Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:01:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080553.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_SRR3080553 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080553.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:01:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080553.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,660,247
Mapped reads	2,194,389 / 82.49%
Unmapped reads	465,858 / 17.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,196 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	118,483 / 4.45%
Duplication rate	4.51%
Clipped reads	1,037,497 / 39%

2.2. ACGT Content

Number/percentage of A's	39,603,982 / 27.32%
Number/percentage of C's	25,562,983 / 17.64%
Number/percentage of T's	47,601,711 / 32.84%
Number/percentage of G's	32,067,776 / 22.12%
Number/percentage of N's	115,721 / 0.08%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0468

Standard Deviation	0.3726

2.4. Mapping Quality

Mean Mapping Quality	47.43

2.5. Mismatches and indels

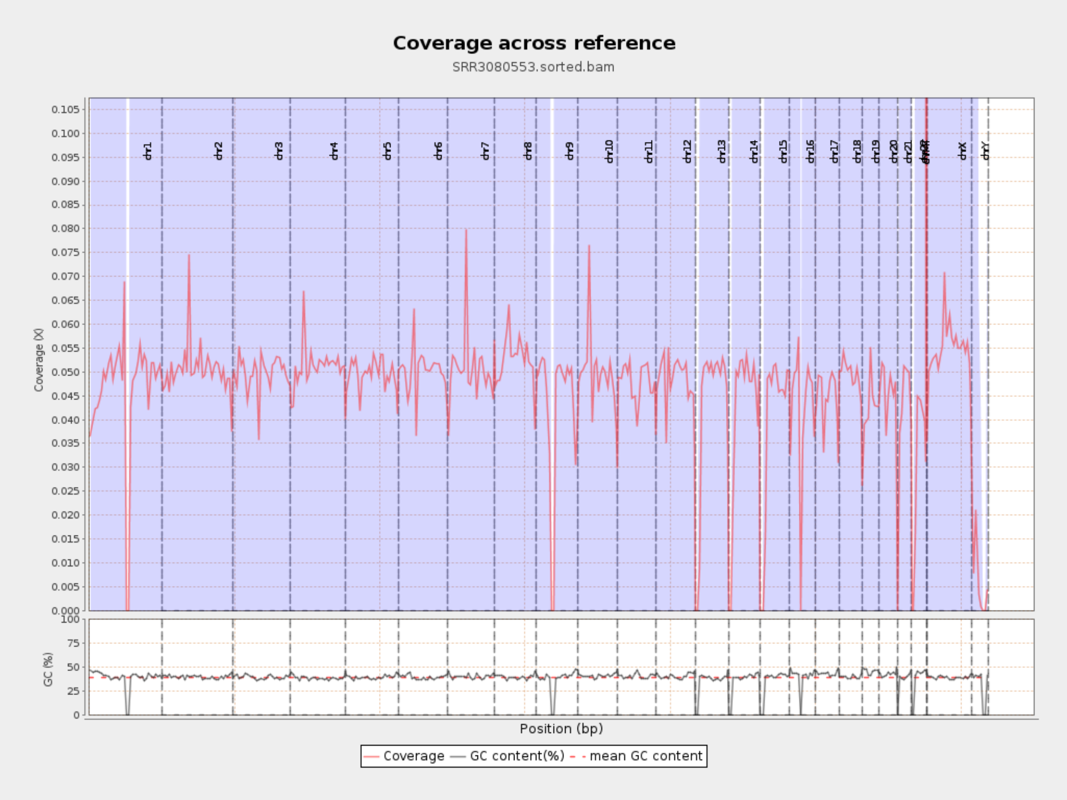
General error rate	0.94%
Mismatches	1,334,924
Insertions	12,387
Mapped reads with at least one insertion	0.56%
Deletions	38,050
Mapped reads with at least one deletion	1.71%
Homopolymer indels	48.07%

2.6. Chromosome stats

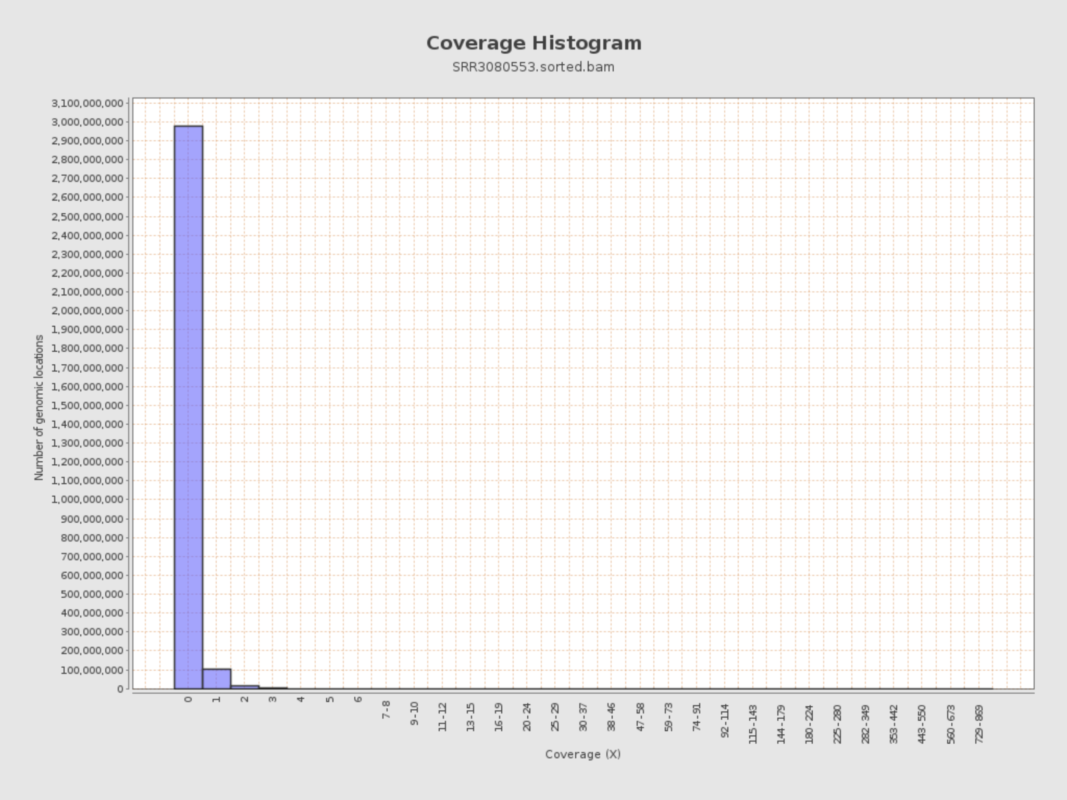
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11548273	0.0463	0.5875
chr2	243199373	12324551	0.0507	0.3689
chr3	198022430	9865670	0.0498	0.2606
chr4	191154276	9772386	0.0511	0.2813
chr5	180915260	8982153	0.0496	0.2595
chr6	171115067	8598504	0.0502	0.3136
chr7	159138663	8108748	0.051	0.5958

chr8	146364022	7690567	0.0525	0.5761
chr9	141213431	5970129	0.0423	0.3322
chr10	135534747	6805766	0.0502	0.3704
chr11	135006516	6451133	0.0478	0.3048
chr12	133851895	6499272	0.0486	0.2602
chr13	115169878	4828017	0.0419	0.2386
chr14	107349540	4403935	0.041	0.2507
chr15	102531392	3994991	0.039	0.2292
chr16	90354753	3814411	0.0422	0.2659
chr17	81195210	3588975	0.0442	0.2651
chr18	78077248	3887761	0.0498	0.538
chr19	59128983	2526744	0.0427	0.4213
chr20	63025520	2878649	0.0457	0.2572
chr21	48129895	1973062	0.041	0.258
chr22	51304566	1502542	0.0293	0.198
chrMT	16571	132318	7.9849	12.269
chrX	155270560	8489900	0.0547	0.2973
chrY	59373566	376483	0.0063	0.1648

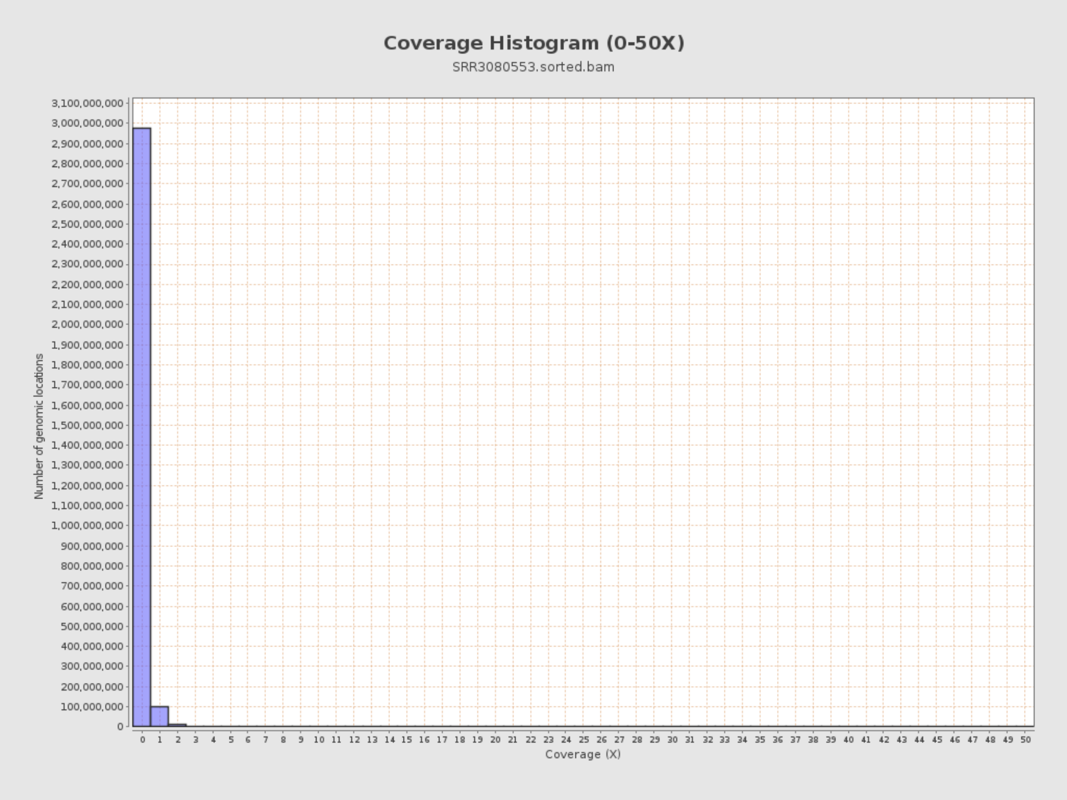
3. Results : Coverage across reference



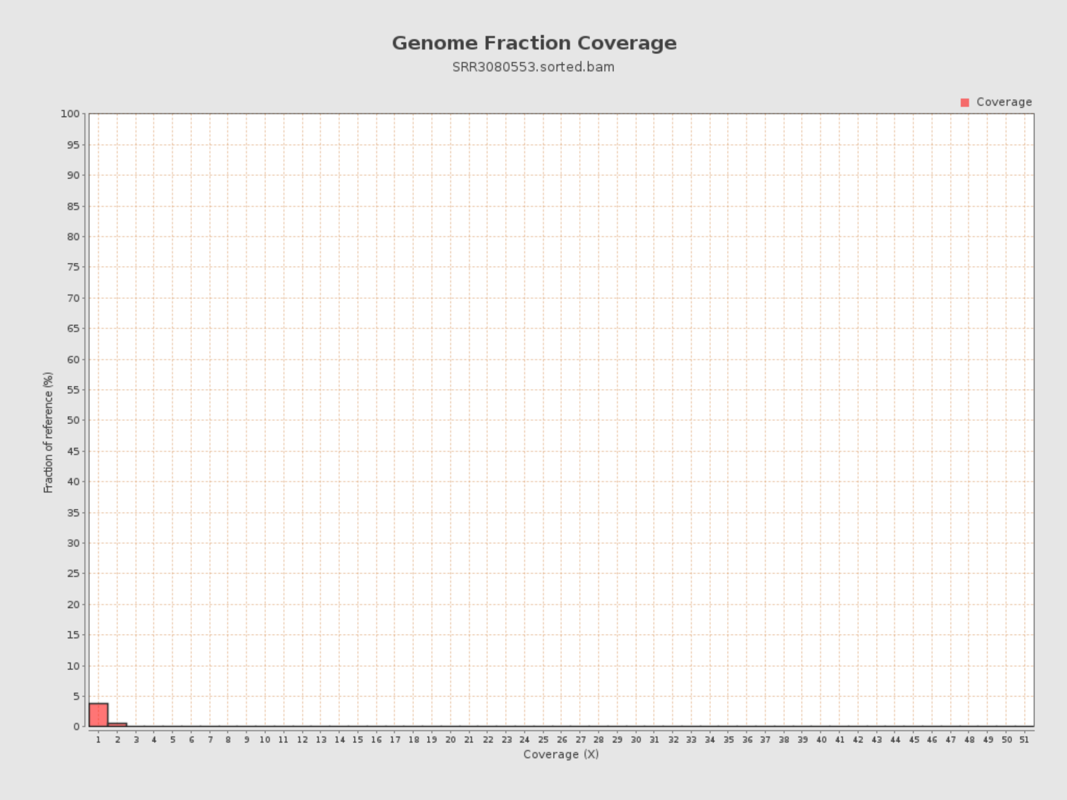
4. Results : Coverage Histogram



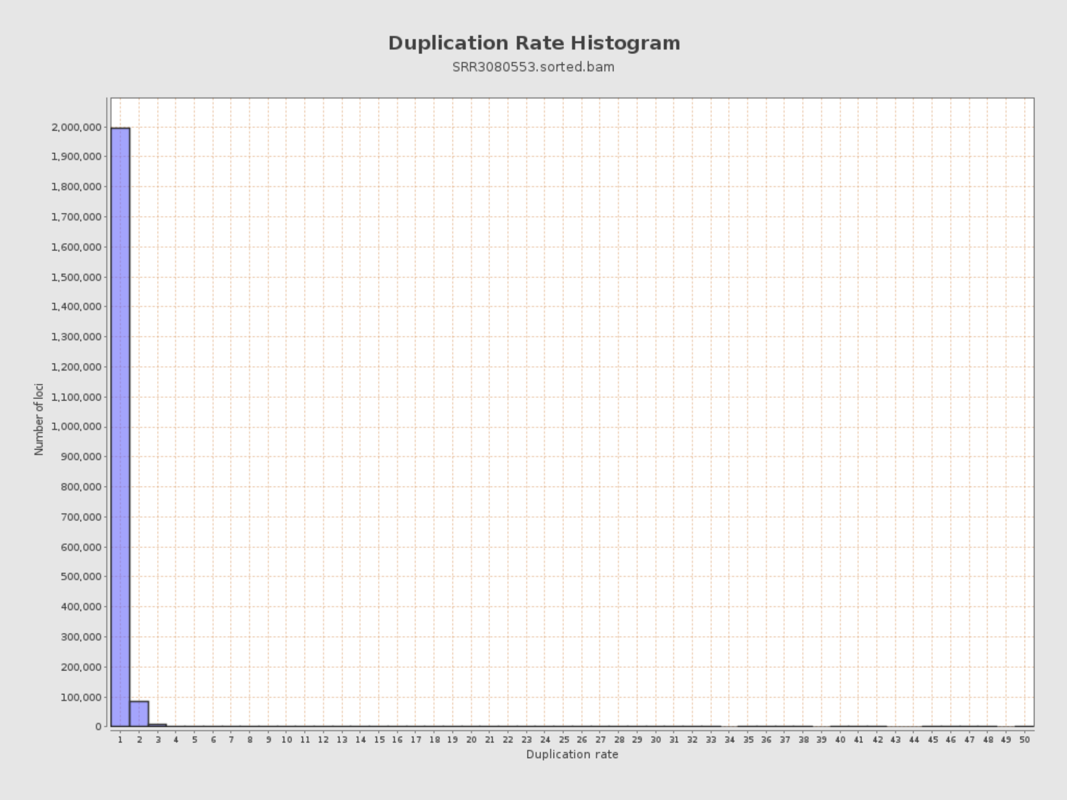
5. Results : Coverage Histogram (0-50X)



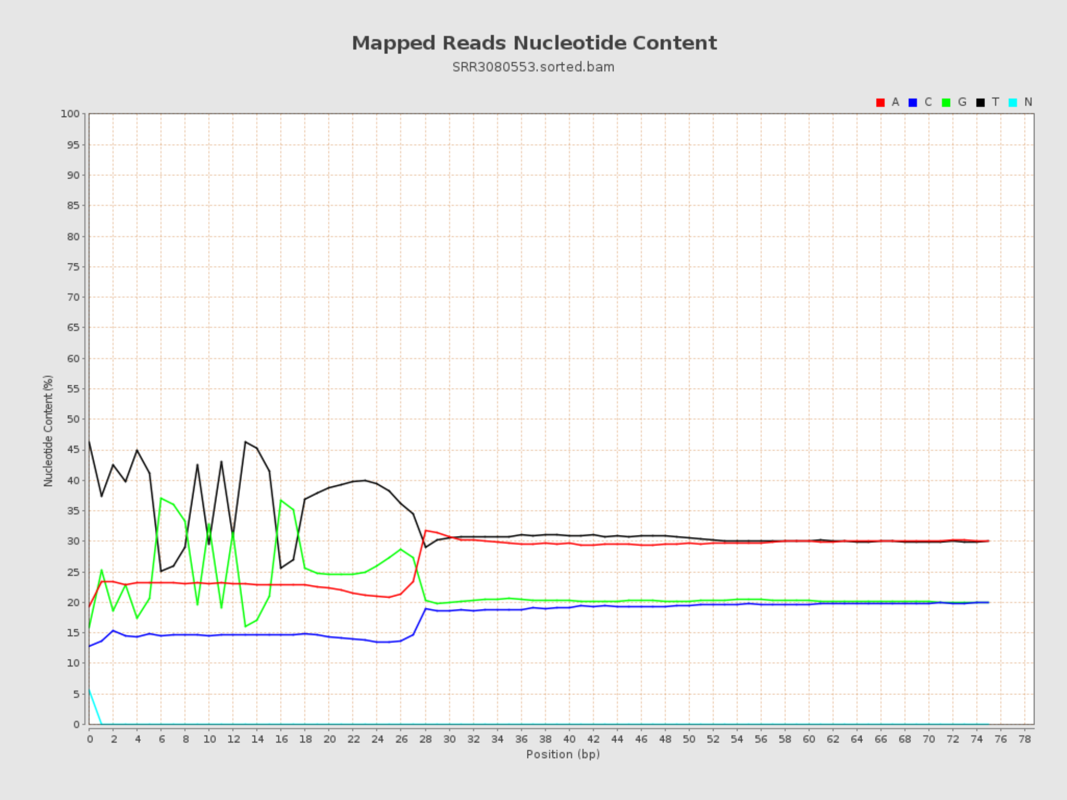
6. Results : Genome Fraction Coverage



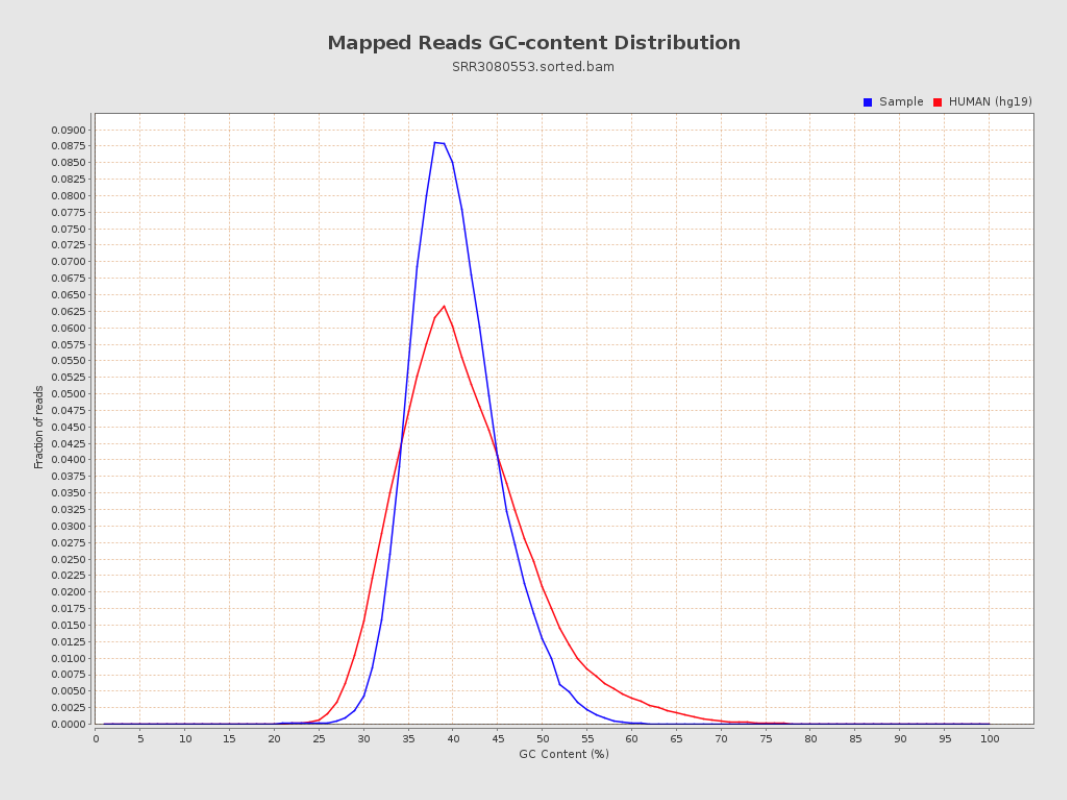
7. Results : Duplication Rate Histogram



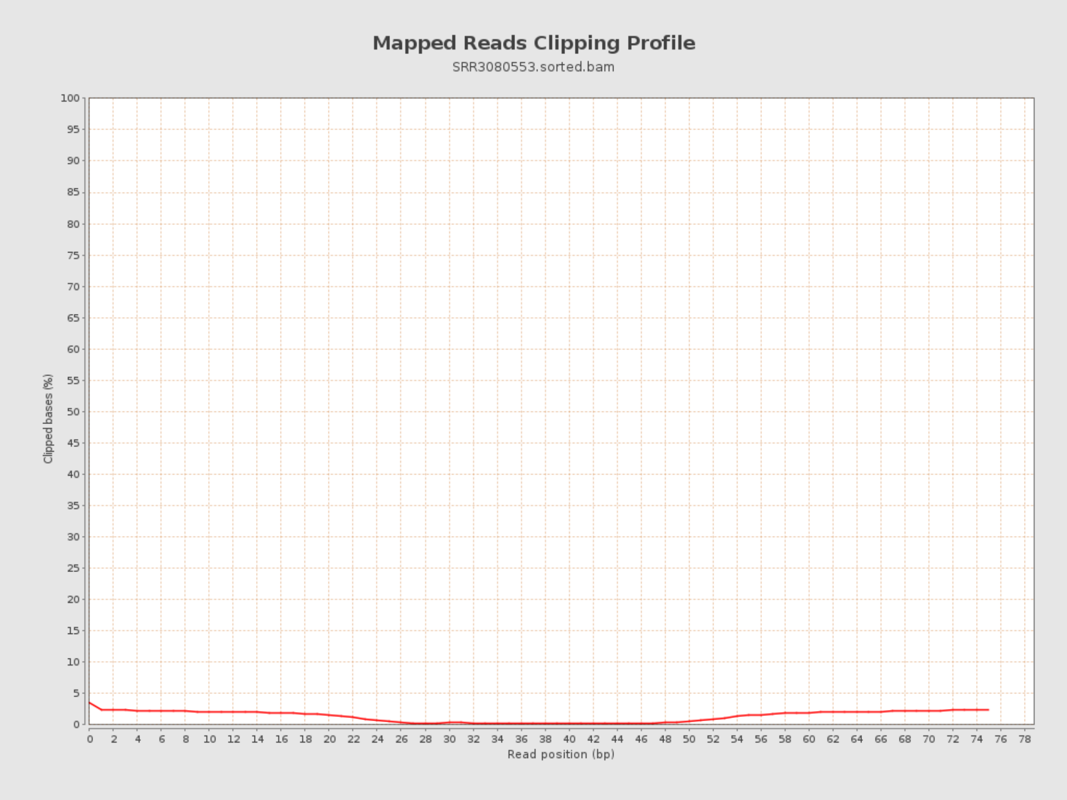
8. Results : Mapped Reads Nucleotide Content



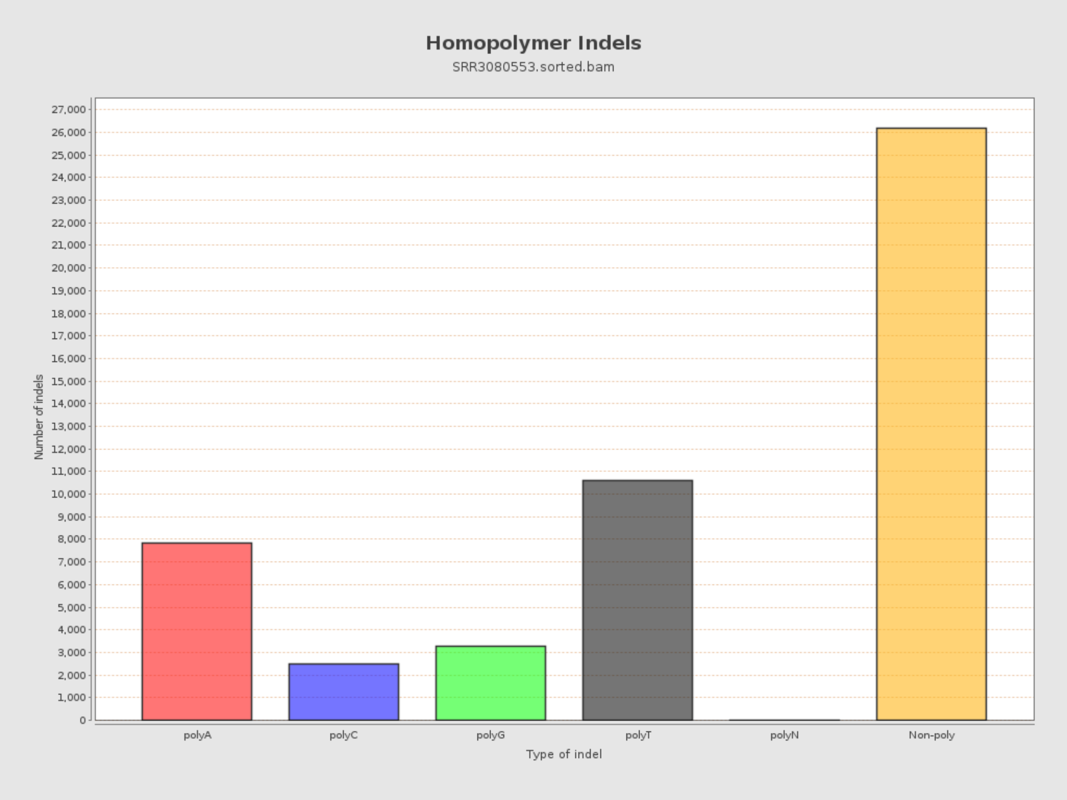
9. Results : Mapped Reads GC-content Distribution



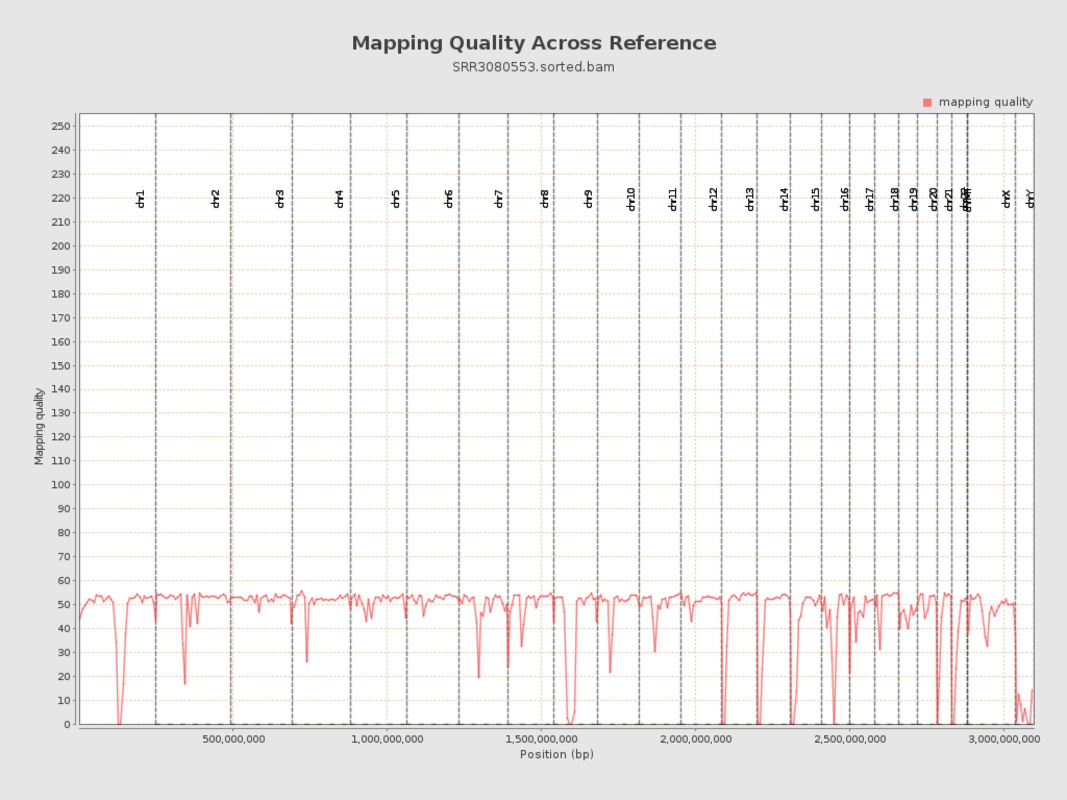
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram