Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 17:33:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006064.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_SRR1006064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006064_1.fastq.gz SRR1006064_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 17:33:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,153,122
Mapped reads	9,713,119 / 87.09%
Unmapped reads	1,440,003 / 12.91%
Mapped paired reads	9,713,119 / 87.09%
Mapped reads, first in pair	4,932,429 / 44.22%
Mapped reads, second in pair	4,780,690 / 42.86%
Mapped reads, both in pair	8,872,630 / 79.55%
Mapped reads, singletons	840,489 / 7.54%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	564,049 / 5.06%
Duplication rate	5.2%
Clipped reads	820,464 / 7.36%

2.2. ACGT Content

Number/percentage of A's	103,113,779 / 27.51%
Number/percentage of C's	80,737,313 / 21.54%
Number/percentage of T's	106,252,142 / 28.34%
Number/percentage of G's	84,752,752 / 22.61%
Number/percentage of N's	15,100 / 0%
GC Percentage	44.15%

2.3. Coverage

Mean	0.1211
Standard Deviation	0.6234

2.4. Mapping Quality

Mean Mapping Quality	47.43

2.5. Insert size

Mean	58,882.69
Standard Deviation	2,360,991.11
P25/Median/P75	70 / 105 / 143

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	1,922,318
Insertions	13,041
Mapped reads with at least one insertion	0.13%
Deletions	34,854
Mapped reads with at least one deletion	0.36%
Homopolymer indels	45.65%

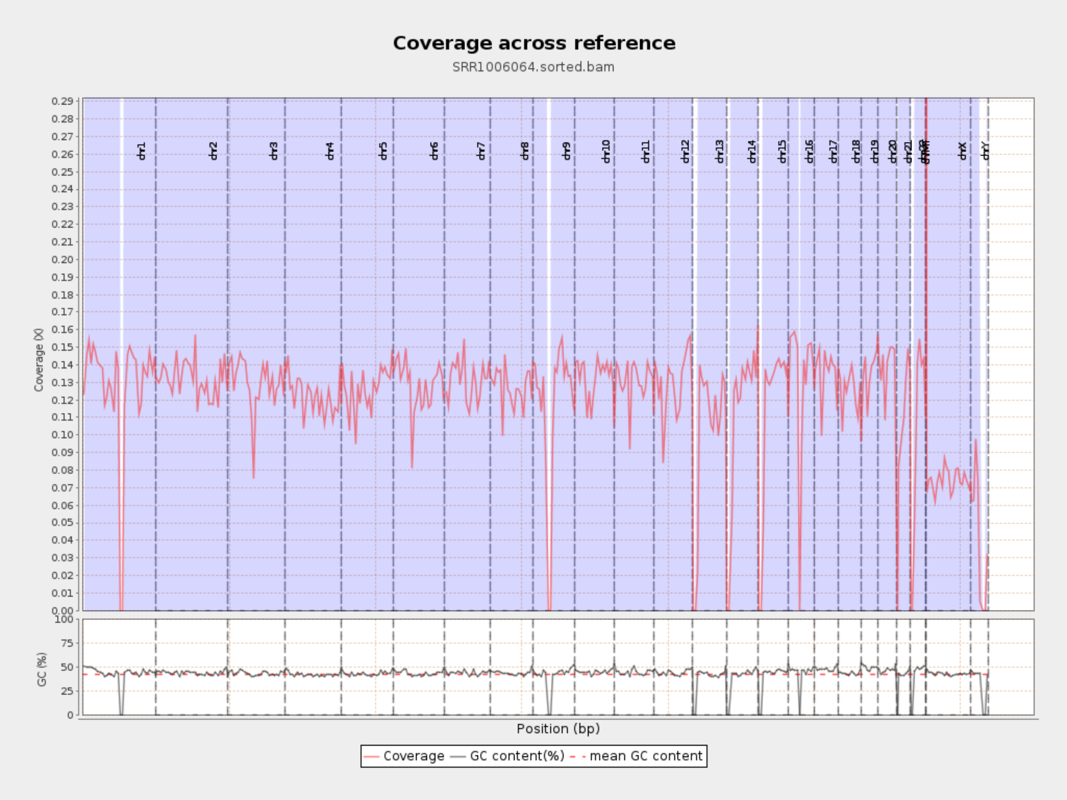
2.7. Chromosome stats

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

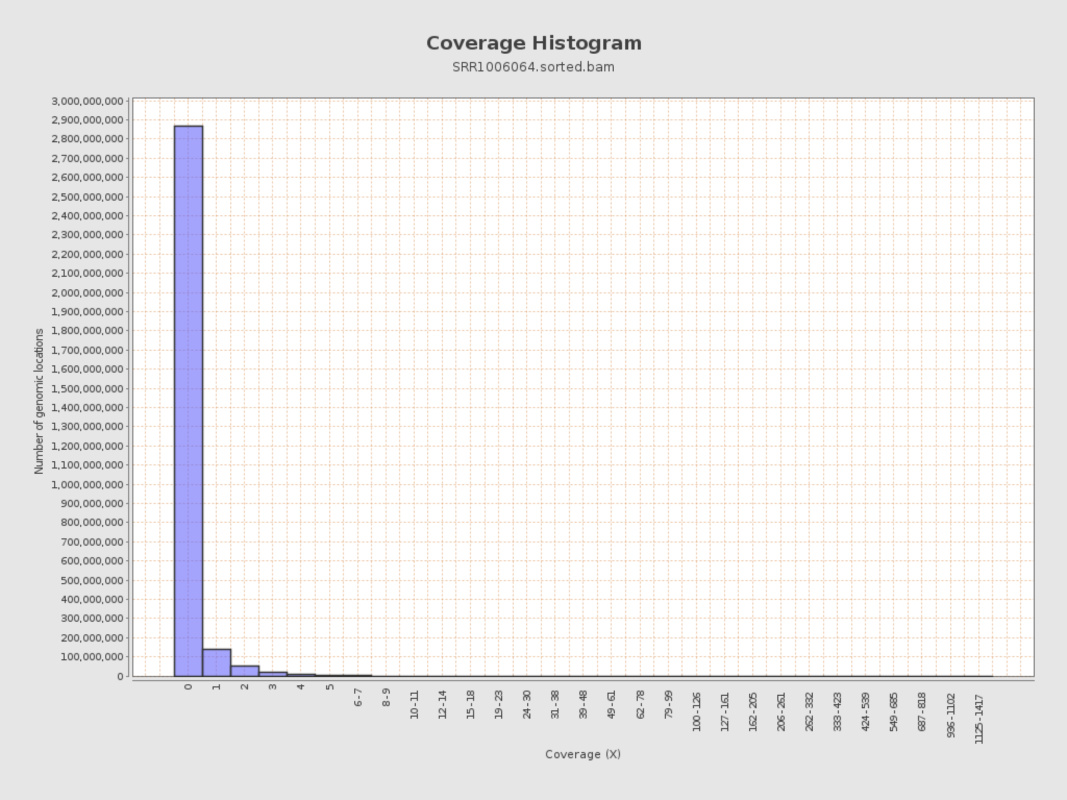
chr1	249250621	31885951	0.1279	0.7002
chr2	243199373	32097575	0.132	0.6783
chr3	198022430	25670612	0.1296	0.5328
chr4	191154276	23343151	0.1221	0.538
chr5	180915260	22929063	0.1267	0.5297
chr6	171115067	21973957	0.1284	0.6102
chr7	159138663	20892017	0.1313	0.8325
chr8	146364022	18538373	0.1267	0.6747
chr9	141213431	16261050	0.1152	0.5772
chr10	135534747	18060449	0.1333	0.5691
chr11	135006516	17621801	0.1305	0.941
chr12	133851895	17495087	0.1307	0.5428
chr13	115169878	11648429	0.1011	0.4756
chr14	107349540	11848864	0.1104	0.5167
chr15	102531392	11343935	0.1106	0.5028
chr16	90354753	11682428	0.1293	0.5885
chr17	81195210	11091191	0.1366	0.634
chr18	78077248	9771921	0.1252	0.8093
chr19	59128983	7952592	0.1345	0.7462
chr20	63025520	8695669	0.138	0.5625
chr21	48129895	5067693	0.1053	0.5451
chr22	51304566	5052214	0.0985	0.5224
chrMT	16571	55266	3.3351	4.9079
chrX	155270560	11509485	0.0741	0.4441

chrY	59373566	2426231	0.0409	0.3453

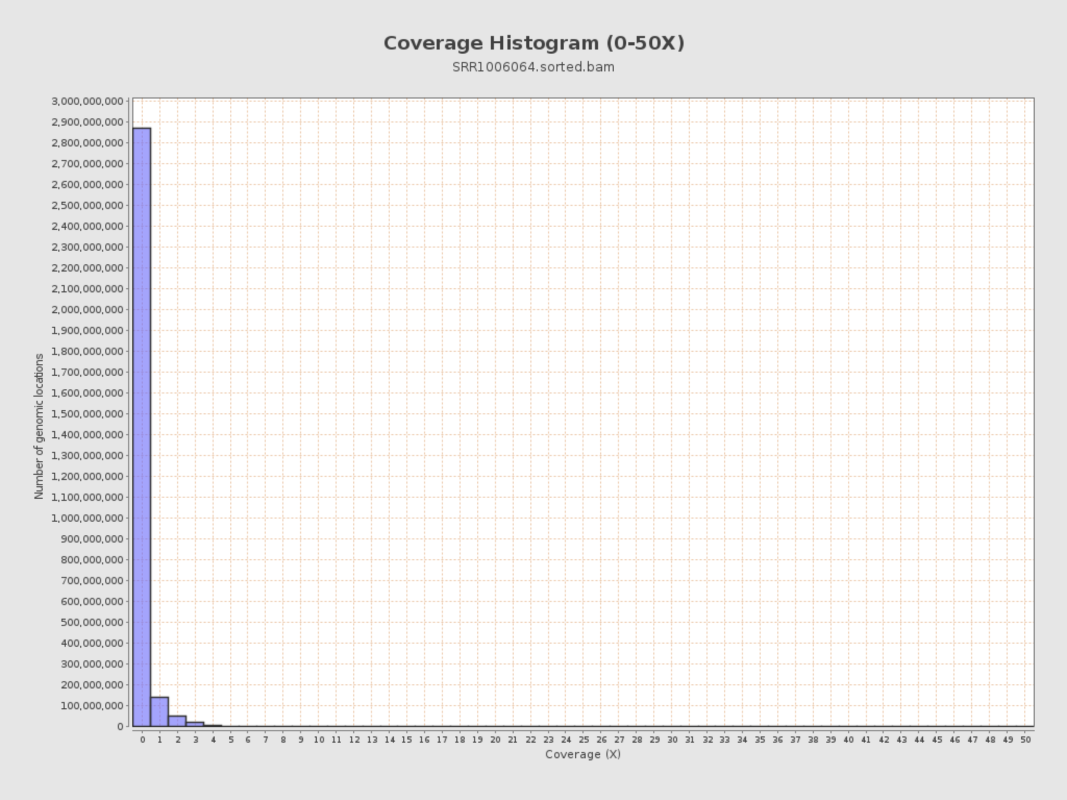
3. Results : Coverage across reference



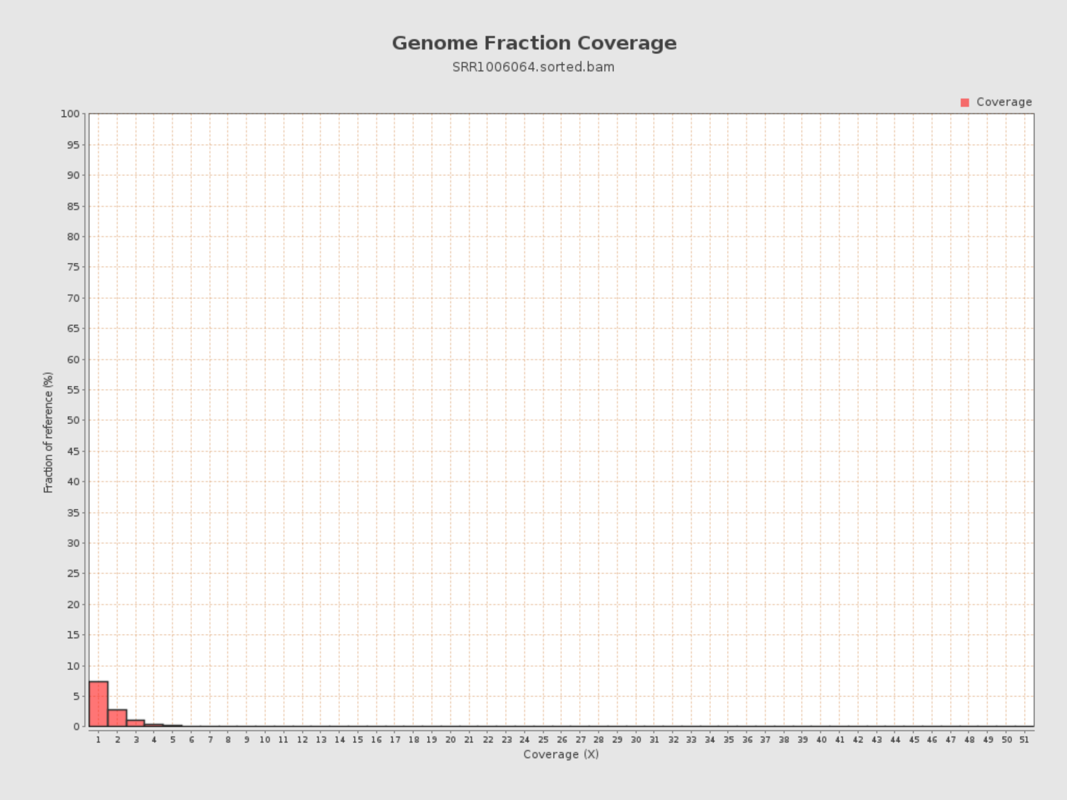
4. Results : Coverage Histogram



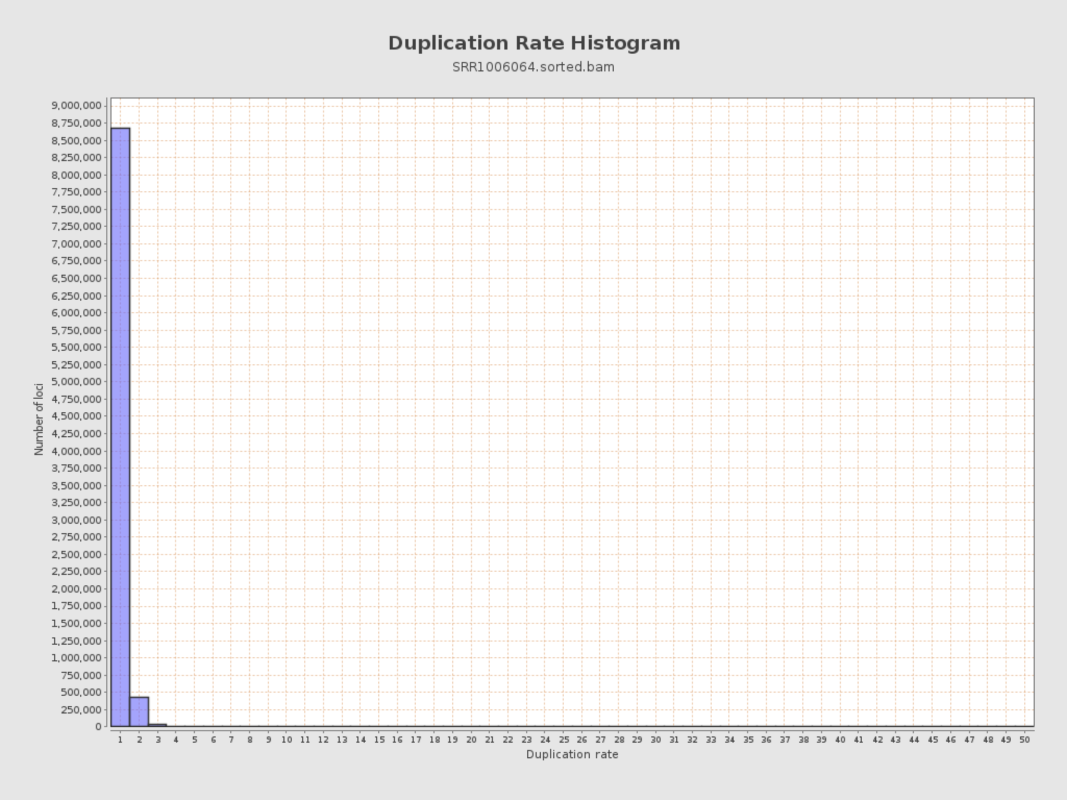
5. Results : Coverage Histogram (0-50X)



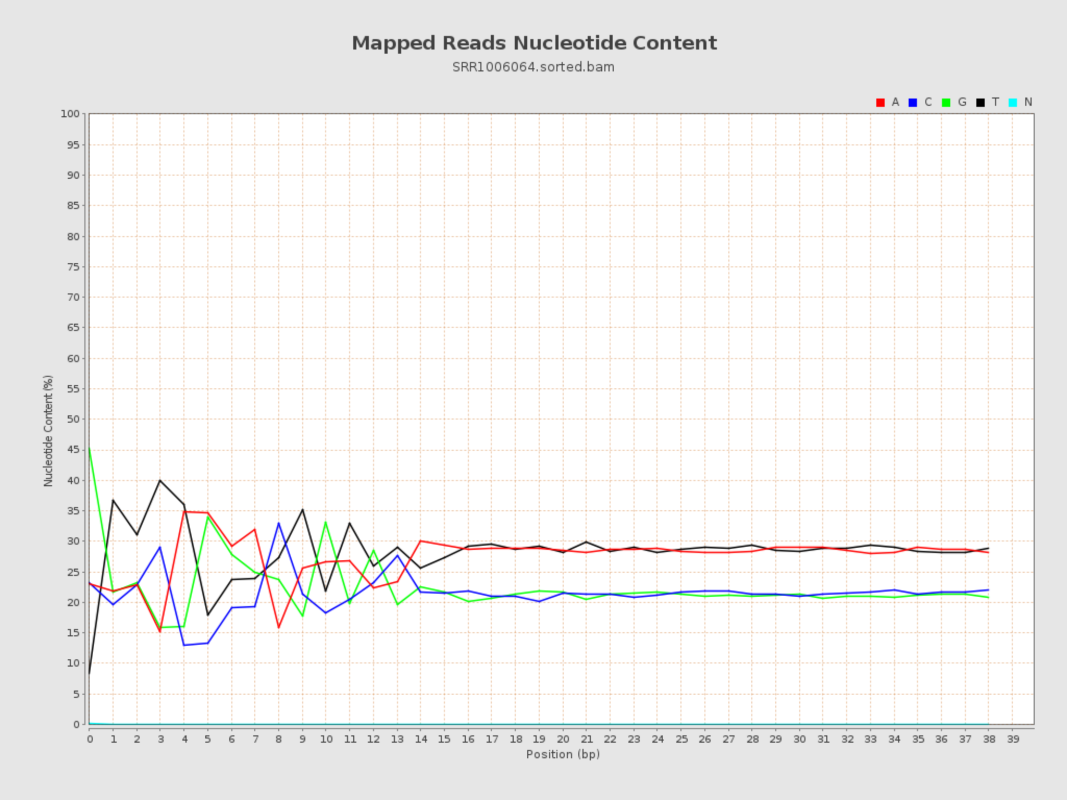
6. Results : Genome Fraction Coverage



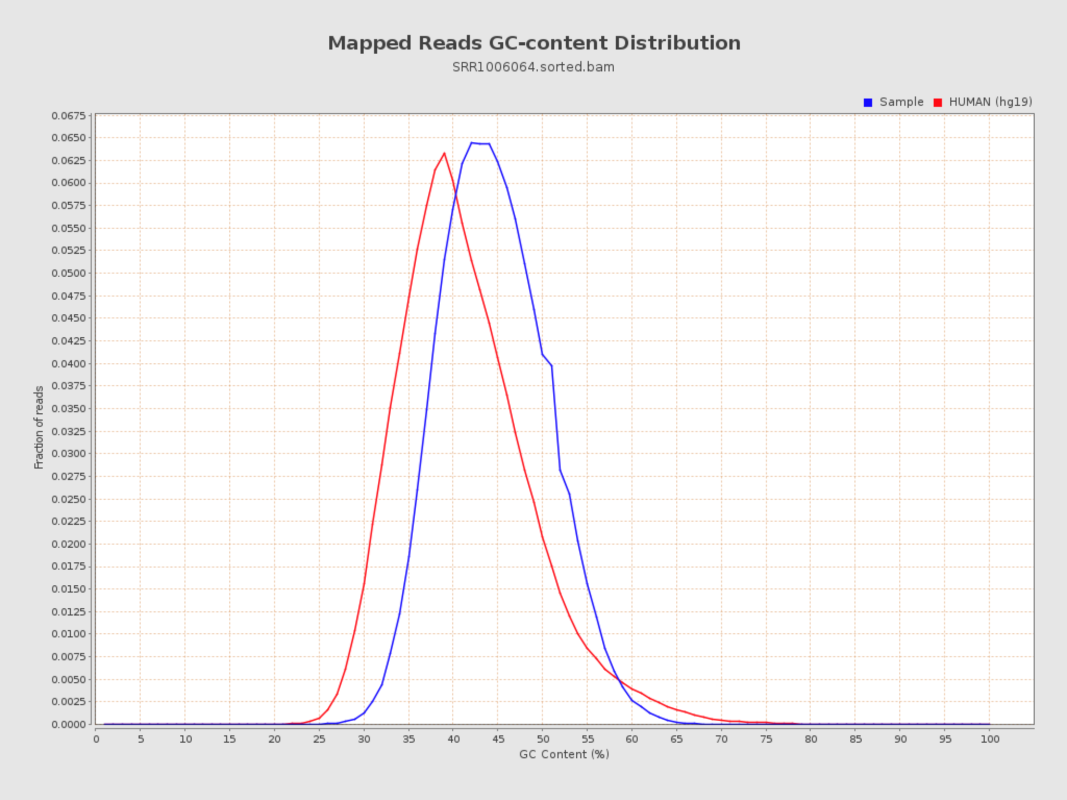
7. Results : Duplication Rate Histogram



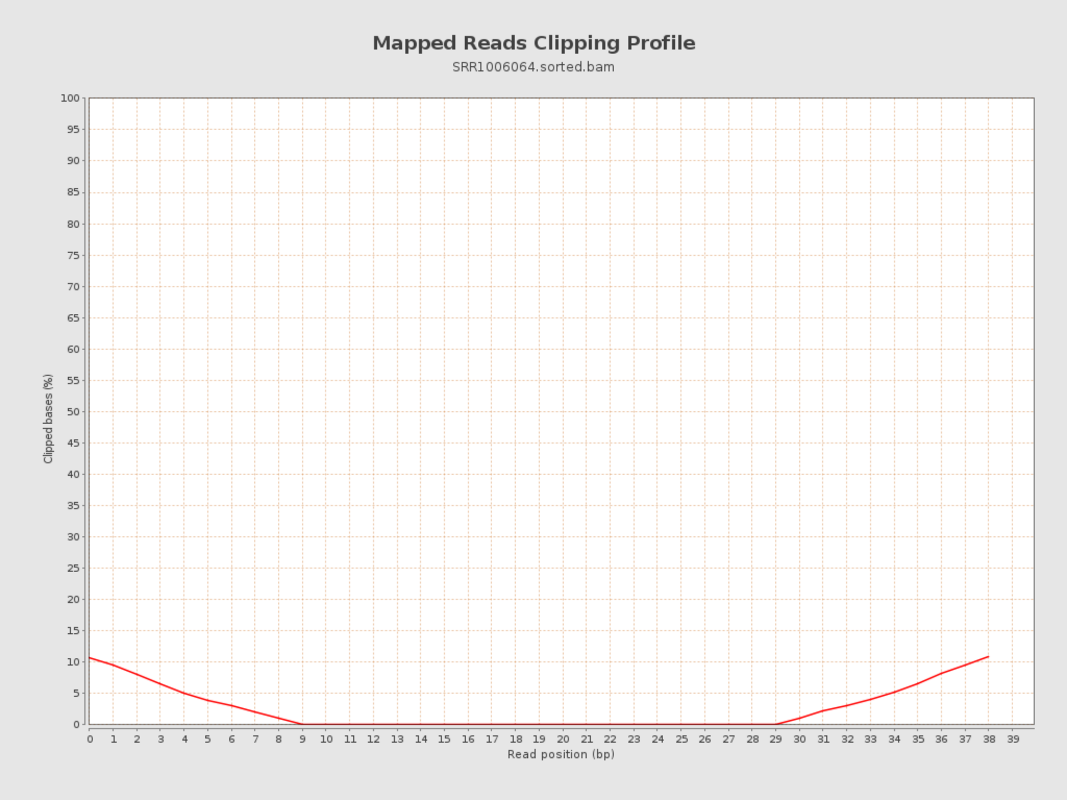
8. Results : Mapped Reads Nucleotide Content



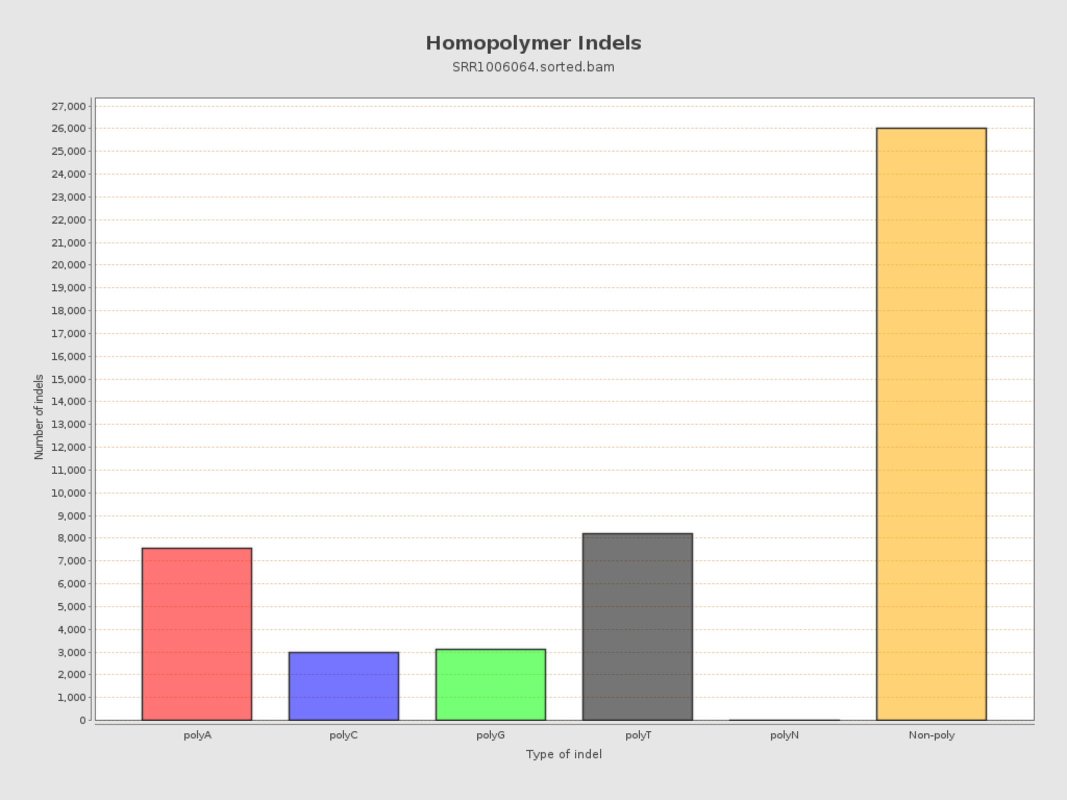
9. Results : Mapped Reads GC-content Distribution



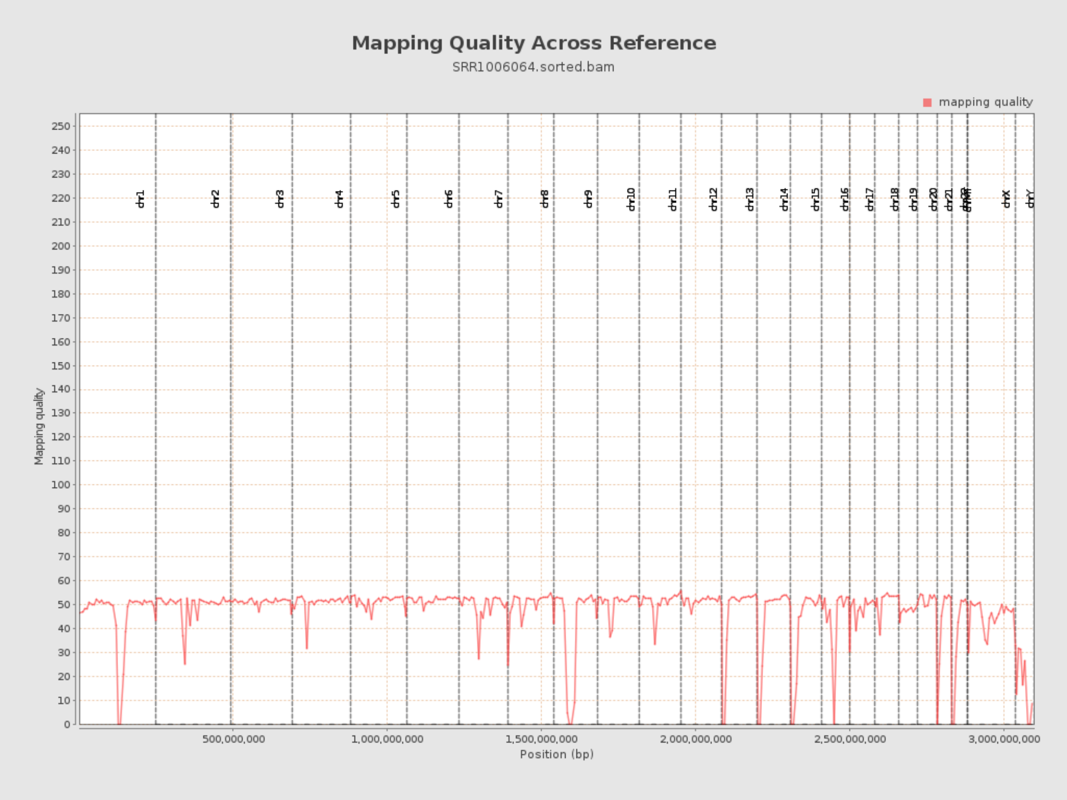
10. Results : Mapped Reads Clipping Profile



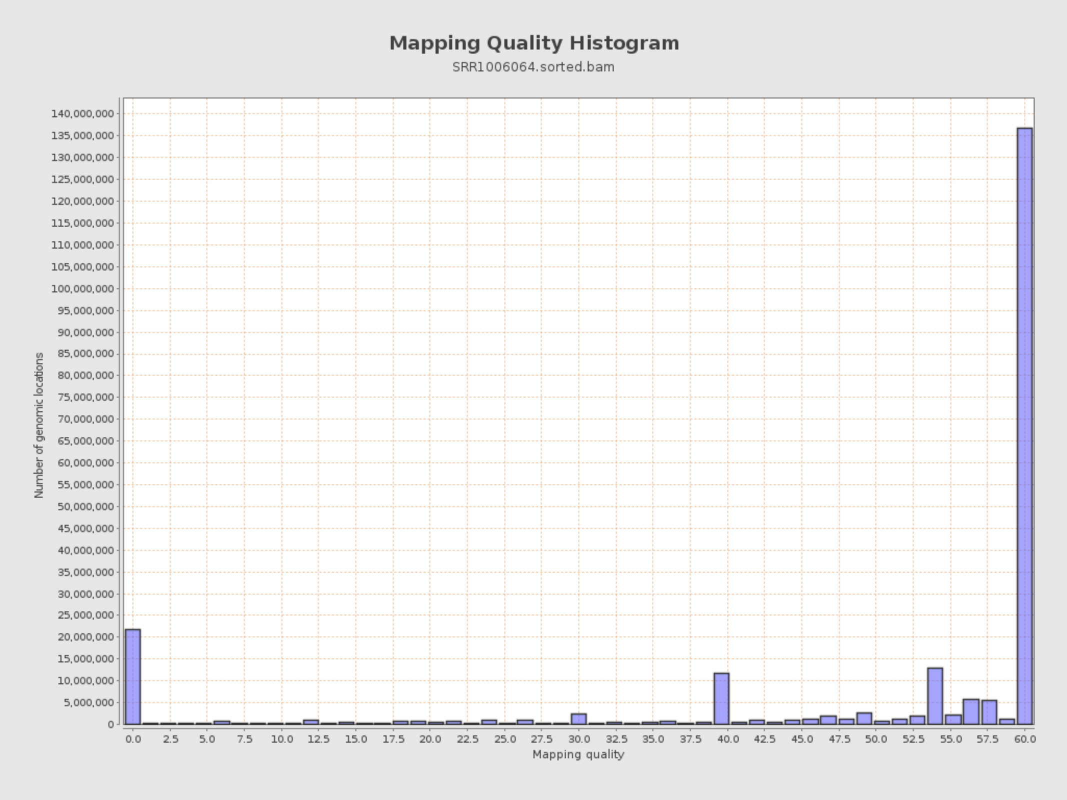
11. Results : Homopolymer Indels



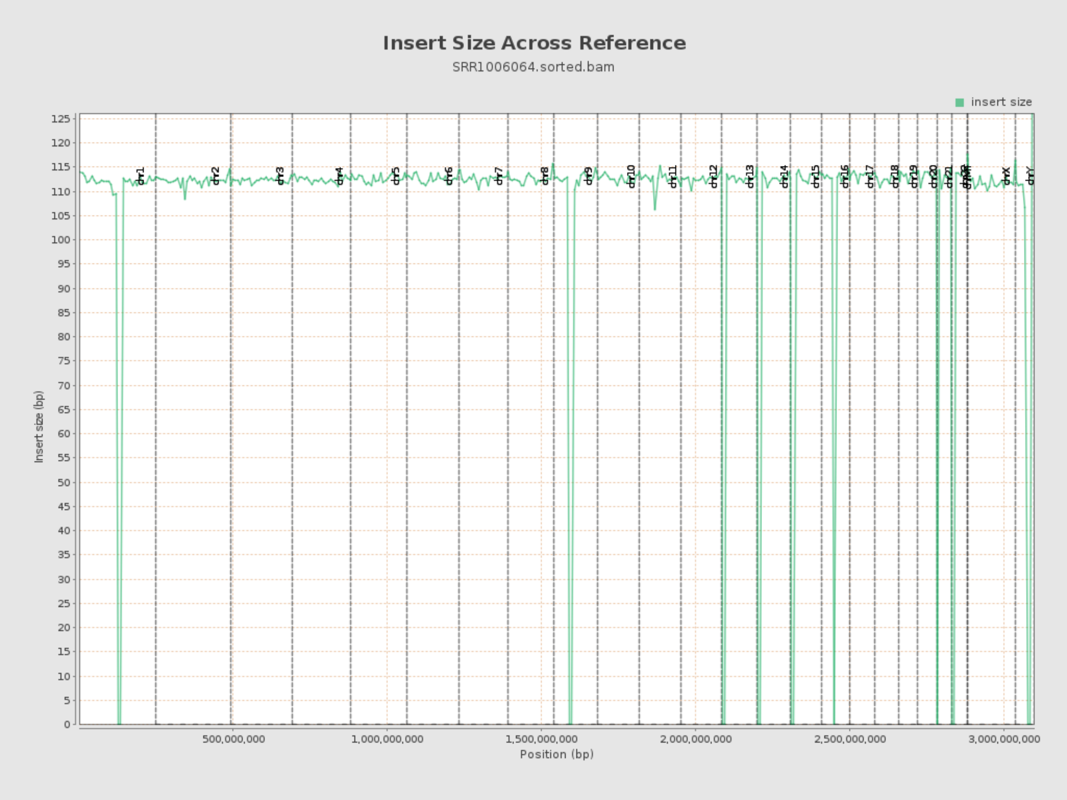
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram