

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/27 06:24:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976568.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_SRR2976568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976568_1.fastq.gz SRR2976568_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Oct 27 06:24:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	366,229,658
Mapped reads	364,007,938 / 99.39%
Unmapped reads	2,221,720 / 0.61%
Mapped paired reads	364,007,938 / 99.39%
Mapped reads, first in pair	182,640,025 / 49.87%
Mapped reads, second in pair	181,367,913 / 49.52%
Mapped reads, both in pair	362,328,536 / 98.93%
Mapped reads, singletons	1,679,402 / 0.46%
Secondary alignments	0
Supplementary alignments	13,874,846 / 3.79%
Read min/max/mean length	20 / 250 / 234.35
Duplicated reads (estimated)	49,748,210 / 13.58%
Duplication rate	11.46%
Clipped reads	45,099,837 / 12.31%

2.2. ACGT Content

Number/percentage of A's	24,382,628,822 / 28.97%
Number/percentage of C's	17,657,219,057 / 20.98%
Number/percentage of T's	24,240,272,130 / 28.8%
Number/percentage of G's	17,893,291,175 / 21.26%
Number/percentage of N's	3,407,390 / 0%

GC Percentage	42.23%
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2.3. Coverage

Mean	27.2015
Standard Deviation	76.4656

2.4. Mapping Quality

Mean Mapping Quality	55.28
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2.5. Insert size

Mean	75,907.44
Standard Deviation	2,663,817.41
P25/Median/P75	488 / 533 / 603

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	607,878,609
Insertions	8,948,072
Mapped reads with at least one insertion	2.3%
Deletions	10,681,774
Mapped reads with at least one deletion	2.77%
Homopolymer indels	45.59%

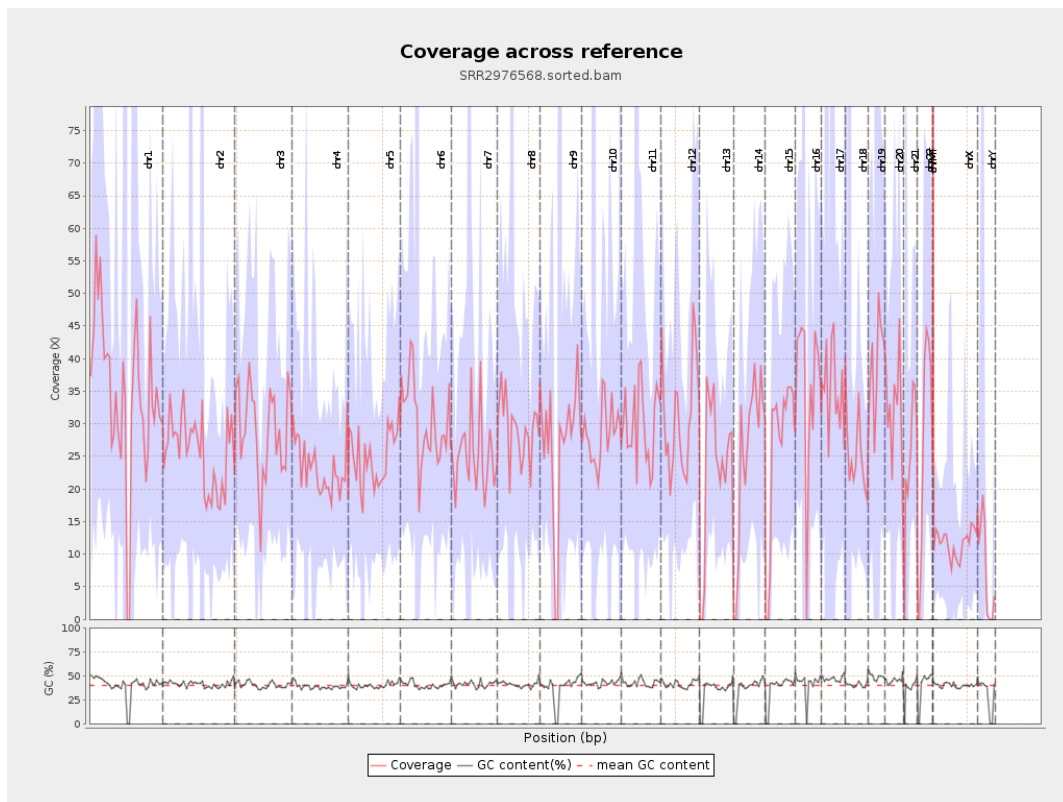
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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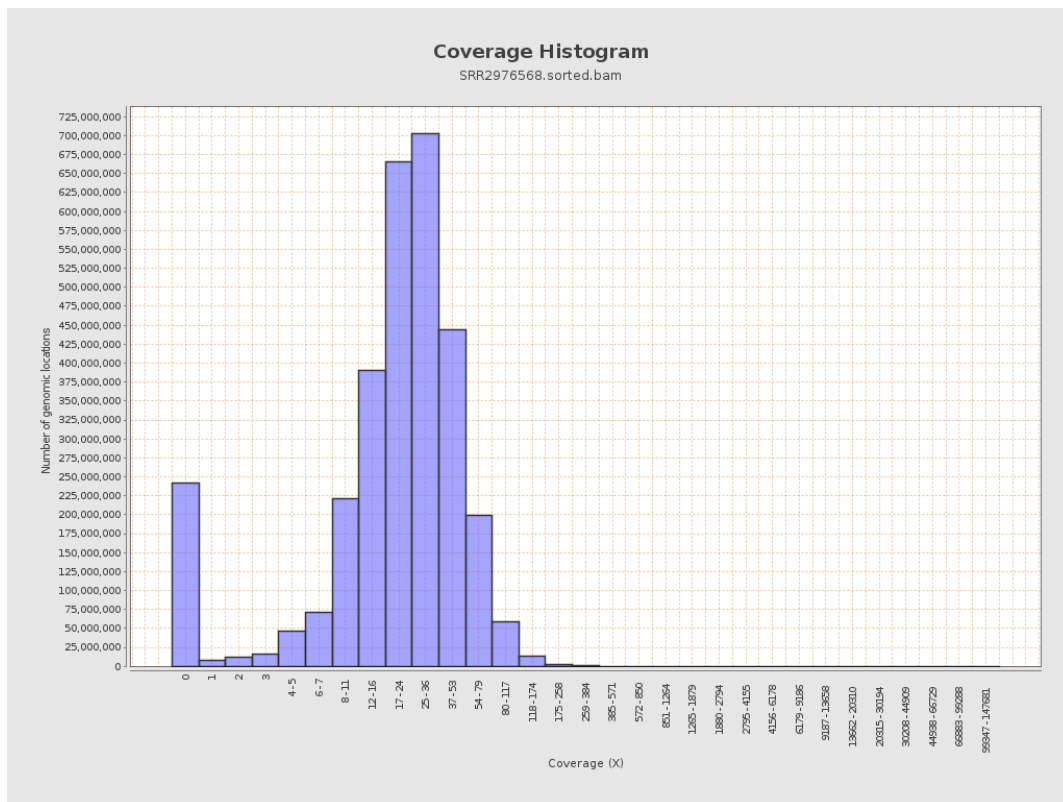
		bases	coverage	deviation
chr1	249250621	8625360041	34.6052	150.2124
chr2	243199373	6235348152	25.6388	51.6267
chr3	198022430	5701825534	28.7938	19.7444
chr4	191154276	4446631843	23.262	21.2203
chr5	180915260	4534819390	25.066	19.0771
chr6	171115067	5177449633	30.2571	53.3073
chr7	159138663	3992009690	25.0851	35.0013
chr8	146364022	4250793379	29.0426	31.4356
chr9	141213431	3777830298	26.7526	179.4988
chr10	135534747	3856774534	28.456	99.7173
chr11	135006516	4030679036	29.8554	67.5958
chr12	133851895	4191204162	31.3123	23.4536
chr13	115169878	2683437905	23.2998	19.5372
chr14	107349540	2778919677	25.8866	23.6737
chr15	102531392	2651871777	25.864	22.281
chr16	90354753	3160911012	34.9833	39.5855
chr17	81195210	2888992161	35.5808	120.5003
chr18	78077248	1945219579	24.914	146.7559
chr19	59128983	2317529419	39.1945	100.3009
chr20	63025520	2030933175	32.224	27.6497
chr21	48129895	1215327474	25.251	37.1696
chr22	51304566	1411009288	27.5026	30.7525
chrMT	16571	2920738	176.256	58.7601
chrX	155270560	1831510027	11.7956	17.2059

chrY	59373566	468092894	7.8839	44.1793
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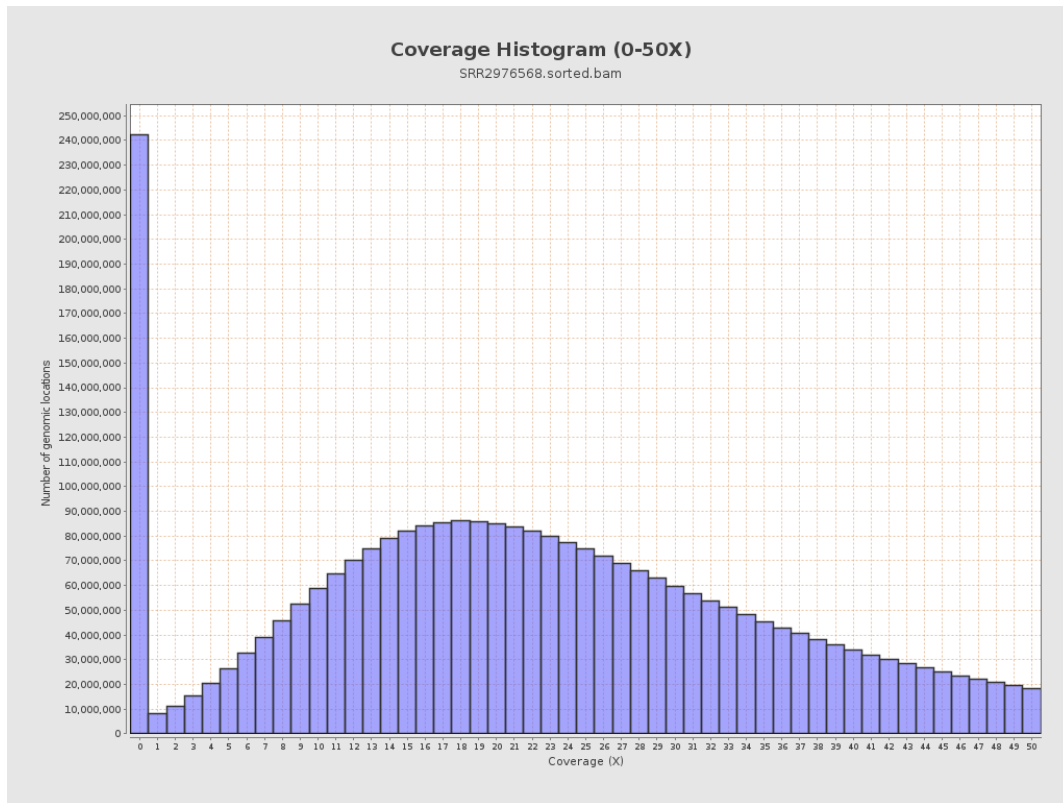
3. Results : Coverage across reference



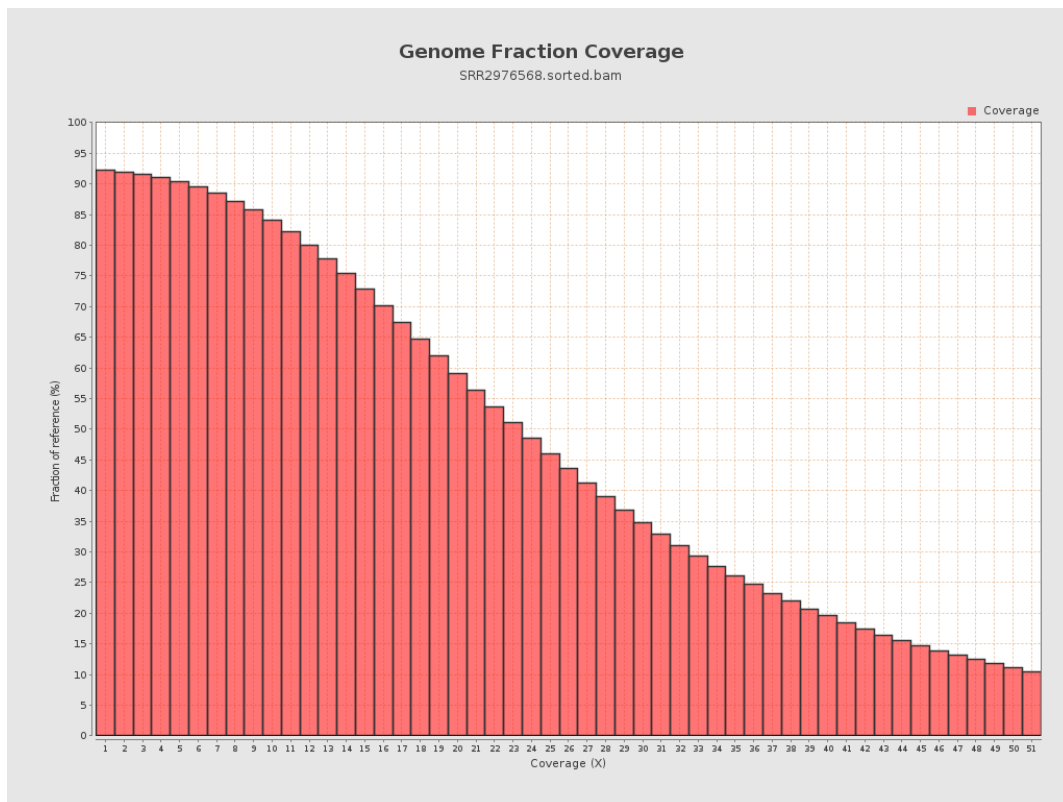
4. Results : Coverage Histogram



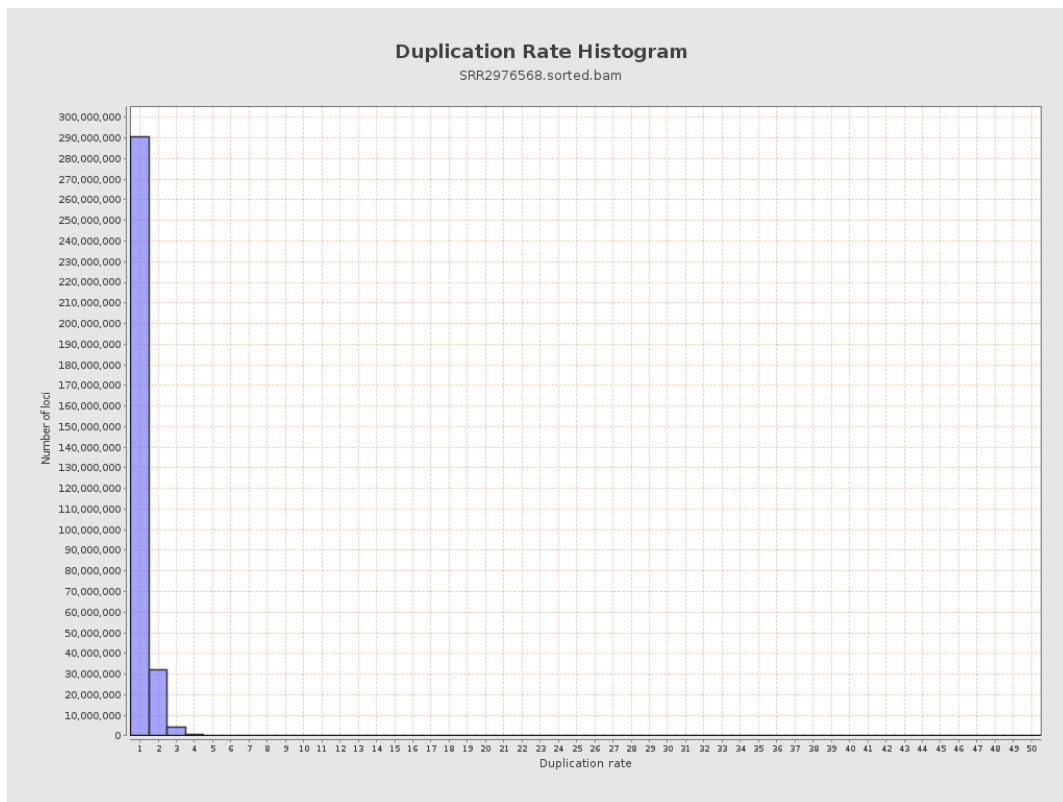
5. Results : Coverage Histogram (0-50X)



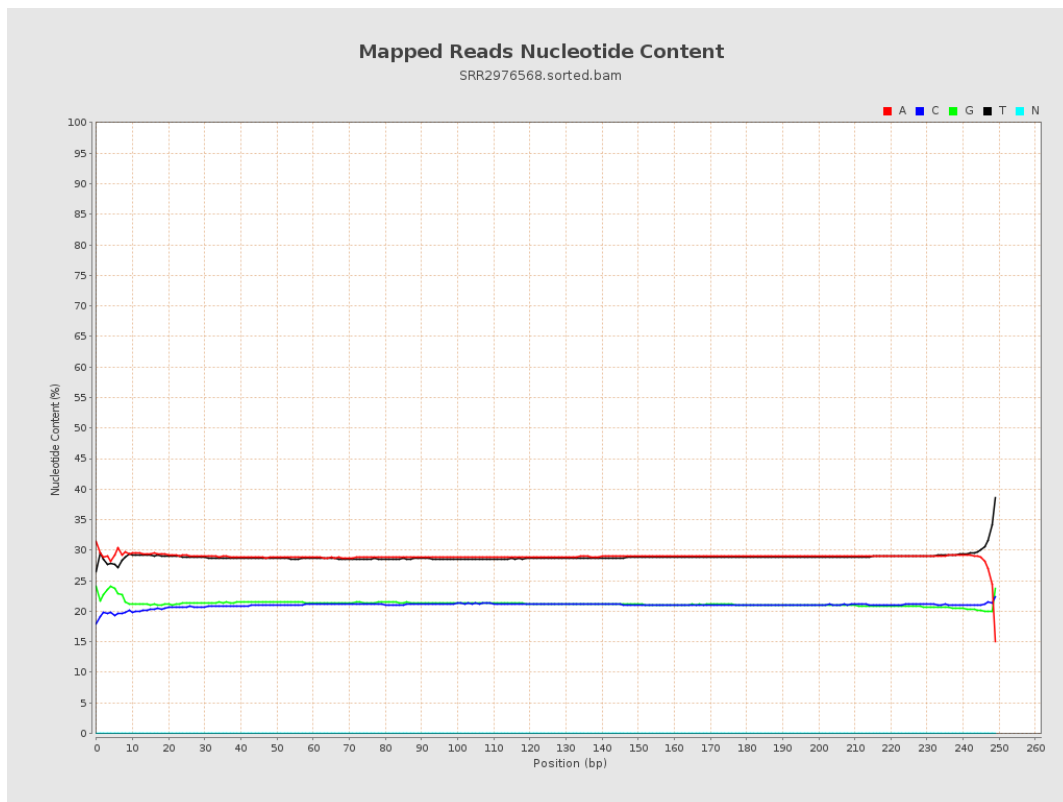
6. Results : Genome Fraction Coverage



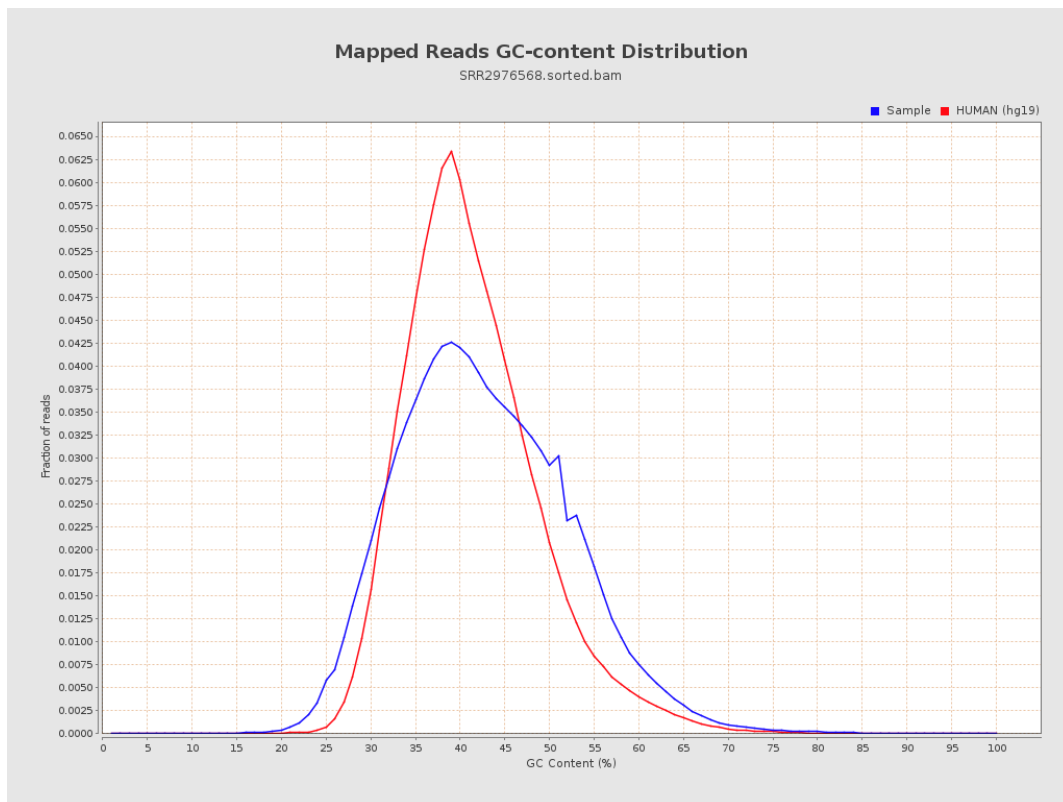
7. Results : Duplication Rate Histogram



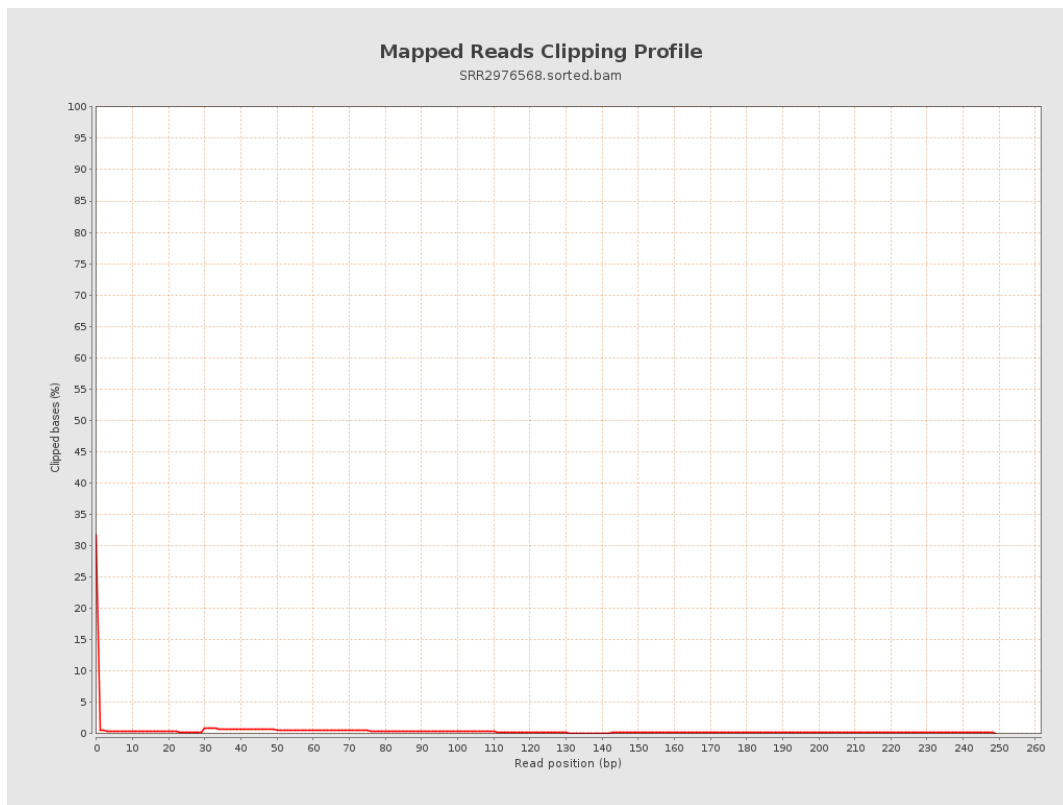
8. Results : Mapped Reads Nucleotide Content



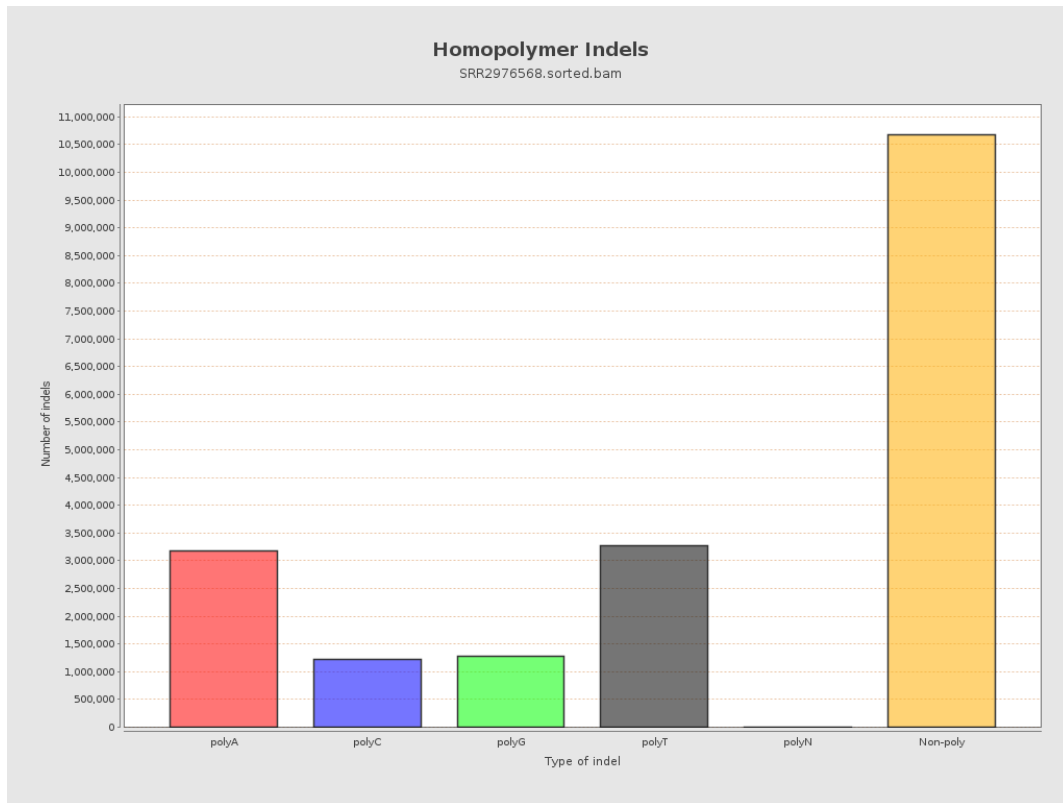
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



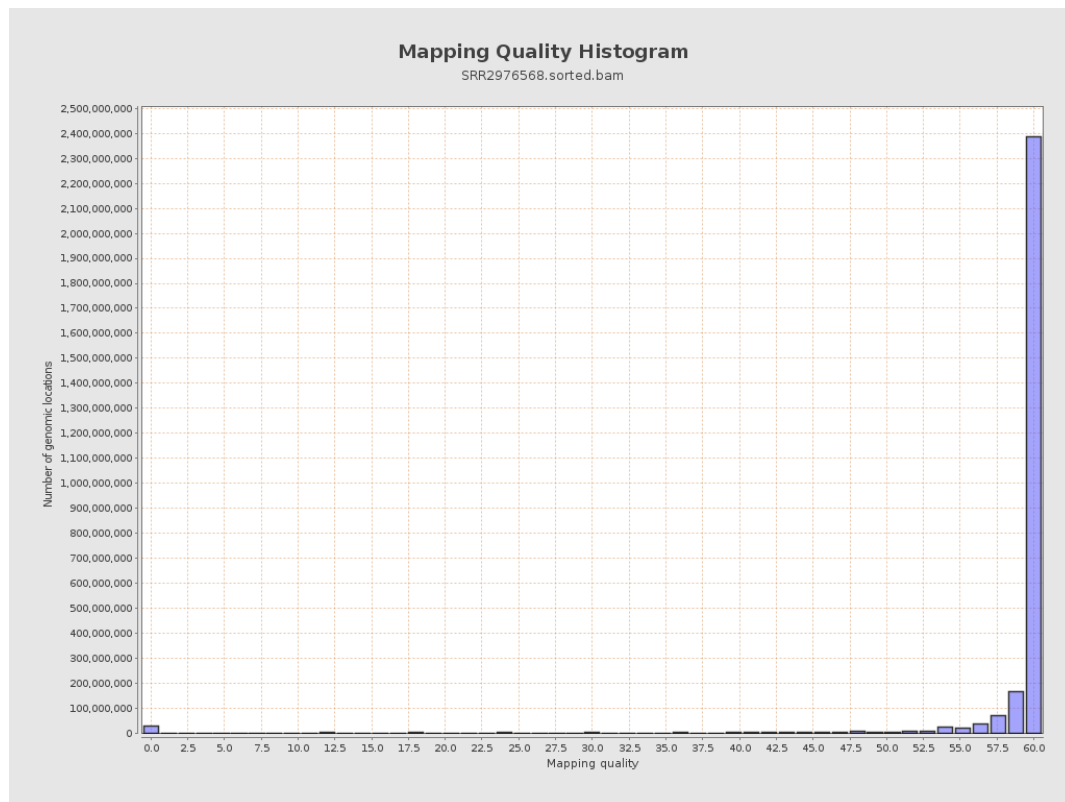
11. Results : Homopolymer Indels



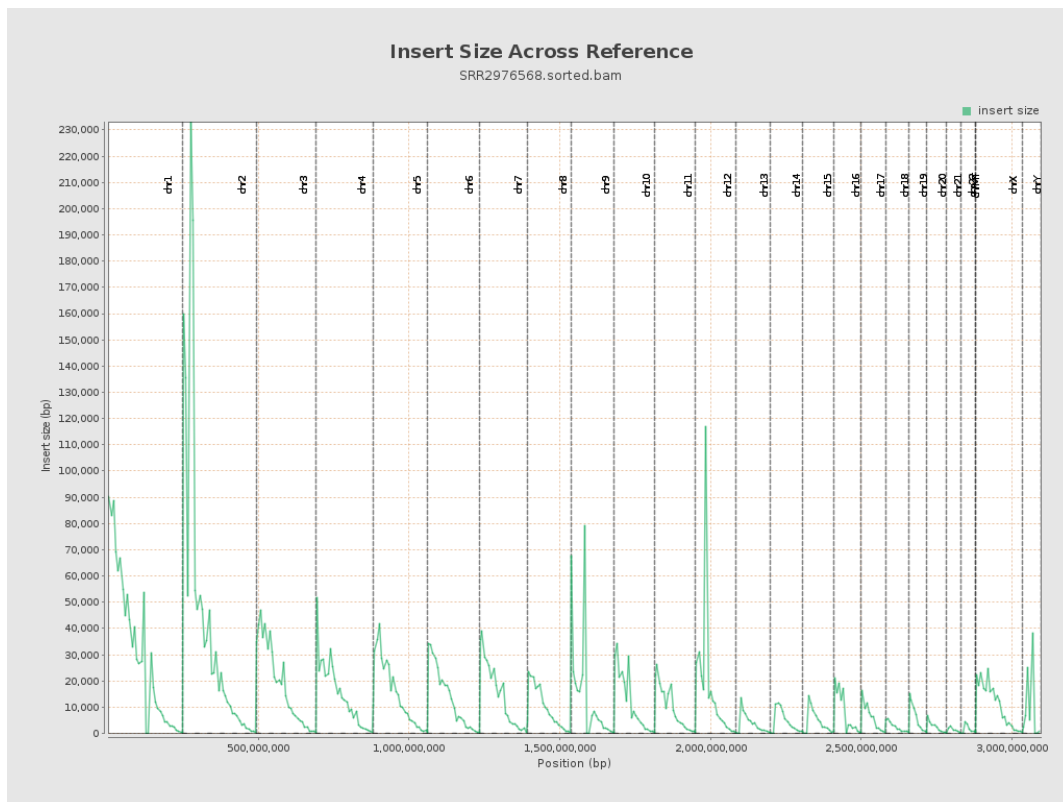
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

