

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/27 15:40:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2976569.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_SRR2976569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2976569_1.fastq.gz SRR2976569_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Oct 27 15:40:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2976569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	353,288,550
Mapped reads	351,000,799 / 99.35%
Unmapped reads	2,287,751 / 0.65%
Mapped paired reads	351,000,799 / 99.35%
Mapped reads, first in pair	176,309,201 / 49.91%
Mapped reads, second in pair	174,691,598 / 49.45%
Mapped reads, both in pair	349,127,168 / 98.82%
Mapped reads, singletons	1,873,631 / 0.53%
Secondary alignments	0
Supplementary alignments	5,765,816 / 1.63%
Read min/max/mean length	20 / 250 / 230.35
Duplicated reads (estimated)	48,075,128 / 13.61%
Duplication rate	12.44%
Clipped reads	27,712,403 / 7.84%

2.2. ACGT Content

Number/percentage of A's	23,811,744,947 / 29.63%
Number/percentage of C's	16,395,465,087 / 20.4%
Number/percentage of T's	23,615,662,244 / 29.38%
Number/percentage of G's	16,538,335,849 / 20.58%
Number/percentage of N's	5,685,911 / 0.01%

GC Percentage	40.98%
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2.3. Coverage

Mean	25.9692
Standard Deviation	37.6088

2.4. Mapping Quality

Mean Mapping Quality	55.6
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2.5. Insert size

Mean	46,158.33
Standard Deviation	2,071,902.39
P25/Median/P75	491 / 530 / 590

2.6. Mismatches and indels

General error rate	0.83%
Mismatches	645,594,109
Insertions	7,291,500
Mapped reads with at least one insertion	1.98%
Deletions	9,231,796
Mapped reads with at least one deletion	2.5%
Homopolymer indels	46.38%

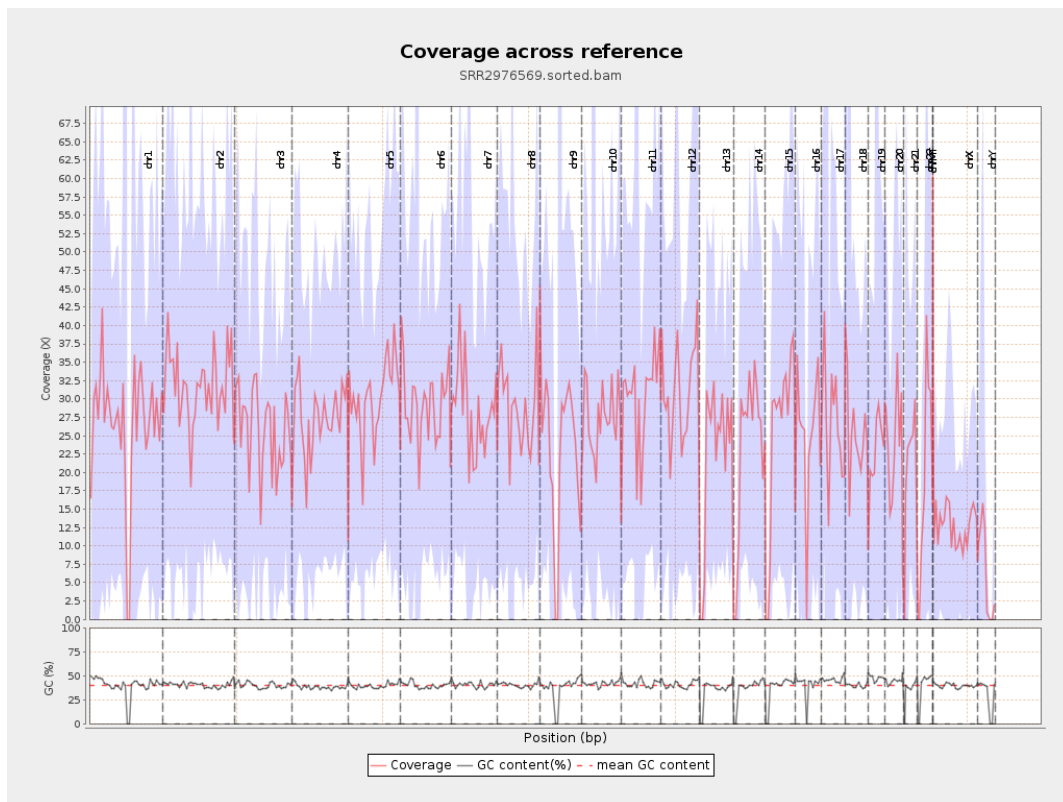
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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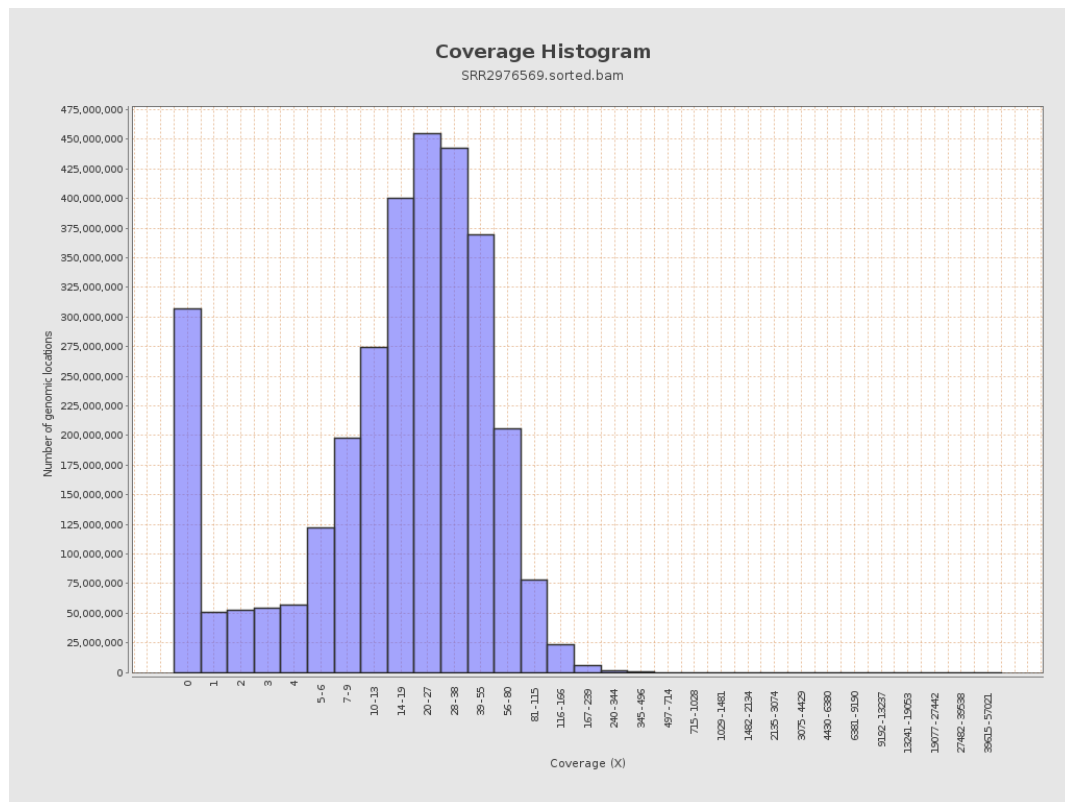
		bases	coverage	deviation
chr1	249250621	6634258543	26.6168	64.2662
chr2	243199373	7709355459	31.6997	29.0006
chr3	198022430	5109311481	25.8017	23.2033
chr4	191154276	5249238807	27.4607	22.5677
chr5	180915260	5427101012	29.998	24.7815
chr6	171115067	4997252143	29.204	33.8663
chr7	159138663	4536632700	28.5074	28.2803
chr8	146364022	4172540178	28.508	27.0602
chr9	141213431	3225669966	22.8425	61.6872
chr10	135534747	3733043738	27.5431	49.4791
chr11	135006516	4078736653	30.2114	35.9872
chr12	133851895	4177505311	31.2099	28.4527
chr13	115169878	2600616760	22.5807	21.5033
chr14	107349540	2551761752	23.7706	24.6815
chr15	102531392	2595433898	25.3136	27.2359
chr16	90354753	2206973161	24.4256	27.7338
chr17	81195210	2196571411	27.053	54.9795
chr18	78077248	1970623728	25.2394	62.6338
chr19	59128983	1379267928	23.3264	46.7465
chr20	63025520	1472012328	23.3558	28.1724
chr21	48129895	978543816	20.3313	30.26
chr22	51304566	1040876041	20.2882	30.4148
chrMT	16571	1003724	60.5711	23.5148
chrX	155270560	1956217894	12.5988	16.0813

chrY	59373566	392086955	6.6037	26.0576
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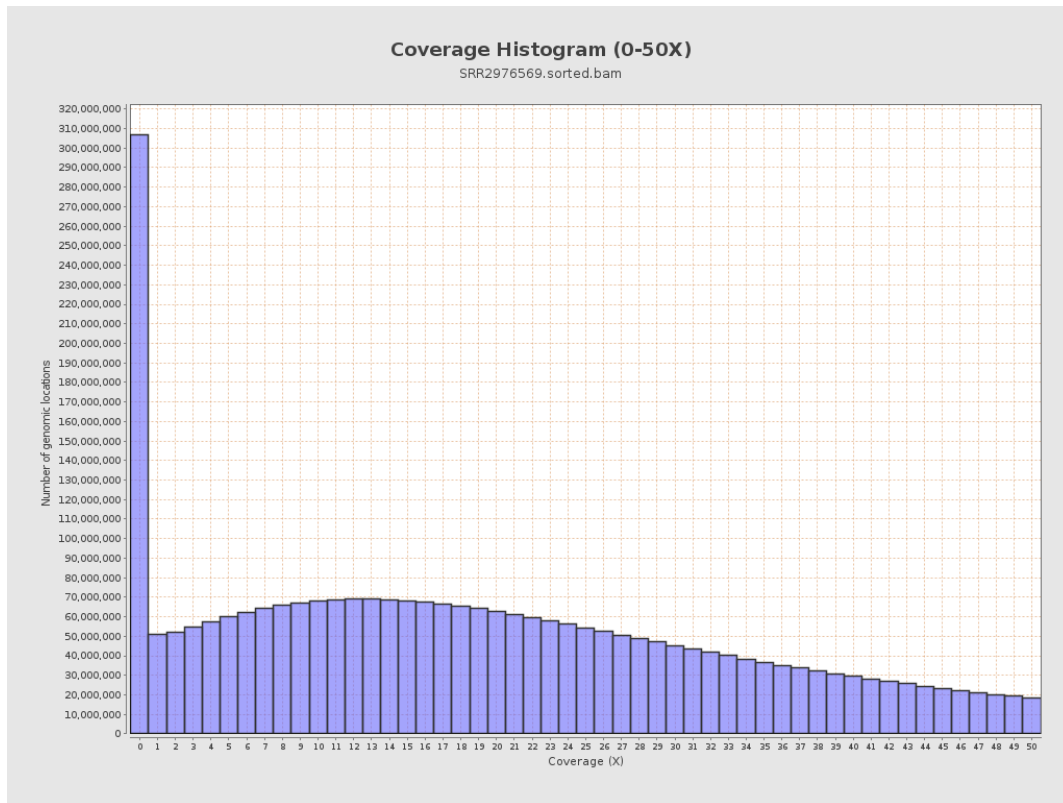
3. Results : Coverage across reference



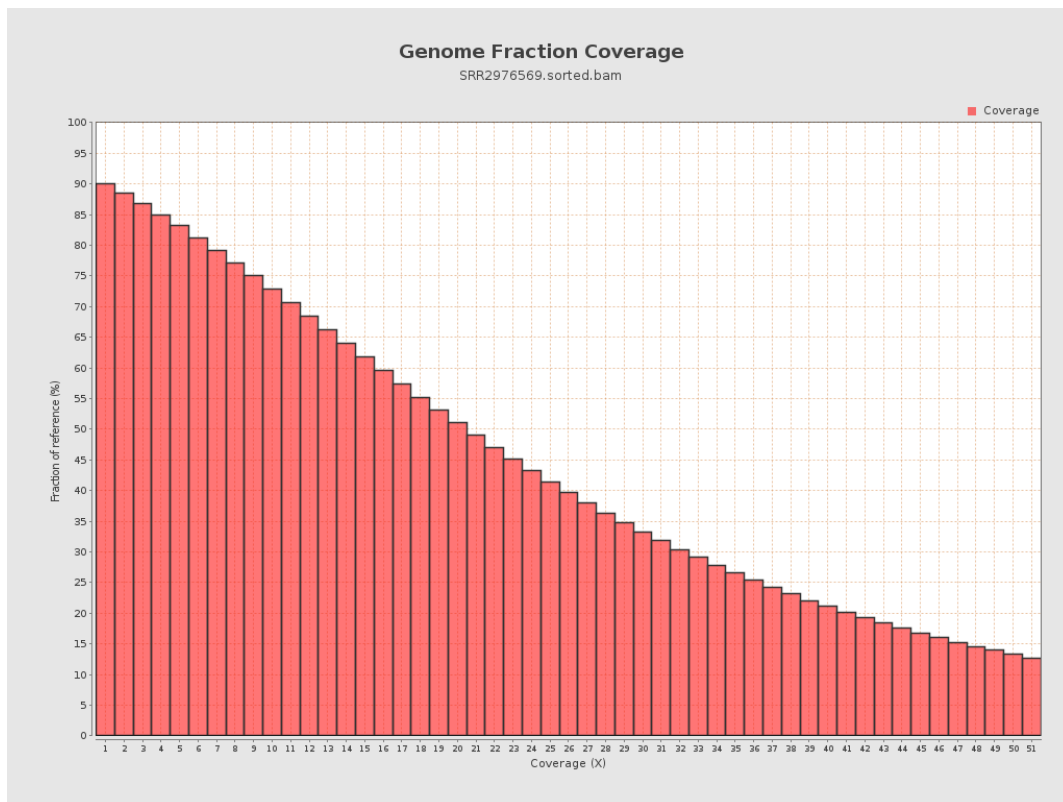
4. Results : Coverage Histogram



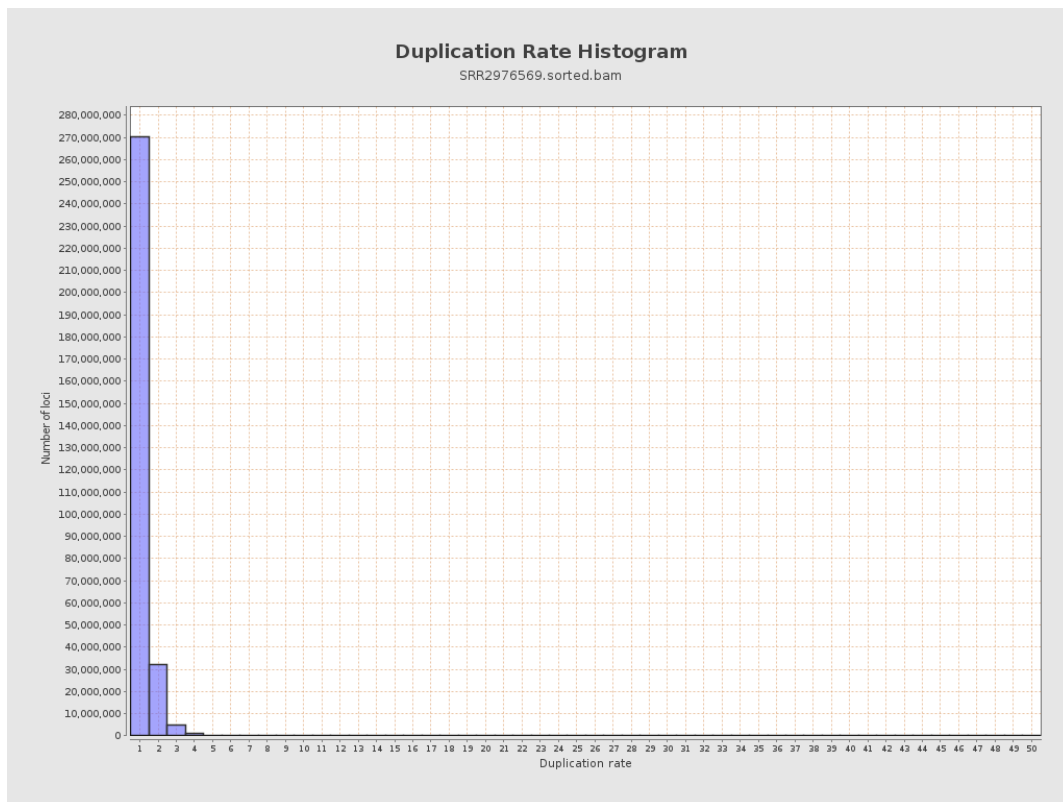
5. Results : Coverage Histogram (0-50X)



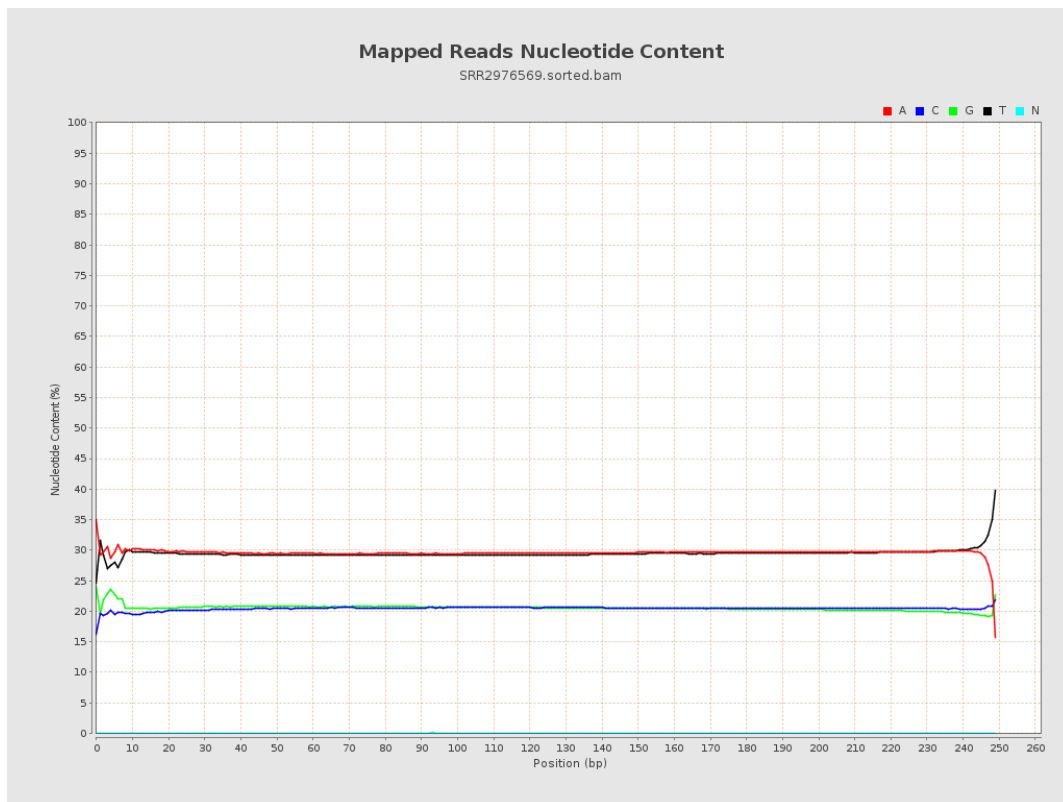
6. Results : Genome Fraction Coverage



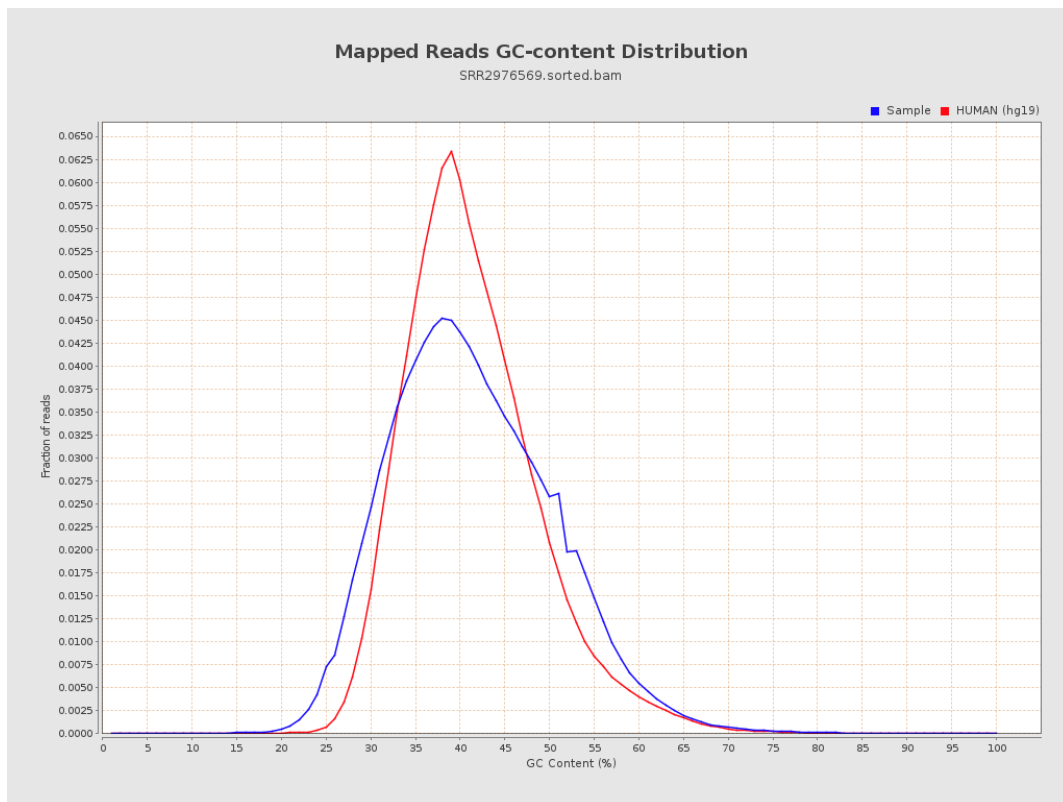
7. Results : Duplication Rate Histogram



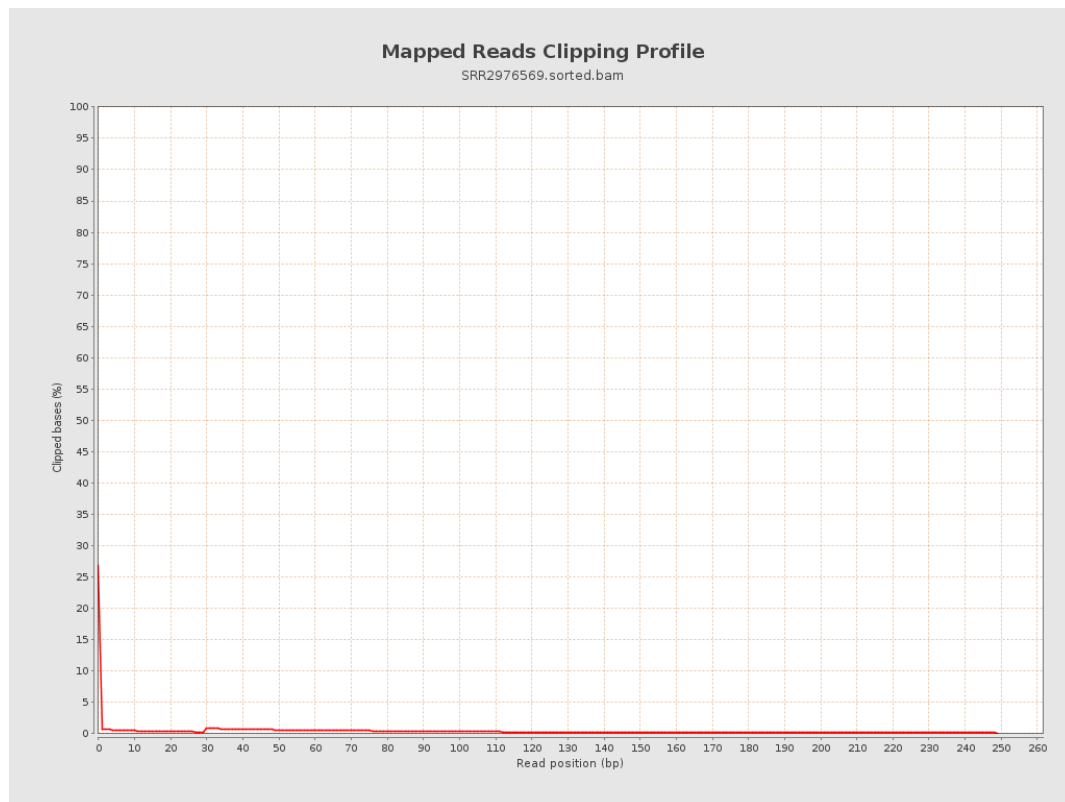
8. Results : Mapped Reads Nucleotide Content



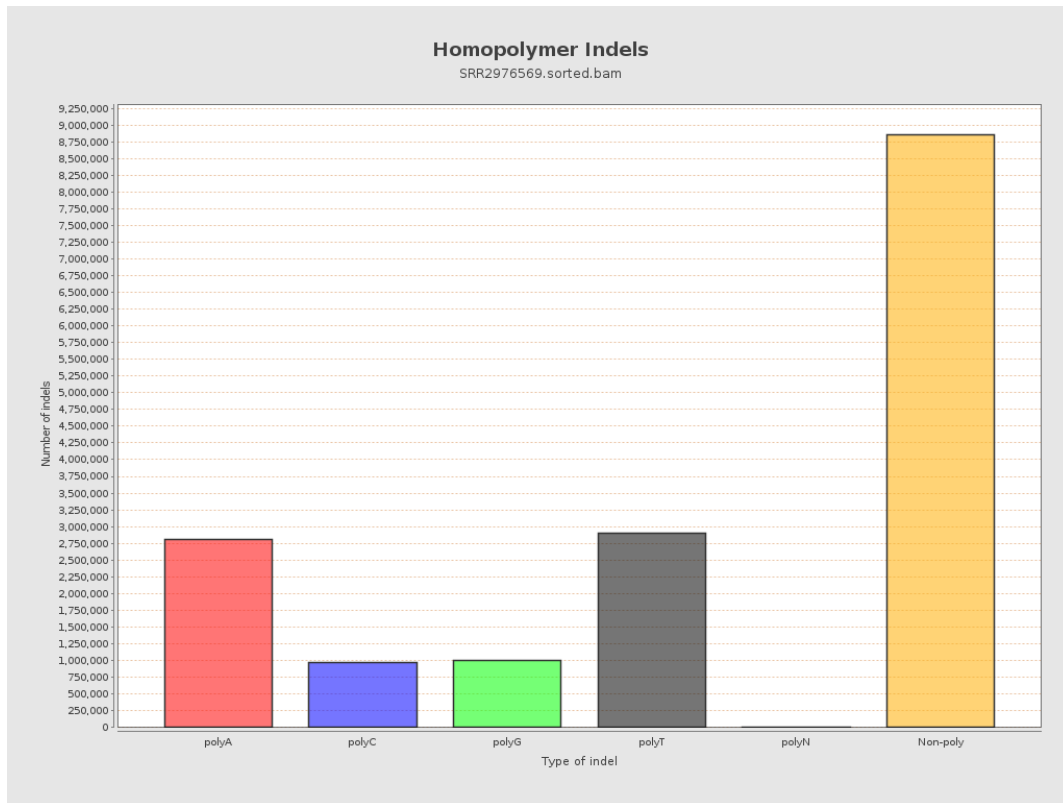
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



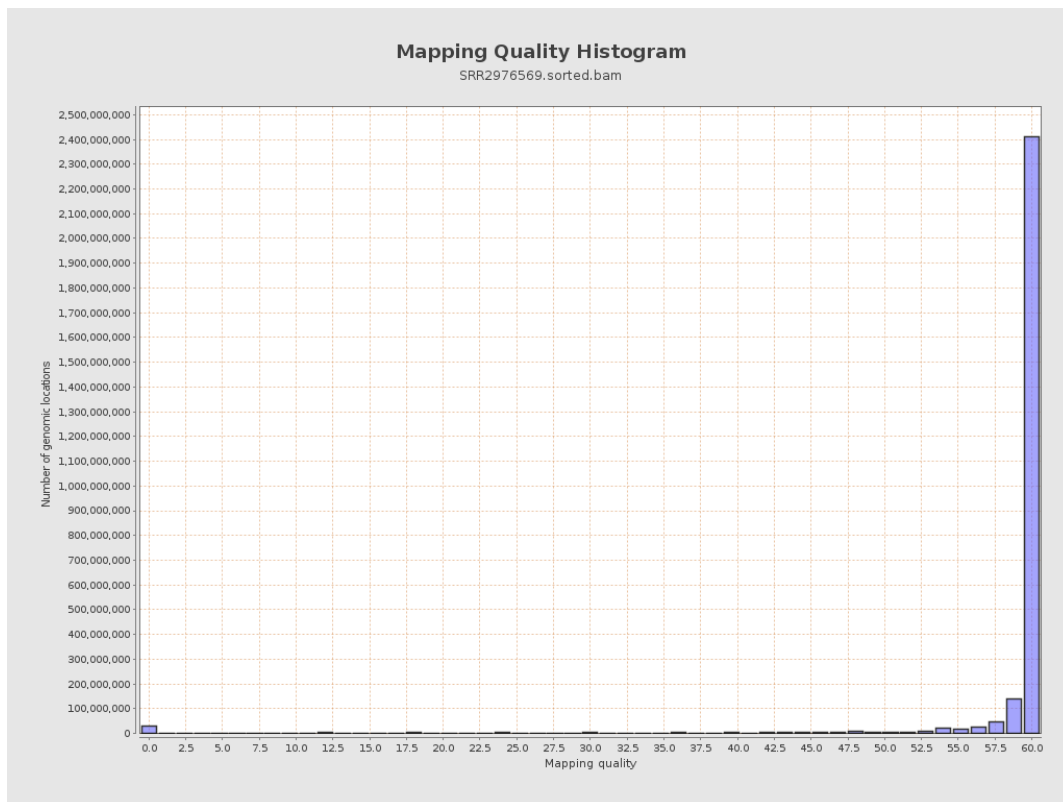
11. Results : Homopolymer Indels



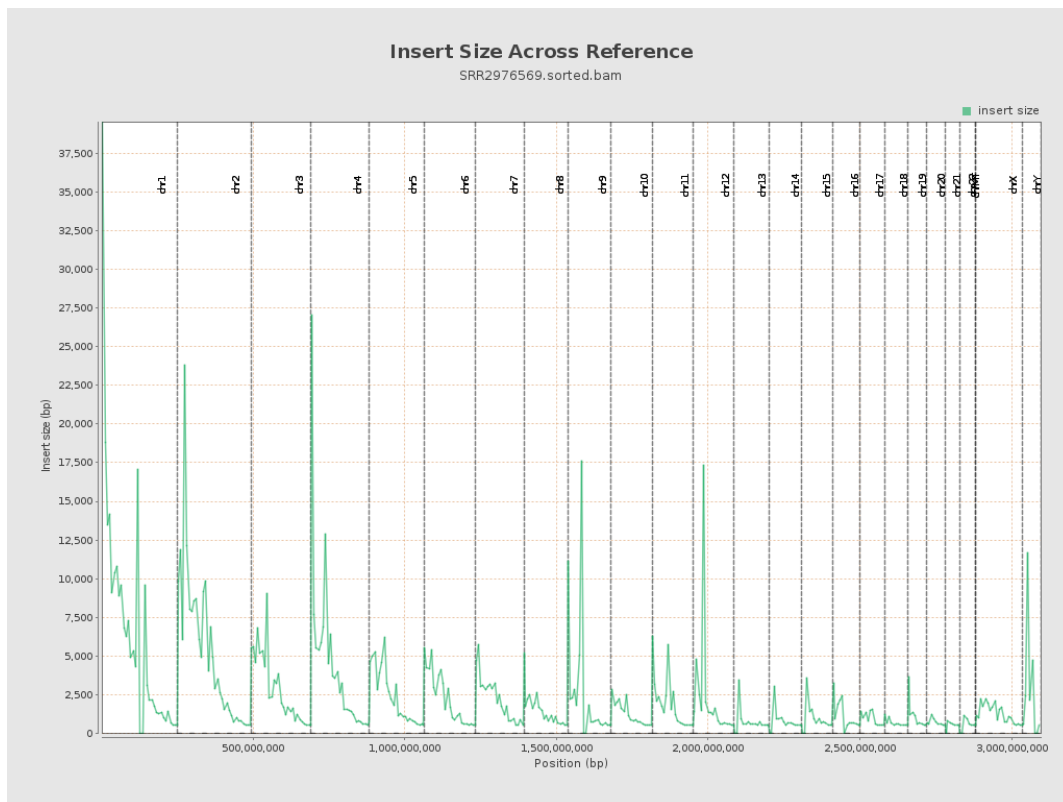
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

