

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/26 16:20:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671988.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_SRR21671988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671988_1.fastq.gz SRR21671988_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 26 16:20:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	300,462,430
Mapped reads	187,840,387 / 62.52%
Unmapped reads	112,622,043 / 37.48%
Mapped paired reads	187,840,387 / 62.52%
Mapped reads, first in pair	93,921,205 / 31.26%
Mapped reads, second in pair	93,919,182 / 31.26%
Mapped reads, both in pair	186,151,848 / 61.96%
Mapped reads, singletons	1,688,539 / 0.56%
Secondary alignments	0
Supplementary alignments	1,301,180 / 0.43%
Read min/max/mean length	15 / 150 / 149.75
Duplicated reads (estimated)	43,978,133 / 14.64%
Duplication rate	19.97%
Clipped reads	10,561,493 / 3.52%

2.2. ACGT Content

Number/percentage of A's	8,165,943,898 / 29.38%
Number/percentage of C's	5,755,153,068 / 20.71%
Number/percentage of T's	8,104,673,101 / 29.16%
Number/percentage of G's	5,765,024,816 / 20.74%
Number/percentage of N's	238,552 / 0%

GC Percentage	41.45%
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2.3. Coverage

Mean	8.9812
Standard Deviation	87.4992

2.4. Mapping Quality

Mean Mapping Quality	54.47
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2.5. Insert size

Mean	110,361.5
Standard Deviation	3,212,764.64
P25/Median/P75	310 / 363 / 415

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	163,198,655
Insertions	4,017,787
Mapped reads with at least one insertion	2.02%
Deletions	4,330,498
Mapped reads with at least one deletion	2.21%
Homopolymer indels	45.78%

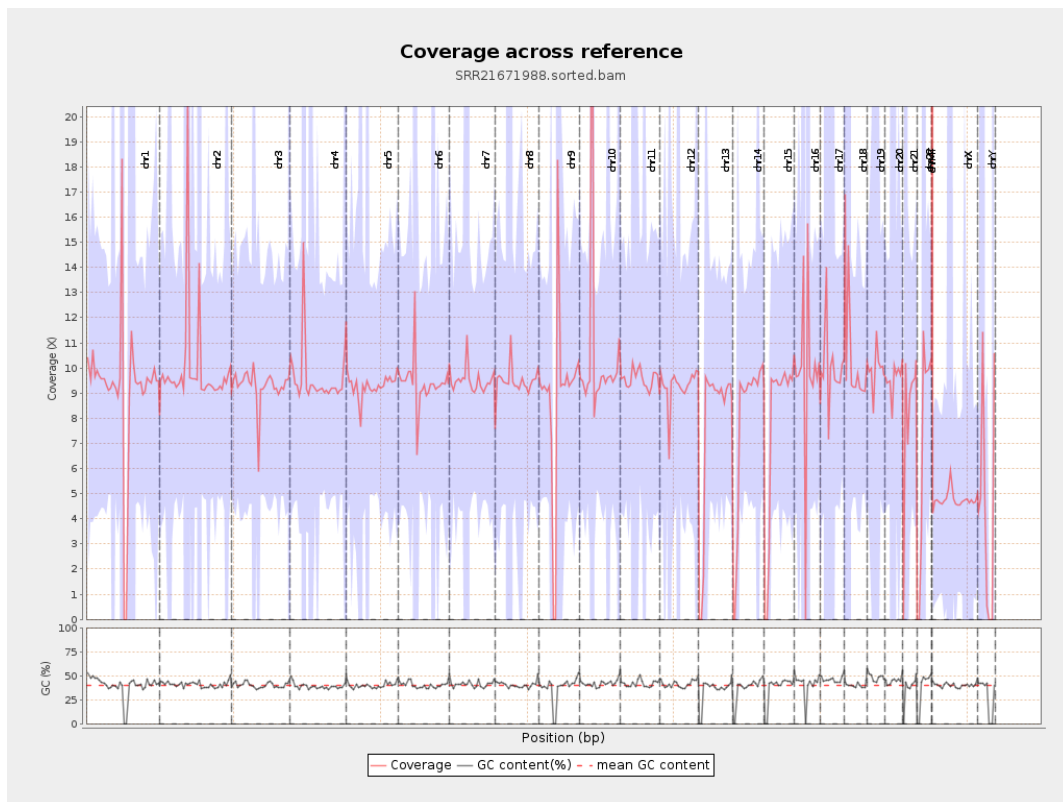
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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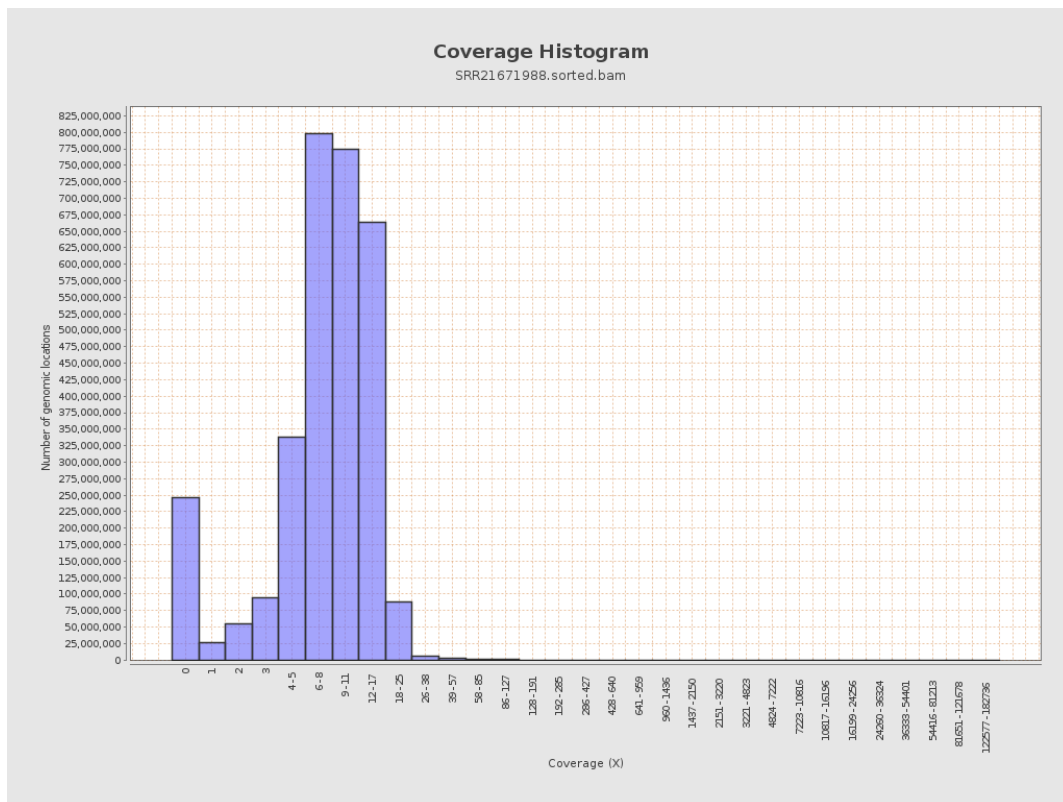
		bases	coverage	deviation
chr1	249250621	2306983198	9.2557	190.2337
chr2	243199373	2427784114	9.9827	64.0398
chr3	198022430	1838000918	9.2818	7.0283
chr4	191154276	1821950127	9.5313	57.1044
chr5	180915260	1682786895	9.3015	8.8607
chr6	171115067	1610237151	9.4103	45.0837
chr7	159138663	1514211436	9.515	52.9854
chr8	146364022	1394533626	9.5278	60.3341
chr9	141213431	1240920709	8.7876	180.58
chr10	135534747	1434889314	10.5869	162.1191
chr11	135006516	1295198255	9.5936	47.0761
chr12	133851895	1239461249	9.2599	9.616
chr13	115169878	886516179	7.6975	6.6547
chr14	107349540	841533081	7.8392	7.974
chr15	102531392	787370968	7.6793	5.858
chr16	90354753	894416025	9.8989	56.5545
chr17	81195210	810949902	9.9877	50.5435
chr18	78077248	798757789	10.2304	149.8336
chr19	59128983	590155721	9.9808	84.1696
chr20	63025520	601384567	9.5419	24.7511
chr21	48129895	400017889	8.3112	36.4741
chr22	51304566	365844155	7.1308	25.8996
chrMT	16571	8627263	520.6242	78.3157
chrX	155270560	739449238	4.7623	16.1273

chrY	59373566	271019023	4.5646	77.7409
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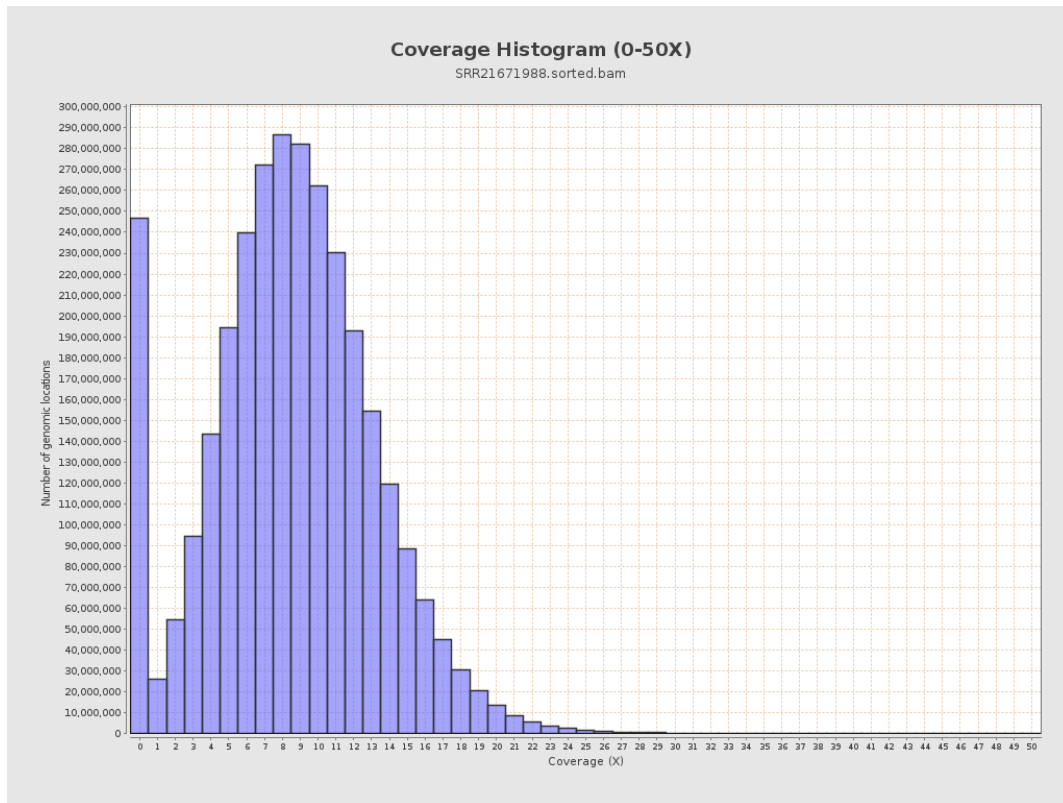
3. Results : Coverage across reference



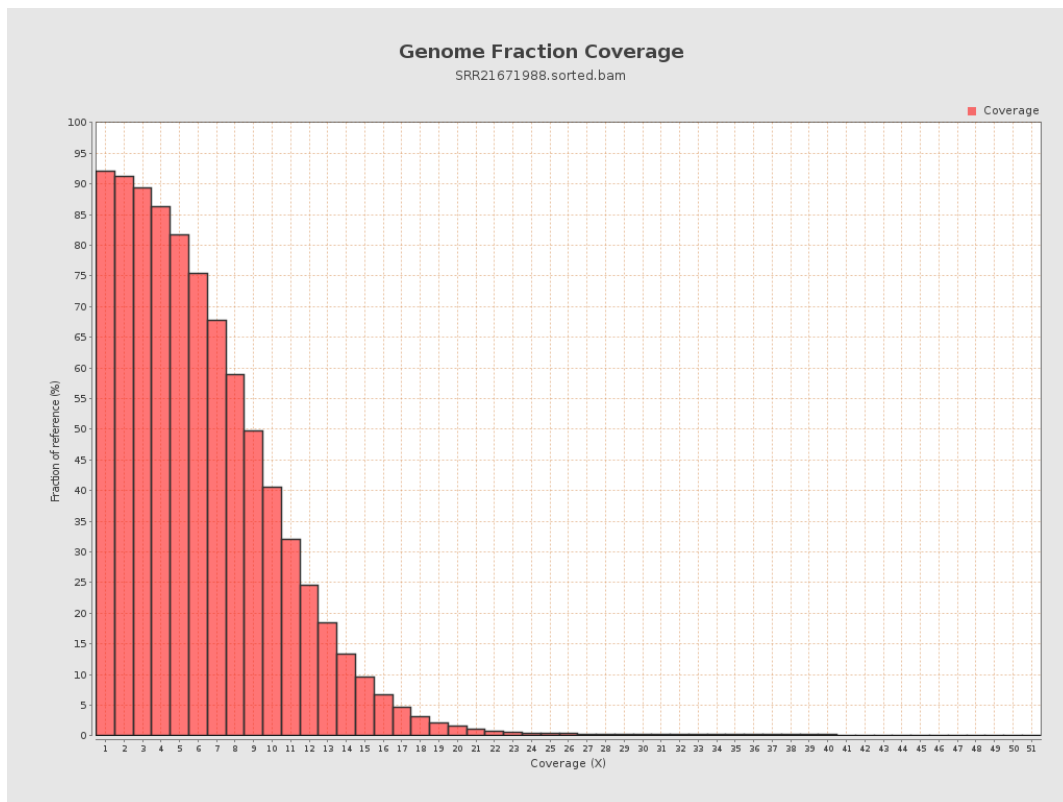
4. Results : Coverage Histogram



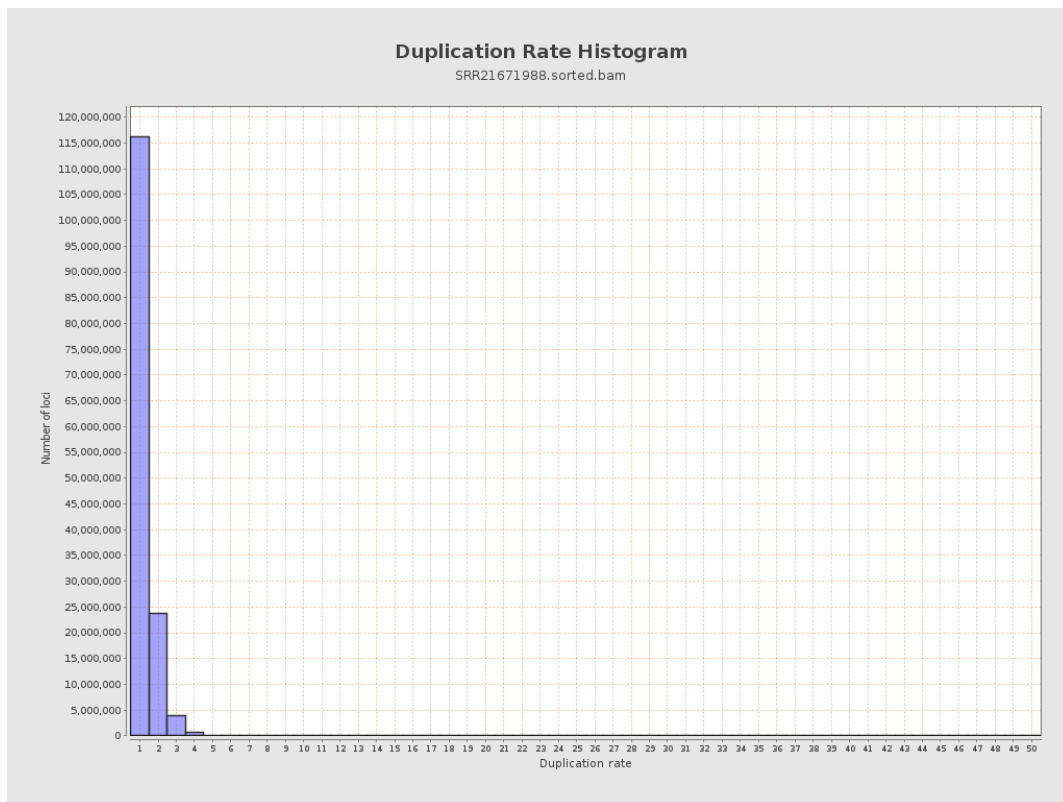
5. Results : Coverage Histogram (0-50X)



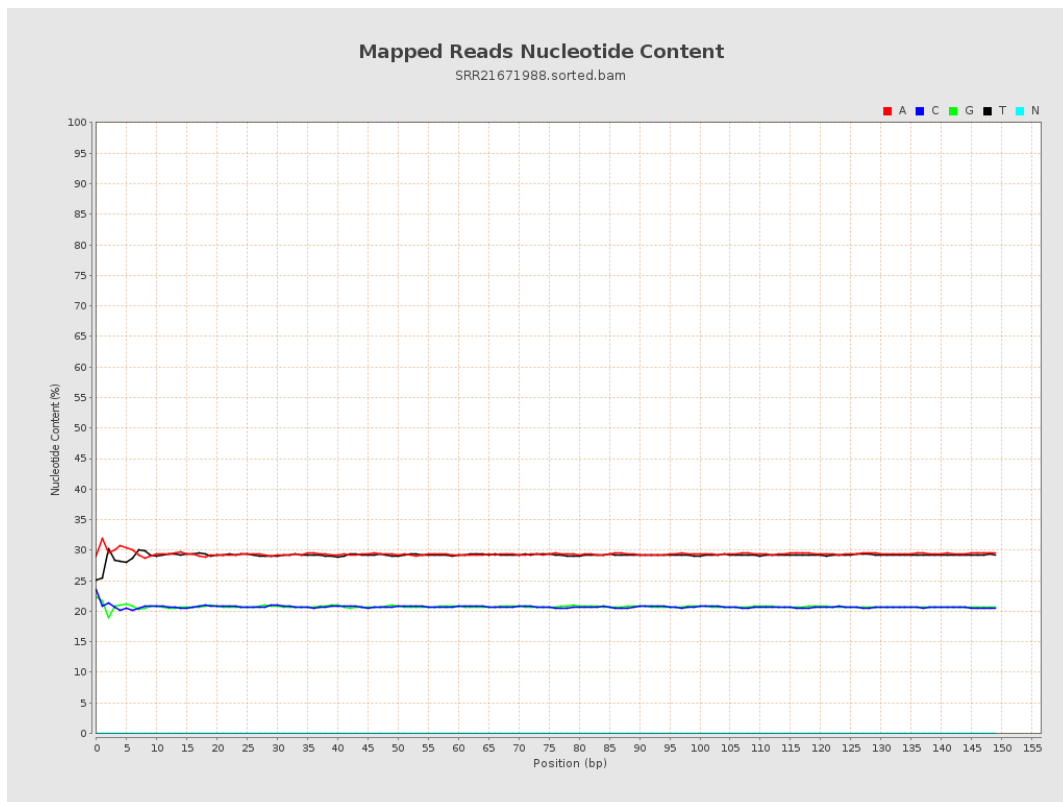
6. Results : Genome Fraction Coverage



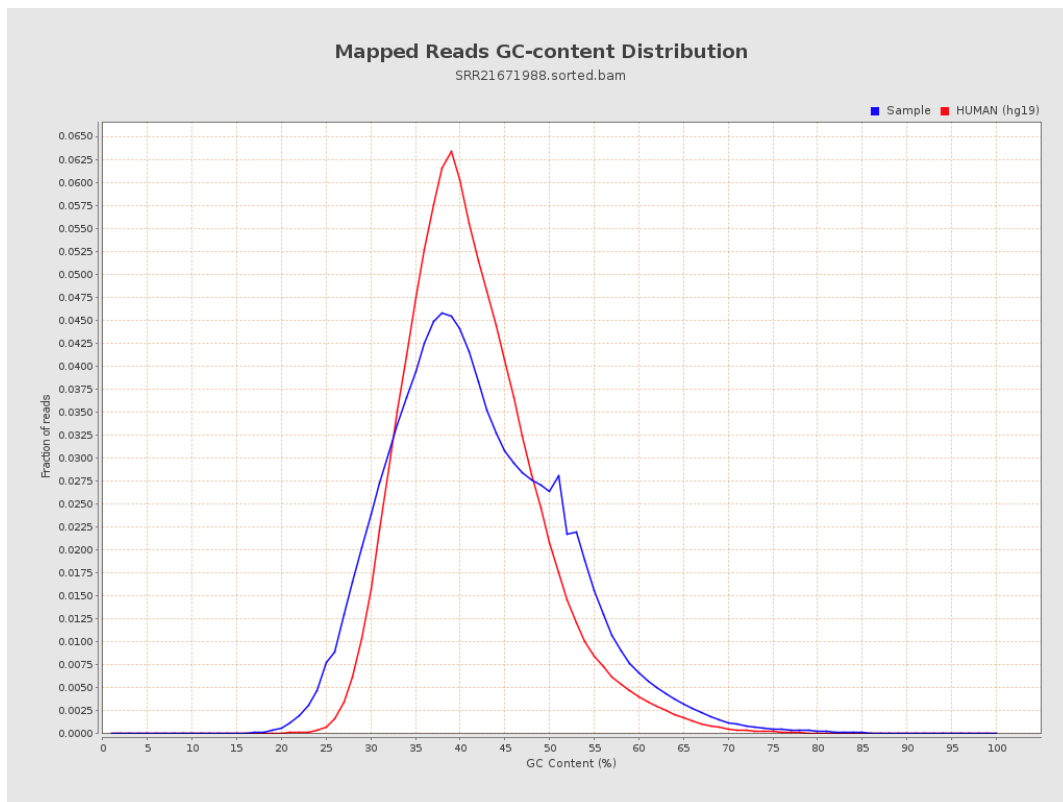
7. Results : Duplication Rate Histogram



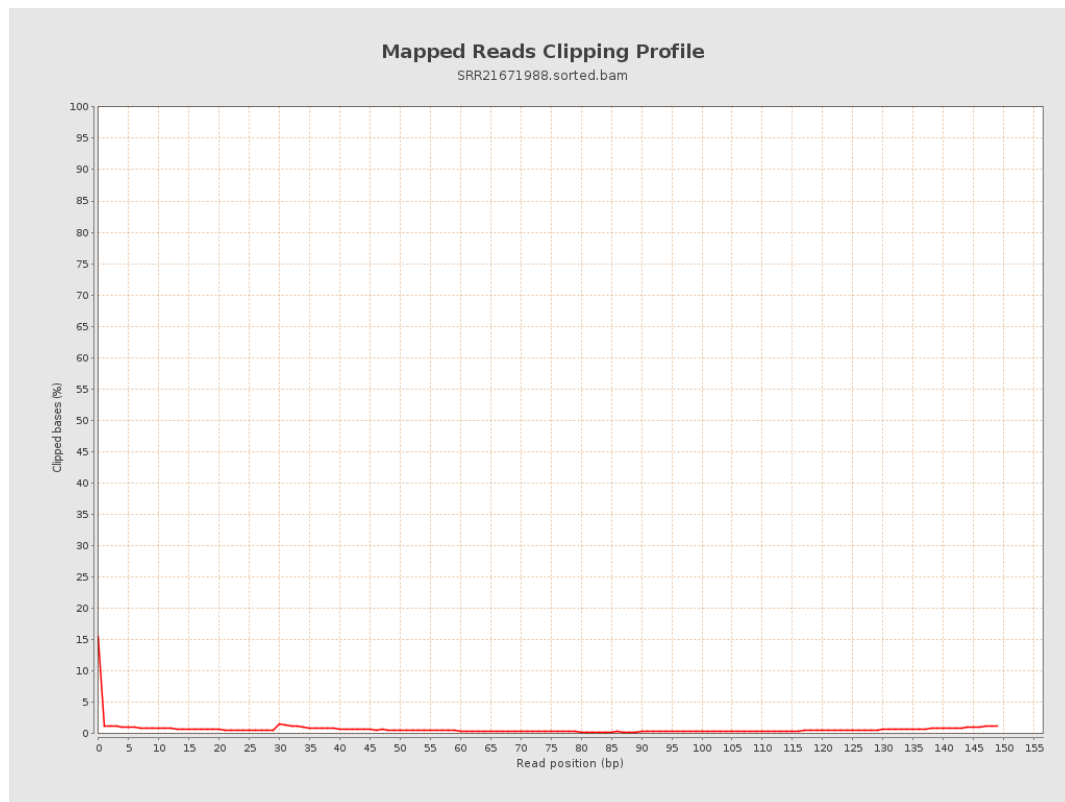
8. Results : Mapped Reads Nucleotide Content



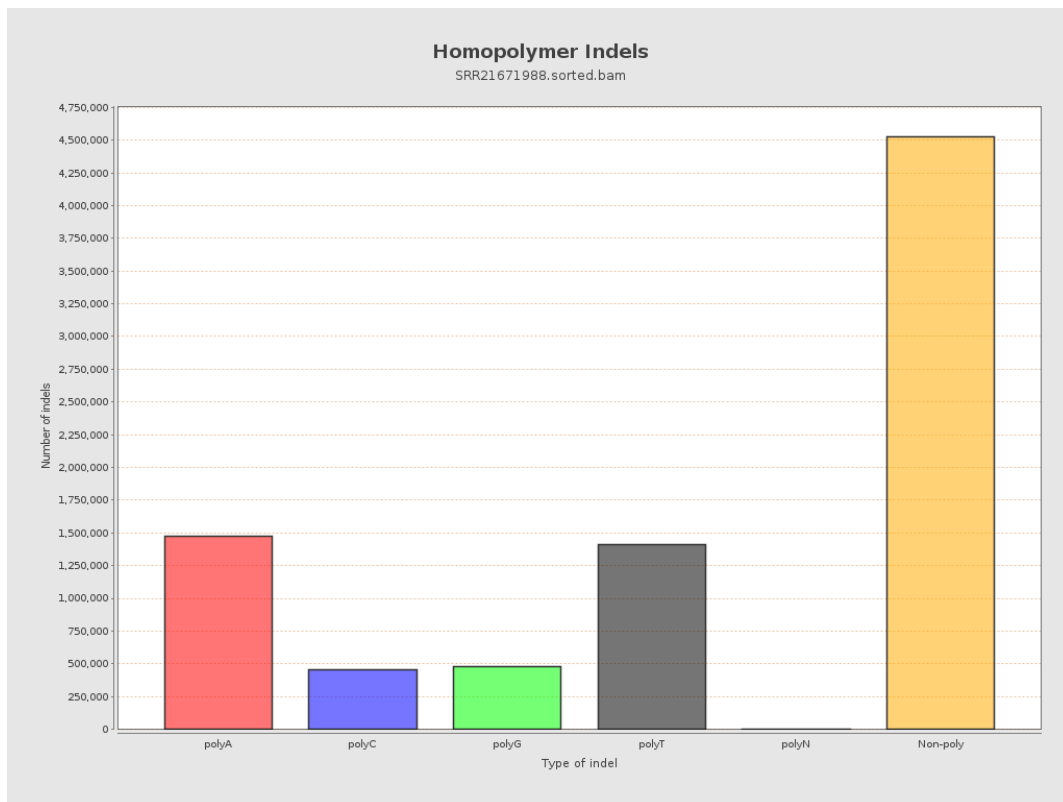
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



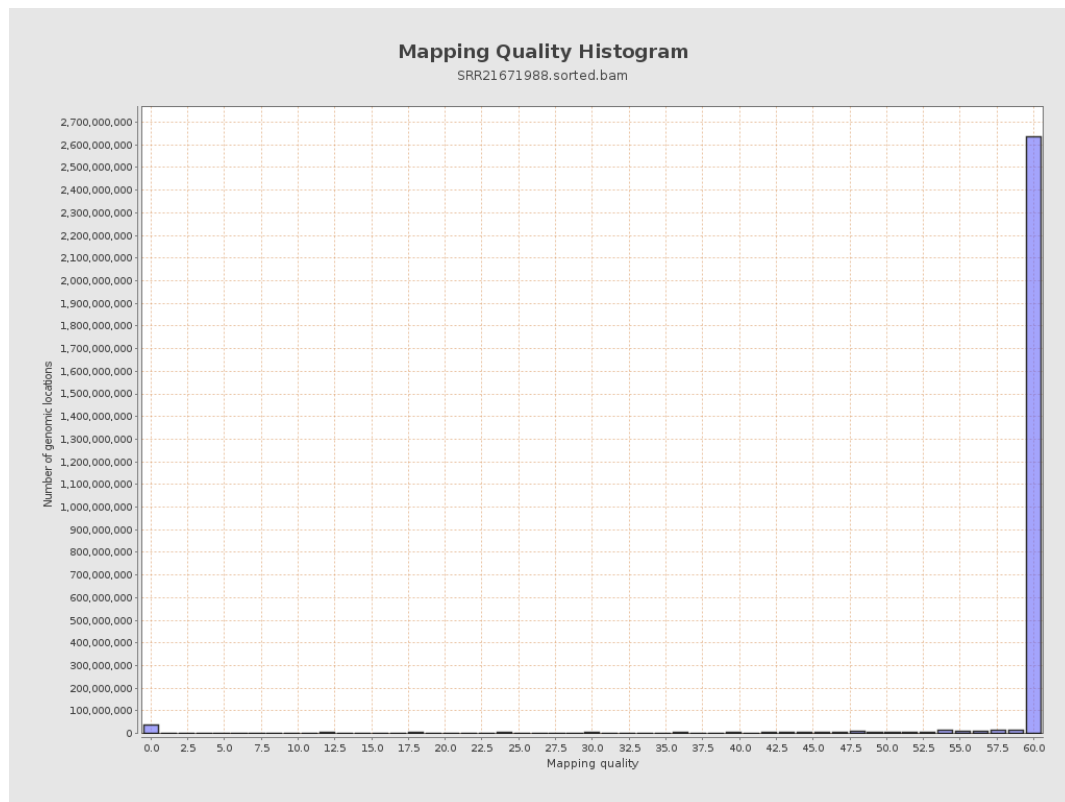
11. Results : Homopolymer Indels



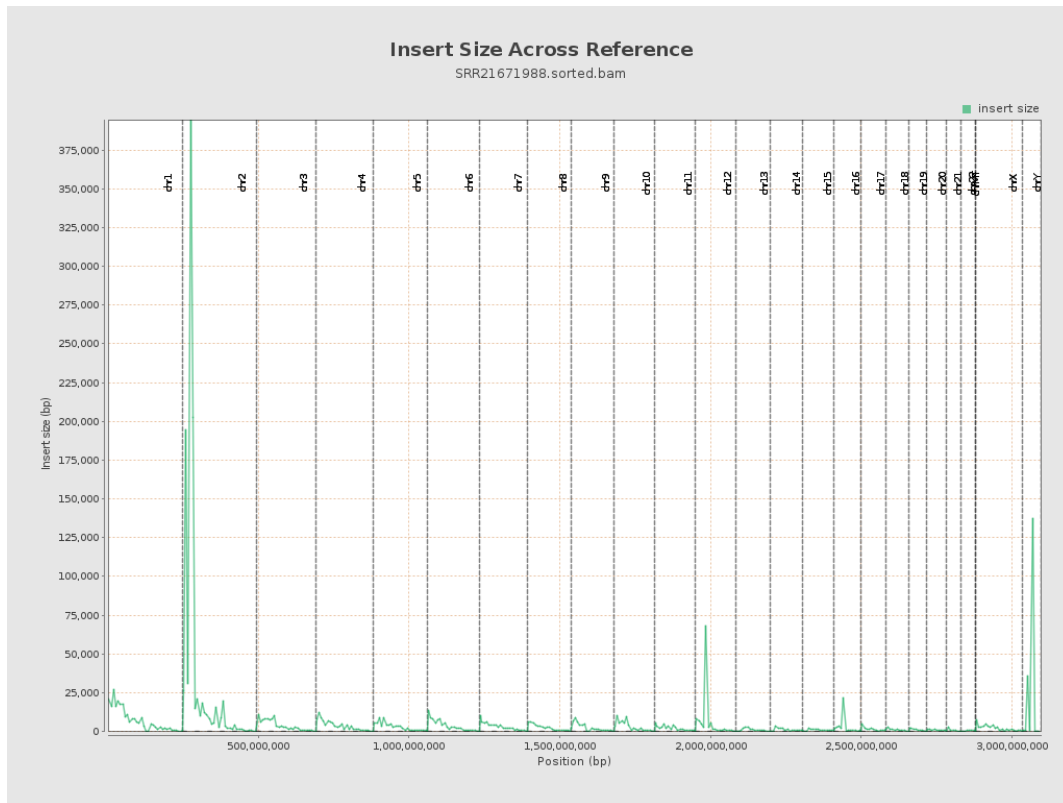
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

