Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:33:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081253.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_SRR3081253 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081253.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:33:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081253.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,793,656
Mapped reads	5,114,692 / 88.28%
Unmapped reads	678,964 / 11.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	58,926 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	318,300 / 5.49%
Duplication rate	4.86%
Clipped reads	1,971,420 / 34.03%

2.2. ACGT Content

Number/percentage of A's	98,624,358 / 28.24%
Number/percentage of C's	64,534,621 / 18.48%
Number/percentage of T's	111,061,923 / 31.8%
Number/percentage of G's	74,939,140 / 21.46%
Number/percentage of N's	96,165 / 0.03%
GC Percentage	39.93%

2.3. Coverage

Mean	0.1129

Standard Deviation	0.7832

2.4. Mapping Quality

Mean Mapping Quality	47.54

2.5. Mismatches and indels

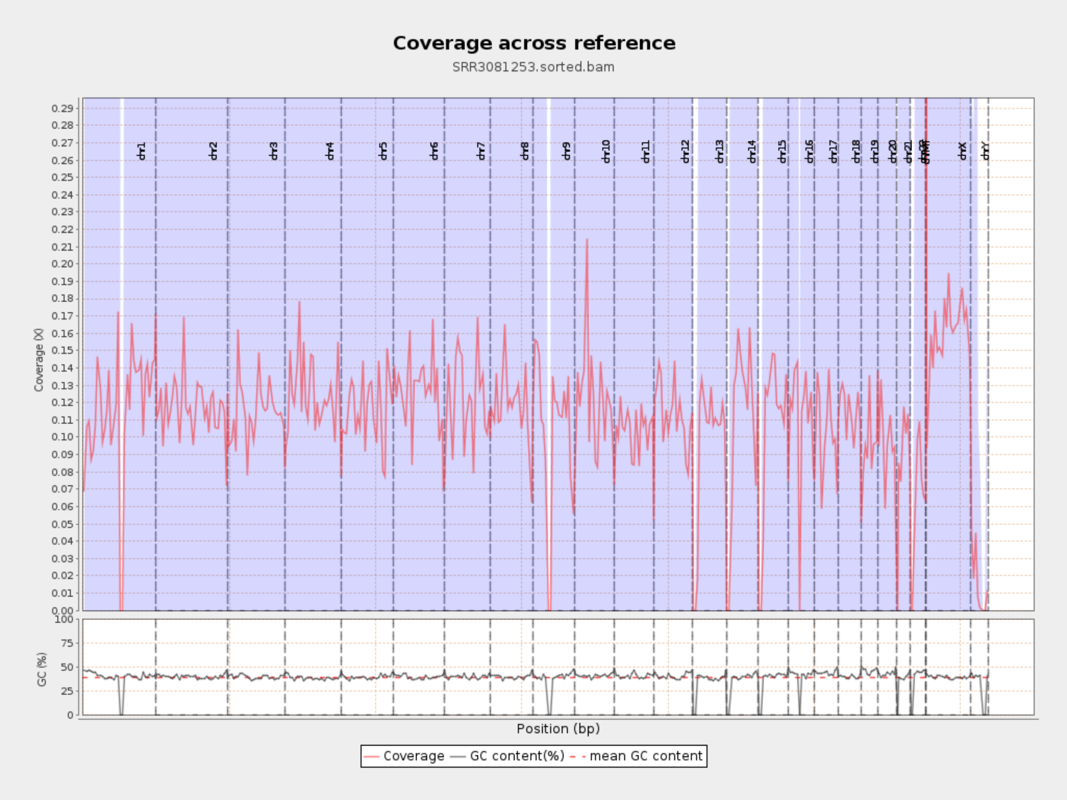
General error rate	0.86%
Mismatches	2,960,700
Insertions	29,043
Mapped reads with at least one insertion	0.56%
Deletions	84,537
Mapped reads with at least one deletion	1.64%
Homopolymer indels	48.52%

2.6. Chromosome stats

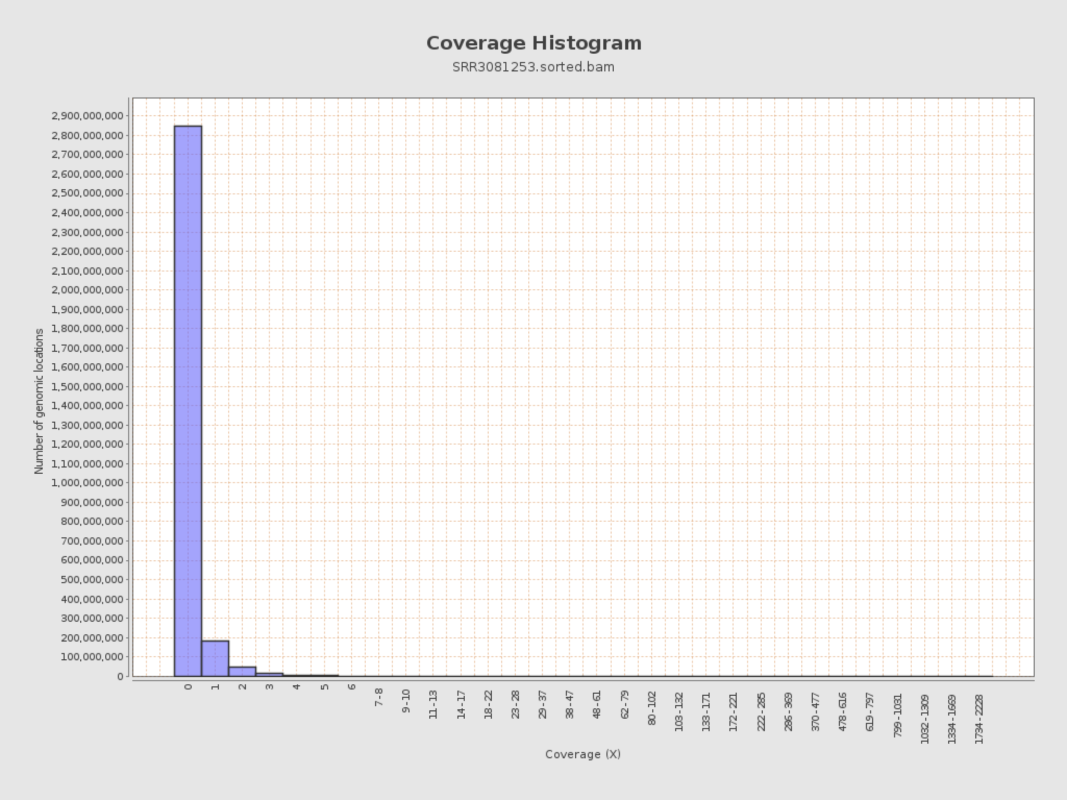
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28687080	0.1151	1.2758
chr2	243199373	28609658	0.1176	0.802
chr3	198022430	22755691	0.1149	0.457
chr4	191154276	23941819	0.1252	0.5323
chr5	180915260	20969855	0.1159	0.4565
chr6	171115067	21836683	0.1276	0.576
chr7	159138663	19398616	0.1219	0.8981

chr8	146364022	17252591	0.1179	1.4217
chr9	141213431	14669454	0.1039	0.7946
chr10	135534747	16650830	0.1229	0.938
chr11	135006516	14035231	0.104	0.7236
chr12	133851895	15233476	0.1138	0.4742
chr13	115169878	10986416	0.0954	0.4084
chr14	107349540	11661981	0.1086	0.5345
chr15	102531392	10594234	0.1033	0.4255
chr16	90354753	9802055	0.1085	0.5213
chr17	81195210	8492646	0.1046	0.5634
chr18	78077248	9005293	0.1153	1.2806
chr19	59128983	5653438	0.0956	1.1104
chr20	63025520	6059194	0.0961	0.4402
chr21	48129895	4201109	0.0873	0.4896
chr22	51304566	3160218	0.0616	0.3243
chrMT	16571	89185	5.382	3.7742
chrX	155270560	24758789	0.1595	0.5982
chrY	59373566	887613	0.0149	0.337

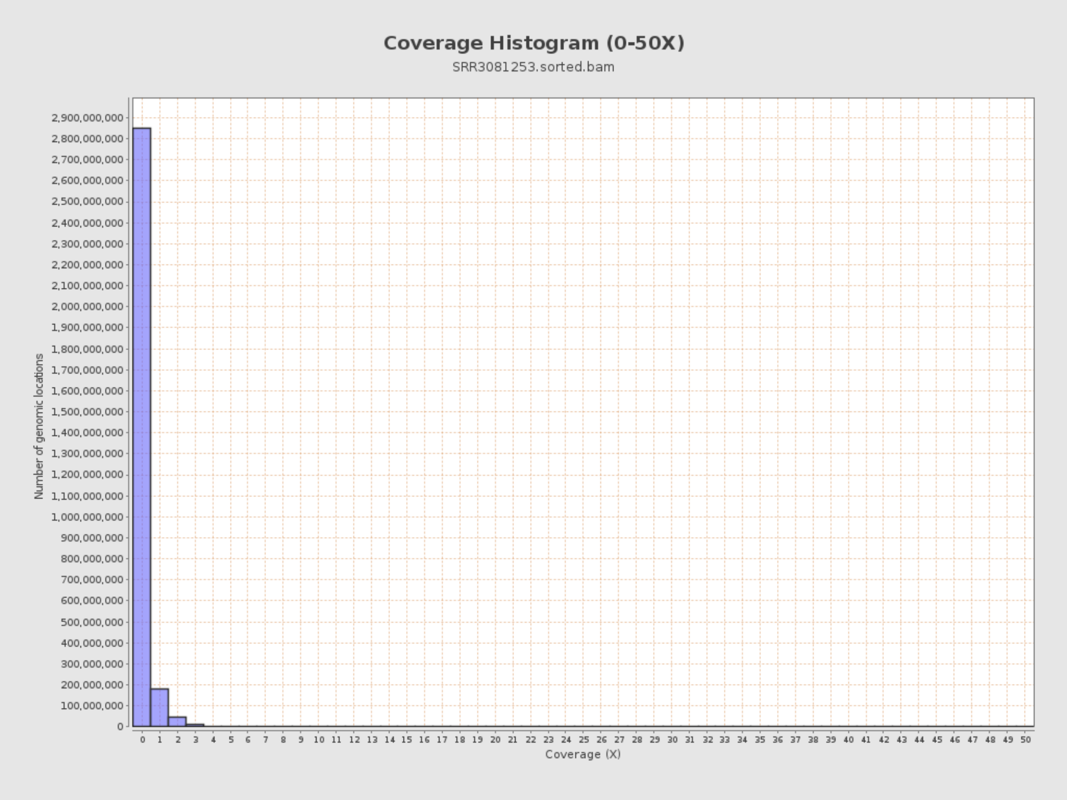
3. Results : Coverage across reference



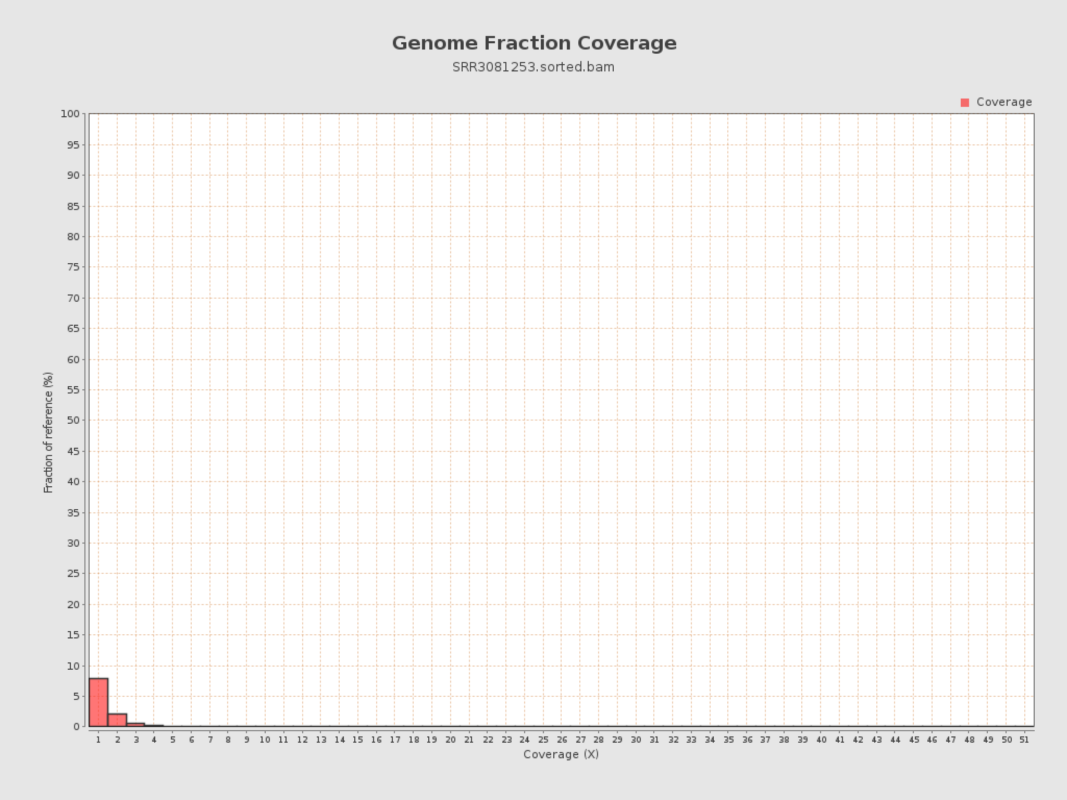
4. Results : Coverage Histogram



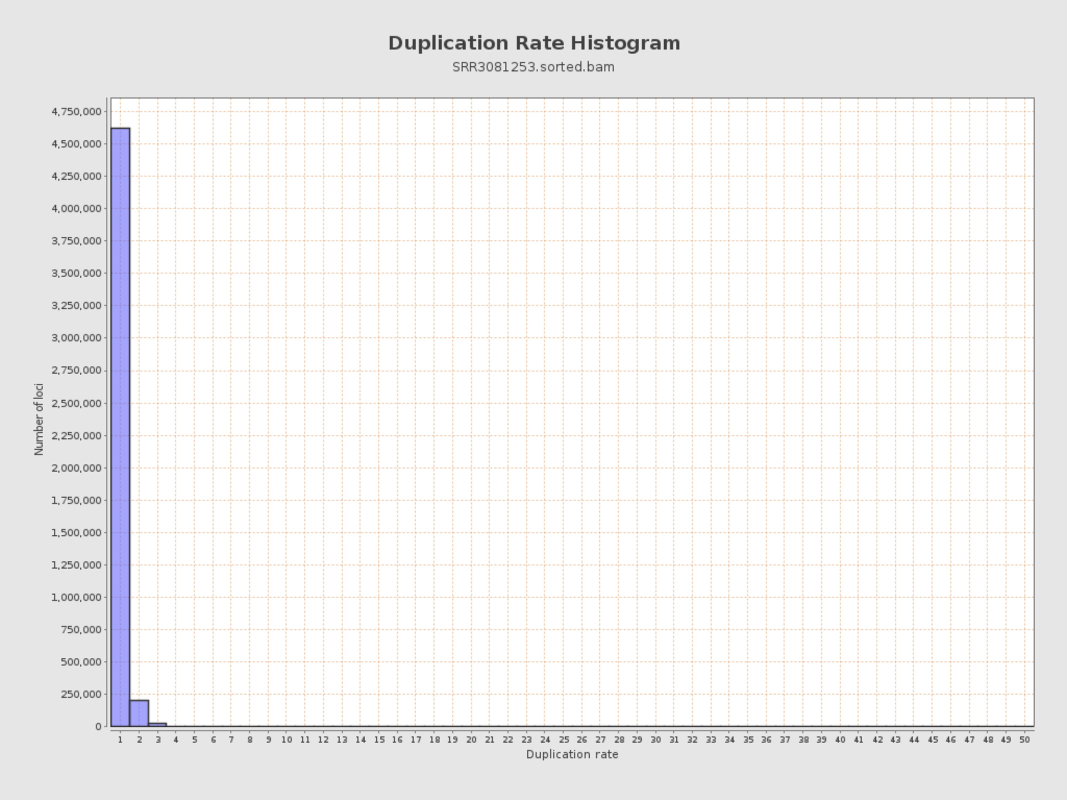
5. Results : Coverage Histogram (0-50X)



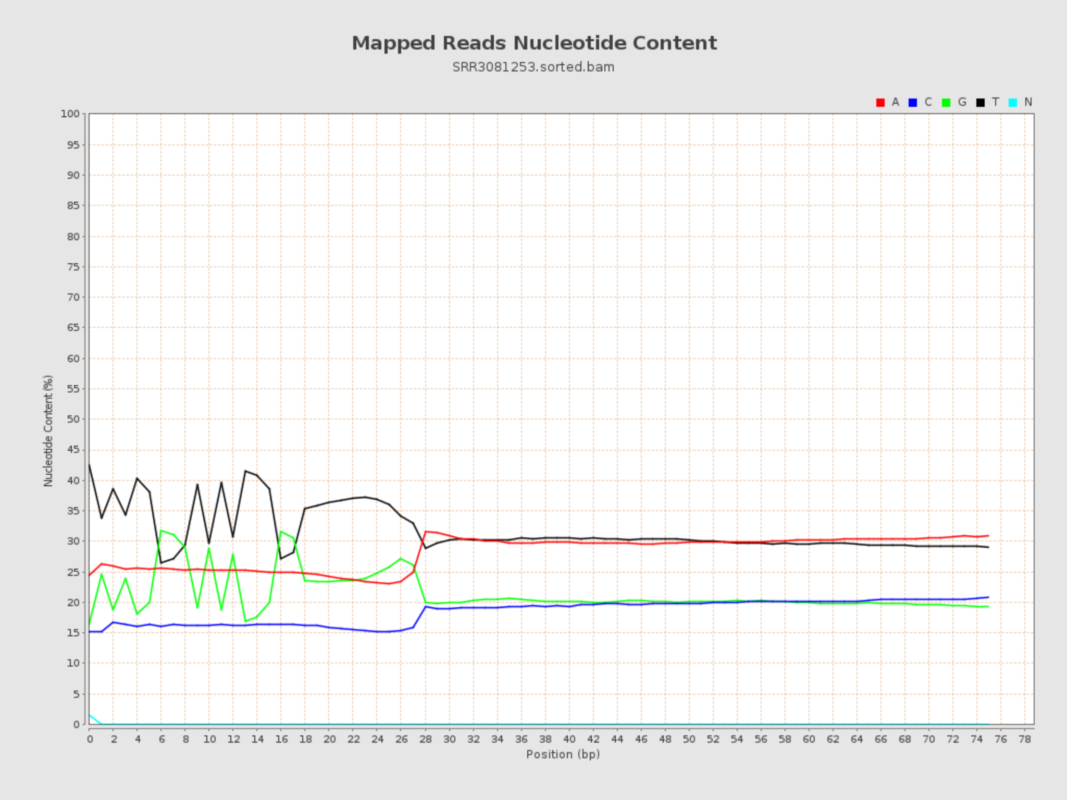
6. Results : Genome Fraction Coverage



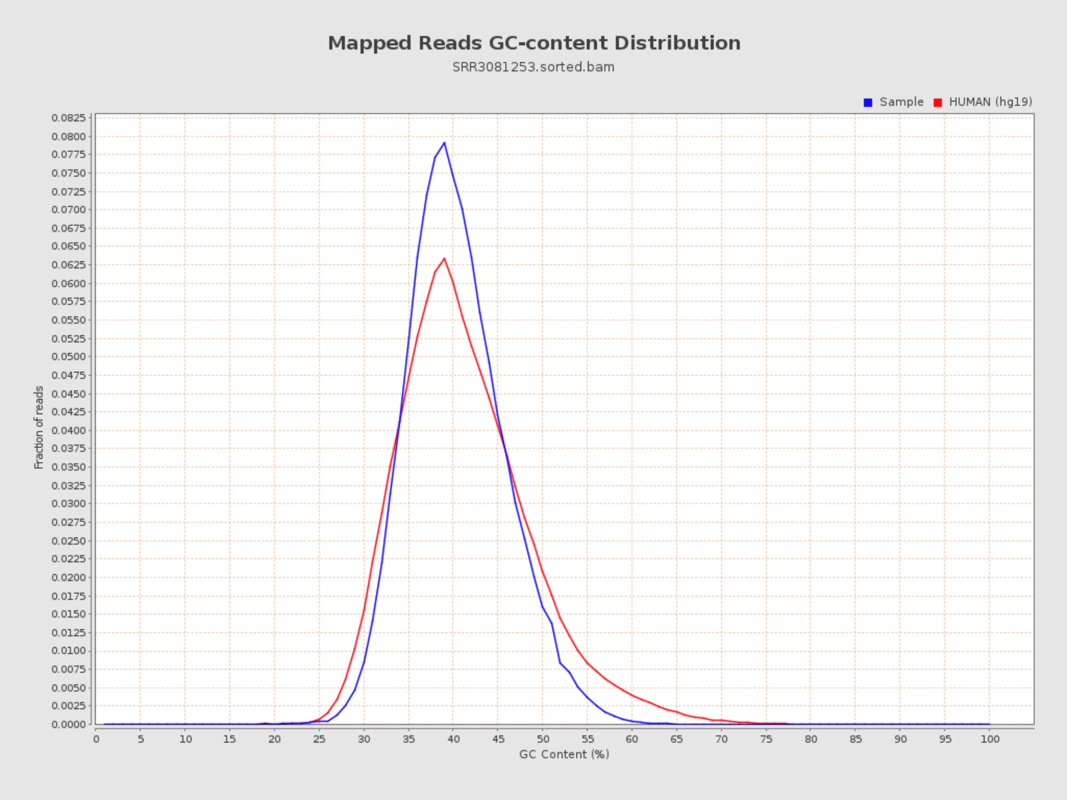
7. Results : Duplication Rate Histogram



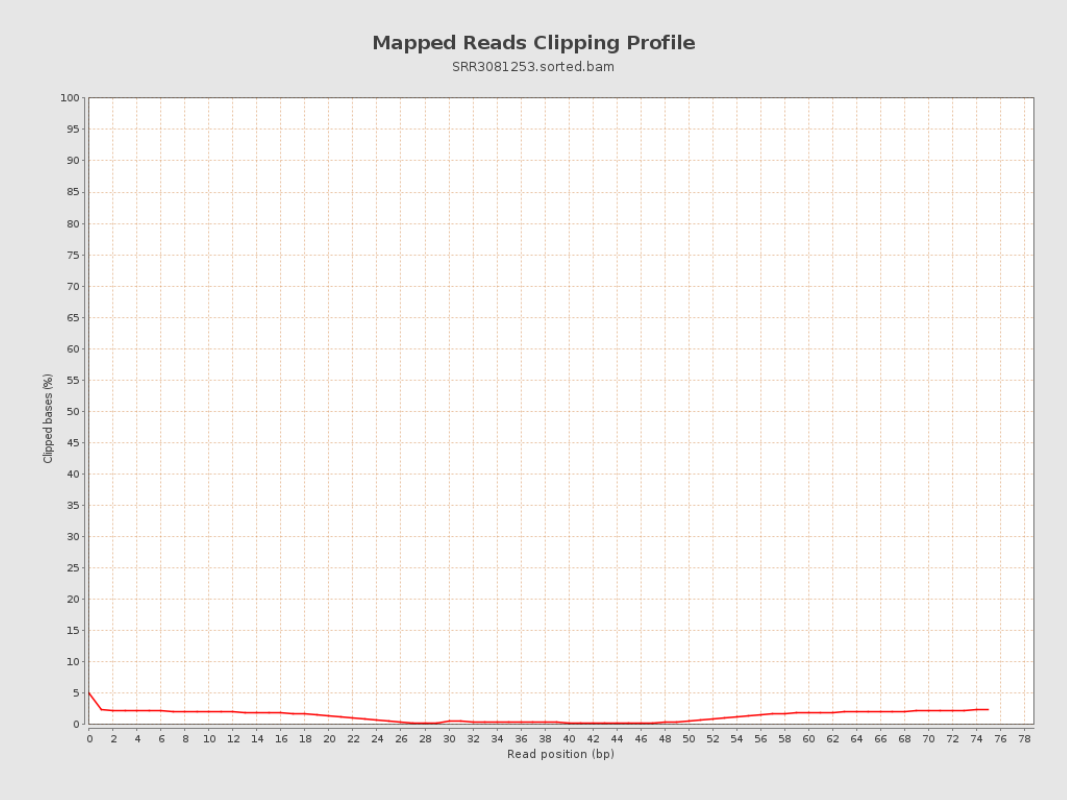
8. Results : Mapped Reads Nucleotide Content



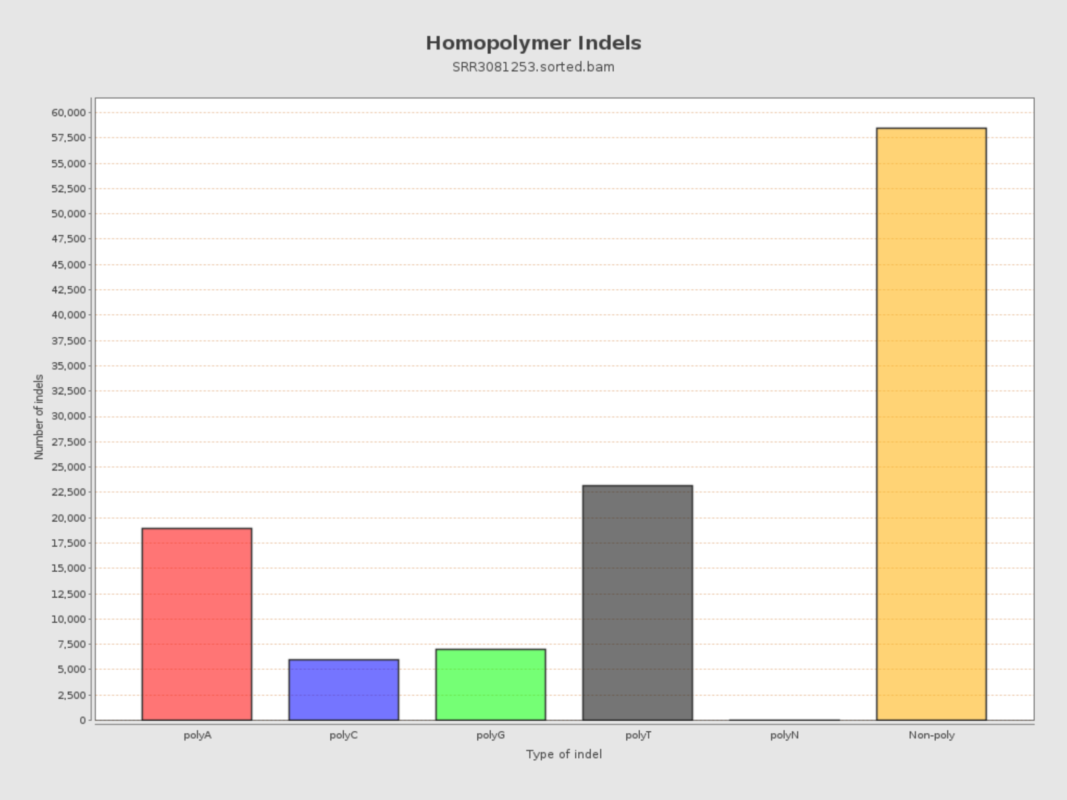
9. Results : Mapped Reads GC-content Distribution



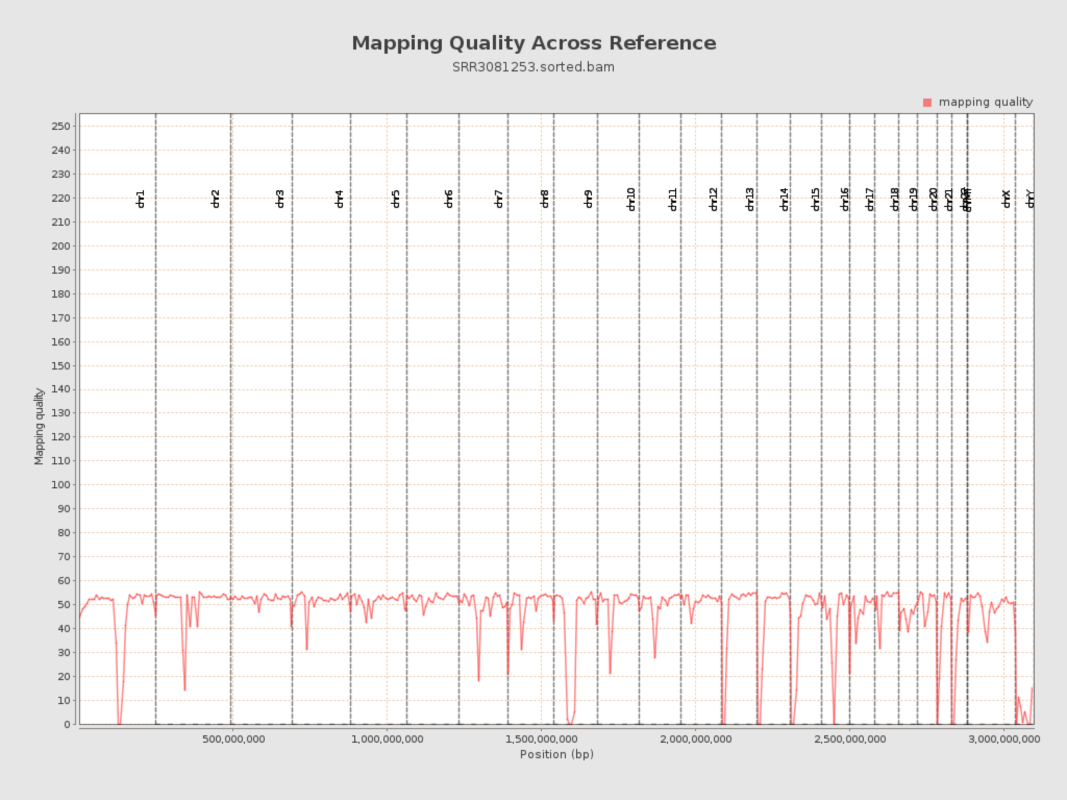
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram