Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 13:33:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777303.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_SRR1777303 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777303_1.fastq.gz SRR1777303_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 13:33:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777303.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	76,362,272
Mapped reads	74,768,497 / 97.91%
Unmapped reads	1,593,775 / 2.09%
Mapped paired reads	74,768,497 / 97.91%
Mapped reads, first in pair	37,495,668 / 49.1%
Mapped reads, second in pair	37,272,829 / 48.81%
Mapped reads, both in pair	74,261,680 / 97.25%
Mapped reads, singletons	506,817 / 0.66%
Secondary alignments	0
Supplementary alignments	3,249,385 / 4.26%
Read min/max/mean length	30 / 101 / 102.76
Duplicated reads (estimated)	17,151,007 / 22.46%
Duplication rate	12.38%
Clipped reads	24,093,744 / 31.55%

2.2. ACGT Content

Number/percentage of A's	2,083,617,584 / 29.07%
Number/percentage of C's	1,503,570,258 / 20.97%
Number/percentage of T's	2,041,638,632 / 28.48%
Number/percentage of G's	1,539,799,910 / 21.48%
Number/percentage of N's	116,346 / 0%

GC Percentage	42.45%

2.3. Coverage

Mean	2.3171
Standard Deviation	41.3661

2.4. Mapping Quality

Mean Mapping Quality	52.45

2.5. Insert size

Mean	139,057.13
Standard Deviation	3,541,603.44
P25/Median/P75	109 / 156 / 220

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	56,484,216
Insertions	2,014,321
Mapped reads with at least one insertion	2.57%
Deletions	1,421,154
Mapped reads with at least one deletion	1.79%
Homopolymer indels	38.02%

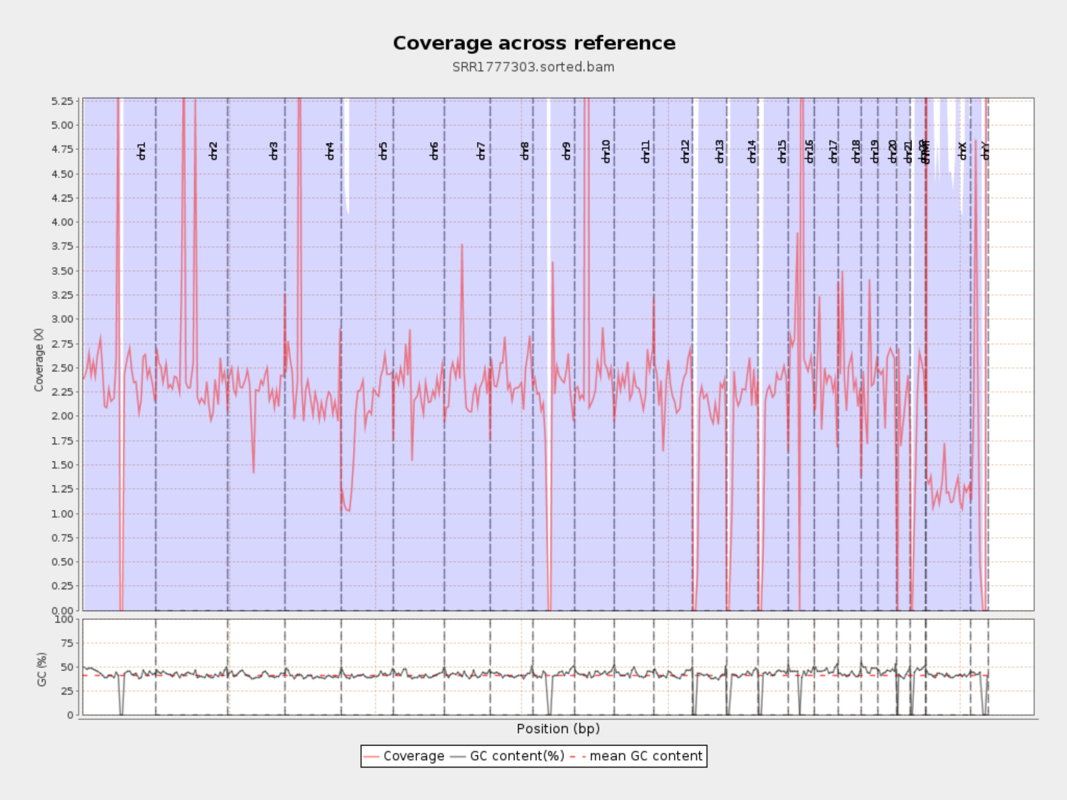
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

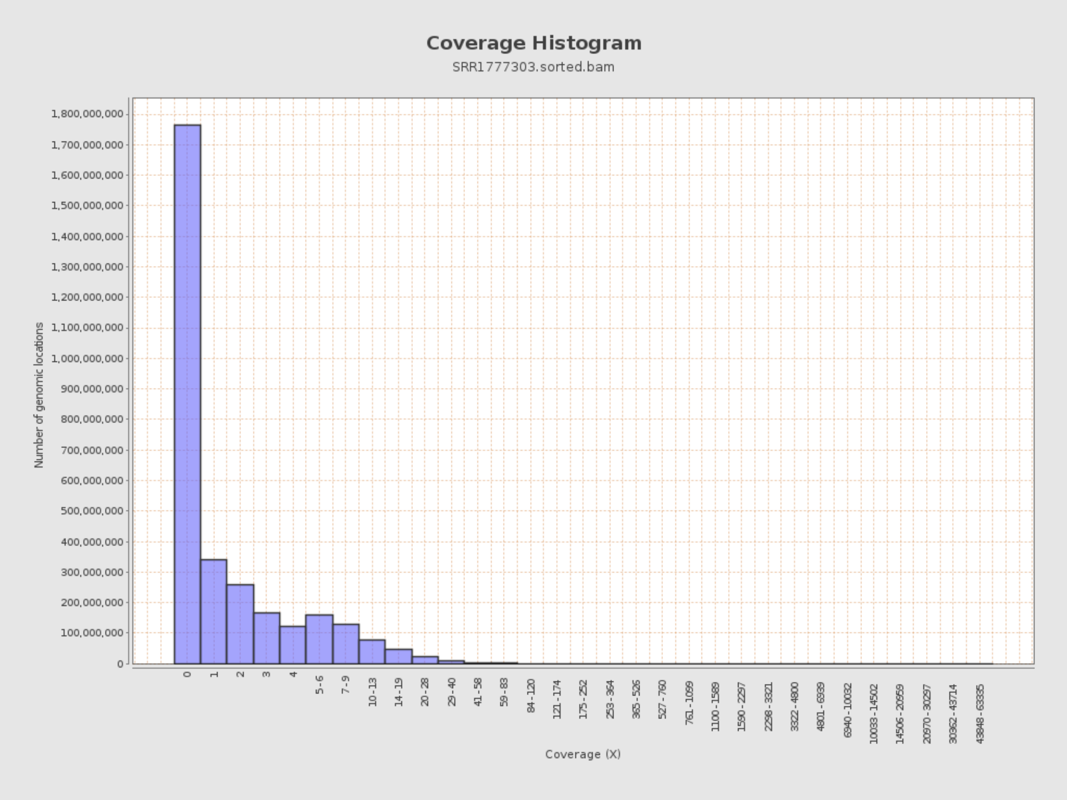
		bases	**coverage**	**deviation**
chr1	249250621	588537246	2.3612	64.5406
chr2	243199373	625821862	2.5733	46.5605
chr3	198022430	451259809	2.2788	13.5306
chr4	191154276	471247201	2.4653	37.6832
chr5	180915260	358900100	1.9838	7.6745
chr6	171115067	394806846	2.3073	11.2039
chr7	159138663	376099786	2.3633	25.9172
chr8	146364022	354453727	2.4217	18.8494
chr9	141213431	295132849	2.09	29.6812
chr10	135534747	428714523	3.1631	118.8048
chr11	135006516	316638212	2.3454	11.672
chr12	133851895	308989445	2.3084	6.4918
chr13	115169878	208345504	1.809	4.991
chr14	107349540	205795844	1.9171	8.7887
chr15	102531392	191297653	1.8657	4.901
chr16	90354753	281203833	3.1122	52.7368
chr17	81195210	192551981	2.3715	14.2328
chr18	78077248	195522979	2.5042	35.8611
chr19	59128983	139531011	2.3598	34.7598
chr20	63025520	153883997	2.4416	11.1606
chr21	48129895	94767130	1.969	15.2366
chr22	51304566	87674889	1.7089	9.5088
chrMT	16571	77248191	4,661.6493	1,142.3823
chrX	155270560	193106599	1.2437	7.1918

chrY	59373566	181646637	3.0594	71.6587

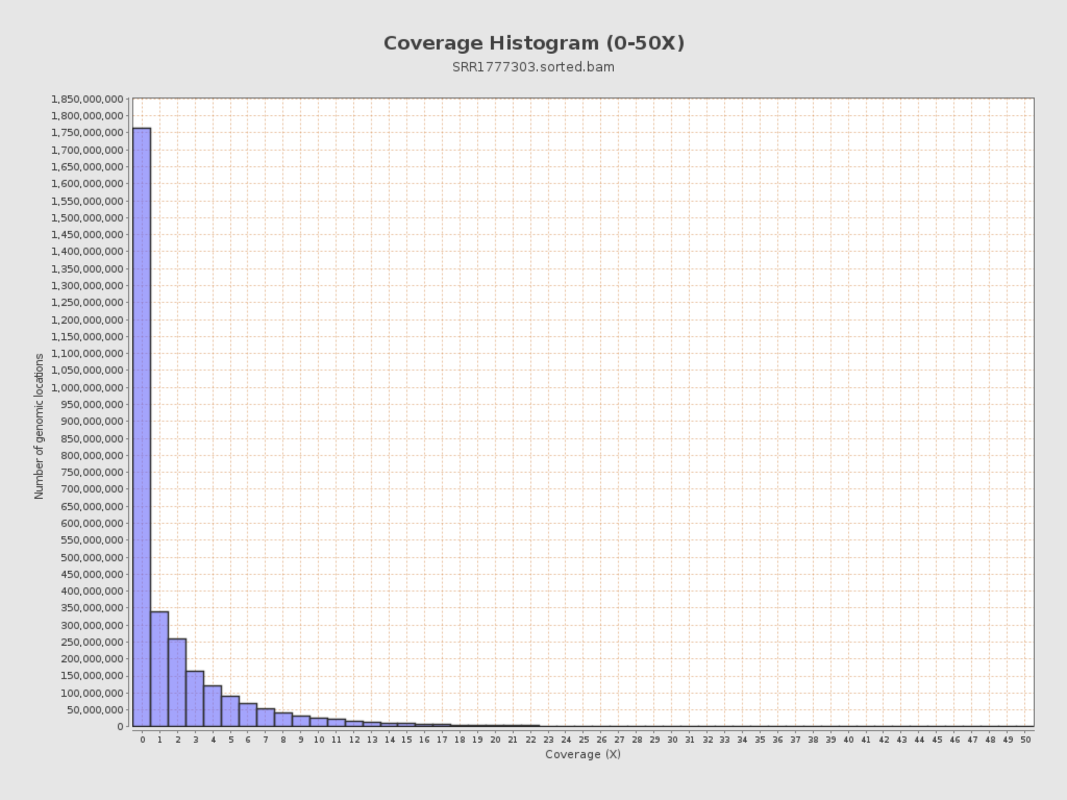
3. Results : Coverage across reference



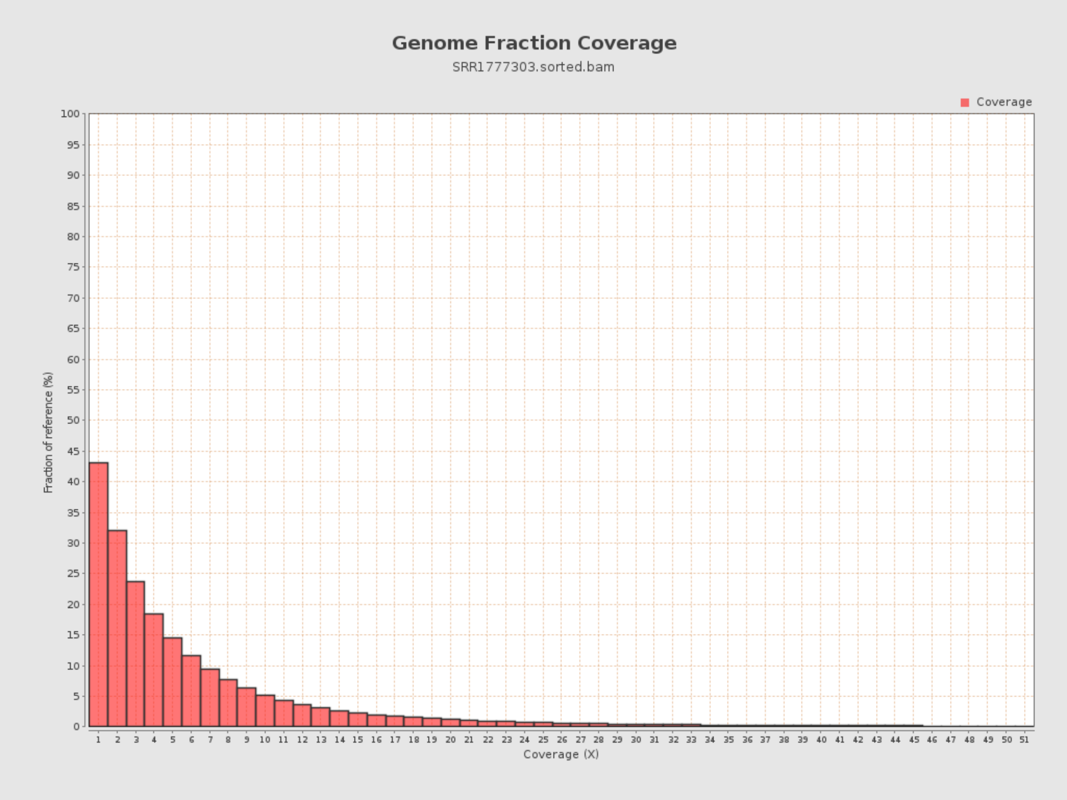
4. Results : Coverage Histogram



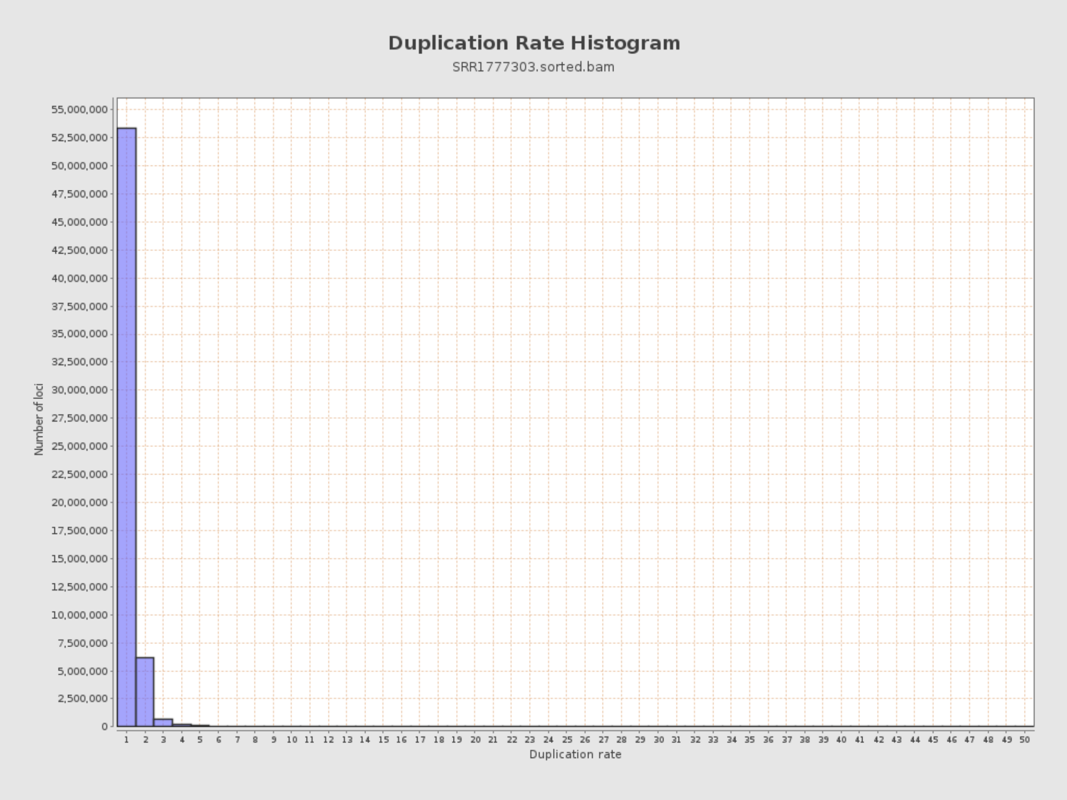
5. Results : Coverage Histogram (0-50X)



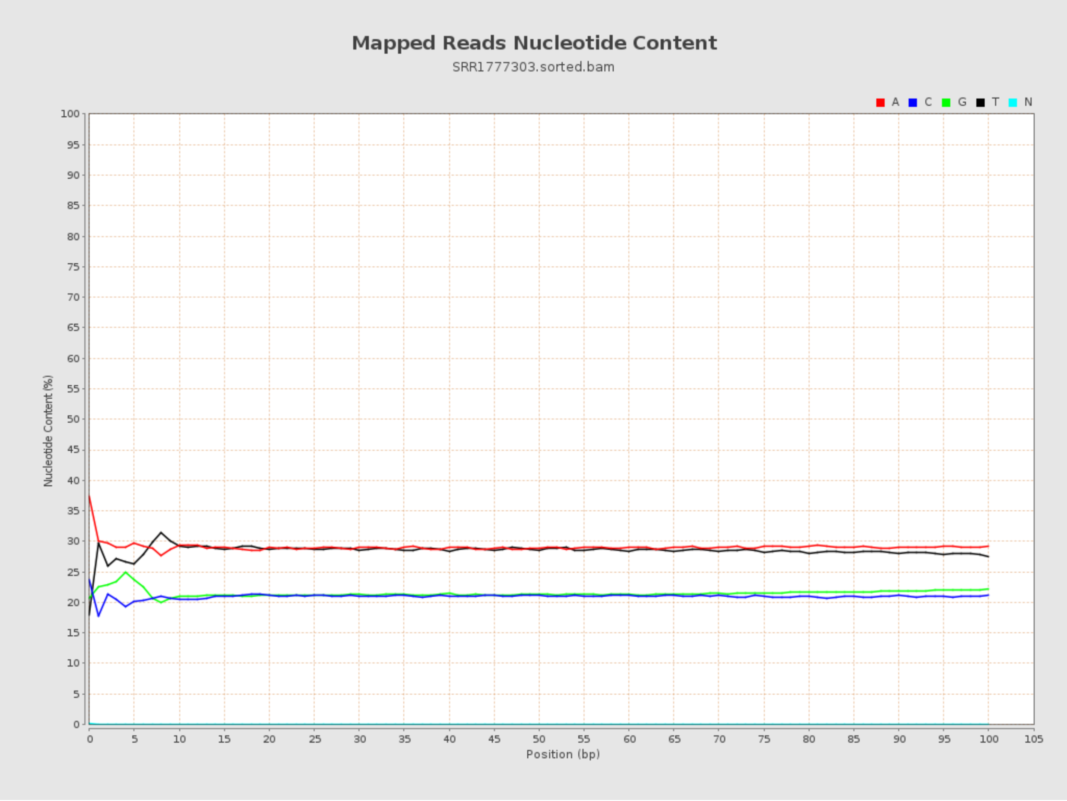
6. Results : Genome Fraction Coverage



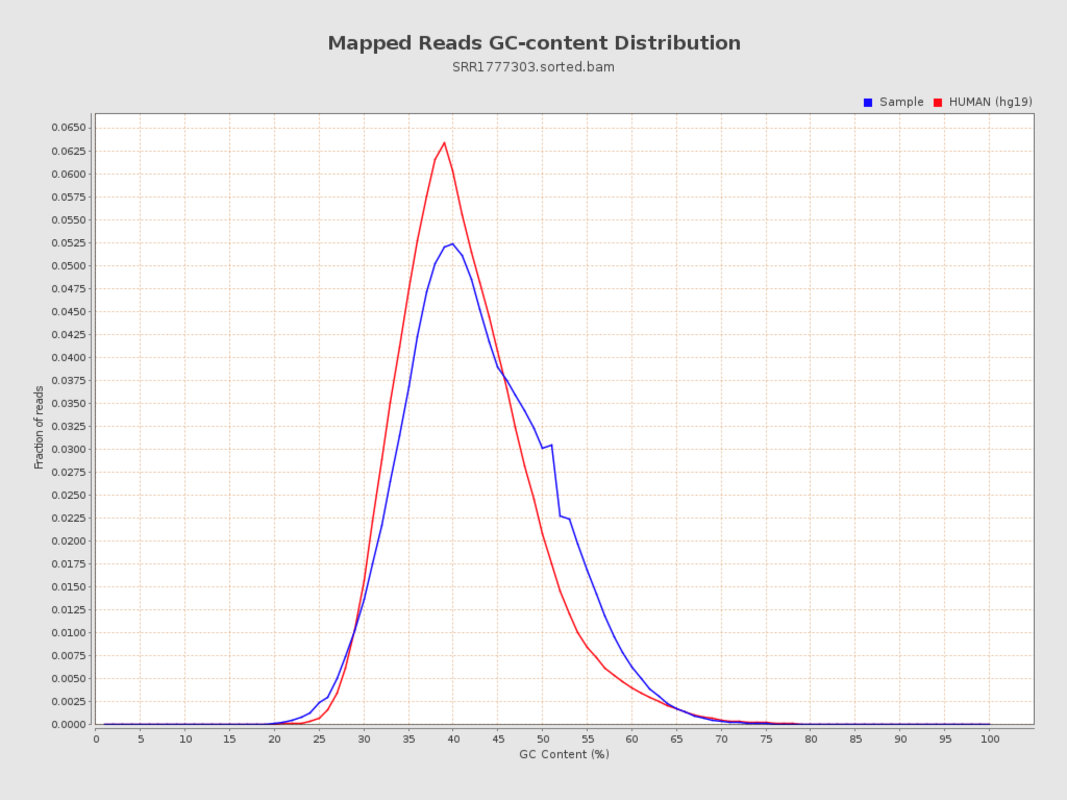
7. Results : Duplication Rate Histogram



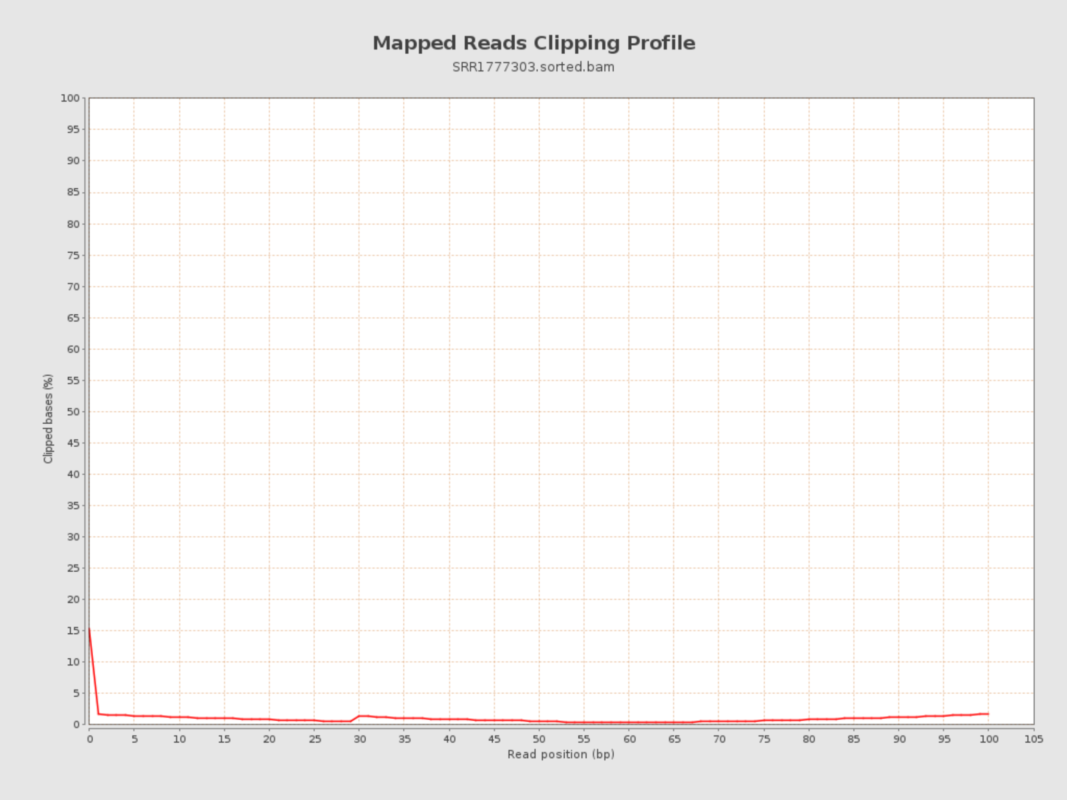
8. Results : Mapped Reads Nucleotide Content



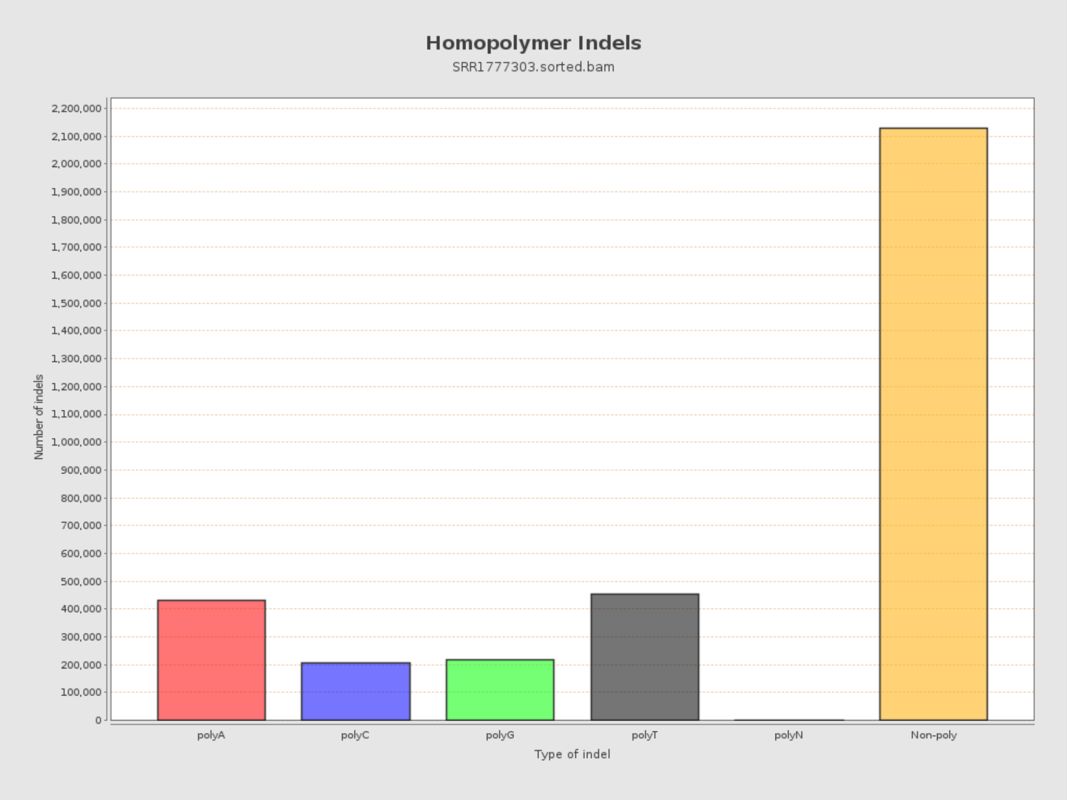
9. Results : Mapped Reads GC-content Distribution



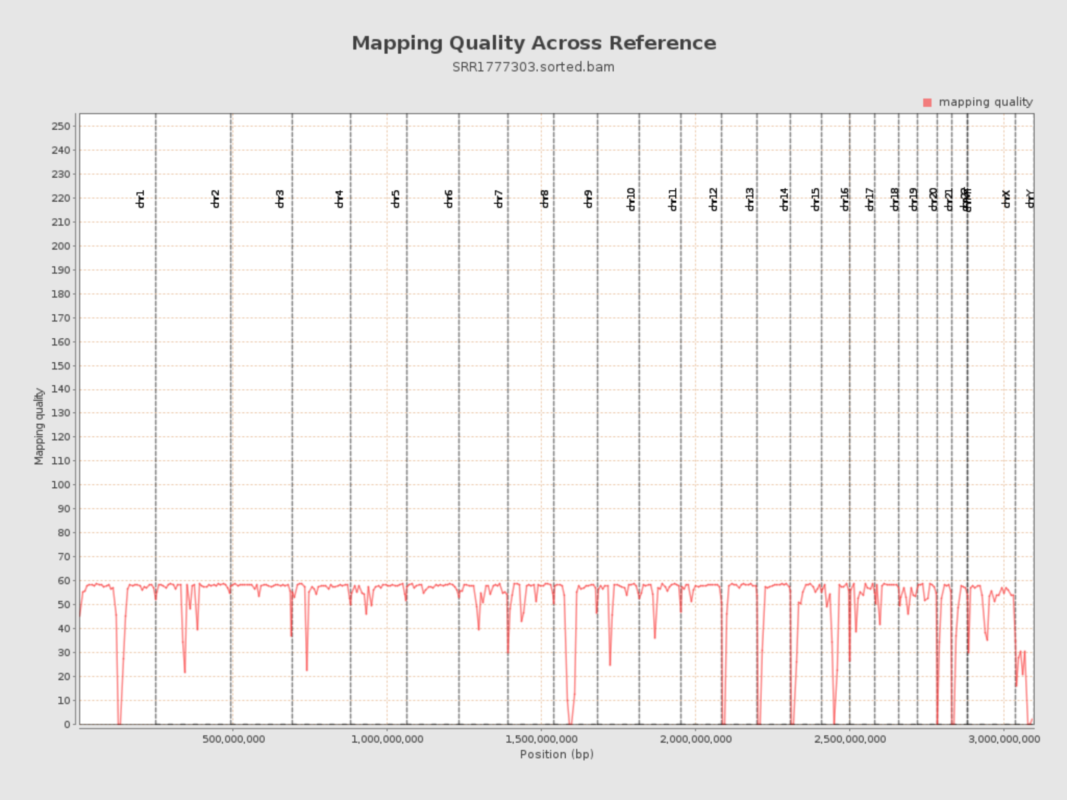
10. Results : Mapped Reads Clipping Profile



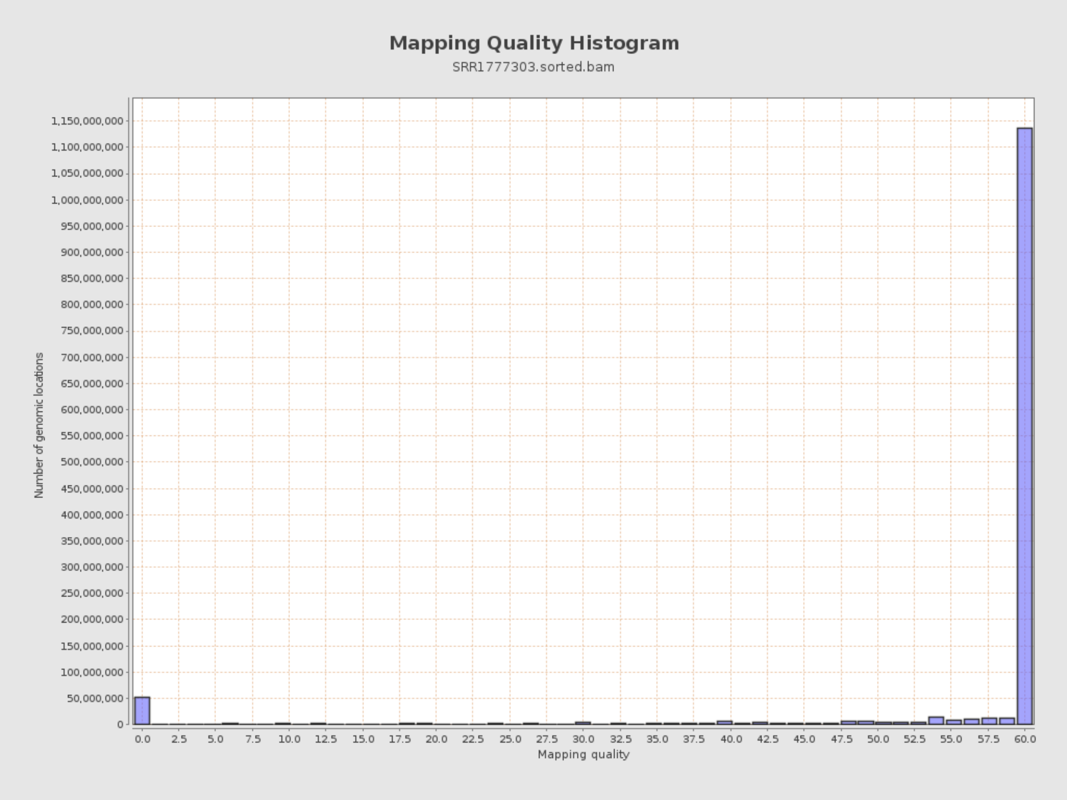
11. Results : Homopolymer Indels



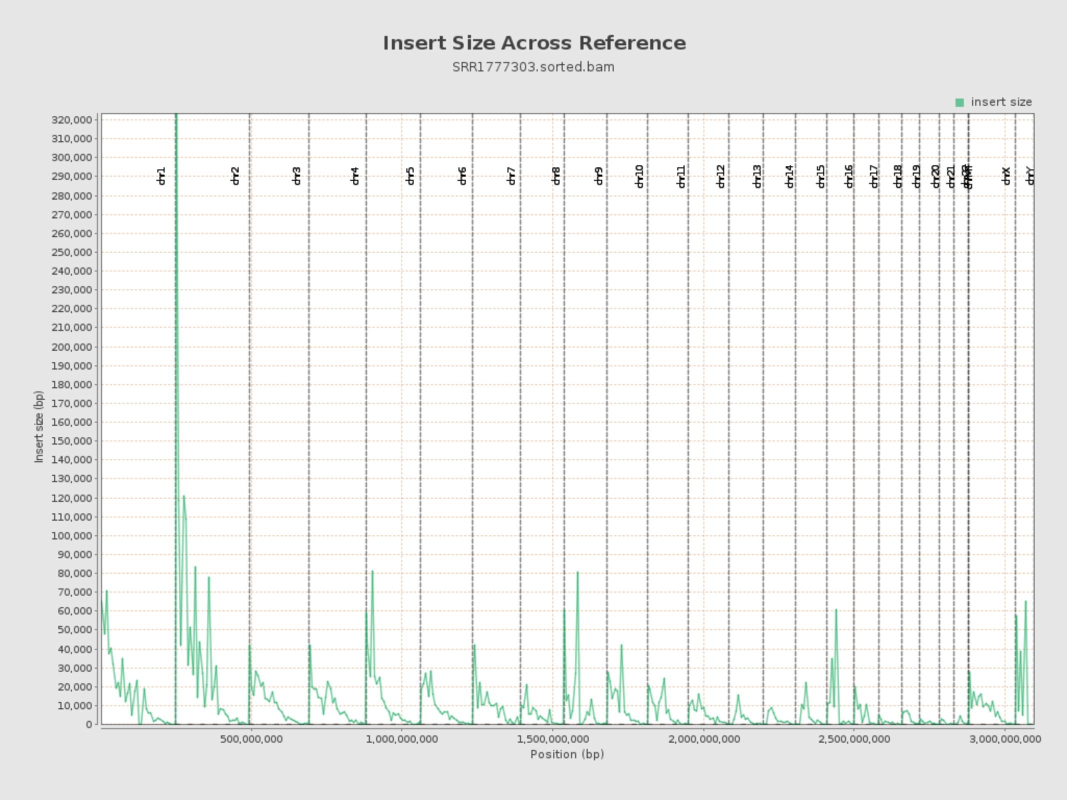
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram