Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:28:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080708.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_SRR3080708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080708.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:28:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,240,492
Mapped reads	2,052,452 / 91.61%
Unmapped reads	188,040 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,179 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	110,205 / 4.92%
Duplication rate	4.61%
Clipped reads	800,772 / 35.74%

2.2. ACGT Content

Number/percentage of A's	38,606,818 / 27.73%
Number/percentage of C's	25,989,432 / 18.67%
Number/percentage of T's	44,049,716 / 31.64%
Number/percentage of G's	30,587,844 / 21.97%
Number/percentage of N's	2,190 / 0%
GC Percentage	40.63%

2.3. Coverage

Mean	0.045

Standard Deviation	0.3619

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

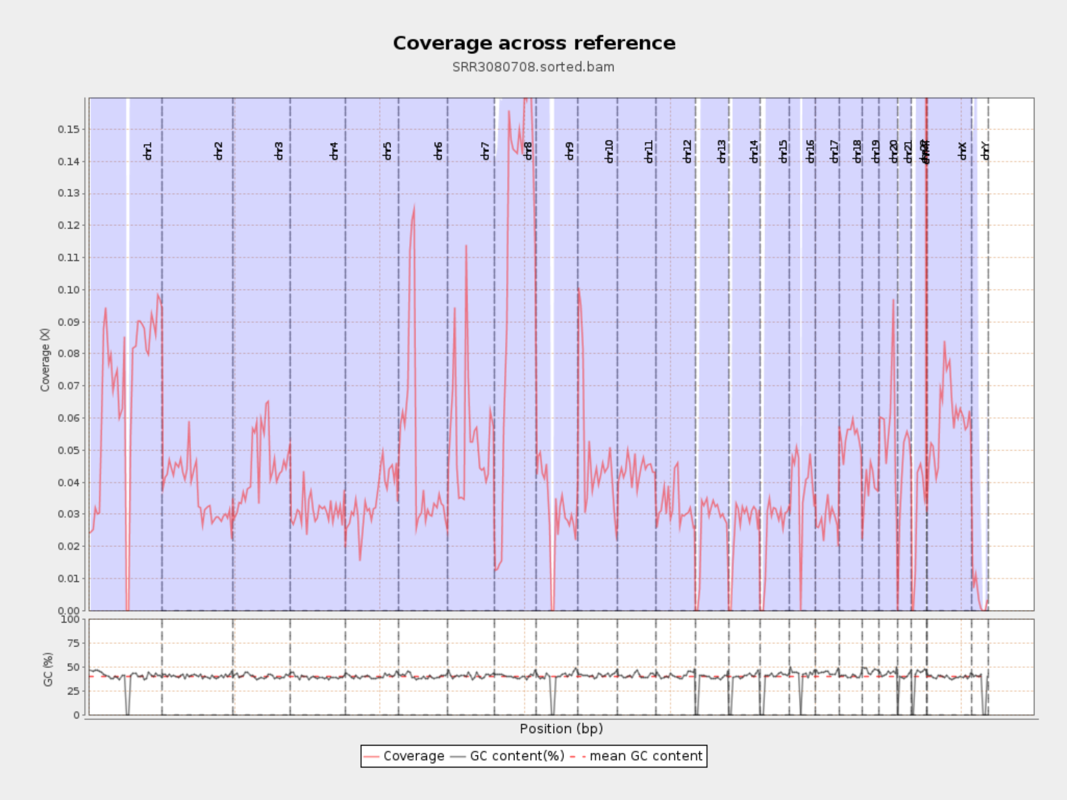
General error rate	0.81%
Mismatches	1,106,627
Insertions	9,893
Mapped reads with at least one insertion	0.48%
Deletions	28,709
Mapped reads with at least one deletion	1.39%
Homopolymer indels	48.59%

2.6. Chromosome stats

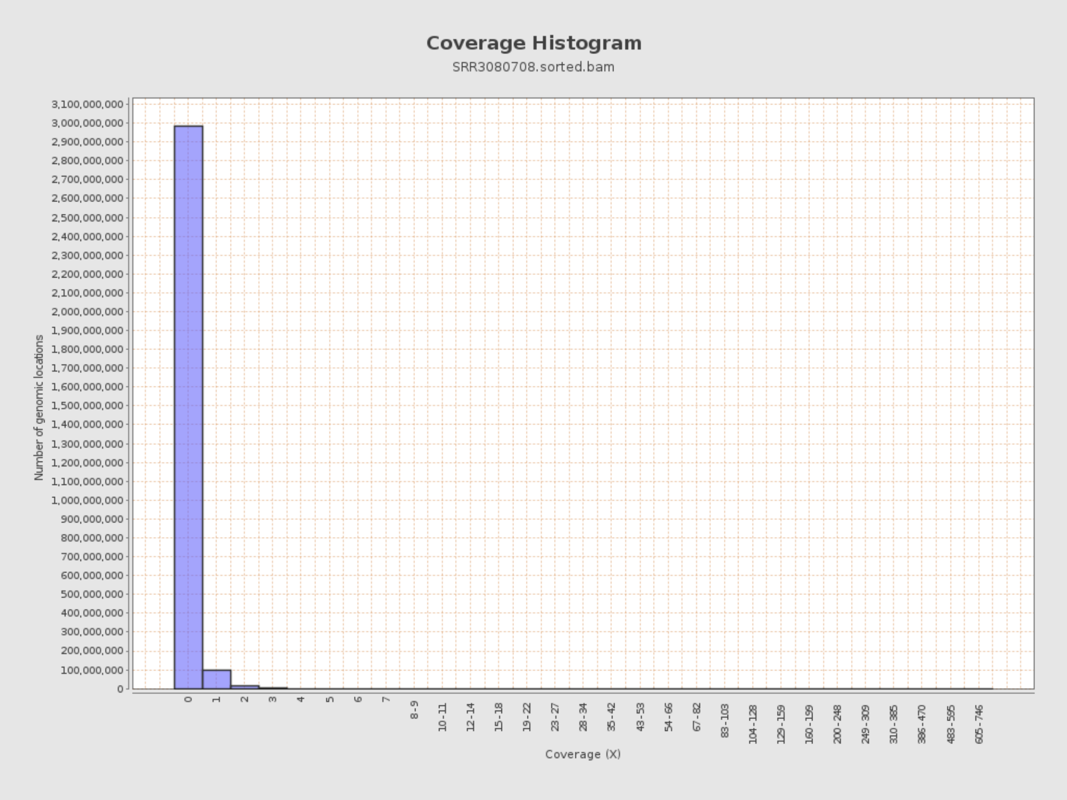
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16905310	0.0678	0.4397
chr2	243199373	9031984	0.0371	0.3712
chr3	198022430	8851612	0.0447	0.247
chr4	191154276	5940353	0.0311	0.2131
chr5	180915260	6224183	0.0344	0.2155
chr6	171115067	8395207	0.0491	0.3474
chr7	159138663	8785214	0.0552	0.8842

chr8	146364022	16444437	0.1124	0.4781
chr9	141213431	4277855	0.0303	0.2555
chr10	135534747	6644393	0.049	0.3204
chr11	135006516	5862953	0.0434	0.2752
chr12	133851895	4307170	0.0322	0.2089
chr13	115169878	3014371	0.0262	0.1895
chr14	107349540	2740111	0.0255	0.1922
chr15	102531392	2534357	0.0247	0.1839
chr16	90354753	3494678	0.0387	0.2458
chr17	81195210	2284763	0.0281	0.204
chr18	78077248	4225757	0.0541	0.3827
chr19	59128983	2324623	0.0393	0.3051
chr20	63025520	3646342	0.0579	0.2857
chr21	48129895	2015068	0.0419	0.2484
chr22	51304566	1448349	0.0282	0.194
chrMT	16571	394342	23.7971	14.7766
chrX	155270560	9224639	0.0594	0.308
chrY	59373566	268611	0.0045	0.1007

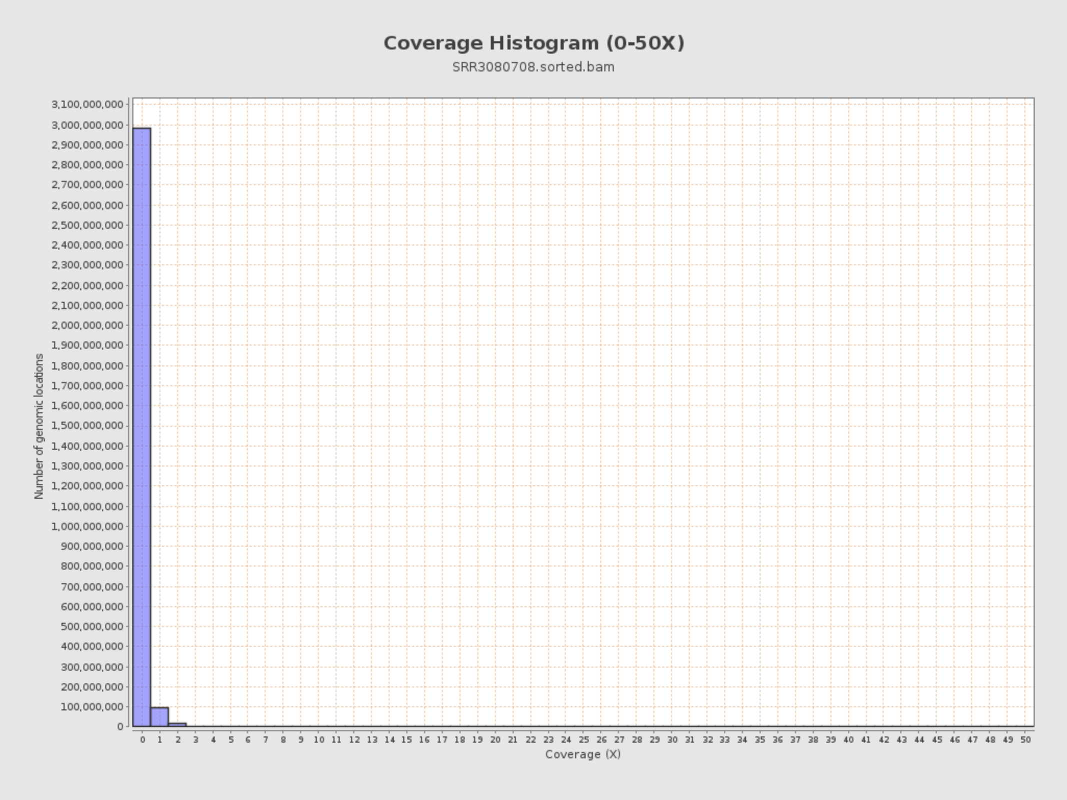
3. Results : Coverage across reference



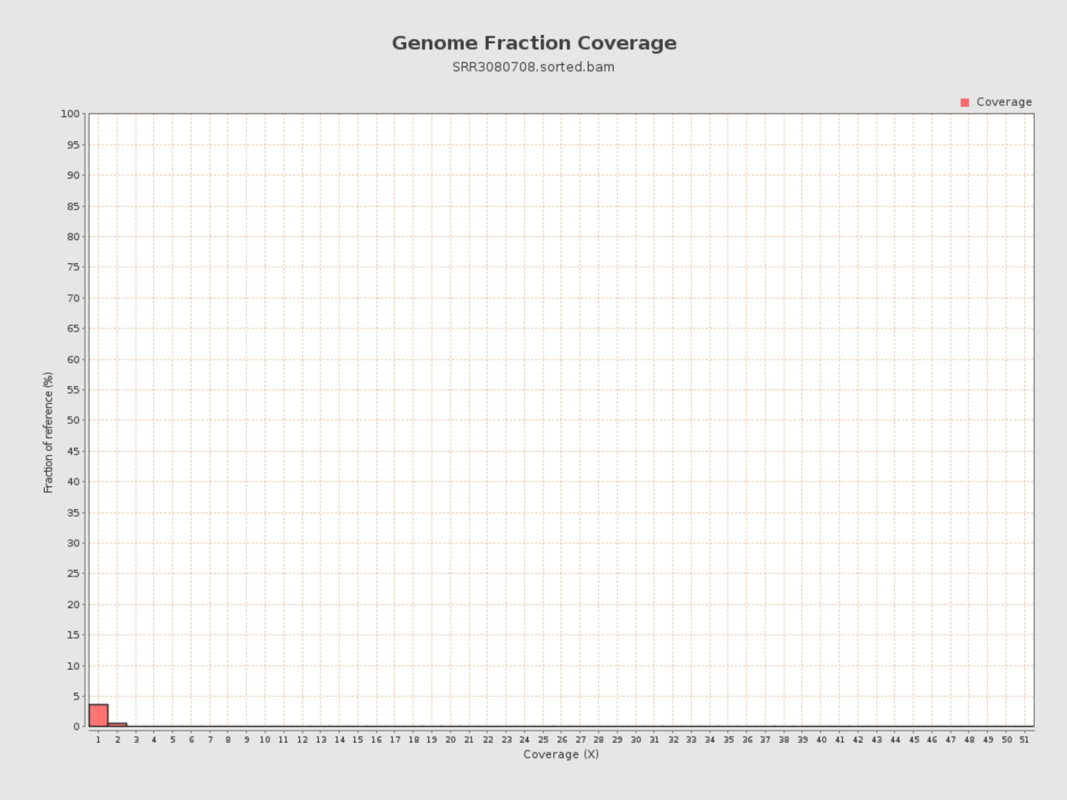
4. Results : Coverage Histogram



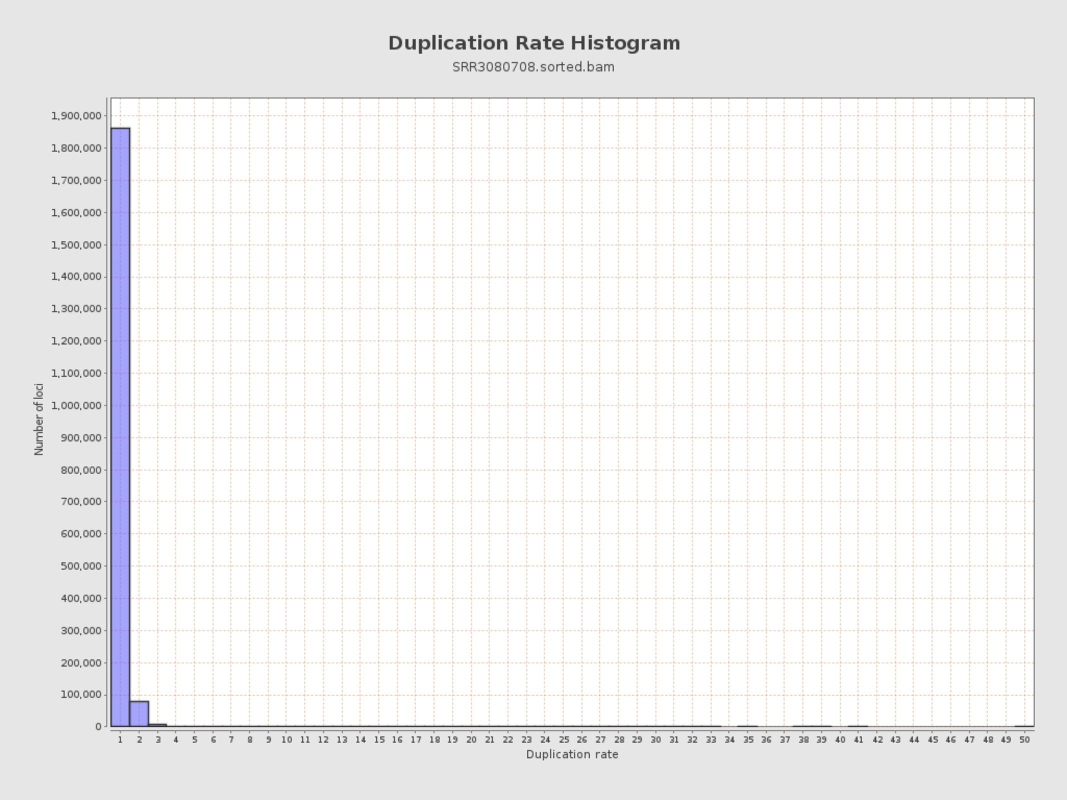
5. Results : Coverage Histogram (0-50X)



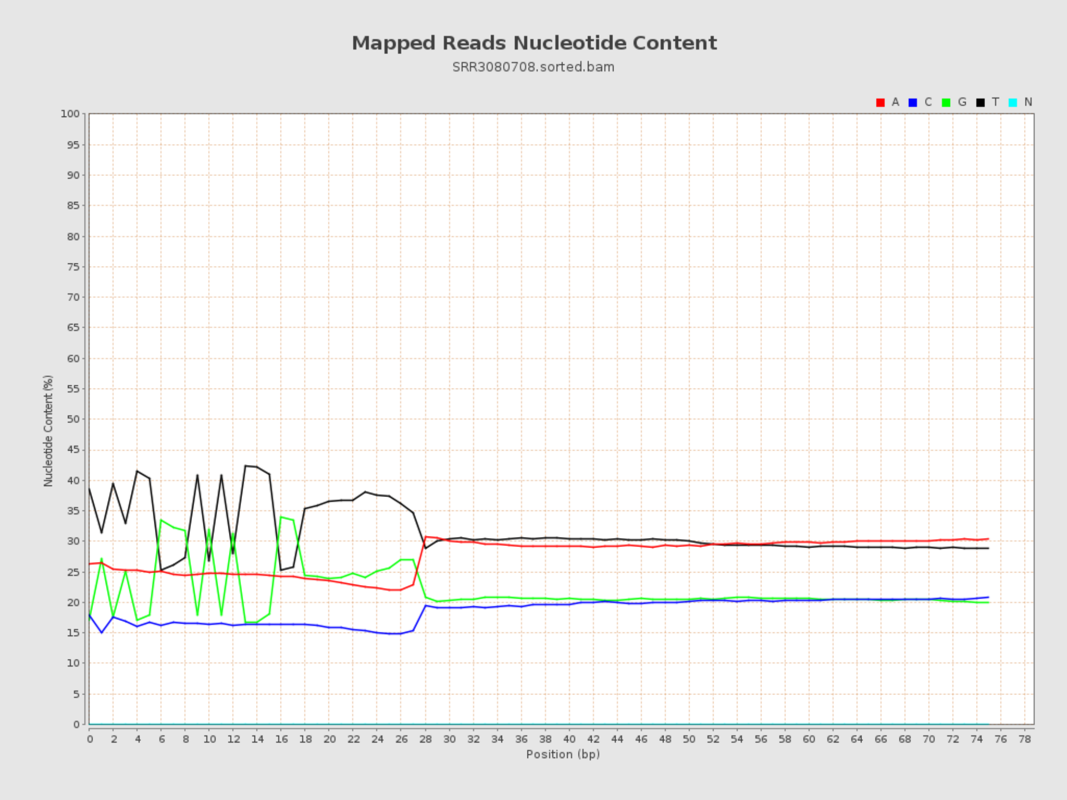
6. Results : Genome Fraction Coverage



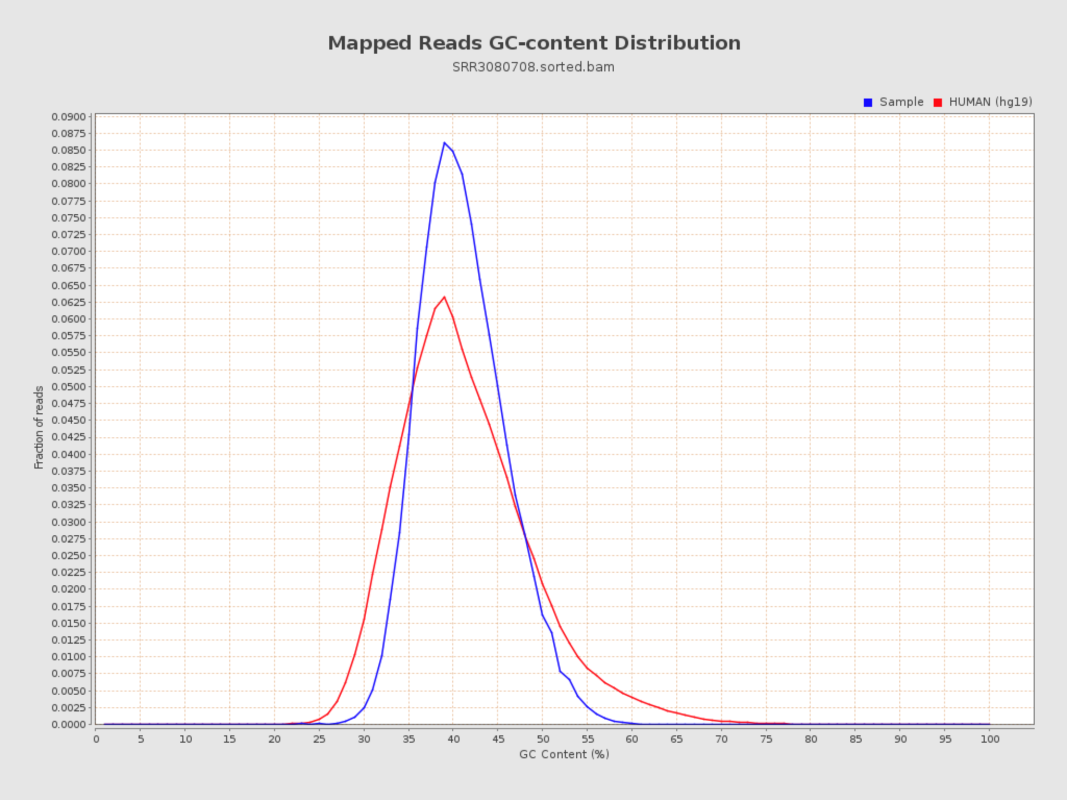
7. Results : Duplication Rate Histogram



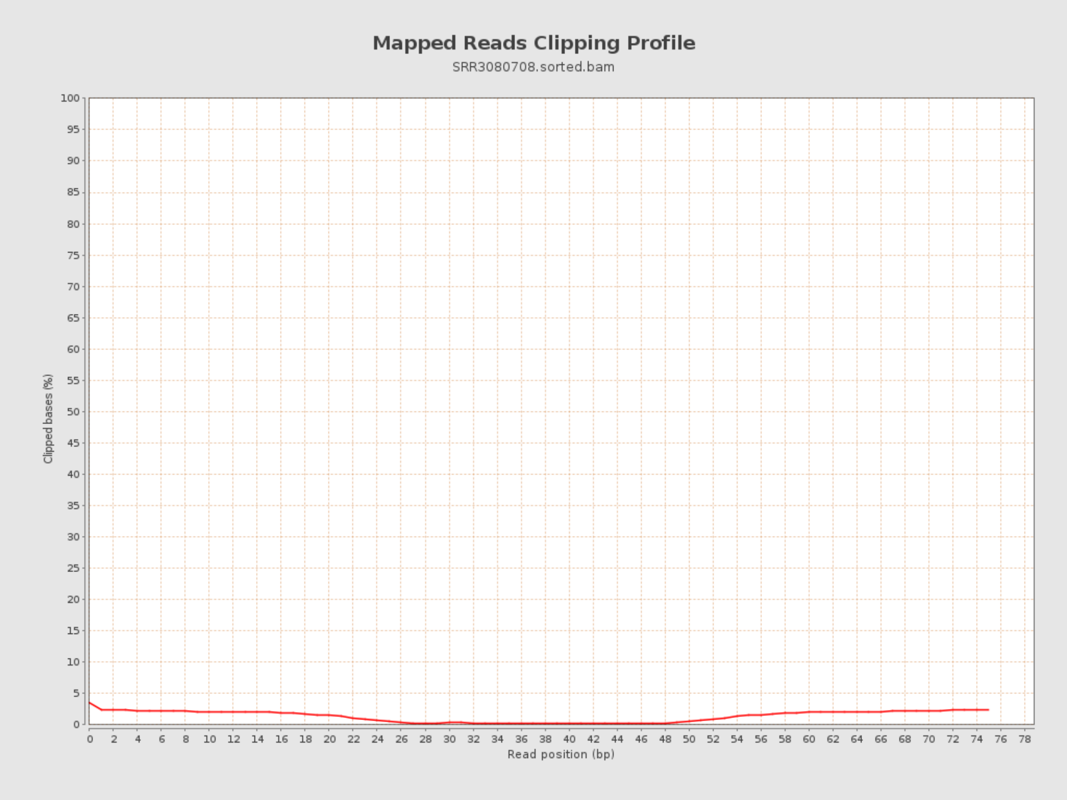
8. Results : Mapped Reads Nucleotide Content



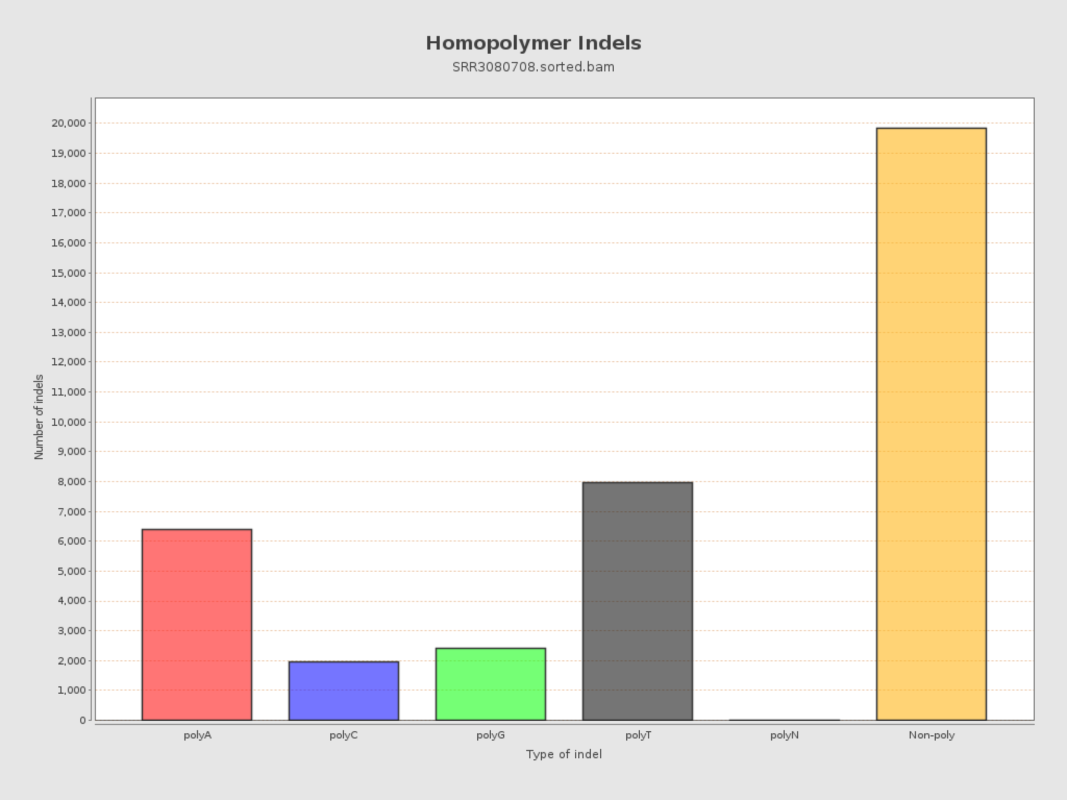
9. Results : Mapped Reads GC-content Distribution



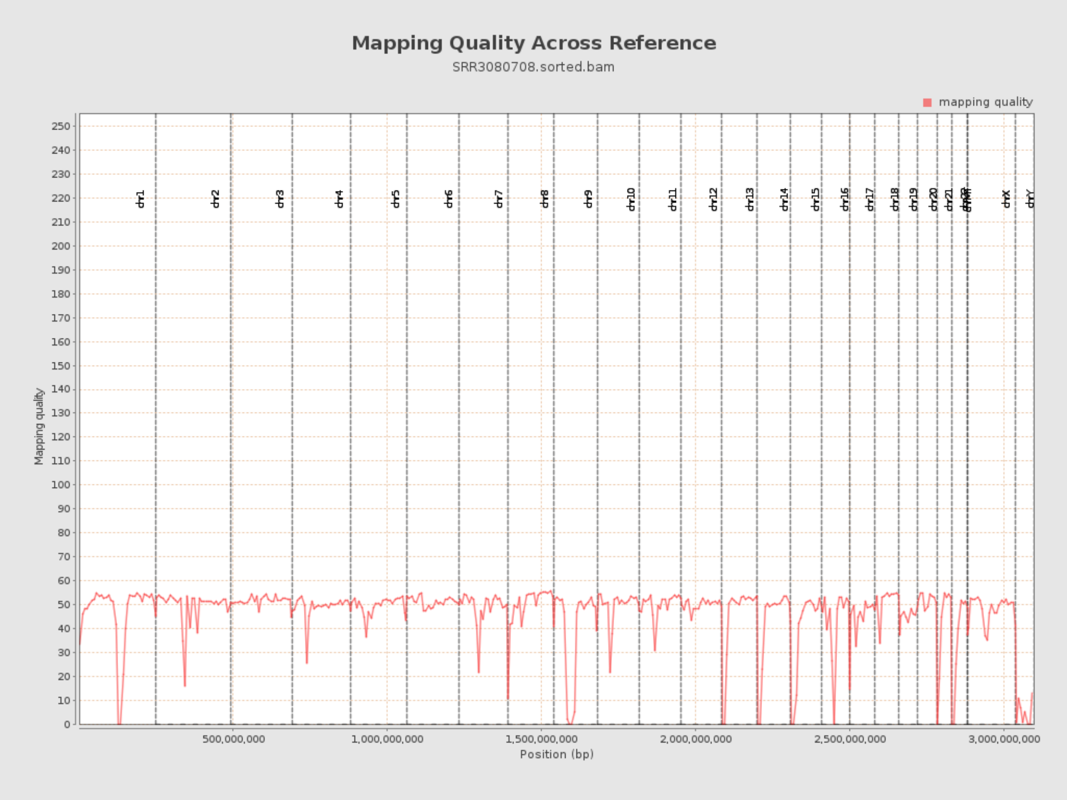
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram