

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 17:07:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006060.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_SRR1006060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006060_1.fastq.gz SRR1006060_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 17:07:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,194,814
Mapped reads	3,697,920 / 88.15%
Unmapped reads	496,894 / 11.85%
Mapped paired reads	3,697,920 / 88.15%
Mapped reads, first in pair	1,882,549 / 44.88%
Mapped reads, second in pair	1,815,371 / 43.28%
Mapped reads, both in pair	3,411,440 / 81.33%
Mapped reads, singletons	286,480 / 6.83%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	160,512 / 3.83%
Duplication rate	3.93%
Clipped reads	274,116 / 6.53%

2.2. ACGT Content

Number/percentage of A's	36,797,706 / 25.75%
Number/percentage of C's	33,195,424 / 23.23%
Number/percentage of T's	38,089,521 / 26.66%
Number/percentage of G's	34,794,815 / 24.35%
Number/percentage of N's	6,894 / 0%
GC Percentage	47.58%

2.3. Coverage

Mean	0.0462
Standard Deviation	0.3132

2.4. Mapping Quality

Mean Mapping Quality	46.12
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2.5. Insert size

Mean	73,270.1
Standard Deviation	2,676,130.26
P25/Median/P75	73 / 96 / 125

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	606,144
Insertions	4,538
Mapped reads with at least one insertion	0.12%
Deletions	11,578
Mapped reads with at least one deletion	0.31%
Homopolymer indels	43.01%

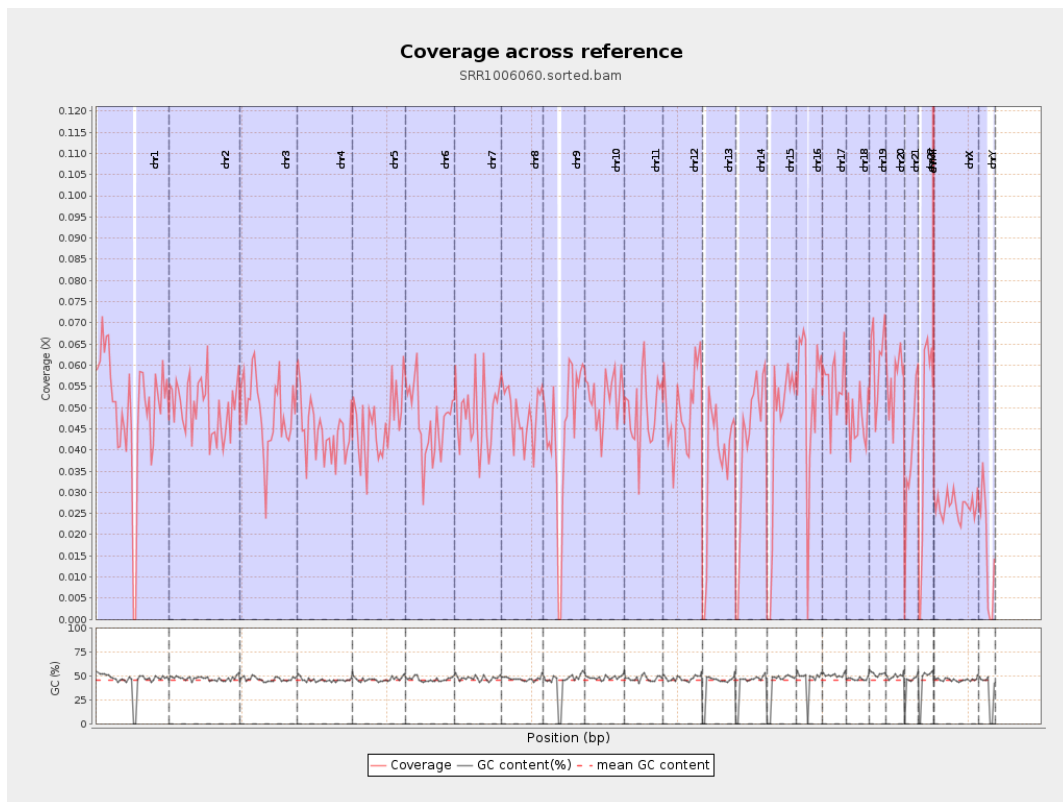
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

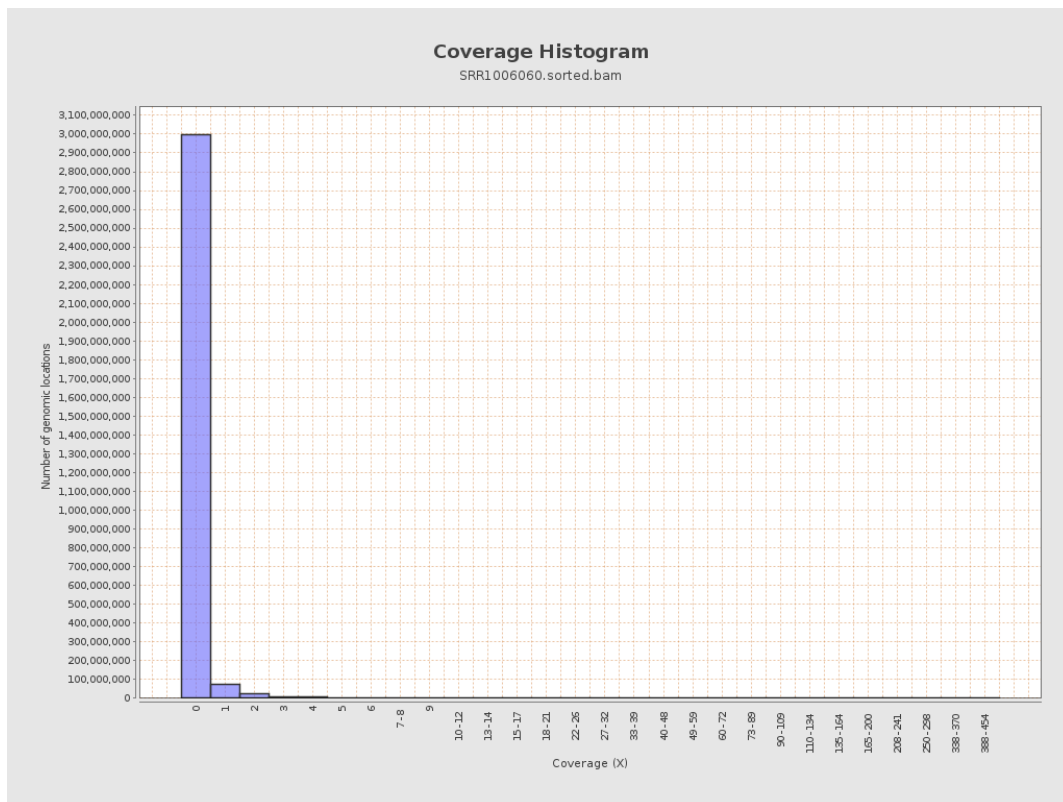
chr1	249250621	12348176	0.0495	0.3204
chr2	243199373	12160534	0.05	0.3557
chr3	198022430	9685502	0.0489	0.2958
chr4	191154276	8423525	0.0441	0.2927
chr5	180915260	8306756	0.0459	0.2884
chr6	171115067	8018600	0.0469	0.3063
chr7	159138663	7635801	0.048	0.3336
chr8	146364022	7108044	0.0486	0.3287
chr9	141213431	6163898	0.0436	0.2904
chr10	135534747	7081557	0.0522	0.3252
chr11	135006516	6642867	0.0492	0.3808
chr12	133851895	6643733	0.0496	0.3034
chr13	115169878	4237366	0.0368	0.2628
chr14	107349540	4514045	0.042	0.282
chr15	102531392	4493467	0.0438	0.2853
chr16	90354753	4839154	0.0536	0.3628
chr17	81195210	4535778	0.0559	0.3394
chr18	78077248	3656133	0.0468	0.3189
chr19	59128983	3623557	0.0613	0.408
chr20	63025520	3532103	0.056	0.3321
chr21	48129895	1885828	0.0392	0.2931
chr22	51304566	2222488	0.0433	0.3222
chrMT	16571	40561	2.4477	3.6256
chrX	155270560	4160394	0.0268	0.2193

chrY	59373566	939511	0.0158	0.2062
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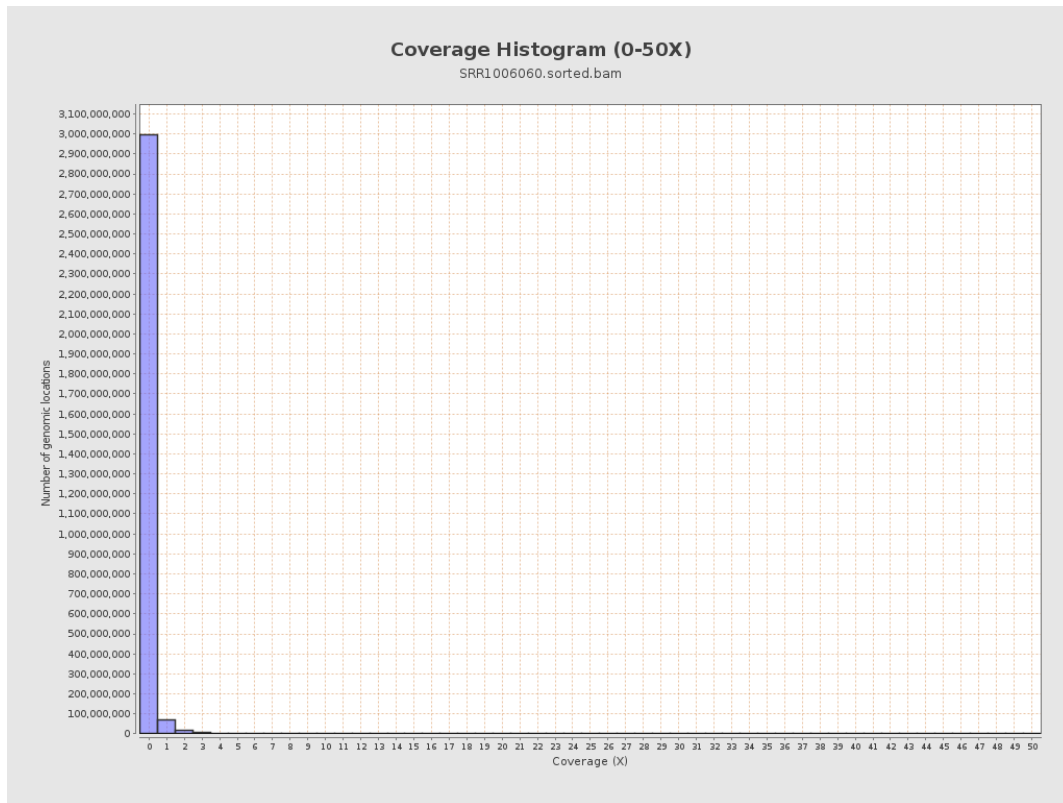
3. Results : Coverage across reference



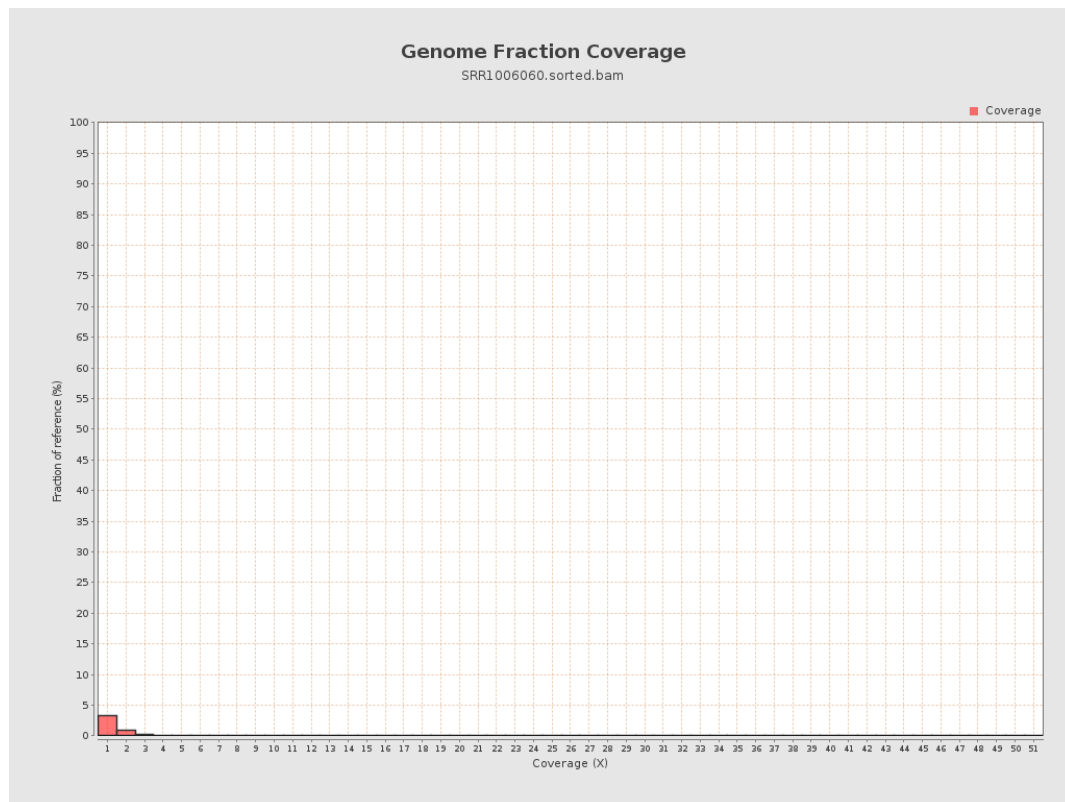
4. Results : Coverage Histogram



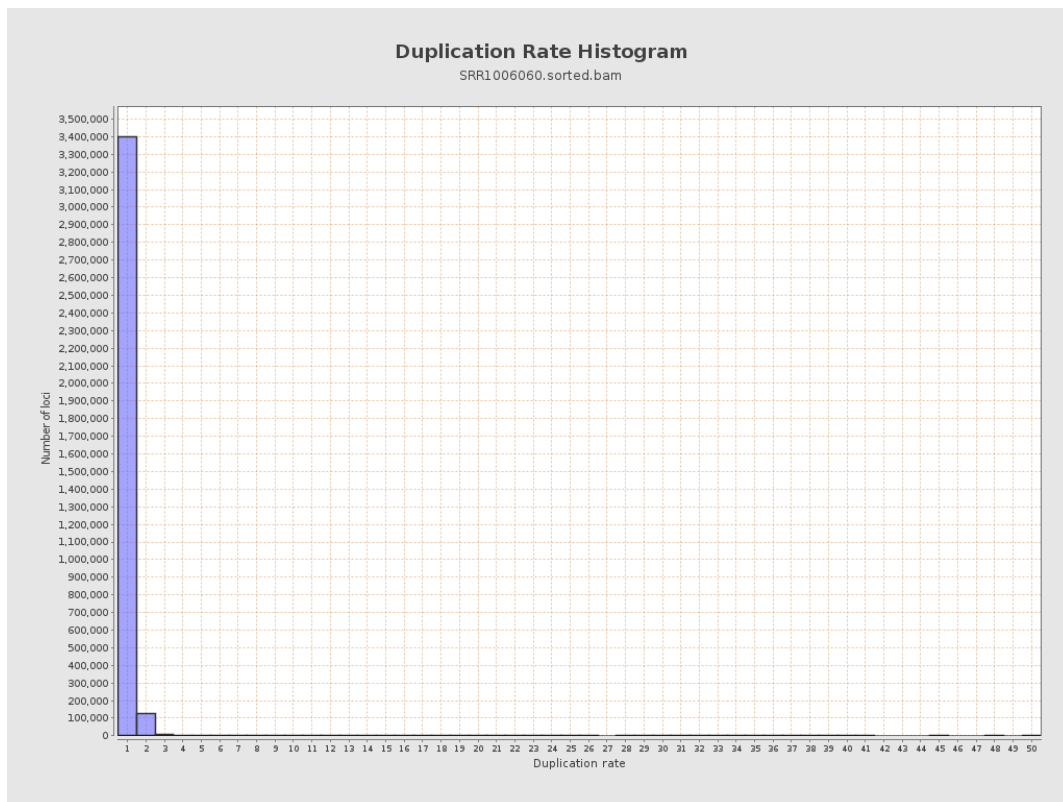
5. Results : Coverage Histogram (0-50X)



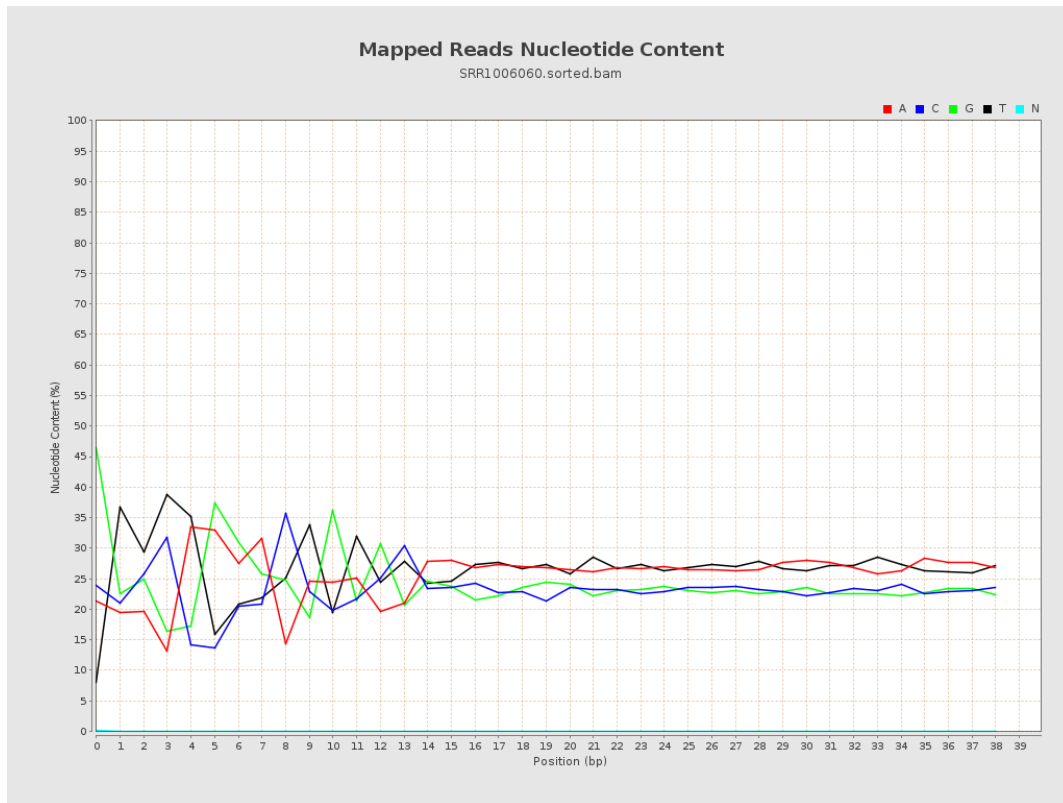
6. Results : Genome Fraction Coverage



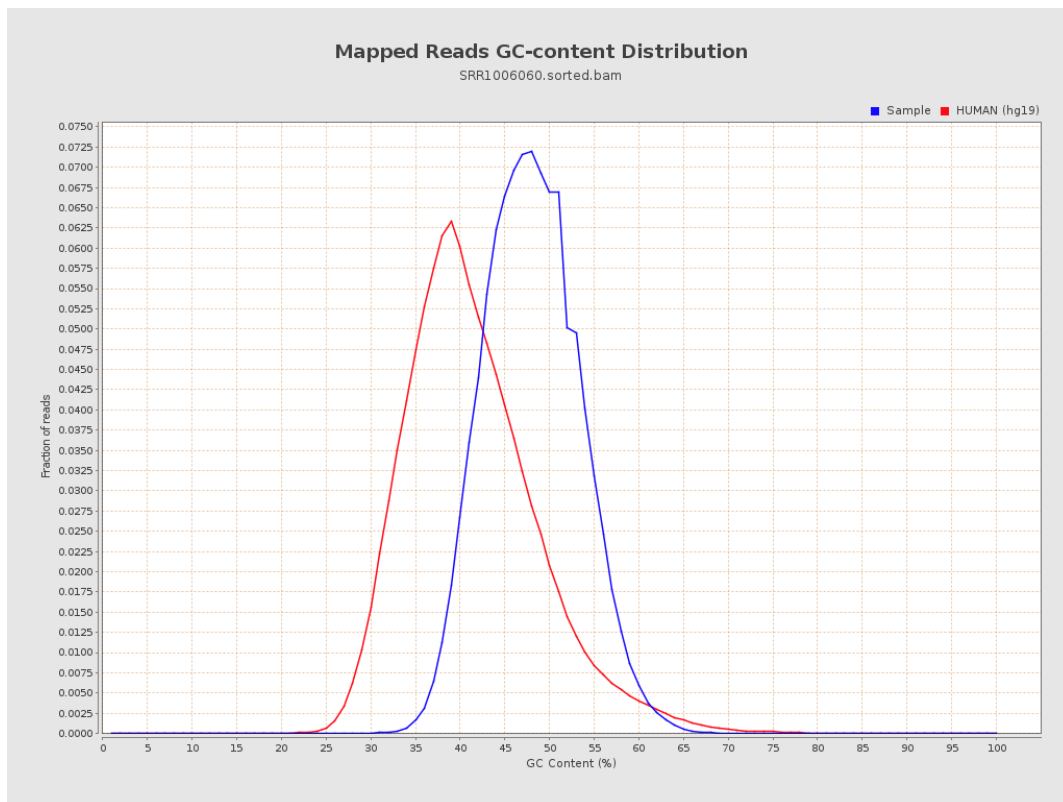
7. Results : Duplication Rate Histogram



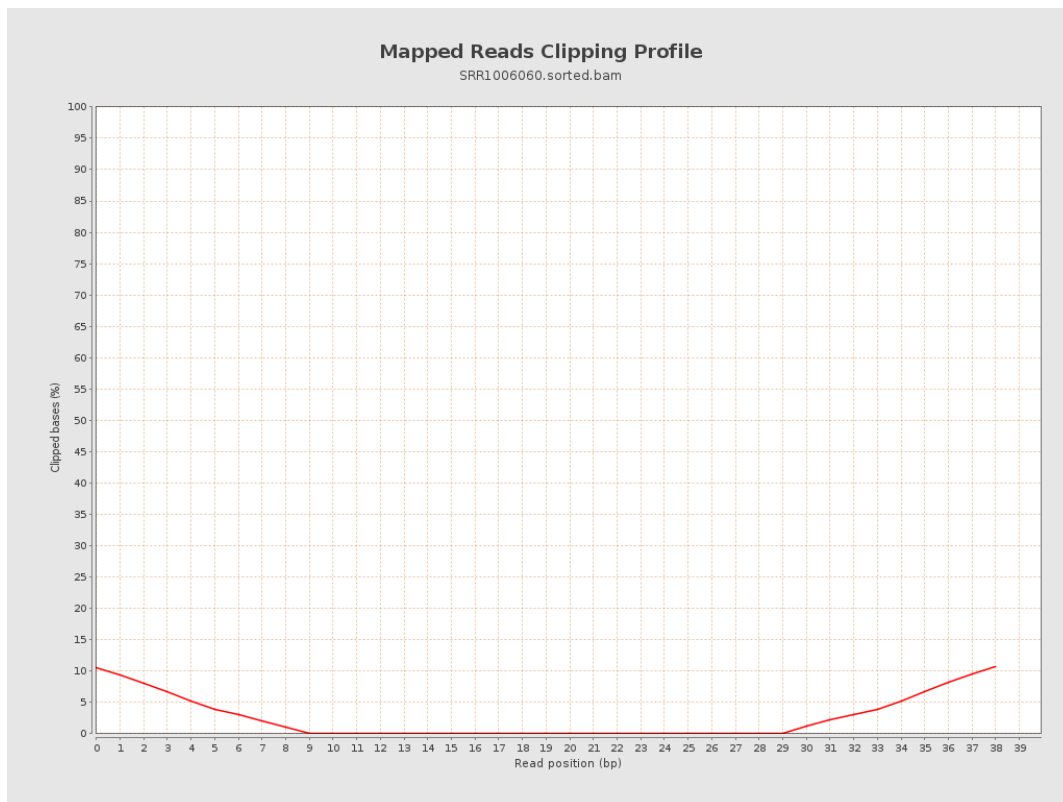
8. Results : Mapped Reads Nucleotide Content



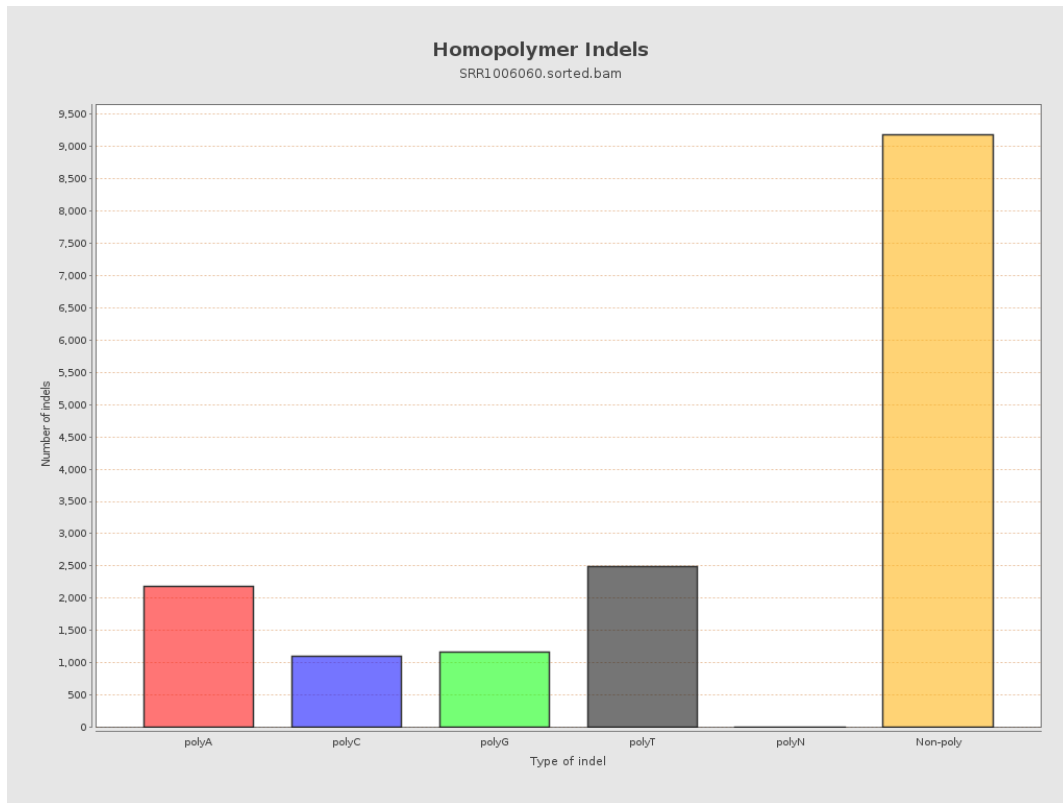
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



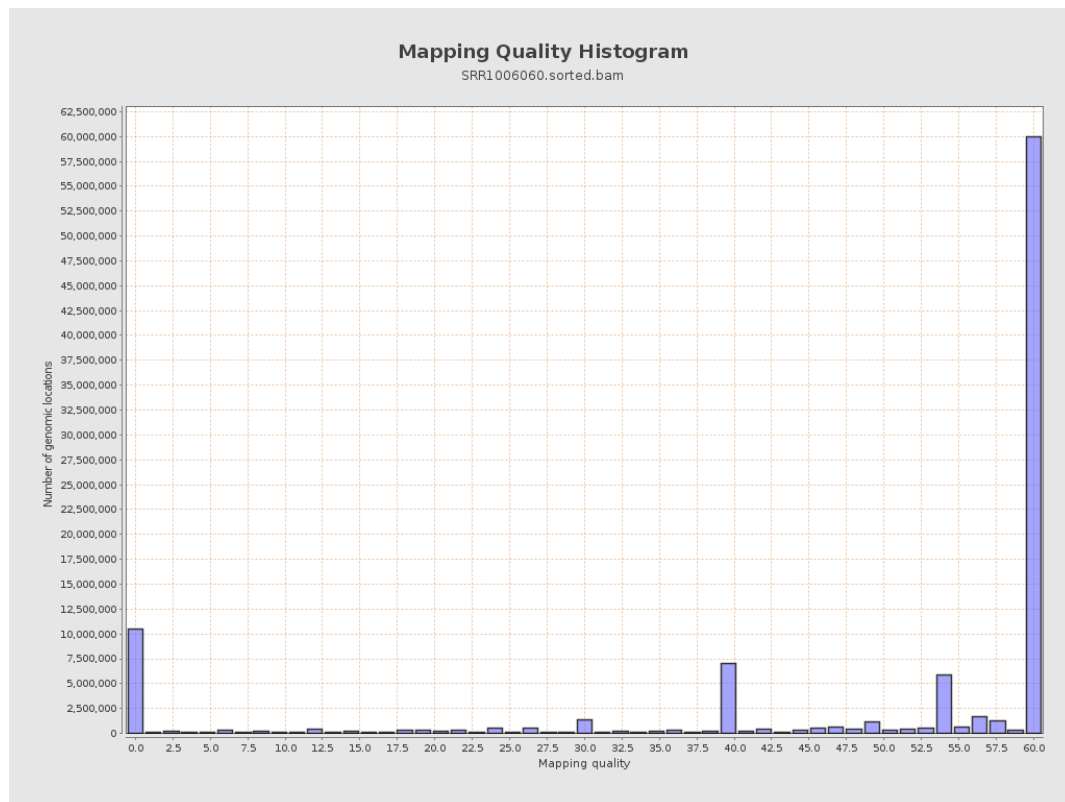
11. Results : Homopolymer Indels



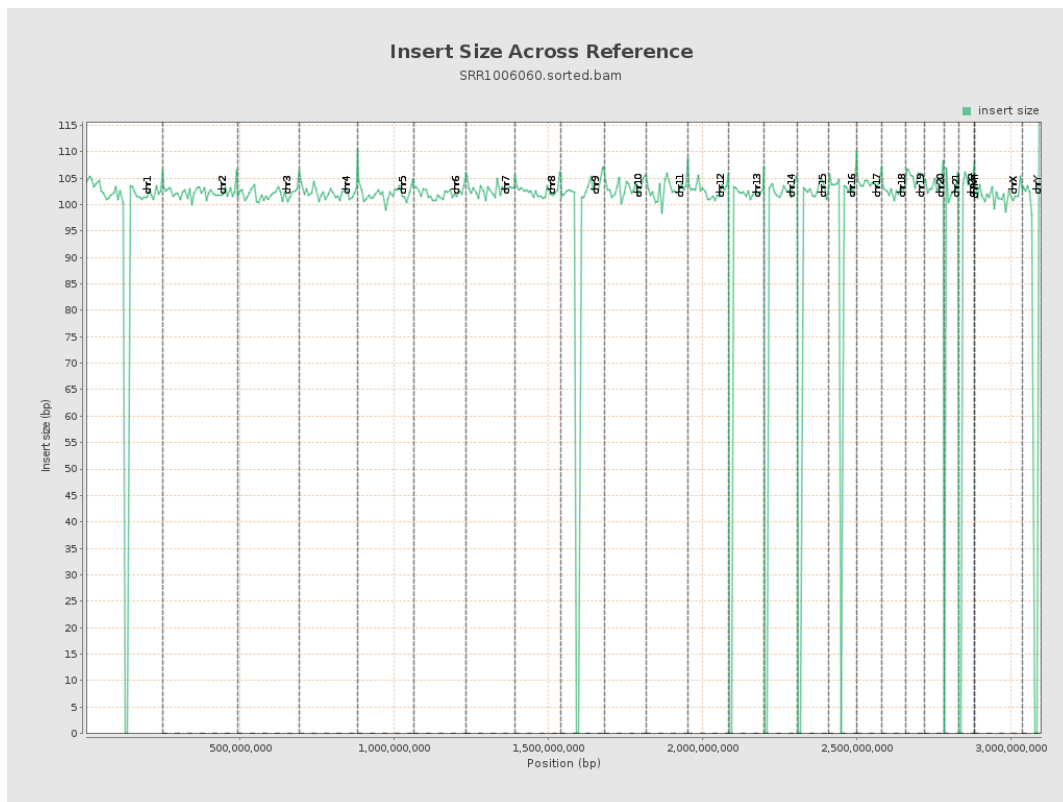
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

