Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:36:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080722.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_SRR3080722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080722.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:36:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,066,222
Mapped reads	3,846,451 / 94.6%
Unmapped reads	219,771 / 5.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,685 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	186,995 / 4.6%
Duplication rate	4.04%
Clipped reads	1,058,295 / 26.03%

2.2. ACGT Content

Number/percentage of A's	80,424,005 / 29.55%
Number/percentage of C's	51,040,296 / 18.76%
Number/percentage of T's	85,842,089 / 31.55%
Number/percentage of G's	54,813,255 / 20.14%
Number/percentage of N's	3,941 / 0%
GC Percentage	38.9%

2.3. Coverage

Mean	0.0879

Standard Deviation	0.6035

2.4. Mapping Quality

Mean Mapping Quality	47.64

2.5. Mismatches and indels

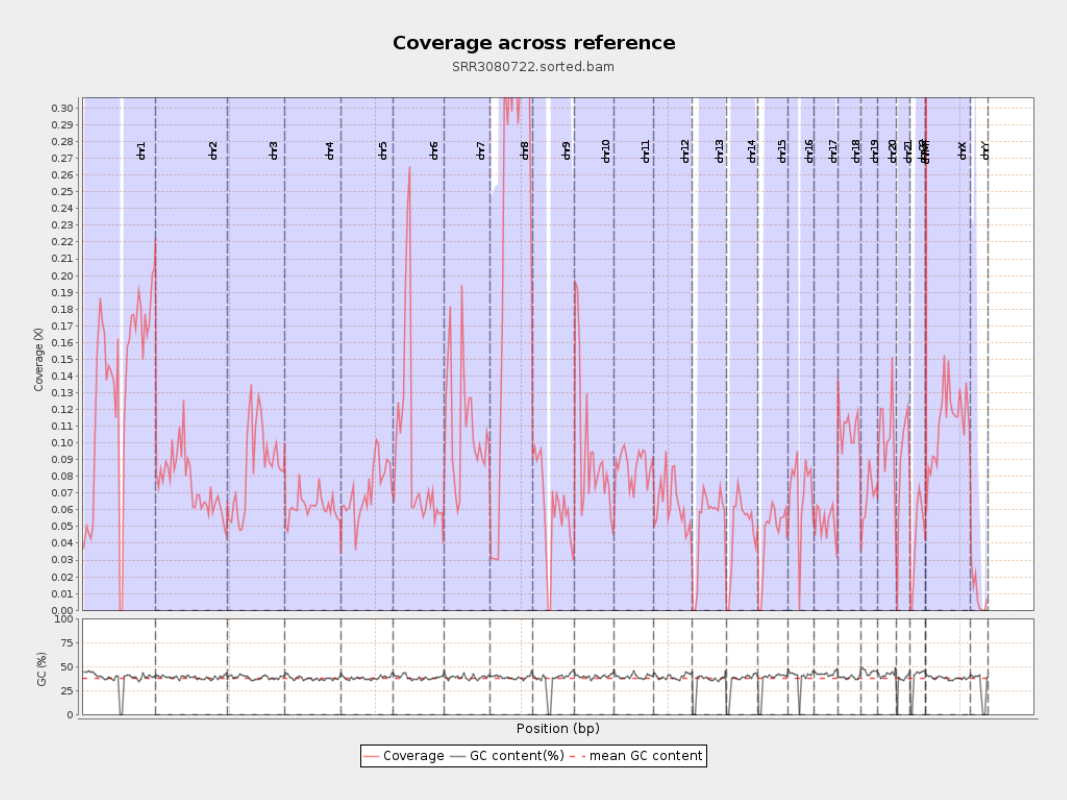
General error rate	0.82%
Mismatches	2,194,946
Insertions	19,515
Mapped reads with at least one insertion	0.5%
Deletions	58,752
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.73%

2.6. Chromosome stats

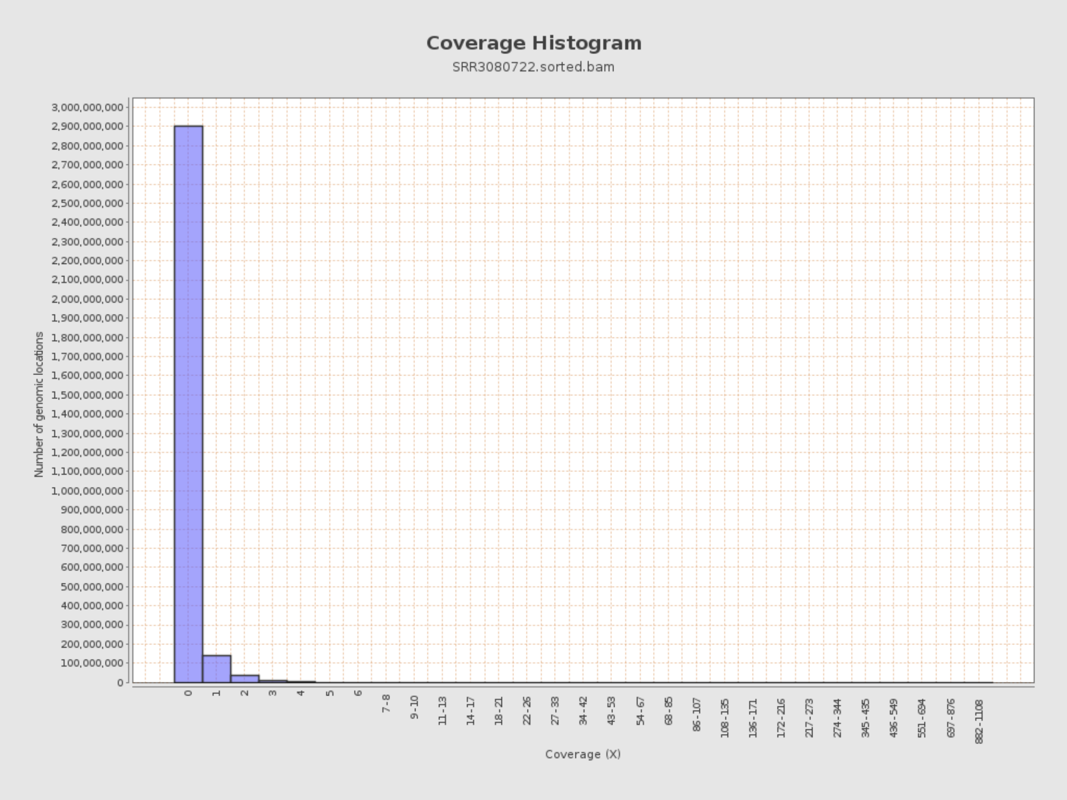
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33210012	0.1332	0.9569
chr2	243199373	18439672	0.0758	0.5263
chr3	198022430	17135817	0.0865	0.3838
chr4	191154276	11842903	0.062	0.3363
chr5	180915260	12882781	0.0712	0.3433
chr6	171115067	16235603	0.0949	0.5885
chr7	159138663	17496686	0.1099	1.2968

chr8	146364022	34021870	0.2324	1.0146
chr9	141213431	8416315	0.0596	0.4176
chr10	135534747	12928486	0.0954	0.5784
chr11	135006516	11557232	0.0856	0.4457
chr12	133851895	8435518	0.063	0.3252
chr13	115169878	6030957	0.0524	0.2947
chr14	107349540	5218153	0.0486	0.2973
chr15	102531392	4538728	0.0443	0.2694
chr16	90354753	6189388	0.0685	0.3632
chr17	81195210	4268128	0.0526	0.3291
chr18	78077248	8494075	0.1088	0.7129
chr19	59128983	4034551	0.0682	0.5775
chr20	63025520	6600151	0.1047	0.4255
chr21	48129895	4145411	0.0861	0.395
chr22	51304566	2251589	0.0439	0.2648
chrMT	16571	23587	1.4234	1.5145
chrX	155270560	17285867	0.1113	0.4739
chrY	59373566	545414	0.0092	0.1599

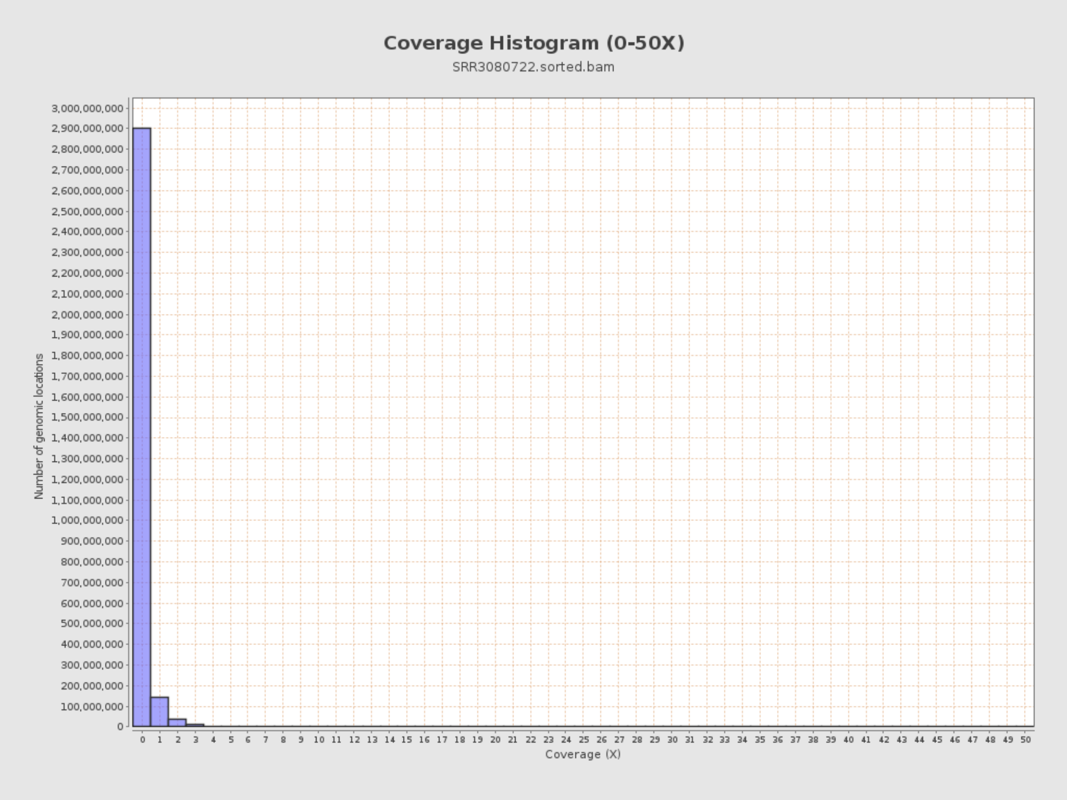
3. Results : Coverage across reference



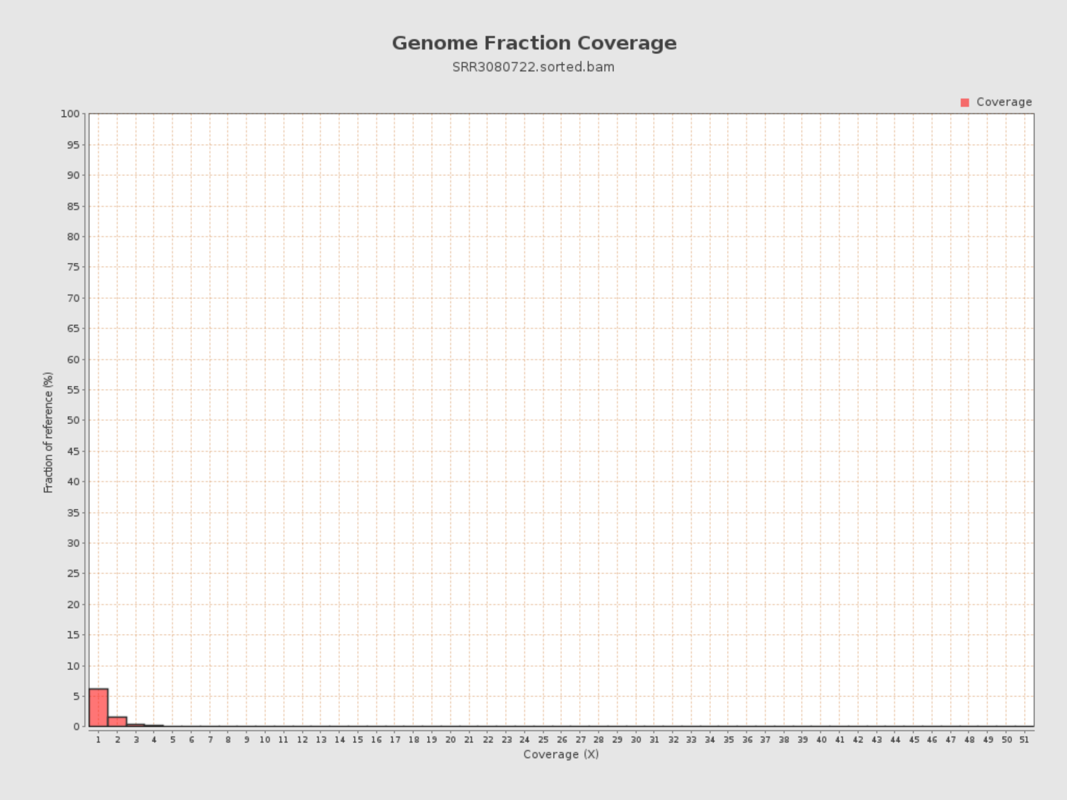
4. Results : Coverage Histogram



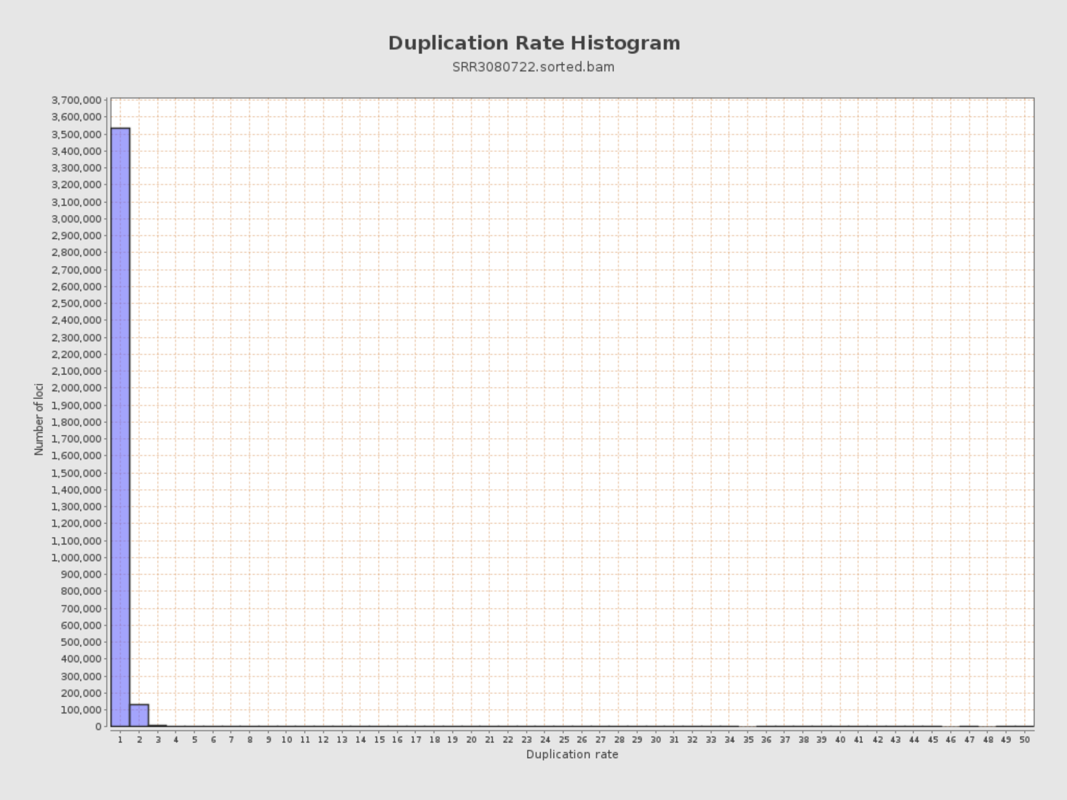
5. Results : Coverage Histogram (0-50X)



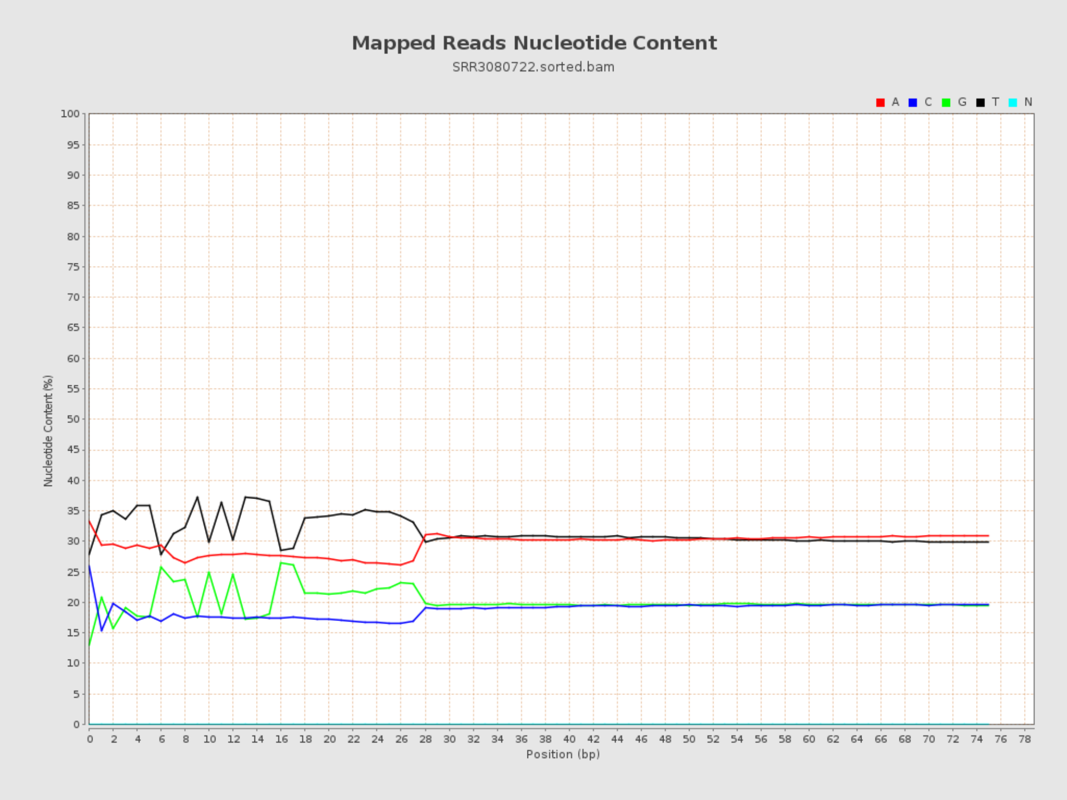
6. Results : Genome Fraction Coverage



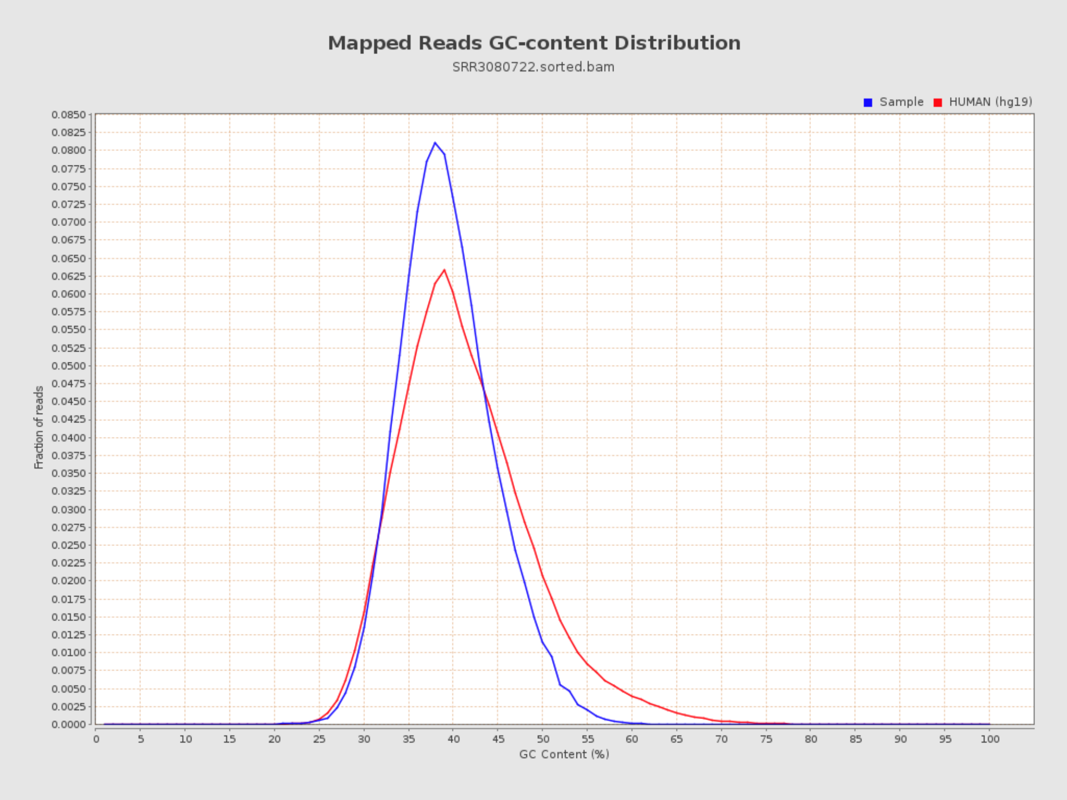
7. Results : Duplication Rate Histogram



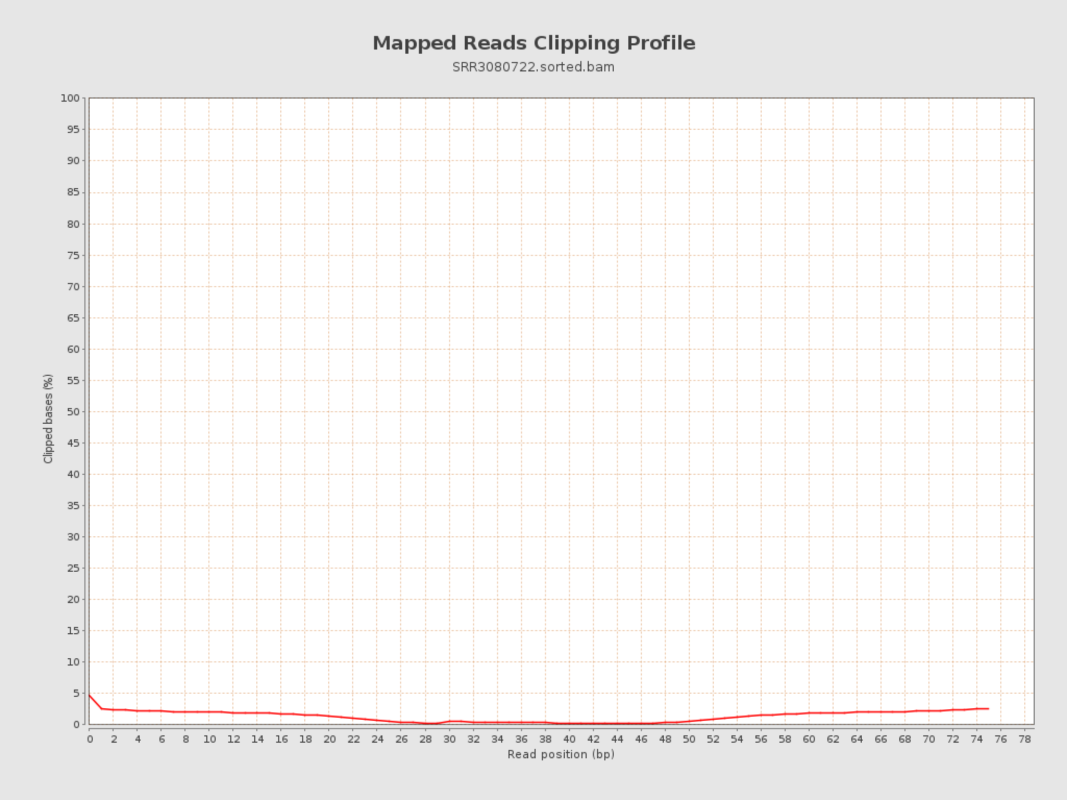
8. Results : Mapped Reads Nucleotide Content



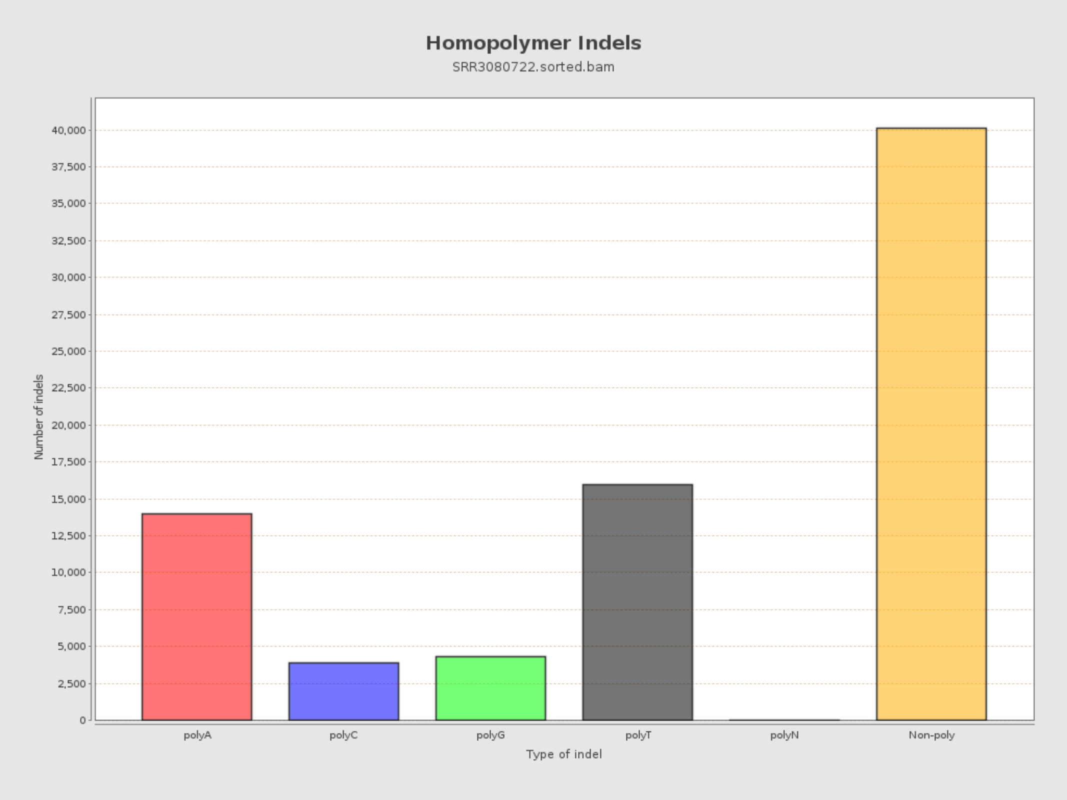
9. Results : Mapped Reads GC-content Distribution



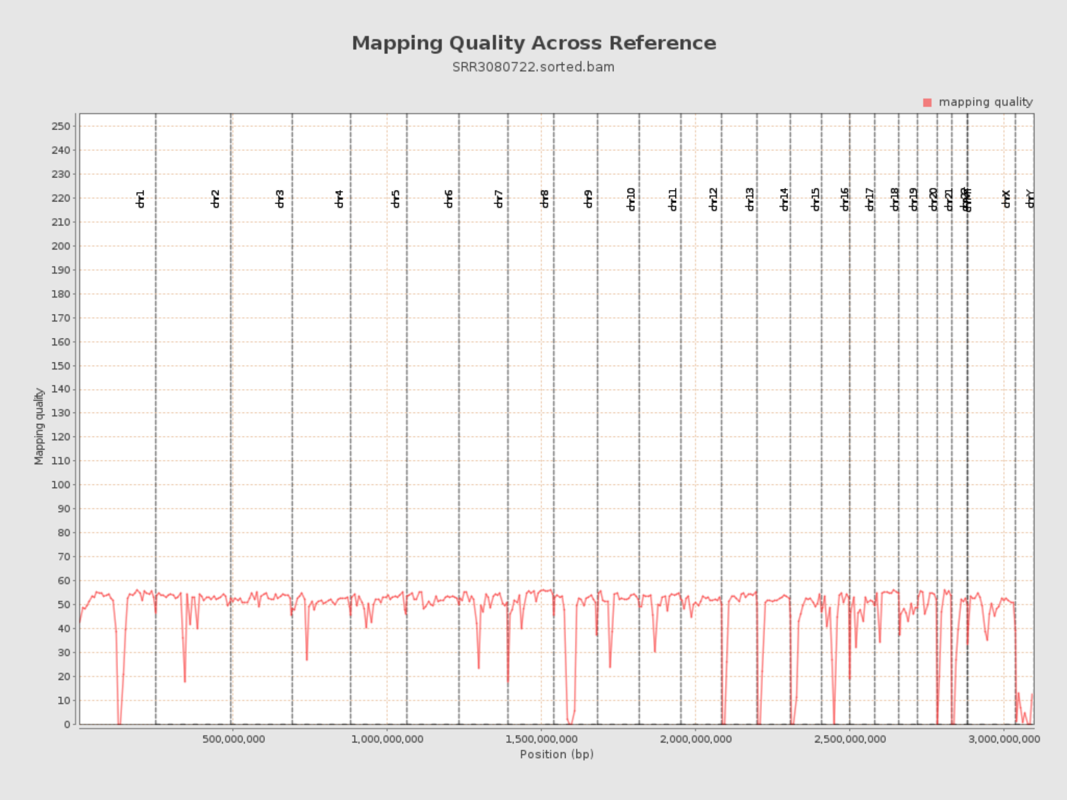
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram