Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 12:01:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779079.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_SRR1779079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779079_1.fastq.gz SRR1779079_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 12:01:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,078,208
Mapped reads	35,926,236 / 96.89%
Unmapped reads	1,151,972 / 3.11%
Mapped paired reads	35,926,236 / 96.89%
Mapped reads, first in pair	18,094,736 / 48.8%
Mapped reads, second in pair	17,831,500 / 48.09%
Mapped reads, both in pair	35,529,380 / 95.82%
Mapped reads, singletons	396,856 / 1.07%
Secondary alignments	0
Supplementary alignments	206,780 / 0.56%
Read min/max/mean length	30 / 101 / 101.22
Duplicated reads (estimated)	1,829,515 / 4.93%
Duplication rate	4.4%
Clipped reads	2,413,494 / 6.51%

2.2. ACGT Content

Number/percentage of A's	1,093,311,619 / 30.49%
Number/percentage of C's	697,586,297 / 19.45%
Number/percentage of T's	1,082,030,619 / 30.17%
Number/percentage of G's	711,828,553 / 19.85%
Number/percentage of N's	1,205,583 / 0.03%

GC Percentage	39.3%

2.3. Coverage

Mean	1.1586
Standard Deviation	3.5152

2.4. Mapping Quality

Mean Mapping Quality	53.68

2.5. Insert size

Mean	75,140.83
Standard Deviation	2,642,912.32
P25/Median/P75	157 / 214 / 294

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	16,549,645
Insertions	300,717
Mapped reads with at least one insertion	0.83%
Deletions	369,978
Mapped reads with at least one deletion	1.01%
Homopolymer indels	46.87%

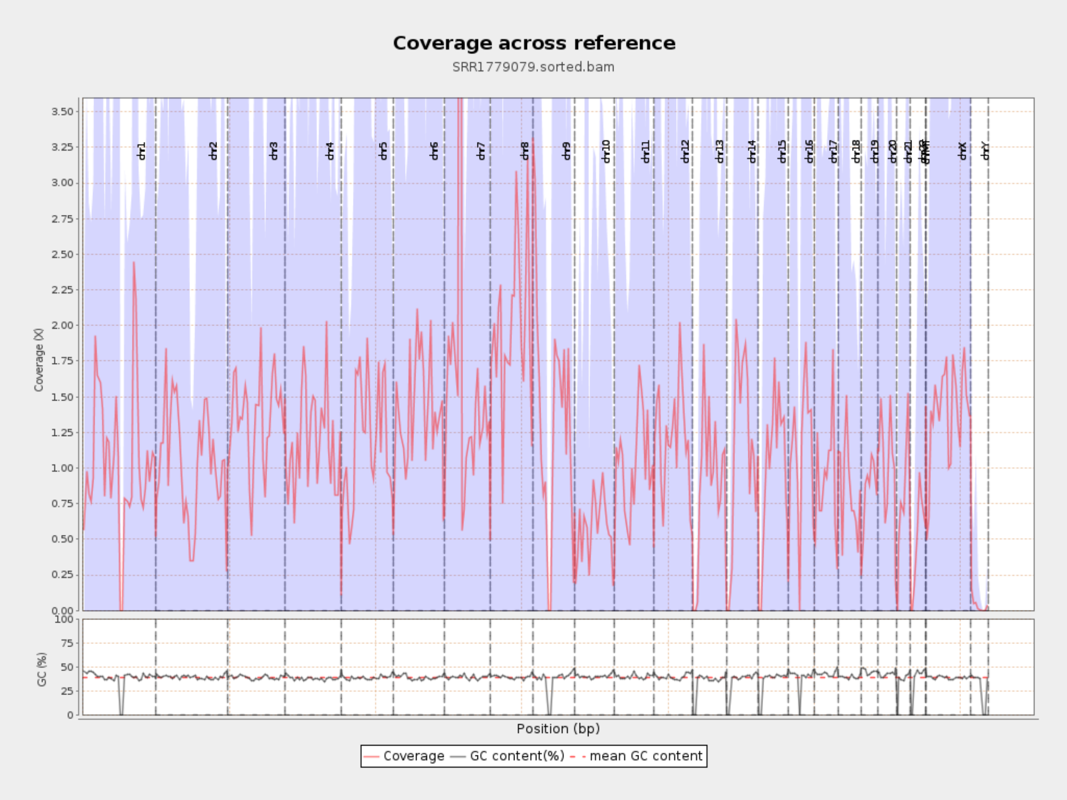
2.7. Chromosome stats

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

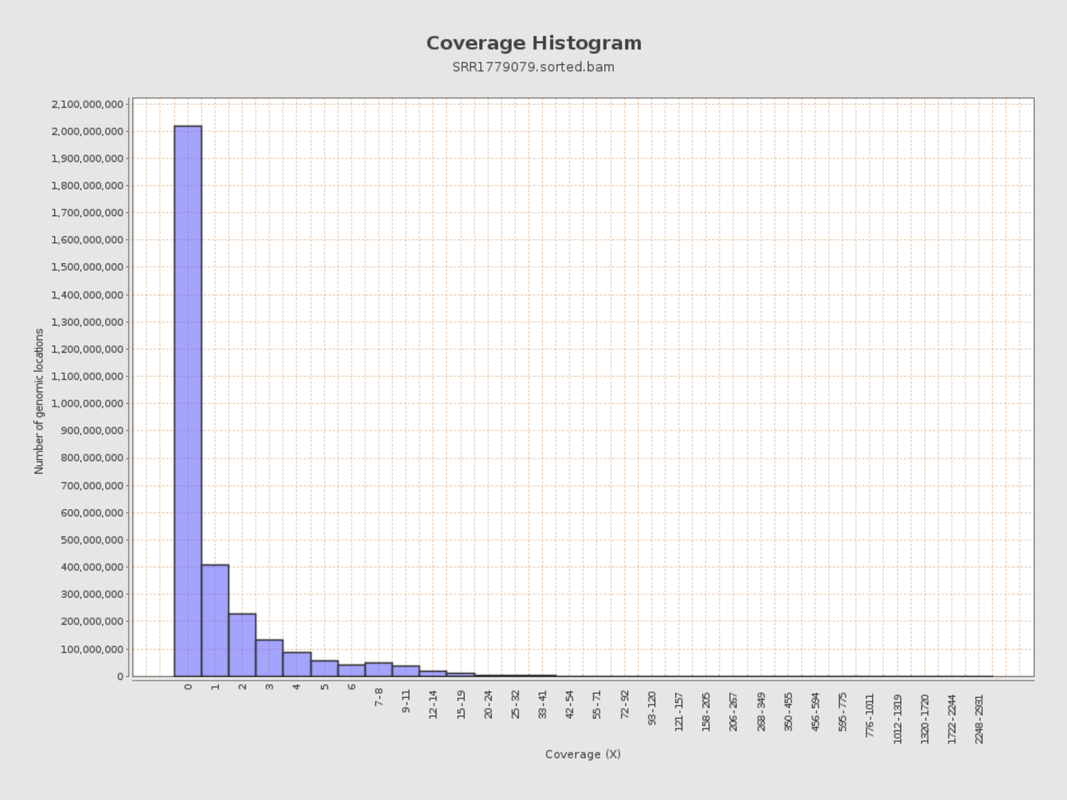
		bases	coverage	deviation
chr1	249250621	261242007	1.0481	3.7906
chr2	243199373	254260002	1.0455	2.762
chr3	198022430	264464547	1.3355	2.7791
chr4	191154276	230187099	1.2042	2.6473
chr5	180915260	215036234	1.1886	2.6527
chr6	171115067	243401291	1.4224	2.9976
chr7	159138663	289447094	1.8188	8.8857
chr8	146364022	292389559	1.9977	3.6646
chr9	141213431	185328227	1.3124	3.1218
chr10	135534747	79020790	0.583	4.3233
chr11	135006516	139612037	1.0341	2.5047
chr12	133851895	164304154	1.2275	2.761
chr13	115169878	102321970	0.8884	2.363
chr14	107349540	123490946	1.1504	2.7056
chr15	102531392	101451118	0.9895	2.6081
chr16	90354753	99296900	1.099	2.6088
chr17	81195210	76346210	0.9403	2.4435
chr18	78077248	66781403	0.8553	2.2827
chr19	59128983	50799549	0.8591	2.5691
chr20	63025520	66027101	1.0476	2.4526
chr21	48129895	38091586	0.7914	2.1858
chr22	51304566	25678458	0.5005	1.4643
chrMT	16571	23889	1.4416	1.3859
chrX	155270560	215824851	1.39	3.2934

chrY	59373566	1963242	0.0331	0.4763

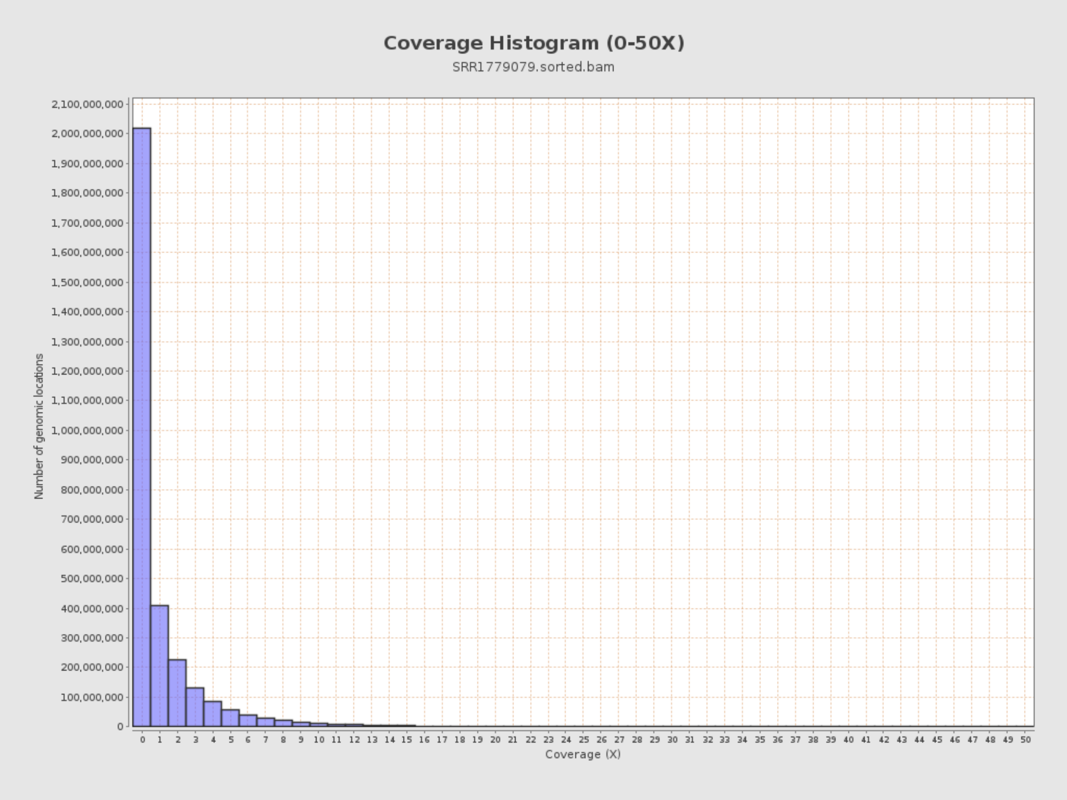
3. Results : Coverage across reference



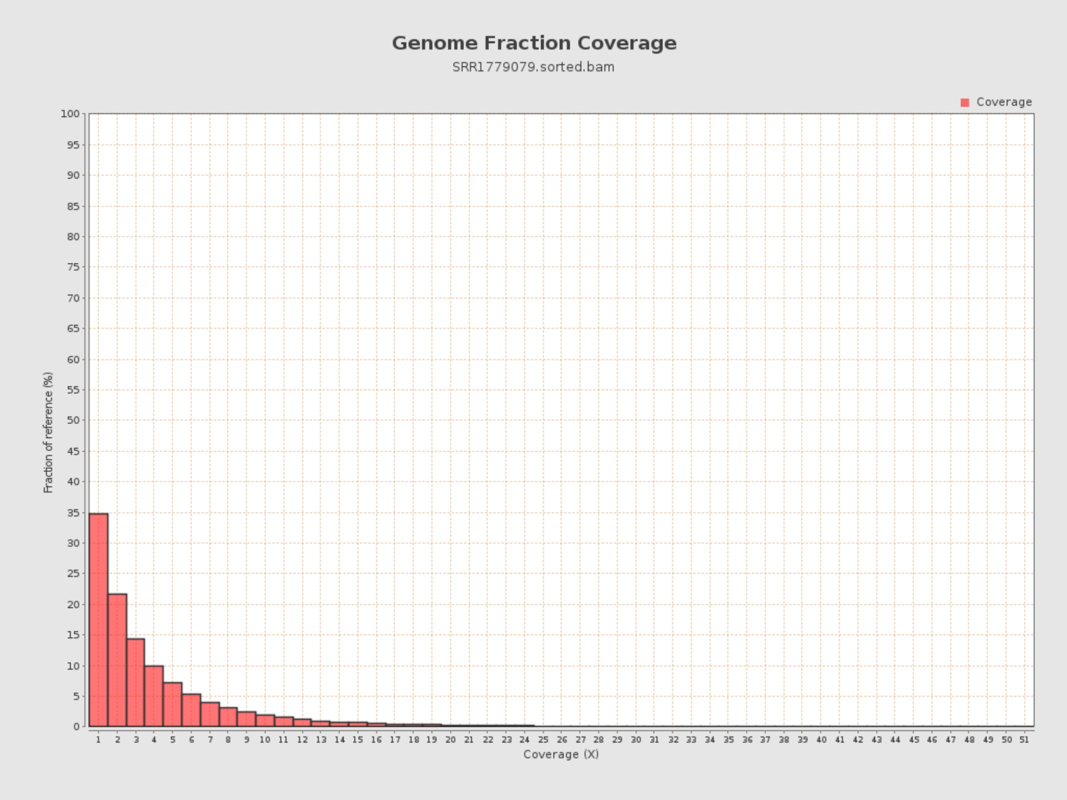
4. Results : Coverage Histogram



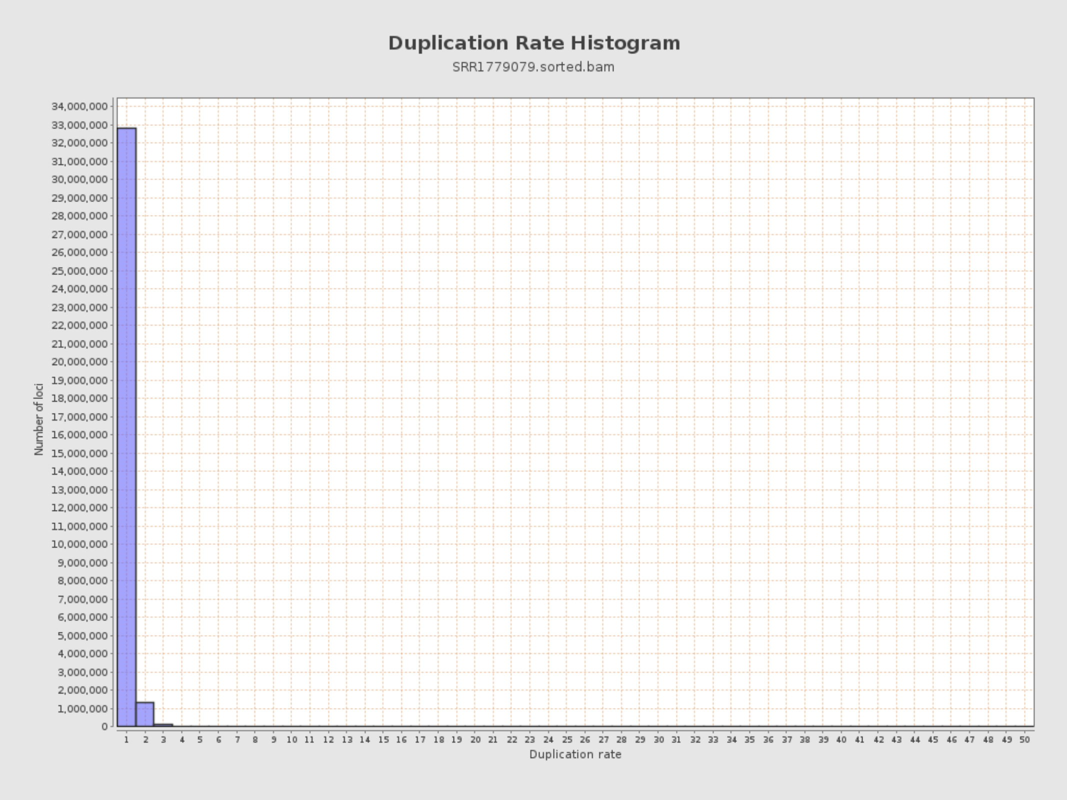
5. Results : Coverage Histogram (0-50X)



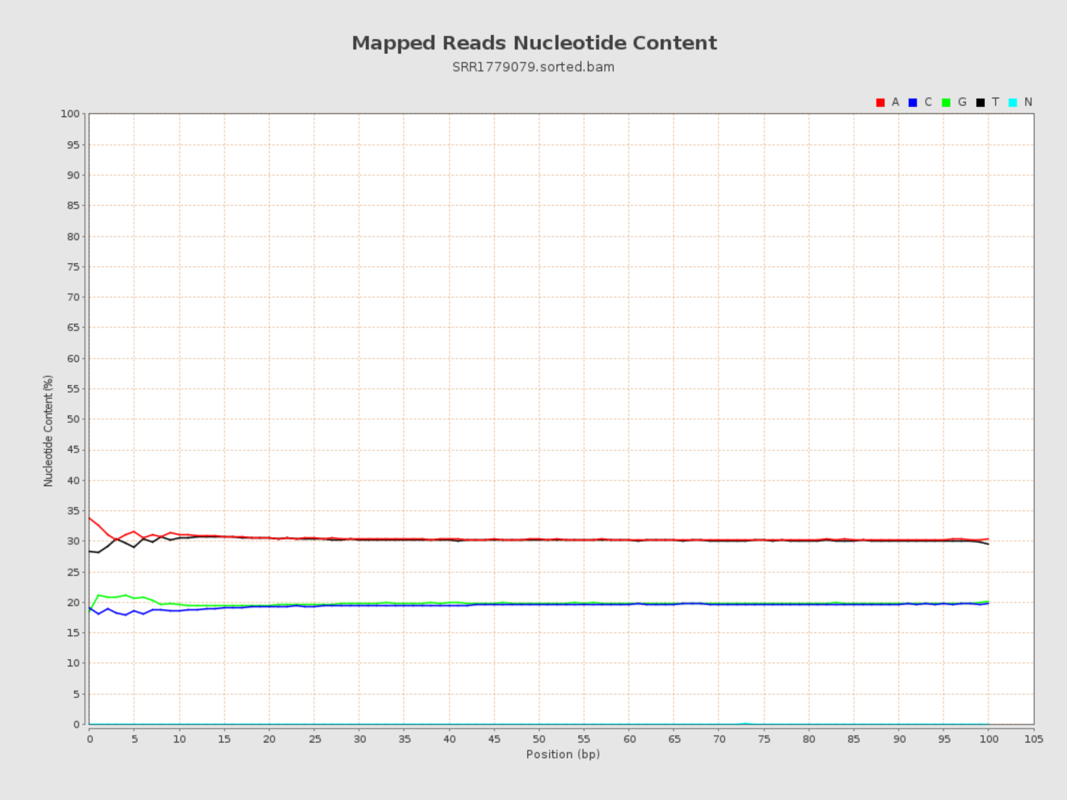
6. Results : Genome Fraction Coverage



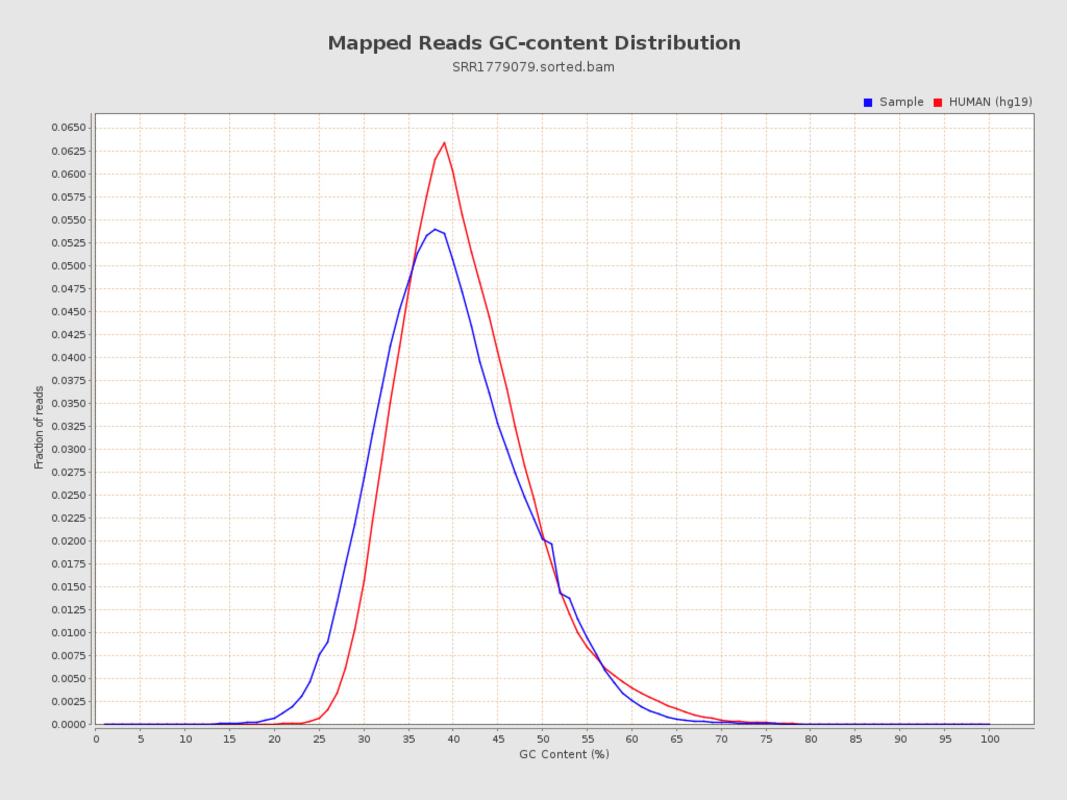
7. Results : Duplication Rate Histogram



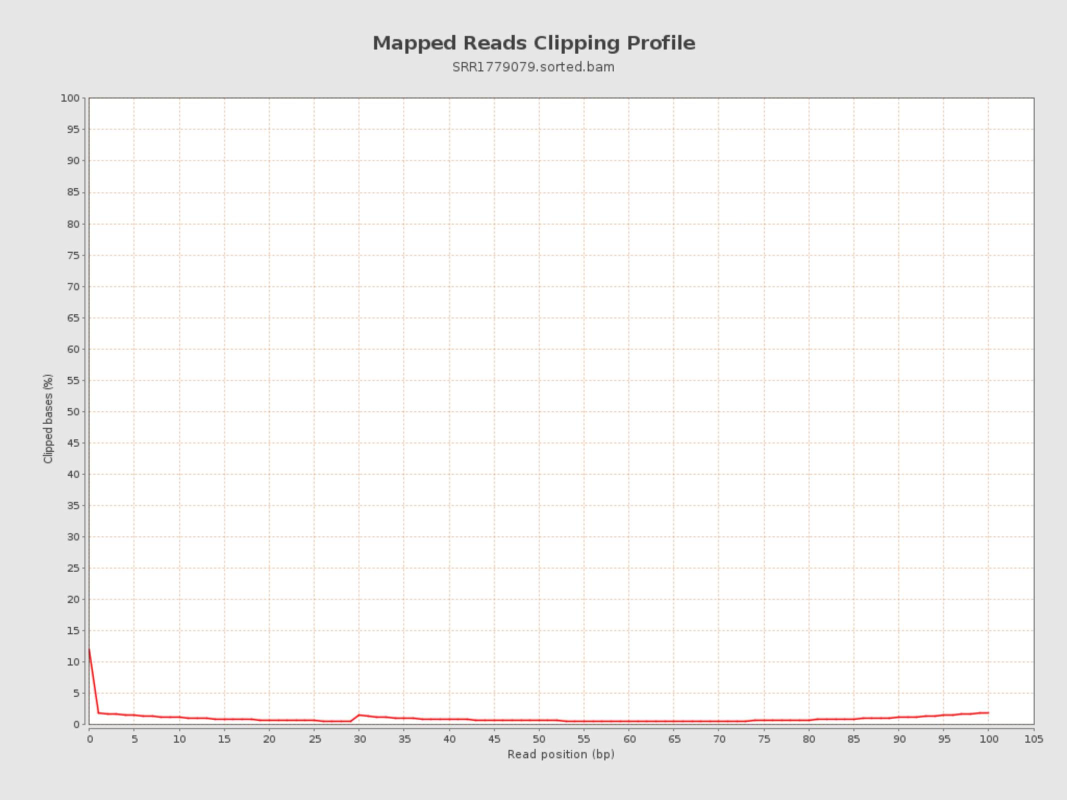
8. Results : Mapped Reads Nucleotide Content



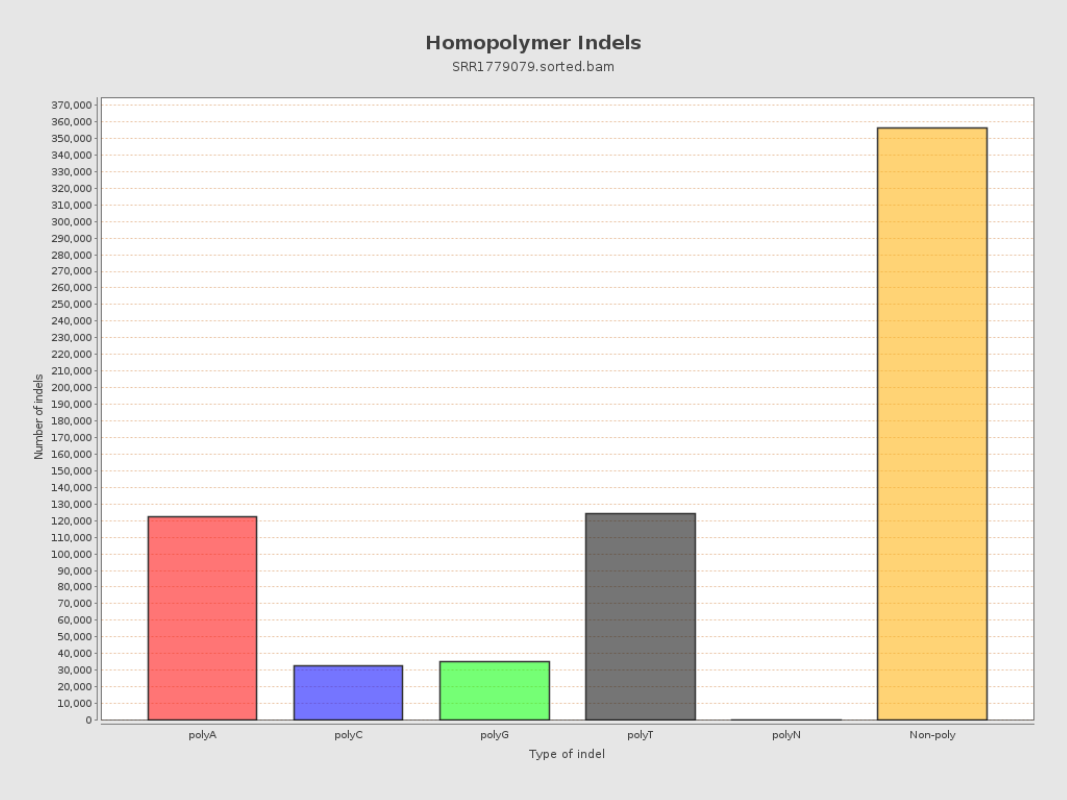
9. Results : Mapped Reads GC-content Distribution



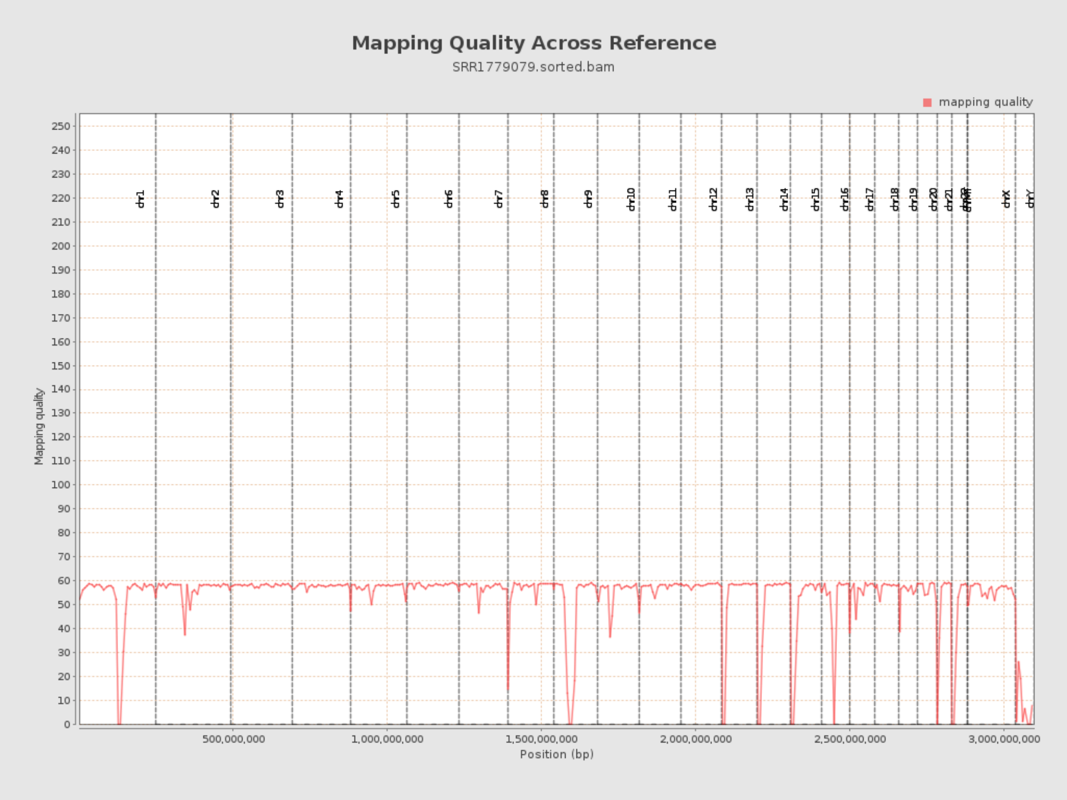
10. Results : Mapped Reads Clipping Profile



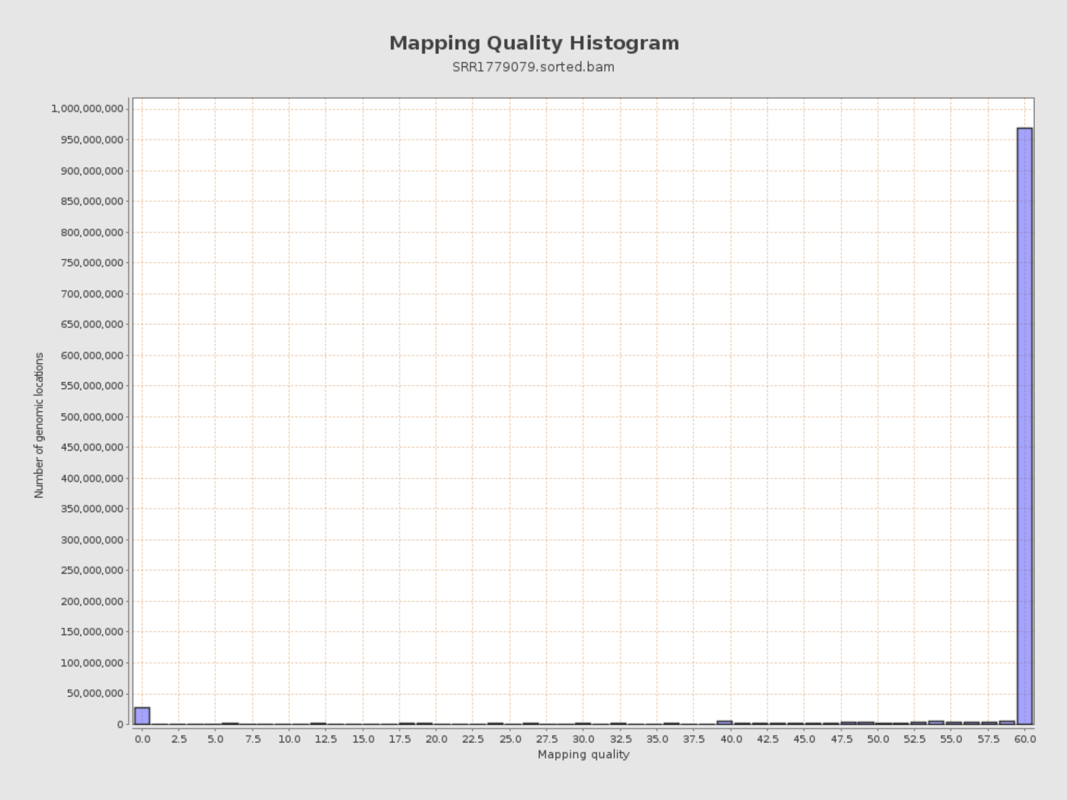
11. Results : Homopolymer Indels



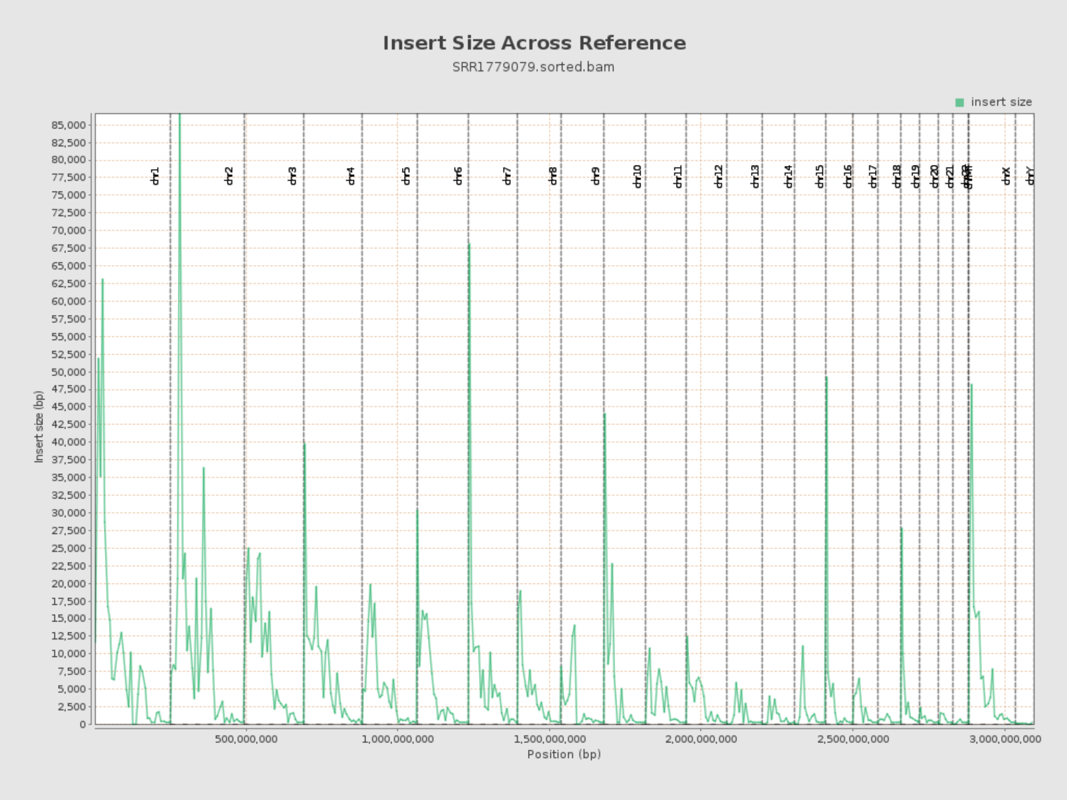
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram