Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:41:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080677.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_SRR3080677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:41:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,461,957
Mapped reads	1,340,421 / 91.69%
Unmapped reads	121,536 / 8.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,200 / 0.97%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	44,720 / 3.06%
Duplication rate	2.86%
Clipped reads	594,053 / 40.63%

2.2. ACGT Content

Number/percentage of A's	24,604,069 / 27.51%
Number/percentage of C's	16,445,472 / 18.38%
Number/percentage of T's	28,416,360 / 31.77%
Number/percentage of G's	19,982,054 / 22.34%
Number/percentage of N's	3,937 / 0%
GC Percentage	40.72%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.231

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

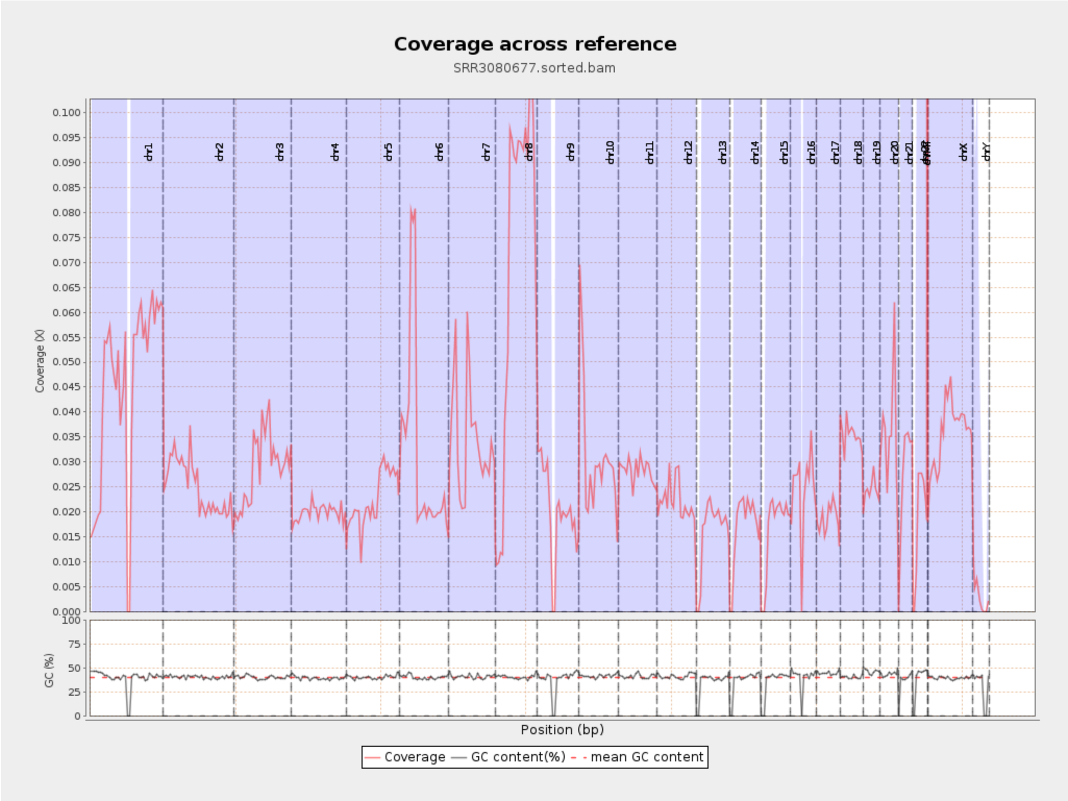
General error rate	0.7%
Mismatches	614,199
Insertions	6,850
Mapped reads with at least one insertion	0.51%
Deletions	21,081
Mapped reads with at least one deletion	1.56%
Homopolymer indels	48.11%

2.6. Chromosome stats

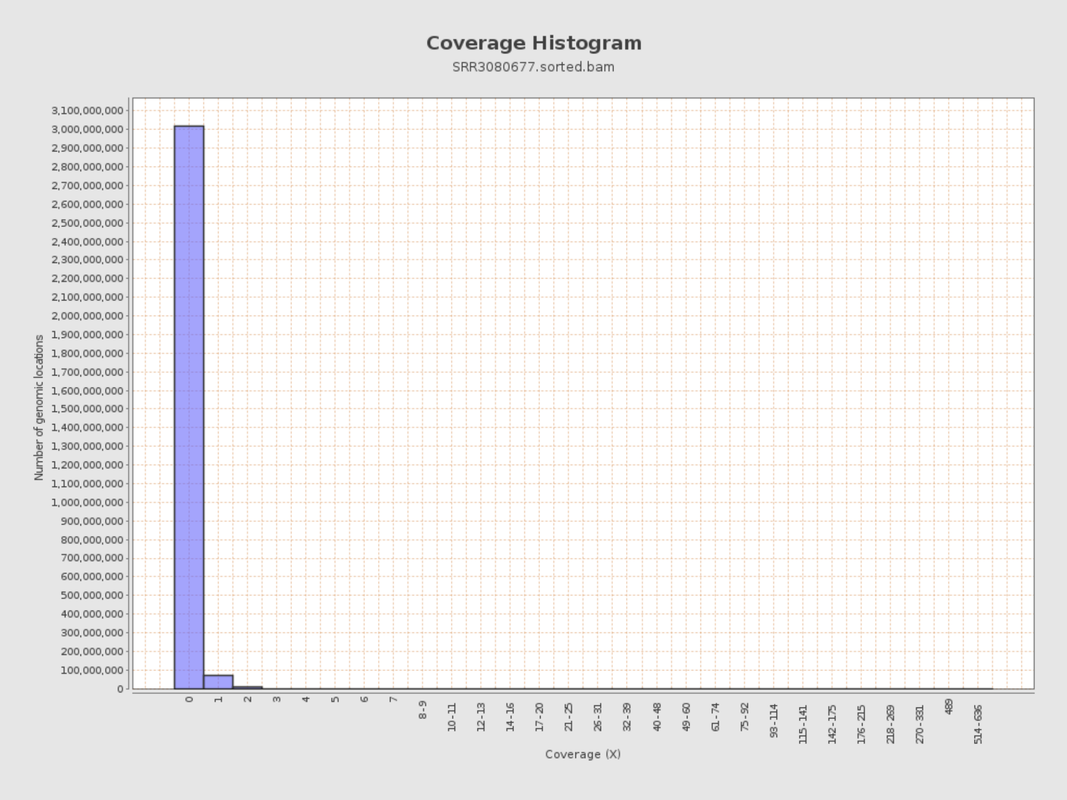
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11147947	0.0447	0.2987
chr2	243199373	6078481	0.025	0.3246
chr3	198022430	5721796	0.0289	0.1859
chr4	191154276	3788892	0.0198	0.157
chr5	180915260	4101423	0.0227	0.1645
chr6	171115067	5397609	0.0315	0.234
chr7	159138663	5576646	0.035	0.3881

chr8	146364022	10366186	0.0708	0.326
chr9	141213431	2803112	0.0199	0.1749
chr10	135534747	4284658	0.0316	0.2094
chr11	135006516	3801739	0.0282	0.2001
chr12	133851895	2927609	0.0219	0.1626
chr13	115169878	1840046	0.016	0.1402
chr14	107349540	1814167	0.0169	0.1455
chr15	102531392	1679389	0.0164	0.1493
chr16	90354753	2222211	0.0246	0.175
chr17	81195210	1501975	0.0185	0.1533
chr18	78077248	2767157	0.0354	0.2634
chr19	59128983	1456258	0.0246	0.2088
chr20	63025520	2253605	0.0358	0.2094
chr21	48129895	1309421	0.0272	0.1844
chr22	51304566	902295	0.0176	0.1443
chrMT	16571	14431	0.8709	1.0769
chrX	155270560	5557287	0.0358	0.2136
chrY	59373566	171891	0.0029	0.0624

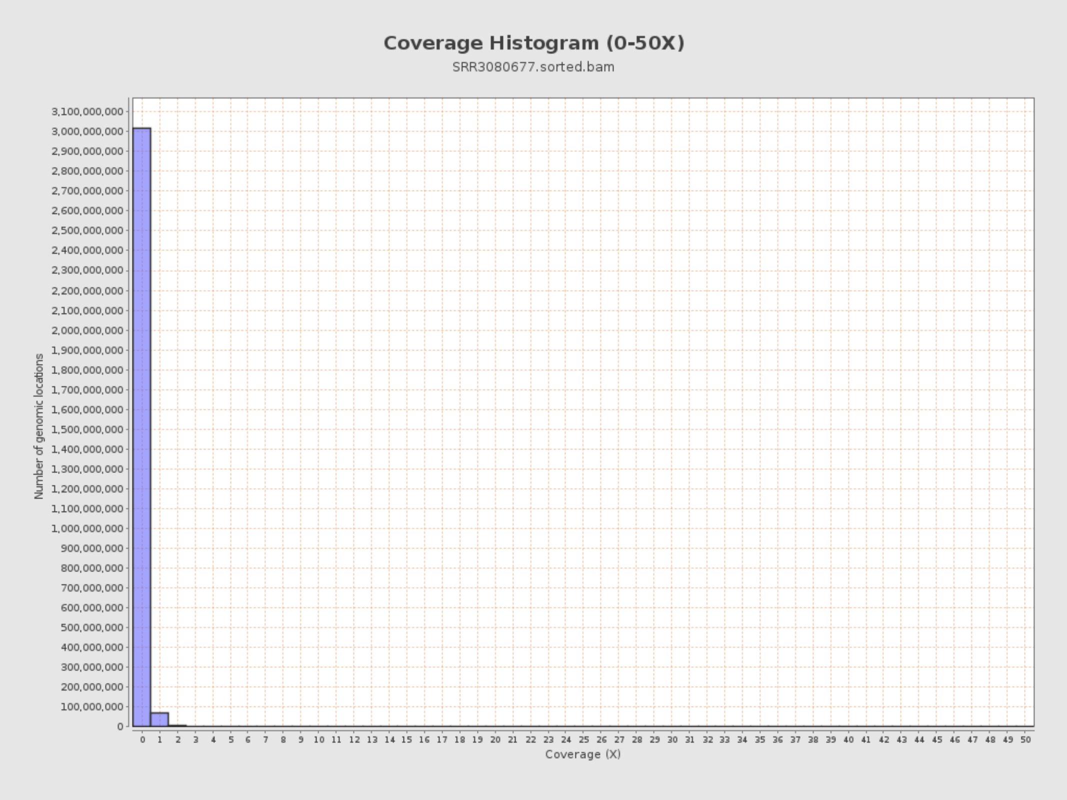
3. Results : Coverage across reference



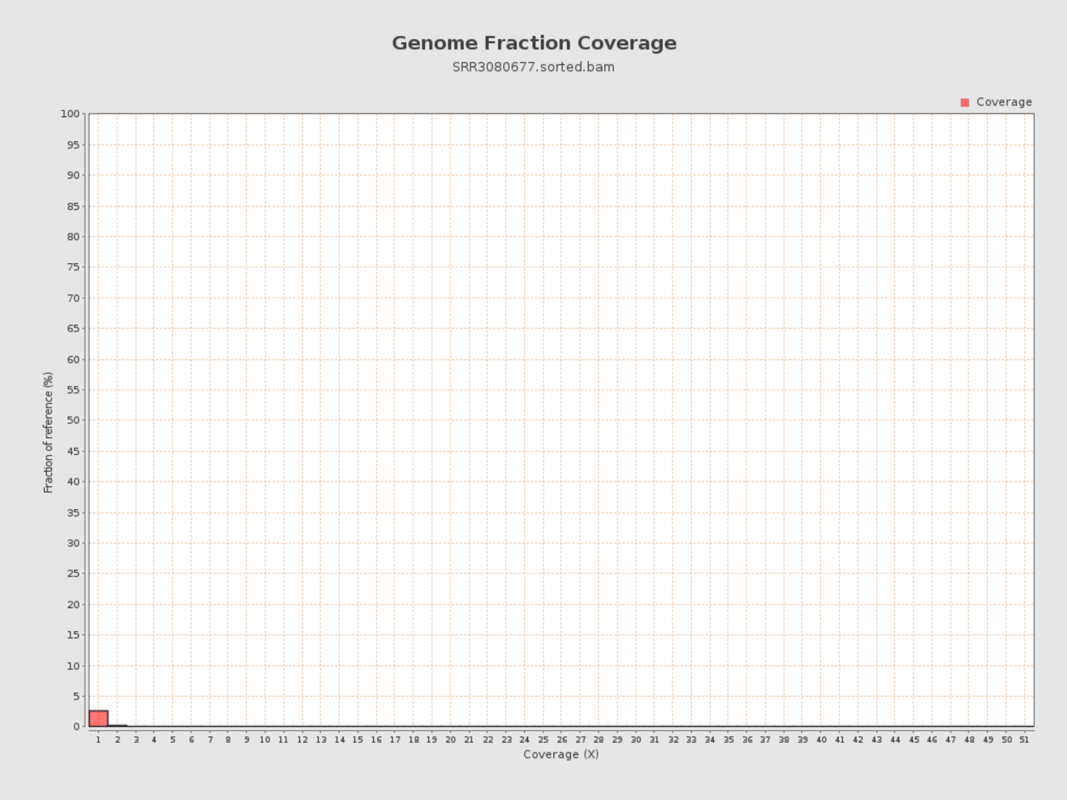
4. Results : Coverage Histogram



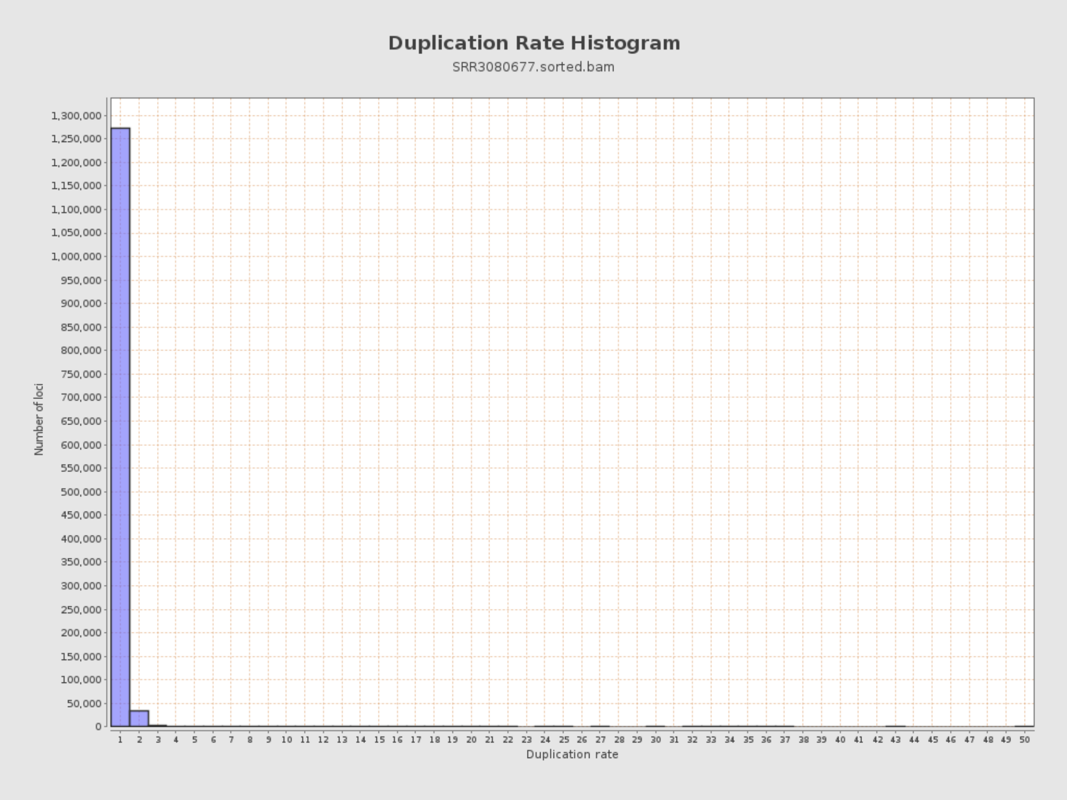
5. Results : Coverage Histogram (0-50X)



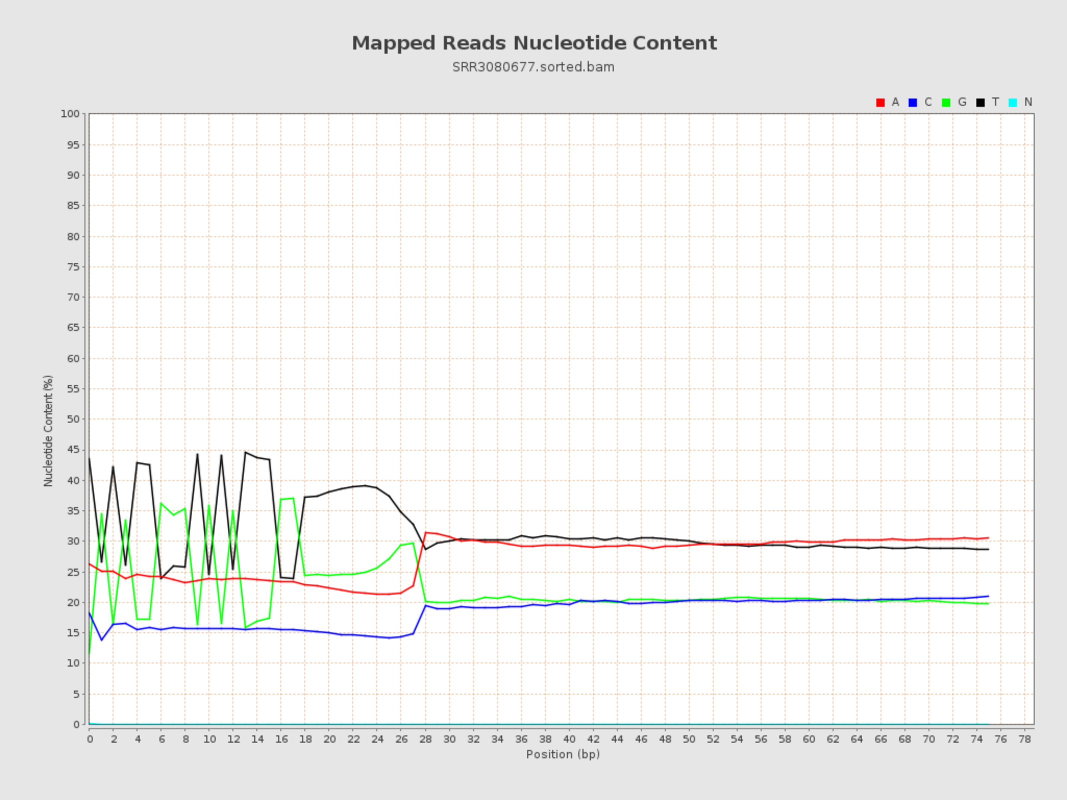
6. Results : Genome Fraction Coverage



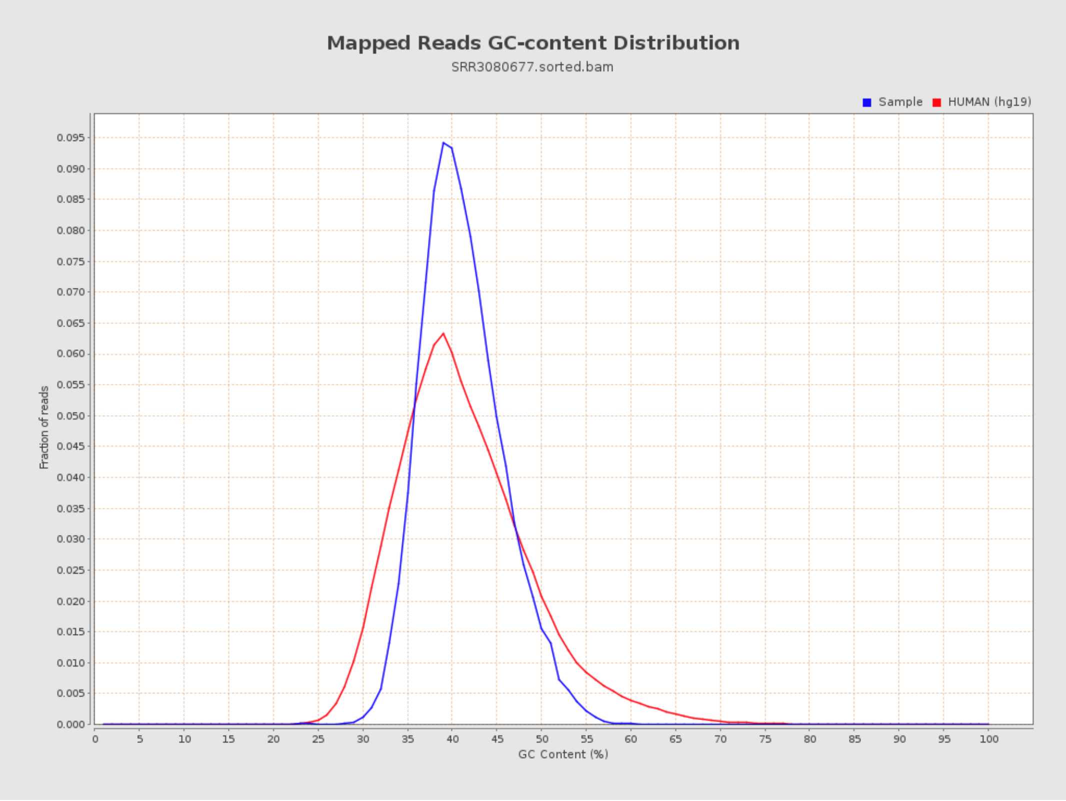
7. Results : Duplication Rate Histogram



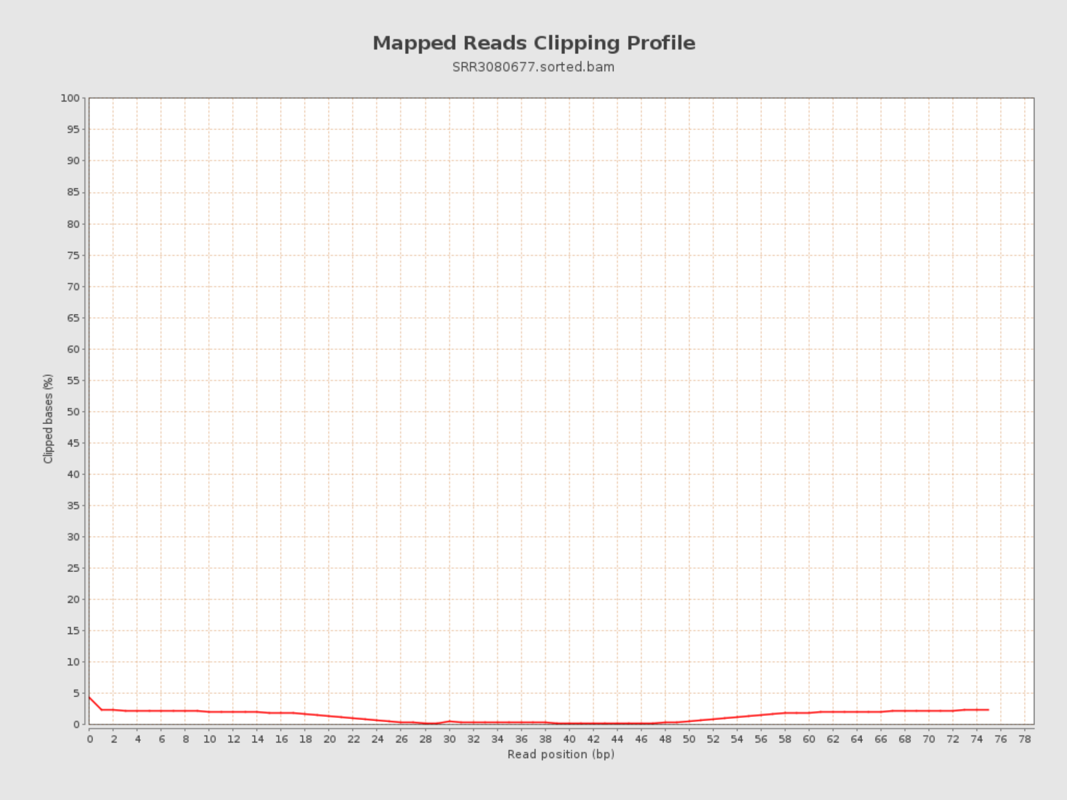
8. Results : Mapped Reads Nucleotide Content



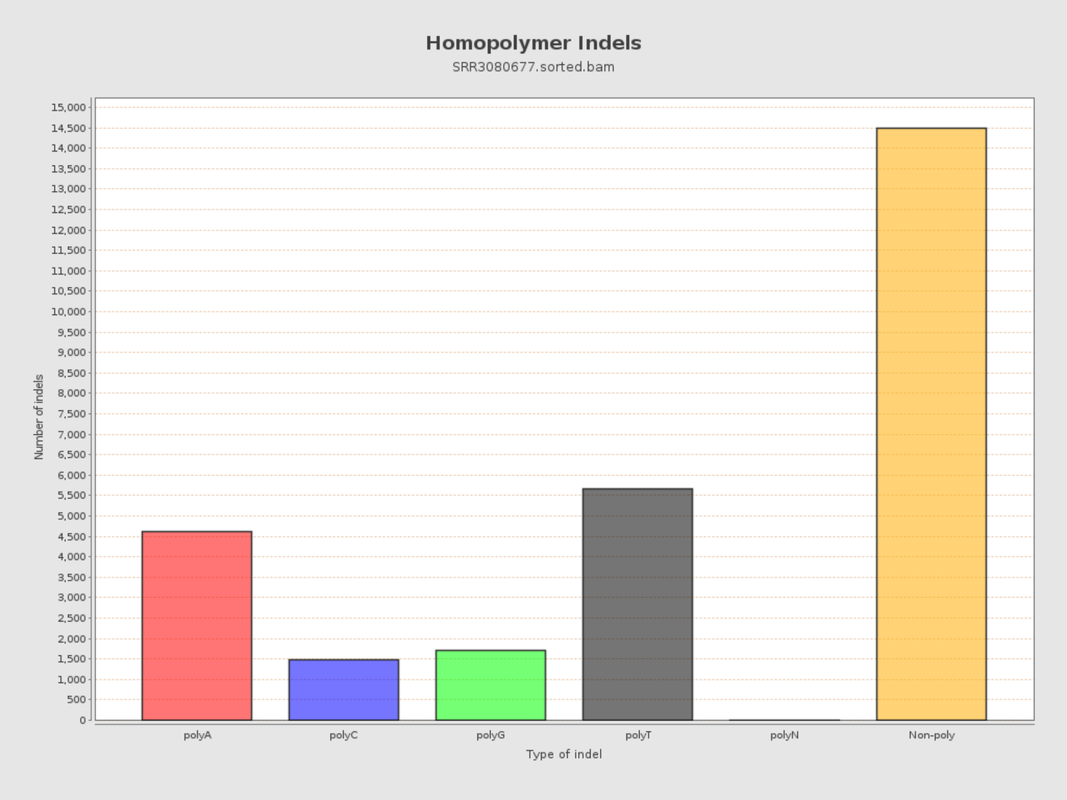
9. Results : Mapped Reads GC-content Distribution



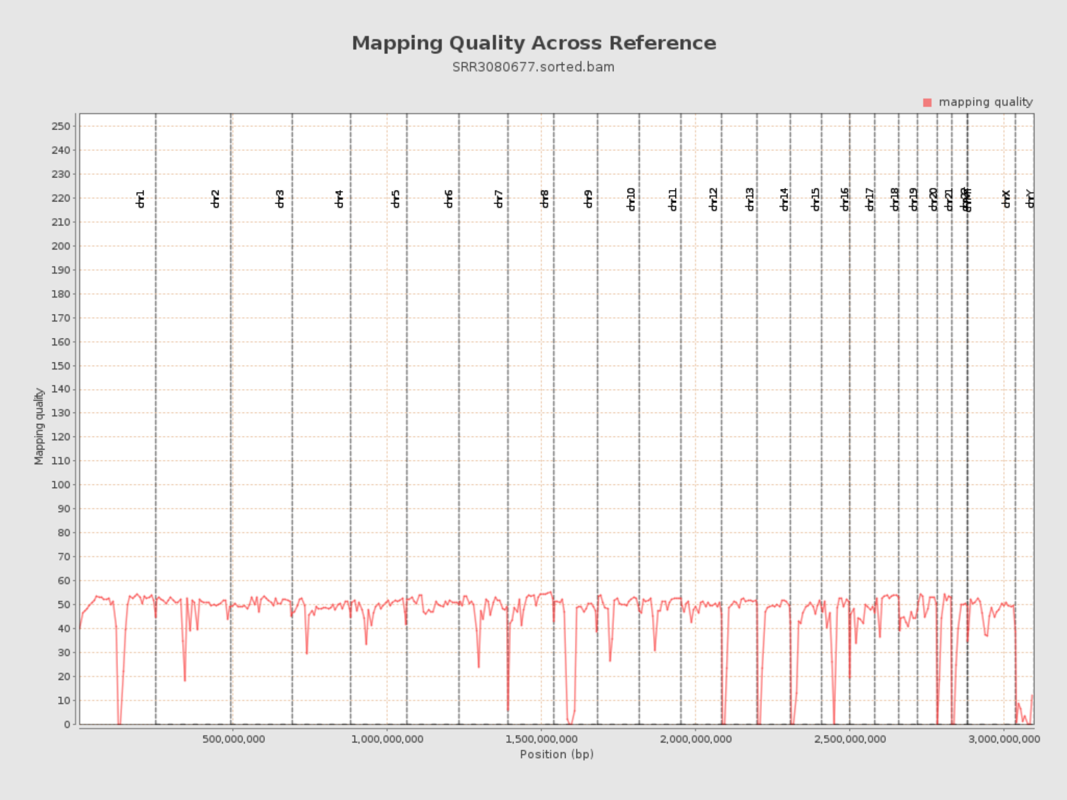
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram