Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 07:43:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083786.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_SRR3083786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 07:43:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,059,544
Mapped reads	2,272,796 / 74.29%
Unmapped reads	786,748 / 25.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,381 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	89,522 / 2.93%
Duplication rate	3.11%
Clipped reads	1,283,184 / 41.94%

2.2. ACGT Content

Number/percentage of A's	40,505,058 / 28.07%
Number/percentage of C's	27,910,197 / 19.34%
Number/percentage of T's	43,453,840 / 30.12%
Number/percentage of G's	32,409,205 / 22.46%
Number/percentage of N's	1,610 / 0%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.3587

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

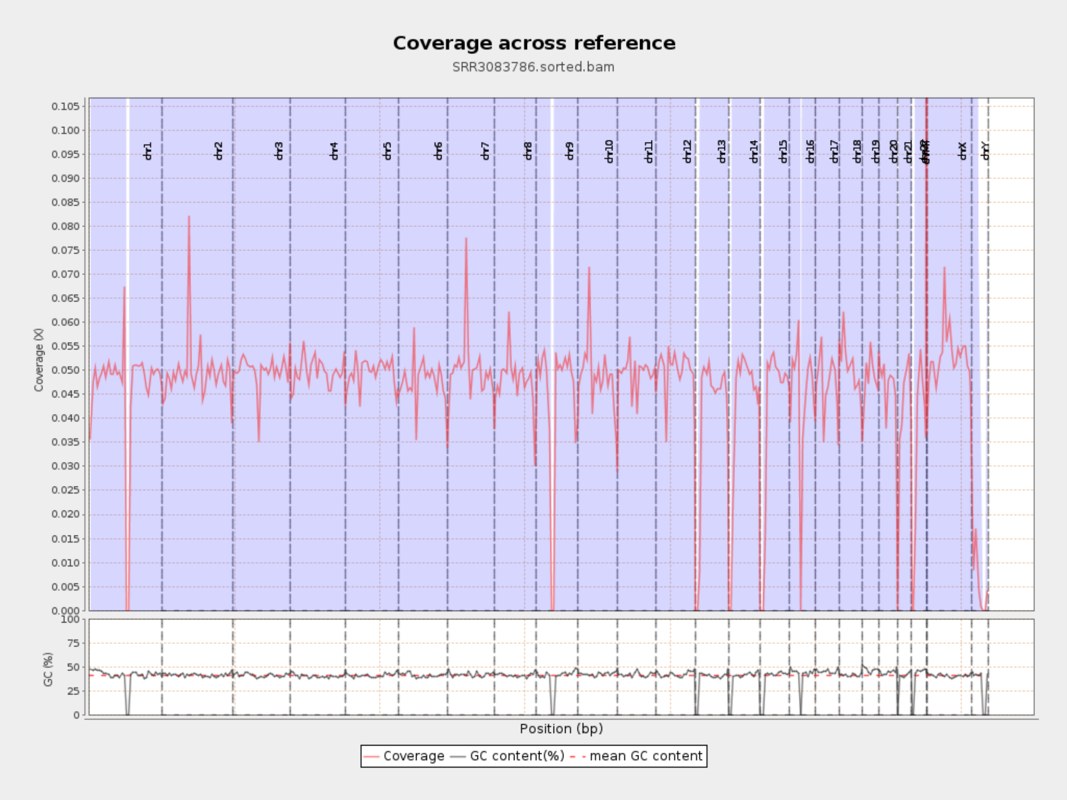
General error rate	0.87%
Mismatches	1,240,529
Insertions	11,154
Mapped reads with at least one insertion	0.49%
Deletions	31,469
Mapped reads with at least one deletion	1.37%
Homopolymer indels	45.3%

2.6. Chromosome stats

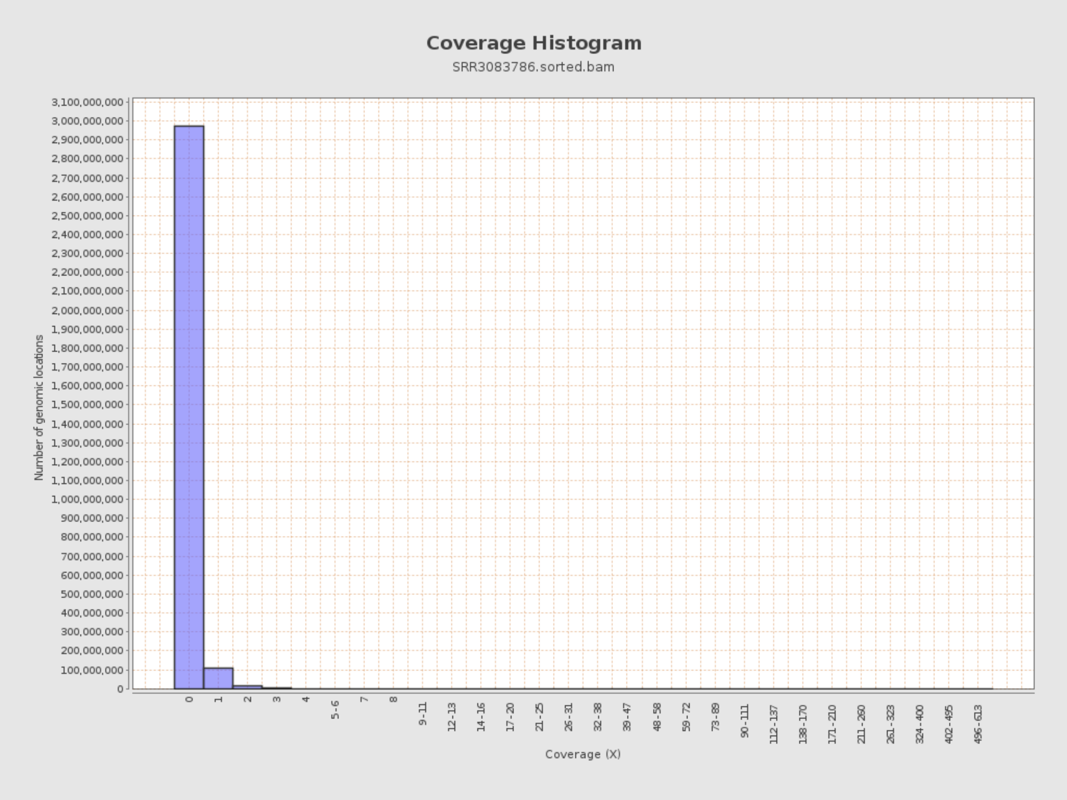
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11536519	0.0463	0.5474
chr2	243199373	12092845	0.0497	0.4652
chr3	198022430	9863572	0.0498	0.2502
chr4	191154276	9498001	0.0497	0.2613
chr5	180915260	8982074	0.0496	0.2518
chr6	171115067	8174122	0.0478	0.2945
chr7	159138663	8064478	0.0507	0.4738

chr8	146364022	7013129	0.0479	0.3694
chr9	141213431	6198128	0.0439	0.3407
chr10	135534747	6669794	0.0492	0.353
chr11	135006516	6655756	0.0493	0.334
chr12	133851895	6707811	0.0501	0.2557
chr13	115169878	4572243	0.0397	0.2233
chr14	107349540	4407404	0.0411	0.2528
chr15	102531392	4138995	0.0404	0.2314
chr16	90354753	4012186	0.0444	0.2662
chr17	81195210	3807263	0.0469	0.2748
chr18	78077248	3981907	0.051	0.7197
chr19	59128983	2872868	0.0486	0.4406
chr20	63025520	2911534	0.0462	0.2529
chr21	48129895	1943503	0.0404	0.2398
chr22	51304566	1667775	0.0325	0.202
chrMT	16571	6684	0.4034	0.7599
chrX	155270560	8191711	0.0528	0.2989
chrY	59373566	359526	0.0061	0.1245

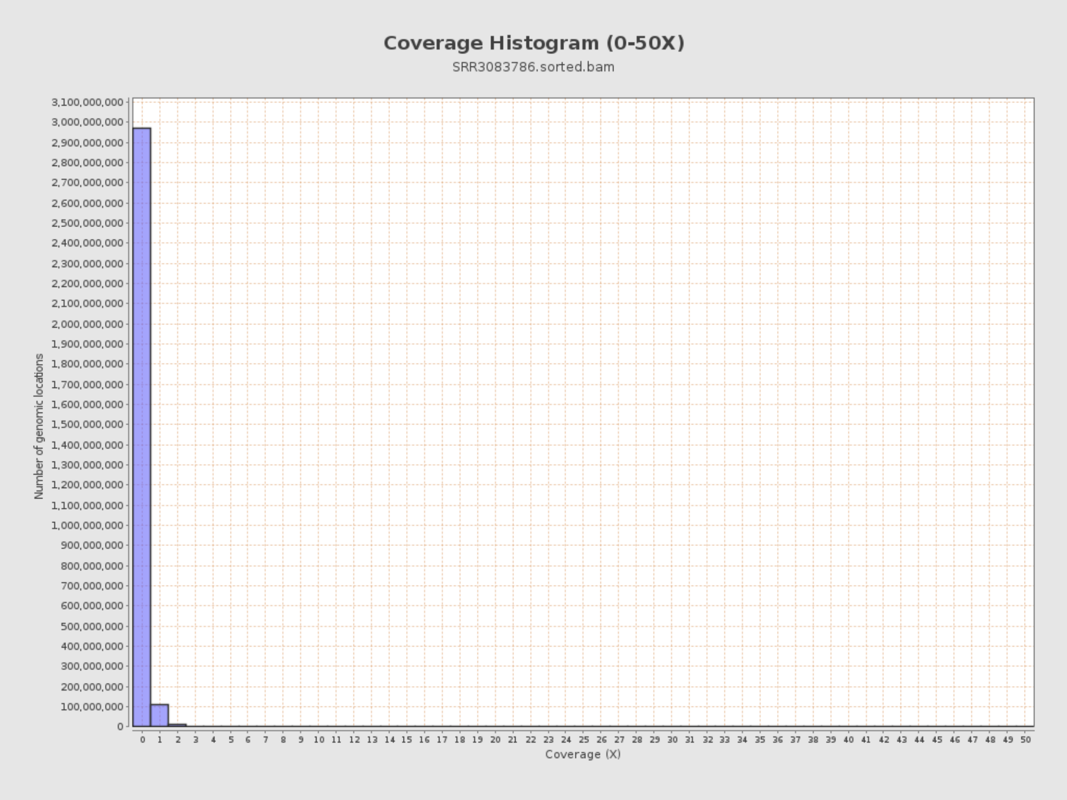
3. Results : Coverage across reference



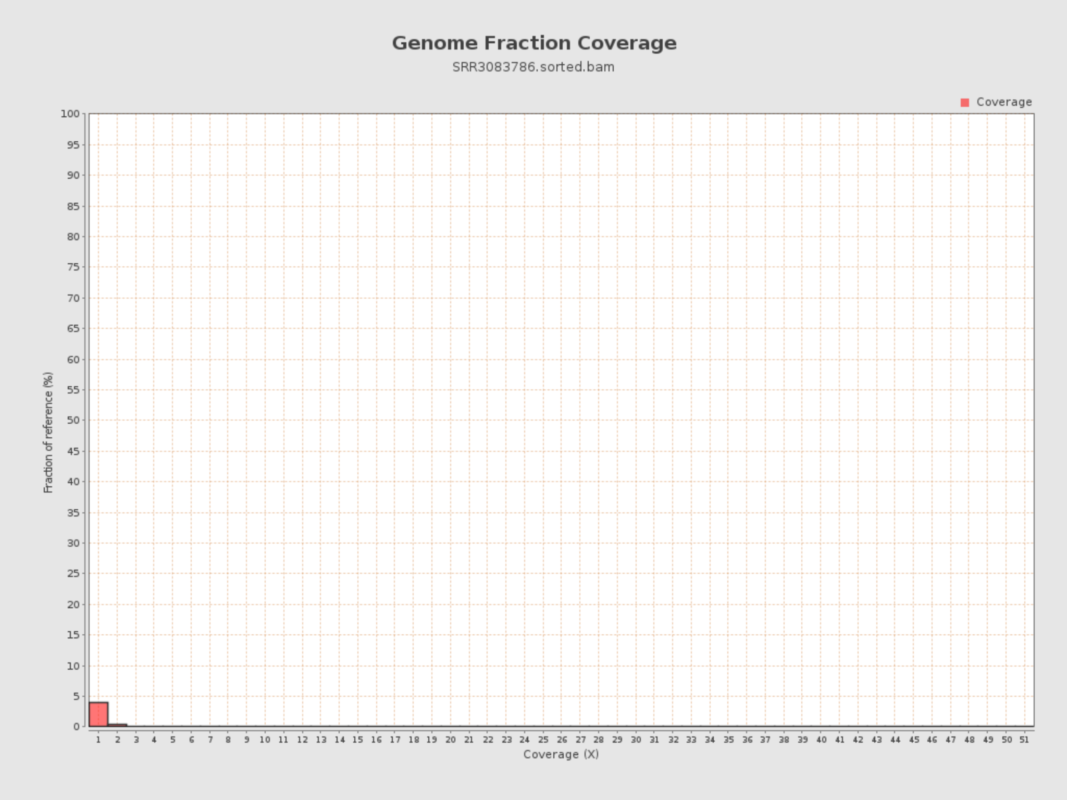
4. Results : Coverage Histogram



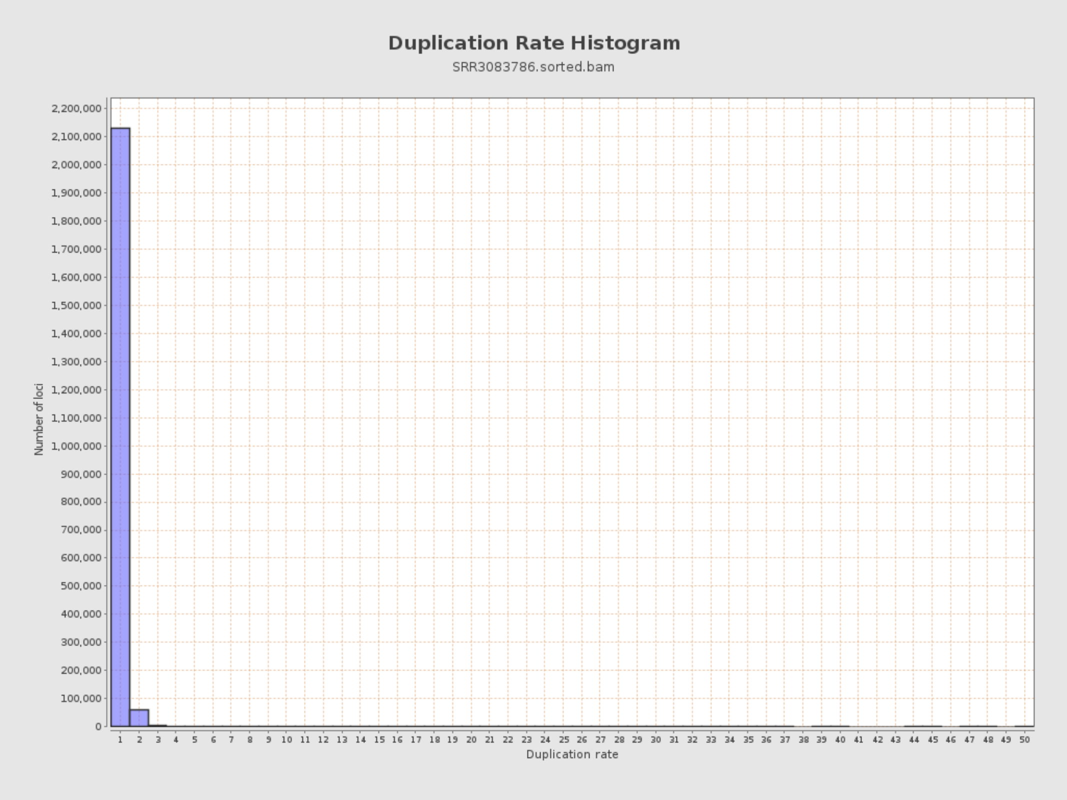
5. Results : Coverage Histogram (0-50X)



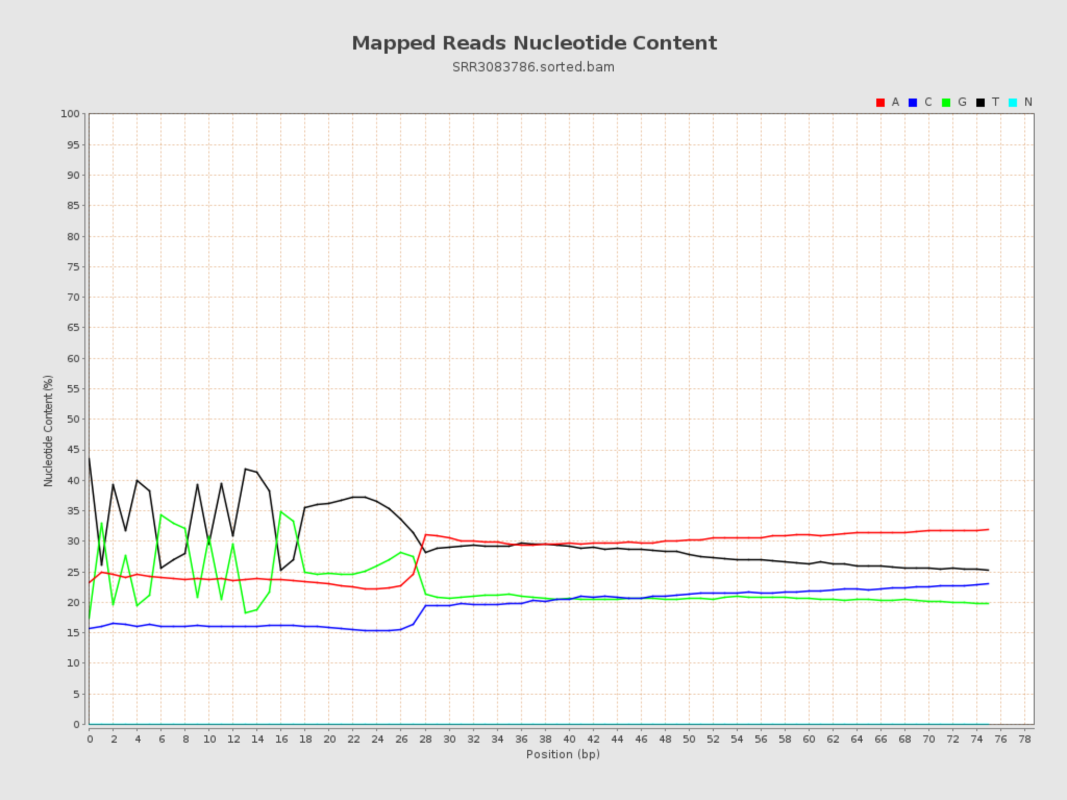
6. Results : Genome Fraction Coverage



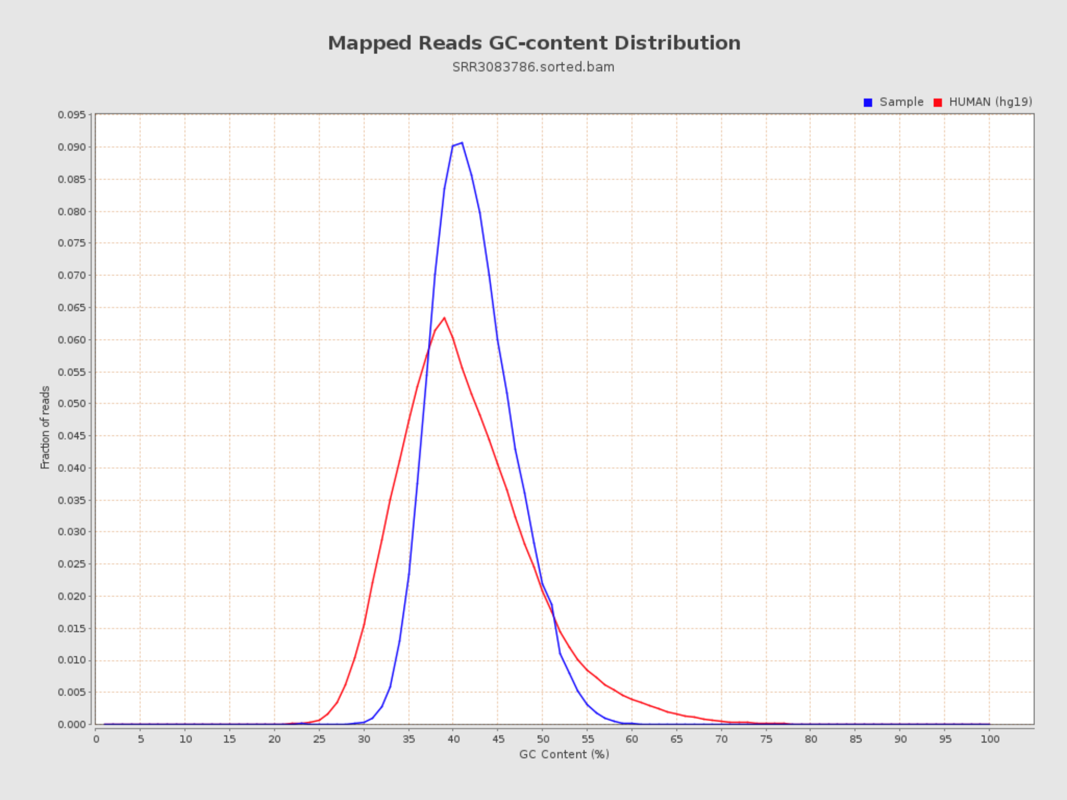
7. Results : Duplication Rate Histogram



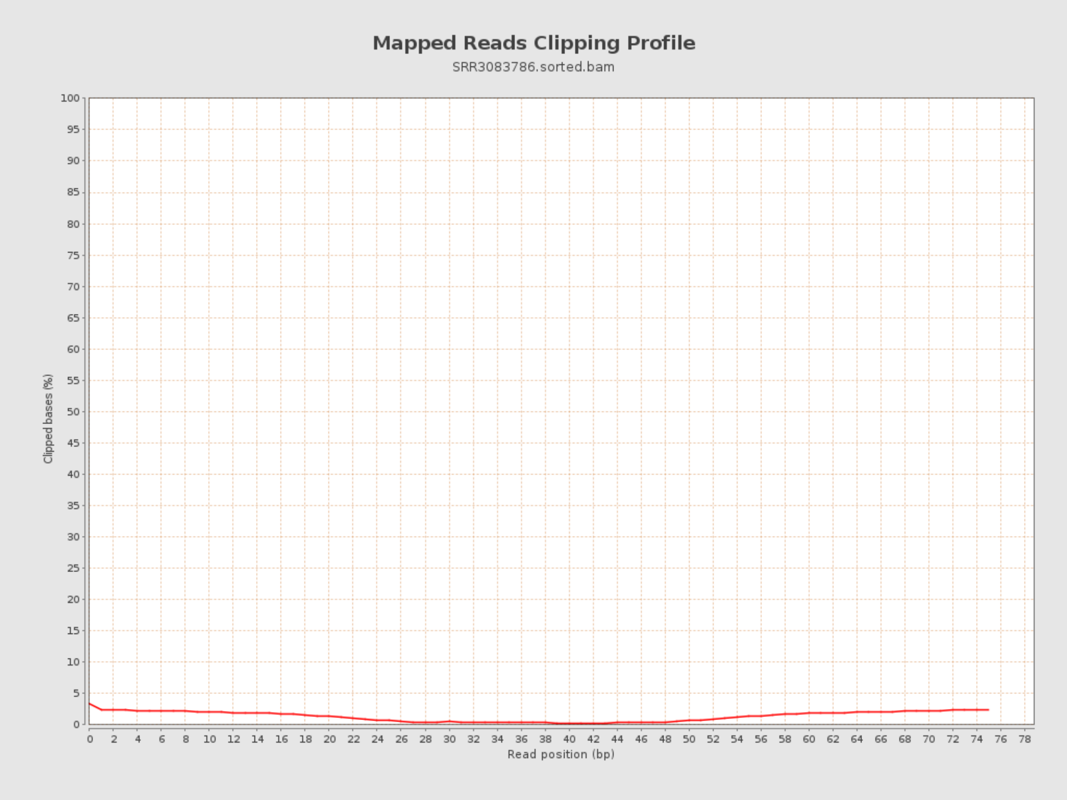
8. Results : Mapped Reads Nucleotide Content



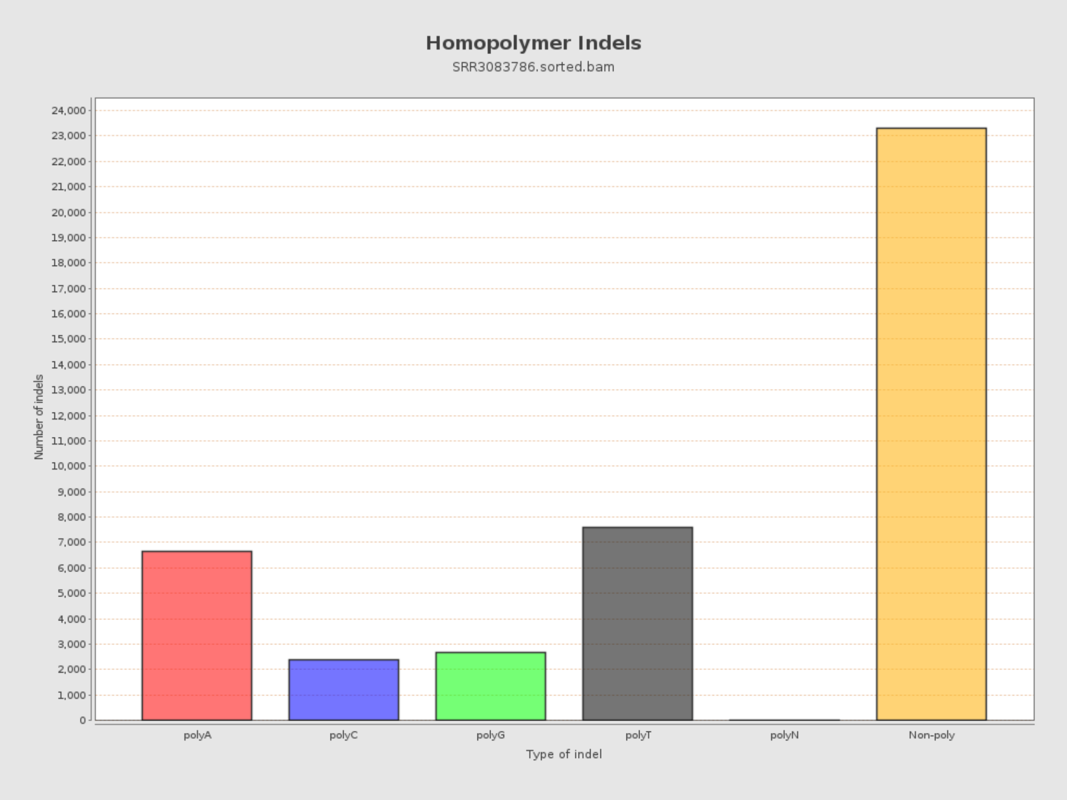
9. Results : Mapped Reads GC-content Distribution



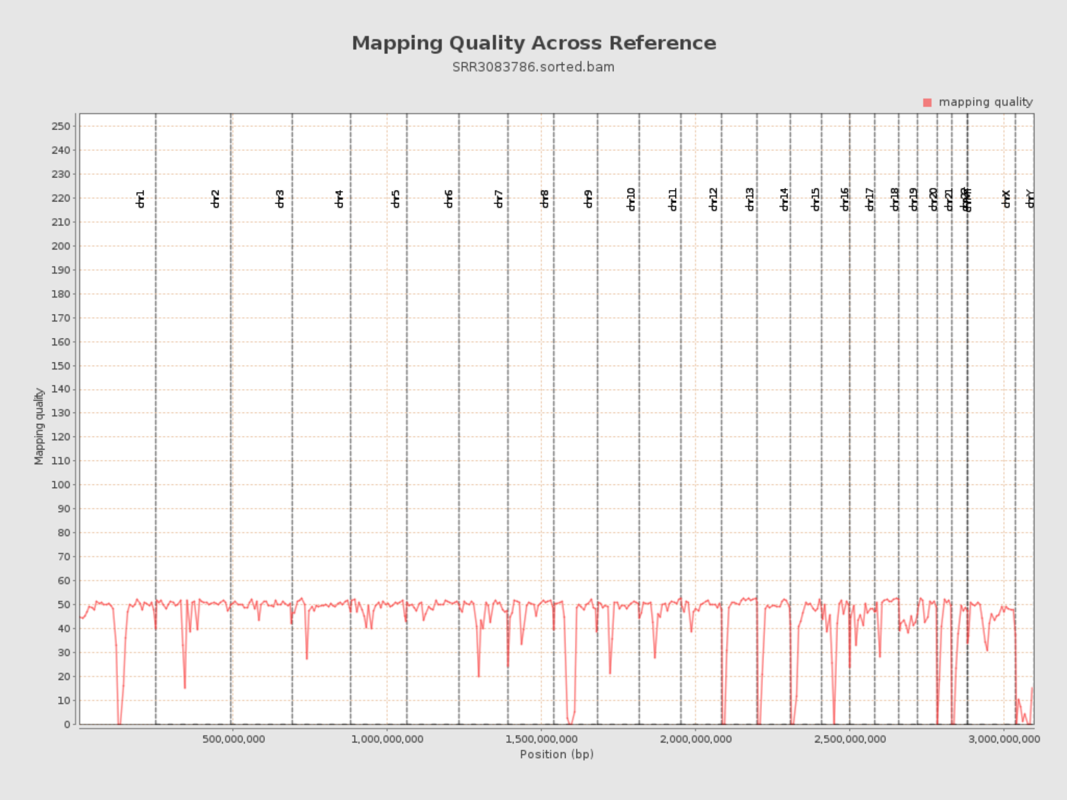
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram