Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:09:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006161.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_SRR1006161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006161_1.fastq.gz SRR1006161_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:09:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,428,862
Mapped reads	4,258,826 / 78.45%
Unmapped reads	1,170,036 / 21.55%
Mapped paired reads	4,258,826 / 78.45%
Mapped reads, first in pair	2,141,764 / 39.45%
Mapped reads, second in pair	2,117,062 / 39%
Mapped reads, both in pair	3,963,970 / 73.02%
Mapped reads, singletons	294,856 / 5.43%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	214,154 / 3.94%
Duplication rate	4.46%
Clipped reads	359,755 / 6.63%

2.2. ACGT Content

Number/percentage of A's	43,459,864 / 26.45%
Number/percentage of C's	37,858,023 / 23.04%
Number/percentage of T's	44,187,002 / 26.89%
Number/percentage of G's	38,785,461 / 23.6%
Number/percentage of N's	22,794 / 0.01%
GC Percentage	46.64%

2.3. Coverage

Mean	0.0531
Standard Deviation	0.4164

2.4. Mapping Quality

Mean Mapping Quality	46.45

2.5. Insert size

Mean	50,363.38
Standard Deviation	2,116,083.03
P25/Median/P75	53 / 73 / 105

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	623,651
Insertions	5,675
Mapped reads with at least one insertion	0.13%
Deletions	14,901
Mapped reads with at least one deletion	0.35%
Homopolymer indels	37.77%

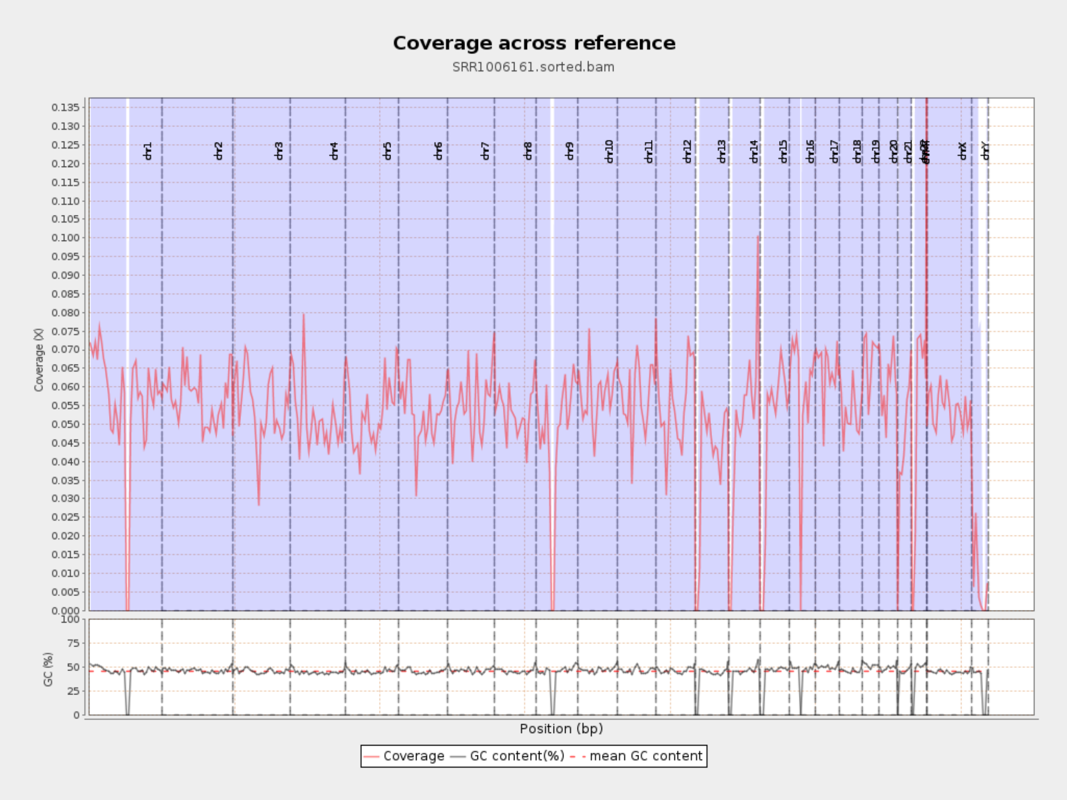
2.7. Chromosome stats

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

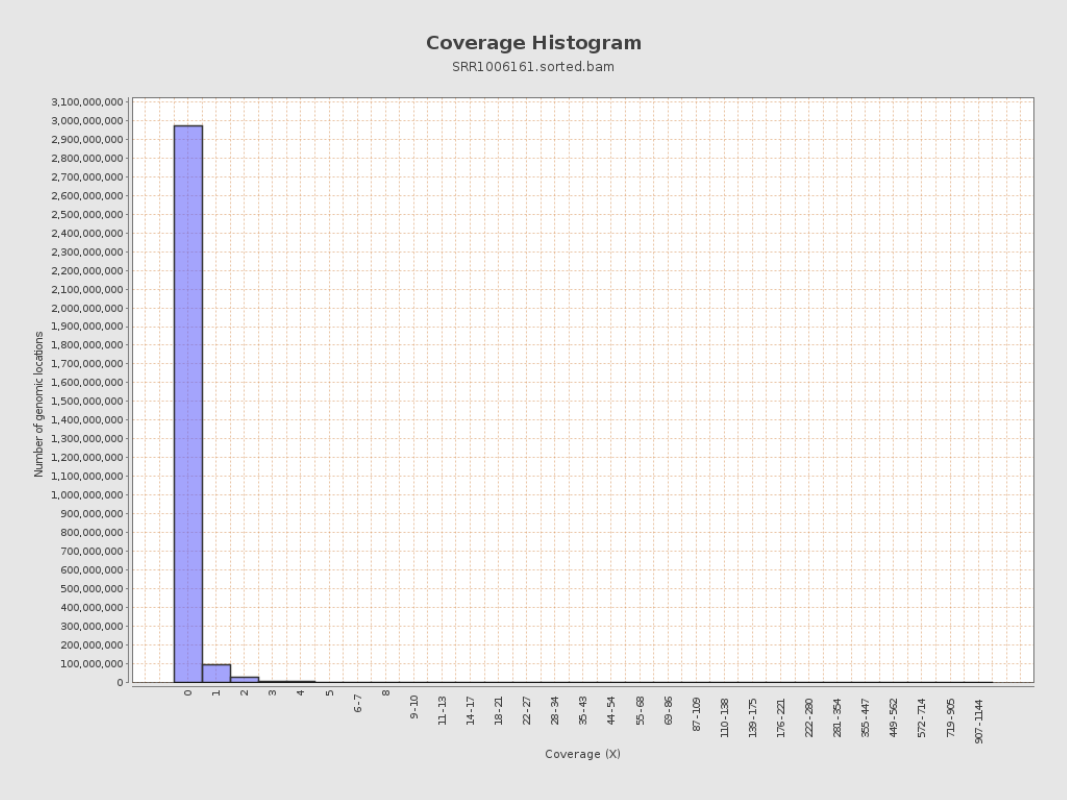
chr1	249250621	13989306	0.0561	0.4122
chr2	243199373	13920852	0.0572	0.3344
chr3	198022430	10787976	0.0545	0.2896
chr4	191154276	9888682	0.0517	0.3127
chr5	180915260	9550879	0.0528	0.2891
chr6	171115067	9125668	0.0533	0.3015
chr7	159138663	8750531	0.055	0.3593
chr8	146364022	7826822	0.0535	0.5415
chr9	141213431	6569474	0.0465	0.2941
chr10	135534747	7793984	0.0575	0.3666
chr11	135006516	7774263	0.0576	0.3229
chr12	133851895	7391593	0.0552	0.298
chr13	115169878	4659052	0.0405	0.253
chr14	107349540	5325733	0.0496	1.3252
chr15	102531392	4917737	0.048	0.2769
chr16	90354753	5333974	0.059	0.3264
chr17	81195210	5242149	0.0646	0.3286
chr18	78077248	4161445	0.0533	0.3801
chr19	59128983	3993510	0.0675	0.3987
chr20	63025520	3833670	0.0608	0.3285
chr21	48129895	2139935	0.0445	0.3142
chr22	51304566	2505354	0.0488	0.4497
chrMT	16571	3107	0.1875	0.5328
chrX	155270560	8382992	0.054	0.2972

chrY	59373566	464290	0.0078	0.2083

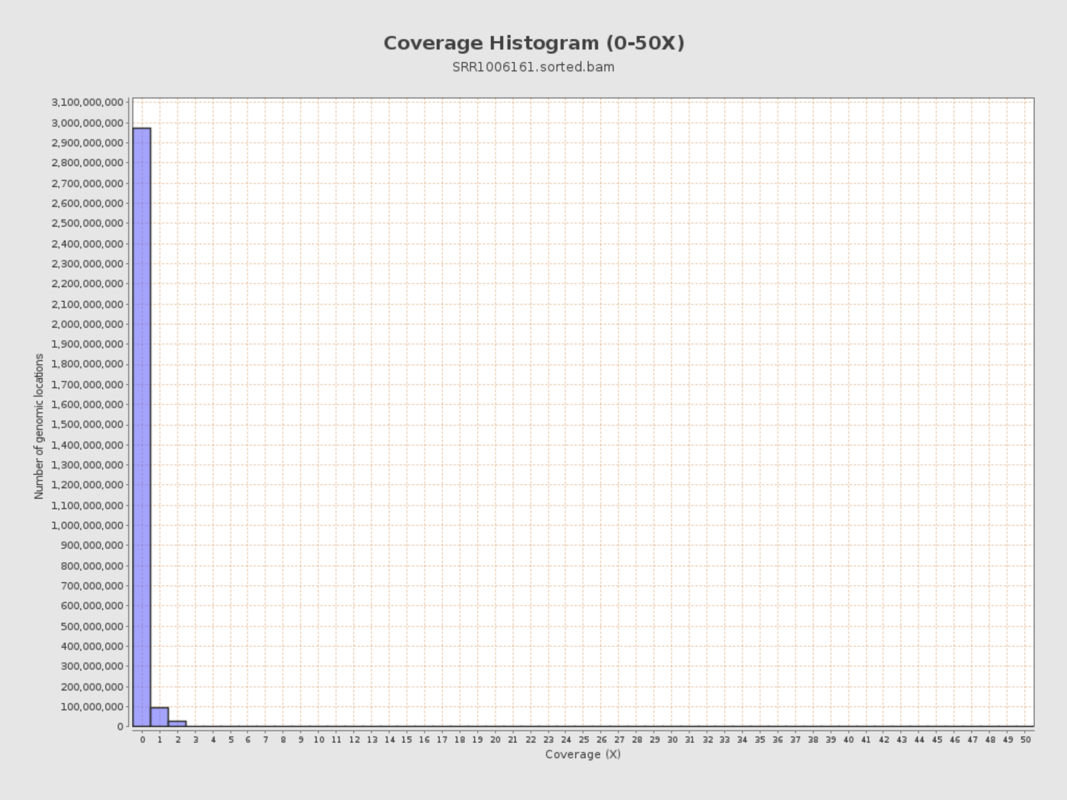
3. Results : Coverage across reference



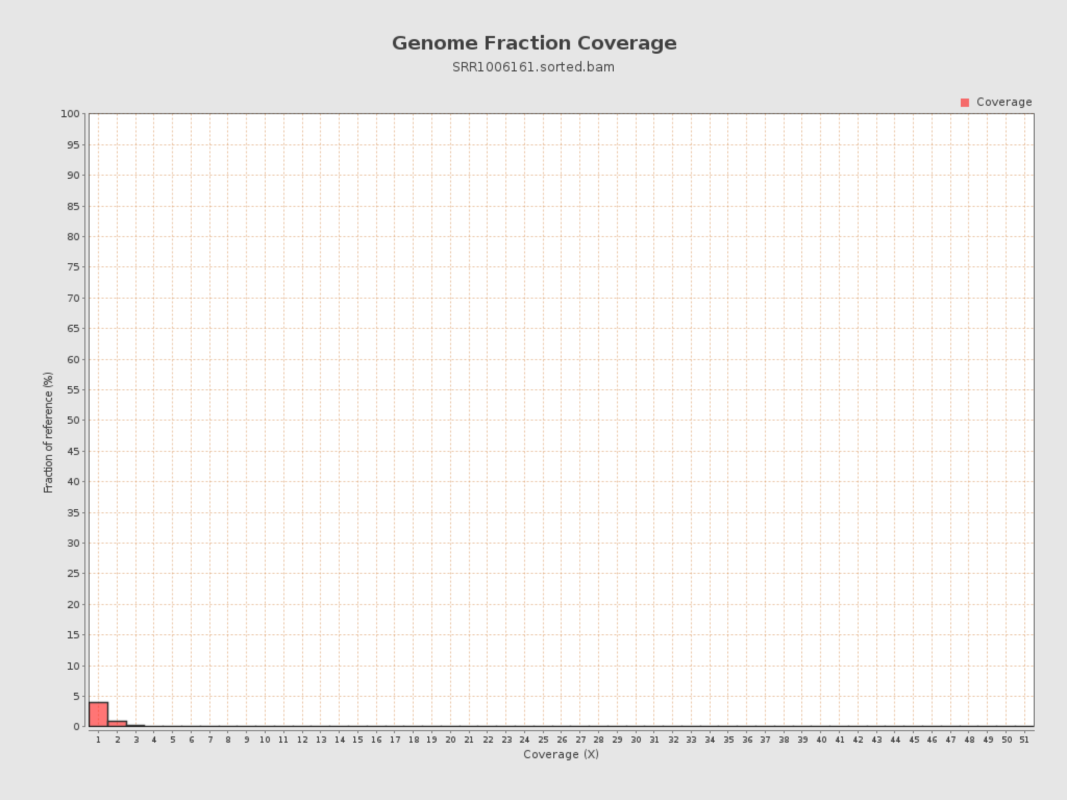
4. Results : Coverage Histogram



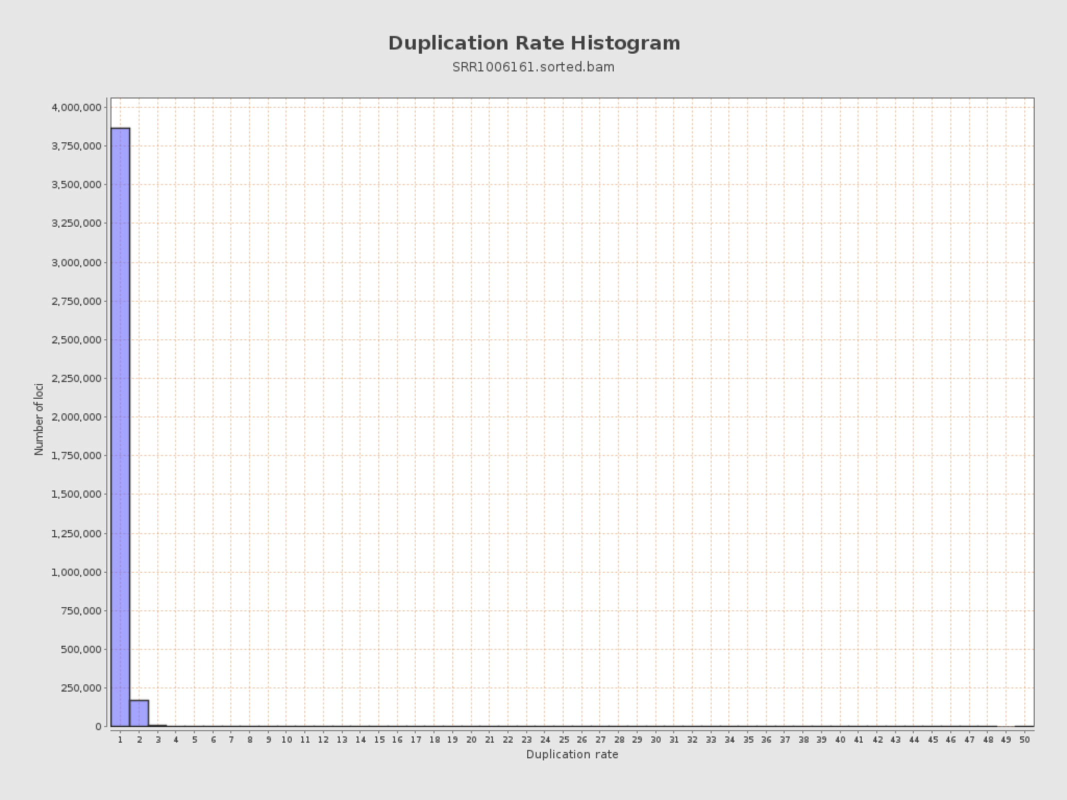
5. Results : Coverage Histogram (0-50X)



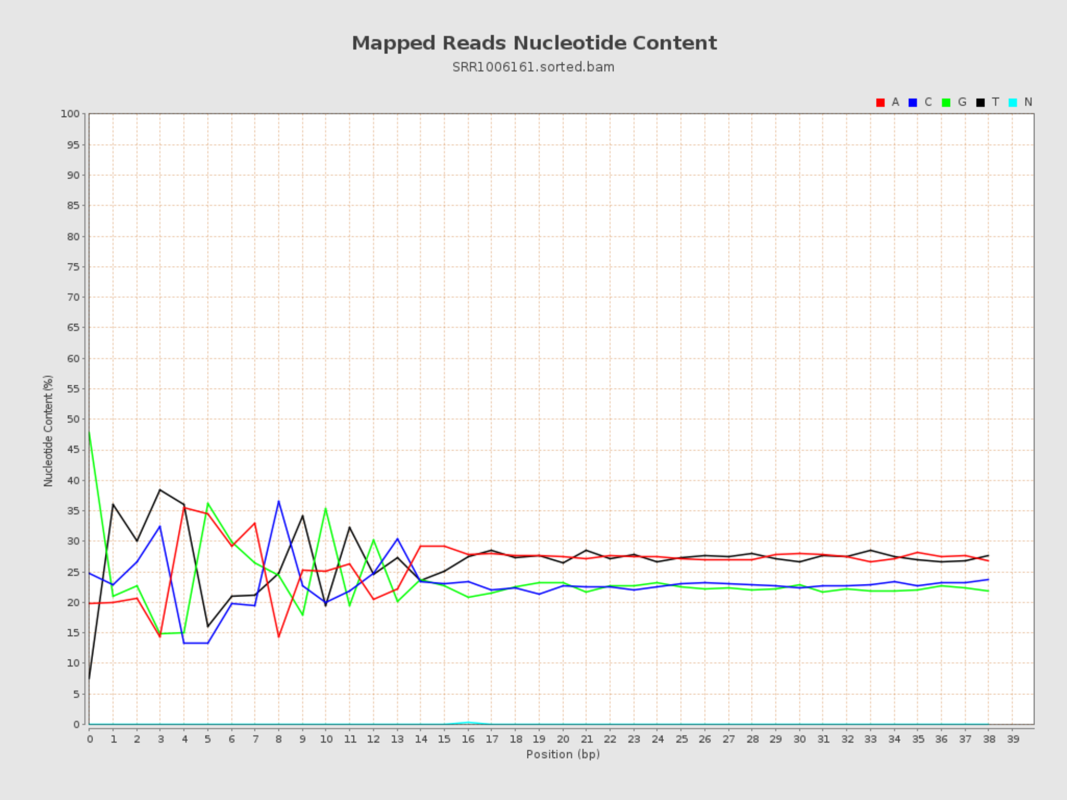
6. Results : Genome Fraction Coverage



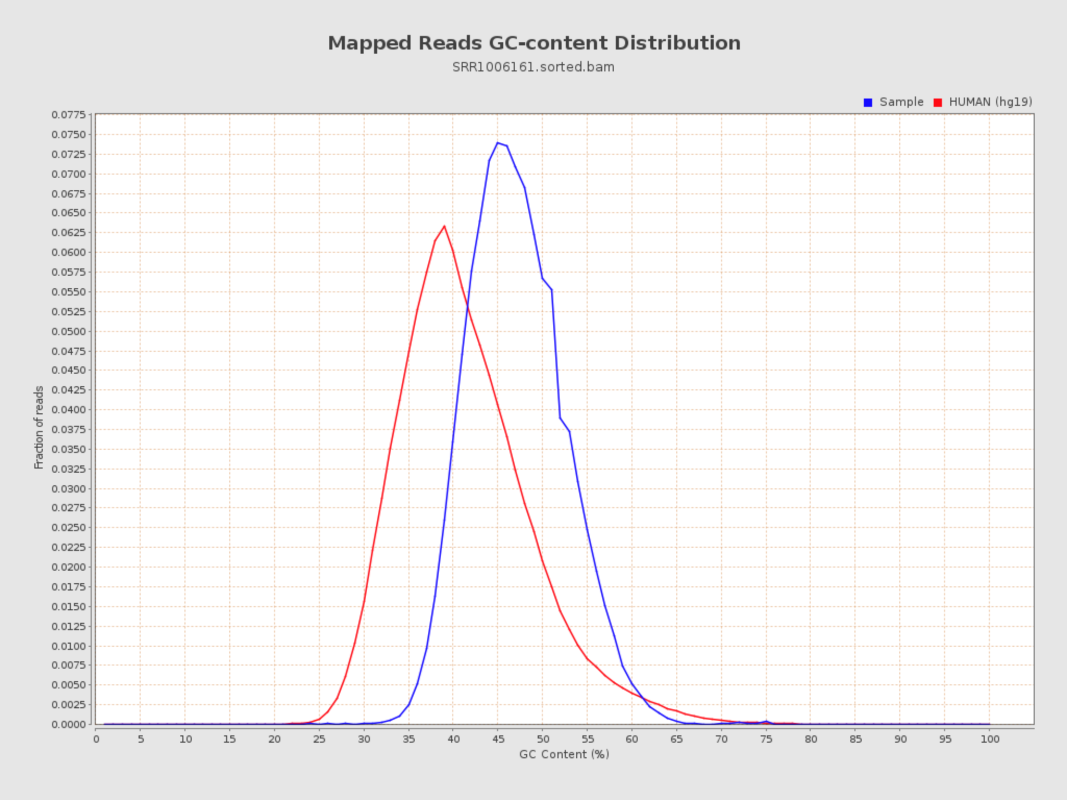
7. Results : Duplication Rate Histogram



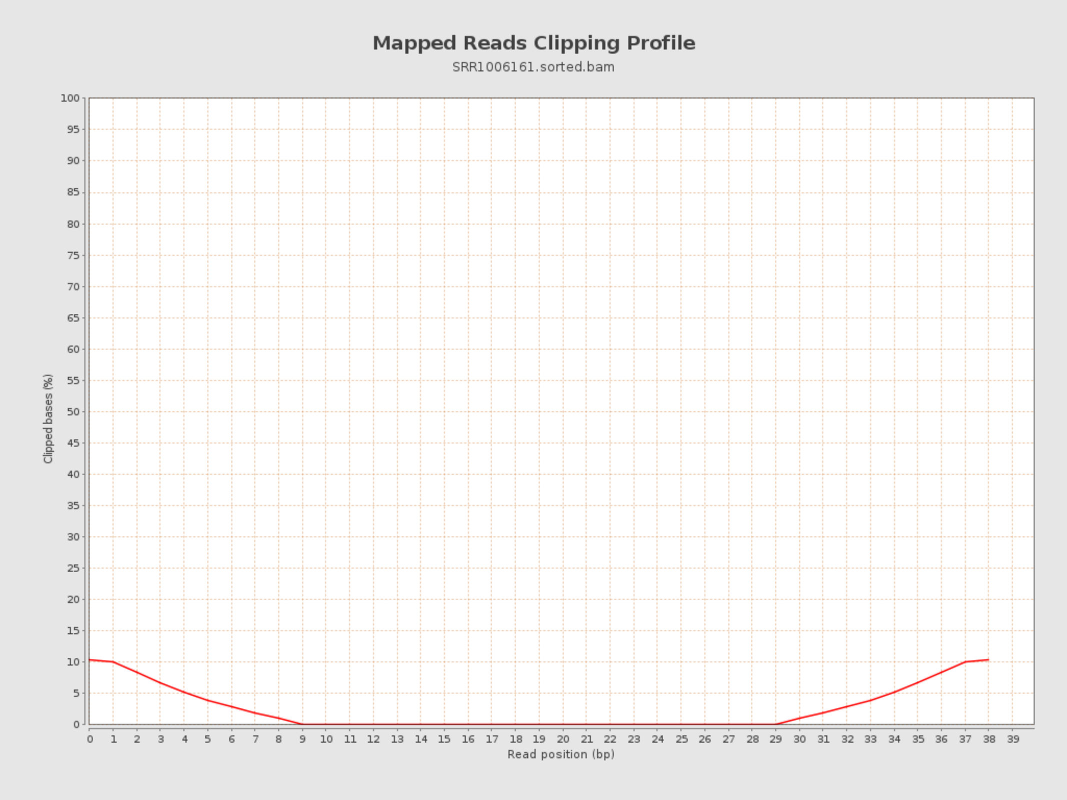
8. Results : Mapped Reads Nucleotide Content



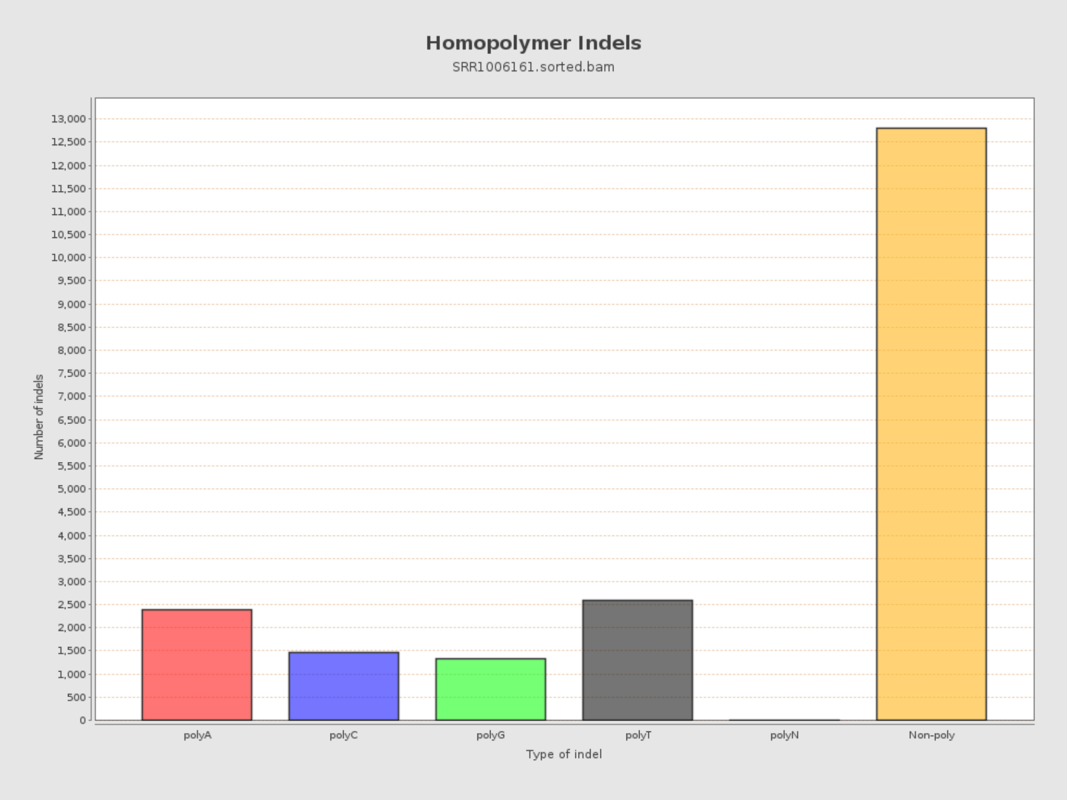
9. Results : Mapped Reads GC-content Distribution



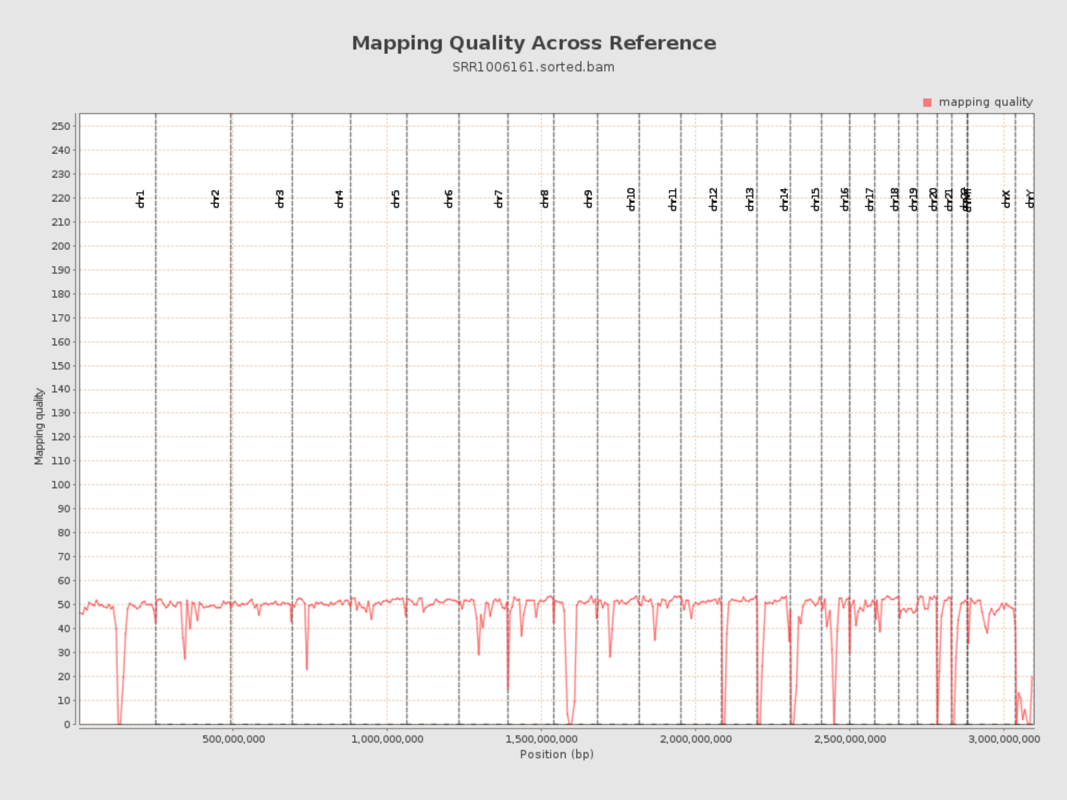
10. Results : Mapped Reads Clipping Profile



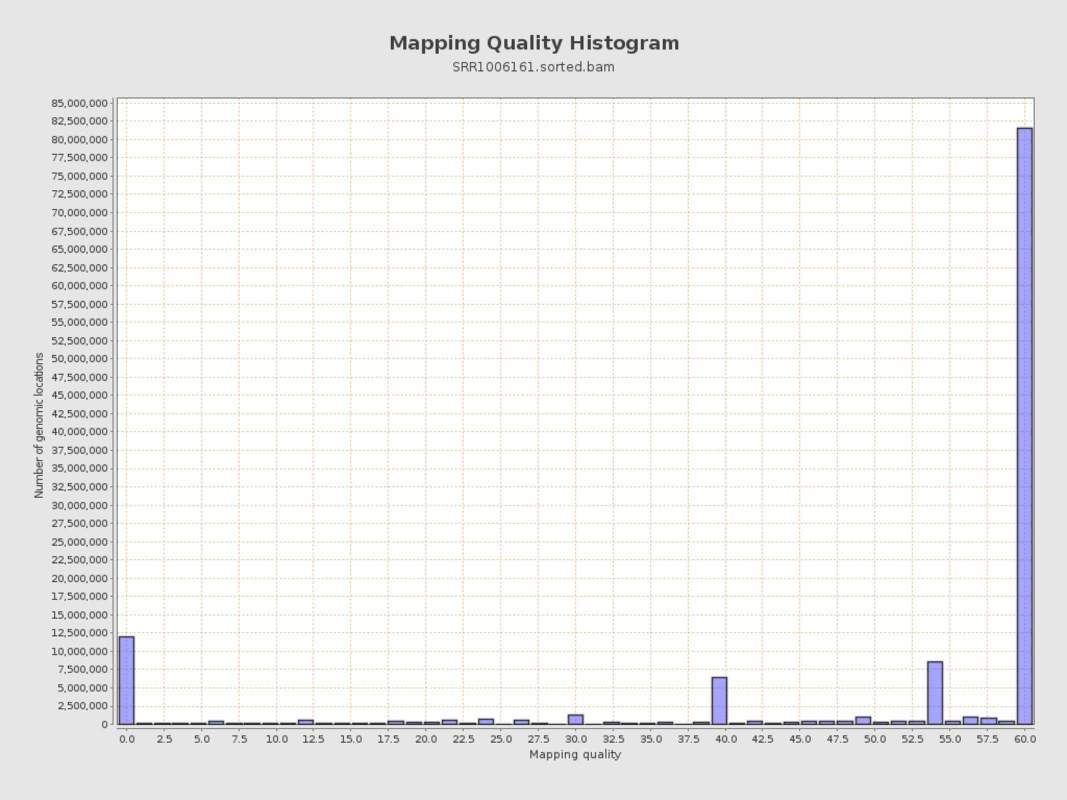
11. Results : Homopolymer Indels



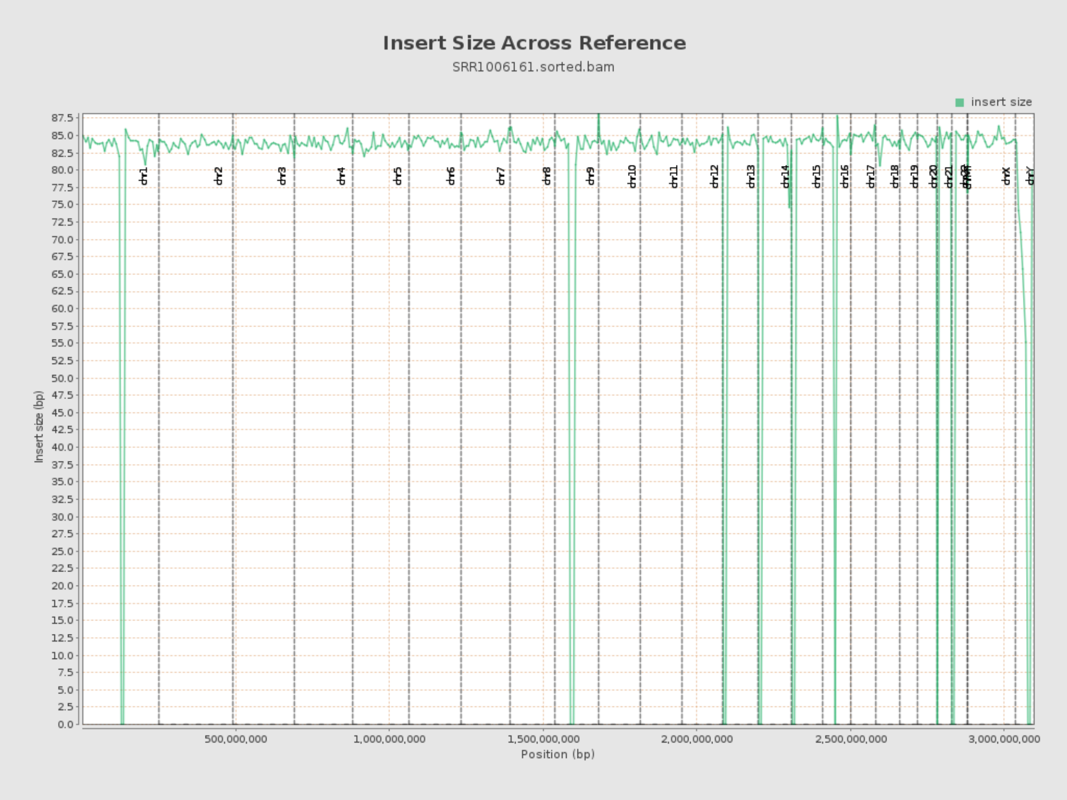
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram