Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:41:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006436.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_SRR1006436 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006436.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:41:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006436.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,299,356
Mapped reads	1,219,202 / 93.83%
Unmapped reads	80,154 / 6.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,223 / 0.25%
Read min/max/mean length	30 / 59 / 56.99
Duplicated reads (estimated)	25,125 / 1.93%
Duplication rate	1.67%
Clipped reads	157,576 / 12.13%

2.2. ACGT Content

Number/percentage of A's	19,097,865 / 28.1%
Number/percentage of C's	14,503,983 / 21.34%
Number/percentage of T's	18,651,622 / 27.45%
Number/percentage of G's	15,633,530 / 23%
Number/percentage of N's	70,697 / 0.1%
GC Percentage	44.35%

2.3. Coverage

Mean	0.022

Standard Deviation	0.2034

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Mismatches and indels

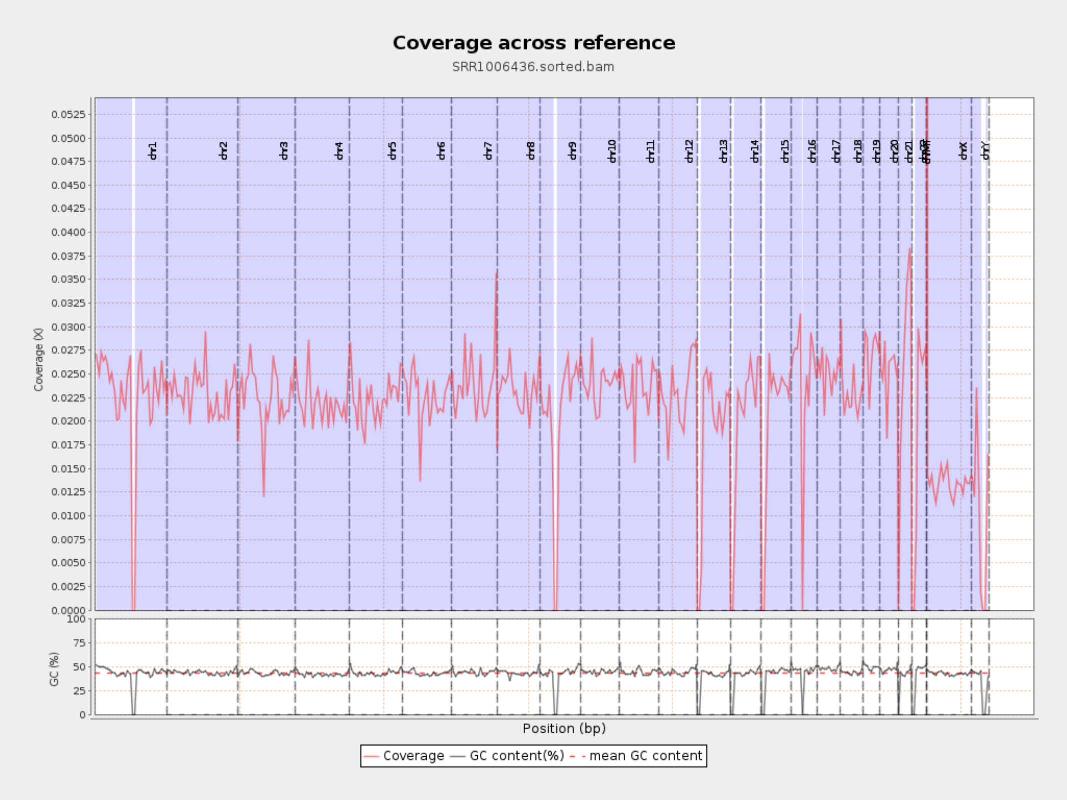
General error rate	0.57%
Mismatches	378,772
Insertions	4,403
Mapped reads with at least one insertion	0.36%
Deletions	12,427
Mapped reads with at least one deletion	1.01%
Homopolymer indels	42.39%

2.6. Chromosome stats

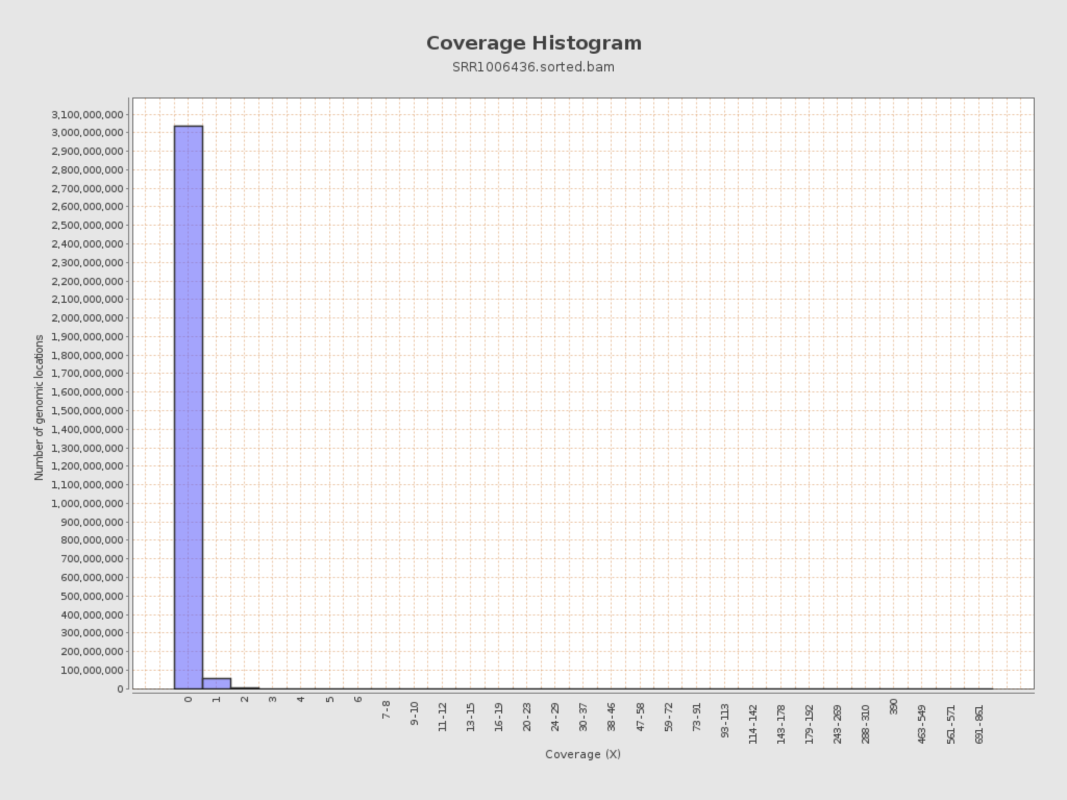
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5622563	0.0226	0.2266
chr2	243199373	5607739	0.0231	0.1832
chr3	198022430	4468549	0.0226	0.1607
chr4	191154276	4228735	0.0221	0.1657
chr5	180915260	4041244	0.0223	0.1602
chr6	171115067	3876762	0.0227	0.1657
chr7	159138663	3833800	0.0241	0.1904

chr8	146364022	3422232	0.0234	0.5054
chr9	141213431	2869125	0.0203	0.1626
chr10	135534747	3267401	0.0241	0.1858
chr11	135006516	3209127	0.0238	0.1753
chr12	133851895	3082647	0.023	0.1635
chr13	115169878	2135831	0.0185	0.1465
chr14	107349540	2114899	0.0197	0.153
chr15	102531392	2024327	0.0197	0.1516
chr16	90354753	2168359	0.024	0.1831
chr17	81195210	2047265	0.0252	0.1775
chr18	78077248	1787173	0.0229	0.2027
chr19	59128983	1606445	0.0272	0.2172
chr20	63025520	1589679	0.0252	0.1853
chr21	48129895	1273518	0.0265	0.1877
chr22	51304566	970086	0.0189	0.1564
chrMT	16571	47213	2.8491	2.1961
chrX	155270560	2082953	0.0134	0.1266
chrY	59373566	601404	0.0101	0.1498

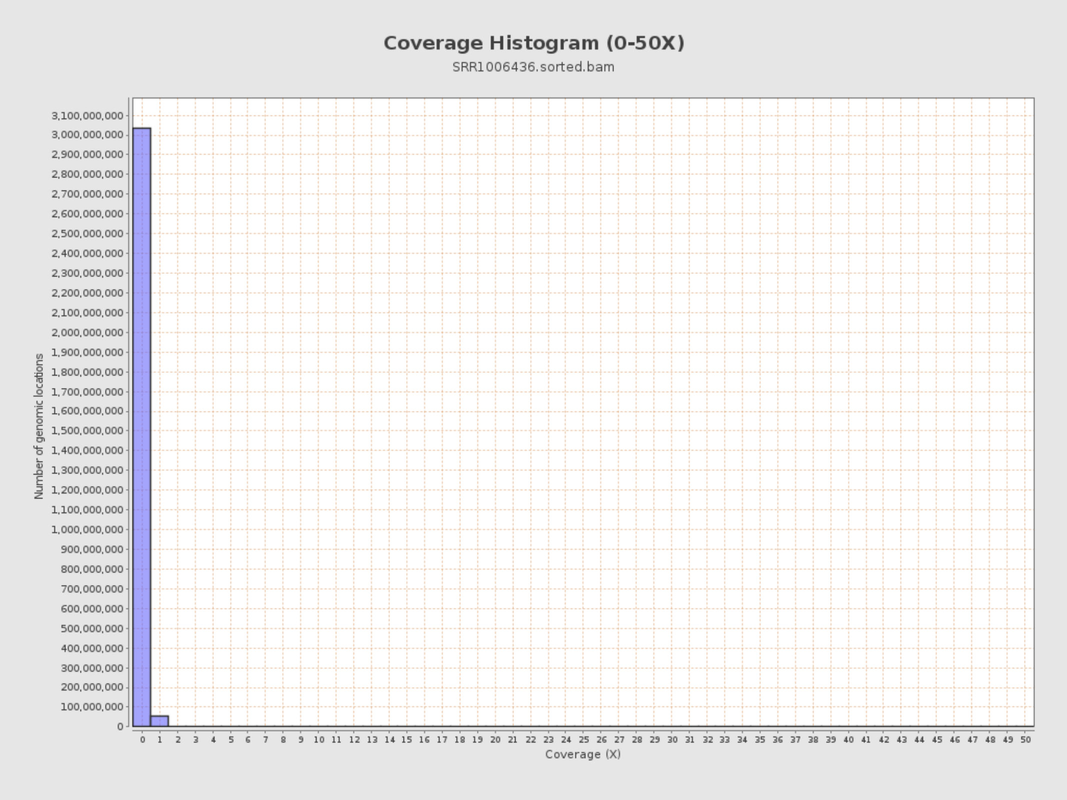
3. Results : Coverage across reference



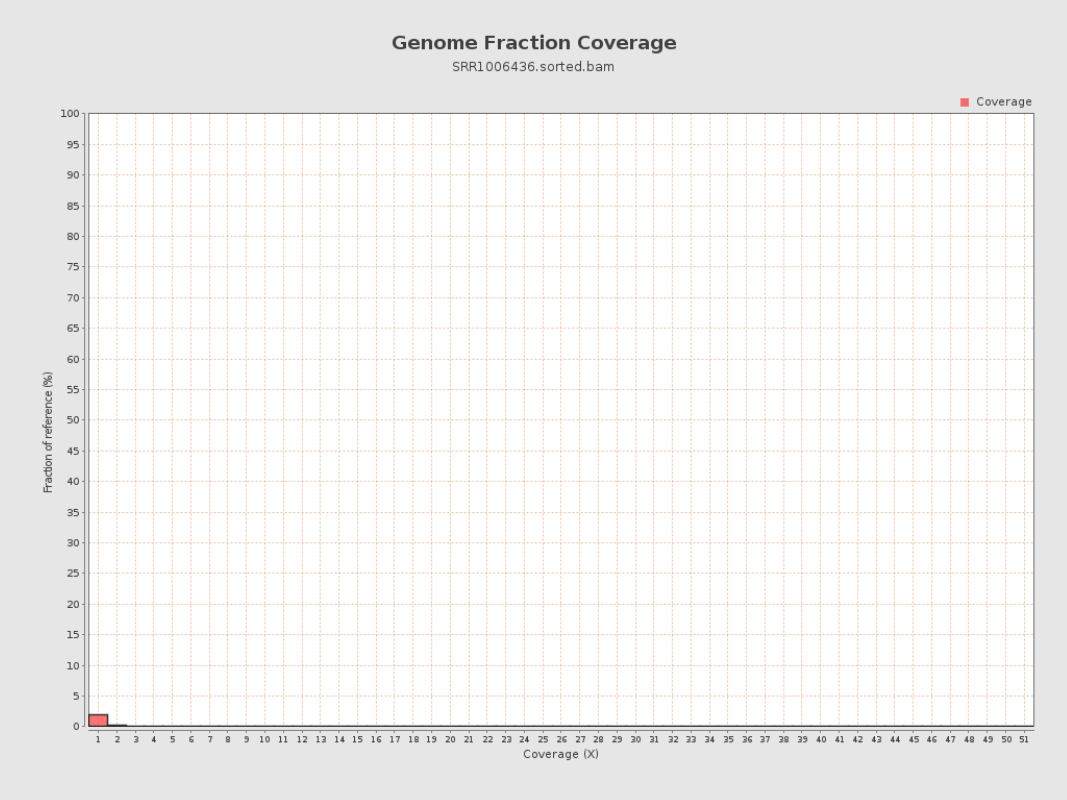
4. Results : Coverage Histogram



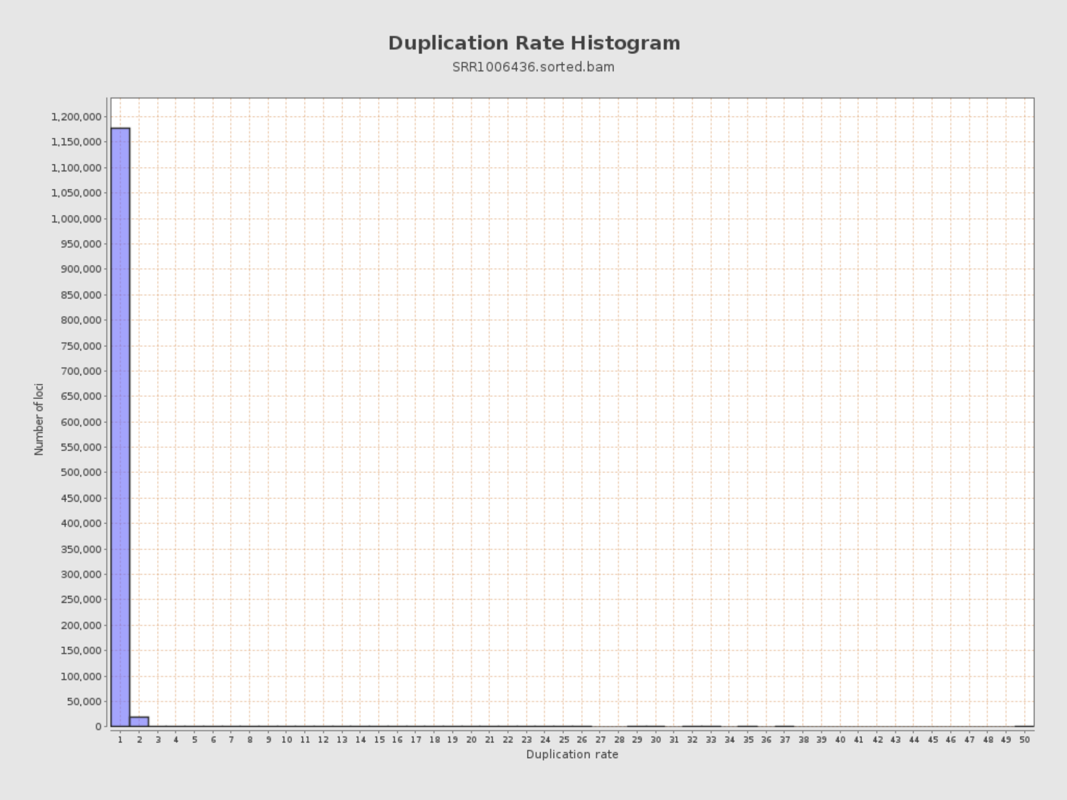
5. Results : Coverage Histogram (0-50X)



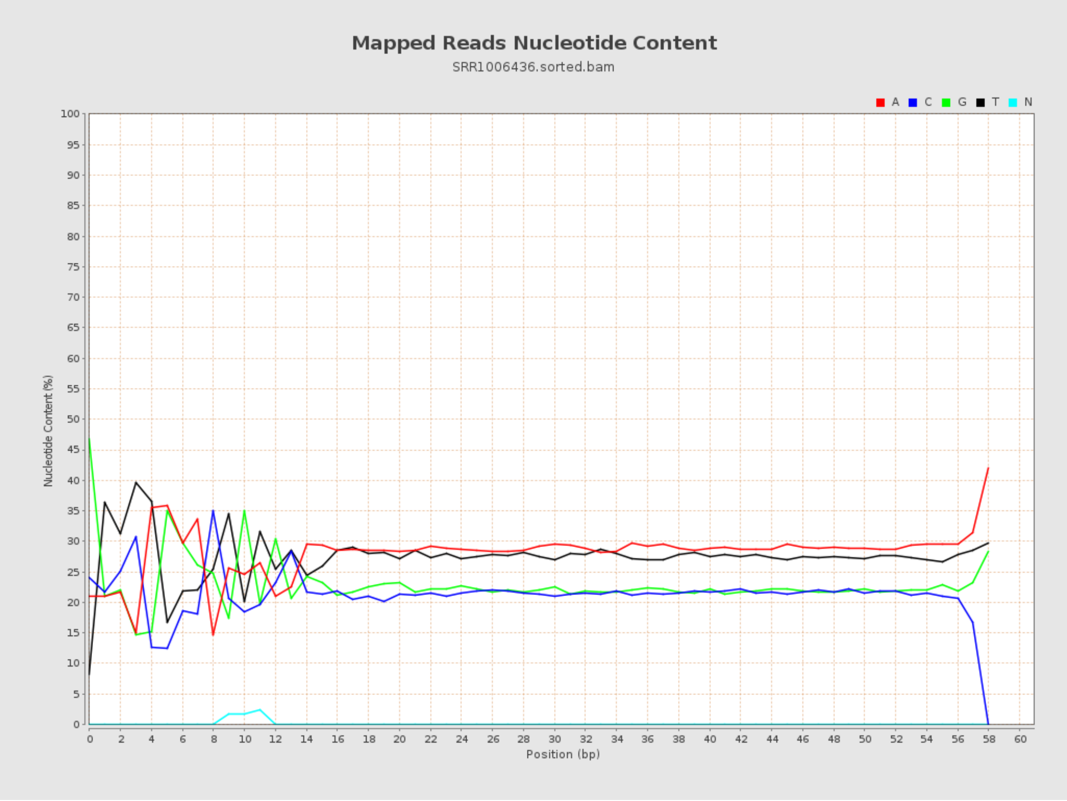
6. Results : Genome Fraction Coverage



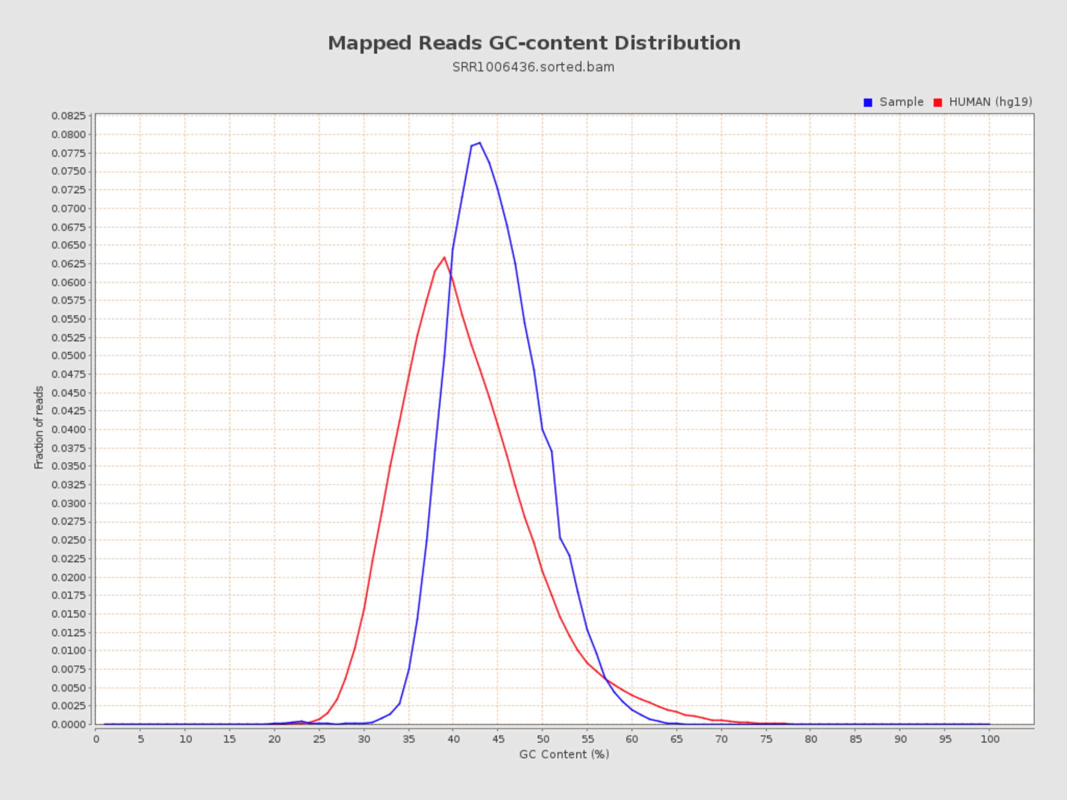
7. Results : Duplication Rate Histogram



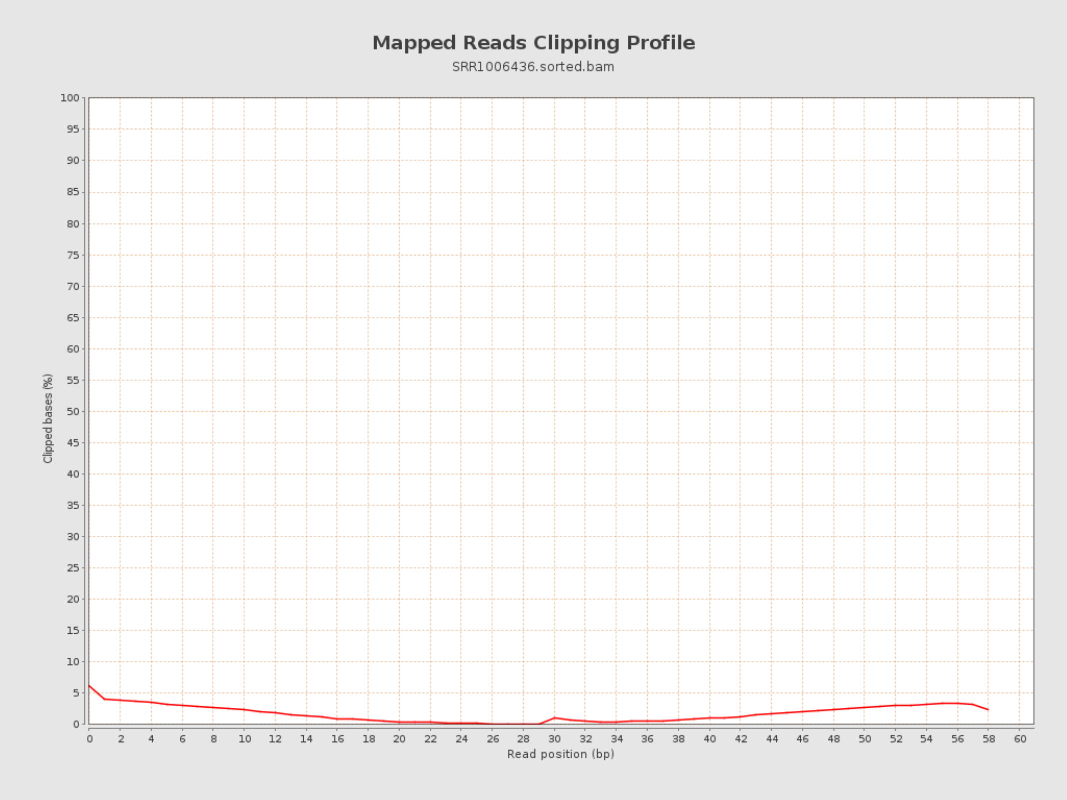
8. Results : Mapped Reads Nucleotide Content



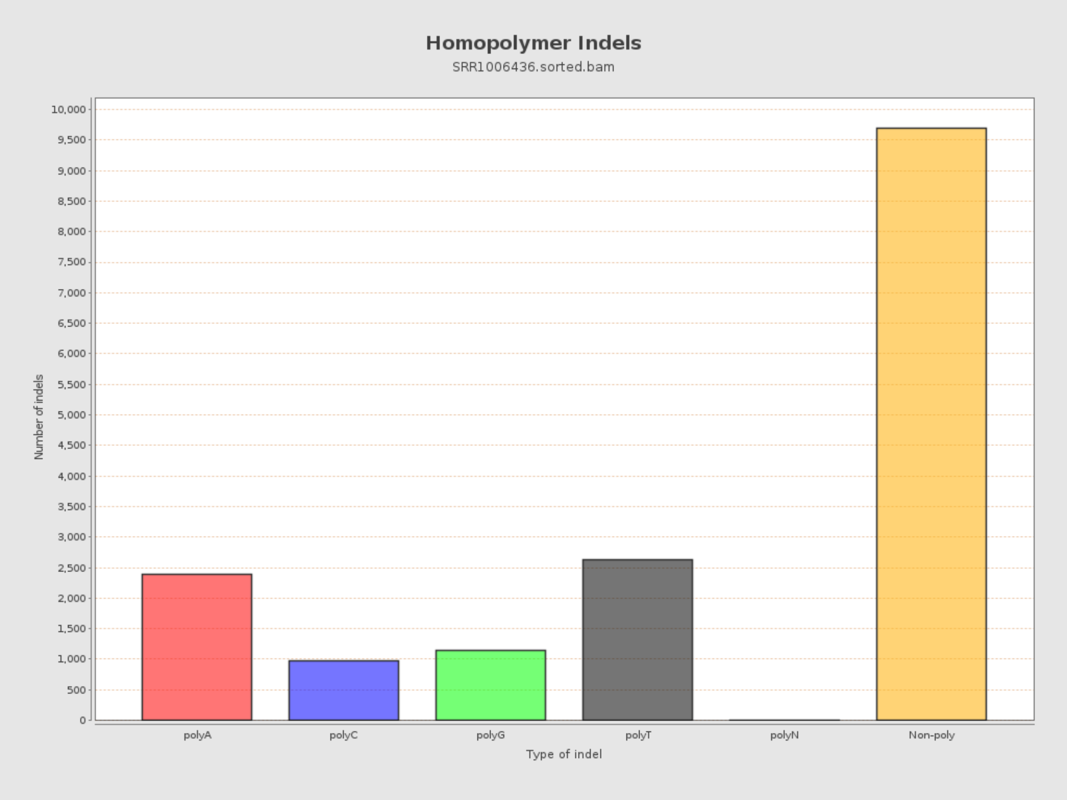
9. Results : Mapped Reads GC-content Distribution



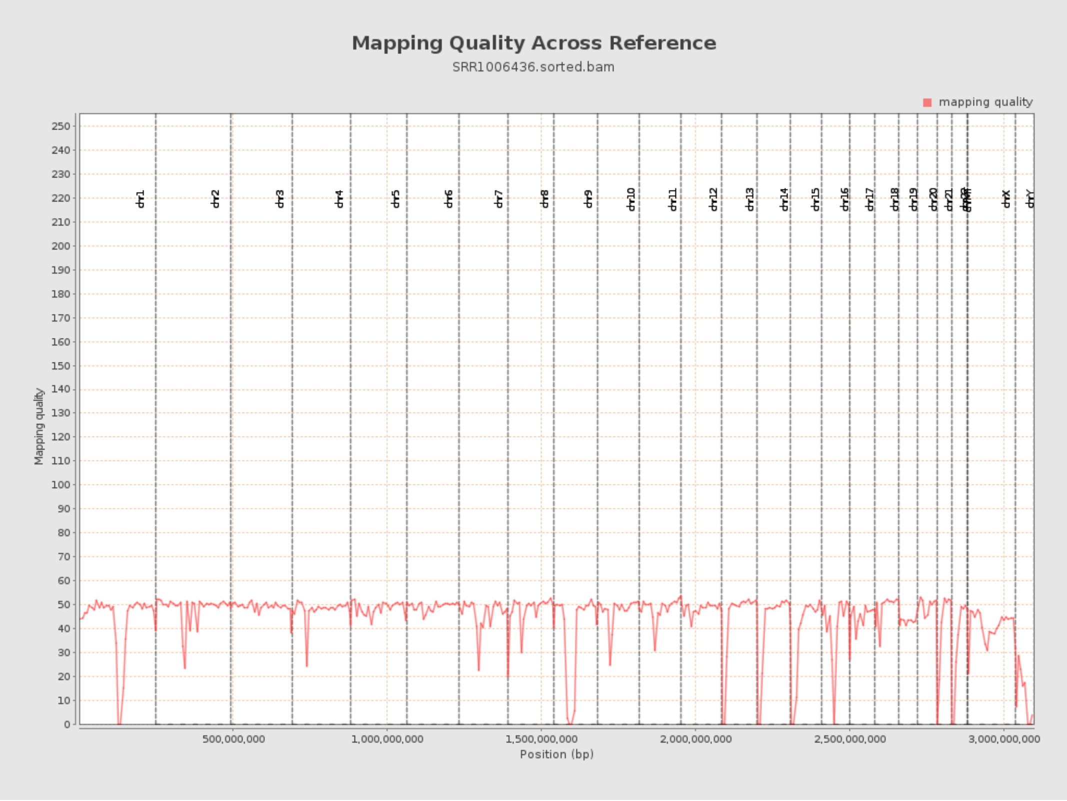
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram