

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 17:18:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046485.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_SRR2046485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046485_1.fastq.gz SRR2046485_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 17:17:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046485.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,887,352
Mapped reads	7,855,708 / 99.6%
Unmapped reads	31,644 / 0.4%
Mapped paired reads	7,855,708 / 99.6%
Mapped reads, first in pair	3,933,835 / 49.88%
Mapped reads, second in pair	3,921,873 / 49.72%
Mapped reads, both in pair	7,833,046 / 99.31%
Mapped reads, singletons	22,662 / 0.29%
Secondary alignments	0
Supplementary alignments	35,107 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	5,273,613 / 66.86%
Duplication rate	39.48%
Clipped reads	940,580 / 11.93%

2.2. ACGT Content

Number/percentage of A's	223,361,330 / 28.98%
Number/percentage of C's	162,635,921 / 21.1%
Number/percentage of T's	224,986,797 / 29.2%
Number/percentage of G's	159,567,606 / 20.71%
Number/percentage of N's	68,345 / 0.01%

GC Percentage	41.81%
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2.3. Coverage

Mean	0.249
Standard Deviation	14.3363

2.4. Mapping Quality

Mean Mapping Quality	53.63
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2.5. Insert size

Mean	17,003.67
Standard Deviation	1,317,105.62
P25/Median/P75	124 / 157 / 197

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	2,799,522
Insertions	62,902
Mapped reads with at least one insertion	0.78%
Deletions	80,751
Mapped reads with at least one deletion	0.99%
Homopolymer indels	49.02%

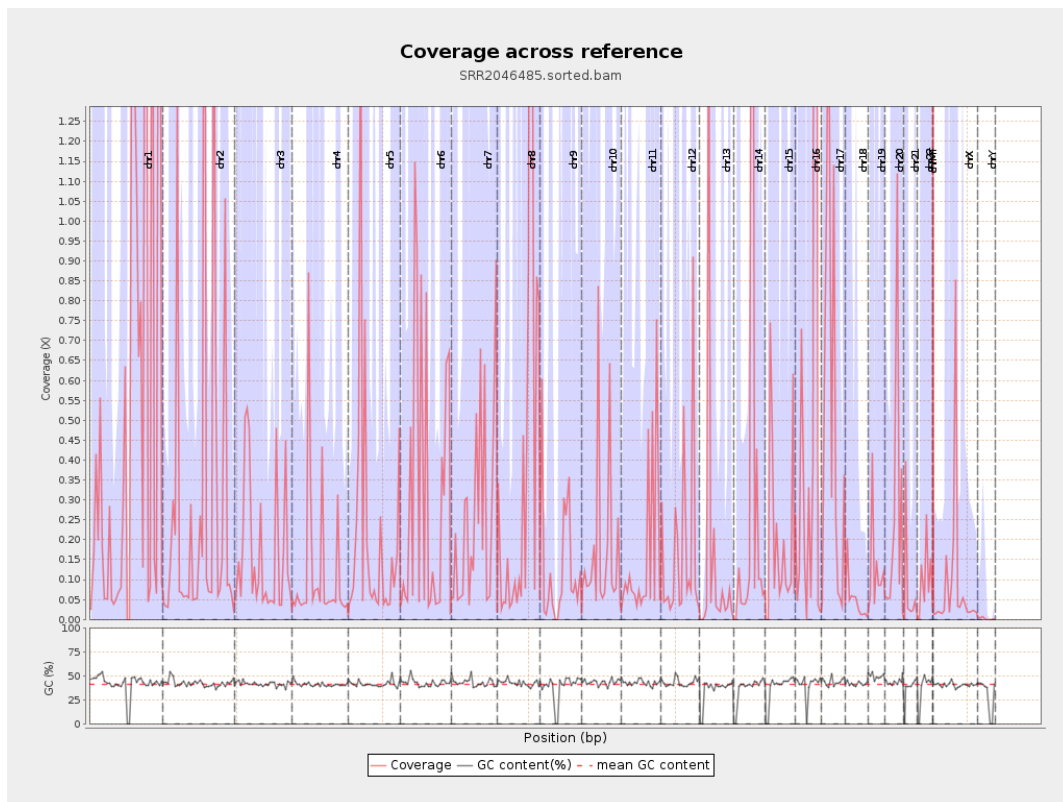
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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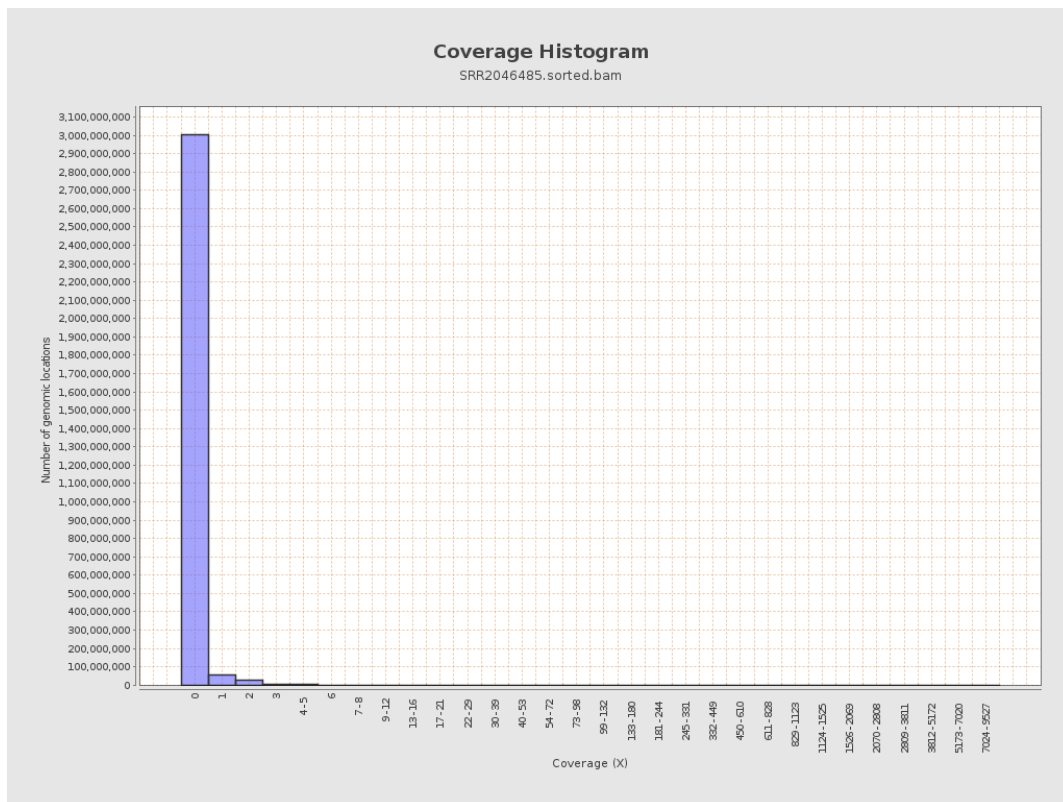
		bases	coverage	deviation
chr1	249250621	133309956	0.5348	24.428
chr2	243199373	75862191	0.3119	15.216
chr3	198022430	33144365	0.1674	8.0021
chr4	191154276	22448672	0.1174	6.7643
chr5	180915260	39455298	0.2181	13.0436
chr6	171115067	54102489	0.3162	14.5828
chr7	159138663	42440378	0.2667	11.6527
chr8	146364022	67892295	0.4639	20.2968
chr9	141213431	17692547	0.1253	7.3654
chr10	135534747	23791192	0.1755	9.2125
chr11	135006516	20432897	0.1513	7.3965
chr12	133851895	22326061	0.1668	11.5563
chr13	115169878	17068105	0.1482	9.3068
chr14	107349540	32901150	0.3065	20.3918
chr15	102531392	21512690	0.2098	11.6973
chr16	90354753	54469761	0.6028	31.2947
chr17	81195210	41605612	0.5124	19.6503
chr18	78077248	3931298	0.0504	1.6096
chr19	59128983	7566820	0.128	4.7091
chr20	63025520	16406466	0.2603	15.4483
chr21	48129895	4039495	0.0839	6.6702
chr22	51304566	5213164	0.1016	4.6963
chrMT	16571	36396	2.1964	2.0309
chrX	155270560	13071649	0.0842	7.1368

chrY	59373566	128291	0.0022	0.1544
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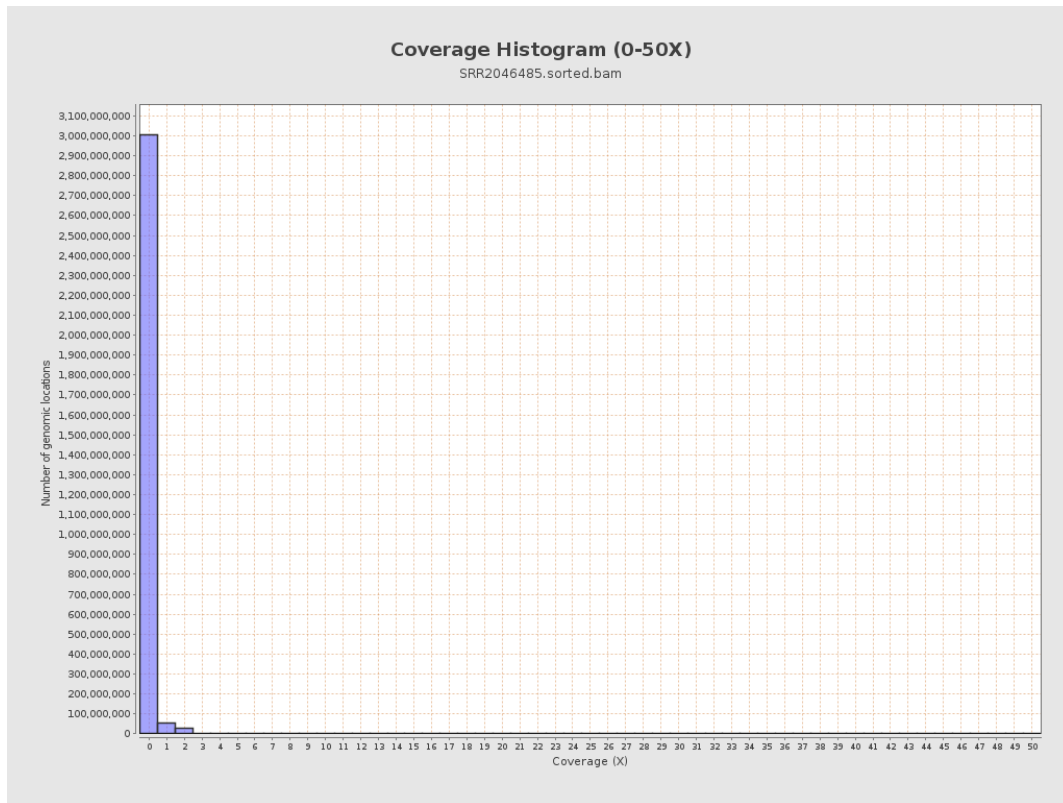
3. Results : Coverage across reference



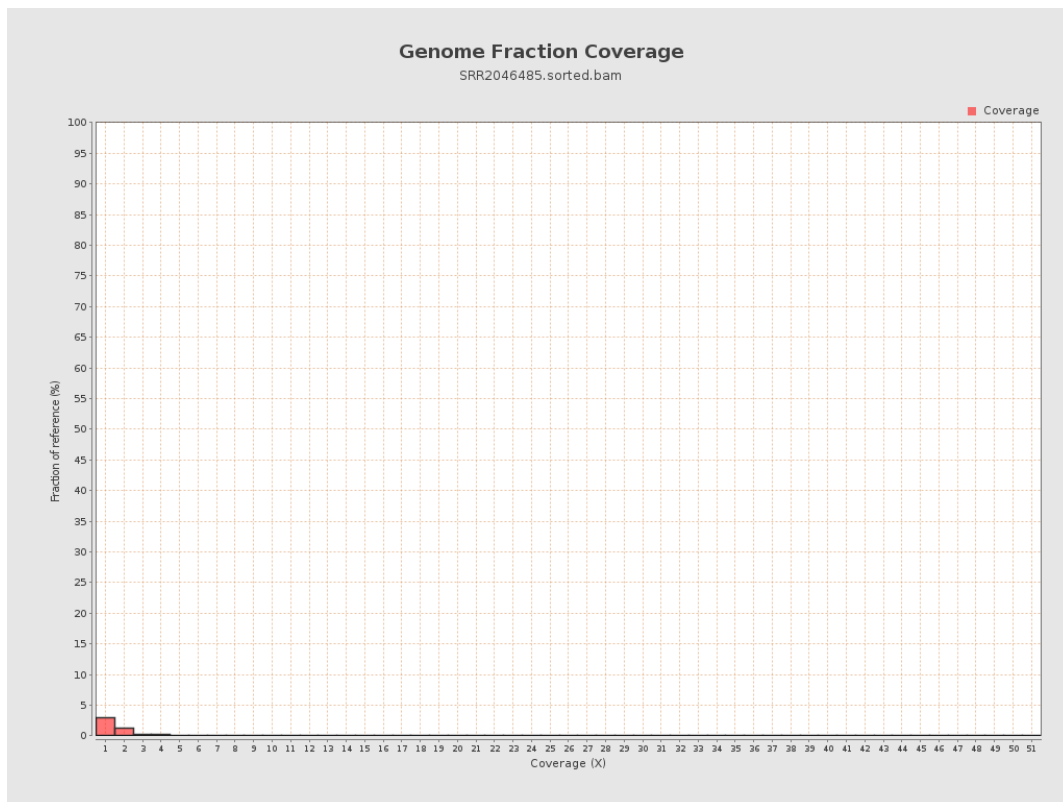
4. Results : Coverage Histogram



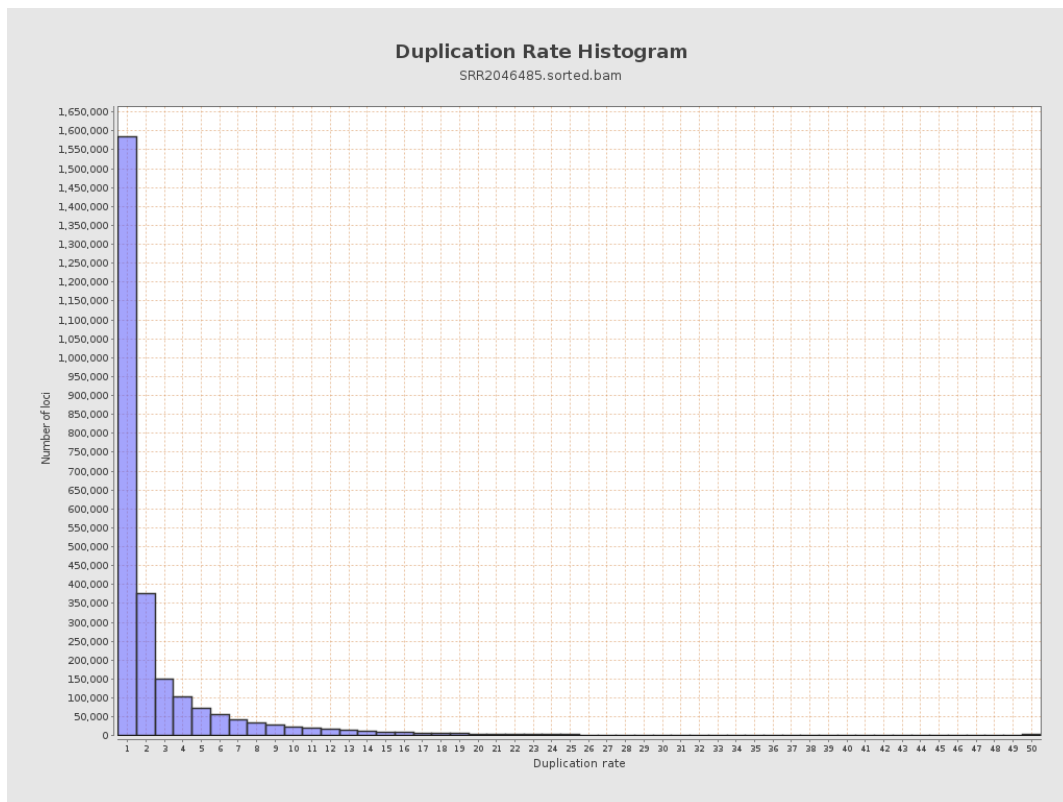
5. Results : Coverage Histogram (0-50X)



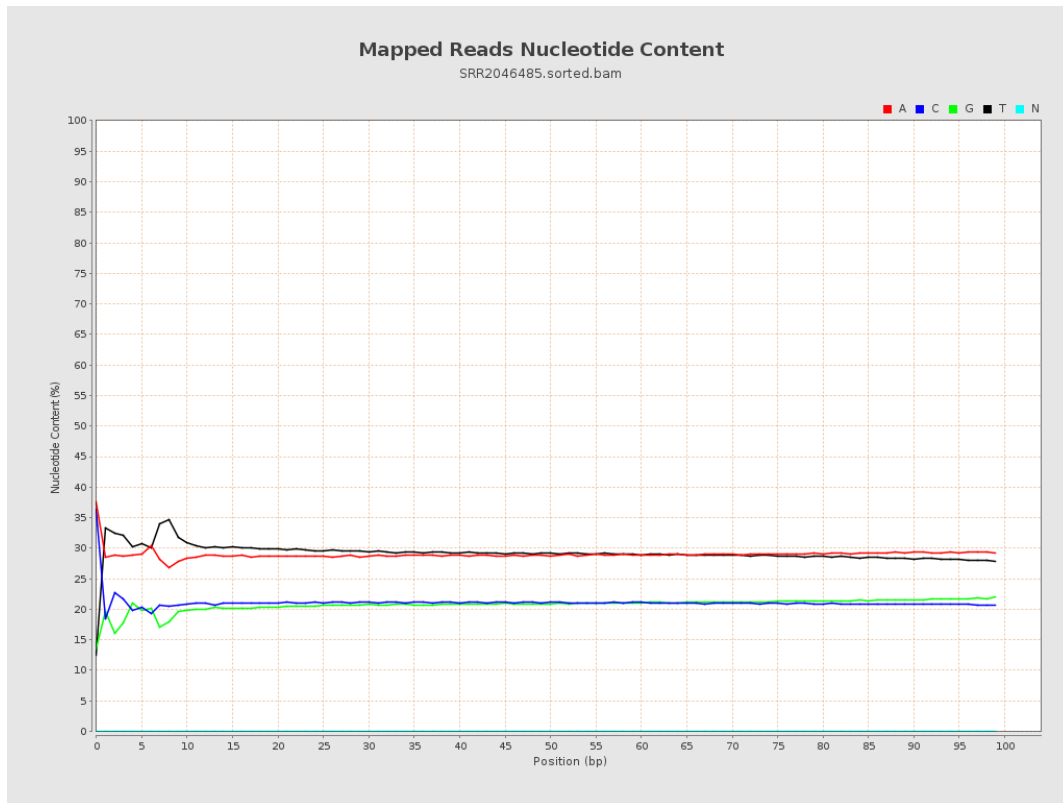
6. Results : Genome Fraction Coverage



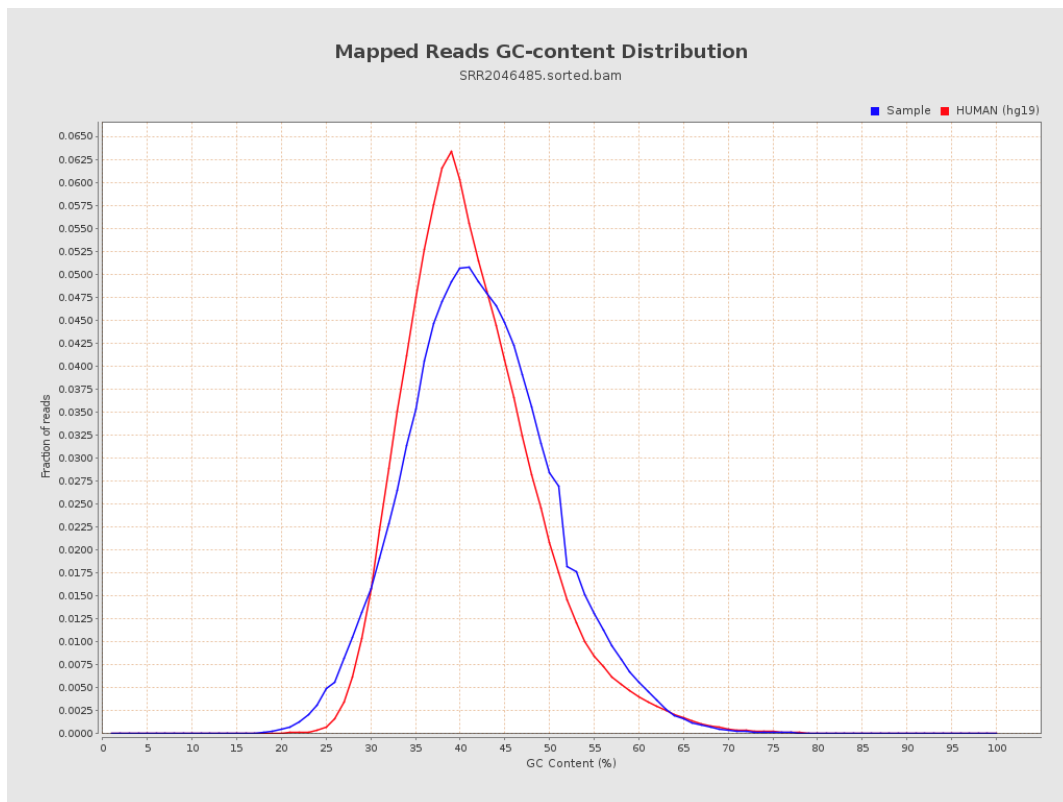
7. Results : Duplication Rate Histogram



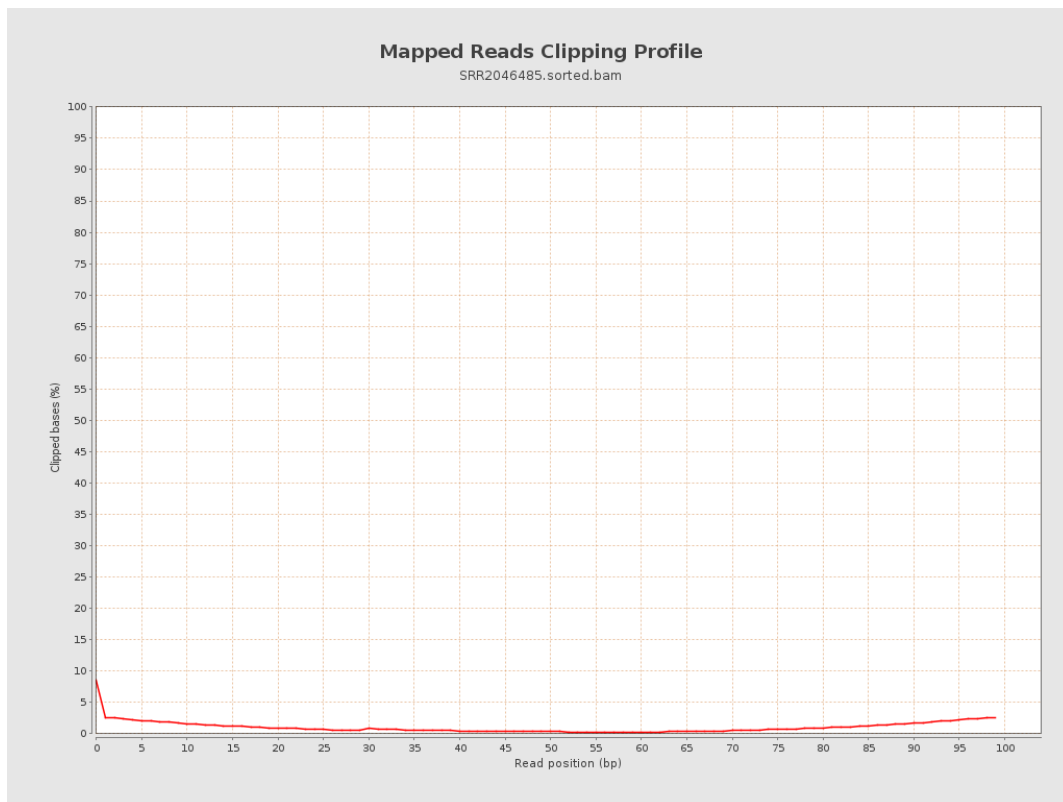
8. Results : Mapped Reads Nucleotide Content



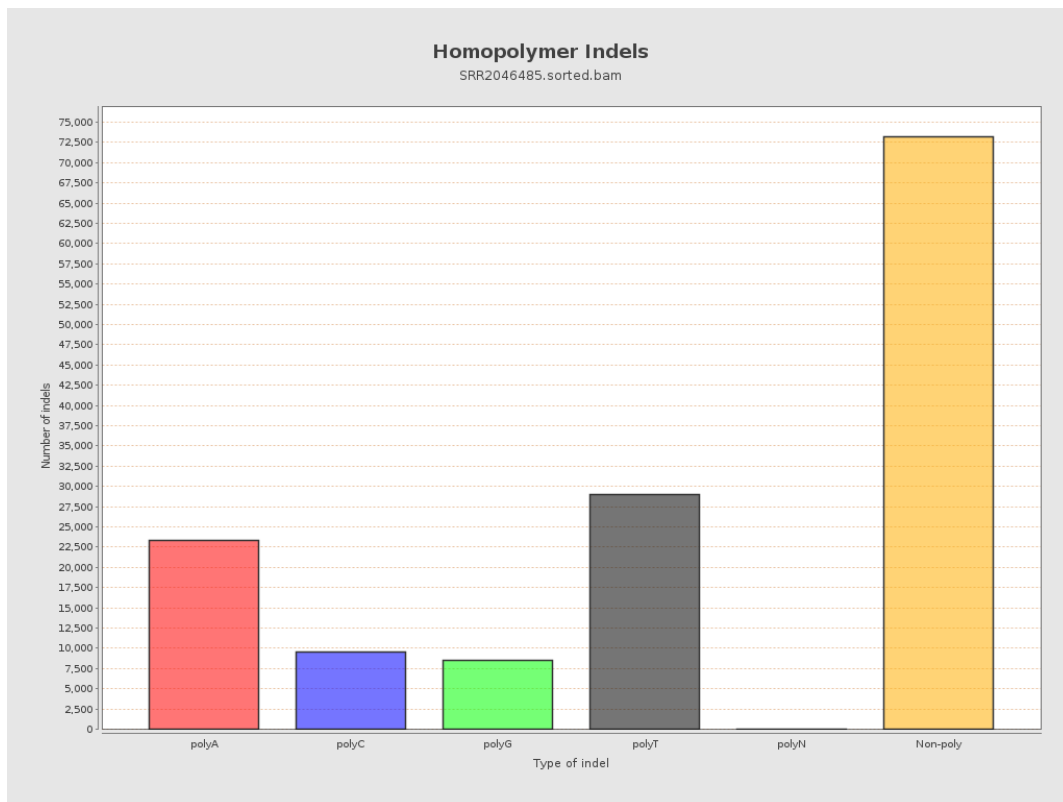
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



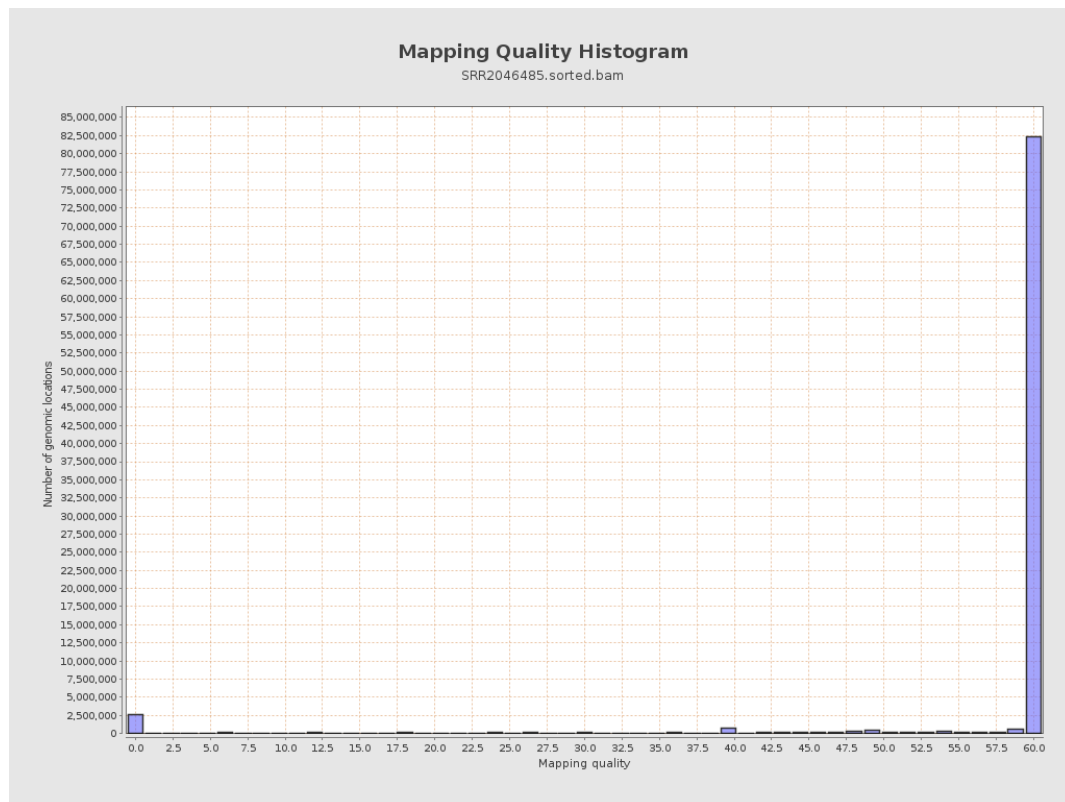
11. Results : Homopolymer Indels



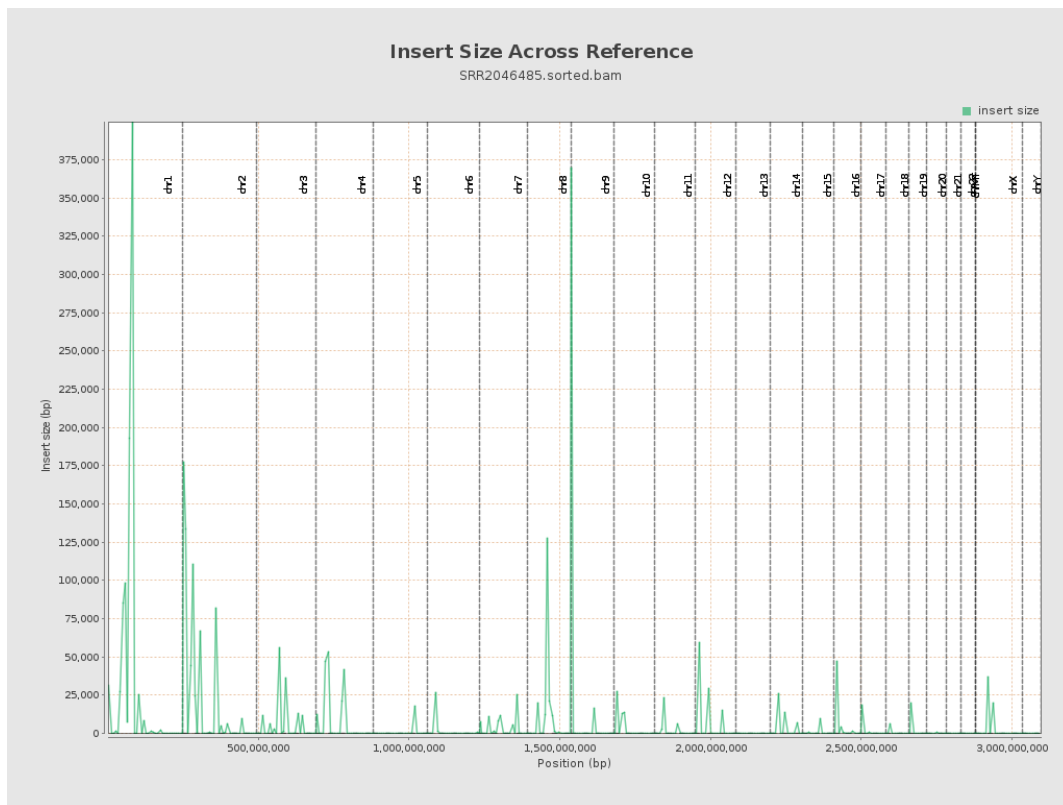
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

