Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 17:15:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779339.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_SRR1779339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779339_1.fastq.gz SRR1779339_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 17:15:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	161,009,040
Mapped reads	155,638,903 / 96.66%
Unmapped reads	5,370,137 / 3.34%
Mapped paired reads	155,638,903 / 96.66%
Mapped reads, first in pair	78,464,376 / 48.73%
Mapped reads, second in pair	77,174,527 / 47.93%
Mapped reads, both in pair	153,454,526 / 95.31%
Mapped reads, singletons	2,184,377 / 1.36%
Secondary alignments	0
Supplementary alignments	880,094 / 0.55%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	11,565,205 / 7.18%
Duplication rate	7.13%
Clipped reads	11,373,095 / 7.06%

2.2. ACGT Content

Number/percentage of A's	4,569,721,353 / 29.68%
Number/percentage of C's	3,118,856,885 / 20.26%
Number/percentage of T's	4,544,328,430 / 29.52%
Number/percentage of G's	3,161,590,575 / 20.54%
Number/percentage of N's	831,275 / 0.01%

GC Percentage	40.79%

2.3. Coverage

Mean	4.9743
Standard Deviation	7.886

2.4. Mapping Quality

Mean Mapping Quality	53.79

2.5. Insert size

Mean	59,928.45
Standard Deviation	2,403,804.17
P25/Median/P75	144 / 187 / 245

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	57,828,558
Insertions	1,549,087
Mapped reads with at least one insertion	0.98%
Deletions	1,575,513
Mapped reads with at least one deletion	0.99%
Homopolymer indels	47.06%

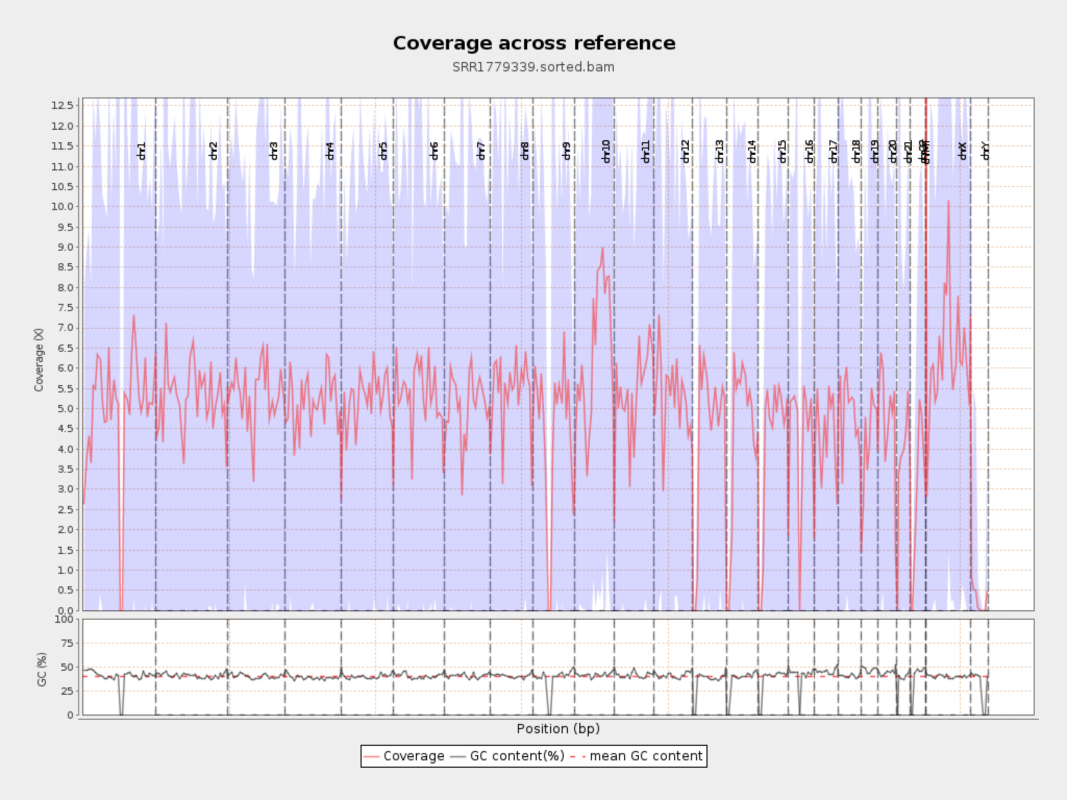
2.7. Chromosome stats

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

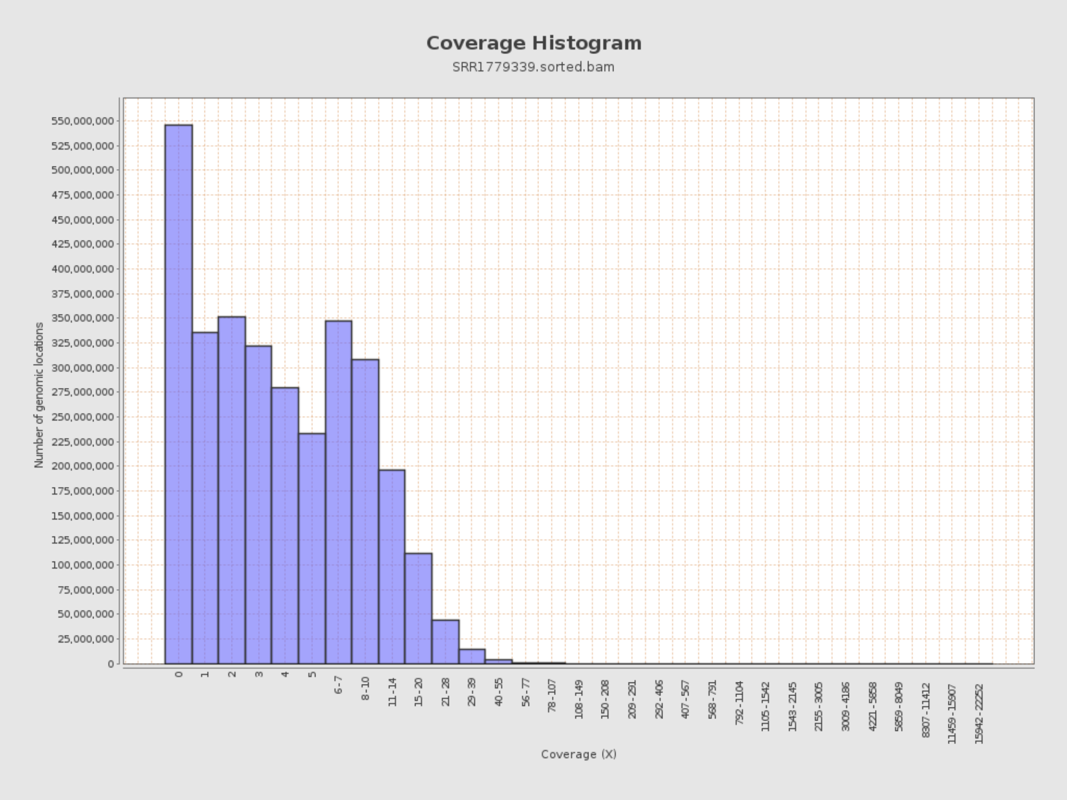
		bases	coverage	deviation
chr1	249250621	1235676898	4.9576	8.7204
chr2	243199373	1285200077	5.2846	18.2596
chr3	198022430	1063922767	5.3727	5.4465
chr4	191154276	993803052	5.199	5.7529
chr5	180915260	937561669	5.1823	5.2441
chr6	171115067	919752898	5.3751	6.0664
chr7	159138663	807243446	5.0726	5.97
chr8	146364022	797288040	5.4473	5.6813
chr9	141213431	628121768	4.448	6.3657
chr10	135534747	875278196	6.458	7.7148
chr11	135006516	733949163	5.4364	5.8314
chr12	133851895	712043572	5.3196	5.9294
chr13	115169878	511023706	4.4371	5.1902
chr14	107349540	472702247	4.4034	5.3843
chr15	102531392	415801400	4.0554	5.0058
chr16	90354753	374213144	4.1416	5.4114
chr17	81195210	361189856	4.4484	6.1346
chr18	78077248	385259074	4.9343	6.2087
chr19	59128983	248238594	4.1983	6.3792
chr20	63025520	313319308	4.9713	5.7988
chr21	48129895	179973181	3.7393	7.177
chr22	51304566	150154411	2.9267	4.4807
chrMT	16571	783666	47.2914	13.0578
chrX	155270560	979831437	6.3105	6.6284

chrY	59373566	16470241	0.2774	2.8196

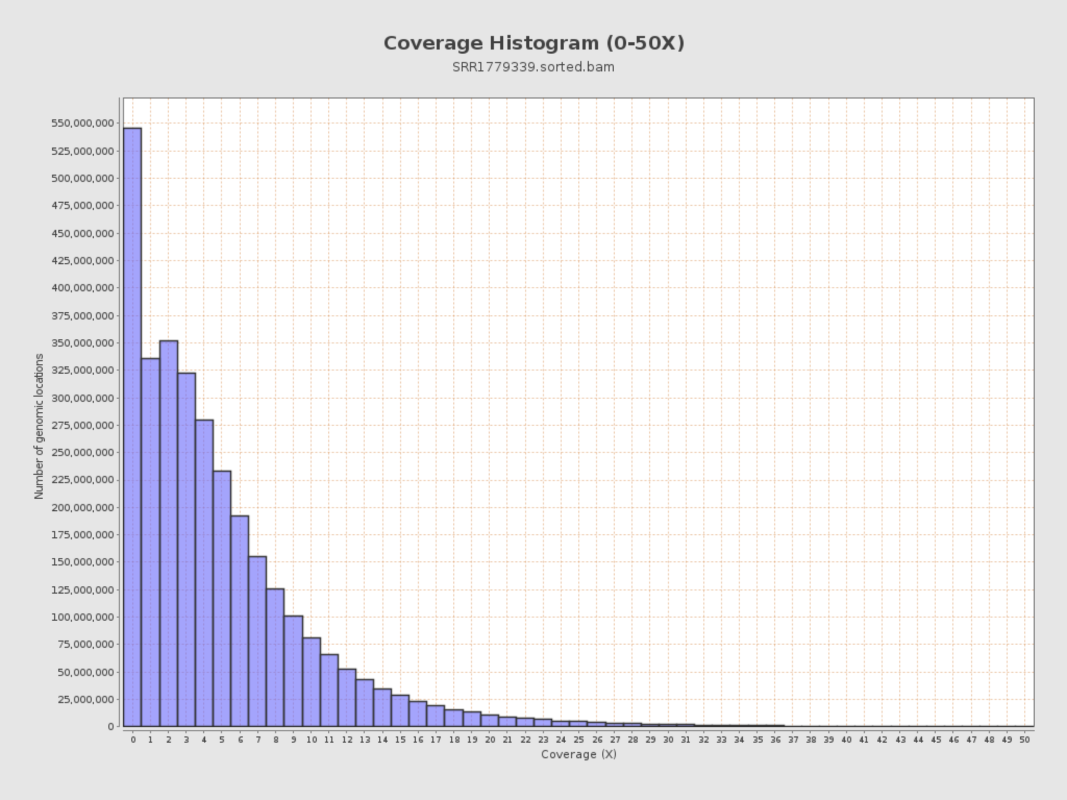
3. Results : Coverage across reference



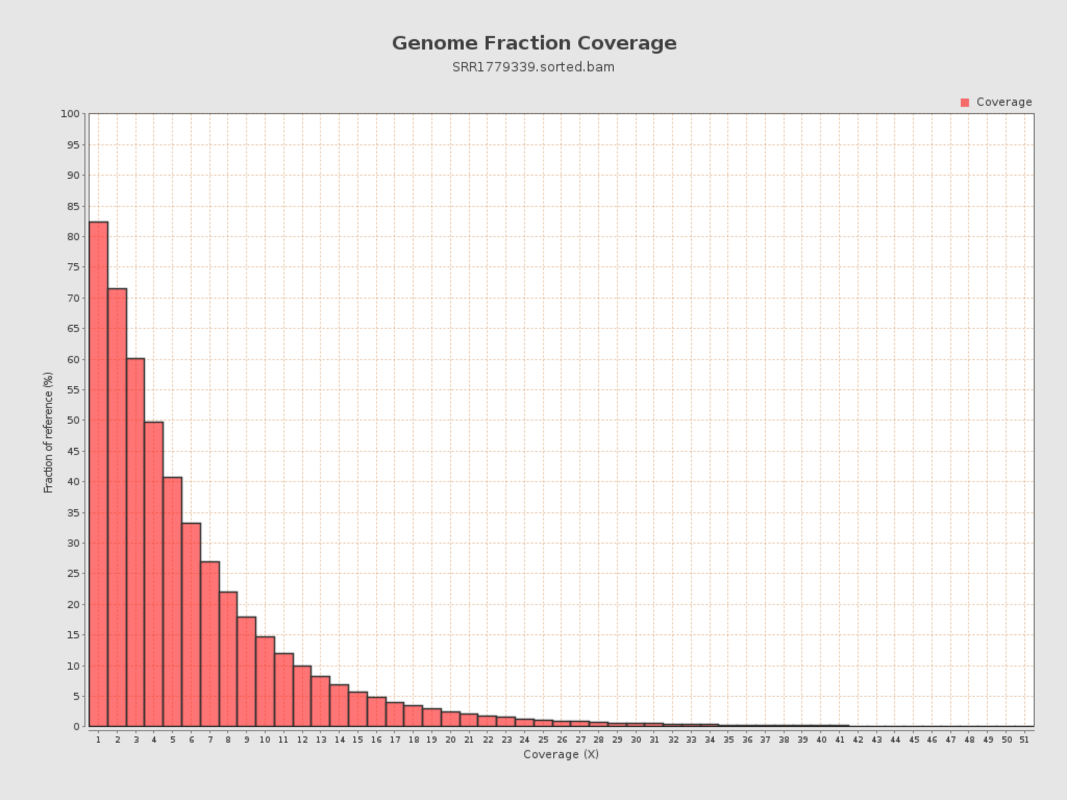
4. Results : Coverage Histogram



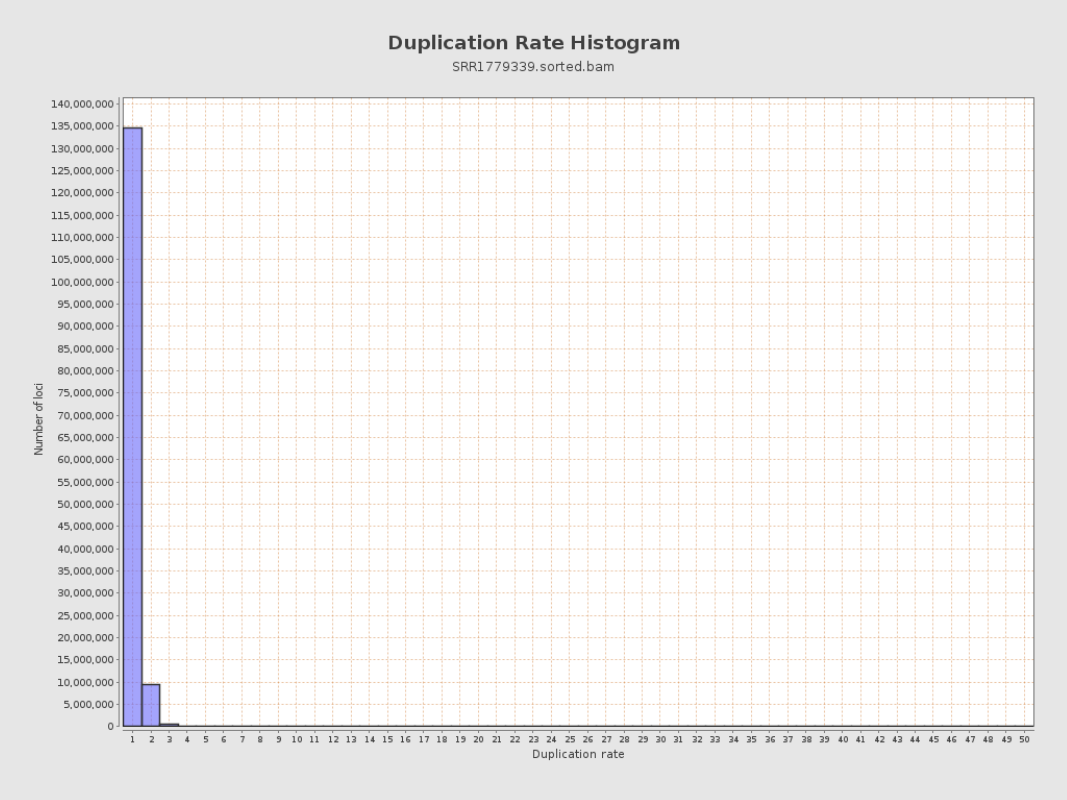
5. Results : Coverage Histogram (0-50X)



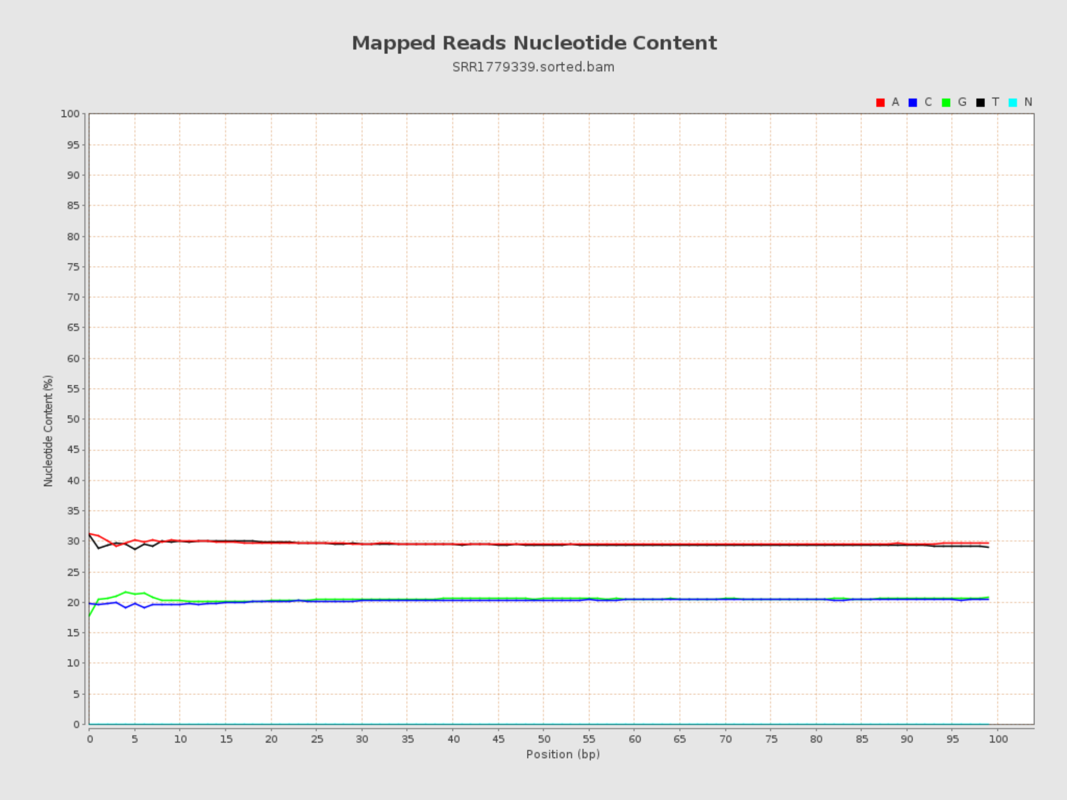
6. Results : Genome Fraction Coverage



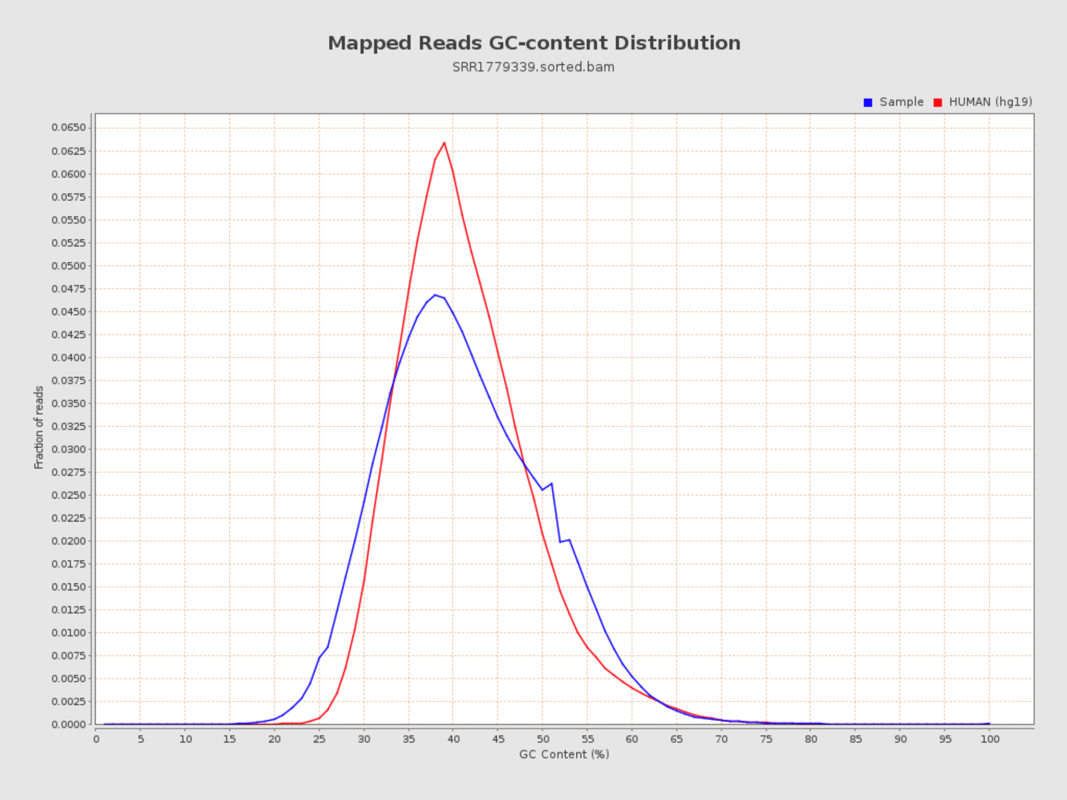
7. Results : Duplication Rate Histogram



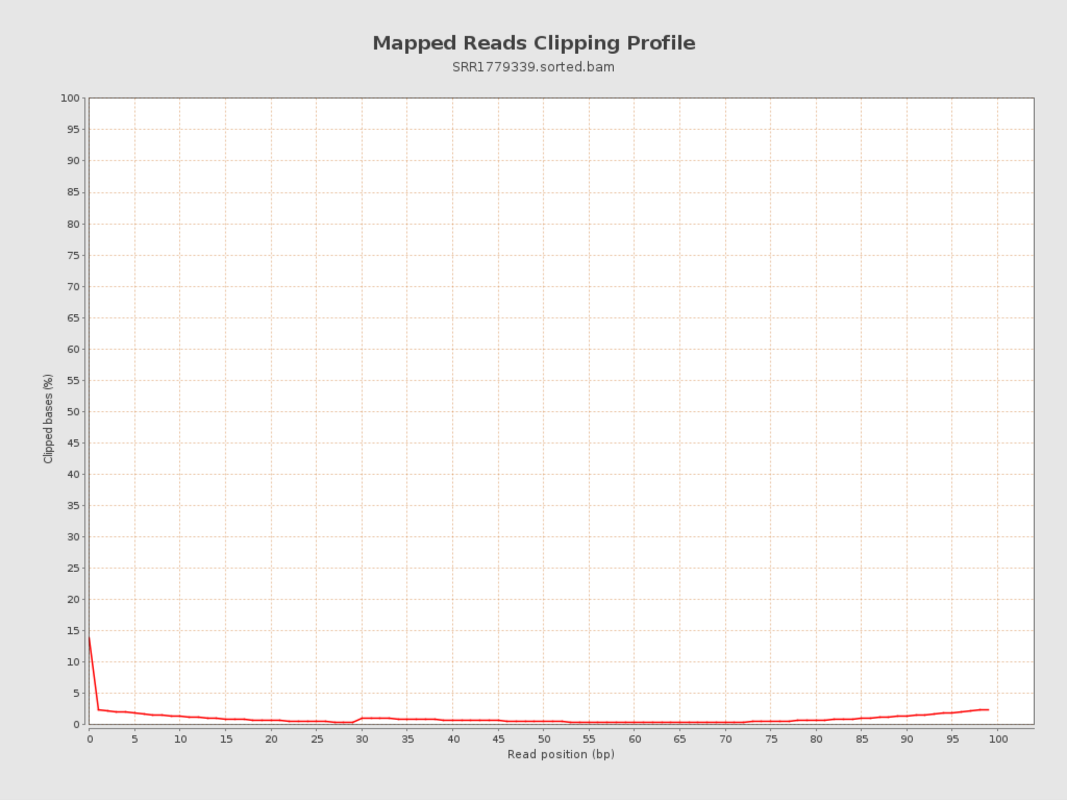
8. Results : Mapped Reads Nucleotide Content



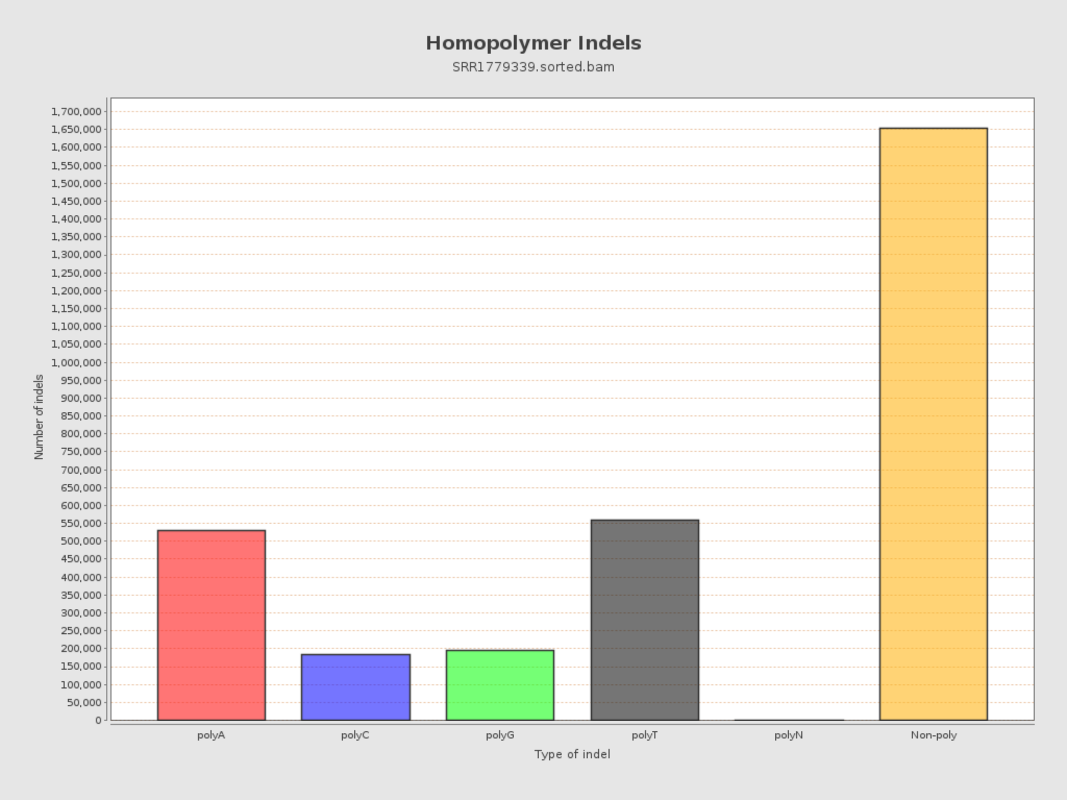
9. Results : Mapped Reads GC-content Distribution



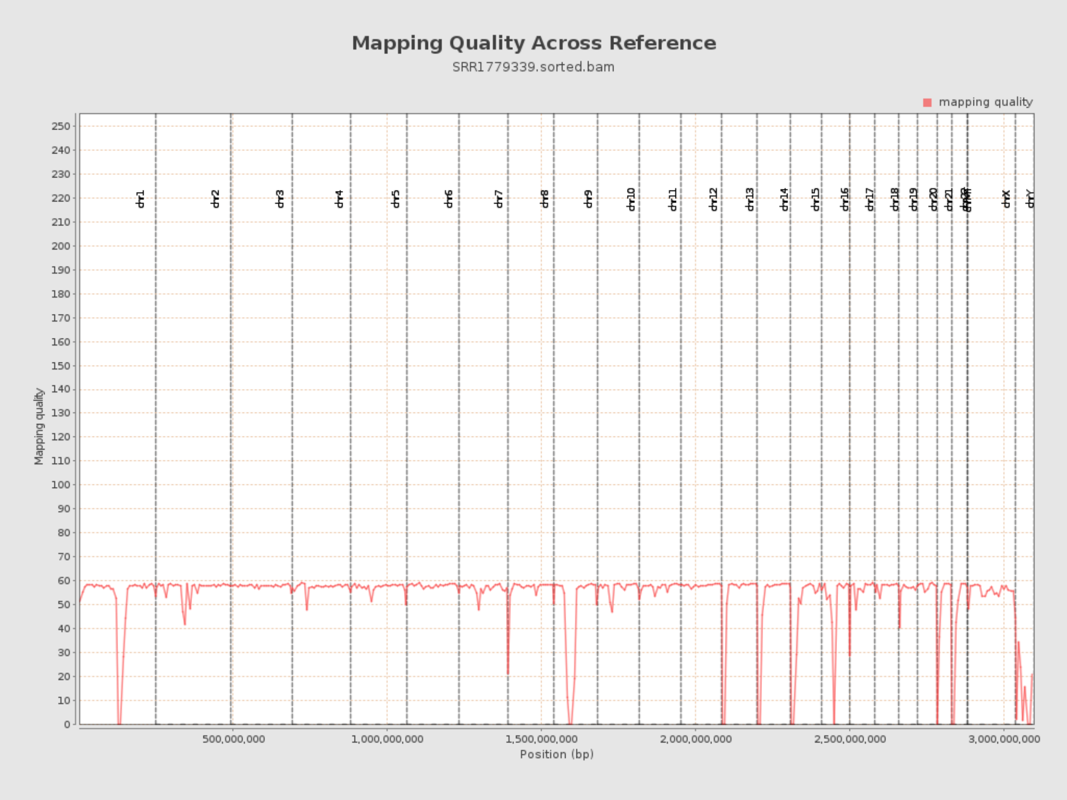
10. Results : Mapped Reads Clipping Profile



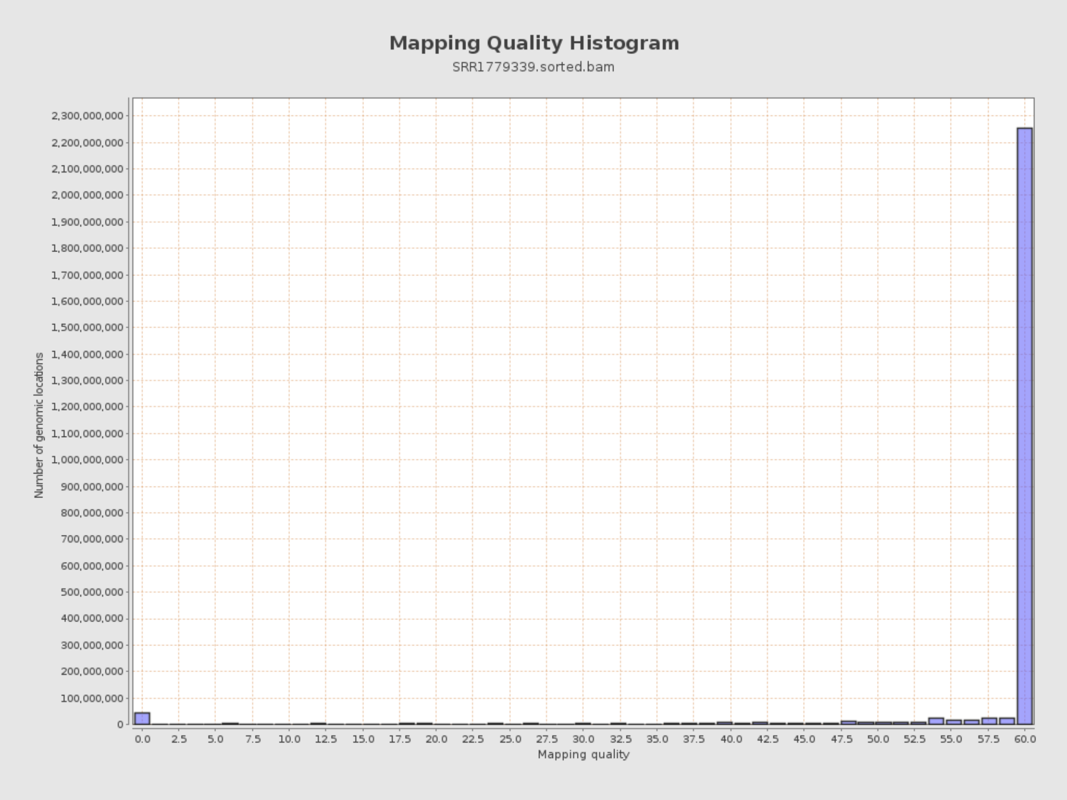
11. Results : Homopolymer Indels



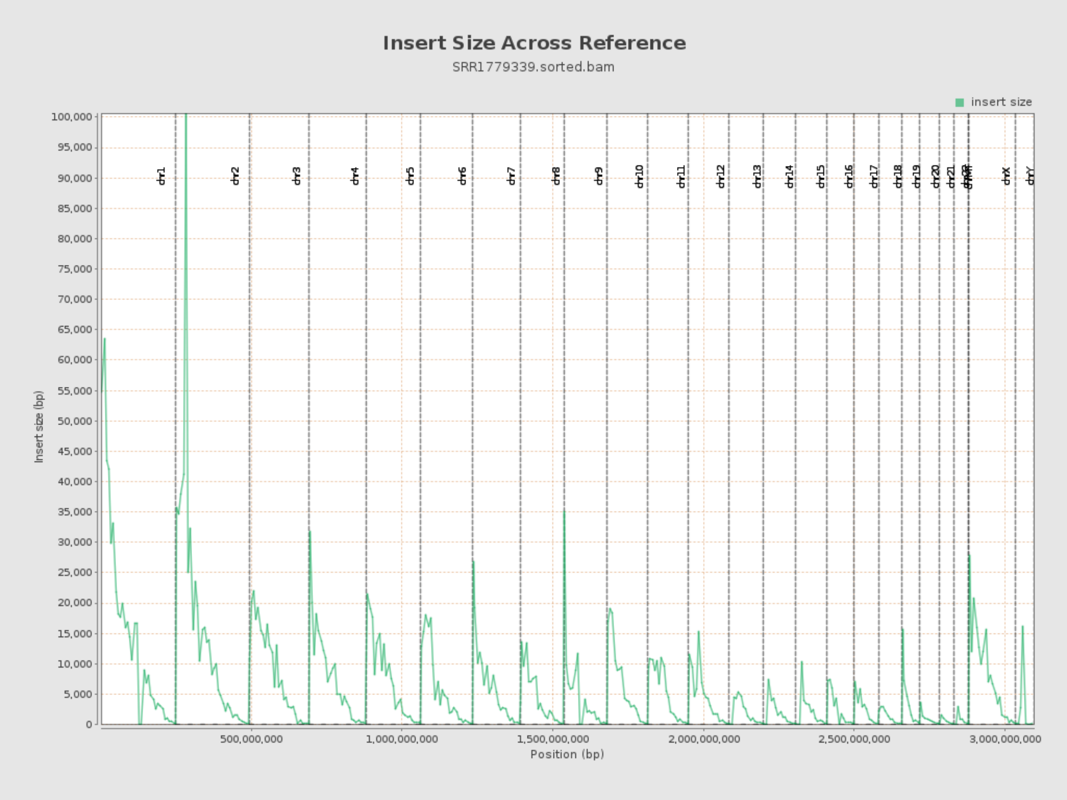
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram