

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 17:56:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926919.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_SRR926919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926919_1.fastq.gz SRR926919_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 17:56:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,409,822
Mapped reads	27,008,414 / 88.81%
Unmapped reads	3,401,408 / 11.19%
Mapped paired reads	27,008,414 / 88.81%
Mapped reads, first in pair	13,570,186 / 44.62%
Mapped reads, second in pair	13,438,228 / 44.19%
Mapped reads, both in pair	26,548,068 / 87.3%
Mapped reads, singletons	460,346 / 1.51%
Secondary alignments	0
Supplementary alignments	500,668 / 1.65%
Read min/max/mean length	30 / 101 / 101.68
Duplicated reads (estimated)	2,131,425 / 7.01%
Duplication rate	6.41%
Clipped reads	10,107,850 / 33.24%

2.2. ACGT Content

Number/percentage of A's	696,688,890 / 28.13%
Number/percentage of C's	496,524,930 / 20.05%
Number/percentage of T's	703,261,200 / 28.4%
Number/percentage of G's	579,698,911 / 23.41%
Number/percentage of N's	216,846 / 0.01%

GC Percentage	43.46%
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2.3. Coverage

Mean	0.8005
Standard Deviation	2.5822

2.4. Mapping Quality

Mean Mapping Quality	52.92
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2.5. Insert size

Mean	189,739.22
Standard Deviation	4,293,401.44
P25/Median/P75	141 / 184 / 249

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	25,402,159
Insertions	392,938
Mapped reads with at least one insertion	1.43%
Deletions	1,272,390
Mapped reads with at least one deletion	4.59%
Homopolymer indels	52.24%

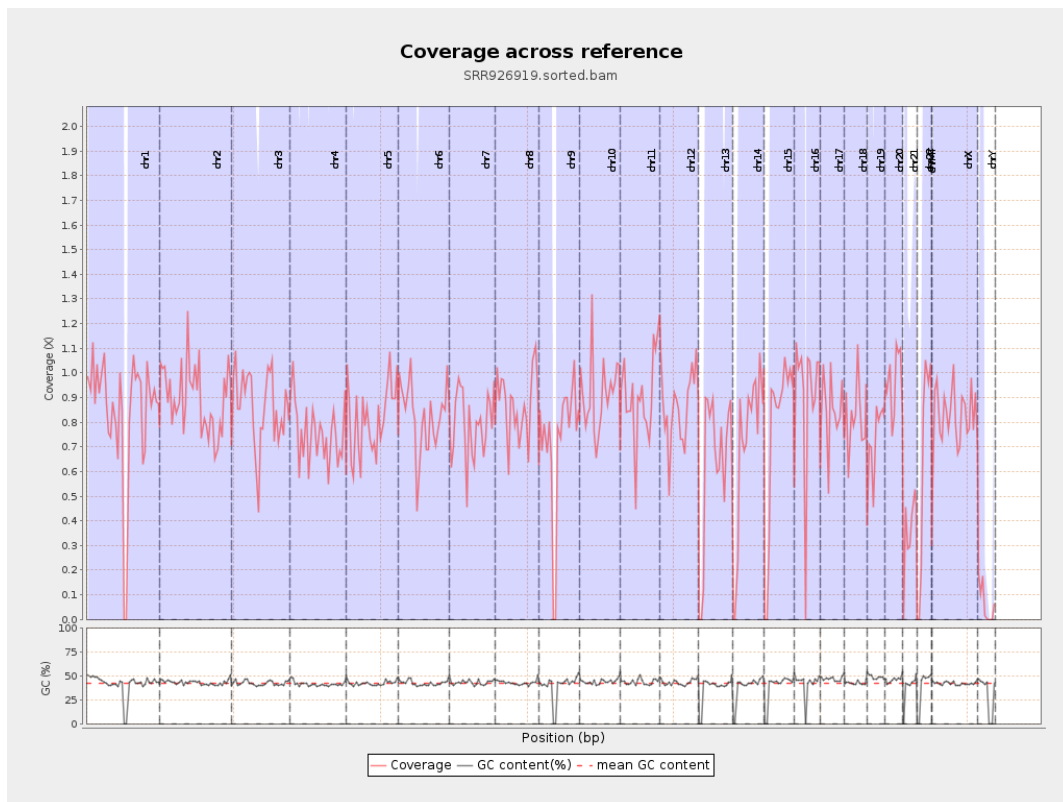
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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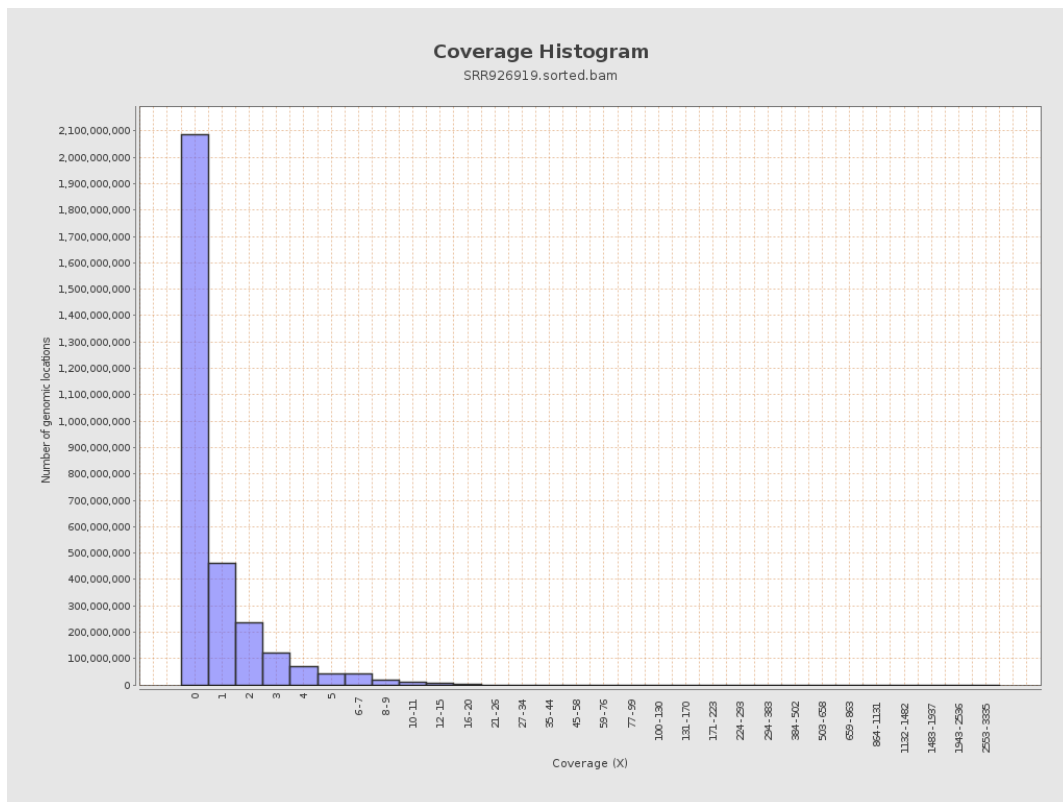
		bases	coverage	deviation
chr1	249250621	211068374	0.8468	2.5357
chr2	243199373	218007342	0.8964	3.592
chr3	198022430	171101277	0.864	1.7771
chr4	191154276	144283990	0.7548	1.8076
chr5	180915260	147574816	0.8157	1.7035
chr6	171115067	141284281	0.8257	1.7189
chr7	159138663	125803491	0.7905	1.8301
chr8	146364022	127546234	0.8714	1.9476
chr9	141213431	102123912	0.7232	2.6623
chr10	135534747	124177362	0.9162	6.7793
chr11	135006516	121041634	0.8966	2.0468
chr12	133851895	115206153	0.8607	1.841
chr13	115169878	73000793	0.6339	1.496
chr14	107349540	75650159	0.7047	1.647
chr15	102531392	78339136	0.7641	1.7729
chr16	90354753	80855388	0.8949	3.469
chr17	81195210	68598699	0.8449	1.9459
chr18	78077248	65083408	0.8336	2.6476
chr19	59128983	43253162	0.7315	1.9298
chr20	63025520	60860656	0.9657	1.9887
chr21	48129895	17666564	0.3671	1.8221
chr22	51304566	33575210	0.6544	1.6786
chrMT	16571	4992	0.3012	0.6923
chrX	155270560	128337328	0.8265	1.7759

chrY	59373566	3774249	0.0636	1.5753
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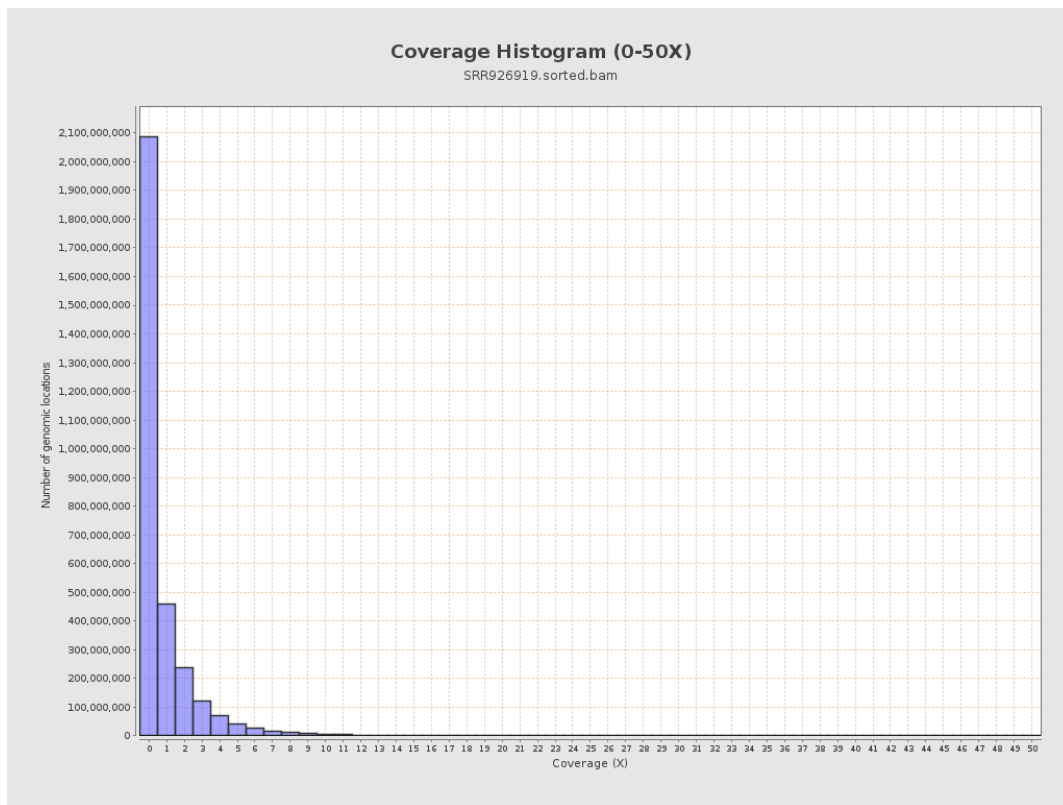
3. Results : Coverage across reference



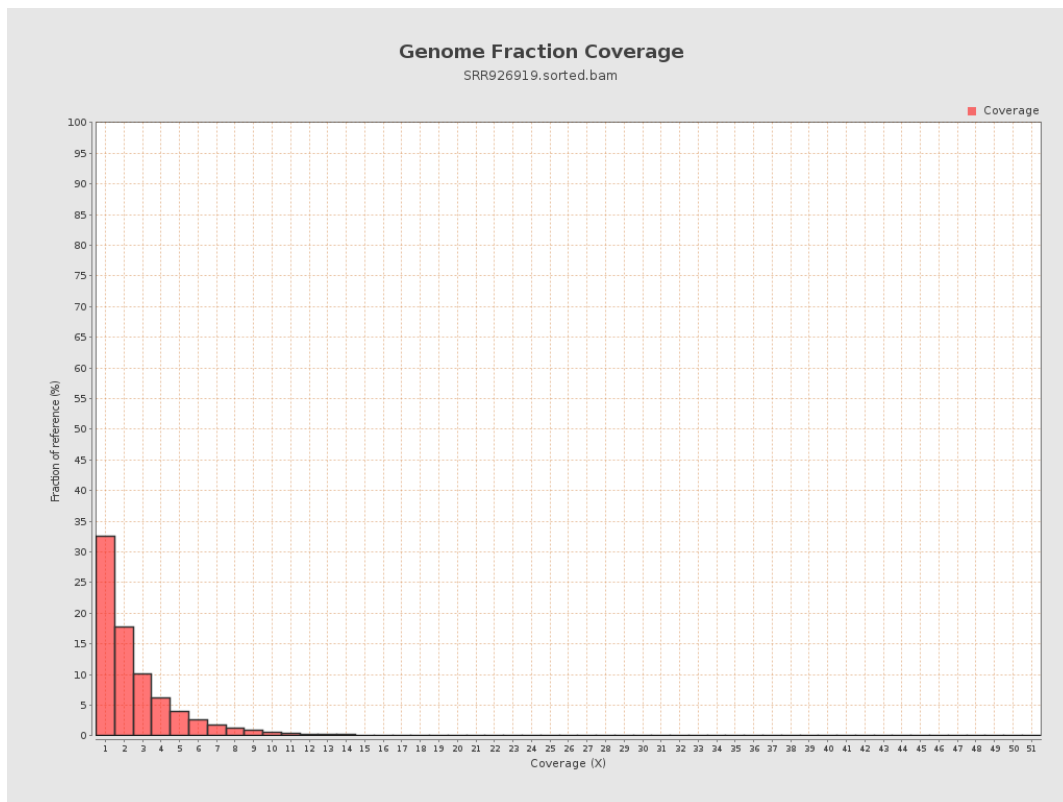
4. Results : Coverage Histogram



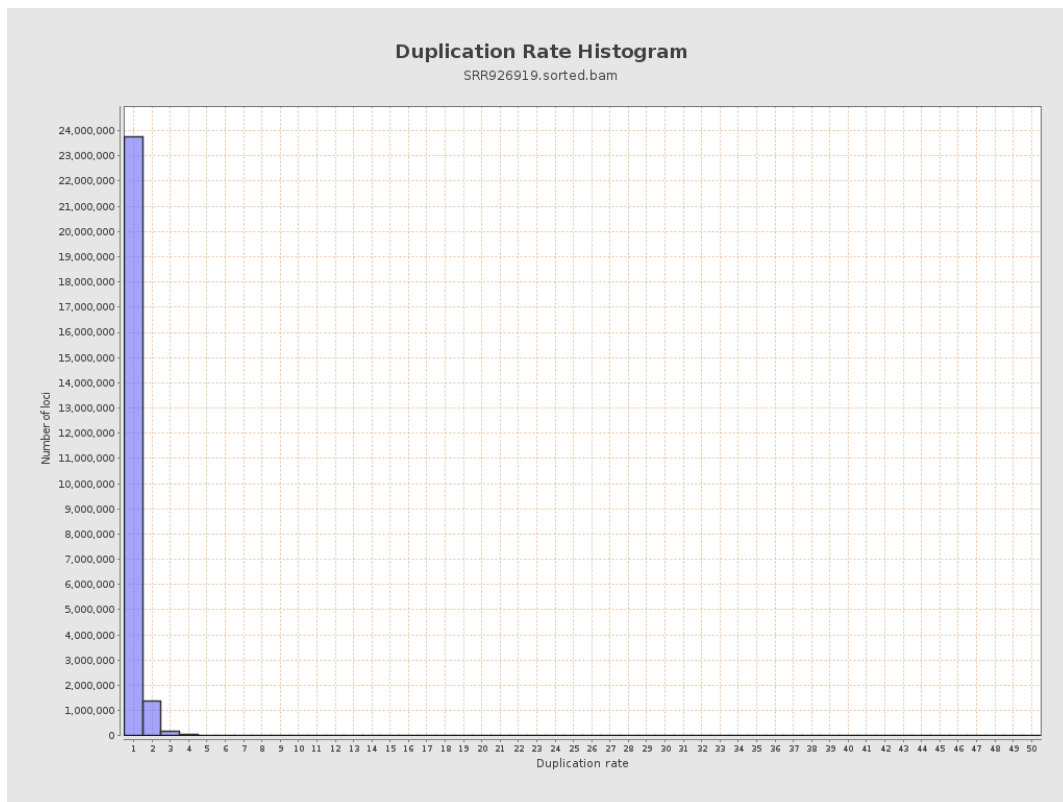
5. Results : Coverage Histogram (0-50X)



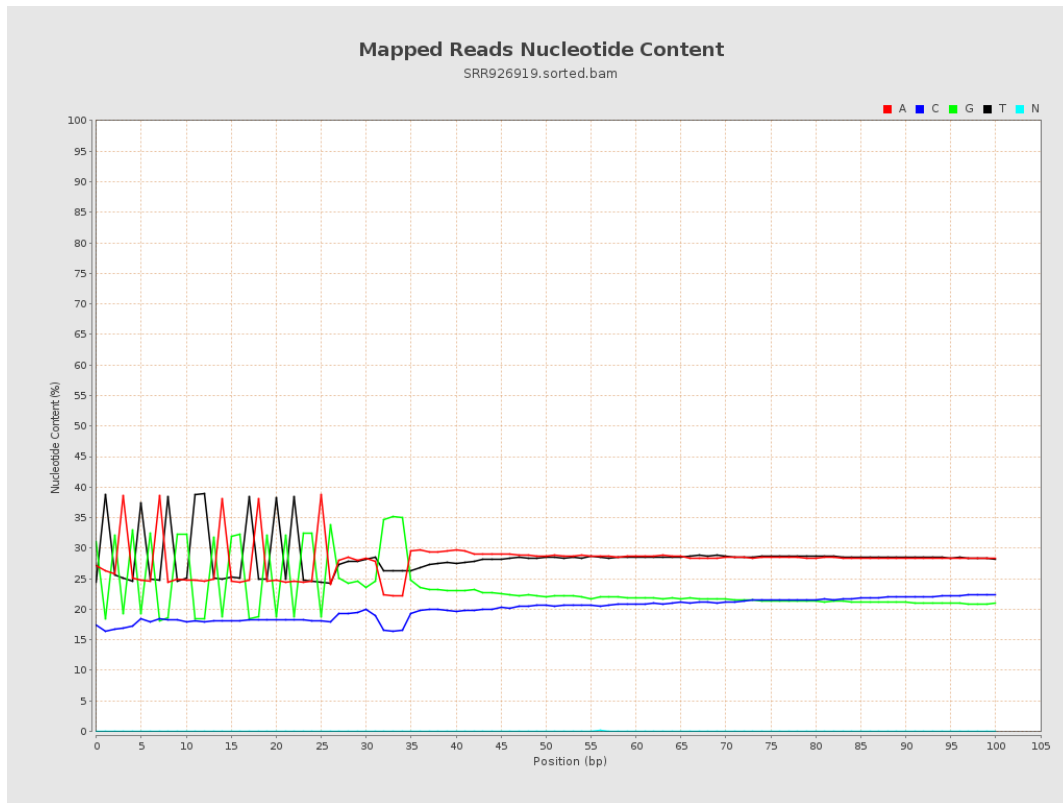
6. Results : Genome Fraction Coverage



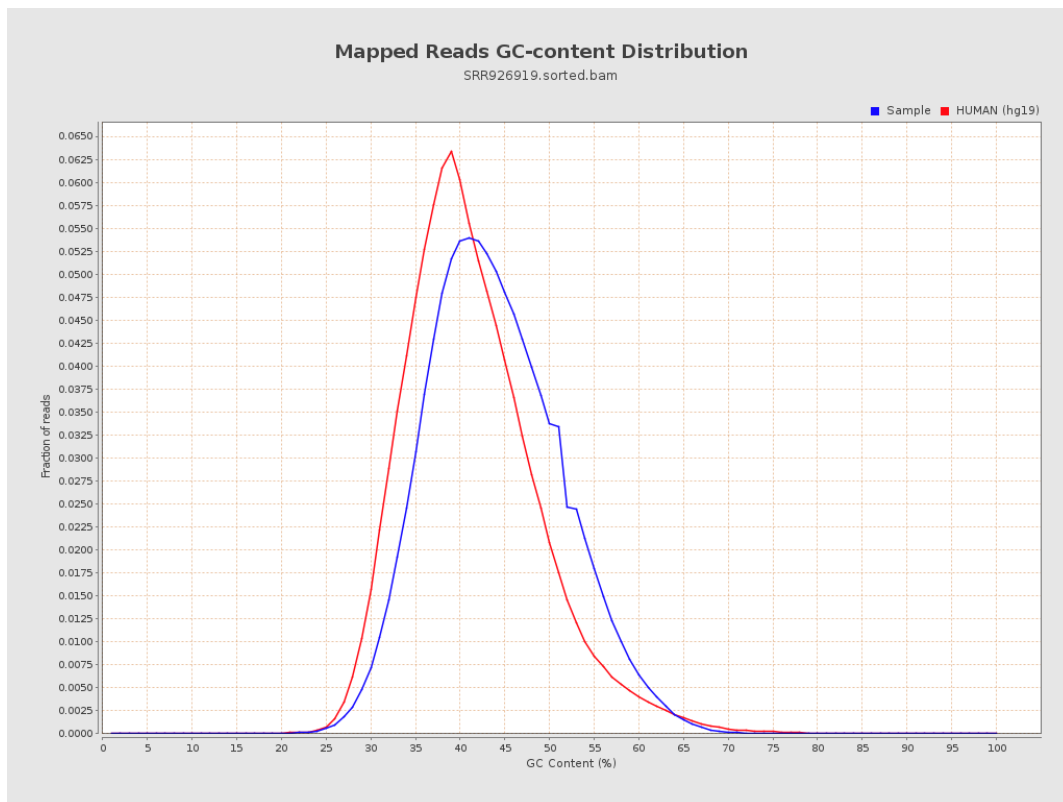
7. Results : Duplication Rate Histogram



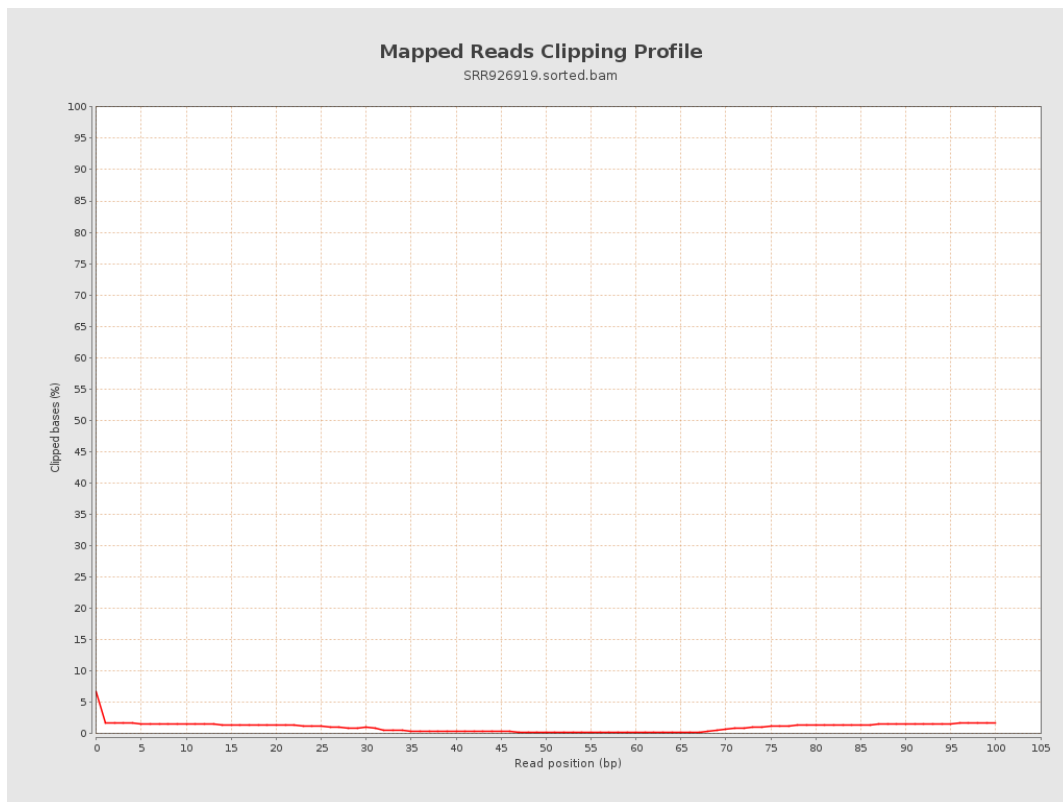
8. Results : Mapped Reads Nucleotide Content



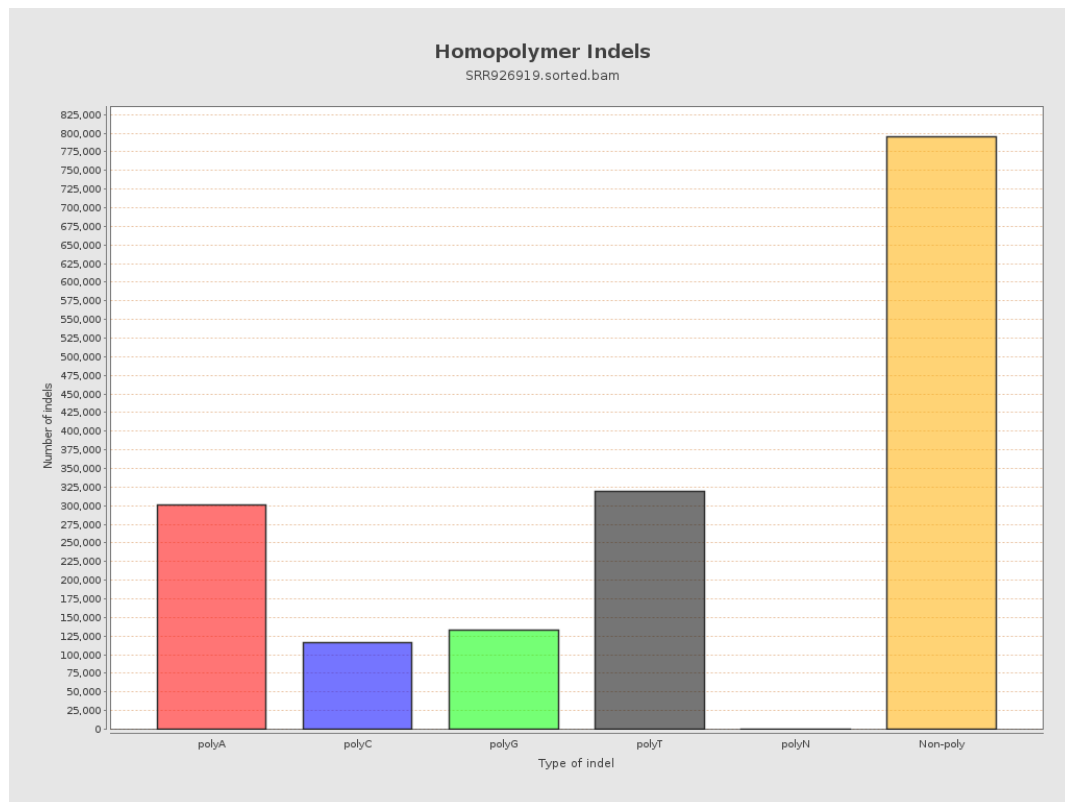
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



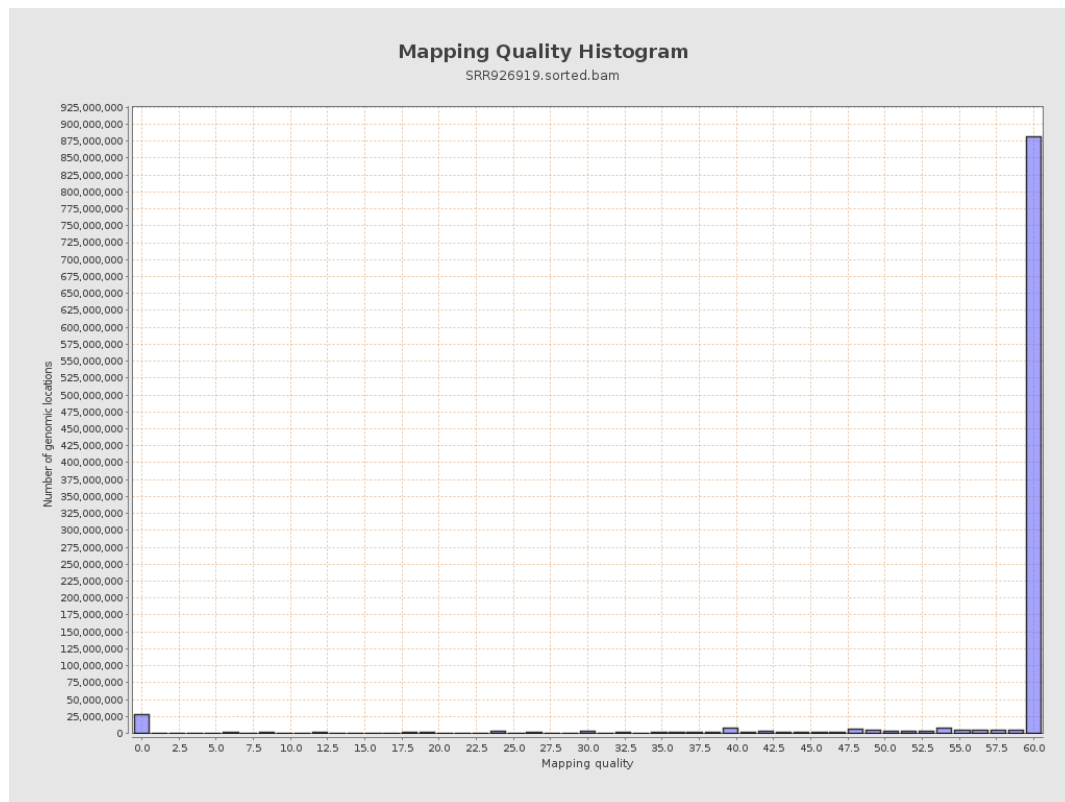
11. Results : Homopolymer Indels



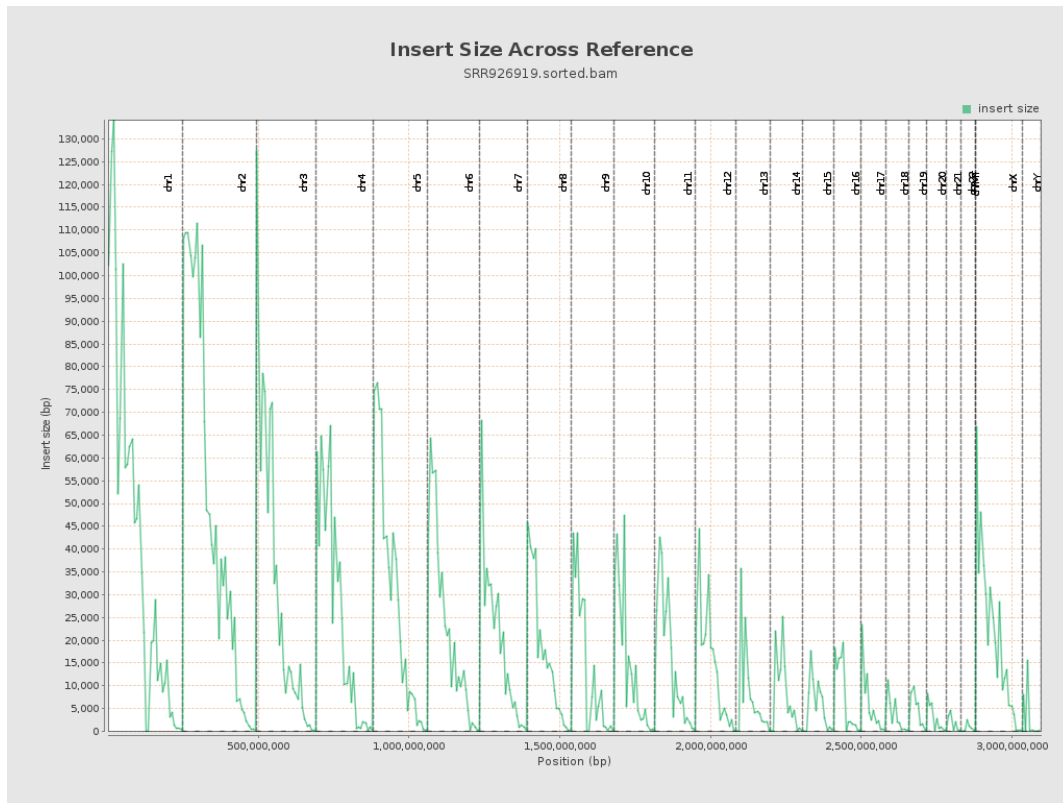
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

