Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 10:11:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779027.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_SRR1779027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779027_1.fastq.gz SRR1779027_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 10:11:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,149,442
Mapped reads	24,428,661 / 97.13%
Unmapped reads	720,781 / 2.87%
Mapped paired reads	24,428,661 / 97.13%
Mapped reads, first in pair	12,293,327 / 48.88%
Mapped reads, second in pair	12,135,334 / 48.25%
Mapped reads, both in pair	24,170,316 / 96.11%
Mapped reads, singletons	258,345 / 1.03%
Secondary alignments	0
Supplementary alignments	135,441 / 0.54%
Read min/max/mean length	30 / 101 / 101.21
Duplicated reads (estimated)	1,102,833 / 4.39%
Duplication rate	4.06%
Clipped reads	1,917,721 / 7.63%

2.2. ACGT Content

Number/percentage of A's	751,294,501 / 30.85%
Number/percentage of C's	464,063,789 / 19.06%
Number/percentage of T's	747,719,492 / 30.7%
Number/percentage of G's	471,386,331 / 19.36%
Number/percentage of N's	824,035 / 0.03%

GC Percentage	38.41%

2.3. Coverage

Mean	0.7869
Standard Deviation	2.6293

2.4. Mapping Quality

Mean Mapping Quality	53.21

2.5. Insert size

Mean	54,074.23
Standard Deviation	2,151,015.35
P25/Median/P75	148 / 202 / 279

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	11,138,420
Insertions	206,974
Mapped reads with at least one insertion	0.83%
Deletions	254,713
Mapped reads with at least one deletion	1.02%
Homopolymer indels	46.71%

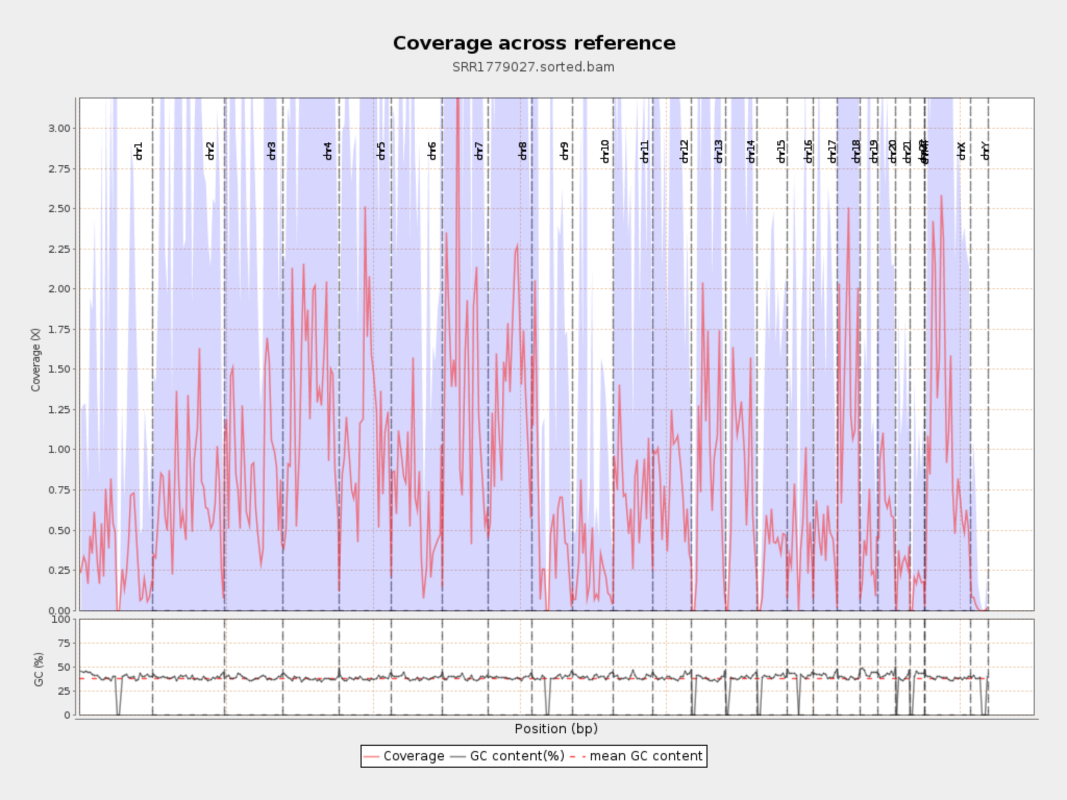
2.7. Chromosome stats

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

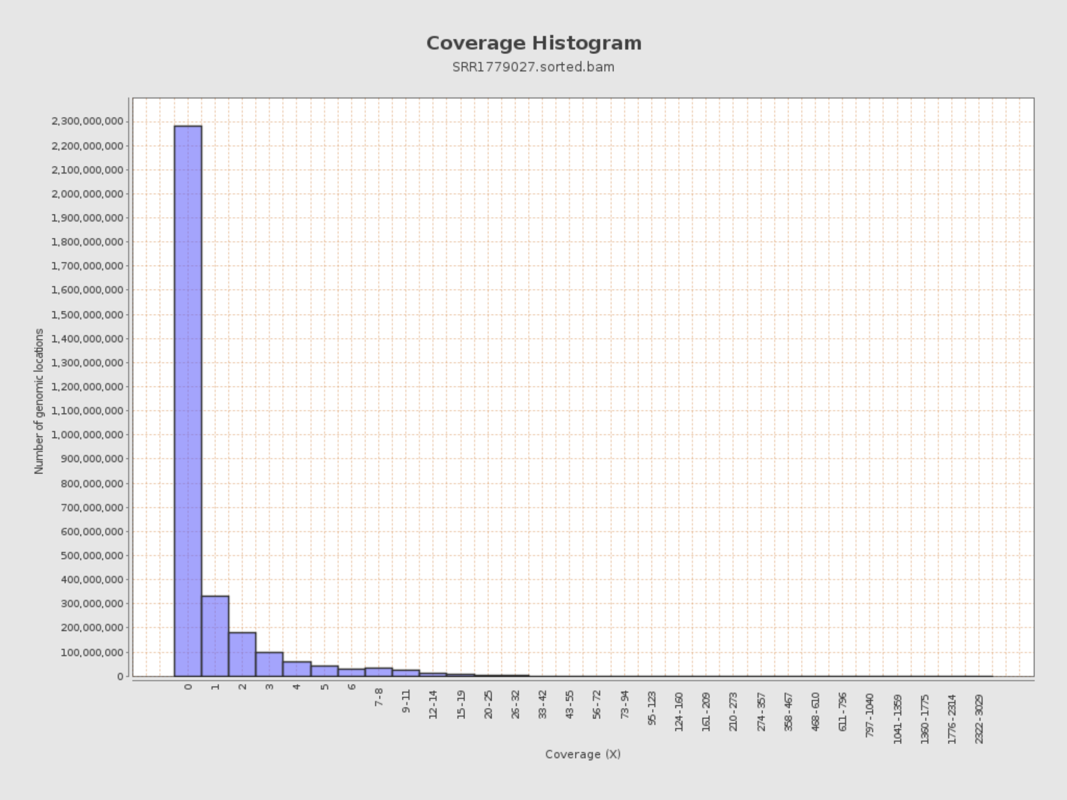
		bases	coverage	deviation
chr1	249250621	82666273	0.3317	3.4184
chr2	243199373	175330211	0.7209	2.1069
chr3	198022430	179909670	0.9085	2.1618
chr4	191154276	257146300	1.3452	2.7047
chr5	180915260	197900007	1.0939	2.4241
chr6	171115067	115029818	0.6722	1.9152
chr7	159138663	224775646	1.4125	5.0312
chr8	146364022	203618804	1.3912	2.7931
chr9	141213431	74366530	0.5266	1.9638
chr10	135534747	32207545	0.2376	3.7093
chr11	135006516	101683345	0.7532	1.9663
chr12	133851895	105119941	0.7853	2.0732
chr13	115169878	103734663	0.9007	2.2268
chr14	107349540	91961638	0.8567	2.1651
chr15	102531392	37175159	0.3626	1.2732
chr16	90354753	37995332	0.4205	1.3884
chr17	81195210	35663188	0.4392	1.6918
chr18	78077248	116531193	1.4925	3.0407
chr19	59128983	18717202	0.3165	2.0367
chr20	63025520	43364213	0.688	1.7851
chr21	48129895	13525718	0.281	1.0872
chr22	51304566	7488457	0.146	0.7908
chrMT	16571	2132	0.1287	0.6322
chrX	155270560	178397695	1.1489	2.9123

chrY	59373566	1541407	0.026	0.4732

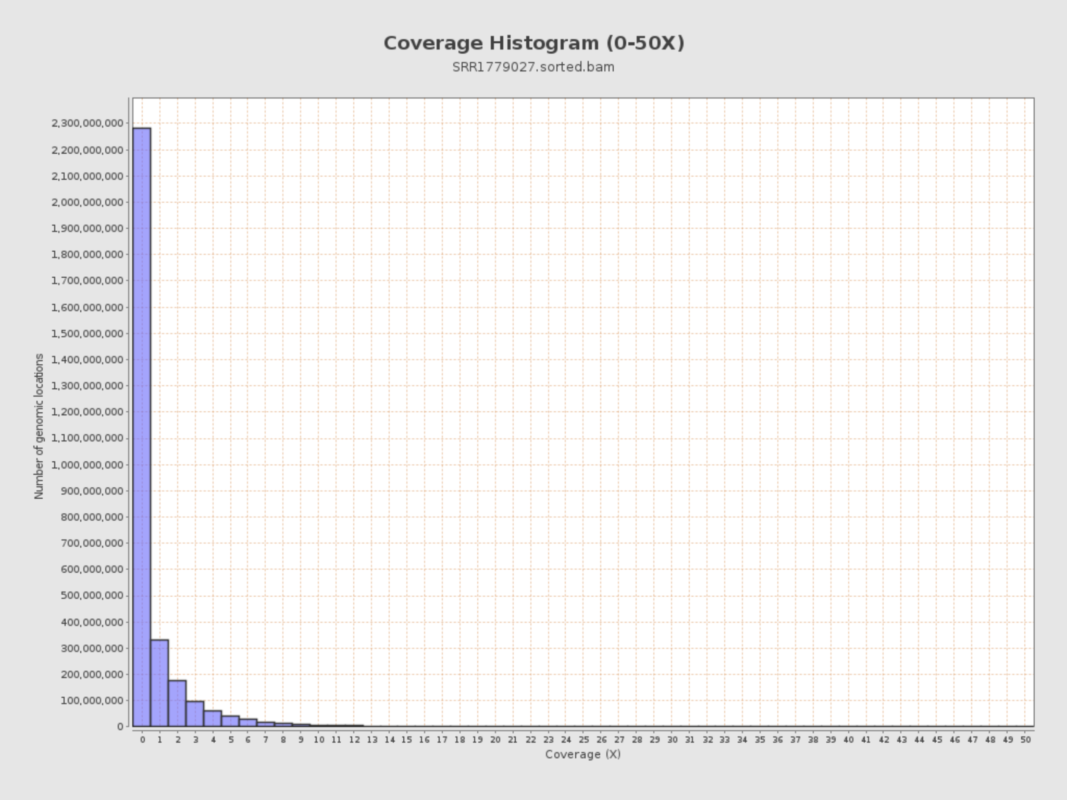
3. Results : Coverage across reference



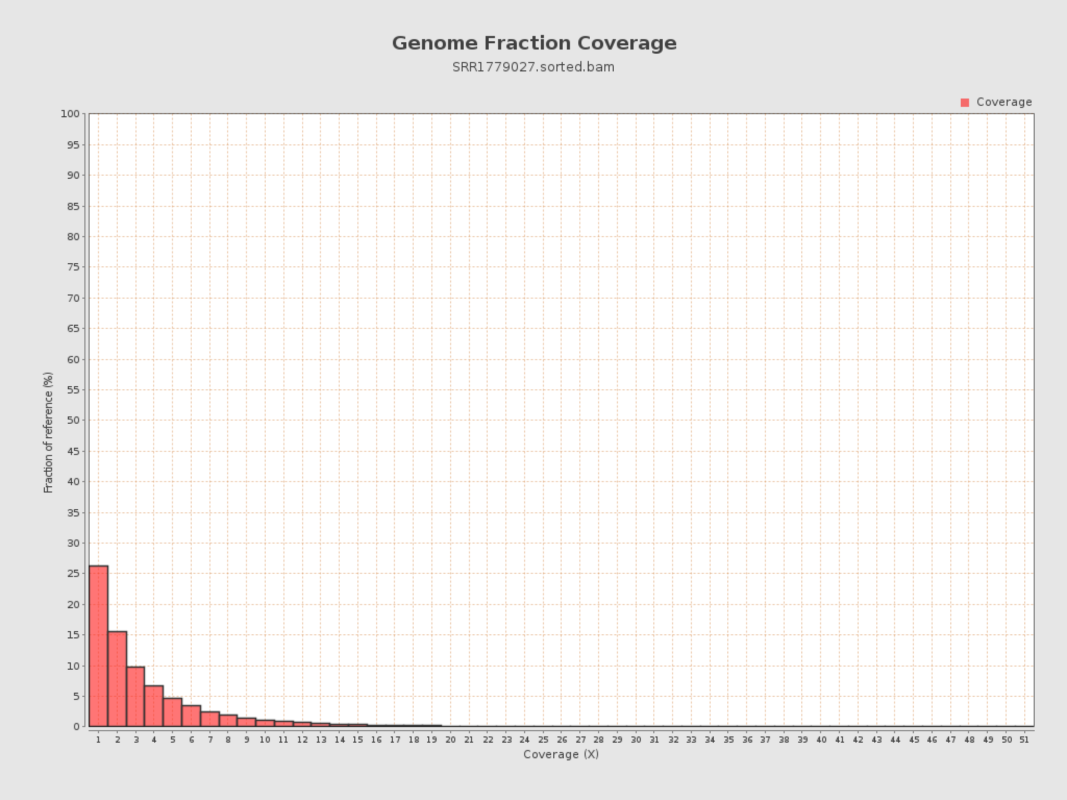
4. Results : Coverage Histogram



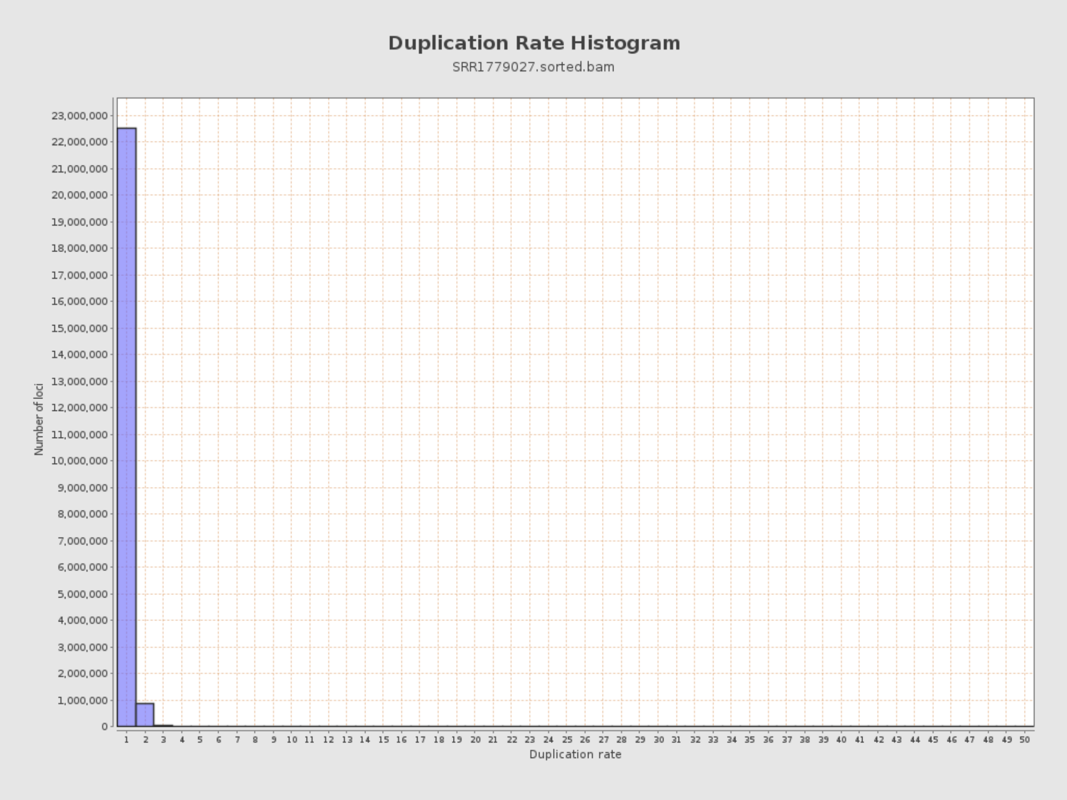
5. Results : Coverage Histogram (0-50X)



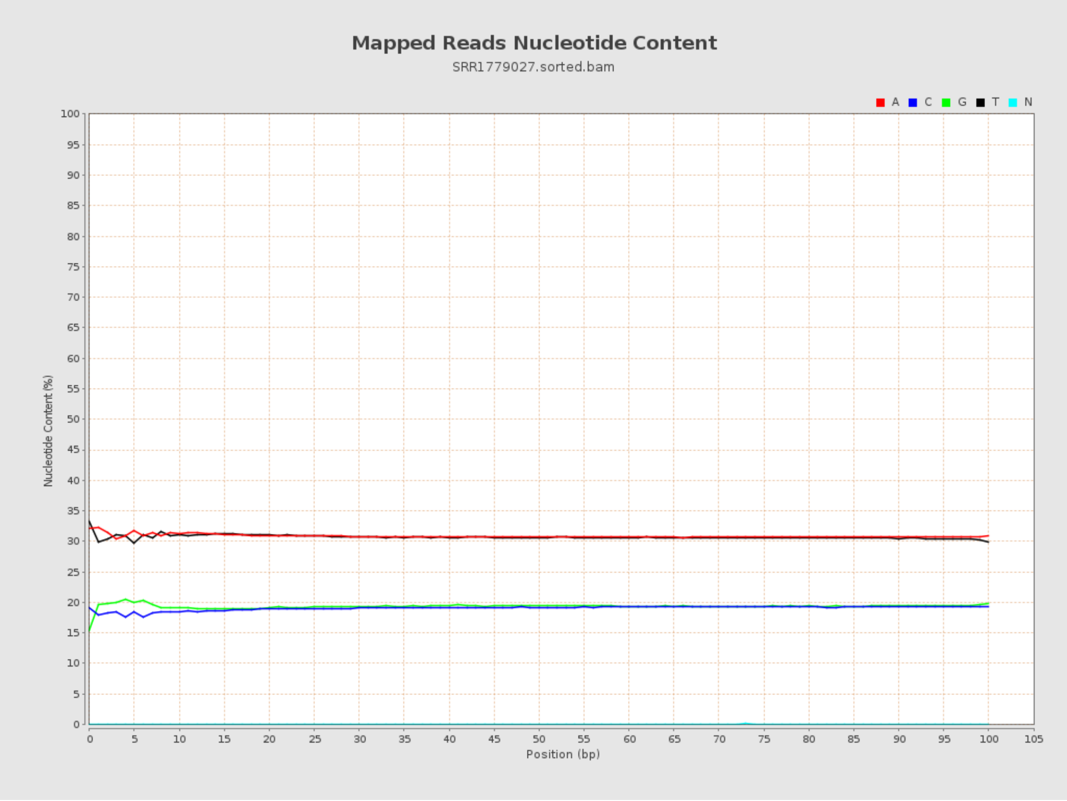
6. Results : Genome Fraction Coverage



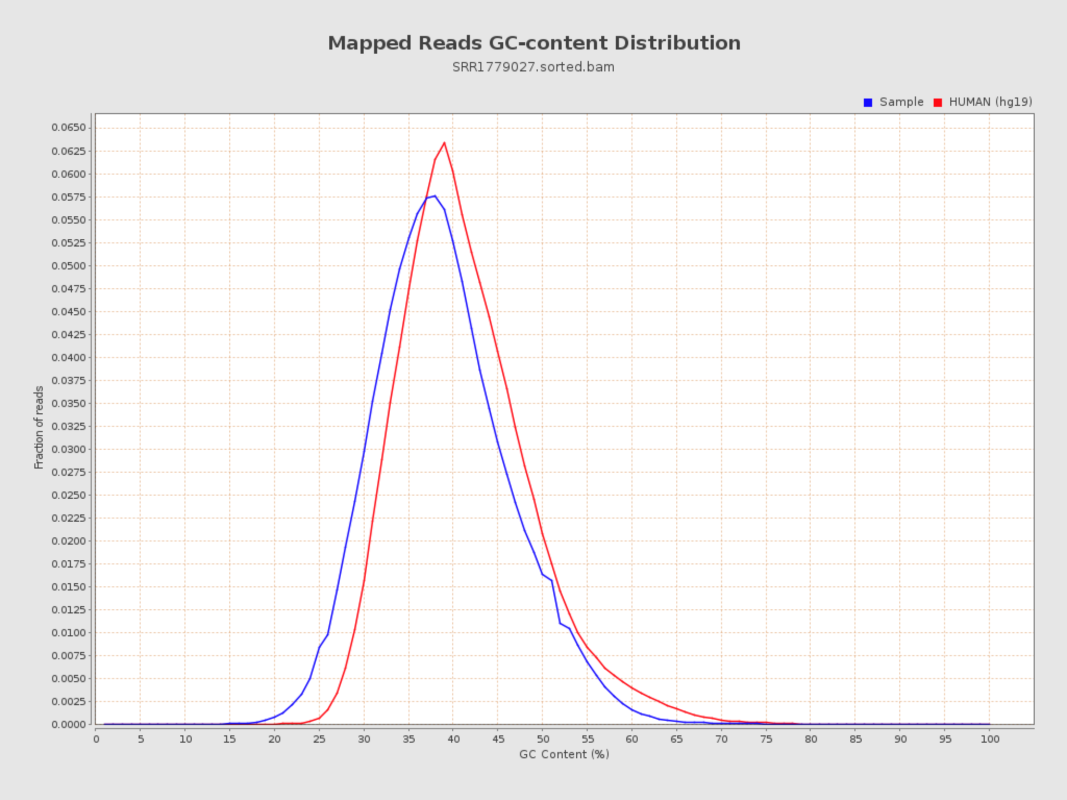
7. Results : Duplication Rate Histogram



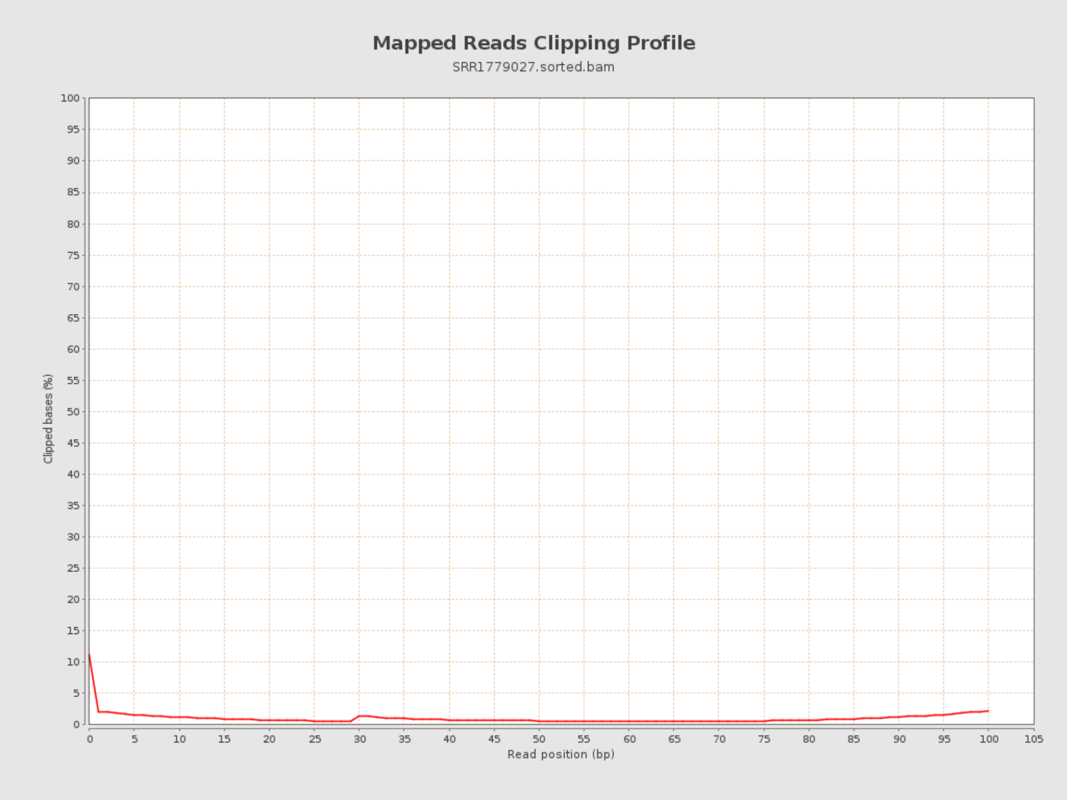
8. Results : Mapped Reads Nucleotide Content



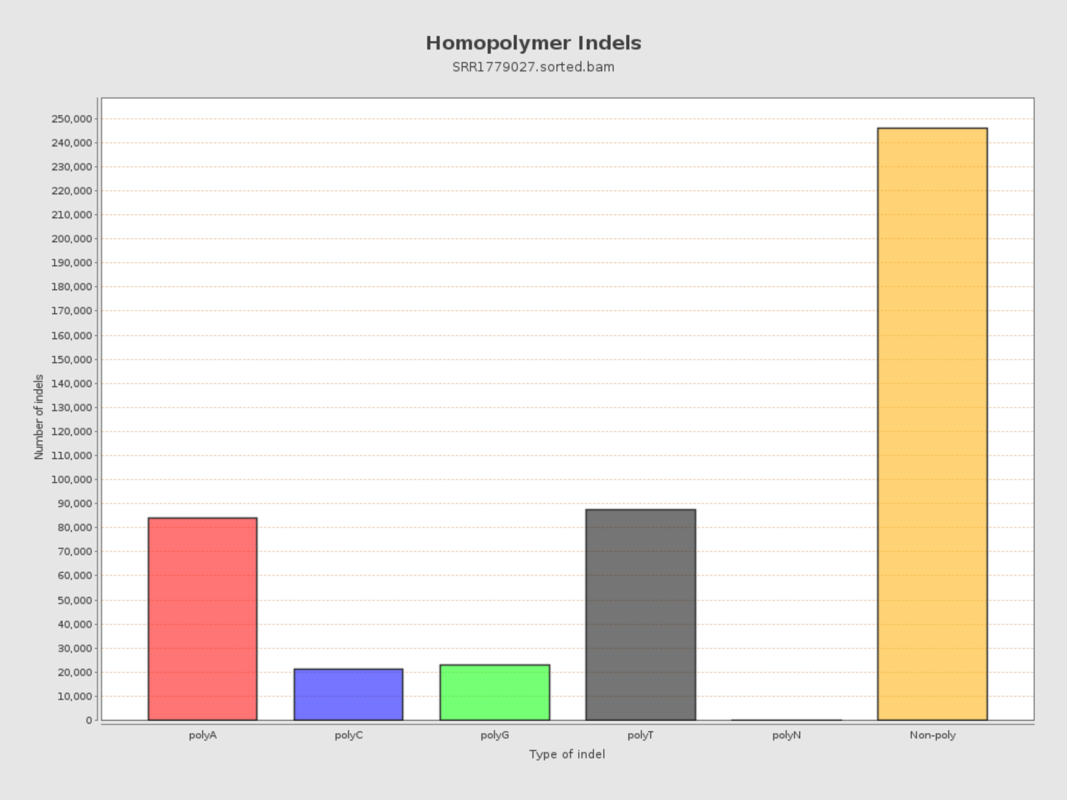
9. Results : Mapped Reads GC-content Distribution



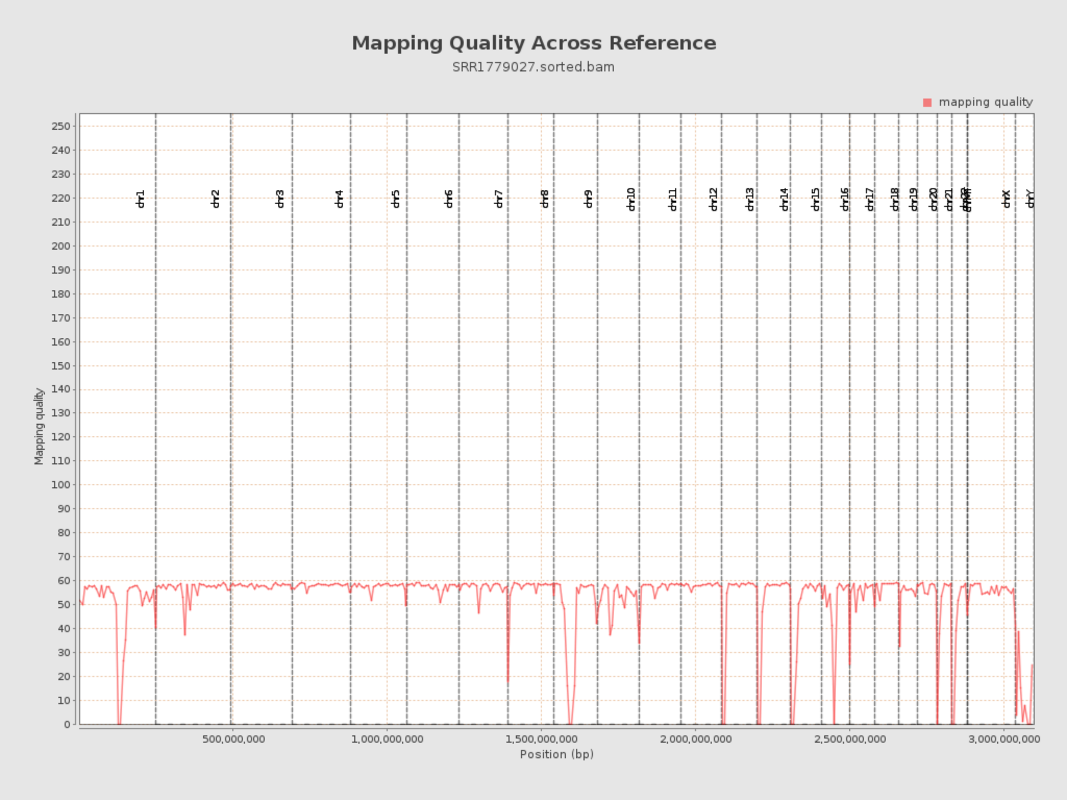
10. Results : Mapped Reads Clipping Profile



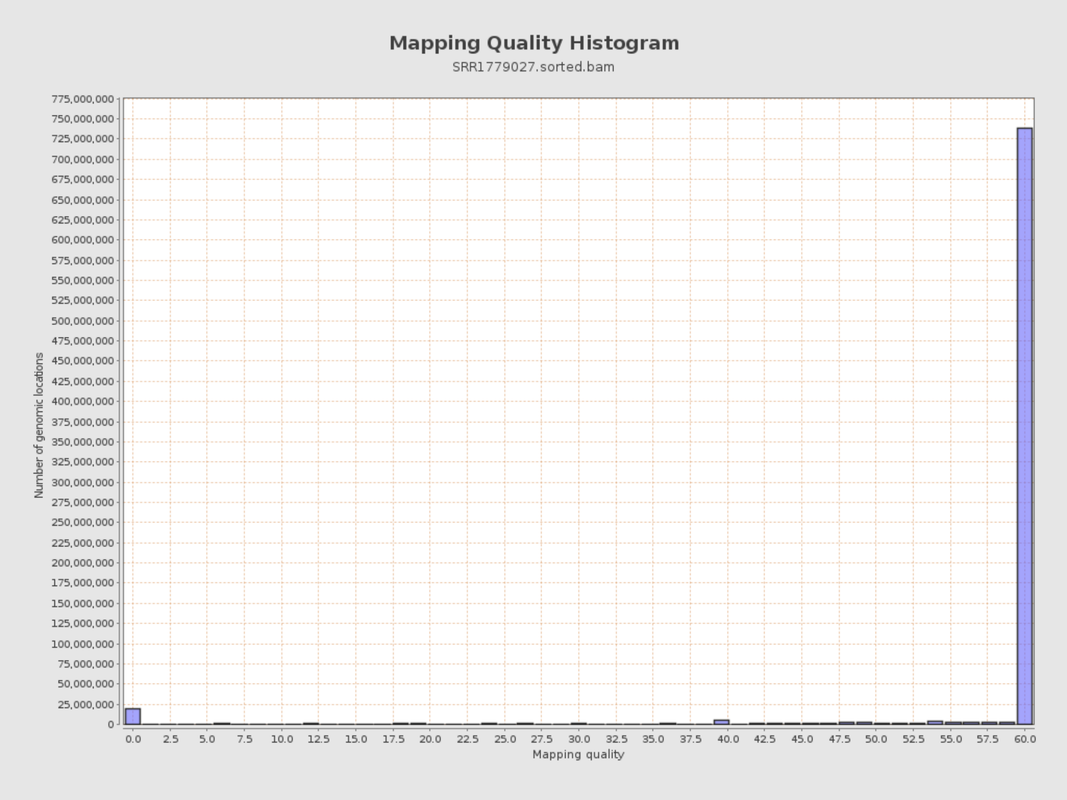
11. Results : Homopolymer Indels



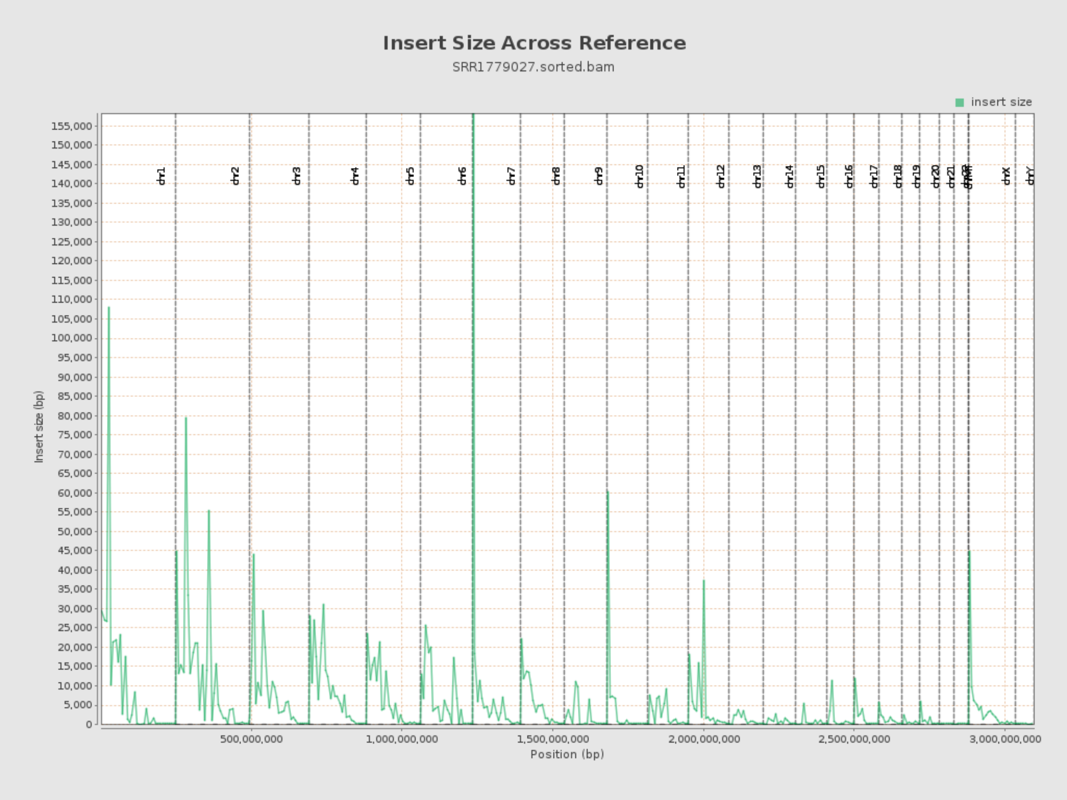
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram