

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 15:38:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104297.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_SRR26104297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104297_1.fastq.gz SRR26104297_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 15:38:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,583,457,124
Mapped reads	2,348,905,187 / 90.92%
Unmapped reads	234,551,937 / 9.08%
Mapped paired reads	2,348,905,187 / 90.92%
Mapped reads, first in pair	1,180,306,461 / 45.69%
Mapped reads, second in pair	1,168,598,726 / 45.23%
Mapped reads, both in pair	2,329,301,380 / 90.16%
Mapped reads, singletons	19,603,807 / 0.76%
Secondary alignments	0
Supplementary alignments	18,559 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	1,791,778,132 / 69.36%
Duplication rate	50.24%
Clipped reads	209,923,815 / 8.13%

2.2. ACGT Content

Number/percentage of A's	28,304,189,664 / 24.46%
Number/percentage of C's	29,582,491,039 / 25.57%
Number/percentage of T's	28,382,098,454 / 24.53%
Number/percentage of G's	29,421,299,631 / 25.43%
Number/percentage of N's	10,679,971 / 0.01%

GC Percentage	51%
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2.3. Coverage

Mean	37.3795
Standard Deviation	1,289.8869

2.4. Mapping Quality

Mean Mapping Quality	52.8
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2.5. Insert size

Mean	7,708
Standard Deviation	945,679.69
P25/Median/P75	74 / 143 / 206

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	321,913,022
Insertions	7,035,685
Mapped reads with at least one insertion	0.3%
Deletions	8,404,302
Mapped reads with at least one deletion	0.36%
Homopolymer indels	45.63%

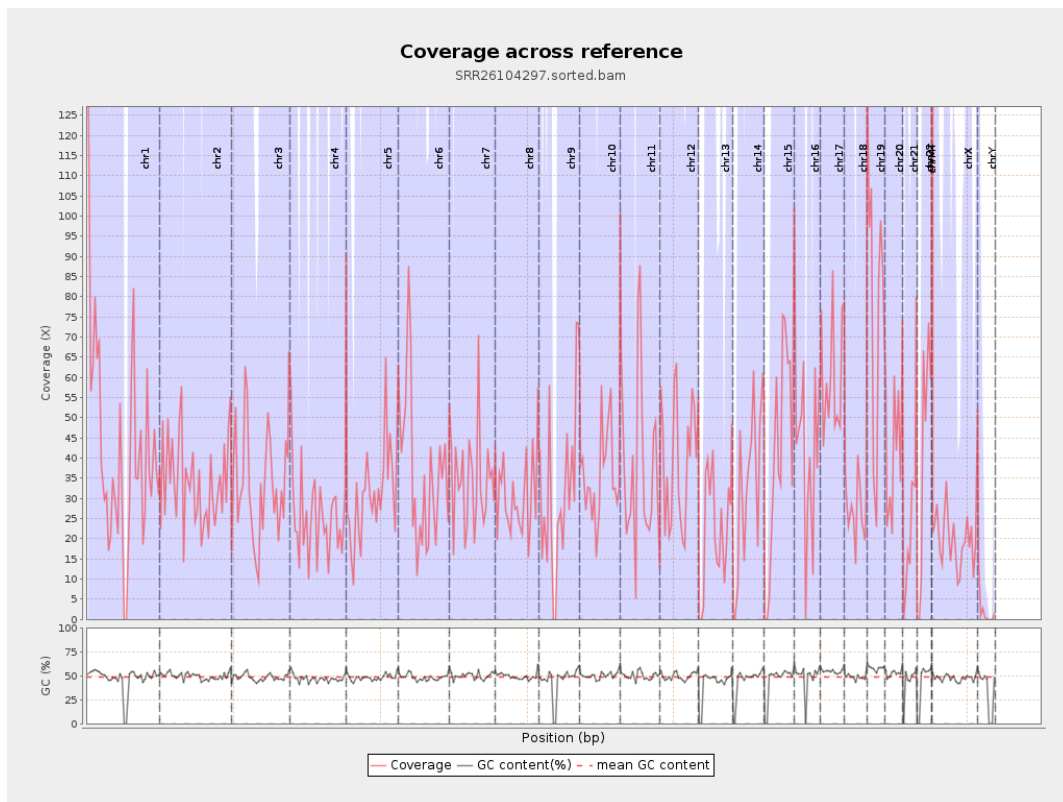
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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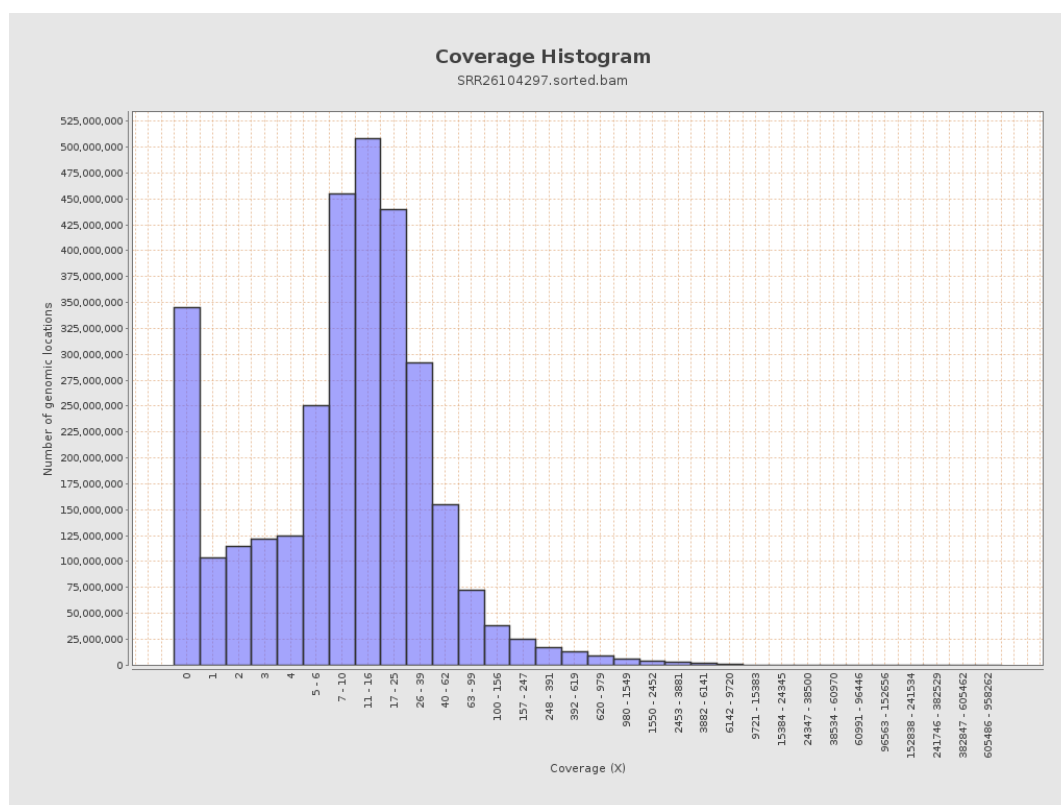
		bases	coverage	deviation
chr1	249250621	10597214669	42.5163	850.747
chr2	243199373	8267995734	33.9968	298.9645
chr3	198022430	6641823942	33.5408	192.2719
chr4	191154276	4818490699	25.2073	148.6069
chr5	180915260	5751323482	31.7902	261.5559
chr6	171115067	6130699121	35.8279	195.7364
chr7	159138663	5478334897	34.4249	236.6454
chr8	146364022	4461829187	30.4845	178.0813
chr9	141213431	4492547430	31.8139	194.4646
chr10	135534747	4813353744	35.5138	190.7449
chr11	135006516	5400290675	40.0002	285.8297
chr12	133851895	5234537826	39.1069	221.8467
chr13	115169878	2525762560	21.9308	303.8189
chr14	107349540	3479612304	32.4139	206.1734
chr15	102531392	4062792457	39.6249	232.5377
chr16	90354753	3960561434	43.8335	249.4057
chr17	81195210	4929863585	60.7162	371.8114
chr18	78077248	2141301875	27.4254	162.6163
chr19	59128983	4674718720	79.0597	403.012
chr20	63025520	2630628308	41.7391	218.8024
chr21	48129895	1197387874	24.8783	184.1796
chr22	51304566	2137150101	41.6561	237.3655
chrMT	16571	8639735157	521,376.8123	137,505.2714
chrX	155270560	3126781491	20.1376	111.715

chrY	59373566	120808897	2.0347	82.2599
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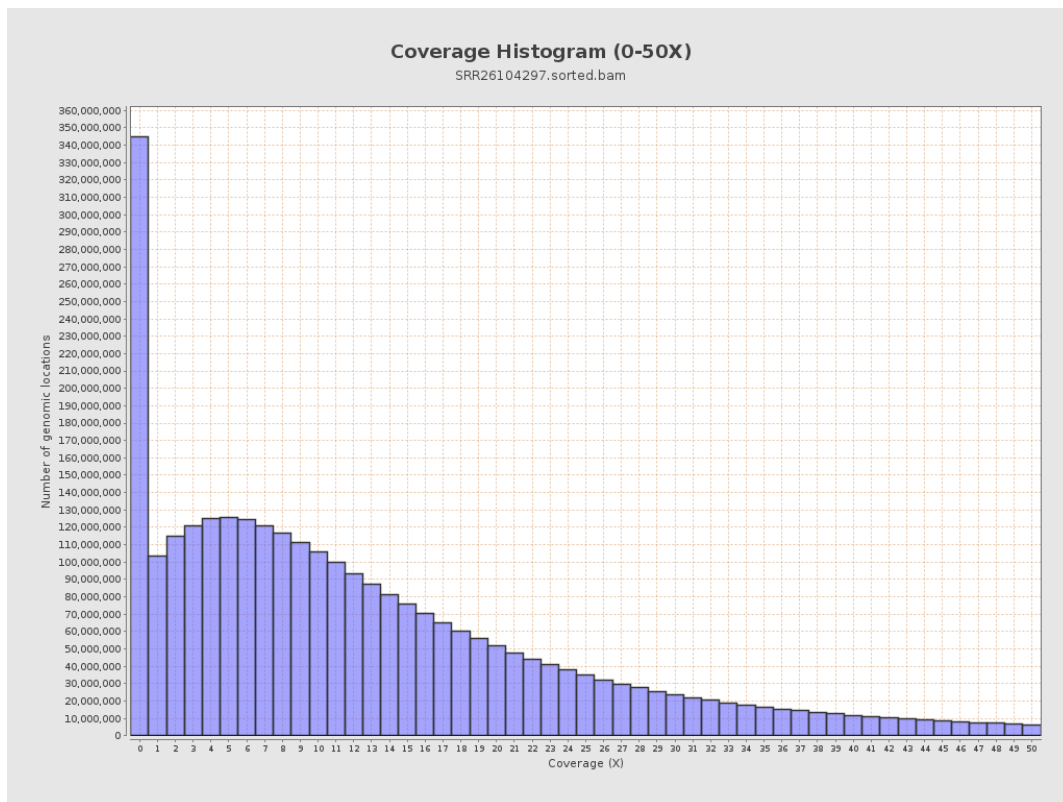
3. Results : Coverage across reference



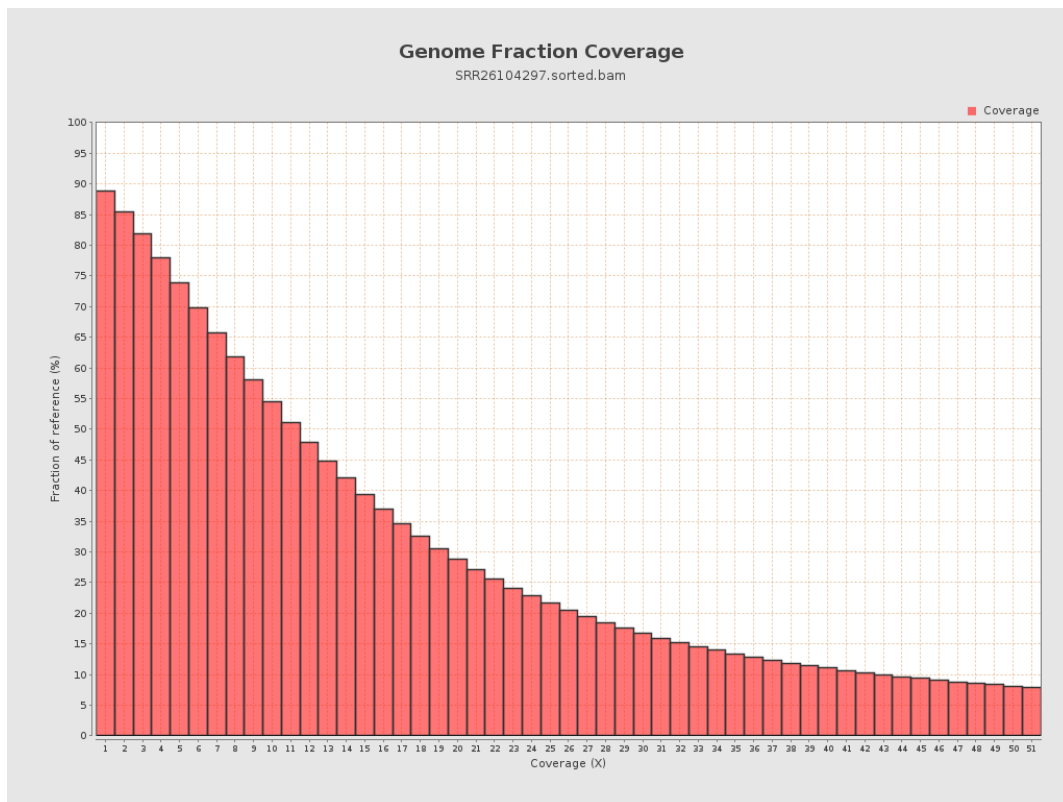
4. Results : Coverage Histogram



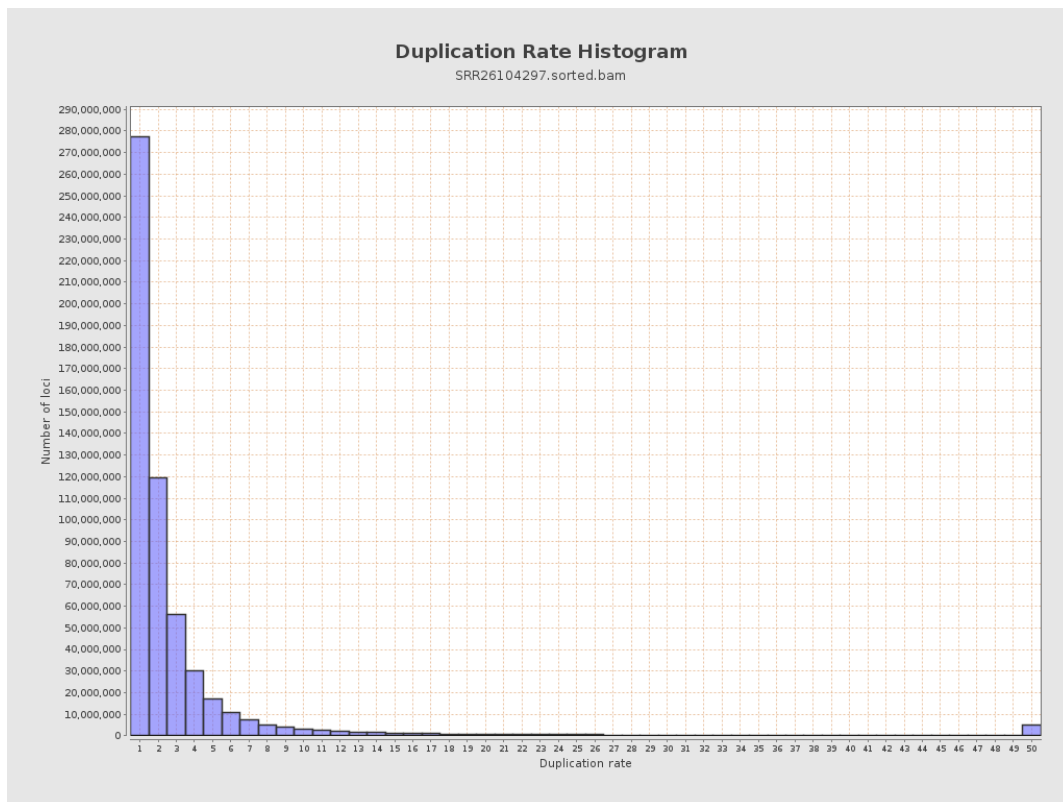
5. Results : Coverage Histogram (0-50X)



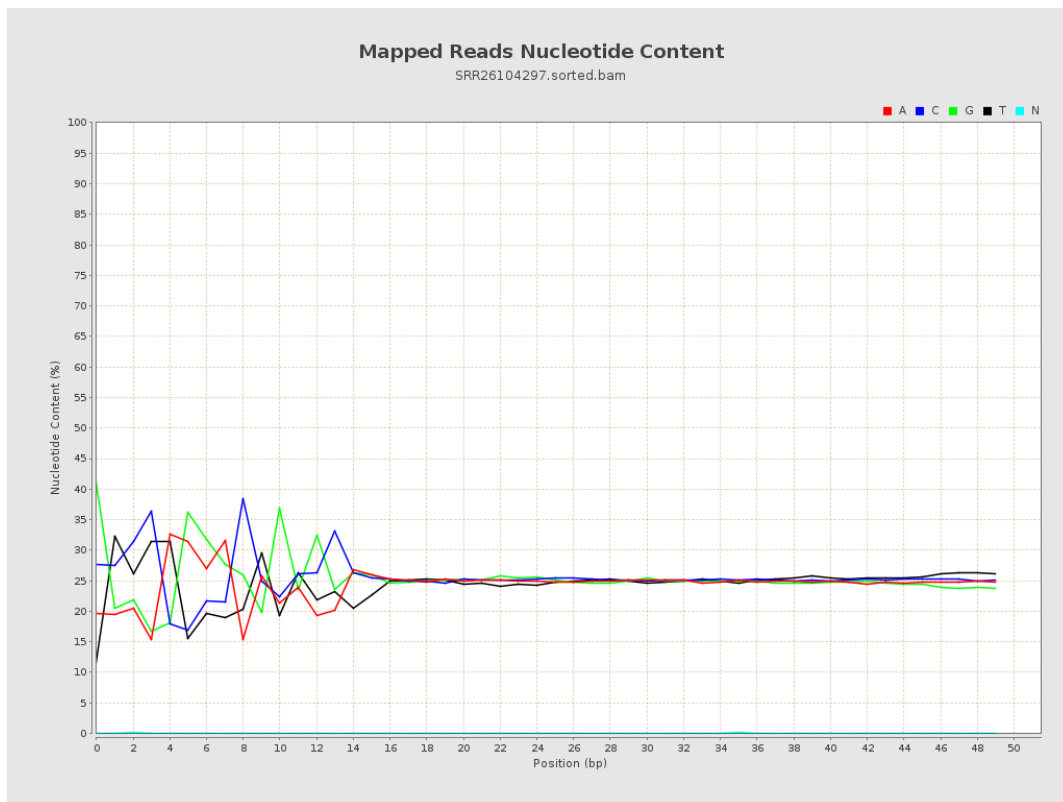
6. Results : Genome Fraction Coverage



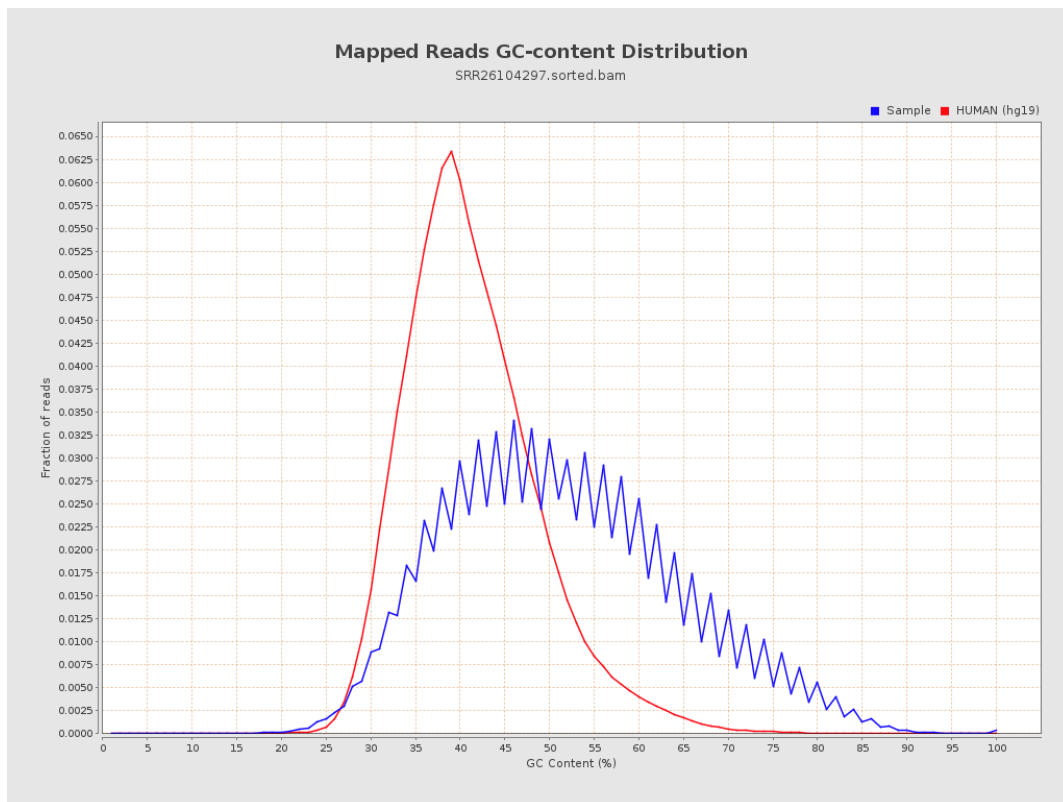
7. Results : Duplication Rate Histogram



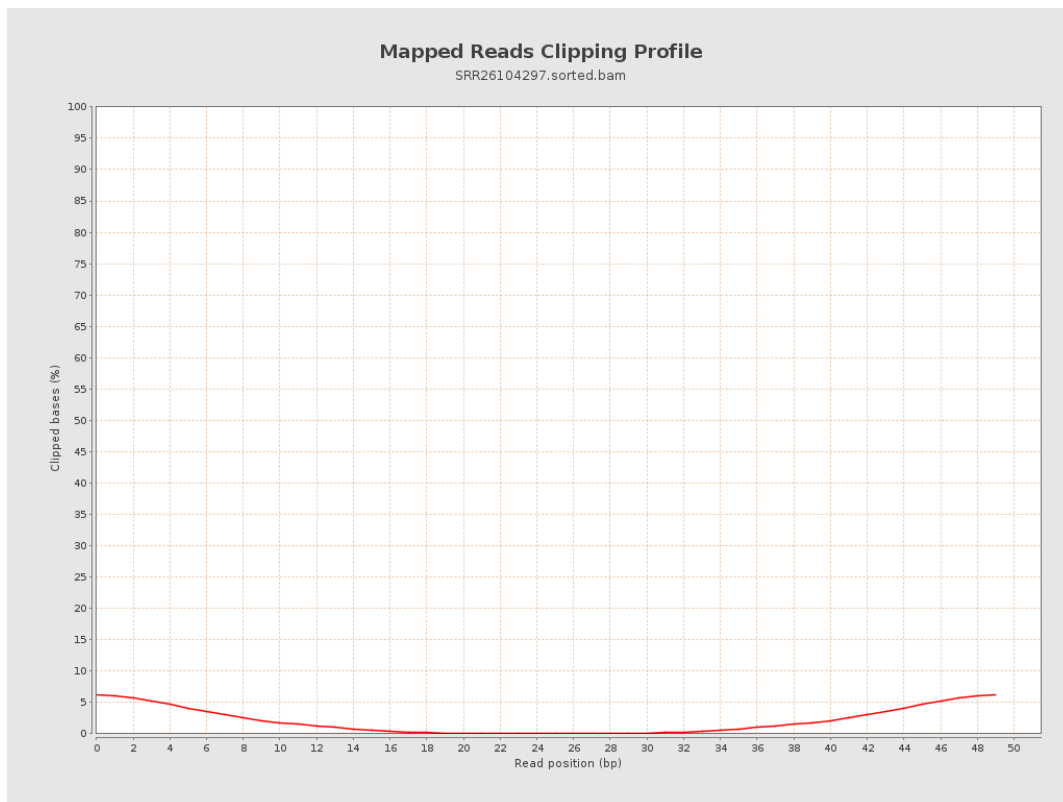
8. Results : Mapped Reads Nucleotide Content



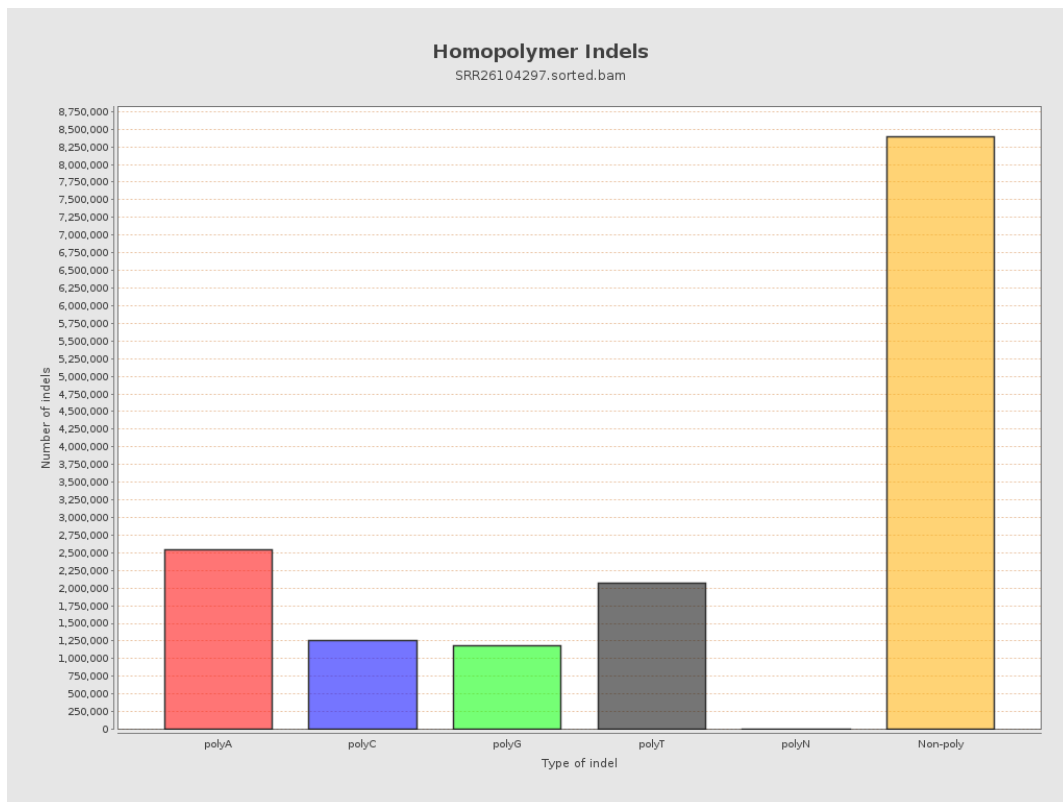
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



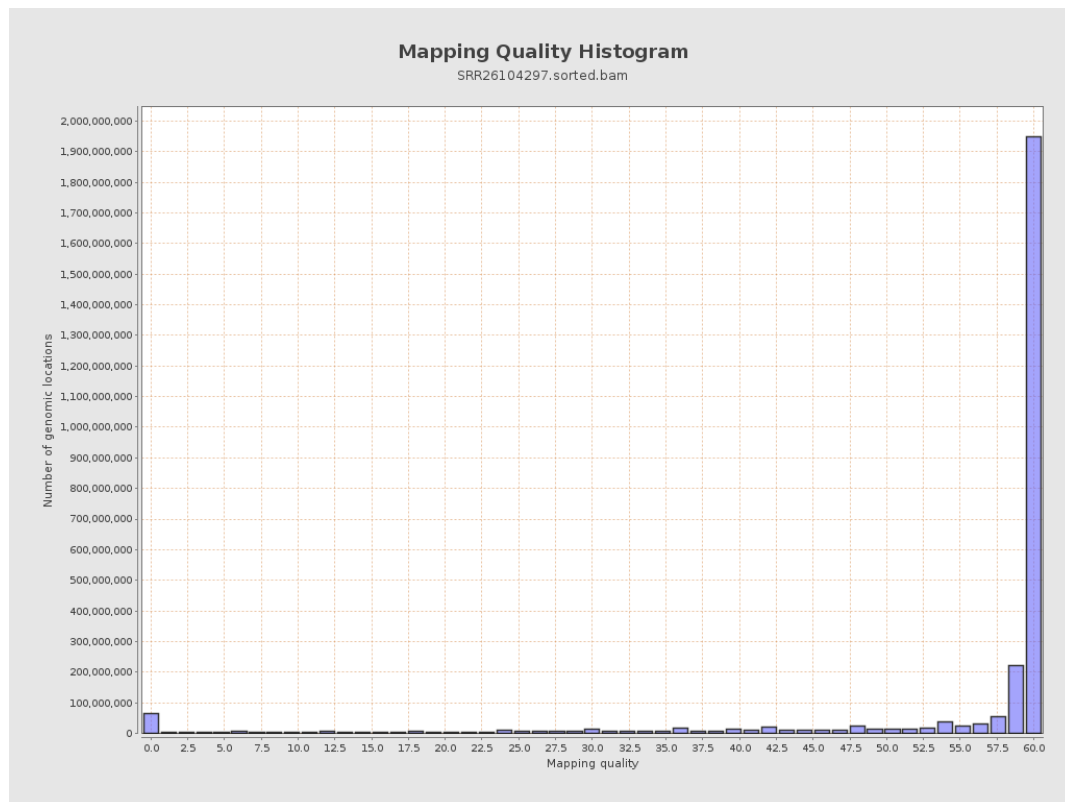
11. Results : Homopolymer Indels



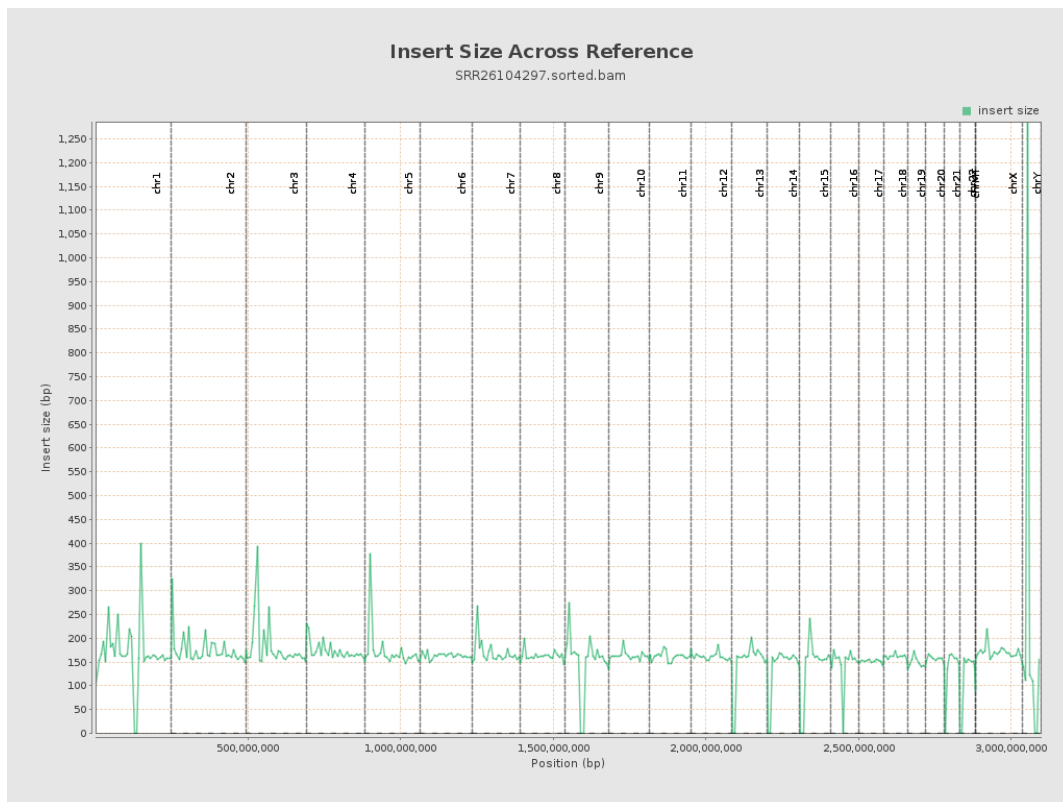
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

