Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:31:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083780.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_SRR3083780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083780.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:30:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,799,519
Mapped reads	1,757,230 / 62.77%
Unmapped reads	1,042,289 / 37.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,022 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	59,981 / 2.14%
Duplication rate	2.84%
Clipped reads	1,007,645 / 35.99%

2.2. ACGT Content

Number/percentage of A's	31,618,244 / 28.59%
Number/percentage of C's	21,112,343 / 19.09%
Number/percentage of T's	33,504,841 / 30.3%
Number/percentage of G's	24,346,508 / 22.02%
Number/percentage of N's	1,303 / 0%
GC Percentage	41.11%

2.3. Coverage

Mean	0.0357

Standard Deviation	0.2727

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

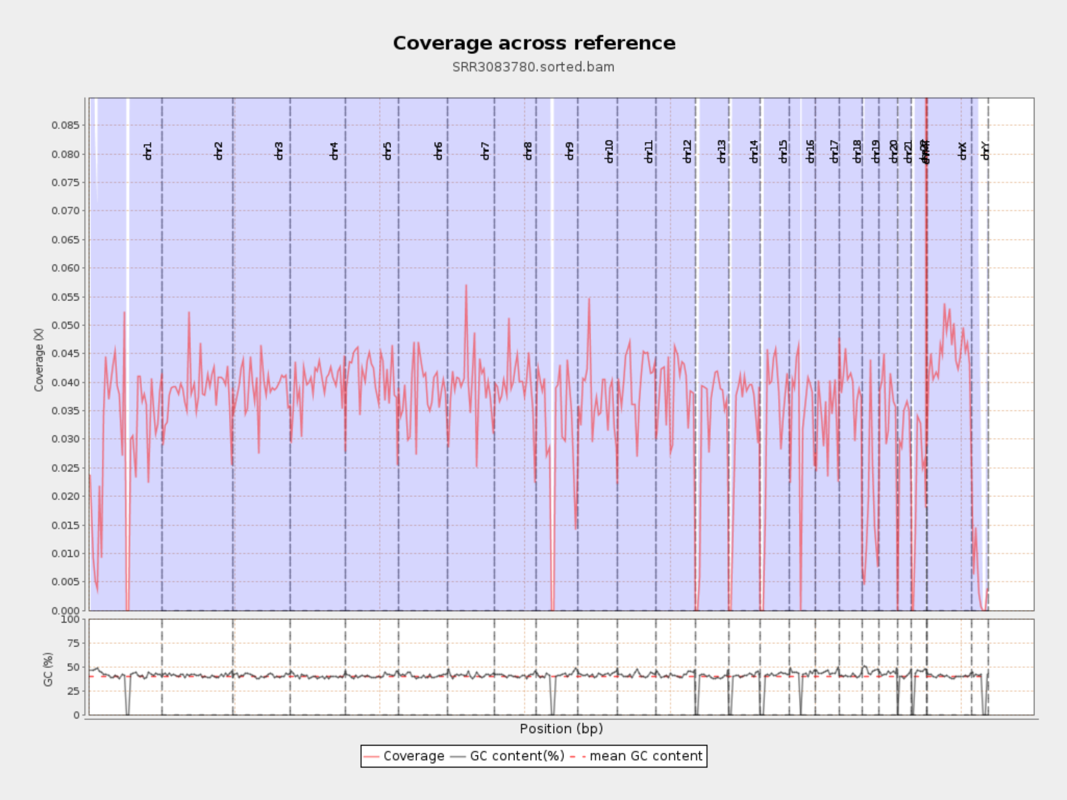
General error rate	0.82%
Mismatches	894,424
Insertions	8,068
Mapped reads with at least one insertion	0.46%
Deletions	22,979
Mapped reads with at least one deletion	1.3%
Homopolymer indels	46.43%

2.6. Chromosome stats

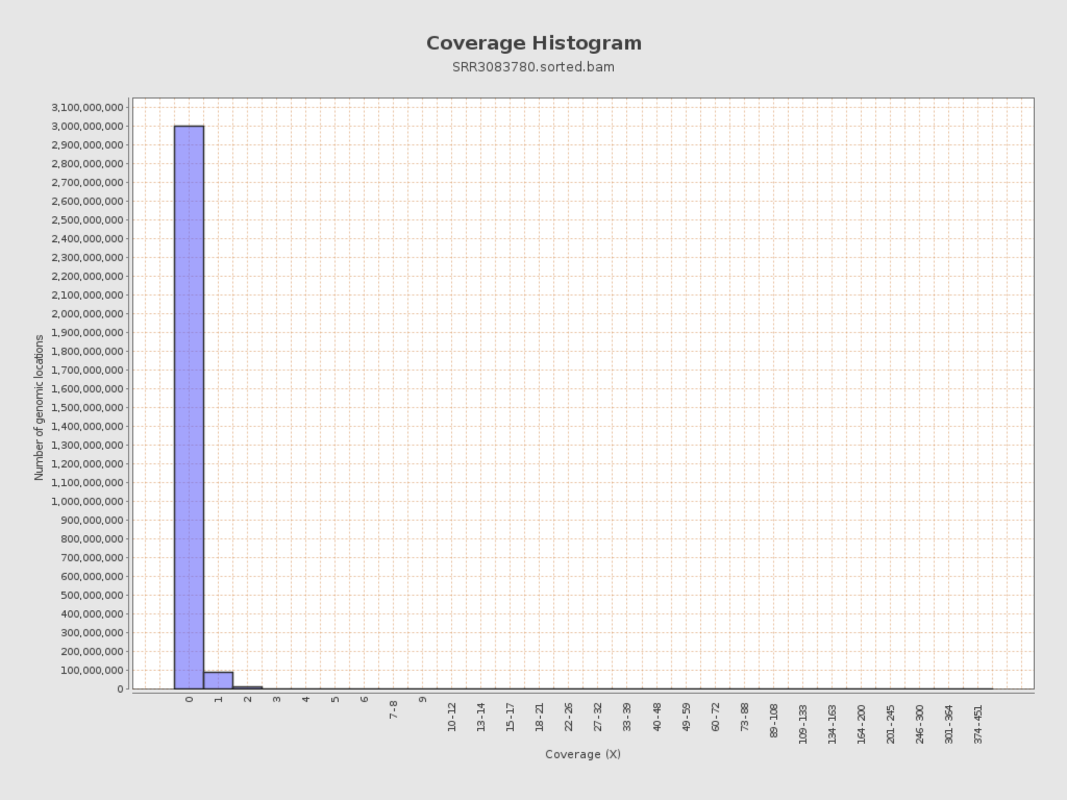
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7432696	0.0298	0.3909
chr2	243199373	9392530	0.0386	0.3288
chr3	198022430	7730370	0.039	0.2178
chr4	191154276	7597503	0.0397	0.2272
chr5	180915260	7476906	0.0413	0.2249
chr6	171115067	6508629	0.038	0.2462
chr7	159138663	6318614	0.0397	0.3271

chr8	146364022	5792119	0.0396	0.282
chr9	141213431	4374676	0.031	0.2448
chr10	135534747	5068047	0.0374	0.2873
chr11	135006516	5446879	0.0403	0.2558
chr12	133851895	5112191	0.0382	0.2169
chr13	115169878	3618400	0.0314	0.1959
chr14	107349540	3367035	0.0314	0.2026
chr15	102531392	3289069	0.0321	0.2004
chr16	90354753	3089768	0.0342	0.2221
chr17	81195210	2660493	0.0328	0.2174
chr18	78077248	3082840	0.0395	0.4654
chr19	59128983	1043247	0.0176	0.2957
chr20	63025520	2291596	0.0364	0.2142
chr21	48129895	1387300	0.0288	0.196
chr22	51304566	1054810	0.0206	0.1572
chrMT	16571	210746	12.7178	7.7554
chrX	155270560	6975226	0.0449	0.251
chrY	59373566	298269	0.005	0.1113

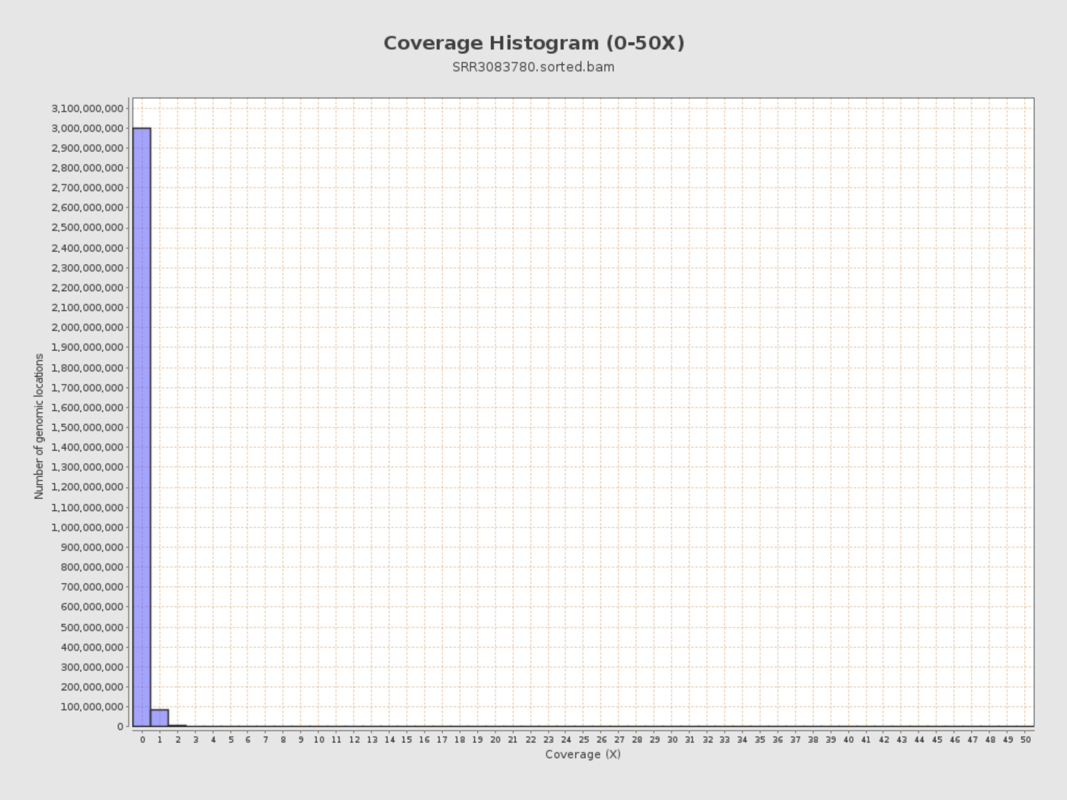
3. Results : Coverage across reference



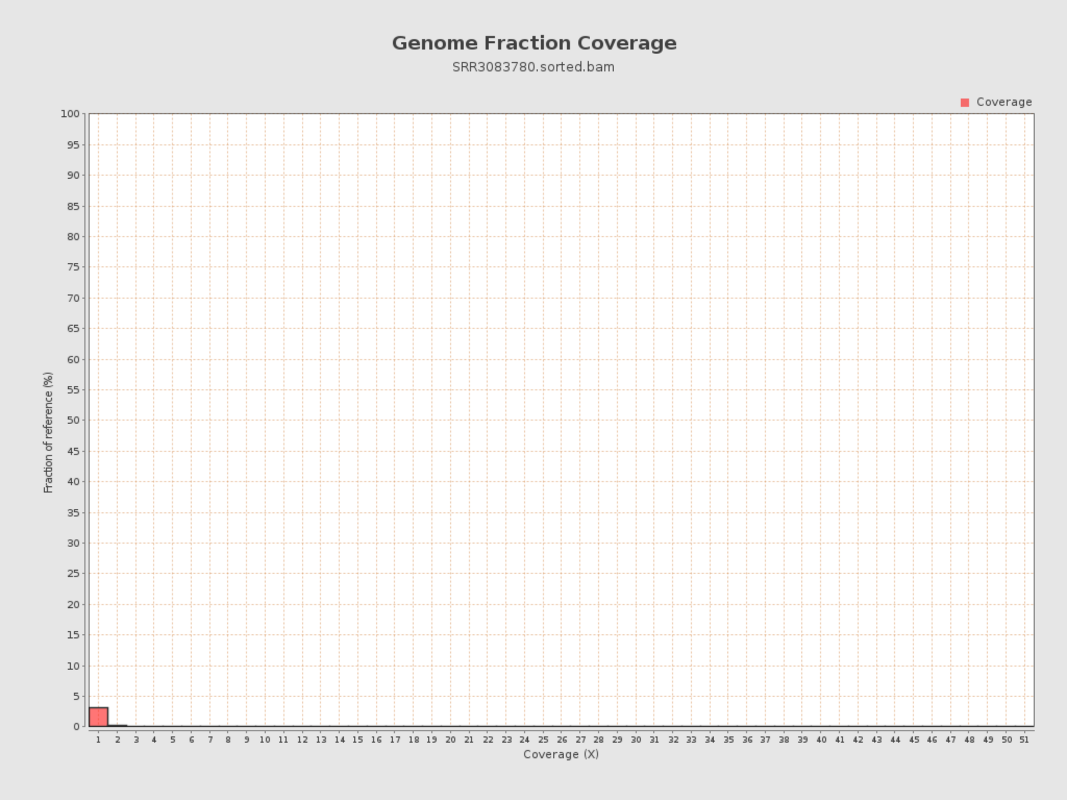
4. Results : Coverage Histogram



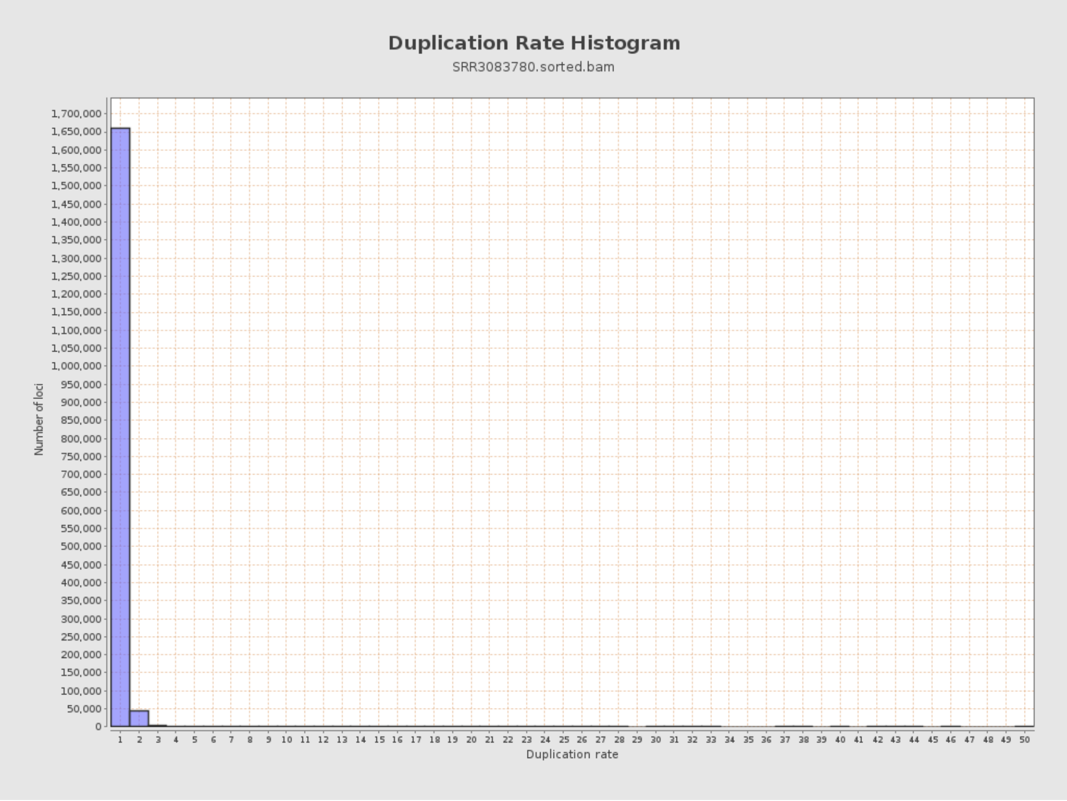
5. Results : Coverage Histogram (0-50X)



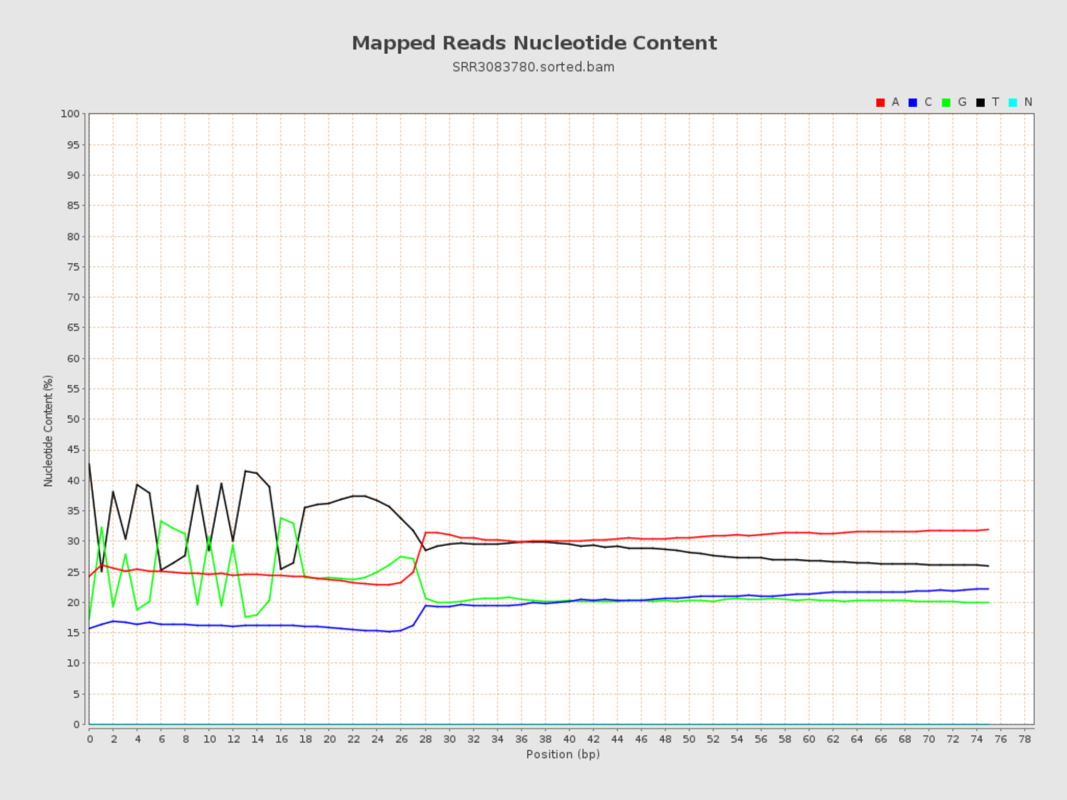
6. Results : Genome Fraction Coverage



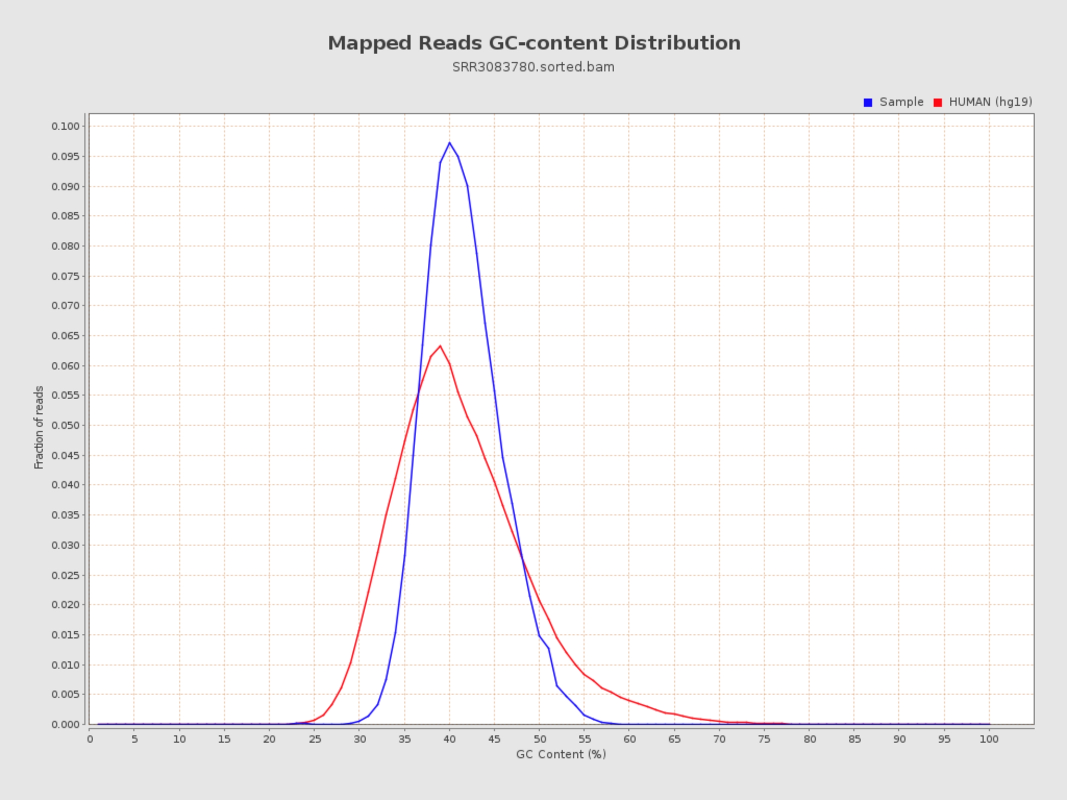
7. Results : Duplication Rate Histogram



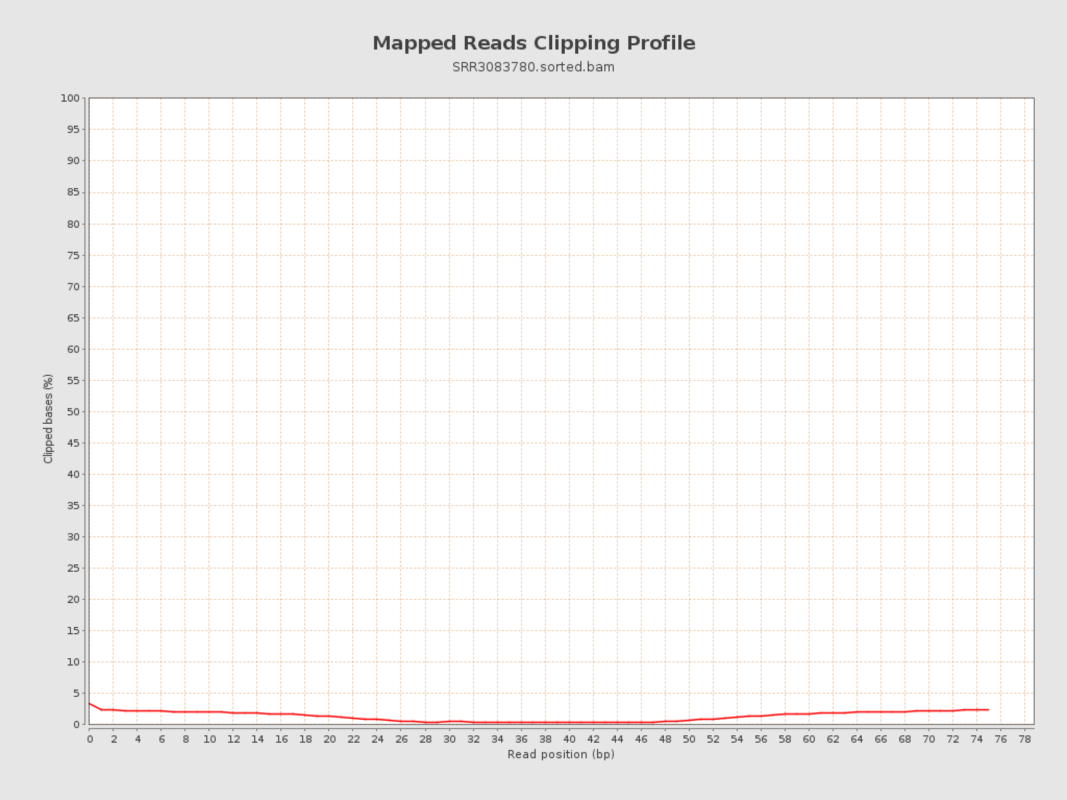
8. Results : Mapped Reads Nucleotide Content



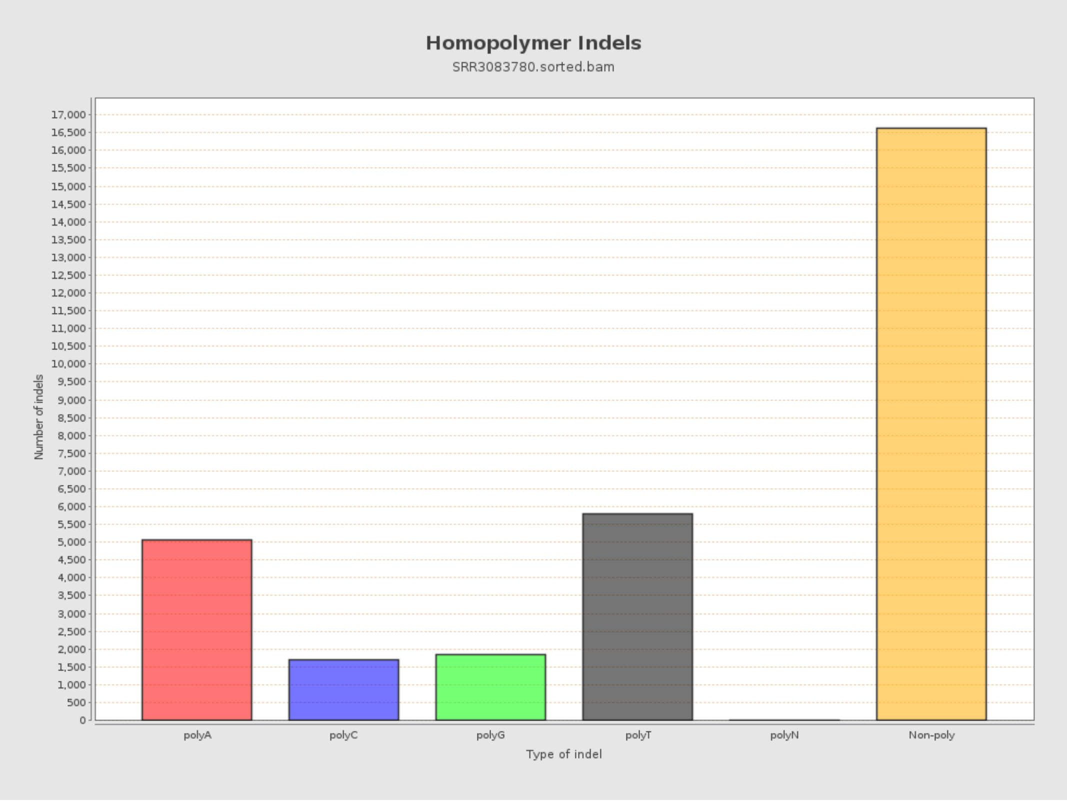
9. Results : Mapped Reads GC-content Distribution



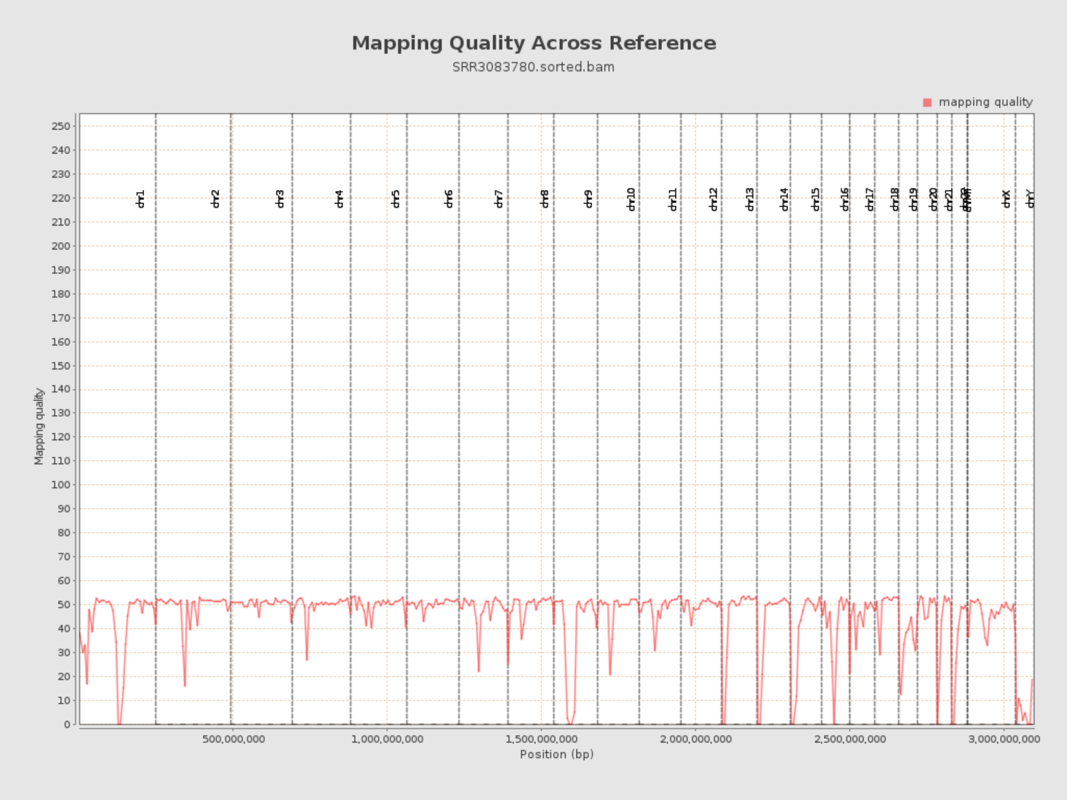
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram