

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 13:34:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1299077.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_SRR1299077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1299077_1.fastq.gz SRR1299077_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 13:34:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1299077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	802,305,020
Mapped reads	706,307,743 / 88.03%
Unmapped reads	95,997,277 / 11.97%
Mapped paired reads	706,307,743 / 88.03%
Mapped reads, first in pair	361,156,846 / 45.01%
Mapped reads, second in pair	345,150,897 / 43.02%
Mapped reads, both in pair	686,616,278 / 85.58%
Mapped reads, singletons	19,691,465 / 2.45%
Secondary alignments	0
Supplementary alignments	630,350 / 0.08%
Read min/max/mean length	30 / 100 / 100.03
Duplicated reads (estimated)	687,543,521 / 85.7%
Duplication rate	75.69%
Clipped reads	696,711,918 / 86.84%

2.2. ACGT Content

Number/percentage of A's	15,882,686,152 / 26.77%
Number/percentage of C's	14,082,306,612 / 23.74%
Number/percentage of T's	15,351,765,817 / 25.88%
Number/percentage of G's	13,992,120,634 / 23.59%
Number/percentage of N's	11,505,297 / 0.02%

GC Percentage	47.33%
---------------	--------

2.3. Coverage

Mean	19.1659
Standard Deviation	1,296.7104

2.4. Mapping Quality

Mean Mapping Quality	54.36
----------------------	-------

2.5. Insert size

Mean	513,019.68
Standard Deviation	7,034,847.51
P25/Median/P75	176 / 234 / 308

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	305,576,740
Insertions	2,637,666
Mapped reads with at least one insertion	0.37%
Deletions	5,490,842
Mapped reads with at least one deletion	0.77%
Homopolymer indels	47.82%

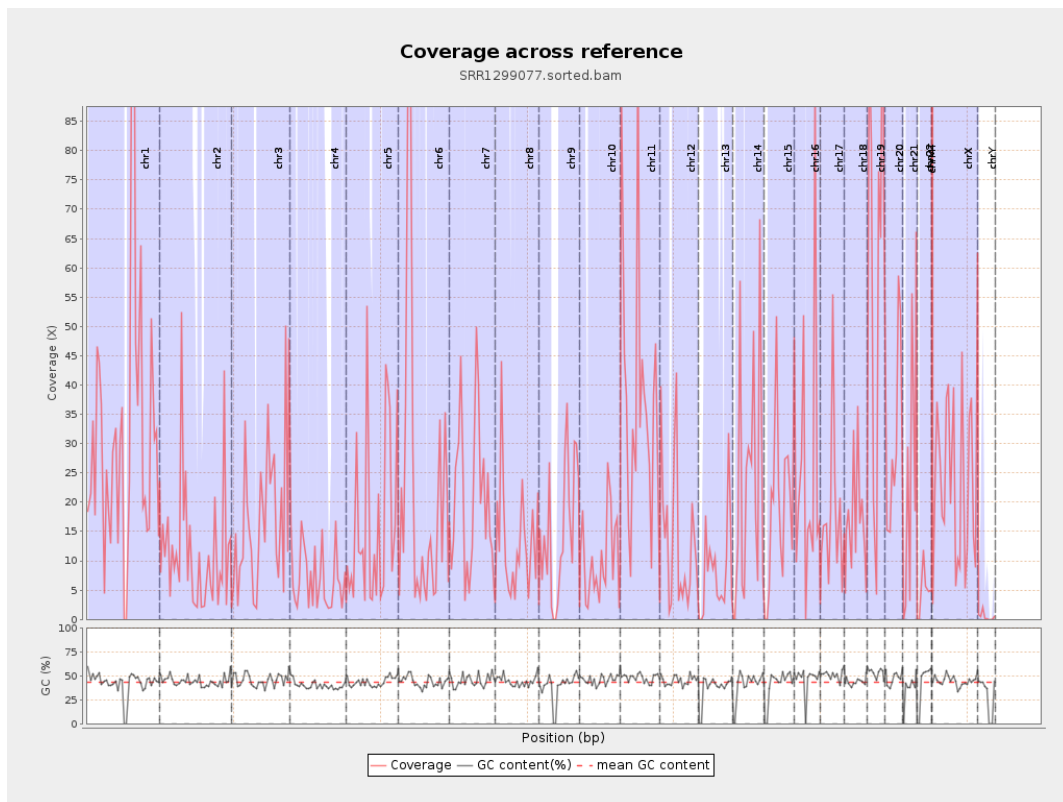
2.7. Chromosome stats

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

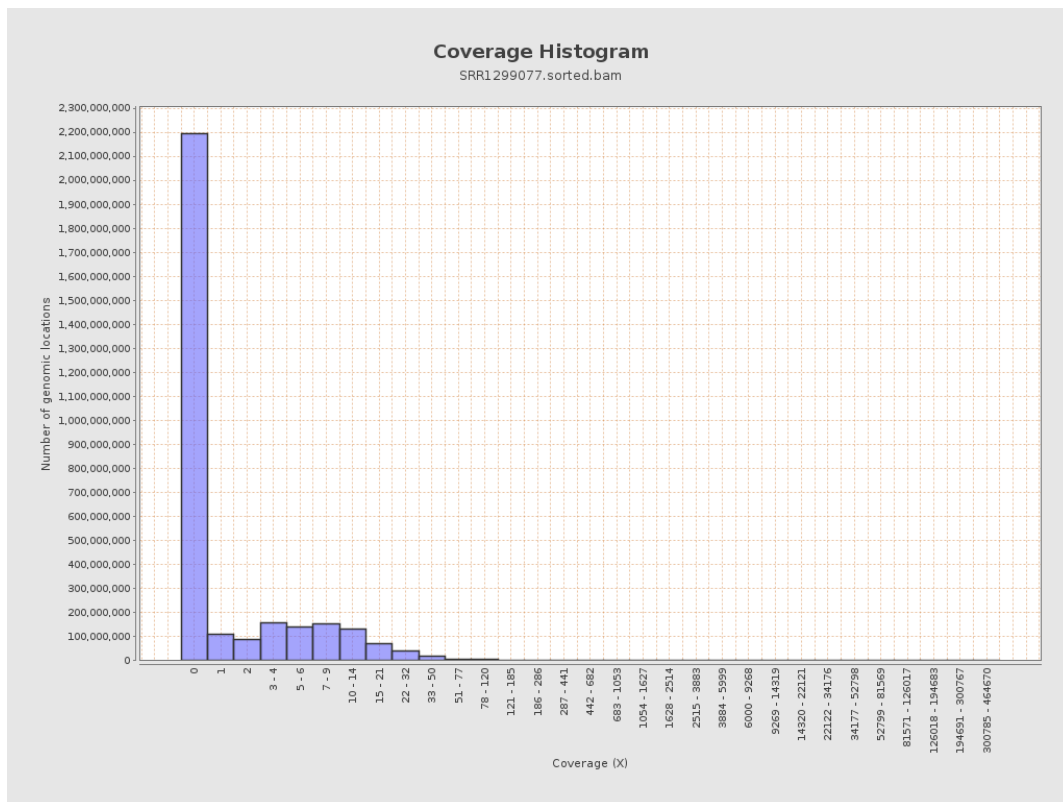
		bases	coverage	deviation
chr1	249250621	7921783408	31.7824	1,881.0349
chr2	243199373	2821775489	11.6027	899.8733
chr3	198022430	3327306726	16.8027	1,220.3286
chr4	191154276	1348827094	7.0562	600.9051
chr5	180915260	3009460021	16.6346	1,190.9067
chr6	171115067	3809108108	22.2605	1,420.4053
chr7	159138663	3316462970	20.8401	1,408.9826
chr8	146364022	1985900553	13.5682	1,010.4115
chr9	141213431	2148465183	15.2143	1,039.3637
chr10	135534747	1390108875	10.2565	711.5486
chr11	135006516	5090729125	37.7073	1,996.1601
chr12	133851895	1849851122	13.8201	860.3962
chr13	115169878	1016520618	8.8263	819.8121
chr14	107349540	2402720773	22.3822	1,456.3958
chr15	102531392	1866825464	18.2074	1,195.1307
chr16	90354753	2360873117	26.1289	1,502.8369
chr17	81195210	1464408801	18.0357	1,023.583
chr18	78077248	1356200158	17.37	1,267.5121
chr19	59128983	3819357837	64.5937	2,409.325
chr20	63025520	1964869786	31.1758	1,685.9088
chr21	48129895	1169086930	24.2902	1,579.7742
chr22	51304566	265755740	5.18	394.9628
chrMT	16571	9920943	598.6931	192.0531
chrX	155270560	3586693676	23.0996	1,435.8869

chrY	59373566	28699954	0.4834	18.7586
------	----------	----------	--------	---------

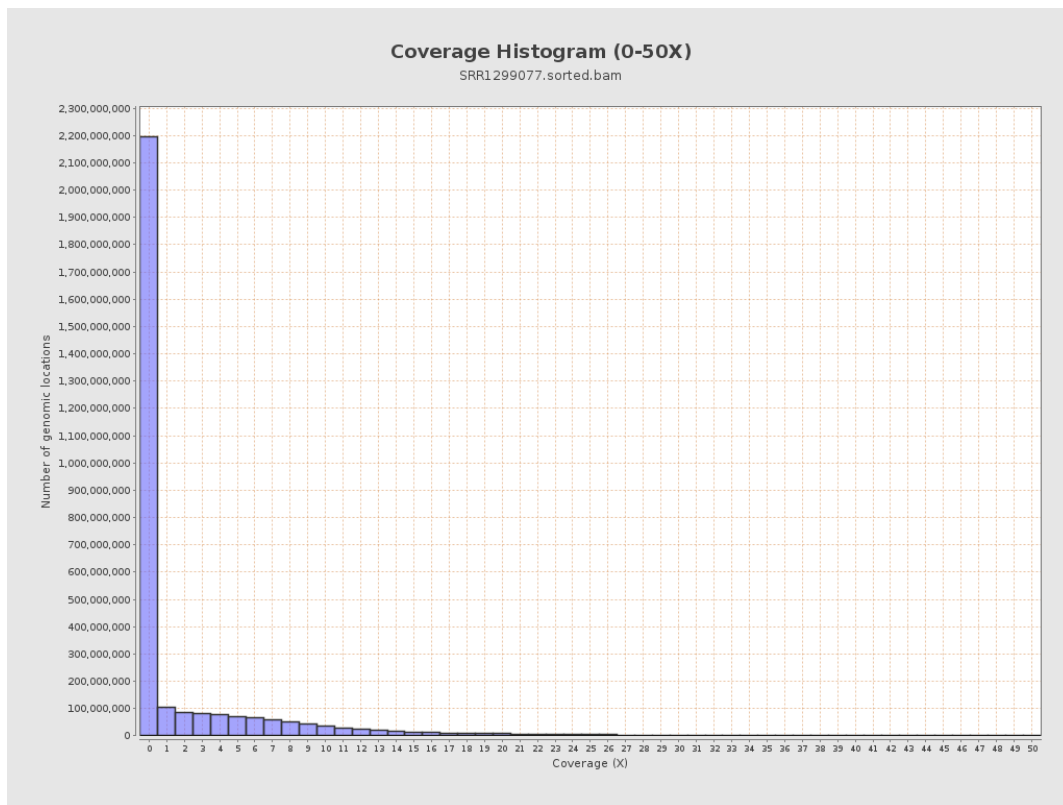
3. Results : Coverage across reference



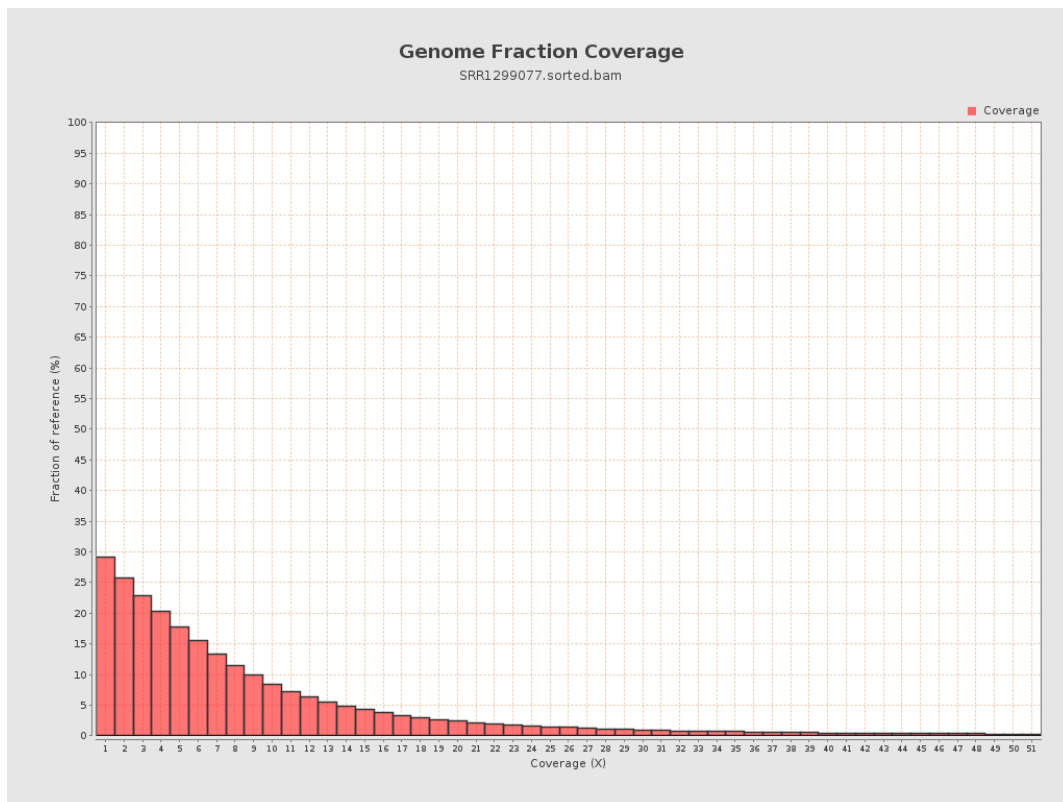
4. Results : Coverage Histogram



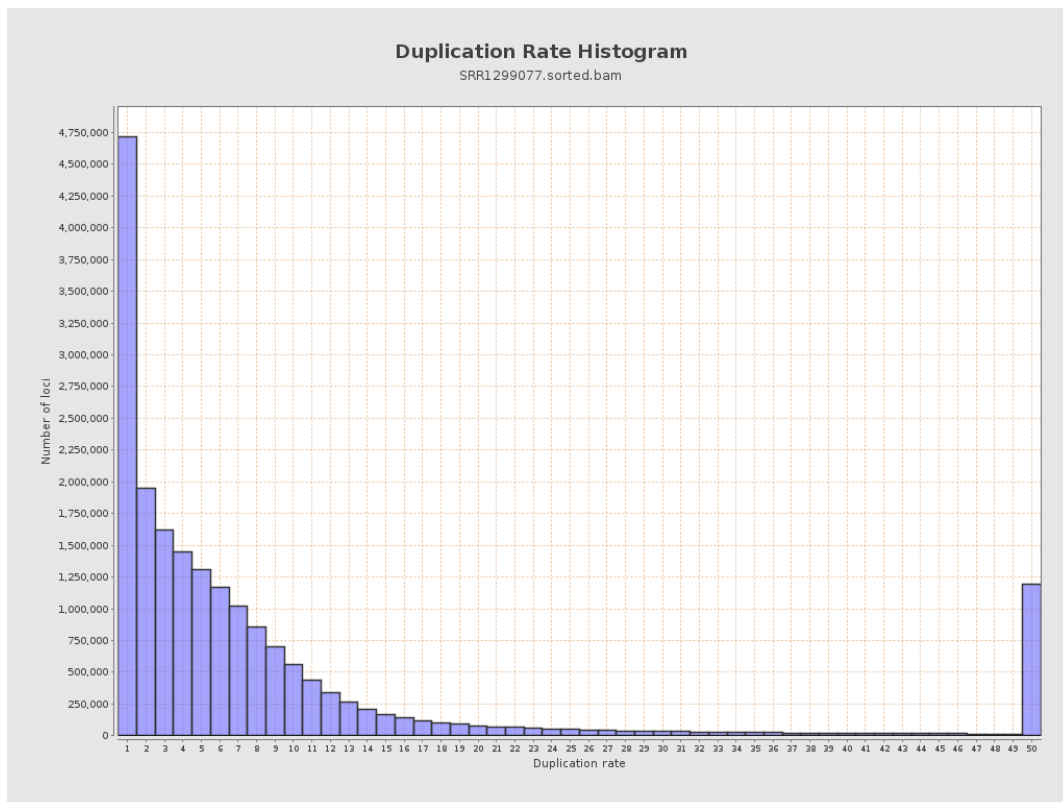
5. Results : Coverage Histogram (0-50X)



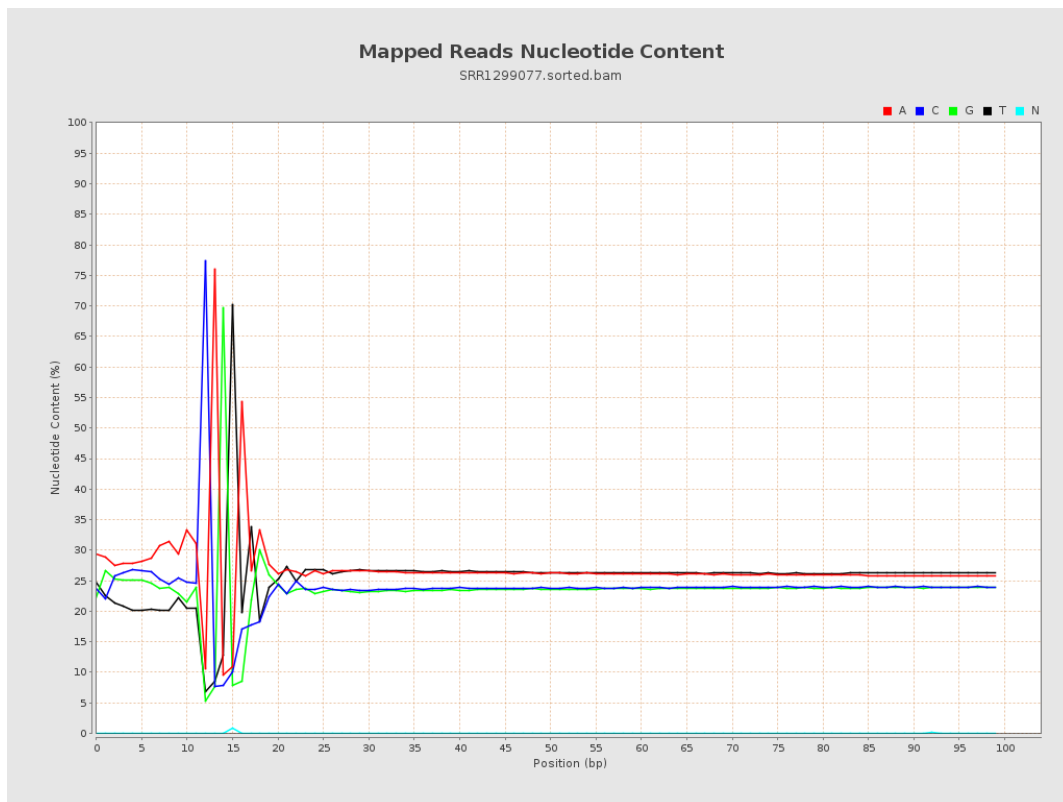
6. Results : Genome Fraction Coverage



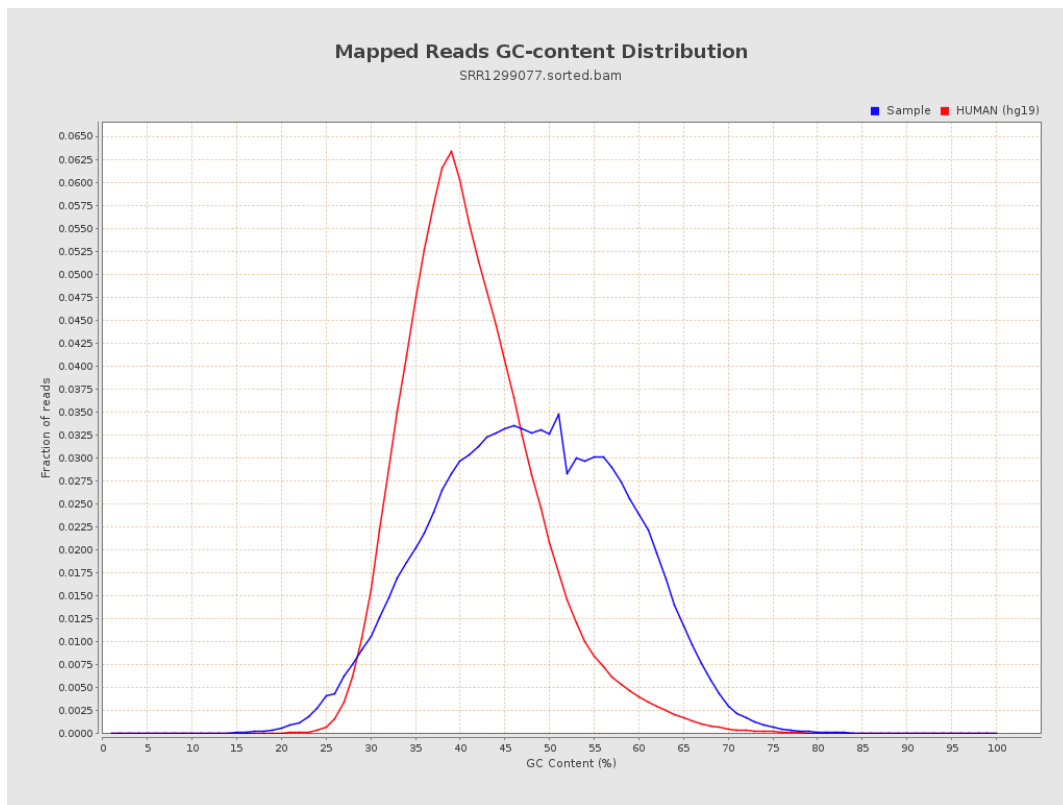
7. Results : Duplication Rate Histogram



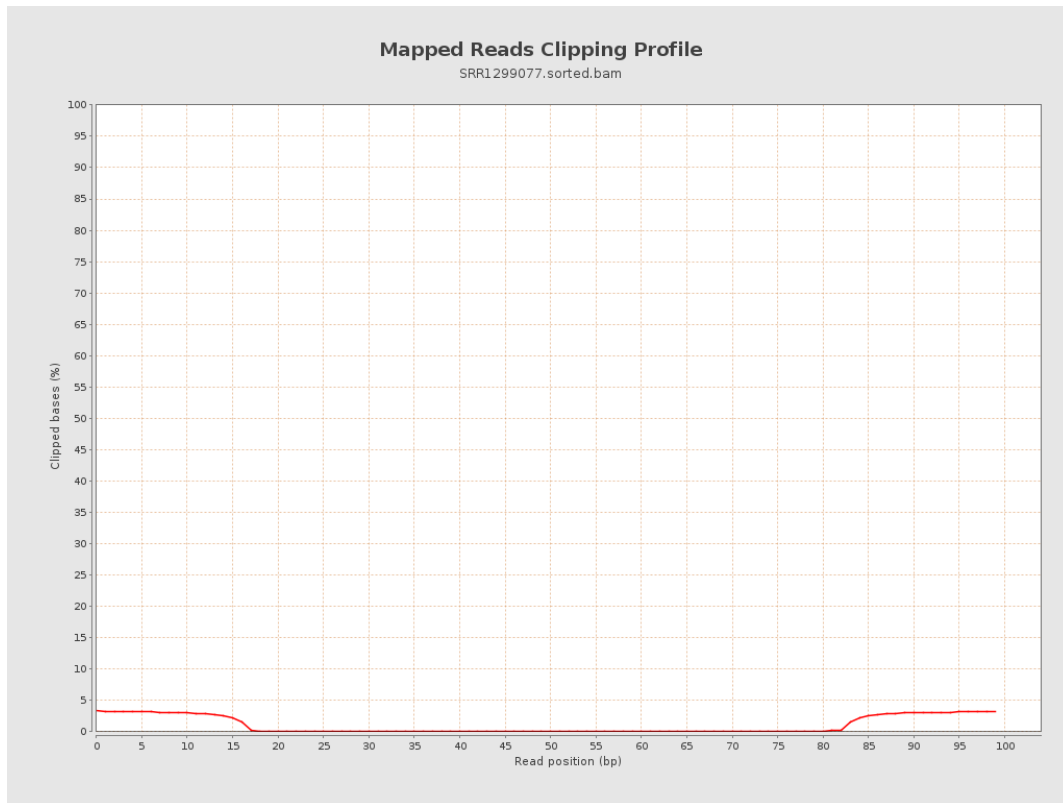
8. Results : Mapped Reads Nucleotide Content



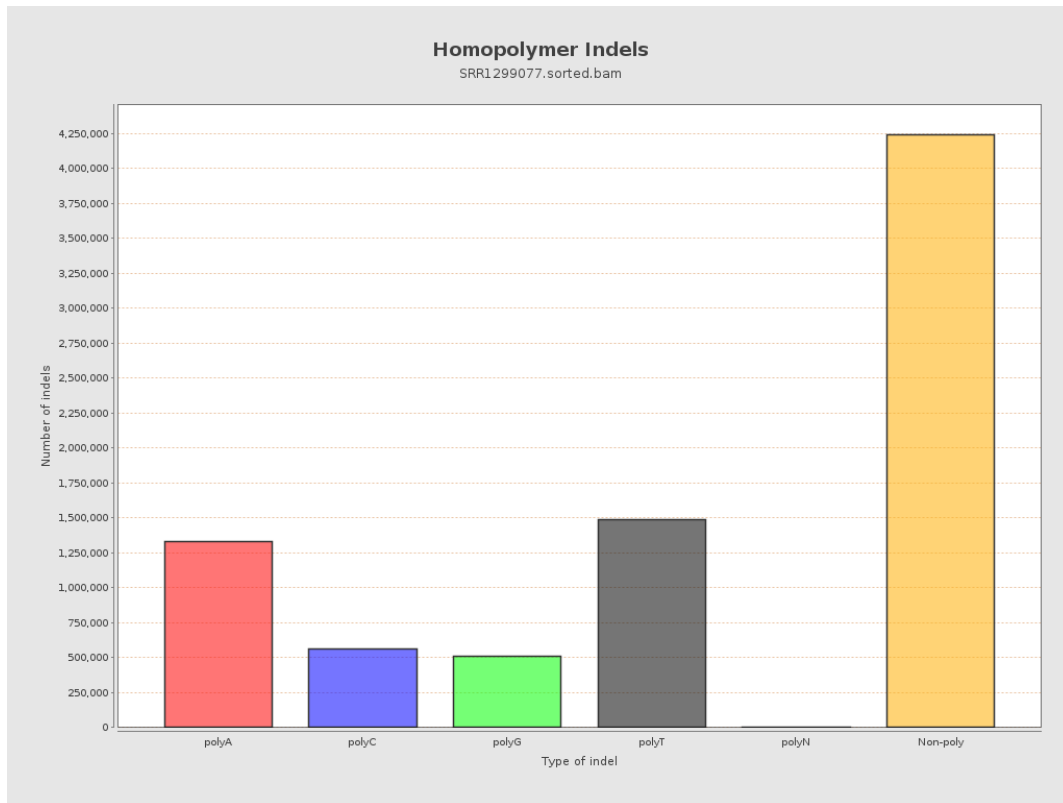
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



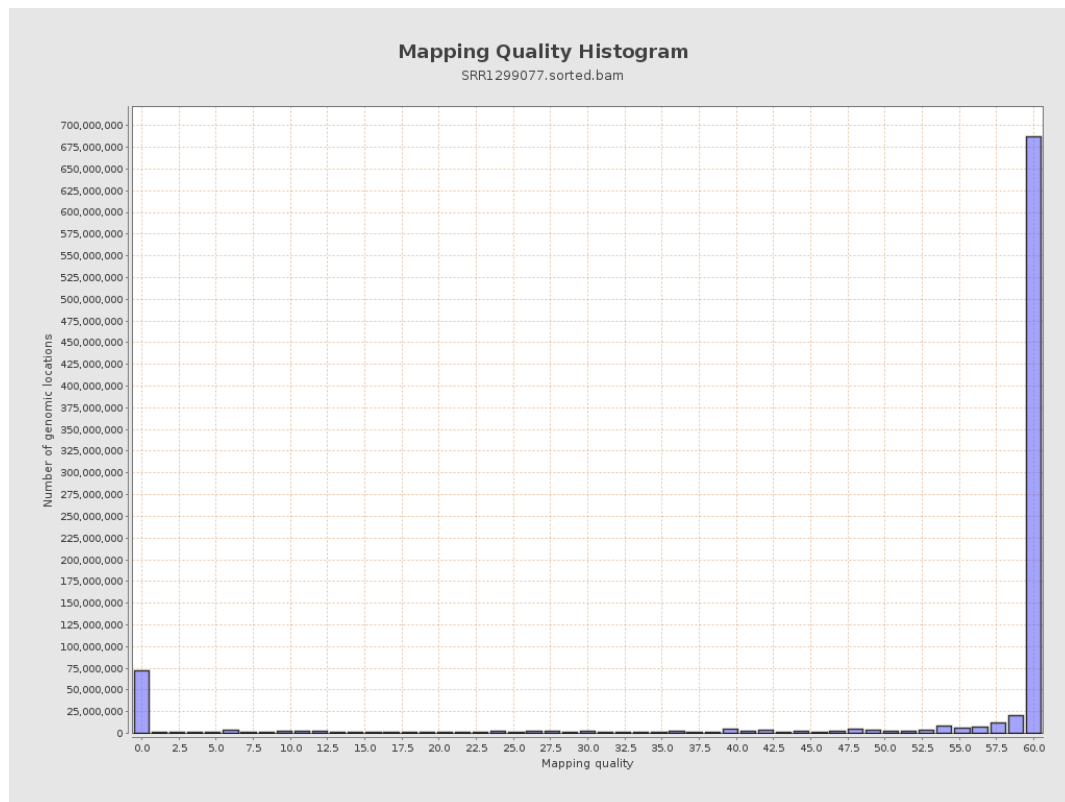
11. Results : Homopolymer Indels



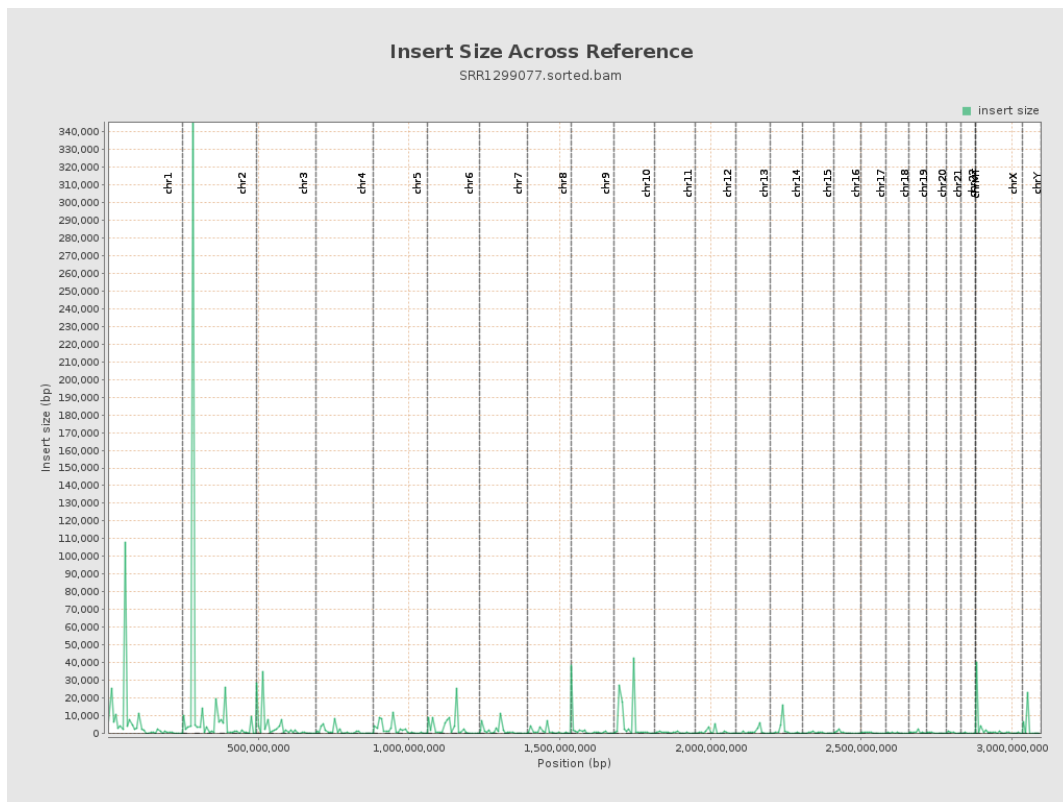
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

