Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 18:41:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084870.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_SRR3084870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084870.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 18:41:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,478,173
Mapped reads	2,216,419 / 89.44%
Unmapped reads	261,754 / 10.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,046 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	101,298 / 4.09%
Duplication rate	3.69%
Clipped reads	743,504 / 30%

2.2. ACGT Content

Number/percentage of A's	44,709,146 / 29.09%
Number/percentage of C's	28,323,075 / 18.43%
Number/percentage of T's	49,088,123 / 31.94%
Number/percentage of G's	31,537,715 / 20.52%
Number/percentage of N's	24,086 / 0.02%
GC Percentage	38.95%

2.3. Coverage

Mean	0.0497

Standard Deviation	0.4573

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

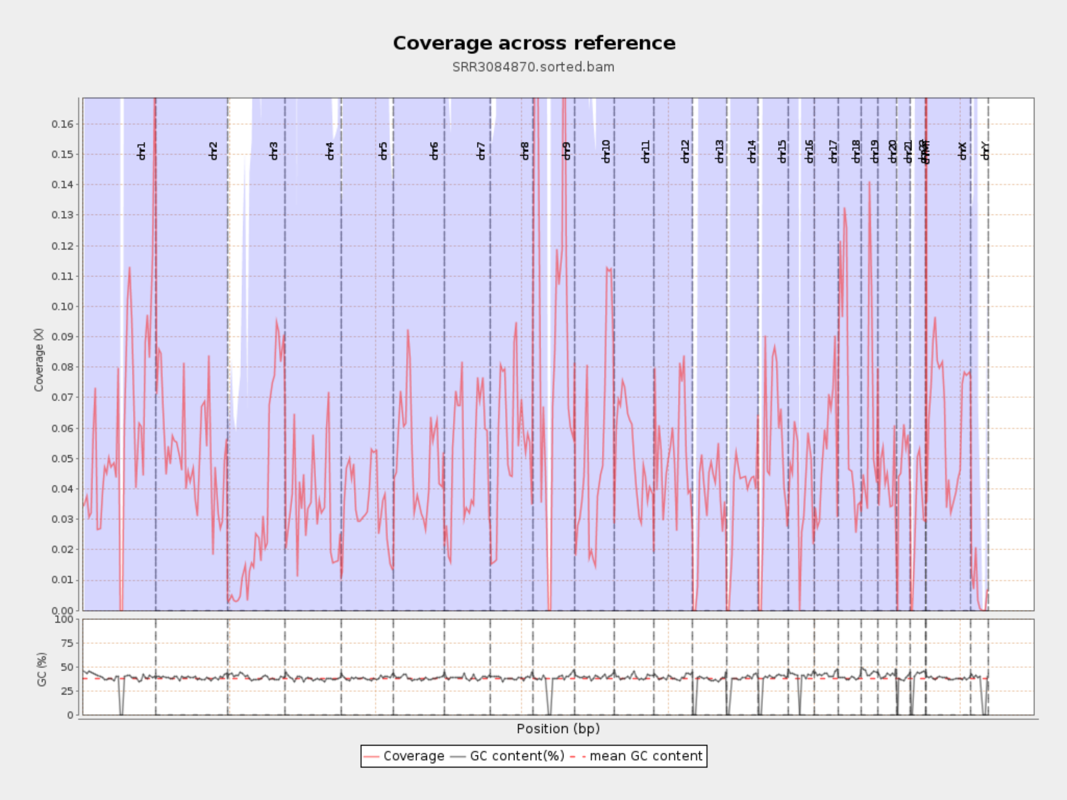
General error rate	0.86%
Mismatches	1,293,795
Insertions	12,676
Mapped reads with at least one insertion	0.57%
Deletions	34,443
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.61%

2.6. Chromosome stats

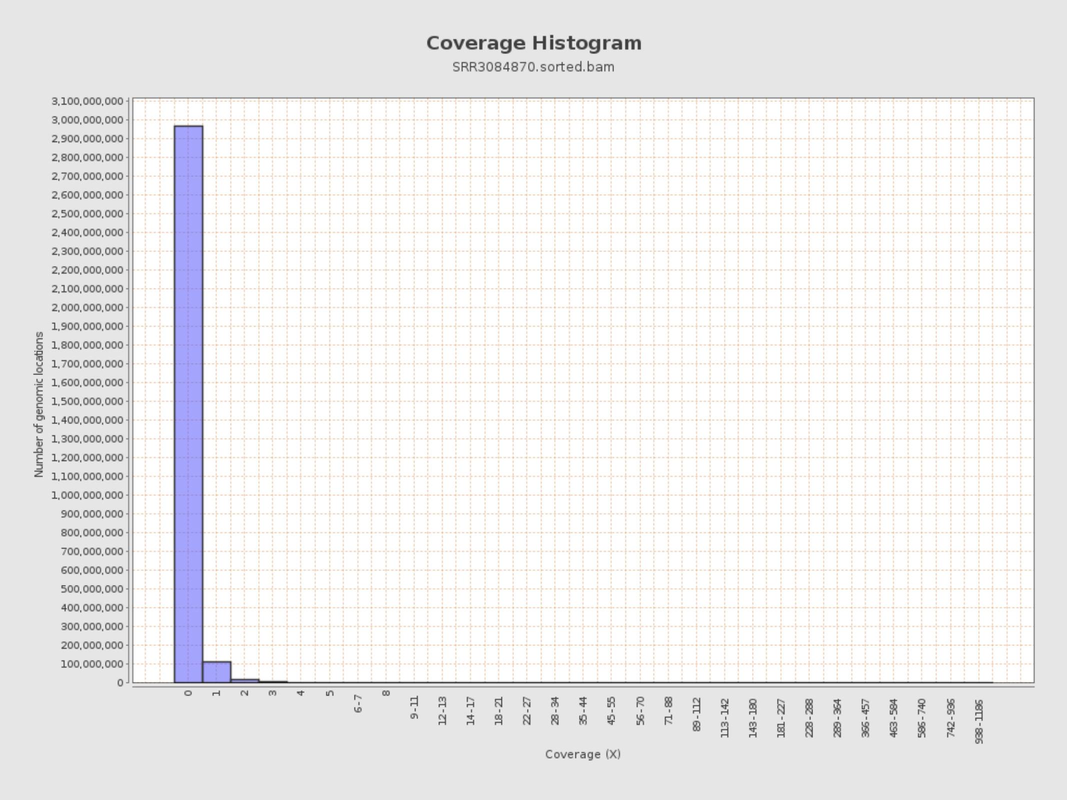
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15153516	0.0608	1.0196
chr2	243199373	12692267	0.0522	0.4381
chr3	198022430	6417751	0.0324	0.2088
chr4	191154276	6629997	0.0347	0.231
chr5	180915260	6262036	0.0346	0.2254
chr6	171115067	8792108	0.0514	0.2635
chr7	159138663	7845934	0.0493	0.409

chr8	146364022	8100994	0.0553	0.7389
chr9	141213431	13276492	0.094	0.4756
chr10	135534747	6953651	0.0513	0.3642
chr11	135006516	7000855	0.0519	0.3198
chr12	133851895	7126898	0.0532	0.2688
chr13	115169878	4021373	0.0349	0.21
chr14	107349540	3959311	0.0369	0.2336
chr15	102531392	5210544	0.0508	0.256
chr16	90354753	3600751	0.0399	0.264
chr17	81195210	4363948	0.0537	0.2758
chr18	78077248	5617714	0.072	0.744
chr19	59128983	3795454	0.0642	0.553
chr20	63025520	2768439	0.0439	0.2508
chr21	48129895	2222052	0.0462	0.2705
chr22	51304566	1537993	0.03	0.1934
chrMT	16571	226465	13.6663	6.8724
chrX	155270560	9802368	0.0631	0.309
chrY	59373566	364355	0.0061	0.1661

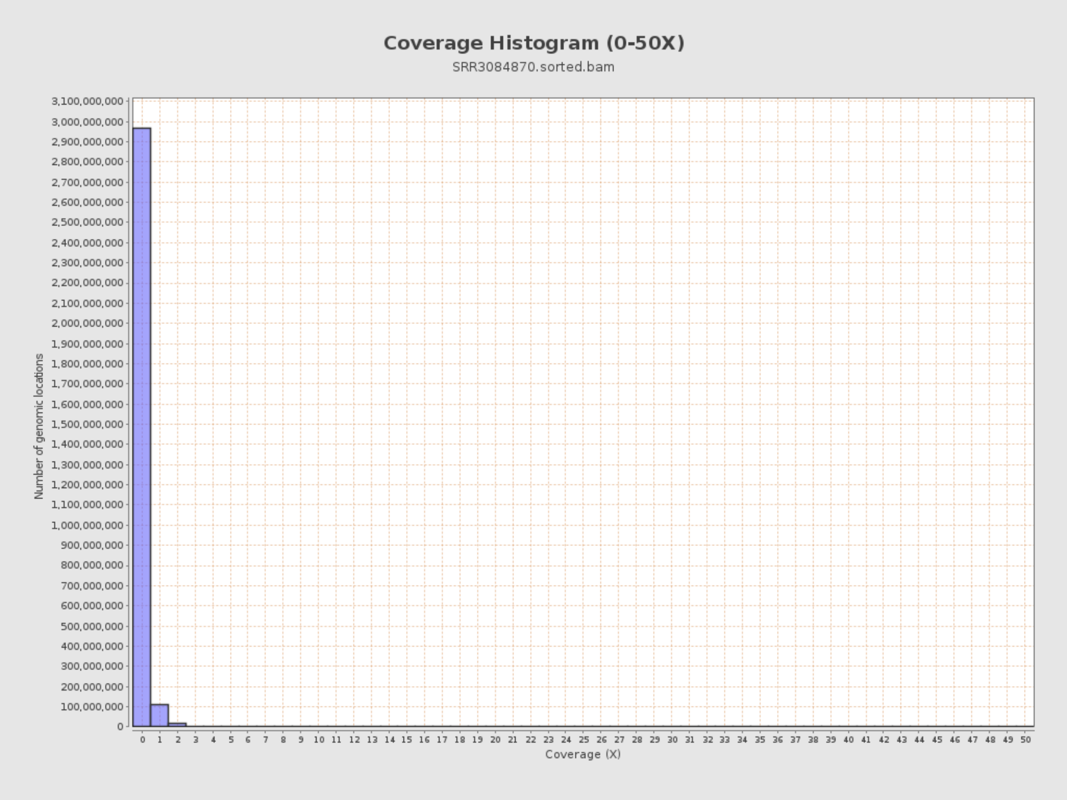
3. Results : Coverage across reference



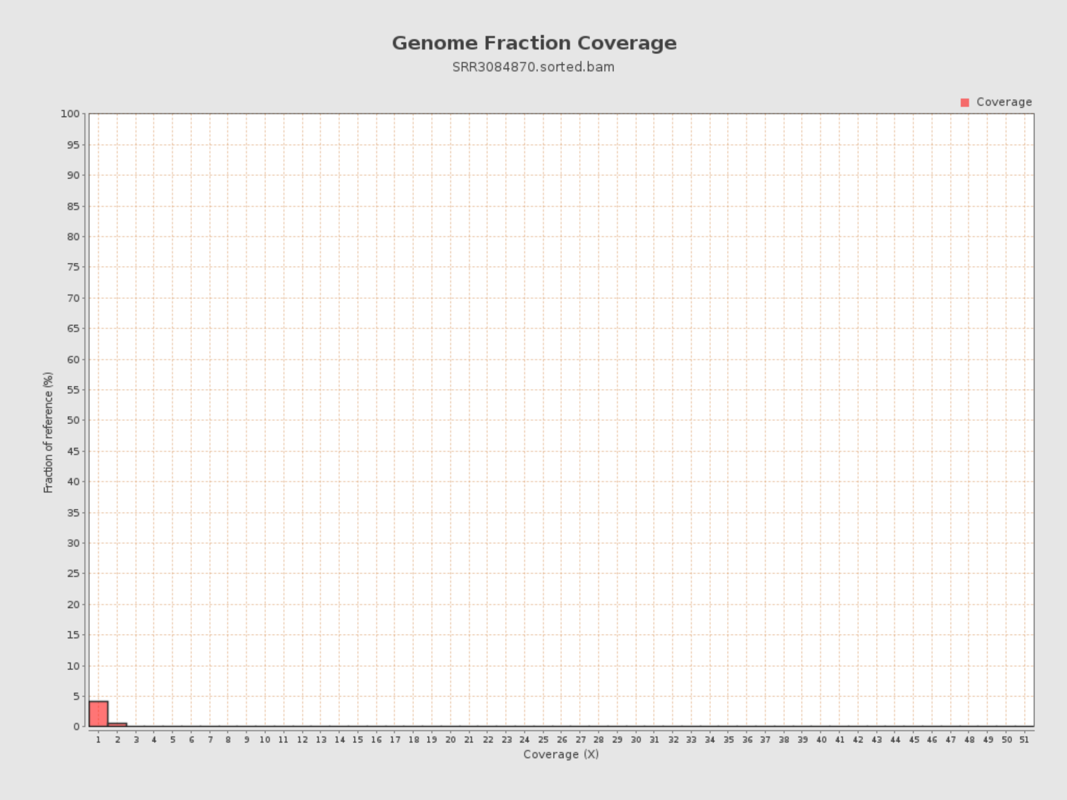
4. Results : Coverage Histogram



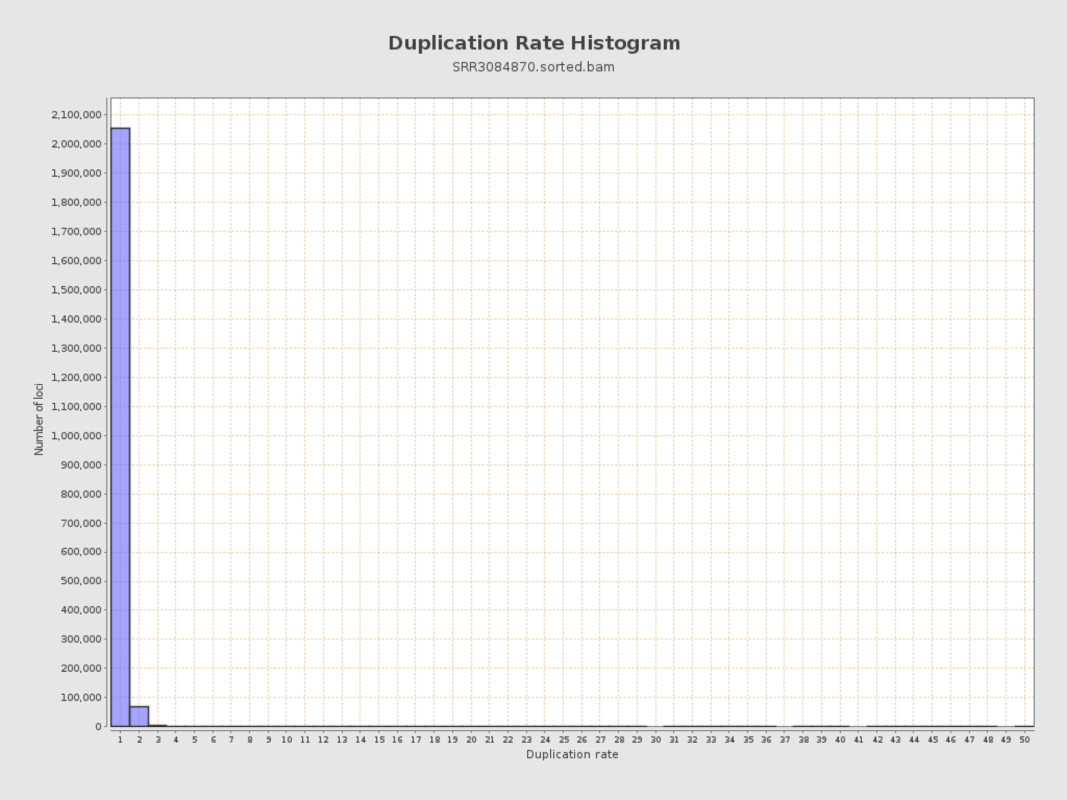
5. Results : Coverage Histogram (0-50X)



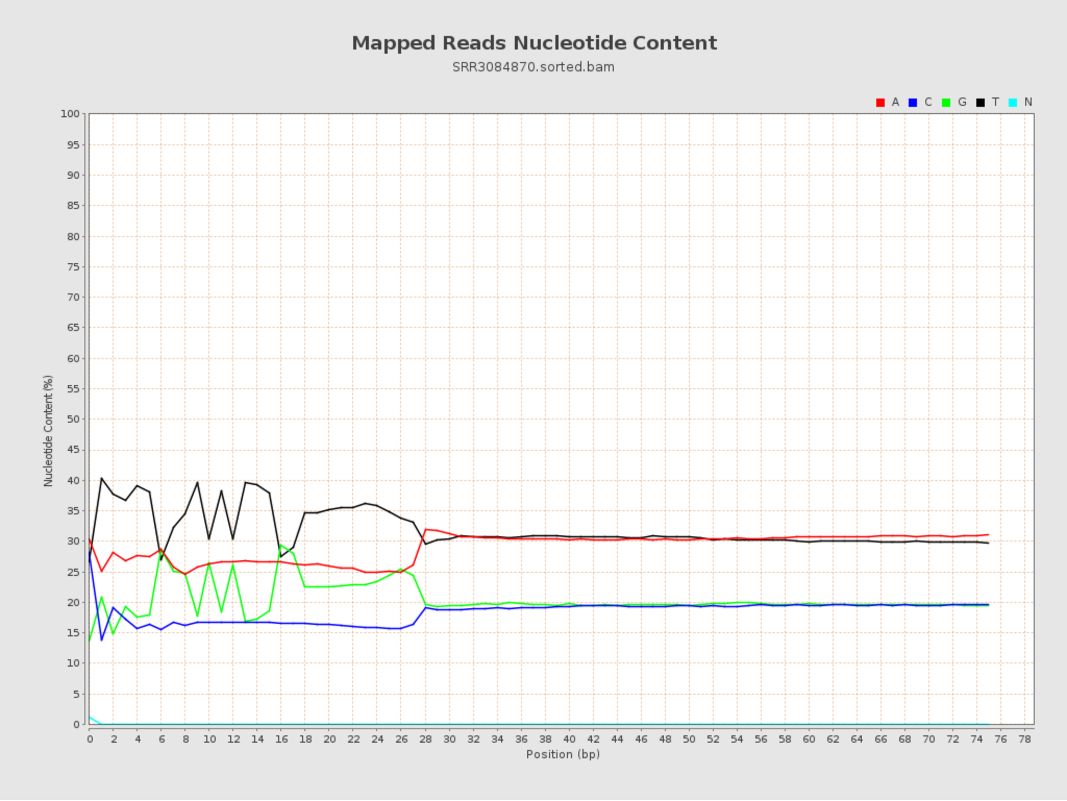
6. Results : Genome Fraction Coverage



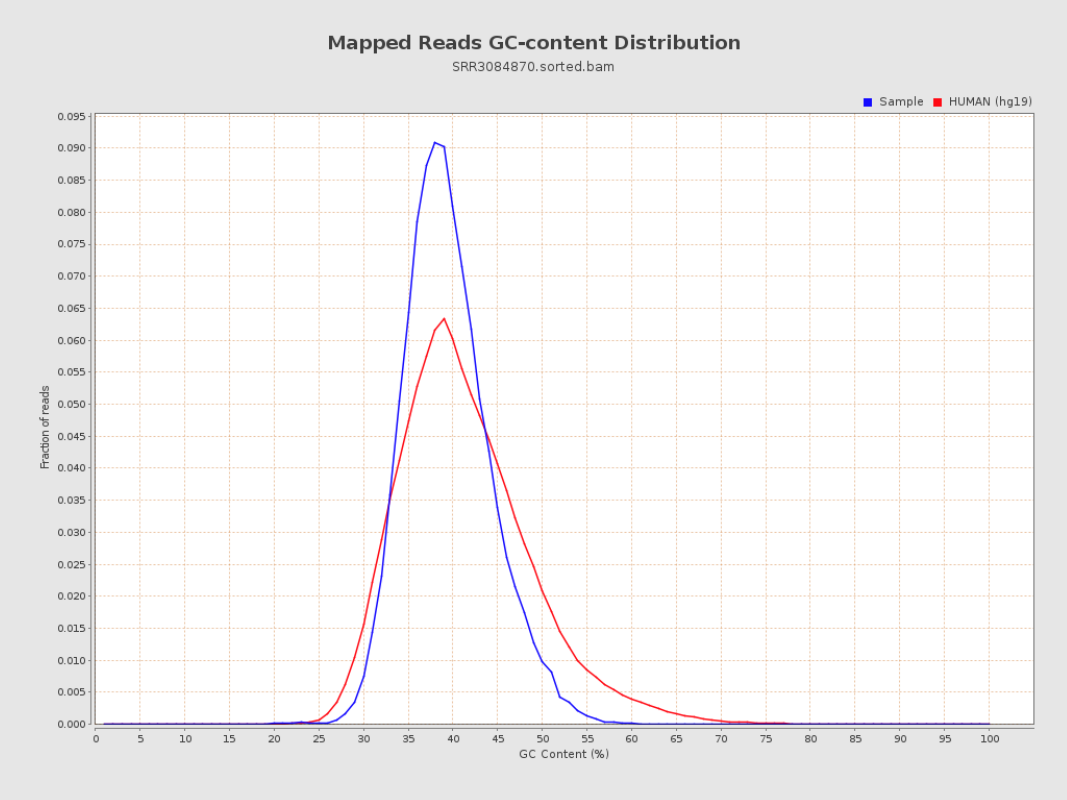
7. Results : Duplication Rate Histogram



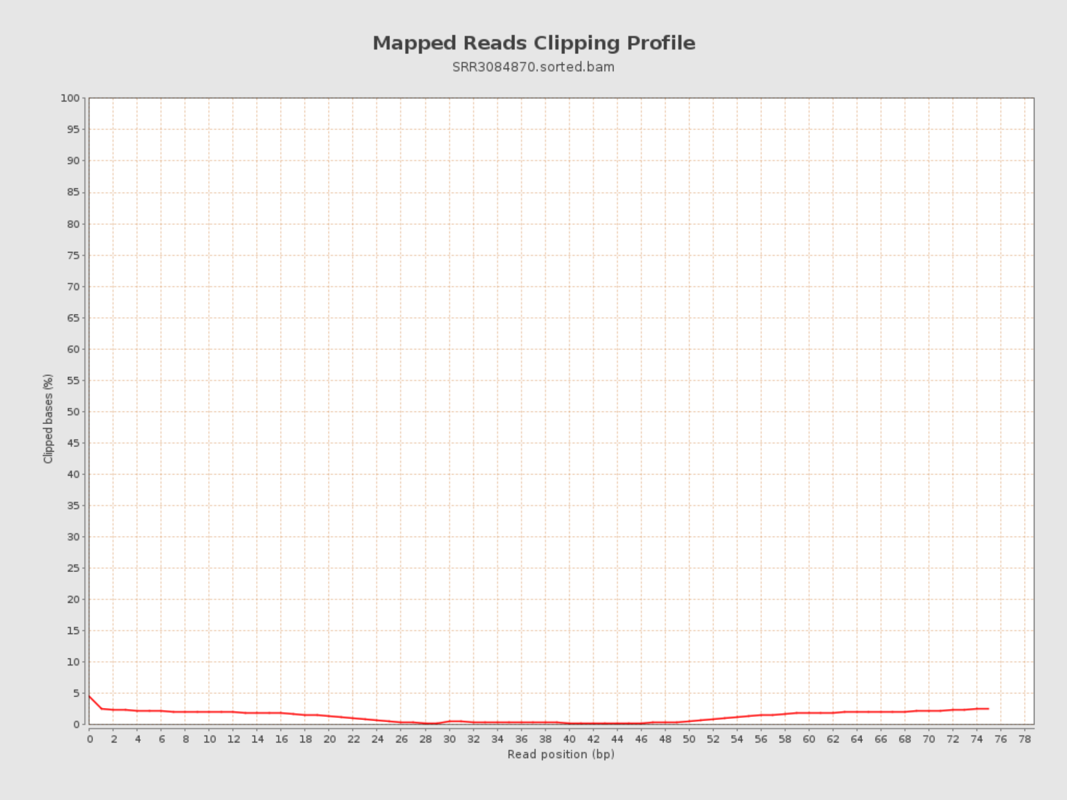
8. Results : Mapped Reads Nucleotide Content



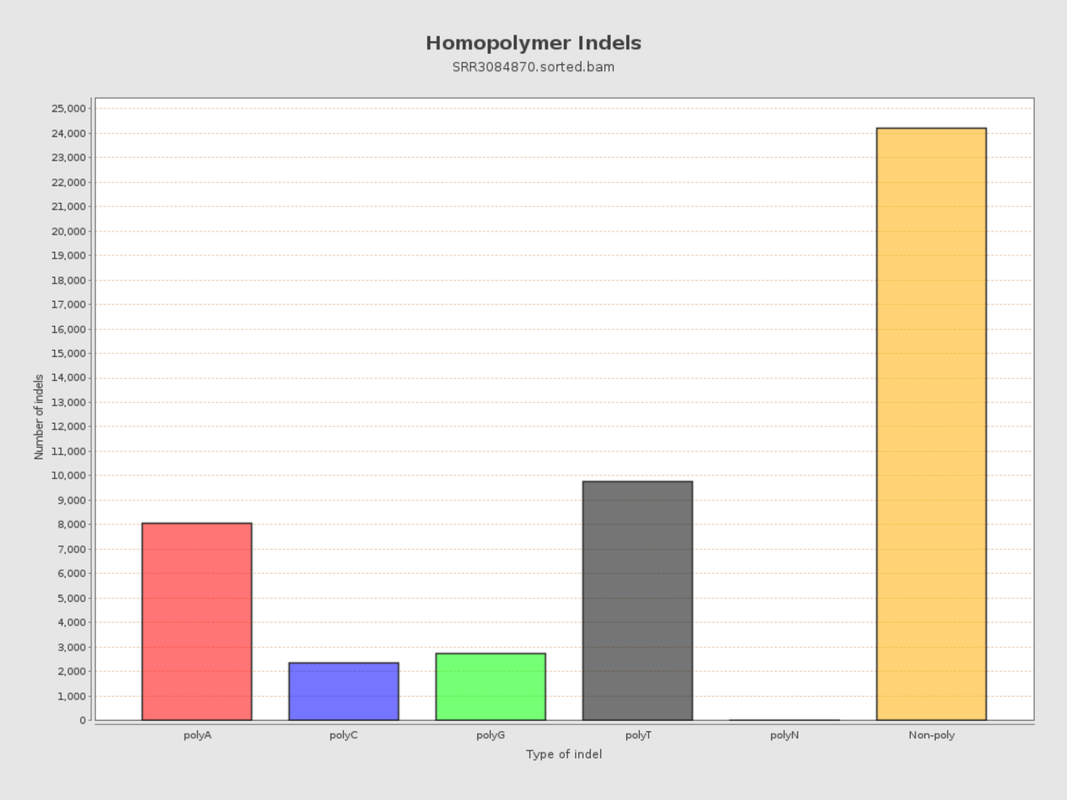
9. Results : Mapped Reads GC-content Distribution



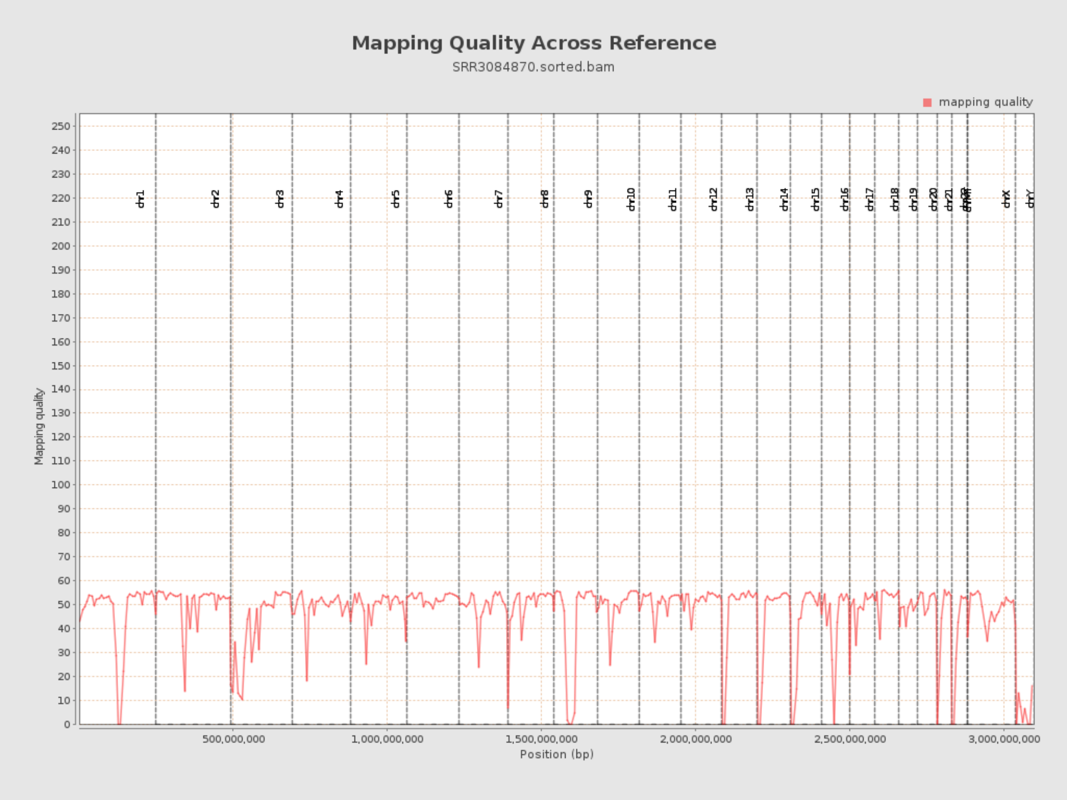
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram