Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:43:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080714.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_SRR3080714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080714.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:43:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,399,528
Mapped reads	2,227,306 / 92.82%
Unmapped reads	172,222 / 7.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,392 / 0.56%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	110,421 / 4.6%
Duplication rate	4.25%
Clipped reads	802,791 / 33.46%

2.2. ACGT Content

Number/percentage of A's	43,130,025 / 28.2%
Number/percentage of C's	28,848,363 / 18.86%
Number/percentage of T's	48,044,830 / 31.41%
Number/percentage of G's	32,939,956 / 21.53%
Number/percentage of N's	2,243 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0494

Standard Deviation	0.3808

2.4. Mapping Quality

Mean Mapping Quality	46.71

2.5. Mismatches and indels

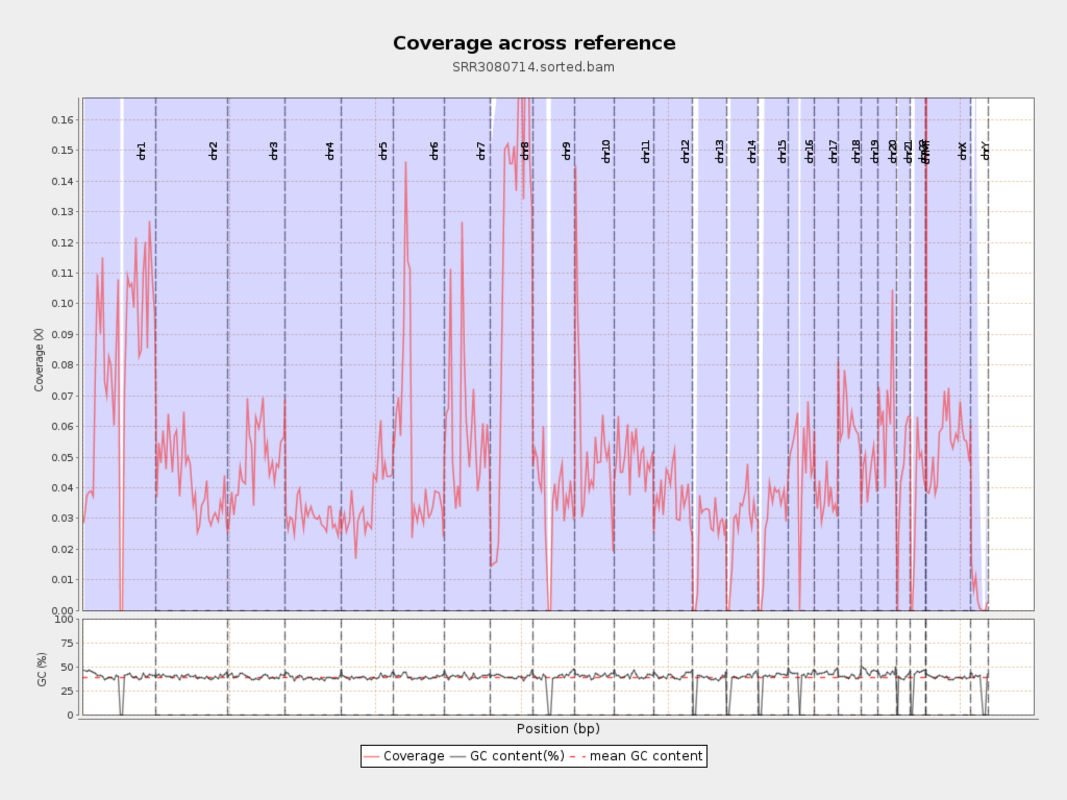
General error rate	0.8%
Mismatches	1,205,936
Insertions	10,842
Mapped reads with at least one insertion	0.48%
Deletions	32,545
Mapped reads with at least one deletion	1.45%
Homopolymer indels	49.03%

2.6. Chromosome stats

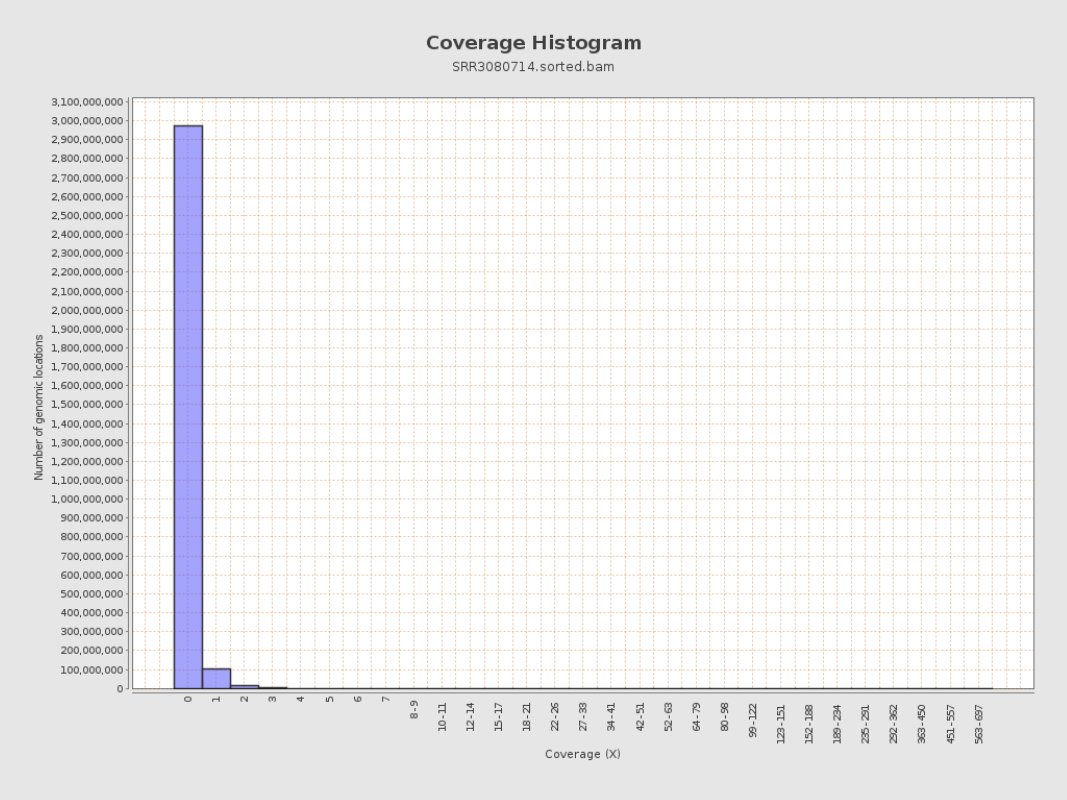
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19940328	0.08	0.5628
chr2	243199373	10290492	0.0423	0.378
chr3	198022430	9619403	0.0486	0.2579
chr4	191154276	5821474	0.0305	0.2092
chr5	180915260	6557109	0.0362	0.2219
chr6	171115067	9025928	0.0527	0.3362
chr7	159138663	9528244	0.0599	0.9096

chr8	146364022	17537291	0.1198	0.5169
chr9	141213431	5046682	0.0357	0.2636
chr10	135534747	7415153	0.0547	0.3381
chr11	135006516	6737303	0.0499	0.3011
chr12	133851895	5080060	0.038	0.2283
chr13	115169878	2937367	0.0255	0.1873
chr14	107349540	2978806	0.0277	0.2021
chr15	102531392	2911960	0.0284	0.1962
chr16	90354753	4331457	0.0479	0.267
chr17	81195210	2982335	0.0367	0.2339
chr18	78077248	4876913	0.0625	0.4065
chr19	59128983	2645715	0.0447	0.3602
chr20	63025520	4088876	0.0649	0.303
chr21	48129895	2154220	0.0448	0.2548
chr22	51304566	1811070	0.0353	0.2205
chrMT	16571	12961	0.7821	1.0385
chrX	155270560	8426256	0.0543	0.287
chrY	59373566	265102	0.0045	0.0927

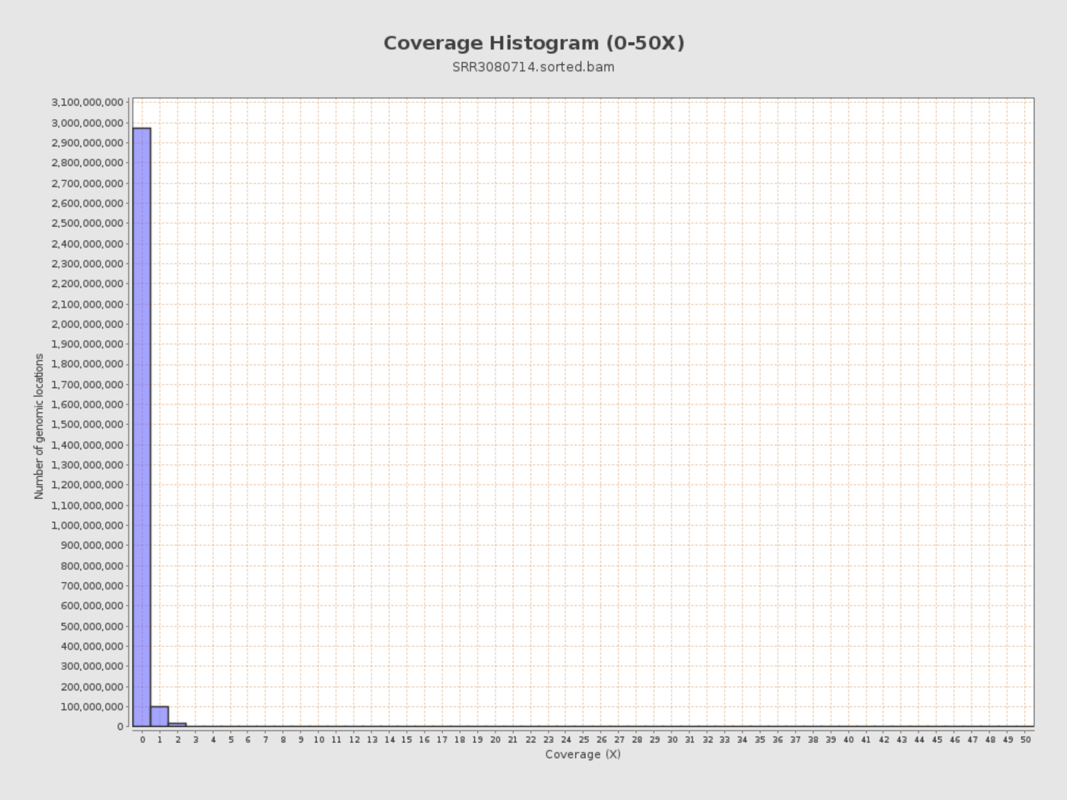
3. Results : Coverage across reference



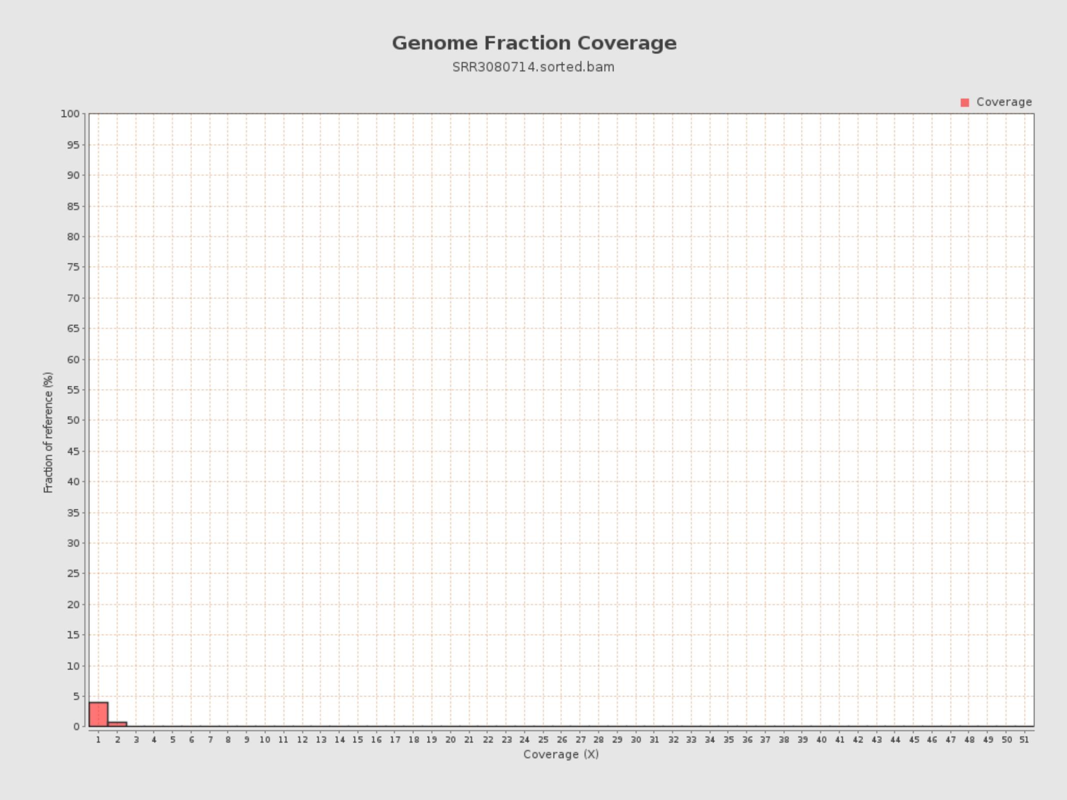
4. Results : Coverage Histogram



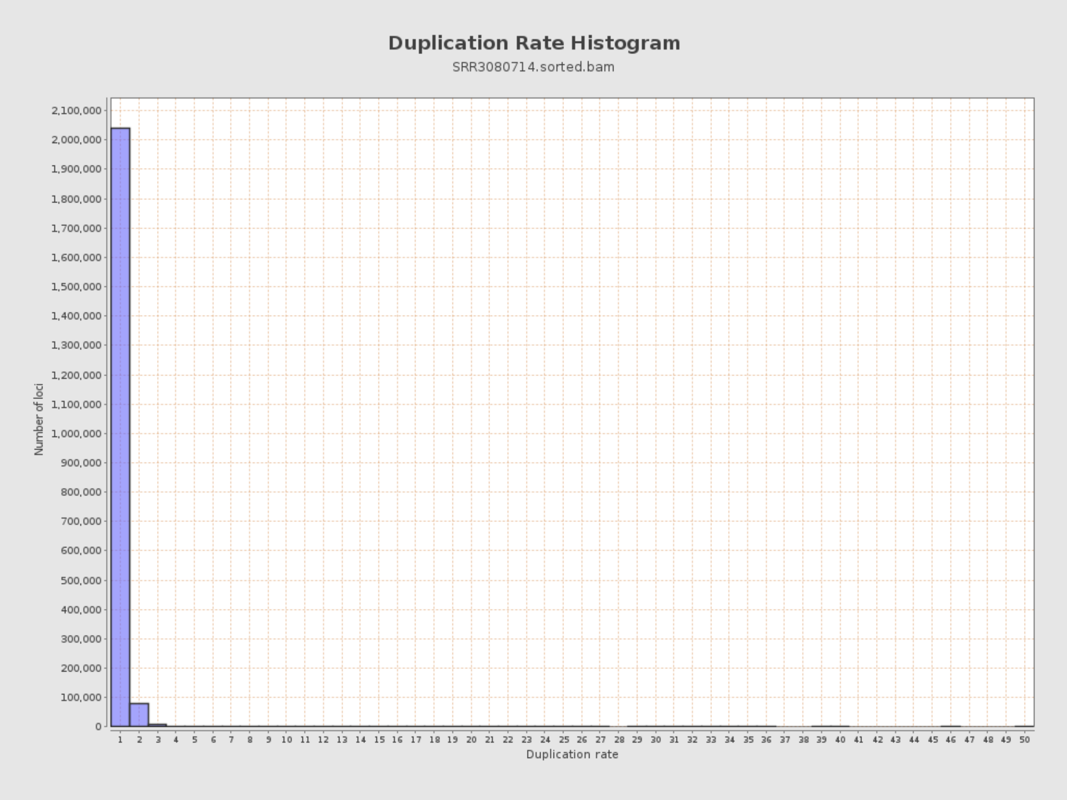
5. Results : Coverage Histogram (0-50X)



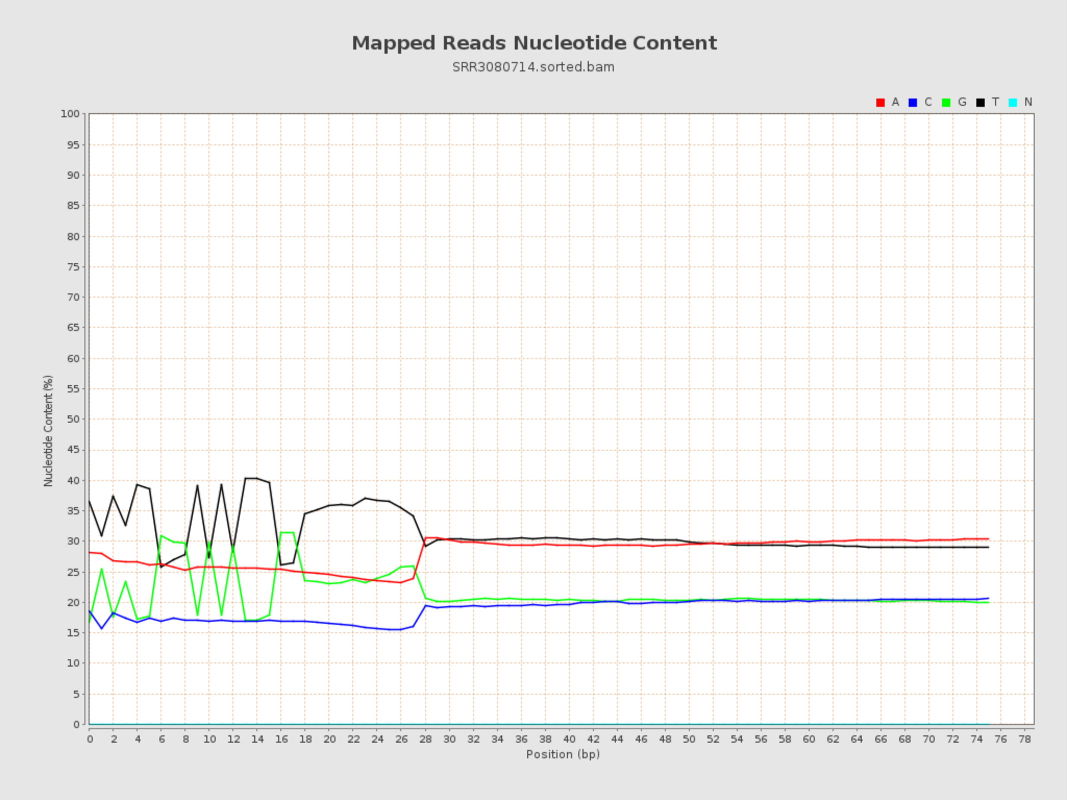
6. Results : Genome Fraction Coverage



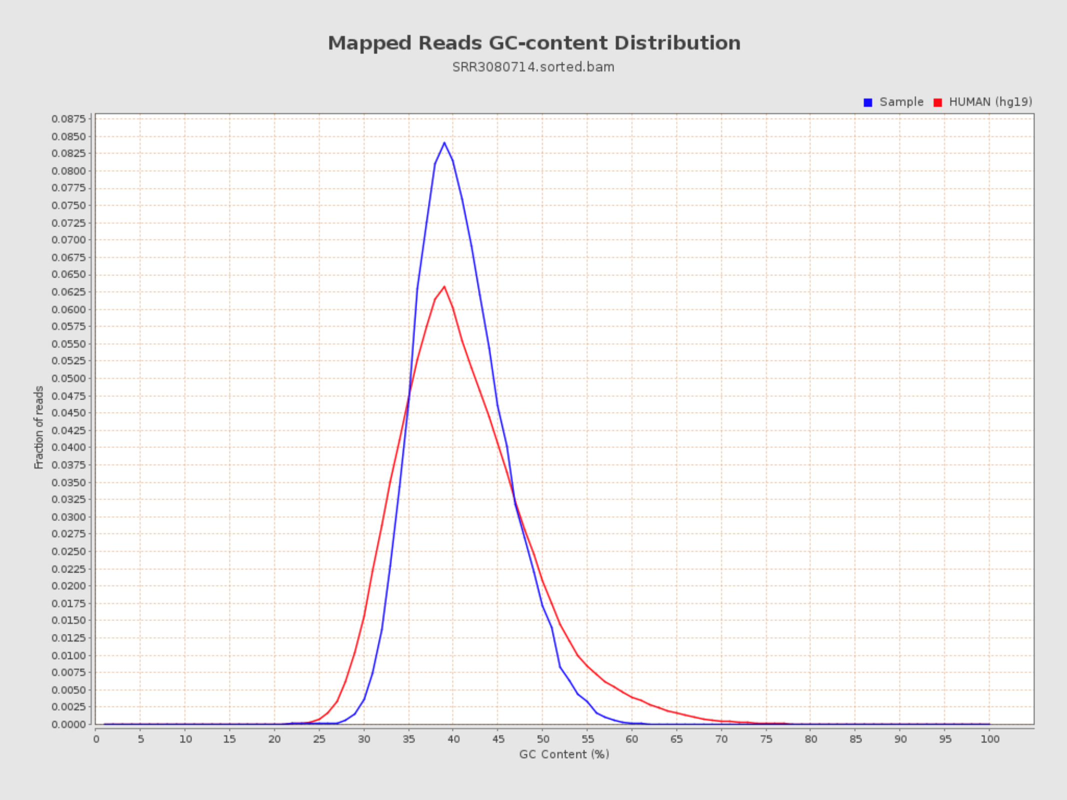
7. Results : Duplication Rate Histogram



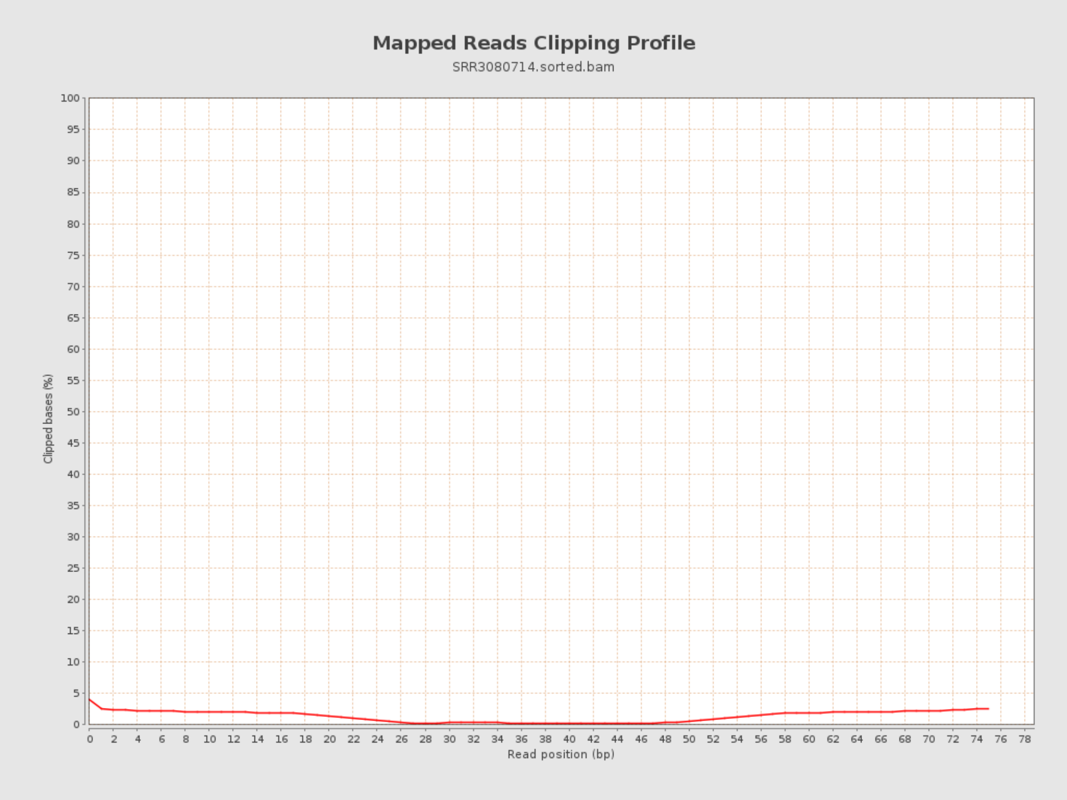
8. Results : Mapped Reads Nucleotide Content



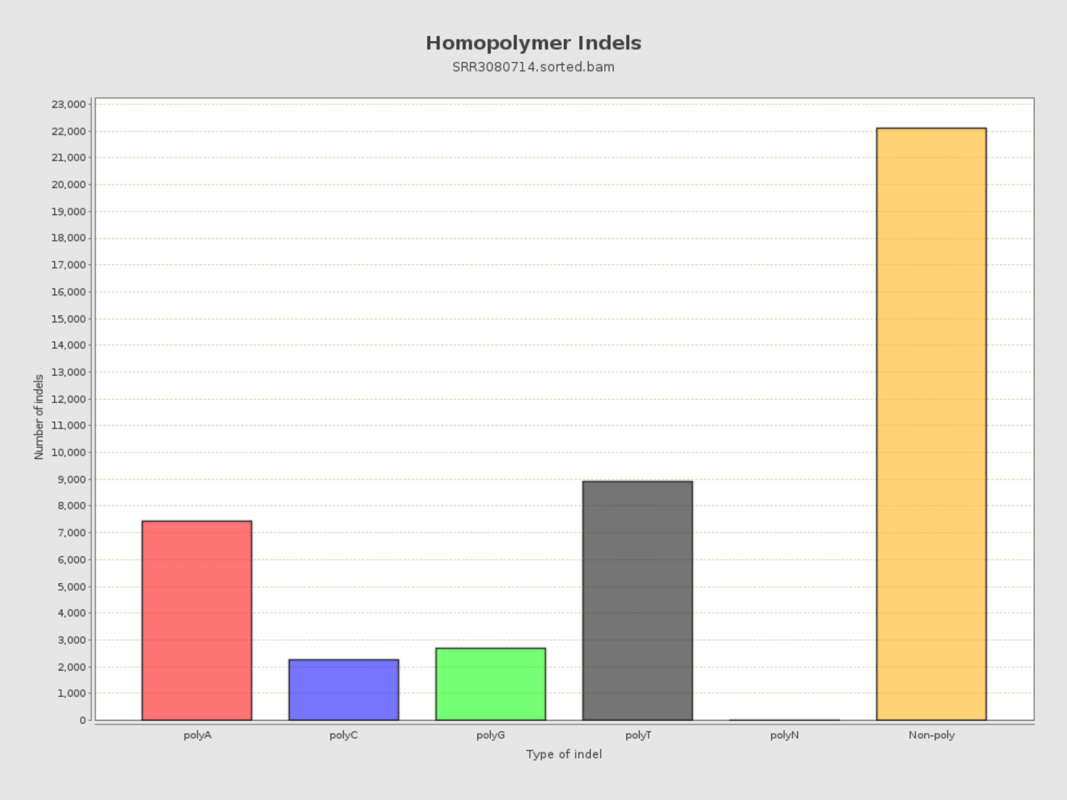
9. Results : Mapped Reads GC-content Distribution



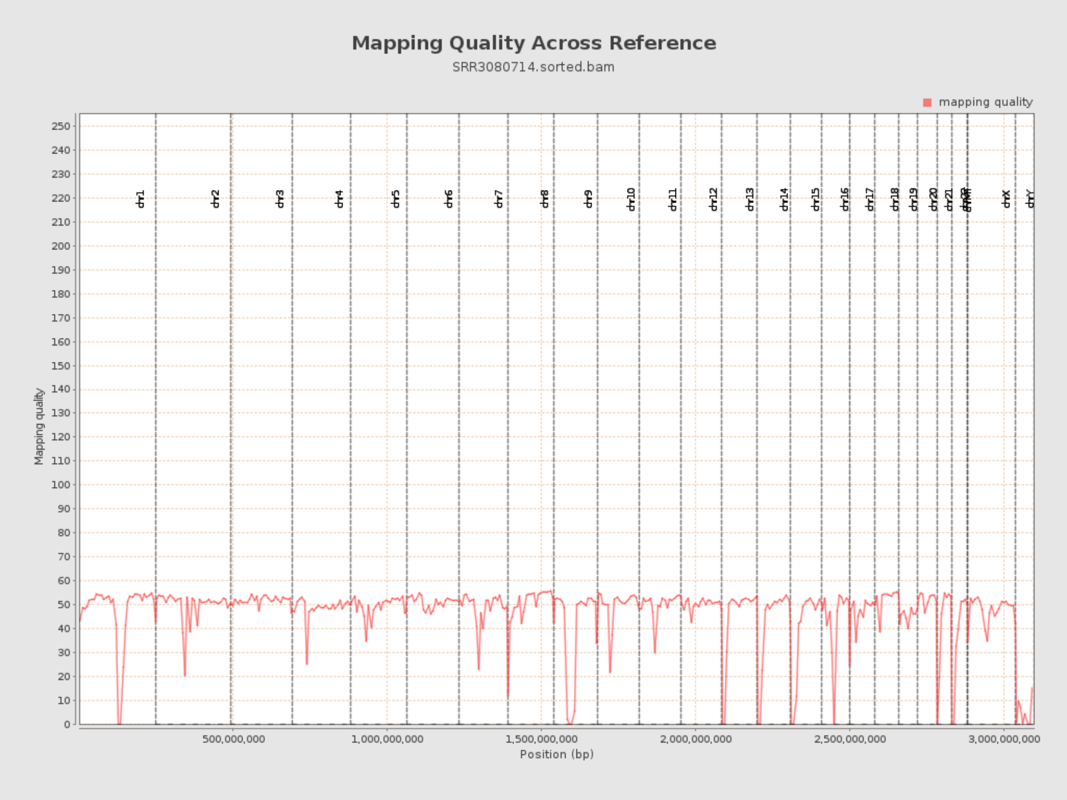
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram