Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 13:41:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779196.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_SRR1779196 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779196_1.fastq.gz SRR1779196_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 13:41:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779196.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,942,624
Mapped reads	11,642,873 / 97.49%
Unmapped reads	299,751 / 2.51%
Mapped paired reads	11,642,873 / 97.49%
Mapped reads, first in pair	5,851,298 / 49%
Mapped reads, second in pair	5,791,575 / 48.49%
Mapped reads, both in pair	11,567,668 / 96.86%
Mapped reads, singletons	75,205 / 0.63%
Secondary alignments	0
Supplementary alignments	29,053 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	152,132 / 1.27%
Duplication rate	1.19%
Clipped reads	382,664 / 3.2%

2.2. ACGT Content

Number/percentage of A's	283,492,269 / 30.6%
Number/percentage of C's	178,968,740 / 19.32%
Number/percentage of T's	281,981,044 / 30.43%
Number/percentage of G's	181,917,020 / 19.63%
Number/percentage of N's	174,072 / 0.02%

GC Percentage	38.95%

2.3. Coverage

Mean	0.2994
Standard Deviation	0.8961

2.4. Mapping Quality

Mean Mapping Quality	52.93

2.5. Insert size

Mean	44,997.82
Standard Deviation	1,983,977.3
P25/Median/P75	150 / 197 / 263

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	3,522,068
Insertions	67,065
Mapped reads with at least one insertion	0.57%
Deletions	84,150
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.64%

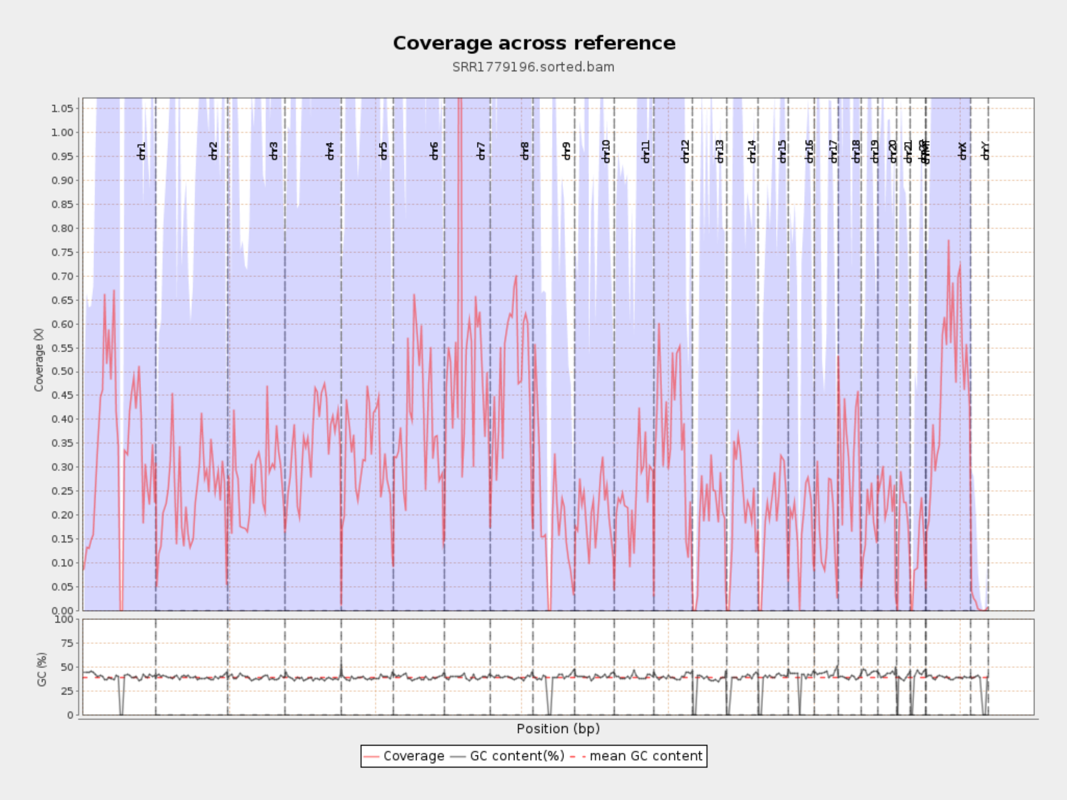
2.7. Chromosome stats

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

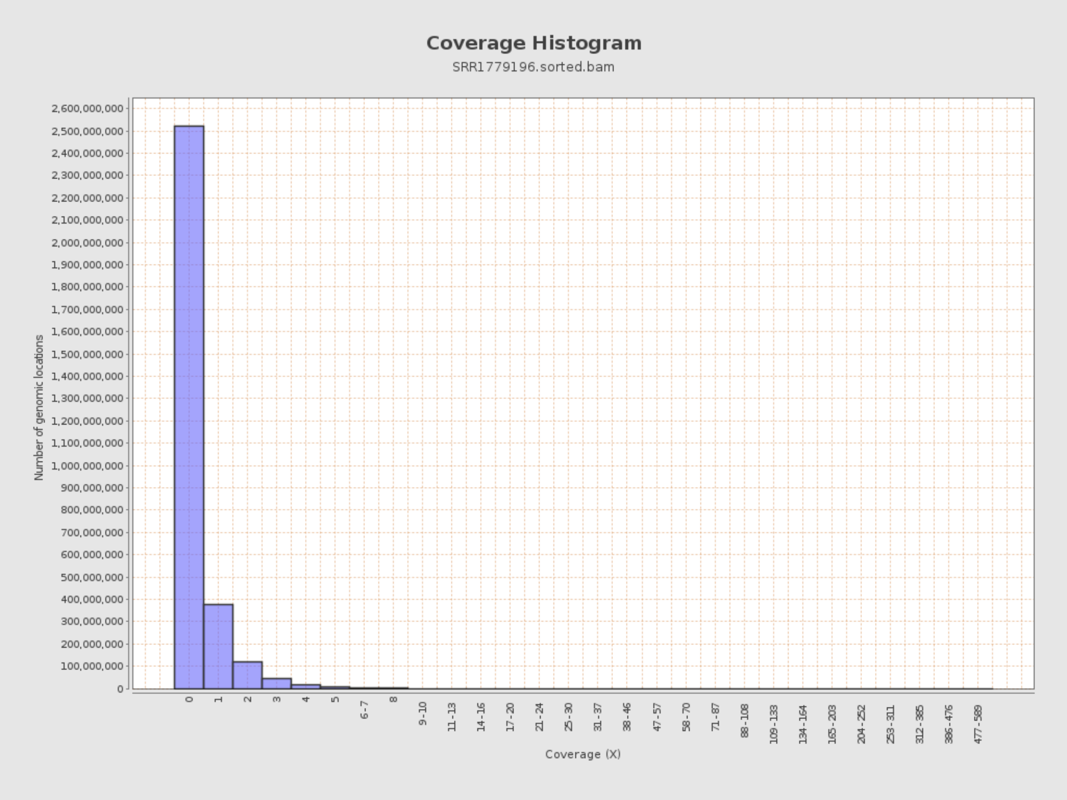
		bases	**coverage**	**deviation**
chr1	249250621	83623319	0.3355	0.9987
chr2	243199373	58524374	0.2406	0.6759
chr3	198022430	53719043	0.2713	0.7241
chr4	191154276	67855571	0.355	0.8247
chr5	180915260	56433117	0.3119	0.7602
chr6	171115067	68313374	0.3992	0.8916
chr7	159138663	89170302	0.5603	1.8841
chr8	146364022	72855834	0.4978	1.0203
chr9	141213431	27817823	0.197	0.6287
chr10	135534747	27753363	0.2048	1.1399
chr11	135006516	32747350	0.2426	0.6889
chr12	133851895	49779946	0.3719	0.8753
chr13	115169878	22120426	0.1921	0.5906
chr14	107349540	23081602	0.215	0.6312
chr15	102531392	20071452	0.1958	0.6128
chr16	90354753	15973871	0.1768	0.5471
chr17	81195210	14514130	0.1788	0.6116
chr18	78077248	26587338	0.3405	0.8251
chr19	59128983	10743363	0.1817	0.6601
chr20	63025520	14942701	0.2371	0.6701
chr21	48129895	8672459	0.1802	0.5773
chr22	51304566	5983305	0.1166	0.4736
chrMT	16571	732	0.0442	0.3024
chrX	155270560	74787623	0.4817	1.0693

chrY	59373566	633924	0.0107	0.1427

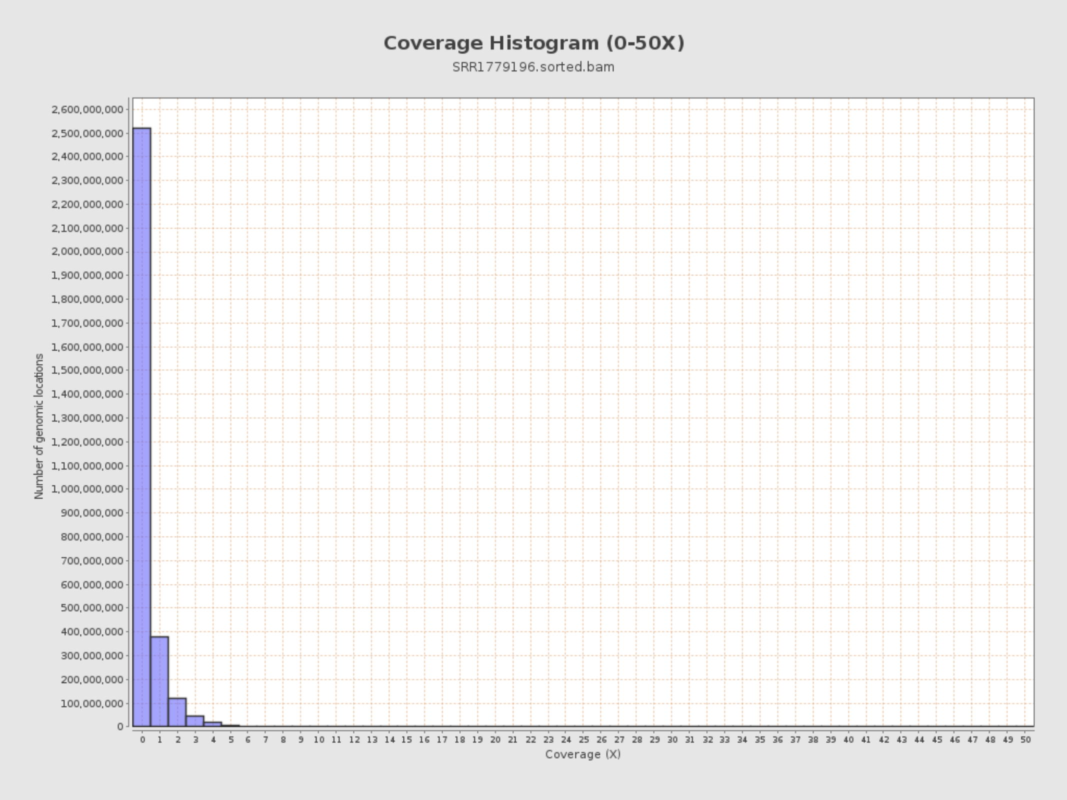
3. Results : Coverage across reference



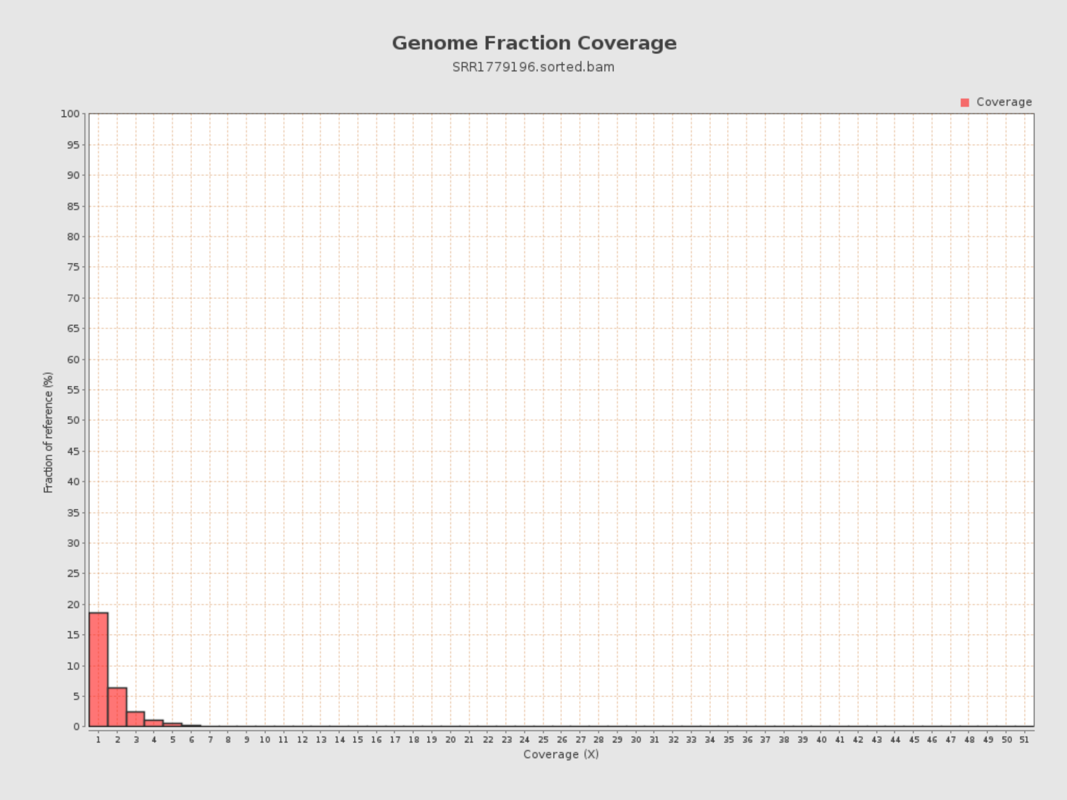
4. Results : Coverage Histogram



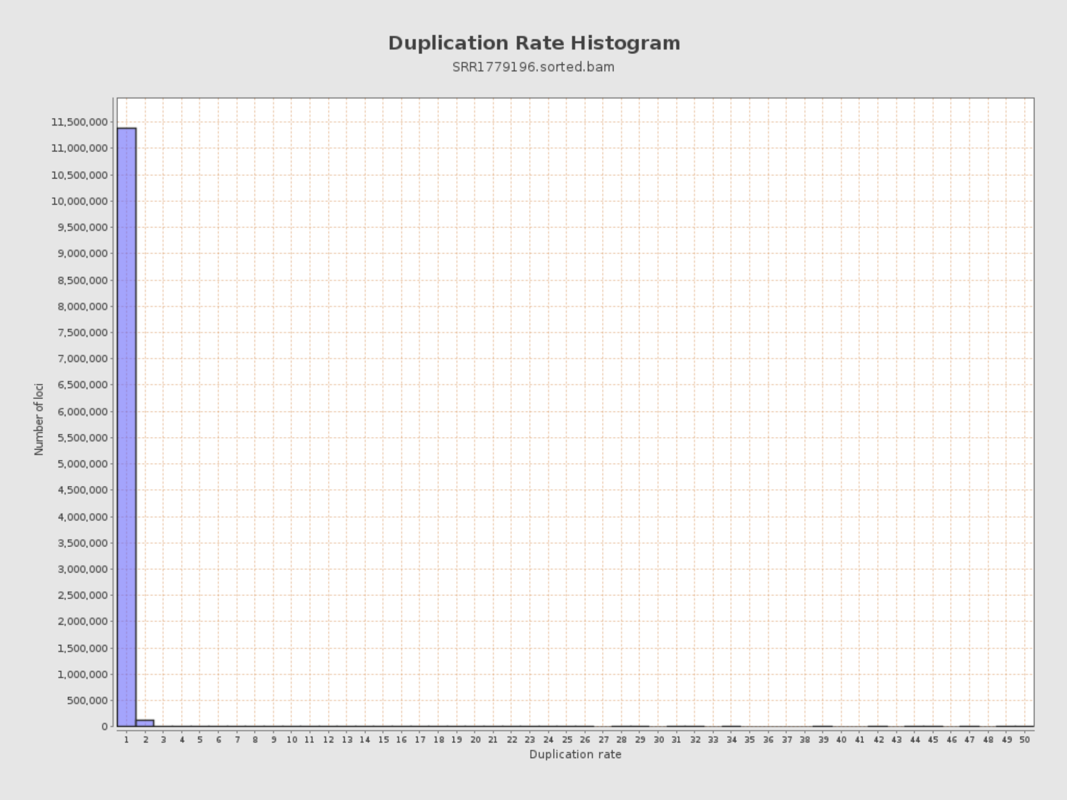
5. Results : Coverage Histogram (0-50X)



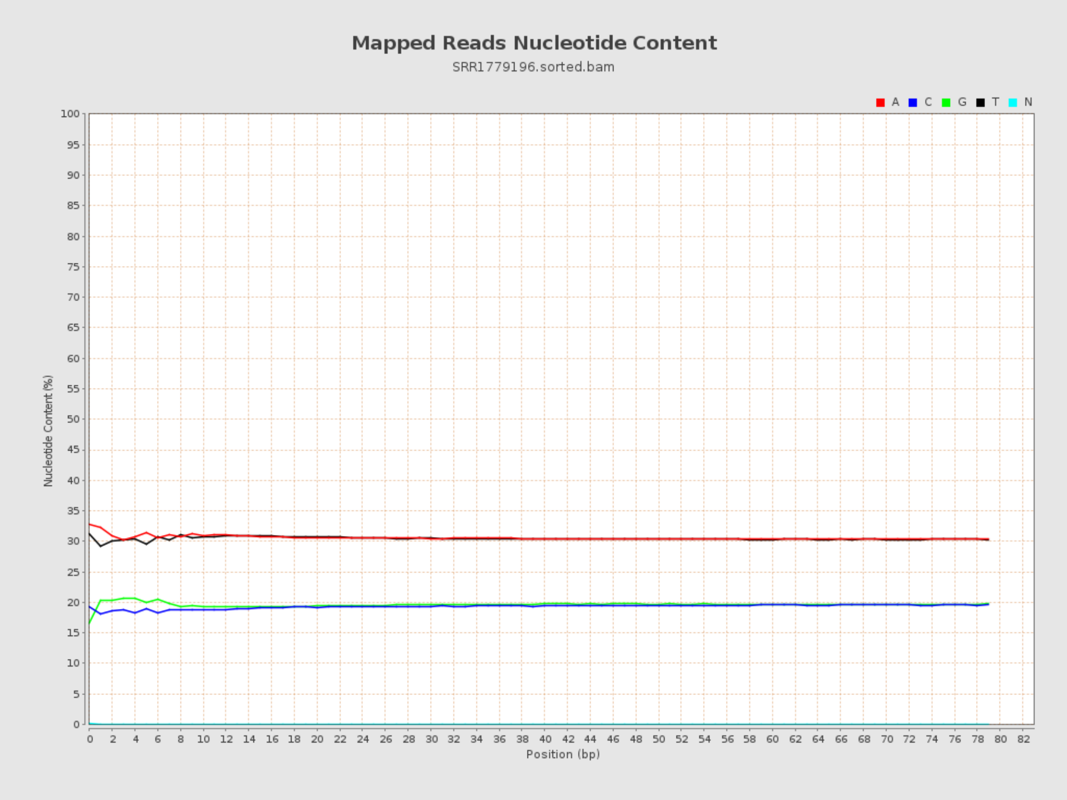
6. Results : Genome Fraction Coverage



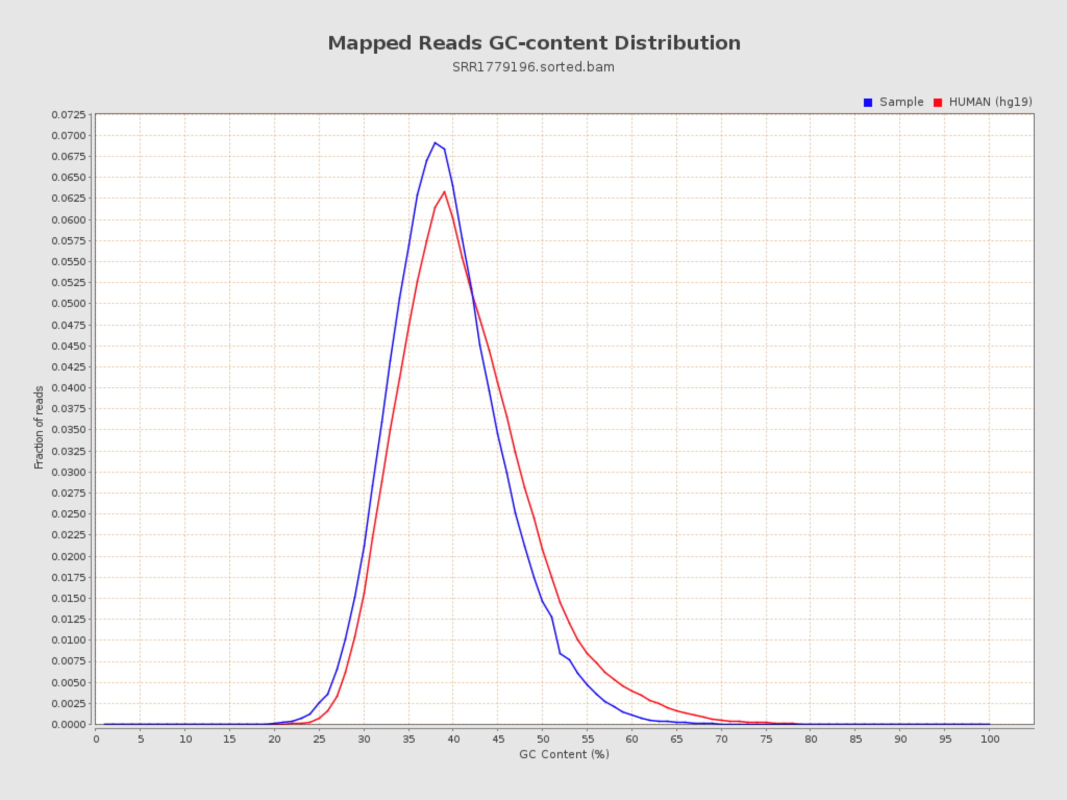
7. Results : Duplication Rate Histogram



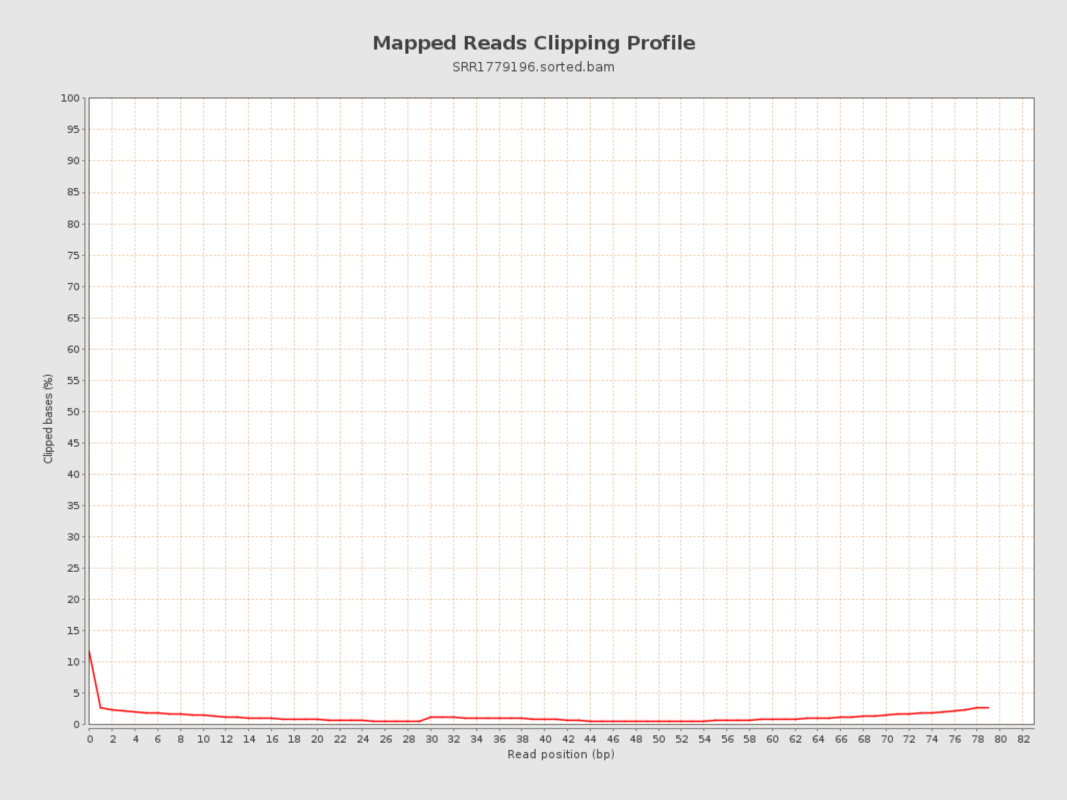
8. Results : Mapped Reads Nucleotide Content



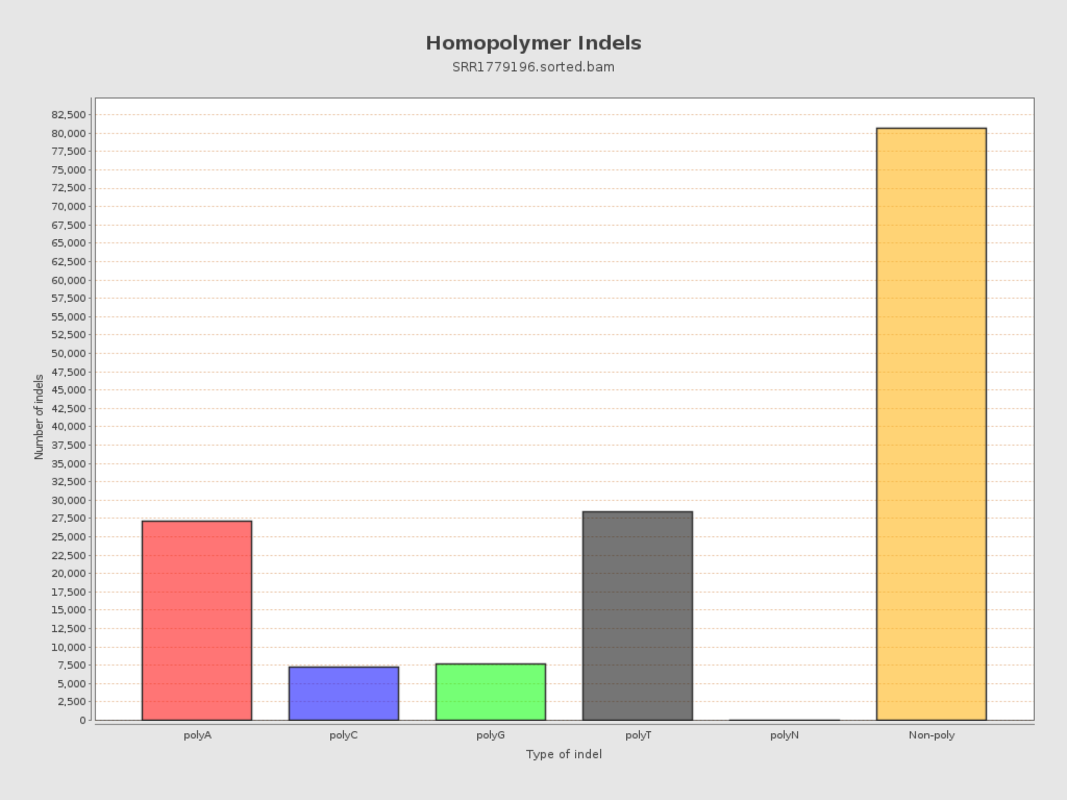
9. Results : Mapped Reads GC-content Distribution



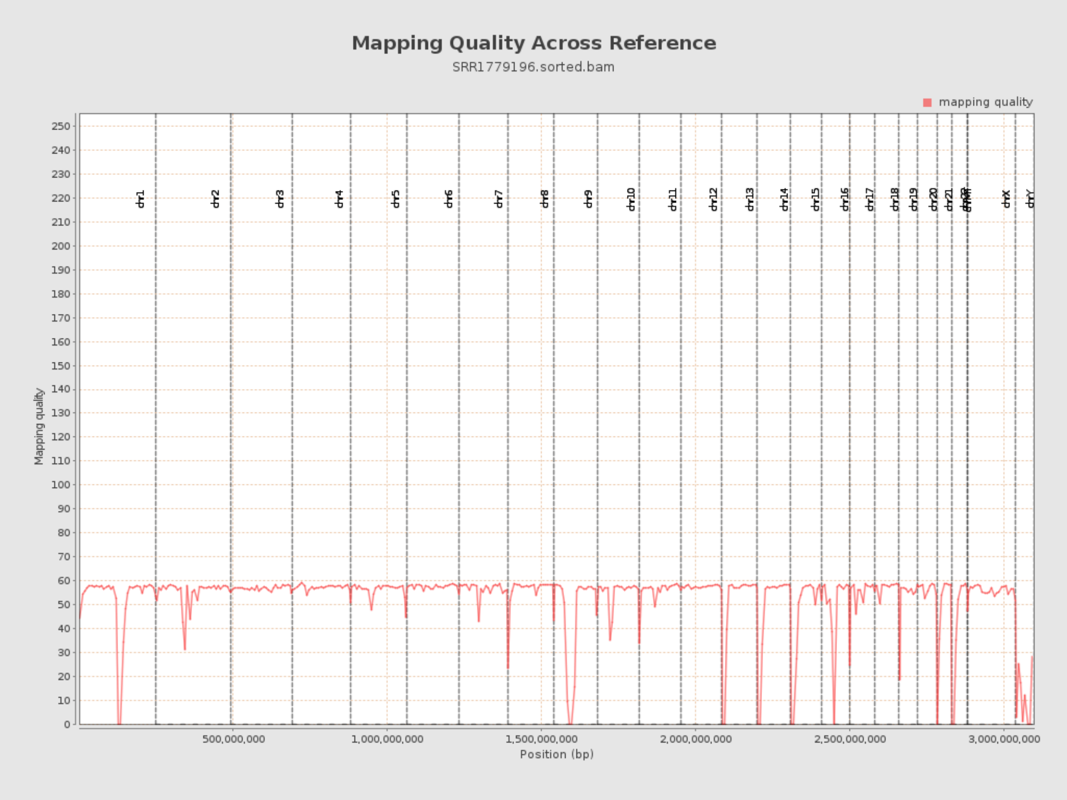
10. Results : Mapped Reads Clipping Profile



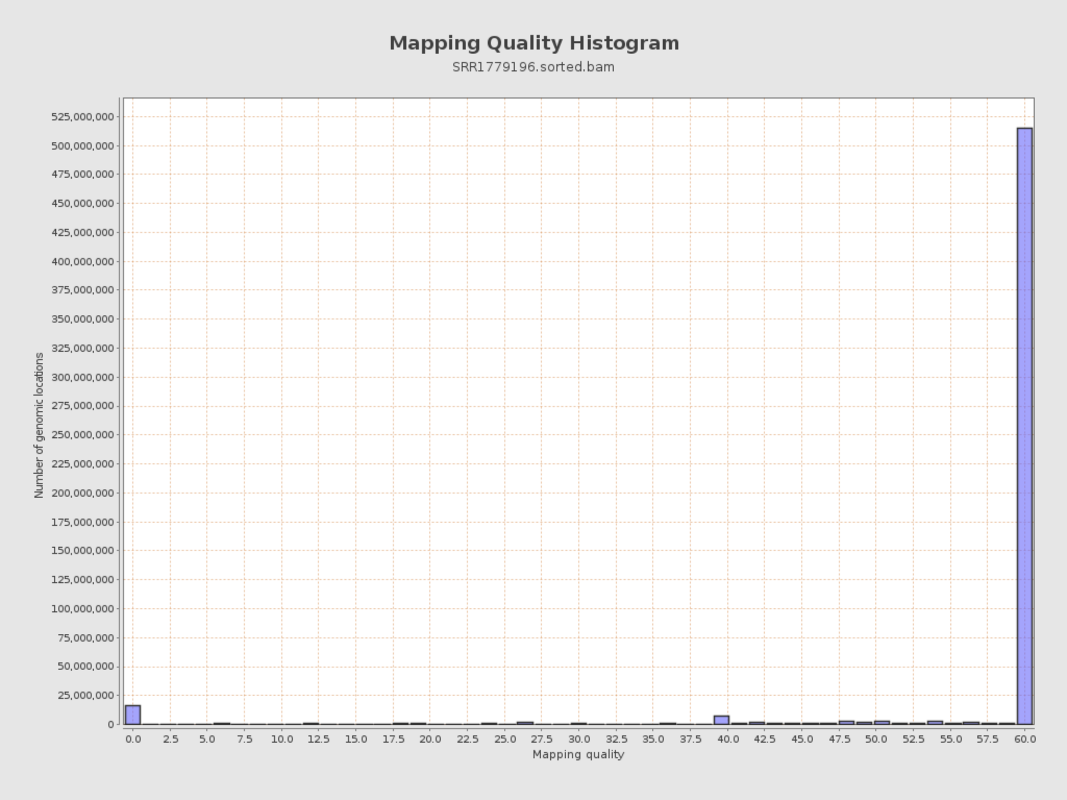
11. Results : Homopolymer Indels



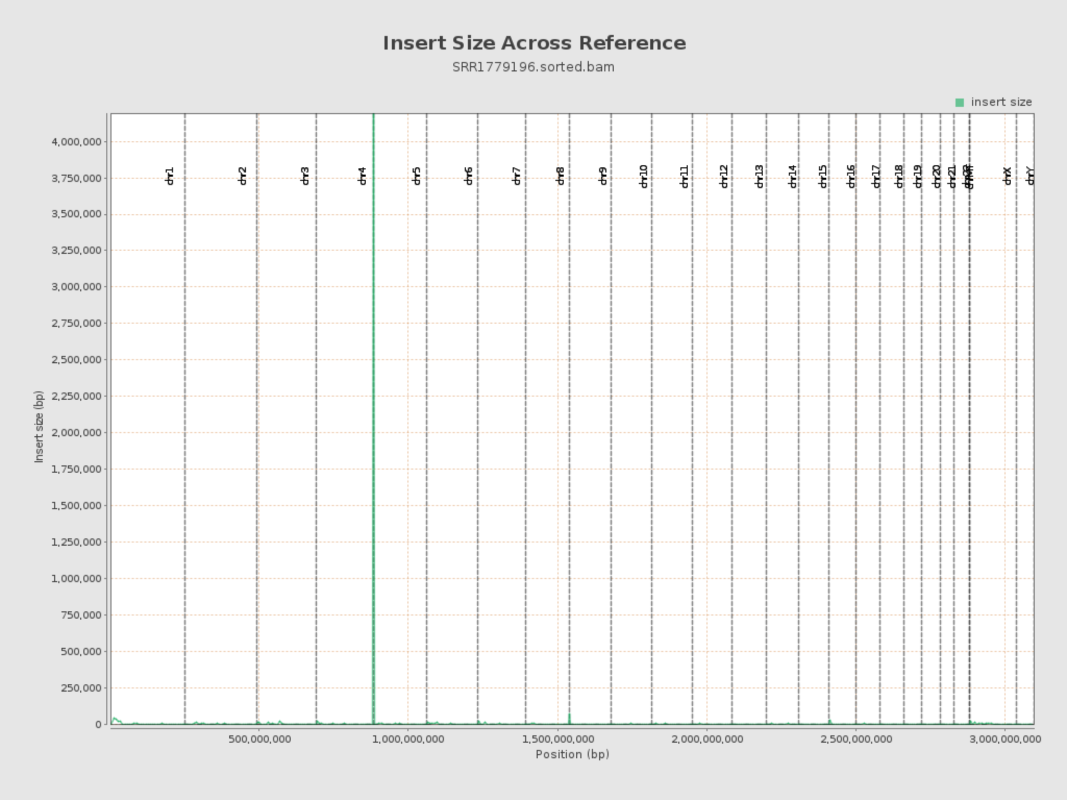
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram