

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 18:01:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926989.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_SRR926989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926989_1.fastq.gz SRR926989_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 18:01:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,427,250
Mapped reads	26,067,779 / 98.64%
Unmapped reads	359,471 / 1.36%
Mapped paired reads	26,067,779 / 98.64%
Mapped reads, first in pair	13,081,239 / 49.5%
Mapped reads, second in pair	12,986,540 / 49.14%
Mapped reads, both in pair	25,870,368 / 97.89%
Mapped reads, singletons	197,411 / 0.75%
Secondary alignments	0
Supplementary alignments	279,467 / 1.06%
Read min/max/mean length	30 / 101 / 101.43
Duplicated reads (estimated)	1,709,723 / 6.47%
Duplication rate	5.07%
Clipped reads	5,079,820 / 19.22%

2.2. ACGT Content

Number/percentage of A's	712,409,975 / 28.4%
Number/percentage of C's	518,511,633 / 20.67%
Number/percentage of T's	719,668,394 / 28.69%
Number/percentage of G's	558,073,307 / 22.24%
Number/percentage of N's	200,582 / 0.01%

GC Percentage	42.91%
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2.3. Coverage

Mean	0.811
Standard Deviation	3.7253

2.4. Mapping Quality

Mean Mapping Quality	53.46
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2.5. Insert size

Mean	105,225.76
Standard Deviation	3,169,403.49
P25/Median/P75	143 / 178 / 231

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	23,275,700
Insertions	390,601
Mapped reads with at least one insertion	1.48%
Deletions	1,331,856
Mapped reads with at least one deletion	4.98%
Homopolymer indels	52.96%

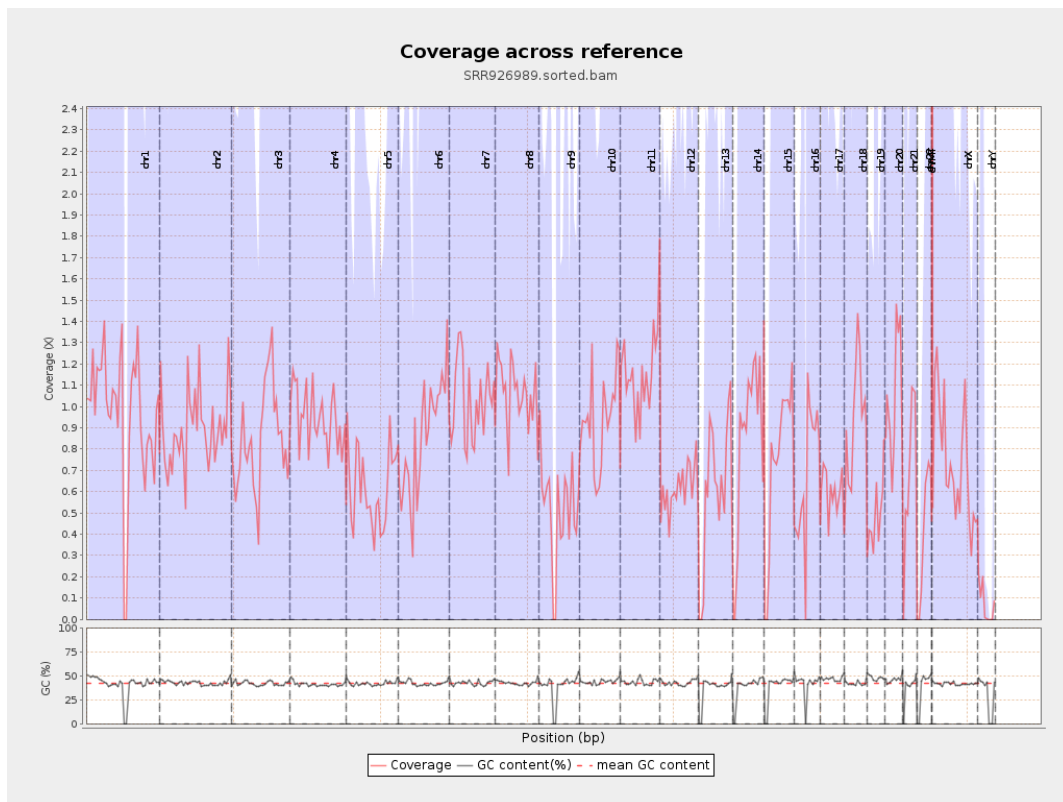
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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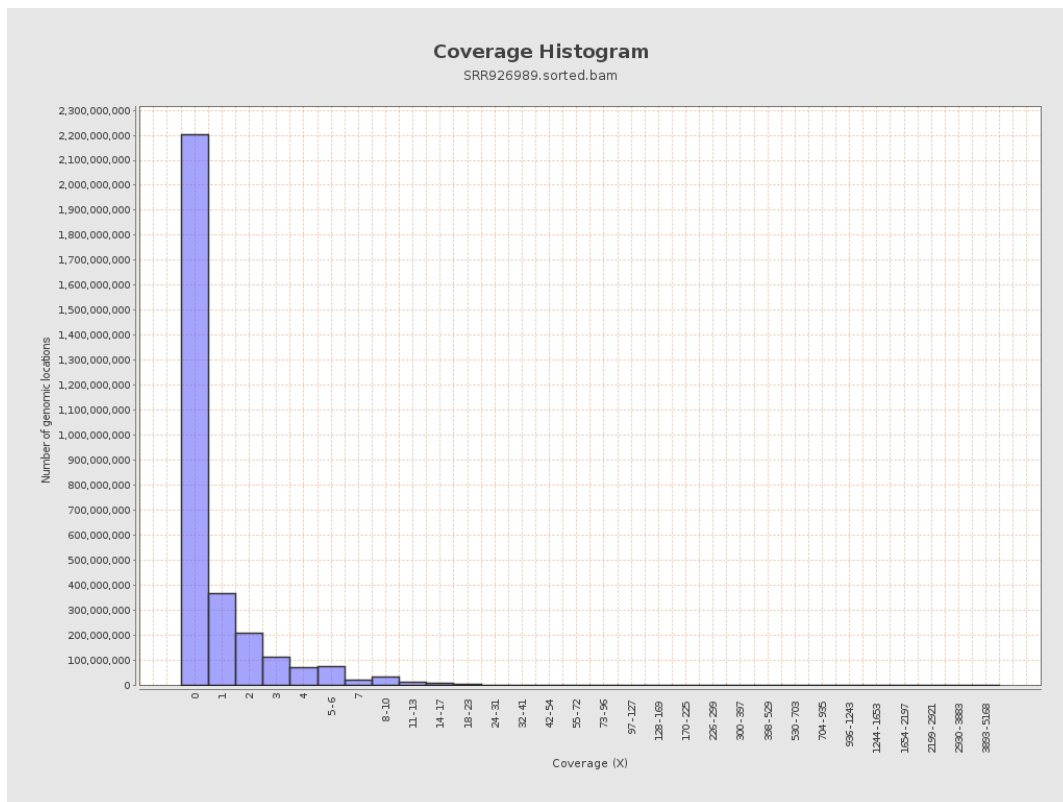
		bases	coverage	deviation
chr1	249250621	240997941	0.9669	5.8906
chr2	243199373	218047189	0.8966	4.7497
chr3	198022430	166744842	0.8421	1.9595
chr4	191154276	181489124	0.9494	2.5636
chr5	180915260	112287616	0.6207	1.6298
chr6	171115067	147141644	0.8599	3.8792
chr7	159138663	163431351	1.027	3.3502
chr8	146364022	156434328	1.0688	2.5945
chr9	141213431	72663163	0.5146	5.1333
chr10	135534747	127659167	0.9419	6.6122
chr11	135006516	152539890	1.1299	4.3239
chr12	133851895	82270597	0.6146	1.8894
chr13	115169878	71126253	0.6176	1.7131
chr14	107349540	90246073	0.8407	2.0279
chr15	102531392	76353605	0.7447	1.9317
chr16	90354753	61567862	0.6814	4.3881
chr17	81195210	48439128	0.5966	2.1442
chr18	78077248	75941858	0.9727	5.5854
chr19	59128983	27840801	0.4708	3.219
chr20	63025520	66199673	1.0504	2.3748
chr21	48129895	33844787	0.7032	3.0051
chr22	51304566	21074178	0.4108	1.4353
chrMT	16571	248599	15.0021	11.0734
chrX	155270560	111890991	0.7206	2.2524

chrY	59373566	4252382	0.0716	1.7722
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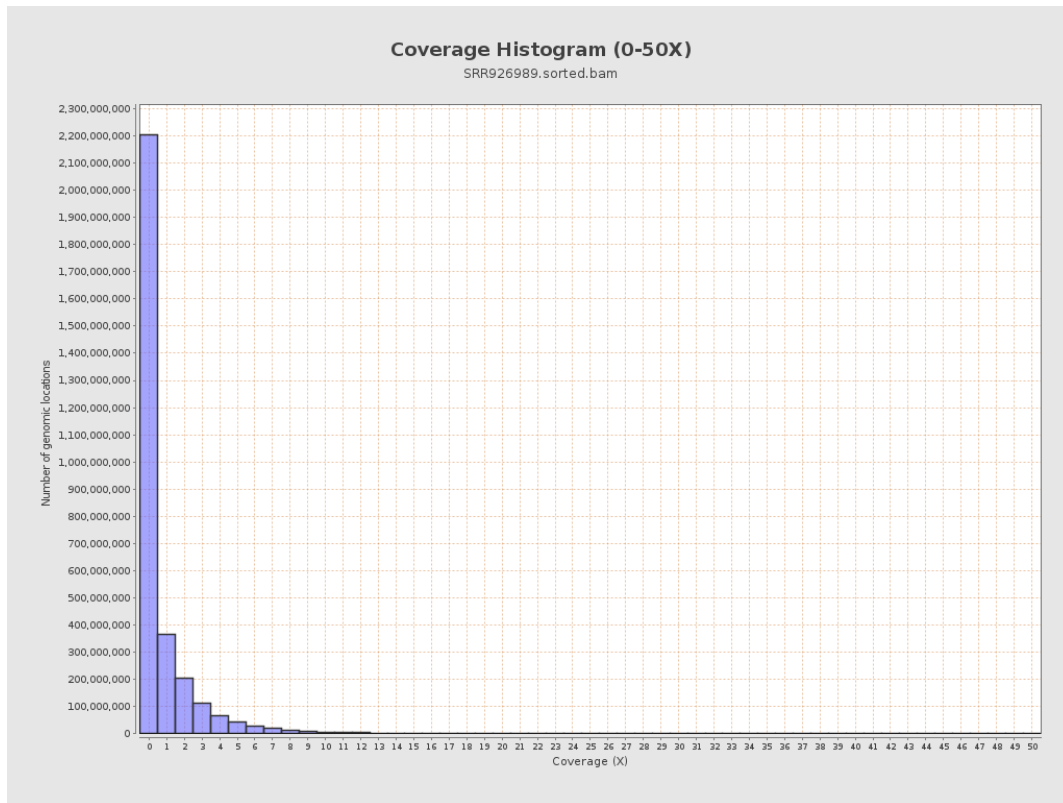
3. Results : Coverage across reference



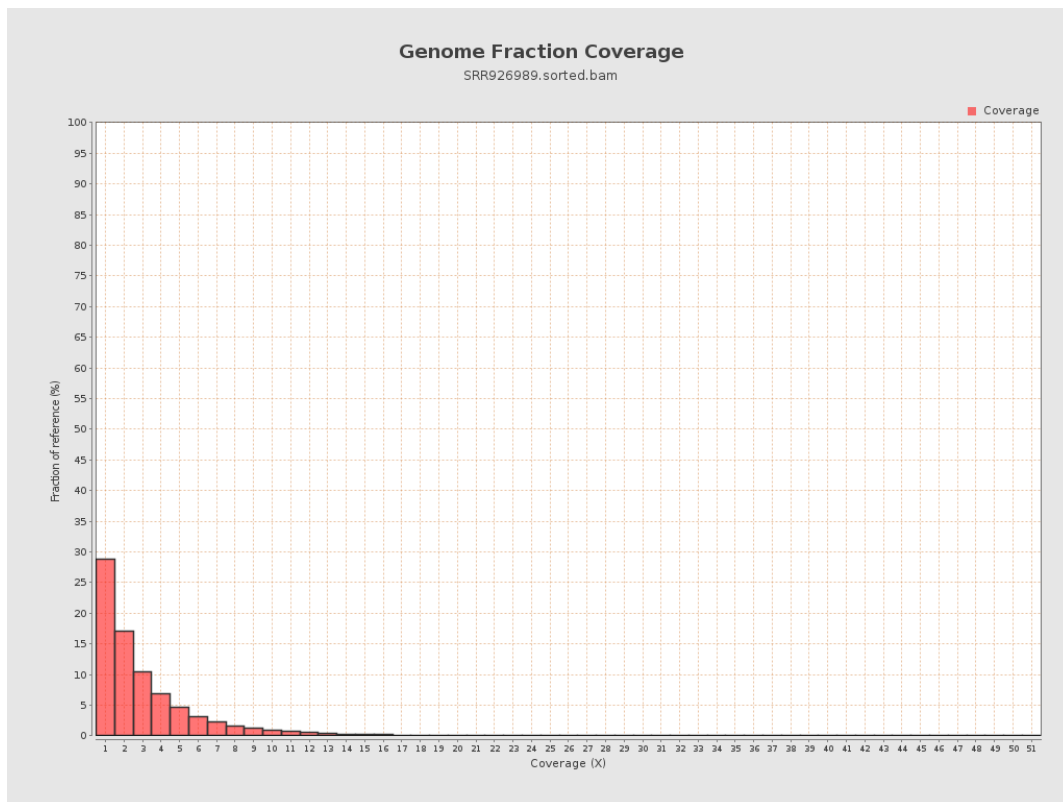
4. Results : Coverage Histogram



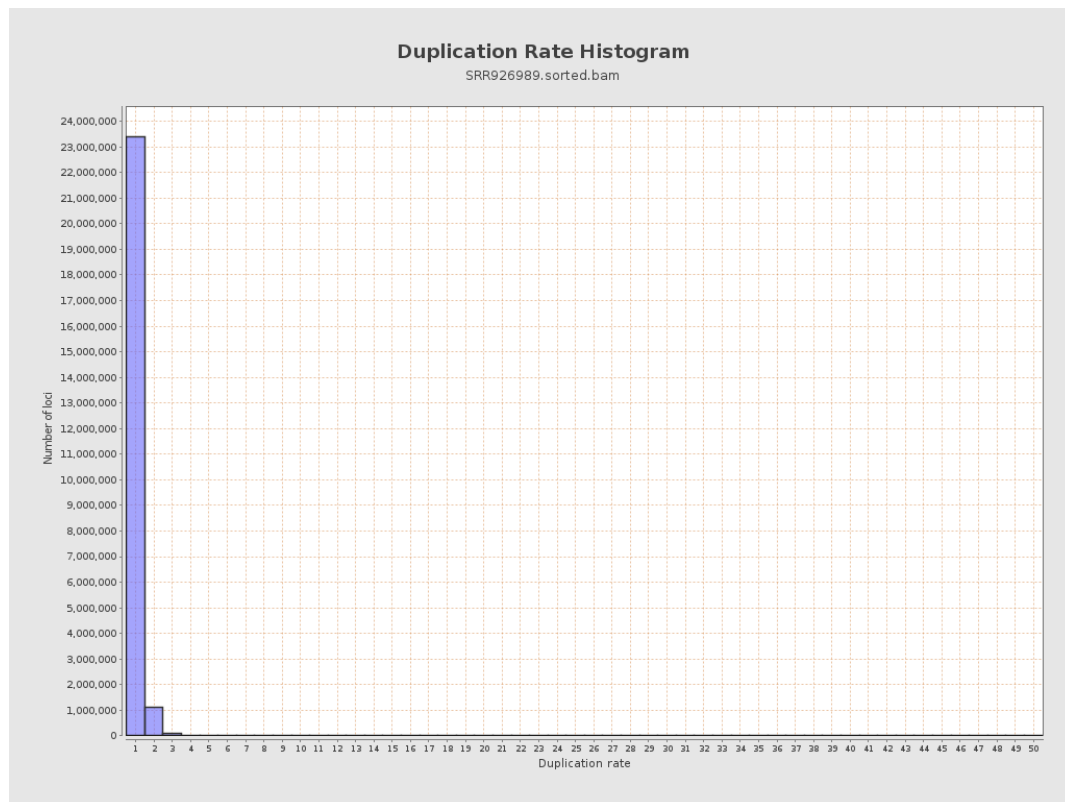
5. Results : Coverage Histogram (0-50X)



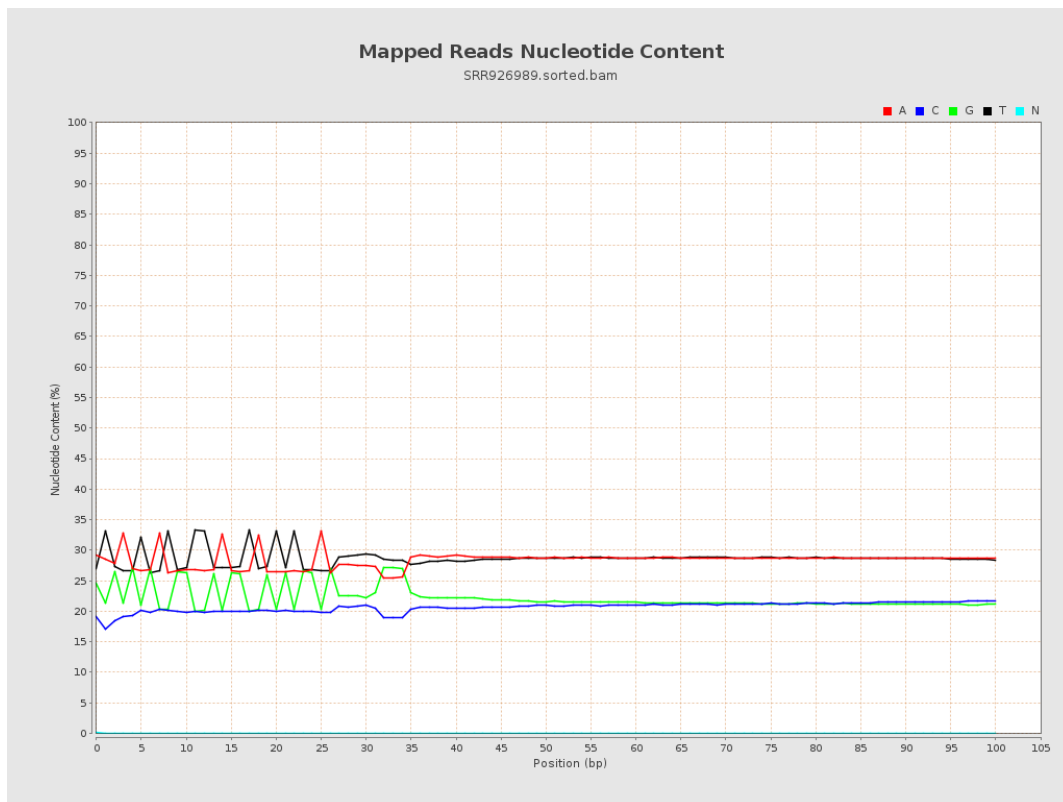
6. Results : Genome Fraction Coverage



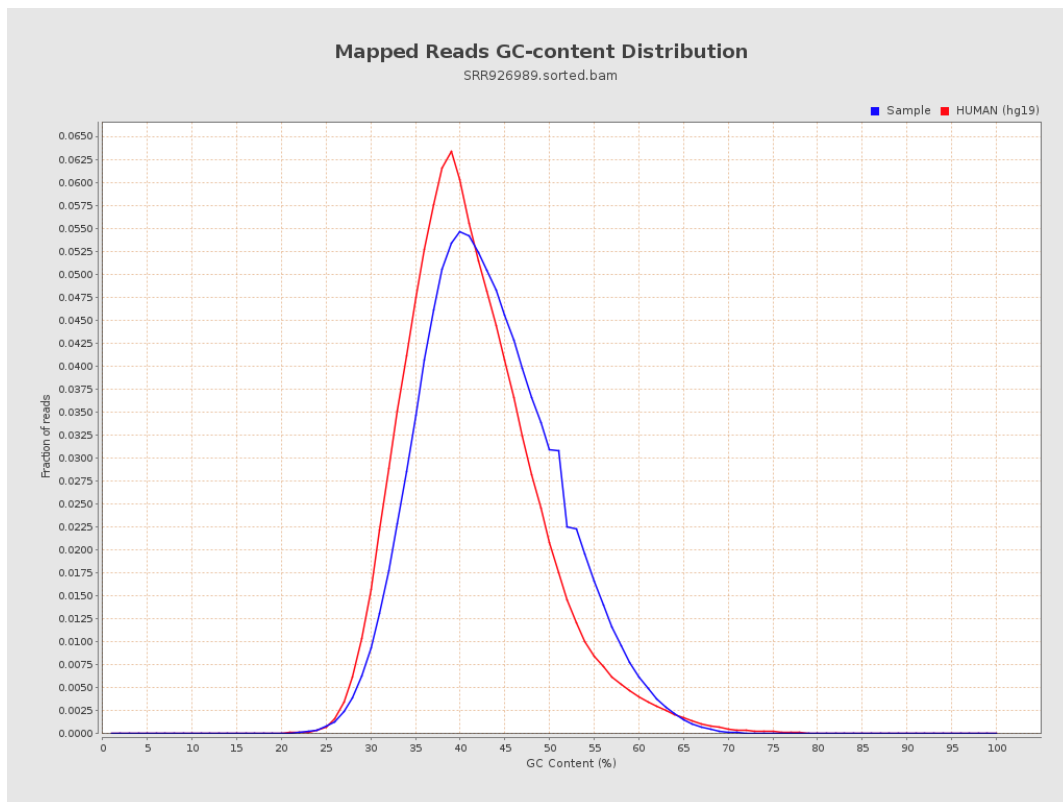
7. Results : Duplication Rate Histogram



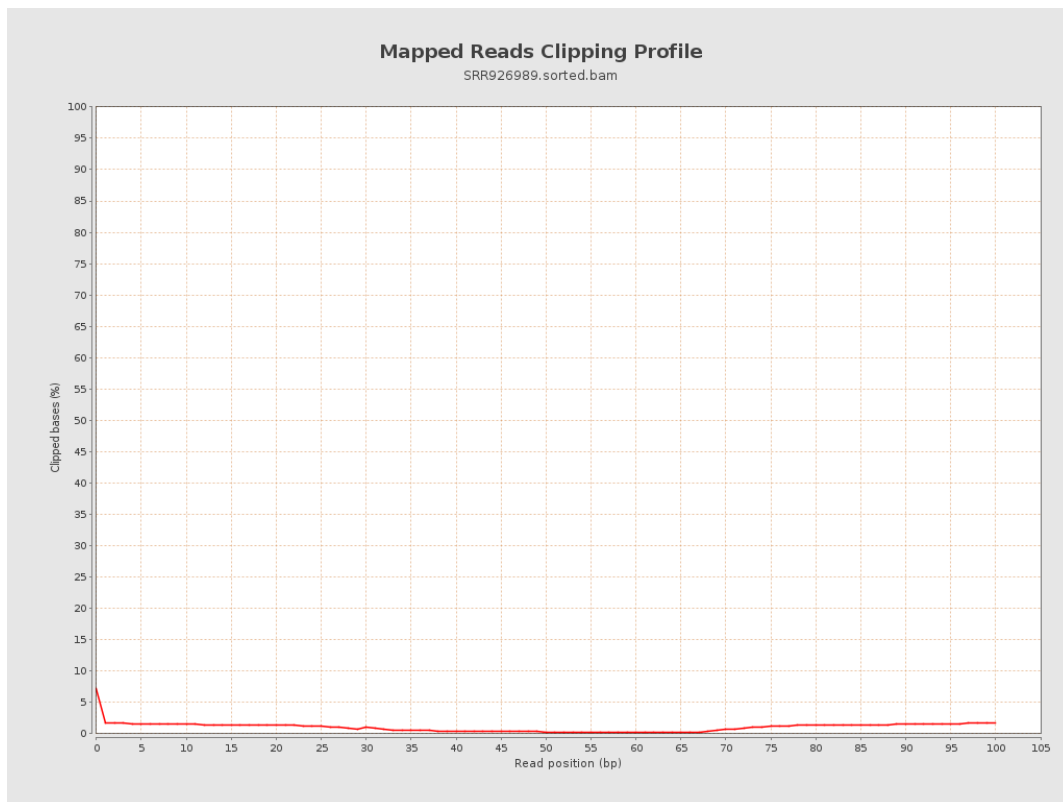
8. Results : Mapped Reads Nucleotide Content



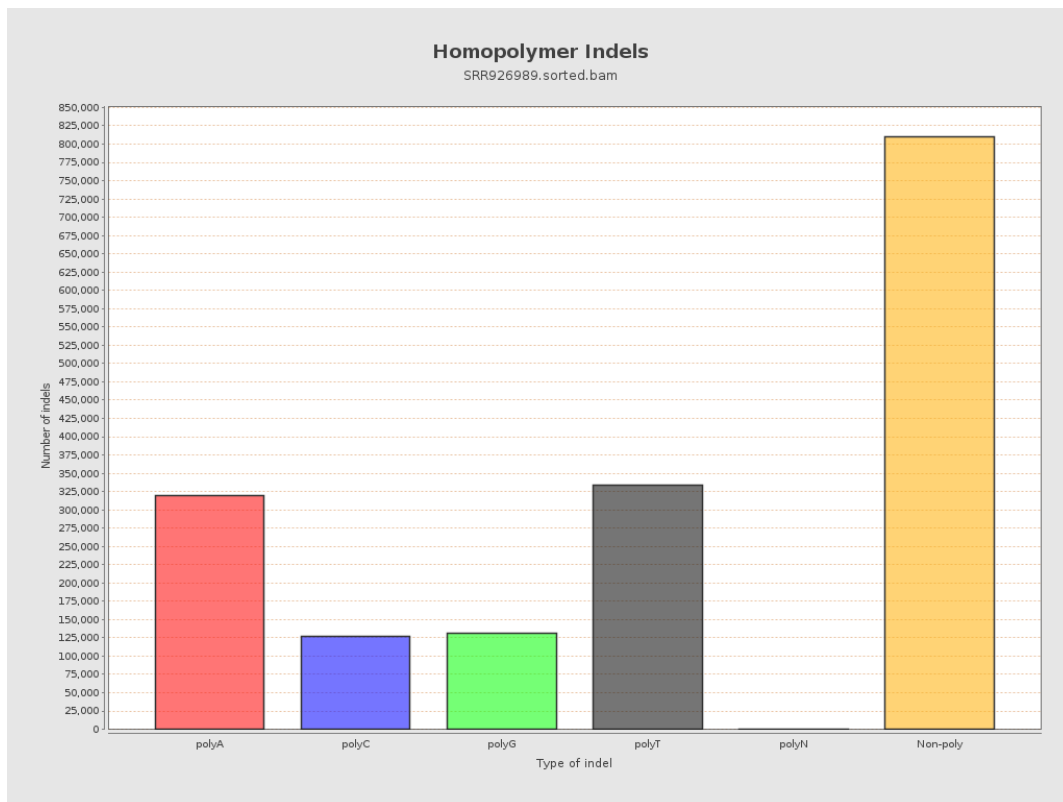
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



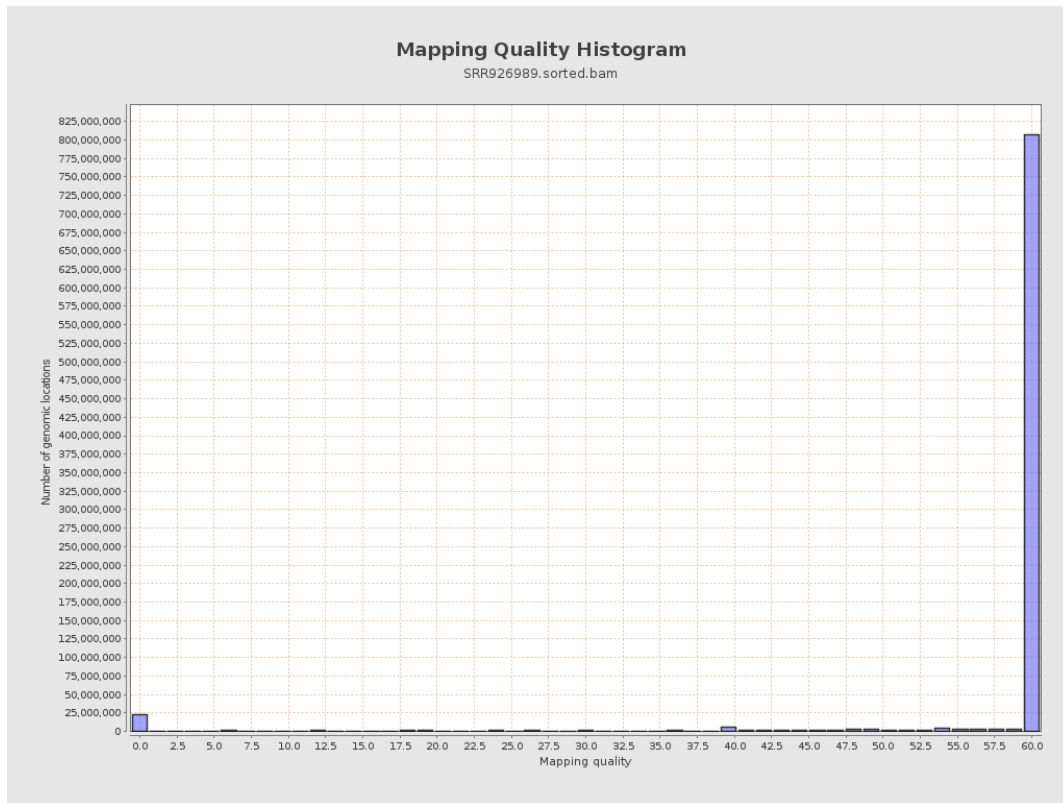
11. Results : Homopolymer Indels



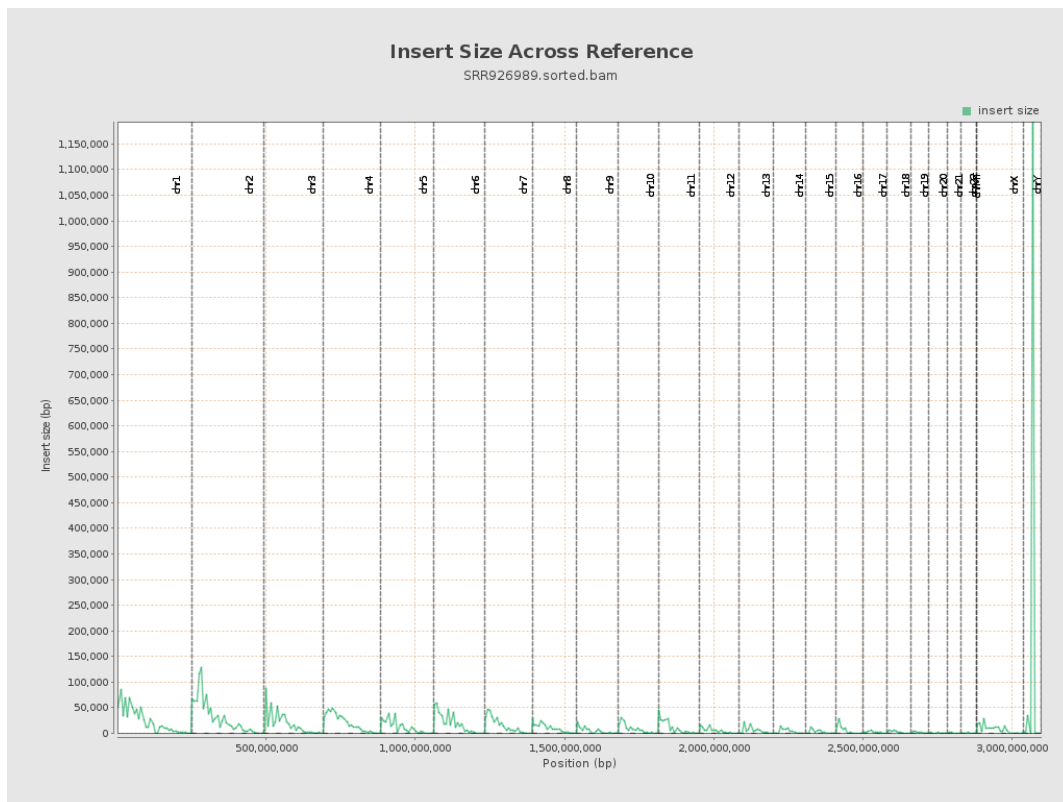
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

