Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 20:53:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006144.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_SRR1006144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006144_1.fastq.gz SRR1006144_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 20:53:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,273,330
Mapped reads	17,774,660 / 87.68%
Unmapped reads	2,498,670 / 12.32%
Mapped paired reads	17,774,660 / 87.68%
Mapped reads, first in pair	9,039,909 / 44.59%
Mapped reads, second in pair	8,734,751 / 43.08%
Mapped reads, both in pair	16,234,374 / 80.08%
Mapped reads, singletons	1,540,286 / 7.6%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,658,446 / 8.18%
Duplication rate	8.25%
Clipped reads	1,260,827 / 6.22%

2.2. ACGT Content

Number/percentage of A's	188,370,243 / 27.42%
Number/percentage of C's	148,401,443 / 21.6%
Number/percentage of T's	194,195,599 / 28.27%
Number/percentage of G's	155,934,909 / 22.7%
Number/percentage of N's	26,755 / 0%
GC Percentage	44.3%

2.3. Coverage

Mean	0.2219
Standard Deviation	1.0377

2.4. Mapping Quality

Mean Mapping Quality	47.56

2.5. Insert size

Mean	61,621.1
Standard Deviation	2,406,839.12
P25/Median/P75	78 / 110 / 148

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	3,001,430
Insertions	20,981
Mapped reads with at least one insertion	0.12%
Deletions	59,113
Mapped reads with at least one deletion	0.33%
Homopolymer indels	47.02%

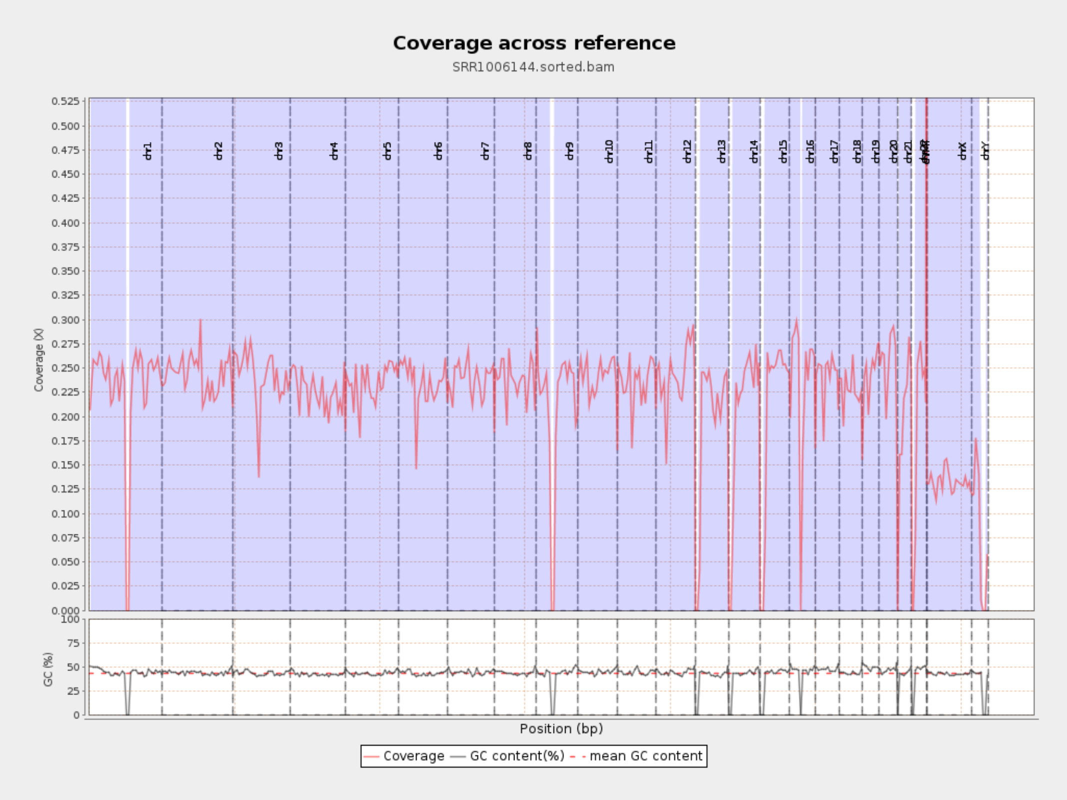
2.7. Chromosome stats

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

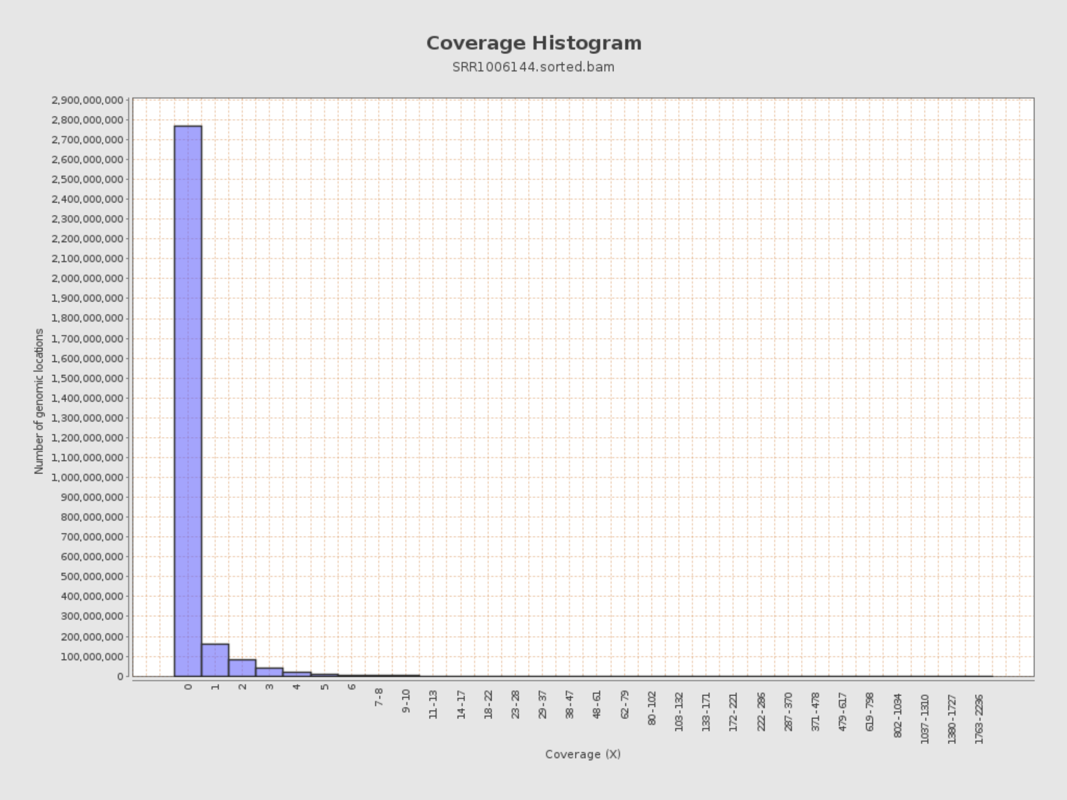
chr1	249250621	56968842	0.2286	1.1294
chr2	243199373	59543435	0.2448	1.1499
chr3	198022430	47768597	0.2412	0.8689
chr4	191154276	43105571	0.2255	0.8886
chr5	180915260	42415004	0.2344	0.86
chr6	171115067	40190539	0.2349	0.978
chr7	159138663	38068036	0.2392	1.5387
chr8	146364022	34965079	0.2389	1.1476
chr9	141213431	29075418	0.2059	0.9747
chr10	135534747	33079100	0.2441	0.9441
chr11	135006516	31721884	0.235	1.5092
chr12	133851895	32581320	0.2434	0.8886
chr13	115169878	21945190	0.1905	0.7738
chr14	107349540	21471571	0.2	0.8327
chr15	102531392	21167674	0.2065	0.8233
chr16	90354753	21320173	0.236	0.9912
chr17	81195210	19634576	0.2418	1.0078
chr18	78077248	17865421	0.2288	1.376
chr19	59128983	14372359	0.2431	1.237
chr20	63025520	16162713	0.2564	0.9291
chr21	48129895	9404913	0.1954	0.9143
chr22	51304566	8915032	0.1738	0.8476
chrMT	16571	33756	2.0371	3.3501
chrX	155270560	20677220	0.1332	0.7191

chrY	59373566	4550481	0.0766	0.5863

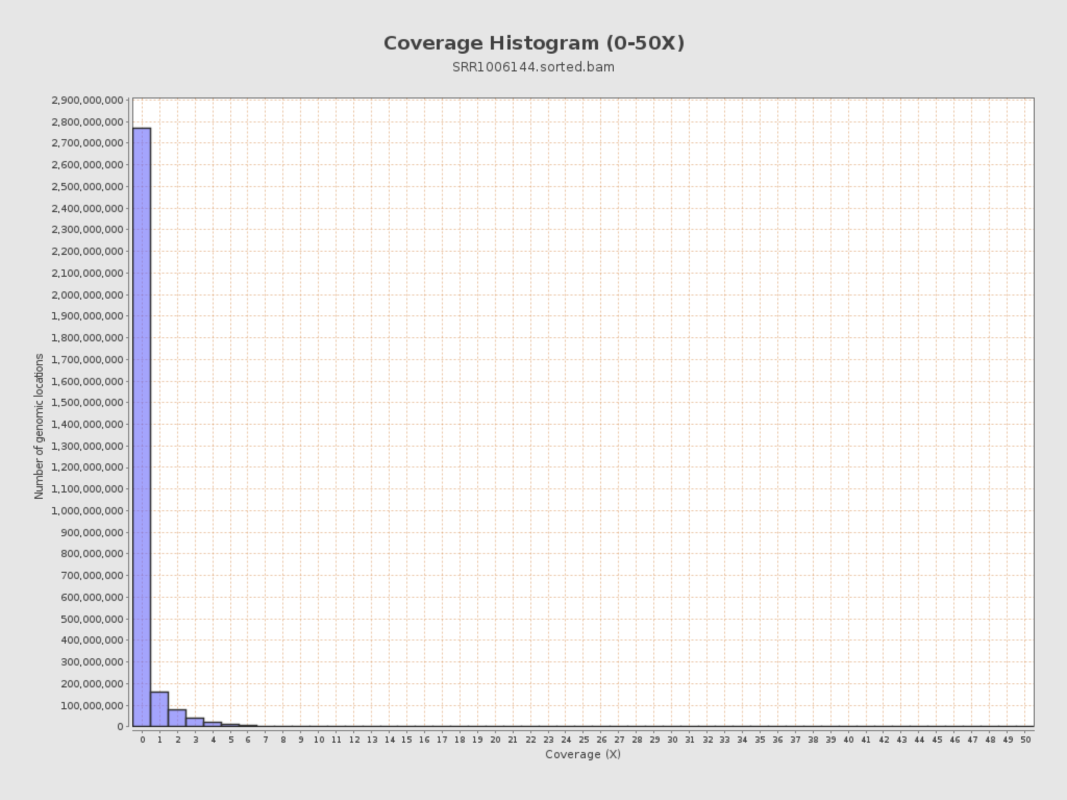
3. Results : Coverage across reference



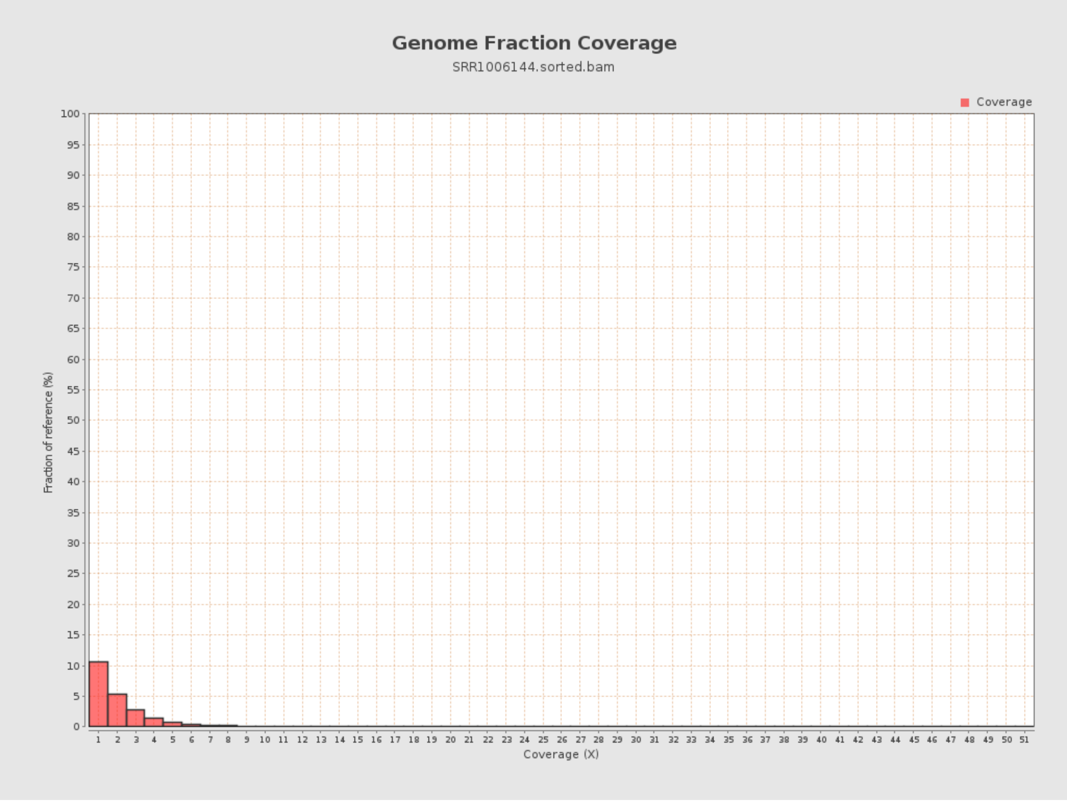
4. Results : Coverage Histogram



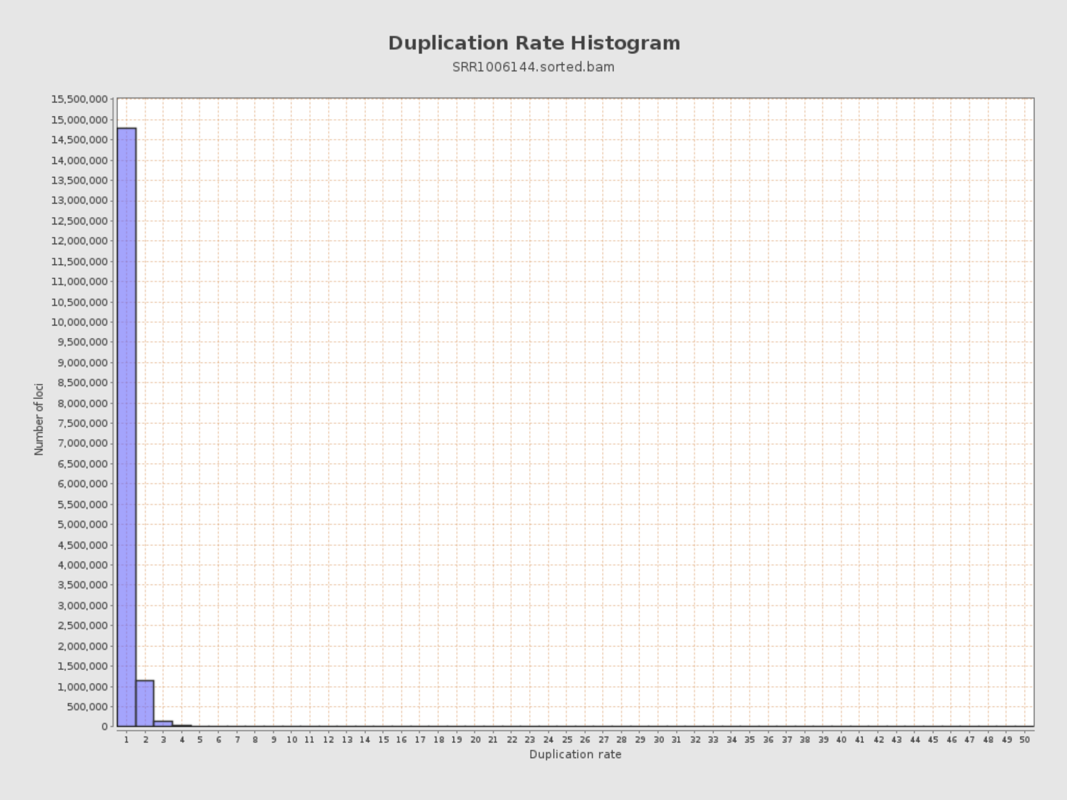
5. Results : Coverage Histogram (0-50X)



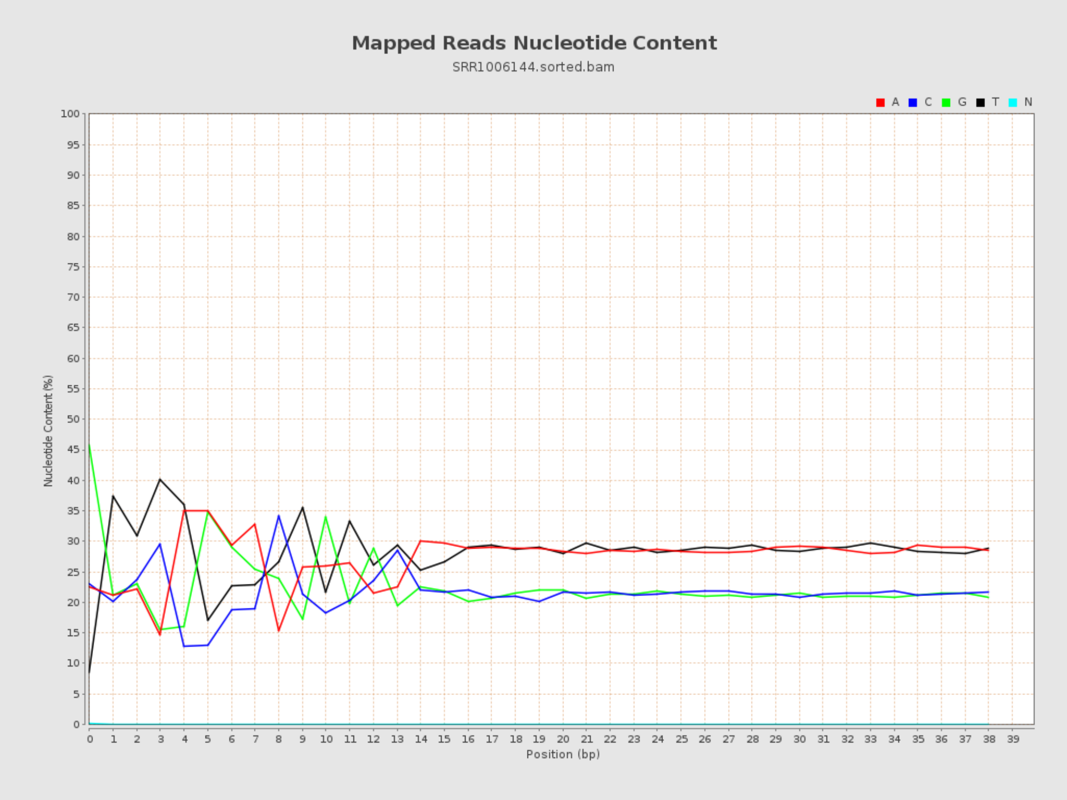
6. Results : Genome Fraction Coverage



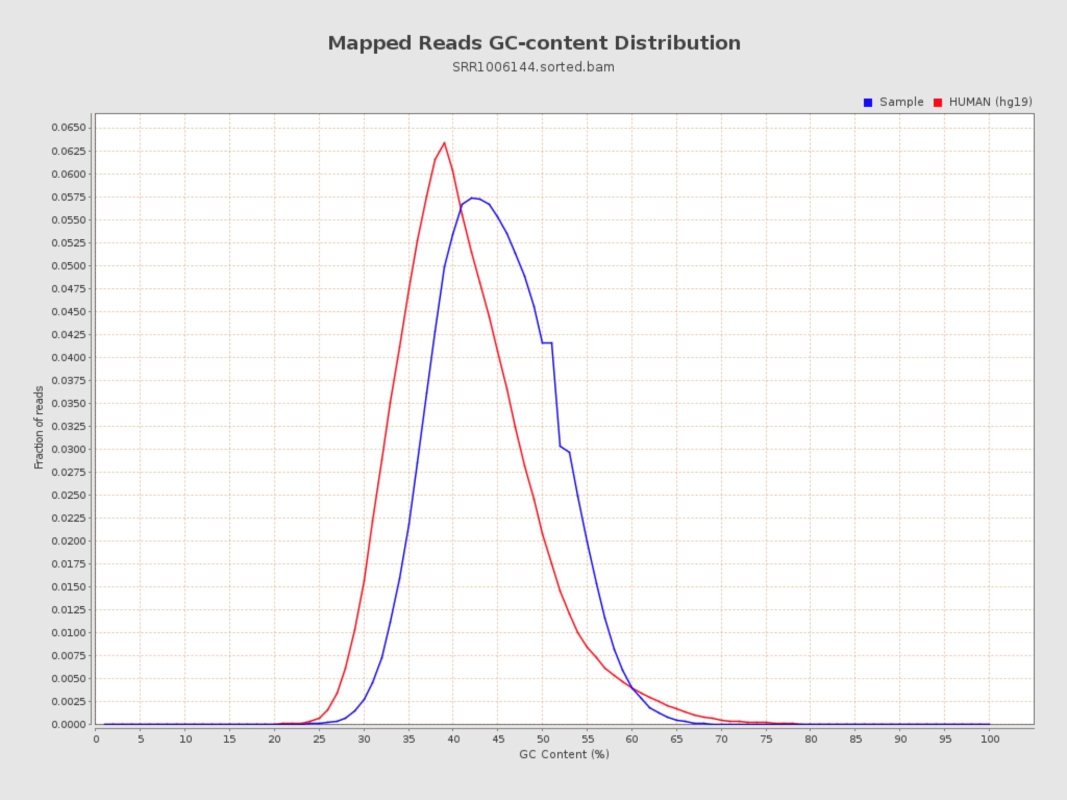
7. Results : Duplication Rate Histogram



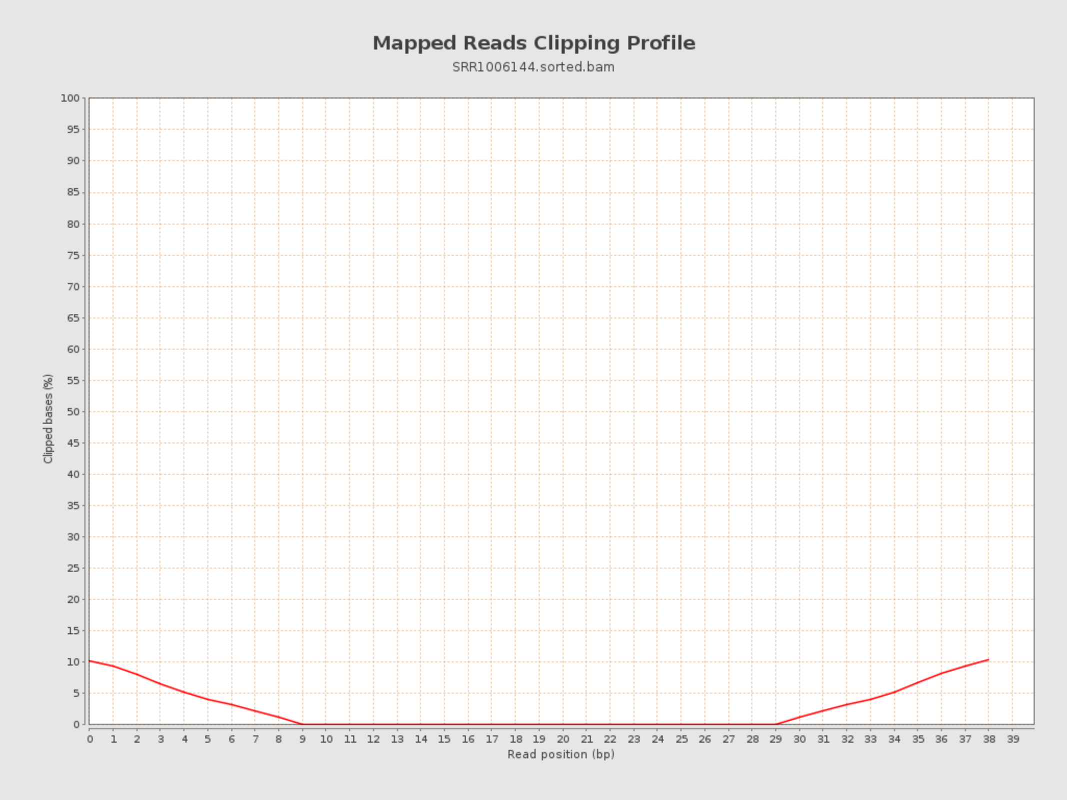
8. Results : Mapped Reads Nucleotide Content



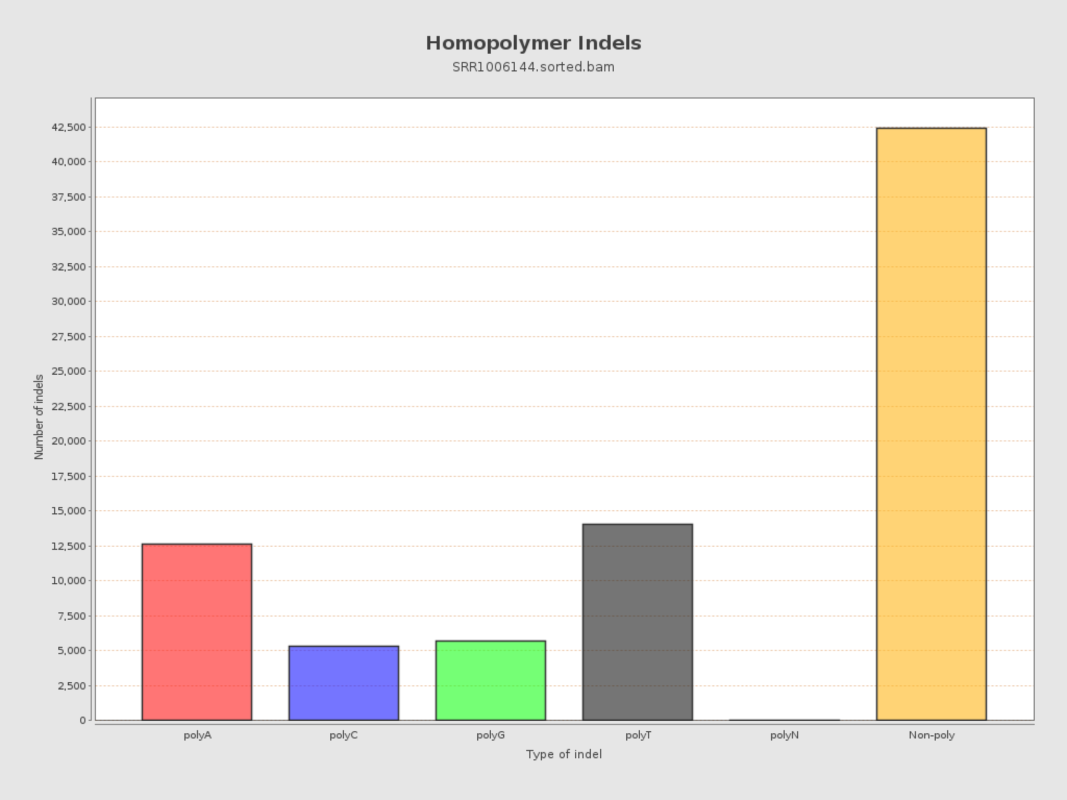
9. Results : Mapped Reads GC-content Distribution



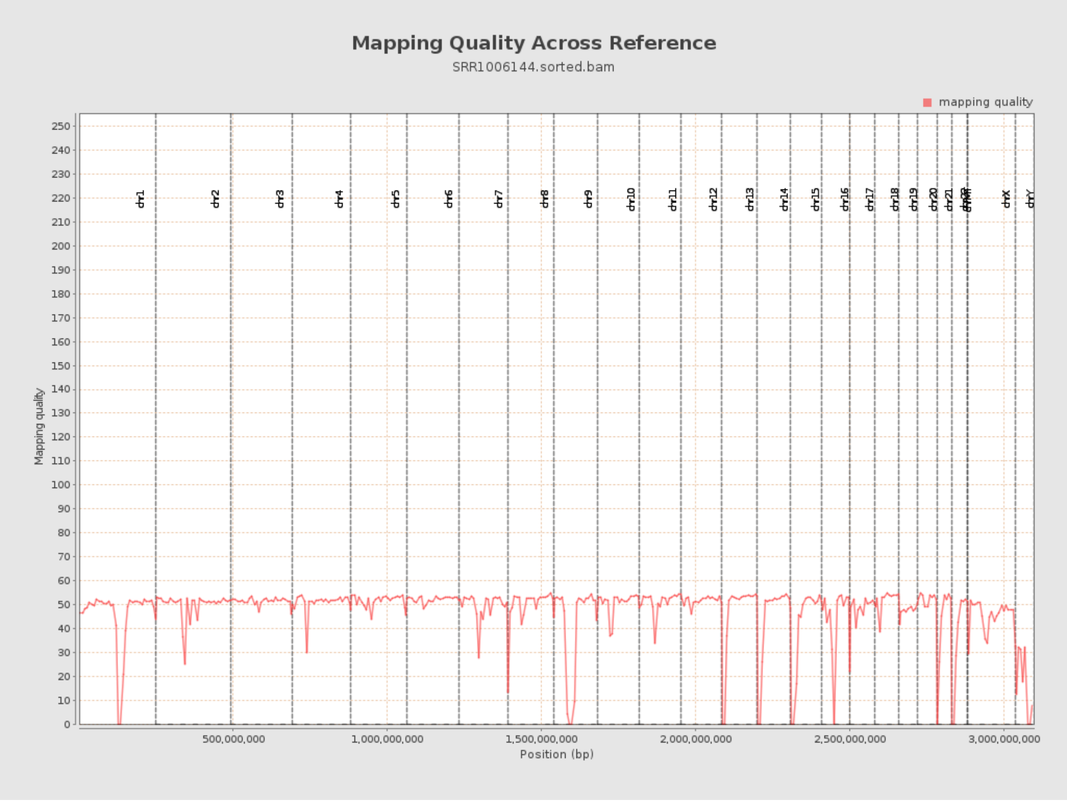
10. Results : Mapped Reads Clipping Profile



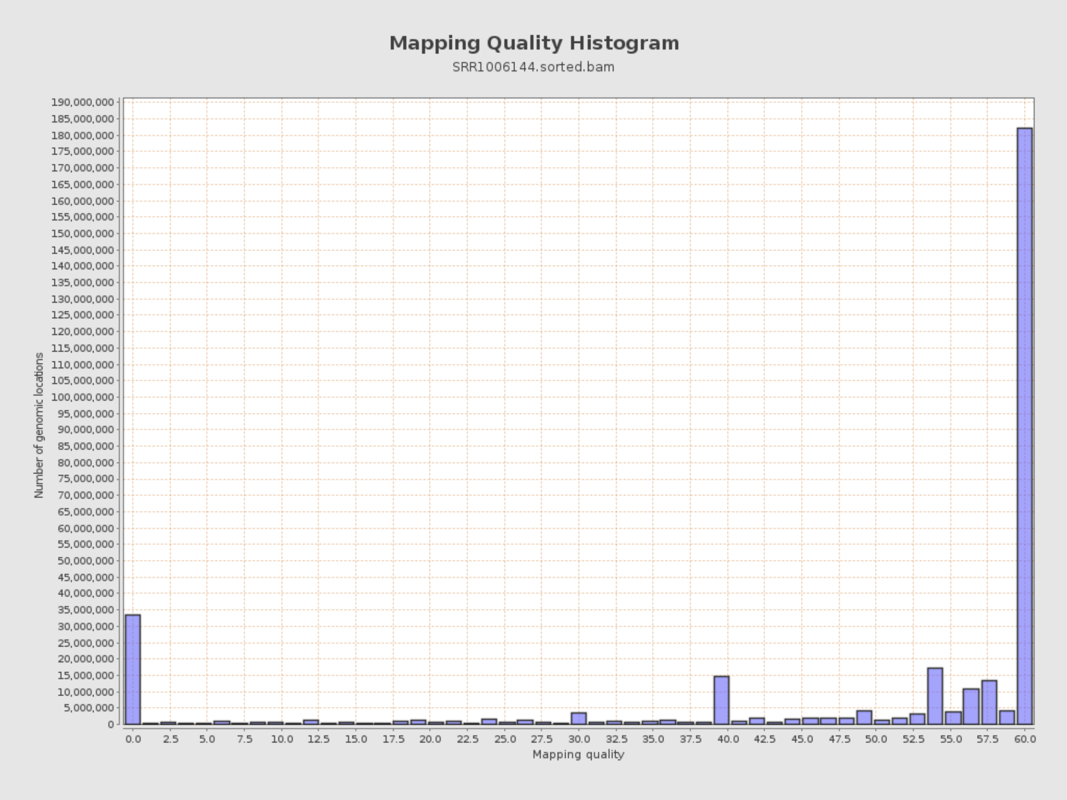
11. Results : Homopolymer Indels



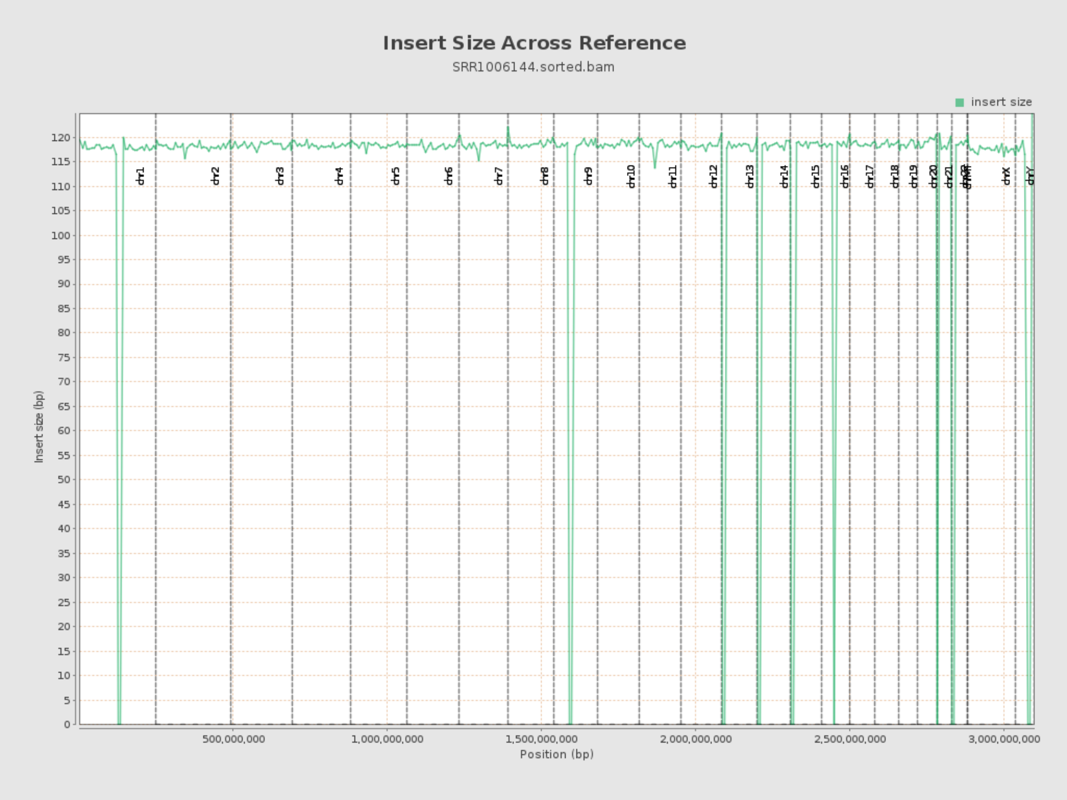
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram