Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:20:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080712.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_SRR3080712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080712.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:20:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,070,923
Mapped reads	1,868,254 / 90.21%
Unmapped reads	202,669 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,419 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	99,861 / 4.82%
Duplication rate	4.55%
Clipped reads	751,027 / 36.27%

2.2. ACGT Content

Number/percentage of A's	35,310,101 / 27.94%
Number/percentage of C's	23,322,414 / 18.46%
Number/percentage of T's	40,281,909 / 31.88%
Number/percentage of G's	27,456,508 / 21.73%
Number/percentage of N's	1,878 / 0%
GC Percentage	40.18%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.3477

2.4. Mapping Quality

Mean Mapping Quality	46.2

2.5. Mismatches and indels

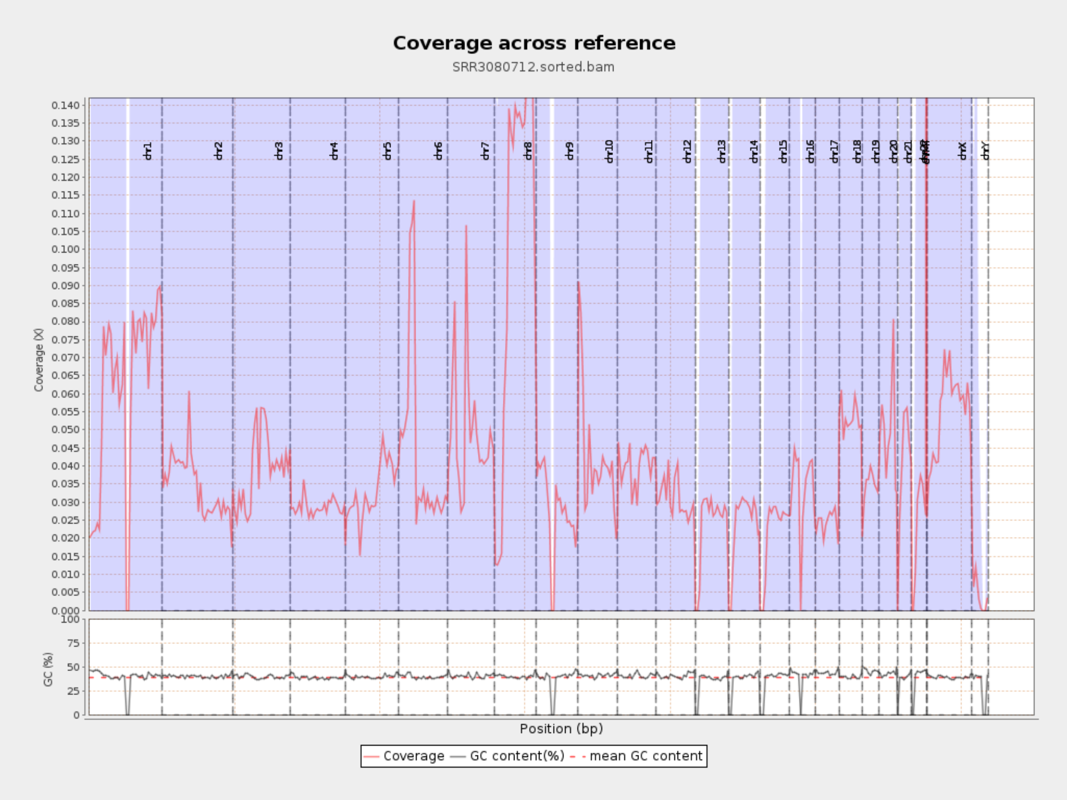
General error rate	0.81%
Mismatches	1,010,678
Insertions	8,912
Mapped reads with at least one insertion	0.47%
Deletions	26,637
Mapped reads with at least one deletion	1.41%
Homopolymer indels	48.38%

2.6. Chromosome stats

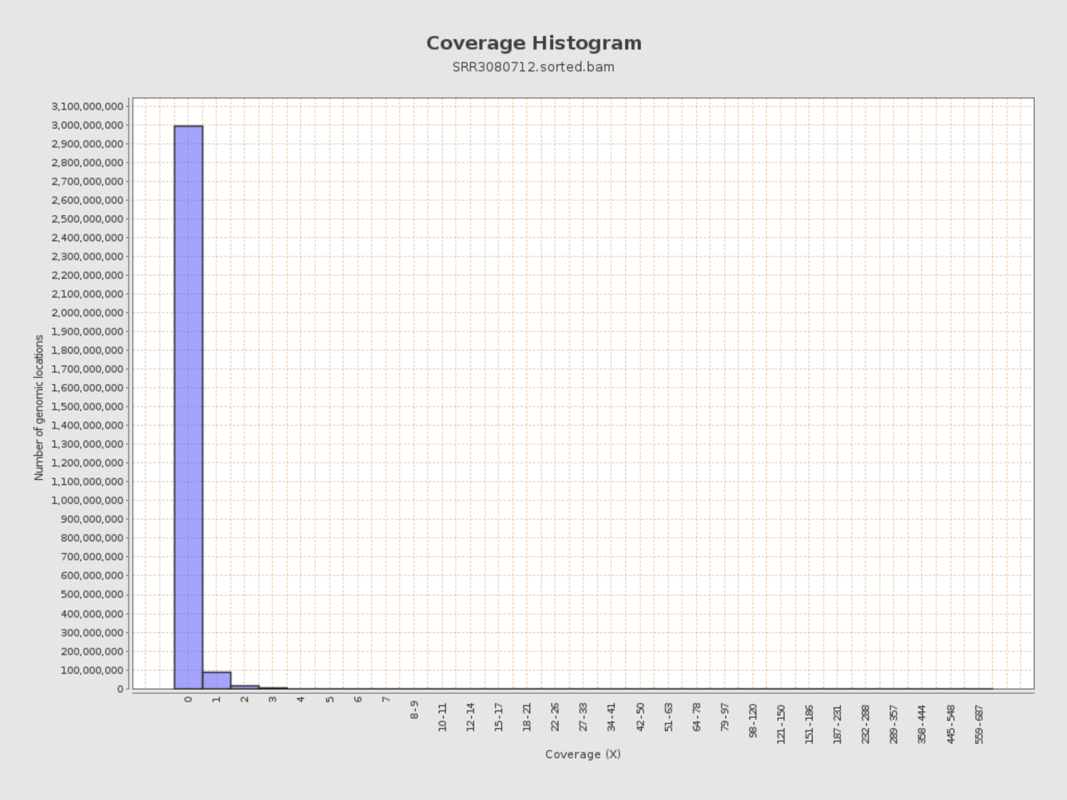
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15200019	0.061	0.4939
chr2	243199373	8410902	0.0346	0.349
chr3	198022430	7783298	0.0393	0.2295
chr4	191154276	5464653	0.0286	0.2008
chr5	180915260	5982532	0.0331	0.2096
chr6	171115067	7614334	0.0445	0.3343
chr7	159138663	8016380	0.0504	0.8398

chr8	146364022	14952154	0.1022	0.4712
chr9	141213431	3856554	0.0273	0.2436
chr10	135534747	5888373	0.0434	0.3142
chr11	135006516	5382888	0.0399	0.2506
chr12	133851895	4113880	0.0307	0.2042
chr13	115169878	2709882	0.0235	0.1776
chr14	107349540	2545514	0.0237	0.1884
chr15	102531392	2206990	0.0215	0.1694
chr16	90354753	3046881	0.0337	0.2273
chr17	81195210	1974755	0.0243	0.1851
chr18	78077248	4182654	0.0536	0.3745
chr19	59128983	2067662	0.035	0.3282
chr20	63025520	3118625	0.0495	0.2611
chr21	48129895	1926152	0.04	0.2371
chr22	51304566	1161747	0.0226	0.1725
chrMT	16571	14760	0.8907	1.1961
chrX	155270560	8528998	0.0549	0.2868
chrY	59373566	269029	0.0045	0.0948

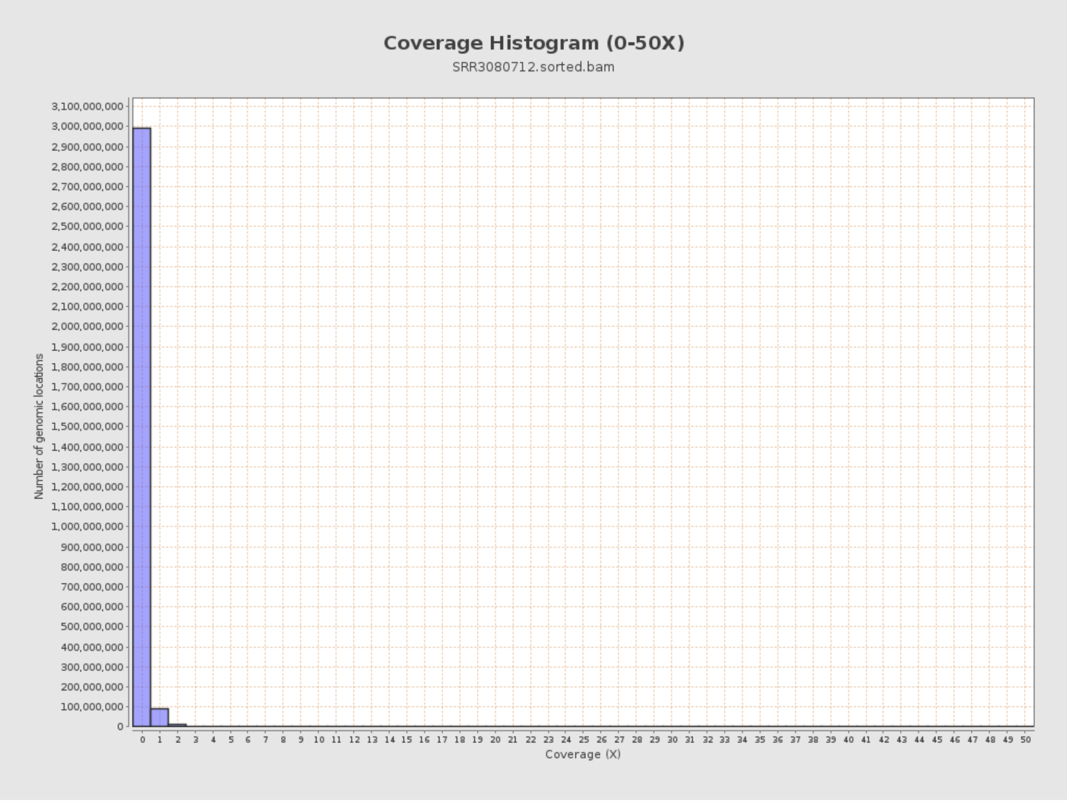
3. Results : Coverage across reference



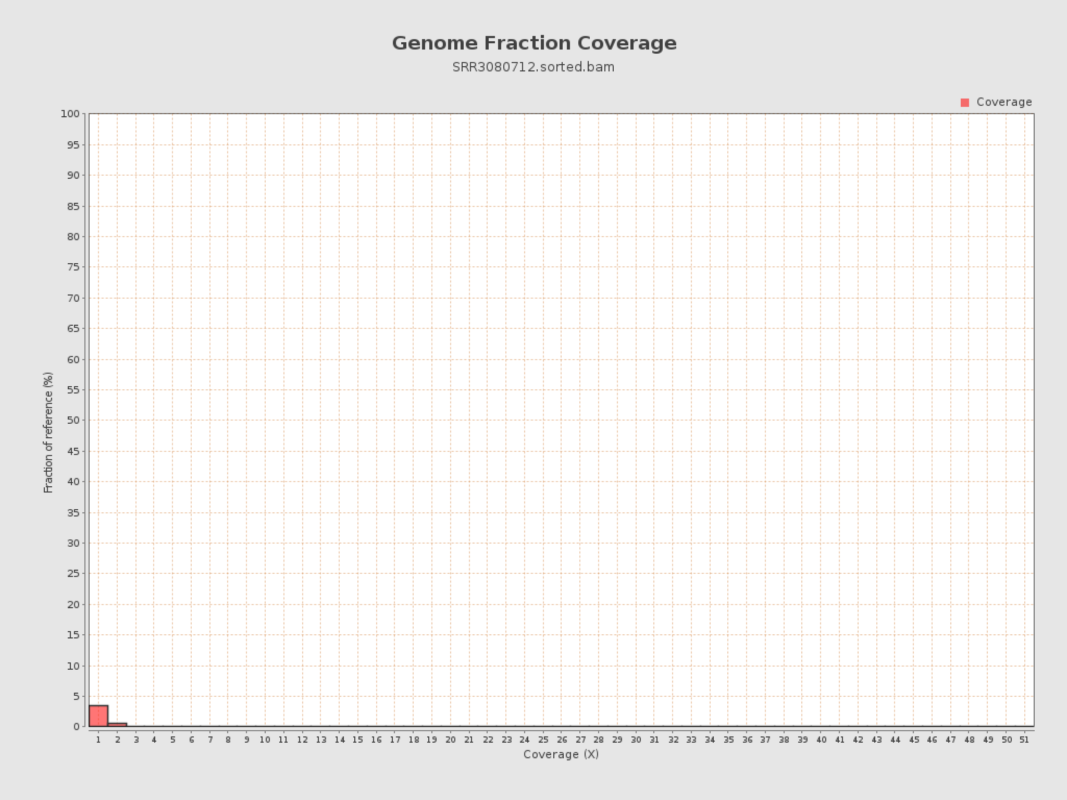
4. Results : Coverage Histogram



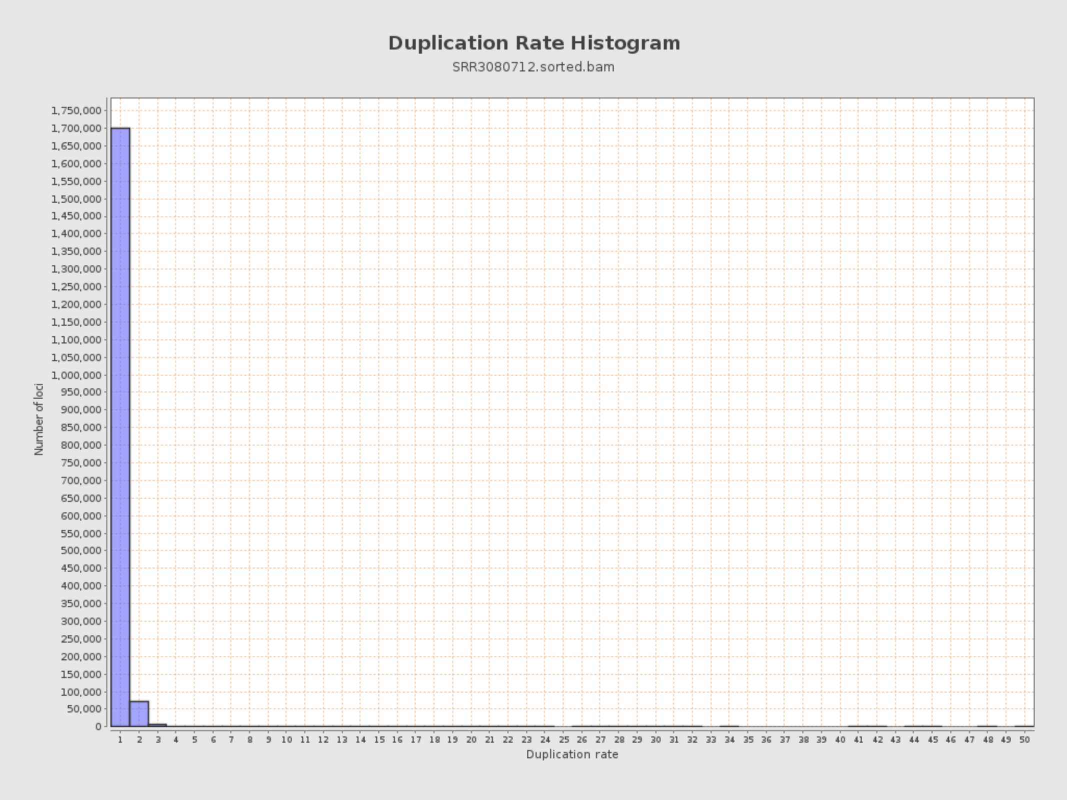
5. Results : Coverage Histogram (0-50X)



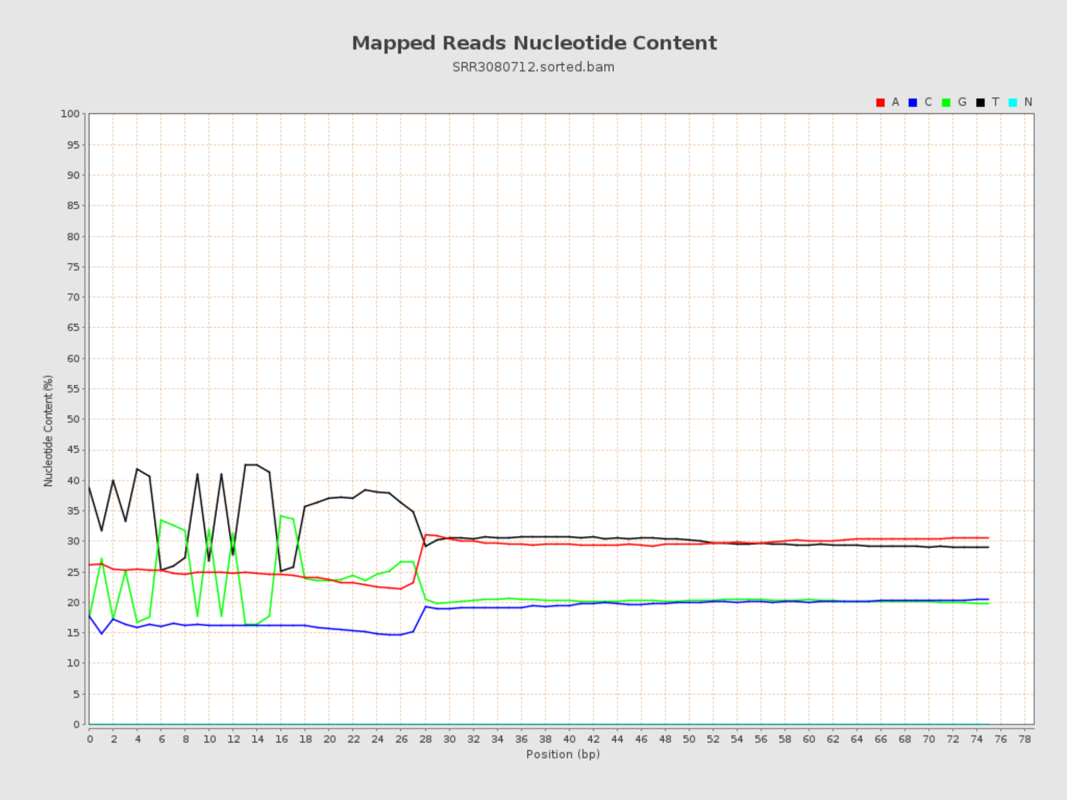
6. Results : Genome Fraction Coverage



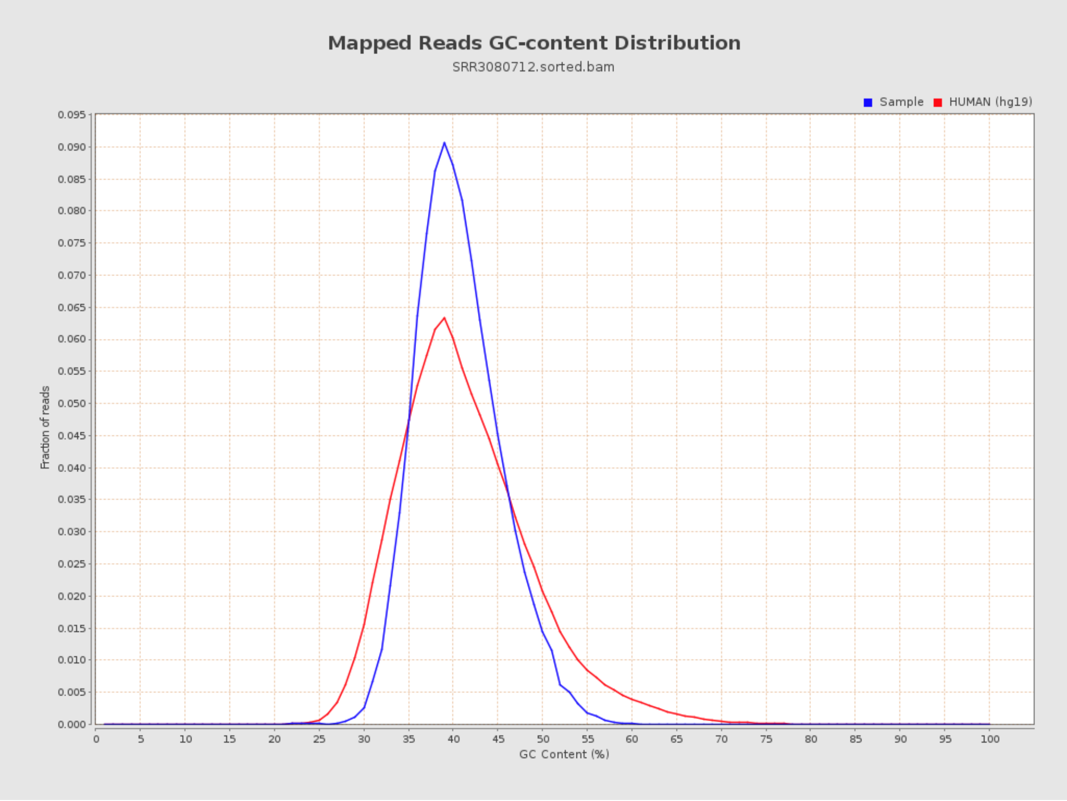
7. Results : Duplication Rate Histogram



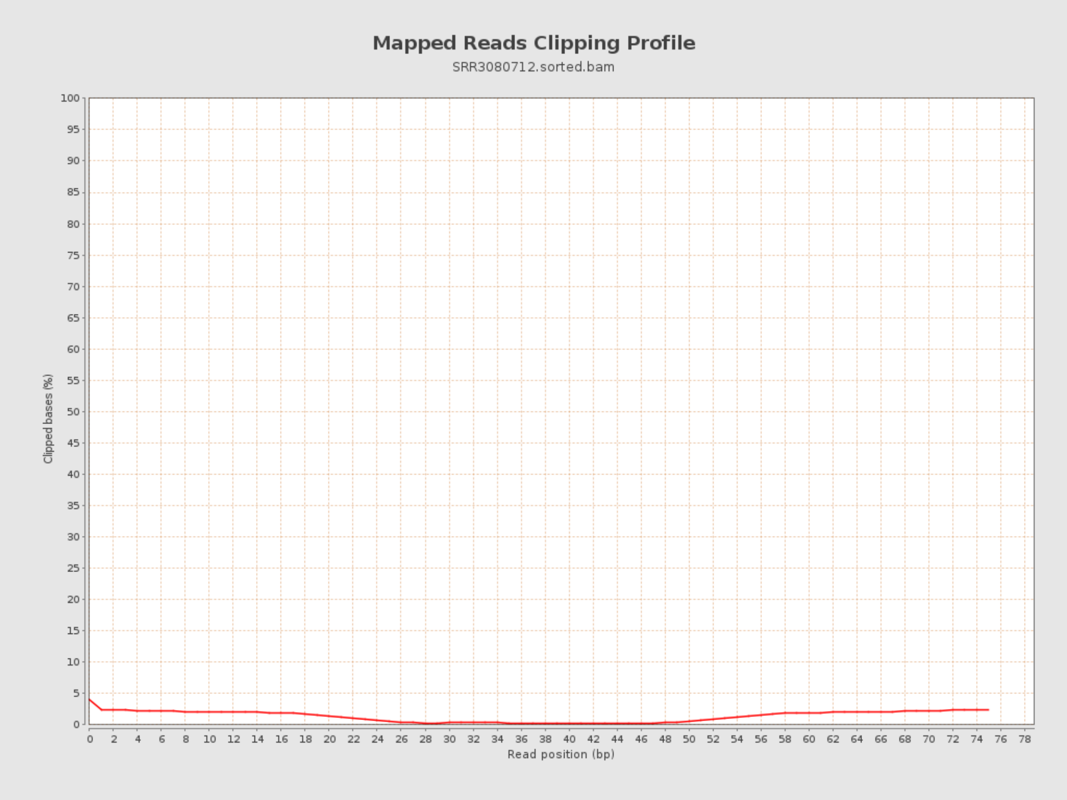
8. Results : Mapped Reads Nucleotide Content



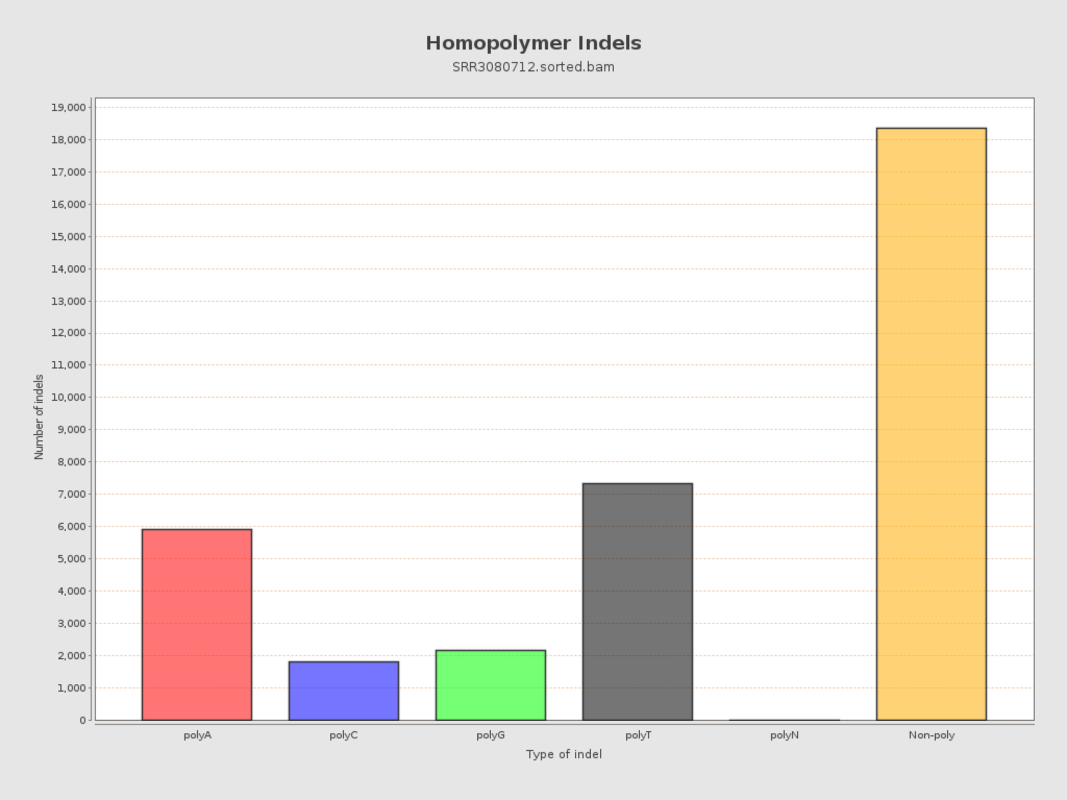
9. Results : Mapped Reads GC-content Distribution



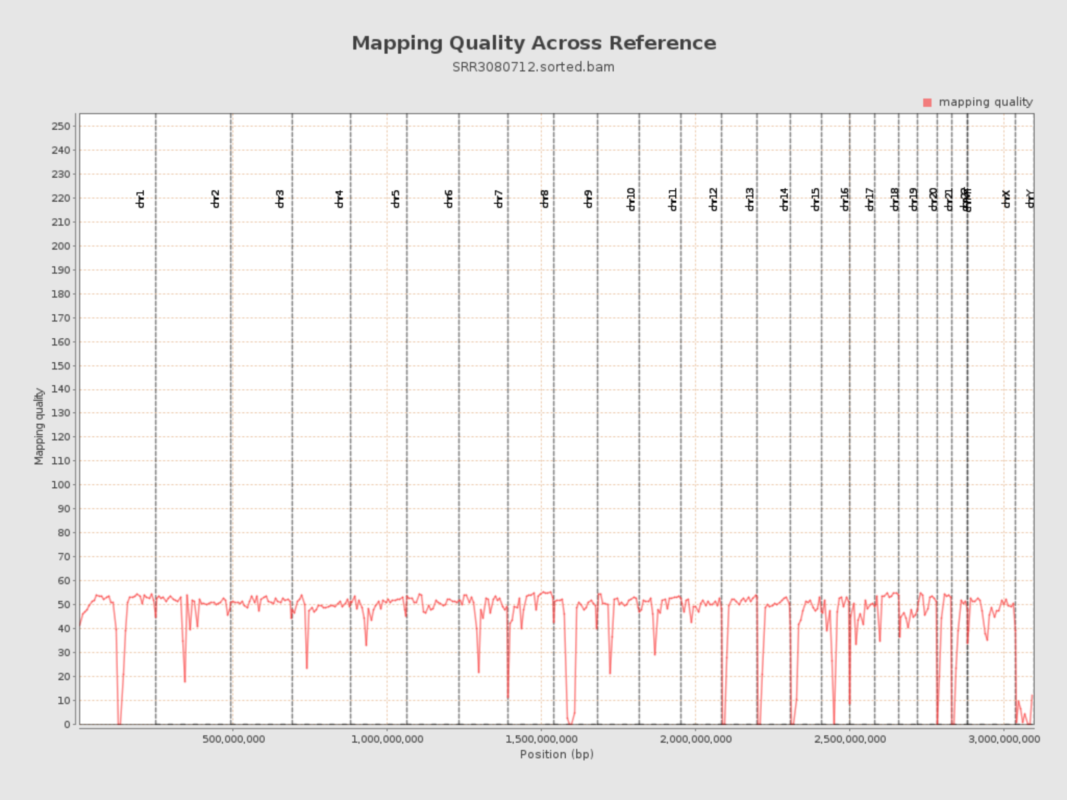
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram