Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 13:50:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173961.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_SRR10173961 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173961_1.fastq.gz SRR10173961_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 13:50:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173961.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,909,564
Mapped reads	10,640,328 / 97.53%
Unmapped reads	269,236 / 2.47%
Mapped paired reads	10,640,328 / 97.53%
Mapped reads, first in pair	5,331,055 / 48.87%
Mapped reads, second in pair	5,309,273 / 48.67%
Mapped reads, both in pair	10,460,672 / 95.89%
Mapped reads, singletons	179,656 / 1.65%
Secondary alignments	0
Supplementary alignments	1,361,027 / 12.48%
Read min/max/mean length	30 / 133 / 125.7
Duplicated reads (estimated)	8,696,338 / 79.71%
Duplication rate	66.65%
Clipped reads	5,449,061 / 49.95%

2.2. ACGT Content

Number/percentage of A's	358,848,455 / 29.75%
Number/percentage of C's	240,710,487 / 19.96%
Number/percentage of T's	356,016,578 / 29.52%
Number/percentage of G's	250,603,057 / 20.78%
Number/percentage of N's	8,789 / 0%

GC Percentage	40.73%

2.3. Coverage

Mean	0.3899
Standard Deviation	6.5741

2.4. Mapping Quality

Mean Mapping Quality	52.61

2.5. Insert size

Mean	988,722.78
Standard Deviation	9,394,795.94
P25/Median/P75	108 / 159 / 247

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	10,440,865
Insertions	133,644
Mapped reads with at least one insertion	1.21%
Deletions	353,732
Mapped reads with at least one deletion	3.24%
Homopolymer indels	41.26%

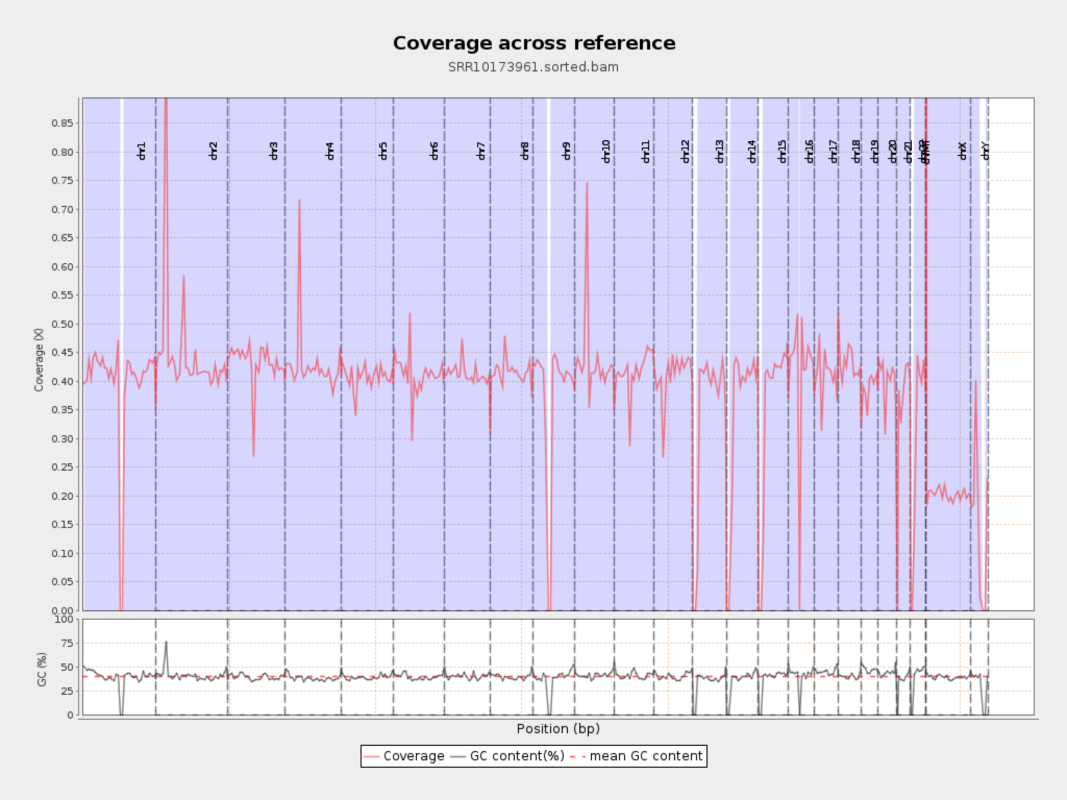
2.7. Chromosome stats

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

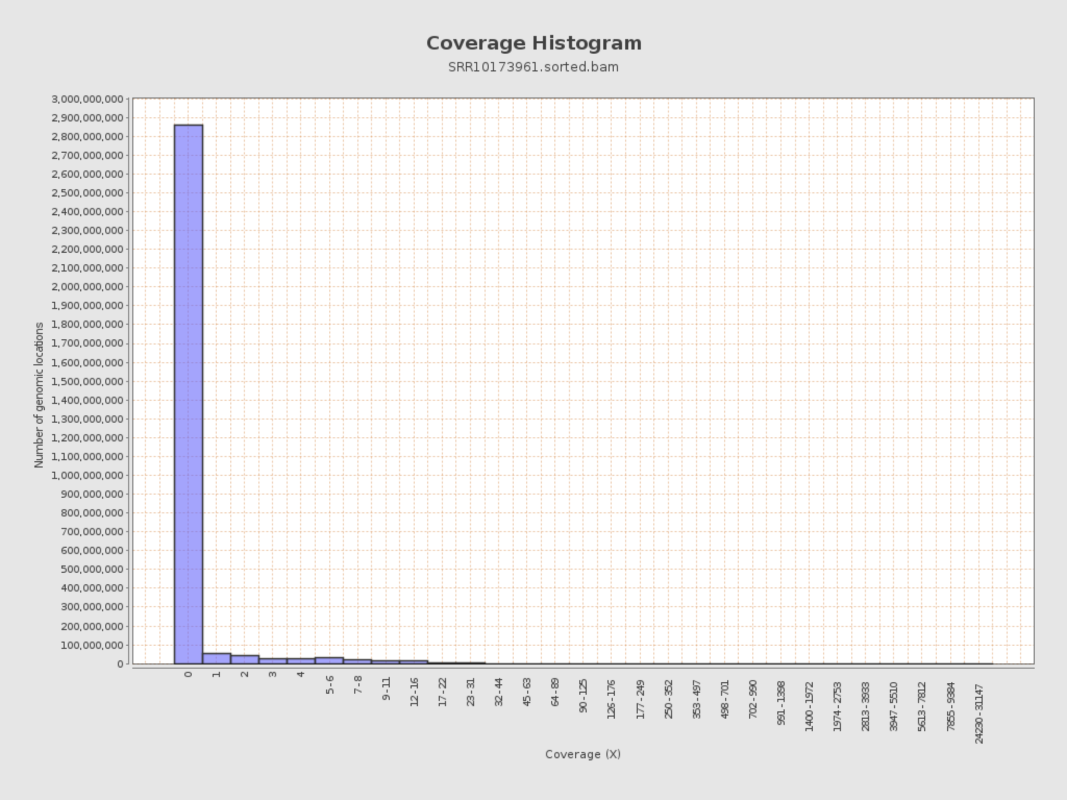
		bases	coverage	deviation
chr1	249250621	98228994	0.3941	3.0381
chr2	243199373	109331779	0.4496	21.6878
chr3	198022430	85744767	0.433	2.0388
chr4	191154276	82077033	0.4294	3.0533
chr5	180915260	73776174	0.4078	1.9648
chr6	171115067	70480973	0.4119	2.3814
chr7	159138663	65780230	0.4134	3.0151
chr8	146364022	60865254	0.4158	3.5508
chr9	141213431	52212996	0.3697	2.9424
chr10	135534747	59071468	0.4358	3.7588
chr11	135006516	56096595	0.4155	2.1229
chr12	133851895	55075284	0.4115	2.1272
chr13	115169878	39302053	0.3413	1.8119
chr14	107349540	37403950	0.3484	1.8901
chr15	102531392	35084284	0.3422	1.9015
chr16	90354753	37201936	0.4117	2.5975
chr17	81195210	33498788	0.4126	2.1524
chr18	78077248	33632969	0.4308	3.6912
chr19	59128983	22854273	0.3865	2.4824
chr20	63025520	25467983	0.4041	2.1792
chr21	48129895	17179822	0.3569	2.7346
chr22	51304566	14955731	0.2915	2.0357
chrMT	16571	1184941	71.5069	51.2915
chrX	155270560	31461018	0.2026	1.4114

chrY	59373566	9062368	0.1526	2.3105

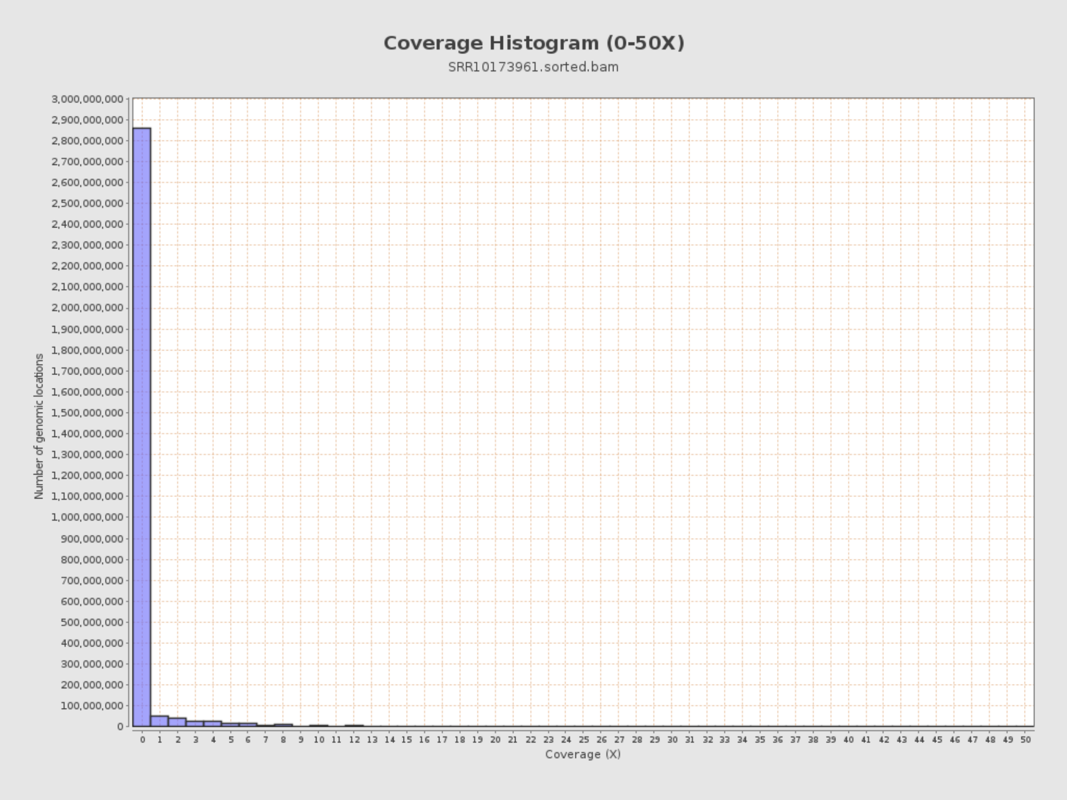
3. Results : Coverage across reference



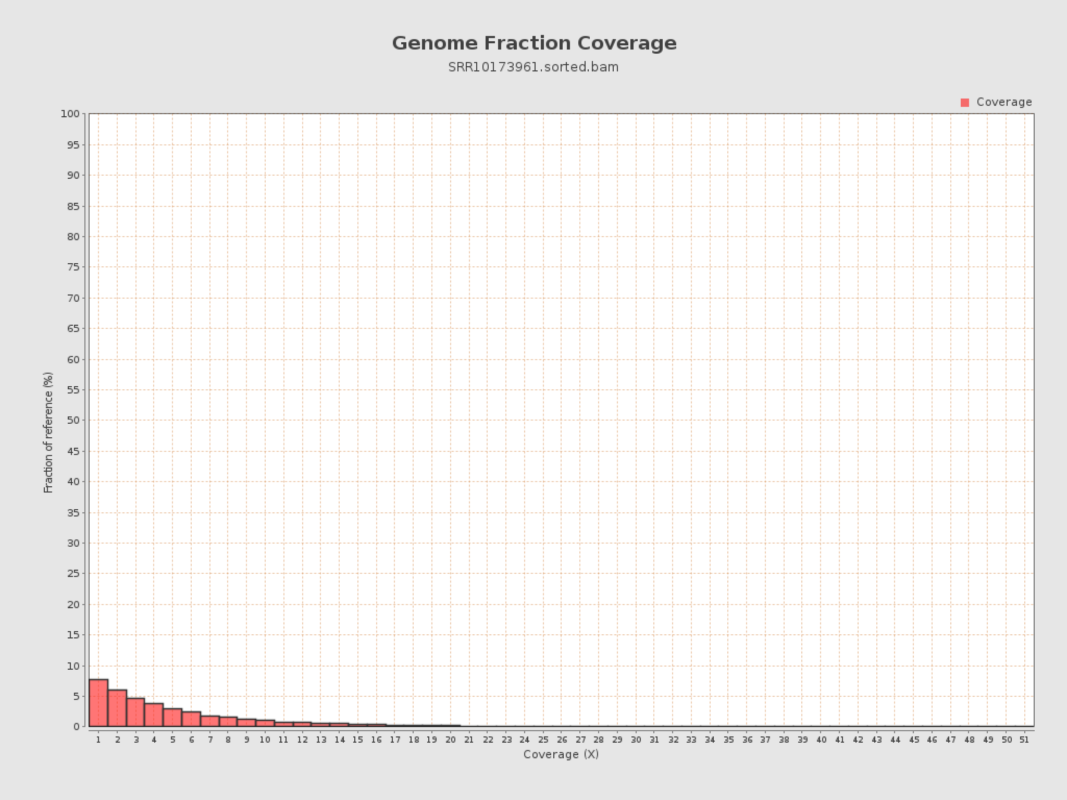
4. Results : Coverage Histogram



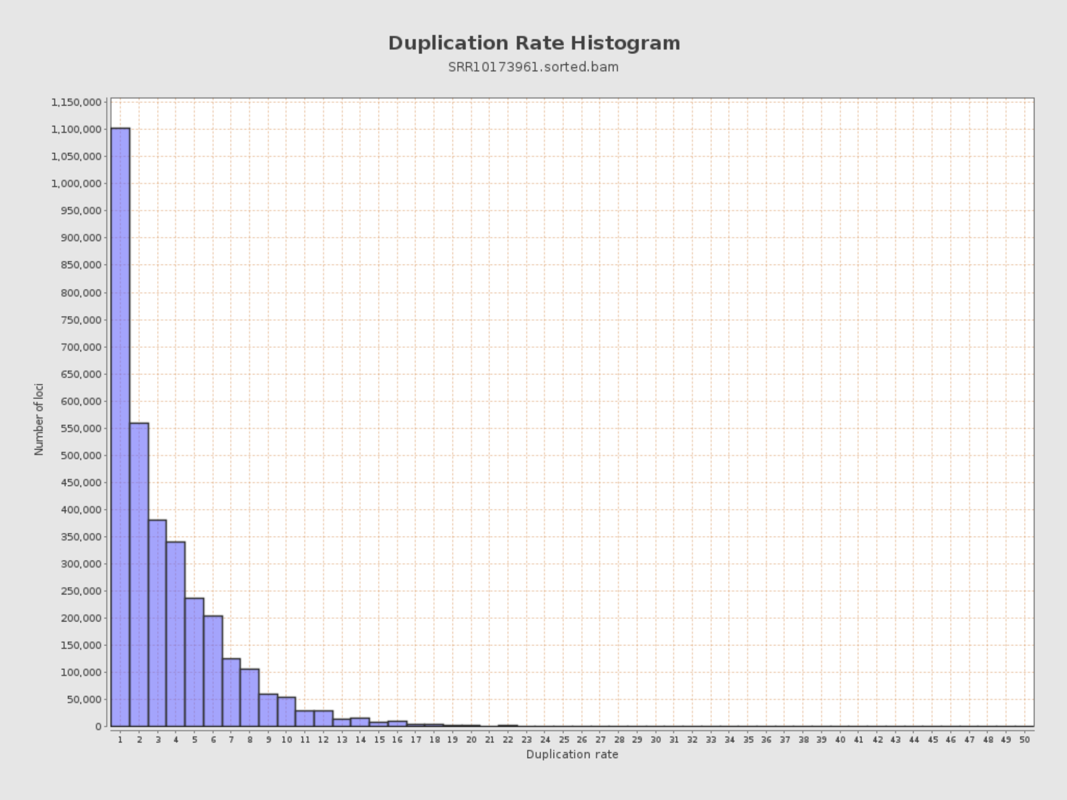
5. Results : Coverage Histogram (0-50X)



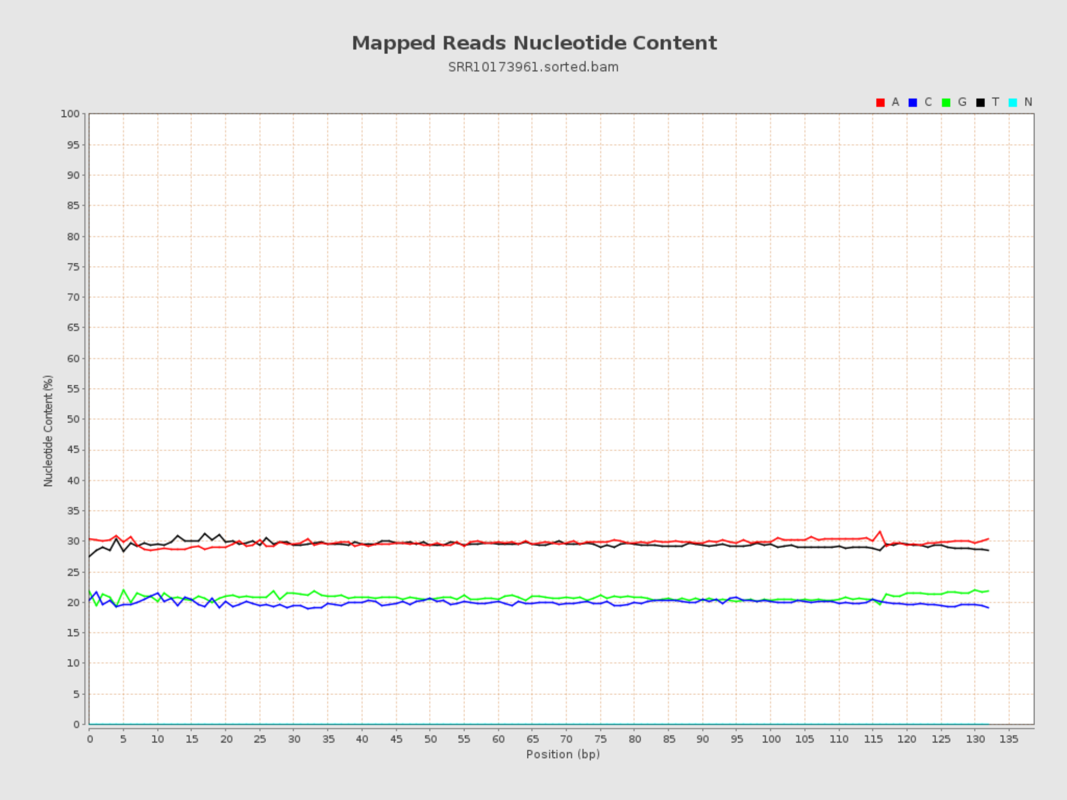
6. Results : Genome Fraction Coverage



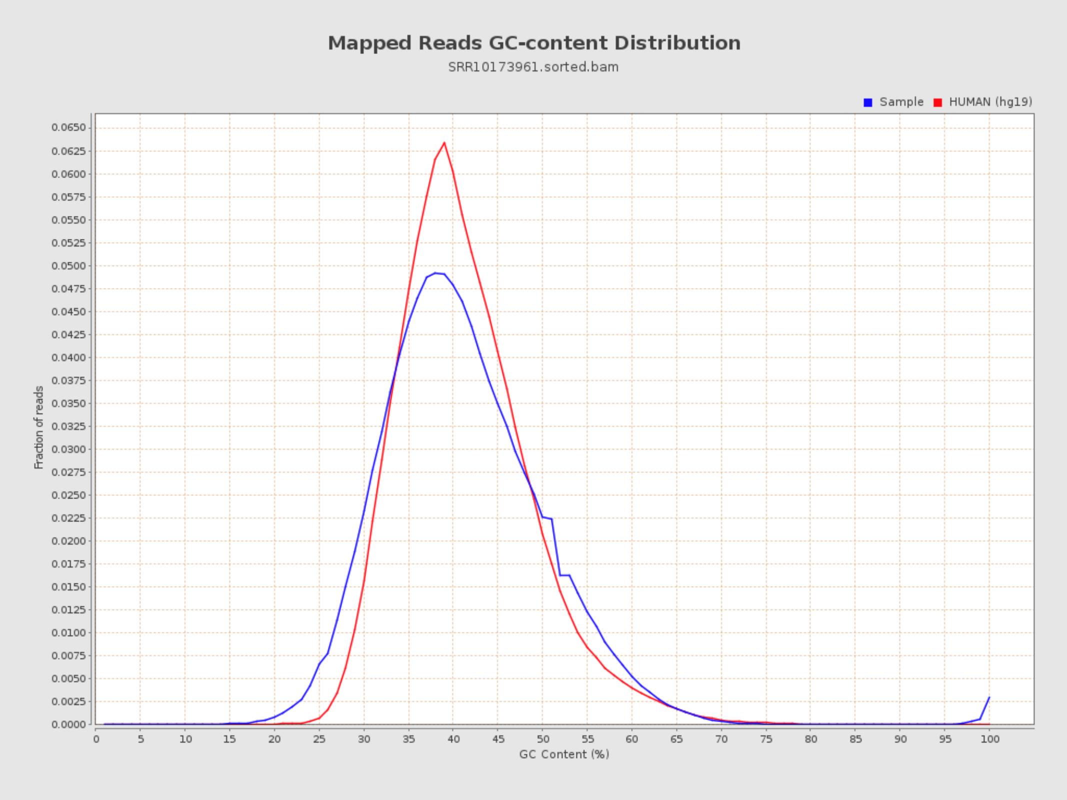
7. Results : Duplication Rate Histogram



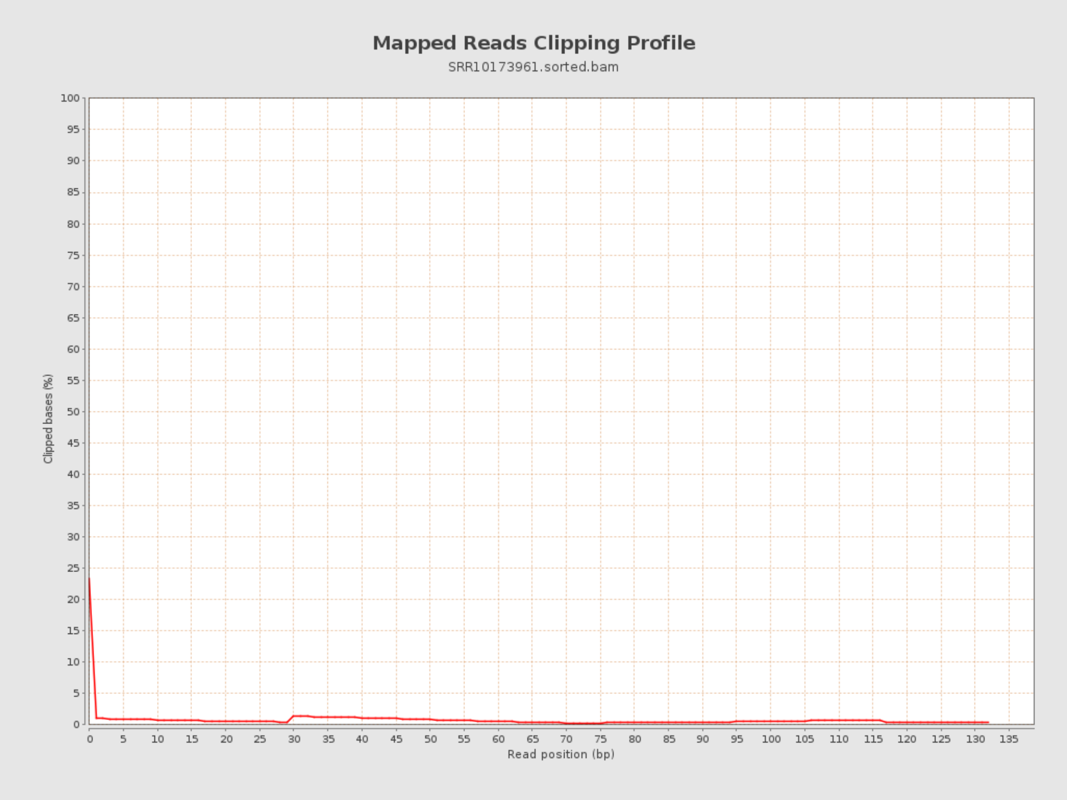
8. Results : Mapped Reads Nucleotide Content



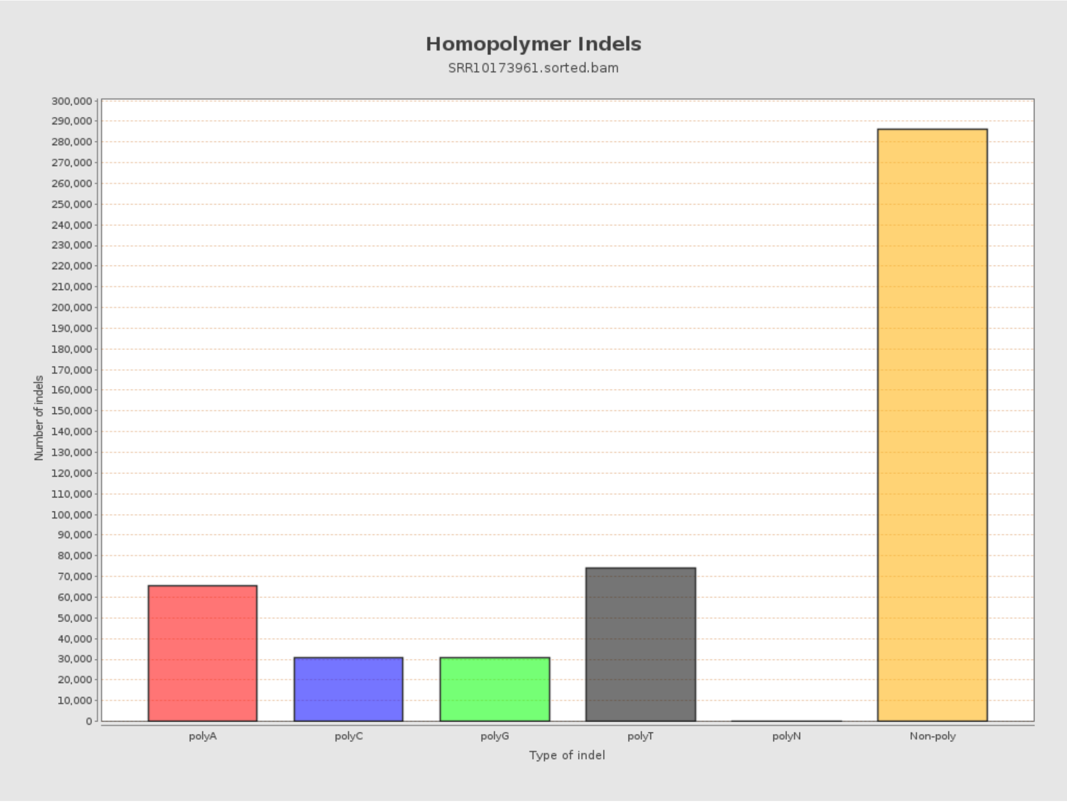
9. Results : Mapped Reads GC-content Distribution



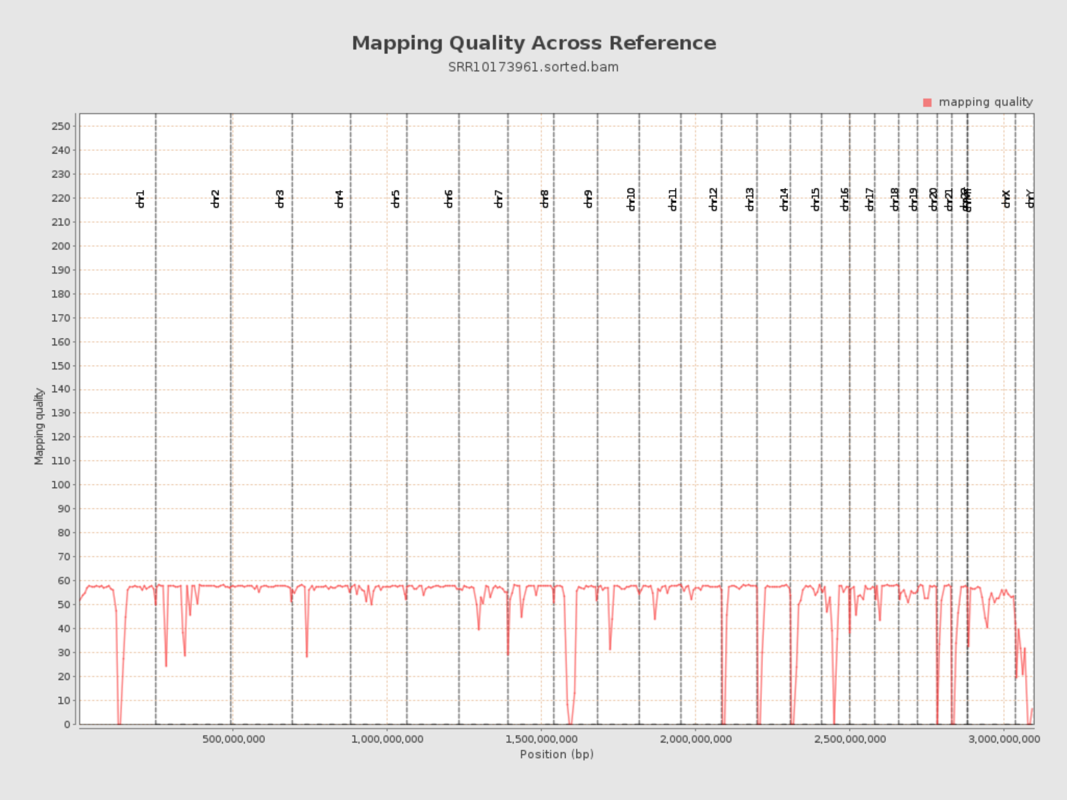
10. Results : Mapped Reads Clipping Profile



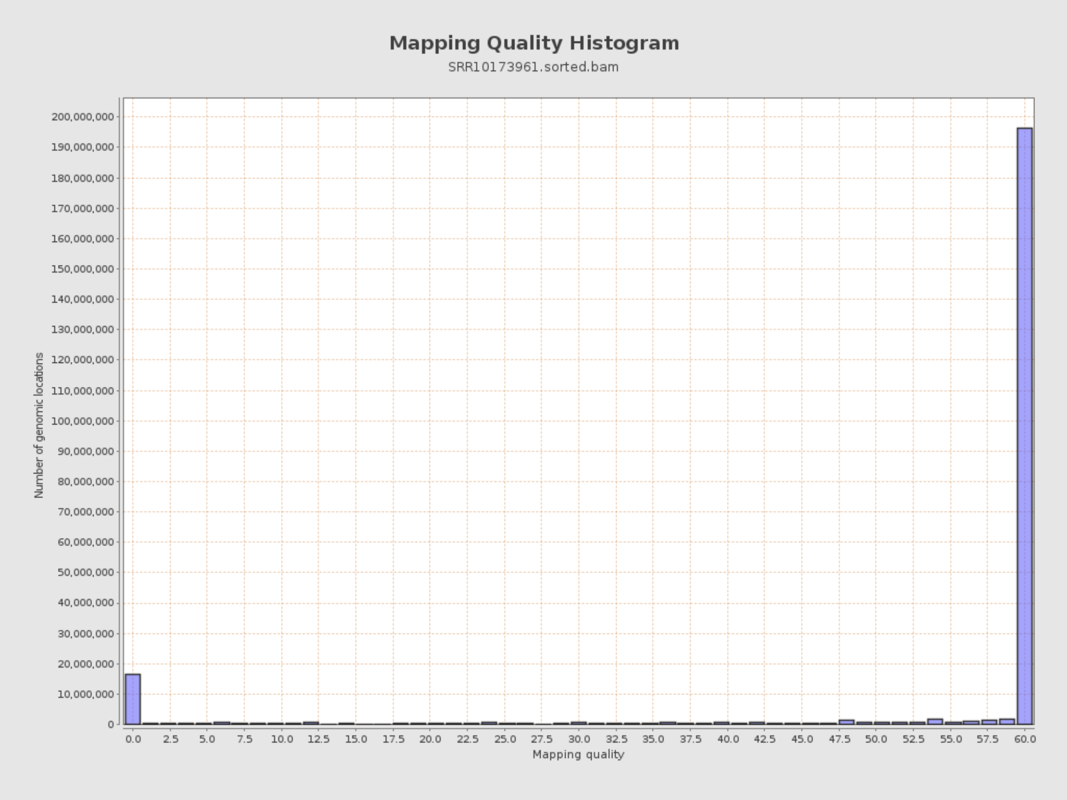
11. Results : Homopolymer Indels



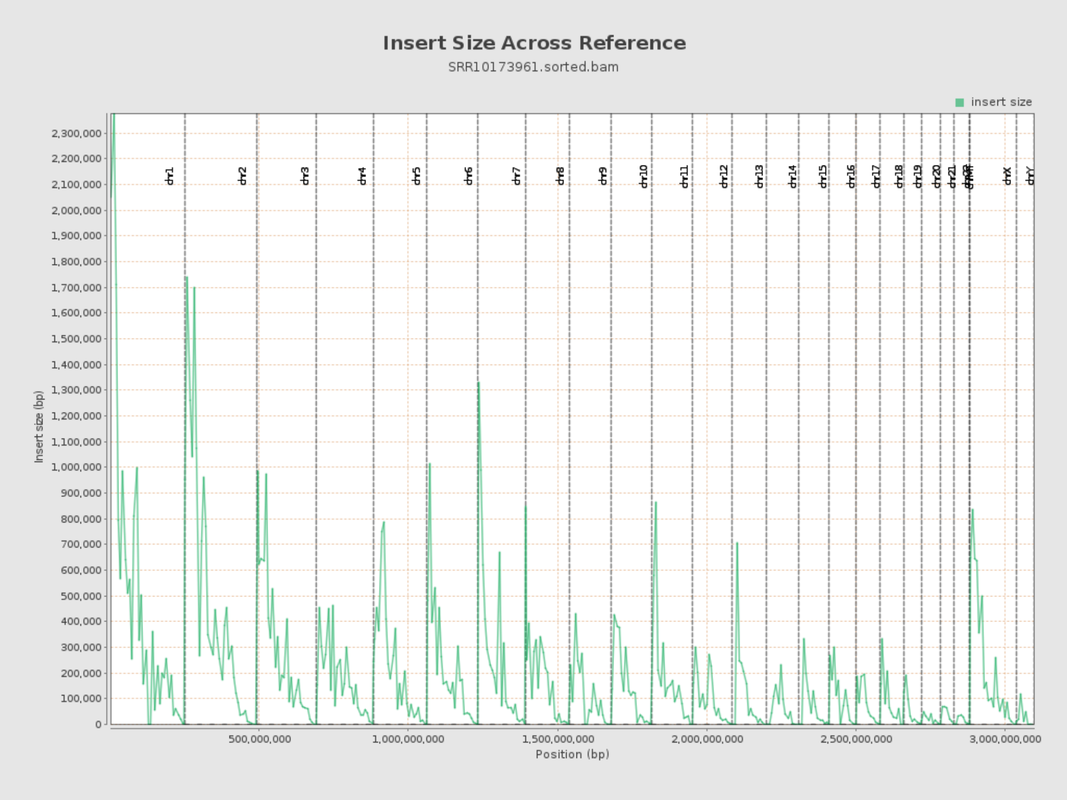
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram