Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:51:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006186.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_SRR1006186 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006186_1.fastq.gz SRR1006186_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:51:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006186.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	927,350
Mapped reads	830,777 / 89.59%
Unmapped reads	96,573 / 10.41%
Mapped paired reads	830,777 / 89.59%
Mapped reads, first in pair	416,301 / 44.89%
Mapped reads, second in pair	414,476 / 44.69%
Mapped reads, both in pair	775,308 / 83.6%
Mapped reads, singletons	55,469 / 5.98%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	13,867 / 1.5%
Duplication rate	1.55%
Clipped reads	39,932 / 4.31%

2.2. ACGT Content

Number/percentage of A's	8,755,725 / 27.2%
Number/percentage of C's	7,111,400 / 22.09%
Number/percentage of T's	8,959,771 / 27.83%
Number/percentage of G's	7,362,113 / 22.87%
Number/percentage of N's	1,216 / 0%
GC Percentage	44.96%

2.3. Coverage

Mean	0.0104
Standard Deviation	0.1124

2.4. Mapping Quality

Mean Mapping Quality	48.22

2.5. Insert size

Mean	59,448.49
Standard Deviation	2,310,158.46
P25/Median/P75	103 / 138 / 183

2.6. Mismatches and indels

General error rate	0.29%
Mismatches	90,968
Insertions	883
Mapped reads with at least one insertion	0.11%
Deletions	2,996
Mapped reads with at least one deletion	0.36%
Homopolymer indels	43.49%

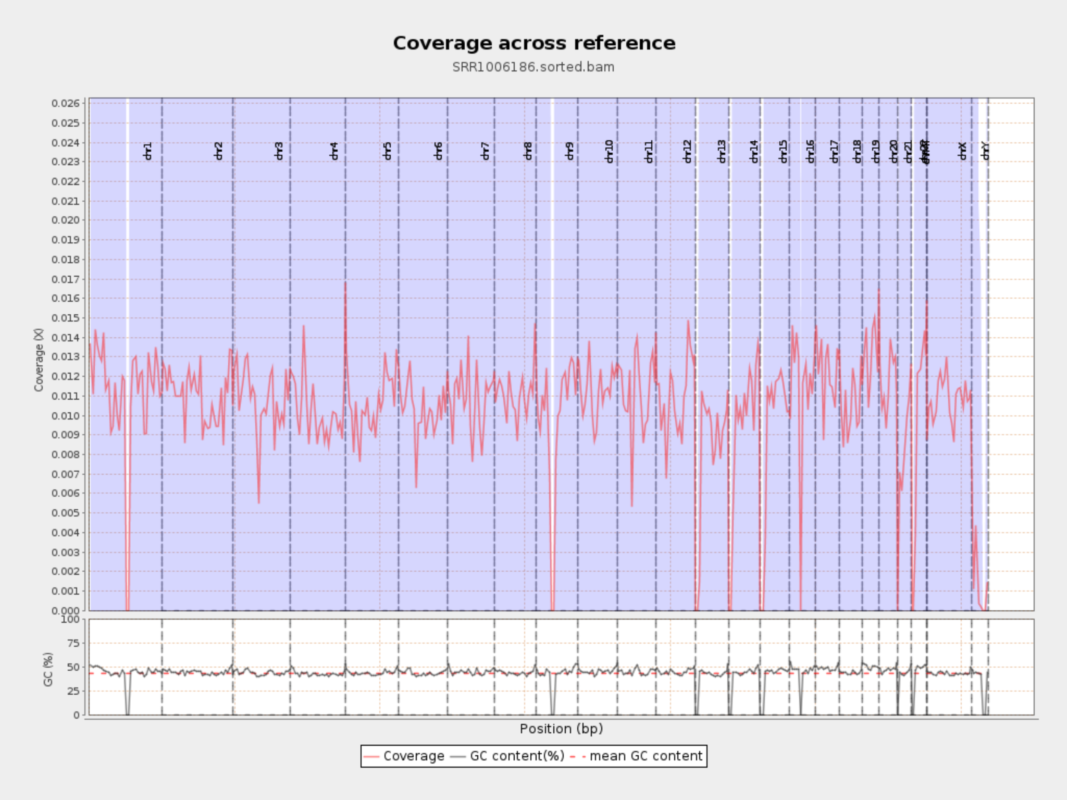
2.7. Chromosome stats

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

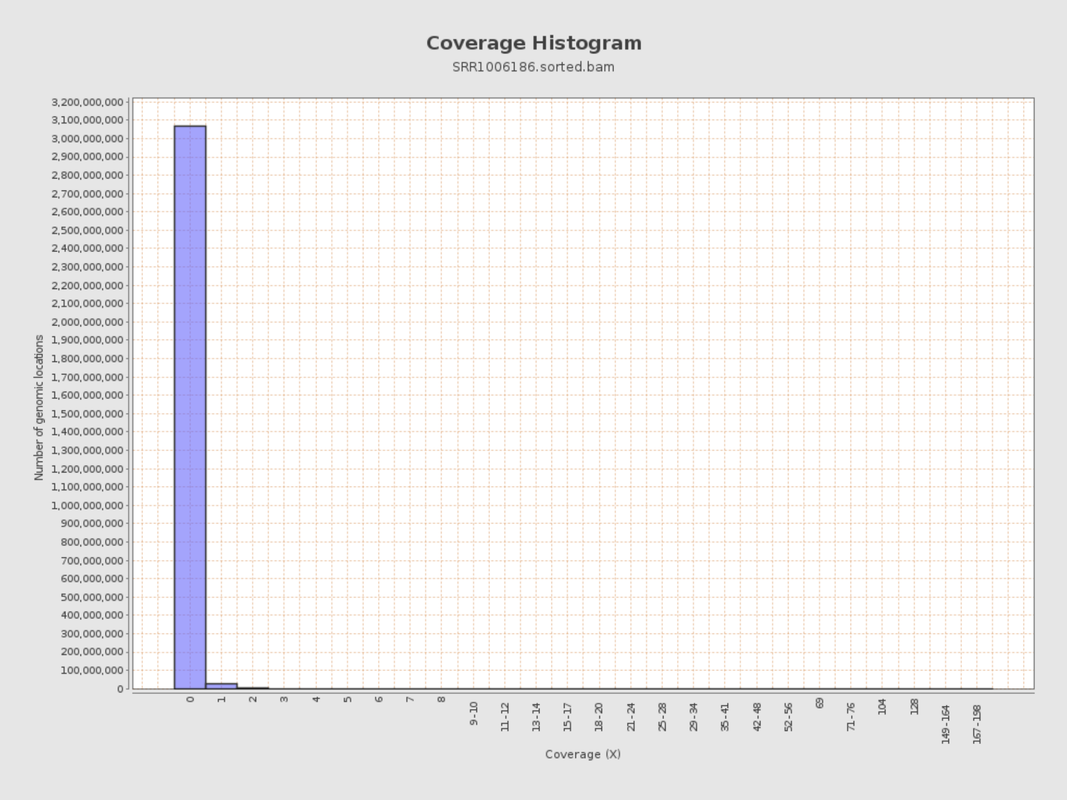
chr1	249250621	2747157	0.011	0.1194
chr2	243199373	2690812	0.0111	0.1146
chr3	198022430	2136864	0.0108	0.1094
chr4	191154276	1942496	0.0102	0.1089
chr5	180915260	1923374	0.0106	0.1088
chr6	171115067	1768852	0.0103	0.1086
chr7	159138663	1709605	0.0107	0.115
chr8	146364022	1622664	0.0111	0.1475
chr9	141213431	1352658	0.0096	0.1048
chr10	135534747	1522673	0.0112	0.1182
chr11	135006516	1506333	0.0112	0.1137
chr12	133851895	1461013	0.0109	0.1108
chr13	115169878	922827	0.008	0.0947
chr14	107349540	990298	0.0092	0.1036
chr15	102531392	932433	0.0091	0.1008
chr16	90354753	1023659	0.0113	0.1159
chr17	81195210	999243	0.0123	0.1183
chr18	78077248	817719	0.0105	0.1182
chr19	59128983	777984	0.0132	0.1259
chr20	63025520	735743	0.0117	0.115
chr21	48129895	385304	0.008	0.0967
chr22	51304566	460837	0.009	0.1011
chrMT	16571	264	0.0159	0.1332
chrX	155270560	1683249	0.0108	0.1106

chrY	59373566	80159	0.0014	0.0487

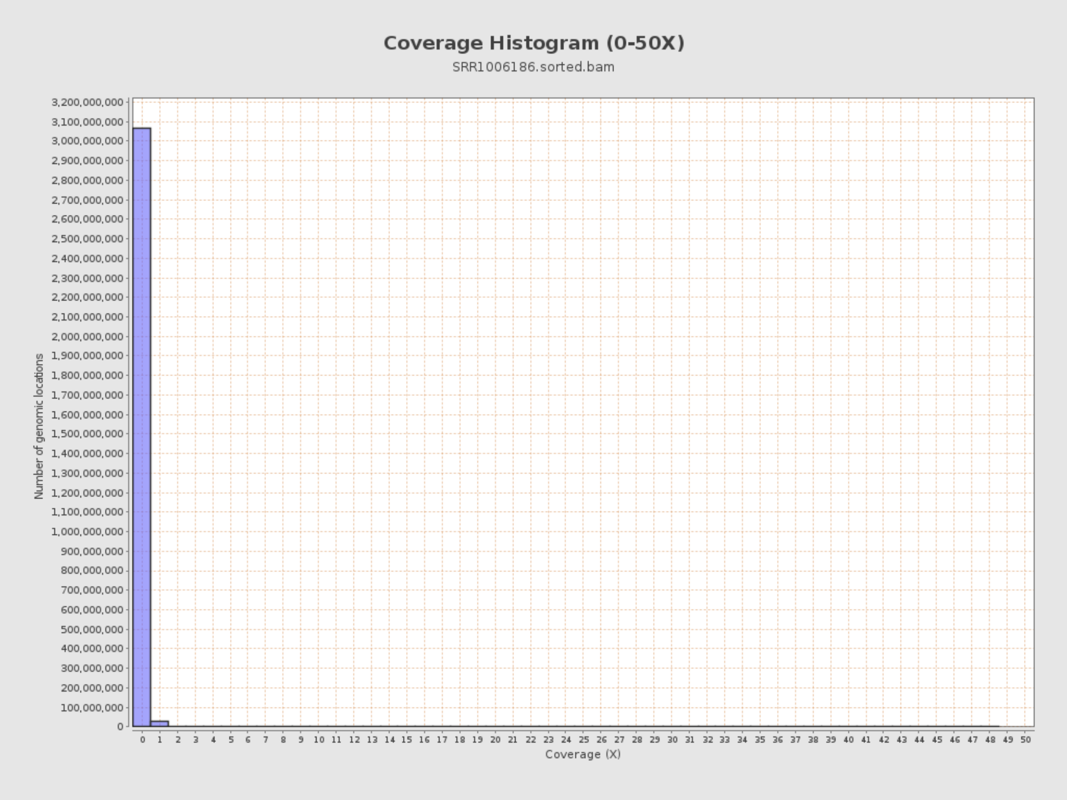
3. Results : Coverage across reference



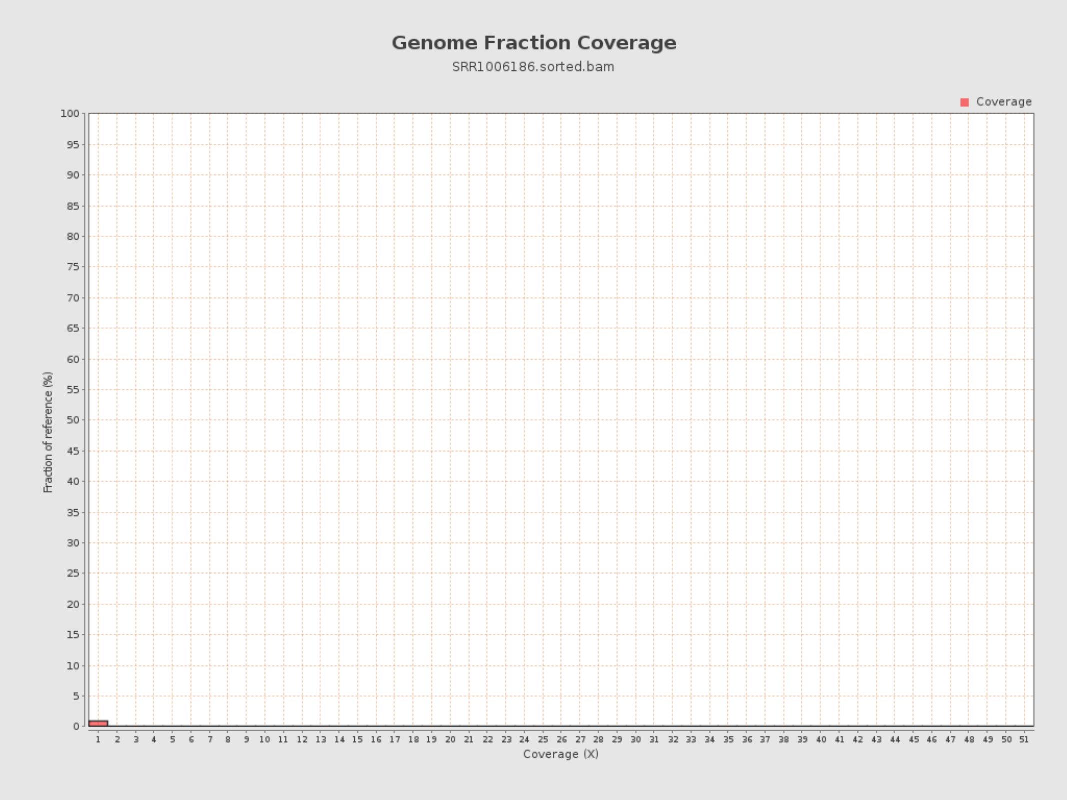
4. Results : Coverage Histogram



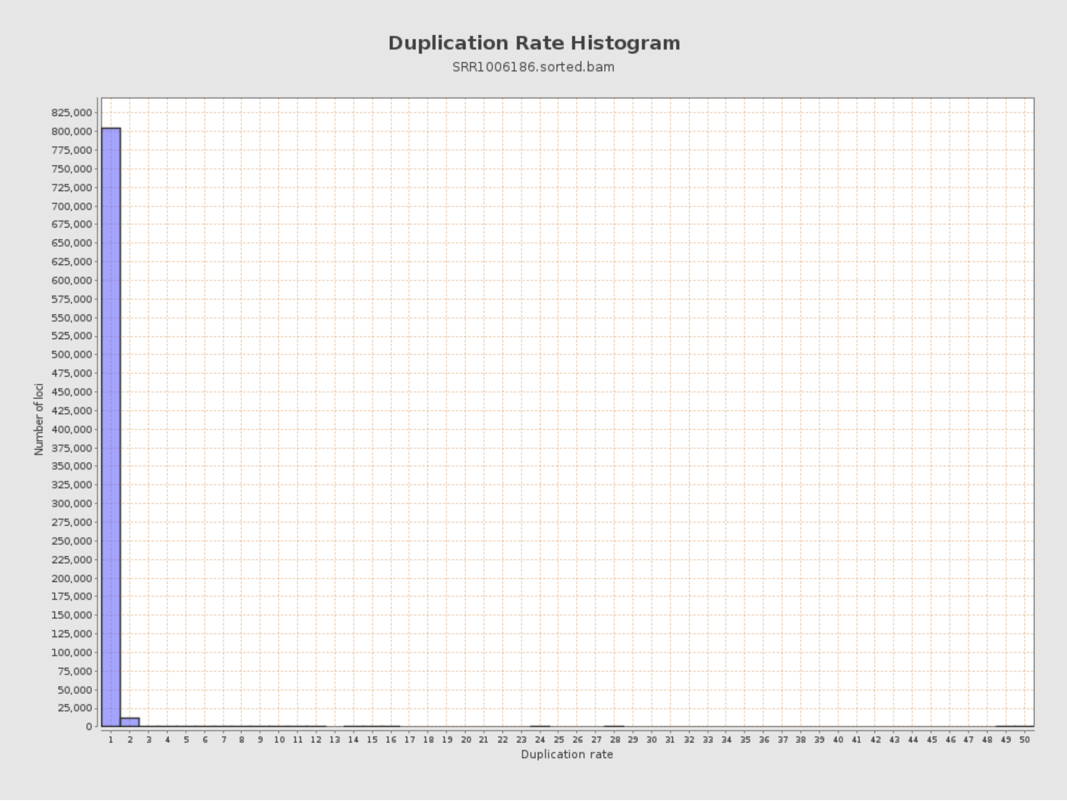
5. Results : Coverage Histogram (0-50X)



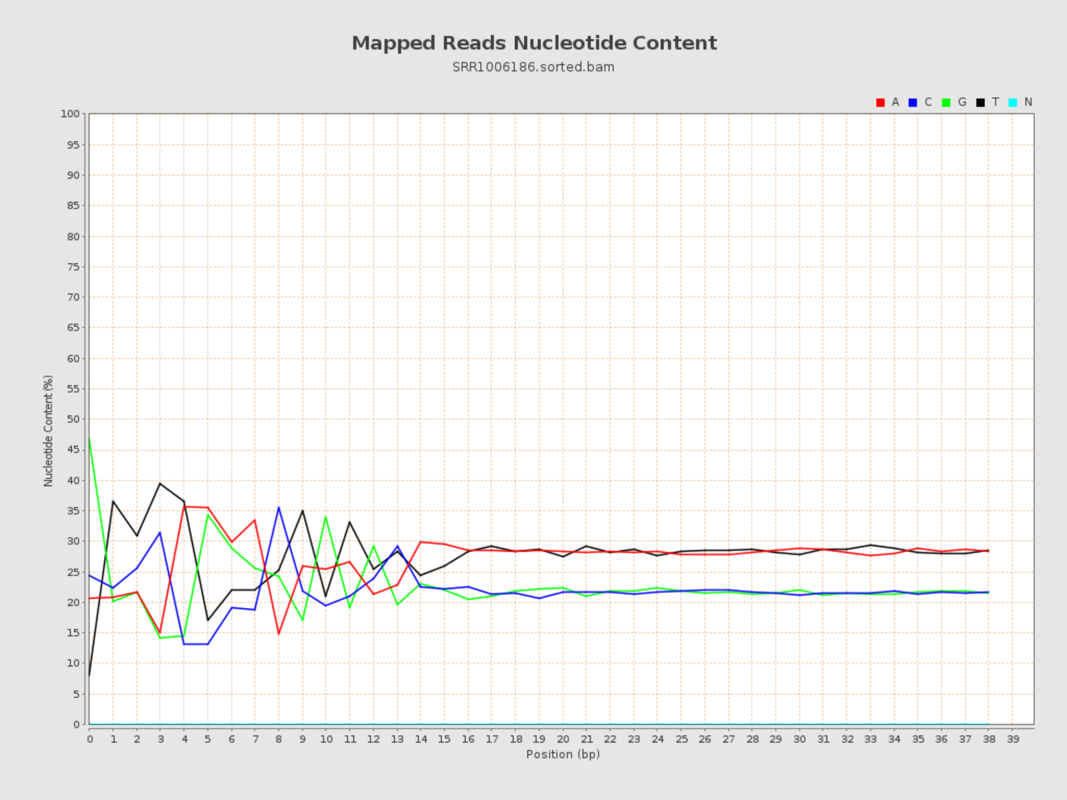
6. Results : Genome Fraction Coverage



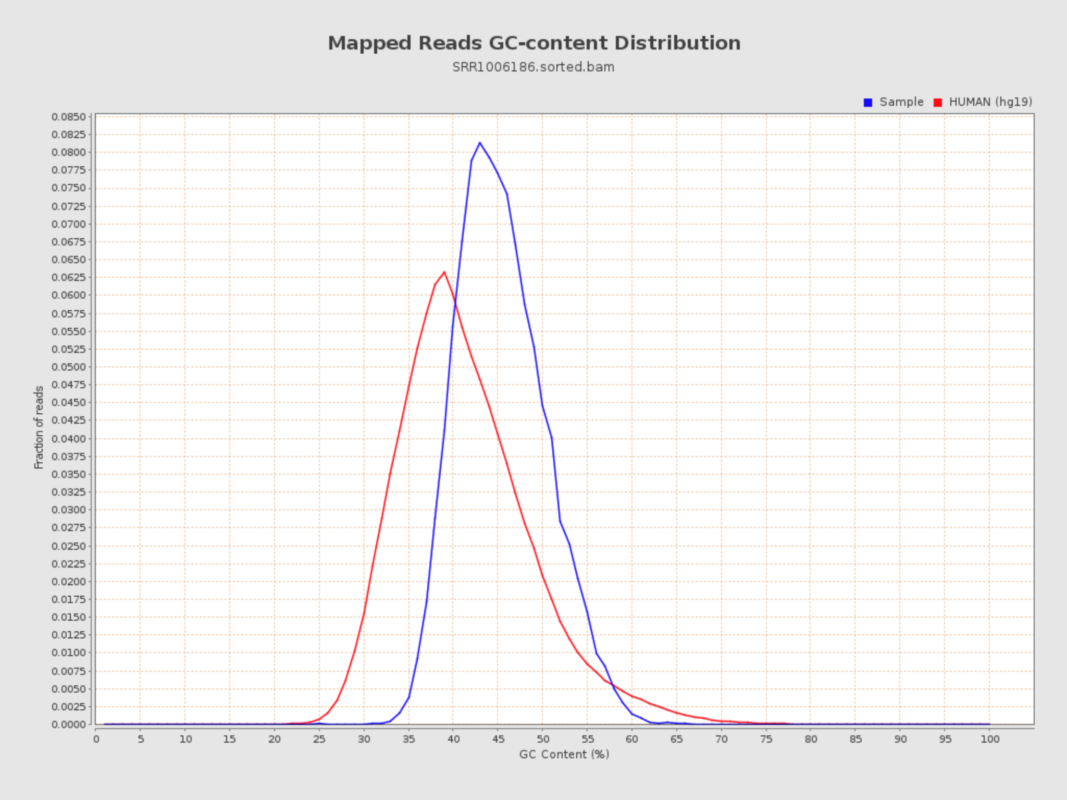
7. Results : Duplication Rate Histogram



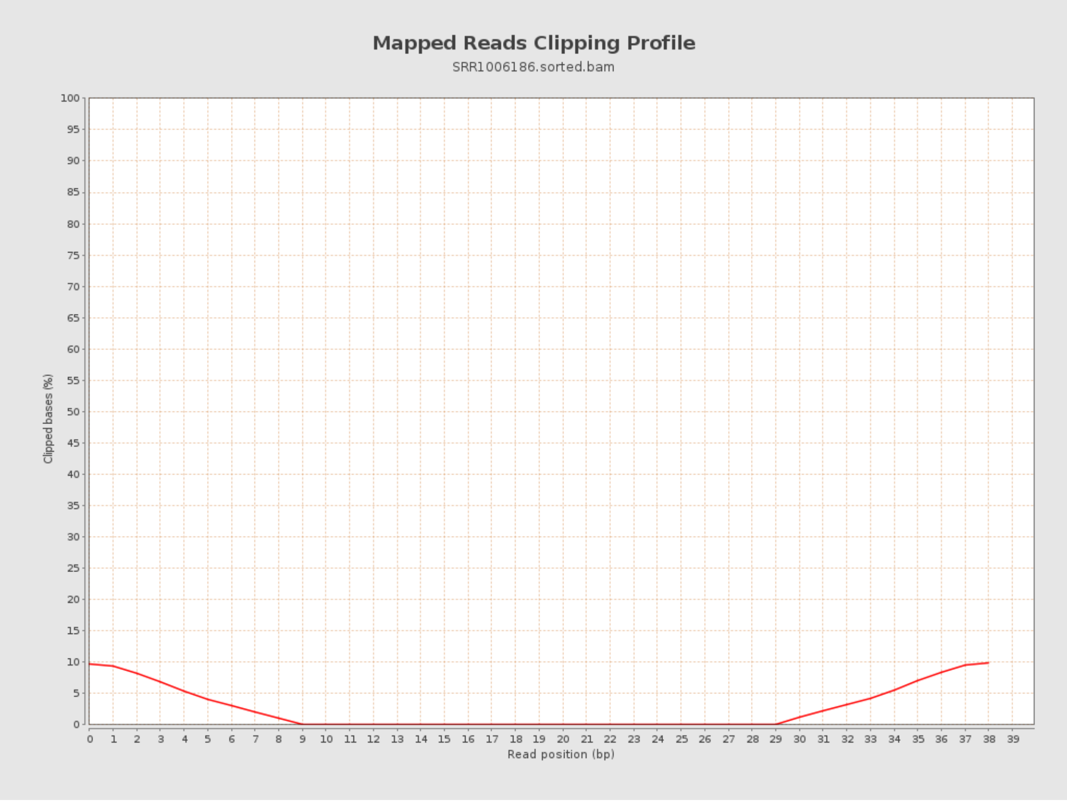
8. Results : Mapped Reads Nucleotide Content



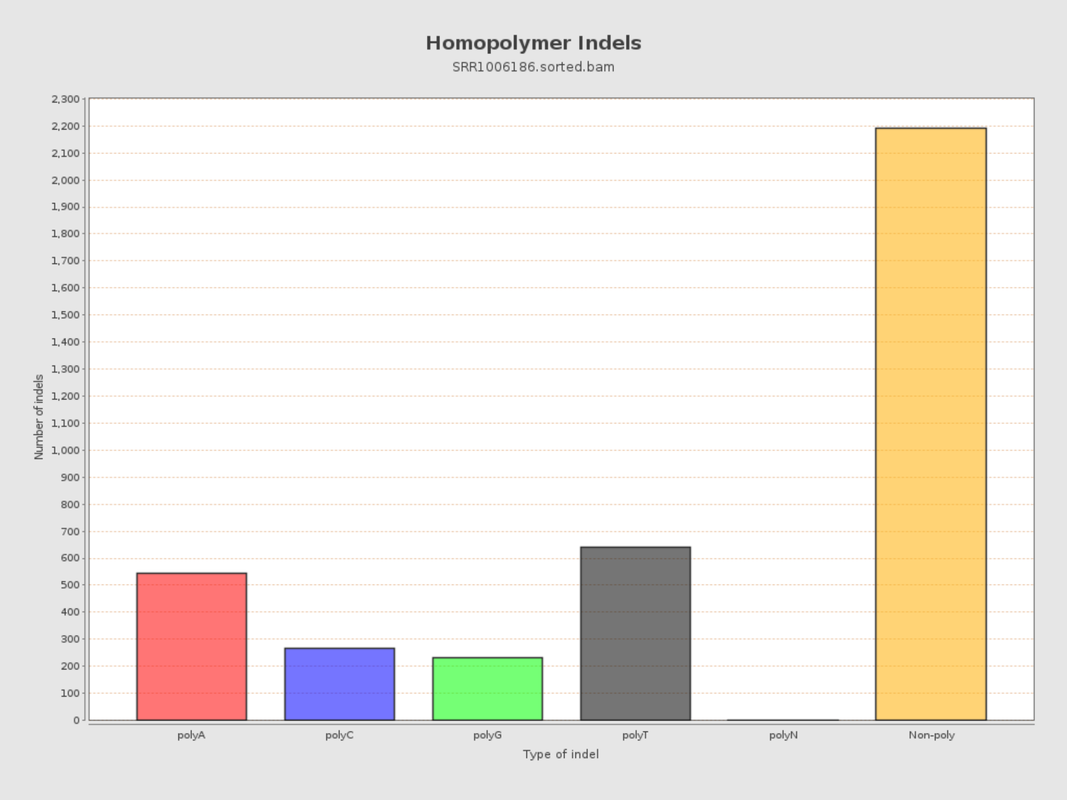
9. Results : Mapped Reads GC-content Distribution



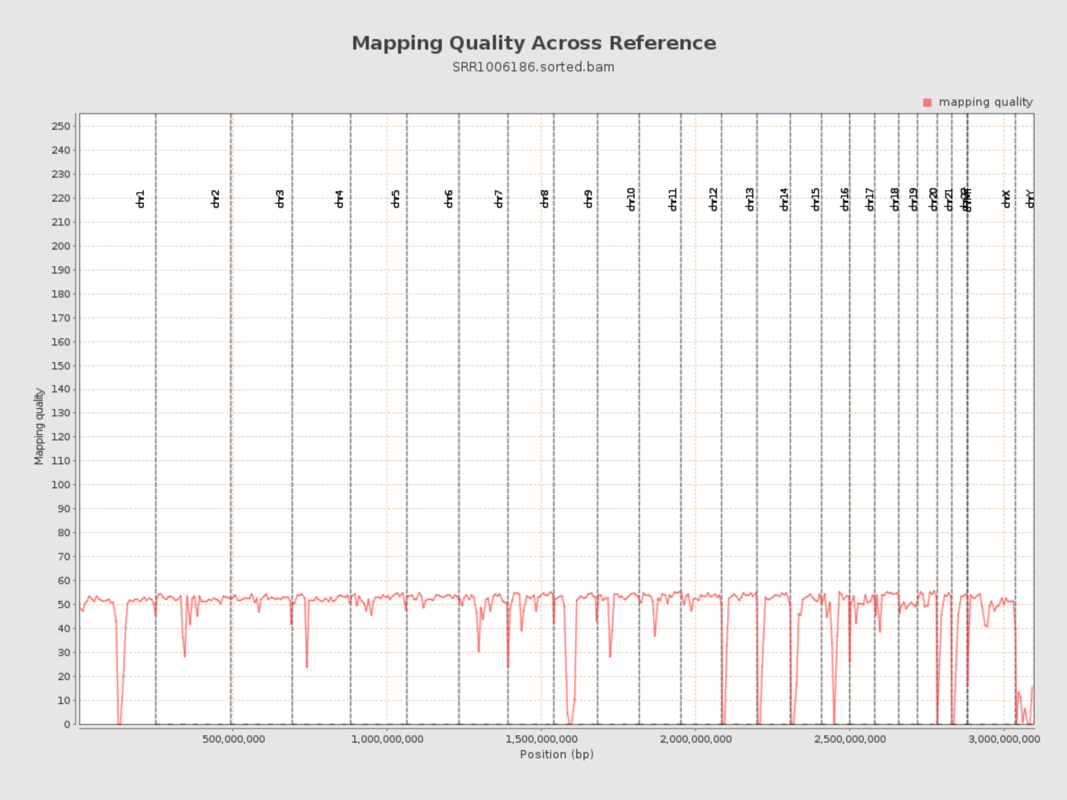
10. Results : Mapped Reads Clipping Profile



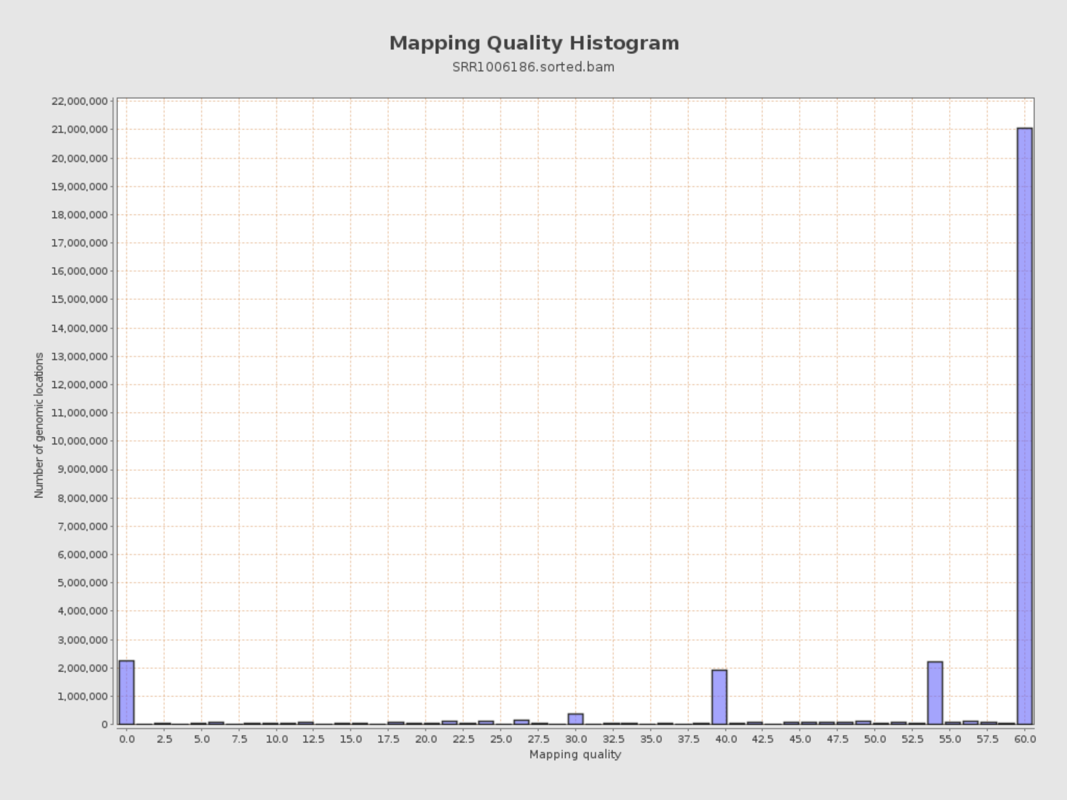
11. Results : Homopolymer Indels



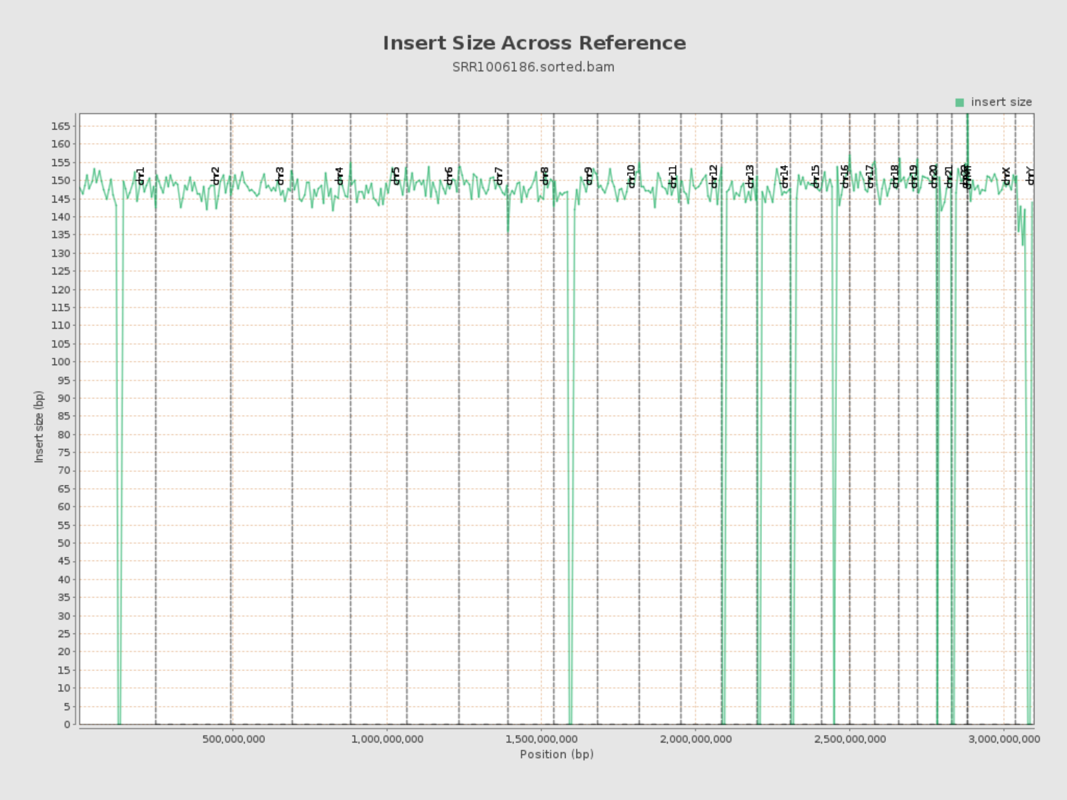
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram