Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 06:16:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083777.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_SRR3083777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 06:15:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,088,200
Mapped reads	1,178,749 / 56.45%
Unmapped reads	909,451 / 43.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,516 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	33,074 / 1.58%
Duplication rate	2.21%
Clipped reads	589,146 / 28.21%

2.2. ACGT Content

Number/percentage of A's	21,595,410 / 28.34%
Number/percentage of C's	14,268,492 / 18.72%
Number/percentage of T's	22,980,087 / 30.16%
Number/percentage of G's	17,357,658 / 22.78%
Number/percentage of N's	901 / 0%
GC Percentage	41.5%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.226

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

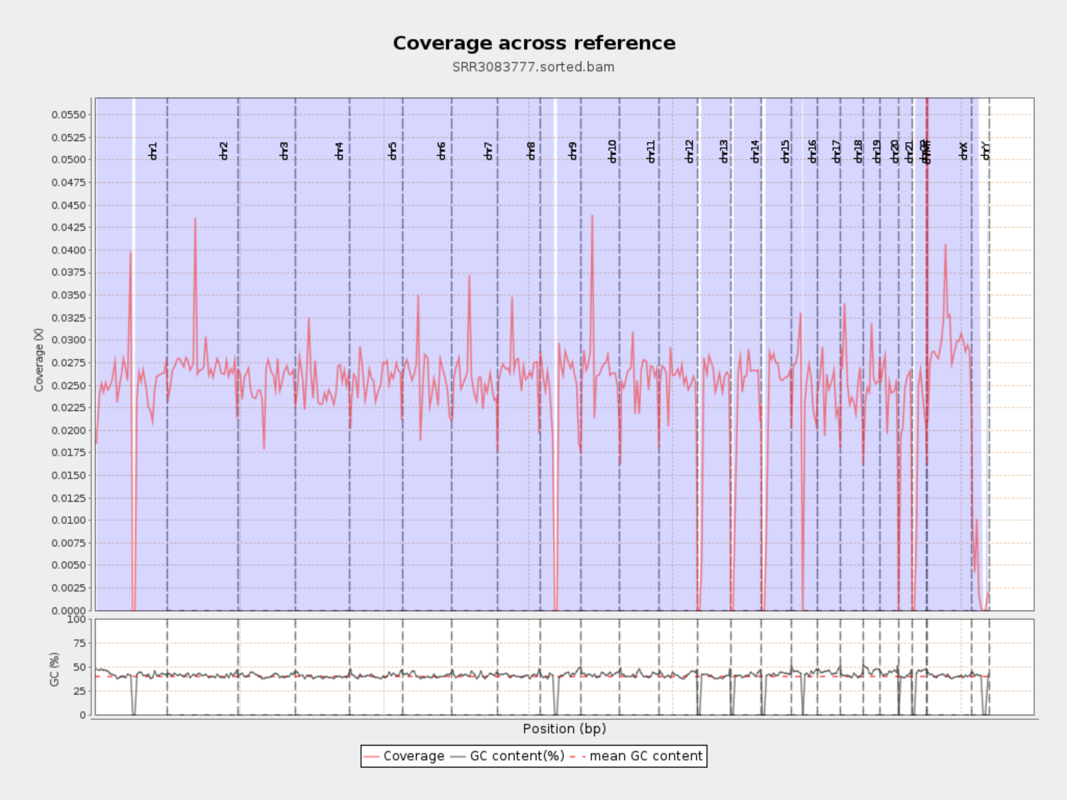
General error rate	0.87%
Mismatches	649,184
Insertions	5,637
Mapped reads with at least one insertion	0.48%
Deletions	17,138
Mapped reads with at least one deletion	1.44%
Homopolymer indels	45.33%

2.6. Chromosome stats

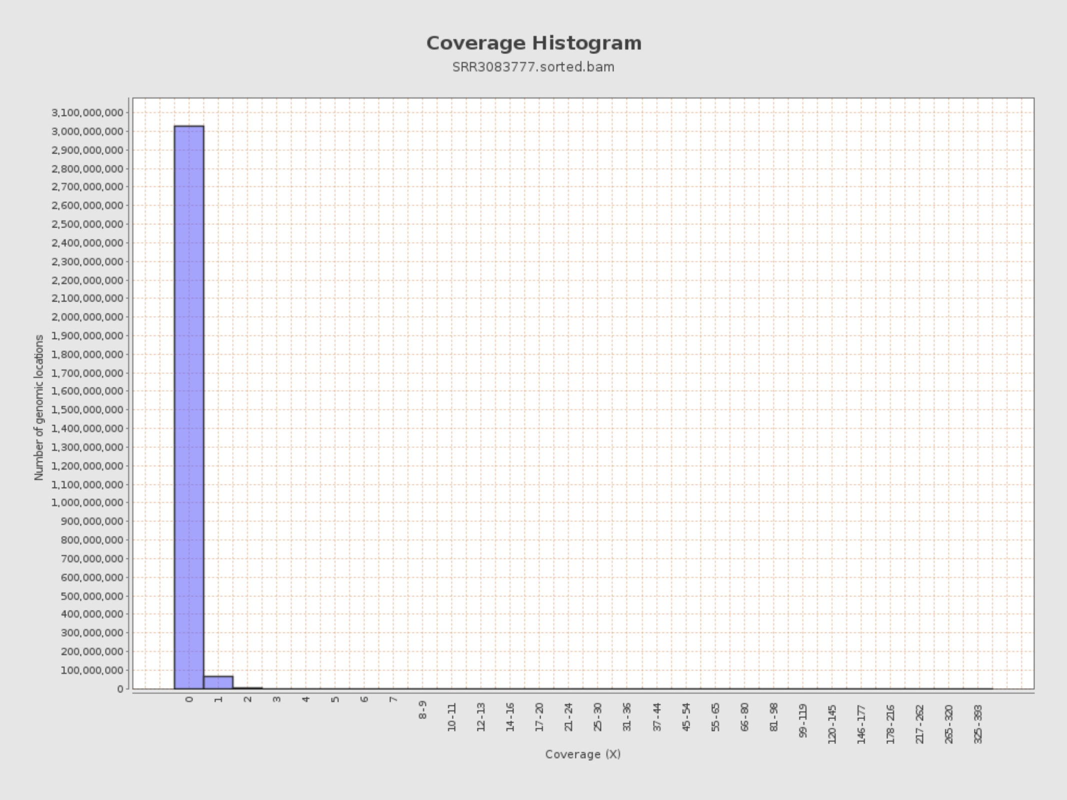
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5946833	0.0239	0.3682
chr2	243199373	6655414	0.0274	0.2727
chr3	198022430	5017574	0.0253	0.17
chr4	191154276	4817351	0.0252	0.1752
chr5	180915260	4663031	0.0258	0.1704
chr6	171115067	4396574	0.0257	0.1955
chr7	159138663	4074138	0.0256	0.2533

chr8	146364022	3907938	0.0267	0.2253
chr9	141213431	3234834	0.0229	0.2133
chr10	135534747	3703468	0.0273	0.247
chr11	135006516	3487391	0.0258	0.198
chr12	133851895	3443040	0.0257	0.1717
chr13	115169878	2520259	0.0219	0.1568
chr14	107349540	2331029	0.0217	0.1623
chr15	102531392	2226223	0.0217	0.1592
chr16	90354753	2128293	0.0236	0.1795
chr17	81195210	1976661	0.0243	0.1821
chr18	78077248	1986232	0.0254	0.3998
chr19	59128983	1504007	0.0254	0.27
chr20	63025520	1542918	0.0245	0.1712
chr21	48129895	1004327	0.0209	0.158
chr22	51304566	836969	0.0163	0.1353
chrMT	16571	26124	1.5765	1.4244
chrX	155270560	4606103	0.0297	0.1998
chrY	59373566	193423	0.0033	0.0796

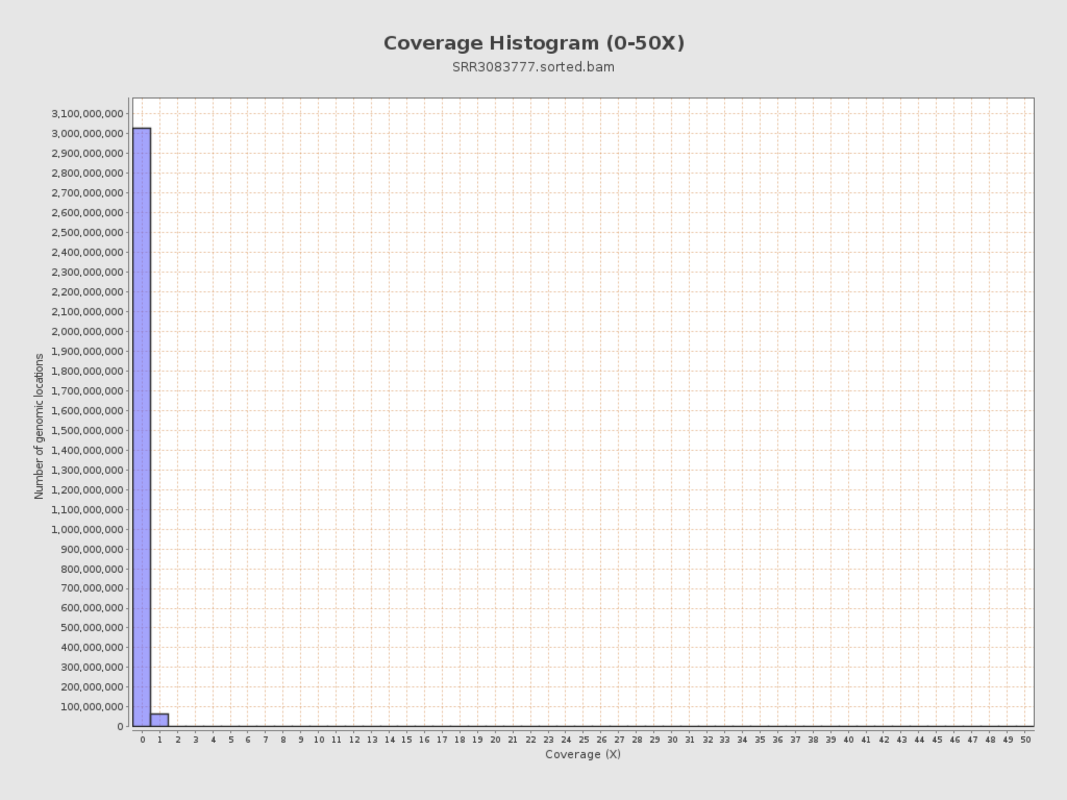
3. Results : Coverage across reference



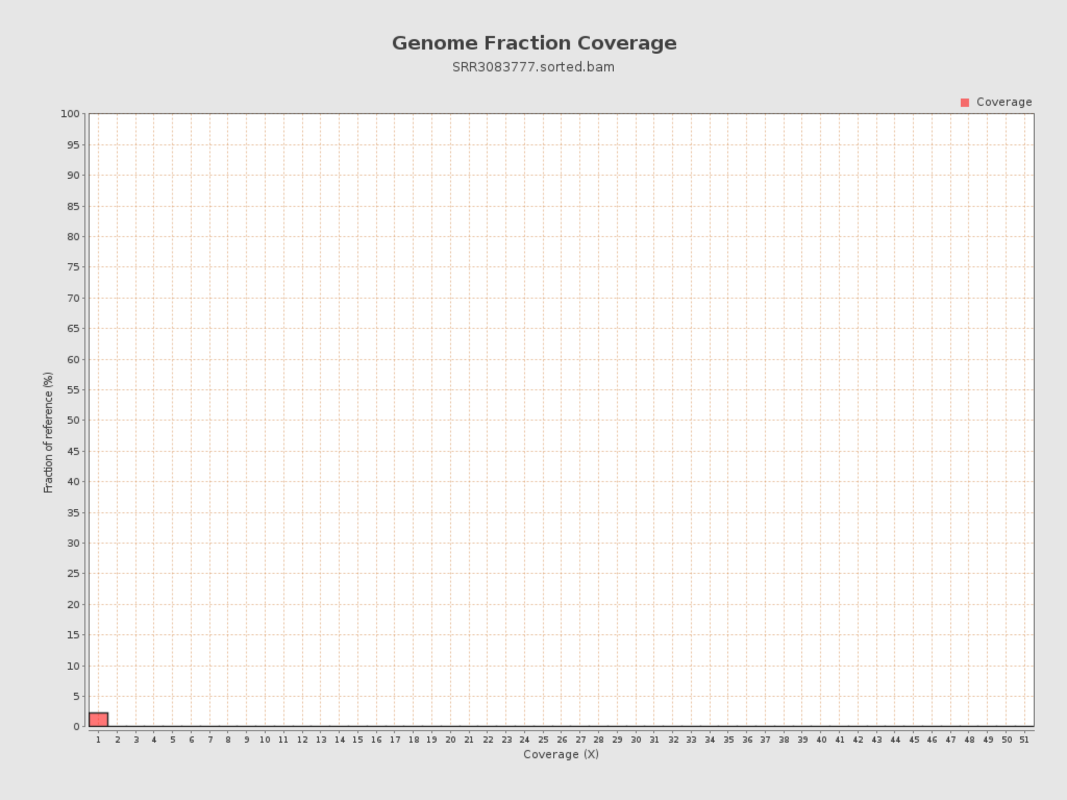
4. Results : Coverage Histogram



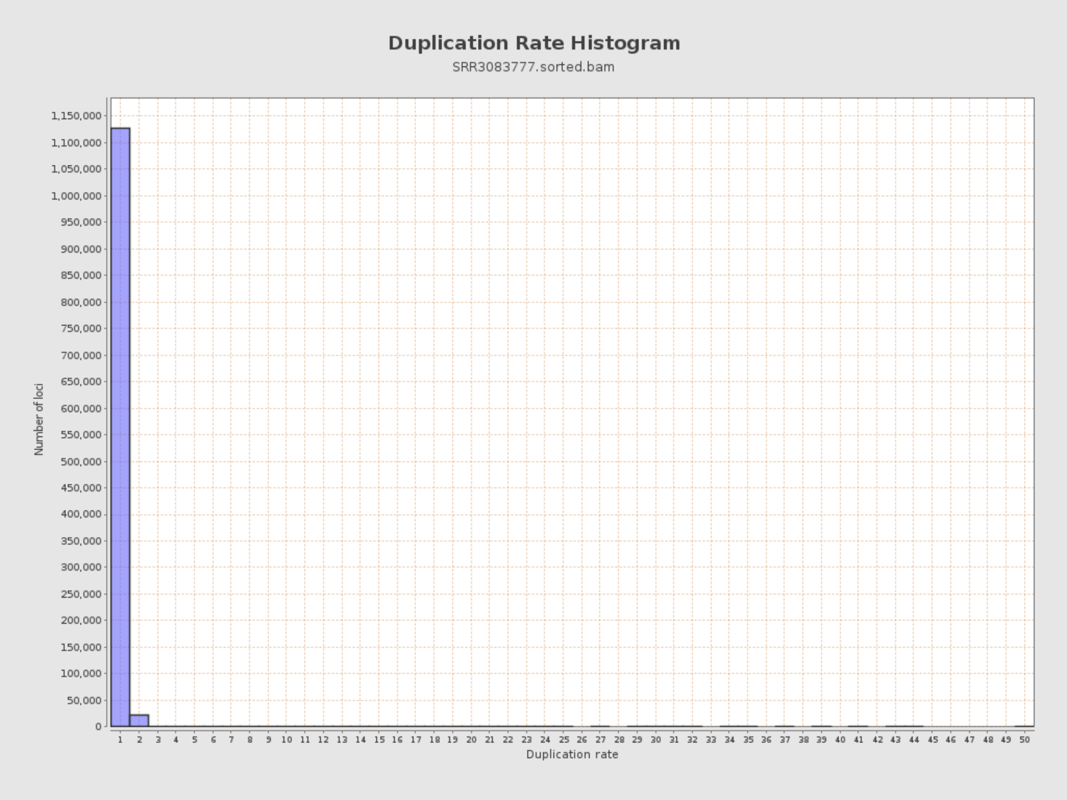
5. Results : Coverage Histogram (0-50X)



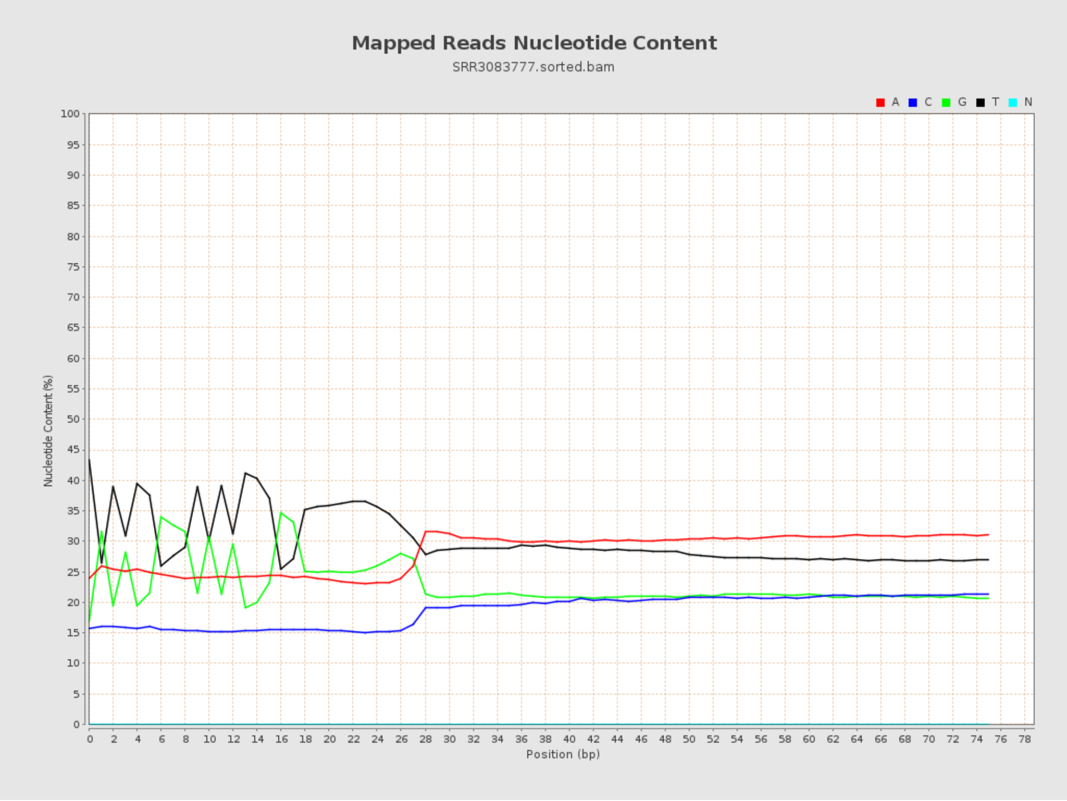
6. Results : Genome Fraction Coverage



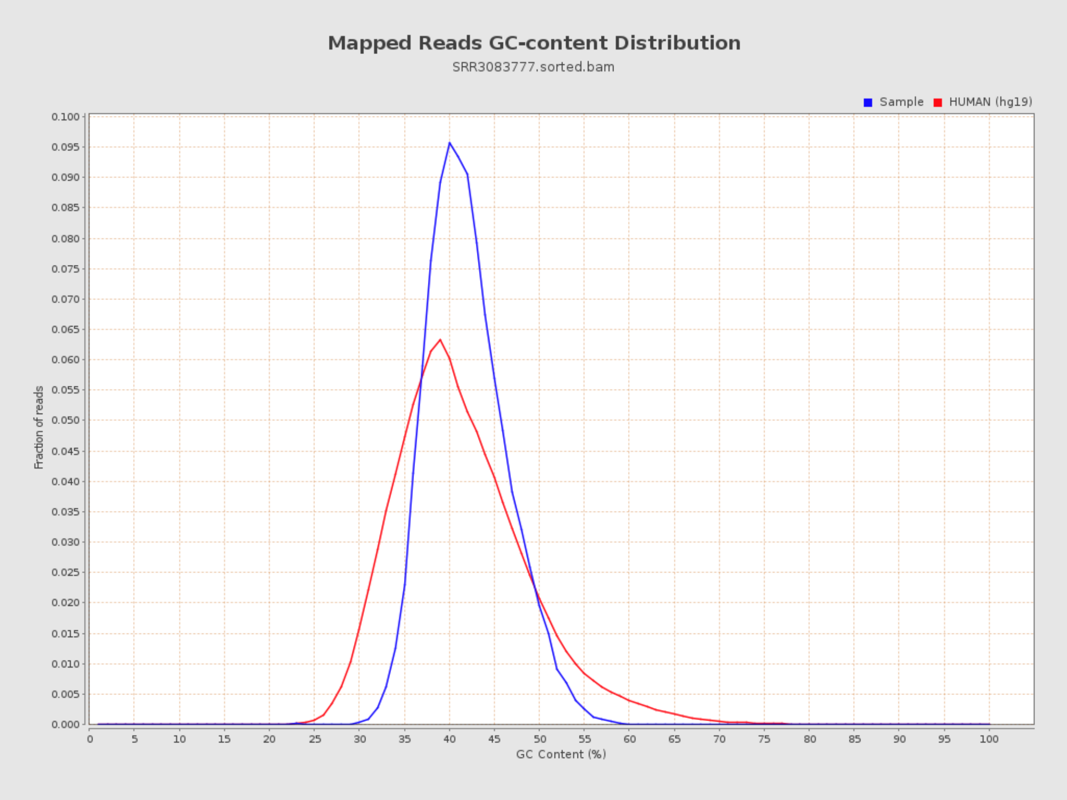
7. Results : Duplication Rate Histogram



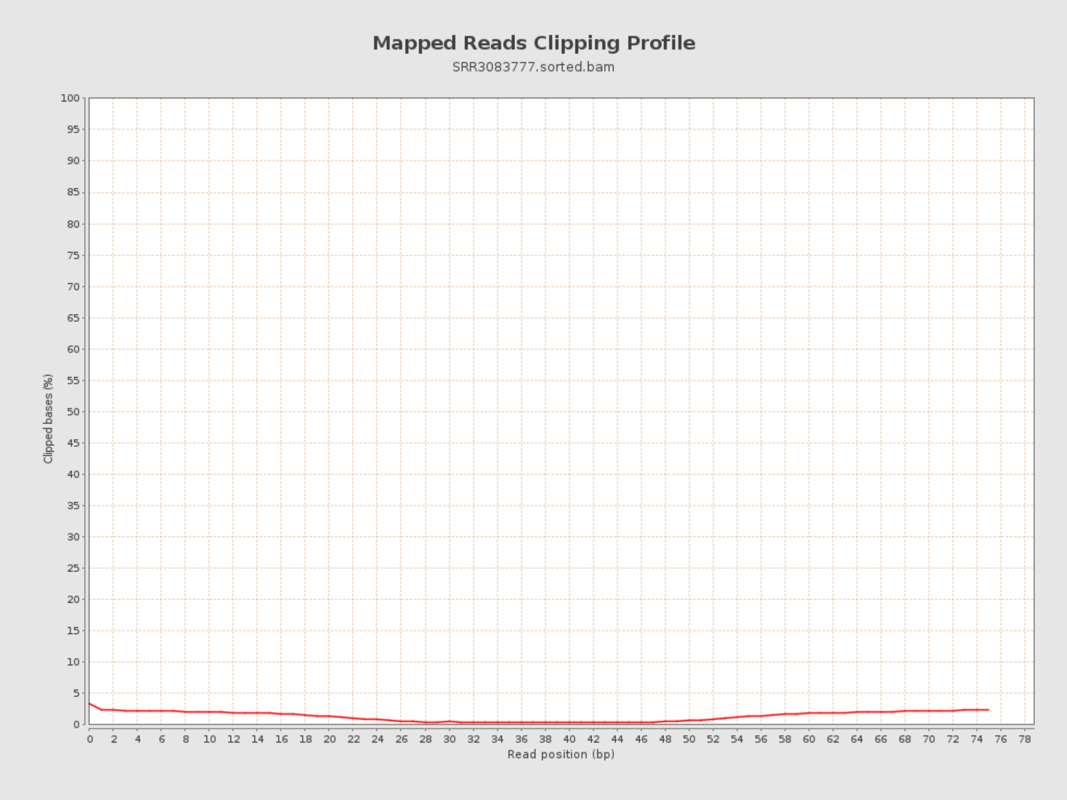
8. Results : Mapped Reads Nucleotide Content



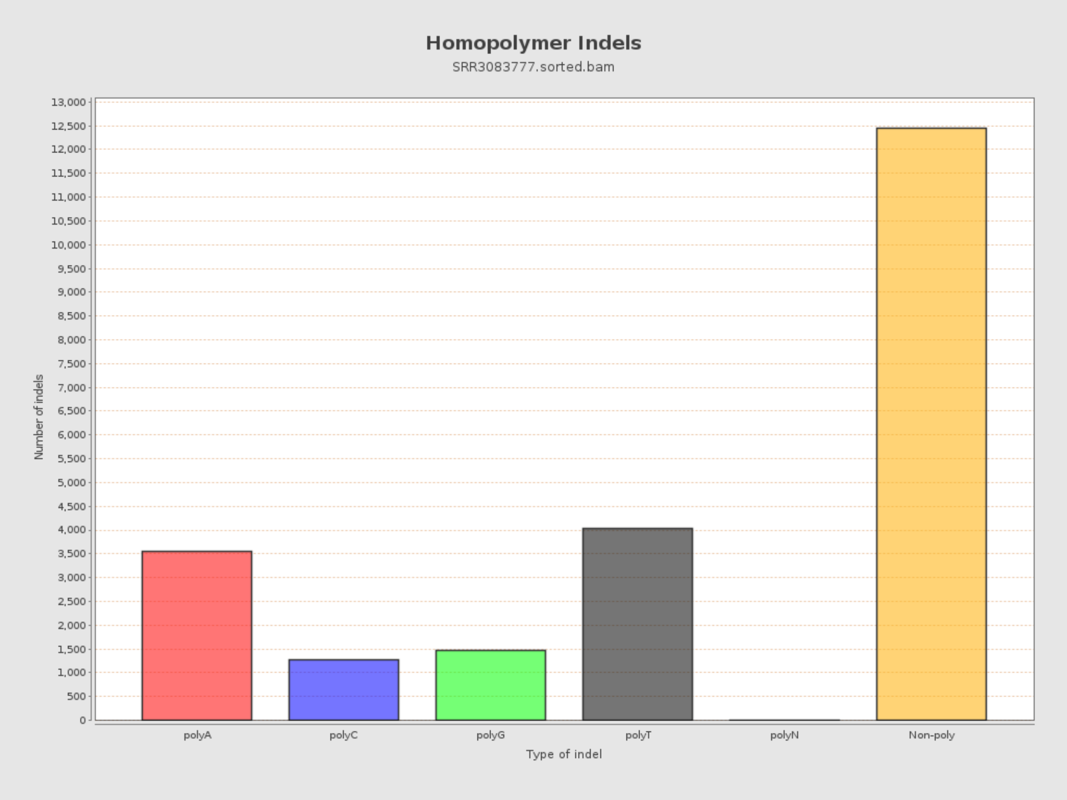
9. Results : Mapped Reads GC-content Distribution



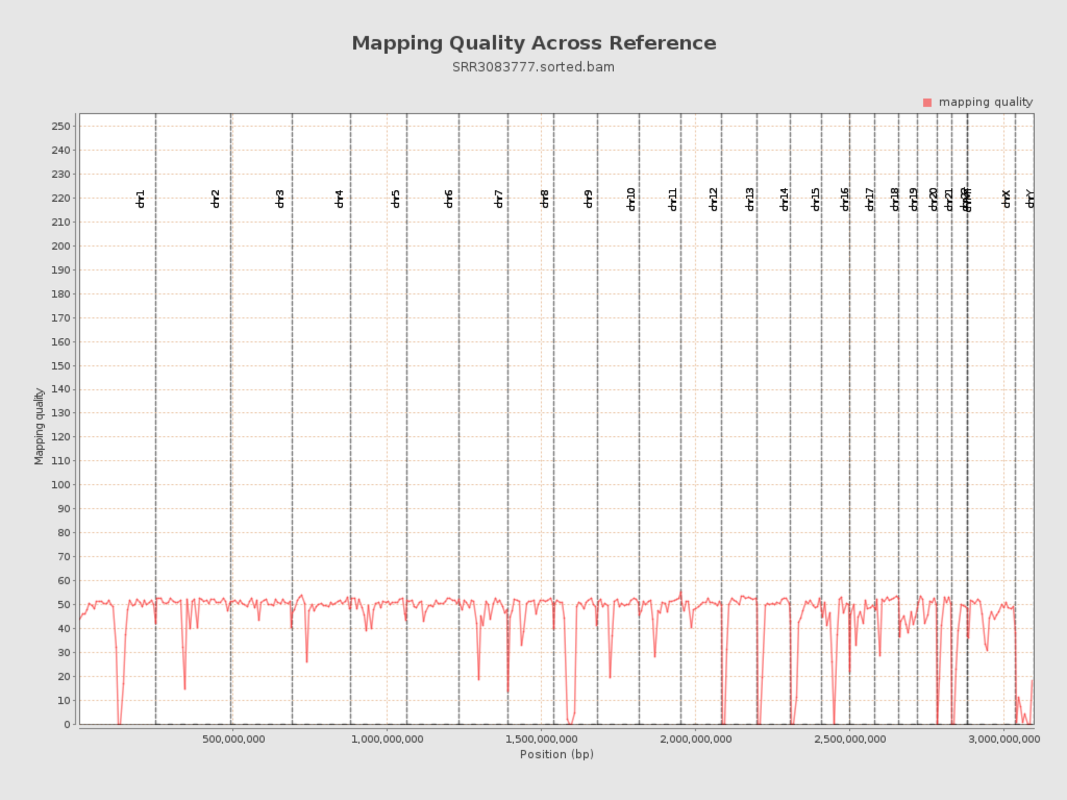
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram