

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 15:24:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046450.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_SRR2046450 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046450_1.fastq.gz SRR2046450_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 15:24:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046450.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,101,054
Mapped reads	8,064,731 / 99.55%
Unmapped reads	36,323 / 0.45%
Mapped paired reads	8,064,731 / 99.55%
Mapped reads, first in pair	4,038,391 / 49.85%
Mapped reads, second in pair	4,026,340 / 49.7%
Mapped reads, both in pair	8,039,256 / 99.24%
Mapped reads, singletons	25,475 / 0.31%
Secondary alignments	0
Supplementary alignments	37,066 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	5,615,396 / 69.32%
Duplication rate	39.12%
Clipped reads	1,125,542 / 13.89%

2.2. ACGT Content

Number/percentage of A's	230,144,135 / 29.27%
Number/percentage of C's	163,553,693 / 20.8%
Number/percentage of T's	230,919,738 / 29.36%
Number/percentage of G's	161,708,382 / 20.56%
Number/percentage of N's	73,347 / 0.01%

GC Percentage	41.36%
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2.3. Coverage

Mean	0.2541
Standard Deviation	17.0613

2.4. Mapping Quality

Mean Mapping Quality	53.51
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2.5. Insert size

Mean	18,705.72
Standard Deviation	1,386,343.1
P25/Median/P75	126 / 165 / 208

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	2,713,240
Insertions	60,873
Mapped reads with at least one insertion	0.74%
Deletions	85,568
Mapped reads with at least one deletion	1.02%
Homopolymer indels	49.47%

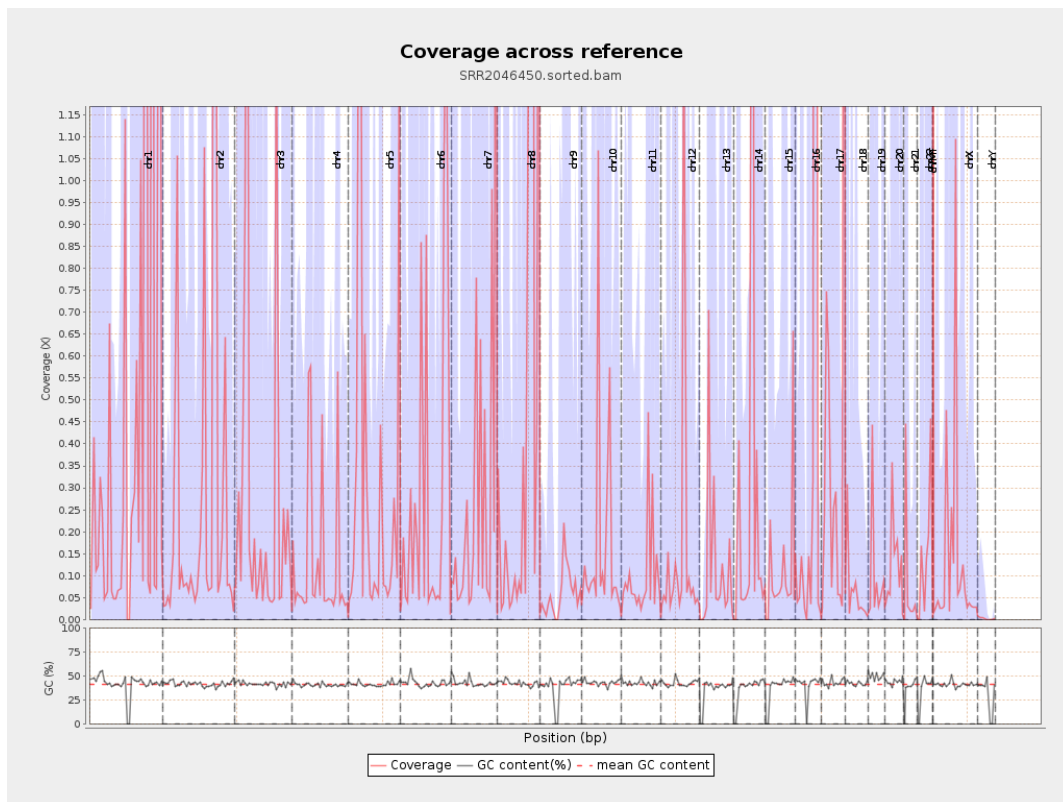
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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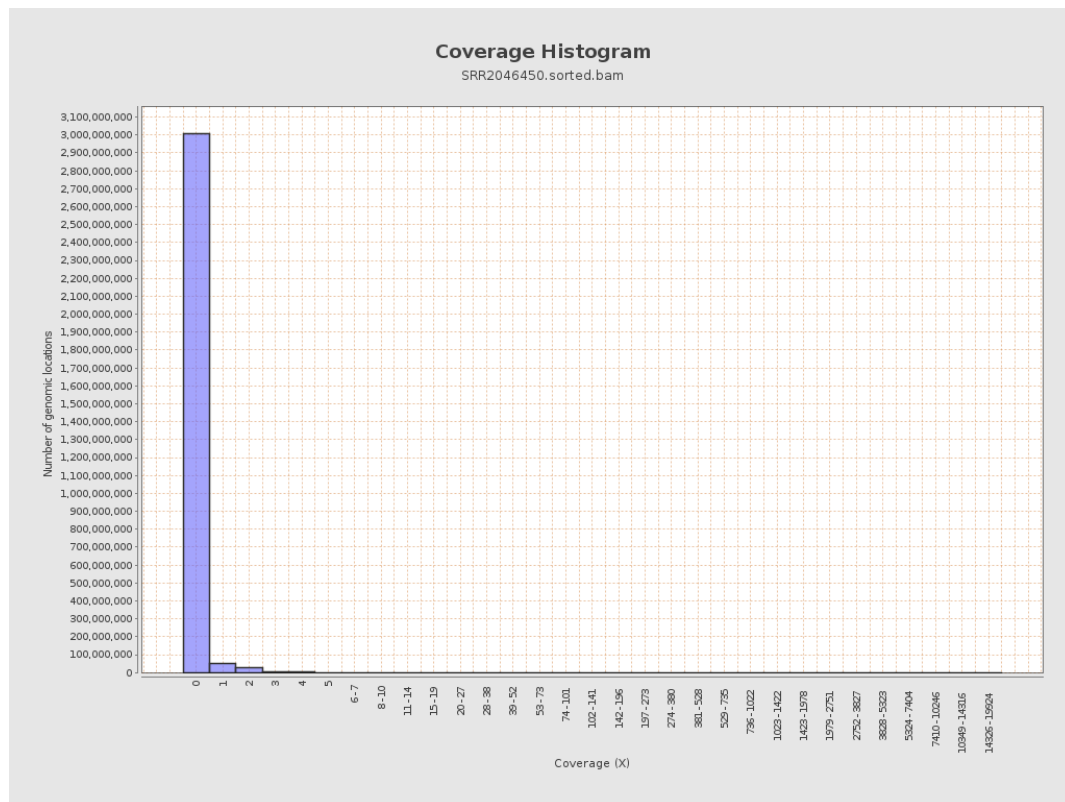
		bases	coverage	deviation
chr1	249250621	128759236	0.5166	25.5782
chr2	243199373	75459042	0.3103	18.9593
chr3	198022430	58218913	0.294	17.6848
chr4	191154276	25756112	0.1347	9.4243
chr5	180915260	59659565	0.3298	18.3966
chr6	171115067	49895996	0.2916	14.4516
chr7	159138663	52949550	0.3327	15.5808
chr8	146364022	87549244	0.5982	38.9474
chr9	141213431	8580759	0.0608	3.0216
chr10	135534747	23474118	0.1732	10.2486
chr11	135006516	13490965	0.0999	4.8759
chr12	133851895	19024595	0.1421	9.5972
chr13	115169878	13172005	0.1144	8.11
chr14	107349540	30951643	0.2883	15.4064
chr15	102531392	12176664	0.1188	7.3856
chr16	90354753	45171706	0.4999	31.2916
chr17	81195210	30966519	0.3814	16.6406
chr18	78077248	5157368	0.0661	2.1493
chr19	59128983	5875032	0.0994	5.8431
chr20	63025520	8226568	0.1305	11.2836
chr21	48129895	4244446	0.0882	9.6514
chr22	51304566	7551768	0.1472	8.2999
chrMT	16571	70177	4.2349	2.6648
chrX	155270560	20155740	0.1298	9.8089

chrY	59373566	101921	0.0017	0.0935
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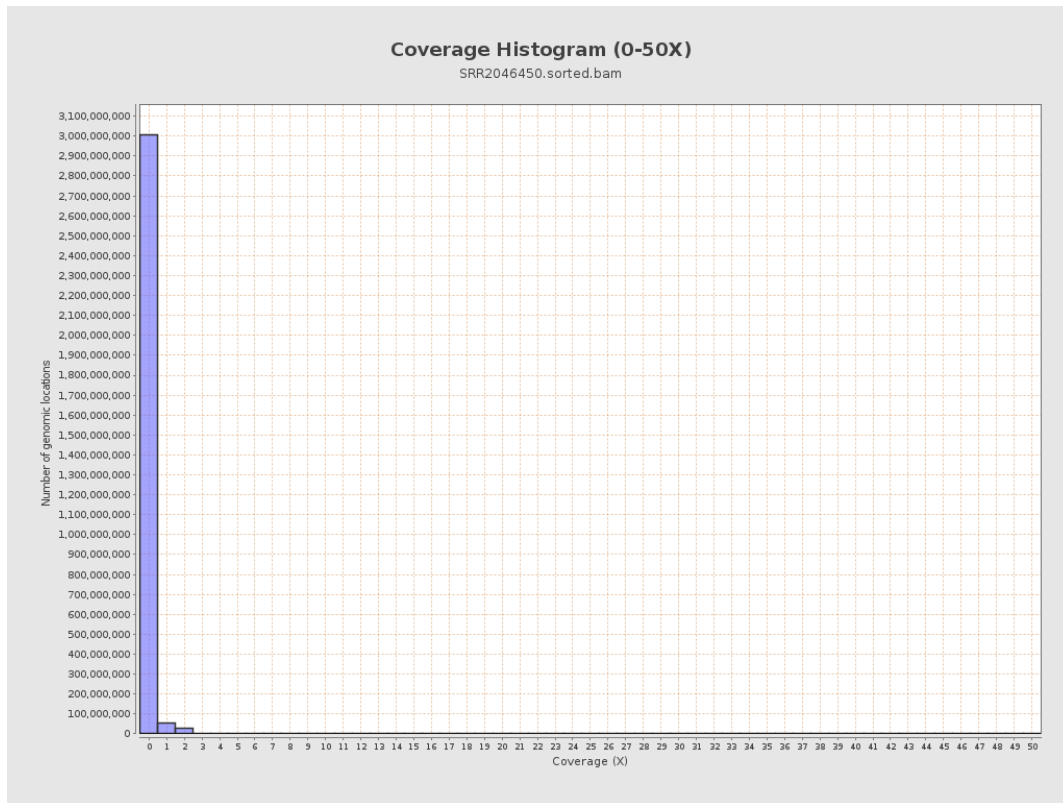
3. Results : Coverage across reference



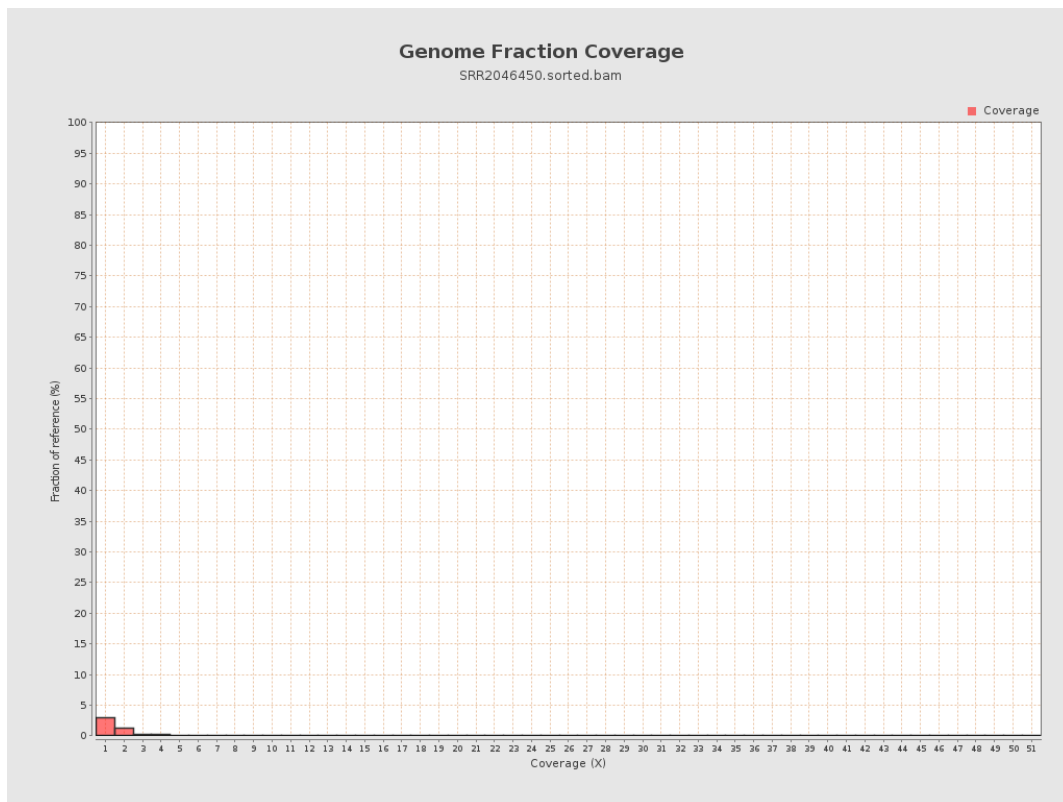
4. Results : Coverage Histogram



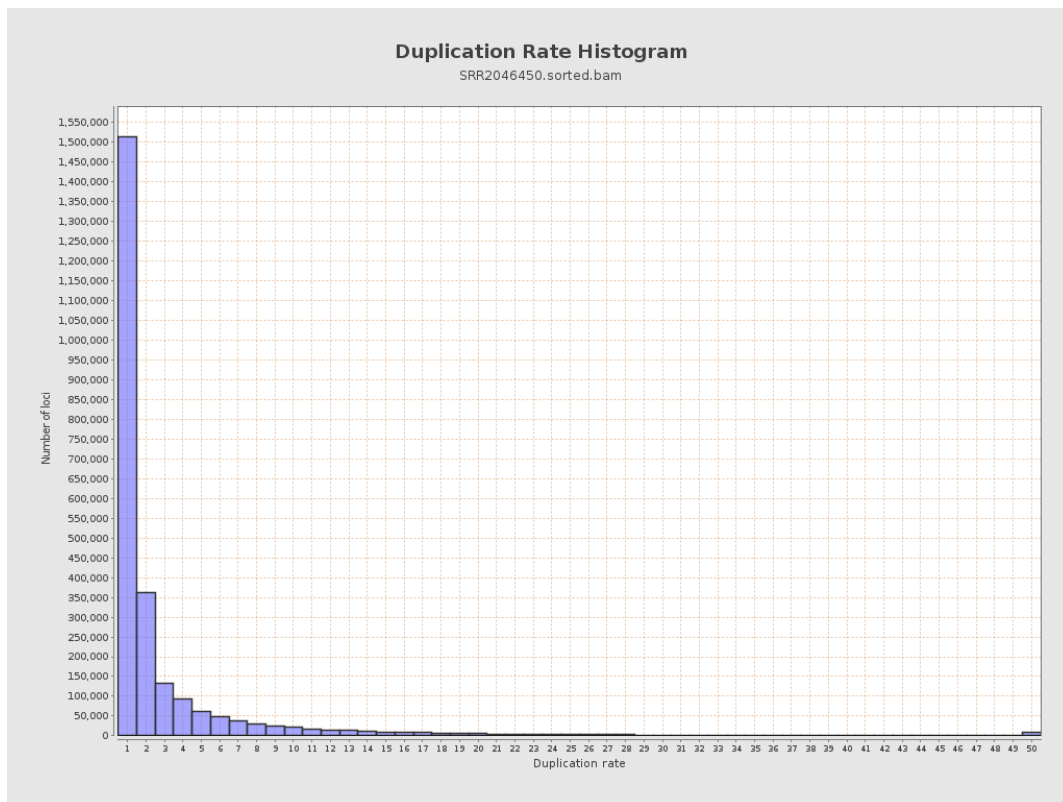
5. Results : Coverage Histogram (0-50X)



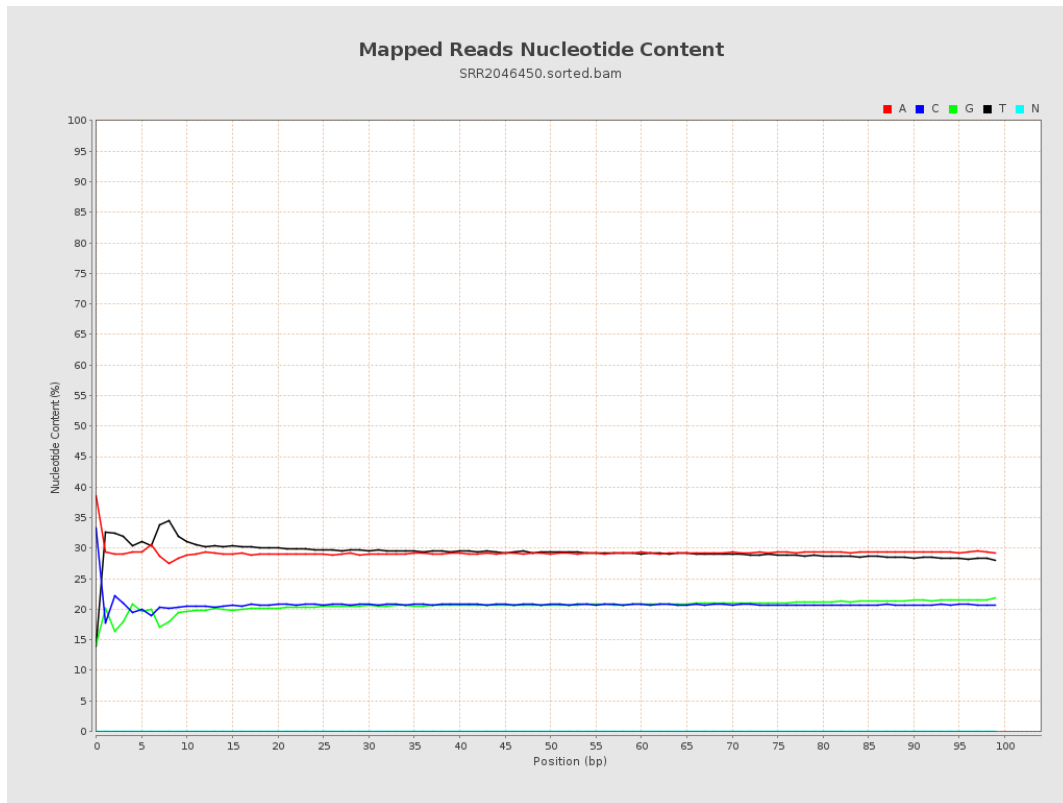
6. Results : Genome Fraction Coverage



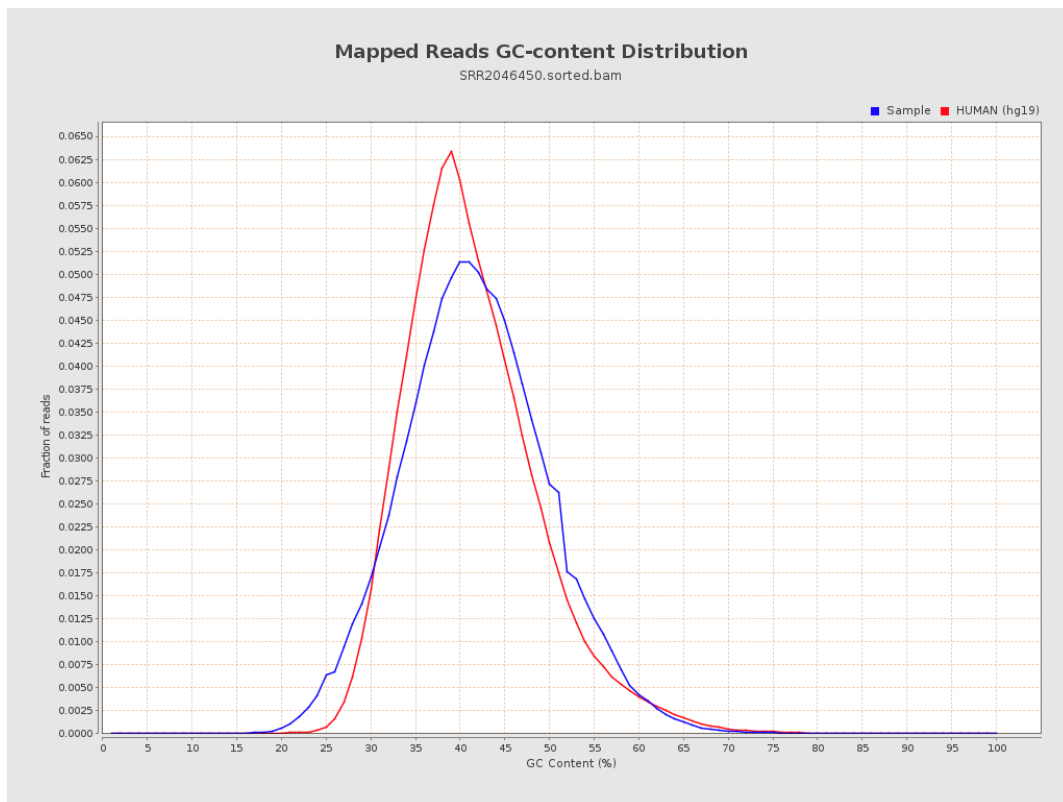
7. Results : Duplication Rate Histogram



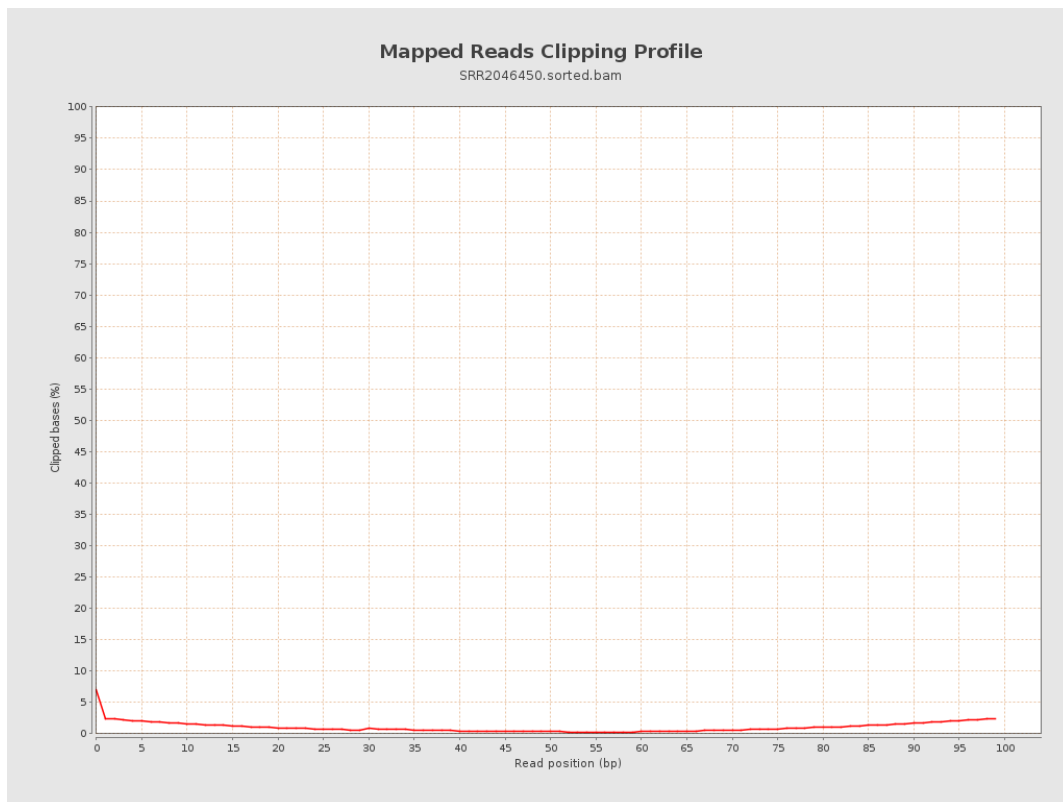
8. Results : Mapped Reads Nucleotide Content



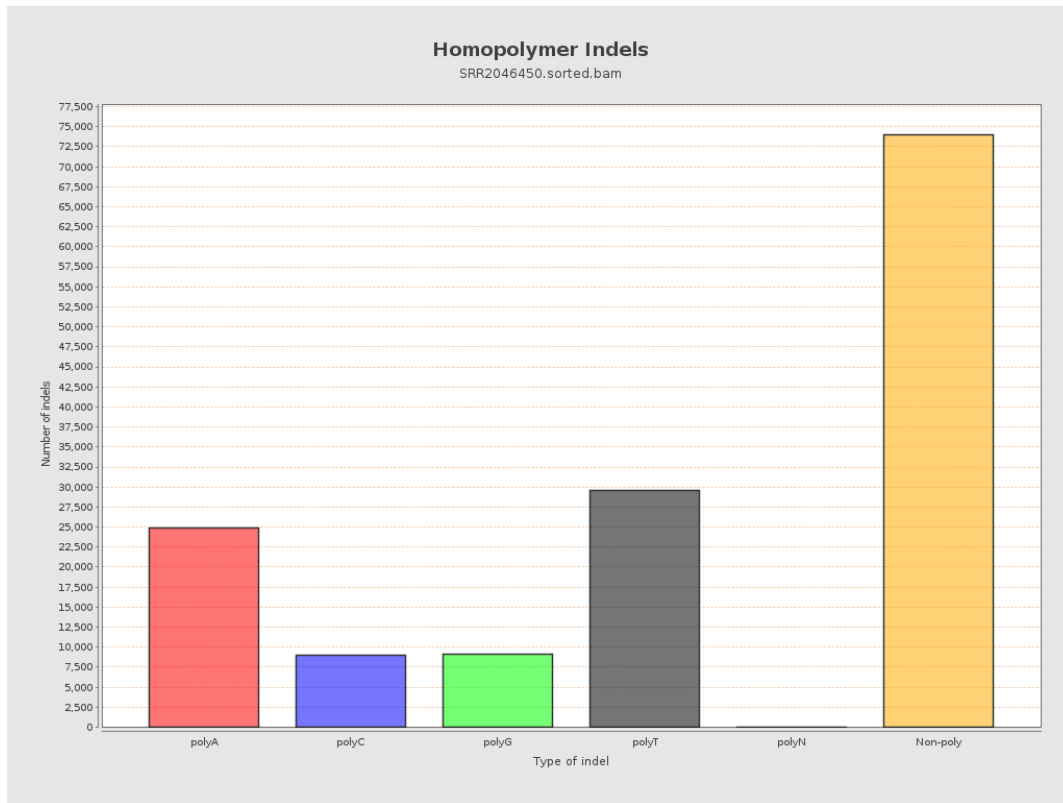
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



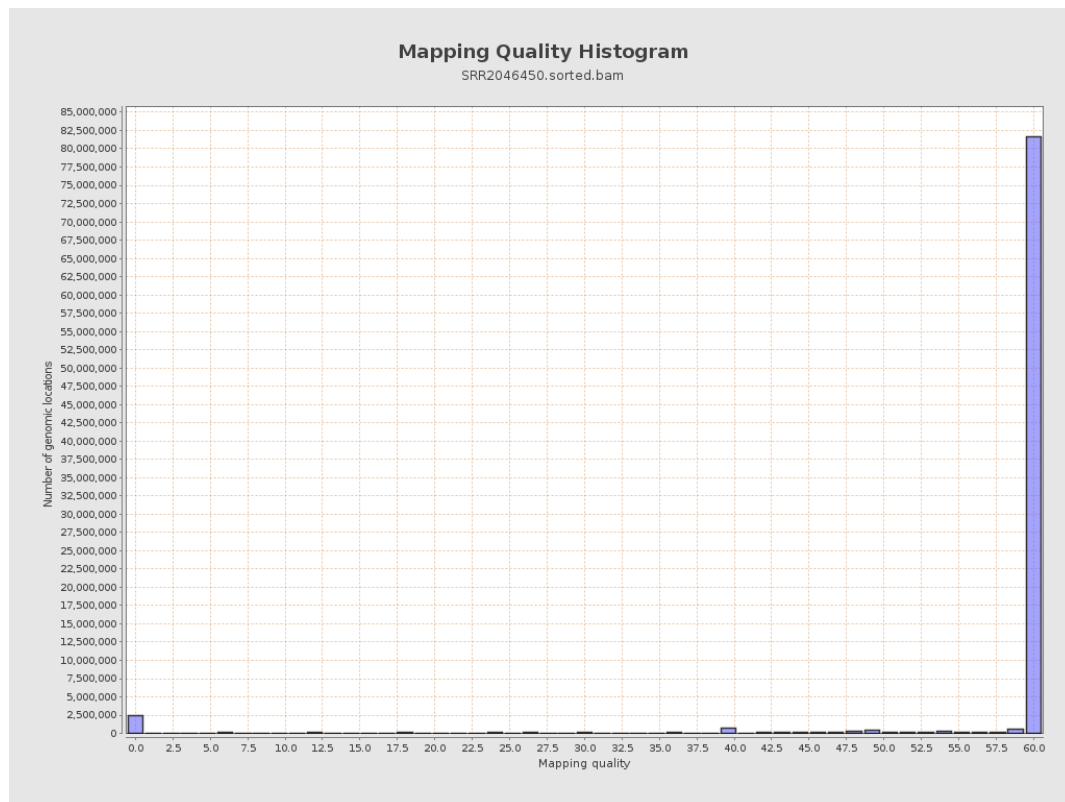
11. Results : Homopolymer Indels



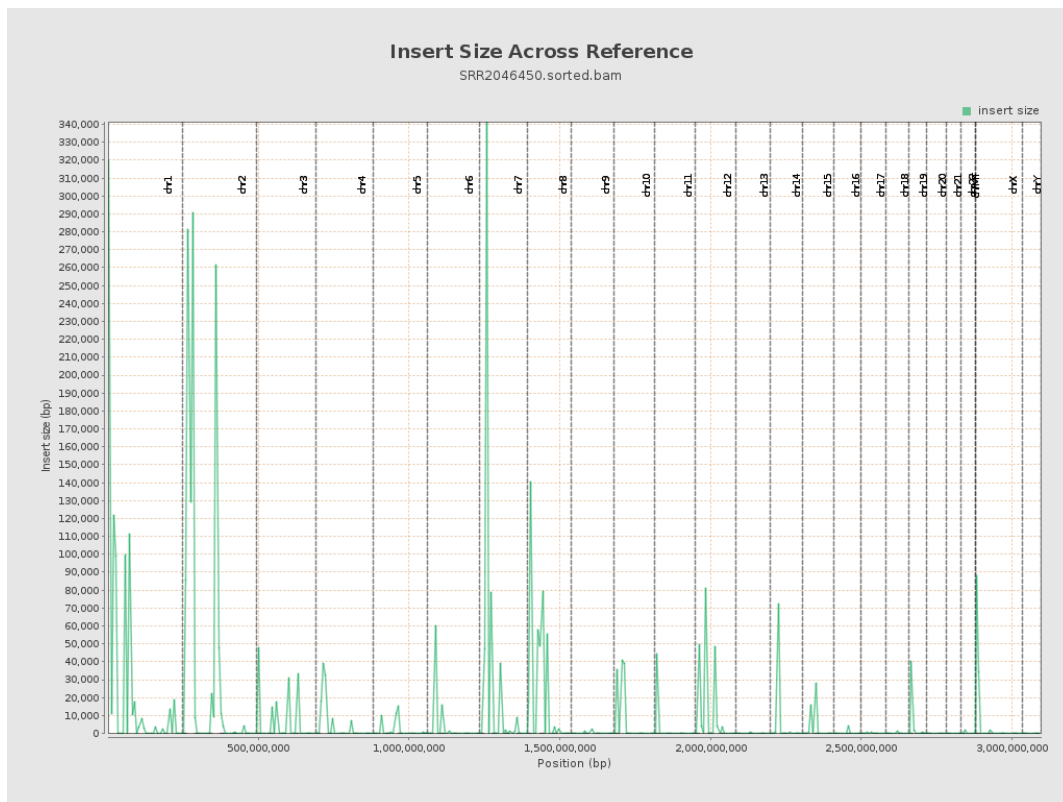
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

