Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:38:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084803.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_SRR3084803 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084803.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:38:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084803.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,901,026
Mapped reads	1,727,659 / 90.88%
Unmapped reads	173,367 / 9.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,748 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	77,677 / 4.09%
Duplication rate	3.91%
Clipped reads	738,238 / 38.83%

2.2. ACGT Content

Number/percentage of A's	32,166,808 / 27.71%
Number/percentage of C's	21,558,618 / 18.57%
Number/percentage of T's	36,723,830 / 31.64%
Number/percentage of G's	25,600,004 / 22.06%
Number/percentage of N's	16,380 / 0.01%
GC Percentage	40.63%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.271

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

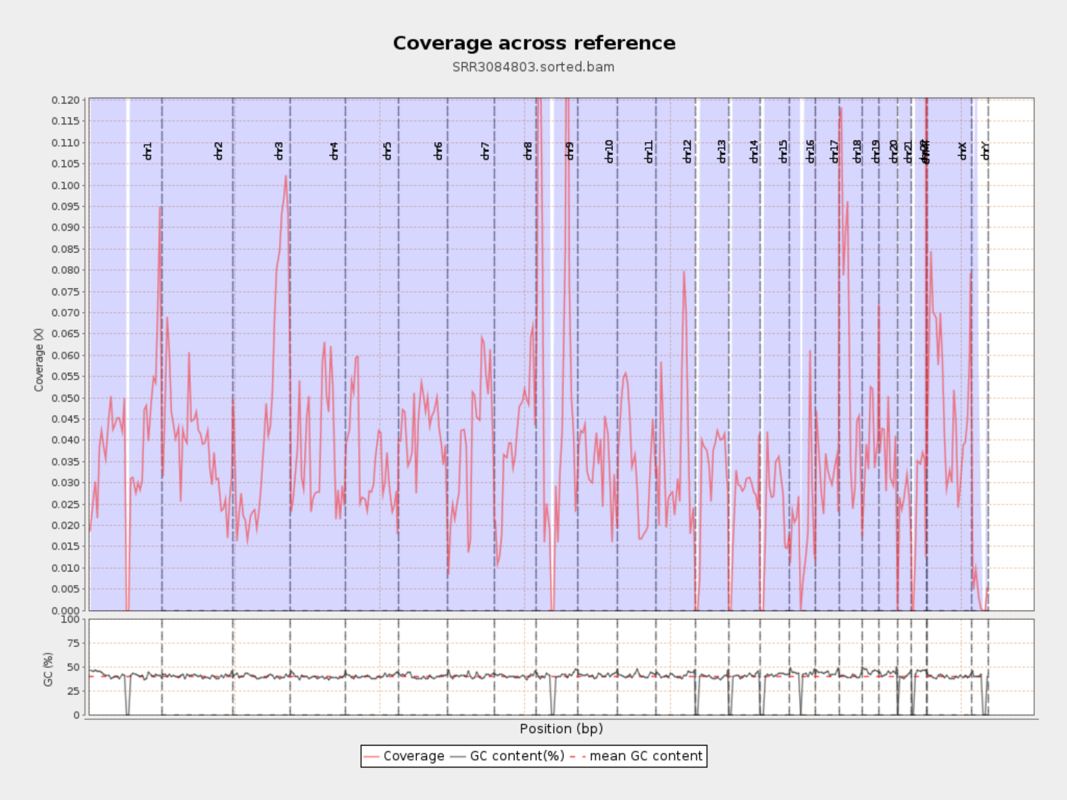
General error rate	0.77%
Mismatches	875,956
Insertions	9,468
Mapped reads with at least one insertion	0.54%
Deletions	26,814
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.43%

2.6. Chromosome stats

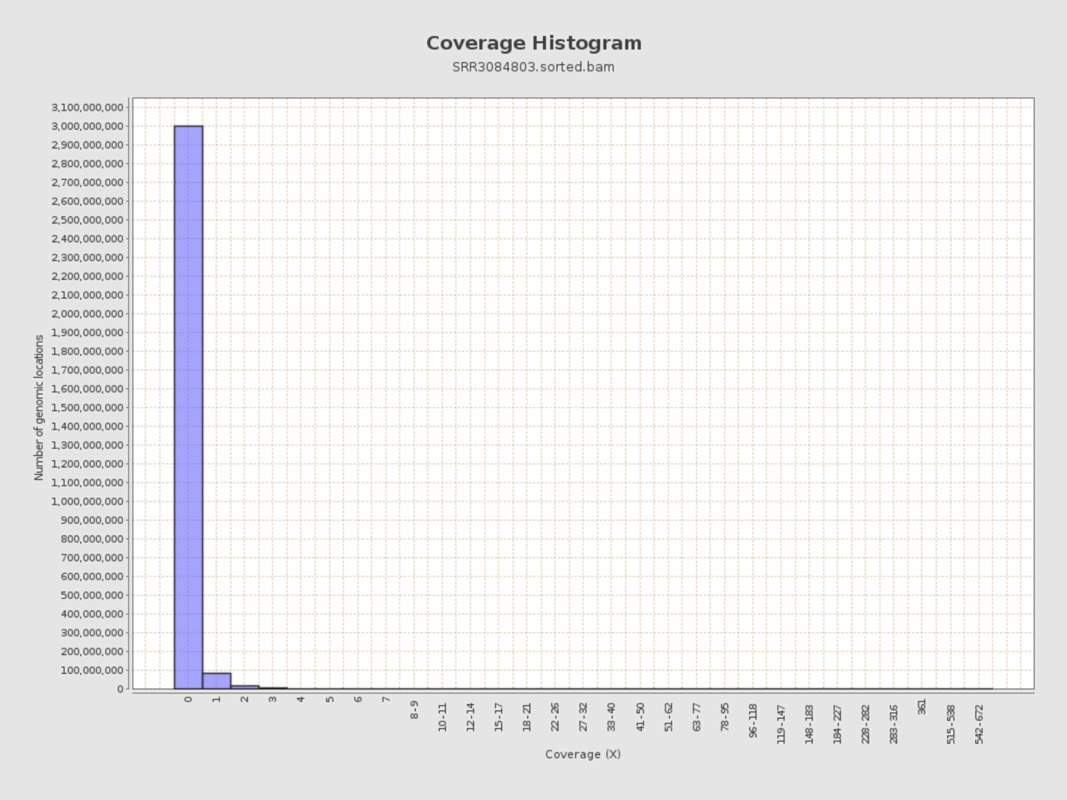
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9770967	0.0392	0.3446
chr2	243199373	9490122	0.039	0.3939
chr3	198022430	9185648	0.0464	0.2549
chr4	191154276	7077202	0.037	0.2298
chr5	180915260	6369163	0.0352	0.2204
chr6	171115067	7286638	0.0426	0.2589
chr7	159138663	6192856	0.0389	0.2669

chr8	146364022	5760693	0.0394	0.2815
chr9	141213431	7690615	0.0545	0.3217
chr10	135534747	4746441	0.035	0.2293
chr11	135006516	4742402	0.0351	0.2631
chr12	133851895	4816537	0.036	0.2234
chr13	115169878	3588709	0.0312	0.2084
chr14	107349540	2634509	0.0245	0.1853
chr15	102531392	2377900	0.0232	0.1845
chr16	90354753	1870797	0.0207	0.1753
chr17	81195210	2690315	0.0331	0.2189
chr18	78077248	4871050	0.0624	0.4205
chr19	59128983	2365037	0.04	0.2819
chr20	63025520	2329900	0.037	0.2301
chr21	48129895	1127285	0.0234	0.1819
chr22	51304566	1231136	0.024	0.1811
chrMT	16571	23535	1.4203	1.5205
chrX	155270560	7631221	0.0491	0.2706
chrY	59373566	239580	0.004	0.0812

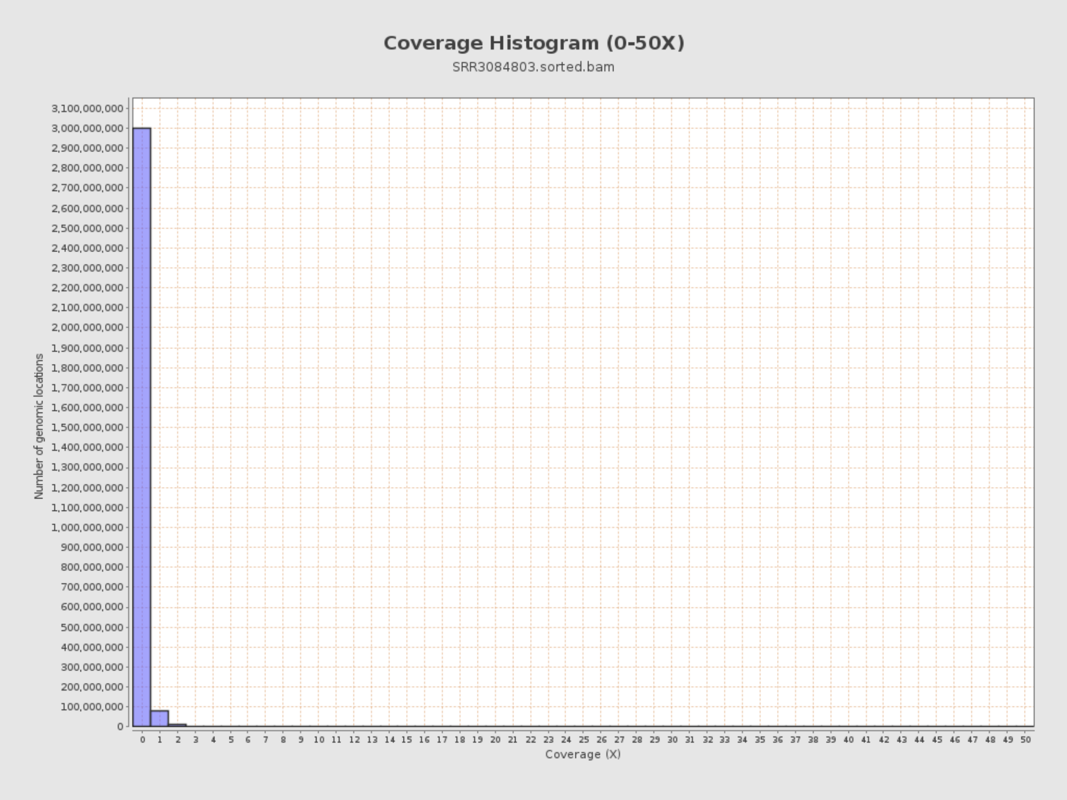
3. Results : Coverage across reference



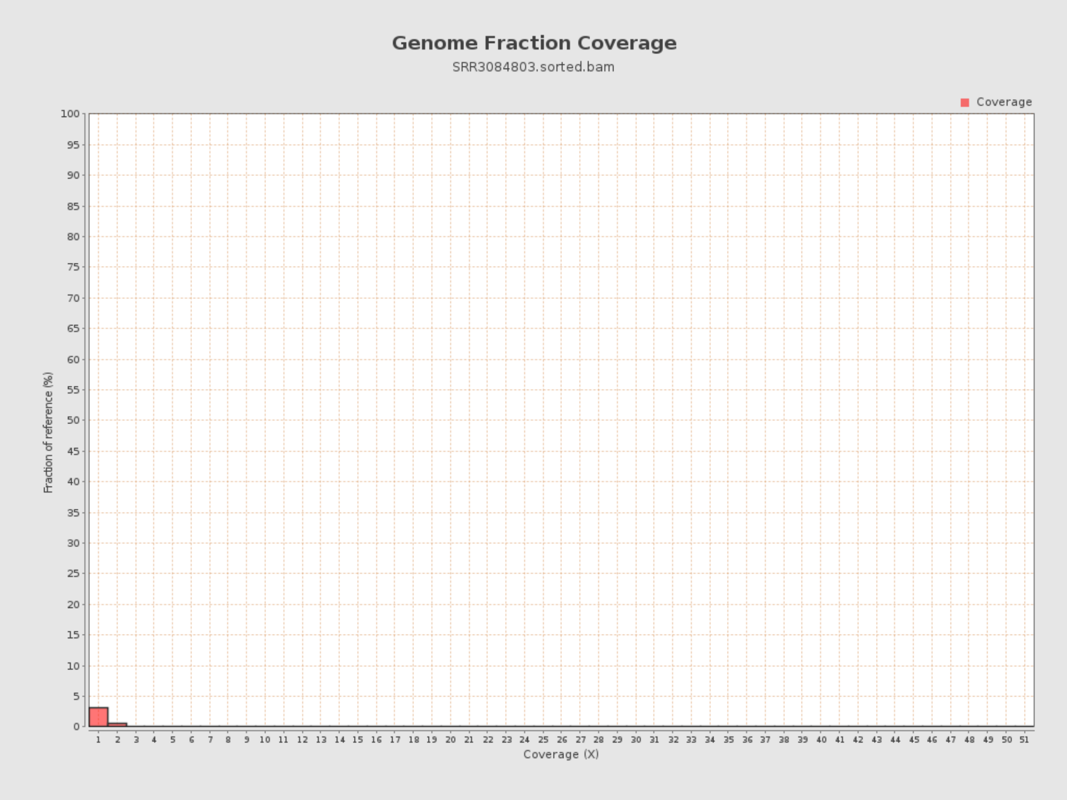
4. Results : Coverage Histogram



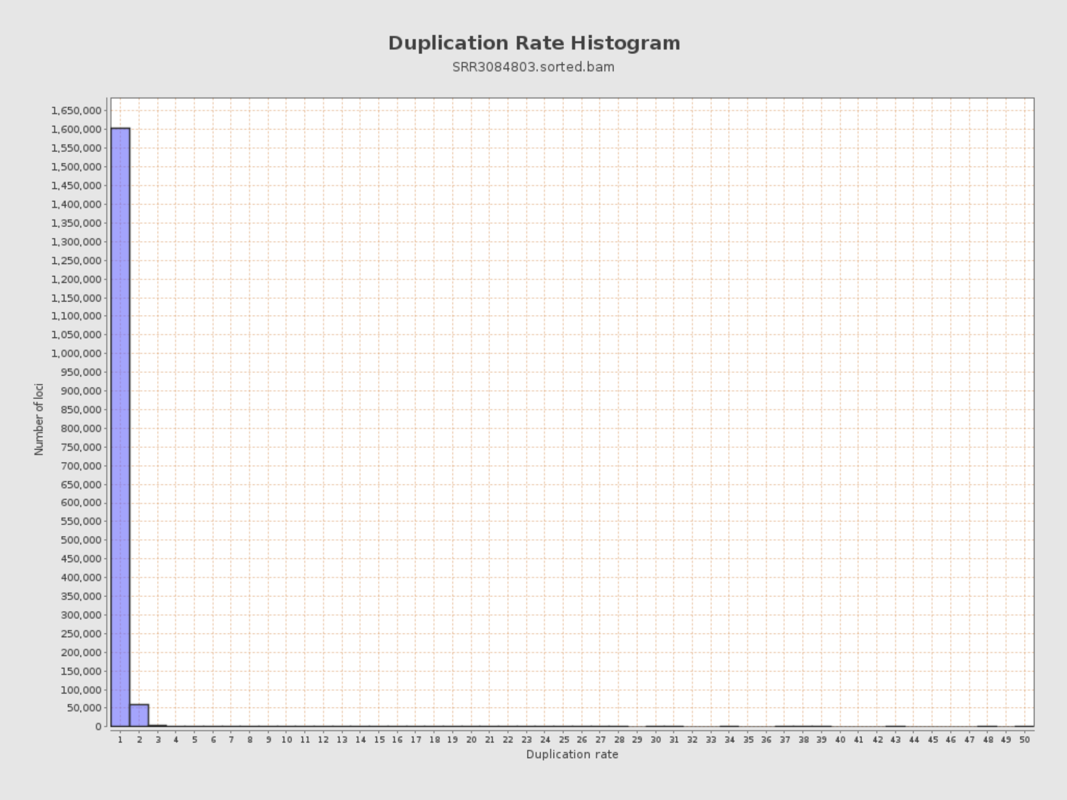
5. Results : Coverage Histogram (0-50X)



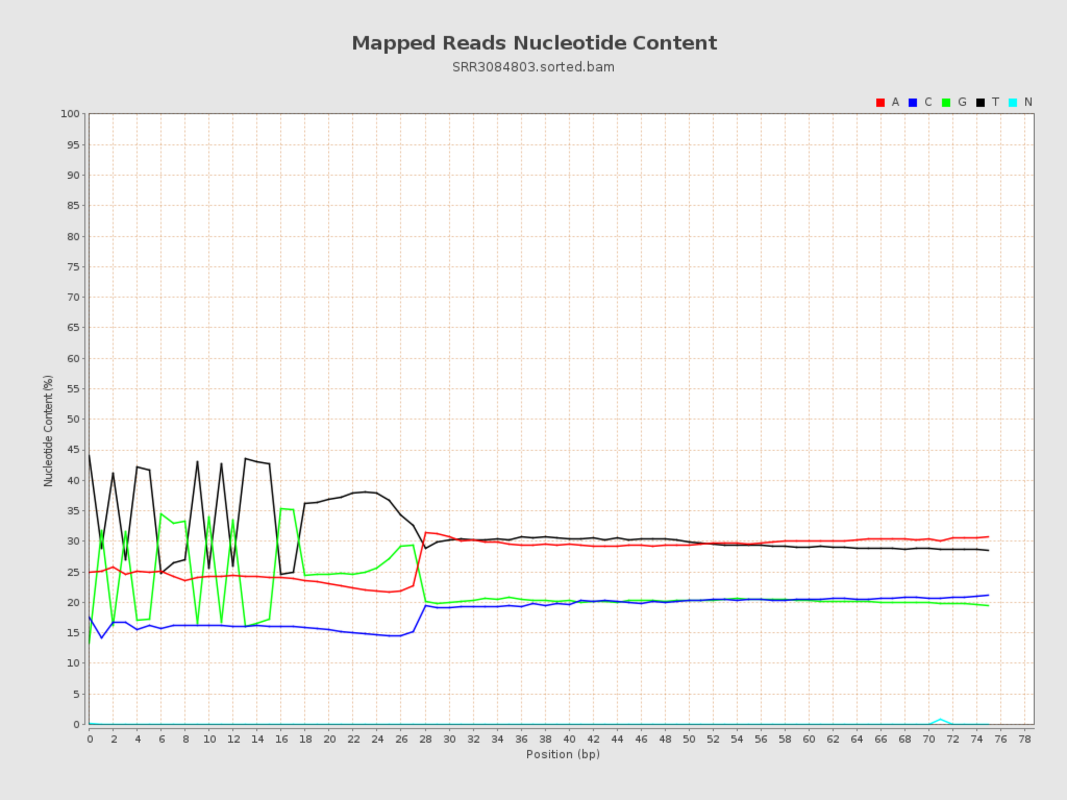
6. Results : Genome Fraction Coverage



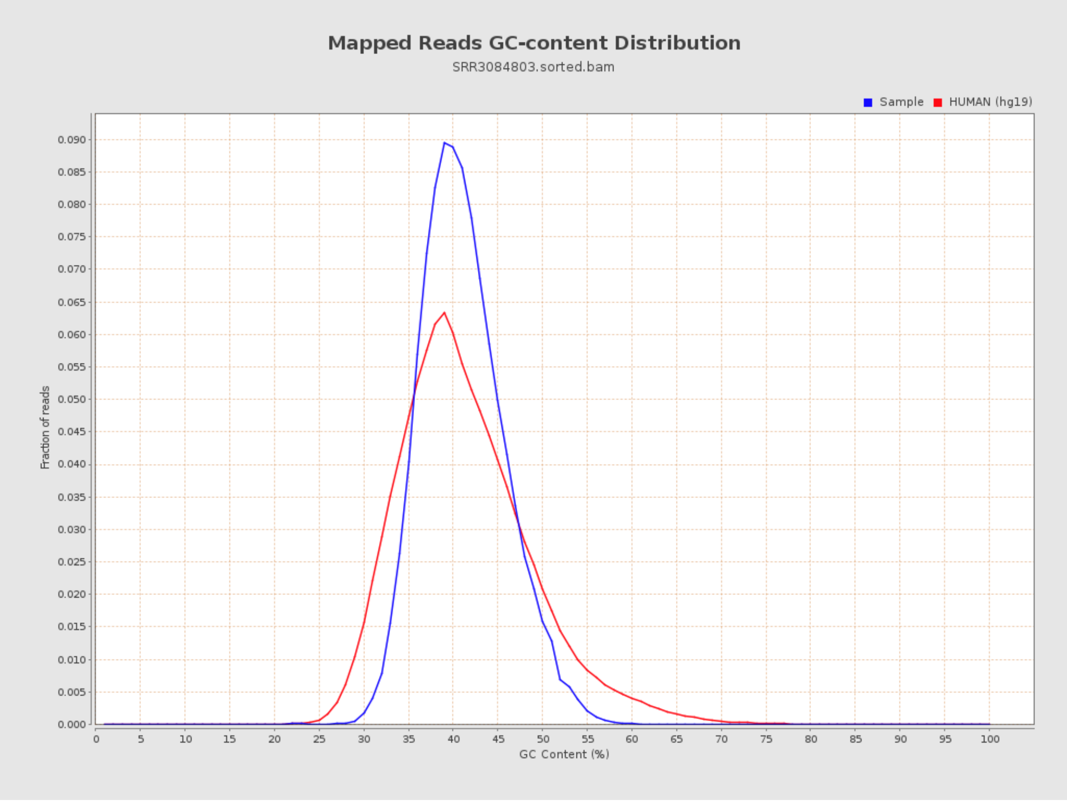
7. Results : Duplication Rate Histogram



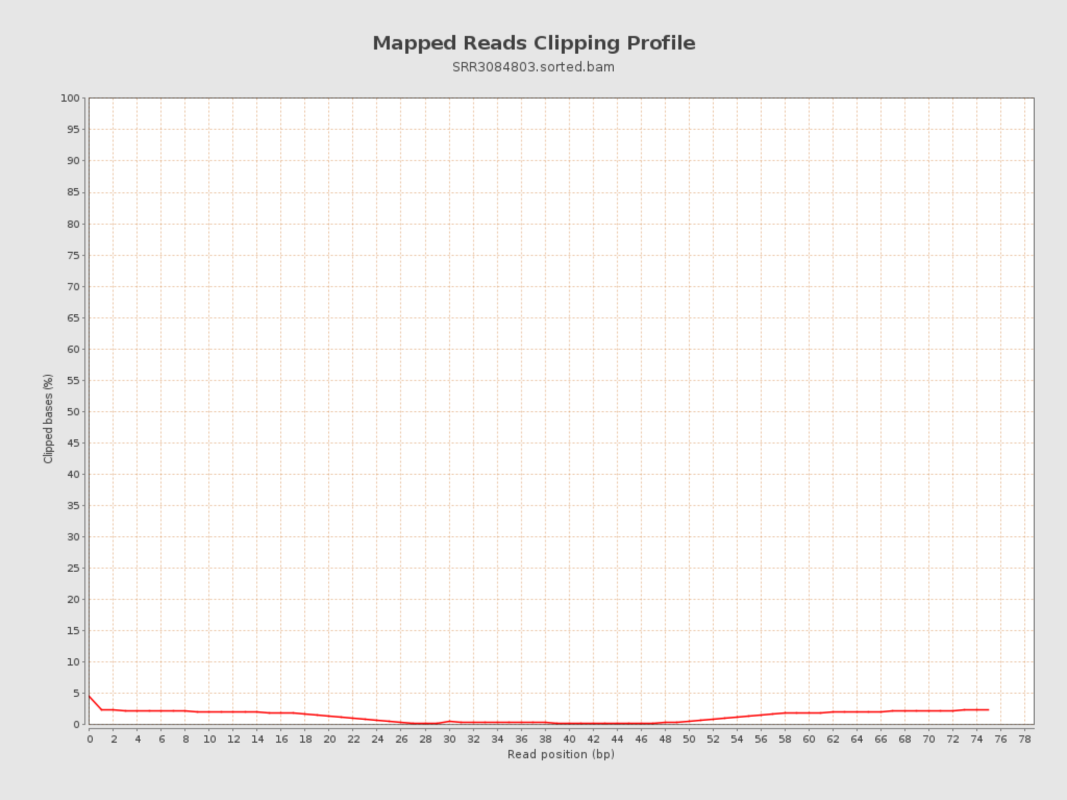
8. Results : Mapped Reads Nucleotide Content



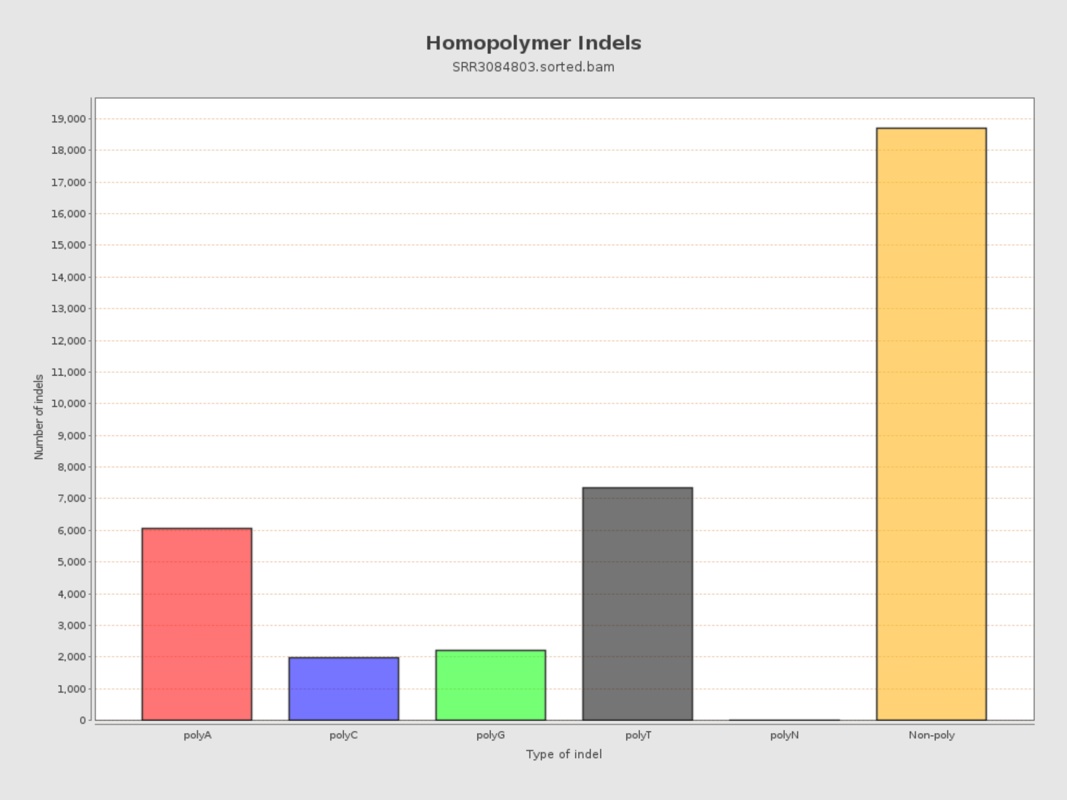
9. Results : Mapped Reads GC-content Distribution



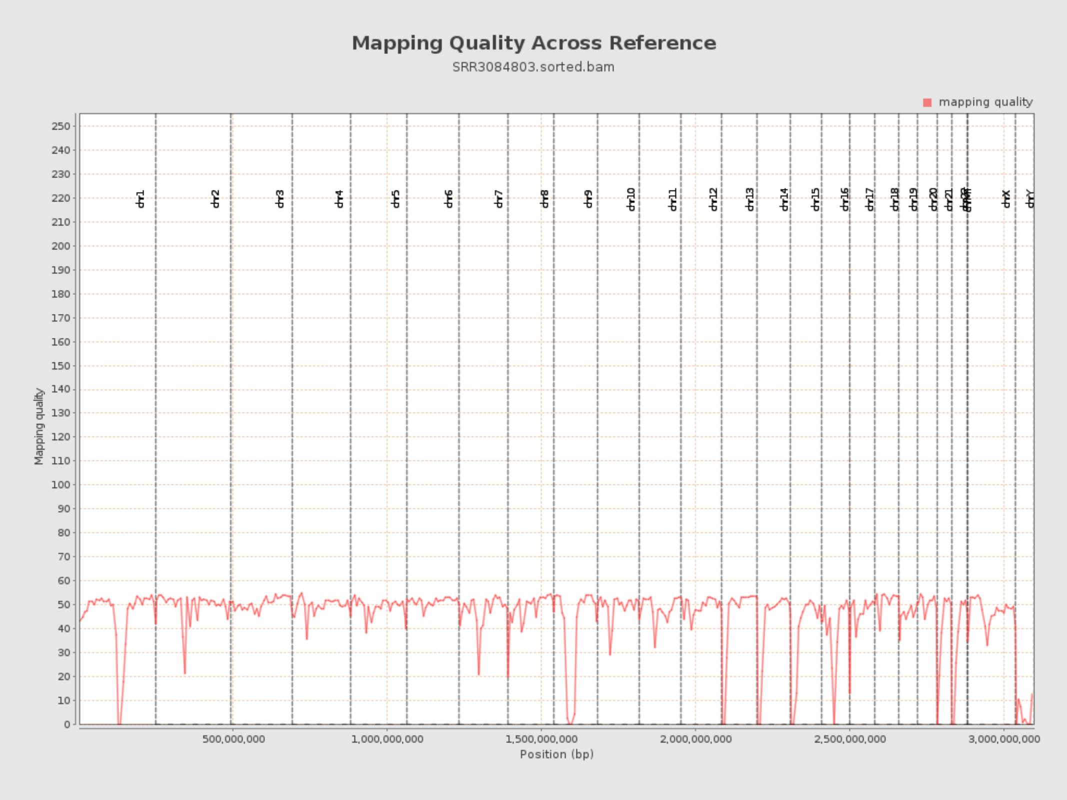
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram