Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:43:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080726.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_SRR3080726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080726.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:43:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,161,006
Mapped reads	1,909,568 / 88.36%
Unmapped reads	251,438 / 11.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,029 / 1.16%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	95,544 / 4.42%
Duplication rate	3.1%
Clipped reads	943,044 / 43.64%

2.2. ACGT Content

Number/percentage of A's	34,617,894 / 27.41%
Number/percentage of C's	24,502,129 / 19.4%
Number/percentage of T's	37,664,511 / 29.82%
Number/percentage of G's	29,517,490 / 23.37%
Number/percentage of N's	1,976 / 0%
GC Percentage	42.77%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.6655

2.4. Mapping Quality

Mean Mapping Quality	40.79

2.5. Mismatches and indels

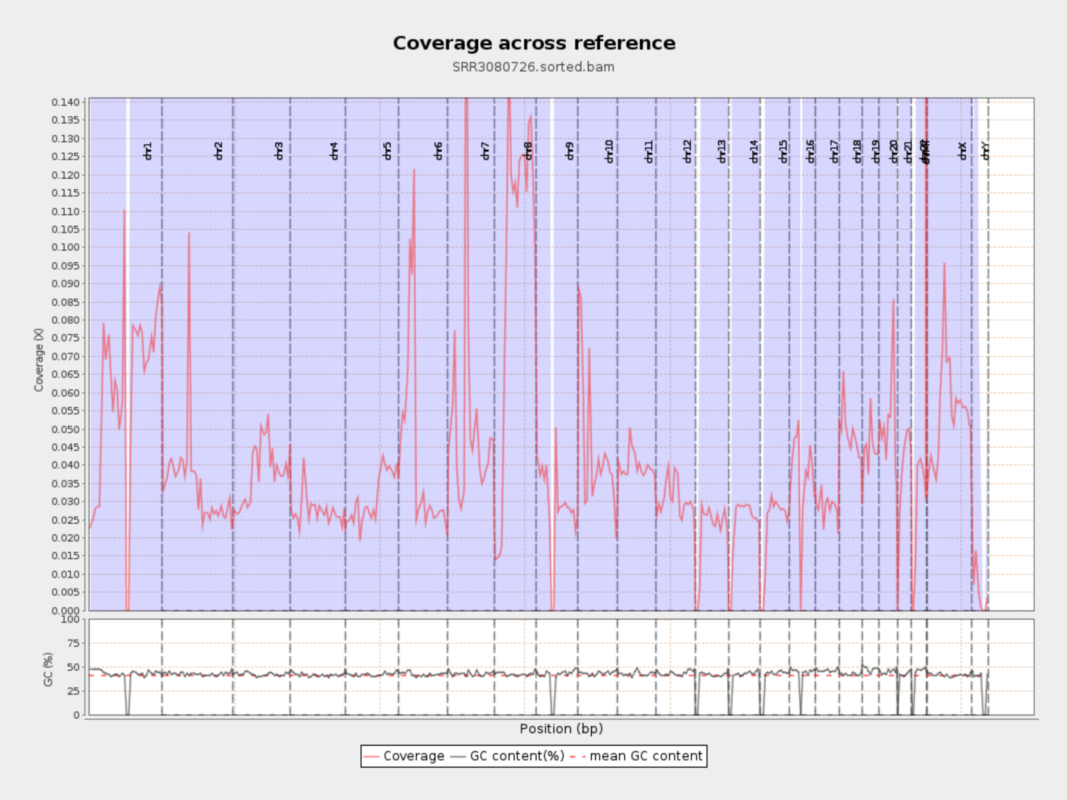
General error rate	0.87%
Mismatches	1,084,689
Insertions	10,694
Mapped reads with at least one insertion	0.55%
Deletions	24,069
Mapped reads with at least one deletion	1.25%
Homopolymer indels	43.94%

2.6. Chromosome stats

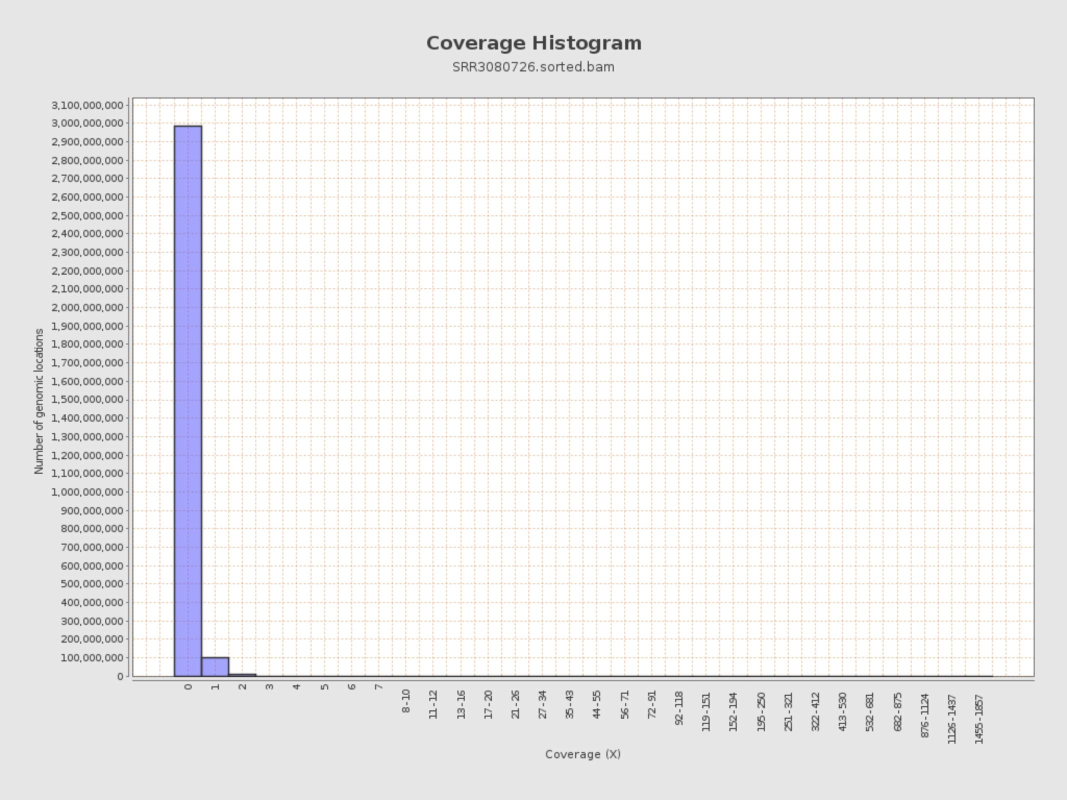
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14943081	0.06	1.0942
chr2	243199373	8539962	0.0351	0.5574
chr3	198022430	7490421	0.0378	0.2138
chr4	191154276	5247016	0.0274	0.2045
chr5	180915260	5671210	0.0313	0.1984
chr6	171115067	7370746	0.0431	0.417
chr7	159138663	8530464	0.0536	2.0608

chr8	146364022	14044866	0.096	0.7063
chr9	141213431	4066028	0.0288	0.4015
chr10	135534747	6093493	0.045	0.4383
chr11	135006516	5348299	0.0396	0.3966
chr12	133851895	4113006	0.0307	0.2092
chr13	115169878	2472705	0.0215	0.1597
chr14	107349540	2500770	0.0233	0.2142
chr15	102531392	2327666	0.0227	0.1872
chr16	90354753	3365965	0.0373	0.2408
chr17	81195210	2308849	0.0284	0.2394
chr18	78077248	3838884	0.0492	0.743
chr19	59128983	2649887	0.0448	0.6463
chr20	63025520	3282642	0.0521	0.2767
chr21	48129895	1828842	0.038	0.2351
chr22	51304566	1373126	0.0268	0.1765
chrMT	16571	69368	4.1861	3.4267
chrX	155270560	8525521	0.0549	0.3372
chrY	59373566	342488	0.0058	0.1283

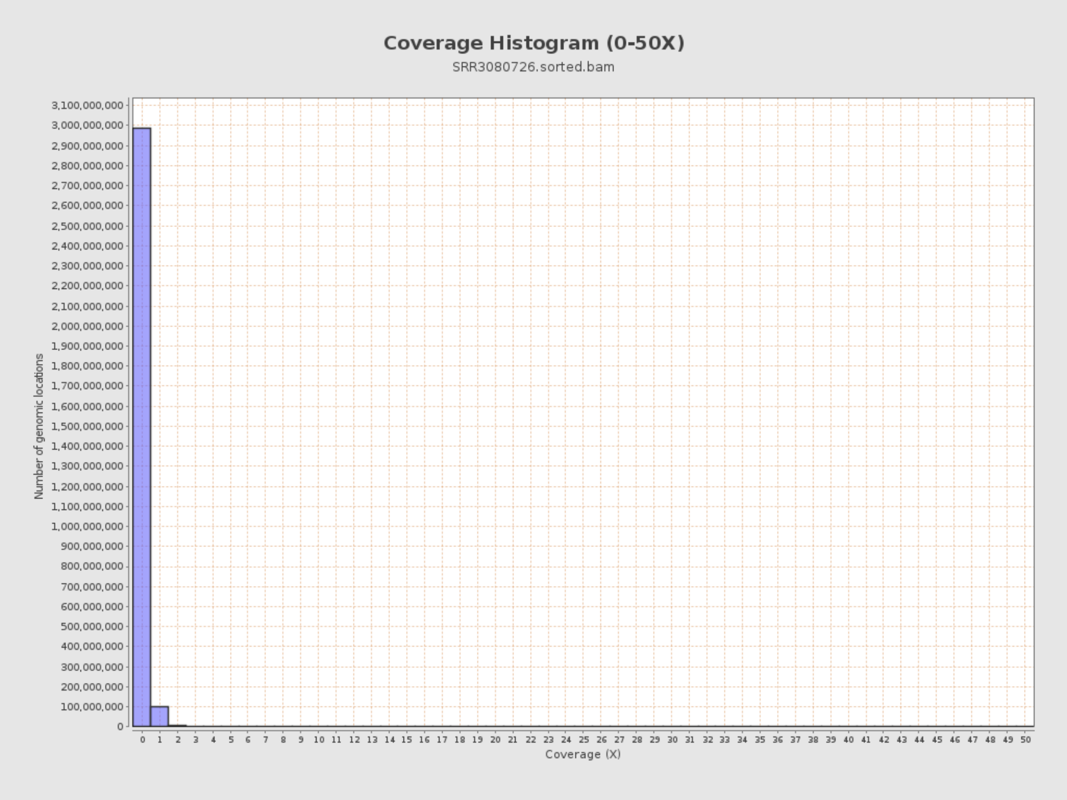
3. Results : Coverage across reference



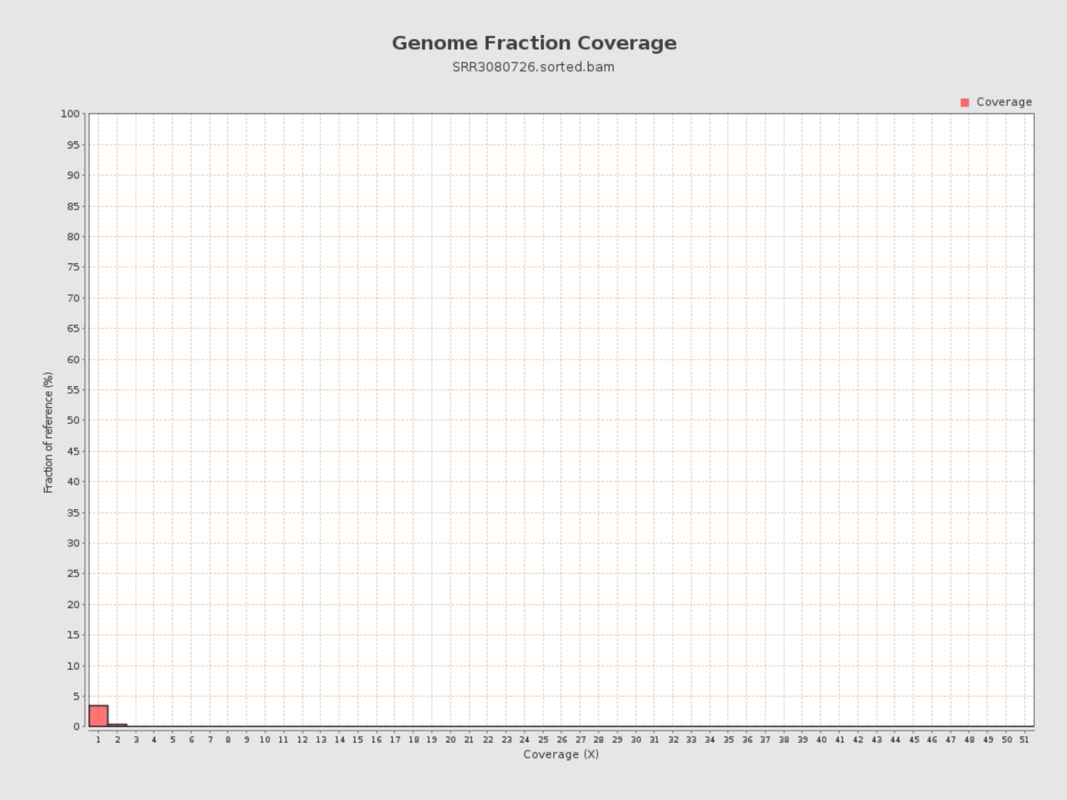
4. Results : Coverage Histogram



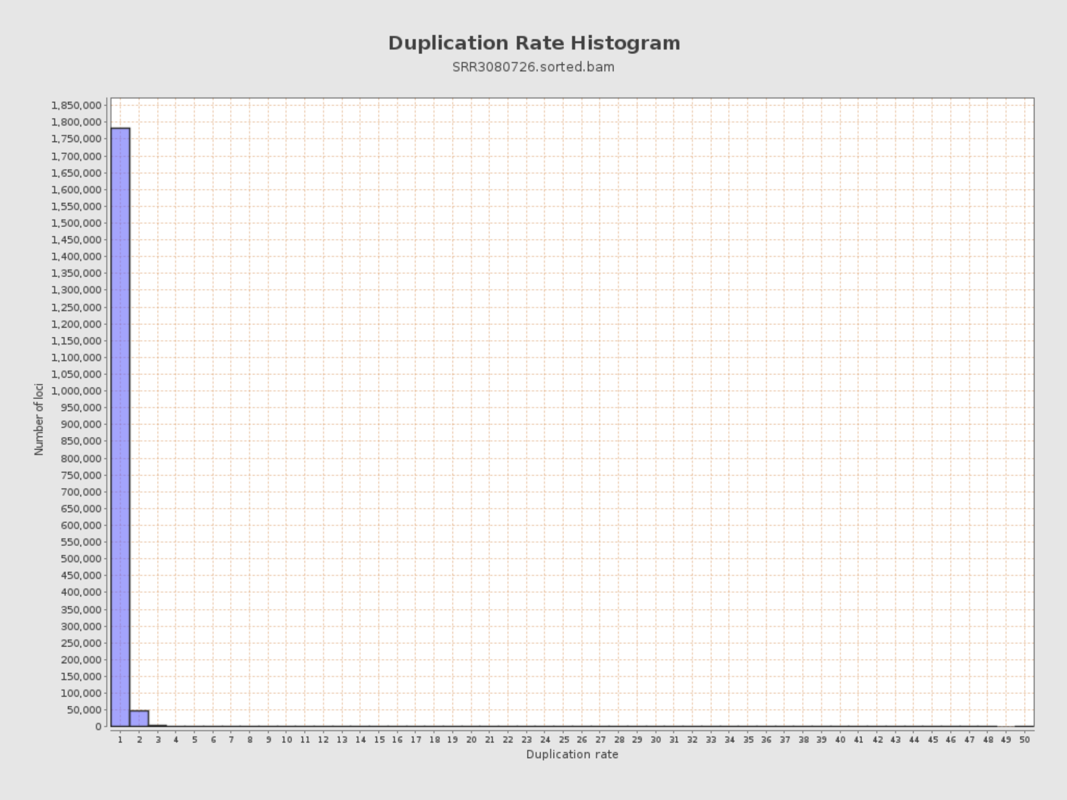
5. Results : Coverage Histogram (0-50X)



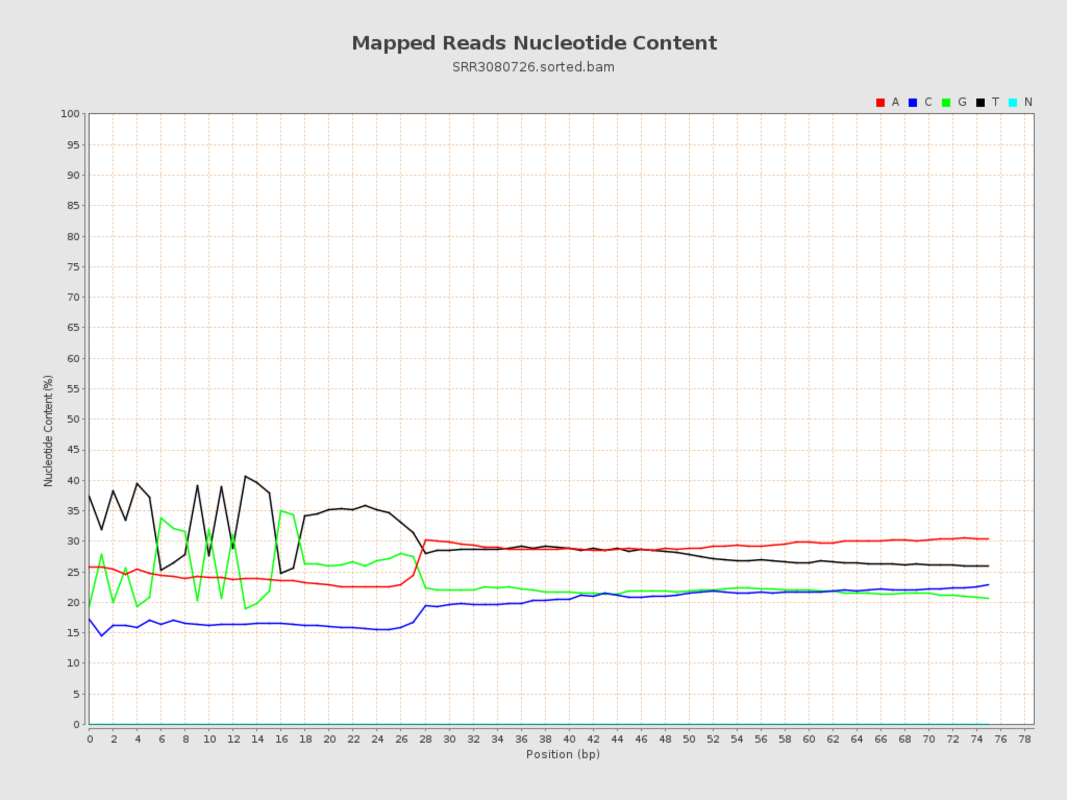
6. Results : Genome Fraction Coverage



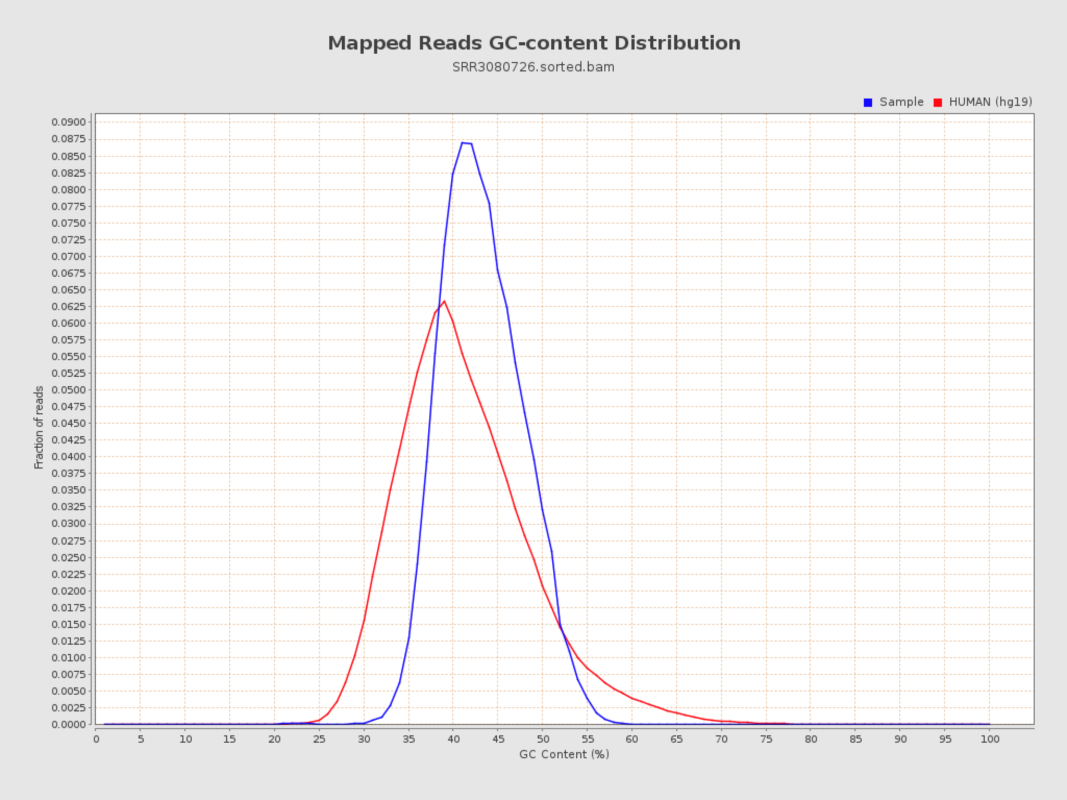
7. Results : Duplication Rate Histogram



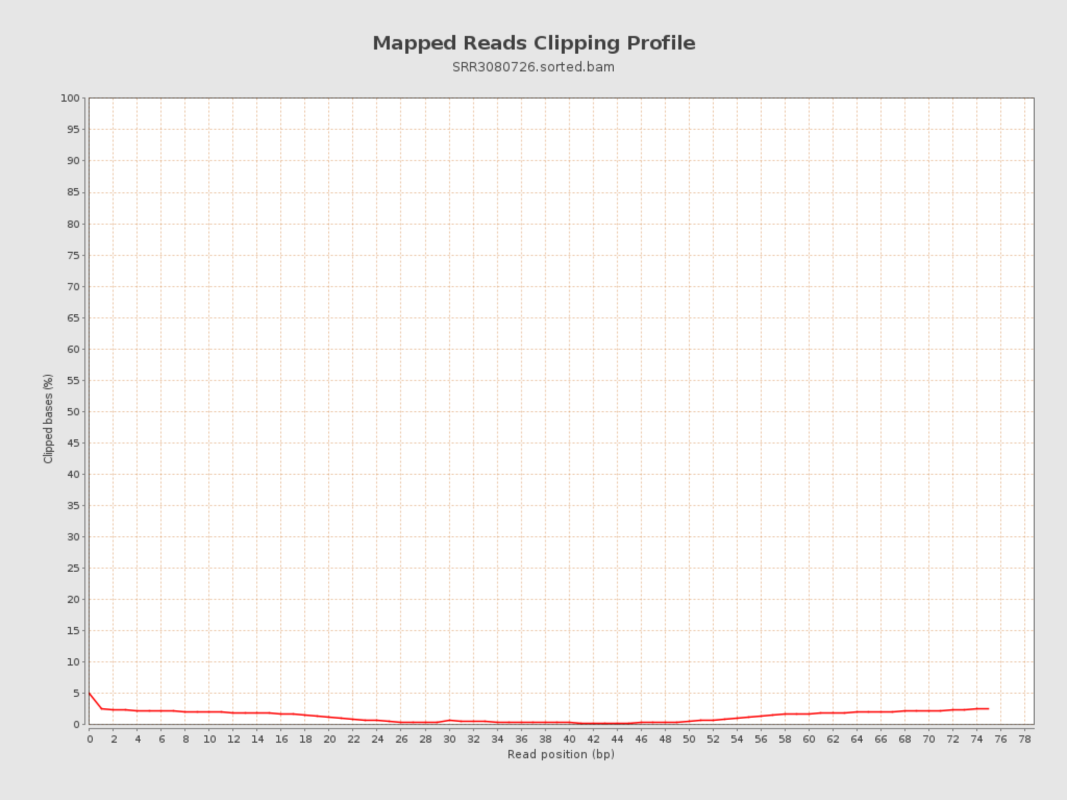
8. Results : Mapped Reads Nucleotide Content



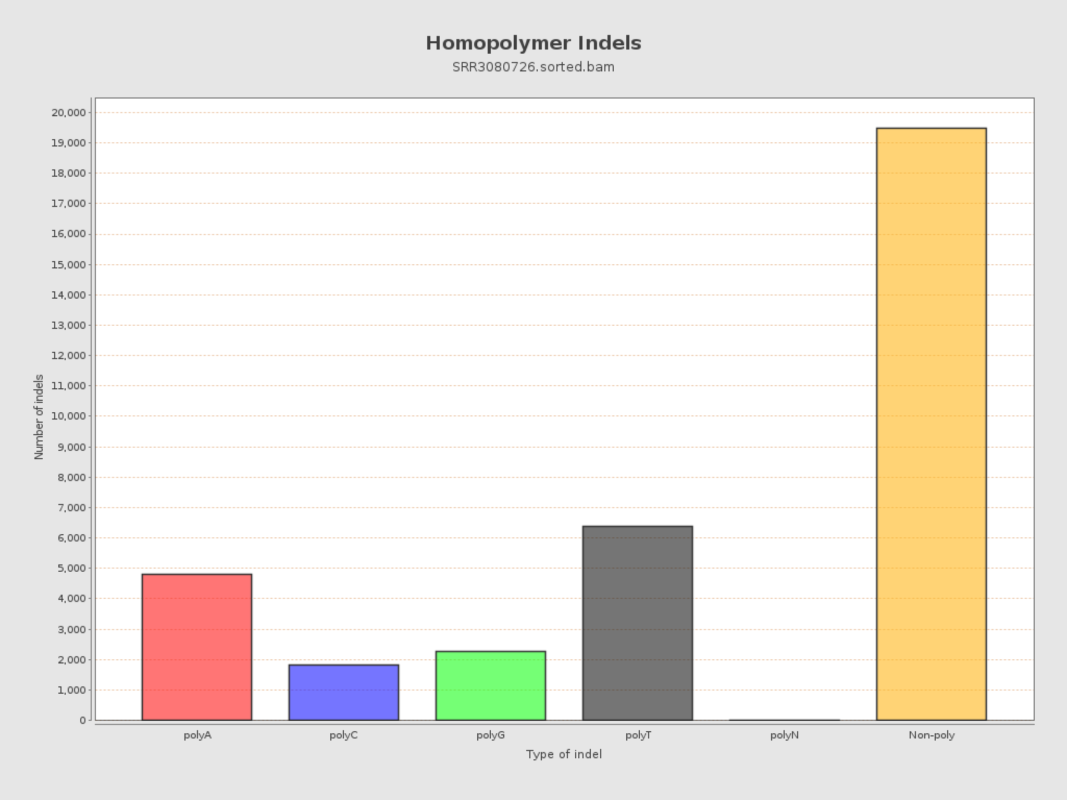
9. Results : Mapped Reads GC-content Distribution



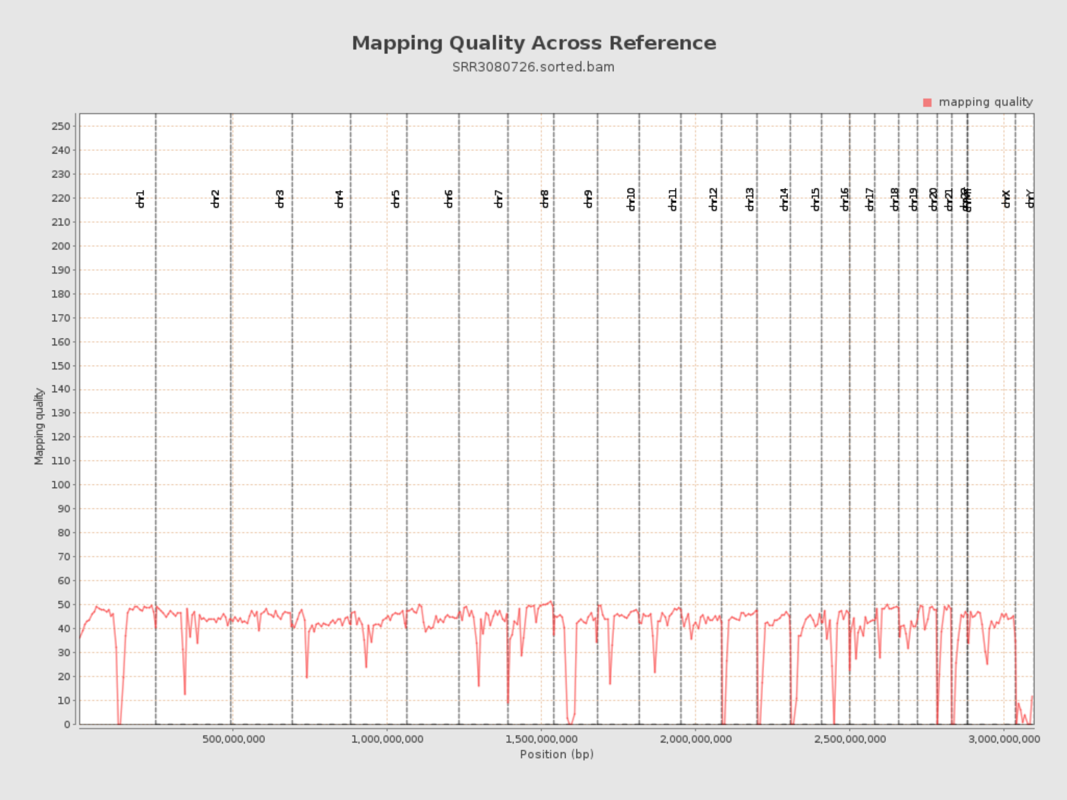
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram