

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 23:23:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104286.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_SRR26104286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104286_1.fastq.gz SRR26104286_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 23:23:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	121,795,034
Mapped reads	119,570,410 / 98.17%
Unmapped reads	2,224,624 / 1.83%
Mapped paired reads	119,570,410 / 98.17%
Mapped reads, first in pair	60,270,199 / 49.48%
Mapped reads, second in pair	59,300,211 / 48.69%
Mapped reads, both in pair	118,377,820 / 97.19%
Mapped reads, singletons	1,192,590 / 0.98%
Secondary alignments	0
Supplementary alignments	107,821 / 0.09%
Read min/max/mean length	30 / 97 / 91.03
Duplicated reads (estimated)	41,660,444 / 34.21%
Duplication rate	28.28%
Clipped reads	23,201,122 / 19.05%

2.2. ACGT Content

Number/percentage of A's	3,227,714,564 / 31.24%
Number/percentage of C's	1,936,616,554 / 18.74%
Number/percentage of T's	3,260,683,973 / 31.56%
Number/percentage of G's	1,901,161,970 / 18.4%
Number/percentage of N's	5,442,535 / 0.05%

GC Percentage	37.15%
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2.3. Coverage

Mean	3.3383
Standard Deviation	28.3538

2.4. Mapping Quality

Mean Mapping Quality	53.26
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2.5. Insert size

Mean	10,855.93
Standard Deviation	967,832.33
P25/Median/P75	105 / 166 / 258

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	65,095,083
Insertions	1,023,551
Mapped reads with at least one insertion	0.85%
Deletions	1,188,428
Mapped reads with at least one deletion	0.98%
Homopolymer indels	44.85%

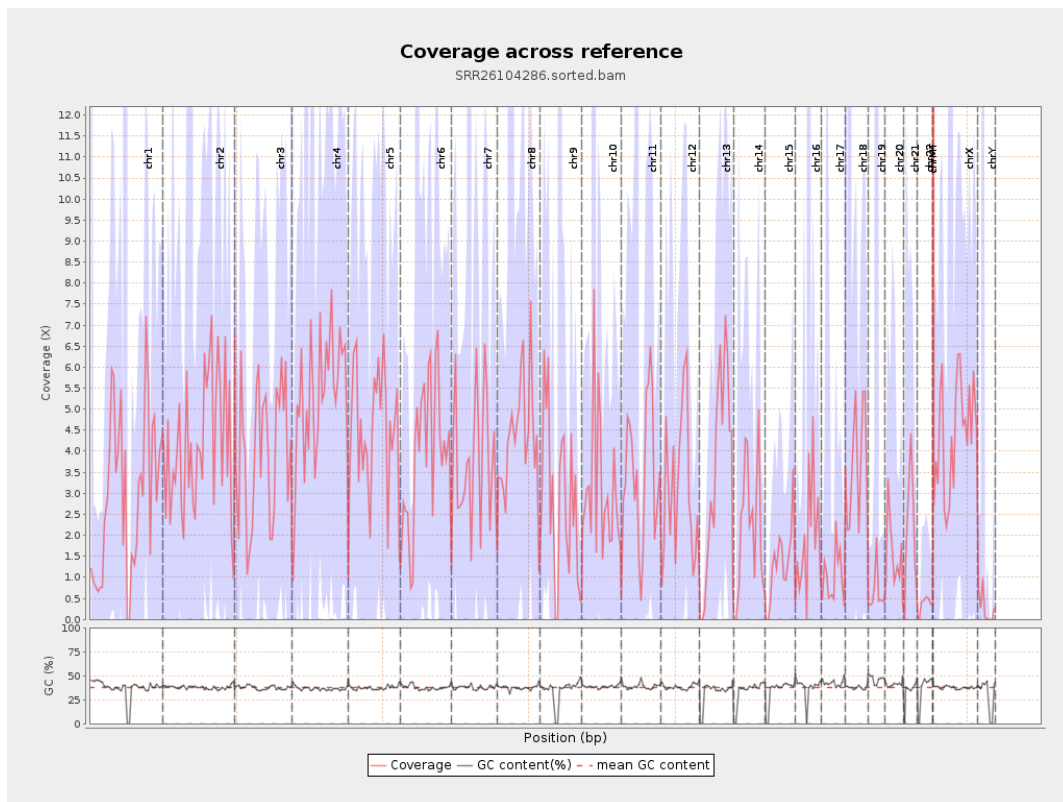
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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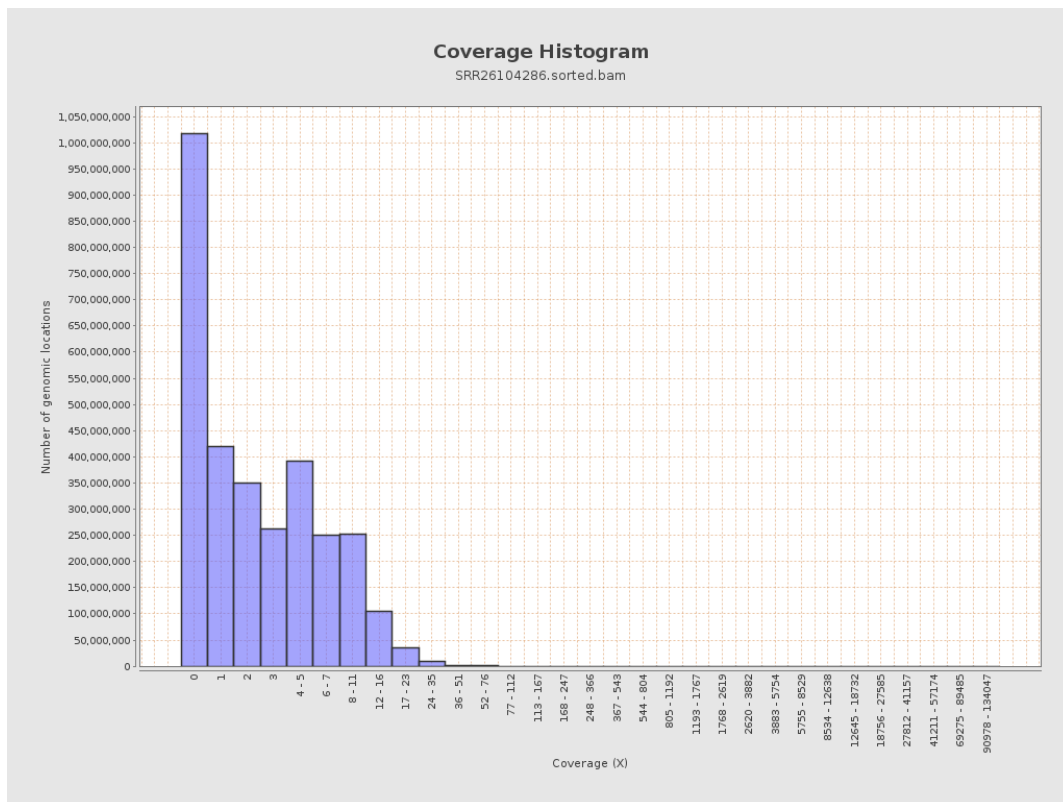
		bases	coverage	deviation
chr1	249250621	734727028	2.9477	46.102
chr2	243199373	1004843008	4.1318	14.6334
chr3	198022430	794962322	4.0145	5.1519
chr4	191154276	1014531276	5.3074	12.5113
chr5	180915260	804218983	4.4453	4.9322
chr6	171115067	681876235	3.9849	11.7989
chr7	159138663	597664818	3.7556	26.379
chr8	146364022	638319530	4.3612	84.2306
chr9	141213431	412687663	2.9224	17.3549
chr10	135534747	416491071	3.0729	39.9565
chr11	135006516	472699235	3.5013	11.4318
chr12	133851895	408461092	3.0516	4.4494
chr13	115169878	406176738	3.5268	4.6527
chr14	107349540	239597783	2.2319	4.4697
chr15	102531392	136906892	1.3353	2.4278
chr16	90354753	170930616	1.8918	15.6747
chr17	81195210	84735502	1.0436	5.4173
chr18	78077248	290389958	3.7193	18.2901
chr19	59128983	39300617	0.6647	29.0529
chr20	63025520	102594796	1.6278	4.2042
chr21	48129895	100706241	2.0924	5.634
chr22	51304566	18191104	0.3546	1.4486
chrMT	16571	67722346	4,086.799	843.6227
chrX	155270560	679589075	4.3768	7.433

chrY	59373566	15929029	0.2683	9.4637
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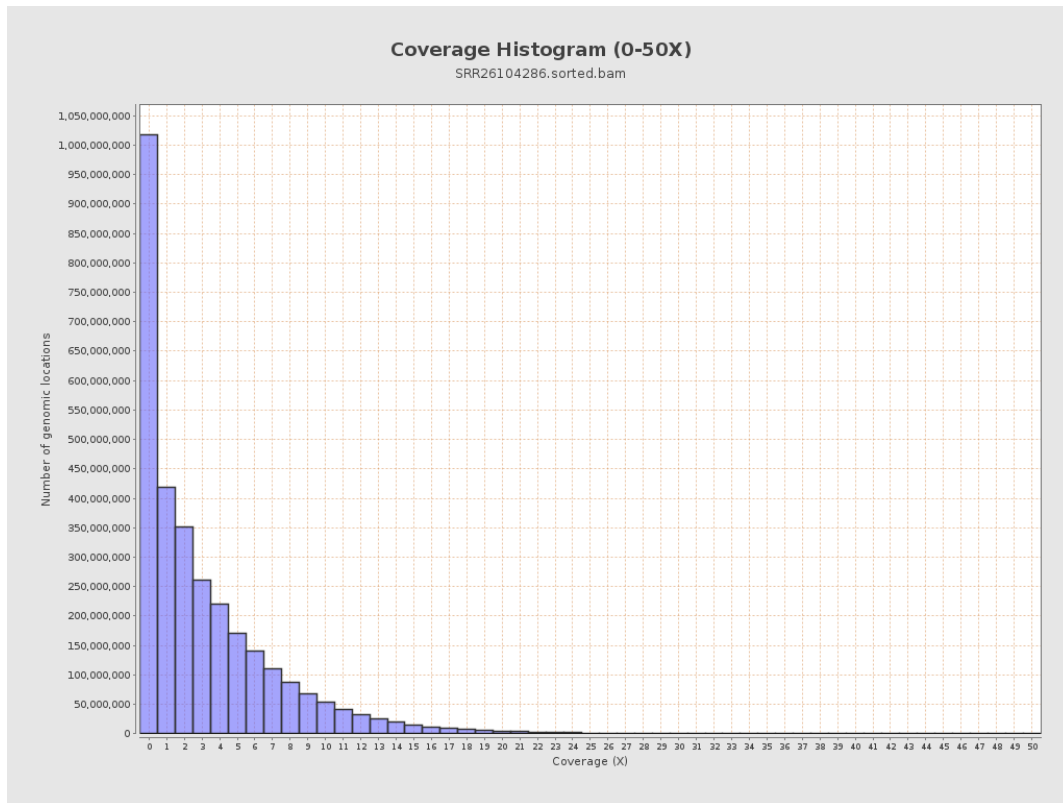
3. Results : Coverage across reference



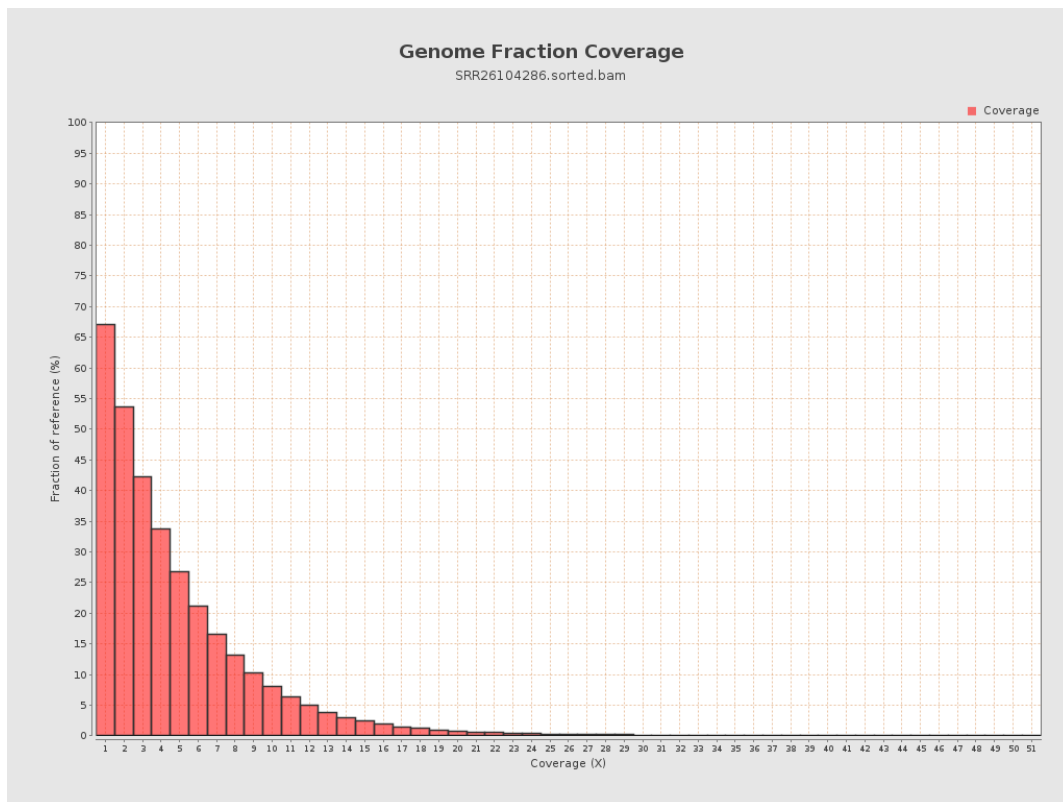
4. Results : Coverage Histogram



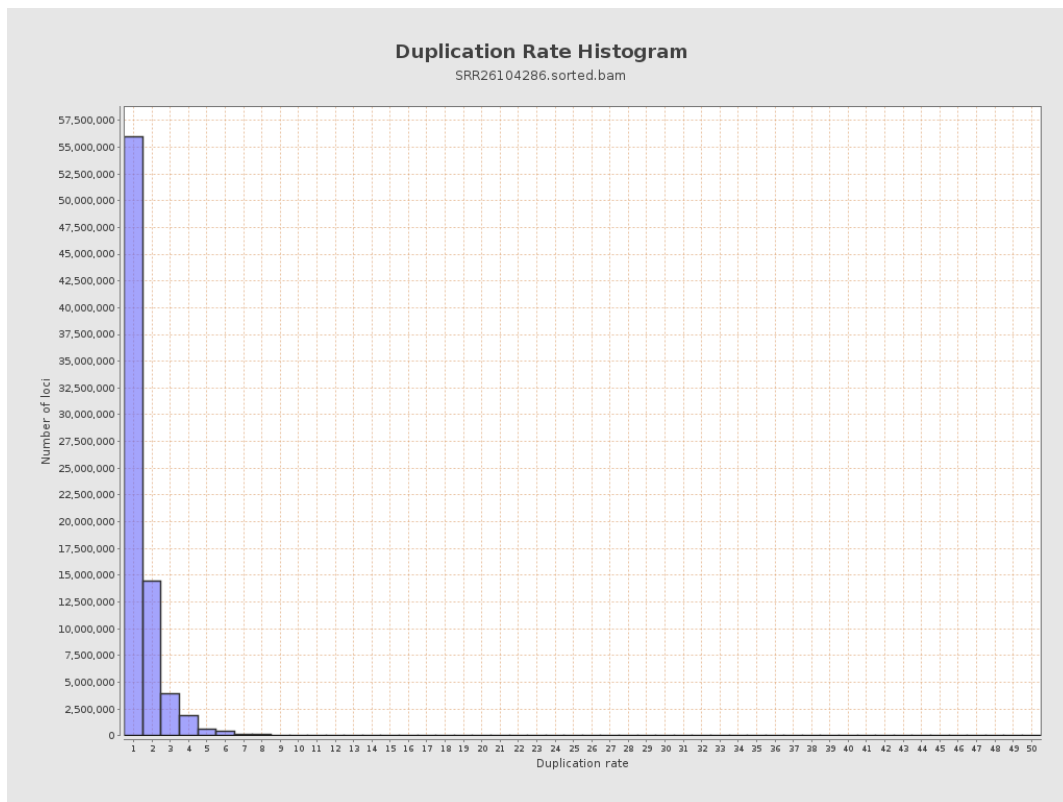
5. Results : Coverage Histogram (0-50X)



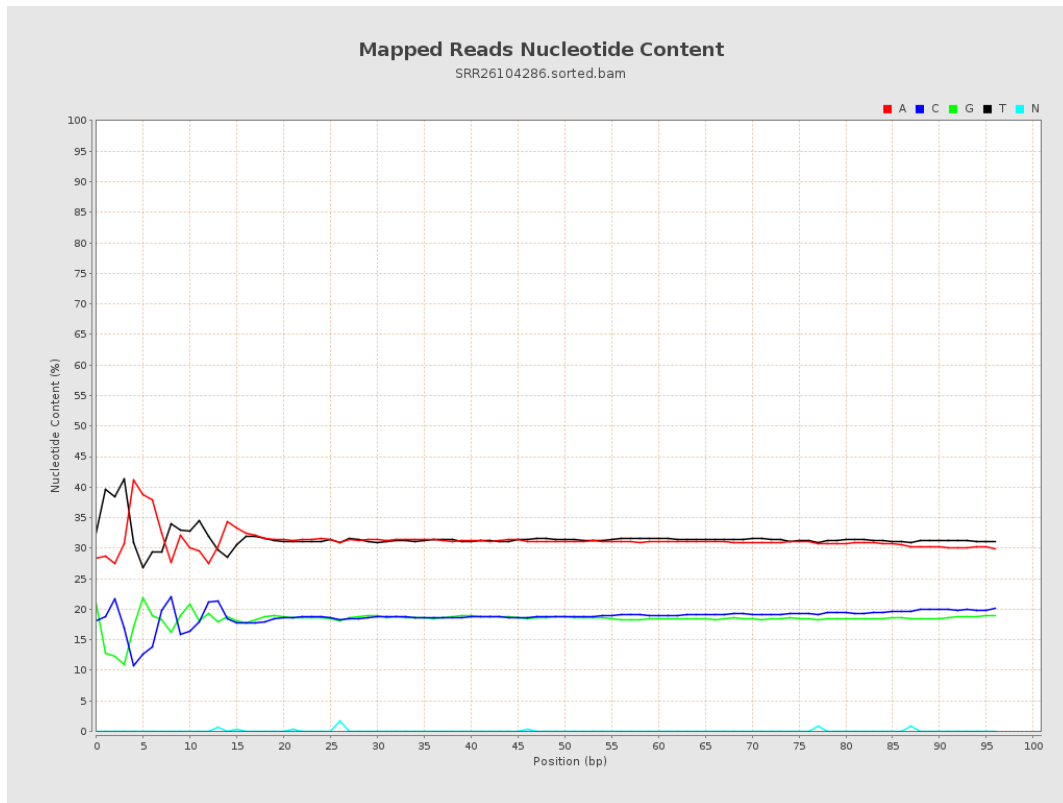
6. Results : Genome Fraction Coverage



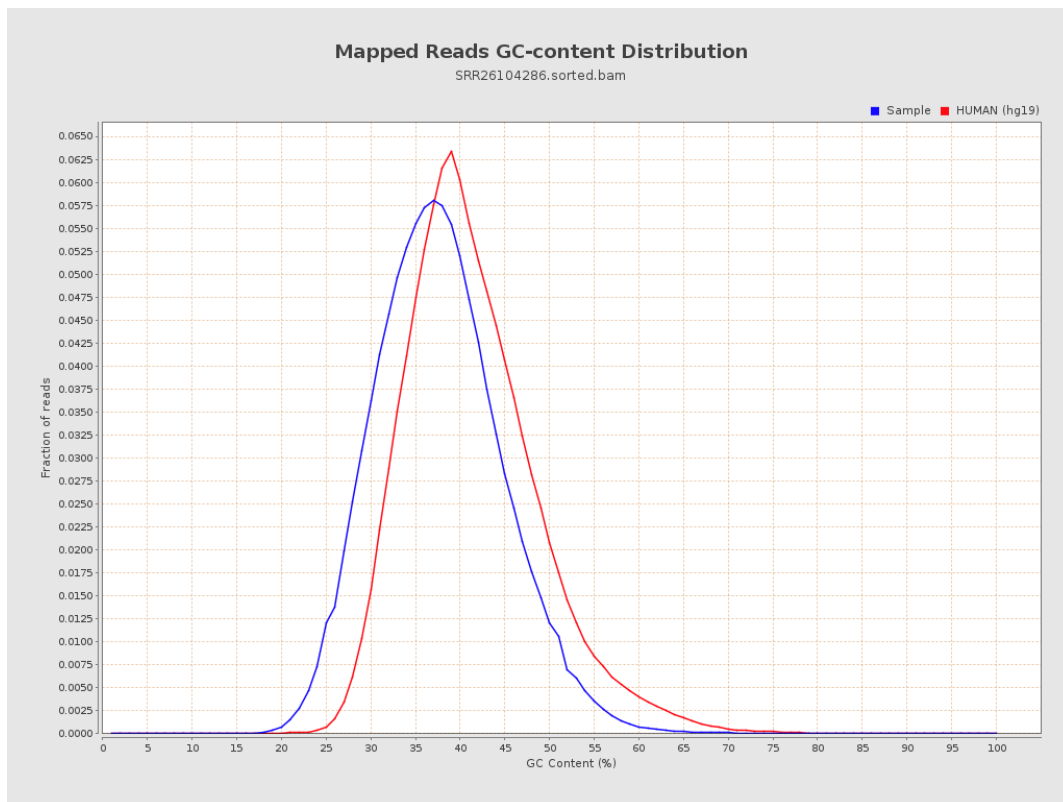
7. Results : Duplication Rate Histogram



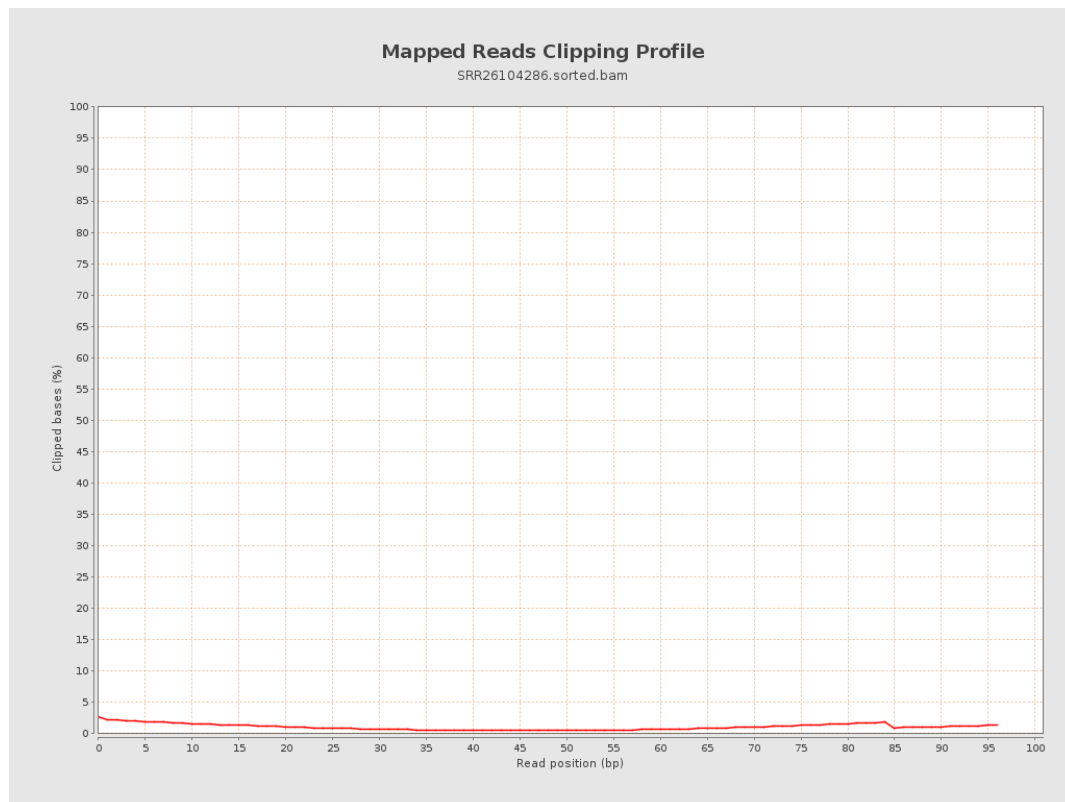
8. Results : Mapped Reads Nucleotide Content



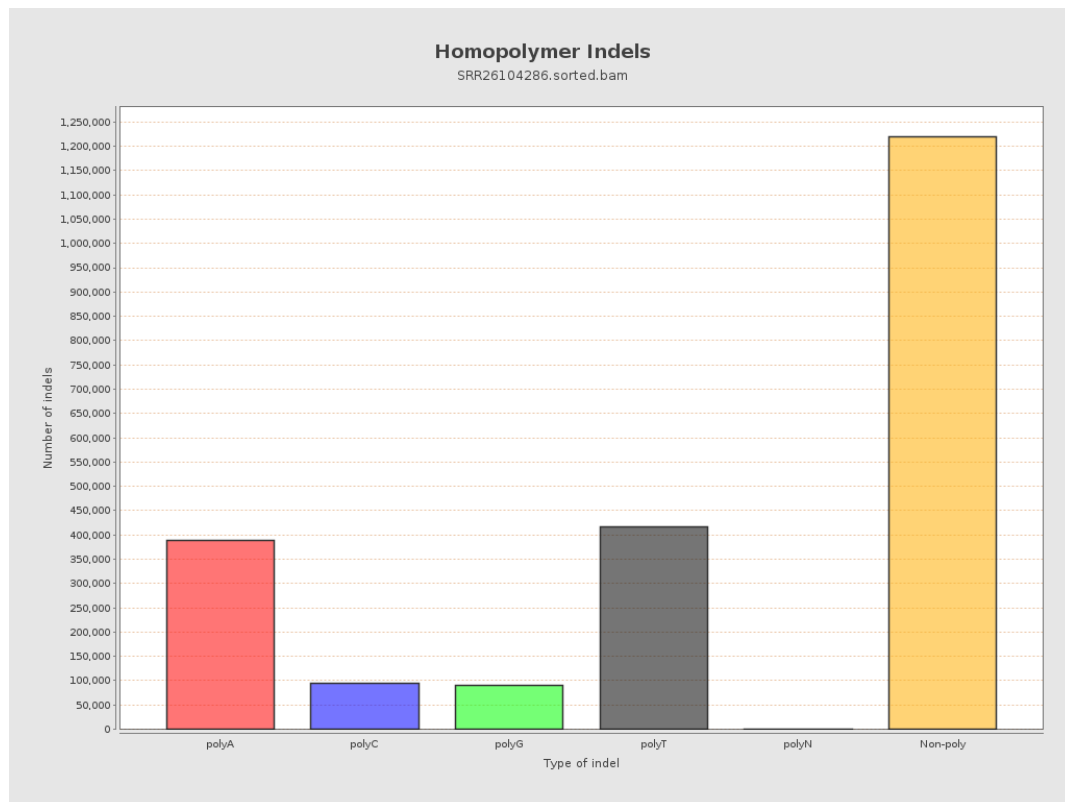
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



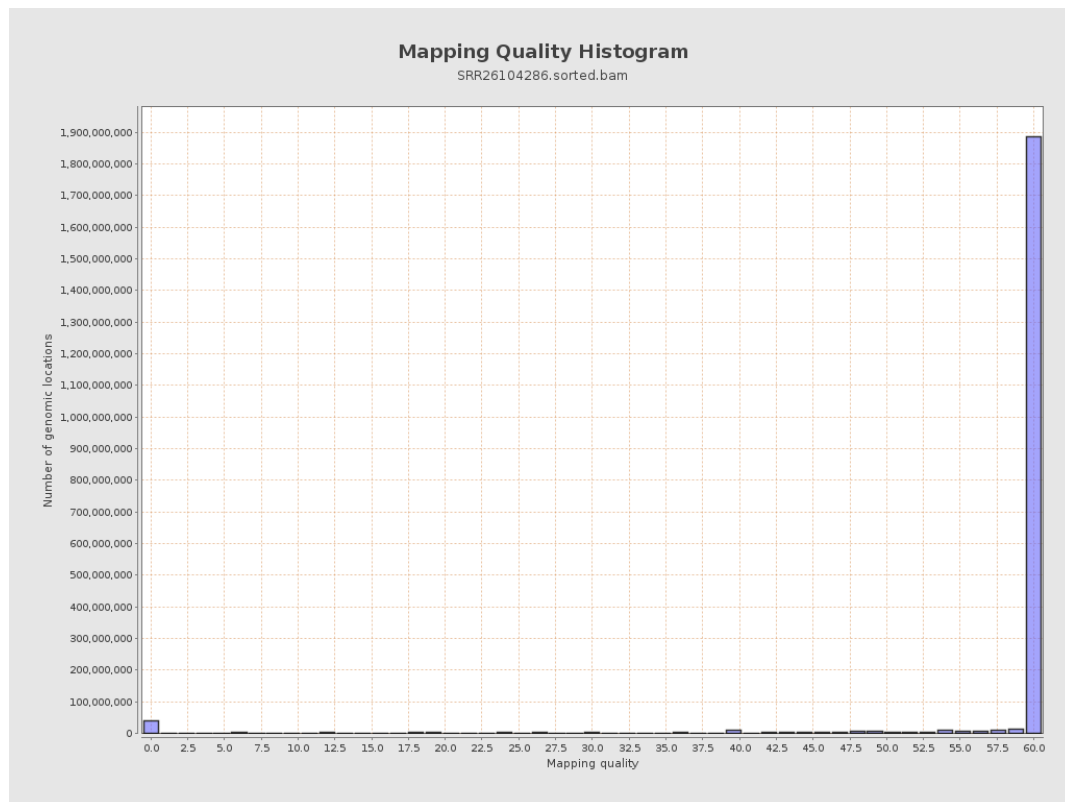
11. Results : Homopolymer Indels



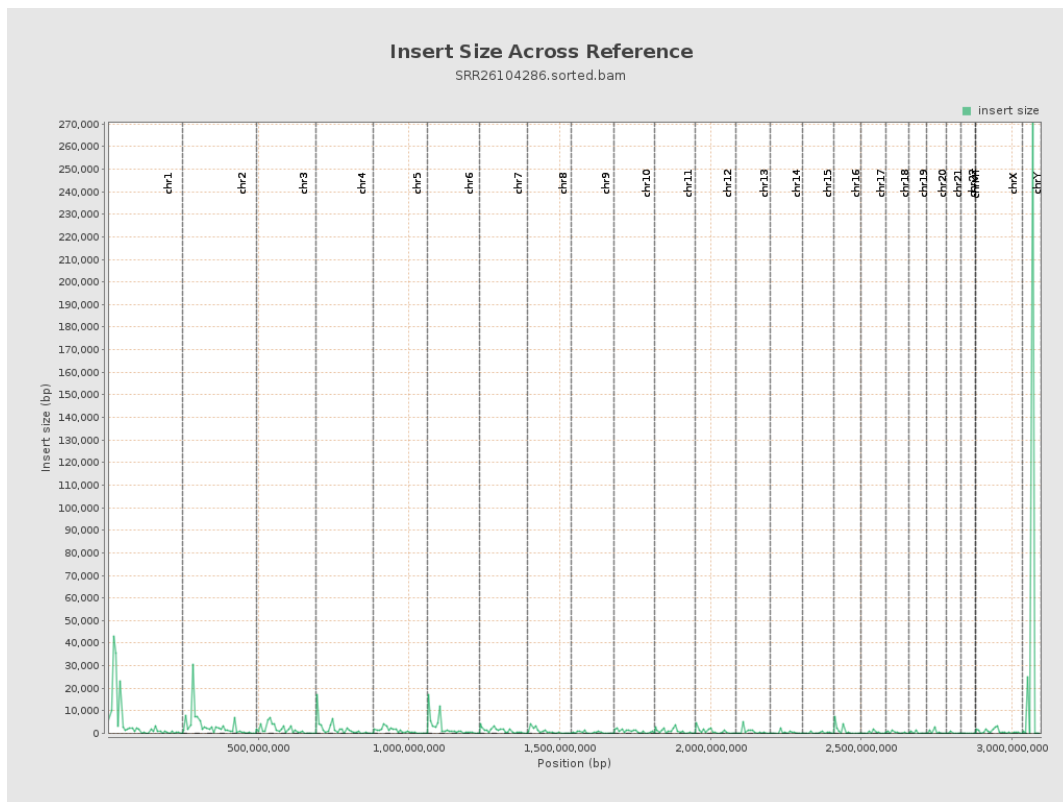
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

