

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/05 02:03:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR26104288.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_SRR26104288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR26104288_1.fastq.gz SRR26104288_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 05 02:03:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR26104288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	157,308,262
Mapped reads	154,218,127 / 98.04%
Unmapped reads	3,090,135 / 1.96%
Mapped paired reads	154,218,127 / 98.04%
Mapped reads, first in pair	77,736,841 / 49.42%
Mapped reads, second in pair	76,481,286 / 48.62%
Mapped reads, both in pair	152,683,450 / 97.06%
Mapped reads, singletons	1,534,677 / 0.98%
Secondary alignments	0
Supplementary alignments	151,510 / 0.1%
Read min/max/mean length	30 / 97 / 91.04
Duplicated reads (estimated)	56,762,573 / 36.08%
Duplication rate	30.2%
Clipped reads	36,071,971 / 22.93%

2.2. ACGT Content

Number/percentage of A's	4,099,029,063 / 31.18%
Number/percentage of C's	2,474,157,830 / 18.82%
Number/percentage of T's	4,148,749,673 / 31.55%
Number/percentage of G's	2,419,496,150 / 18.4%
Number/percentage of N's	6,940,761 / 0.05%

GC Percentage	37.22%
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2.3. Coverage

Mean	4.2484
Standard Deviation	38.0928

2.4. Mapping Quality

Mean Mapping Quality	53.07
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2.5. Insert size

Mean	10,457.54
Standard Deviation	955,167.53
P25/Median/P75	96 / 148 / 229

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	81,590,337
Insertions	1,287,405
Mapped reads with at least one insertion	0.82%
Deletions	1,477,971
Mapped reads with at least one deletion	0.94%
Homopolymer indels	44.97%

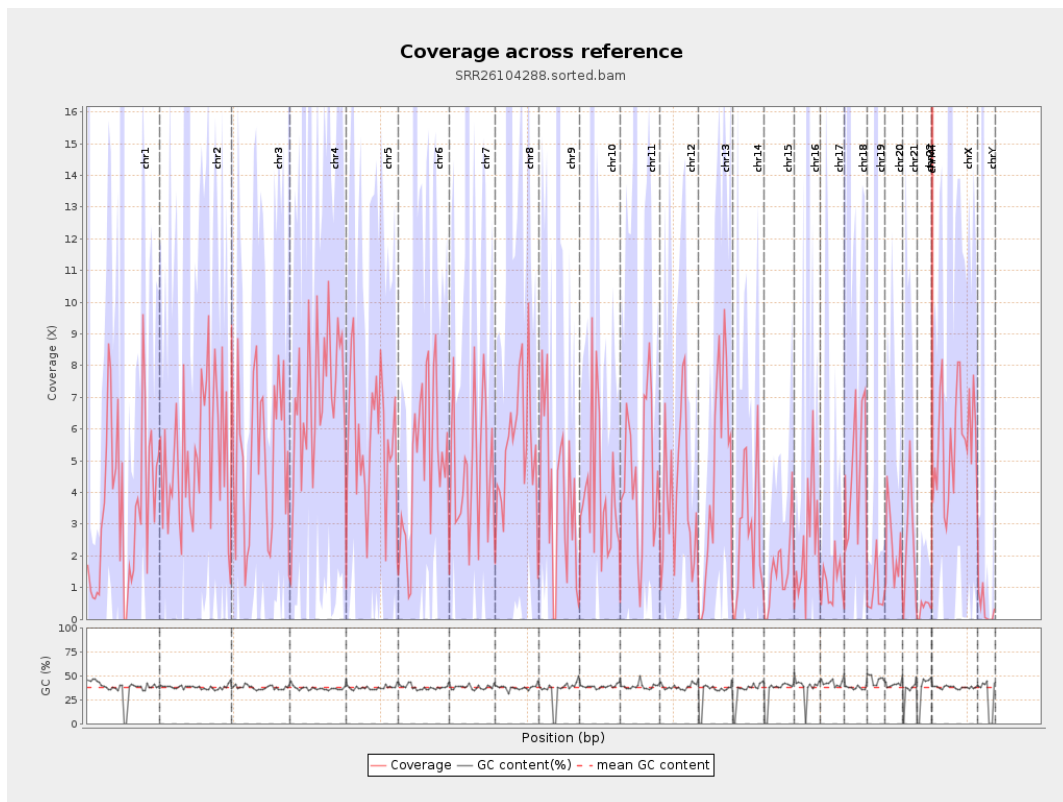
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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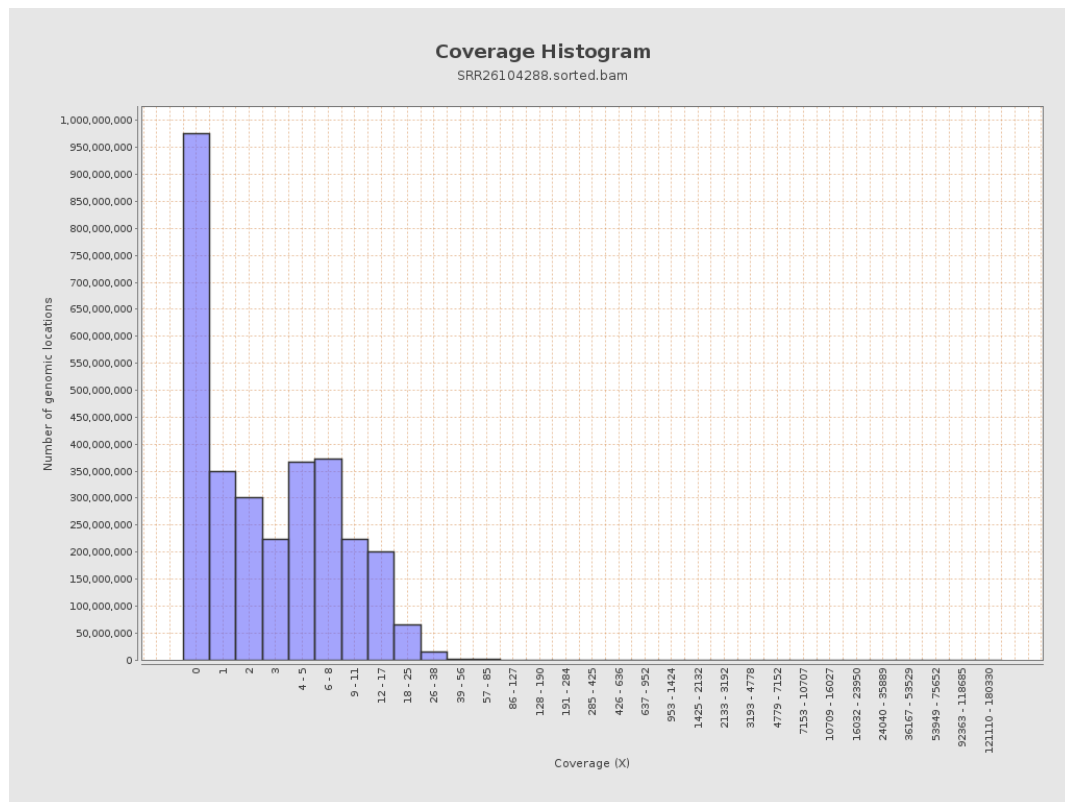
		bases	coverage	deviation
chr1	249250621	892440560	3.5805	54.5308
chr2	243199373	1253191050	5.1529	18.9534
chr3	198022430	1028010734	5.1914	6.5423
chr4	191154276	1337110399	6.9949	14.7529
chr5	180915260	1011496076	5.591	6.292
chr6	171115067	854016247	4.9909	15.0786
chr7	159138663	753433798	4.7344	32.8885
chr8	146364022	803438935	5.4893	112.923
chr9	141213431	525318430	3.72	21.3957
chr10	135534747	545371136	4.0238	47.7703
chr11	135006516	617085002	4.5708	14.962
chr12	133851895	520881176	3.8915	5.5813
chr13	115169878	527797254	4.5828	6.1496
chr14	107349540	298088918	2.7768	5.8169
chr15	102531392	162559805	1.5855	2.8606
chr16	90354753	211490310	2.3407	17.5225
chr17	81195210	90199965	1.1109	6.3542
chr18	78077248	370147637	4.7408	22.6125
chr19	59128983	46378214	0.7844	35.4924
chr20	63025520	139927333	2.2202	5.3005
chr21	48129895	123009244	2.5558	6.6951
chr22	51304566	18793972	0.3663	1.5598
chrMT	16571	121984342	7,361.3145	1,432.3214
chrX	155270560	879452745	5.664	10.0548

chrY	59373566	19983896	0.3366	11.4831
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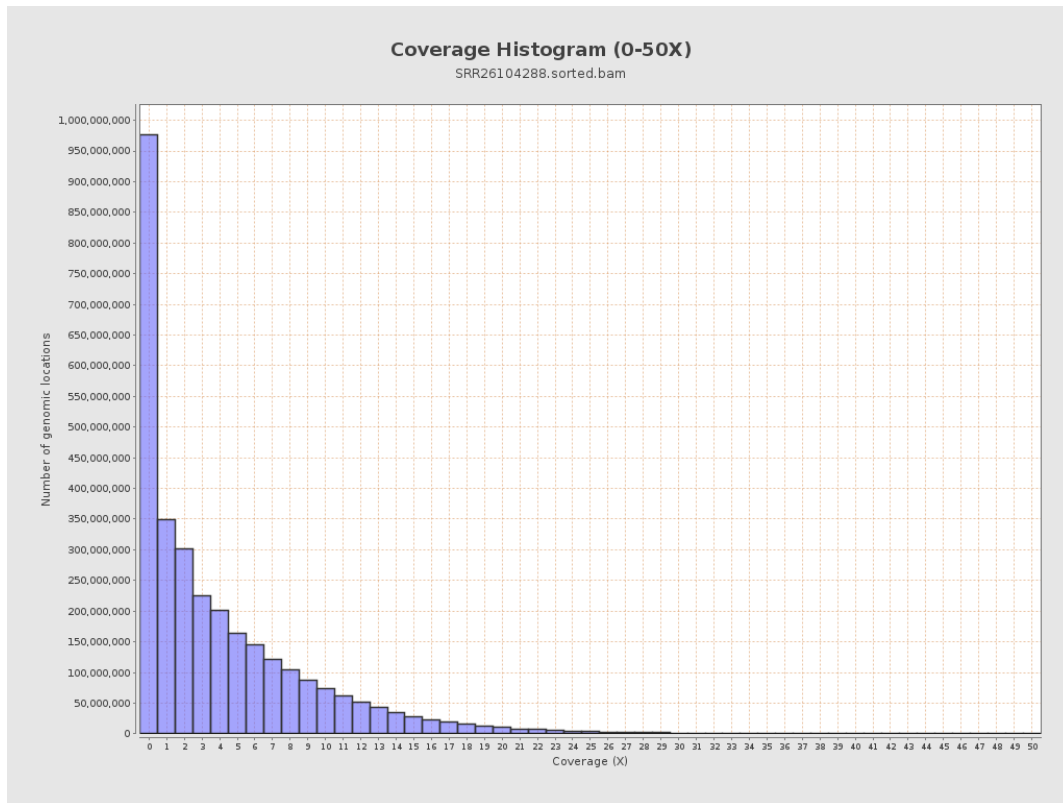
3. Results : Coverage across reference



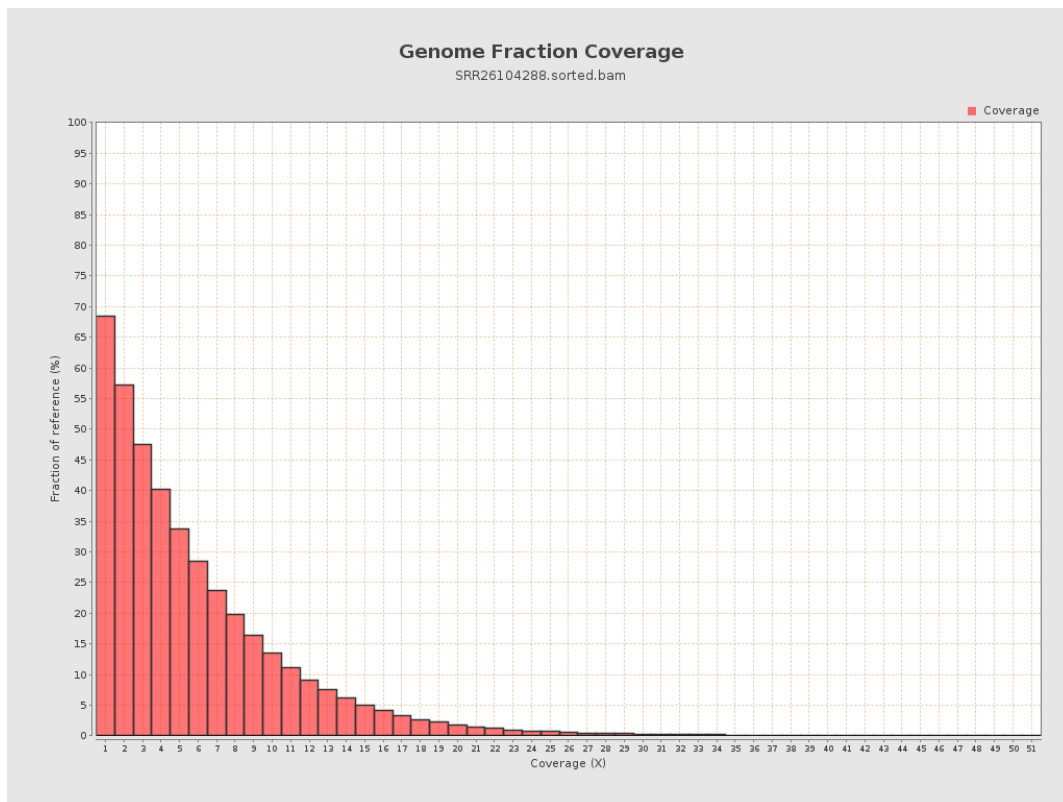
4. Results : Coverage Histogram



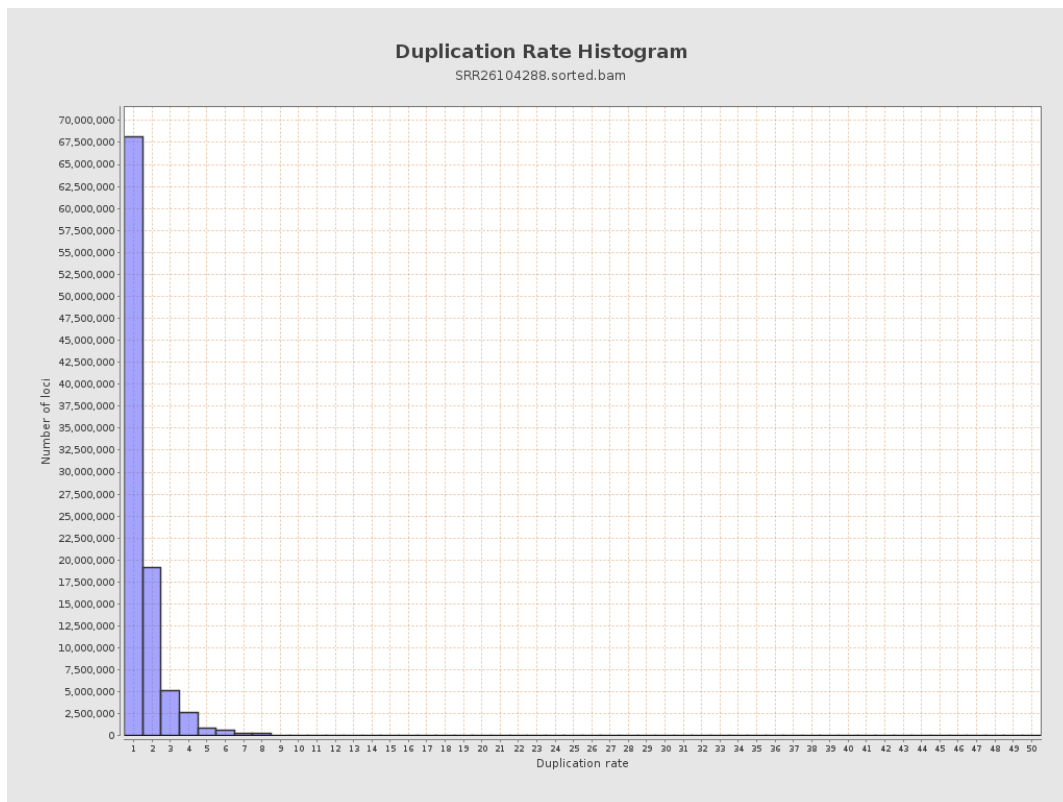
5. Results : Coverage Histogram (0-50X)



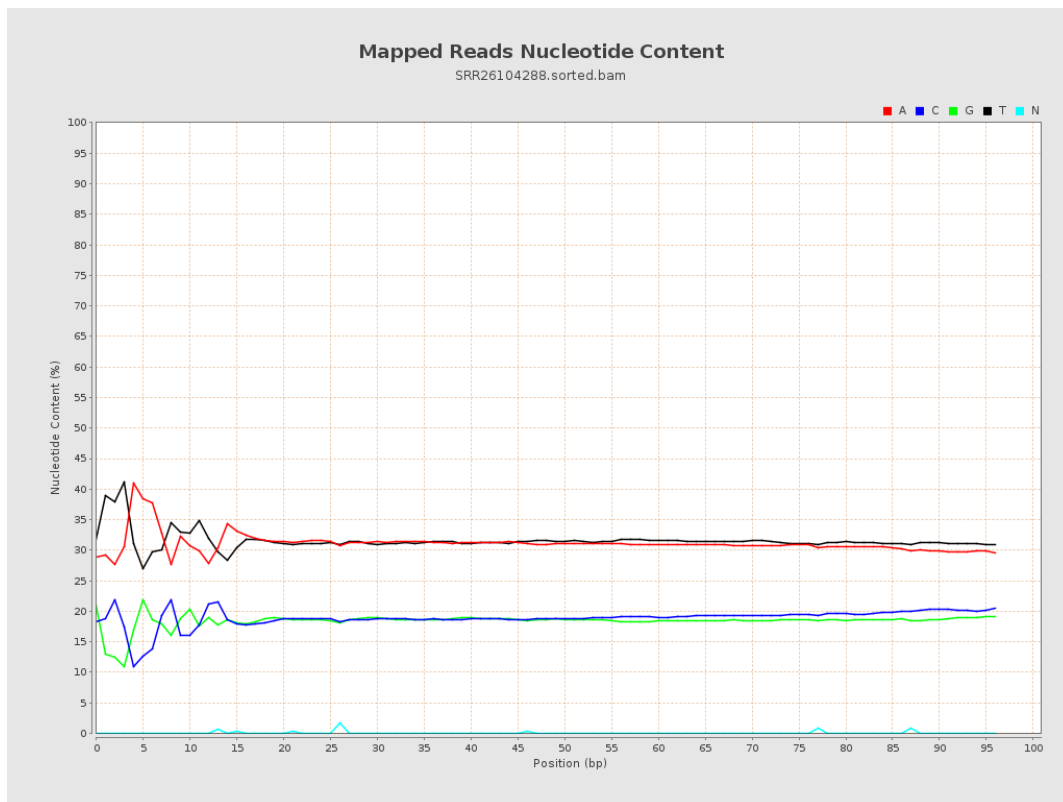
6. Results : Genome Fraction Coverage



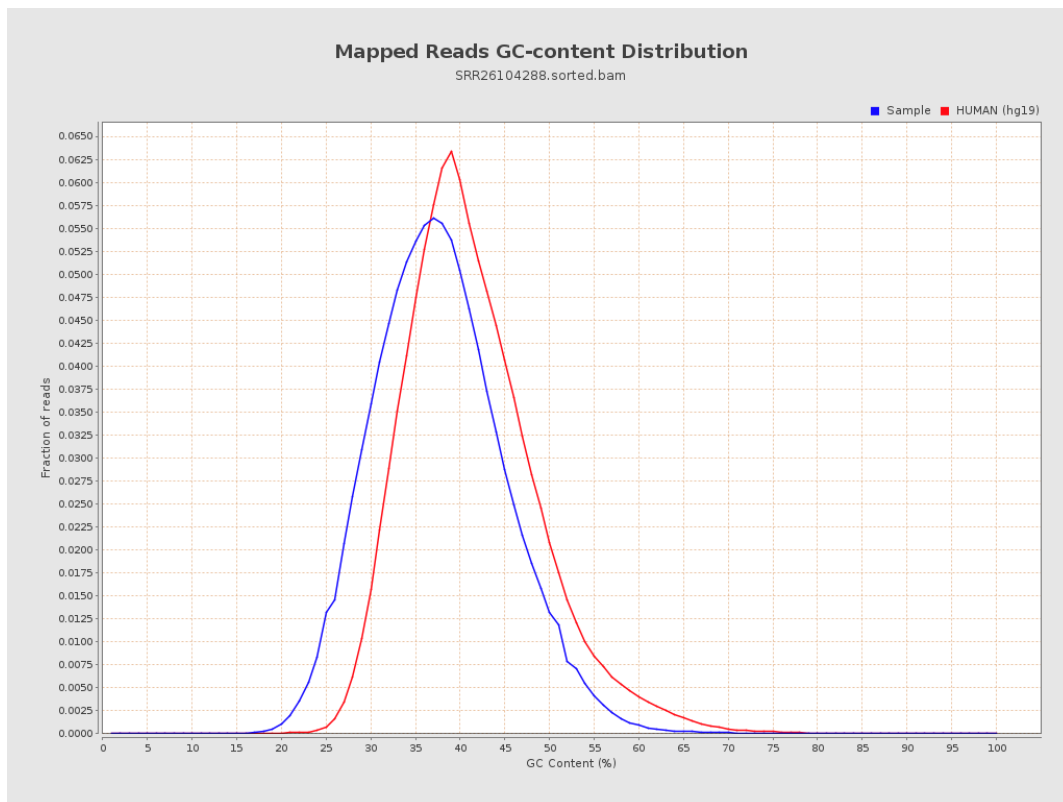
7. Results : Duplication Rate Histogram



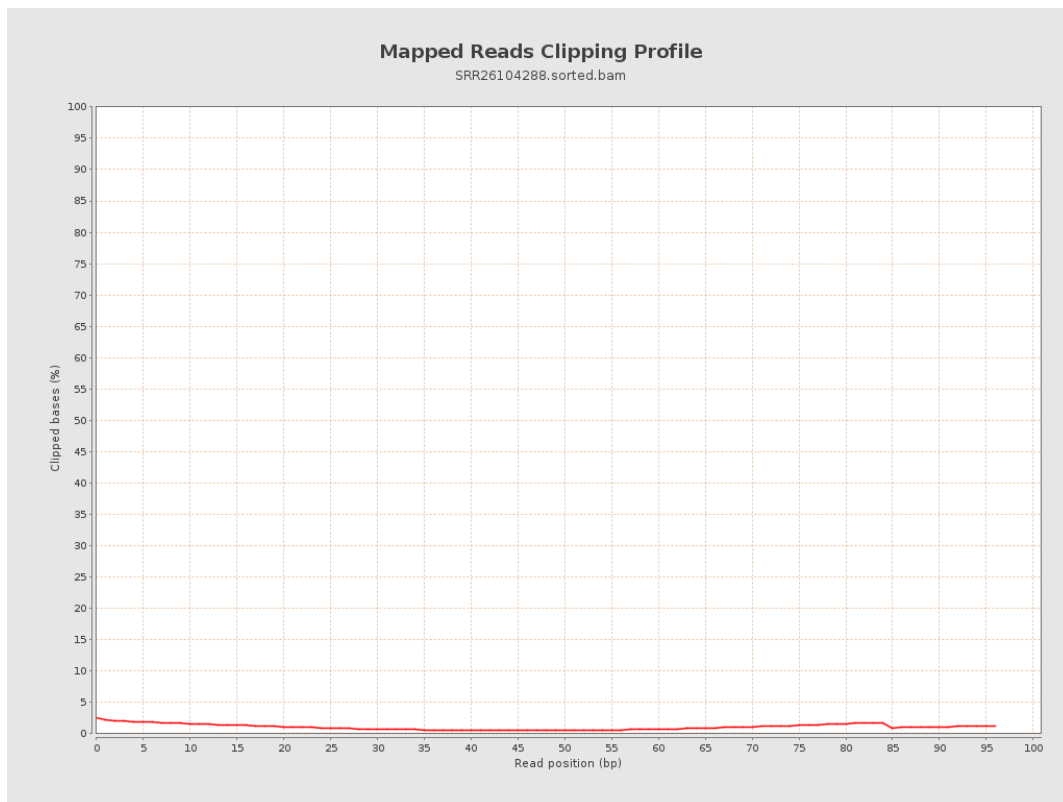
8. Results : Mapped Reads Nucleotide Content



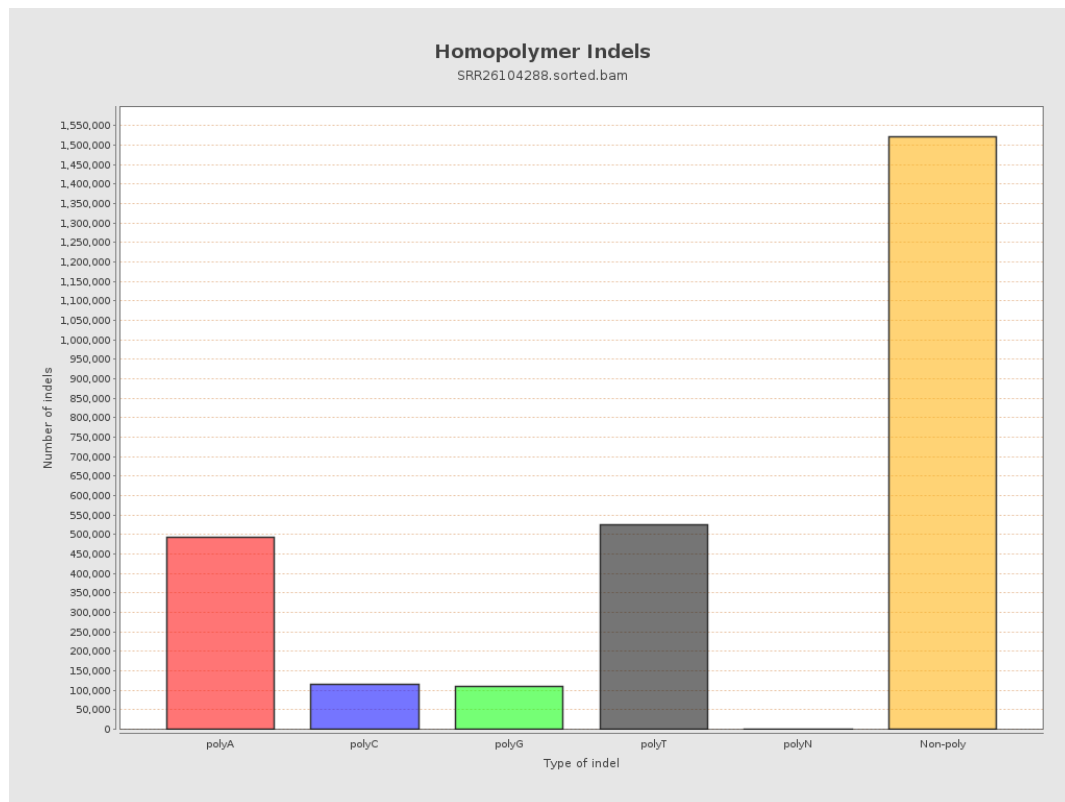
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



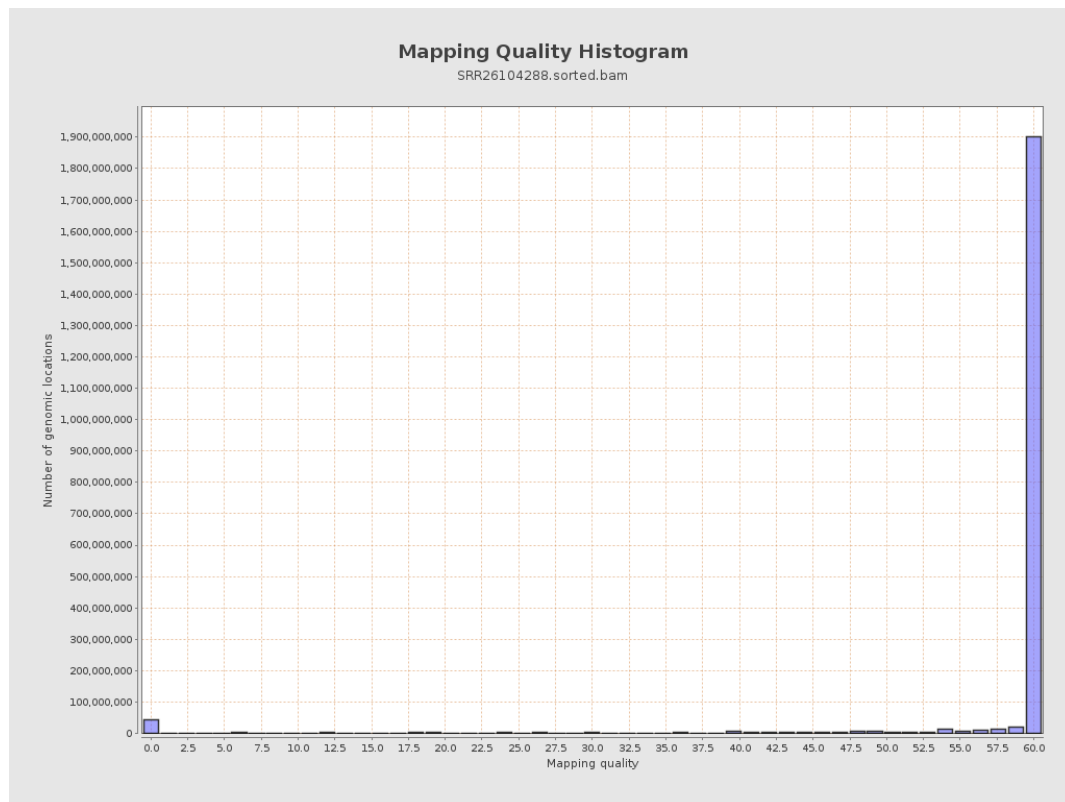
11. Results : Homopolymer Indels



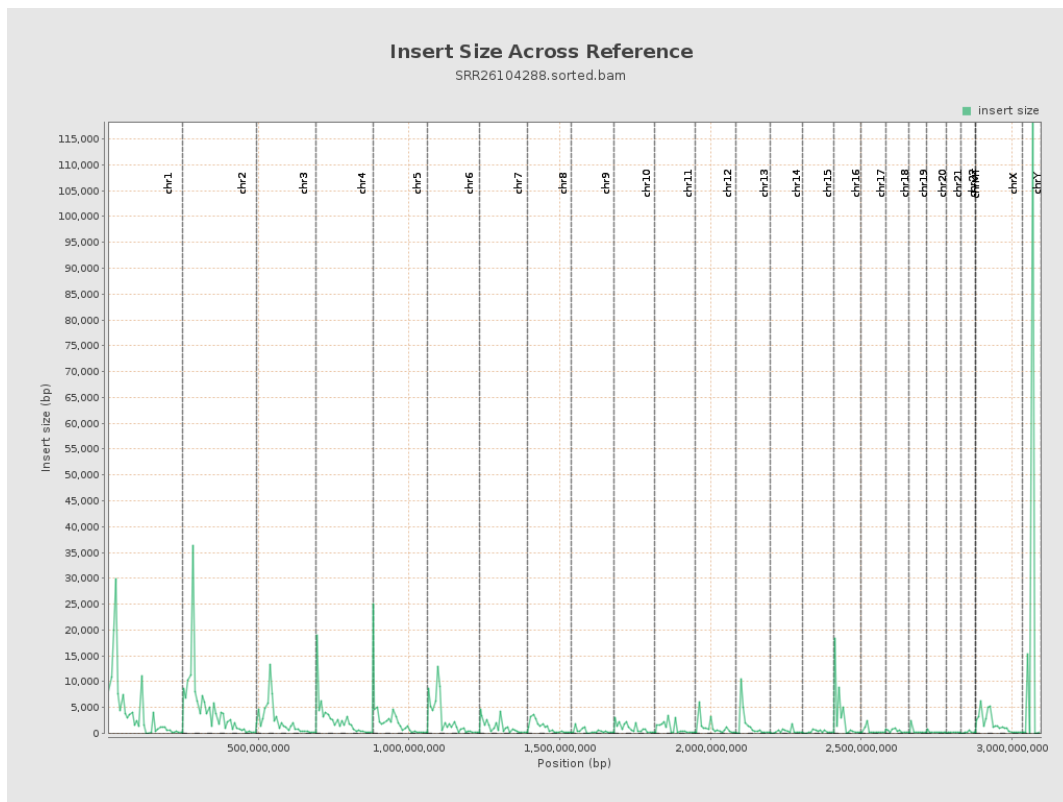
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

