

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 02:52:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472668.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_SRR3472668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472668_1.fastq.gz SRR3472668_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 02:52:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,158,152
Mapped reads	19,022,128 / 99.29%
Unmapped reads	136,024 / 0.71%
Mapped paired reads	19,022,128 / 99.29%
Mapped reads, first in pair	9,529,272 / 49.74%
Mapped reads, second in pair	9,492,856 / 49.55%
Mapped reads, both in pair	18,933,236 / 98.83%
Mapped reads, singletons	88,892 / 0.46%
Secondary alignments	0
Supplementary alignments	118,030 / 0.62%
Read min/max/mean length	30 / 101 / 99.52
Duplicated reads (estimated)	13,943,784 / 72.78%
Duplication rate	49.78%
Clipped reads	1,638,221 / 8.55%

2.2. ACGT Content

Number/percentage of A's	506,724,972 / 27.22%
Number/percentage of C's	426,182,103 / 22.89%
Number/percentage of T's	507,373,691 / 27.25%
Number/percentage of G's	420,957,609 / 22.61%
Number/percentage of N's	350,909 / 0.02%

GC Percentage	45.51%
---------------	--------

2.3. Coverage

Mean	0.6014
Standard Deviation	30.6835

2.4. Mapping Quality

Mean Mapping Quality	54.64
----------------------	-------

2.5. Insert size

Mean	22,485.28
Standard Deviation	1,450,614.37
P25/Median/P75	138 / 192 / 261

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	10,506,271
Insertions	115,555
Mapped reads with at least one insertion	0.6%
Deletions	92,763
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45.89%

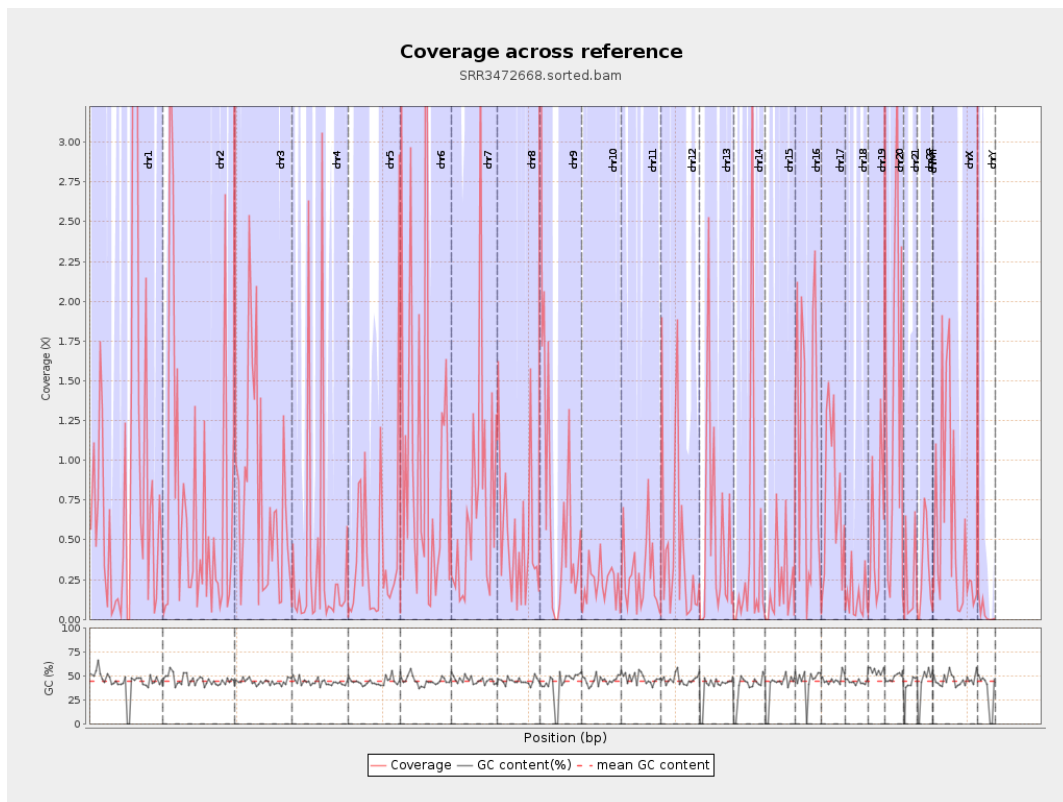
2.7. Chromosome stats

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

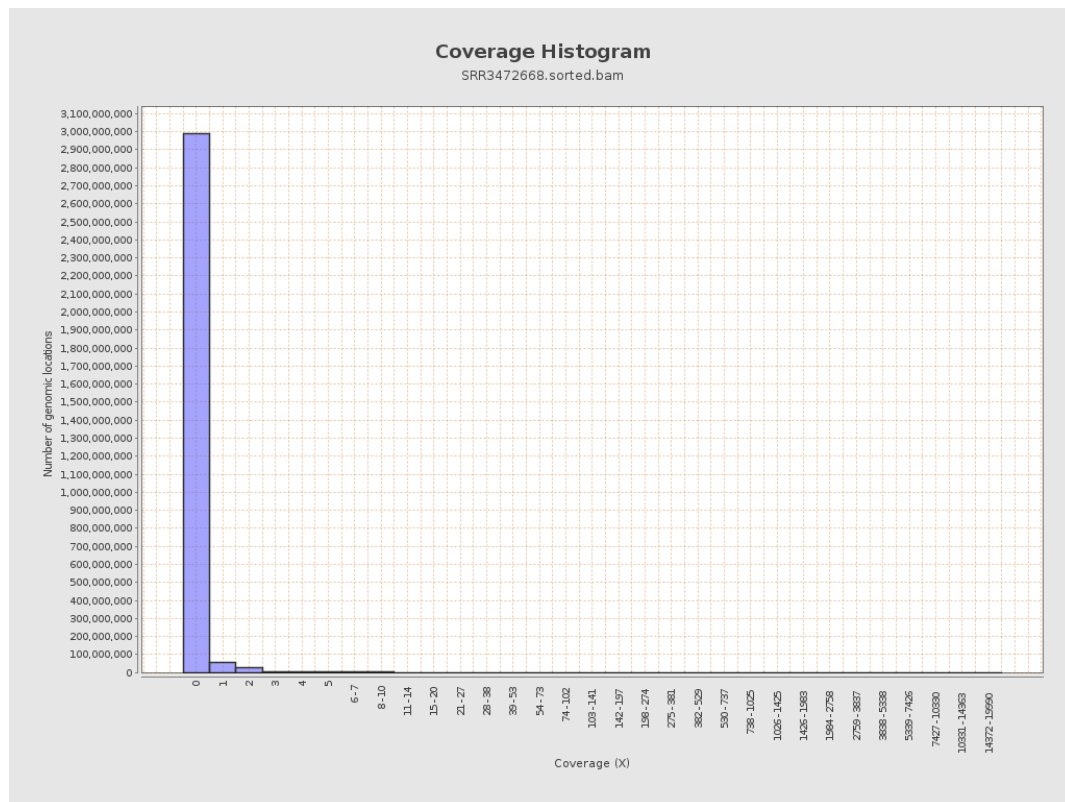
		bases	coverage	deviation
chr1	249250621	225304096	0.9039	41.4394
chr2	243199373	163599386	0.6727	43.5427
chr3	198022430	164046949	0.8284	30.8127
chr4	191154276	70953457	0.3712	22.9668
chr5	180915260	77115181	0.4263	28.8638
chr6	171115067	190041840	1.1106	49.4861
chr7	159138663	117663597	0.7394	38.2569
chr8	146364022	75070071	0.5129	26.3167
chr9	141213431	94777761	0.6712	24.6939
chr10	135534747	31423479	0.2318	11.6064
chr11	135006516	37867823	0.2805	13.3052
chr12	133851895	64085189	0.4788	18.6153
chr13	115169878	61645223	0.5353	21.8331
chr14	107349540	43141204	0.4019	25.5952
chr15	102531392	22279732	0.2173	11.9741
chr16	90354753	96784705	1.0712	44.584
chr17	81195210	64167646	0.7903	29.3068
chr18	78077248	10912176	0.1398	9.668
chr19	59128983	38999473	0.6596	25.9834
chr20	63025520	85759045	1.3607	42.5948
chr21	48129895	12027101	0.2499	18.2415
chr22	51304566	16383858	0.3193	9.6851
chrMT	16571	4336	0.2617	0.6013
chrX	155270560	95346550	0.6141	23.4587

chrY	59373566	2413582	0.0407	2.9443
------	----------	---------	--------	--------

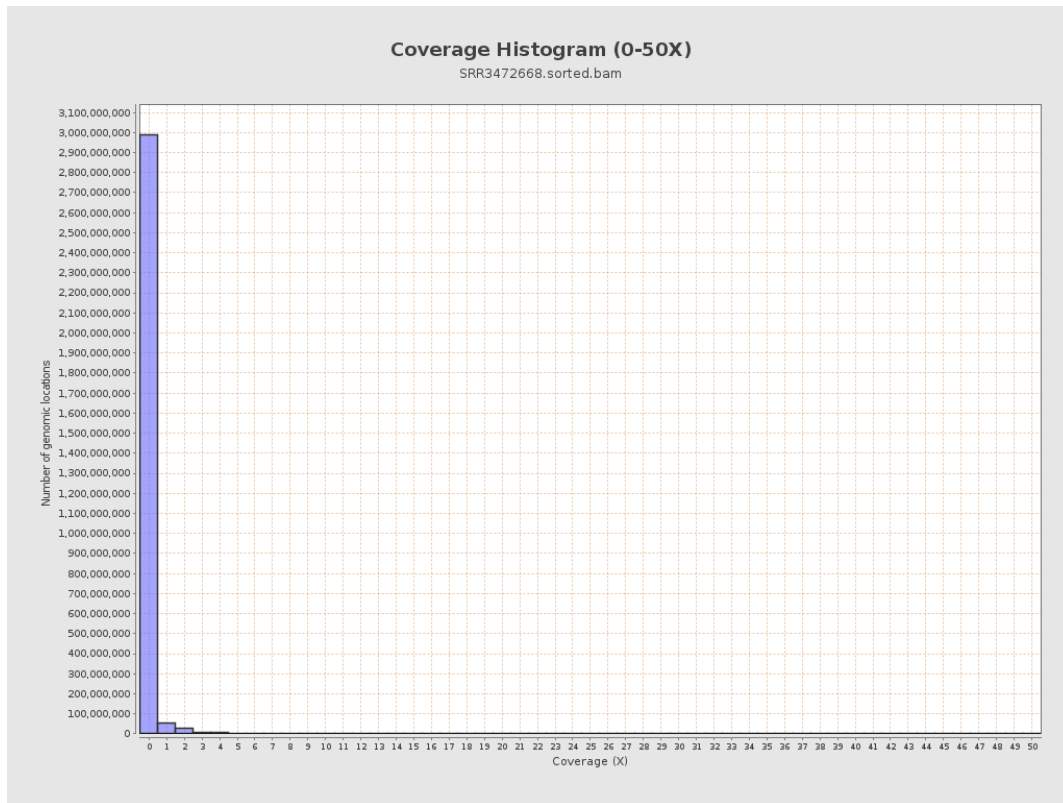
3. Results : Coverage across reference



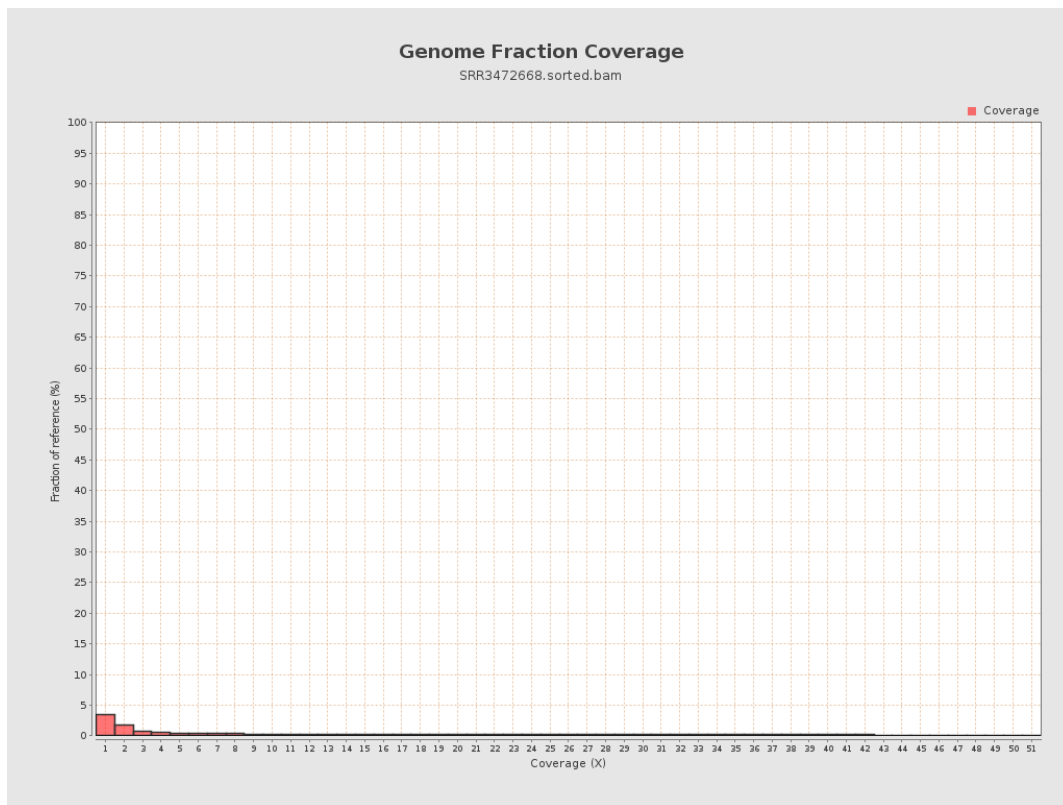
4. Results : Coverage Histogram



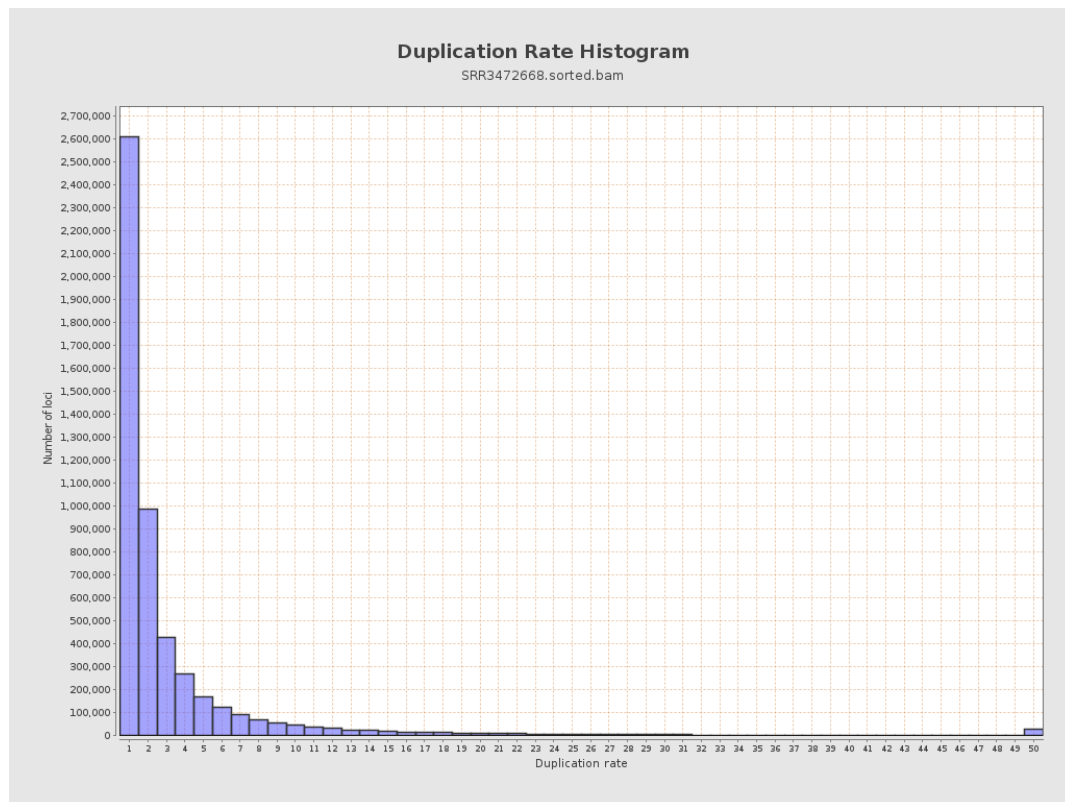
5. Results : Coverage Histogram (0-50X)



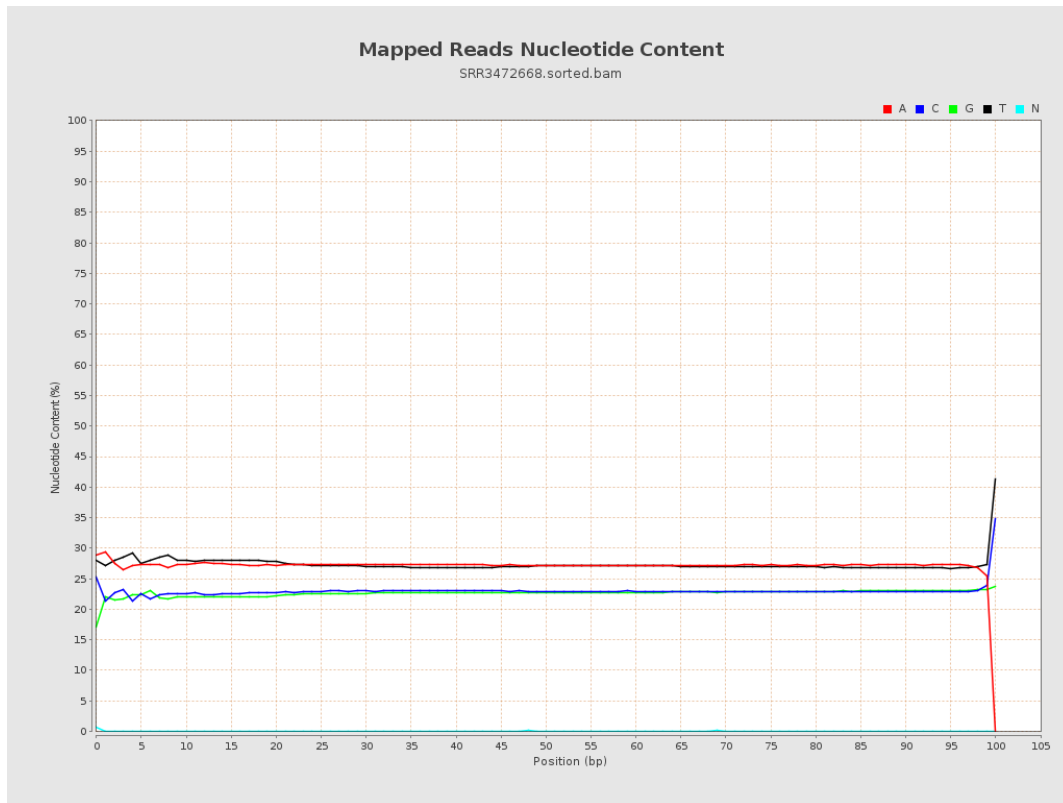
6. Results : Genome Fraction Coverage



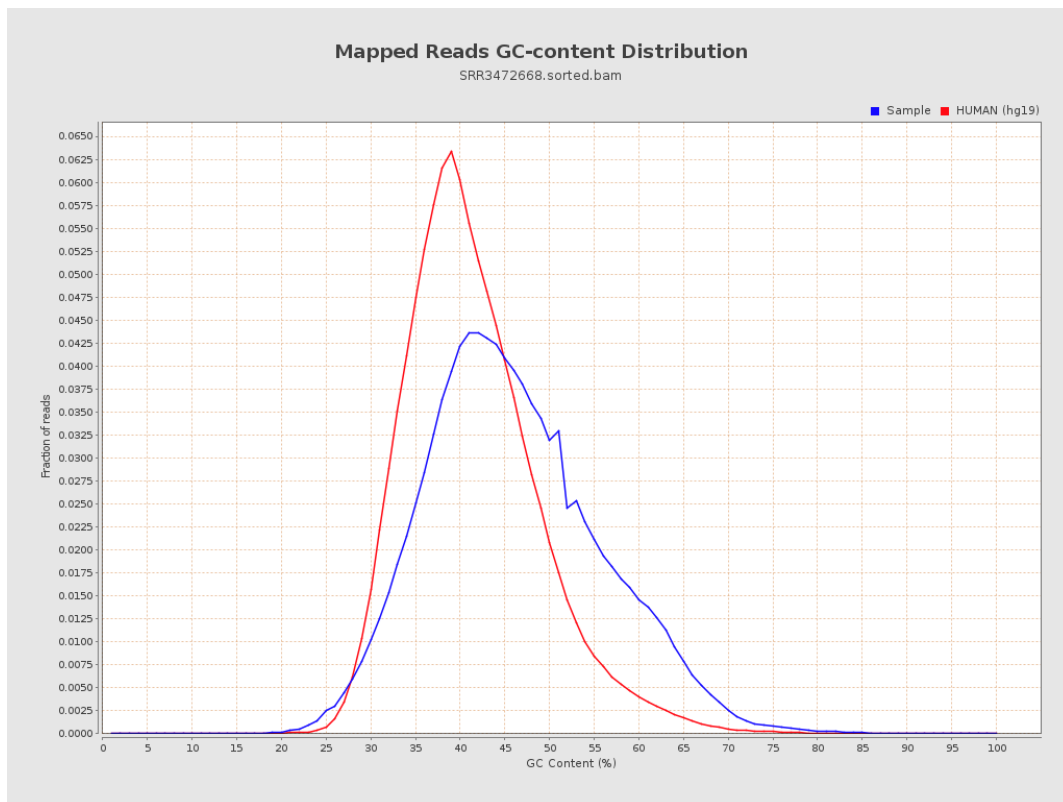
7. Results : Duplication Rate Histogram



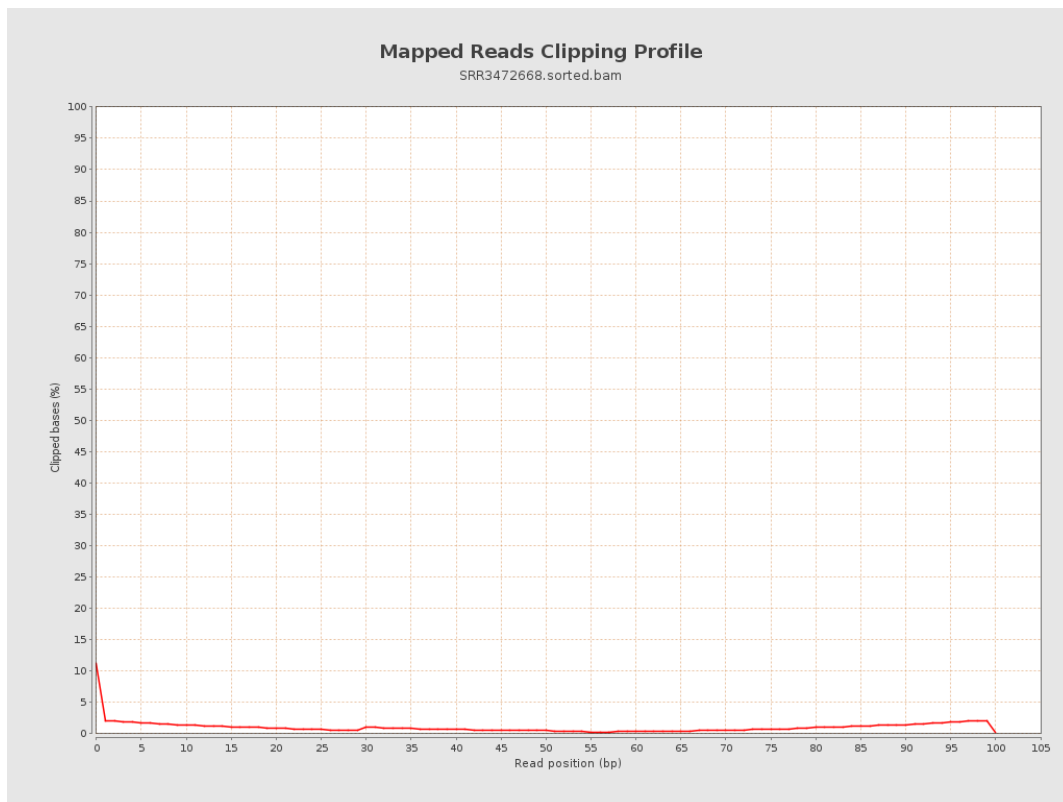
8. Results : Mapped Reads Nucleotide Content



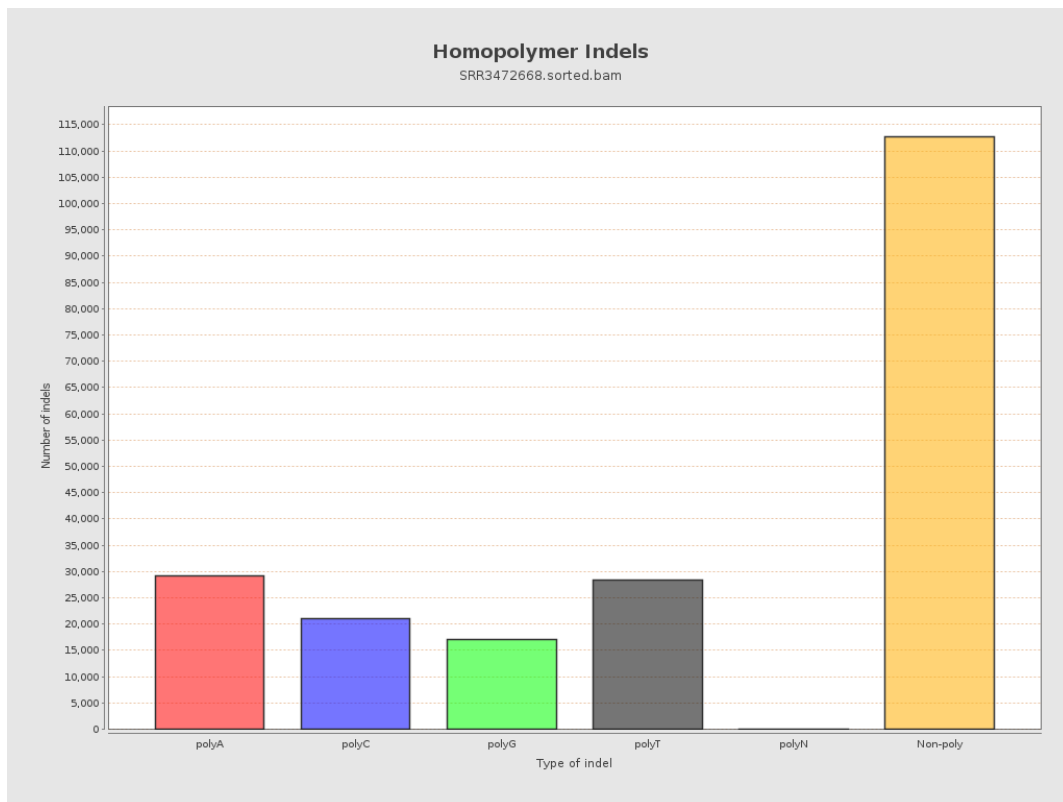
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



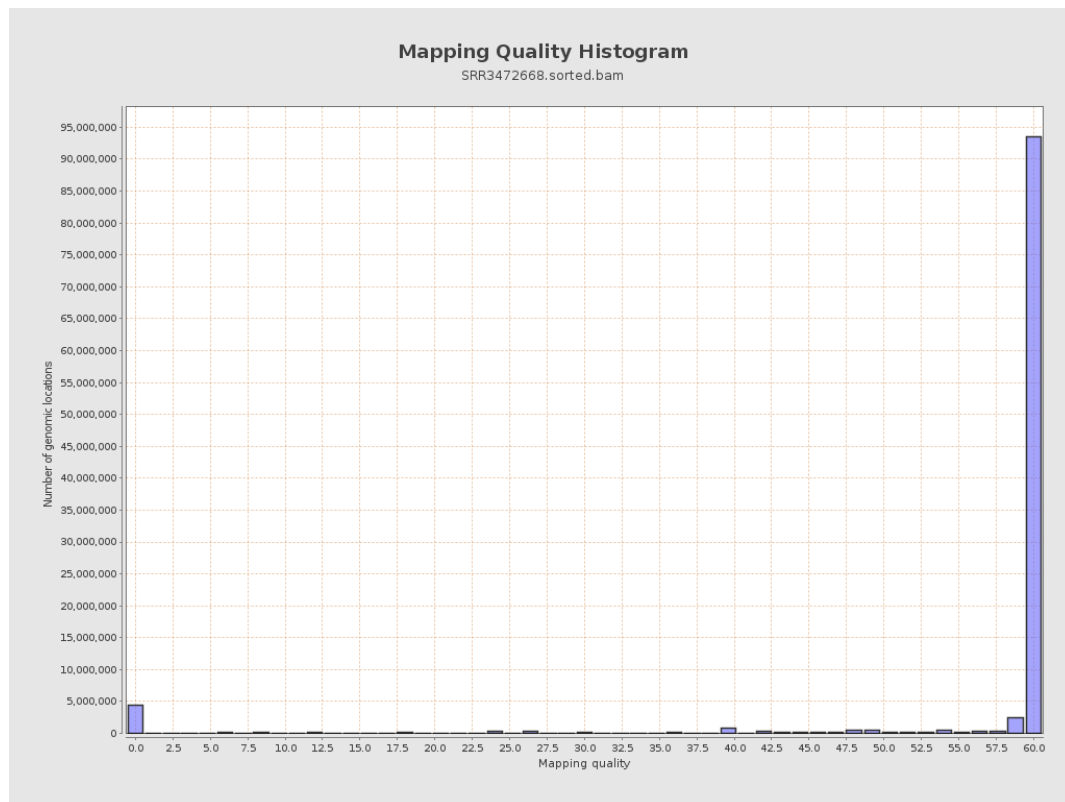
11. Results : Homopolymer Indels



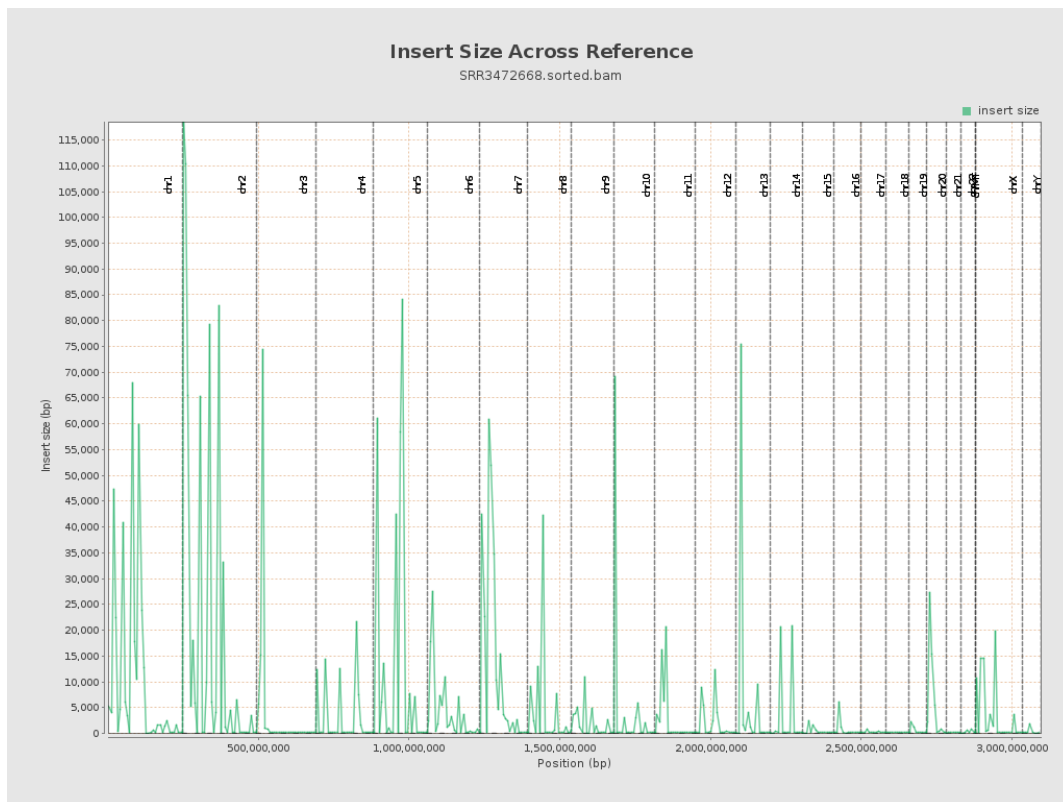
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

