

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 00:11:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104287.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_SRR26104287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104287_1.fastq.gz SRR26104287_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 00:11:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,910,938
Mapped reads	17,215,006 / 96.11%
Unmapped reads	695,932 / 3.89%
Mapped paired reads	17,215,006 / 96.11%
Mapped reads, first in pair	8,725,930 / 48.72%
Mapped reads, second in pair	8,489,076 / 47.4%
Mapped reads, both in pair	16,954,452 / 94.66%
Mapped reads, singletons	260,554 / 1.45%
Secondary alignments	0
Supplementary alignments	20,218 / 0.11%
Read min/max/mean length	30 / 97 / 91.04
Duplicated reads (estimated)	7,786,581 / 43.47%
Duplication rate	33.94%
Clipped reads	8,687,583 / 48.5%

2.2. ACGT Content

Number/percentage of A's	340,300,453 / 26.74%
Number/percentage of C's	299,845,215 / 23.56%
Number/percentage of T's	344,388,695 / 27.06%
Number/percentage of G's	287,289,676 / 22.58%
Number/percentage of N's	671,162 / 0.05%

GC Percentage	46.14%
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2.3. Coverage

Mean	0.4112
Standard Deviation	7.8551

2.4. Mapping Quality

Mean Mapping Quality	53.56
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2.5. Insert size

Mean	13,431.08
Standard Deviation	1,120,177.27
P25/Median/P75	54 / 93 / 177

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	6,980,303
Insertions	140,756
Mapped reads with at least one insertion	0.81%
Deletions	149,602
Mapped reads with at least one deletion	0.86%
Homopolymer indels	45.03%

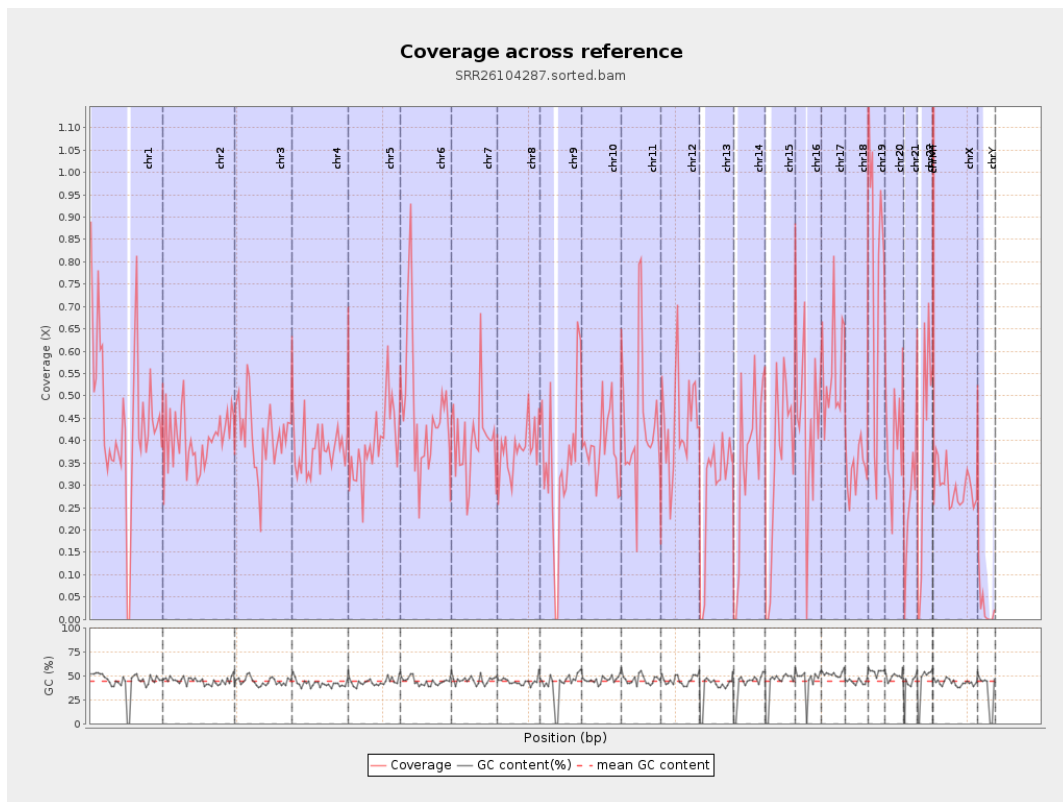
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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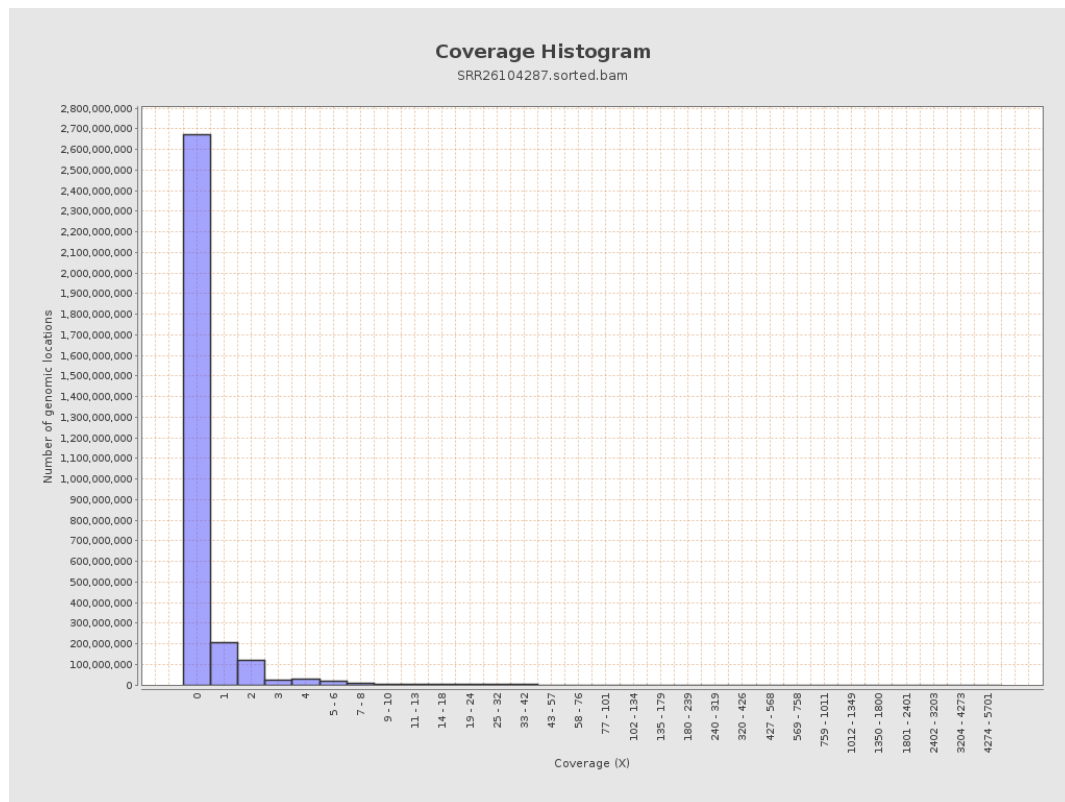
		bases	coverage	deviation
chr1	249250621	111172754	0.446	5.0706
chr2	243199373	977111178	0.4018	2.2706
chr3	198022430	81430709	0.4112	2.2182
chr4	191154276	72251337	0.378	1.8288
chr5	180915260	72037629	0.3982	2.3838
chr6	171115067	78568028	0.4592	2.4935
chr7	159138663	63402517	0.3984	2.4575
chr8	146364022	55606723	0.3799	3.1955
chr9	141213431	48905505	0.3463	2.2648
chr10	135534747	52395597	0.3866	2.5633
chr11	135006516	58891085	0.4362	2.7505
chr12	133851895	59810714	0.4468	2.6107
chr13	115169878	33465467	0.2906	2.1414
chr14	107349540	38065502	0.3546	2.4111
chr15	102531392	34308304	0.3346	2.3025
chr16	90354753	40683391	0.4503	2.9149
chr17	81195210	45264455	0.5575	3.6037
chr18	78077248	26383326	0.3379	1.9401
chr19	59128983	45624599	0.7716	5.0463
chr20	63025520	24559306	0.3897	2.3955
chr21	48129895	13068345	0.2715	2.1426
chr22	51304566	19964645	0.3891	2.8857
chrMT	16571	51081788	3,082.6014	756.633
chrX	155270560	46582274	0.3	1.5538

chrY	59373566	1580053	0.0266	0.8194
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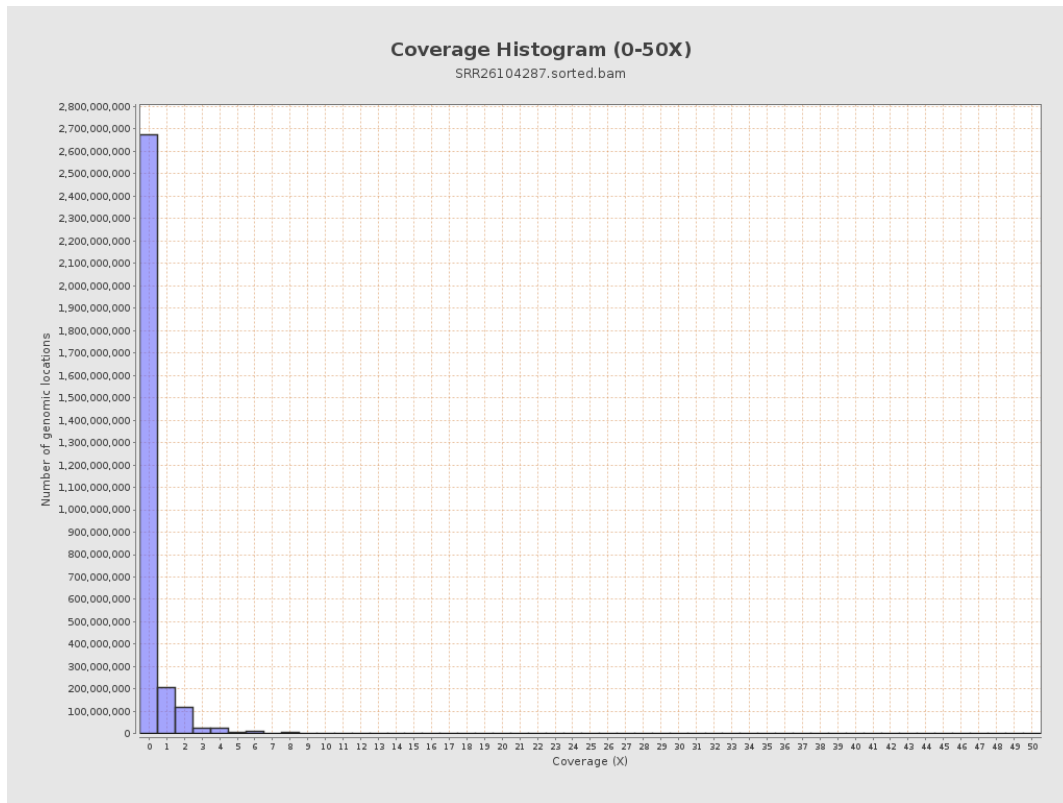
3. Results : Coverage across reference



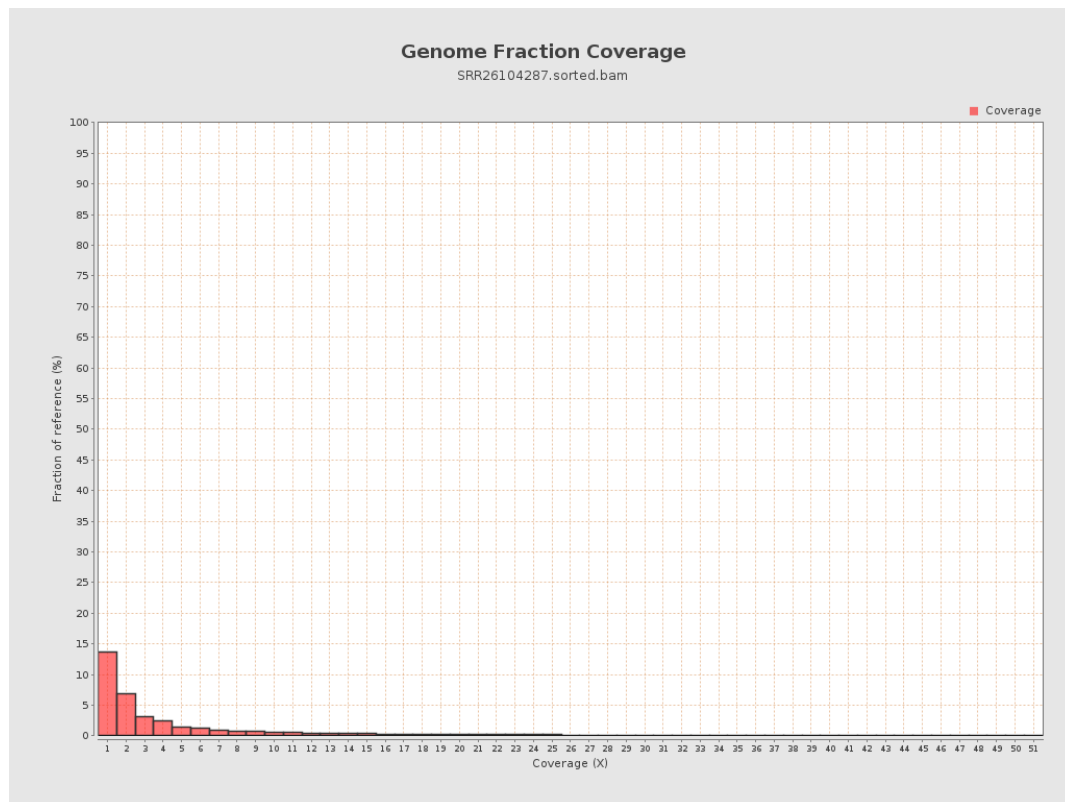
4. Results : Coverage Histogram



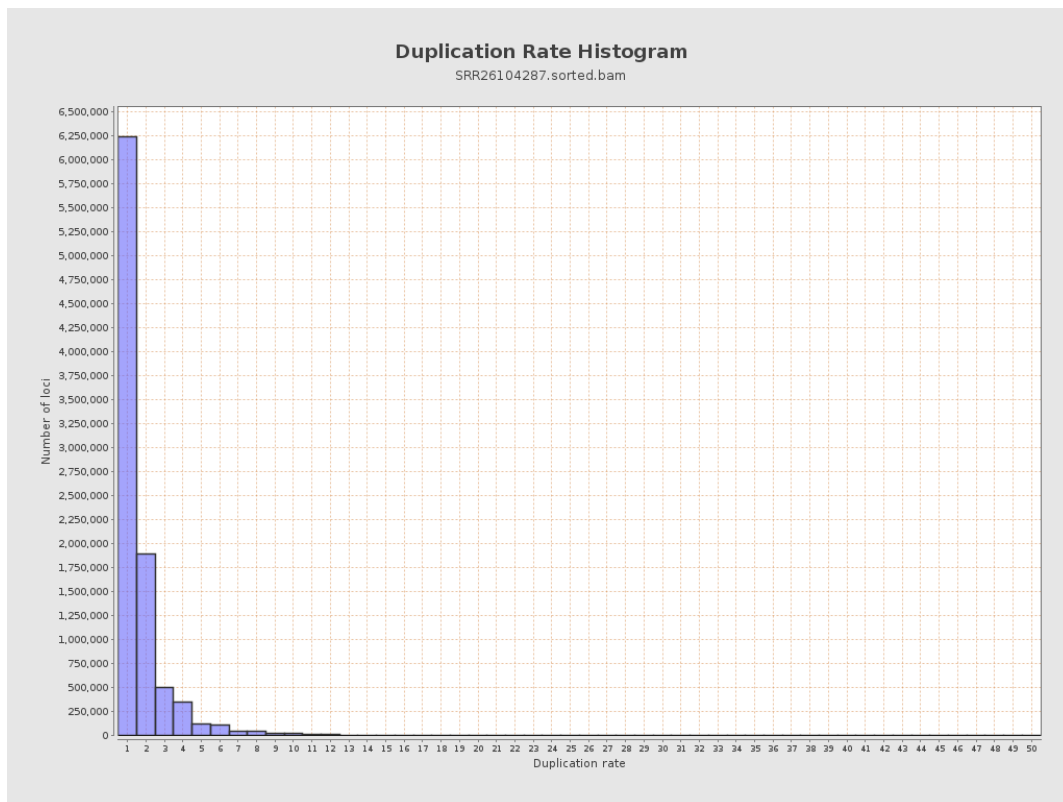
5. Results : Coverage Histogram (0-50X)



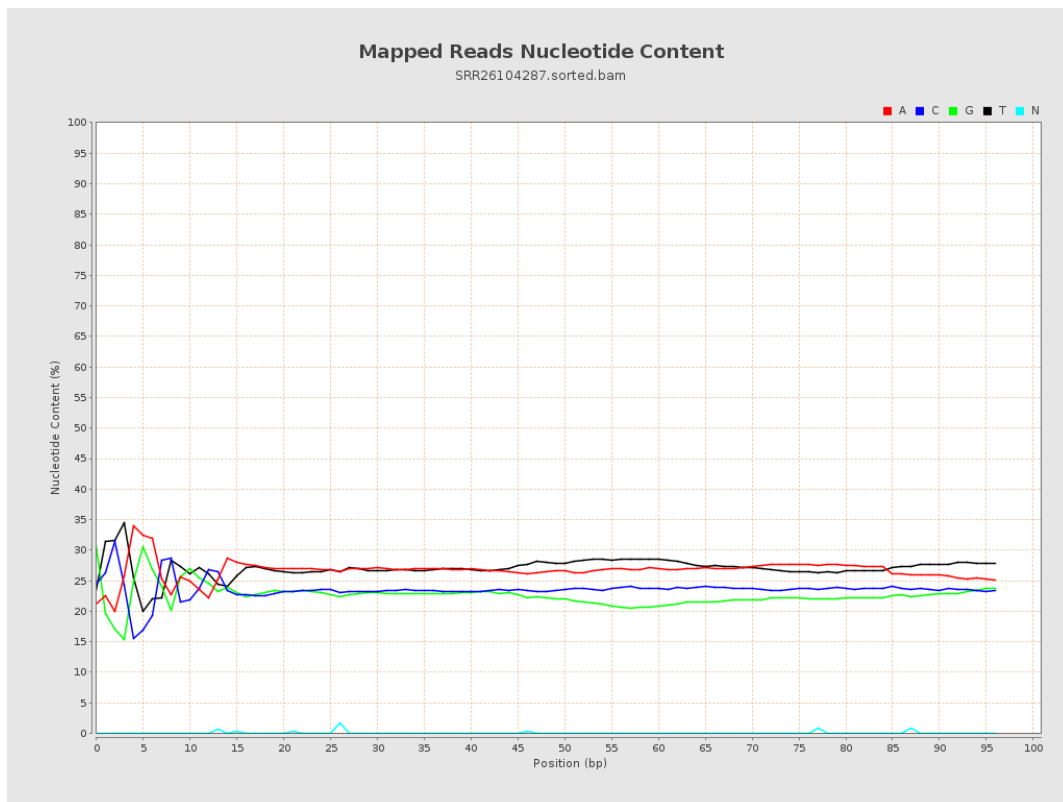
6. Results : Genome Fraction Coverage



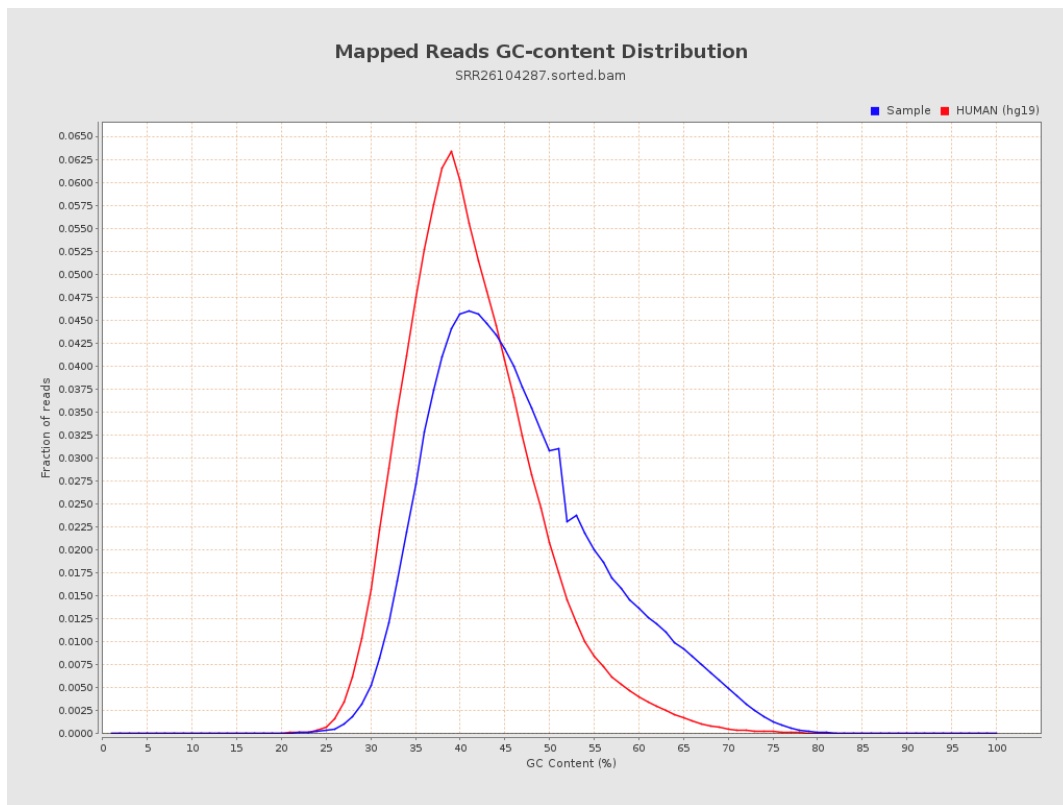
7. Results : Duplication Rate Histogram



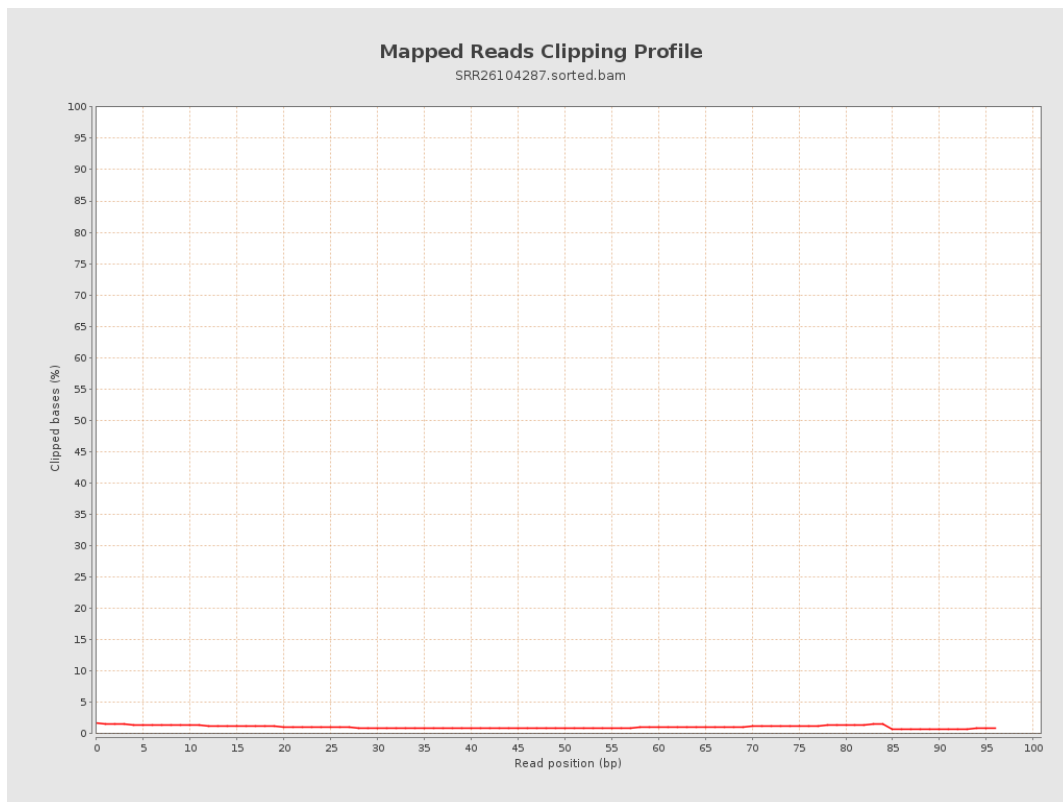
8. Results : Mapped Reads Nucleotide Content



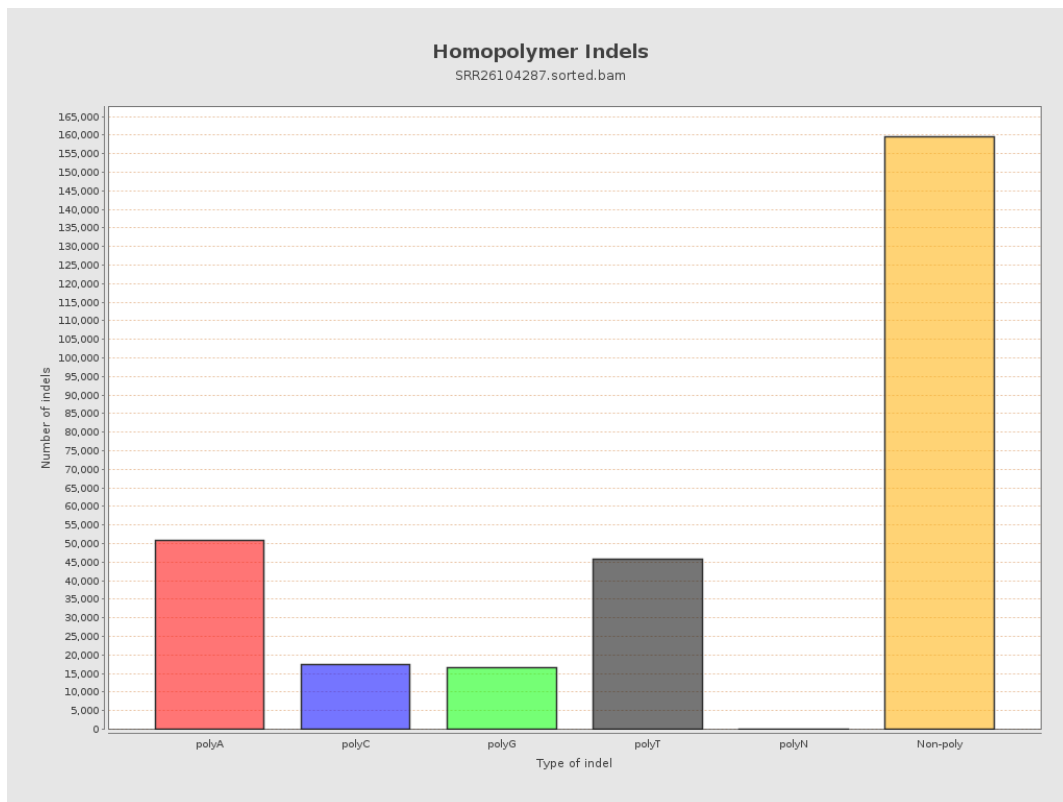
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



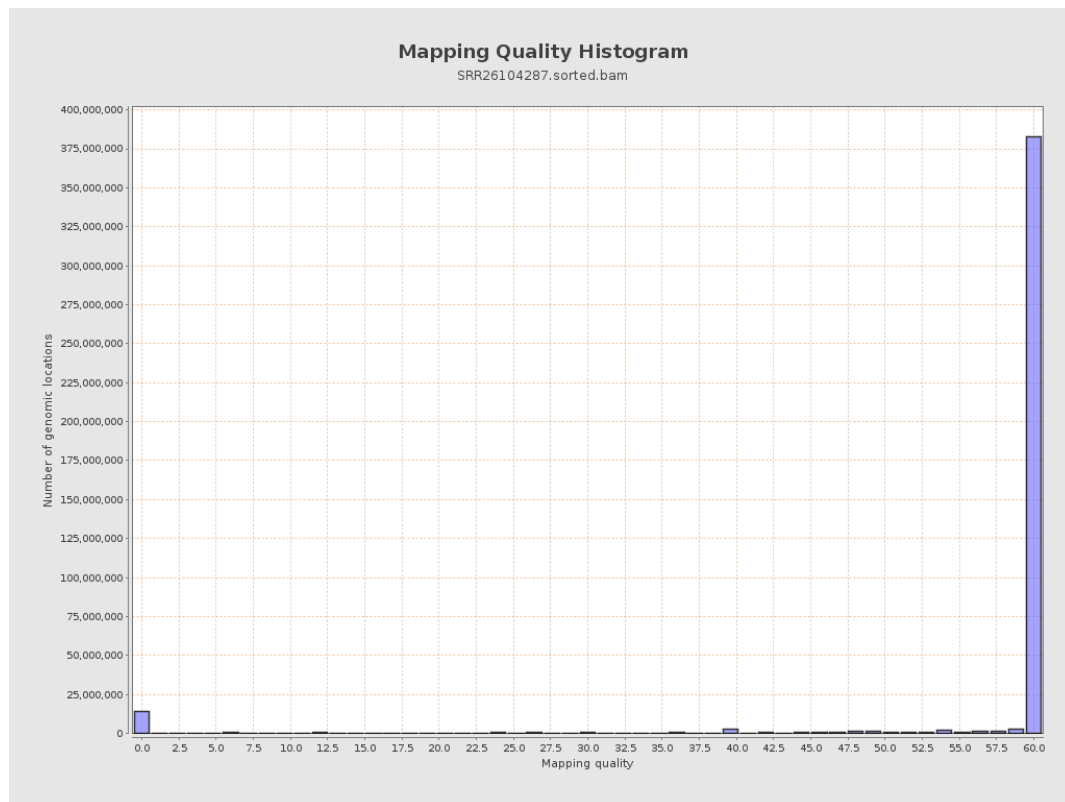
11. Results : Homopolymer Indels



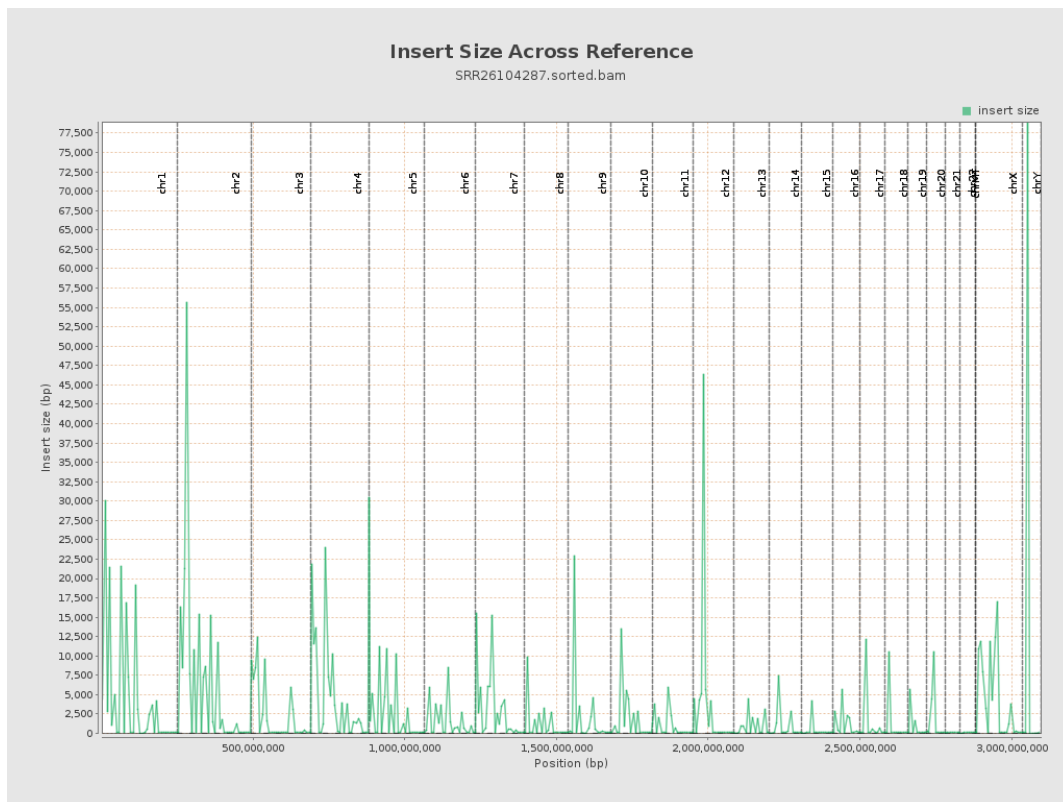
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

