Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 01:48:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779100.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_SRR1779100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779100_1.fastq.gz SRR1779100_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 01:48:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,088,712
Mapped reads	21,497,071 / 97.32%
Unmapped reads	591,641 / 2.68%
Mapped paired reads	21,497,071 / 97.32%
Mapped reads, first in pair	10,826,506 / 49.01%
Mapped reads, second in pair	10,670,565 / 48.31%
Mapped reads, both in pair	21,265,304 / 96.27%
Mapped reads, singletons	231,767 / 1.05%
Secondary alignments	0
Supplementary alignments	117,348 / 0.53%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	558,800 / 2.53%
Duplication rate	2.25%
Clipped reads	1,329,962 / 6.02%

2.2. ACGT Content

Number/percentage of A's	655,617,835 / 30.54%
Number/percentage of C's	415,624,708 / 19.36%
Number/percentage of T's	653,626,619 / 30.44%
Number/percentage of G's	421,344,129 / 19.62%
Number/percentage of N's	865,015 / 0.04%

GC Percentage	38.98%

2.3. Coverage

Mean	0.6937
Standard Deviation	1.8444

2.4. Mapping Quality

Mean Mapping Quality	53.67

2.5. Insert size

Mean	64,570.02
Standard Deviation	2,437,081.29
P25/Median/P75	159 / 212 / 287

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	8,948,088
Insertions	179,954
Mapped reads with at least one insertion	0.83%
Deletions	221,672
Mapped reads with at least one deletion	1.01%
Homopolymer indels	46.71%

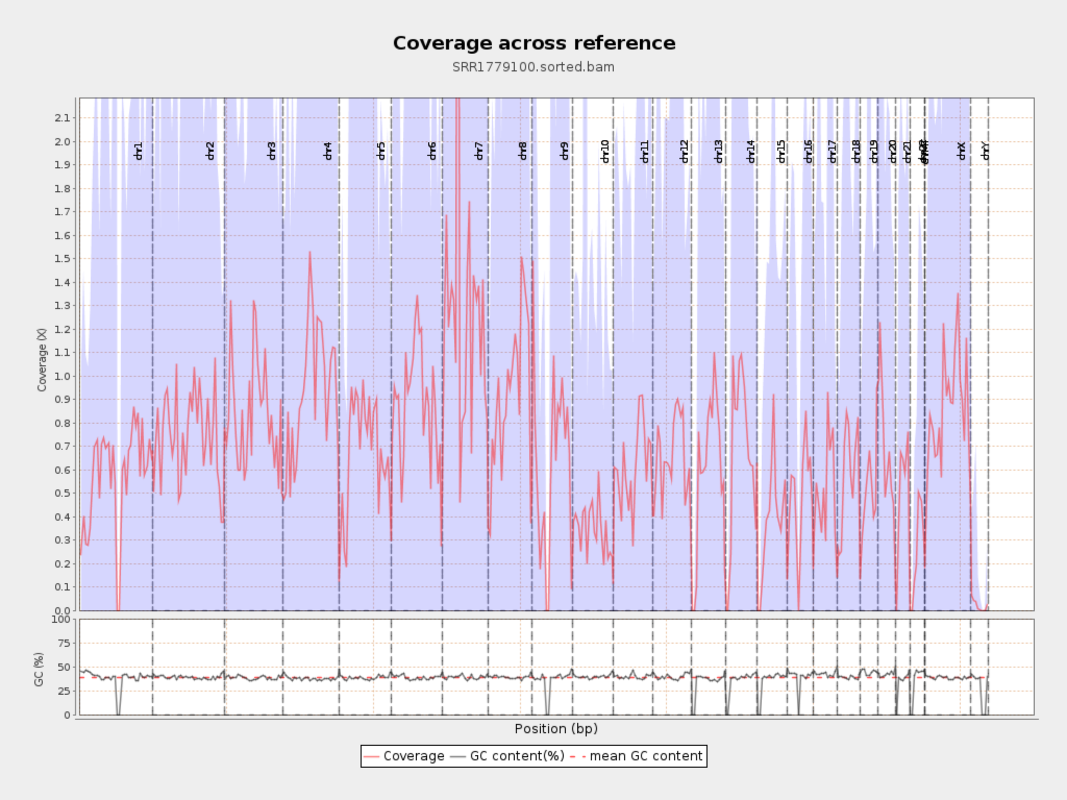
2.7. Chromosome stats

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

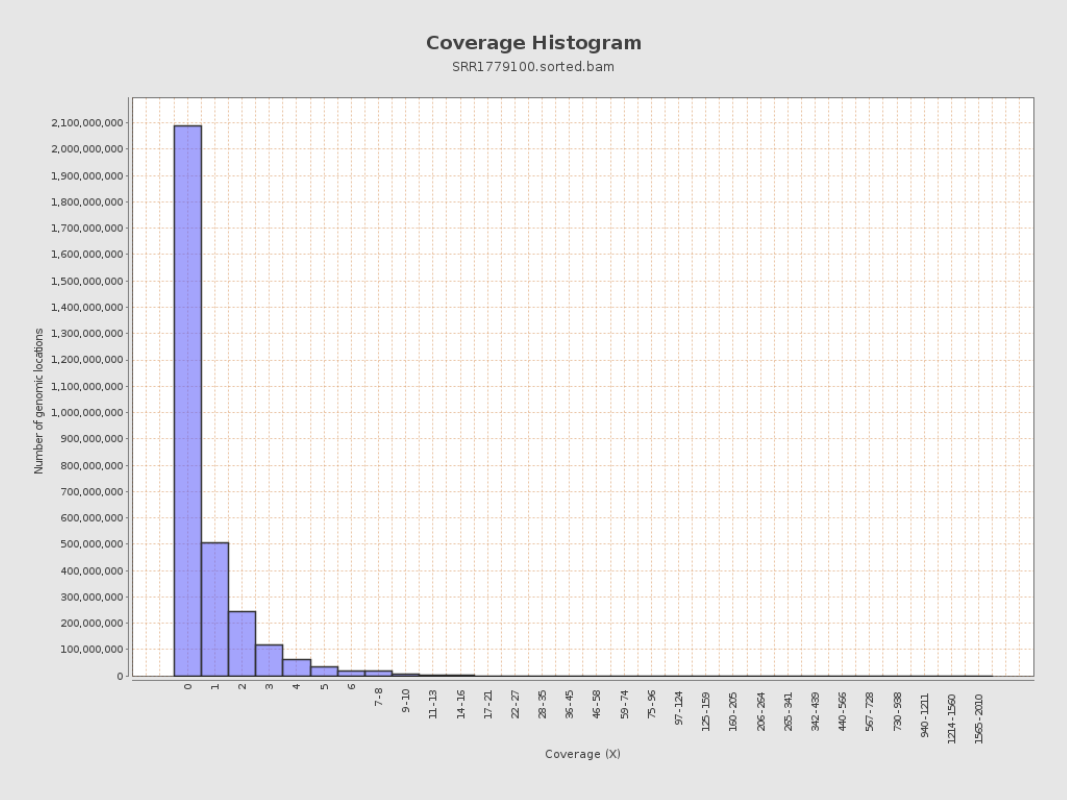
		bases	coverage	deviation
chr1	249250621	142033436	0.5698	2.4098
chr2	243199373	181346109	0.7457	1.6573
chr3	198022430	167313224	0.8449	1.5382
chr4	191154276	178537472	0.934	1.6377
chr5	180915260	121367792	0.6709	1.3275
chr6	171115067	153618751	0.8978	1.6452
chr7	159138663	212042040	1.3324	3.9164
chr8	146364022	136742690	0.9343	1.6435
chr9	141213431	86695329	0.6139	1.4403
chr10	135534747	47330608	0.3492	2.885
chr11	135006516	81840736	0.6062	1.2892
chr12	133851895	86589796	0.6469	1.3397
chr13	115169878	70014639	0.6079	1.3059
chr14	107349540	71730041	0.6682	1.4016
chr15	102531392	39669909	0.3869	1.1119
chr16	90354753	41844665	0.4631	1.0816
chr17	81195210	40523842	0.4991	1.3907
chr18	78077248	45221482	0.5792	1.2904
chr19	59128983	28247727	0.4777	1.6311
chr20	63025520	42912952	0.6809	1.4061
chr21	48129895	24813997	0.5156	1.2218
chr22	51304566	12901278	0.2515	0.8002
chrMT	16571	3020	0.1822	0.5047
chrX	155270560	133005858	0.8566	1.6585

chrY	59373566	1226744	0.0207	0.3317

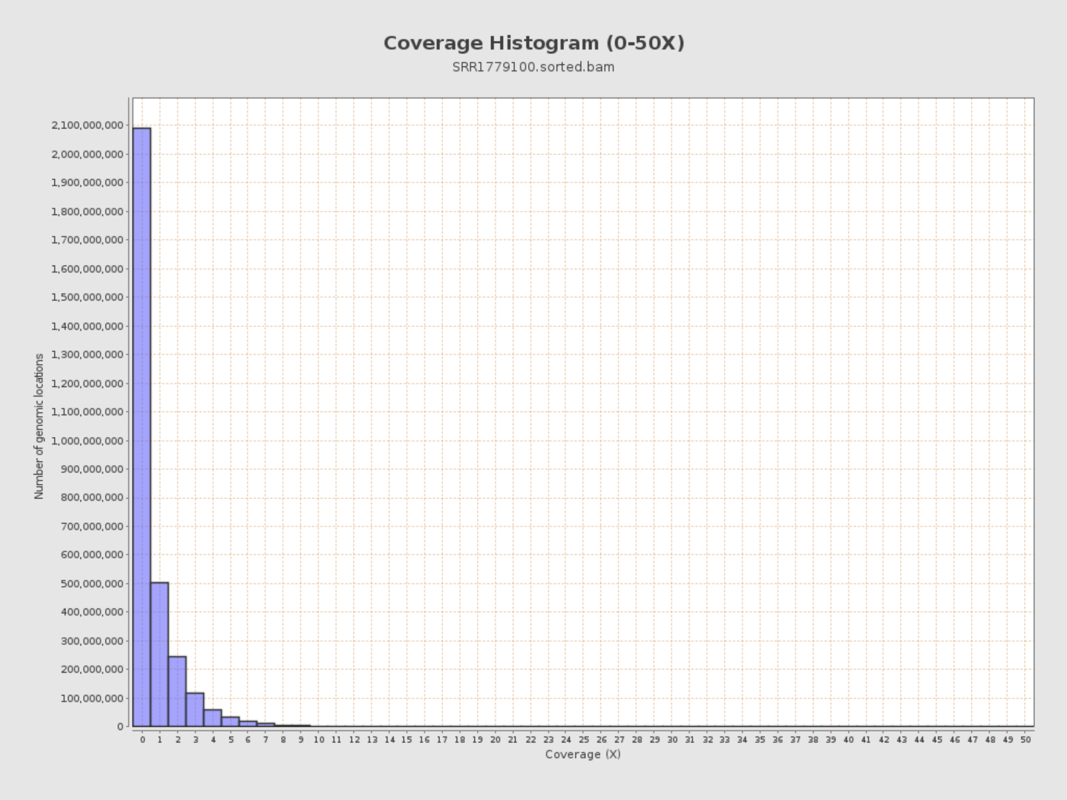
3. Results : Coverage across reference



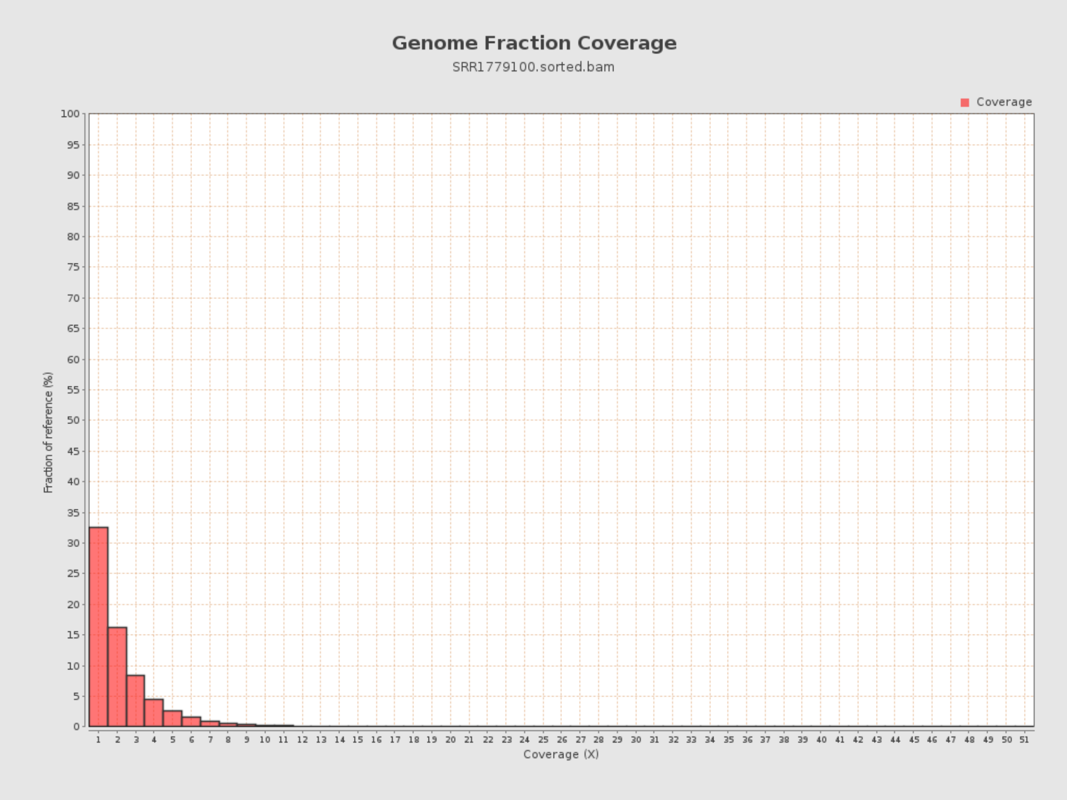
4. Results : Coverage Histogram



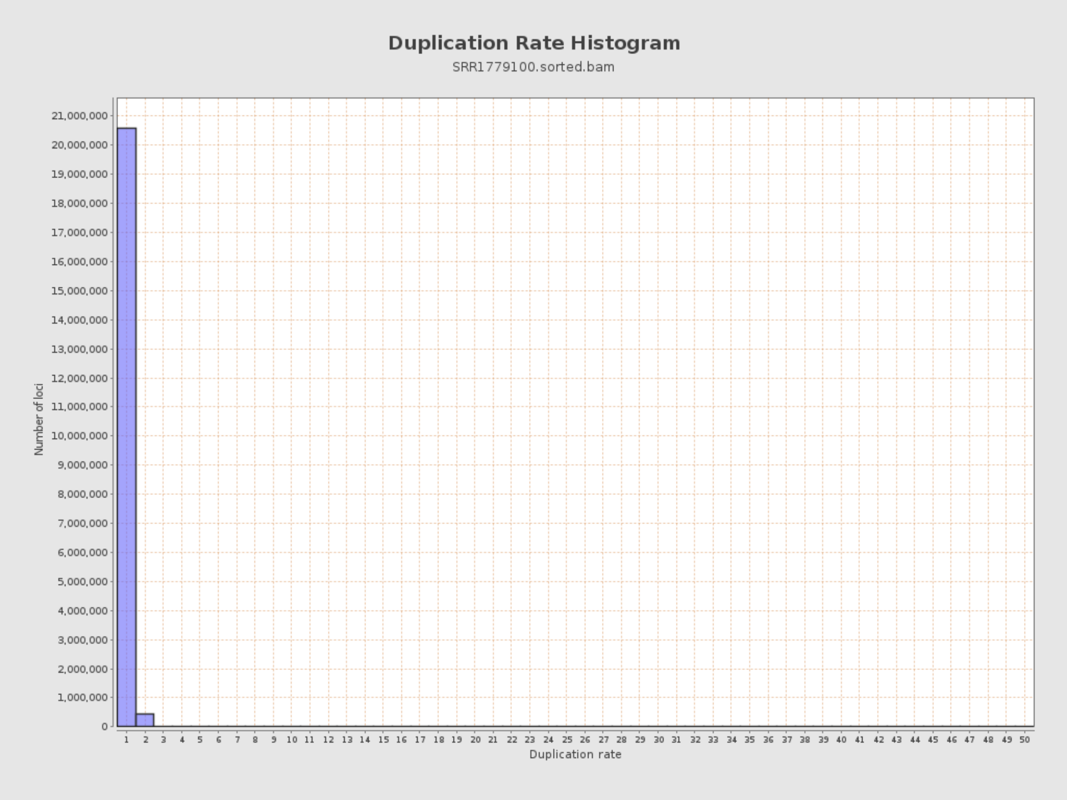
5. Results : Coverage Histogram (0-50X)



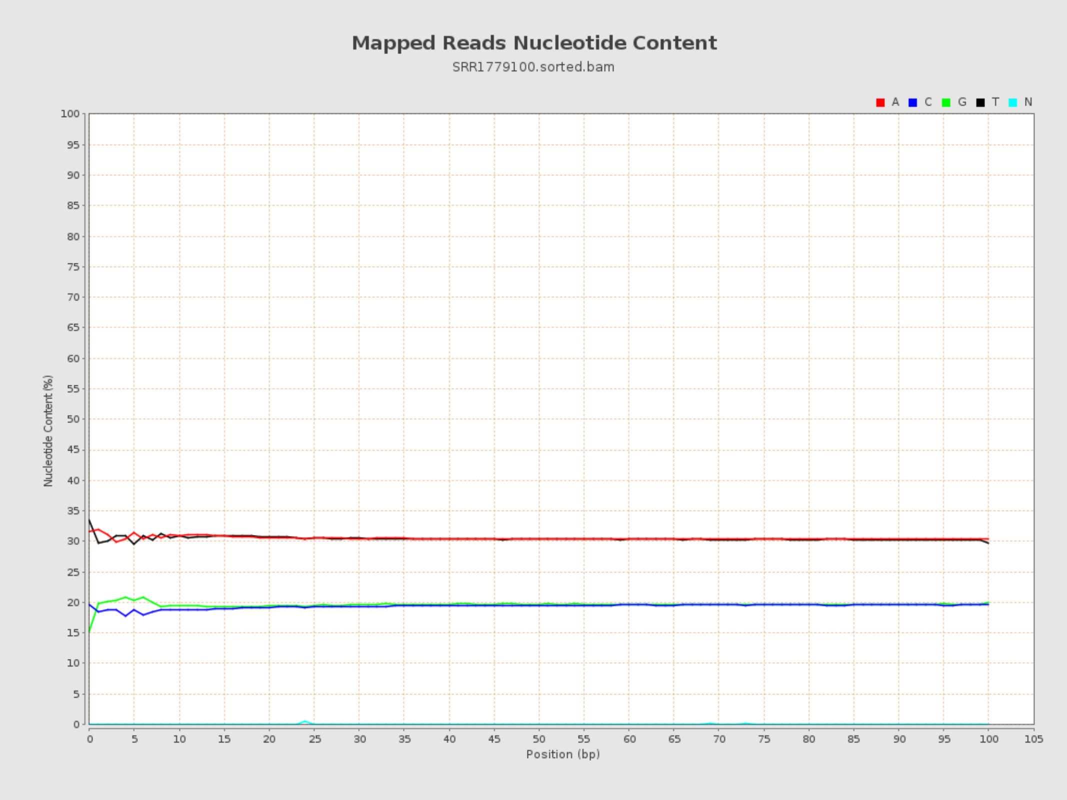
6. Results : Genome Fraction Coverage



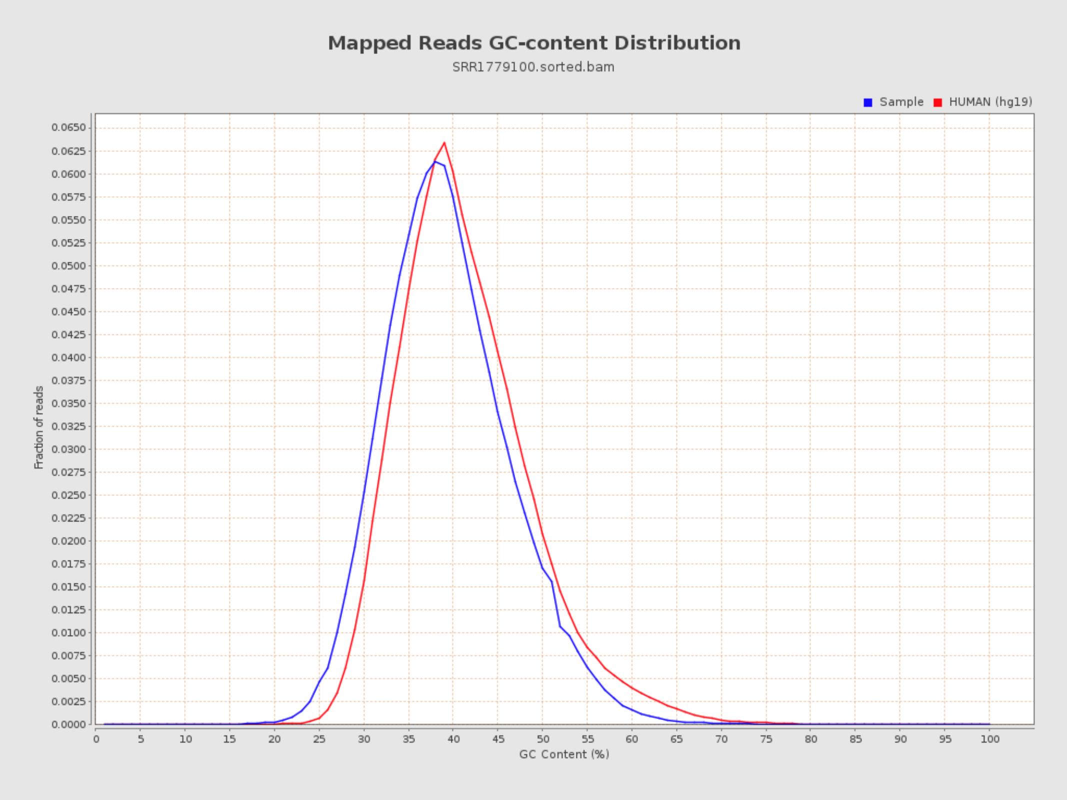
7. Results : Duplication Rate Histogram



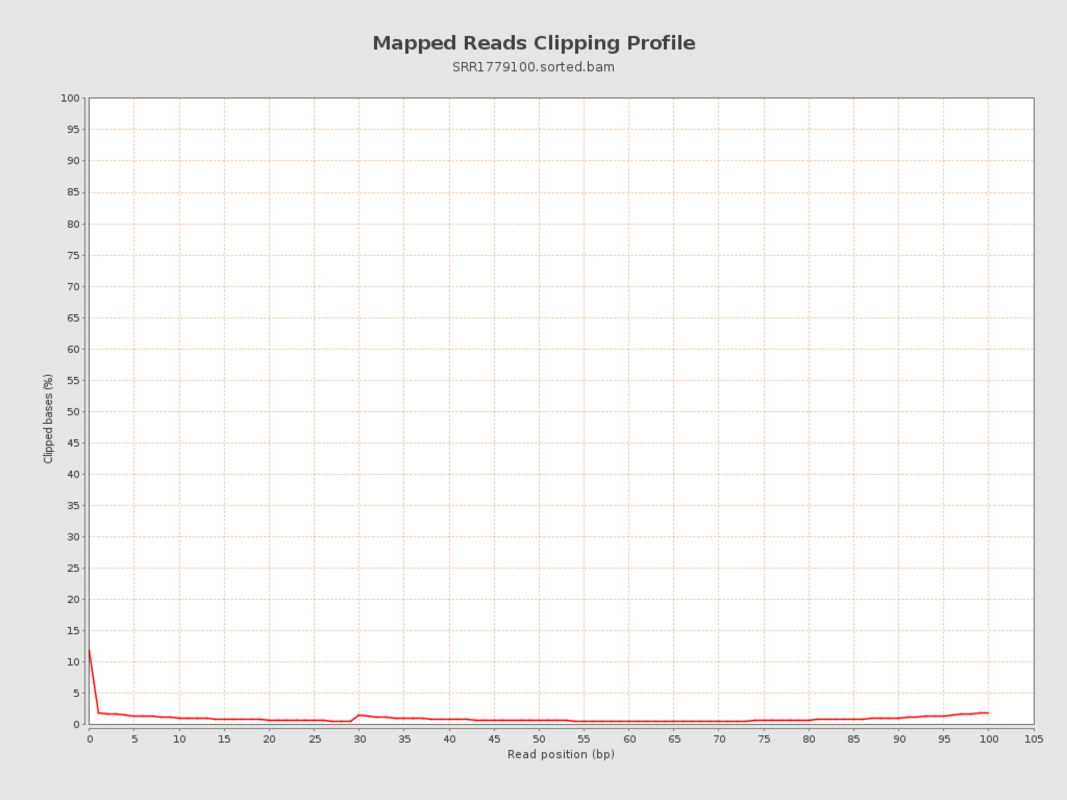
8. Results : Mapped Reads Nucleotide Content



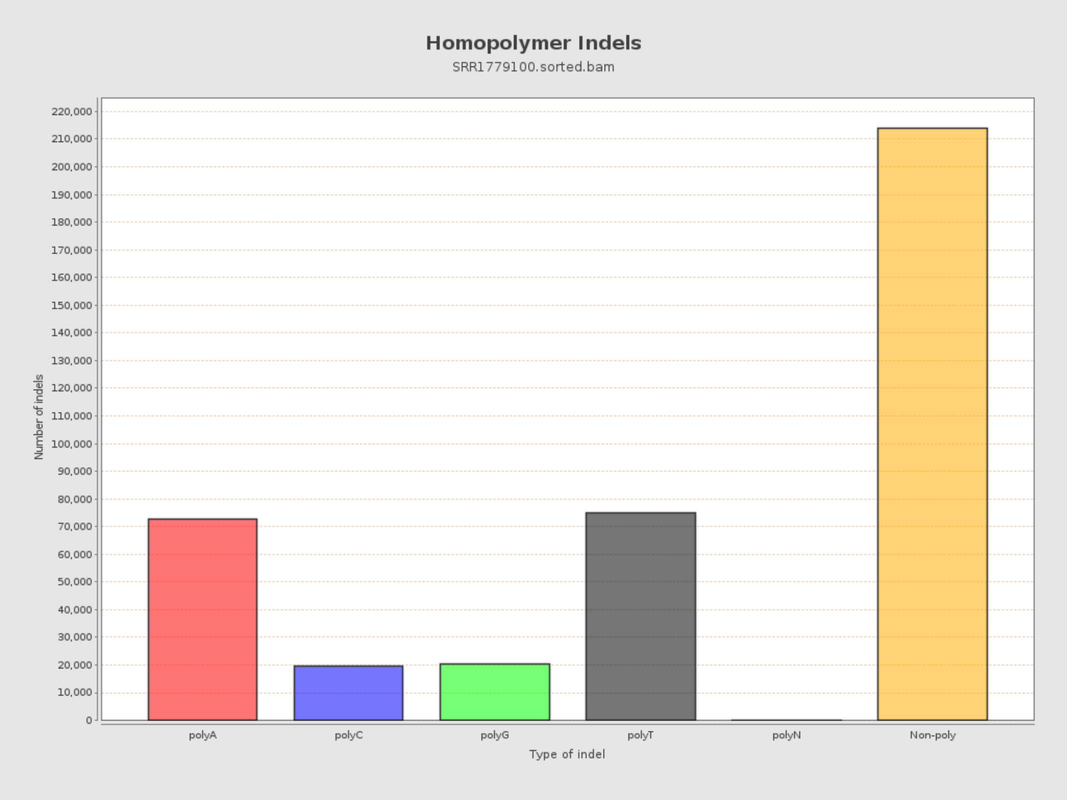
9. Results : Mapped Reads GC-content Distribution



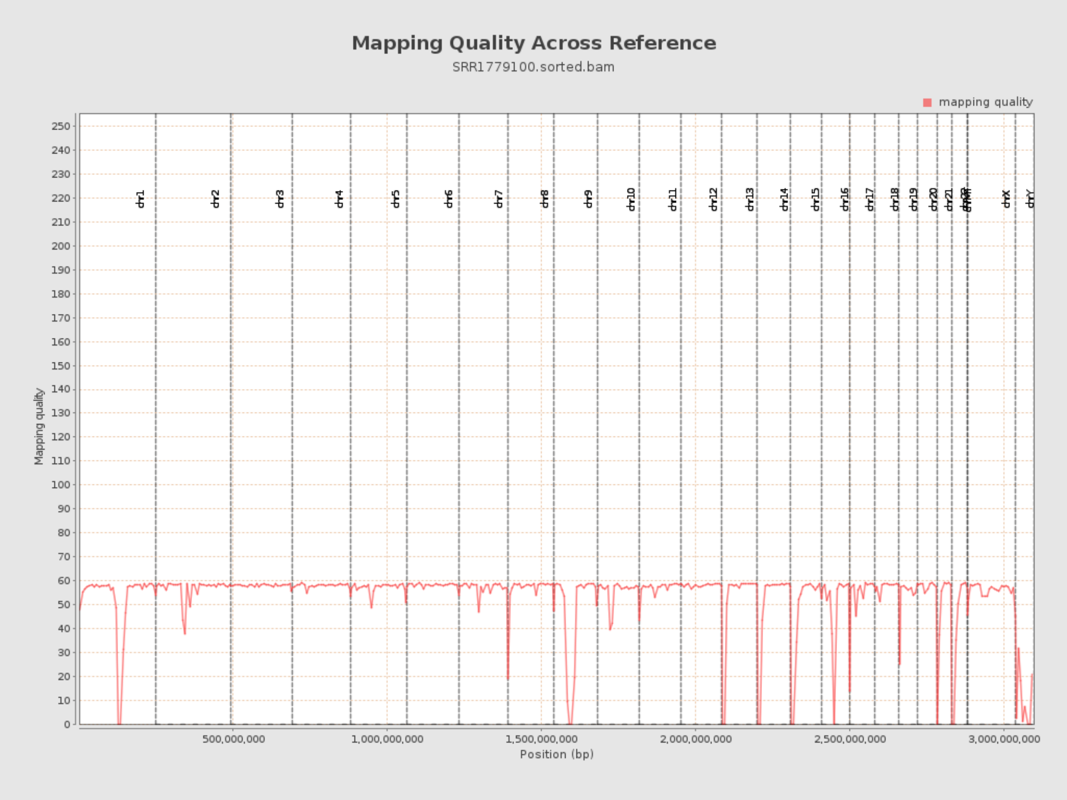
10. Results : Mapped Reads Clipping Profile



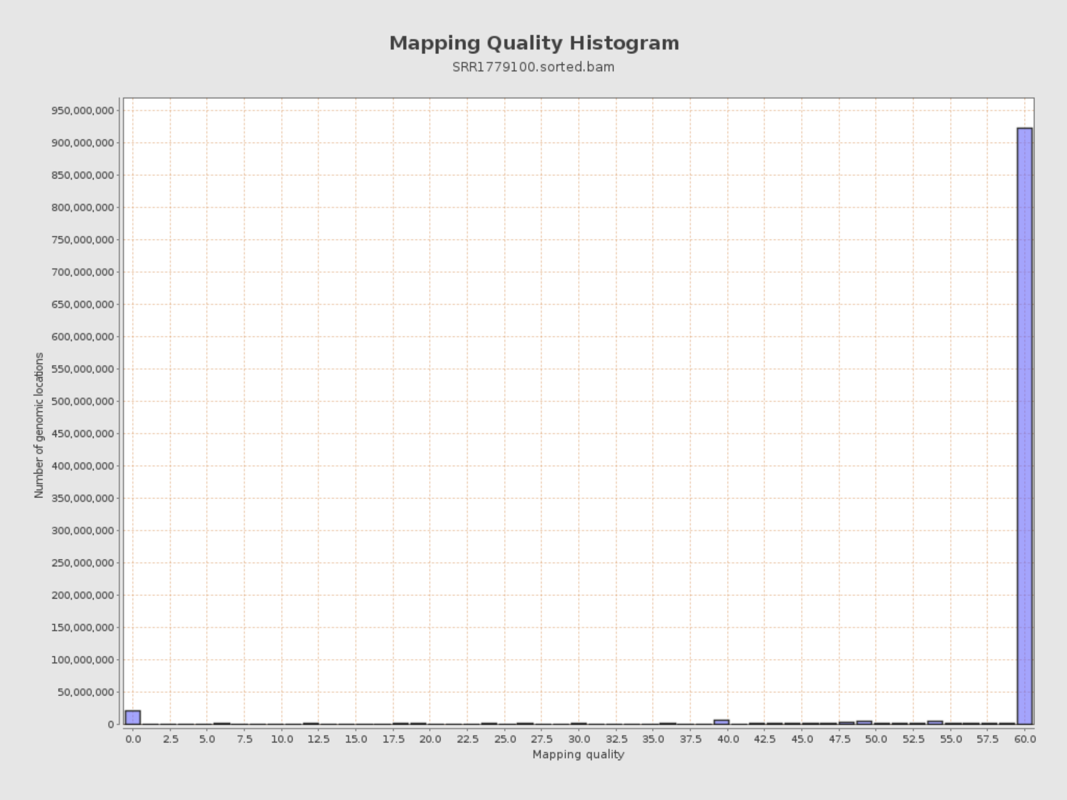
11. Results : Homopolymer Indels



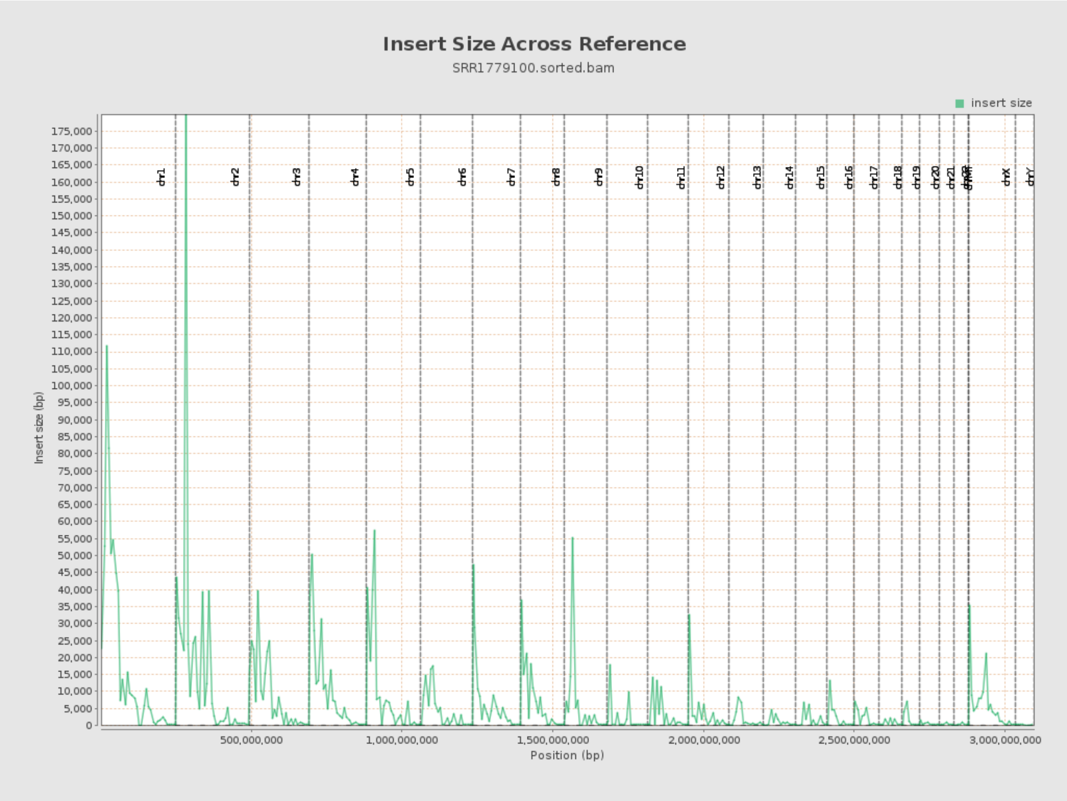
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram