Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 20:51:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779330.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_SRR1779330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779330_1.fastq.gz SRR1779330_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 20:51:19 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	152,400,940
Mapped reads	150,024,676 / 98.44%
Unmapped reads	2,376,264 / 1.56%
Mapped paired reads	150,024,676 / 98.44%
Mapped reads, first in pair	75,494,797 / 49.54%
Mapped reads, second in pair	74,529,879 / 48.9%
Mapped reads, both in pair	148,935,820 / 97.73%
Mapped reads, singletons	1,088,856 / 0.71%
Secondary alignments	0
Supplementary alignments	501,515 / 0.33%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	11,331,049 / 7.44%
Duplication rate	7.33%
Clipped reads	11,929,990 / 7.83%

2.2. ACGT Content

Number/percentage of A's	4,540,049,957 / 30.32%
Number/percentage of C's	2,940,601,726 / 19.64%
Number/percentage of T's	4,500,326,742 / 30.05%
Number/percentage of G's	2,990,194,142 / 19.97%
Number/percentage of N's	3,785,032 / 0.03%

GC Percentage	39.6%

2.3. Coverage

Mean	4.8384
Standard Deviation	6.8715

2.4. Mapping Quality

Mean Mapping Quality	53.8

2.5. Insert size

Mean	43,255.75
Standard Deviation	1,975,417.45
P25/Median/P75	151 / 208 / 283

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	43,099,070
Insertions	1,143,562
Mapped reads with at least one insertion	0.75%
Deletions	1,466,086
Mapped reads with at least one deletion	0.96%
Homopolymer indels	46.96%

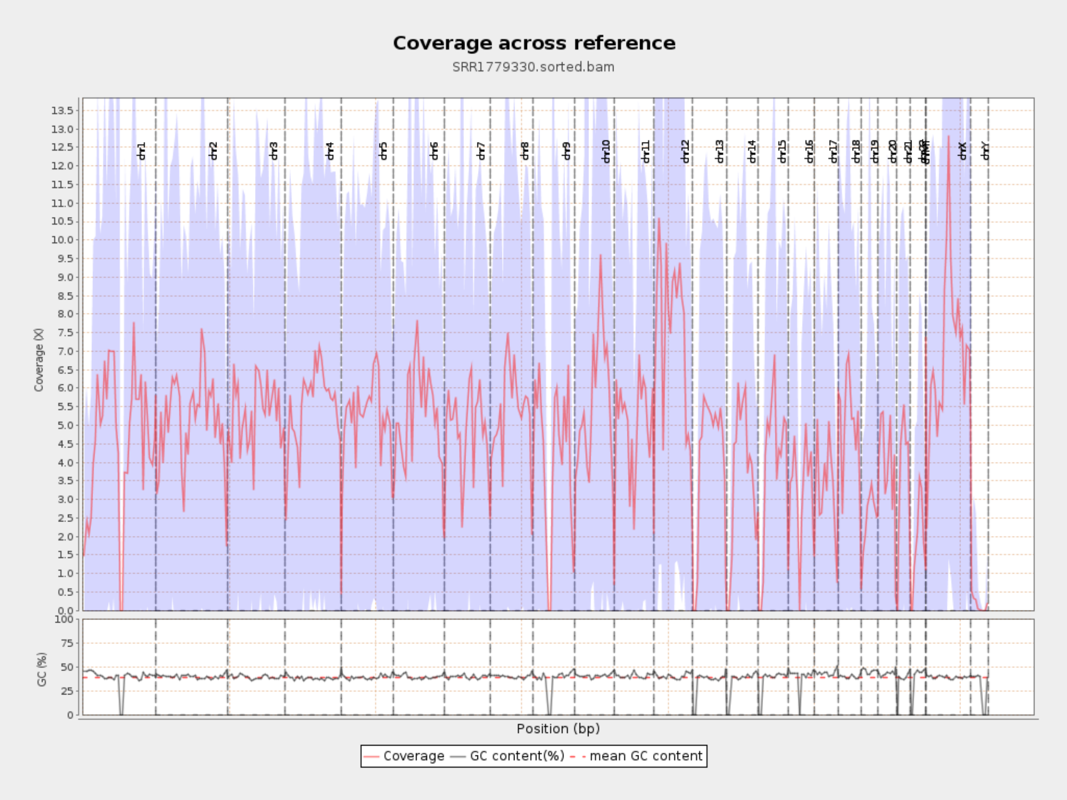
2.7. Chromosome stats

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

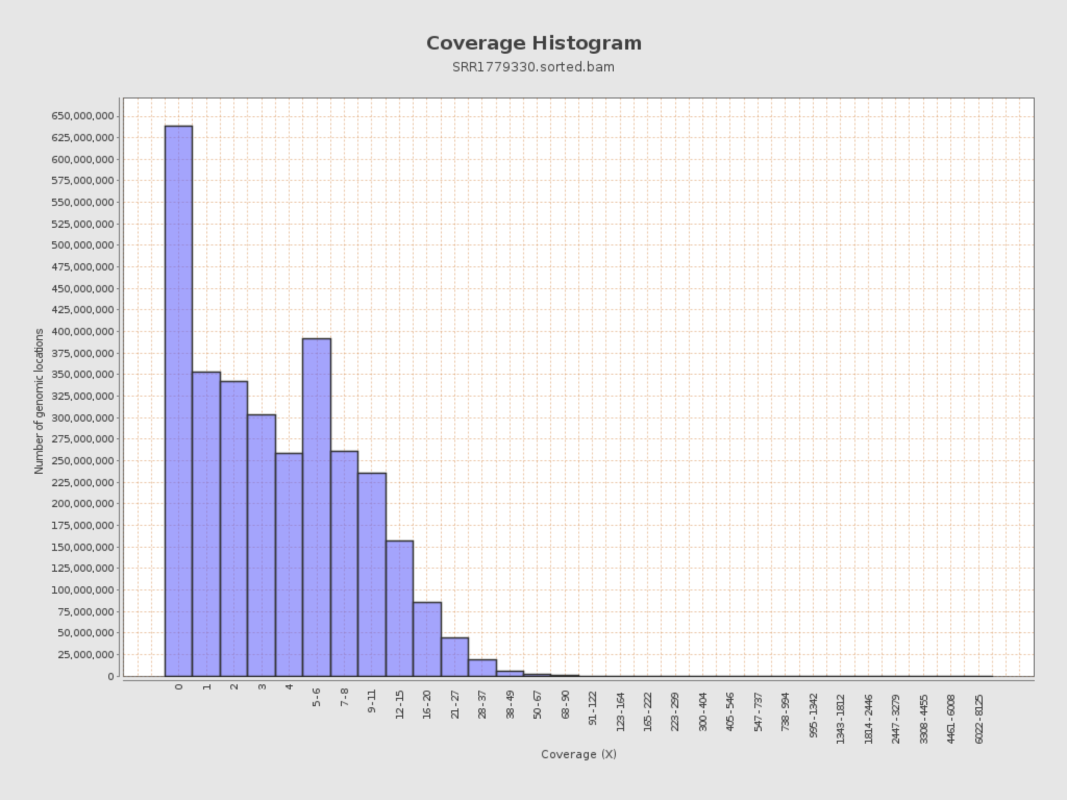
		bases	coverage	deviation
chr1	249250621	1151057640	4.6181	8.2943
chr2	243199373	1249295298	5.1369	6.0348
chr3	198022430	1051875754	5.3119	5.5515
chr4	191154276	1059315864	5.5417	5.7524
chr5	180915260	942040984	5.2071	5.3039
chr6	171115067	914756992	5.3459	5.8112
chr7	159138663	768834959	4.8312	6.7199
chr8	146364022	787658519	5.3815	5.6259
chr9	141213431	594295735	4.2085	6.0494
chr10	135534747	771602491	5.693	15.3831
chr11	135006516	677412643	5.0176	5.7791
chr12	133851895	1013506868	7.5719	7.9865
chr13	115169878	475939665	4.1325	4.934
chr14	107349540	391490129	3.6469	4.9074
chr15	102531392	397293556	3.8748	5.3735
chr16	90354753	286142608	3.1669	4.4197
chr17	81195210	276399889	3.4041	4.8357
chr18	78077248	396182647	5.0742	5.7654
chr19	59128983	149748976	2.5326	5.5743
chr20	63025520	253003157	4.0143	5.7498
chr21	48129895	170817369	3.5491	5.2972
chr22	51304566	95523216	1.8619	3.5558
chrMT	16571	122354	7.3836	3.5901
chrX	155270560	1094479543	7.0489	7.6071

chrY	59373566	9400281	0.1583	1.4694

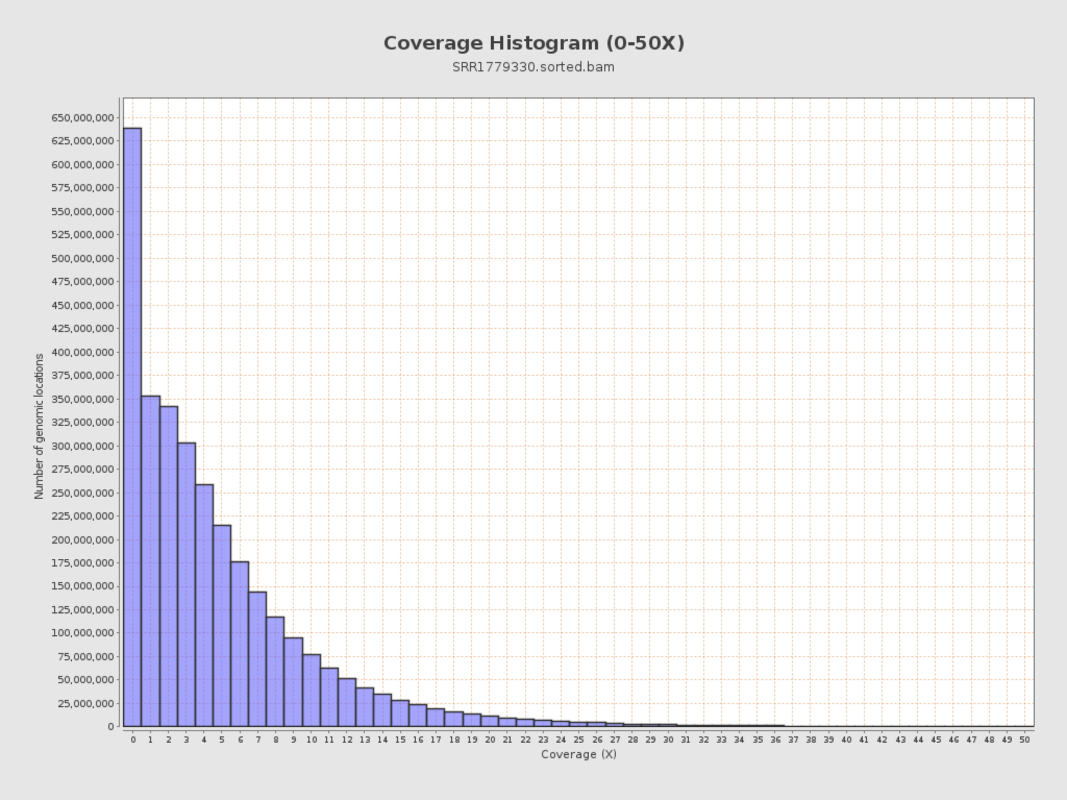
3. Results : Coverage across reference



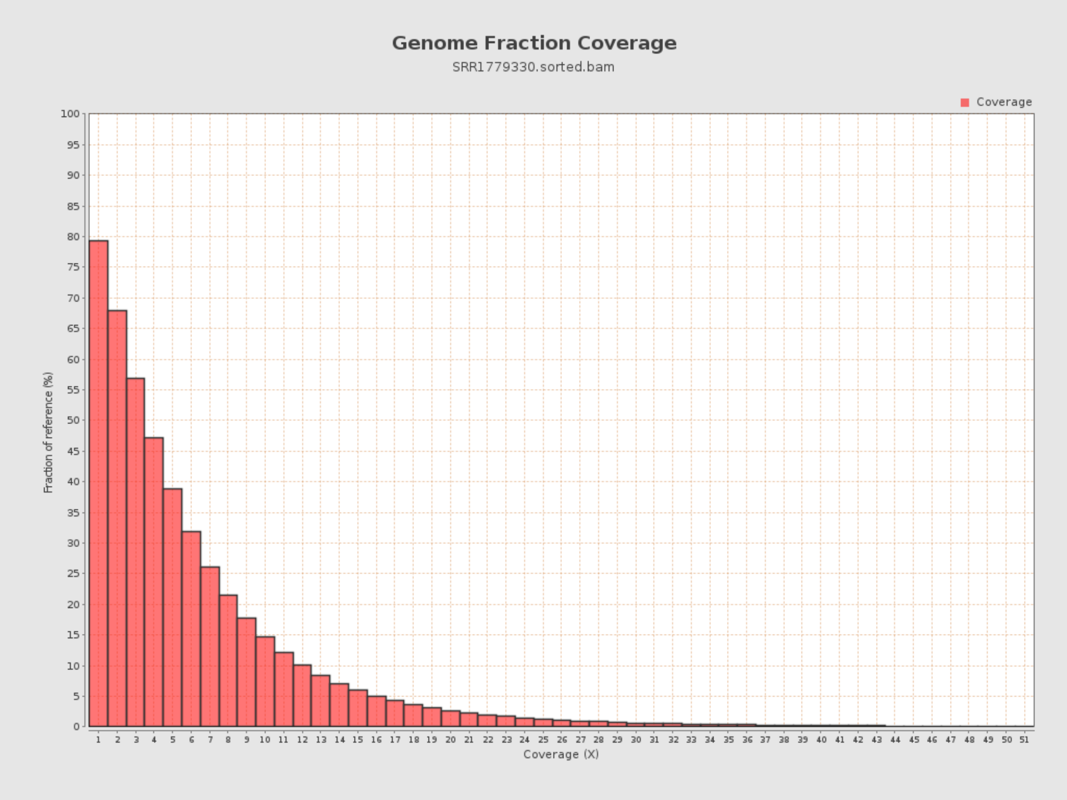
4. Results : Coverage Histogram



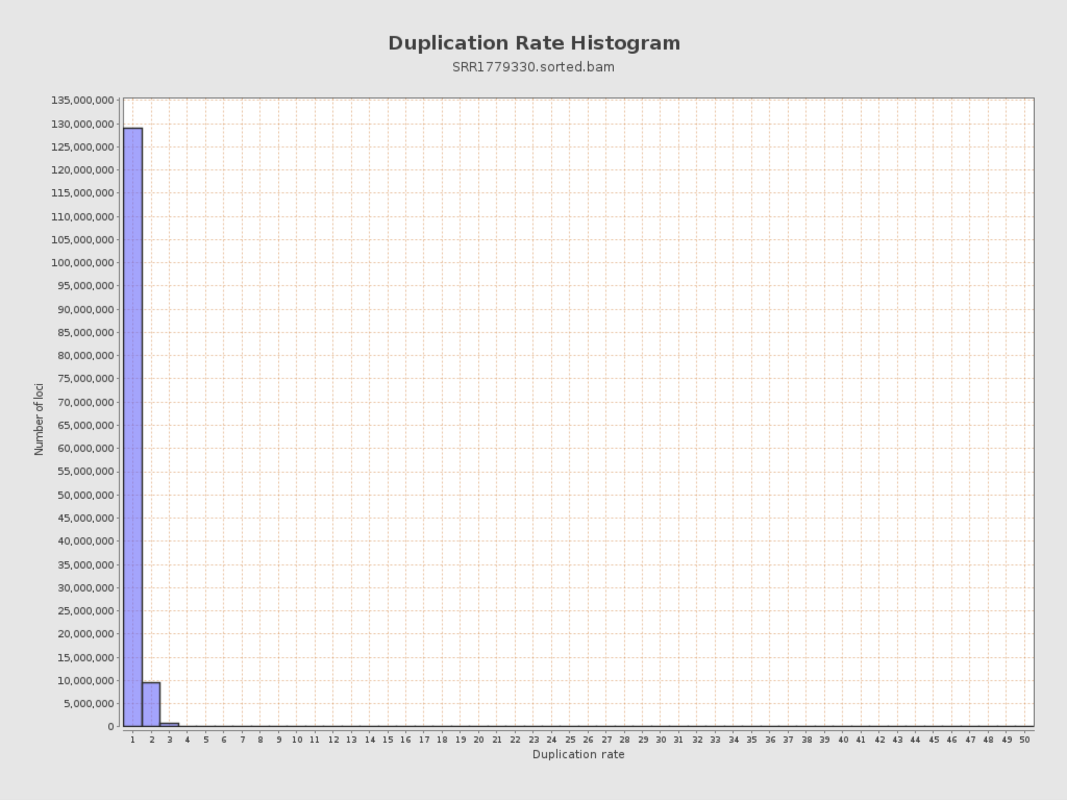
5. Results : Coverage Histogram (0-50X)



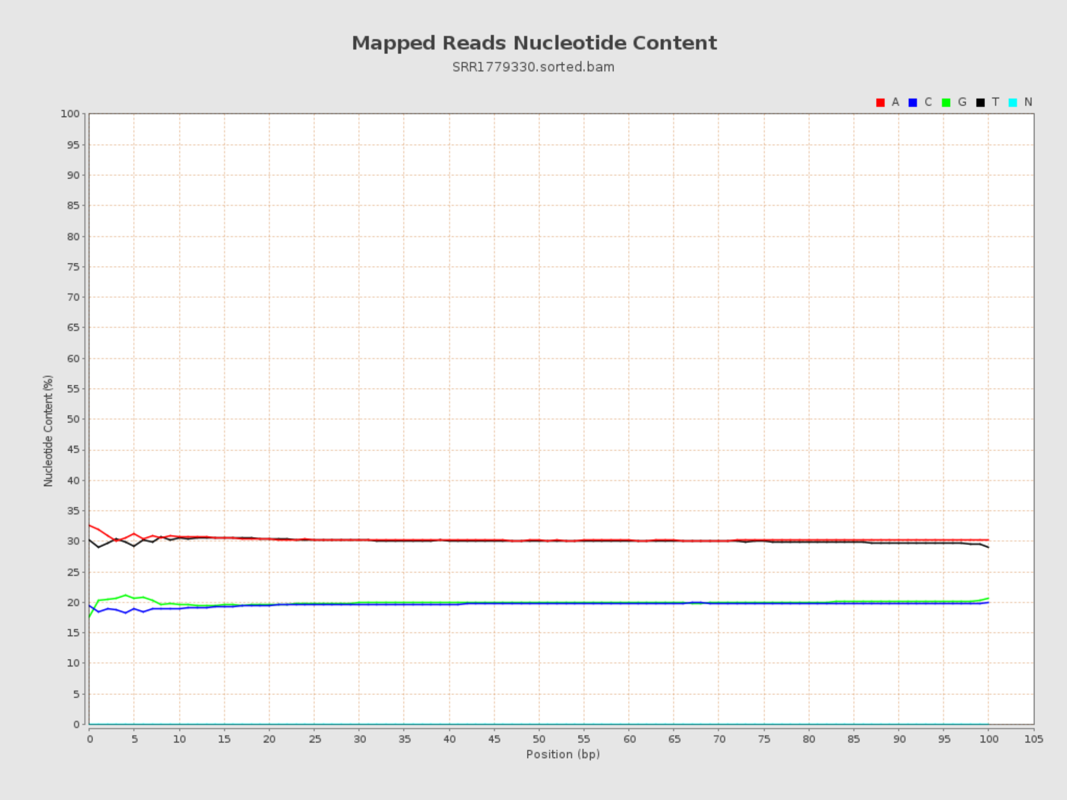
6. Results : Genome Fraction Coverage



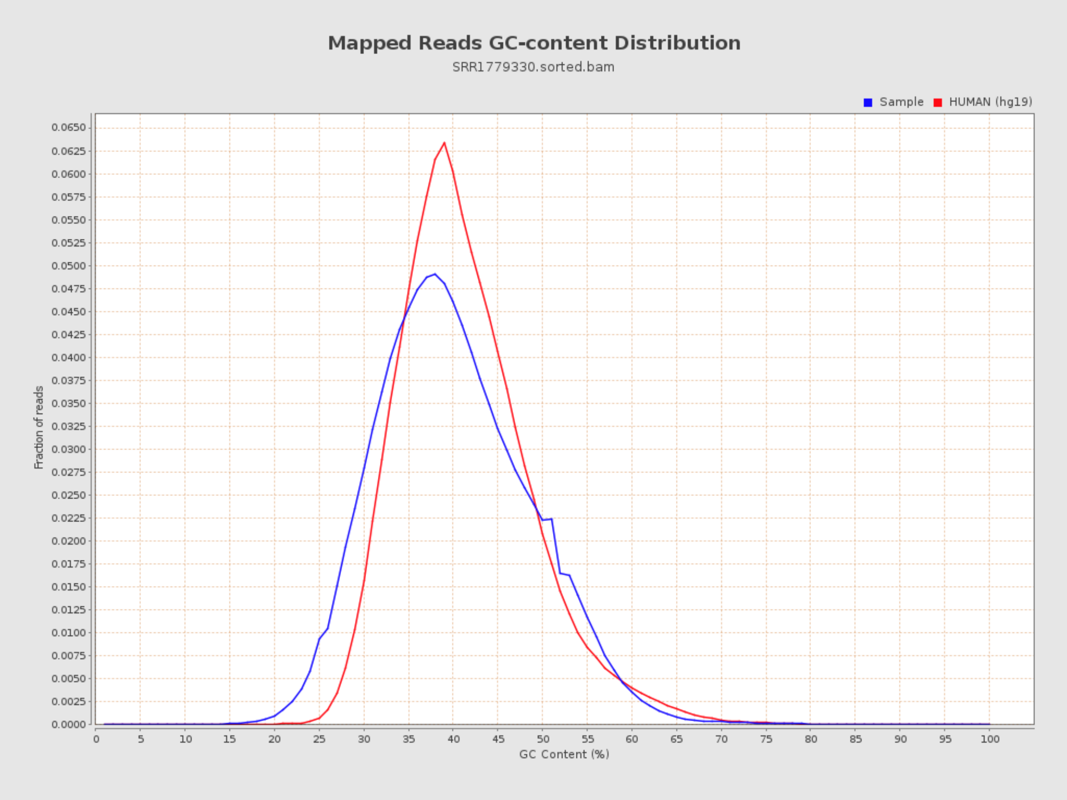
7. Results : Duplication Rate Histogram



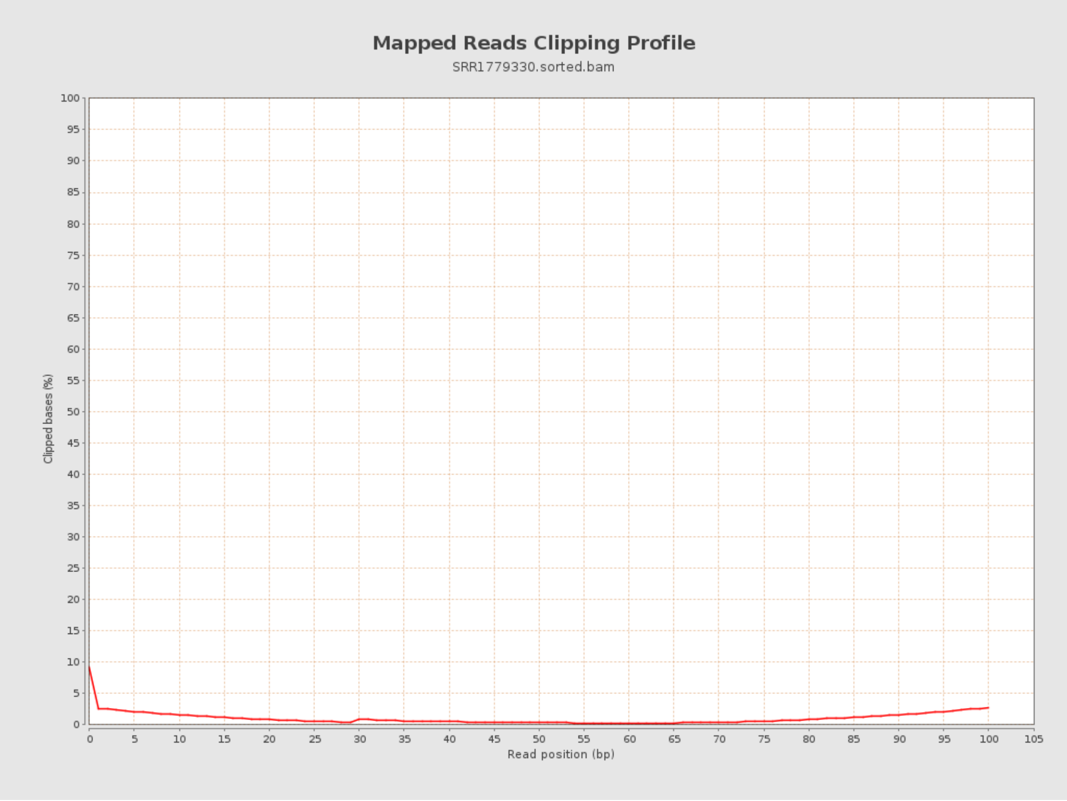
8. Results : Mapped Reads Nucleotide Content



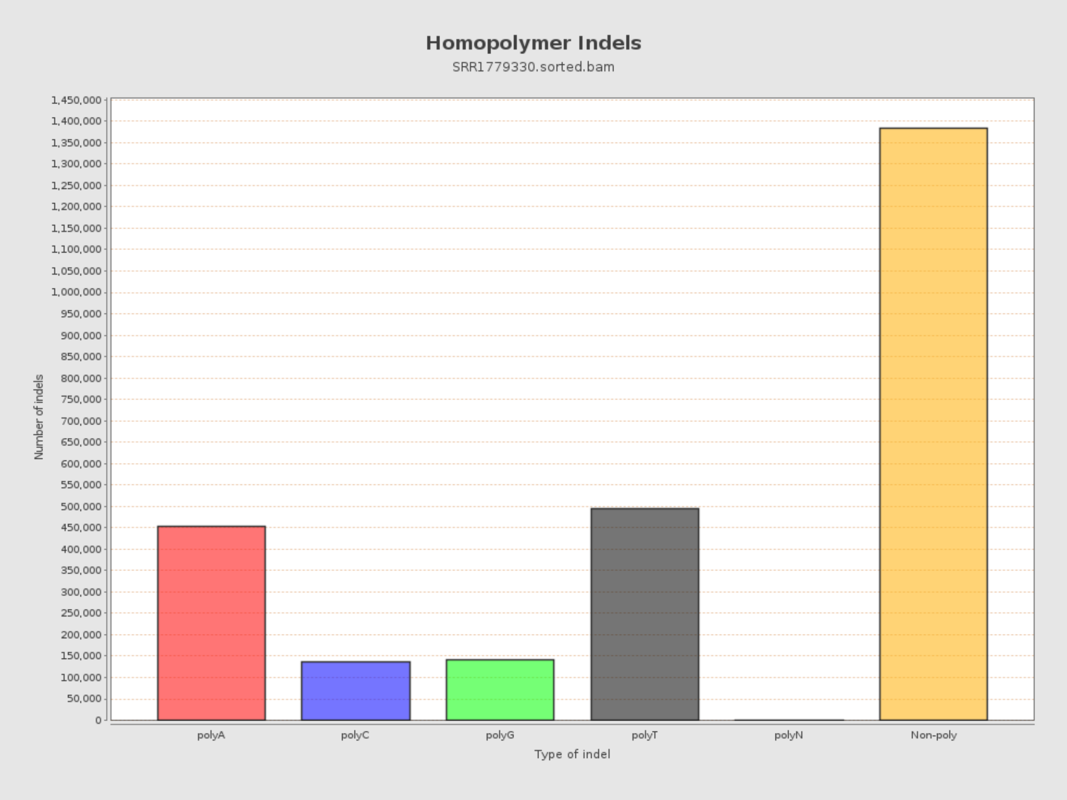
9. Results : Mapped Reads GC-content Distribution



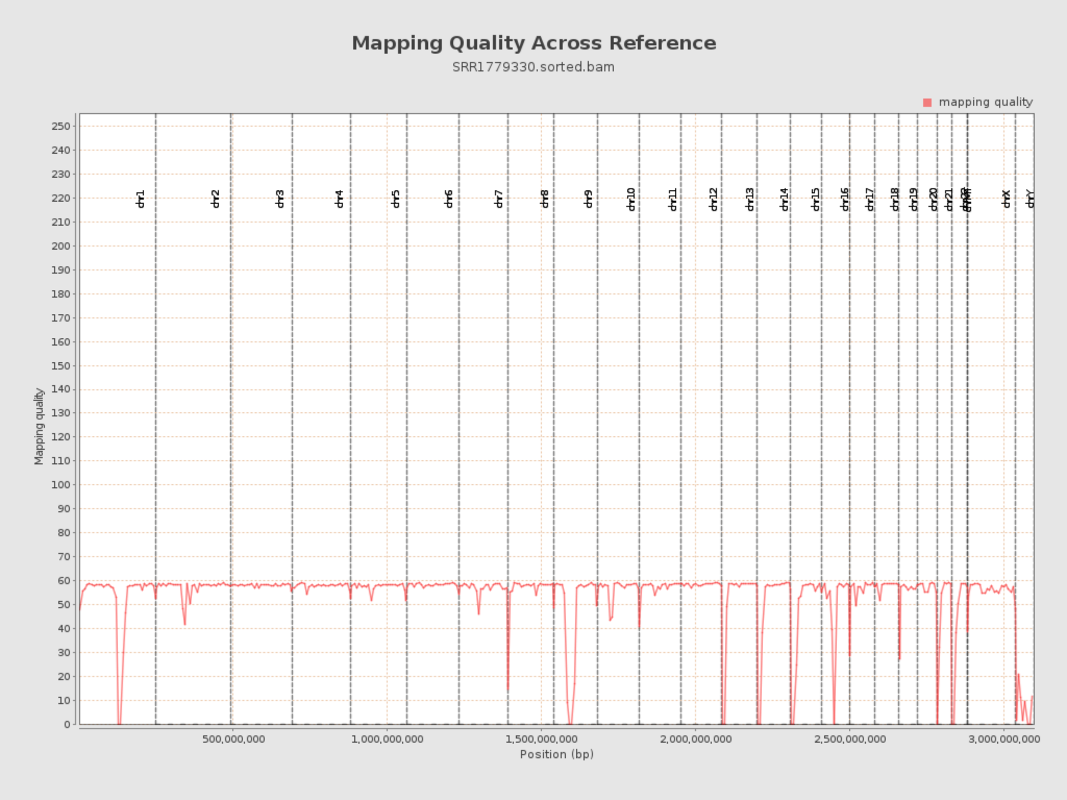
10. Results : Mapped Reads Clipping Profile



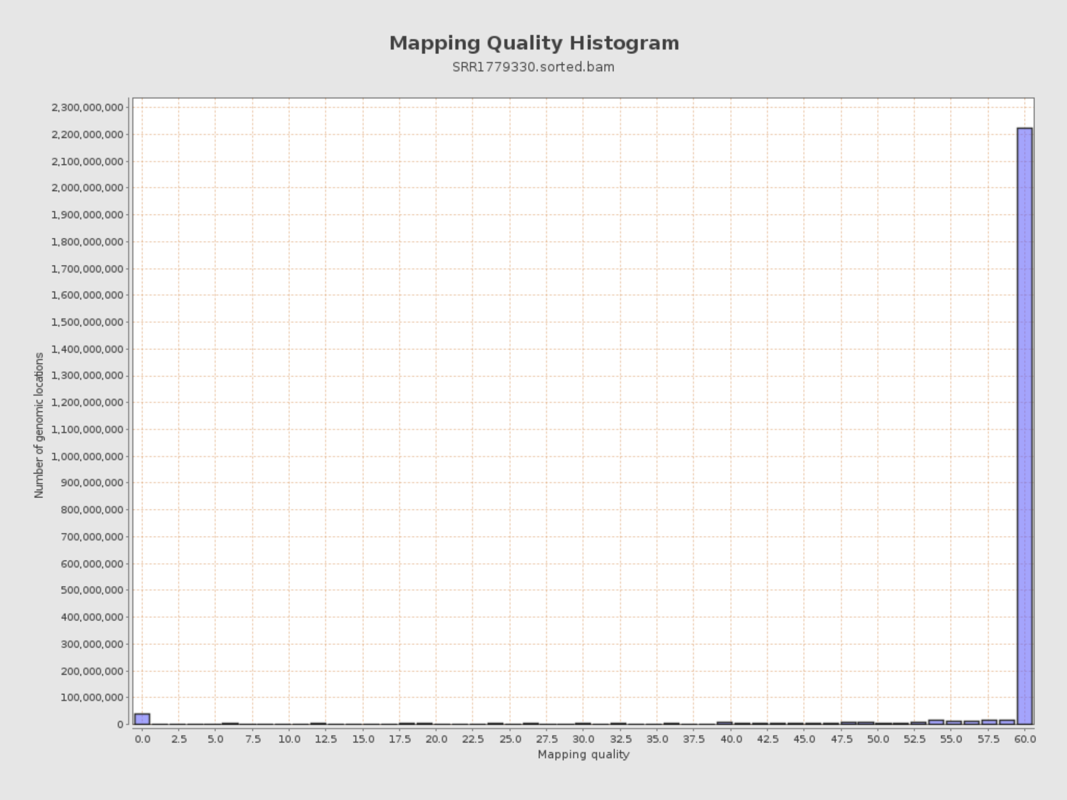
11. Results : Homopolymer Indels



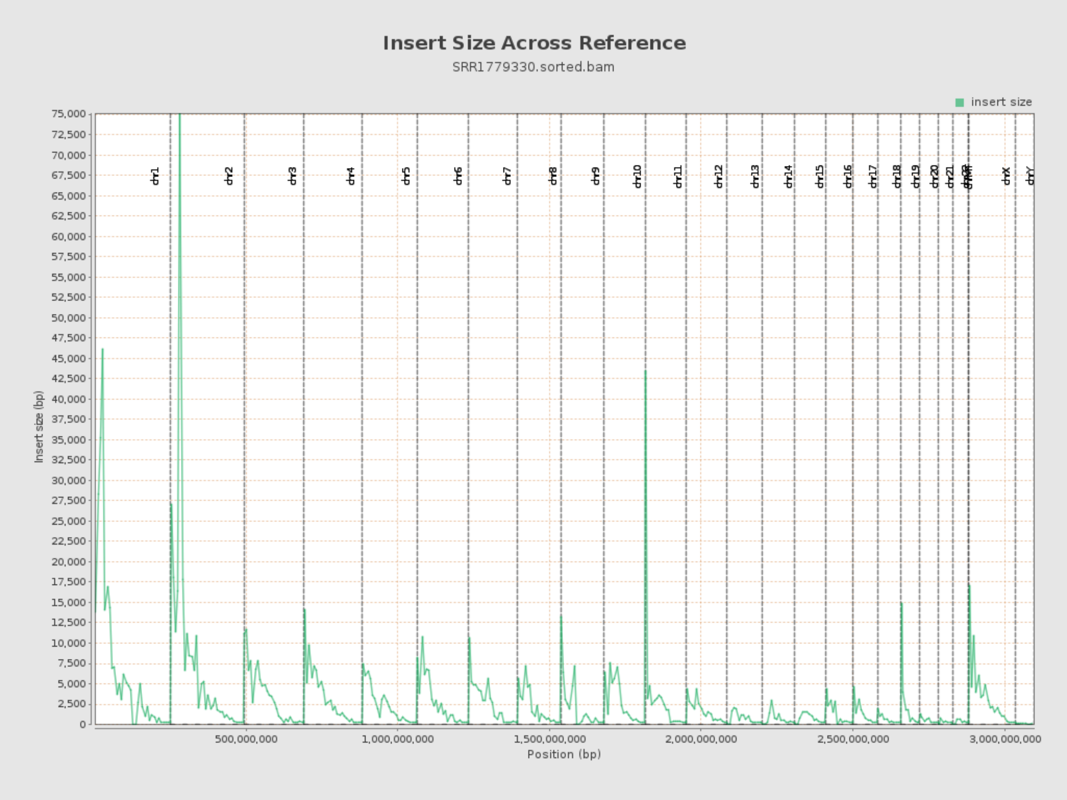
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram