

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 22:07:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104285.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_SRR26104285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104285_1.fastq.gz SRR26104285_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 22:07:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,412,594
Mapped reads	5,222,337 / 96.48%
Unmapped reads	190,257 / 3.52%
Mapped paired reads	5,222,337 / 96.48%
Mapped reads, first in pair	2,645,421 / 48.88%
Mapped reads, second in pair	2,576,916 / 47.61%
Mapped reads, both in pair	5,147,232 / 95.1%
Mapped reads, singletons	75,105 / 1.39%
Secondary alignments	0
Supplementary alignments	5,452 / 0.1%
Read min/max/mean length	30 / 97 / 91.04
Duplicated reads (estimated)	2,177,206 / 40.22%
Duplication rate	31.85%
Clipped reads	2,445,546 / 45.18%

2.2. ACGT Content

Number/percentage of A's	103,896,921 / 26.31%
Number/percentage of C's	93,939,324 / 23.79%
Number/percentage of T's	105,891,855 / 26.82%
Number/percentage of G's	90,939,140 / 23.03%
Number/percentage of N's	206,593 / 0.05%

GC Percentage	46.82%
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2.3. Coverage

Mean	0.1276
Standard Deviation	3.1662

2.4. Mapping Quality

Mean Mapping Quality	53.96
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2.5. Insert size

Mean	10,974.32
Standard Deviation	981,935.88
P25/Median/P75	58 / 101 / 196

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	2,247,662
Insertions	42,030
Mapped reads with at least one insertion	0.8%
Deletions	46,462
Mapped reads with at least one deletion	0.88%
Homopolymer indels	45.35%

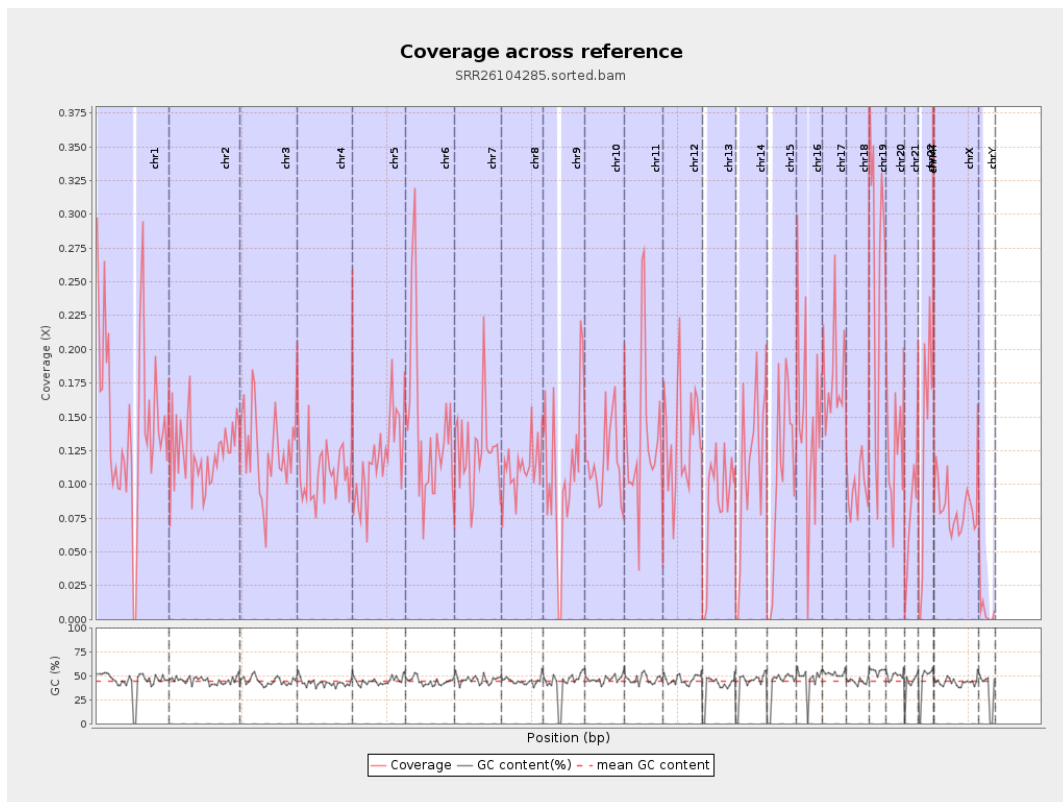
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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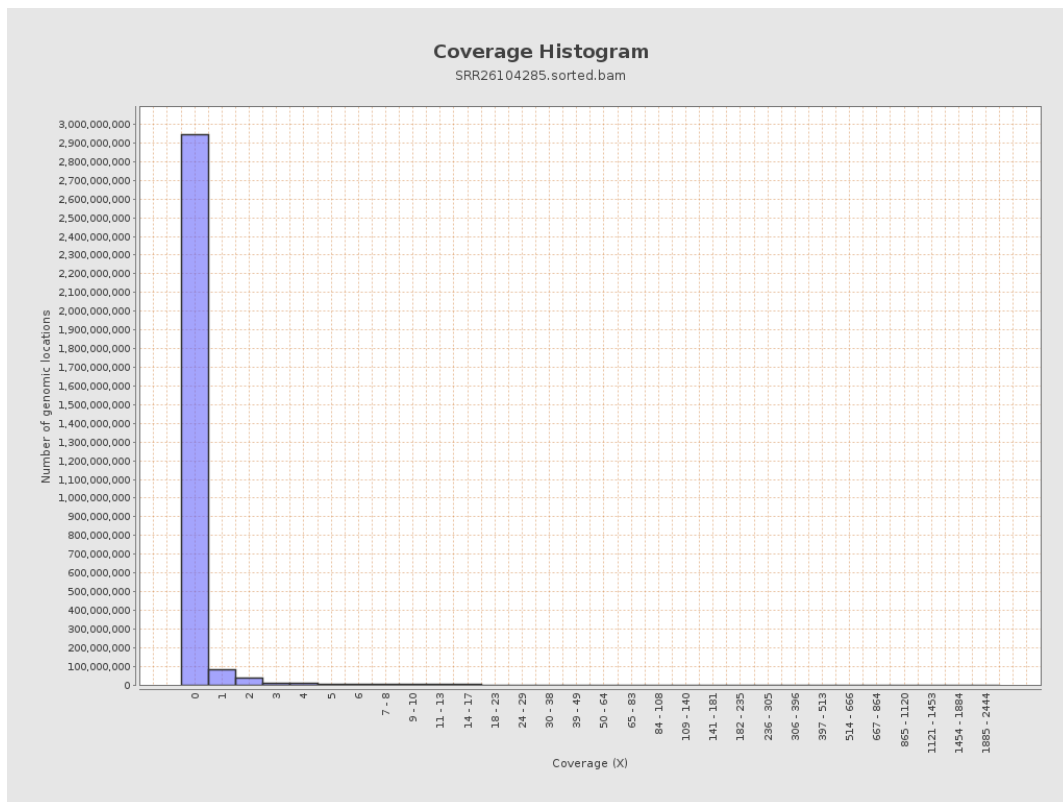
		bases	coverage	deviation
chr1	249250621	35784659	0.1436	1.8953
chr2	243199373	29924444	0.123	0.9546
chr3	198022430	24544392	0.1239	0.9553
chr4	191154276	20736343	0.1085	0.8104
chr5	180915260	21551968	0.1191	1.0105
chr6	171115067	23808724	0.1391	1.0457
chr7	159138663	19864841	0.1248	1.0064
chr8	146364022	16482237	0.1126	1.1091
chr9	141213431	15200510	0.1076	0.9412
chr10	135534747	15786292	0.1165	0.9989
chr11	135006516	18156350	0.1345	1.1442
chr12	133851895	18024815	0.1347	1.0979
chr13	115169878	9810111	0.0852	0.8707
chr14	107349540	11863104	0.1105	1.0339
chr15	102531392	10664960	0.104	0.9677
chr16	90354753	13071482	0.1447	1.2537
chr17	81195210	14852481	0.1829	1.4879
chr18	78077248	7602686	0.0974	0.8075
chr19	59128983	15211607	0.2573	1.9932
chr20	63025520	7750165	0.123	1.0476
chr21	48129895	3948137	0.082	0.9094
chr22	51304566	6507981	0.1268	1.1986
chrMT	16571	20522861	1,238.4805	322.5296
chrX	155270560	12858733	0.0828	0.6775

chrY	59373566	442367	0.0075	0.3055
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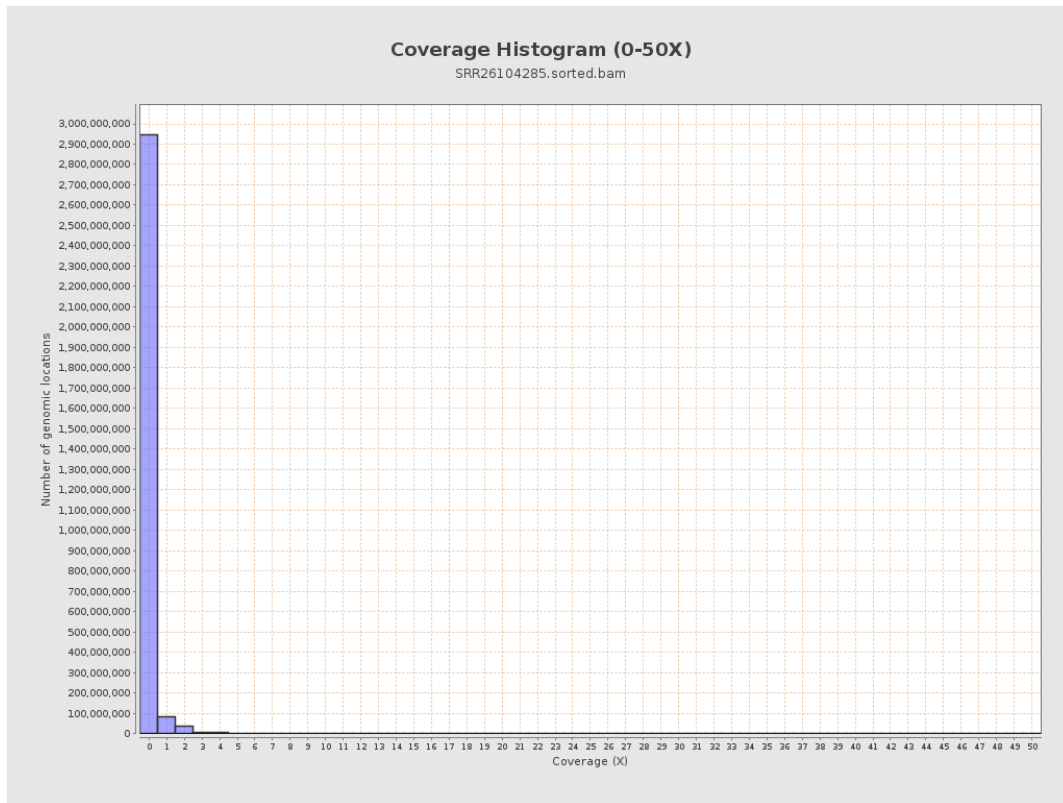
3. Results : Coverage across reference



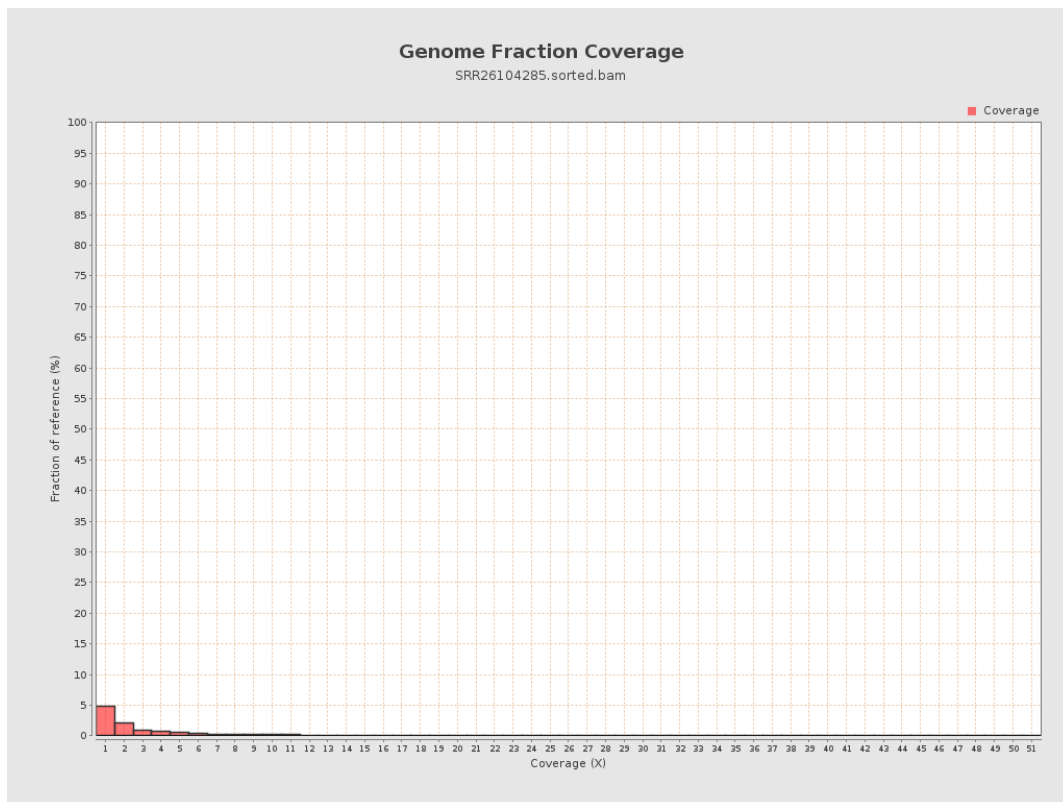
4. Results : Coverage Histogram



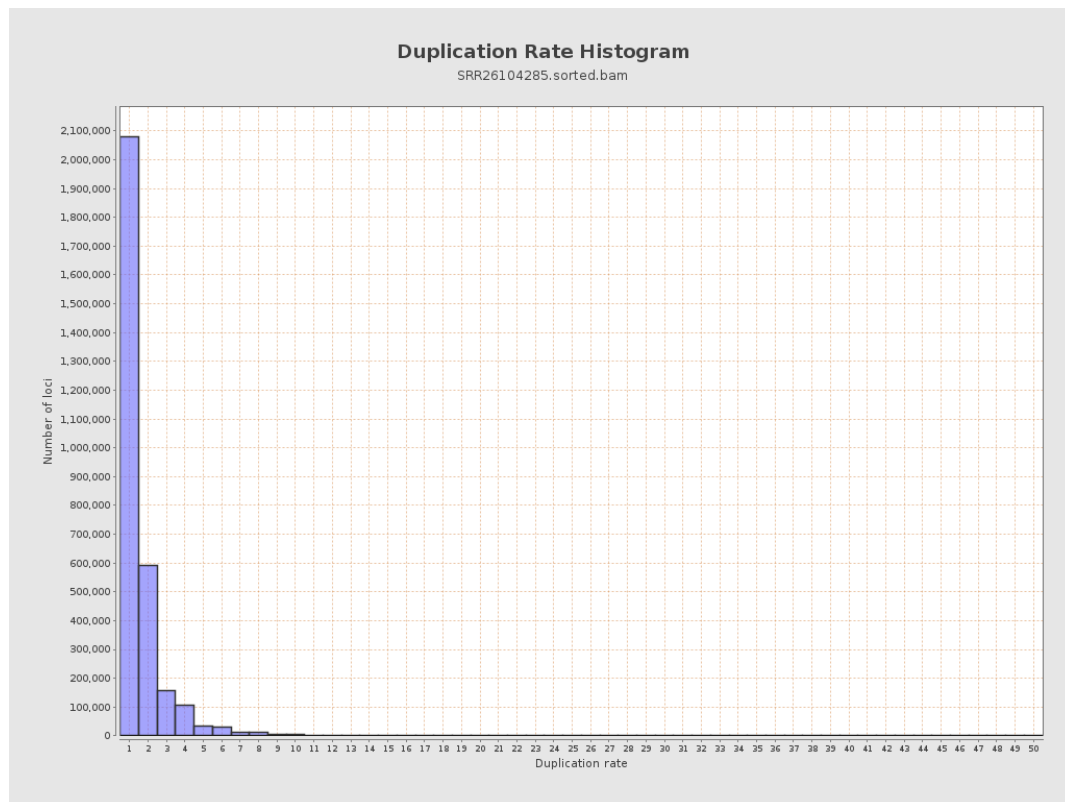
5. Results : Coverage Histogram (0-50X)



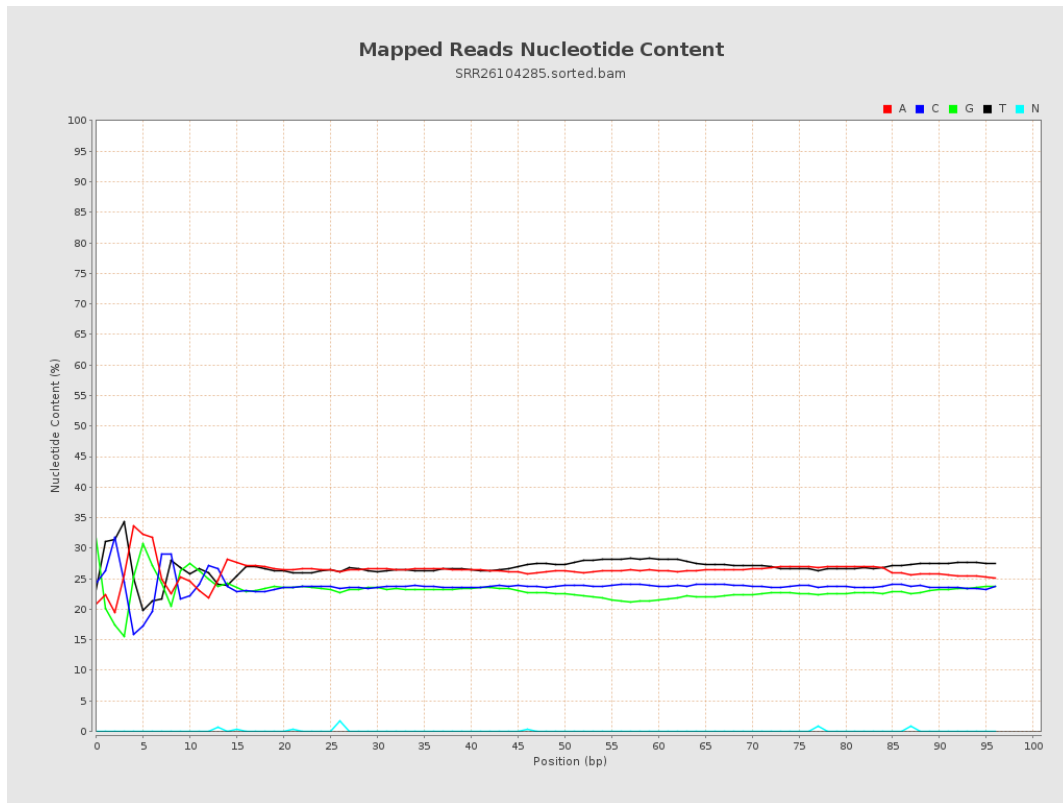
6. Results : Genome Fraction Coverage



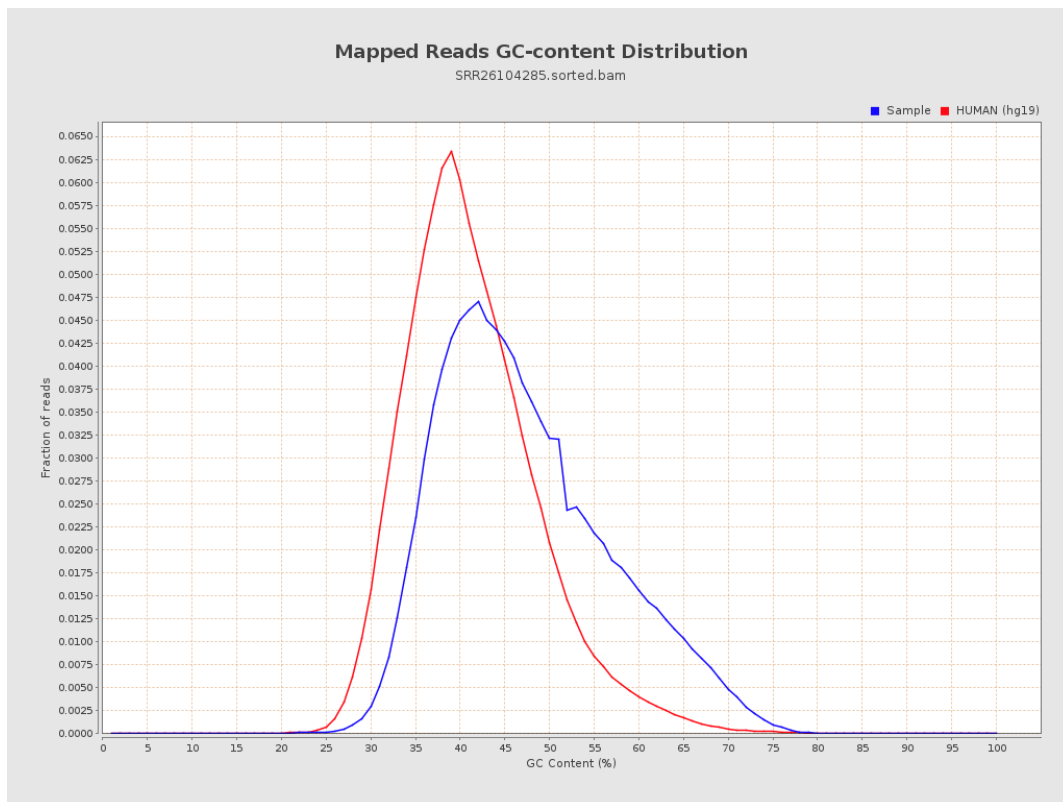
7. Results : Duplication Rate Histogram



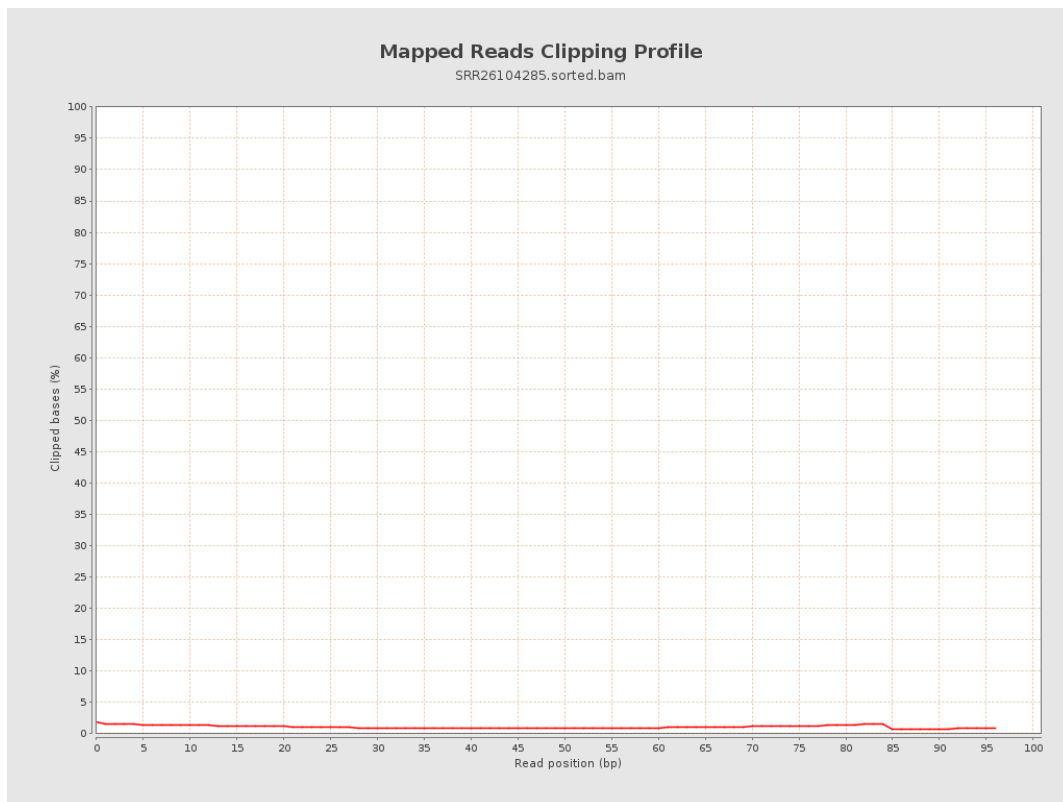
8. Results : Mapped Reads Nucleotide Content



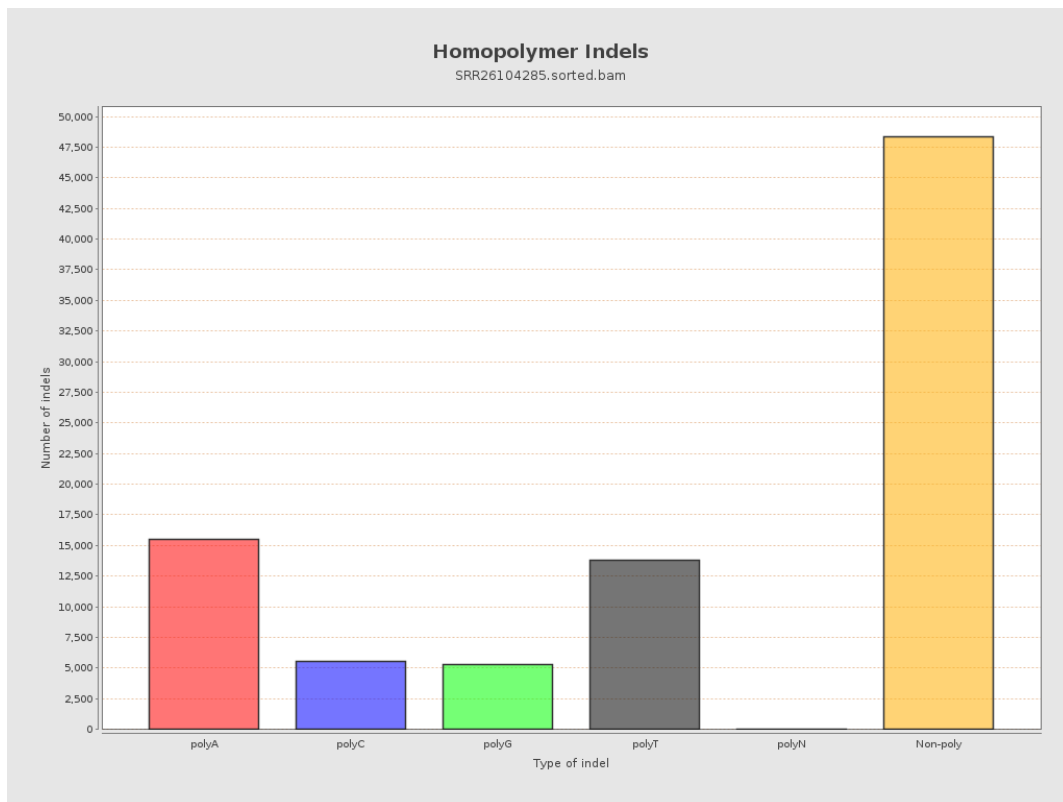
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



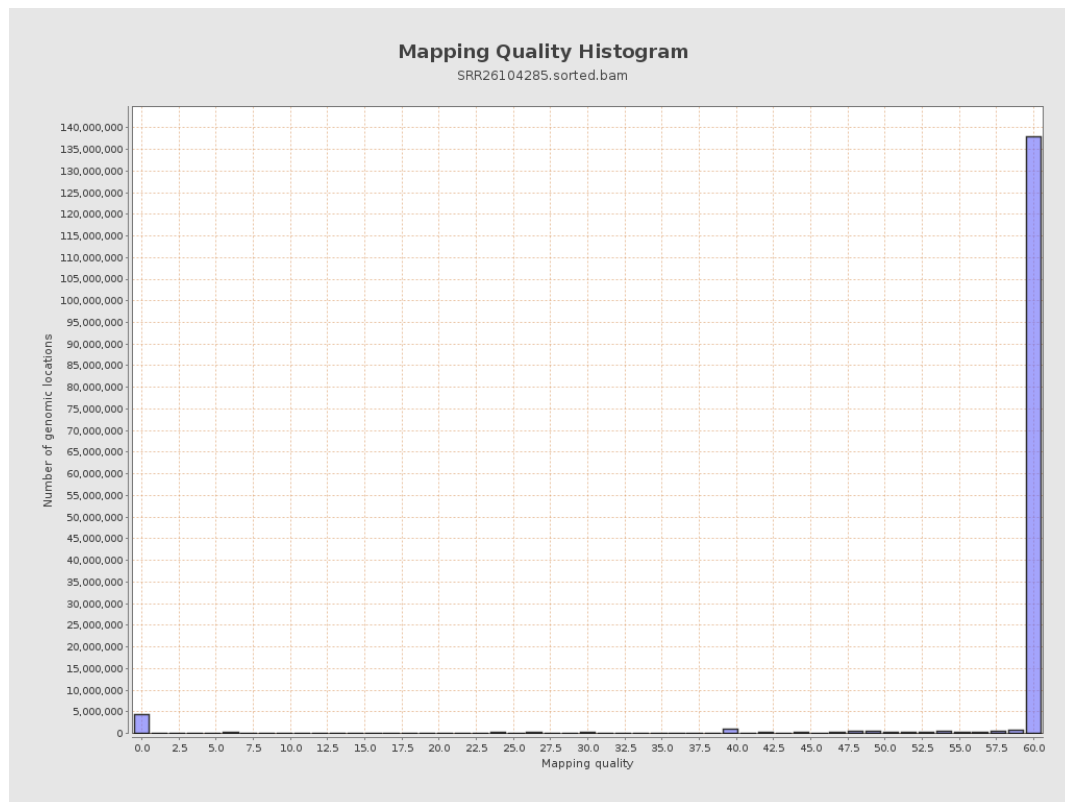
11. Results : Homopolymer Indels



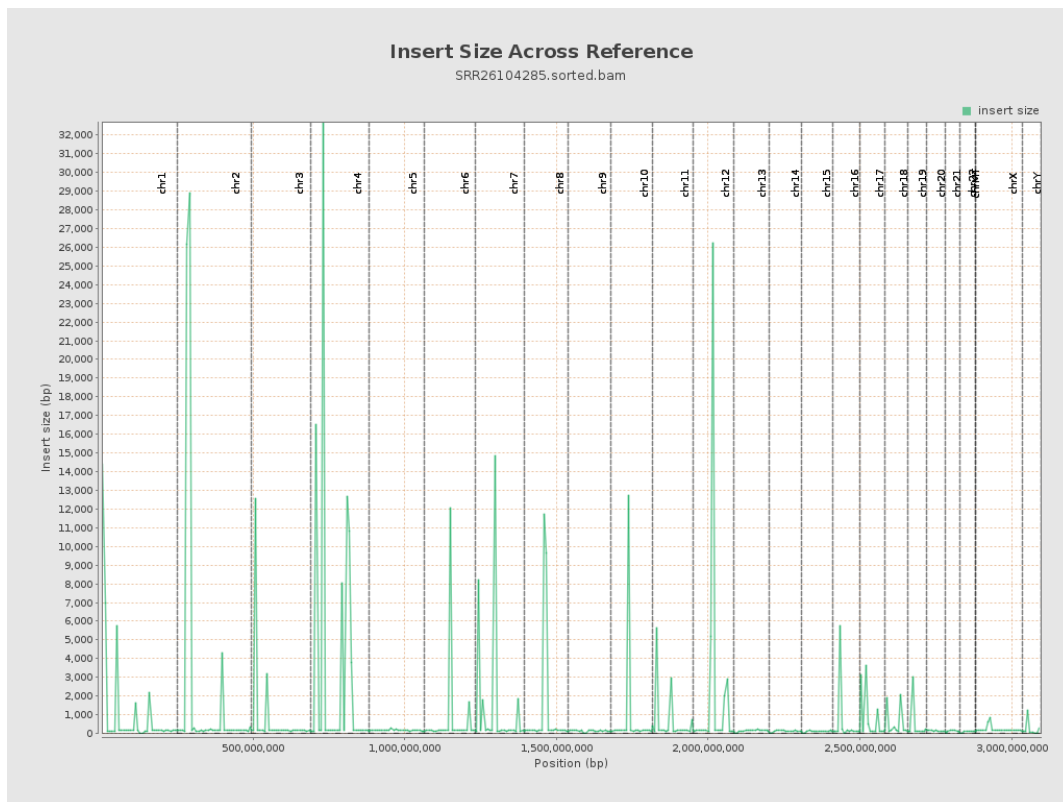
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

