Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:12:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008803.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_SRR6008803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008803.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:12:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,677,474
Mapped reads	1,451,083 / 86.5%
Unmapped reads	226,391 / 13.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,446 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	130,644 / 7.79%
Duplication rate	6.91%
Clipped reads	736,376 / 43.9%

2.2. ACGT Content

Number/percentage of A's	25,528,452 / 26.96%
Number/percentage of C's	18,623,124 / 19.67%
Number/percentage of T's	28,812,628 / 30.43%
Number/percentage of G's	21,566,755 / 22.78%
Number/percentage of N's	148,927 / 0.16%
GC Percentage	42.45%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.3816

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

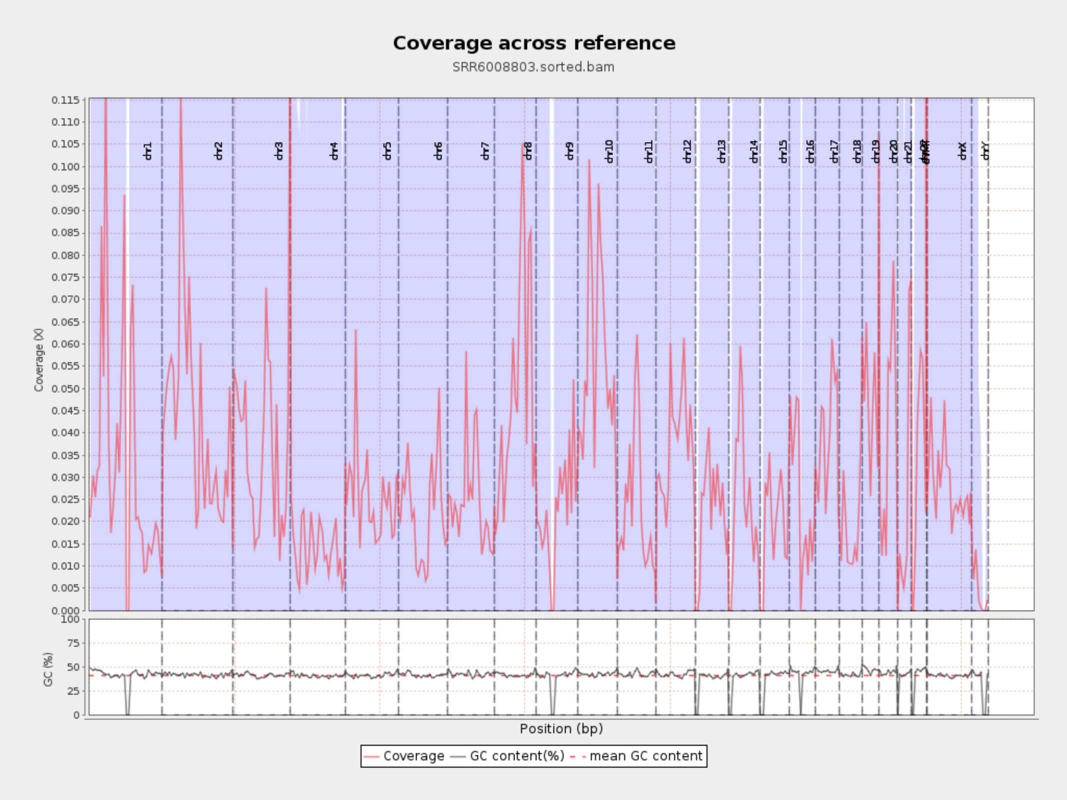
General error rate	0.93%
Mismatches	865,427
Insertions	7,382
Mapped reads with at least one insertion	0.5%
Deletions	31,364
Mapped reads with at least one deletion	2.14%
Homopolymer indels	44.31%

2.6. Chromosome stats

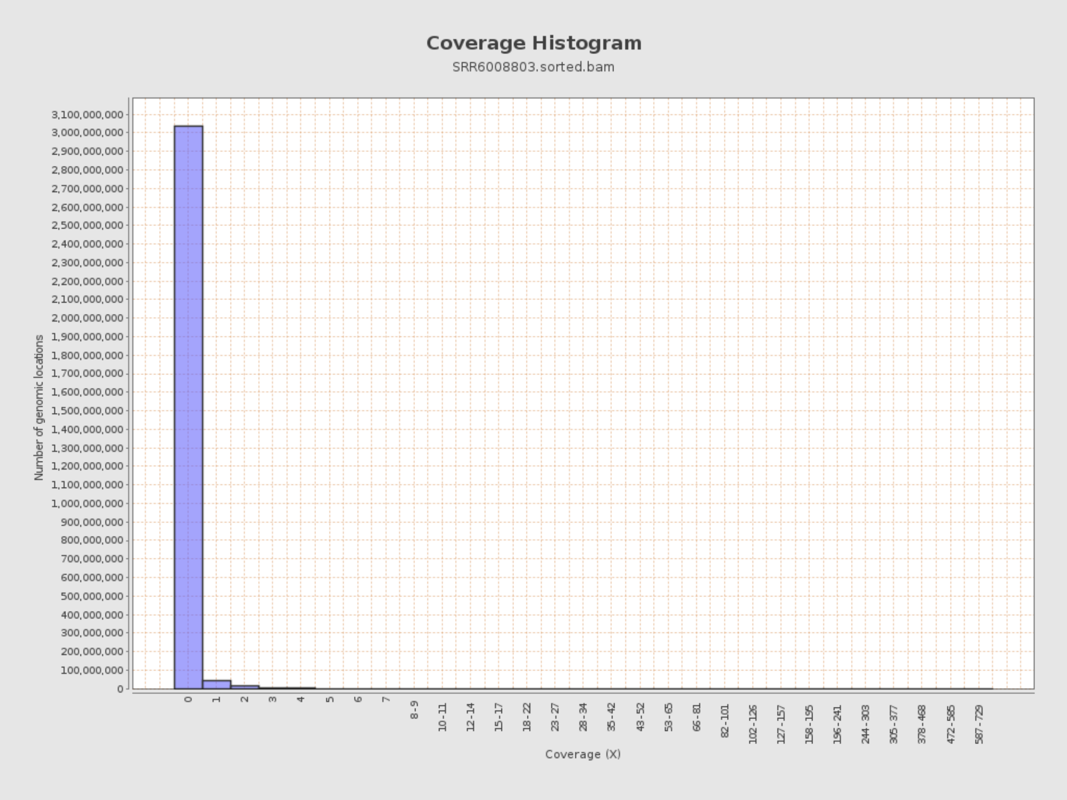
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8259472	0.0331	0.649
chr2	243199373	10697264	0.044	0.4935
chr3	198022430	7113017	0.0359	0.282
chr4	191154276	2587561	0.0135	0.1682
chr5	180915260	4677850	0.0259	0.2305
chr6	171115067	3815475	0.0223	0.241
chr7	159138663	3958367	0.0249	0.4526

chr8	146364022	7219640	0.0493	0.415
chr9	141213431	3145498	0.0223	0.272
chr10	135534747	7733472	0.0571	0.6155
chr11	135006516	3156973	0.0234	0.2628
chr12	133851895	5137790	0.0384	0.2826
chr13	115169878	2528782	0.022	0.2145
chr14	107349540	2587893	0.0241	0.2274
chr15	102531392	2043519	0.0199	0.203
chr16	90354753	2232794	0.0247	0.3675
chr17	81195210	3223521	0.0397	0.3414
chr18	78077248	1394199	0.0179	0.4977
chr19	59128983	2858475	0.0483	0.535
chr20	63025520	2496442	0.0396	0.2924
chr21	48129895	1217517	0.0253	0.2373
chr22	51304566	1660384	0.0324	0.2587
chrMT	16571	320405	19.3353	12.3534
chrX	155270560	4417470	0.0285	0.2584
chrY	59373566	251365	0.0042	0.1907

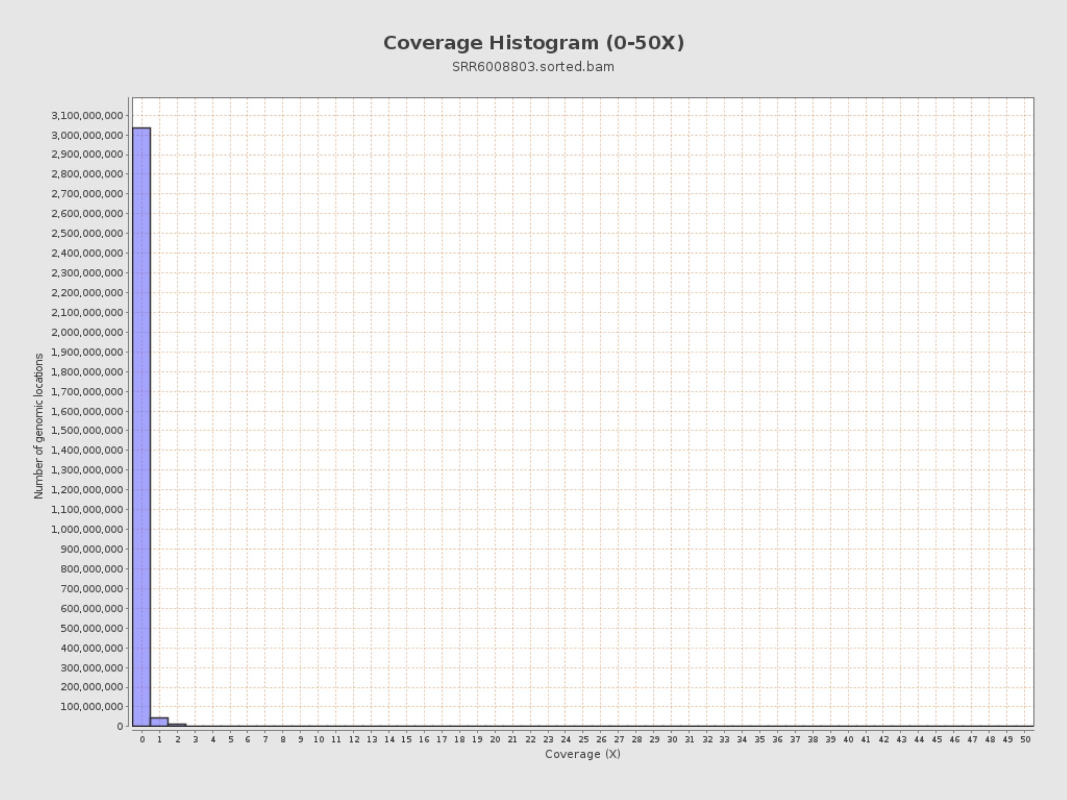
3. Results : Coverage across reference



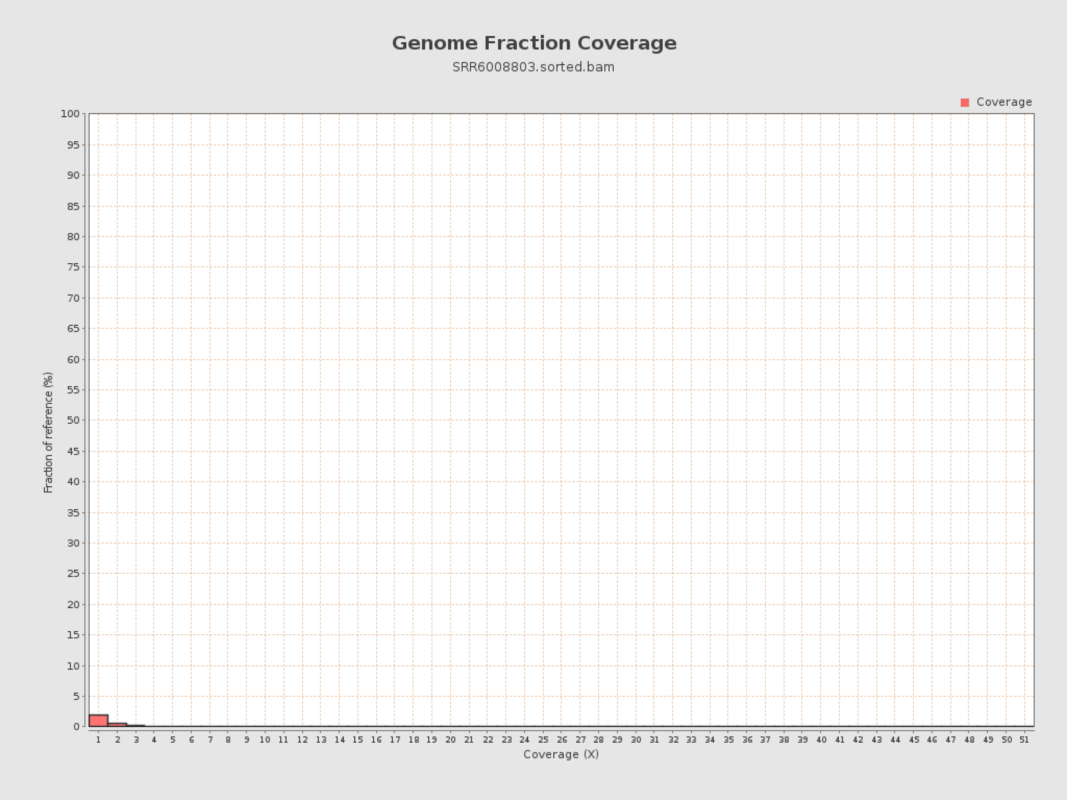
4. Results : Coverage Histogram



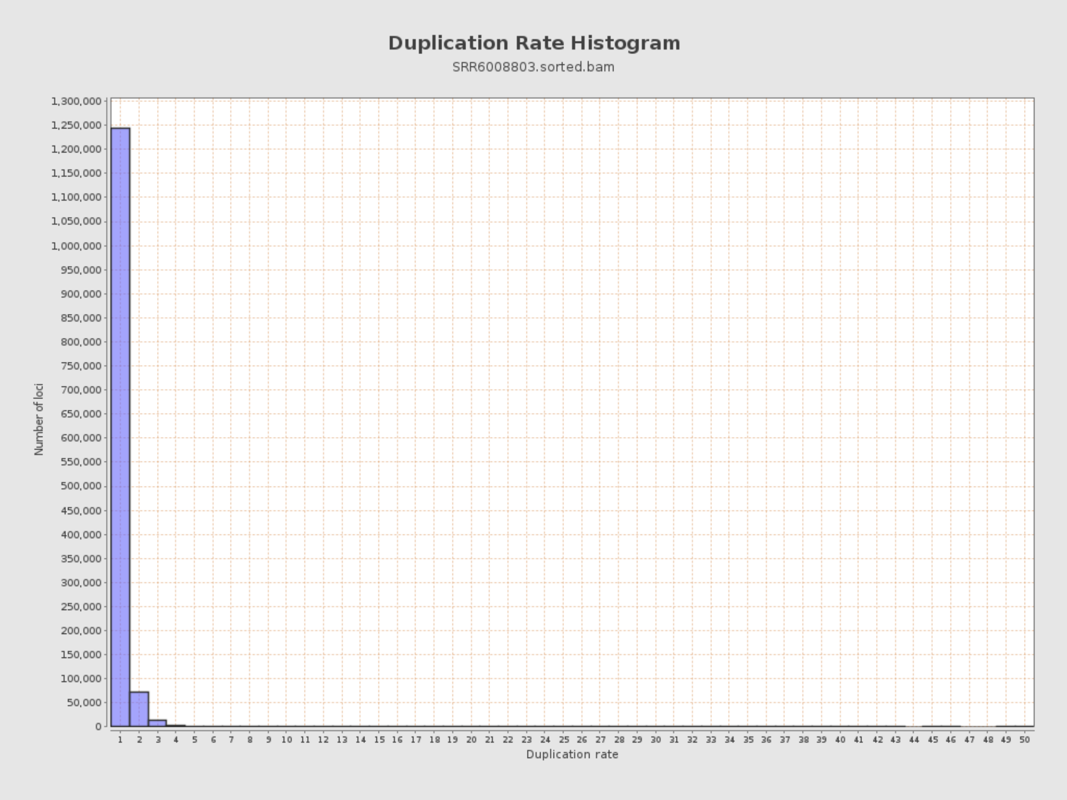
5. Results : Coverage Histogram (0-50X)



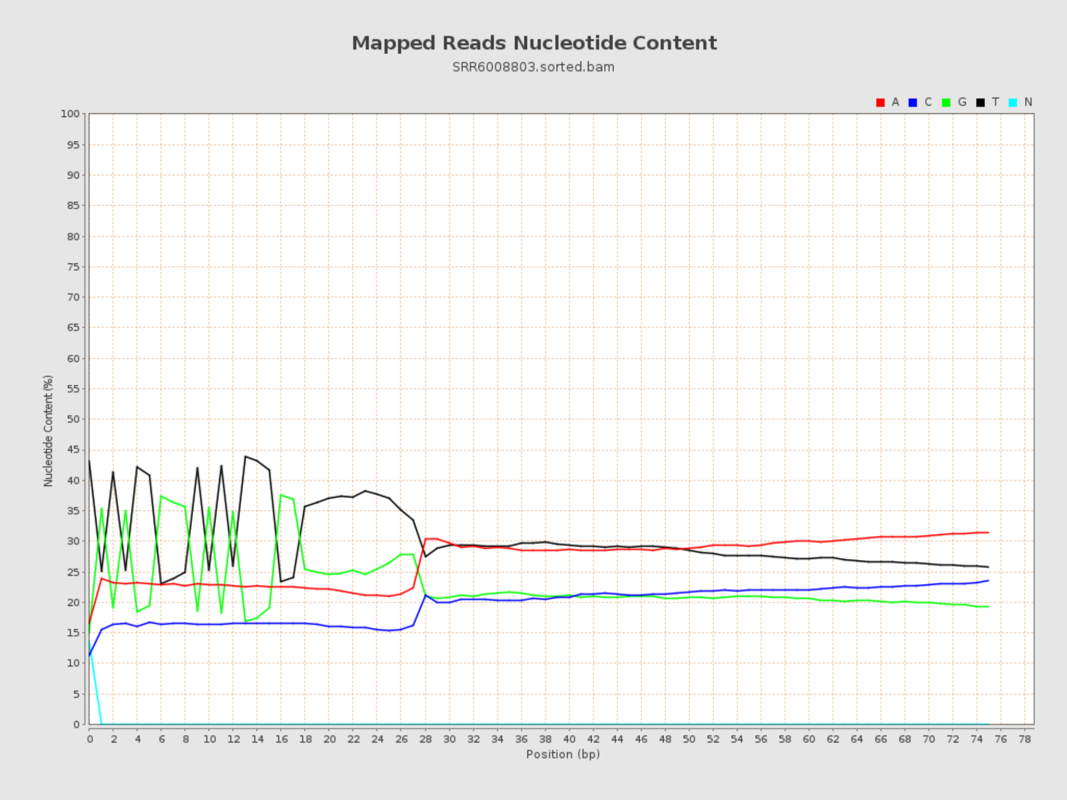
6. Results : Genome Fraction Coverage



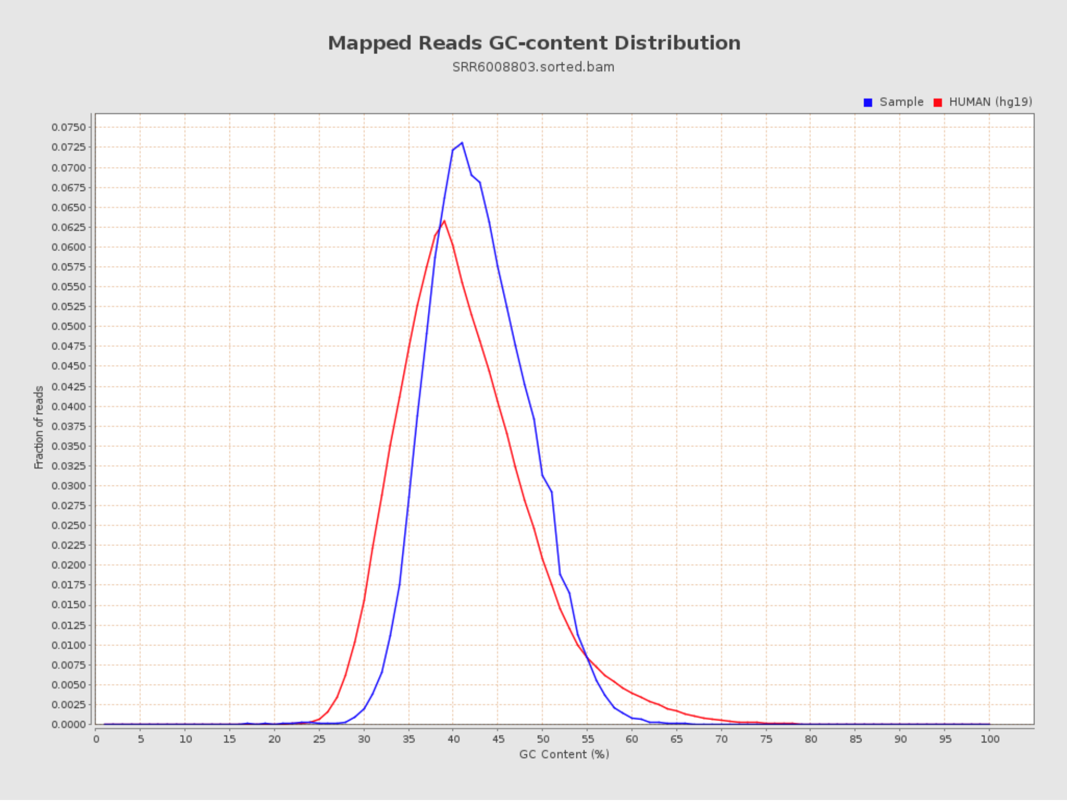
7. Results : Duplication Rate Histogram



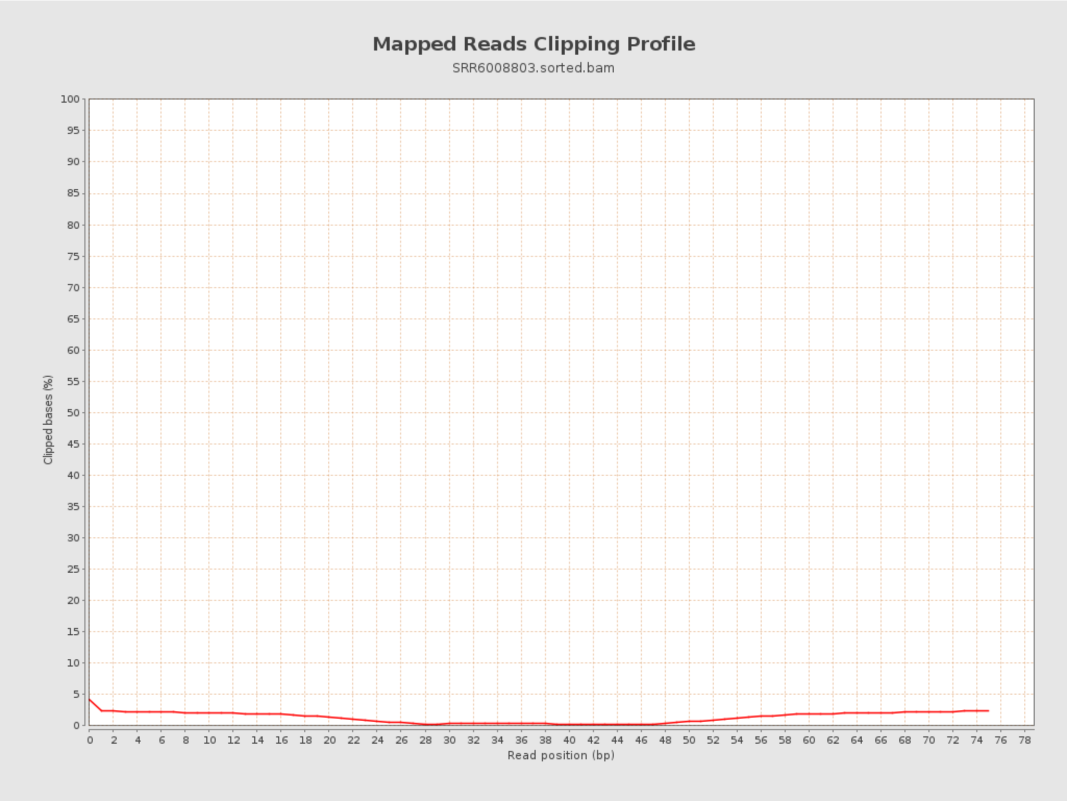
8. Results : Mapped Reads Nucleotide Content



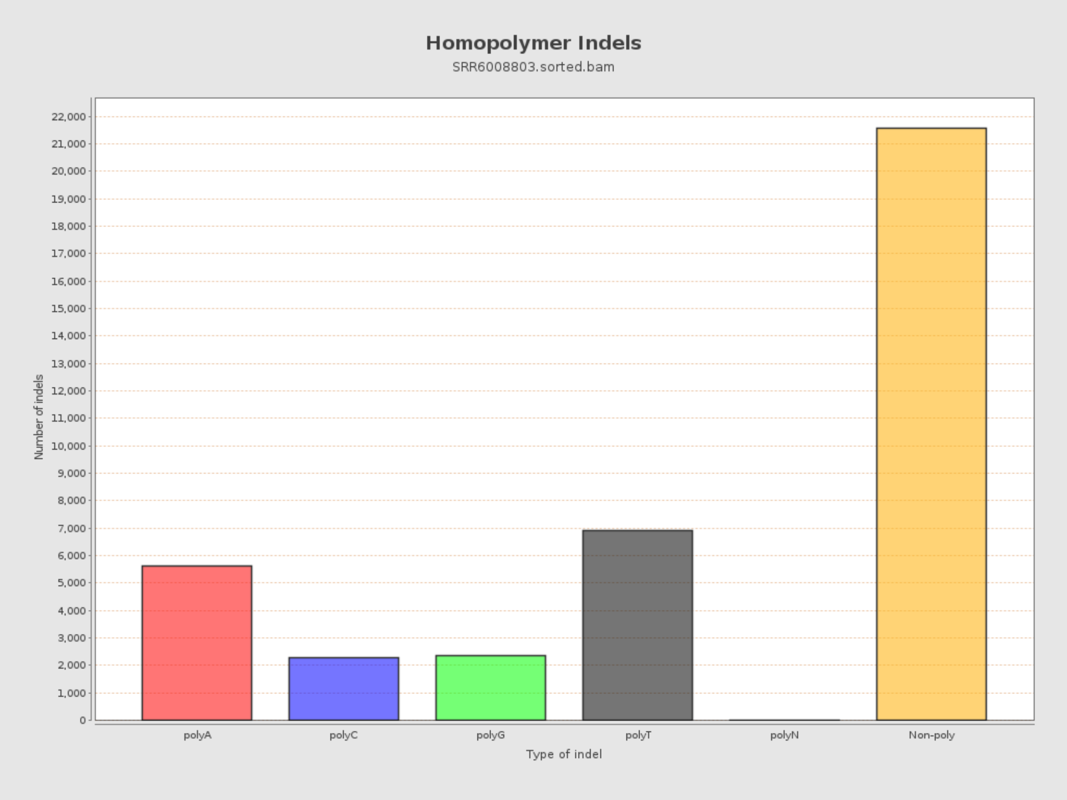
9. Results : Mapped Reads GC-content Distribution



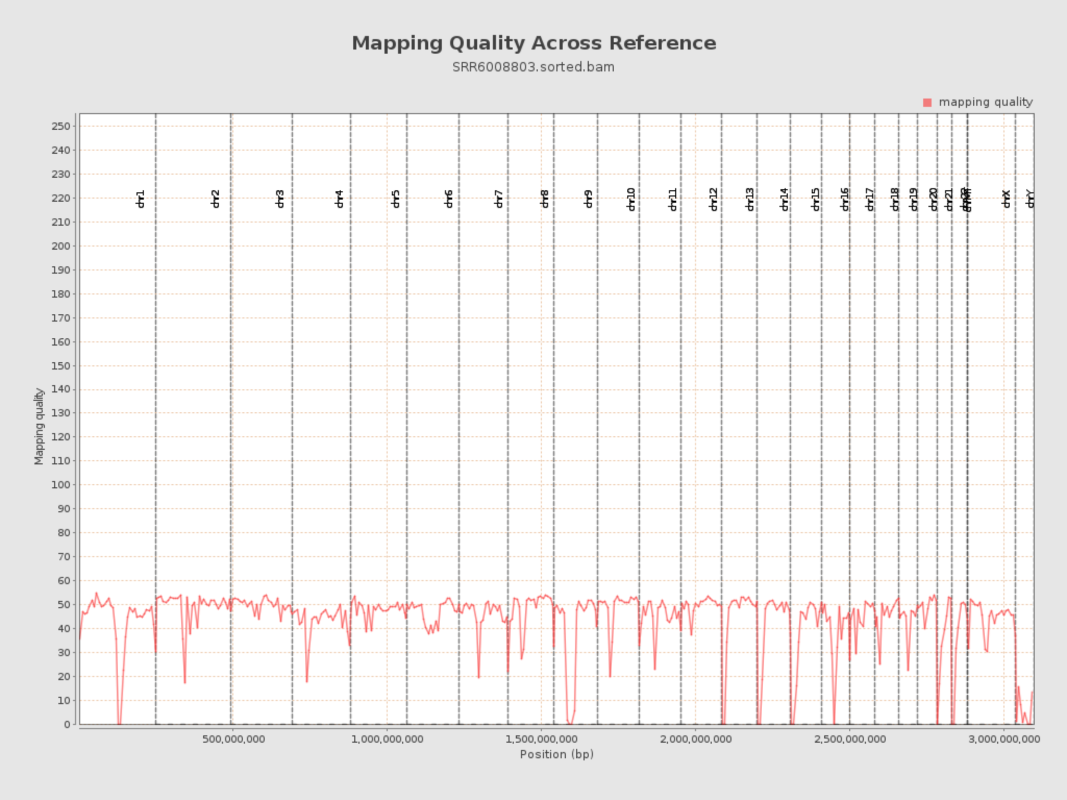
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram