Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:16:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080919.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_SRR3080919 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080919.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:16:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080919.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,566,974
Mapped reads	3,213,699 / 90.1%
Unmapped reads	353,275 / 9.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,068 / 1.12%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	136,507 / 3.83%
Duplication rate	3.43%
Clipped reads	1,066,204 / 29.89%

2.2. ACGT Content

Number/percentage of A's	64,908,144 / 29.11%
Number/percentage of C's	39,948,217 / 17.92%
Number/percentage of T's	70,772,667 / 31.74%
Number/percentage of G's	46,238,589 / 20.74%
Number/percentage of N's	1,093,217 / 0.49%
GC Percentage	38.66%

2.3. Coverage

Mean	0.072

Standard Deviation	0.4733

2.4. Mapping Quality

Mean Mapping Quality	47.93

2.5. Mismatches and indels

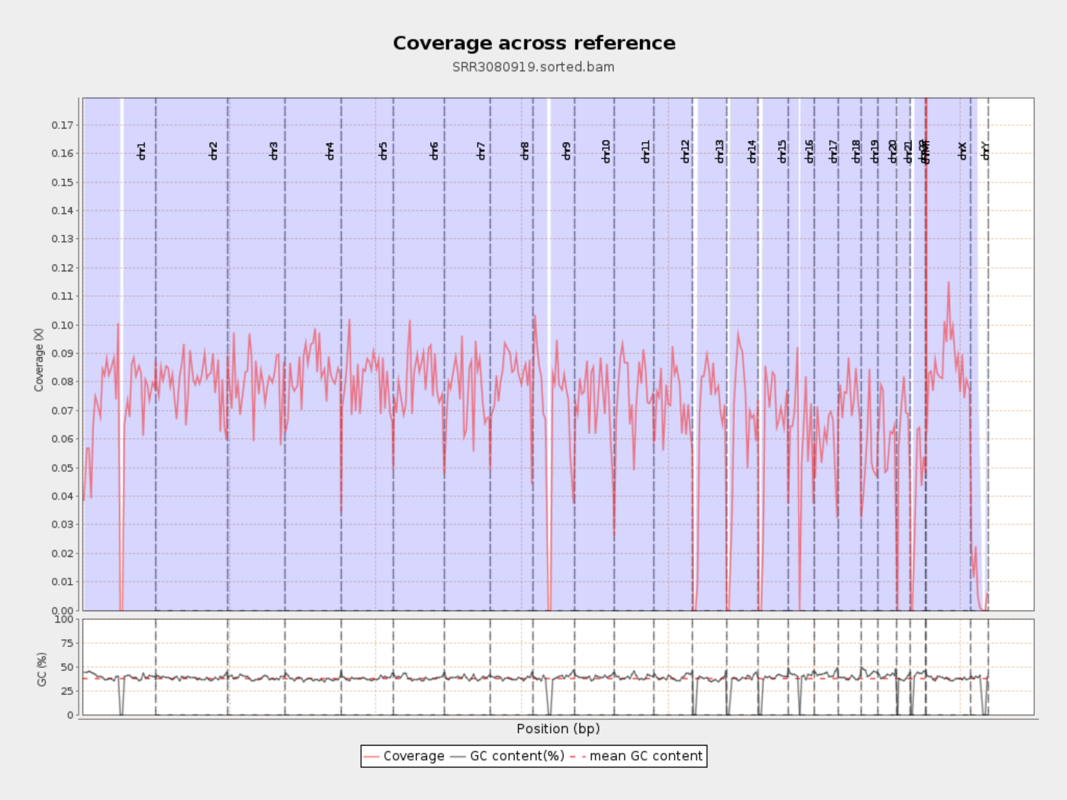
General error rate	1.14%
Mismatches	2,519,792
Insertions	17,031
Mapped reads with at least one insertion	0.53%
Deletions	49,305
Mapped reads with at least one deletion	1.52%
Homopolymer indels	50.44%

2.6. Chromosome stats

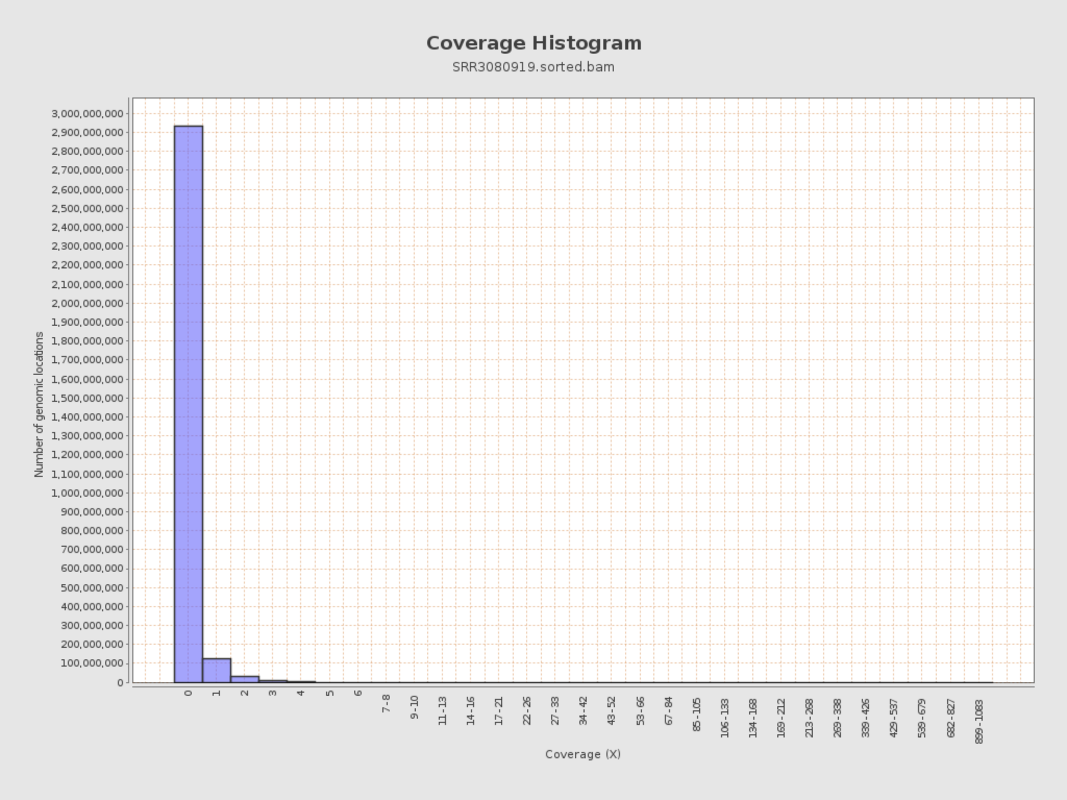
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17494682	0.0702	0.7526
chr2	243199373	19416556	0.0798	0.4747
chr3	198022430	15888637	0.0802	0.3651
chr4	191154276	15974301	0.0836	0.3874
chr5	180915260	14427249	0.0797	0.3662
chr6	171115067	13849539	0.0809	0.4239
chr7	159138663	12123892	0.0762	0.5783

chr8	146364022	11855991	0.081	0.7627
chr9	141213431	9702057	0.0687	0.4395
chr10	135534747	10036138	0.074	0.4379
chr11	135006516	10365720	0.0768	0.4297
chr12	133851895	9763825	0.0729	0.3524
chr13	115169878	7384070	0.0641	0.3289
chr14	107349540	6738391	0.0628	0.3395
chr15	102531392	6162459	0.0601	0.3167
chr16	90354753	5253523	0.0581	0.3339
chr17	81195210	4814229	0.0593	0.3395
chr18	78077248	5888293	0.0754	0.7238
chr19	59128983	3196785	0.0541	0.5125
chr20	63025520	3912816	0.0621	0.3296
chr21	48129895	2896967	0.0602	0.347
chr22	51304566	2006656	0.0391	0.251
chrMT	16571	119826	7.2311	4.2769
chrX	155270560	13298149	0.0856	0.395
chrY	59373566	471360	0.0079	0.1544

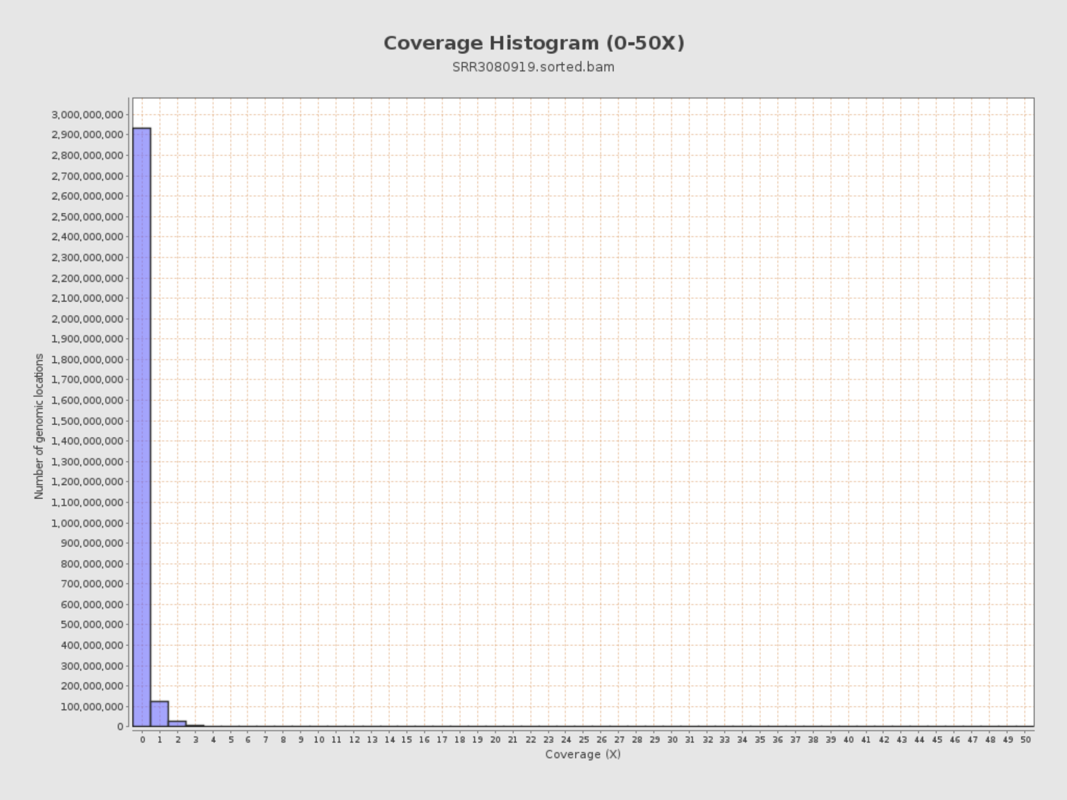
3. Results : Coverage across reference



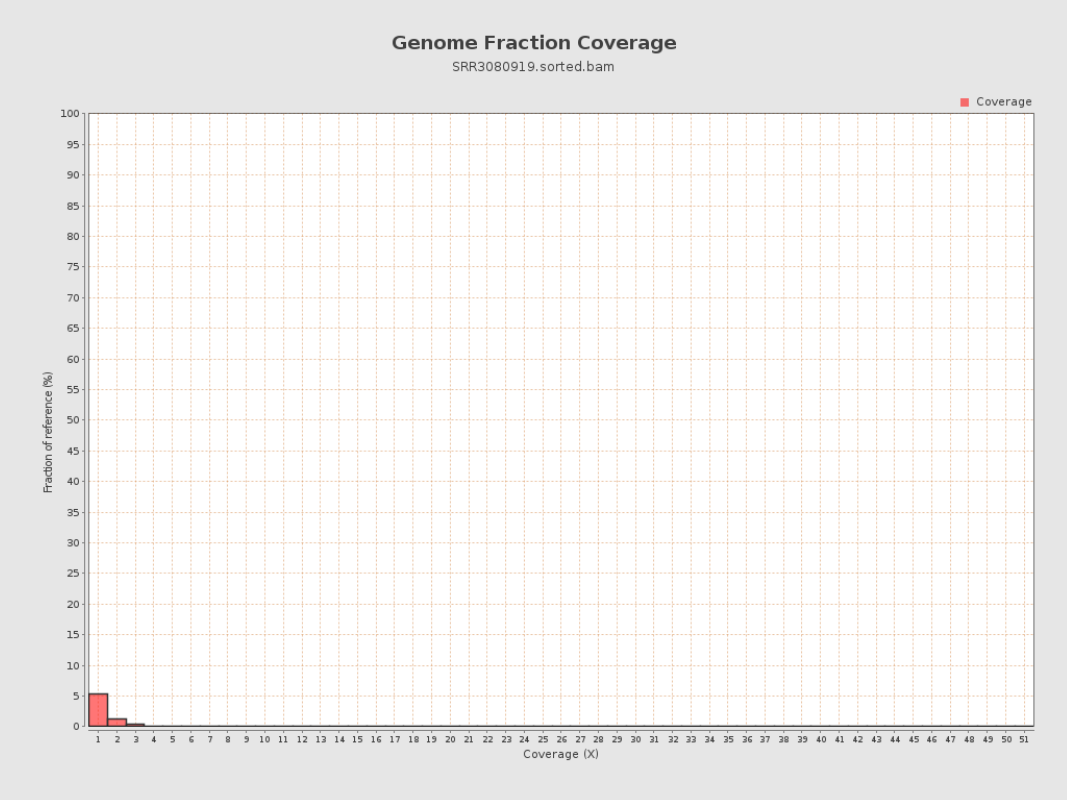
4. Results : Coverage Histogram



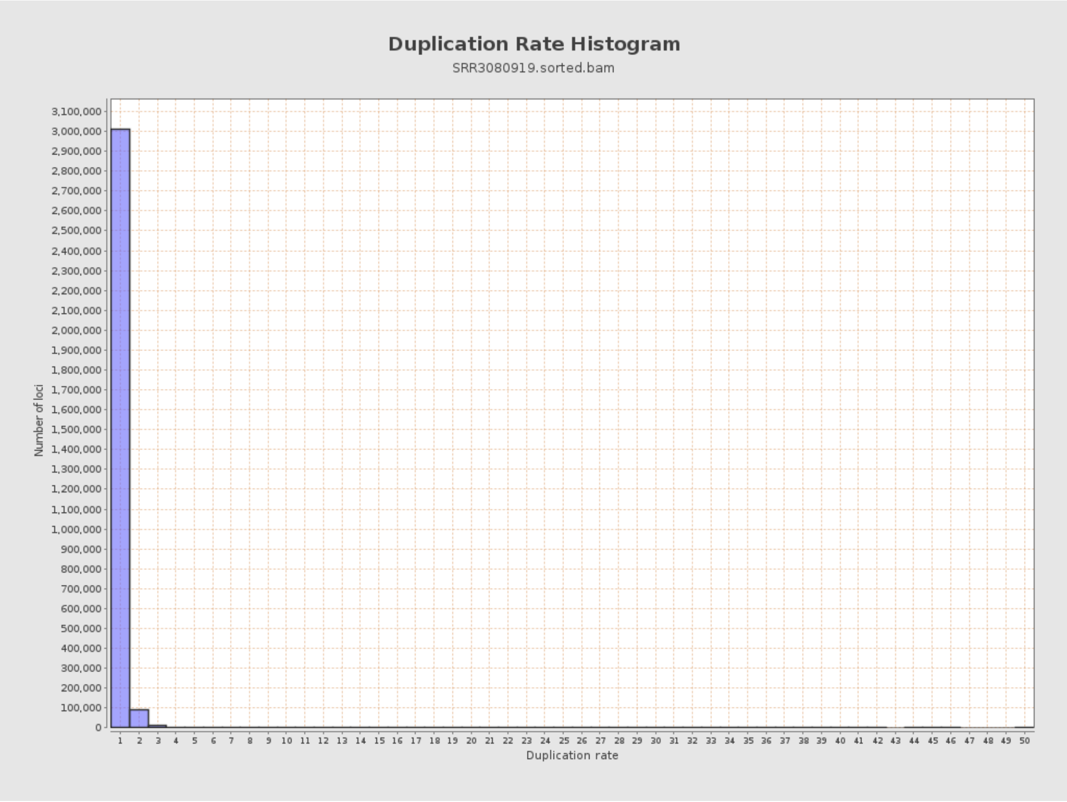
5. Results : Coverage Histogram (0-50X)



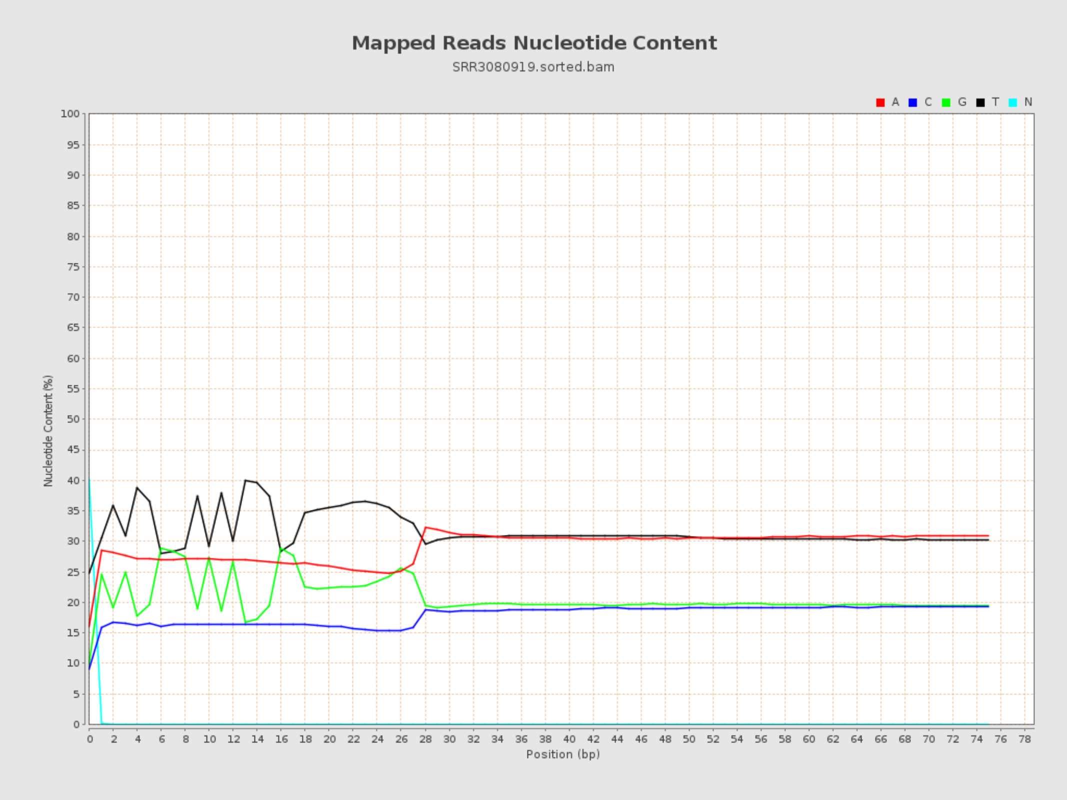
6. Results : Genome Fraction Coverage



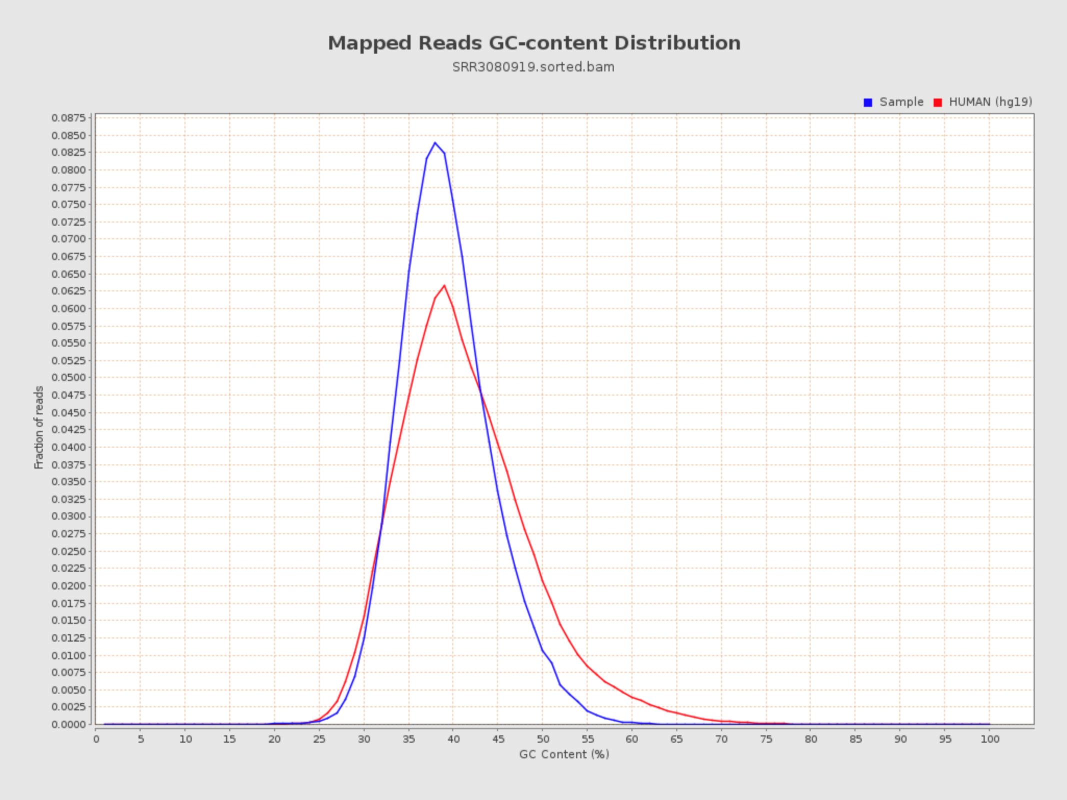
7. Results : Duplication Rate Histogram



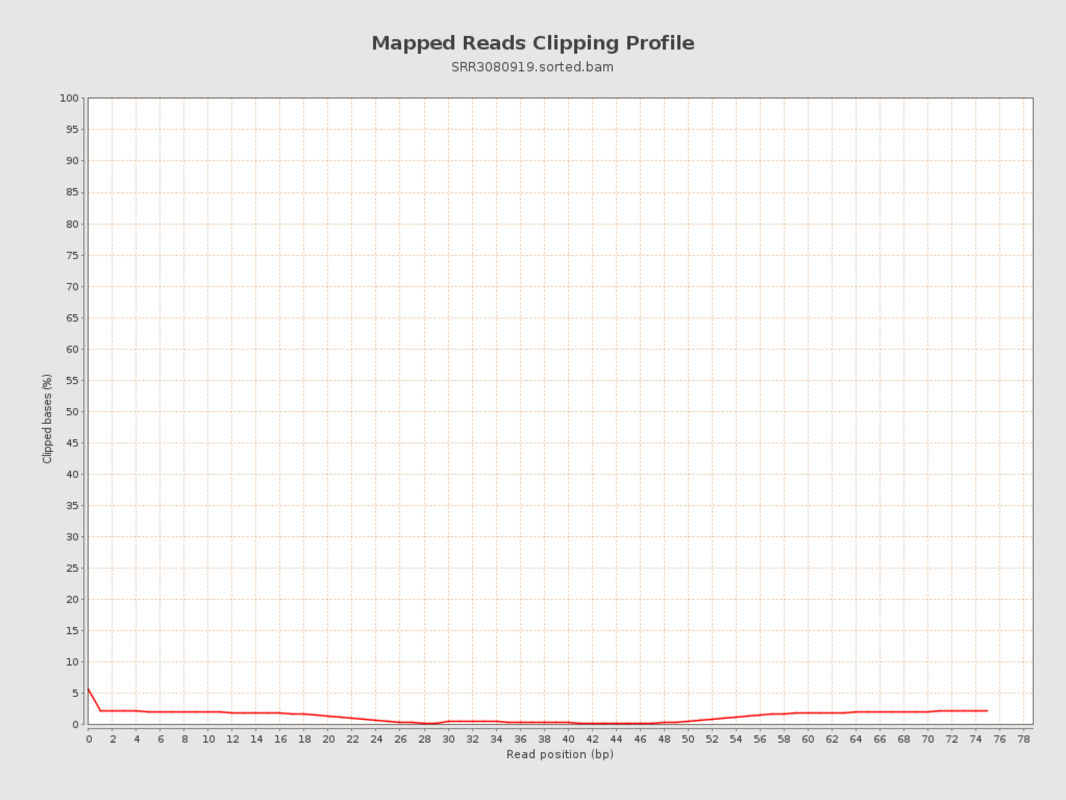
8. Results : Mapped Reads Nucleotide Content



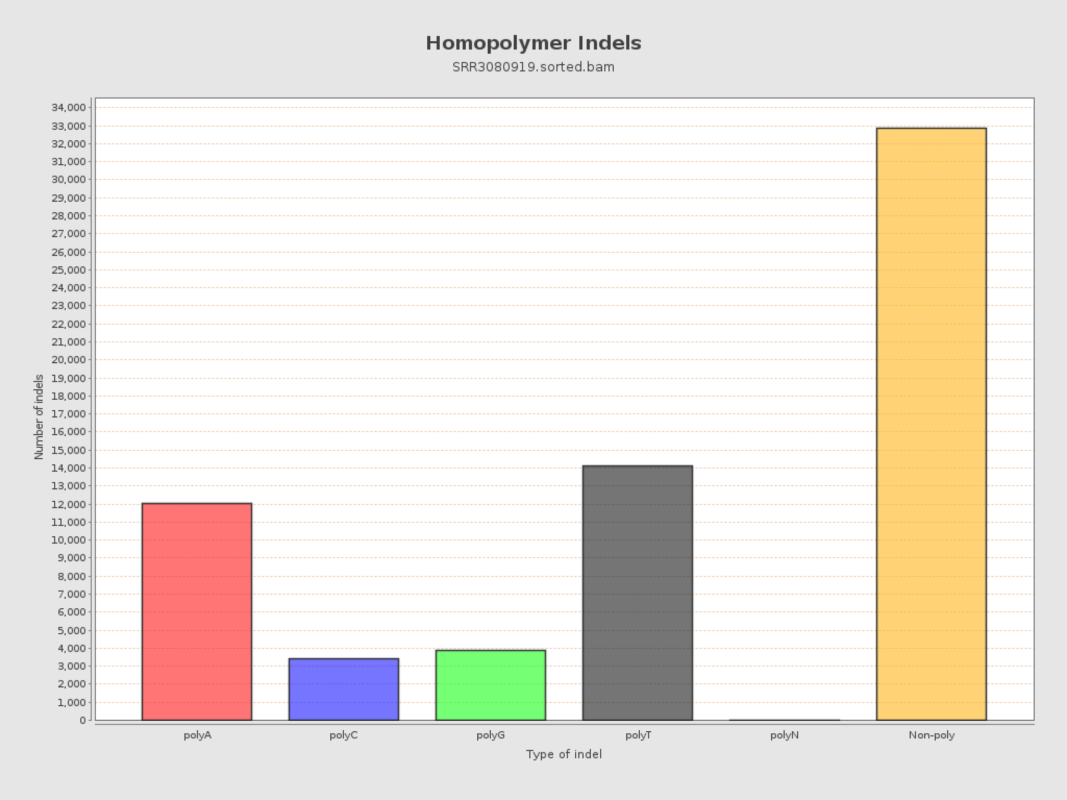
9. Results : Mapped Reads GC-content Distribution



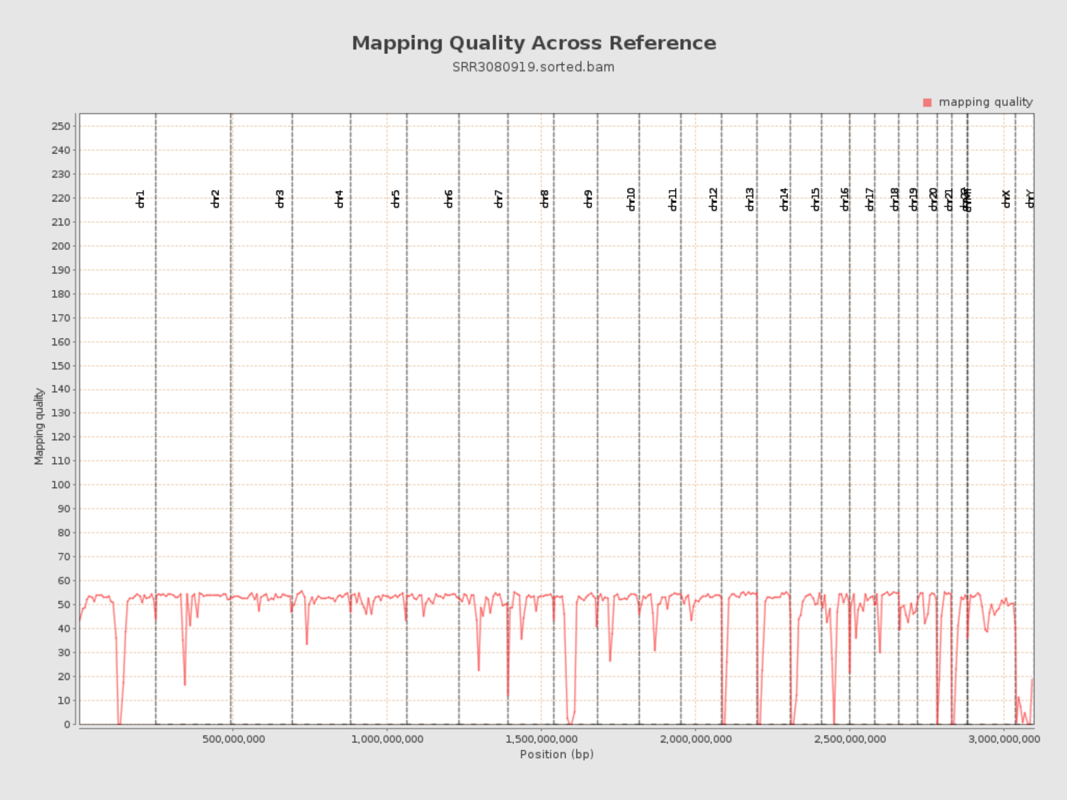
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram