Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:45:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084871.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_SRR3084871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084871.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:45:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,736,781
Mapped reads	2,493,789 / 91.12%
Unmapped reads	242,992 / 8.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,945 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	122,363 / 4.47%
Duplication rate	4.02%
Clipped reads	820,097 / 29.97%

2.2. ACGT Content

Number/percentage of A's	50,732,160 / 29.28%
Number/percentage of C's	31,571,781 / 18.22%
Number/percentage of T's	55,835,270 / 32.23%
Number/percentage of G's	35,097,285 / 20.26%
Number/percentage of N's	27,032 / 0.02%
GC Percentage	38.48%

2.3. Coverage

Mean	0.056

Standard Deviation	0.4908

2.4. Mapping Quality

Mean Mapping Quality	46.97

2.5. Mismatches and indels

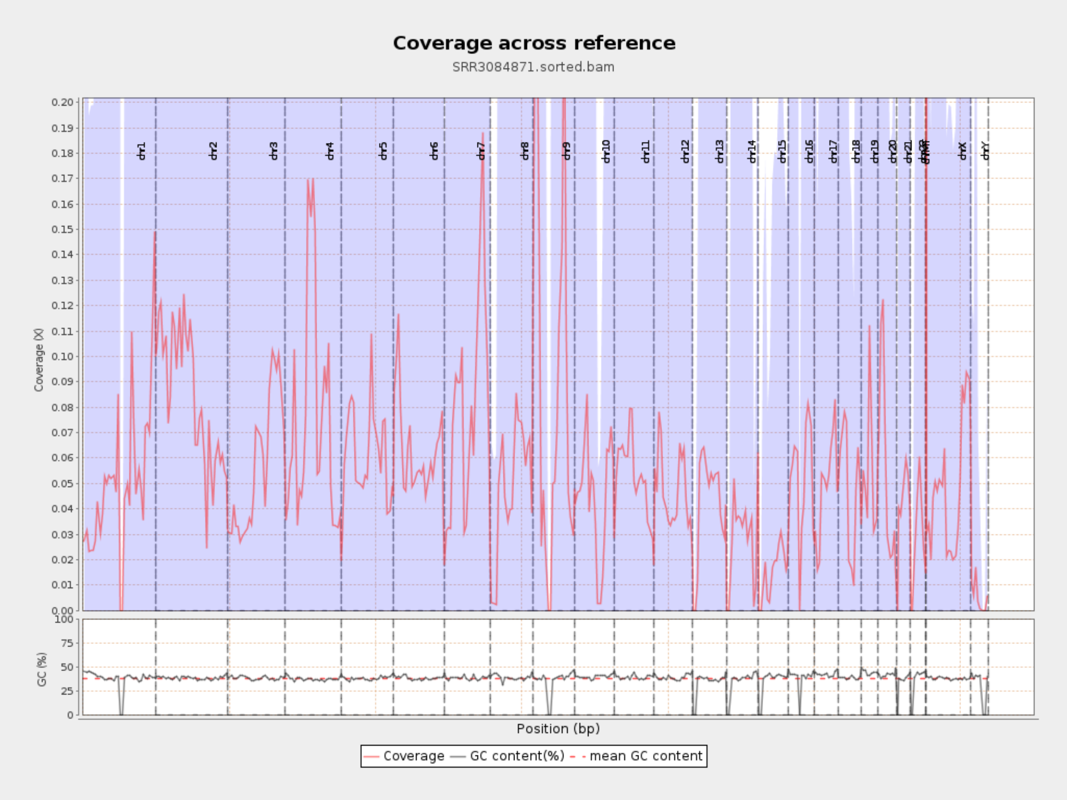
General error rate	0.84%
Mismatches	1,428,431
Insertions	13,963
Mapped reads with at least one insertion	0.56%
Deletions	38,255
Mapped reads with at least one deletion	1.52%
Homopolymer indels	48.53%

2.6. Chromosome stats

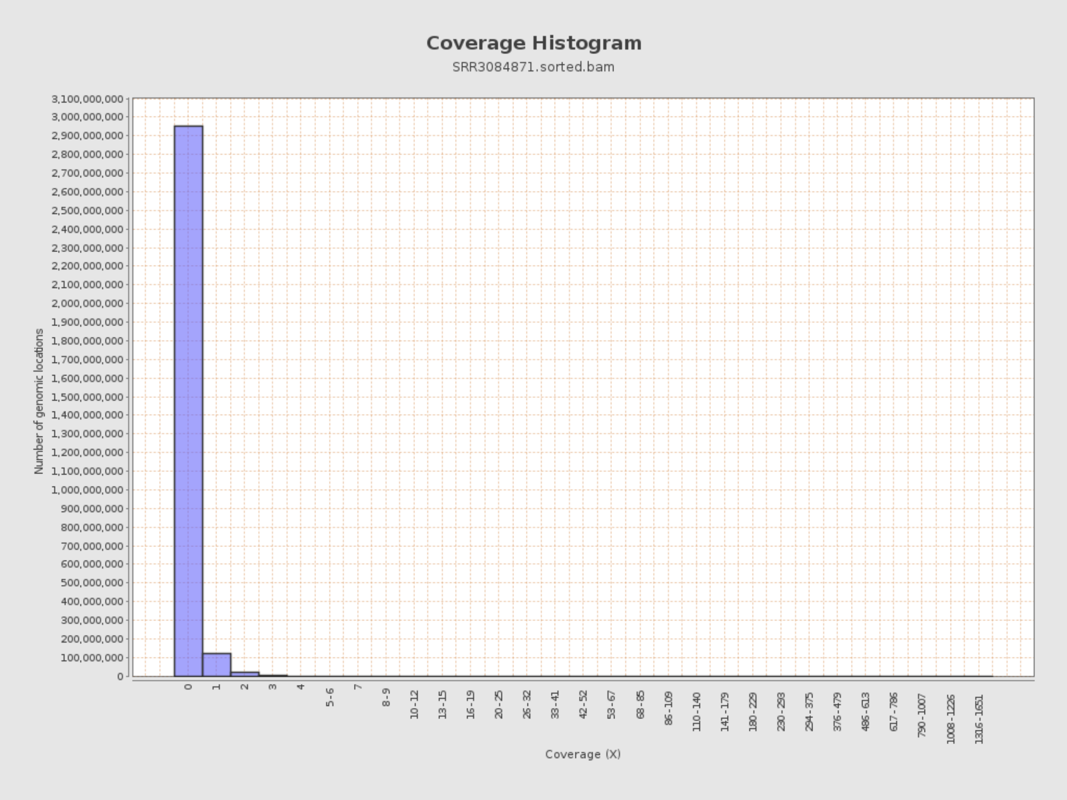
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12881045	0.0517	0.9436
chr2	243199373	20504996	0.0843	0.4924
chr3	198022430	11204038	0.0566	0.2758
chr4	191154276	14270642	0.0747	0.3318
chr5	180915260	11146669	0.0616	0.2942
chr6	171115067	10871302	0.0635	0.3007
chr7	159138663	12797174	0.0804	0.5095

chr8	146364022	7249339	0.0495	1.0824
chr9	141213431	12757765	0.0903	0.4602
chr10	135534747	6166815	0.0455	0.3967
chr11	135006516	7247286	0.0537	0.3826
chr12	133851895	6352983	0.0475	0.253
chr13	115169878	4811763	0.0418	0.2347
chr14	107349540	2899686	0.027	0.2019
chr15	102531392	1516792	0.0148	0.1395
chr16	90354753	4571815	0.0506	0.2767
chr17	81195210	3984920	0.0491	0.2704
chr18	78077248	3859717	0.0494	0.6978
chr19	59128983	3250937	0.055	0.5368
chr20	63025520	3605122	0.0572	0.2878
chr21	48129895	2069355	0.043	0.2547
chr22	51304566	1514570	0.0295	0.1951
chrMT	16571	84427	5.0949	3.4433
chrX	155270560	7398883	0.0477	0.2749
chrY	59373566	312935	0.0053	0.1202

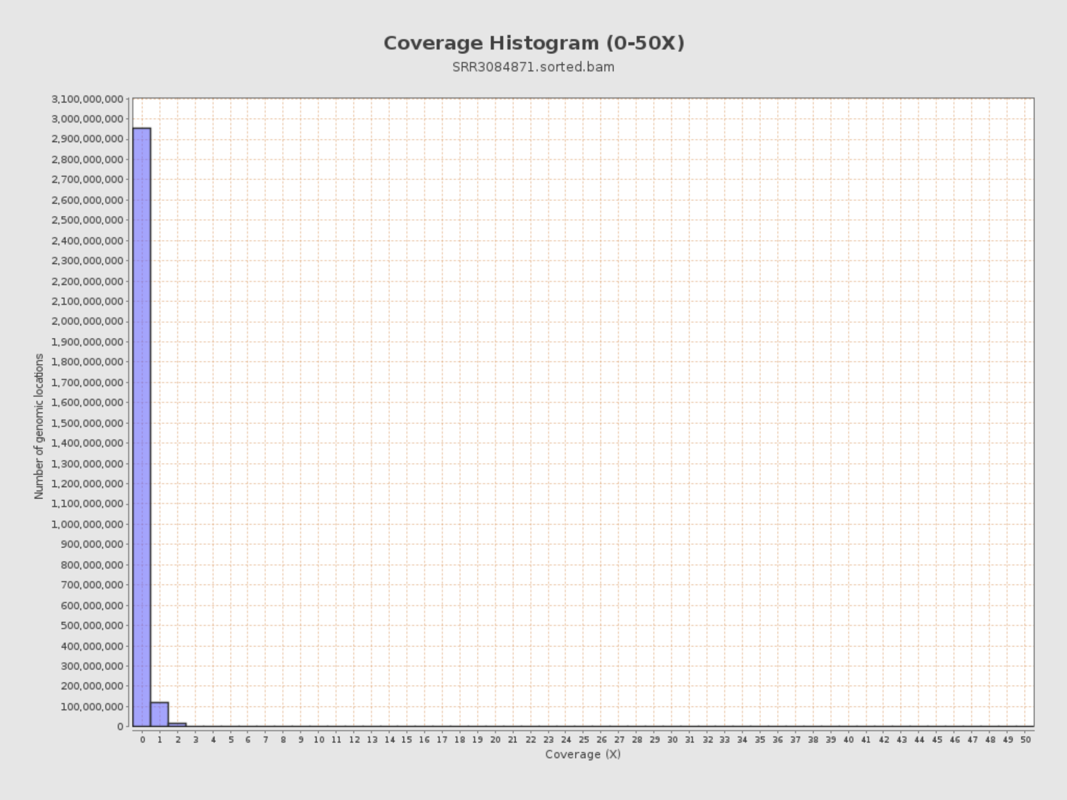
3. Results : Coverage across reference



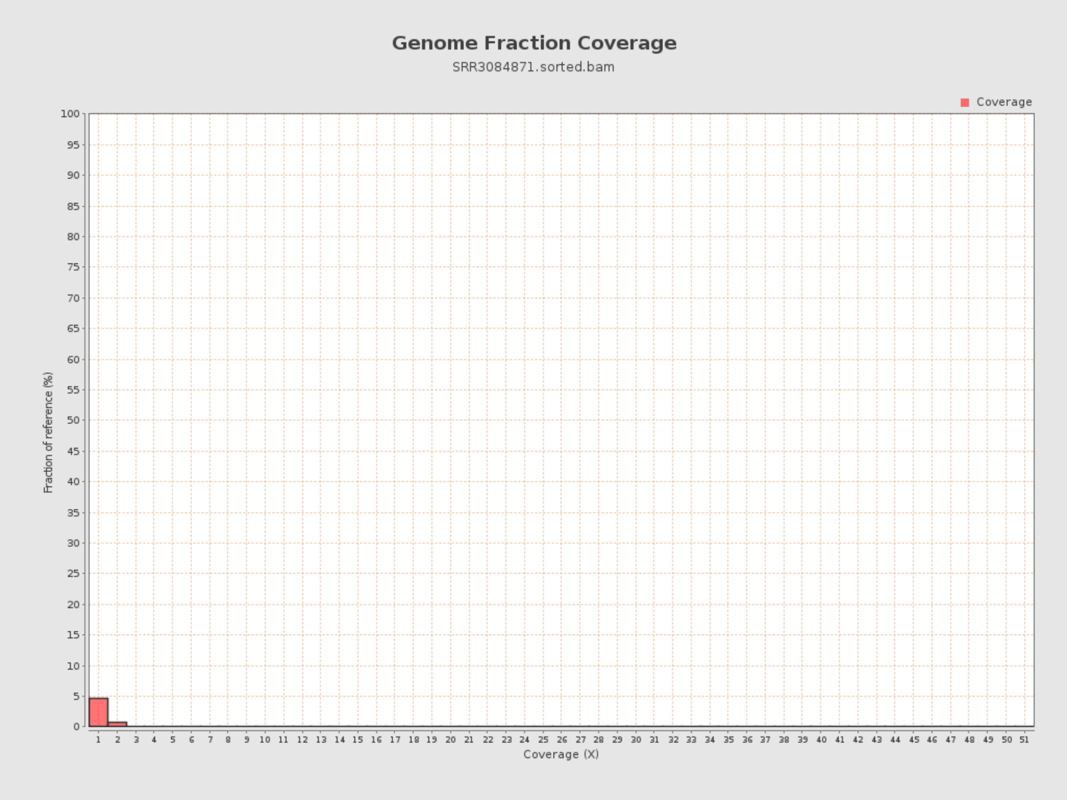
4. Results : Coverage Histogram



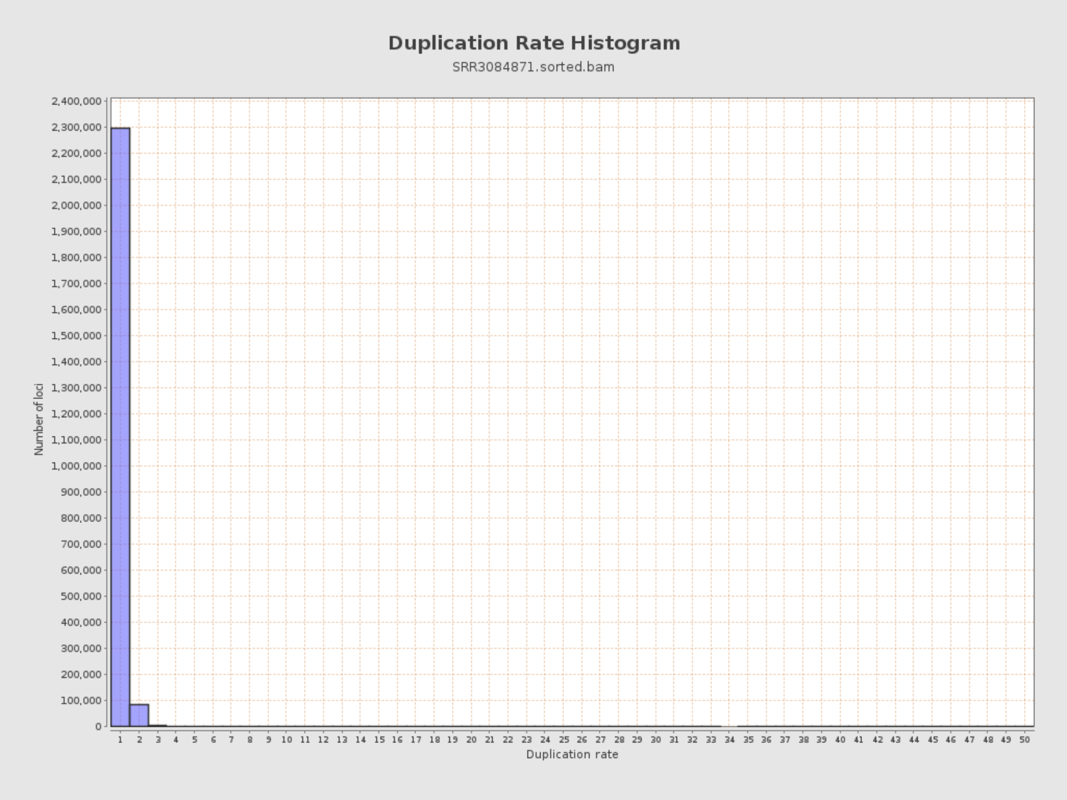
5. Results : Coverage Histogram (0-50X)



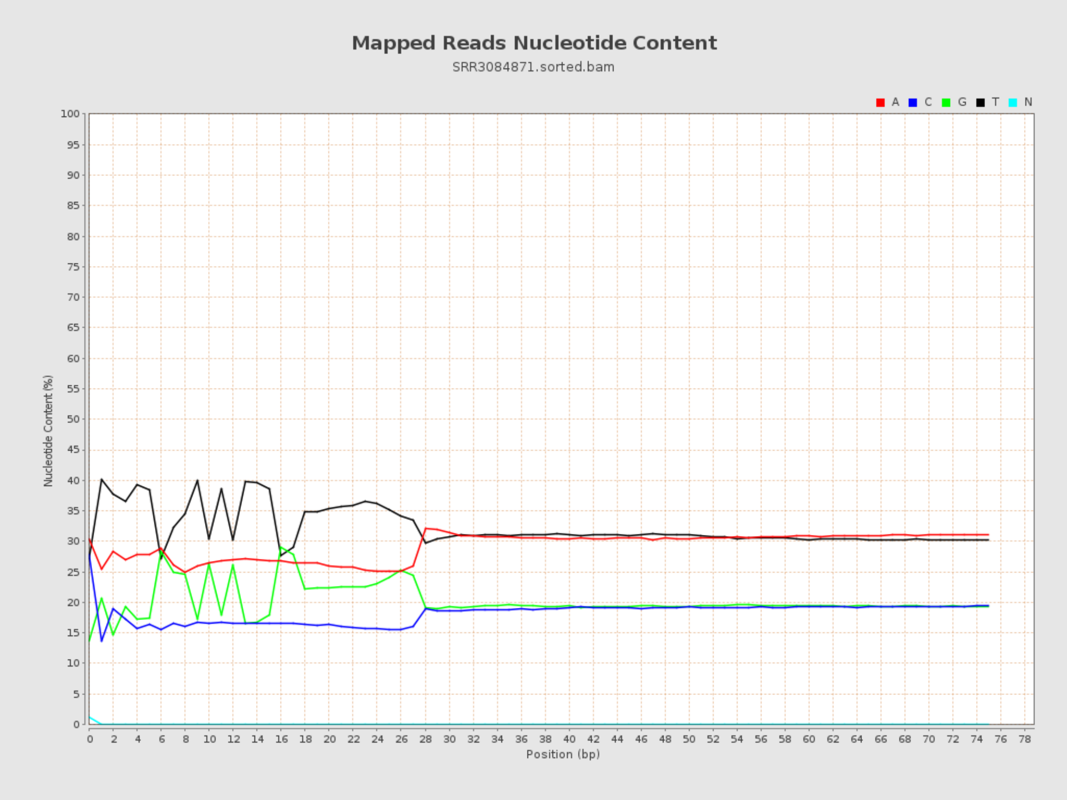
6. Results : Genome Fraction Coverage



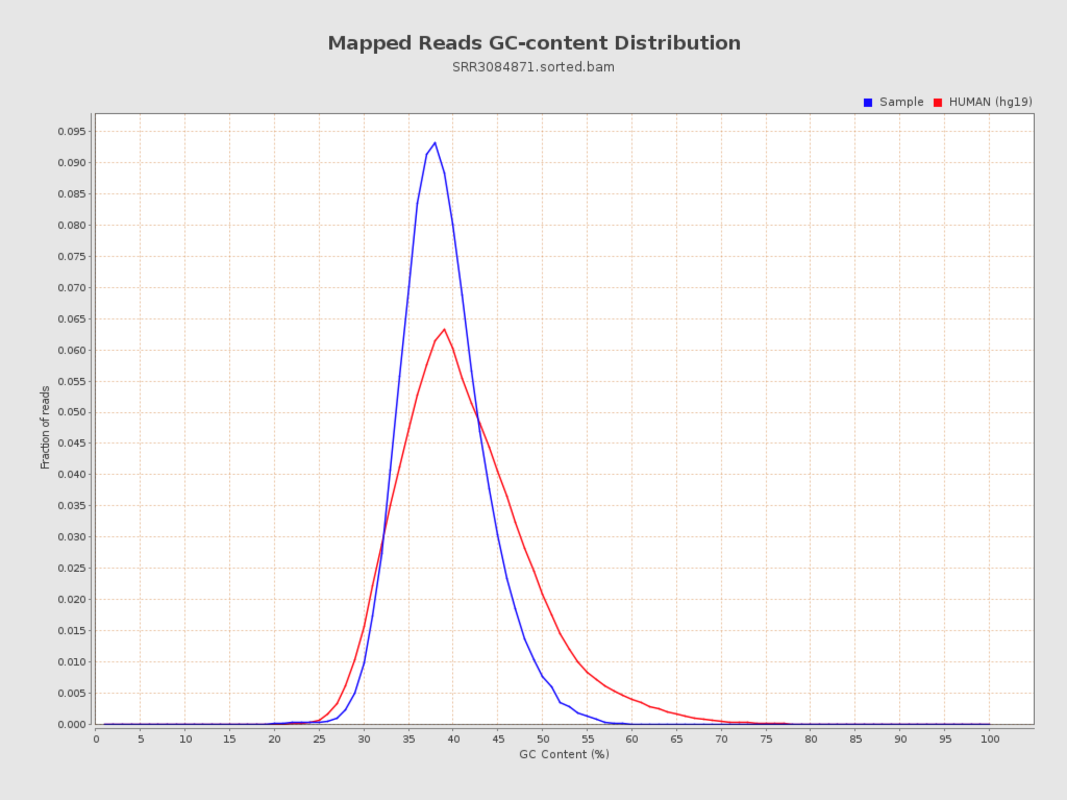
7. Results : Duplication Rate Histogram



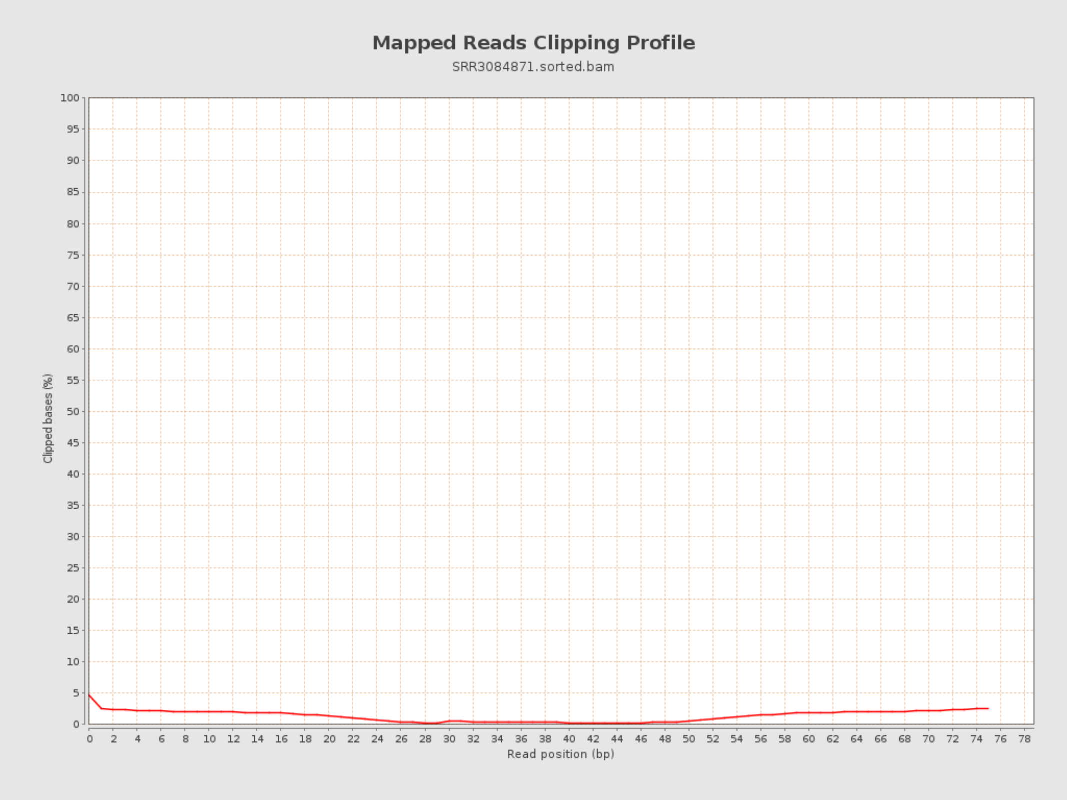
8. Results : Mapped Reads Nucleotide Content



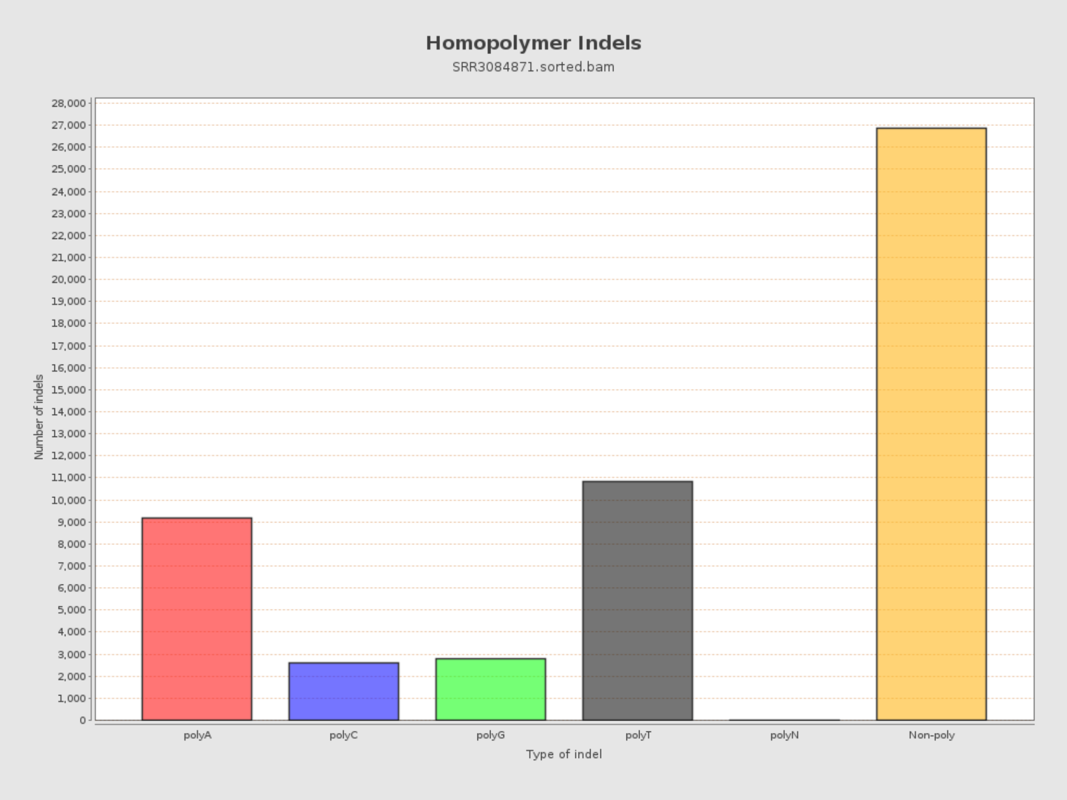
9. Results : Mapped Reads GC-content Distribution



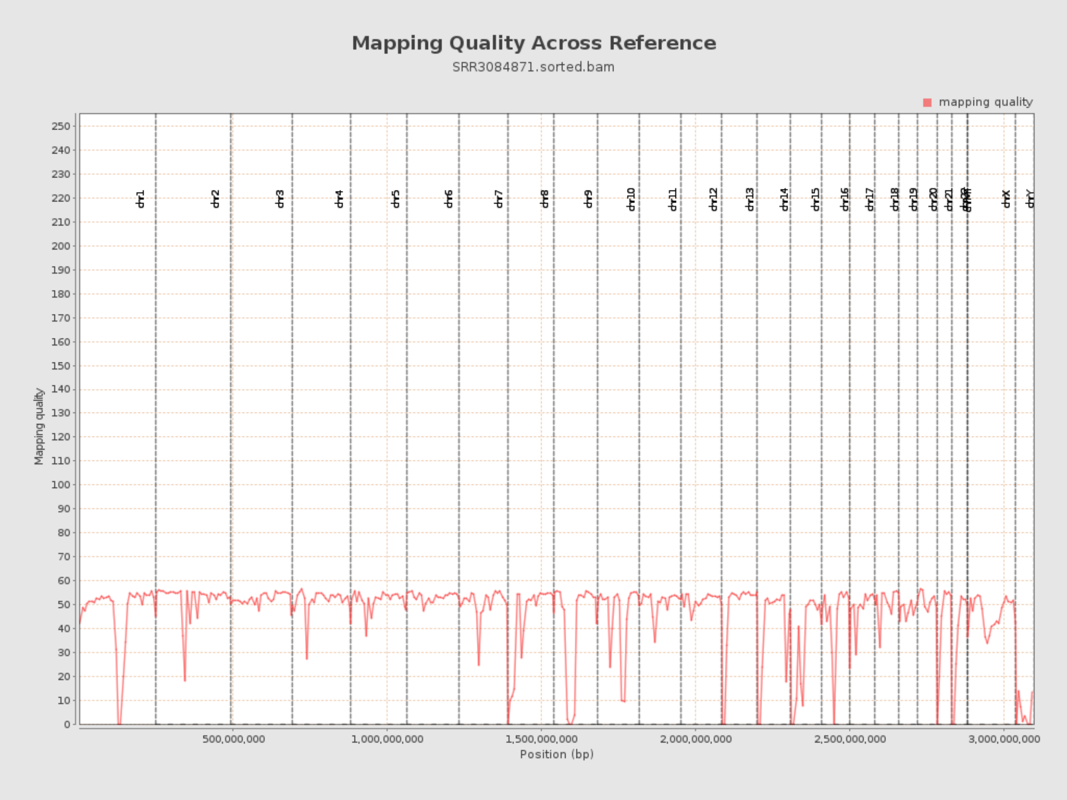
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram