Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:16:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084886.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_SRR3084886 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084886.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:16:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084886.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,539,412
Mapped reads	2,279,817 / 89.78%
Unmapped reads	259,595 / 10.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,129 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	102,249 / 4.03%
Duplication rate	3.63%
Clipped reads	729,291 / 28.72%

2.2. ACGT Content

Number/percentage of A's	46,580,093 / 29.33%
Number/percentage of C's	29,110,496 / 18.33%
Number/percentage of T's	50,910,691 / 32.05%
Number/percentage of G's	32,201,528 / 20.27%
Number/percentage of N's	25,297 / 0.02%
GC Percentage	38.6%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.4368

2.4. Mapping Quality

Mean Mapping Quality	47.96

2.5. Mismatches and indels

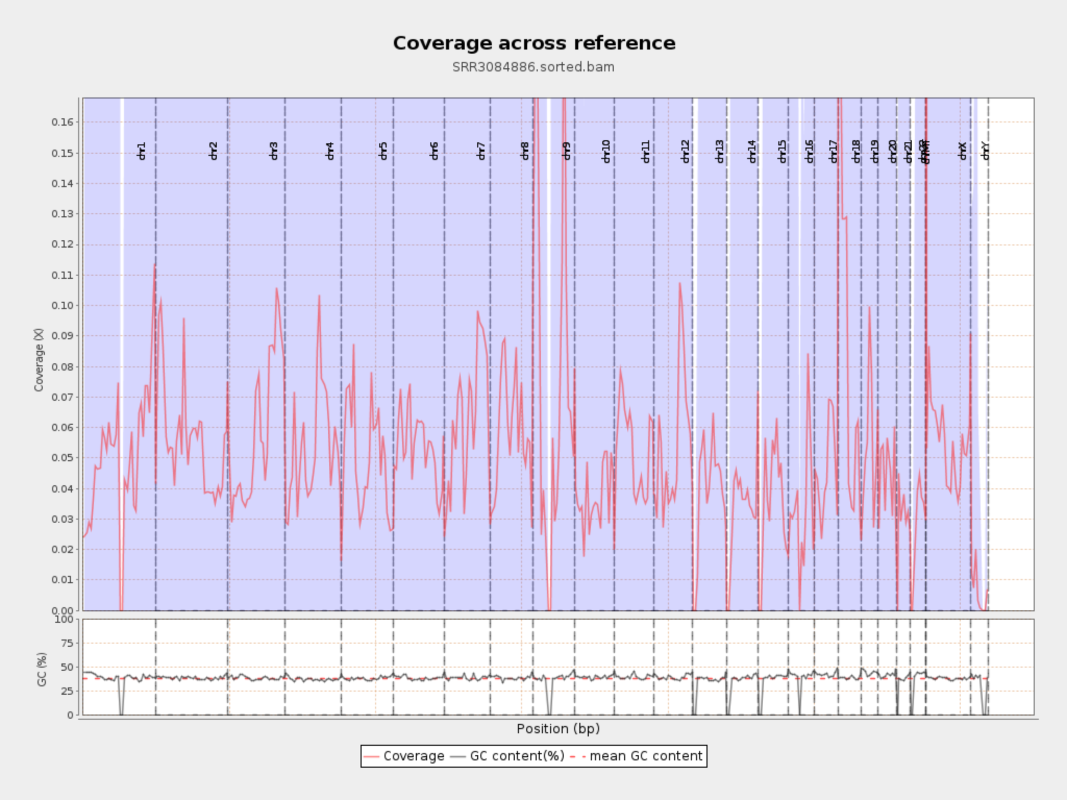
General error rate	0.84%
Mismatches	1,312,147
Insertions	12,734
Mapped reads with at least one insertion	0.55%
Deletions	36,502
Mapped reads with at least one deletion	1.58%
Homopolymer indels	47.98%

2.6. Chromosome stats

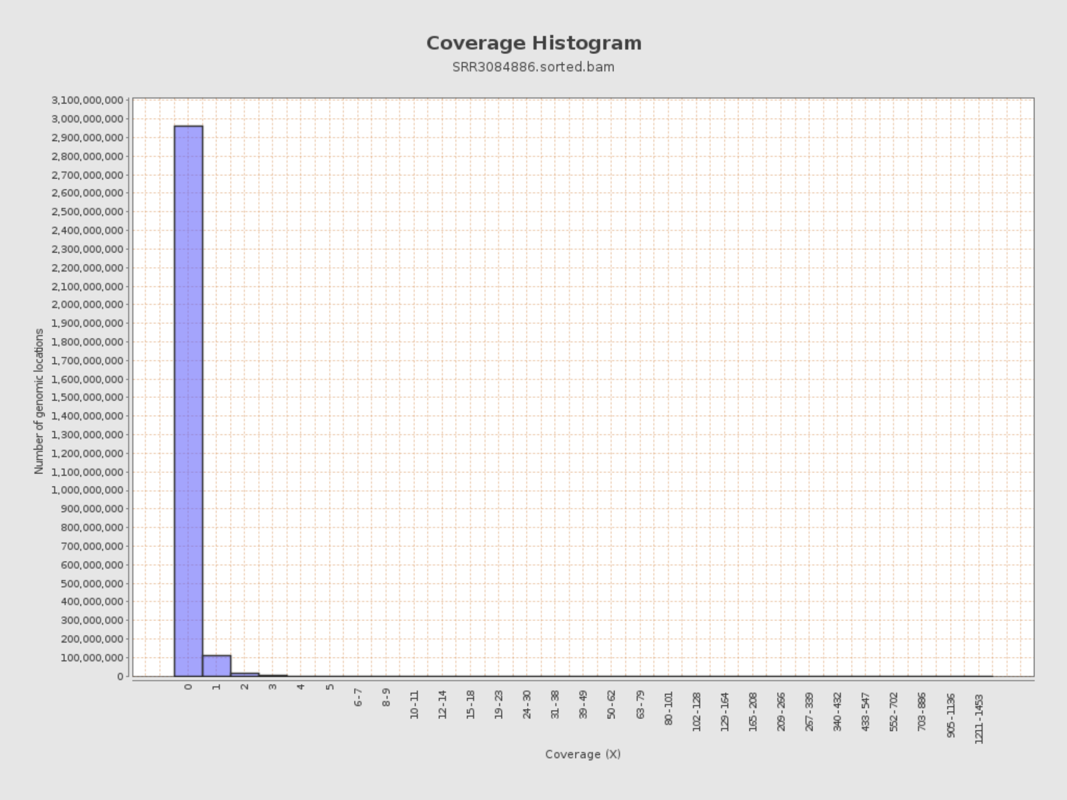
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12604598	0.0506	0.7185
chr2	243199373	13675112	0.0562	0.4751
chr3	198022430	11668991	0.0589	0.2779
chr4	191154276	10243574	0.0536	0.2691
chr5	180915260	9002136	0.0498	0.264
chr6	171115067	9233031	0.054	0.2739
chr7	159138663	10014981	0.0629	0.4045

chr8	146364022	8615566	0.0589	0.9881
chr9	141213431	10912113	0.0773	0.454
chr10	135534747	5056698	0.0373	0.2843
chr11	135006516	7151704	0.053	0.3614
chr12	133851895	7336250	0.0548	0.275
chr13	115169878	4502941	0.0391	0.2245
chr14	107349540	3455192	0.0322	0.2258
chr15	102531392	3603751	0.0351	0.2144
chr16	90354753	2878365	0.0319	0.2365
chr17	81195210	3860976	0.0476	0.2639
chr18	78077248	7082843	0.0907	0.8189
chr19	59128983	3281260	0.0555	0.444
chr20	63025520	2840877	0.0451	0.259
chr21	48129895	1467472	0.0305	0.2157
chr22	51304566	1385932	0.027	0.1839
chrMT	16571	64450	3.8893	2.6216
chrX	155270560	8594273	0.0554	0.3028
chrY	59373566	359313	0.0061	0.1699

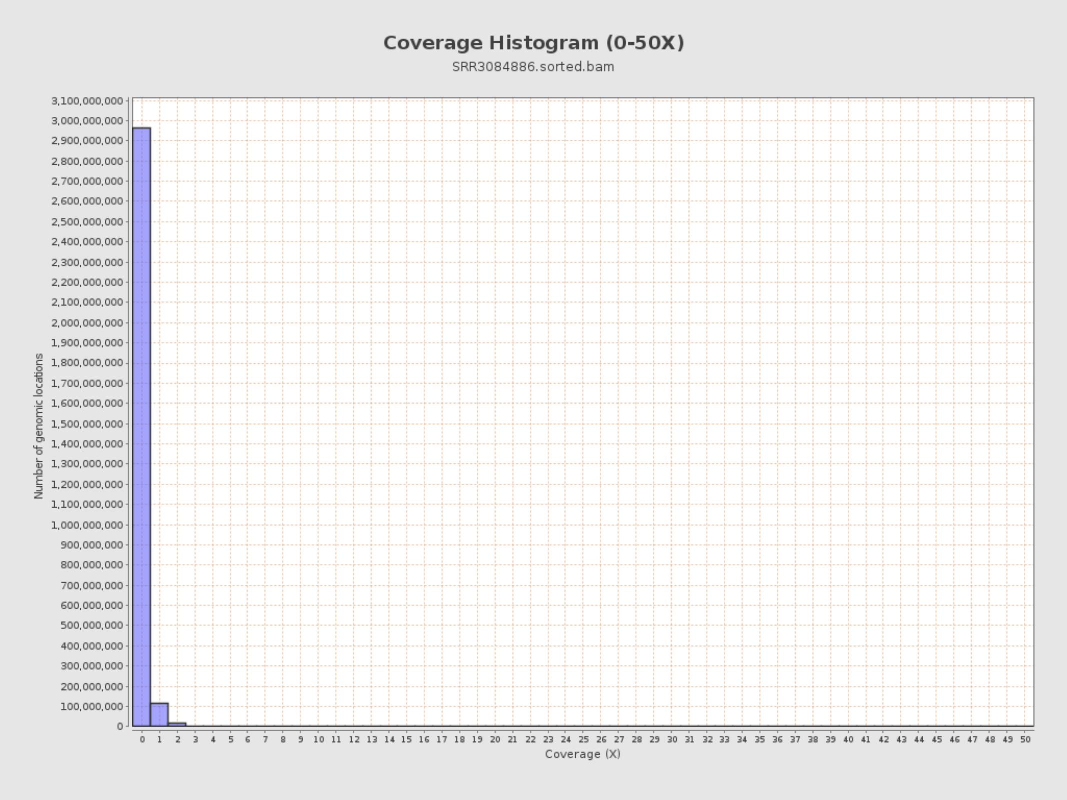
3. Results : Coverage across reference



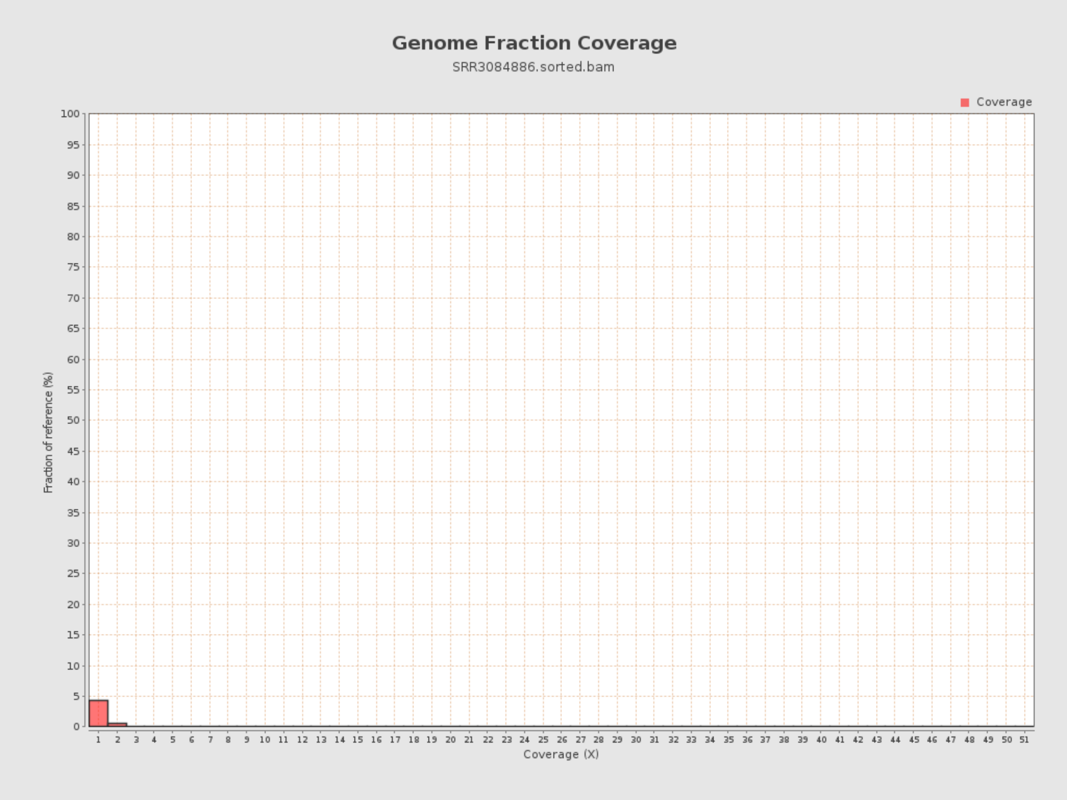
4. Results : Coverage Histogram



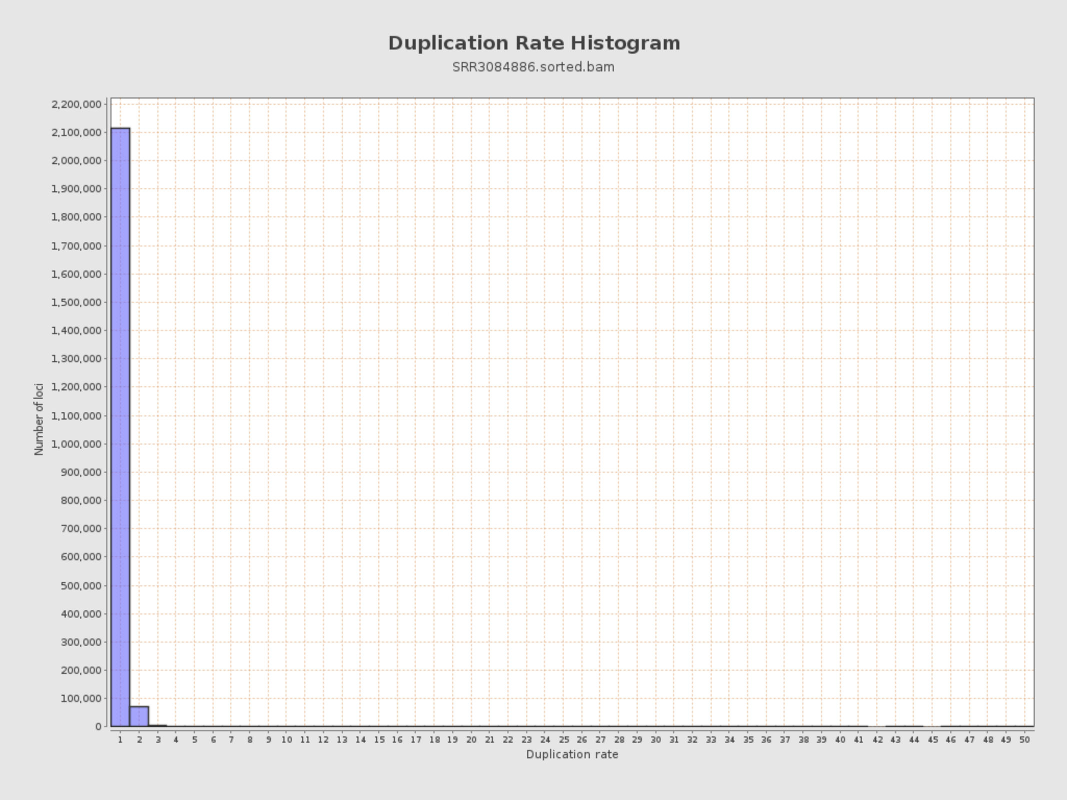
5. Results : Coverage Histogram (0-50X)



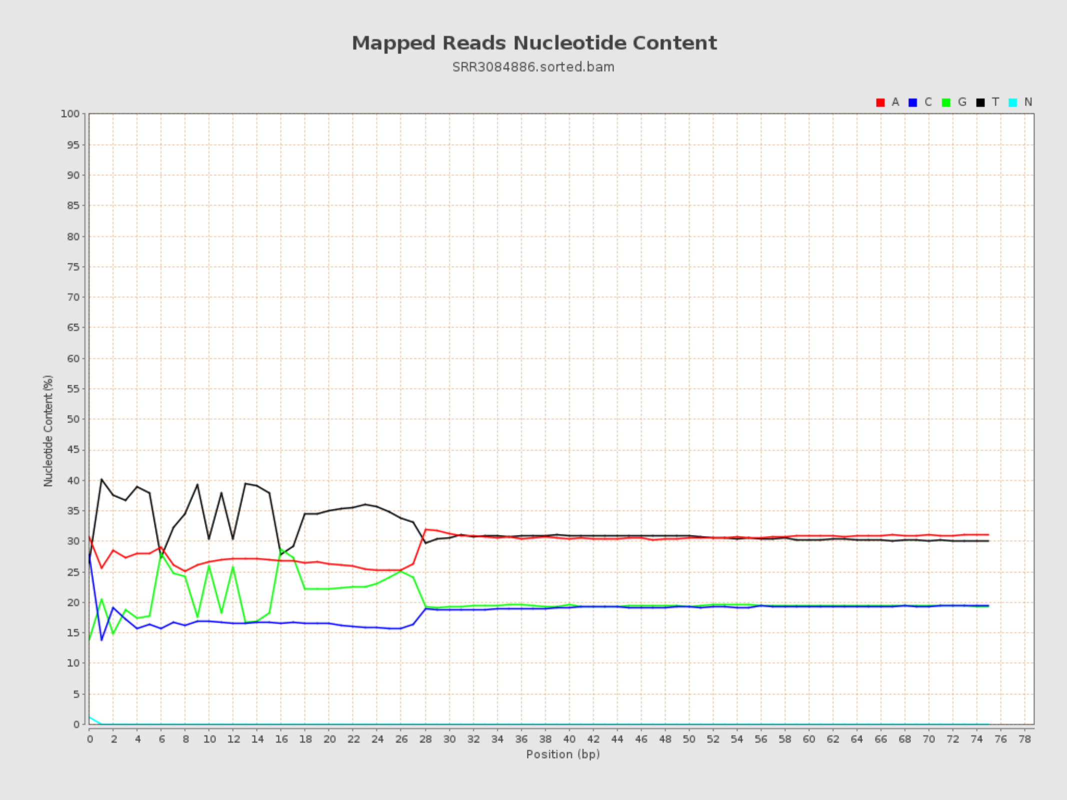
6. Results : Genome Fraction Coverage



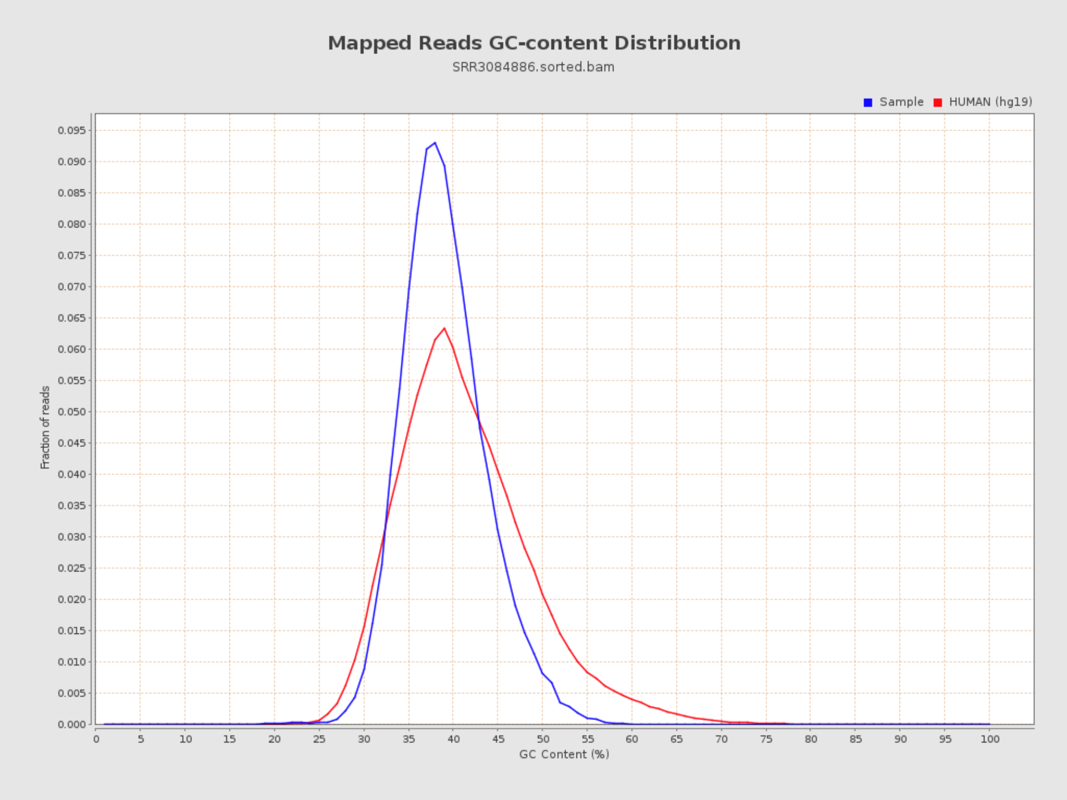
7. Results : Duplication Rate Histogram



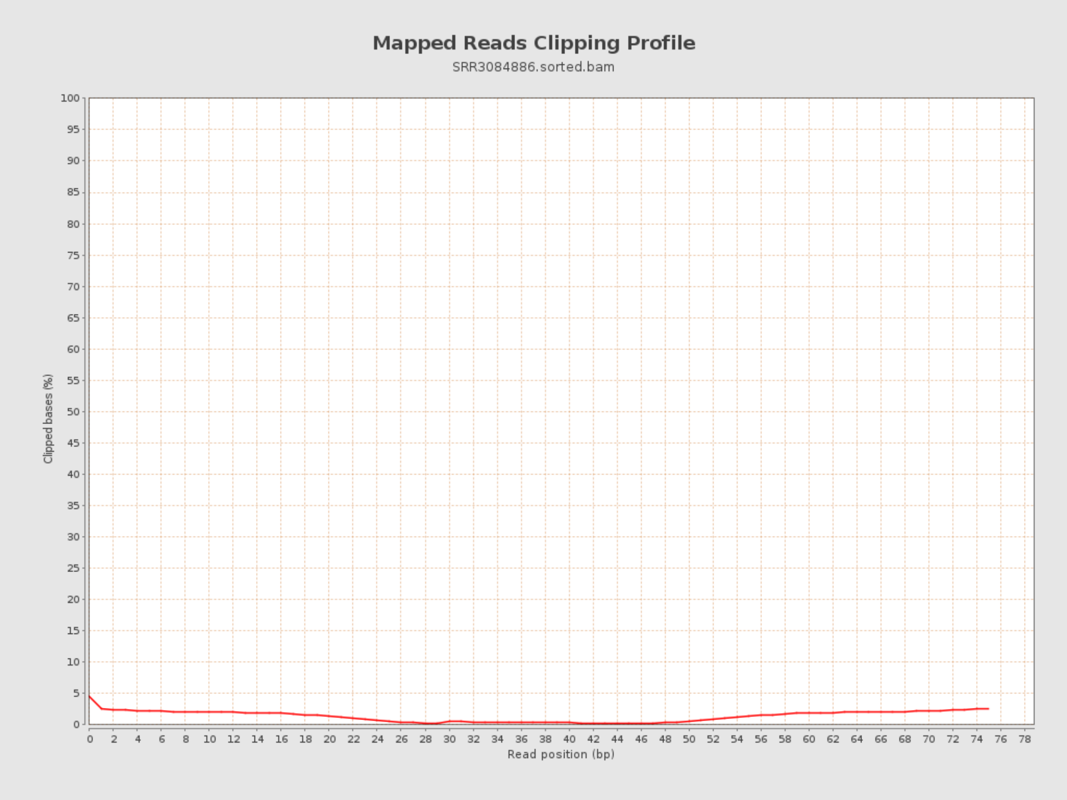
8. Results : Mapped Reads Nucleotide Content



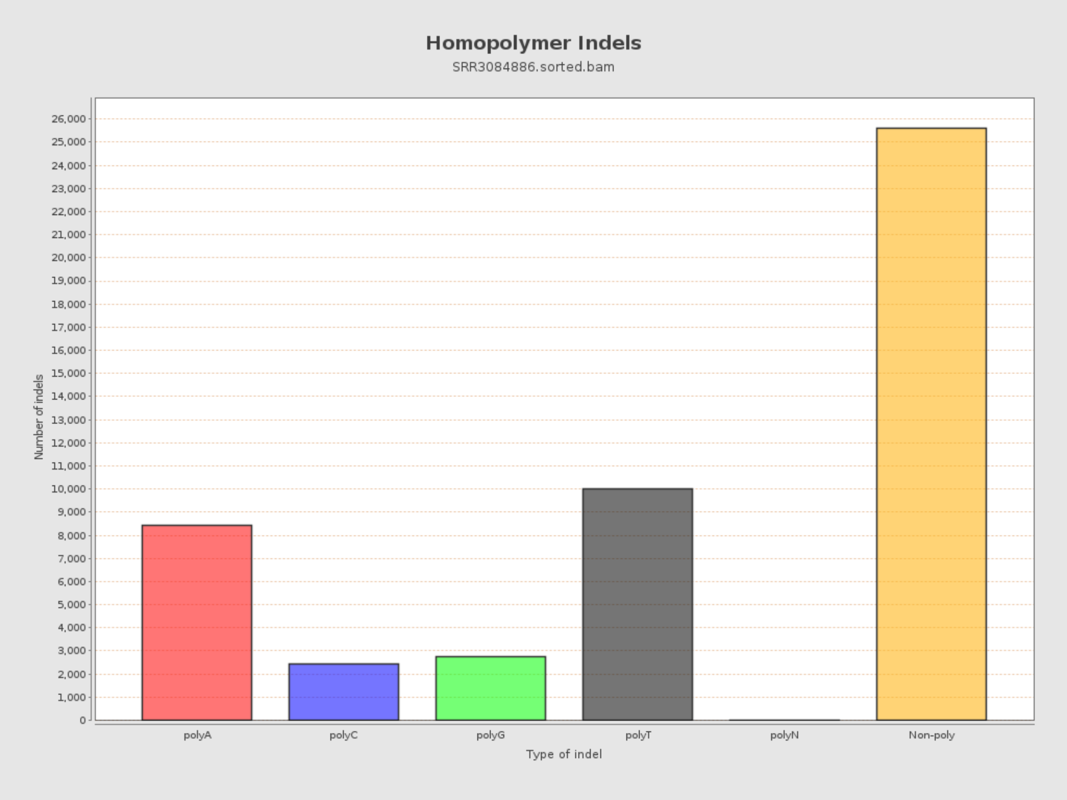
9. Results : Mapped Reads GC-content Distribution



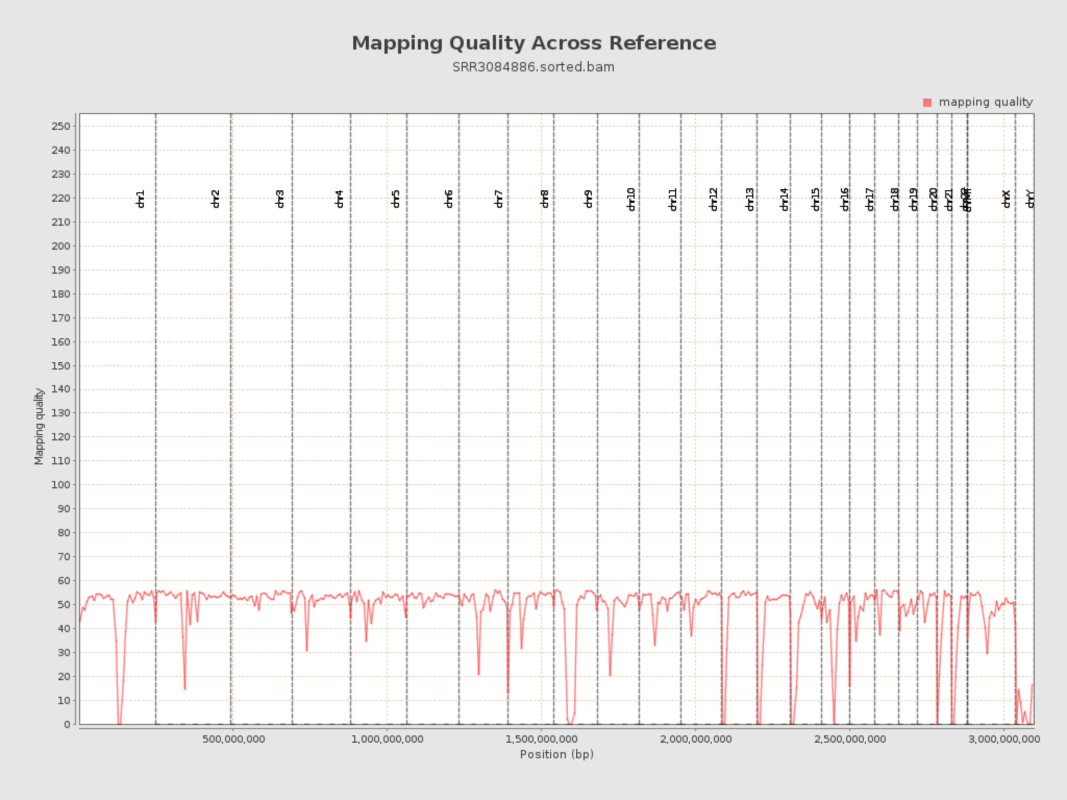
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram