Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:44:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081774.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_SRR3081774 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081774.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:44:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081774.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,163,594
Mapped reads	1,943,598 / 89.83%
Unmapped reads	219,996 / 10.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,110 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	79,321 / 3.67%
Duplication rate	3.08%
Clipped reads	868,062 / 40.12%

2.2. ACGT Content

Number/percentage of A's	35,716,436 / 27.63%
Number/percentage of C's	24,441,152 / 18.91%
Number/percentage of T's	40,180,117 / 31.08%
Number/percentage of G's	28,937,577 / 22.38%
Number/percentage of N's	1,533 / 0%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.3675

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

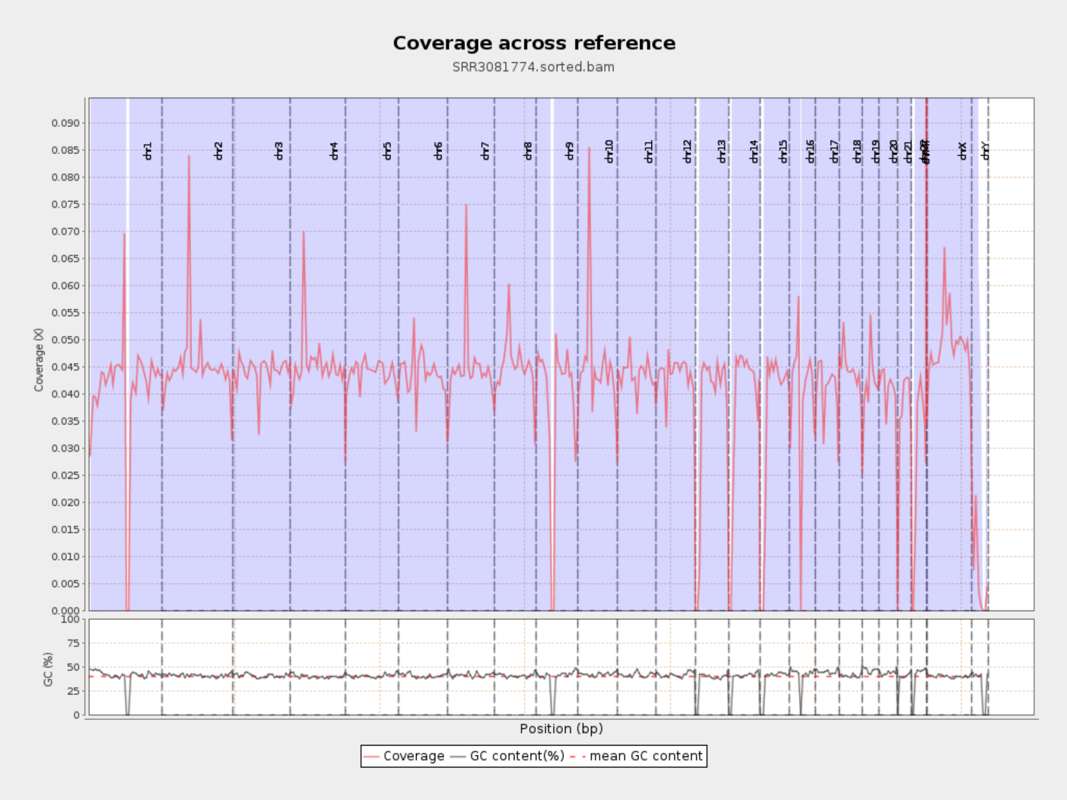
General error rate	0.81%
Mismatches	1,030,946
Insertions	9,667
Mapped reads with at least one insertion	0.49%
Deletions	26,043
Mapped reads with at least one deletion	1.32%
Homopolymer indels	46.93%

2.6. Chromosome stats

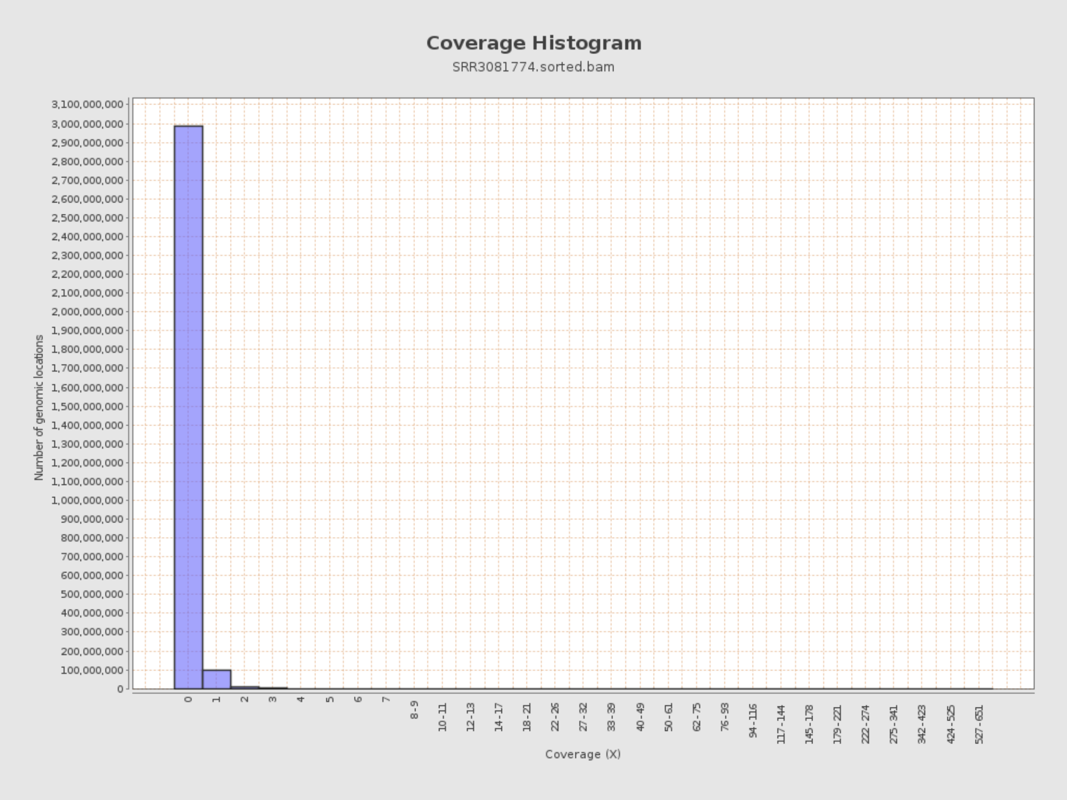
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10149216	0.0407	0.6061
chr2	243199373	11064851	0.0455	0.4617
chr3	198022430	8763447	0.0443	0.24
chr4	191154276	8696679	0.0455	0.2738
chr5	180915260	7938970	0.0439	0.2364
chr6	171115067	7463639	0.0436	0.2768
chr7	159138663	7173086	0.0451	0.513

chr8	146364022	6597819	0.0451	0.4336
chr9	141213431	5413619	0.0383	0.357
chr10	135534747	6171596	0.0455	0.4302
chr11	135006516	5851883	0.0433	0.3234
chr12	133851895	5809234	0.0434	0.2369
chr13	115169878	4136450	0.0359	0.2117
chr14	107349540	3963074	0.0369	0.2331
chr15	102531392	3658504	0.0357	0.2154
chr16	90354753	3595127	0.0398	0.266
chr17	81195210	3296121	0.0406	0.249
chr18	78077248	3490991	0.0447	0.5952
chr19	59128983	2495337	0.0422	0.4938
chr20	63025520	2545009	0.0404	0.2396
chr21	48129895	1703876	0.0354	0.2409
chr22	51304566	1371919	0.0267	0.1824
chrMT	16571	4577	0.2762	0.687
chrX	155270560	7596808	0.0489	0.2807
chrY	59373566	371210	0.0063	0.1757

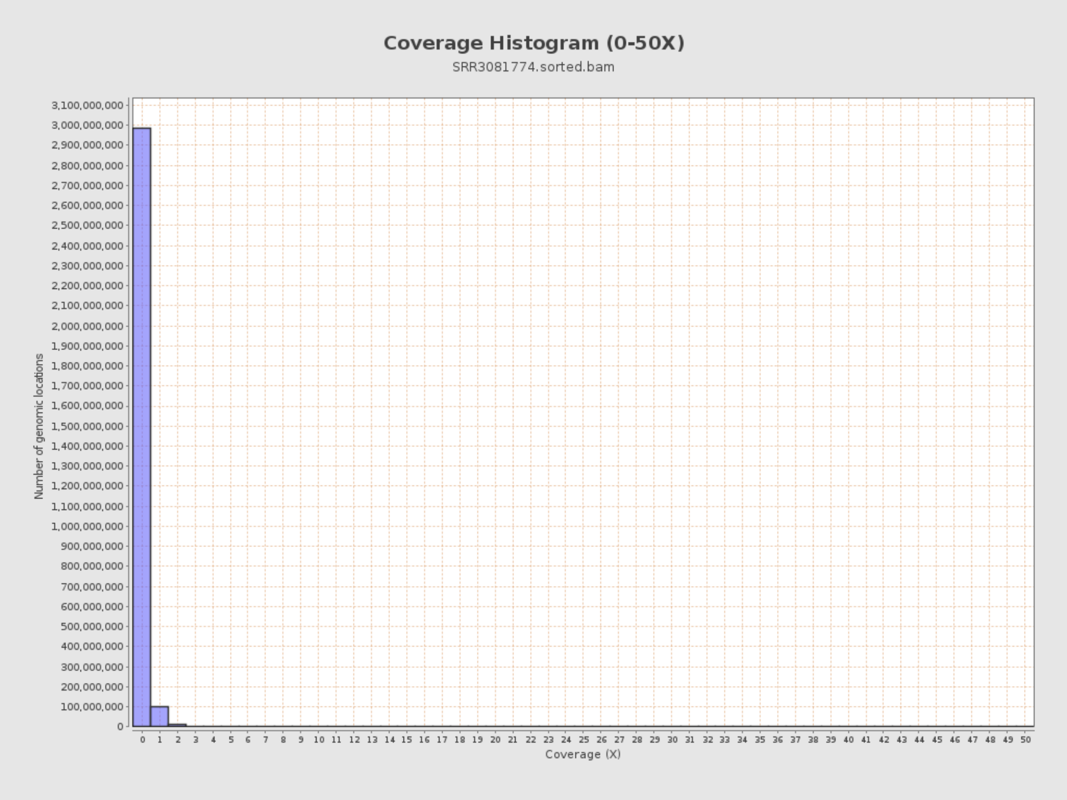
3. Results : Coverage across reference



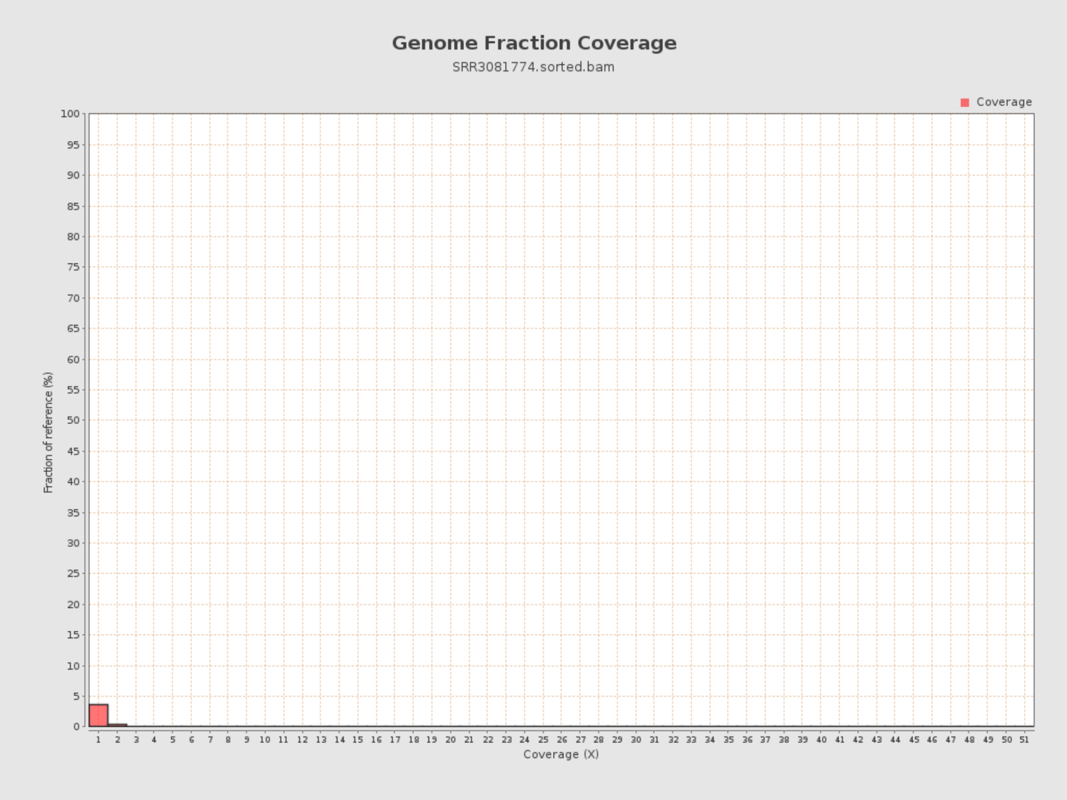
4. Results : Coverage Histogram



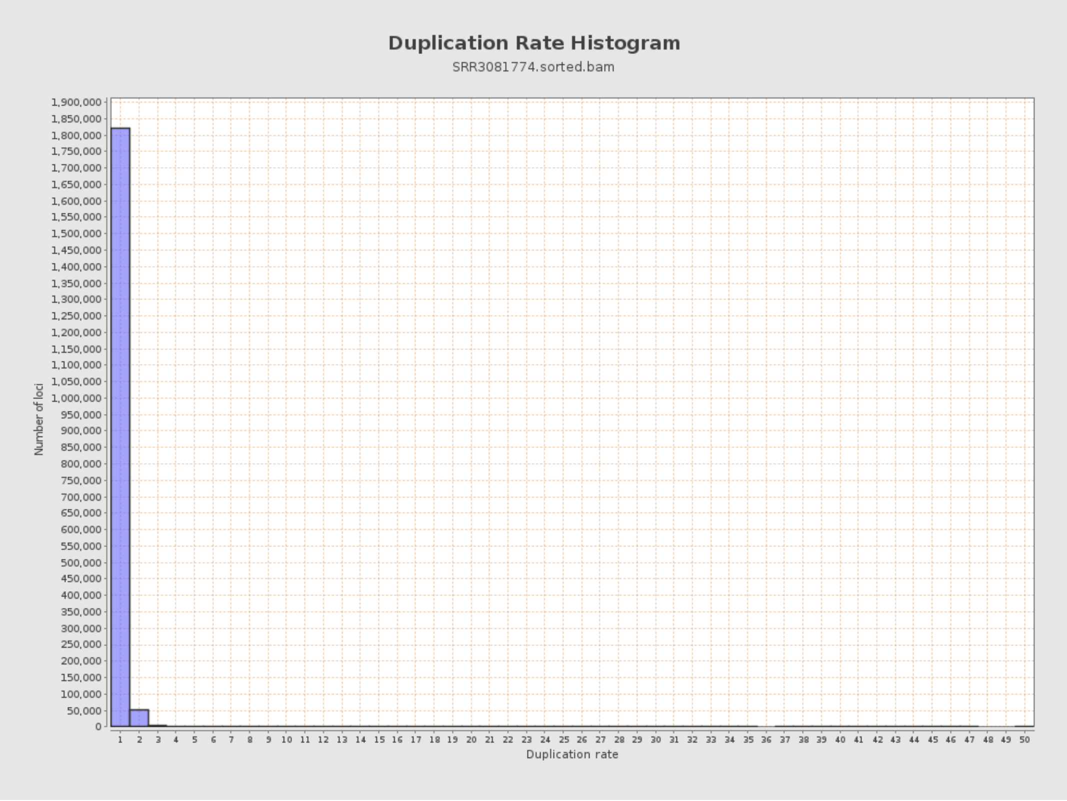
5. Results : Coverage Histogram (0-50X)



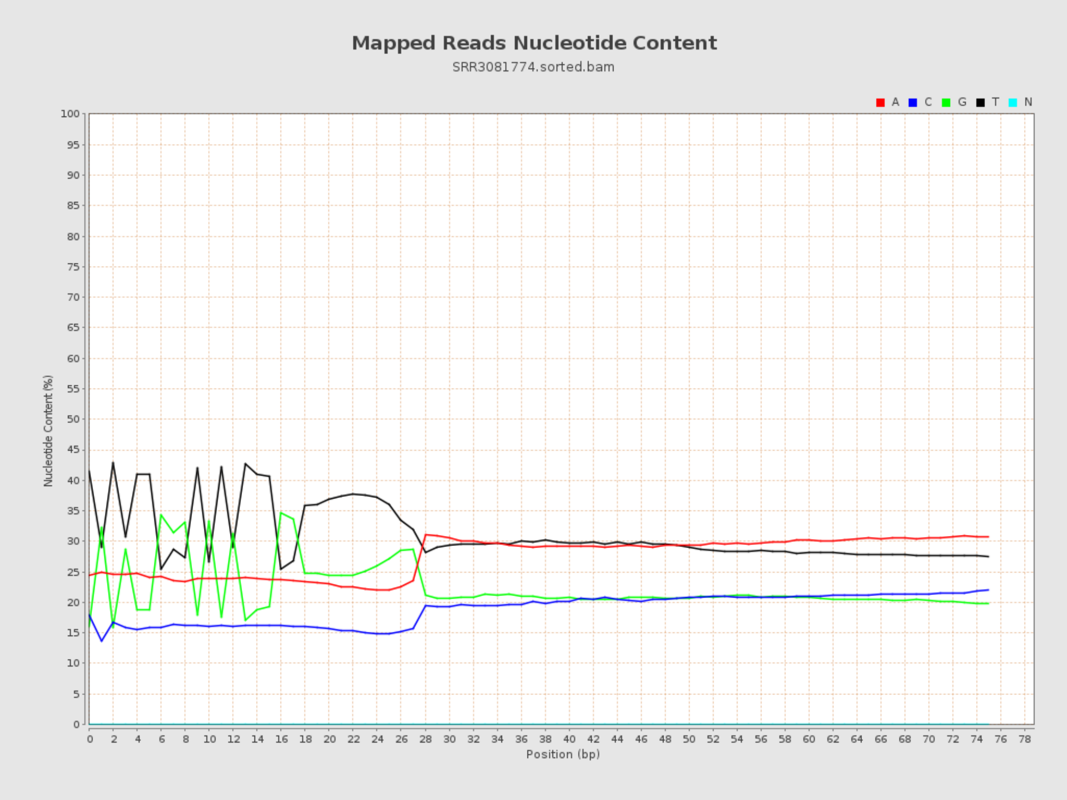
6. Results : Genome Fraction Coverage



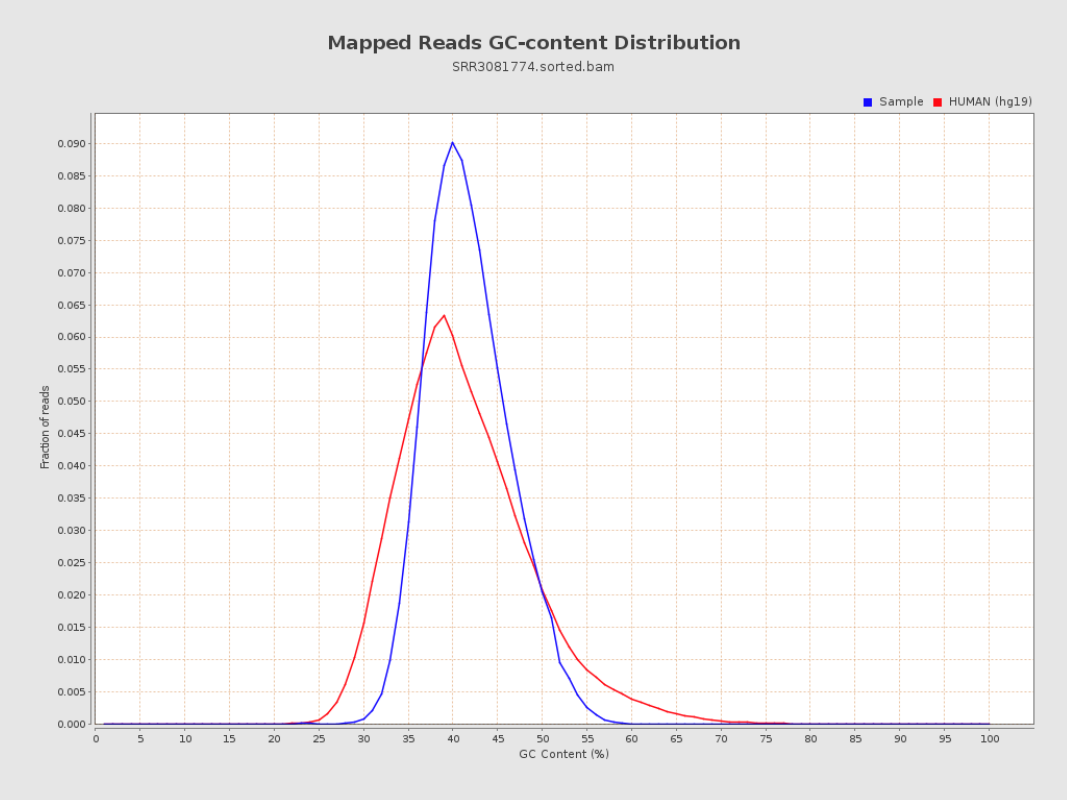
7. Results : Duplication Rate Histogram



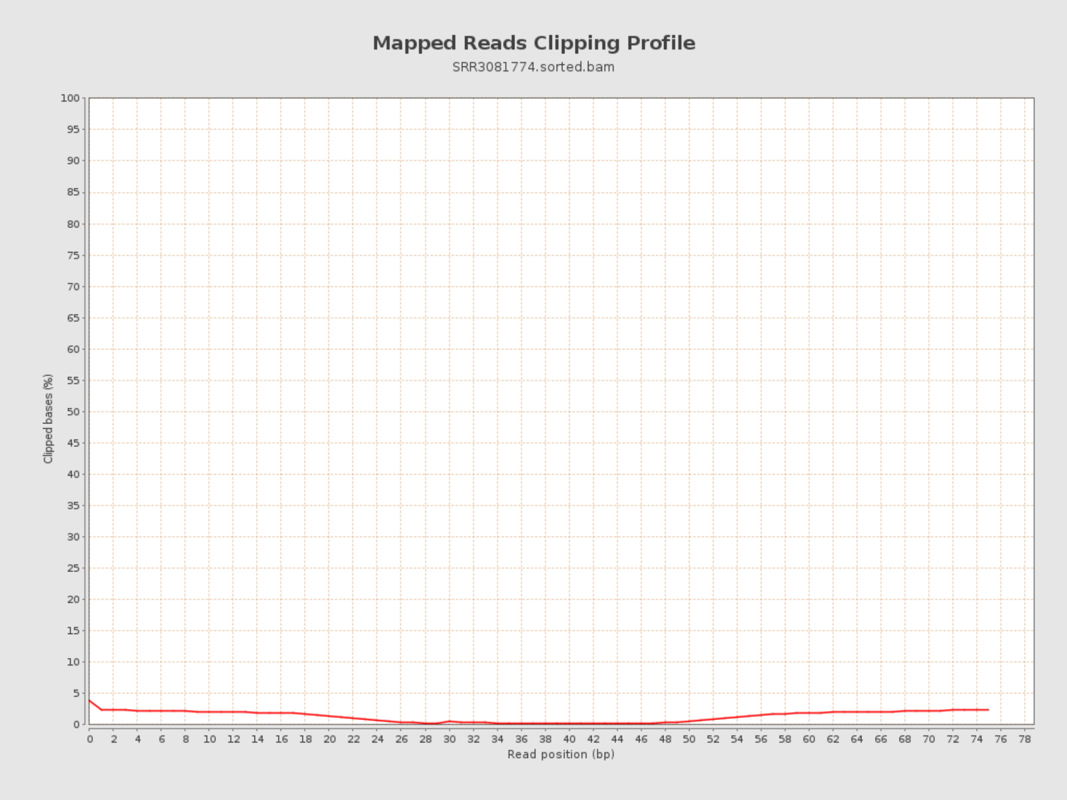
8. Results : Mapped Reads Nucleotide Content



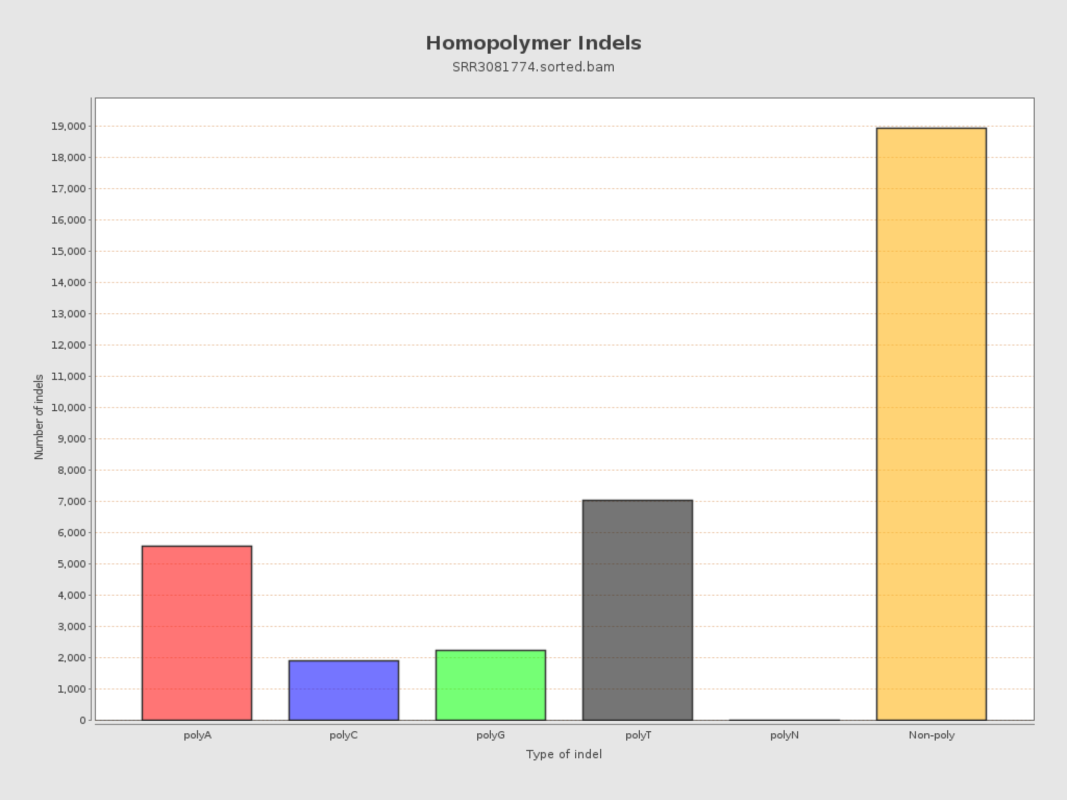
9. Results : Mapped Reads GC-content Distribution



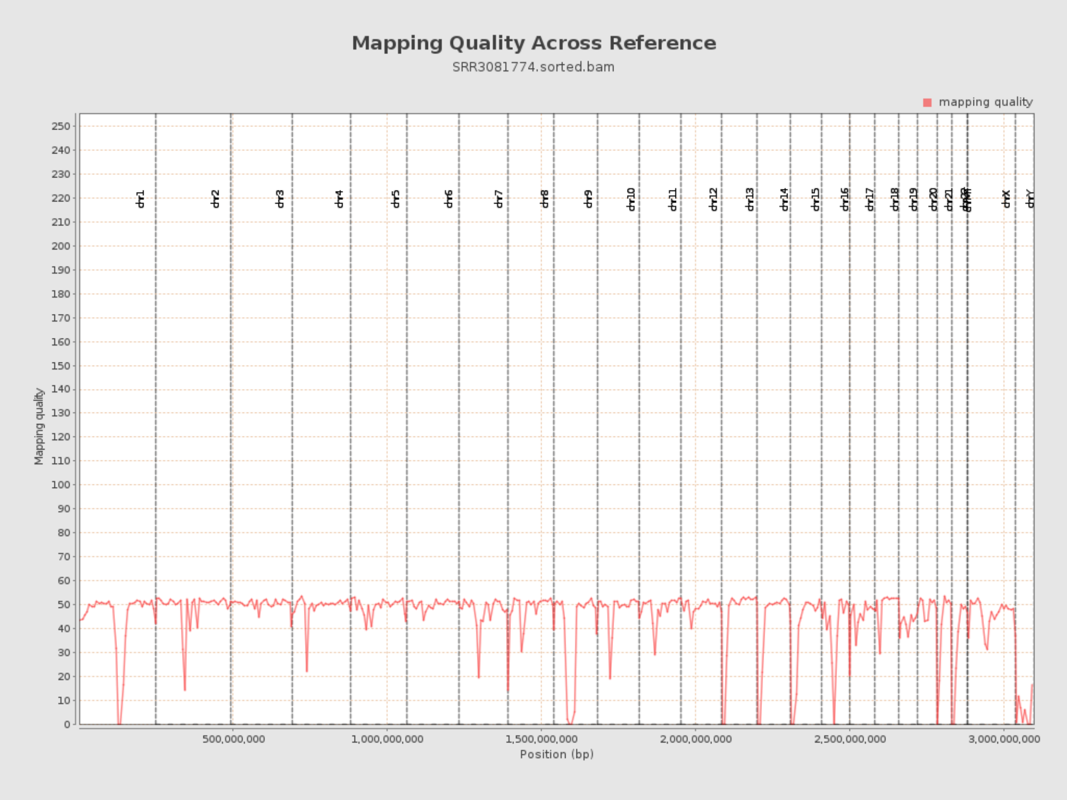
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram