

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 19:51:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046488.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_SRR2046488 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046488_1.fastq.gz SRR2046488_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 19:51:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046488.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,591,848
Mapped reads	8,557,733 / 99.6%
Unmapped reads	34,115 / 0.4%
Mapped paired reads	8,557,733 / 99.6%
Mapped reads, first in pair	4,285,260 / 49.88%
Mapped reads, second in pair	4,272,473 / 49.73%
Mapped reads, both in pair	8,534,238 / 99.33%
Mapped reads, singletons	23,495 / 0.27%
Secondary alignments	0
Supplementary alignments	49,880 / 0.58%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	6,165,812 / 71.76%
Duplication rate	43.21%
Clipped reads	2,357,533 / 27.44%

2.2. ACGT Content

Number/percentage of A's	238,512,174 / 29.3%
Number/percentage of C's	169,071,909 / 20.77%
Number/percentage of T's	235,240,621 / 28.9%
Number/percentage of G's	171,205,718 / 21.03%
Number/percentage of N's	77,563 / 0.01%

GC Percentage	41.8%
---------------	-------

2.3. Coverage

Mean	0.2631
Standard Deviation	18.659

2.4. Mapping Quality

Mean Mapping Quality	53.04
----------------------	-------

2.5. Insert size

Mean	17,326.1
Standard Deviation	1,262,395.78
P25/Median/P75	98 / 121 / 150

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	3,312,373
Insertions	67,810
Mapped reads with at least one insertion	0.77%
Deletions	89,952
Mapped reads with at least one deletion	1.02%
Homopolymer indels	48.02%

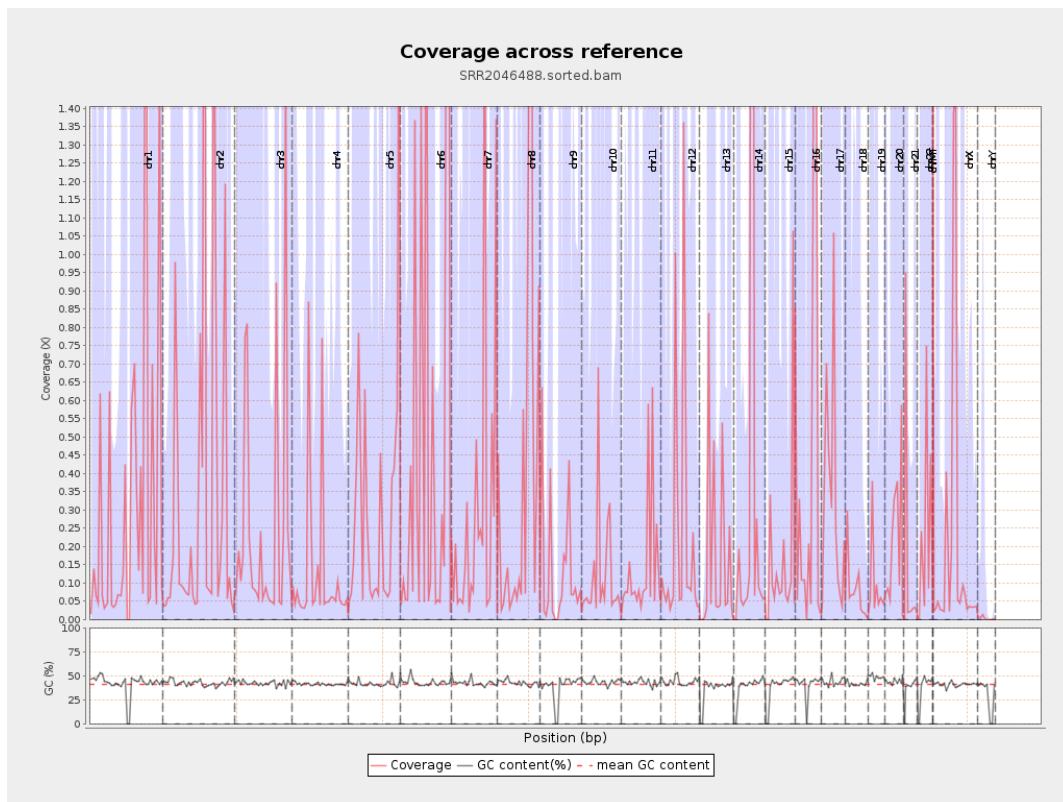
2.7. Chromosome stats

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

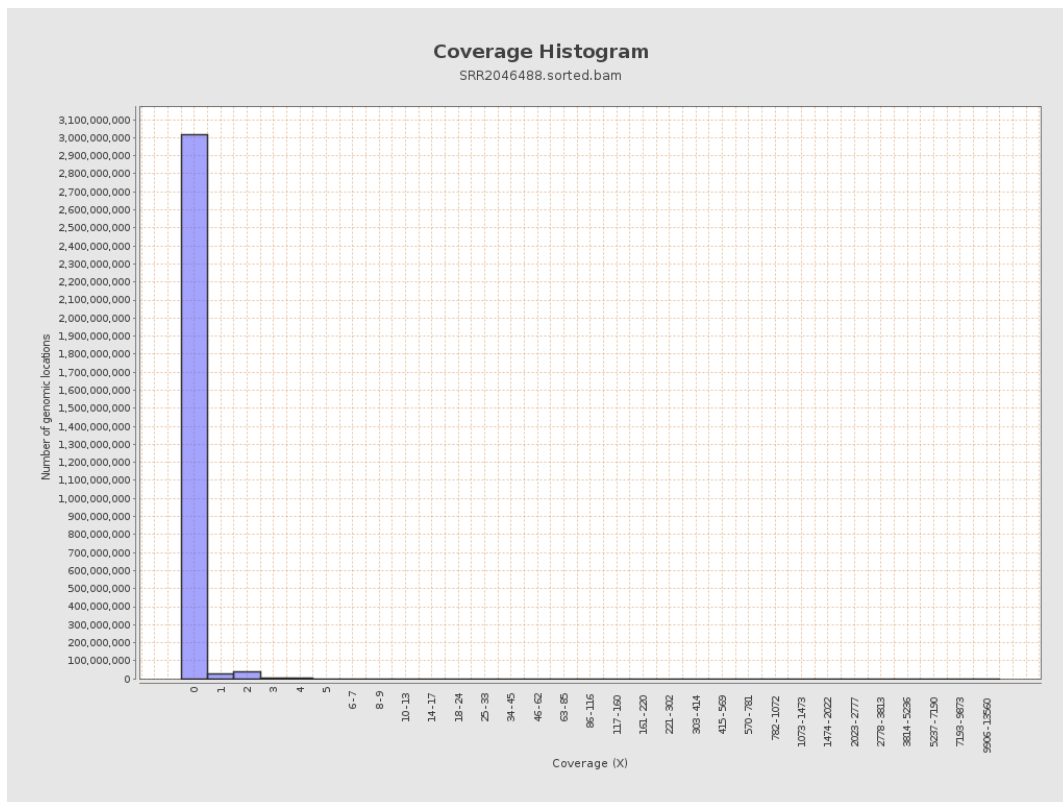
		bases	coverage	deviation
chr1	249250621	77007057	0.309	19.5918
chr2	243199373	88996546	0.3659	21.556
chr3	198022430	49280409	0.2489	15.6279
chr4	191154276	24916380	0.1303	8.7969
chr5	180915260	57716009	0.319	19.5026
chr6	171115067	84120230	0.4916	28.4688
chr7	159138663	50905763	0.3199	22.7285
chr8	146364022	71924487	0.4914	27.4163
chr9	141213431	18458881	0.1307	9.8951
chr10	135534747	16481939	0.1216	8.8308
chr11	135006516	19443231	0.144	7.7762
chr12	133851895	29745271	0.2222	13.528
chr13	115169878	18787359	0.1631	9.9936
chr14	107349540	41651769	0.388	23.1491
chr15	102531392	17603863	0.1717	11.1053
chr16	90354753	42175762	0.4668	28.4377
chr17	81195210	27351840	0.3369	15.2512
chr18	78077248	6167971	0.079	3.2292
chr19	59128983	5597222	0.0947	4.6717
chr20	63025520	14071537	0.2233	14.3267
chr21	48129895	8271517	0.1719	21.0532
chr22	51304566	12155605	0.2369	13.8693
chrMT	16571	38108	2.2997	2.4708
chrX	155270560	31299257	0.2016	28.8515

chrY	59373566	188669	0.0032	0.4495
------	----------	--------	--------	--------

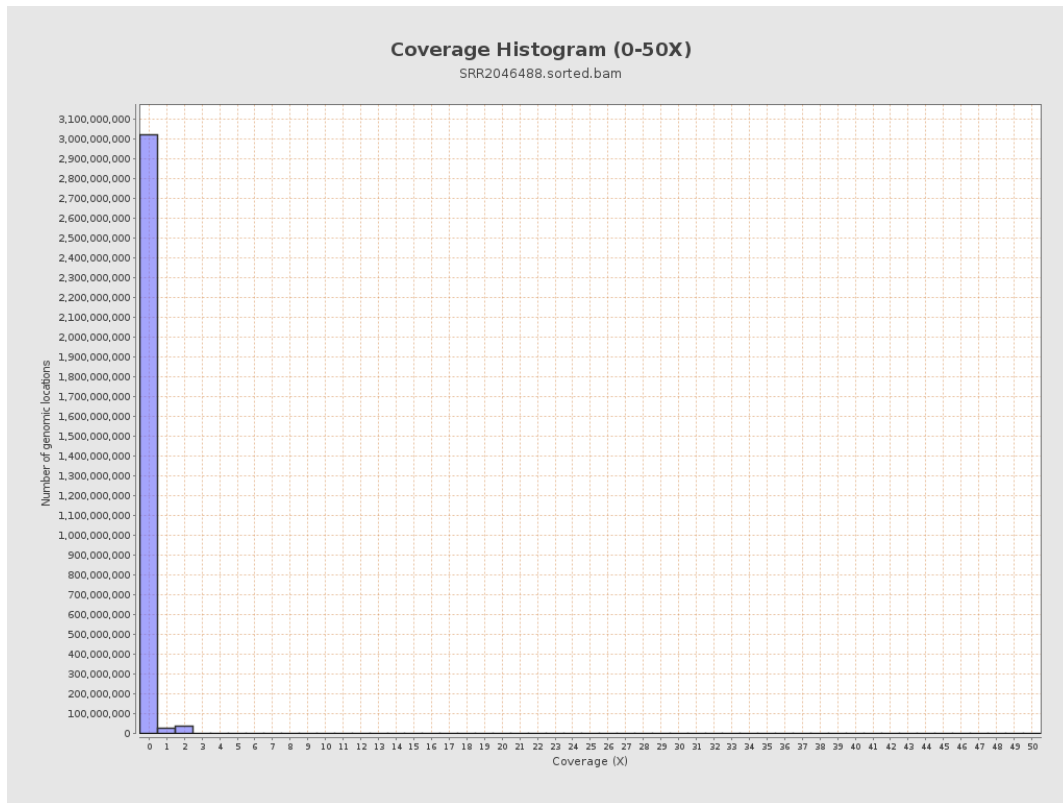
3. Results : Coverage across reference



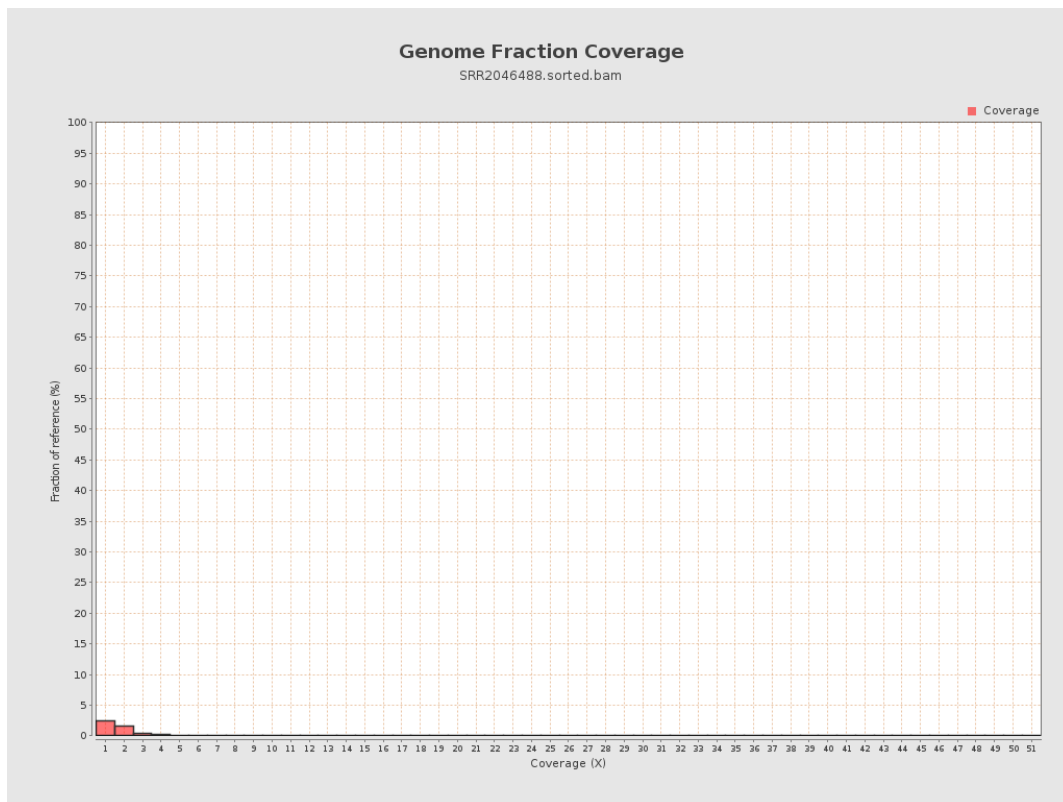
4. Results : Coverage Histogram



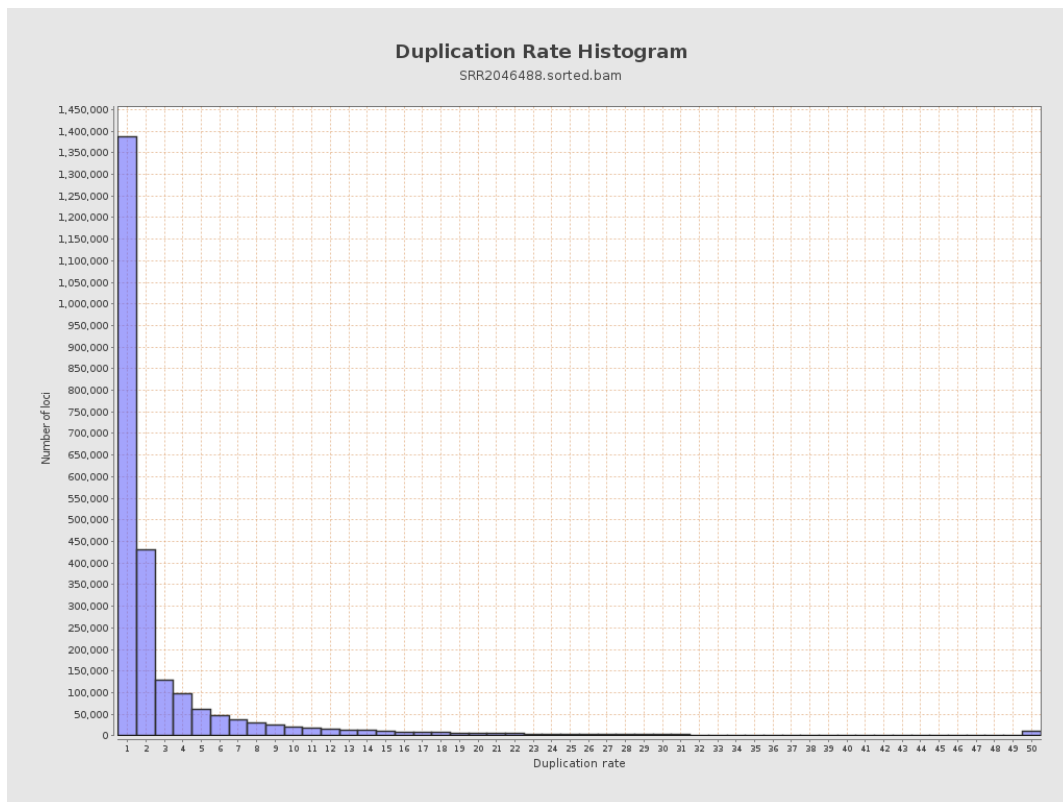
5. Results : Coverage Histogram (0-50X)



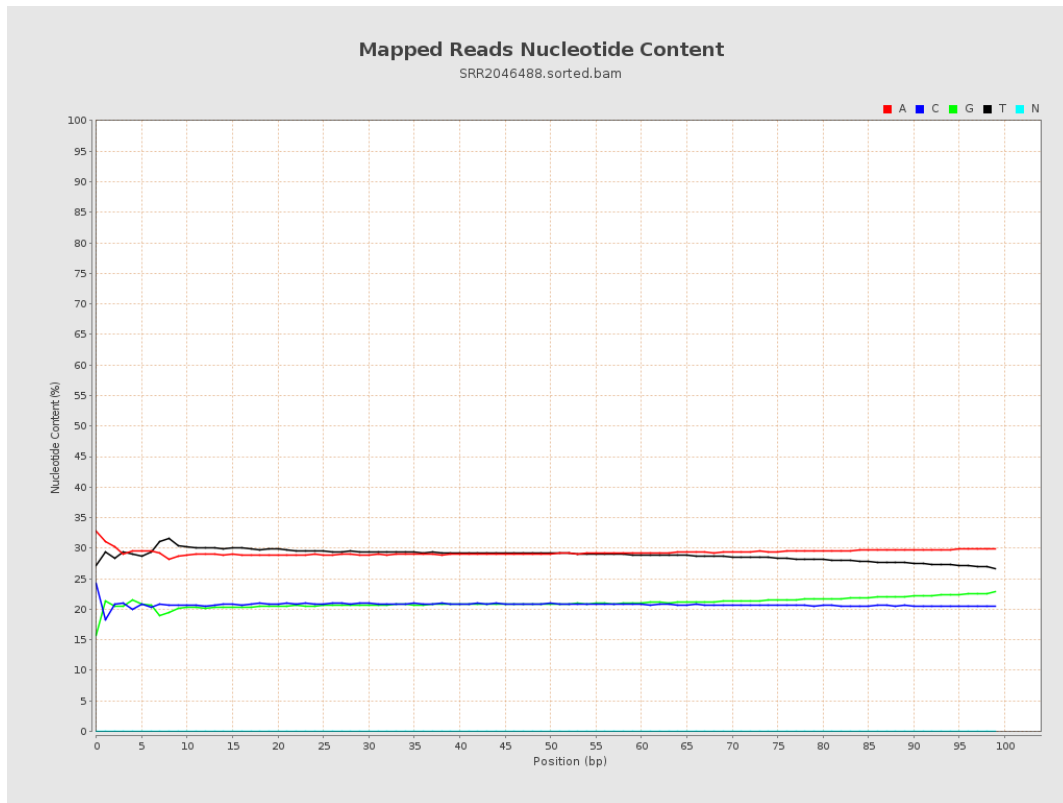
6. Results : Genome Fraction Coverage



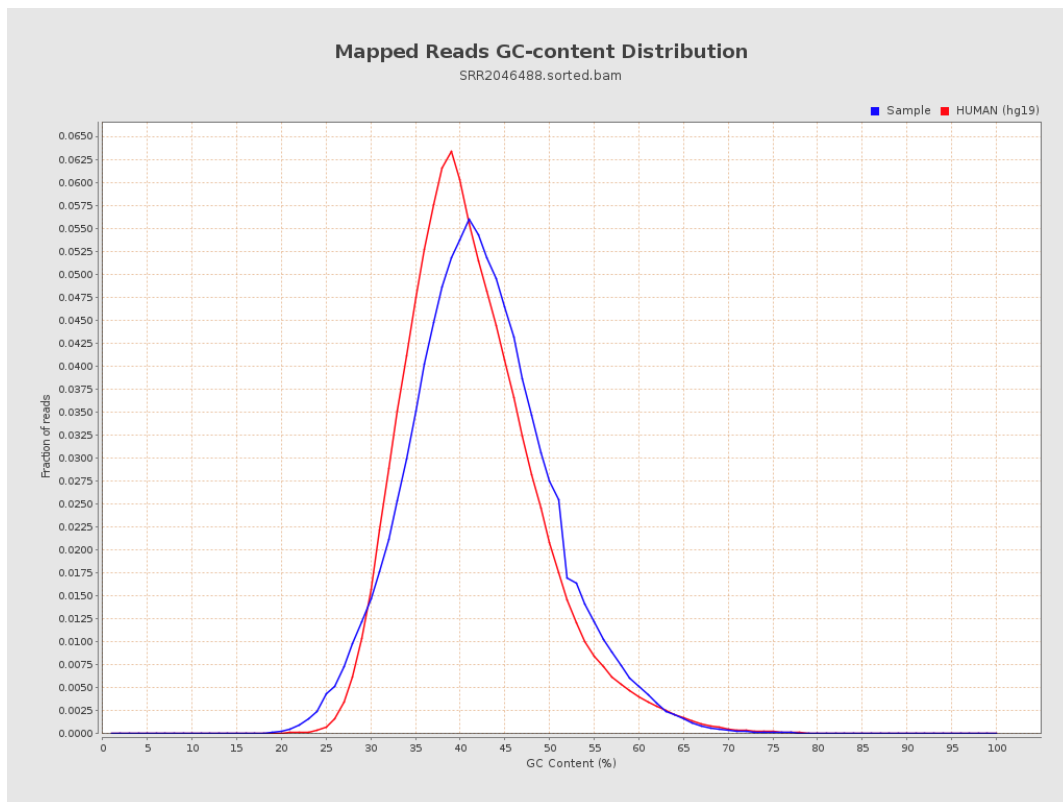
7. Results : Duplication Rate Histogram



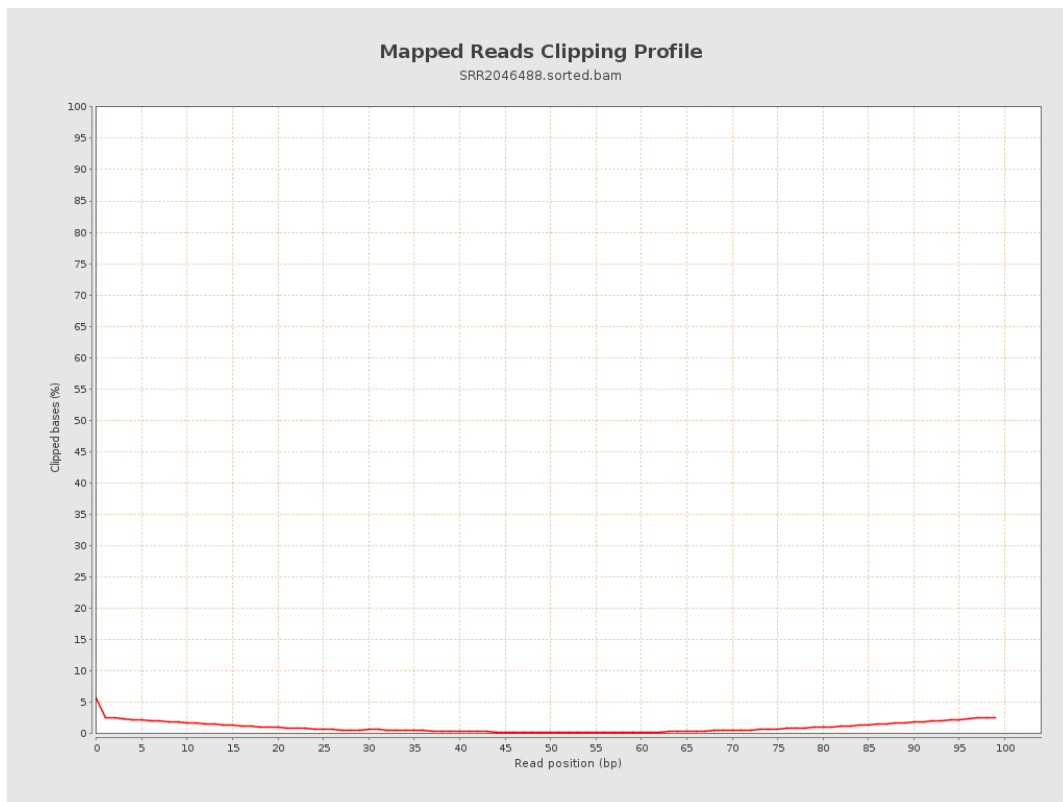
8. Results : Mapped Reads Nucleotide Content



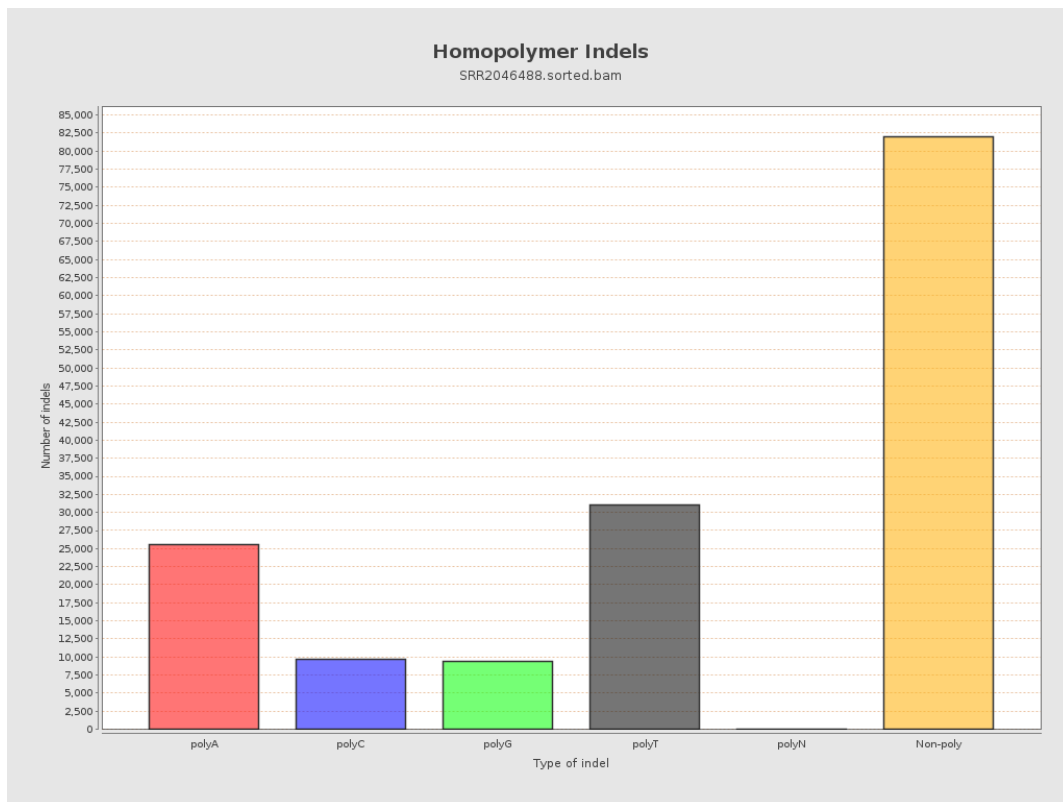
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



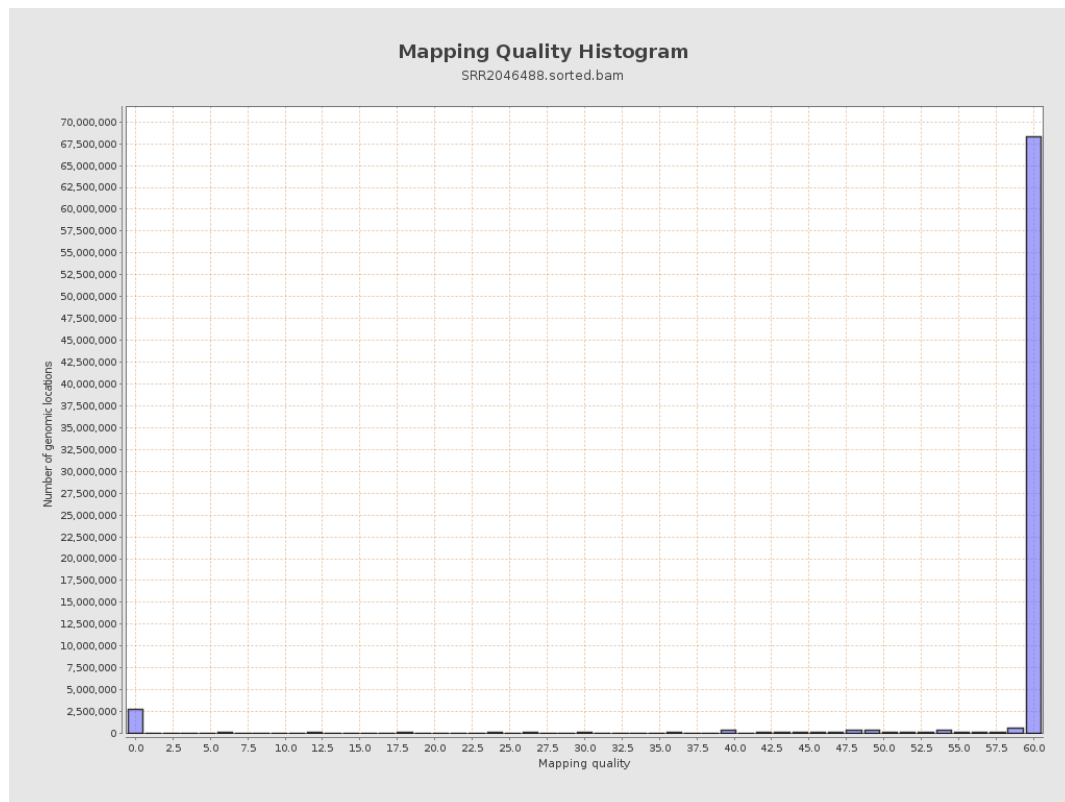
11. Results : Homopolymer Indels



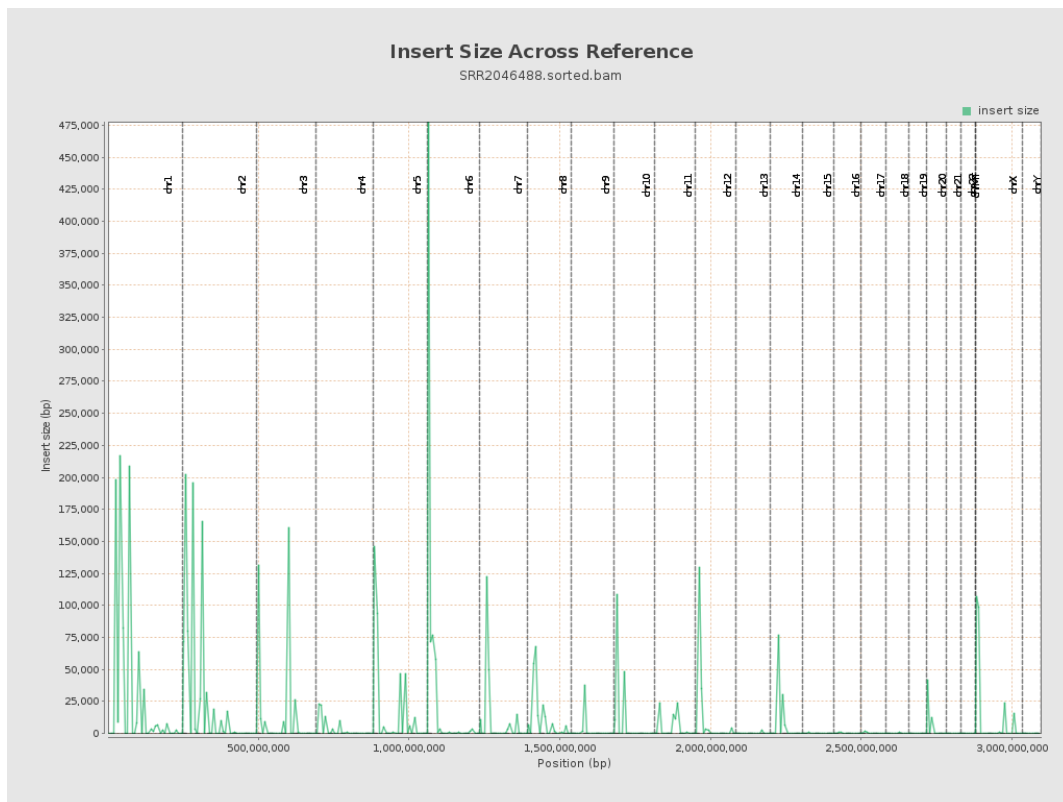
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

