Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 04:24:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083752.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_SRR3083752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 04:24:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,755,848
Mapped reads	1,418,479 / 80.79%
Unmapped reads	337,369 / 19.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,575 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	30,490 / 1.74%
Duplication rate	1.73%
Clipped reads	651,199 / 37.09%

2.2. ACGT Content

Number/percentage of A's	27,960,341 / 29.81%
Number/percentage of C's	17,387,503 / 18.54%
Number/percentage of T's	27,123,793 / 28.91%
Number/percentage of G's	21,323,792 / 22.73%
Number/percentage of N's	13,171 / 0.01%
GC Percentage	41.27%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.2583

2.4. Mapping Quality

Mean Mapping Quality	47.06

2.5. Mismatches and indels

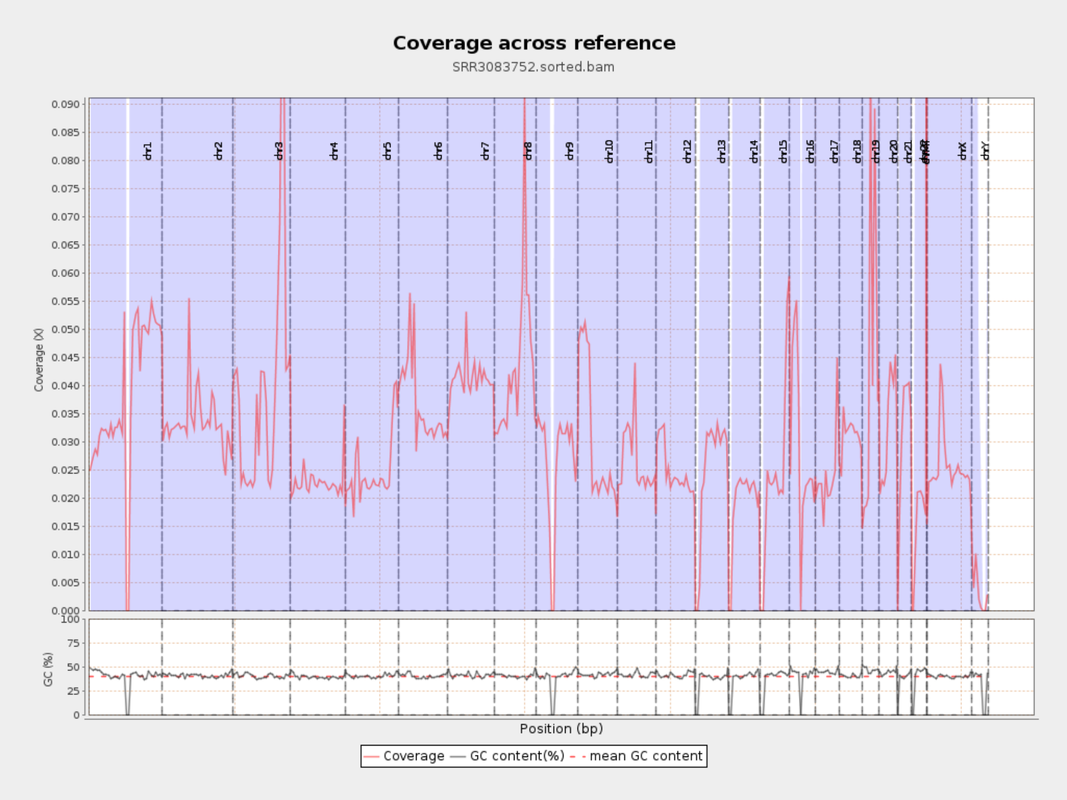
General error rate	0.9%
Mismatches	829,724
Insertions	6,647
Mapped reads with at least one insertion	0.46%
Deletions	17,818
Mapped reads with at least one deletion	1.25%
Homopolymer indels	46.11%

2.6. Chromosome stats

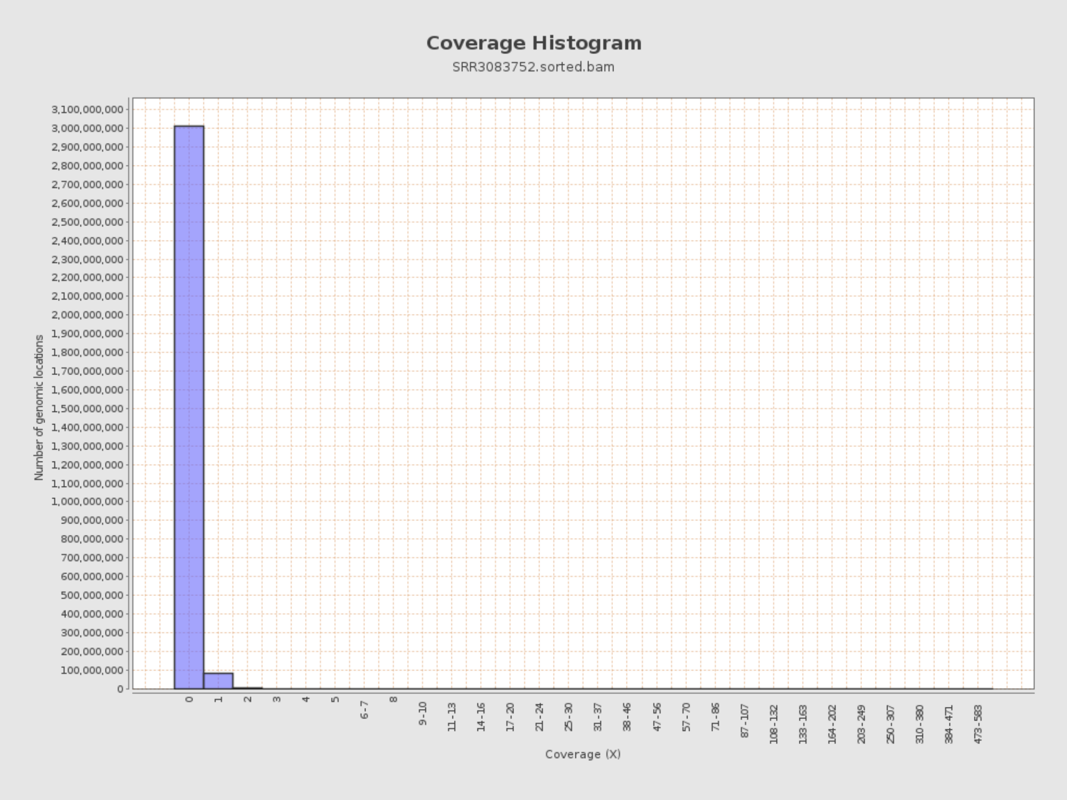
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9434994	0.0379	0.525
chr2	243199373	8172142	0.0336	0.2427
chr3	198022430	7827542	0.0395	0.2127
chr4	191154276	4365481	0.0228	0.1621
chr5	180915260	4494519	0.0248	0.1672
chr6	171115067	6302787	0.0368	0.2336
chr7	159138663	6617890	0.0416	0.3565

chr8	146364022	6399486	0.0437	0.2971
chr9	141213431	3714577	0.0263	0.1963
chr10	135534747	4218325	0.0311	0.2377
chr11	135006516	3561901	0.0264	0.1985
chr12	133851895	3320446	0.0248	0.1673
chr13	115169878	2839205	0.0247	0.1654
chr14	107349540	2022634	0.0188	0.1486
chr15	102531392	2394522	0.0234	0.1625
chr16	90354753	2622263	0.029	0.1892
chr17	81195210	1986593	0.0245	0.1706
chr18	78077248	2436330	0.0312	0.3385
chr19	59128983	2621050	0.0443	0.3378
chr20	63025520	2071338	0.0329	0.194
chr21	48129895	1481961	0.0308	0.1896
chr22	51304566	739710	0.0144	0.1268
chrMT	16571	4667	0.2816	0.5562
chrX	155270560	3998305	0.0258	0.1759
chrY	59373566	189036	0.0032	0.0821

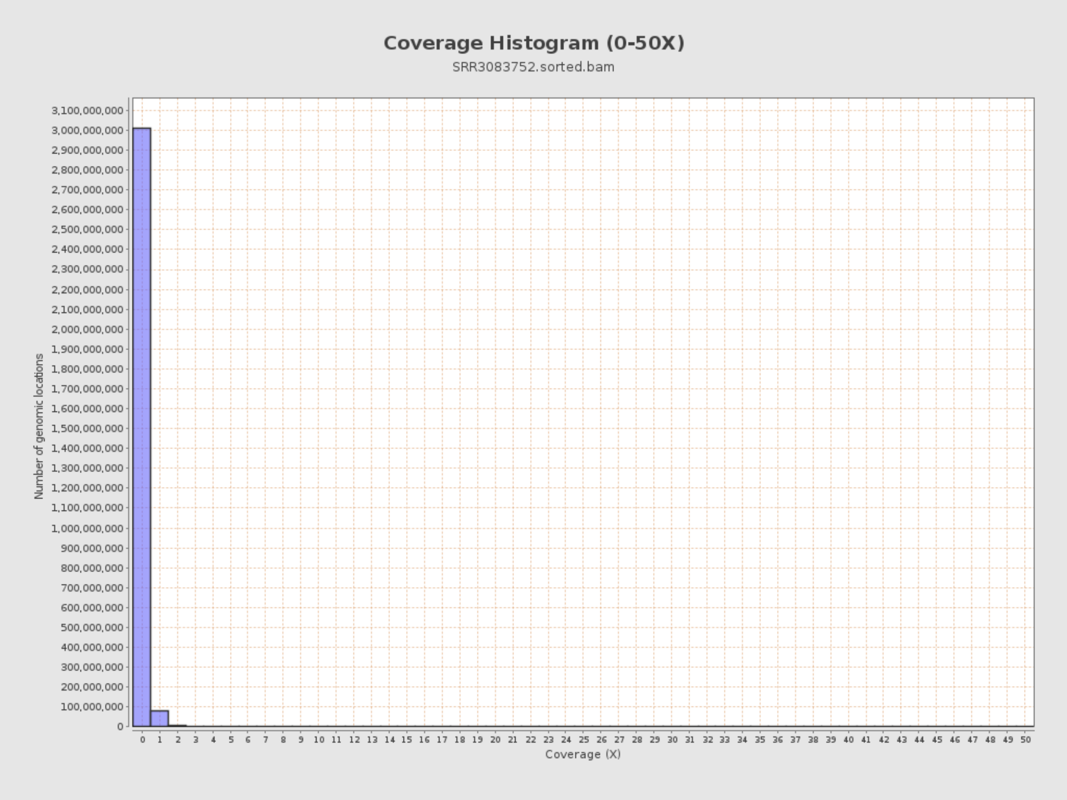
3. Results : Coverage across reference



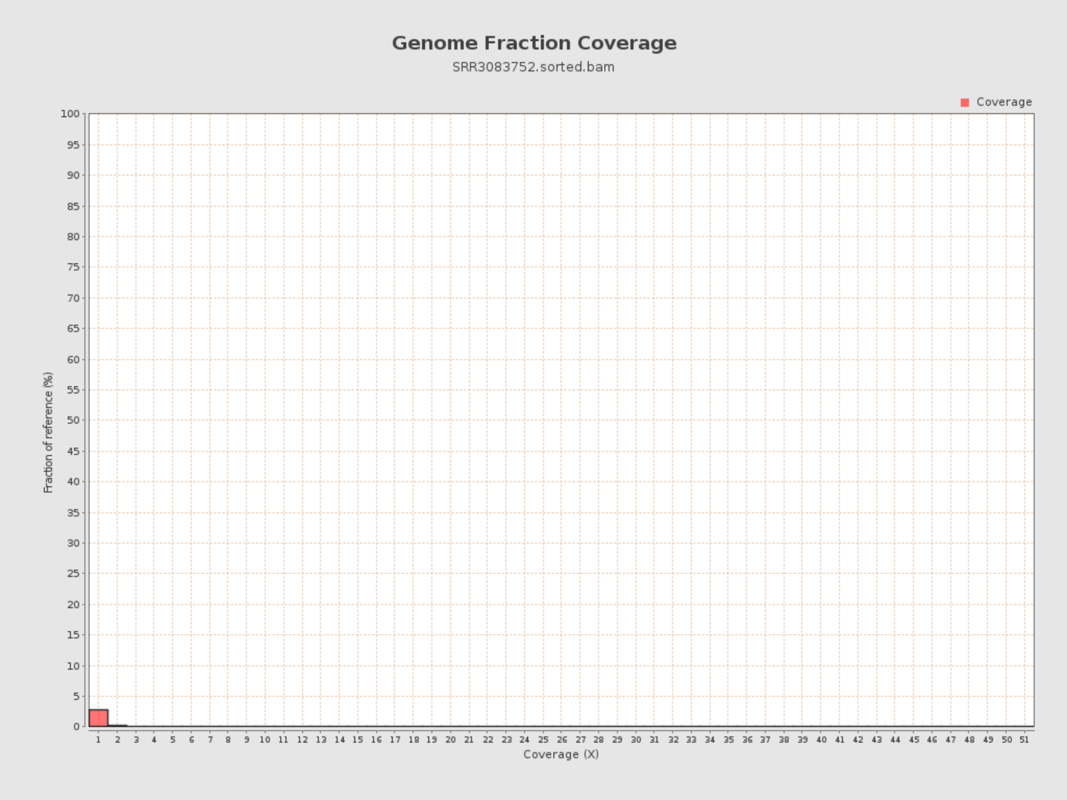
4. Results : Coverage Histogram



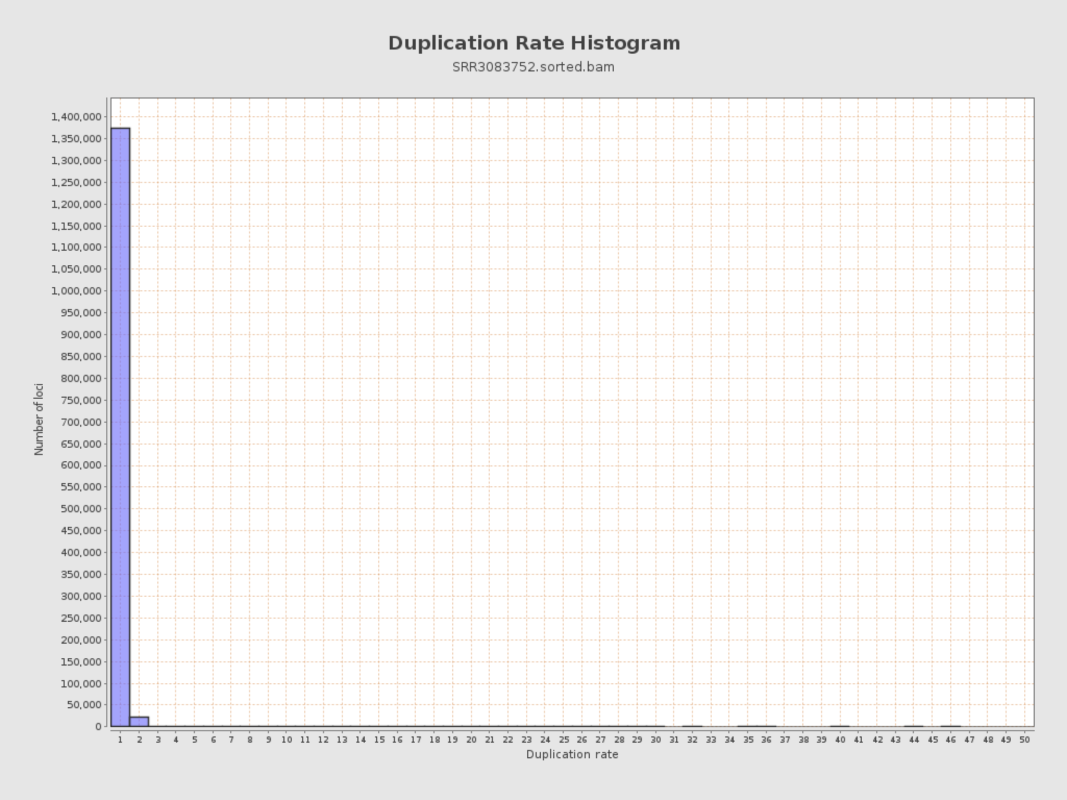
5. Results : Coverage Histogram (0-50X)



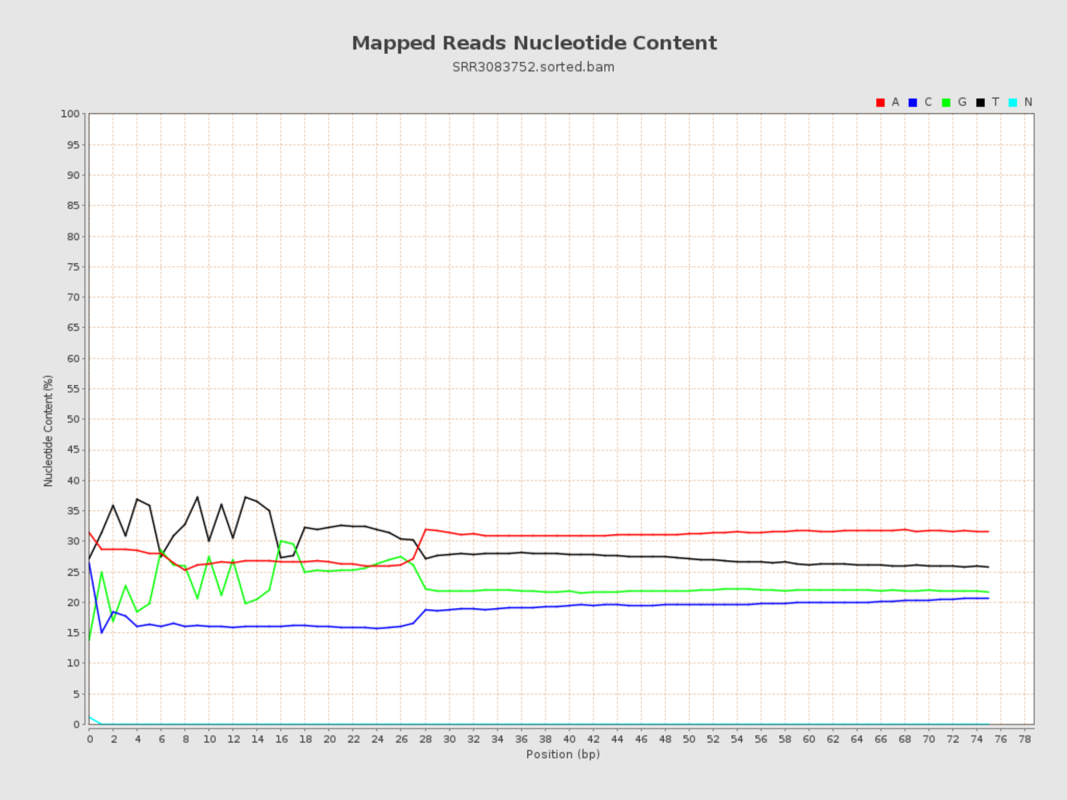
6. Results : Genome Fraction Coverage



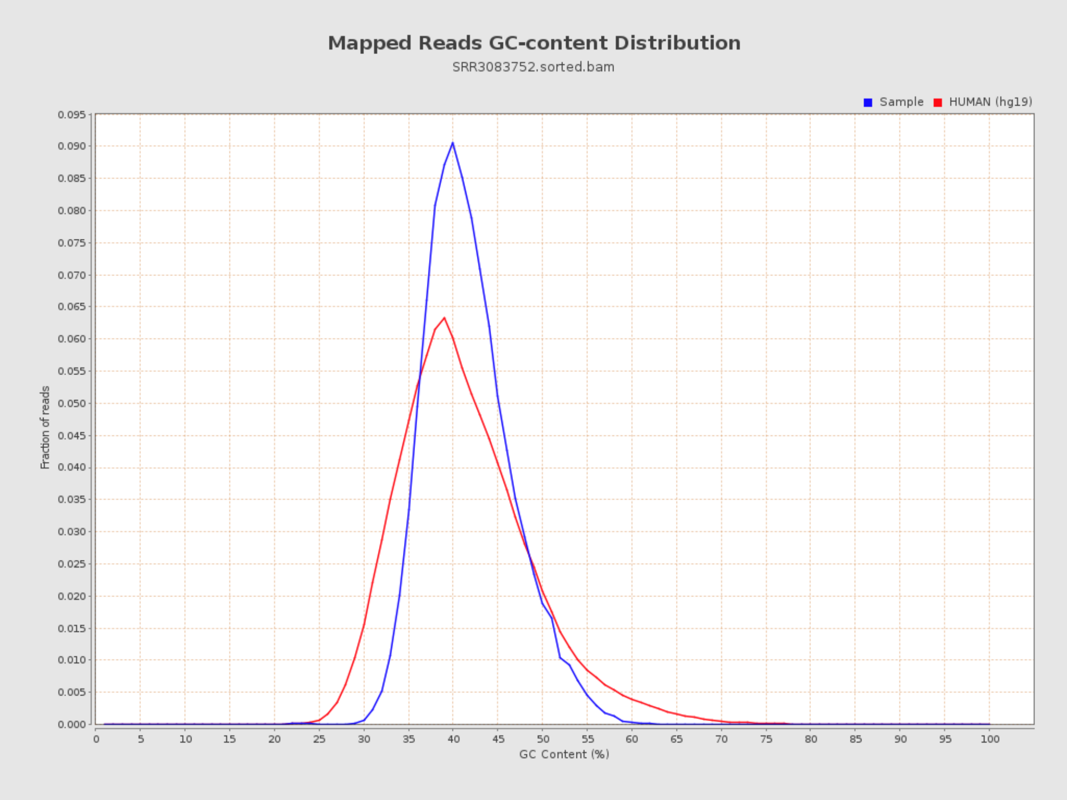
7. Results : Duplication Rate Histogram



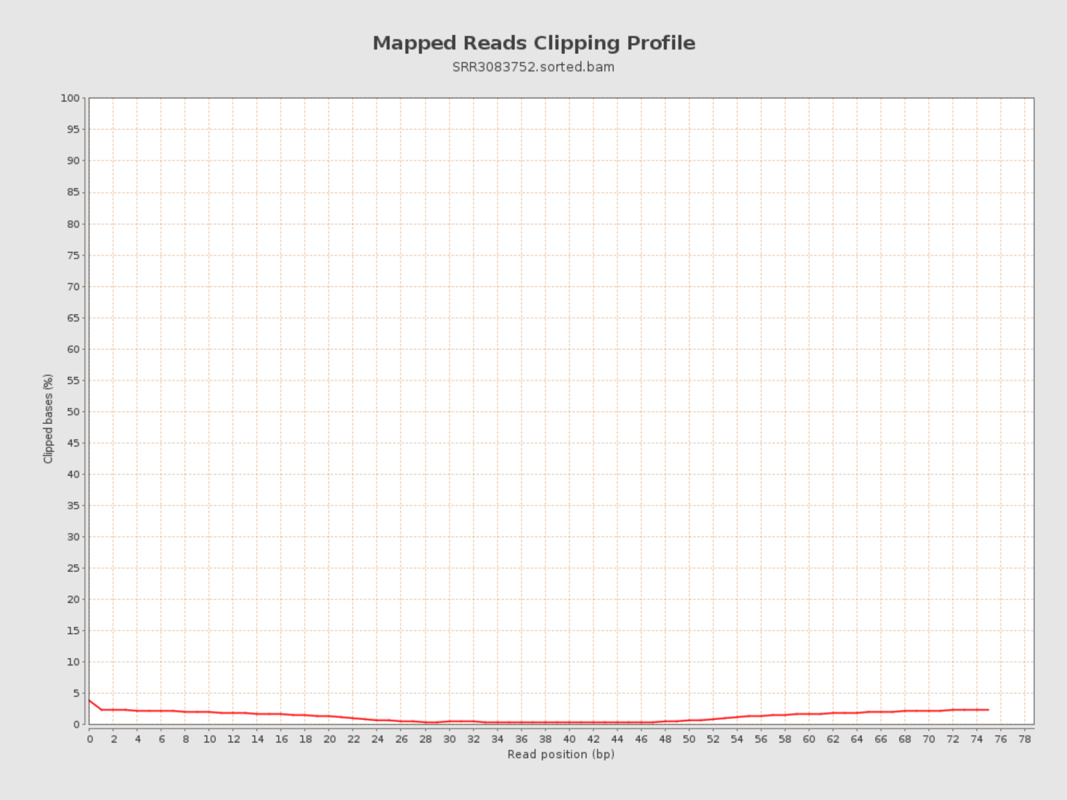
8. Results : Mapped Reads Nucleotide Content



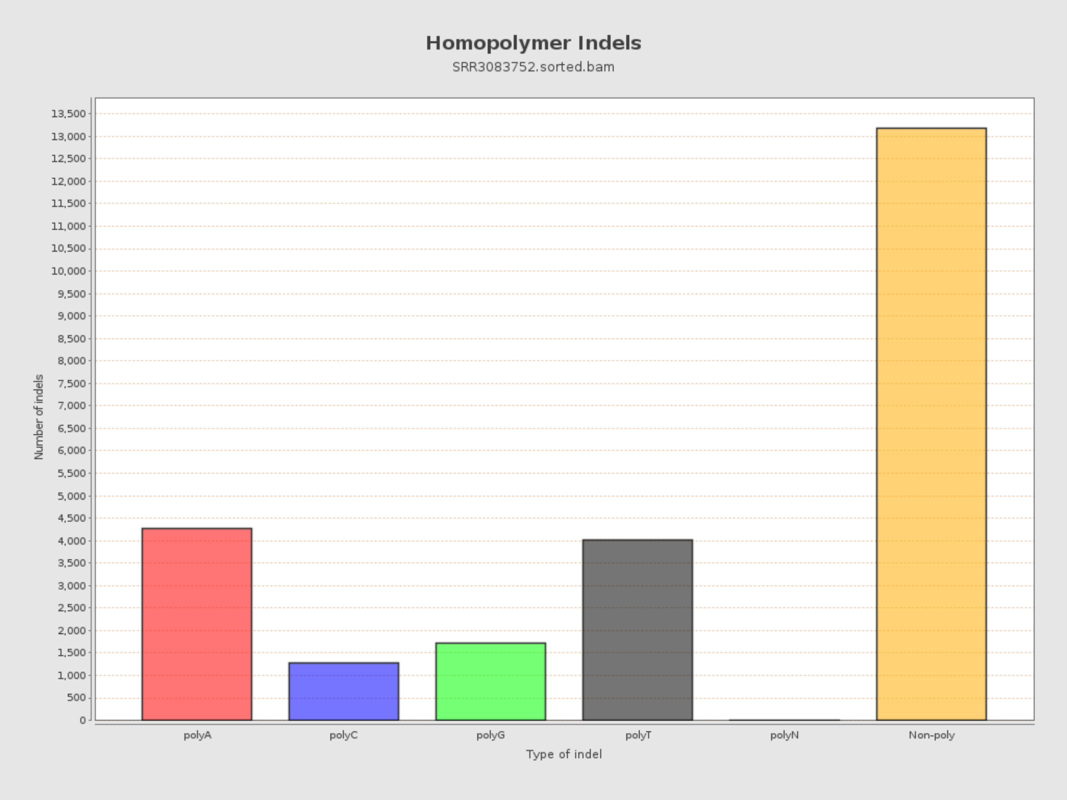
9. Results : Mapped Reads GC-content Distribution



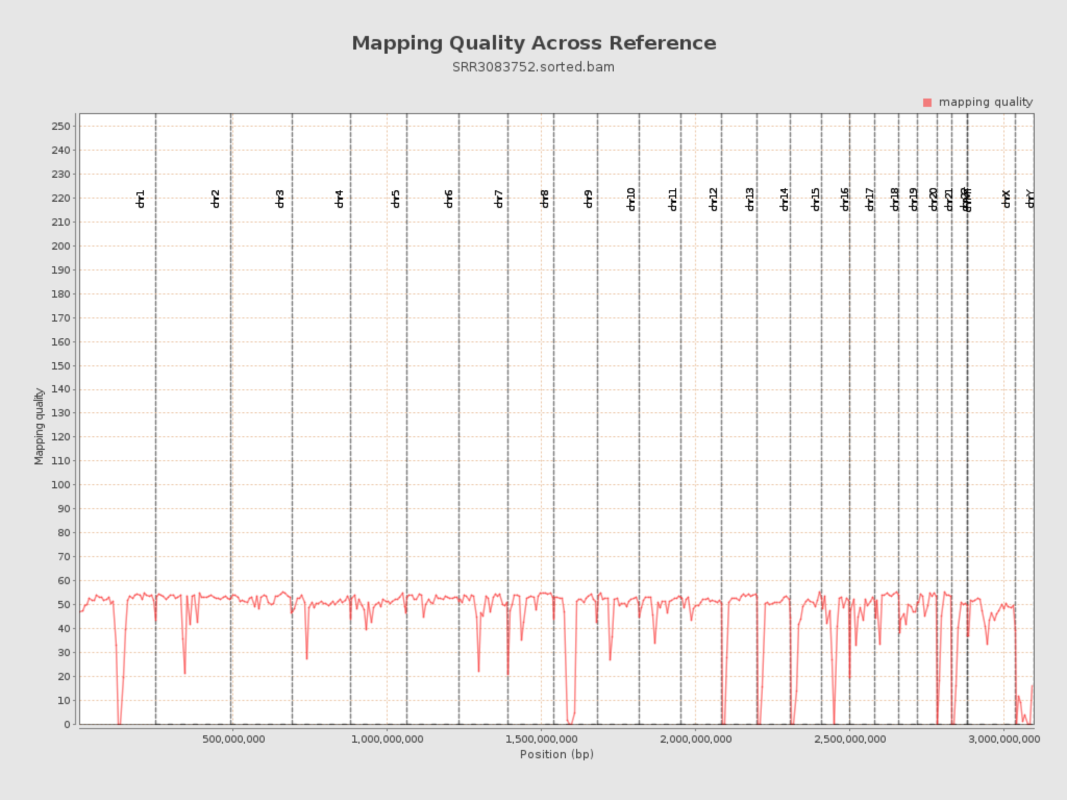
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram