Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:10:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006446.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_SRR1006446 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006446.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:10:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006446.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,927,913
Mapped reads	1,848,613 / 95.89%
Unmapped reads	79,300 / 4.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,081 / 0.32%
Read min/max/mean length	30 / 59 / 58.13
Duplicated reads (estimated)	44,191 / 2.29%
Duplication rate	1.84%
Clipped reads	208,773 / 10.83%

2.2. ACGT Content

Number/percentage of A's	30,253,219 / 28.81%
Number/percentage of C's	21,726,788 / 20.69%
Number/percentage of T's	30,290,532 / 28.85%
Number/percentage of G's	22,720,440 / 21.64%
Number/percentage of N's	2,944 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0339

Standard Deviation	0.2866

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

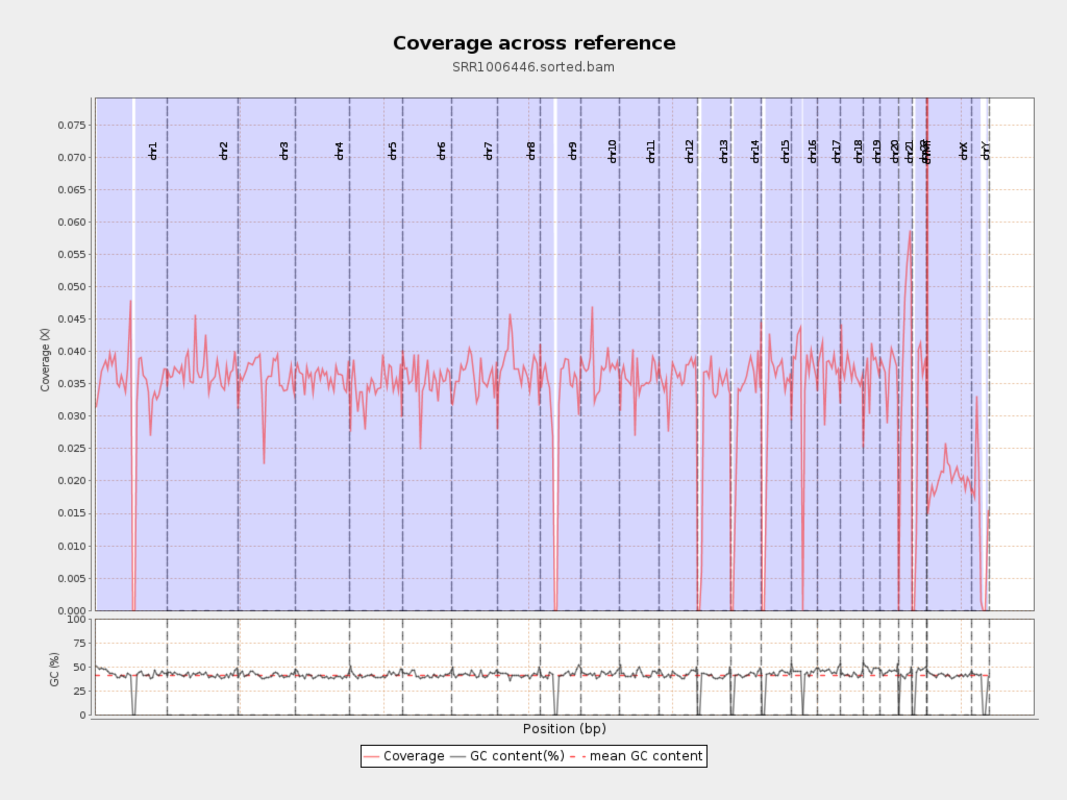
General error rate	0.42%
Mismatches	427,655
Insertions	6,399
Mapped reads with at least one insertion	0.35%
Deletions	18,336
Mapped reads with at least one deletion	0.99%
Homopolymer indels	47.06%

2.6. Chromosome stats

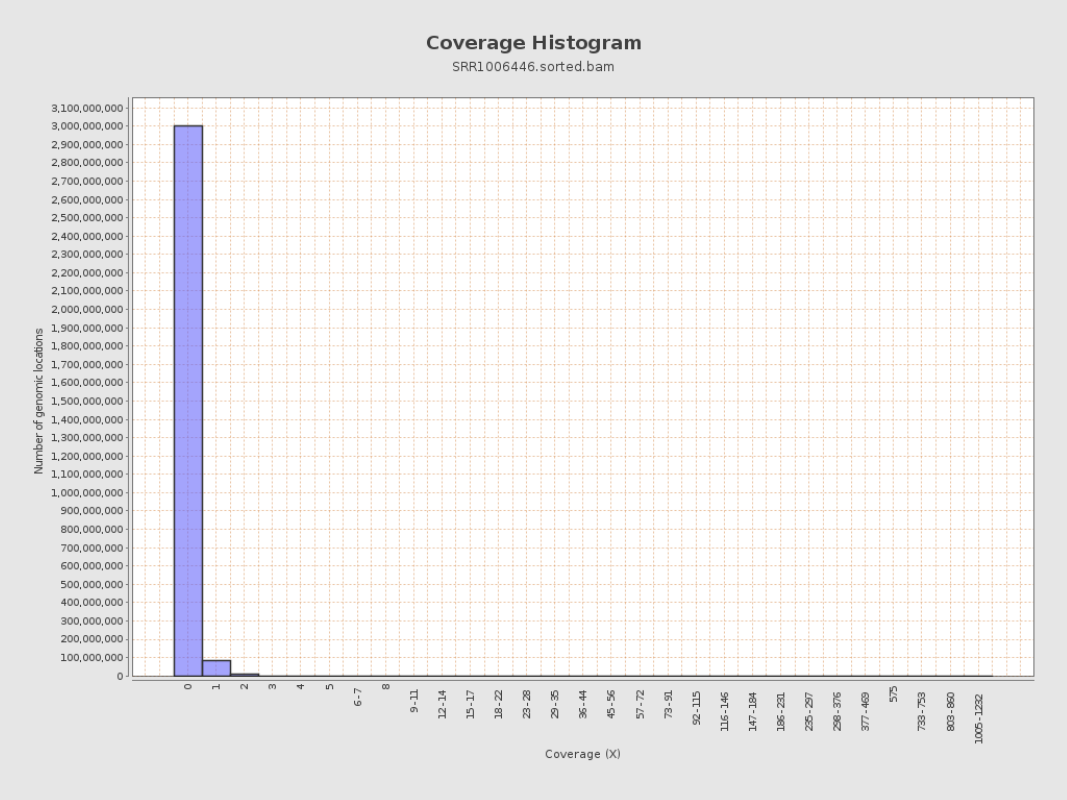
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8409180	0.0337	0.3924
chr2	243199373	9018133	0.0371	0.2453
chr3	198022430	7136165	0.036	0.2072
chr4	191154276	6901176	0.0361	0.2106
chr5	180915260	6309594	0.0349	0.2046
chr6	171115067	6085261	0.0356	0.2174
chr7	159138663	5740127	0.0361	0.2693

chr8	146364022	5516995	0.0377	0.7282
chr9	141213431	4431756	0.0314	0.226
chr10	135534747	5090477	0.0376	0.2634
chr11	135006516	4820568	0.0357	0.2367
chr12	133851895	4818457	0.036	0.2102
chr13	115169878	3427846	0.0298	0.1895
chr14	107349540	3222112	0.03	0.1985
chr15	102531392	3148961	0.0307	0.1916
chr16	90354753	3166249	0.035	0.2214
chr17	81195210	3032114	0.0373	0.2324
chr18	78077248	2891917	0.037	0.3386
chr19	59128983	2170151	0.0367	0.3164
chr20	63025520	2317982	0.0368	0.2124
chr21	48129895	1993079	0.0414	0.2386
chr22	51304566	1369570	0.0267	0.1931
chrMT	16571	66796	4.0309	2.7249
chrX	155270560	3152124	0.0203	0.1643
chrY	59373566	787119	0.0133	0.1576

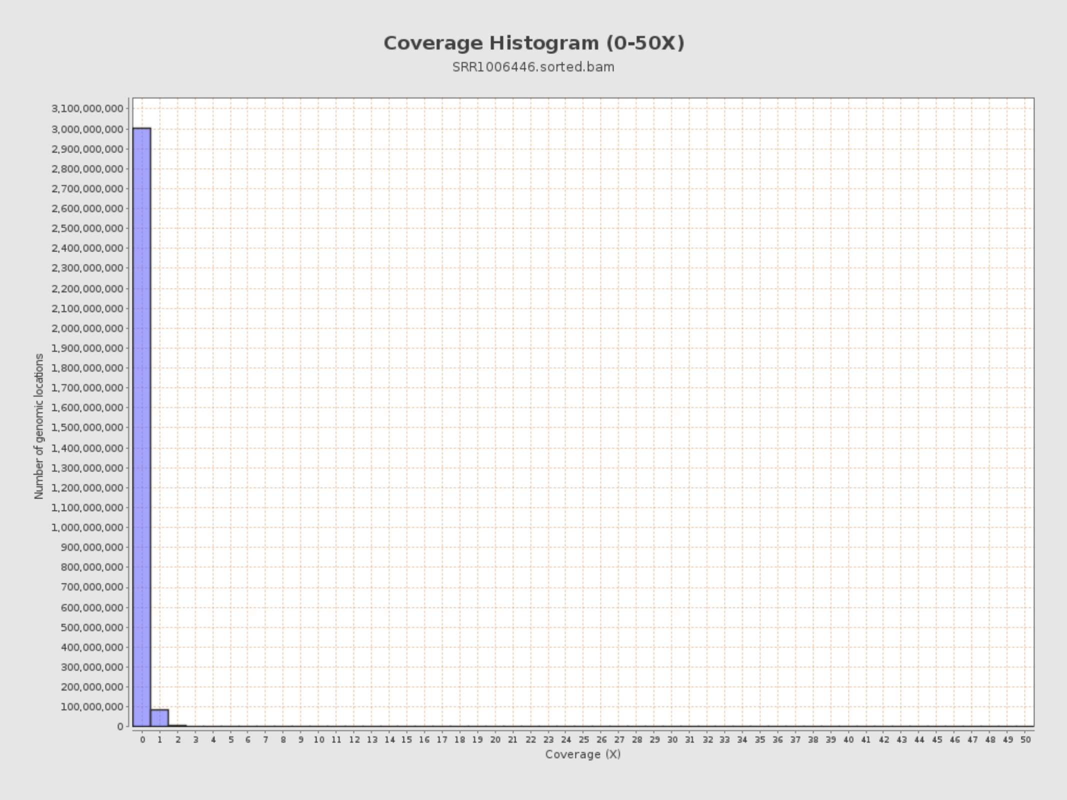
3. Results : Coverage across reference



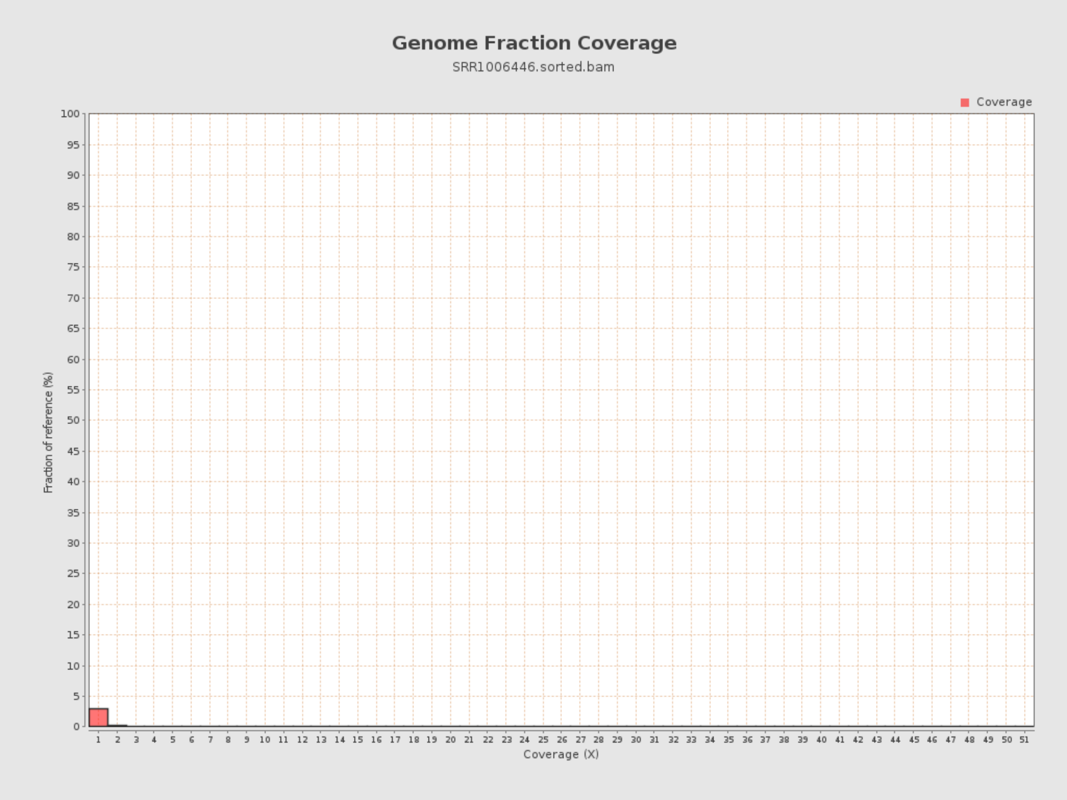
4. Results : Coverage Histogram



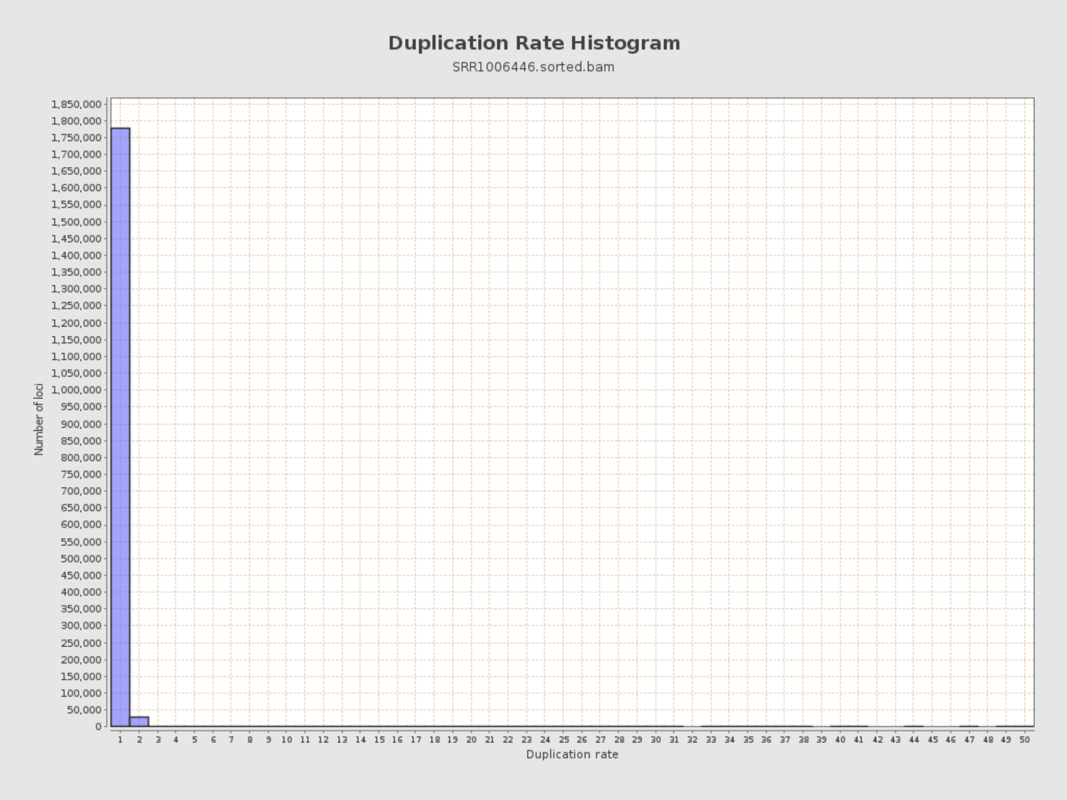
5. Results : Coverage Histogram (0-50X)



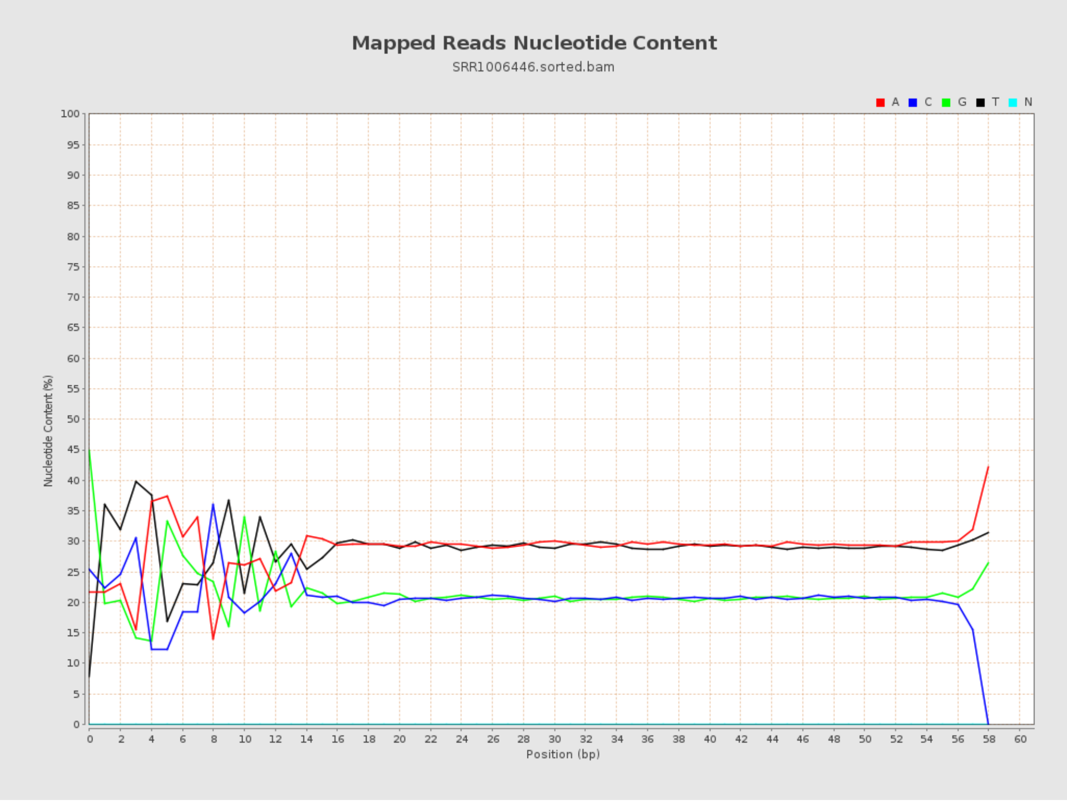
6. Results : Genome Fraction Coverage



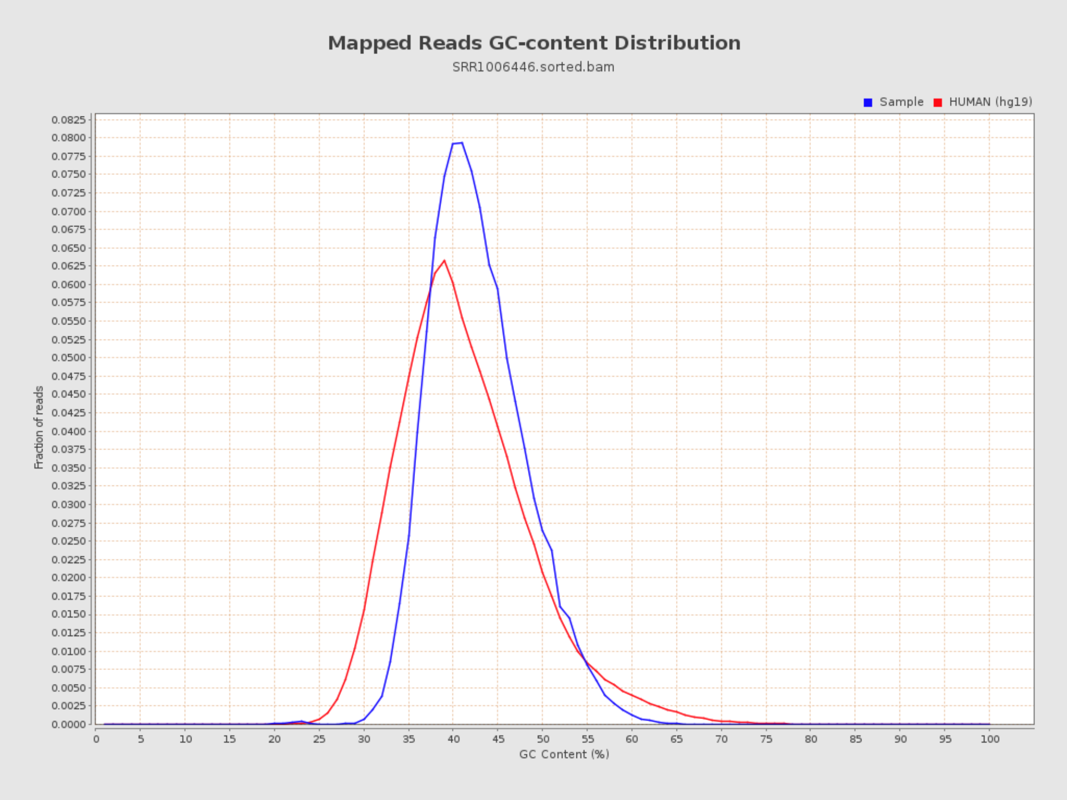
7. Results : Duplication Rate Histogram



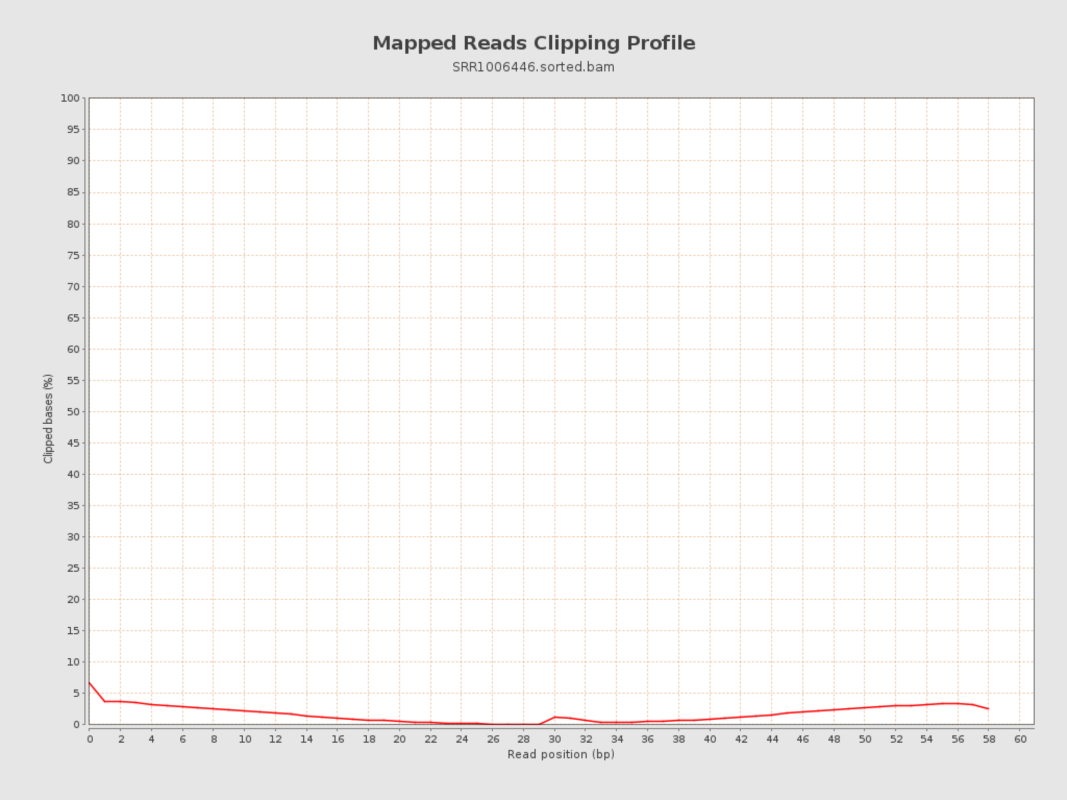
8. Results : Mapped Reads Nucleotide Content



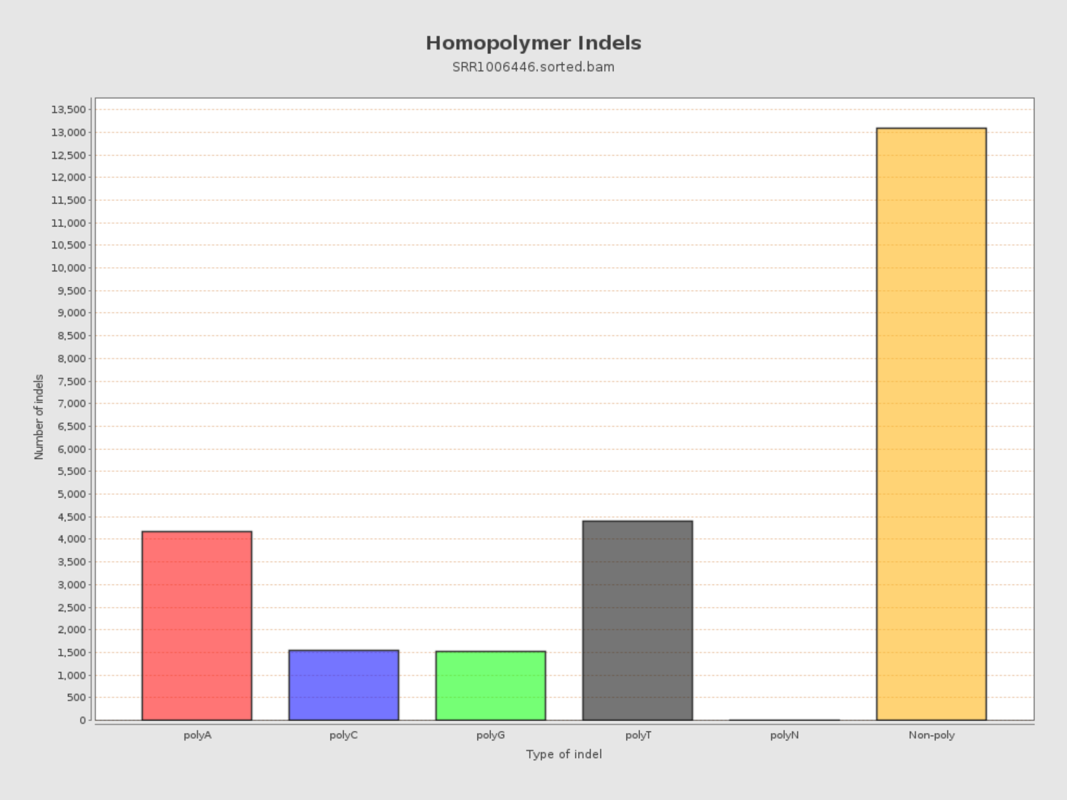
9. Results : Mapped Reads GC-content Distribution



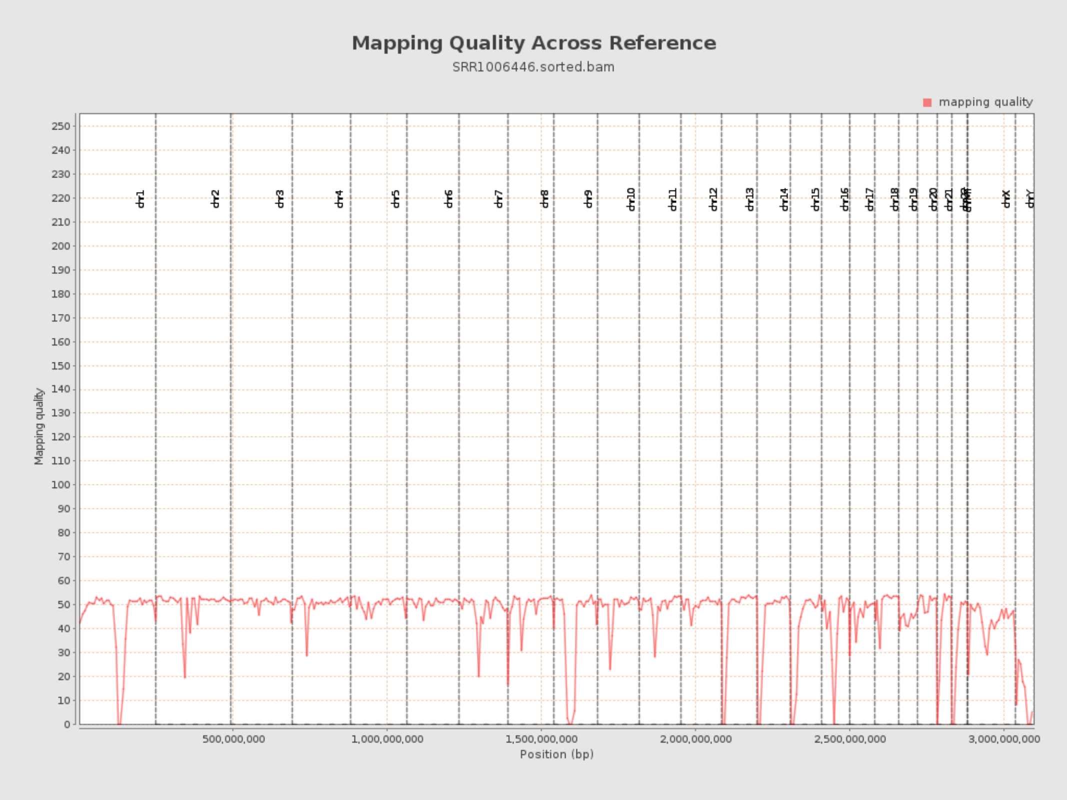
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram