Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:33:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080818.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_SRR3080818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:33:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,296,686
Mapped reads	2,044,498 / 89.02%
Unmapped reads	252,188 / 10.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,482 / 0.76%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	126,614 / 5.51%
Duplication rate	5.06%
Clipped reads	862,442 / 37.55%

2.2. ACGT Content

Number/percentage of A's	38,595,852 / 28.07%
Number/percentage of C's	25,311,894 / 18.41%
Number/percentage of T's	43,858,644 / 31.9%
Number/percentage of G's	29,701,555 / 21.6%
Number/percentage of N's	19,062 / 0.01%
GC Percentage	40.01%

2.3. Coverage

Mean	0.0444

Standard Deviation	0.4623

2.4. Mapping Quality

Mean Mapping Quality	46.39

2.5. Mismatches and indels

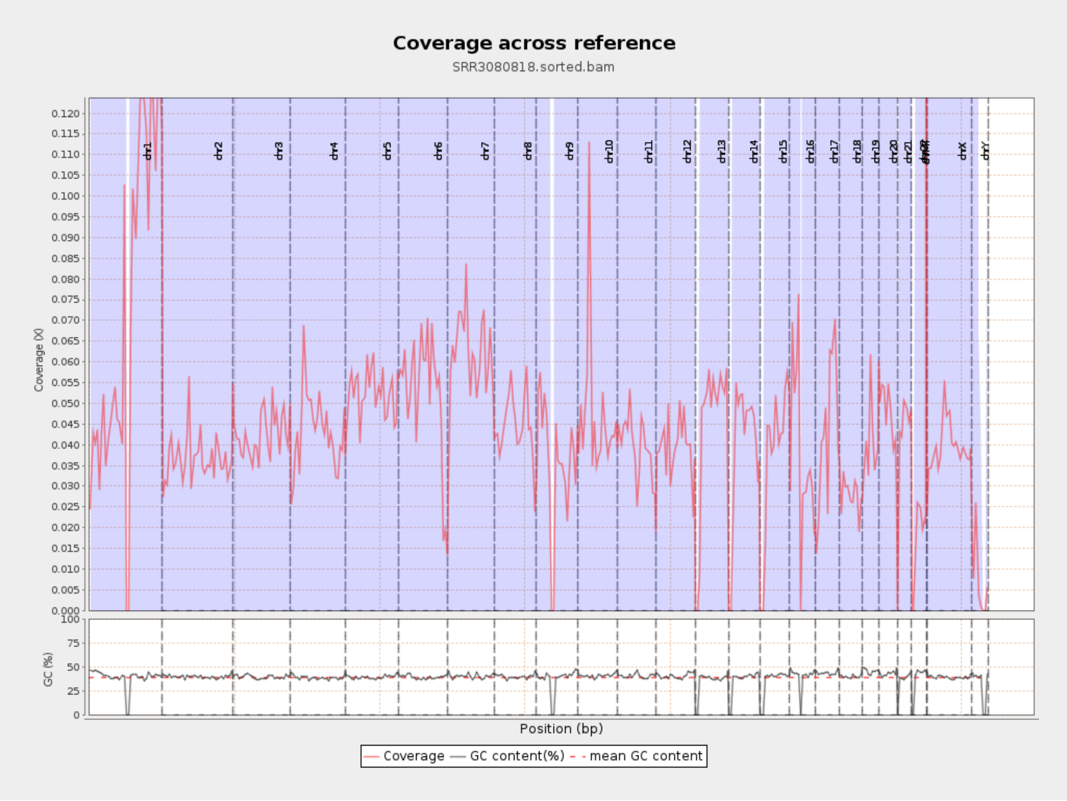
General error rate	0.86%
Mismatches	1,159,878
Insertions	10,643
Mapped reads with at least one insertion	0.51%
Deletions	30,506
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.29%

2.6. Chromosome stats

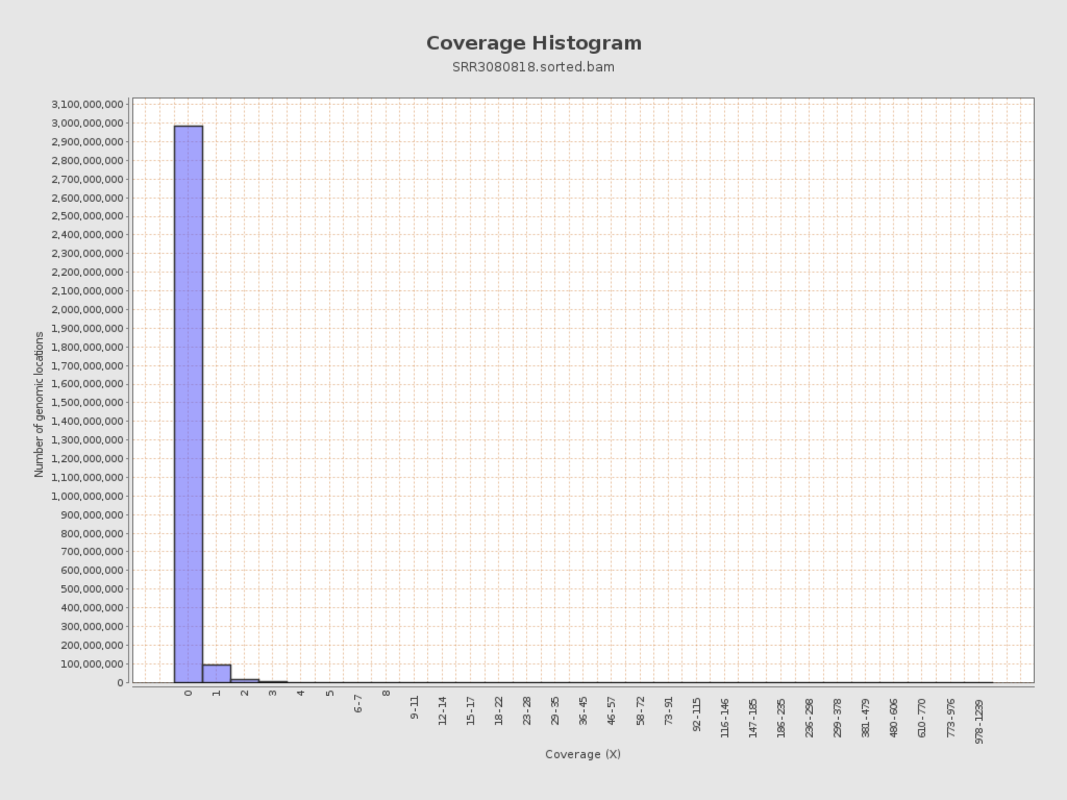
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17996561	0.0722	1.1381
chr2	243199373	8893210	0.0366	0.3601
chr3	198022430	8405817	0.0424	0.2599
chr4	191154276	8260784	0.0432	0.2682
chr5	180915260	9455504	0.0523	0.2679
chr6	171115067	9066034	0.053	0.3046
chr7	159138663	9905582	0.0622	0.4939

chr8	146364022	6544654	0.0447	0.5285
chr9	141213431	5007257	0.0355	0.2821
chr10	135534747	6340468	0.0468	0.5644
chr11	135006516	5348309	0.0396	0.2726
chr12	133851895	5286729	0.0395	0.2355
chr13	115169878	5069528	0.044	0.2464
chr14	107349540	4195262	0.0391	0.2408
chr15	102531392	3802461	0.0371	0.2244
chr16	90354753	3461283	0.0383	0.2645
chr17	81195210	3522359	0.0434	0.2524
chr18	78077248	2191258	0.0281	0.4651
chr19	59128983	2416372	0.0409	0.7377
chr20	63025520	2982924	0.0473	0.2617
chr21	48129895	2016943	0.0419	0.2626
chr22	51304566	856604	0.0167	0.1479
chrMT	16571	12016	0.7251	1.0349
chrX	155270560	6102169	0.0393	0.2401
chrY	59373566	400740	0.0067	0.2076

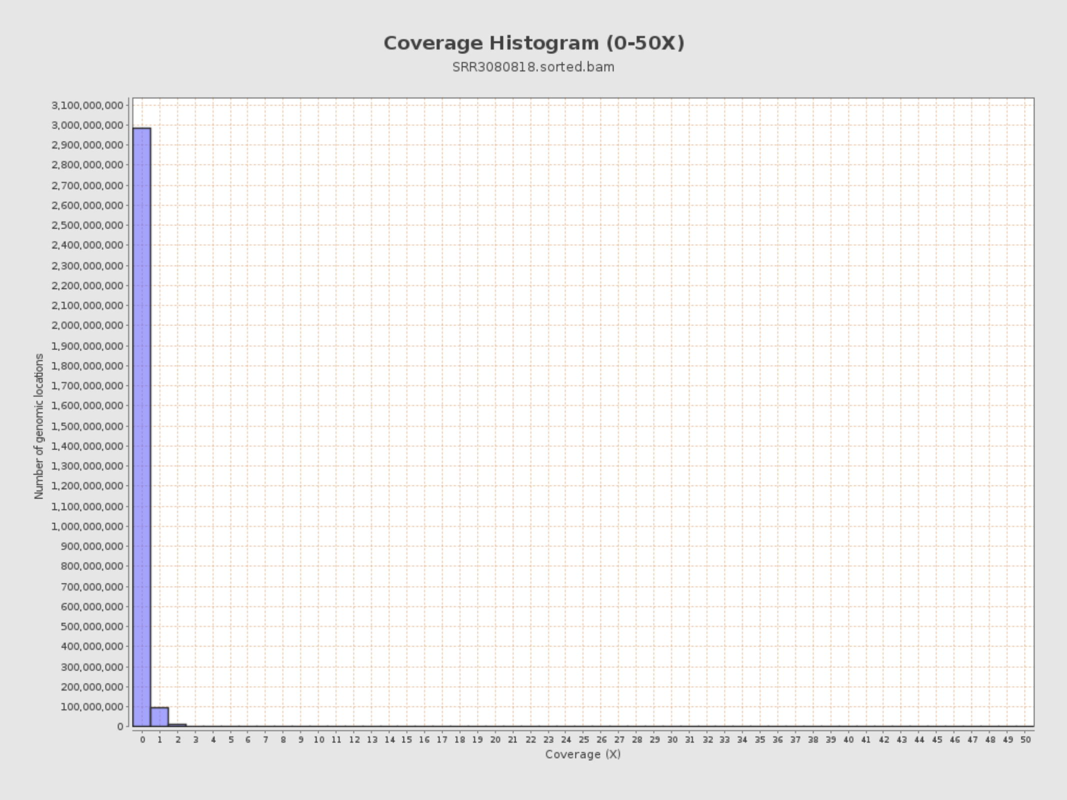
3. Results : Coverage across reference



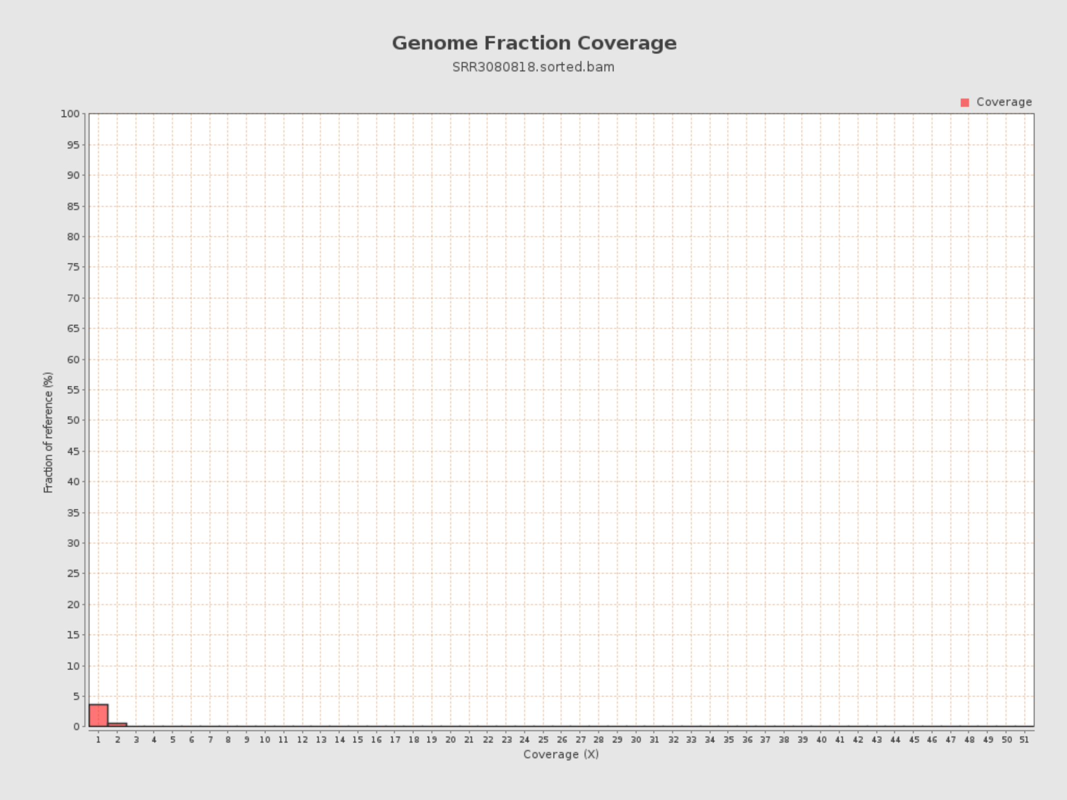
4. Results : Coverage Histogram



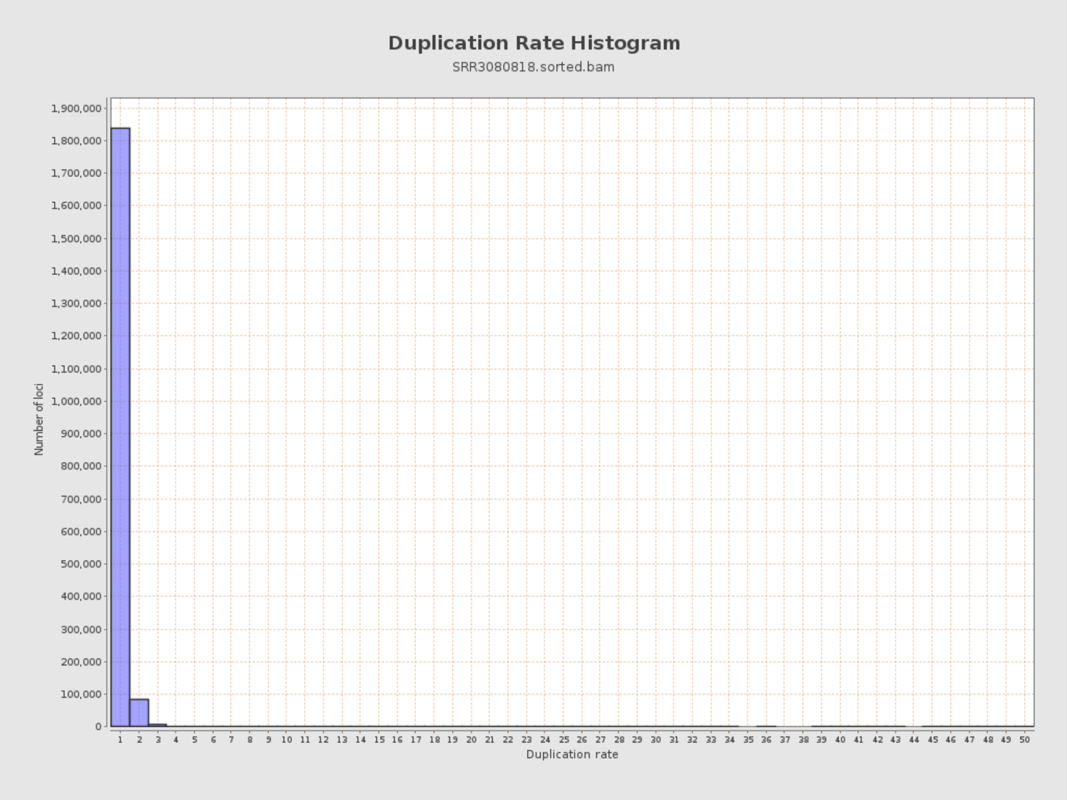
5. Results : Coverage Histogram (0-50X)



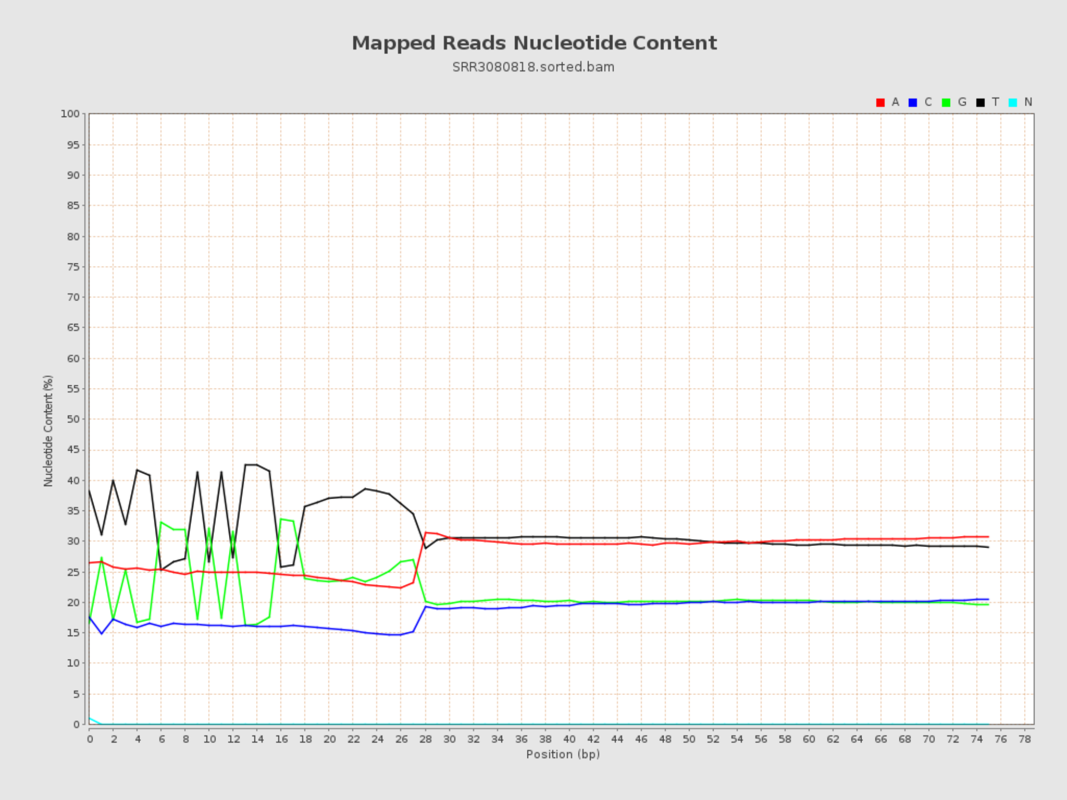
6. Results : Genome Fraction Coverage



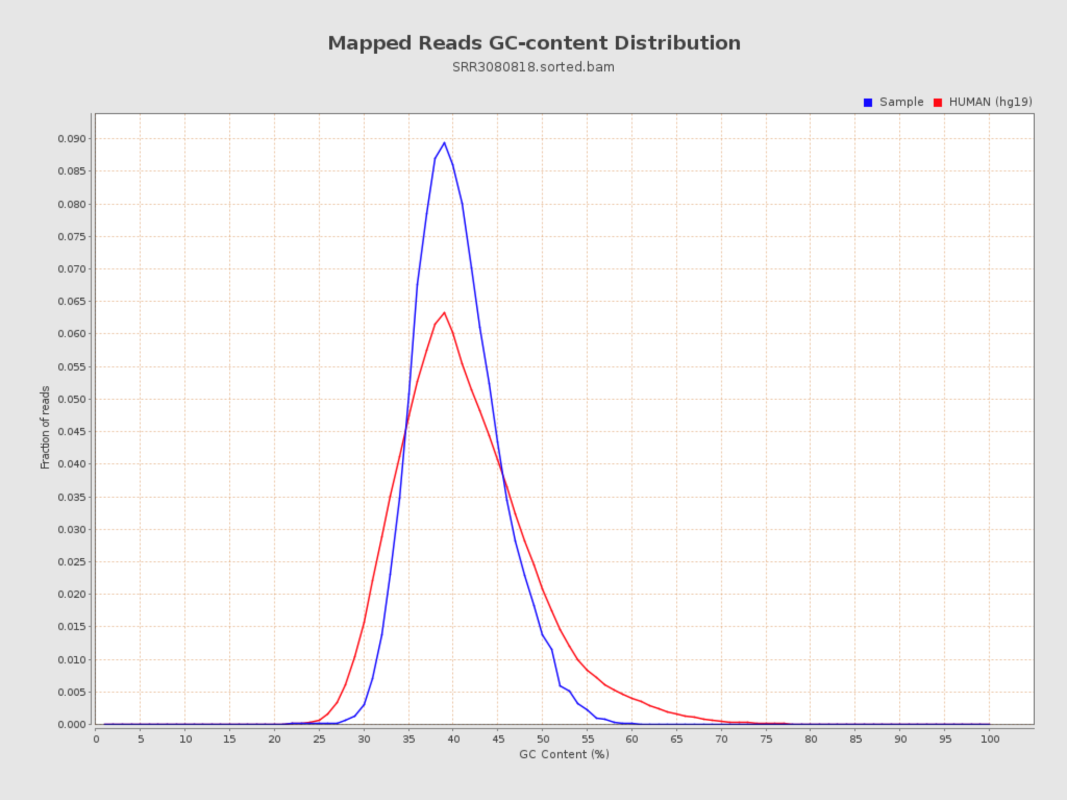
7. Results : Duplication Rate Histogram



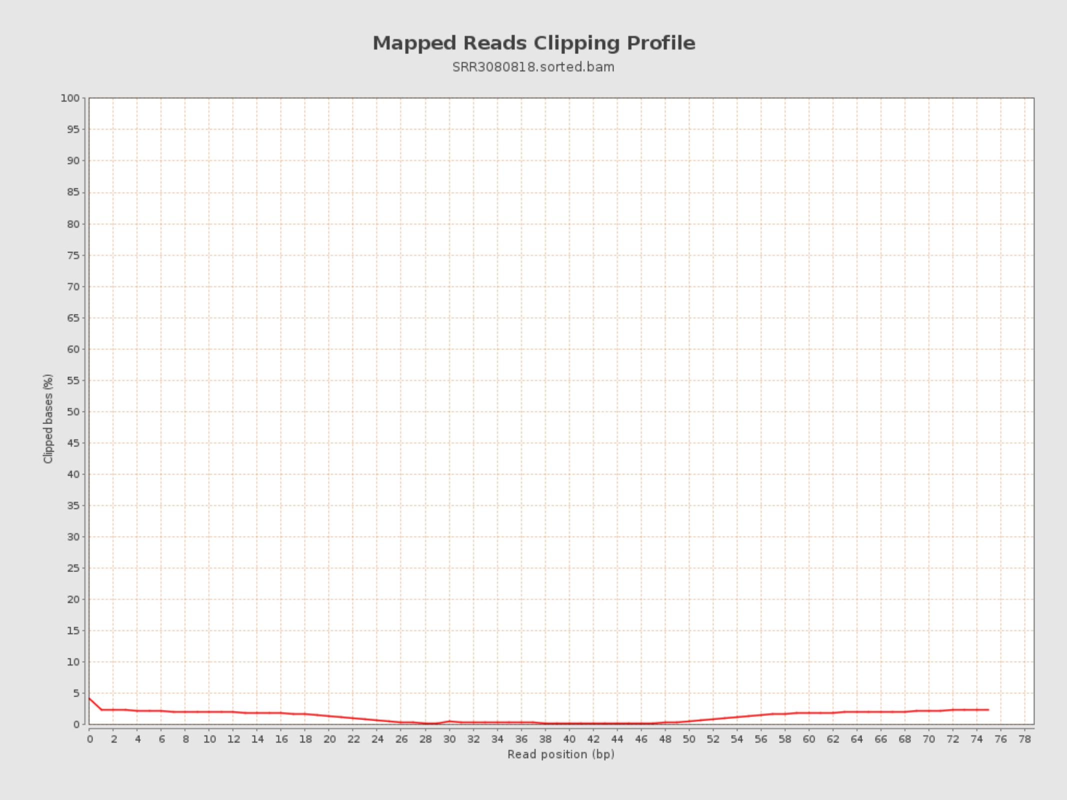
8. Results : Mapped Reads Nucleotide Content



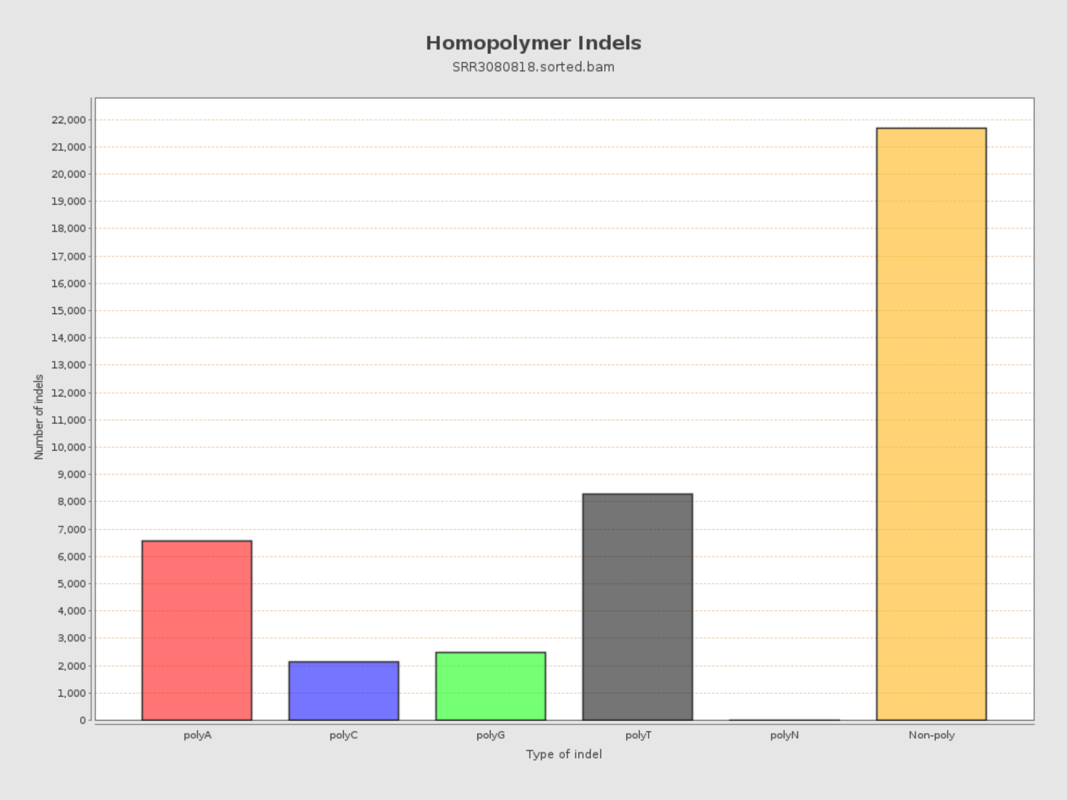
9. Results : Mapped Reads GC-content Distribution



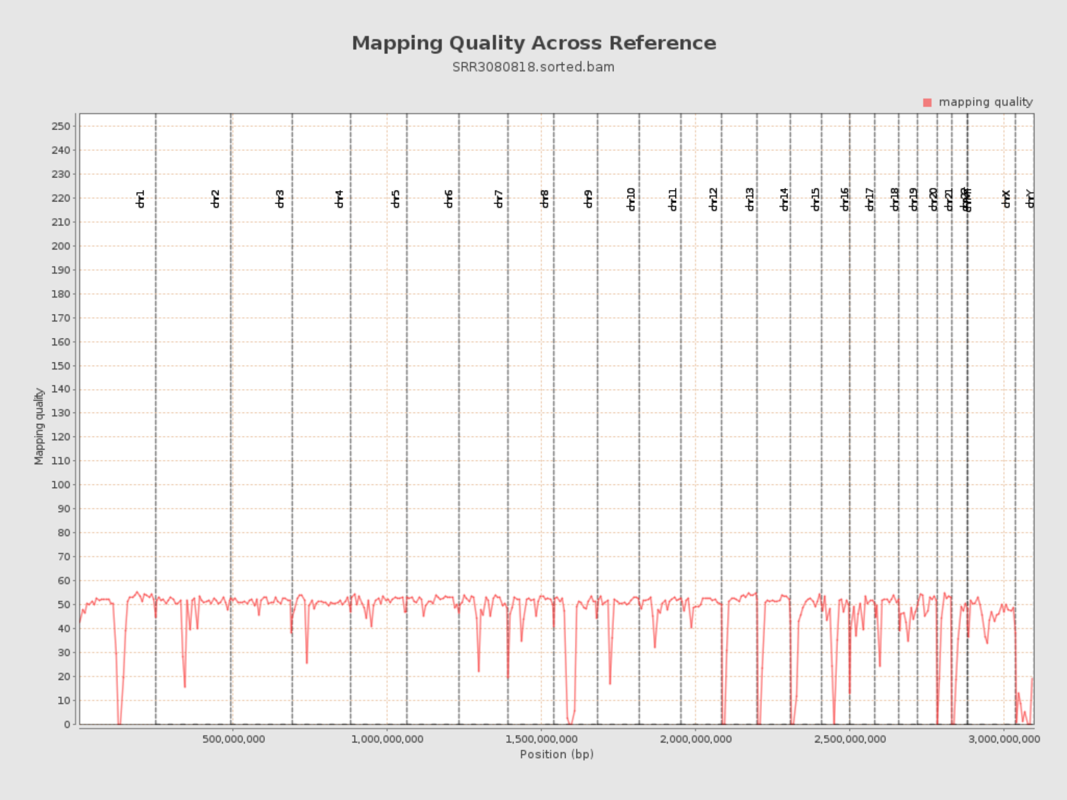
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram