Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:29:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081779.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_SRR3081779 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081779.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:29:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081779.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,951,393
Mapped reads	2,666,308 / 90.34%
Unmapped reads	285,085 / 9.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,347 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	119,683 / 4.06%
Duplication rate	3.09%
Clipped reads	1,175,995 / 39.85%

2.2. ACGT Content

Number/percentage of A's	48,772,211 / 27.35%
Number/percentage of C's	34,287,618 / 19.23%
Number/percentage of T's	54,497,241 / 30.56%
Number/percentage of G's	40,788,210 / 22.87%
Number/percentage of N's	2,083 / 0%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0576

Standard Deviation	0.5503

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

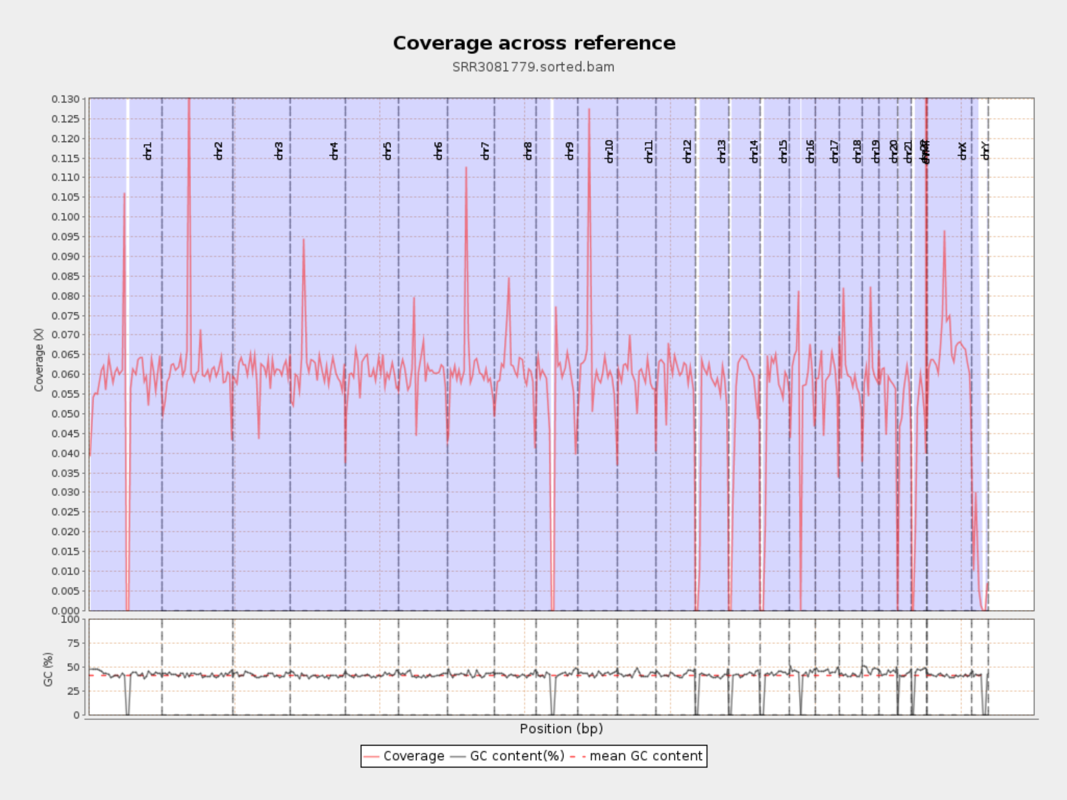
General error rate	0.86%
Mismatches	1,506,346
Insertions	12,965
Mapped reads with at least one insertion	0.48%
Deletions	34,522
Mapped reads with at least one deletion	1.28%
Homopolymer indels	46.22%

2.6. Chromosome stats

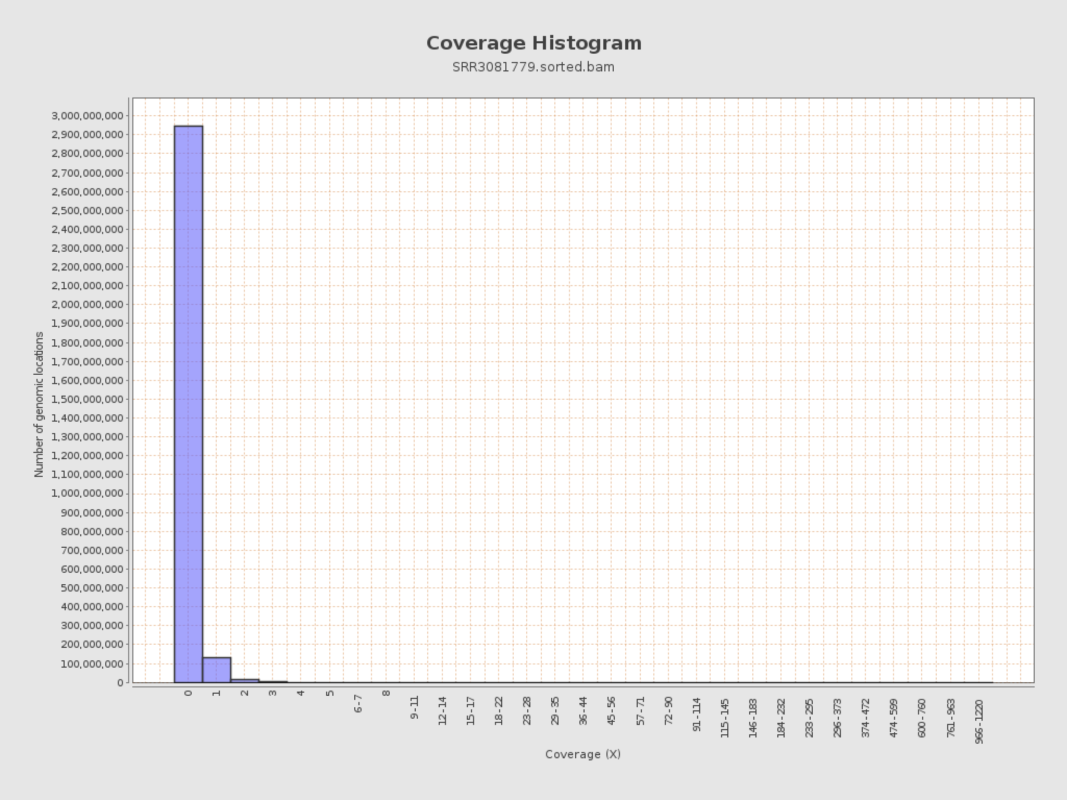
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14182143	0.0569	1.0307
chr2	243199373	15265925	0.0628	0.7257
chr3	198022430	12021985	0.0607	0.2879
chr4	191154276	11762067	0.0615	0.3409
chr5	180915260	10917187	0.0603	0.2837
chr6	171115067	10379392	0.0607	0.3484
chr7	159138663	9947165	0.0625	0.7967

chr8	146364022	8981461	0.0614	0.5872
chr9	141213431	7500817	0.0531	0.5229
chr10	135534747	8537037	0.063	0.6398
chr11	135006516	8011991	0.0593	0.4365
chr12	133851895	8076246	0.0603	0.2888
chr13	115169878	5649276	0.0491	0.2516
chr14	107349540	5389859	0.0502	0.2974
chr15	102531392	4991912	0.0487	0.2617
chr16	90354753	5064559	0.0561	0.3398
chr17	81195210	4667412	0.0575	0.3212
chr18	78077248	4761115	0.061	0.9573
chr19	59128983	3619752	0.0612	0.7843
chr20	63025520	3508365	0.0557	0.2883
chr21	48129895	2326156	0.0483	0.2979
chr22	51304566	1904777	0.0371	0.2177
chrMT	16571	53977	3.2573	2.4612
chrX	155270560	10351888	0.0667	0.3734
chrY	59373566	536754	0.009	0.2423

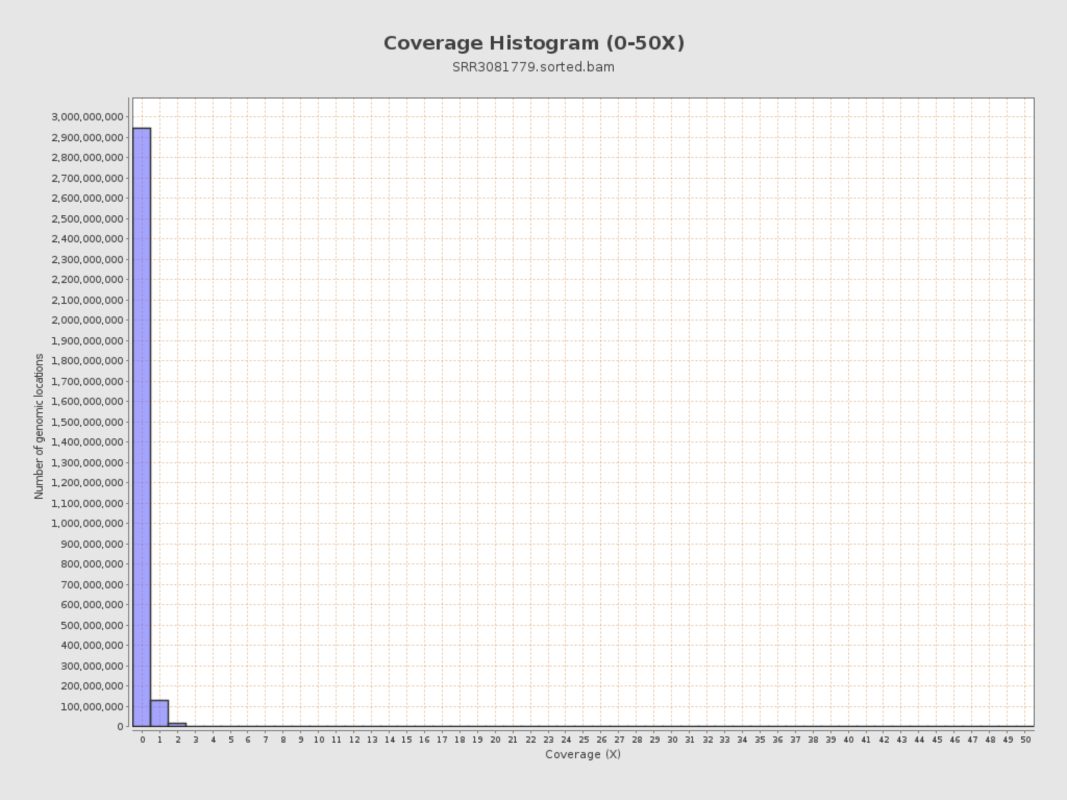
3. Results : Coverage across reference



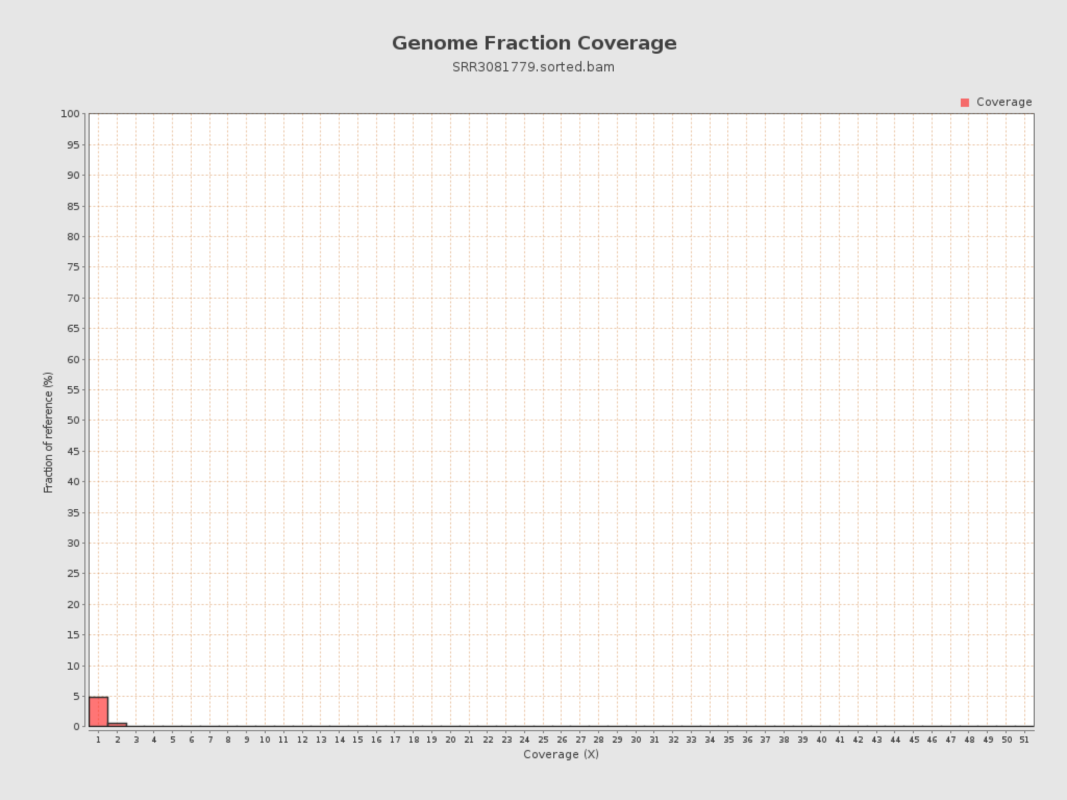
4. Results : Coverage Histogram



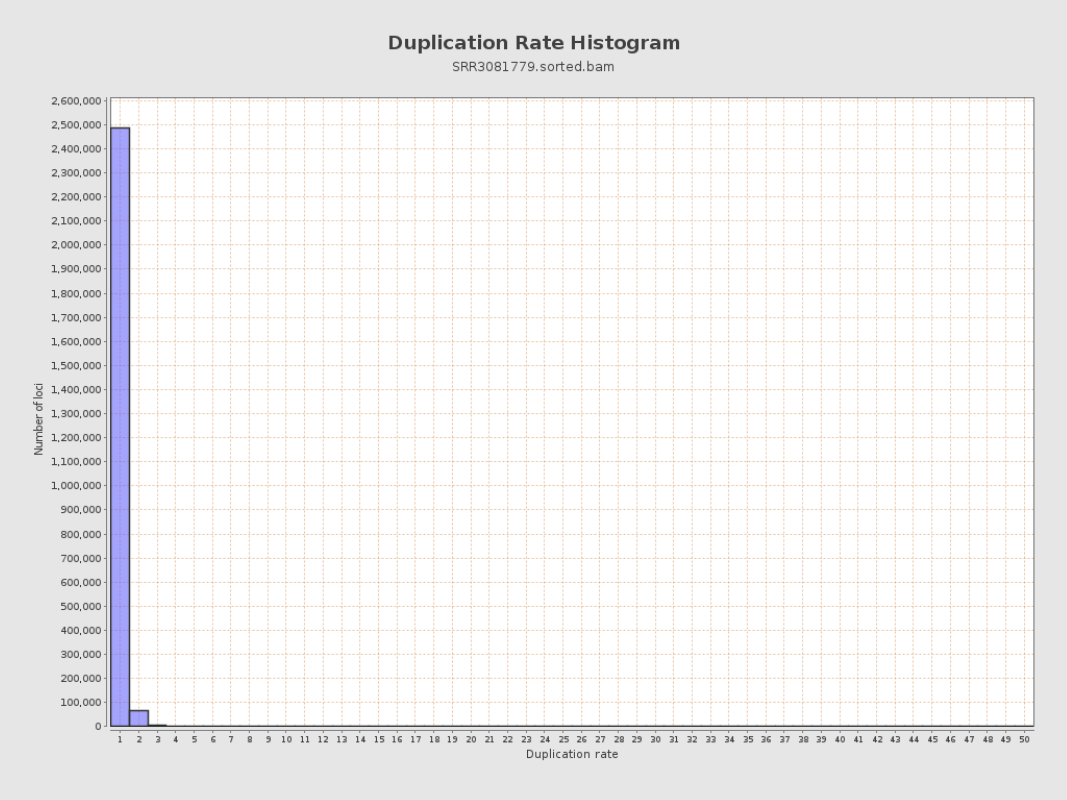
5. Results : Coverage Histogram (0-50X)



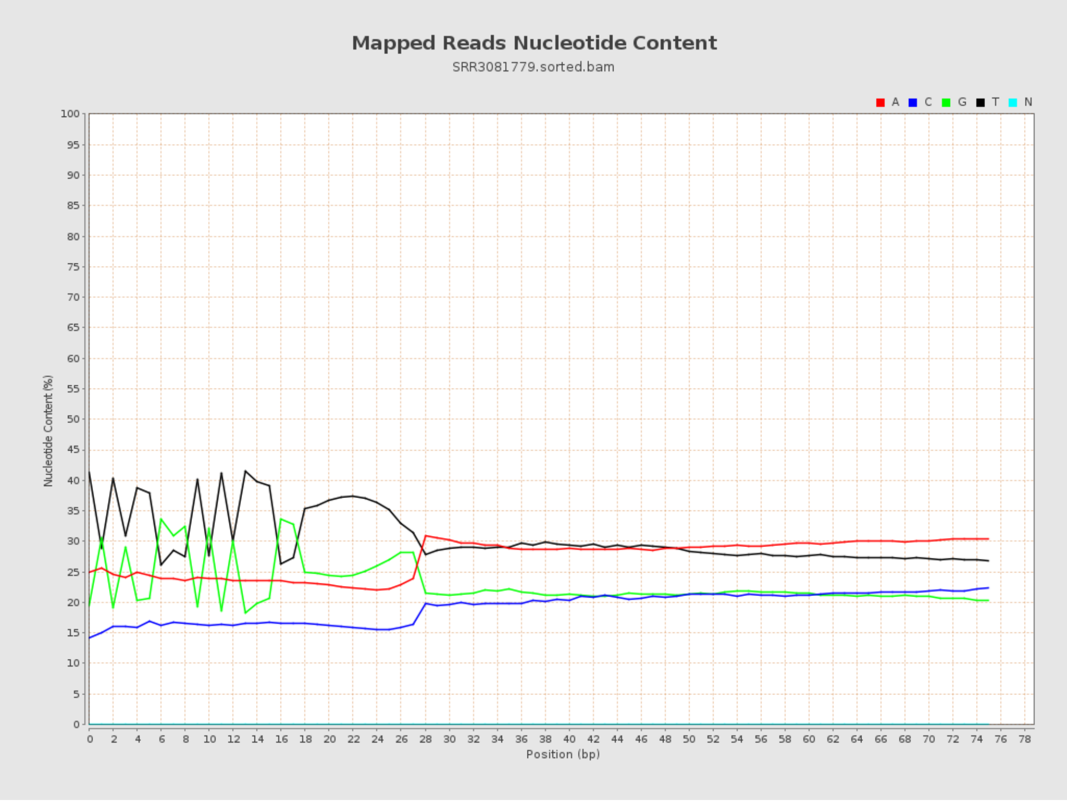
6. Results : Genome Fraction Coverage



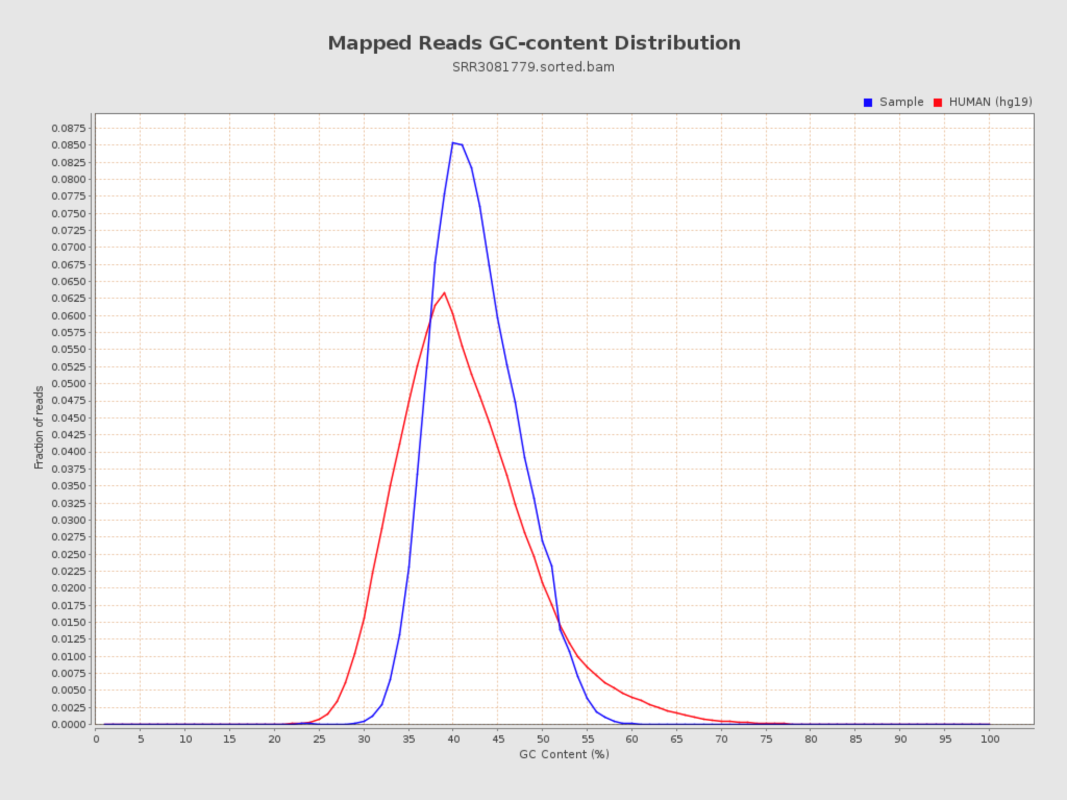
7. Results : Duplication Rate Histogram



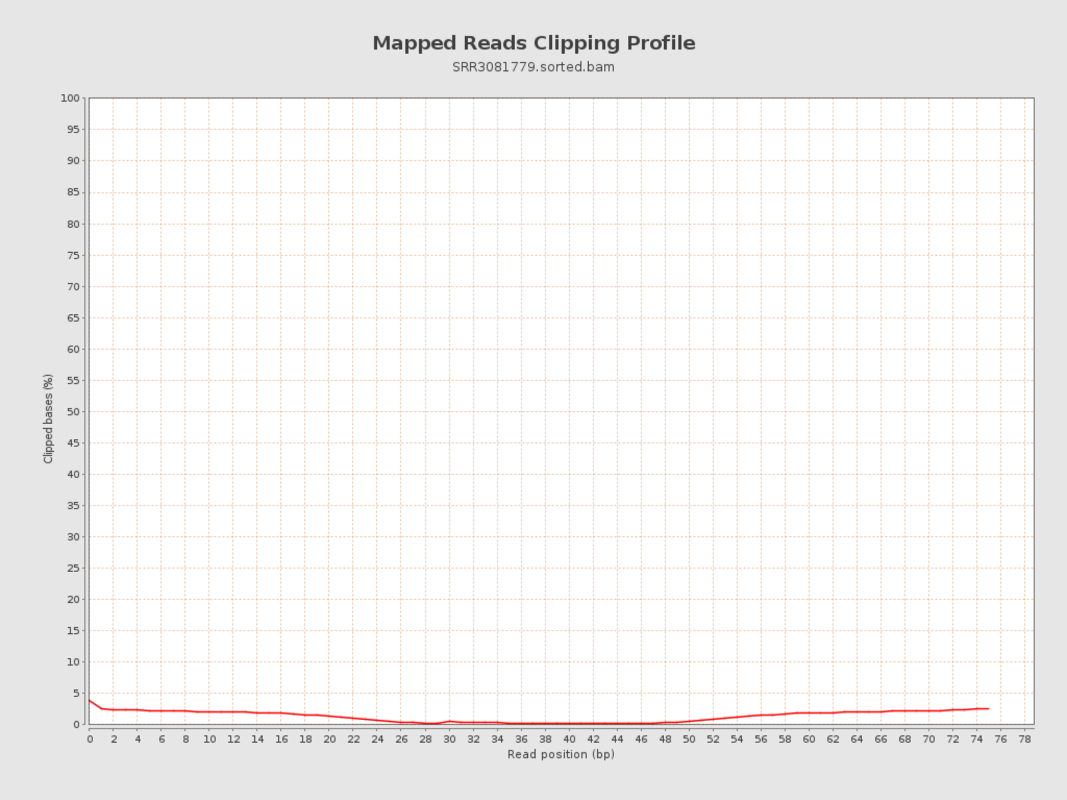
8. Results : Mapped Reads Nucleotide Content



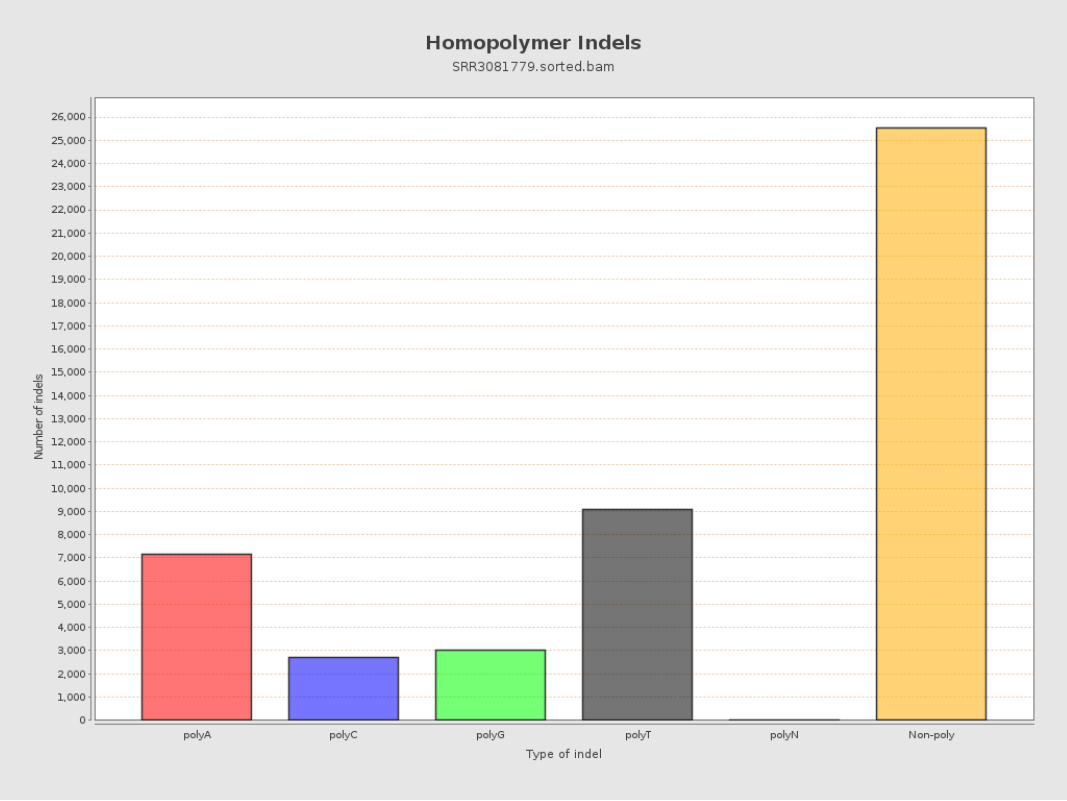
9. Results : Mapped Reads GC-content Distribution



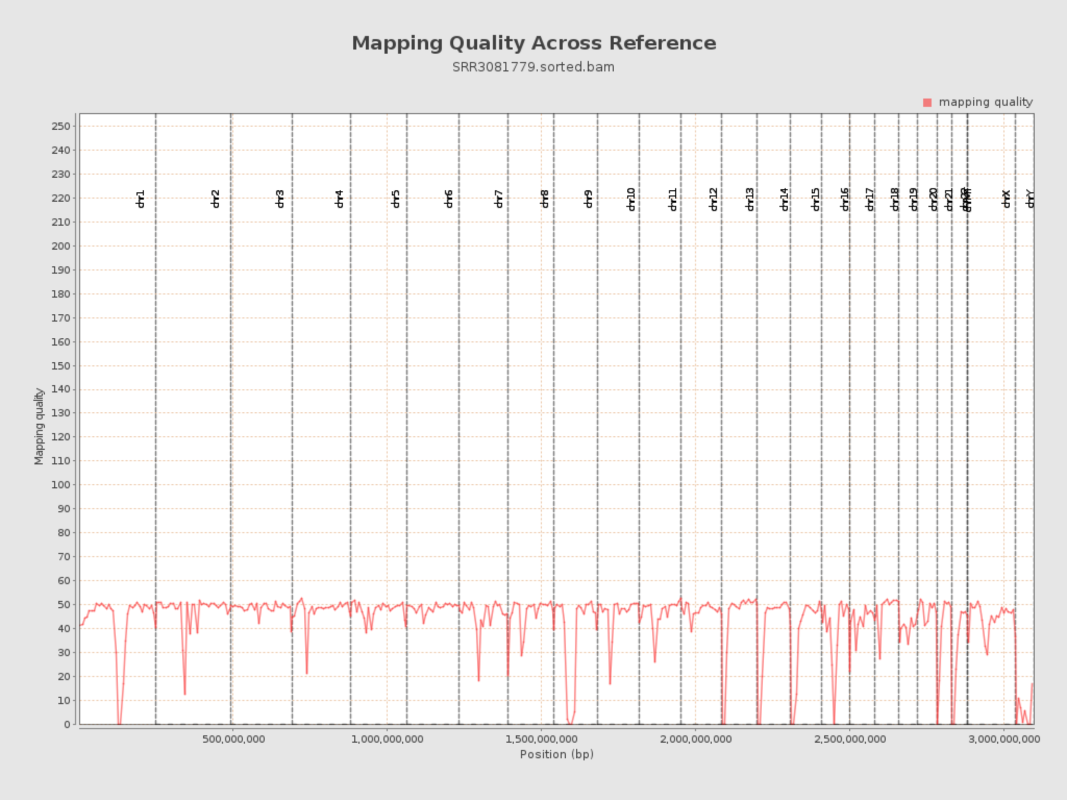
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram