Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:22:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083778.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_SRR3083778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:22:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,138,554
Mapped reads	1,275,071 / 59.62%
Unmapped reads	863,483 / 40.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,859 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	35,028 / 1.64%
Duplication rate	2.32%
Clipped reads	672,265 / 31.44%

2.2. ACGT Content

Number/percentage of A's	23,302,803 / 28.69%
Number/percentage of C's	15,207,812 / 18.72%
Number/percentage of T's	24,652,430 / 30.35%
Number/percentage of G's	18,065,785 / 22.24%
Number/percentage of N's	905 / 0%
GC Percentage	40.96%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.2089

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

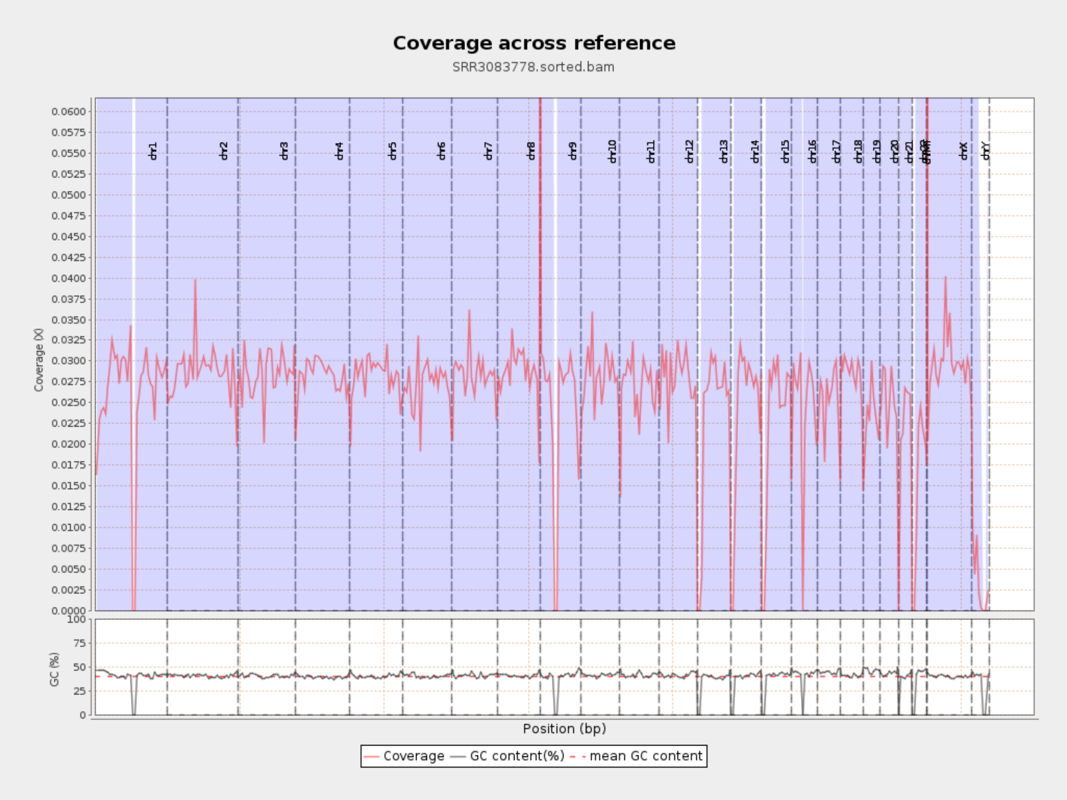
General error rate	0.85%
Mismatches	681,760
Insertions	5,773
Mapped reads with at least one insertion	0.45%
Deletions	16,732
Mapped reads with at least one deletion	1.3%
Homopolymer indels	46.39%

2.6. Chromosome stats

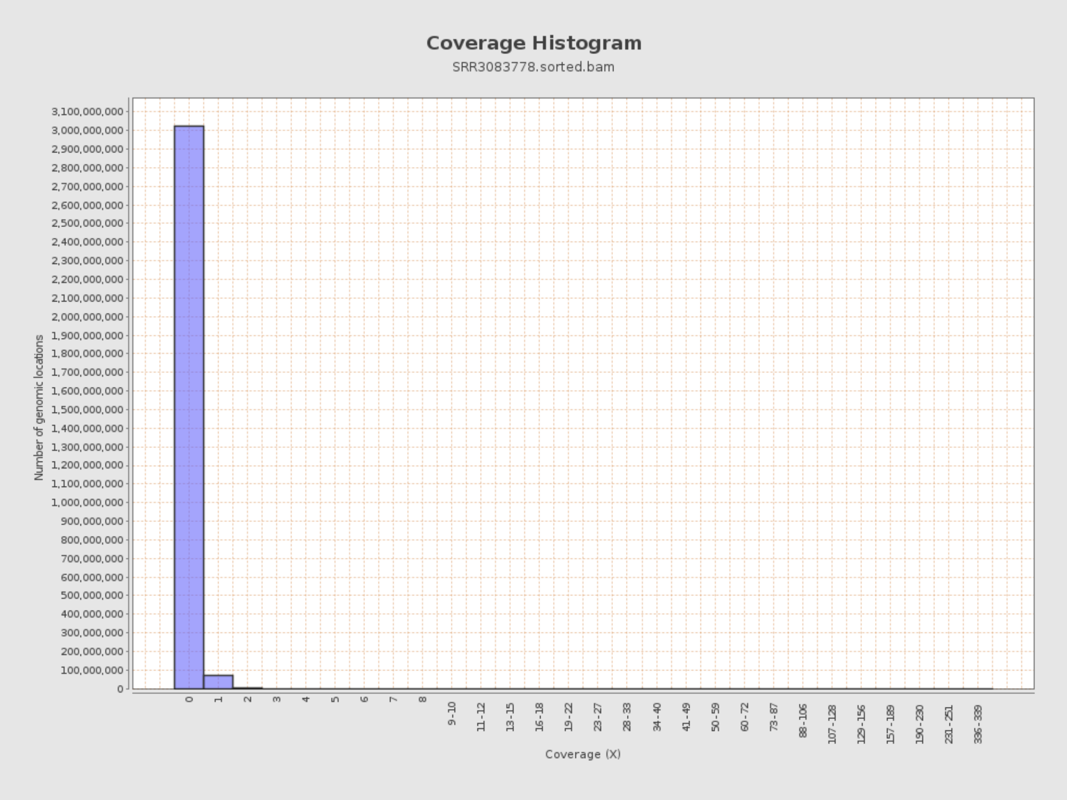
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6481652	0.026	0.2755
chr2	243199373	7009578	0.0288	0.258
chr3	198022430	5626553	0.0284	0.1814
chr4	191154276	5382686	0.0282	0.183
chr5	180915260	5149836	0.0285	0.1824
chr6	171115067	4650012	0.0272	0.1922
chr7	159138663	4515724	0.0284	0.2379

chr8	146364022	4205474	0.0287	0.2155
chr9	141213431	3465810	0.0245	0.2078
chr10	135534747	3822518	0.0282	0.2148
chr11	135006516	3656517	0.0271	0.1953
chr12	133851895	3751561	0.028	0.1806
chr13	115169878	2650066	0.023	0.1635
chr14	107349540	2523478	0.0235	0.1704
chr15	102531392	2291482	0.0223	0.1667
chr16	90354753	2169491	0.024	0.1768
chr17	81195210	2047197	0.0252	0.1784
chr18	78077248	2243053	0.0287	0.3401
chr19	59128983	1384221	0.0234	0.2259
chr20	63025520	1572340	0.0249	0.1741
chr21	48129895	1026279	0.0213	0.1611
chr22	51304566	788661	0.0154	0.1323
chrMT	16571	18911	1.1412	1.2849
chrX	155270560	4627875	0.0298	0.1979
chrY	59373566	195166	0.0033	0.0748

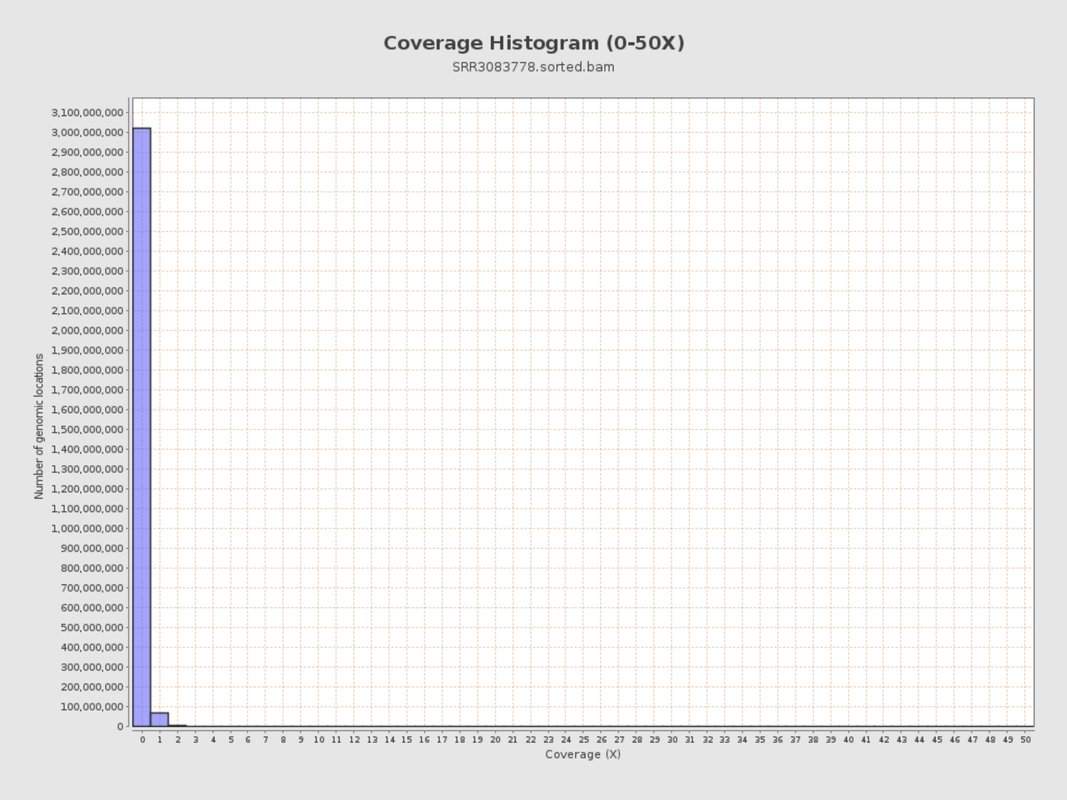
3. Results : Coverage across reference



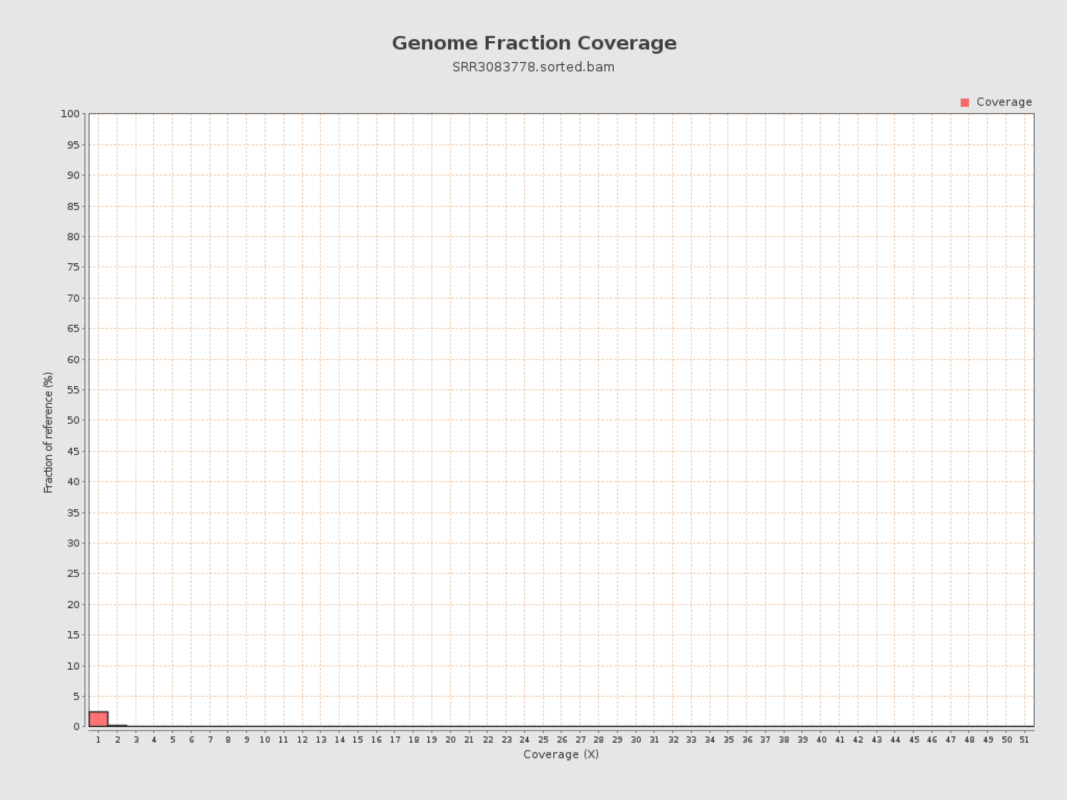
4. Results : Coverage Histogram



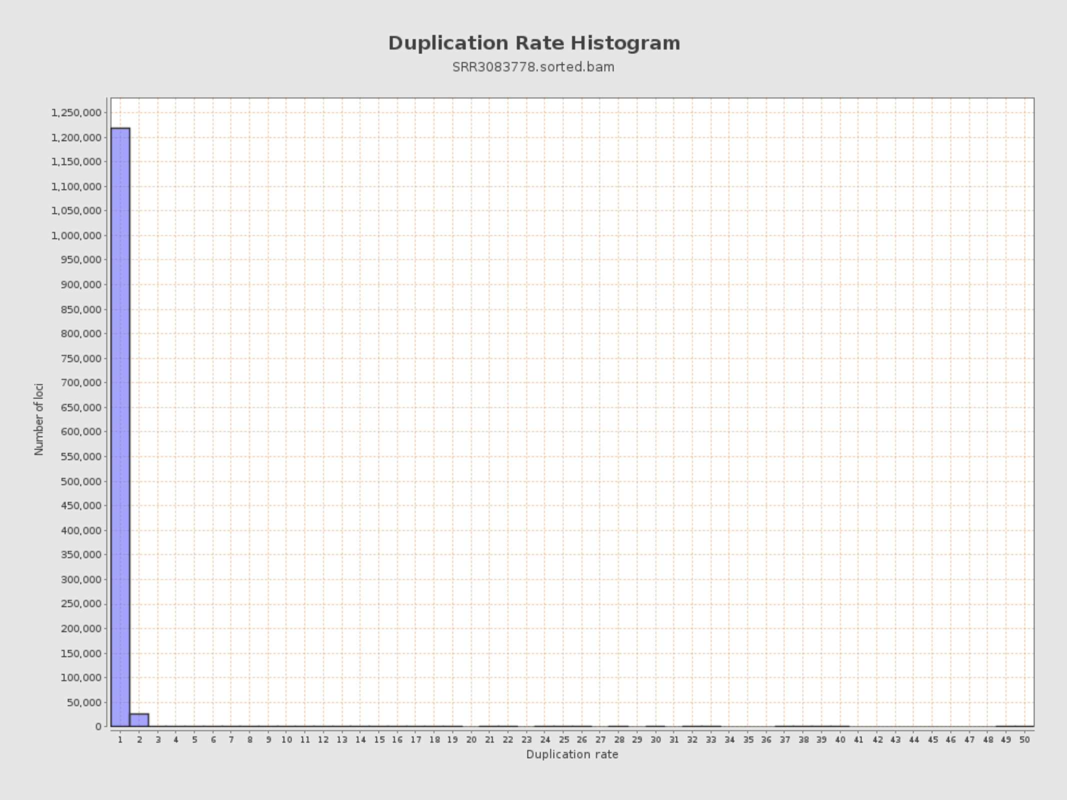
5. Results : Coverage Histogram (0-50X)



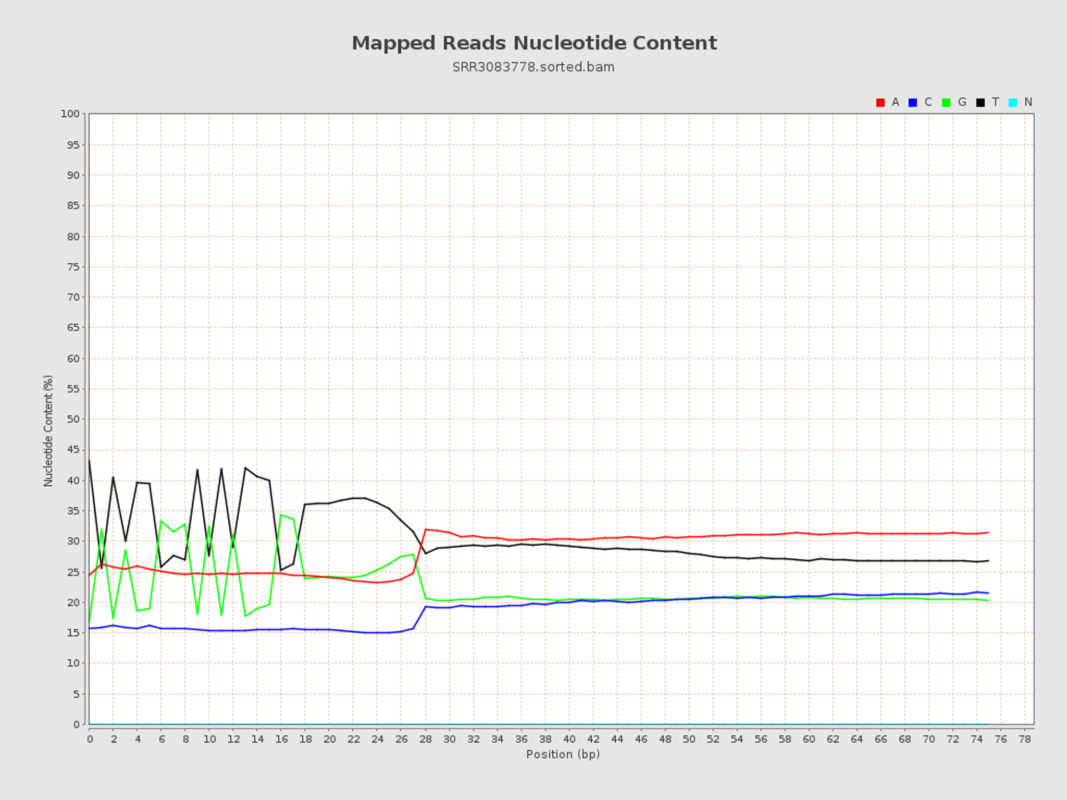
6. Results : Genome Fraction Coverage



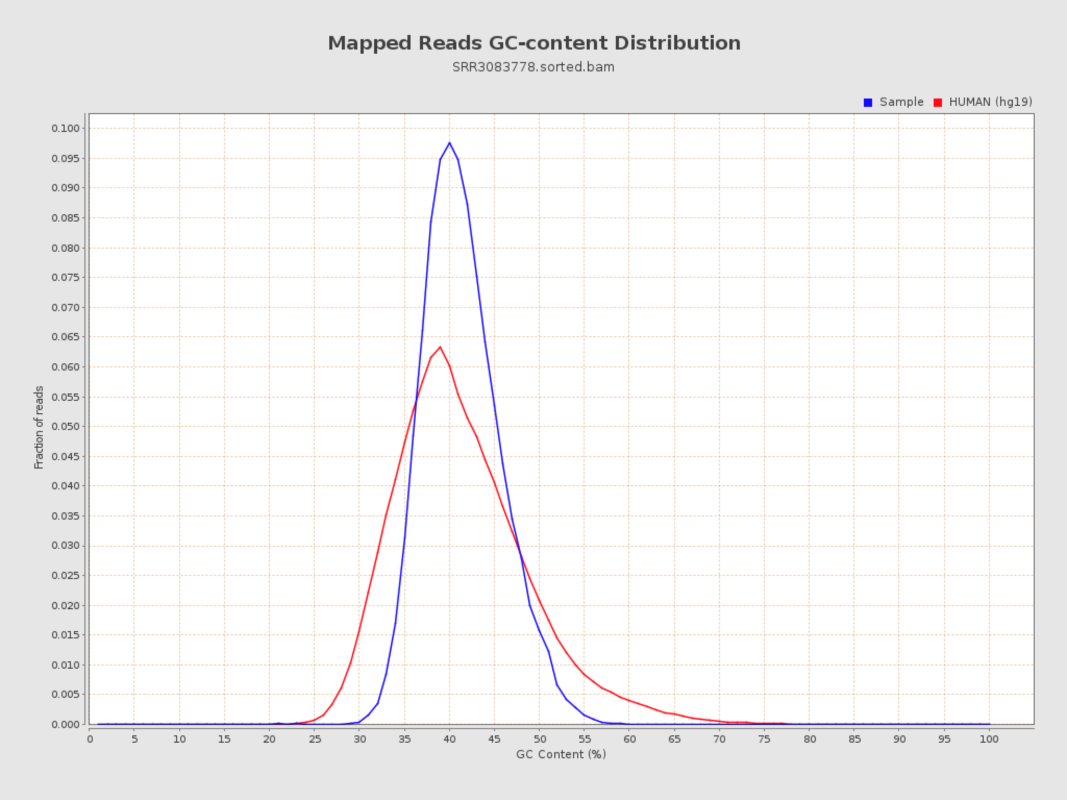
7. Results : Duplication Rate Histogram



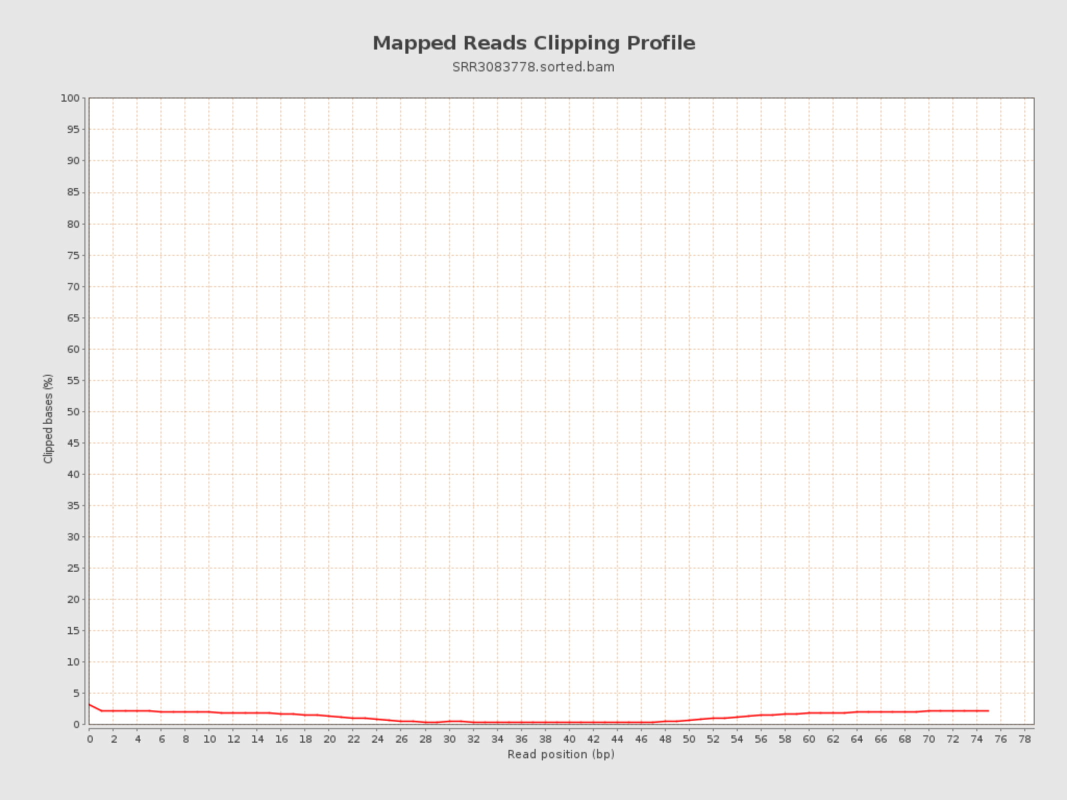
8. Results : Mapped Reads Nucleotide Content



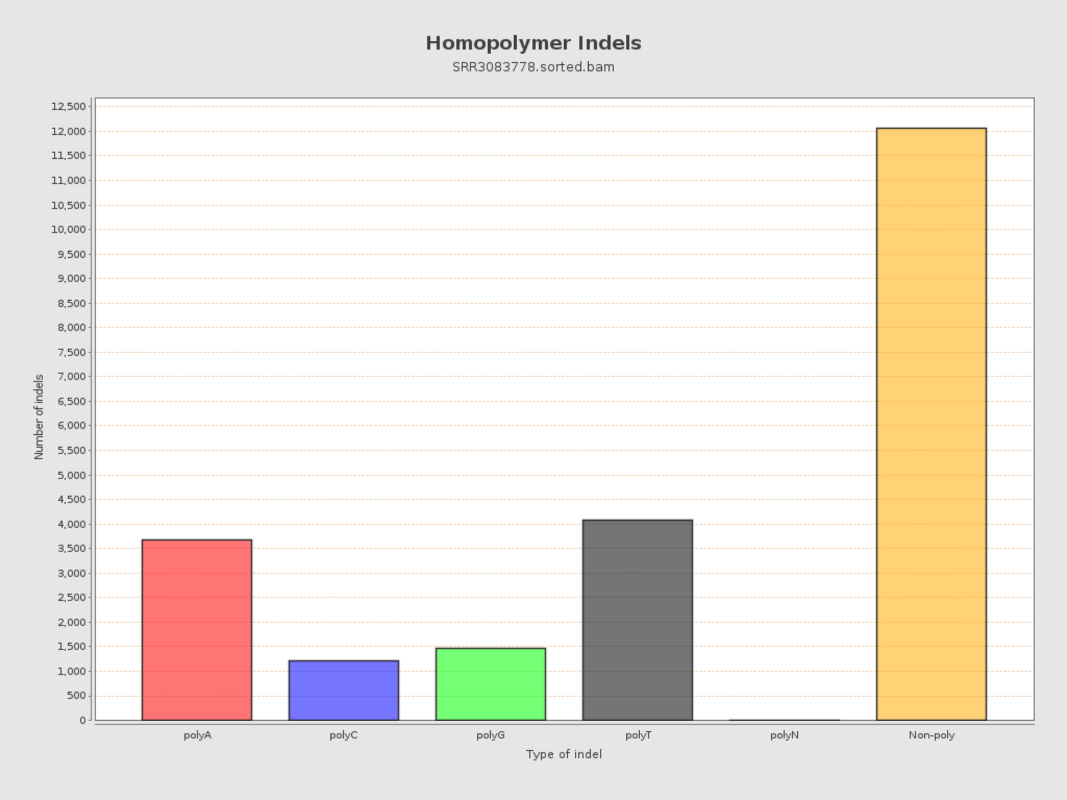
9. Results : Mapped Reads GC-content Distribution



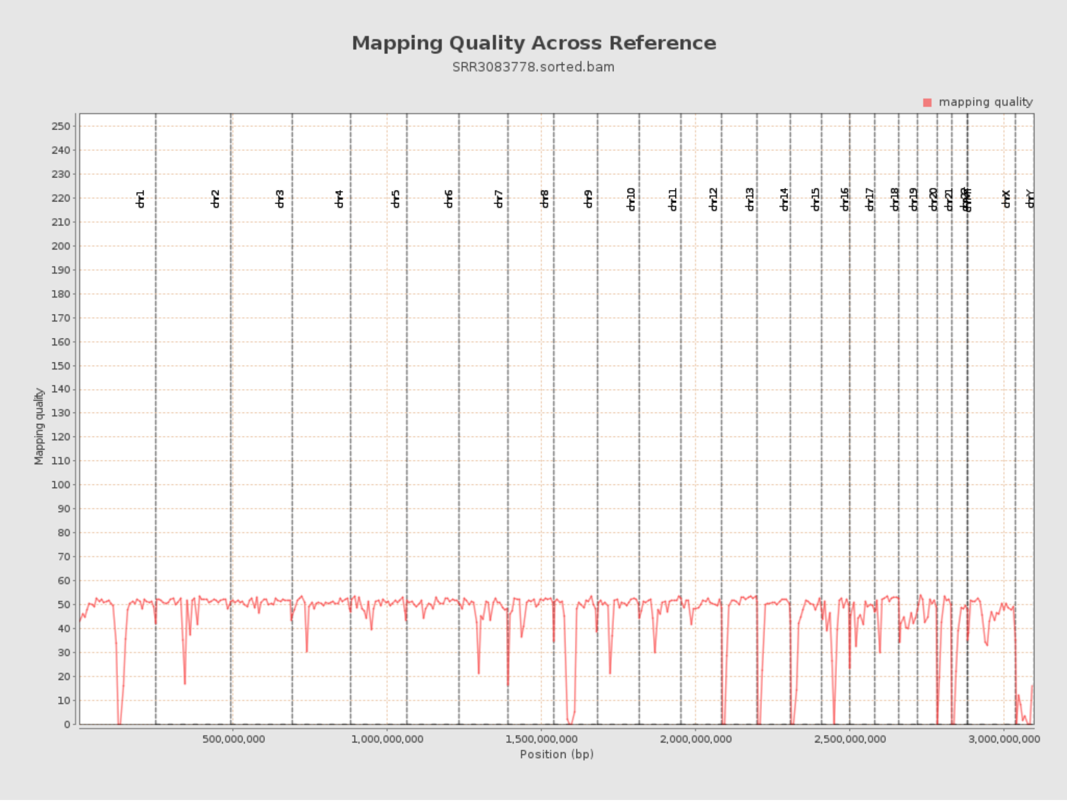
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram