

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 04:15:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777300.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_SRR1777300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777300_1.fastq.gz SRR1777300_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 04:15:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,515,744
Mapped reads	1,486,089 / 98.04%
Unmapped reads	29,655 / 1.96%
Mapped paired reads	1,486,089 / 98.04%
Mapped reads, first in pair	744,577 / 49.12%
Mapped reads, second in pair	741,512 / 48.92%
Mapped reads, both in pair	1,478,406 / 97.54%
Mapped reads, singletons	7,683 / 0.51%
Secondary alignments	0
Supplementary alignments	59,373 / 3.92%
Read min/max/mean length	30 / 101 / 102.62
Duplicated reads (estimated)	140,644 / 9.28%
Duplication rate	7.66%
Clipped reads	441,283 / 29.11%

2.2. ACGT Content

Number/percentage of A's	42,701,918 / 29.79%
Number/percentage of C's	29,116,038 / 20.31%
Number/percentage of T's	41,910,589 / 29.24%
Number/percentage of G's	29,594,591 / 20.65%
Number/percentage of N's	2,236 / 0%

GC Percentage	40.96%
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2.3. Coverage

Mean	0.0463
Standard Deviation	0.6903

2.4. Mapping Quality

Mean Mapping Quality	52.83
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2.5. Insert size

Mean	162,320.16
Standard Deviation	3,847,368.32
P25/Median/P75	112 / 157 / 220

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	888,724
Insertions	36,088
Mapped reads with at least one insertion	2.34%
Deletions	22,350
Mapped reads with at least one deletion	1.44%
Homopolymer indels	42.18%

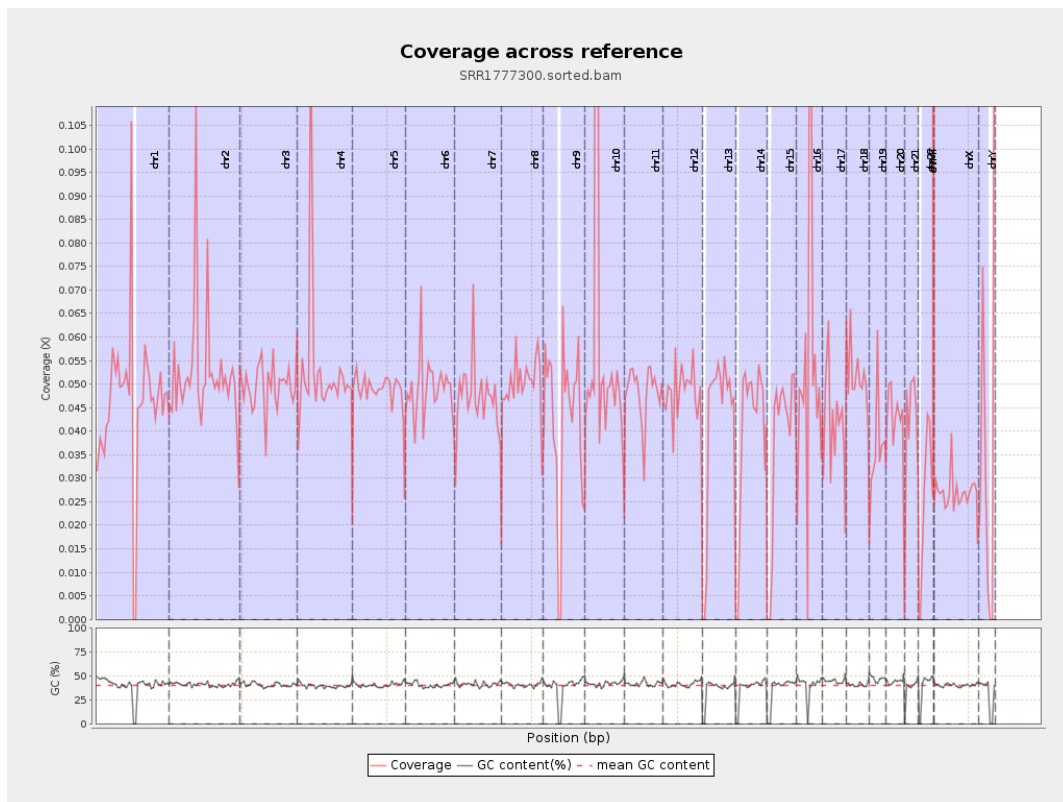
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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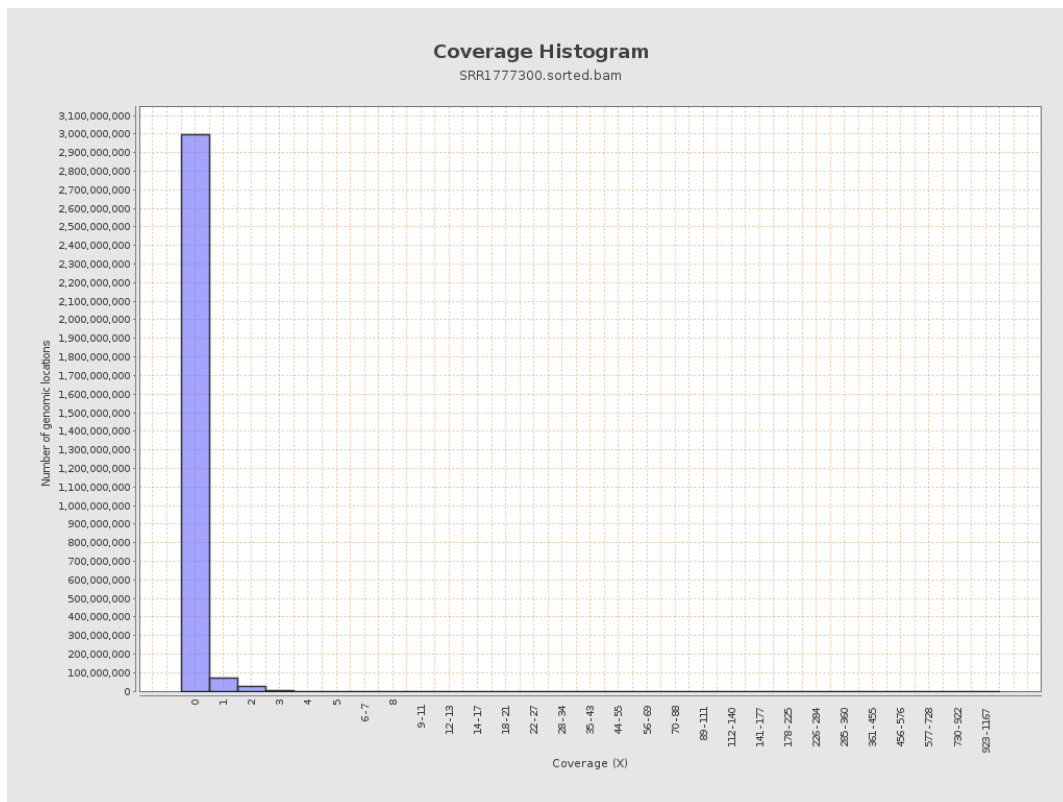
		bases	coverage	deviation
chr1	249250621	11473647	0.046	1.1493
chr2	243199373	12793233	0.0526	0.6344
chr3	198022430	9826197	0.0496	0.3514
chr4	191154276	10025428	0.0524	0.6384
chr5	180915260	8805333	0.0487	0.2841
chr6	171115067	8378293	0.049	0.3434
chr7	159138663	7563604	0.0475	0.4732
chr8	146364022	7340233	0.0502	0.4339
chr9	141213431	6013997	0.0426	0.5636
chr10	135534747	8143930	0.0601	1.9552
chr11	135006516	6469033	0.0479	0.3293
chr12	133851895	6445875	0.0482	0.2903
chr13	115169878	4762482	0.0414	0.2633
chr14	107349540	4279154	0.0399	0.266
chr15	102531392	3790321	0.037	0.2439
chr16	90354753	4943776	0.0547	0.9223
chr17	81195210	3316634	0.0408	0.3791
chr18	78077248	4052849	0.0519	0.7292
chr19	59128983	2165842	0.0366	0.6549
chr20	63025520	2729971	0.0433	0.2952
chr21	48129895	1954828	0.0406	0.3464
chr22	51304566	1282092	0.025	0.2168
chrMT	16571	555998	33.5525	11.4373
chrX	155270560	4186725	0.027	0.2325

chrY	59373566	2088707	0.0352	0.8081
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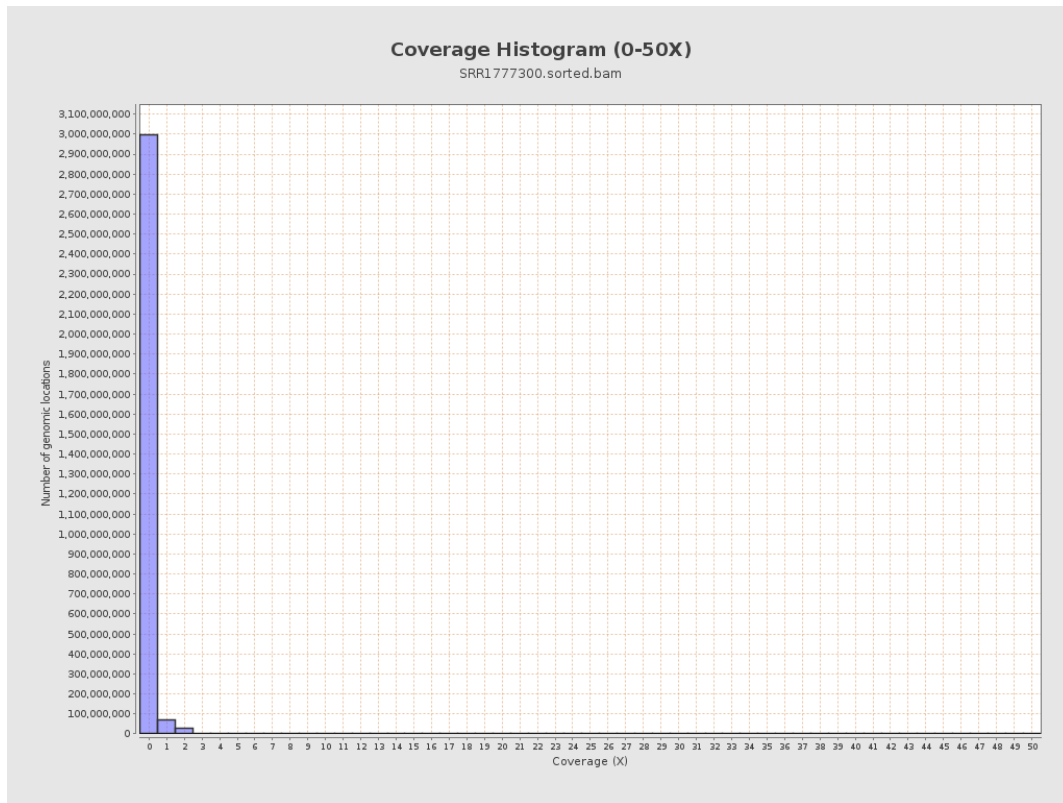
3. Results : Coverage across reference



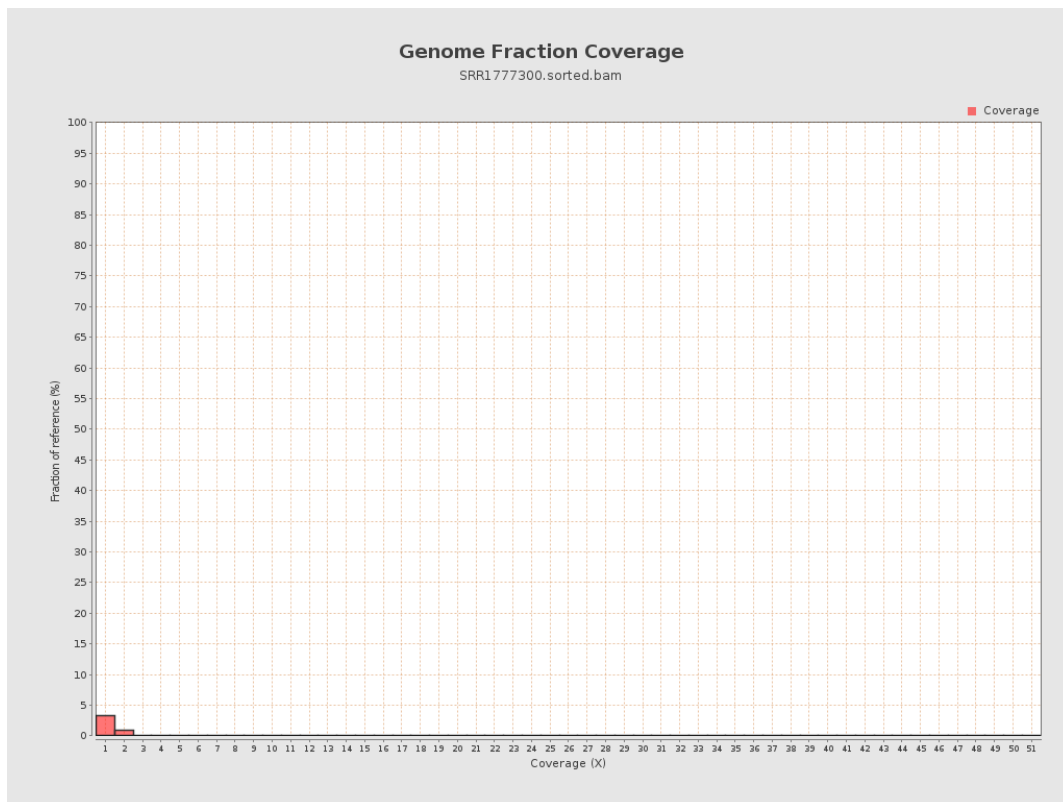
4. Results : Coverage Histogram



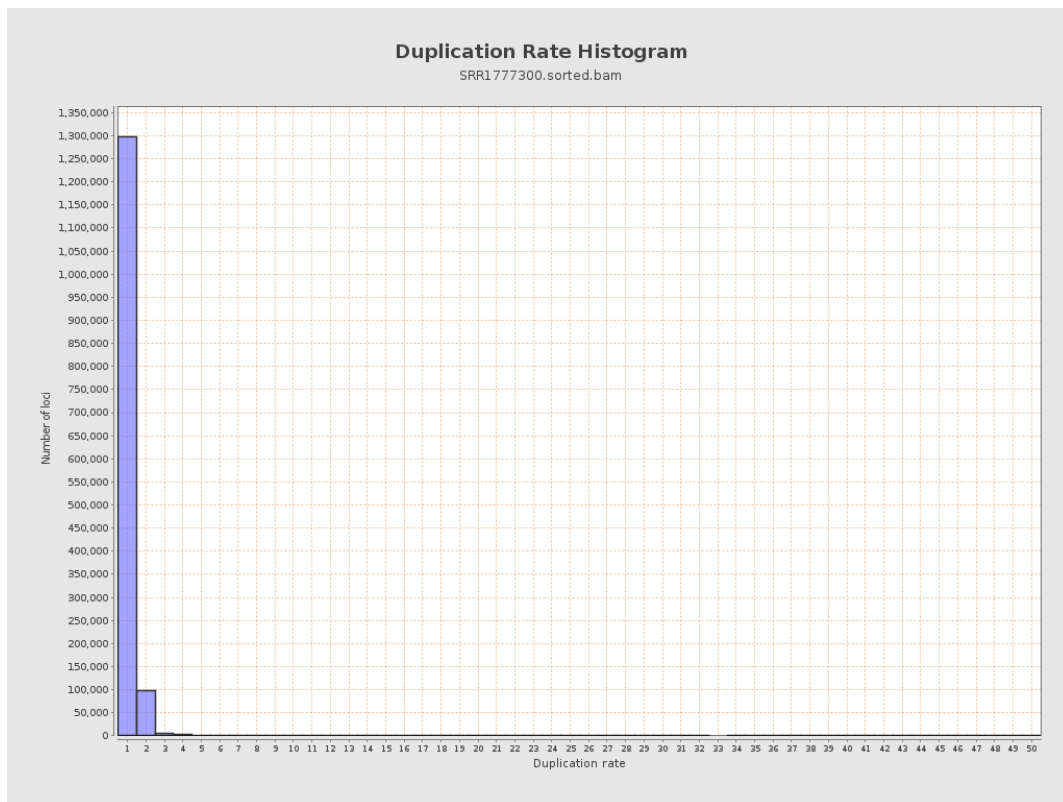
5. Results : Coverage Histogram (0-50X)



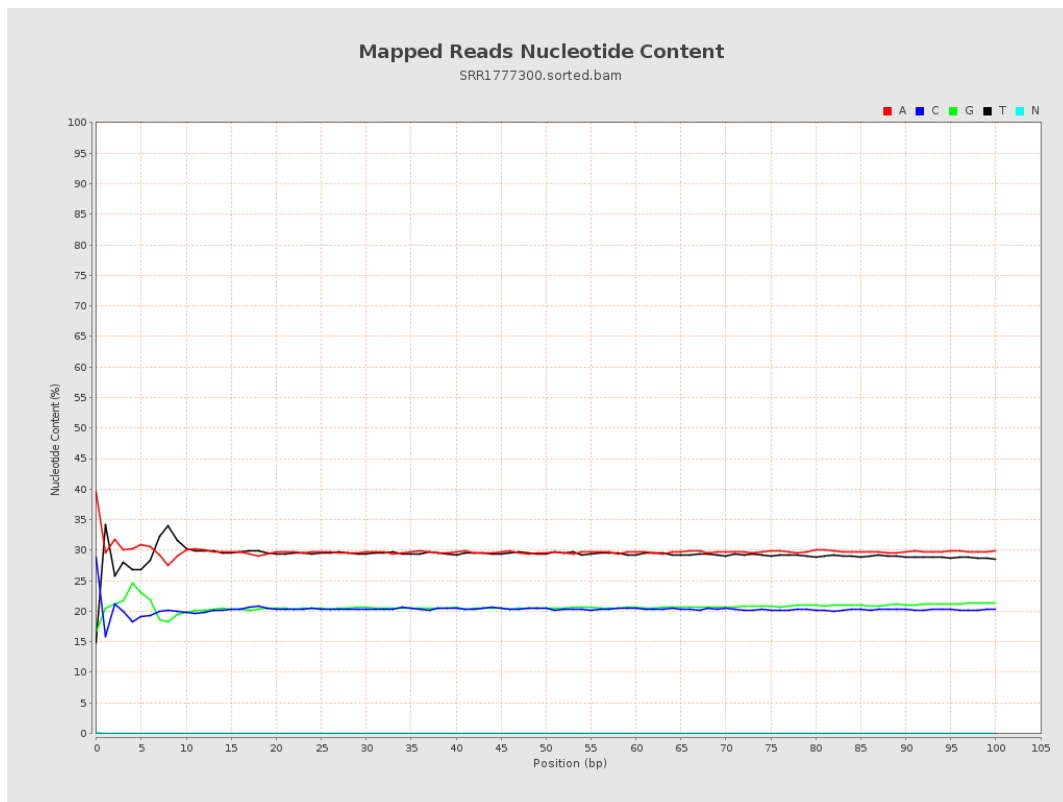
6. Results : Genome Fraction Coverage



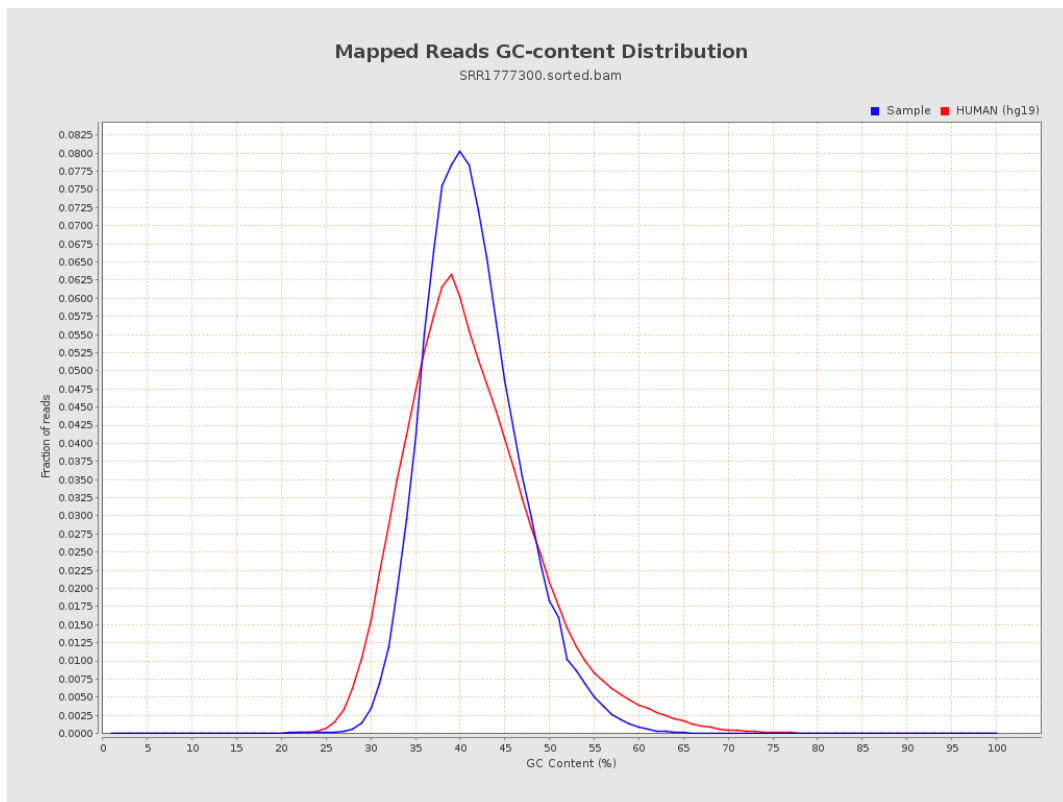
7. Results : Duplication Rate Histogram



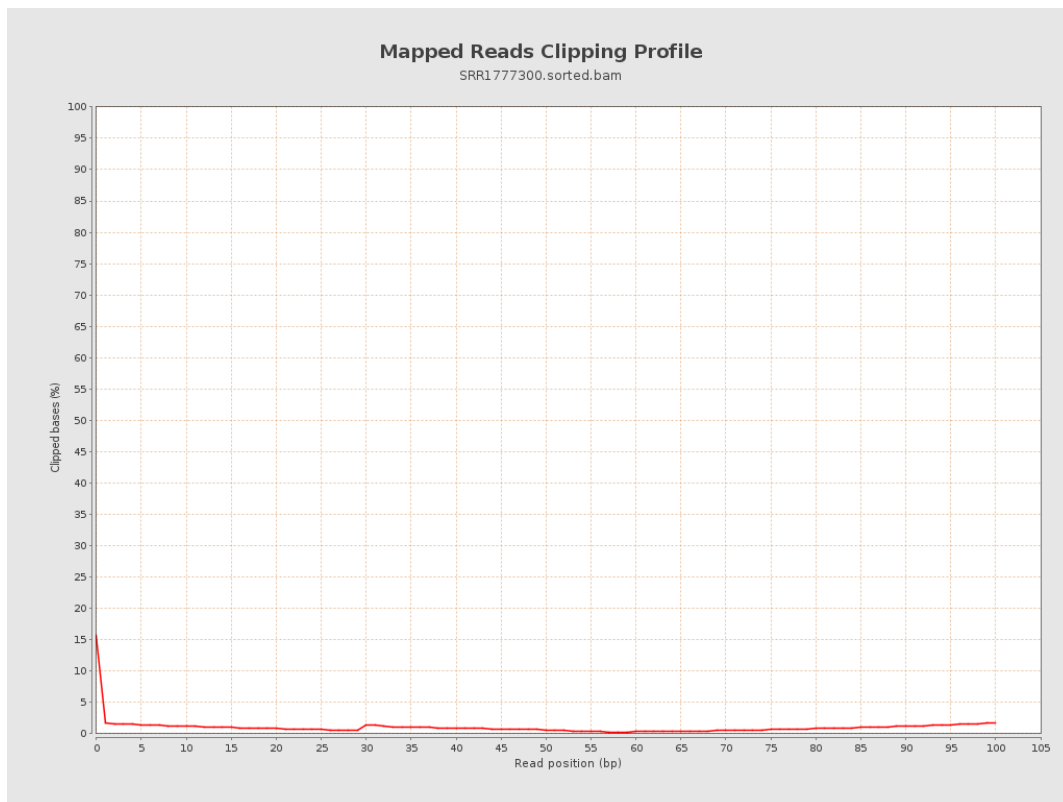
8. Results : Mapped Reads Nucleotide Content



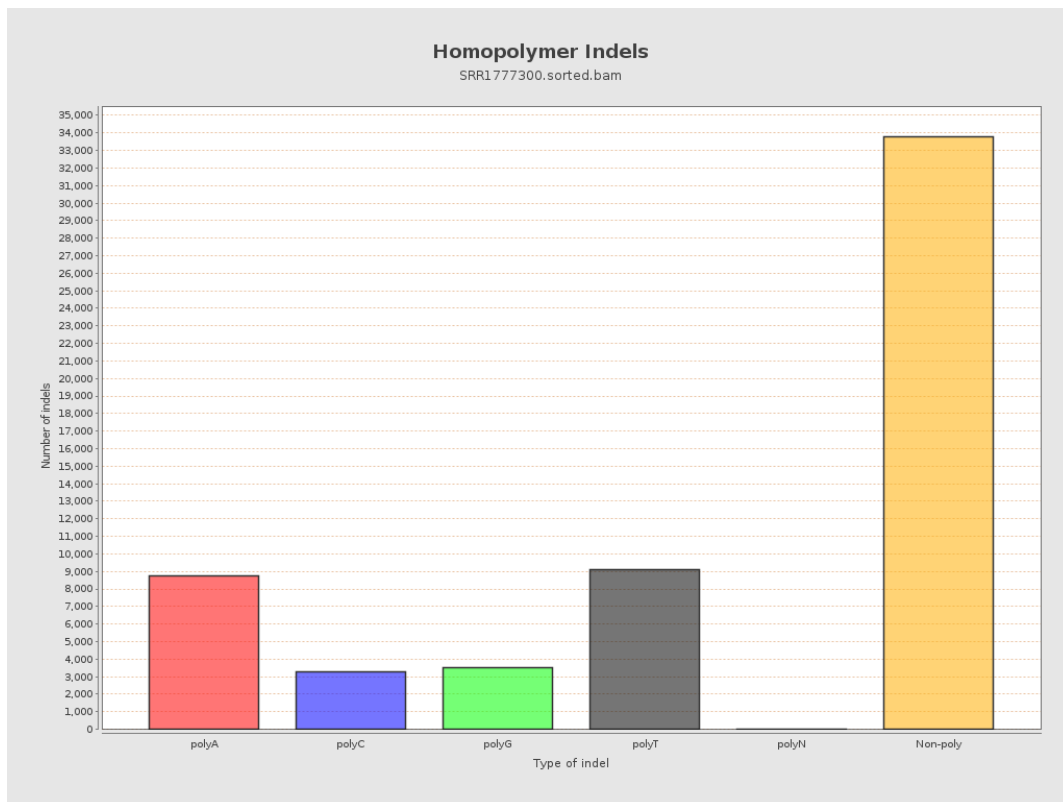
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



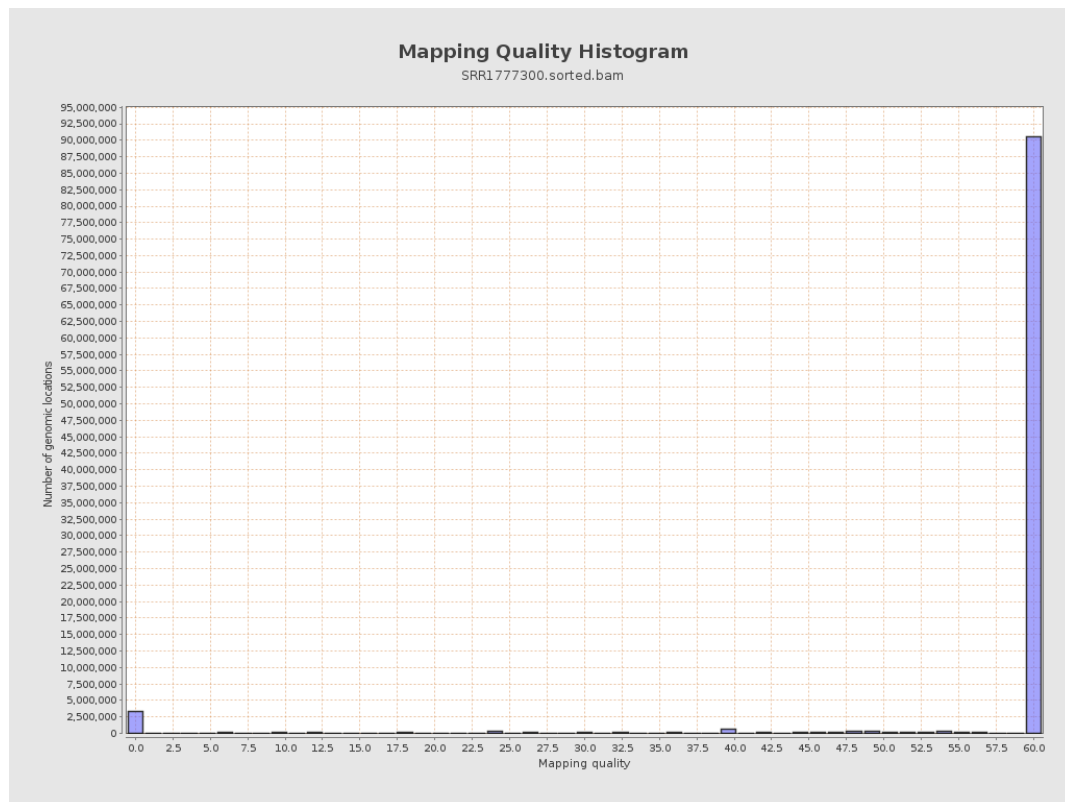
11. Results : Homopolymer Indels



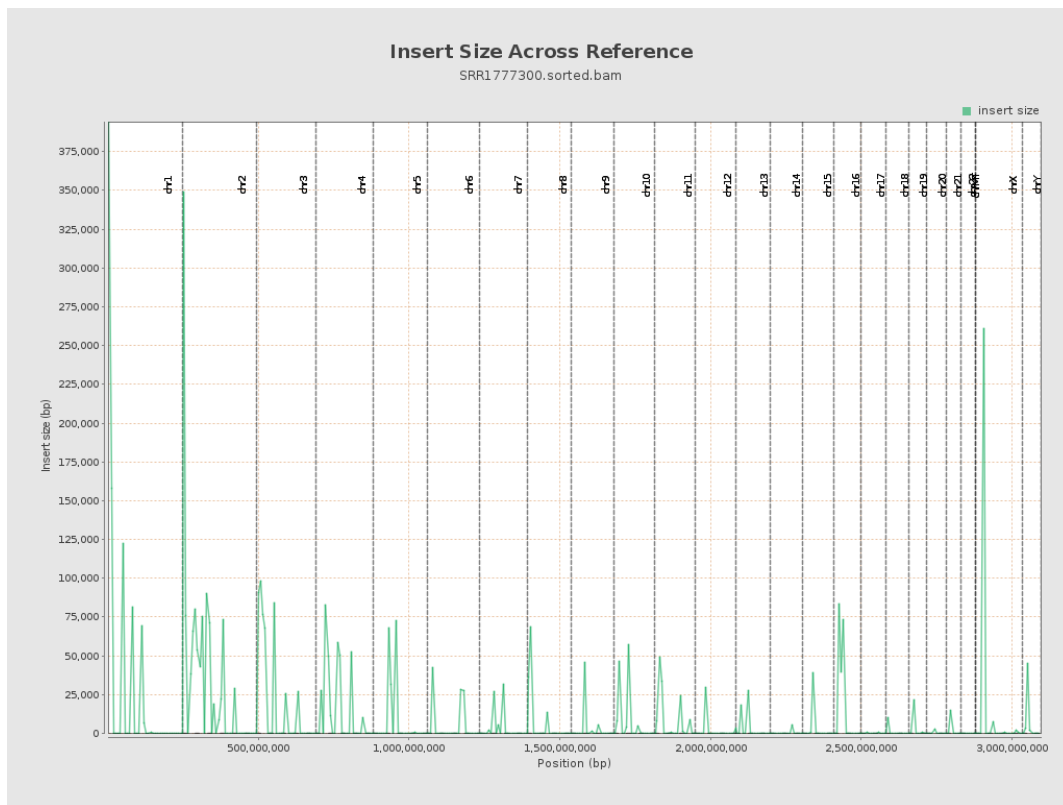
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

