Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:52:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080786.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_SRR3080786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:52:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,686,376
Mapped reads	2,396,527 / 89.21%
Unmapped reads	289,849 / 10.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,074 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	114,383 / 4.26%
Duplication rate	3.91%
Clipped reads	1,129,553 / 42.05%

2.2. ACGT Content

Number/percentage of A's	45,921,583 / 28.82%
Number/percentage of C's	30,927,668 / 19.41%
Number/percentage of T's	48,415,148 / 30.38%
Number/percentage of G's	34,091,884 / 21.39%
Number/percentage of N's	3,239 / 0%
GC Percentage	40.8%

2.3. Coverage

Mean	0.0515

Standard Deviation	0.3827

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

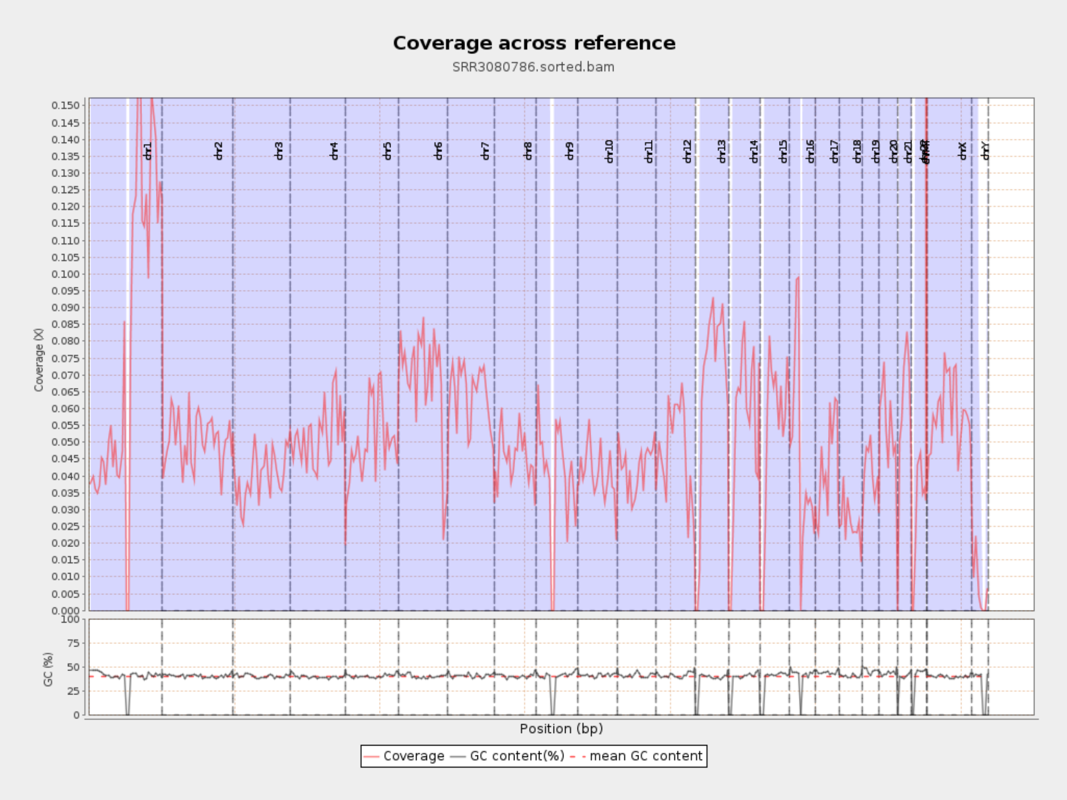
General error rate	0.76%
Mismatches	1,184,754
Insertions	12,183
Mapped reads with at least one insertion	0.5%
Deletions	34,905
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.55%

2.6. Chromosome stats

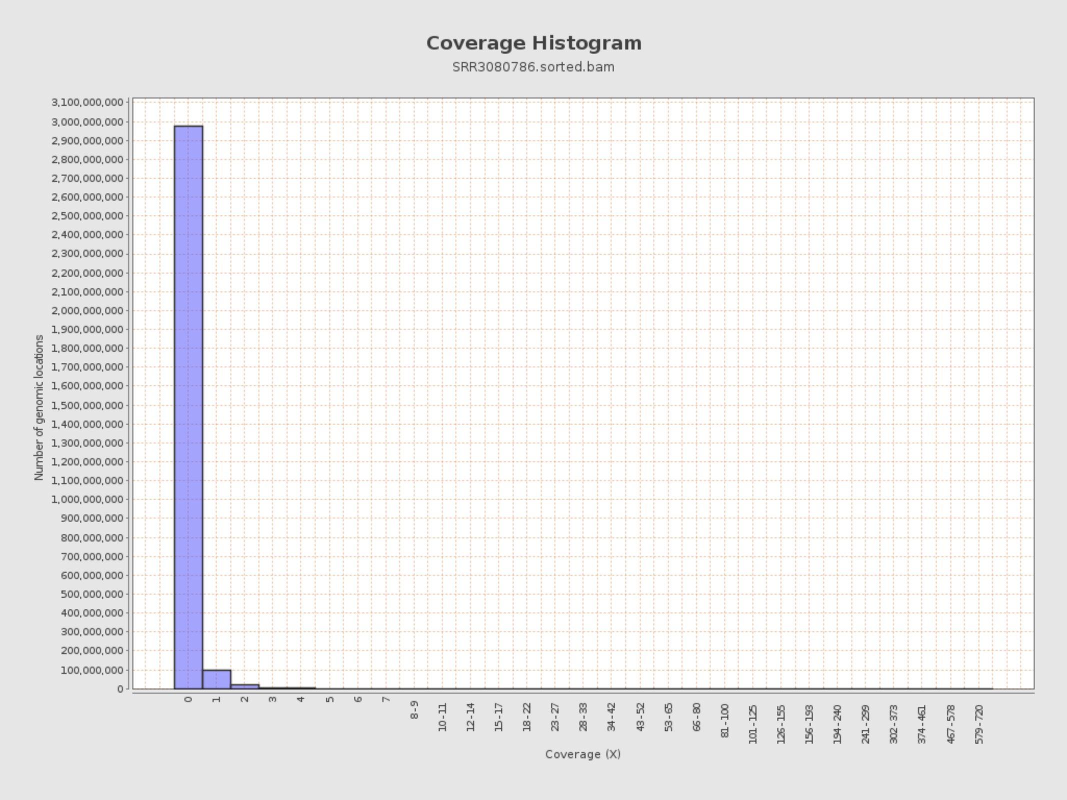
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19651415	0.0788	0.6972
chr2	243199373	12353982	0.0508	0.4102
chr3	198022430	8005435	0.0404	0.251
chr4	191154276	9921686	0.0519	0.2937
chr5	180915260	9173322	0.0507	0.2817
chr6	171115067	11662227	0.0682	0.3562
chr7	159138663	10254725	0.0644	0.3853

chr8	146364022	6652223	0.0454	0.4368
chr9	141213431	5577613	0.0395	0.3223
chr10	135534747	5529739	0.0408	0.3018
chr11	135006516	5751967	0.0426	0.2898
chr12	133851895	6379577	0.0477	0.2739
chr13	115169878	7630902	0.0663	0.3244
chr14	107349540	5718776	0.0533	0.3005
chr15	102531392	5443985	0.0531	0.2916
chr16	90354753	4096631	0.0453	0.2869
chr17	81195210	3521336	0.0434	0.2753
chr18	78077248	2033370	0.026	0.5587
chr19	59128983	2461220	0.0416	0.5031
chr20	63025520	3476668	0.0552	0.2958
chr21	48129895	2826248	0.0587	0.3143
chr22	51304566	1455116	0.0284	0.2068
chrMT	16571	415487	25.0731	12.7057
chrX	155270560	9004975	0.058	0.3131
chrY	59373566	416597	0.007	0.1671

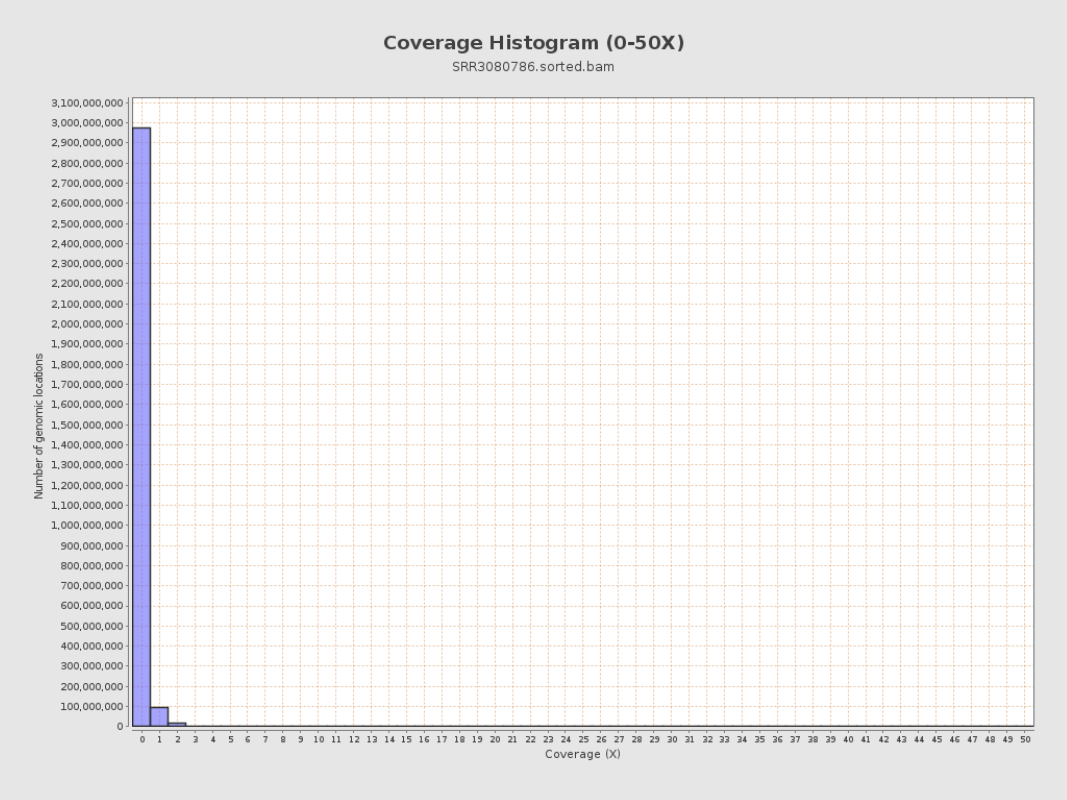
3. Results : Coverage across reference



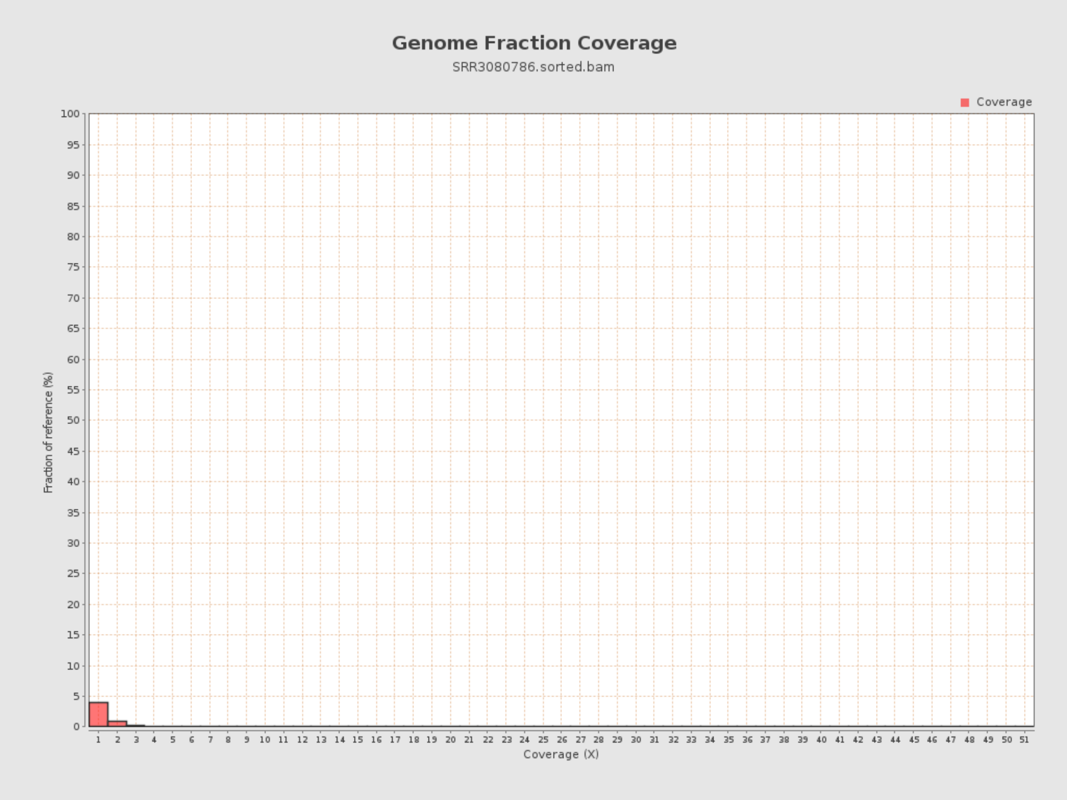
4. Results : Coverage Histogram



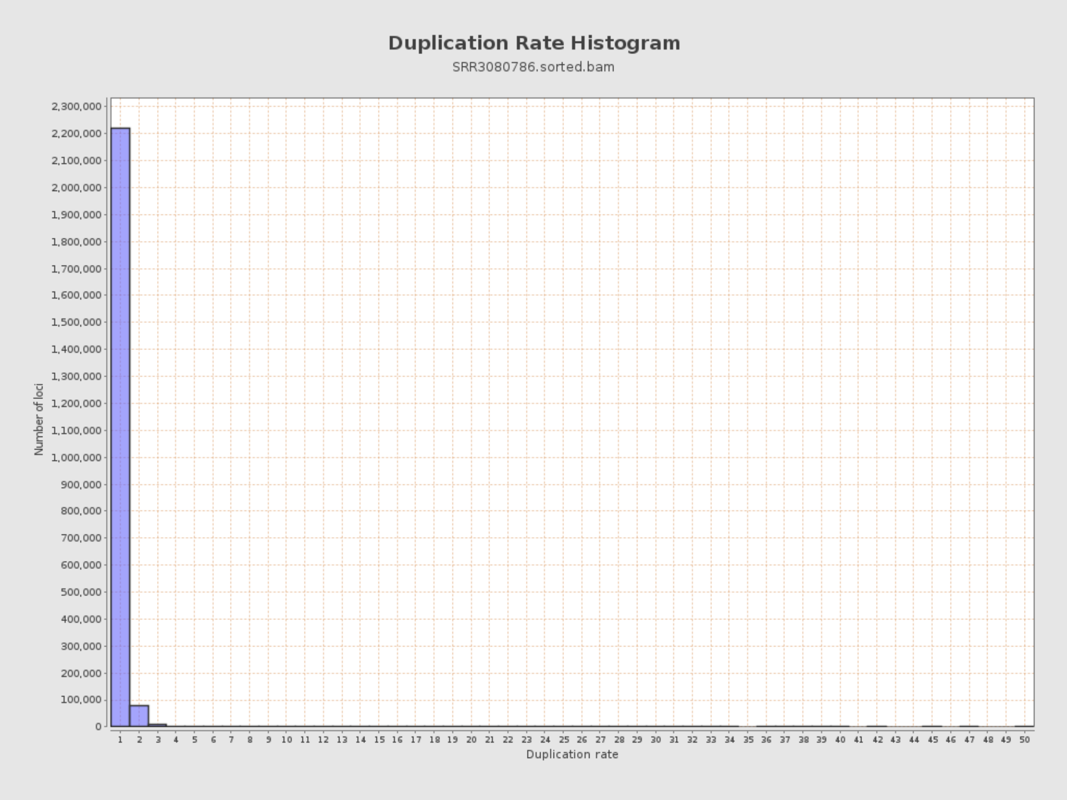
5. Results : Coverage Histogram (0-50X)



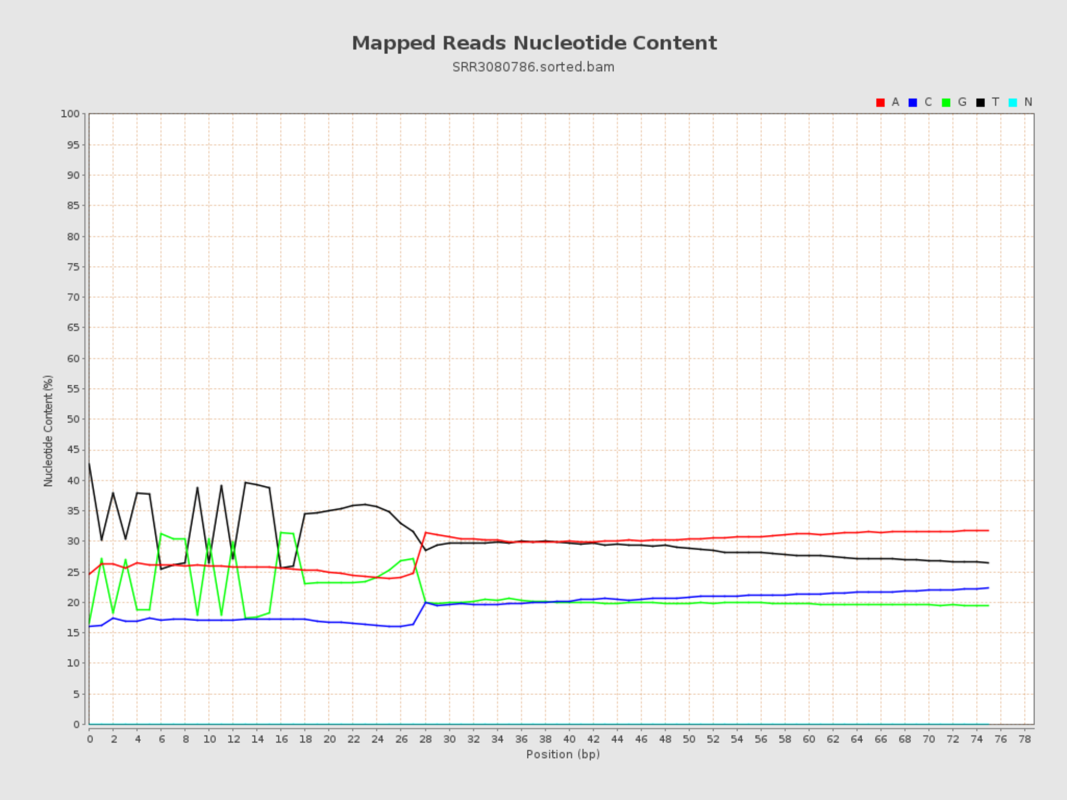
6. Results : Genome Fraction Coverage



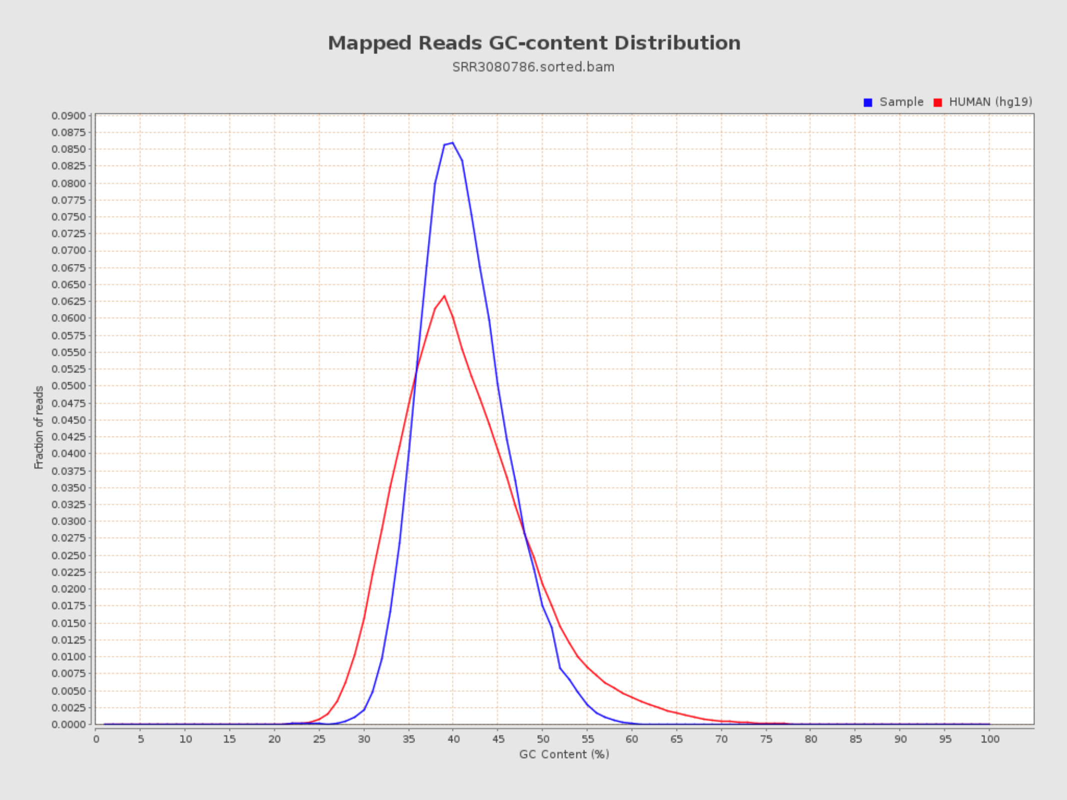
7. Results : Duplication Rate Histogram



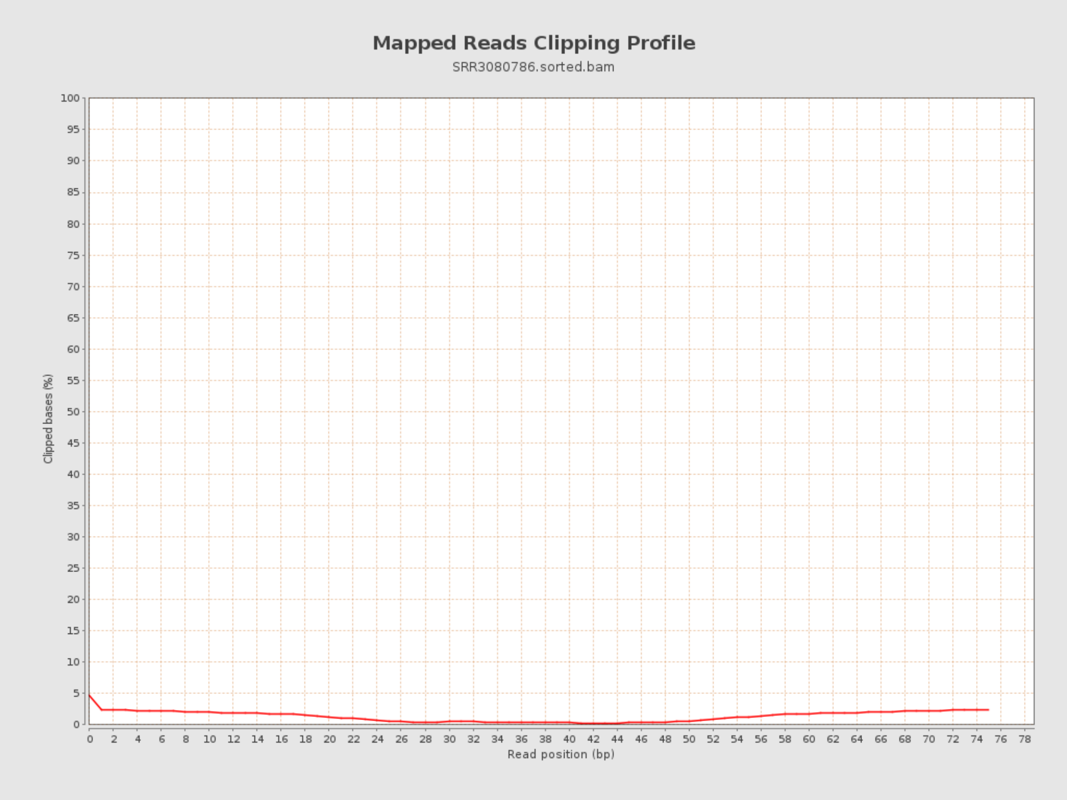
8. Results : Mapped Reads Nucleotide Content



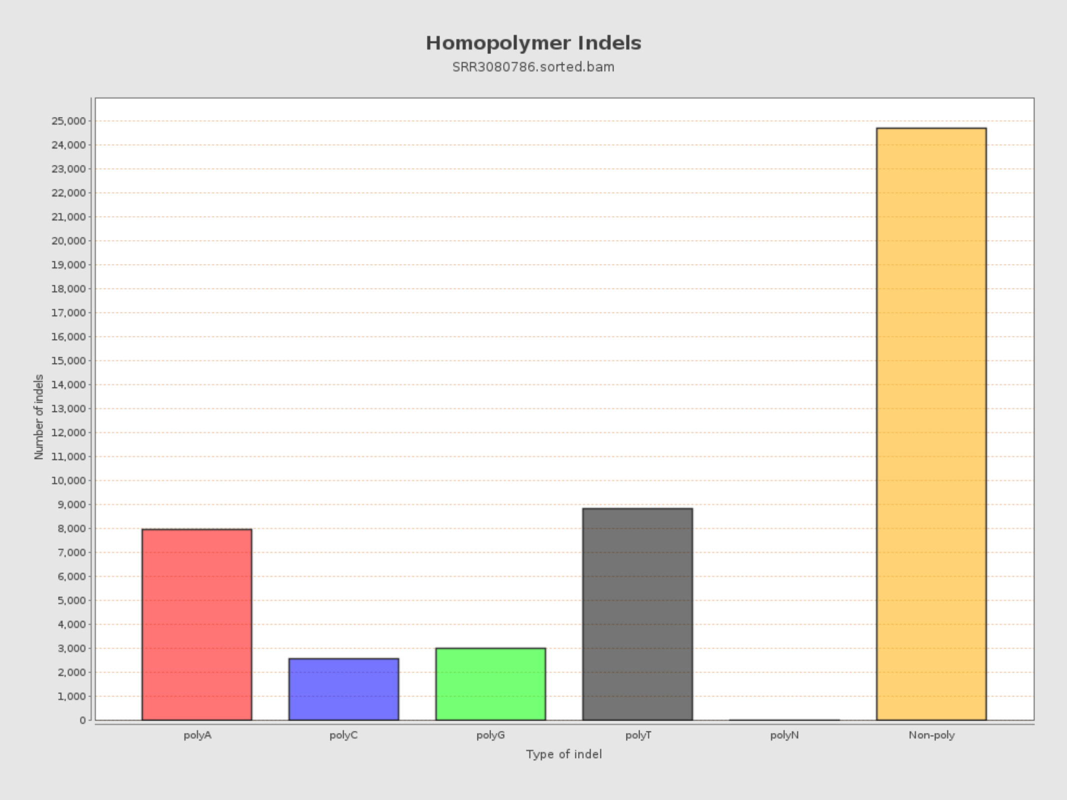
9. Results : Mapped Reads GC-content Distribution



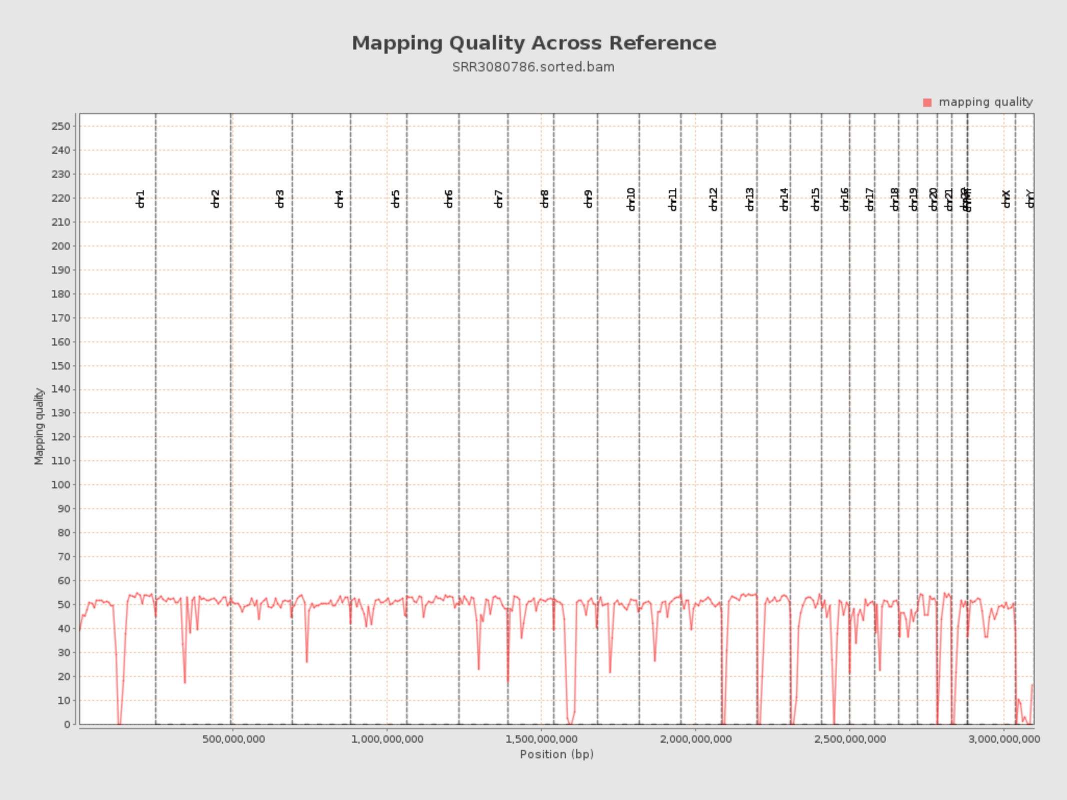
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram