Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 13:51:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006019.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_SRR1006019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006019_1.fastq.gz SRR1006019_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 13:51:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,148,626
Mapped reads	8,196,723 / 73.52%
Unmapped reads	2,951,903 / 26.48%
Mapped paired reads	8,196,723 / 73.52%
Mapped reads, first in pair	4,125,727 / 37.01%
Mapped reads, second in pair	4,070,996 / 36.52%
Mapped reads, both in pair	7,433,808 / 66.68%
Mapped reads, singletons	762,915 / 6.84%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	283,027 / 2.54%
Duplication rate	2.85%
Clipped reads	661,444 / 5.93%

2.2. ACGT Content

Number/percentage of A's	90,124,430 / 28.48%
Number/percentage of C's	66,920,987 / 21.14%
Number/percentage of T's	91,412,469 / 28.88%
Number/percentage of G's	67,986,452 / 21.48%
Number/percentage of N's	43,006 / 0.01%
GC Percentage	42.63%

2.3. Coverage

Mean	0.1022
Standard Deviation	0.5498

2.4. Mapping Quality

Mean Mapping Quality	46.68

2.5. Insert size

Mean	60,190.24
Standard Deviation	2,380,532.98
P25/Median/P75	54 / 72 / 101

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	1,628,572
Insertions	9,870
Mapped reads with at least one insertion	0.12%
Deletions	29,838
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.75%

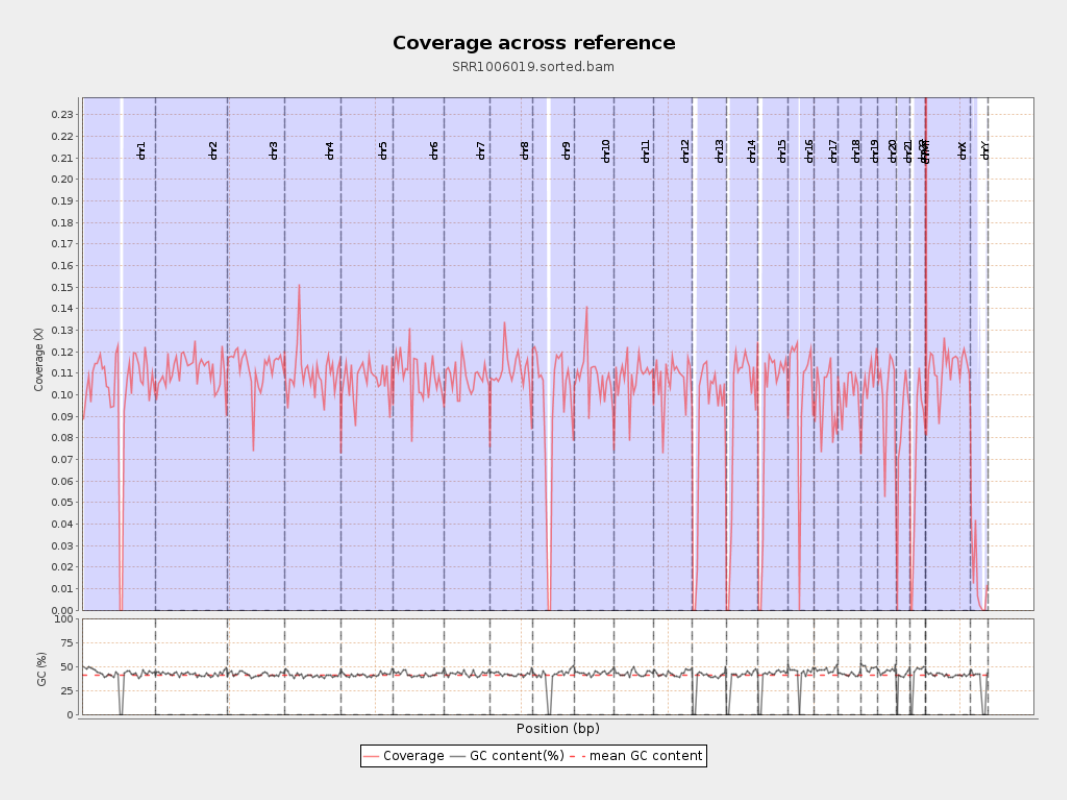
2.7. Chromosome stats

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

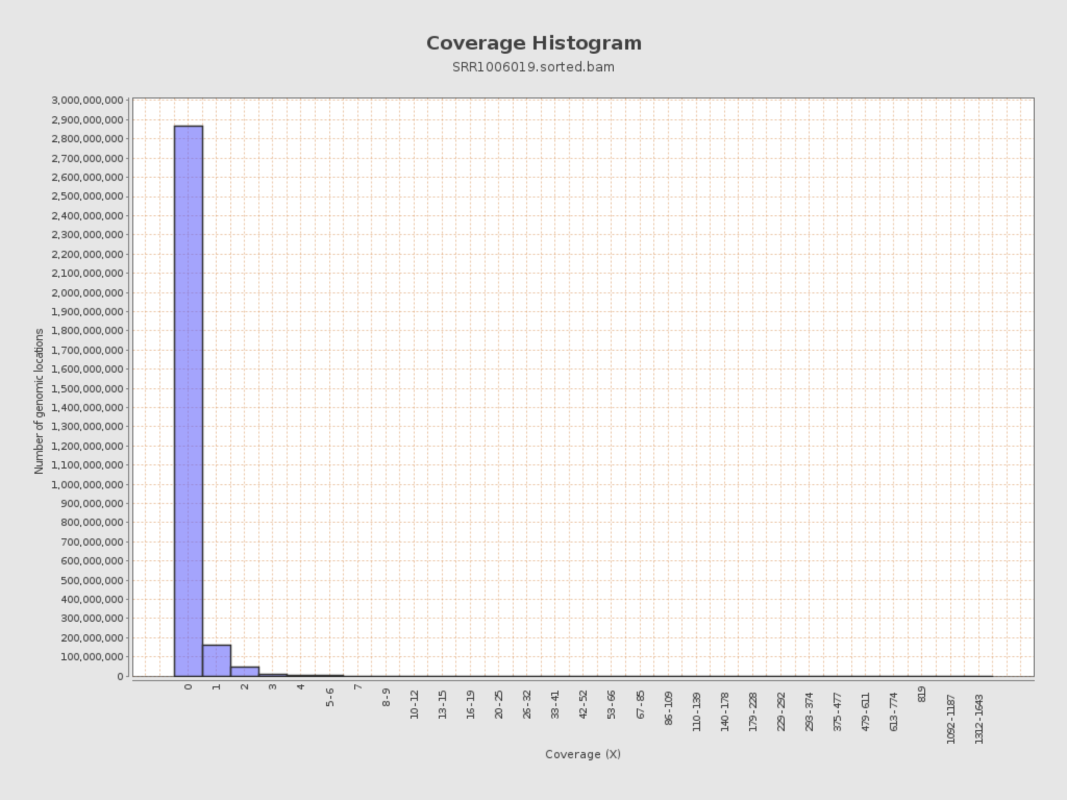
chr1	249250621	25282086	0.1014	0.7458
chr2	243199373	27069921	0.1113	0.546
chr3	198022430	22240511	0.1123	0.4297
chr4	191154276	21118010	0.1105	0.4789
chr5	180915260	19350309	0.107	0.4195
chr6	171115067	18638856	0.1089	0.6076
chr7	159138663	17150313	0.1078	0.6758
chr8	146364022	16173759	0.1105	0.9251
chr9	141213431	13269499	0.094	0.4649
chr10	135534747	14716528	0.1086	0.6246
chr11	135006516	14537849	0.1077	0.487
chr12	133851895	14325764	0.107	0.4226
chr13	115169878	10039221	0.0872	0.378
chr14	107349540	9892407	0.0922	0.4128
chr15	102531392	9284277	0.0906	0.3884
chr16	90354753	9175436	0.1015	0.467
chr17	81195210	7975831	0.0982	0.4139
chr18	78077248	7881732	0.1009	0.6555
chr19	59128983	6312102	0.1068	0.7004
chr20	63025520	6312104	0.1002	0.4254
chr21	48129895	4020956	0.0835	0.4229
chr22	51304566	3543680	0.0691	0.3675
chrMT	16571	28543	1.7225	2.2054
chrX	155270560	17393145	0.112	0.4621

chrY	59373566	792731	0.0134	0.2817

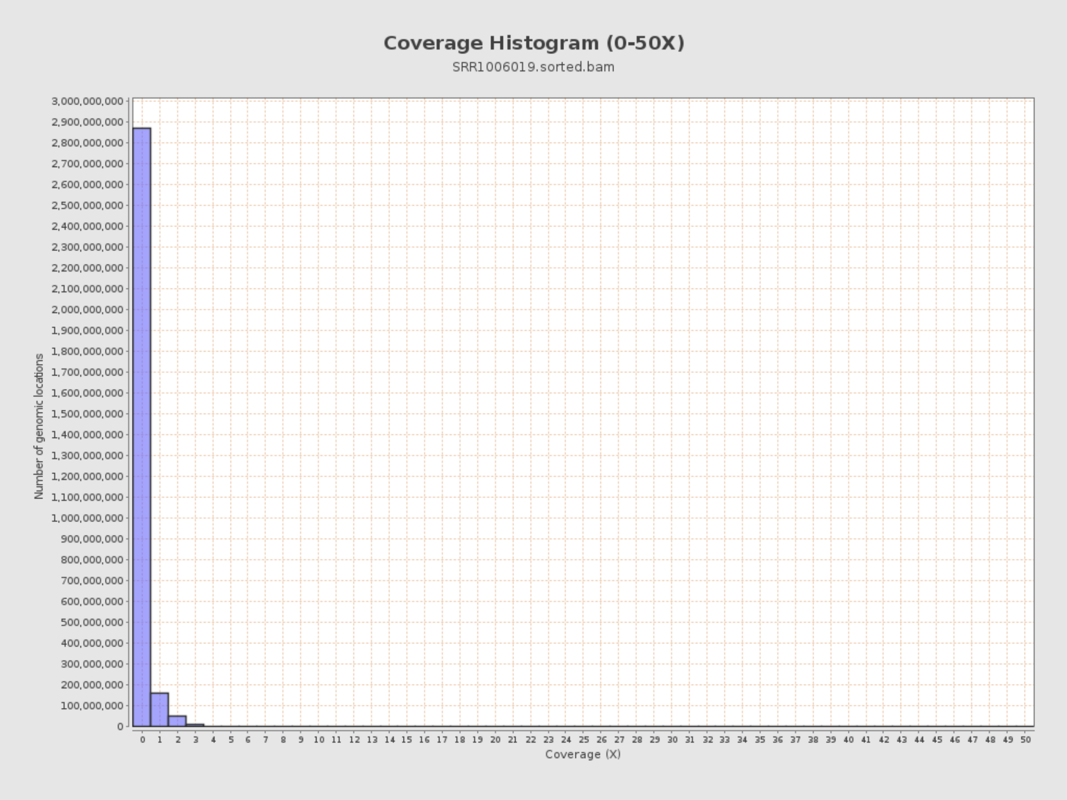
3. Results : Coverage across reference



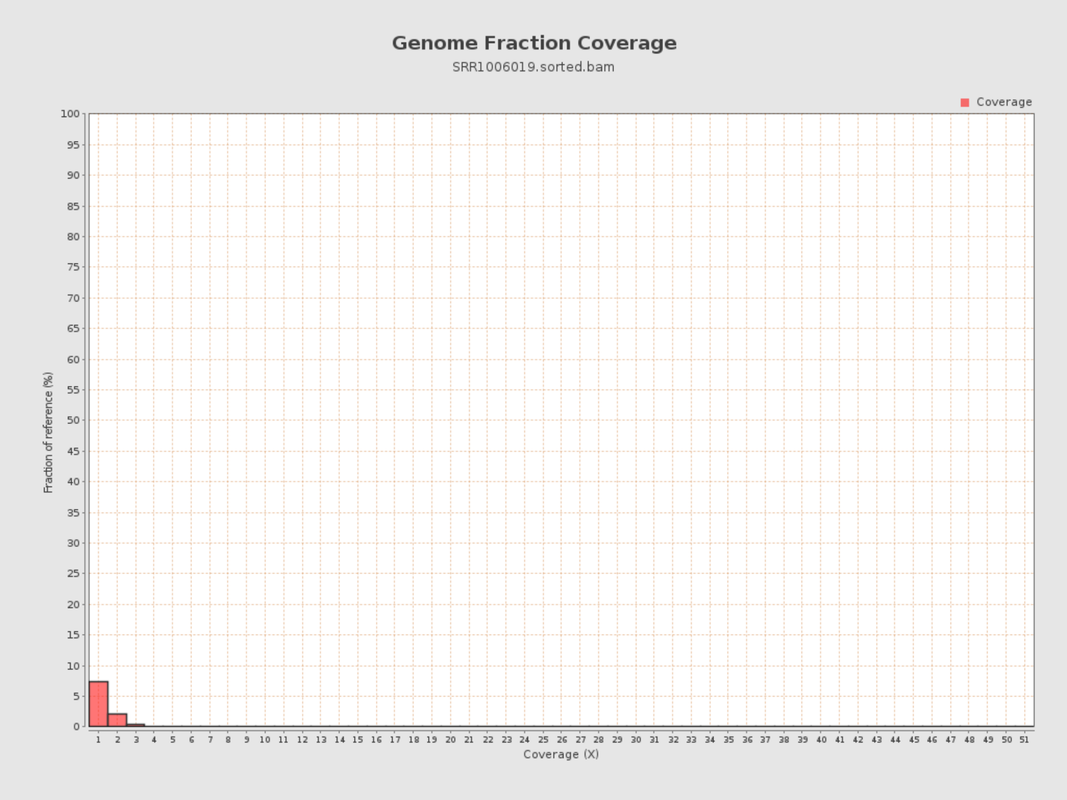
4. Results : Coverage Histogram



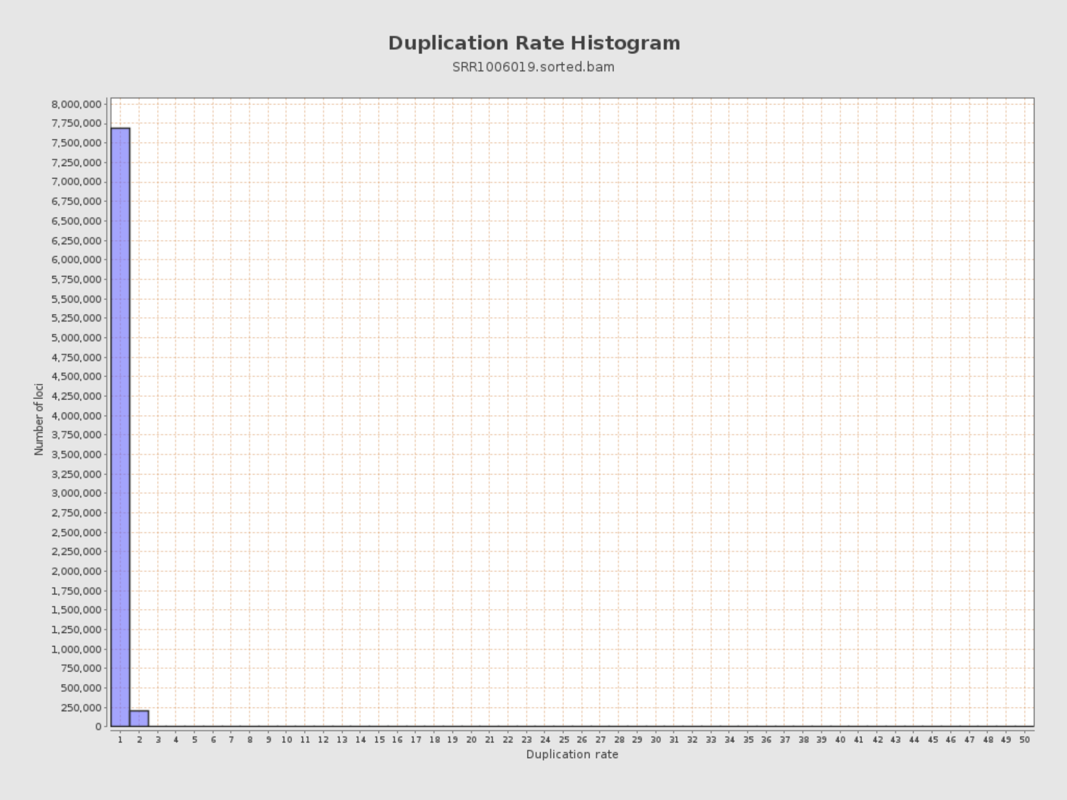
5. Results : Coverage Histogram (0-50X)



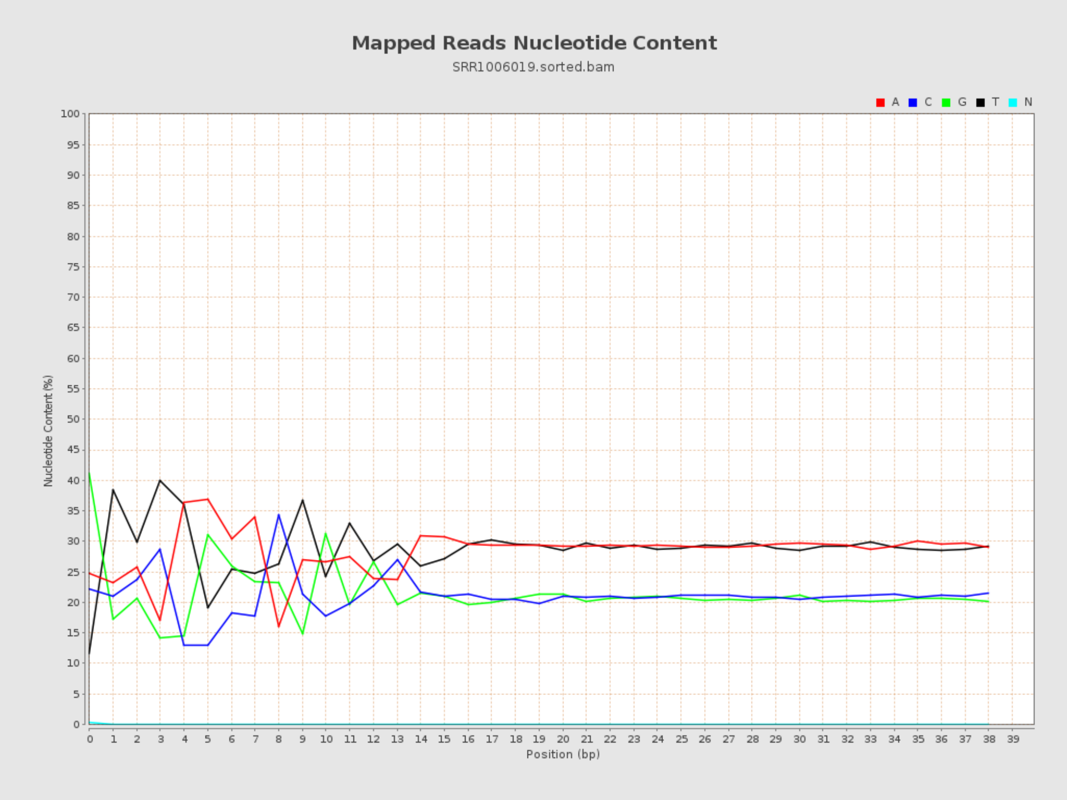
6. Results : Genome Fraction Coverage



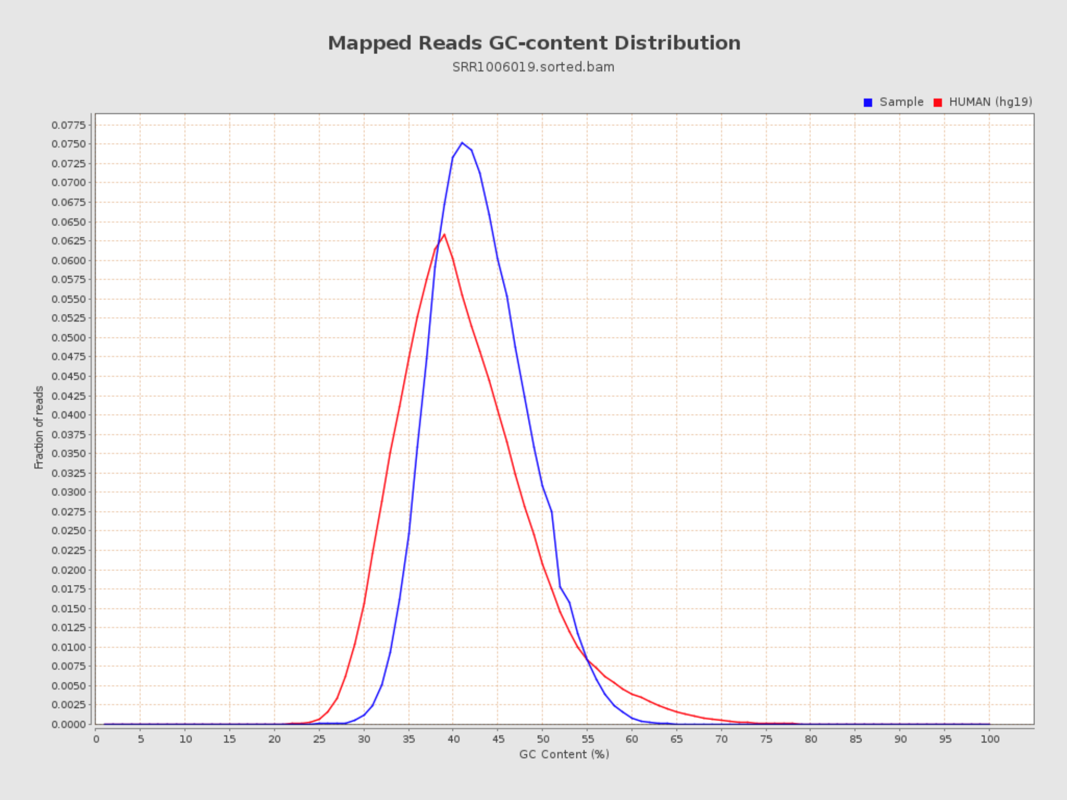
7. Results : Duplication Rate Histogram



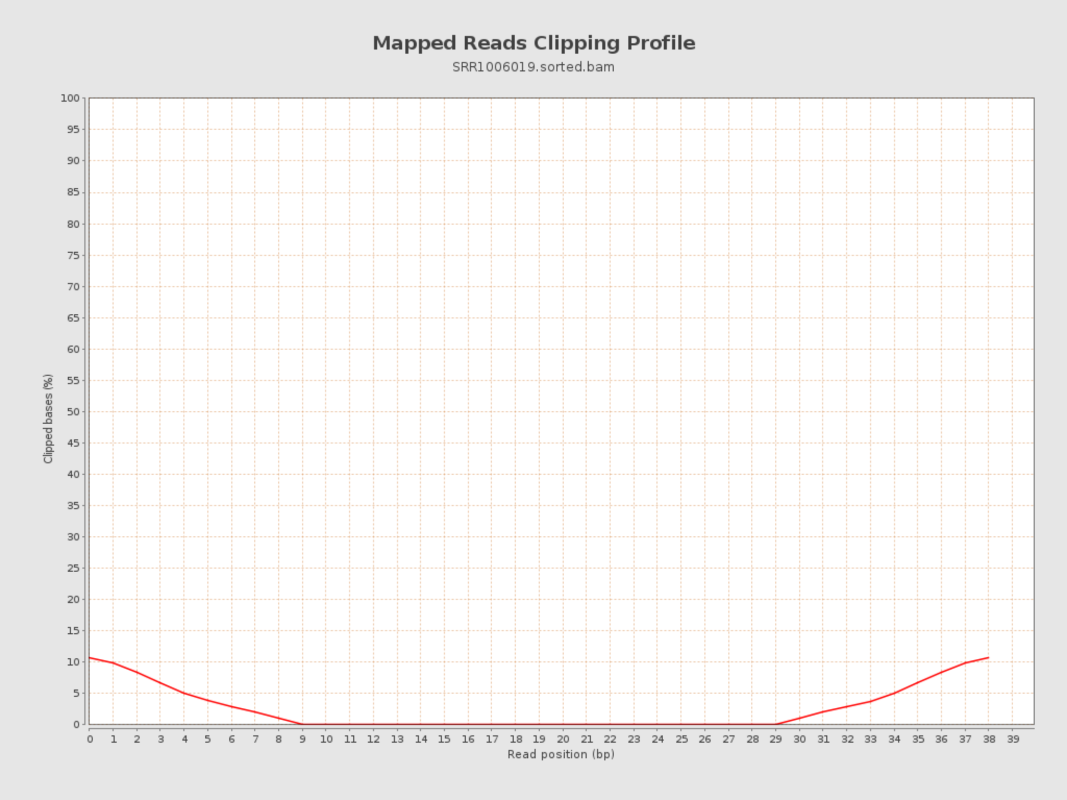
8. Results : Mapped Reads Nucleotide Content



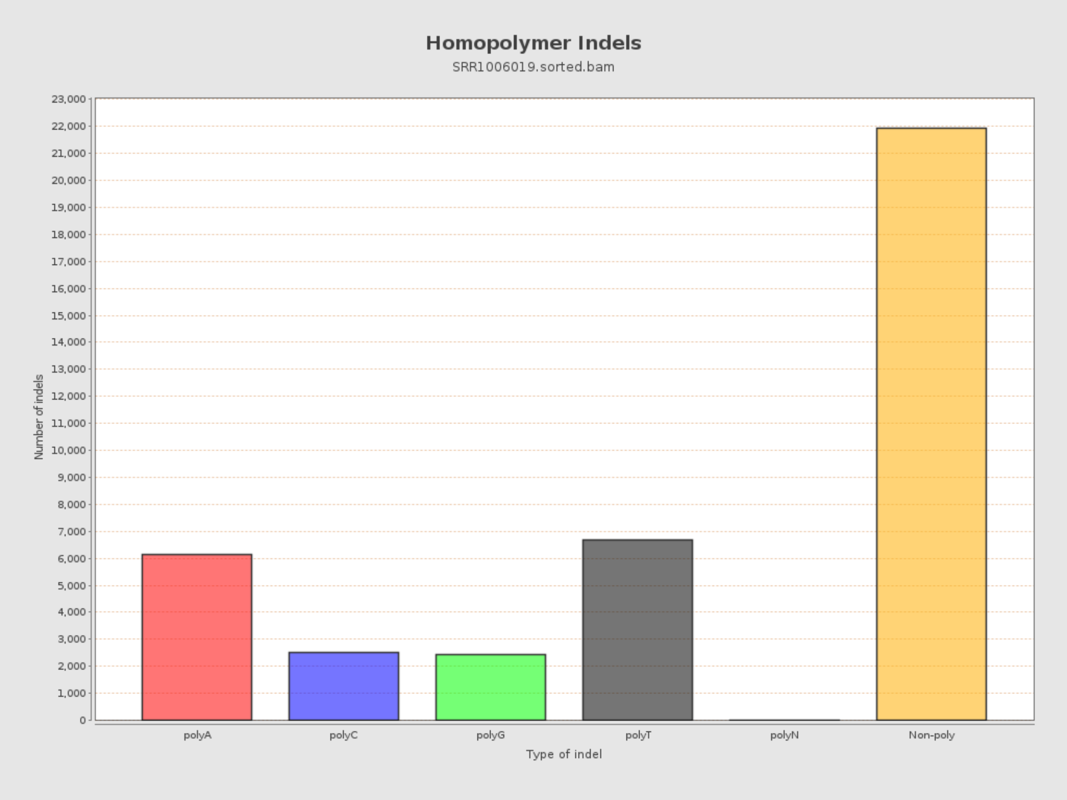
9. Results : Mapped Reads GC-content Distribution



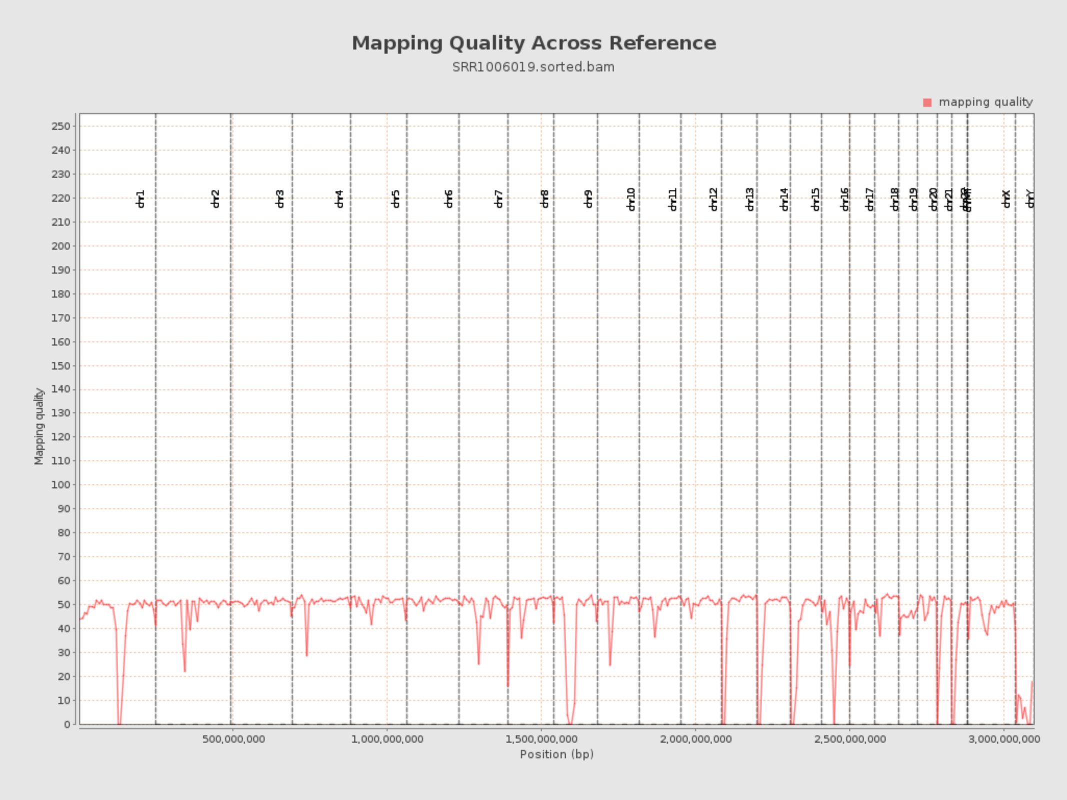
10. Results : Mapped Reads Clipping Profile



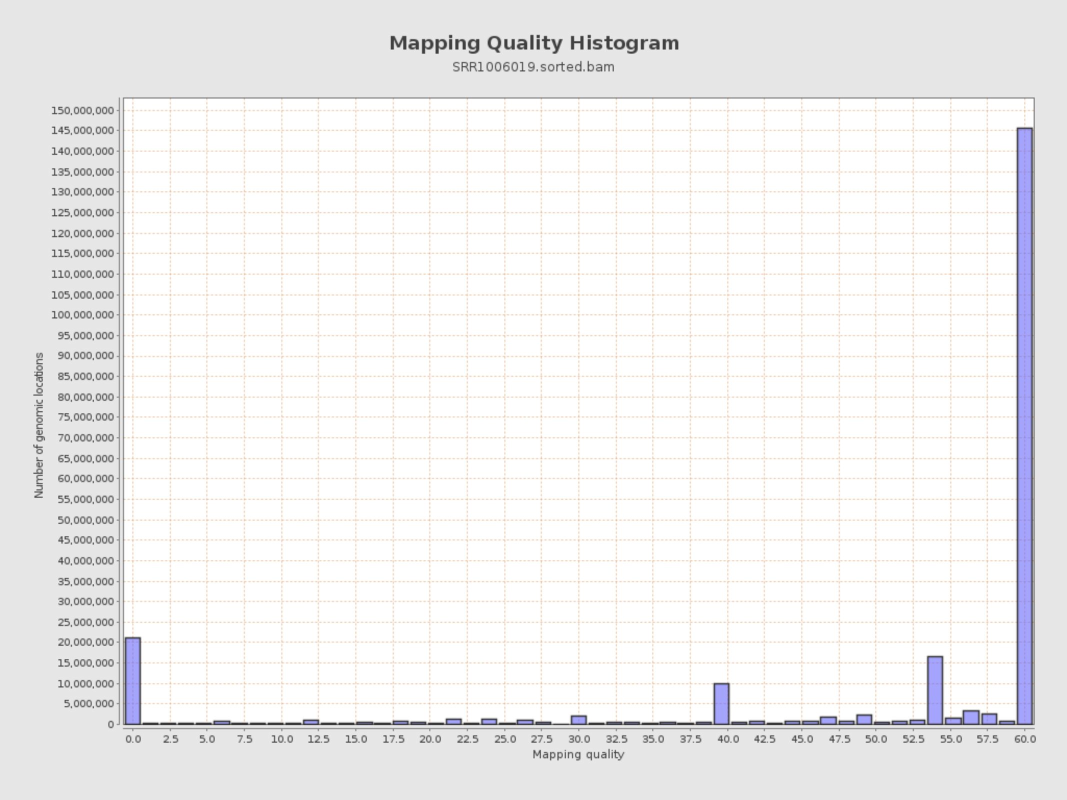
11. Results : Homopolymer Indels



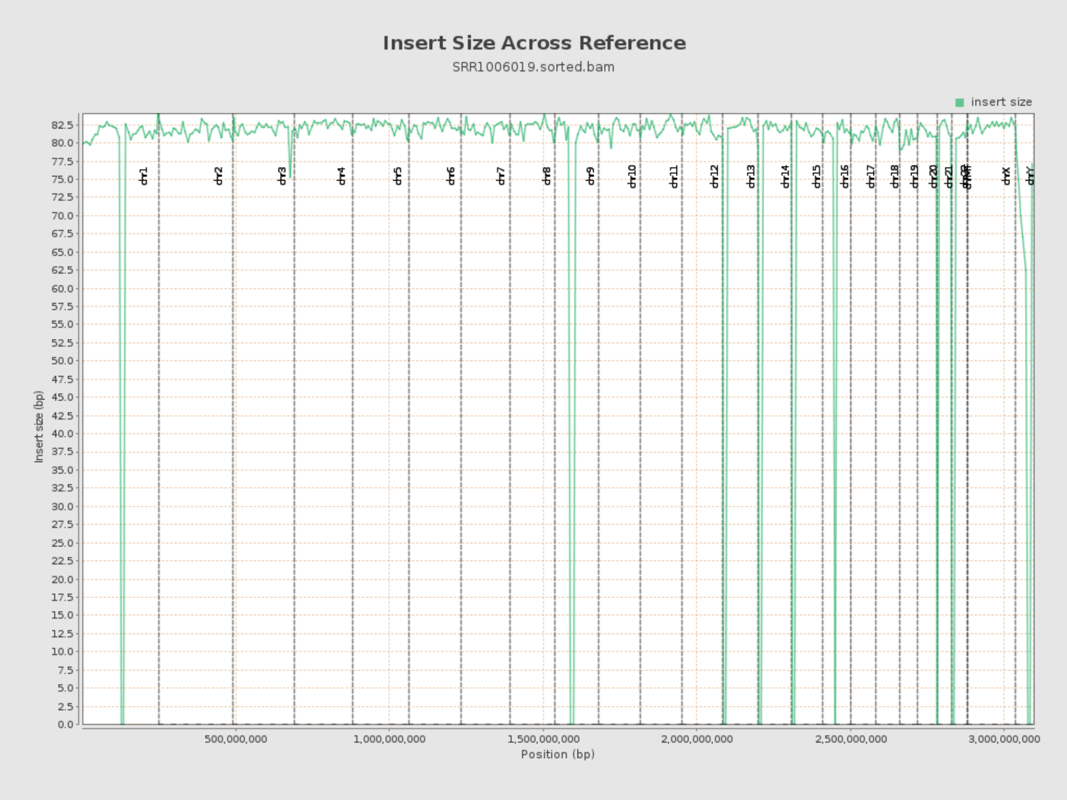
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram