

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:19:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006163.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_SRR1006163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006163_1.fastq.gz SRR1006163_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:19:23 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,019,272
Mapped reads	3,518,443 / 87.54%
Unmapped reads	500,829 / 12.46%
Mapped paired reads	3,518,443 / 87.54%
Mapped reads, first in pair	1,767,532 / 43.98%
Mapped reads, second in pair	1,750,911 / 43.56%
Mapped reads, both in pair	3,284,080 / 81.71%
Mapped reads, singletons	234,363 / 5.83%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	123,474 / 3.07%
Duplication rate	3.02%
Clipped reads	230,122 / 5.73%

2.2. ACGT Content

Number/percentage of A's	36,247,804 / 26.64%
Number/percentage of C's	31,061,049 / 22.83%
Number/percentage of T's	36,772,252 / 27.03%
Number/percentage of G's	31,961,625 / 23.49%
Number/percentage of N's	18,126 / 0.01%
GC Percentage	46.32%

2.3. Coverage

Mean	0.044
Standard Deviation	0.3083

2.4. Mapping Quality

Mean Mapping Quality	47
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2.5. Insert size

Mean	60,774.24
Standard Deviation	2,380,817.86
P25/Median/P75	63 / 84 / 119

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	503,212
Insertions	4,199
Mapped reads with at least one insertion	0.12%
Deletions	12,545
Mapped reads with at least one deletion	0.36%
Homopolymer indels	38.92%

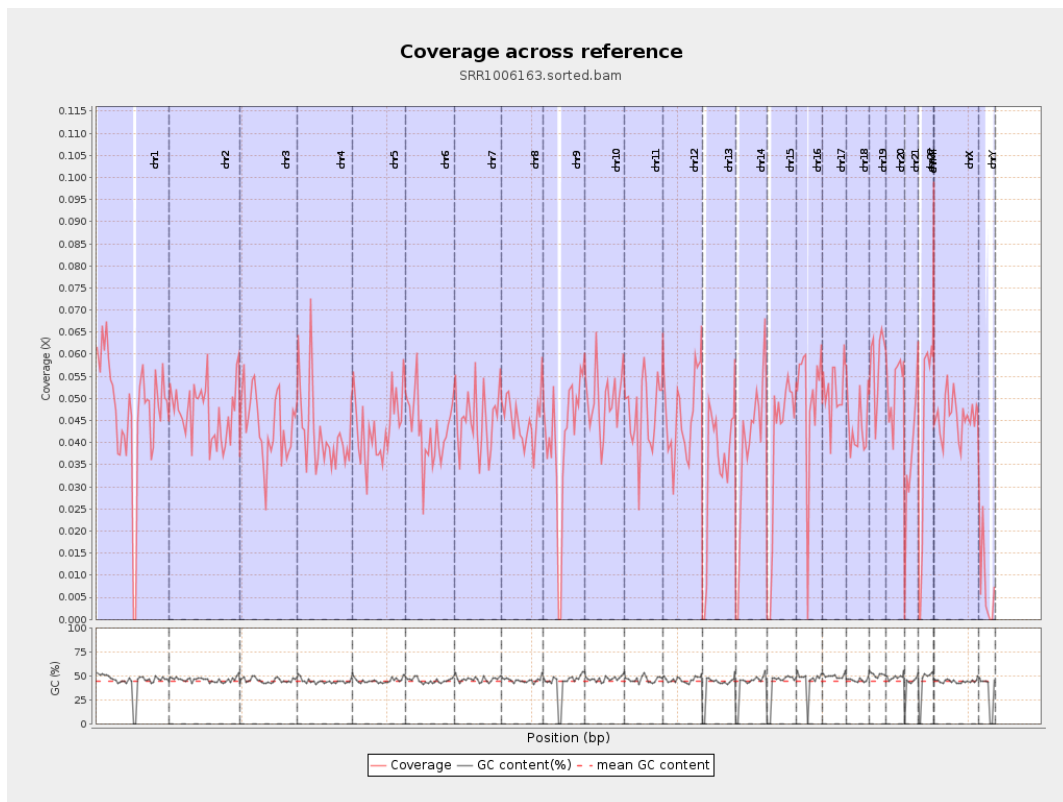
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

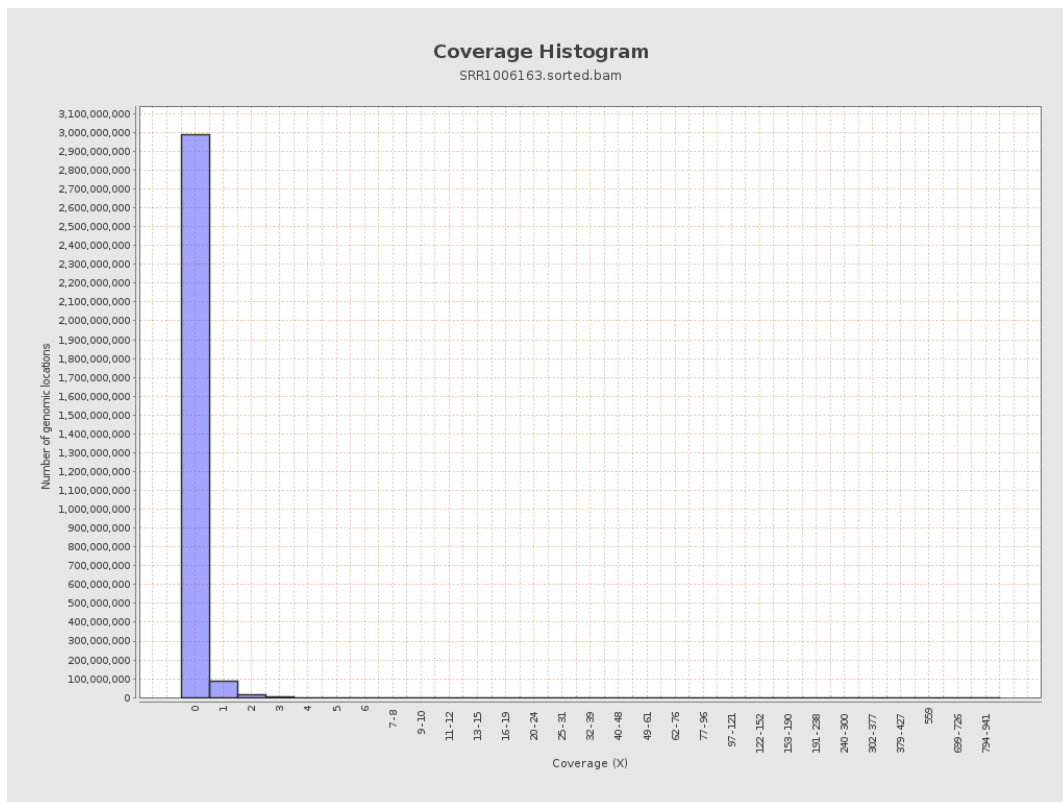
chr1	249250621	11718876	0.047	0.3471
chr2	243199373	11419051	0.047	0.293
chr3	198022430	8681651	0.0438	0.2483
chr4	191154276	8011357	0.0419	0.2743
chr5	180915260	7843033	0.0434	0.2511
chr6	171115067	7365143	0.043	0.2575
chr7	159138663	7135946	0.0448	0.3032
chr8	146364022	6607294	0.0451	0.5259
chr9	141213431	5667179	0.0401	0.2536
chr10	135534747	6671890	0.0492	0.3372
chr11	135006516	6304873	0.0467	0.2767
chr12	133851895	6131286	0.0458	0.2601
chr13	115169878	3938188	0.0342	0.2235
chr14	107349540	4195524	0.0391	0.5063
chr15	102531392	4056013	0.0396	0.2404
chr16	90354753	4537890	0.0502	0.295
chr17	81195210	4226385	0.0521	0.2838
chr18	78077248	3396361	0.0435	0.3303
chr19	59128983	3428190	0.058	0.333
chr20	63025520	3280206	0.052	0.2949
chr21	48129895	1788457	0.0372	0.2692
chr22	51304566	2093327	0.0408	0.2895
chrMT	16571	1643	0.0991	0.3579
chrX	155270560	7127564	0.0459	0.2588

chrY	59373566	450666	0.0076	0.2095
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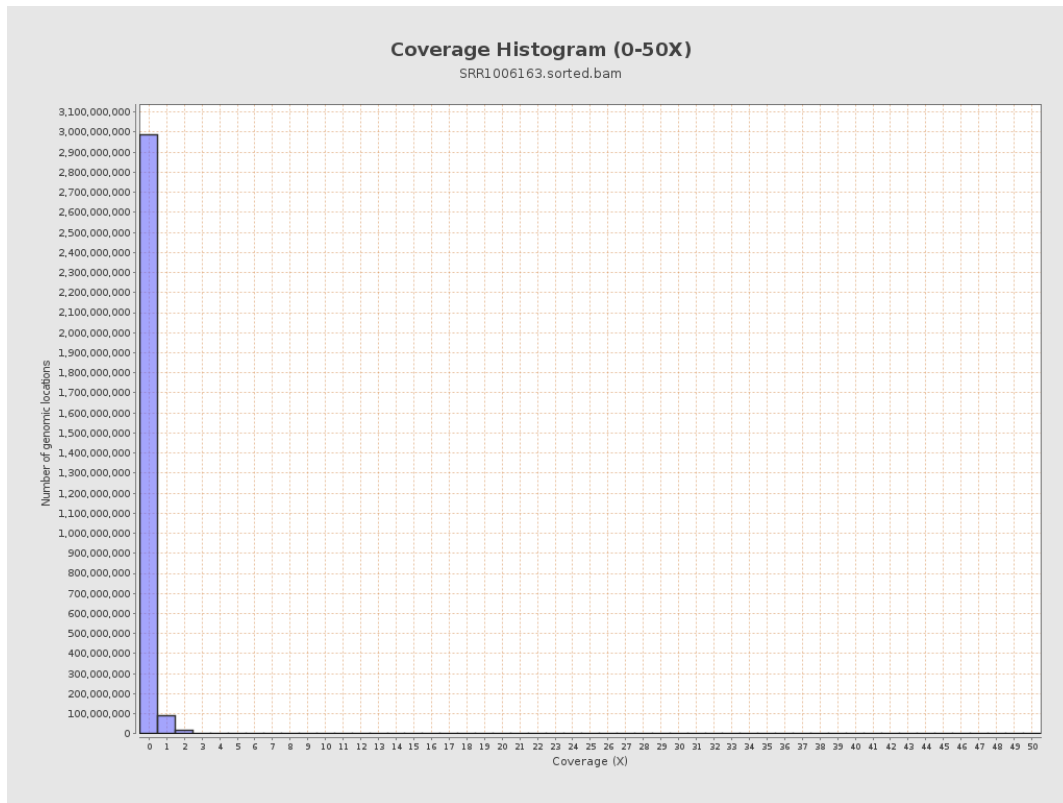
3. Results : Coverage across reference



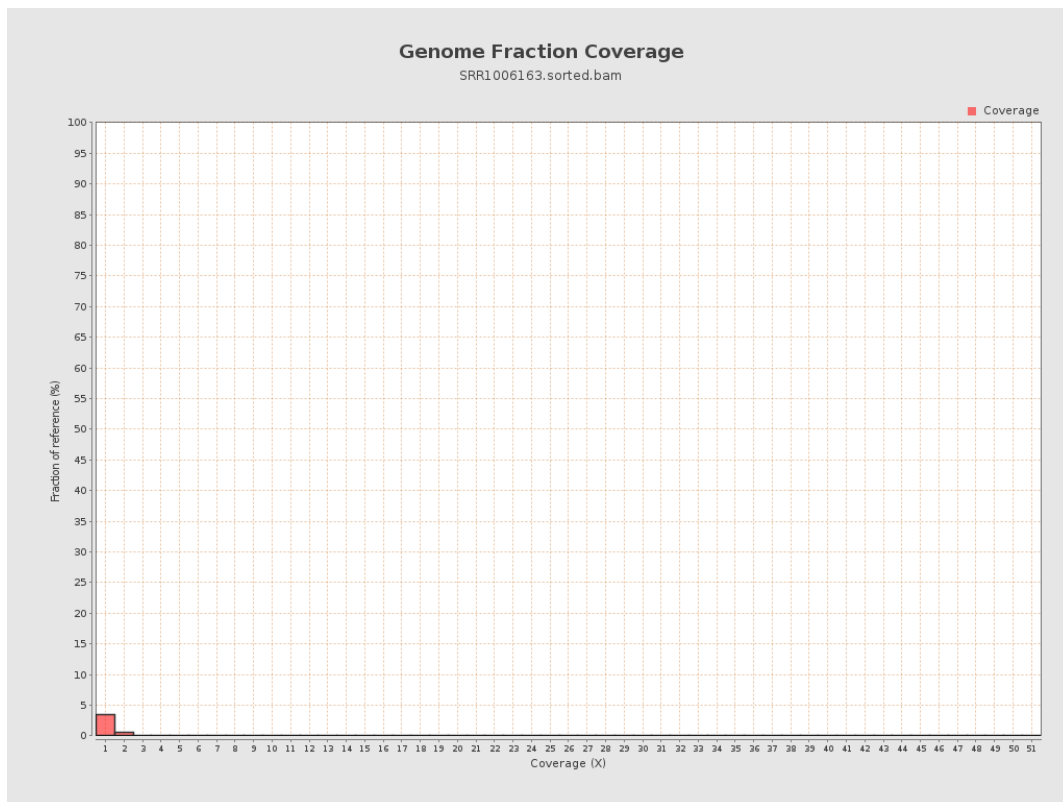
4. Results : Coverage Histogram



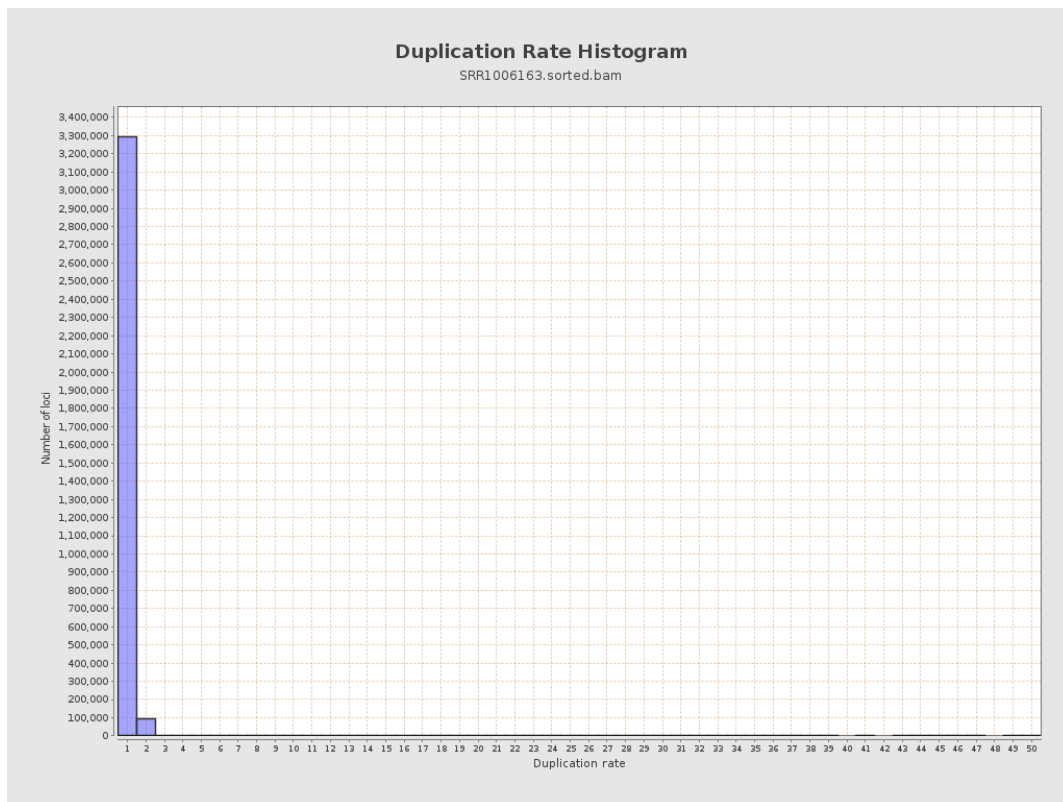
5. Results : Coverage Histogram (0-50X)



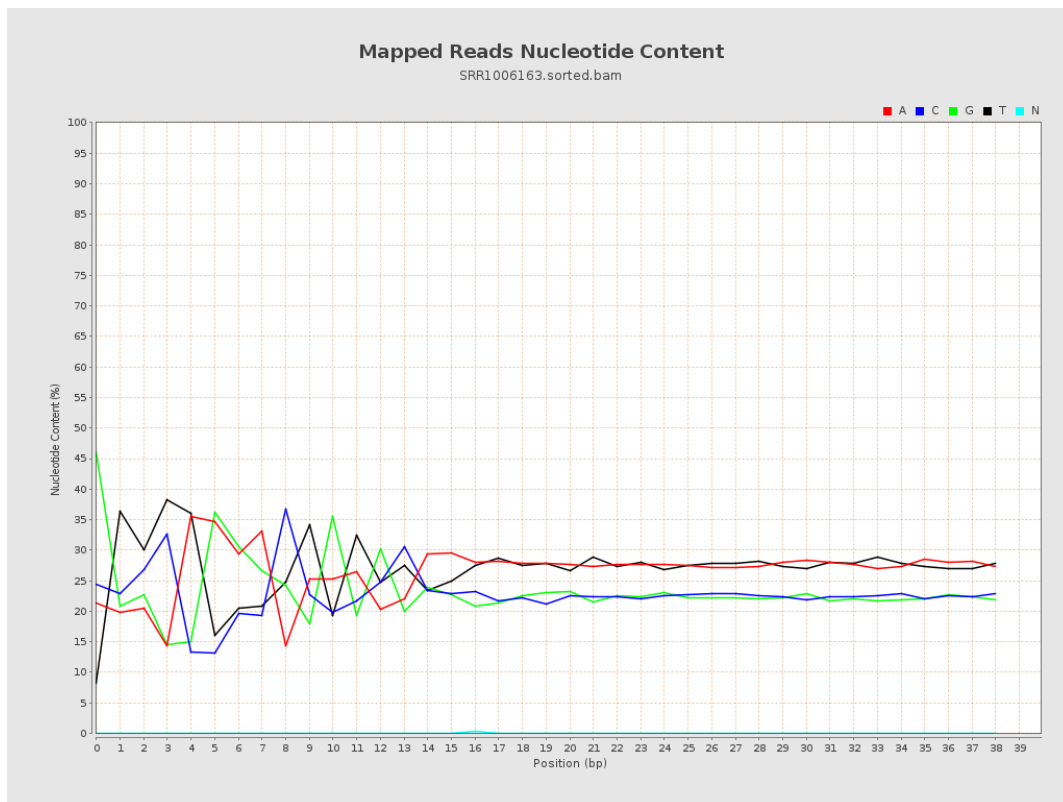
6. Results : Genome Fraction Coverage



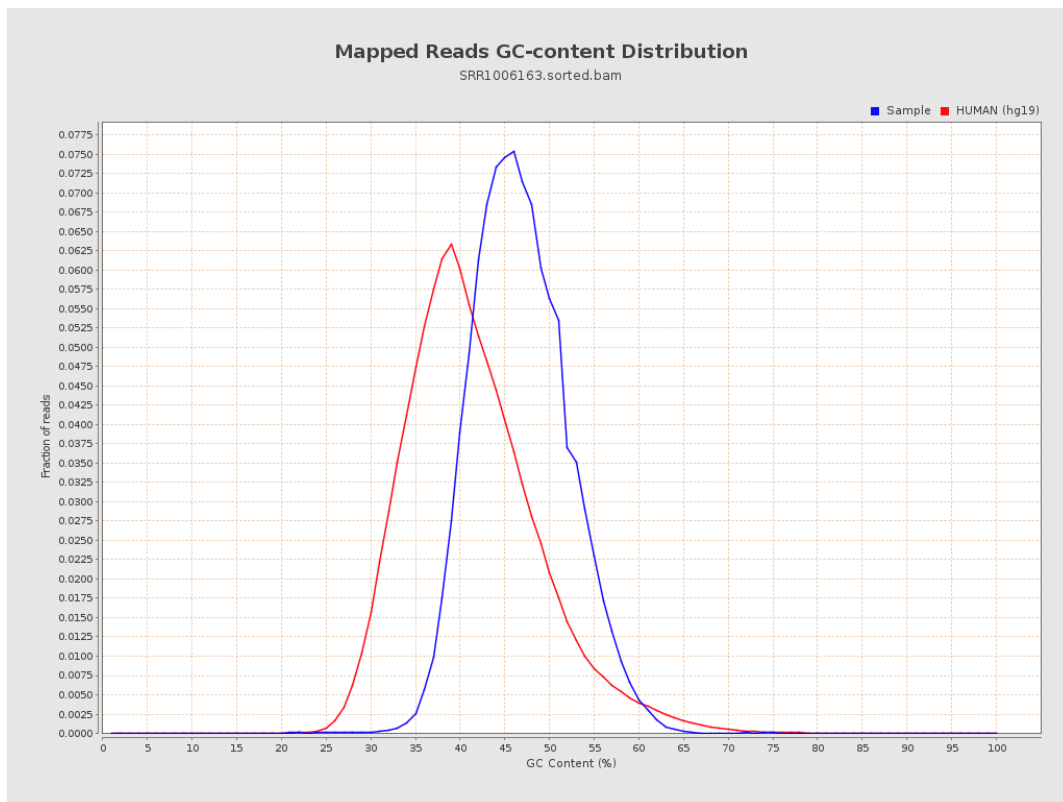
7. Results : Duplication Rate Histogram



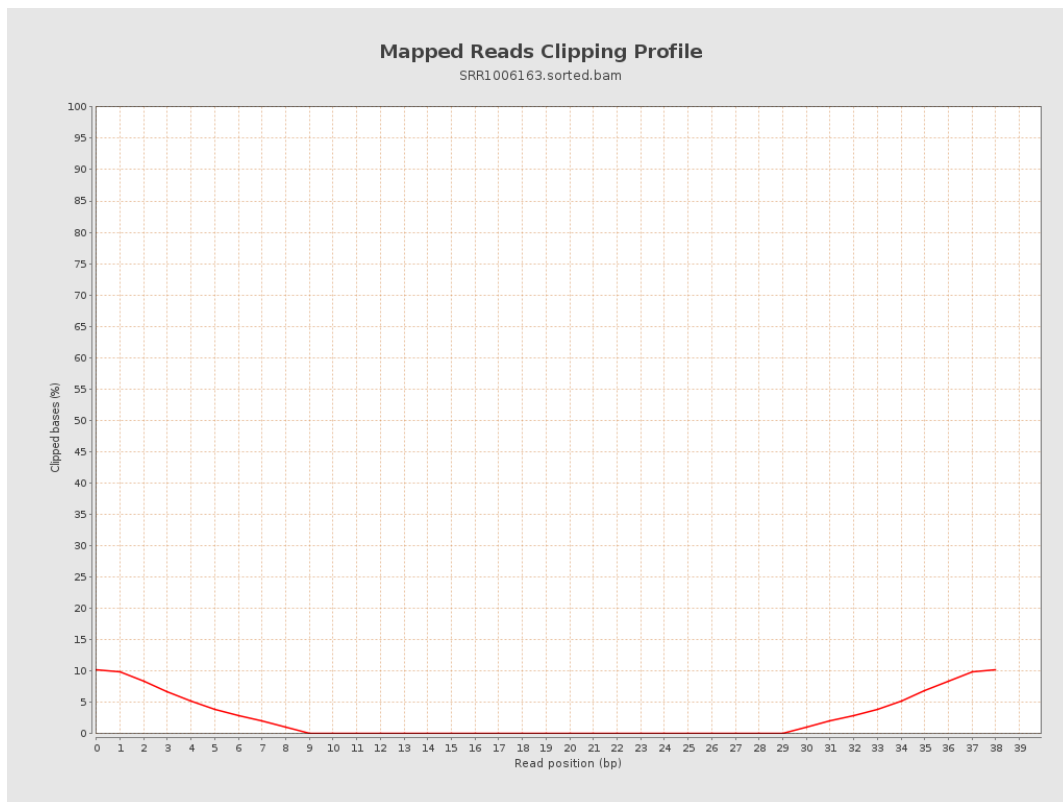
8. Results : Mapped Reads Nucleotide Content



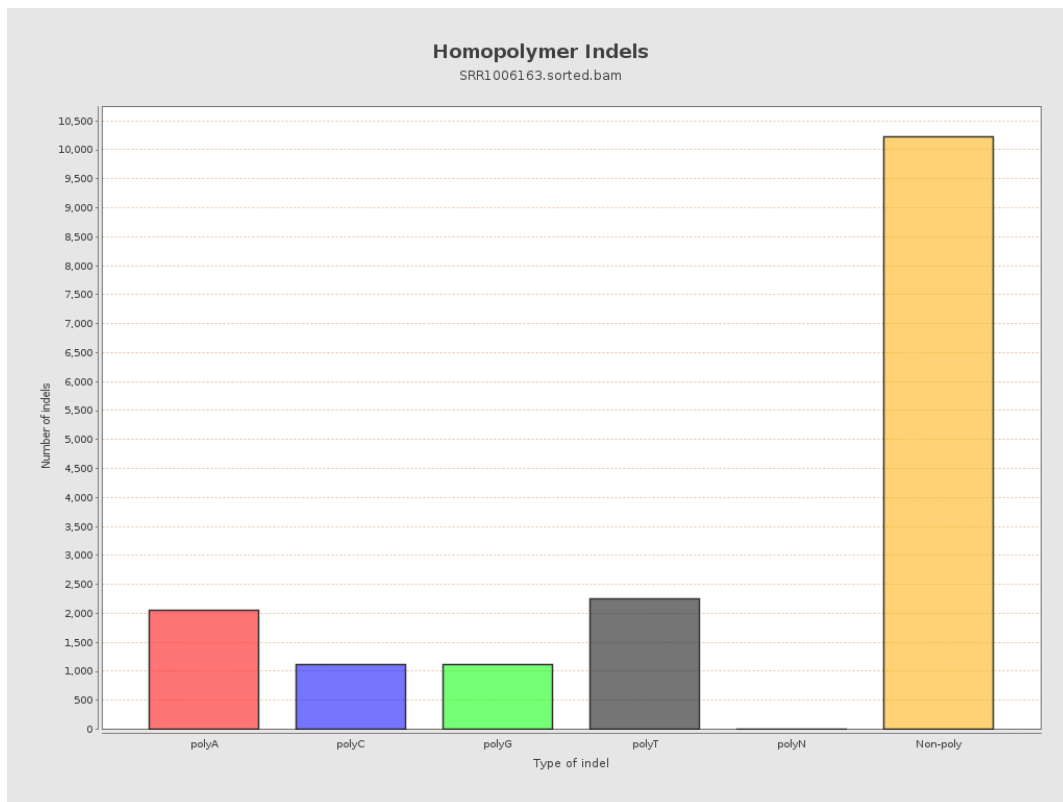
9. Results : Mapped Reads GC-content Distribution



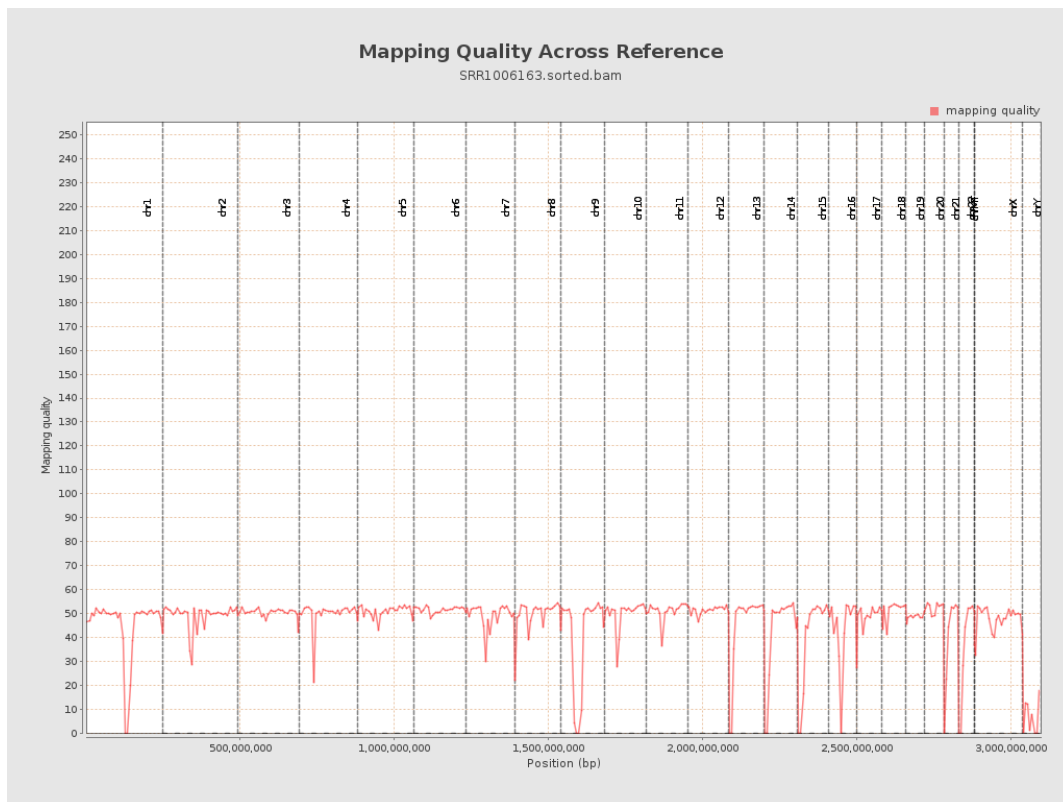
10. Results : Mapped Reads Clipping Profile



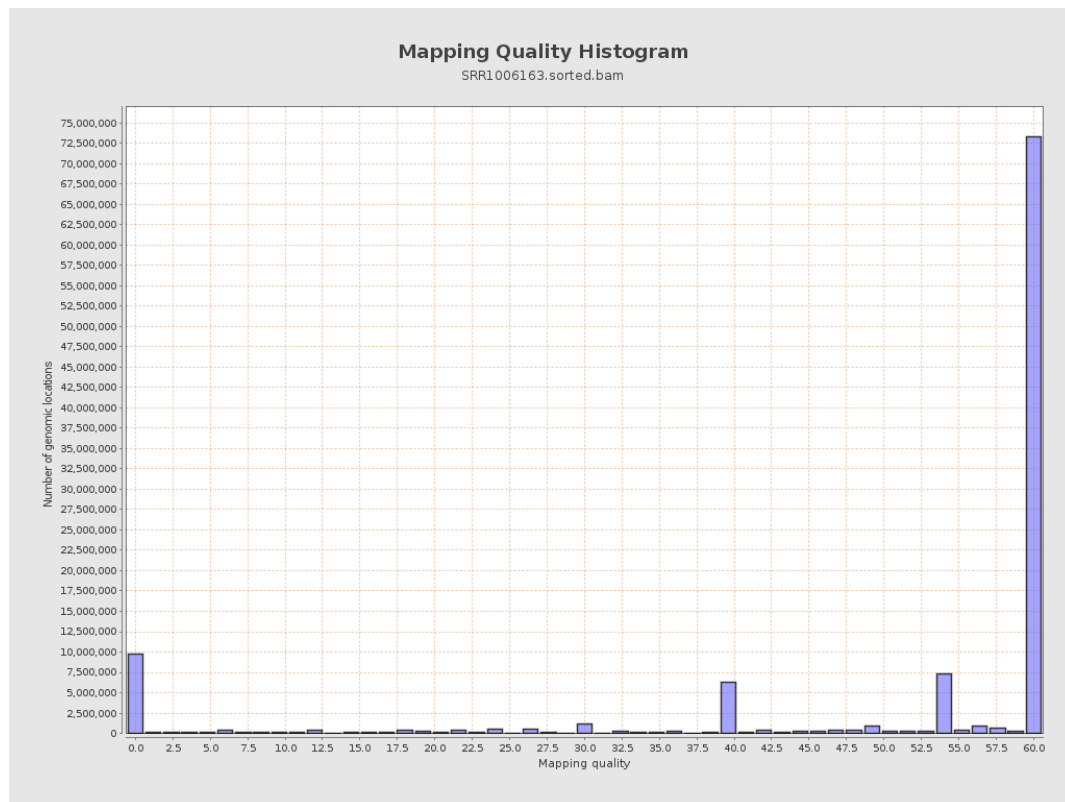
11. Results : Homopolymer Indels



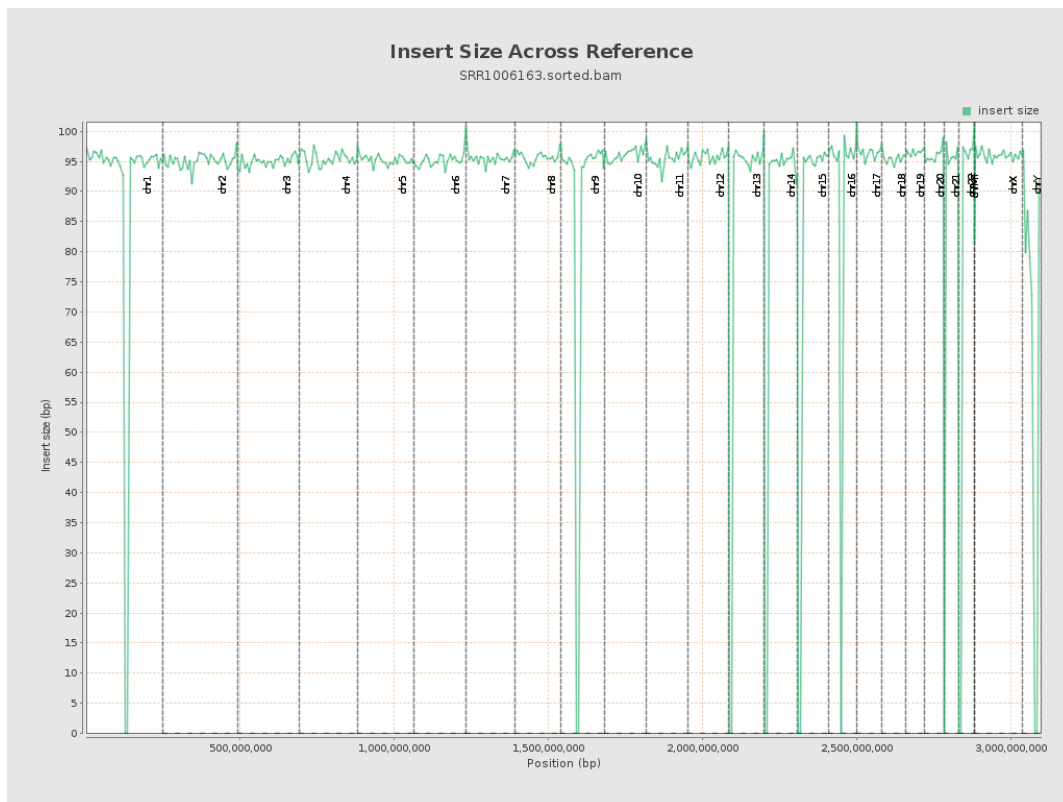
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

