Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 11:46:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080661.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_SRR3080661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080661.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 11:46:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,457,643
Mapped reads	1,304,144 / 89.47%
Unmapped reads	153,499 / 10.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,760 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	47,931 / 3.29%
Duplication rate	3.18%
Clipped reads	623,662 / 42.79%

2.2. ACGT Content

Number/percentage of A's	23,254,699 / 27.06%
Number/percentage of C's	15,730,166 / 18.31%
Number/percentage of T's	27,381,774 / 31.87%
Number/percentage of G's	19,556,850 / 22.76%
Number/percentage of N's	3,607 / 0%
GC Percentage	41.07%

2.3. Coverage

Mean	0.0278

Standard Deviation	0.2269

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

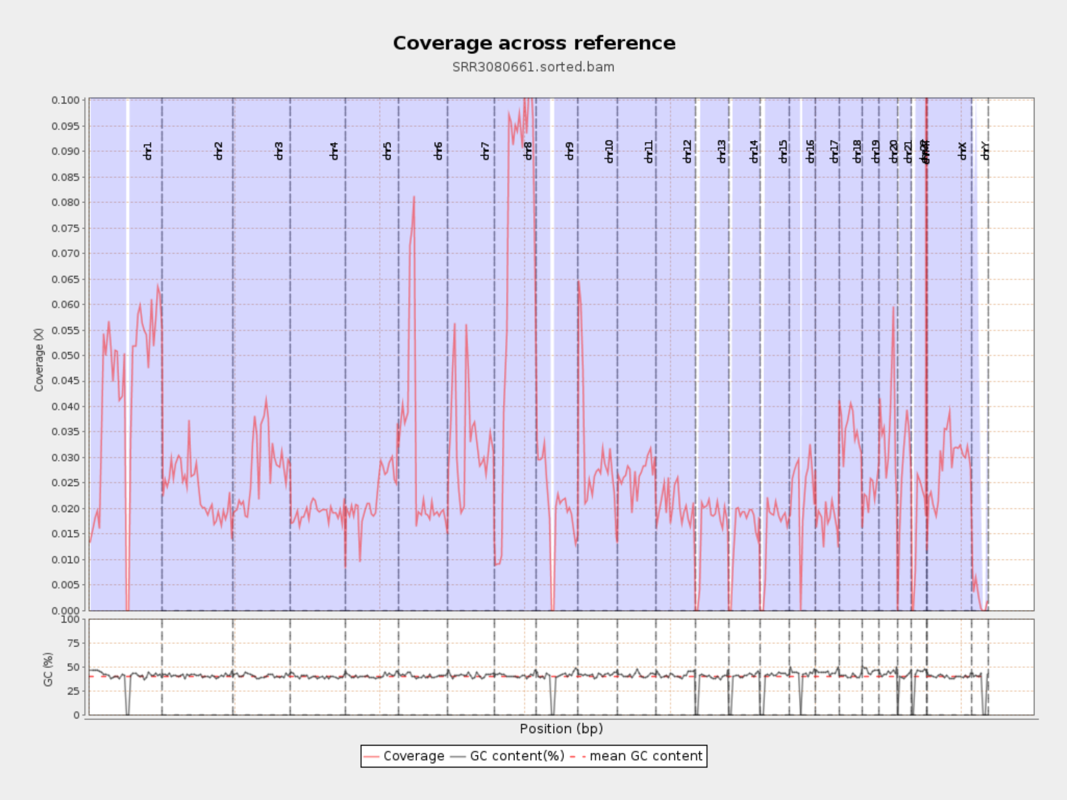
General error rate	0.71%
Mismatches	600,855
Insertions	6,344
Mapped reads with at least one insertion	0.48%
Deletions	19,939
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.7%

2.6. Chromosome stats

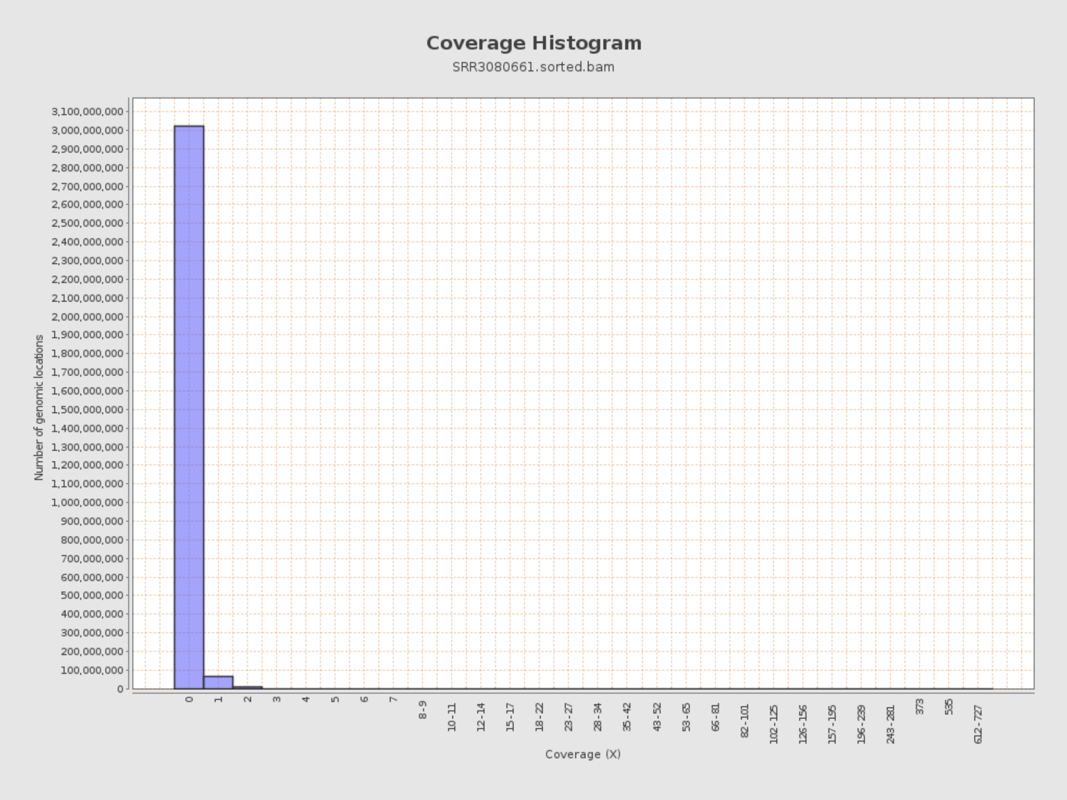
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10737141	0.0431	0.2726
chr2	243199373	5716161	0.0235	0.3505
chr3	198022430	5537696	0.028	0.1852
chr4	191154276	3668640	0.0192	0.156
chr5	180915260	4049598	0.0224	0.1654
chr6	171115067	5227606	0.0306	0.2282
chr7	159138663	5425913	0.0341	0.3631

chr8	146364022	10441988	0.0713	0.3293
chr9	141213431	2839639	0.0201	0.1753
chr10	135534747	4196899	0.031	0.2049
chr11	135006516	3586278	0.0266	0.1922
chr12	133851895	2724104	0.0204	0.1592
chr13	115169878	1868764	0.0162	0.1417
chr14	107349540	1661138	0.0155	0.1398
chr15	102531392	1575318	0.0154	0.1457
chr16	90354753	2148931	0.0238	0.1735
chr17	81195210	1428200	0.0176	0.1494
chr18	78077248	2777058	0.0356	0.2532
chr19	59128983	1381465	0.0234	0.2012
chr20	63025520	2254247	0.0358	0.2108
chr21	48129895	1280298	0.0266	0.1825
chr22	51304566	849877	0.0166	0.1415
chrMT	16571	10694	0.6453	0.9482
chrX	155270560	4418985	0.0285	0.192
chrY	59373566	152592	0.0026	0.0587

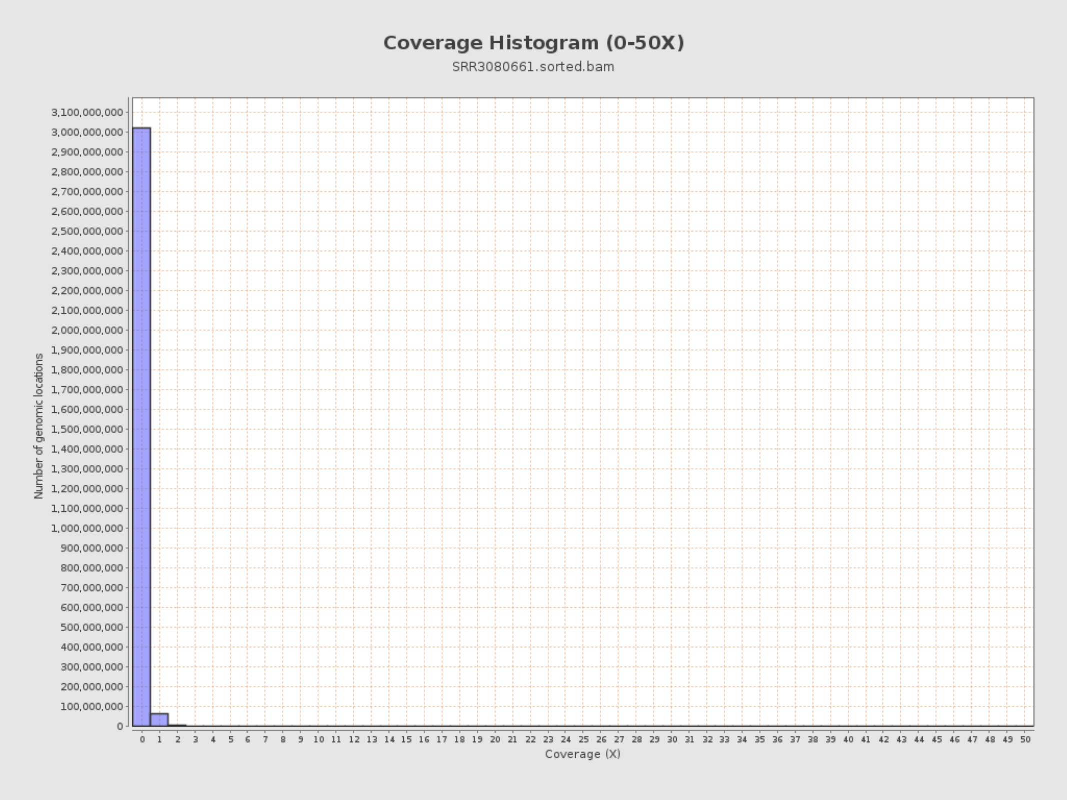
3. Results : Coverage across reference



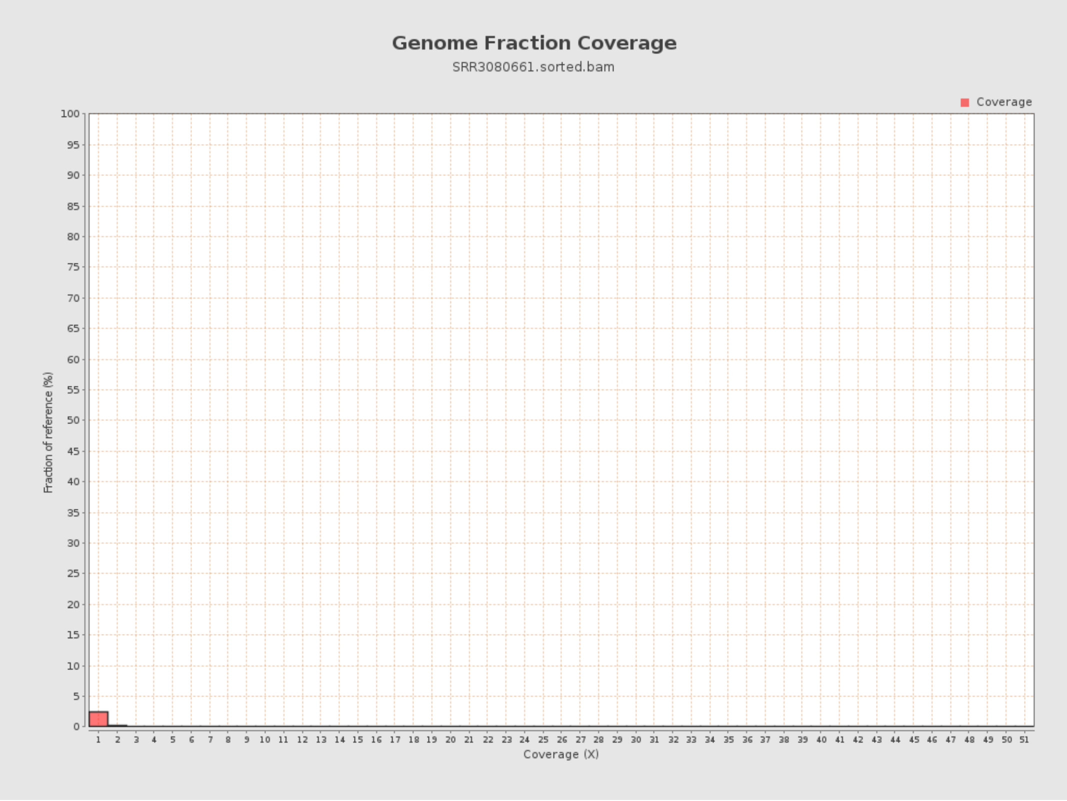
4. Results : Coverage Histogram



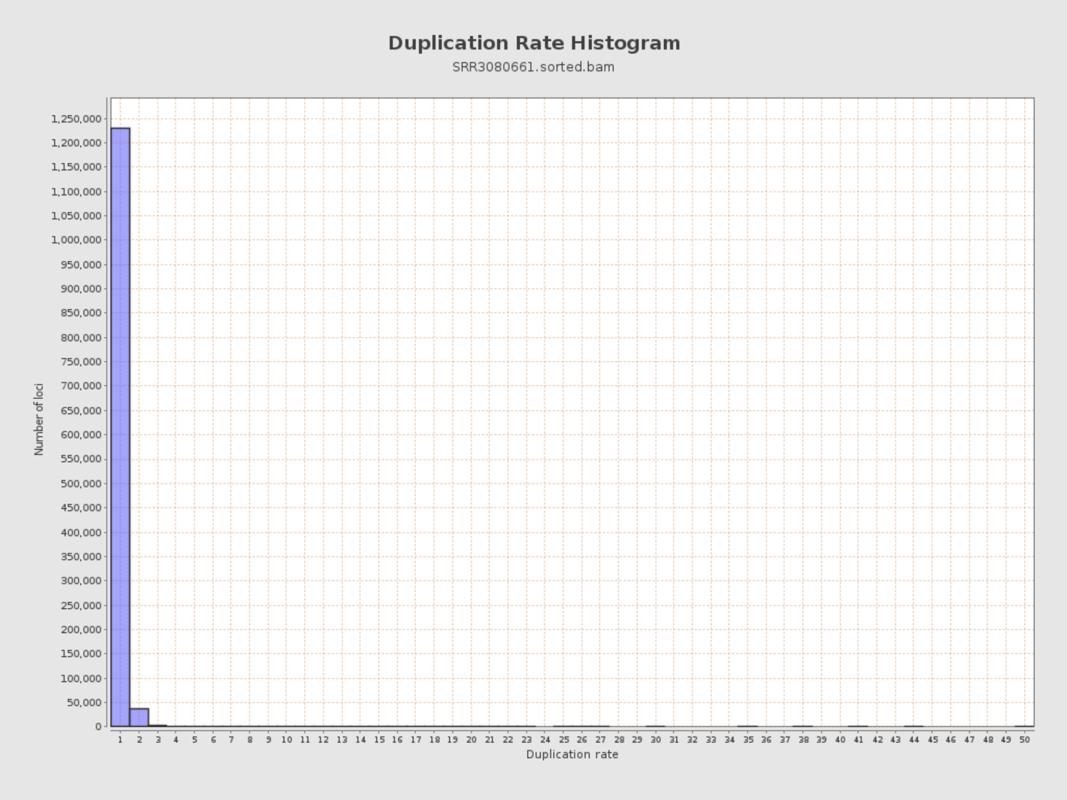
5. Results : Coverage Histogram (0-50X)



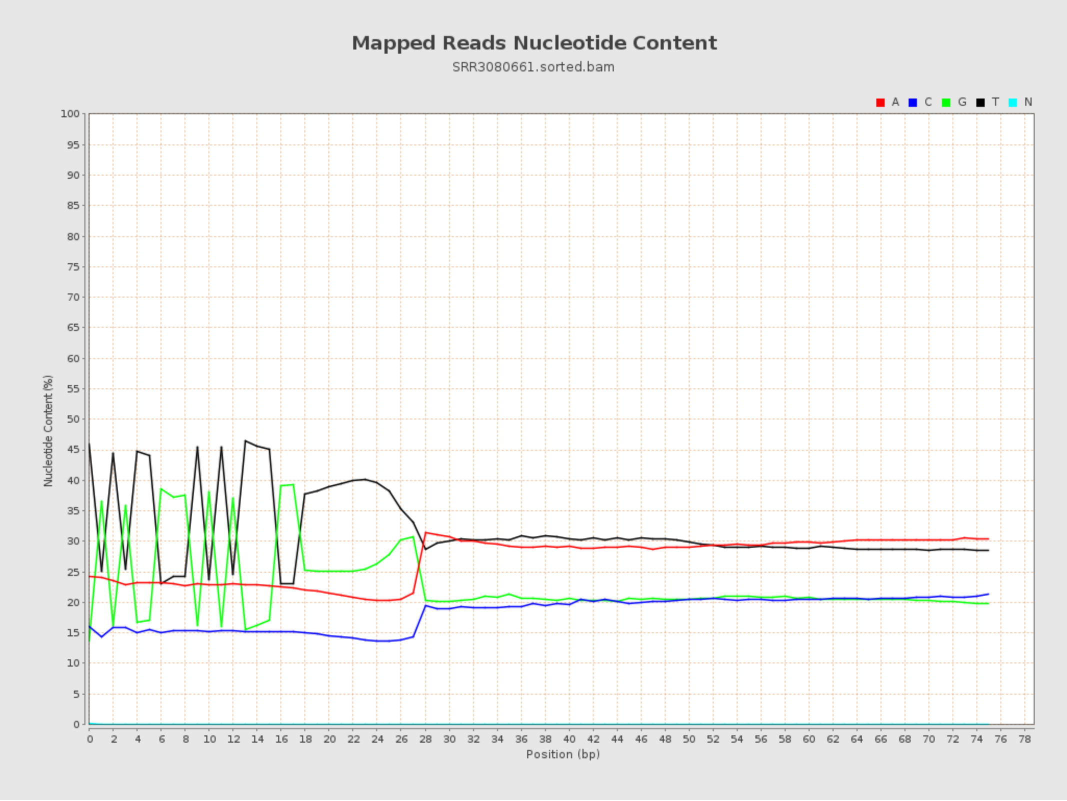
6. Results : Genome Fraction Coverage



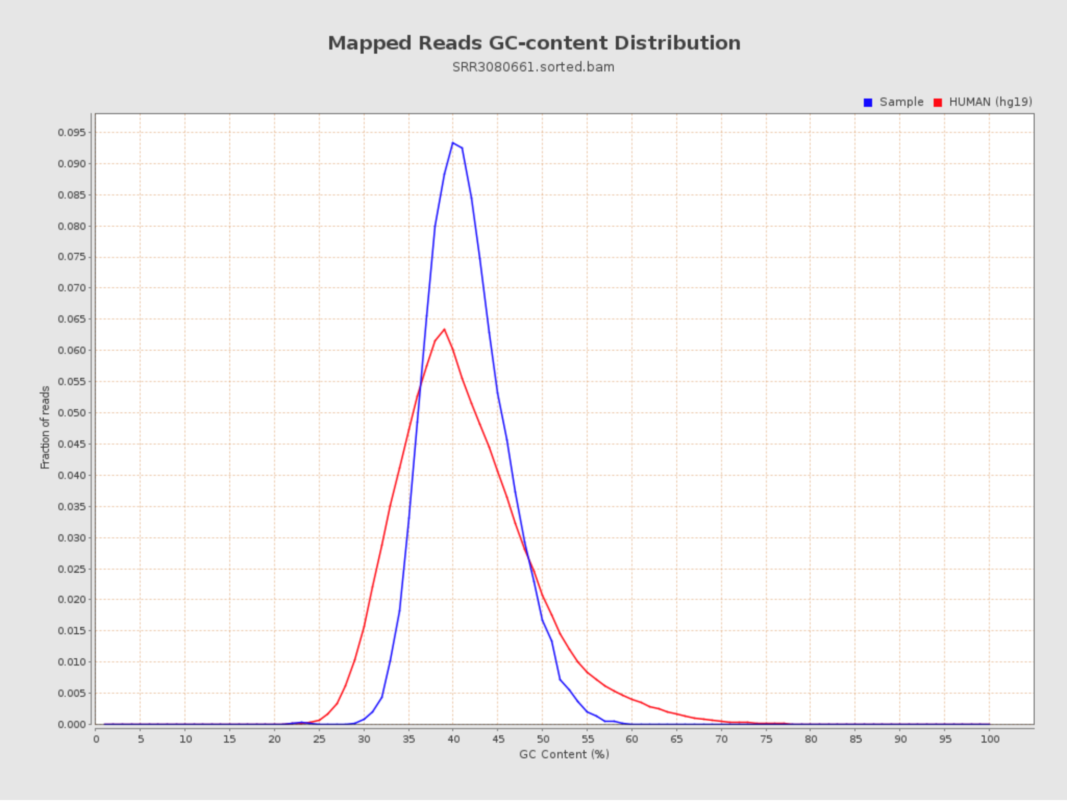
7. Results : Duplication Rate Histogram



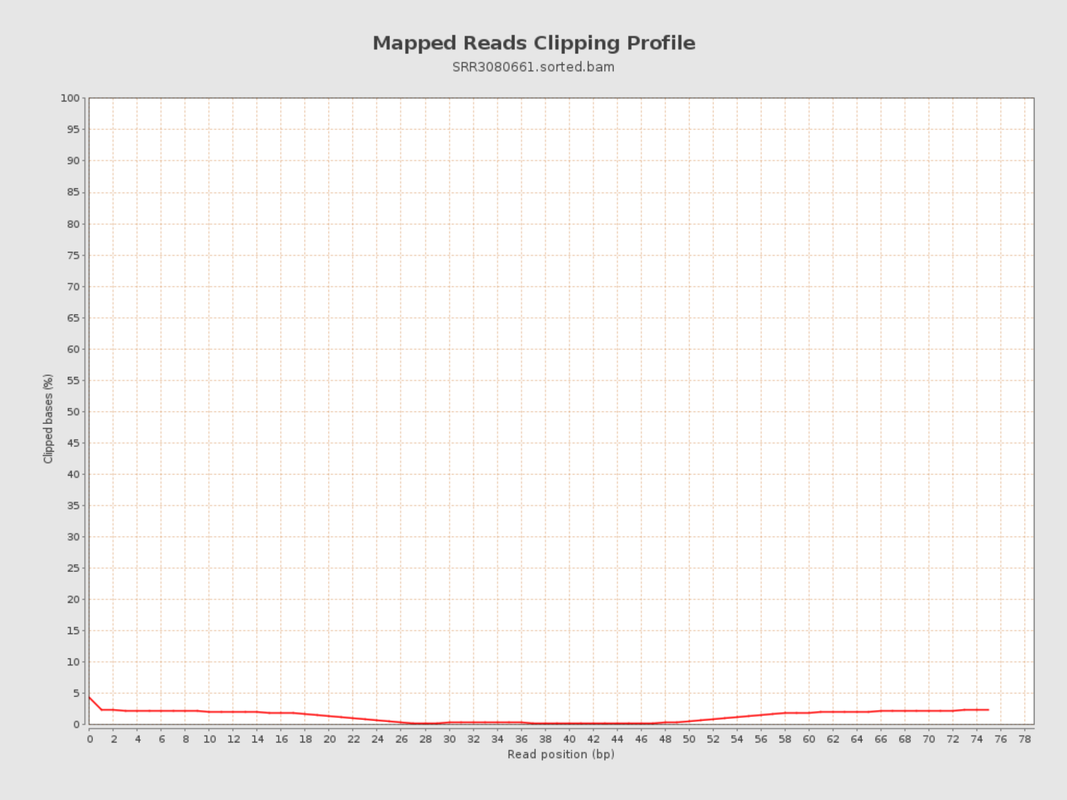
8. Results : Mapped Reads Nucleotide Content



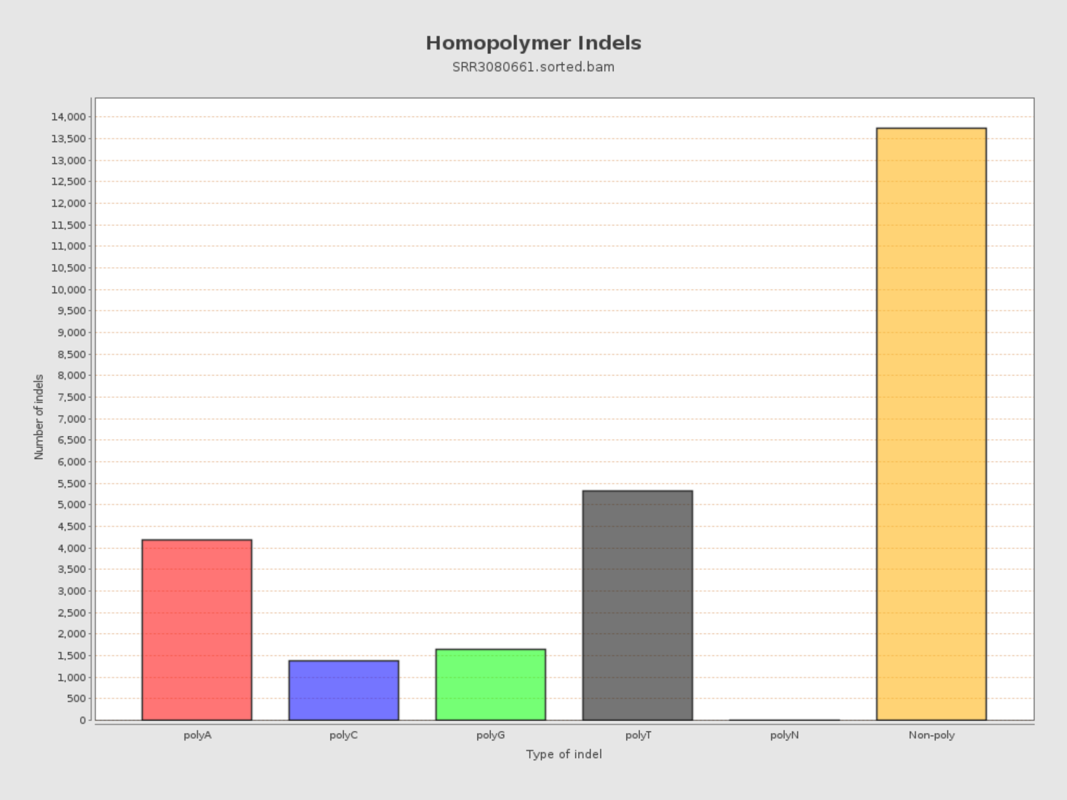
9. Results : Mapped Reads GC-content Distribution



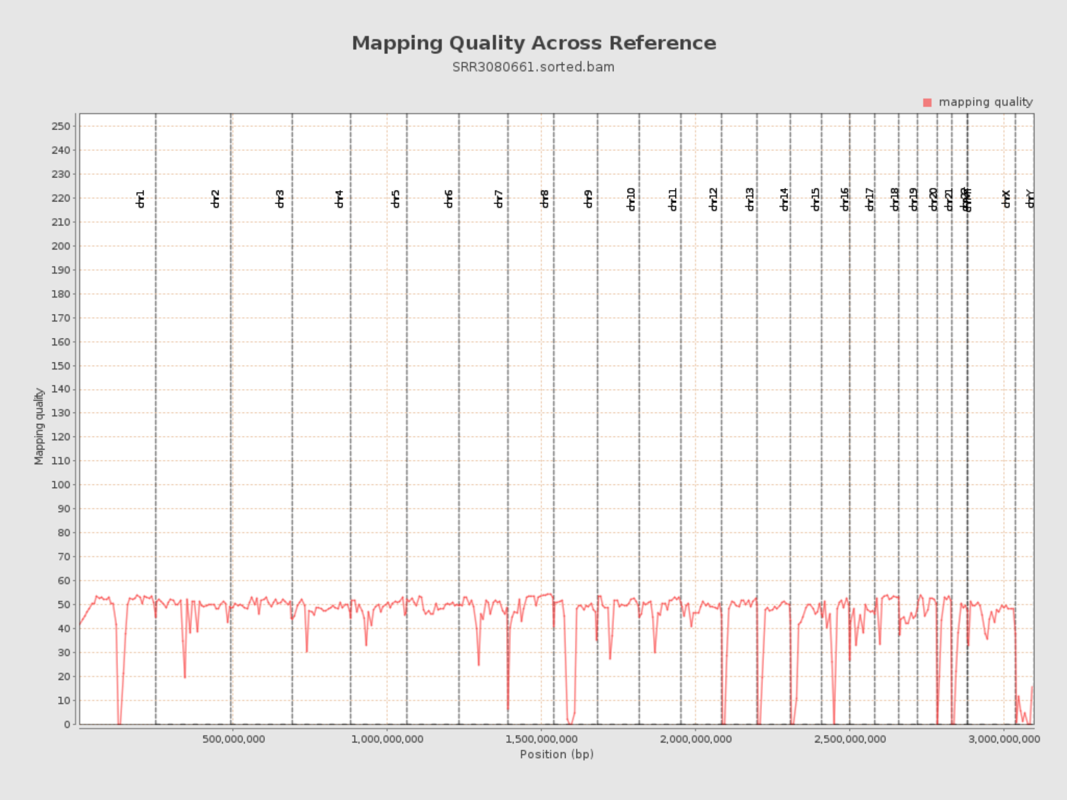
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram