

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 18:59:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926991.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_SRR926991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926991_1.fastq.gz SRR926991_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 18:59:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926991.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,499,884
Mapped reads	21,074,927 / 98.02%
Unmapped reads	424,957 / 1.98%
Mapped paired reads	21,074,927 / 98.02%
Mapped reads, first in pair	10,582,129 / 49.22%
Mapped reads, second in pair	10,492,798 / 48.8%
Mapped reads, both in pair	20,814,386 / 96.81%
Mapped reads, singletons	260,541 / 1.21%
Secondary alignments	0
Supplementary alignments	581,620 / 2.71%
Read min/max/mean length	30 / 101 / 102.12
Duplicated reads (estimated)	1,493,628 / 6.95%
Duplication rate	5.59%
Clipped reads	7,429,085 / 34.55%

2.2. ACGT Content

Number/percentage of A's	559,684,812 / 28.55%
Number/percentage of C's	390,434,118 / 19.92%
Number/percentage of T's	568,065,333 / 28.98%
Number/percentage of G's	441,810,170 / 22.54%
Number/percentage of N's	149,903 / 0.01%

GC Percentage	42.46%
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2.3. Coverage

Mean	0.6337
Standard Deviation	2.5532

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	279,197.91
Standard Deviation	5,200,780.21
P25/Median/P75	136 / 173 / 227

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	18,230,167
Insertions	331,167
Mapped reads with at least one insertion	1.55%
Deletions	1,000,842
Mapped reads with at least one deletion	4.63%
Homopolymer indels	52.25%

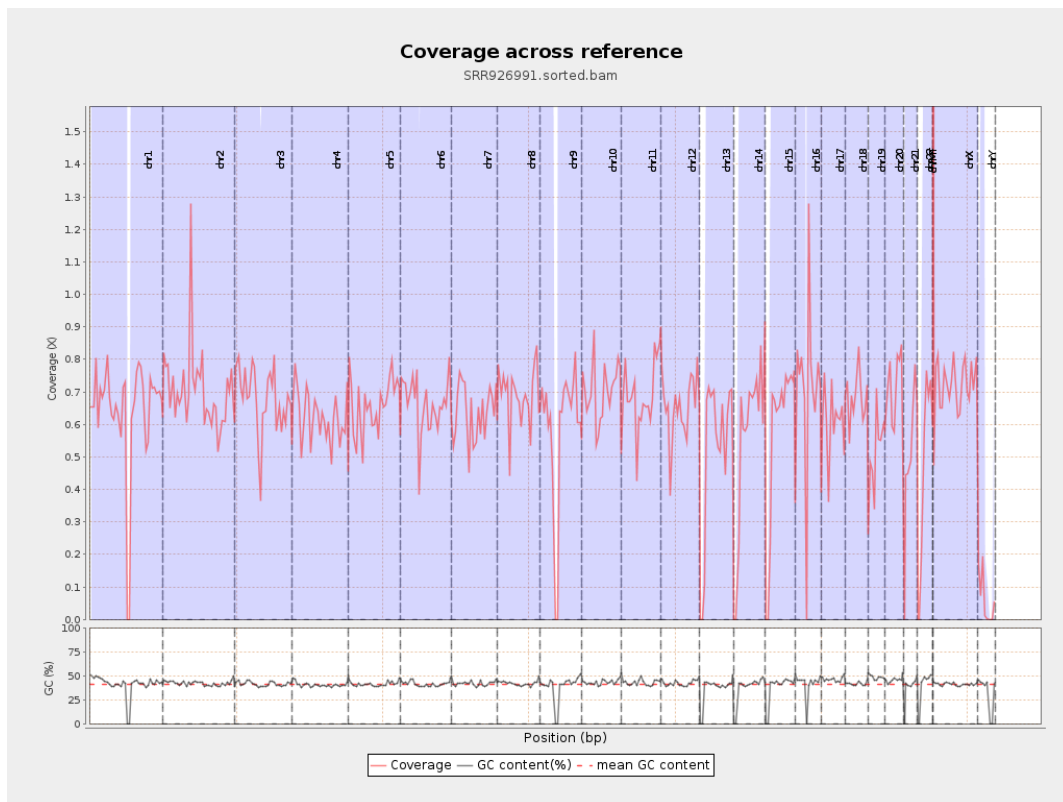
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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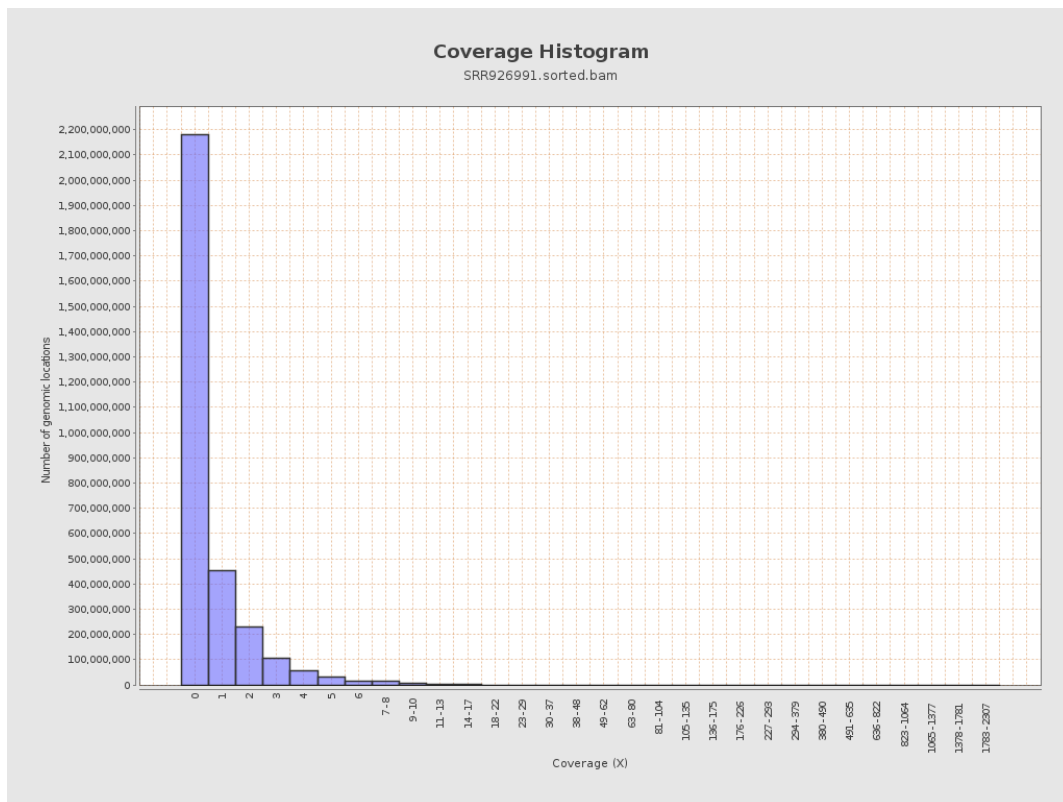
		bases	coverage	deviation
chr1	249250621	159640269	0.6405	2.8426
chr2	243199373	171510363	0.7052	4.5601
chr3	198022430	133757307	0.6755	1.3913
chr4	191154276	119409207	0.6247	2.0317
chr5	180915260	119253212	0.6592	1.3607
chr6	171115067	113360582	0.6625	2.0192
chr7	159138663	100826050	0.6336	2.2107
chr8	146364022	100884344	0.6893	1.6997
chr9	141213431	82786672	0.5863	3.41
chr10	135534747	94773130	0.6993	3.4417
chr11	135006516	92459475	0.6849	2.2103
chr12	133851895	88022135	0.6576	1.6879
chr13	115169878	60286393	0.5235	1.286
chr14	107349540	59580414	0.555	1.3083
chr15	102531392	58070462	0.5664	1.3806
chr16	90354753	63743335	0.7055	5.039
chr17	81195210	49652321	0.6115	1.7206
chr18	78077248	53151677	0.6808	3.6325
chr19	59128983	30636245	0.5181	1.9149
chr20	63025520	45221895	0.7175	1.537
chr21	48129895	25083852	0.5212	2.0033
chr22	51304566	24234867	0.4724	1.2488
chrMT	16571	216779	13.0818	10.4845
chrX	155270560	111550252	0.7184	1.6424

chrY	59373566	3492837	0.0588	1.7806
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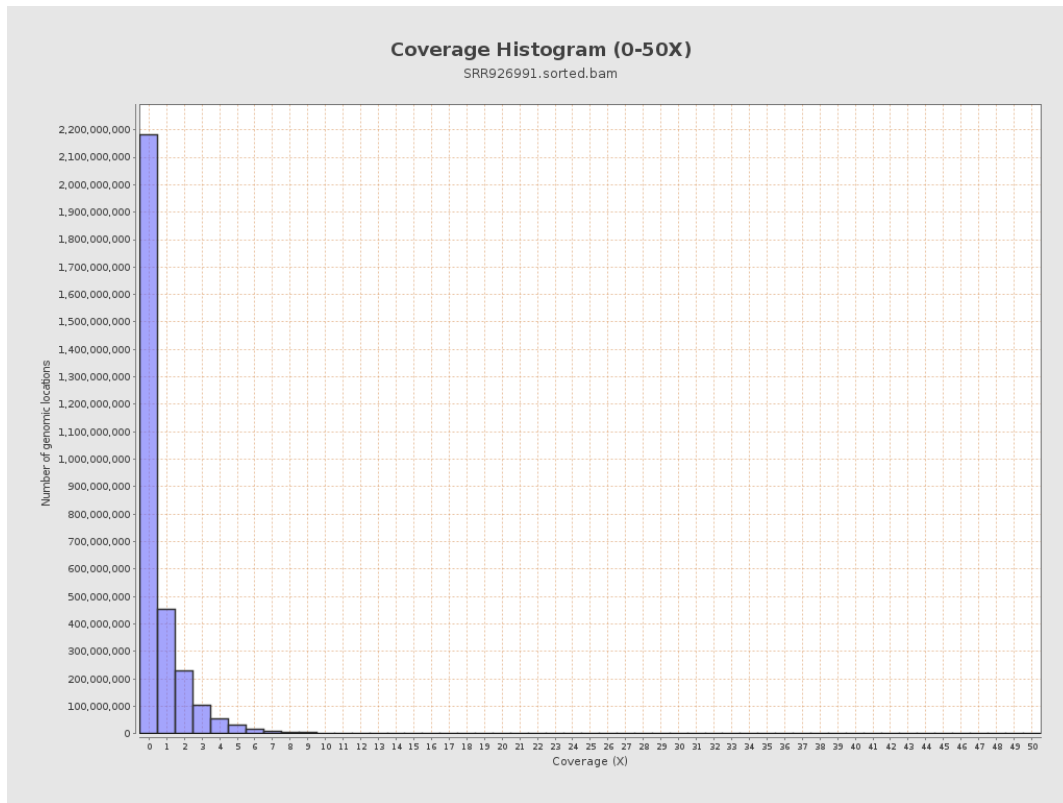
3. Results : Coverage across reference



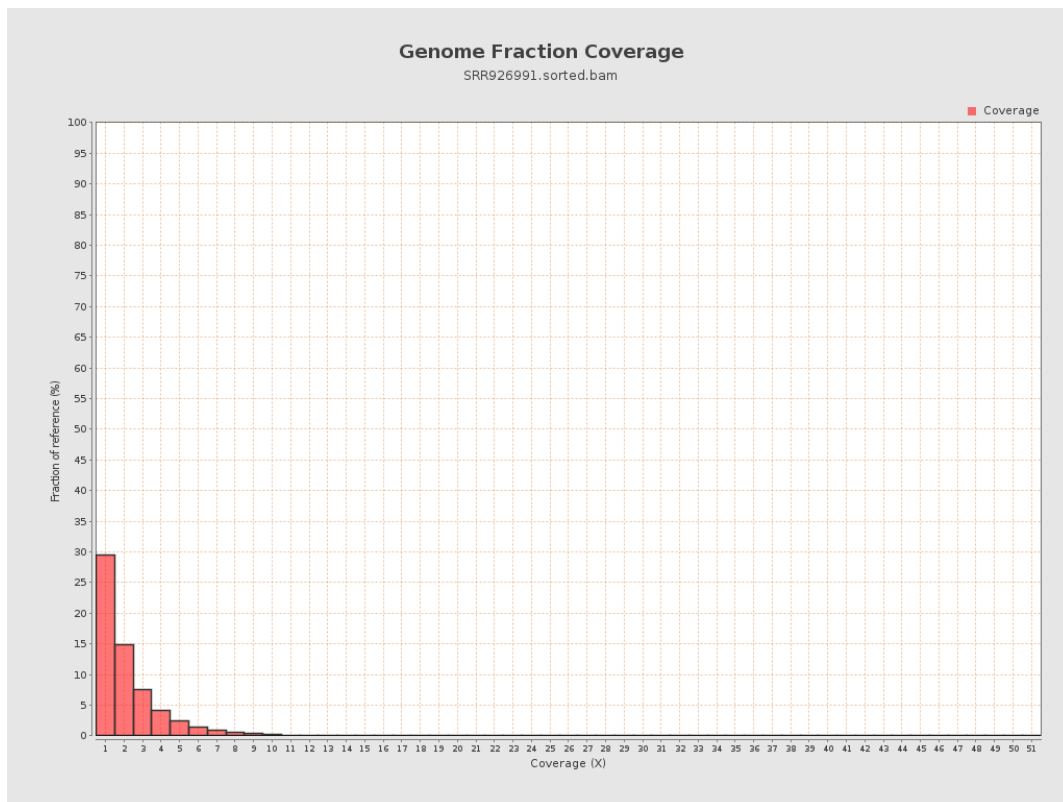
4. Results : Coverage Histogram



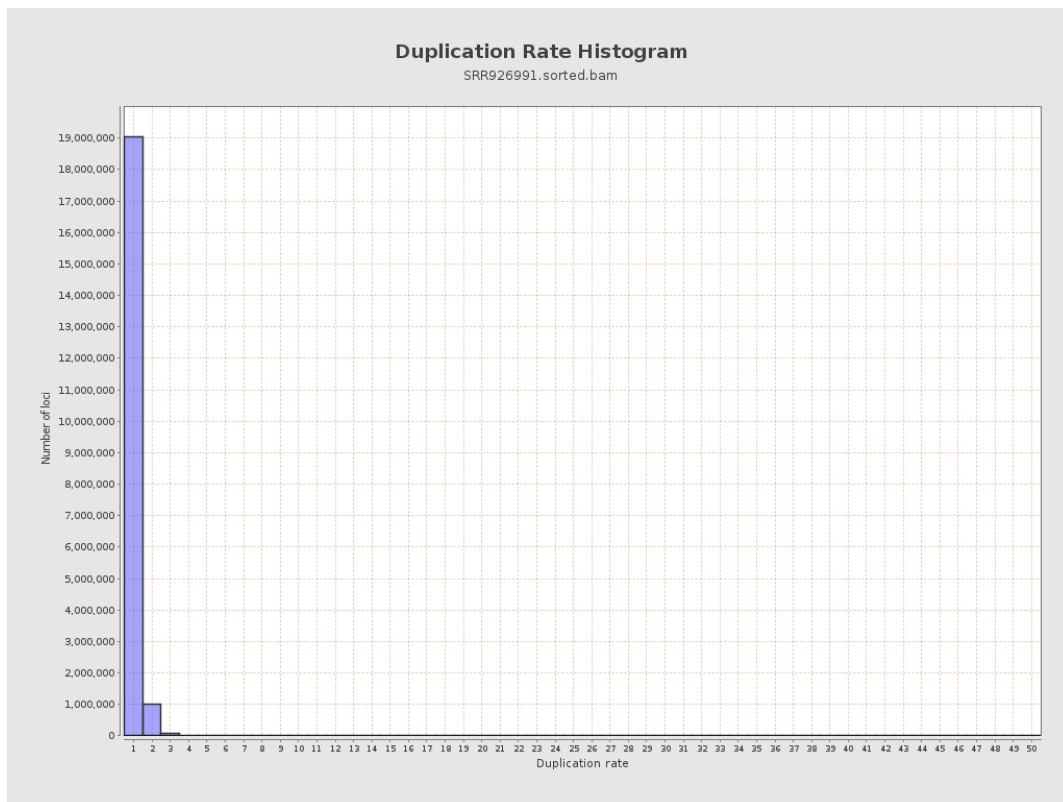
5. Results : Coverage Histogram (0-50X)



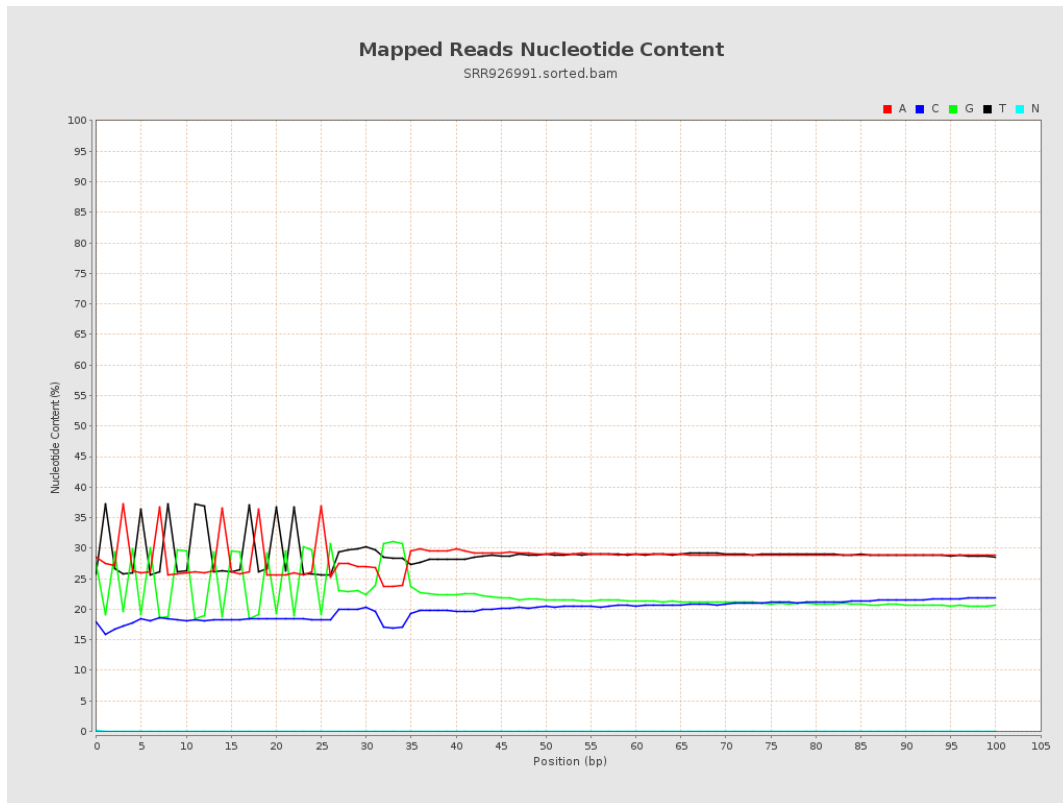
6. Results : Genome Fraction Coverage



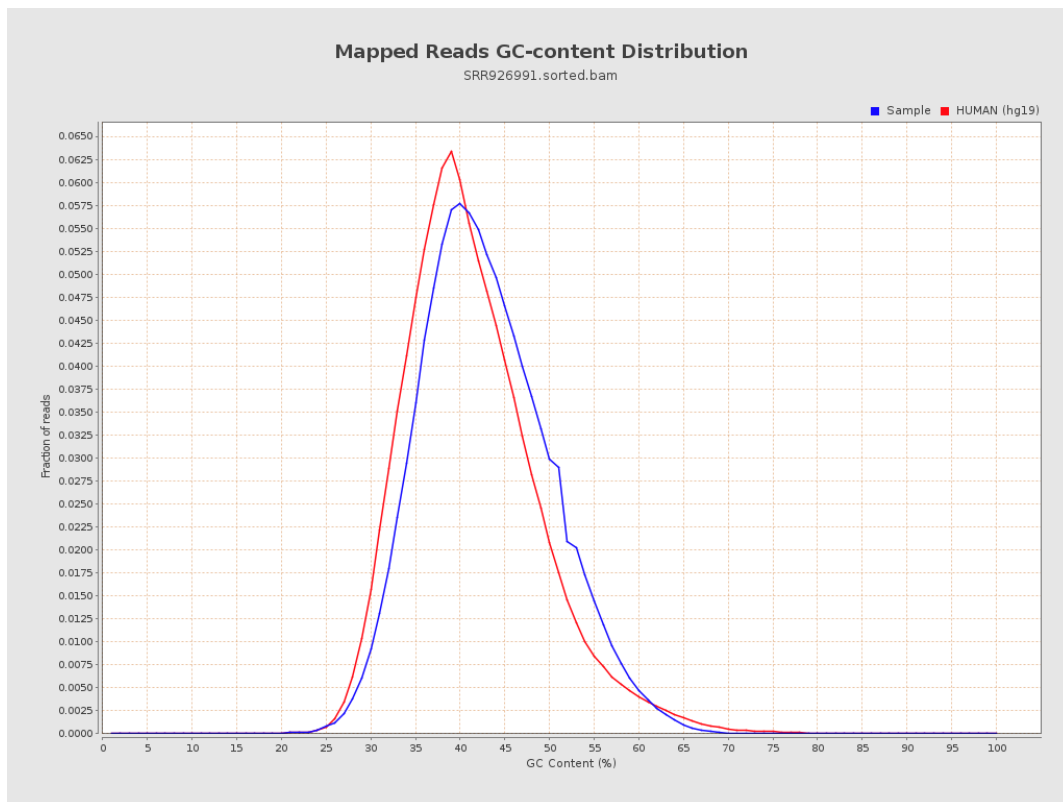
7. Results : Duplication Rate Histogram



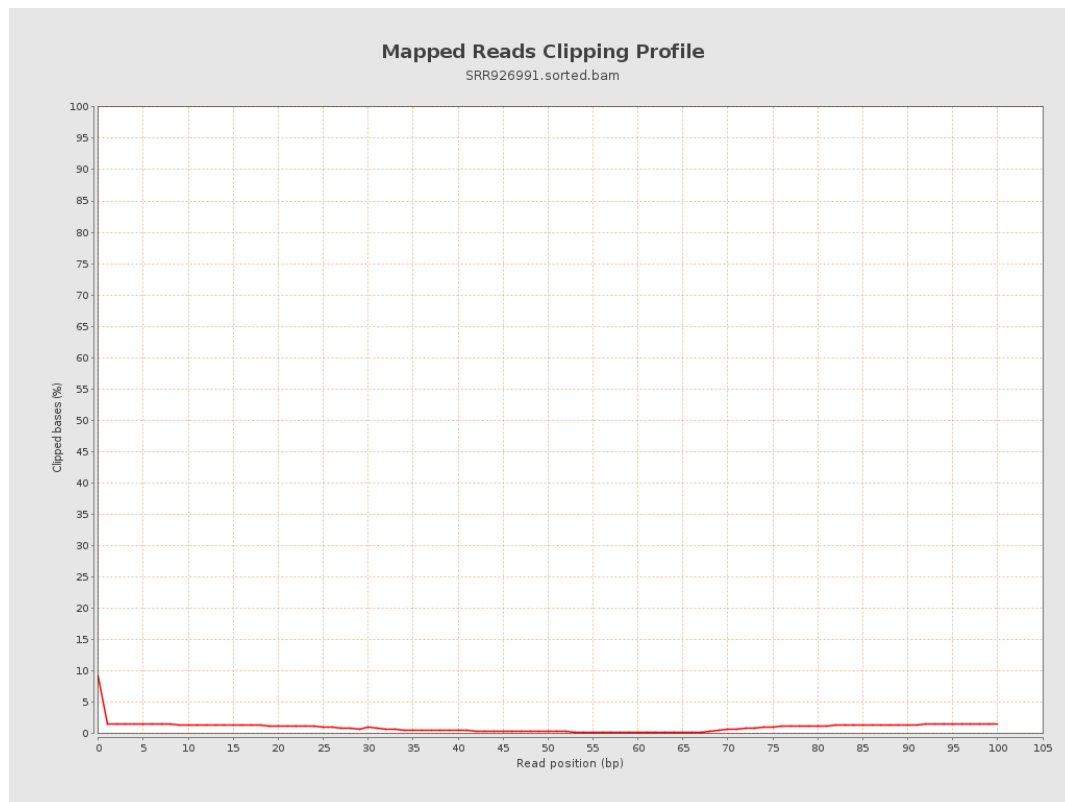
8. Results : Mapped Reads Nucleotide Content



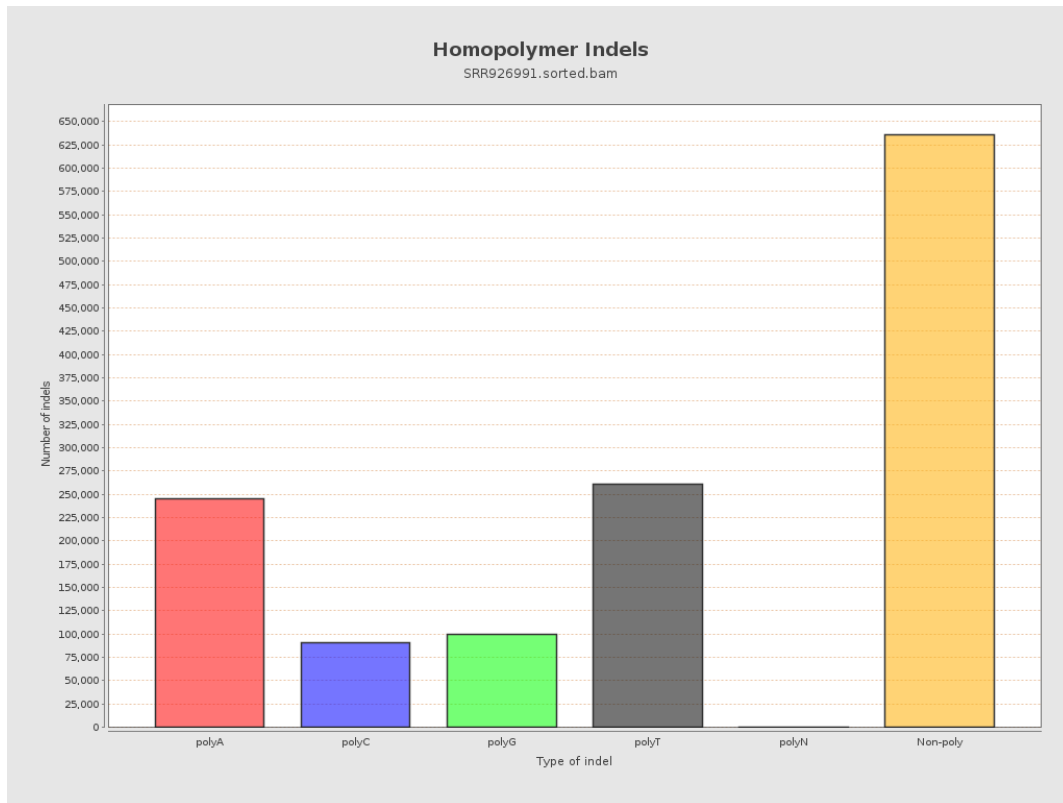
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



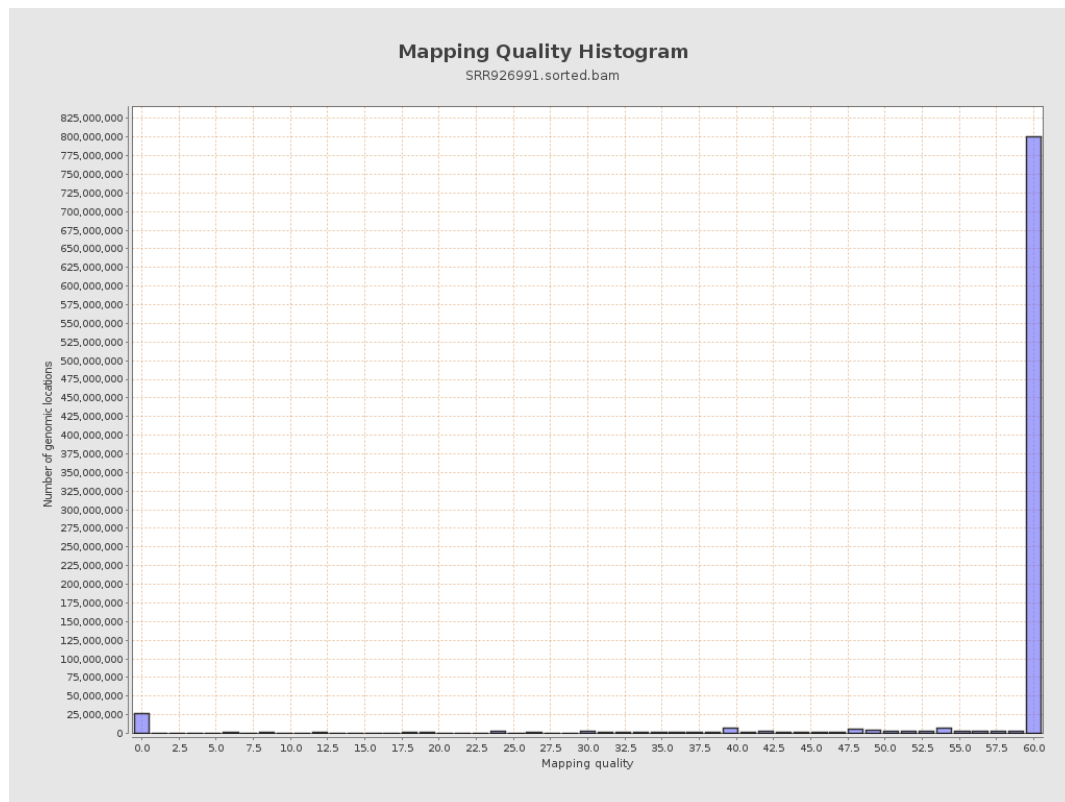
11. Results : Homopolymer Indels



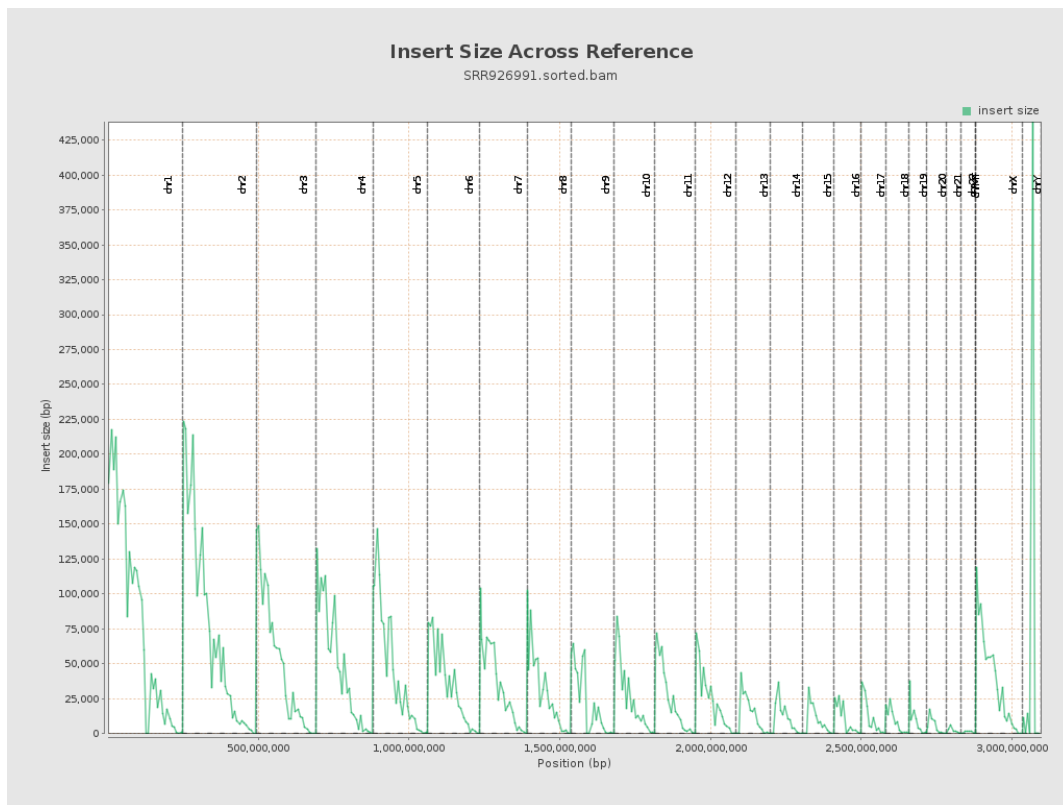
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

