

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 10:51:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777305.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_SRR1777305 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777305_1.fastq.gz SRR1777305_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 10:51:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777305.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	212,237,082
Mapped reads	207,283,362 / 97.67%
Unmapped reads	4,953,720 / 2.33%
Mapped paired reads	207,283,362 / 97.67%
Mapped reads, first in pair	103,976,322 / 48.99%
Mapped reads, second in pair	103,307,040 / 48.68%
Mapped reads, both in pair	206,410,686 / 97.25%
Mapped reads, singletons	872,676 / 0.41%
Secondary alignments	0
Supplementary alignments	759,098 / 0.36%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	46,972,424 / 22.13%
Duplication rate	20.73%
Clipped reads	40,862,386 / 19.25%

2.2. ACGT Content

Number/percentage of A's	5,557,044,599 / 27.77%
Number/percentage of C's	4,436,758,411 / 22.17%
Number/percentage of T's	5,454,794,327 / 27.26%
Number/percentage of G's	4,559,084,898 / 22.78%
Number/percentage of N's	1,950,207 / 0.01%

GC Percentage	44.96%
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2.3. Coverage

Mean	6.468
Standard Deviation	17.5516

2.4. Mapping Quality

Mean Mapping Quality	54.12
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2.5. Insert size

Mean	84,032.36
Standard Deviation	2,948,341.94
P25/Median/P75	119 / 163 / 222

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	147,351,989
Insertions	3,253,275
Mapped reads with at least one insertion	1.55%
Deletions	9,485,138
Mapped reads with at least one deletion	4.47%
Homopolymer indels	54.19%

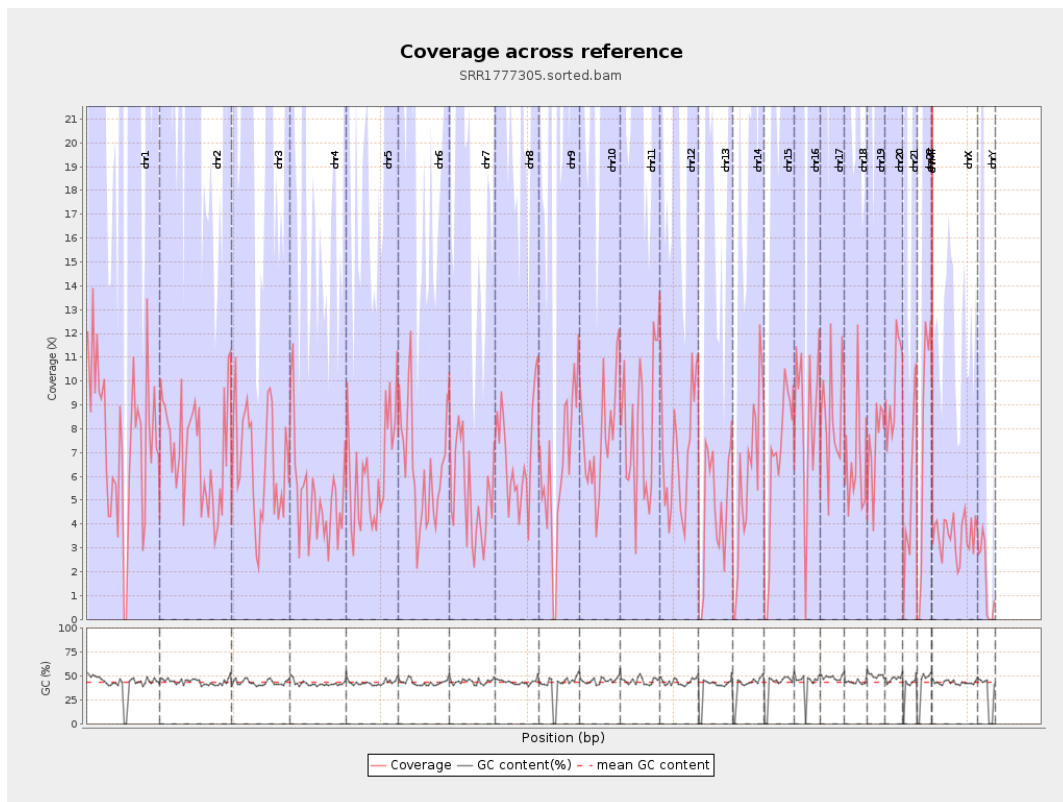
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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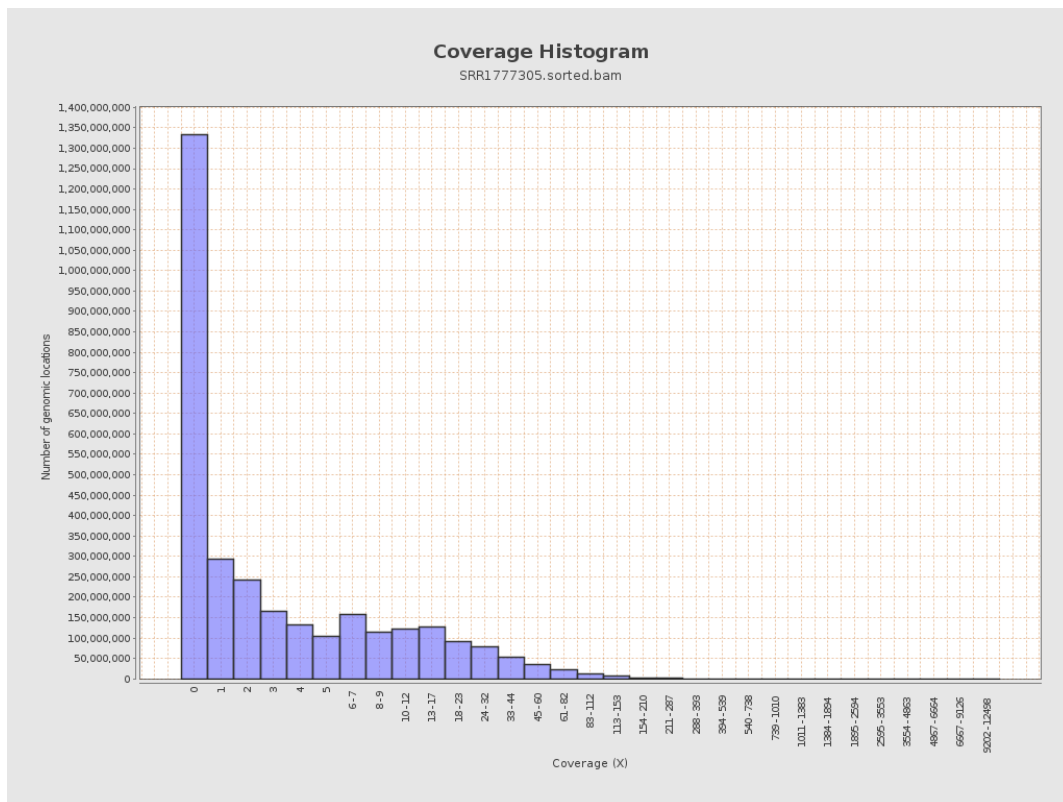
		bases	coverage	deviation
chr1	249250621	1869171963	7.4992	21.4421
chr2	243199373	1713199533	7.0444	21.2317
chr3	198022430	1306517180	6.5978	14.9628
chr4	191154276	982805905	5.1414	17.2921
chr5	180915260	1135370473	6.2757	14.3253
chr6	171115067	1080544790	6.3147	14.5565
chr7	159138663	840310298	5.2804	12.8749
chr8	146364022	1006996010	6.8801	15.8823
chr9	141213431	906599023	6.4201	19.5374
chr10	135534747	1037447641	7.6545	18.0779
chr11	135006516	1079437187	7.9954	18.5653
chr12	133851895	935593201	6.9898	16.0572
chr13	115169878	520784846	4.5219	11.928
chr14	107349540	630078094	5.8694	14.7986
chr15	102531392	663070204	6.467	15.7488
chr16	90354753	756383106	8.3713	22.5965
chr17	81195210	694619018	8.5549	20.3806
chr18	78077248	518812783	6.6449	19.8148
chr19	59128983	438009878	7.4077	18.6877
chr20	63025520	614787021	9.7546	20.5286
chr21	48129895	259547642	5.3926	29.9482
chr22	51304566	388785129	7.578	19.2581
chrMT	16571	3915000	236.2561	183.188
chrX	155270560	540801534	3.483	8.5886

chrY	59373566	99218268	1.6711	11.3409
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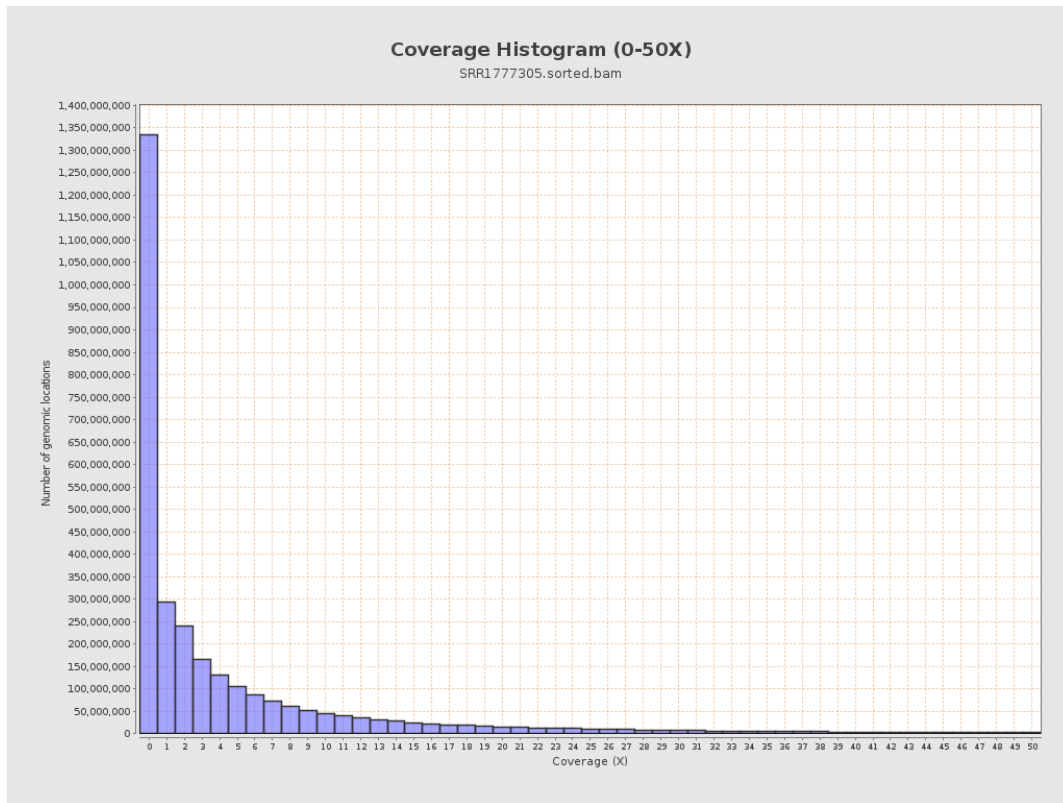
3. Results : Coverage across reference



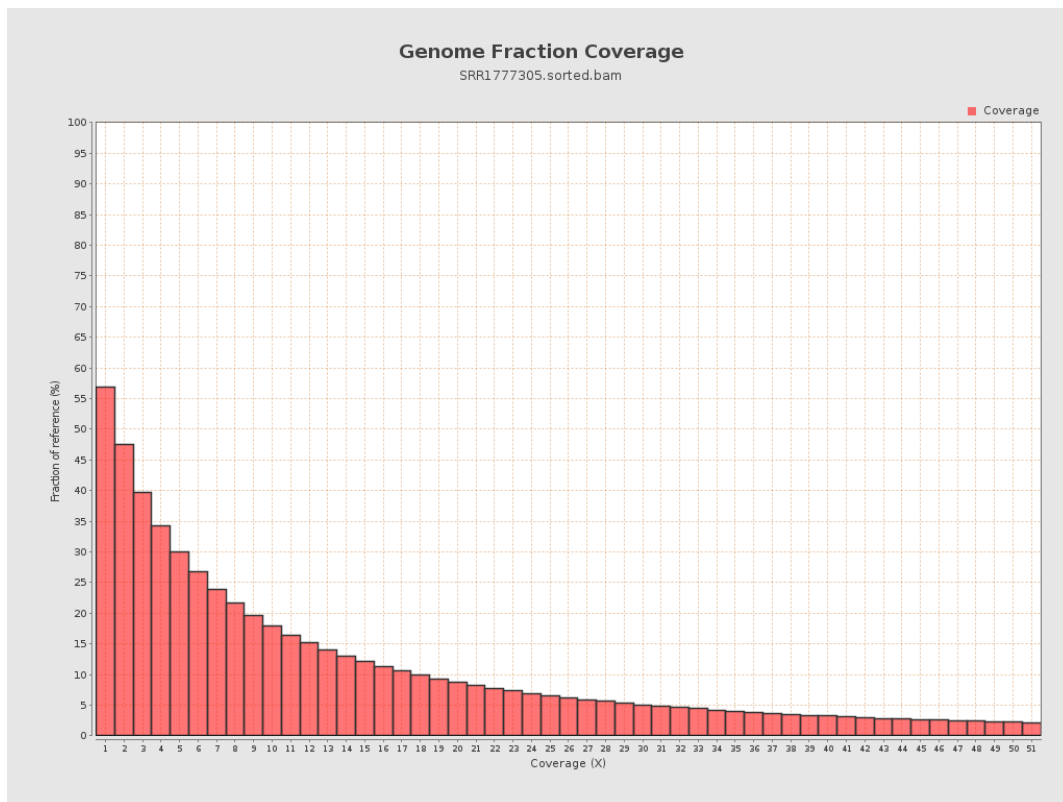
4. Results : Coverage Histogram



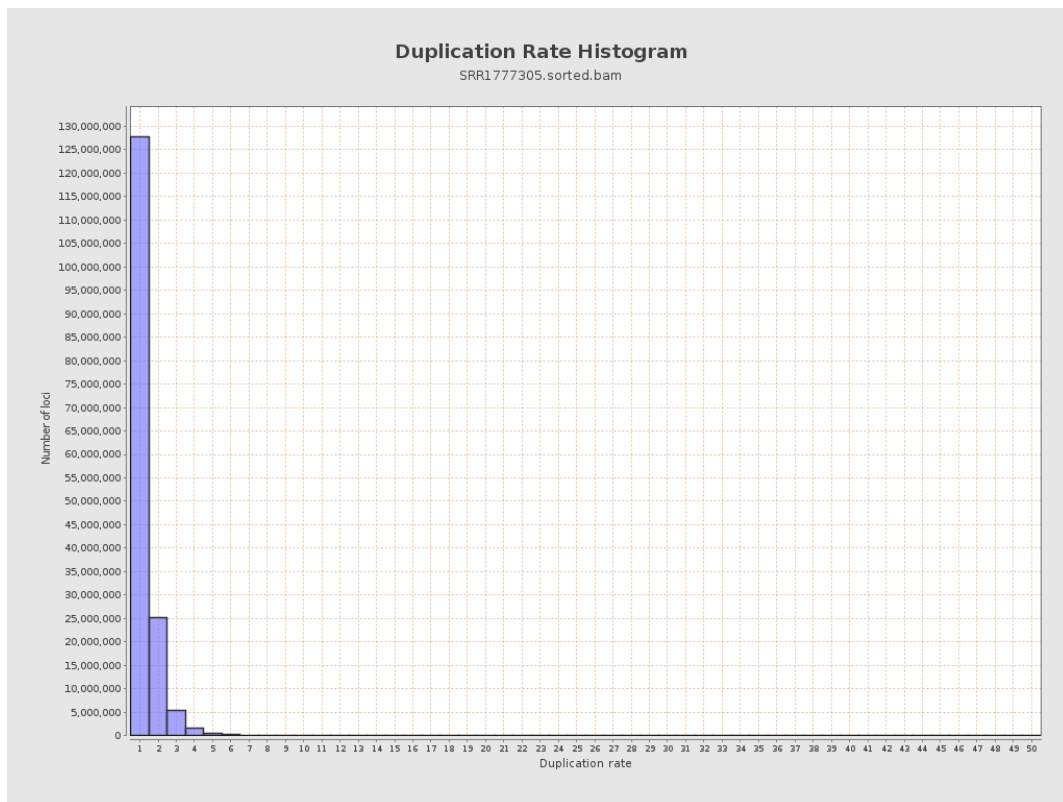
5. Results : Coverage Histogram (0-50X)



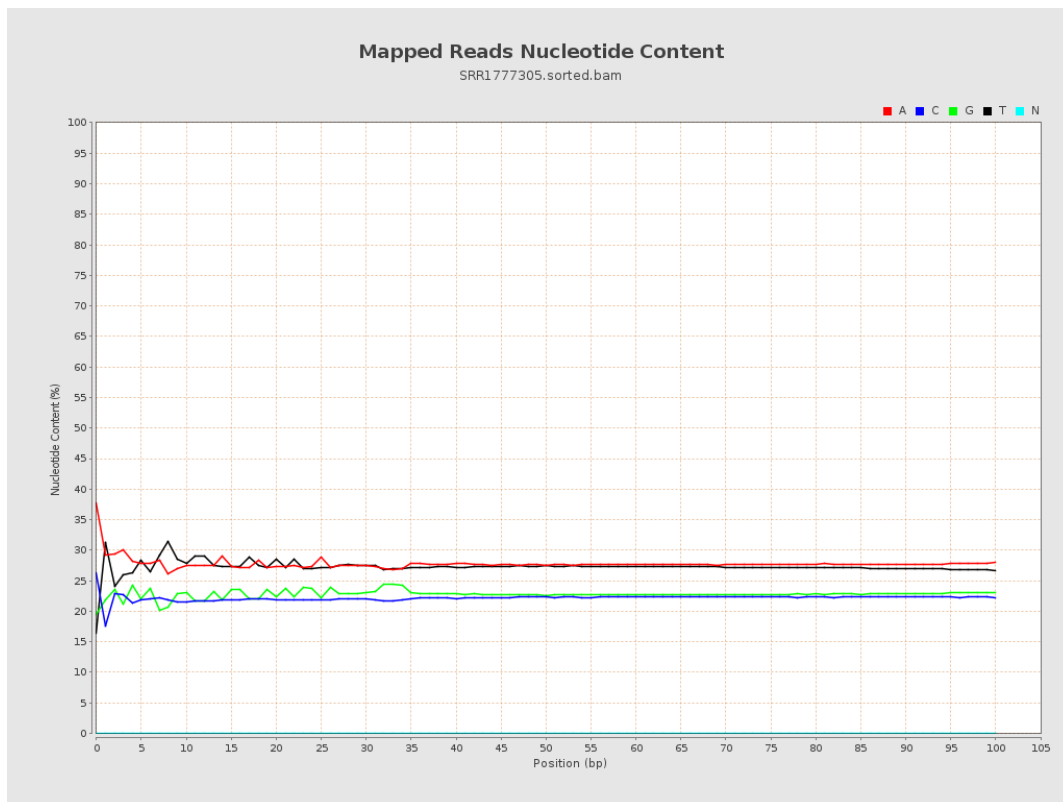
6. Results : Genome Fraction Coverage



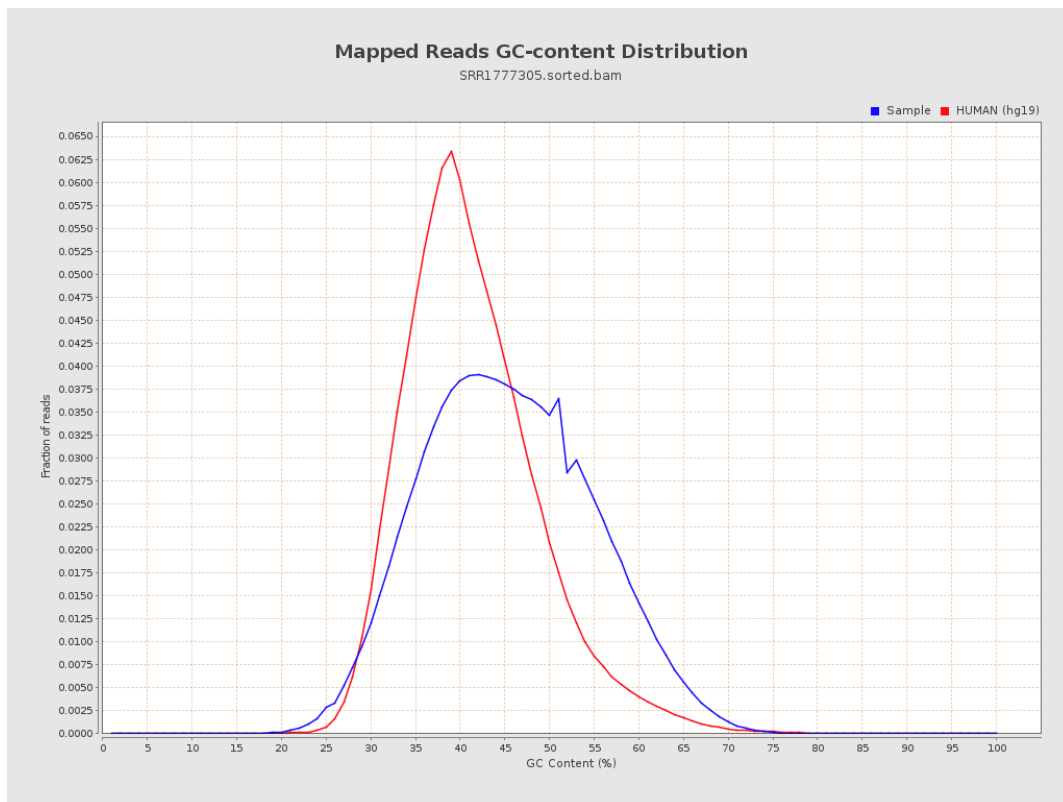
7. Results : Duplication Rate Histogram



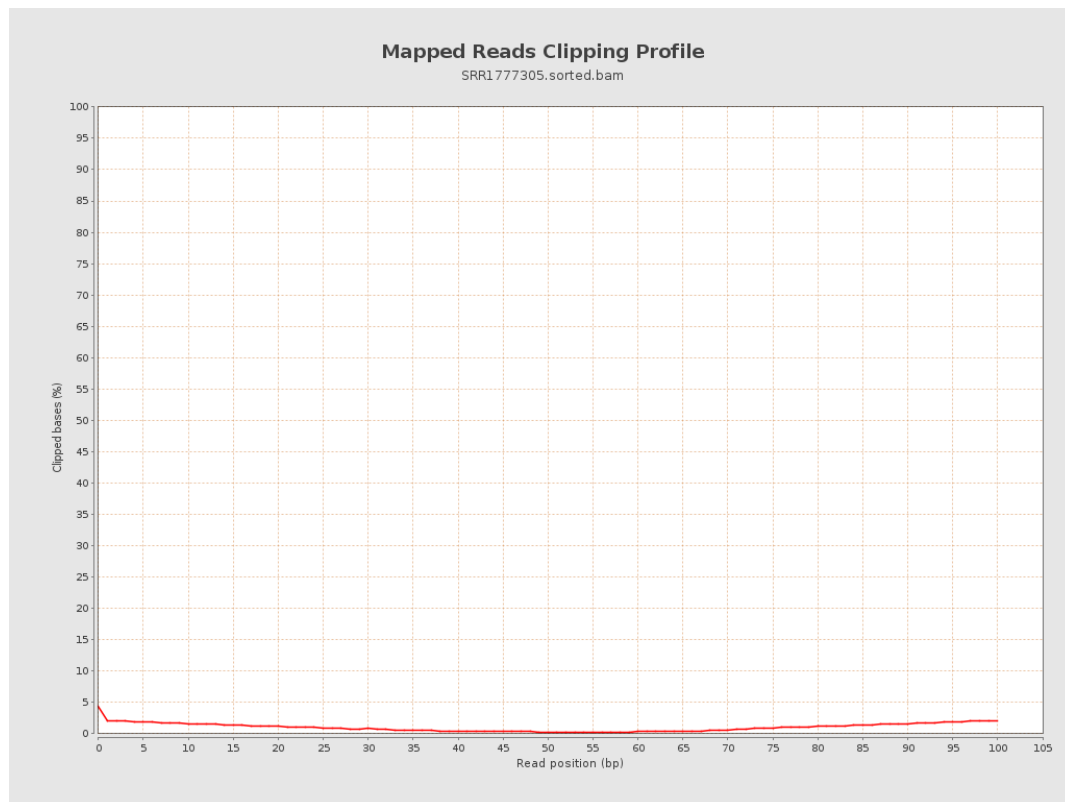
8. Results : Mapped Reads Nucleotide Content



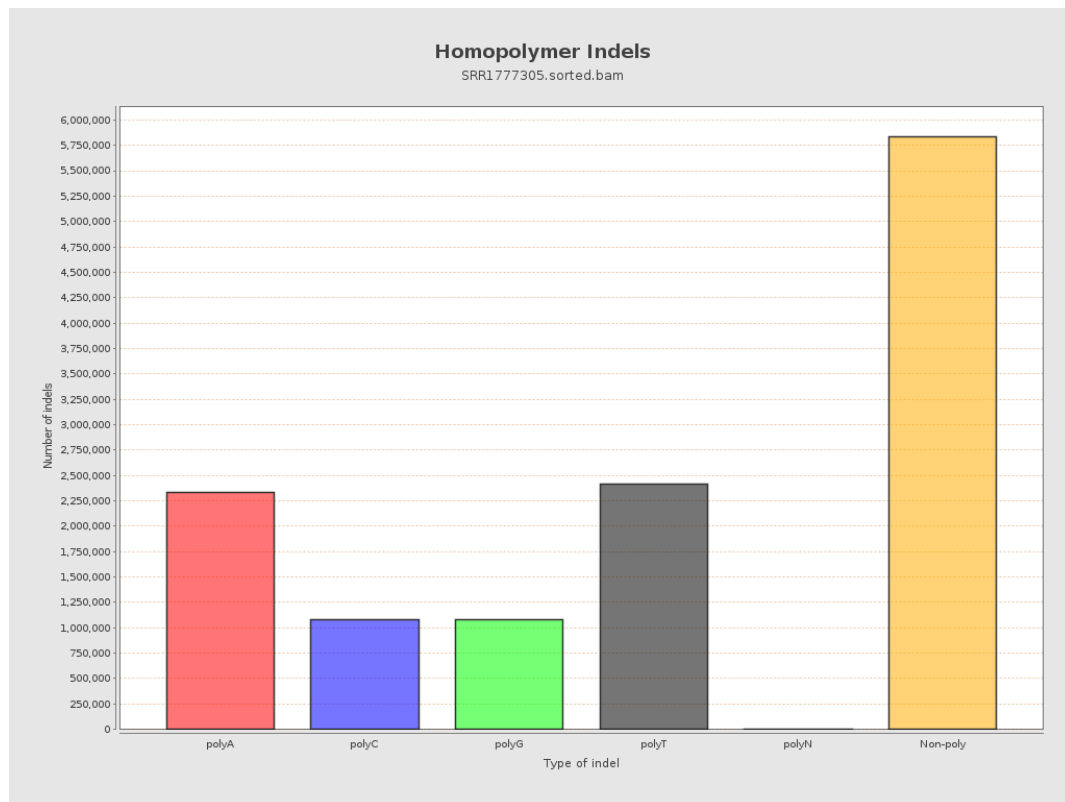
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



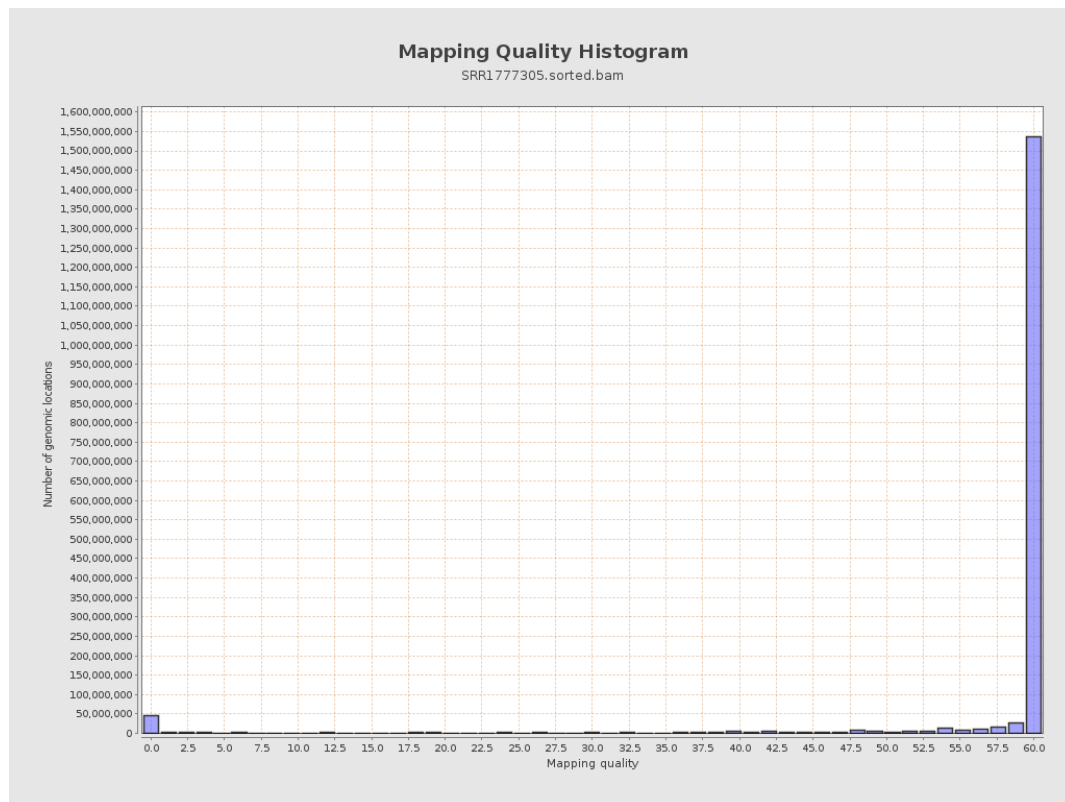
11. Results : Homopolymer Indels



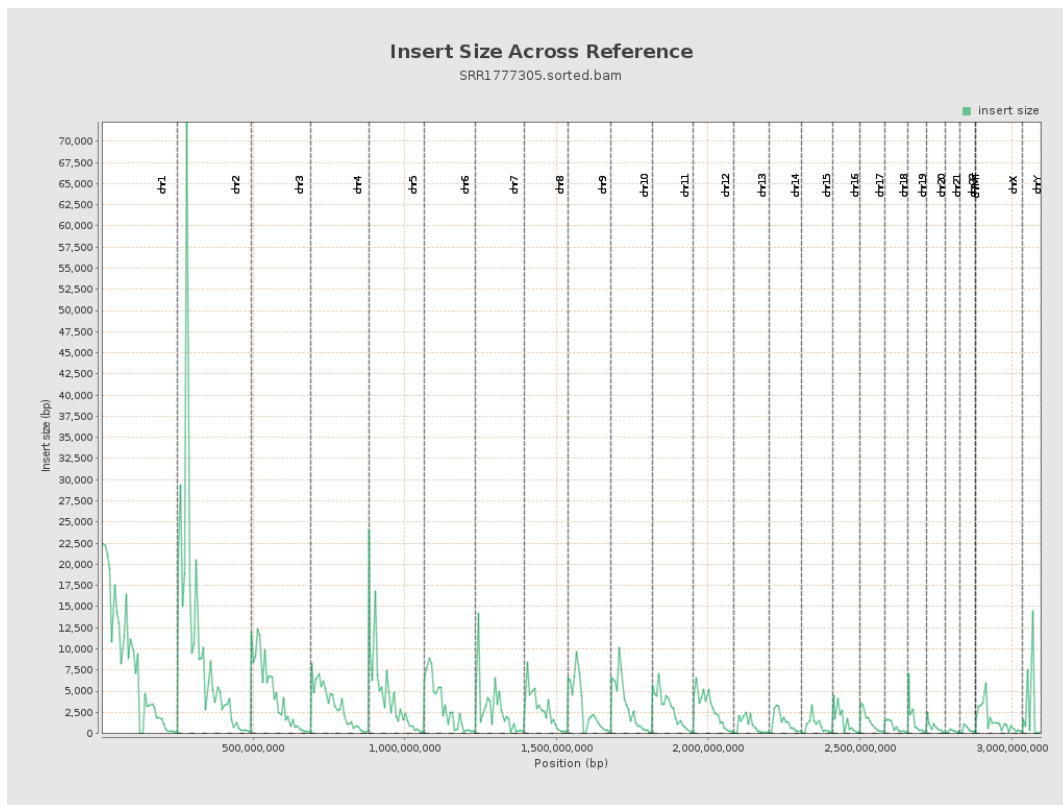
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

