Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 08:50:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779169.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_SRR1779169 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779169_1.fastq.gz SRR1779169_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 08:50:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779169.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	68,290,020
Mapped reads	66,036,114 / 96.7%
Unmapped reads	2,253,906 / 3.3%
Mapped paired reads	66,036,114 / 96.7%
Mapped reads, first in pair	33,357,074 / 48.85%
Mapped reads, second in pair	32,679,040 / 47.85%
Mapped reads, both in pair	65,115,976 / 95.35%
Mapped reads, singletons	920,138 / 1.35%
Secondary alignments	0
Supplementary alignments	366,089 / 0.54%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	3,747,136 / 5.49%
Duplication rate	4.96%
Clipped reads	3,900,787 / 5.71%

2.2. ACGT Content

Number/percentage of A's	2,014,886,640 / 30.54%
Number/percentage of C's	1,277,105,200 / 19.36%
Number/percentage of T's	2,009,104,020 / 30.45%
Number/percentage of G's	1,293,749,130 / 19.61%
Number/percentage of N's	2,663,863 / 0.04%

GC Percentage	38.97%

2.3. Coverage

Mean	2.1317
Standard Deviation	4.94

2.4. Mapping Quality

Mean Mapping Quality	53.47

2.5. Insert size

Mean	63,627.32
Standard Deviation	2,441,255.06
P25/Median/P75	162 / 213 / 284

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	27,061,681
Insertions	539,666
Mapped reads with at least one insertion	0.81%
Deletions	650,538
Mapped reads with at least one deletion	0.97%
Homopolymer indels	46.72%

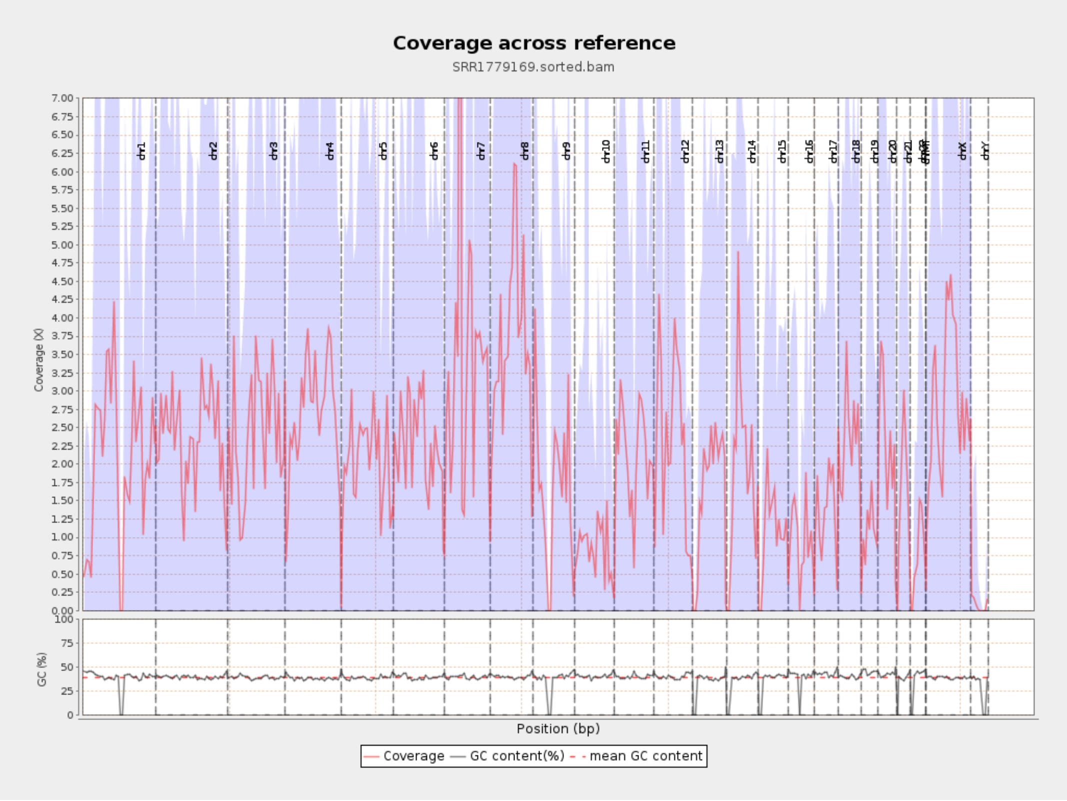
2.7. Chromosome stats

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

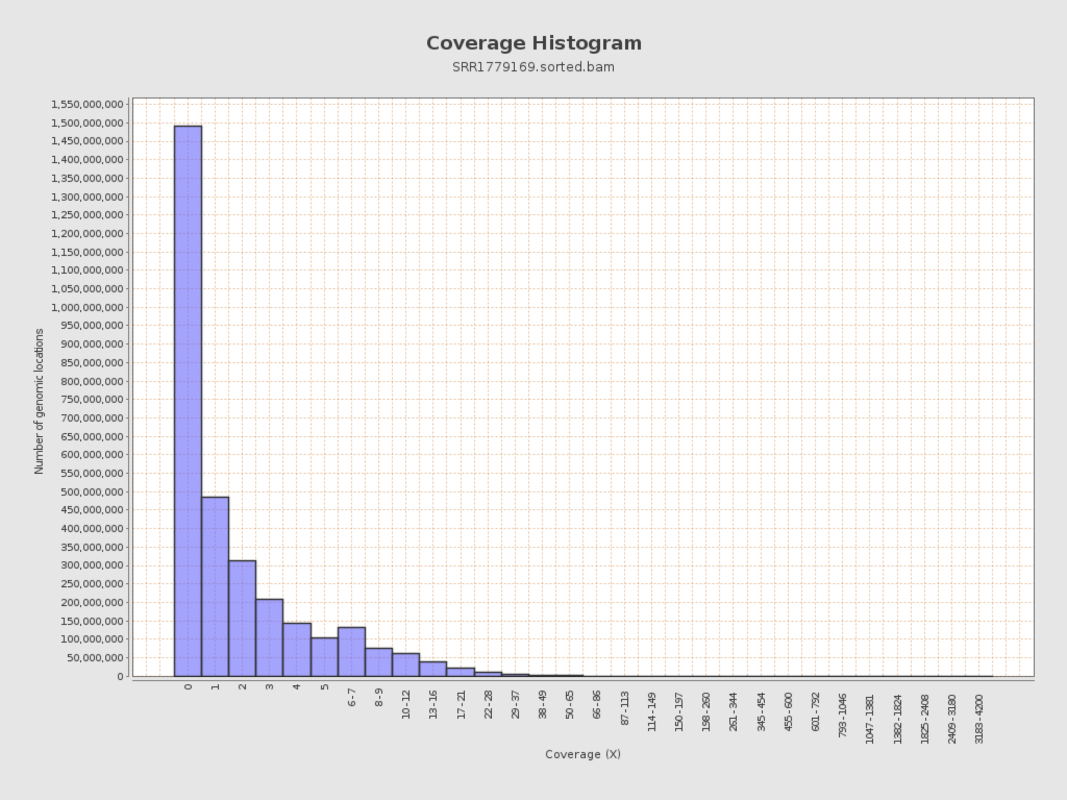
		bases	coverage	deviation
chr1	249250621	514773054	2.0653	4.6703
chr2	243199373	575480548	2.3663	4.7944
chr3	198022430	479390319	2.4209	4.1425
chr4	191154276	518338143	2.7116	4.478
chr5	180915260	370193399	2.0462	3.638
chr6	171115067	395528468	2.3115	3.9586
chr7	159138663	563631333	3.5418	11.6757
chr8	146364022	543682418	3.7146	5.3182
chr9	141213431	242263639	1.7156	3.6785
chr10	135534747	114334803	0.8436	6.3945
chr11	135006516	287224354	2.1275	3.7956
chr12	133851895	310808539	2.322	4.2312
chr13	115169878	195272609	1.6955	3.3824
chr14	107349540	209217461	1.9489	3.7675
chr15	102531392	111804597	1.0904	2.9626
chr16	90354753	84416547	0.9343	2.2982
chr17	81195210	112790816	1.3891	3.2009
chr18	78077248	186019845	2.3825	3.9005
chr19	59128983	64677222	1.0938	2.9865
chr20	63025520	149461117	2.3714	4.2513
chr21	48129895	74273509	1.5432	3.0861
chr22	51304566	40171835	0.783	2.1496
chrMT	16571	4639	0.2799	0.7098
chrX	155270560	450507242	2.9014	5.1012

chrY	59373566	4698851	0.0791	1.0837

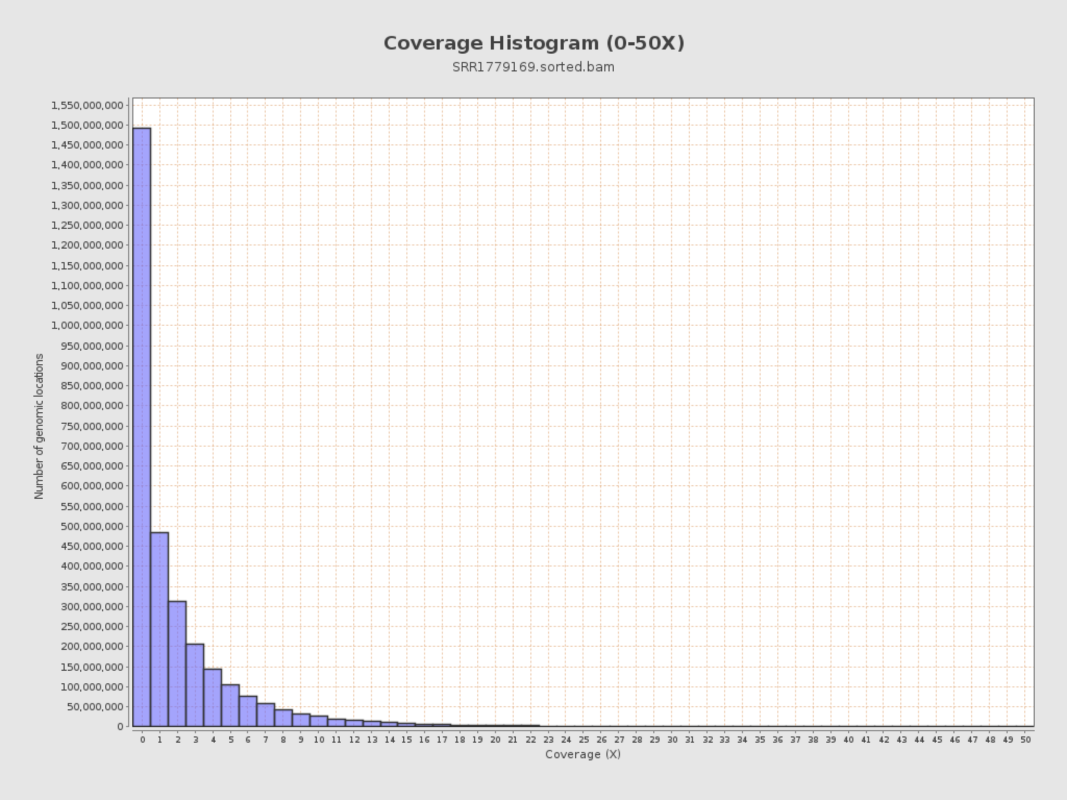
3. Results : Coverage across reference



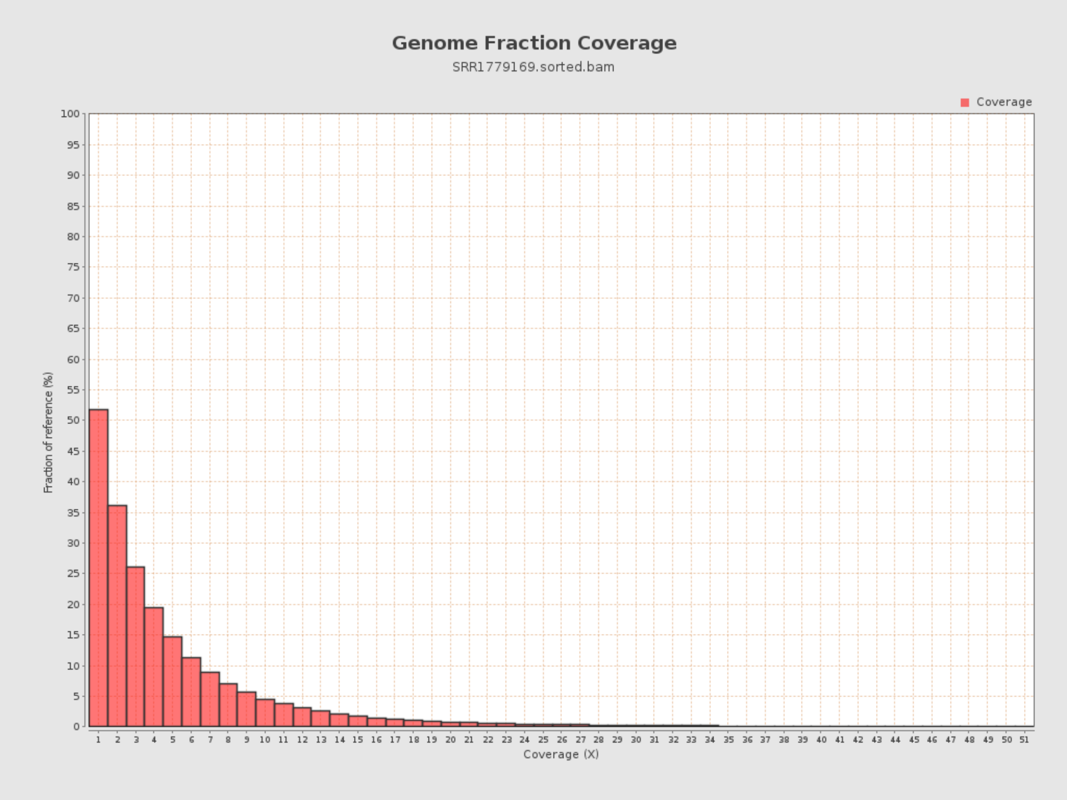
4. Results : Coverage Histogram



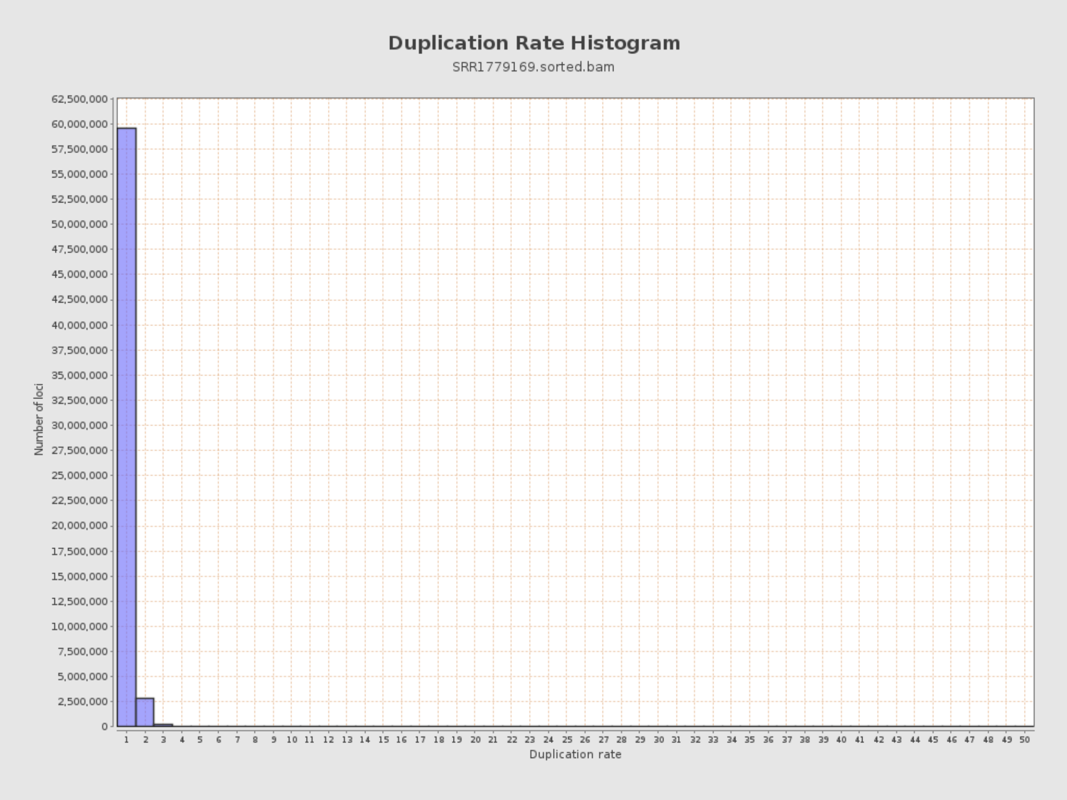
5. Results : Coverage Histogram (0-50X)



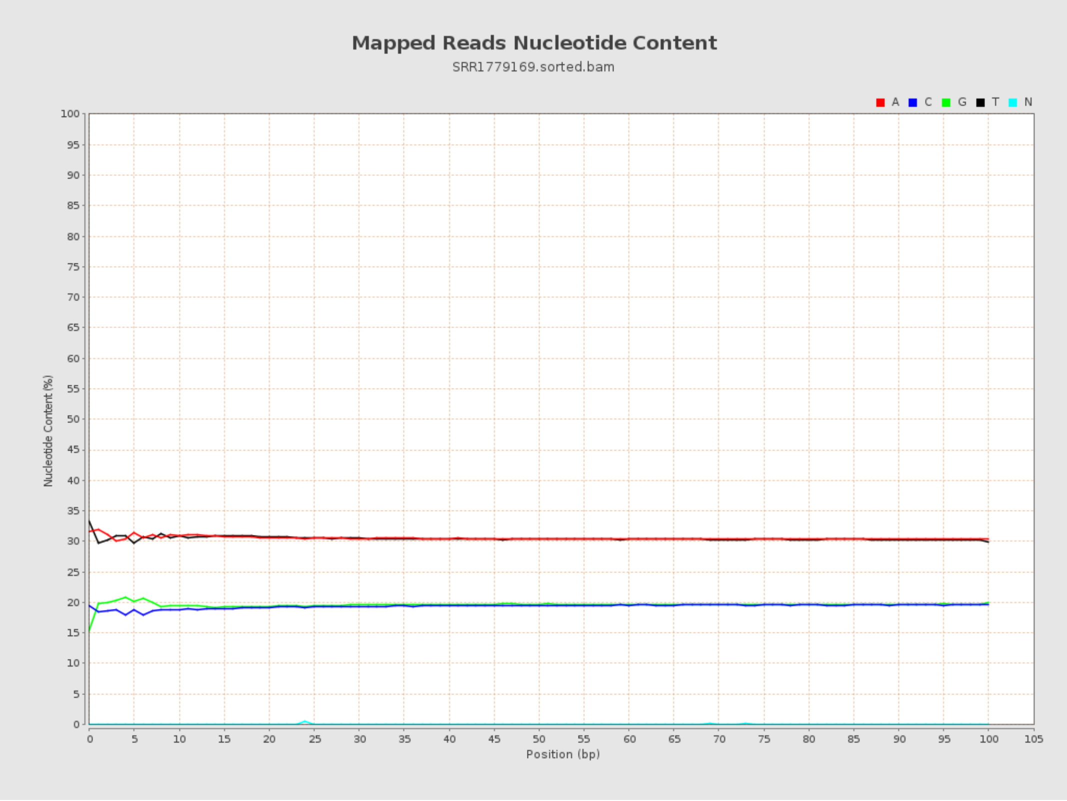
6. Results : Genome Fraction Coverage



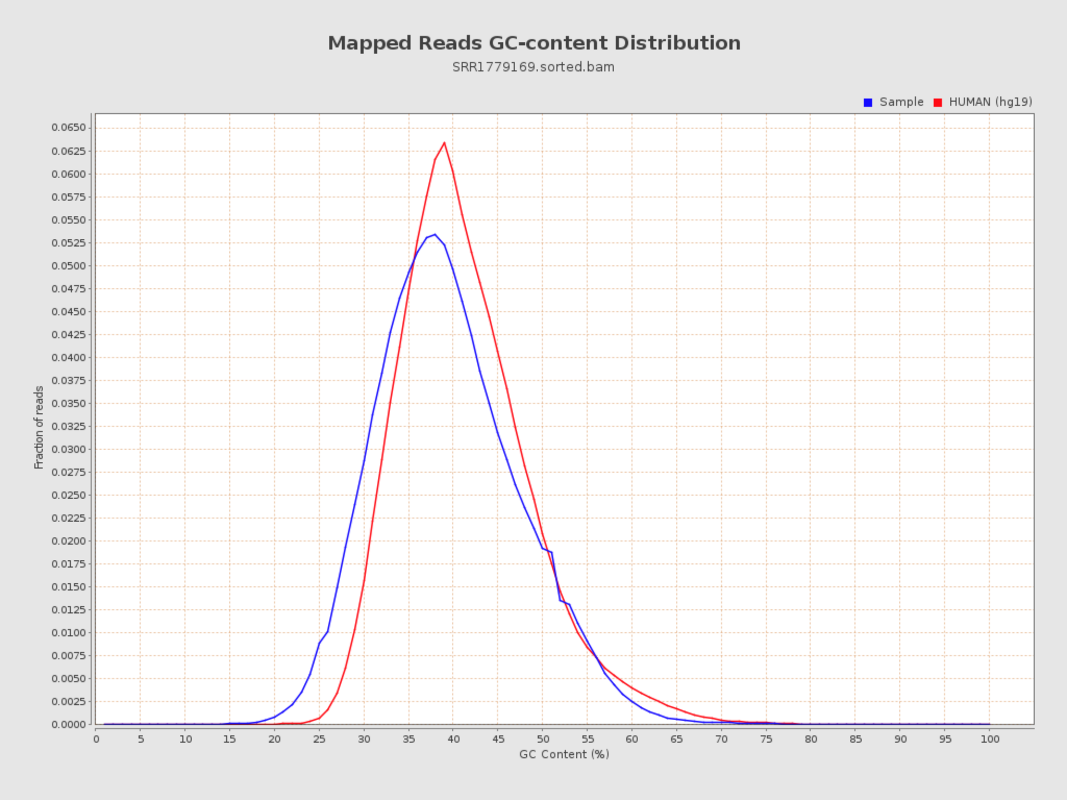
7. Results : Duplication Rate Histogram



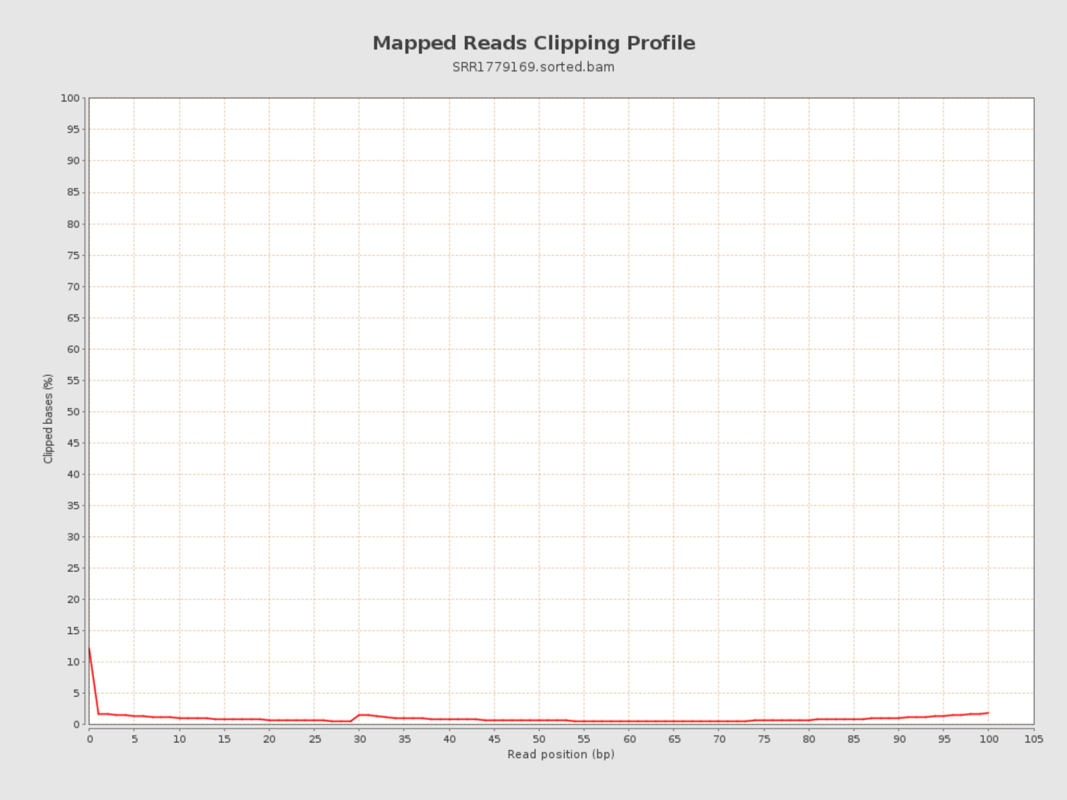
8. Results : Mapped Reads Nucleotide Content



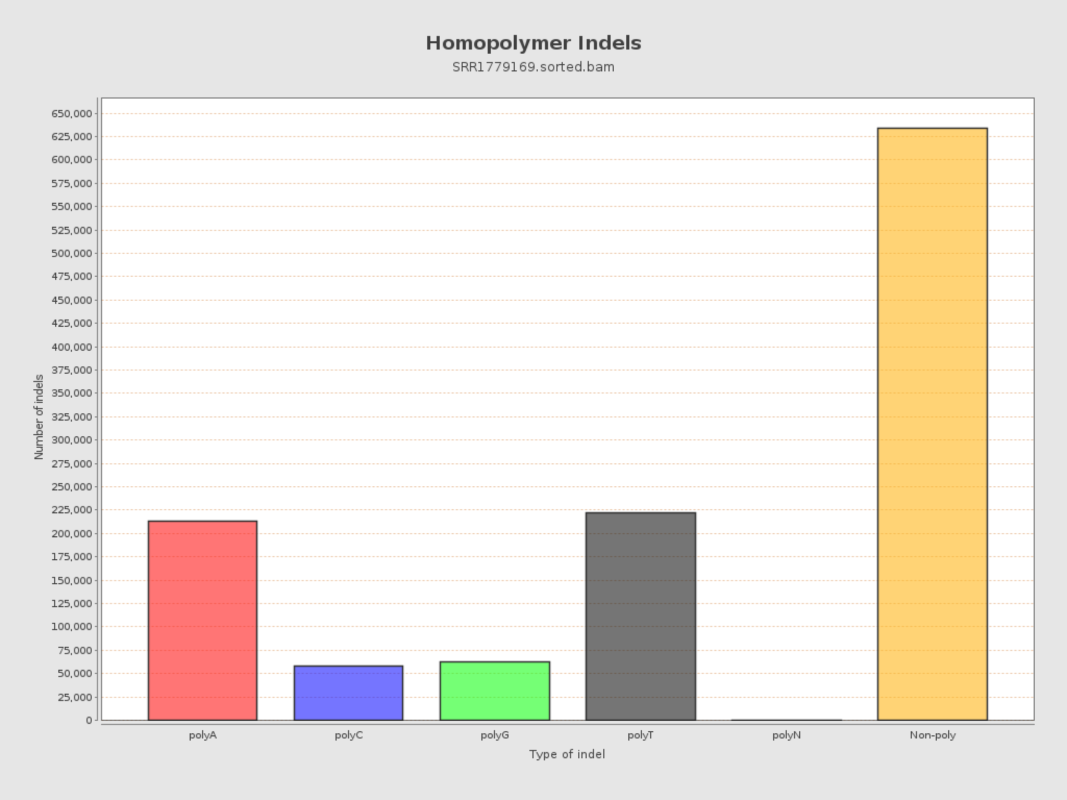
9. Results : Mapped Reads GC-content Distribution



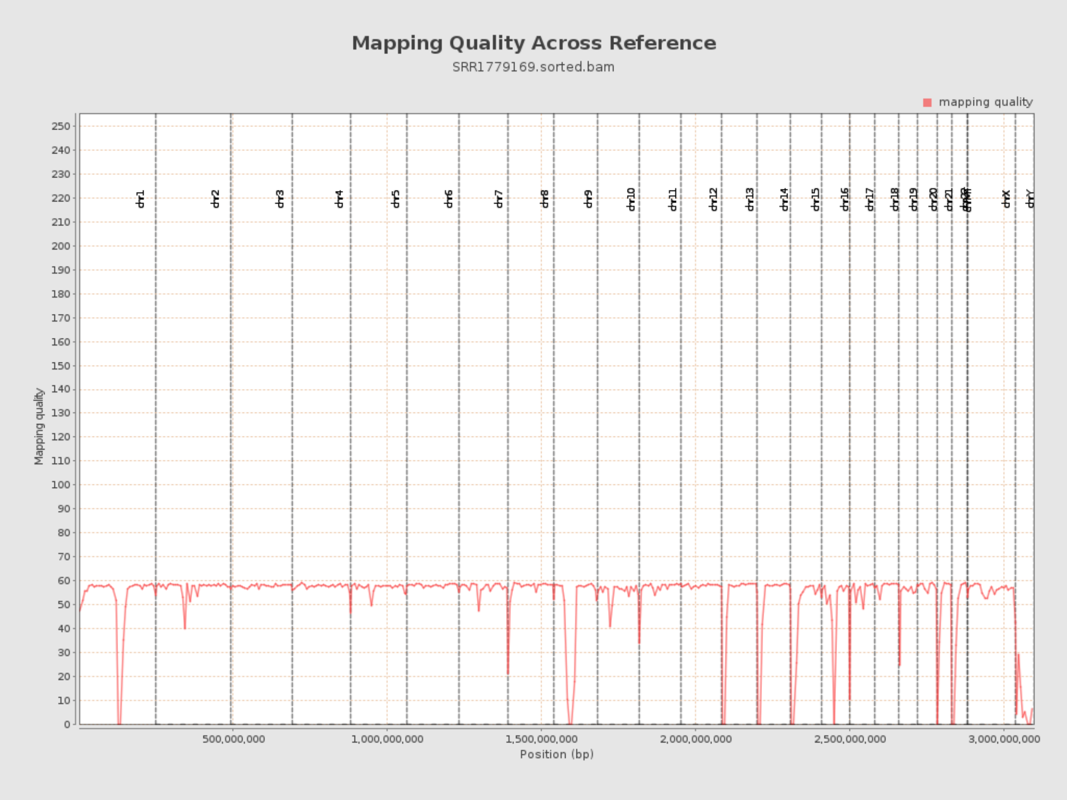
10. Results : Mapped Reads Clipping Profile



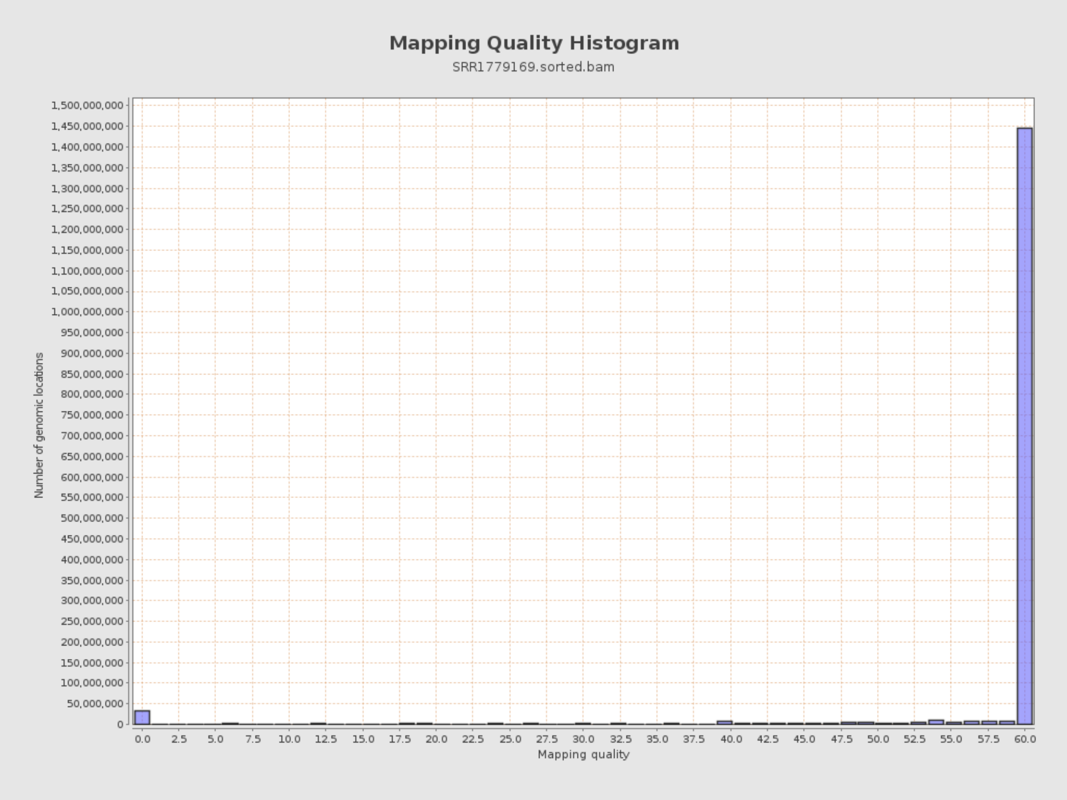
11. Results : Homopolymer Indels



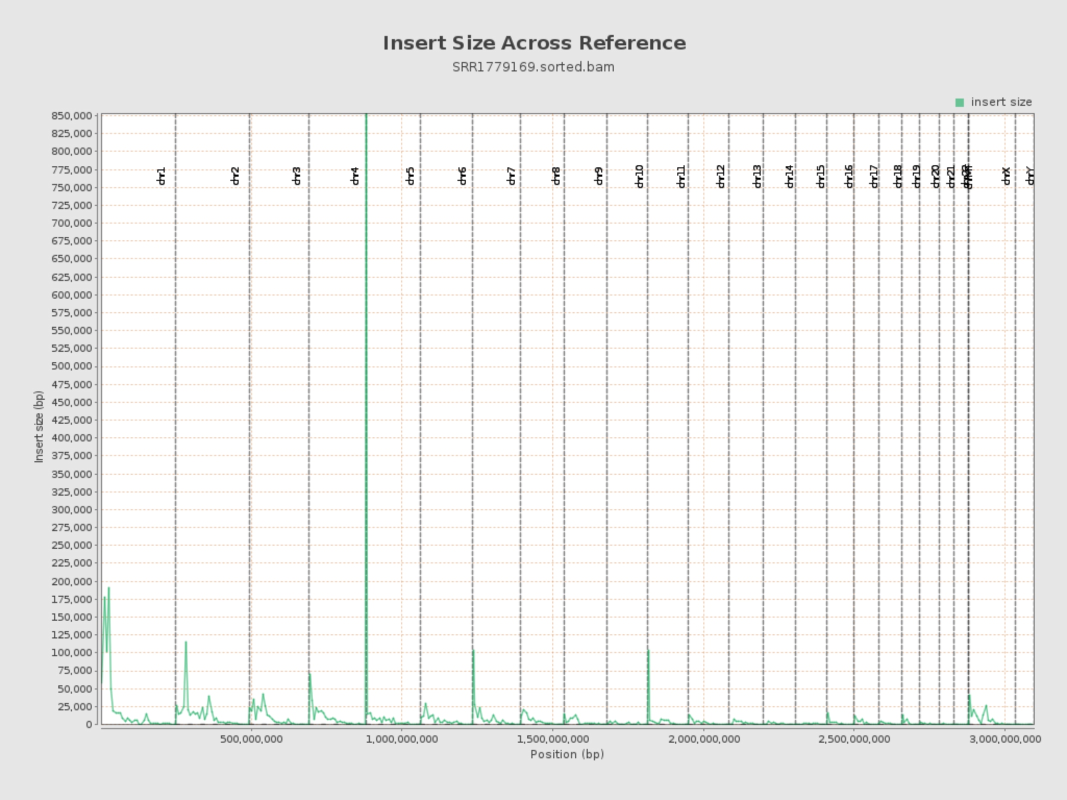
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram