

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/31 10:39:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16352027.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_SRR16352027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16352027_1.fastq.gz SRR16352027_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 31 10:39:42 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16352027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	593,065,306
Mapped reads	543,248,702 / 91.6%
Unmapped reads	49,816,604 / 8.4%
Mapped paired reads	543,248,702 / 91.6%
Mapped reads, first in pair	273,381,645 / 46.1%
Mapped reads, second in pair	269,867,057 / 45.5%
Mapped reads, both in pair	538,187,212 / 90.75%
Mapped reads, singletons	5,061,490 / 0.85%
Secondary alignments	0
Supplementary alignments	24,918,992 / 4.2%
Read min/max/mean length	30 / 150 / 152.1
Duplicated reads (estimated)	215,052,816 / 36.26%
Duplication rate	34.29%
Clipped reads	357,310,076 / 60.25%

2.2. ACGT Content

Number/percentage of A's	21,707,991,040 / 28.82%
Number/percentage of C's	15,905,223,099 / 21.12%
Number/percentage of T's	21,578,515,589 / 28.65%
Number/percentage of G's	16,120,256,541 / 21.4%
Number/percentage of N's	5,776,698 / 0.01%

GC Percentage	42.52%
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2.3. Coverage

Mean	24.3505
Standard Deviation	246.5427

2.4. Mapping Quality

Mean Mapping Quality	53.77
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2.5. Insert size

Mean	155,545.46
Standard Deviation	3,831,043.92
P25/Median/P75	183 / 238 / 318

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	652,317,871
Insertions	12,647,231
Mapped reads with at least one insertion	2.21%
Deletions	35,995,930
Mapped reads with at least one deletion	6.36%
Homopolymer indels	44.62%

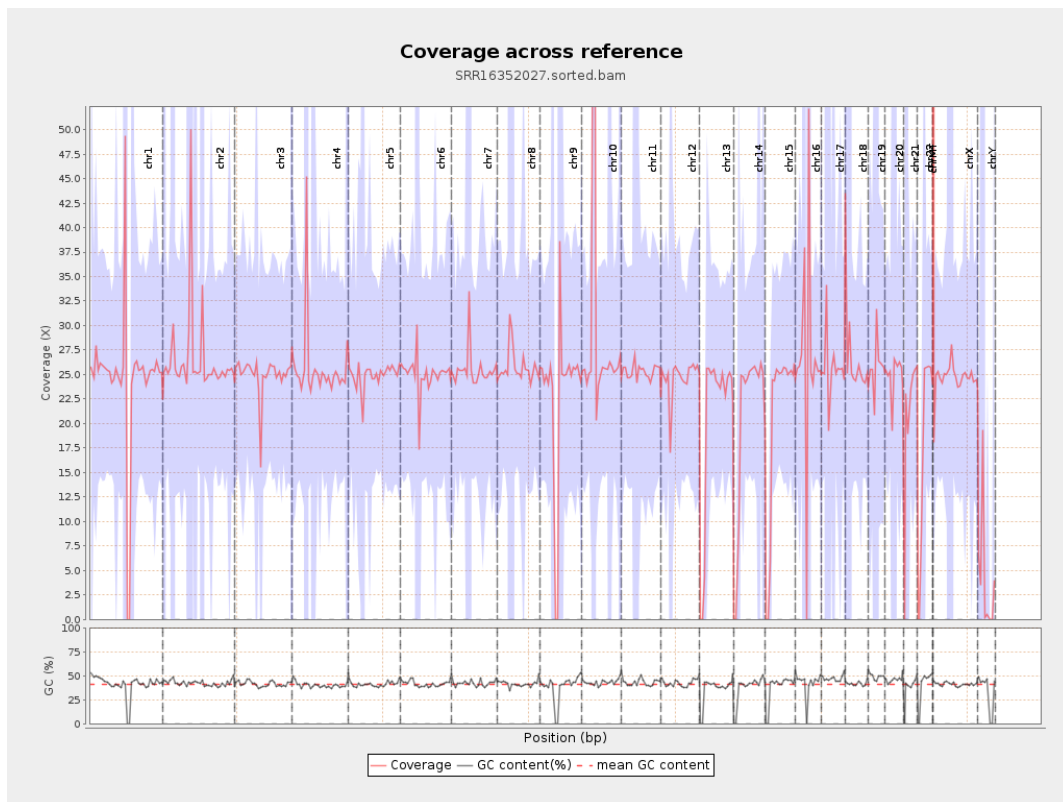
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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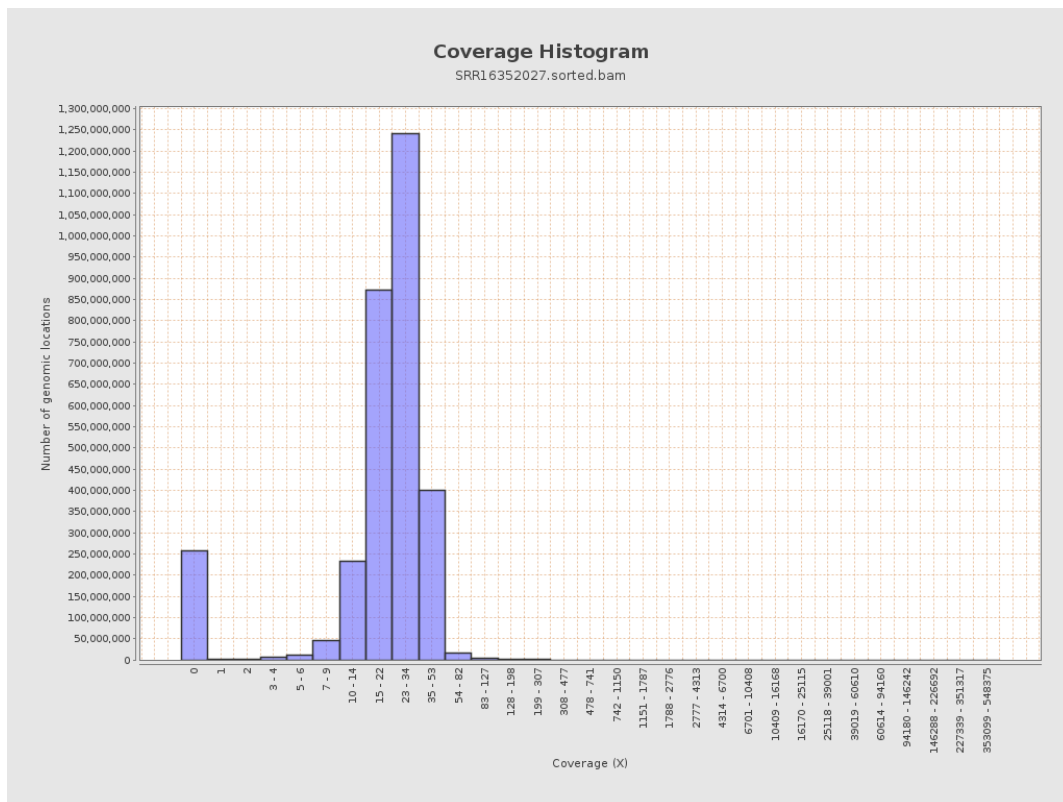
		bases	coverage	deviation
chr1	249250621	6111747156	24.5205	549.5515
chr2	243199373	6450324829	26.5228	217.5327
chr3	198022430	4936806009	24.9305	26.2774
chr4	191154276	4901968382	25.644	180.198
chr5	180915260	4509940097	24.9285	19.7257
chr6	171115067	4277040489	24.9951	68.1014
chr7	159138663	4059688335	25.5104	185.1413
chr8	146364022	3772264831	25.7732	347.6064
chr9	141213431	3254258552	23.045	276.1247
chr10	135534747	3889955615	28.7008	524.4621
chr11	135006516	3413539188	25.2843	105.5558
chr12	133851895	3309349859	24.724	16.266
chr13	115169878	2371854466	20.5944	14.3342
chr14	107349540	2238252246	20.8501	22.8242
chr15	102531392	2067775420	20.1672	14.304
chr16	90354753	2411628588	26.6907	197.5951
chr17	81195210	2090455803	25.746	122.1452
chr18	78077248	2048209644	26.2331	273.2913
chr19	59128983	1528717175	25.8539	310.0227
chr20	63025520	1567230402	24.8666	51.1919
chr21	48129895	1024776890	21.2919	80.9925
chr22	51304566	912881307	17.7934	21.7256
chrMT	16571	154330321	9,313.2775	1,314.1126
chrX	155270560	3832077895	24.68	56.4436

chrY	59373566	246759992	4.1561	209.2354
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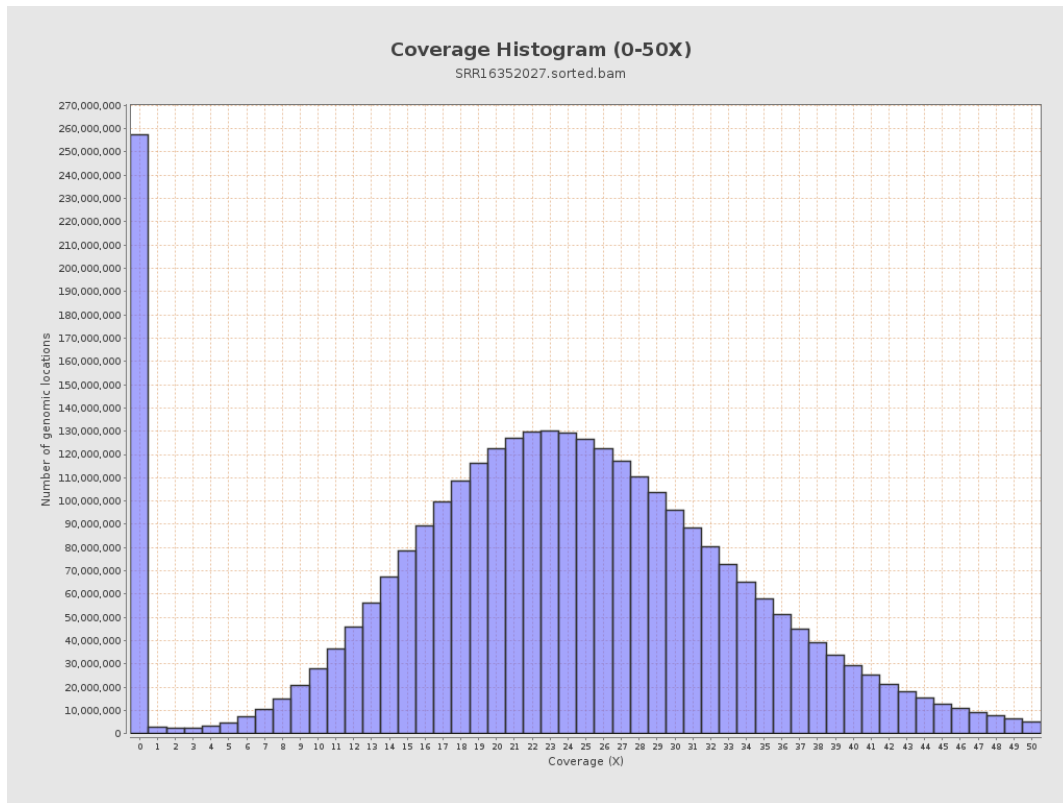
3. Results : Coverage across reference



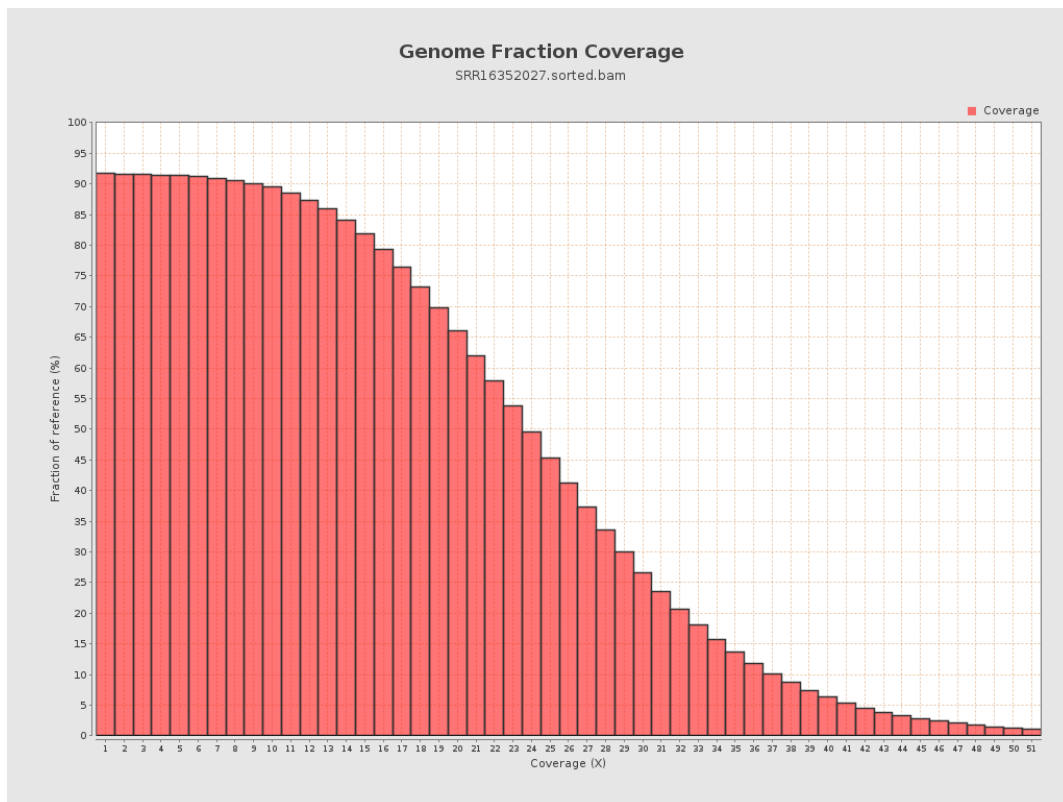
4. Results : Coverage Histogram



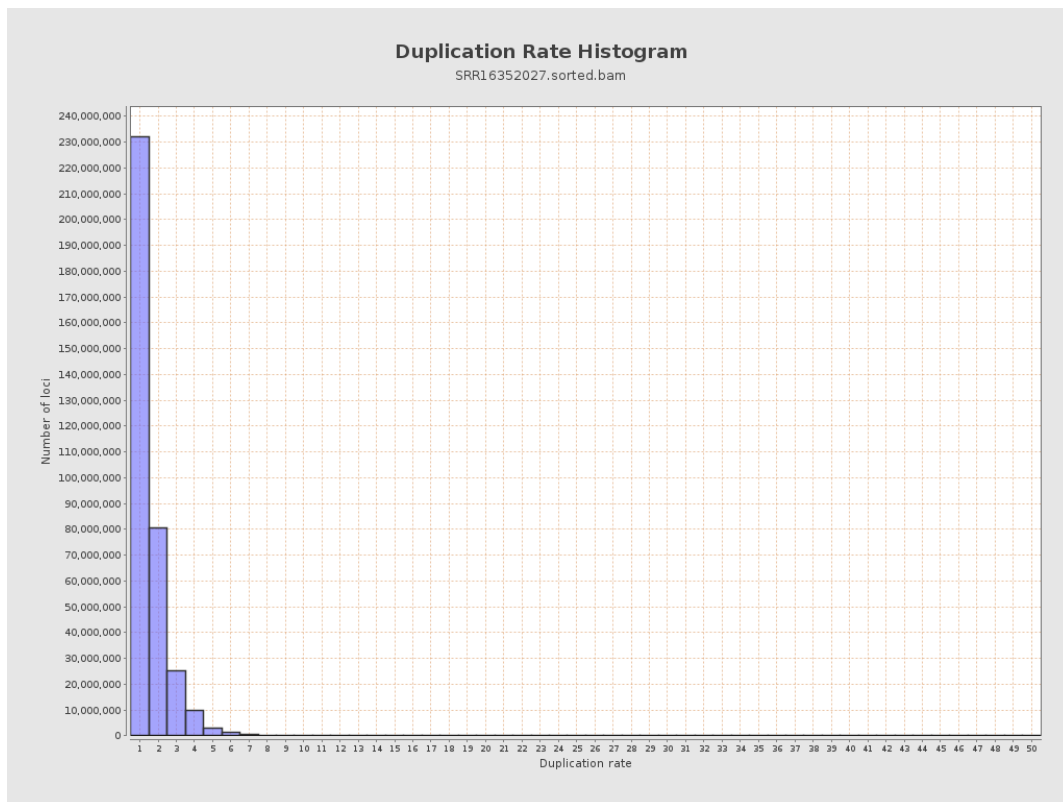
5. Results : Coverage Histogram (0-50X)



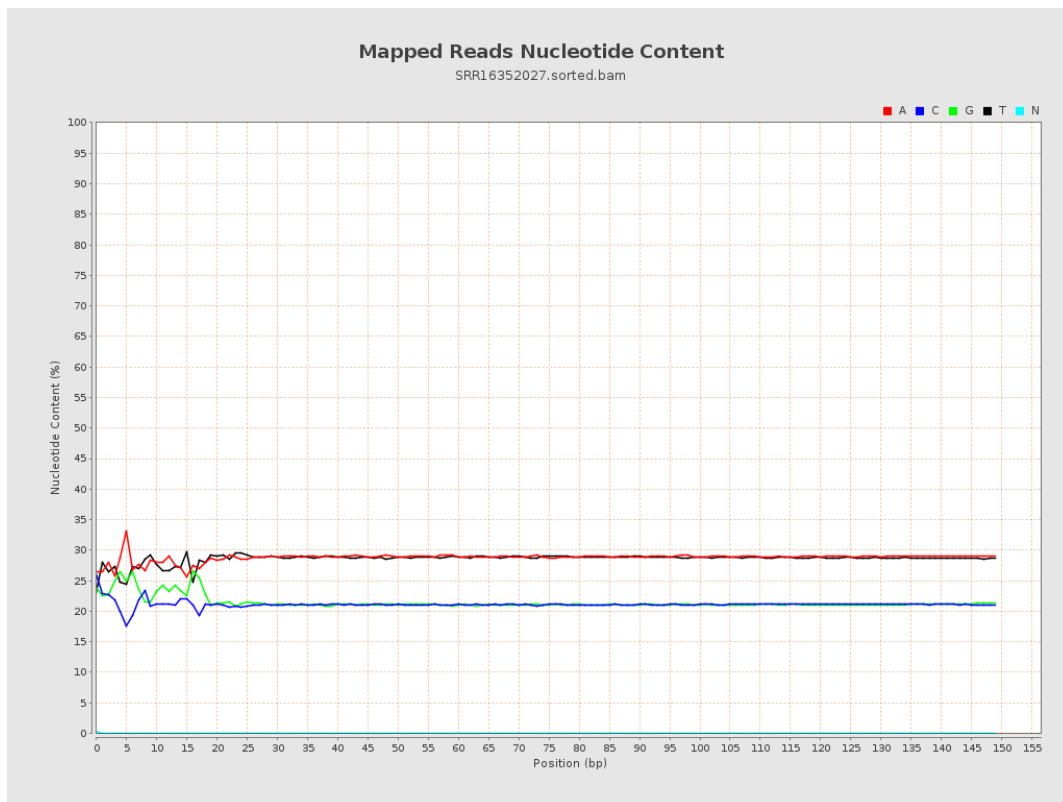
6. Results : Genome Fraction Coverage



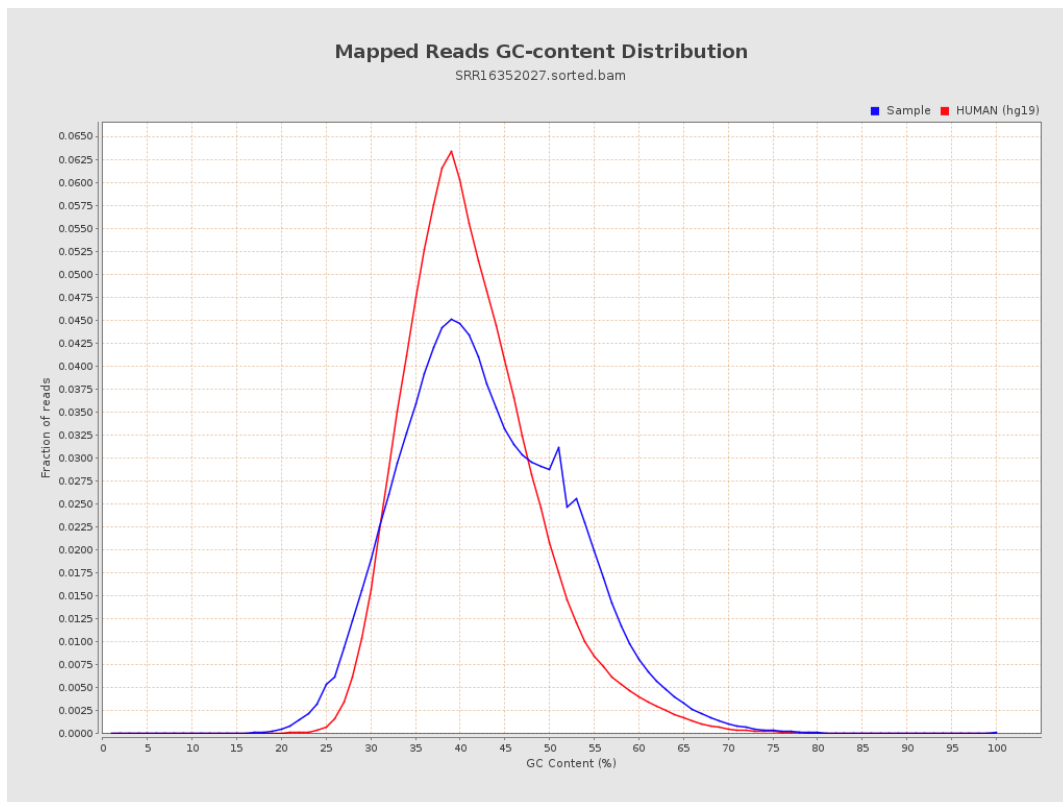
7. Results : Duplication Rate Histogram



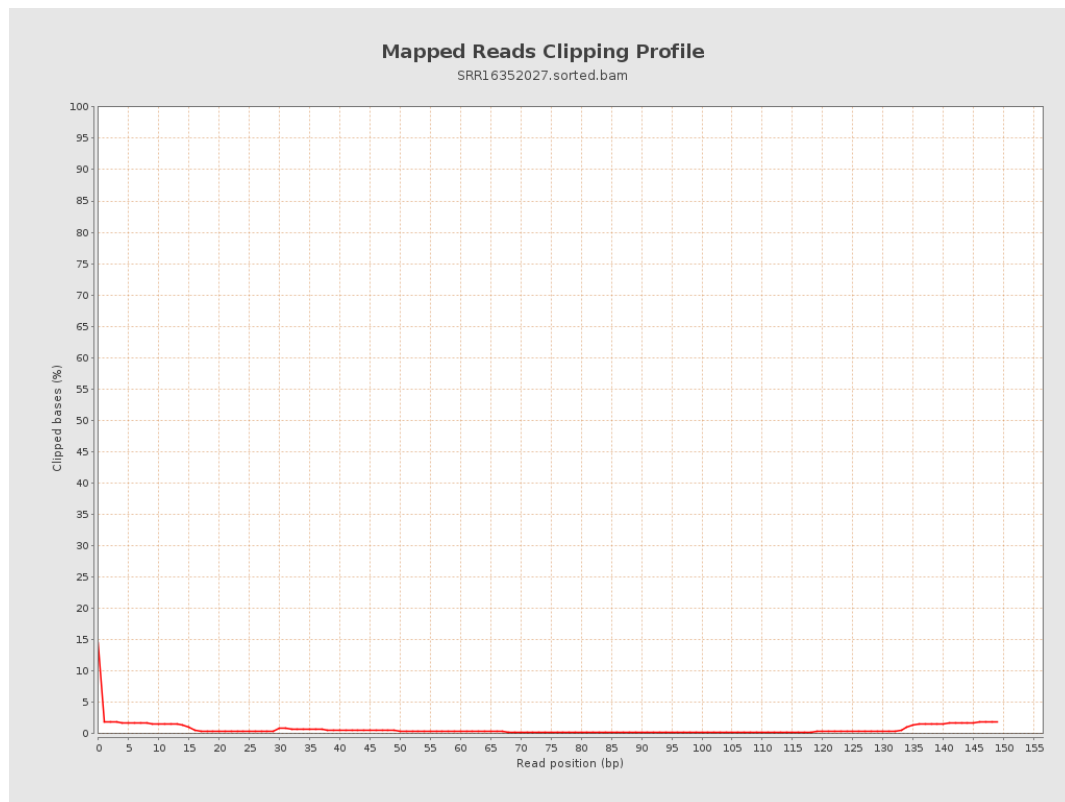
8. Results : Mapped Reads Nucleotide Content



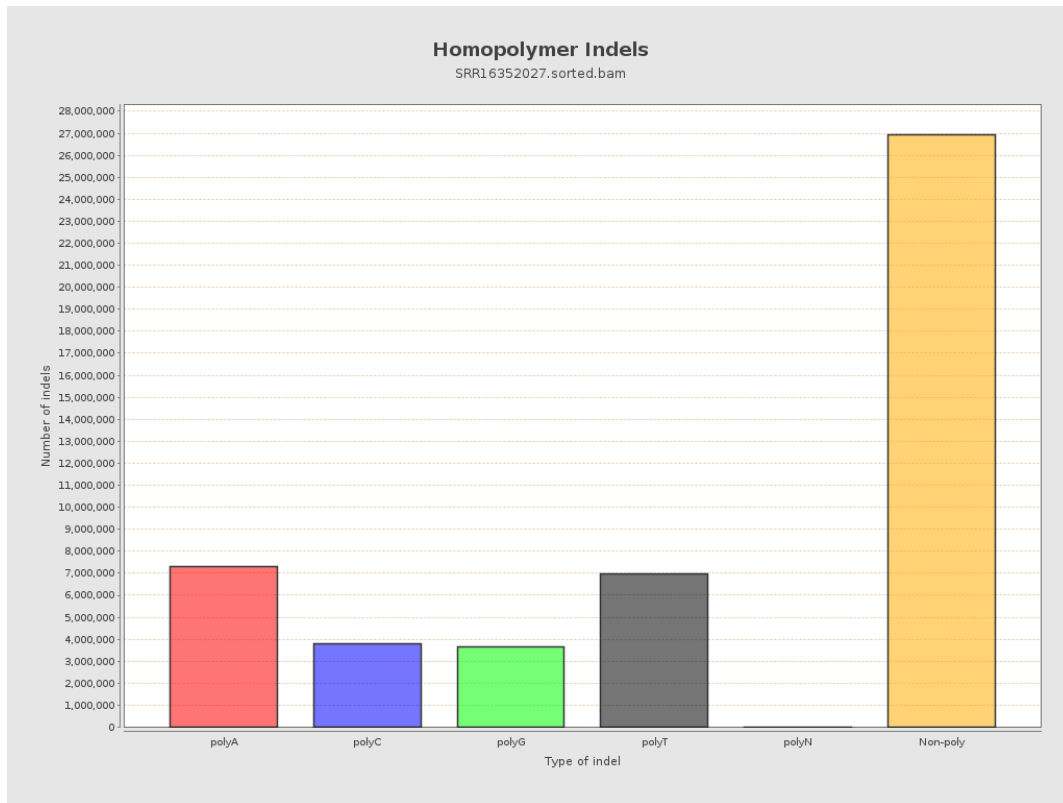
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



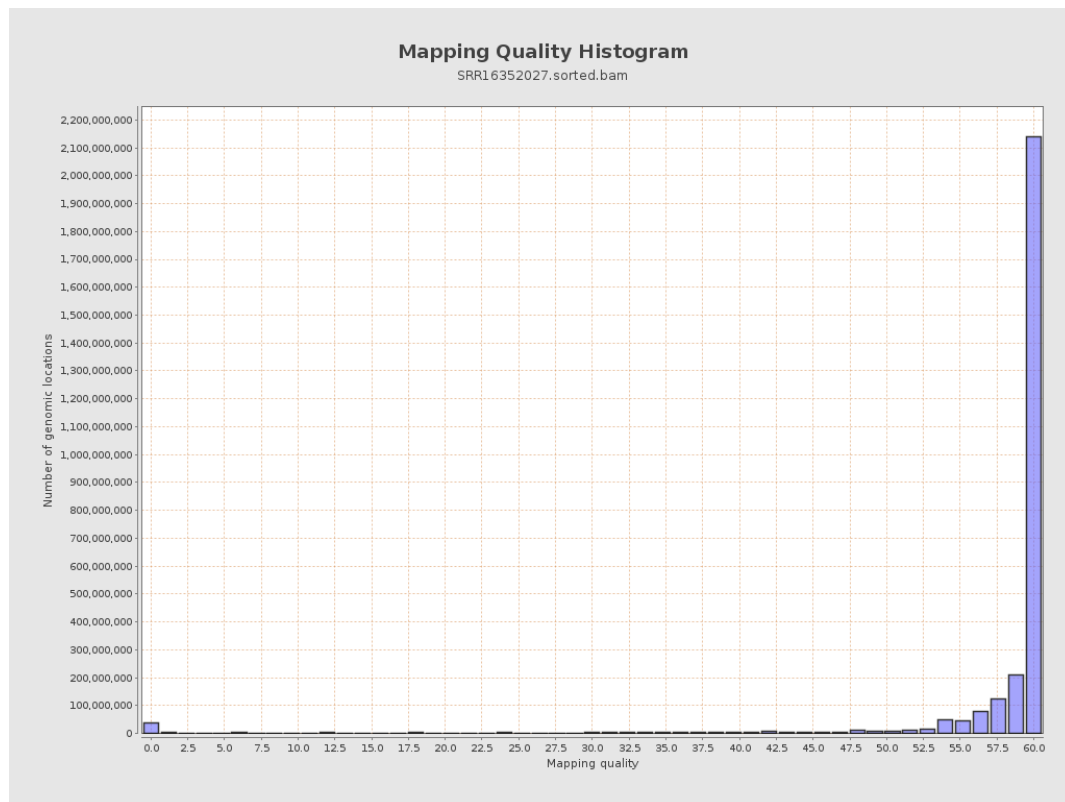
11. Results : Homopolymer Indels



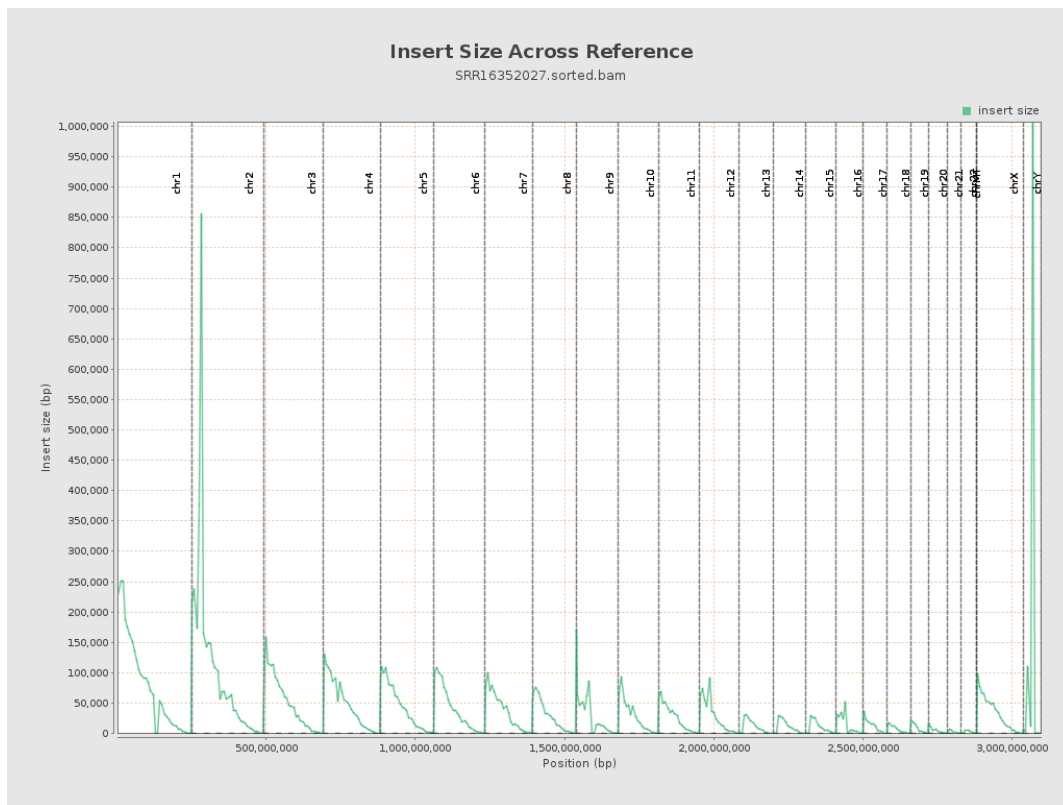
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

