Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 02:56:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006441.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_SRR1006441 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006441.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 02:56:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006441.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,263,973
Mapped reads	6,819,531 / 93.88%
Unmapped reads	444,442 / 6.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,479 / 0.3%
Read min/max/mean length	30 / 59 / 57.58
Duplicated reads (estimated)	955,893 / 13.16%
Duplication rate	12.47%
Clipped reads	1,051,791 / 14.48%

2.2. ACGT Content

Number/percentage of A's	108,105,126 / 28.37%
Number/percentage of C's	78,472,275 / 20.59%
Number/percentage of T's	111,628,126 / 29.29%
Number/percentage of G's	82,836,019 / 21.74%
Number/percentage of N's	8,072 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.1231

Standard Deviation	1.2714

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

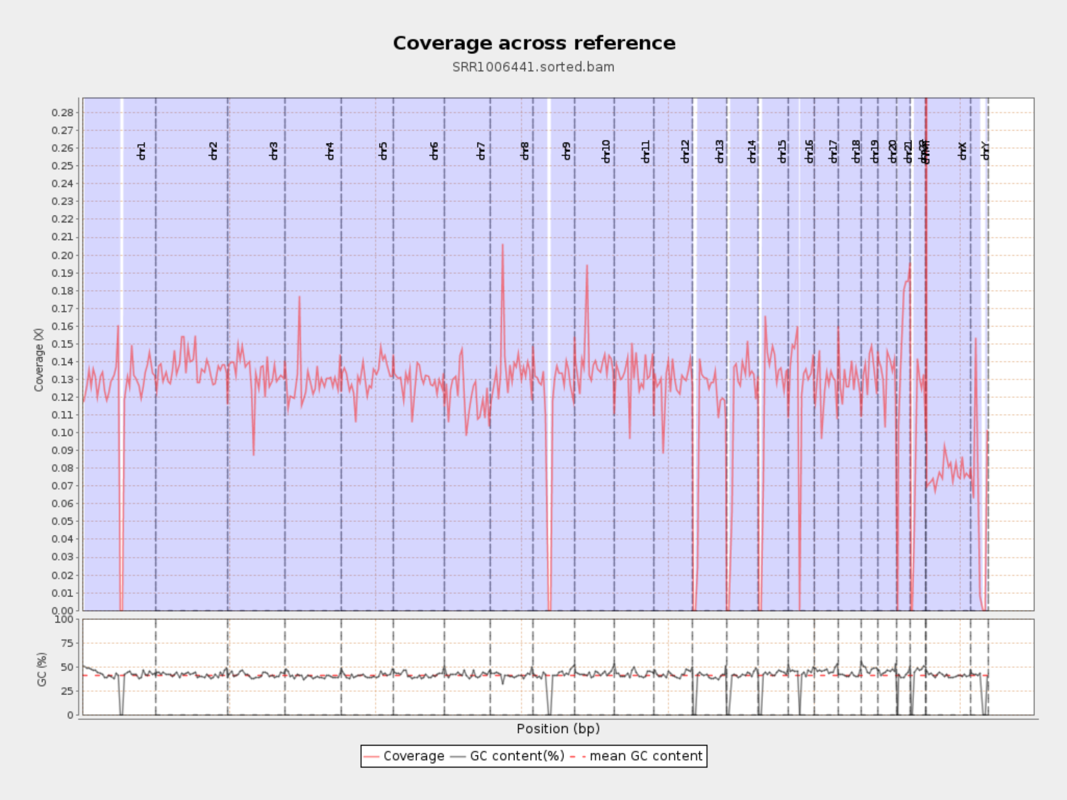
General error rate	0.43%
Mismatches	1,591,460
Insertions	24,908
Mapped reads with at least one insertion	0.36%
Deletions	80,005
Mapped reads with at least one deletion	1.17%
Homopolymer indels	43.69%

2.6. Chromosome stats

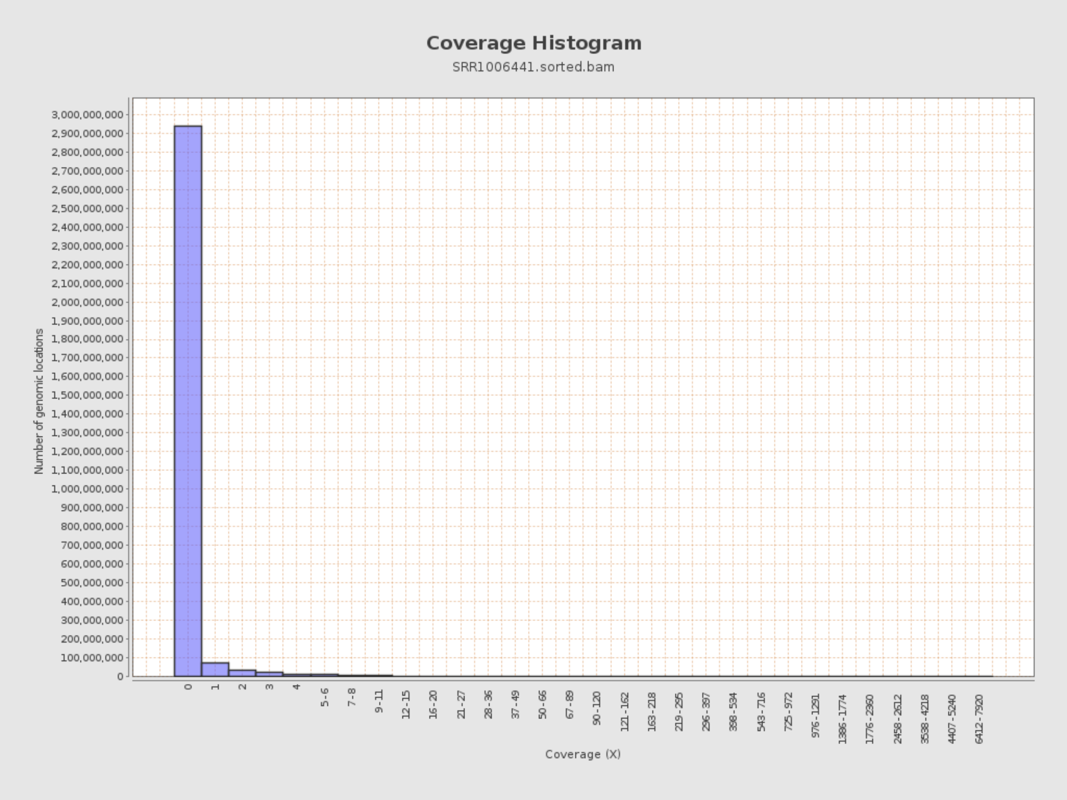
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30576401	0.1227	1.2507
chr2	243199373	33250691	0.1367	0.8749
chr3	198022430	26303364	0.1328	0.7415
chr4	191154276	24582768	0.1286	0.7657
chr5	180915260	23808392	0.1316	0.7362
chr6	171115067	21993484	0.1285	0.7515
chr7	159138663	19162934	0.1204	0.9168

chr8	146364022	19918505	0.1361	4.4583
chr9	141213431	16263015	0.1152	0.7901
chr10	135534747	18921982	0.1396	0.9891
chr11	135006516	17879063	0.1324	0.8093
chr12	133851895	17230965	0.1287	0.7291
chr13	115169878	12135760	0.1054	0.6571
chr14	107349540	11974115	0.1115	0.6955
chr15	102531392	11747580	0.1146	0.7047
chr16	90354753	11345091	0.1256	0.7788
chr17	81195210	10244144	0.1262	0.795
chr18	78077248	10140391	0.1299	1.0183
chr19	59128983	7934173	0.1342	1.0626
chr20	63025520	8378771	0.1329	0.7821
chr21	48129895	7104774	0.1476	0.866
chr22	51304566	4646901	0.0906	0.7016
chrMT	16571	127206	7.6764	6.5479
chrX	155270560	11994117	0.0772	0.5614
chrY	59373566	3518402	0.0593	0.725

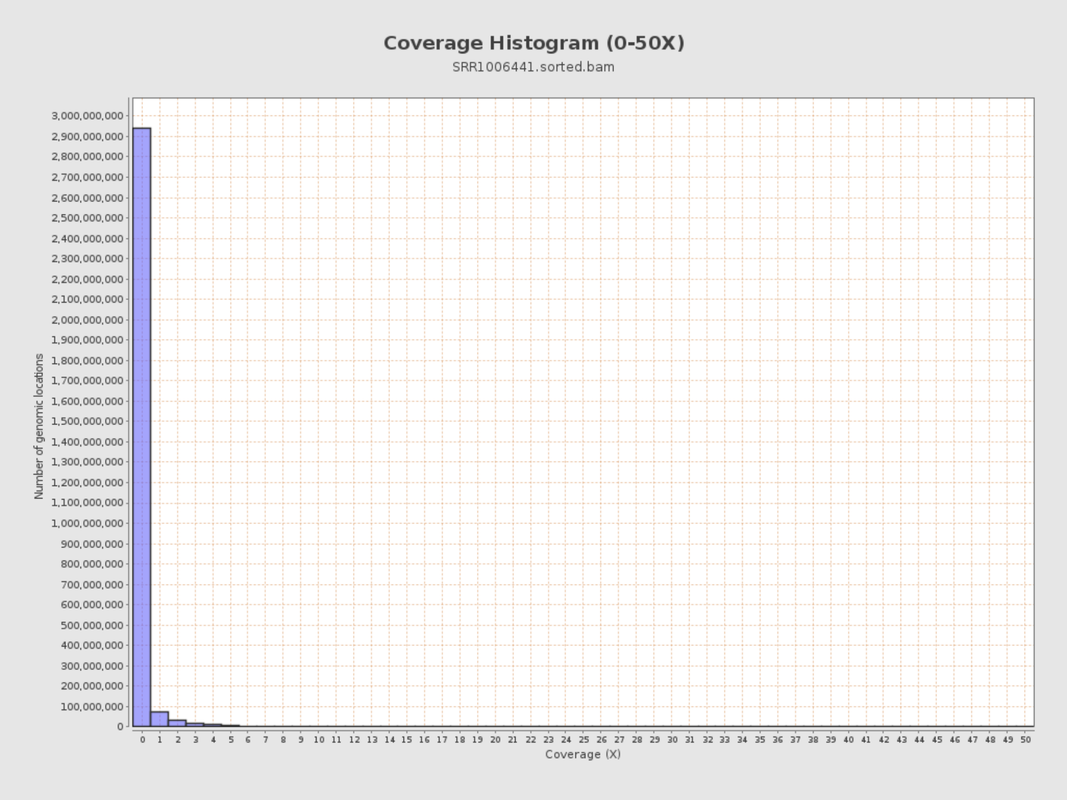
3. Results : Coverage across reference



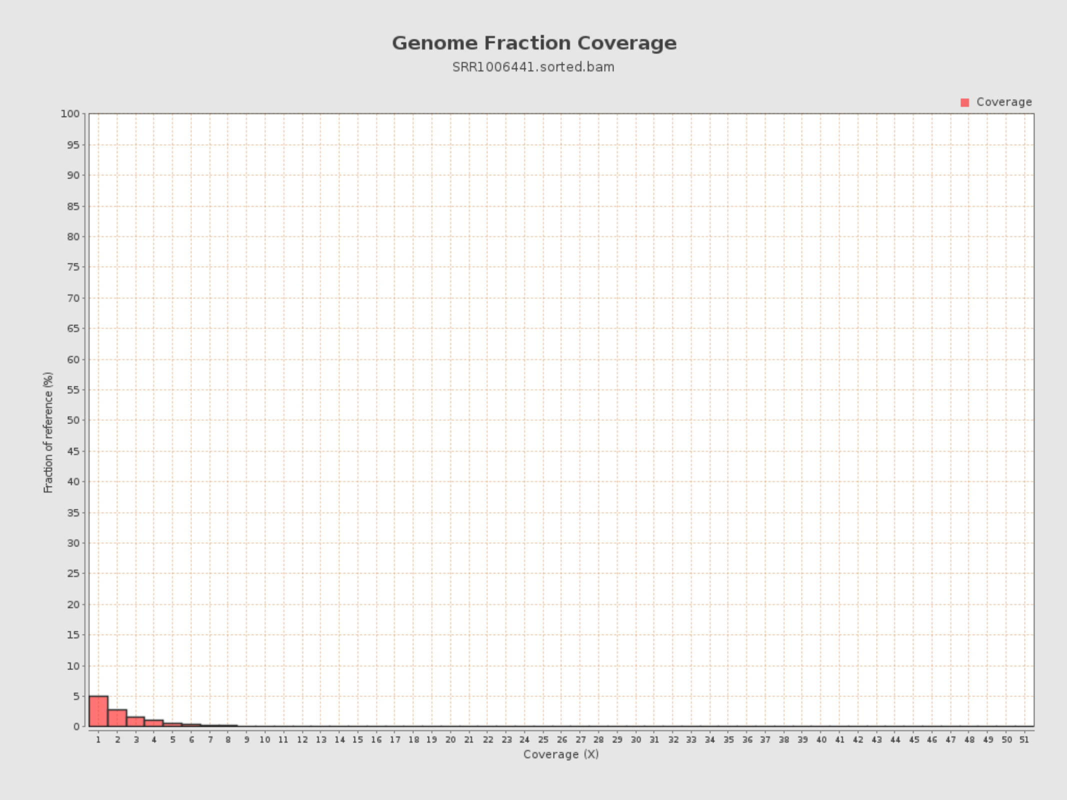
4. Results : Coverage Histogram



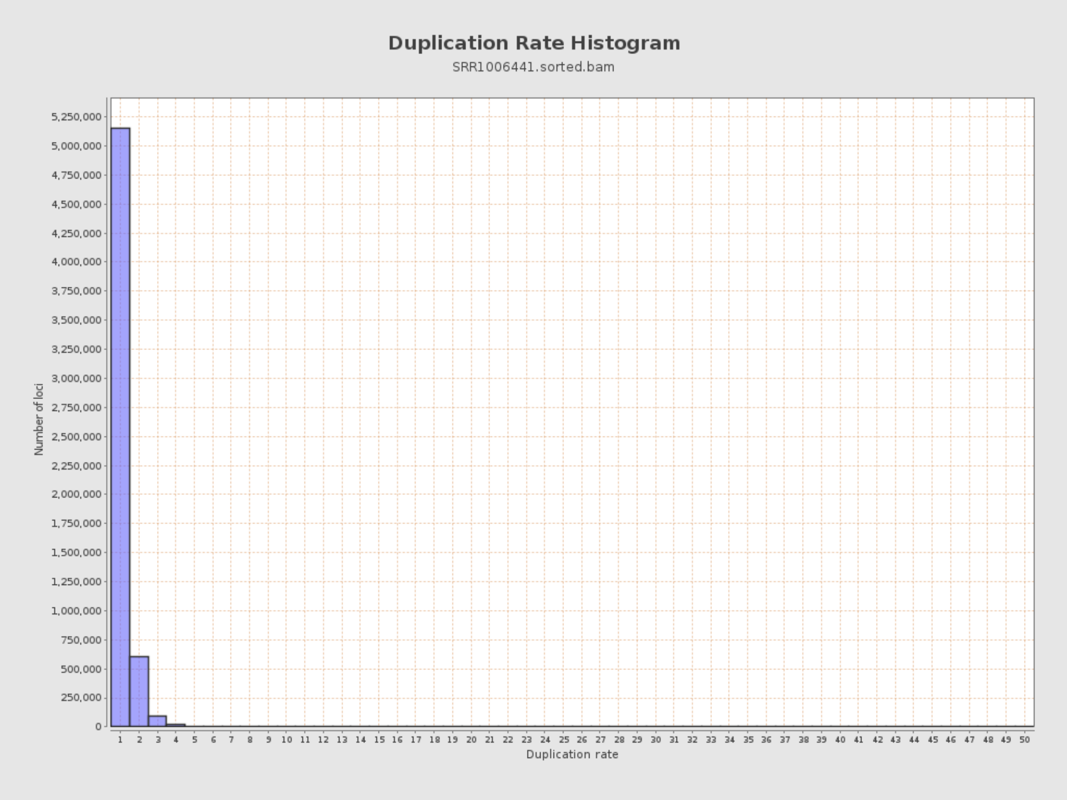
5. Results : Coverage Histogram (0-50X)



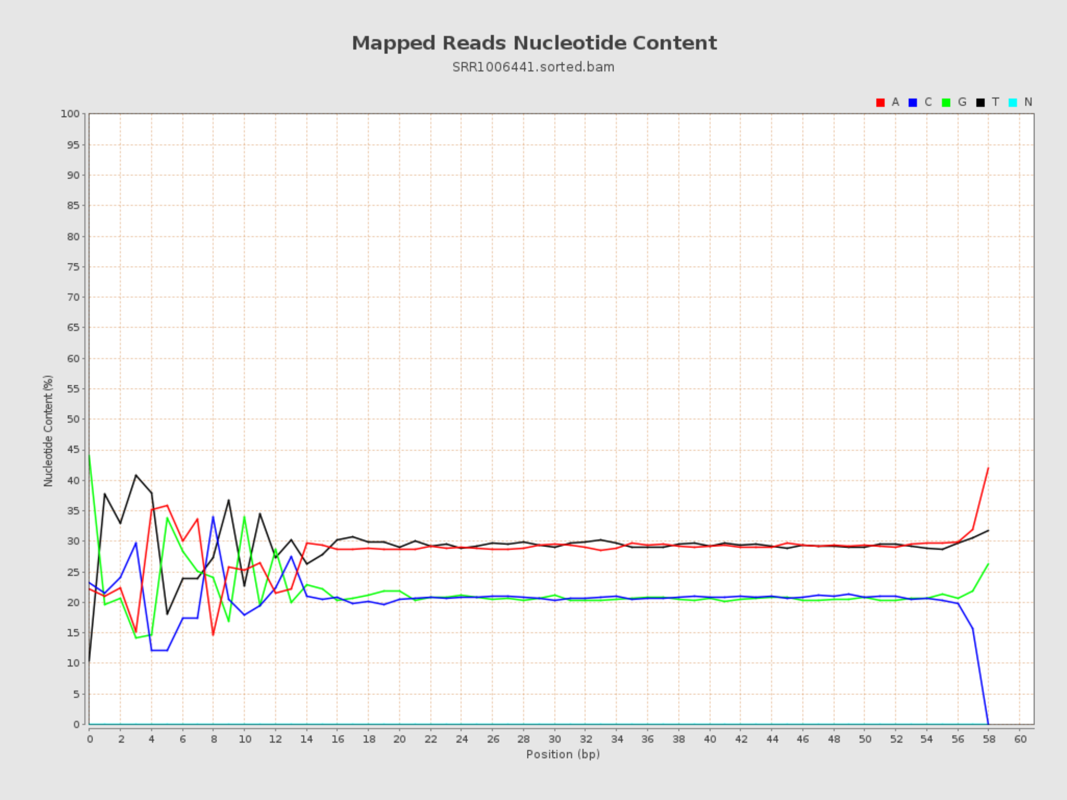
6. Results : Genome Fraction Coverage



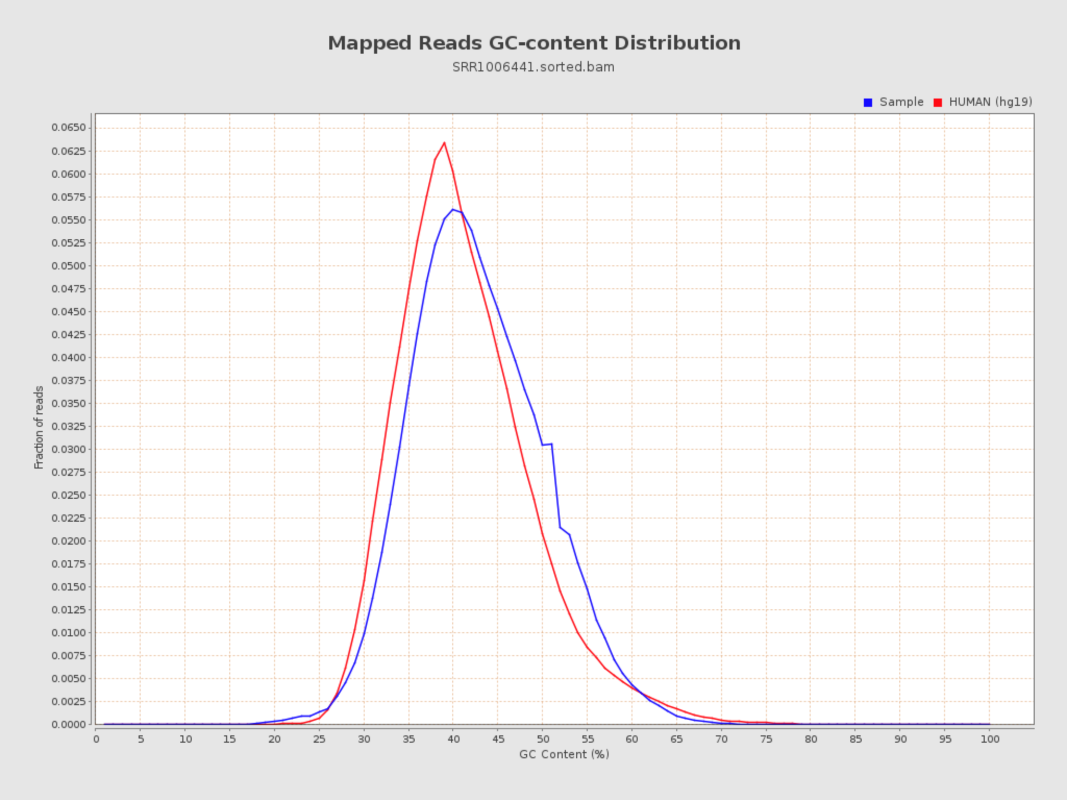
7. Results : Duplication Rate Histogram



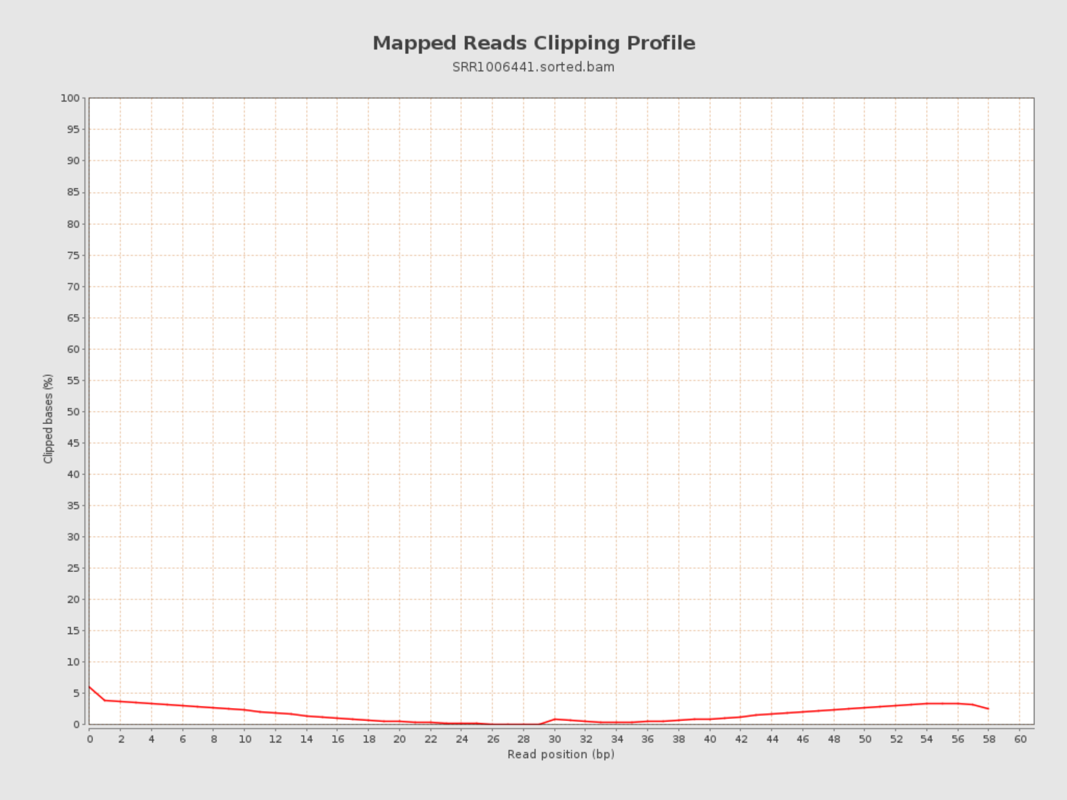
8. Results : Mapped Reads Nucleotide Content



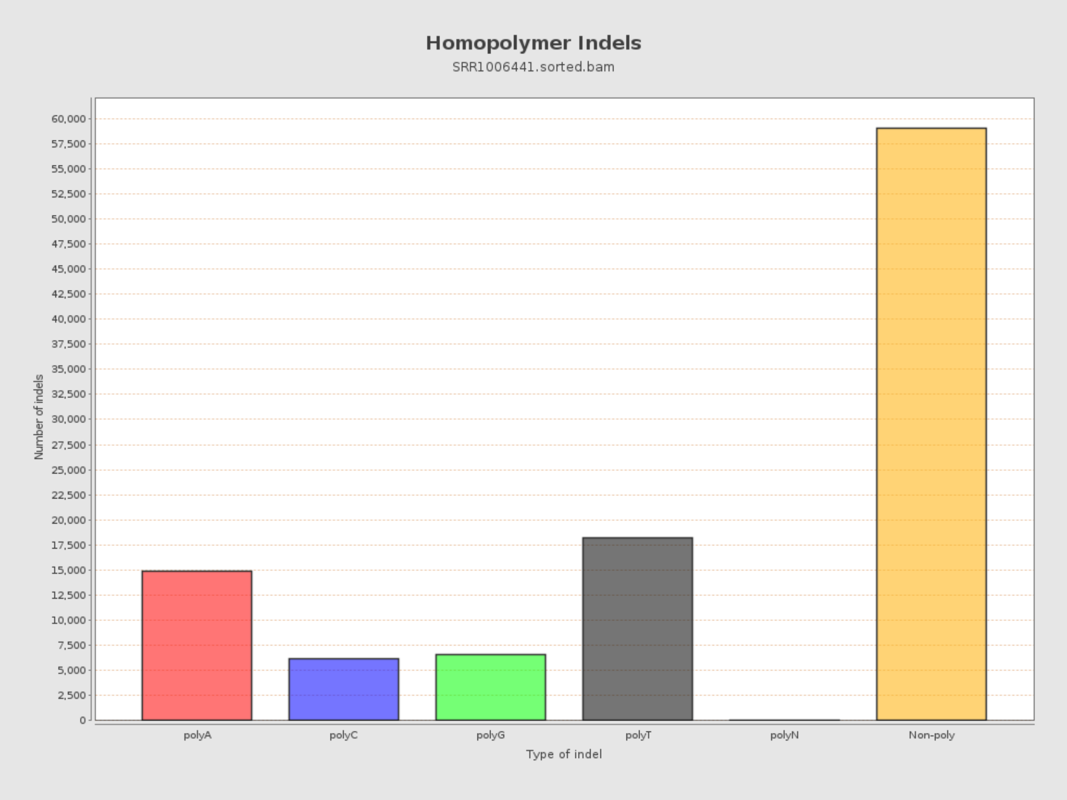
9. Results : Mapped Reads GC-content Distribution



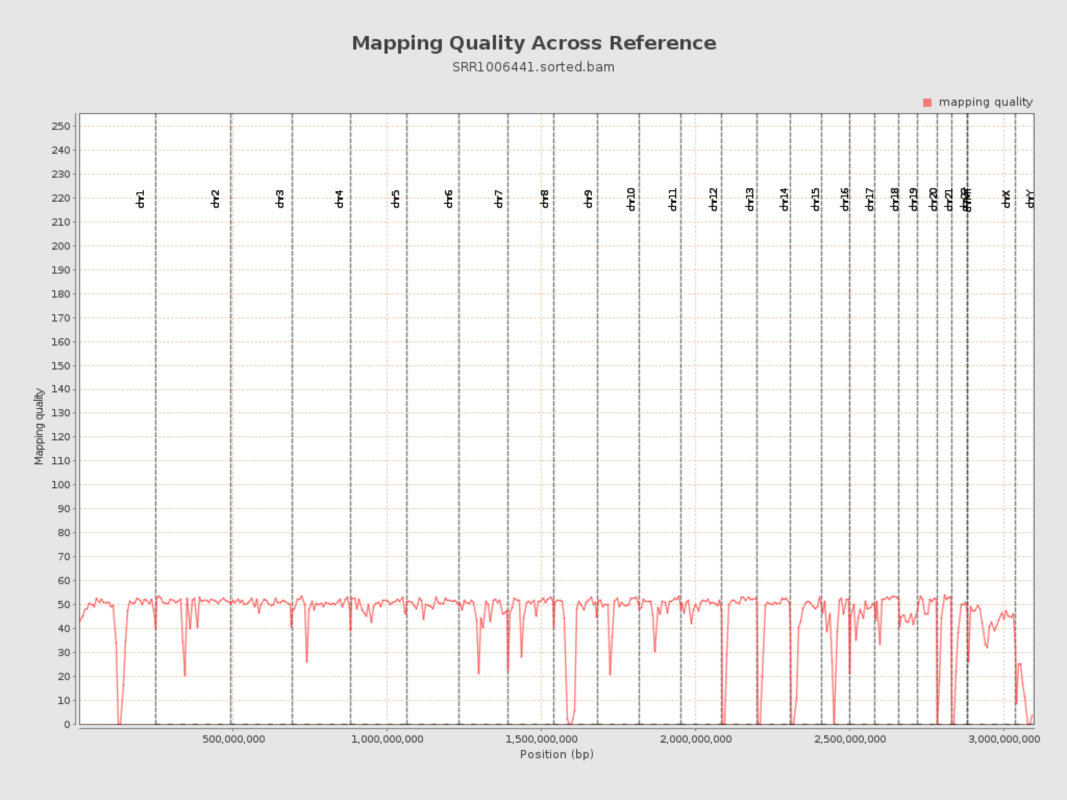
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram