

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 16:11:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046482.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_SRR2046482 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046482_1.fastq.gz SRR2046482_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 16:11:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046482.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,931,742
Mapped reads	7,900,090 / 99.6%
Unmapped reads	31,652 / 0.4%
Mapped paired reads	7,900,090 / 99.6%
Mapped reads, first in pair	3,954,145 / 49.85%
Mapped reads, second in pair	3,945,945 / 49.75%
Mapped reads, both in pair	7,879,392 / 99.34%
Mapped reads, singletons	20,698 / 0.26%
Secondary alignments	0
Supplementary alignments	36,133 / 0.46%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	5,731,660 / 72.26%
Duplication rate	38.98%
Clipped reads	2,425,592 / 30.58%

2.2. ACGT Content

Number/percentage of A's	217,338,906 / 29.12%
Number/percentage of C's	156,045,159 / 20.91%
Number/percentage of T's	214,228,445 / 28.7%
Number/percentage of G's	158,740,341 / 21.27%
Number/percentage of N's	56,346 / 0.01%

GC Percentage	42.17%
---------------	--------

2.3. Coverage

Mean	0.2412
Standard Deviation	22.8569

2.4. Mapping Quality

Mean Mapping Quality	51.6
----------------------	------

2.5. Insert size

Mean	15,322.71
Standard Deviation	1,232,895.66
P25/Median/P75	95 / 116 / 142

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	2,665,810
Insertions	70,505
Mapped reads with at least one insertion	0.88%
Deletions	84,535
Mapped reads with at least one deletion	1.04%
Homopolymer indels	47.15%

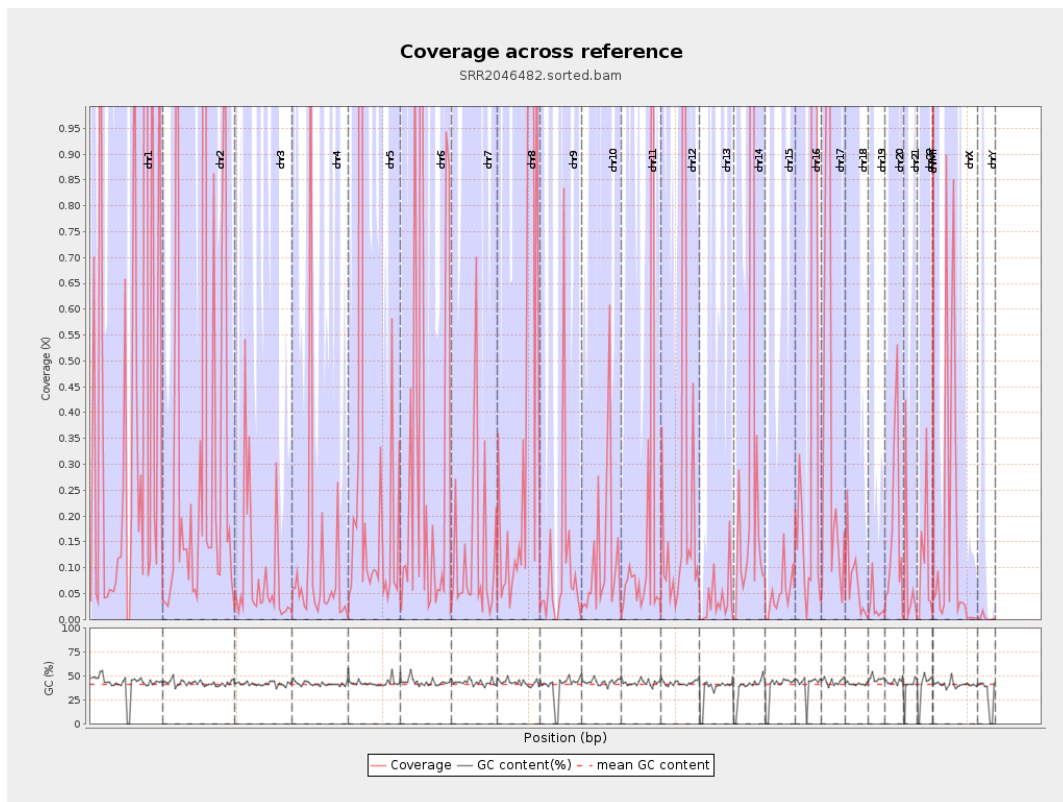
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

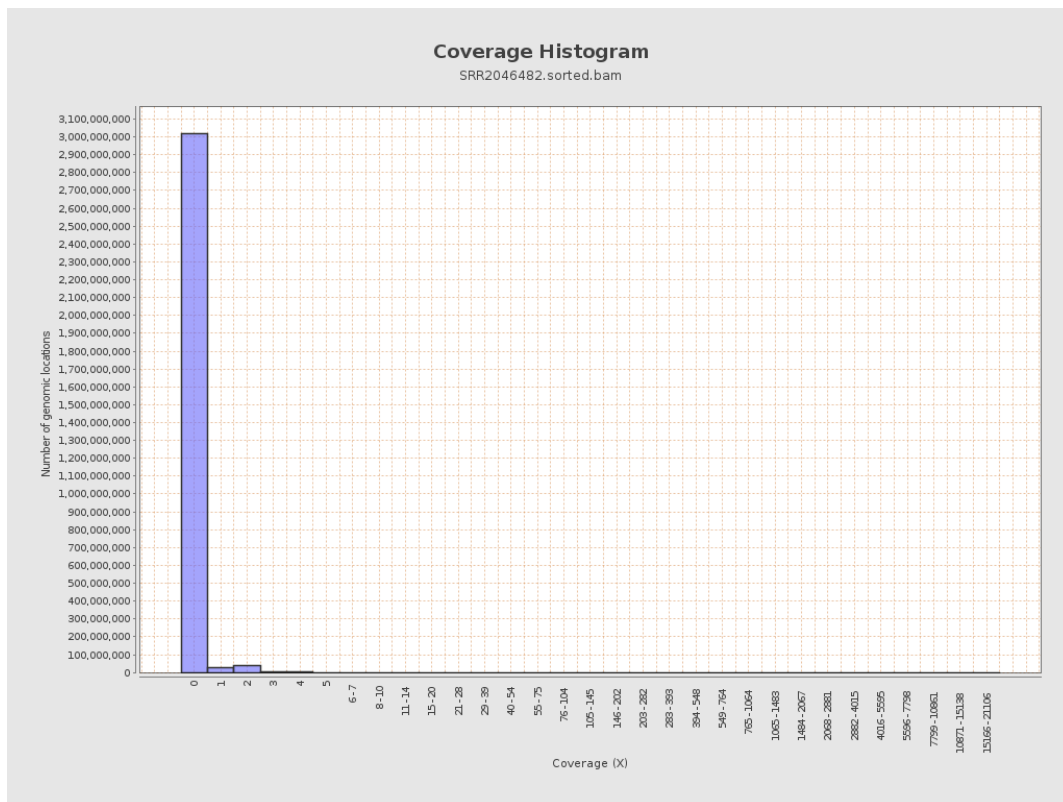
		bases	coverage	deviation
chr1	249250621	102111620	0.4097	28.6935
chr2	243199373	110449460	0.4542	32.1083
chr3	198022430	16444932	0.083	7.0706
chr4	191154276	21210479	0.111	13.6416
chr5	180915260	76964942	0.4254	43.7921
chr6	171115067	56055781	0.3276	21.7189
chr7	159138663	20704003	0.1301	9.2427
chr8	146364022	63424345	0.4333	29.5478
chr9	141213431	14141551	0.1001	20.046
chr10	135534747	16653202	0.1229	10.344
chr11	135006516	28874147	0.2139	16.3673
chr12	133851895	33883587	0.2531	18.4912
chr13	115169878	4444894	0.0386	3.4908
chr14	107349540	41220307	0.384	21.7075
chr15	102531392	5357888	0.0523	3.0249
chr16	90354753	48814118	0.5402	44.8601
chr17	81195210	34206739	0.4213	22.2738
chr18	78077248	5531812	0.0709	2.411
chr19	59128983	1554541	0.0263	1.7607
chr20	63025520	11125752	0.1765	12.1859
chr21	48129895	4248917	0.0883	10.7235
chr22	51304566	5586053	0.1089	7.911
chrMT	16571	83254	5.0241	3.6168
chrX	155270560	23348160	0.1504	25.3506

chrY	59373566	209769	0.0035	0.5863
------	----------	--------	--------	--------

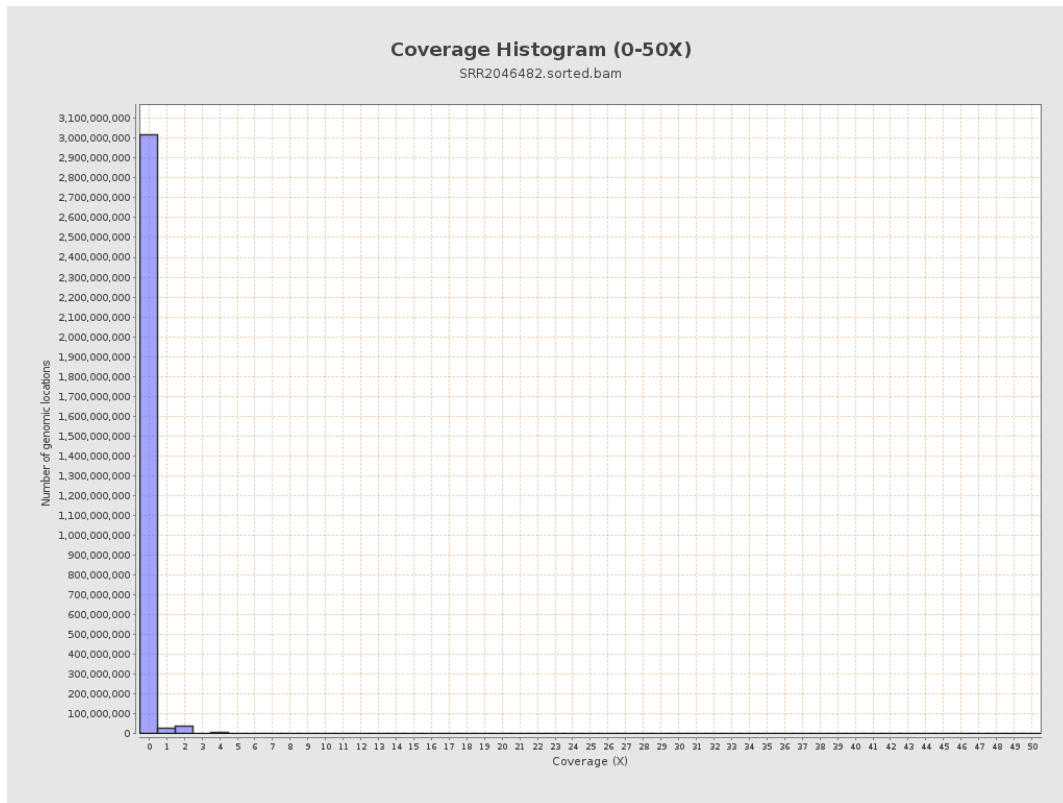
3. Results : Coverage across reference



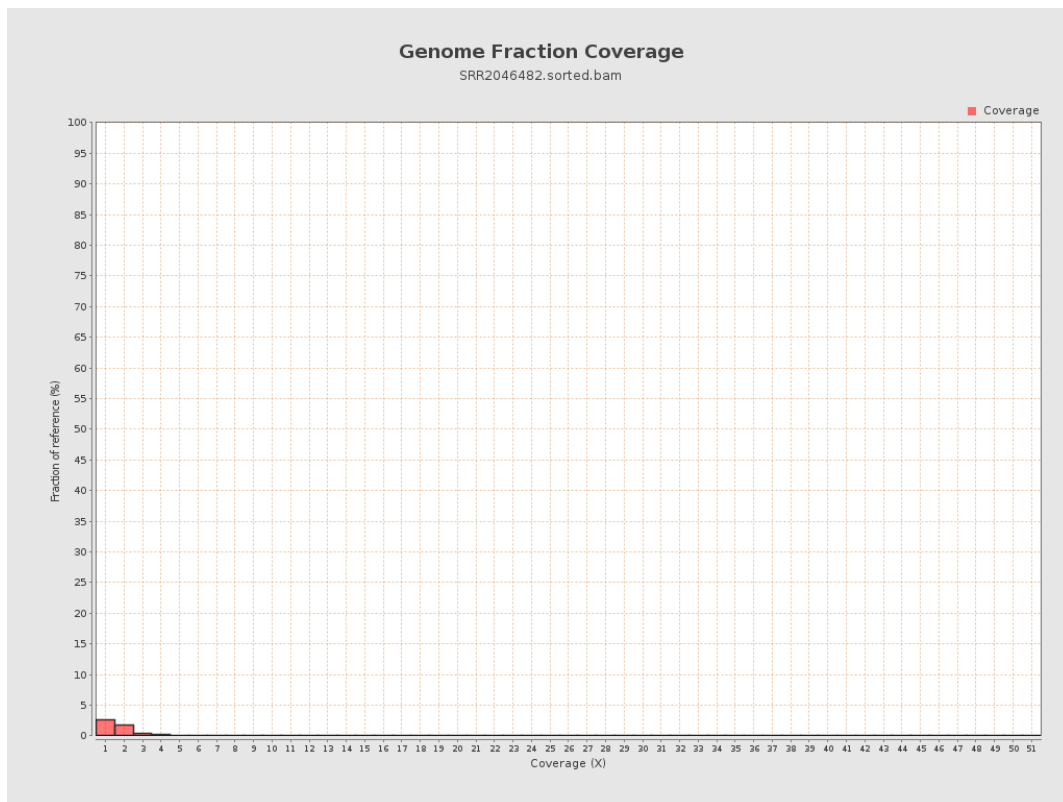
4. Results : Coverage Histogram



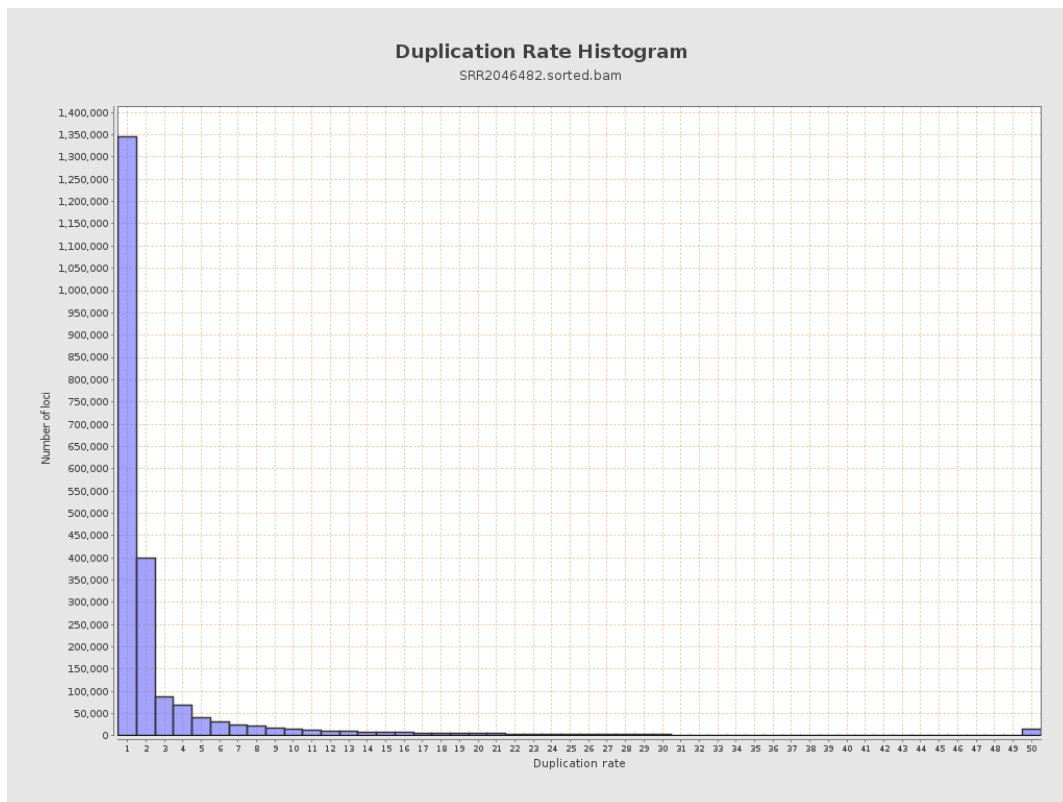
5. Results : Coverage Histogram (0-50X)



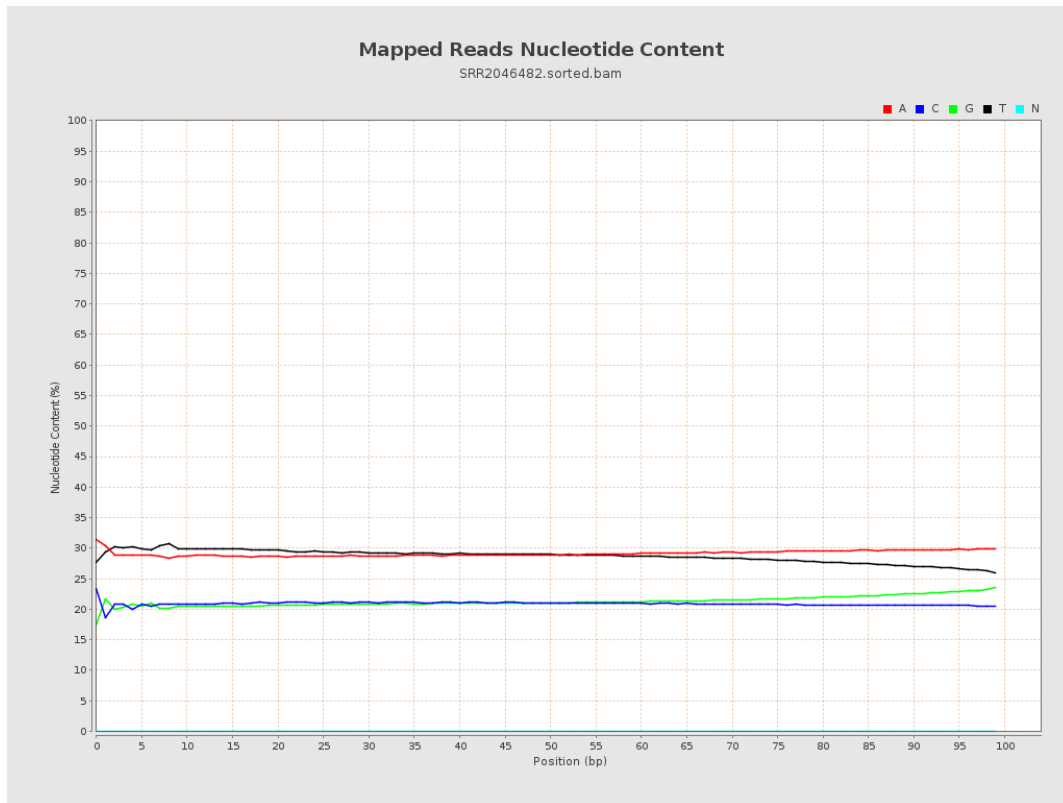
6. Results : Genome Fraction Coverage



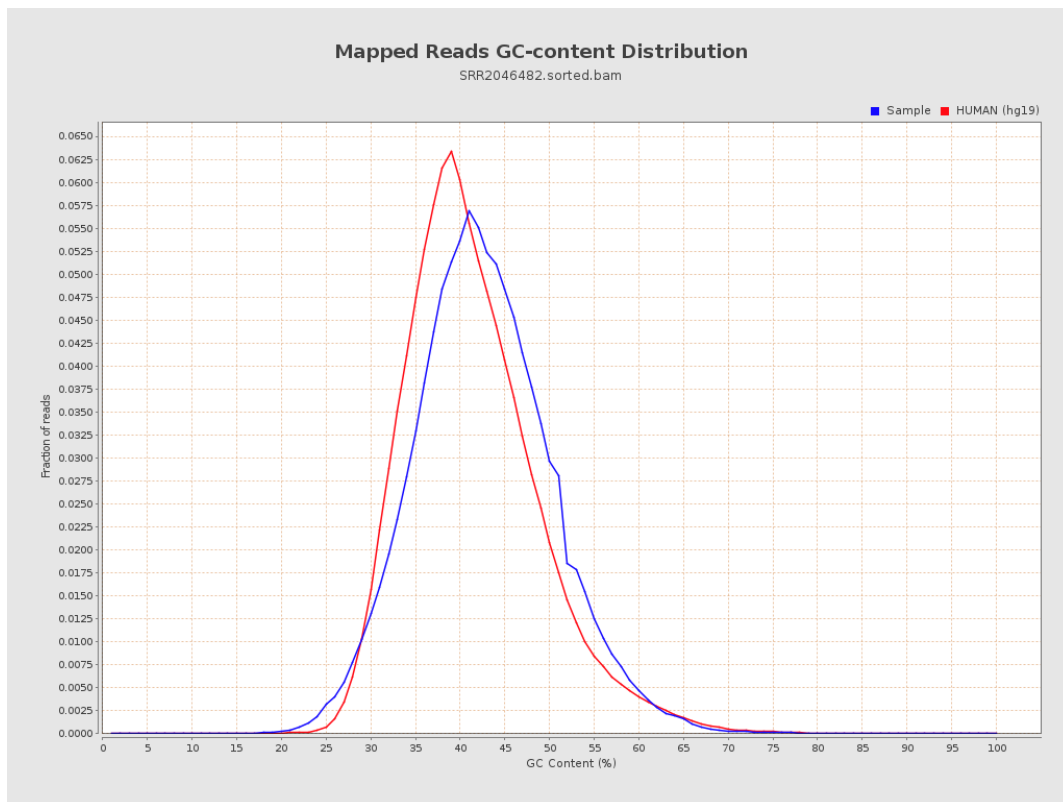
7. Results : Duplication Rate Histogram



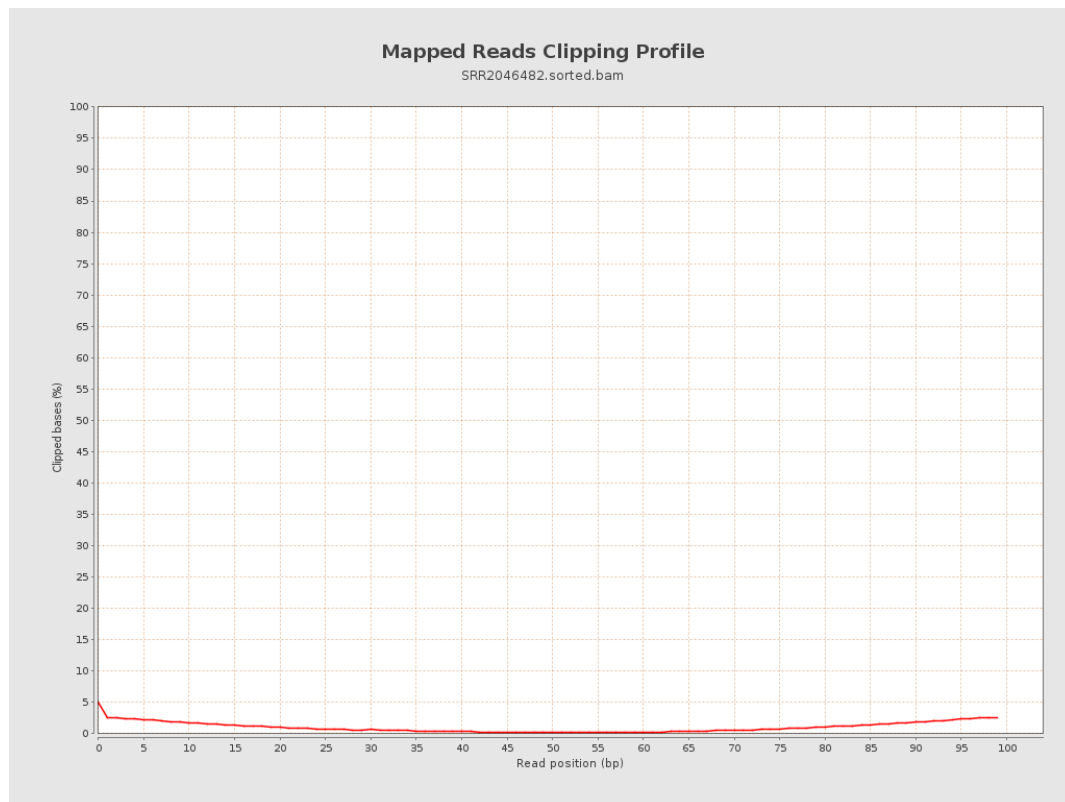
8. Results : Mapped Reads Nucleotide Content



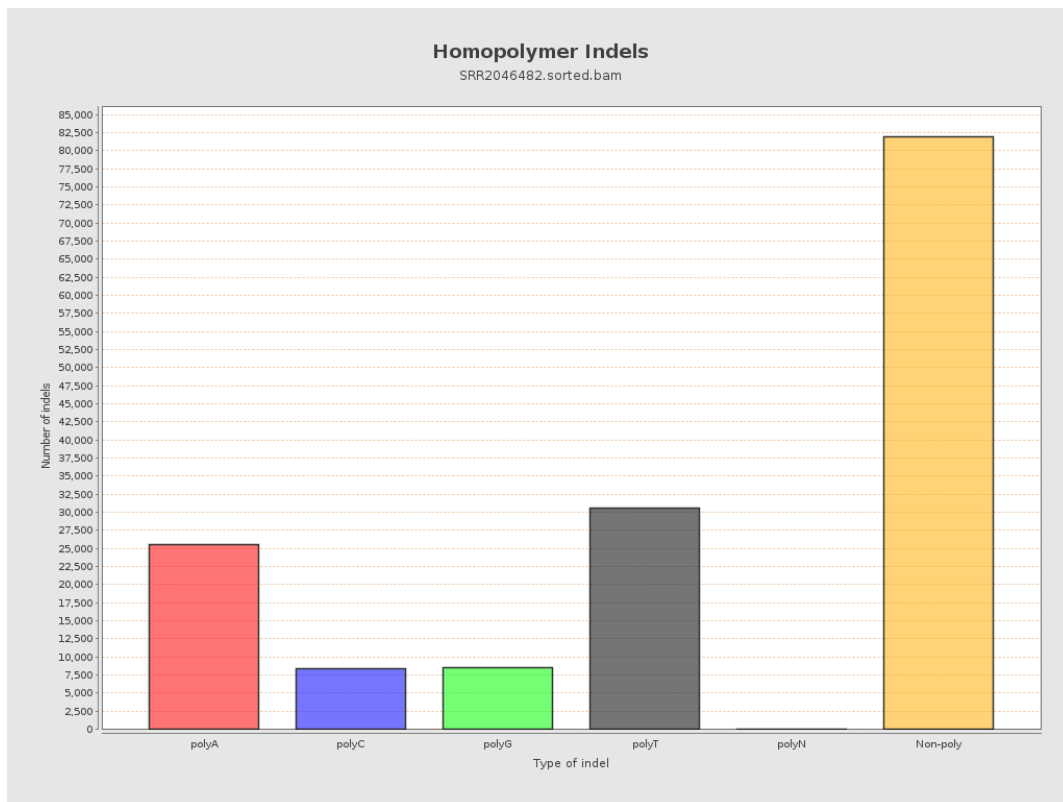
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



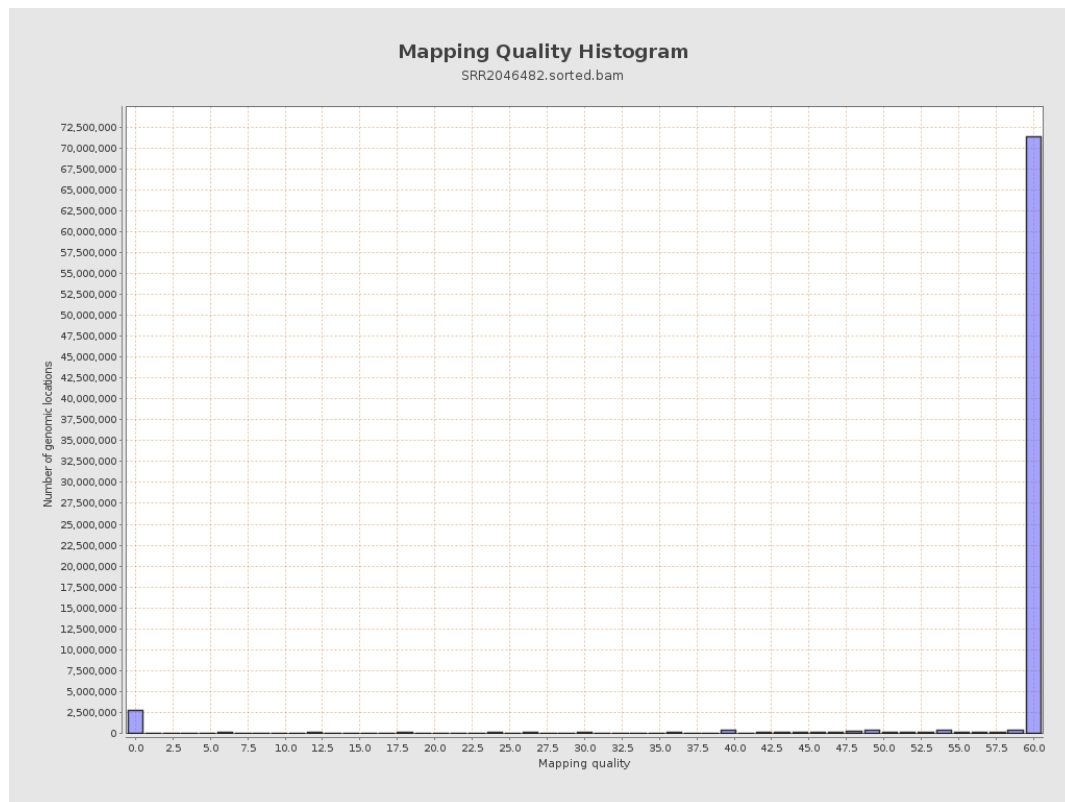
11. Results : Homopolymer Indels



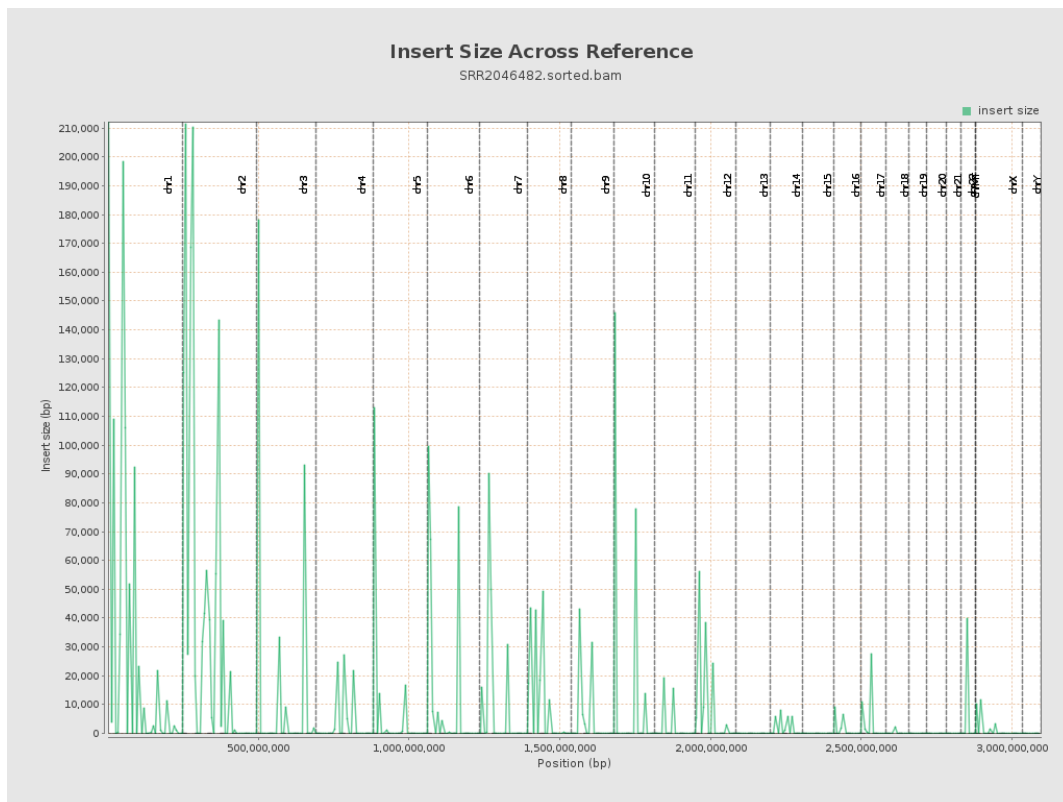
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

