Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 13:44:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779376.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_SRR1779376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779376_1.fastq.gz SRR1779376_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 13:44:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,912,028
Mapped reads	18,327,900 / 83.64%
Unmapped reads	3,584,128 / 16.36%
Mapped paired reads	18,327,900 / 83.64%
Mapped reads, first in pair	9,224,093 / 42.1%
Mapped reads, second in pair	9,103,807 / 41.55%
Mapped reads, both in pair	18,005,268 / 82.17%
Mapped reads, singletons	322,632 / 1.47%
Secondary alignments	0
Supplementary alignments	222,151 / 1.01%
Read min/max/mean length	30 / 80 / 80.37
Duplicated reads (estimated)	8,884,823 / 40.55%
Duplication rate	16.93%
Clipped reads	1,581,418 / 7.22%

2.2. ACGT Content

Number/percentage of A's	455,770,879 / 31.42%
Number/percentage of C's	271,074,441 / 18.68%
Number/percentage of T's	446,175,881 / 30.75%
Number/percentage of G's	277,448,450 / 19.12%
Number/percentage of N's	313,818 / 0.02%

GC Percentage	37.81%

2.3. Coverage

Mean	0.4688
Standard Deviation	44.8753

2.4. Mapping Quality

Mean Mapping Quality	52.33

2.5. Insert size

Mean	289,455.98
Standard Deviation	5,193,049.24
P25/Median/P75	126 / 162 / 207

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	4,846,303
Insertions	172,280
Mapped reads with at least one insertion	0.93%
Deletions	162,002
Mapped reads with at least one deletion	0.84%
Homopolymer indels	46.27%

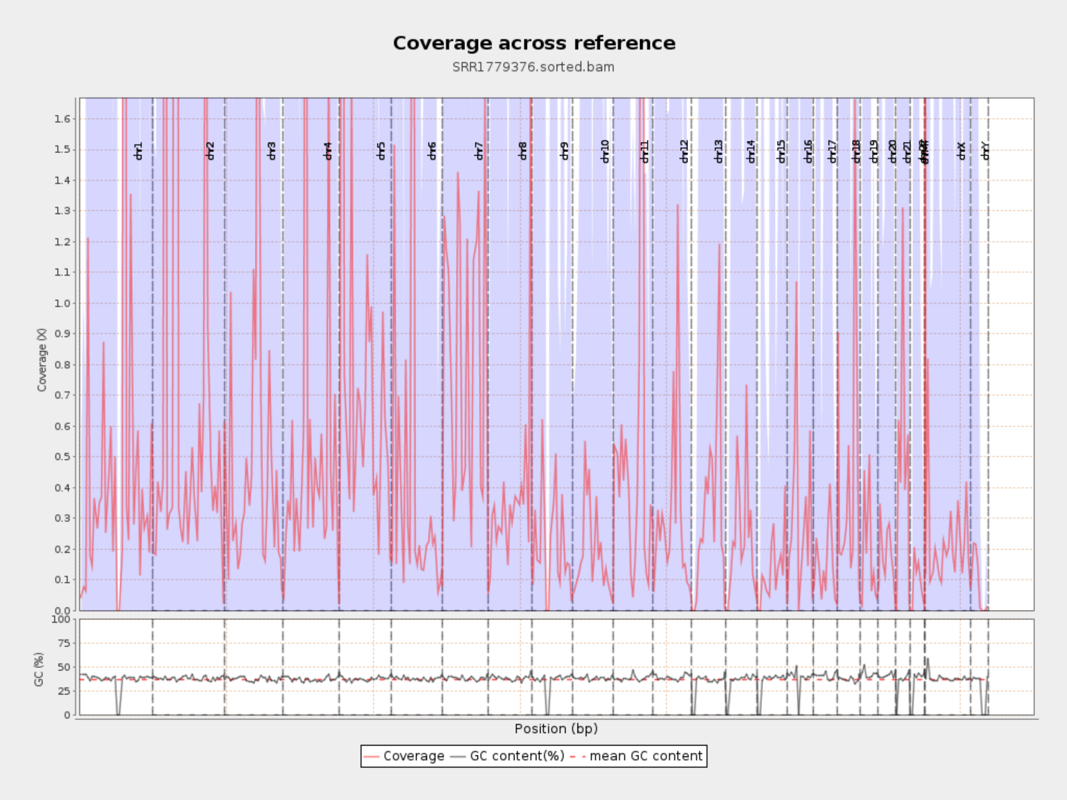
2.7. Chromosome stats

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

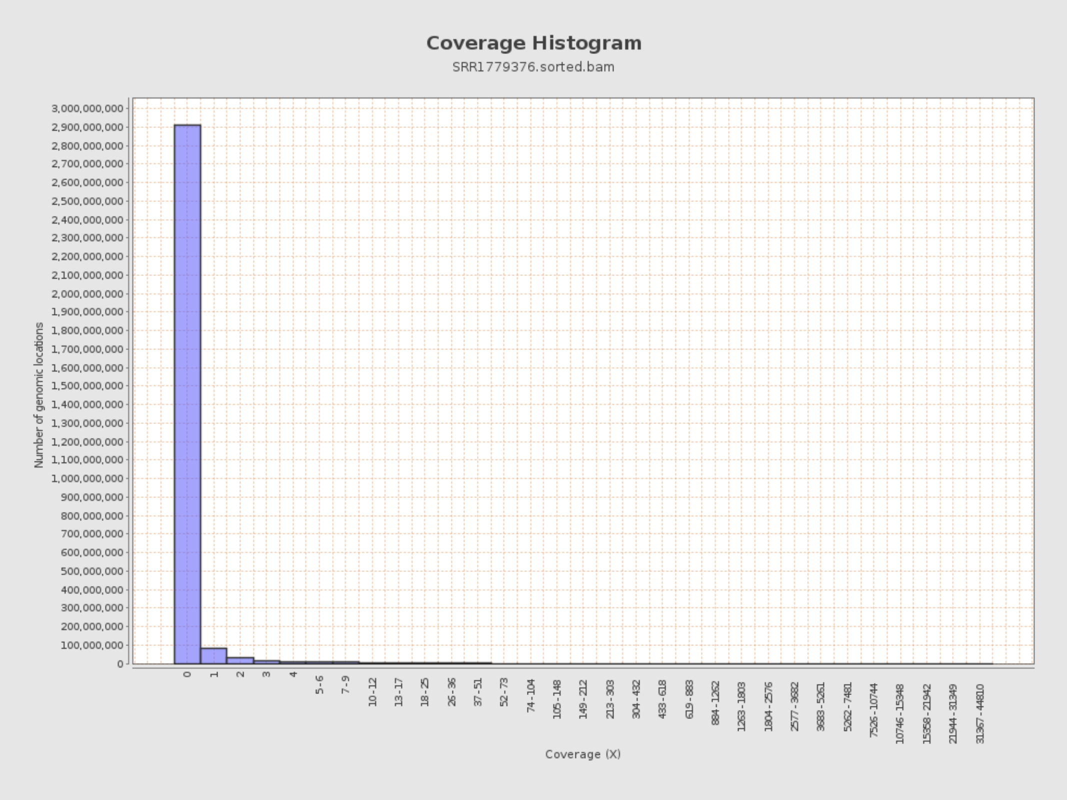
		bases	coverage	deviation
chr1	249250621	152701851	0.6126	77.0044
chr2	243199373	244922037	1.0071	125.2656
chr3	198022430	100592741	0.508	15.8363
chr4	191154276	105401908	0.5514	29.8274
chr5	180915260	154266842	0.8527	35.07
chr6	171115067	79359508	0.4638	8.2135
chr7	159138663	134196594	0.8433	20.6464
chr8	146364022	57348222	0.3918	32.3913
chr9	141213431	30027343	0.2126	9.7064
chr10	135534747	26392269	0.1947	5.558
chr11	135006516	80741688	0.5981	23.0873
chr12	133851895	41106482	0.3071	5.0724
chr13	115169878	39292133	0.3412	18.3332
chr14	107349540	26106364	0.2432	3.4836
chr15	102531392	13905101	0.1356	2.6101
chr16	90354753	26862479	0.2973	20.8019
chr17	81195210	11828239	0.1457	3.9376
chr18	78077248	32897379	0.4213	20.0009
chr19	59128983	11055984	0.187	9.8913
chr20	63025520	11795894	0.1872	2.882
chr21	48129895	25757937	0.5352	27.7555
chr22	51304566	4519171	0.0881	1.8027
chrMT	16571	196103	11.8341	6.9423
chrX	155270560	34579473	0.2227	9.8624

chrY	59373566	5272927	0.0888	3.408

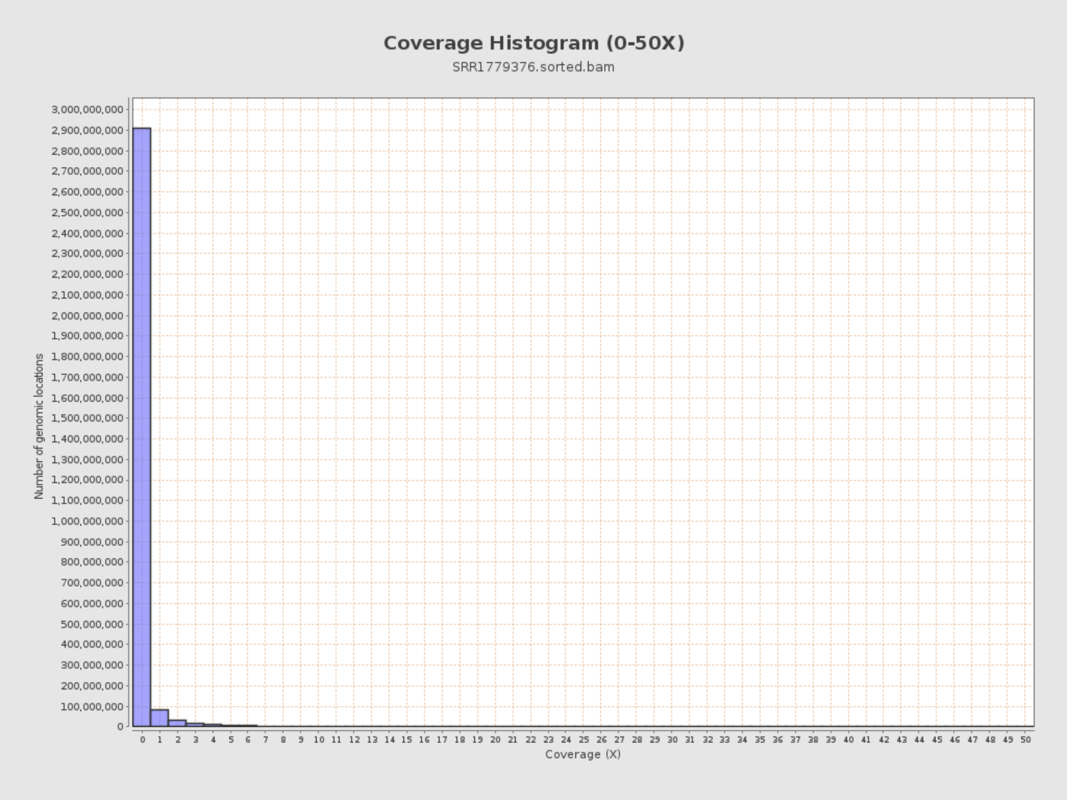
3. Results : Coverage across reference



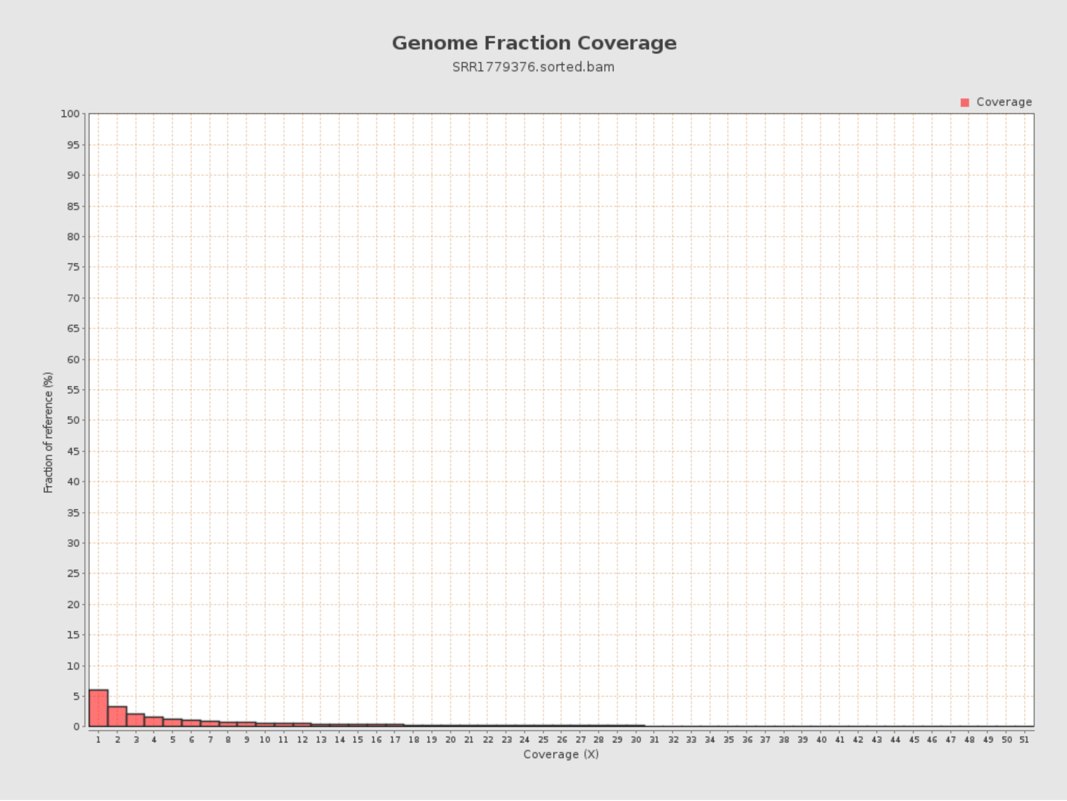
4. Results : Coverage Histogram



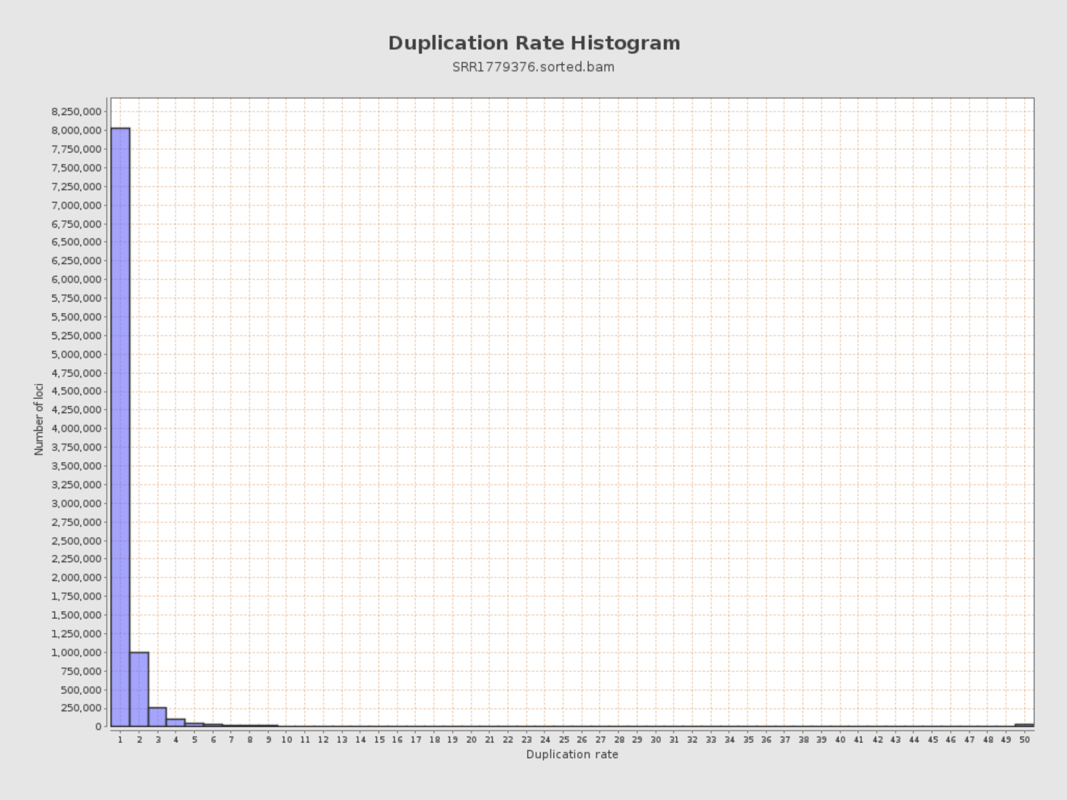
5. Results : Coverage Histogram (0-50X)



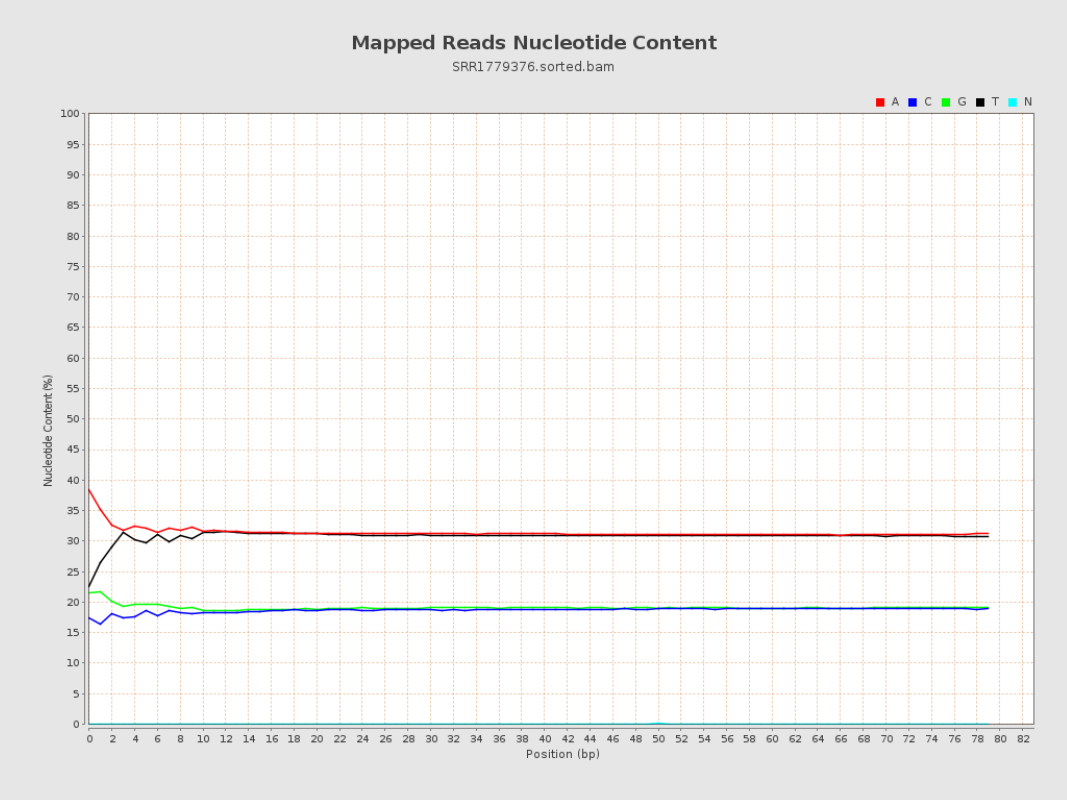
6. Results : Genome Fraction Coverage



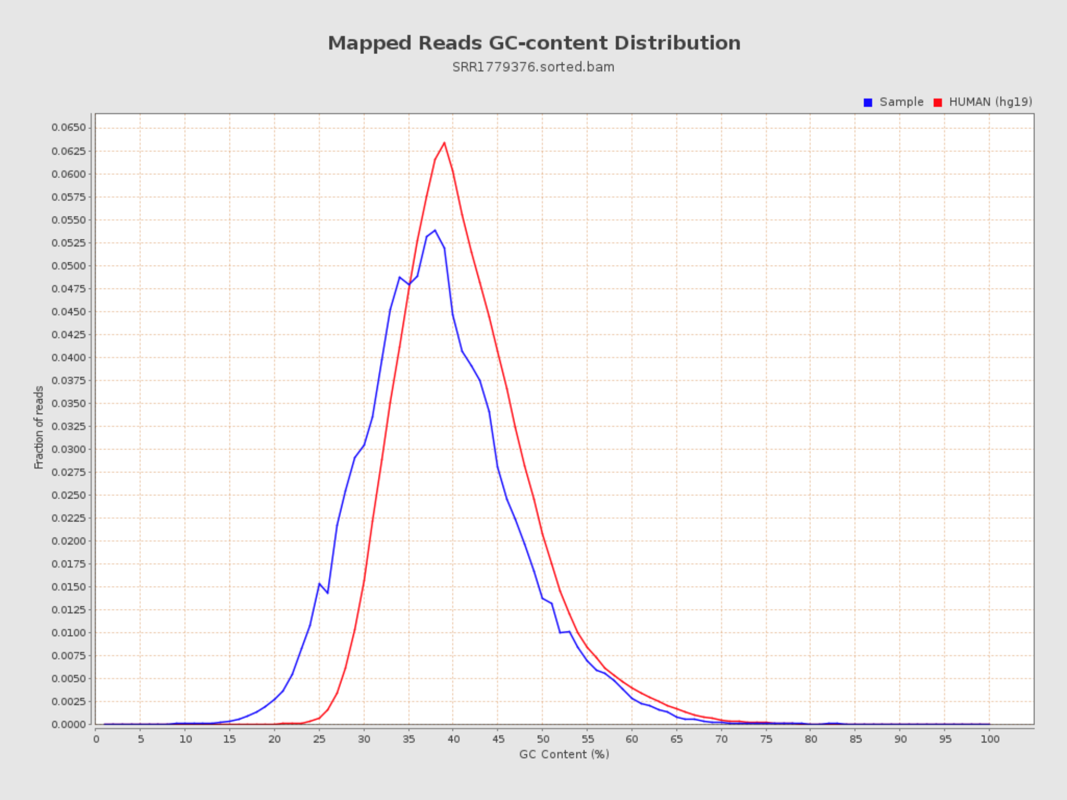
7. Results : Duplication Rate Histogram



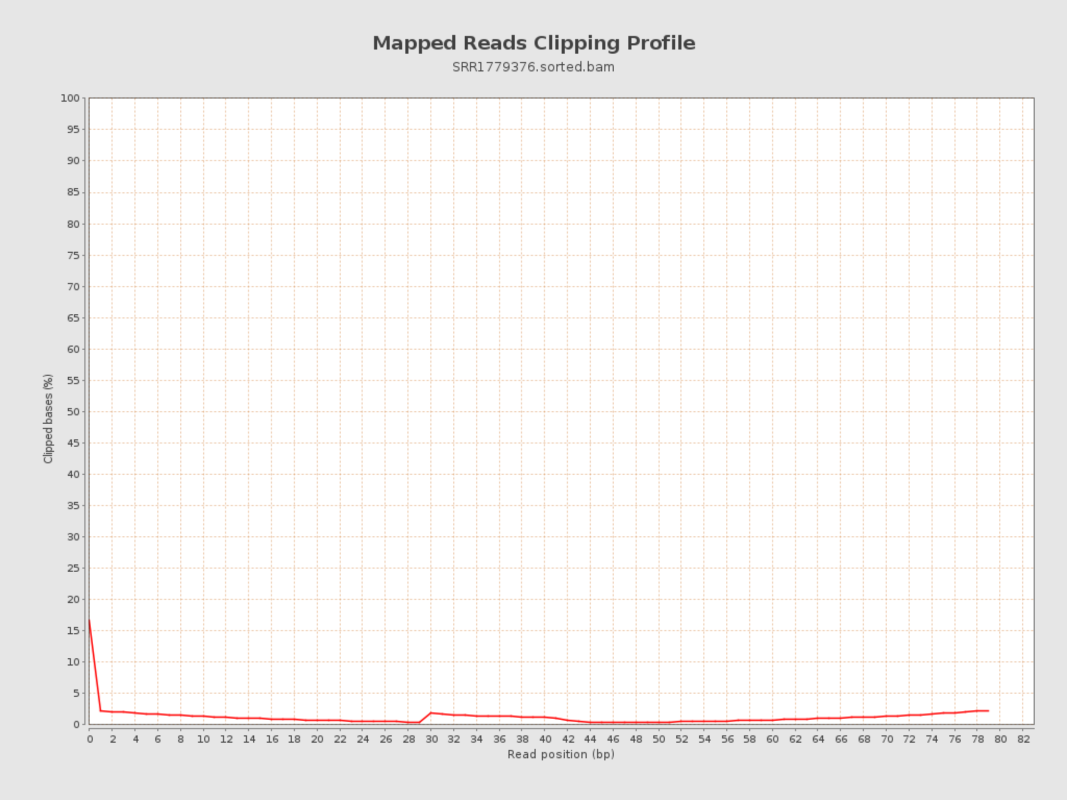
8. Results : Mapped Reads Nucleotide Content



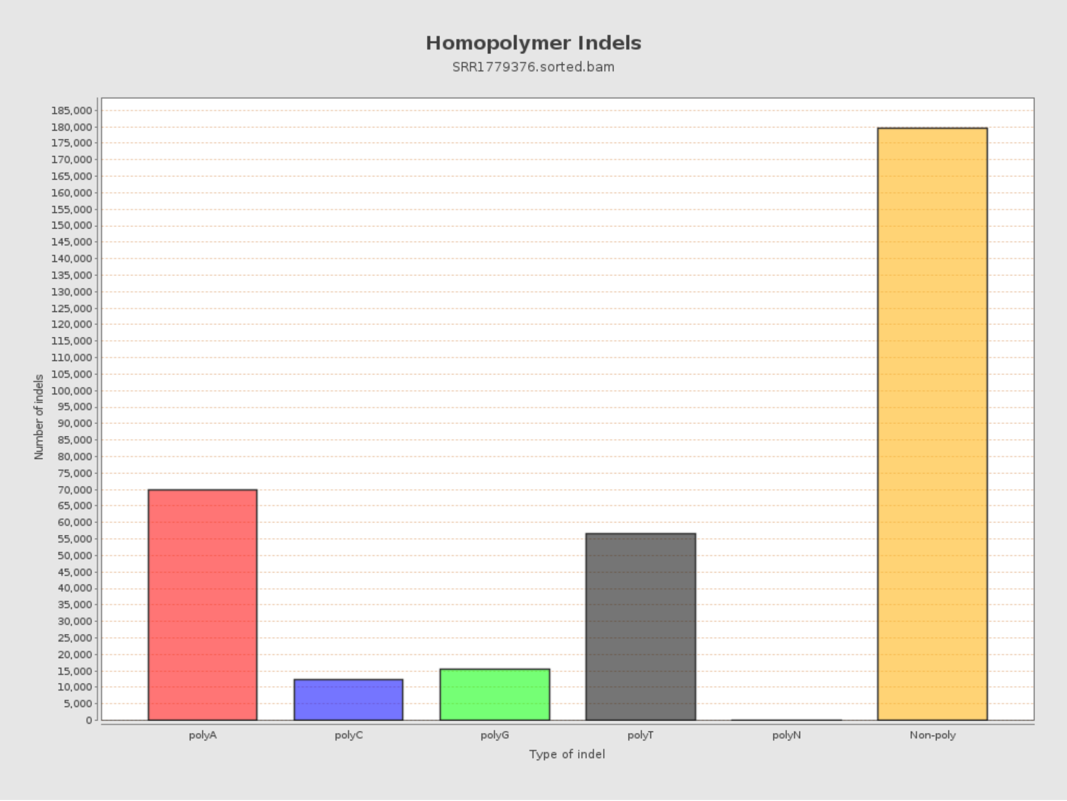
9. Results : Mapped Reads GC-content Distribution



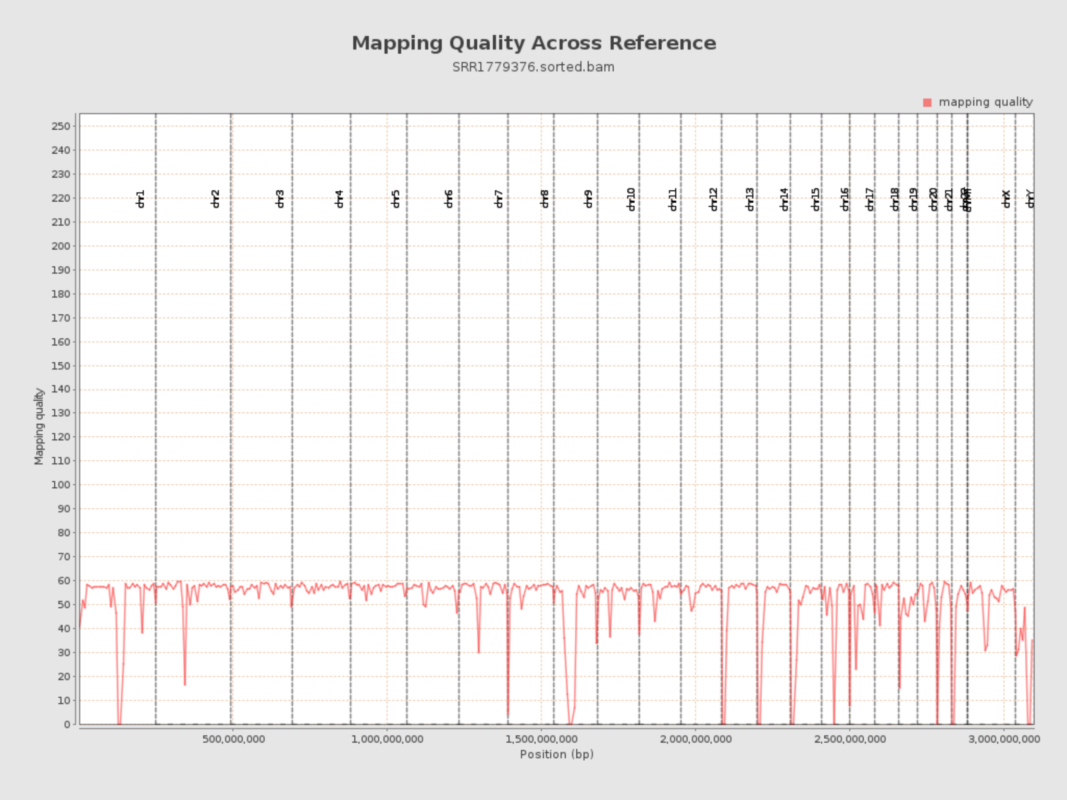
10. Results : Mapped Reads Clipping Profile



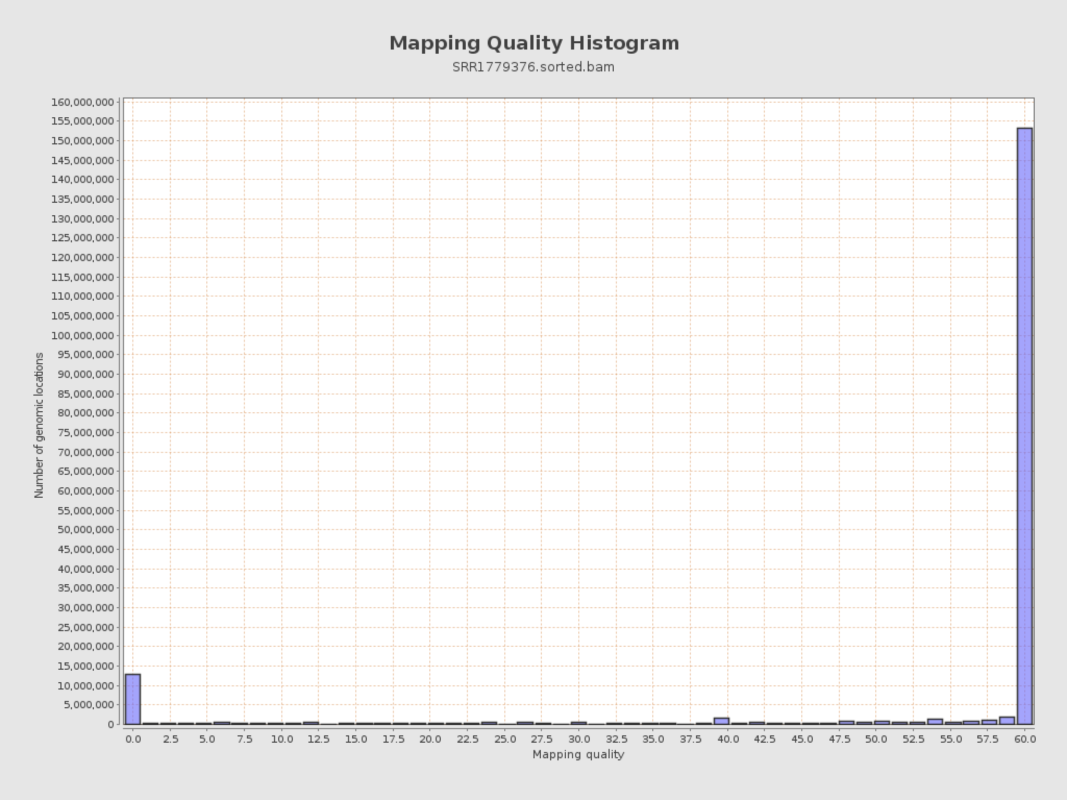
11. Results : Homopolymer Indels



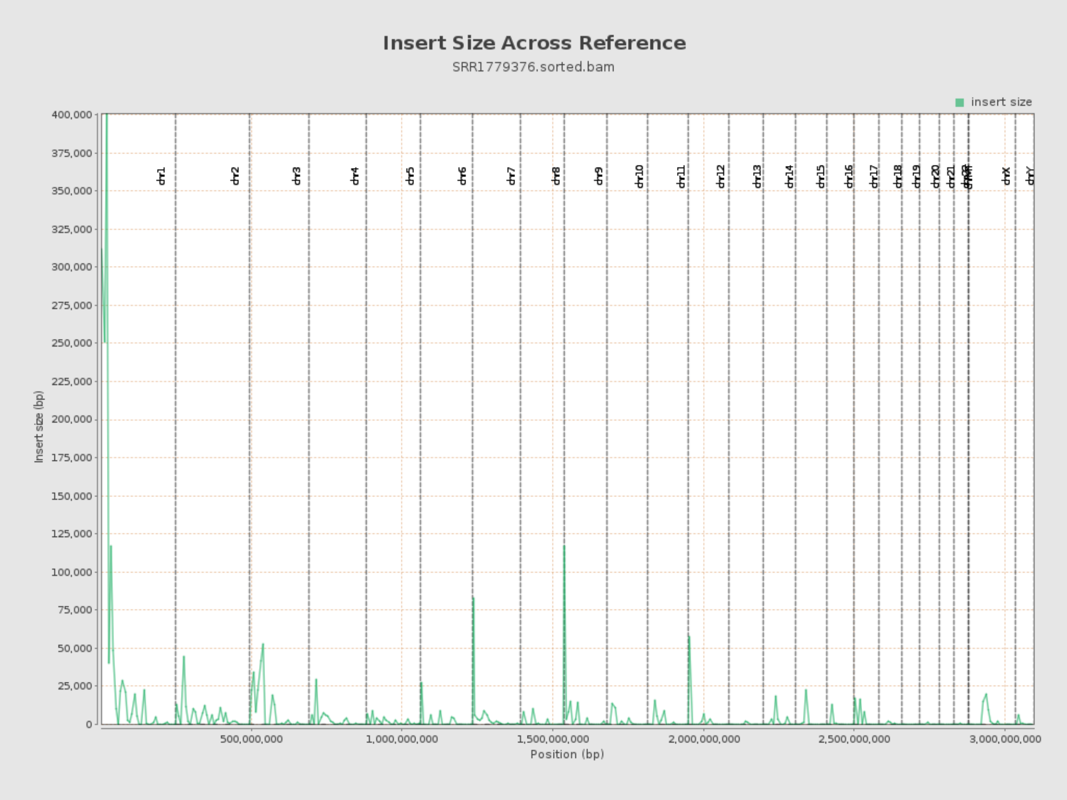
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram