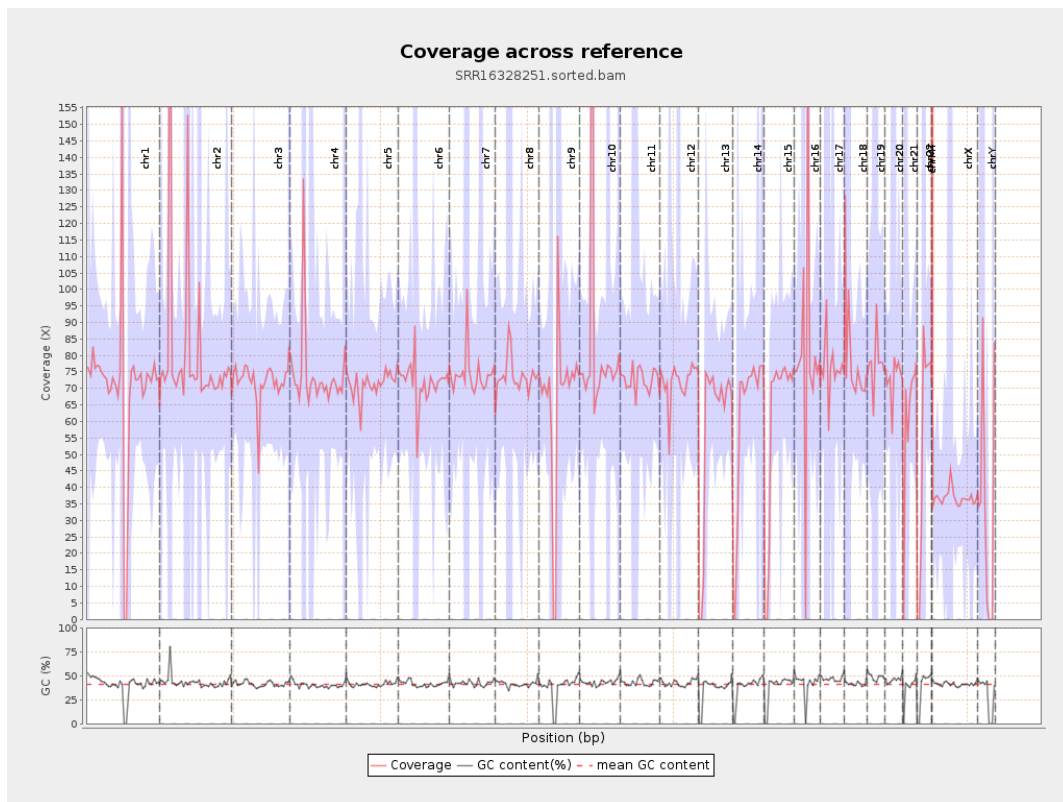
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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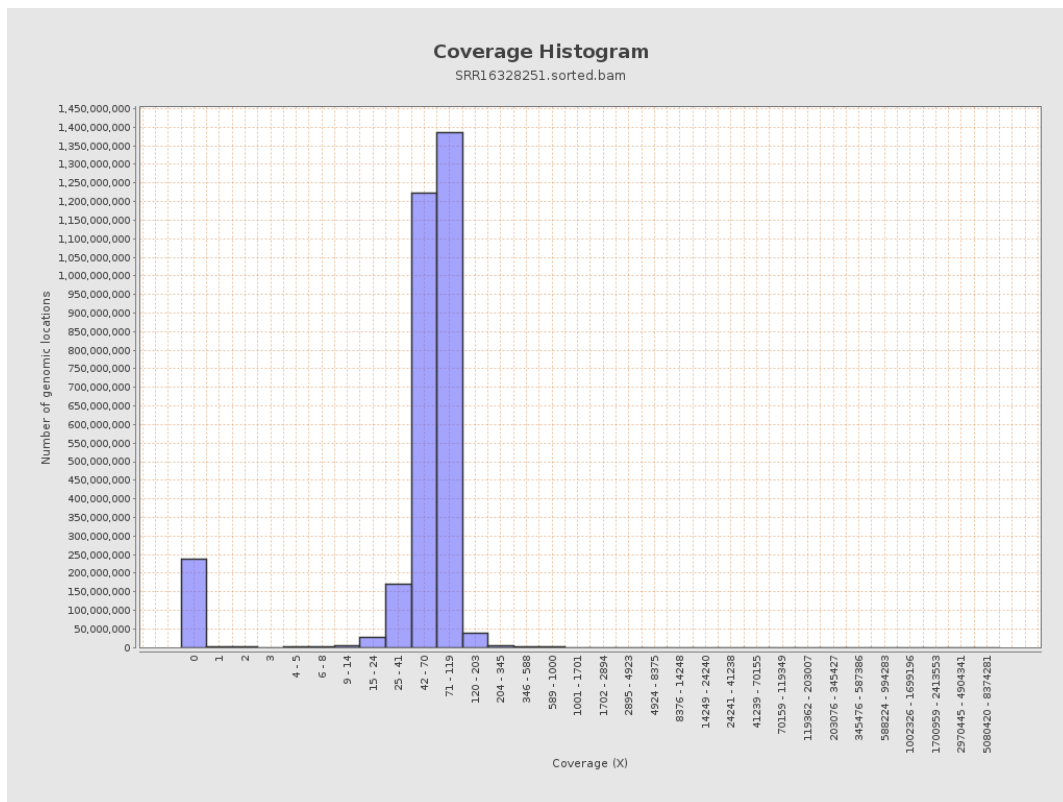
		bases	coverage	deviation
chr1	249250621	17801801562	71.4213	1,928.2363
chr2	243199373	19815653875	81.4791	5,652.3331
chr3	198022430	14229930659	71.8602	76.3185
chr4	191154276	14111943898	73.8249	570.2564
chr5	180915260	12913470258	71.3786	50.5894
chr6	171115067	12296006047	71.8581	228.6008
chr7	159138663	11834984723	74.369	579.4213
chr8	146364022	10835614920	74.032	989.354
chr9	141213431	9322106720	66.0143	1,022.8121
chr10	135534747	11402734162	84.1314	1,583.9393
chr11	135006516	9833148377	72.8346	263.0794
chr12	133851895	9621161914	71.8792	106.9569
chr13	115169878	6751547001	58.6225	39.2782
chr14	107349540	6541140809	60.9331	78.1268
chr15	102531392	6087265630	59.3698	43.2975
chr16	90354753	7292281308	80.7072	707.0376
chr17	81195210	6178402282	76.0932	293.063
chr18	78077248	6015261591	77.0424	956.5505
chr19	59128983	4600413690	77.803	1,043.2245
chr20	63025520	4602430182	73.0249	165.527
chr21	48129895	2996405132	62.2566	352.1602
chr22	51304566	2831932304	55.1984	299.7684
chrMT	16571	640326012	38,641.3621	5,292.9544
chrX	155270560	5715229816	36.8082	107.6574

chrY	59373566	2121044225	35.7237	665.5816
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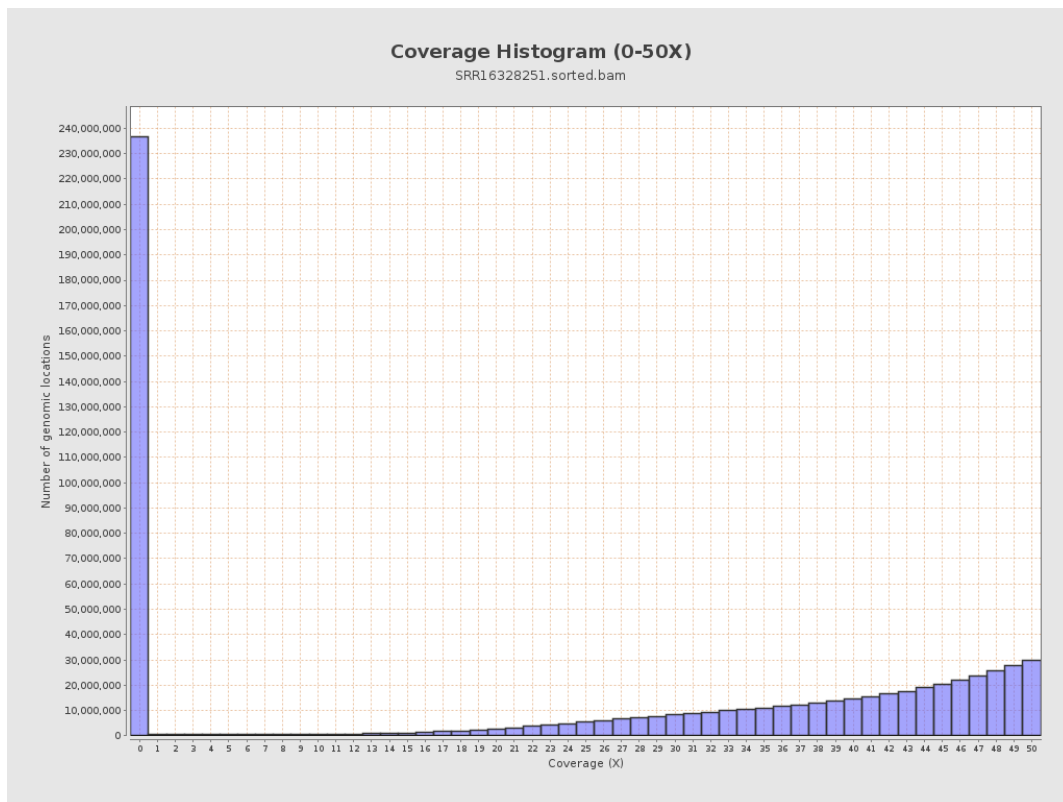
3. Results : Coverage across reference



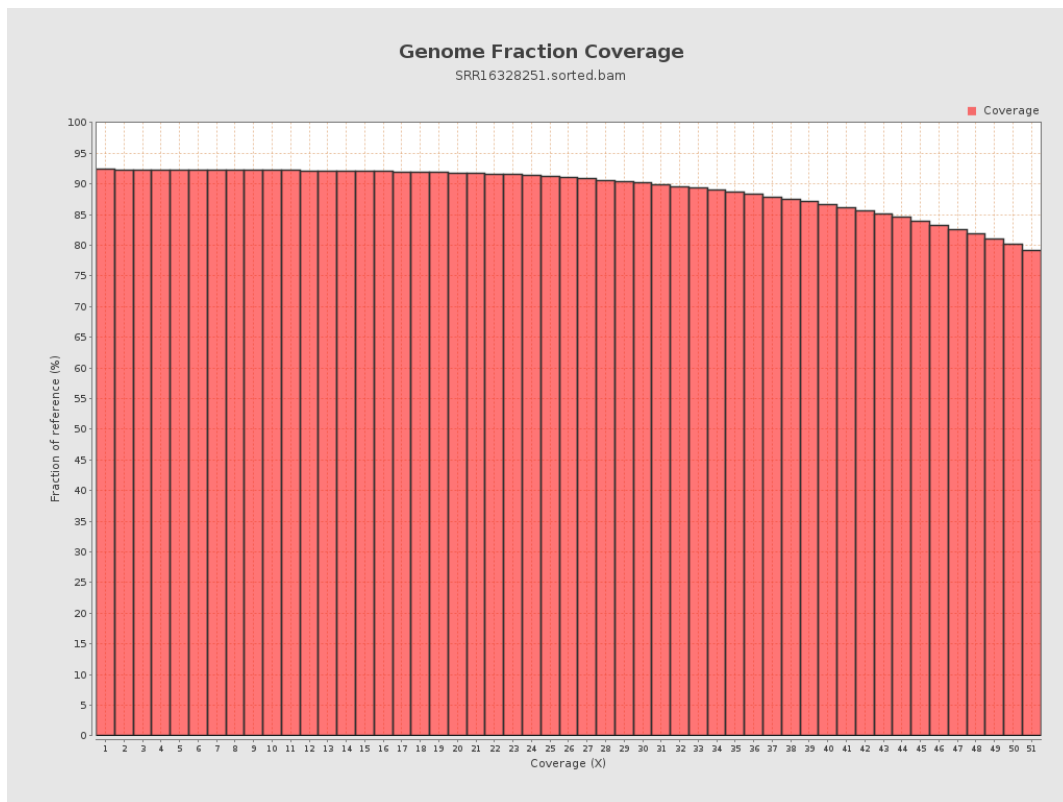
4. Results : Coverage Histogram



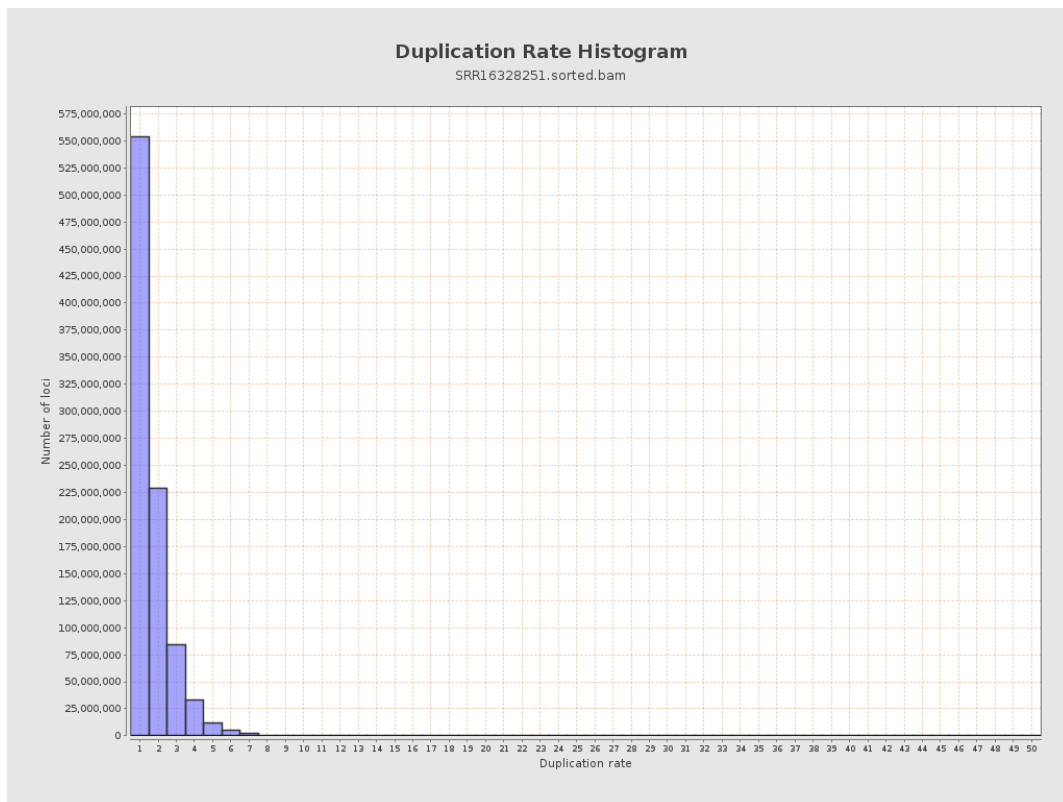
5. Results : Coverage Histogram (0-50X)



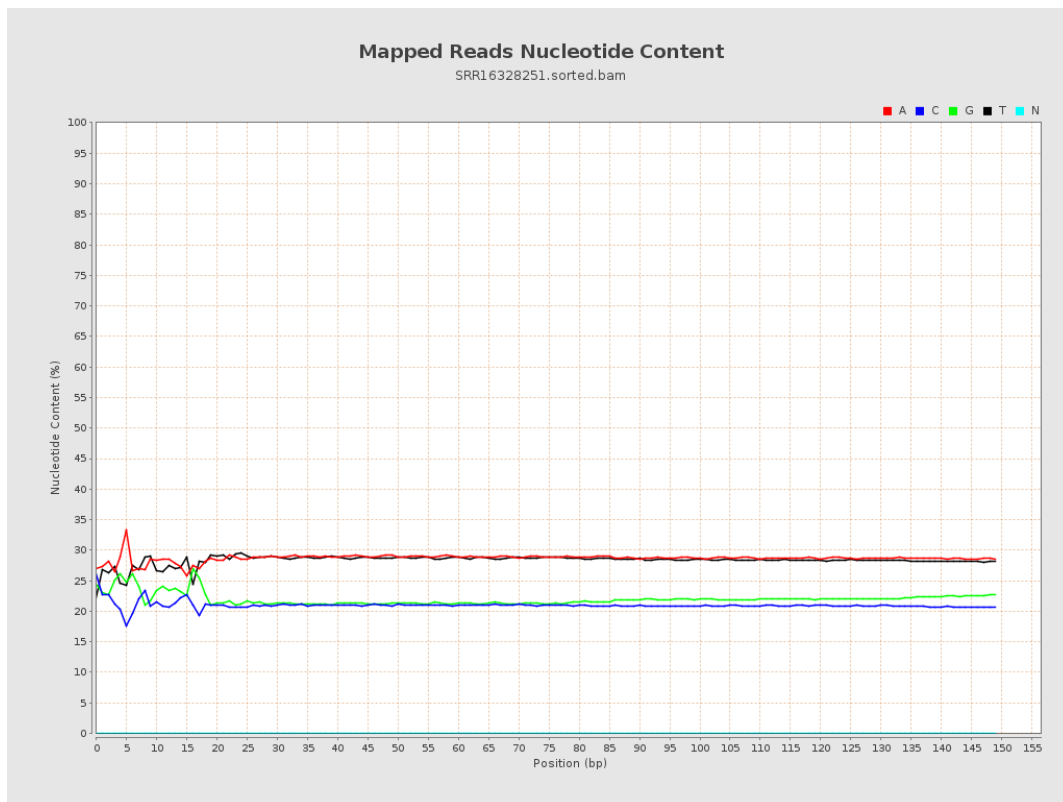
6. Results : Genome Fraction Coverage



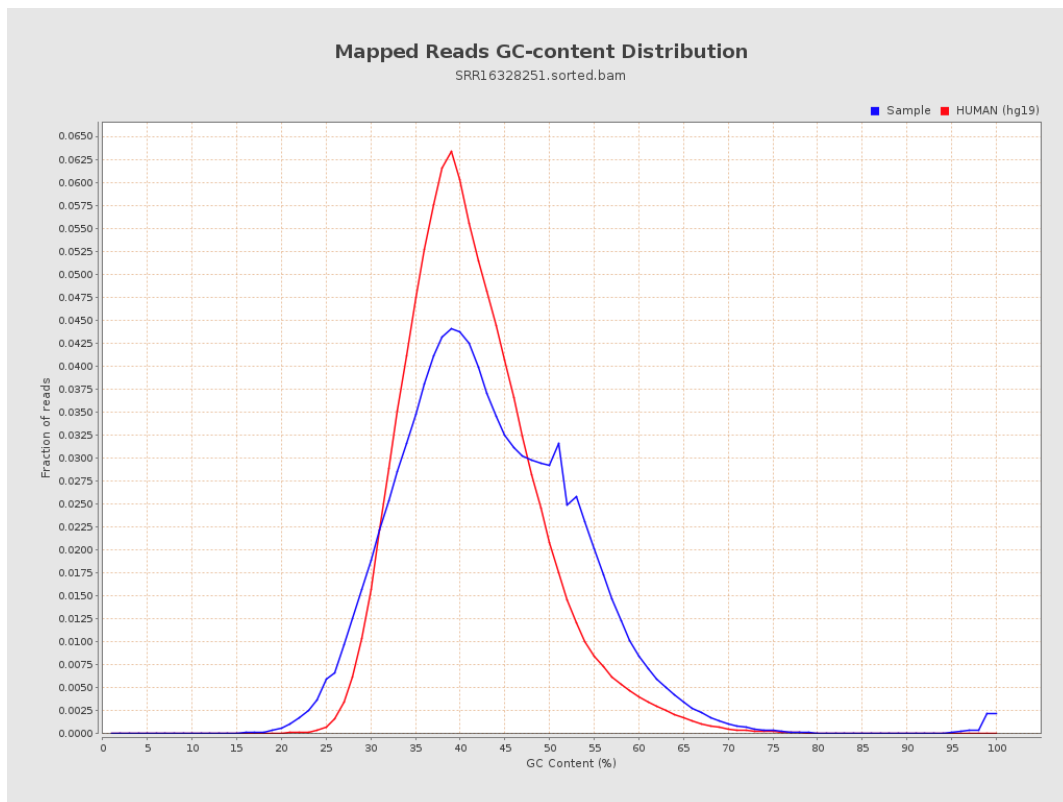
7. Results : Duplication Rate Histogram



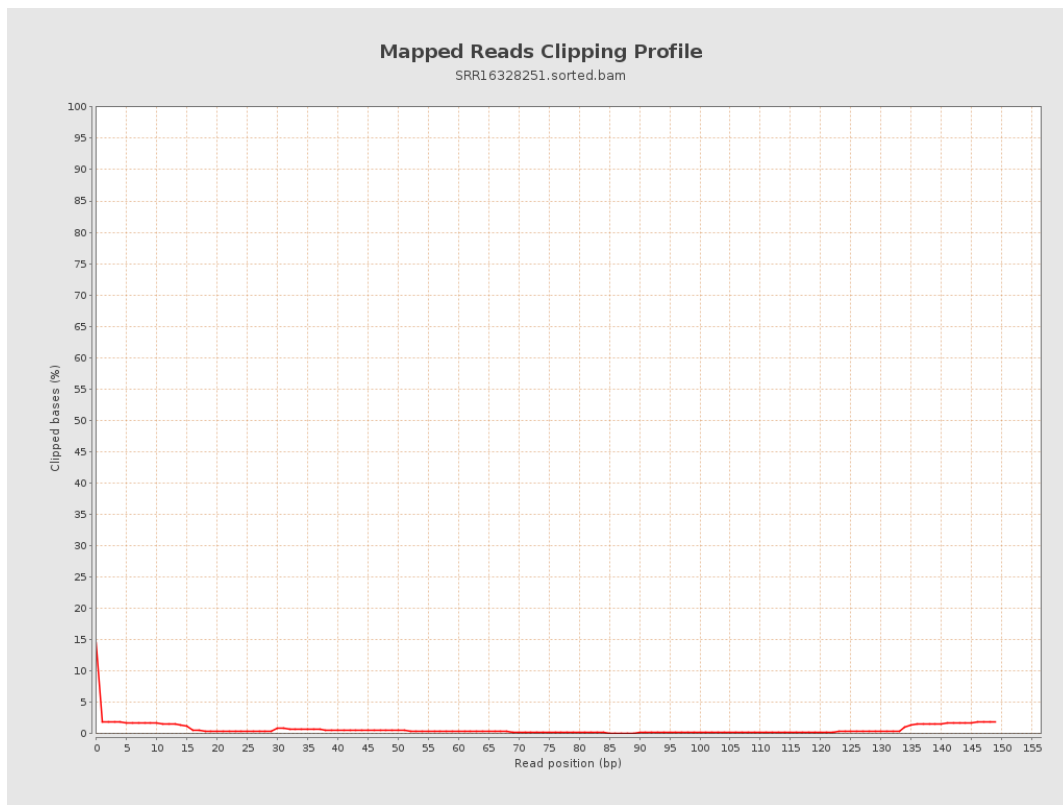
8. Results : Mapped Reads Nucleotide Content



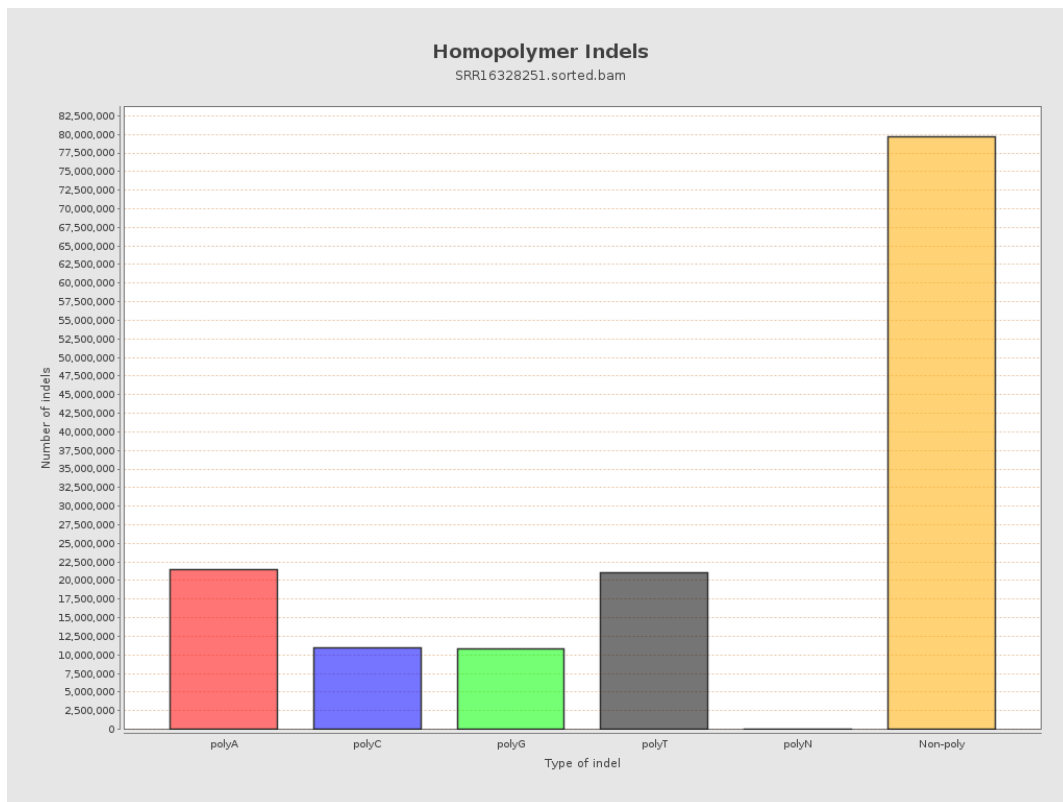
9. Results : Mapped Reads GC-content Distribution



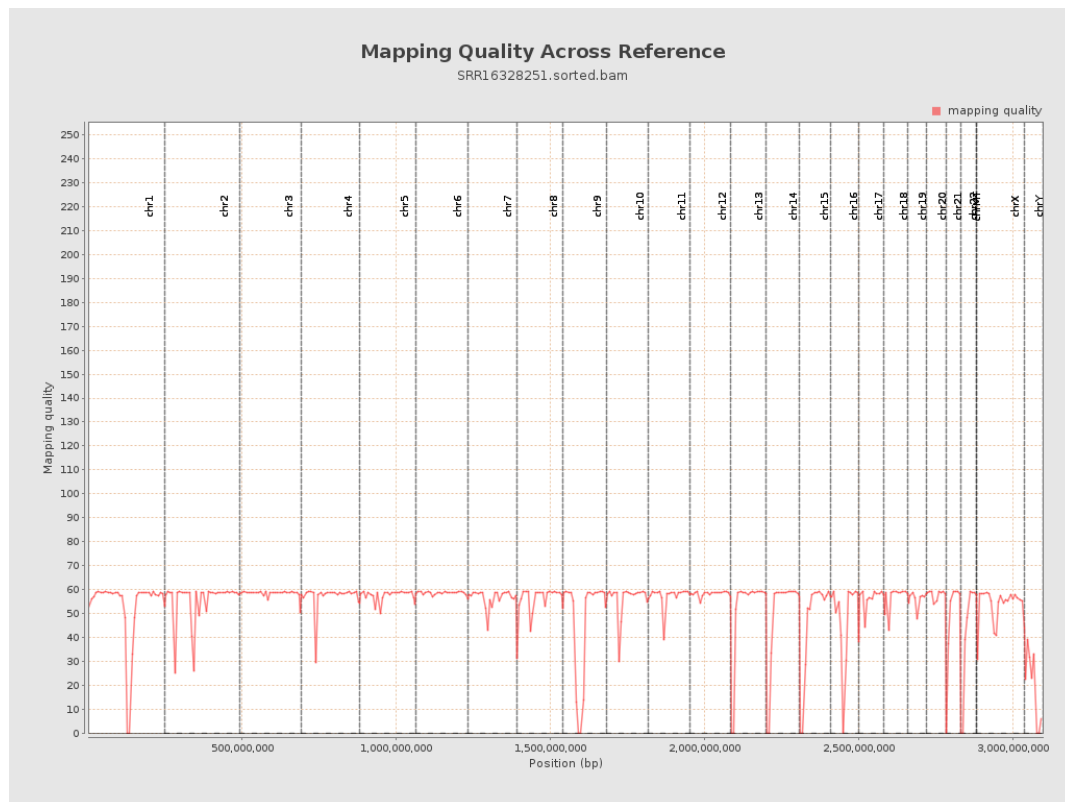
10. Results : Mapped Reads Clipping Profile



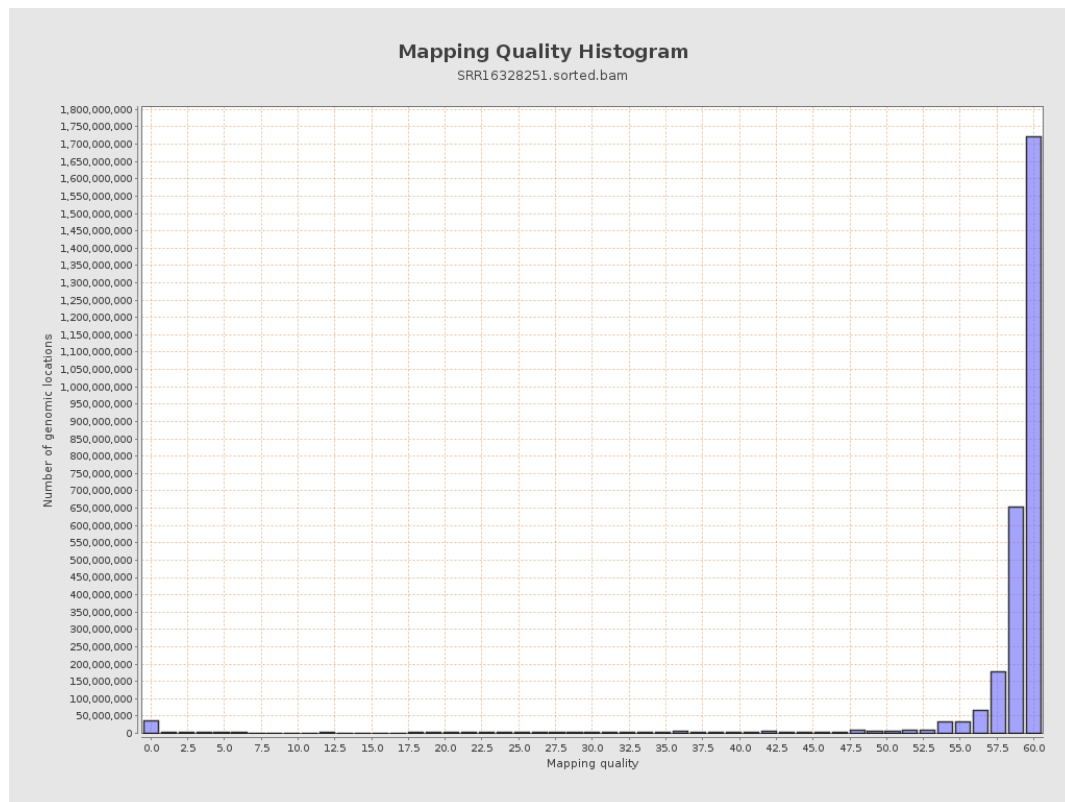
11. Results : Homopolymer Indels



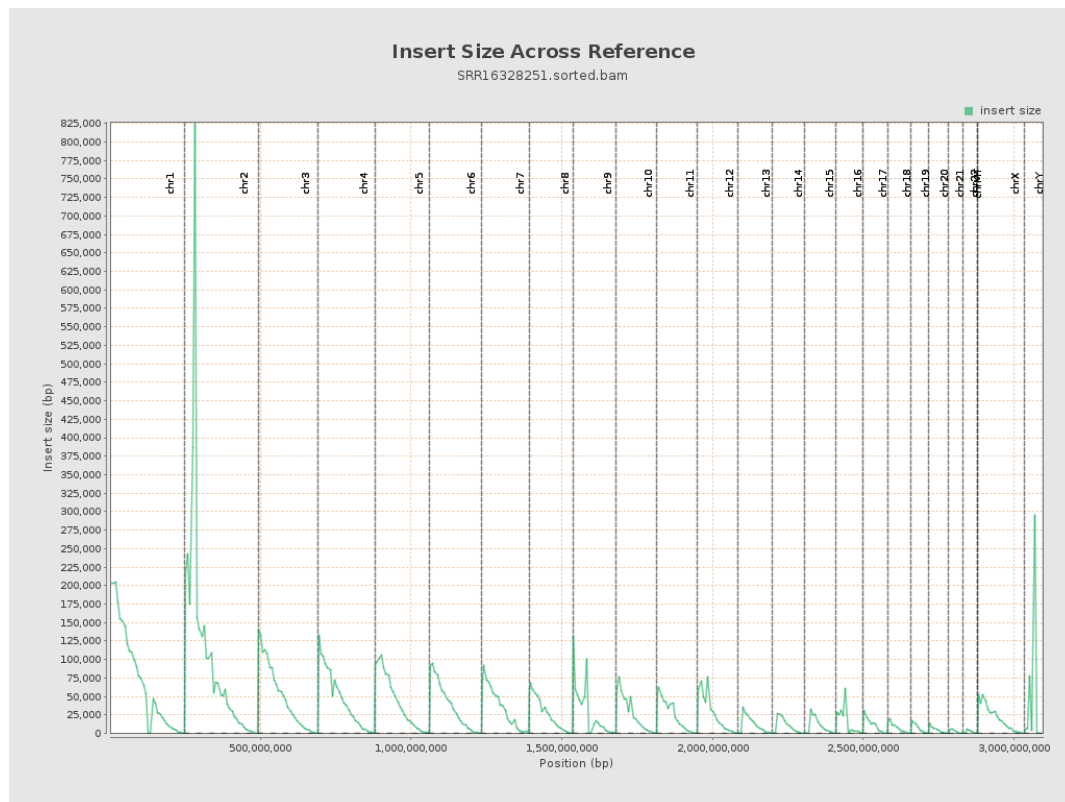
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

