Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 06:58:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777304.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_SRR1777304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777304_1.fastq.gz SRR1777304_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 06:58:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	215,557,934
Mapped reads	210,317,445 / 97.57%
Unmapped reads	5,240,489 / 2.43%
Mapped paired reads	210,317,445 / 97.57%
Mapped reads, first in pair	105,513,852 / 48.95%
Mapped reads, second in pair	104,803,593 / 48.62%
Mapped reads, both in pair	209,393,030 / 97.14%
Mapped reads, singletons	924,415 / 0.43%
Secondary alignments	0
Supplementary alignments	767,342 / 0.36%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	47,962,487 / 22.25%
Duplication rate	20.85%
Clipped reads	41,440,908 / 19.22%

2.2. ACGT Content

Number/percentage of A's	5,642,206,972 / 27.79%
Number/percentage of C's	4,497,970,402 / 22.16%
Number/percentage of T's	5,538,152,112 / 27.28%
Number/percentage of G's	4,621,215,206 / 22.76%
Number/percentage of N's	2,255,106 / 0.01%

GC Percentage	44.92%

2.3. Coverage

Mean	6.5624
Standard Deviation	17.8051

2.4. Mapping Quality

Mean Mapping Quality	54.12

2.5. Insert size

Mean	84,199.05
Standard Deviation	2,949,933.27
P25/Median/P75	119 / 163 / 222

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	150,579,836
Insertions	3,291,409
Mapped reads with at least one insertion	1.54%
Deletions	9,622,993
Mapped reads with at least one deletion	4.47%
Homopolymer indels	54.16%

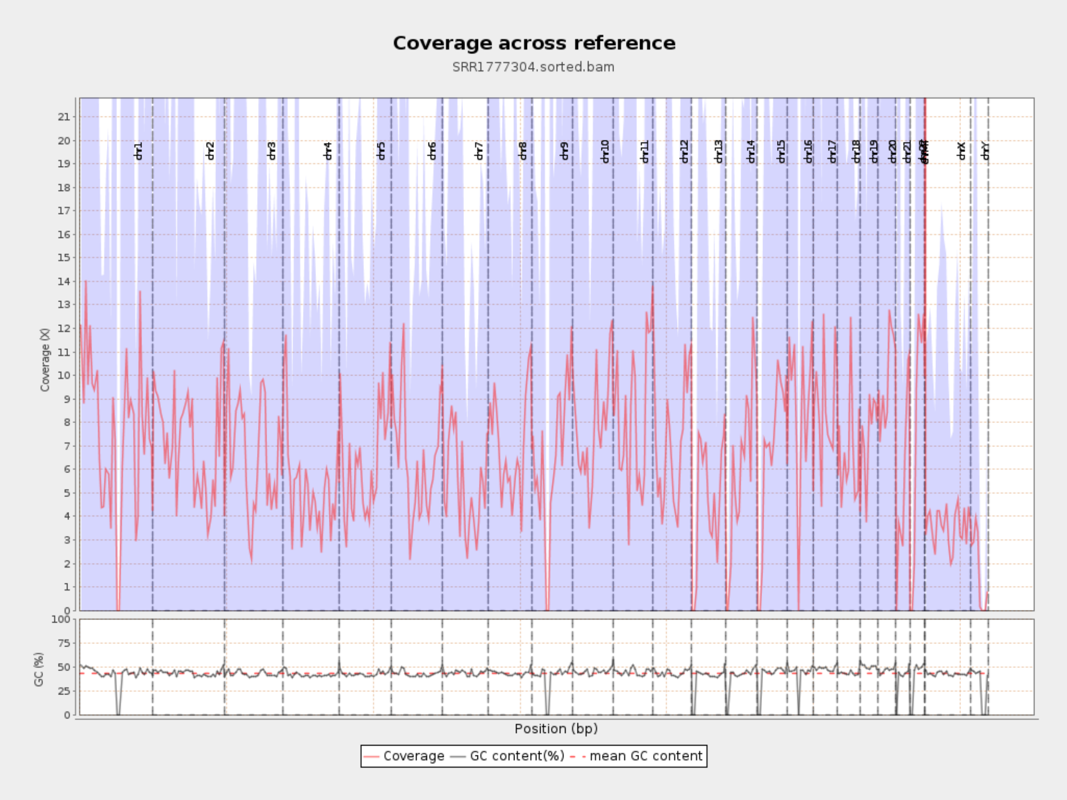
2.7. Chromosome stats

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

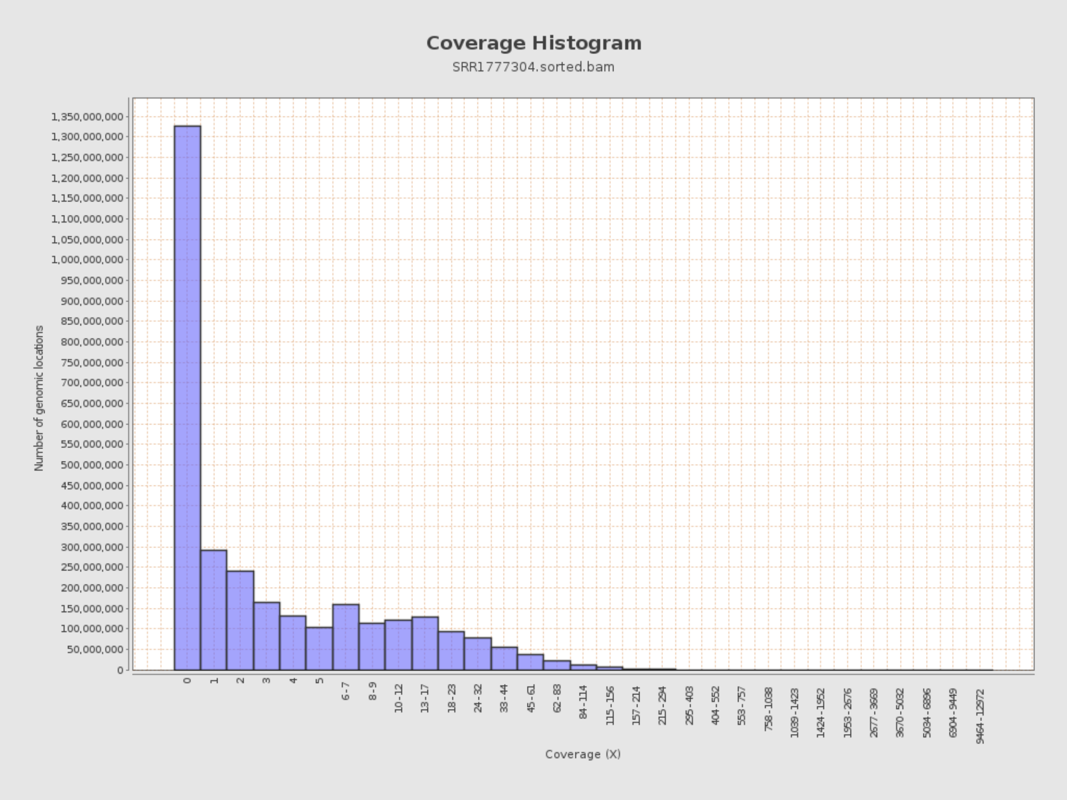
		bases	coverage	deviation
chr1	249250621	1895513598	7.6049	21.7336
chr2	243199373	1739185989	7.1513	21.6019
chr3	198022430	1326784135	6.7002	15.1701
chr4	191154276	998233158	5.2221	17.4989
chr5	180915260	1152324982	6.3694	14.5176
chr6	171115067	1096652748	6.4089	14.7448
chr7	159138663	852959051	5.3598	13.0739
chr8	146364022	1022003326	6.9826	16.1074
chr9	141213431	920150076	6.516	19.9259
chr10	135534747	1052372871	7.7646	18.314
chr11	135006516	1095651718	8.1155	18.7657
chr12	133851895	948975356	7.0897	16.2008
chr13	115169878	529057259	4.5937	12.1091
chr14	107349540	638883878	5.9514	14.9792
chr15	102531392	672284373	6.5569	15.9233
chr16	90354753	766074195	8.4785	22.7547
chr17	81195210	703800056	8.668	20.6425
chr18	78077248	527539346	6.7566	20.183
chr19	59128983	442836839	7.4893	18.9378
chr20	63025520	623649006	9.8952	20.7663
chr21	48129895	263249257	5.4696	30.8493
chr22	51304566	392312992	7.6467	19.3969
chrMT	16571	3889154	234.6964	181.09
chrX	155270560	550056325	3.5426	8.7444

chrY	59373566	100698200	1.696	11.6412

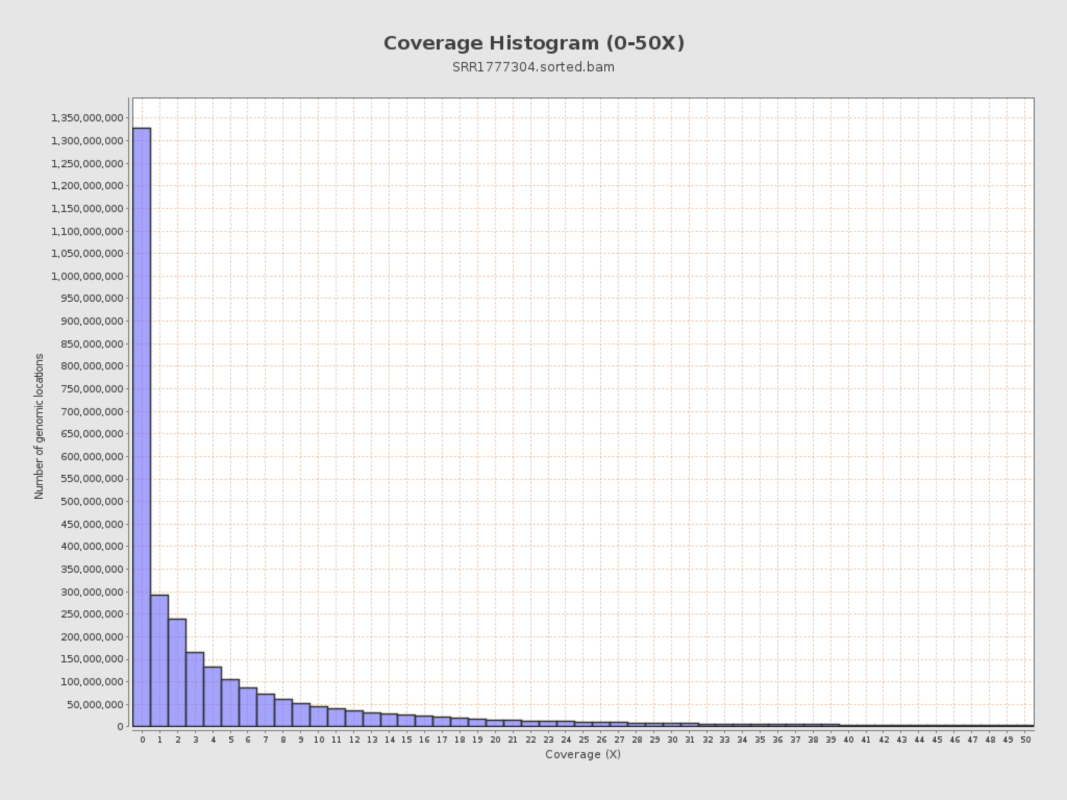
3. Results : Coverage across reference



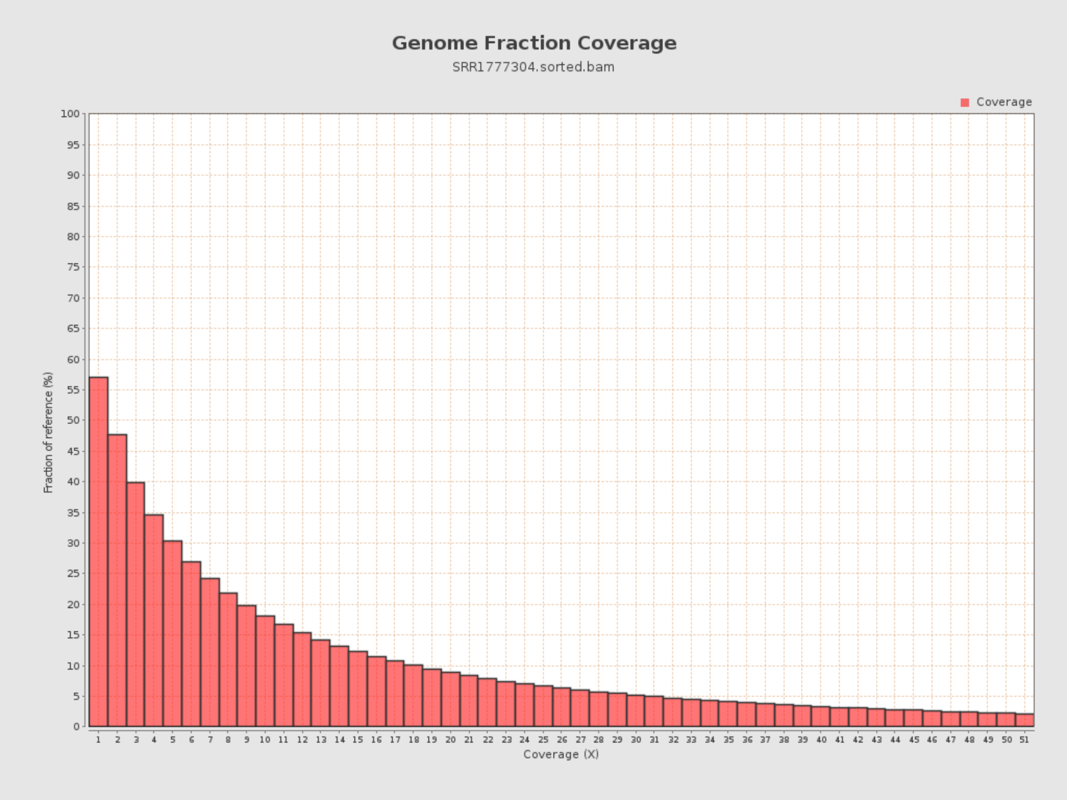
4. Results : Coverage Histogram



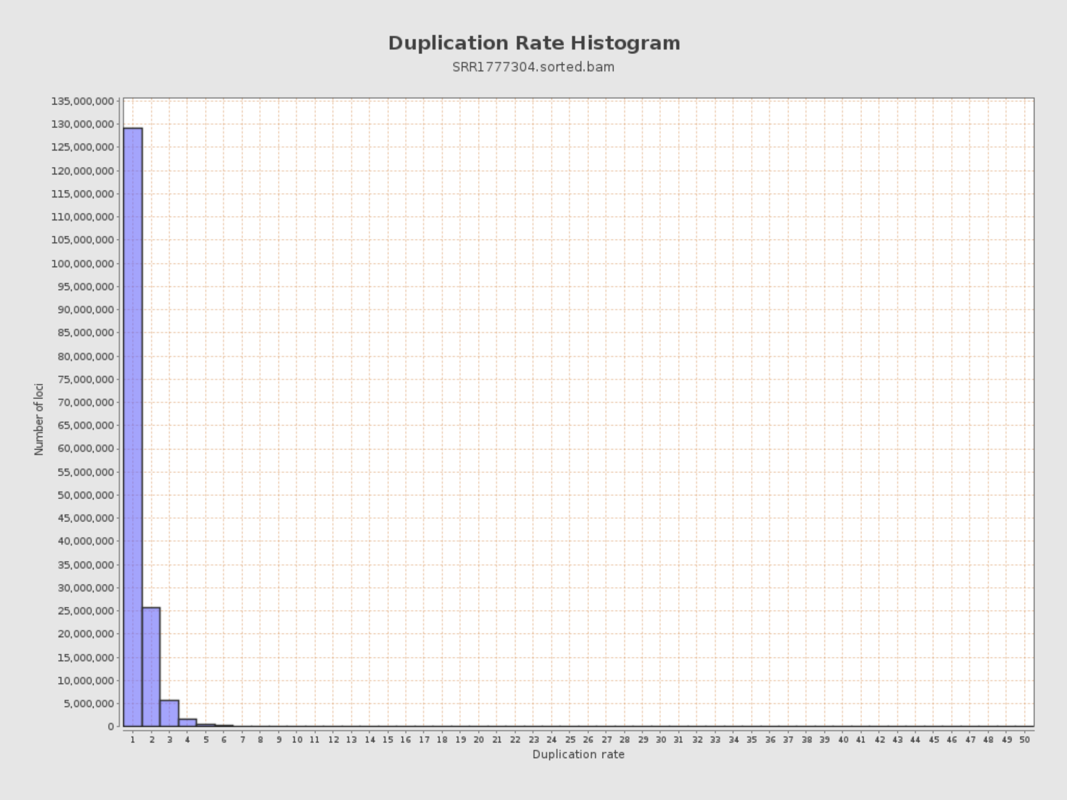
5. Results : Coverage Histogram (0-50X)



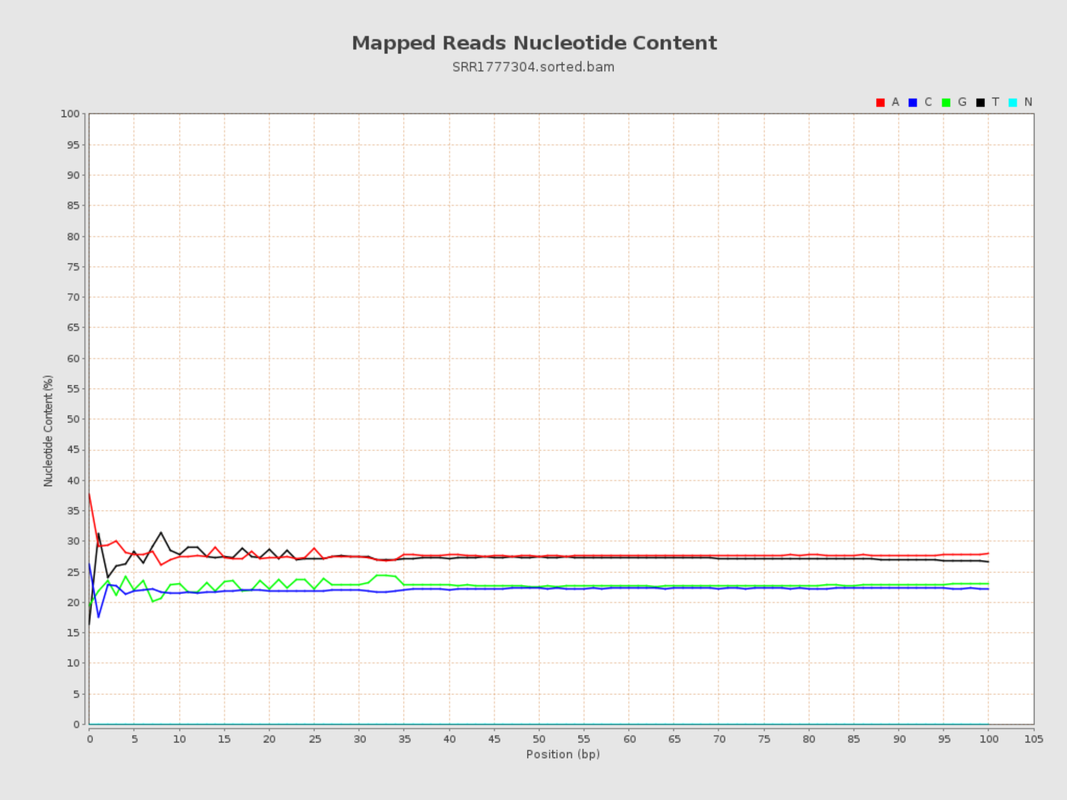
6. Results : Genome Fraction Coverage



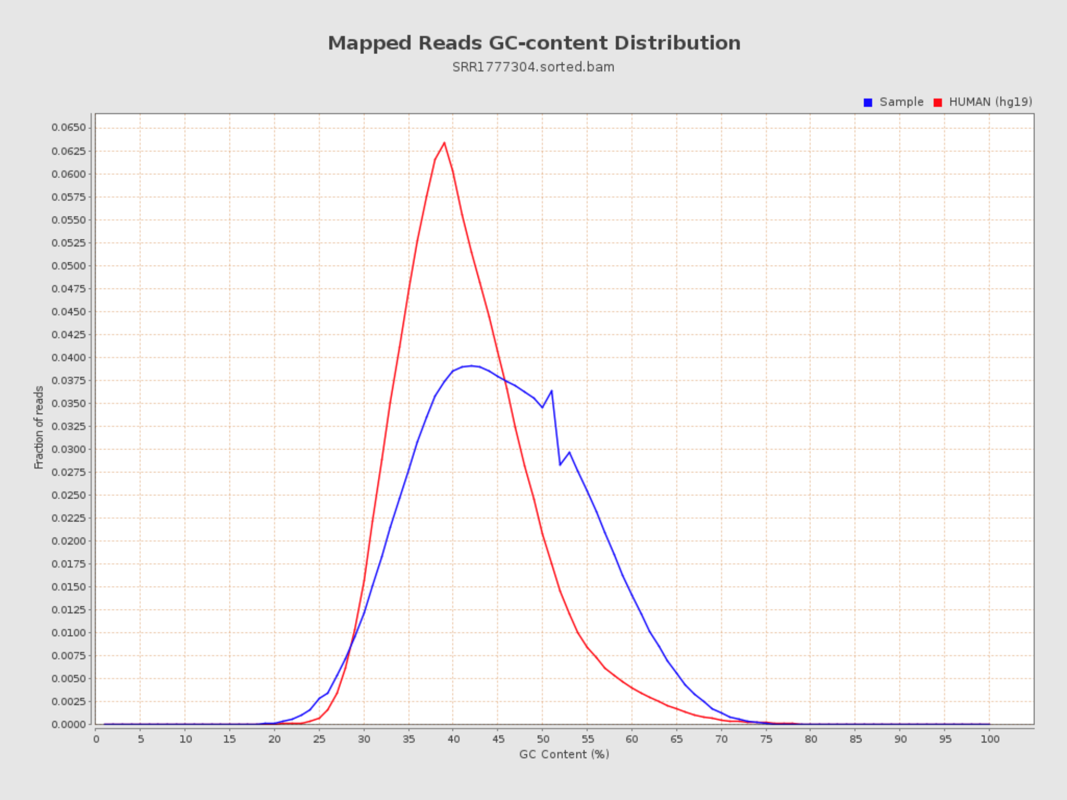
7. Results : Duplication Rate Histogram



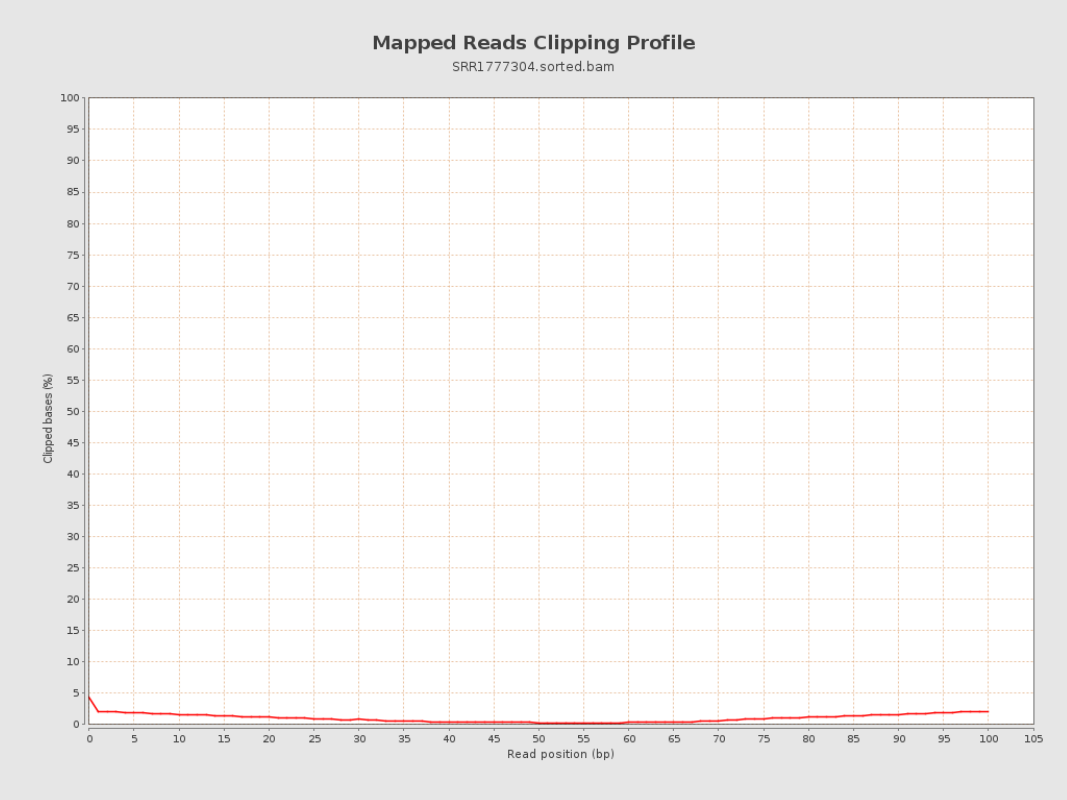
8. Results : Mapped Reads Nucleotide Content



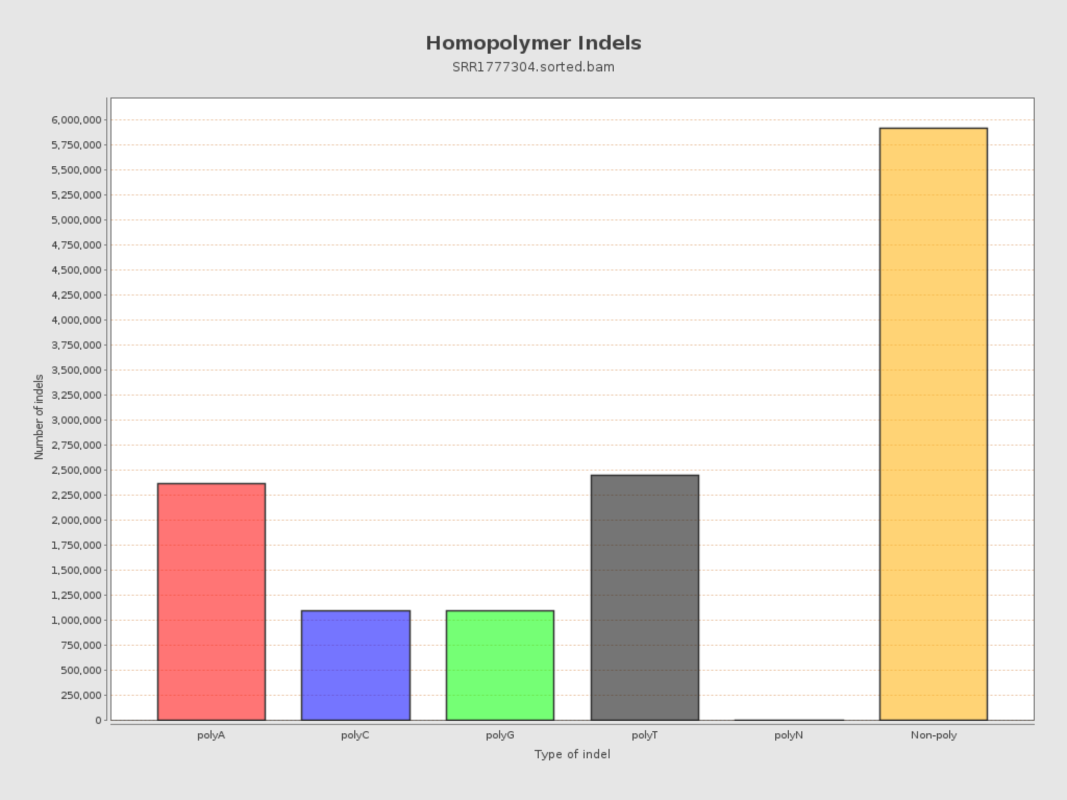
9. Results : Mapped Reads GC-content Distribution



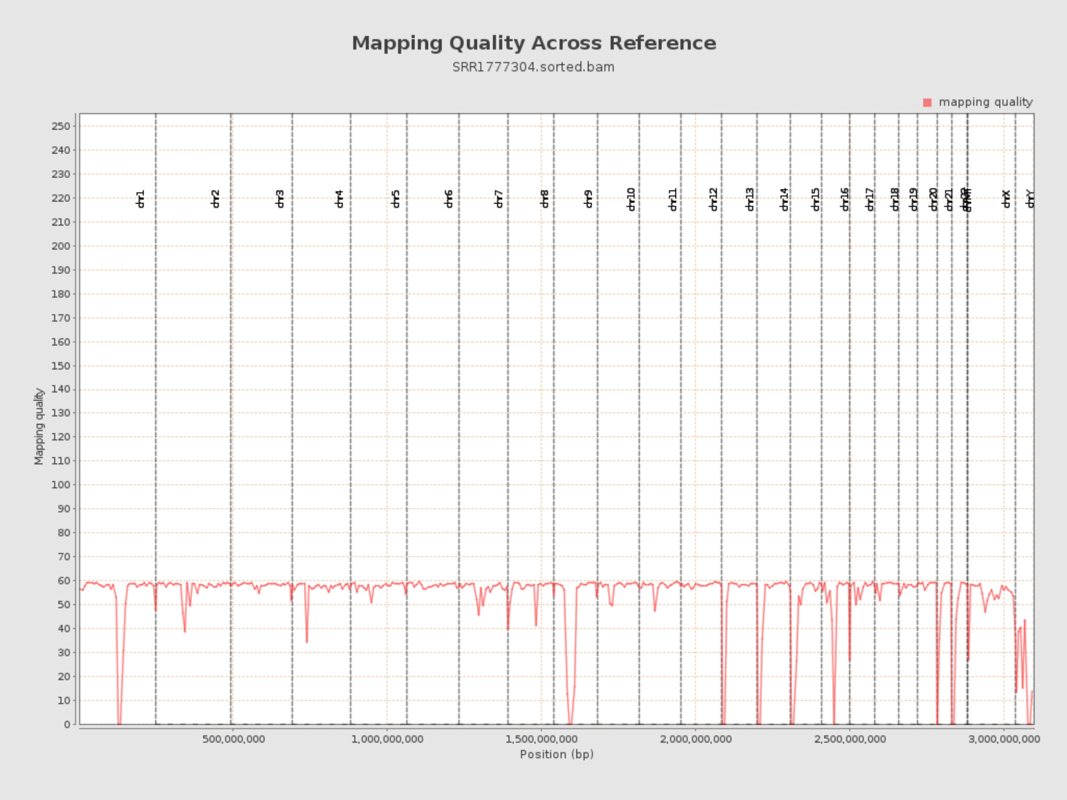
10. Results : Mapped Reads Clipping Profile



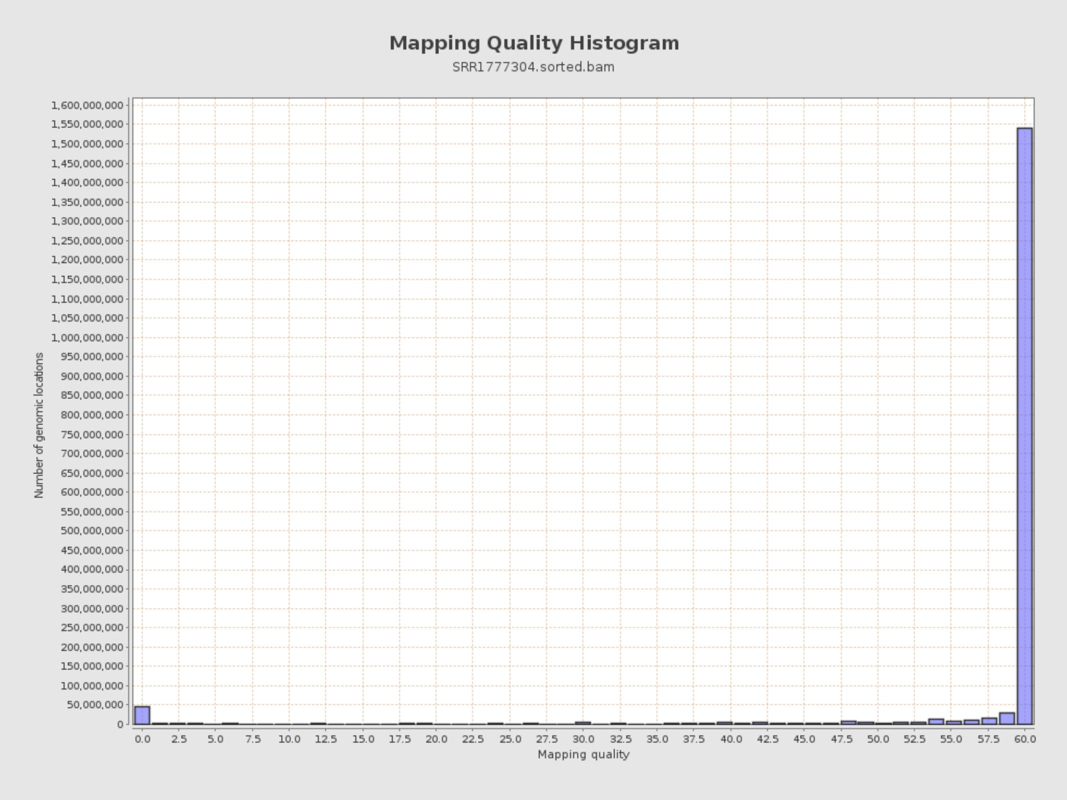
11. Results : Homopolymer Indels



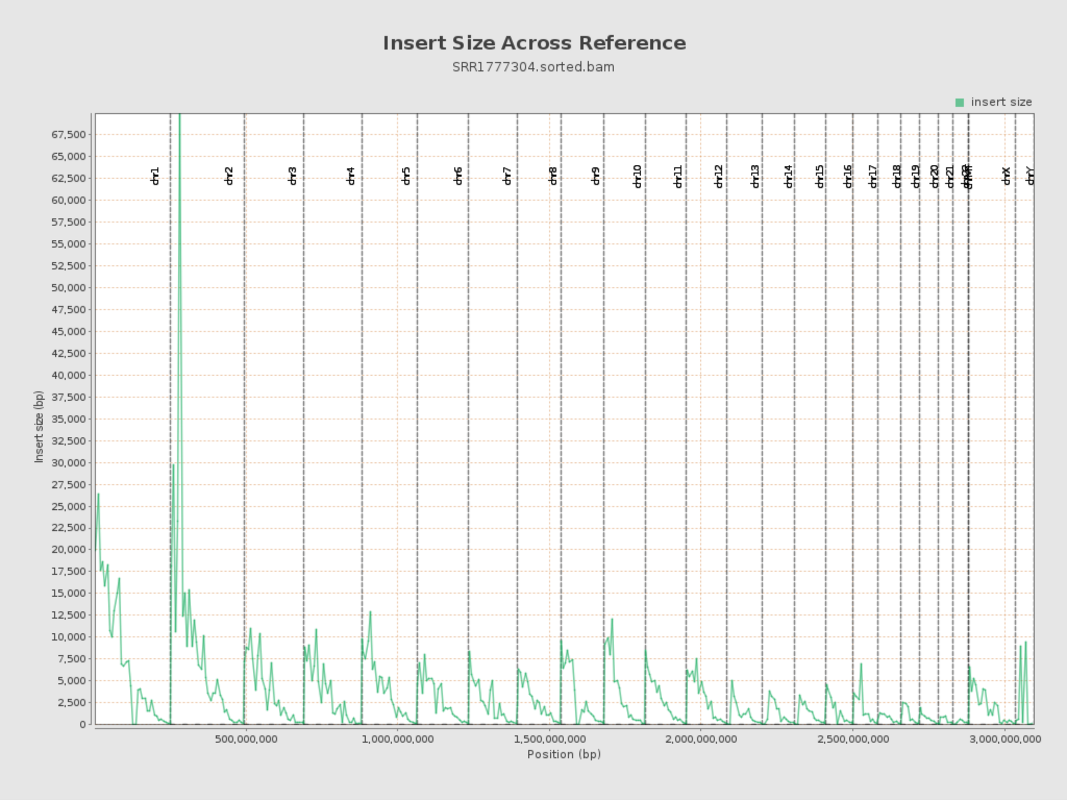
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram