Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:42:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084804.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_SRR3084804 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084804.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:42:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084804.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,072,403
Mapped reads	1,840,404 / 88.81%
Unmapped reads	231,999 / 11.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,627 / 1.19%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	104,318 / 5.03%
Duplication rate	4.84%
Clipped reads	839,582 / 40.51%

2.2. ACGT Content

Number/percentage of A's	33,552,736 / 27.36%
Number/percentage of C's	22,839,688 / 18.62%
Number/percentage of T's	38,713,310 / 31.56%
Number/percentage of G's	27,530,462 / 22.45%
Number/percentage of N's	17,361 / 0.01%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.2962

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

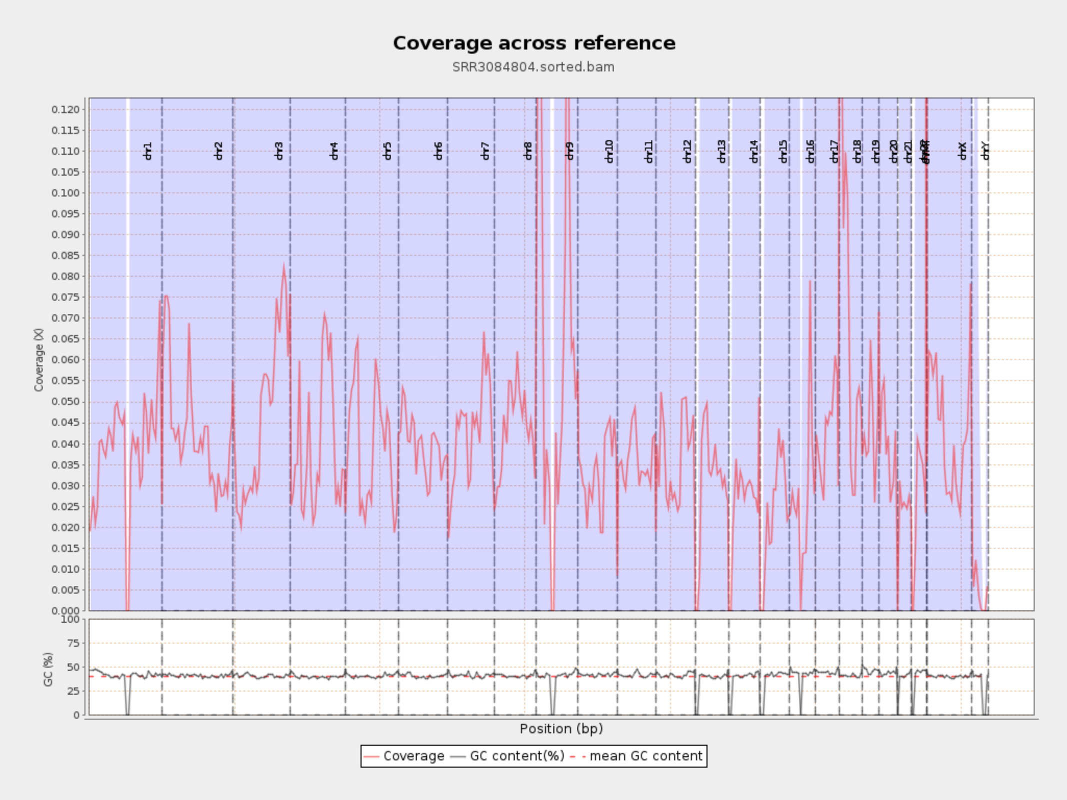
General error rate	0.81%
Mismatches	971,694
Insertions	9,845
Mapped reads with at least one insertion	0.53%
Deletions	28,366
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.09%

2.6. Chromosome stats

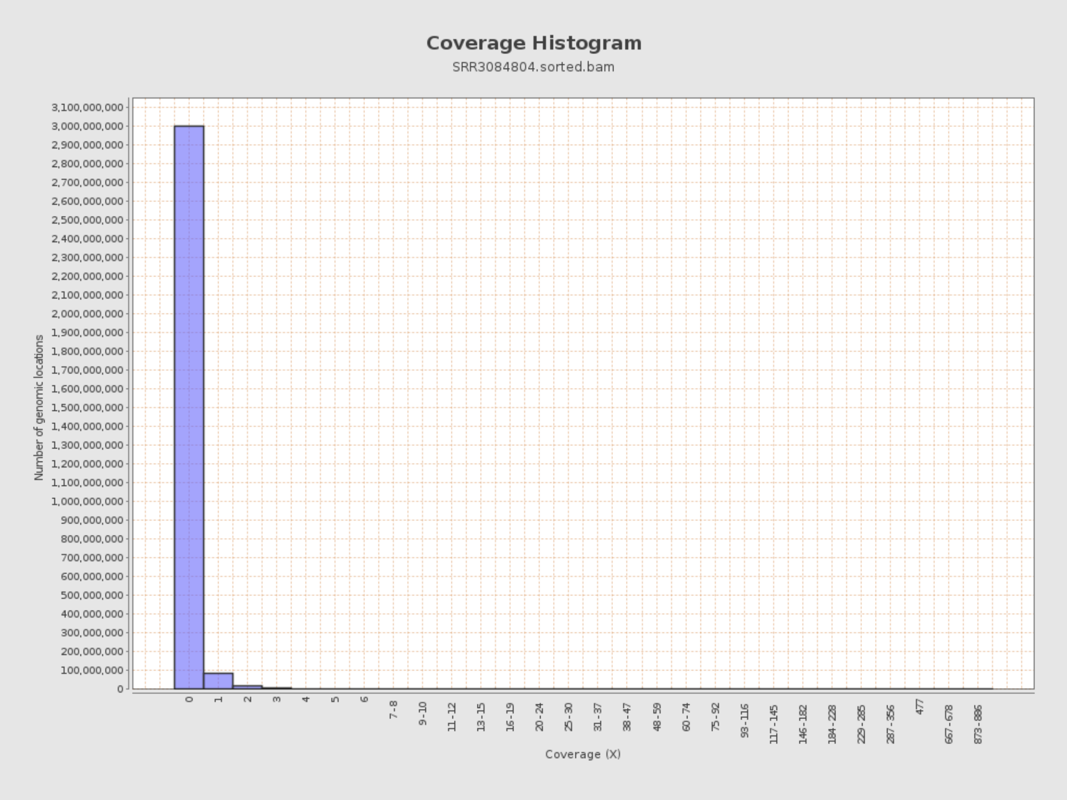
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9586992	0.0385	0.347
chr2	243199373	10386803	0.0427	0.4885
chr3	198022430	9314849	0.047	0.2616
chr4	191154276	7559259	0.0395	0.2426
chr5	180915260	7152886	0.0395	0.2407
chr6	171115067	6771396	0.0396	0.2586
chr7	159138663	6884589	0.0433	0.276

chr8	146364022	6415161	0.0438	0.3238
chr9	141213431	9553776	0.0677	0.3757
chr10	135534747	4498567	0.0332	0.233
chr11	135006516	4798597	0.0355	0.264
chr12	133851895	4929499	0.0368	0.2331
chr13	115169878	3478320	0.0302	0.2099
chr14	107349540	2701754	0.0252	0.1991
chr15	102531392	2415188	0.0236	0.19
chr16	90354753	2521112	0.0279	0.2102
chr17	81195210	3509200	0.0432	0.2608
chr18	78077248	5722186	0.0733	0.4869
chr19	59128983	2620488	0.0443	0.3043
chr20	63025520	2506580	0.0398	0.2424
chr21	48129895	1149910	0.0239	0.1918
chr22	51304566	1268464	0.0247	0.1879
chrMT	16571	16036	0.9677	1.2302
chrX	155270560	6670666	0.043	0.2611
chrY	59373566	268113	0.0045	0.0987

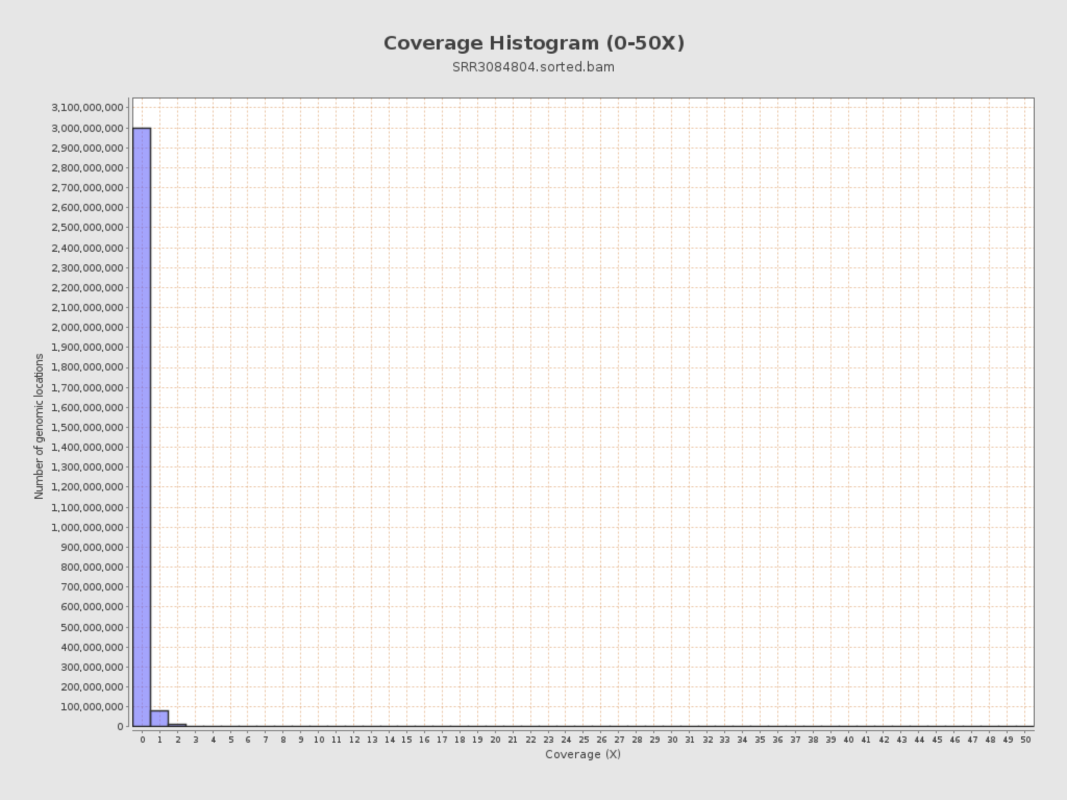
3. Results : Coverage across reference



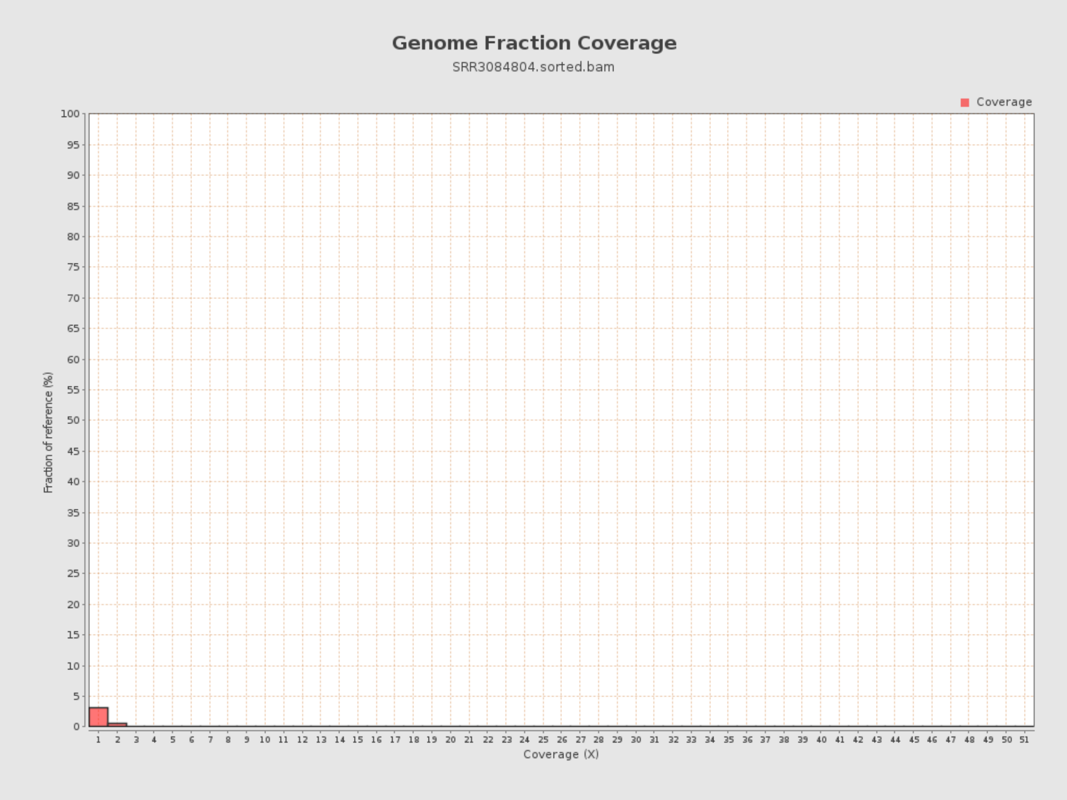
4. Results : Coverage Histogram



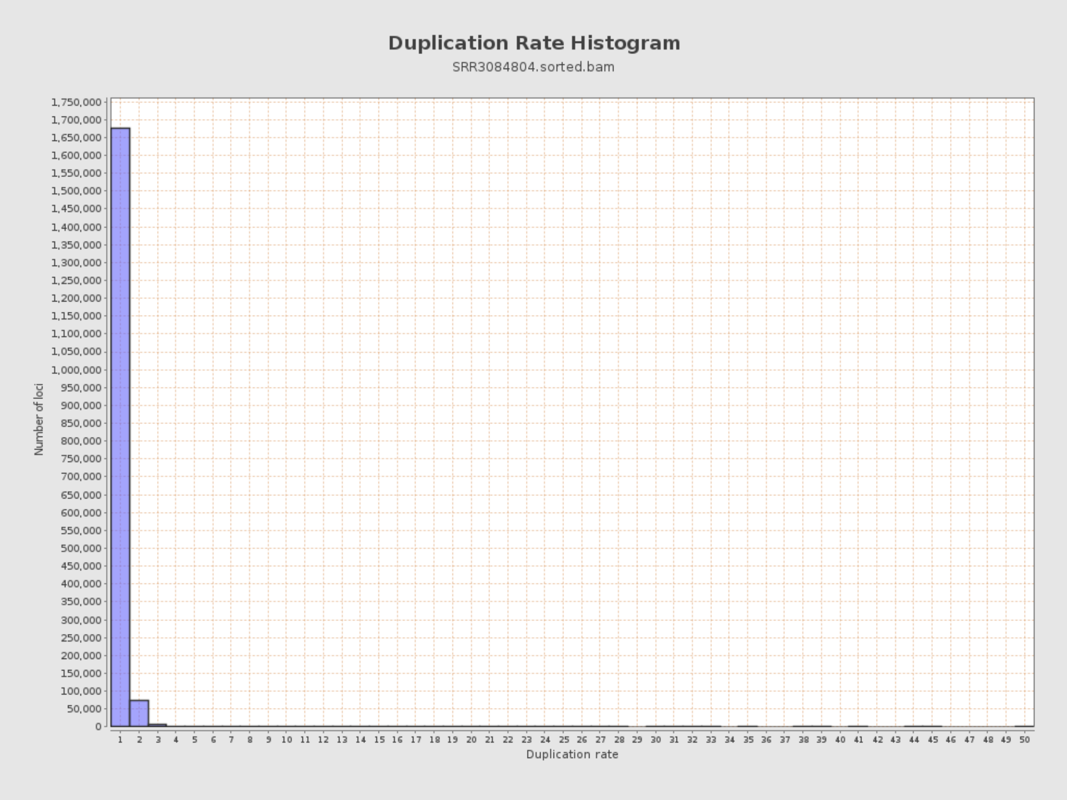
5. Results : Coverage Histogram (0-50X)



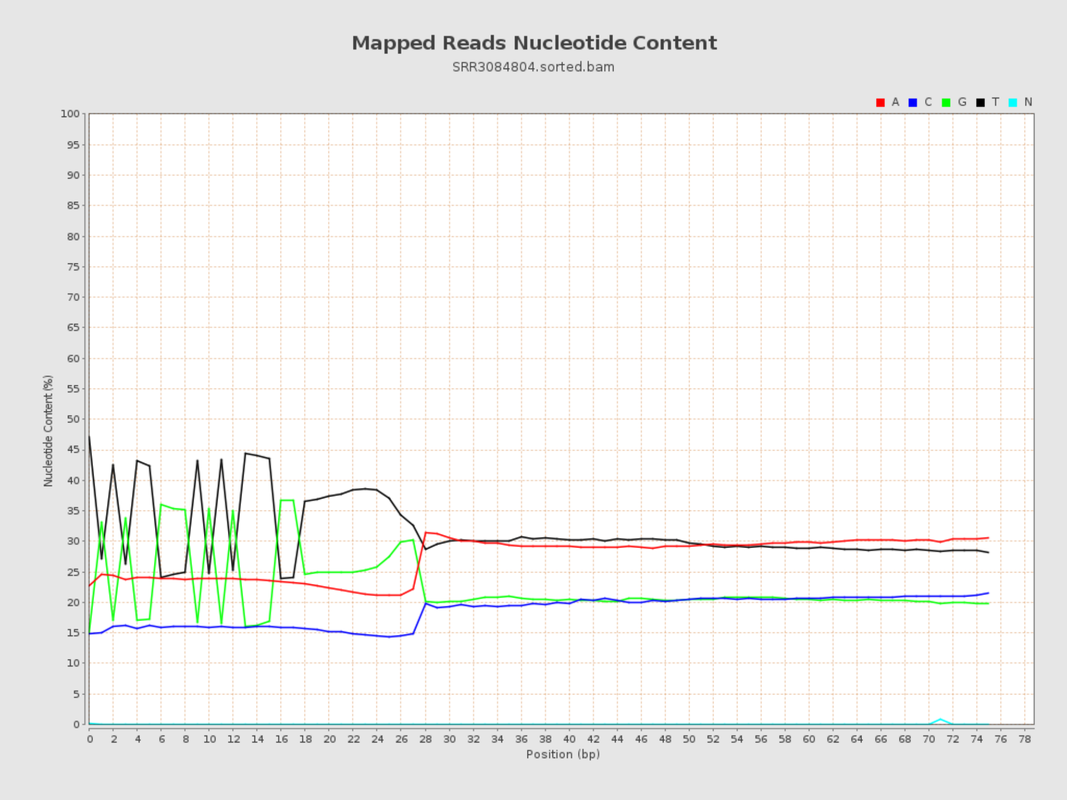
6. Results : Genome Fraction Coverage



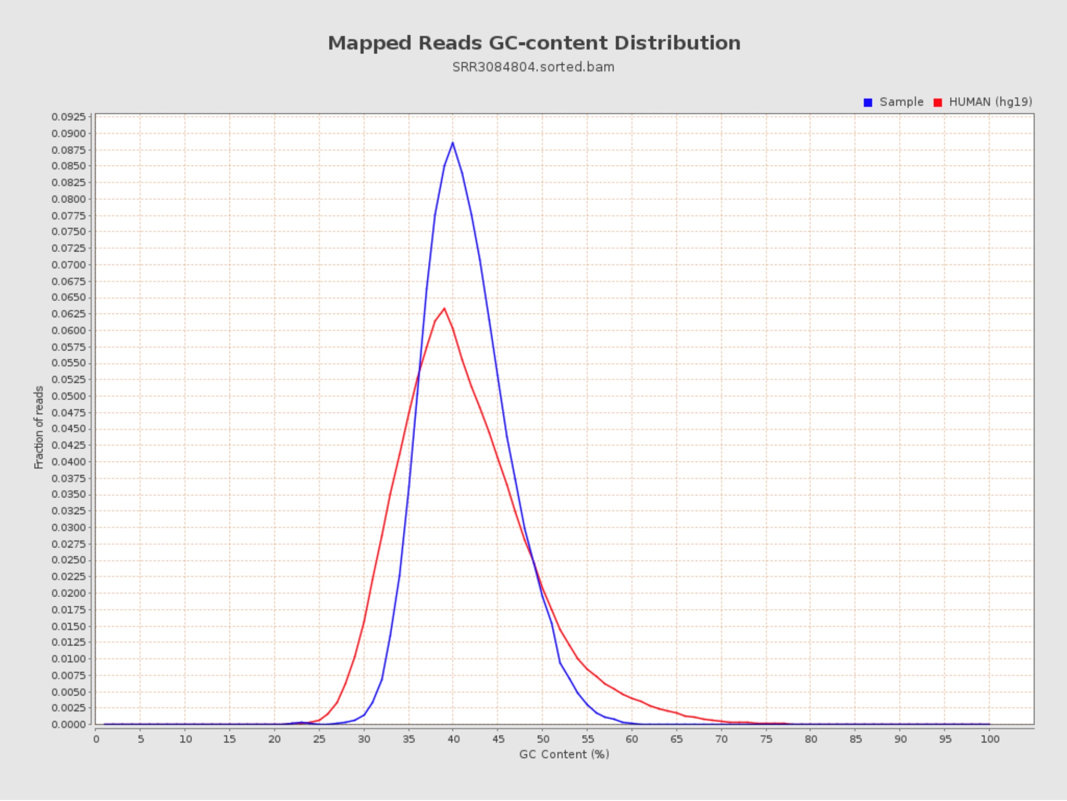
7. Results : Duplication Rate Histogram



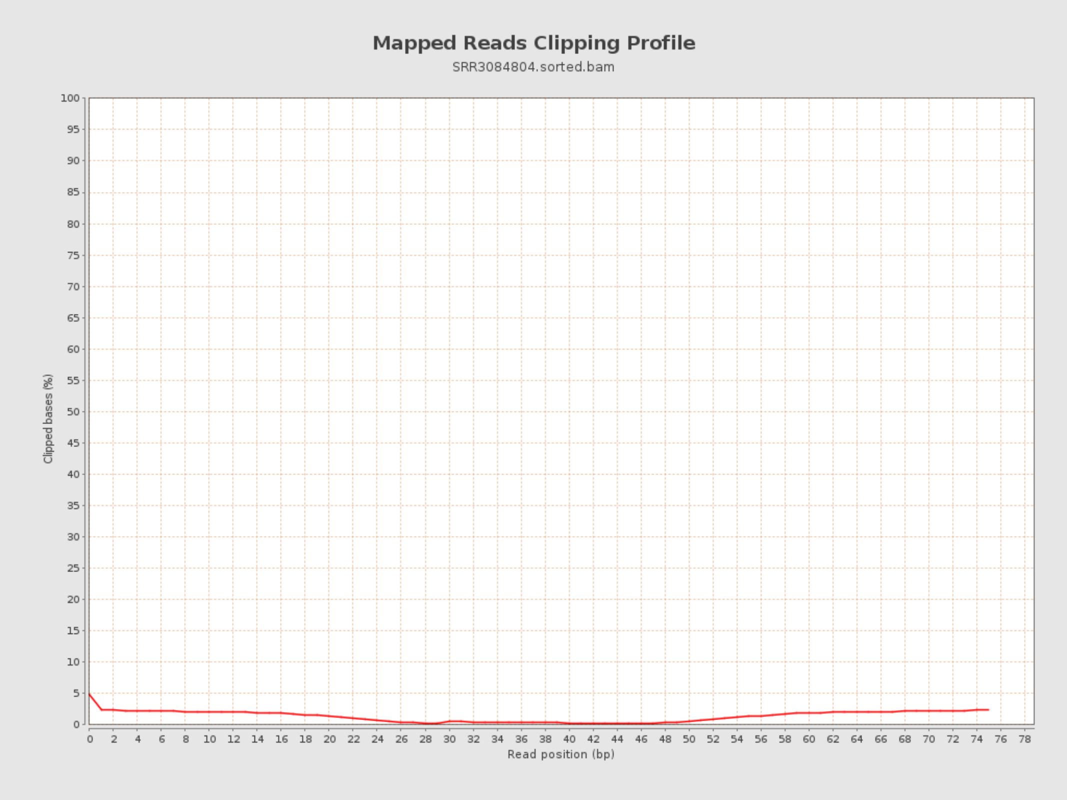
8. Results : Mapped Reads Nucleotide Content



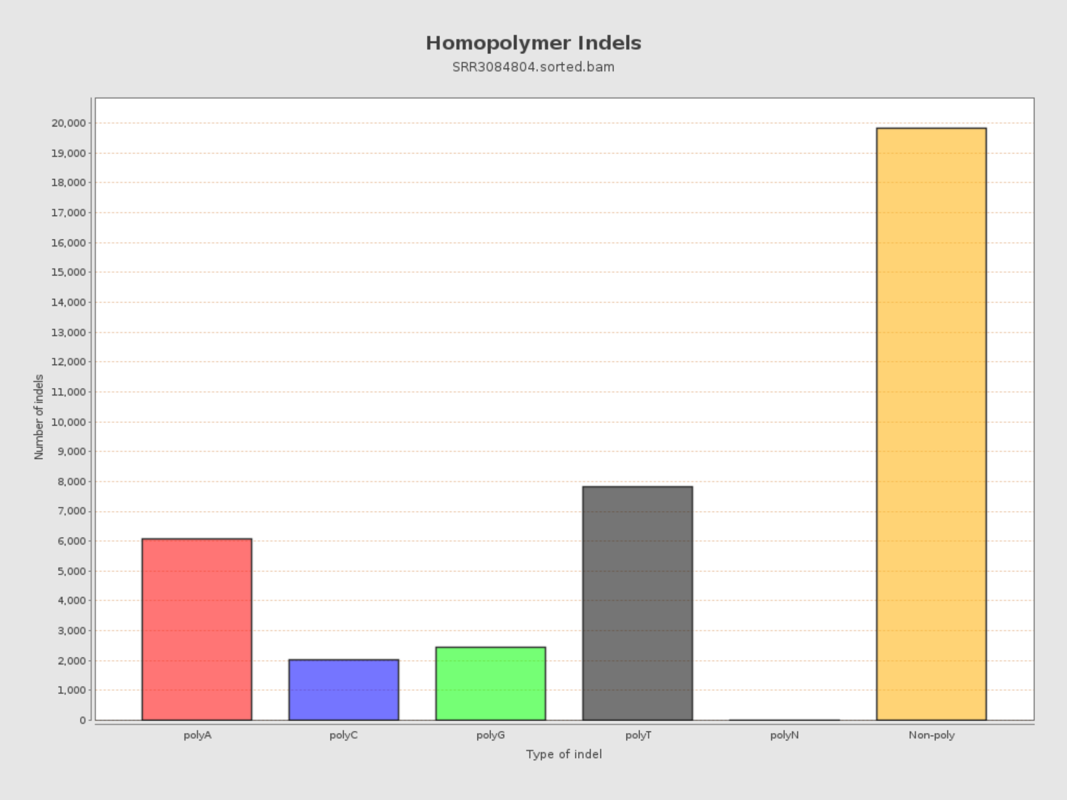
9. Results : Mapped Reads GC-content Distribution



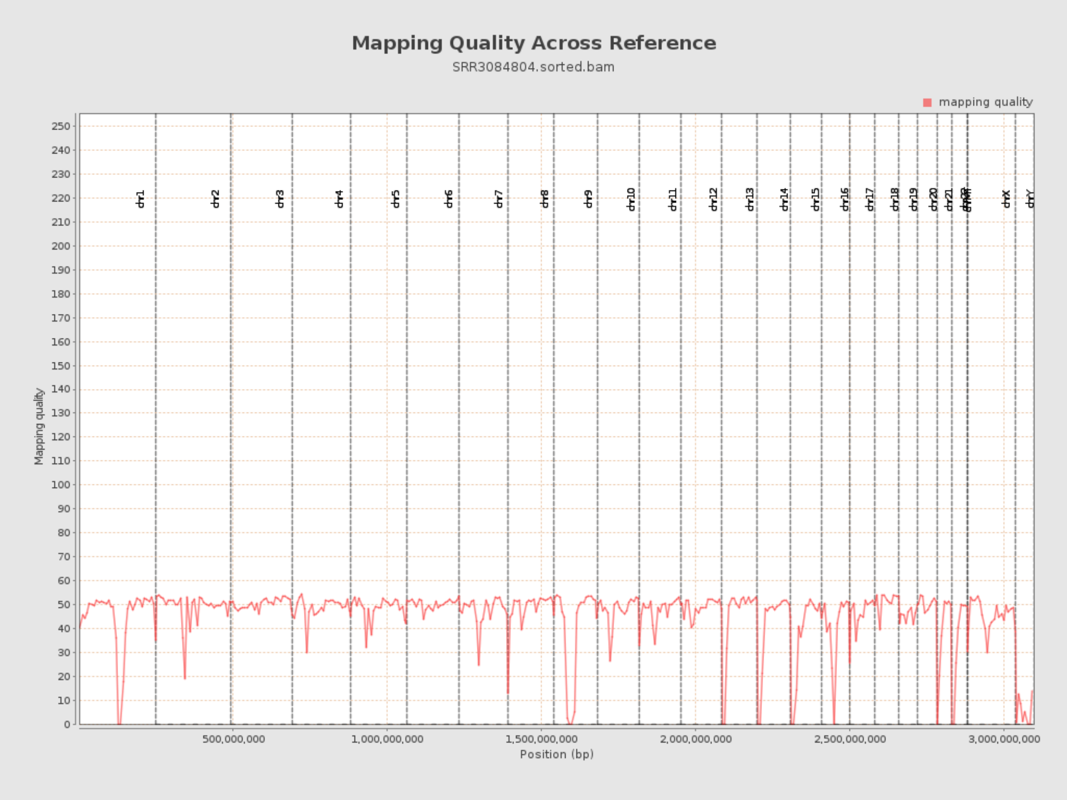
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram