Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:56:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084776.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_SRR3084776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084776.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:56:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,131,675
Mapped reads	1,902,655 / 89.26%
Unmapped reads	229,020 / 10.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,571 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	80,236 / 3.76%
Duplication rate	3.34%
Clipped reads	796,307 / 37.36%

2.2. ACGT Content

Number/percentage of A's	34,759,152 / 27.06%
Number/percentage of C's	24,892,660 / 19.38%
Number/percentage of T's	39,547,318 / 30.79%
Number/percentage of G's	29,215,871 / 22.74%
Number/percentage of N's	41,635 / 0.03%
GC Percentage	42.12%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.3478

2.4. Mapping Quality

Mean Mapping Quality	46.63

2.5. Mismatches and indels

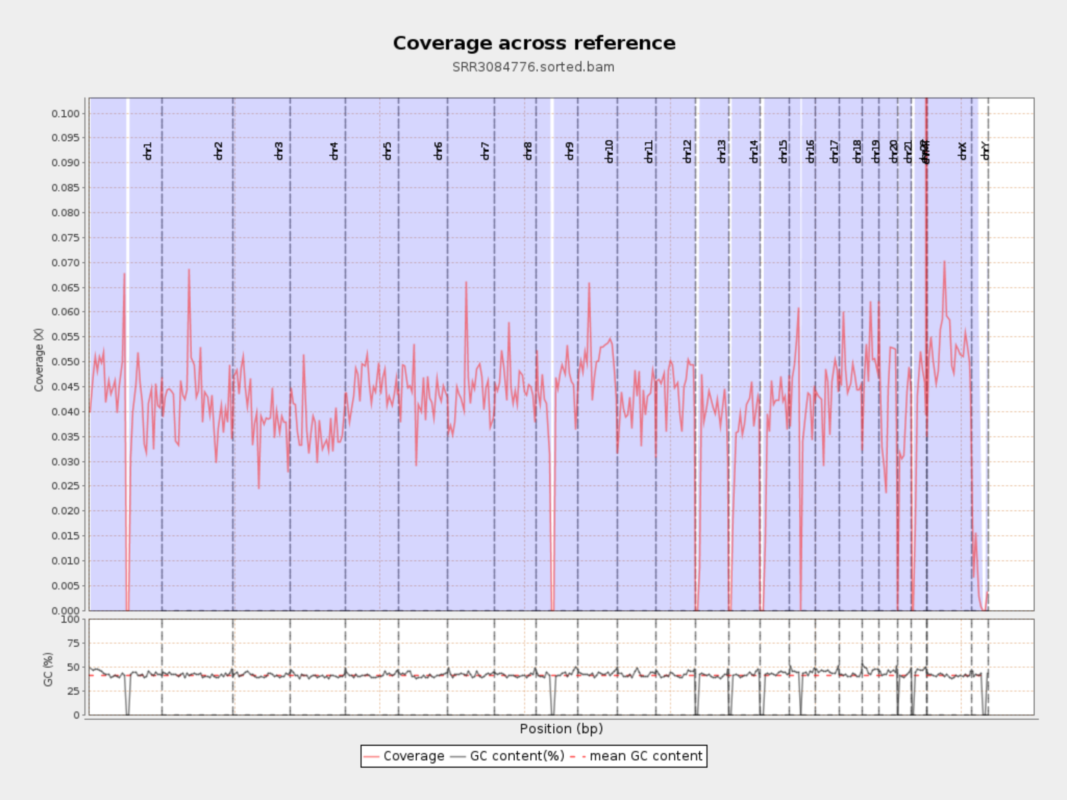
General error rate	0.89%
Mismatches	1,121,184
Insertions	9,330
Mapped reads with at least one insertion	0.49%
Deletions	30,707
Mapped reads with at least one deletion	1.6%
Homopolymer indels	46.99%

2.6. Chromosome stats

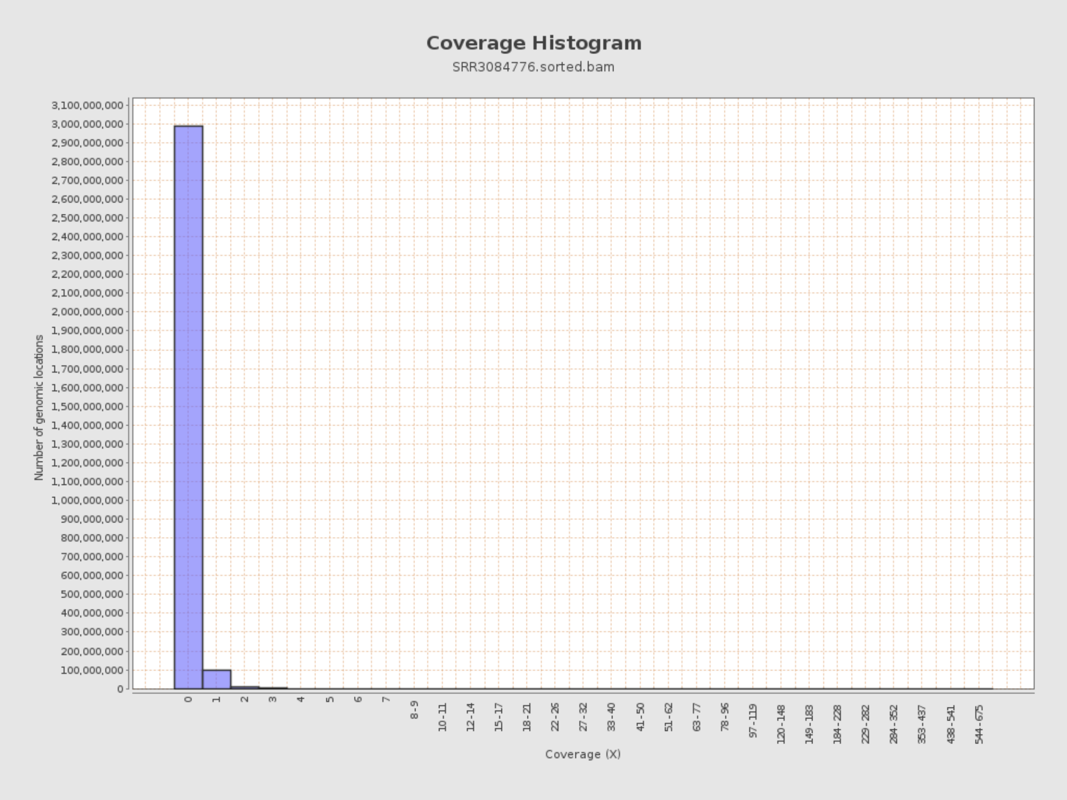
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10389301	0.0417	0.6166
chr2	243199373	10367970	0.0426	0.4119
chr3	198022430	7896848	0.0399	0.224
chr4	191154276	6998334	0.0366	0.2301
chr5	180915260	8136660	0.045	0.2405
chr6	171115067	7427675	0.0434	0.2842
chr7	159138663	6963469	0.0438	0.4263

chr8	146364022	6659292	0.0455	0.3298
chr9	141213431	5612917	0.0397	0.3207
chr10	135534747	6925508	0.0511	0.3486
chr11	135006516	5637336	0.0418	0.3191
chr12	133851895	6097856	0.0456	0.2436
chr13	115169878	3969881	0.0345	0.2111
chr14	107349540	3549371	0.0331	0.2238
chr15	102531392	3465334	0.0338	0.2092
chr16	90354753	3693998	0.0409	0.2561
chr17	81195210	3525393	0.0434	0.2413
chr18	78077248	3710275	0.0475	0.6646
chr19	59128983	2986473	0.0505	0.4836
chr20	63025520	2617609	0.0415	0.2418
chr21	48129895	1658027	0.0344	0.2211
chr22	51304566	1680369	0.0328	0.2031
chrMT	16571	34632	2.0899	1.8644
chrX	155270560	8184510	0.0527	0.2926
chrY	59373566	318031	0.0054	0.119

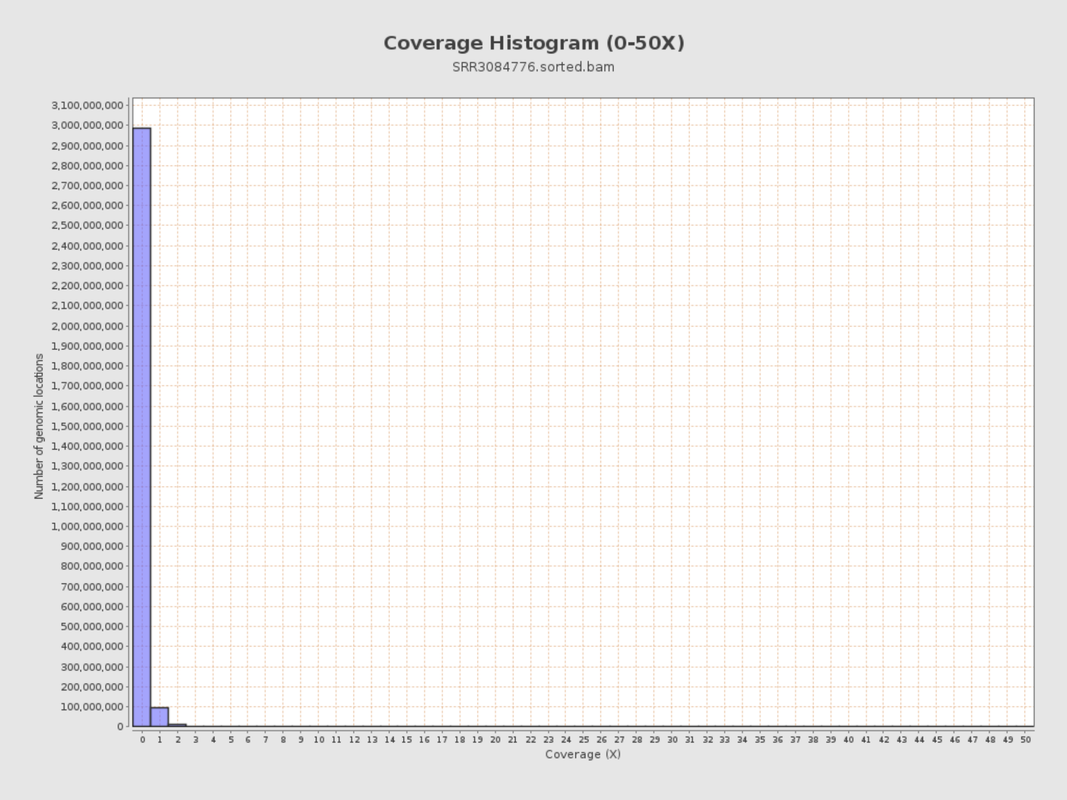
3. Results : Coverage across reference



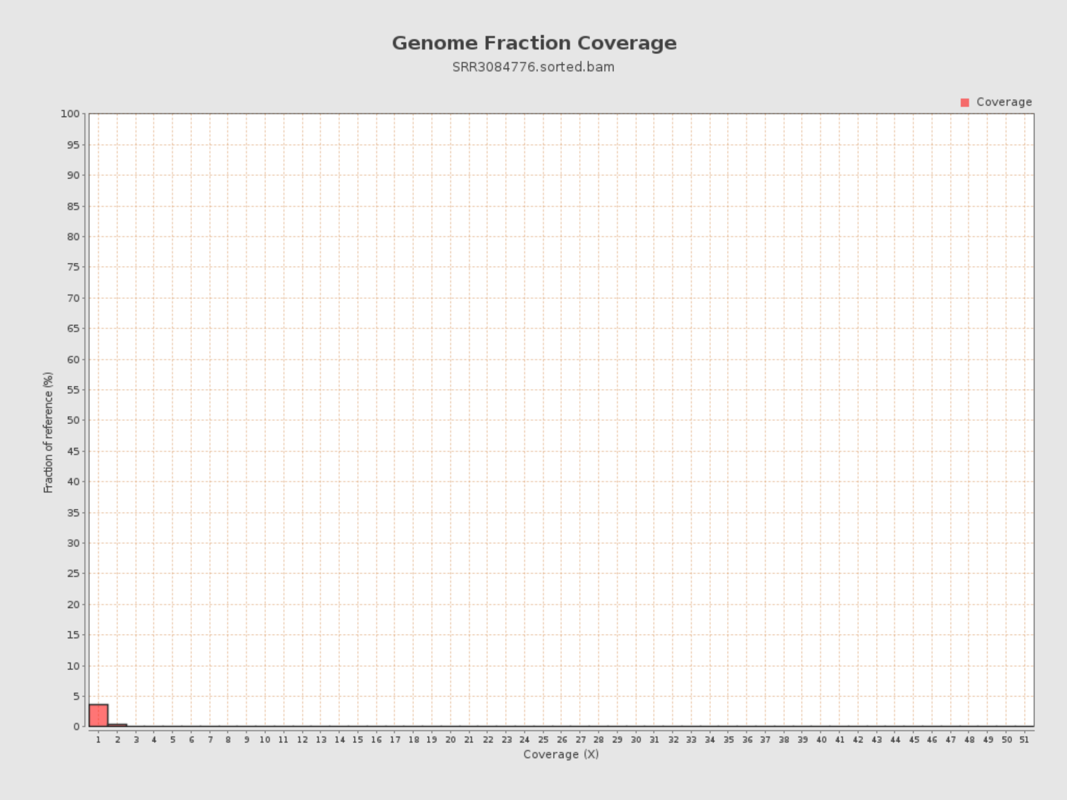
4. Results : Coverage Histogram



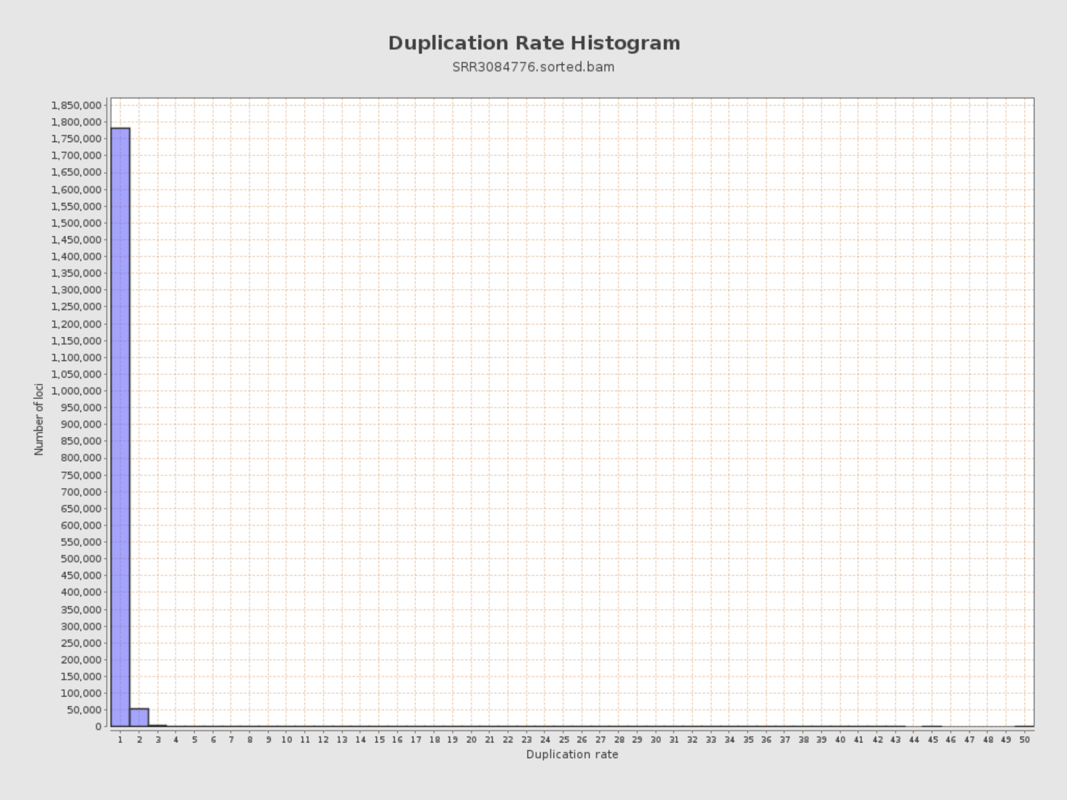
5. Results : Coverage Histogram (0-50X)



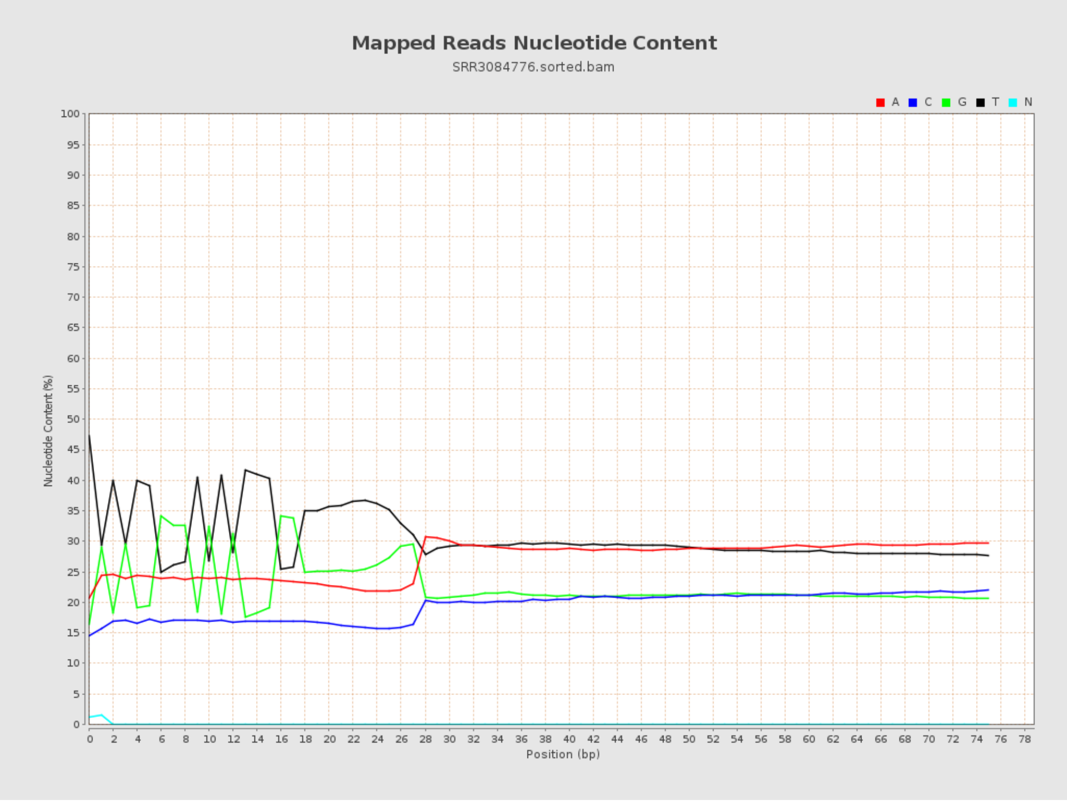
6. Results : Genome Fraction Coverage



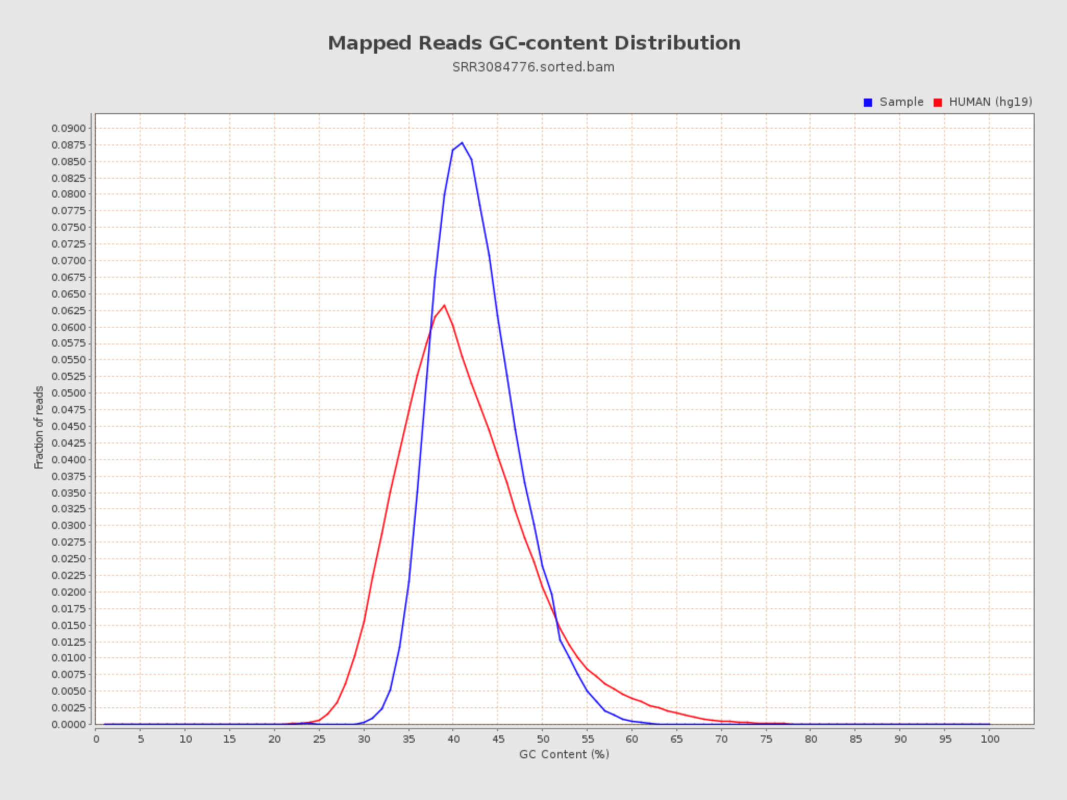
7. Results : Duplication Rate Histogram



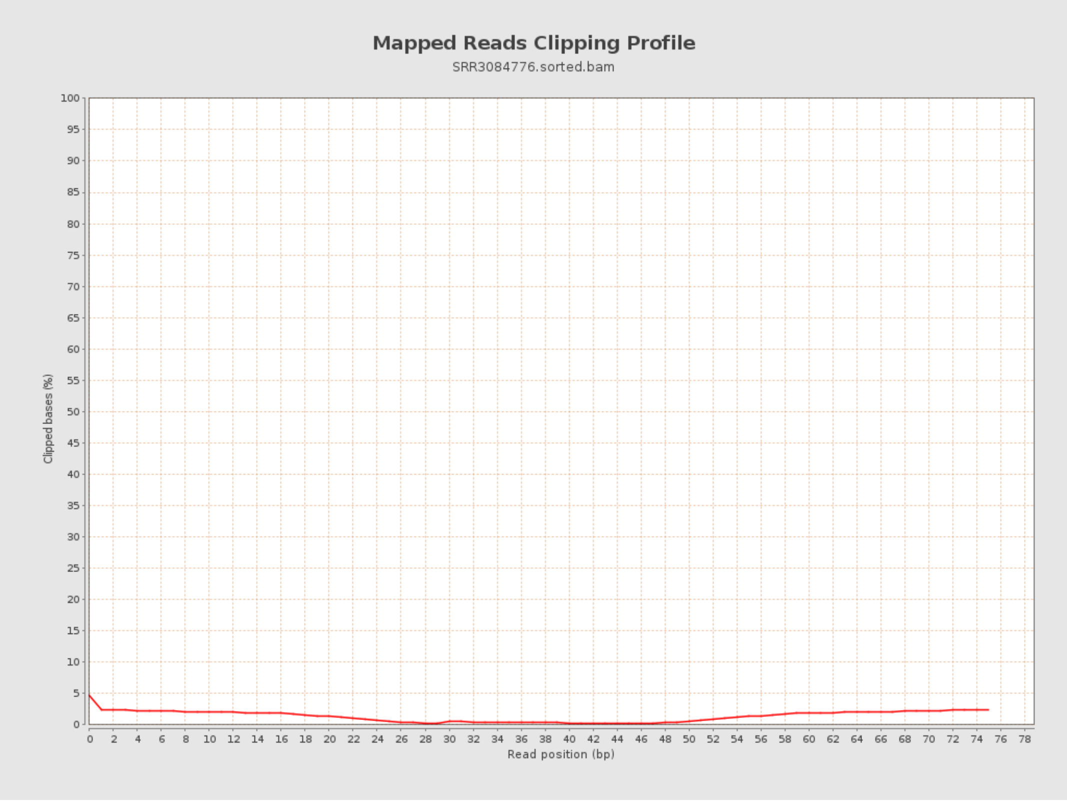
8. Results : Mapped Reads Nucleotide Content



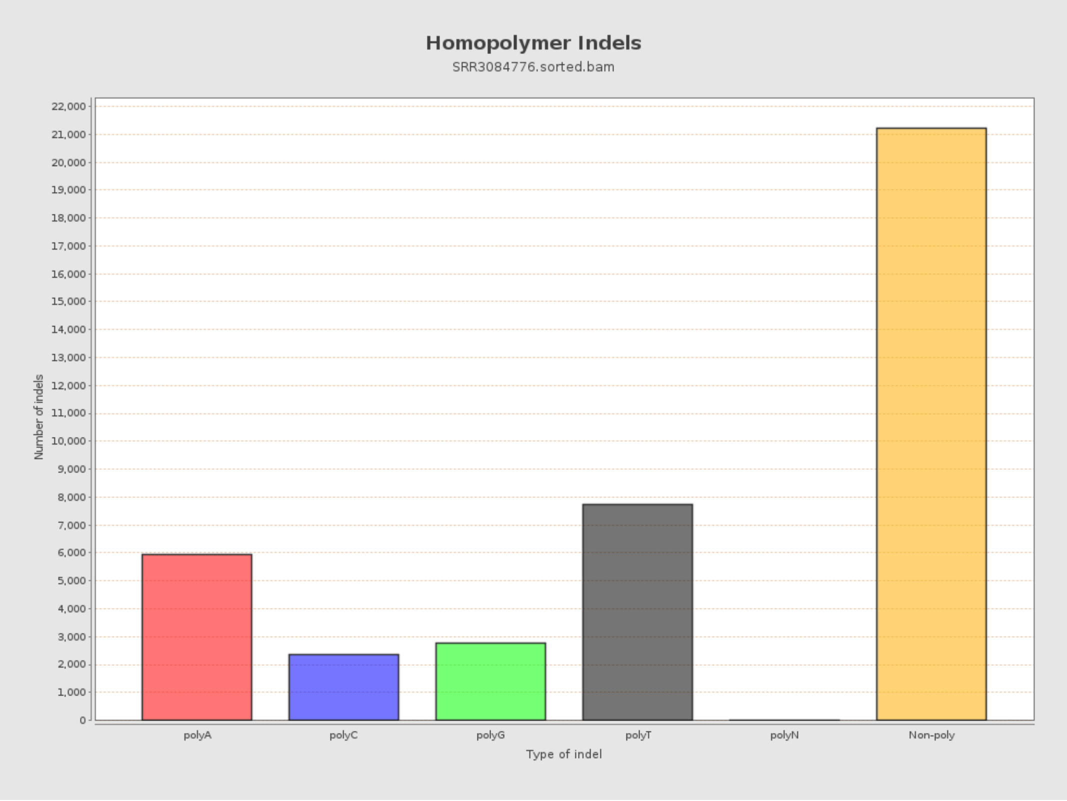
9. Results : Mapped Reads GC-content Distribution



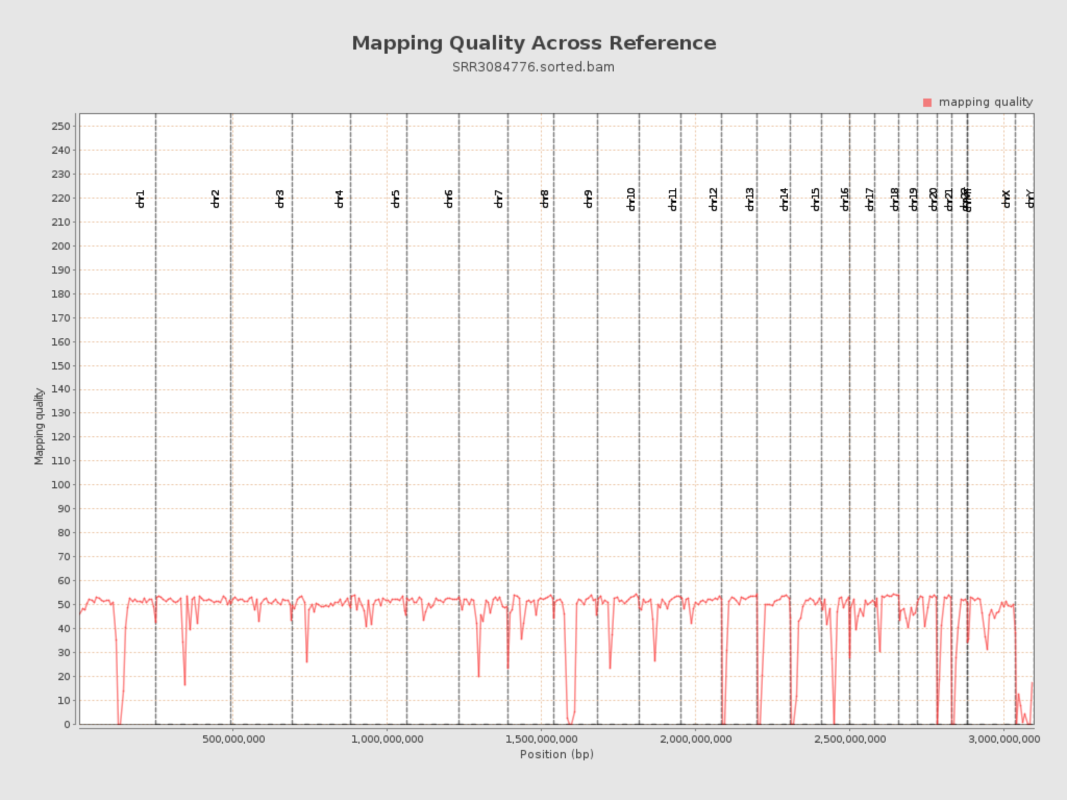
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram