

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 00:28:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779293.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_SRR1779293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779293_1.fastq.gz SRR1779293_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 00:28:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,305,734
Mapped reads	13,772,663 / 96.27%
Unmapped reads	533,071 / 3.73%
Mapped paired reads	13,772,663 / 96.27%
Mapped reads, first in pair	6,926,099 / 48.41%
Mapped reads, second in pair	6,846,564 / 47.86%
Mapped reads, both in pair	13,672,514 / 95.57%
Mapped reads, singletons	100,149 / 0.7%
Secondary alignments	0
Supplementary alignments	38,333 / 0.27%
Read min/max/mean length	30 / 80 / 80.1
Duplicated reads (estimated)	189,600 / 1.33%
Duplication rate	1.28%
Clipped reads	478,100 / 3.34%

2.2. ACGT Content

Number/percentage of A's	333,995,052 / 30.48%
Number/percentage of C's	213,680,929 / 19.5%
Number/percentage of T's	329,894,072 / 30.1%
Number/percentage of G's	218,066,086 / 19.9%
Number/percentage of N's	208,206 / 0.02%

GC Percentage	39.4%
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2.3. Coverage

Mean	0.3541
Standard Deviation	0.9635

2.4. Mapping Quality

Mean Mapping Quality	52.91
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2.5. Insert size

Mean	61,462.58
Standard Deviation	2,315,468.77
P25/Median/P75	141 / 186 / 252

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	4,089,577
Insertions	77,921
Mapped reads with at least one insertion	0.56%
Deletions	98,771
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.39%

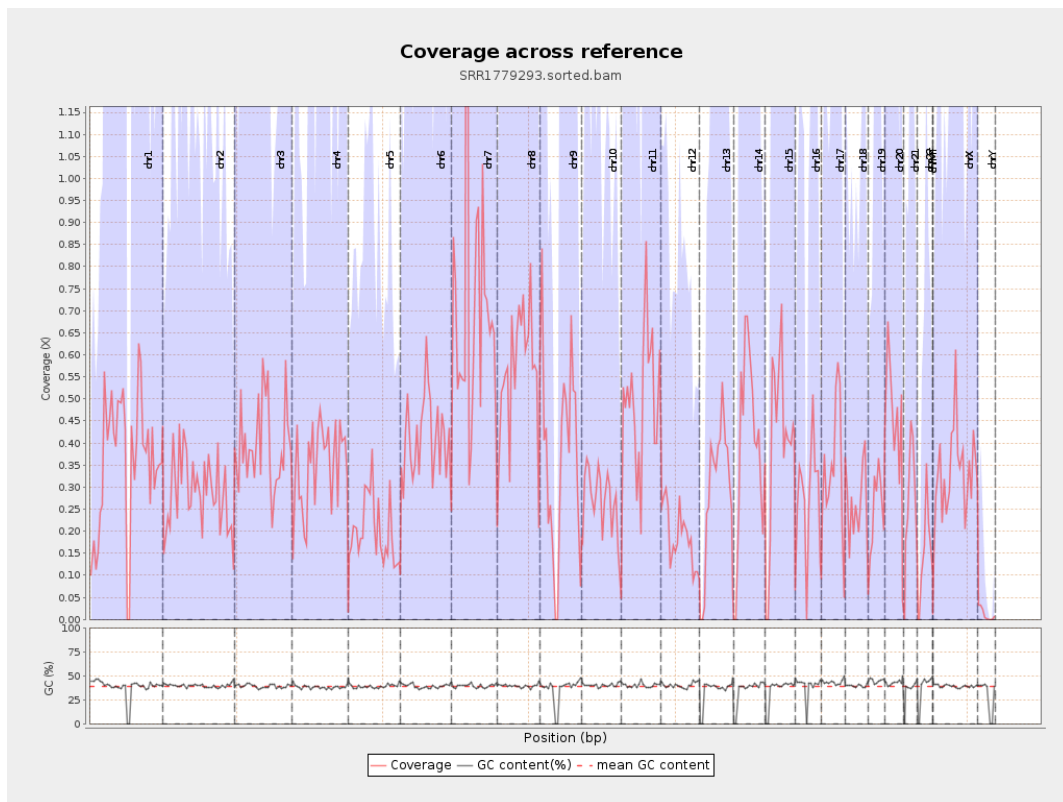
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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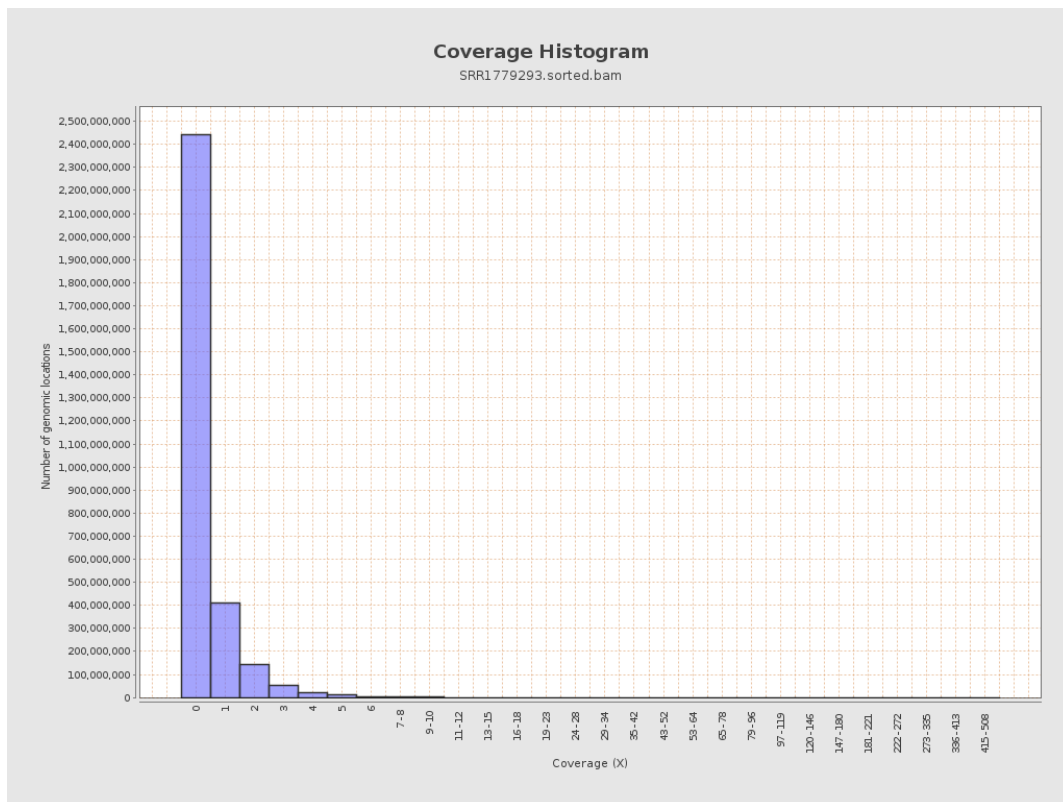
		bases	coverage	deviation
chr1	249250621	88619825	0.3555	1.0143
chr2	243199373	69163416	0.2844	0.7438
chr3	198022430	77972970	0.3938	0.9002
chr4	191154276	67170219	0.3514	0.8394
chr5	180915260	36113303	0.1996	0.6036
chr6	171115067	71077897	0.4154	0.9297
chr7	159138663	113338333	0.7122	1.9833
chr8	146364022	83035914	0.5673	1.1031
chr9	141213431	51466712	0.3645	0.9117
chr10	135534747	36450449	0.2689	1.0143
chr11	135006516	66753406	0.4944	1.0268
chr12	133851895	25245998	0.1886	0.5993
chr13	115169878	33424564	0.2902	0.7676
chr14	107349540	43020036	0.4007	0.925
chr15	102531392	41042313	0.4003	0.9721
chr16	90354753	24466005	0.2708	0.7133
chr17	81195210	28674463	0.3532	0.865
chr18	78077248	20771798	0.266	0.711
chr19	59128983	15116756	0.2557	0.7831
chr20	63025520	29516638	0.4683	1.0903
chr21	48129895	12843775	0.2669	0.7339
chr22	51304566	7975825	0.1555	0.5434
chrMT	16571	187	0.0113	0.126
chrX	155270560	52113985	0.3356	0.8485

chrY	59373566	673424	0.0113	0.1712
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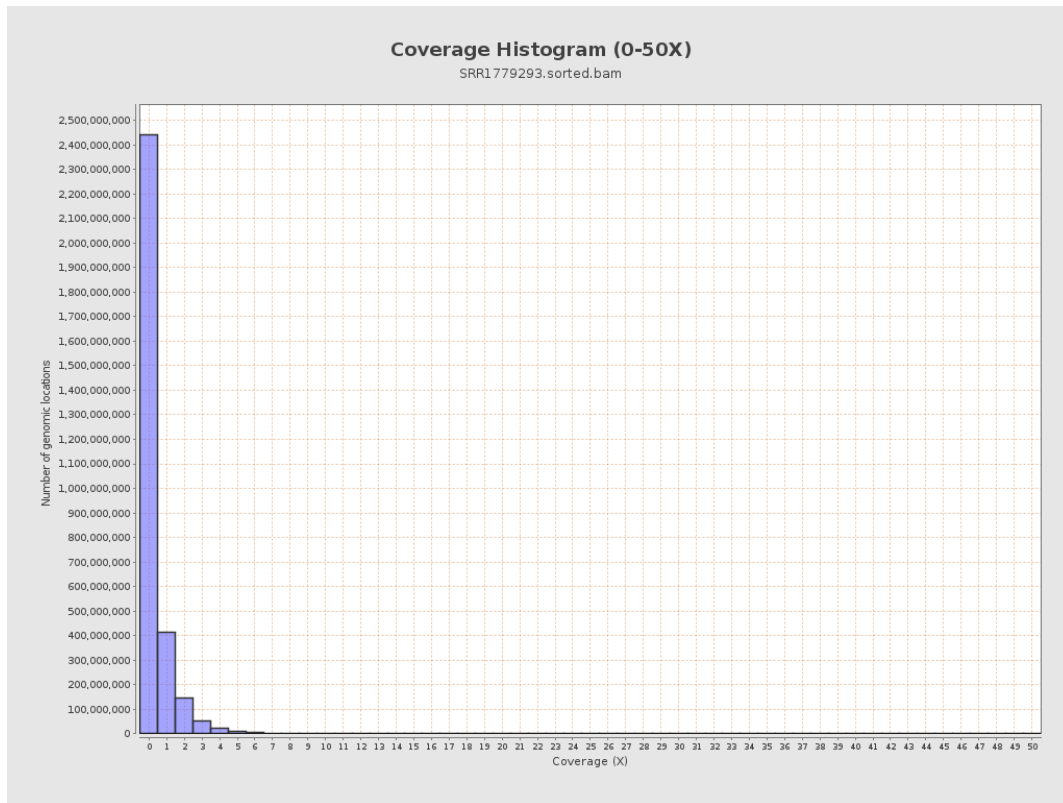
3. Results : Coverage across reference



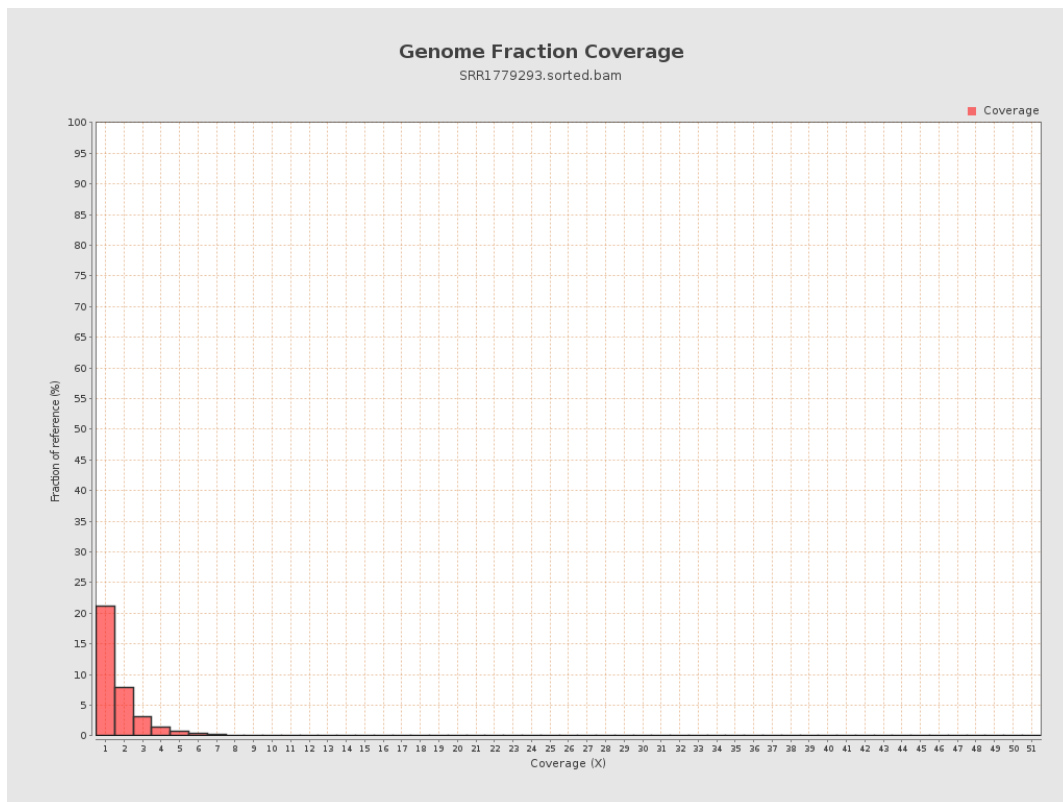
4. Results : Coverage Histogram



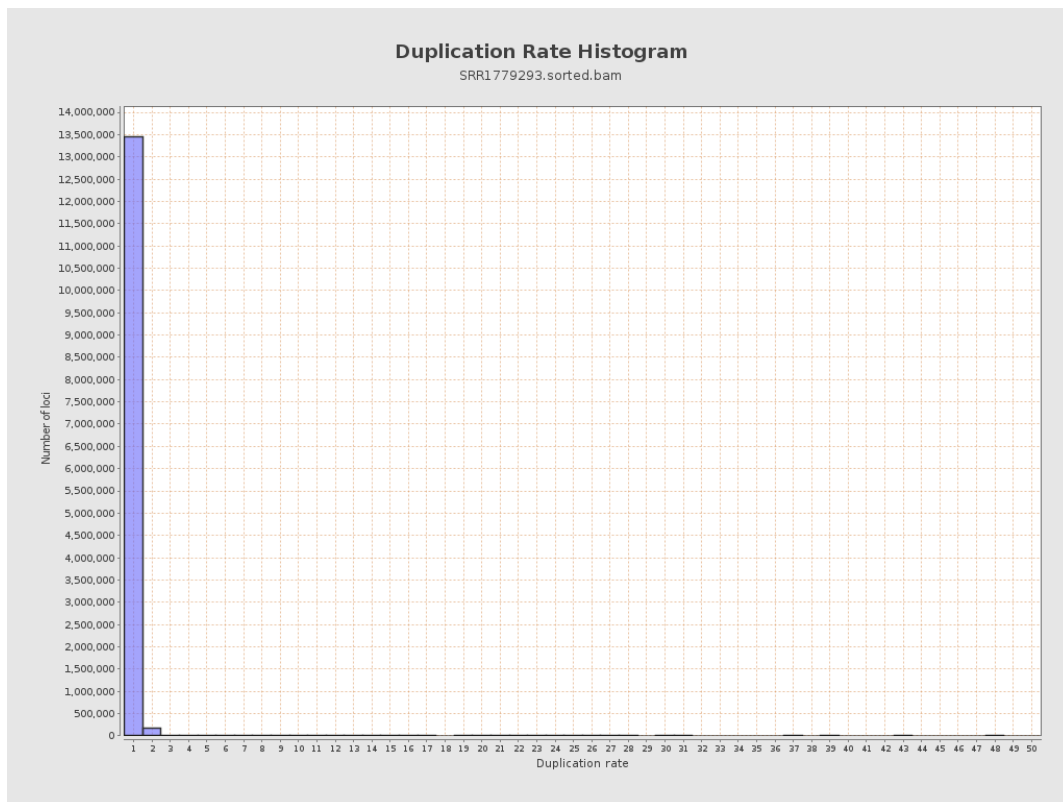
5. Results : Coverage Histogram (0-50X)



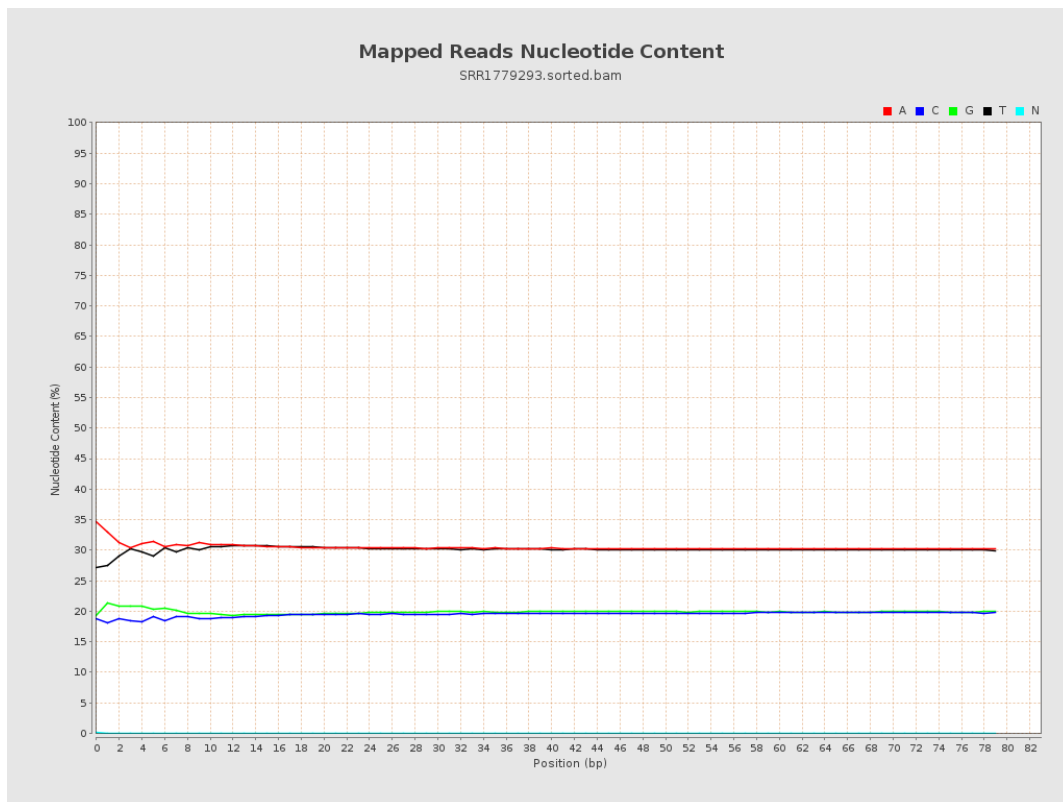
6. Results : Genome Fraction Coverage



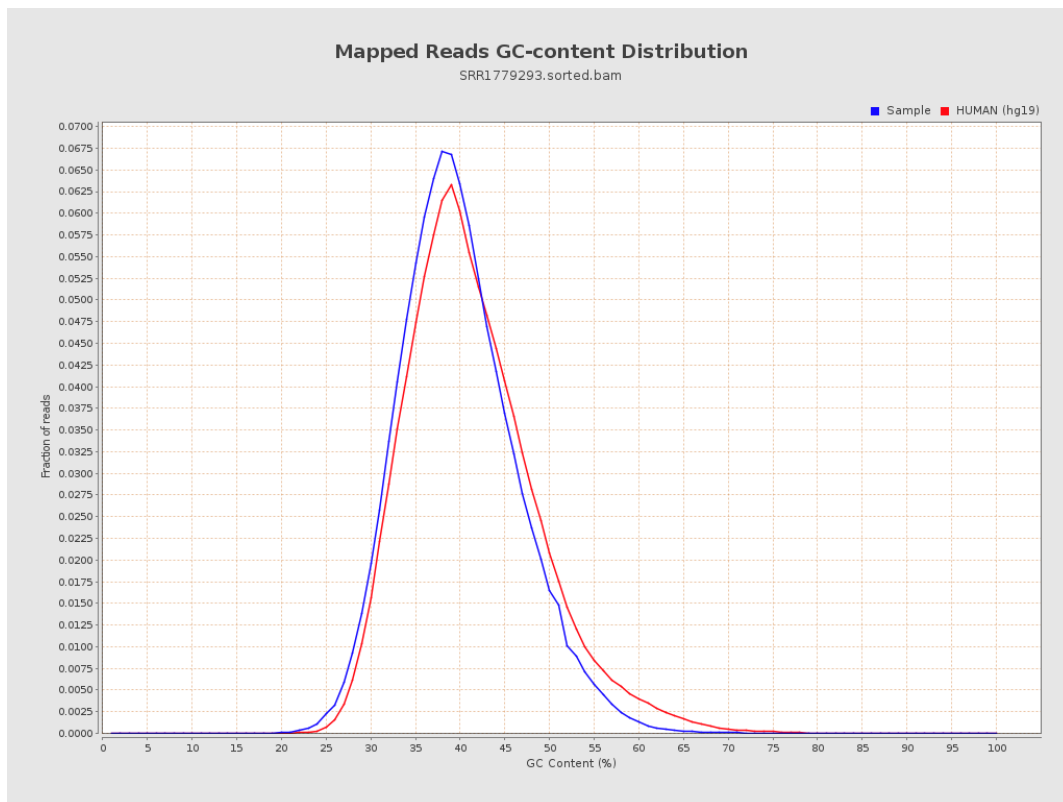
7. Results : Duplication Rate Histogram



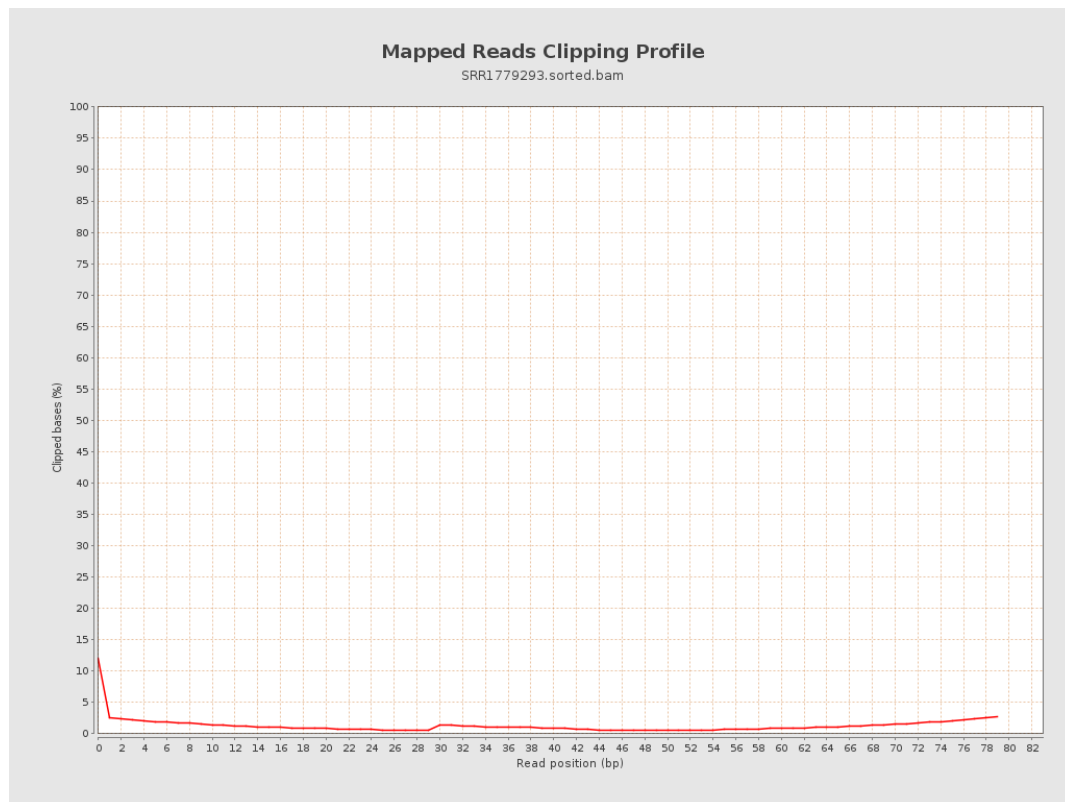
8. Results : Mapped Reads Nucleotide Content



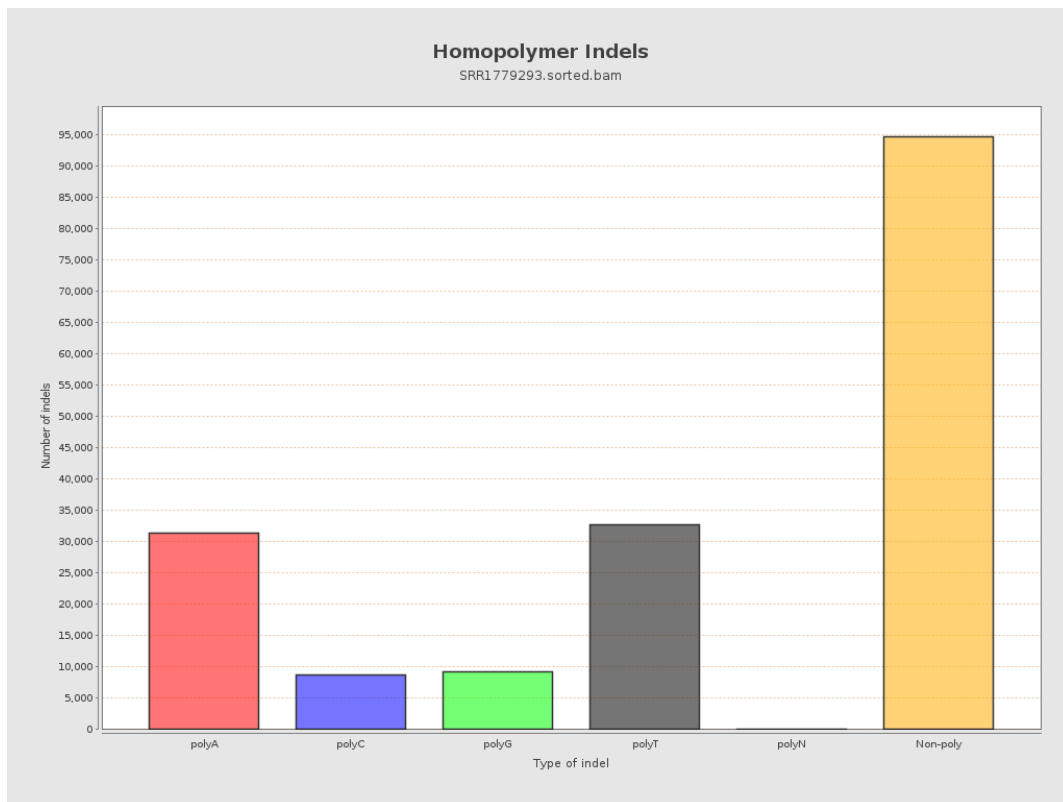
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



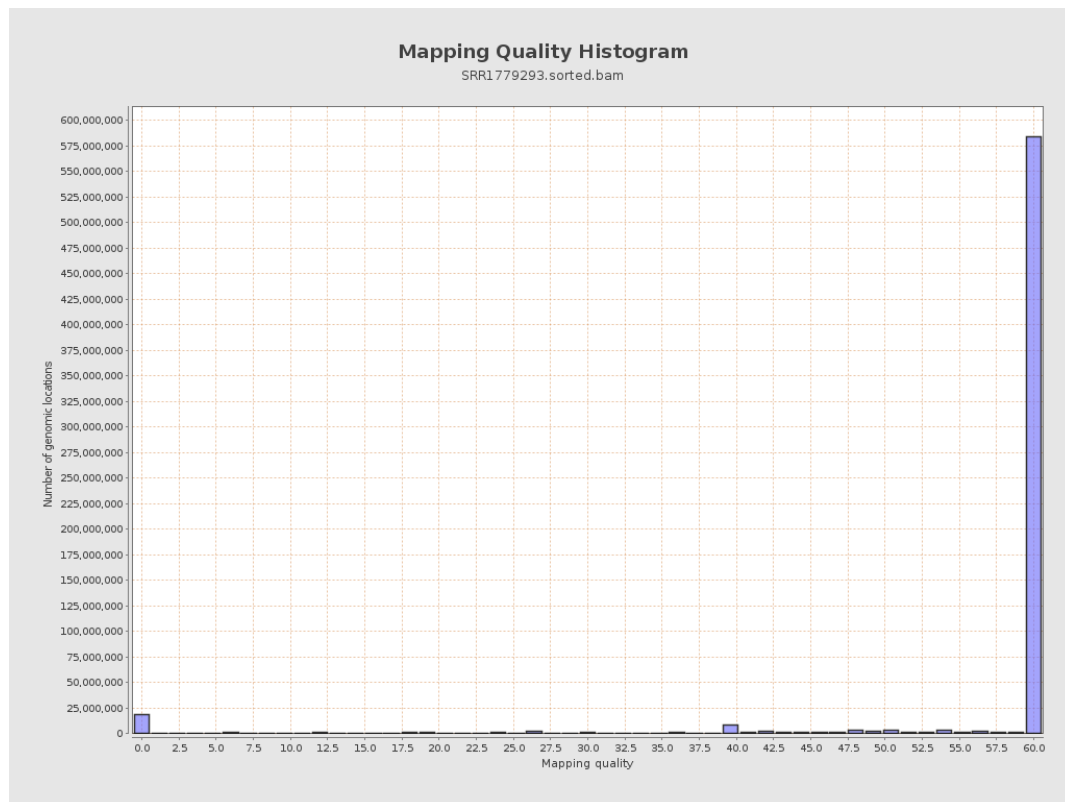
11. Results : Homopolymer Indels



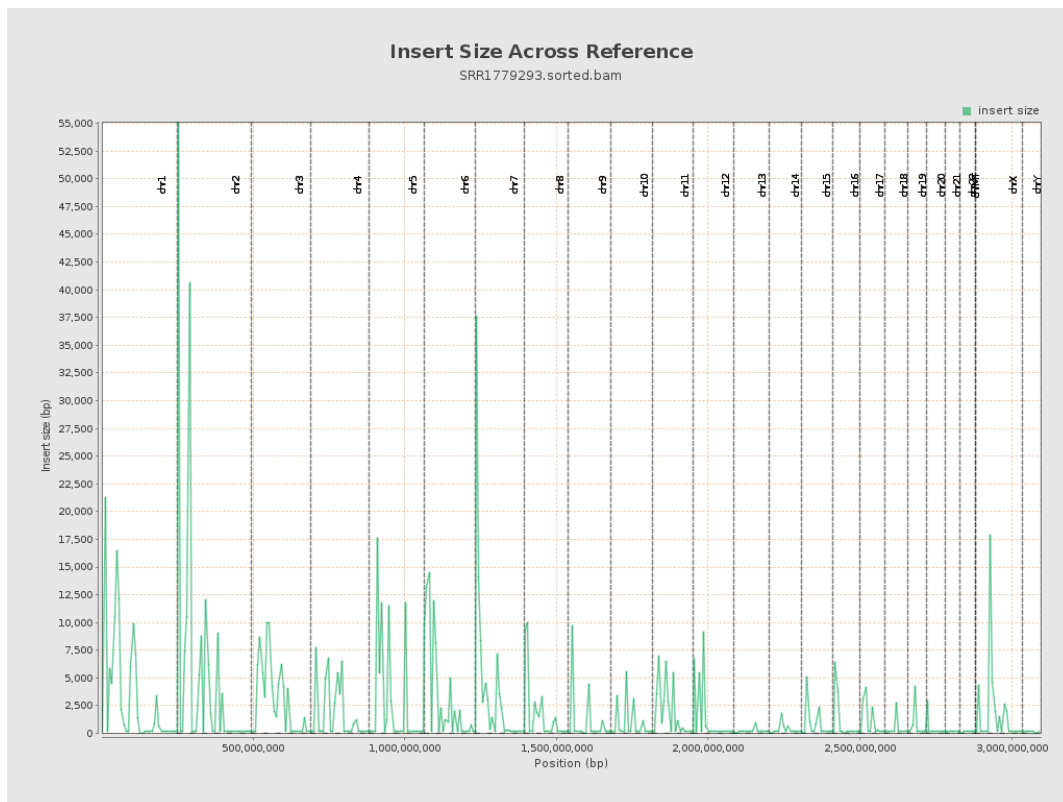
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

