Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:57:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084270.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_SRR3084270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084270.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:57:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,073,975
Mapped reads	887,865 / 82.67%
Unmapped reads	186,110 / 17.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,022 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	21,590 / 2.01%
Duplication rate	2.03%
Clipped reads	453,612 / 42.24%

2.2. ACGT Content

Number/percentage of A's	16,640,223 / 28.98%
Number/percentage of C's	10,616,291 / 18.49%
Number/percentage of T's	17,510,989 / 30.5%
Number/percentage of G's	12,652,236 / 22.03%
Number/percentage of N's	682 / 0%
GC Percentage	40.52%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.1732

2.4. Mapping Quality

Mean Mapping Quality	46.23

2.5. Mismatches and indels

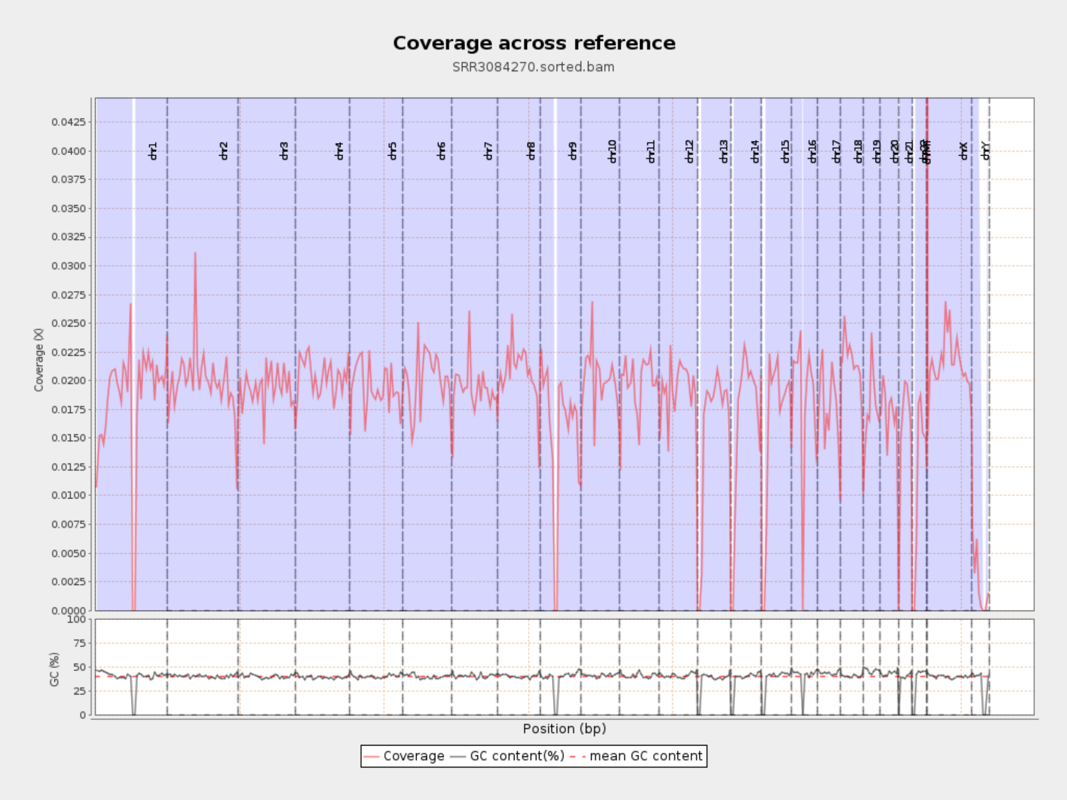
General error rate	0.86%
Mismatches	489,276
Insertions	4,238
Mapped reads with at least one insertion	0.47%
Deletions	12,224
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.85%

2.6. Chromosome stats

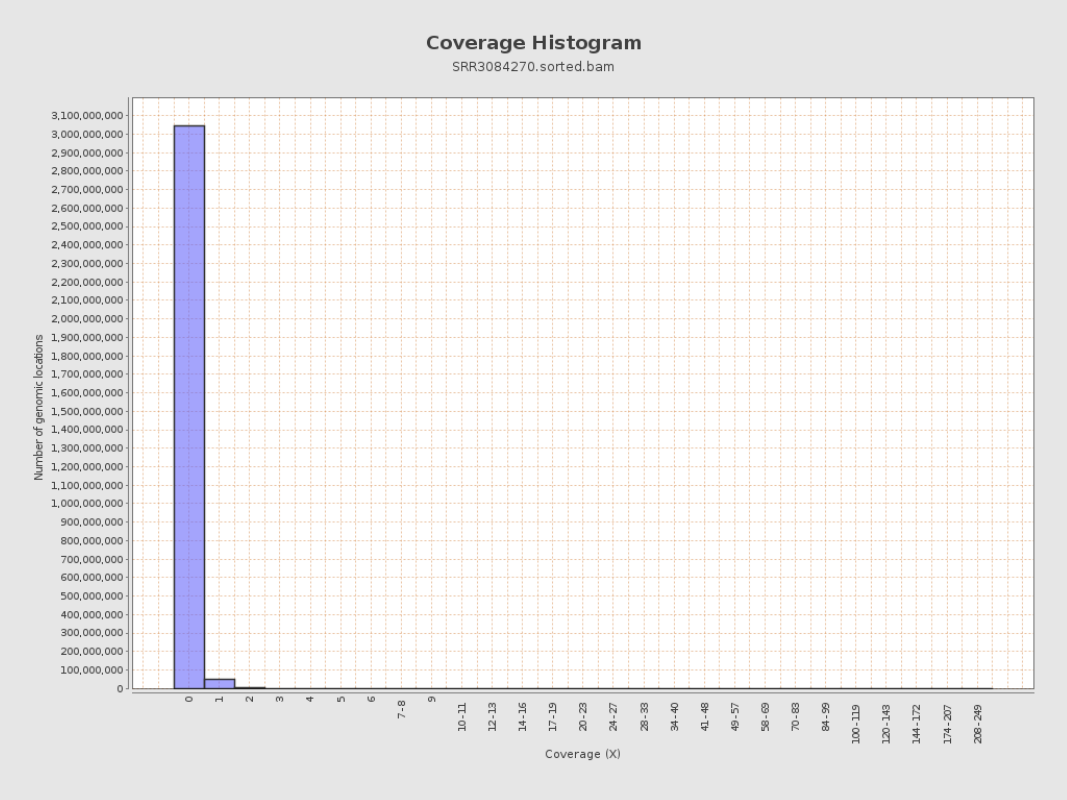
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4563640	0.0183	0.2332
chr2	243199373	4877047	0.0201	0.2047
chr3	198022430	3831745	0.0194	0.1469
chr4	191154276	3885922	0.0203	0.1524
chr5	180915260	3531535	0.0195	0.1476
chr6	171115067	3444554	0.0201	0.1627
chr7	159138663	3076954	0.0193	0.194

chr8	146364022	3034212	0.0207	0.1877
chr9	141213431	2239114	0.0159	0.1618
chr10	135534747	2728527	0.0201	0.1789
chr11	135006516	2689912	0.0199	0.1606
chr12	133851895	2583939	0.0193	0.1472
chr13	115169878	1797762	0.0156	0.132
chr14	107349540	1750355	0.0163	0.1396
chr15	102531392	1652039	0.0161	0.1357
chr16	90354753	1642888	0.0182	0.1516
chr17	81195210	1442508	0.0178	0.1499
chr18	78077248	1700171	0.0218	0.3044
chr19	59128983	1048482	0.0177	0.1971
chr20	63025520	1082652	0.0172	0.1398
chr21	48129895	762565	0.0158	0.1354
chr22	51304566	589220	0.0115	0.1127
chrMT	16571	4037	0.2436	0.497
chrX	155270560	3345455	0.0215	0.1609
chrY	59373566	134390	0.0023	0.0576

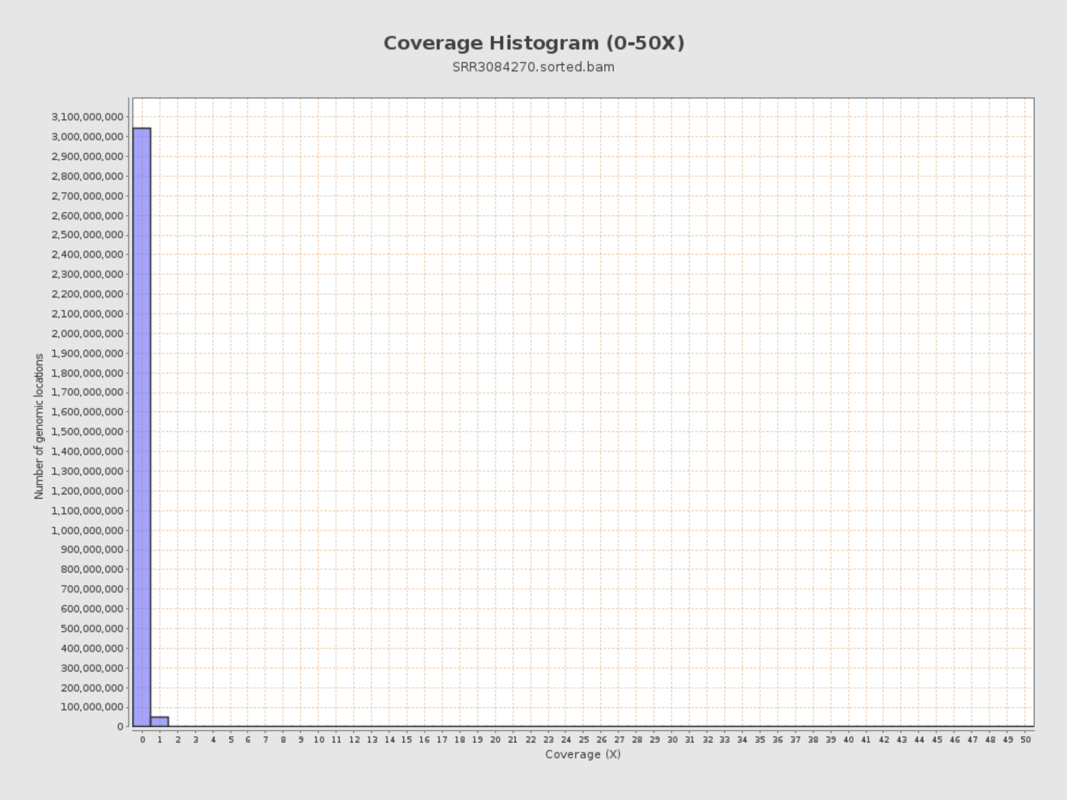
3. Results : Coverage across reference



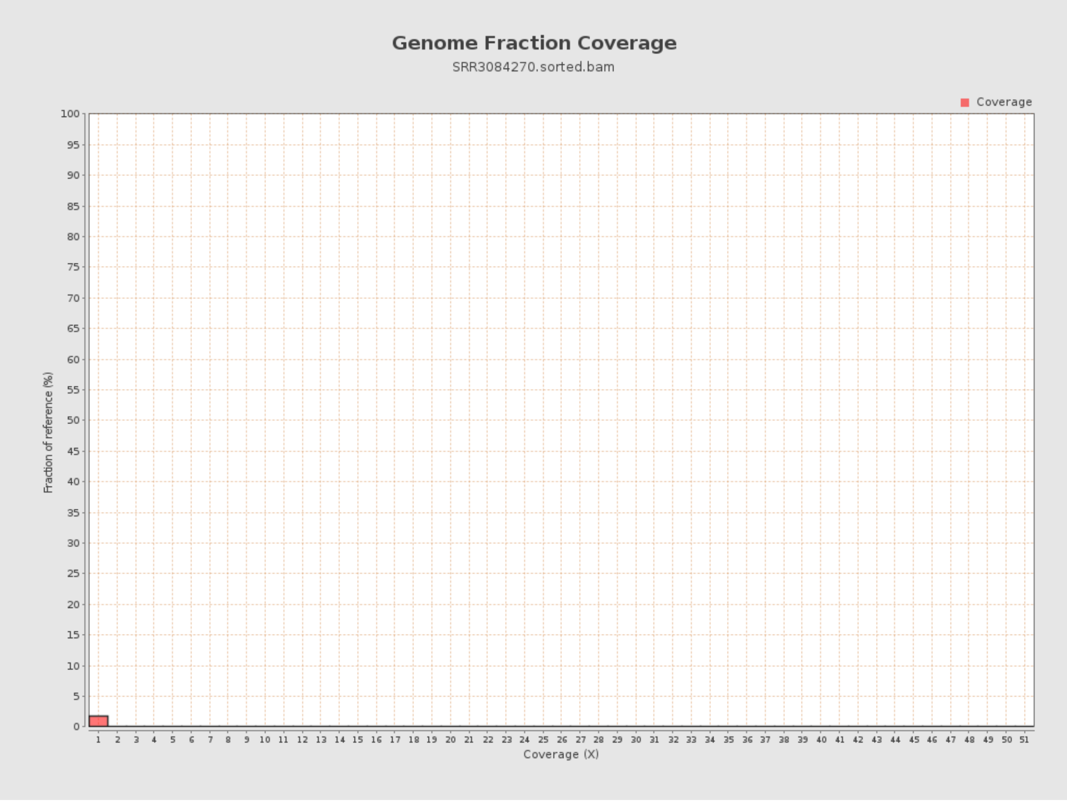
4. Results : Coverage Histogram



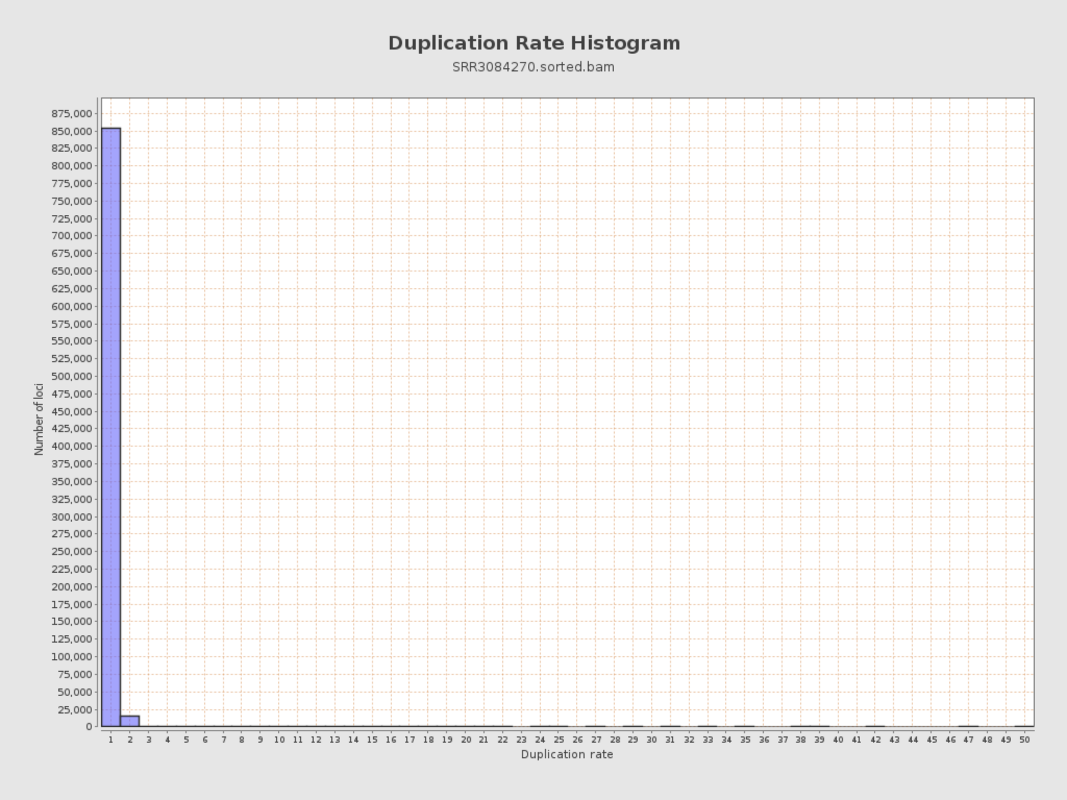
5. Results : Coverage Histogram (0-50X)



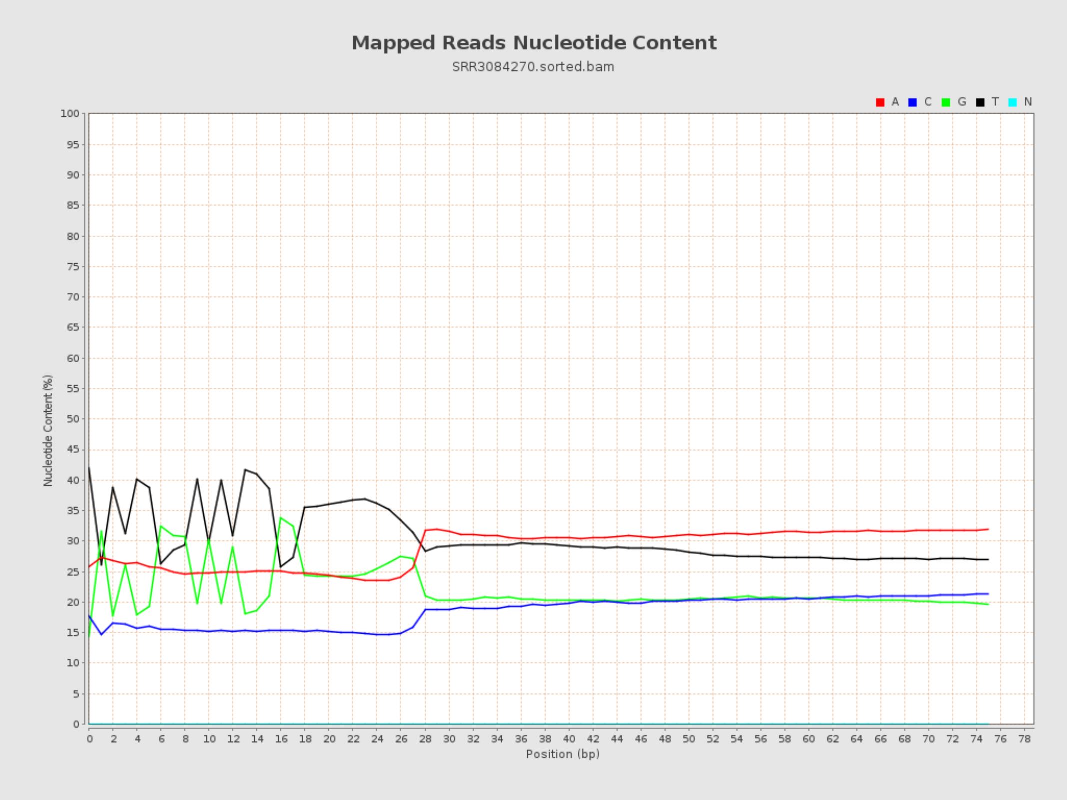
6. Results : Genome Fraction Coverage



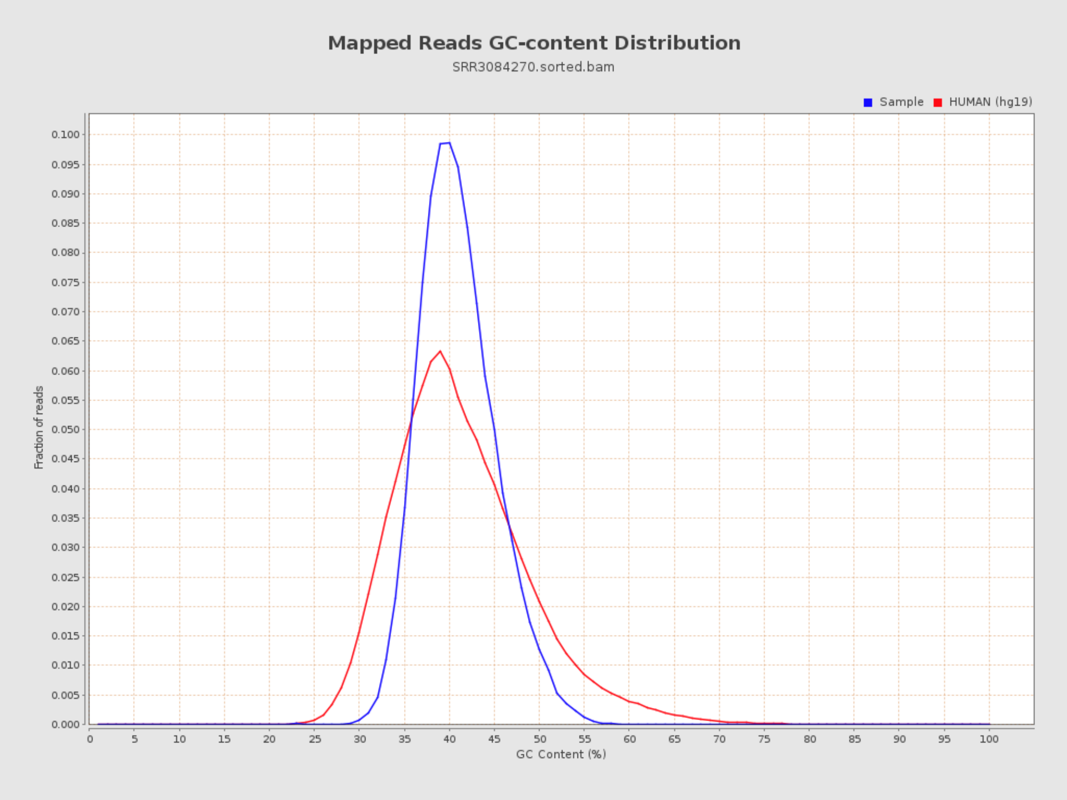
7. Results : Duplication Rate Histogram



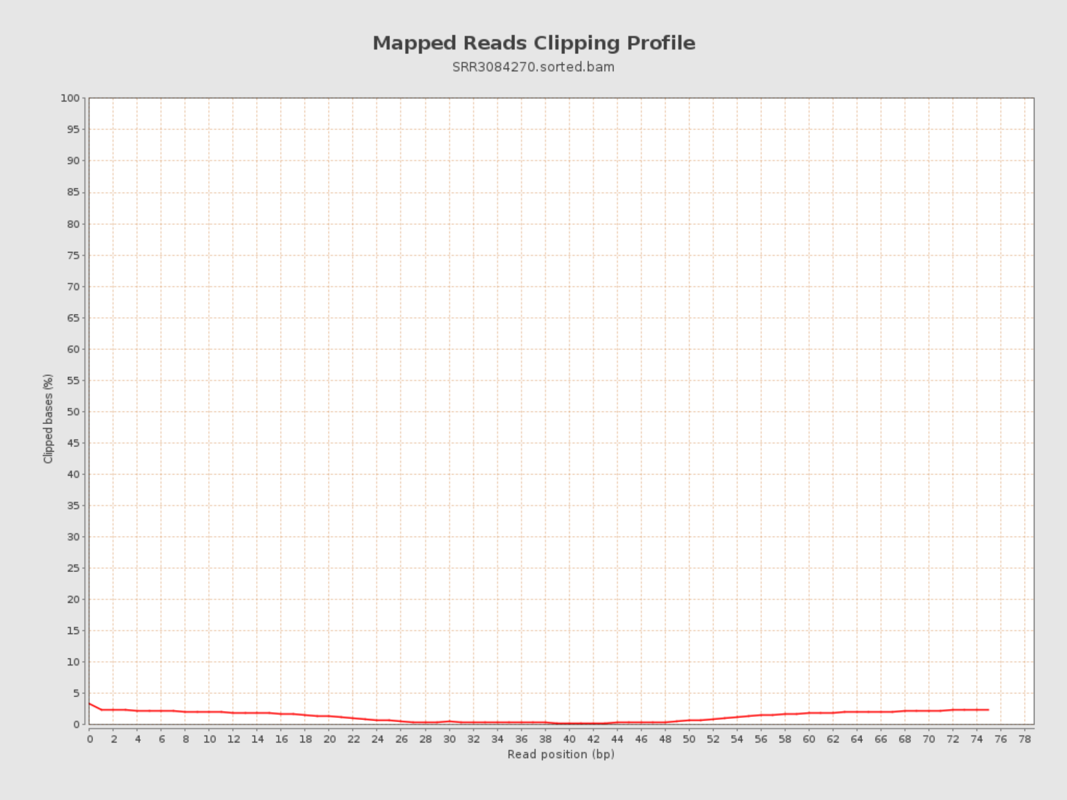
8. Results : Mapped Reads Nucleotide Content



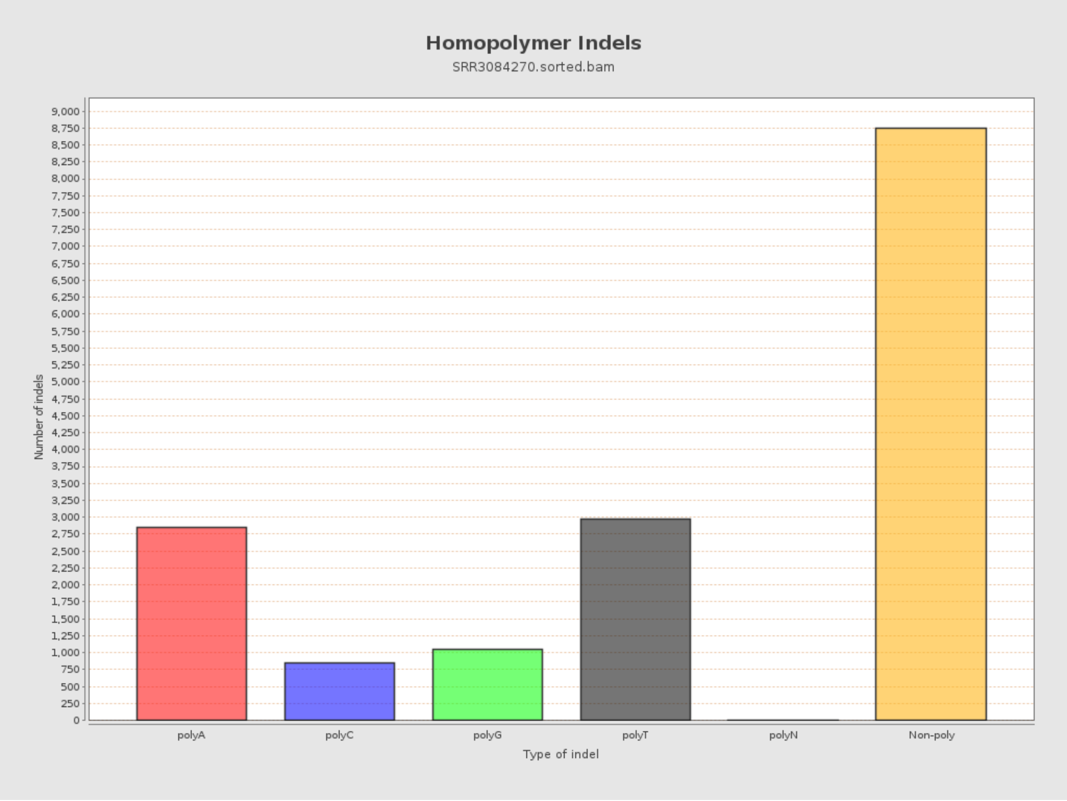
9. Results : Mapped Reads GC-content Distribution



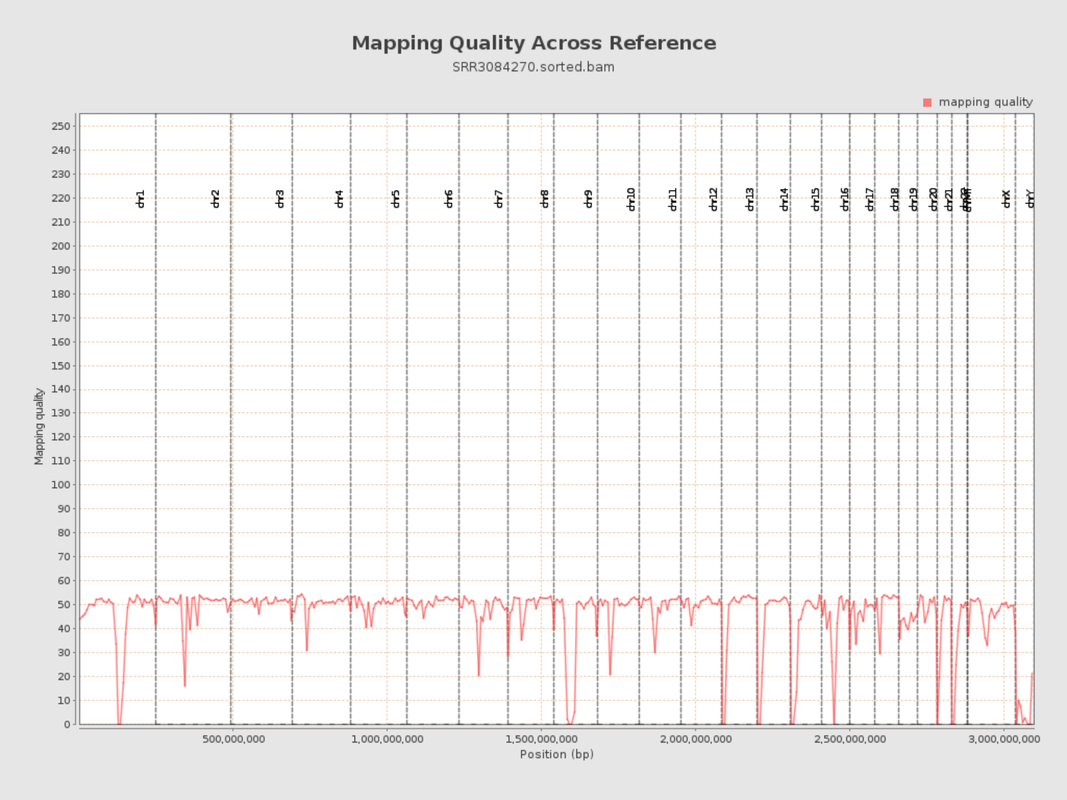
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram