Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:28:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084800.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_SRR3084800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:28:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,188,967
Mapped reads	1,989,025 / 90.87%
Unmapped reads	199,942 / 9.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,664 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	87,524 / 4%
Duplication rate	3.75%
Clipped reads	898,847 / 41.06%

2.2. ACGT Content

Number/percentage of A's	35,847,987 / 27.05%
Number/percentage of C's	24,970,005 / 18.84%
Number/percentage of T's	41,432,089 / 31.26%
Number/percentage of G's	30,264,853 / 22.84%
Number/percentage of N's	18,463 / 0.01%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.3037

2.4. Mapping Quality

Mean Mapping Quality	45.2

2.5. Mismatches and indels

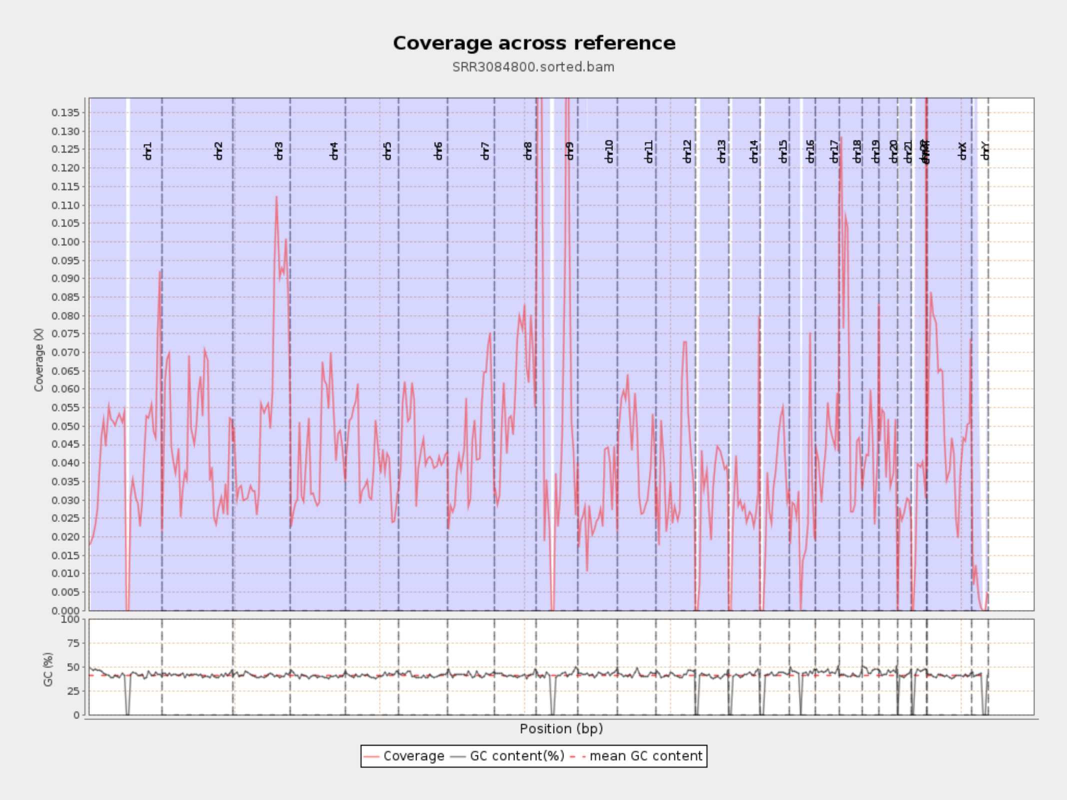
General error rate	0.79%
Mismatches	1,026,562
Insertions	10,412
Mapped reads with at least one insertion	0.52%
Deletions	30,295
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.42%

2.6. Chromosome stats

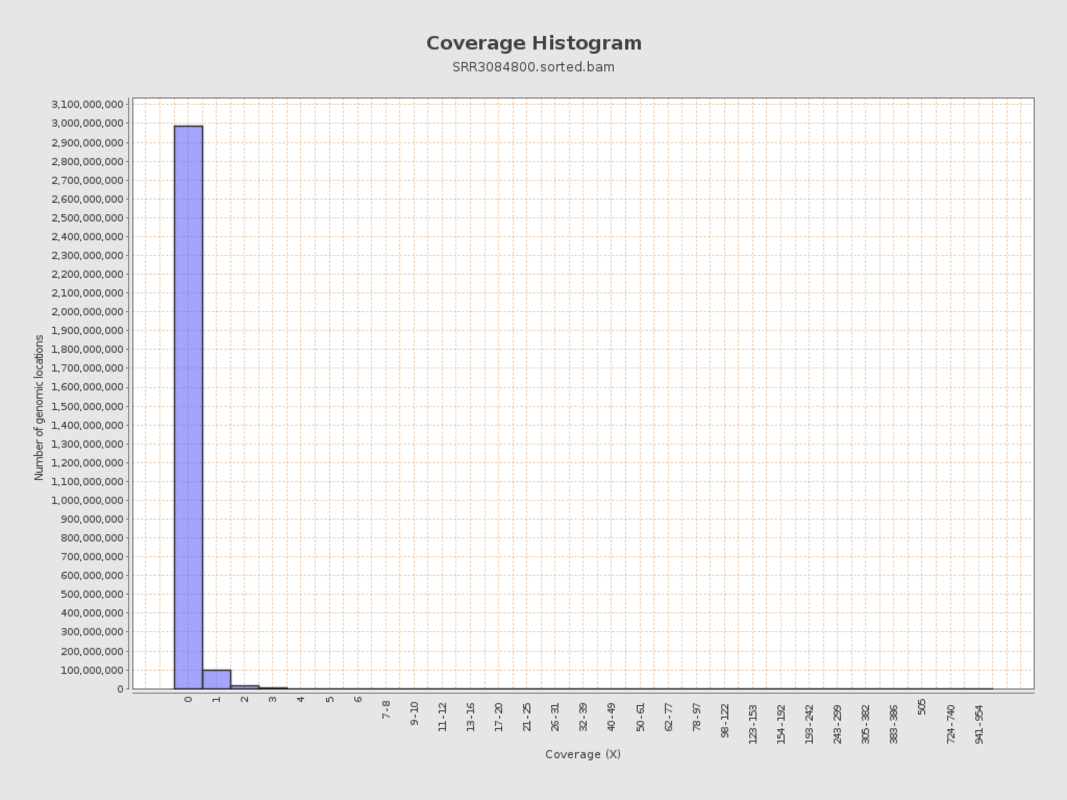
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10360313	0.0416	0.3499
chr2	243199373	10862417	0.0447	0.5109
chr3	198022430	10997869	0.0555	0.2723
chr4	191154276	8154191	0.0427	0.2417
chr5	180915260	7232553	0.04	0.2303
chr6	171115067	7604329	0.0444	0.2639
chr7	159138663	7175676	0.0451	0.3341

chr8	146364022	8508264	0.0581	0.3337
chr9	141213431	9644316	0.0683	0.3752
chr10	135534747	3834224	0.0283	0.2176
chr11	135006516	6009721	0.0445	0.3051
chr12	133851895	5243455	0.0392	0.2311
chr13	115169878	3534341	0.0307	0.2016
chr14	107349540	2695514	0.0251	0.1893
chr15	102531392	3201678	0.0312	0.2154
chr16	90354753	2412310	0.0267	0.2007
chr17	81195210	3666807	0.0452	0.2591
chr18	78077248	5158545	0.0661	0.4524
chr19	59128983	2569598	0.0435	0.2965
chr20	63025520	2804863	0.0445	0.246
chr21	48129895	1194416	0.0248	0.1881
chr22	51304566	1348619	0.0263	0.184
chrMT	16571	21042	1.2698	1.3793
chrX	155270560	8052476	0.0519	0.2809
chrY	59373566	294918	0.005	0.1007

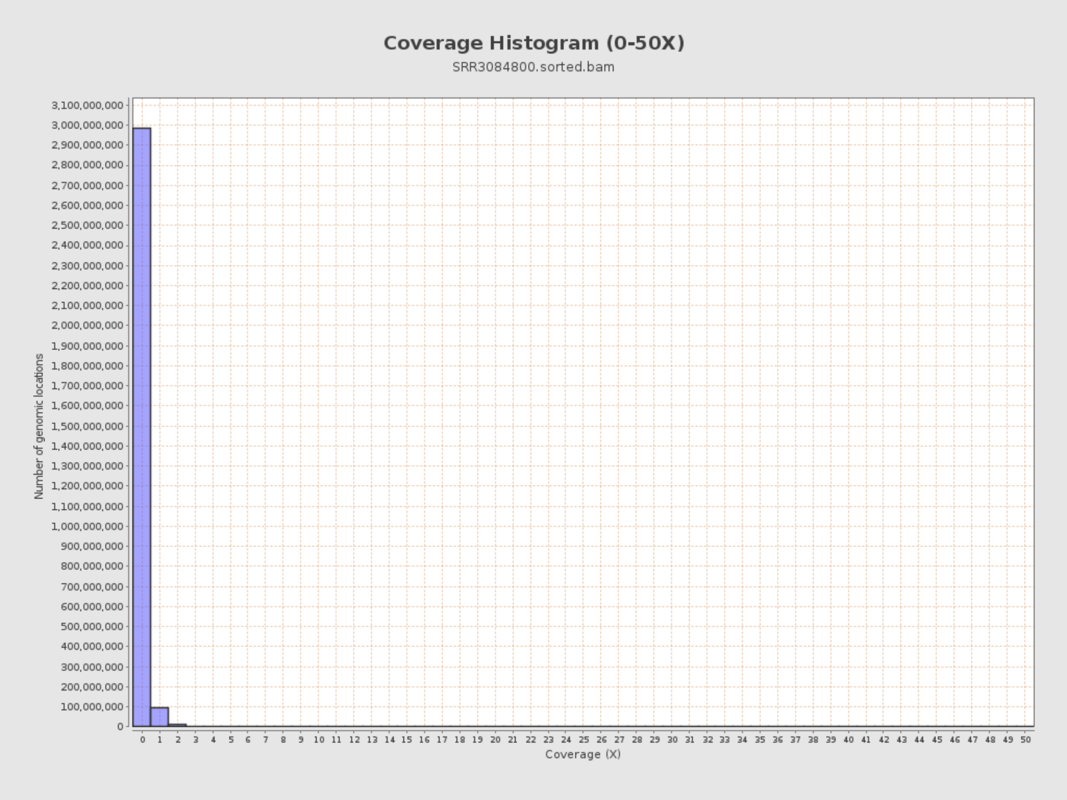
3. Results : Coverage across reference



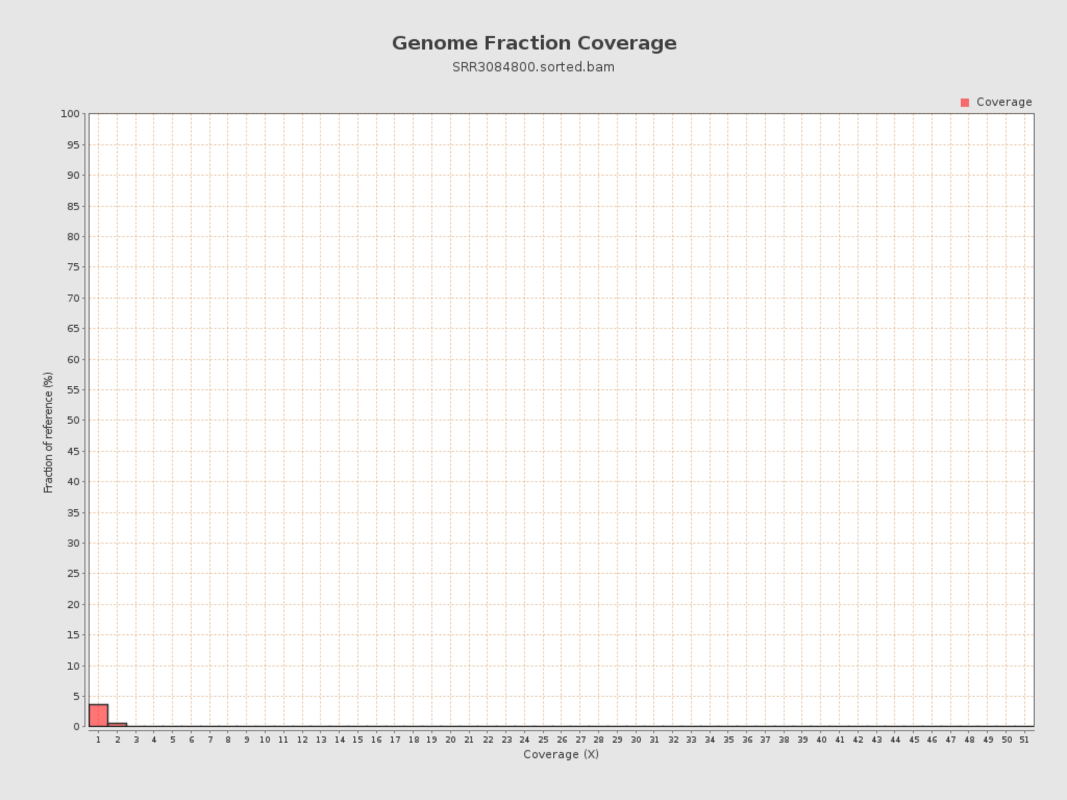
4. Results : Coverage Histogram



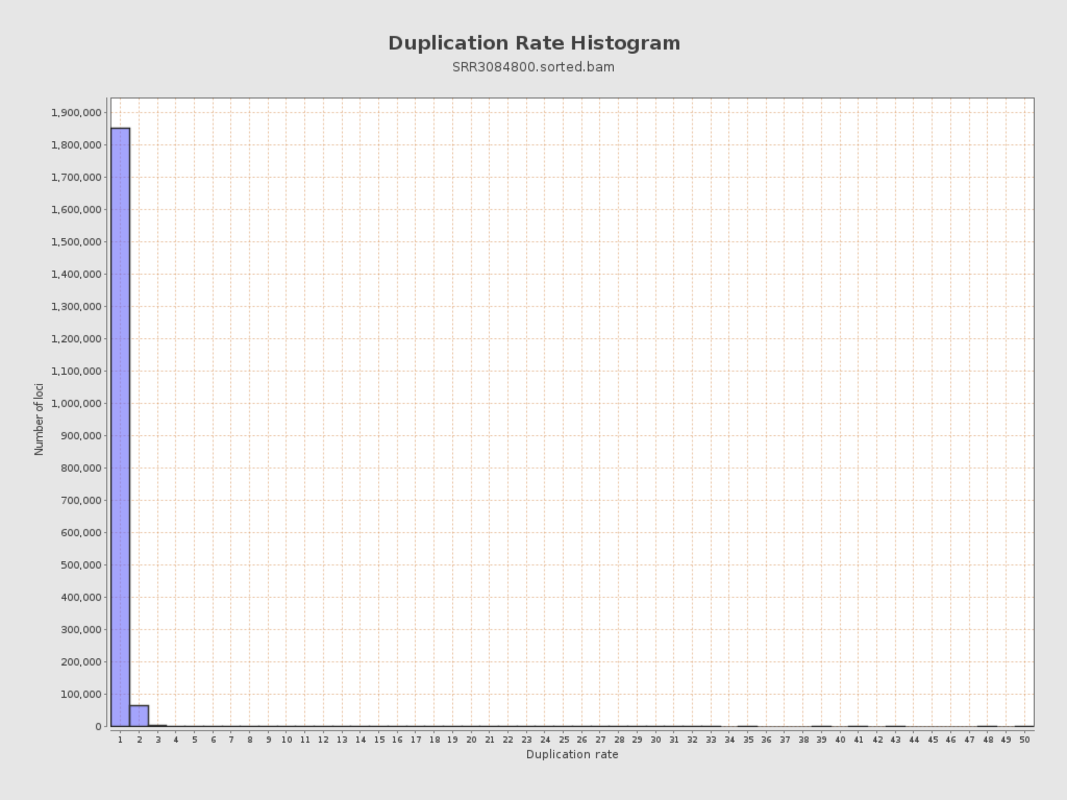
5. Results : Coverage Histogram (0-50X)



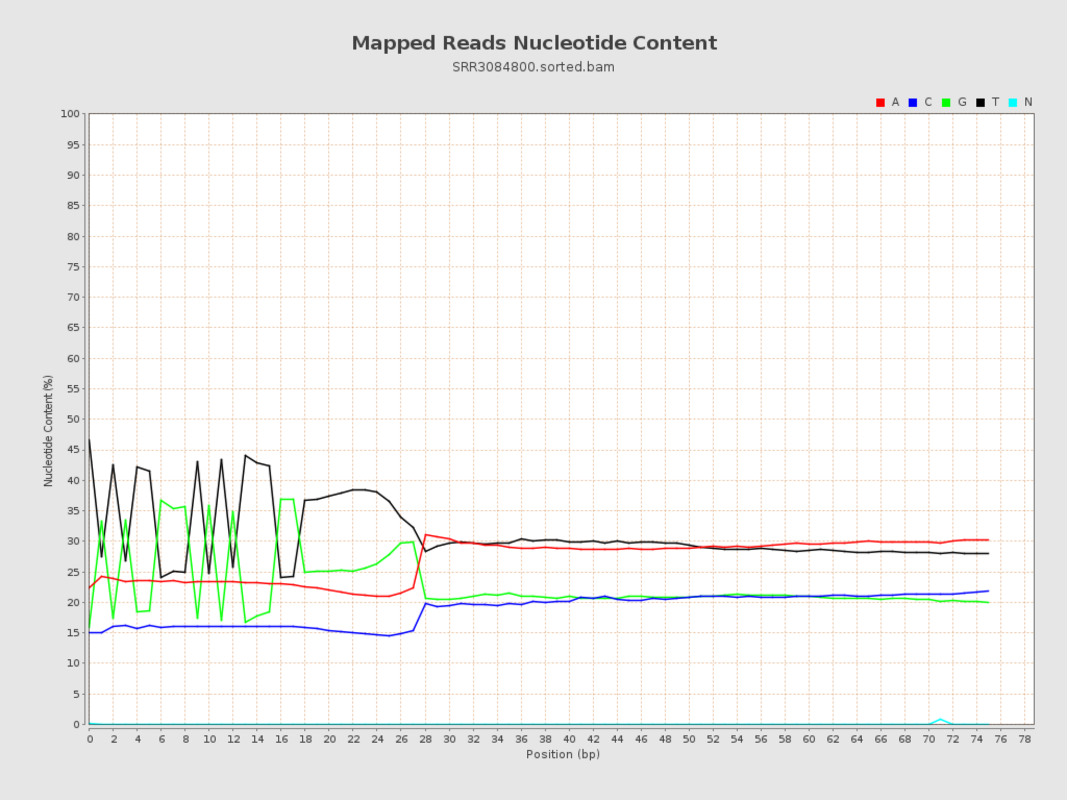
6. Results : Genome Fraction Coverage



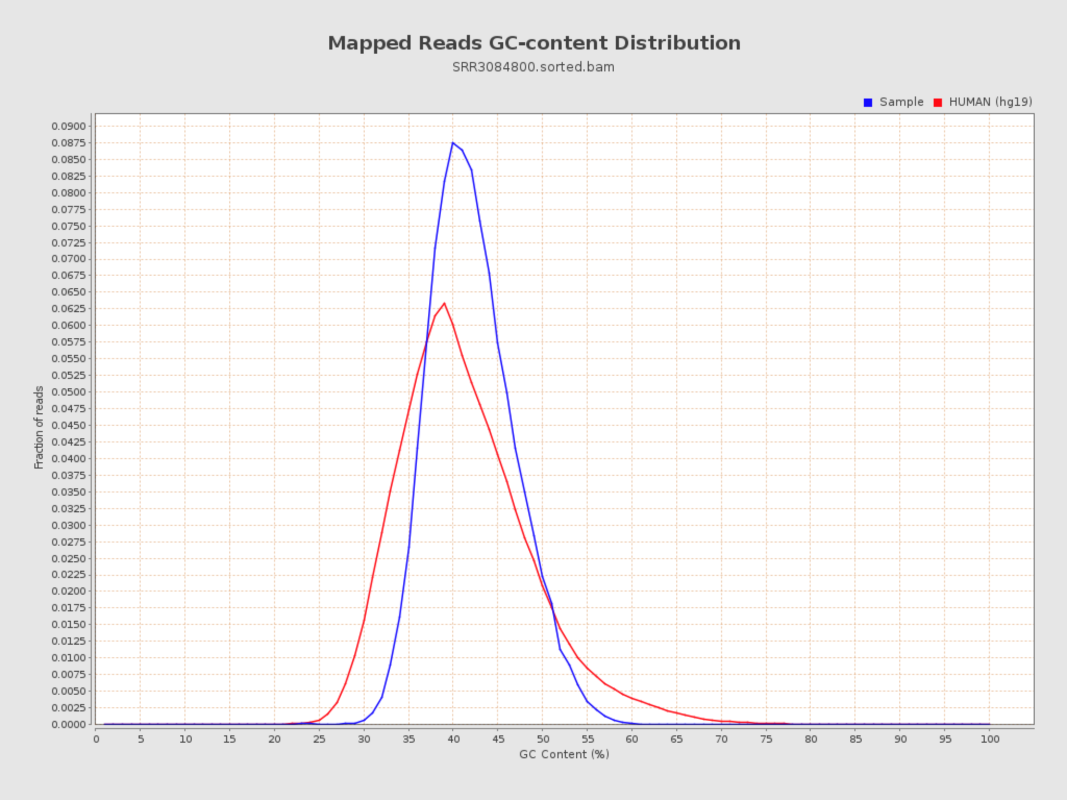
7. Results : Duplication Rate Histogram



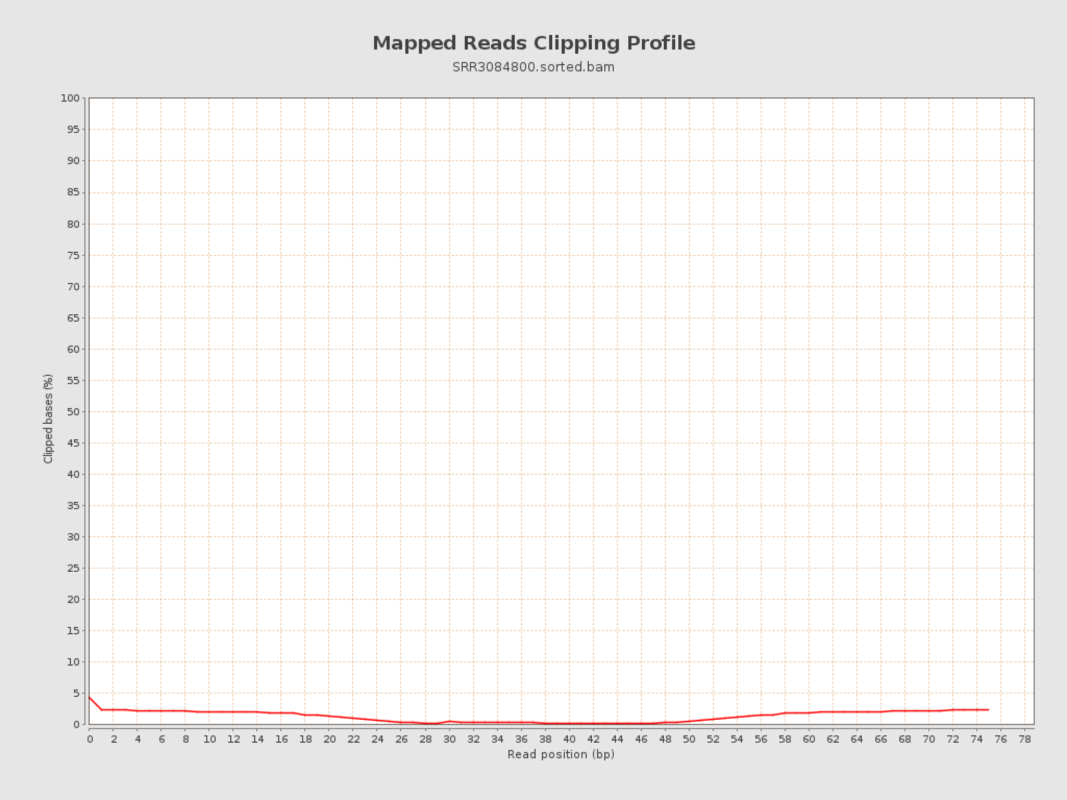
8. Results : Mapped Reads Nucleotide Content



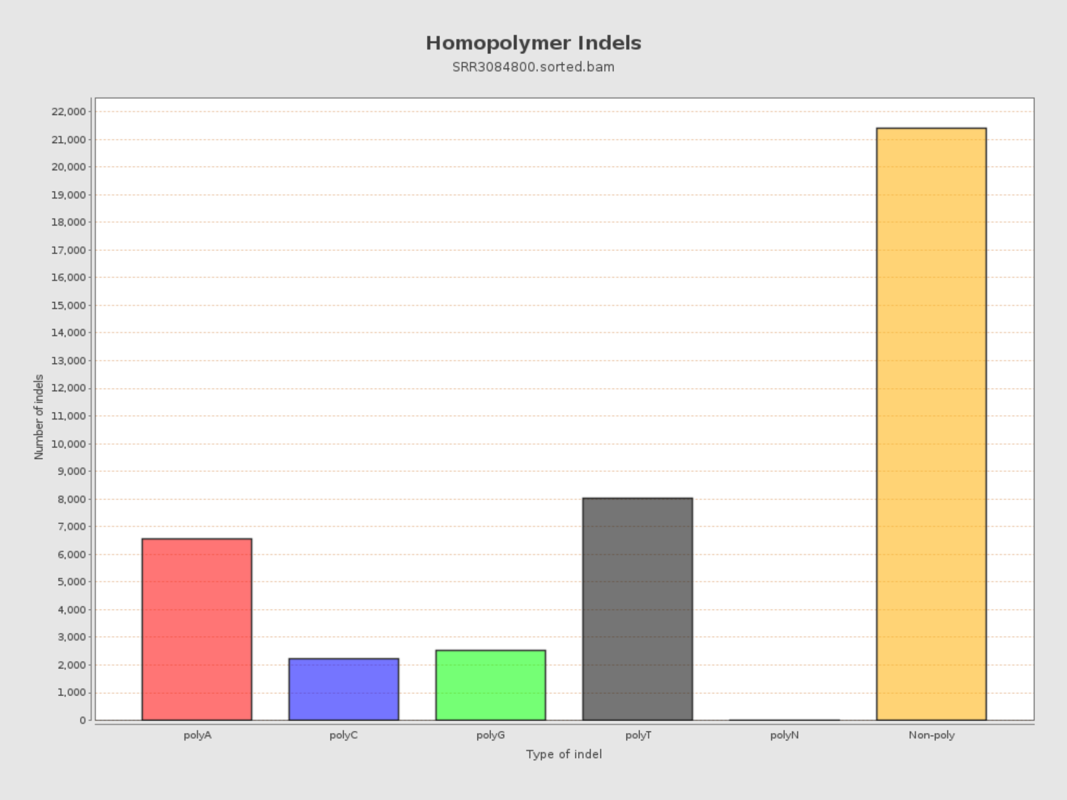
9. Results : Mapped Reads GC-content Distribution



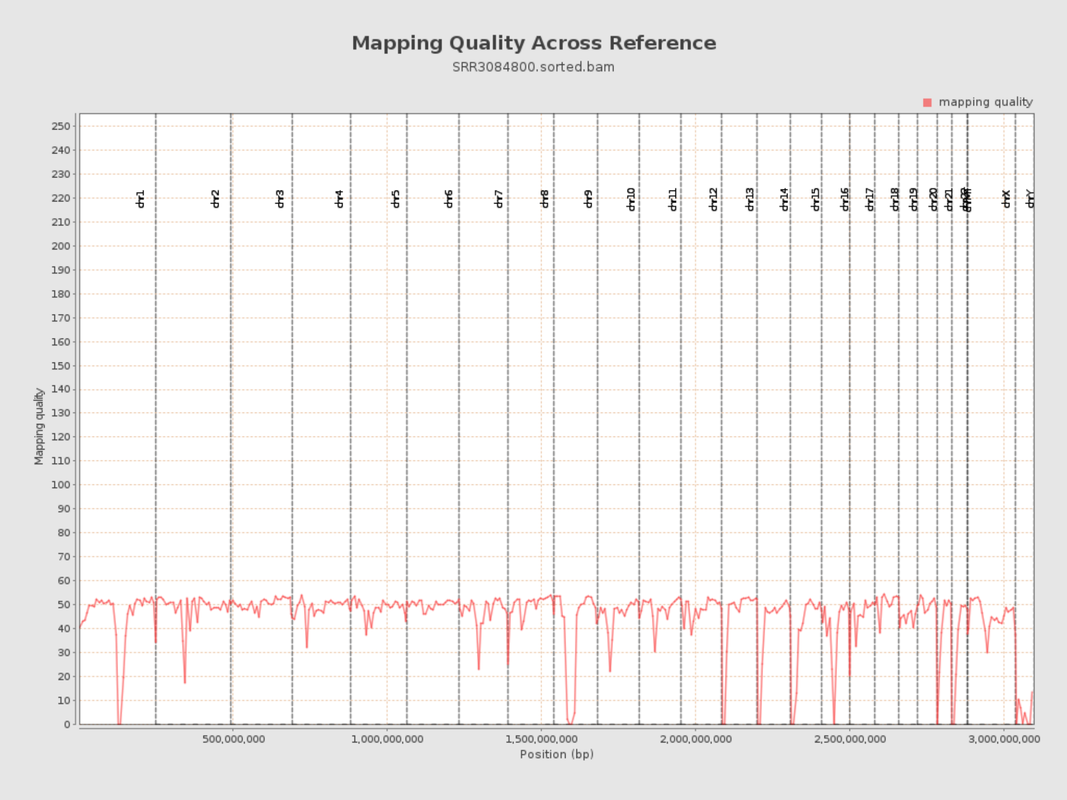
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram