Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:06:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080641.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_SRR3080641 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080641.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:06:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080641.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,487,891
Mapped reads	4,531,079 / 82.57%
Unmapped reads	956,812 / 17.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,700 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	251,976 / 4.59%
Duplication rate	4.22%
Clipped reads	2,174,021 / 39.61%

2.2. ACGT Content

Number/percentage of A's	81,654,759 / 27.17%
Number/percentage of C's	54,077,008 / 17.99%
Number/percentage of T's	96,959,734 / 32.26%
Number/percentage of G's	67,651,609 / 22.51%
Number/percentage of N's	242,963 / 0.08%
GC Percentage	40.5%

2.3. Coverage

Mean	0.0971

Standard Deviation	0.779

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

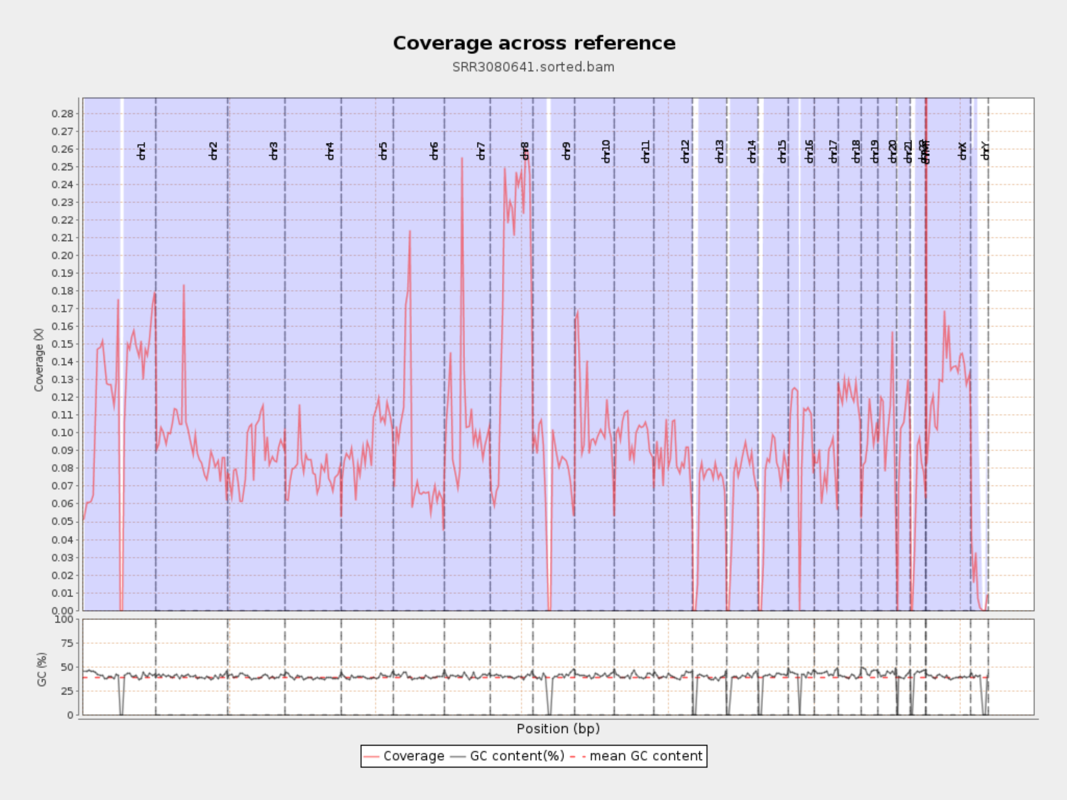
General error rate	0.93%
Mismatches	2,743,384
Insertions	26,335
Mapped reads with at least one insertion	0.58%
Deletions	71,226
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.84%

2.6. Chromosome stats

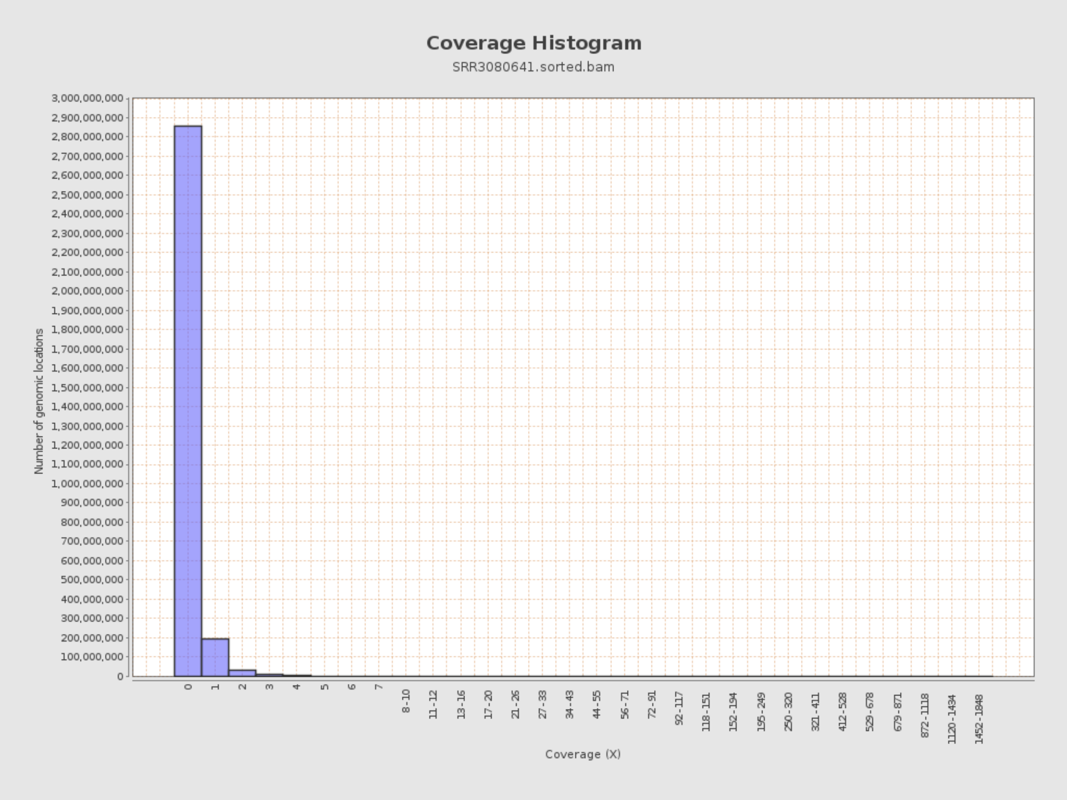
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30287113	0.1215	1.0509
chr2	243199373	23154521	0.0952	0.853
chr3	198022430	17335349	0.0875	0.3559
chr4	191154276	15027383	0.0786	0.3739
chr5	180915260	16969870	0.0938	0.3722
chr6	171115067	15153665	0.0886	0.6277
chr7	159138663	17086879	0.1074	2.1397

chr8	146364022	27578661	0.1884	0.8586
chr9	141213431	10856977	0.0769	0.6564
chr10	135534747	14754384	0.1089	0.6418
chr11	135006516	13239739	0.0981	0.5688
chr12	133851895	11597475	0.0866	0.3685
chr13	115169878	7358514	0.0639	0.3022
chr14	107349540	7398250	0.0689	0.3867
chr15	102531392	6986795	0.0681	0.3169
chr16	90354753	8845734	0.0979	0.4323
chr17	81195210	6573518	0.081	0.4199
chr18	78077248	9491309	0.1216	1.0799
chr19	59128983	5643703	0.0954	0.754
chr20	63025520	6760736	0.1073	0.422
chr21	48129895	4577382	0.0951	0.4197
chr22	51304566	3064385	0.0597	0.2894
chrMT	16571	112678	6.7997	7.8333
chrX	155270560	20132954	0.1297	0.5254
chrY	59373566	714592	0.012	0.223

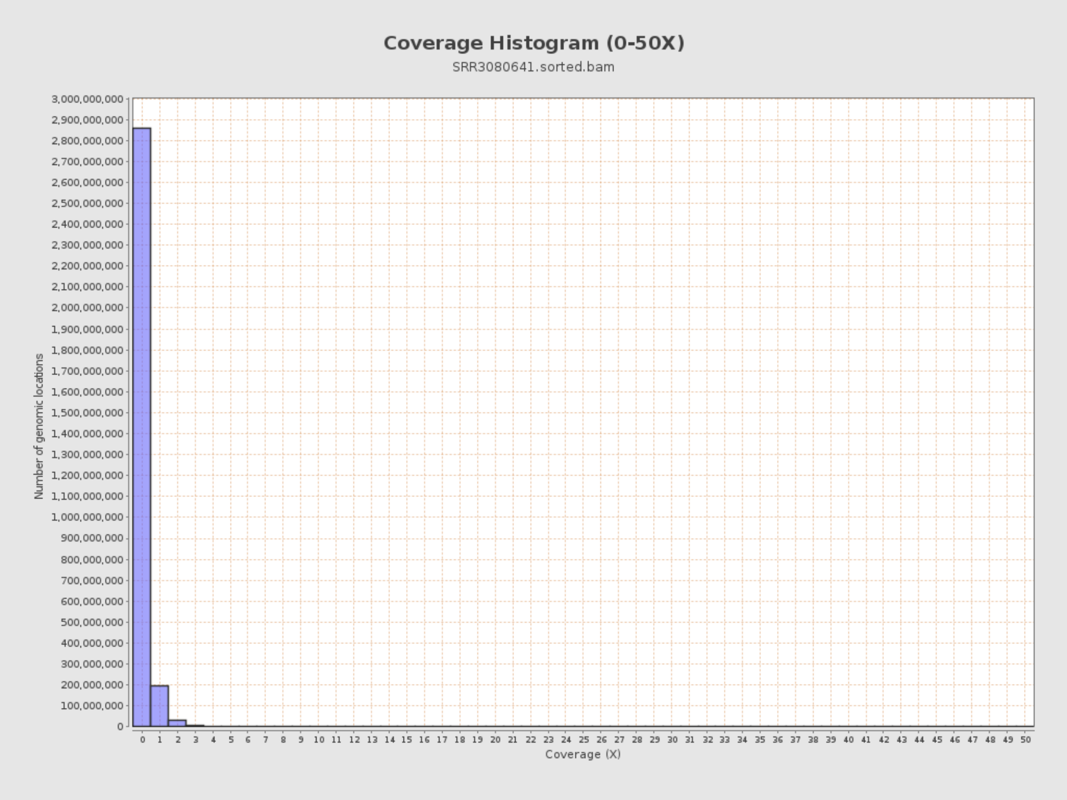
3. Results : Coverage across reference



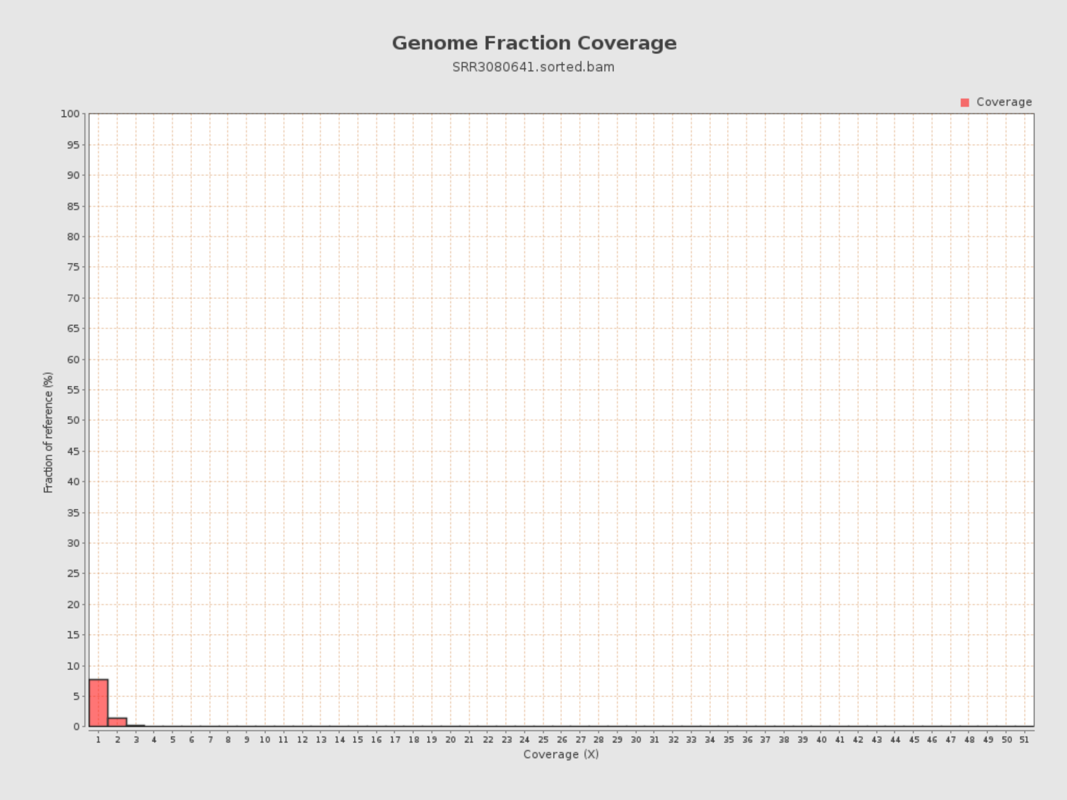
4. Results : Coverage Histogram



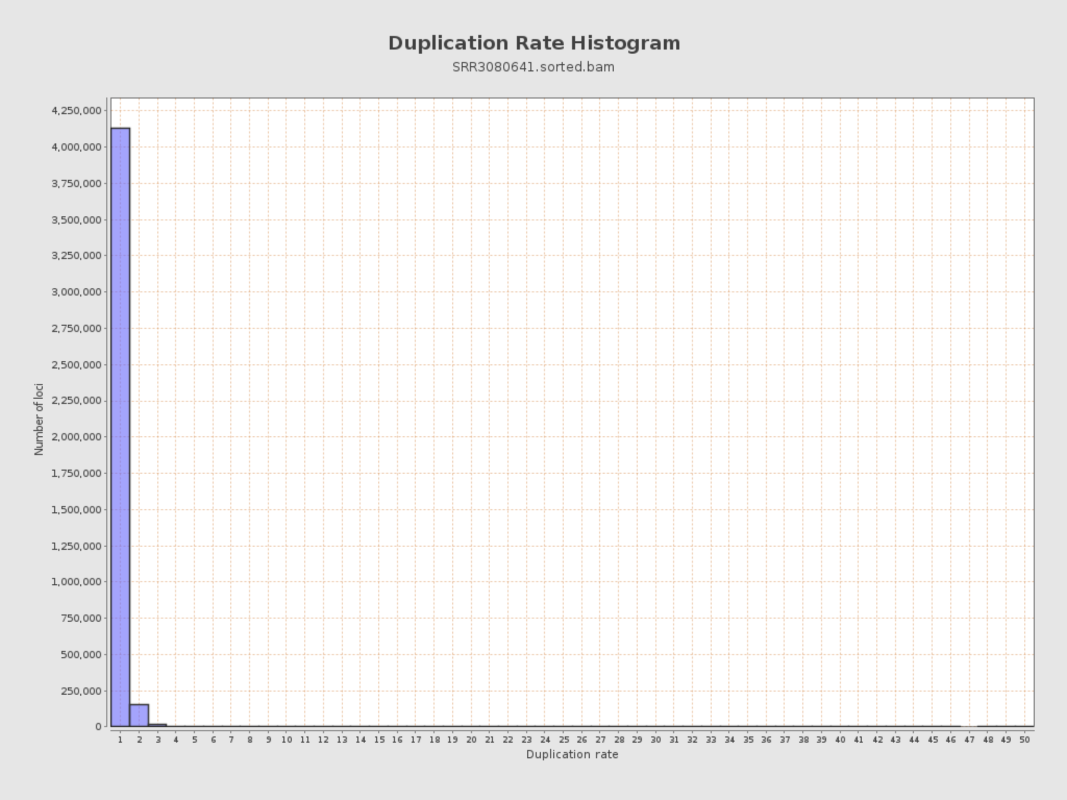
5. Results : Coverage Histogram (0-50X)



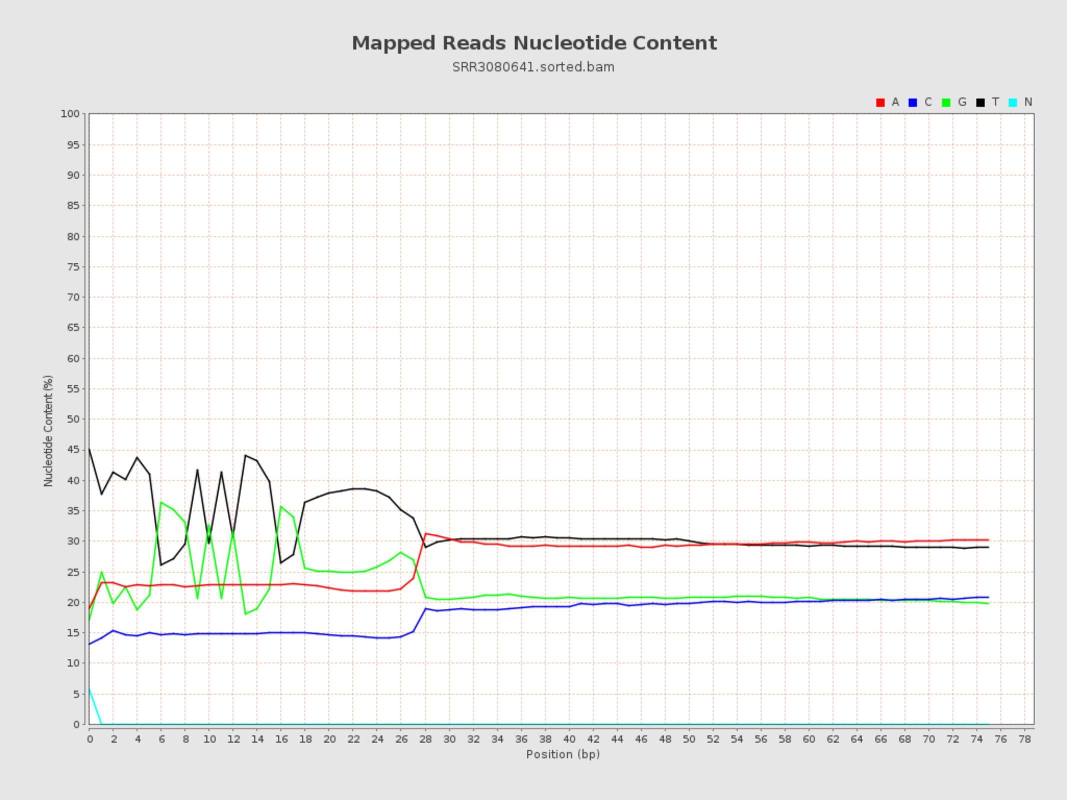
6. Results : Genome Fraction Coverage



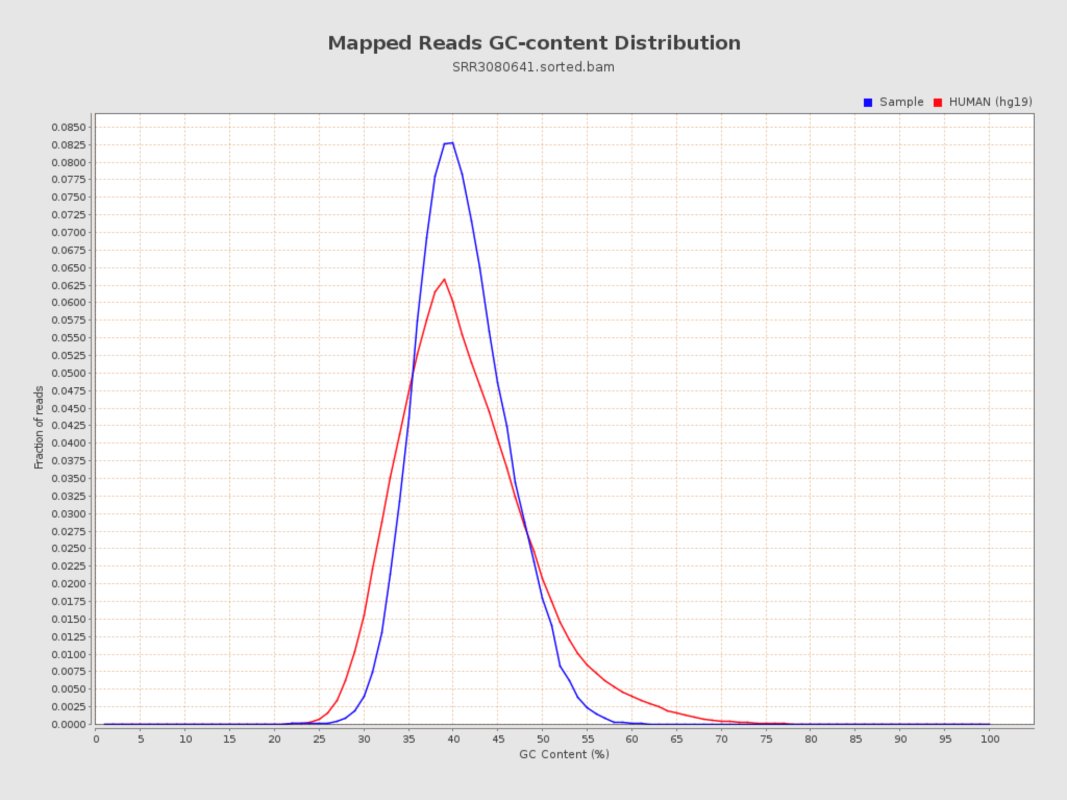
7. Results : Duplication Rate Histogram



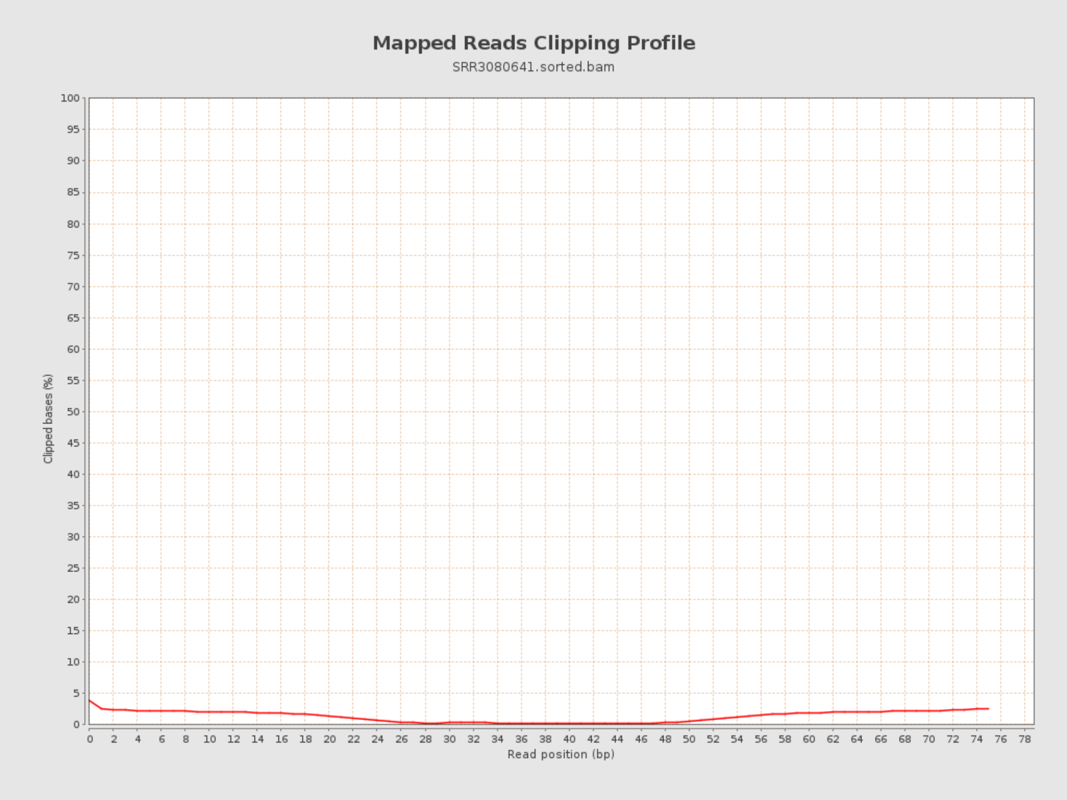
8. Results : Mapped Reads Nucleotide Content



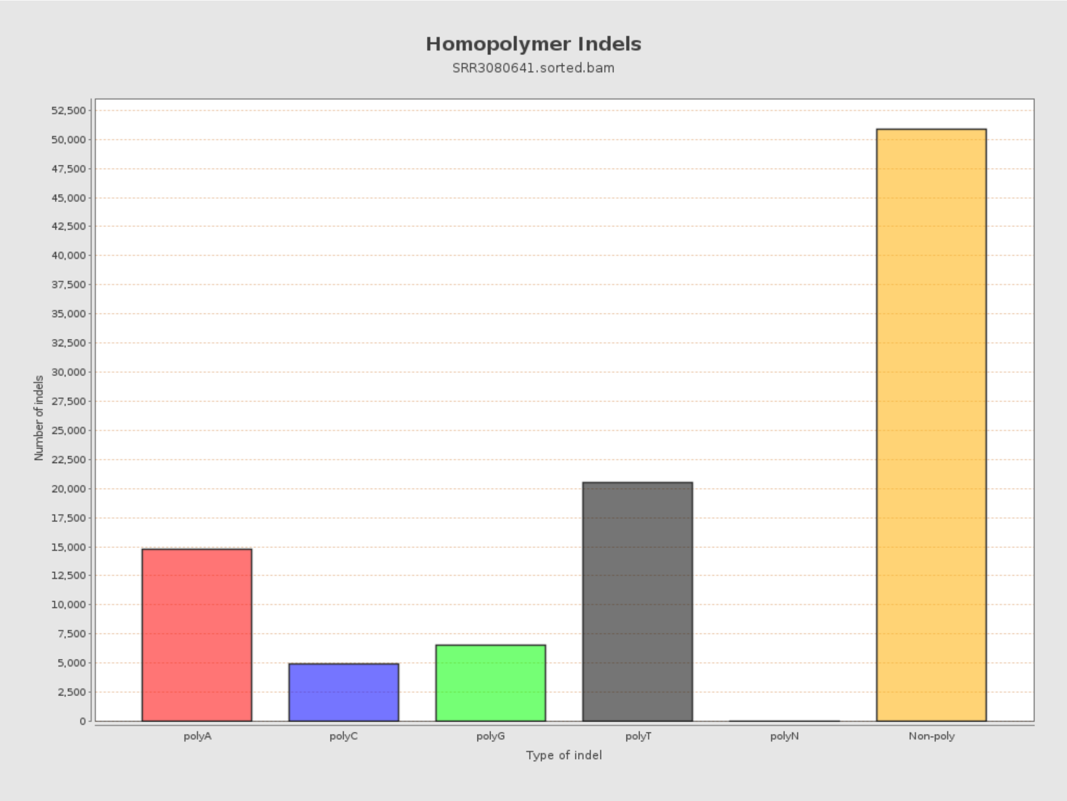
9. Results : Mapped Reads GC-content Distribution



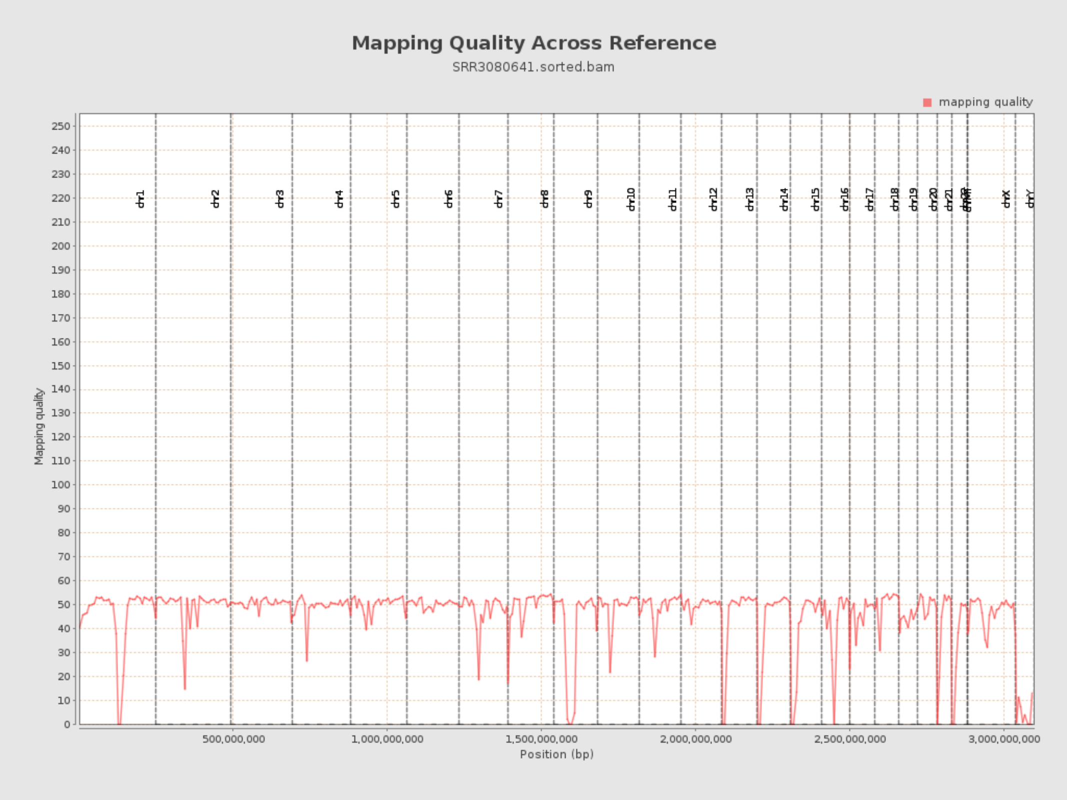
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram