

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 03:35:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472544.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_SRR3472544 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472544_1.fastq.gz SRR3472544_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 03:35:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472544.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,476,916
Mapped reads	15,249,447 / 98.53%
Unmapped reads	227,469 / 1.47%
Mapped paired reads	15,249,447 / 98.53%
Mapped reads, first in pair	7,642,713 / 49.38%
Mapped reads, second in pair	7,606,734 / 49.15%
Mapped reads, both in pair	15,151,774 / 97.9%
Mapped reads, singletons	97,673 / 0.63%
Secondary alignments	0
Supplementary alignments	65,669 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	9,912,847 / 64.05%
Duplication rate	42.88%
Clipped reads	1,409,976 / 9.11%

2.2. ACGT Content

Number/percentage of A's	410,676,636 / 27.44%
Number/percentage of C's	340,195,904 / 22.73%
Number/percentage of T's	407,599,700 / 27.23%
Number/percentage of G's	338,160,868 / 22.59%
Number/percentage of N's	233,434 / 0.02%

GC Percentage	45.32%
---------------	--------

2.3. Coverage

Mean	0.4836
Standard Deviation	26.2179

2.4. Mapping Quality

Mean Mapping Quality	54.89
----------------------	-------

2.5. Insert size

Mean	37,503.71
Standard Deviation	1,900,692.92
P25/Median/P75	159 / 220 / 295

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	8,453,024
Insertions	68,724
Mapped reads with at least one insertion	0.45%
Deletions	72,074
Mapped reads with at least one deletion	0.47%
Homopolymer indels	42.93%

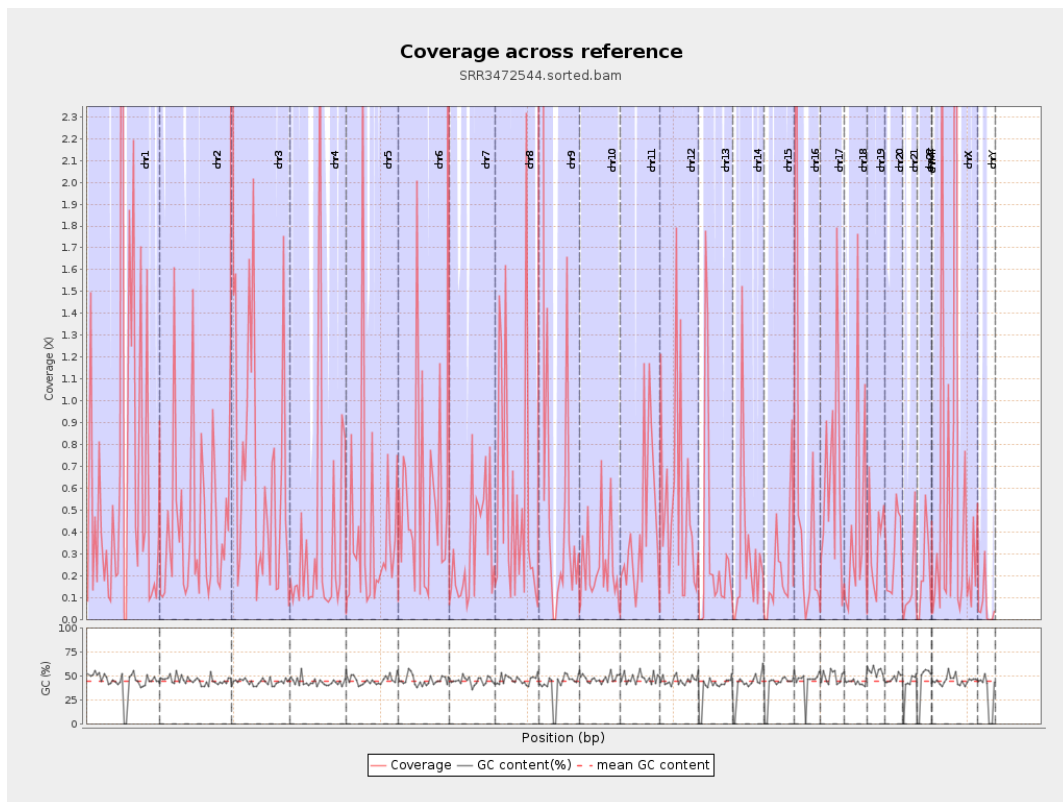
2.7. Chromosome stats

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

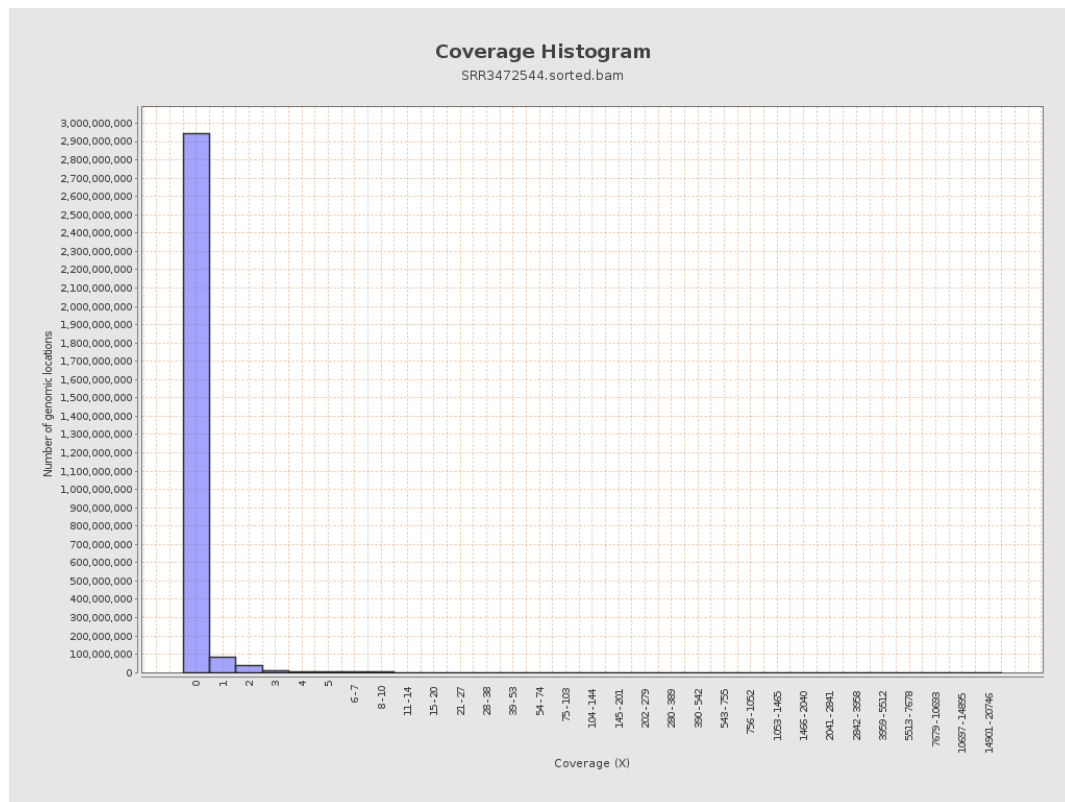
		bases	coverage	deviation
chr1	249250621	167783847	0.6732	33.8386
chr2	243199373	104802811	0.4309	20.5135
chr3	198022430	152240811	0.7688	22.5234
chr4	191154276	66192348	0.3463	21.8873
chr5	180915260	74904507	0.414	20.1111
chr6	171115067	105281899	0.6153	23.3569
chr7	159138663	51396317	0.323	12.0113
chr8	146364022	83325154	0.5693	22.0251
chr9	141213431	130993857	0.9276	46.7603
chr10	135534747	34255727	0.2527	11.0547
chr11	135006516	57726286	0.4276	17.1884
chr12	133851895	72888954	0.5445	17.2829
chr13	115169878	38917097	0.3379	20.1299
chr14	107349540	31688922	0.2952	16.7554
chr15	102531392	25337615	0.2471	9.2592
chr16	90354753	48605246	0.5379	21.526
chr17	81195210	49841718	0.6139	20.2272
chr18	78077248	34360121	0.4401	26.5543
chr19	59128983	21048632	0.356	11.6125
chr20	63025520	19252075	0.3055	9.1049
chr21	48129895	7495485	0.1557	6.1632
chr22	51304566	10524171	0.2051	7.5087
chrMT	16571	7524	0.454	1.6454
chrX	155270560	104345399	0.672	64.5809

chrY	59373566	3820533	0.0643	4.3119
------	----------	---------	--------	--------

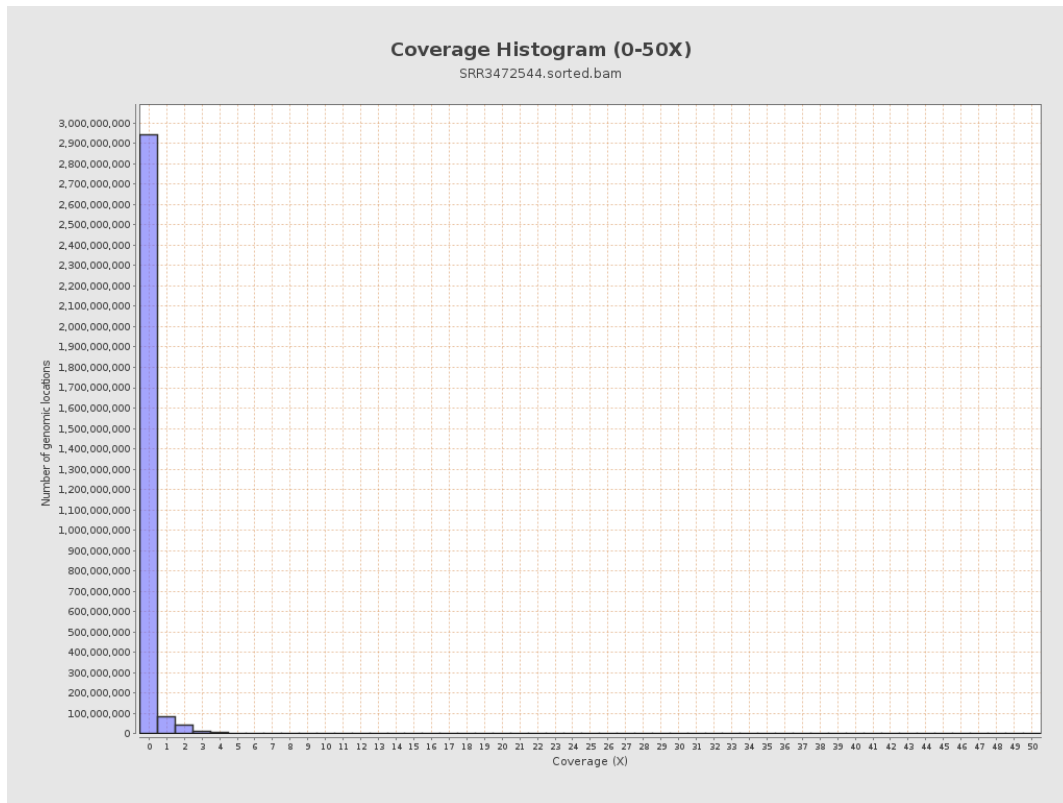
3. Results : Coverage across reference



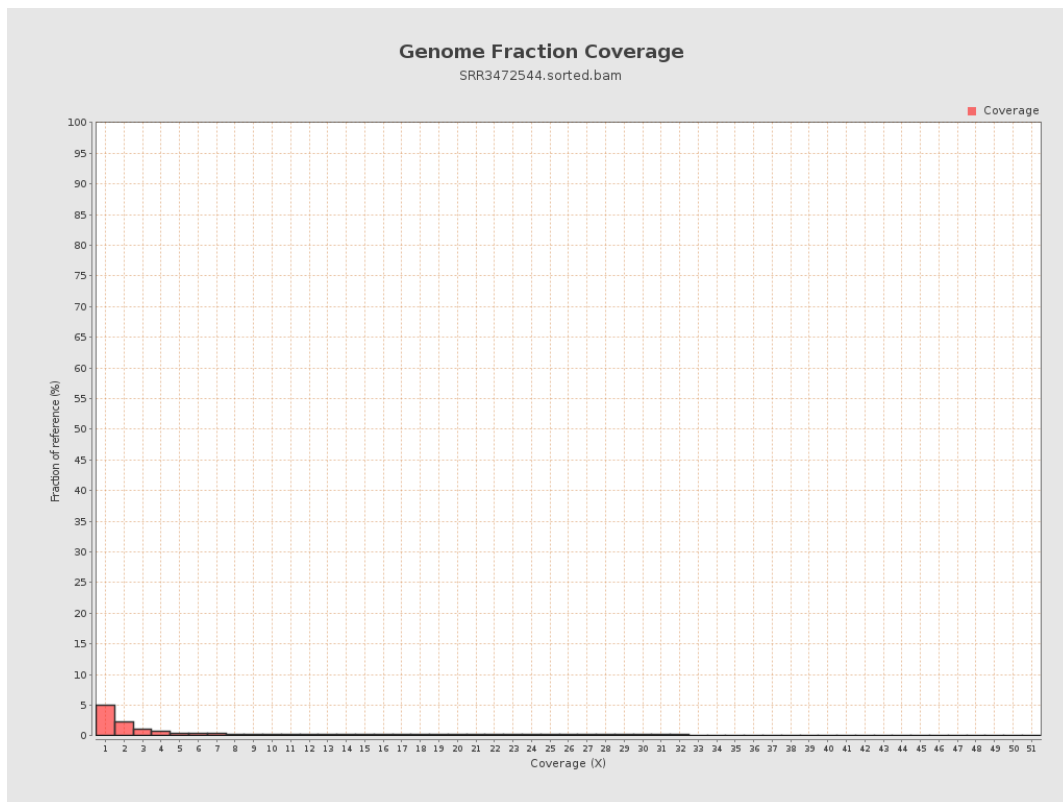
4. Results : Coverage Histogram



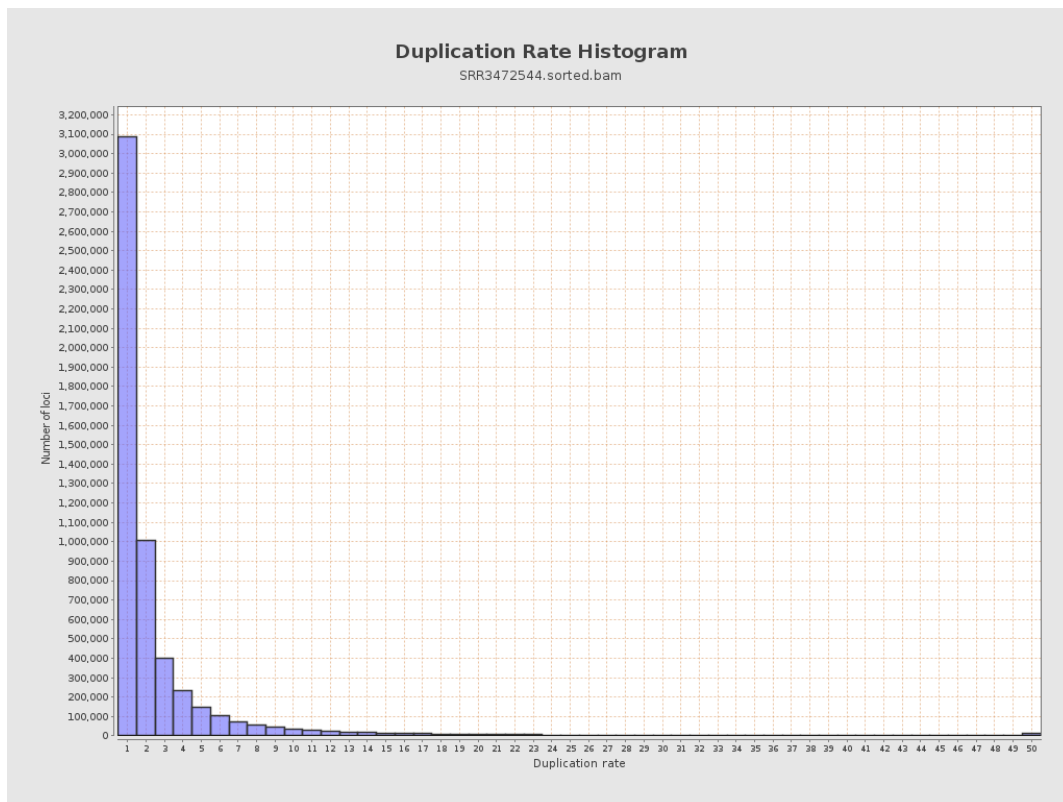
5. Results : Coverage Histogram (0-50X)



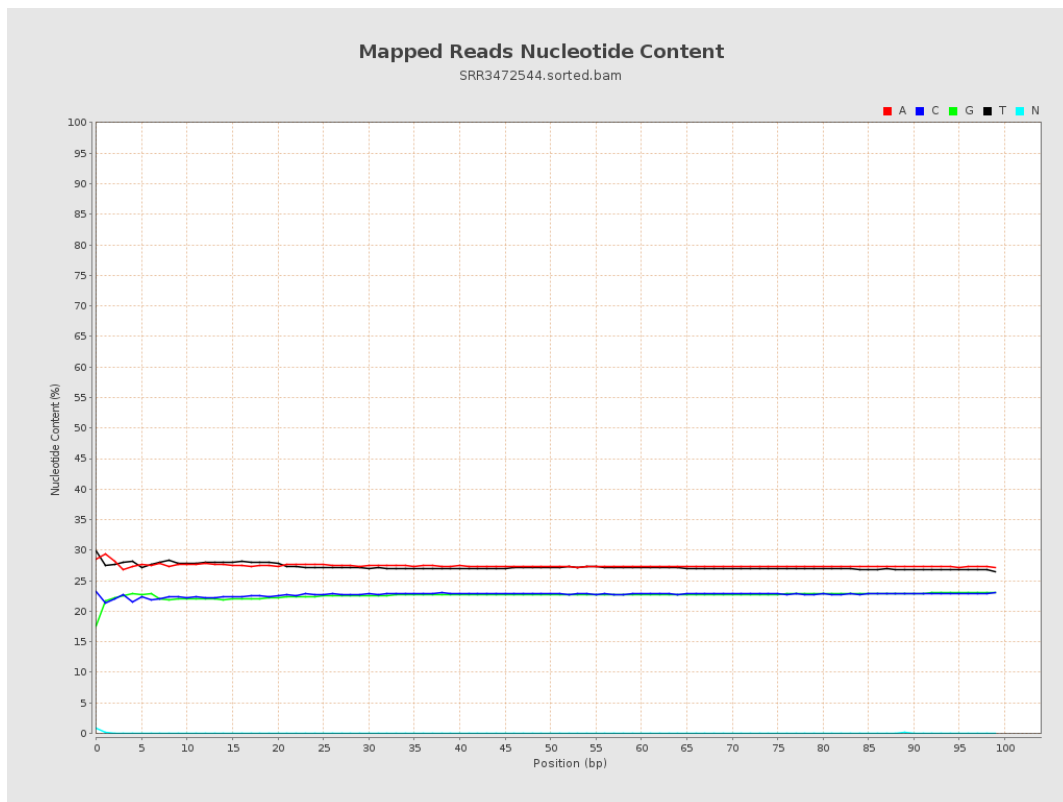
6. Results : Genome Fraction Coverage



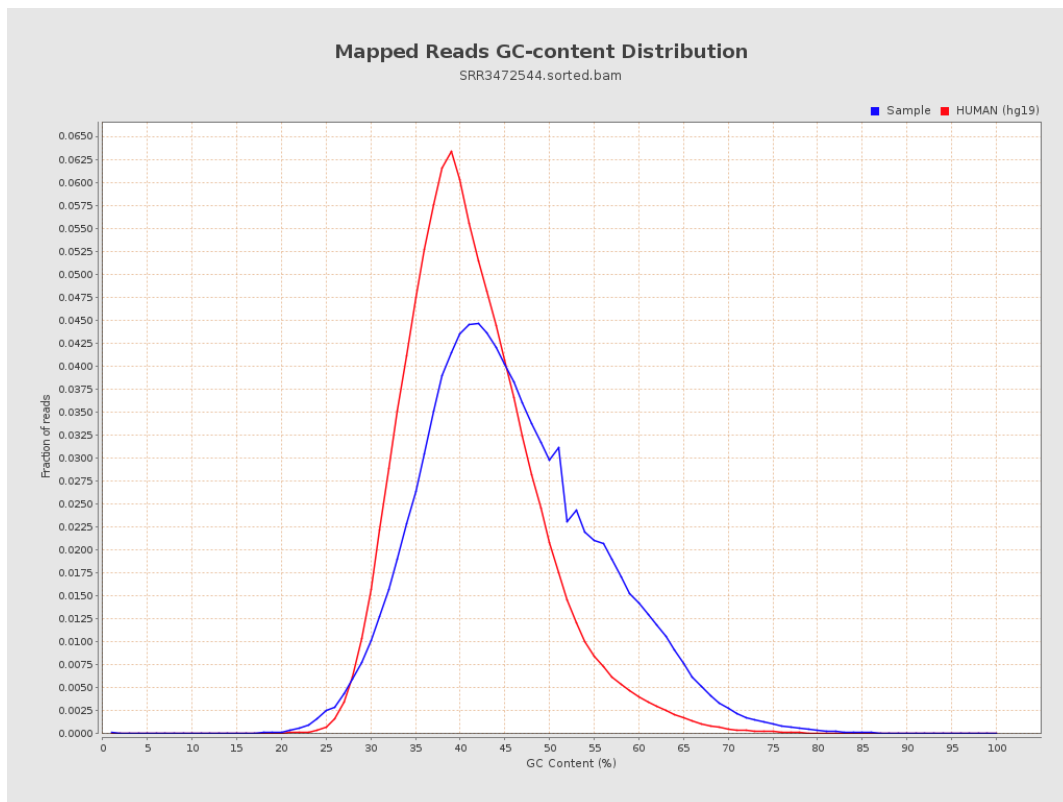
7. Results : Duplication Rate Histogram



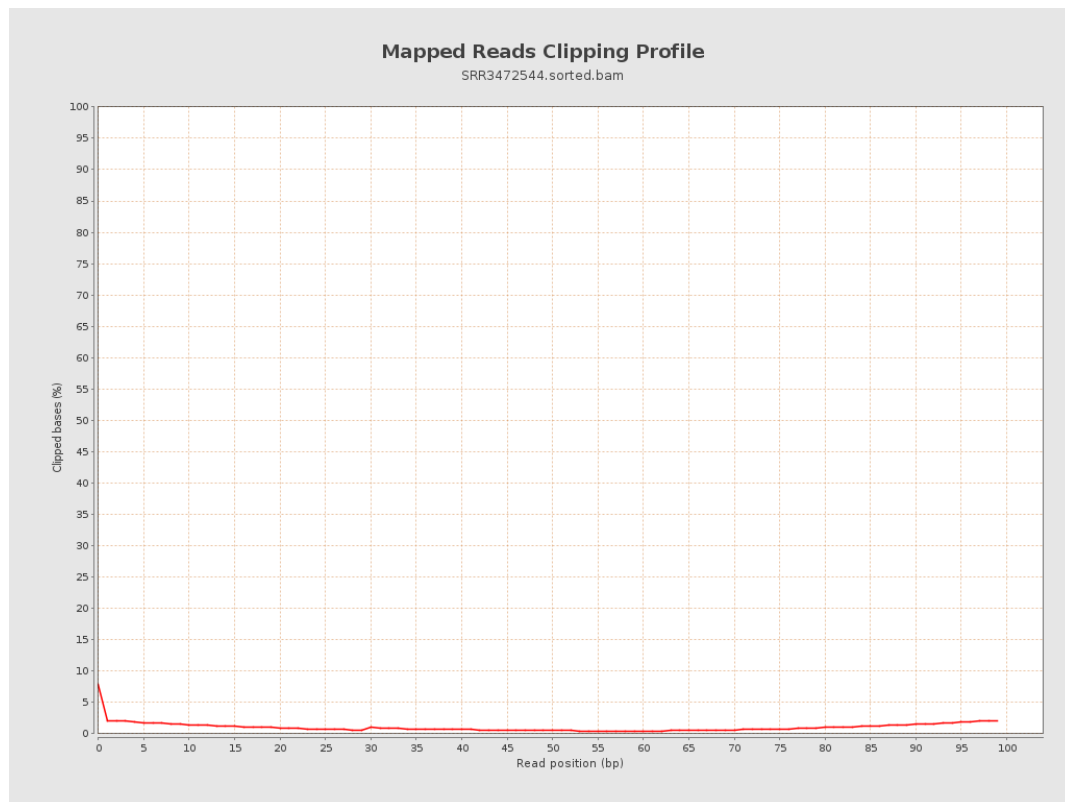
8. Results : Mapped Reads Nucleotide Content



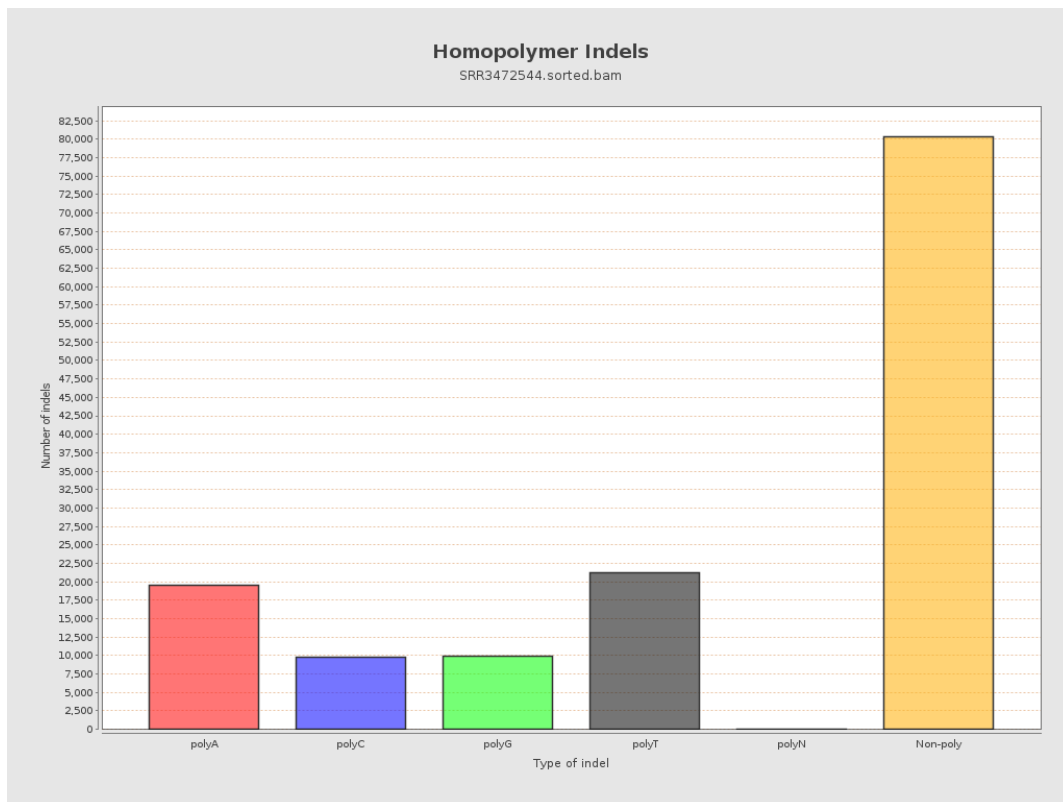
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



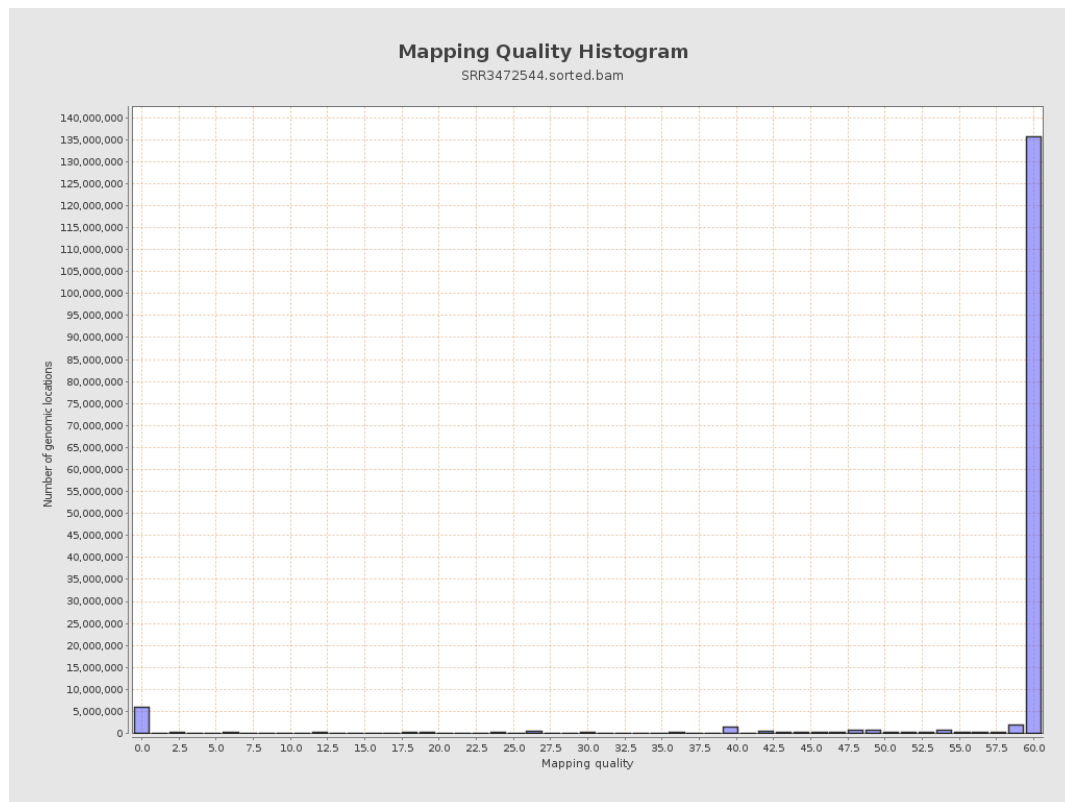
11. Results : Homopolymer Indels



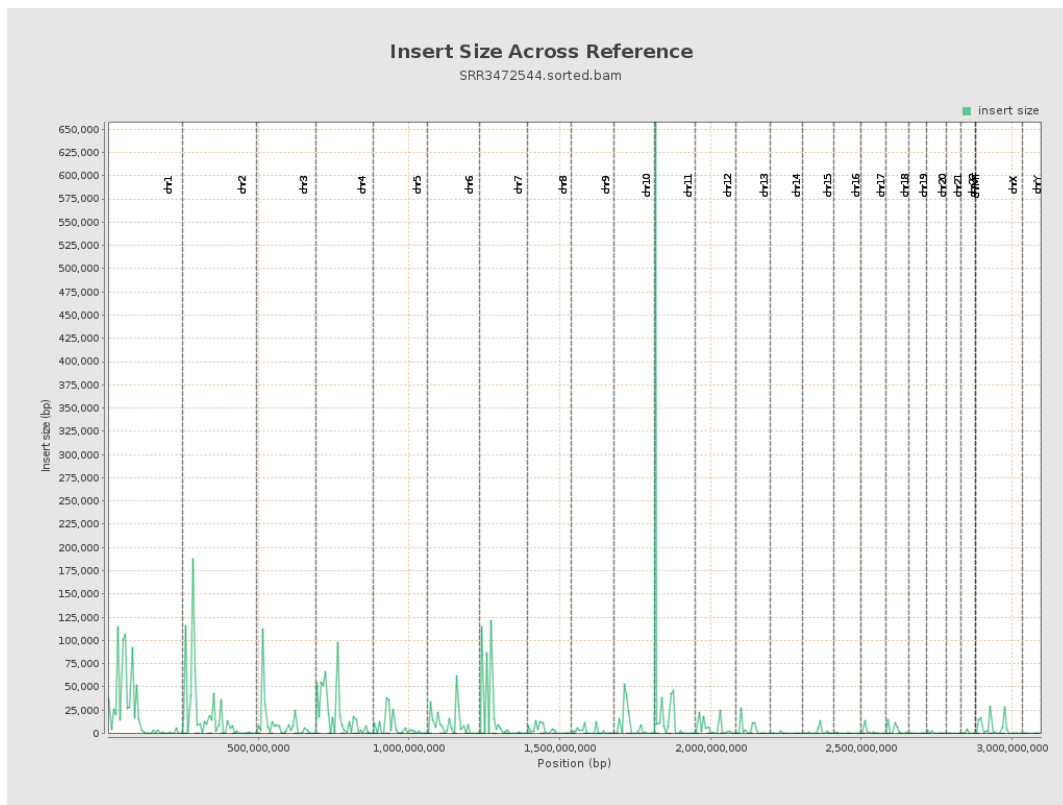
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

