Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:30:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084761.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_SRR3084761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:30:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,233,345
Mapped reads	1,911,449 / 85.59%
Unmapped reads	321,896 / 14.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,631 / 1.19%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	59,412 / 2.66%
Duplication rate	1.87%
Clipped reads	975,569 / 43.68%

2.2. ACGT Content

Number/percentage of A's	35,679,778 / 28.5%
Number/percentage of C's	24,264,732 / 19.38%
Number/percentage of T's	36,783,422 / 29.38%
Number/percentage of G's	28,406,290 / 22.69%
Number/percentage of N's	44,320 / 0.04%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0404

Standard Deviation	0.4255

2.4. Mapping Quality

Mean Mapping Quality	43.4

2.5. Mismatches and indels

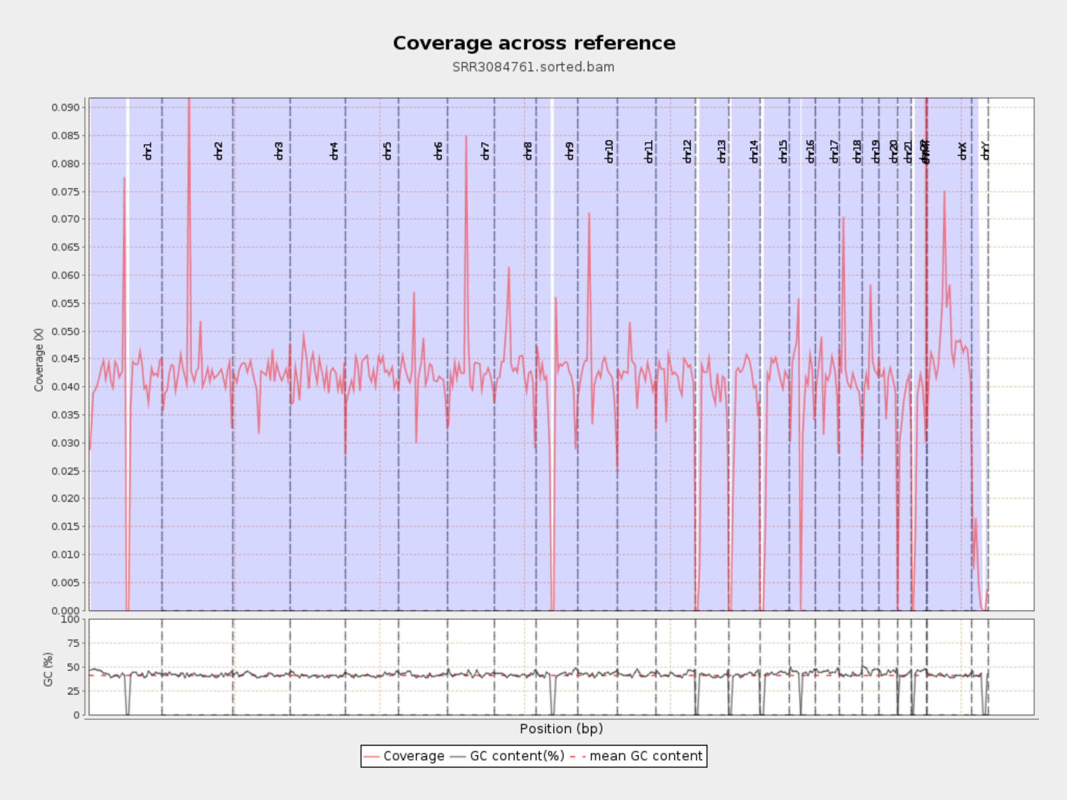
General error rate	0.87%
Mismatches	1,075,135
Insertions	10,468
Mapped reads with at least one insertion	0.54%
Deletions	24,927
Mapped reads with at least one deletion	1.29%
Homopolymer indels	43.44%

2.6. Chromosome stats

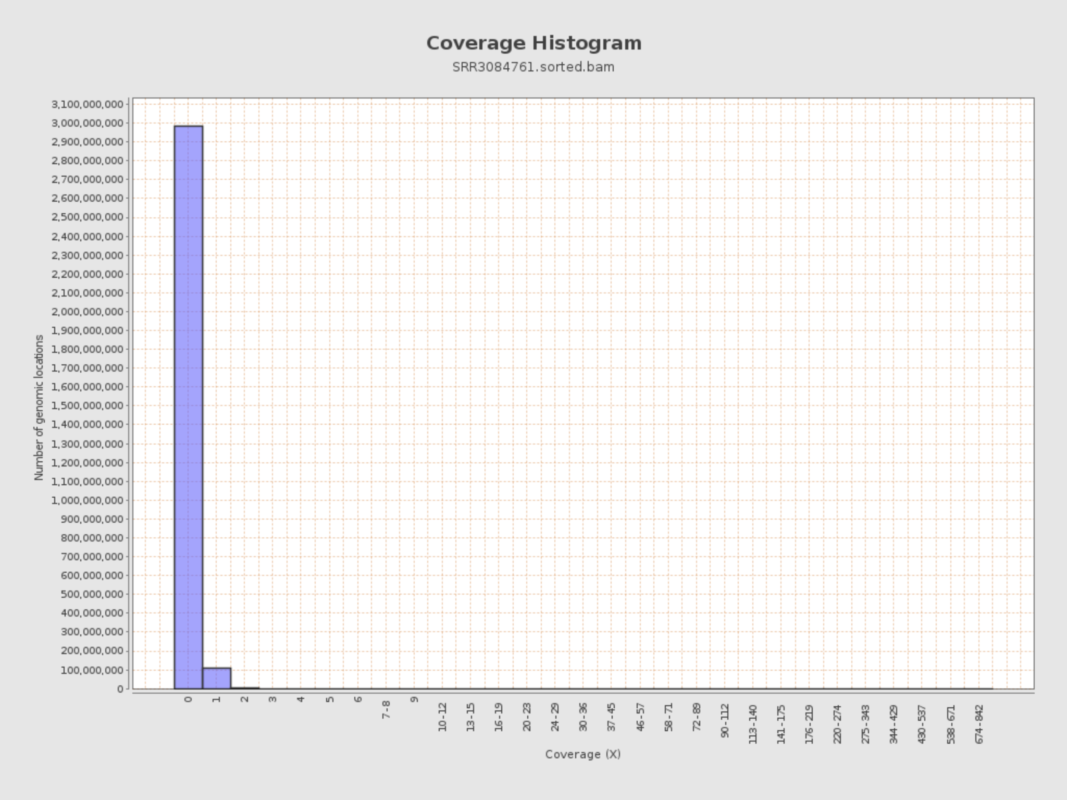
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10032030	0.0402	0.7677
chr2	243199373	10656112	0.0438	0.5292
chr3	198022430	8368875	0.0423	0.2188
chr4	191154276	8038233	0.0421	0.232
chr5	180915260	7659483	0.0423	0.2234
chr6	171115067	7246515	0.0423	0.2882
chr7	159138663	7049968	0.0443	0.6047

chr8	146364022	6377652	0.0436	0.4706
chr9	141213431	5293882	0.0375	0.4198
chr10	135534747	5837979	0.0431	0.3912
chr11	135006516	5698055	0.0422	0.379
chr12	133851895	5620021	0.042	0.2256
chr13	115169878	3898387	0.0338	0.1951
chr14	107349540	3787908	0.0353	0.2523
chr15	102531392	3529058	0.0344	0.2156
chr16	90354753	3503319	0.0388	0.2612
chr17	81195210	3321404	0.0409	0.265
chr18	78077248	3433230	0.044	0.9503
chr19	59128983	2568407	0.0434	0.5734
chr20	63025520	2513420	0.0399	0.2455
chr21	48129895	1587612	0.033	0.2096
chr22	51304566	1372598	0.0268	0.1725
chrMT	16571	19799	1.1948	1.3386
chrX	155270560	7470452	0.0481	0.2981
chrY	59373566	335546	0.0057	0.1173

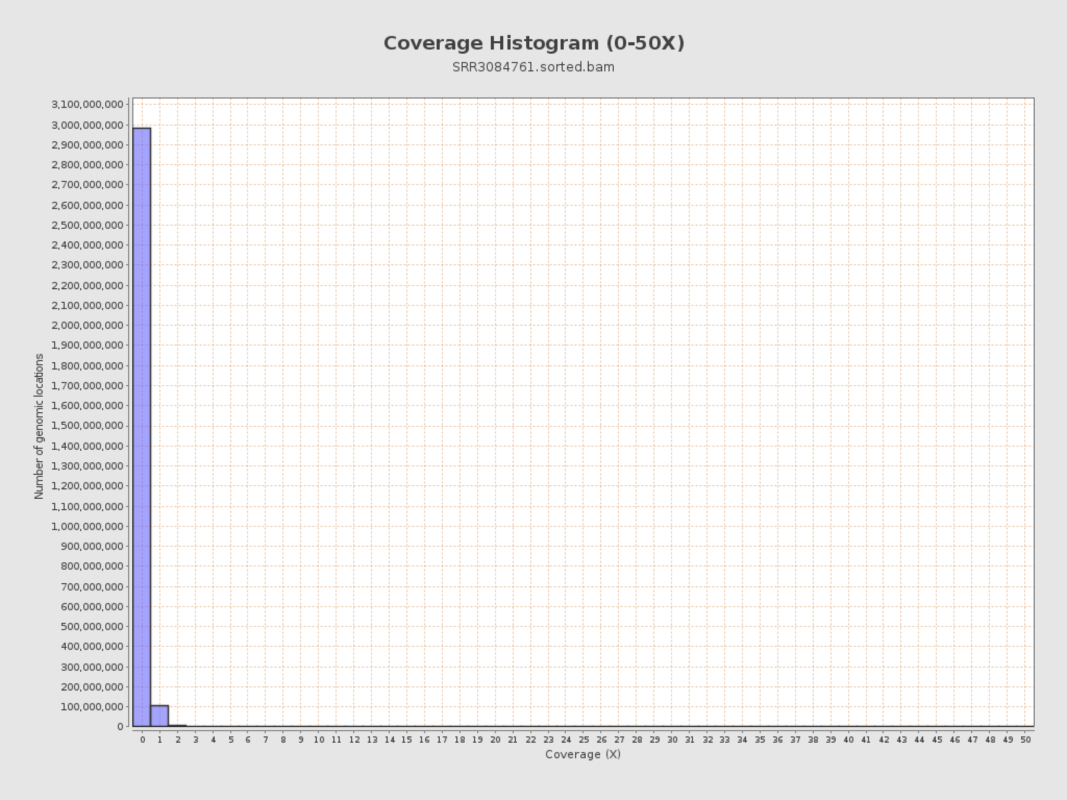
3. Results : Coverage across reference



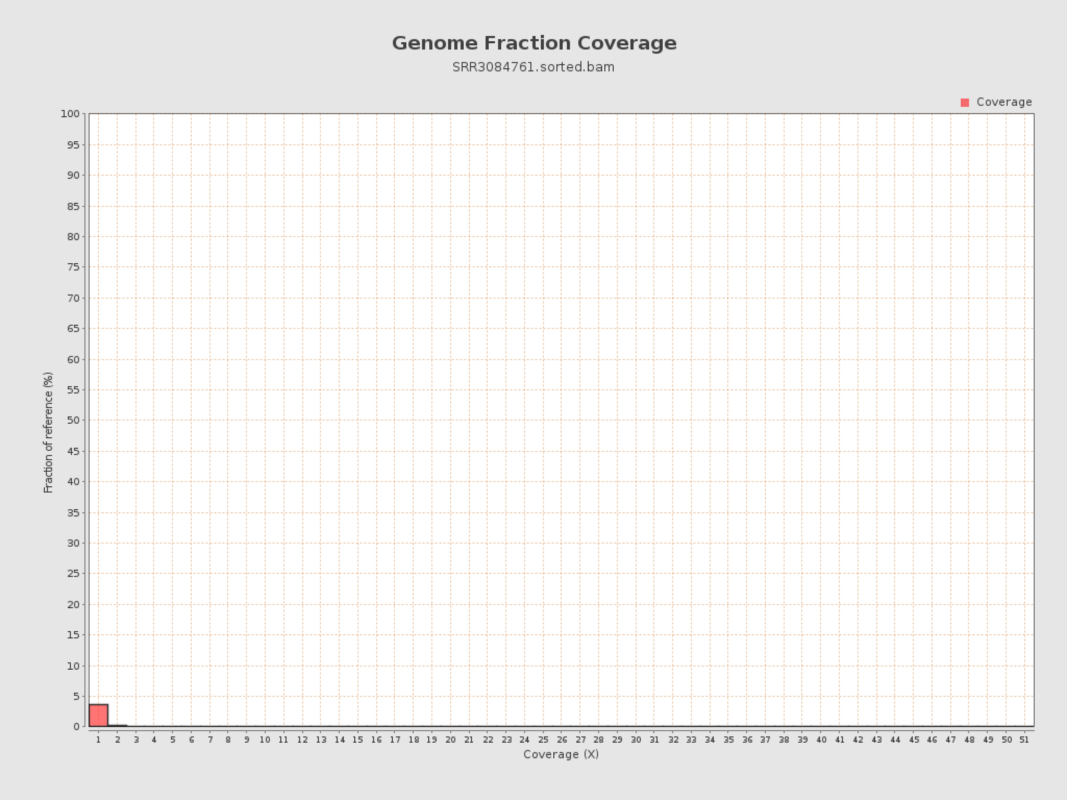
4. Results : Coverage Histogram



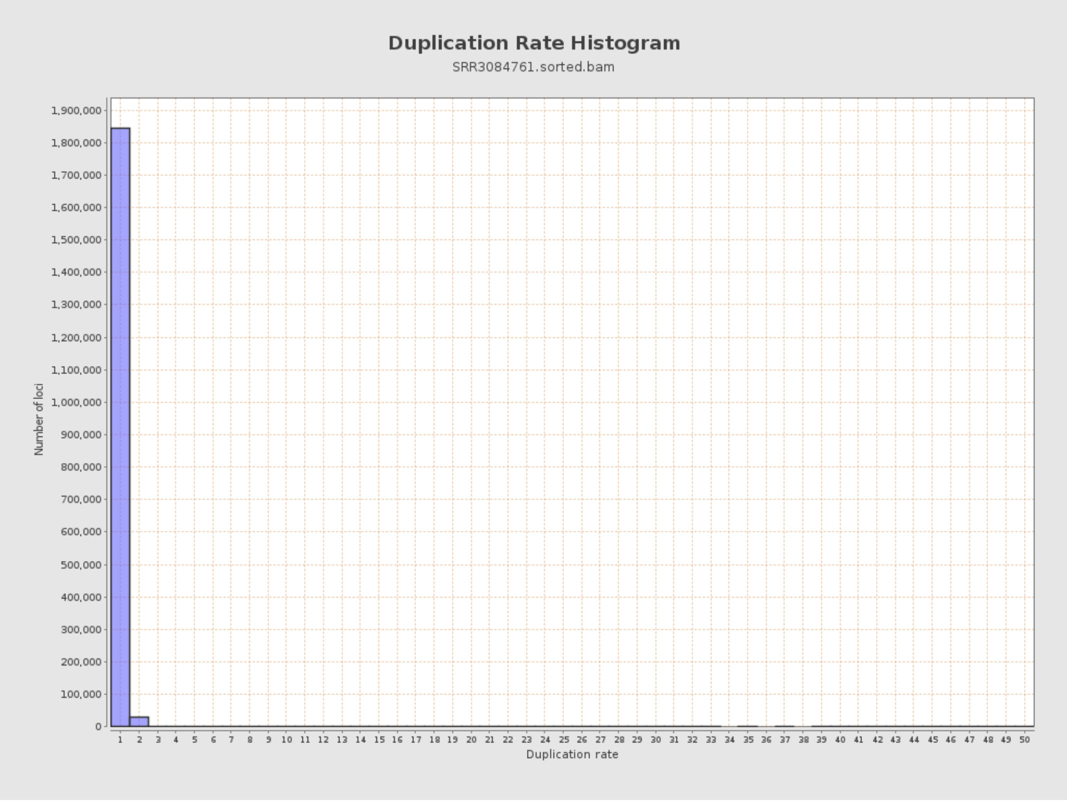
5. Results : Coverage Histogram (0-50X)



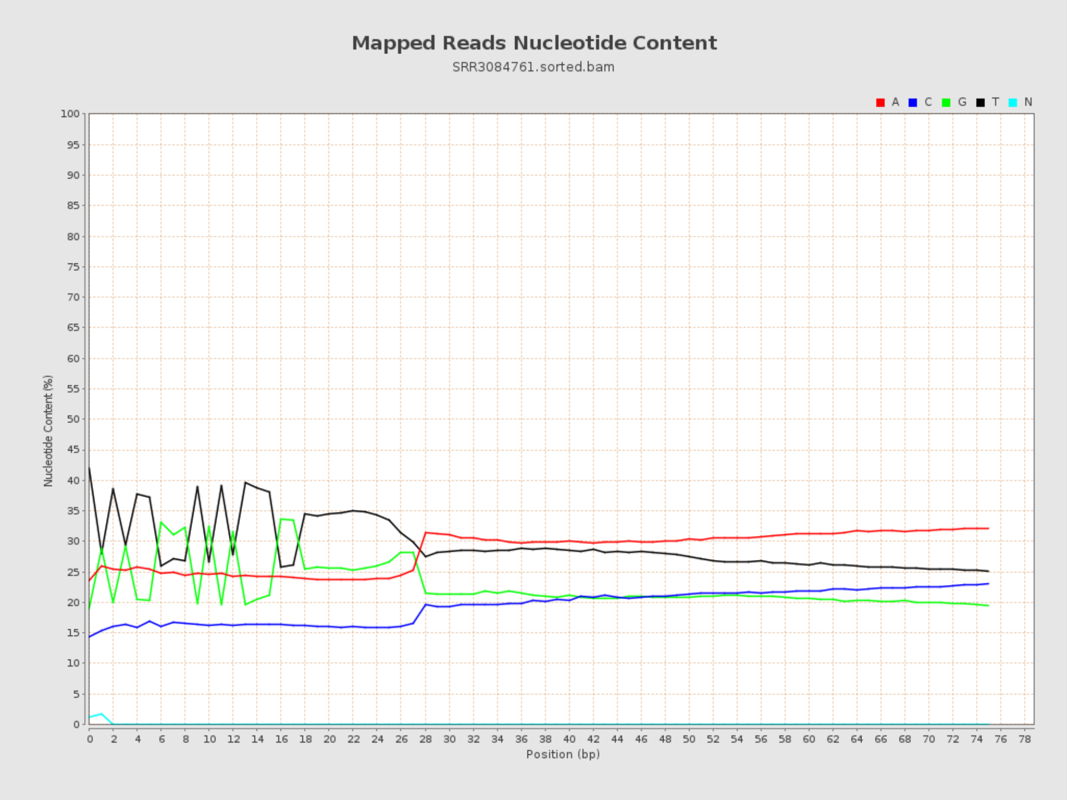
6. Results : Genome Fraction Coverage



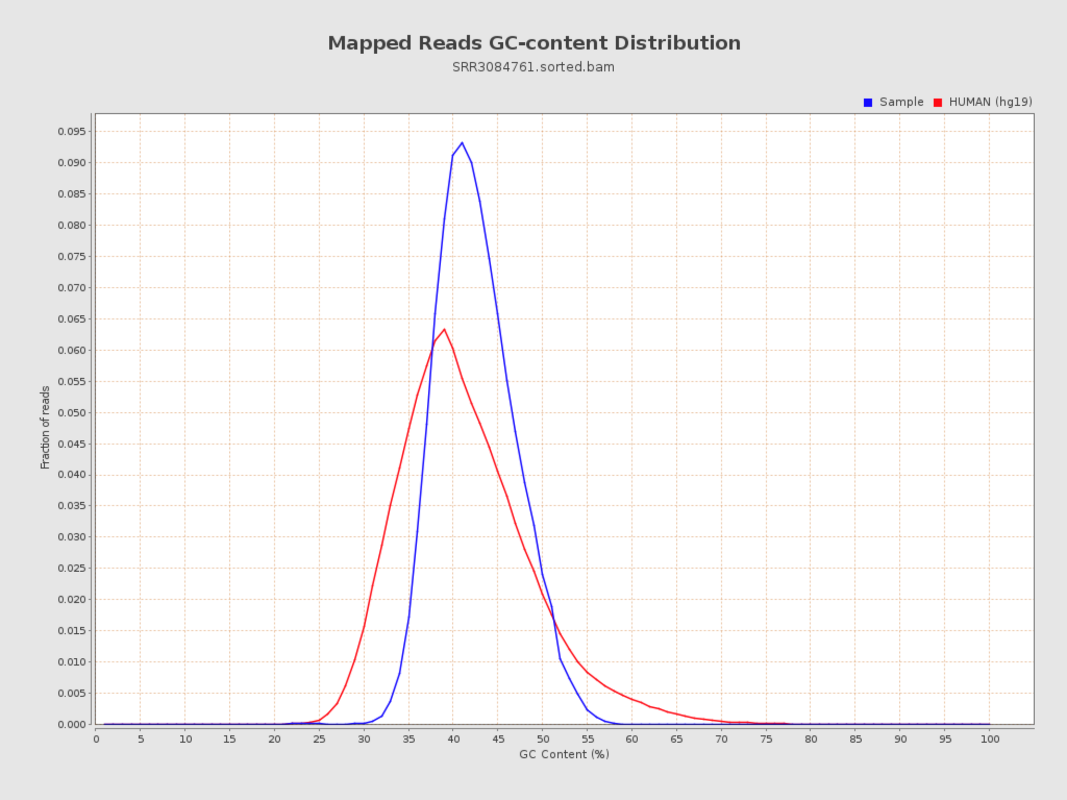
7. Results : Duplication Rate Histogram



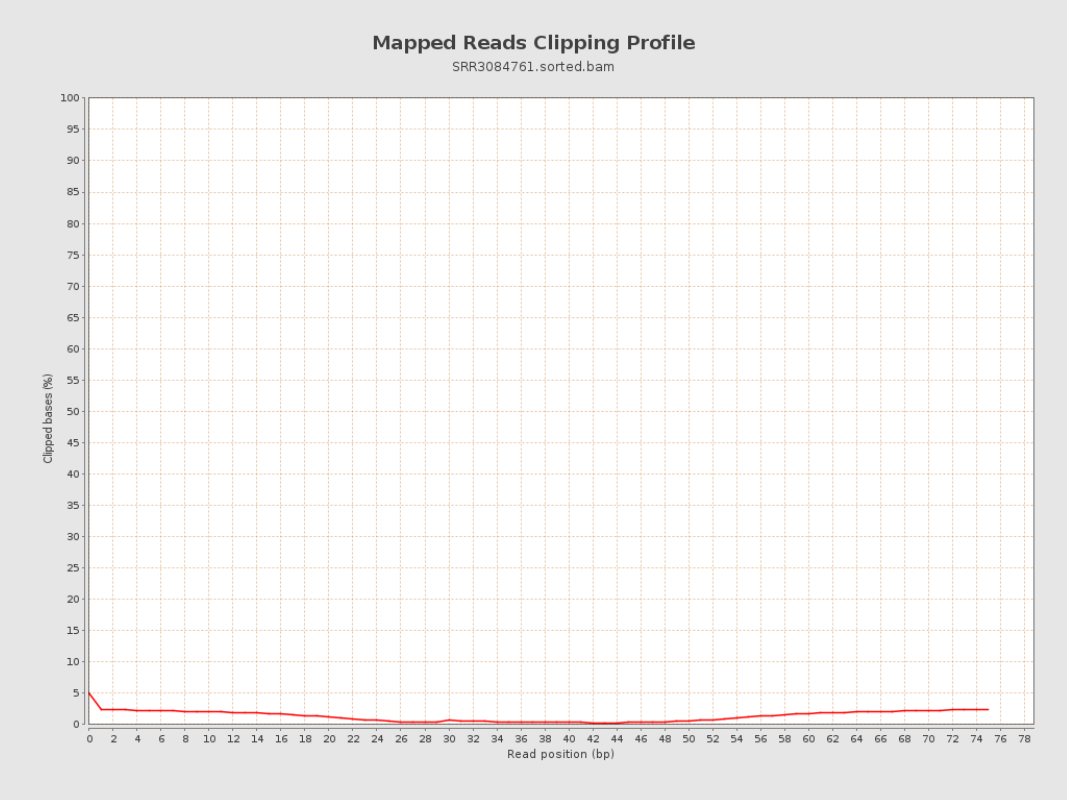
8. Results : Mapped Reads Nucleotide Content



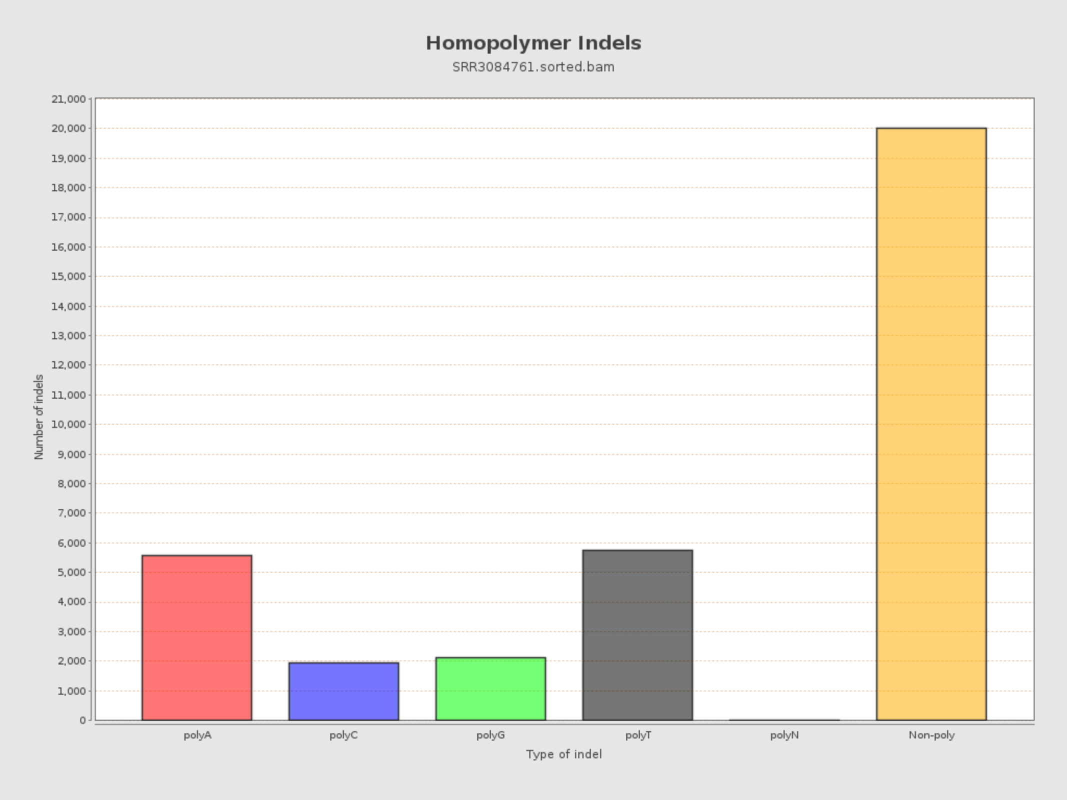
9. Results : Mapped Reads GC-content Distribution



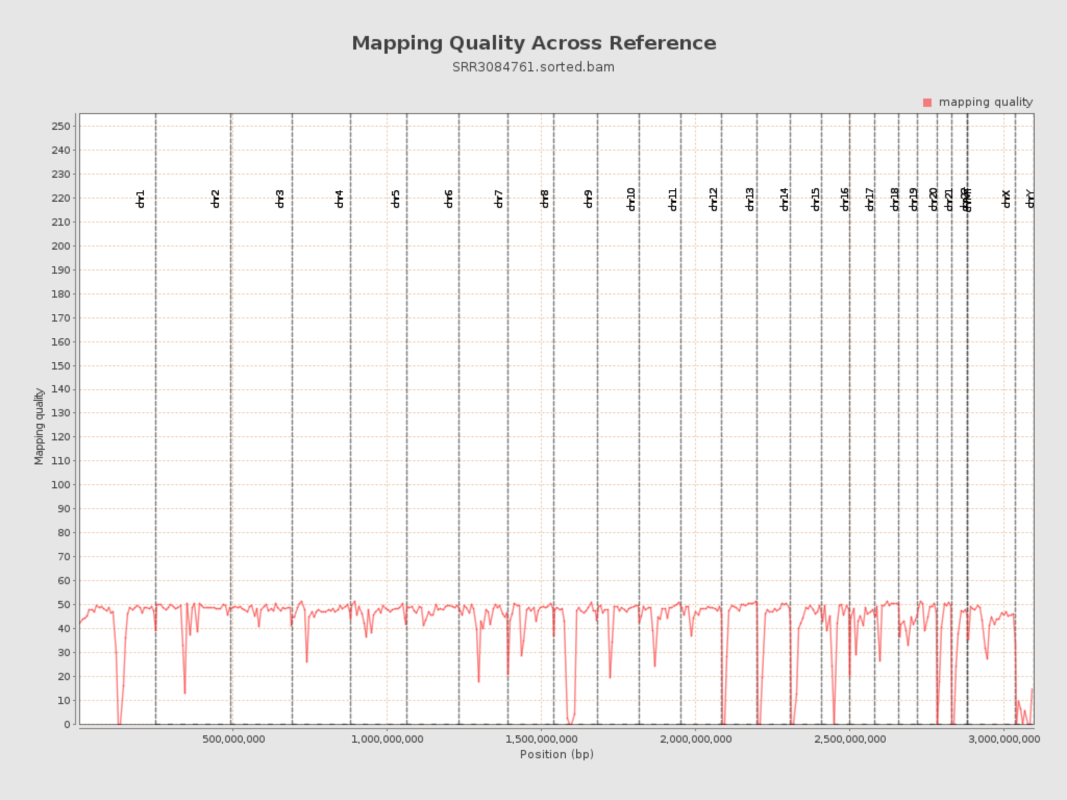
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram