Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 05:39:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777263.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_SRR1777263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777263_1.fastq.gz SRR1777263_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 05:39:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	61,526,560
Mapped reads	61,334,618 / 99.69%
Unmapped reads	191,942 / 0.31%
Mapped paired reads	61,334,618 / 99.69%
Mapped reads, first in pair	30,670,384 / 49.85%
Mapped reads, second in pair	30,664,234 / 49.84%
Mapped reads, both in pair	61,255,314 / 99.56%
Mapped reads, singletons	79,304 / 0.13%
Secondary alignments	0
Supplementary alignments	1,994,815 / 3.24%
Read min/max/mean length	30 / 101 / 102.34
Duplicated reads (estimated)	29,053,361 / 47.22%
Duplication rate	40.73%
Clipped reads	7,343,838 / 11.94%

2.2. ACGT Content

Number/percentage of A's	1,684,254,948 / 27.39%
Number/percentage of C's	1,376,580,585 / 22.38%
Number/percentage of T's	1,671,470,259 / 27.18%
Number/percentage of G's	1,388,503,204 / 22.58%
Number/percentage of N's	28,950,737 / 0.47%

GC Percentage	44.96%

2.3. Coverage

Mean	1.9868
Standard Deviation	16.7195

2.4. Mapping Quality

Mean Mapping Quality	54.67

2.5. Insert size

Mean	314,370.57
Standard Deviation	5,474,873.32
P25/Median/P75	188 / 238 / 300

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	43,186,467
Insertions	953,489
Mapped reads with at least one insertion	1.53%
Deletions	418,047
Mapped reads with at least one deletion	0.67%
Homopolymer indels	50.16%

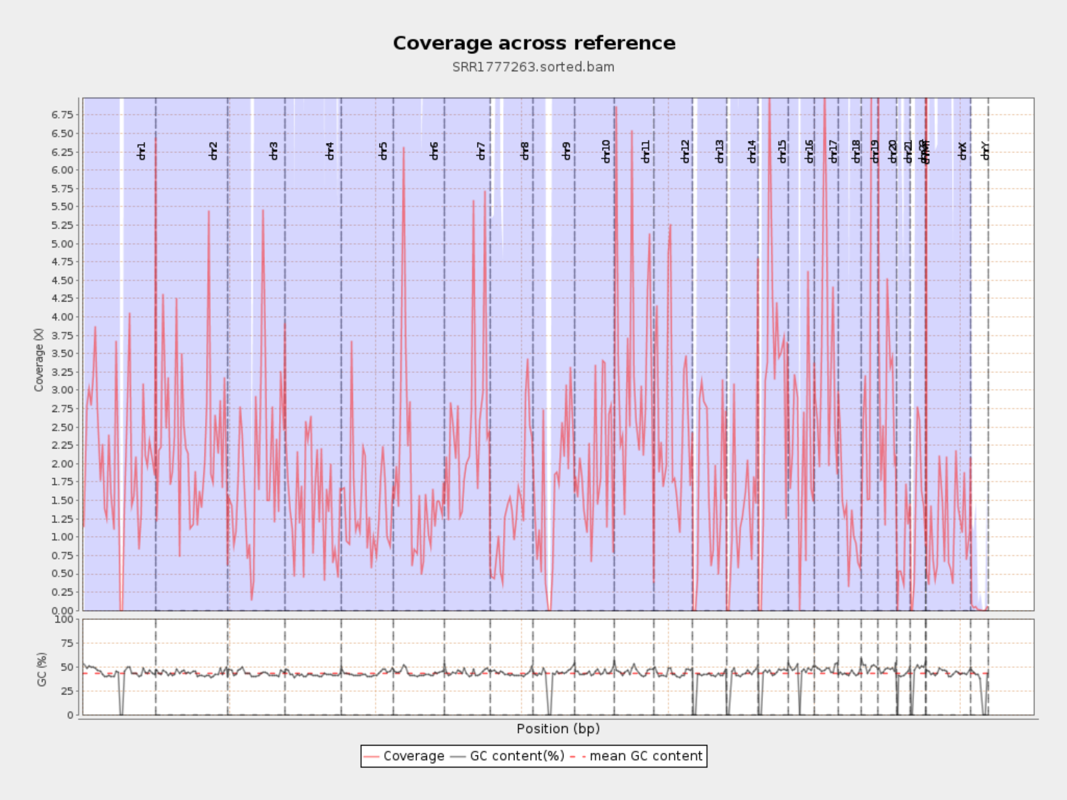
2.7. Chromosome stats

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

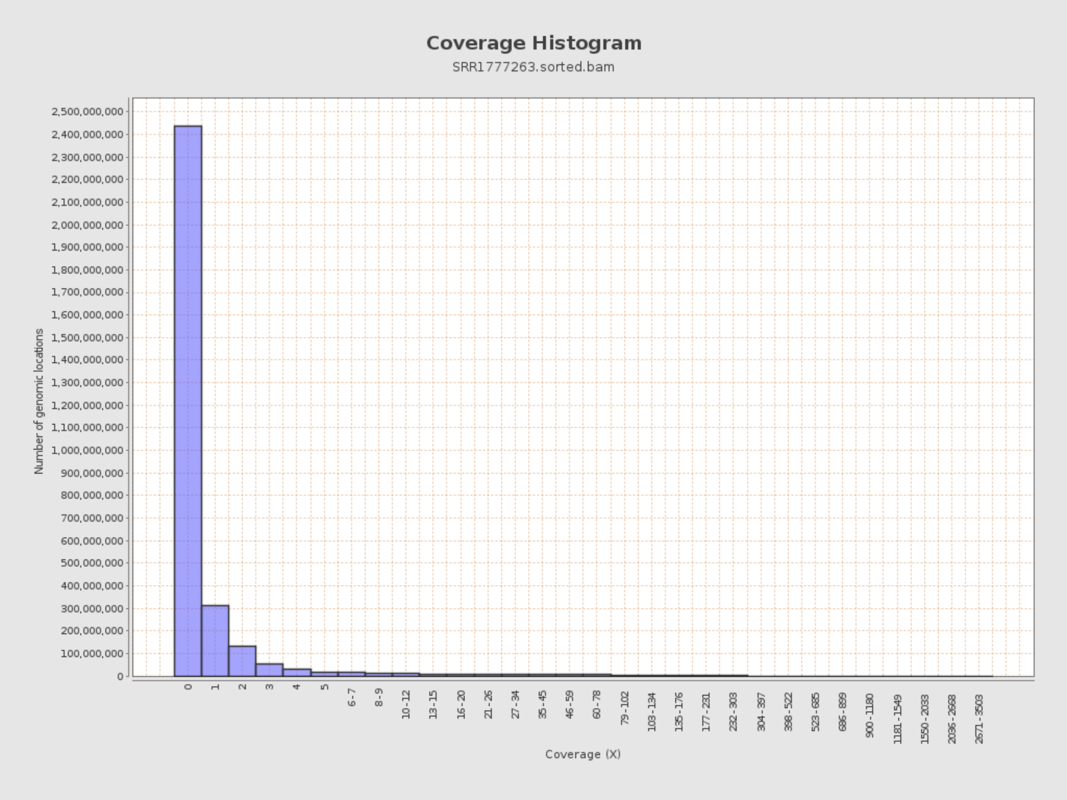
		bases	coverage	deviation
chr1	249250621	521047394	2.0905	15.6589
chr2	243199373	561931080	2.3106	18.2818
chr3	198022430	385355908	1.946	16.7767
chr4	191154276	282431314	1.4775	14.1125
chr5	180915260	262191462	1.4493	13.1447
chr6	171115067	297771643	1.7402	14.6473
chr7	159138663	398515985	2.5042	19.8916
chr8	146364022	207407027	1.4171	14.0631
chr9	141213431	220225348	1.5595	14.0569
chr10	135534747	265955455	1.9623	15.8441
chr11	135006516	441341364	3.269	24.1935
chr12	133851895	352491367	2.6334	18.8286
chr13	115169878	185779613	1.6131	16.031
chr14	107349540	137877219	1.2844	11.3428
chr15	102531392	307360357	2.9977	23.2444
chr16	90354753	189286619	2.0949	15.5511
chr17	81195210	280690542	3.457	22.9985
chr18	78077248	98219452	1.258	11.9014
chr19	59128983	297154571	5.0255	28.9967
chr20	63025520	173154007	2.7474	20.4862
chr21	48129895	40569671	0.8429	8.9744
chr22	51304566	70054512	1.3655	10.9915
chrMT	16571	1527585	92.1842	32.6024
chrX	155270560	170601662	1.0987	10.715

chrY	59373566	1699589	0.0286	0.9868

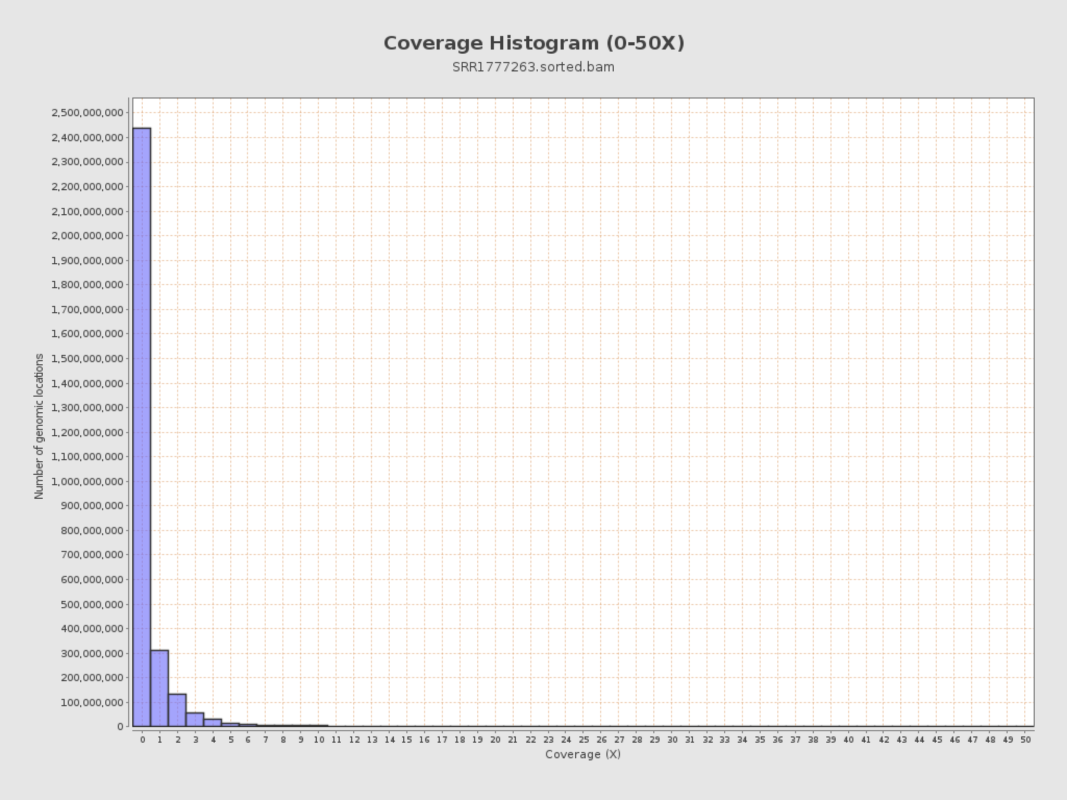
3. Results : Coverage across reference



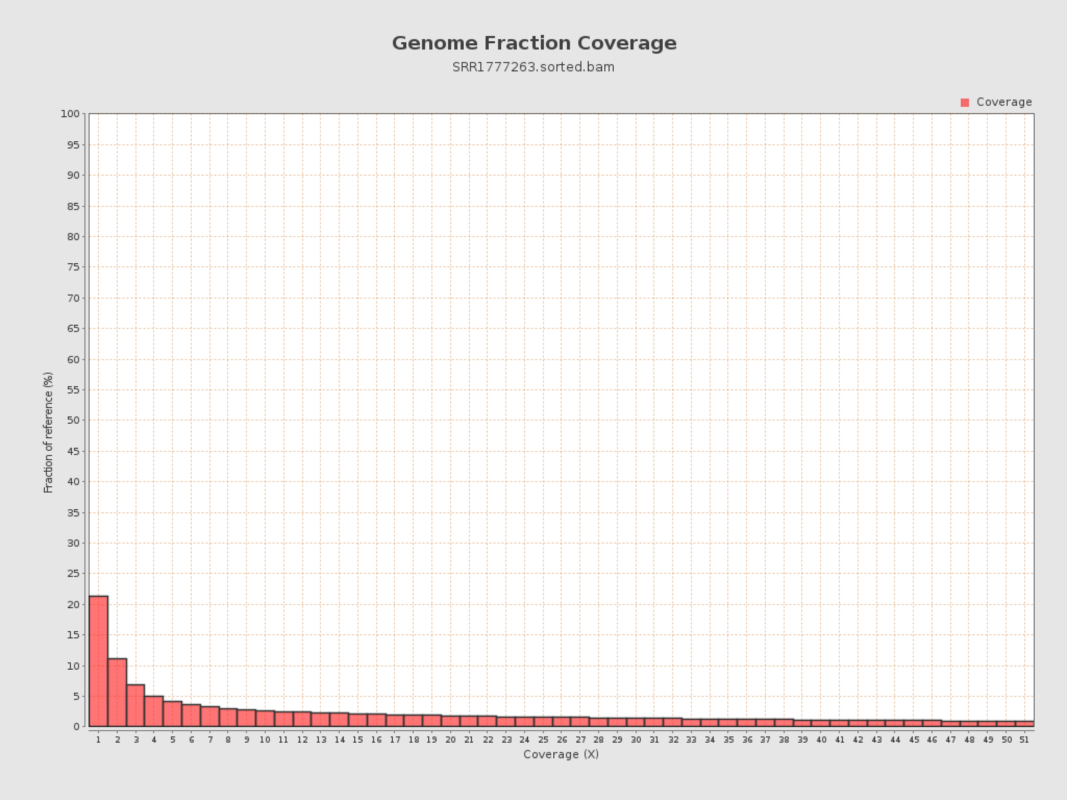
4. Results : Coverage Histogram



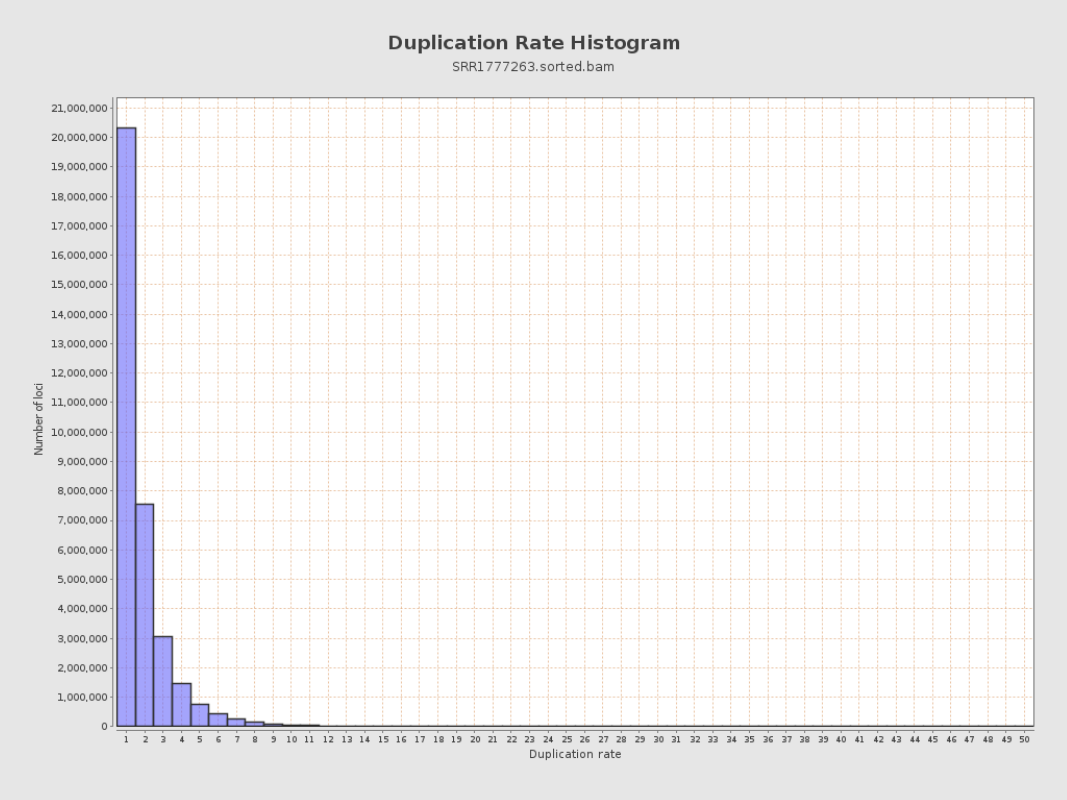
5. Results : Coverage Histogram (0-50X)



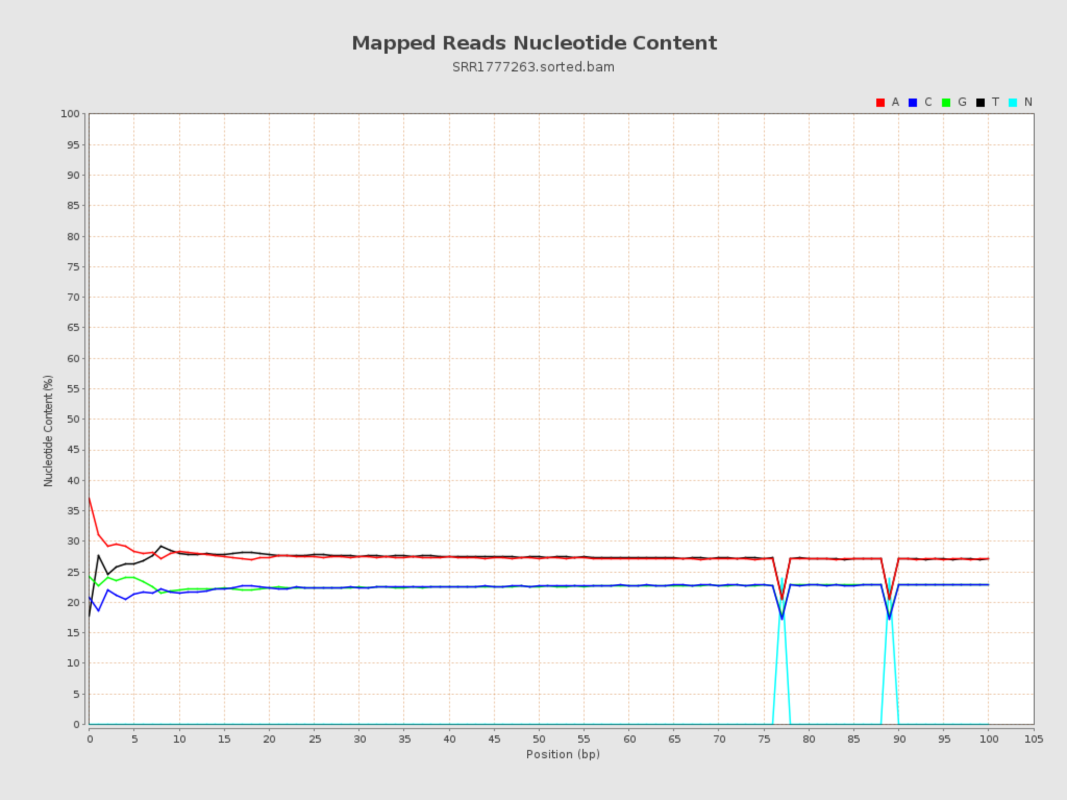
6. Results : Genome Fraction Coverage



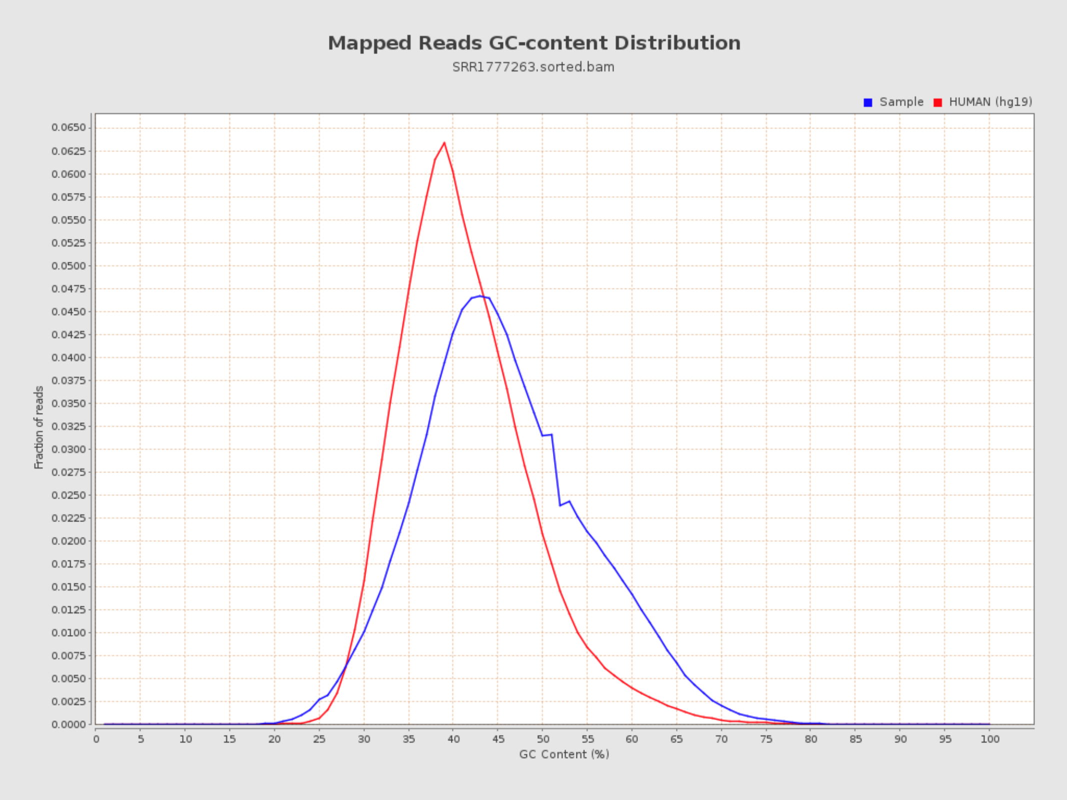
7. Results : Duplication Rate Histogram



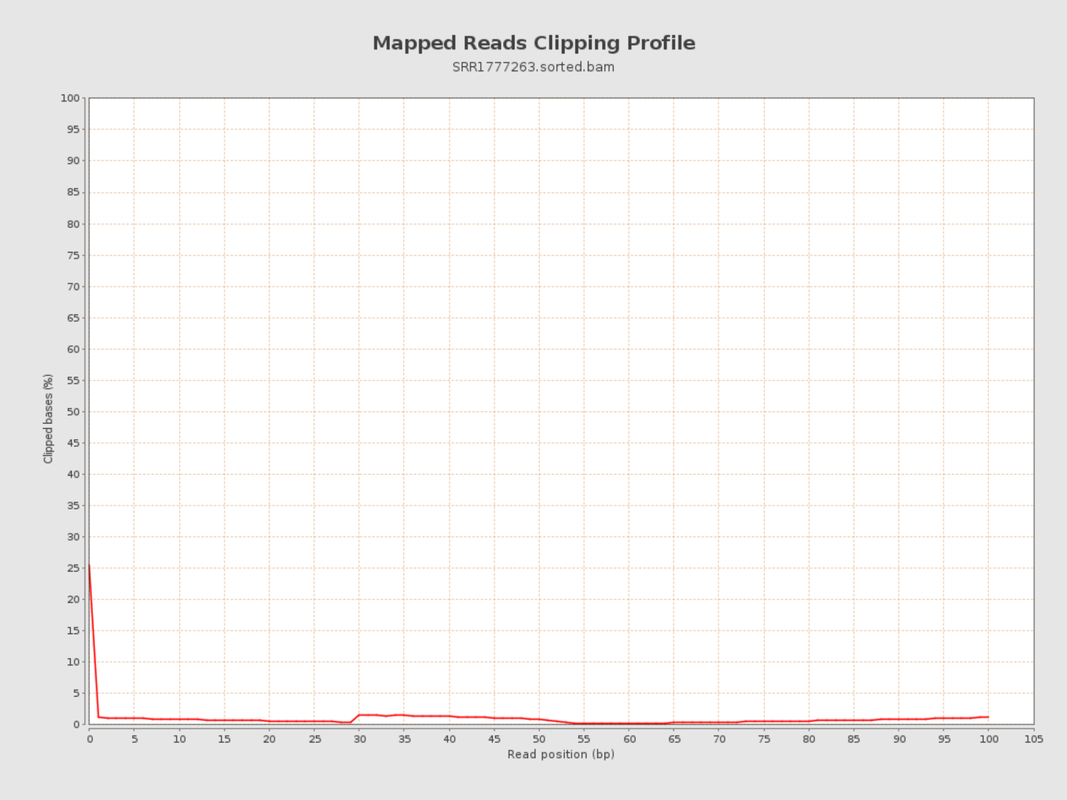
8. Results : Mapped Reads Nucleotide Content



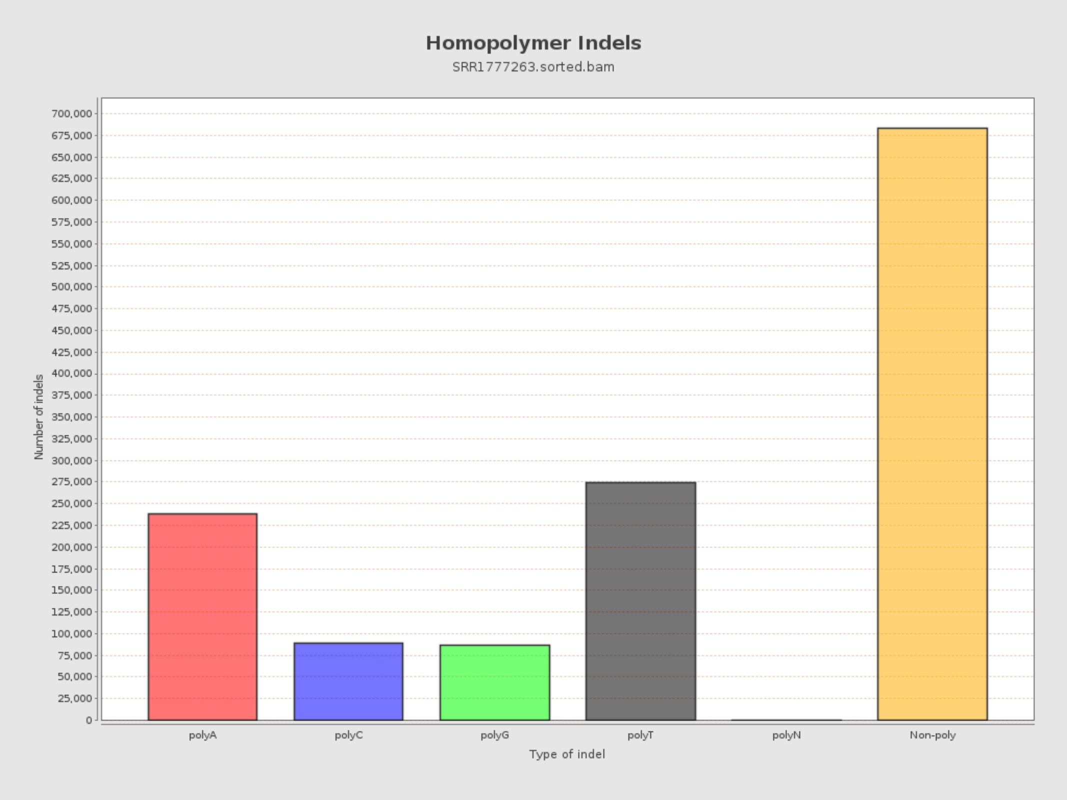
9. Results : Mapped Reads GC-content Distribution



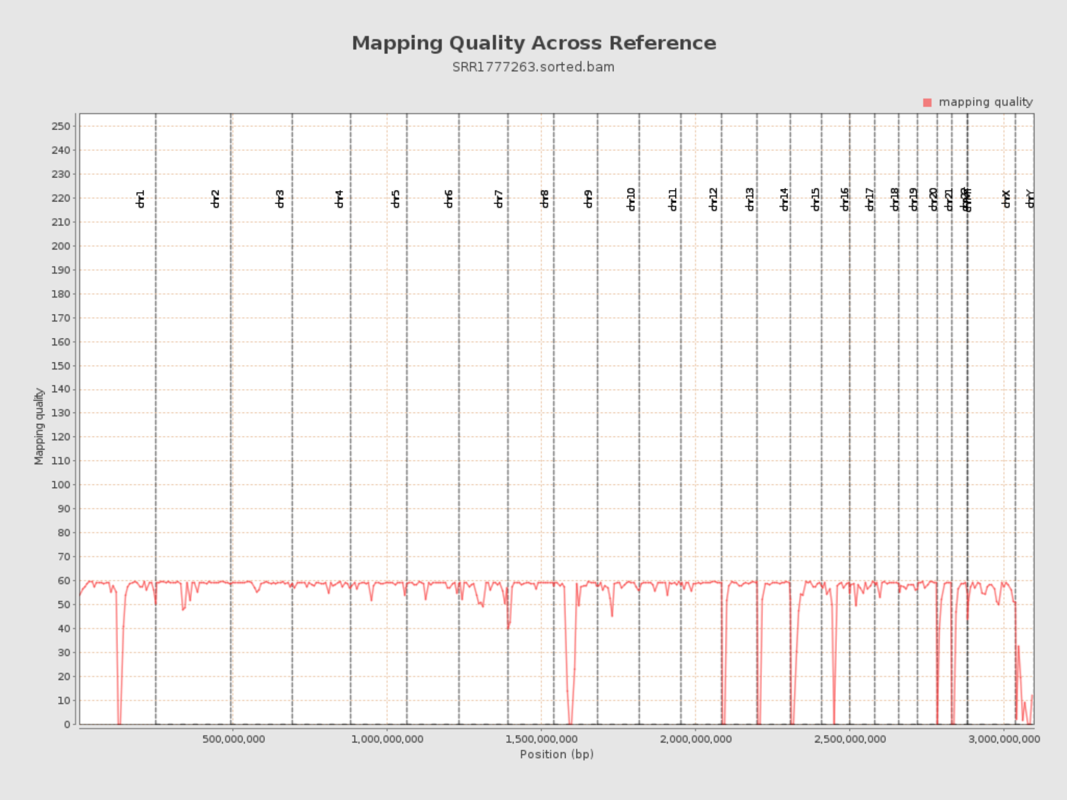
10. Results : Mapped Reads Clipping Profile



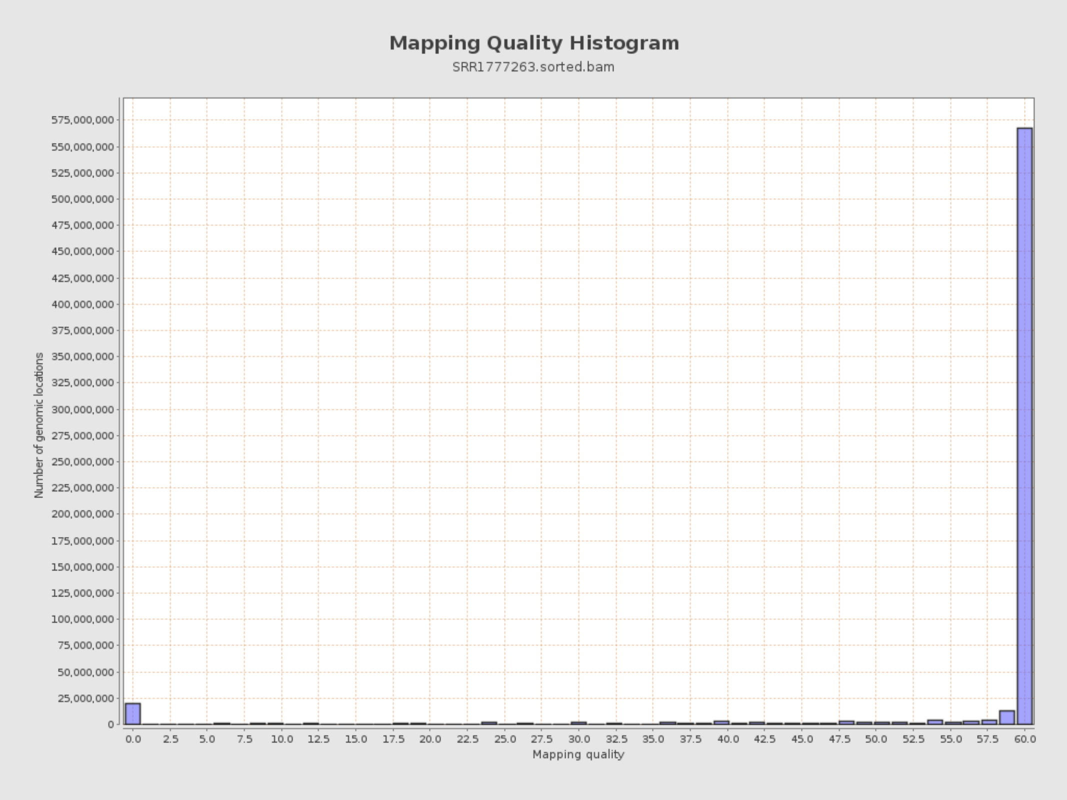
11. Results : Homopolymer Indels



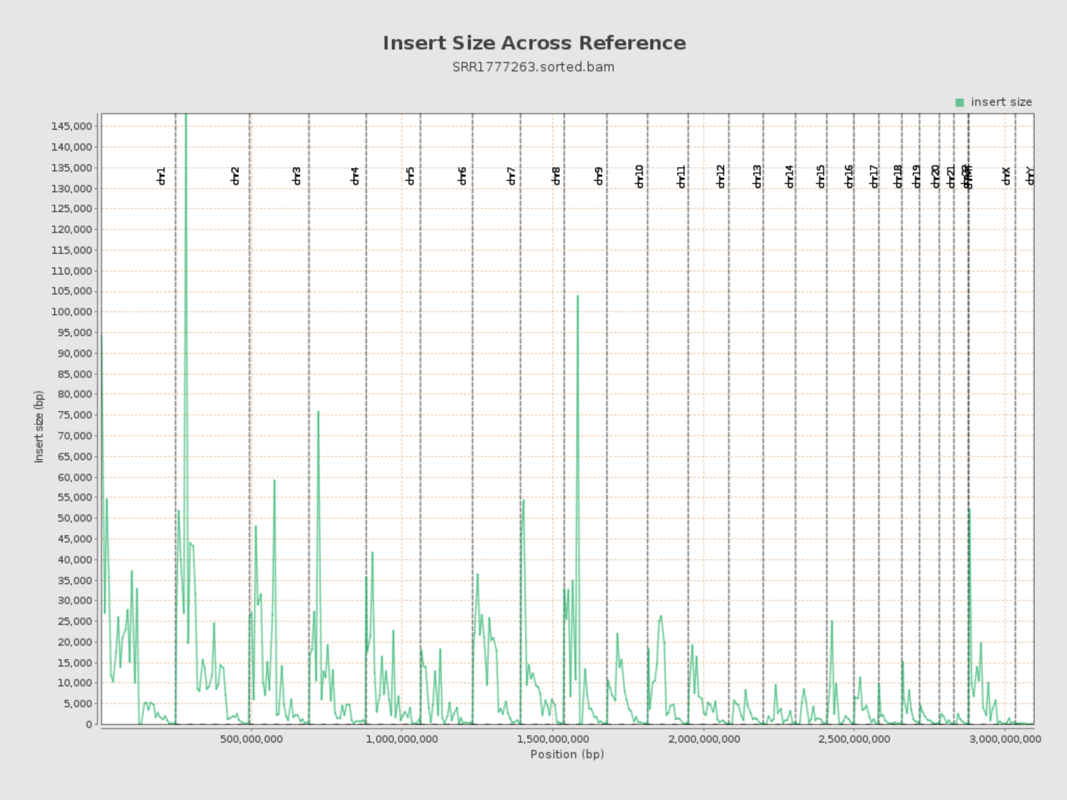
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram