Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 17:01:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006058.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_SRR1006058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006058_1.fastq.gz SRR1006058_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 17:01:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,314,664
Mapped reads	4,557,294 / 85.75%
Unmapped reads	757,370 / 14.25%
Mapped paired reads	4,557,294 / 85.75%
Mapped reads, first in pair	2,327,320 / 43.79%
Mapped reads, second in pair	2,229,974 / 41.96%
Mapped reads, both in pair	4,155,692 / 78.19%
Mapped reads, singletons	401,602 / 7.56%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	260,752 / 4.91%
Duplication rate	5.21%
Clipped reads	399,757 / 7.52%

2.2. ACGT Content

Number/percentage of A's	45,265,212 / 25.75%
Number/percentage of C's	40,611,305 / 23.1%
Number/percentage of T's	47,012,955 / 26.74%
Number/percentage of G's	42,899,134 / 24.4%
Number/percentage of N's	8,359 / 0%
GC Percentage	47.5%

2.3. Coverage

Mean	0.0568
Standard Deviation	0.3813

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Insert size

Mean	79,187.19
Standard Deviation	2,808,528.72
P25/Median/P75	69 / 91 / 118

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	841,434
Insertions	5,867
Mapped reads with at least one insertion	0.13%
Deletions	14,894
Mapped reads with at least one deletion	0.33%
Homopolymer indels	43.87%

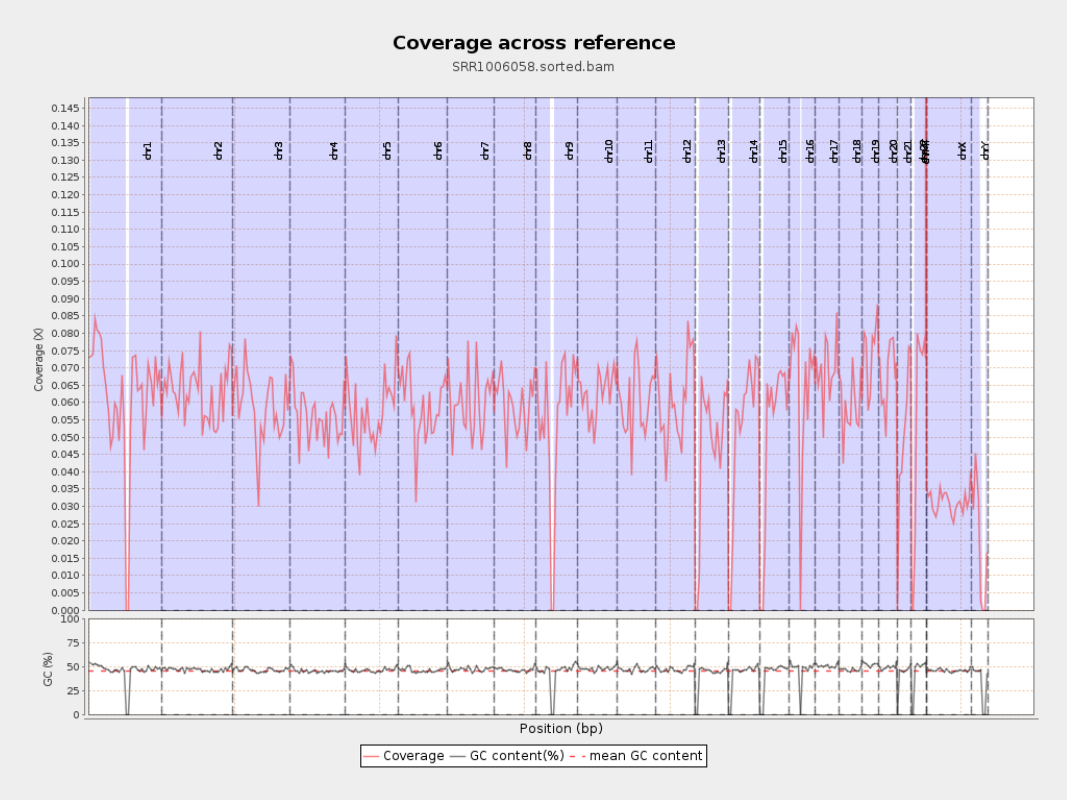
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

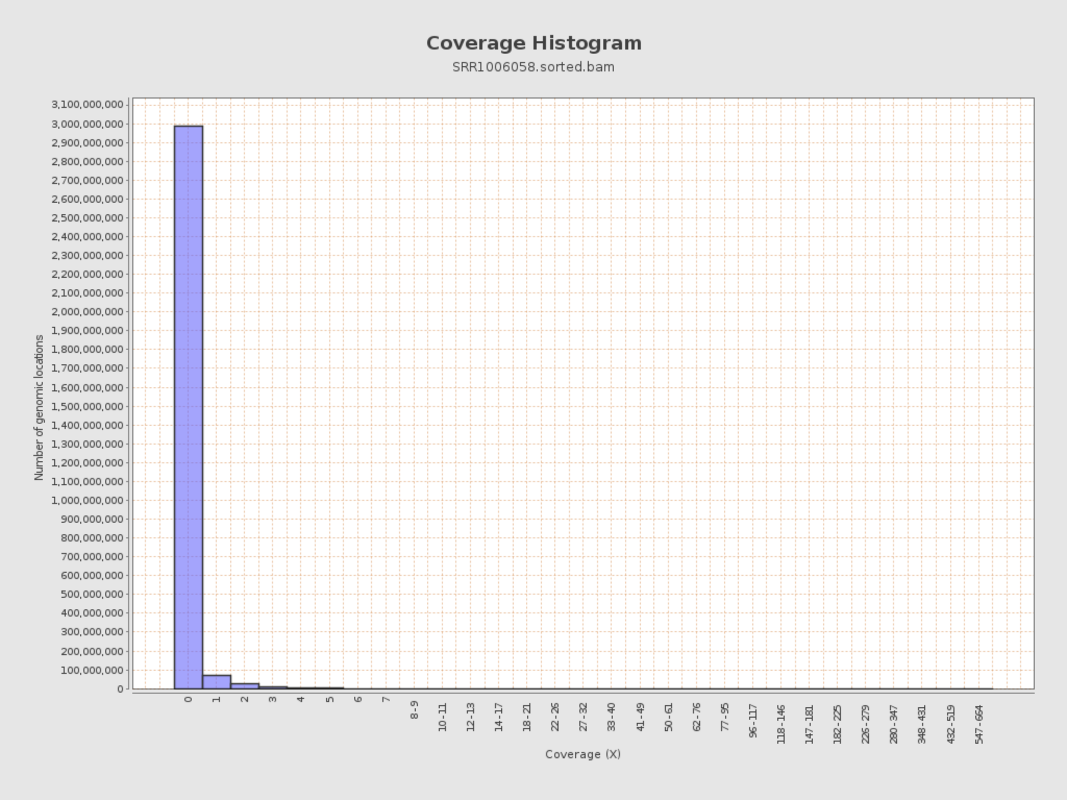
chr1	249250621	15167910	0.0609	0.3941
chr2	243199373	15360182	0.0632	0.4386
chr3	198022430	11614499	0.0587	0.3533
chr4	191154276	10670189	0.0558	0.3546
chr5	180915260	10401114	0.0575	0.352
chr6	171115067	10128597	0.0592	0.3848
chr7	159138663	9475496	0.0595	0.3991
chr8	146364022	8723601	0.0596	0.4053
chr9	141213431	7527766	0.0533	0.3475
chr10	135534747	8476293	0.0625	0.3859
chr11	135006516	8159758	0.0604	0.4992
chr12	133851895	8113003	0.0606	0.365
chr13	115169878	5328622	0.0463	0.3165
chr14	107349540	5555648	0.0518	0.3418
chr15	102531392	5277486	0.0515	0.3382
chr16	90354753	5840851	0.0646	0.4276
chr17	81195210	5665126	0.0698	0.4185
chr18	78077248	4605113	0.059	0.3814
chr19	59128983	4375285	0.074	0.4944
chr20	63025520	4252950	0.0675	0.4026
chr21	48129895	2405824	0.05	0.3588
chr22	51304566	2681845	0.0523	0.3858
chrMT	16571	10293	0.6211	1.2392
chrX	155270560	4848234	0.0312	0.2553

chrY	59373566	1150334	0.0194	0.2314

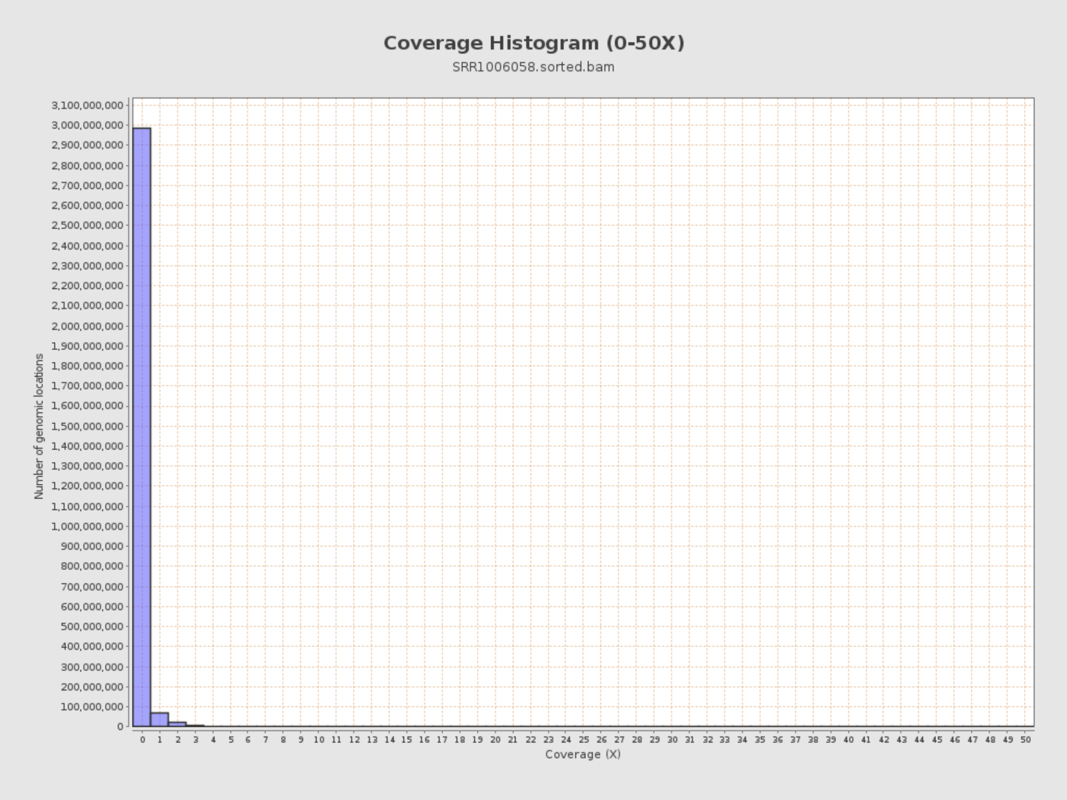
3. Results : Coverage across reference



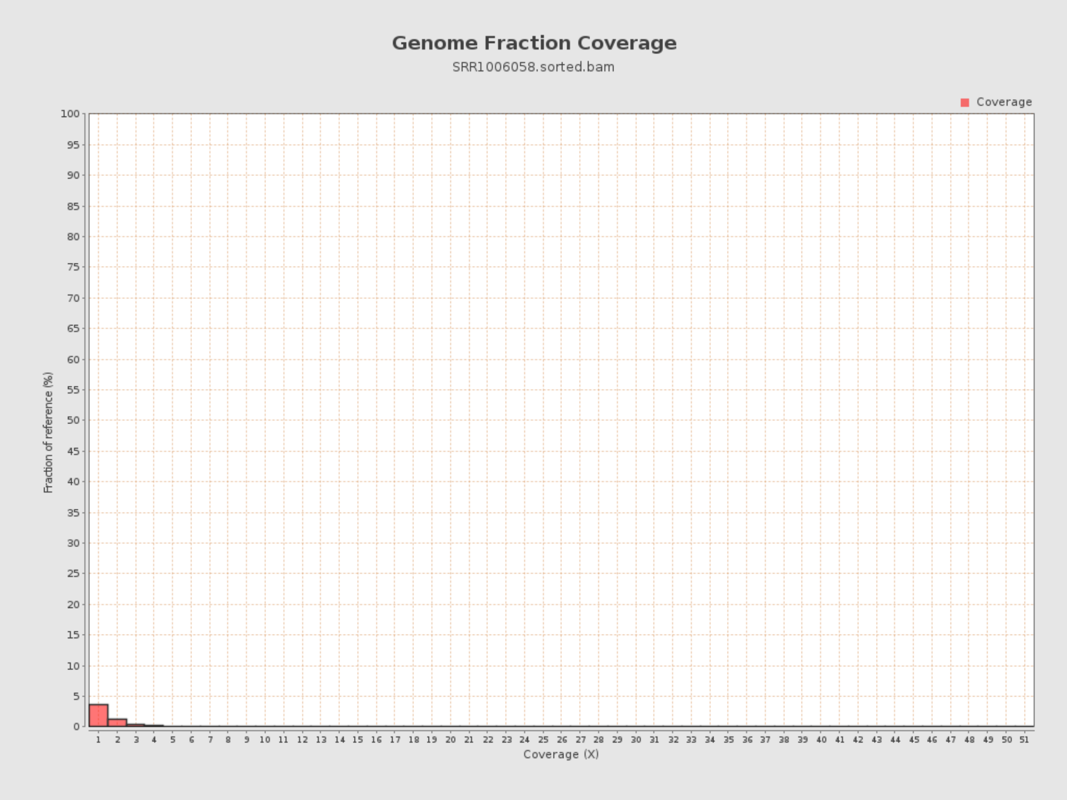
4. Results : Coverage Histogram



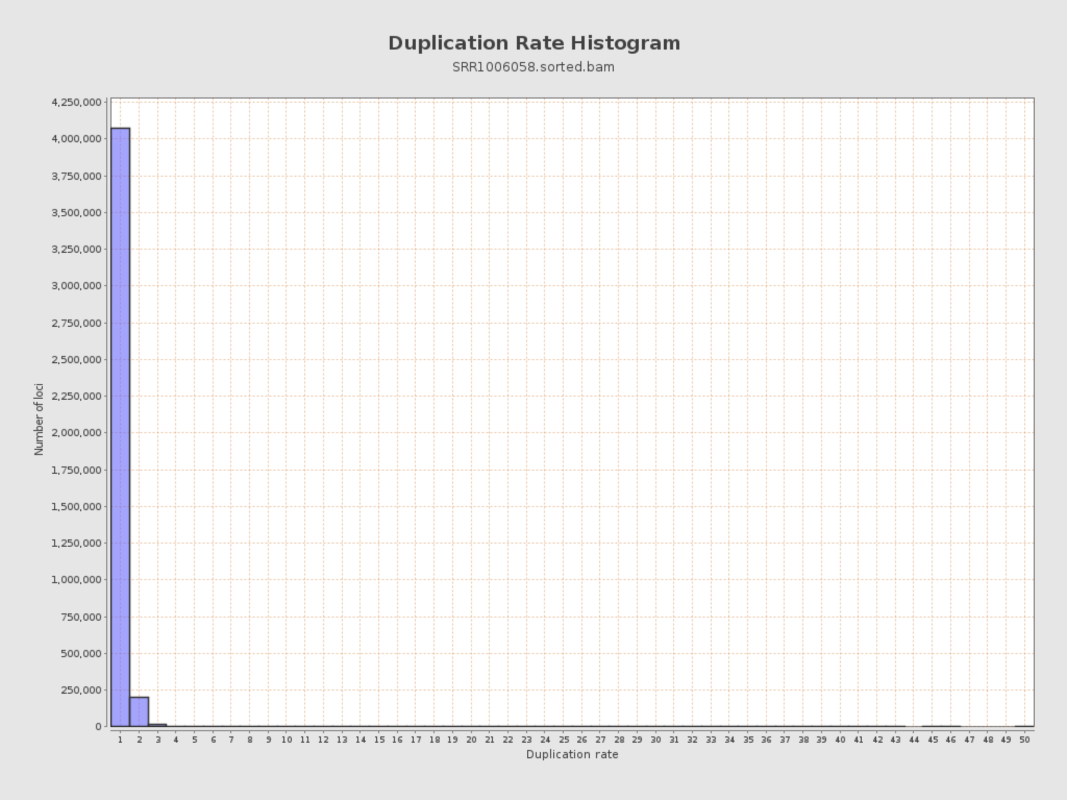
5. Results : Coverage Histogram (0-50X)



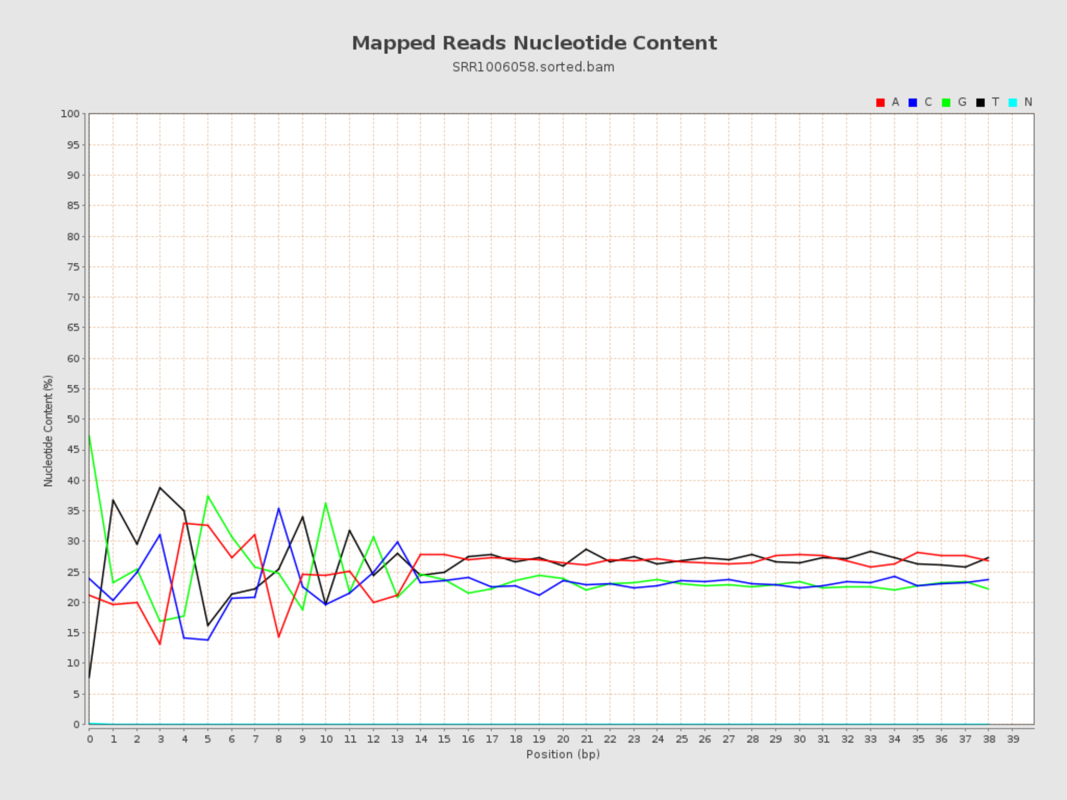
6. Results : Genome Fraction Coverage



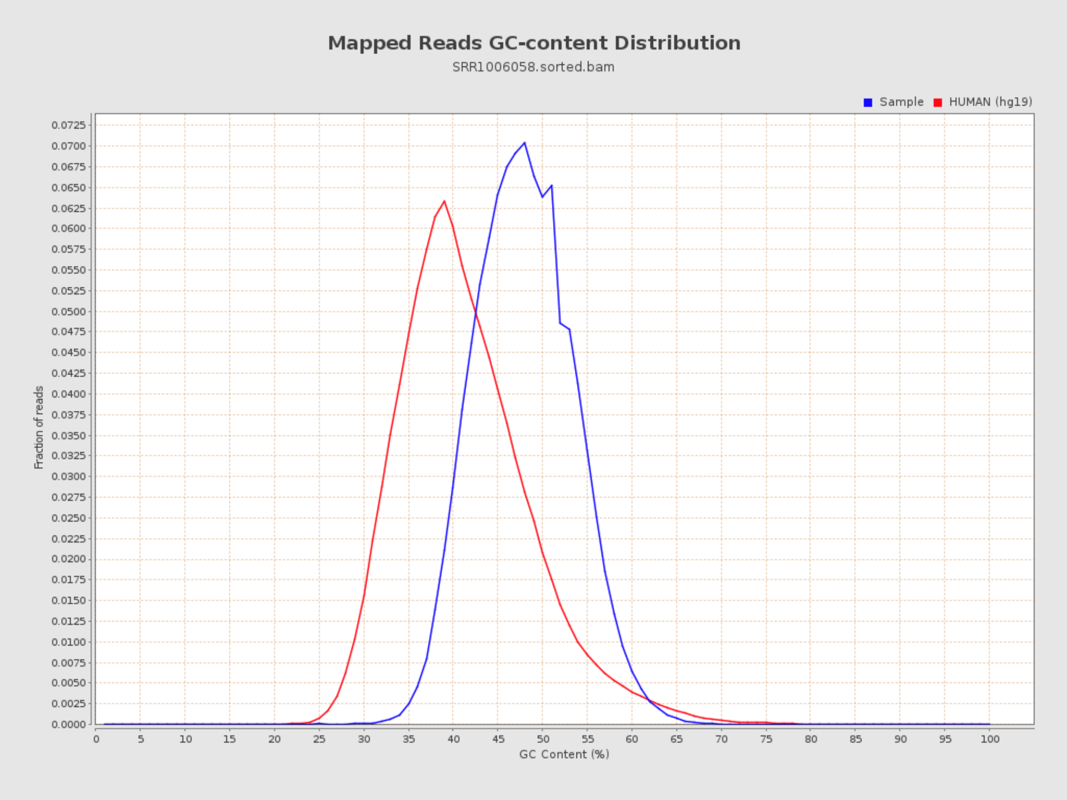
7. Results : Duplication Rate Histogram



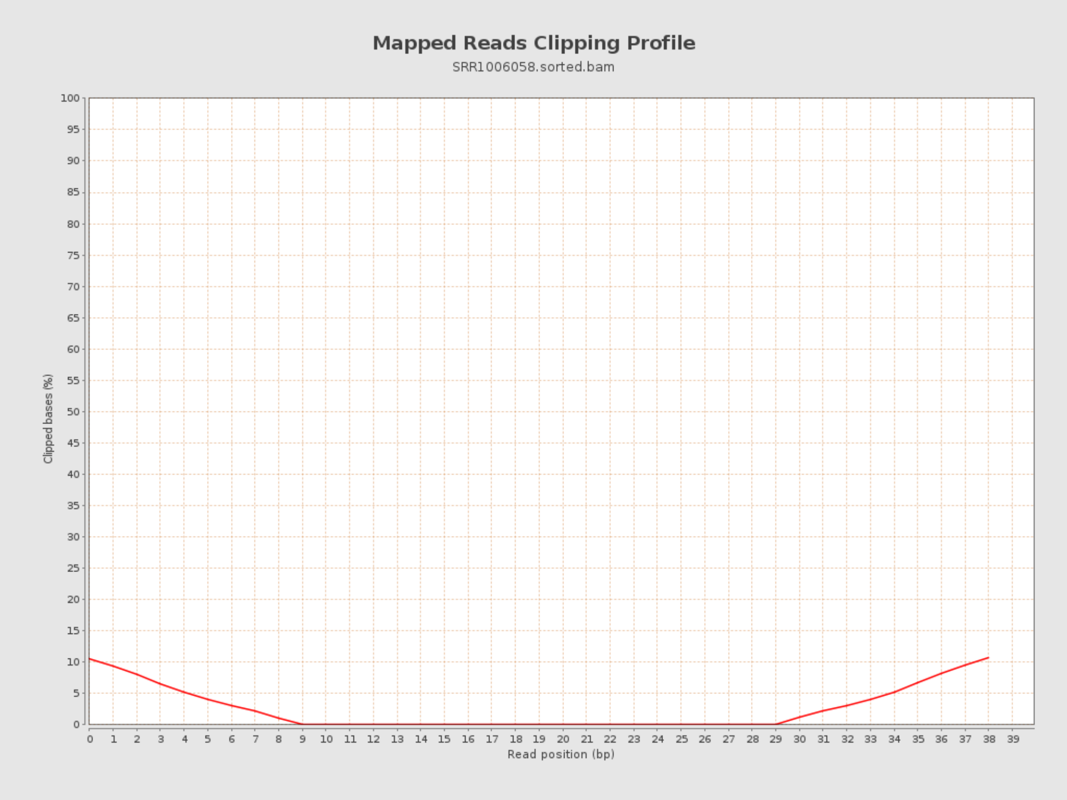
8. Results : Mapped Reads Nucleotide Content



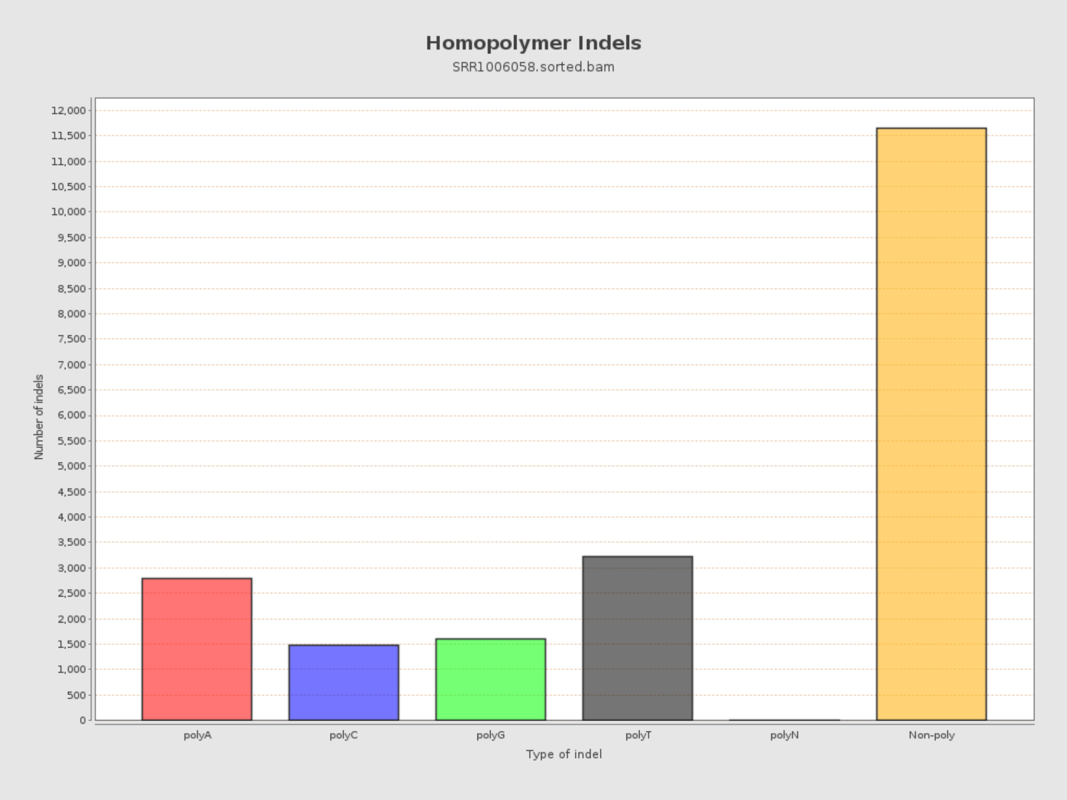
9. Results : Mapped Reads GC-content Distribution



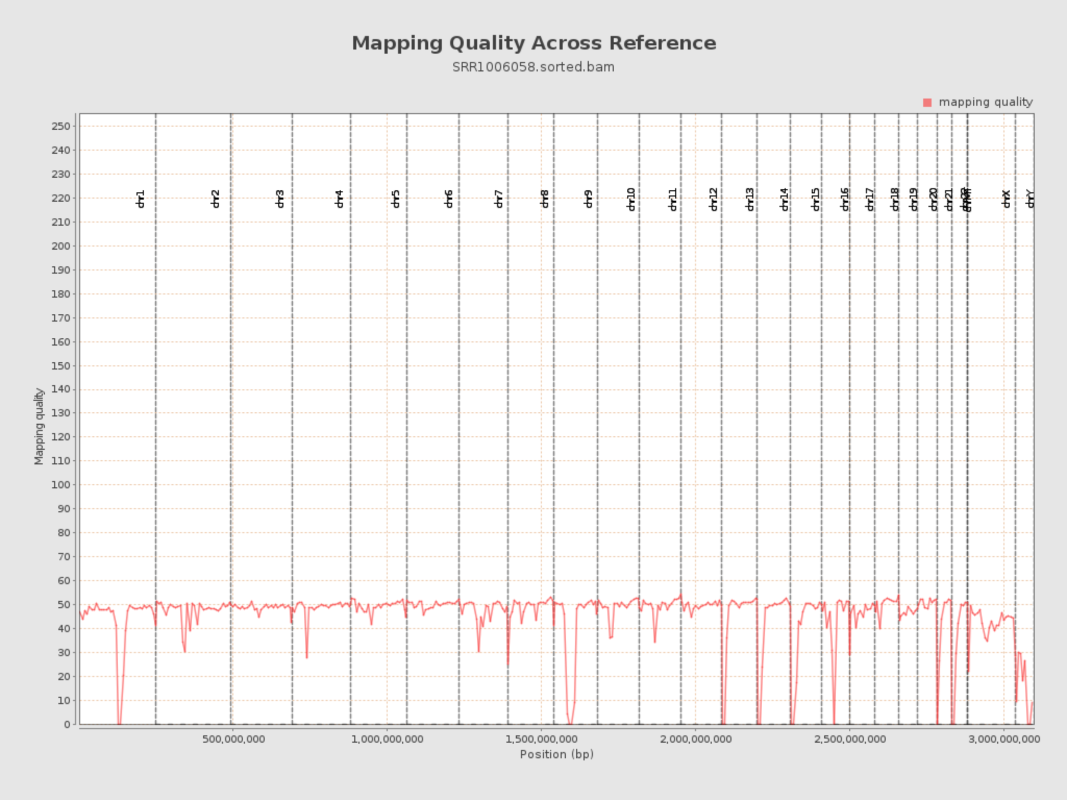
10. Results : Mapped Reads Clipping Profile



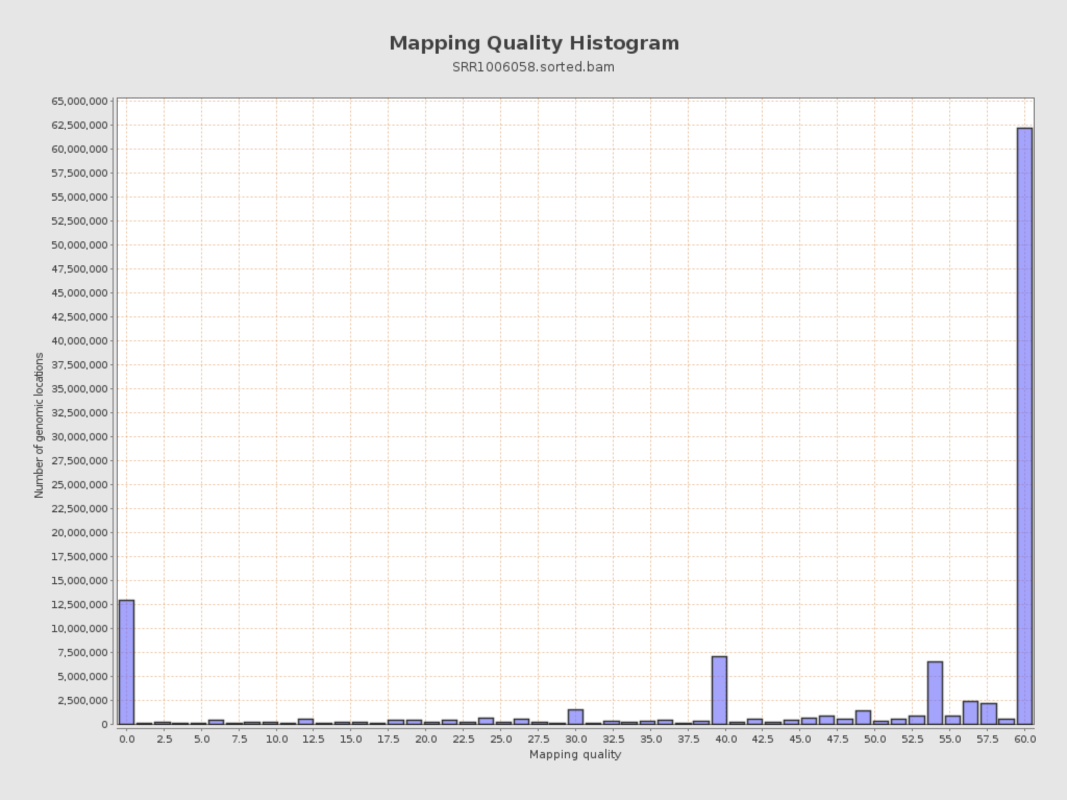
11. Results : Homopolymer Indels



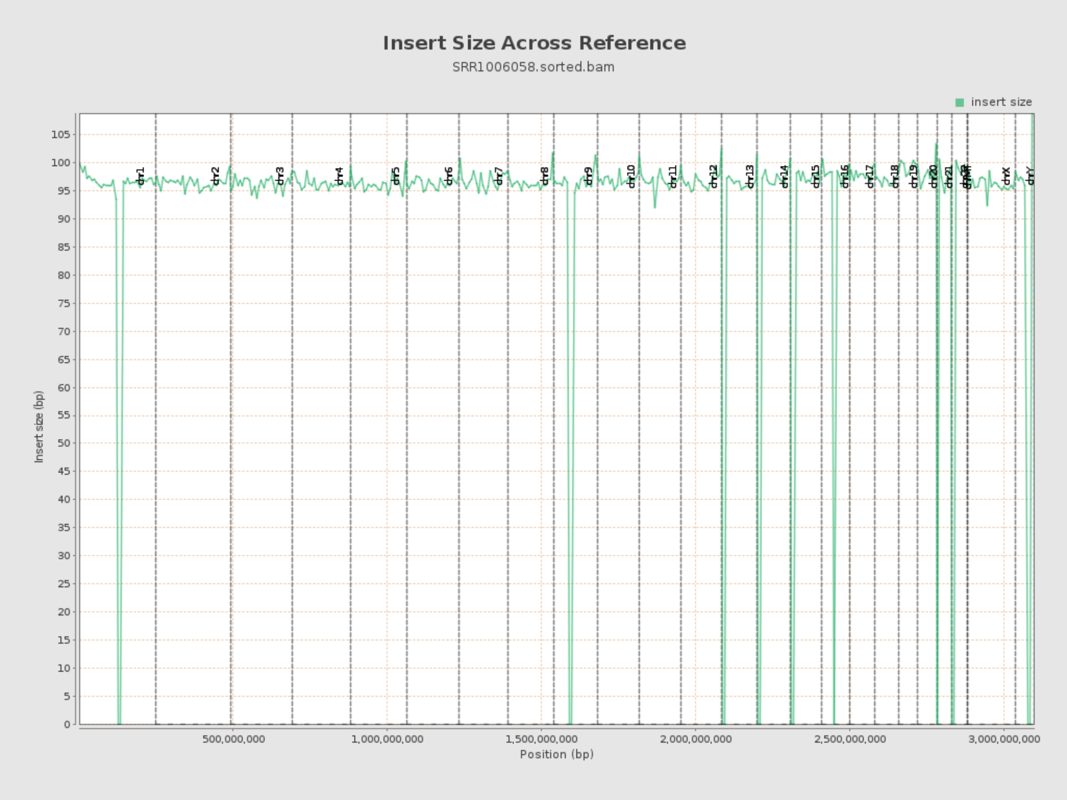
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram