

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 07:25:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472683.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_SRR3472683 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472683_1.fastq.gz SRR3472683_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 07:25:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472683.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,768,862
Mapped reads	27,525,991 / 99.13%
Unmapped reads	242,871 / 0.87%
Mapped paired reads	27,525,991 / 99.13%
Mapped reads, first in pair	13,800,034 / 49.7%
Mapped reads, second in pair	13,725,957 / 49.43%
Mapped reads, both in pair	27,361,336 / 98.53%
Mapped reads, singletons	164,655 / 0.59%
Secondary alignments	0
Supplementary alignments	165,360 / 0.6%
Read min/max/mean length	30 / 101 / 99.79
Duplicated reads (estimated)	20,462,015 / 73.69%
Duplication rate	50.54%
Clipped reads	1,992,594 / 7.18%

2.2. ACGT Content

Number/percentage of A's	730,928,659 / 27%
Number/percentage of C's	626,794,387 / 23.15%
Number/percentage of T's	731,705,224 / 27.03%
Number/percentage of G's	617,486,599 / 22.81%
Number/percentage of N's	524,068 / 0.02%

GC Percentage	45.96%
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2.3. Coverage

Mean	0.8747
Standard Deviation	42.038

2.4. Mapping Quality

Mean Mapping Quality	54.58
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2.5. Insert size

Mean	27,365.99
Standard Deviation	1,636,387.9
P25/Median/P75	165 / 229 / 305

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	17,255,455
Insertions	183,636
Mapped reads with at least one insertion	0.66%
Deletions	148,666
Mapped reads with at least one deletion	0.53%
Homopolymer indels	46.78%

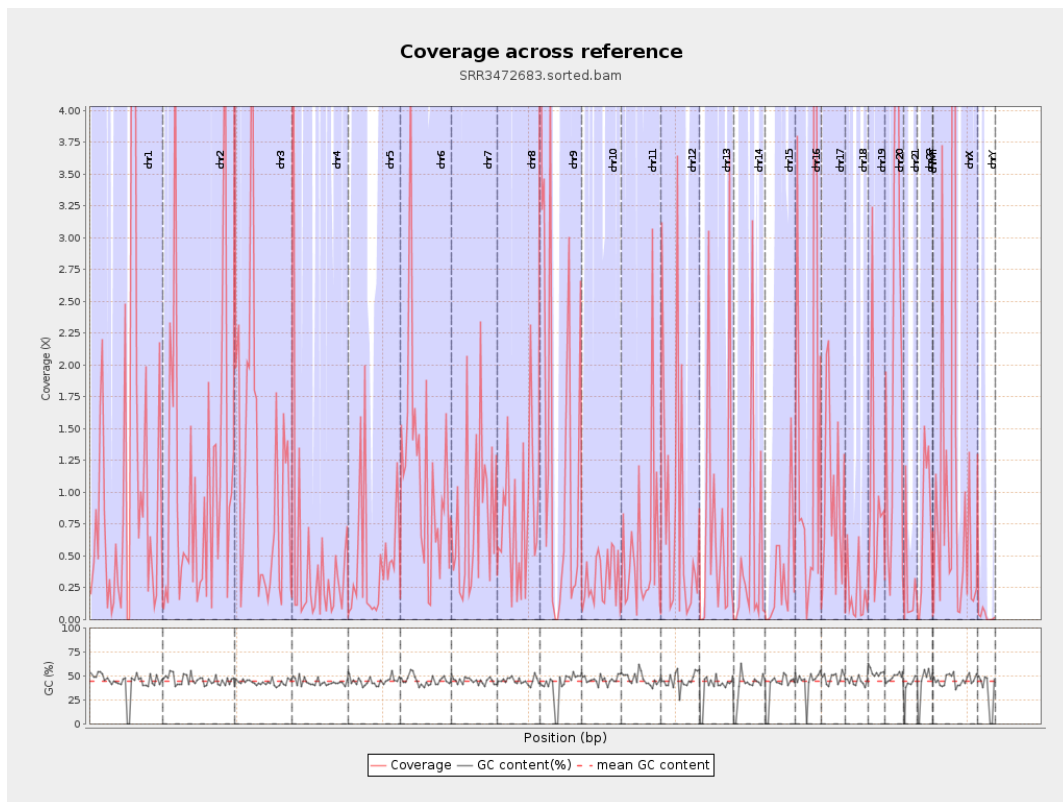
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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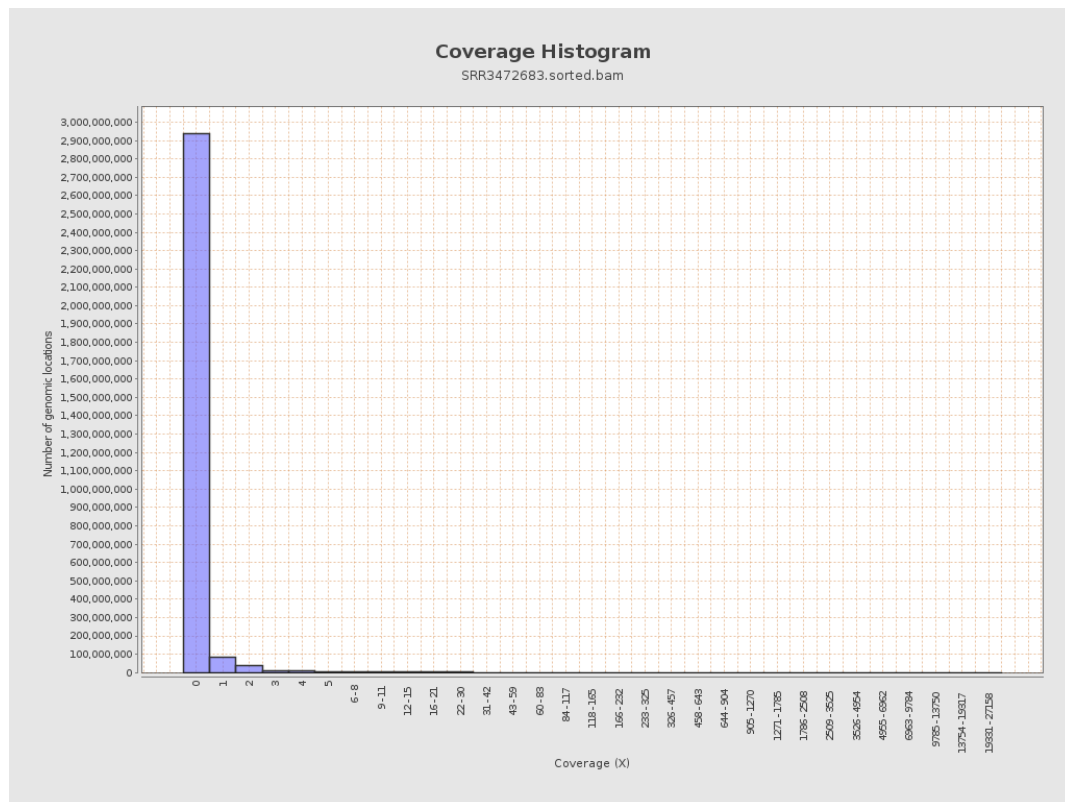
		bases	coverage	deviation
chr1	249250621	257655310	1.0337	37.8103
chr2	243199373	258296979	1.0621	52.5715
chr3	198022430	235053563	1.187	34.3184
chr4	191154276	99326013	0.5196	35.1386
chr5	180915260	82606145	0.4566	18.4386
chr6	171115067	196565656	1.1487	31.5135
chr7	159138663	131066368	0.8236	29.0253
chr8	146364022	120424570	0.8228	28.4206
chr9	141213431	180058746	1.2751	40.7488
chr10	135534747	43711301	0.3225	11.5818
chr11	135006516	74869931	0.5546	29.7937
chr12	133851895	118303344	0.8838	30.7058
chr13	115169878	90939218	0.7896	39.9496
chr14	107349540	48351598	0.4504	24.0706
chr15	102531392	34498261	0.3365	16.9057
chr16	90354753	144696329	1.6014	62.8439
chr17	81195210	79307032	0.9767	27.2607
chr18	78077248	15587698	0.1996	11.3398
chr19	59128983	57085993	0.9654	29.6286
chr20	63025520	138656717	2.2	62.6663
chr21	48129895	14032460	0.2916	20.0167
chr22	51304566	39215867	0.7644	33.2258
chrMT	16571	11469	0.6921	1.47
chrX	155270560	245807017	1.5831	110.9617

chrY	59373566	1723909	0.029	2.4051
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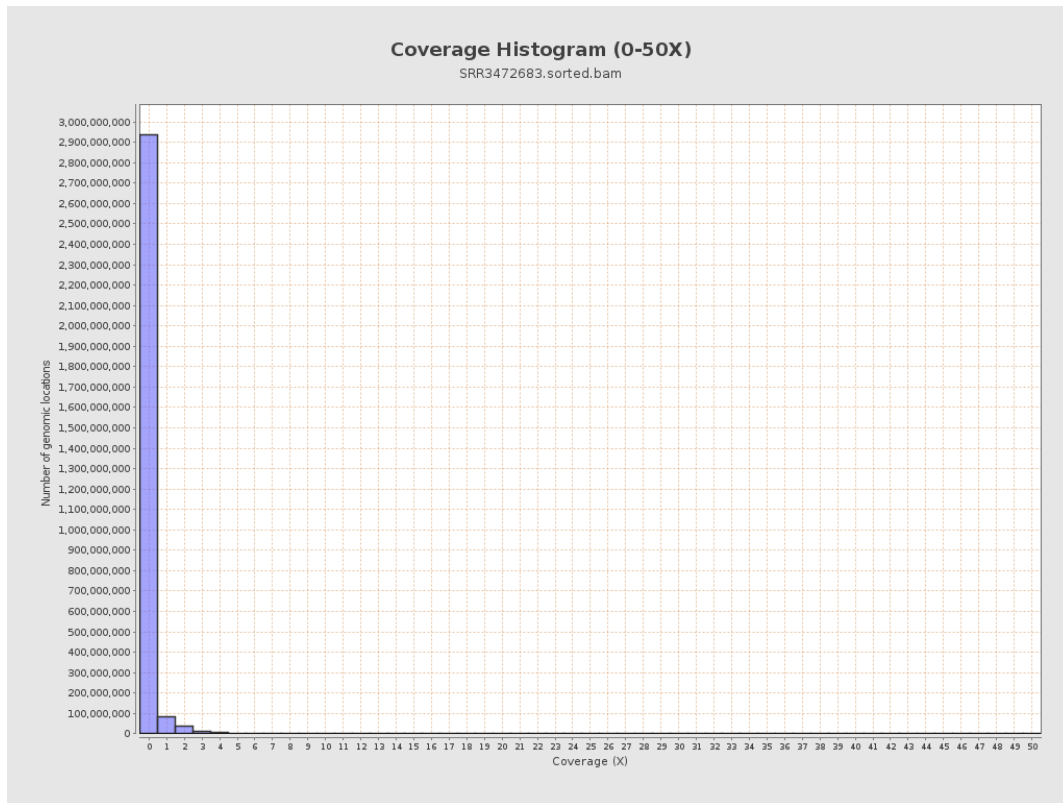
3. Results : Coverage across reference



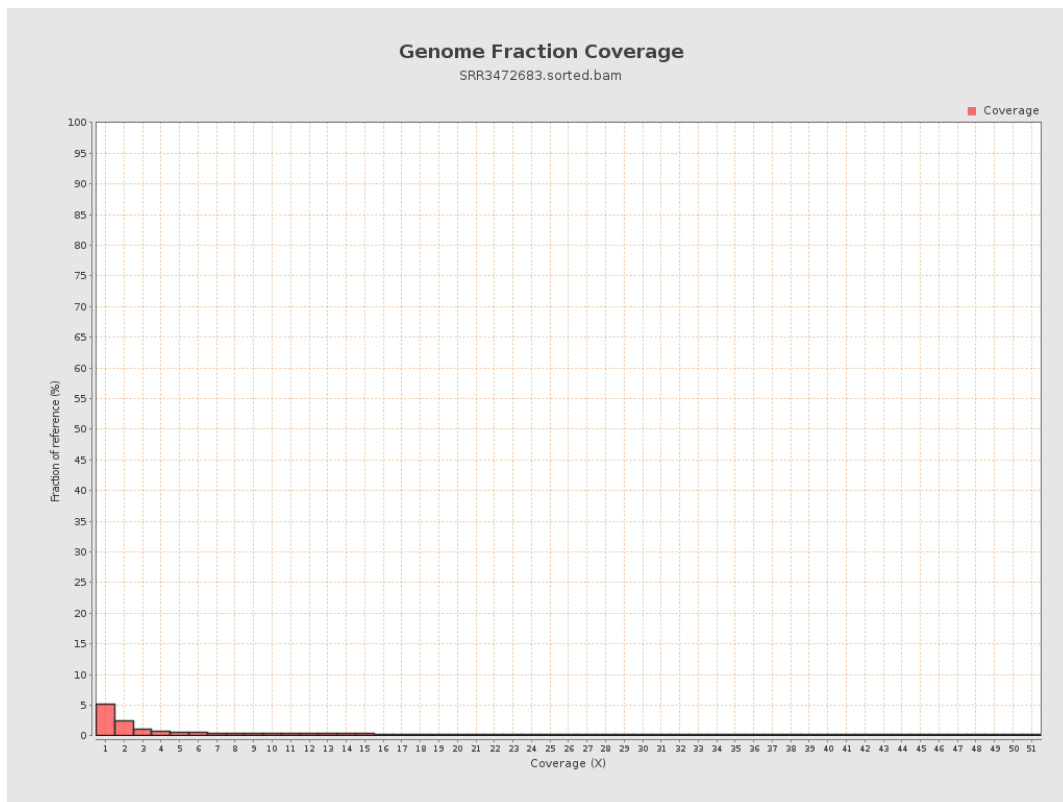
4. Results : Coverage Histogram



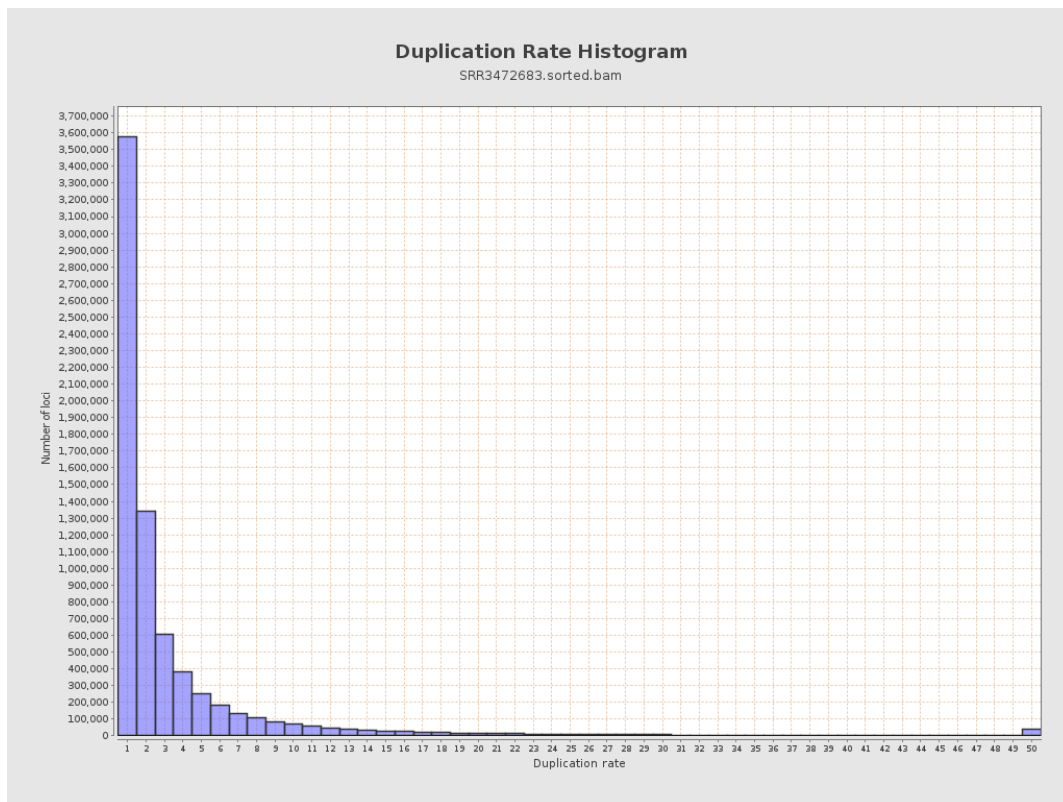
5. Results : Coverage Histogram (0-50X)



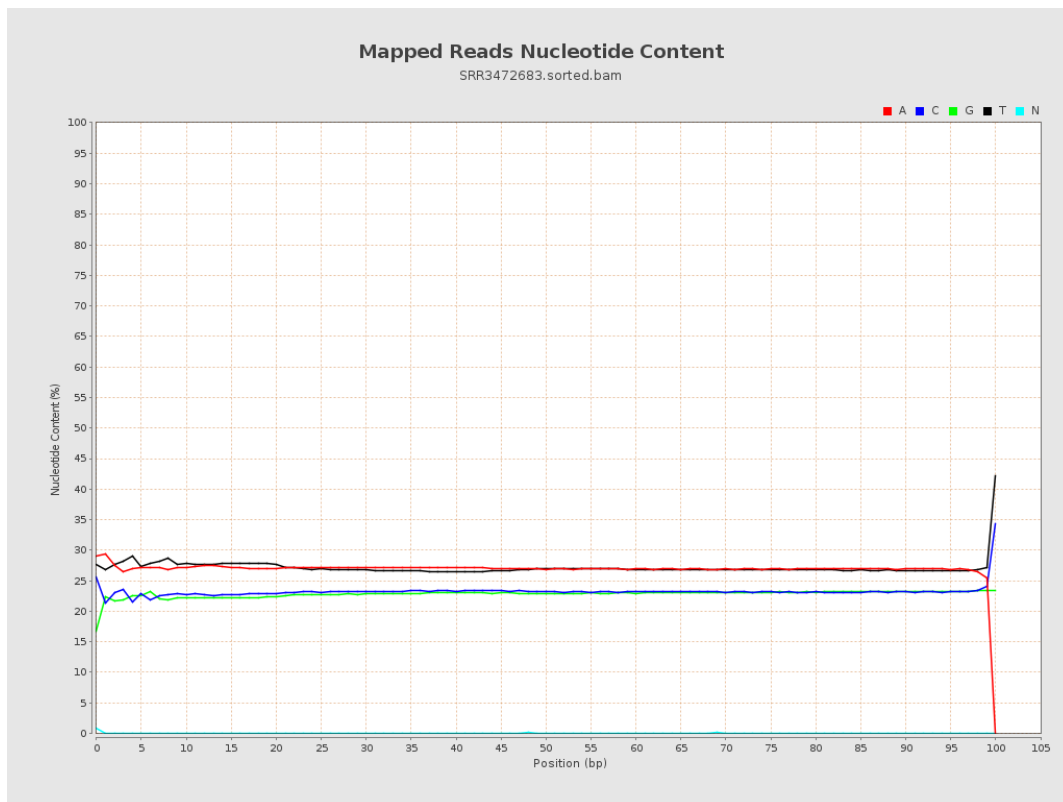
6. Results : Genome Fraction Coverage



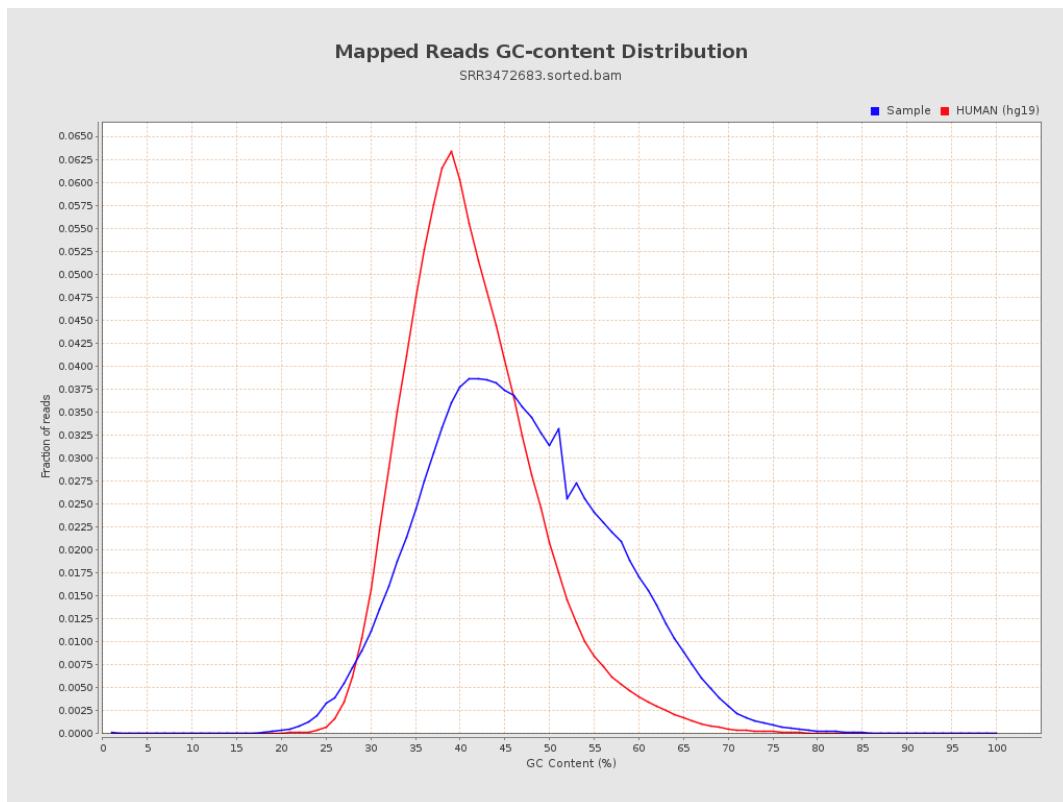
7. Results : Duplication Rate Histogram



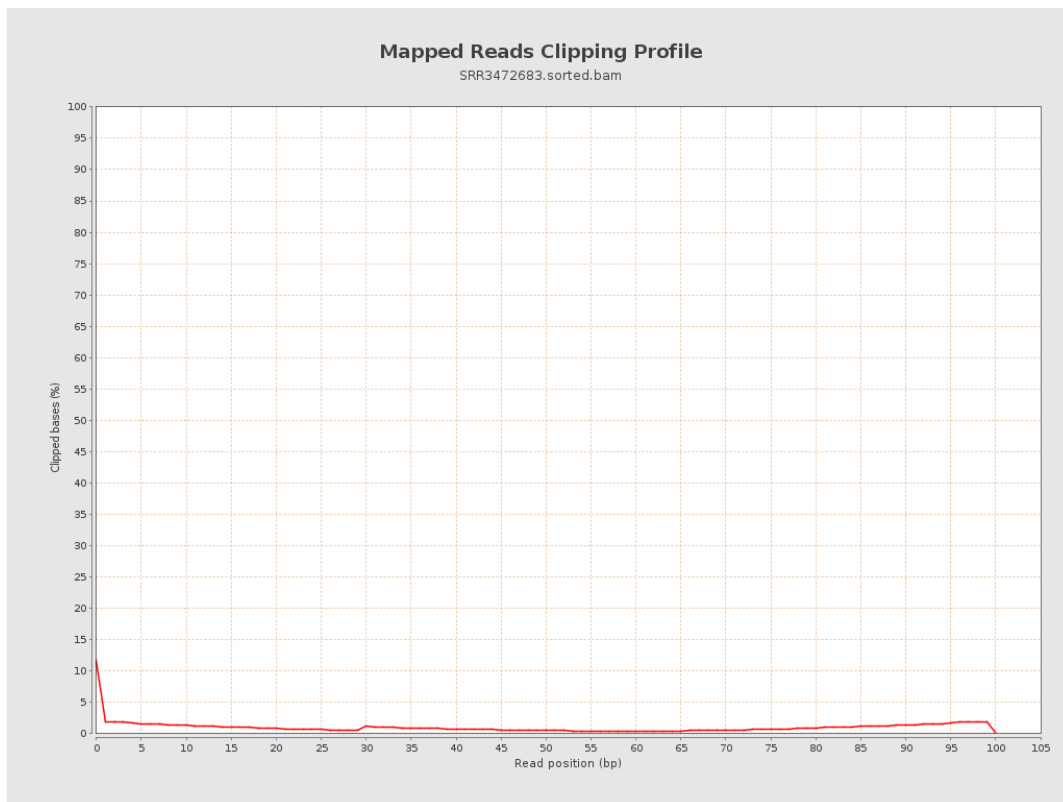
8. Results : Mapped Reads Nucleotide Content



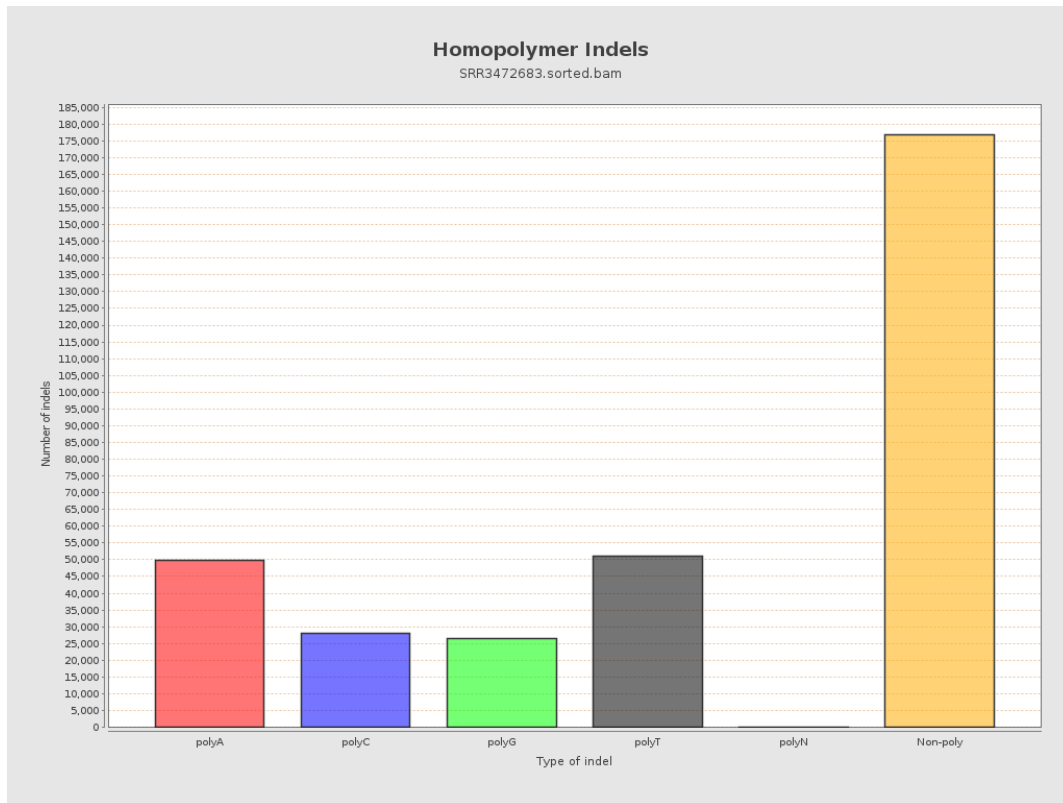
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



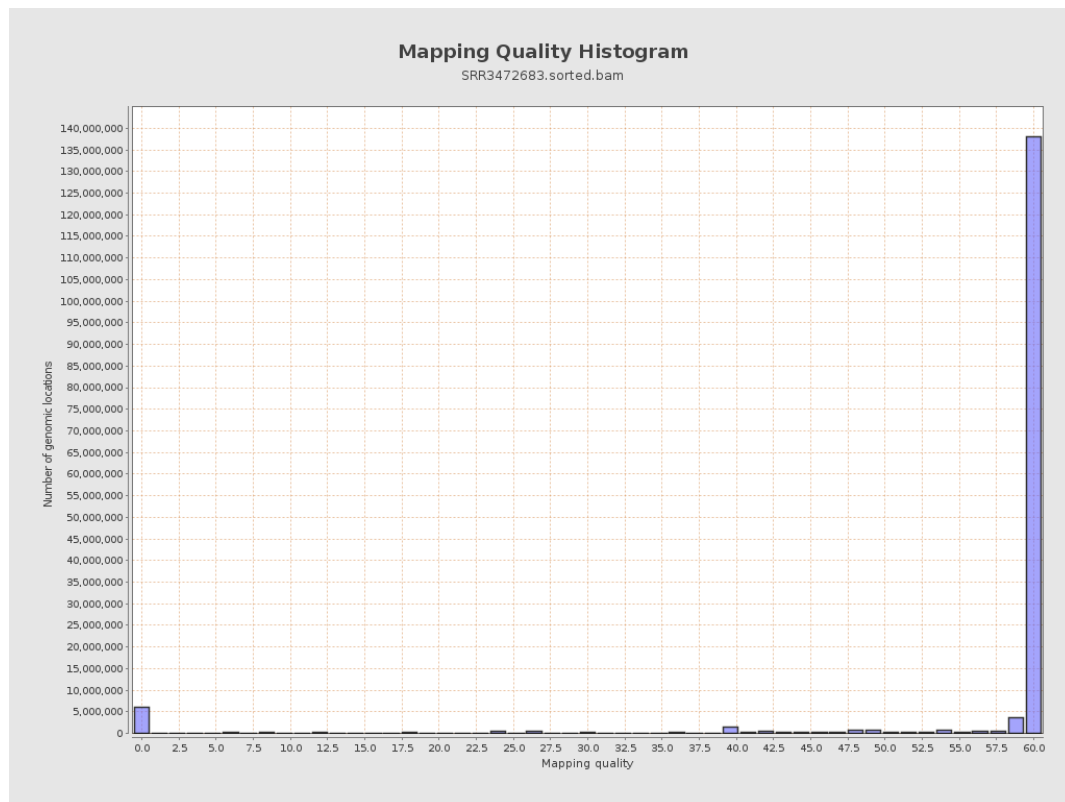
11. Results : Homopolymer Indels



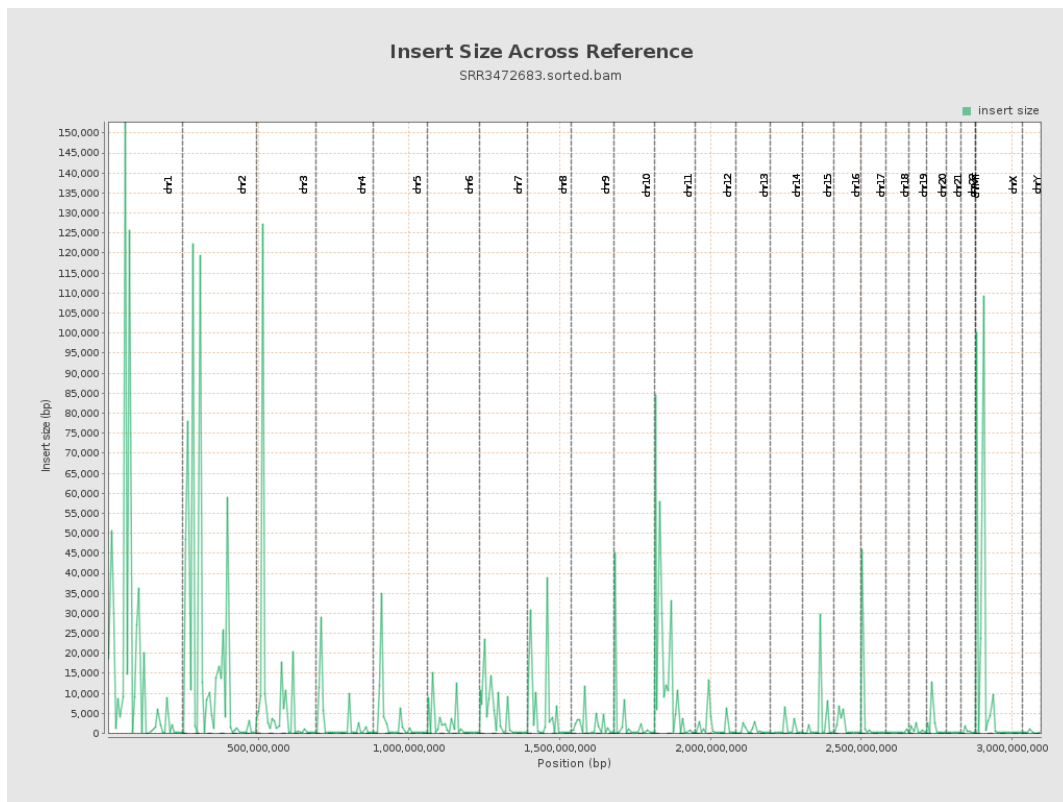
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

