

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 09:34:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926971.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_SRR926971 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926971_1.fastq.gz SRR926971_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 09:34:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926971.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,453,622
Mapped reads	23,058,854 / 98.32%
Unmapped reads	394,768 / 1.68%
Mapped paired reads	23,058,854 / 98.32%
Mapped reads, first in pair	11,584,625 / 49.39%
Mapped reads, second in pair	11,474,229 / 48.92%
Mapped reads, both in pair	22,872,860 / 97.52%
Mapped reads, singletons	185,994 / 0.79%
Secondary alignments	0
Supplementary alignments	130,176 / 0.56%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	1,301,512 / 5.55%
Duplication rate	4.32%
Clipped reads	3,610,020 / 15.39%

2.2. ACGT Content

Number/percentage of A's	642,088,885 / 28.72%
Number/percentage of C's	458,196,918 / 20.5%
Number/percentage of T's	646,967,276 / 28.94%
Number/percentage of G's	488,039,780 / 21.83%
Number/percentage of N's	181,236 / 0.01%

GC Percentage	42.33%
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2.3. Coverage

Mean	0.7227
Standard Deviation	3.2031

2.4. Mapping Quality

Mean Mapping Quality	53.5
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2.5. Insert size

Mean	60,305.28
Standard Deviation	2,389,018.93
P25/Median/P75	147 / 183 / 236

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	20,708,695
Insertions	364,809
Mapped reads with at least one insertion	1.55%
Deletions	1,205,144
Mapped reads with at least one deletion	5.09%
Homopolymer indels	53.2%

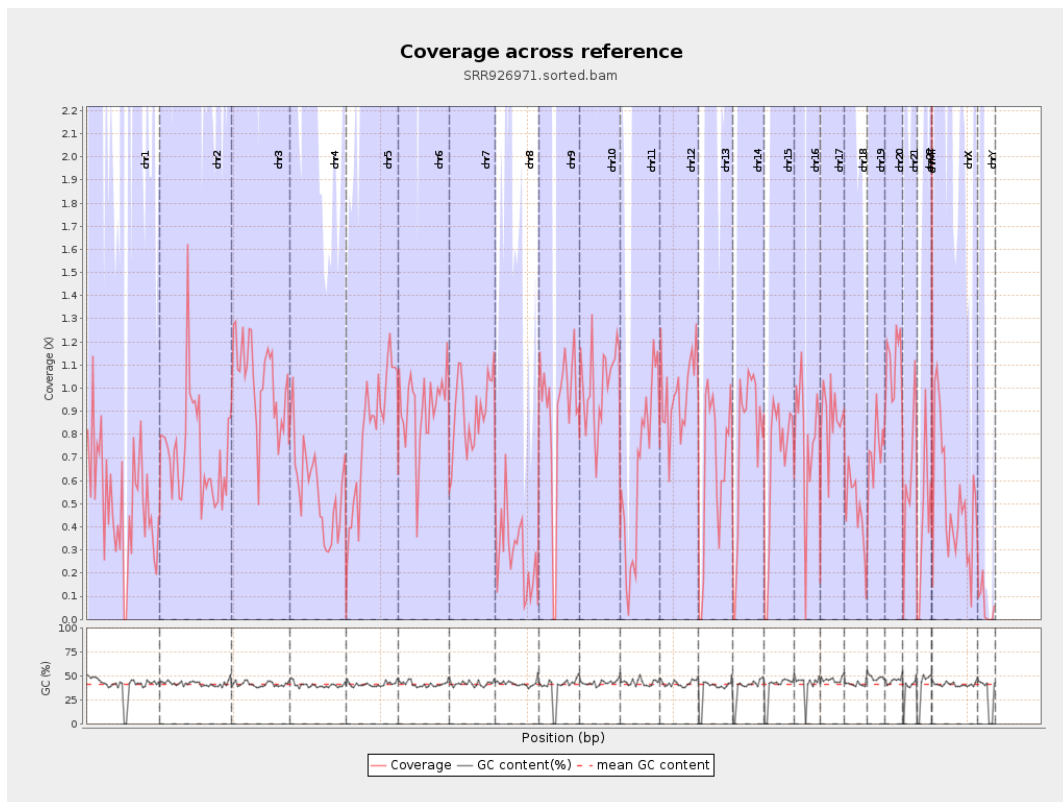
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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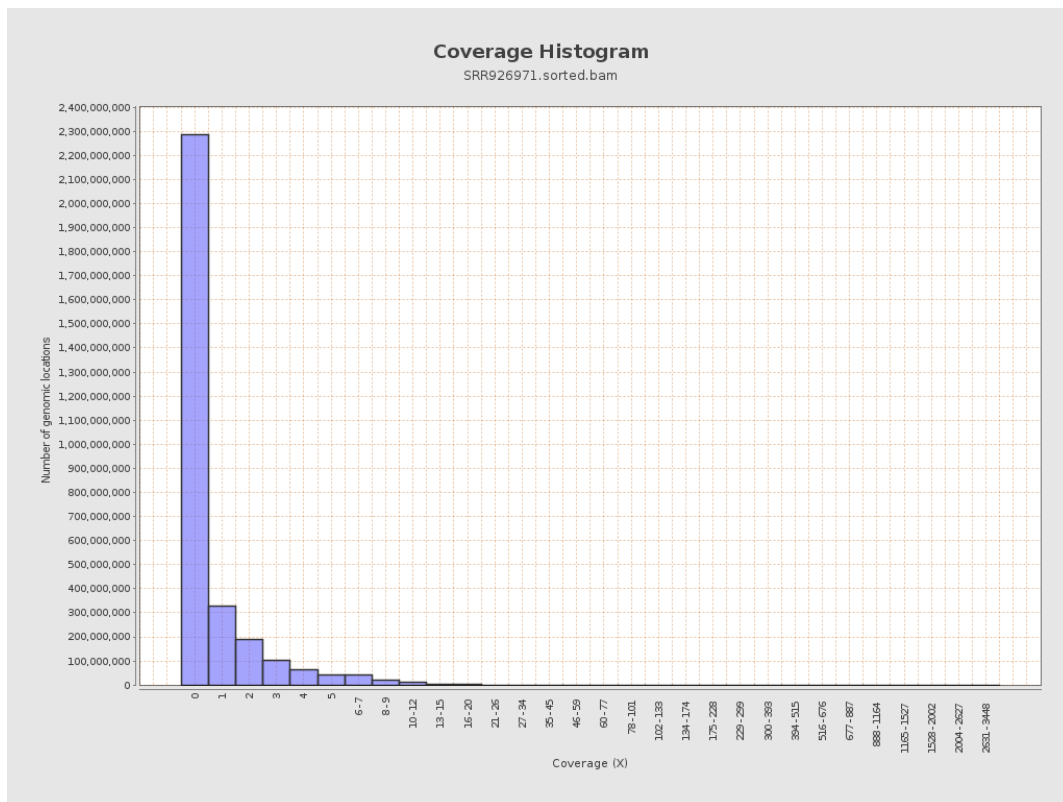
		bases	coverage	deviation
chr1	249250621	126493244	0.5075	3.5567
chr2	243199373	175062305	0.7198	5.8722
chr3	198022430	203766913	1.029	2.046
chr4	191154276	107342445	0.5615	2.3642
chr5	180915260	146343822	0.8089	1.8273
chr6	171115067	157631369	0.9212	2.5651
chr7	159138663	142225616	0.8937	3.1043
chr8	146364022	40000695	0.2733	1.4054
chr9	141213431	126011645	0.8923	5.1537
chr10	135534747	138585449	1.0225	4.7912
chr11	135006516	87177091	0.6457	2.0125
chr12	133851895	130896796	0.9779	2.2536
chr13	115169878	75864121	0.6587	1.7261
chr14	107349540	83607464	0.7788	1.8602
chr15	102531392	69376456	0.6766	1.8007
chr16	90354753	70486730	0.7801	3.3718
chr17	81195210	71057454	0.8751	2.8904
chr18	78077248	36541765	0.468	4.9801
chr19	59128983	43218997	0.7309	2.4407
chr20	63025520	69852049	1.1083	2.3175
chr21	48129895	31092873	0.646	2.576
chr22	51304566	22142643	0.4316	1.5188
chrMT	16571	39619	2.3909	2.4014
chrX	155270560	78782038	0.5074	1.6855

chrY	59373566	3584977	0.0604	2.1172
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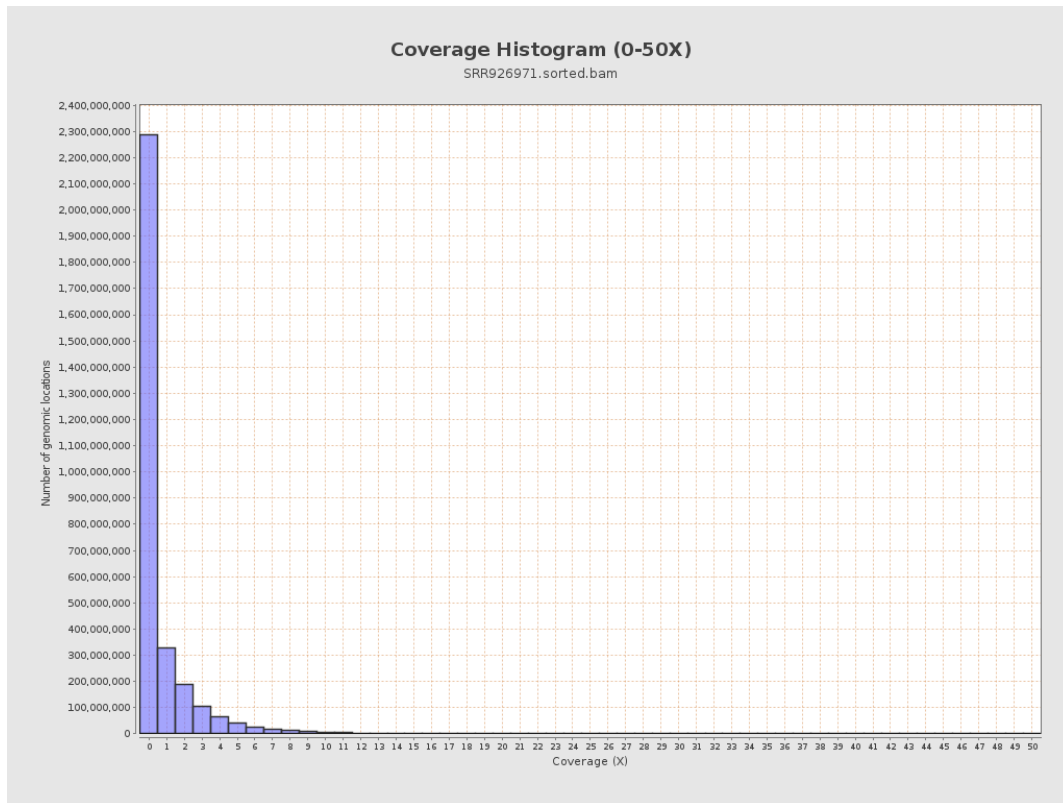
3. Results : Coverage across reference



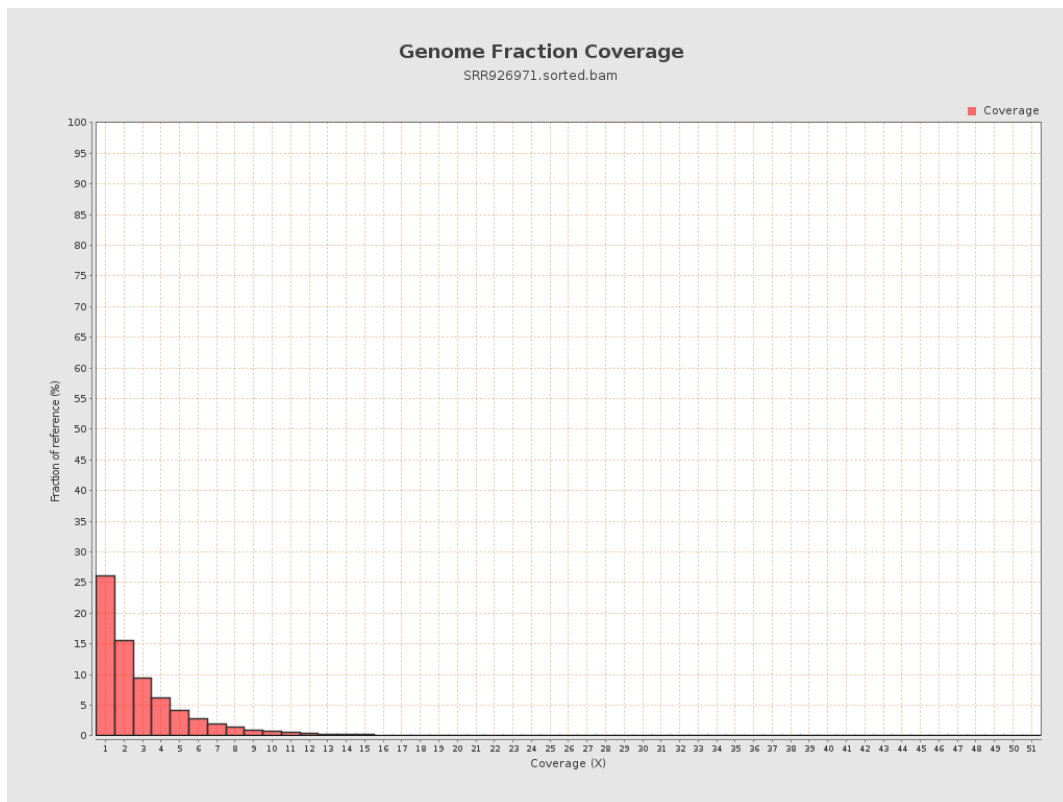
4. Results : Coverage Histogram



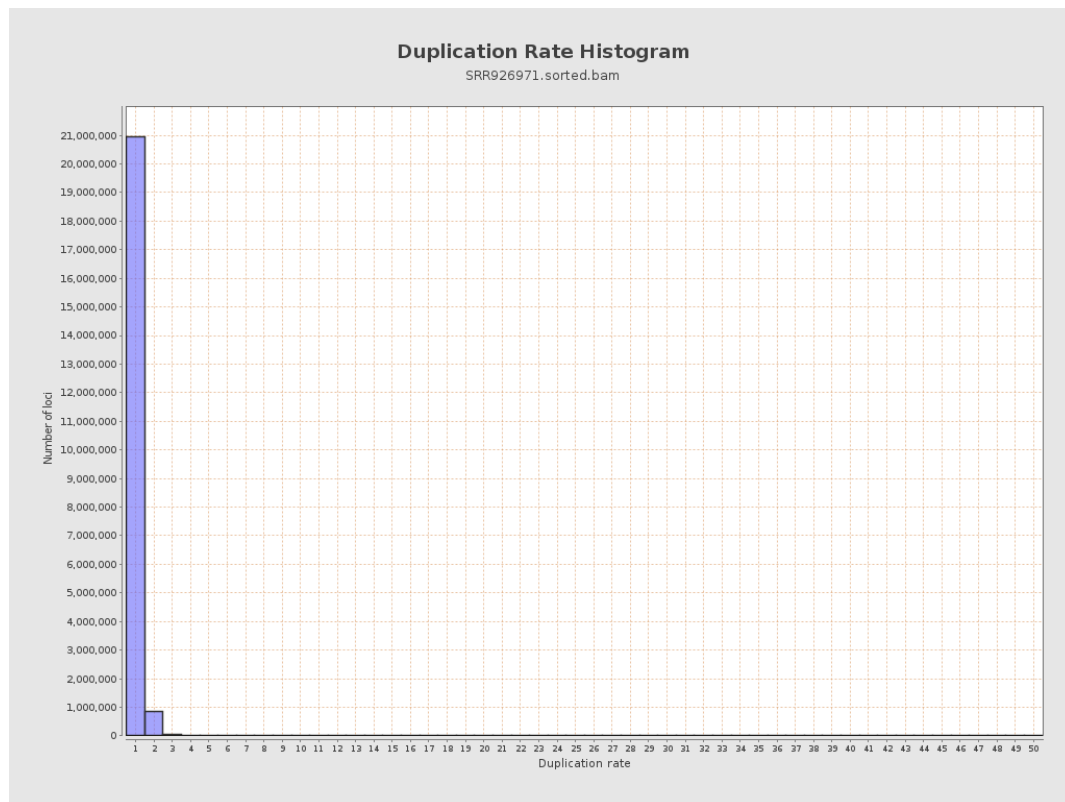
5. Results : Coverage Histogram (0-50X)



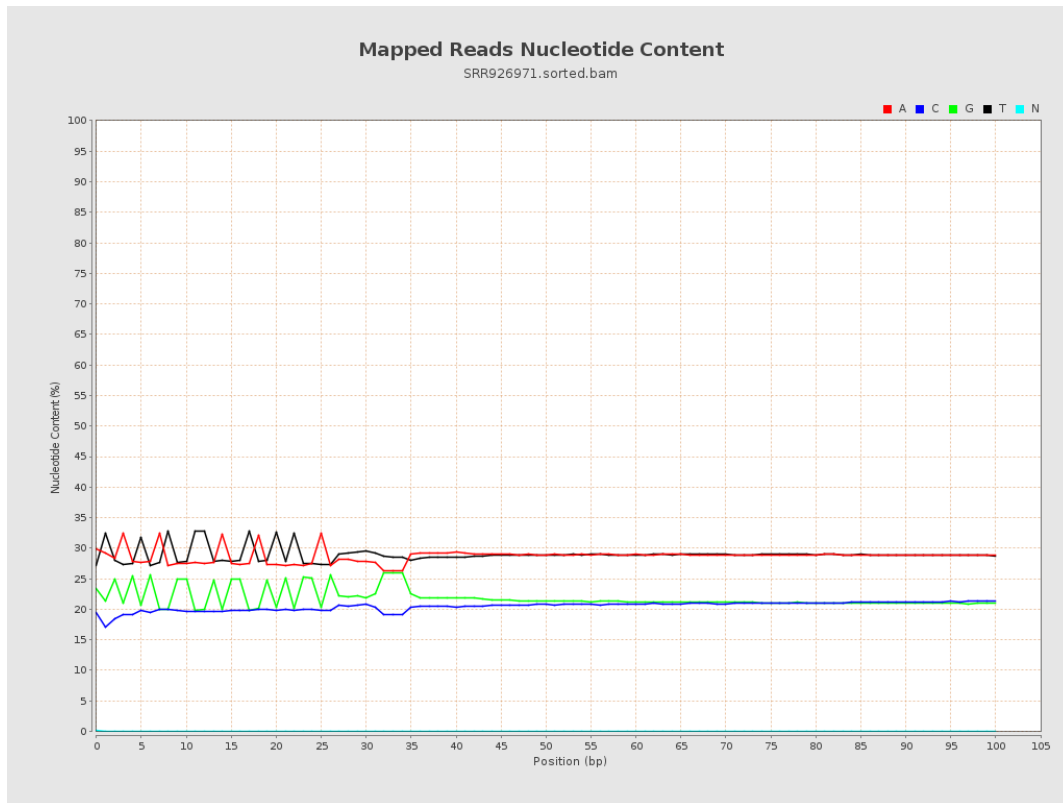
6. Results : Genome Fraction Coverage



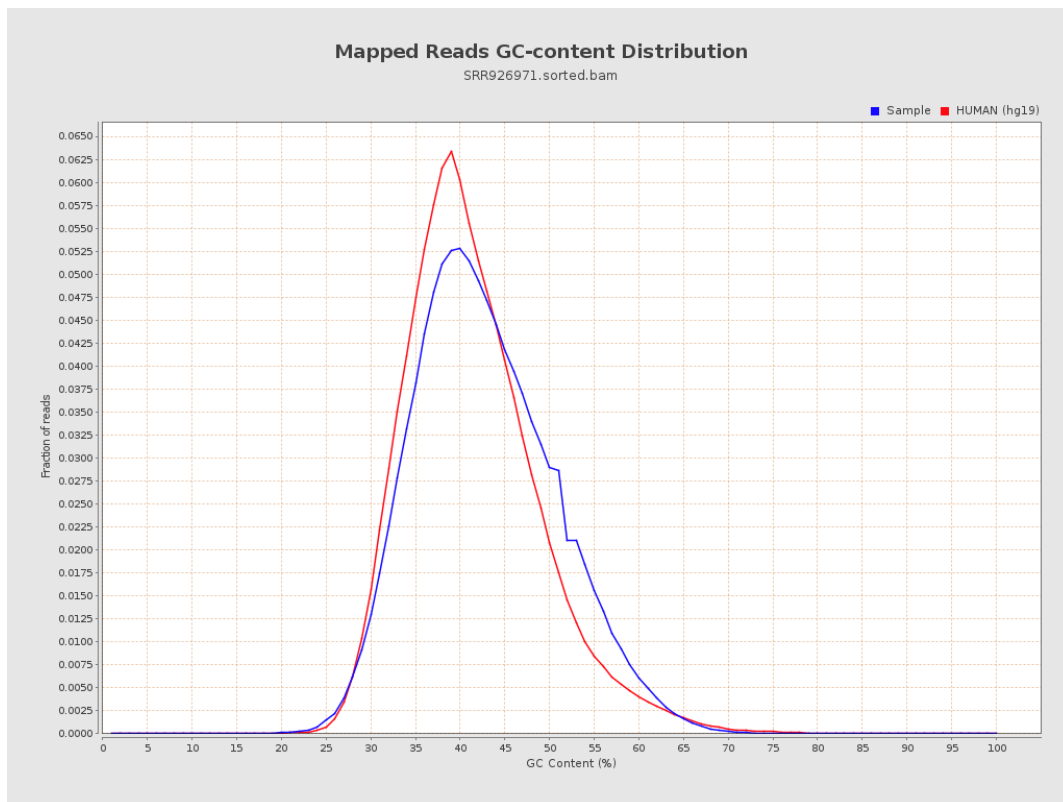
7. Results : Duplication Rate Histogram



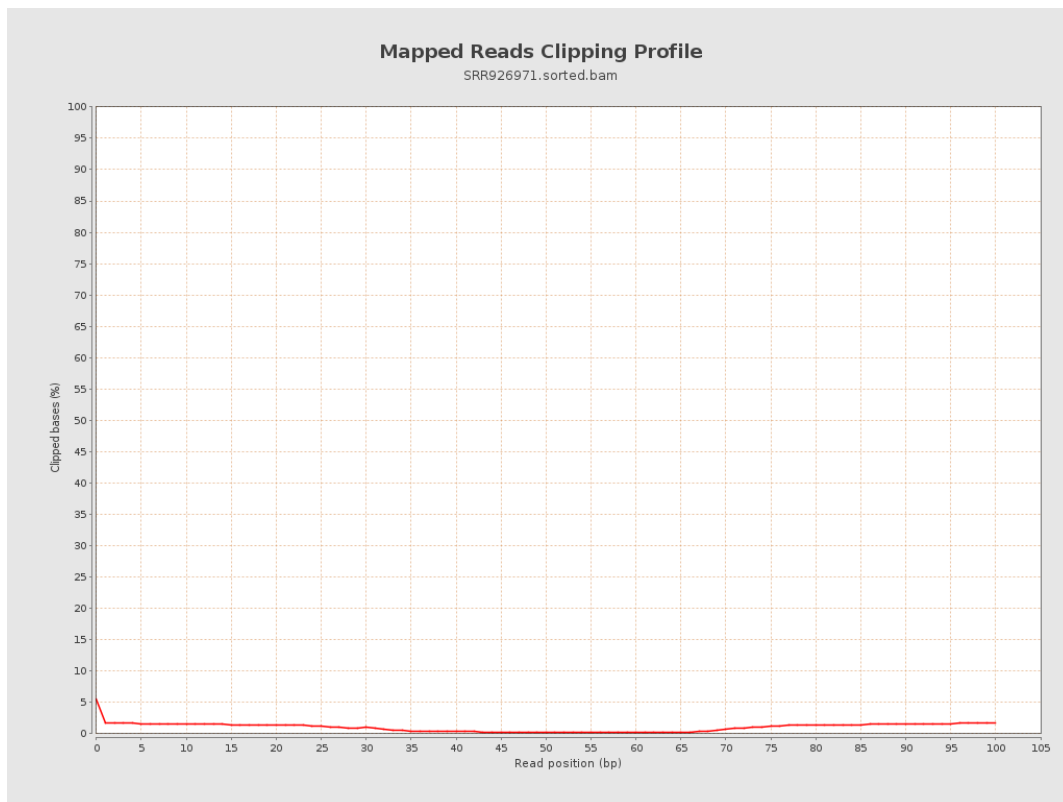
8. Results : Mapped Reads Nucleotide Content



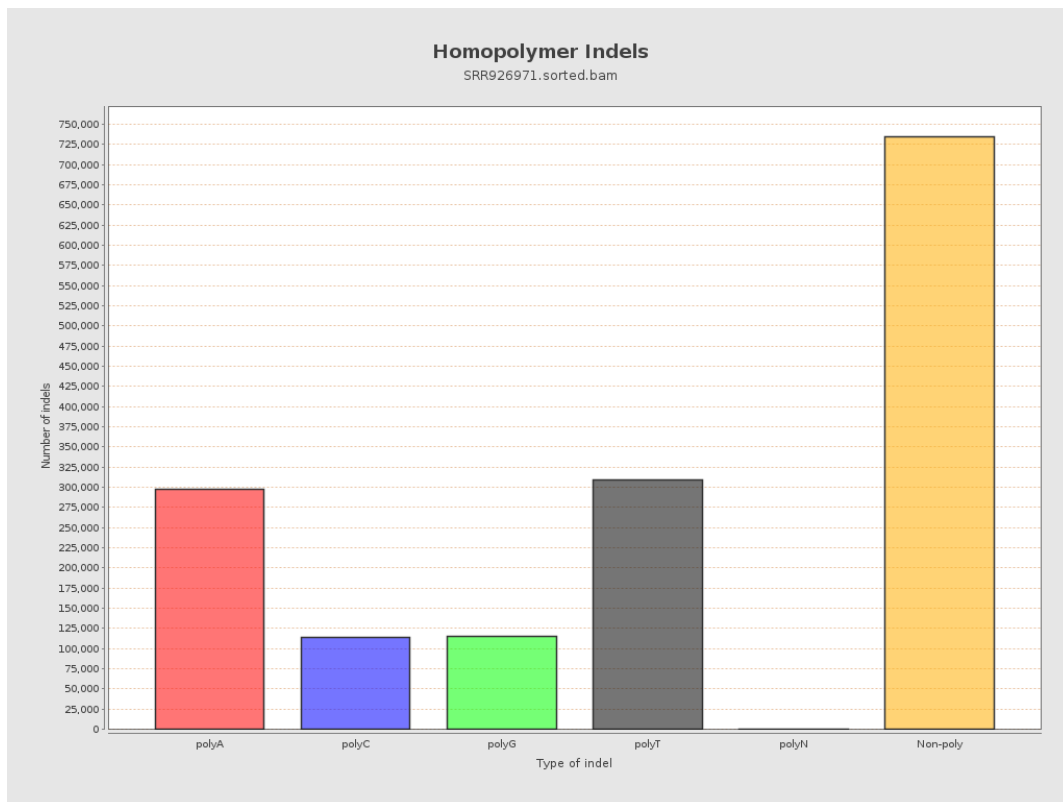
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



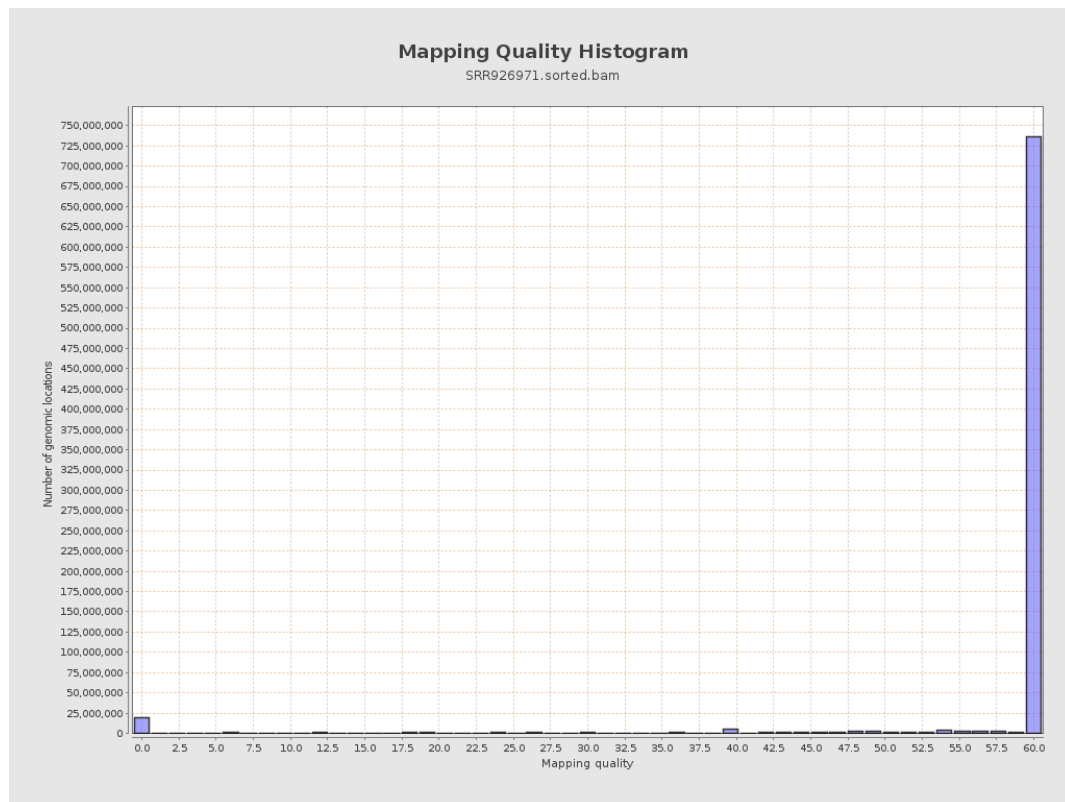
11. Results : Homopolymer Indels



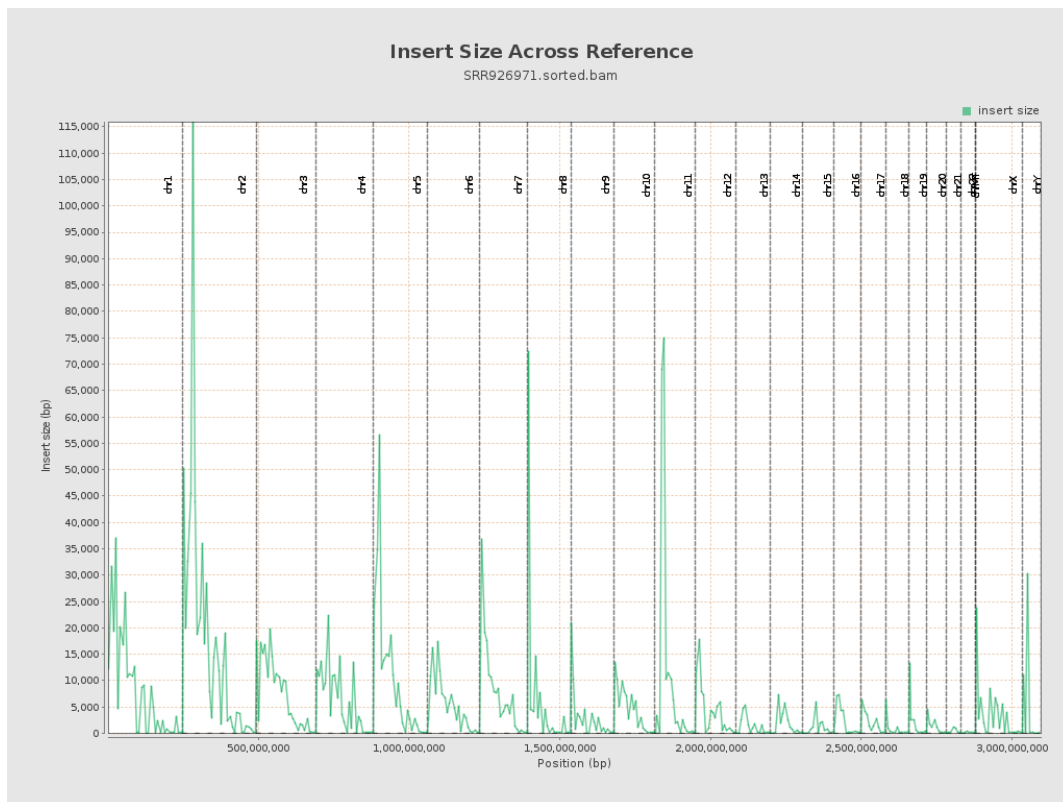
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

