Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 06:15:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777264.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_SRR1777264 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777264_1.fastq.gz SRR1777264_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 06:15:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777264.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,955,548
Mapped reads	3,788,672 / 95.78%
Unmapped reads	166,876 / 4.22%
Mapped paired reads	3,788,672 / 95.78%
Mapped reads, first in pair	1,901,387 / 48.07%
Mapped reads, second in pair	1,887,285 / 47.71%
Mapped reads, both in pair	3,763,538 / 95.15%
Mapped reads, singletons	25,134 / 0.64%
Secondary alignments	0
Supplementary alignments	73,202 / 1.85%
Read min/max/mean length	30 / 76 / 76.65
Duplicated reads (estimated)	79,038 / 2%
Duplication rate	1.95%
Clipped reads	531,592 / 13.44%

2.2. ACGT Content

Number/percentage of A's	84,140,257 / 29.77%
Number/percentage of C's	57,617,835 / 20.38%
Number/percentage of T's	82,368,758 / 29.14%
Number/percentage of G's	58,527,844 / 20.71%
Number/percentage of N's	16,556 / 0.01%

GC Percentage	41.09%

2.3. Coverage

Mean	0.0913
Standard Deviation	0.404

2.4. Mapping Quality

Mean Mapping Quality	52.61

2.5. Insert size

Mean	169,483.96
Standard Deviation	4,001,265.12
P25/Median/P75	115 / 157 / 214

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	1,530,885
Insertions	55,535
Mapped reads with at least one insertion	1.45%
Deletions	26,083
Mapped reads with at least one deletion	0.68%
Homopolymer indels	49.45%

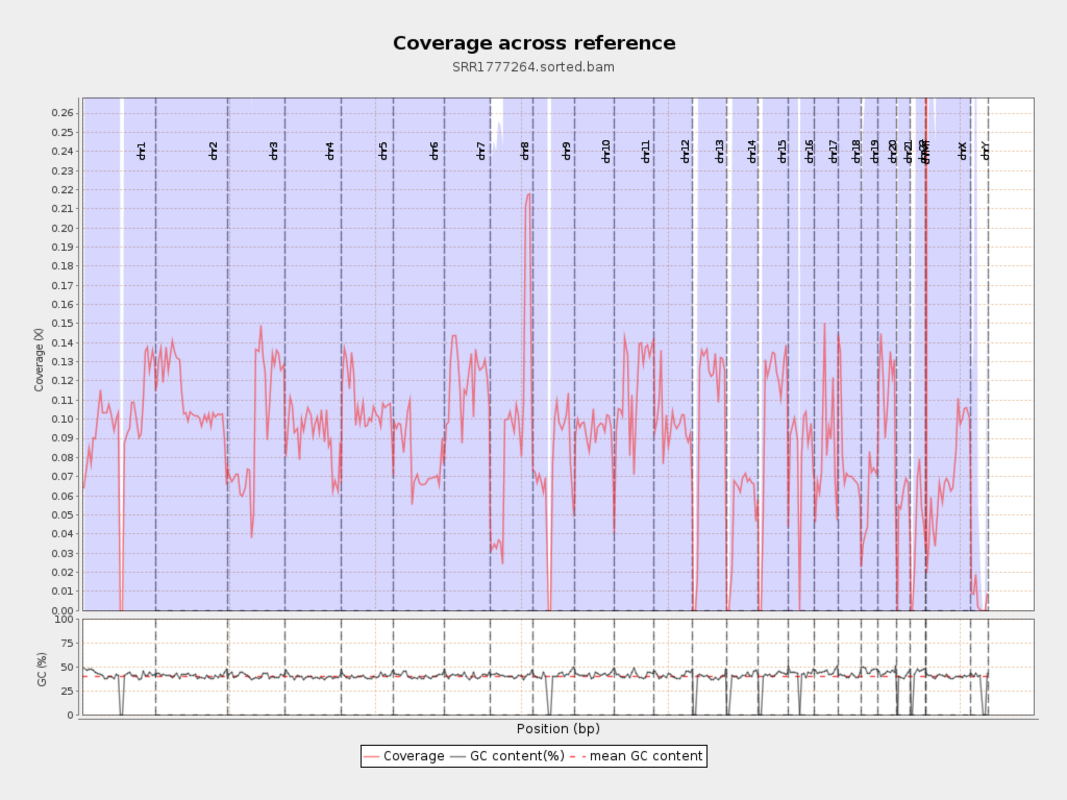
2.7. Chromosome stats

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

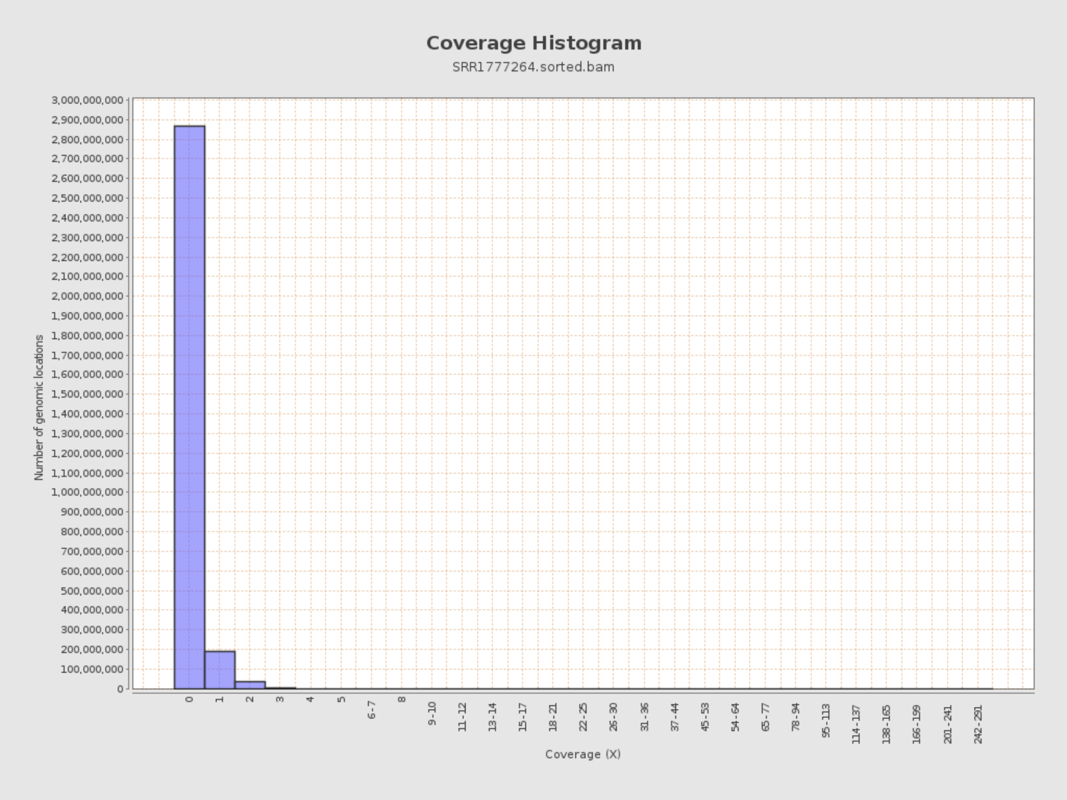
		bases	coverage	deviation
chr1	249250621	23917728	0.096	0.468
chr2	243199373	26976628	0.1109	0.3991
chr3	198022430	19195871	0.0969	0.3557
chr4	191154276	17629979	0.0922	0.3496
chr5	180915260	19465907	0.1076	0.375
chr6	171115067	13518651	0.079	0.3567
chr7	159138663	19071163	0.1198	0.4256
chr8	146364022	14131321	0.0965	0.3639
chr9	141213431	10437326	0.0739	0.4225
chr10	135534747	12841482	0.0947	0.4211
chr11	135006516	15732058	0.1165	0.4075
chr12	133851895	13008432	0.0972	0.3553
chr13	115169878	12157218	0.1056	0.3733
chr14	107349540	5775116	0.0538	0.2641
chr15	102531392	10595013	0.1033	0.3704
chr16	90354753	7381352	0.0817	0.3494
chr17	81195210	6789234	0.0836	0.3572
chr18	78077248	6181256	0.0792	0.4305
chr19	59128983	3488074	0.059	0.3554
chr20	63025520	7439513	0.118	0.3935
chr21	48129895	2577039	0.0535	0.2776
chr22	51304566	2126633	0.0415	0.2328
chrMT	16571	1001949	60.464	16.2495
chrX	155270560	10935981	0.0704	0.3077

chrY	59373566	347952	0.0059	0.1551

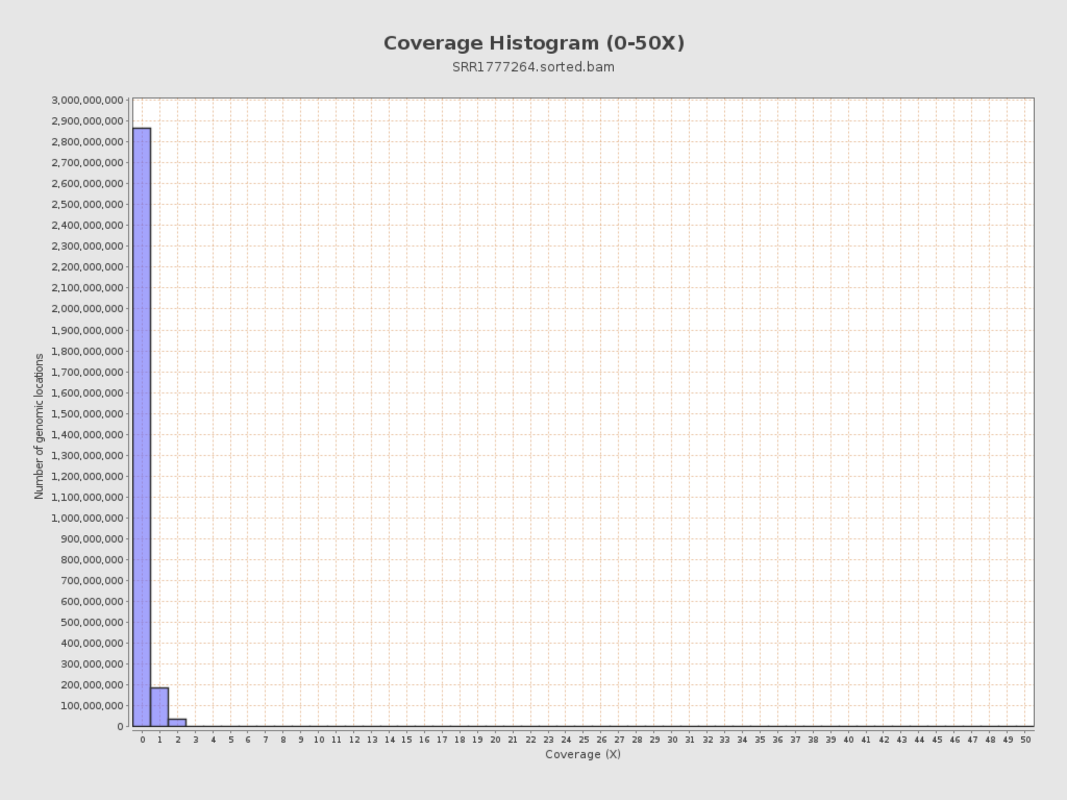
3. Results : Coverage across reference



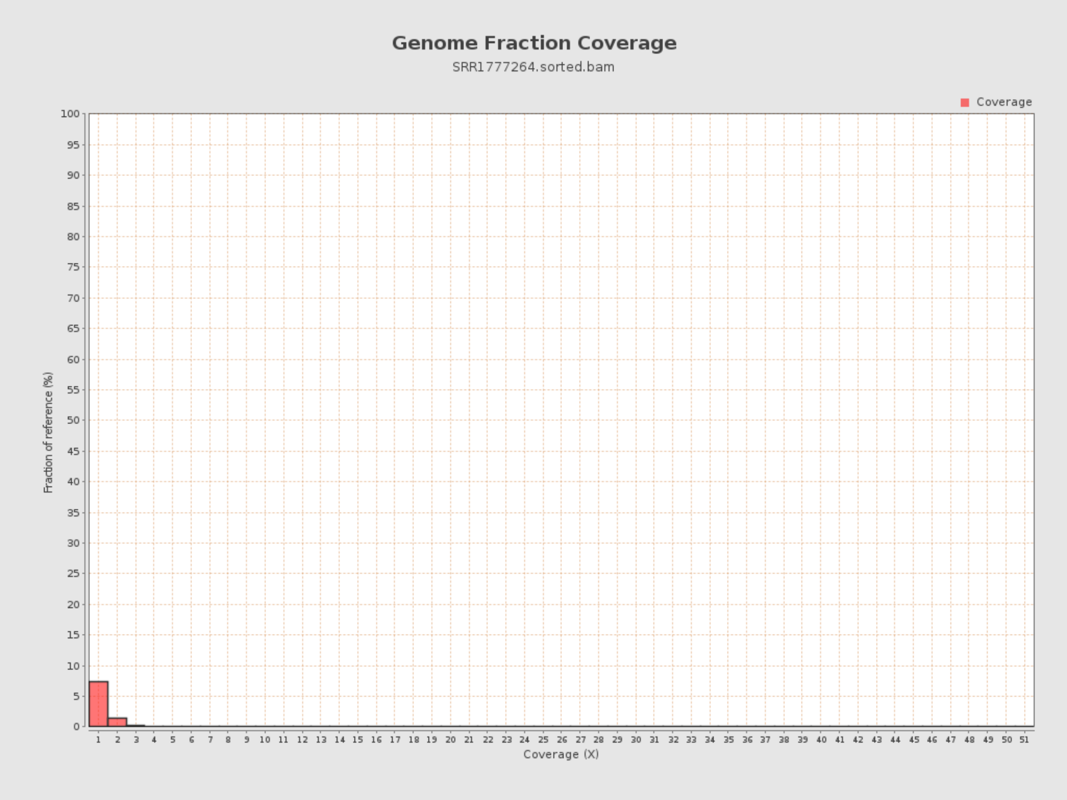
4. Results : Coverage Histogram



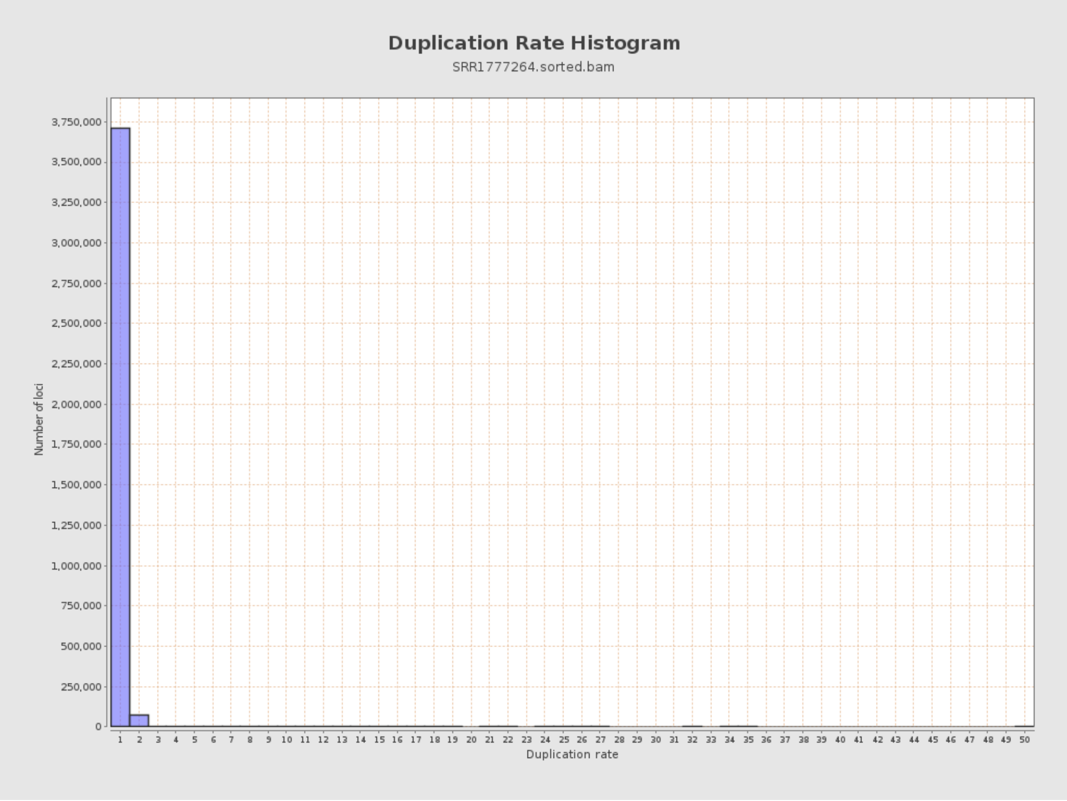
5. Results : Coverage Histogram (0-50X)



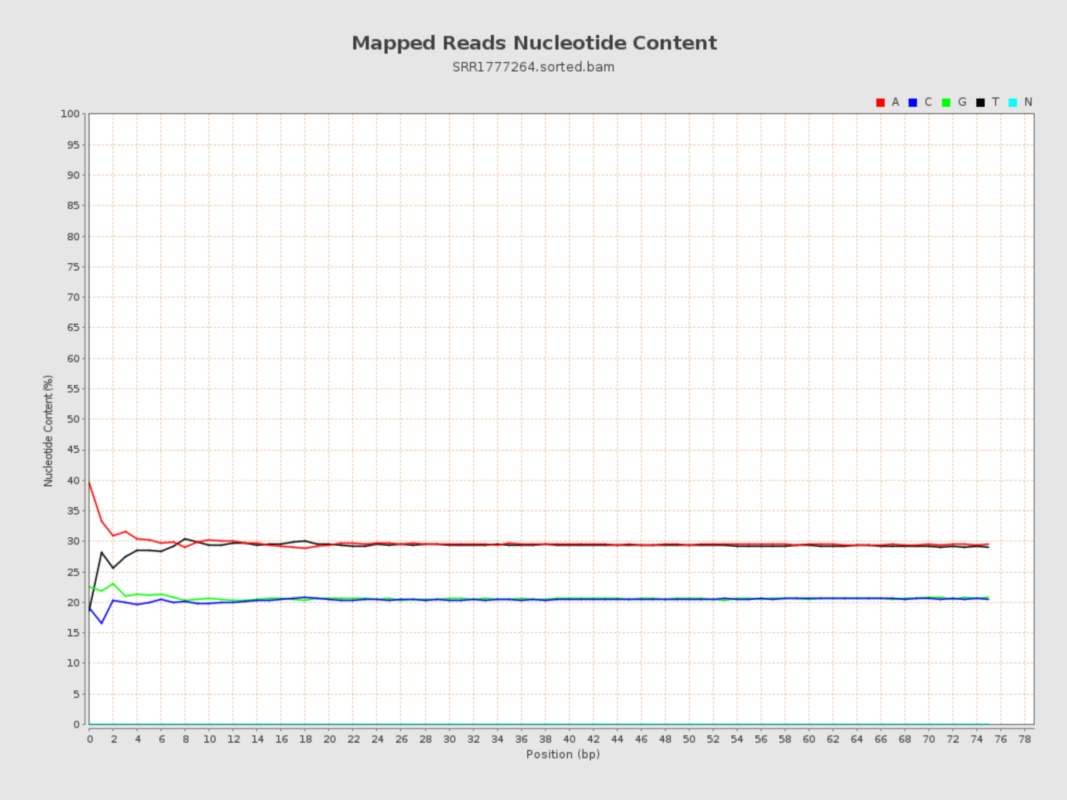
6. Results : Genome Fraction Coverage



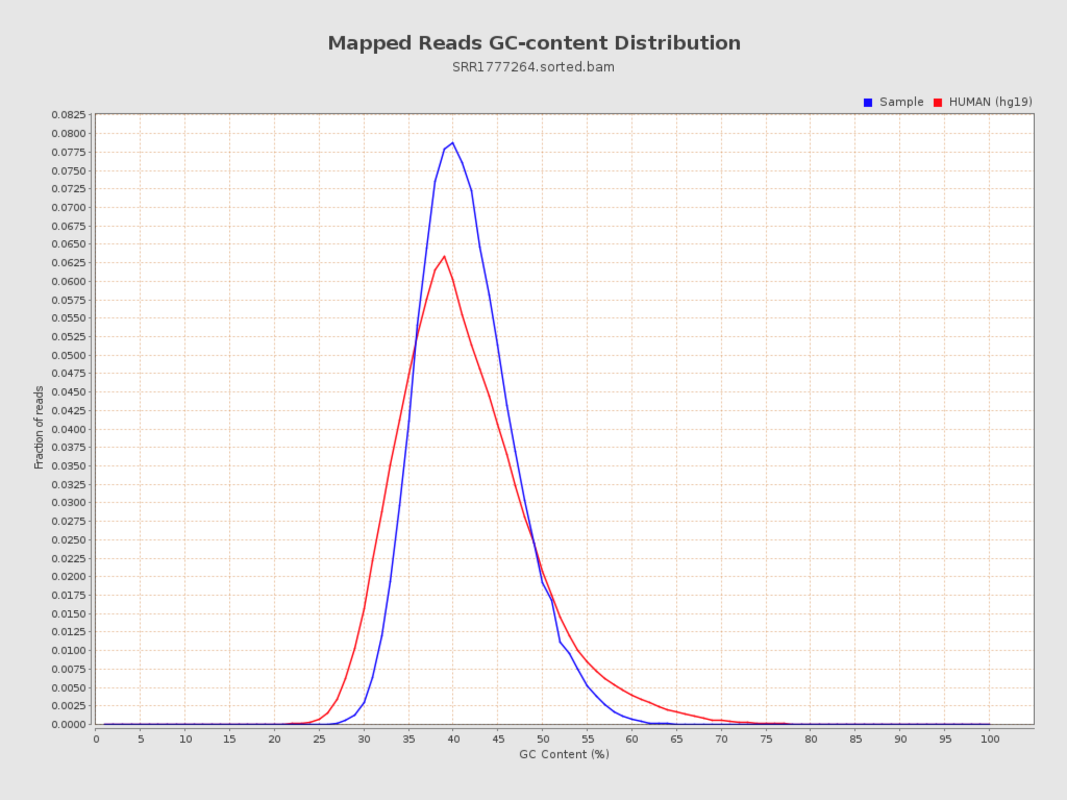
7. Results : Duplication Rate Histogram



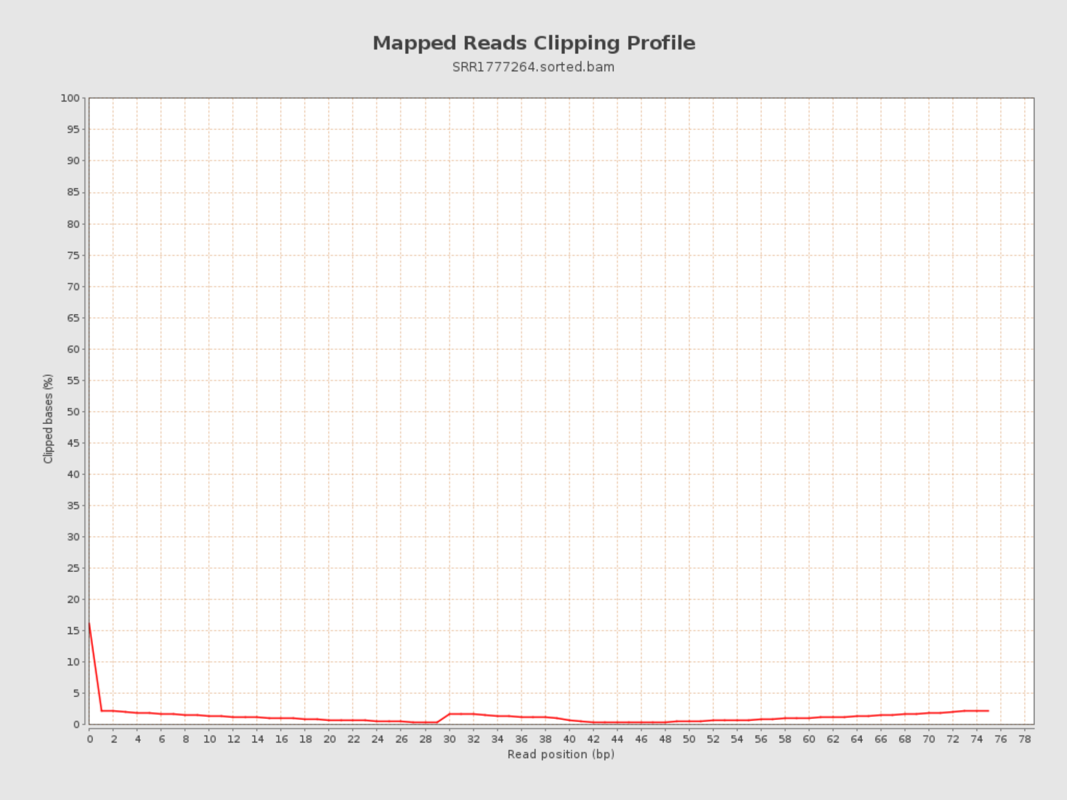
8. Results : Mapped Reads Nucleotide Content



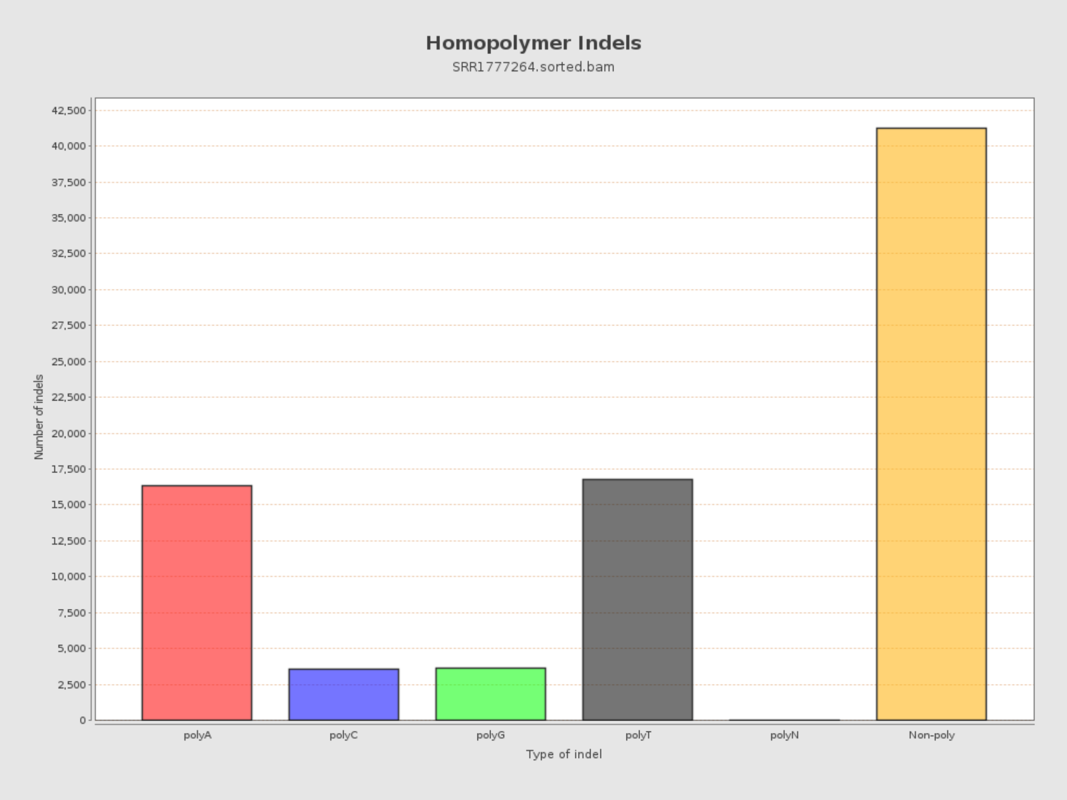
9. Results : Mapped Reads GC-content Distribution



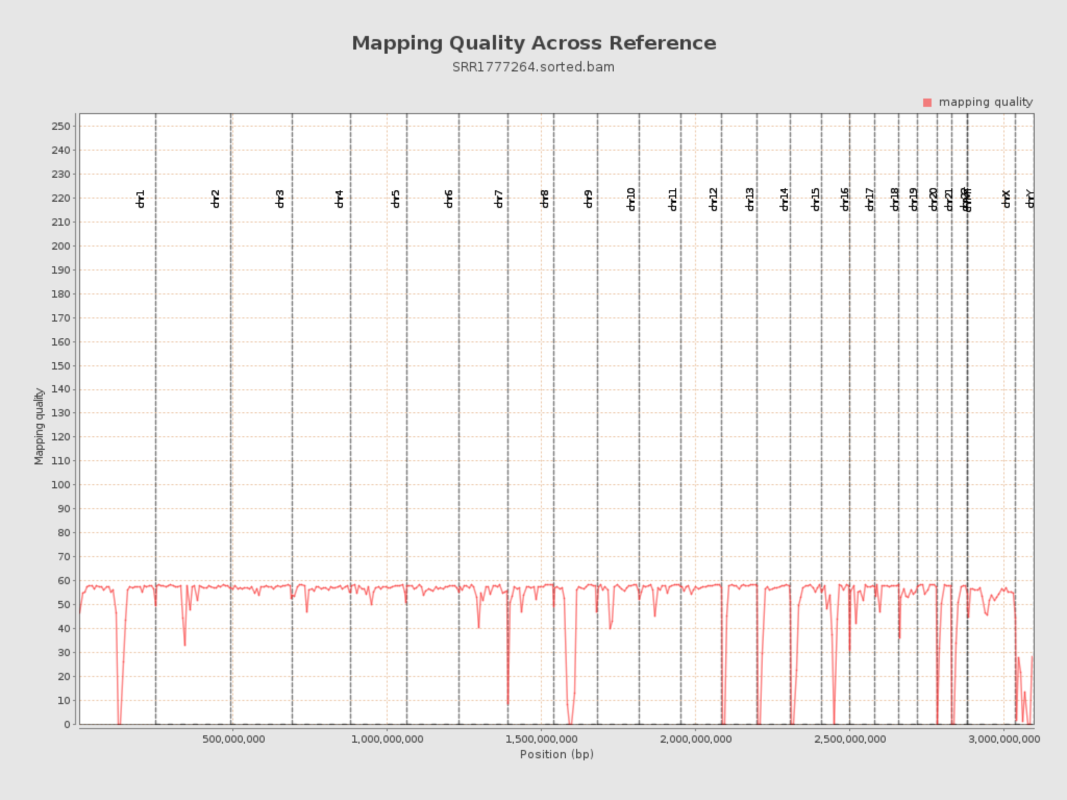
10. Results : Mapped Reads Clipping Profile



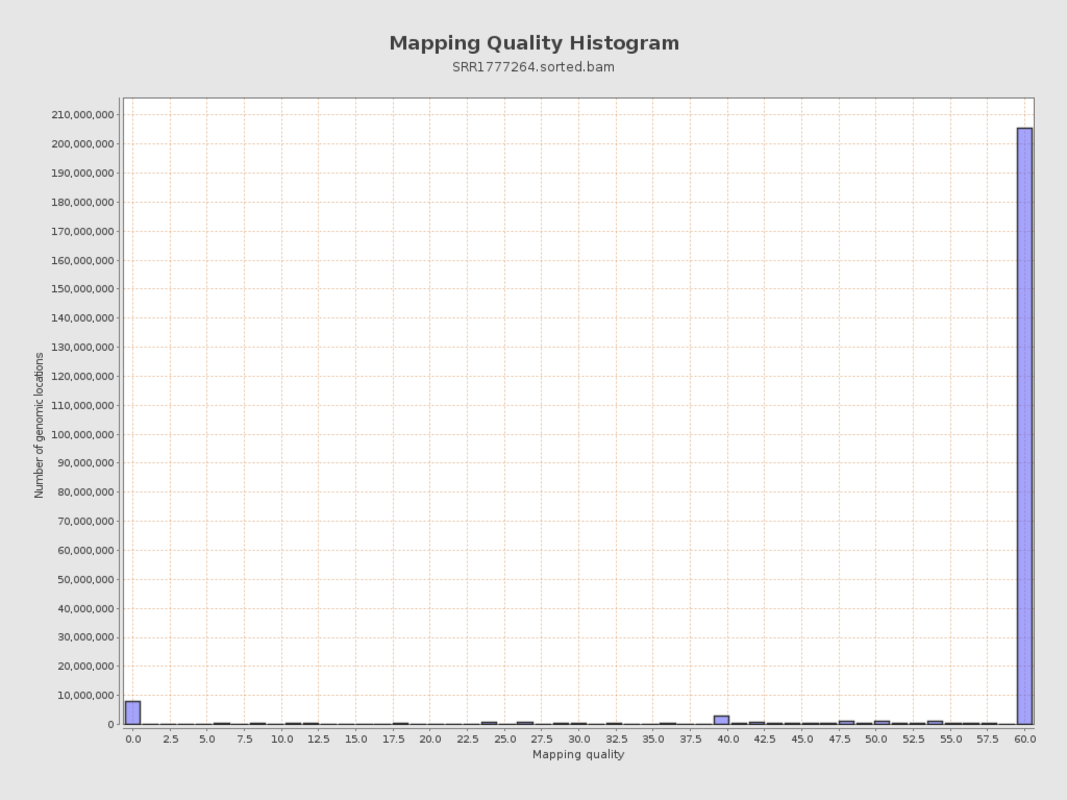
11. Results : Homopolymer Indels



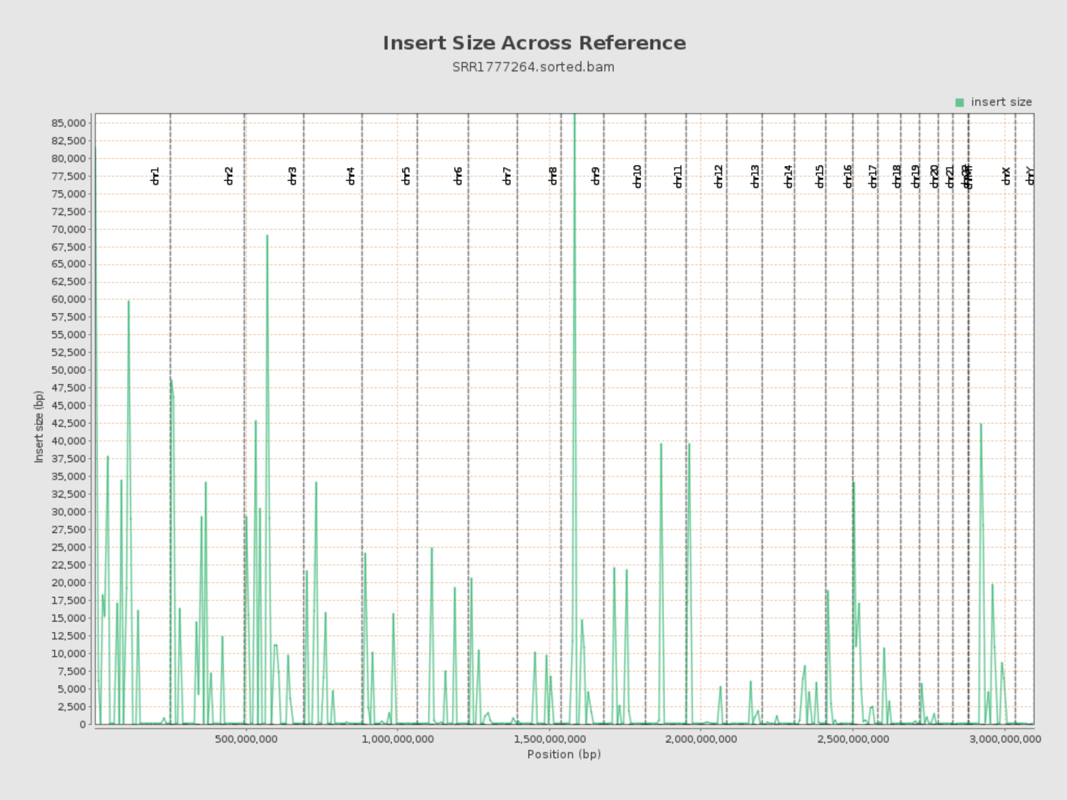
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram