

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 06:21:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21671990.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_SRR21671990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21671990_1.fastq.gz SRR21671990_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 06:21:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21671990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	299,983,516
Mapped reads	298,549,094 / 99.52%
Unmapped reads	1,434,422 / 0.48%
Mapped paired reads	298,549,094 / 99.52%
Mapped reads, first in pair	149,307,363 / 49.77%
Mapped reads, second in pair	149,241,731 / 49.75%
Mapped reads, both in pair	298,021,140 / 99.35%
Mapped reads, singletons	527,954 / 0.18%
Secondary alignments	0
Supplementary alignments	1,279,015 / 0.43%
Read min/max/mean length	15 / 150 / 149.68
Duplicated reads (estimated)	74,074,898 / 24.69%
Duplication rate	21.52%
Clipped reads	13,318,260 / 4.44%

2.2. ACGT Content

Number/percentage of A's	12,966,135,106 / 29.28%
Number/percentage of C's	9,203,078,297 / 20.78%
Number/percentage of T's	12,887,154,337 / 29.1%
Number/percentage of G's	9,228,406,428 / 20.84%
Number/percentage of N's	376,721 / 0%

GC Percentage	41.62%
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2.3. Coverage

Mean	14.3112
Standard Deviation	149.0137

2.4. Mapping Quality

Mean Mapping Quality	54.56
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2.5. Insert size

Mean	75,506.53
Standard Deviation	2,650,567.22
P25/Median/P75	297 / 346 / 395

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	257,276,749
Insertions	5,959,861
Mapped reads with at least one insertion	1.89%
Deletions	6,510,727
Mapped reads with at least one deletion	2.09%
Homopolymer indels	45.79%

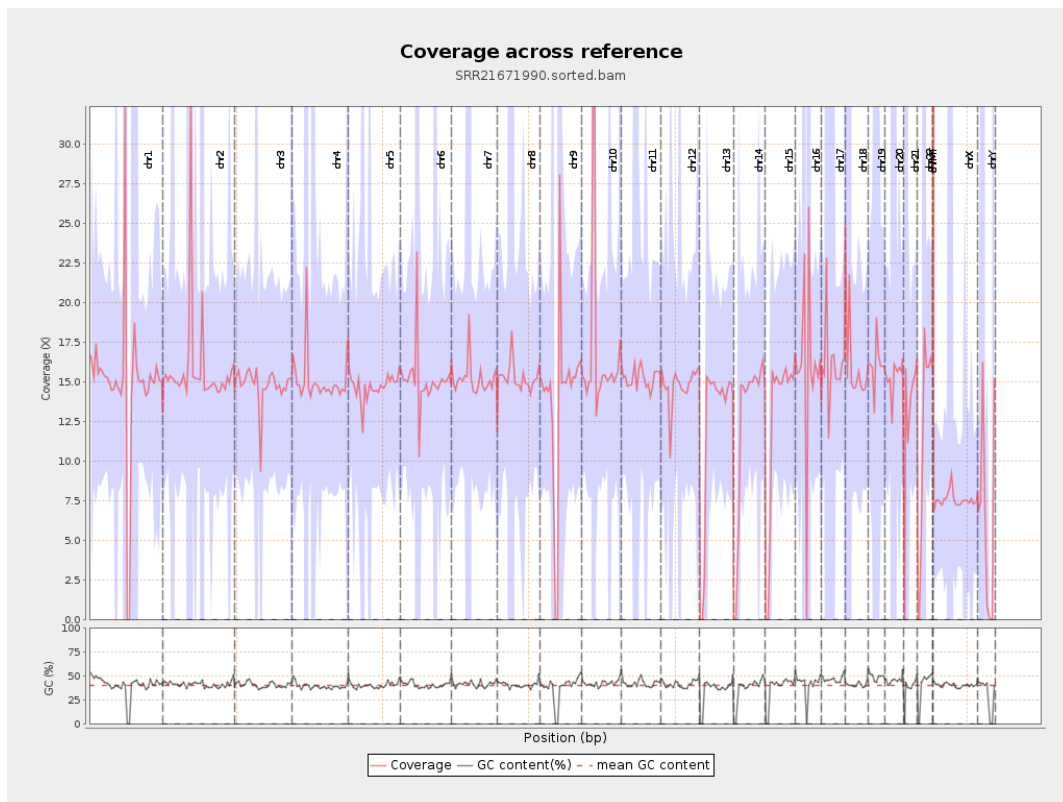
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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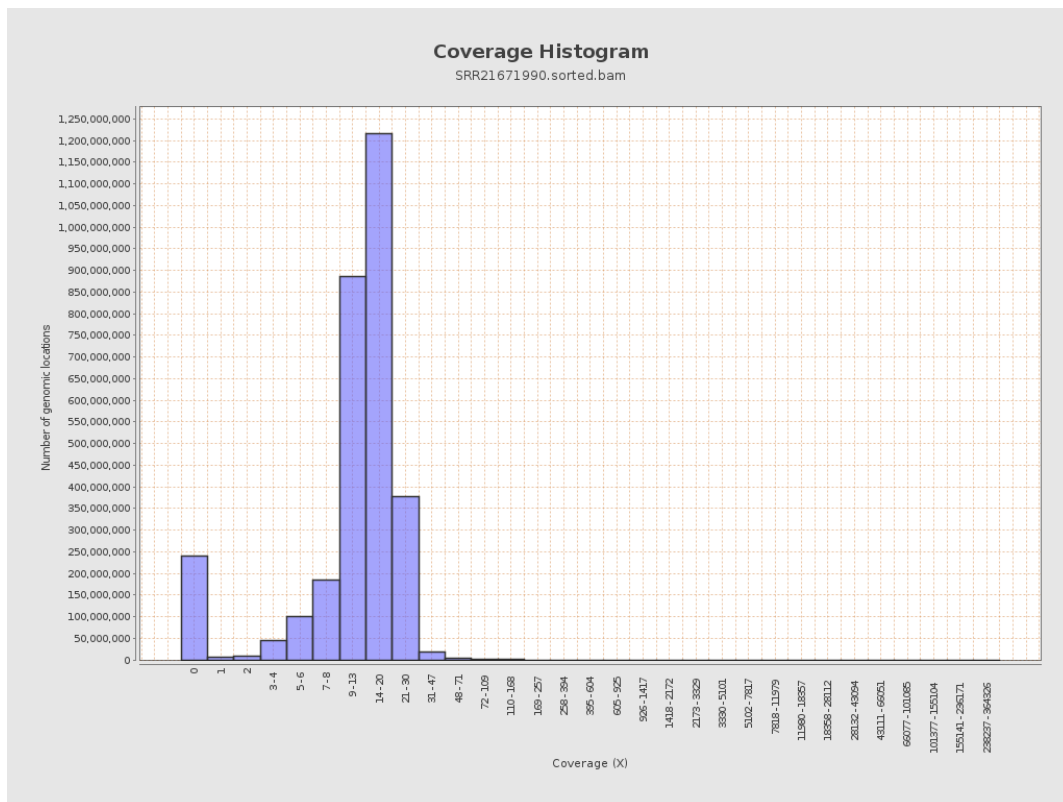
		bases	coverage	deviation
chr1	249250621	3707735041	14.8755	371.0069
chr2	243199373	3842970877	15.8017	97.2151
chr3	198022430	2927436419	14.7834	9.067
chr4	191154276	2885623519	15.0958	79.4298
chr5	180915260	2663877913	14.7245	11.0795
chr6	171115067	2586845450	15.1176	96.9047
chr7	159138663	2422555450	15.2229	105.4486
chr8	146364022	2234253145	15.265	128.0882
chr9	141213431	1977206096	14.0015	262.4872
chr10	135534747	2256040453	16.6455	233.002
chr11	135006516	2055671911	15.2265	64.1309
chr12	133851895	1976749662	14.7682	11.7999
chr13	115169878	1412939800	12.2683	8.5833
chr14	107349540	1347795711	12.5552	10.9757
chr15	102531392	1274507053	12.4304	8.7247
chr16	90354753	1437578589	15.9104	91.9943
chr17	81195210	1306760079	16.0941	84.8479
chr18	78077248	1251511792	16.0291	205.6558
chr19	59128983	951495456	16.0919	169.1144
chr20	63025520	958994047	15.216	32.0979
chr21	48129895	634971530	13.1929	51.186
chr22	51304566	590768228	11.5149	41.7887
chrMT	16571	23612965	1,424.9572	147.5785
chrX	155270560	1174148486	7.562	23.4657

chrY	59373566	400955524	6.7531	105.6855
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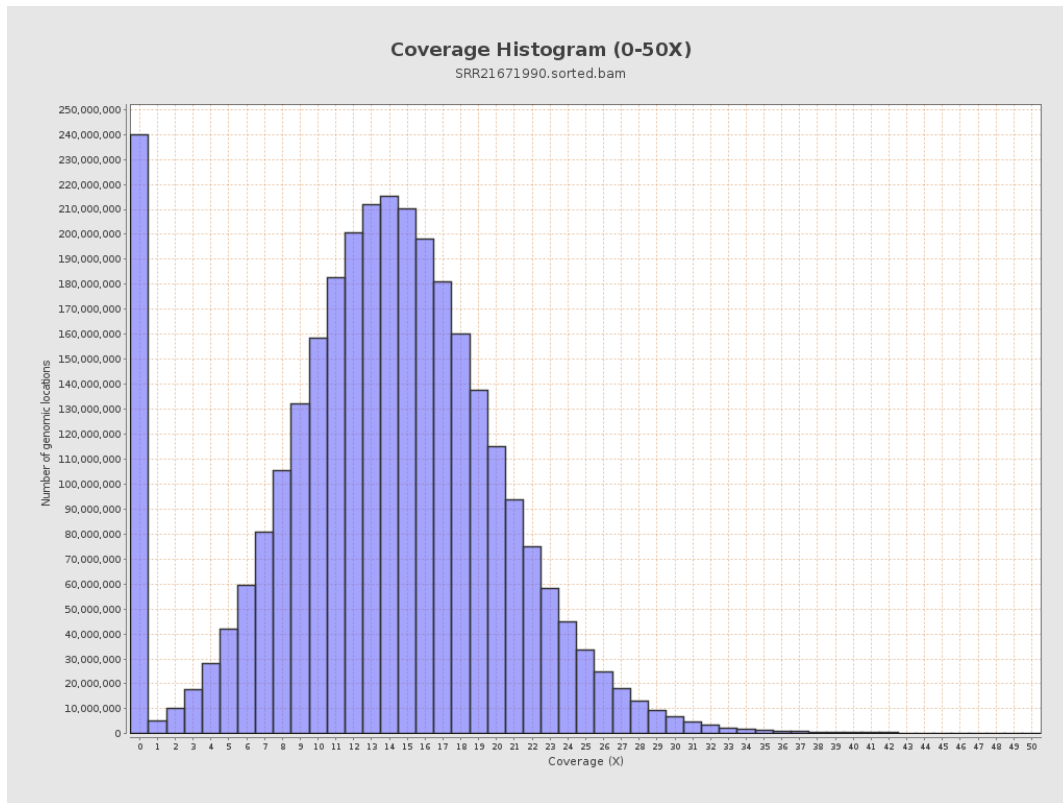
3. Results : Coverage across reference



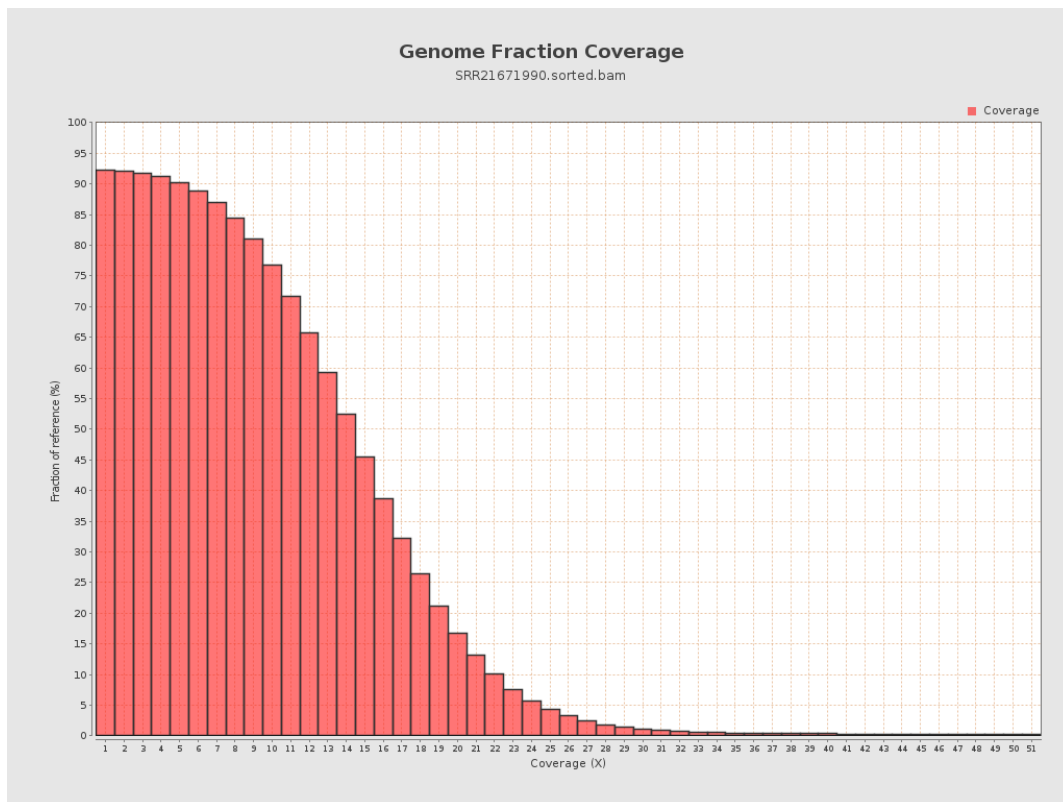
4. Results : Coverage Histogram



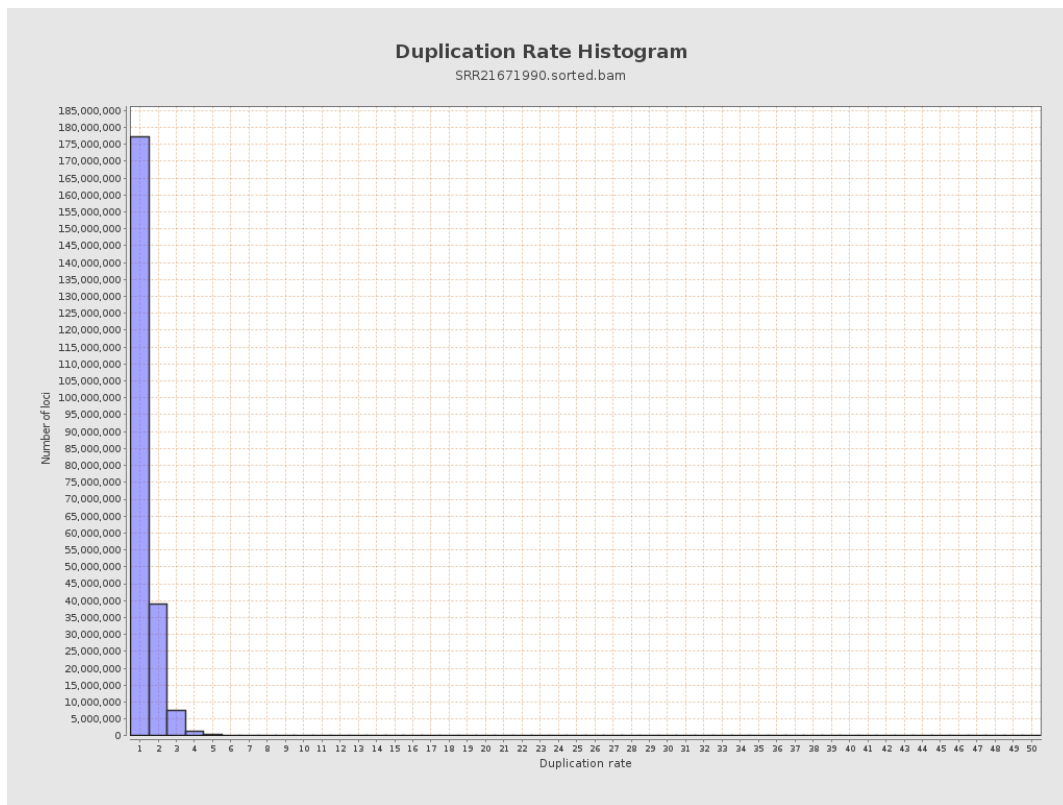
5. Results : Coverage Histogram (0-50X)



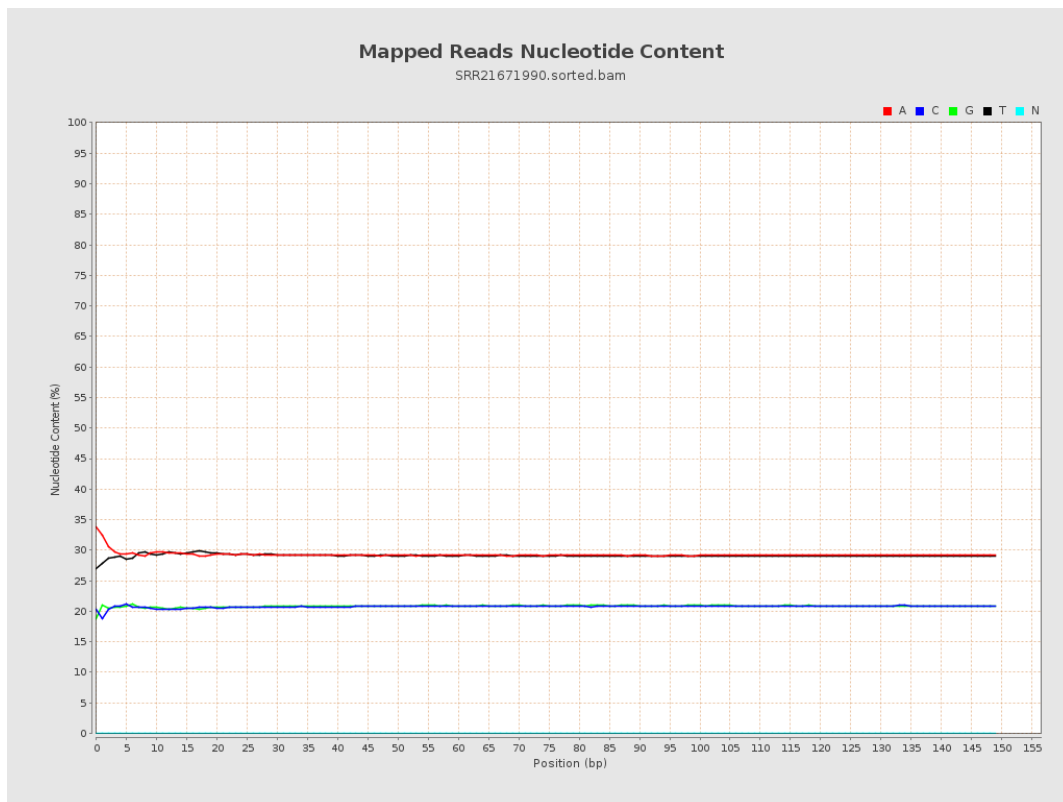
6. Results : Genome Fraction Coverage



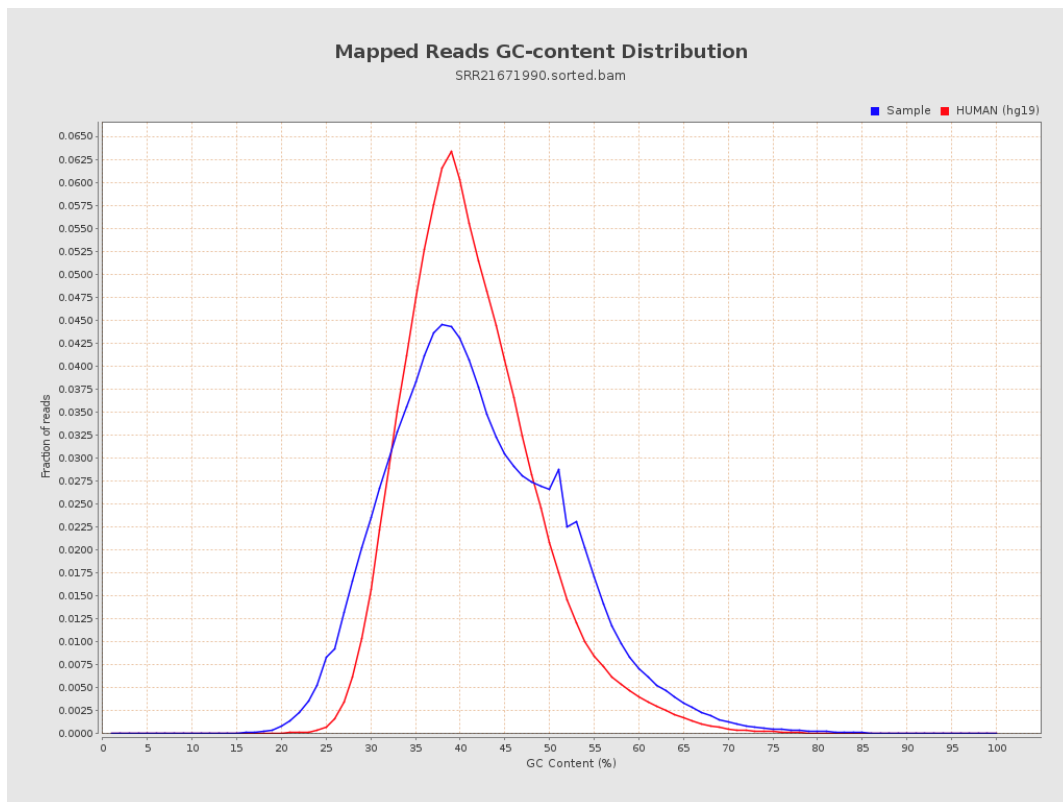
7. Results : Duplication Rate Histogram



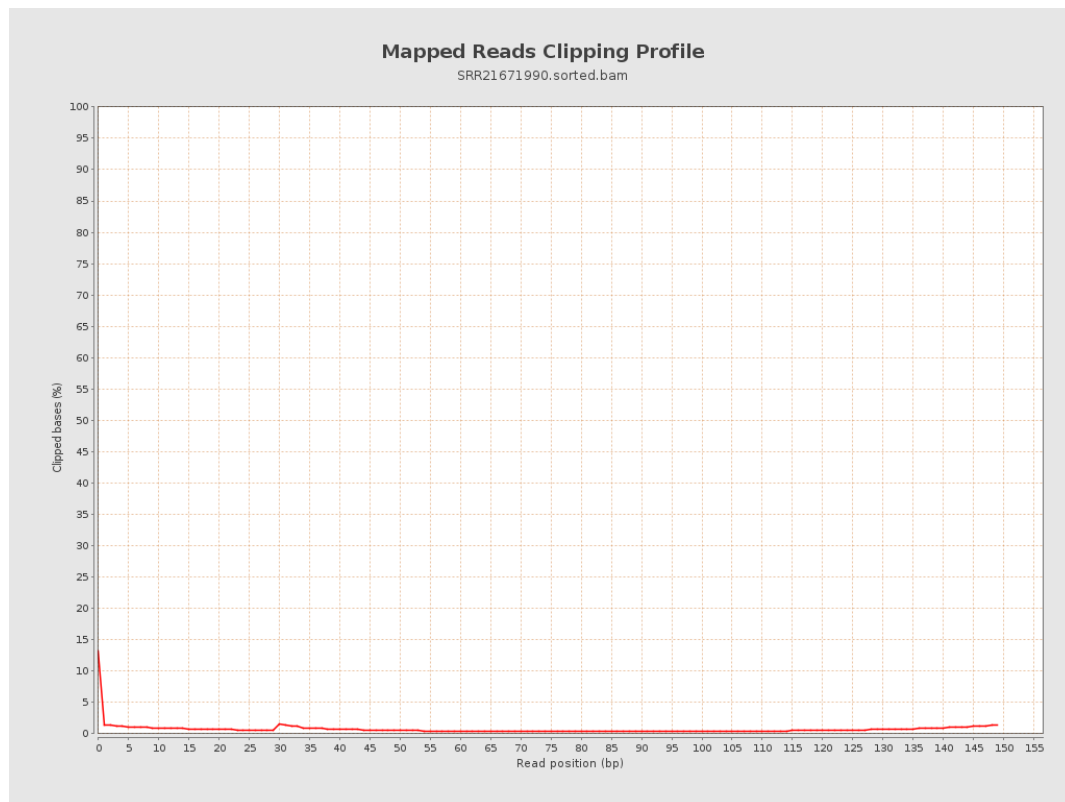
8. Results : Mapped Reads Nucleotide Content



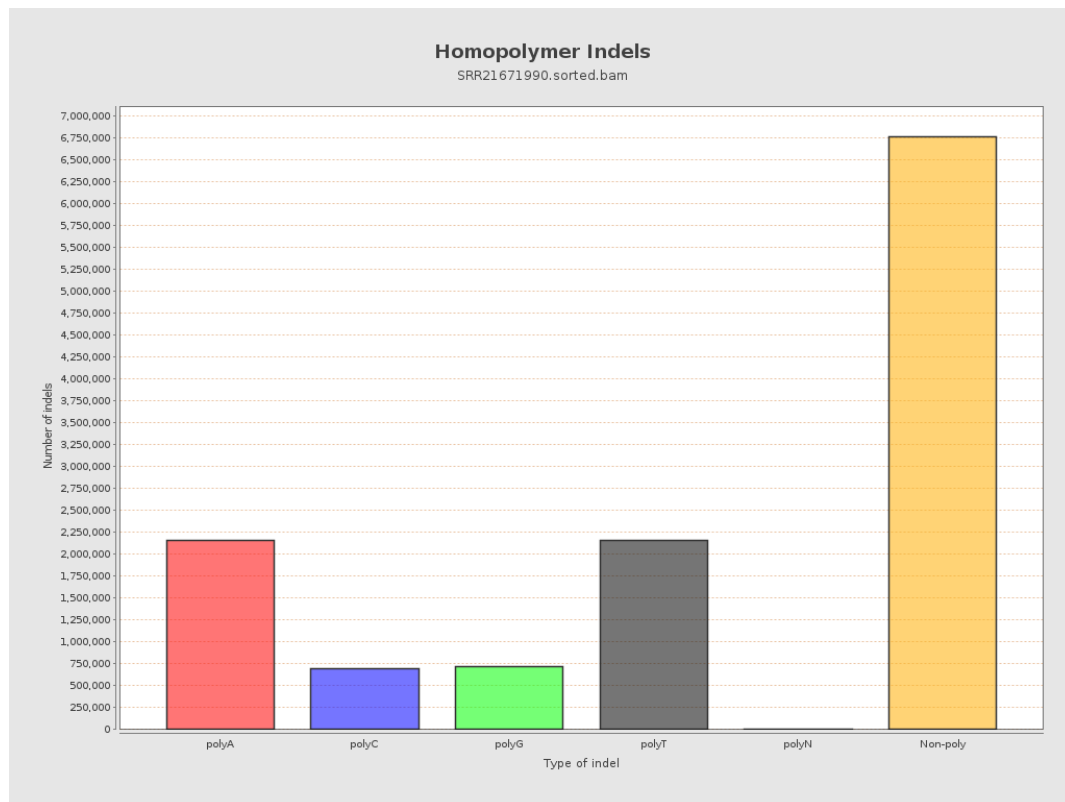
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



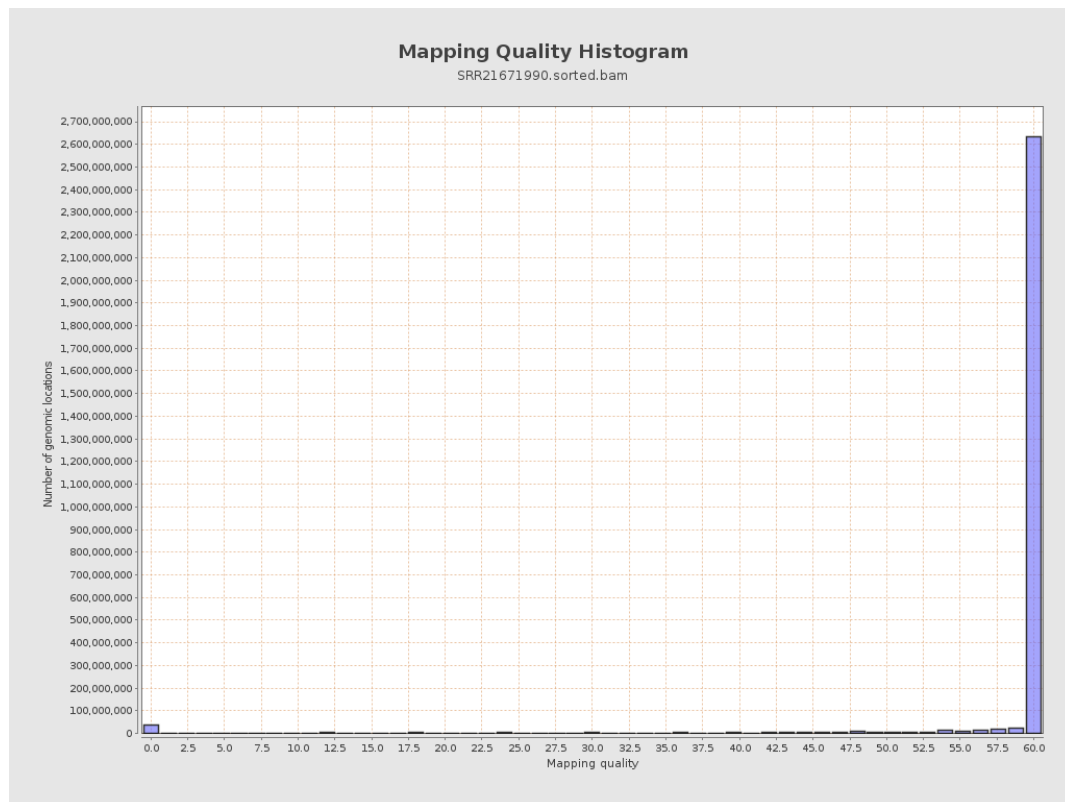
11. Results : Homopolymer Indels



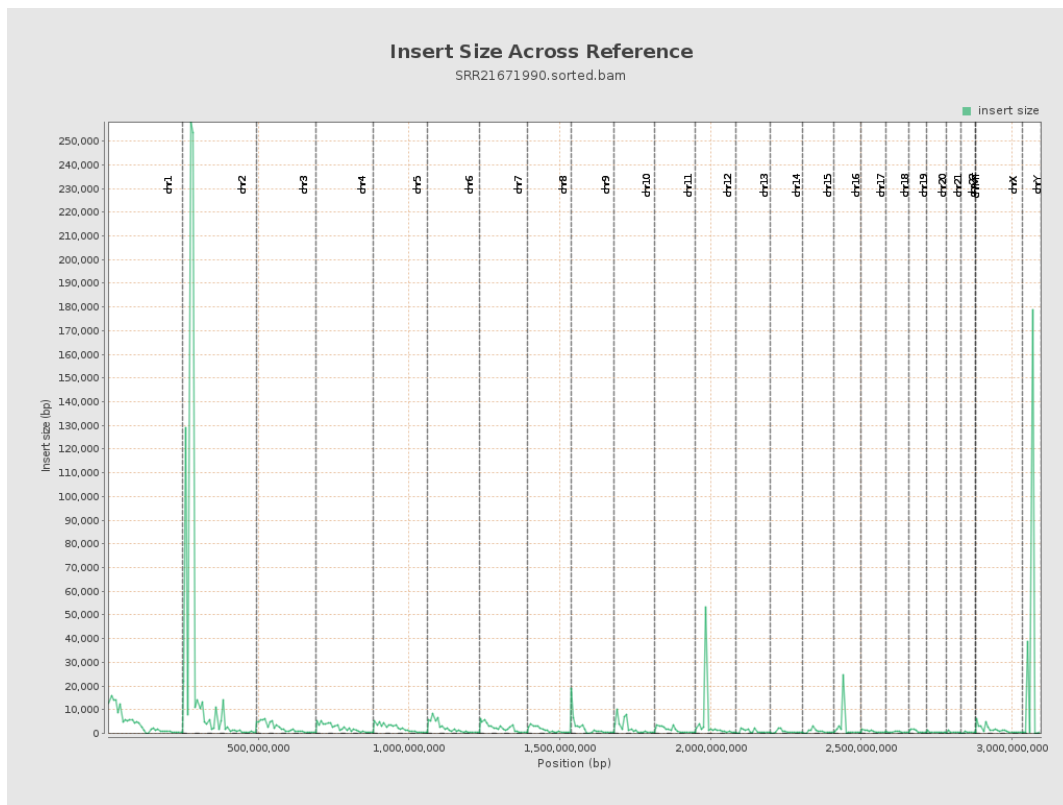
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

