Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 17:32:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779089.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_SRR1779089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779089_1.fastq.gz SRR1779089_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 17:32:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	28,083,946
Mapped reads	27,115,386 / 96.55%
Unmapped reads	968,560 / 3.45%
Mapped paired reads	27,115,386 / 96.55%
Mapped reads, first in pair	13,739,200 / 48.92%
Mapped reads, second in pair	13,376,186 / 47.63%
Mapped reads, both in pair	26,650,094 / 94.89%
Mapped reads, singletons	465,292 / 1.66%
Secondary alignments	0
Supplementary alignments	205,304 / 0.73%
Read min/max/mean length	30 / 101 / 101.3
Duplicated reads (estimated)	801,420 / 2.85%
Duplication rate	2.21%
Clipped reads	1,852,175 / 6.6%

2.2. ACGT Content

Number/percentage of A's	813,851,489 / 30.08%
Number/percentage of C's	534,838,218 / 19.77%
Number/percentage of T's	810,669,812 / 29.96%
Number/percentage of G's	545,602,663 / 20.16%
Number/percentage of N's	901,986 / 0.03%

GC Percentage	39.93%

2.3. Coverage

Mean	0.8743
Standard Deviation	3.3082

2.4. Mapping Quality

Mean Mapping Quality	53.84

2.5. Insert size

Mean	70,421.39
Standard Deviation	2,549,215.14
P25/Median/P75	220 / 286 / 360

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	15,029,851
Insertions	273,923
Mapped reads with at least one insertion	1%
Deletions	315,882
Mapped reads with at least one deletion	1.14%
Homopolymer indels	47.21%

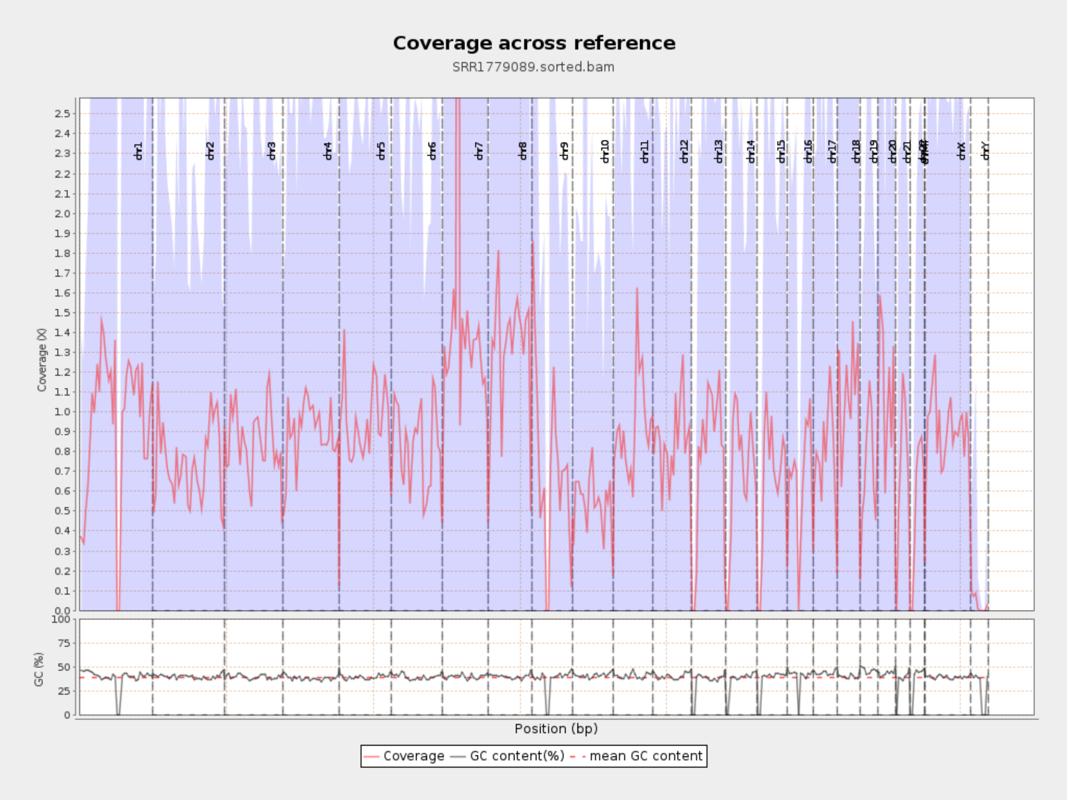
2.7. Chromosome stats

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

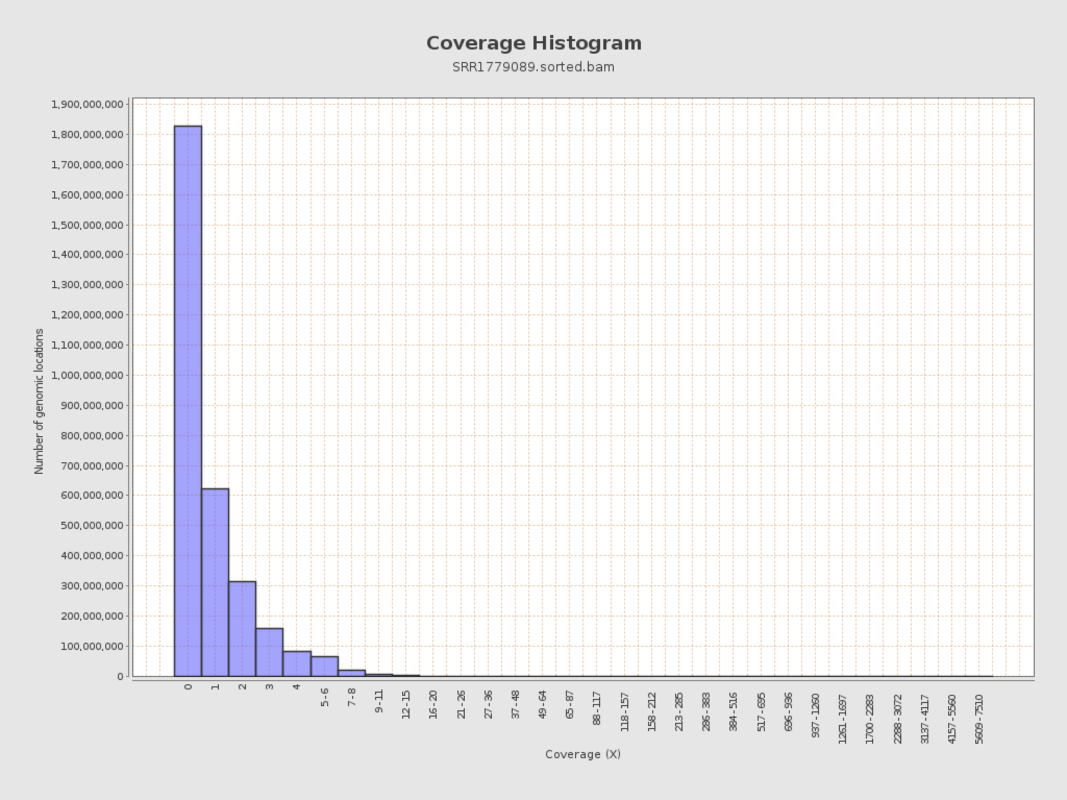
		bases	coverage	deviation
chr1	249250621	241618243	0.9694	8.1716
chr2	243199373	180014564	0.7402	1.9076
chr3	198022430	170376785	0.8604	1.3915
chr4	191154276	172701082	0.9035	1.4431
chr5	180915260	171250157	0.9466	1.4714
chr6	171115067	143130743	0.8365	1.6988
chr7	159138663	264101203	1.6596	6.1949
chr8	146364022	195853829	1.3381	1.9365
chr9	141213431	100689755	0.713	2.0893
chr10	135534747	74452495	0.5493	3.7821
chr11	135006516	123024710	0.9113	1.6901
chr12	133851895	113013884	0.8443	1.4925
chr13	115169878	90929834	0.7895	1.4055
chr14	107349540	74499489	0.694	1.3055
chr15	102531392	66314511	0.6468	1.3345
chr16	90354753	57719363	0.6388	1.3248
chr17	81195210	63515735	0.7823	3.5563
chr18	78077248	85993759	1.1014	2.4345
chr19	59128983	41979680	0.71	4.9863
chr20	63025520	68645472	1.0892	1.7034
chr21	48129895	35274323	0.7329	1.4164
chr22	51304566	26932288	0.5249	1.165
chrMT	16571	5202	0.3139	0.6236
chrX	155270560	142490729	0.9177	1.7649

chrY	59373566	2036955	0.0343	0.5168

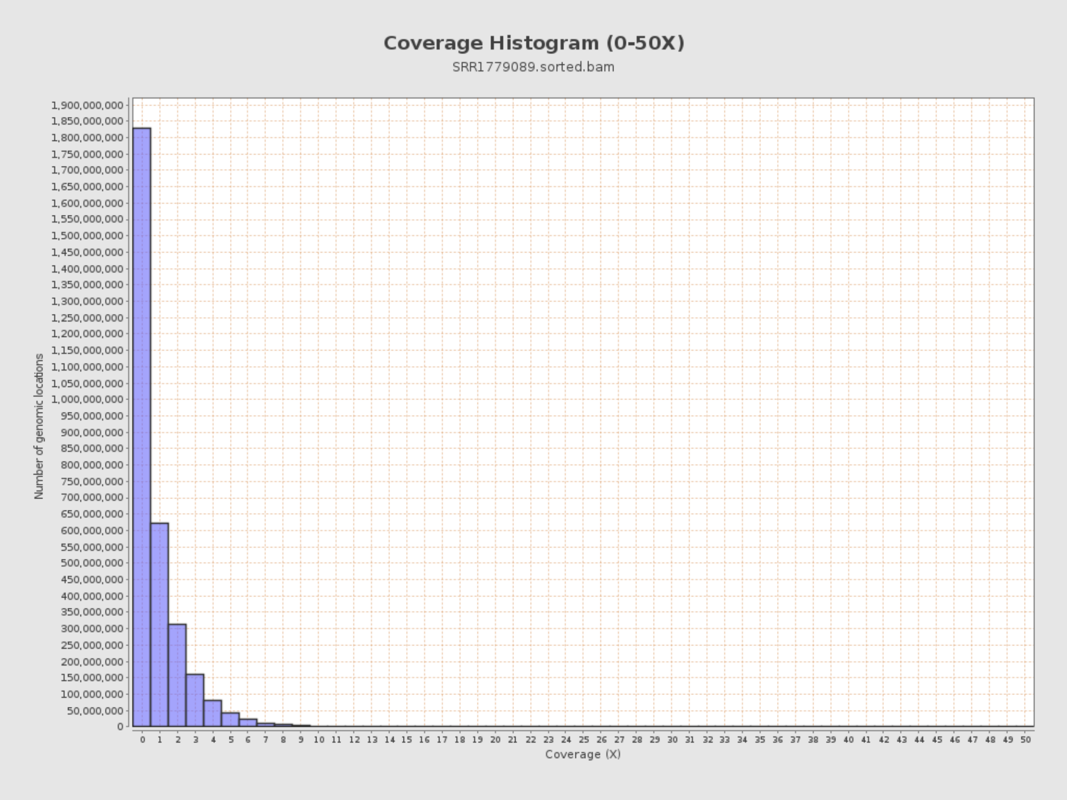
3. Results : Coverage across reference



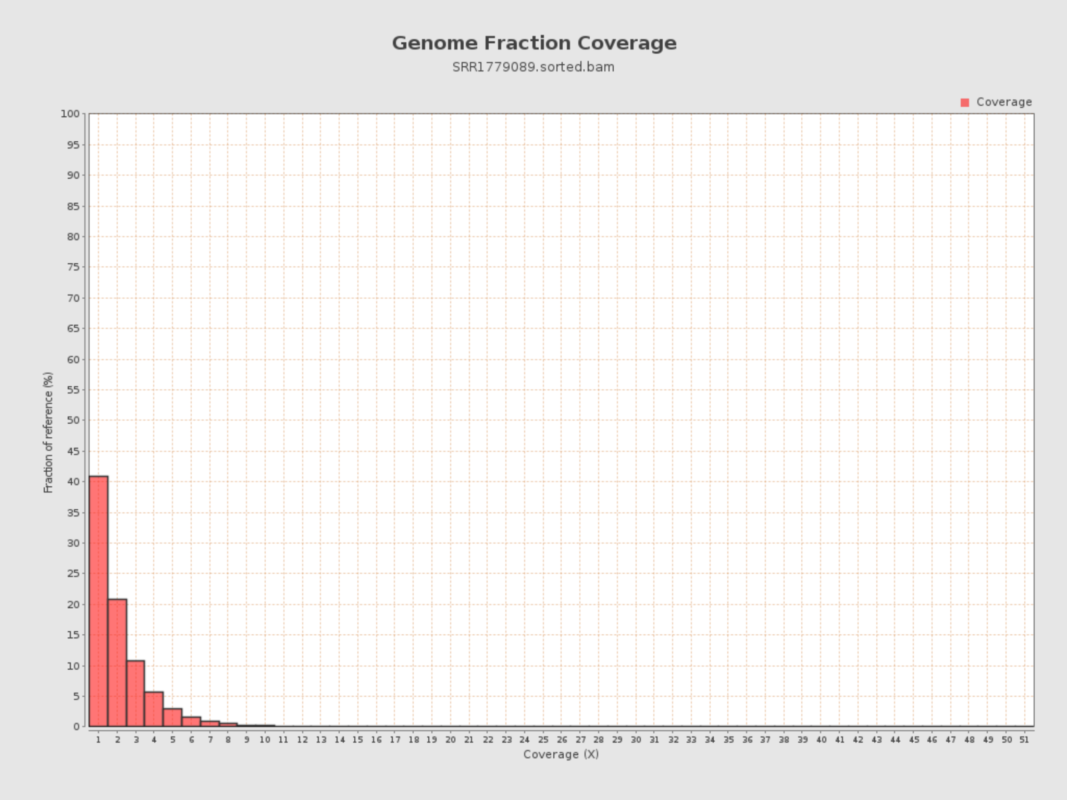
4. Results : Coverage Histogram



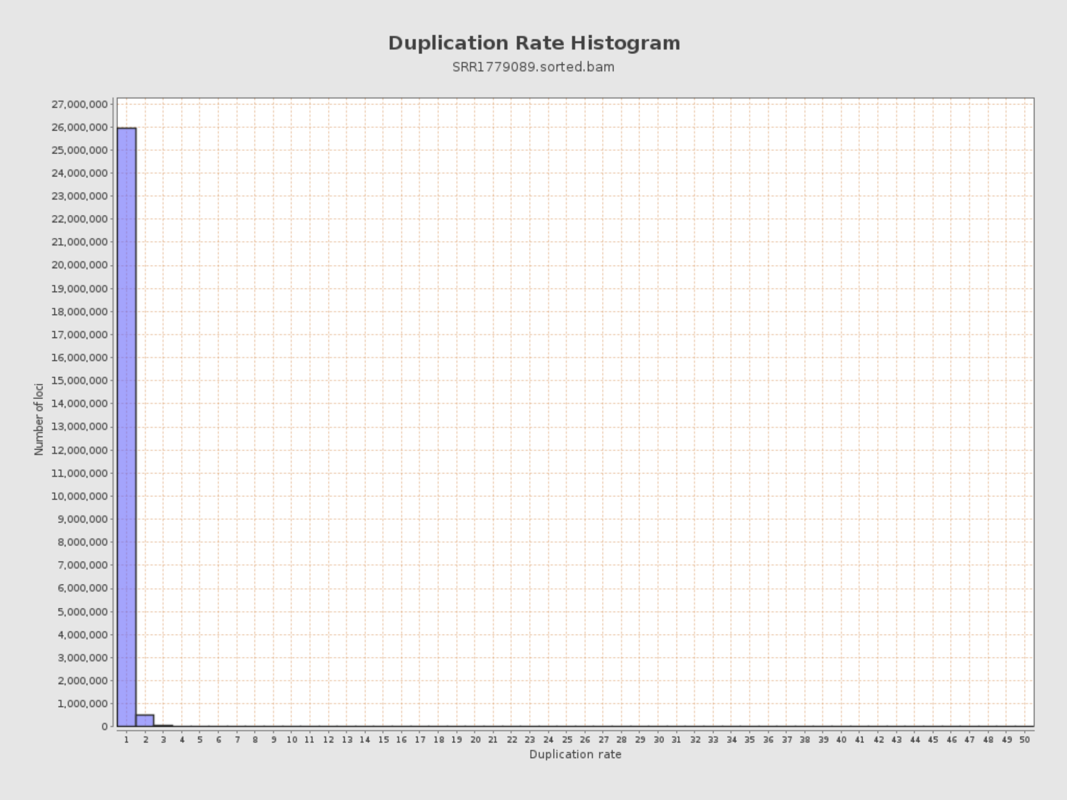
5. Results : Coverage Histogram (0-50X)



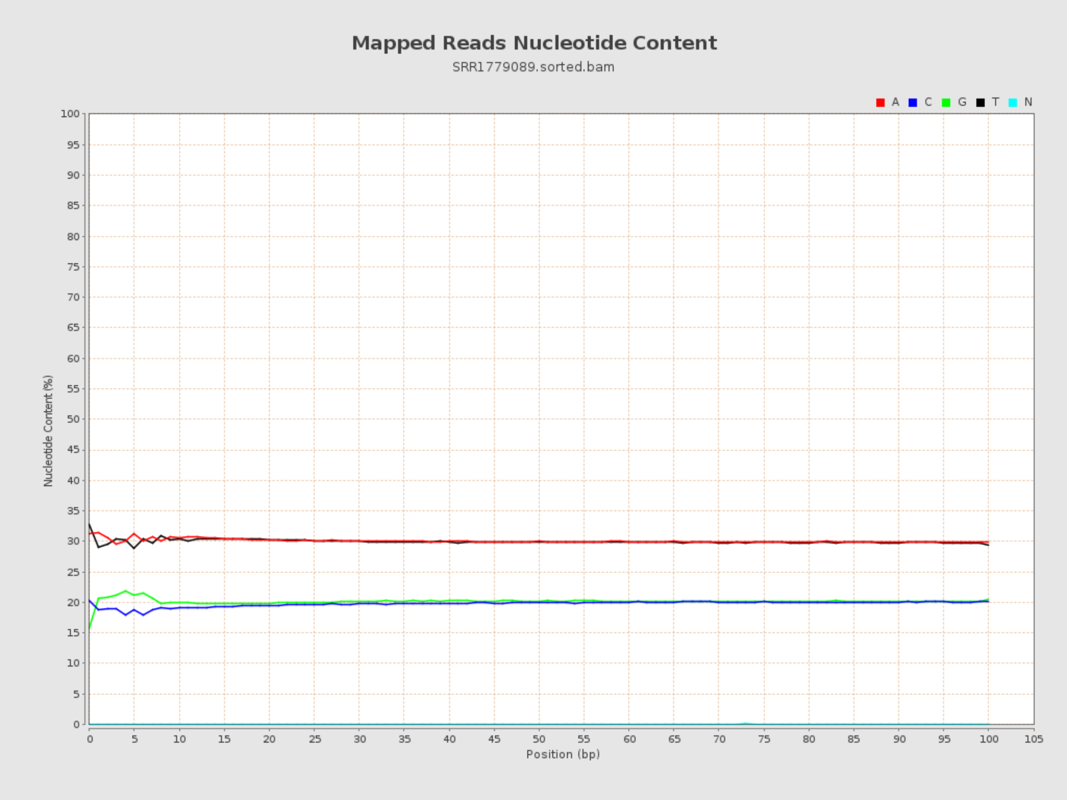
6. Results : Genome Fraction Coverage



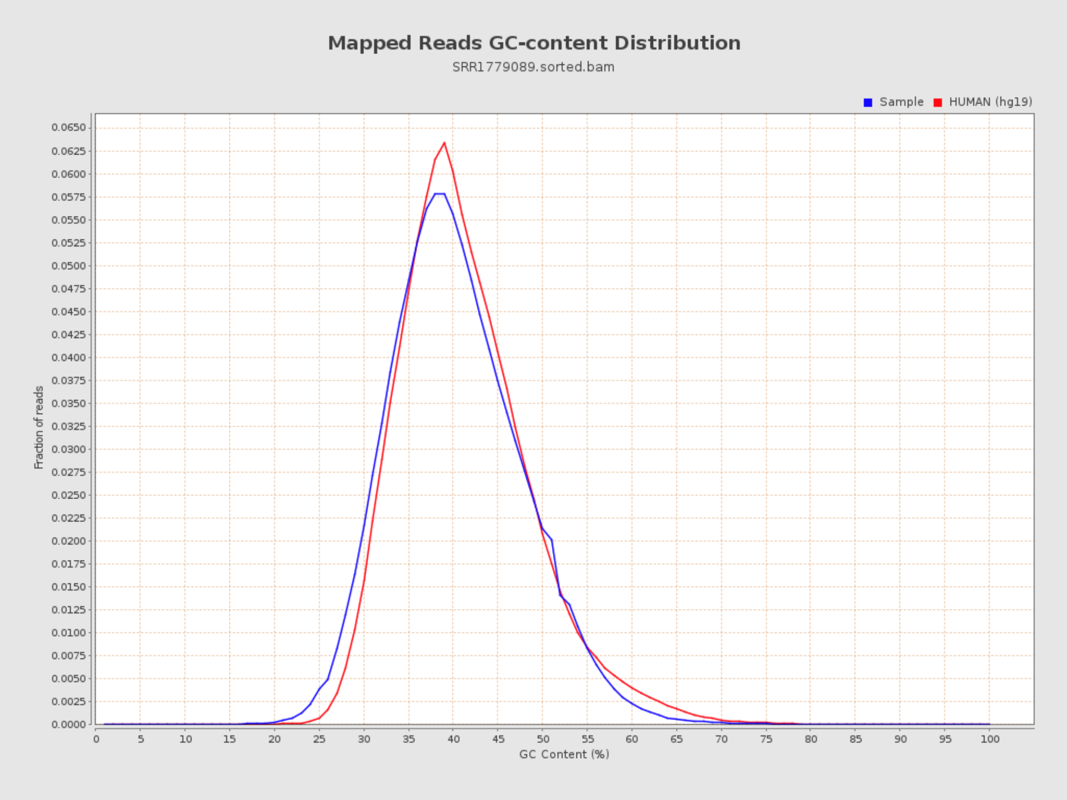
7. Results : Duplication Rate Histogram



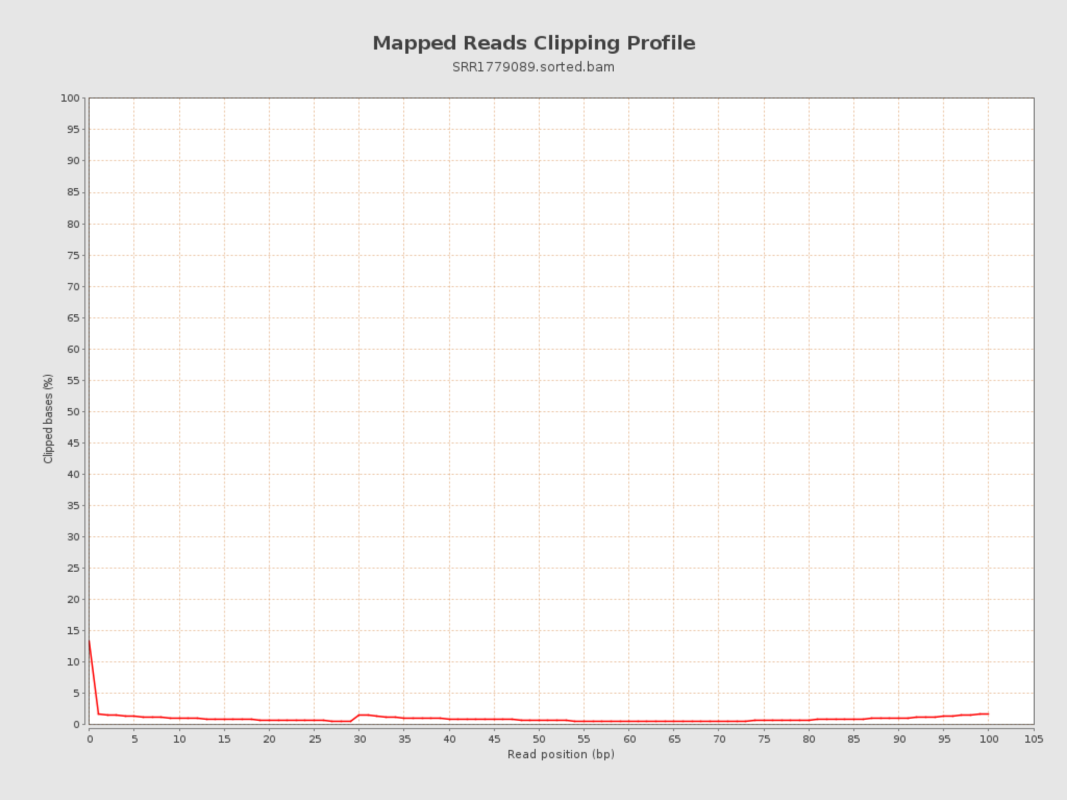
8. Results : Mapped Reads Nucleotide Content



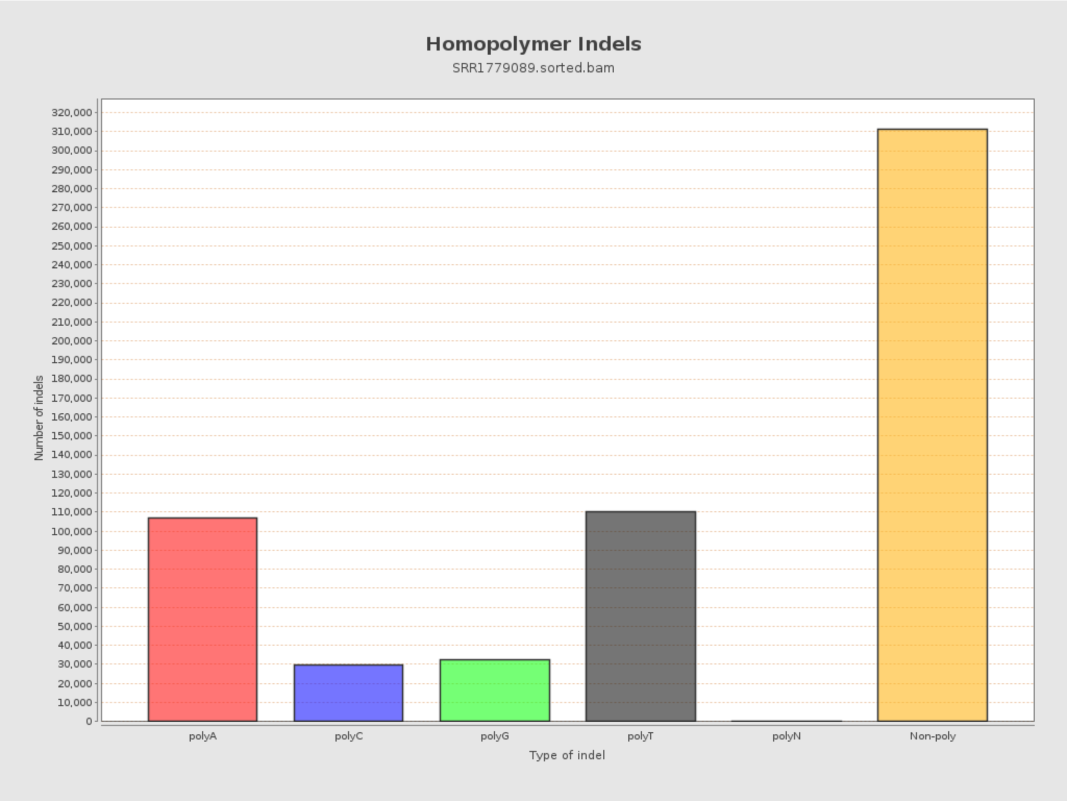
9. Results : Mapped Reads GC-content Distribution



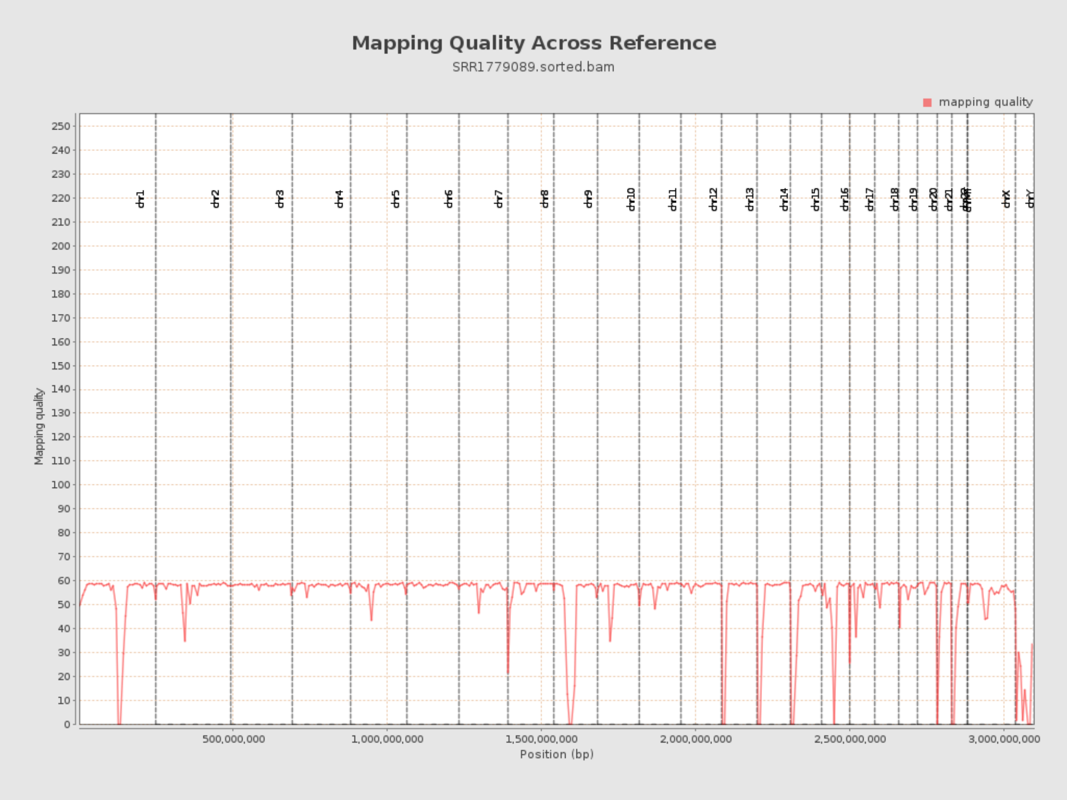
10. Results : Mapped Reads Clipping Profile



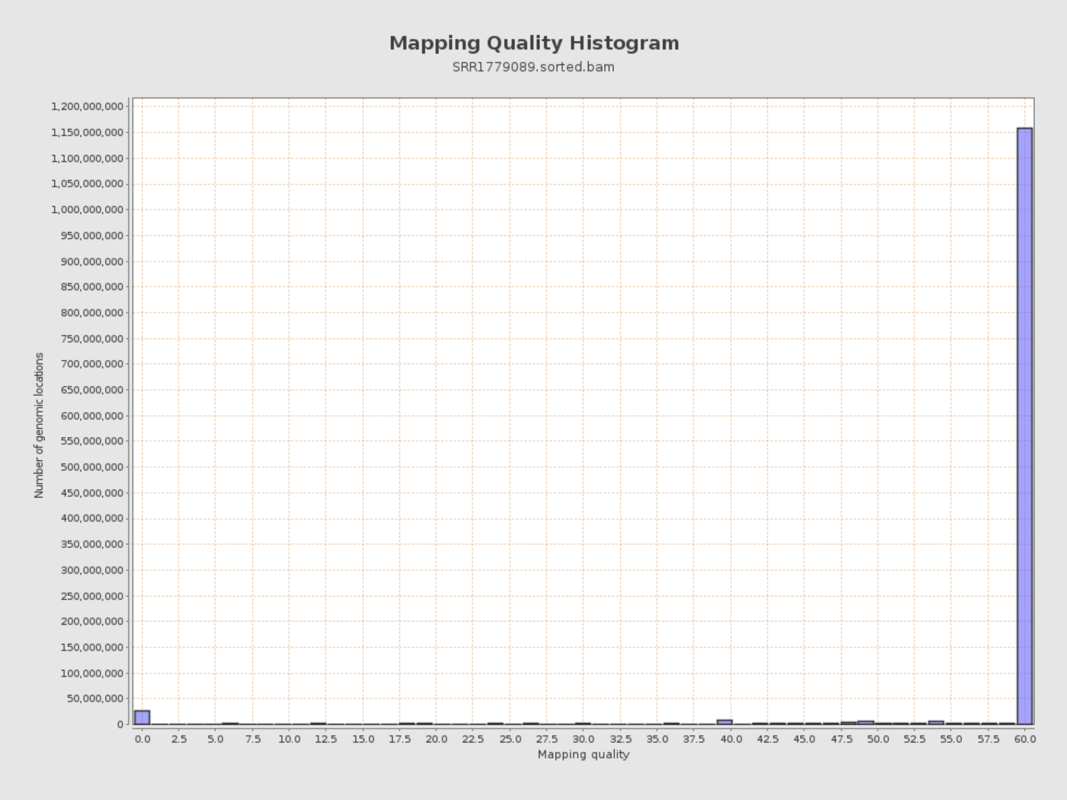
11. Results : Homopolymer Indels



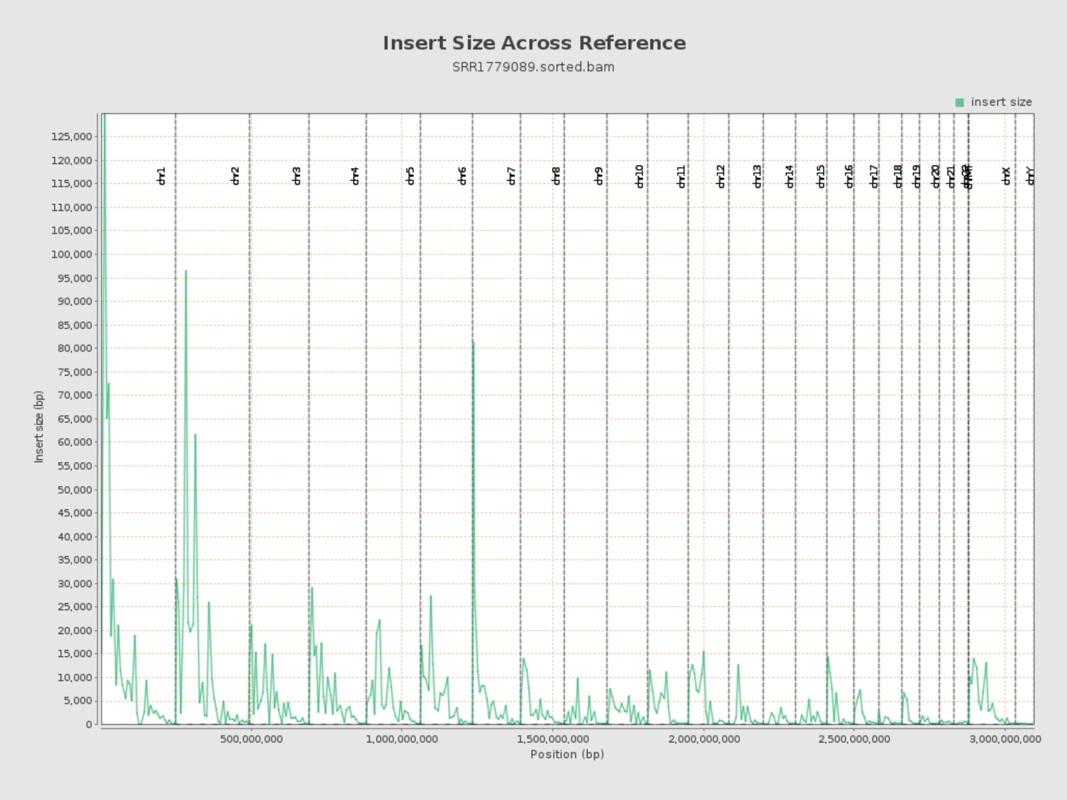
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram