Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 16:42:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779088.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_SRR1779088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779088_1.fastq.gz SRR1779088_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 16:42:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,033,794
Mapped reads	30,001,506 / 96.67%
Unmapped reads	1,032,288 / 3.33%
Mapped paired reads	30,001,506 / 96.67%
Mapped reads, first in pair	15,179,774 / 48.91%
Mapped reads, second in pair	14,821,732 / 47.76%
Mapped reads, both in pair	29,537,452 / 95.18%
Mapped reads, singletons	464,054 / 1.5%
Secondary alignments	0
Supplementary alignments	220,564 / 0.71%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	796,734 / 2.57%
Duplication rate	1.99%
Clipped reads	2,034,944 / 6.56%

2.2. ACGT Content

Number/percentage of A's	896,414,092 / 29.94%
Number/percentage of C's	595,633,593 / 19.89%
Number/percentage of T's	893,664,600 / 29.85%
Number/percentage of G's	607,265,612 / 20.28%
Number/percentage of N's	991,614 / 0.03%

GC Percentage	40.18%

2.3. Coverage

Mean	0.9674
Standard Deviation	3.4109

2.4. Mapping Quality

Mean Mapping Quality	53.95

2.5. Insert size

Mean	71,020.44
Standard Deviation	2,584,636.26
P25/Median/P75	216 / 285 / 360

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	16,511,274
Insertions	295,748
Mapped reads with at least one insertion	0.97%
Deletions	342,223
Mapped reads with at least one deletion	1.12%
Homopolymer indels	47.19%

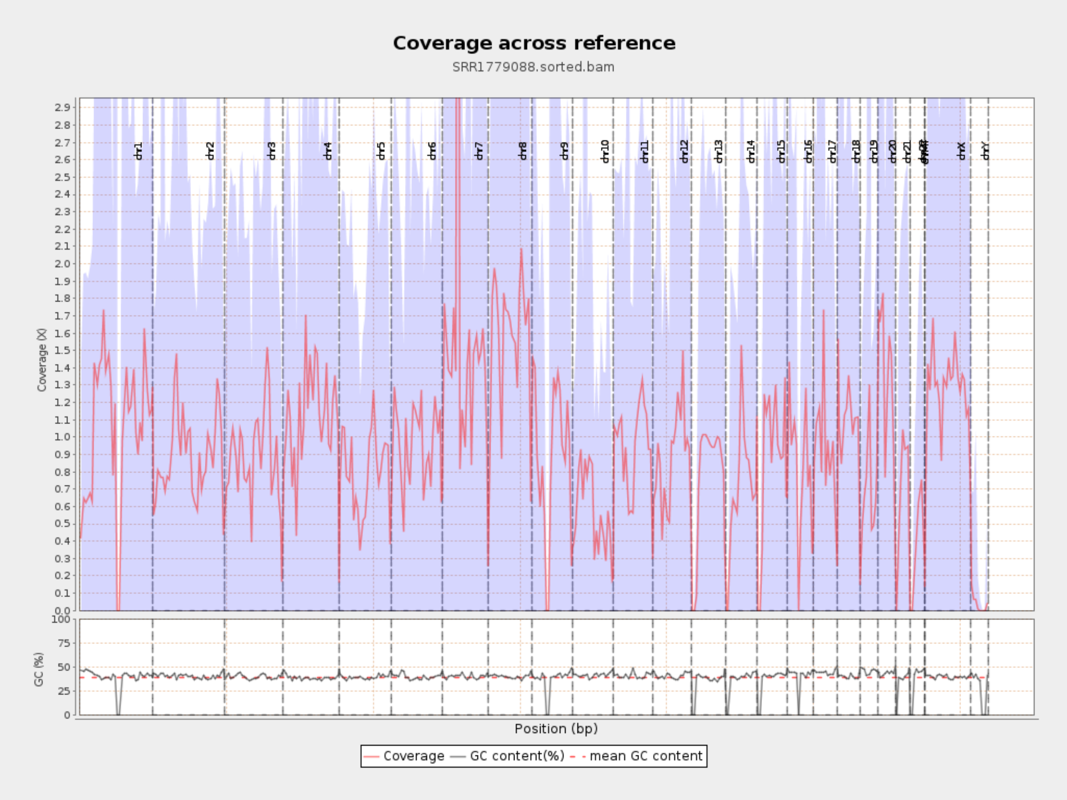
2.7. Chromosome stats

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

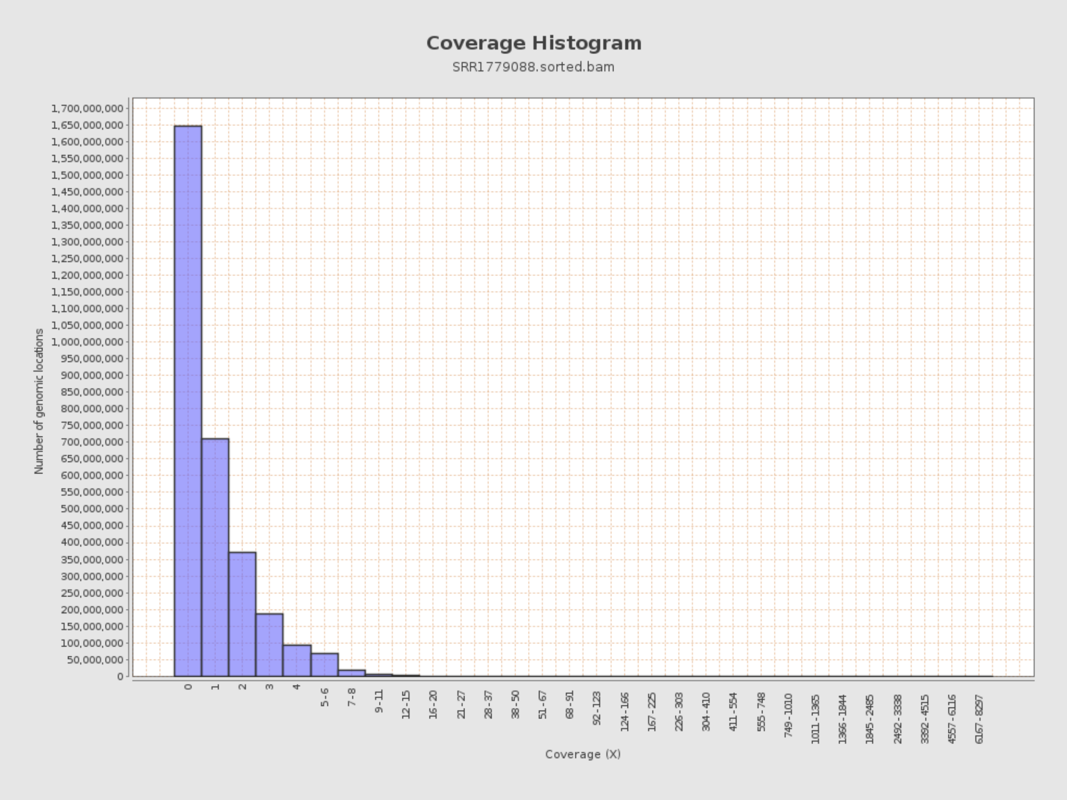
		bases	coverage	deviation
chr1	249250621	262118052	1.0516	8.6891
chr2	243199373	219340630	0.9019	2.1198
chr3	198022430	176850428	0.8931	1.3231
chr4	191154276	217009378	1.1353	1.5348
chr5	180915260	142512986	0.7877	1.2128
chr6	171115067	166608848	0.9737	1.9519
chr7	159138663	262249994	1.6479	5.2328
chr8	146364022	234821535	1.6044	1.9176
chr9	141213431	125196455	0.8866	2.5161
chr10	135534747	77872749	0.5746	4.5386
chr11	135006516	127968993	0.9479	1.5632
chr12	133851895	117156797	0.8753	1.4324
chr13	115169878	88235378	0.7661	1.2688
chr14	107349540	74811062	0.6969	1.236
chr15	102531392	89466552	0.8726	1.4654
chr16	90354753	72106670	0.798	1.3661
chr17	81195210	75835376	0.934	3.2435
chr18	78077248	86577238	1.1089	2.6005
chr19	59128983	39174630	0.6625	5.8296
chr20	63025520	84295509	1.3375	1.7641
chr21	48129895	33481737	0.6957	1.2411
chr22	51304566	19247148	0.3752	0.8975
chrMT	16571	2250	0.1358	0.5051
chrX	155270560	199587189	1.2854	1.7152

chrY	59373566	2202919	0.0371	0.4855

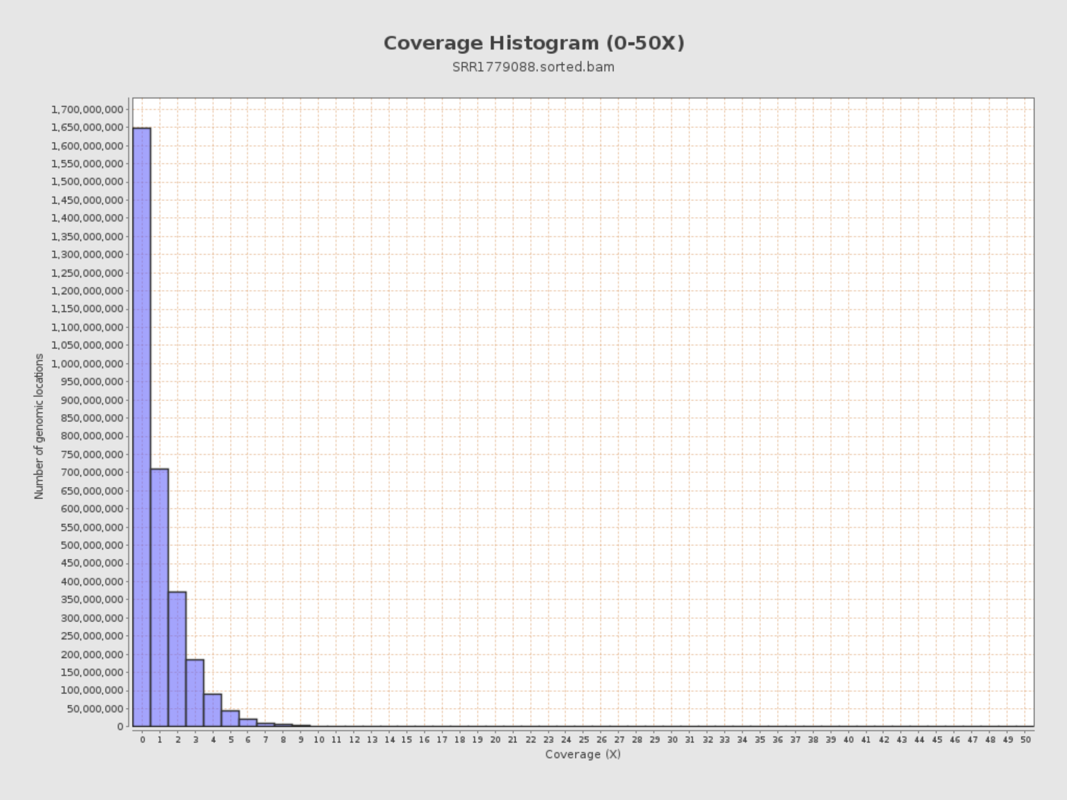
3. Results : Coverage across reference



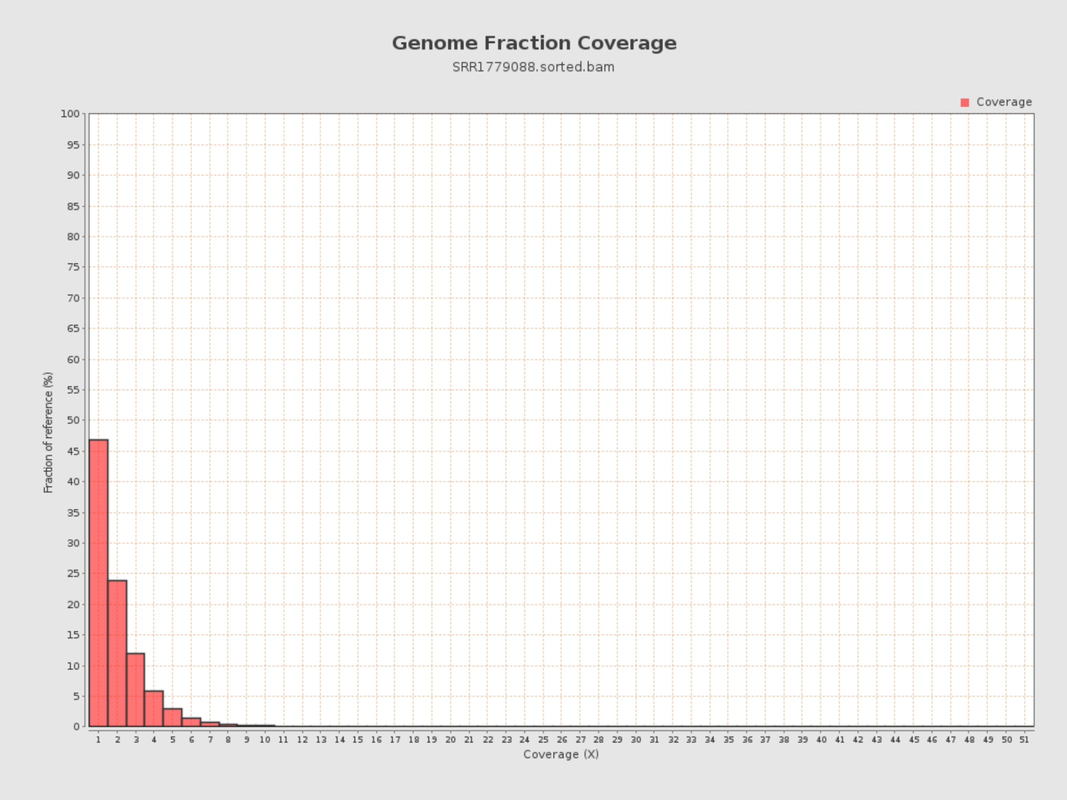
4. Results : Coverage Histogram



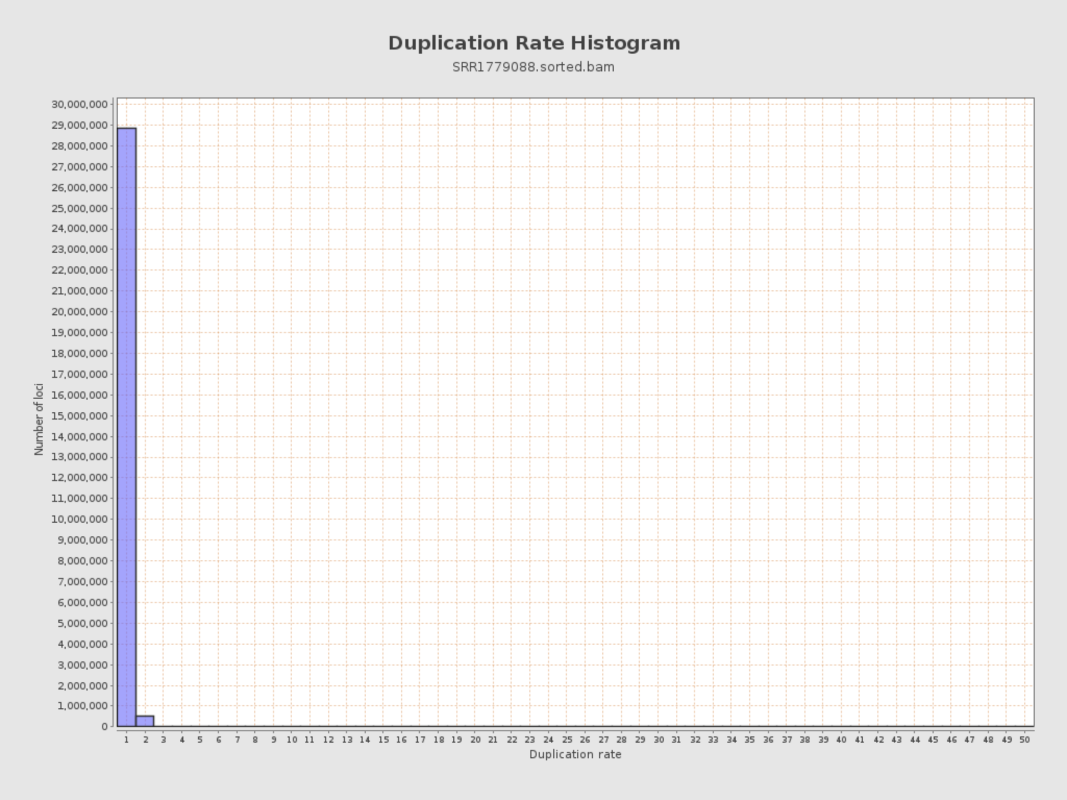
5. Results : Coverage Histogram (0-50X)



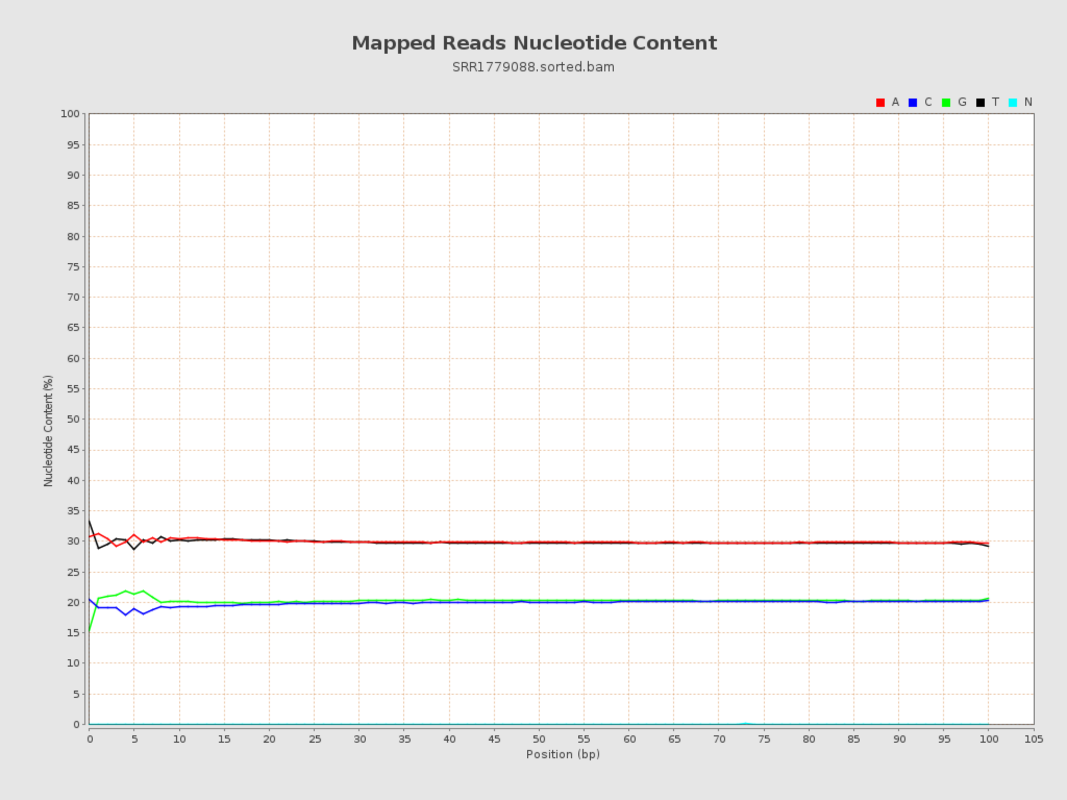
6. Results : Genome Fraction Coverage



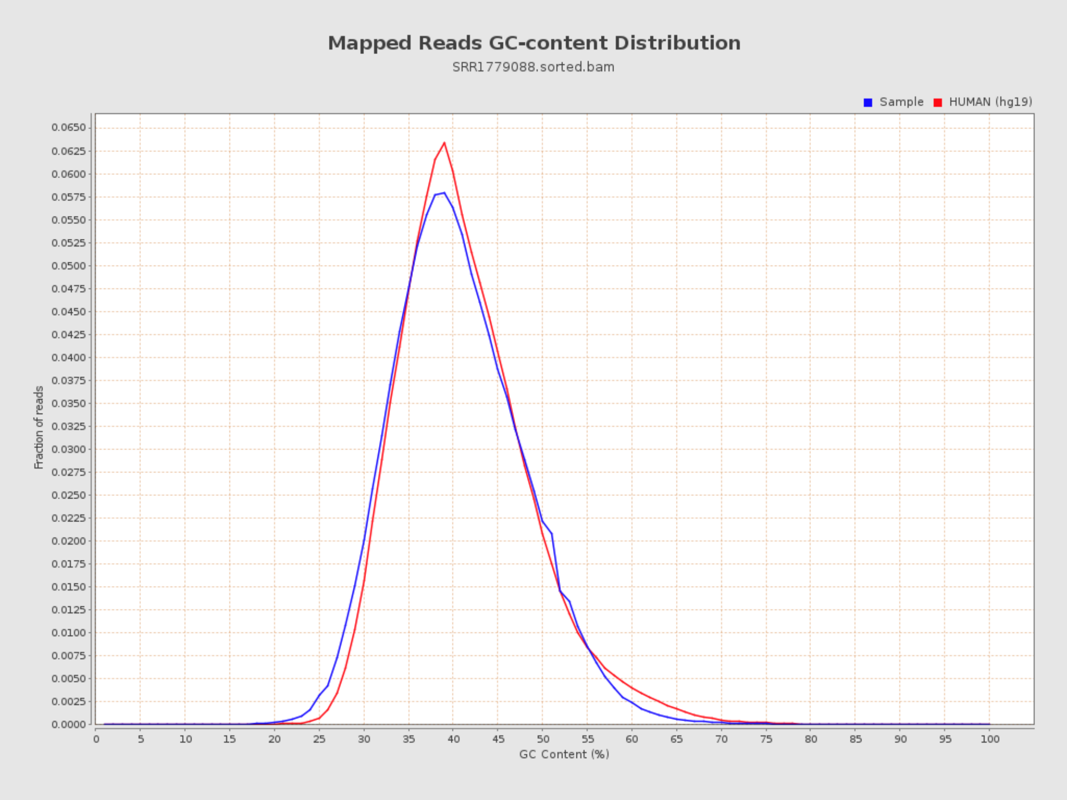
7. Results : Duplication Rate Histogram



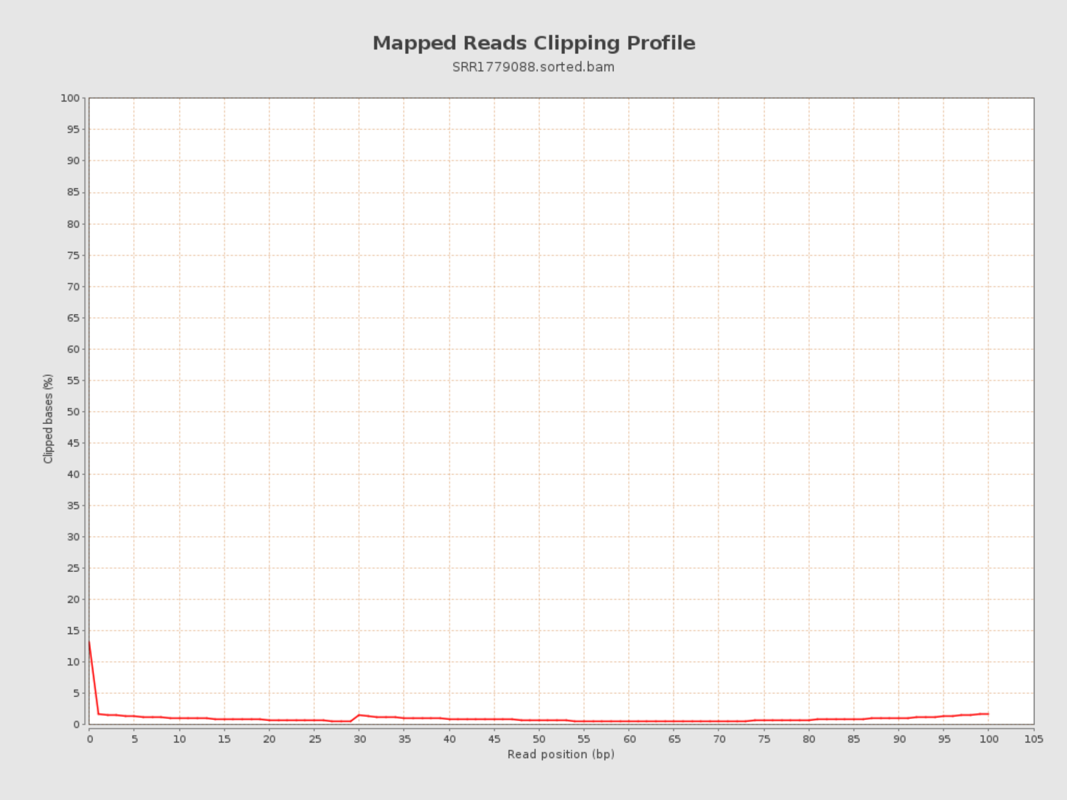
8. Results : Mapped Reads Nucleotide Content



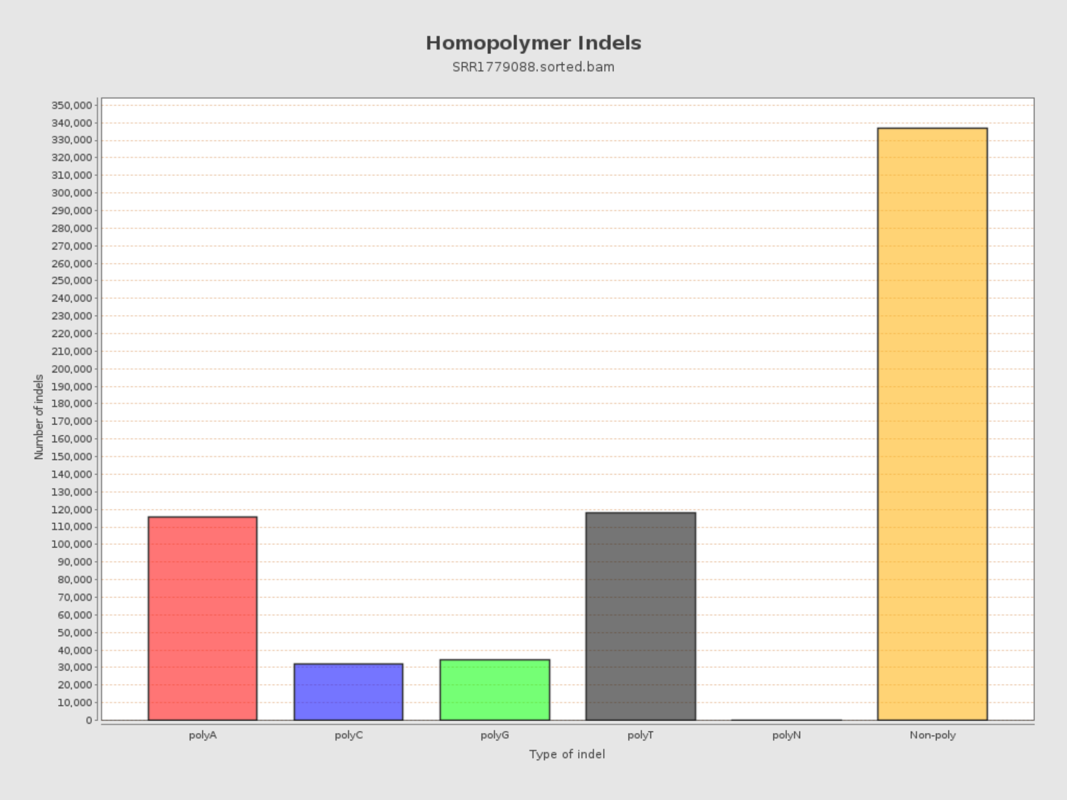
9. Results : Mapped Reads GC-content Distribution



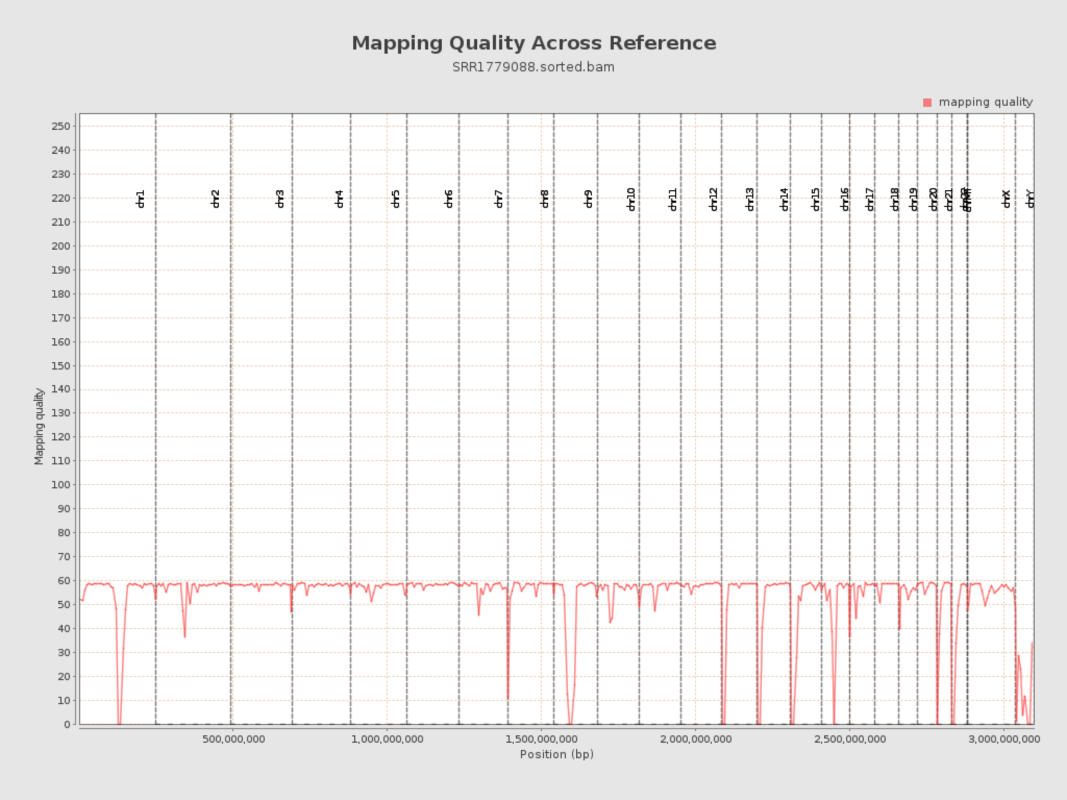
10. Results : Mapped Reads Clipping Profile



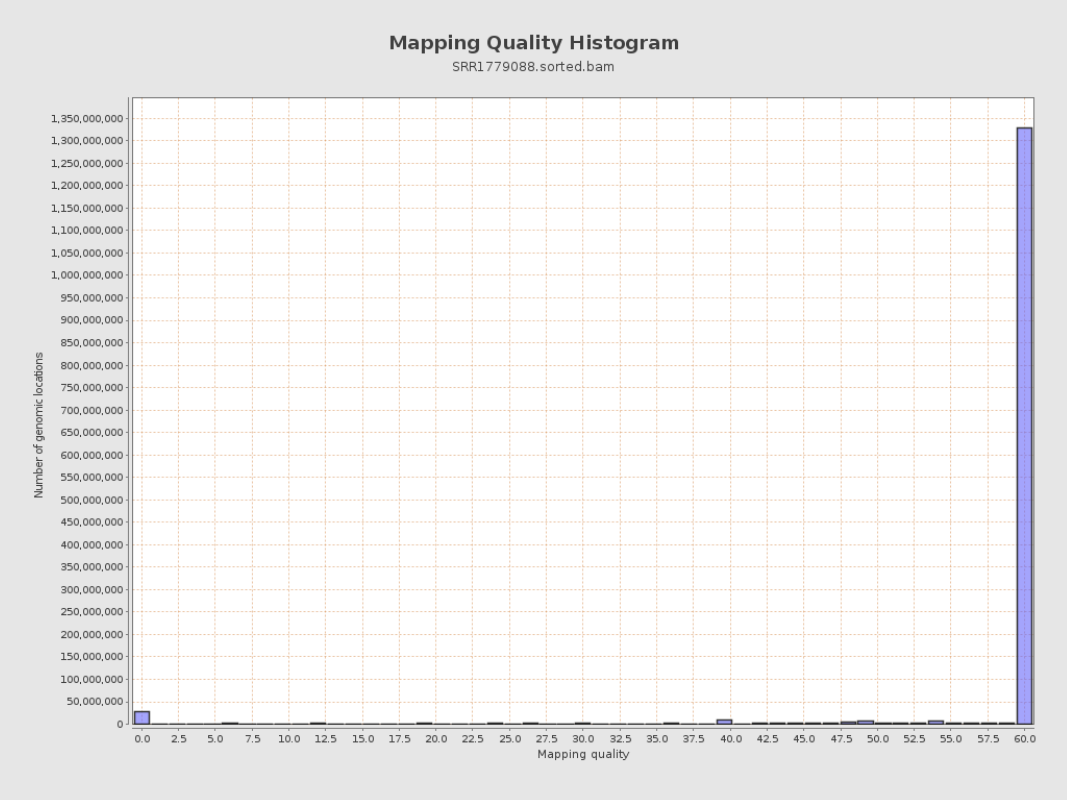
11. Results : Homopolymer Indels



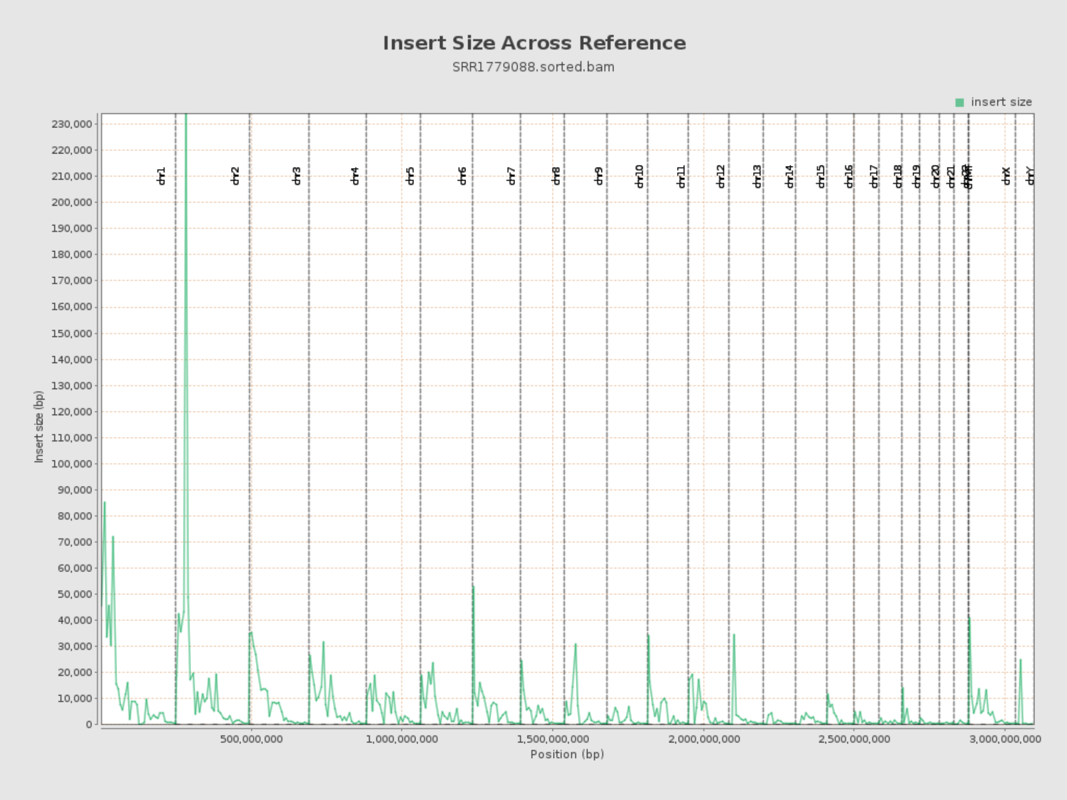
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram