Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:25:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006164.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_SRR1006164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006164_1.fastq.gz SRR1006164_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:25:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,329,604
Mapped reads	7,421,148 / 79.54%
Unmapped reads	1,908,456 / 20.46%
Mapped paired reads	7,421,148 / 79.54%
Mapped reads, first in pair	3,738,137 / 40.07%
Mapped reads, second in pair	3,683,011 / 39.48%
Mapped reads, both in pair	6,862,098 / 73.55%
Mapped reads, singletons	559,050 / 5.99%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	473,246 / 5.07%
Duplication rate	5.63%
Clipped reads	461,449 / 4.95%

2.2. ACGT Content

Number/percentage of A's	77,956,250 / 27.16%
Number/percentage of C's	63,856,659 / 22.24%
Number/percentage of T's	79,240,968 / 27.6%
Number/percentage of G's	65,968,190 / 22.98%
Number/percentage of N's	39,615 / 0.01%
GC Percentage	45.23%

2.3. Coverage

Mean	0.0927
Standard Deviation	0.5738

2.4. Mapping Quality

Mean Mapping Quality	47.41

2.5. Insert size

Mean	58,262.55
Standard Deviation	2,316,335.73
P25/Median/P75	65 / 89 / 129

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	1,054,604
Insertions	8,434
Mapped reads with at least one insertion	0.11%
Deletions	27,049
Mapped reads with at least one deletion	0.36%
Homopolymer indels	40.61%

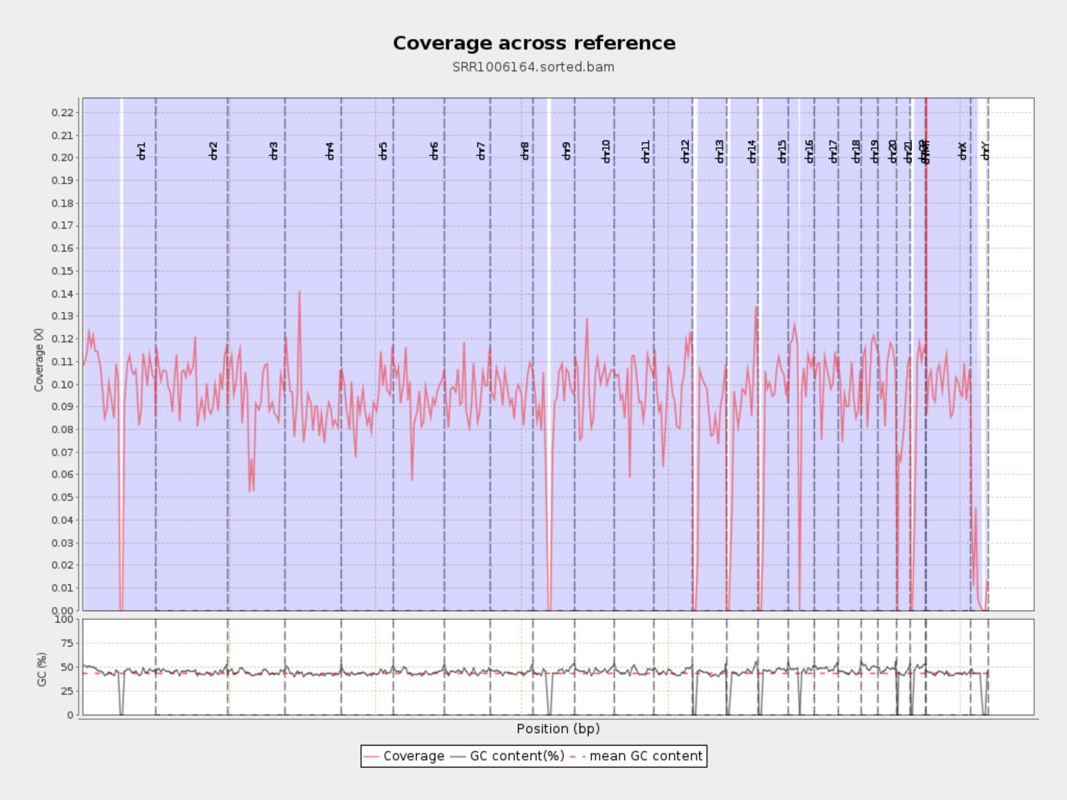
2.7. Chromosome stats

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

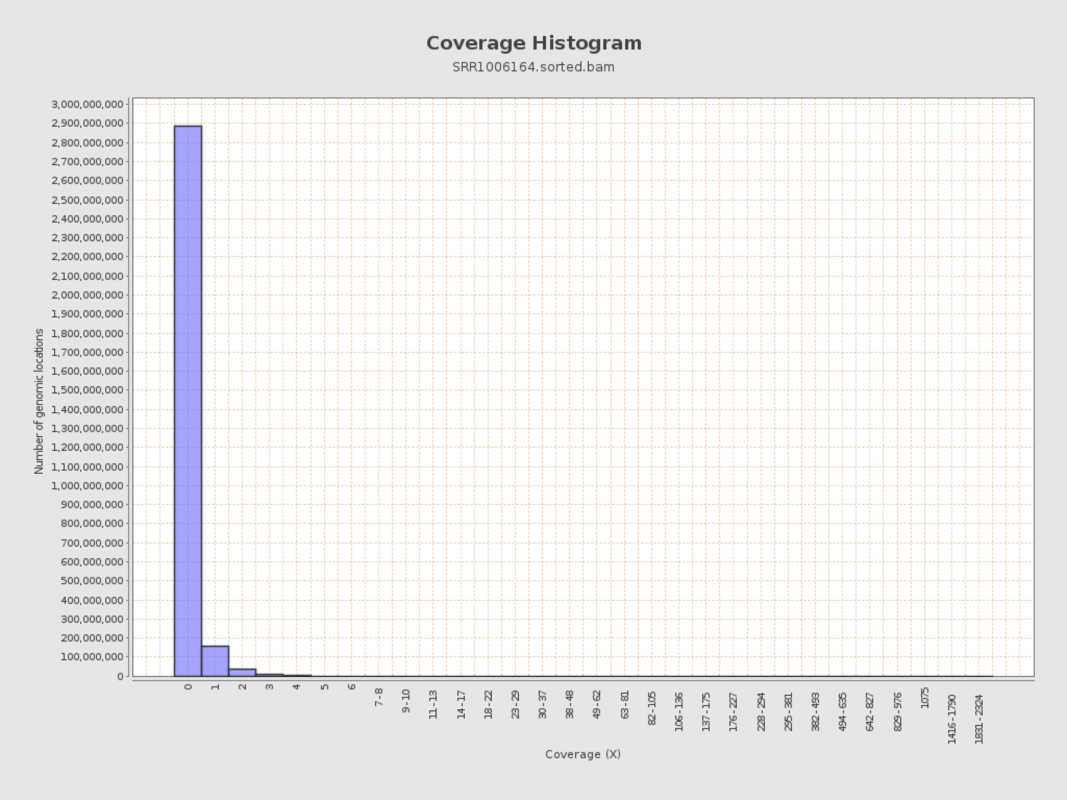
chr1	249250621	24315591	0.0976	0.6289
chr2	243199373	24322208	0.1	0.5004
chr3	198022430	18481456	0.0933	0.3972
chr4	191154276	17460863	0.0913	0.462
chr5	180915260	16924395	0.0935	0.4107
chr6	171115067	16102090	0.0941	0.4316
chr7	159138663	15371230	0.0966	0.5534
chr8	146364022	14253497	0.0974	1.204
chr9	141213431	11765991	0.0833	0.4246
chr10	135534747	13564238	0.1001	0.5665
chr11	135006516	13253144	0.0982	0.4825
chr12	133851895	13141083	0.0982	0.4168
chr13	115169878	8865230	0.077	0.3871
chr14	107349540	8846890	0.0824	1.205
chr15	102531392	8445098	0.0824	0.3762
chr16	90354753	9090404	0.1006	0.4677
chr17	81195210	8392843	0.1034	0.4544
chr18	78077248	7313572	0.0937	0.5885
chr19	59128983	6399450	0.1082	0.5575
chr20	63025520	6629909	0.1052	0.4578
chr21	48129895	3805140	0.0791	0.4563
chr22	51304566	4021022	0.0784	0.4541
chrMT	16571	44026	2.6568	2.3792
chrX	155270560	15467064	0.0996	0.4385

chrY	59373566	822110	0.0138	0.3387

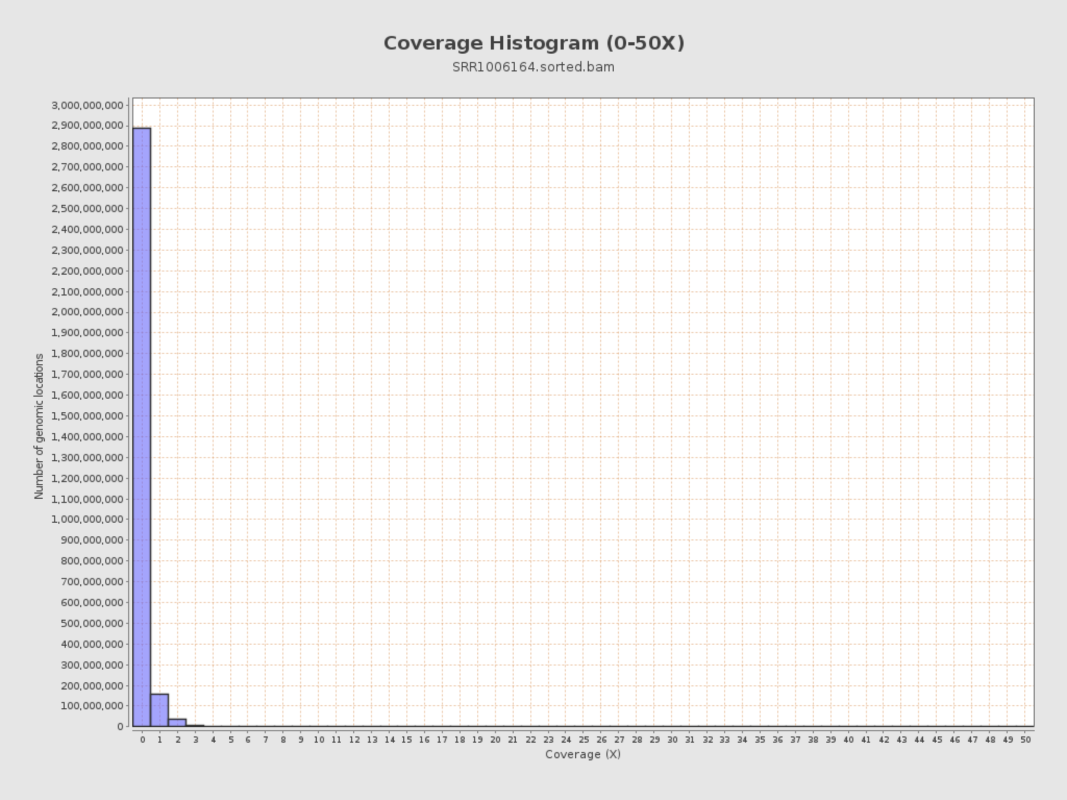
3. Results : Coverage across reference



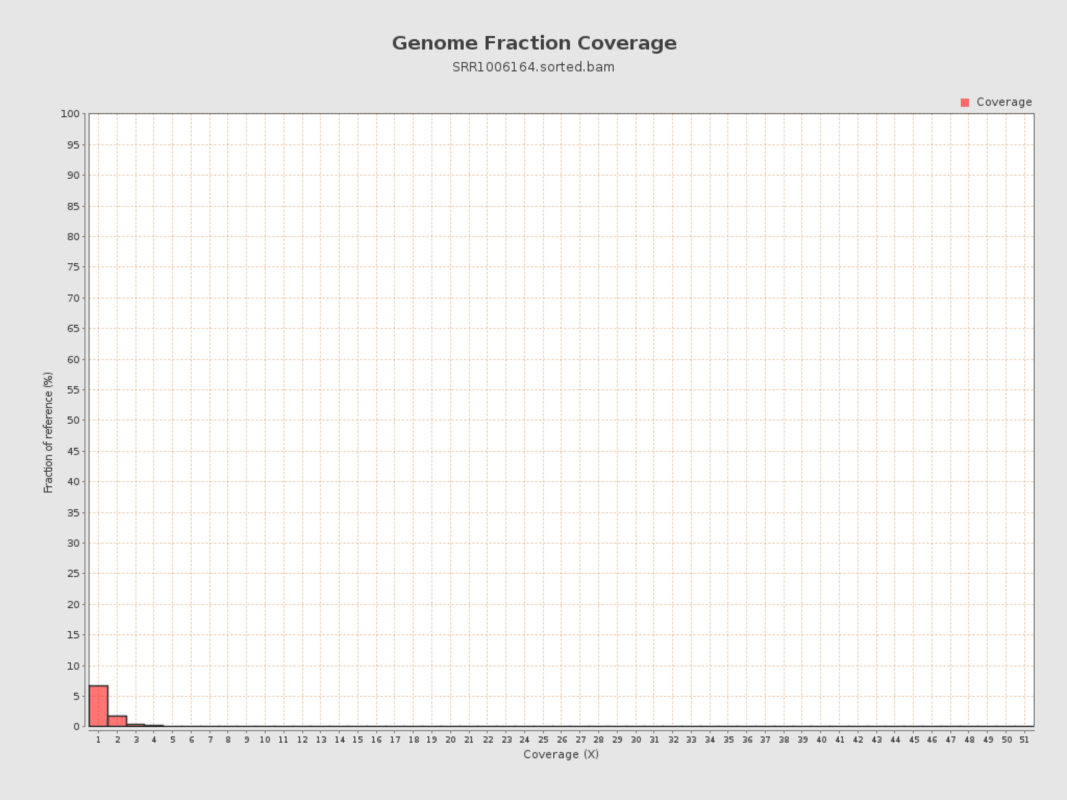
4. Results : Coverage Histogram



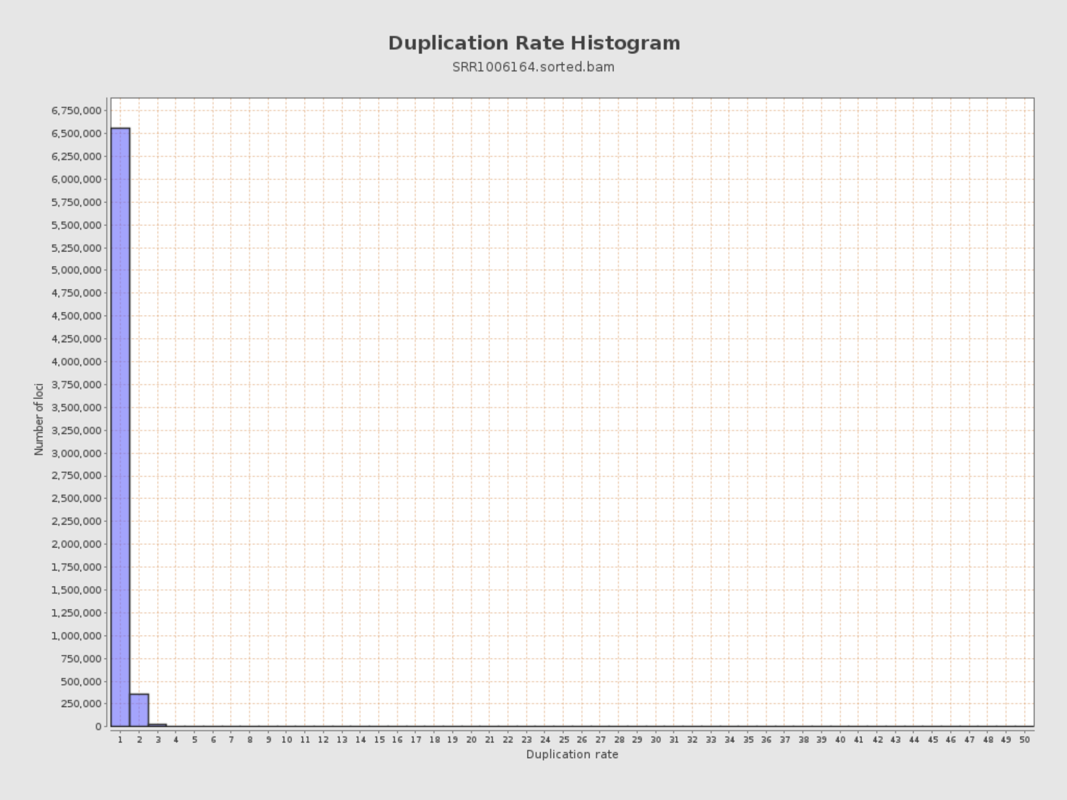
5. Results : Coverage Histogram (0-50X)



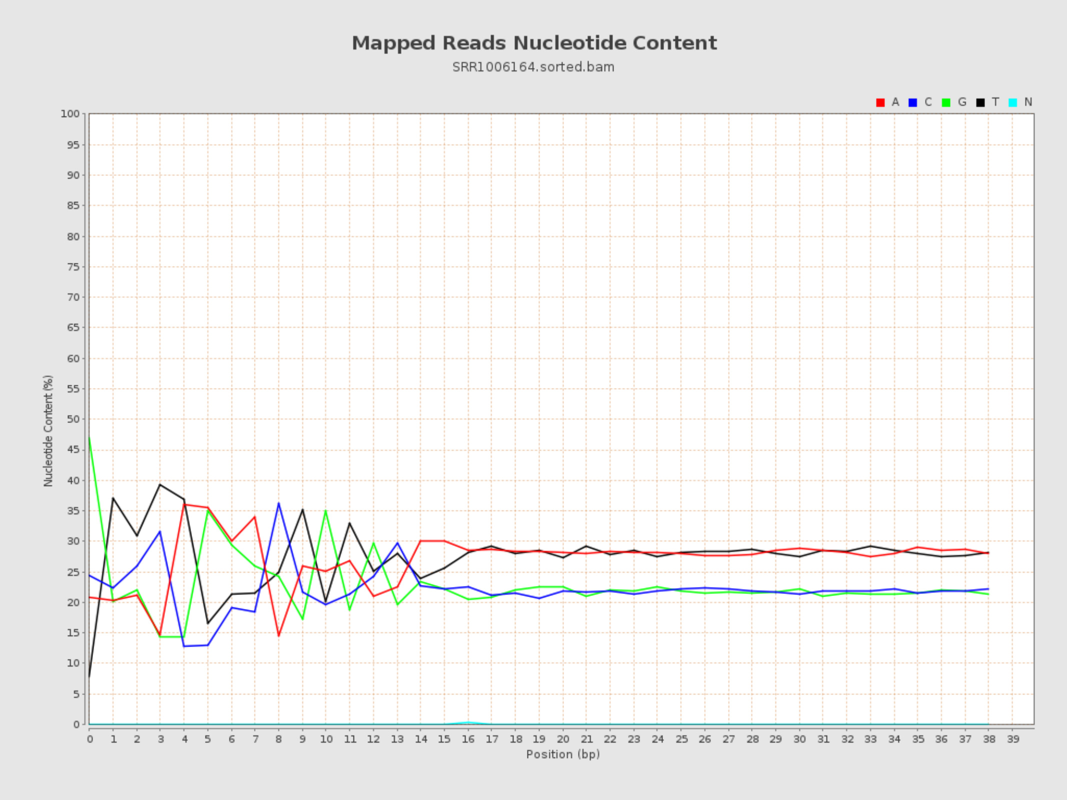
6. Results : Genome Fraction Coverage



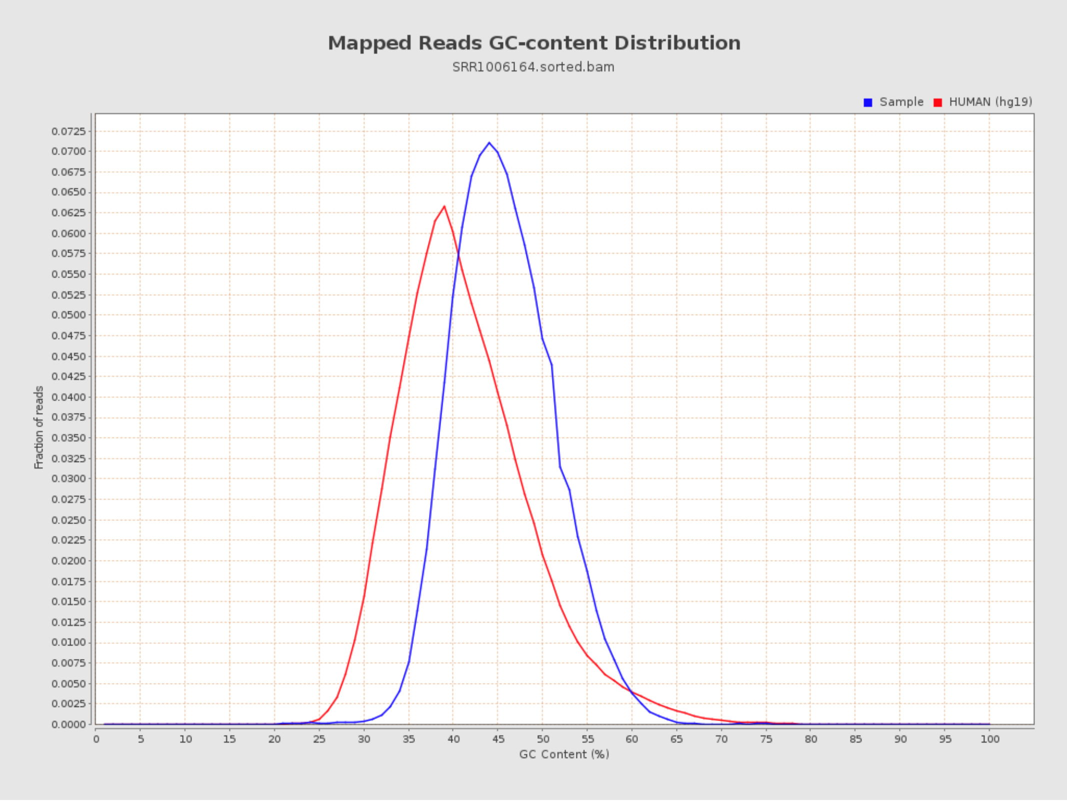
7. Results : Duplication Rate Histogram



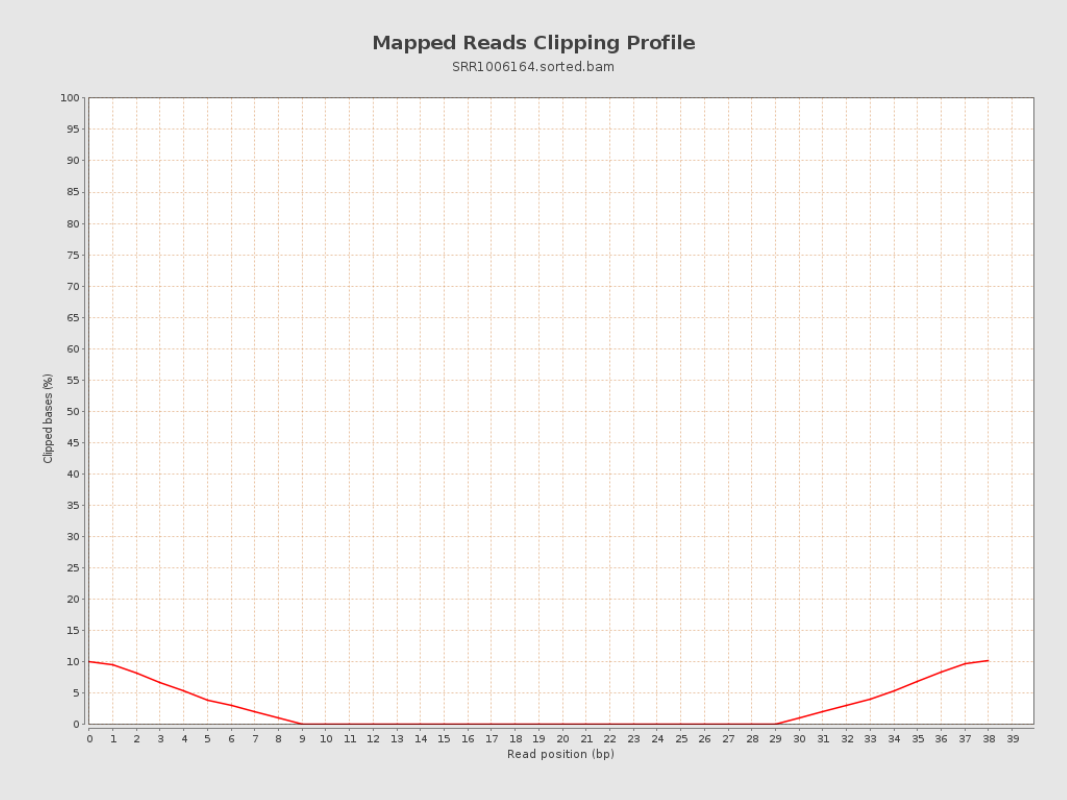
8. Results : Mapped Reads Nucleotide Content



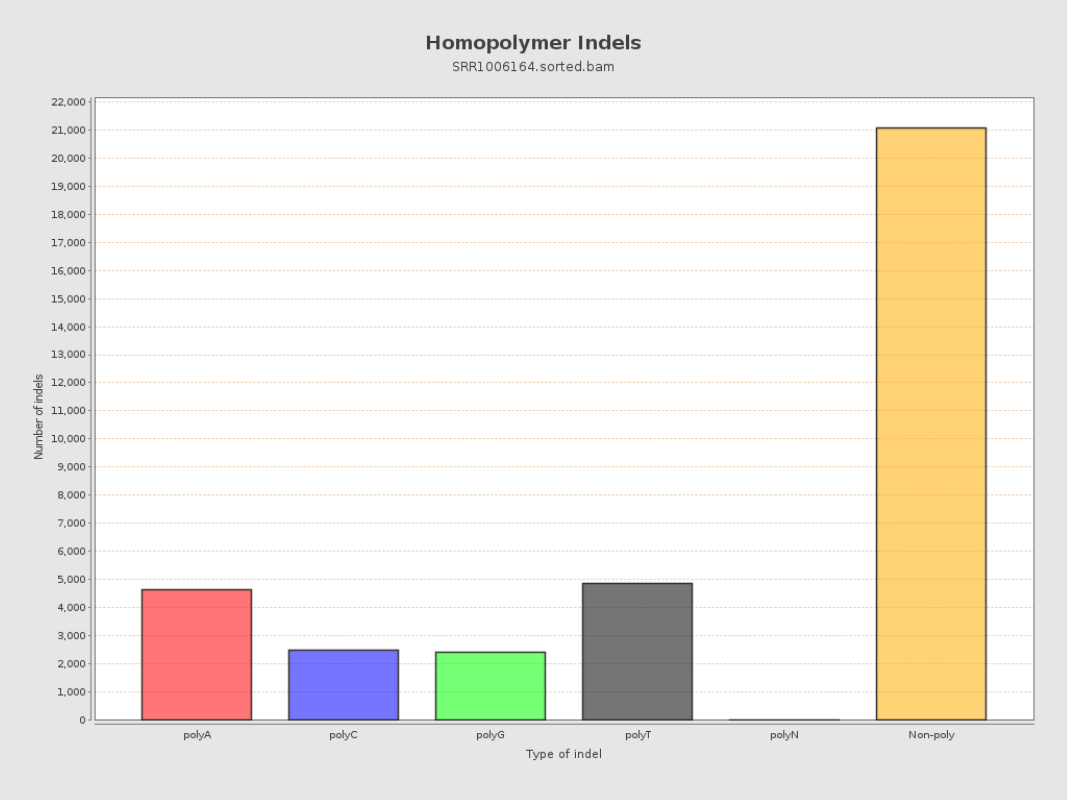
9. Results : Mapped Reads GC-content Distribution



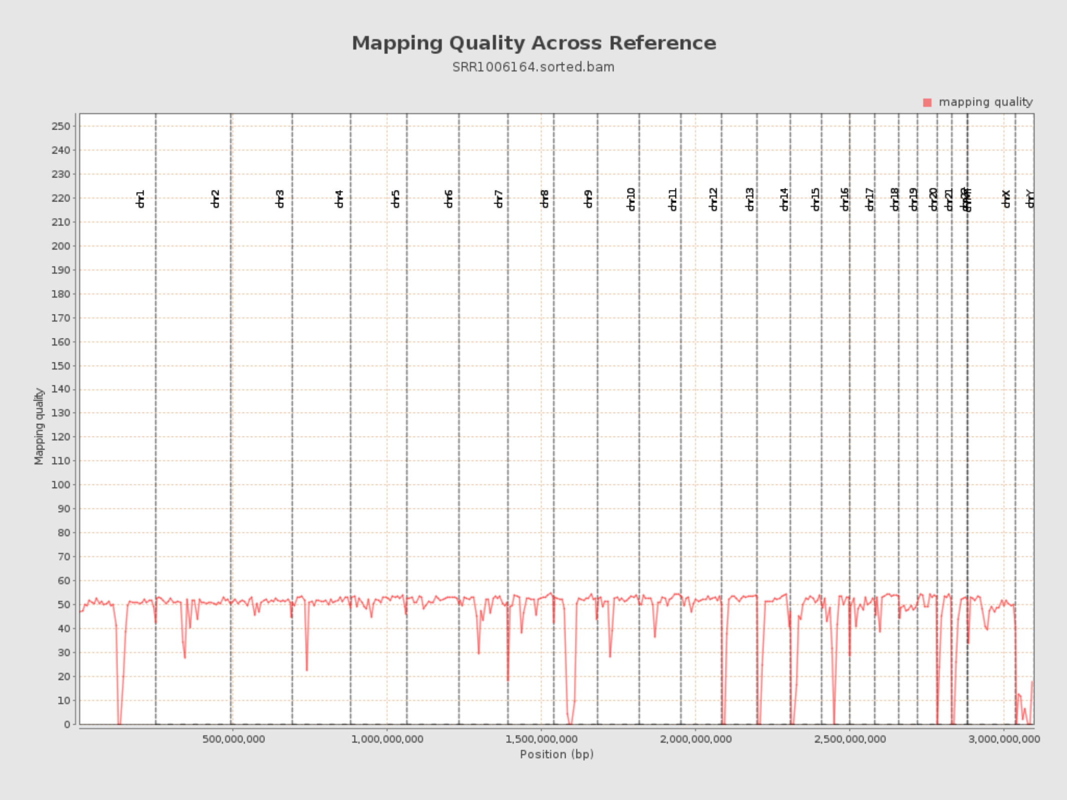
10. Results : Mapped Reads Clipping Profile



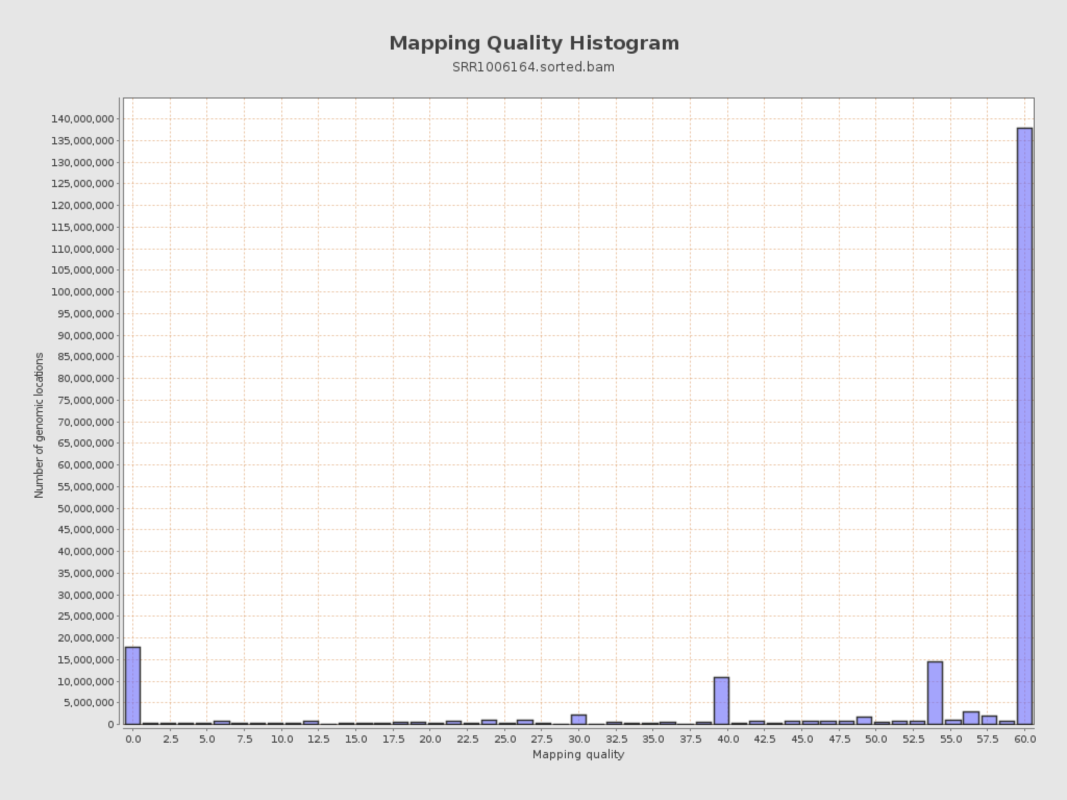
11. Results : Homopolymer Indels



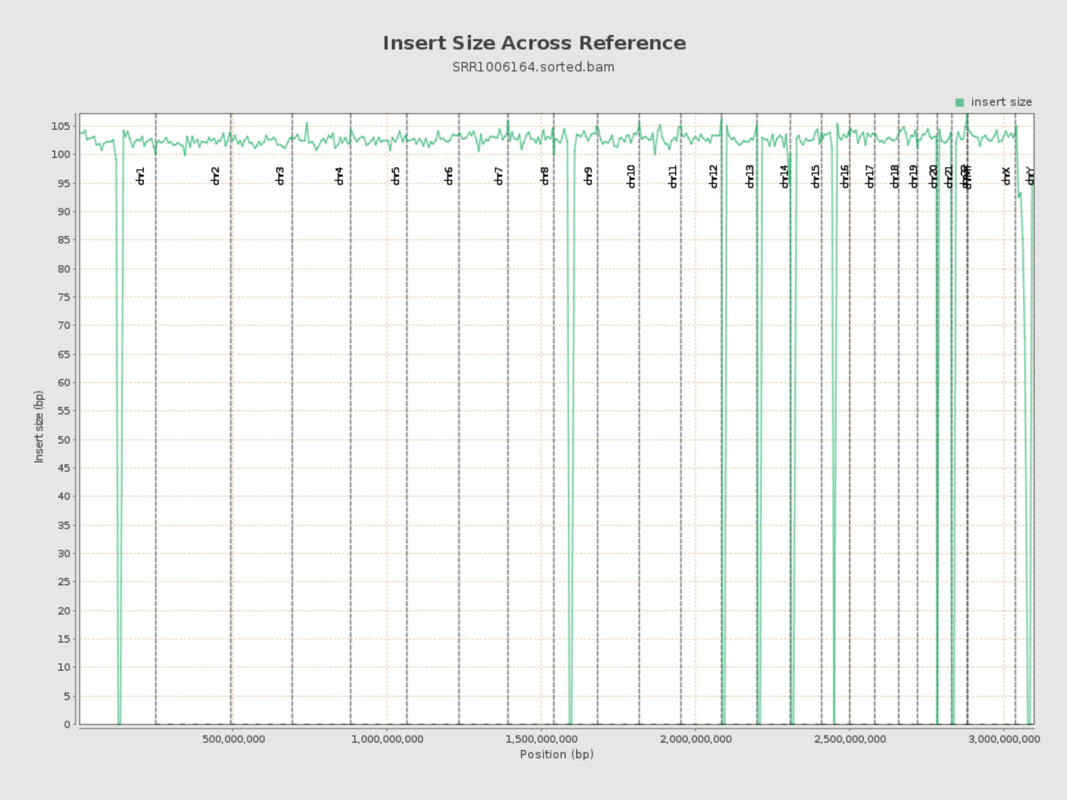
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram